SUPPLEMENTARY INFORMATION

CHEMICAL CROSSLINKING EXTENDS AND COMPLEMENTS UV CROSSLINKING IN ANALYSIS OF RNA/DNA NUCLEIC ACID–PROTEIN INTERACTION SITES BY MASS SPECTROMETRY

AUTHORS

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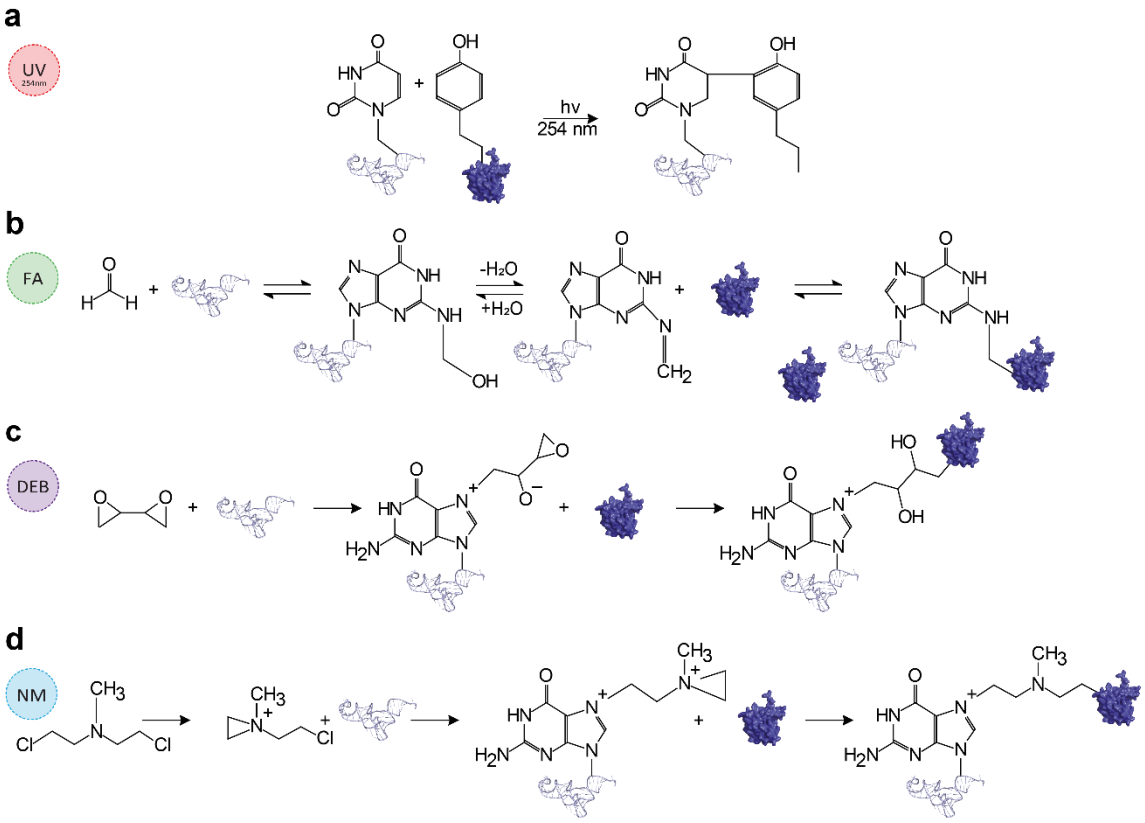
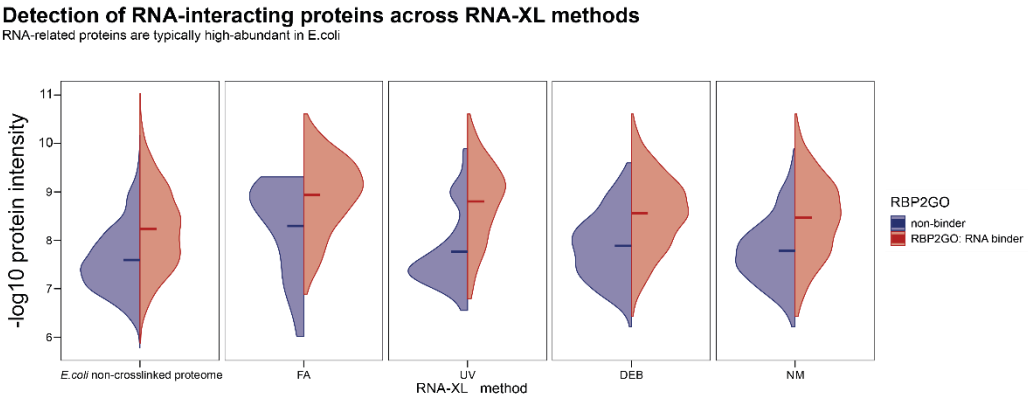
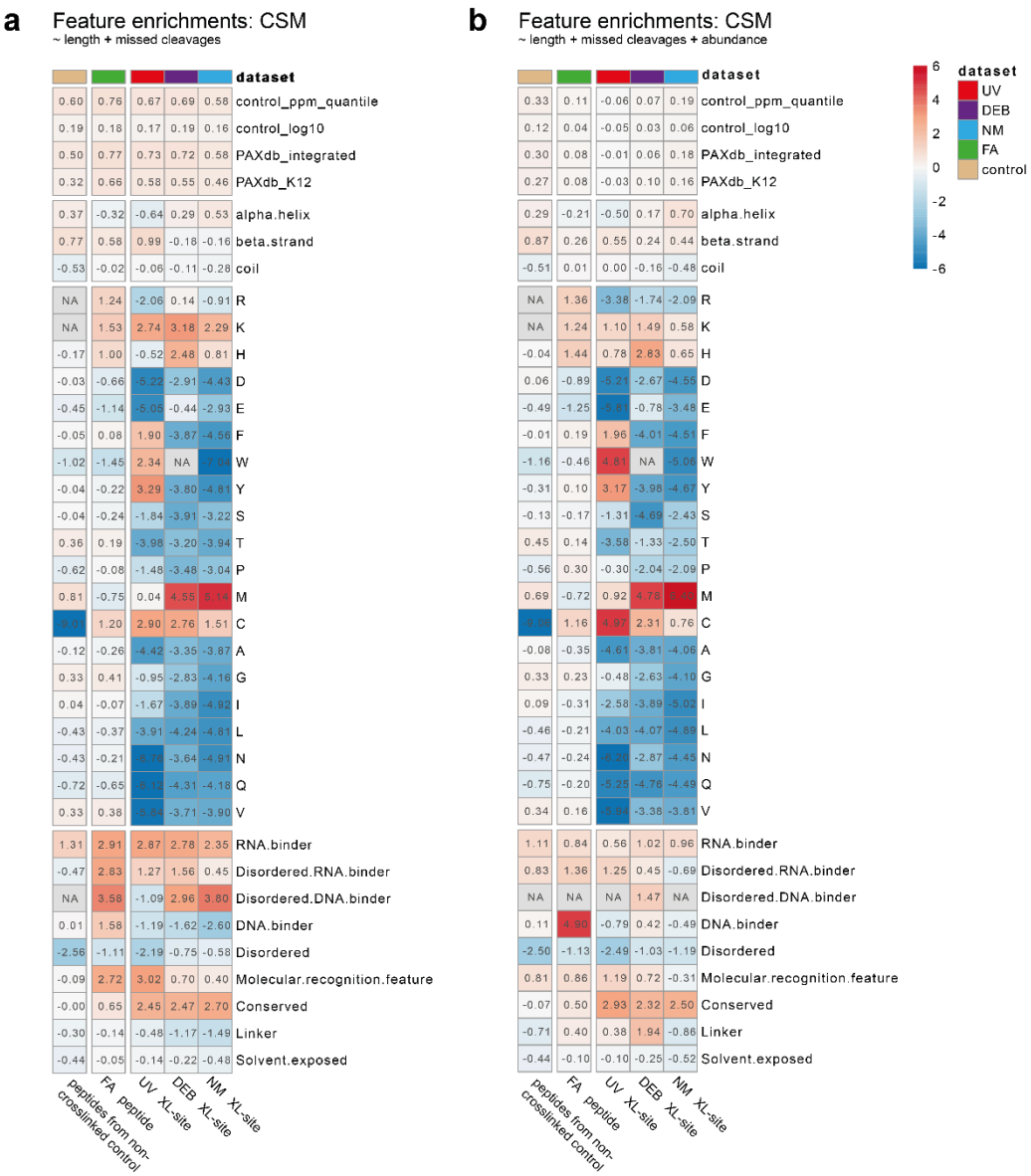
SUPPLEMENTARY FIGURES



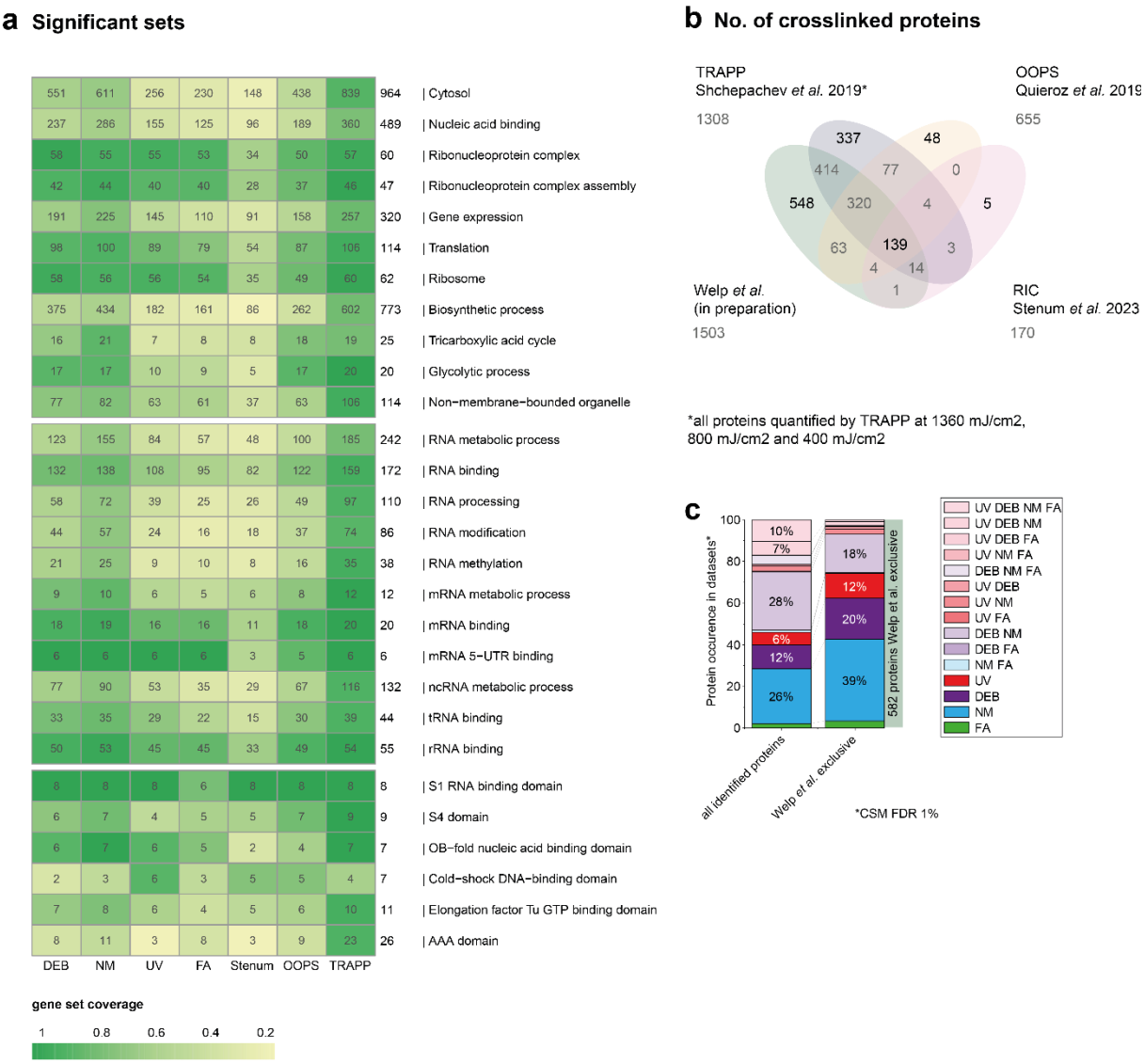
Supplementary Figure S1. Proposed chemical protein-RNA crosslinking reaction mechanisms. *Reaction mechanisms for* **(a)** UV light at λ=254 nm (adapted from Kramer *et al.,* 2011(1)), **(b)** formaldehyde (FA) (adapted from Hoffman *et al.,* 2015(2)), **(c)** 1,2:3,4-diepoxybutane (DEB) (adapted from Gherezghiher *et al.,* 2013(3)), **(d)** mechlorethamine (nitrogen mustard, NM) (adapted from Tretyakova *et al.,* 2015(4)).



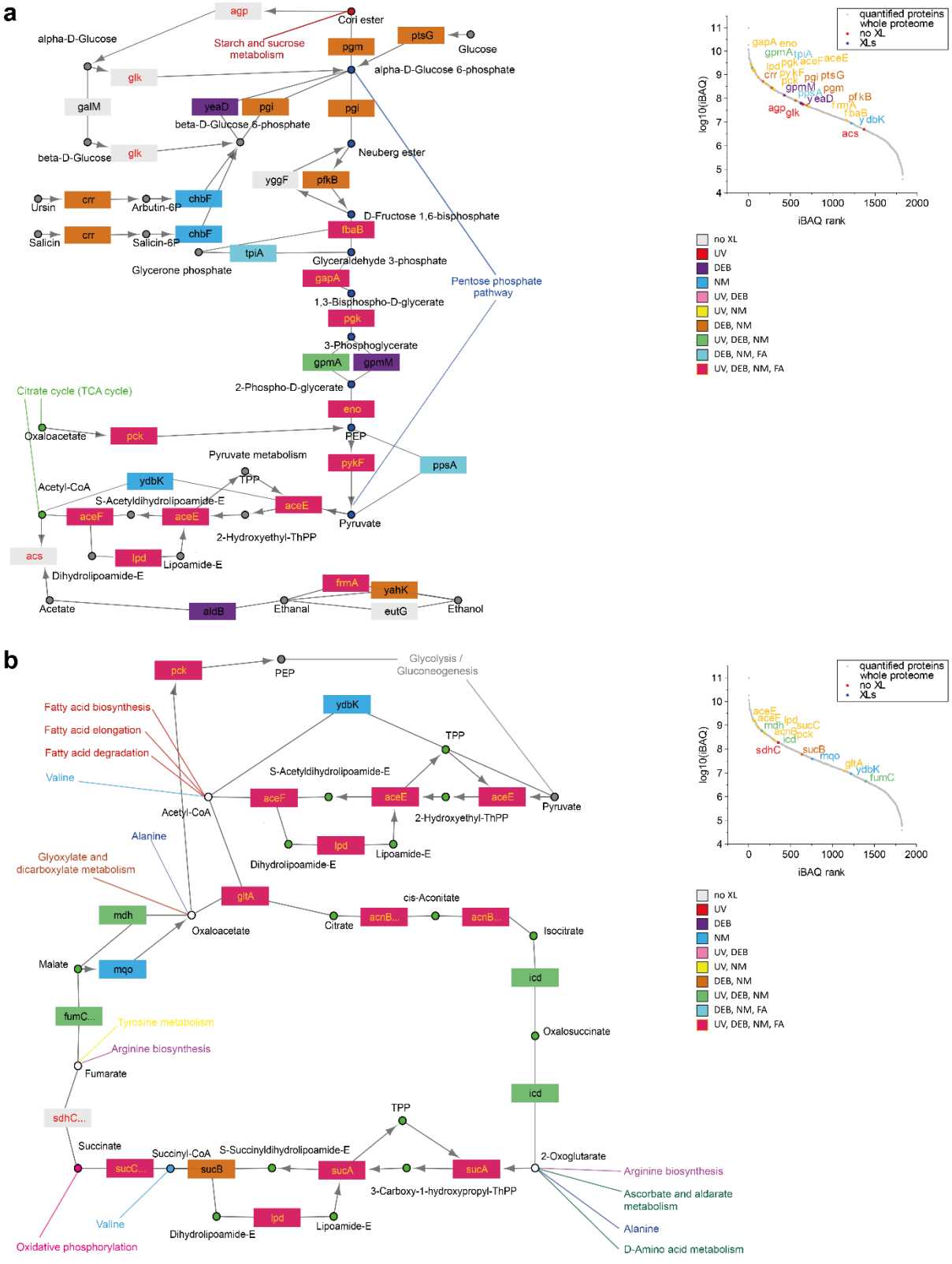
Supplementary Figure S2. Crosslinked protein abundances. Distributions of the *E. coli* protein abundance measured by label-free MS1 intensity and stratified by the annotation in Caudron-Herger et al., 2021 and detection across the crosslinking methods(5). Highlighted are the distribution means.



Supplementary Figure S3. The log2FoldChanges between the experimental and an *in-silico* background distribution mean feature counts per residue. The background sampling was performed with regards to: **(a)** the experimentally observed peptide length and missed cleavage distribution and **(b)** the experimentally observed peptide length, missed cleavage distribution and source protein abundance. The tryptic and FA datasets were enriched on the peptide level, whilst the UV, NM and DEB enrichment was done on crosslinked residue level. The NA values correspond to the cases where the sampling or statistical testing could not be performed due to the feature distribution violating the method assumptions. Crosslinker specific feature enrichment. Control, non-crosslinked *E. coli* proteome.

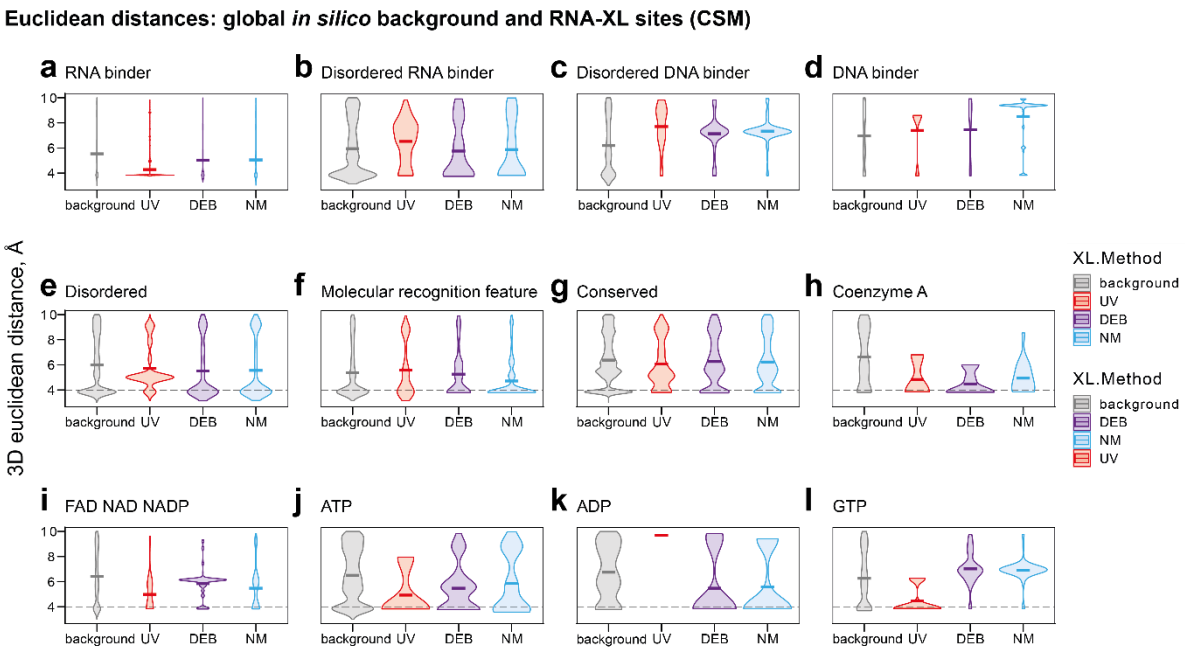


Supplementary Figure S4. Protein-RNA XL-MS dataset comparison. **(a)** GO term and domain gene set coverage by E. coli UV, DEB, NM and FA XL-MS datasets presented in this study and *E. coli* XL-MS datasets from (6-8) The terms are selected from those significantly enriched in at least one of the UV, DEB, NM or FA XL-MS datasets (padj, ≤ 0.01 for GO terms; padj, ≤ 0.05 for domains). **(b)** Venn diagram of *E. coli* RNA-crosslinked proteins identified in this study compared to proteins identified as RNA-binding in Stenum *et al.* 2023 (RIC, protocol used)(8), Quieroz *et al.* 2019 (OOPS)(7) and/or Shchepachev *et al.* 2029 (TRAPP)(6). **(c)** 100% stacked bar plot of all RNA-crosslinked proteins identified in this study and proteins found crosslinked to RNA but not identified as interaction partners in OOPS or TRAPP (Welp *et al.* exclusive). Relative numbers of proteins occurring in UV, DEB, NM and FA are indicated.

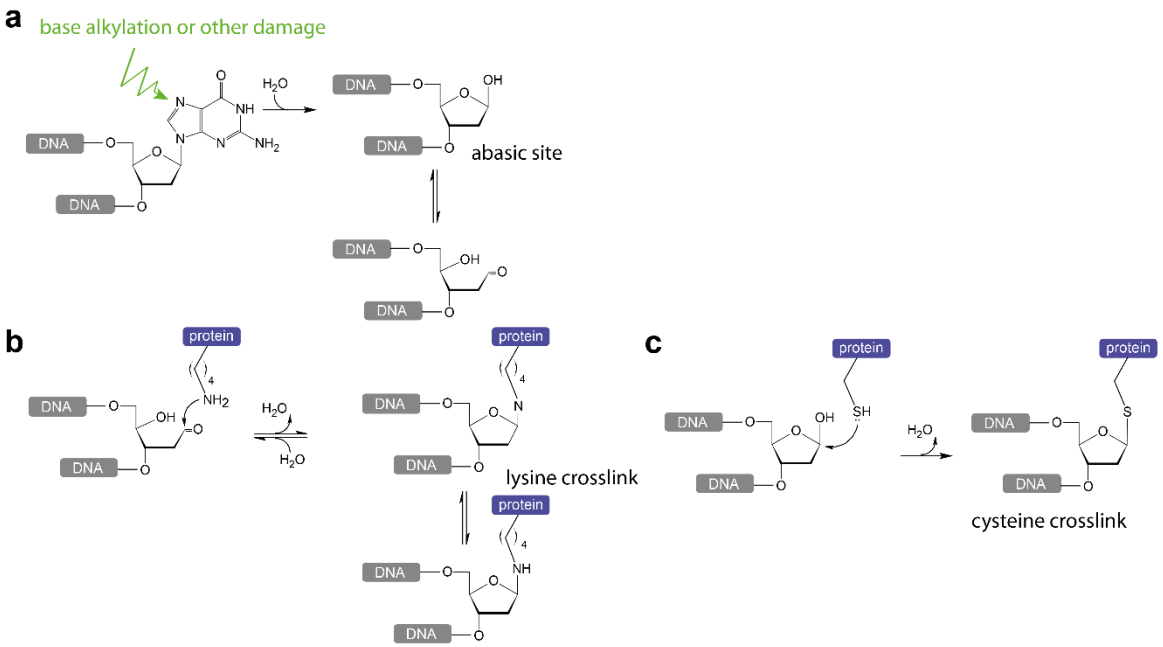


Supplementary Figure S5. Coverage of glycolysis- and TCA-cycle-involved enzymes by protein-RNA XL-MS. **(a)** KEGG pathway of glycolysis and gluconeogenesis. Genes are indicated by rectangles. Colours encode respective protein occurrence in UV, DEB, NM and/or FA dataset.

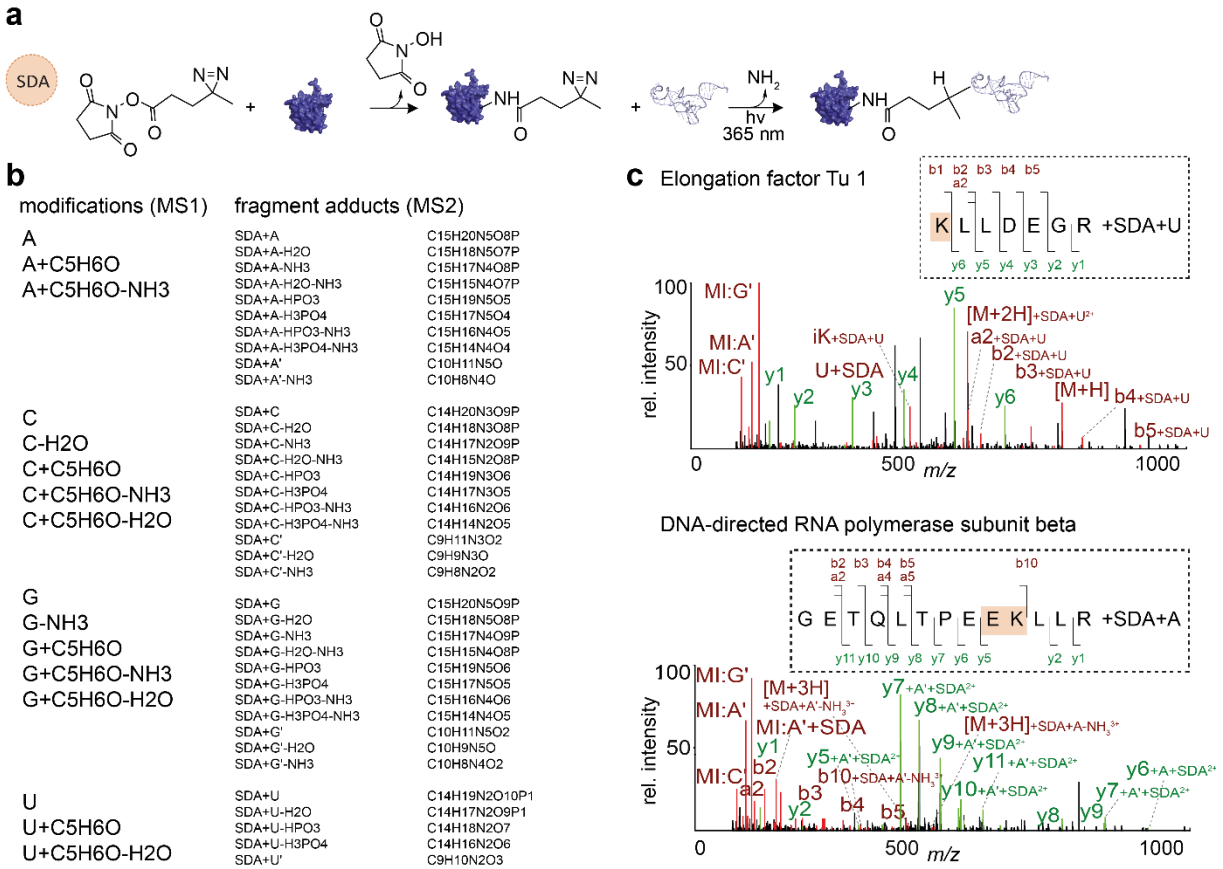
Grey boxes indicate proteins not found as crosslinked. Genes highlighted by red font colour were not identified as crosslinked but were quantified in the proteomics dataset. Right panel: Ranked plot of proteins quantified in the *E. coli* proteomics control experiment. Font colour code matches the rectangle colour code in KEGG pathway. Glycolysis-involved proteins not found as crosslinked are indicated by red font color. **(b)** KEGG pathway of the tricarboxylic acid cycle (TCA-cycle) as in a. Right panel: Ranked plot as in a with TCA-cycle-involved proteins highlighted as in a.



Supplementary Figure S6. 3D distances of crosslinked amino acids to protein sequence features. The distributions of 3D Euclidean distances between the Cα atom pairs of crosslinked residues and nearest feature residue Cα annotated in DESCRIBEPROT **(a-g)** and InterPro (**h-l**) Highlighted are the group means. The 4 Å range is marked, corresponding to the typical distance to the nearest residue across the proteome.



Supplementary Figure S7. Depurination and abasic site reactions in DNA. **(a)** Guanosine base alkylation or other forms of base damage weaking N-glyosidic bond, leading to base hydrolysis. Abasic sites exist in ring-opened aldehyde and the closed hemi-acetal form. **(b)** The acetal form of an abasic site can be attacked at the C1' position by the nucleophilic ε-amino group of lysines to create a crosslink via a reversible Schiff-base intermediate(9). **(c)** The acetal form of an abasic site can be attacked at the C1' position by the nucleophilic thiol group in cysteines to form a stable covalent linkage(10).



Supplementary Figure S8. Protein-nucleic acid XL-MS using SDA. **(a)** Proposed chemical protein-RNA crosslinking reaction mechanism for SDA. **(b)** Sum formula of SDA RNA-crosslink adducts for NuXL analysis. Expected modifications on MS1 level and fragment adducts in MS2 scans. **(c)** MS2 crosslink spectra for SDA-crosslinked peptide-RNA-(oligo)nucleotides from *E. coli* ribosomes resulting from SDA XL-MS and NuXL analysis using settings listed in b. Upper panel: MS2 spectrum of elongation factor Tu 1 peptide KLLDEGR crosslinked to uridine-monophosphate by SDA. Lower panel: MS2 spectrum of DNA-directed RNA polymerase subunit beta peptide GETQLTPEEKLLR crosslinked to adenosine-monophosphate by SDA. Annotated peaks are highlighted in green (y-ions) or red (marker ions and a-/b-ions). Crosslinked amino acids are highlighted in orange.

SUPPLEMENTARY TABLES

Supplementary Table S1. Crosslinker-specific presets in NuXL. Table including all sum formula for RNA/DNA adducts defined as presets in NuXL. Sheets contain different presets. Columns include: target_nucleotides, definitions (sum formula) of monophosphate-nucleotides/deoxyribose; modifications, definitions (sum formula) of RNA/DNA adducts on peptide precursor (MS1); fragment_adducts, definitions (sum formula) of RNA/DNA adducts on peptide fragments (MS2).

Supplementary Table S2. Protein-RNA crosslinks in *E. coli* ribosomes. Table including RNA-crosslink spectrum matches (CSMs) from UV, DEB, NM and FA XL-MS data from purified *E. coli* ribosomes. CSMs are filtered for 1% FDR and rescored by Percolator. Among other values, the table includes: idxml, source file; index, spectrum index number; RT, retention time; precursor *m/z*; score, main score calibrated by percolator algorithm using subscores; PeakAnnotations, MS2 peaks *m/z* values, annotations and intensities; NuXL:NA, RNA adduct on peptide precursor (MS1); NuXL:NT, crosslinked nucleobase.

Supplementary Table S3. List of all subscores used in Percolator-based rescoring. List of all subscores used in Percolator-based rescoring.

Supplementary Table S4. Protein-RNA crosslinks in *in vitro* protein-RNA complexes. Table including RNA-crosslink spectrum matches (CSMs) from UV, DEB, NM and FA XL-MS data from *in vitro* analysed protein-RNA complexes. Sheets include results from: Hsh49-Cus1-U2RNA; Dnmt2-tRNA^{Asp}, NELF-TAR complexes separately. CSMs are filtered for 1% FDR and rescored by Percolator. Among other values, the table includes: idxml, source file; index, spectrum index number; RT, retention time; precursor *m/z*; score, main score calibrated by percolator algorithm using subscores; PeakAnnotations, MS2 peaks *m/z* values, annotations and intensities; NuXL:NA, RNA adduct on peptide precursor (MS1); NuXL:NT, crosslinked nucleobase.

Supplementary Table S5. Protein-RNA crosslinks from *E. coli*. Table including RNA-crosslink spectrum matches (CSMs) from UV, DEB, NM and FA XL-MS data from *E. coli* cells. CSMs are filtered for 1% FDR and rescored by Percolator. Among other values, the table includes: fraction, S30/S100 fraction of lysate; idxml, source file; index, spectrum index number; RT,

retention time; precursor *m/z*; score, main score calibrated by percolator algorithm using subscores; PeakAnnotations, MS2 peaks *m/z* values, annotations and intensities; NuXL:NA, RNA adduct on peptide precursor (MS1); NuXL:NT, crosslinked nucleobase.

Supplementary Table S6. Label-free quantitative *E. coli* proteomics results. Table including modified proteingroups.txt output from MaxQuant search of *E. coli* label-free quantitative proteomics dataset. Among others, columns include iBAQ values for identified proteins.

Supplementary Table S7. Amino acid / sequence feature tests. Table with enrichment analysis of RNA-crosslinks against sequence features of *E. coli* proteome. Secondary structure counts from S4PRED, amino acid counts, feature counts from DESCRIBEPROT and InterPro are included together with the distances to the next feature in 10 Å radius (1D, 3D-euclidean and 3D-SAS distances). The analysis is performed on the detected peptide and crosslinked residue levels, with and without consideration of crosslink-spectrum match counts in a variety of background assumptions. Residue-level enrichment only considers the CSMs with the NuXL best localization threshold >= 1. Provided are the average values of the detected crosslinks, expected background values, t-test outputs, nonparametric goodness-of-fit test outputs, adjusted p-values for both tests (BH procedure) and sample sizes.

Supplementary Table S8. Gene set overrepresentation analysis. Table with a hypergeometric test overrepresentation analysis of identified *E. coli* proteins across crosslinking methods. The proteins were filtered for the detection of at least 1 unique peptide sequence. Provided are the gene set names together with the overlap size, significance of the overlap and the estimates of the gene set redundancy.

Supplementary Table S9. Proximal feature enrichment. Table with significance of co-localization of crosslinked residues and annotated protein sequence features. Reported are the outcomes of binomial tests with feature frequency weights: set sizes of foreground and background within and outside the 4 Å radius, the p-value of enrichment, adjusted p-value (BH method) and 0.95 confidence interval.

Supplementary Table S10. Protein-DNA crosslinks in HeLa nucleosomes. Table including DNA-crosslink spectrum matches (CSMs) from UV, DEB, NM and FA XL-MS data from purified HeLa nucleosomes. CSMs are filtered for 1% FDR and rescored by Percolator. Among other values,

the table includes: idxml, source file; index, spectrum index number; RT, retention time; precursor *m/z*; score, main score calibrated by percolator algorithm using subscores; PeakAnnotations, MS2 peaks *m/z* values, annotations and intensities; NuXL:NA, DNA adduct on peptide precursor (MS1); NuXL:NT, crosslinked nucleobase/deoxyribose.

Supplementary Table S11. Protein-DNA crosslinks from *E. coli*. Table including DNA-crosslink spectrum matches (CSMs) from UV, DEB, NM and FA XL-MS data from *E. coli* cells. CSMs are filtered for 1% FDR and rescored by Percolator. Among other values, the table includes: fraction, S30/S100 fraction of lysate; idxml, source file; index, spectrum index number; RT, retention time; precursor *m/z*; score, main score calibrated by percolator algorithm using subscores; PeakAnnotations, MS2 peaks *m/z* values, annotations and intensities; NuXL:NA, DNA adduct on peptide precursor (MS1); NuXL:NT, crosslinked nucleobase.

Supplementary Table S12. Ambiguous RNA/DNA mass adducts in XL-MS. Table containing ambiguous RNA/DNA mass adducts in XL-MS. Sum formula corresponding to ambiguous mass adducts are listed with respective monoisotopic masses and possible RNA/DNA adducts.

SUPPLEMENTARY DATA

Supplementary Data S1. Visualisation of RNA-crosslinks in *E. coli*. PDF file displaying 1D Sequence representations of all crosslinked proteins from UV, DEB, NM and FA XL-MS *E. coli in vivo* datasets containing at least one crosslink site with a localisation score ≥ 1. The header provides information on: protein accession, protein name, protein abundance (log10 iBAQ values) from label-free quantitative proteomics dataset presented in this study ("tryptic"), PAXdb K12 strain protein abundance in ppm, PAXdb *E. coli* protein abundance in ppm. For all abundance values, the respective abundance quantile the values correspond to is given. The plot includes the protein sequence plotted schematically in 1D, including positions of UV, DEB and NM crosslink sites (localisation score ≥) and indicated CSM counts (y axis), UV, DEB, NM and FA crosslinked peptide positions, potential tryptic cleavages.

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7. Queiroz, R.M.L., Smith, T., Villanueva, E., Marti-Solano, M., Monti, M., Pizzinga, M., Mirea, D.M., Ramakrishna, M., Harvey, R.F., Dezi, V. *et al.* (2019) Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS). *Nat Biotechnol*, **37**, 169-178.
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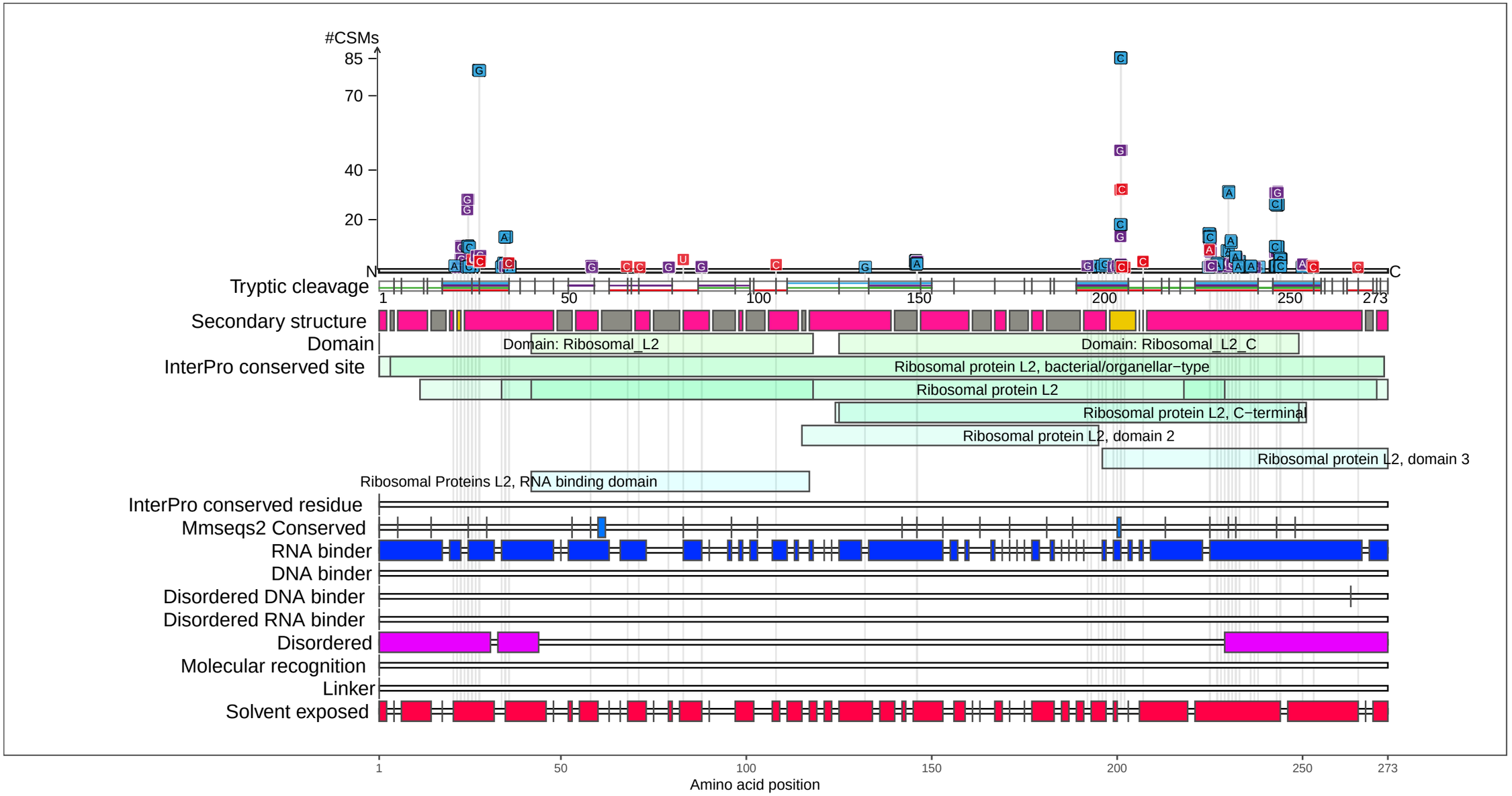
9. Sczepanski, J.T., Wong, R.S., McKnight, J.N., Bowman, G.D. and Greenberg, M.M. (2010) Rapid DNA-protein cross-linking and strand scission by an abasic site in a nucleosome core particle. *Proc Natl Acad Sci U S A*, **107**, 22475-22480.
10. Chan, W., Ham, Y.-H., Jin, L., Chan, H.W., Wong, Y.-L., Chan, C.-K. and Chung, P.-Y. (2019) Quantification of a Novel DNA–Protein Cross-Link Product Formed by Reacting Apurinic/Apyrimidinic Sites in DNA with Cysteine Residues in Protein by Liquid Chromatography-Tandem Mass Spectrometry Coupled with the Stable Isotope-Dilution Method. *Analytical Chemistry*, **91**, 4987-4994.

P60422
RL2_ECOLI 50S ribosomal protein L2

− Abundance:
tryptic [log10 Intensity]: 9.26 (Q 93)
PAXdb K12 strain [ppm]: 3.89 (Q 100)
PAXdb E.coli [ppm]: 3.33 (Q 98)

− RNA functions:
Ribosomal Proteins L2, RNA binding domain; RNA binding; rRNA binding



P0A7V3
RS3_ECOLI 30S ribosomal protein S3

− Abundance:
tryptic [log10 Intensity]: 9.66 (Q 98)
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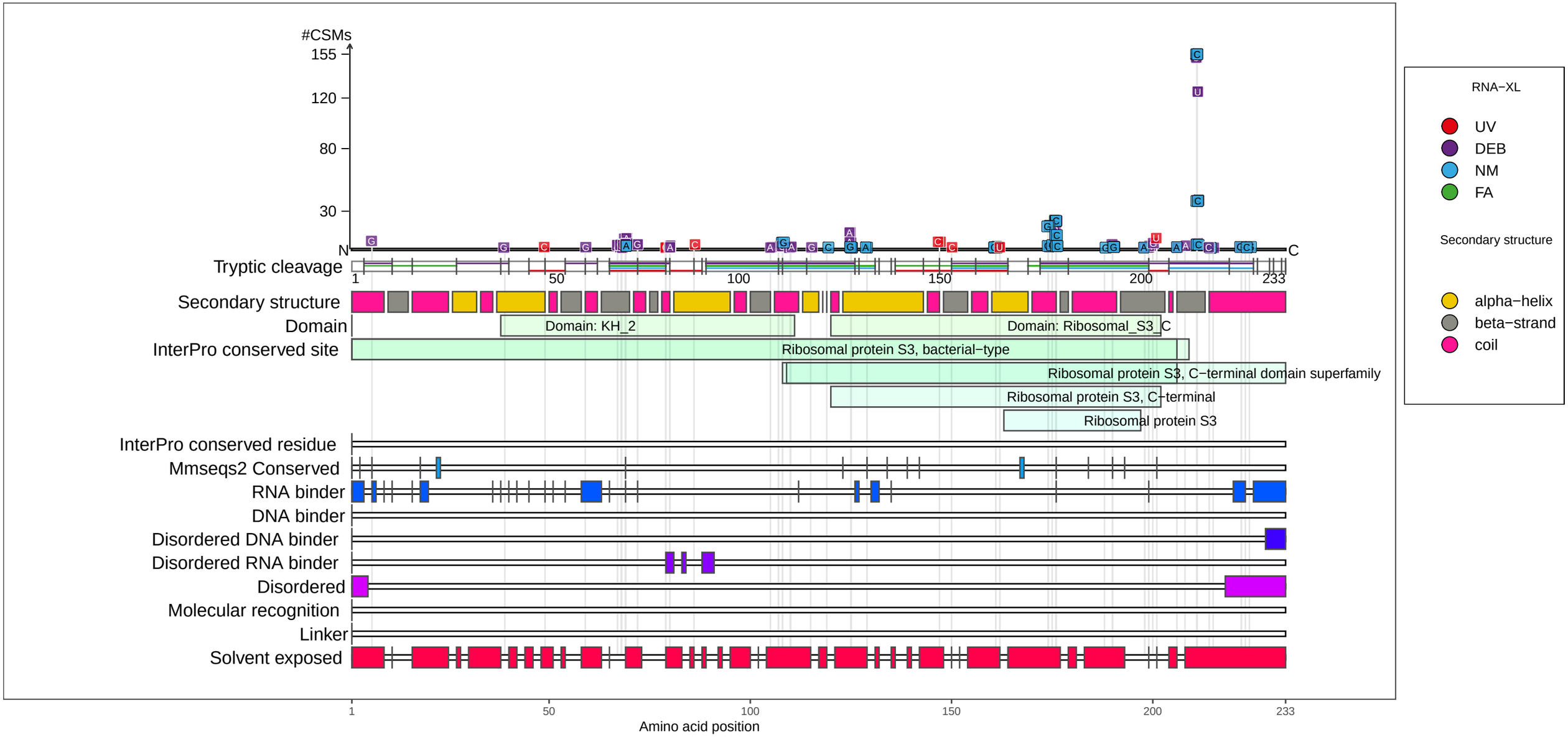
PAXdb E.coli [ppm]: 3.45 (Q 98)

− RNA functions:
mRNA binding; RNA binding; rRNA binding



P0A6Y8
DNAK_ECOLI Chaperone protein DnaK

− Abundance:
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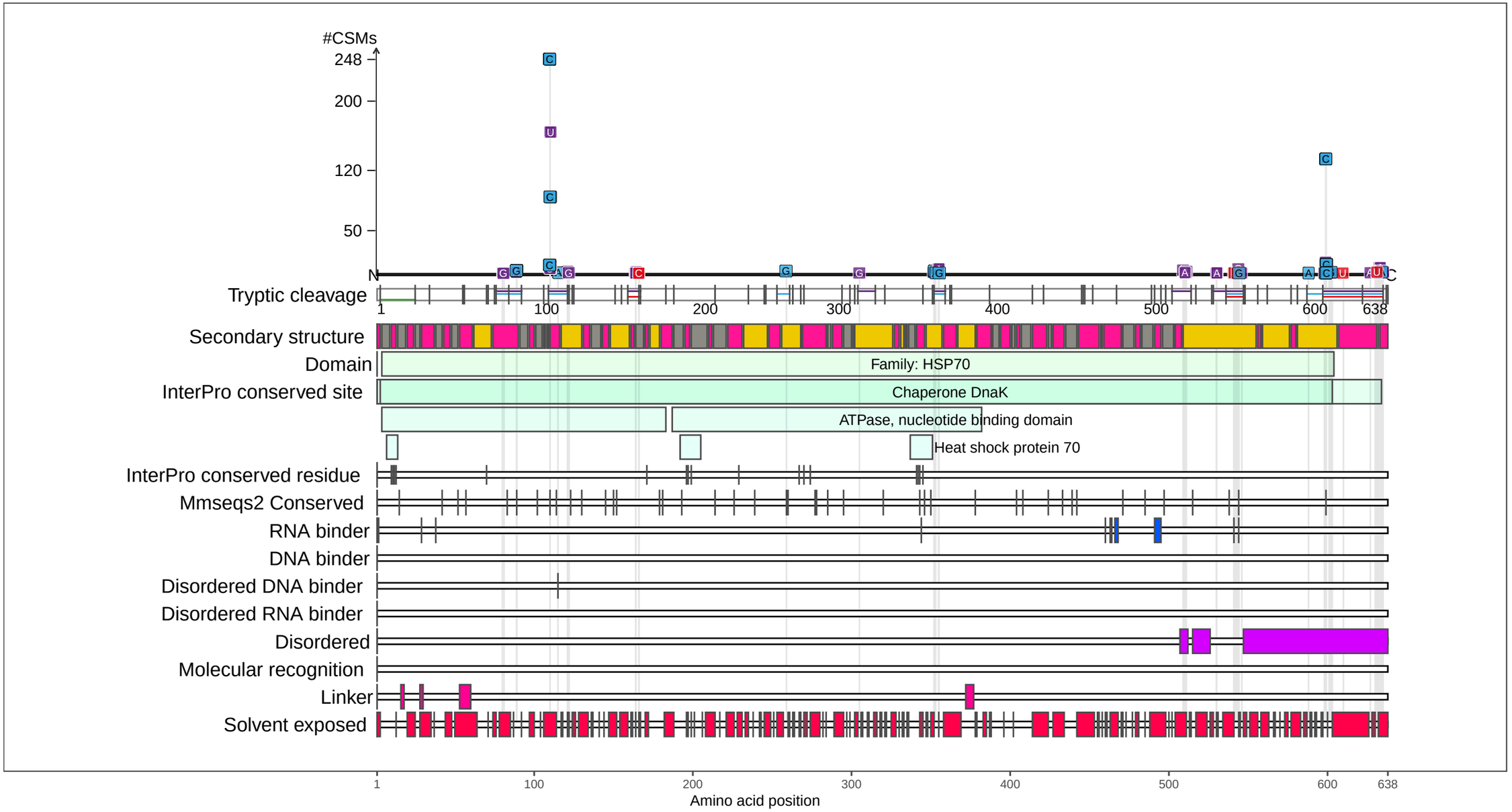
PAXdb E.coli [ppm]: 3.89 (Q 100)

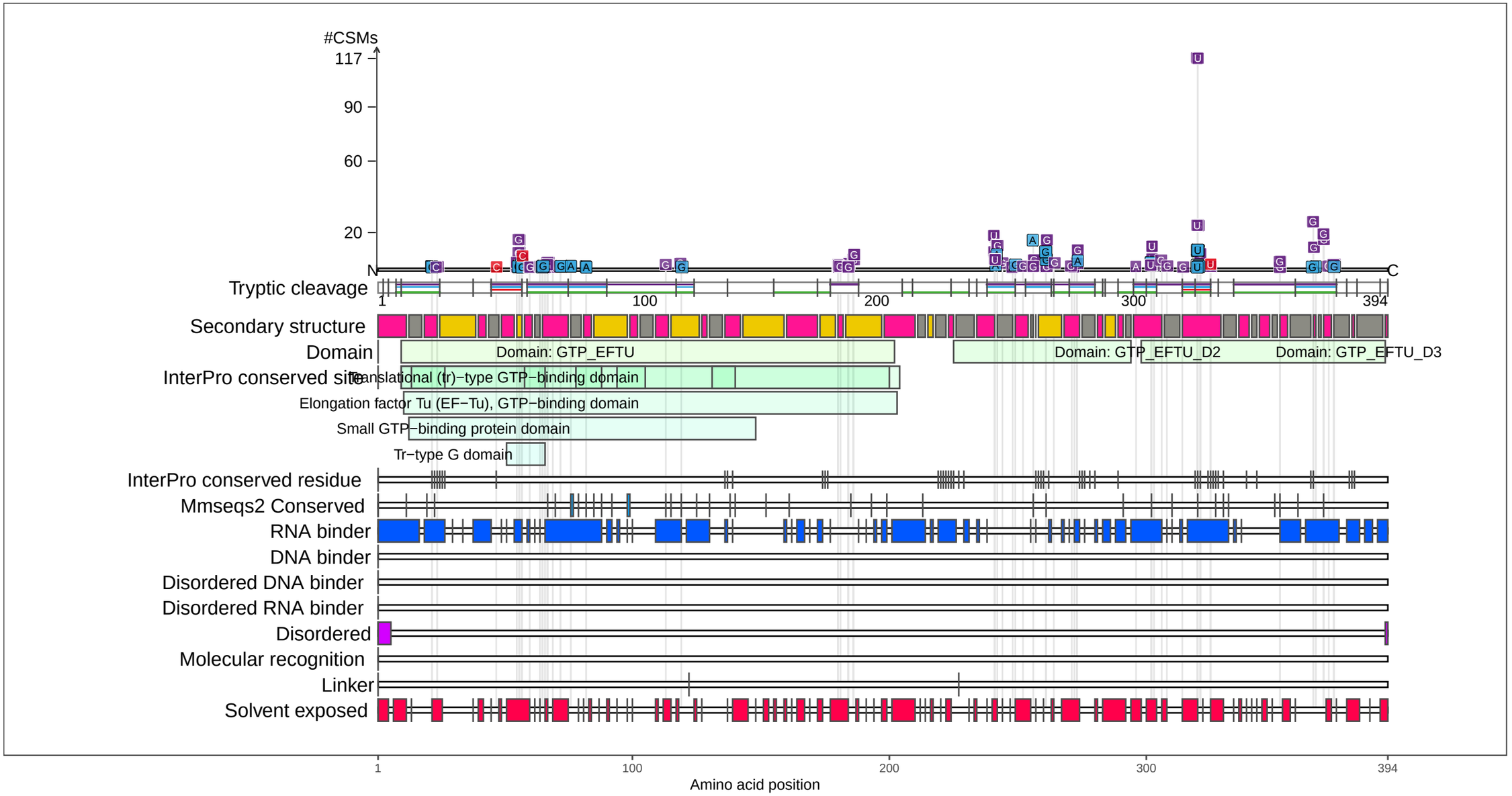
− RNA functions: not annotated

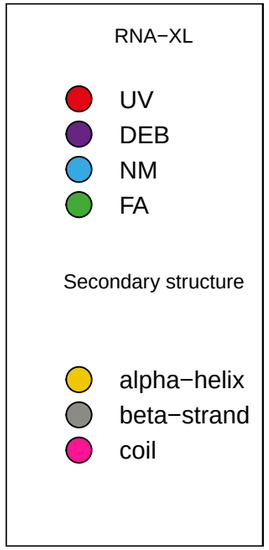


P0CE47
EFTU1_ECOLI Elongation factor Tu 1

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 3.7 (Q 99)
PAXdb E.coli [ppm]: 4.27 (Q 100)

− RNA functions:
RNA binding

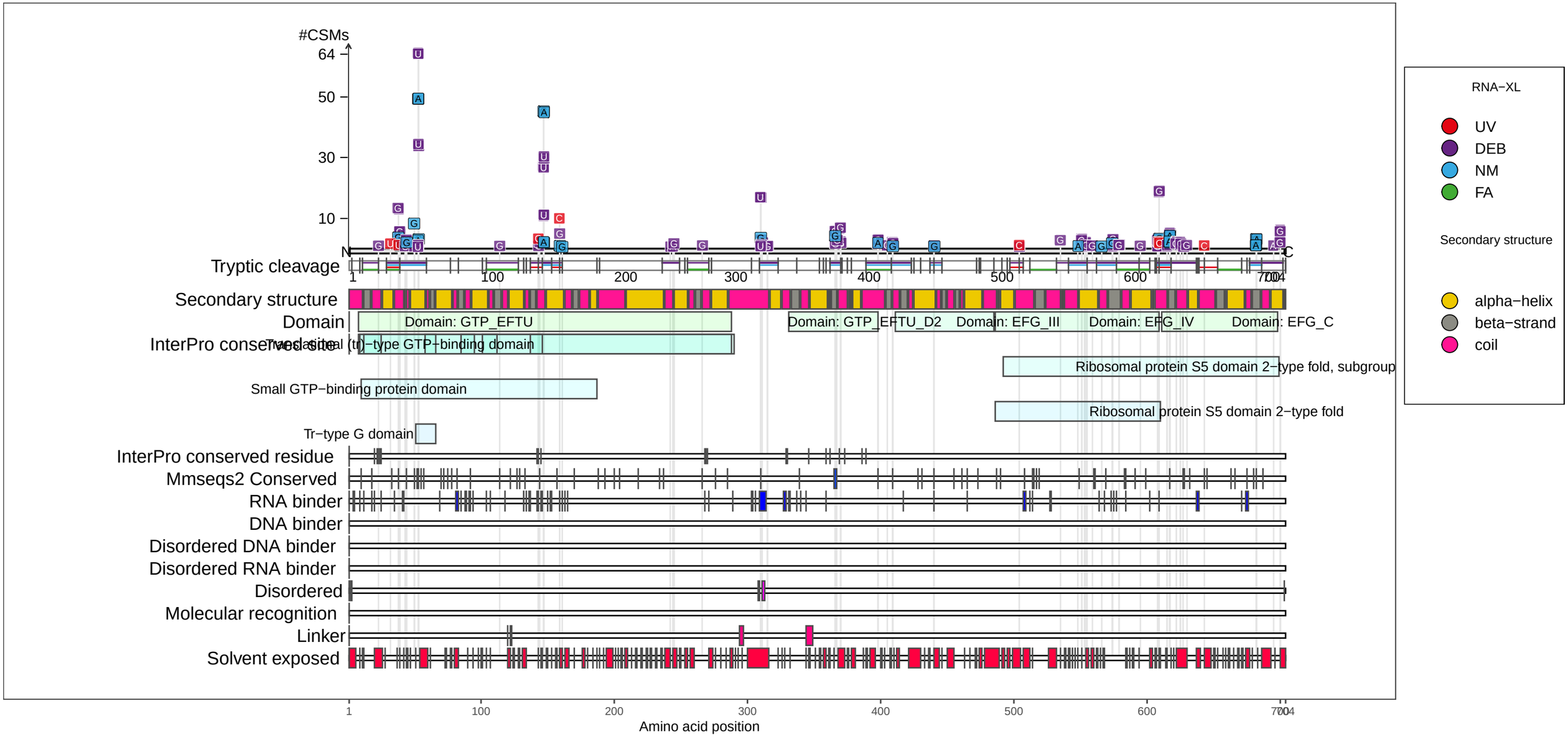




P0A6M8
EFG_ECOLI Elongation factor G

− Abundance:
tryptic [log10 Intensity]: 10.41 (Q 100)
PAXdb K12 strain [ppm]: 3.24 (Q 94)
PAXdb E.coli [ppm]: 3.48 (Q 99)

− RNA functions:
RNA binding



P0AG67
RS1_ECOLI 30S ribosomal protein S1

− Abundance:
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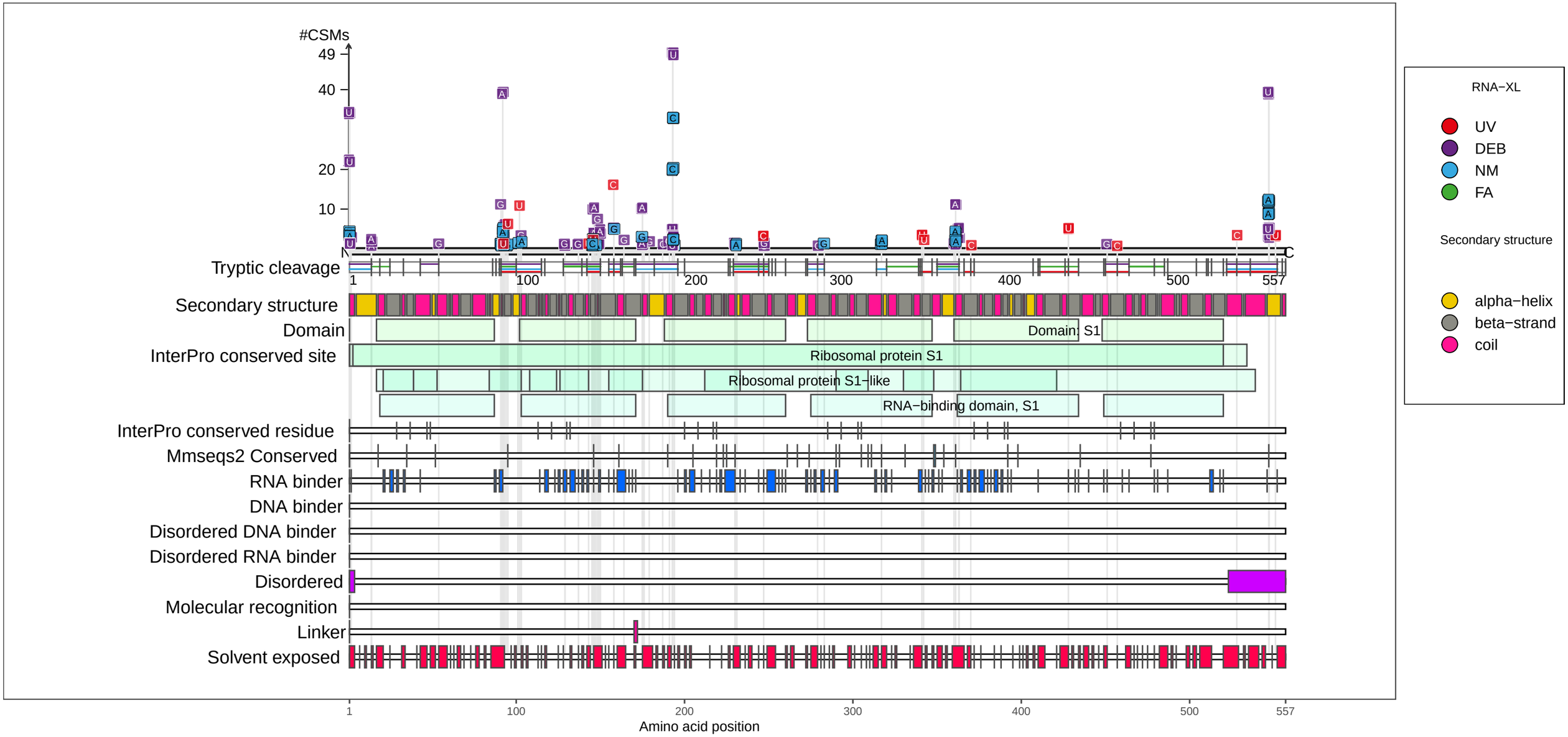
PAXdb K12 strain [ppm]: 3.53 (Q 98)
PAXdb E.coli [ppm]: 3.38 (Q 98)

− RNA functions:
mRNA binding; RNA binding; S1 RNA binding domain



P61175
RL22_ECOLI 50S ribosomal protein L22

− Abundance:
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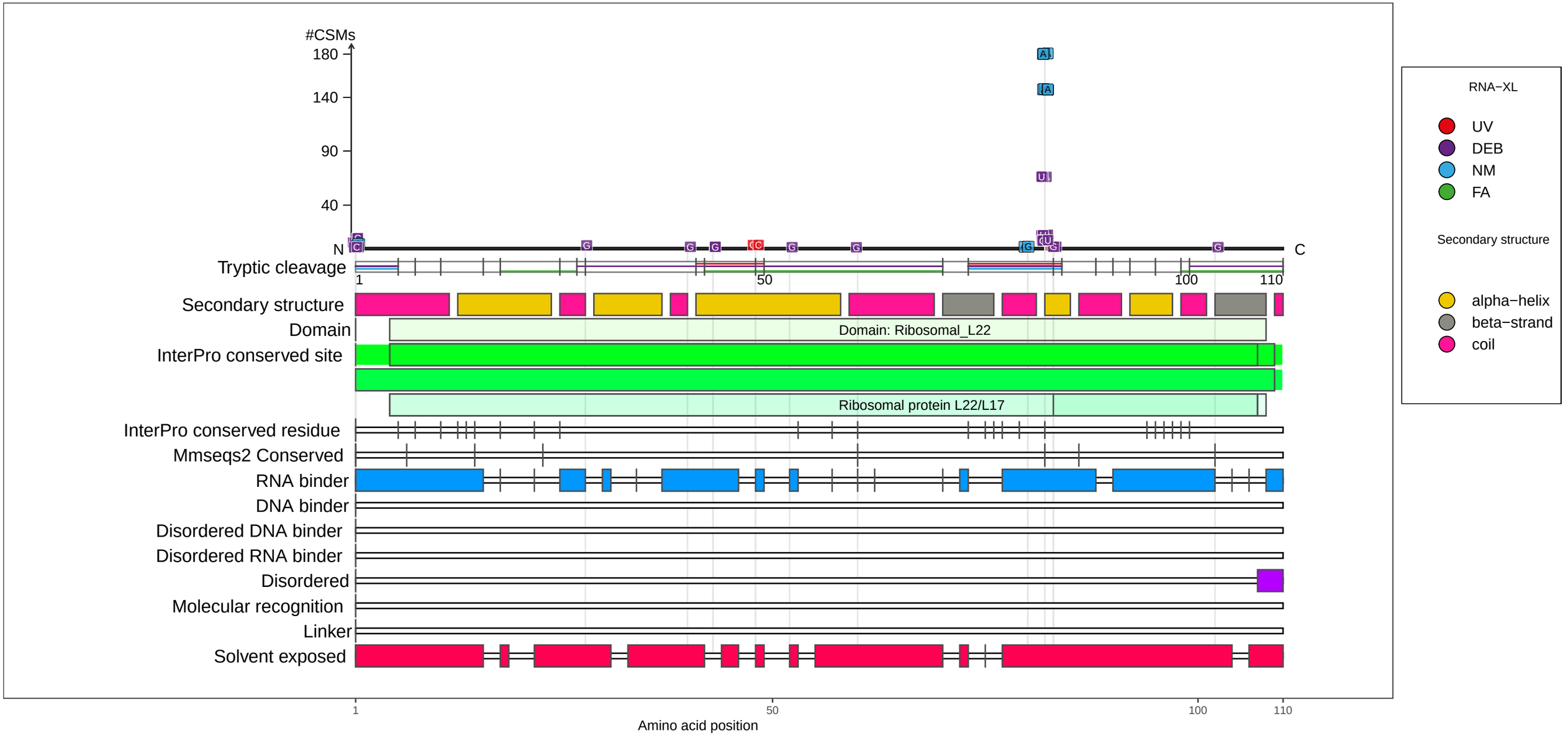
PAXdb K12 strain [ppm]: 4.03 (Q 100)
PAXdb E.coli [ppm]: 3.62 (Q 100)

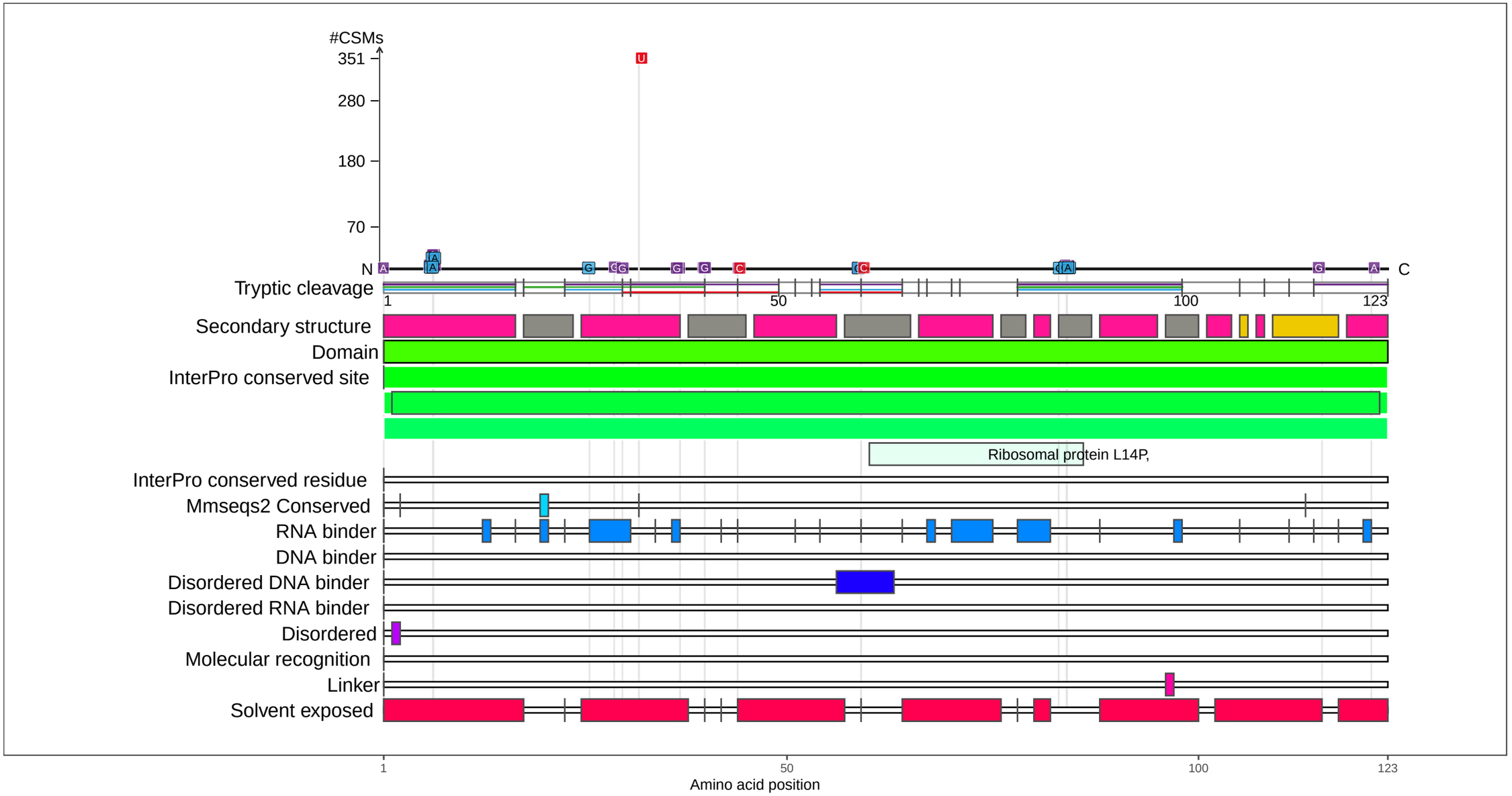
− RNA functions:
RNA binding; rRNA binding



P0ADY3
RL14_ECOLI 50S ribosomal protein L14

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 3.68 (Q 99)
PAXdb E.coli [ppm]: 3.57 (Q 99)

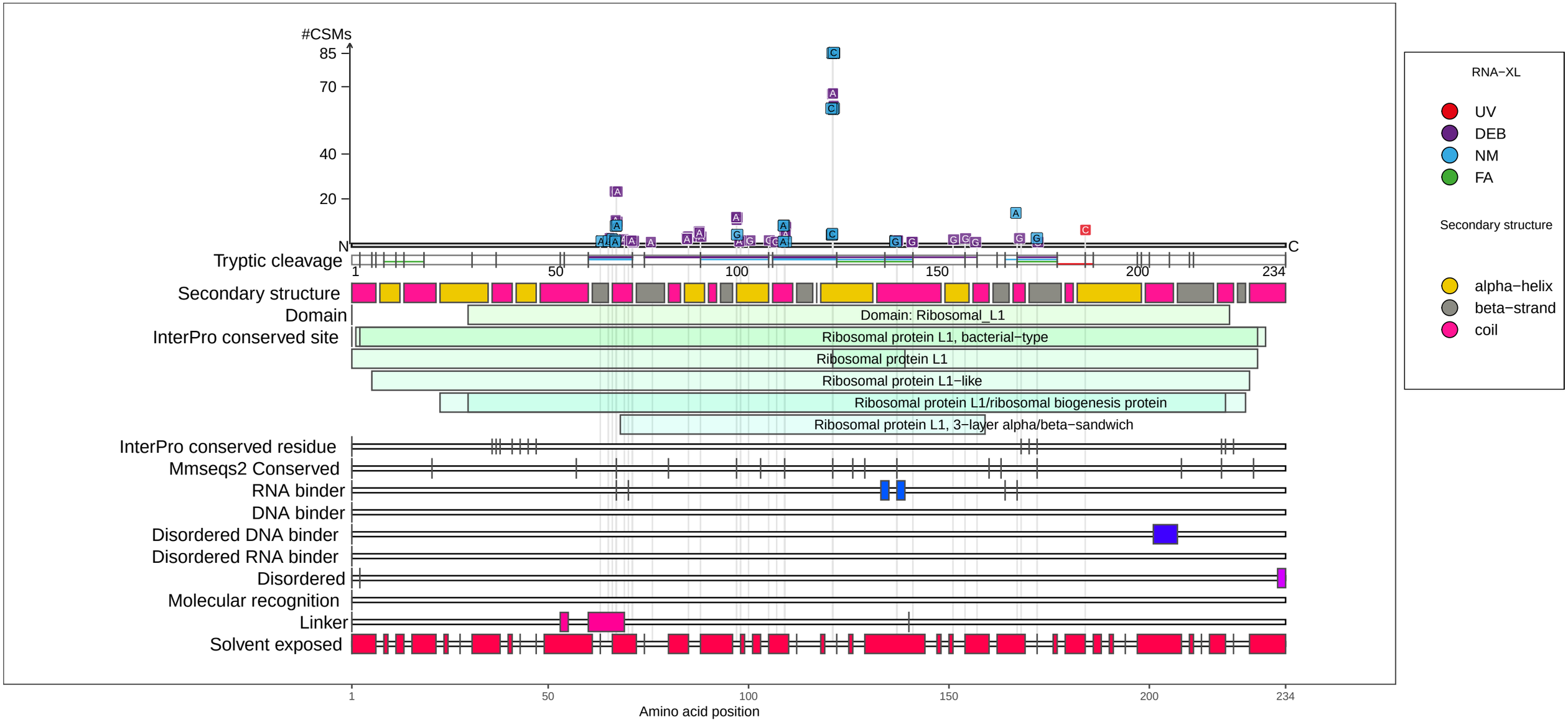
− RNA functions:
RNA binding; rRNA binding



P0A7L0
RL1_ECOLI 50S ribosomal protein L1

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 3.48 (Q 97)
PAXdb E.coli [ppm]: 3.37 (Q 98)

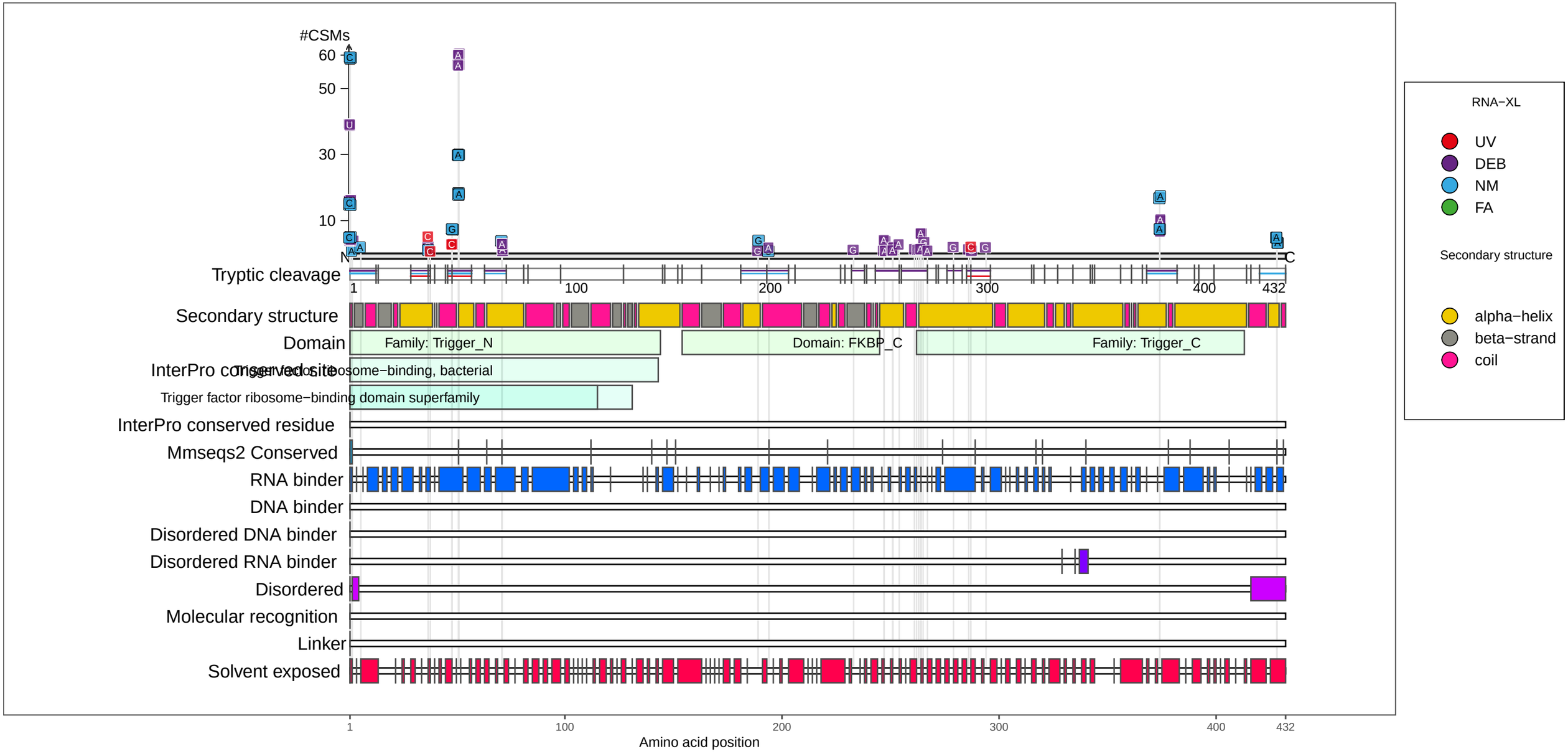
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA processing; rRNA binding; rRNA metabolic process; rRNA processing; tRNA binding



P0A850
TIG_ECOLI Trigger factor

− Abundance:
tryptic [log10 Intensity]: 10.15 (Q 100)
PAXdb K12 strain [ppm]: 3.53 (Q 98)
PAXdb E.coli [ppm]: 3.52 (Q 99)

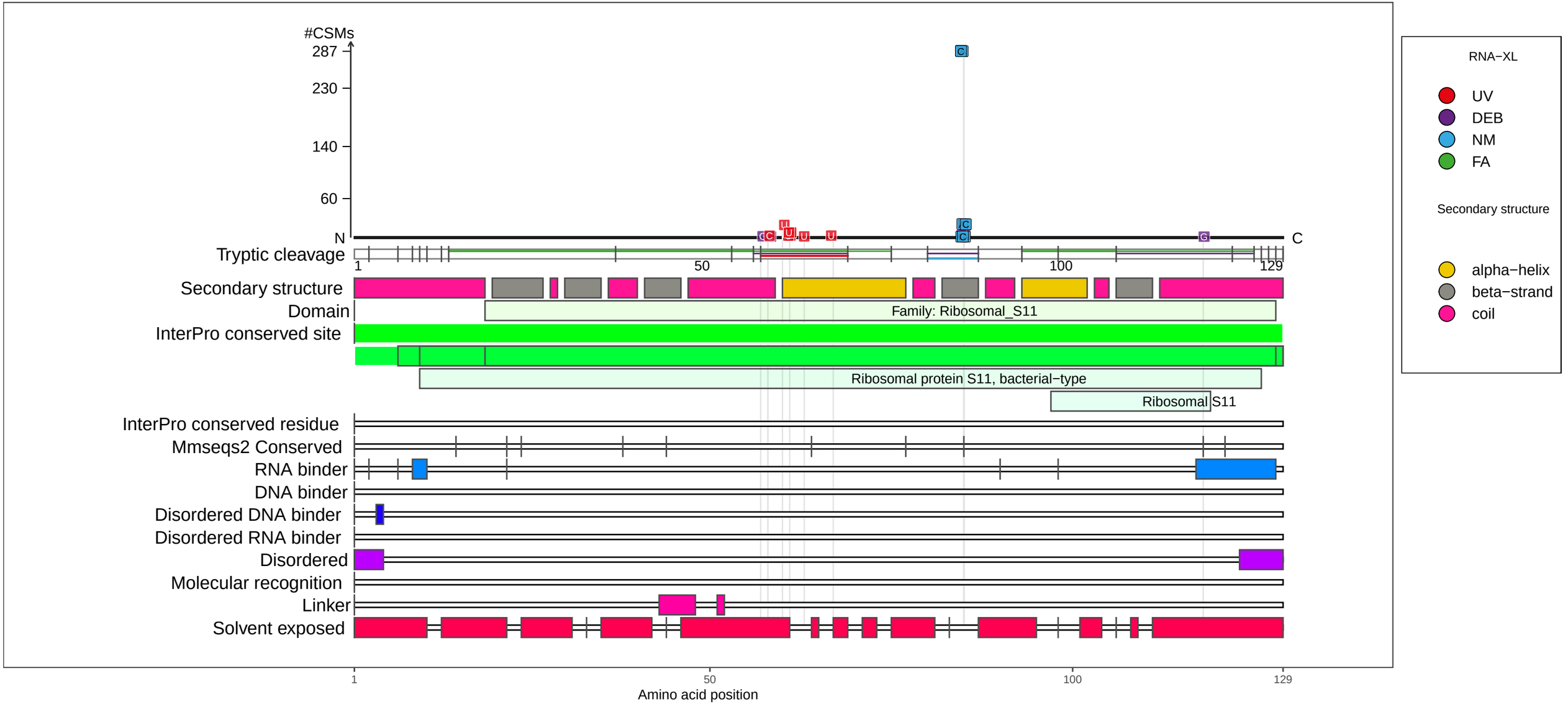
− RNA functions: not annotated



P0A7R9
RS11_ECOLI 30S ribosomal protein S11

− Abundance:
tryptic [log10 Intensity]: 8.89 (Q 86)
PAXdb K12 strain [ppm]: 3.47 (Q 97)
PAXdb E.coli [ppm]: 3.04 (Q 95)

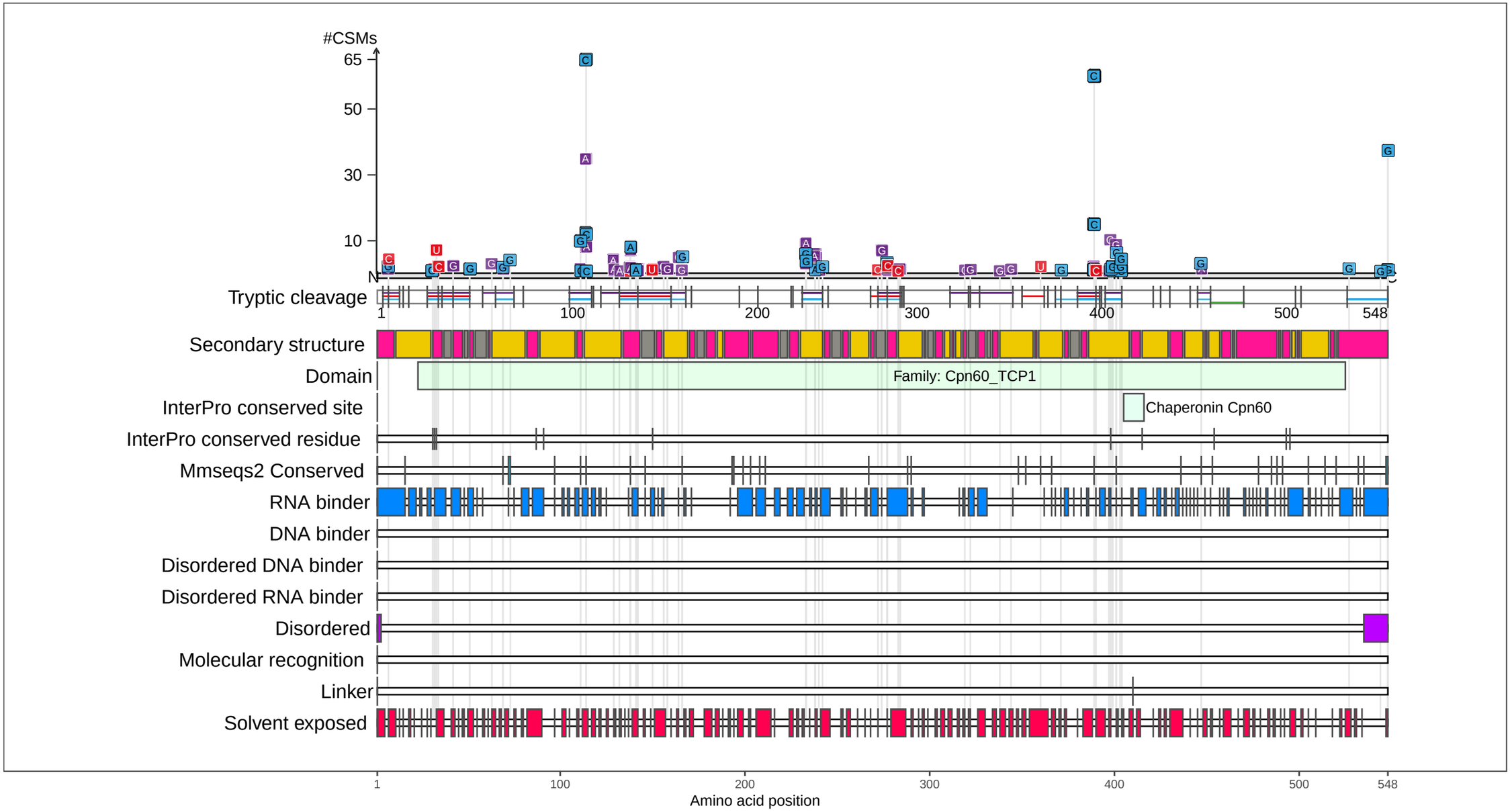
− RNA functions:
mRNA 5−UTR binding; mRNA binding; ncRNA metabolic process; ncRNA processing; RNA binding
RNA metabolic process; RNA processing; rRNA binding; rRNA metabolic process
rRNA processing

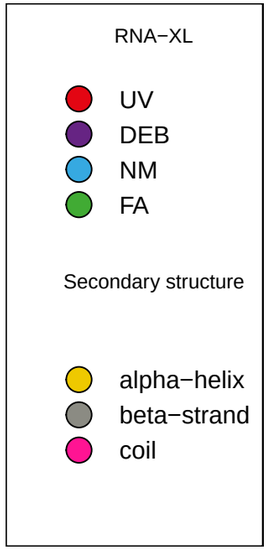


P0A6F5
CH60_ECOLI Chaperonin GroEL

− Abundance:
tryptic [log10 Intensity]: 10.15 (Q 100)
PAXdb K12 strain [ppm]: 3.48 (Q 97)
PAXdb E.coli [ppm]: 3.53 (Q 99)

− RNA functions: not annotated

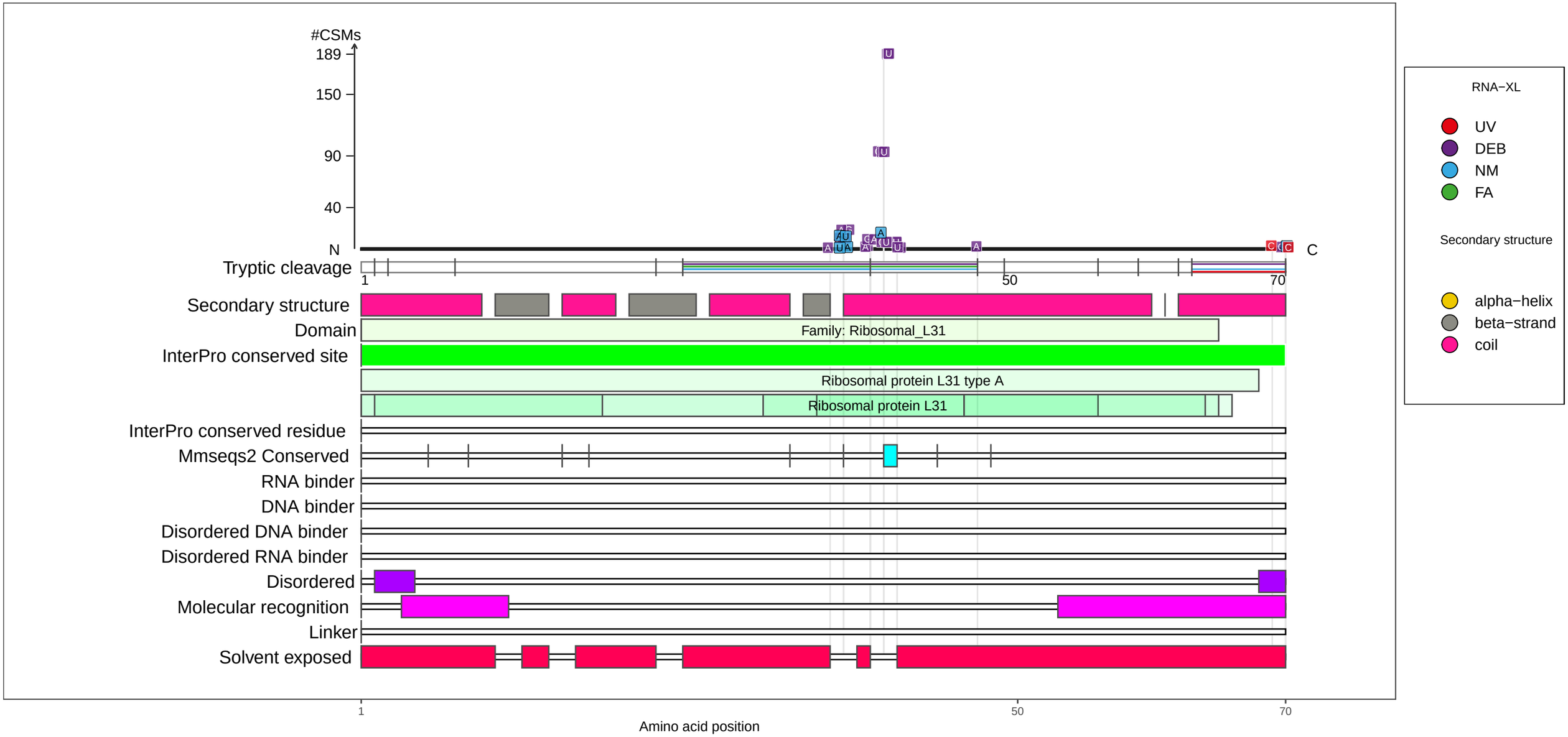




P0A7M9
RL31_ECOLI 50S ribosomal protein L31

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 3.53 (Q 98)
PAXdb E.coli [ppm]: 2.89 (Q 93)

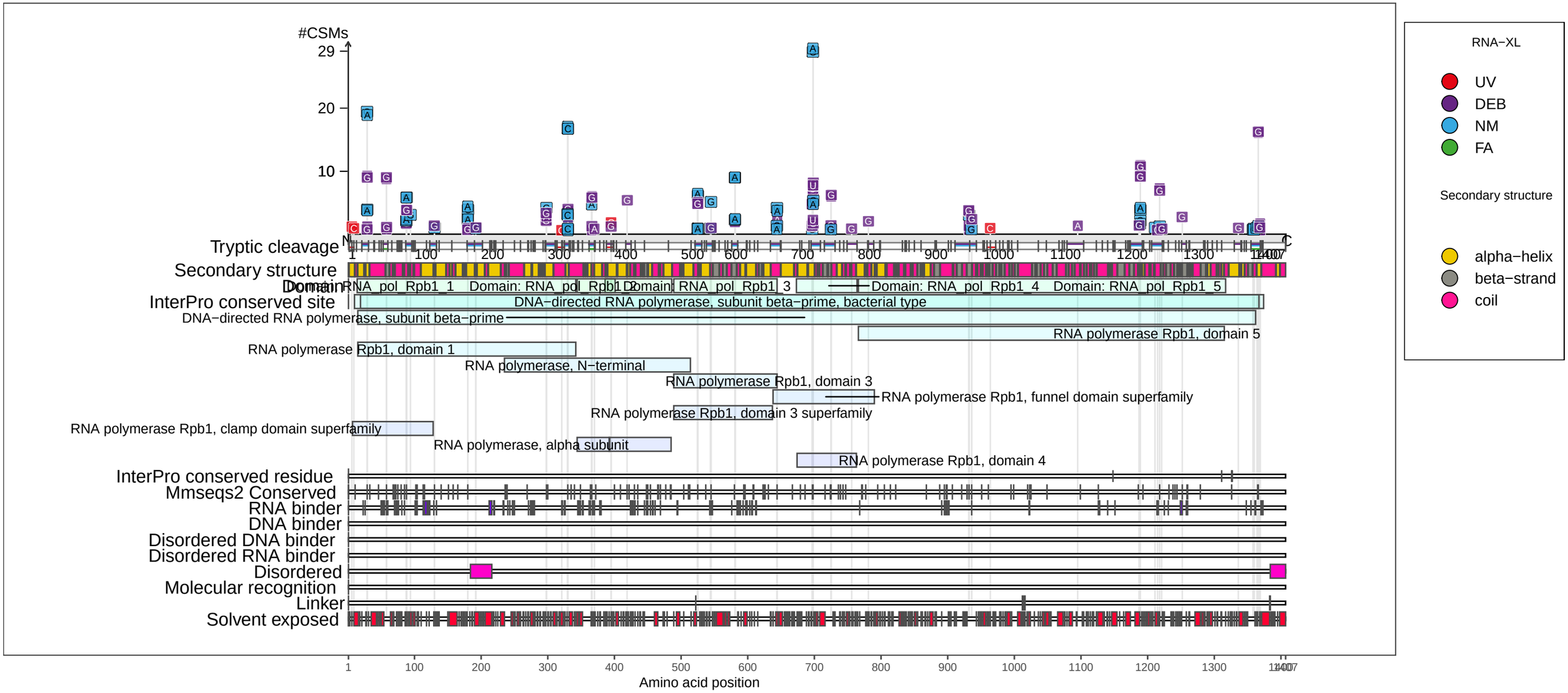
− RNA functions:
RNA binding; rRNA binding



P0A8T7
RPOC_ECOLI DNA−directed RNA polymerase subunit beta'

− Abundance:
tryptic [log10 Intensity]: 9.82 (Q 99)
PAXdb K12 strain [ppm]: 3.18 (Q 94)
PAXdb E.coli [ppm]: 2.9 (Q 93)

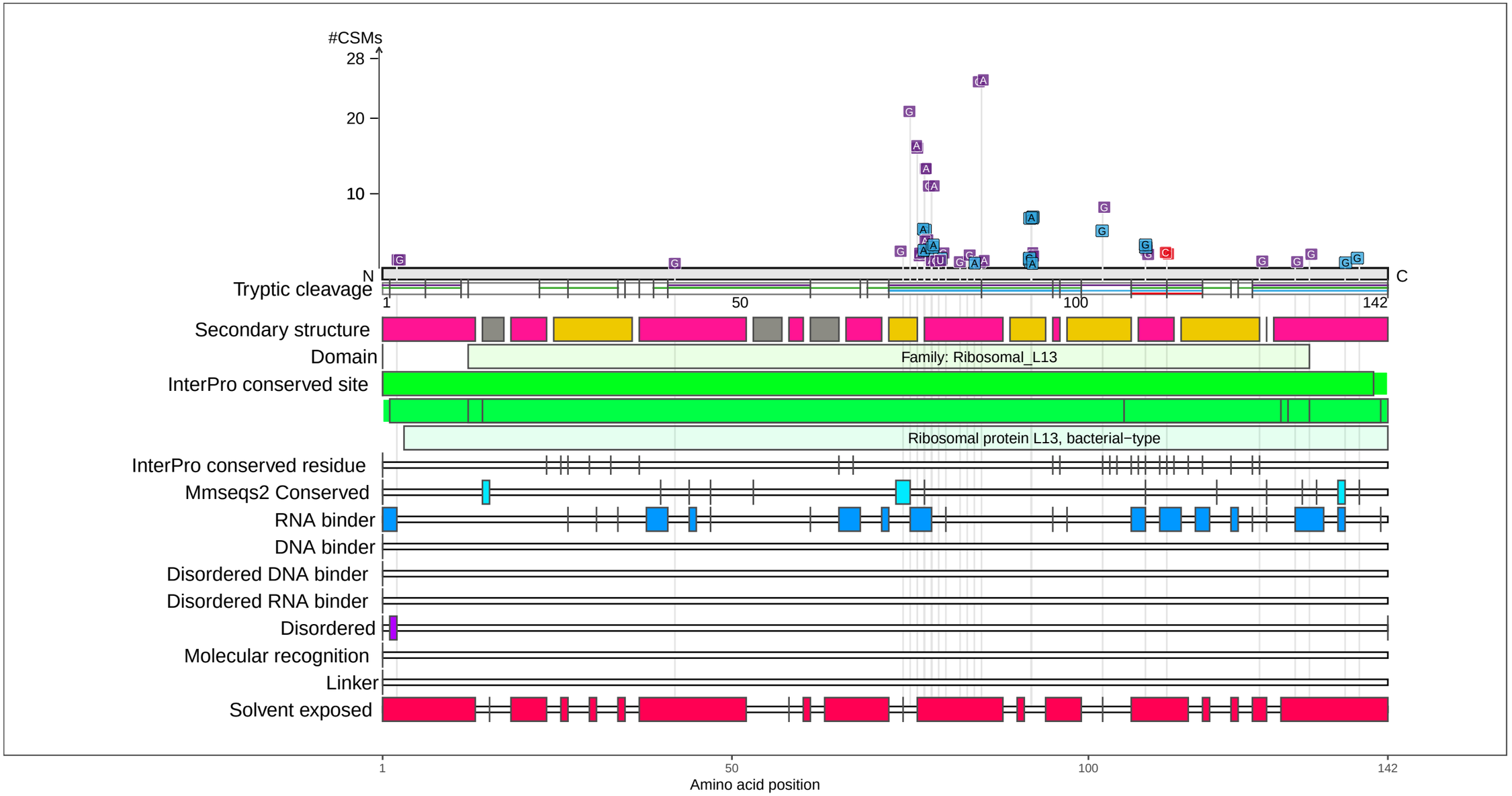
− RNA functions:
5−3 RNA polymerase activity; DNA−directed 5−3 RNA polymerase activity
RNA biosynthetic process; RNA metabolic process; RNA polymerase activity
RNA polymerase Rpb1, domain 1; RNA polymerase Rpb1, domain 2; RNA polymerase Rpb1, domain 3
RNA polymerase Rpb1, domain 4; RNA polymerase Rpb1, domain 5



P0AA10
RL13_ECOLI 50S ribosomal protein L13

− Abundance:
tryptic [log10 Intensity]: 9.11 (Q 91)
PAXdb K12 strain [ppm]: 3.67 (Q 99)
PAXdb E.coli [ppm]: 3.44 (Q 98)

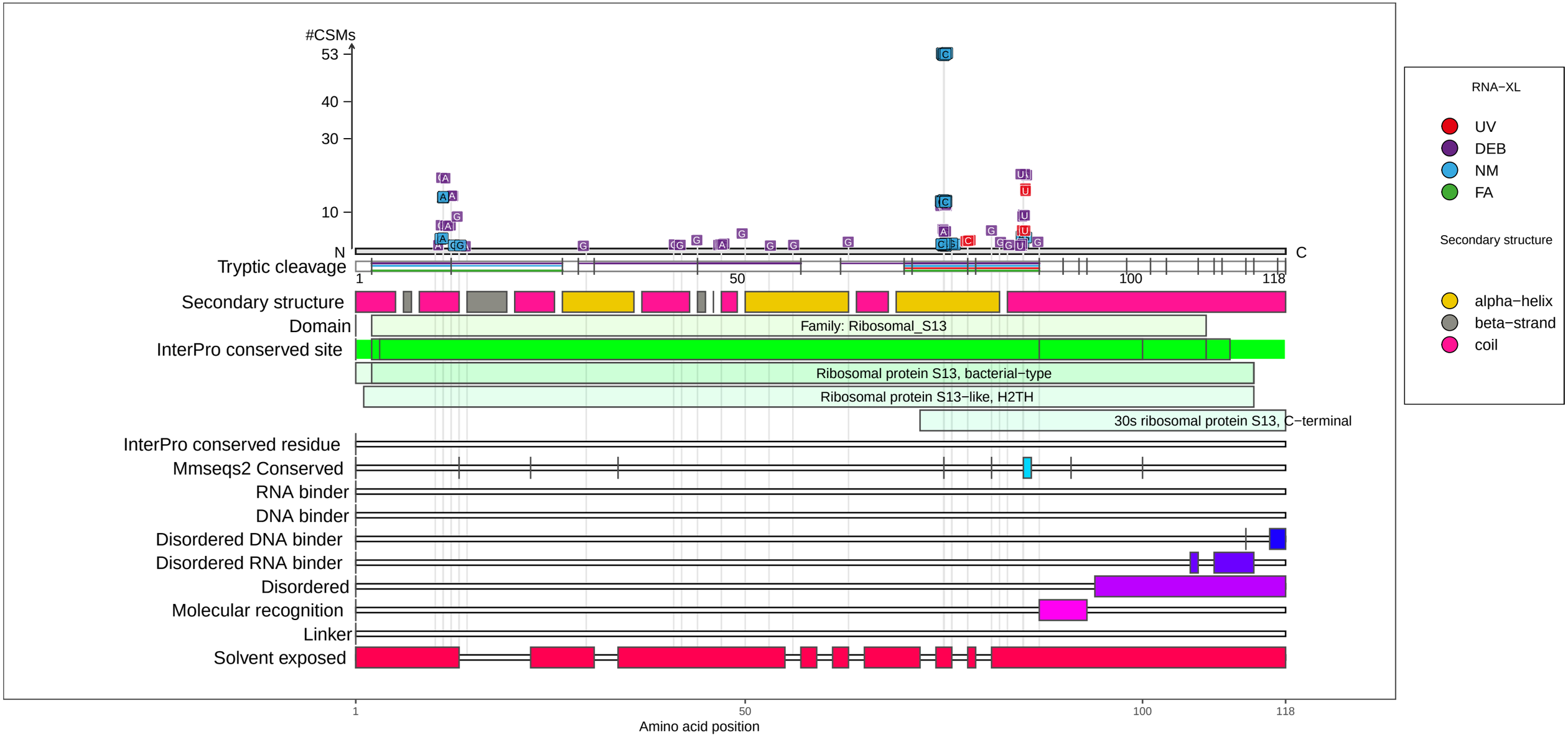
− RNA functions:
mRNA binding; RNA binding; rRNA binding



P0A7S9
RS13_ECOLI 30S ribosomal protein S13

− Abundance:
tryptic [log10 Intensity]: 9.56 (Q 97)
PAXdb K12 strain [ppm]: 3.69 (Q 99)
PAXdb E.coli [ppm]: 3.59 (Q 100)

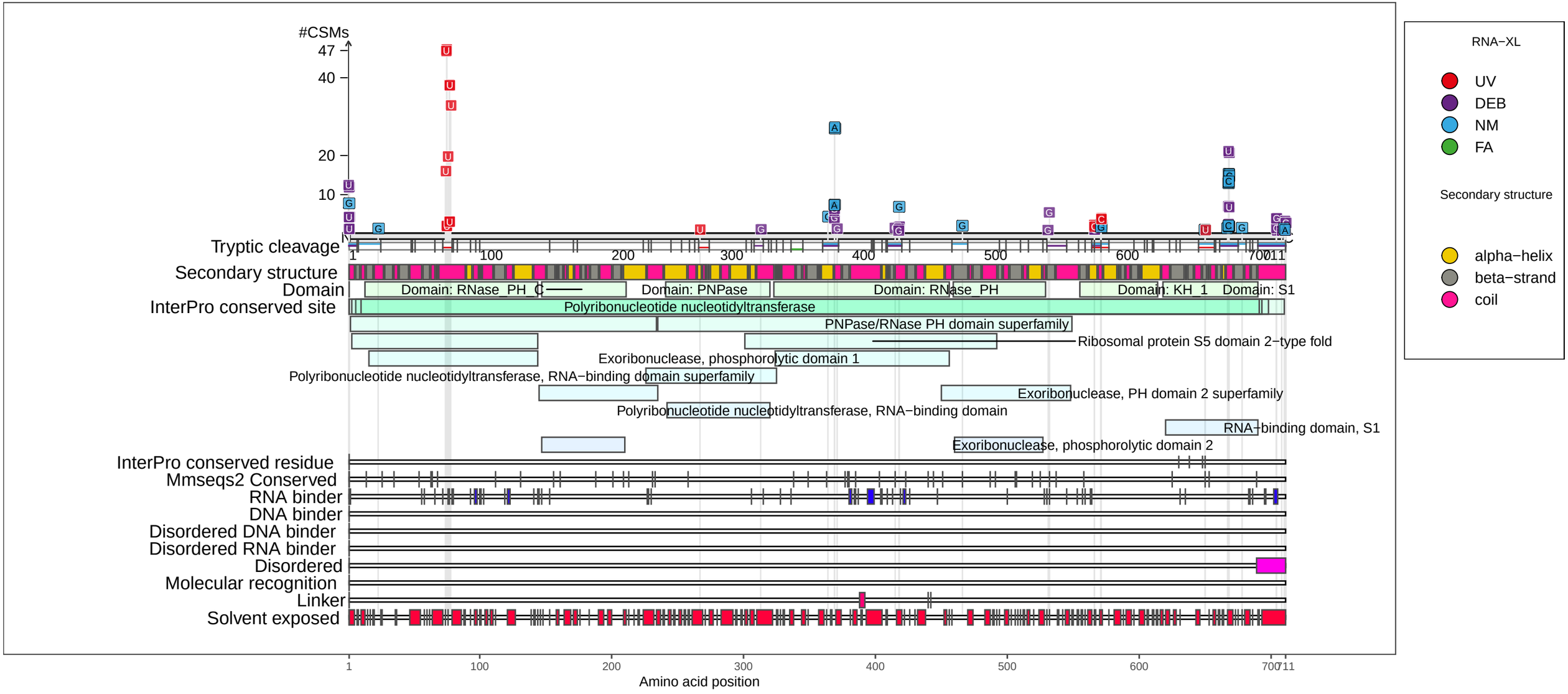
− RNA functions:
RNA binding; rRNA binding; tRNA binding



P05055
PNP_ECOLI Polyribonucleotide nucleotidyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.59 (Q 97)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 3.43 (Q 98)

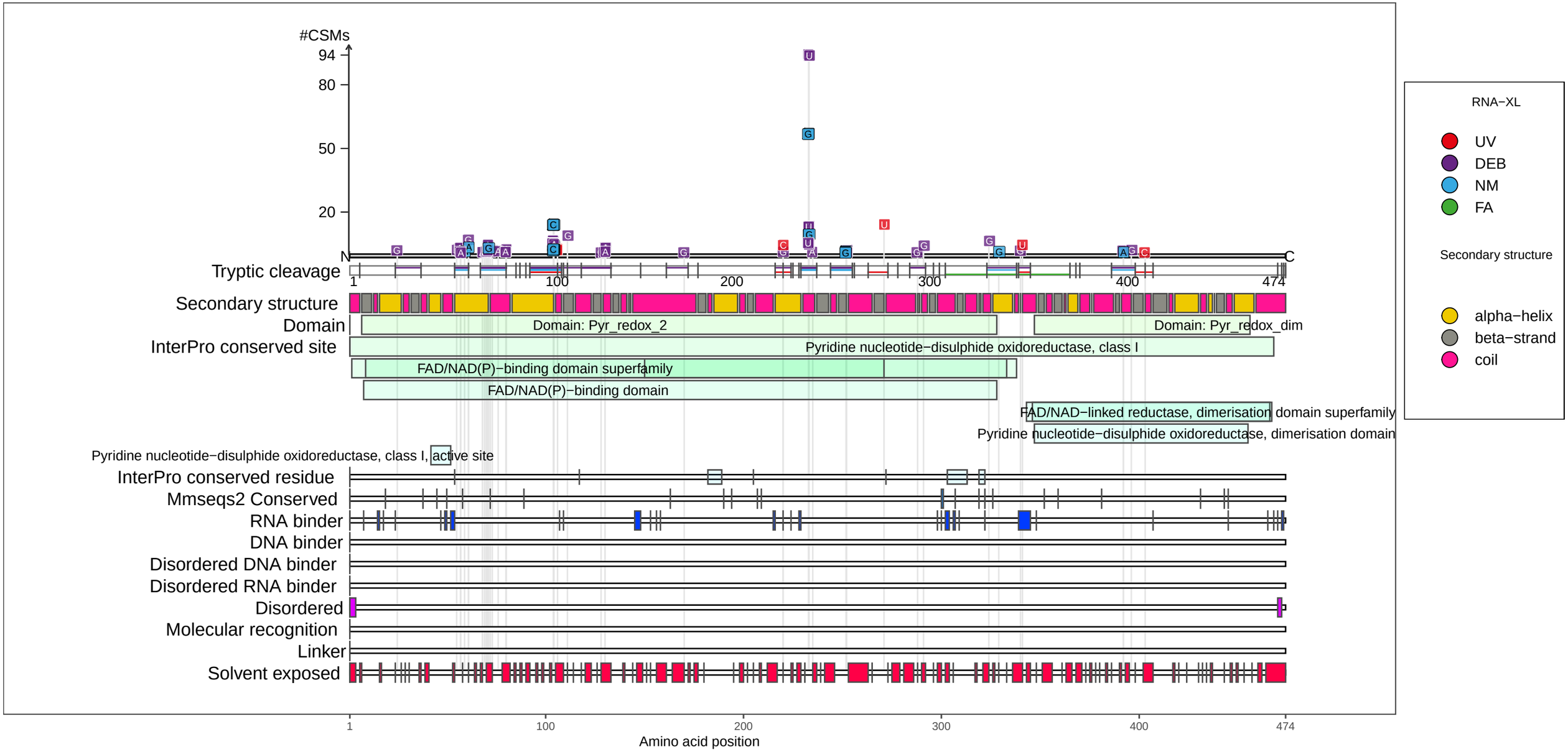
− RNA functions:
mRNA catabolic process; mRNA metabolic process
Polyribonucleotide nucleotidyltransferase, RNA binding domain; RNA binding; RNA catabolic process; RNA metabolic process
RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, exonucleolytic; RNA processing; S1 RNA binding domain



P0A9P0
DLDH_ECOLI Dihydrolipoyl dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.67 (Q 98)
PAXdb K12 strain [ppm]: 3.46 (Q 97)
PAXdb E.coli [ppm]: 3.4 (Q 98)

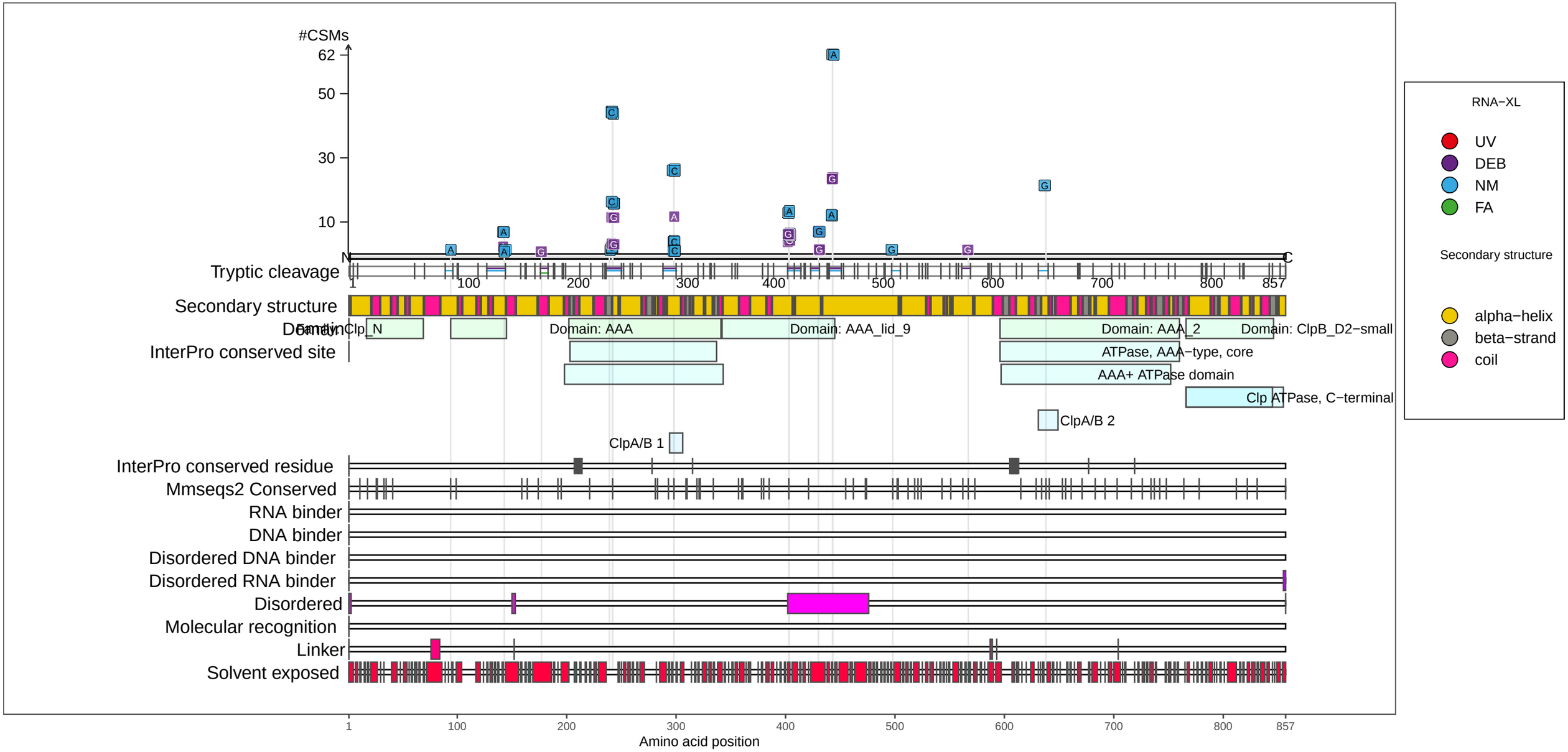
− RNA functions: not annotated



P63284
CLPB_ECOLI Chaperone protein ClpB

− Abundance:
tryptic [log10 Intensity]: 9.37 (Q 95)
PAXdb K12 strain [ppm]: 3.48 (Q 97)
PAXdb E.coli [ppm]: 2.97 (Q 94)

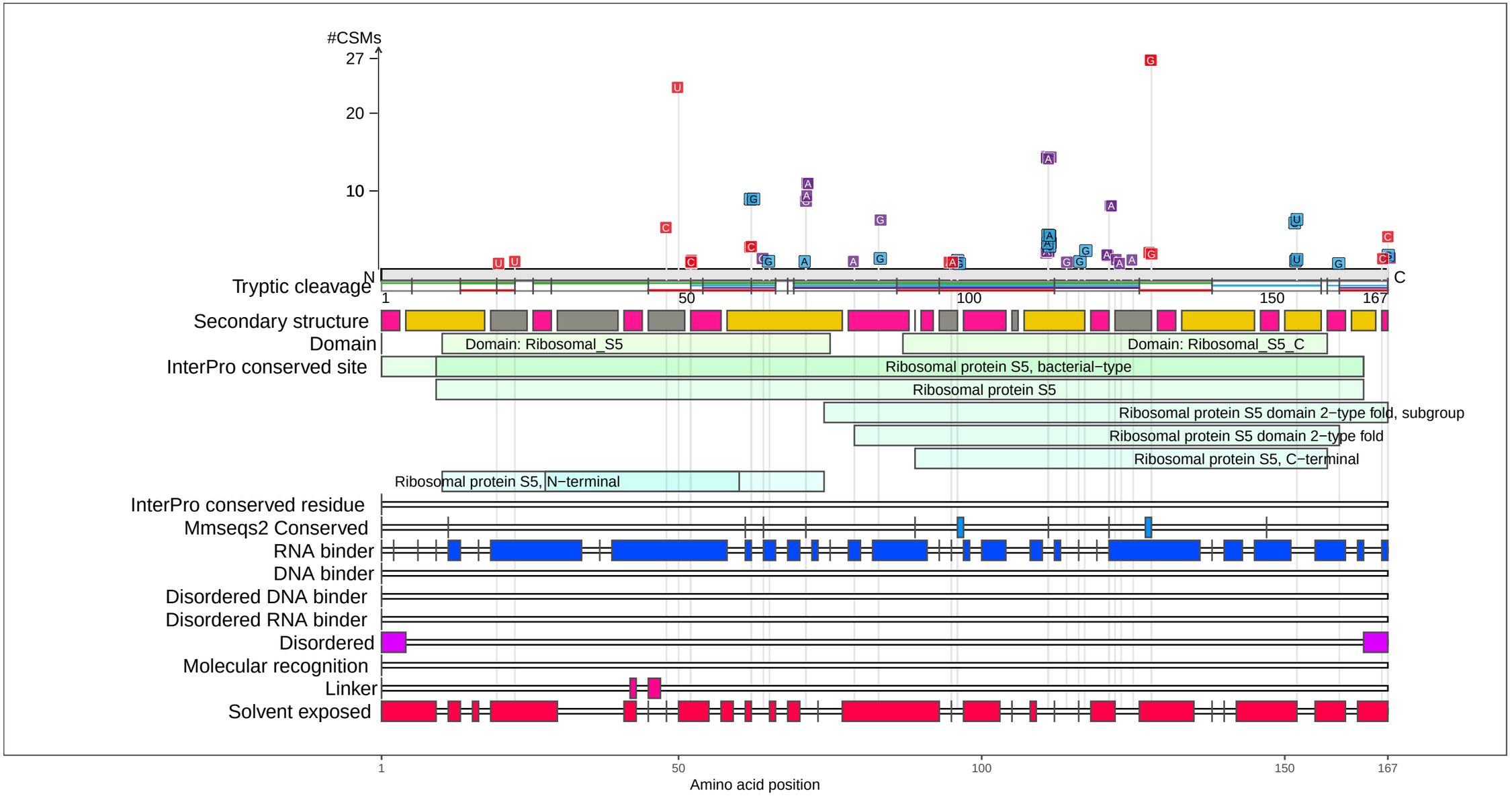
− RNA functions: not annotated



P0A7W1
RS5_ECOLI 30S ribosomal protein S5

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.8 (Q 100)
PAXdb E.coli [ppm]: 3.89 (Q 100)

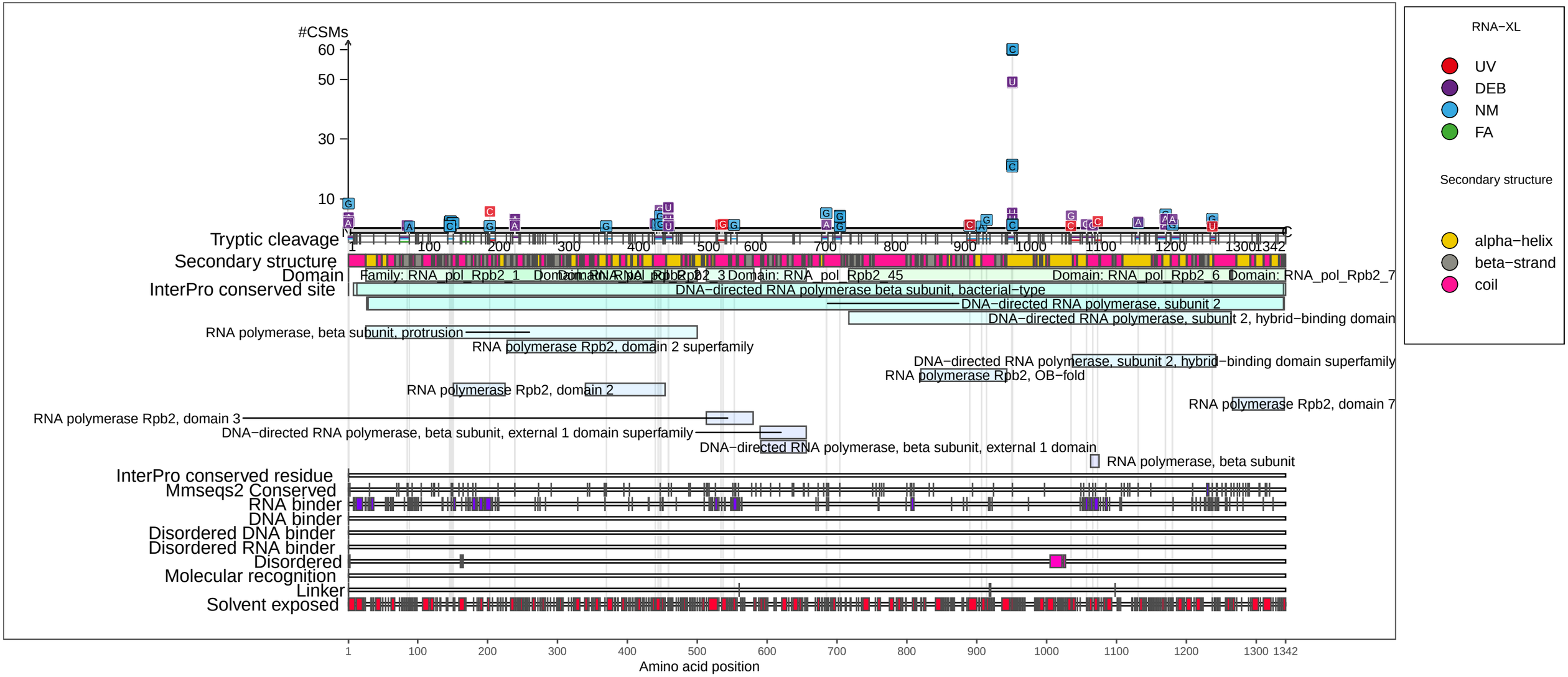
− RNA functions:
RNA binding; rRNA binding



P0A8V2
RPOB_ECOLI DNA−directed RNA polymerase subunit beta

− Abundance:
tryptic [log10 Intensity]: 9.69 (Q 98)
PAXdb K12 strain [ppm]: 2.92 (Q 89)
PAXdb E.coli [ppm]: 3.25 (Q 97)

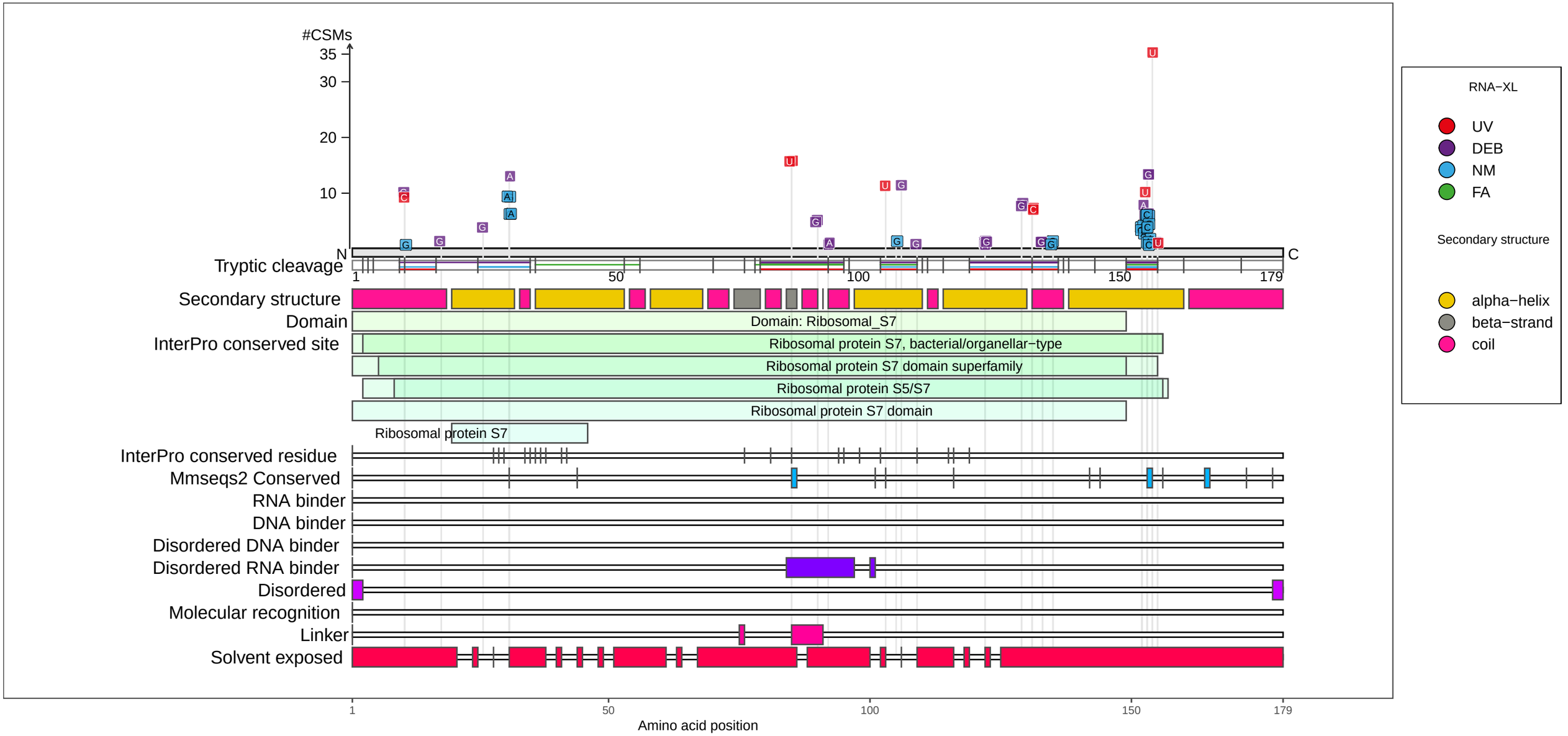
− RNA functions:
5−3 RNA polymerase activity; DNA−directed 5−3 RNA polymerase activity
RNA biosynthetic process; RNA metabolic process; RNA polymerase activity
RNA polymerase beta subunit; RNA polymerase beta subunit external 1 domain; RNA polymerase Rpb2, domain 2
RNA polymerase Rpb2, domain 3; RNA polymerase Rpb2, domain 6
RNA polymerase Rpb2, domain 7



P02359
RS7_ECOLI 30S ribosomal protein S7

− Abundance:
tryptic [log10 Intensity]: 9.12 (Q 91)
PAXdb K12 strain [ppm]: 3.86 (Q 100)
PAXdb E.coli [ppm]: 3.72 (Q 100)

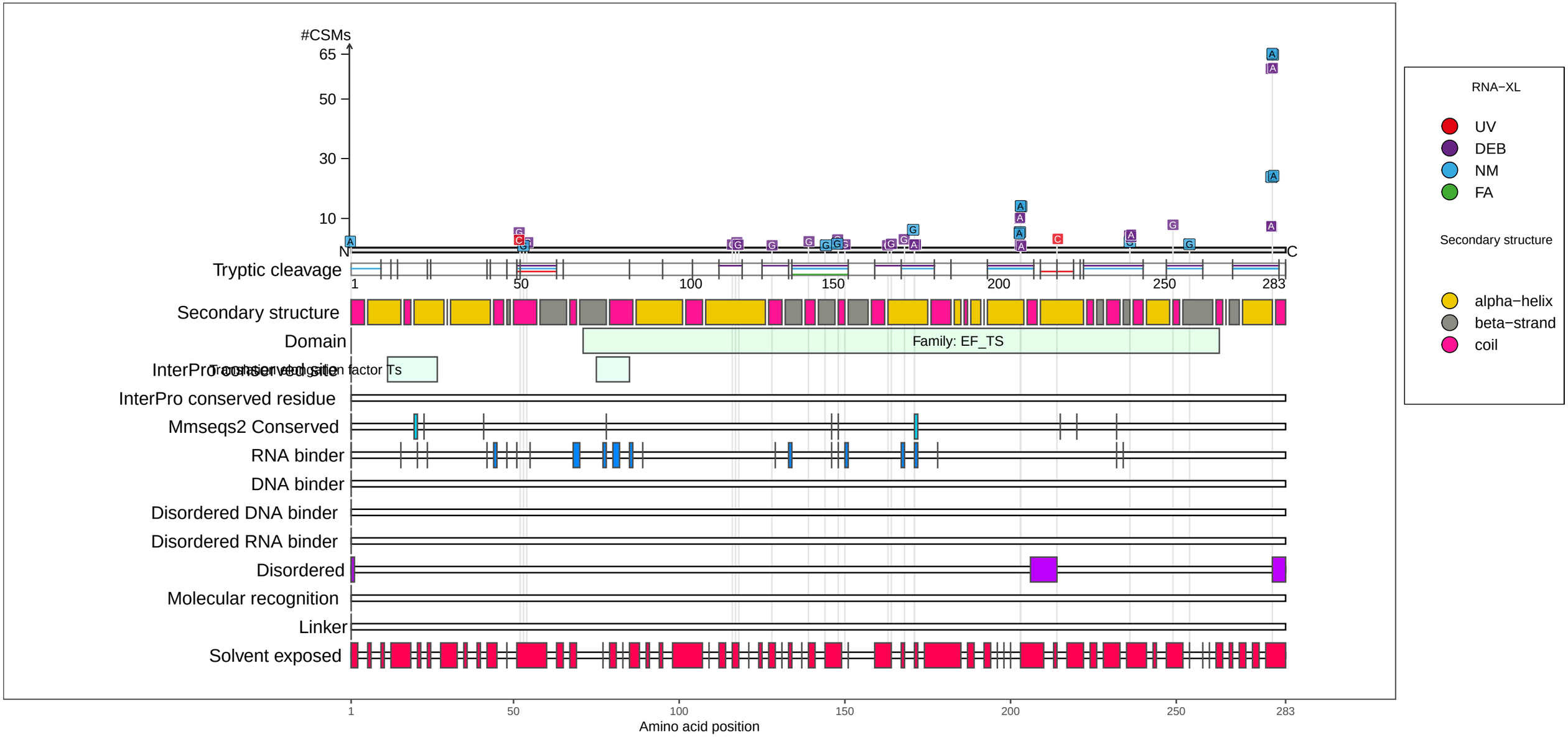
− RNA functions:
mRNA binding; RNA binding; rRNA binding; tRNA binding



P0A6P1
EFTS_ECOLI Elongation factor Ts

− Abundance:
tryptic [log10 Intensity]: 9.7 (Q 98)
PAXdb K12 strain [ppm]: 3.4 (Q 96)
PAXdb E.coli [ppm]: 3.65 (Q 100)

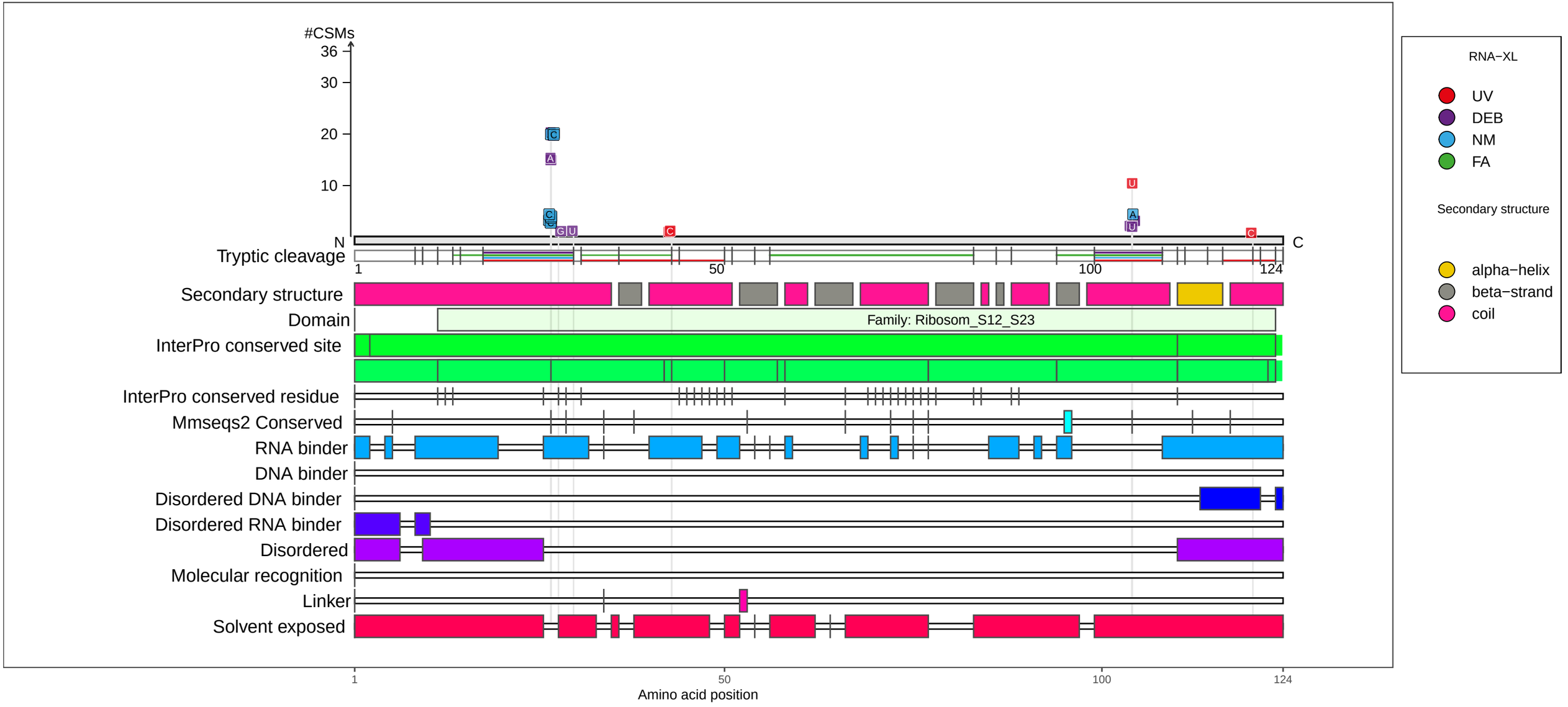
− RNA functions:
RNA binding



P0A7S3
RS12_ECOLI 30S ribosomal protein S12

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 76)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 3.06 (Q 95)

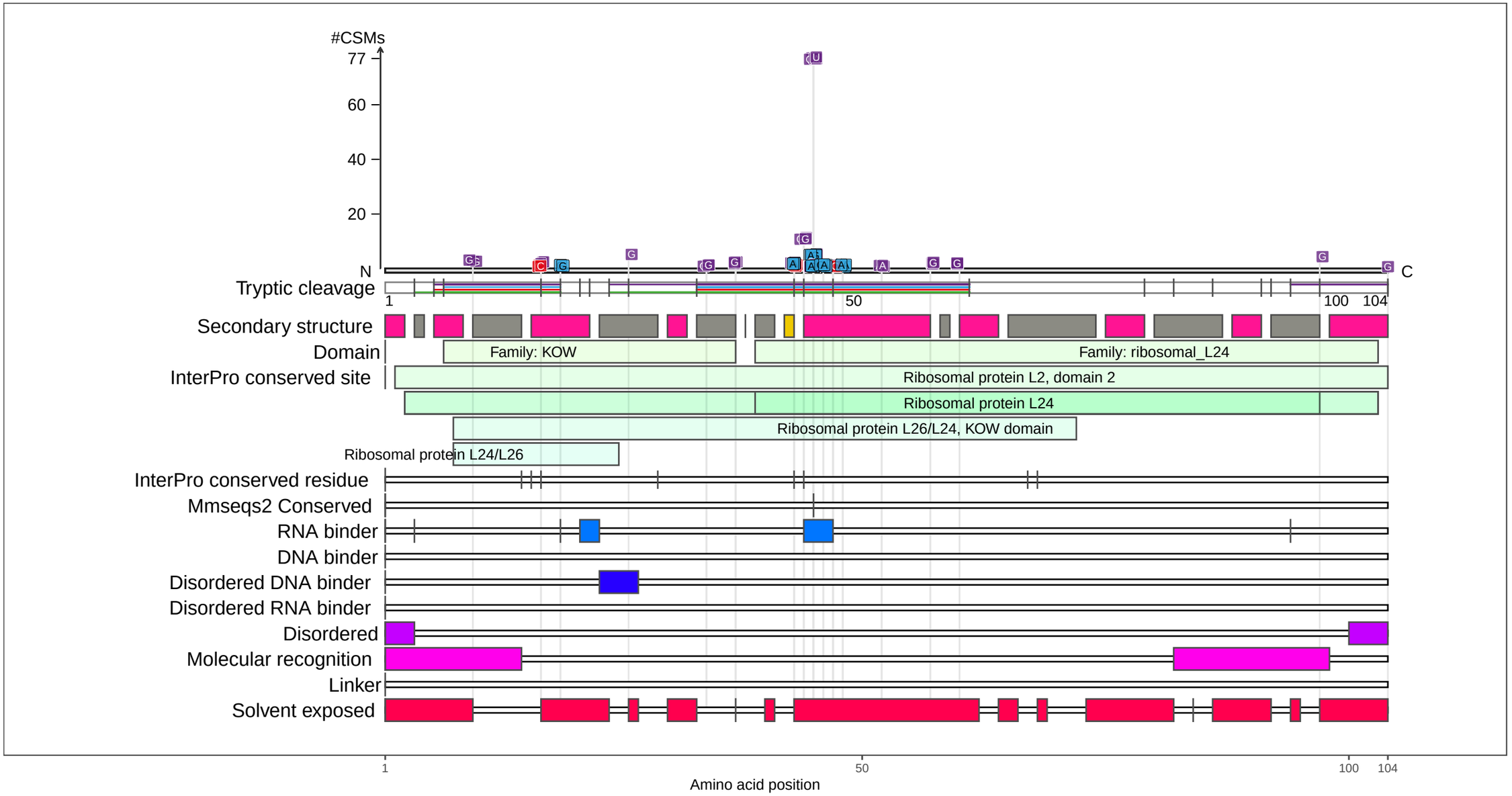
− RNA functions:
RNA binding; RNA folding; RNA metabolic process; RNA processing; RNA splicing
RNA splicing, via transesterification reactions
RNA splicing, via transesterification reactions with guanosine as nucleophile; rRNA binding; tRNA binding



P60624
RL24_ECOLI 50S ribosomal protein L24

− Abundance:
tryptic [log10 Intensity]: 9.65 (Q 97)
PAXdb K12 strain [ppm]: 3.74 (Q 99)
PAXdb E.coli [ppm]: 3.57 (Q 99)

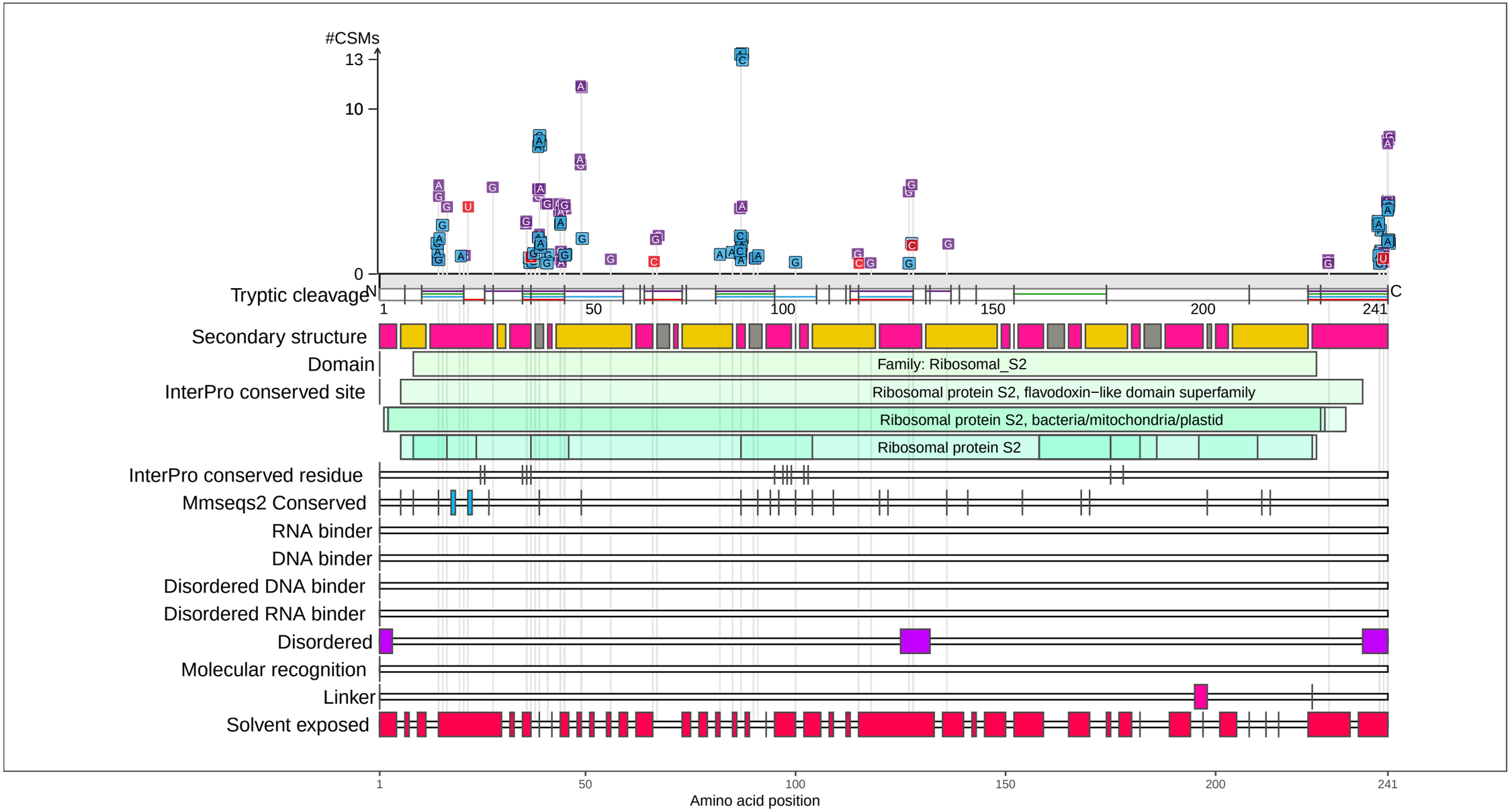
− RNA functions:
RNA binding; rRNA binding



P0A7V0
RS2_ECOLI 30S ribosomal protein S2

− Abundance:
tryptic [log10 Intensity]: 9.45 (Q 96)
PAXdb K12 strain [ppm]: 3.71 (Q 99)
PAXdb E.coli [ppm]: 3.45 (Q 98)

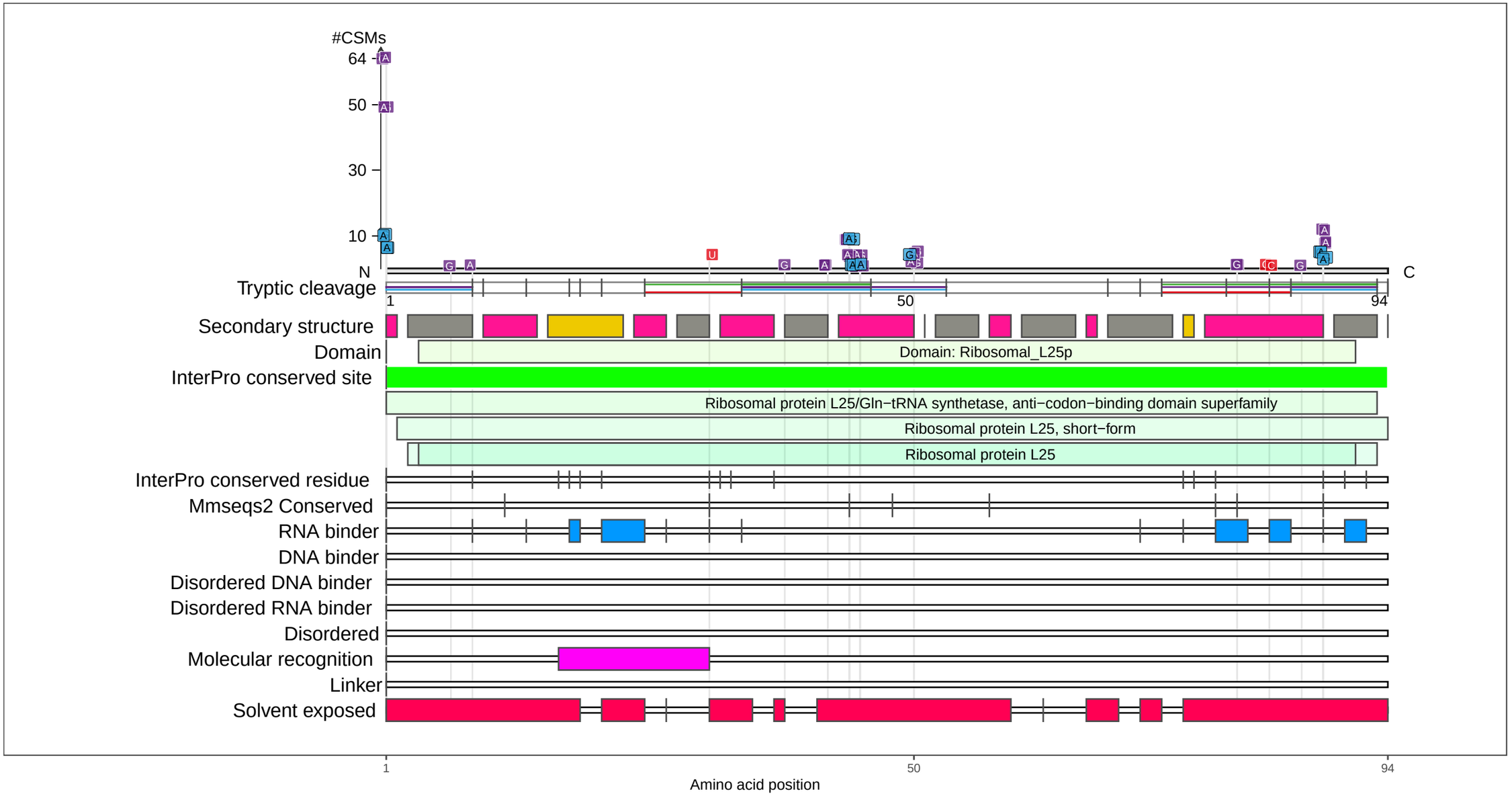
− RNA functions: not annotated



P68919
RL25_ECOLI 50S ribosomal protein L25

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 87)
PAXdb K12 strain [ppm]: 3.79 (Q 99)
PAXdb E.coli [ppm]: 3.84 (Q 100)

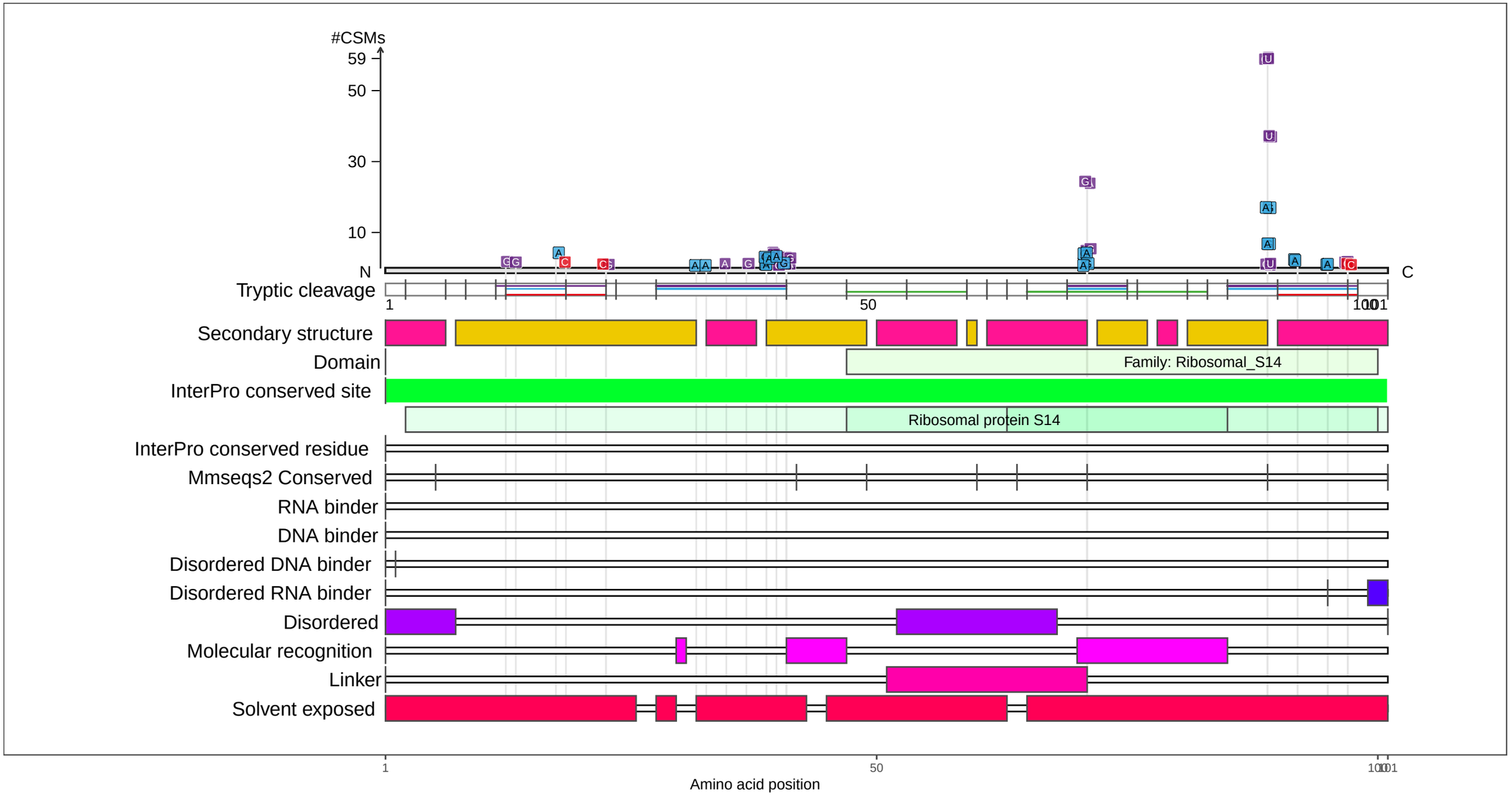
− RNA functions:
5S rRNA binding; RNA binding; rRNA binding



P0AG59
RS14_ECOLI 30S ribosomal protein S14

− Abundance:
tryptic [log10 Intensity]: 8.34 (Q 71)
PAXdb K12 strain [ppm]: 3.8 (Q 100)
PAXdb E.coli [ppm]: 3.35 (Q 98)

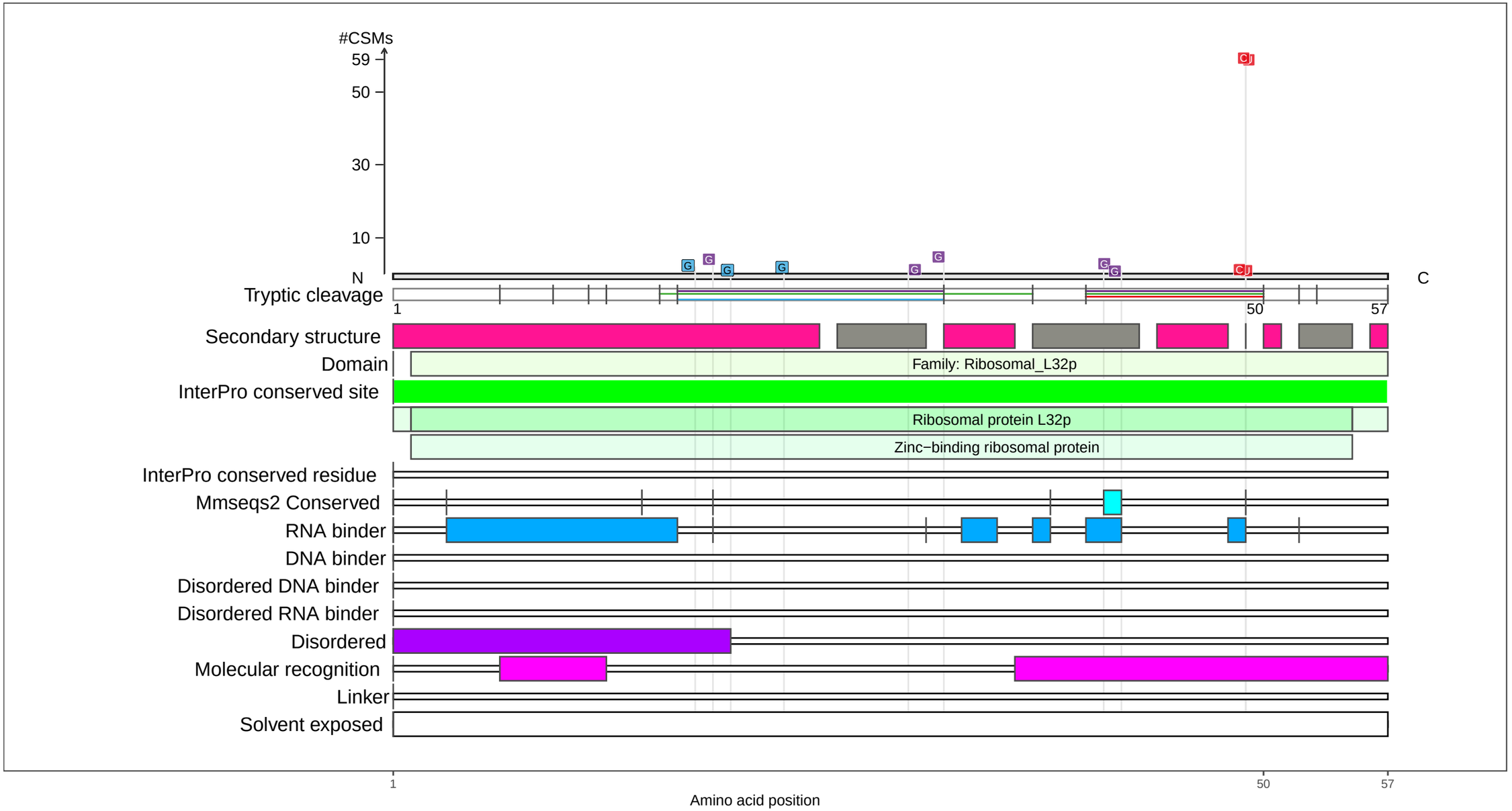
− RNA functions:
RNA binding; rRNA binding



P0A7N4
RL32_ECOLI 50S ribosomal protein L32

− Abundance:
tryptic [log10 Intensity]: 8.26 (Q 68)
PAXdb K12 strain [ppm]: 3.87 (Q 100)
PAXdb E.coli [ppm]: 3.47 (Q 99)

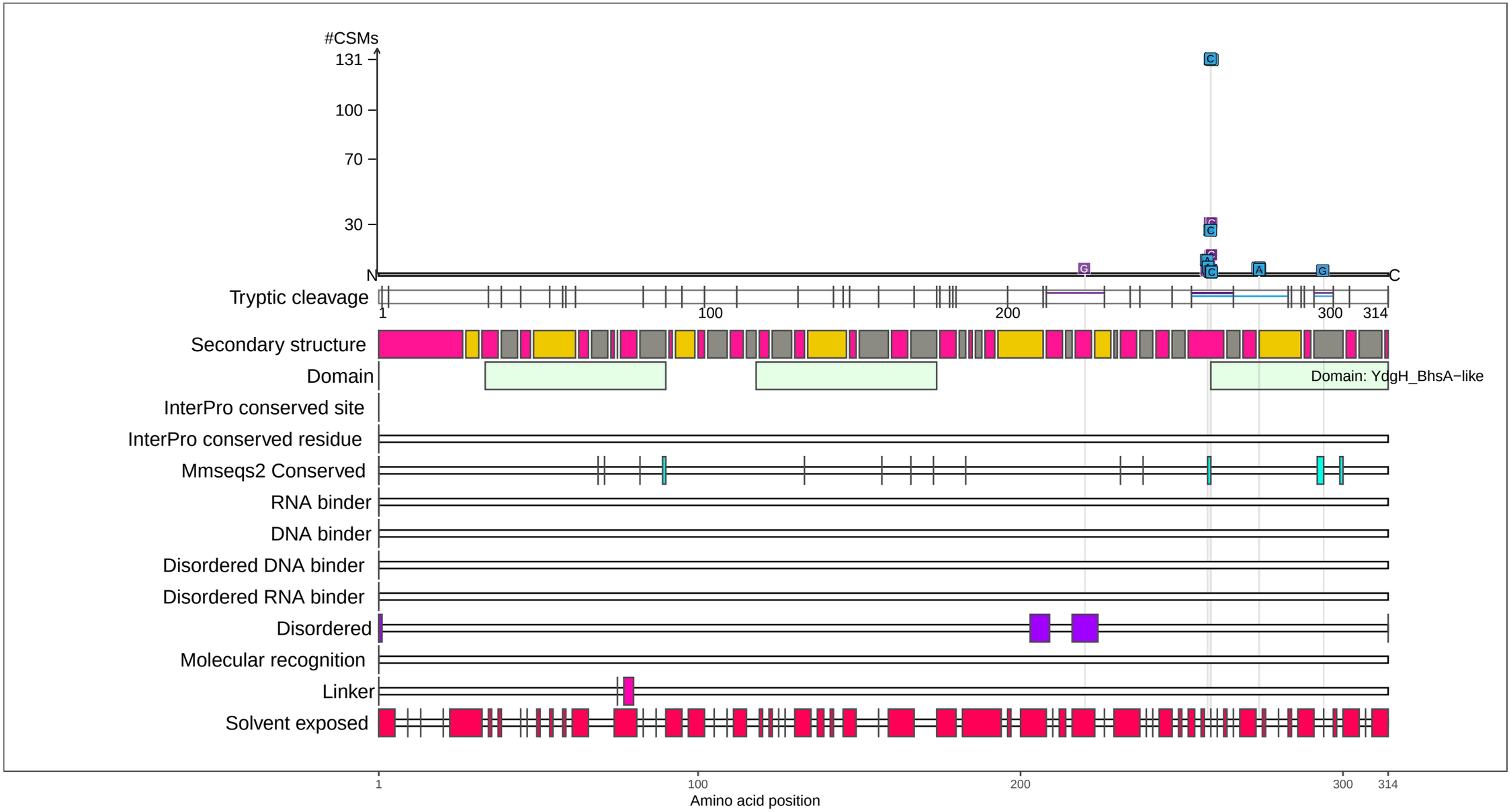
− RNA functions: not annotated



P76177
YDGH_ECOLI Protein YdgH

− Abundance:
tryptic [log10 Intensity]: 8.35 (Q 71)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.84 (Q 92)

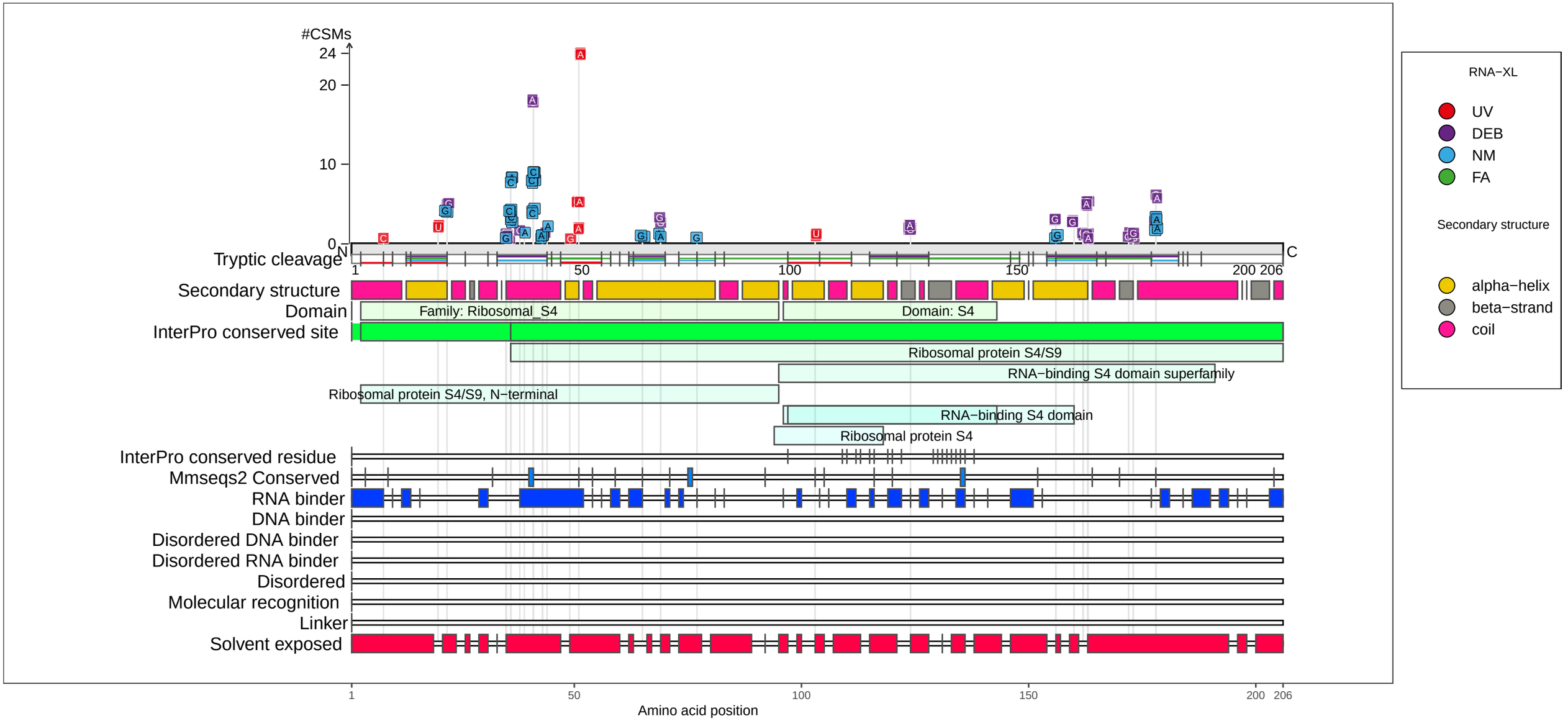
− RNA functions: not annotated



P0A7V8
RS4_ECOLI 30S ribosomal protein S4

− Abundance:
tryptic [log10 Intensity]: 9.07 (Q 90)
PAXdb K12 strain [ppm]: 3.57 (Q 98)
PAXdb E.coli [ppm]: 3.5 (Q 99)

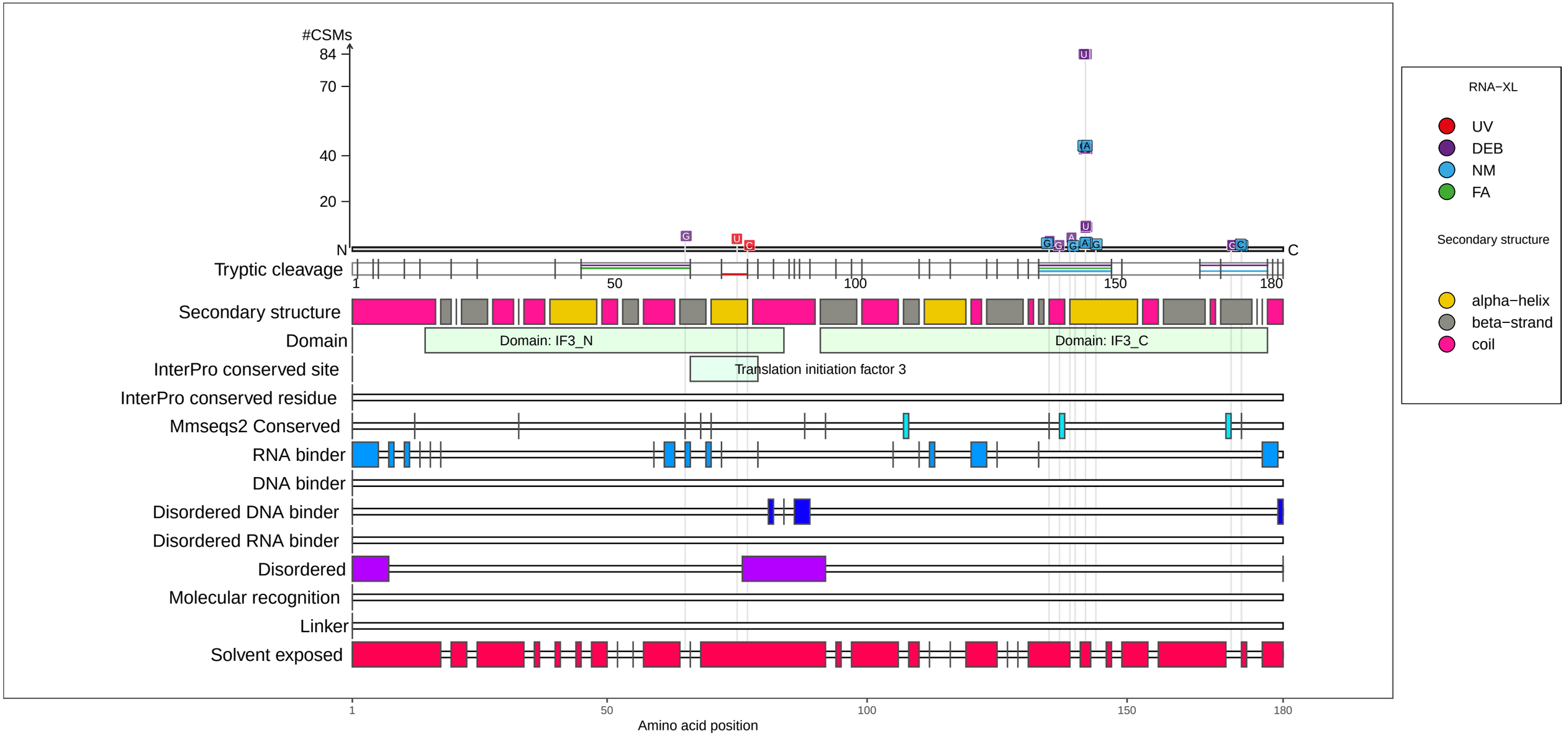
− RNA functions:
mRNA 5−UTR binding; mRNA binding; RNA binding; RNA biosynthetic process
RNA metabolic process; rRNA binding



P0A707
IF3_ECOLI Translation initiation factor IF−3

− Abundance:
tryptic [log10 Intensity]: 8.76 (Q 82)
PAXdb K12 strain [ppm]: 3.48 (Q 97)
PAXdb E.coli [ppm]: 2.97 (Q 94)

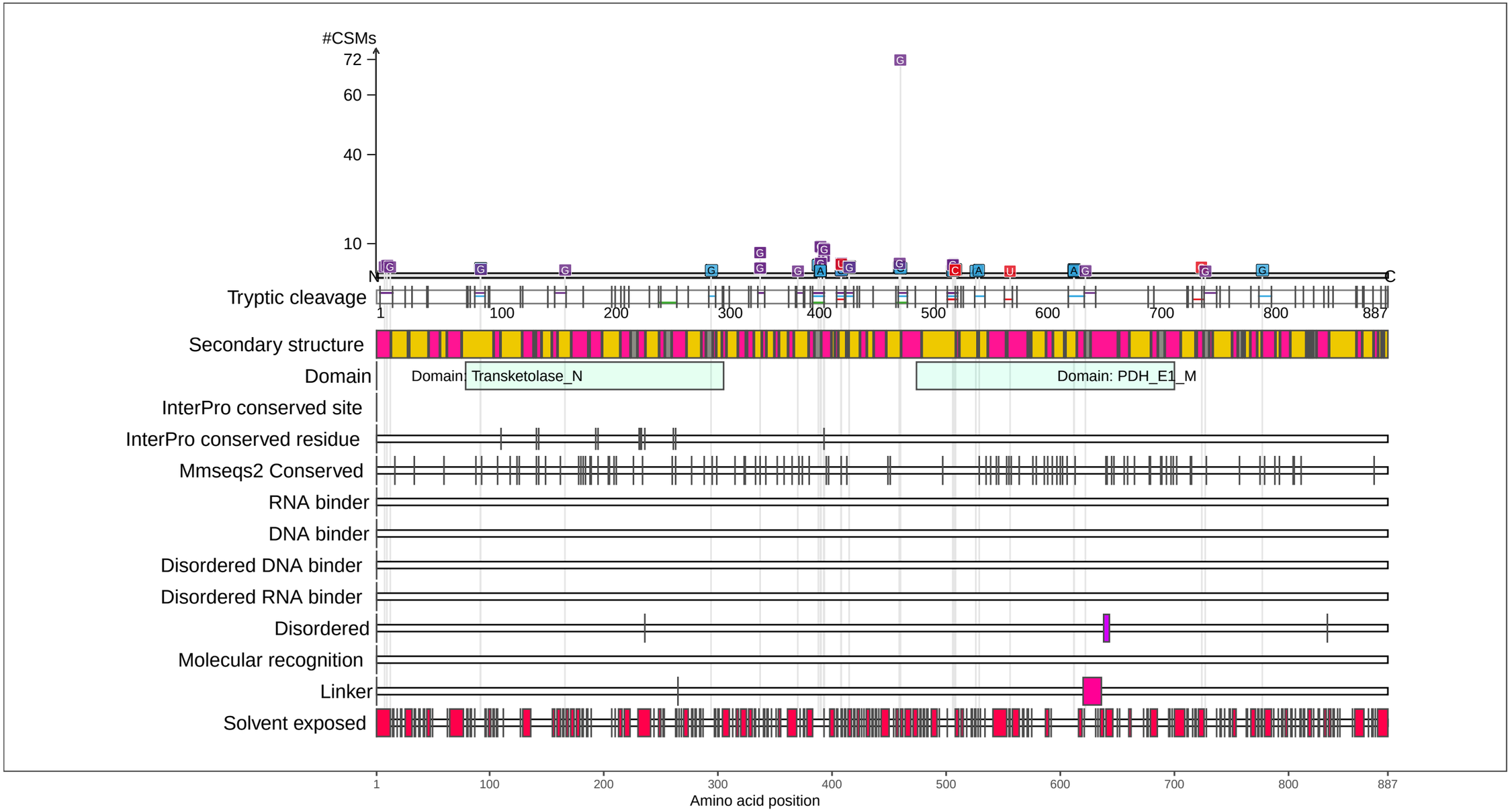
− RNA functions:
RNA binding



P0AFG8
ODP1_ECOLI Pyruvate dehydrogenase E1 component

− Abundance:
tryptic [log10 Intensity]: 10.3 (Q 100)
PAXdb K12 strain [ppm]: 3.47 (Q 97)
PAXdb E.coli [ppm]: 3.5 (Q 99)

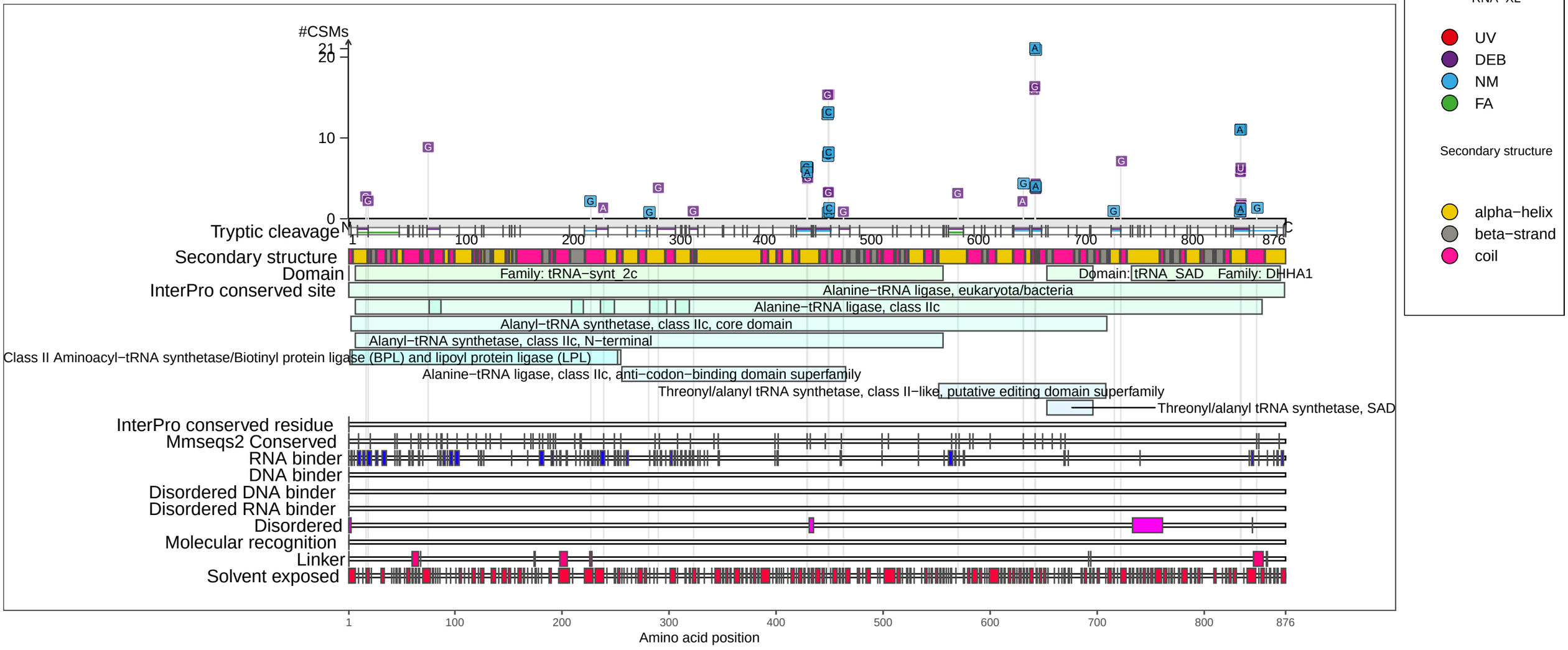
− RNA functions: not annotated



P00957
SYA_ECOLI Alanine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.68 (Q 98)
PAXdb K12 strain [ppm]: 3.01 (Q 91)
PAXdb E.coli [ppm]: 2.78 (Q 91)

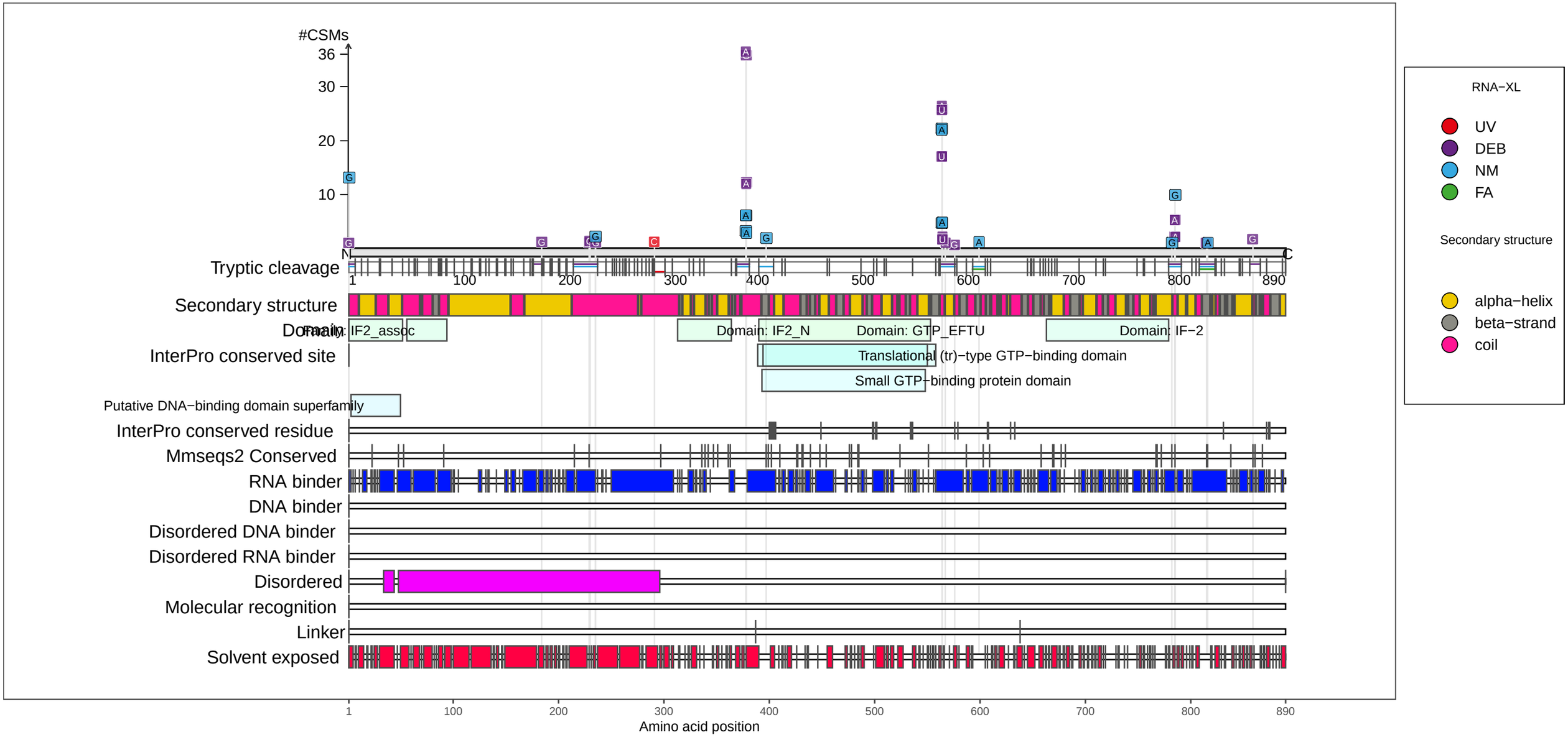
− RNA functions:
alanine−tRNA ligase activity; alanyl−tRNA aminoacylation
aminoacyl−tRNA editing activity; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; ncRNA metabolic process; ncRNA processing; RNA binding
RNA metabolic process; RNA modification; RNA processing; Ser−tRNA(Ala) hydrolase activity
Threonyl and Alanyl tRNA synthetase second additional domain; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA modification; tRNA processing; tRNA synthetases class II (A)



P0A705
IF2_ECOLI Translation initiation factor IF−2

− Abundance:
tryptic [log10 Intensity]: 9.78 (Q 99)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 2.67 (Q 89)

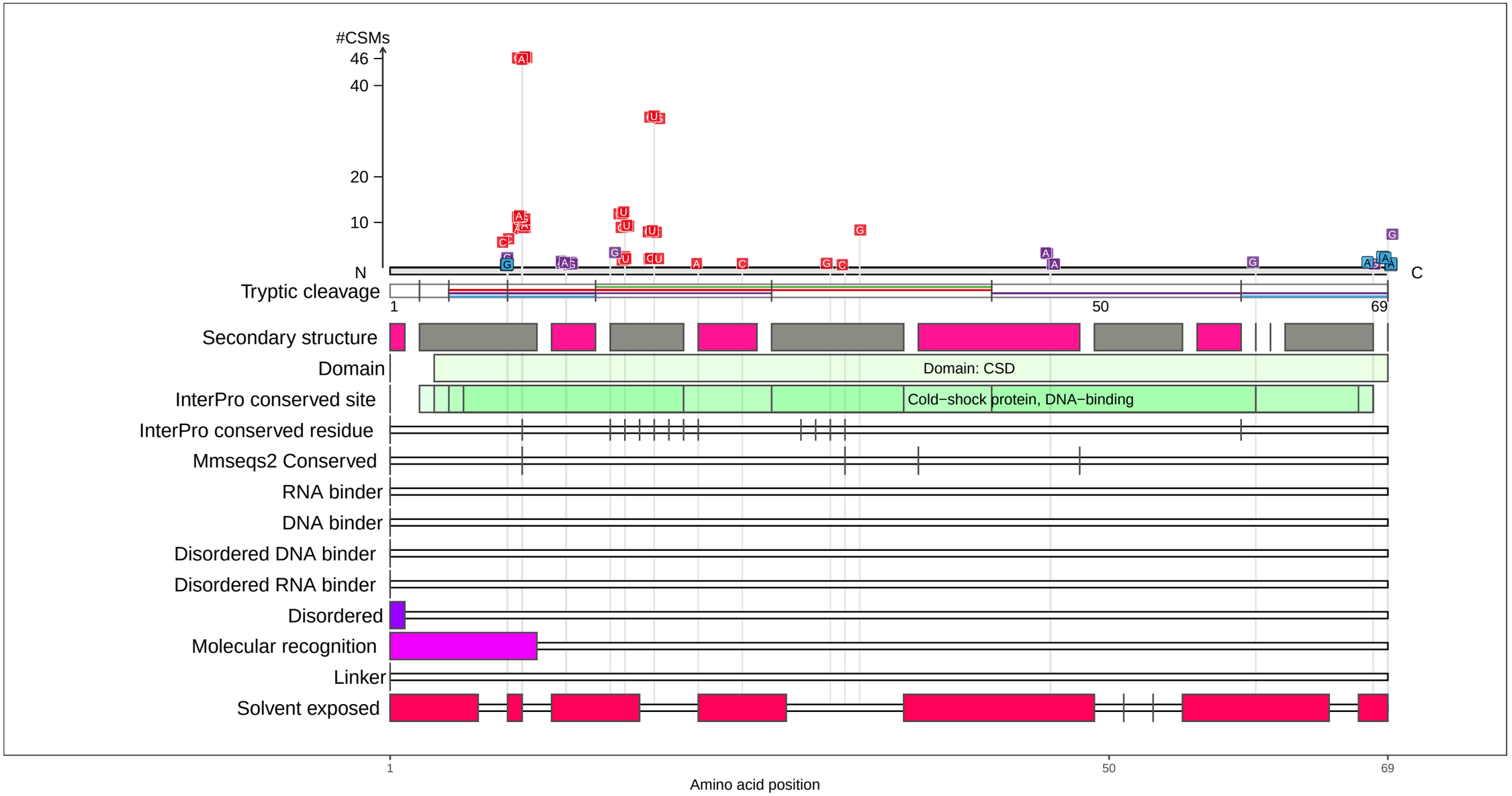
− RNA functions:
RNA binding



P0A9Y6
CSPC_ECOLI Cold shock−like protein CspC

− Abundance:
tryptic [log10 Intensity]: 9.87 (Q 99)
PAXdb K12 strain [ppm]: 3.46 (Q 97)
PAXdb E.coli [ppm]: 4.32 (Q 100)

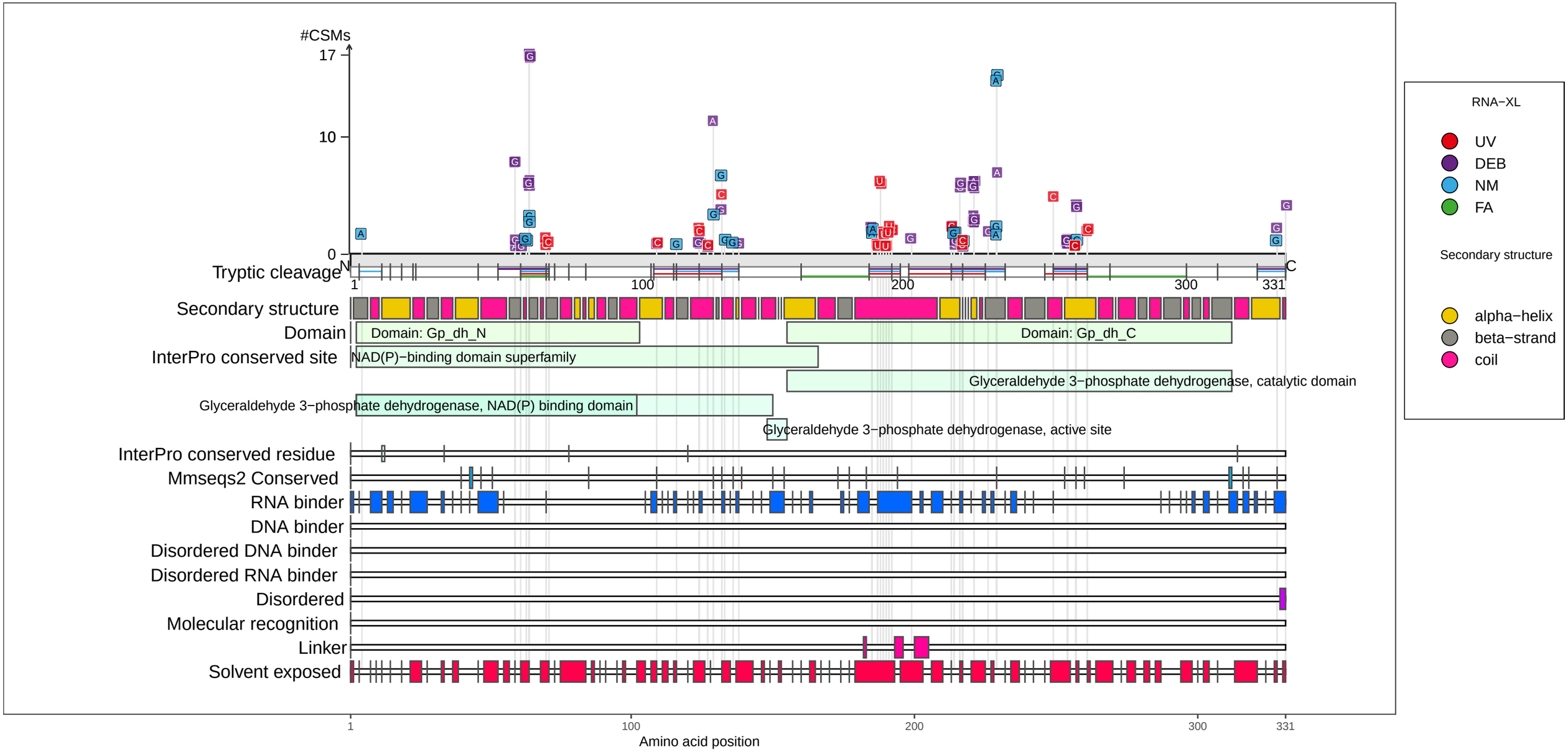
− RNA functions:
RNA binding



P0A9B2
G3P1_ECOLI Glyceraldehyde−3−phosphate dehydrogenase A

− Abundance:
tryptic [log10 Intensity]: 10.17 (Q 100)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 4.03 (Q 100)

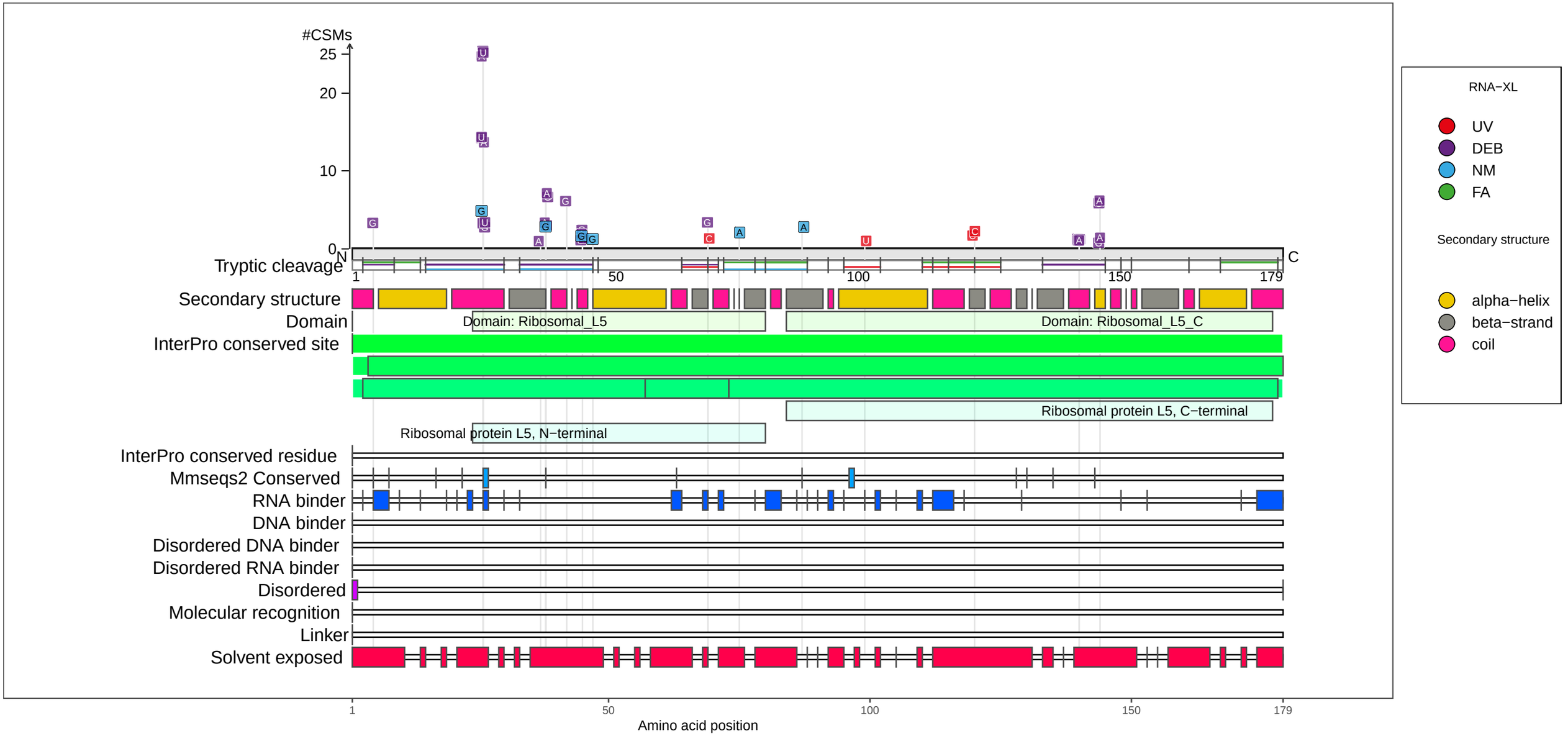
− RNA functions: not annotated



P62399
RL5_ECOLI 50S ribosomal protein L5

− Abundance:
tryptic [log10 Intensity]: 9.56 (Q 97)
PAXdb K12 strain [ppm]: 3.79 (Q 99)
PAXdb E.coli [ppm]: 3.56 (Q 99)

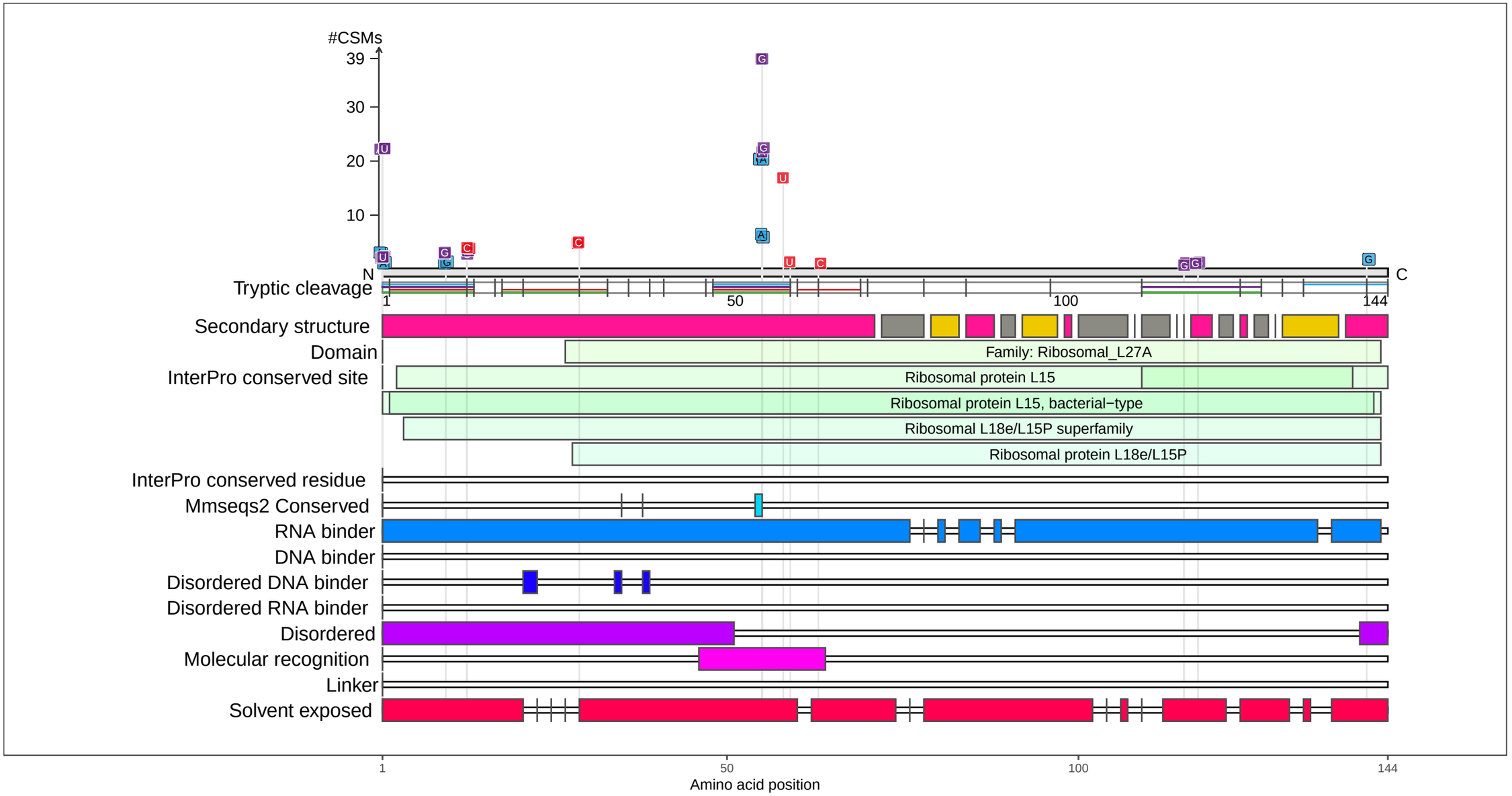
− RNA functions:
5S rRNA binding; RNA binding; rRNA binding; tRNA binding



P02413
RL15_ECOLI 50S ribosomal protein L15

− Abundance:
tryptic [log10 Intensity]: 9.45 (Q 96)
PAXdb K12 strain [ppm]: 3.41 (Q 96)
PAXdb E.coli [ppm]: 3.45 (Q 99)

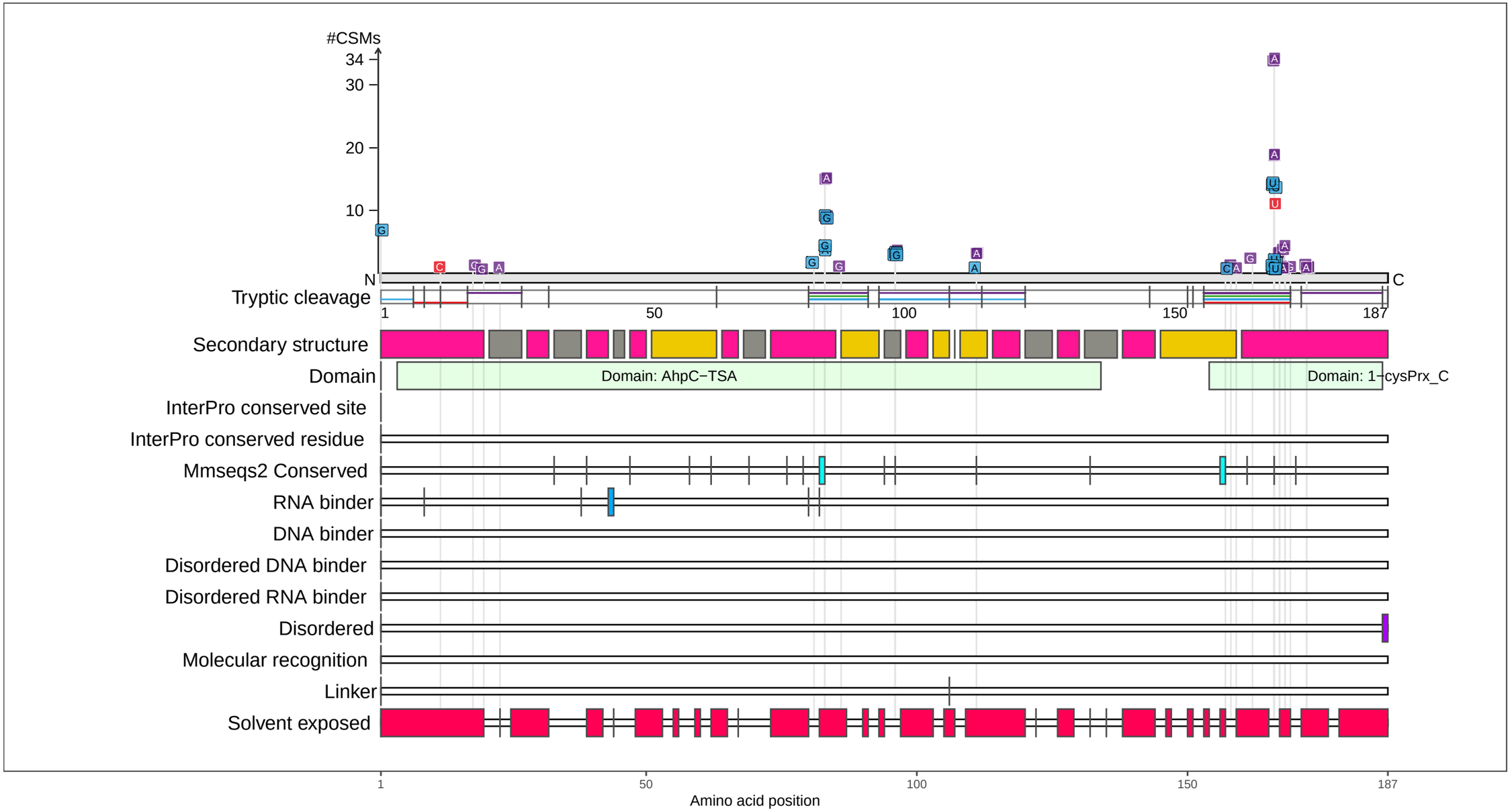
− RNA functions:
RNA binding; rRNA binding



P0AE08
AHPC_ECOLI Alkyl hydroperoxide reductase C

− Abundance:
tryptic [log10 Intensity]: 9.82 (Q 99)
PAXdb K12 strain [ppm]: 4.01 (Q 100)
PAXdb E.coli [ppm]: 3.6 (Q 100)

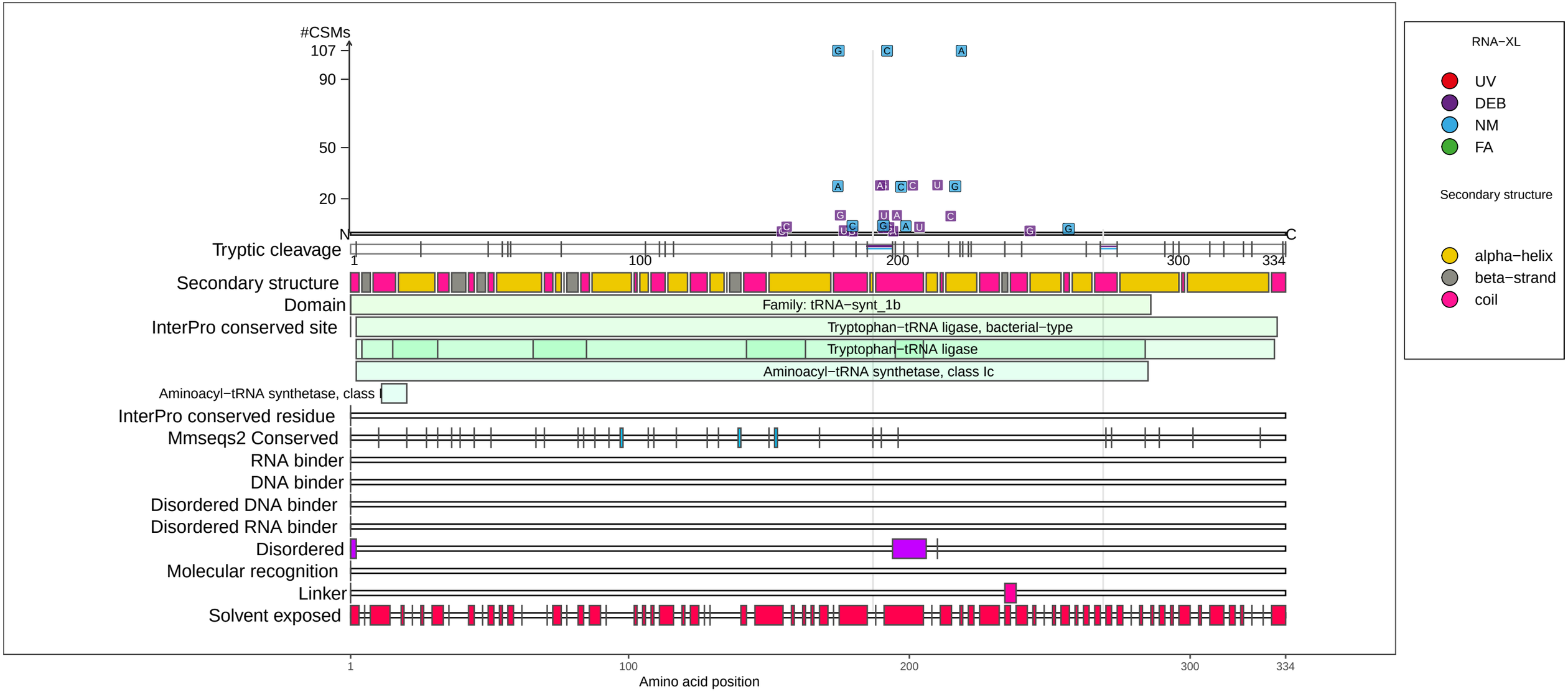
− RNA functions: not annotated



P00954
SYW_ECOLI Tryptophan−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 8.6 (Q 79)
PAXdb K12 strain [ppm]: 3.33 (Q 96)
PAXdb E.coli [ppm]: 2.83 (Q 92)

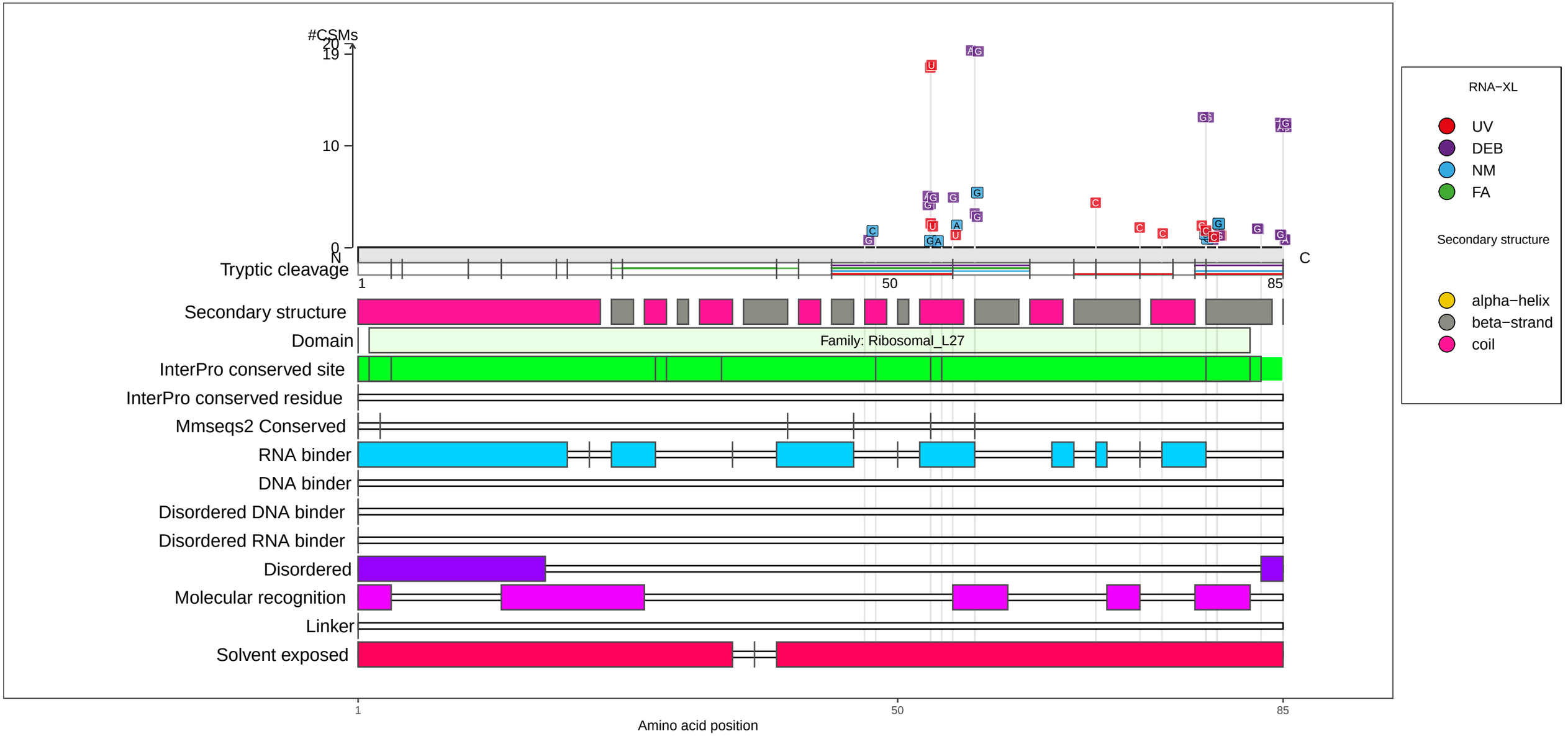
− RNA functions:
aminoacyl−tRNA ligase activity; ncRNA metabolic process; RNA metabolic process
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetases class I (W and Y); tryptophan−tRNA ligase activity
tryptophanyl−tRNA aminoacylation



P0A7L8
RL27_ECOLI 50S ribosomal protein L27

− Abundance:
tryptic [log10 Intensity]: 8.89 (Q 86)
PAXdb K12 strain [ppm]: 3.89 (Q 100)
PAXdb E.coli [ppm]: 3.24 (Q 97)

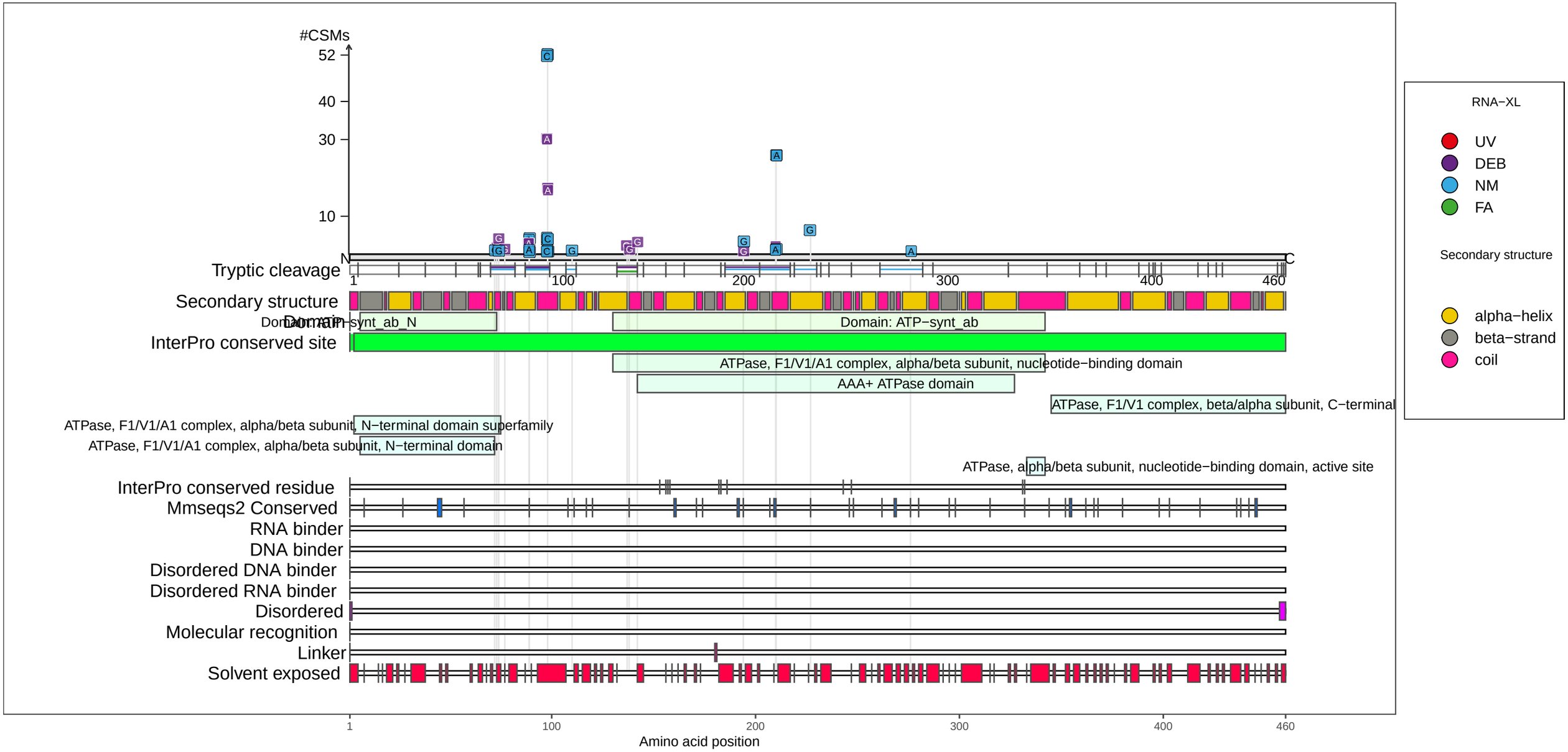
− RNA functions:
RNA binding; rRNA binding; tRNA binding



P0ABB4
ATPB_ECOLI ATP synthase subunit beta

− Abundance:
tryptic [log10 Intensity]: 10.24 (Q 100)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 3.62 (Q 100)

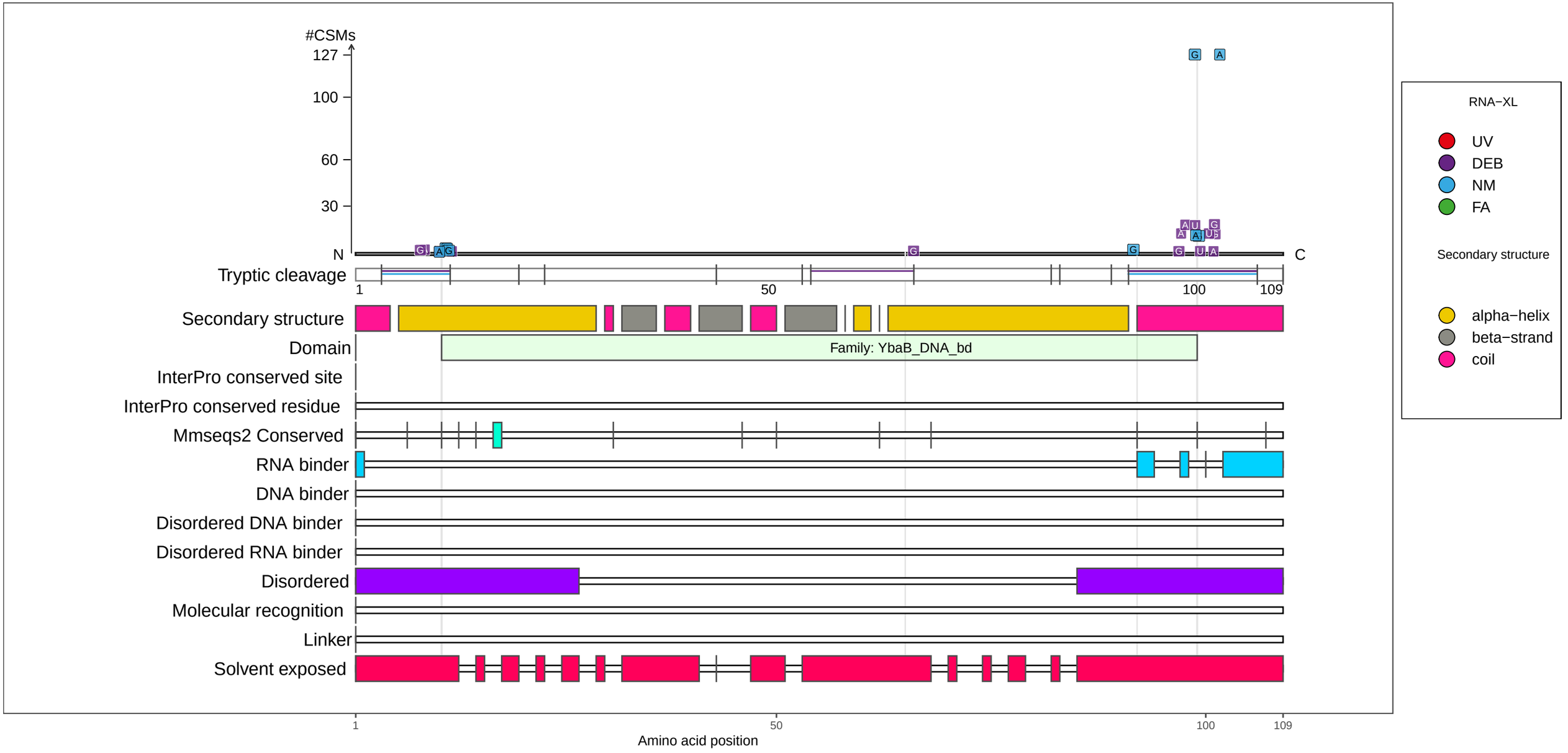
− RNA functions: not annotated



P0A8B5
YBAB_ECOLI Nucleoid−associated protein YbaB

− Abundance:
tryptic [log10 Intensity]: 8.79 (Q 83)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 3.28 (Q 97)

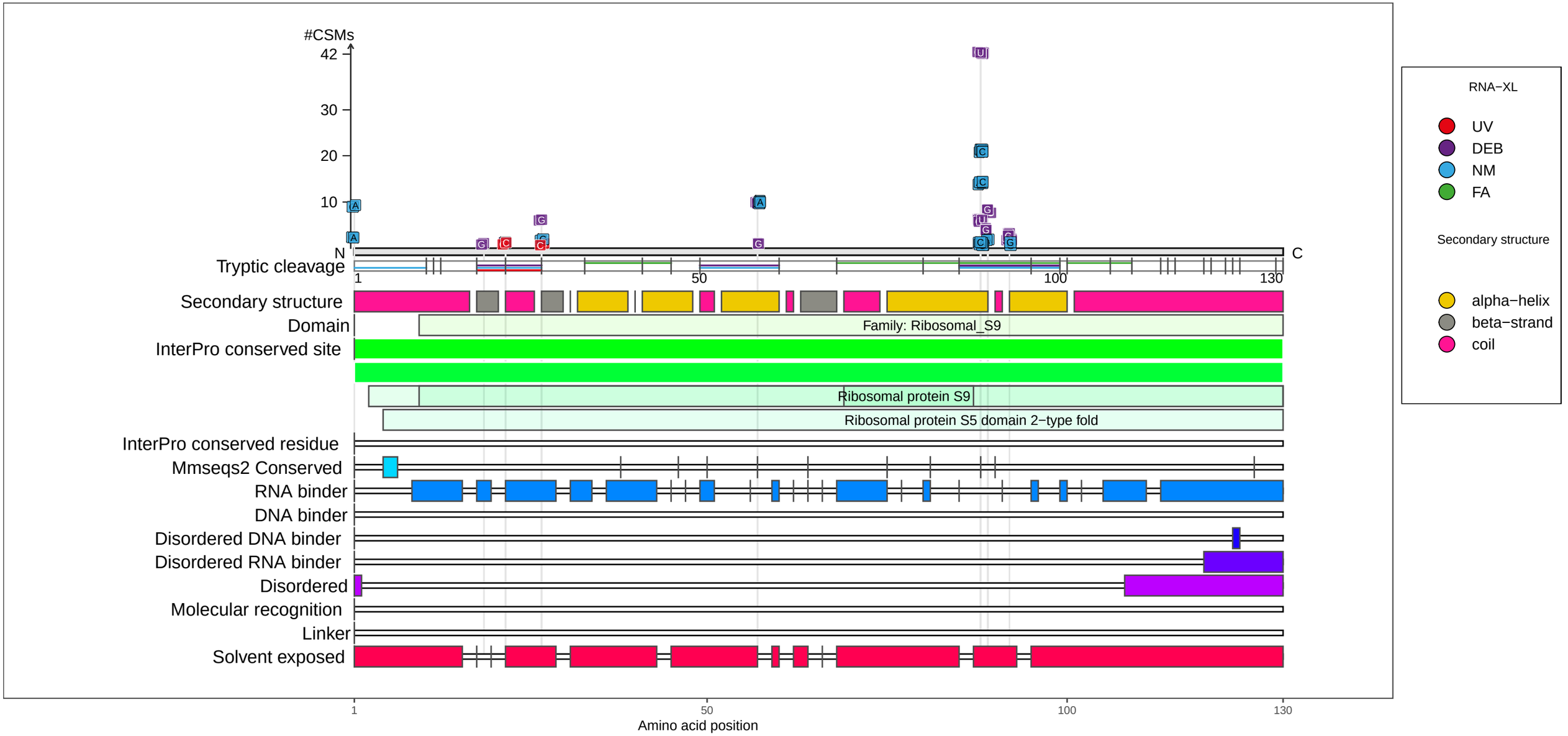
− RNA functions: not annotated



P0A7X3
RS9_ECOLI 30S ribosomal protein S9

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.71 (Q 99)
PAXdb E.coli [ppm]: 3.25 (Q 97)

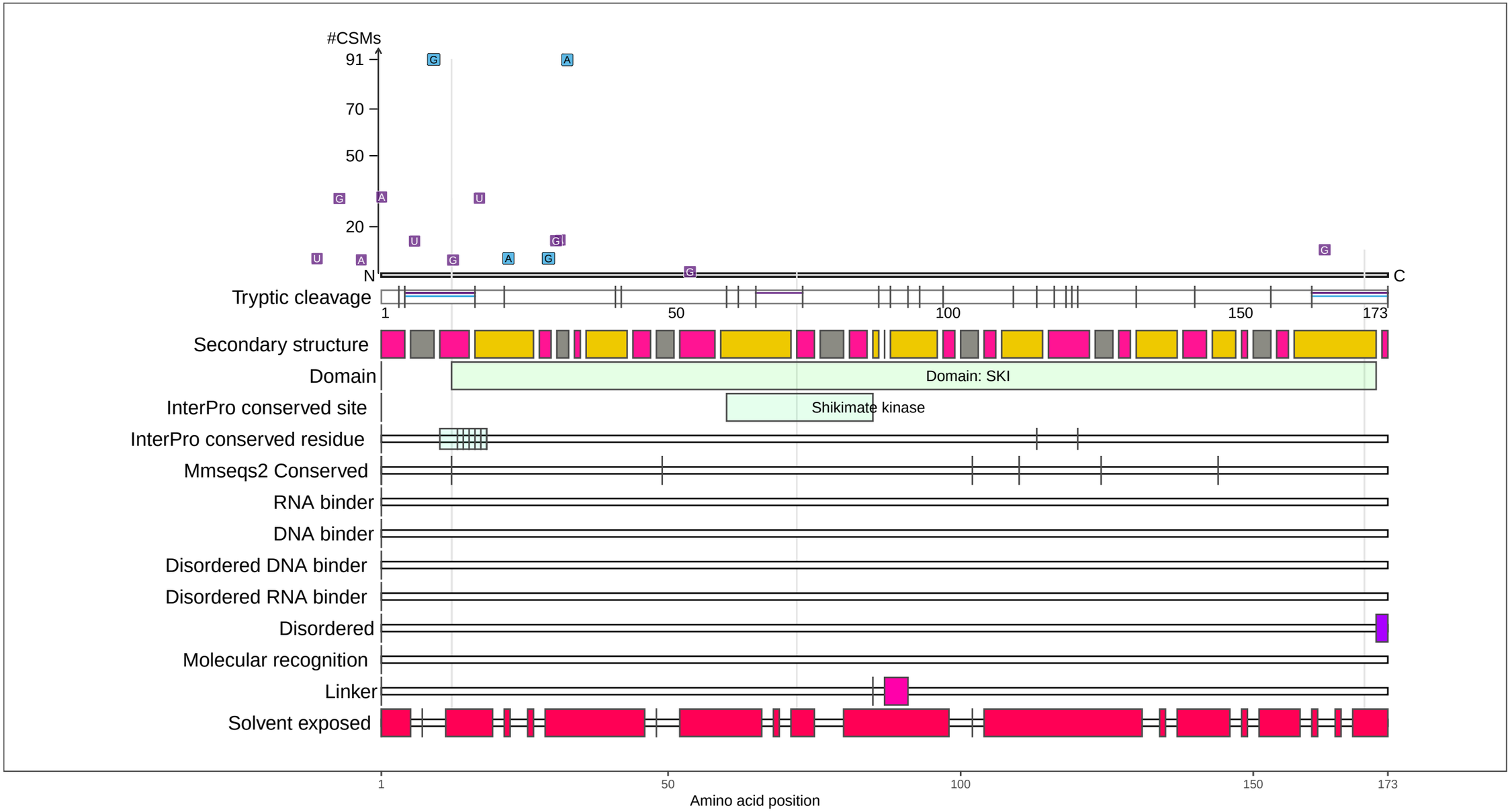
− RNA functions:
RNA binding; tRNA binding



P0A6D7
AROK_ECOLI Shikimate kinase 1

− Abundance:
tryptic [log10 Intensity]: 9 (Q 88)
PAXdb K12 strain [ppm]: 2.81 (Q 86)
PAXdb E.coli [ppm]: 2.32 (Q 81)

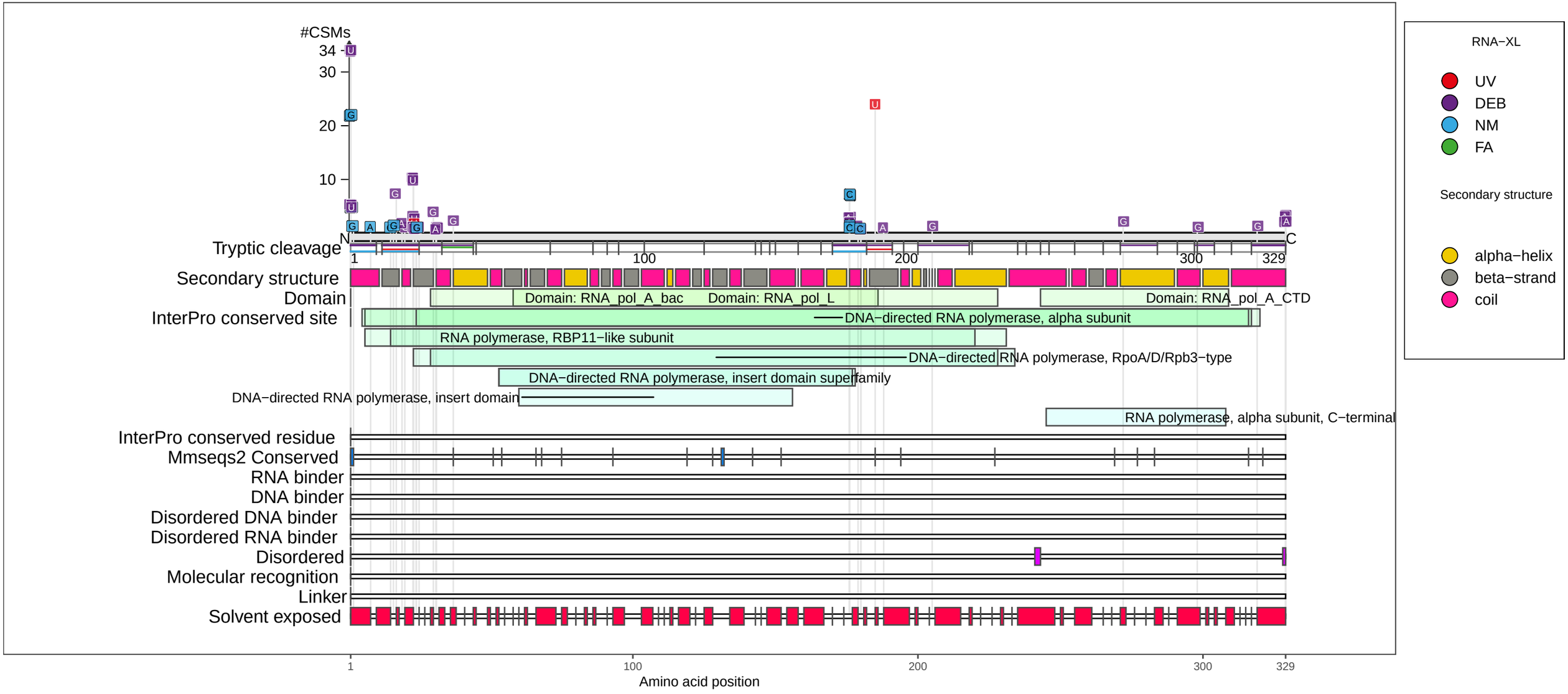
− RNA functions: not annotated



P0A7Z4
RPOA_ECOLI DNA−directed RNA polymerase subunit alpha

− Abundance:
tryptic [log10 Intensity]: 9.79 (Q 99)
PAXdb K12 strain [ppm]: 3.34 (Q 96)
PAXdb E.coli [ppm]: 3.16 (Q 96)

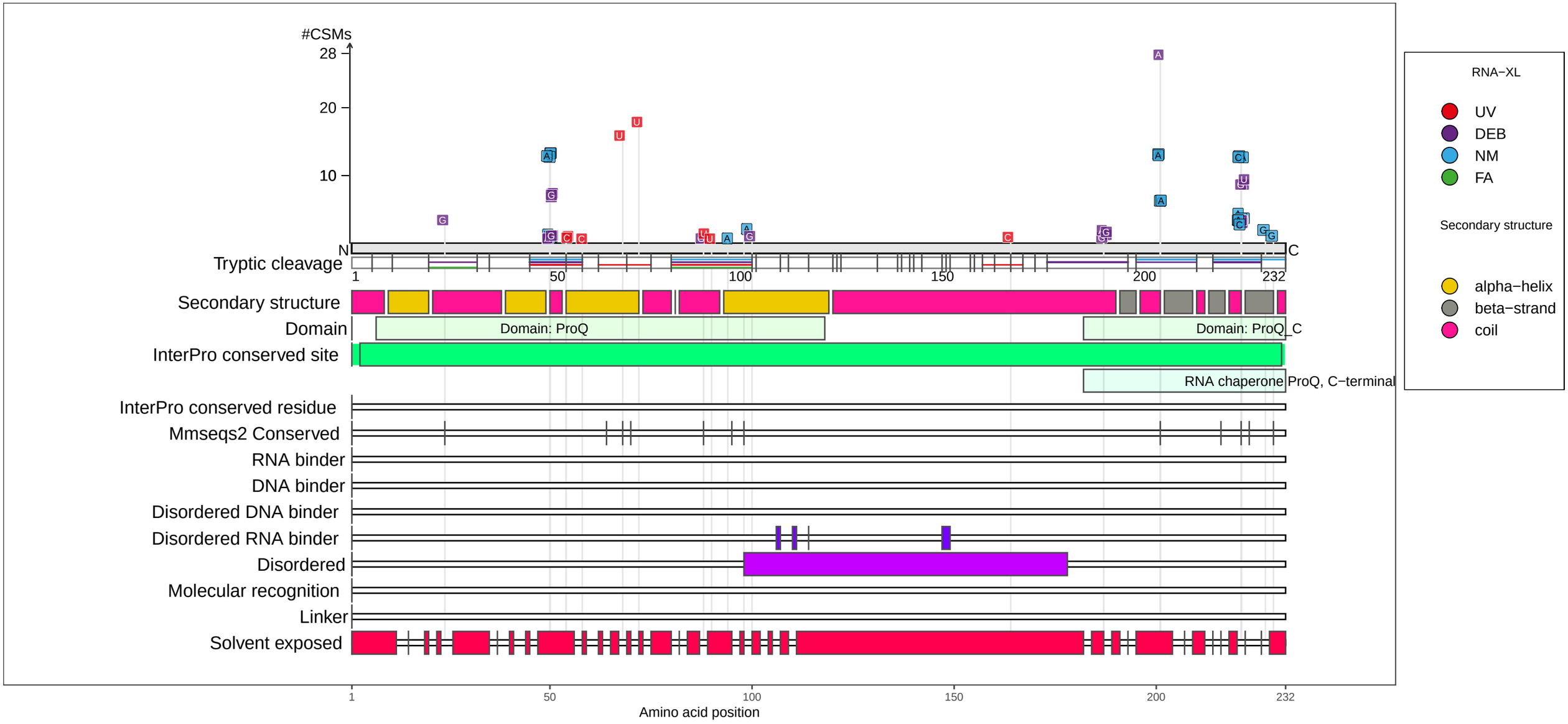
− RNA functions:
5−3 RNA polymerase activity
Bacterial RNA polymerase, alpha chain C terminal domain; DNA−directed 5−3 RNA polymerase activity; RNA biosynthetic process
RNA metabolic process; RNA polymerase activity; RNA polymerase Rpb3/Rpb11 dimerisation domain
RNA polymerase Rpb3/RpoA insert domain



P45577
PROQ_ECOLI RNA chaperone ProQ

− Abundance:
tryptic [log10 Intensity]: 8.59 (Q 78)
PAXdb K12 strain [ppm]: 3.45 (Q 97)
PAXdb E.coli [ppm]: 2.78 (Q 91)

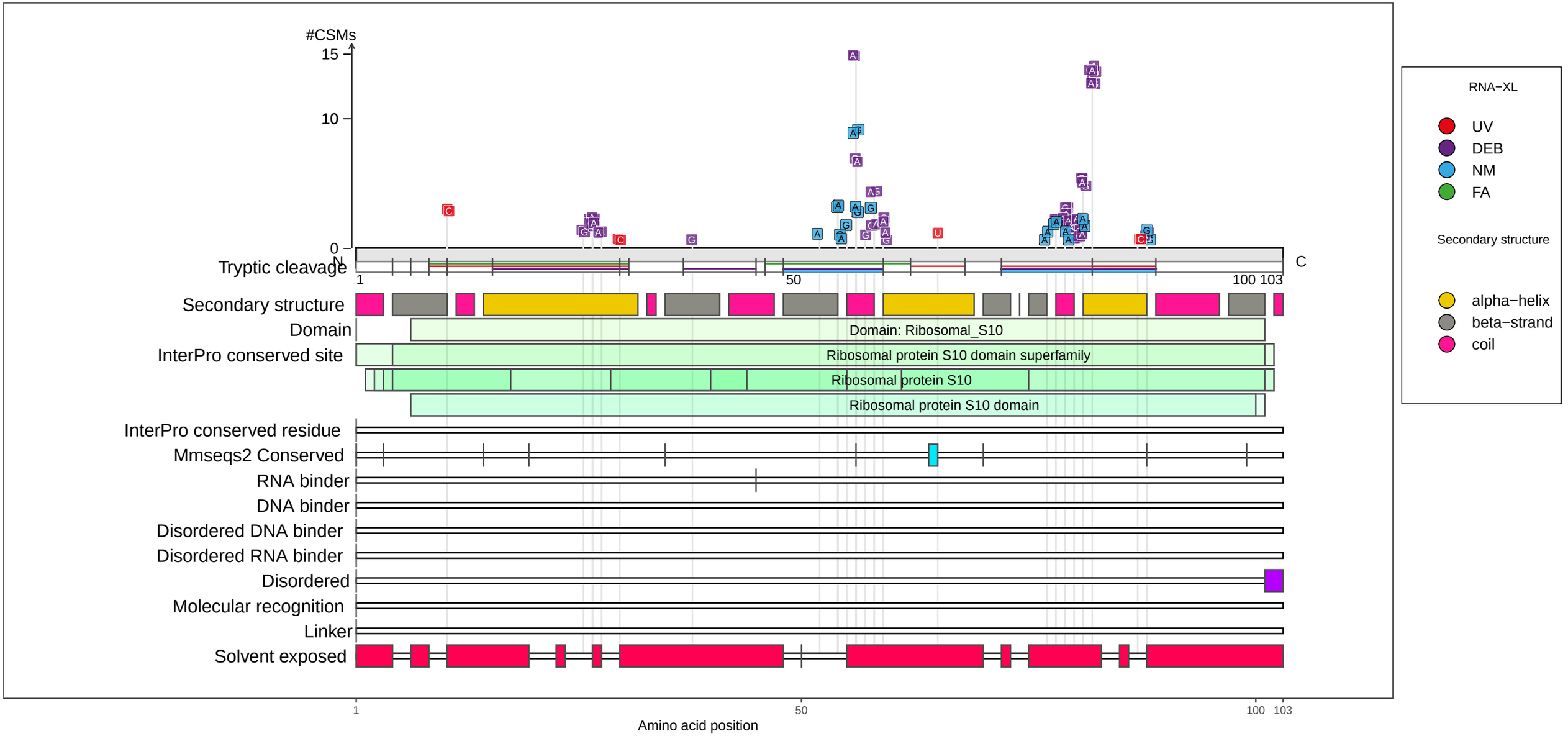
− RNA functions:
mRNA 3−UTR binding; mRNA binding; RNA binding; RNA strand annealing activity
RNA strand−exchange activity



P0A7R5
RS10_ECOLI 30S ribosomal protein S10

− Abundance:
tryptic [log10 Intensity]: 9.4 (Q 95)
PAXdb K12 strain [ppm]: 3.82 (Q 100)
PAXdb E.coli [ppm]: 3.45 (Q 98)

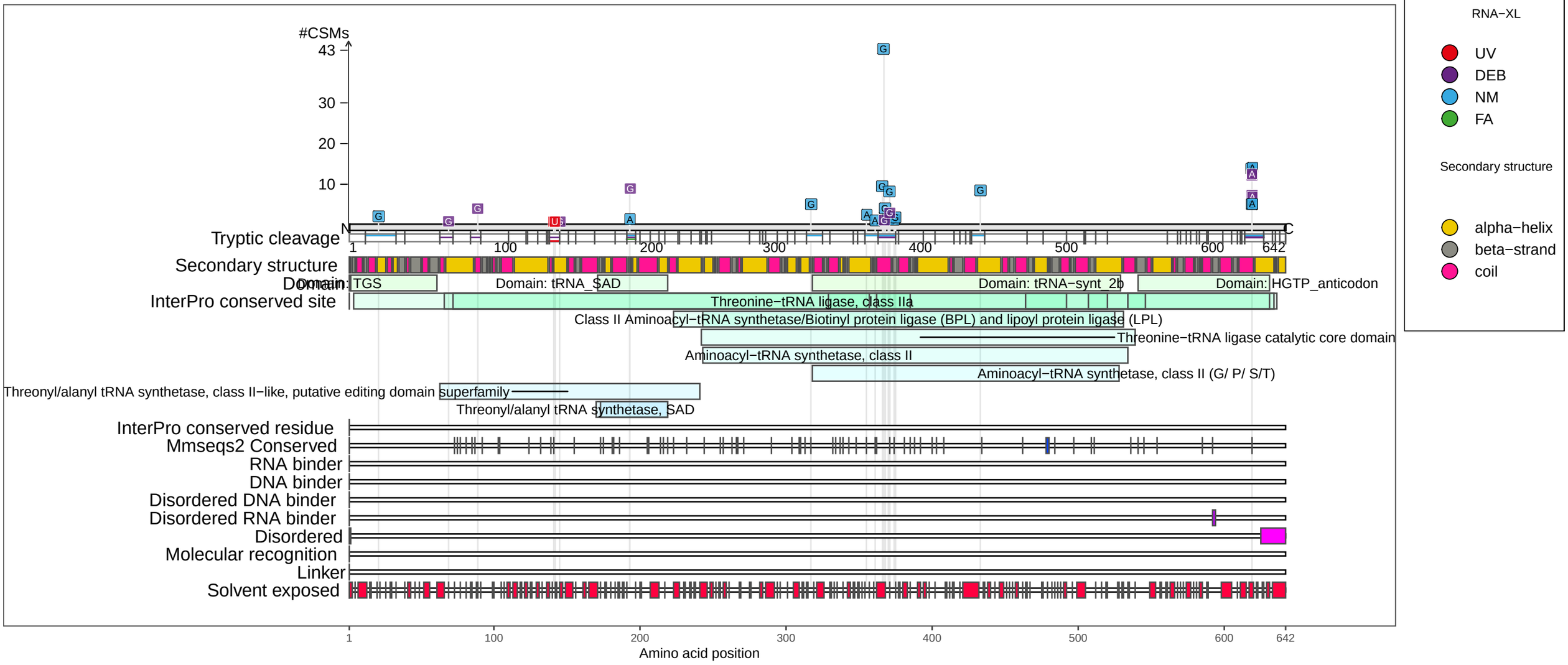
− RNA functions:
RNA binding; tRNA binding



P0A8M3
SYT_ECOLI Threonine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.3 (Q 94)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 3.29 (Q 97)

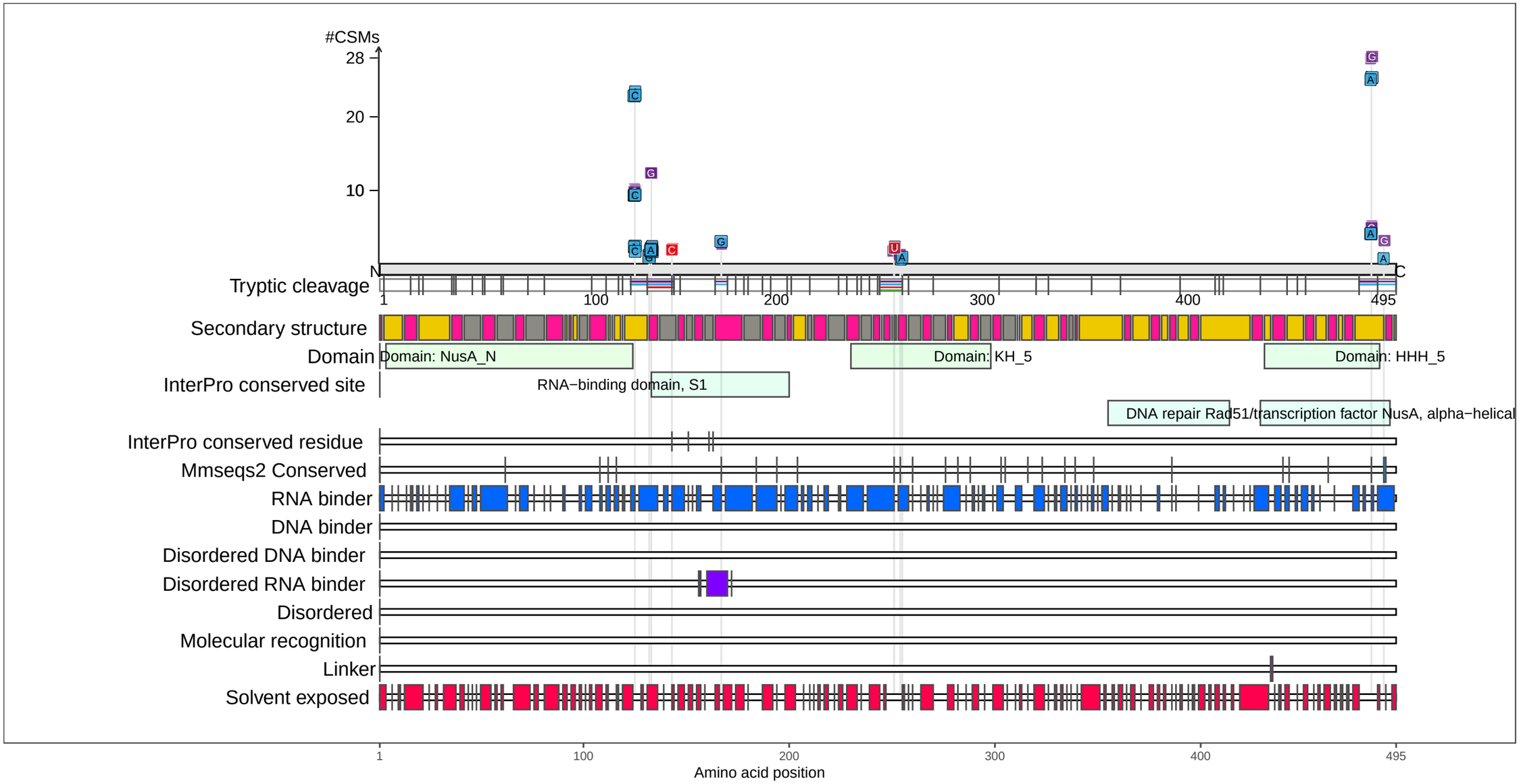
− RNA functions:
aminoacyl−tRNA editing activity; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; mRNA 5−UTR binding; mRNA binding
ncRNA metabolic process; RNA binding; RNA metabolic process; threonine−tRNA ligase activity
Threonyl and Alanyl tRNA synthetase second additional domain
threonyl−tRNA aminoacylation; tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA binding
tRNA metabolic process; tRNA synthetase class II core domain (G, H, P, S and T)

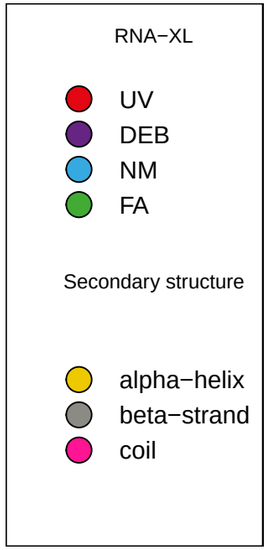


P0AFF6
NUSA_ECOLI Transcription termination/antitermination protein NusA

− Abundance:
tryptic [log10 Intensity]: 9.04 (Q 89)
PAXdb K12 strain [ppm]: 3.17 (Q 94)
PAXdb E.coli [ppm]: 3.21 (Q 97)

− RNA functions:
RNA binding; RNA biosynthetic process; RNA metabolic process; RNA polymerase binding
RNA polymerase core enzyme binding; S1 RNA binding domain

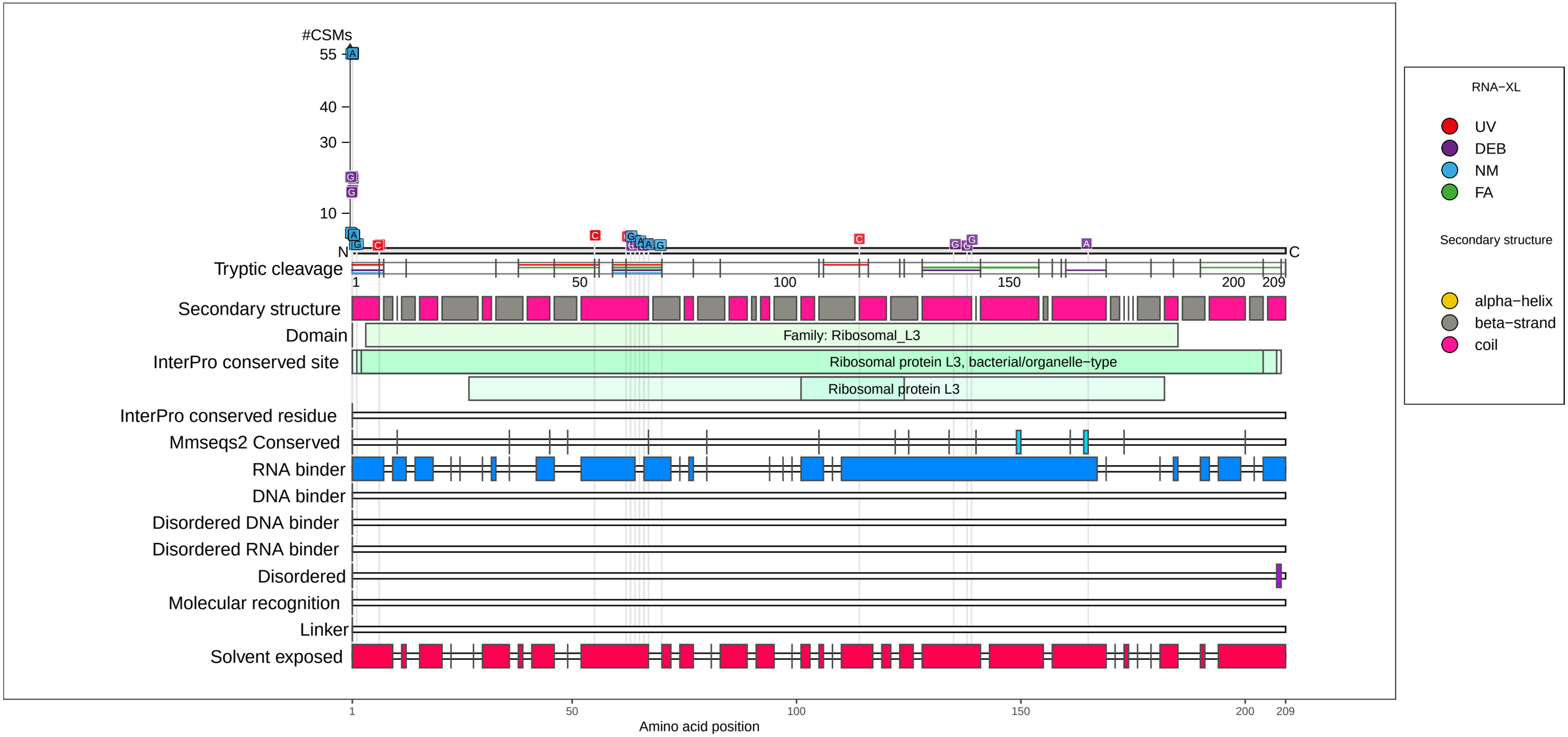




P60438
RL3_ECOLI 50S ribosomal protein L3

− Abundance:
tryptic [log10 Intensity]: 9.42 (Q 96)
PAXdb K12 strain [ppm]: 3.38 (Q 96)
PAXdb E.coli [ppm]: 3.49 (Q 99)

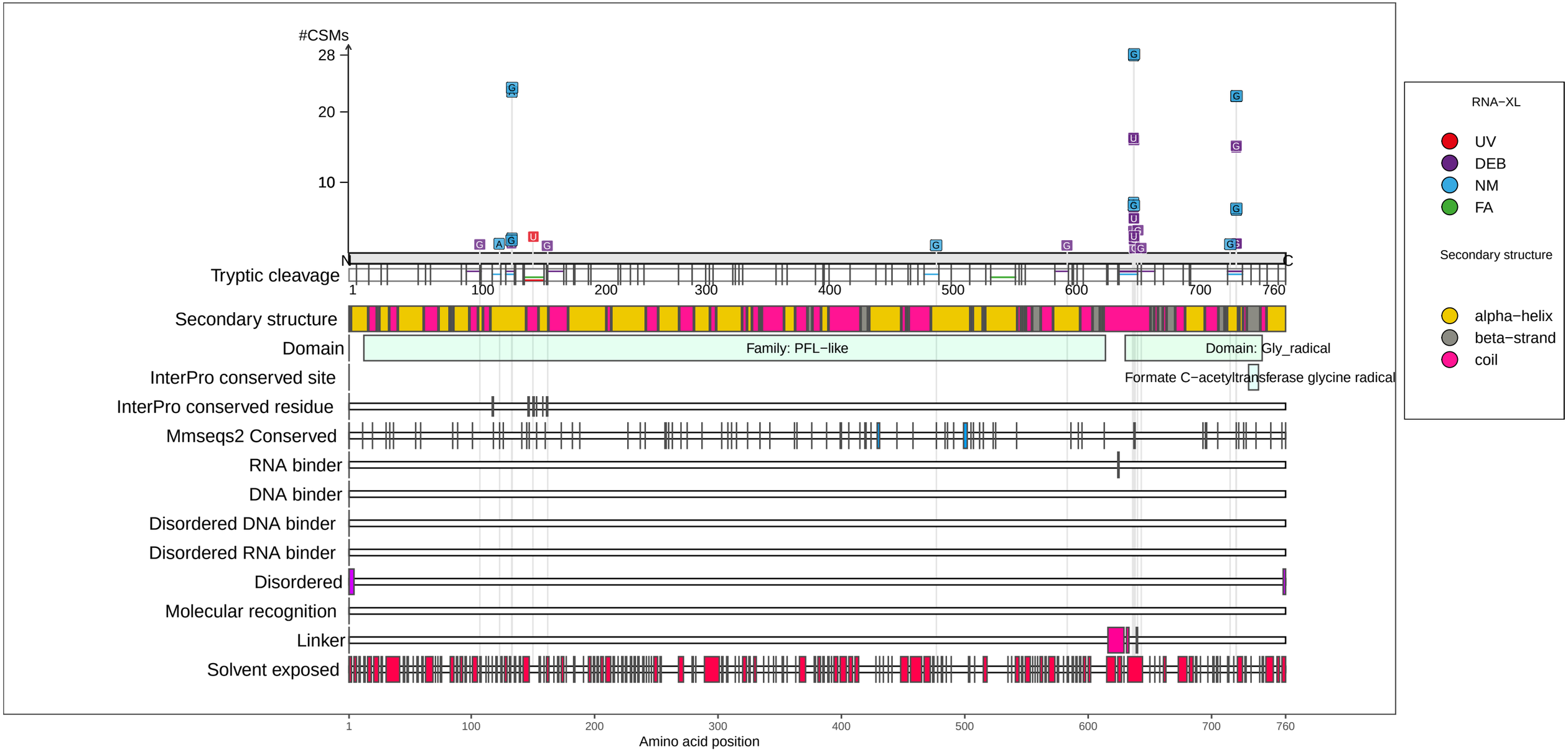
− RNA functions:
RNA binding; rRNA binding



P09373
PFLB_ECOLI Formate acetyltransferase 1

− Abundance:
tryptic [log10 Intensity]: 9.93 (Q 99)
PAXdb K12 strain [ppm]: 3.15 (Q 93)
PAXdb E.coli [ppm]: 3.52 (Q 99)

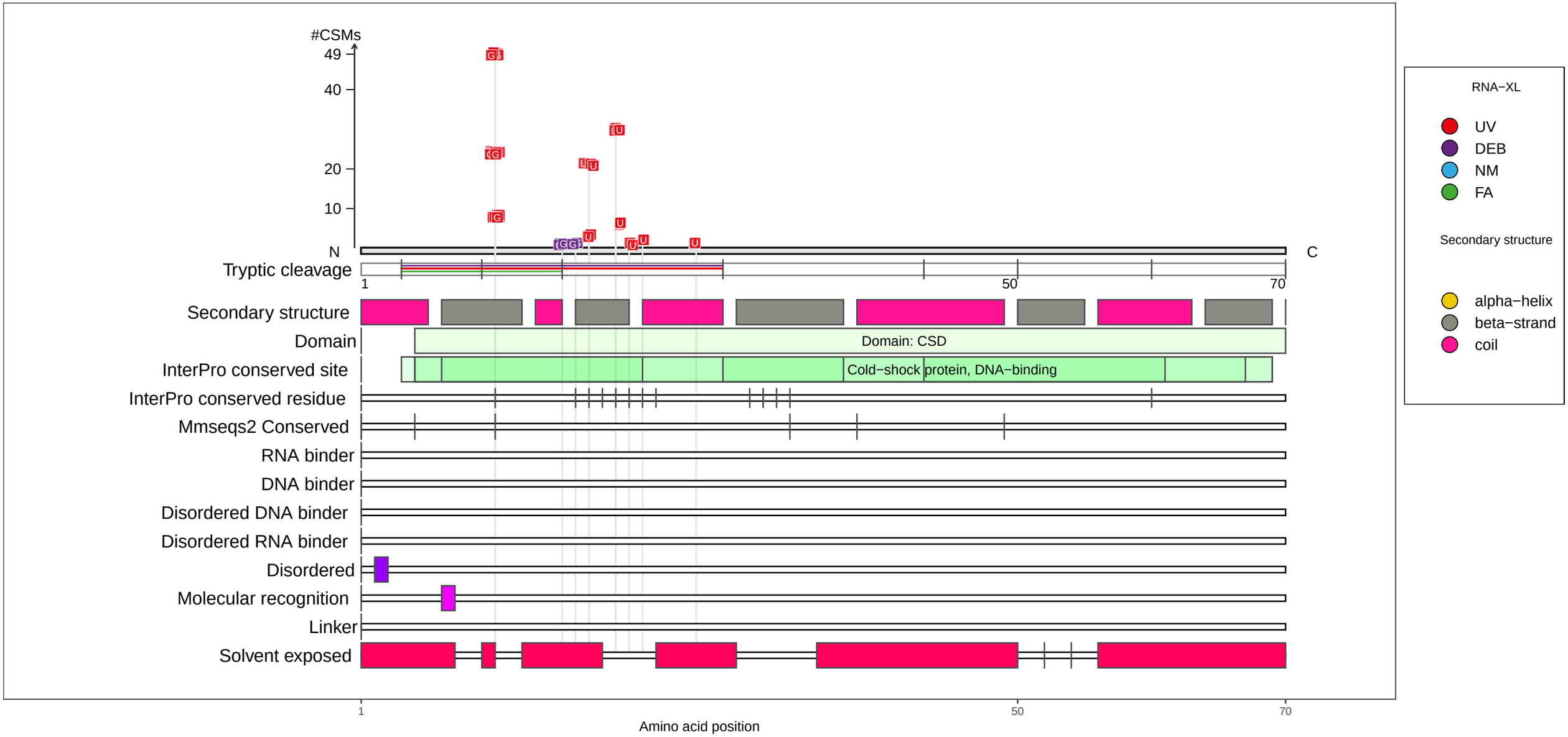
− RNA functions: not annotated



P0A978
CSPG_ECOLI Cold shock−like protein CspG

− Abundance:
tryptic [log10 Intensity]: 9.15 (Q 92)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 1.73 (Q 65)

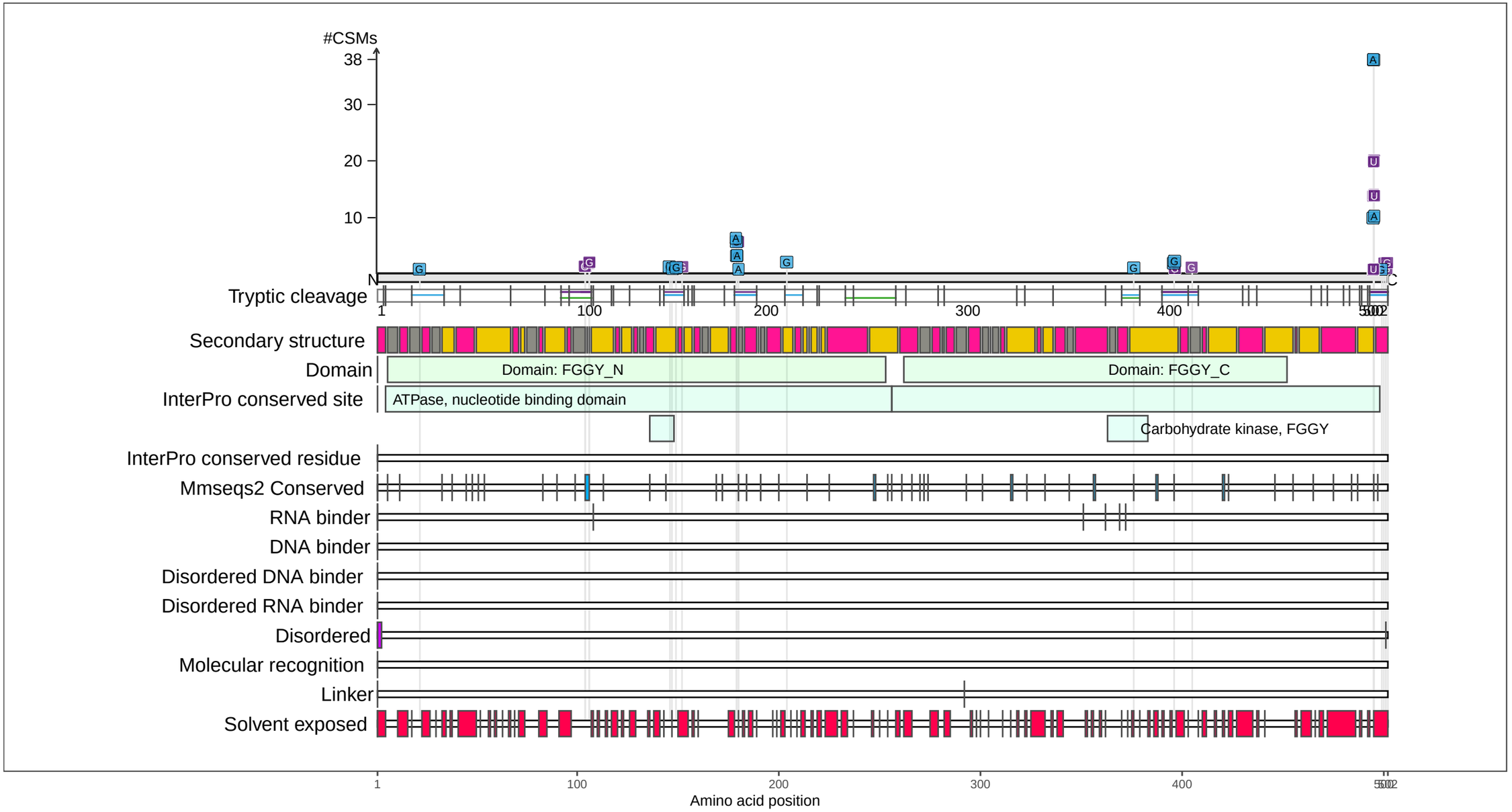
− RNA functions:
RNA binding



P0A6F3
GLPK_ECOLI Glycerol kinase

− Abundance:
tryptic [log10 Intensity]: 9.91 (Q 99)
PAXdb K12 strain [ppm]: 3.28 (Q 95)
PAXdb E.coli [ppm]: 2.75 (Q 91)

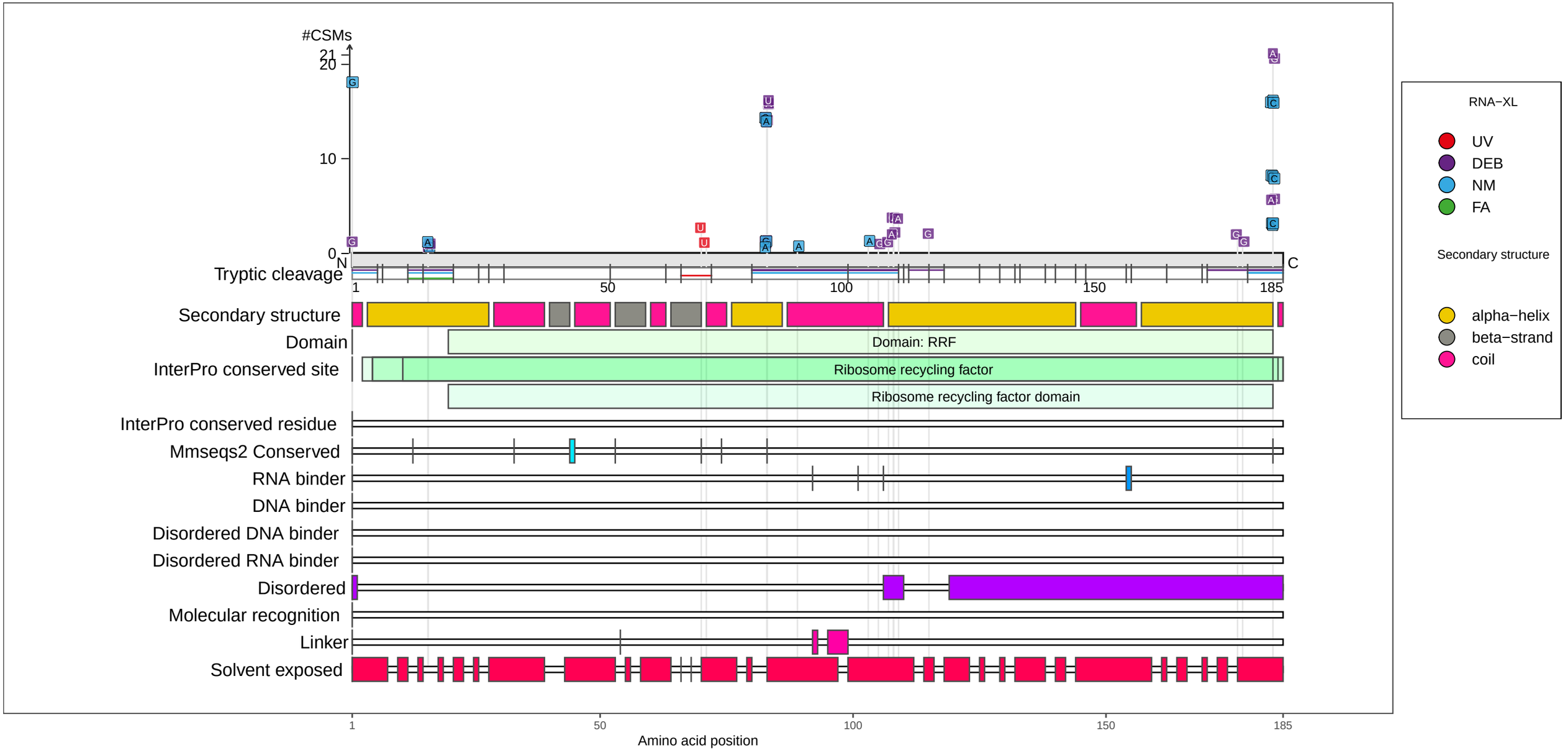
− RNA functions: not annotated



P0A805
RRF_ECOLI Ribosome−recycling factor

− Abundance:
tryptic [log10 Intensity]: 8.51 (Q 76)
PAXdb K12 strain [ppm]: 3.53 (Q 98)
PAXdb E.coli [ppm]: 3.08 (Q 96)

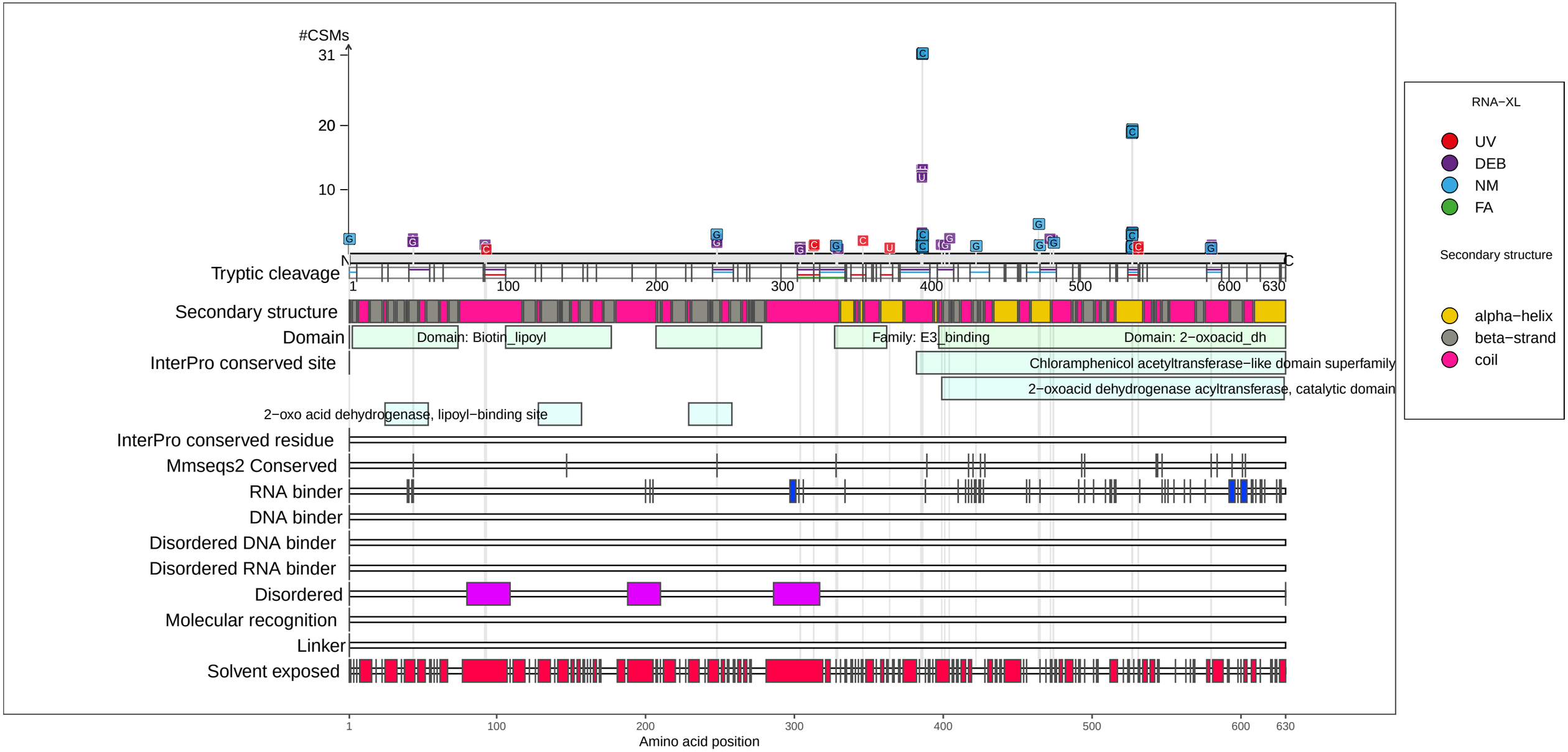
− RNA functions: not annotated



P06959
ODP2_ECOLI Dihydrolipoyllysine−residue acetyltransferase component of pyruvate dehydrogenase complex

− Abundance:
tryptic [log10 Intensity]: 10.12 (Q 100)
PAXdb K12 strain [ppm]: 3.12 (Q 93)
PAXdb E.coli [ppm]: 3.45 (Q 99)

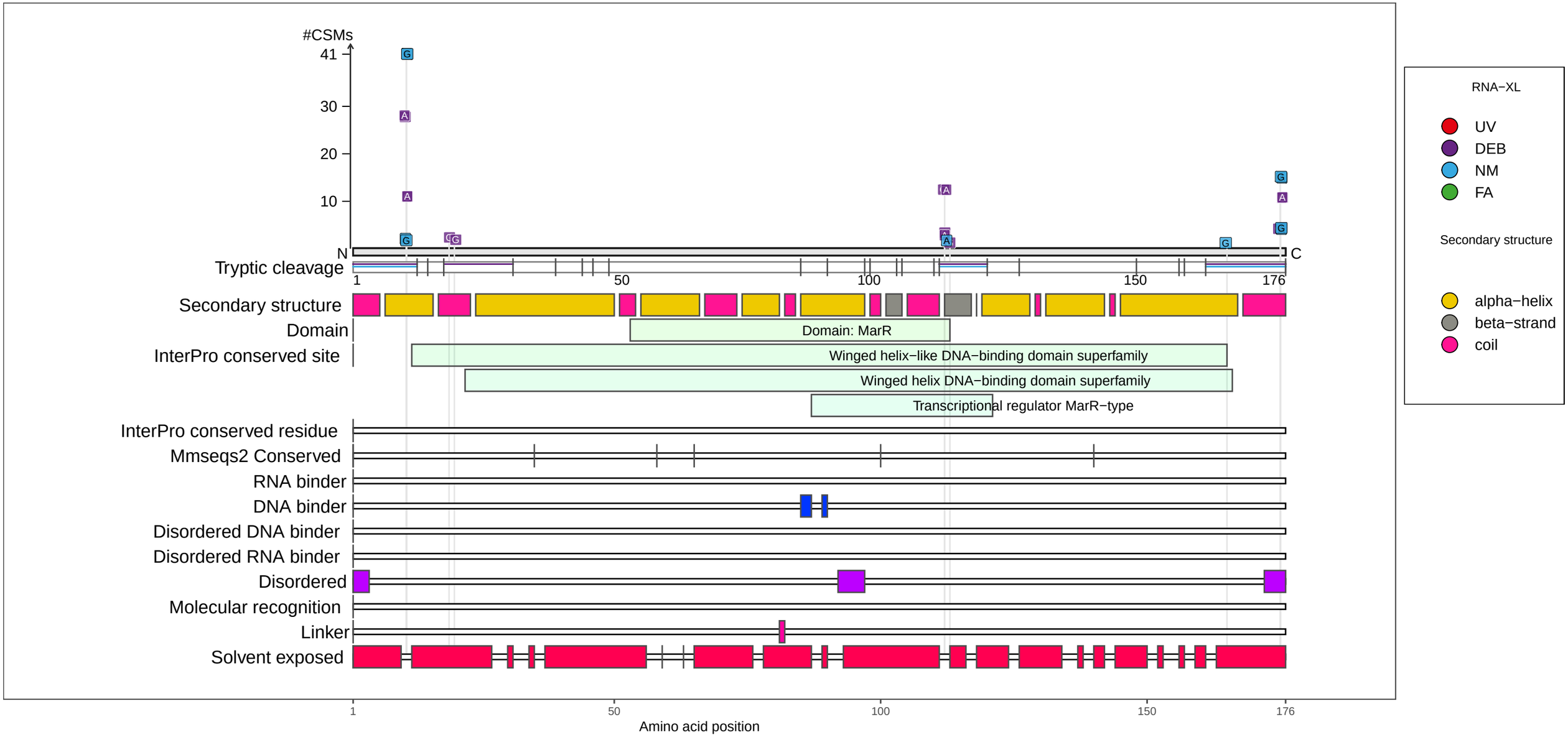
− RNA functions: not annotated



P0ACR9
MPRA_ECOLI Transcriptional repressor MprA

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 2.79 (Q 86)
PAXdb E.coli [ppm]: 2.16 (Q 76)

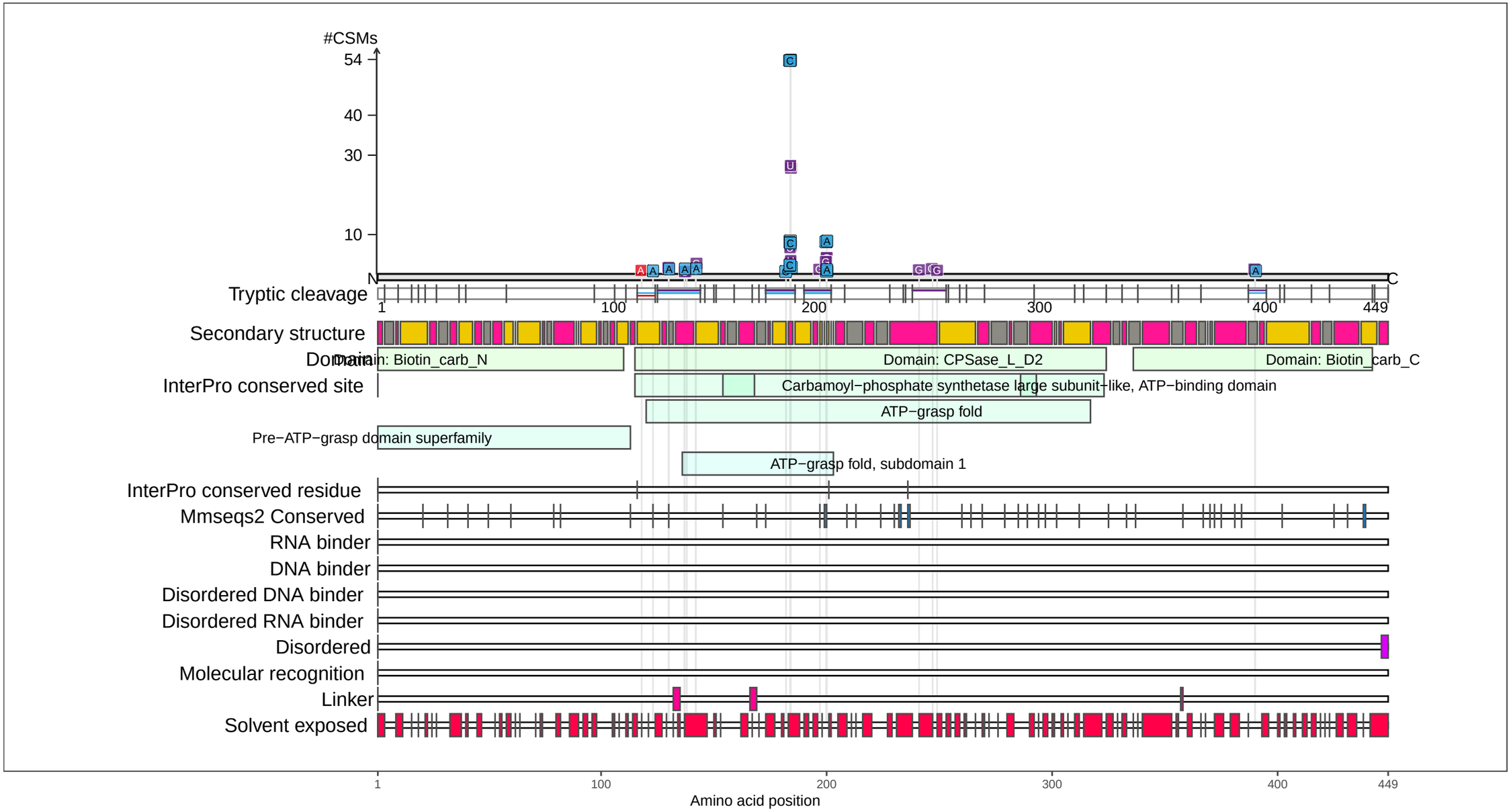
− RNA functions:
RNA biosynthetic process; RNA metabolic process

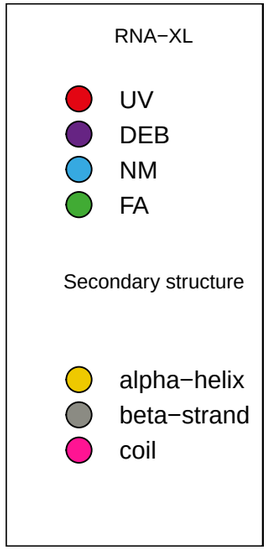


P24182
ACCC_ECOLI Biotin carboxylase

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 3.47 (Q 97)
PAXdb E.coli [ppm]: 2.4 (Q 83)

− RNA functions: not annotated

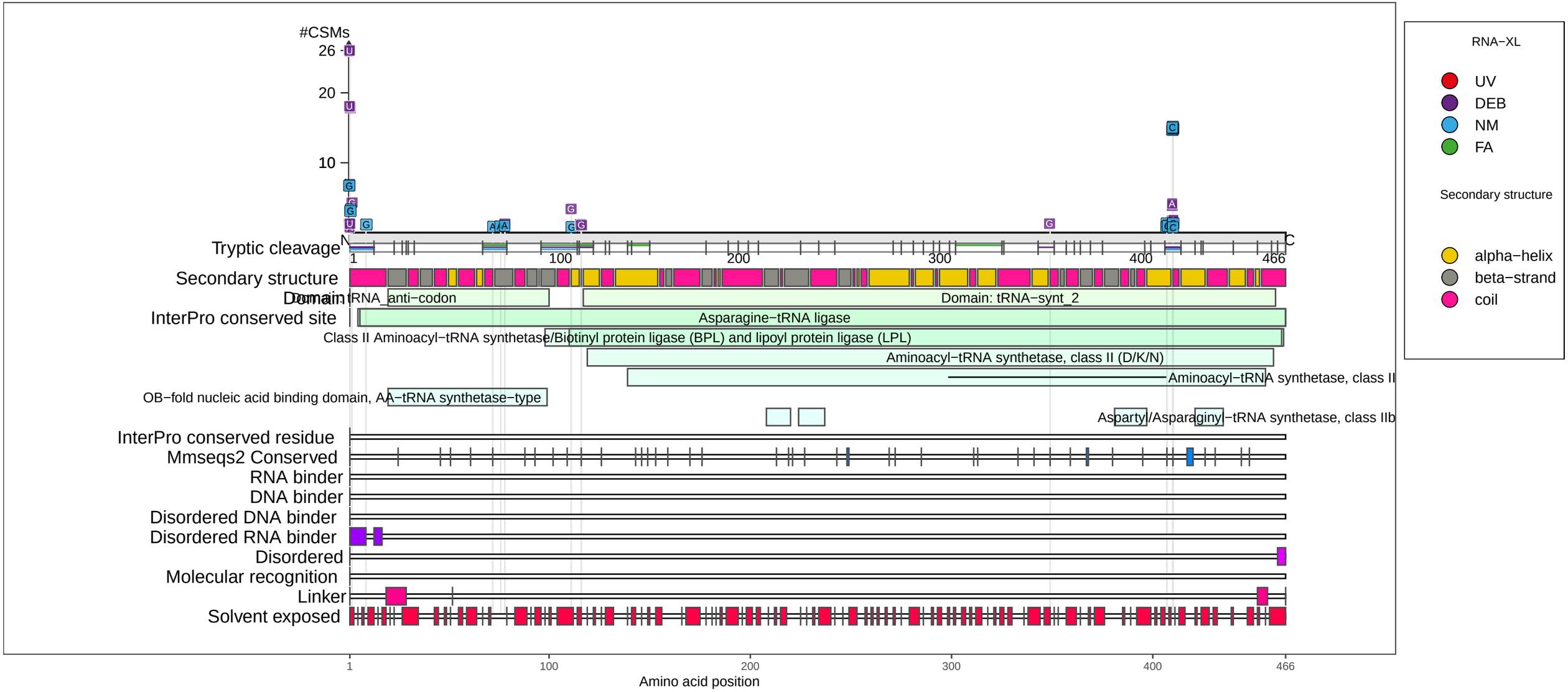




P0A8M0
SYN_ECOLI Asparagine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.34 (Q 95)
PAXdb K12 strain [ppm]: 3.26 (Q 95)
PAXdb E.coli [ppm]: 2.78 (Q 91)

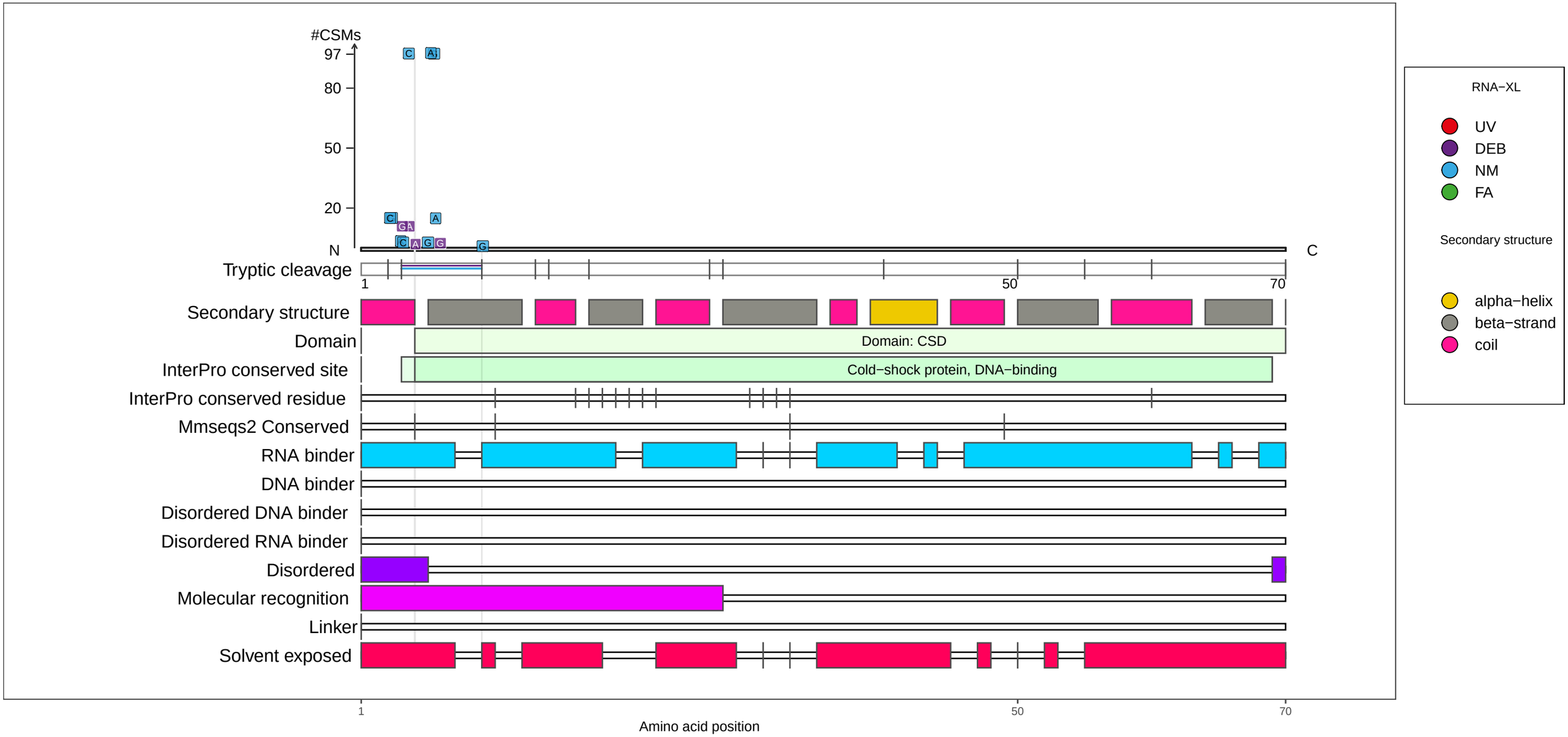
− RNA functions:
aminoacyl−tRNA ligase activity; asparagine−tRNA ligase activity
asparaginyl−tRNA aminoacylation; ncRNA metabolic process; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetases class II (D, K and N)



P0A982
CSPH_ECOLI Cold shock−like protein CspH

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.48 (Q 4)

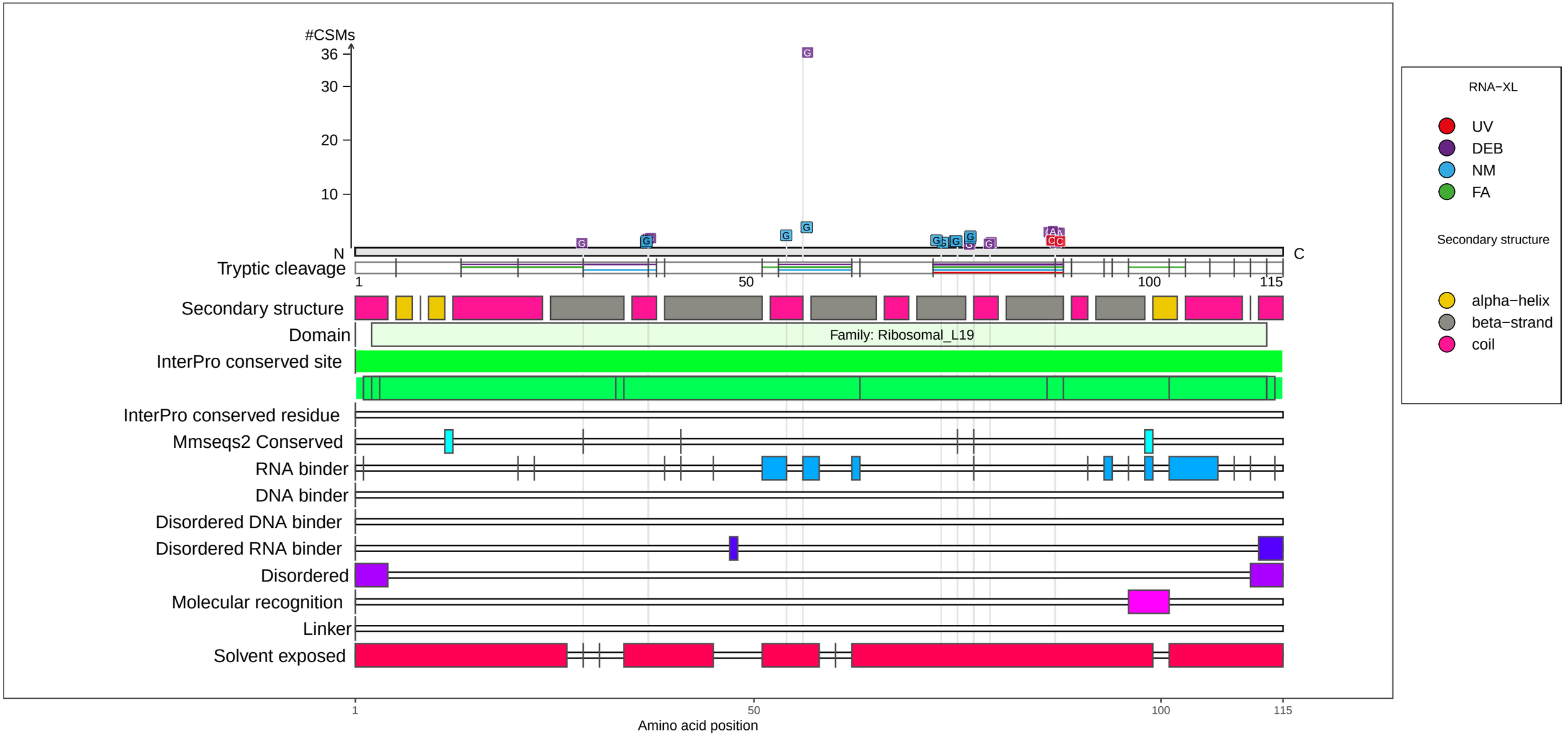
− RNA functions:
RNA binding



P0A7K6
RL19_ECOLI 50S ribosomal protein L19

− Abundance:
tryptic [log10 Intensity]: 9.12 (Q 91)
PAXdb K12 strain [ppm]: 3.73 (Q 99)
PAXdb E.coli [ppm]: 3.34 (Q 98)

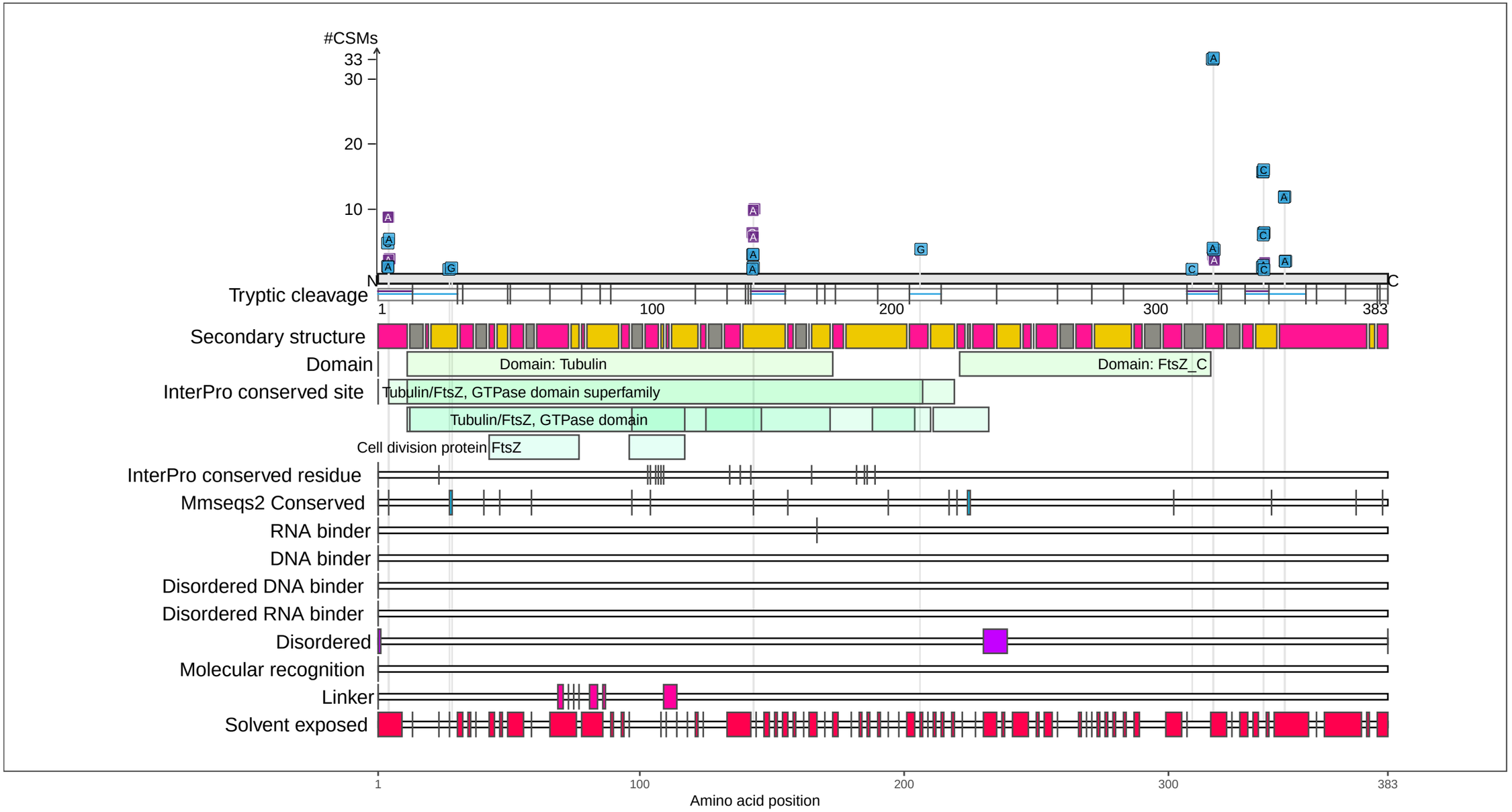
− RNA functions:
RNA binding; rRNA binding



P0A9A6
FTSZ_ECOLI Cell division protein FtsZ

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 90)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 2.95 (Q 94)

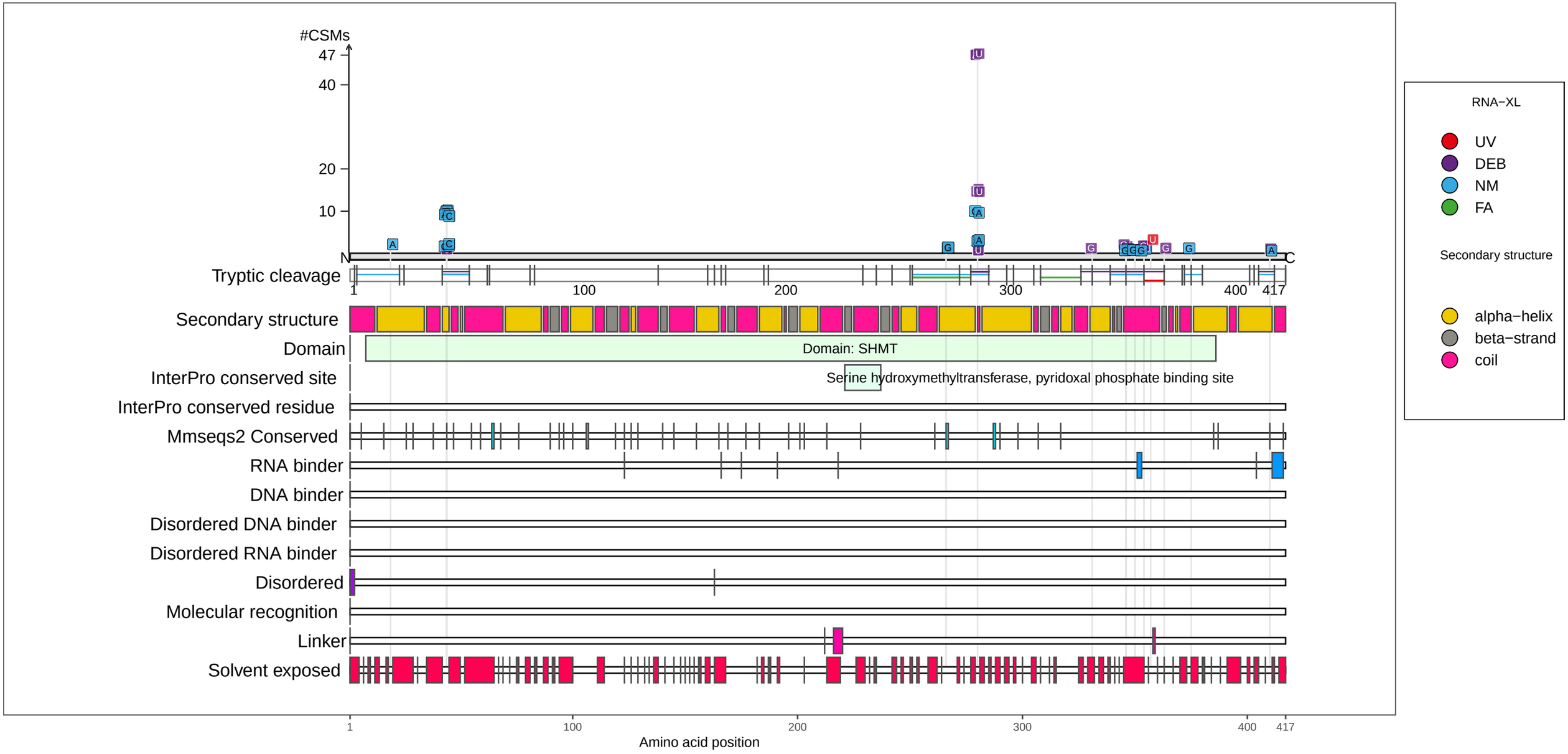
− RNA functions: not annotated



P0A825
GLYA_ECOLI Serine hydroxymethyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.34 (Q 95)
PAXdb K12 strain [ppm]: 3.54 (Q 98)
PAXdb E.coli [ppm]: 3.7 (Q 100)

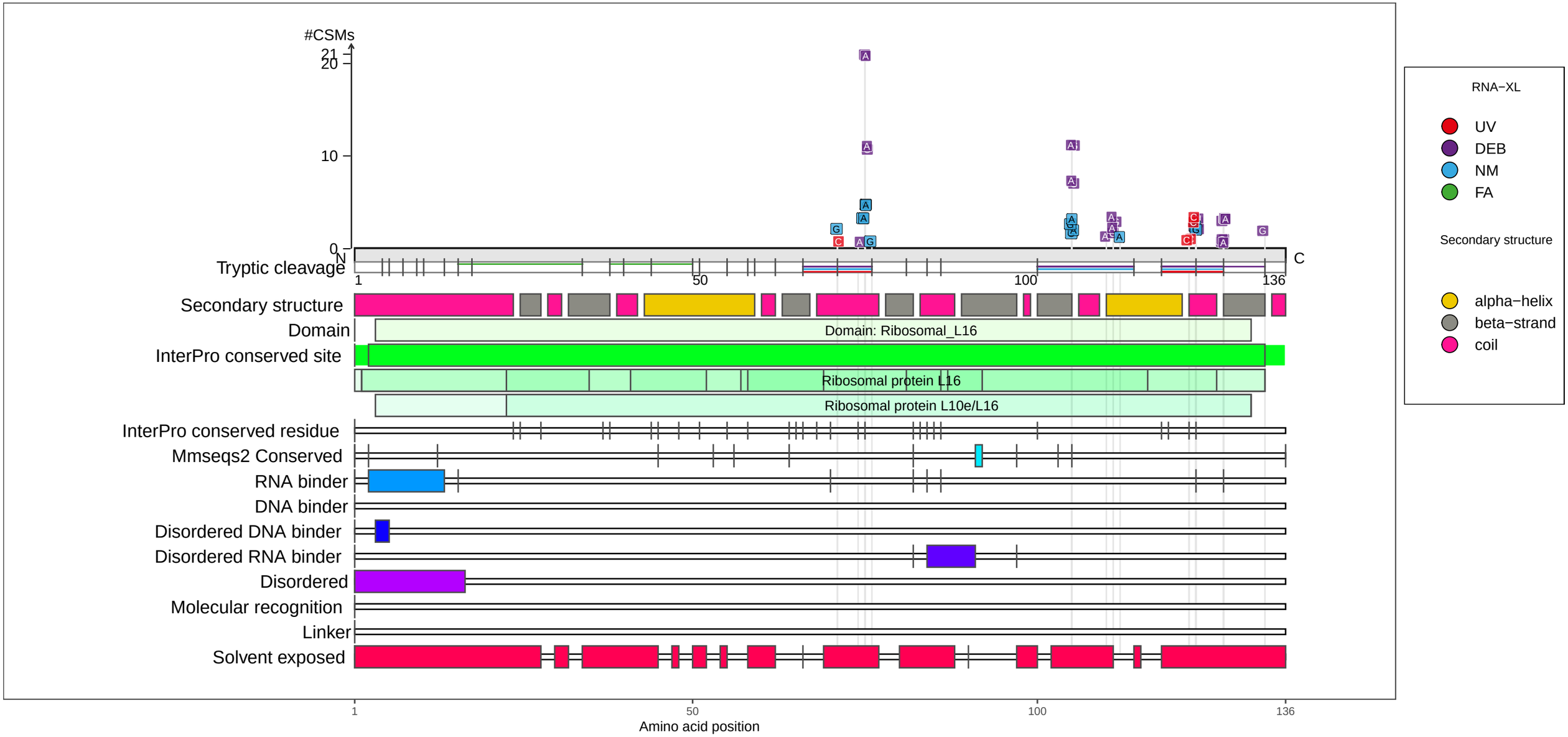
− RNA functions: not annotated



P0ADY7
RL16_ECOLI 50S ribosomal protein L16

− Abundance:
tryptic [log10 Intensity]: 8.89 (Q 86)
PAXdb K12 strain [ppm]: 3.85 (Q 100)
PAXdb E.coli [ppm]: 3.16 (Q 96)

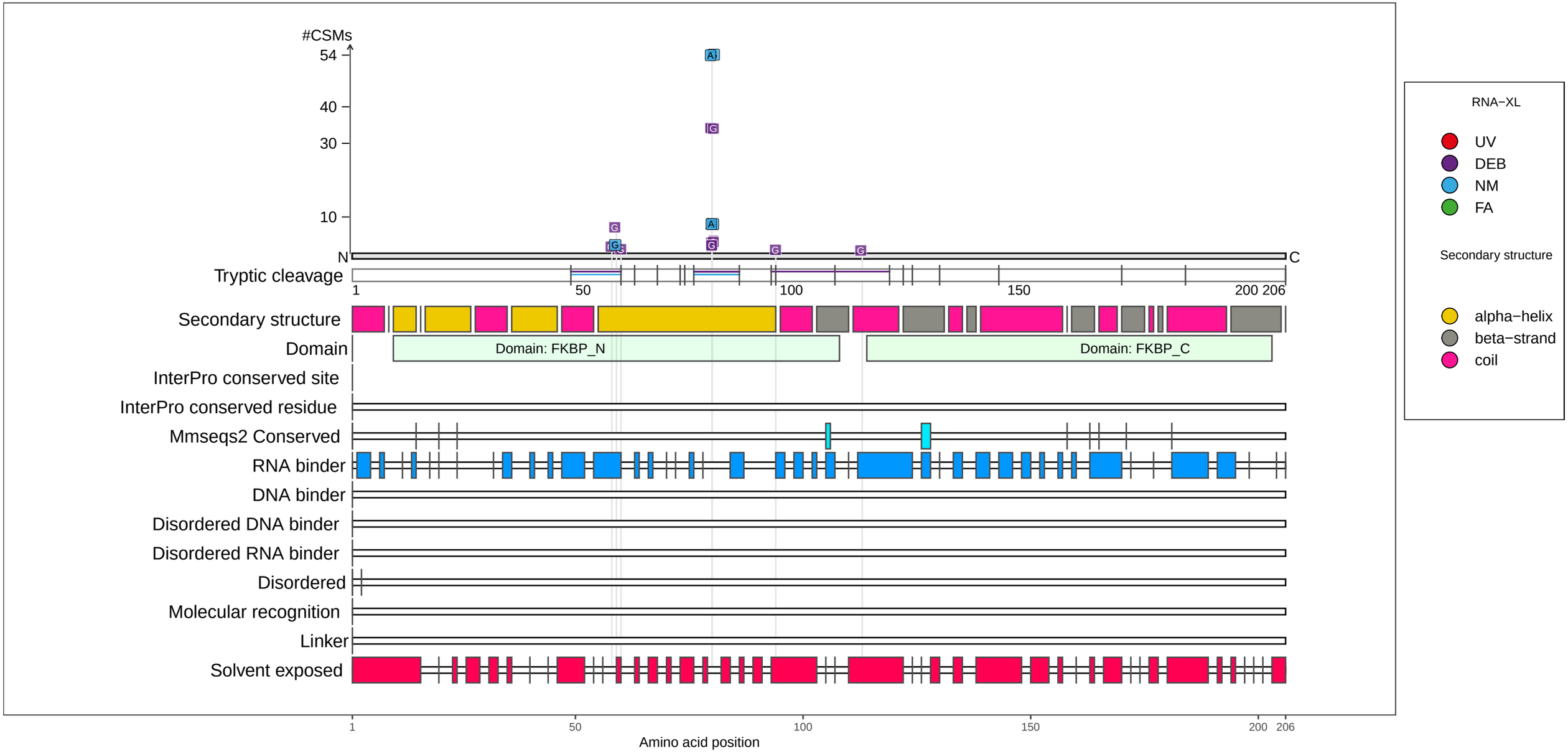
− RNA functions:
RNA binding; rRNA binding; tRNA binding



P0A9L3
FKBB_ECOLI FKBP−type 22 kDa peptidyl−prolyl cis−trans isomerase

− Abundance:
tryptic [log10 Intensity]: 8.32 (Q 70)
PAXdb K12 strain [ppm]: 2.71 (Q 83)
PAXdb E.coli [ppm]: 2.97 (Q 94)

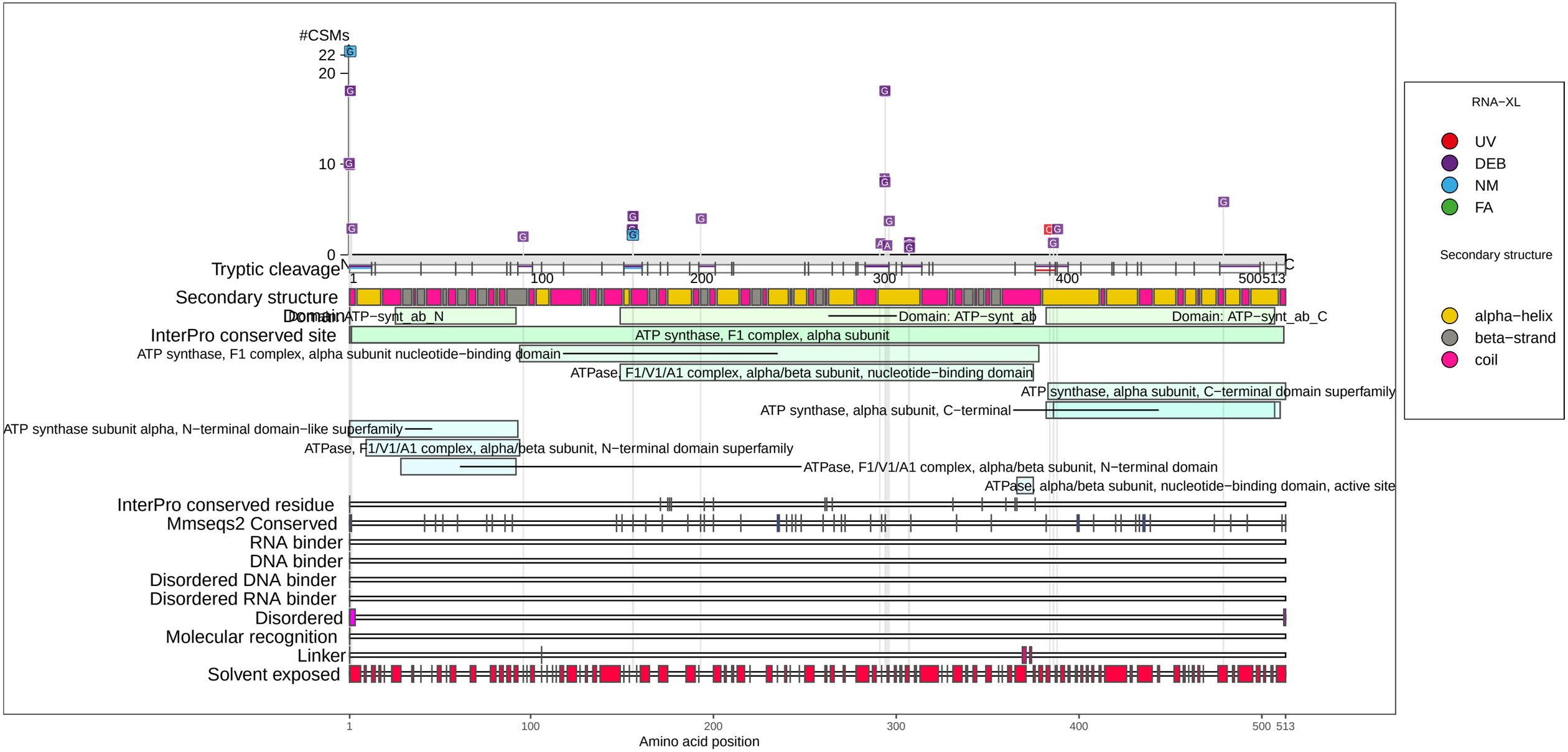
− RNA functions: not annotated



P0ABB0
ATPA_ECOLI ATP synthase subunit alpha

− Abundance:
tryptic [log10 Intensity]: 9.73 (Q 98)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 3.39 (Q 98)

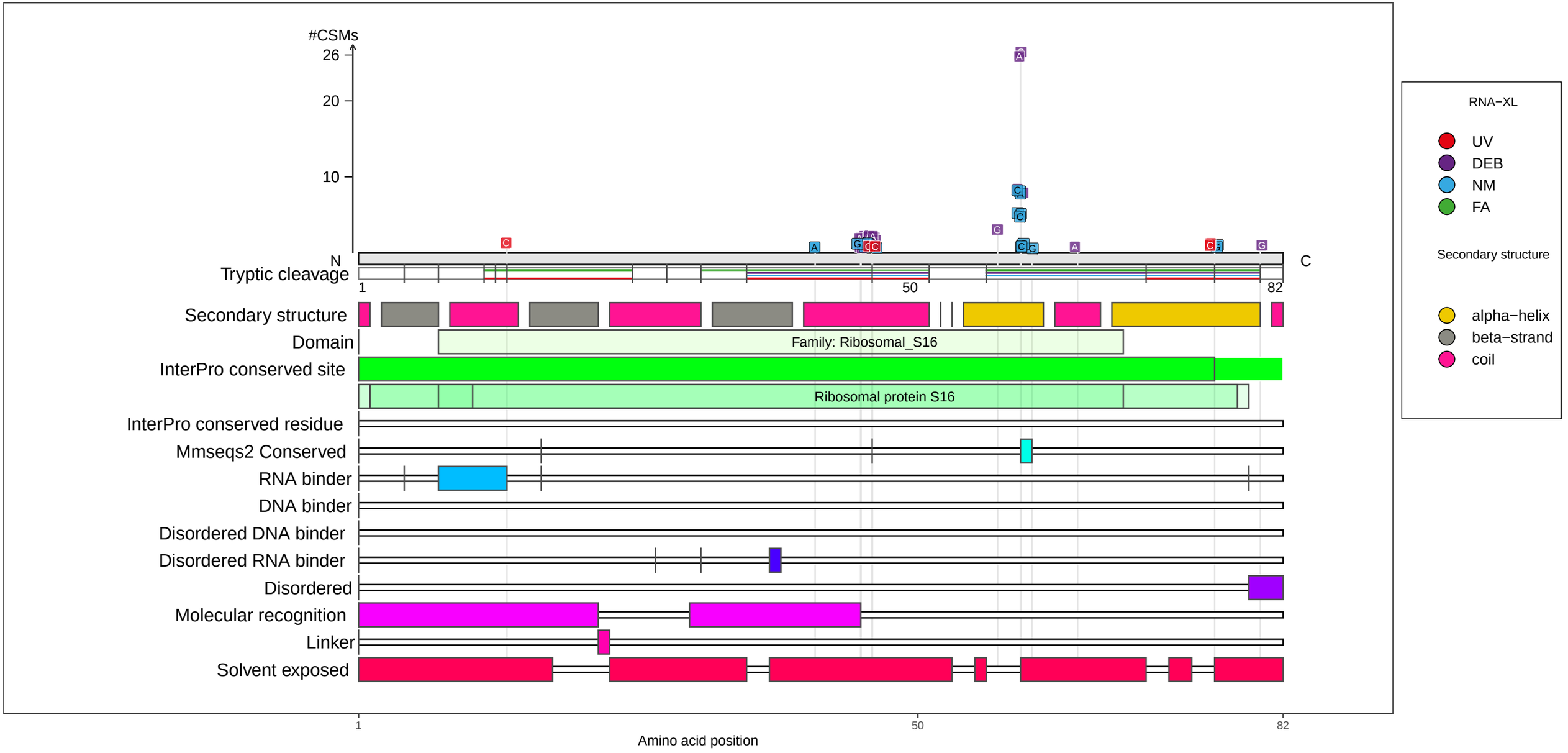
− RNA functions: not annotated



P0A7T3
RS16_ECOLI 30S ribosomal protein S16

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 3.66 (Q 98)
PAXdb E.coli [ppm]: 3.45 (Q 99)

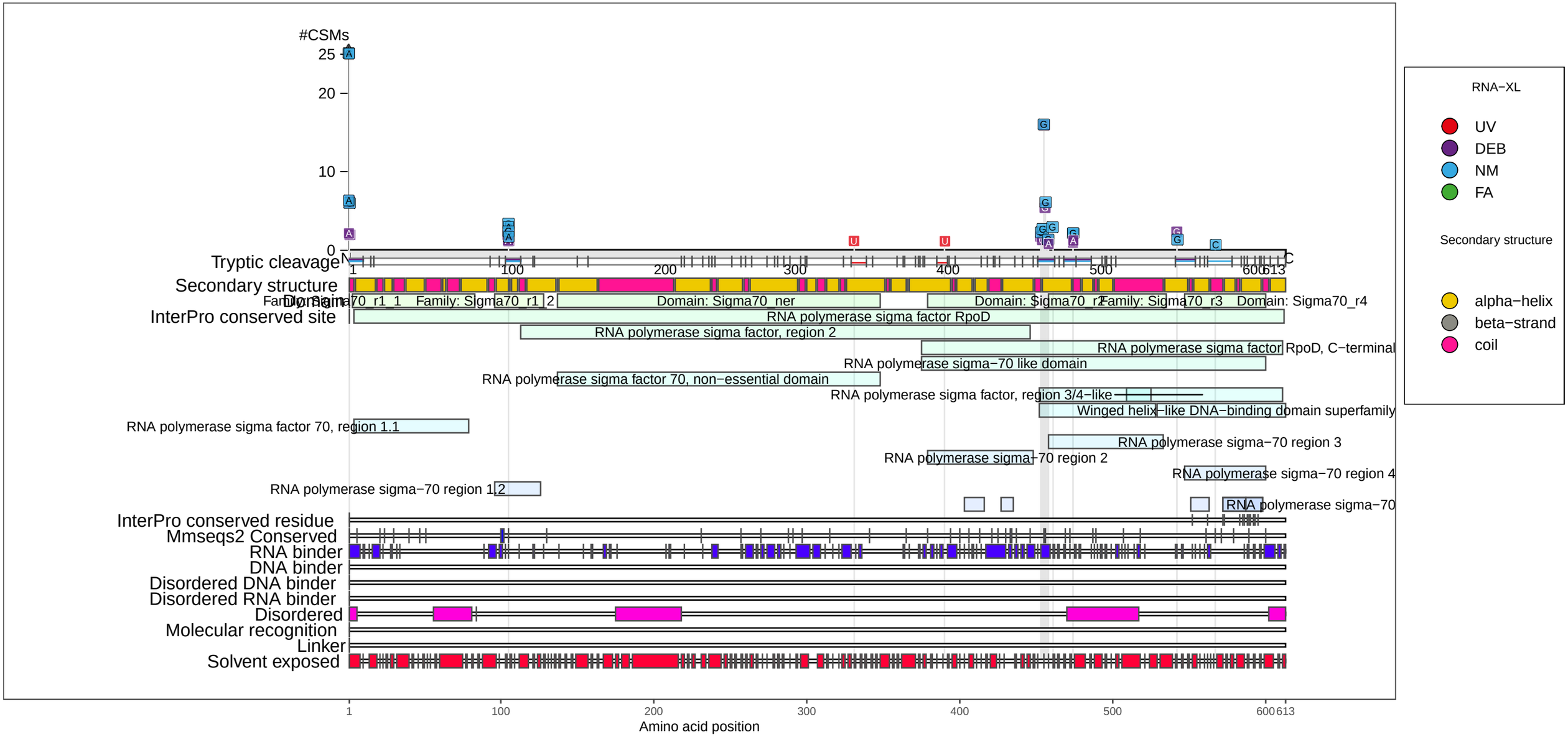
− RNA functions: not annotated



P00579
RPOD_ECOLI RNA polymerase sigma factor RpoD

− Abundance:
tryptic [log10 Intensity]: 8.98 (Q 88)
PAXdb K12 strain [ppm]: 2.99 (Q 91)
PAXdb E.coli [ppm]: 2.57 (Q 87)

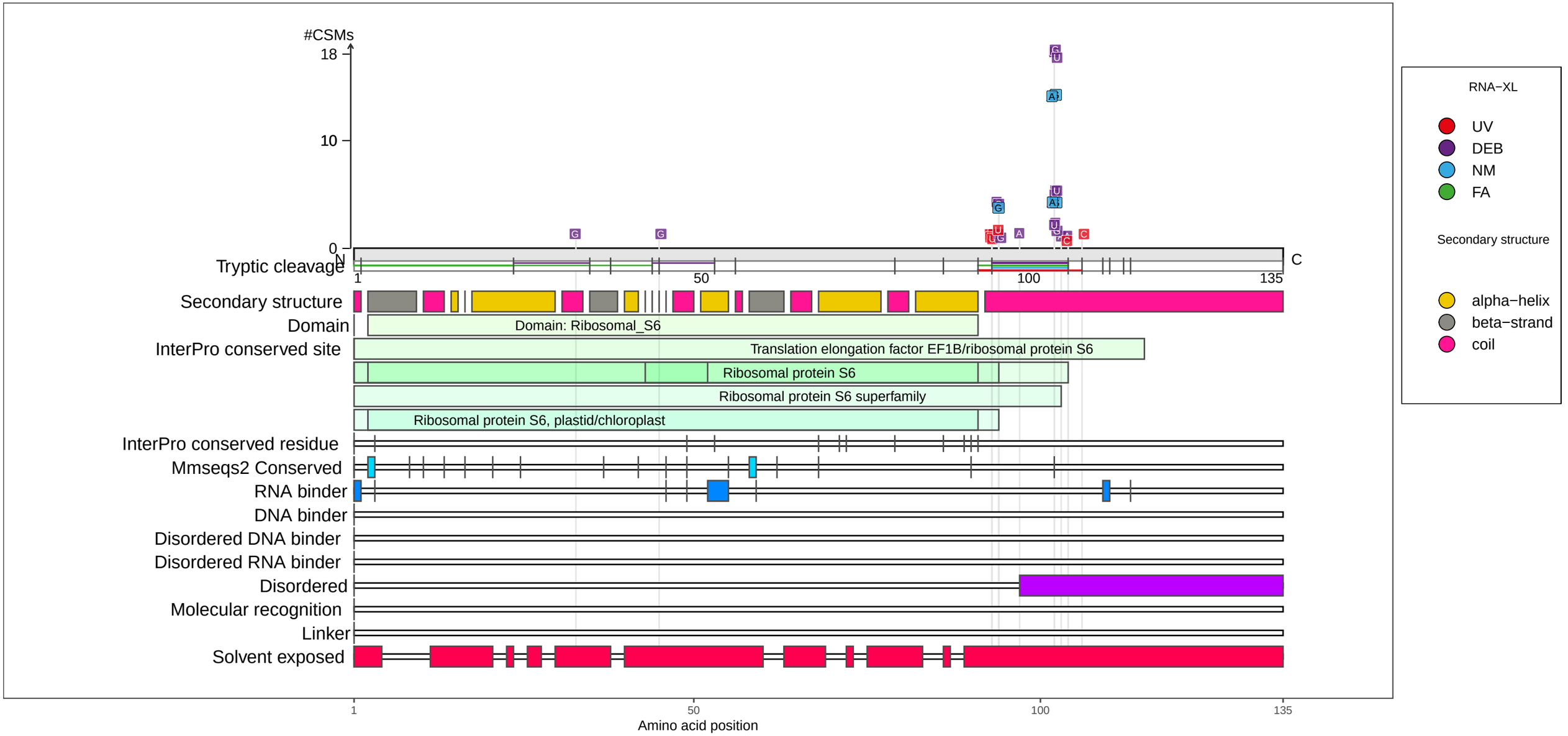
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P02358
RS6_ECOLI 30S ribosomal protein S6

− Abundance:
tryptic [log10 Intensity]: 8.99 (Q 88)
PAXdb K12 strain [ppm]: 3.01 (Q 91)
PAXdb E.coli [ppm]: 3.48 (Q 99)

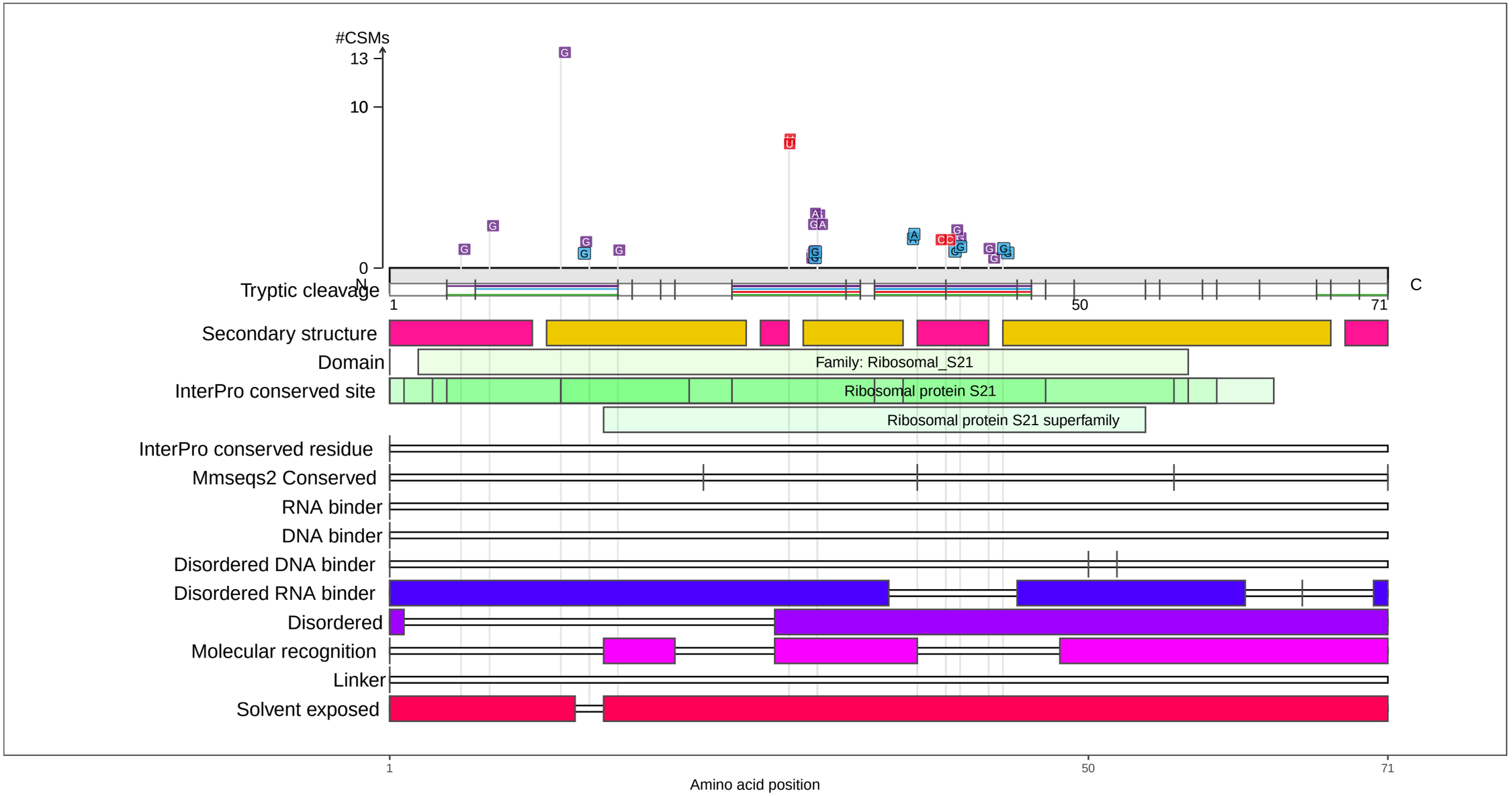
− RNA functions:
mRNA 5−UTR binding; mRNA binding; RNA binding; rRNA binding



P68679
RS21_ECOLI 30S ribosomal protein S21

− Abundance:
tryptic [log10 Intensity]: 8.65 (Q 80)
PAXdb K12 strain [ppm]: 4.2 (Q 100)
PAXdb E.coli [ppm]: 3.54 (Q 99)

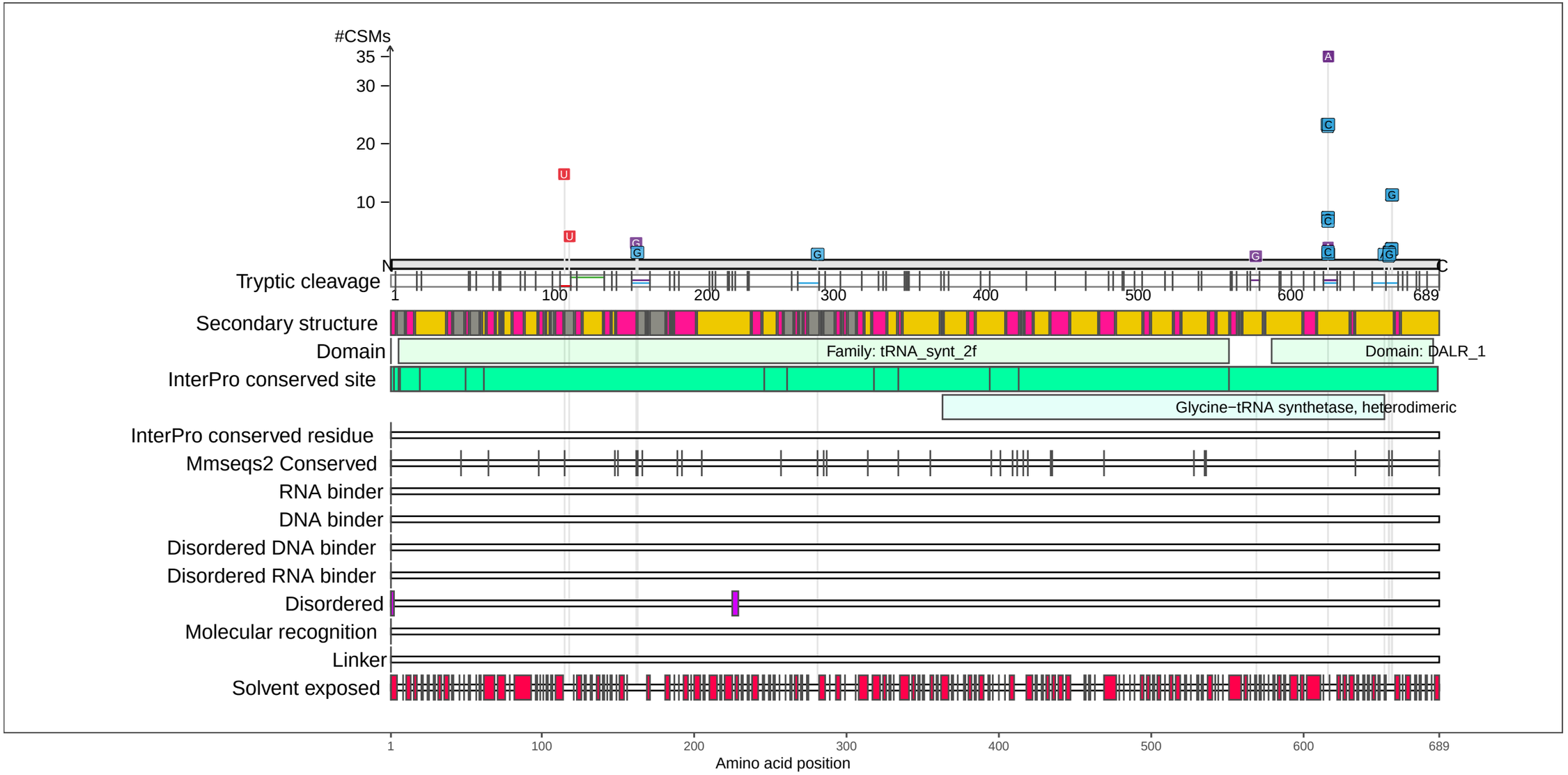
− RNA functions:
RNA binding; rRNA binding

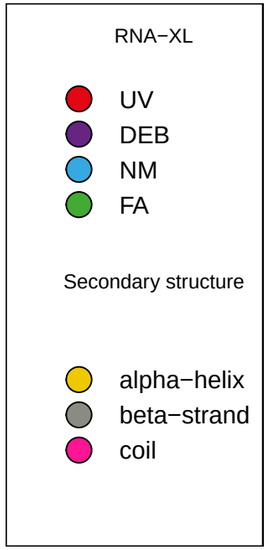


P00961
SYGB_ECOLI Glycine−−tRNA ligase beta subunit

− Abundance:
tryptic [log10 Intensity]: 8.74 (Q 82)
PAXdb K12 strain [ppm]: 3 (Q 91)
PAXdb E.coli [ppm]: 2.71 (Q 90)

− RNA functions:
aminoacyl−tRNA ligase activity; arginine−tRNA ligase activity
arginyl−tRNA aminoacylation; glycine−tRNA ligase activity; glycyl−tRNA aminoacylation
Glycyl−tRNA synthetase beta subunit; ncRNA metabolic process; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process

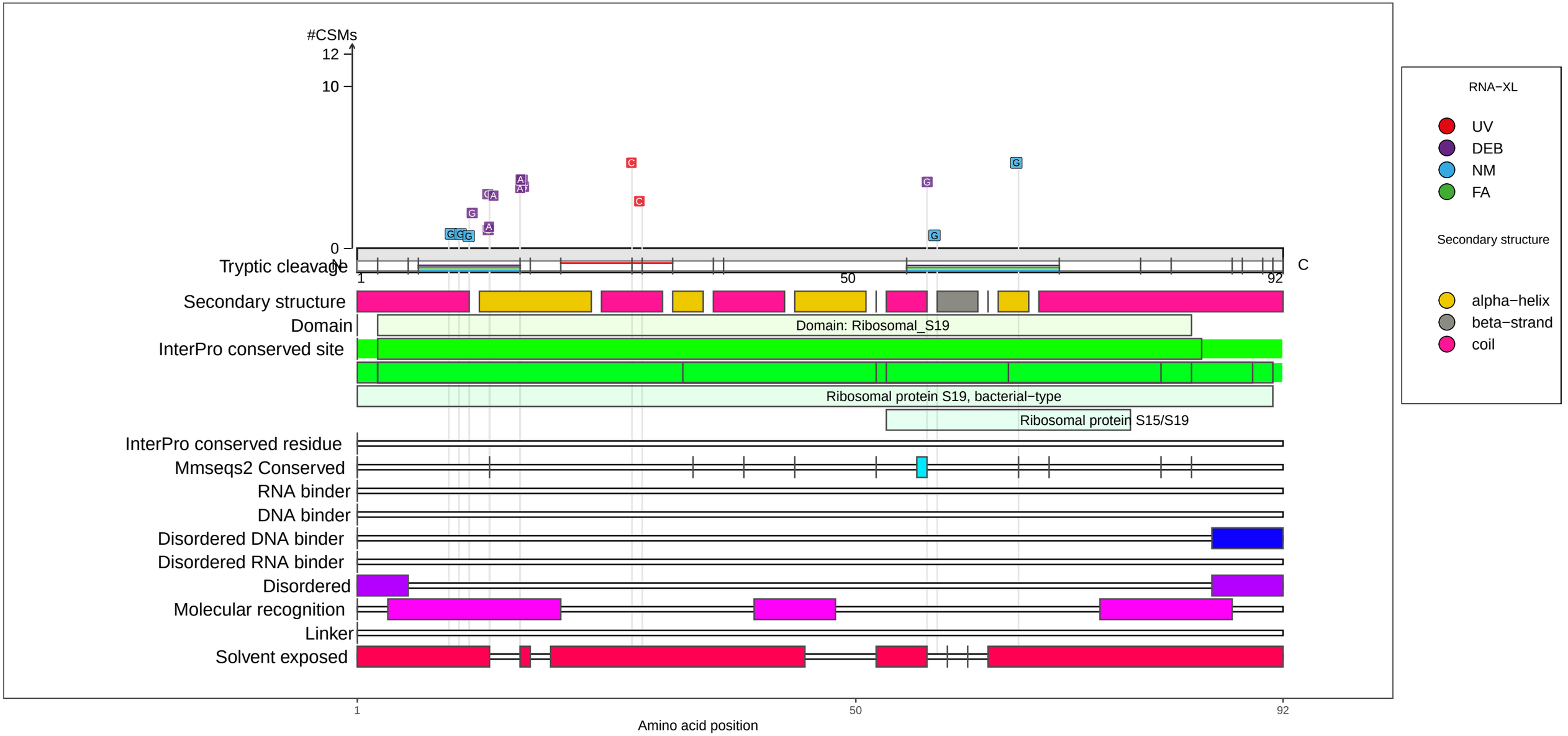




P0A7U3
RS19_ECOLI 30S ribosomal protein S19

− Abundance:
tryptic [log10 Intensity]: 8.56 (Q 78)
PAXdb K12 strain [ppm]: 3.73 (Q 99)
PAXdb E.coli [ppm]: 3.6 (Q 100)

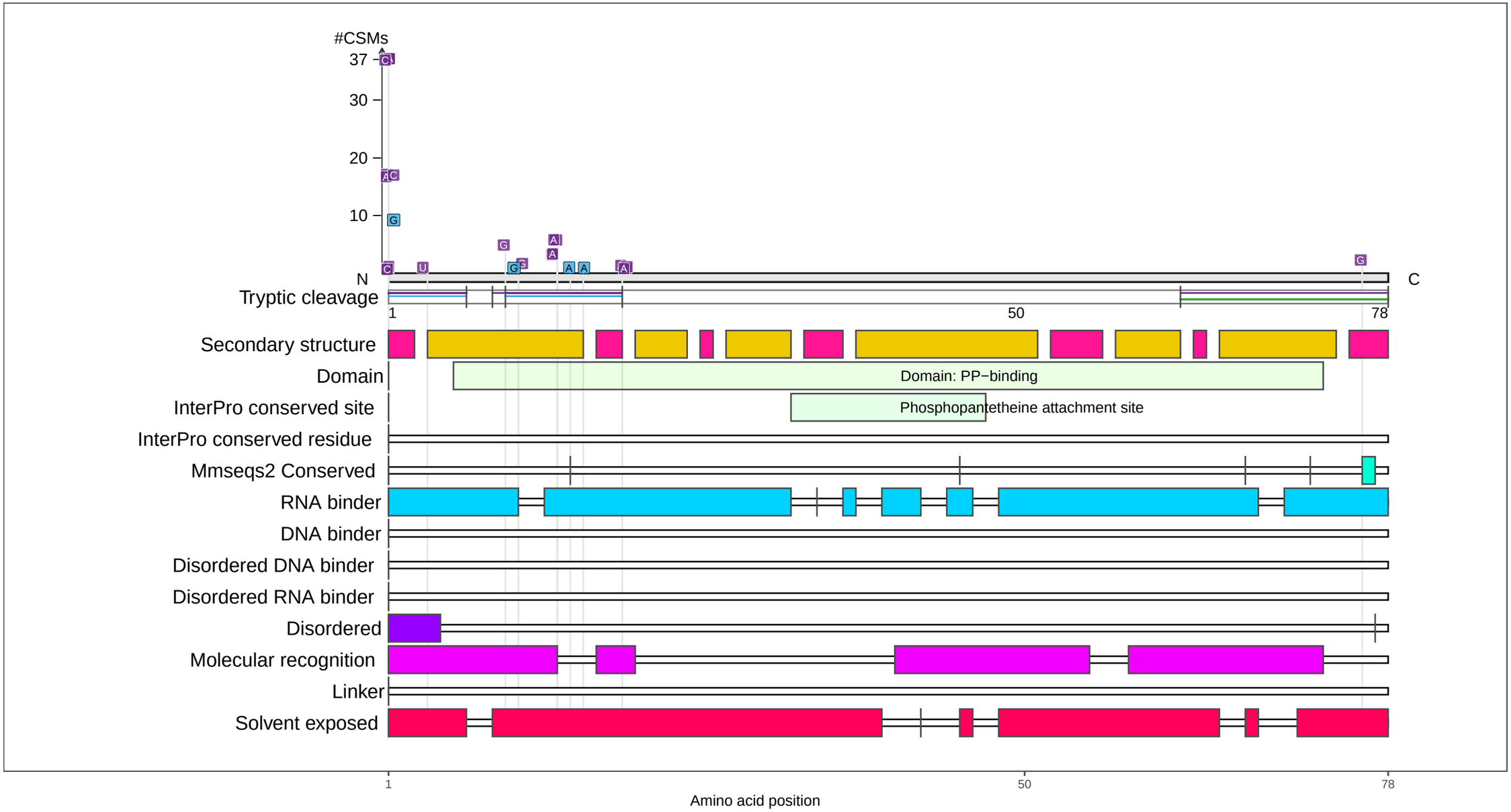
− RNA functions:
RNA binding; rRNA binding; tRNA binding



P0A6A8
ACP_ECOLI Acyl carrier protein

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.67 (Q 99)
PAXdb E.coli [ppm]: 3.53 (Q 99)

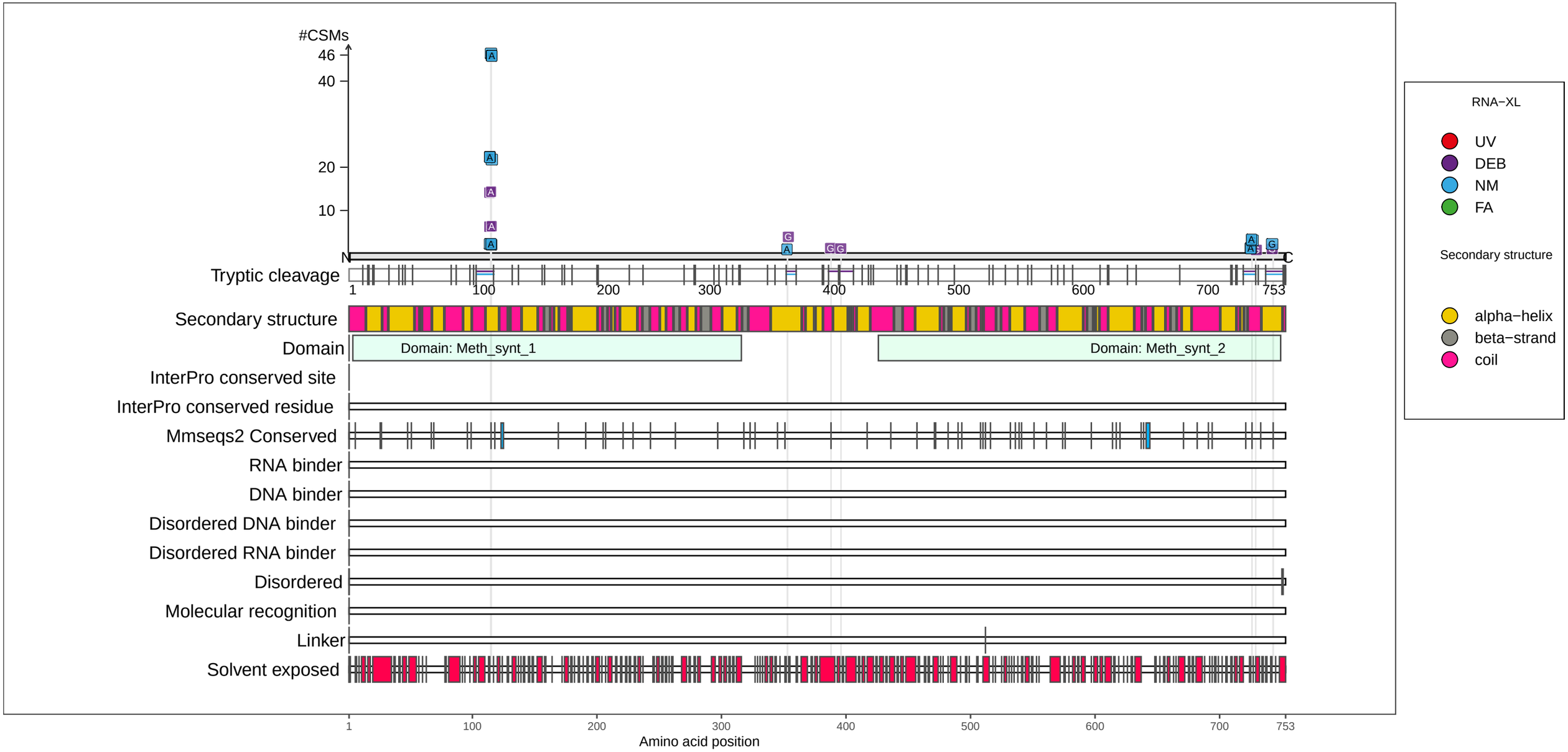
− RNA functions: not annotated



P25665
METE_ECOLI 5−methyltetrahydropteroyltriglutamate−−homocysteine methyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.26 (Q 93)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 3.18 (Q 96)

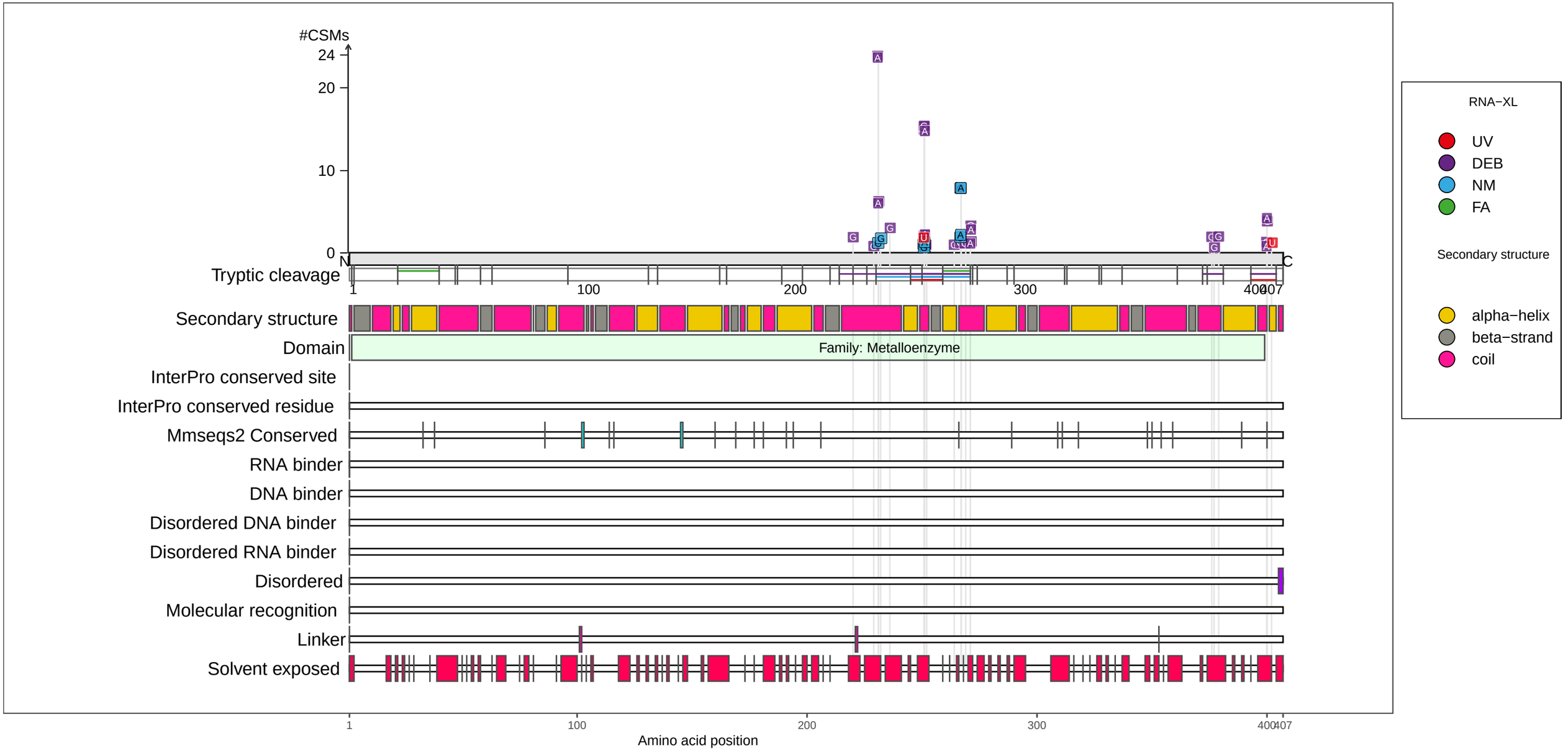
− RNA functions: not annotated



P0A6K6
DEOB_ECOLI Phosphopentomutase

− Abundance:
tryptic [log10 Intensity]: 9.44 (Q 96)
PAXdb K12 strain [ppm]: 3.28 (Q 95)
PAXdb E.coli [ppm]: 2.95 (Q 94)

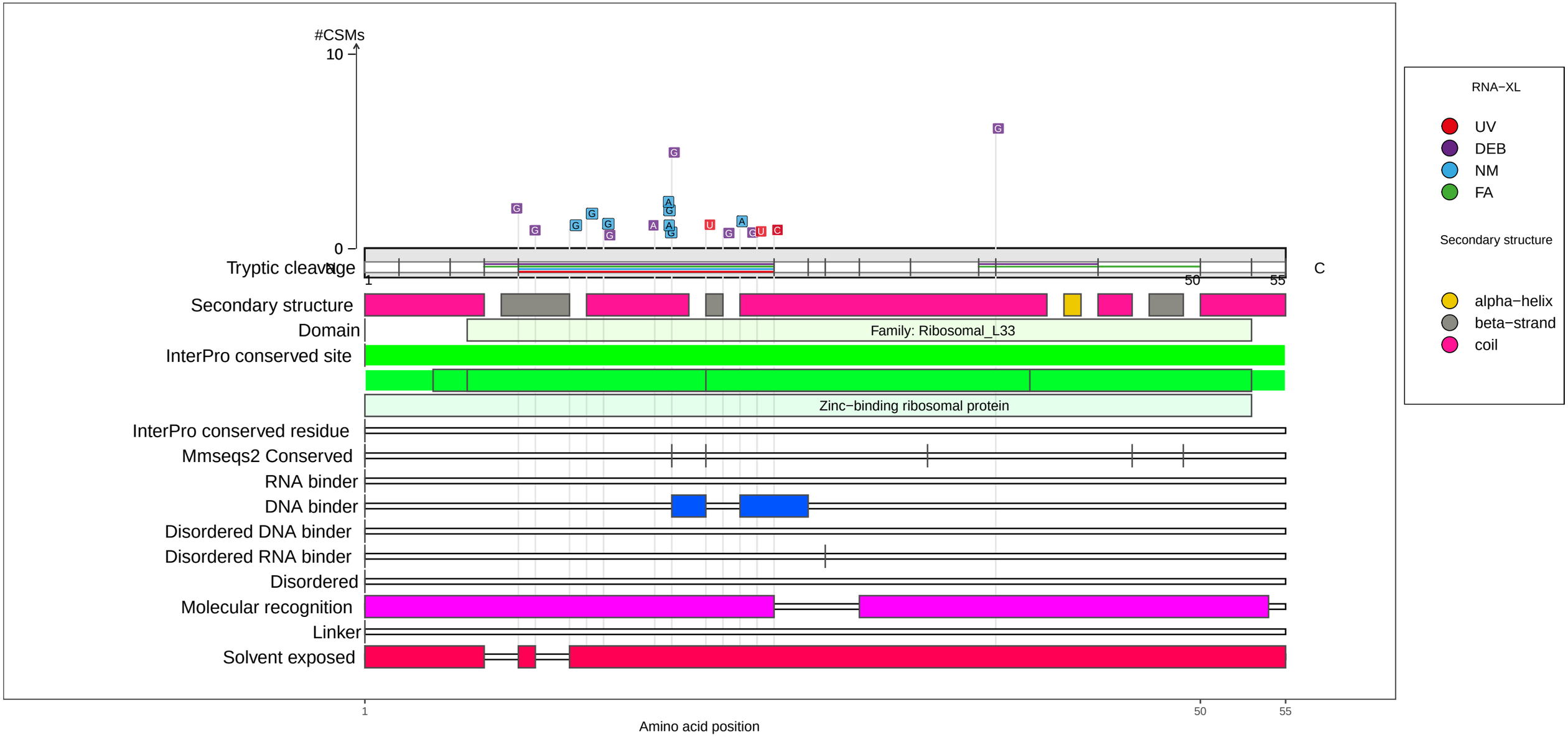
− RNA functions: not annotated



P0A7N9
RL33_ECOLI 50S ribosomal protein L33

− Abundance:
tryptic [log10 Intensity]: 10.61 (Q 100)
PAXdb K12 strain [ppm]: 3.75 (Q 99)
PAXdb E.coli [ppm]: 3.2 (Q 96)

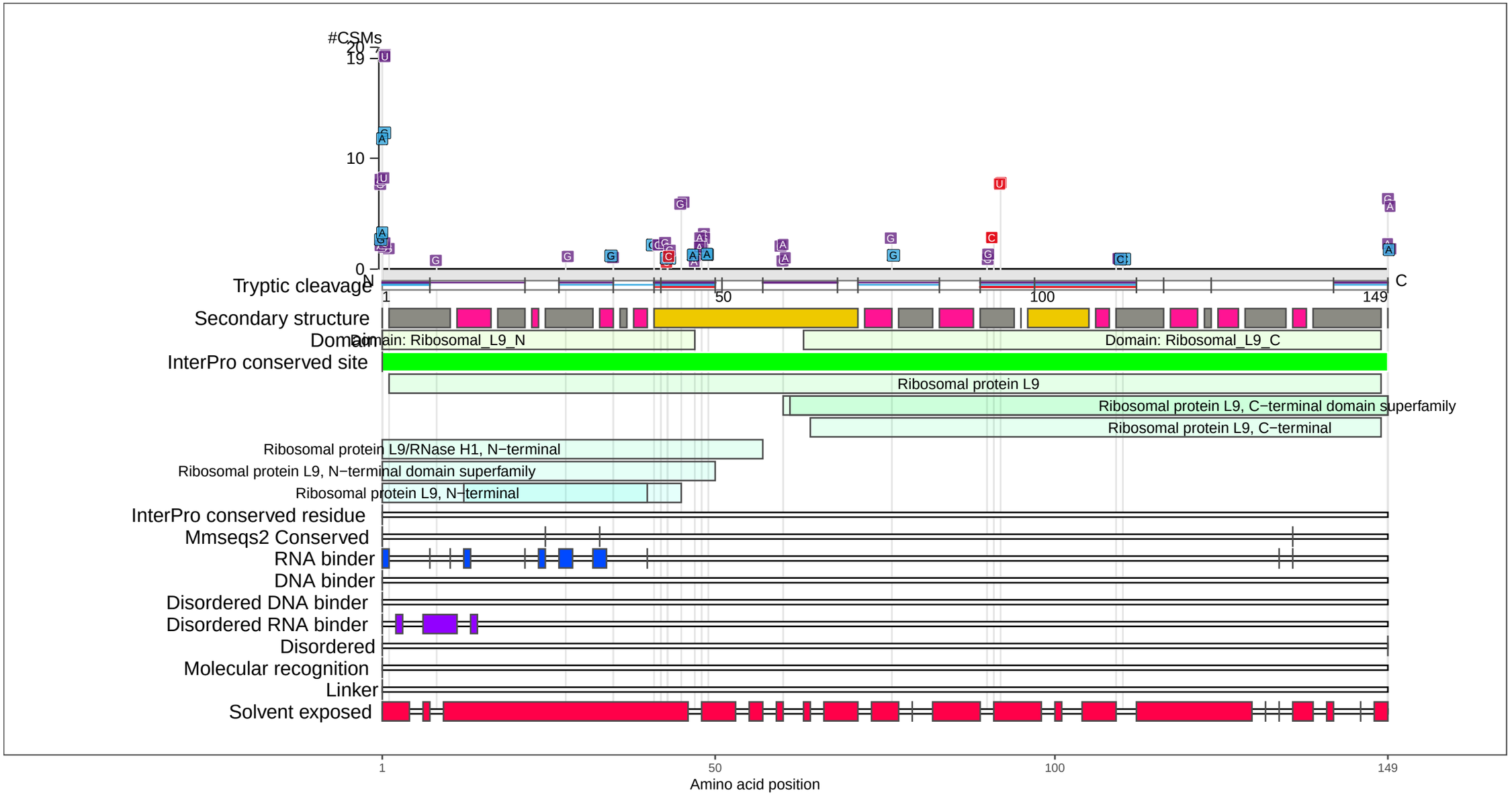
− RNA functions:
RNA binding; tRNA binding

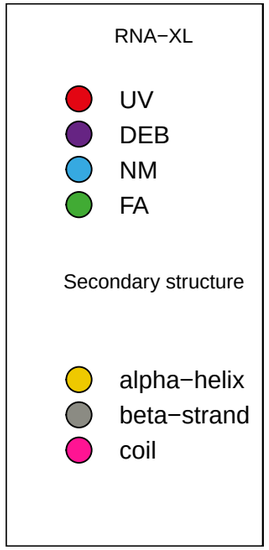


P0A7R1
RL9_ECOLI 50S ribosomal protein L9

− Abundance:
tryptic [log10 Intensity]: 9.46 (Q 96)
PAXdb K12 strain [ppm]: 3.61 (Q 98)
PAXdb E.coli [ppm]: 3.51 (Q 99)

− RNA functions:
RNA binding; rRNA binding

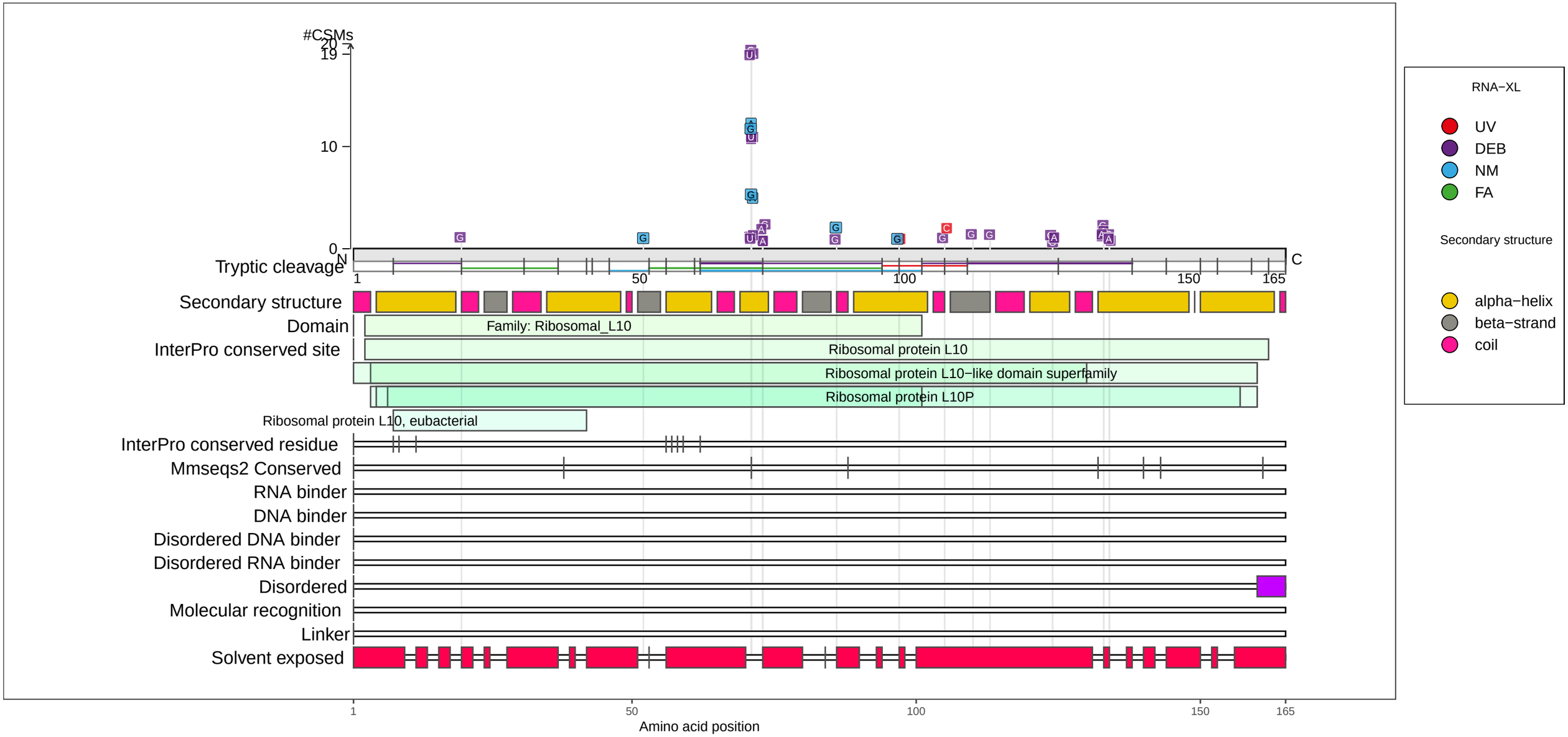




P0A7J3
RL10_ECOLI 50S ribosomal protein L10

− Abundance:
tryptic [log10 Intensity]: 9.09 (Q 90)
PAXdb K12 strain [ppm]: 3.58 (Q 98)
PAXdb E.coli [ppm]: 3.44 (Q 98)

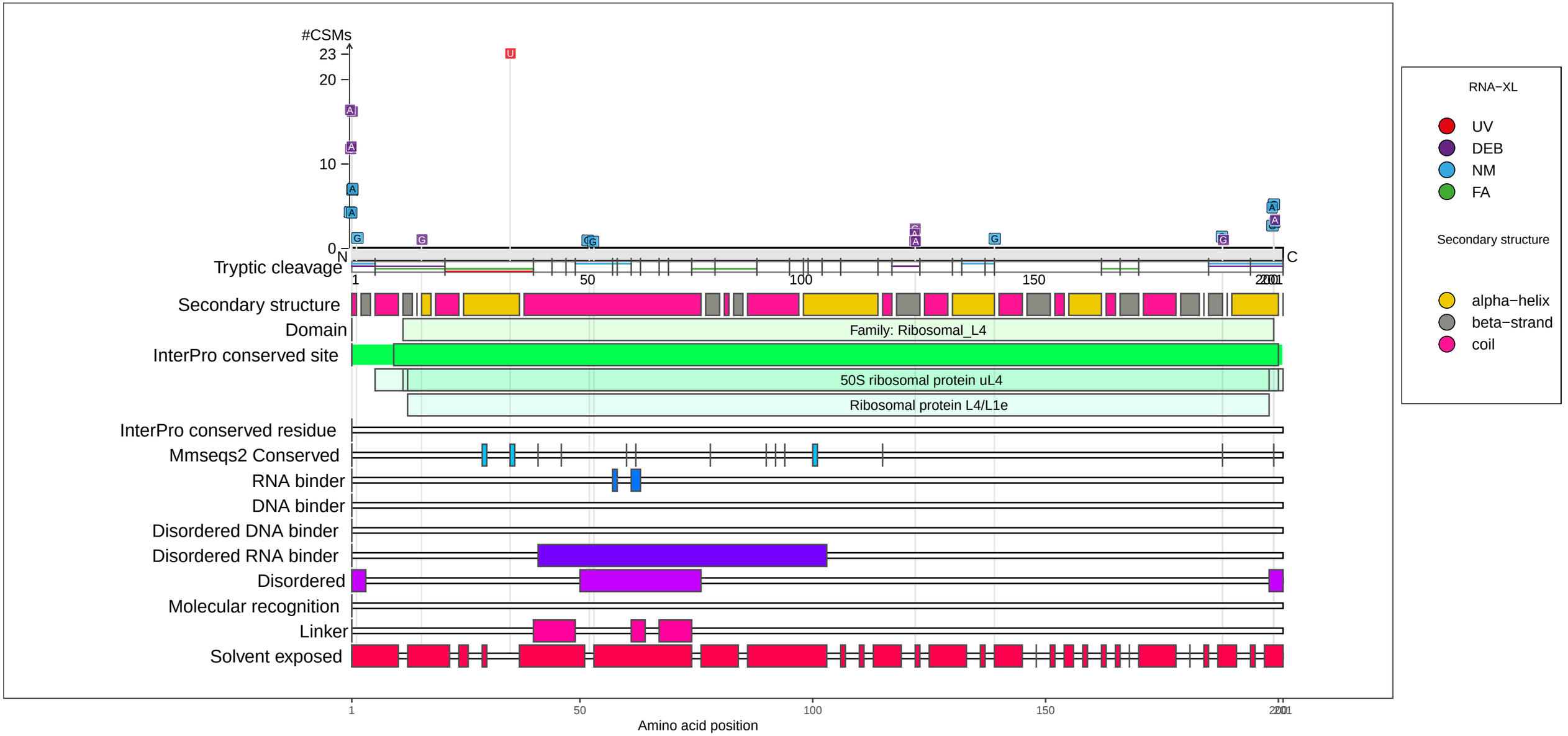
− RNA functions:
RNA binding; rRNA binding



P60723
RL4_ECOLI 50S ribosomal protein L4

− Abundance:
tryptic [log10 Intensity]: 9.3 (Q 94)
PAXdb K12 strain [ppm]: 3.44 (Q 97)
PAXdb E.coli [ppm]: 3.32 (Q 98)

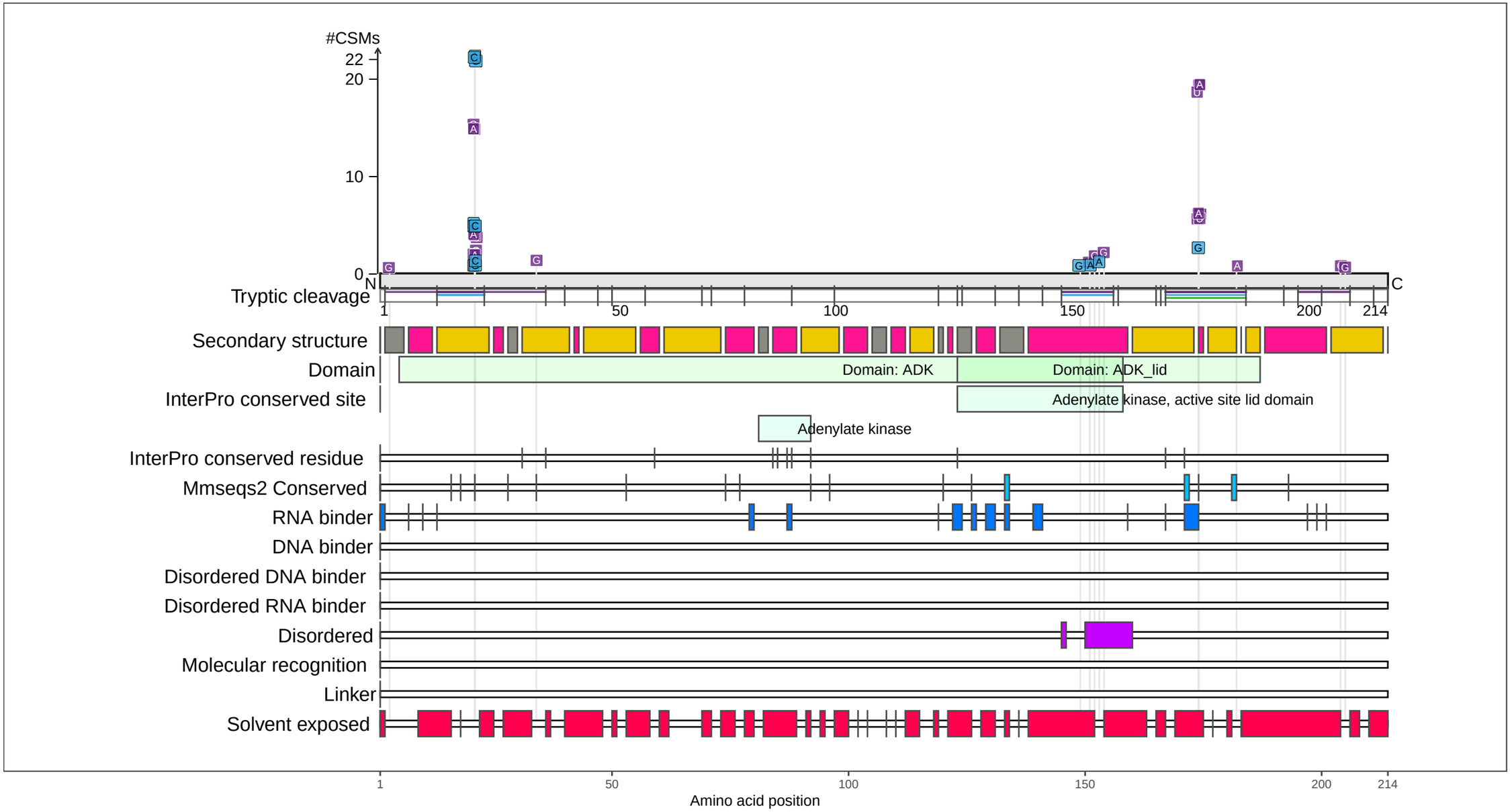
− RNA functions:
RNA binding; RNA biosynthetic process; RNA metabolic process; rRNA binding



P69441
KAD_ECOLI Adenylate kinase

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 90)
PAXdb K12 strain [ppm]: 3.7 (Q 99)
PAXdb E.coli [ppm]: 3.41 (Q 98)

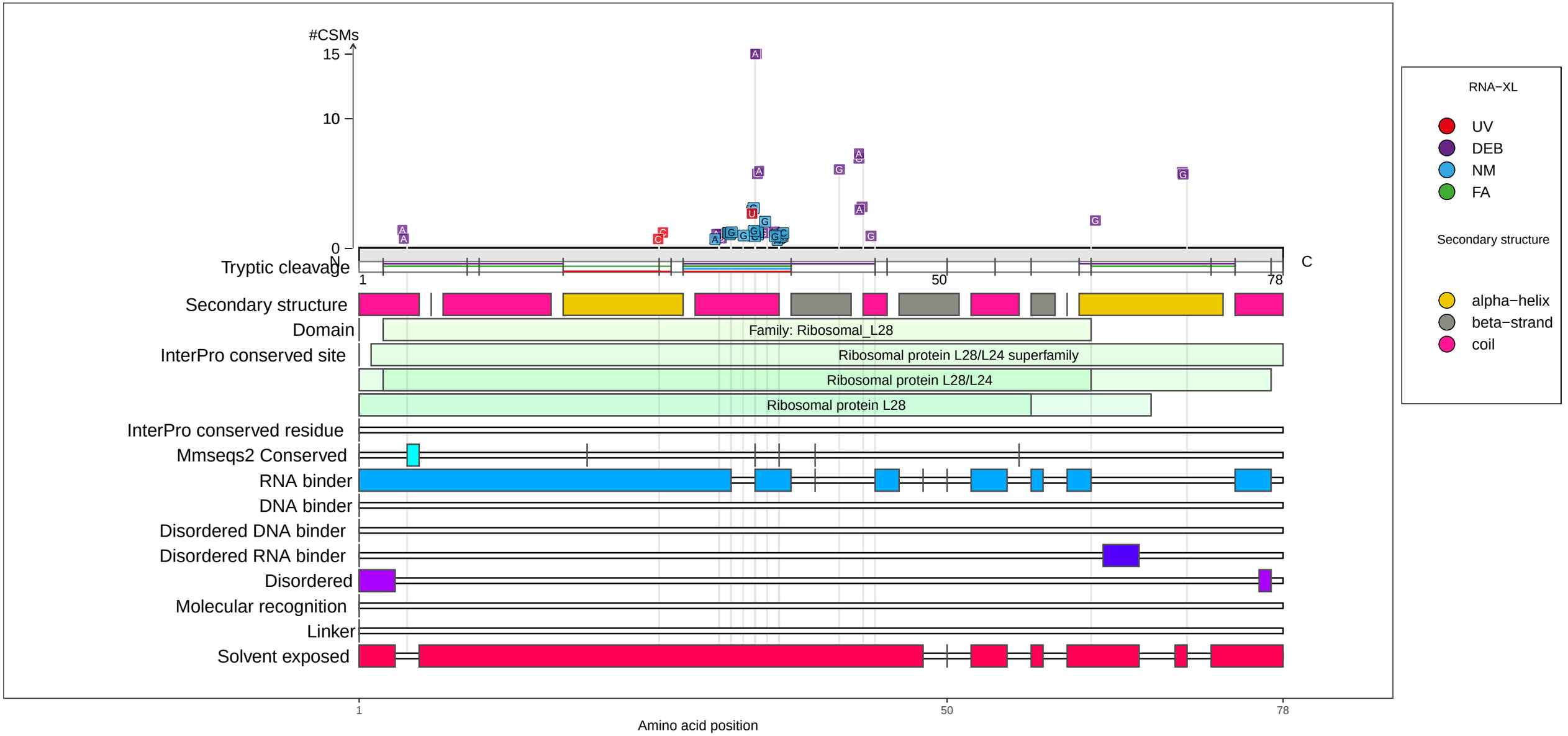
− RNA functions: not annotated



P0A7M2
RL28_ECOLI 50S ribosomal protein L28

− Abundance:
tryptic [log10 Intensity]: 8.99 (Q 88)
PAXdb K12 strain [ppm]: 3.71 (Q 99)
PAXdb E.coli [ppm]: 3.5 (Q 99)

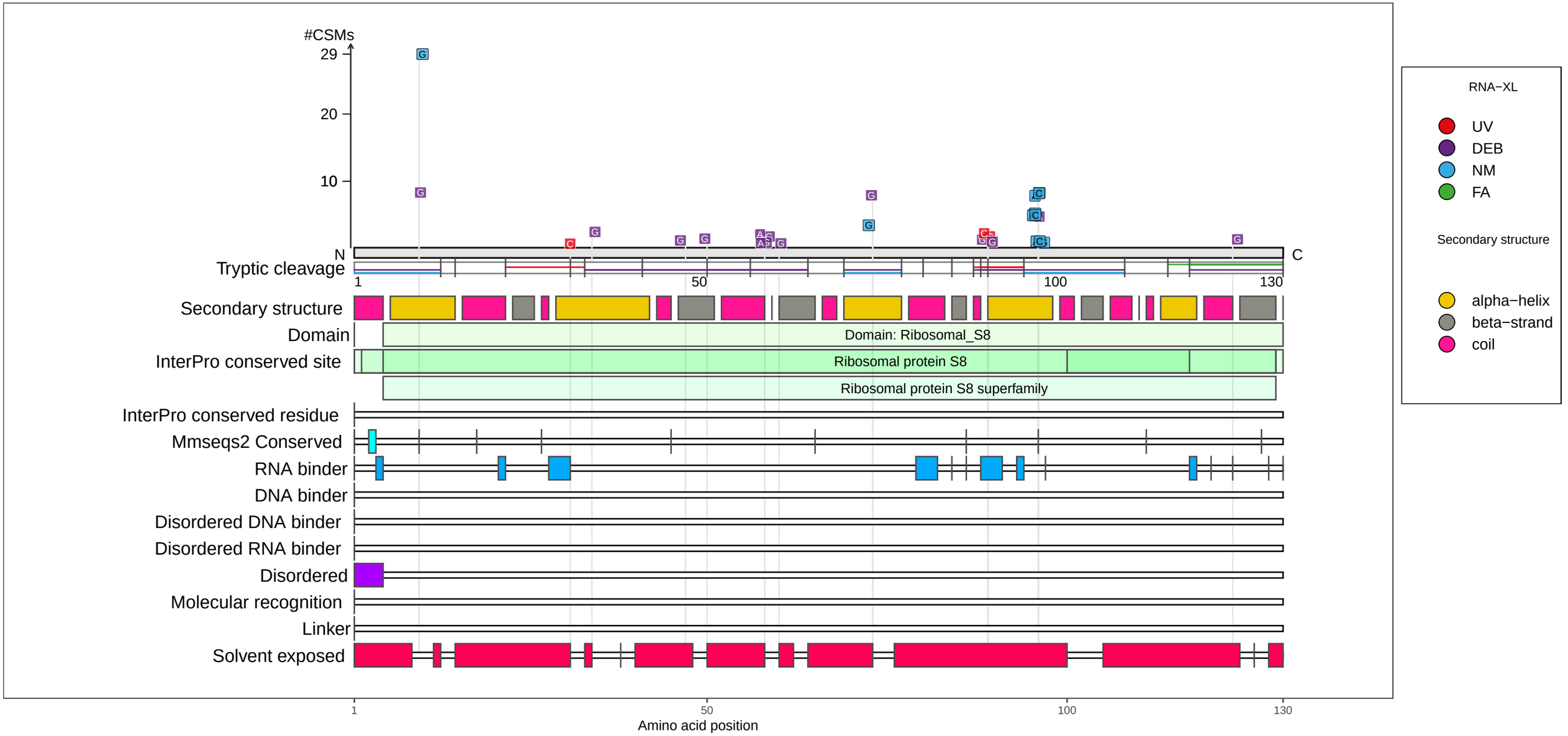
− RNA functions:
RNA binding; rRNA binding



P0A7W7
RS8_ECOLI 30S ribosomal protein S8

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 3.34 (Q 96)
PAXdb E.coli [ppm]: 3.31 (Q 97)

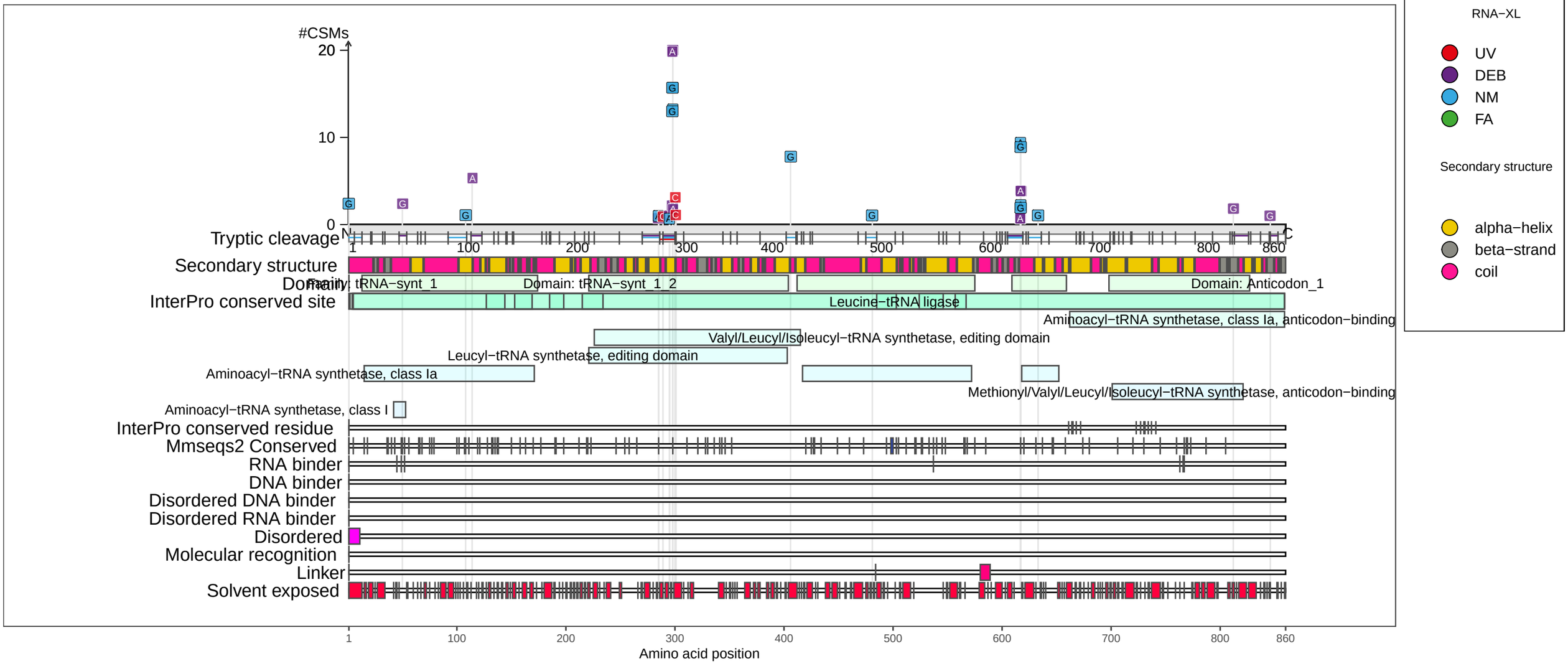
− RNA functions:
RNA binding; rRNA binding



P07813
SYL_ECOLI Leucine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.26 (Q 93)
PAXdb K12 strain [ppm]: 2.91 (Q 89)
PAXdb E.coli [ppm]: 2.79 (Q 92)

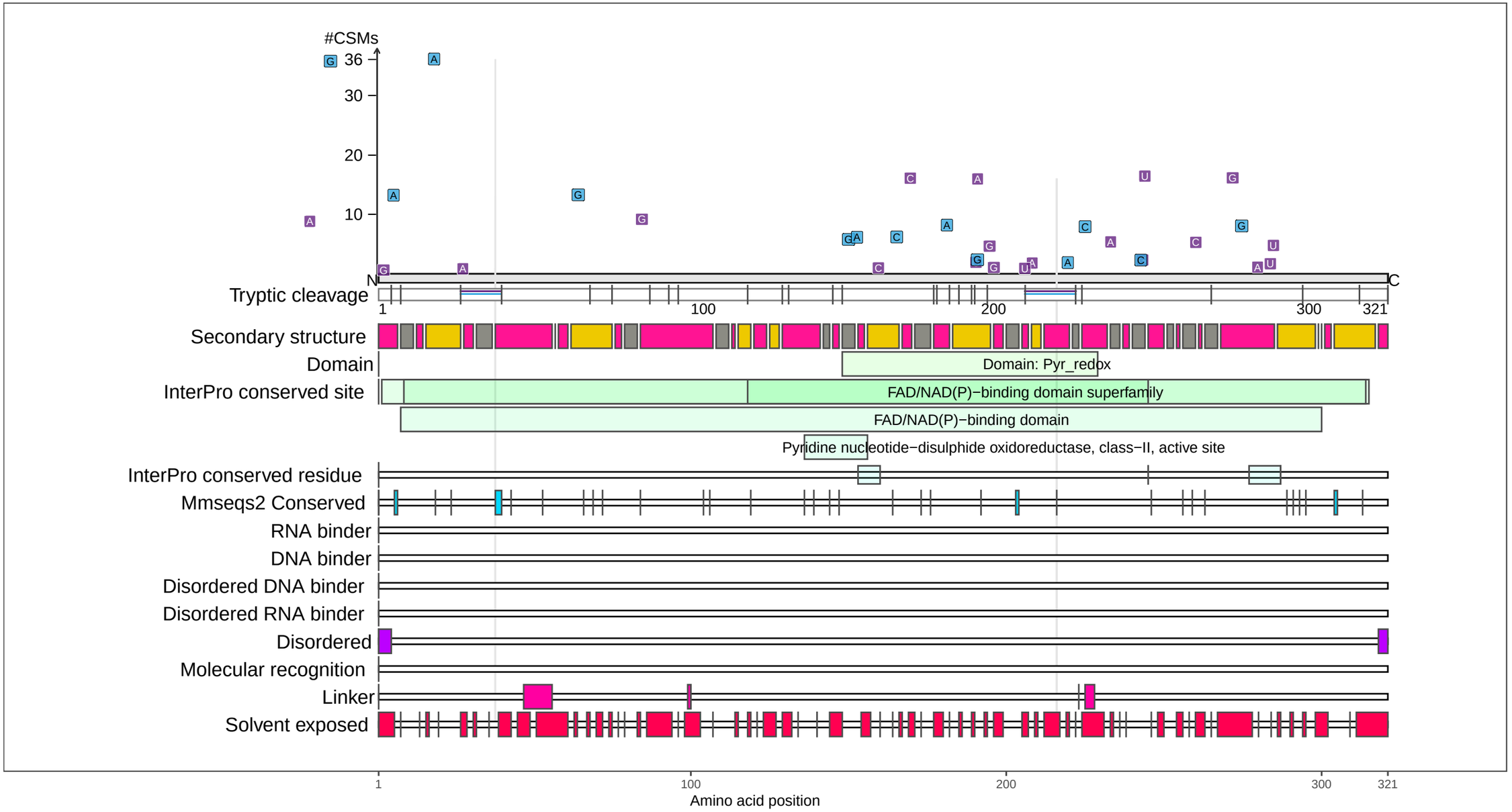
− RNA functions:
aminoacyl−tRNA editing activity; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; Anticodon−binding domain of tRNA
leucine−tRNA ligase activity; leucyl−tRNA aminoacylation; Leucyl−tRNA synthetase, Domain 2
ncRNA metabolic process; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetases class I (I, L, M and V); tRNA synthetases class I (M)



P0A9P4
TRXB_ECOLI Thioredoxin reductase

− Abundance:
tryptic [log10 Intensity]: 9.18 (Q 92)
PAXdb K12 strain [ppm]: 3.24 (Q 94)
PAXdb E.coli [ppm]: 2.62 (Q 88)

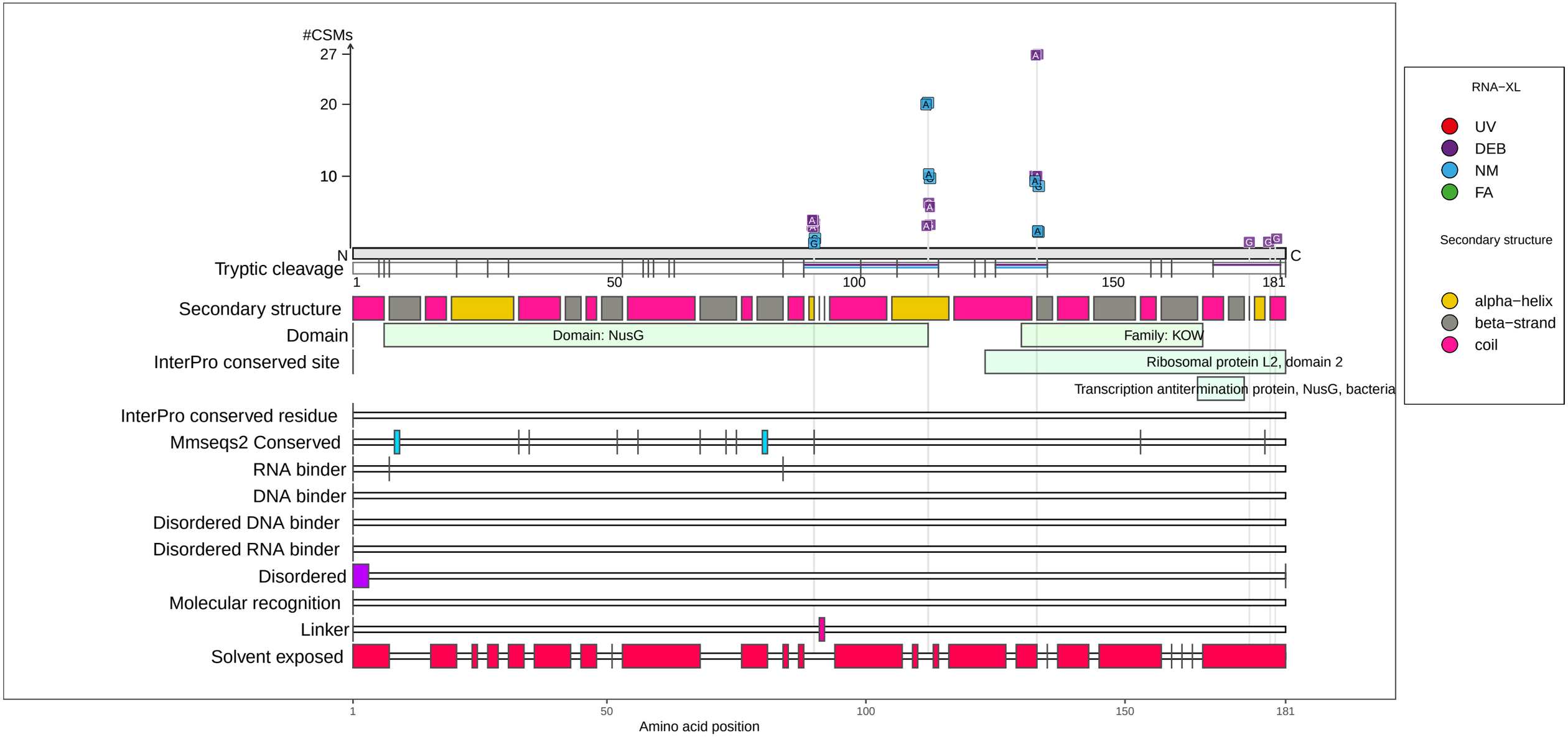
− RNA functions: not annotated



P0AFG0
NUSG_ECOLI Transcription termination/antitermination protein NusG

− Abundance:
tryptic [log10 Intensity]: 9.04 (Q 89)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 3.03 (Q 95)

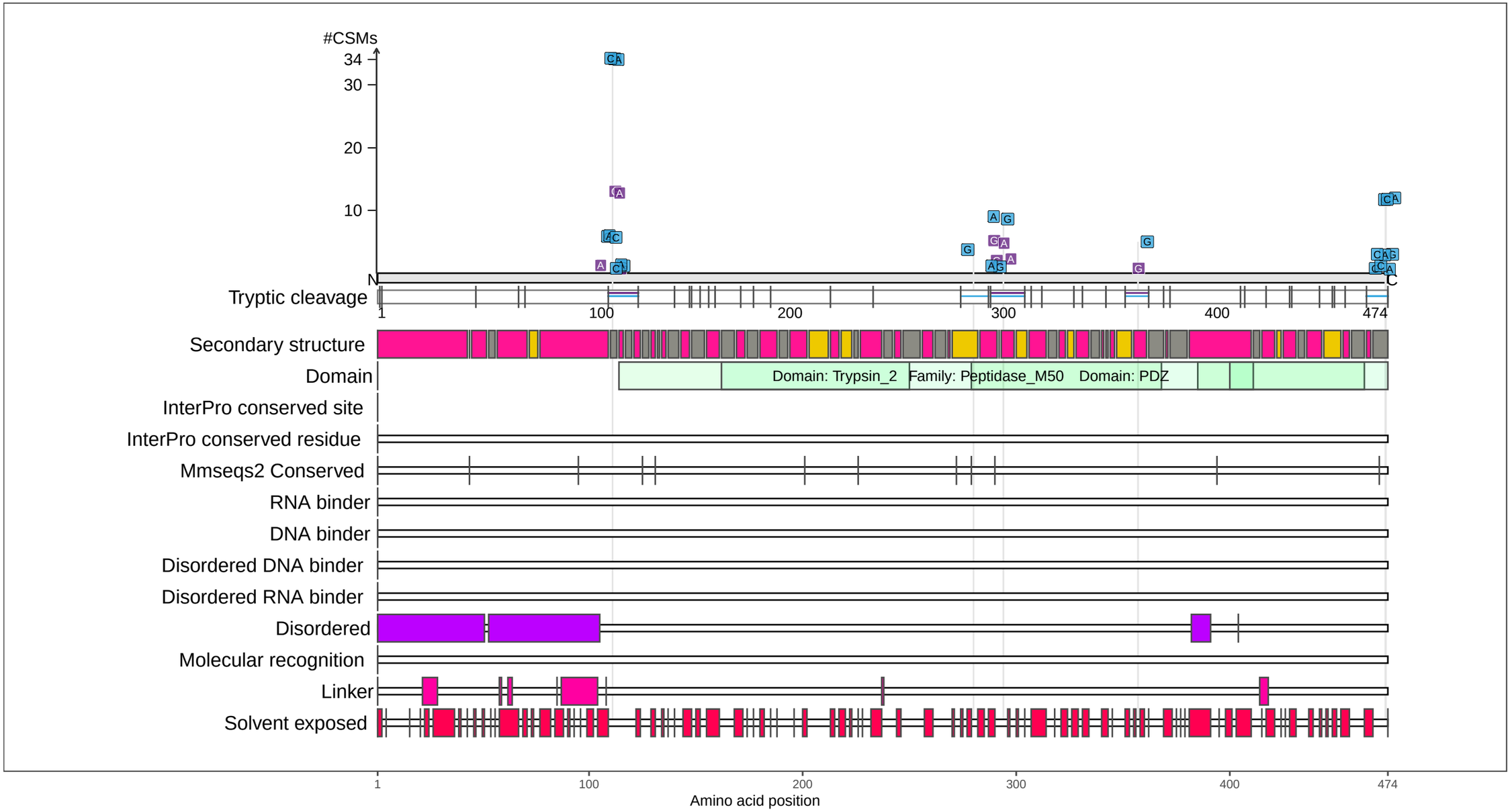
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0C0V0
DEGP_ECOLI Periplasmic serine endoprotease DegP

− Abundance:
tryptic [log10 Intensity]: 8.81 (Q 84)
PAXdb K12 strain [ppm]: 2.86 (Q 88)
PAXdb E.coli [ppm]: 2.77 (Q 91)

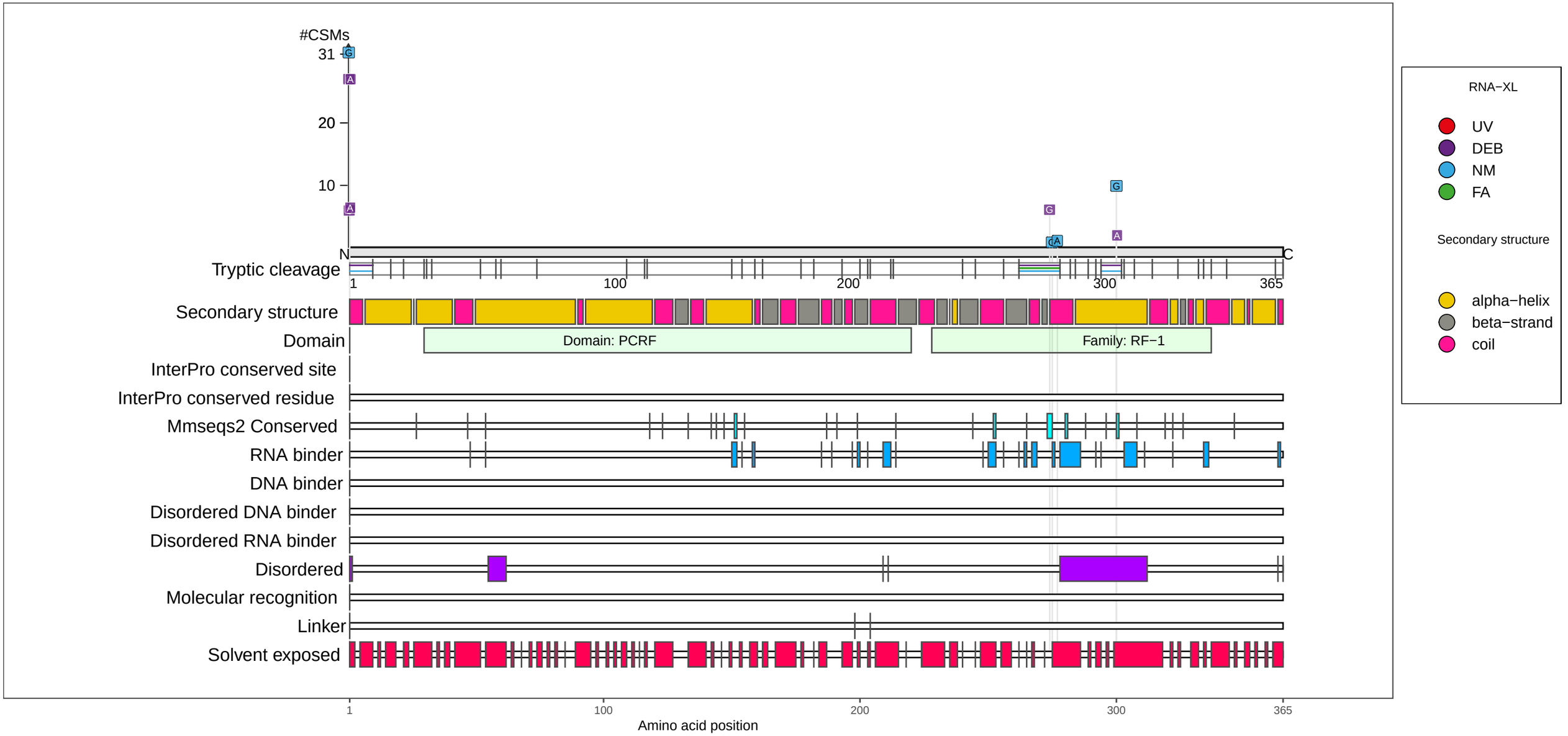
− RNA functions: not annotated



P07012
RF2_ECOLI Peptide chain release factor RF2

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 86)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 2.51 (Q 86)

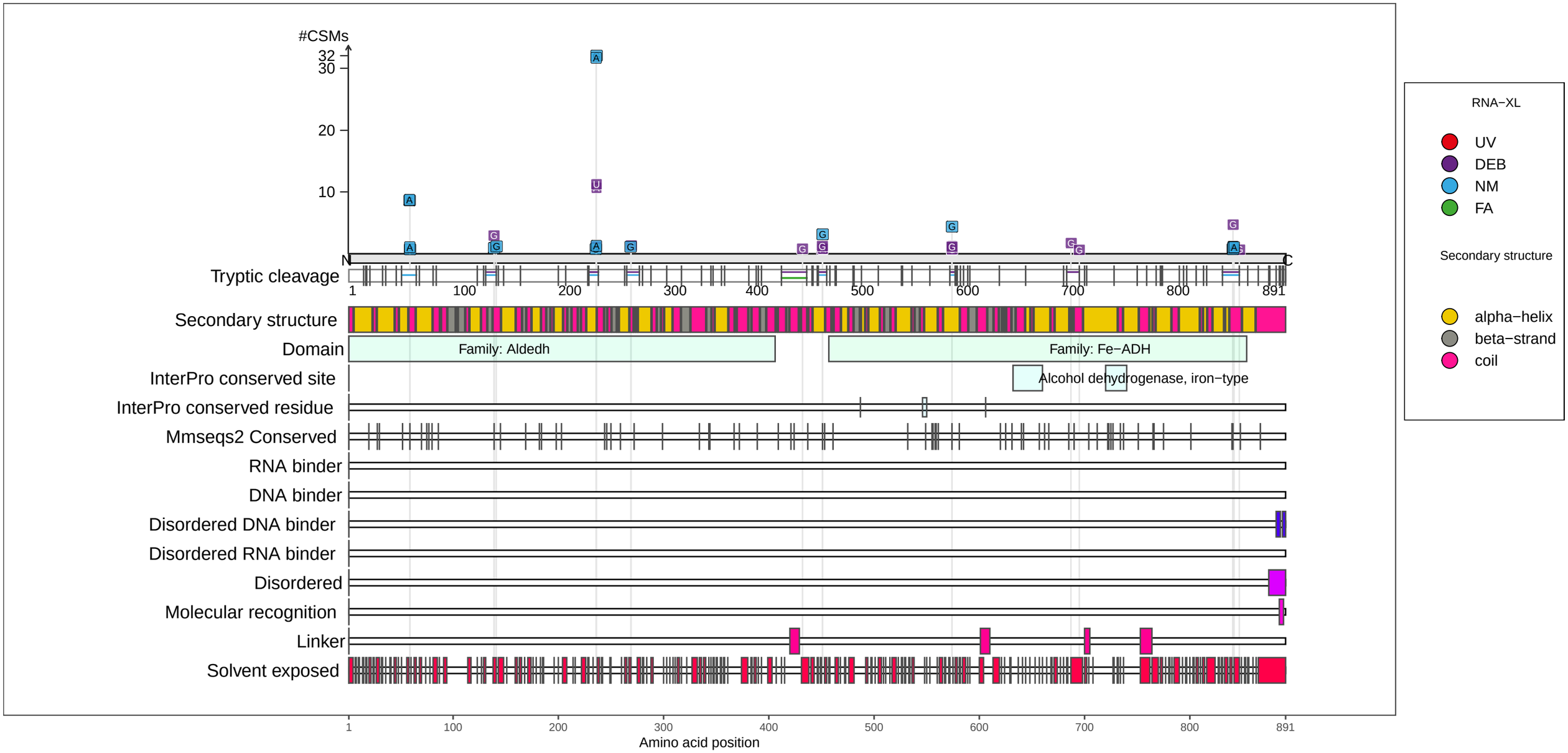
− RNA functions:
RNA binding



P0A9Q7
ADHE_ECOLI Aldehyde−alcohol dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 3.05 (Q 91)
PAXdb E.coli [ppm]: 3.22 (Q 97)

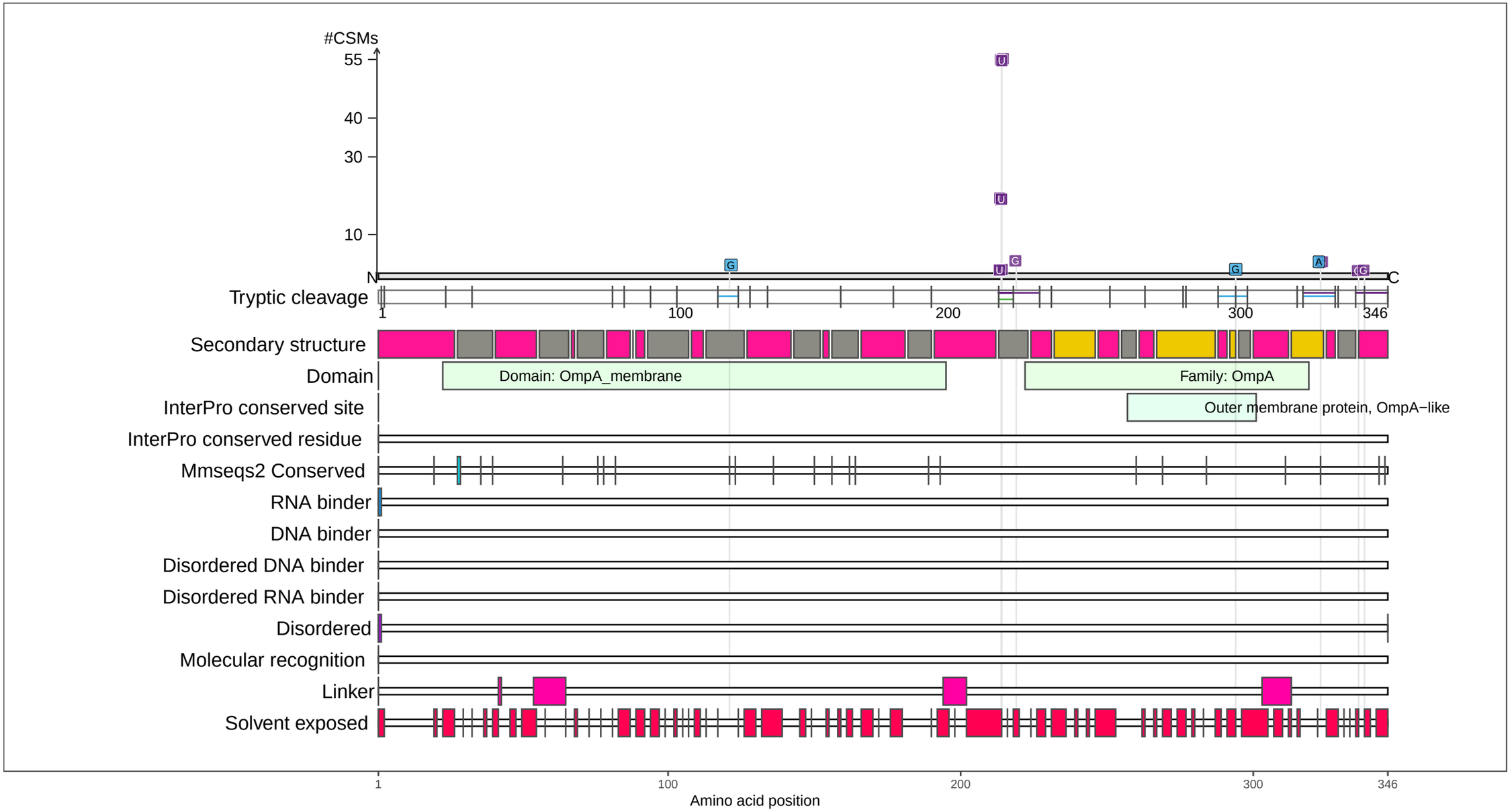
− RNA functions: not annotated



P0A910
OMPA_ECOLI Outer membrane protein A

− Abundance:
tryptic [log10 Intensity]: 10.15 (Q 100)
PAXdb K12 strain [ppm]: 3.17 (Q 94)
PAXdb E.coli [ppm]: 3.55 (Q 99)

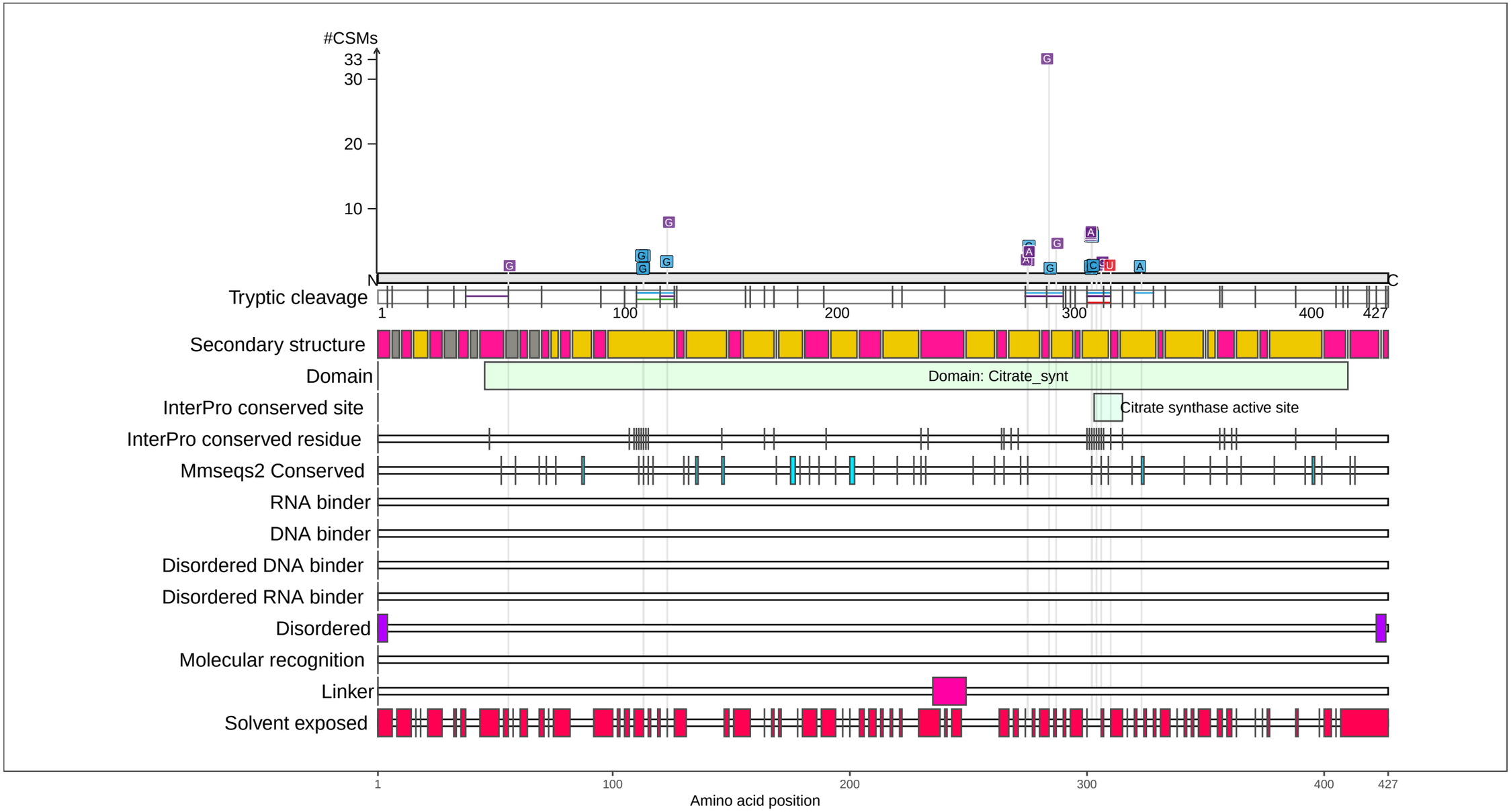
− RNA functions: not annotated



P0ABH7
CISY_ECOLI Citrate synthase

− Abundance:
tryptic [log10 Intensity]: 9.52 (Q 97)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 3.03 (Q 95)

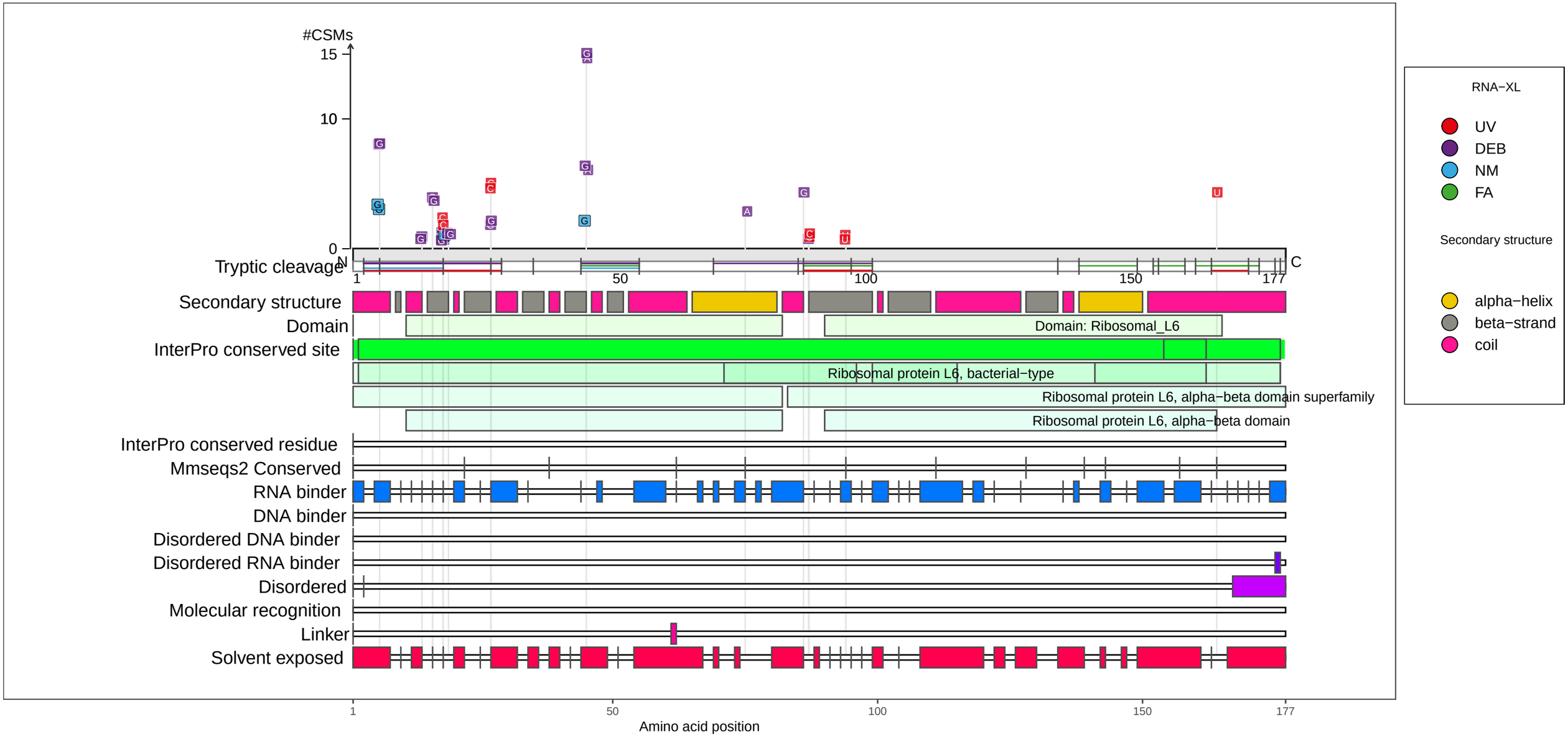
− RNA functions: not annotated



P0AG55
RL6_ECOLI 50S ribosomal protein L6

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 3.67 (Q 99)
PAXdb E.coli [ppm]: 3.43 (Q 98)

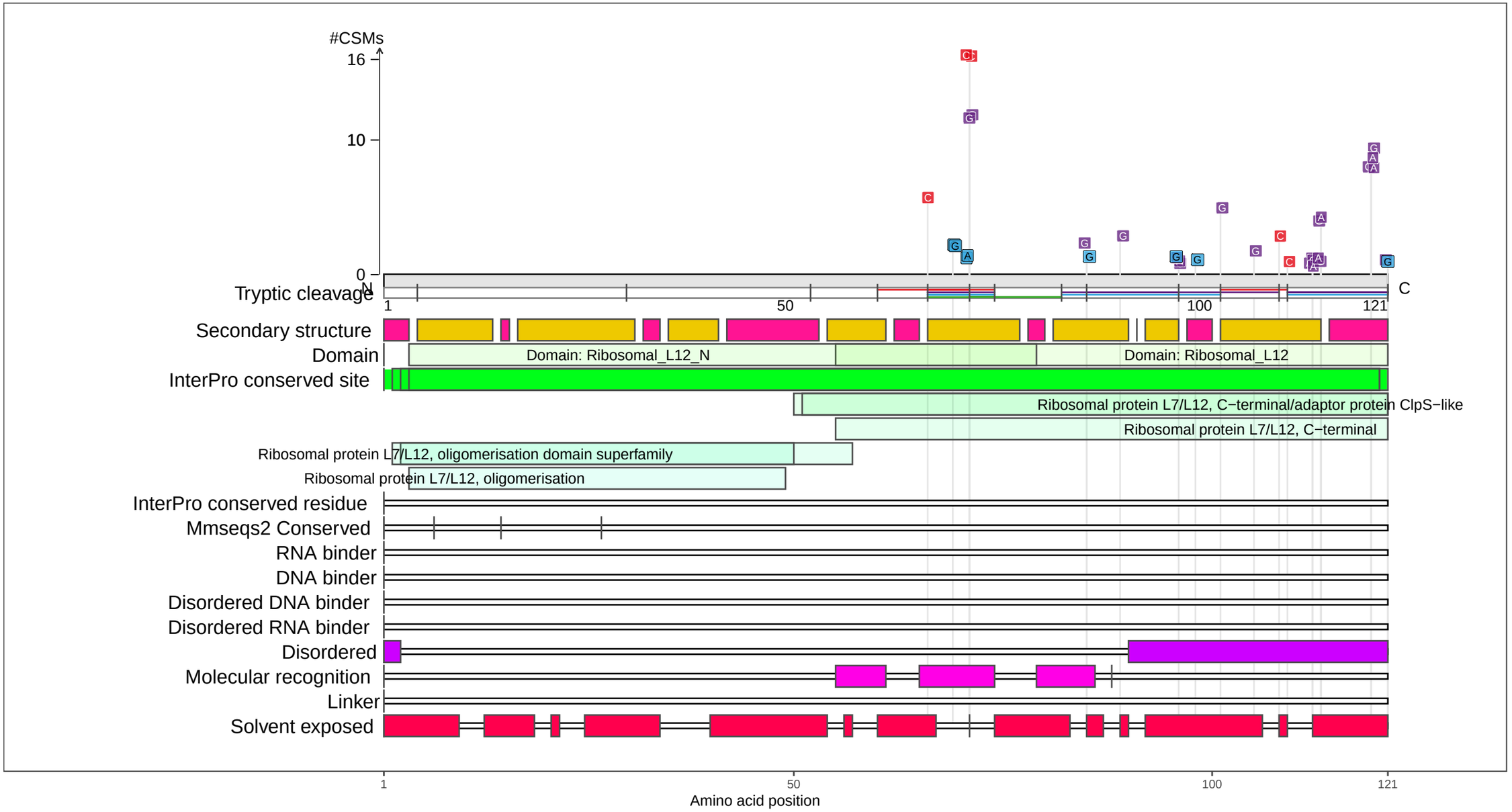
− RNA functions:
RNA binding; rRNA binding



P0A7K2
RL7_ECOLI 50S ribosomal protein L7/L12

− Abundance:
tryptic [log10 Intensity]: 10.08 (Q 100)
PAXdb K12 strain [ppm]: 3.8 (Q 99)
PAXdb E.coli [ppm]: 3.86 (Q 100)

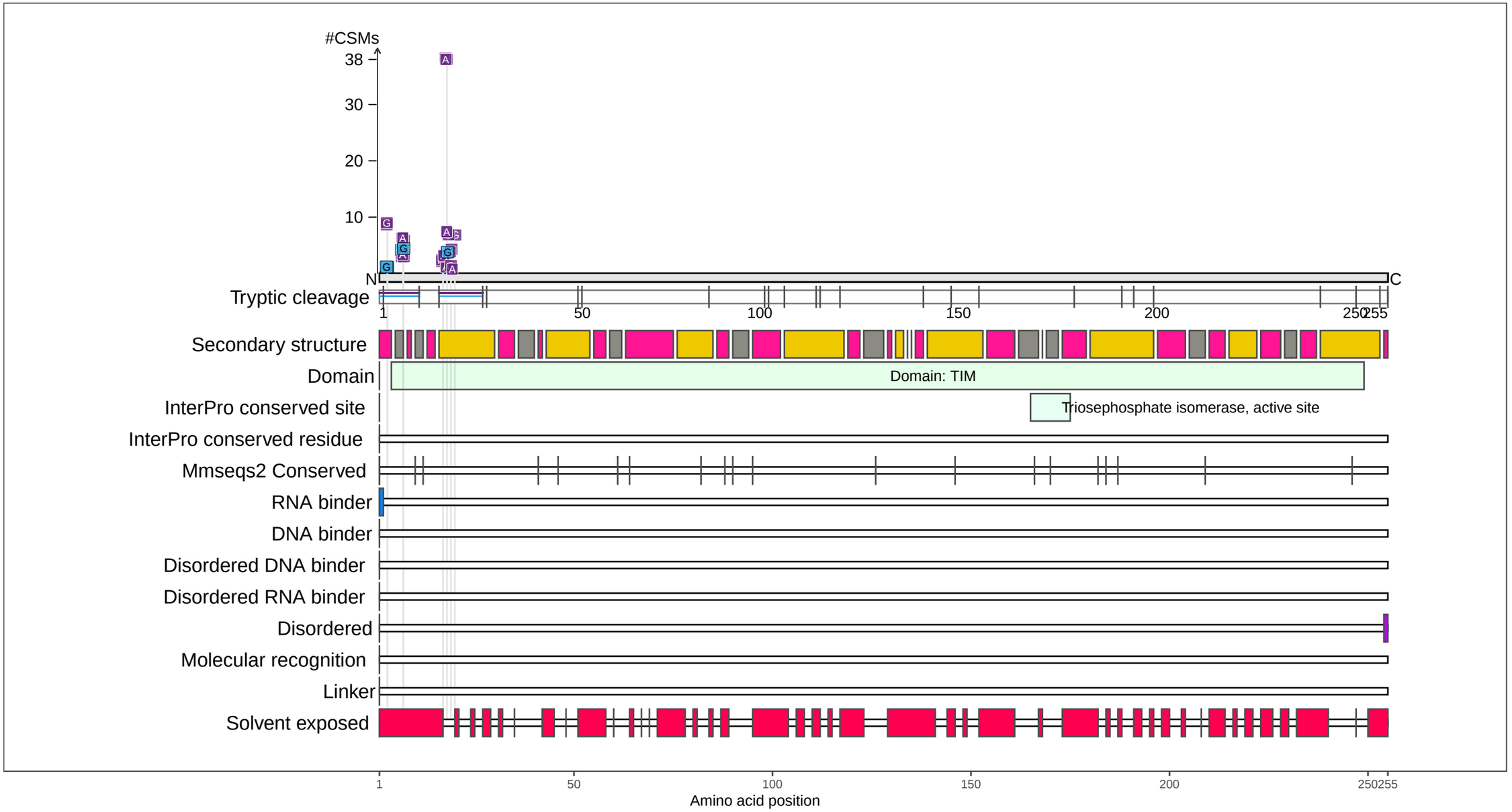
− RNA functions: not annotated



P0A858
TPIS_ECOLI Triosephosphate isomerase

− Abundance:
tryptic [log10 Intensity]: 10.02 (Q 99)
PAXdb K12 strain [ppm]: 2.58 (Q 80)
PAXdb E.coli [ppm]: 3.54 (Q 99)

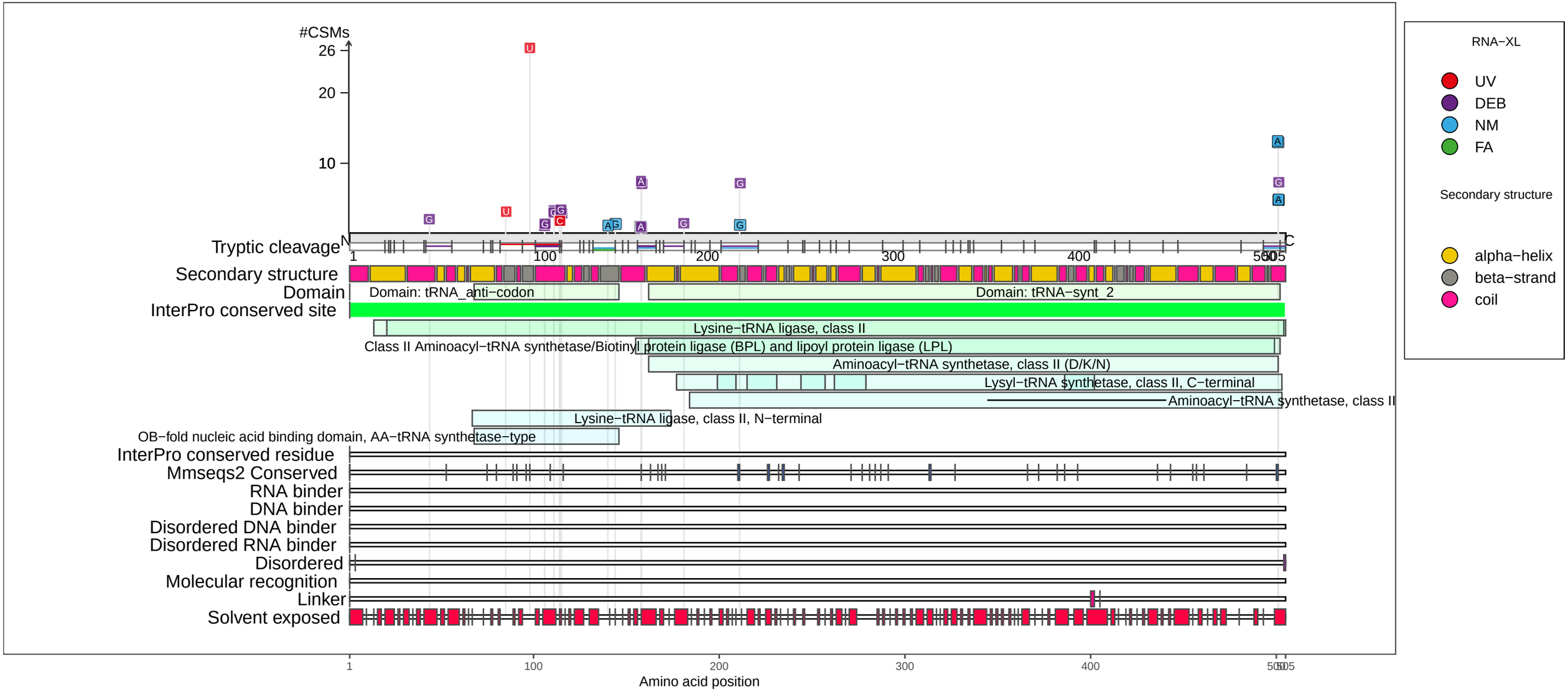
− RNA functions: not annotated



P0A8N3
SYK1_ECOLI Lysine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.64 (Q 97)
PAXdb K12 strain [ppm]: 3.15 (Q 93)
PAXdb E.coli [ppm]: 2.92 (Q 93)

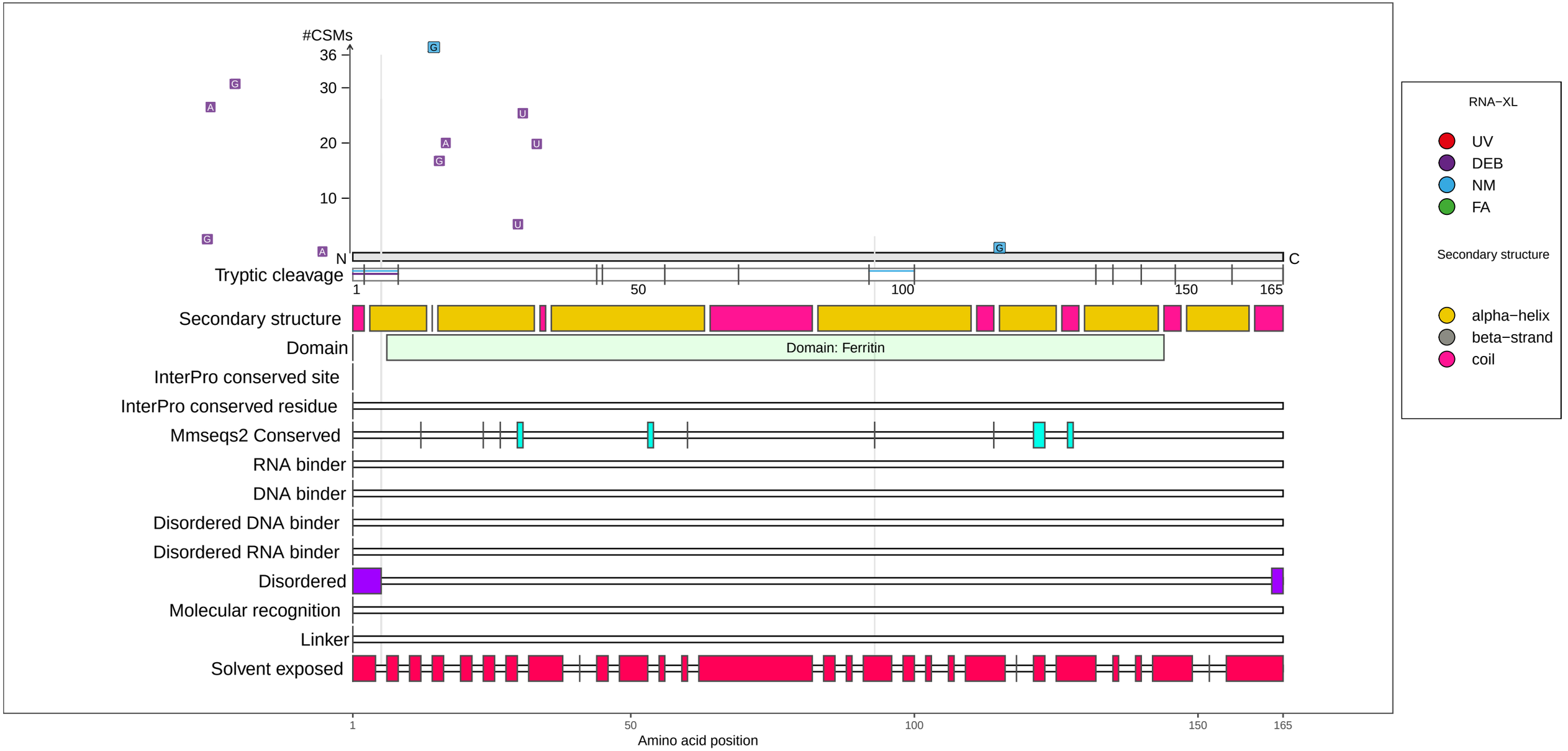
− RNA functions:
aminoacyl−tRNA ligase activity; lysine−tRNA ligase activity
lysyl−tRNA aminoacylation; ncRNA metabolic process; RNA binding; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA synthetases class II (D, K and N)



P0A998
FTNA_ECOLI Bacterial non−heme ferritin

− Abundance:
tryptic [log10 Intensity]: 9.36 (Q 95)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 2.83 (Q 92)

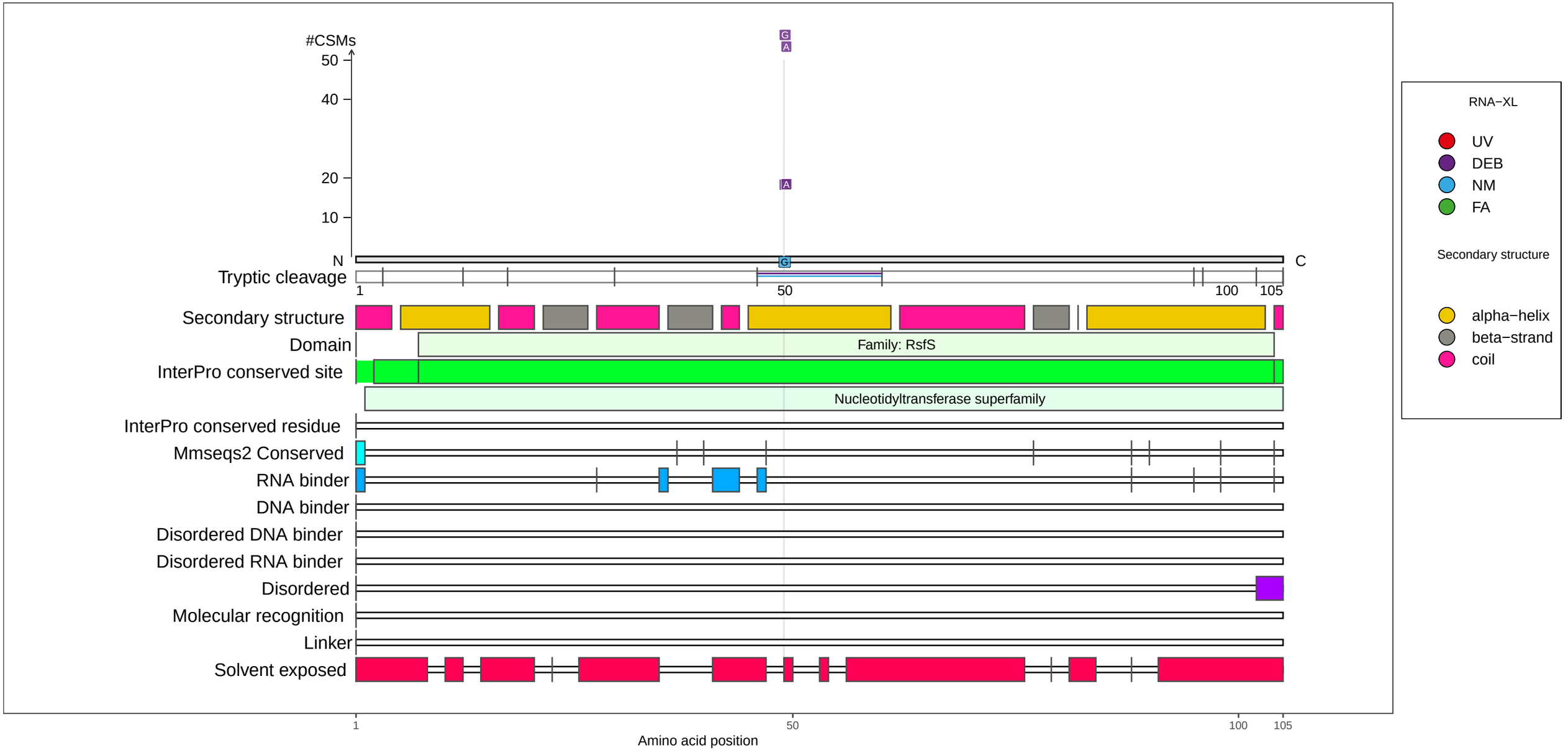
− RNA functions: not annotated



P0AAT6
IOJAP_ECOLI Ribosomal silencing factor RsfS

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 2.53 (Q 78)
PAXdb E.coli [ppm]: 2.36 (Q 82)

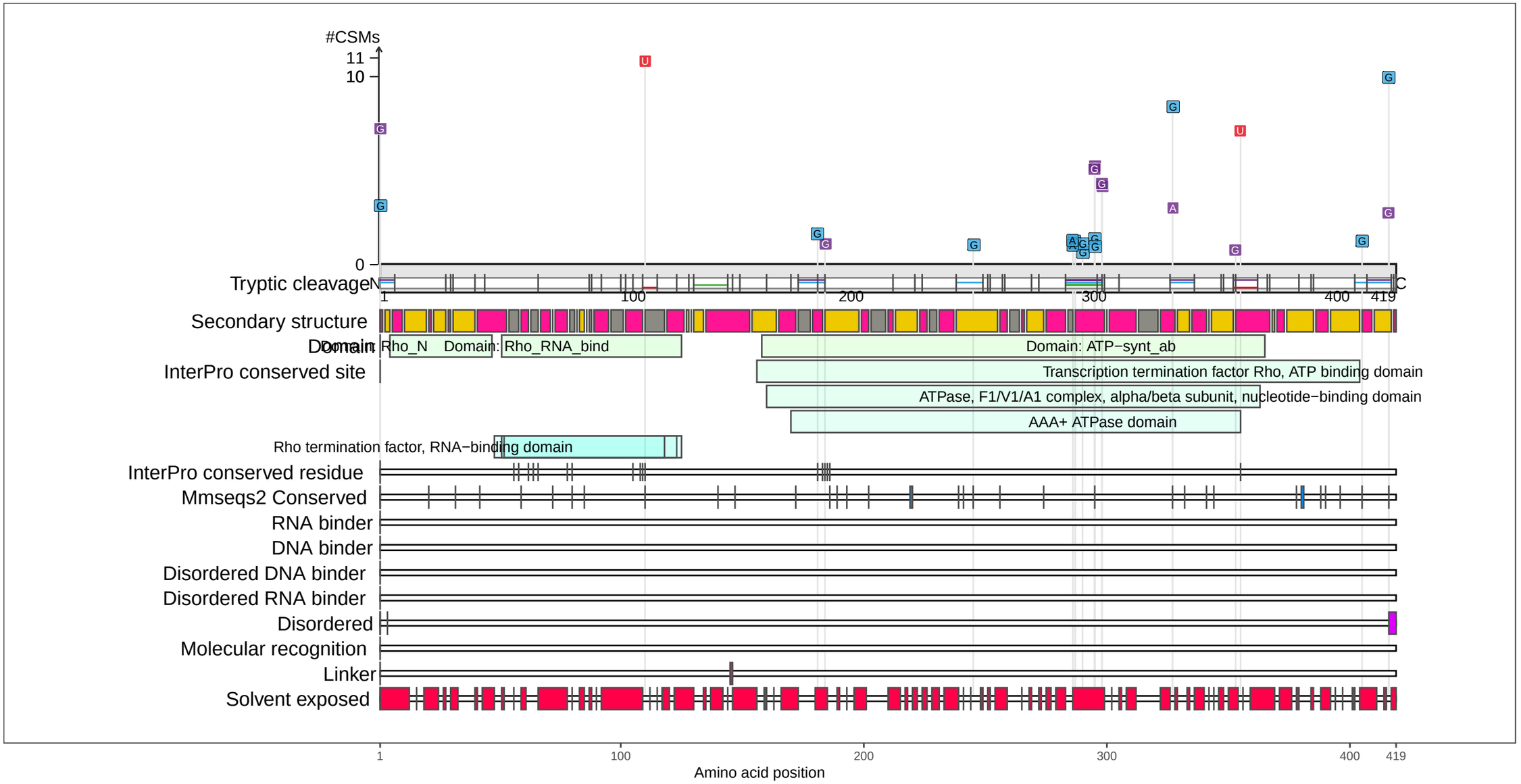
− RNA functions: not annotated

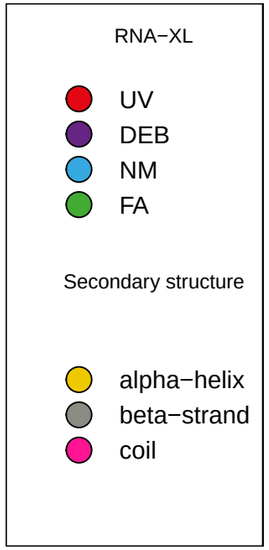


P0AG30
RHO_ECOLI Transcription termination factor Rho

− Abundance:
tryptic [log10 Intensity]: 8.54 (Q 77)
PAXdb K12 strain [ppm]: 3.4 (Q 96)
PAXdb E.coli [ppm]: 3.73 (Q 100)

− RNA functions:
Rho termination factor, RNA−binding domain; RNA binding; RNA biosynthetic process
RNA metabolic process; RNA−dependent ATPase activity

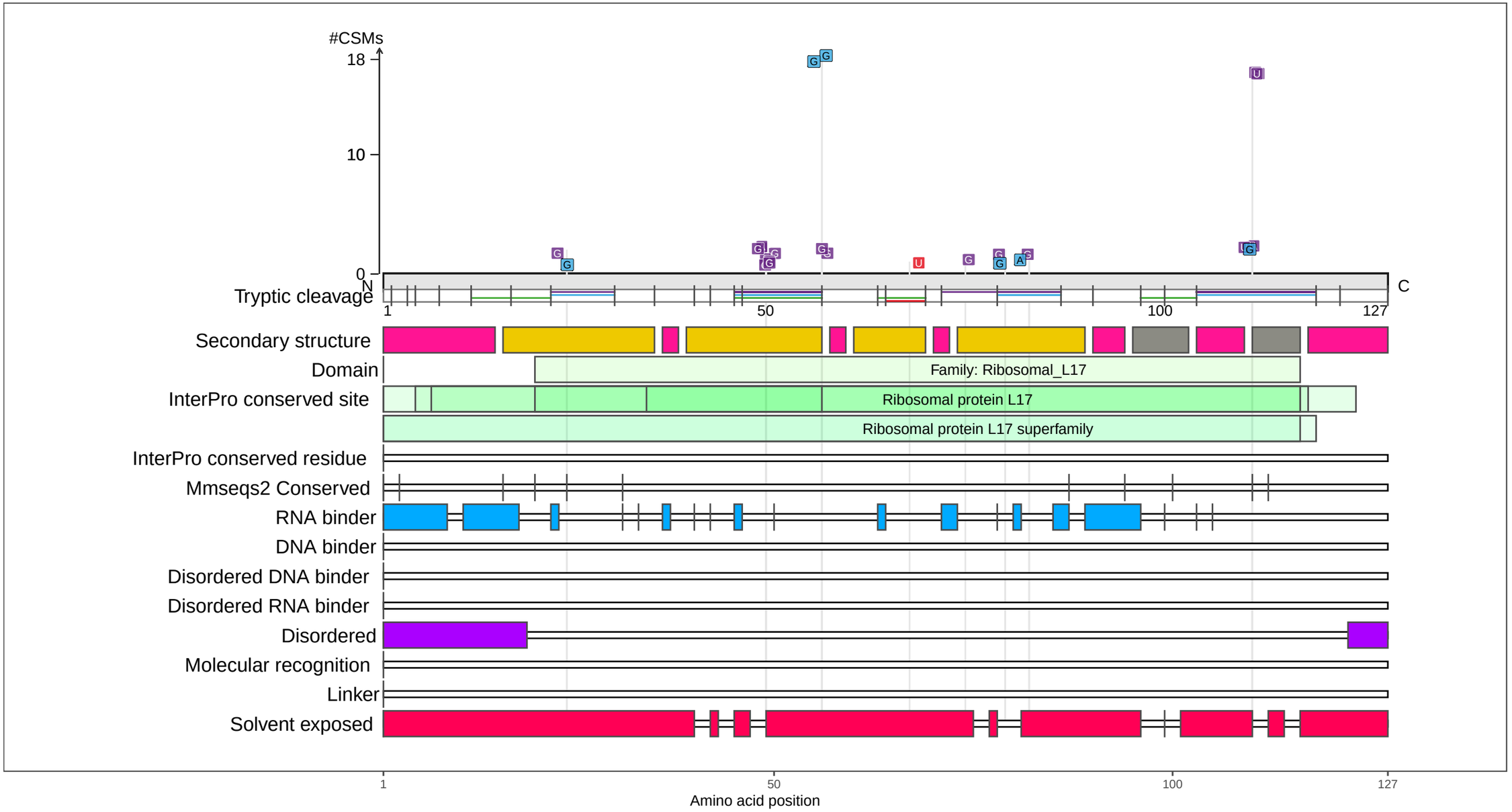


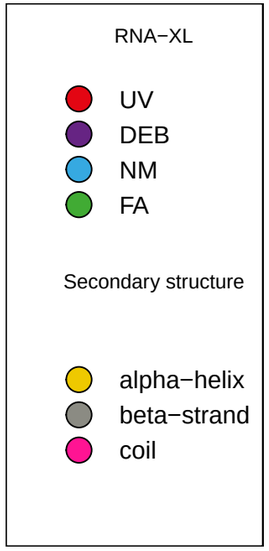


P0AG44
RL17_ECOLI 50S ribosomal protein L17

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: 3.85 (Q 100)
PAXdb E.coli [ppm]: 3.33 (Q 98)

− RNA functions: not annotated

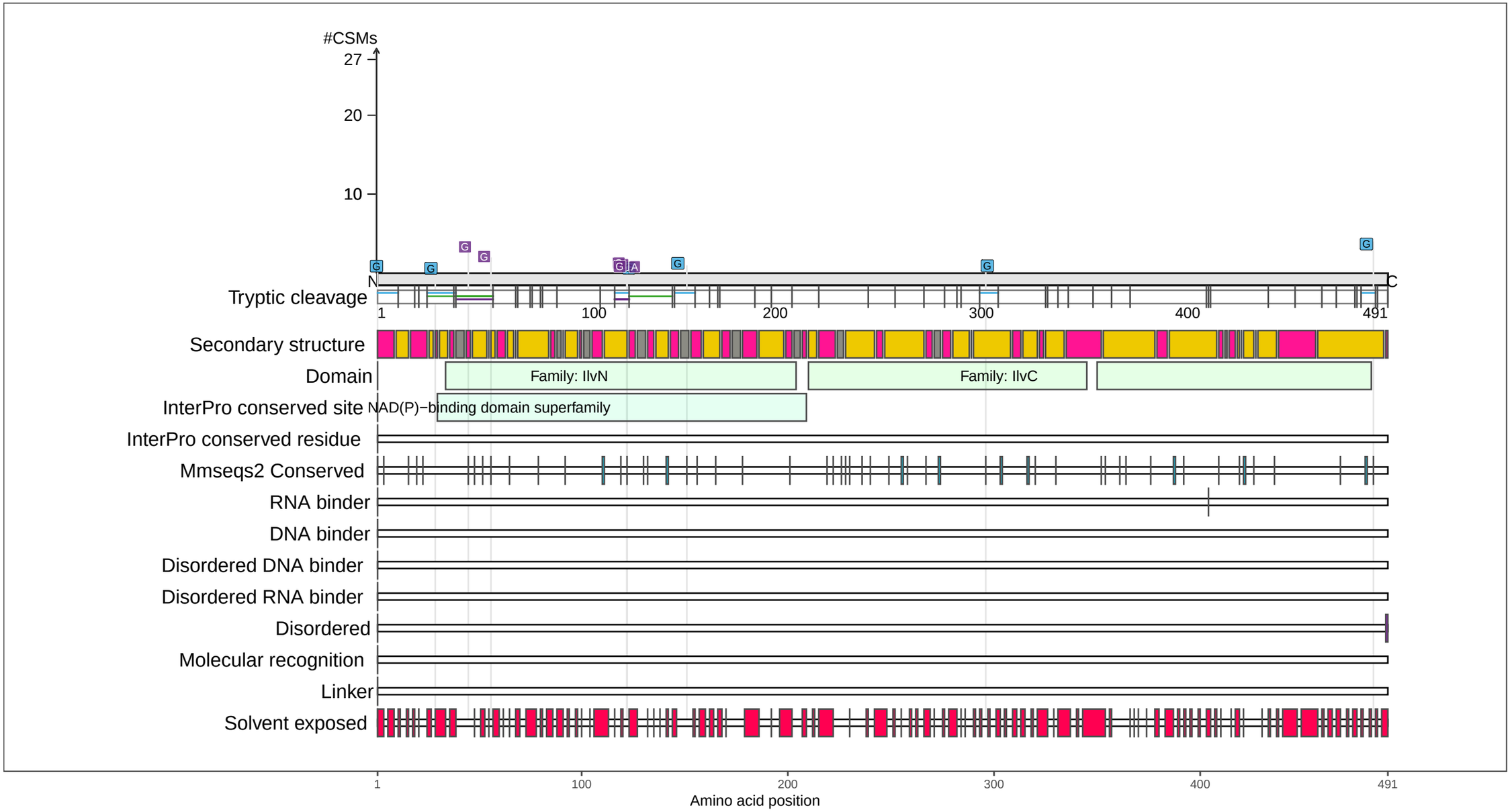


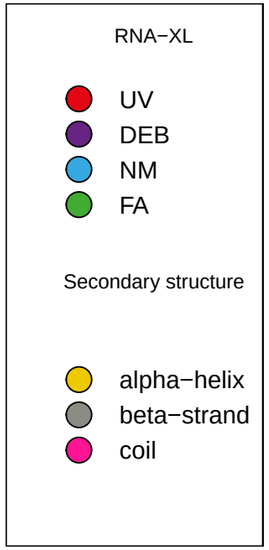


P05793
ILVC_ECOLI Ketol−acid reductoisomerase (NADP(+))

− Abundance:
tryptic [log10 Intensity]: 9.75 (Q 98)
PAXdb K12 strain [ppm]: 2.99 (Q 91)
PAXdb E.coli [ppm]: 3.28 (Q 97)

− RNA functions: not annotated

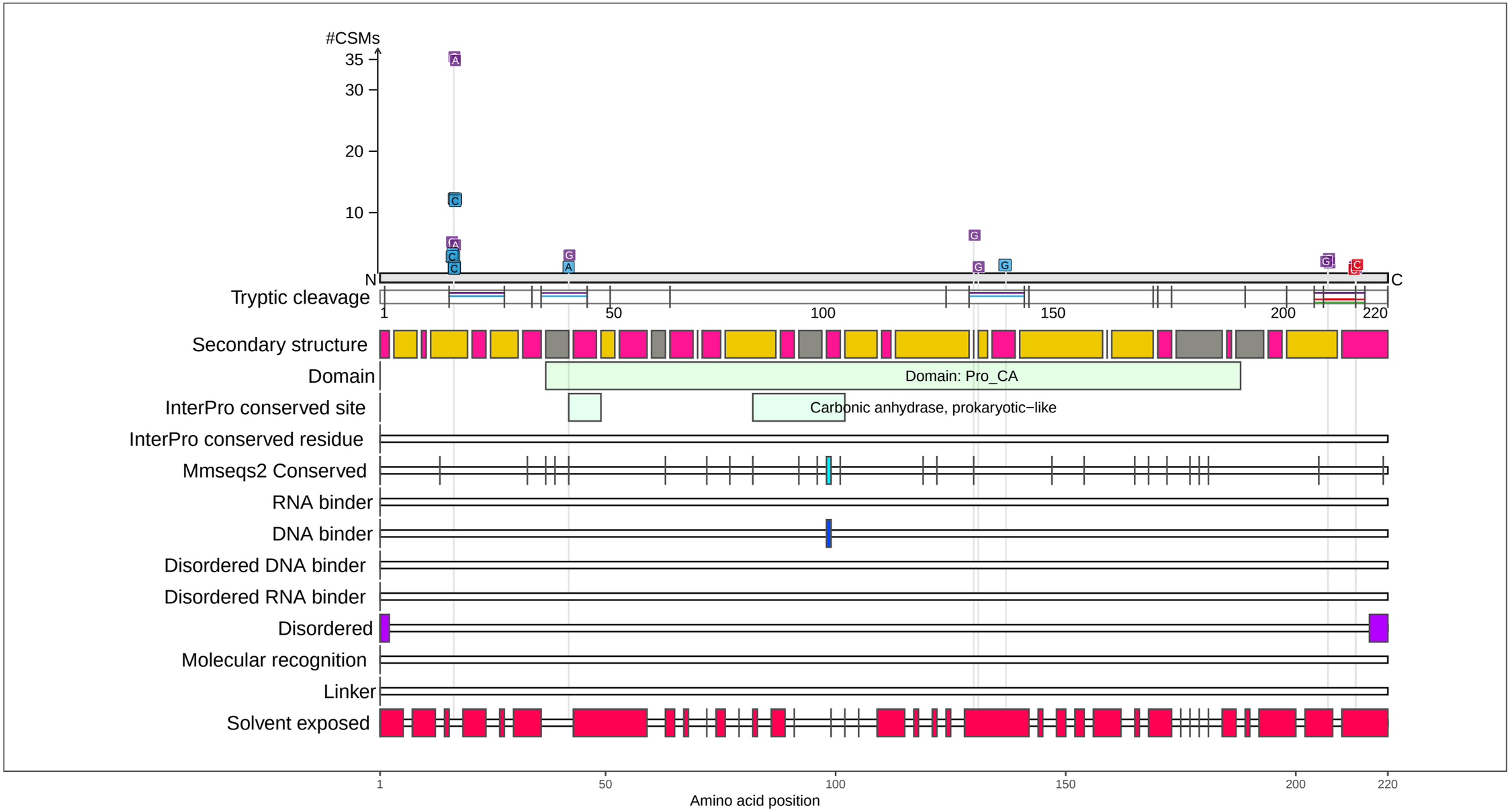




P61517
CAN_ECOLI Carbonic anhydrase 2

− Abundance:
tryptic [log10 Intensity]: 9.61 (Q 97)
PAXdb K12 strain [ppm]: 2.5 (Q 78)
PAXdb E.coli [ppm]: 2.73 (Q 90)

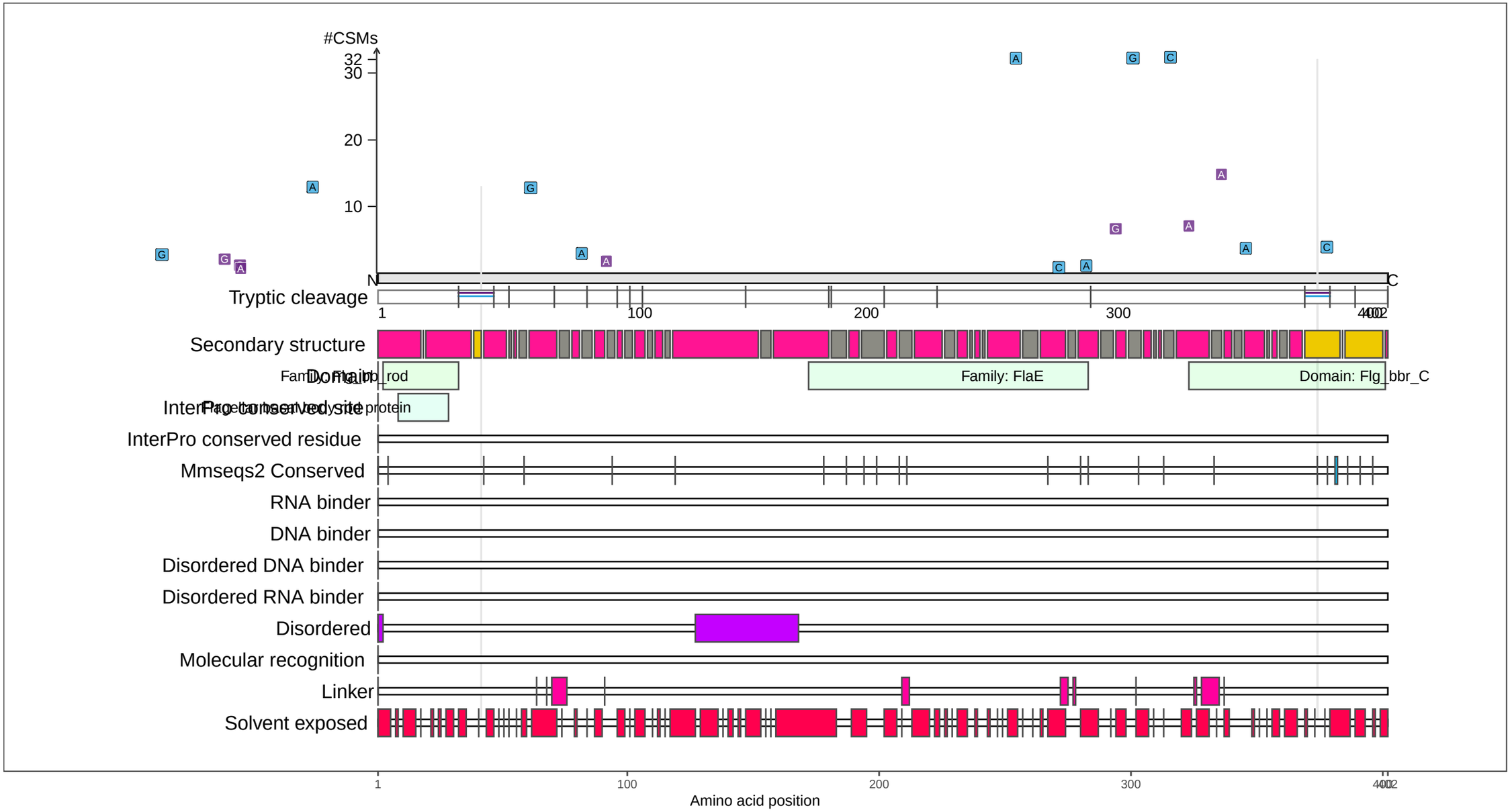
− RNA functions: not annotated



P75937
FLGE_ECOLI Flagellar hook protein FlgE

− Abundance:
tryptic [log10 Intensity]: 8.02 (Q 58)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 1.17 (Q 52)

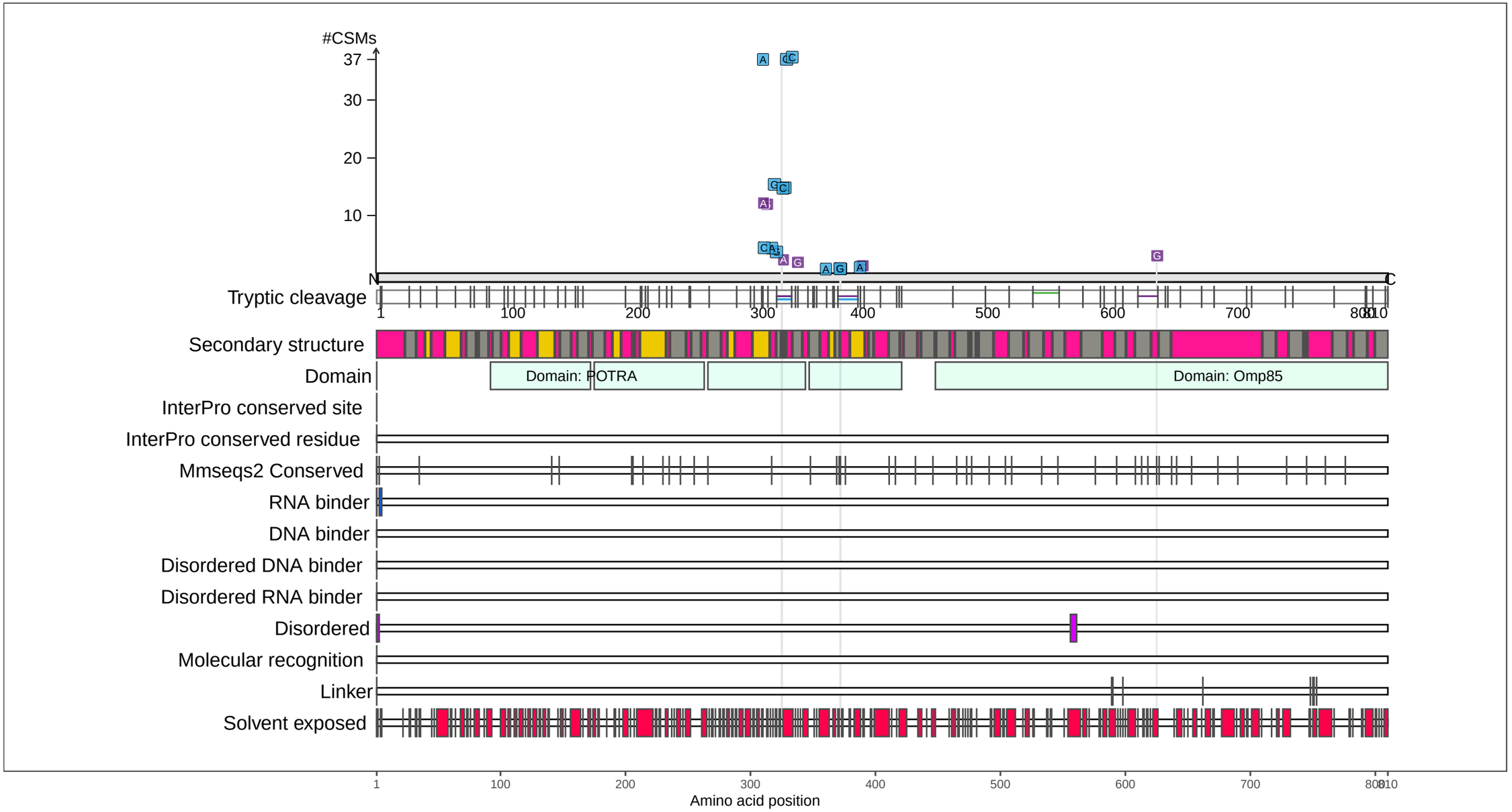
− RNA functions: not annotated



P0A940
BAMA_ECOLI Outer membrane protein assembly factor BamA

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 2 (Q 60)
PAXdb E.coli [ppm]: 2.28 (Q 80)

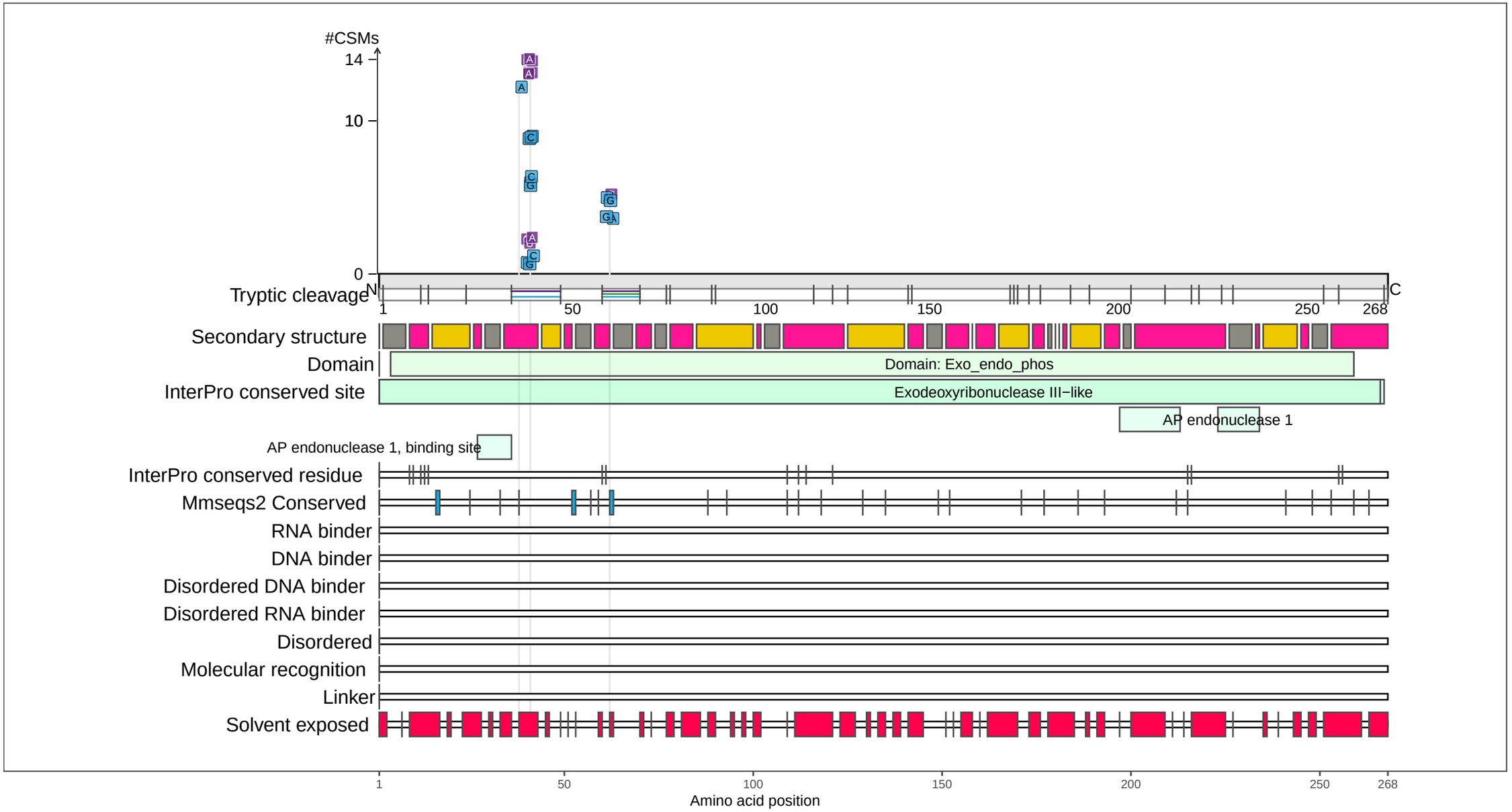
− RNA functions: not annotated



P09030
EX3_ECOLI Exodeoxyribonuclease III

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 2.77 (Q 85)
PAXdb E.coli [ppm]: 2.42 (Q 84)

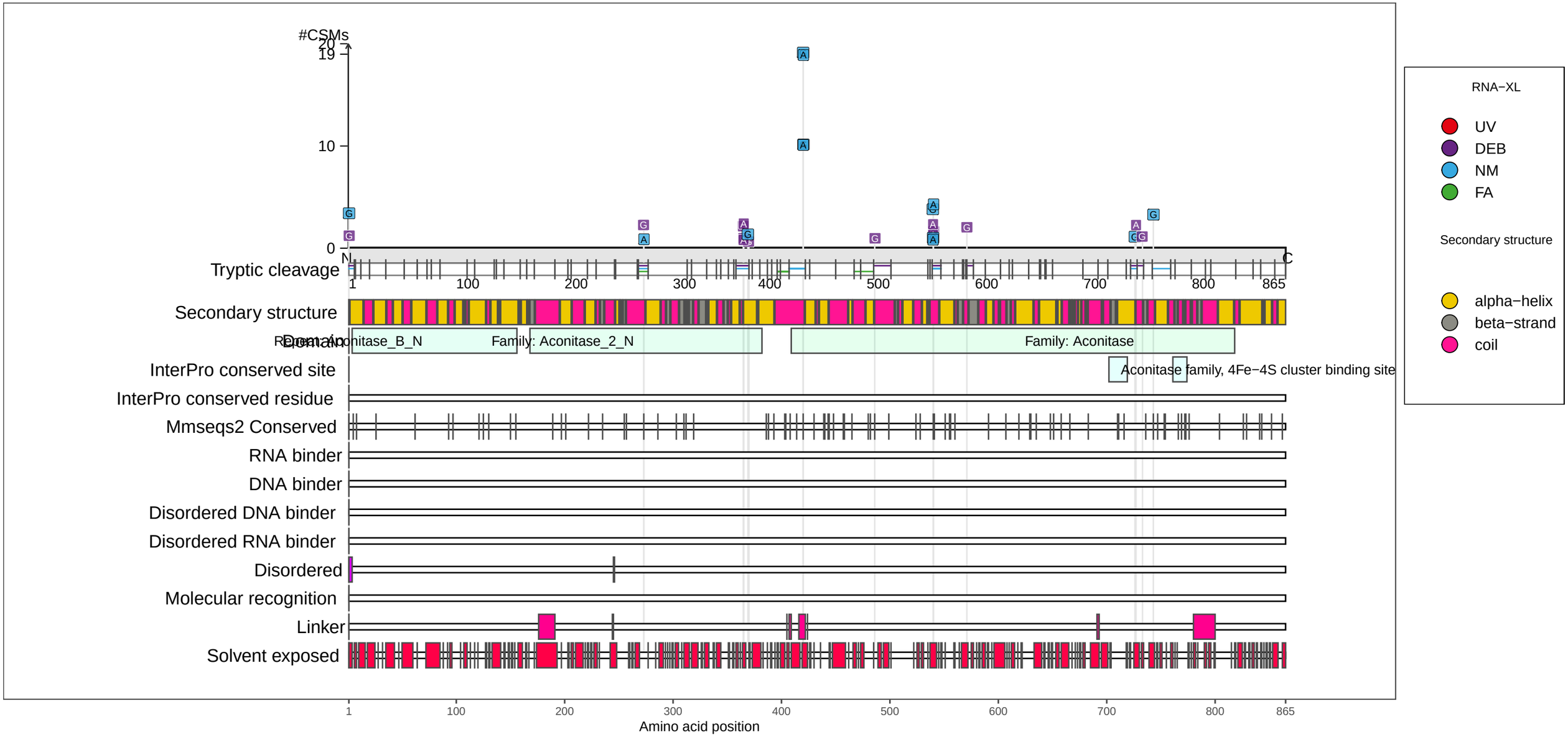
− RNA functions: not annotated



P36683
ACNB_ECOLI Aconitate hydratase B

− Abundance:
tryptic [log10 Intensity]: 9.47 (Q 96)
PAXdb K12 strain [ppm]: 3.11 (Q 93)
PAXdb E.coli [ppm]: 3.36 (Q 98)

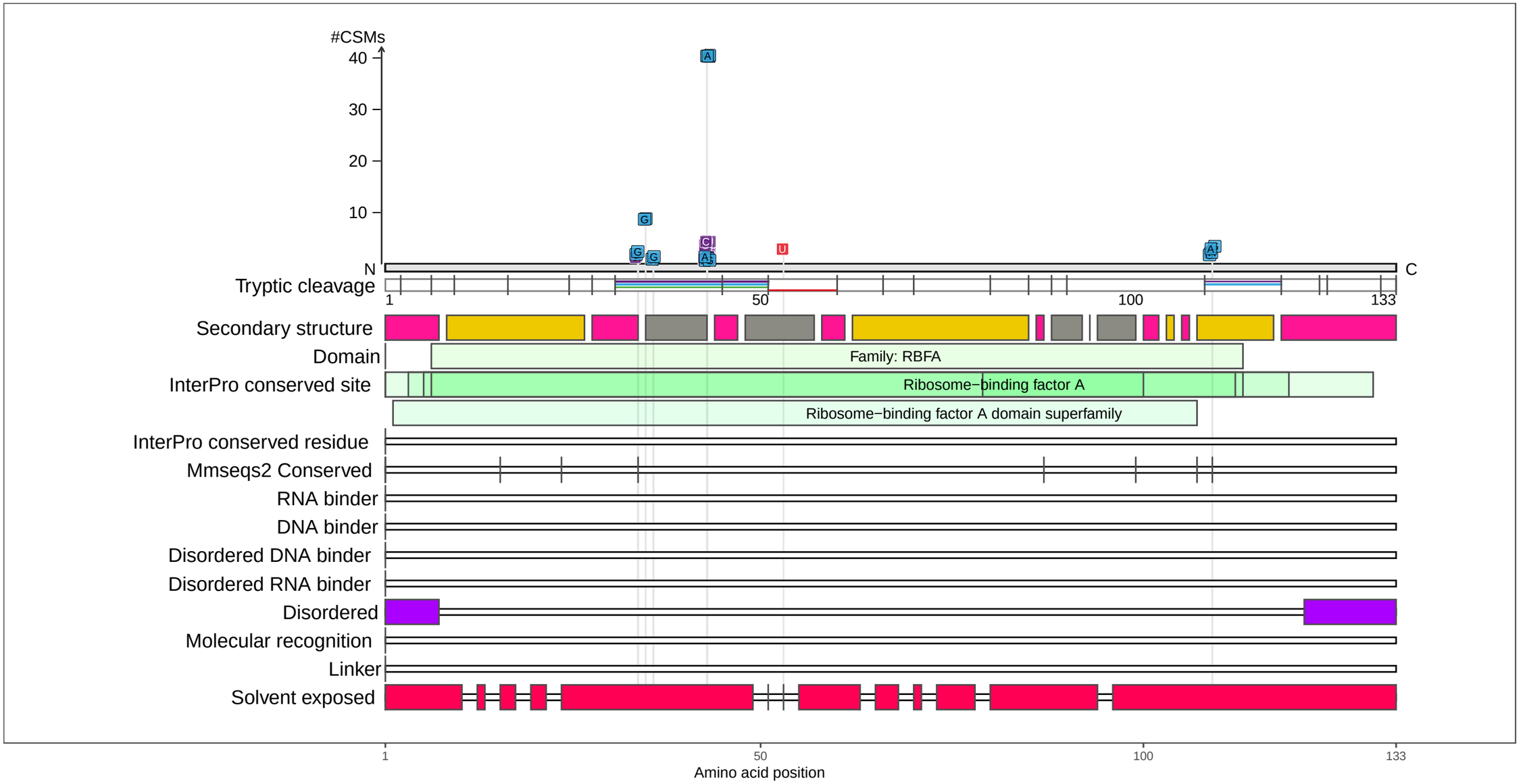
− RNA functions:
mRNA 3−UTR binding; mRNA binding; RNA binding

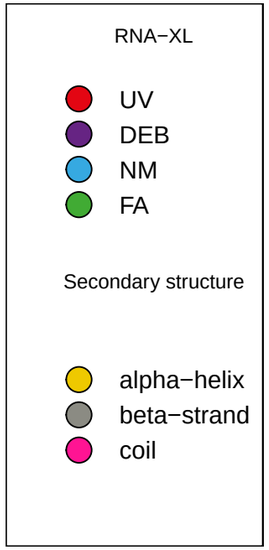


P0A7G2
RBFA_ECOLI 30S ribosome−binding factor

− Abundance:
tryptic [log10 Intensity]: 8.03 (Q 59)
PAXdb K12 strain [ppm]: 3.08 (Q 92)
PAXdb E.coli [ppm]: 2.81 (Q 92)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA processing
rRNA metabolic process; rRNA processing

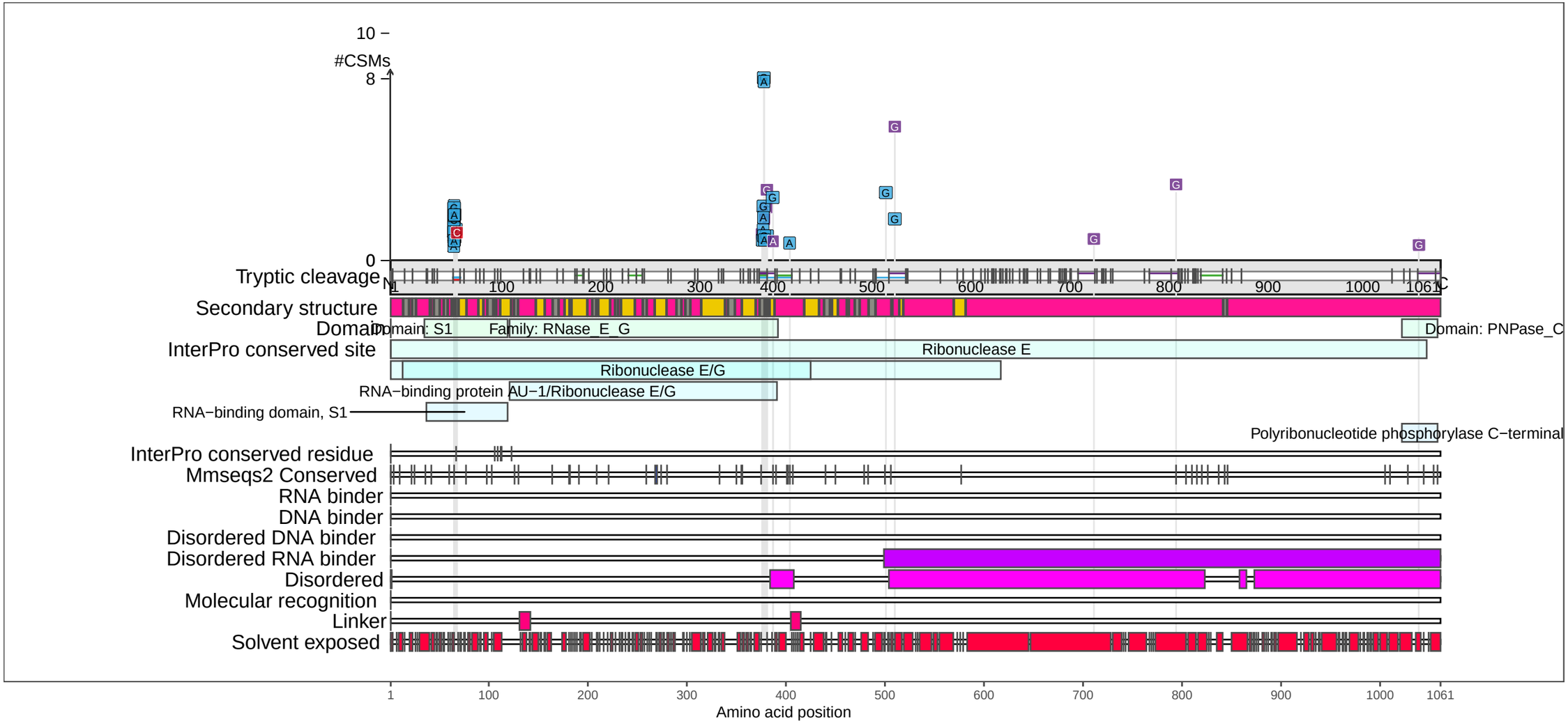


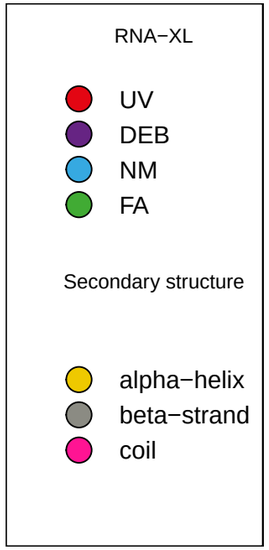


P21513
RNE_ECOLI Ribonuclease E

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 87)
PAXdb K12 strain [ppm]: 2.48 (Q 77)
PAXdb E.coli [ppm]: 2.43 (Q 84)

− RNA functions:
7S RNA binding; DEAD/H−box RNA helicase binding; mRNA catabolic process
mRNA metabolic process; ncRNA 5−end processing; ncRNA metabolic process; ncRNA processing
Ribosomal protein S1−like RNA−binding domain; RNA 5−end processing; RNA binding
RNA catabolic process; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic; RNA processing; rRNA 5−end processing
rRNA metabolic process; rRNA processing; S1 RNA binding domain; tRNA metabolic process
tRNA processing

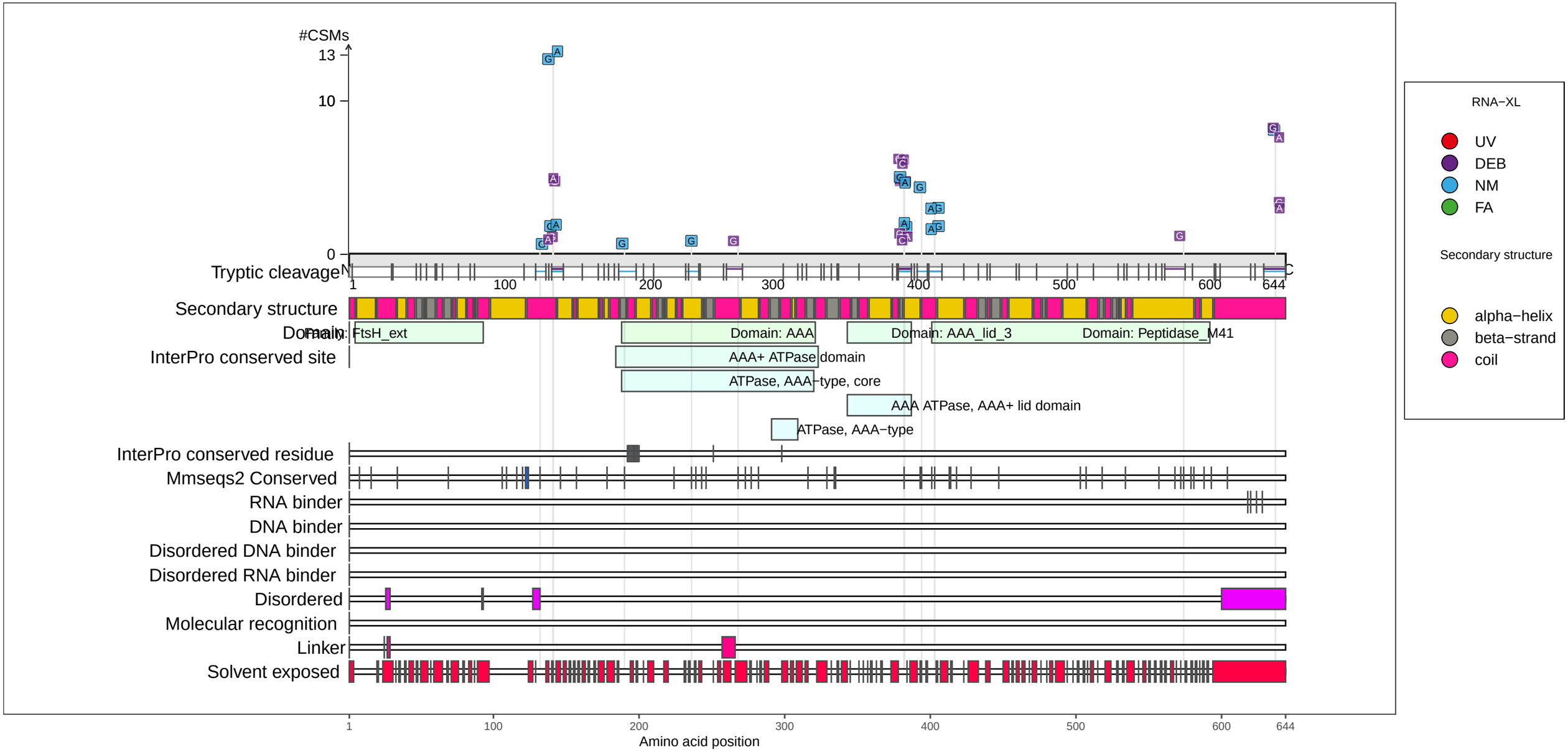




P0AAI3
FTSH_ECOLI ATP−dependent zinc metalloprotease FtsH

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: 2.56 (Q 79)
PAXdb E.coli [ppm]: 2.66 (Q 89)

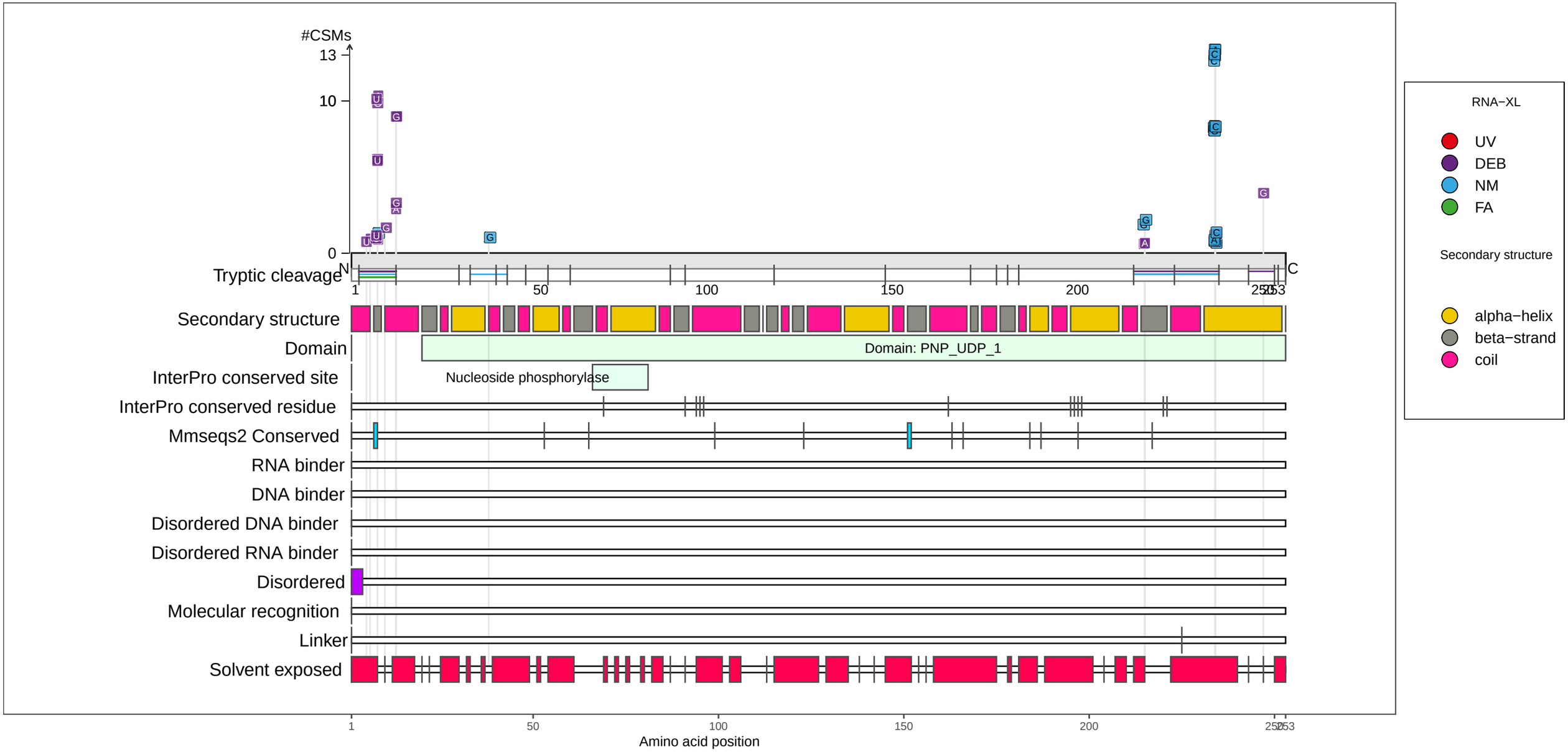
− RNA functions: not annotated



P12758
UDP_ECOLI Uridine phosphorylase

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 3.18 (Q 96)

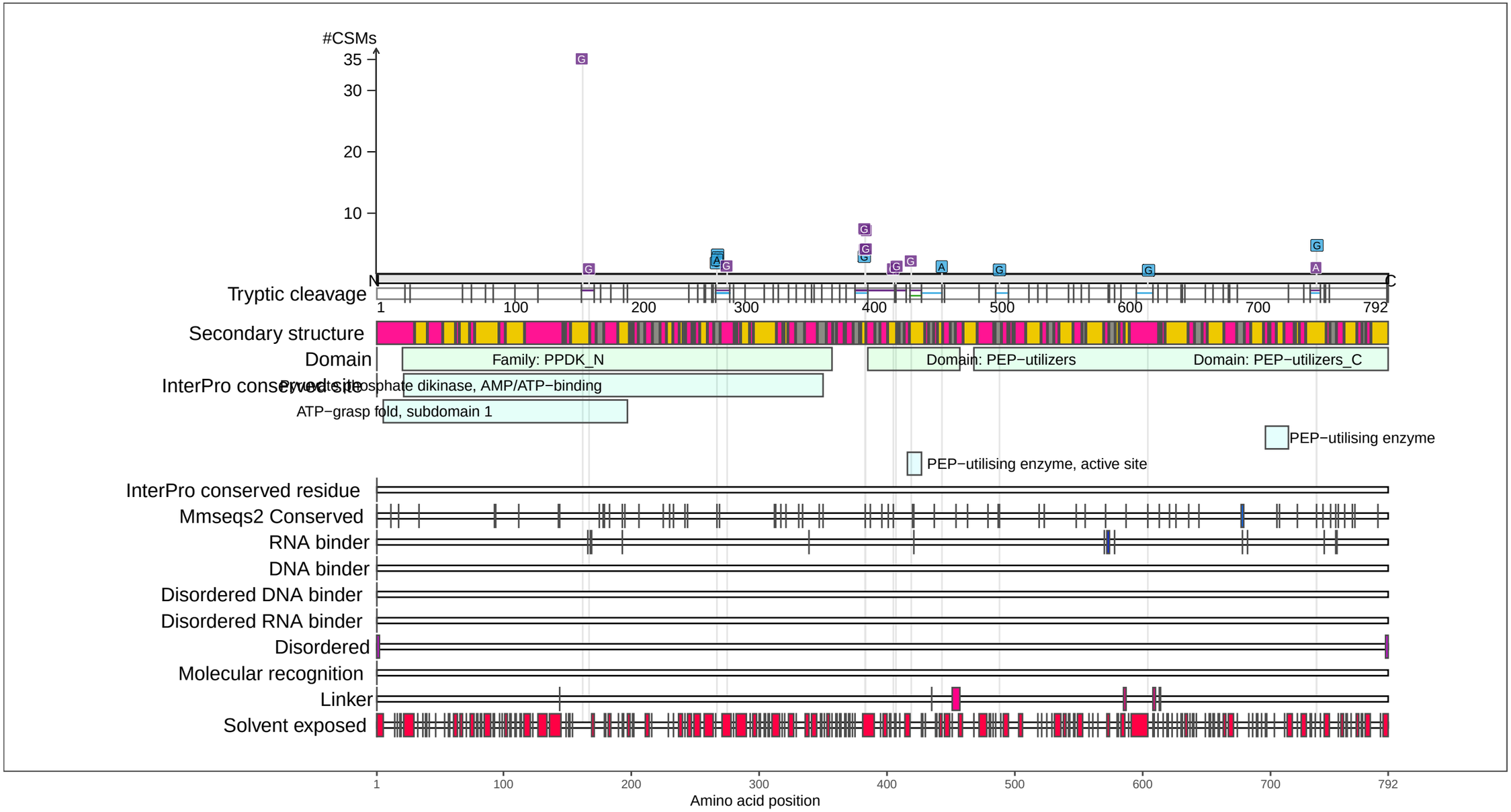
− RNA functions: not annotated

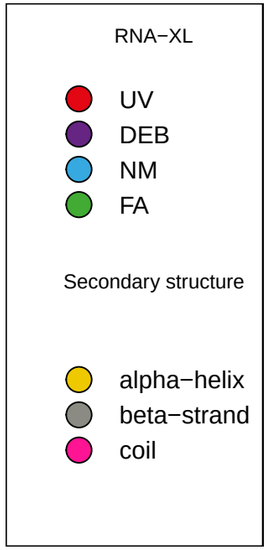


P23538
PPSA_ECOLI Phosphoenolpyruvate synthase

− Abundance:
tryptic [log10 Intensity]: 8.59 (Q 78)
PAXdb K12 strain [ppm]: 2.35 (Q 72)
PAXdb E.coli [ppm]: 2.89 (Q 93)

− RNA functions: not annotated

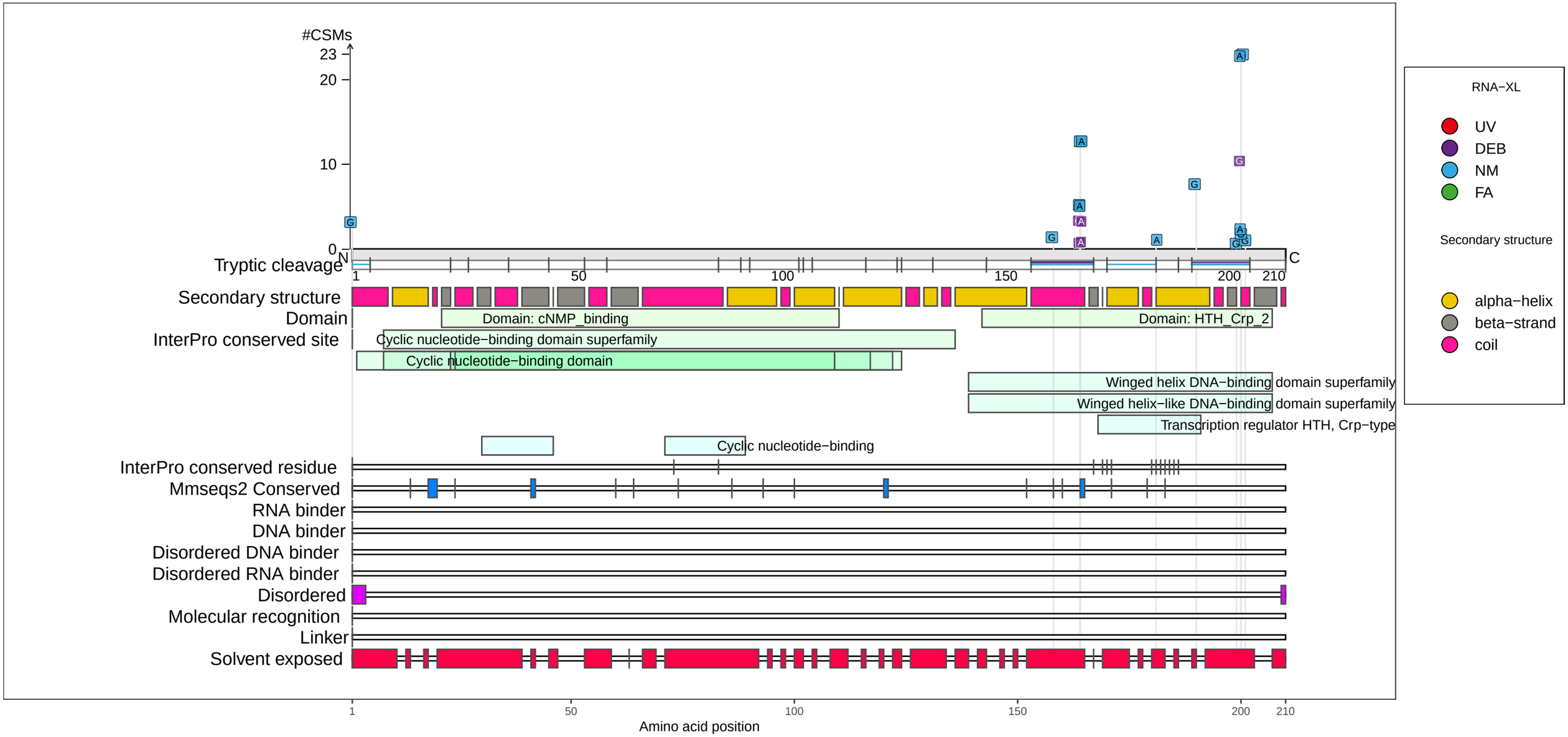




P0ACJ8
CRP_ECOLI cAMP−activated global transcriptional regulator CRP

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 80)
PAXdb K12 strain [ppm]: 2.95 (Q 90)
PAXdb E.coli [ppm]: 2.92 (Q 93)

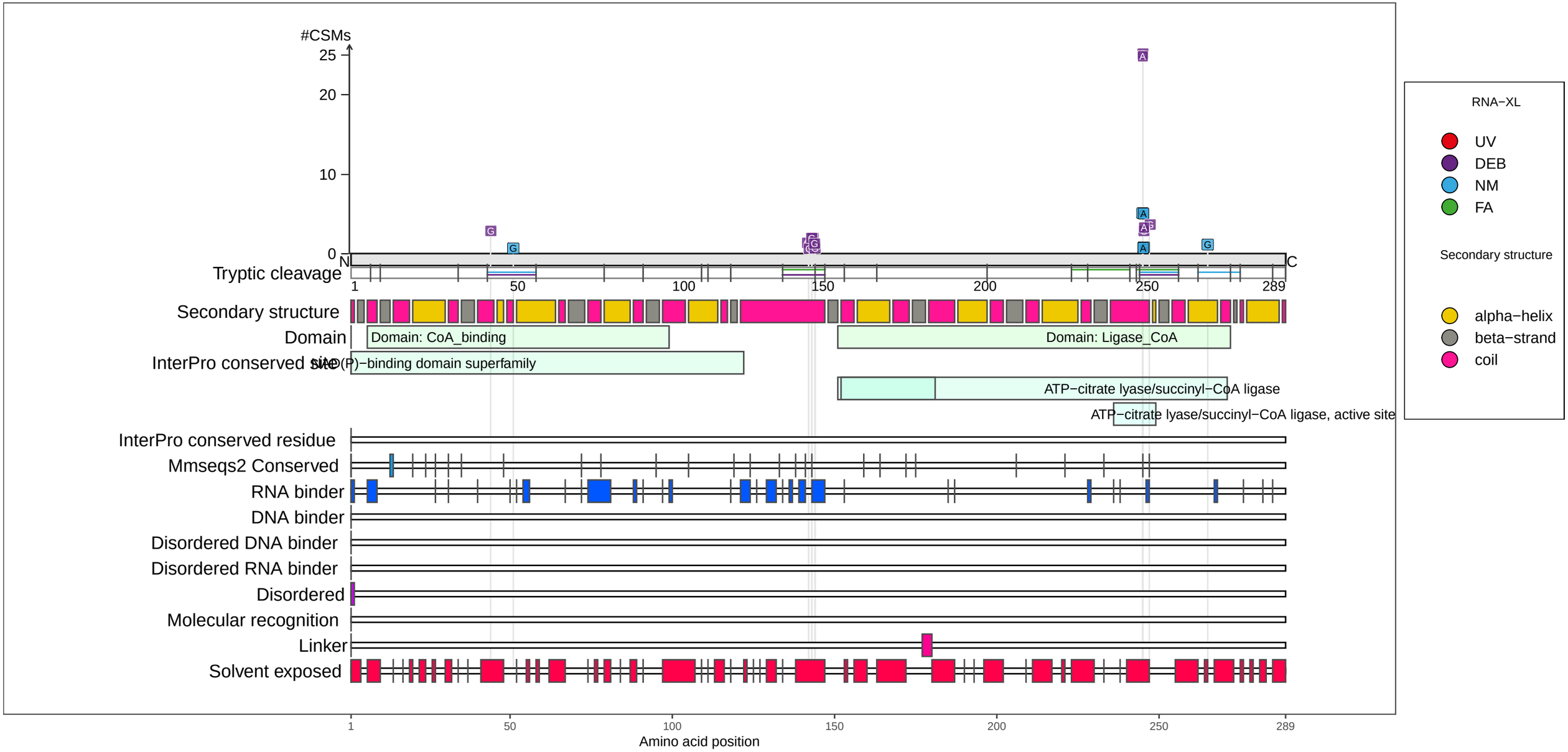
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0AGE9
SUCD_ECOLI Succinate−−CoA ligase [ADP−forming] subunit alpha

− Abundance:
tryptic [log10 Intensity]: 9.07 (Q 90)
PAXdb K12 strain [ppm]: 3.32 (Q 95)
PAXdb E.coli [ppm]: 3.31 (Q 97)

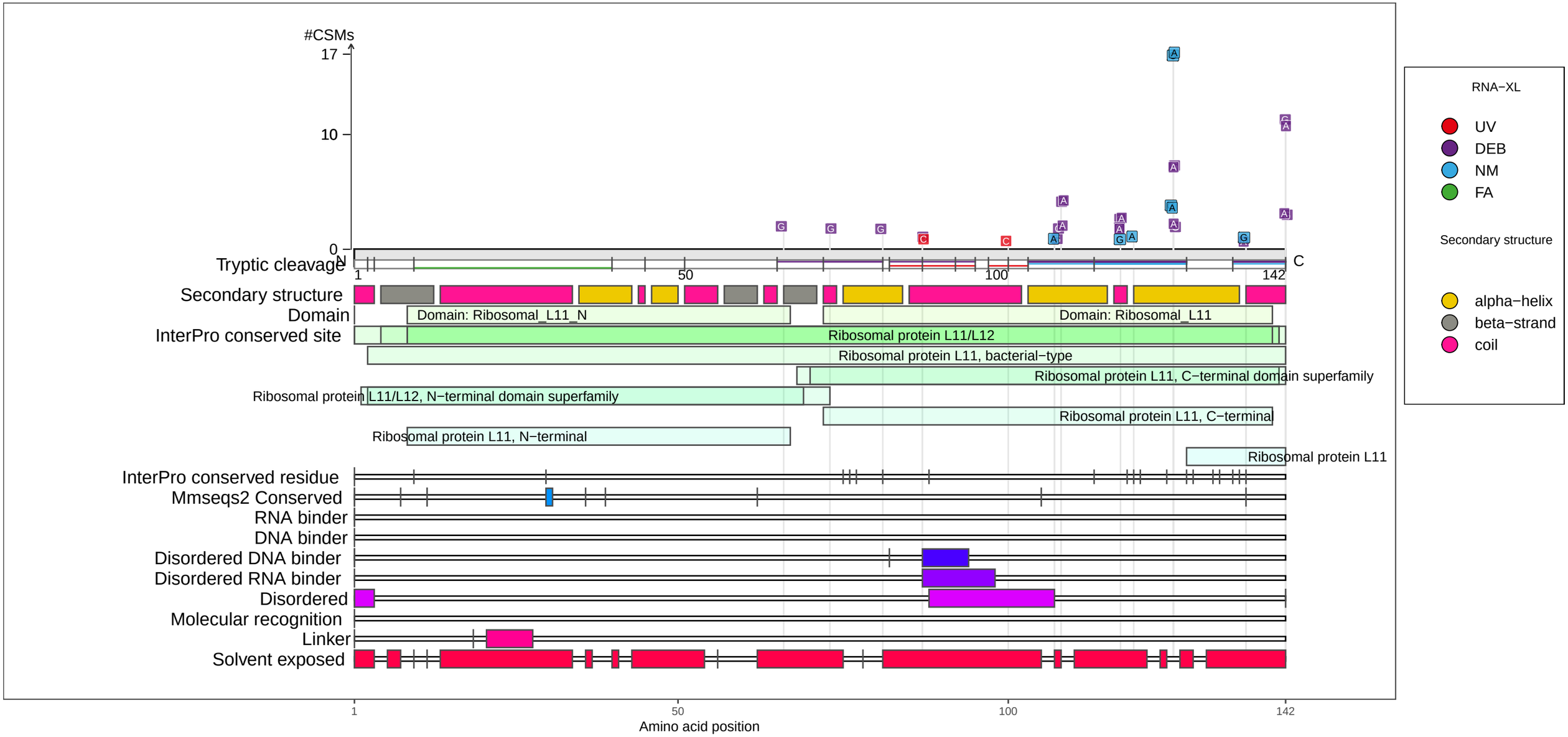
− RNA functions: not annotated



P0A7J7
RL11_ECOLI 50S ribosomal protein L11

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 3.51 (Q 98)
PAXdb E.coli [ppm]: 3.28 (Q 97)

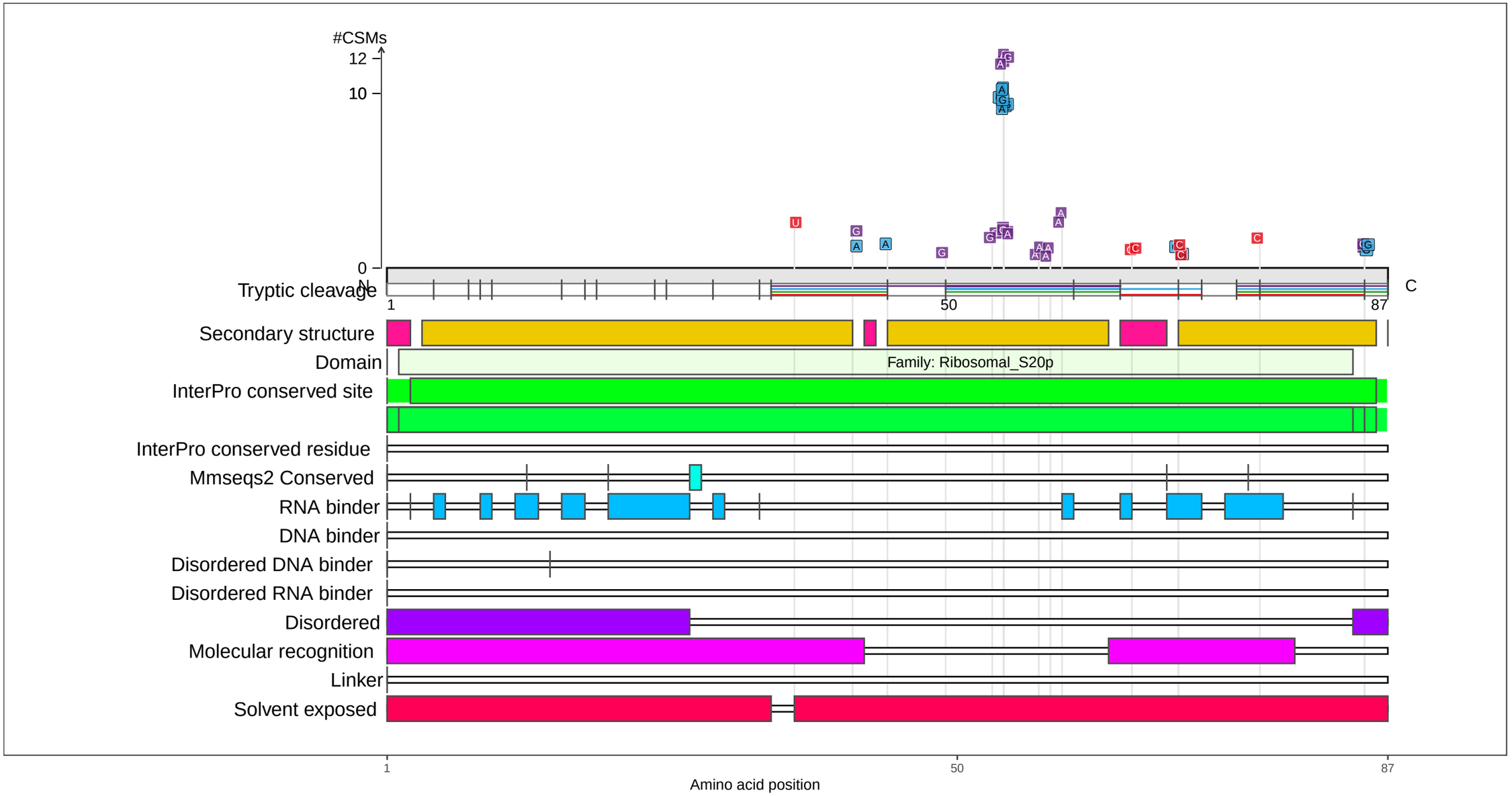
− RNA functions:
Ribosomal protein L11, RNA binding domain; RNA binding; rRNA binding

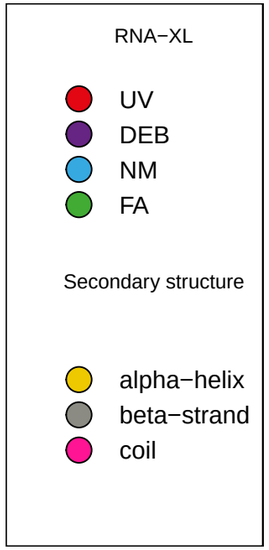


P0A7U7
RS20_ECOLI 30S ribosomal protein S20

− Abundance:
tryptic [log10 Intensity]: 8.9 (Q 86)
PAXdb K12 strain [ppm]: 3.85 (Q 100)
PAXdb E.coli [ppm]: 3.49 (Q 99)

− RNA functions:
RNA binding; rRNA binding

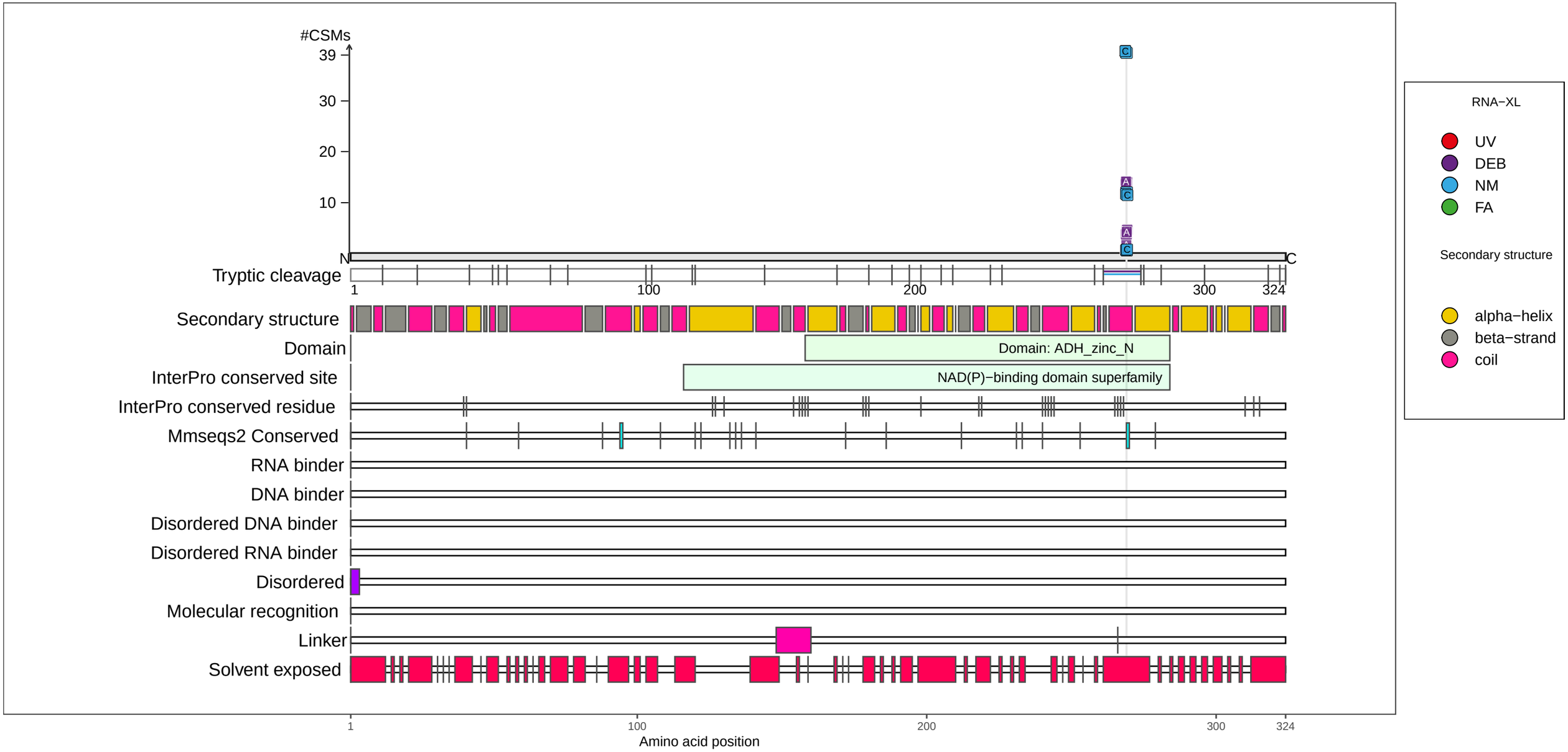




P26646
ACUI_ECOLI Probable acrylyl−CoA reductase AcuI

− Abundance:
tryptic [log10 Intensity]: 8.64 (Q 80)
PAXdb K12 strain [ppm]: 2.75 (Q 84)
PAXdb E.coli [ppm]: 2.63 (Q 89)

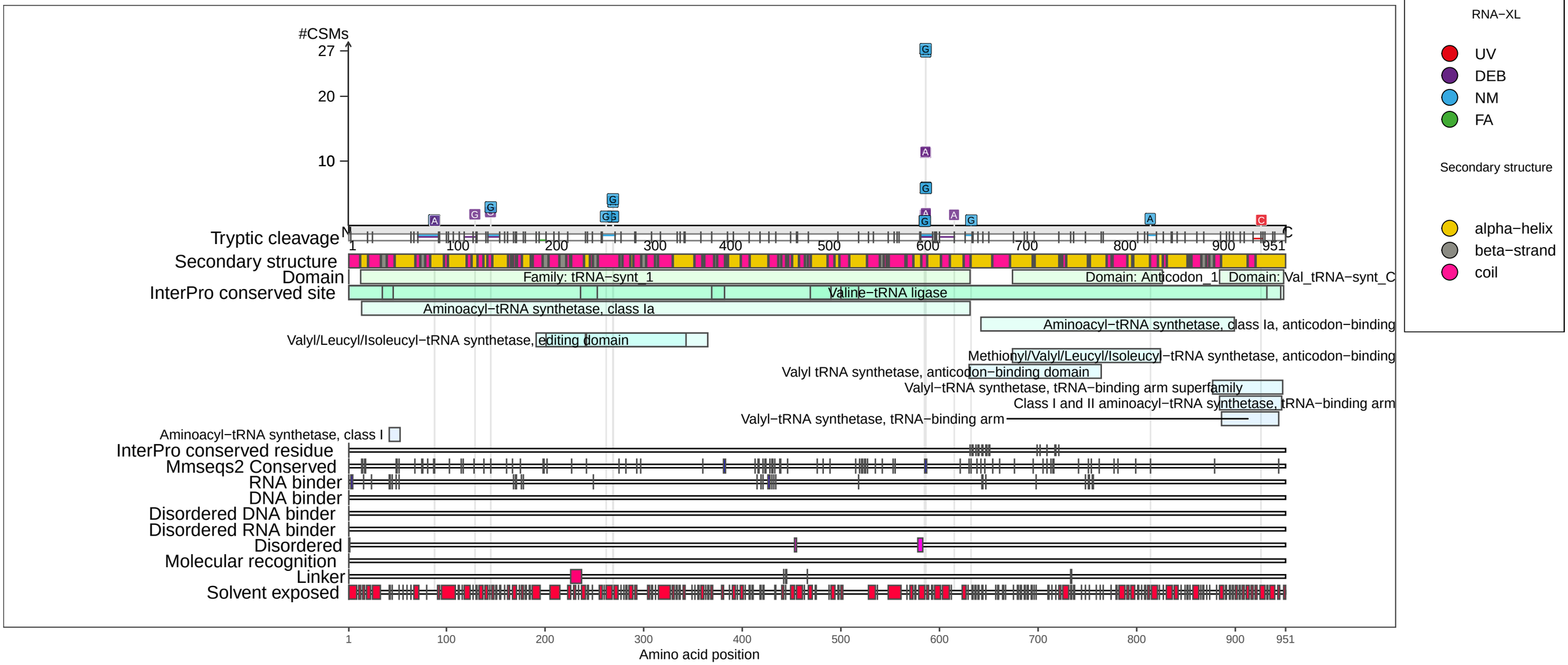
− RNA functions: not annotated



P07118
SYV_ECOLI Valine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.77 (Q 99)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 2.67 (Q 89)

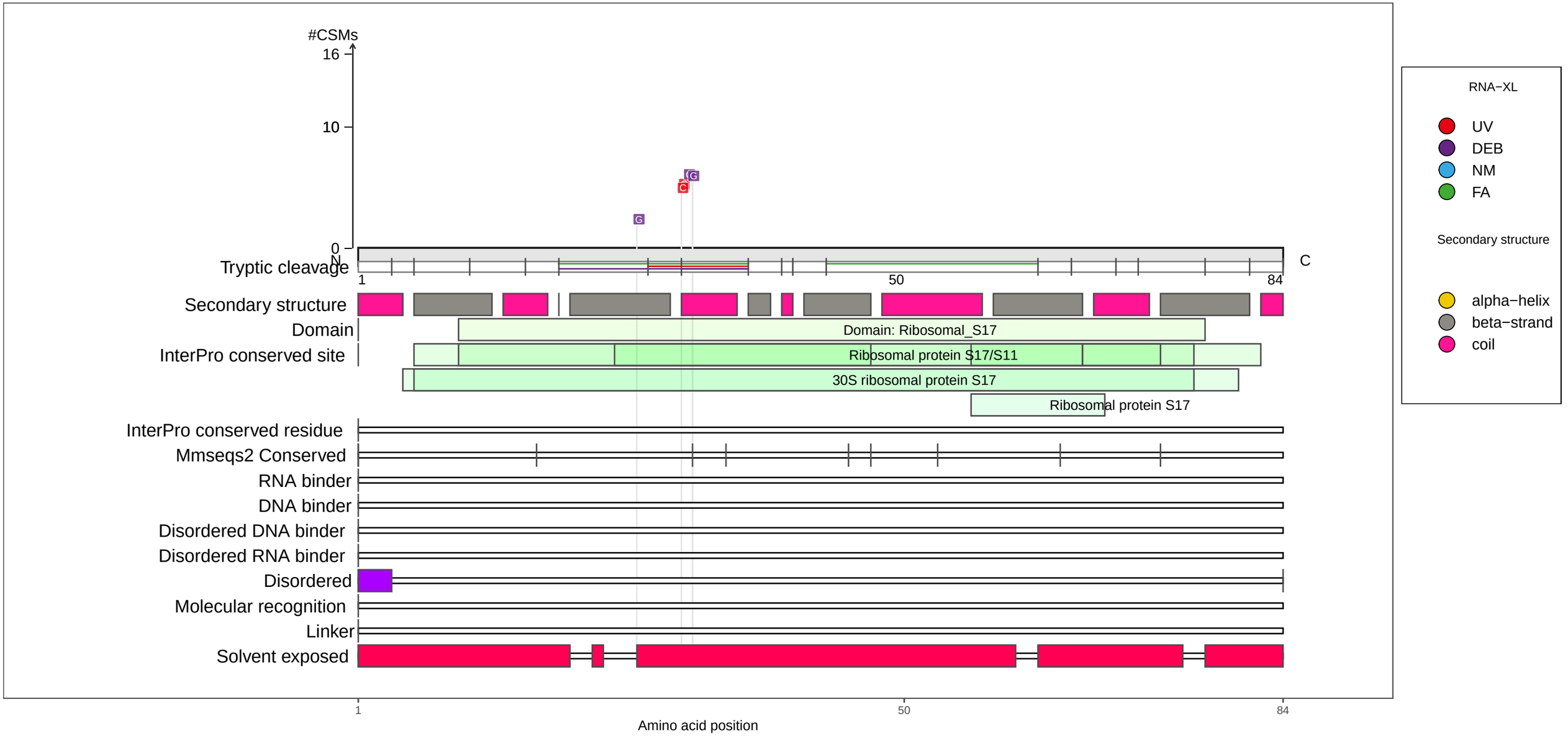
− RNA functions:
aminoacyl−tRNA editing activity; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; Anticodon−binding domain of tRNA
Leucyl−tRNA synthetase, Domain 2; ncRNA metabolic process; RNA metabolic process
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetases class I (I, L, M and V); tRNA synthetases class I (M)
valine−tRNA ligase activity; Valyl tRNA synthetase tRNA binding arm; valyl−tRNA aminoacylation



P0AG63
RS17_ECOLI 30S ribosomal protein S17

− Abundance:
tryptic [log10 Intensity]: 9.84 (Q 99)
PAXdb K12 strain [ppm]: 3.83 (Q 100)
PAXdb E.coli [ppm]: 2.92 (Q 94)

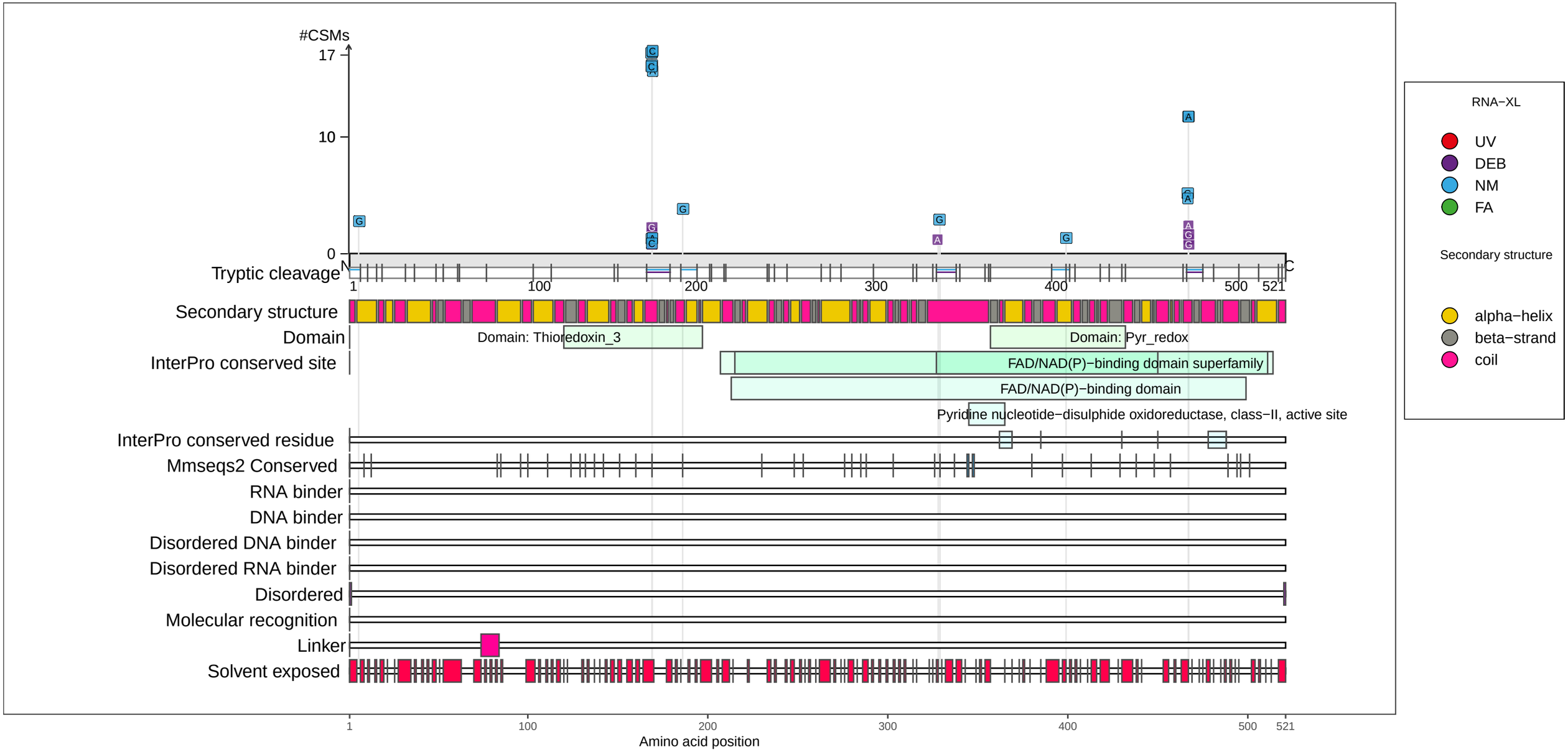
− RNA functions:
RNA binding; rRNA binding



P35340
AHPF_ECOLI Alkyl hydroperoxide reductase subunit F

− Abundance:
tryptic [log10 Intensity]: 9.34 (Q 95)
PAXdb K12 strain [ppm]: 2.69 (Q 83)
PAXdb E.coli [ppm]: 2.45 (Q 84)

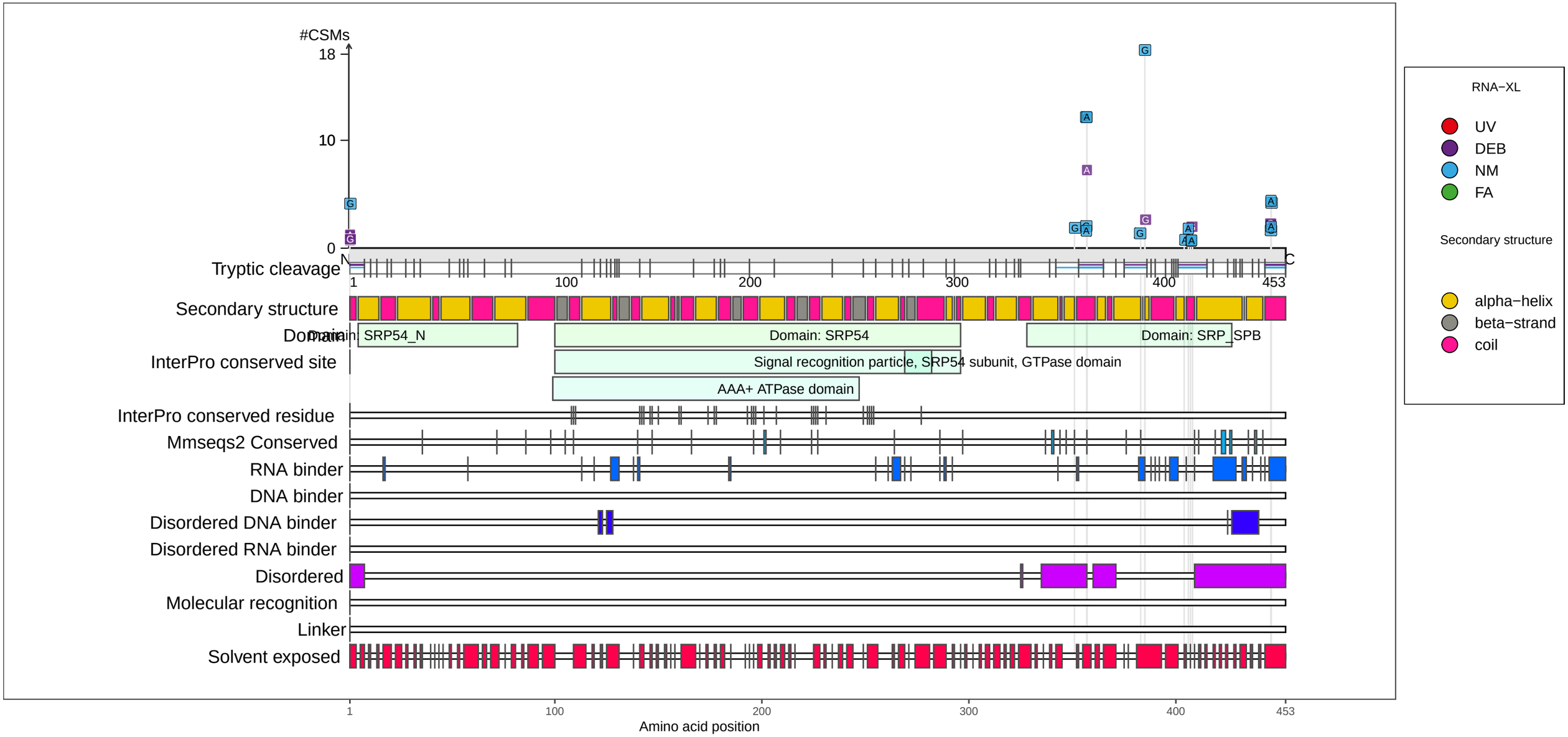
− RNA functions: not annotated



P0AGD7
SRP54_ECOLI Signal recognition particle protein

− Abundance:
tryptic [log10 Intensity]: 6.56 (Q 3)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 2.31 (Q 81)

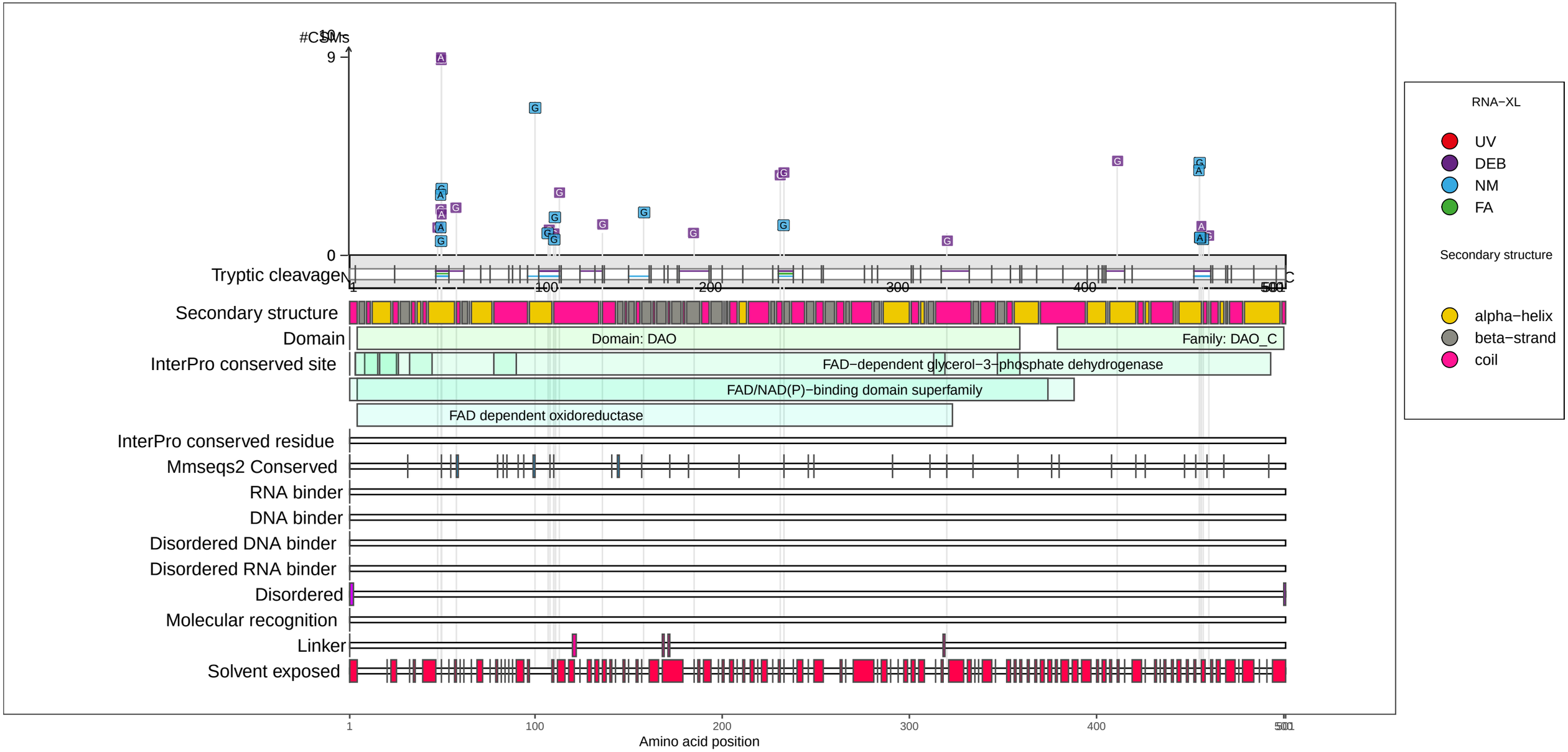
− RNA functions:
7S RNA binding; RNA binding



P13035
GLPD_ECOLI Aerobic glycerol−3−phosphate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.67 (Q 98)
PAXdb K12 strain [ppm]: 2.25 (Q 68)
PAXdb E.coli [ppm]: 2.55 (Q 87)

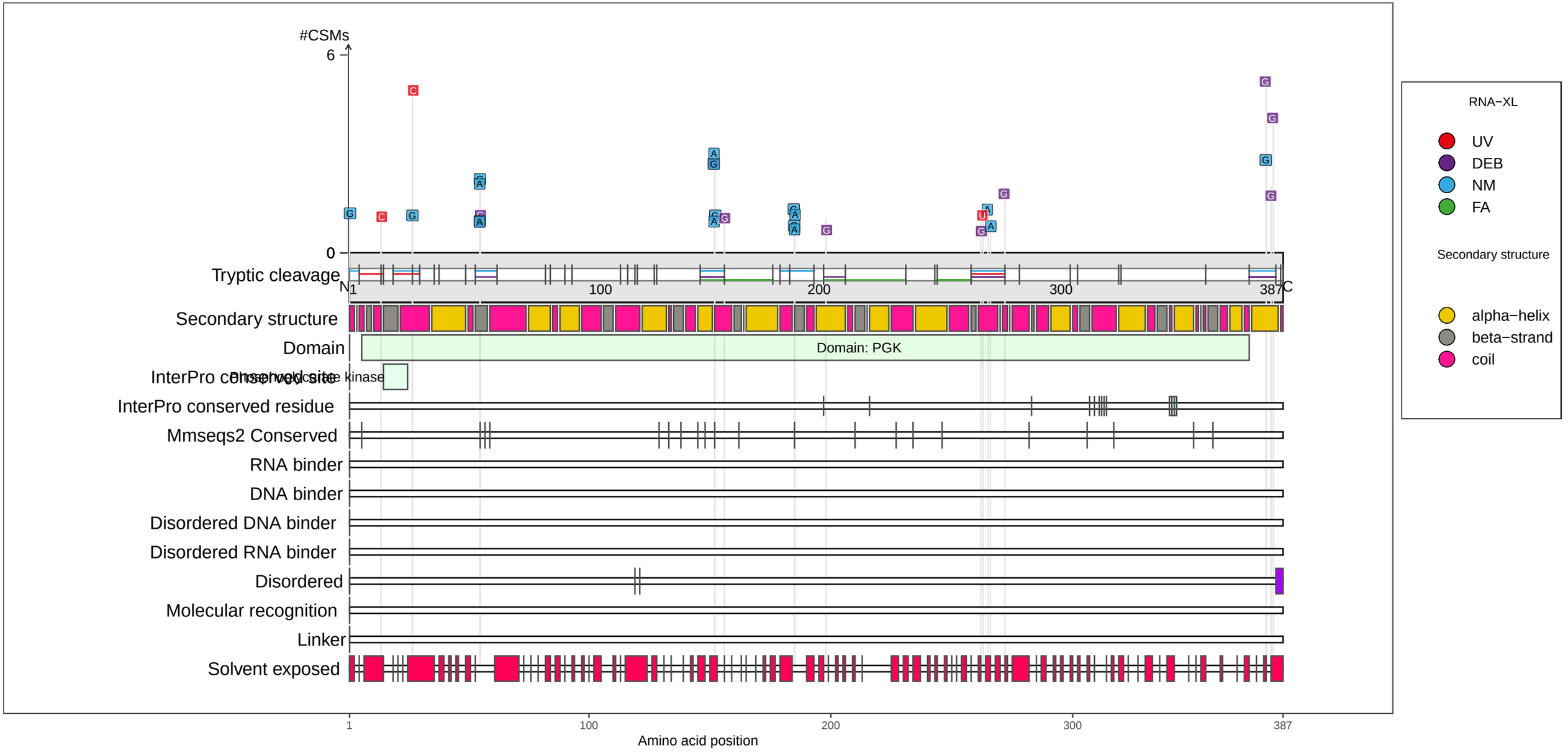
− RNA functions: not annotated



P0A799
PGK_ECOLI Phosphoglycerate kinase

− Abundance:
tryptic [log10 Intensity]: 9.45 (Q 96)
PAXdb K12 strain [ppm]: 3.17 (Q 94)
PAXdb E.coli [ppm]: 3.74 (Q 100)

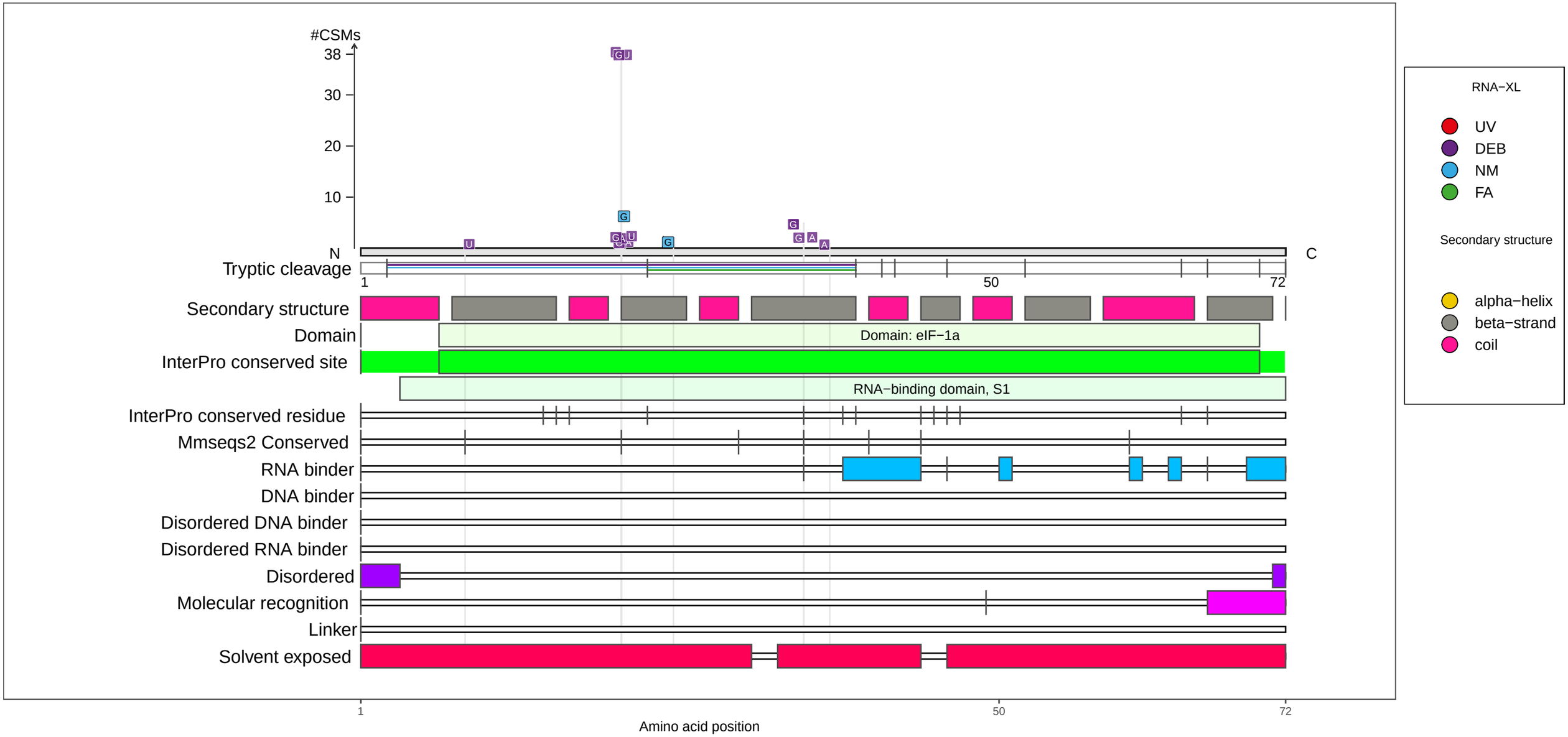
− RNA functions: not annotated



P69222
IF1_ECOLI Translation initiation factor IF−1

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 3.5 (Q 97)
PAXdb E.coli [ppm]: 3.3 (Q 97)

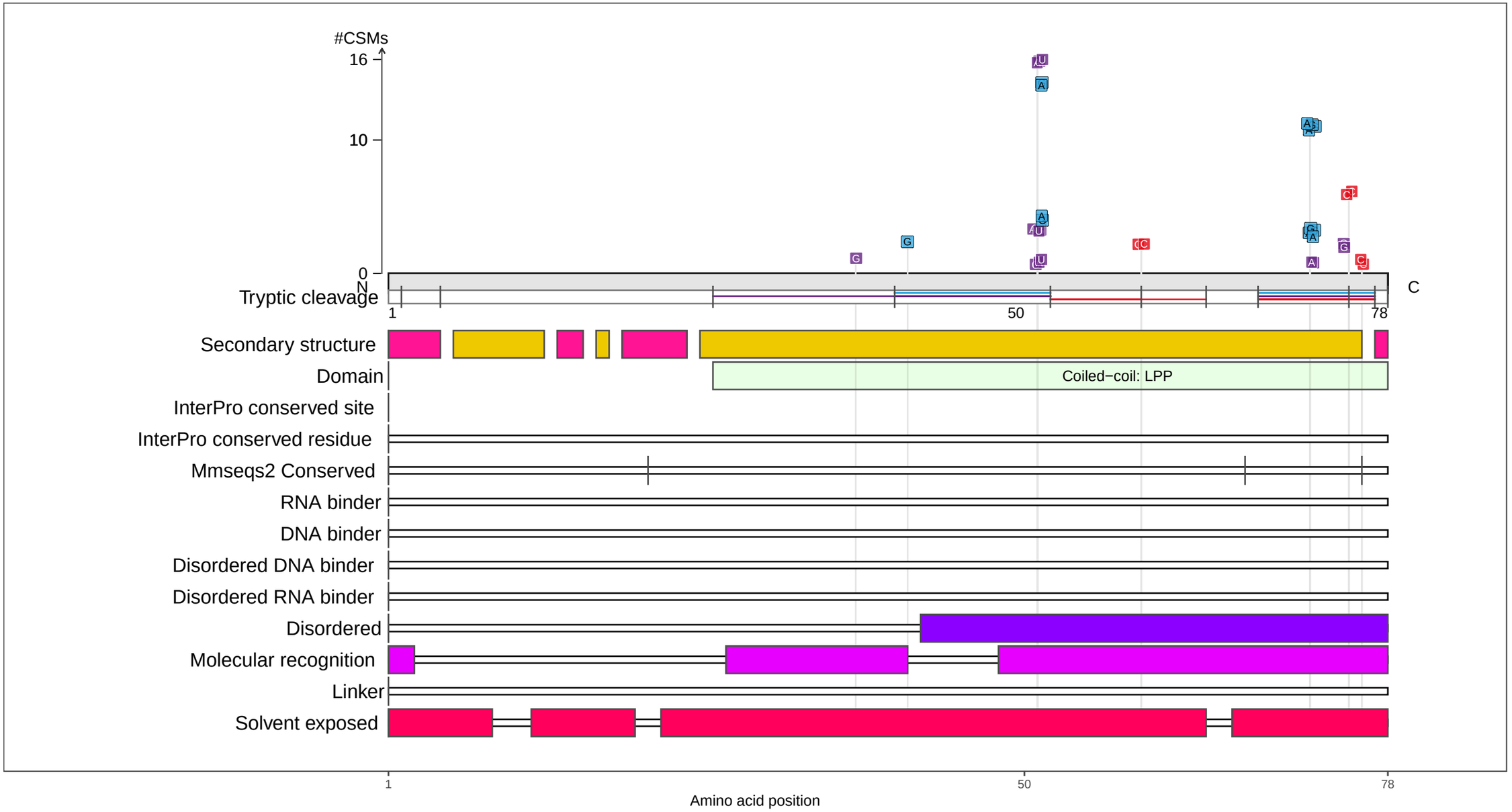
− RNA functions:
RNA binding; rRNA binding

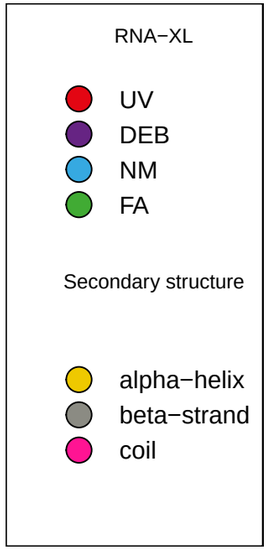


P69776
LPP_ECOLI Major outer membrane lipoprotein Lpp

− Abundance:
tryptic [log10 Intensity]: 10.6 (Q 100)
PAXdb K12 strain [ppm]: 2.77 (Q 85)
PAXdb E.coli [ppm]: 3.58 (Q 100)

− RNA functions: not annotated

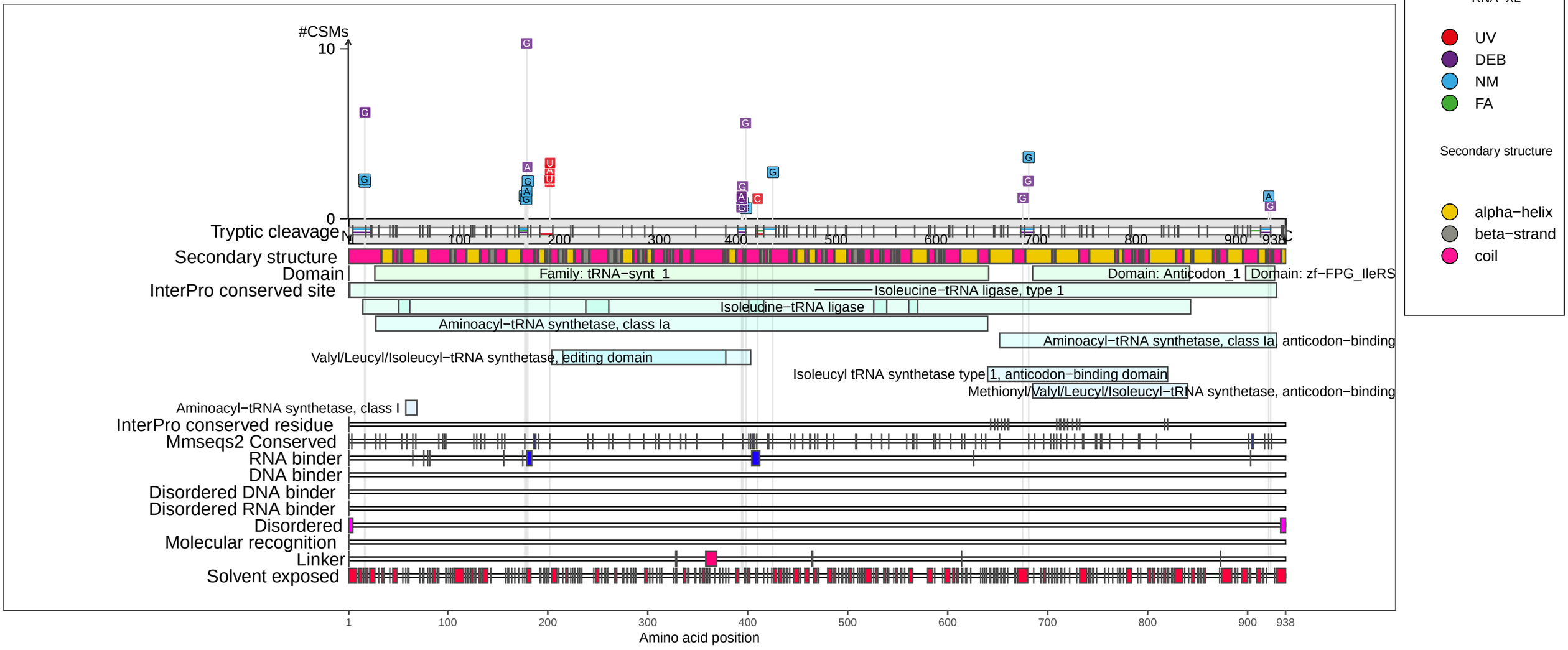




P00956
SYI_ECOLI Isoleucine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.76 (Q 99)
PAXdb K12 strain [ppm]: 3 (Q 91)
PAXdb E.coli [ppm]: 2.74 (Q 90)

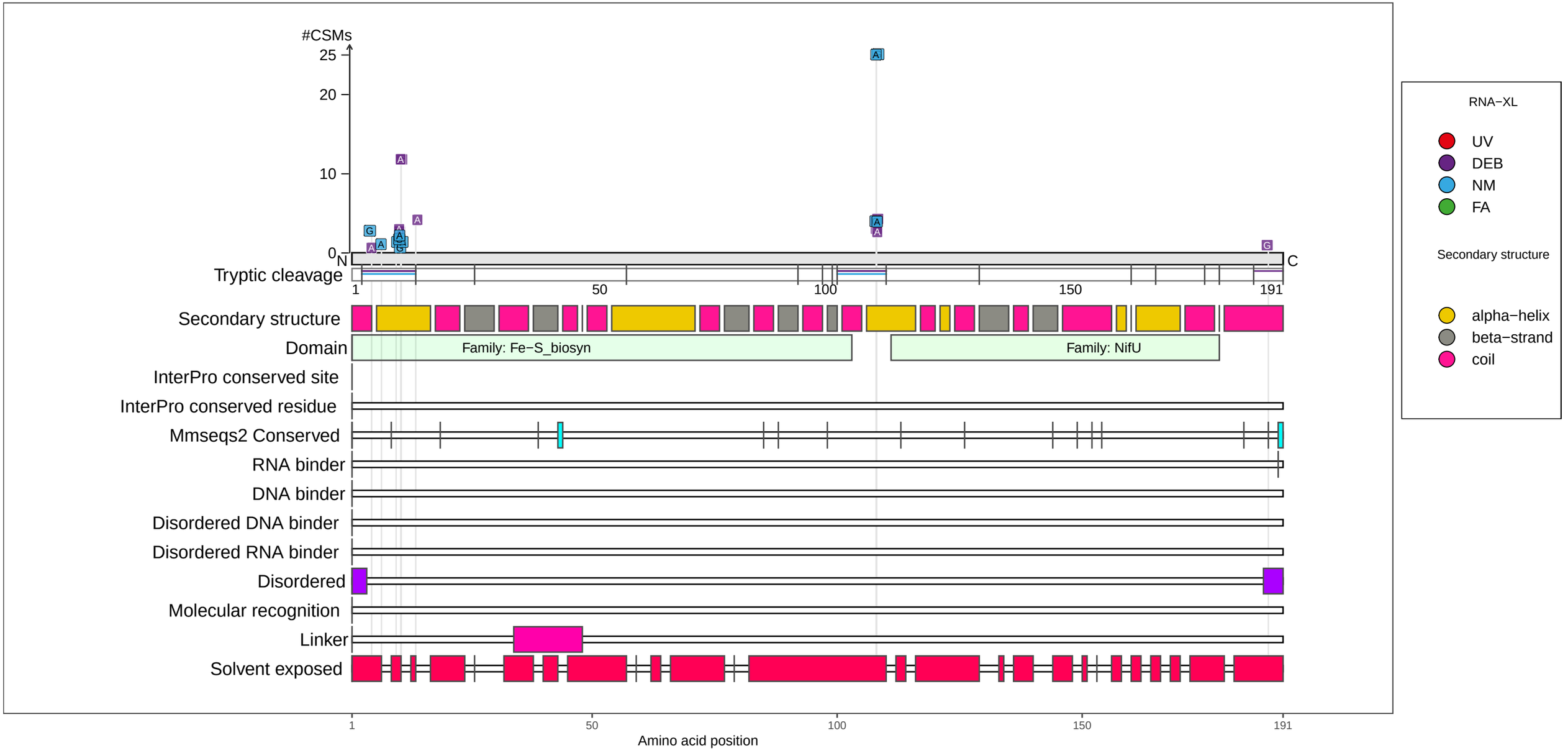
− RNA functions:
aminoacyl−tRNA editing activity; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; Anticodon−binding domain of tRNA
isoleucine−tRNA ligase activity; isoleucyl−tRNA aminoacylation
Leucyl−tRNA synthetase, Domain 2; ncRNA metabolic process; RNA binding; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA synthetases class I (C) catalytic domain
tRNA synthetases class I (I, L, M and V); tRNA synthetases class I (K); tRNA synthetases class I (M)



P63020
NFUA_ECOLI Fe/S biogenesis protein NfuA

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 2.66 (Q 82)
PAXdb E.coli [ppm]: 3.09 (Q 96)

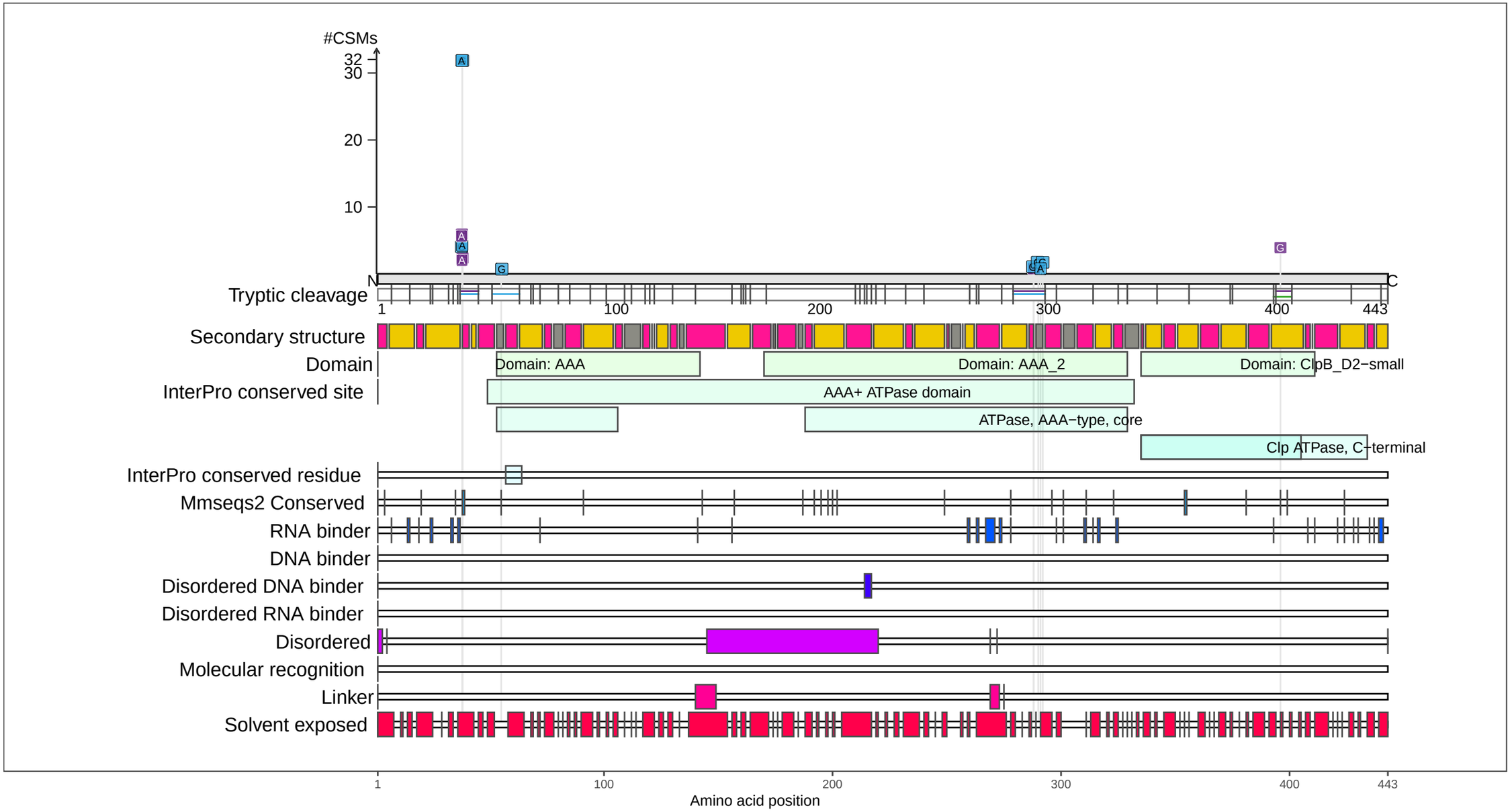
− RNA functions: not annotated

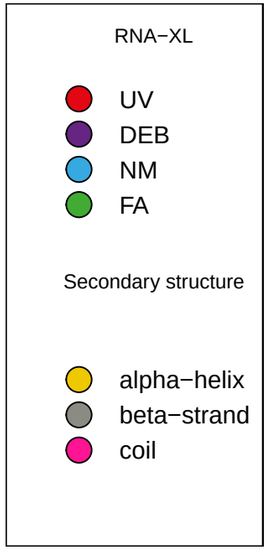


P0A6H5
HSLU_ECOLI ATP−dependent protease ATPase subunit HslU

− Abundance:
tryptic [log10 Intensity]: 9.37 (Q 95)
PAXdb K12 strain [ppm]: 3.26 (Q 95)
PAXdb E.coli [ppm]: 2.8 (Q 92)

− RNA functions: not annotated

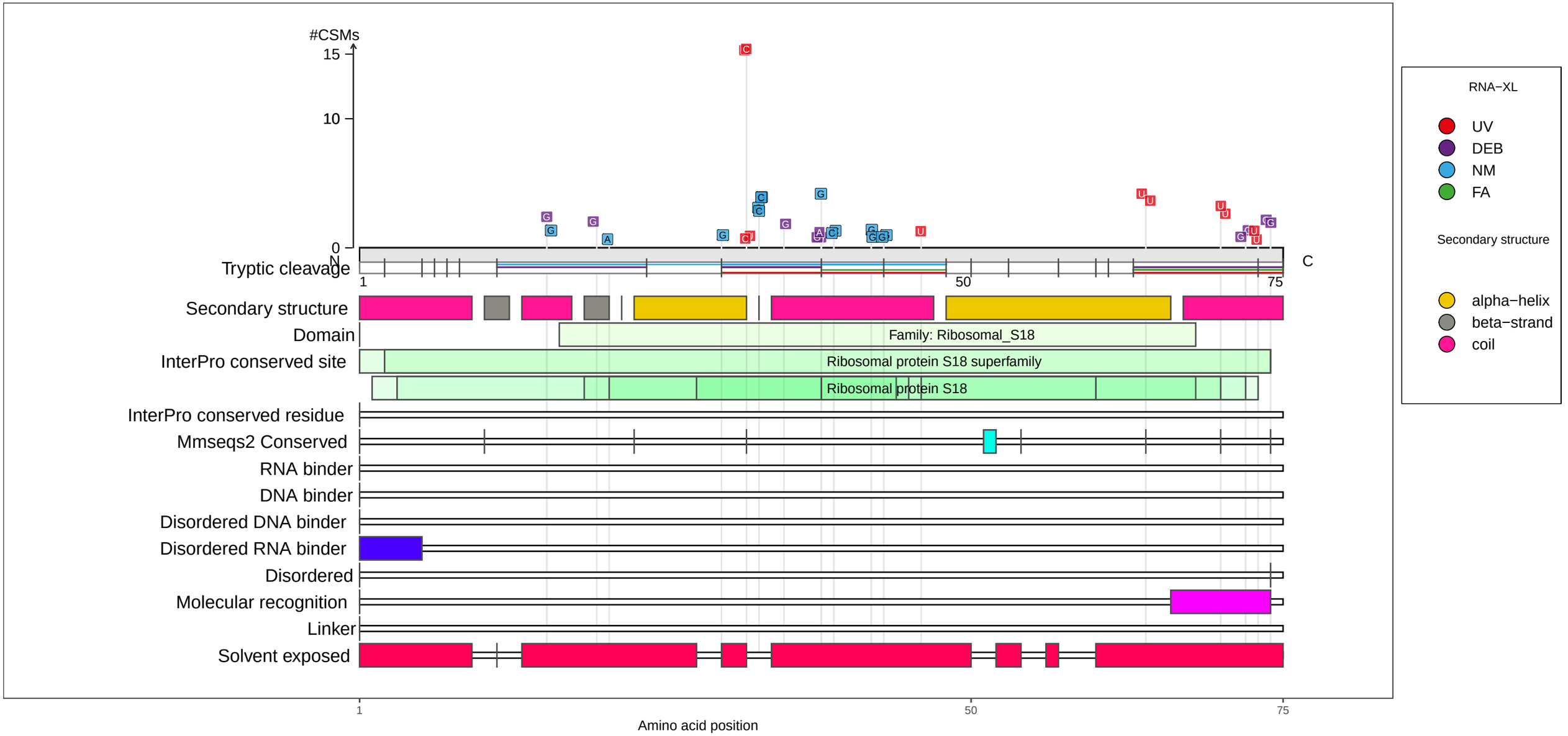




P0A7T7
RS18_ECOLI 30S ribosomal protein S18

− Abundance:
tryptic [log10 Intensity]: 8.82 (Q 84)
PAXdb K12 strain [ppm]: 3.88 (Q 100)
PAXdb E.coli [ppm]: 3.48 (Q 99)

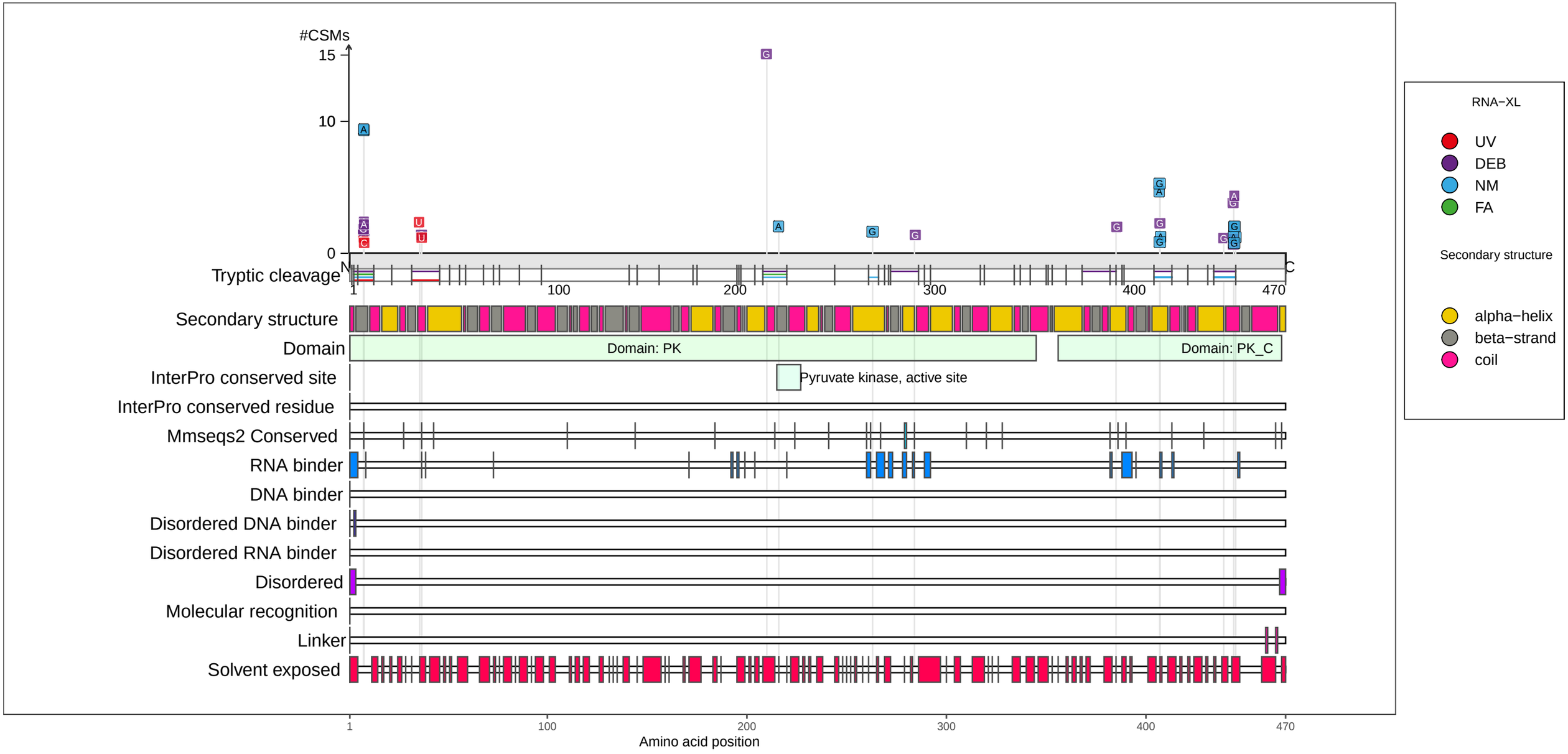
− RNA functions:
mRNA 5−UTR binding; mRNA binding; RNA binding; rRNA binding



P0AD61
KPYK1_ECOLI Pyruvate kinase I

− Abundance:
tryptic [log10 Intensity]: 9.41 (Q 95)
PAXdb K12 strain [ppm]: 2.78 (Q 86)
PAXdb E.coli [ppm]: 3.18 (Q 96)

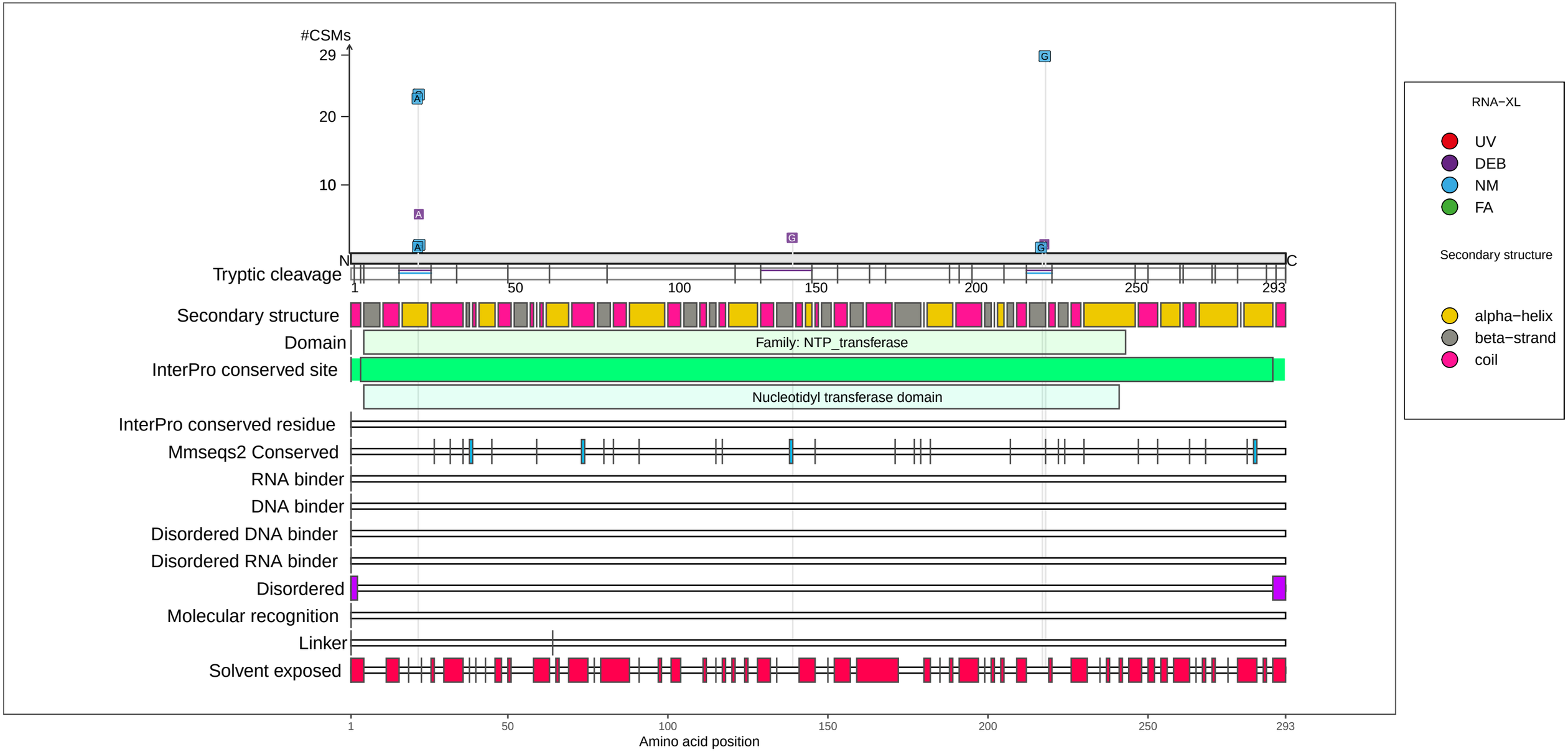
− RNA functions: not annotated



P37744
RMLA1_ECOLI Glucose−1−phosphate thymidylyltransferase 1

− Abundance:
tryptic [log10 Intensity]: 8.4 (Q 72)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 2.39 (Q 83)

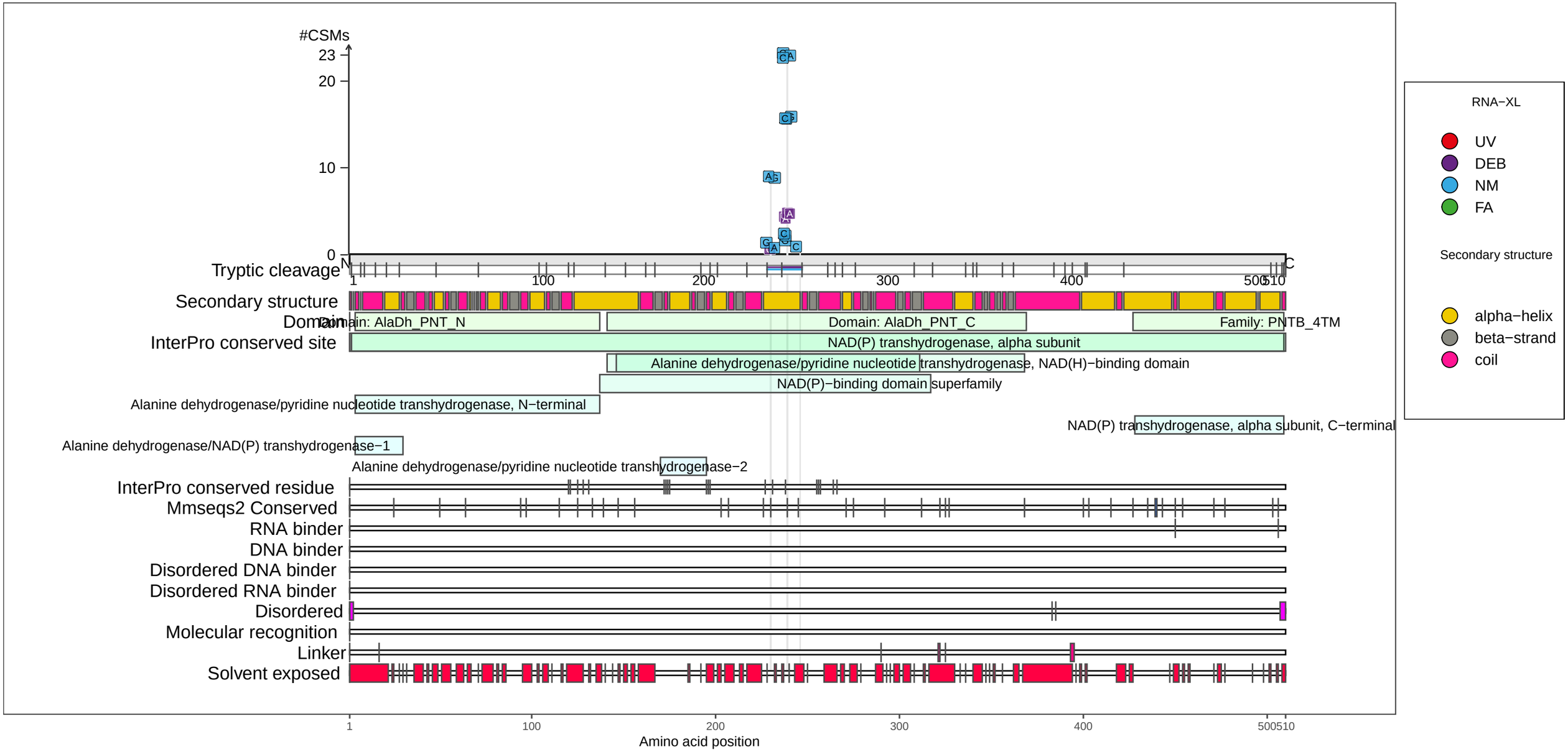
− RNA functions: not annotated



P07001
PNTA_ECOLI NAD(P) transhydrogenase subunit alpha

− Abundance:
tryptic [log10 Intensity]: 9 (Q 88)
PAXdb K12 strain [ppm]: 1.3 (Q 26)
PAXdb E.coli [ppm]: 2.4 (Q 83)

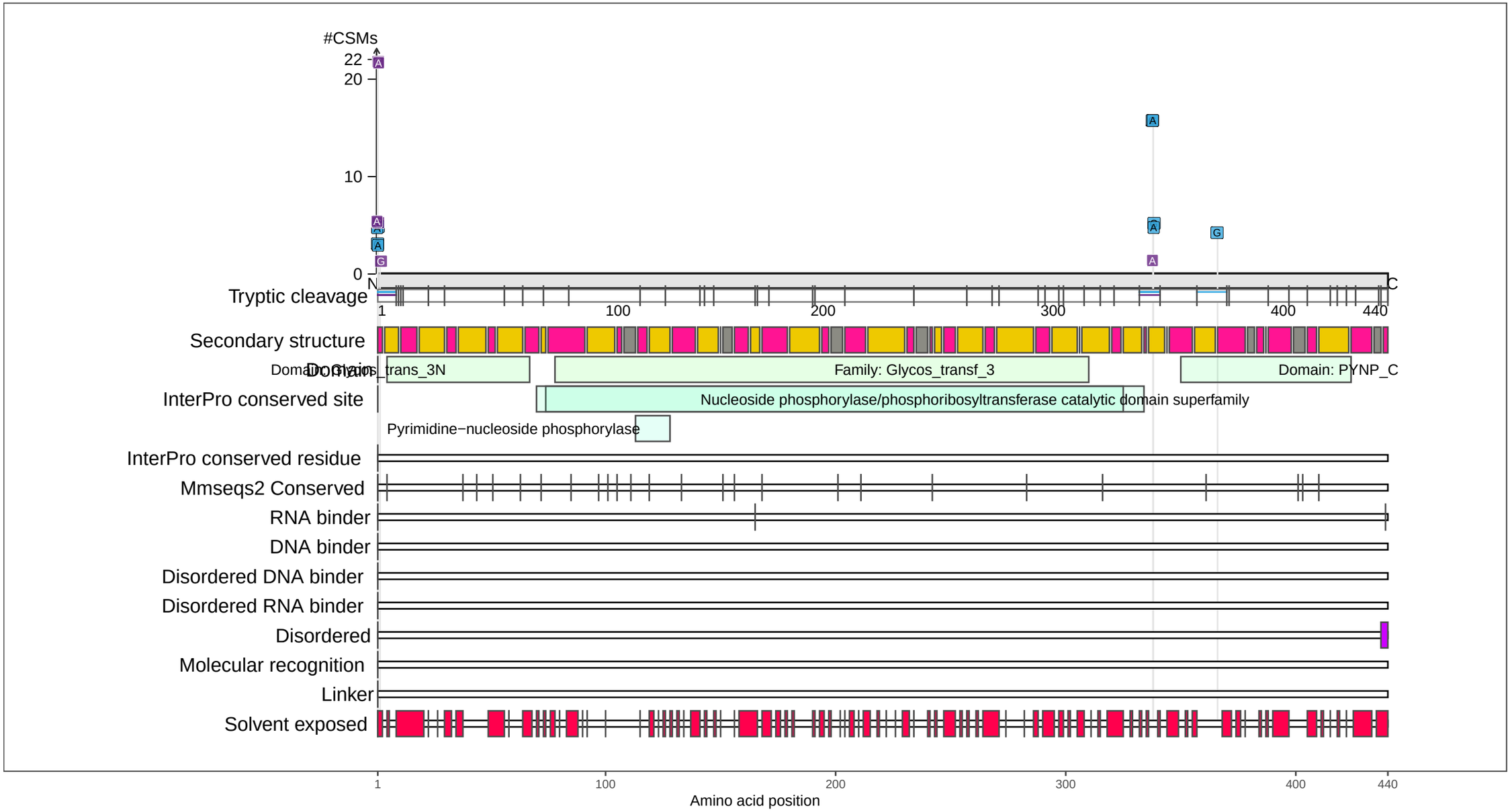
− RNA functions: not annotated



P07650
TYPH_ECOLI Thymidine phosphorylase

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 86)
PAXdb K12 strain [ppm]: 2.61 (Q 81)
PAXdb E.coli [ppm]: 2.19 (Q 77)

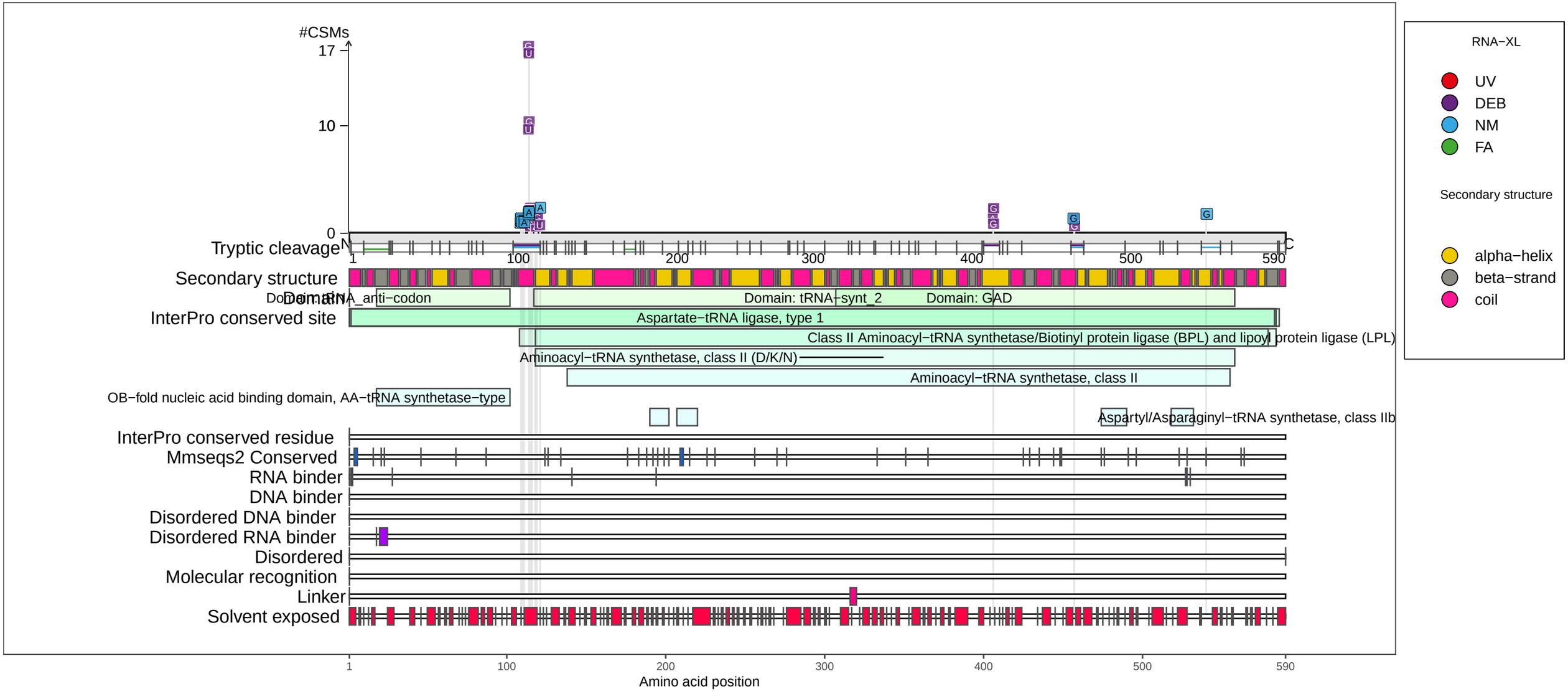
− RNA functions: not annotated



P21889
SYD_ECOLI Aspartate−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.25 (Q 93)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 2.9 (Q 93)

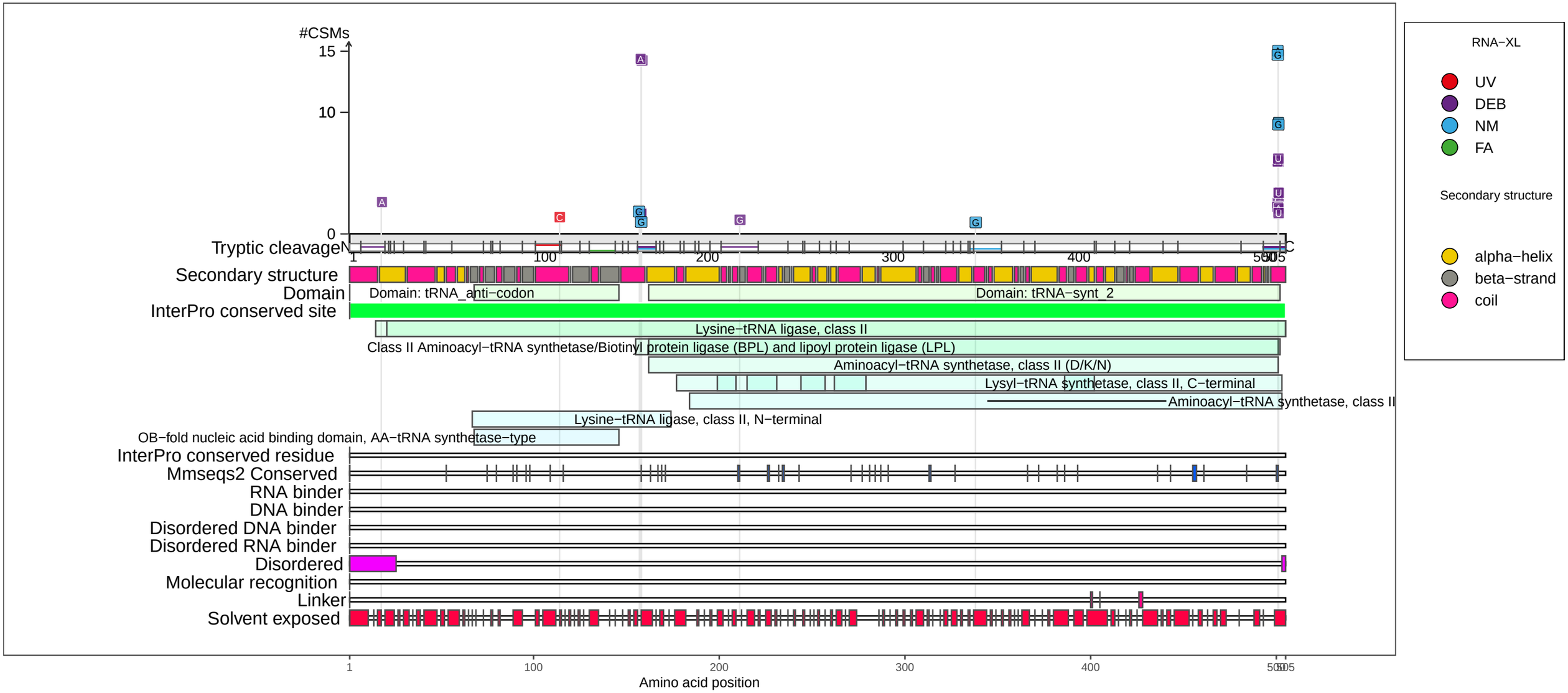
− RNA functions:
aminoacyl−tRNA ligase activity; aspartate−tRNA ligase activity
aspartyl−tRNA aminoacylation; ncRNA metabolic process; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetases class II (D, K and N)



P0A8N5
SYK2_ECOLI Lysine−−tRNA ligase, heat inducible

− Abundance:
tryptic [log10 Intensity]: 9.36 (Q 95)
PAXdb K12 strain [ppm]: 3.3 (Q 95)
PAXdb E.coli [ppm]: 2.34 (Q 82)

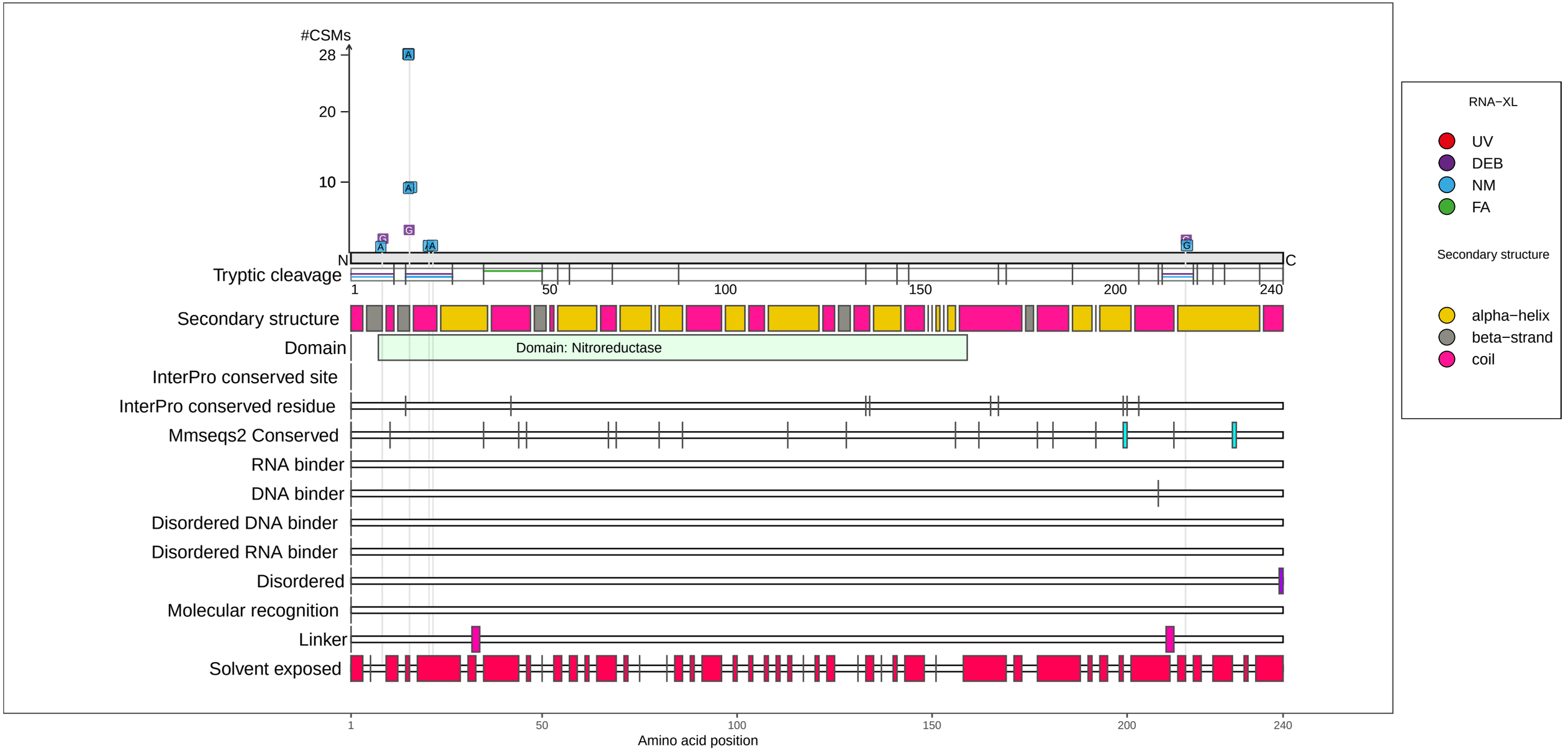
− RNA functions:
aminoacyl−tRNA ligase activity; lysine−tRNA ligase activity
lysyl−tRNA aminoacylation; ncRNA metabolic process; RNA binding; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA synthetases class II (D, K and N)



P17117
NFSA_ECOLI Oxygen−insensitive NADPH nitroreductase

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 87)
PAXdb K12 strain [ppm]: 2.86 (Q 88)
PAXdb E.coli [ppm]: 2 (Q 72)

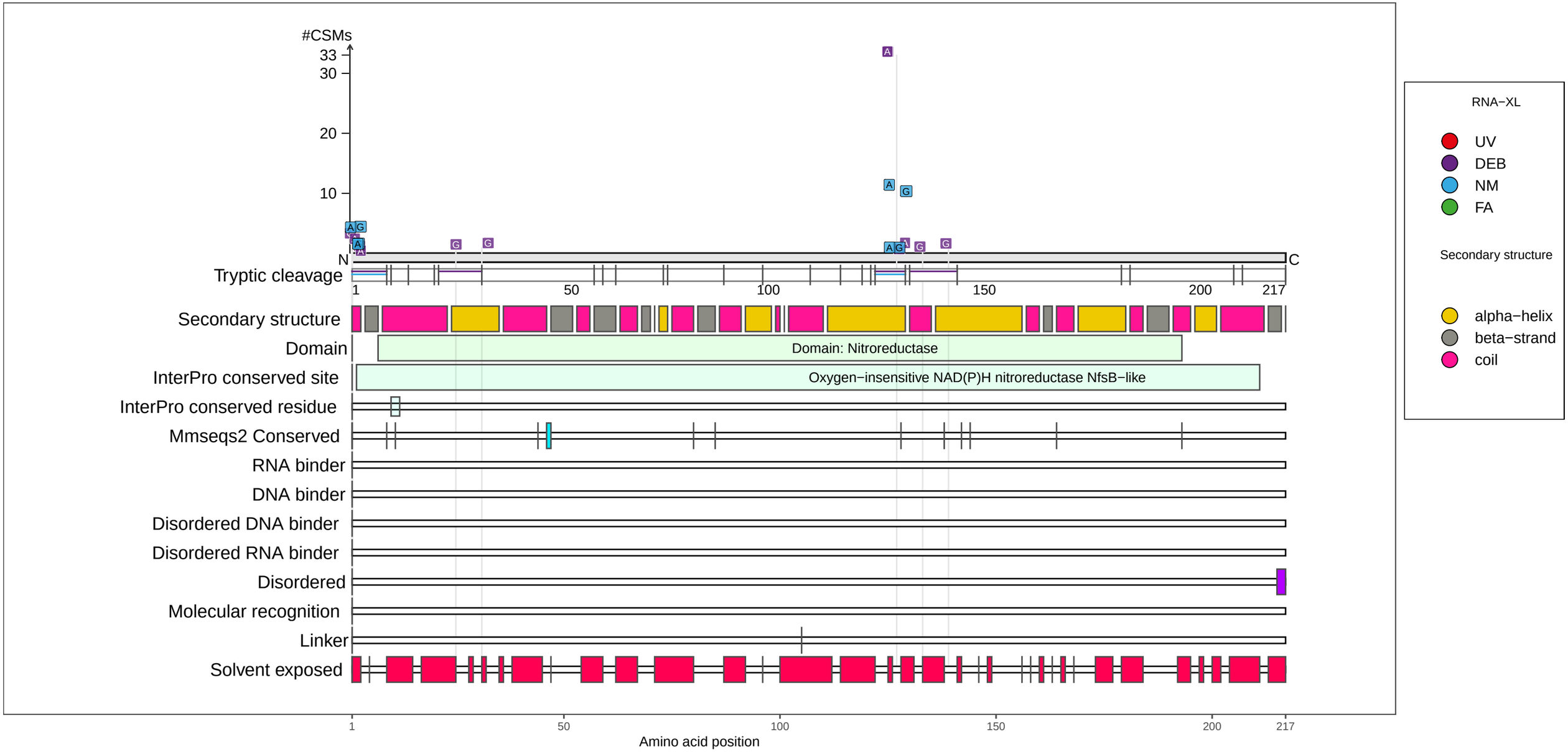
− RNA functions: not annotated



P38489
NFSB_ECOLI Oxygen−insensitive NAD(P)H nitroreductase

− Abundance:
tryptic [log10 Intensity]: 8.98 (Q 88)
PAXdb K12 strain [ppm]: 3.52 (Q 98)
PAXdb E.coli [ppm]: 2.84 (Q 92)

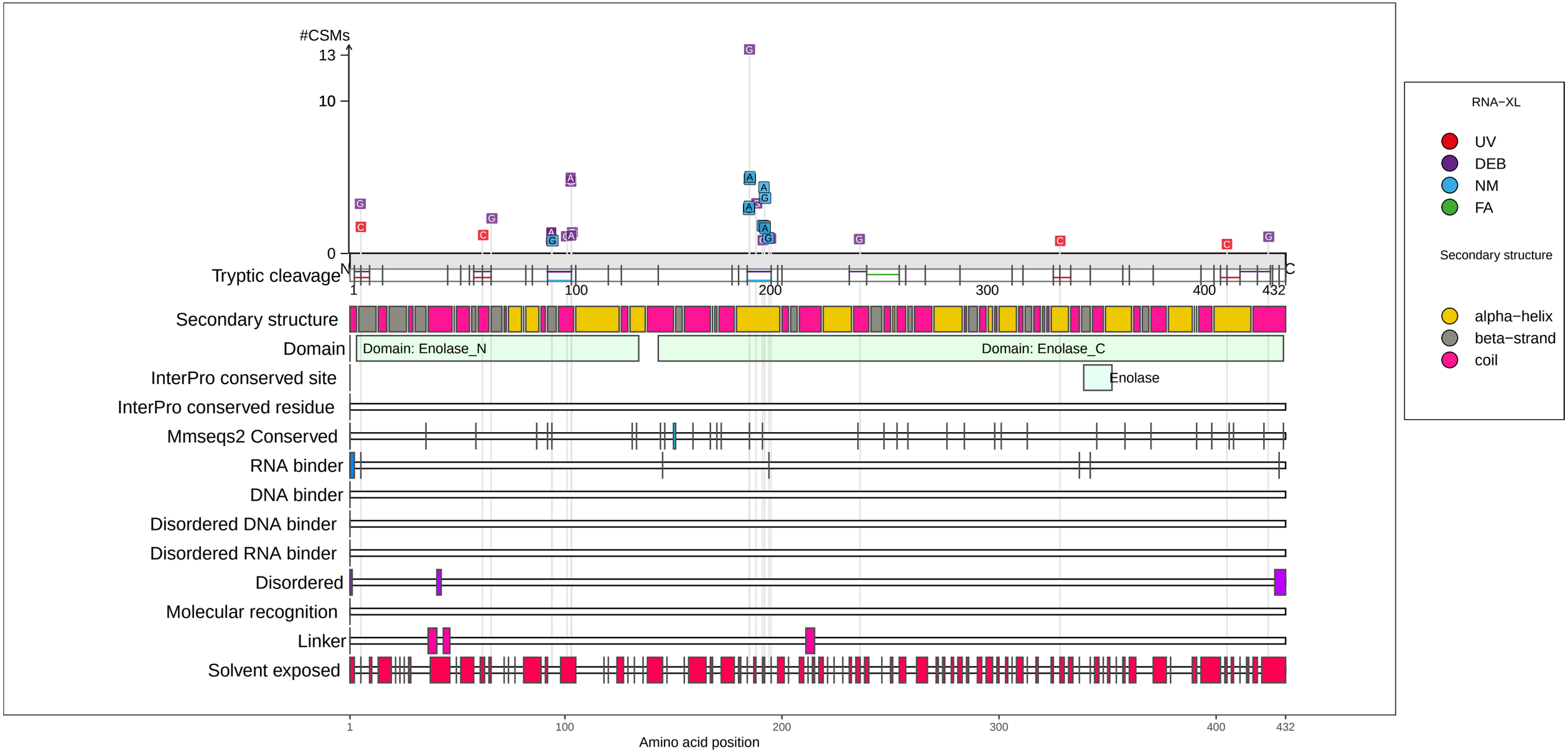
− RNA functions: not annotated



P0A6P9
ENO_ECOLI Enolase

− Abundance:
tryptic [log10 Intensity]: 9.84 (Q 99)
PAXdb K12 strain [ppm]: 3.79 (Q 99)
PAXdb E.coli [ppm]: 3.69 (Q 100)

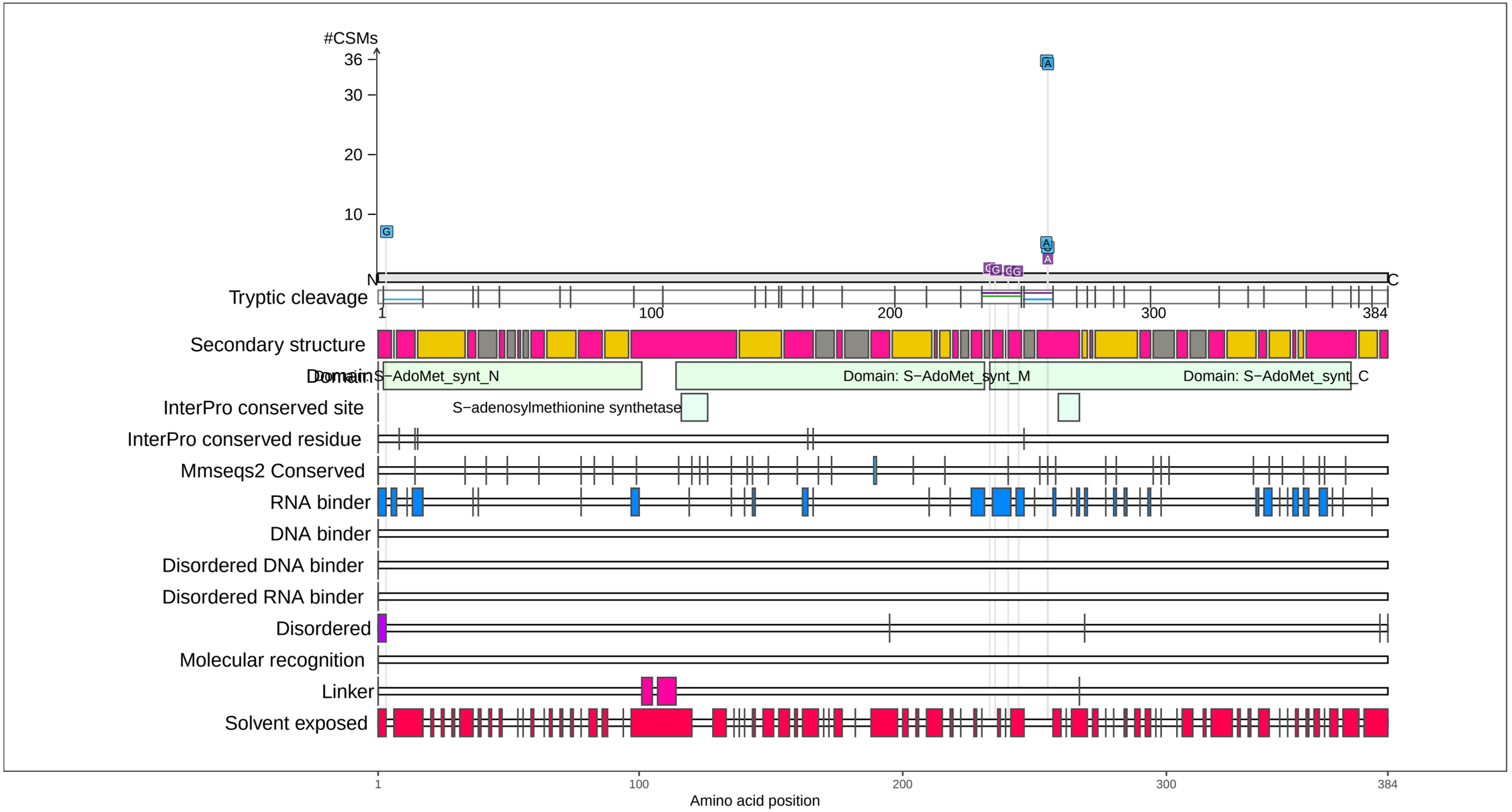
− RNA functions: not annotated



P0A817
METK_ECOLI S−adenosylmethionine synthase

− Abundance:
tryptic [log10 Intensity]: 9.37 (Q 95)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 3.21 (Q 97)

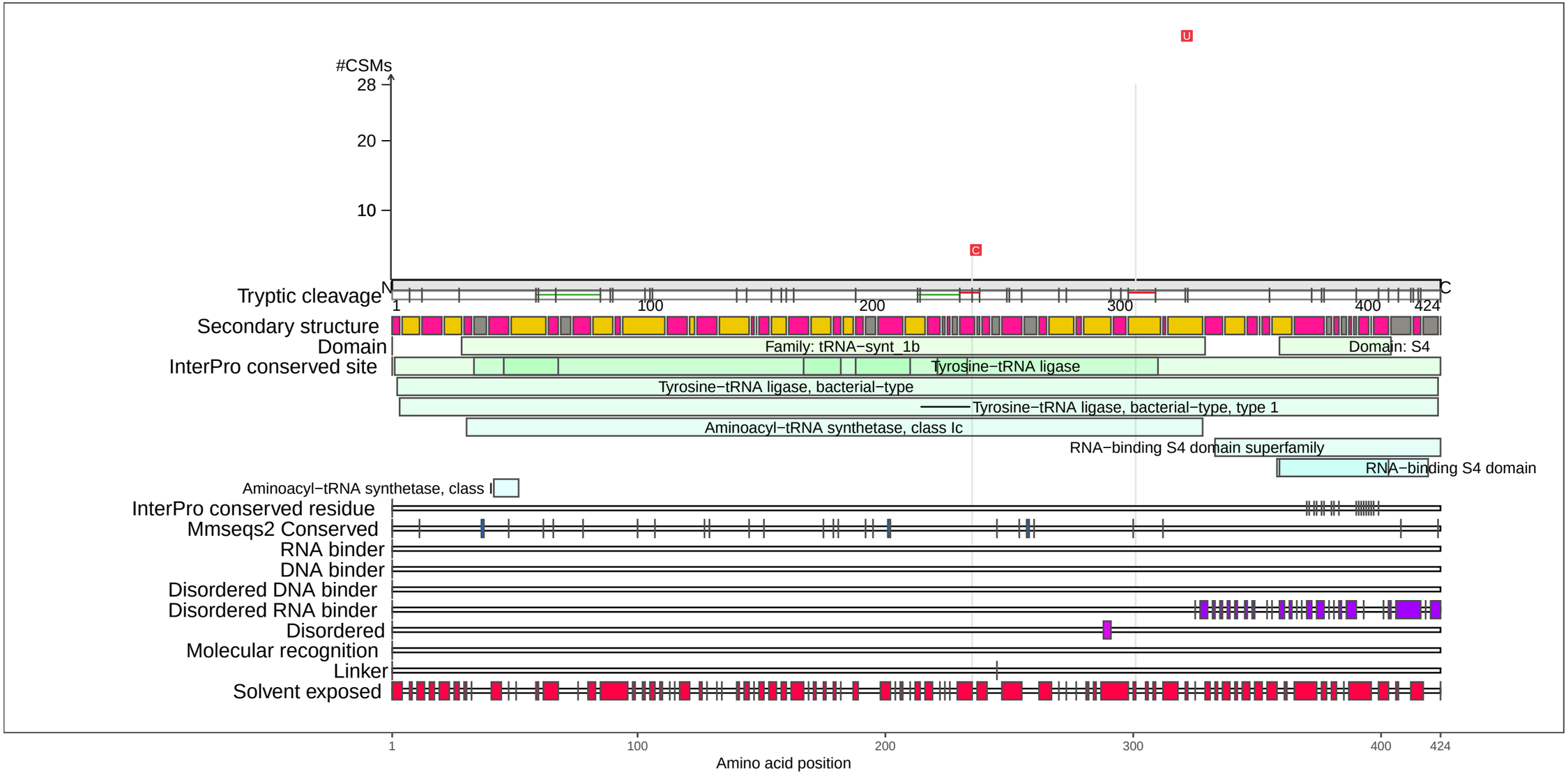
− RNA functions: not annotated



P0AGJ9
SYY_ECOLI Tyrosine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 7.94 (Q 56)
PAXdb K12 strain [ppm]: 3.05 (Q 92)
PAXdb E.coli [ppm]: 2.46 (Q 85)

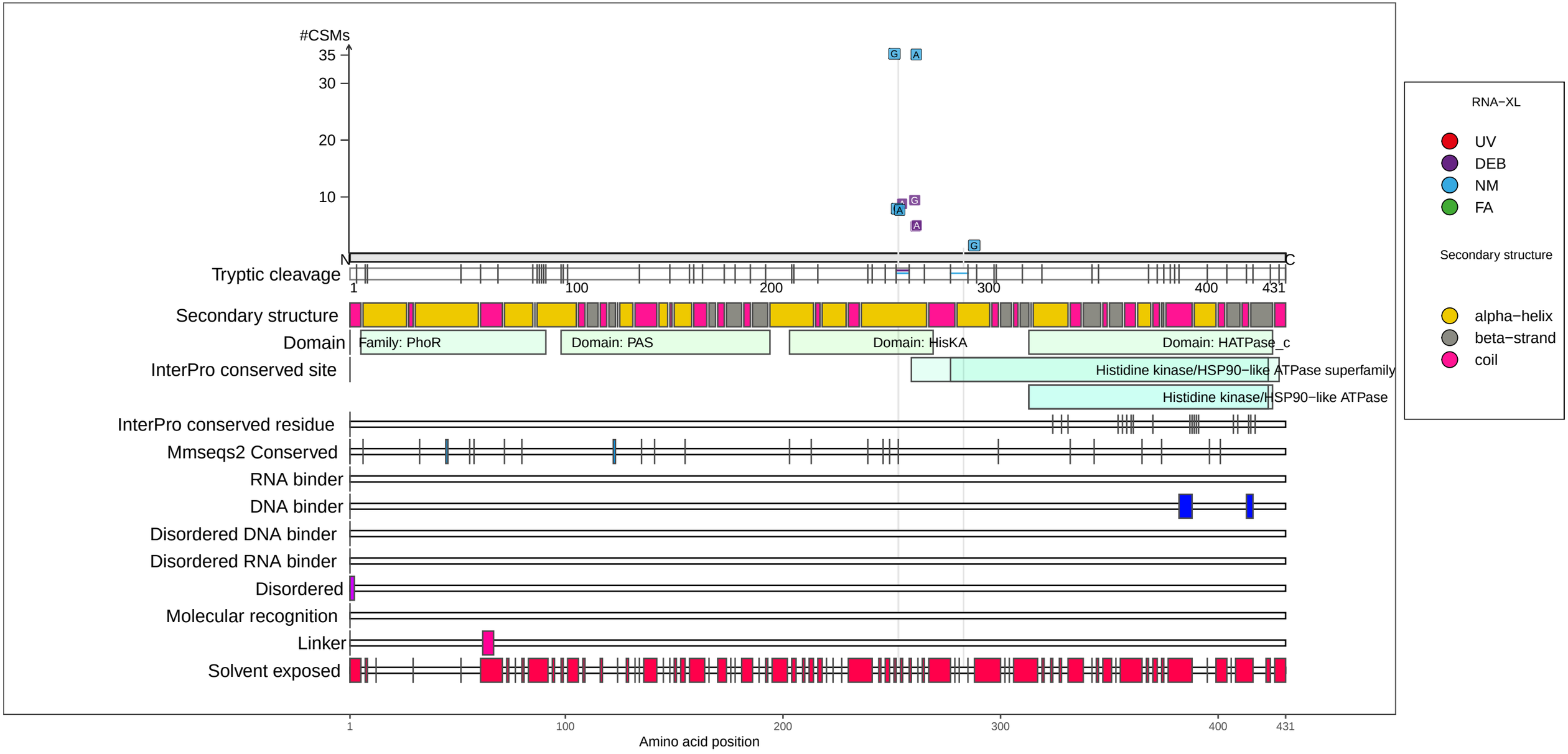
− RNA functions:
aminoacyl−tRNA ligase activity; ncRNA metabolic process; RNA binding
RNA metabolic process; S4 RNA−binding domain; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process; tRNA synthetases class I (W and Y)
tyrosine−tRNA ligase activity; tyrosyl−tRNA aminoacylation



P08400
PHOR_ECOLI Phosphate regulon sensor protein PhoR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.45 (Q 58)

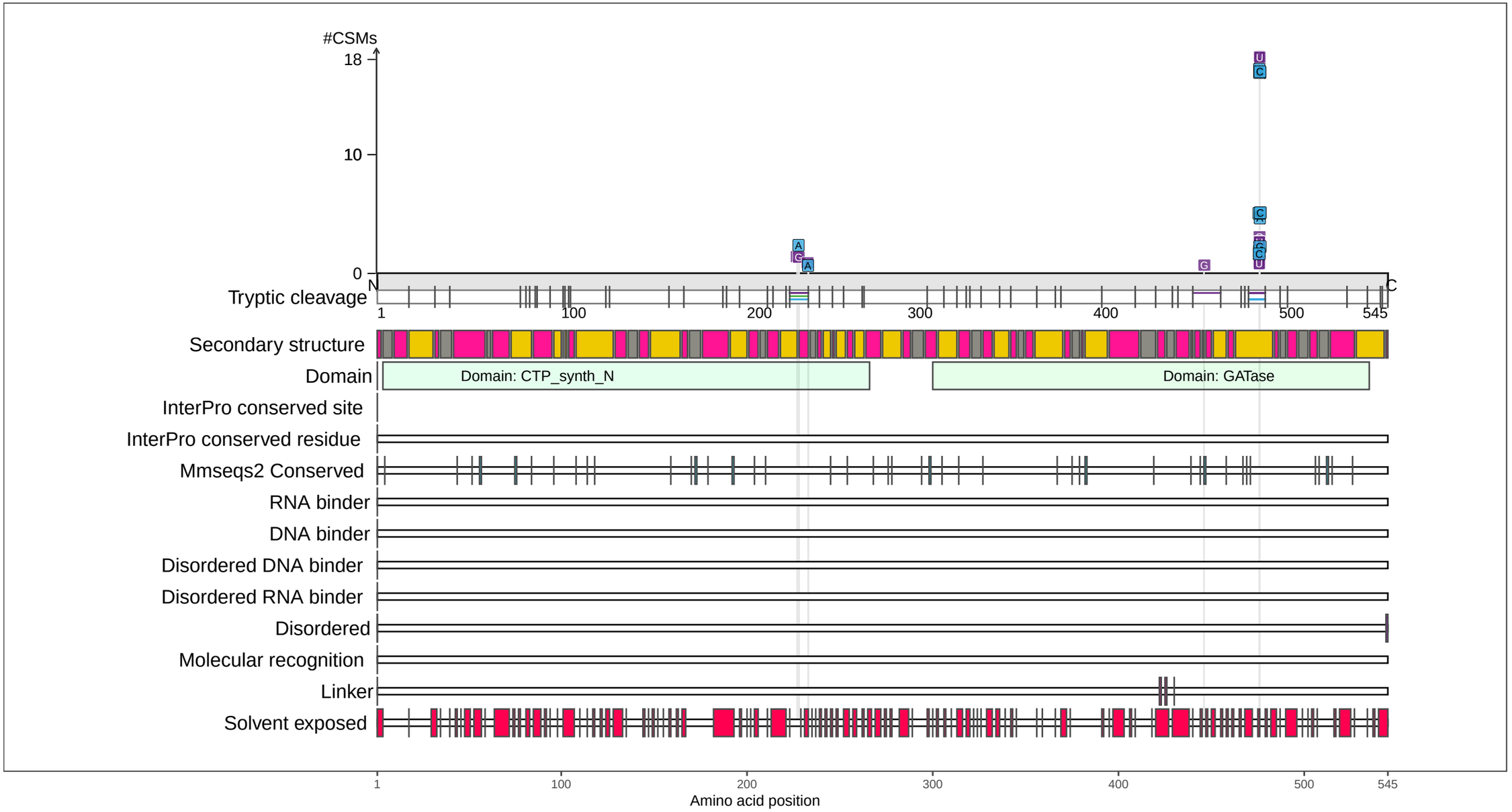
− RNA functions: not annotated



P0A7E5
PYRG_ECOLI CTP synthase

− Abundance:
tryptic [log10 Intensity]: 9.42 (Q 96)
PAXdb K12 strain [ppm]: 3.23 (Q 94)
PAXdb E.coli [ppm]: 2.32 (Q 81)

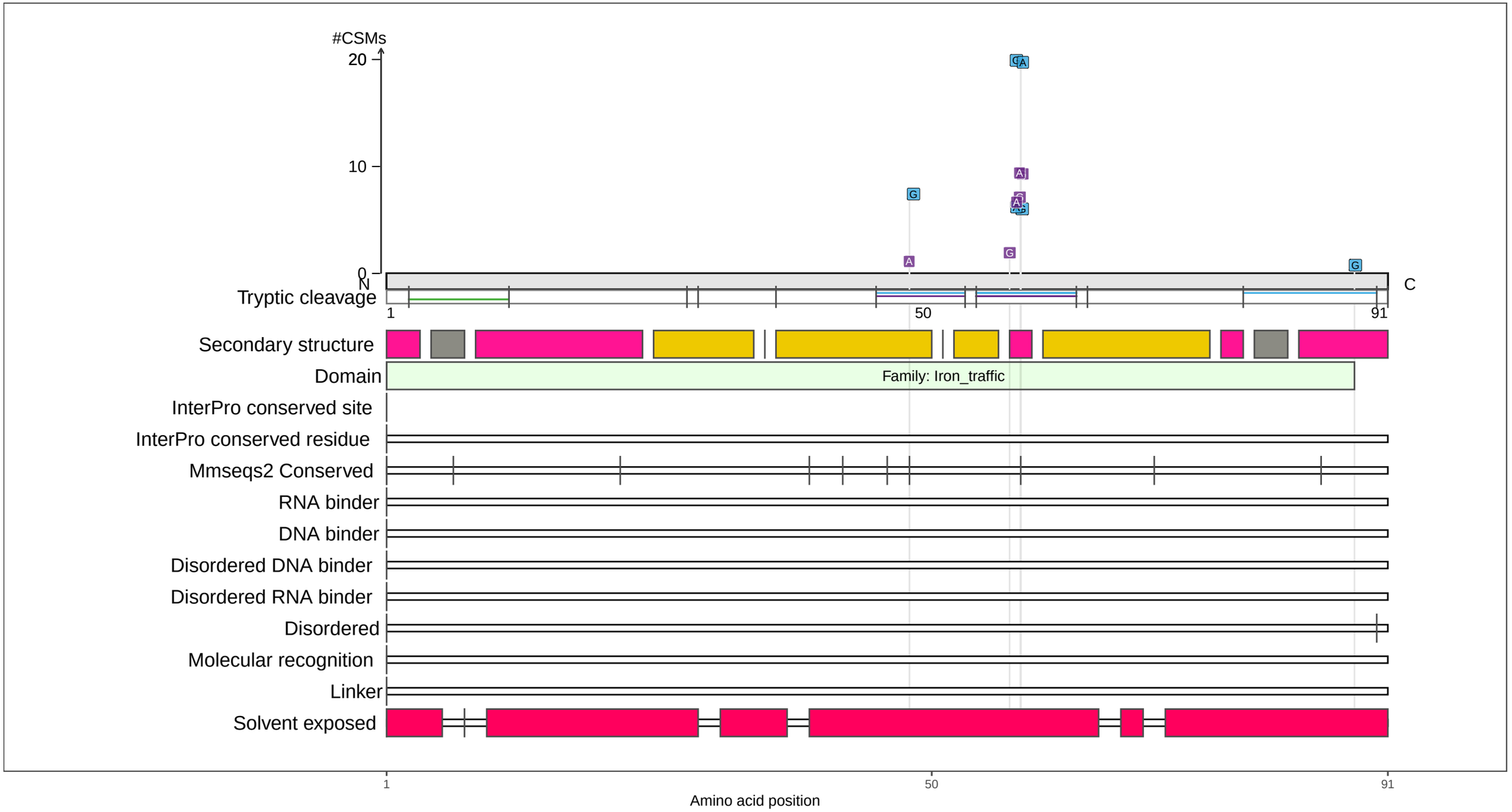
− RNA functions: not annotated

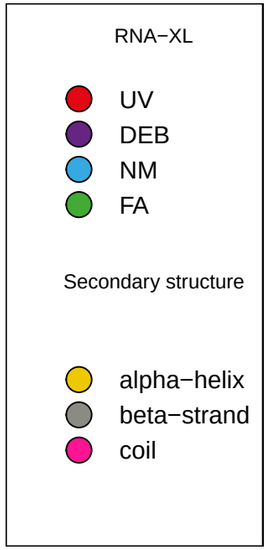


P0A8P3
FETP_ECOLI Probable Fe(2+)−trafficking protein

− Abundance:
tryptic [log10 Intensity]: 8.29 (Q 69)
PAXdb K12 strain [ppm]: 2.7 (Q 83)
PAXdb E.coli [ppm]: 3.16 (Q 96)

− RNA functions: not annotated

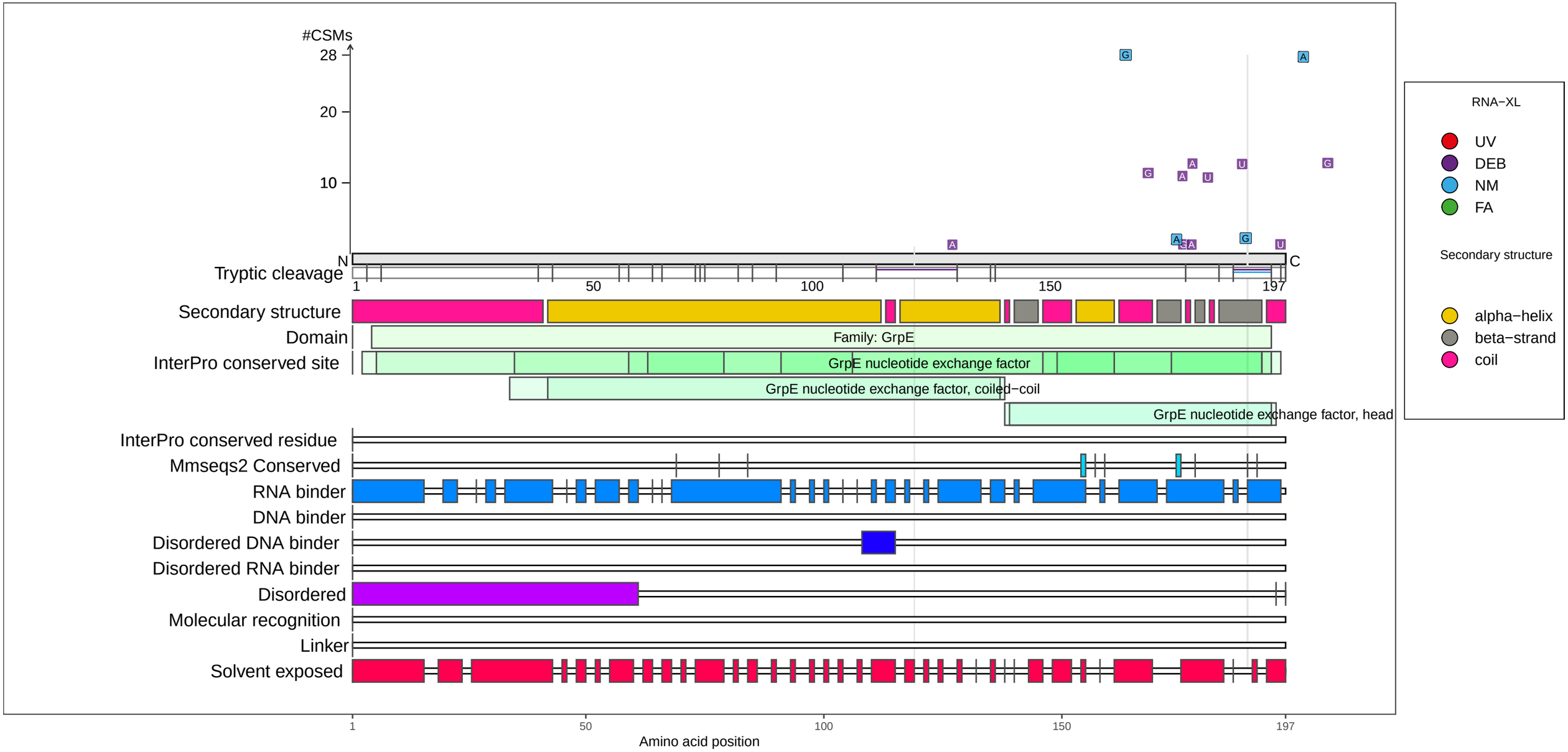




P09372
GRPE_ECOLI Protein GrpE

− Abundance:
tryptic [log10 Intensity]: 8.79 (Q 83)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 3.01 (Q 95)

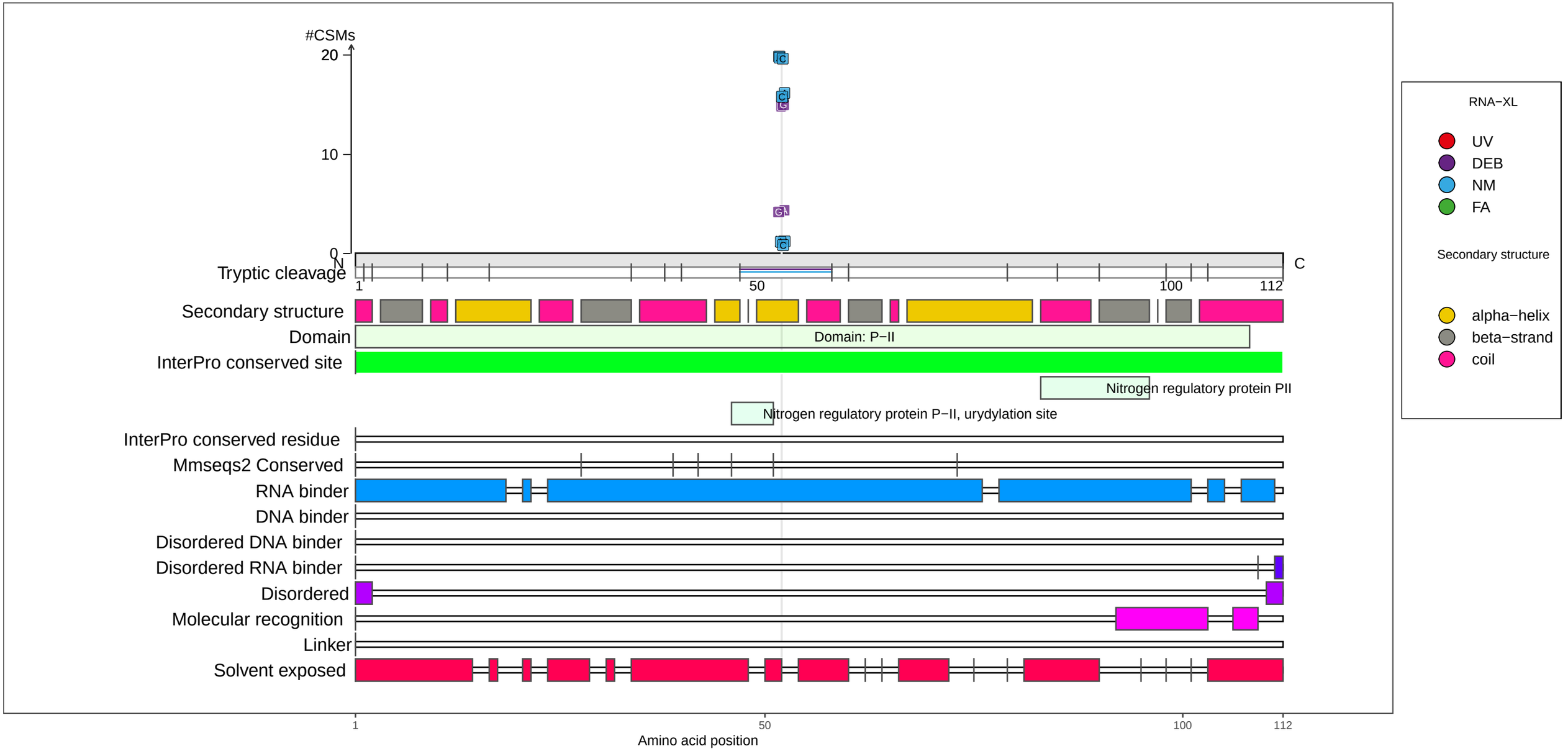
− RNA functions: not annotated



P0A9Z1
GLNB_ECOLI Nitrogen regulatory protein P−II 1

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 2.66 (Q 89)

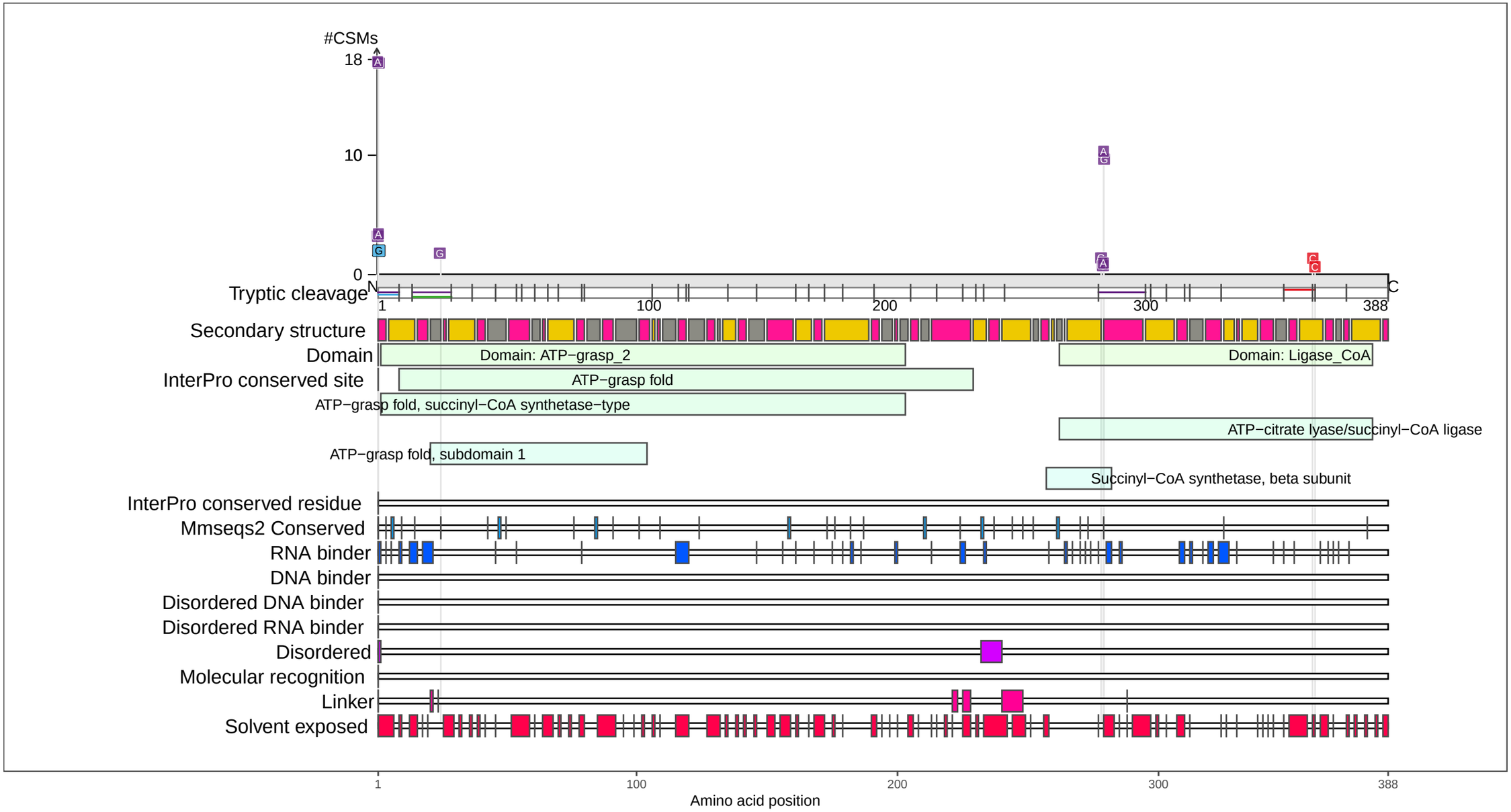
− RNA functions: not annotated



P0A836
SUCC_ECOLI Succinate−−CoA ligase [ADP−forming] subunit beta

− Abundance:
tryptic [log10 Intensity]: 9.18 (Q 92)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 3.27 (Q 97)

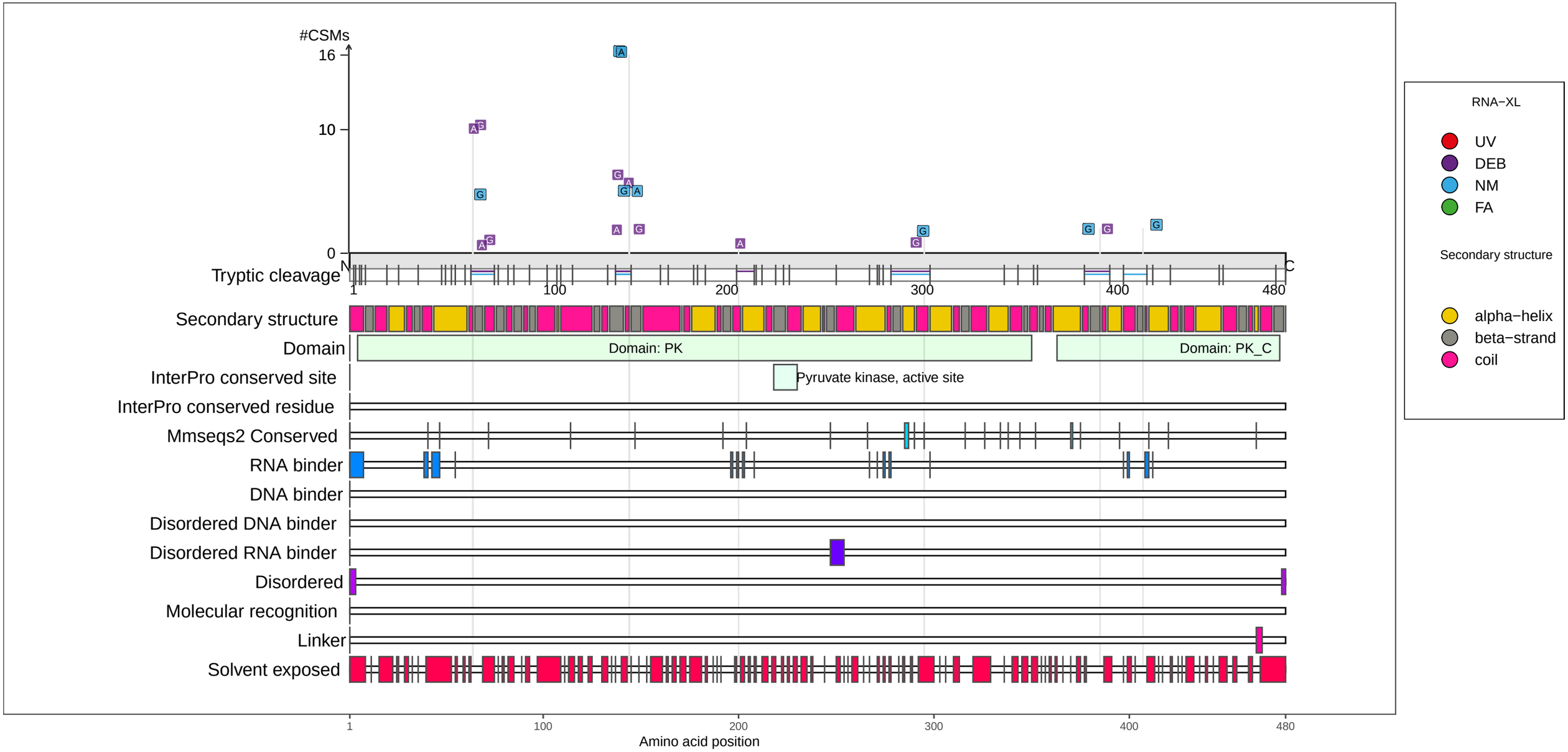
− RNA functions: not annotated



P21599
KPYK2_ECOLI Pyruvate kinase II

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 93)
PAXdb K12 strain [ppm]: 3.17 (Q 93)
PAXdb E.coli [ppm]: 2.91 (Q 93)

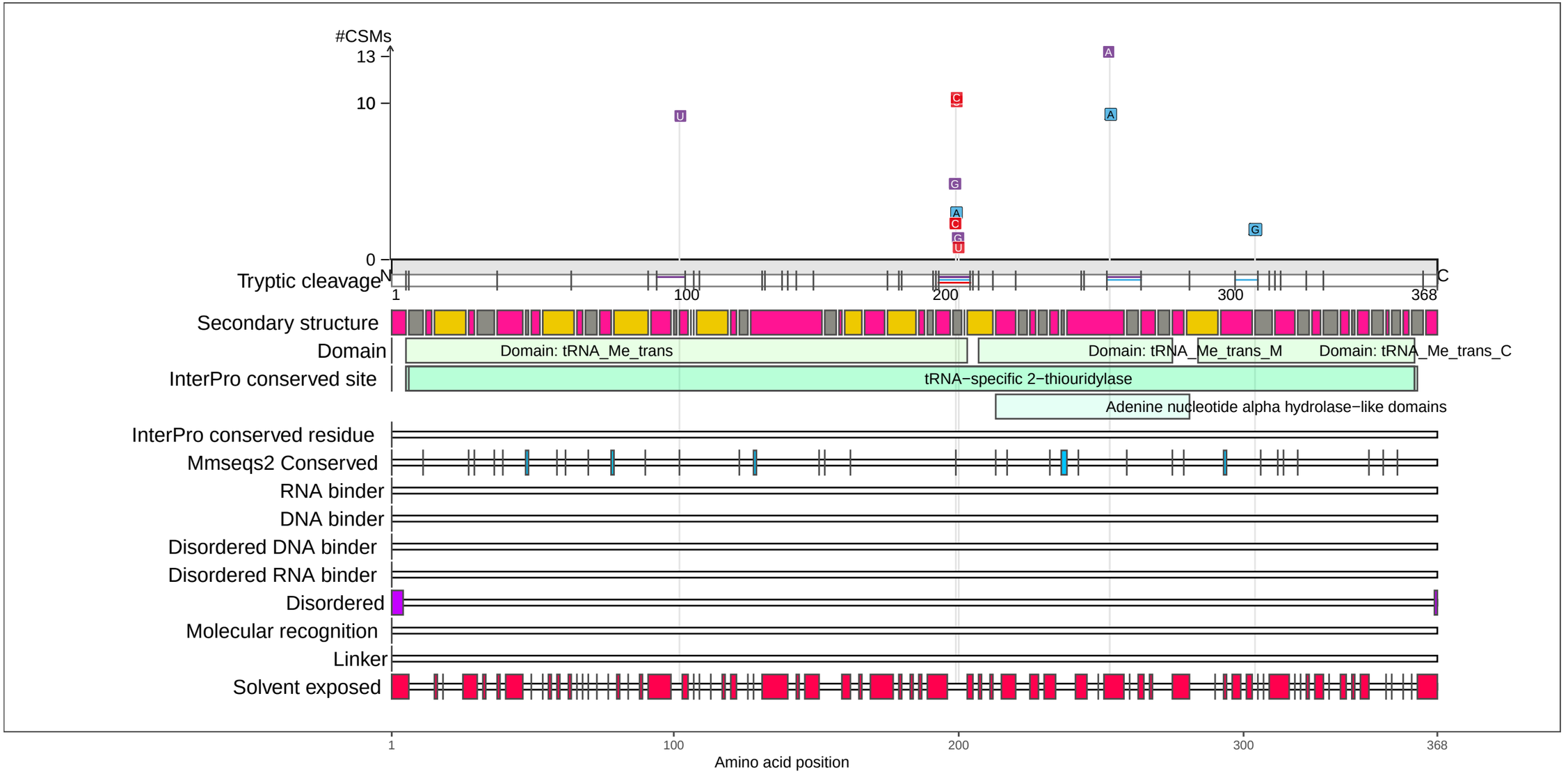
− RNA functions: not annotated



P25745
MNMA_ECOLI tRNA−specific 2−thiouridylase MnmA

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 2.21 (Q 67)
PAXdb E.coli [ppm]: 2.31 (Q 80)

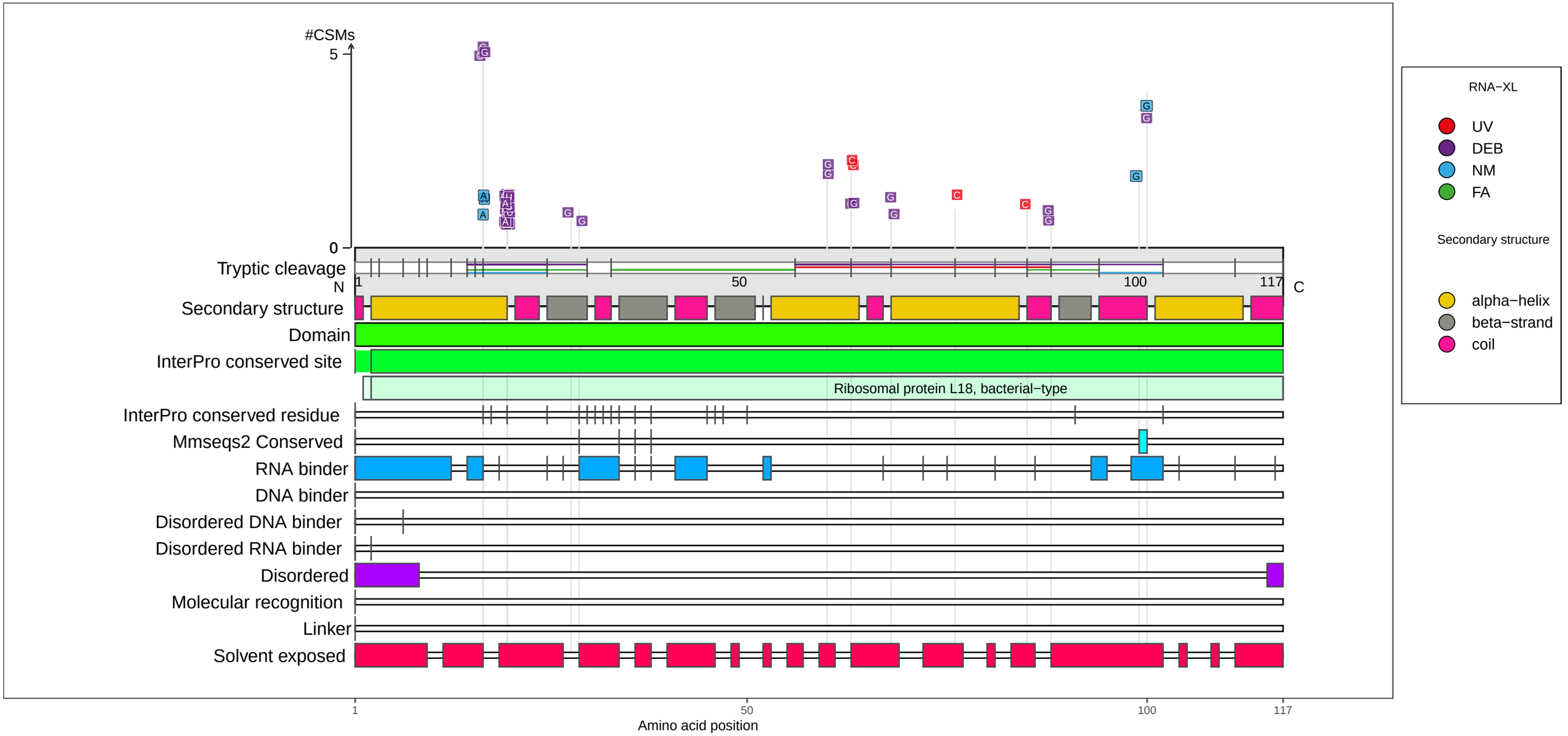
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; tRNA binding; tRNA metabolic process; tRNA methyl transferase
tRNA modification; tRNA processing; tRNA thio−modification
tRNA wobble base modification; tRNA wobble position uridine thiolation; tRNA wobble uridine modification



P0C018
RL18_ECOLI 50S ribosomal protein L18

− Abundance:
tryptic [log10 Intensity]: 8.7 (Q 81)
PAXdb K12 strain [ppm]: 3.89 (Q 100)
PAXdb E.coli [ppm]: 3.39 (Q 98)

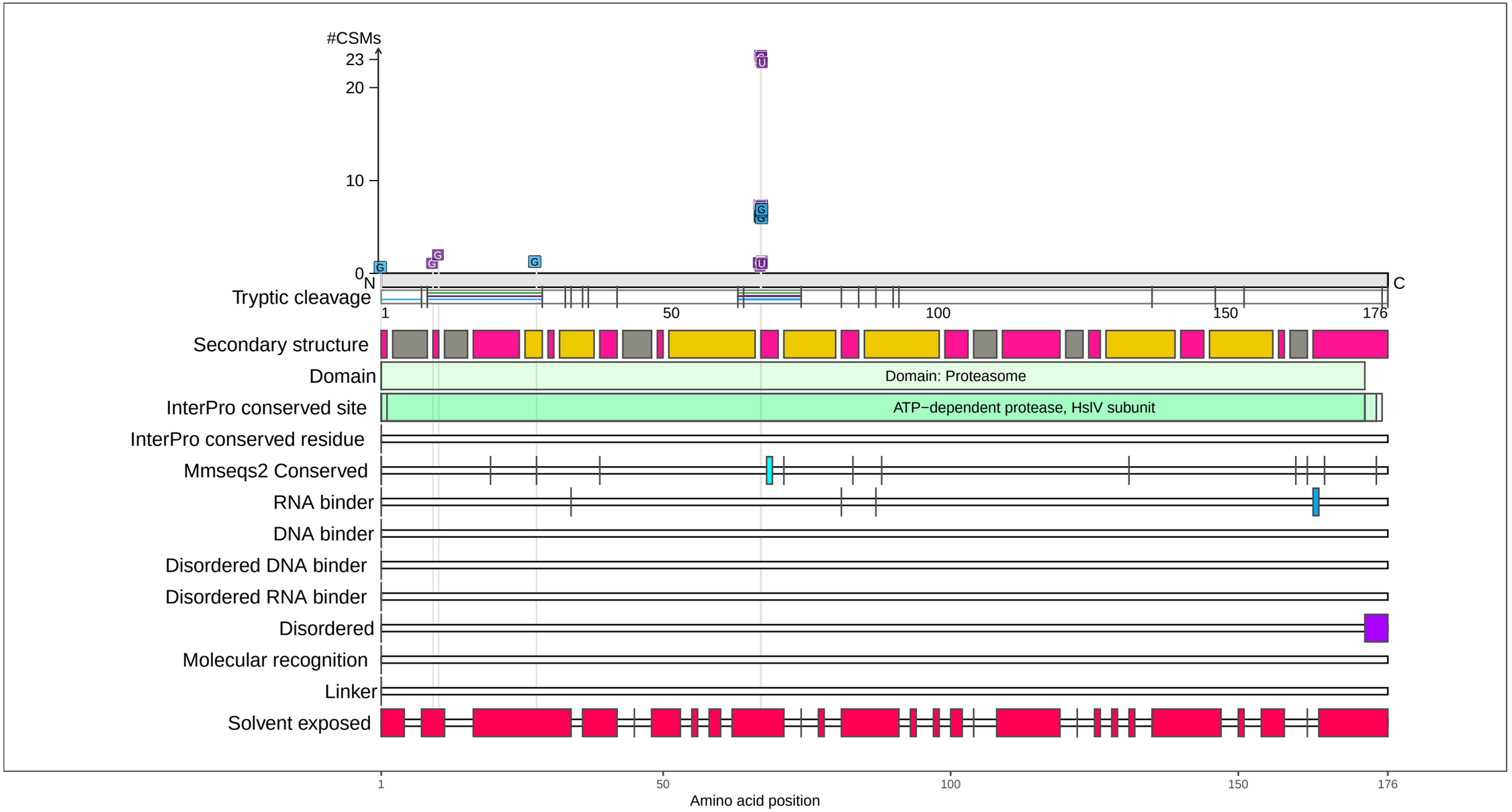
− RNA functions:
5S rRNA binding; RNA binding; rRNA binding

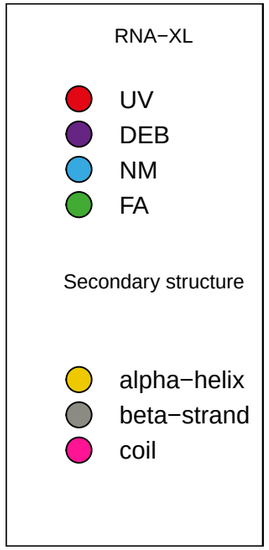


P0A7B8
HSLV_ECOLI ATP−dependent protease subunit HslV

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 2.16 (Q 76)

− RNA functions: not annotated

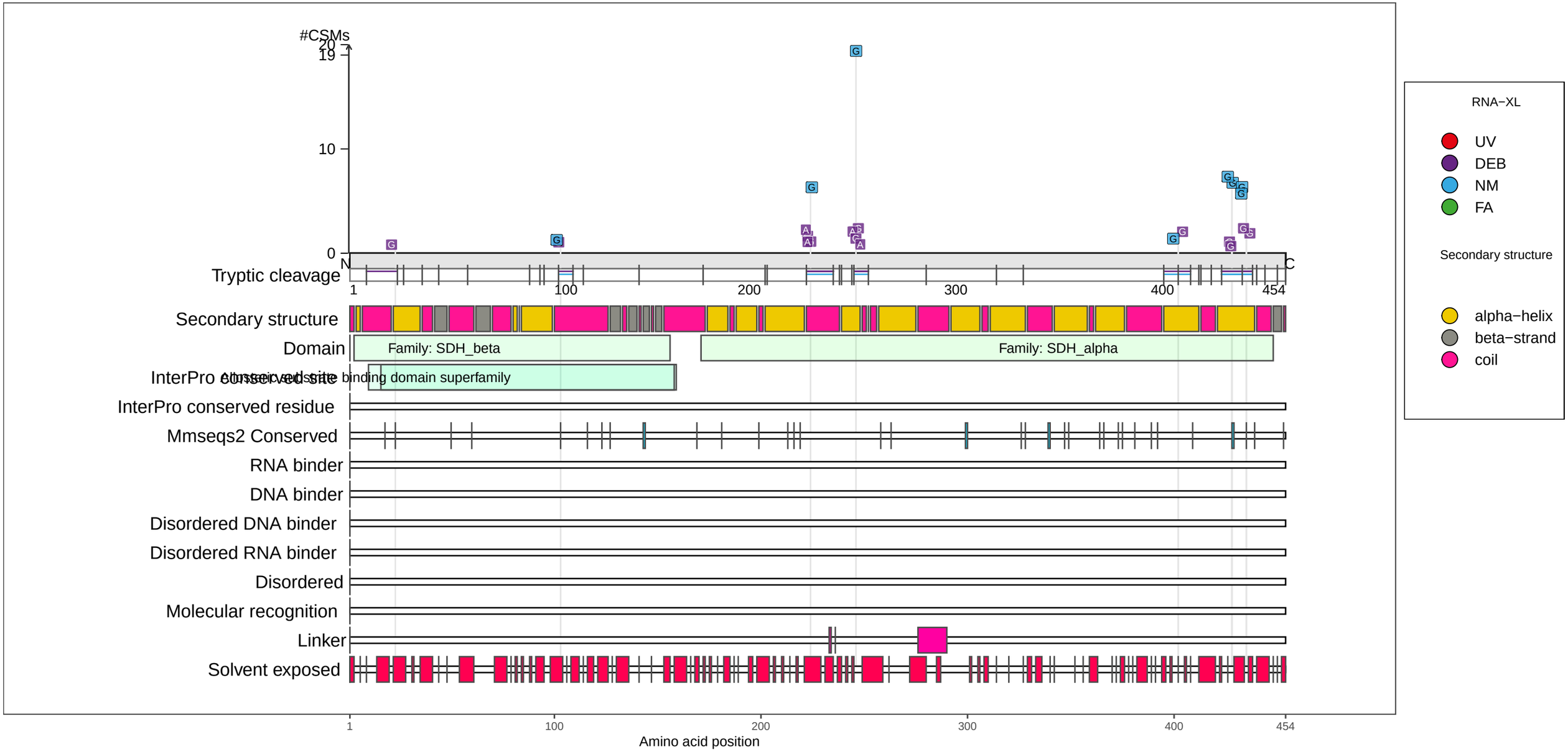




P16095
SDHL_ECOLI L−serine dehydratase 1

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 77)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 1.44 (Q 58)

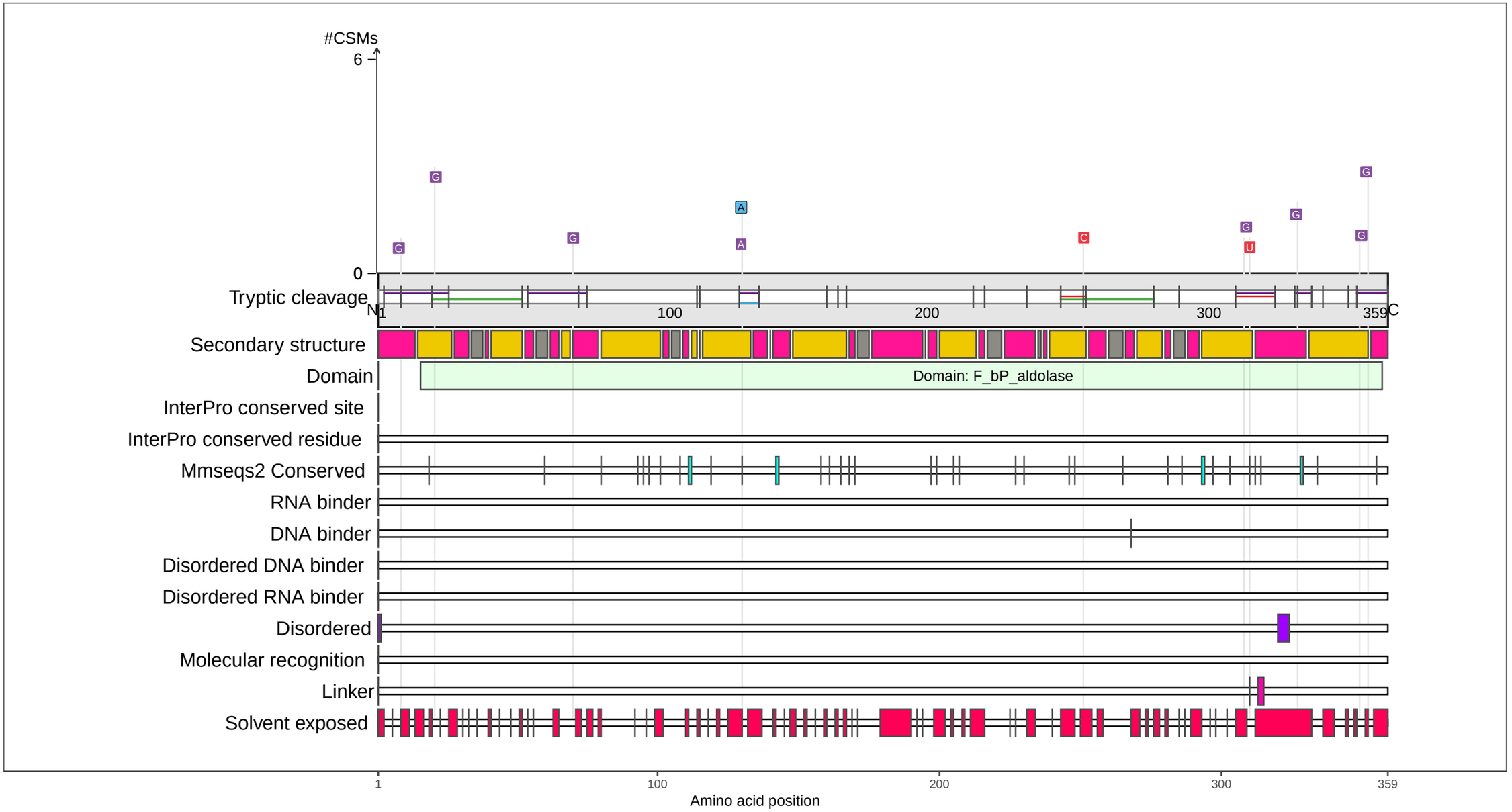
− RNA functions: not annotated

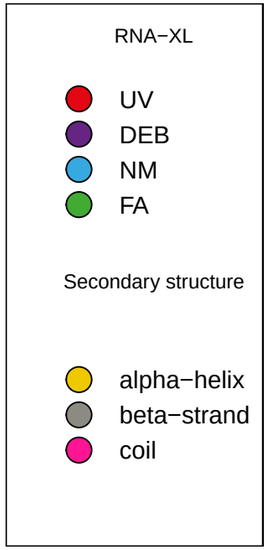


P0AB71
ALF_ECOLI Fructose−bisphosphate aldolase class 2

− Abundance:
tryptic [log10 Intensity]: 10.21 (Q 100)
PAXdb K12 strain [ppm]: 3.52 (Q 98)
PAXdb E.coli [ppm]: 3.5 (Q 99)

− RNA functions: not annotated

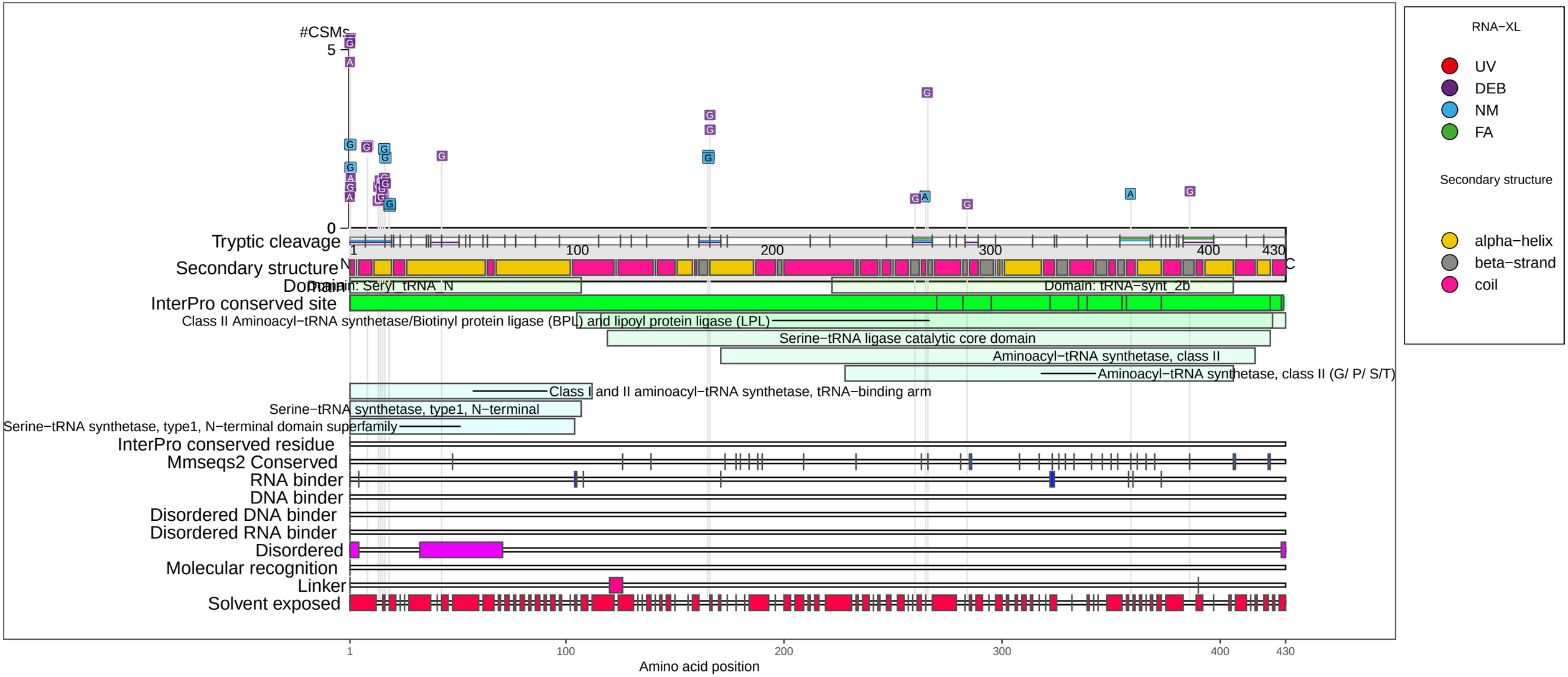




P0A8L1
SYS_ECOLI Serine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.34 (Q 95)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 2.93 (Q 94)

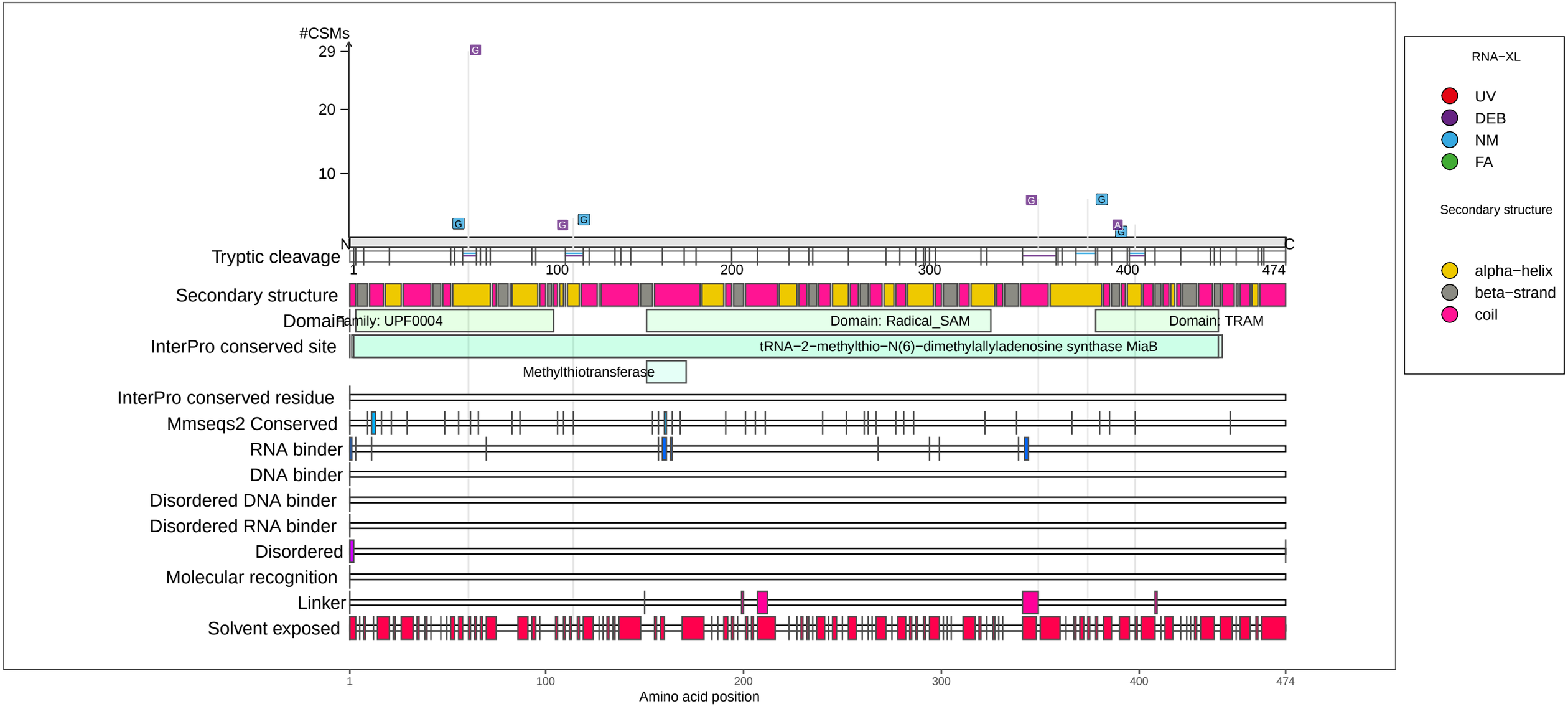
− RNA functions:
aminoacyl−tRNA ligase activity; ncRNA metabolic process; RNA biosynthetic process
RNA metabolic process; selenocysteinyl−tRNA(Sec) biosynthetic process
serine−tRNA ligase activity; seryl−tRNA aminoacylation; Seryl−tRNA synthetase N−terminal domain
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetase class II core domain (G, H, P, S and T)



P0AEI1
MIAB_ECOLI tRNA−2−methylthio−N(6)−dimethylallyladenosine synthase

− Abundance:
tryptic [log10 Intensity]: 8.78 (Q 83)
PAXdb K12 strain [ppm]: 1.45 (Q 35)
PAXdb E.coli [ppm]: 1.5 (Q 60)

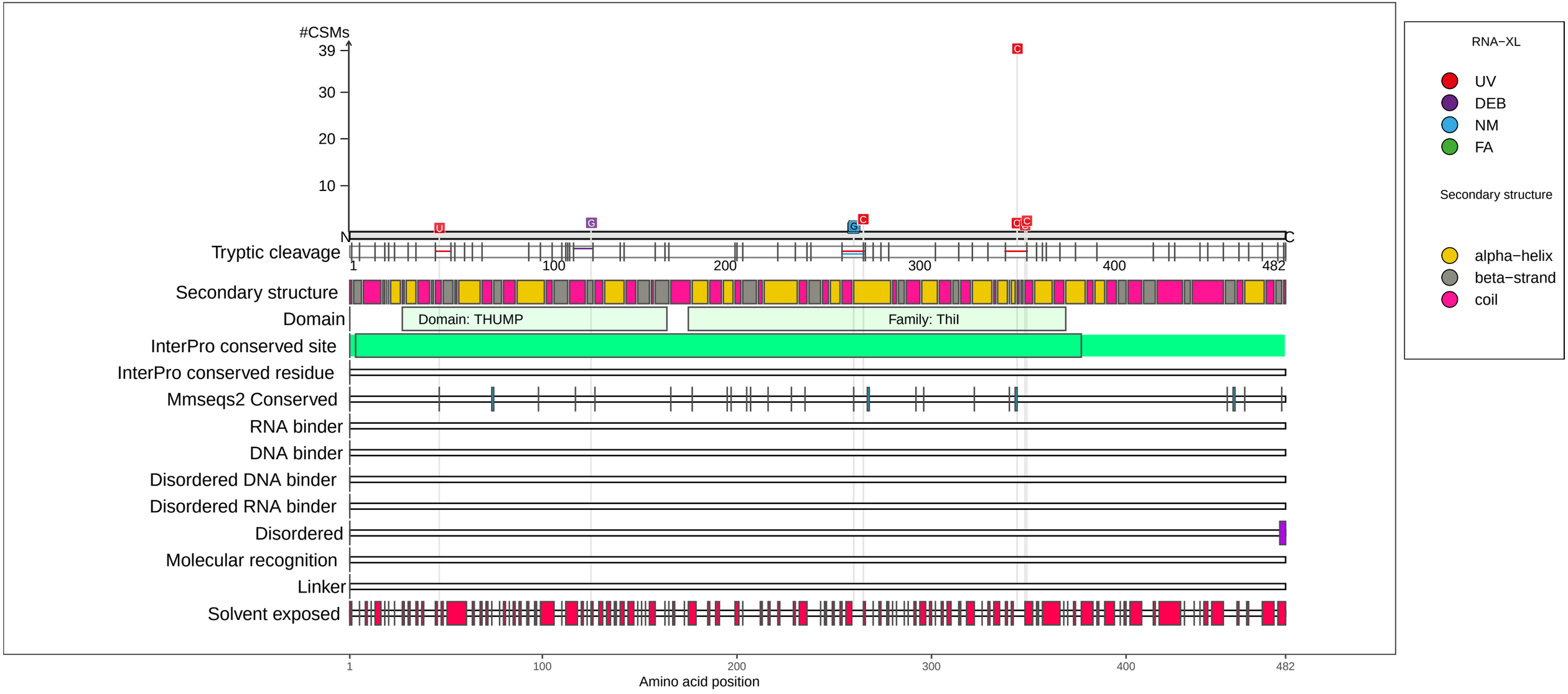
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA methylation
RNA modification; RNA processing; tRNA metabolic process; tRNA methylation
tRNA methylthiolation; tRNA modification; tRNA processing



P77718
THII_ECOLI tRNA sulfurtransferase

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 1.51 (Q 60)

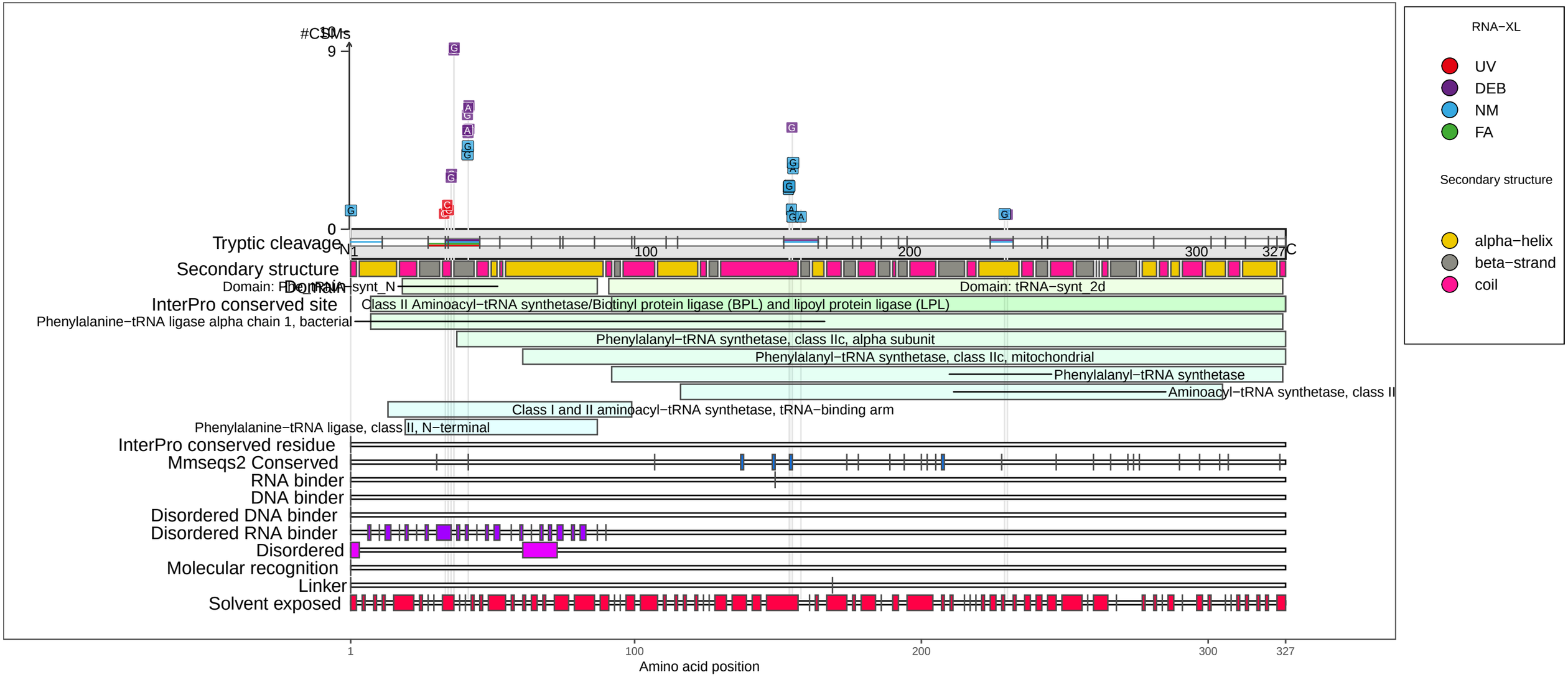
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA adenylyltransferase activity
RNA binding; RNA metabolic process; RNA modification; RNA processing
tRNA 4−thiouridine biosynthesis; tRNA adenylyltransferase activity; tRNA binding; tRNA metabolic process
tRNA modification; tRNA processing; tRNA thio−modification



P08312
SYFA_ECOLI Phenylalanine−−tRNA ligase alpha subunit

− Abundance:
tryptic [log10 Intensity]: 9.12 (Q 91)
PAXdb K12 strain [ppm]: 2.97 (Q 90)
PAXdb E.coli [ppm]: 2.61 (Q 88)

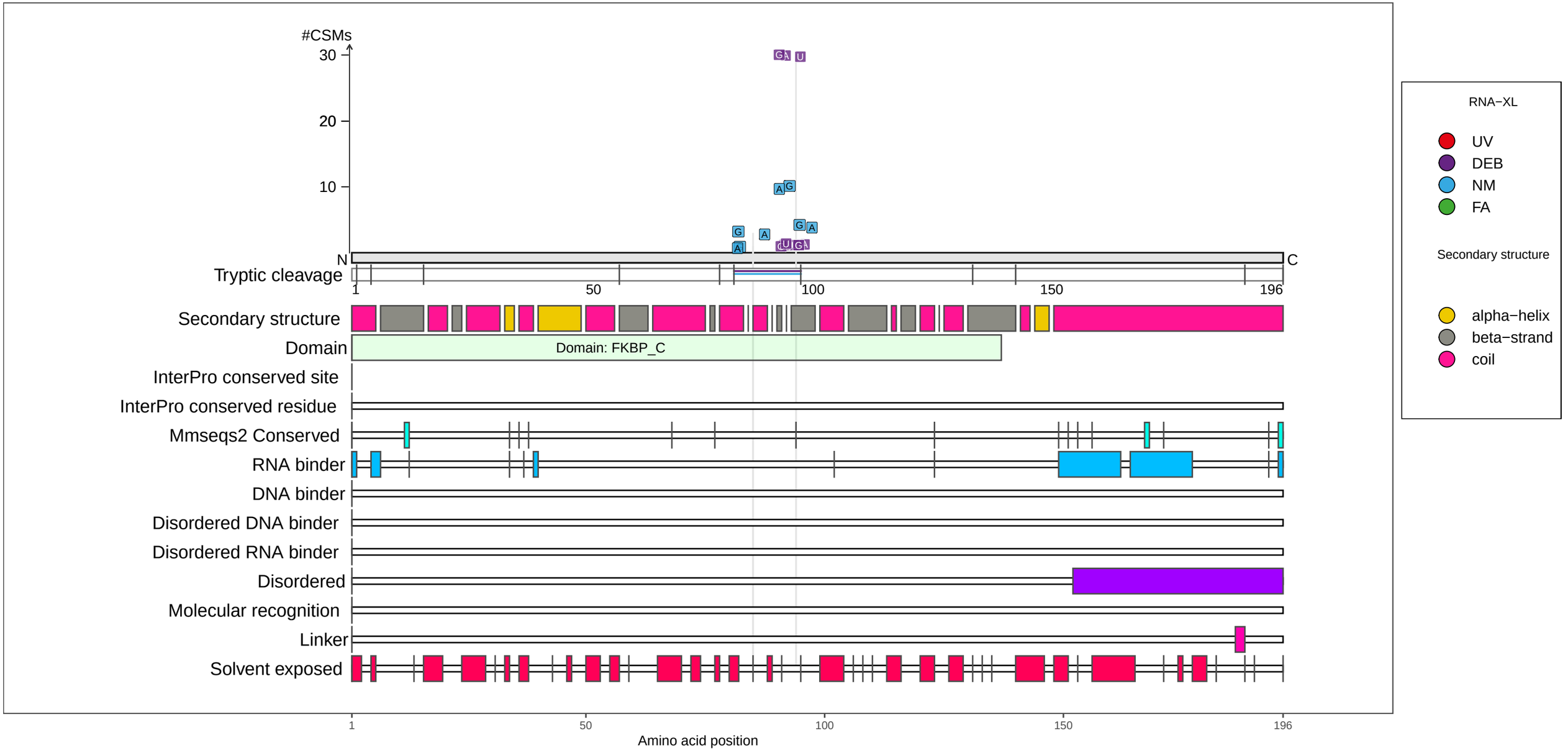
− RNA functions:
Aminoacyl tRNA synthetase class II, N−terminal domain
aminoacyl−tRNA ligase activity; ncRNA metabolic process; phenylalanine−tRNA ligase activity
phenylalanine−tRNA ligase complex; phenylalanyl−tRNA aminoacylation; RNA binding; RNA metabolic process
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA binding
tRNA metabolic process; tRNA synthetases class II core domain (F)



P0A9K9
SLYD_ECOLI FKBP−type peptidyl−prolyl cis−trans isomerase SlyD

− Abundance:
tryptic [log10 Intensity]: 9.87 (Q 99)
PAXdb K12 strain [ppm]: 3.39 (Q 96)
PAXdb E.coli [ppm]: 3.2 (Q 96)

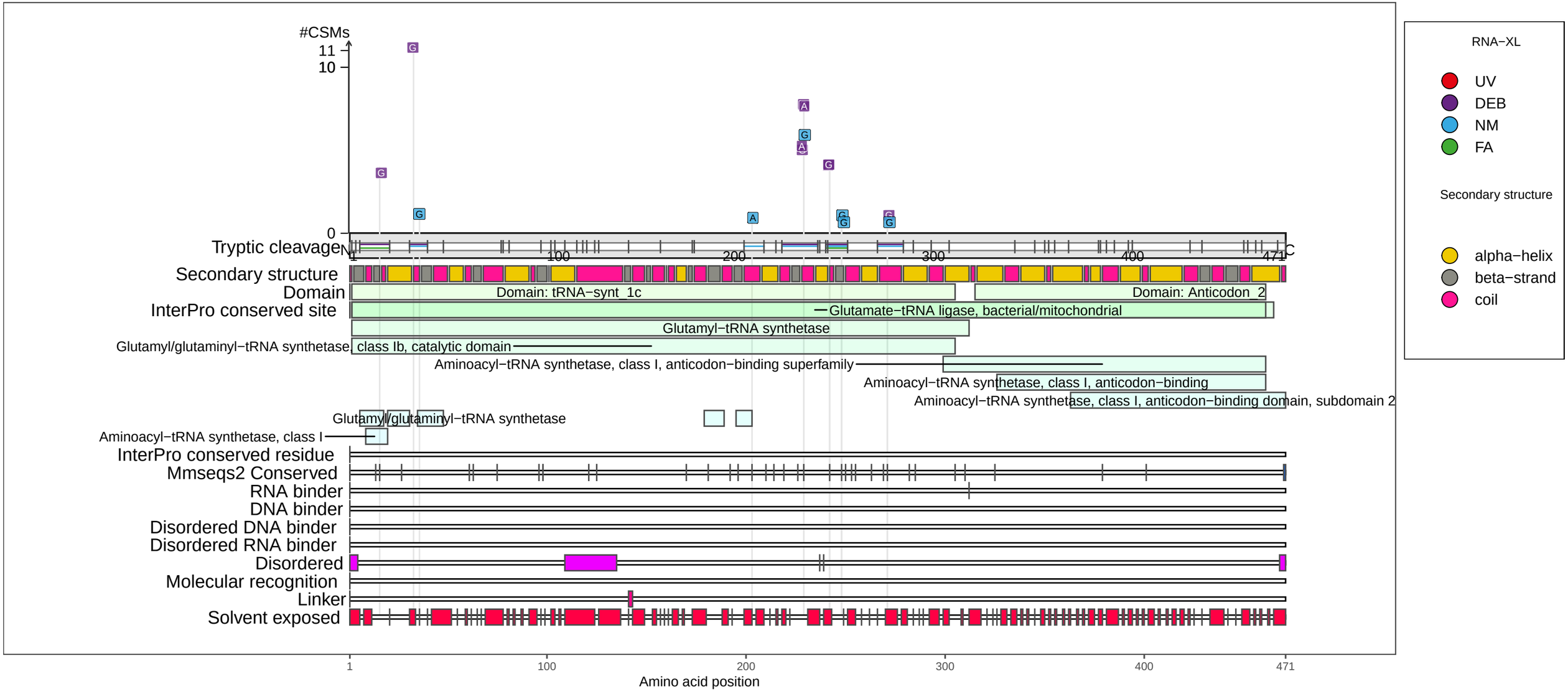
− RNA functions: not annotated



P04805
SYE_ECOLI Glutamate−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 2.92 (Q 89)
PAXdb E.coli [ppm]: 2.56 (Q 87)

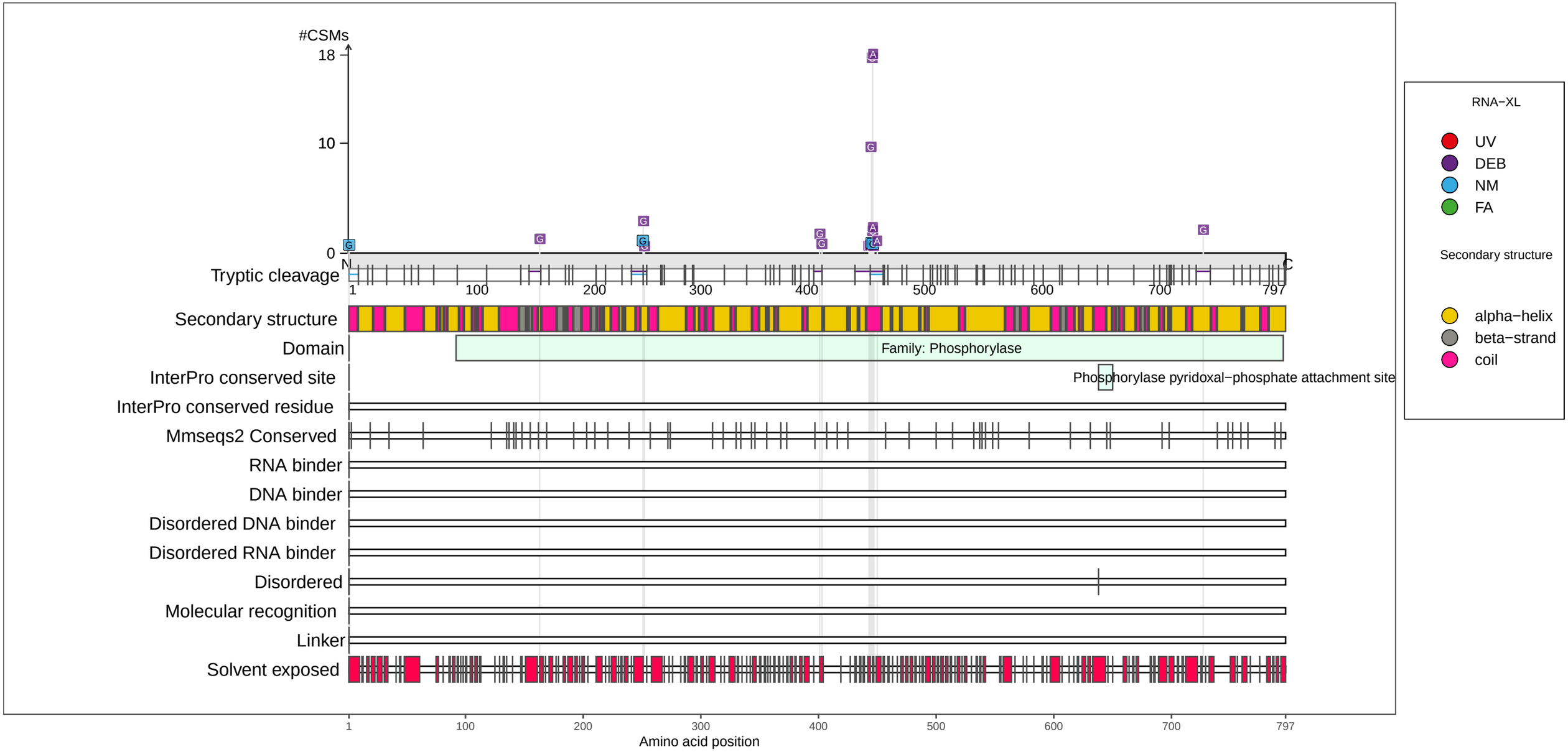
− RNA functions:
aminoacyl−tRNA ligase activity; glutamate−tRNA ligase activity
glutamyl−tRNA aminoacylation; ncRNA metabolic process; RNA binding; RNA metabolic process
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA synthetases class I (E and Q), catalytic domain



P00490
PHSM_ECOLI Maltodextrin phosphorylase

− Abundance:
tryptic [log10 Intensity]: 8.8 (Q 83)
PAXdb K12 strain [ppm]: 1.85 (Q 55)
PAXdb E.coli [ppm]: 2.17 (Q 77)

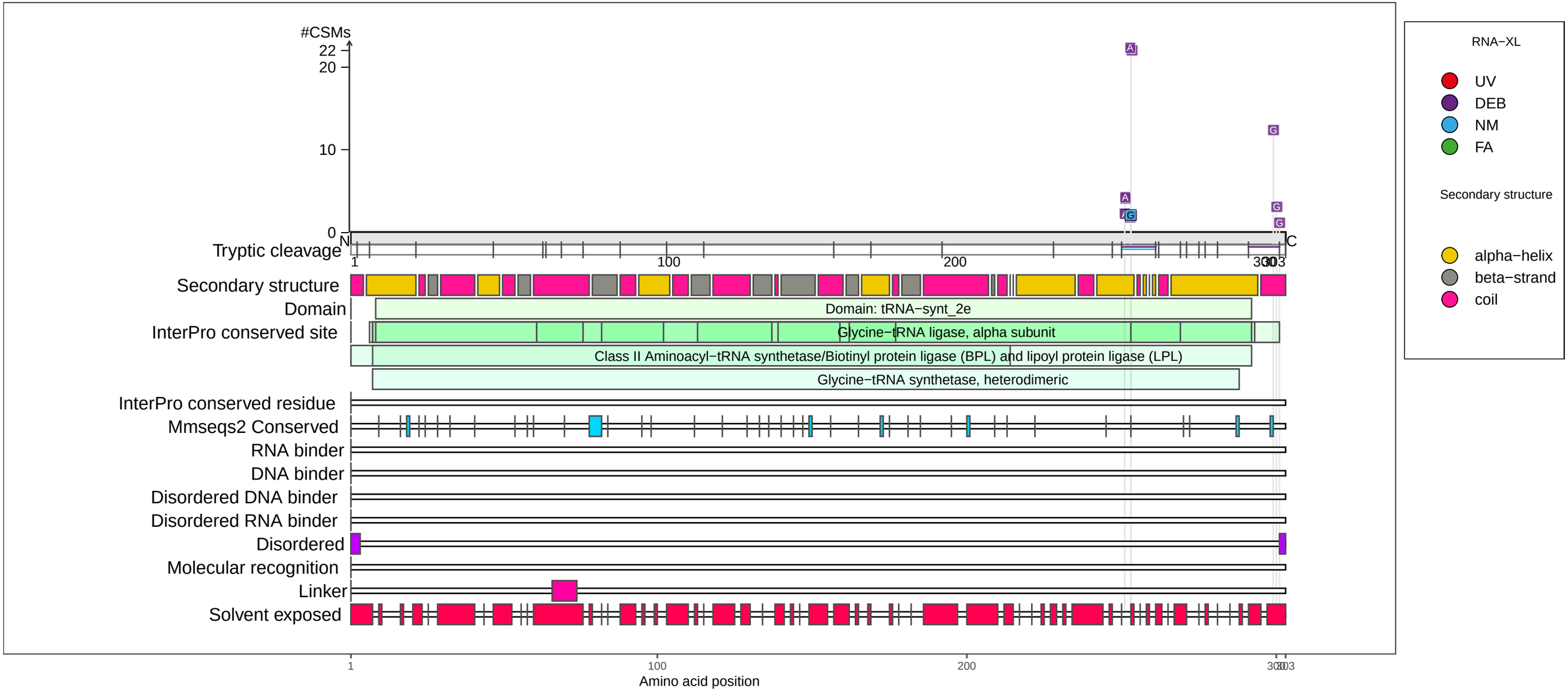
− RNA functions: not annotated



P00960
SYGA_ECOLI Glycine−−tRNA ligase alpha subunit

− Abundance:
tryptic [log10 Intensity]: 9.38 (Q 95)
PAXdb K12 strain [ppm]: 2.2 (Q 67)
PAXdb E.coli [ppm]: 2.57 (Q 87)

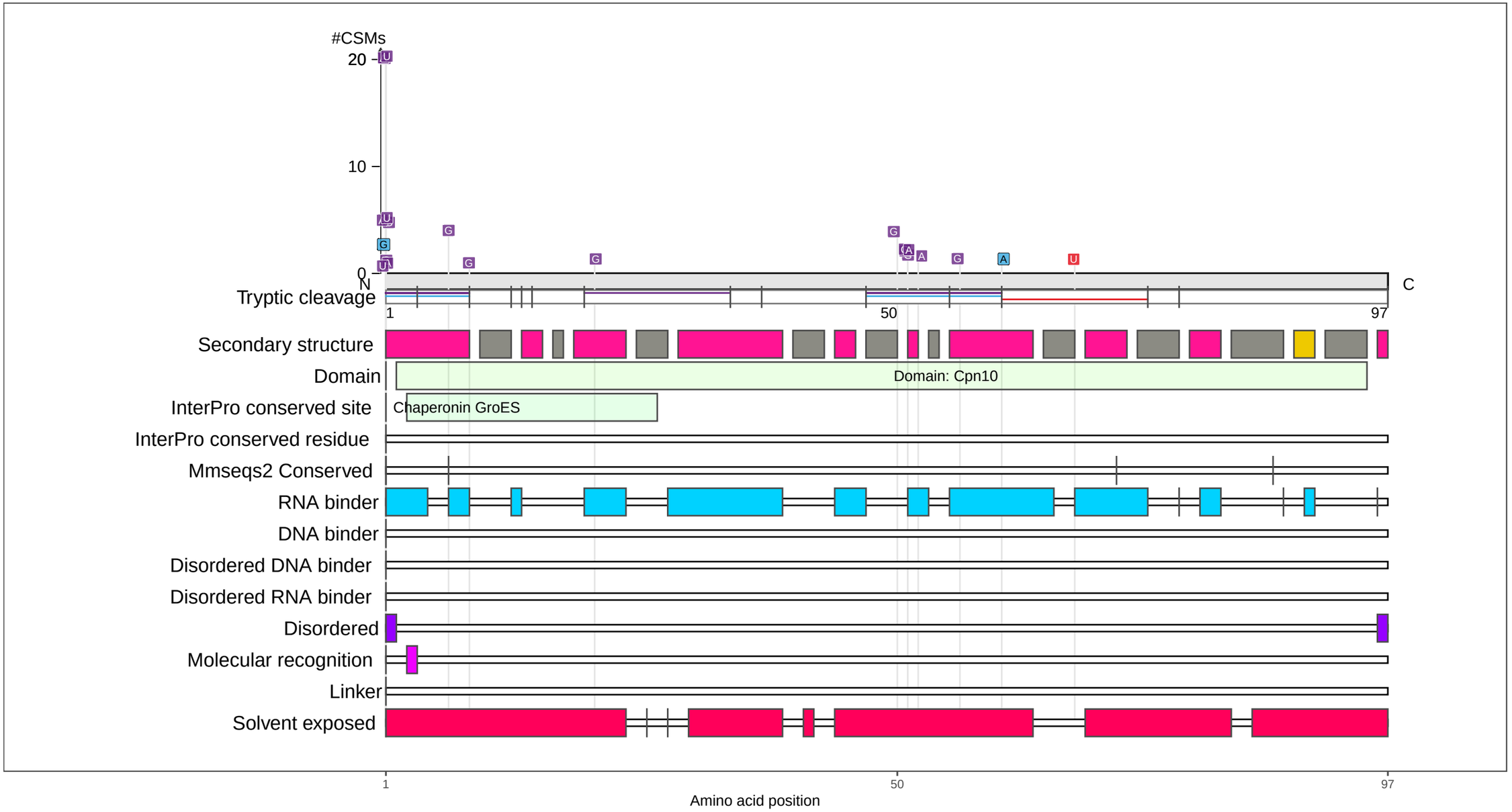
− RNA functions:
aminoacyl−tRNA ligase activity; glycine−tRNA ligase activity
glycyl−tRNA aminoacylation; Glycyl−tRNA synthetase alpha subunit; ncRNA metabolic process
RNA metabolic process; tRNA aminoacylation; tRNA aminoacylation for protein translation
tRNA metabolic process



P0A6F9
CH10_ECOLI Co−chaperonin GroES

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 3.64 (Q 98)
PAXdb E.coli [ppm]: 3.85 (Q 100)

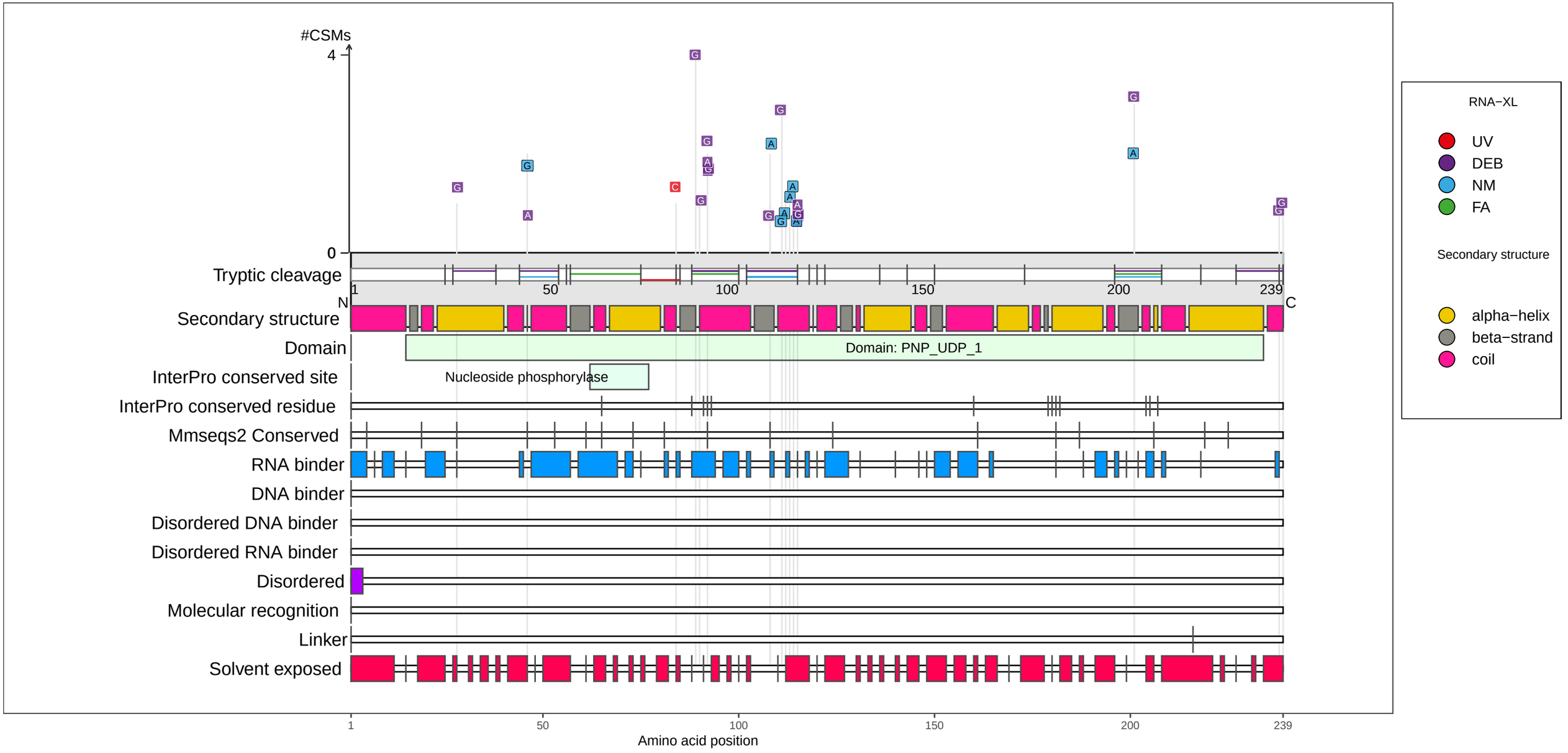
− RNA functions: not annotated



P0ABP8
DEOD_ECOLI Purine nucleoside phosphorylase DeoD−type

− Abundance:
tryptic [log10 Intensity]: 9.22 (Q 93)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 3.2 (Q 96)

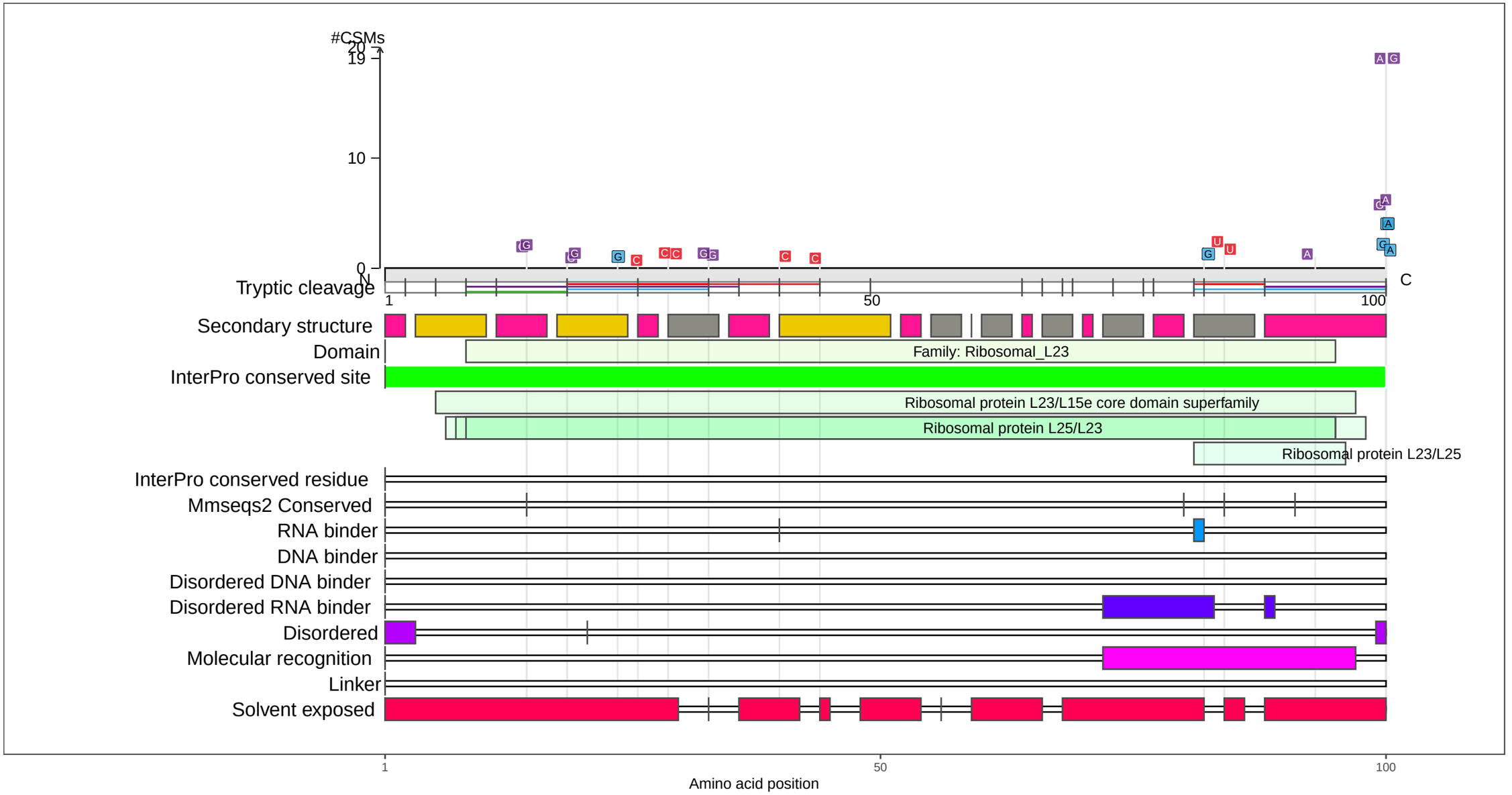
− RNA functions: not annotated



P0ADZ0
RL23_ECOLI 50S ribosomal protein L23

− Abundance:
tryptic [log10 Intensity]: 8.78 (Q 83)
PAXdb K12 strain [ppm]: 2.89 (Q 88)
PAXdb E.coli [ppm]: 2.81 (Q 92)

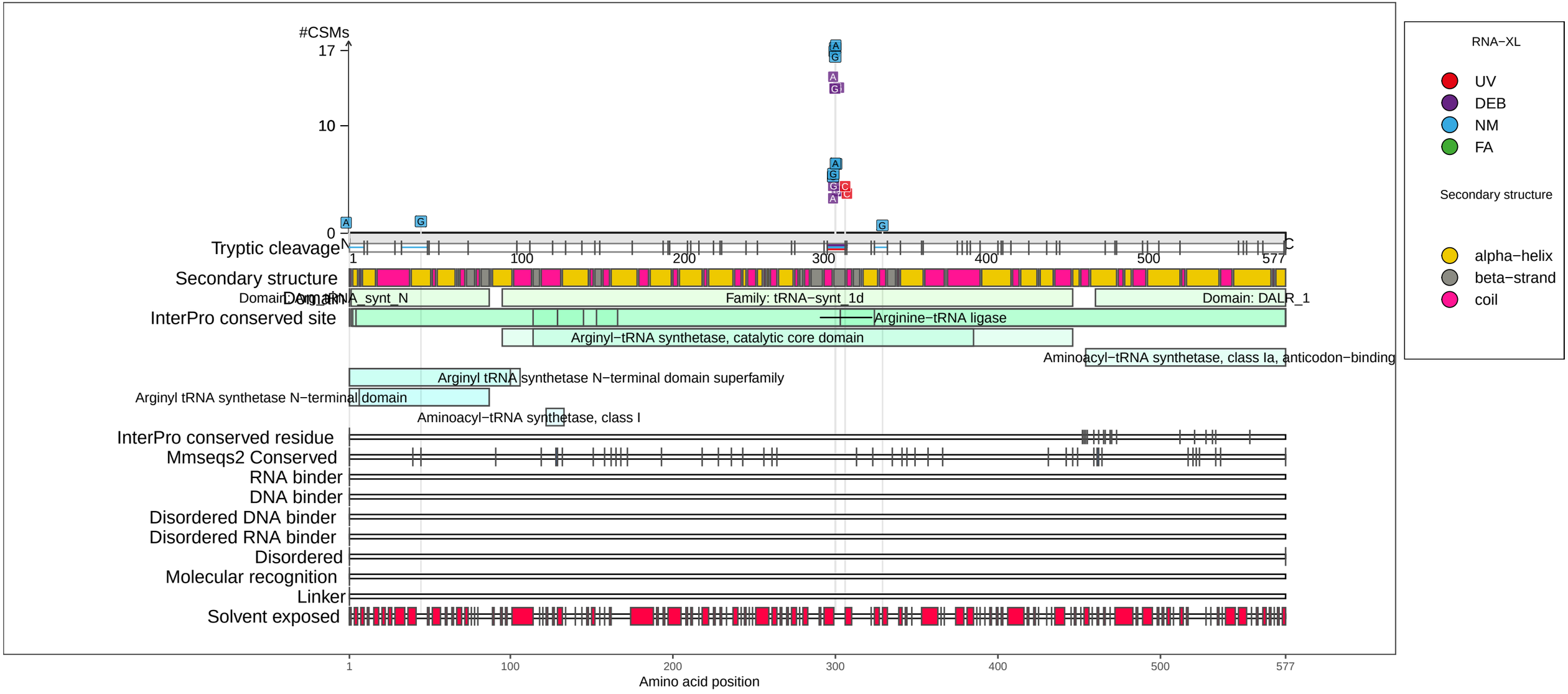
− RNA functions:
RNA binding; rRNA binding



P11875
SYR_ECOLI Arginine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 8.36 (Q 71)
PAXdb K12 strain [ppm]: 2.16 (Q 66)
PAXdb E.coli [ppm]: 2.23 (Q 78)

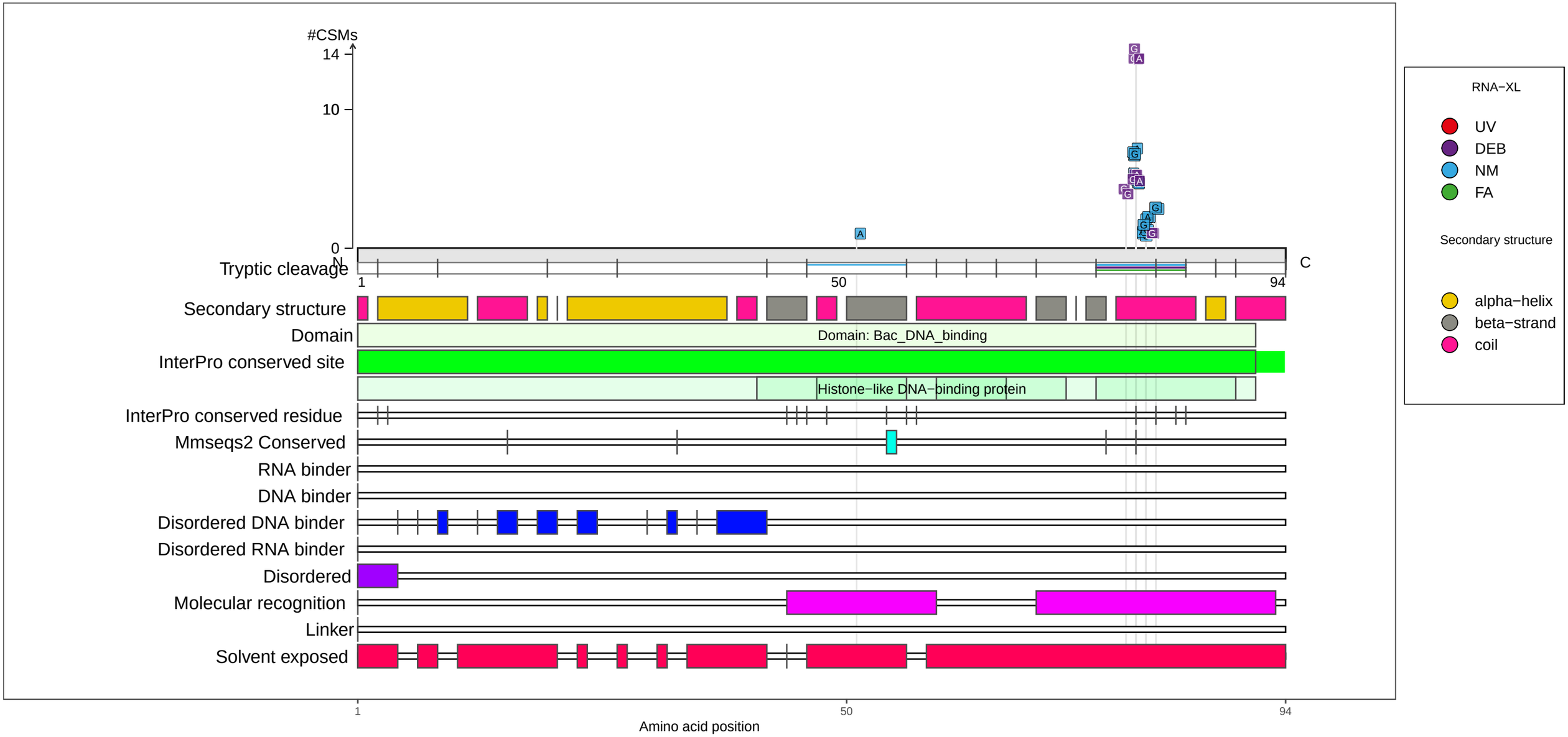
− RNA functions:
aminoacyl−tRNA ligase activity; arginine−tRNA ligase activity
Arginyl tRNA synthetase N terminal domain; arginyl−tRNA aminoacylation; ncRNA metabolic process
RNA metabolic process; tRNA aminoacylation; tRNA aminoacylation for protein translation
tRNA metabolic process; tRNA synthetases class I (R)



P0A6Y1
IHFB_ECOLI Integration host factor subunit beta

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 51)
PAXdb K12 strain [ppm]: 3.42 (Q 96)
PAXdb E.coli [ppm]: 3.18 (Q 96)

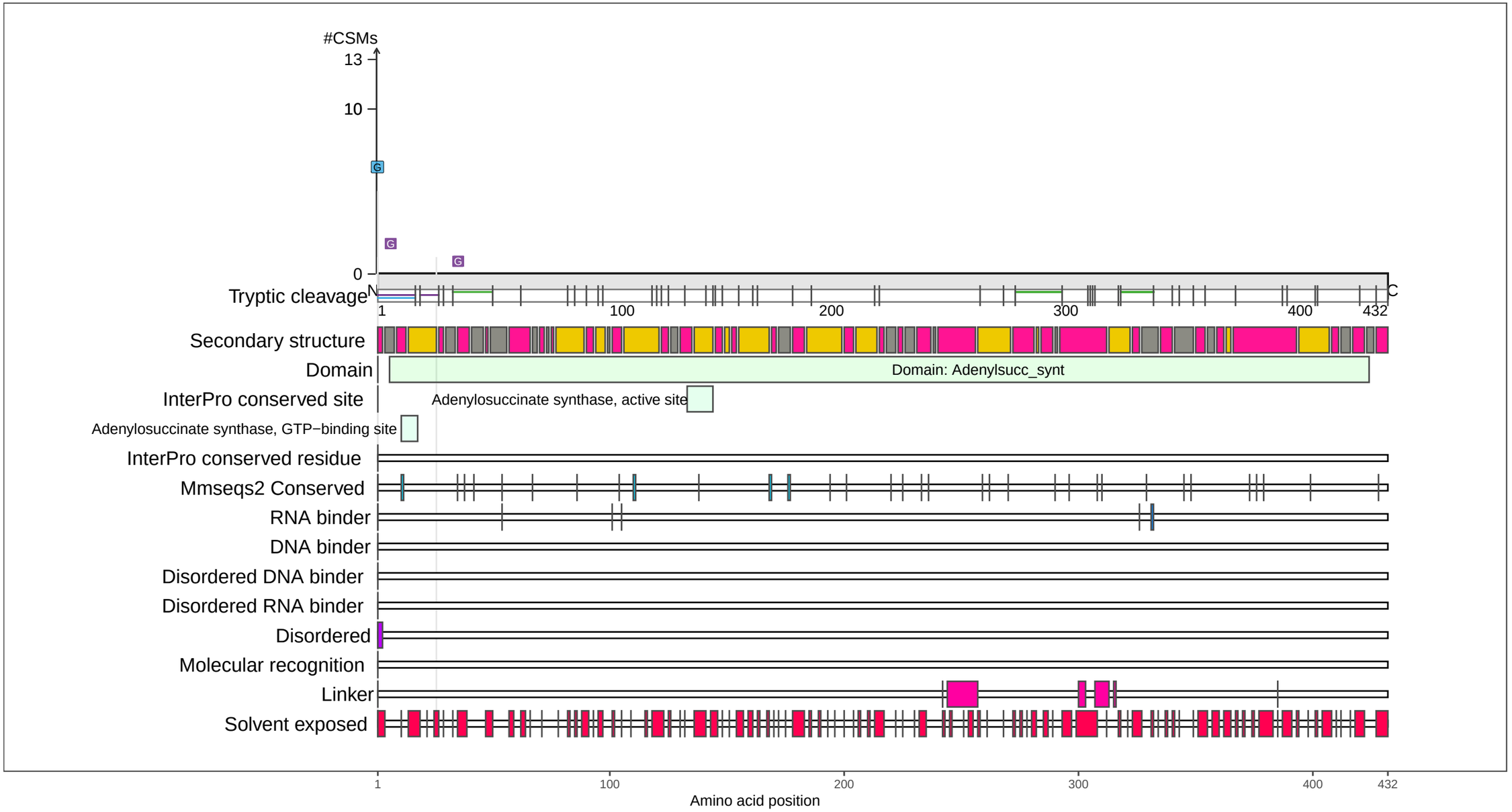
− RNA functions:
RNA biosynthetic process; RNA metabolic process

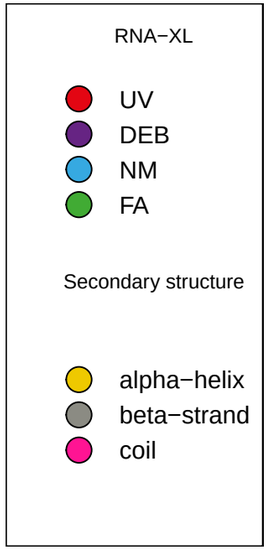


P0A7D4
PURA_ECOLI Adenylosuccinate synthetase

− Abundance:
tryptic [log10 Intensity]: 9.69 (Q 98)
PAXdb K12 strain [ppm]: 3.38 (Q 96)
PAXdb E.coli [ppm]: 3.32 (Q 98)

− RNA functions: not annotated

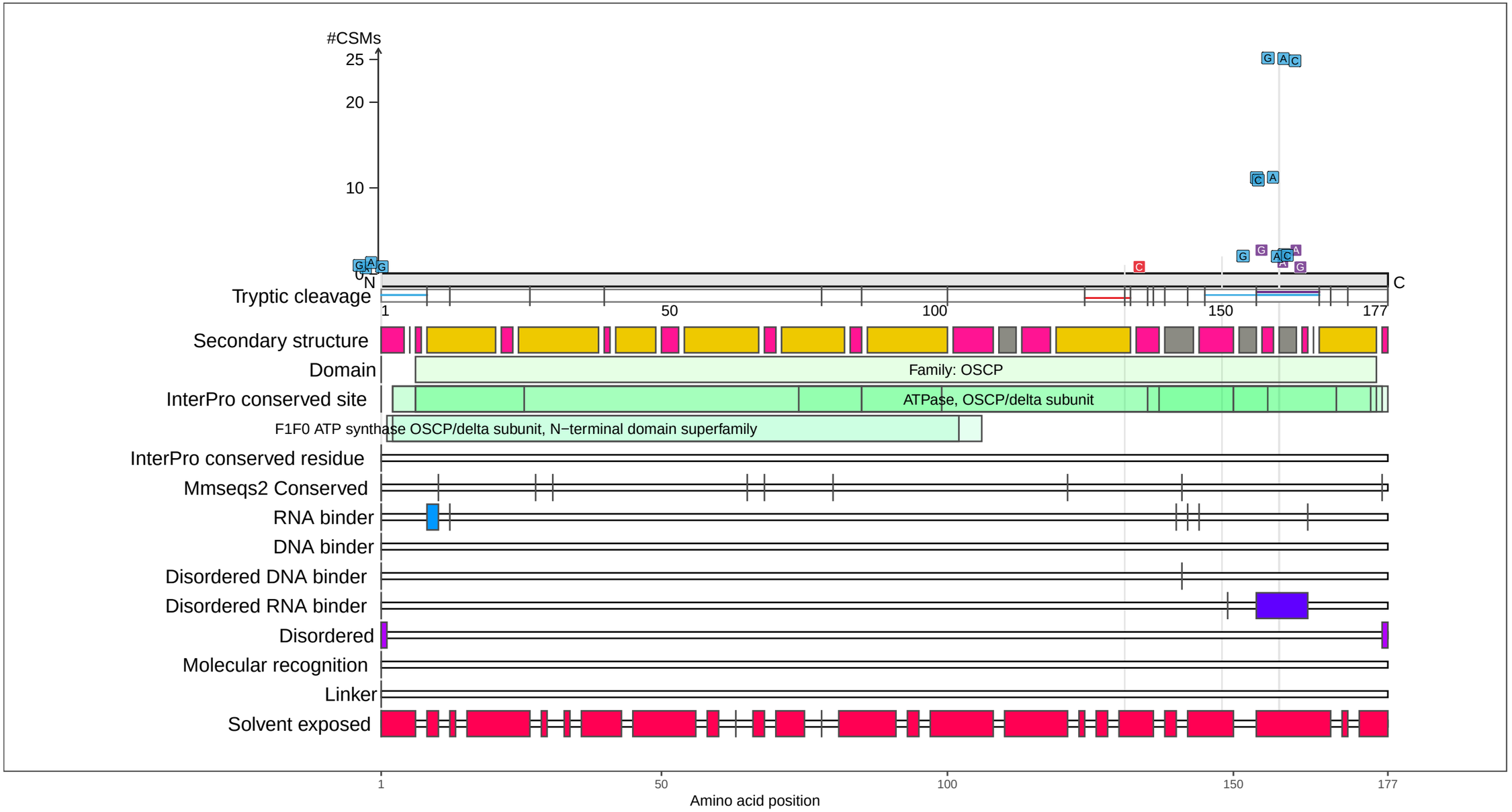




P0ABA4
ATPD_ECOLI ATP synthase subunit delta

− Abundance:
tryptic [log10 Intensity]: 9 (Q 88)
PAXdb K12 strain [ppm]: 2.87 (Q 88)
PAXdb E.coli [ppm]: 3.01 (Q 95)

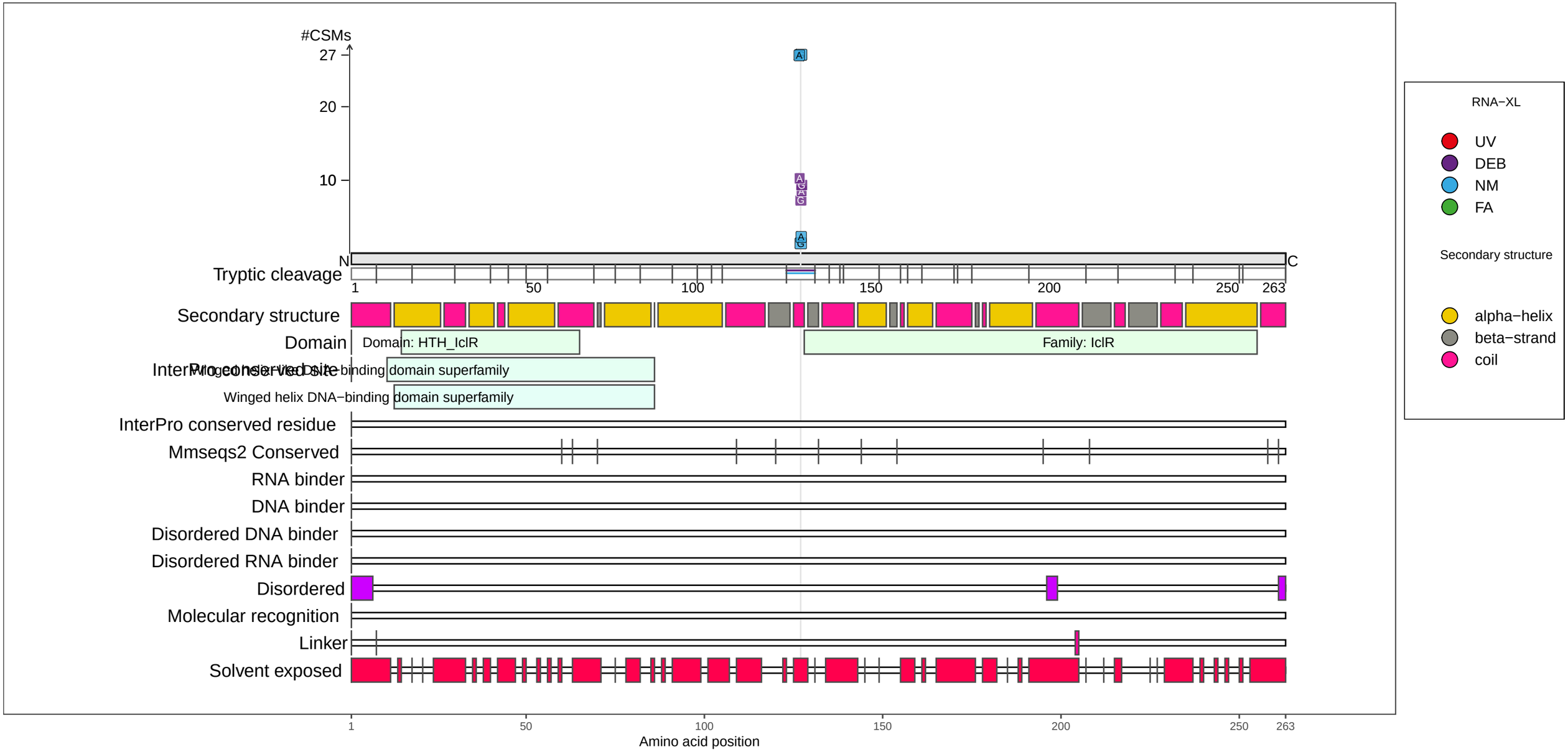
− RNA functions: not annotated



P76268
KDGR_ECOLI Transcriptional regulator KdgR

− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.48 (Q 85)

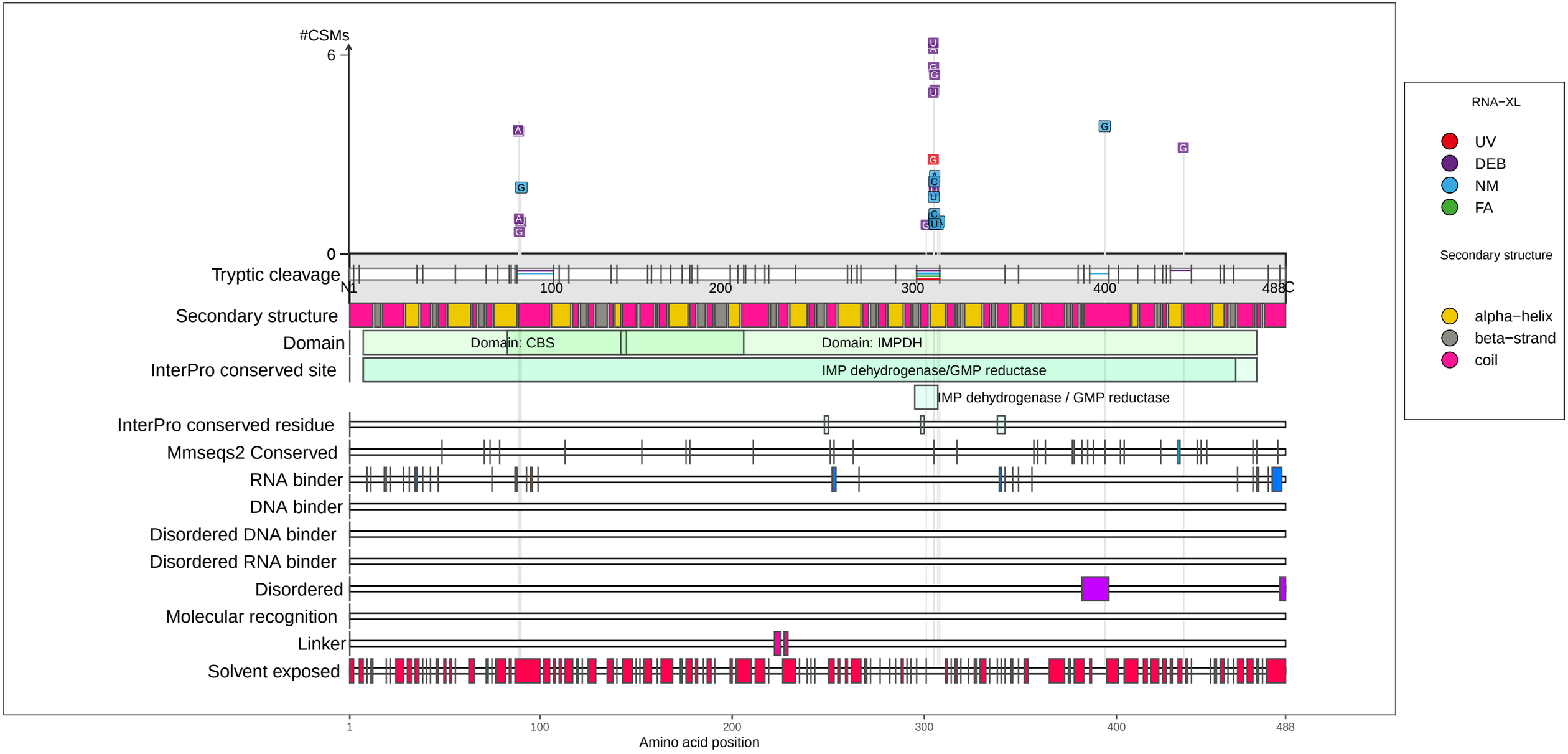
− RNA functions: not annotated



P0ADG7
IMDH_ECOLI Inosine−5'−monophosphate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.54 (Q 97)
PAXdb K12 strain [ppm]: 2.83 (Q 87)
PAXdb E.coli [ppm]: 2.94 (Q 94)

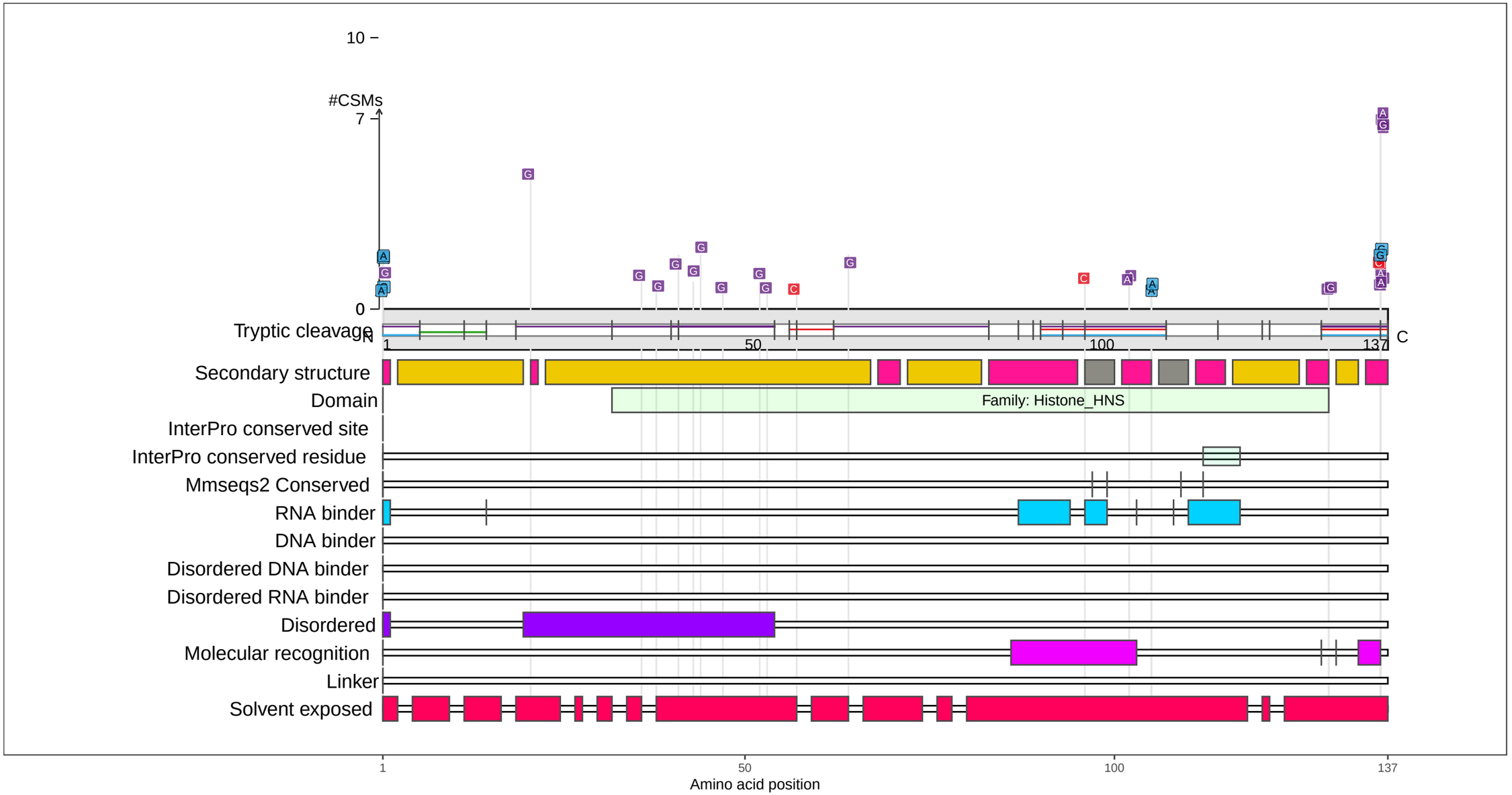
− RNA functions: not annotated



P0ACF8
HNS_ECOLI DNA−binding protein H−NS

− Abundance:
tryptic [log10 Intensity]: 9.73 (Q 98)
PAXdb K12 strain [ppm]: 3.95 (Q 100)
PAXdb E.coli [ppm]: 3.82 (Q 100)

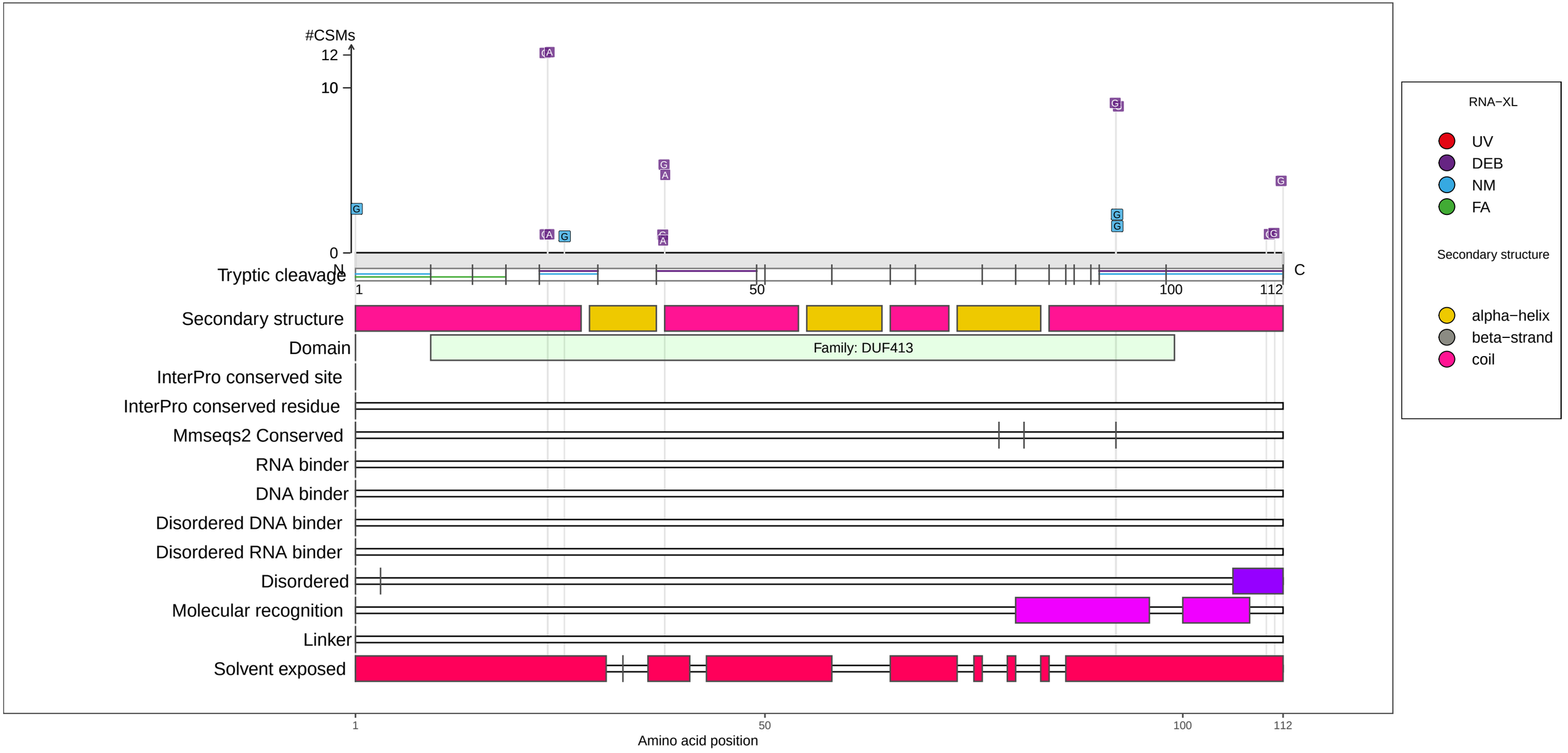
− RNA functions:
RNA binding



P0ADN2
YIFE_ECOLI UPF0438 protein YifE

− Abundance:
tryptic [log10 Intensity]: 8.72 (Q 81)
PAXdb K12 strain [ppm]: 3.47 (Q 97)
PAXdb E.coli [ppm]: 2.98 (Q 94)

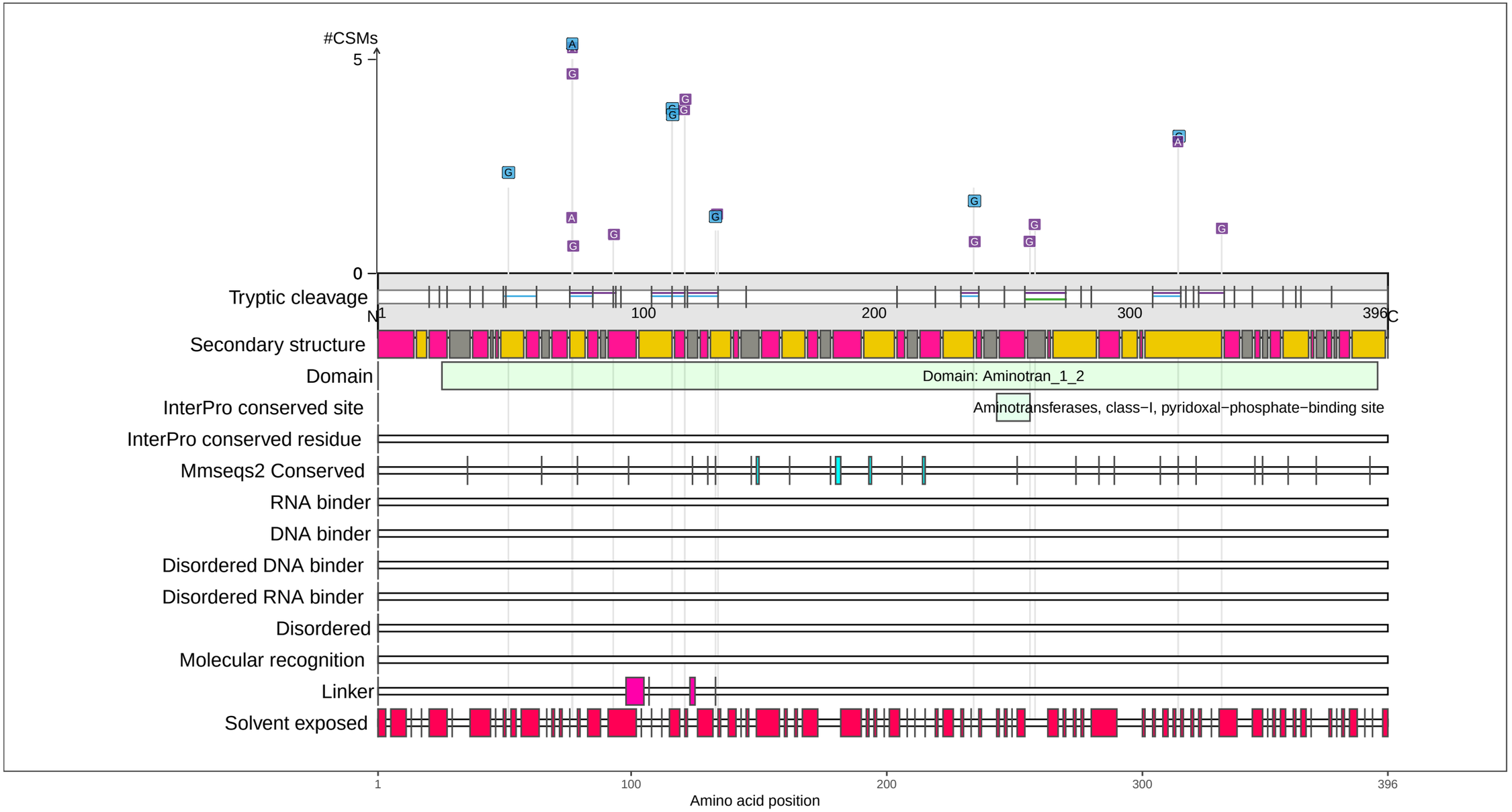
− RNA functions: not annotated

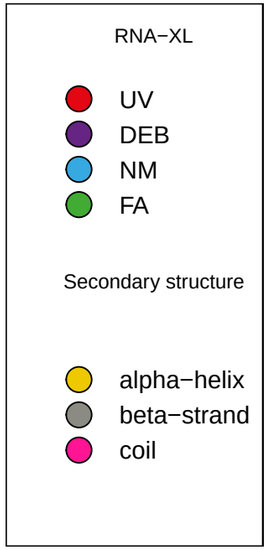


P00509
AAT_ECOLI Aspartate aminotransferase

− Abundance:
tryptic [log10 Intensity]: 9.75 (Q 98)
PAXdb K12 strain [ppm]: 3.43 (Q 96)
PAXdb E.coli [ppm]: 3.24 (Q 97)

− RNA functions: not annotated

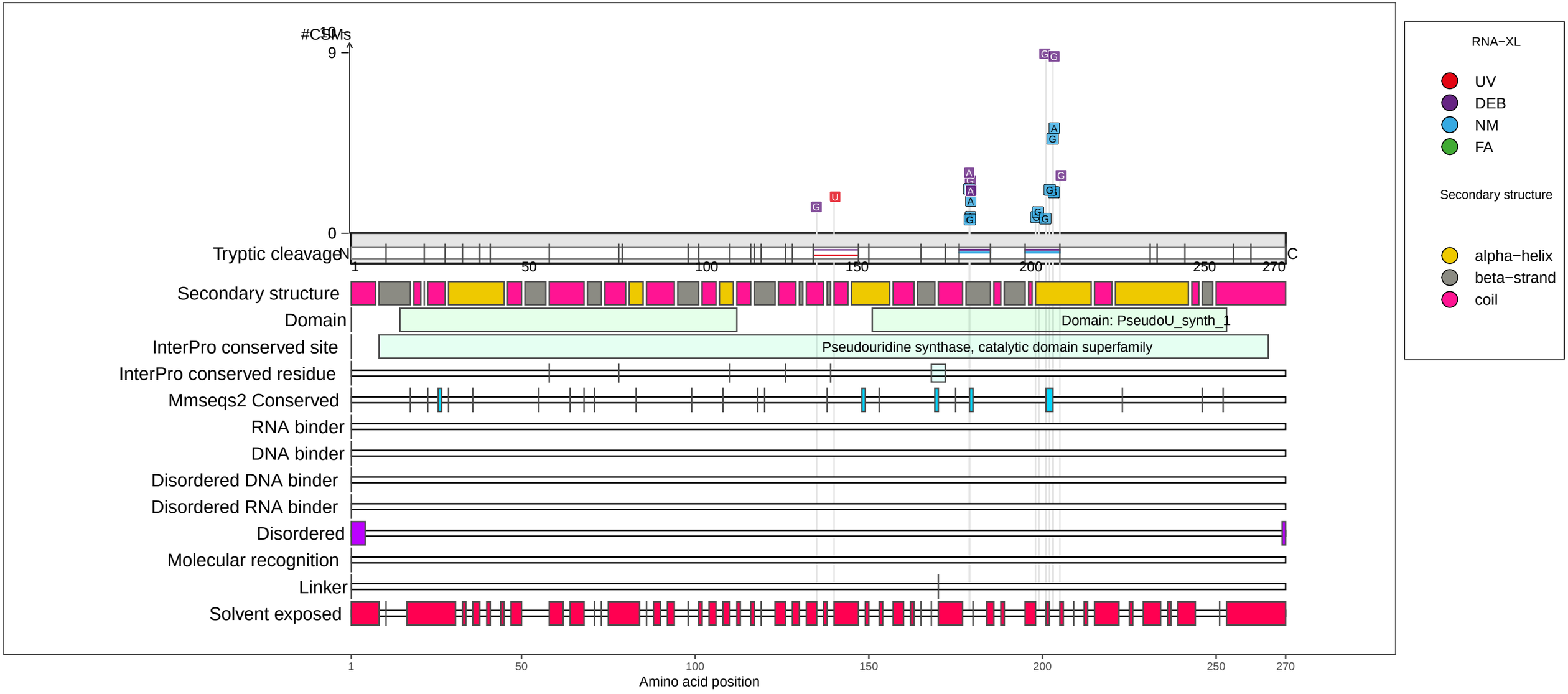




P07649
TRUA_ECOLI tRNA pseudouridine synthase A

− Abundance:
tryptic [log10 Intensity]: 8.89 (Q 86)
PAXdb K12 strain [ppm]: 2.11 (Q 64)
PAXdb E.coli [ppm]: 1.18 (Q 52)

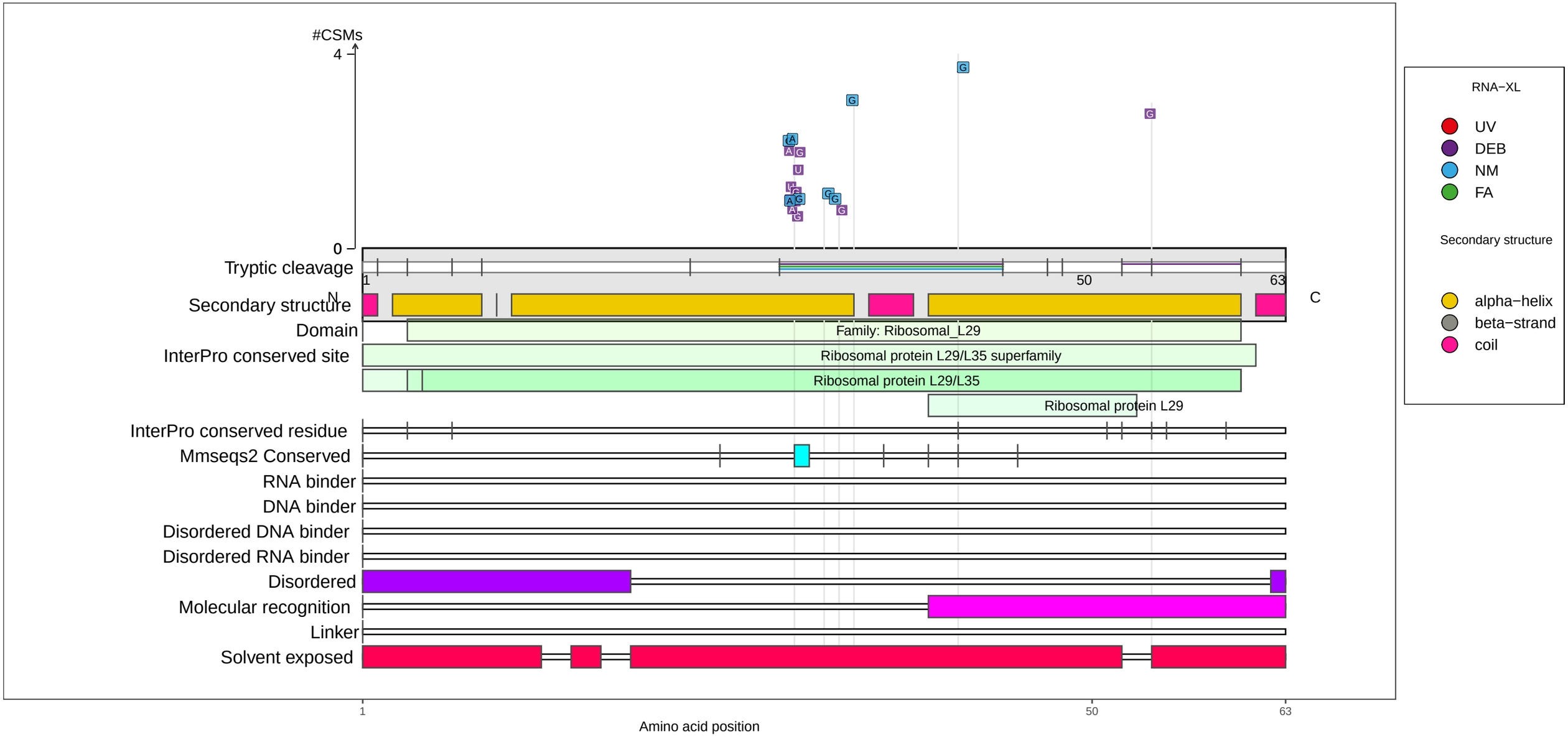
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; tRNA binding; tRNA metabolic process; tRNA modification
tRNA processing; tRNA pseudouridine synthase; tRNA pseudouridine synthase activity
tRNA pseudouridine synthesis



P0A7M6
RL29_ECOLI 50S ribosomal protein L29

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 3.37 (Q 96)
PAXdb E.coli [ppm]: 3.37 (Q 98)

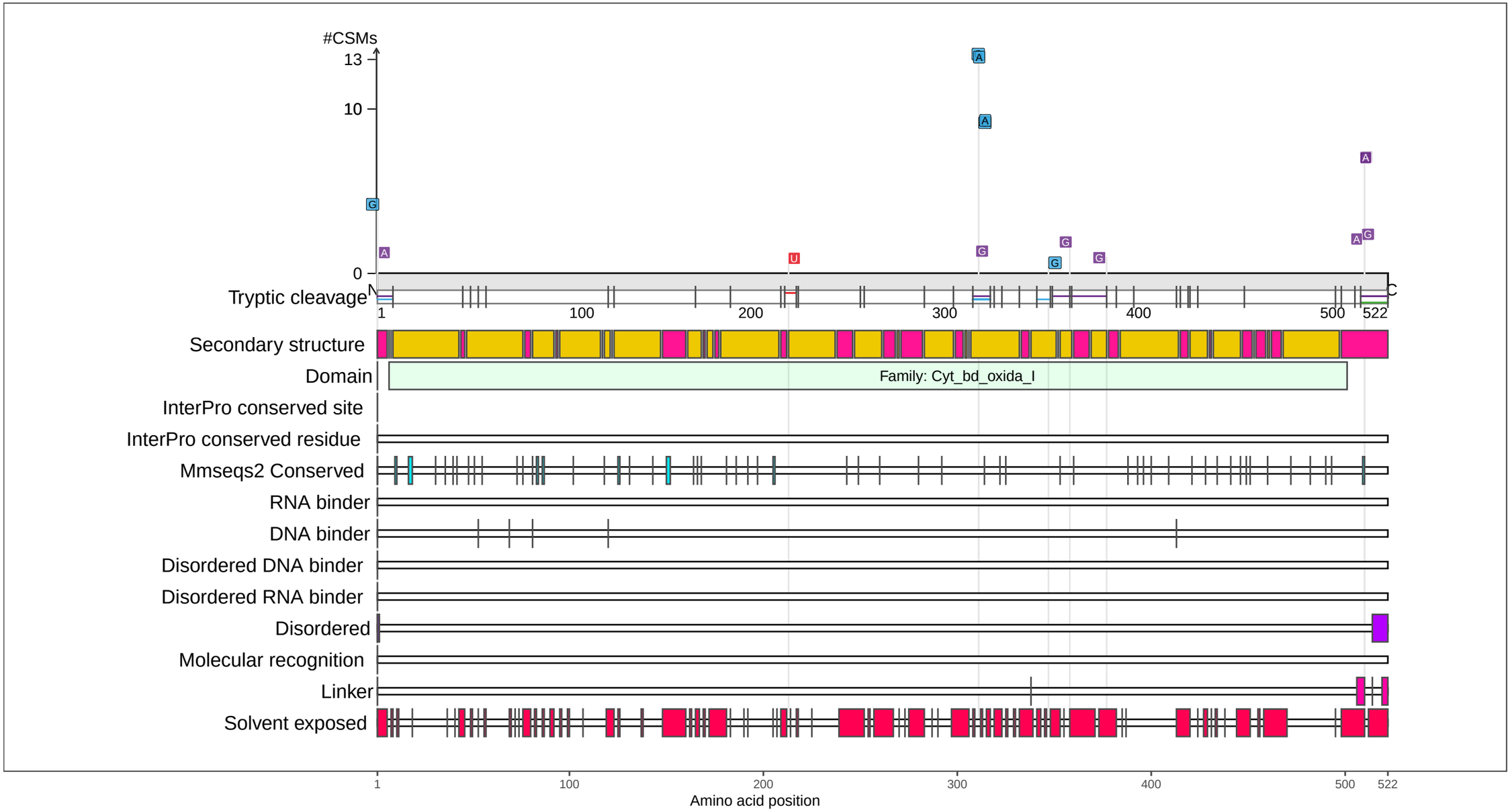
− RNA functions:
RNA binding; rRNA binding



P0ABJ9
CYDA_ECOLI Cytochrome bd−I ubiquinol oxidase subunit 1

− Abundance:
tryptic [log10 Intensity]: 10.13 (Q 100)
PAXdb K12 strain [ppm]: 2.32 (Q 70)
PAXdb E.coli [ppm]: 3.12 (Q 96)

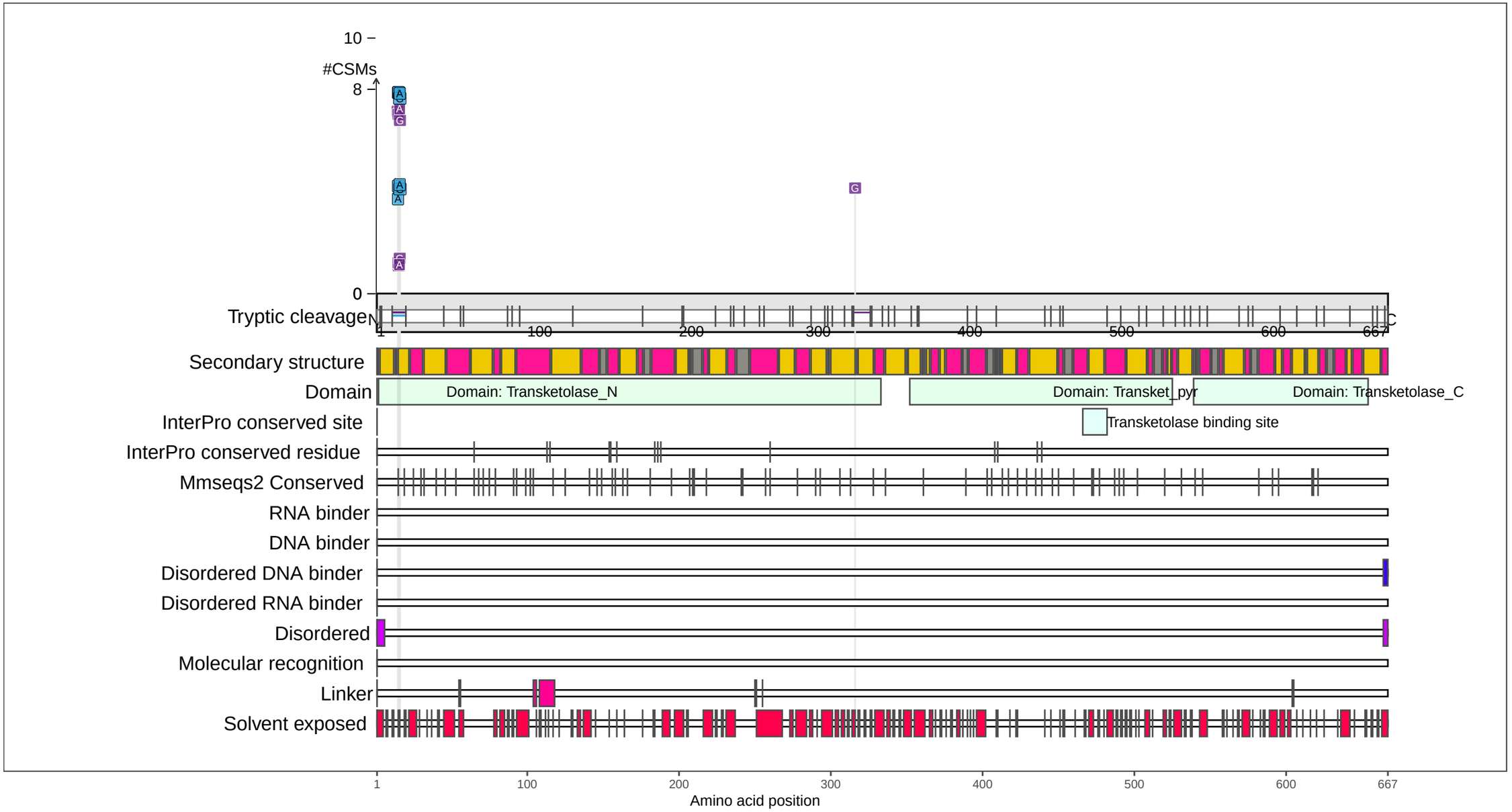
− RNA functions: not annotated

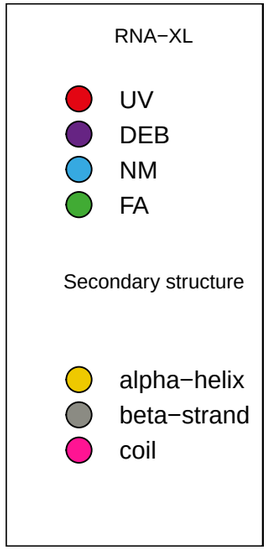


P33570
TKT2_ECOLI Transketolase 2

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 2.61 (Q 81)
PAXdb E.coli [ppm]: 2.82 (Q 92)

− RNA functions: not annotated

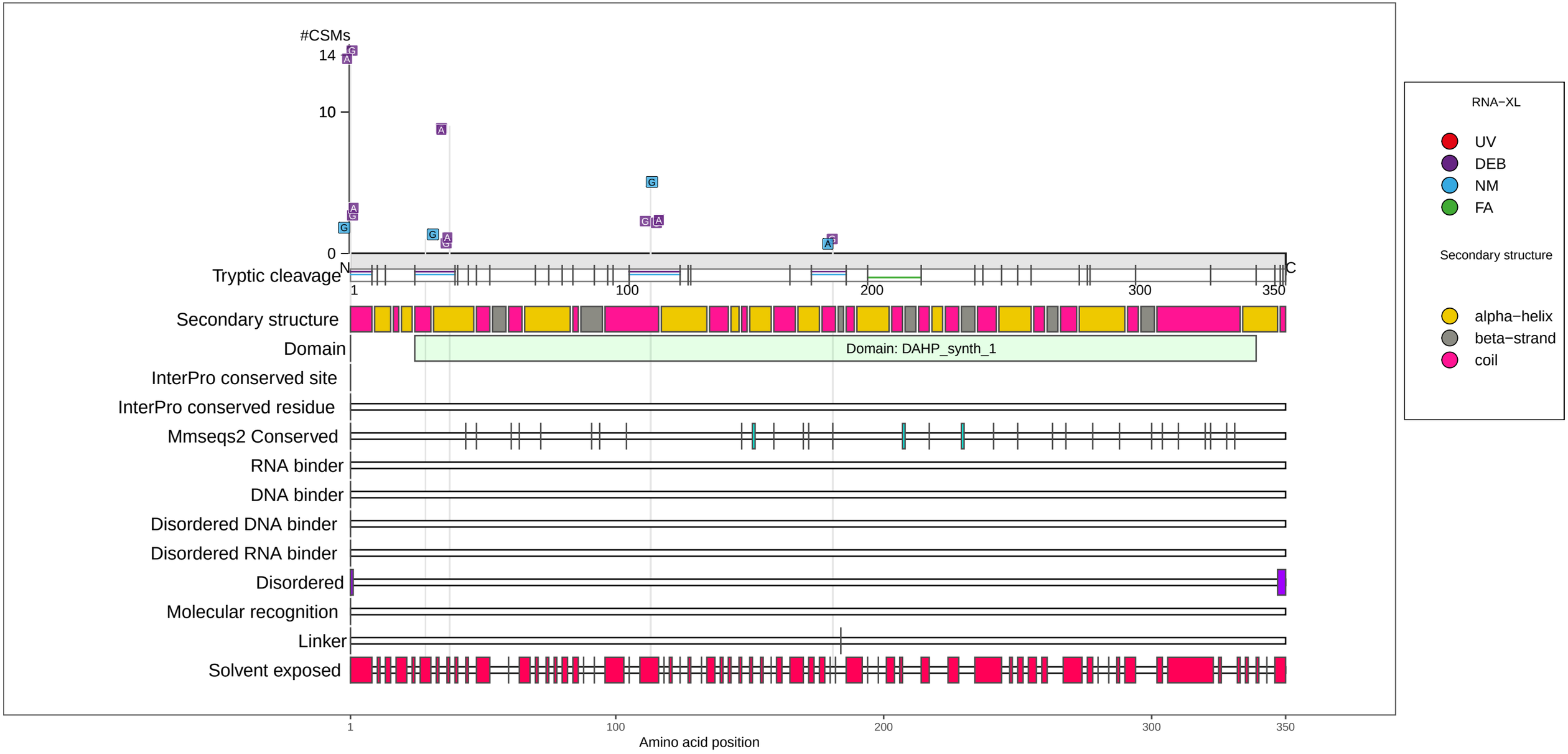




P0AB91
AROG_ECOLI Phospho−2−dehydro−3−deoxyheptonate aldolase, Phe−sensitive

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 3.14 (Q 93)
PAXdb E.coli [ppm]: 2.7 (Q 90)

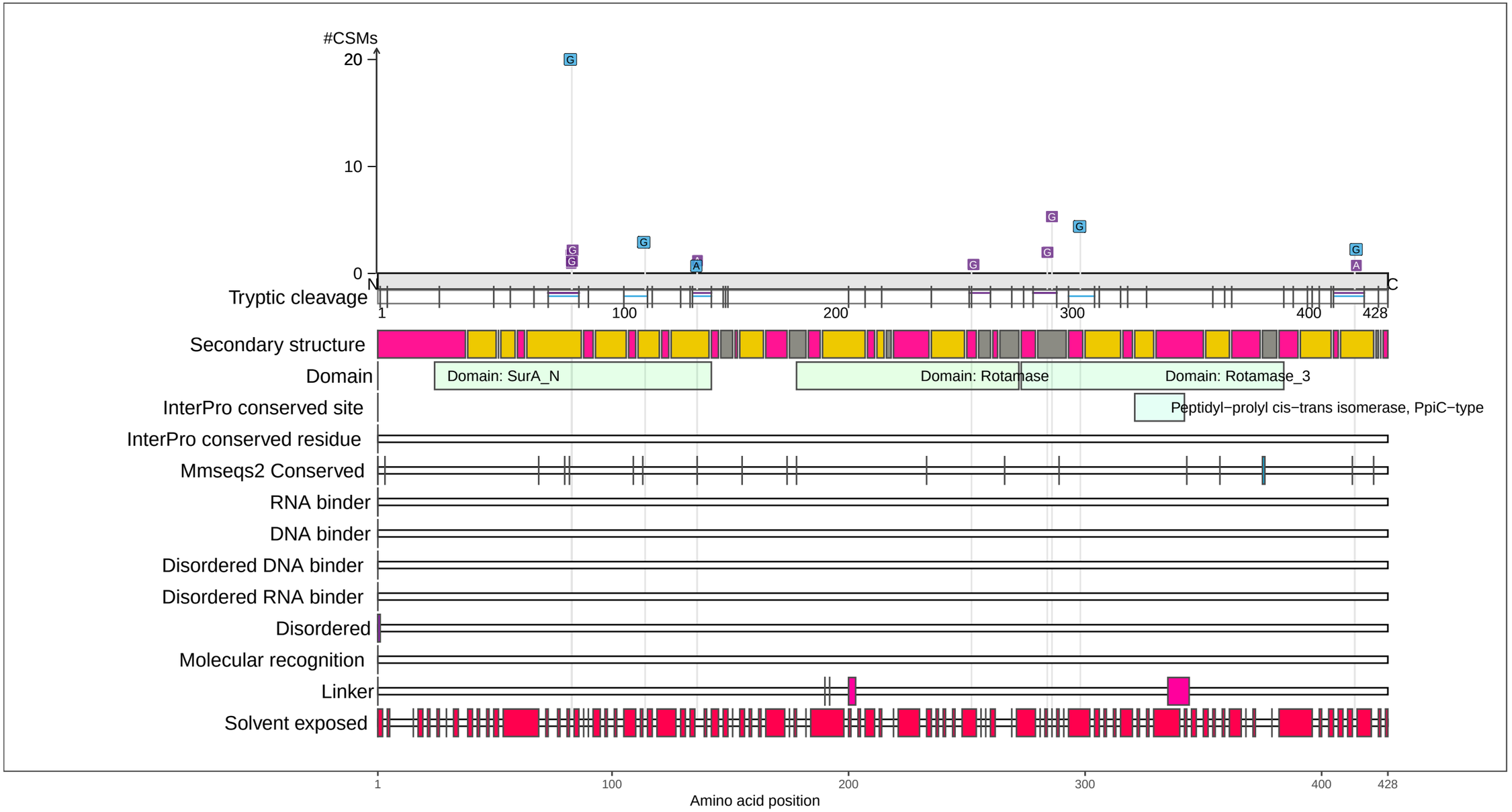
− RNA functions: not annotated

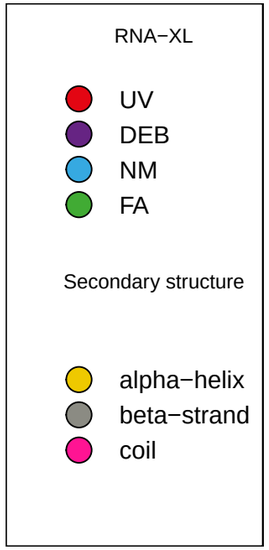


P0ABZ6
SURA_ECOLI Chaperone SurA

− Abundance:
tryptic [log10 Intensity]: 8.37 (Q 71)
PAXdb K12 strain [ppm]: 3.07 (Q 92)
PAXdb E.coli [ppm]: 2.76 (Q 91)

− RNA functions: not annotated

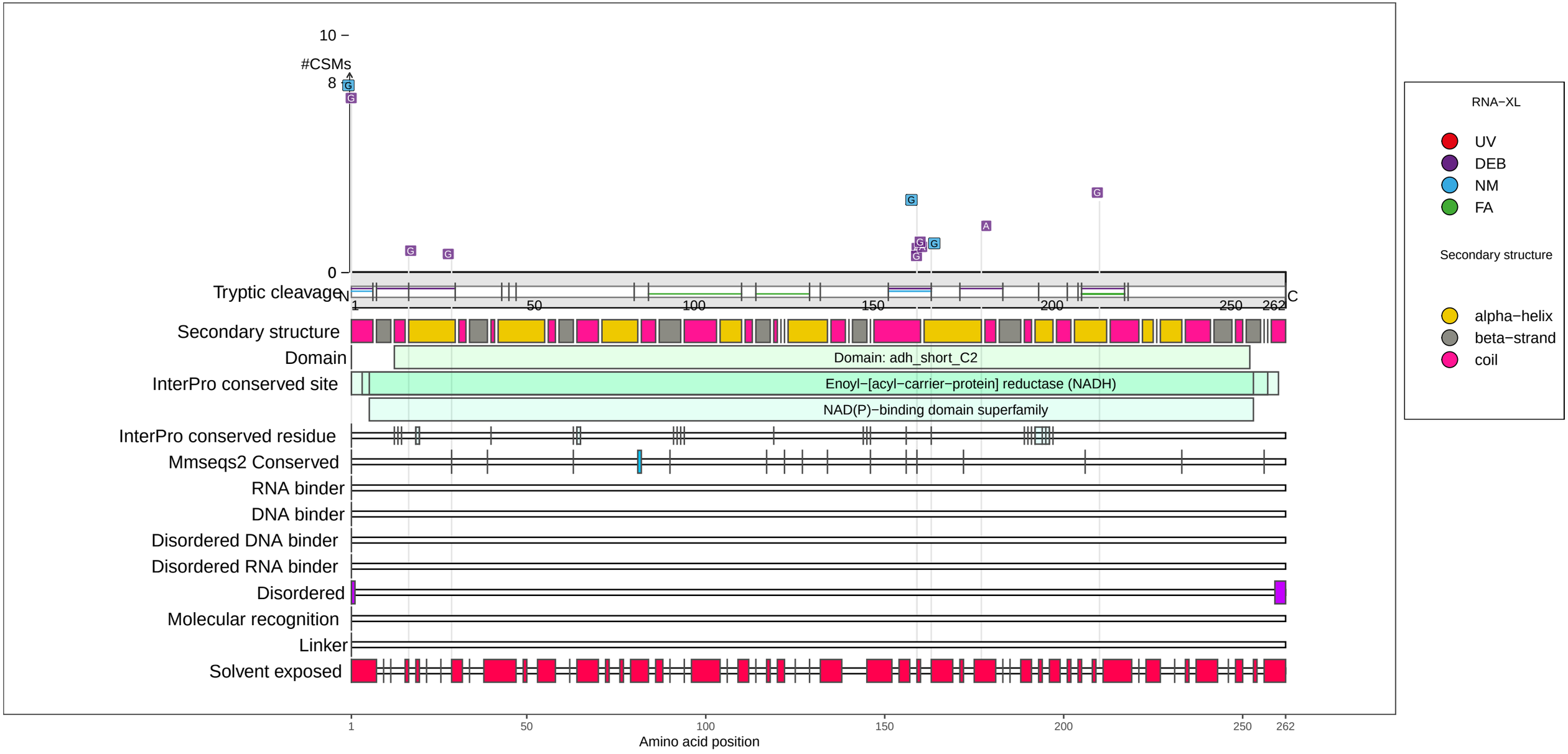




P0AEK4
FABI_ECOLI Enoyl−[acyl−carrier−protein] reductase [NADH] FabI

− Abundance:
tryptic [log10 Intensity]: 9.75 (Q 98)
PAXdb K12 strain [ppm]: 3.29 (Q 95)
PAXdb E.coli [ppm]: 3.31 (Q 97)

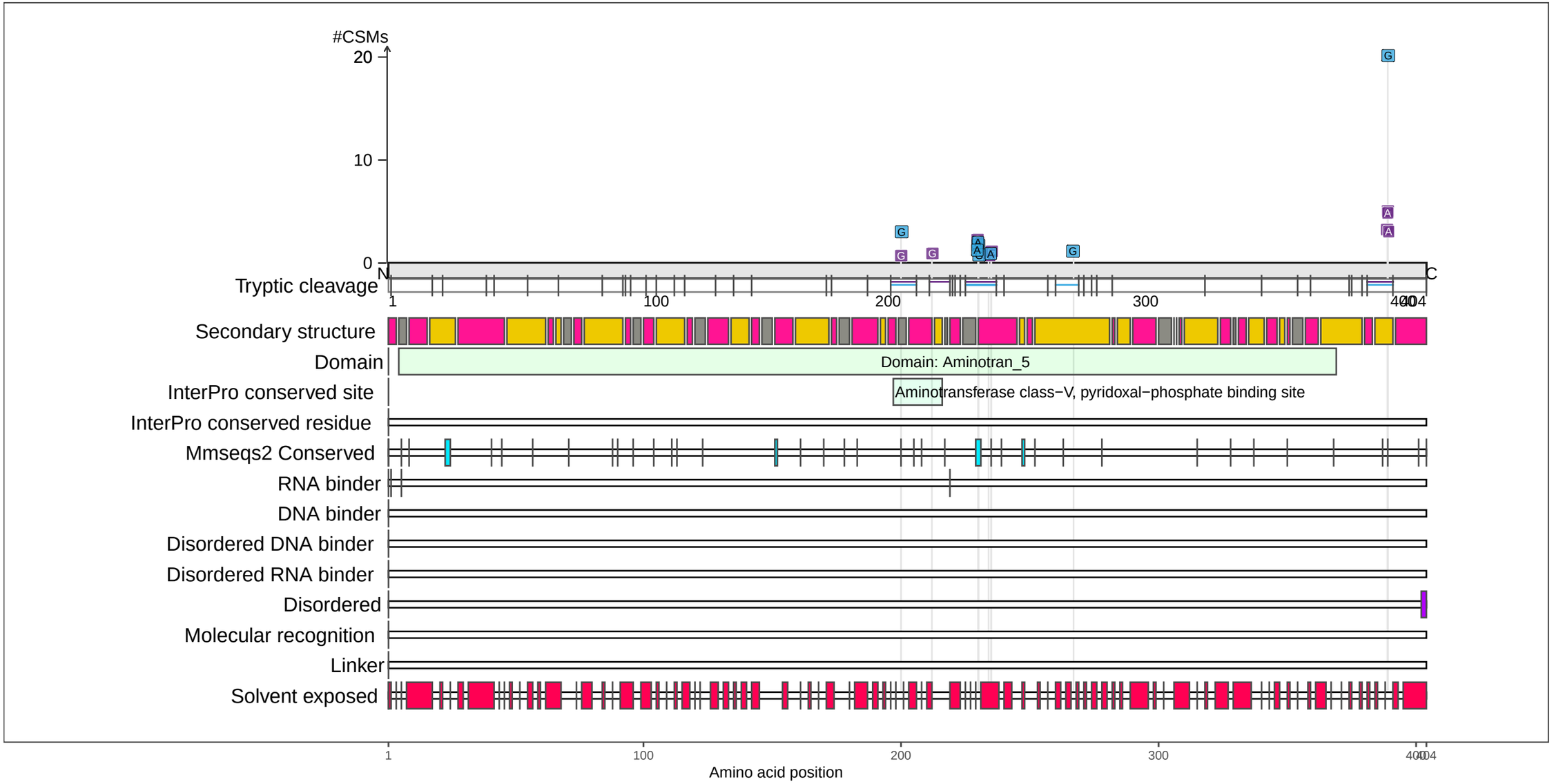
− RNA functions: not annotated

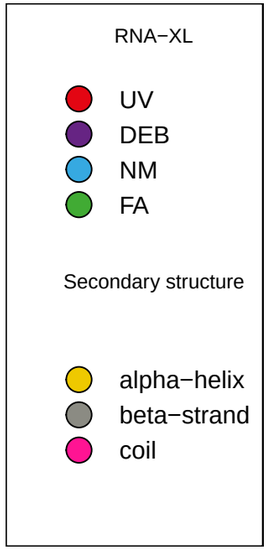


P0A6B7
ISCS_ECOLI Cysteine desulfurase IscS

− Abundance:
tryptic [log10 Intensity]: 9.17 (Q 92)
PAXdb K12 strain [ppm]: 3.19 (Q 94)
PAXdb E.coli [ppm]: 3.4 (Q 98)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA pseudouridine synthesis

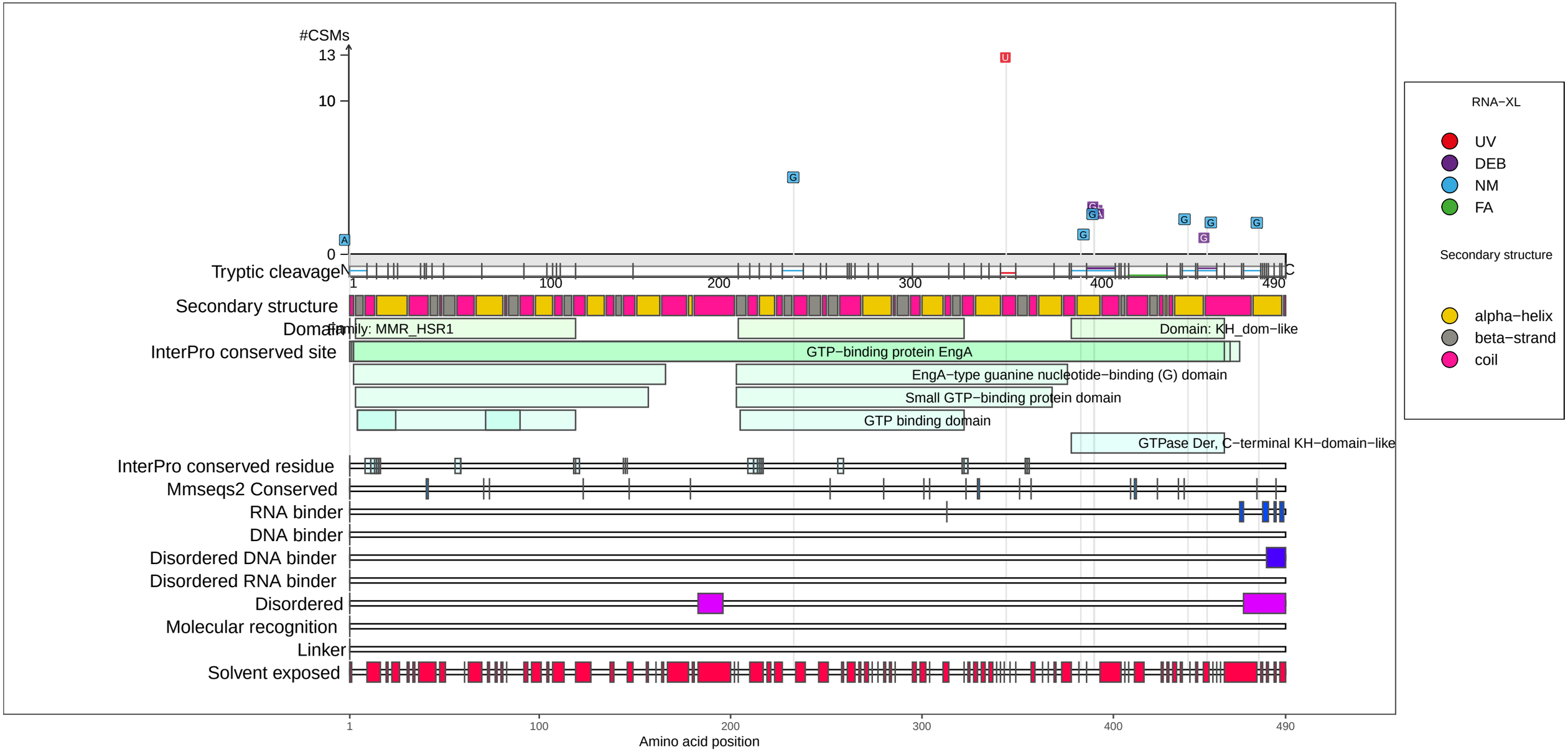




P0A6P5
DER_ECOLI GTPase Der

− Abundance:
tryptic [log10 Intensity]: 7.51 (Q 35)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 2.4 (Q 83)

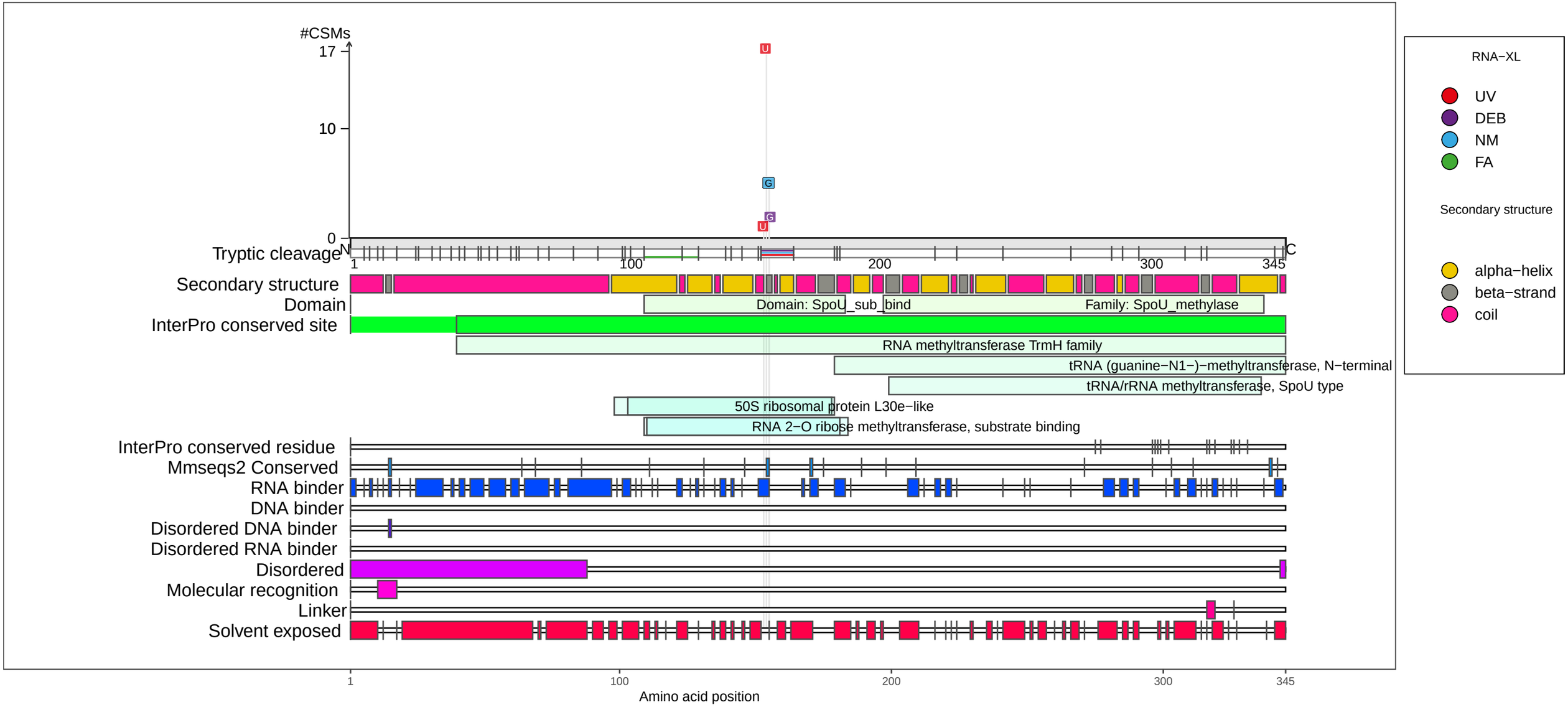
− RNA functions: not annotated



P0AGJ5
YFIF_ECOLI Uncharacterized tRNA/rRNA methyltransferase YfiF

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 2.39 (Q 83)

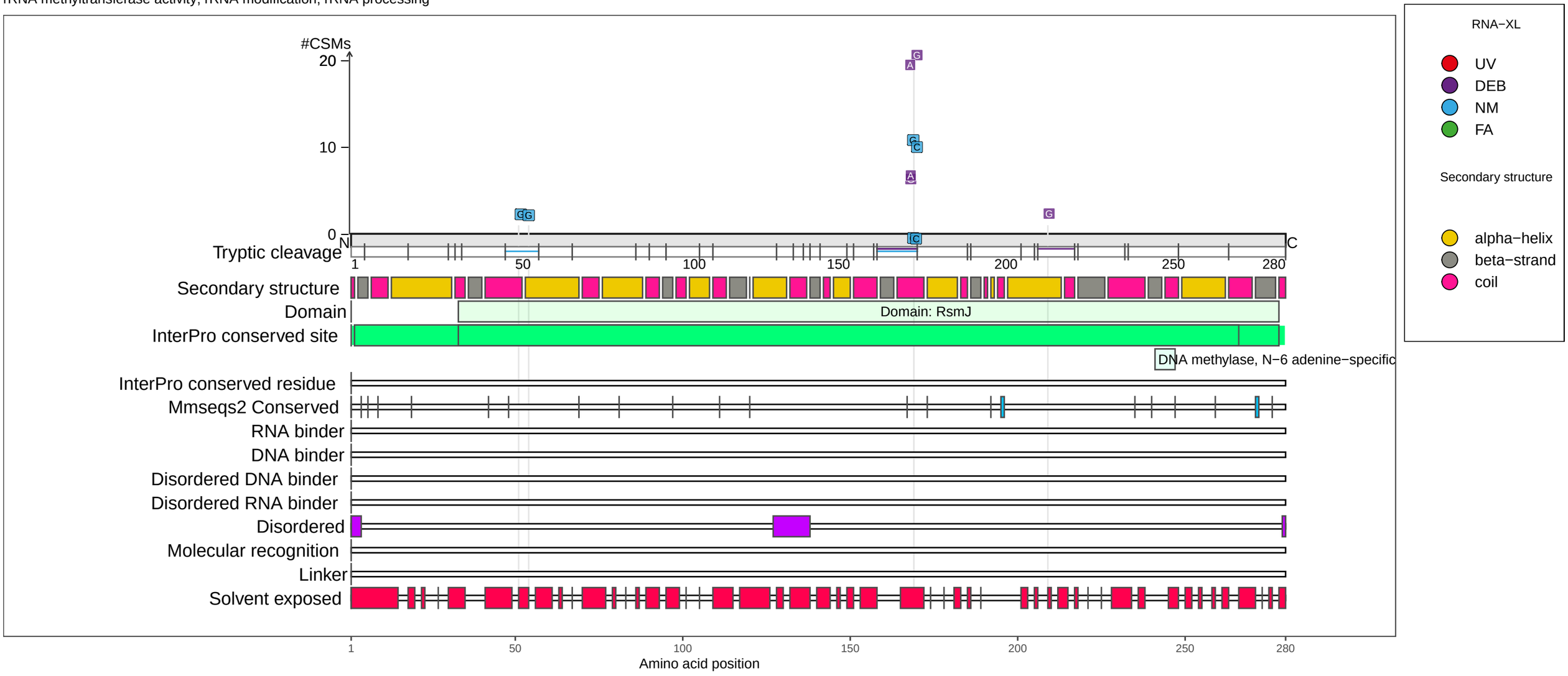
− RNA functions:
RNA 2−O ribose methyltransferase substrate binding; RNA binding
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification; RNA processing
SpoU rRNA Methylase family



P37634
RLMJ_ECOLI Ribosomal RNA large subunit methyltransferase J

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.55 (Q 61)

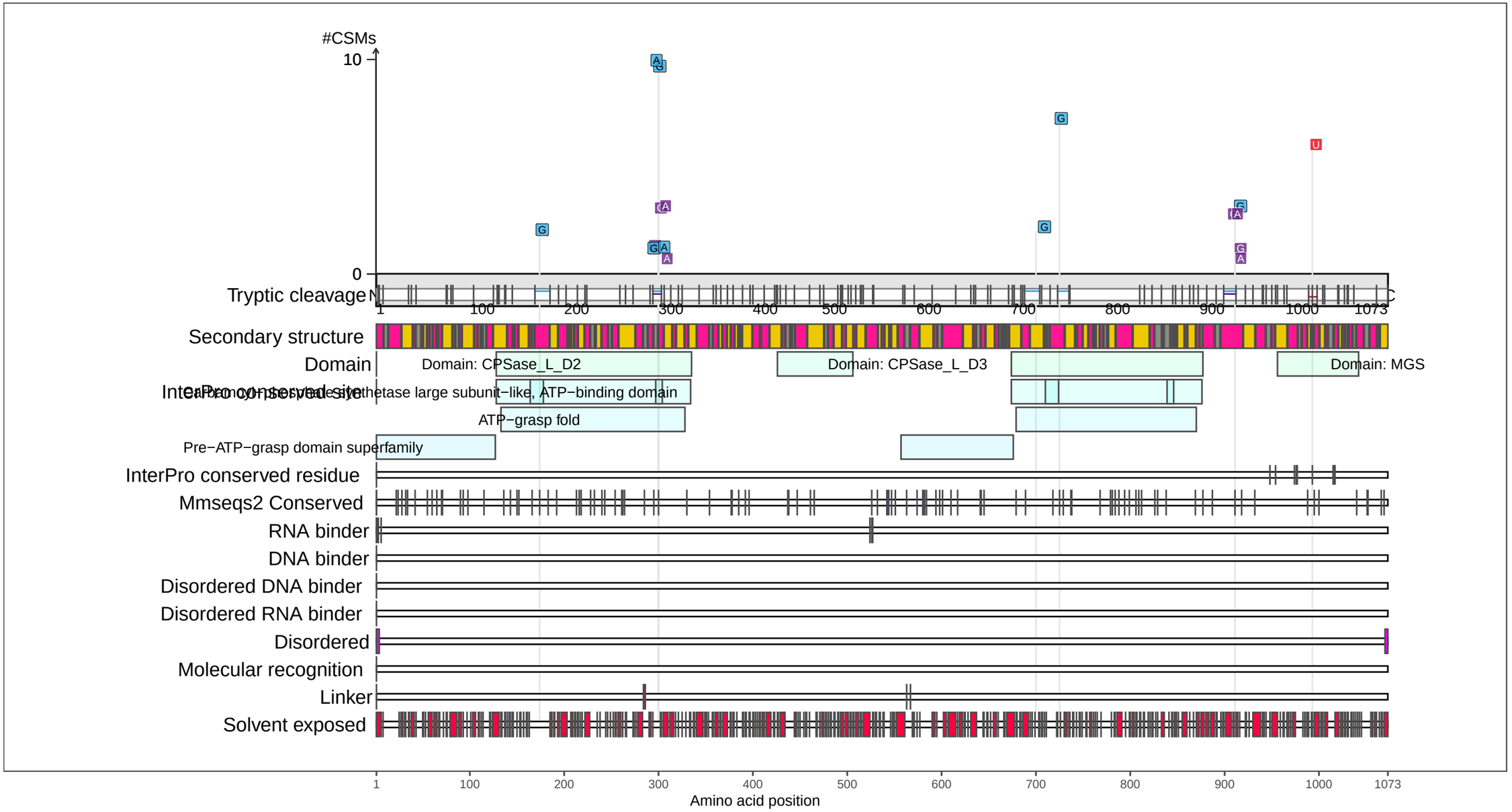
− RNA functions:
23S rRNA (adenine(2030)−N(6))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; Ribosomal RNA large subunit methyltransferase D, RlmJ; RNA binding
RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (adenine−N6−)−methyltransferase activity
rRNA (adenine) methyltransferase activity; rRNA base methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing

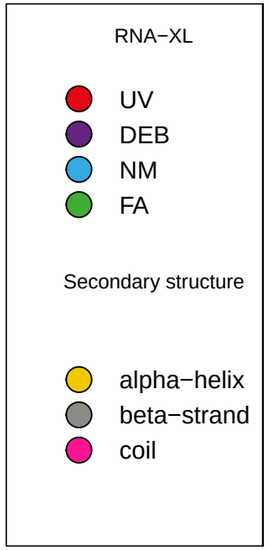


P00968
CARB_ECOLI Carbamoyl−phosphate synthase large chain

− Abundance:
tryptic [log10 Intensity]: 9.04 (Q 89)
PAXdb K12 strain [ppm]: 3.08 (Q 92)
PAXdb E.coli [ppm]: 2.57 (Q 87)

− RNA functions: not annotated

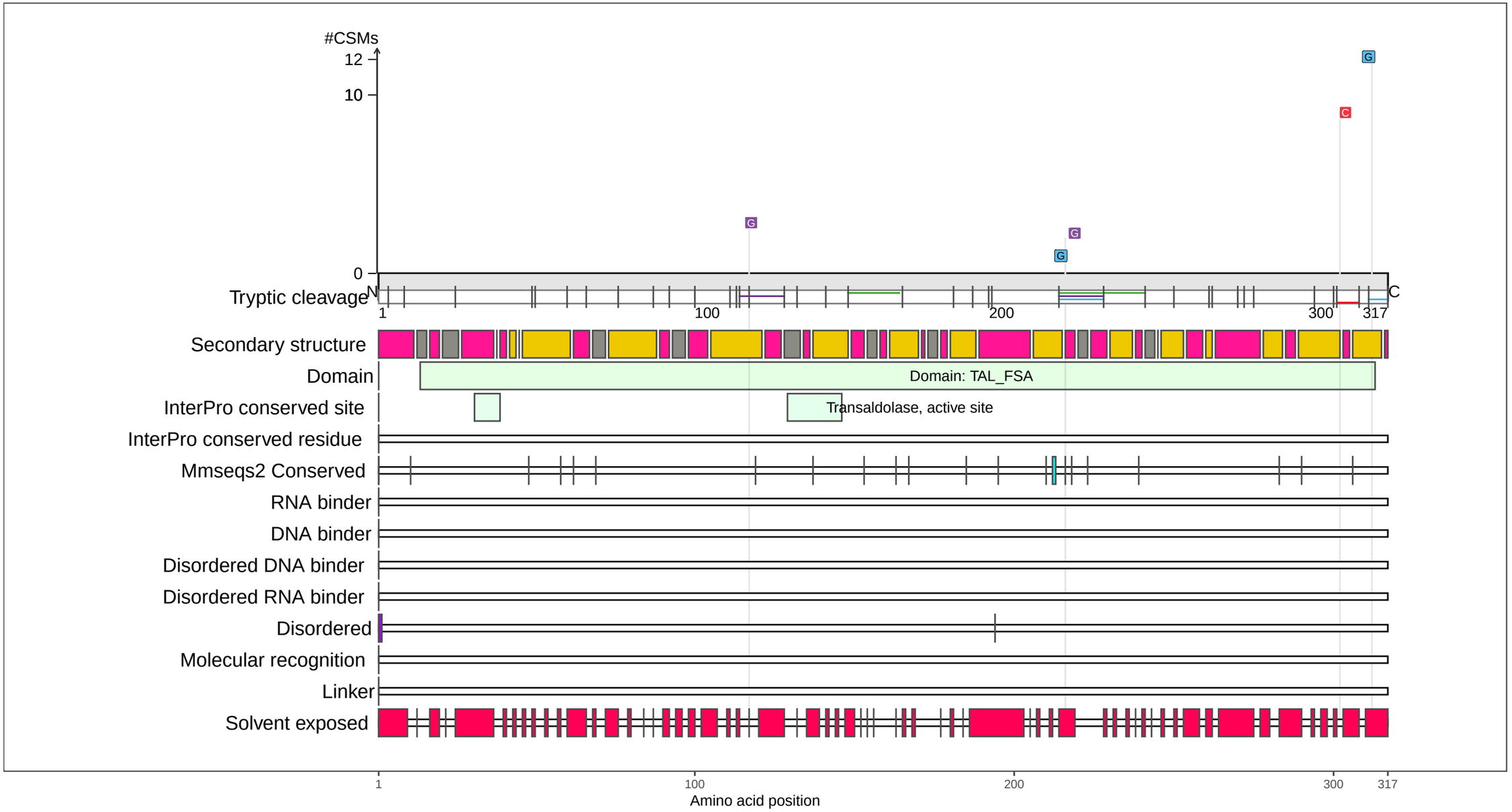


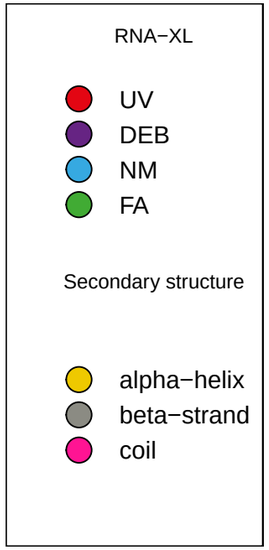


P0A870
TALB_ECOLI Transaldolase B

− Abundance:
tryptic [log10 Intensity]: 9.67 (Q 98)
PAXdb K12 strain [ppm]: 3.09 (Q 92)
PAXdb E.coli [ppm]: 3.33 (Q 98)

− RNA functions: not annotated

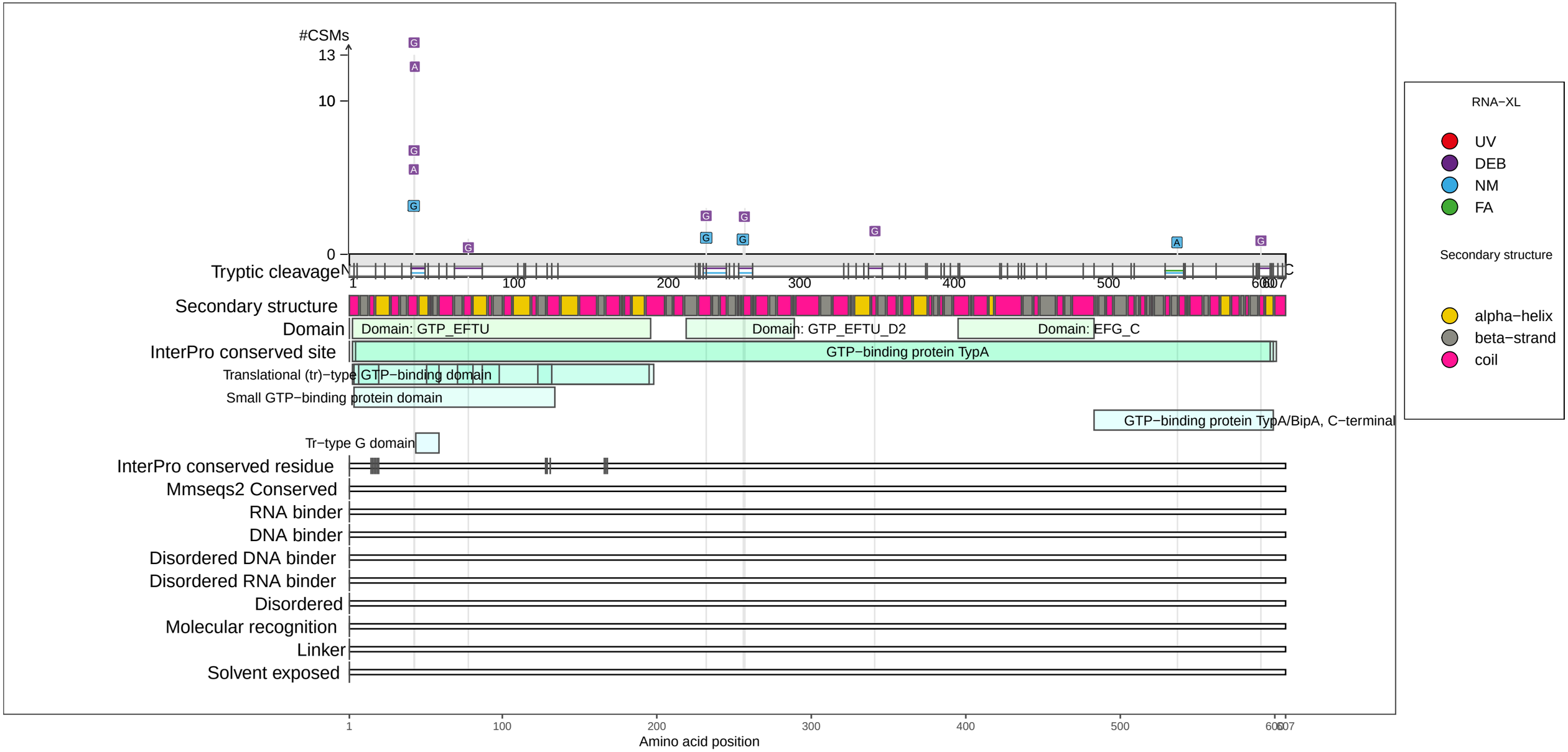




P0DTT0
BIPA_ECOLI 50S ribosomal subunit assembly factor BipA

− Abundance:
tryptic [log10 Intensity]: 9.85 (Q 99)
PAXdb K12 strain [ppm]: 3.13 (Q 93)
PAXdb E.coli [ppm]: 2.73 (Q 90)

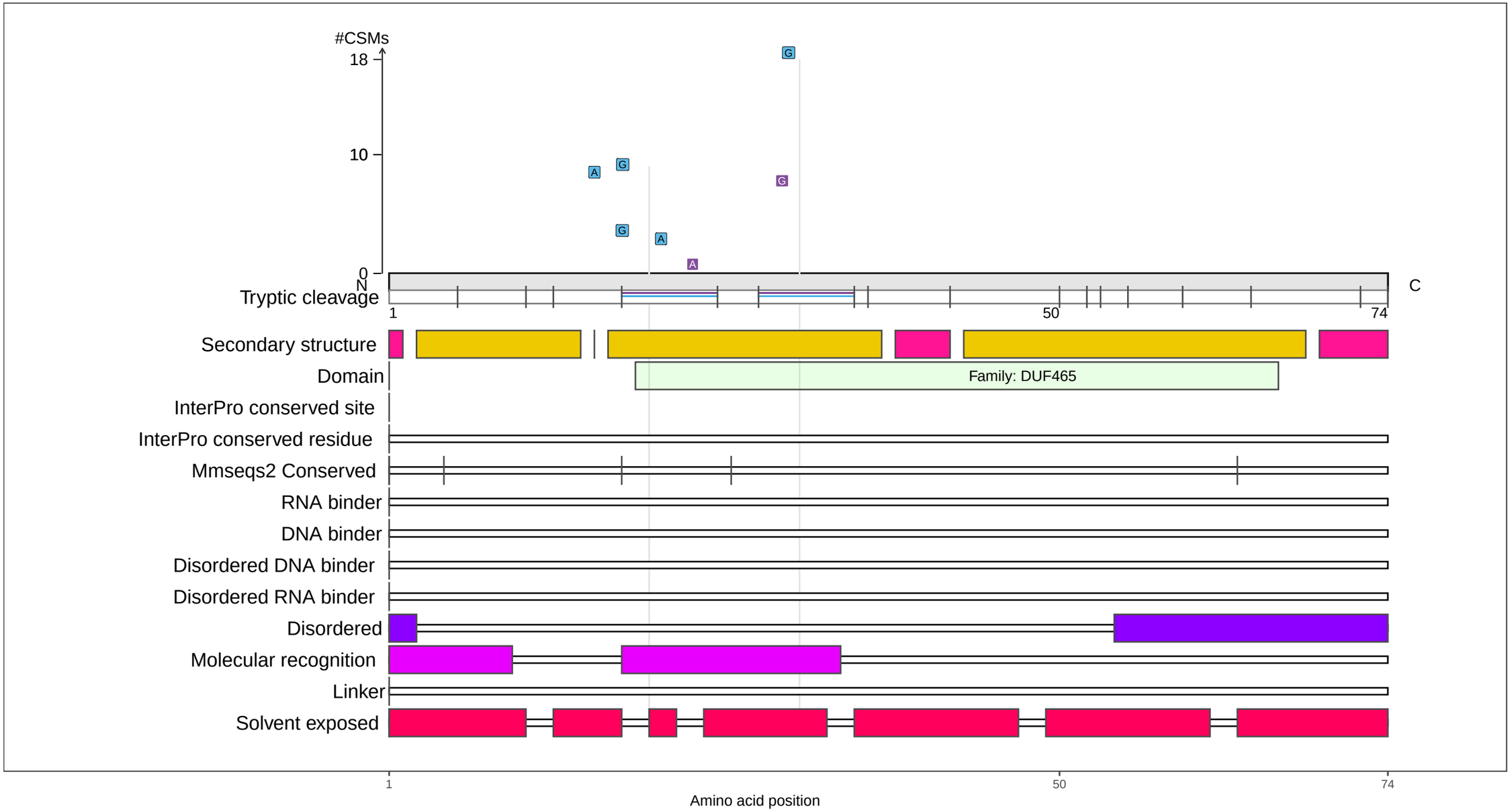
− RNA functions: not annotated

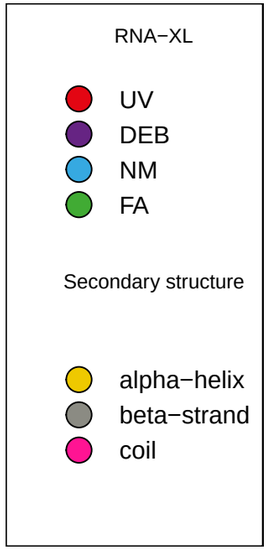


P0ACW6
YDCH_ECOLI Uncharacterized protein YdcH

− Abundance:
tryptic [log10 Intensity]: 6.94 (Q 11)
PAXdb K12 strain [ppm]: 2.77 (Q 85)
PAXdb E.coli [ppm]: 2.69 (Q 90)

− RNA functions: not annotated

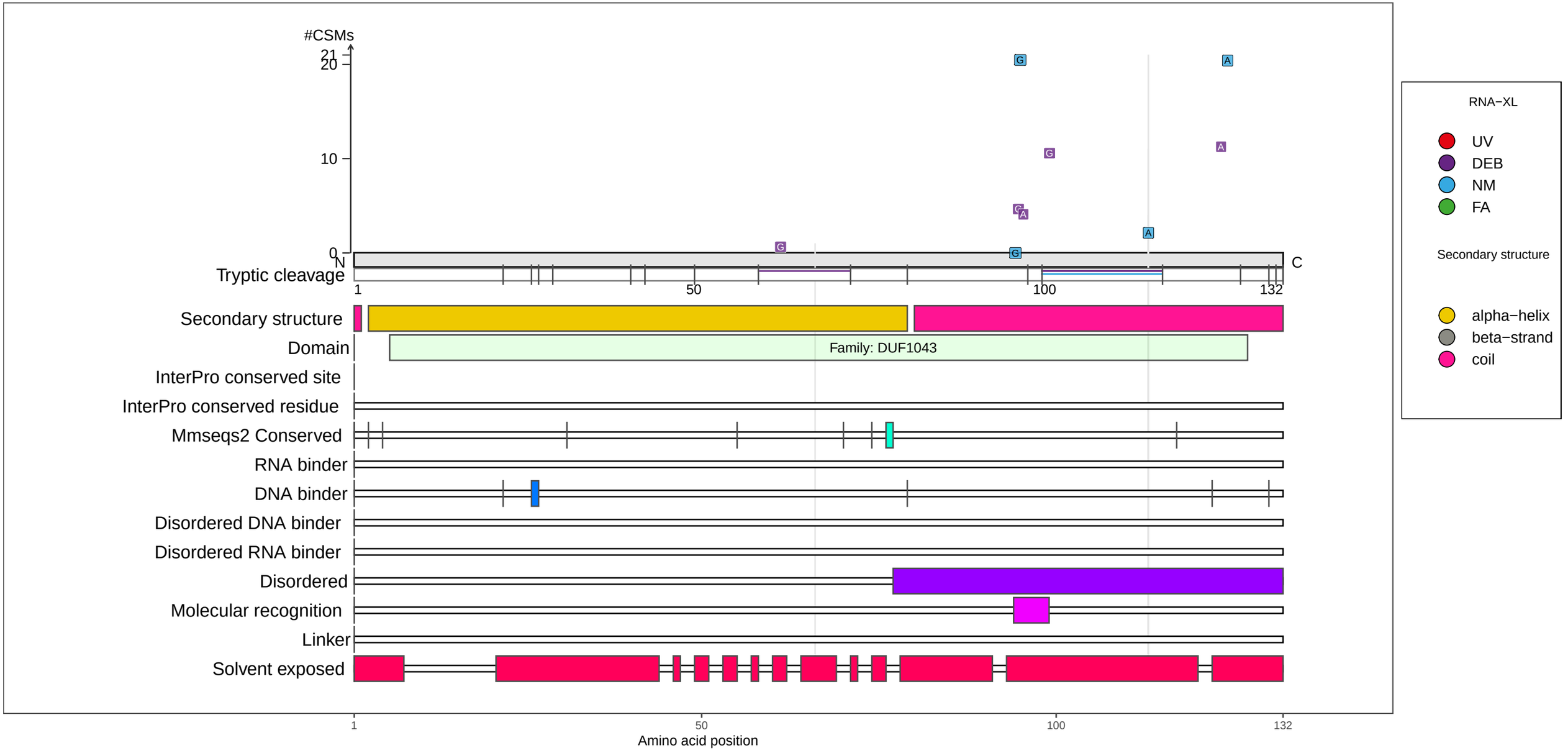




P0ADW3
YHCB_ECOLI Inner membrane protein YhcB

− Abundance:
tryptic [log10 Intensity]: 8.54 (Q 77)
PAXdb K12 strain [ppm]: 2.41 (Q 74)
PAXdb E.coli [ppm]: 2.75 (Q 91)

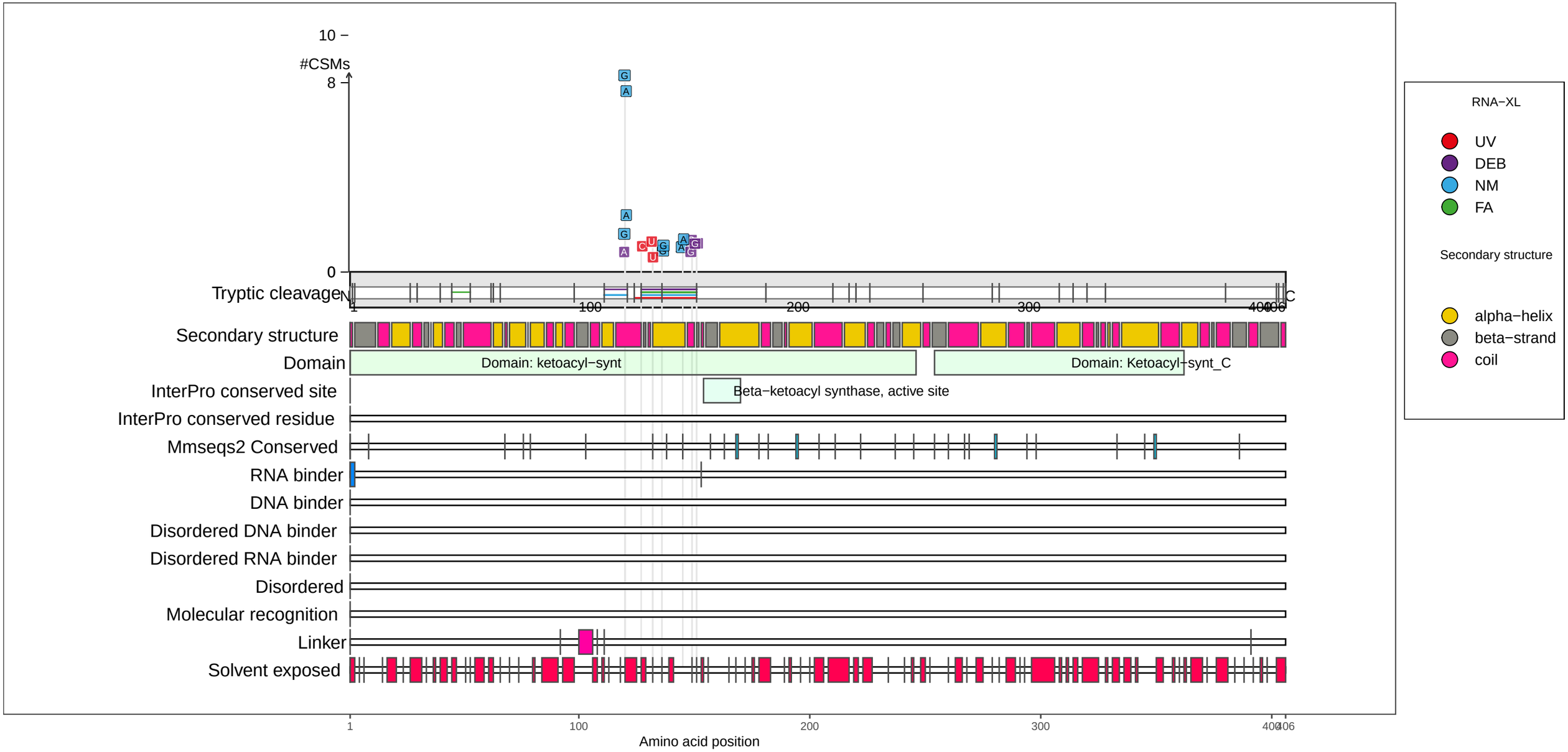
− RNA functions: not annotated



P0A953
FABB_ECOLI 3−oxoacyl−[acyl−carrier−protein] synthase 1

− Abundance:
tryptic [log10 Intensity]: 9.48 (Q 96)
PAXdb K12 strain [ppm]: 3.29 (Q 95)
PAXdb E.coli [ppm]: 3.19 (Q 96)

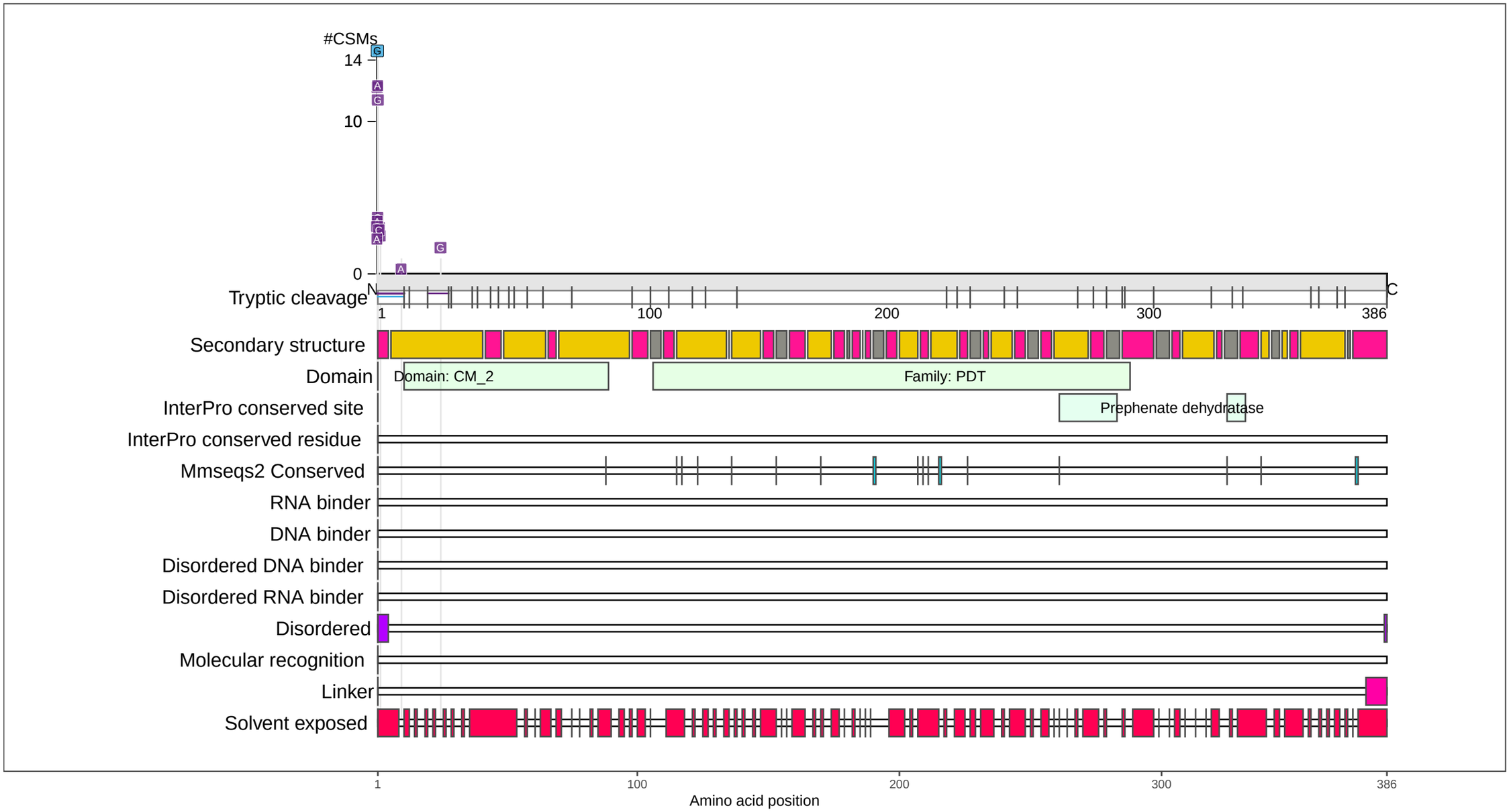
− RNA functions: not annotated



P0A9J8
CMPDT_ECOLI Bifunctional chorismate mutase/prephenate dehydratase

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 61)
PAXdb K12 strain [ppm]: 2.2 (Q 67)
PAXdb E.coli [ppm]: 2.38 (Q 83)

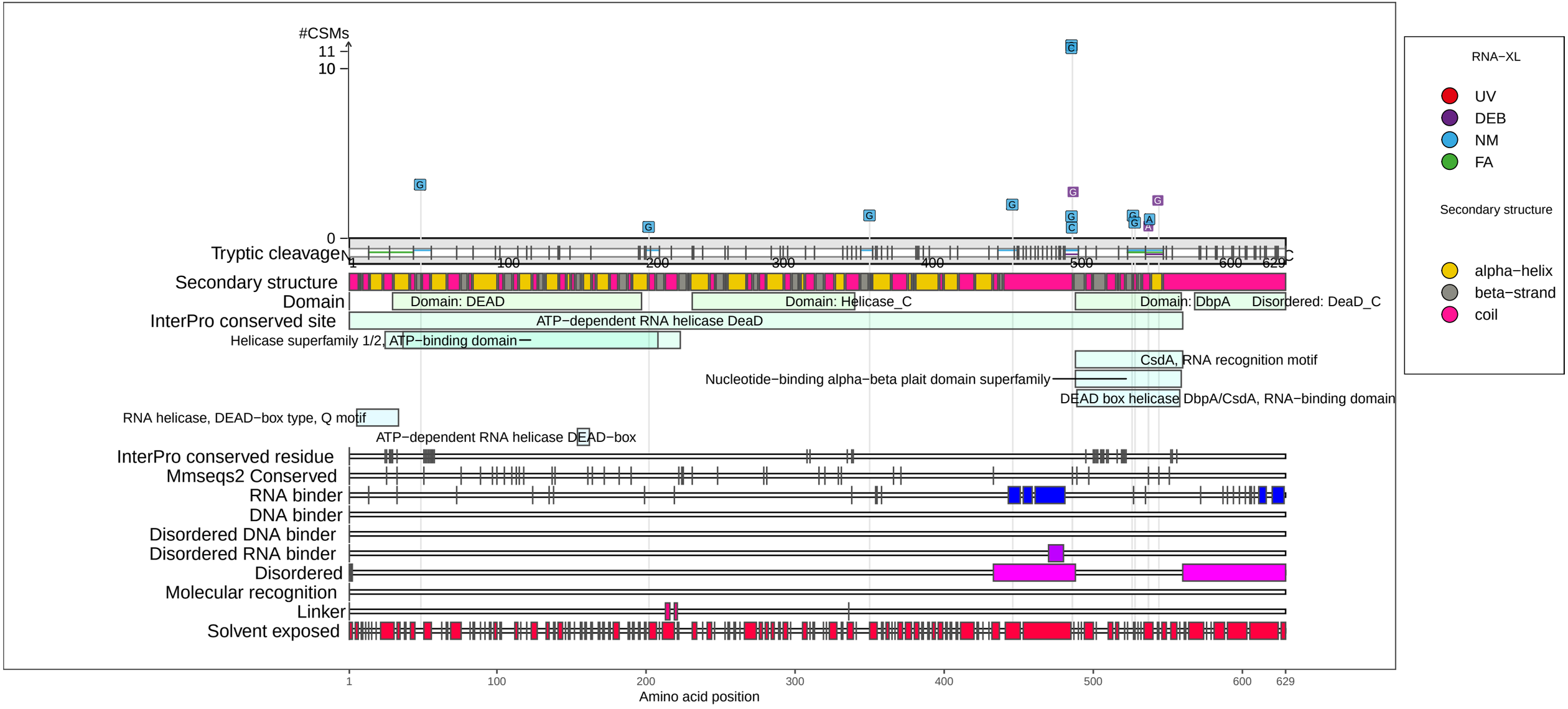
− RNA functions: not annotated



P0A9P6
DEAD_ECOLI ATP−dependent RNA helicase DeaD

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 2.66 (Q 82)
PAXdb E.coli [ppm]: 2.29 (Q 80)

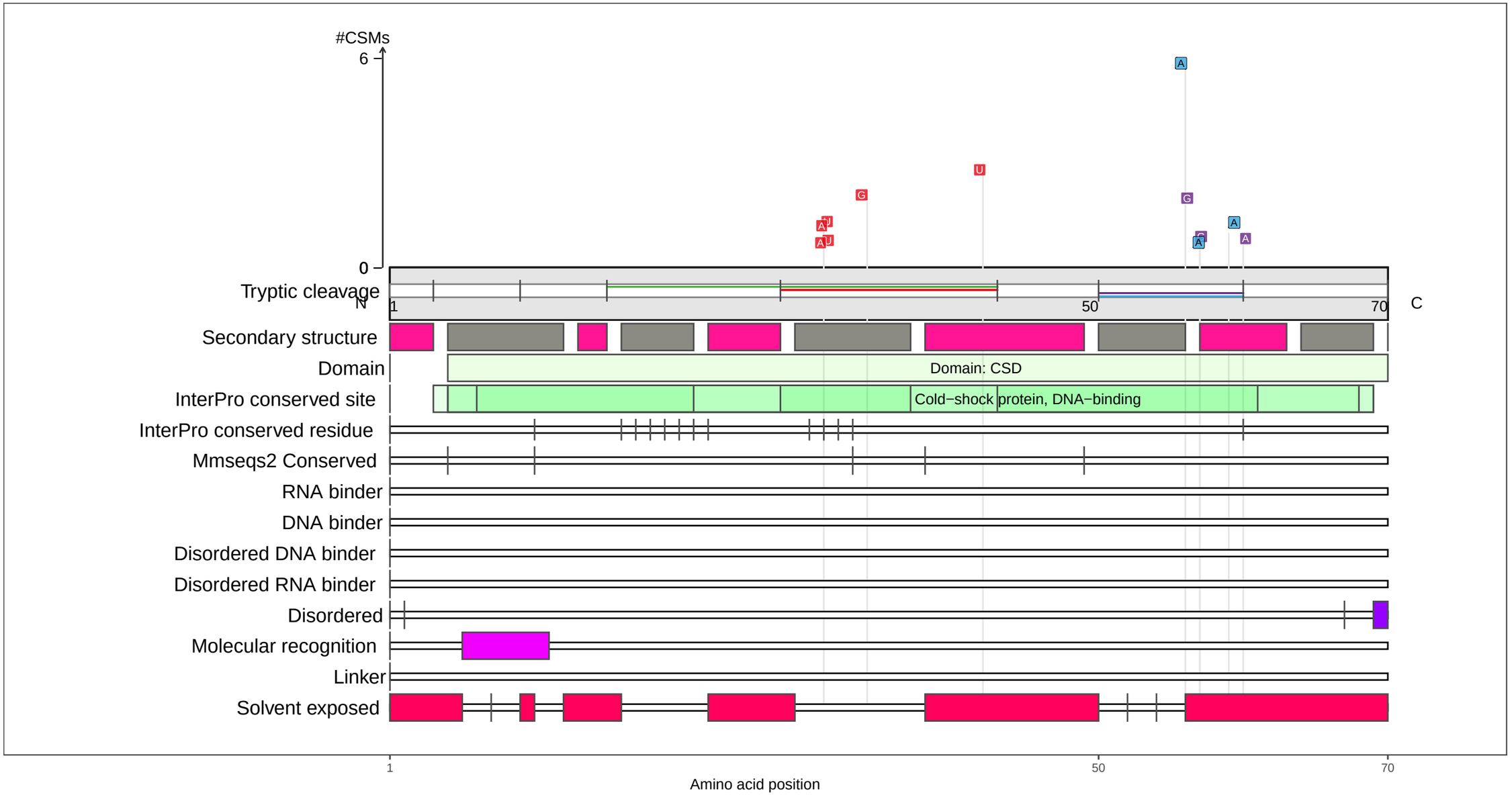
− RNA functions:
DbpA RNA binding domain; mRNA stabilization; RNA binding; RNA catabolic process
RNA helicase activity; RNA metabolic process; RNA stabilization
RNA strand annealing activity

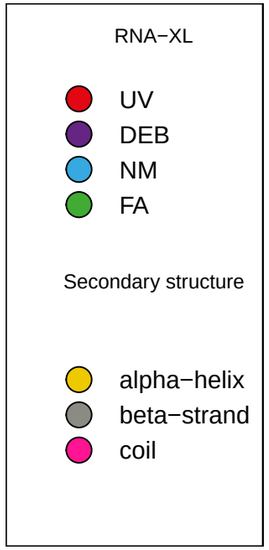


P0A9X9
CSPA_ECOLI Cold shock protein CspA

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 95)
PAXdb K12 strain [ppm]: 3.49 (Q 97)
PAXdb E.coli [ppm]: 3.24 (Q 97)

− RNA functions:
RNA binding; RNA biosynthetic process; RNA metabolic process

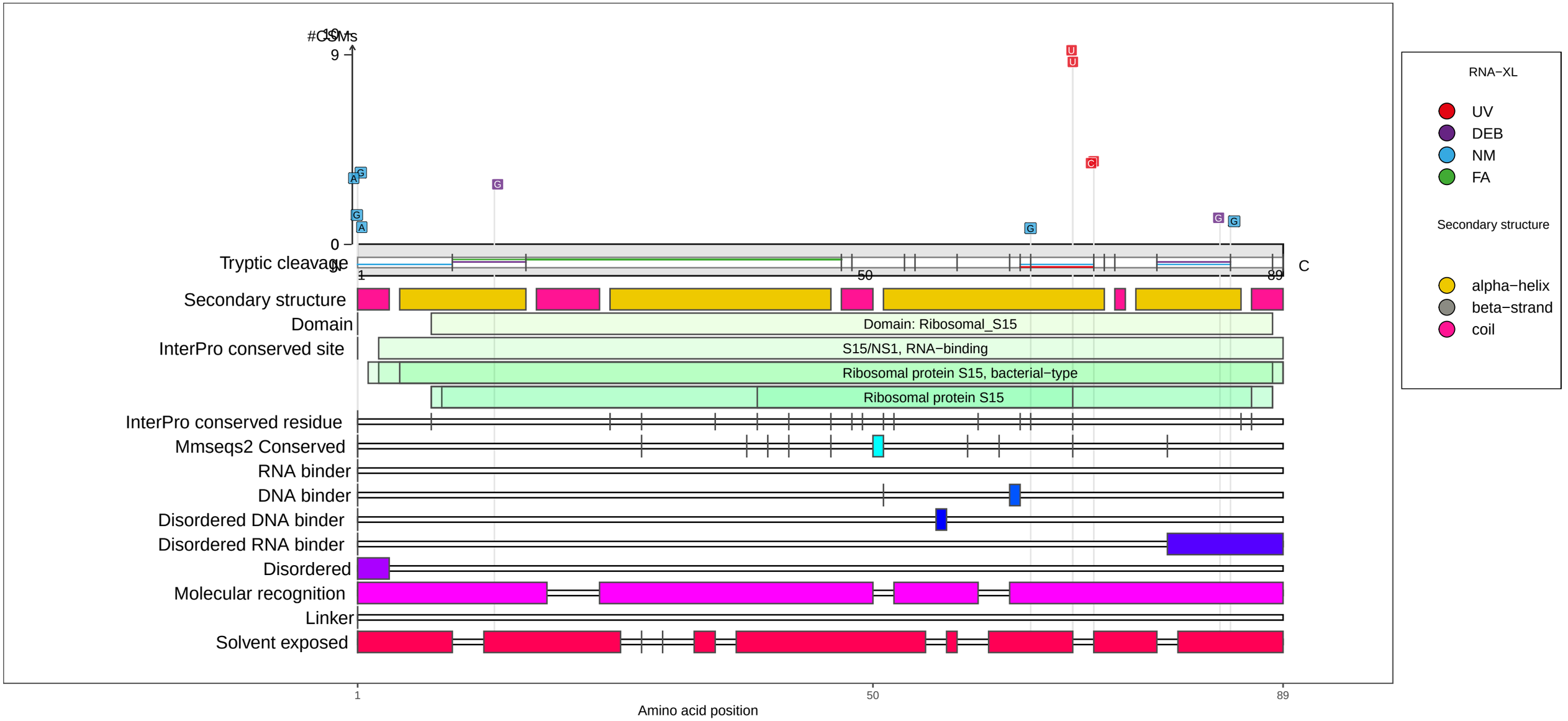




P0ADZ4
RS15_ECOLI 30S ribosomal protein S15

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 2.69 (Q 83)
PAXdb E.coli [ppm]: 3.22 (Q 97)

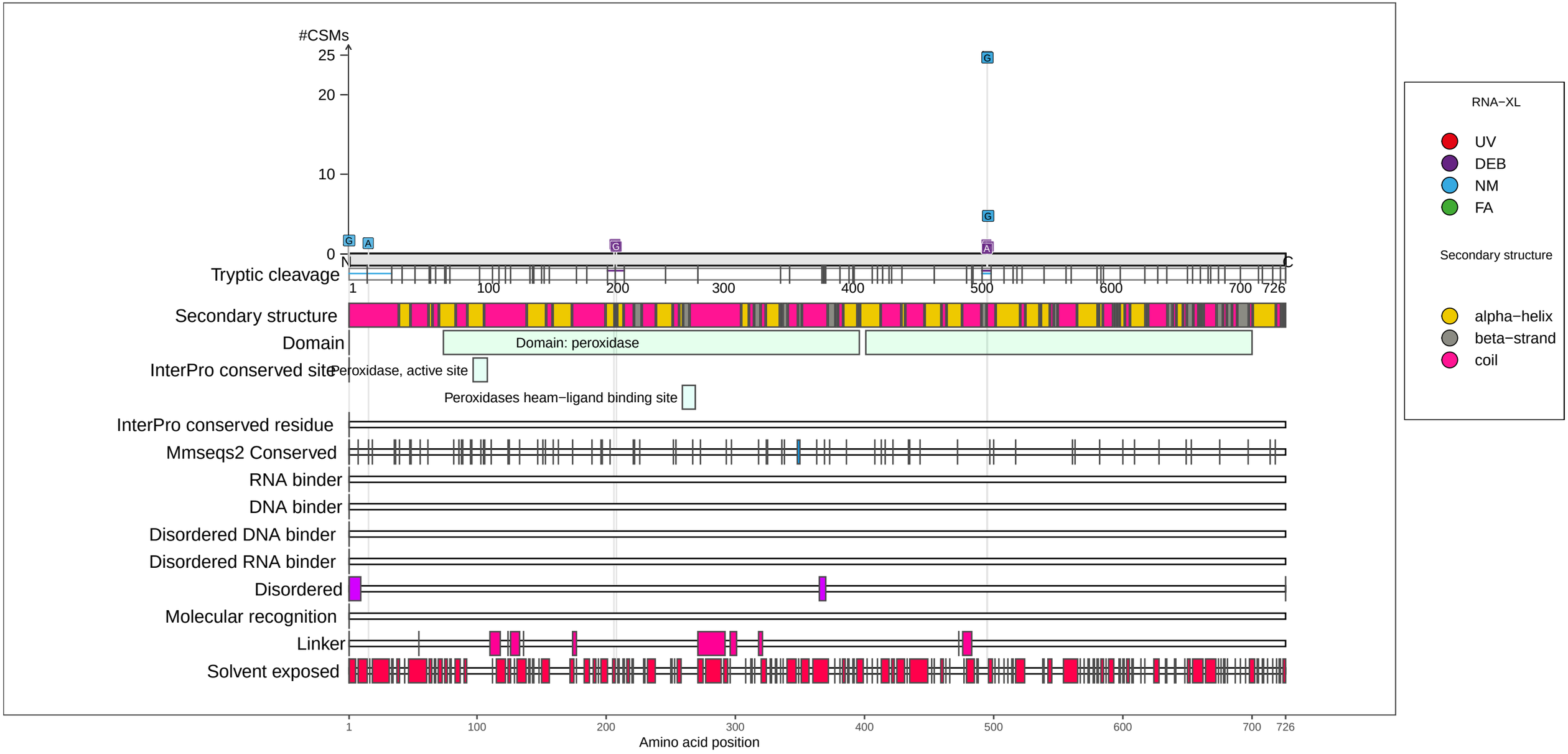
− RNA functions:
mRNA binding; mRNA binding involved in posttranscriptional gene silencing
RNA binding; RNA binding involved in posttranscriptional gene silencing; rRNA binding



P13029
KATG_ECOLI Catalase−peroxidase

− Abundance:
tryptic [log10 Intensity]: 8.91 (Q 86)
PAXdb K12 strain [ppm]: 2.82 (Q 87)
PAXdb E.coli [ppm]: 3.04 (Q 95)

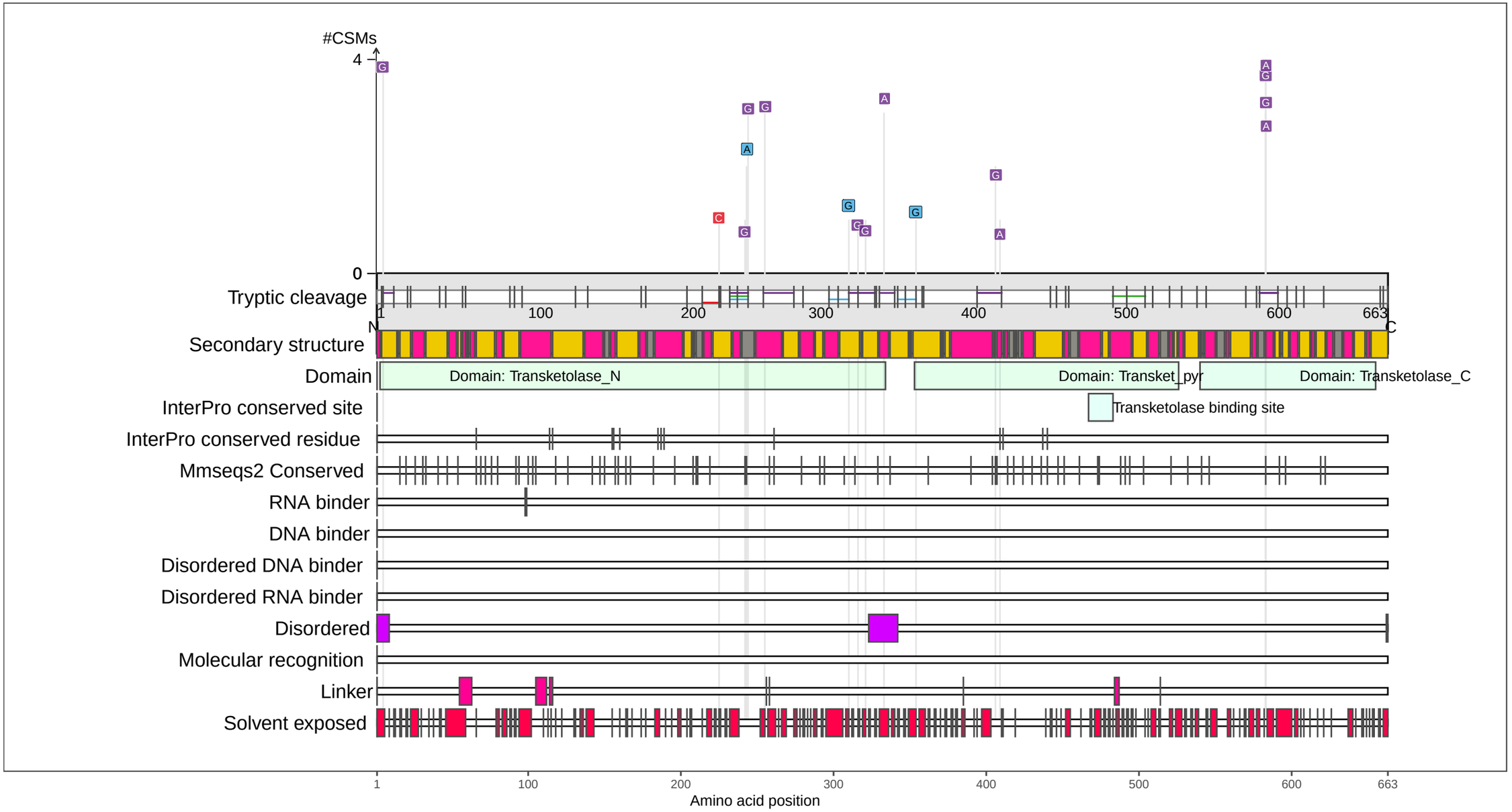
− RNA functions: not annotated

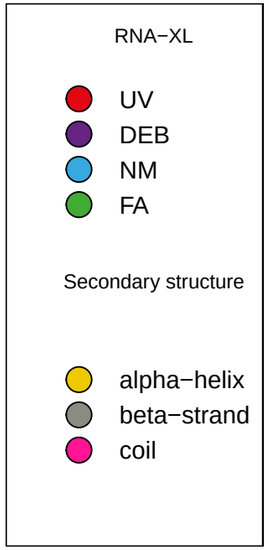


P27302
TKT1_ECOLI Transketolase 1

− Abundance:
tryptic [log10 Intensity]: 10.15 (Q 100)
PAXdb K12 strain [ppm]: 3.1 (Q 92)
PAXdb E.coli [ppm]: 3.04 (Q 95)

− RNA functions: not annotated

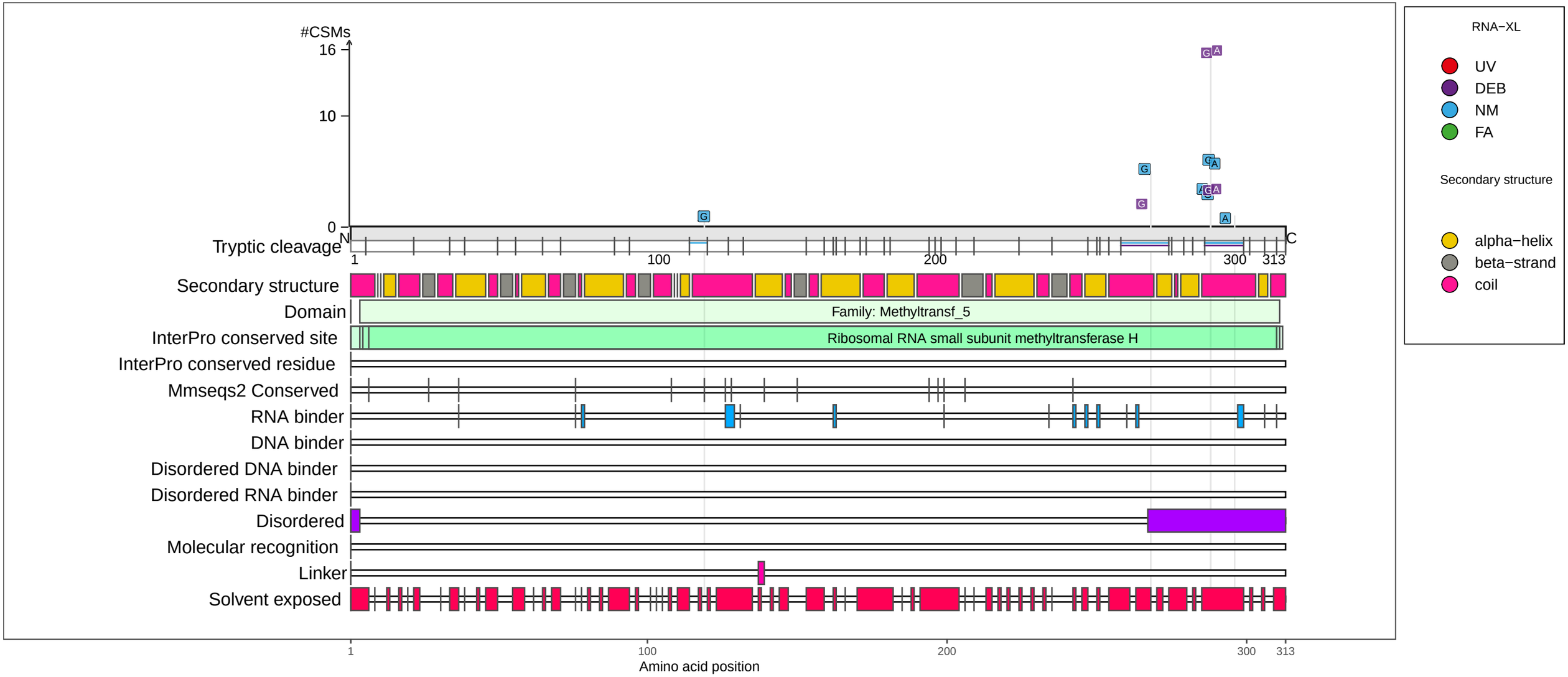




P60390
RSMH_ECOLI Ribosomal RNA small subunit methyltransferase H

− Abundance:
tryptic [log10 Intensity]: 7.04 (Q 15)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 2.06 (Q 74)

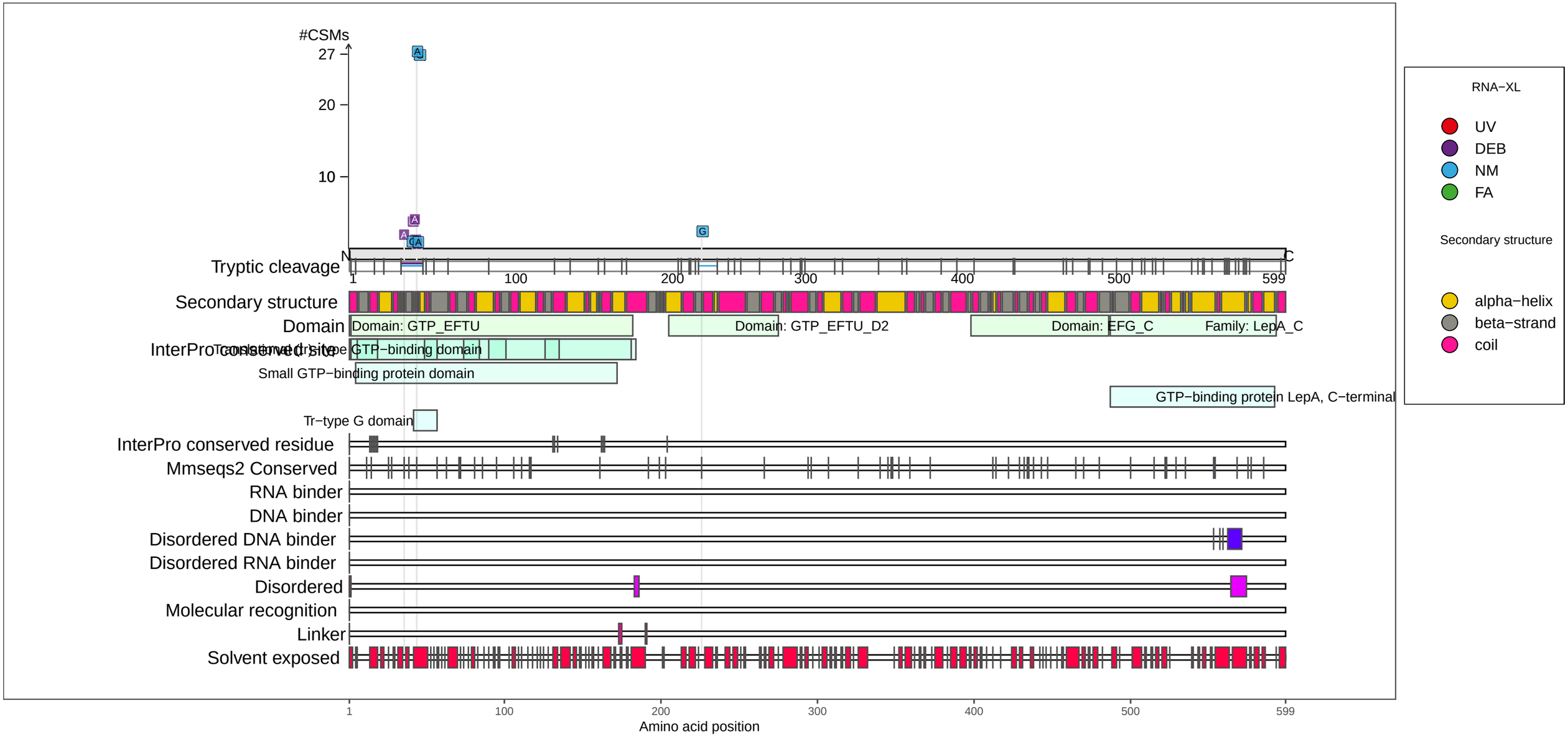
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA methylation
RNA methyltransferase activity; RNA modification; RNA processing
rRNA (cytosine−N4−)−methyltransferase activity; rRNA (cytosine) methyltransferase activity
rRNA base methylation; rRNA metabolic process; rRNA methylation; rRNA methyltransferase activity
rRNA modification; rRNA processing



P60785
LEPA_ECOLI Elongation factor 4

− Abundance:
tryptic [log10 Intensity]: 8.87 (Q 85)
PAXdb K12 strain [ppm]: 2.06 (Q 63)
PAXdb E.coli [ppm]: 2.49 (Q 85)

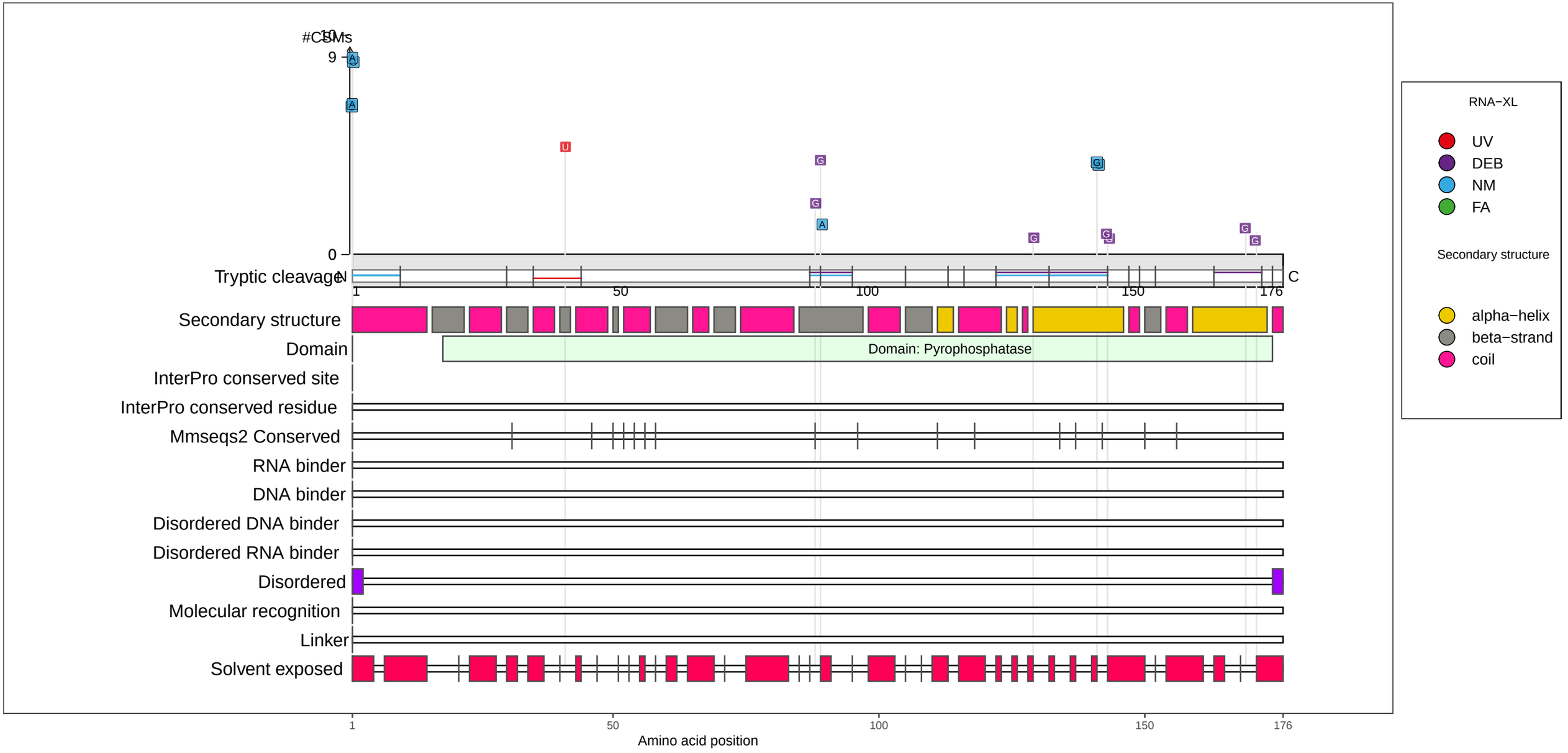
− RNA functions:
RNA binding



P0A7A9
IPYR_ECOLI Inorganic pyrophosphatase

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 2.82 (Q 86)
PAXdb E.coli [ppm]: 3.42 (Q 98)

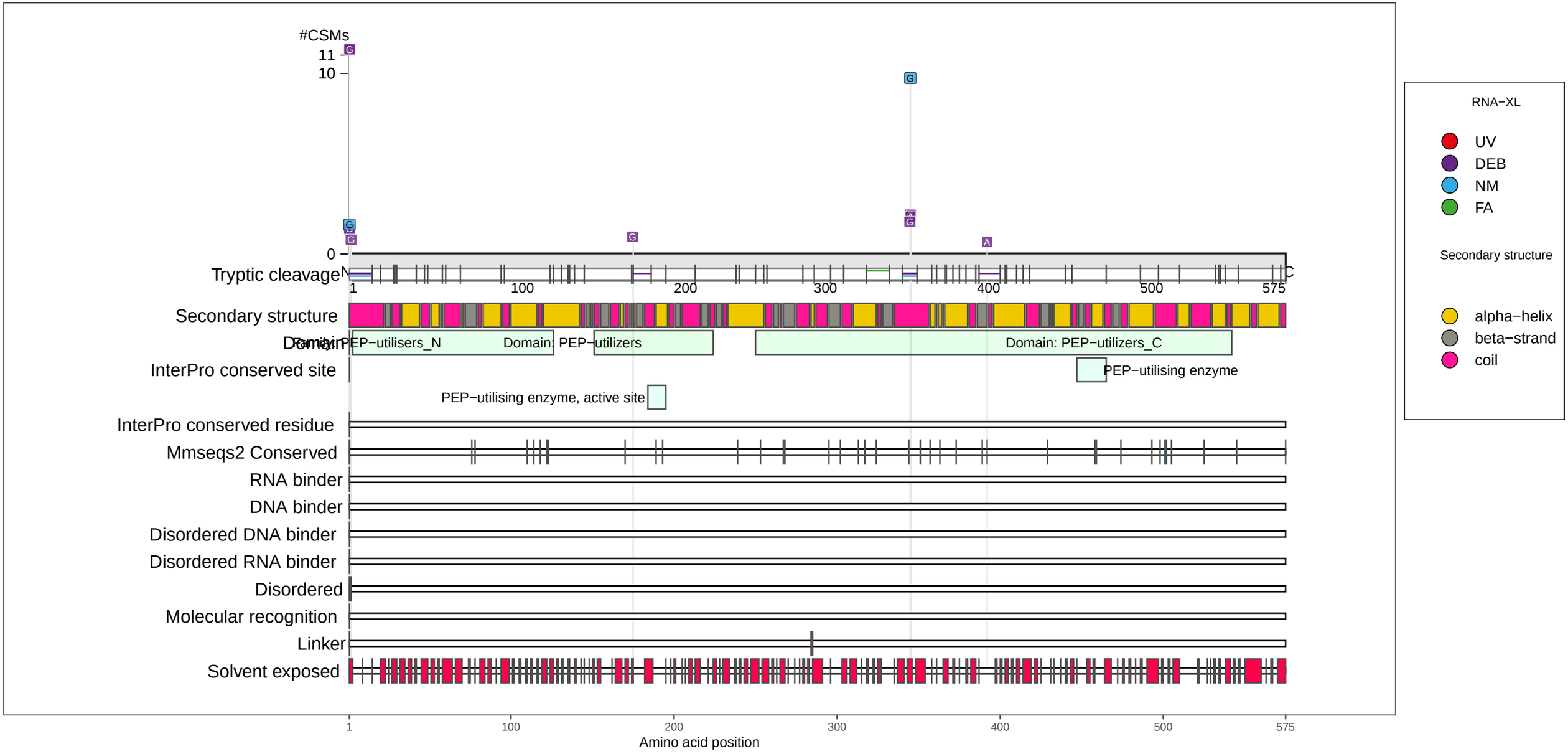
− RNA functions: not annotated



P08839
PT1_ECOLI Phosphoenolpyruvate−protein phosphotransferase

− Abundance:
tryptic [log10 Intensity]: 9.02 (Q 89)
PAXdb K12 strain [ppm]: 3.27 (Q 95)
PAXdb E.coli [ppm]: 3.04 (Q 95)

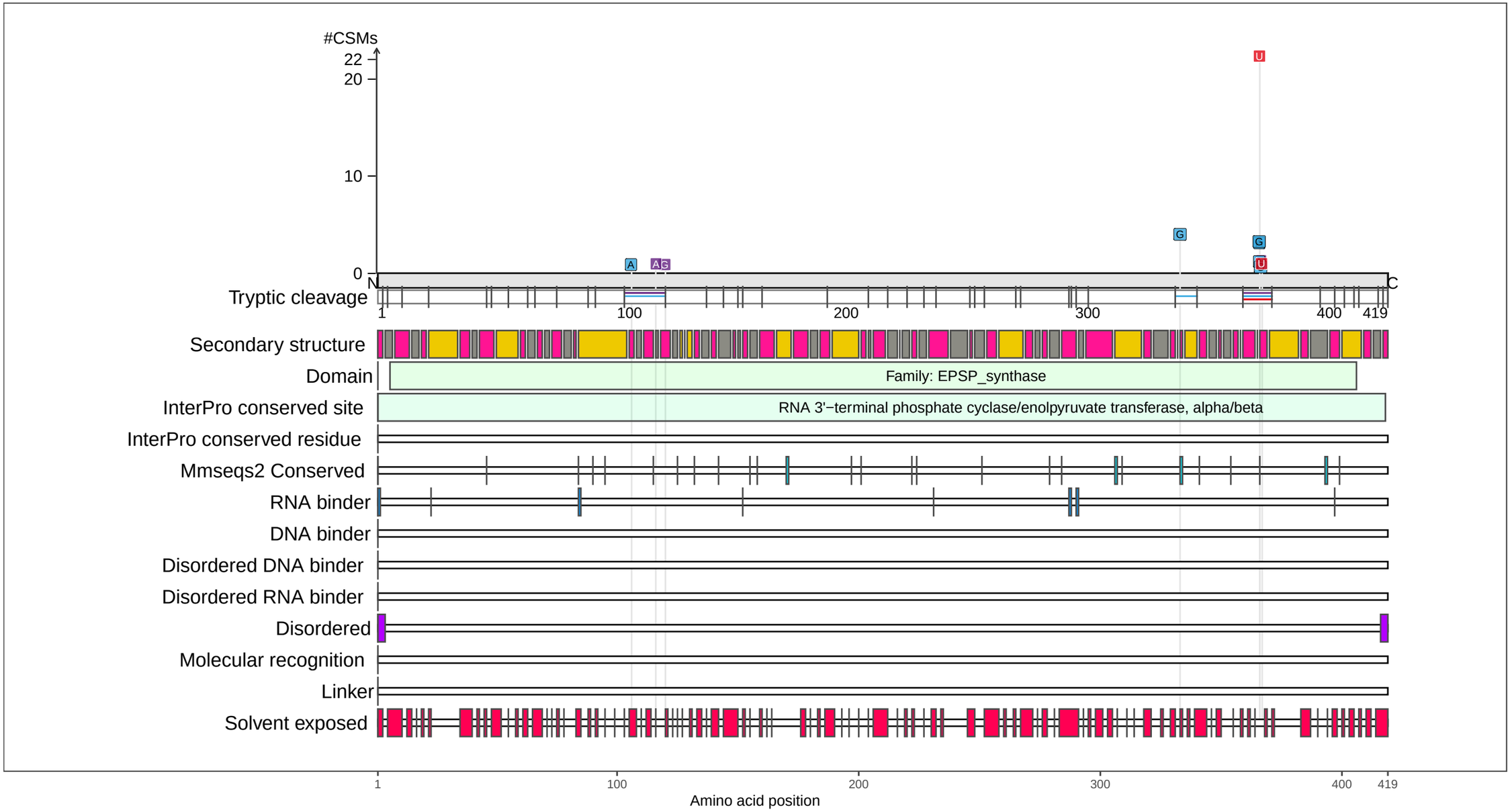
− RNA functions: not annotated



P0A749
MURA_ECOLI UDP−N−acetylglucosamine 1−carboxyvinyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.31 (Q 25)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 2.27 (Q 79)

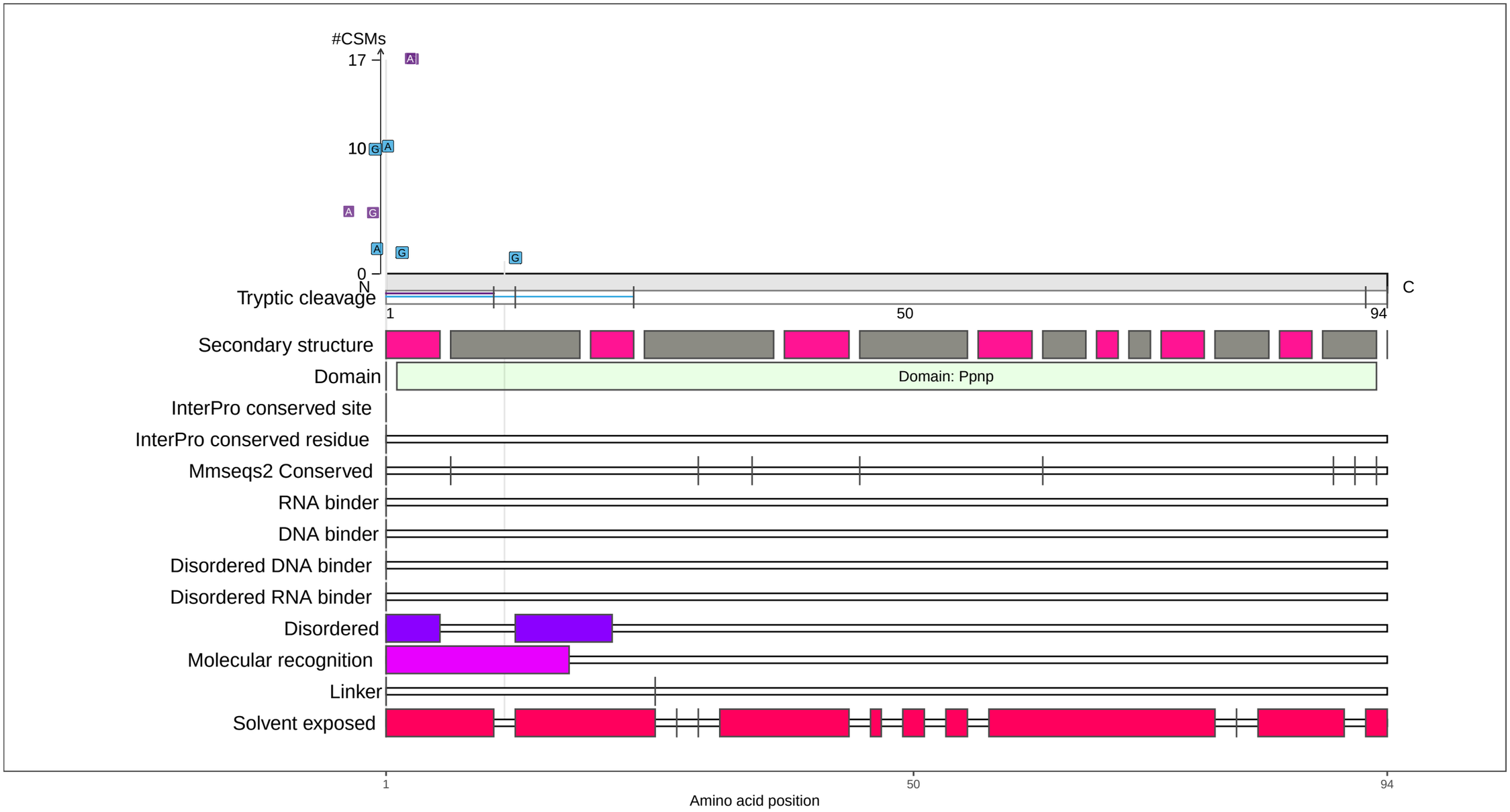
− RNA functions: not annotated

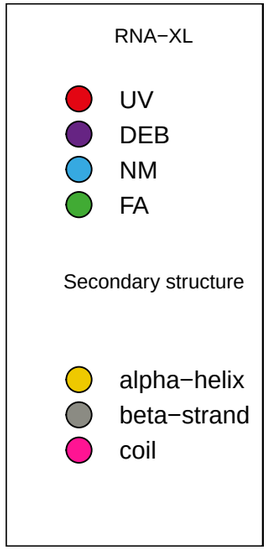


P0C037
PPNP_ECOLI Pyrimidine/purine nucleoside phosphorylase

− Abundance:
tryptic [log10 Intensity]: 8.23 (Q 67)
PAXdb K12 strain [ppm]: 2.42 (Q 75)
PAXdb E.coli [ppm]: 2.85 (Q 92)

− RNA functions: not annotated

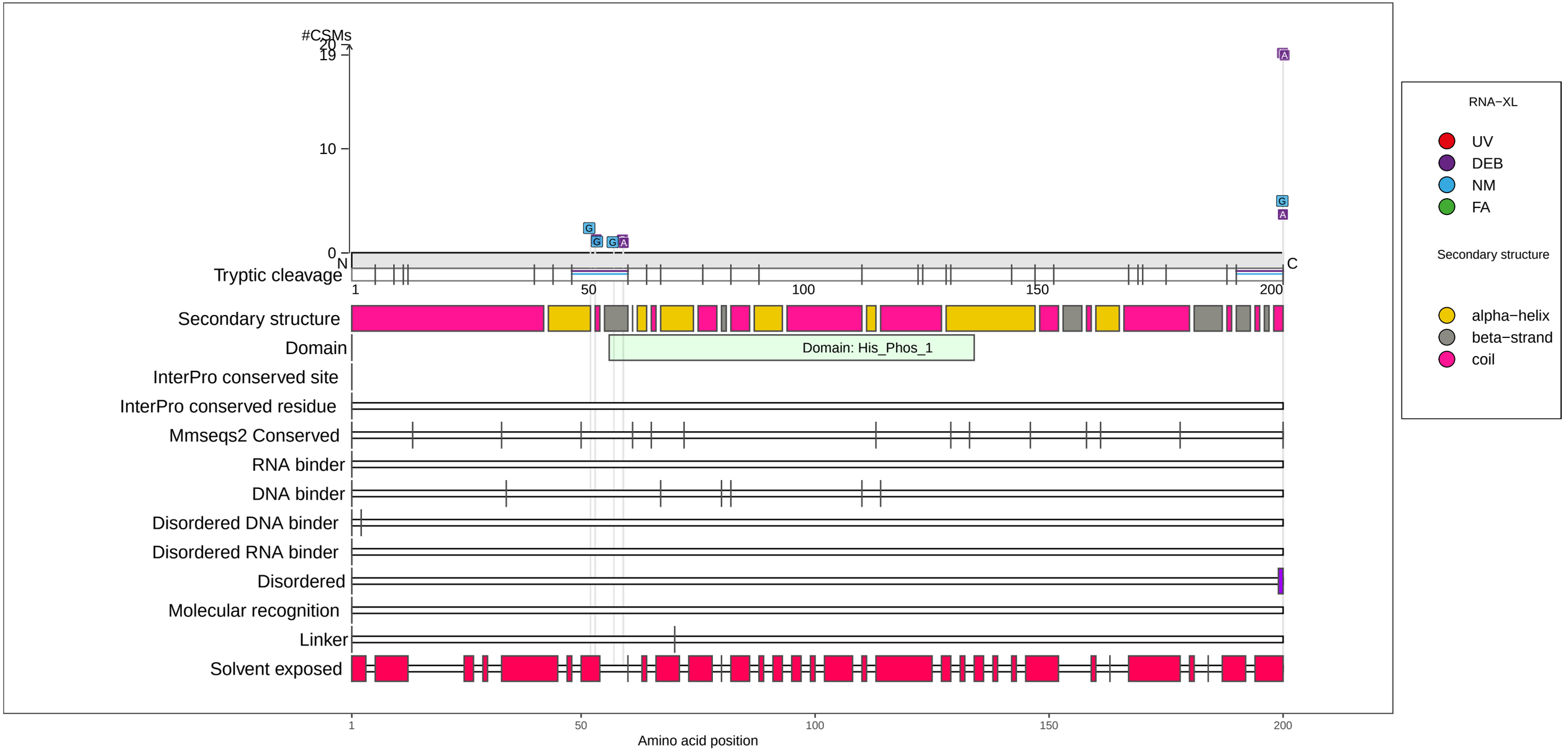




P45565
AIS_ECOLI Lipopolysaccharide core heptose(II)−phosphate phosphatase

− Abundance:
tryptic [log10 Intensity]: 8.98 (Q 88)
PAXdb K12 strain [ppm]: 3.22 (Q 94)
PAXdb E.coli [ppm]: 1.69 (Q 64)

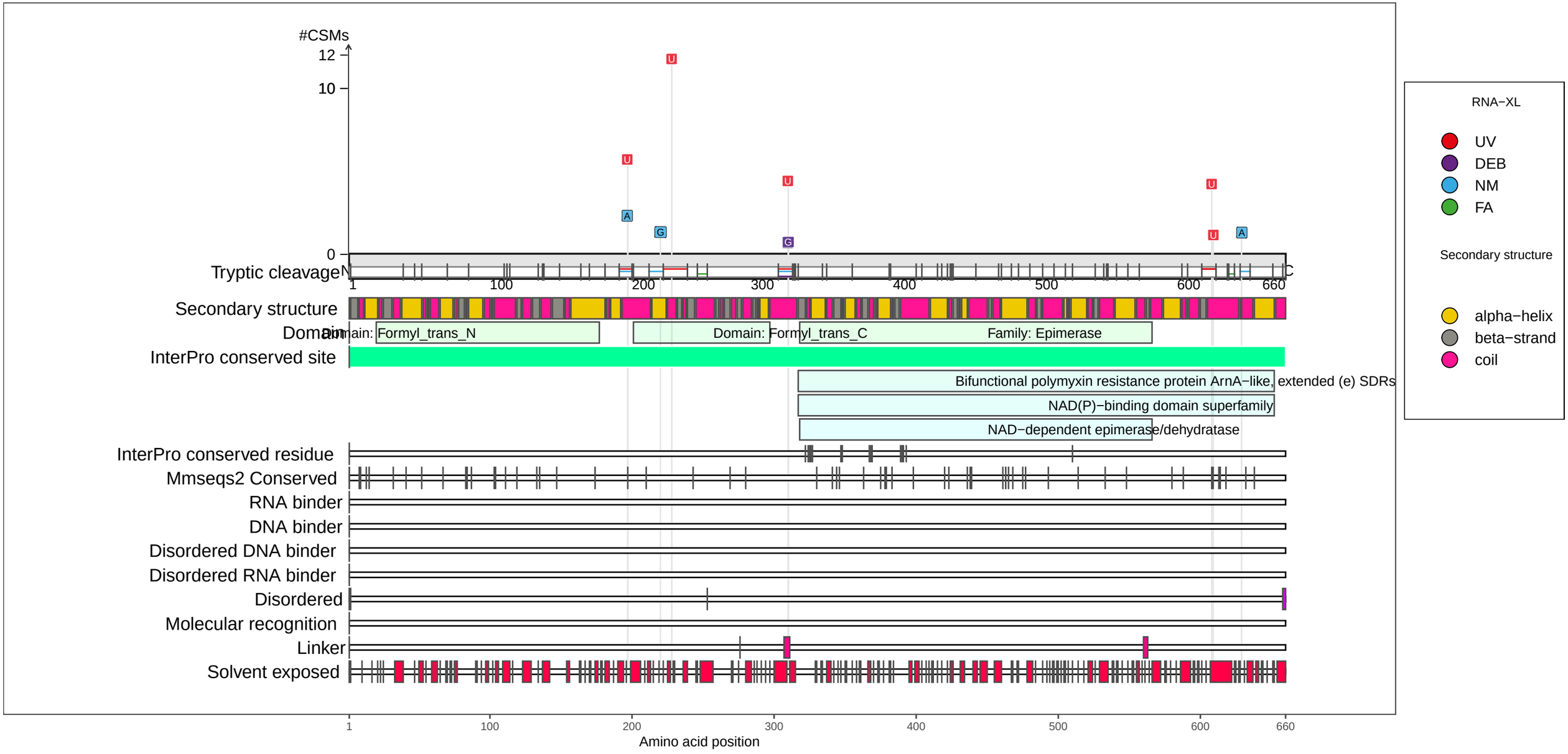
− RNA functions: not annotated



P77398
ARNA_ECOLI Bifunctional polymyxin resistance protein ArnA

− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: 2.86 (Q 88)
PAXdb E.coli [ppm]: 1.73 (Q 65)

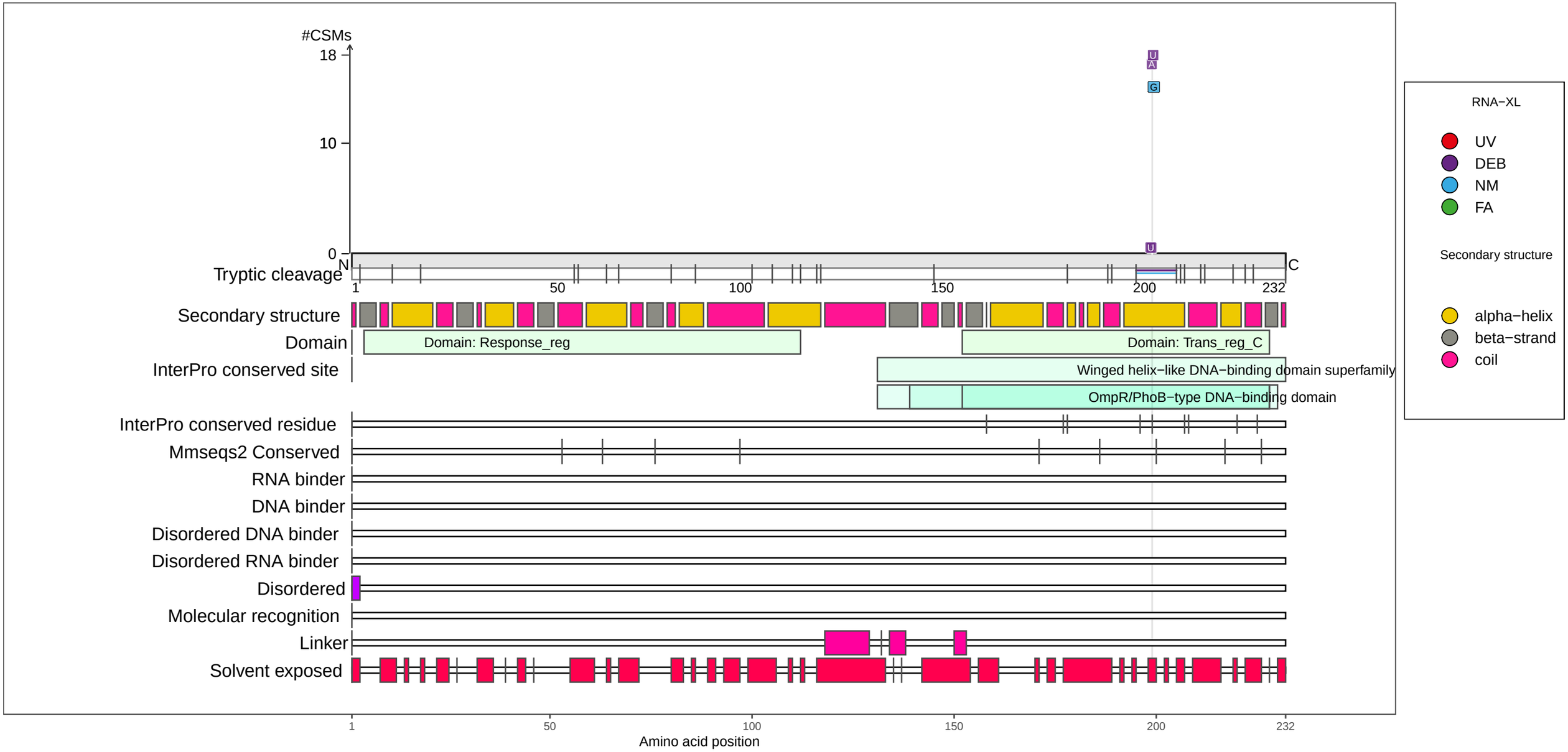
− RNA functions: not annotated



P0AE88
CPXR_ECOLI Transcriptional regulatory protein CpxR

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 44)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.77 (Q 91)

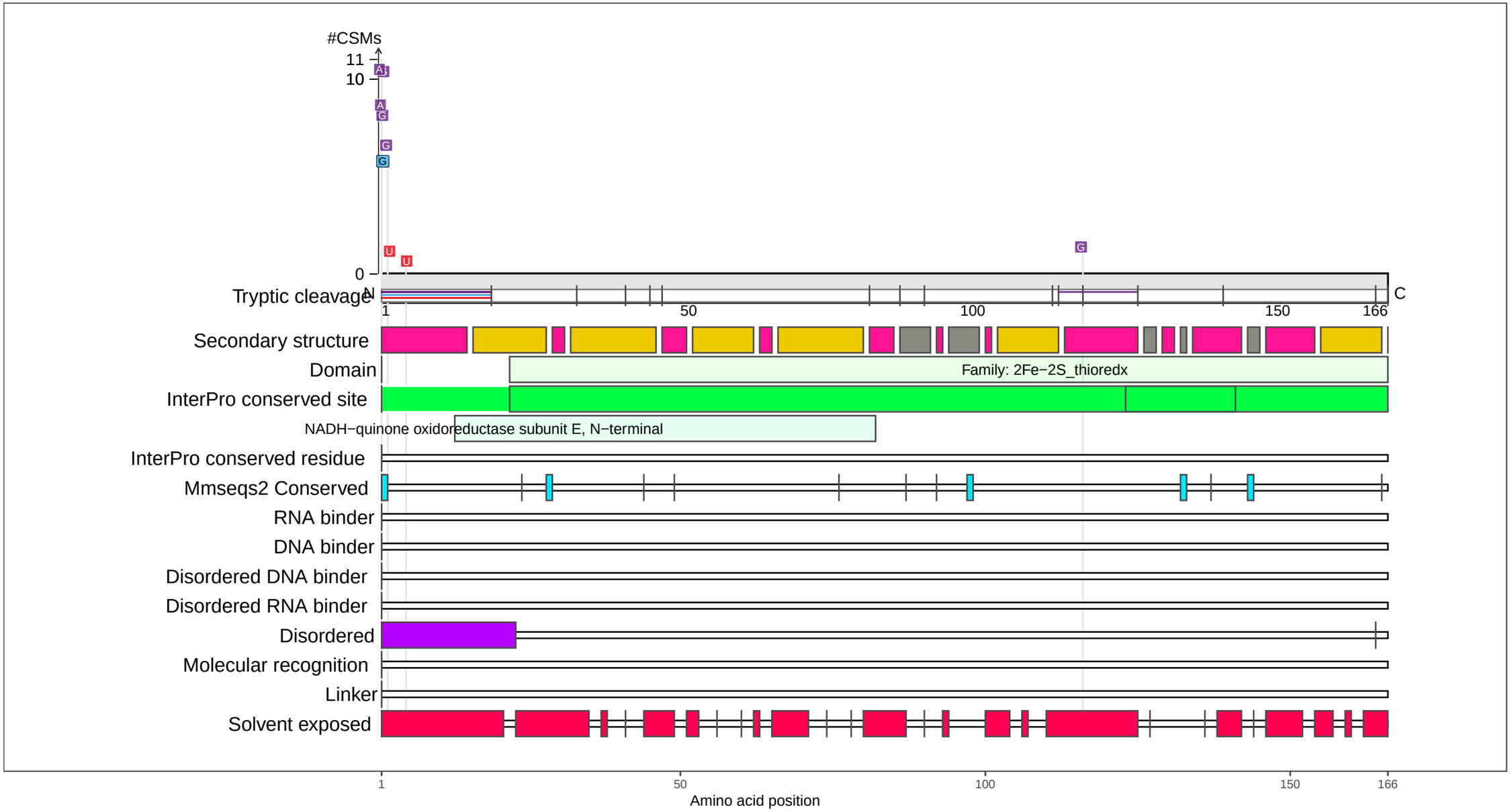
− RNA functions: not annotated



P0AFD1
NUOE_ECOLI NADH−quinone oxidoreductase subunit E

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 2.07 (Q 63)
PAXdb E.coli [ppm]: 2.46 (Q 84)

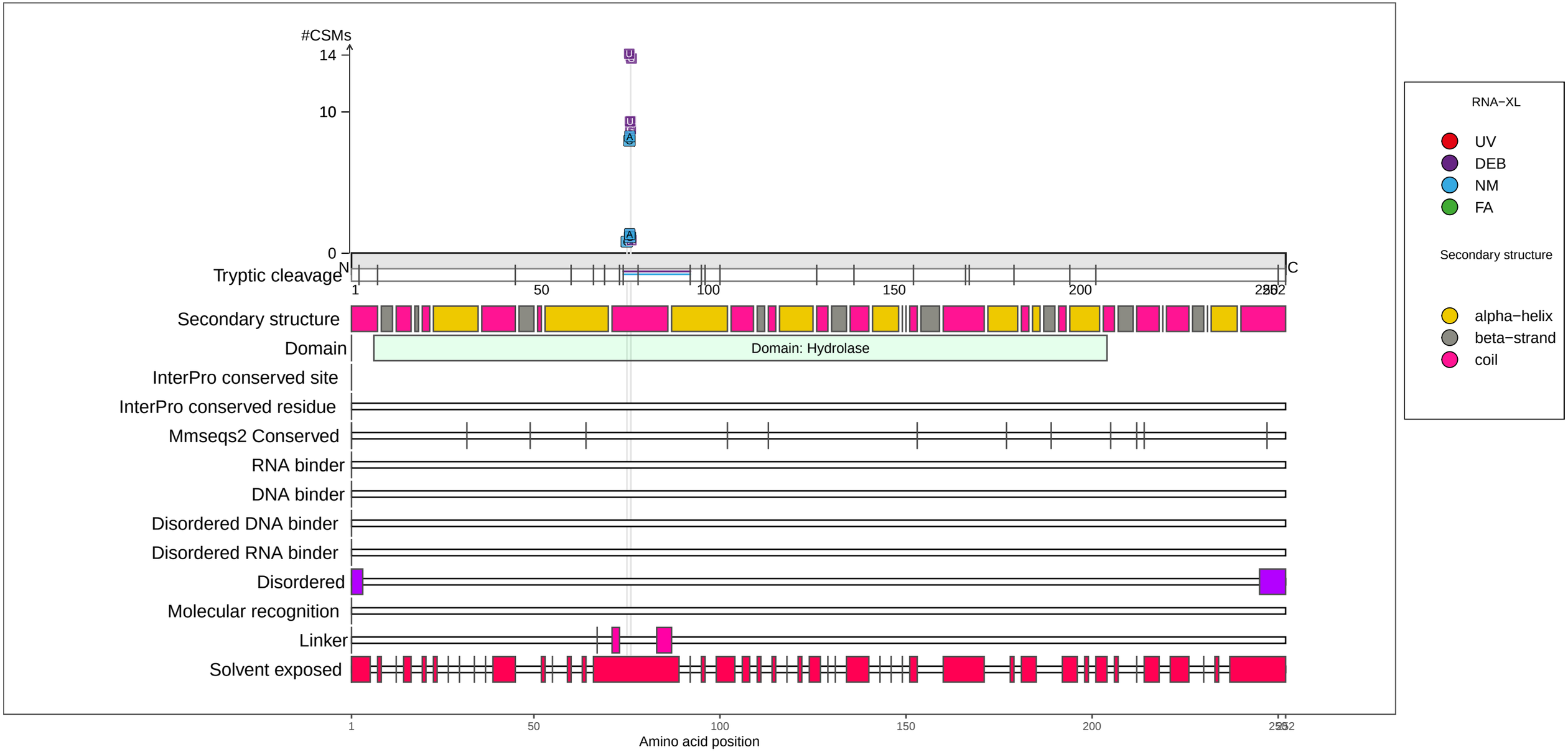
− RNA functions: not annotated



P32662
GPH_ECOLI Phosphoglycolate phosphatase

− Abundance:
tryptic [log10 Intensity]: 7.94 (Q 55)
PAXdb K12 strain [ppm]: 2.05 (Q 62)
PAXdb E.coli [ppm]: 1.97 (Q 71)

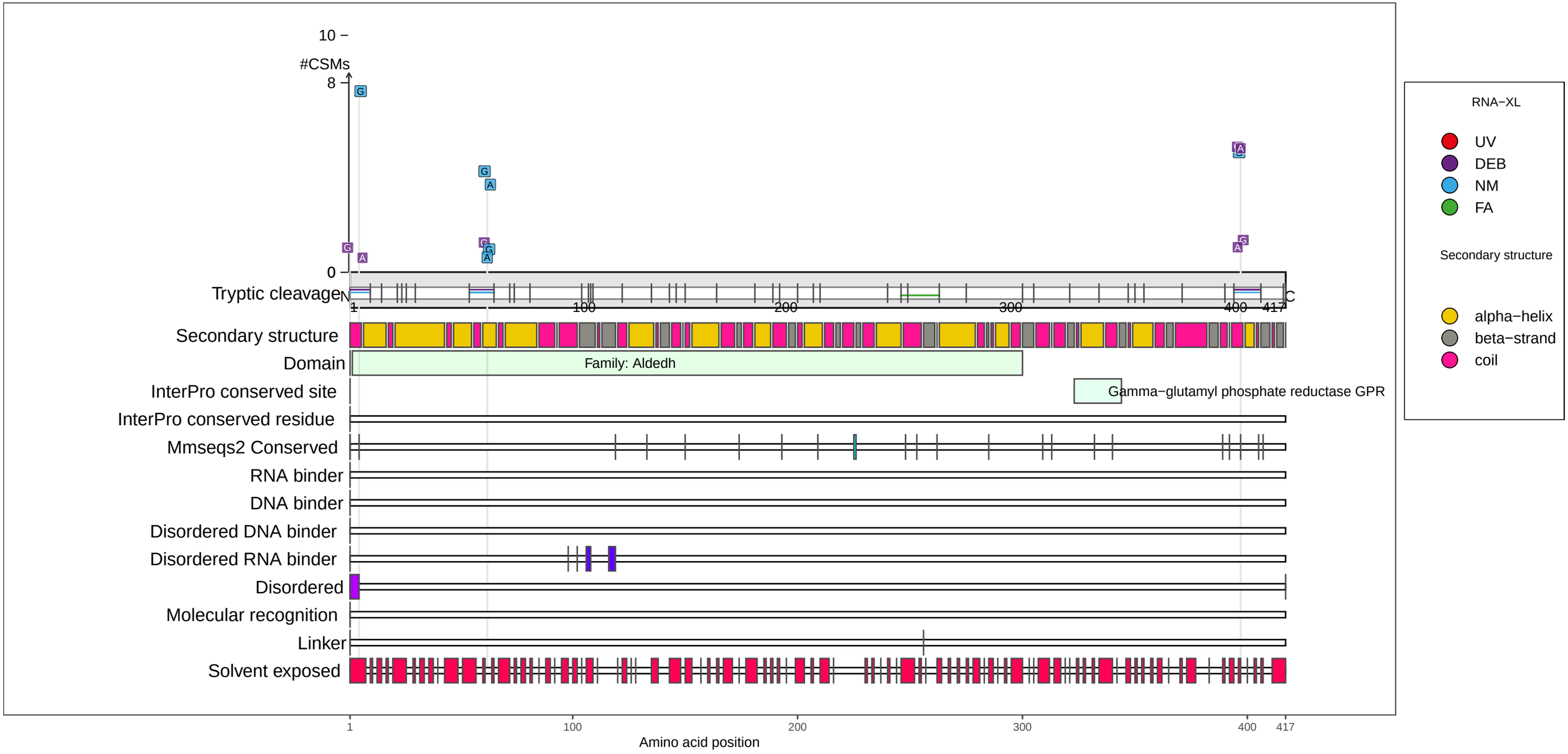
− RNA functions: not annotated



P07004
PROA_ECOLI Gamma−glutamyl phosphate reductase

− Abundance:
tryptic [log10 Intensity]: 8.59 (Q 78)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 2.58 (Q 87)

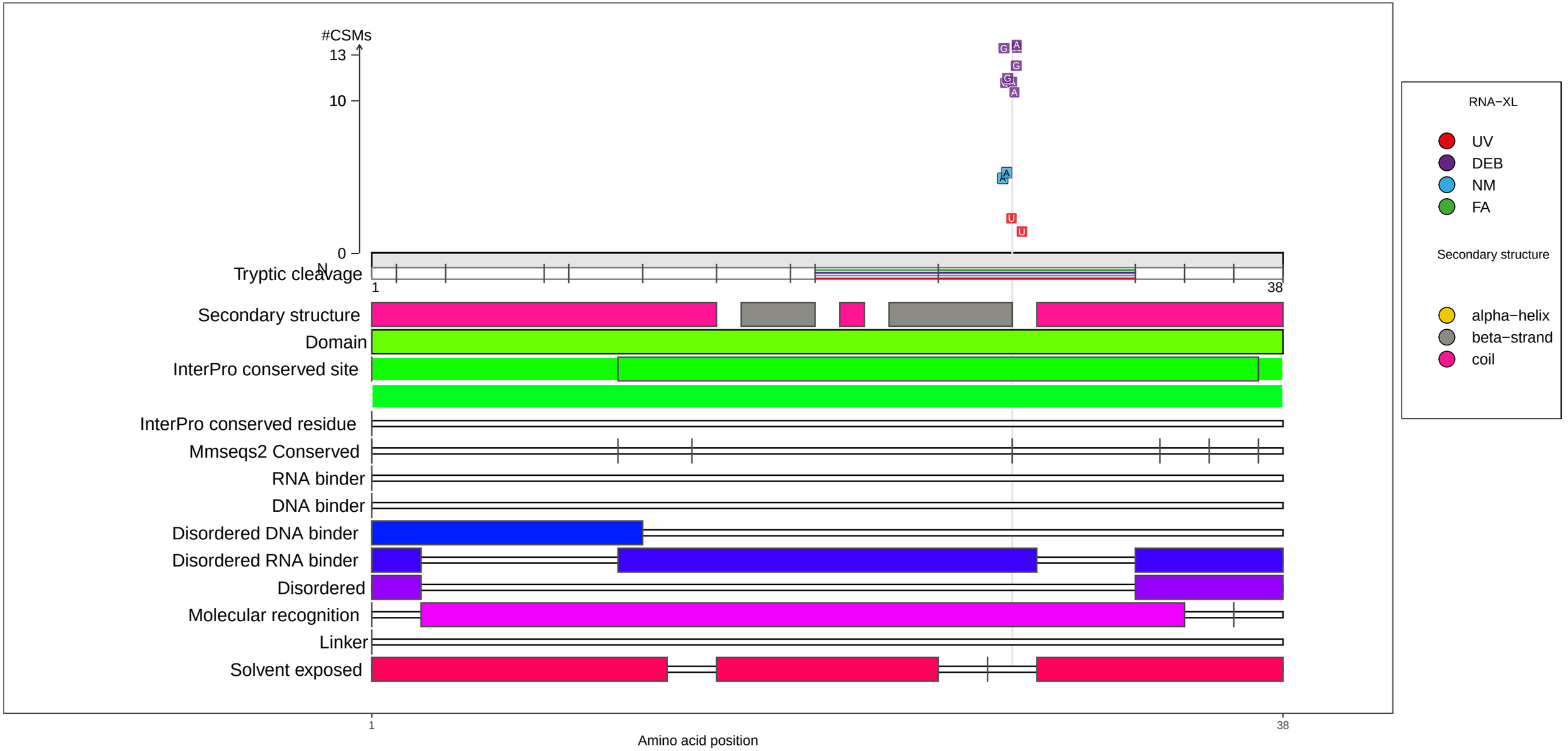
− RNA functions: not annotated



P0A7Q6
RL36_ECOLI 50S ribosomal protein L36

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.63 (Q 89)

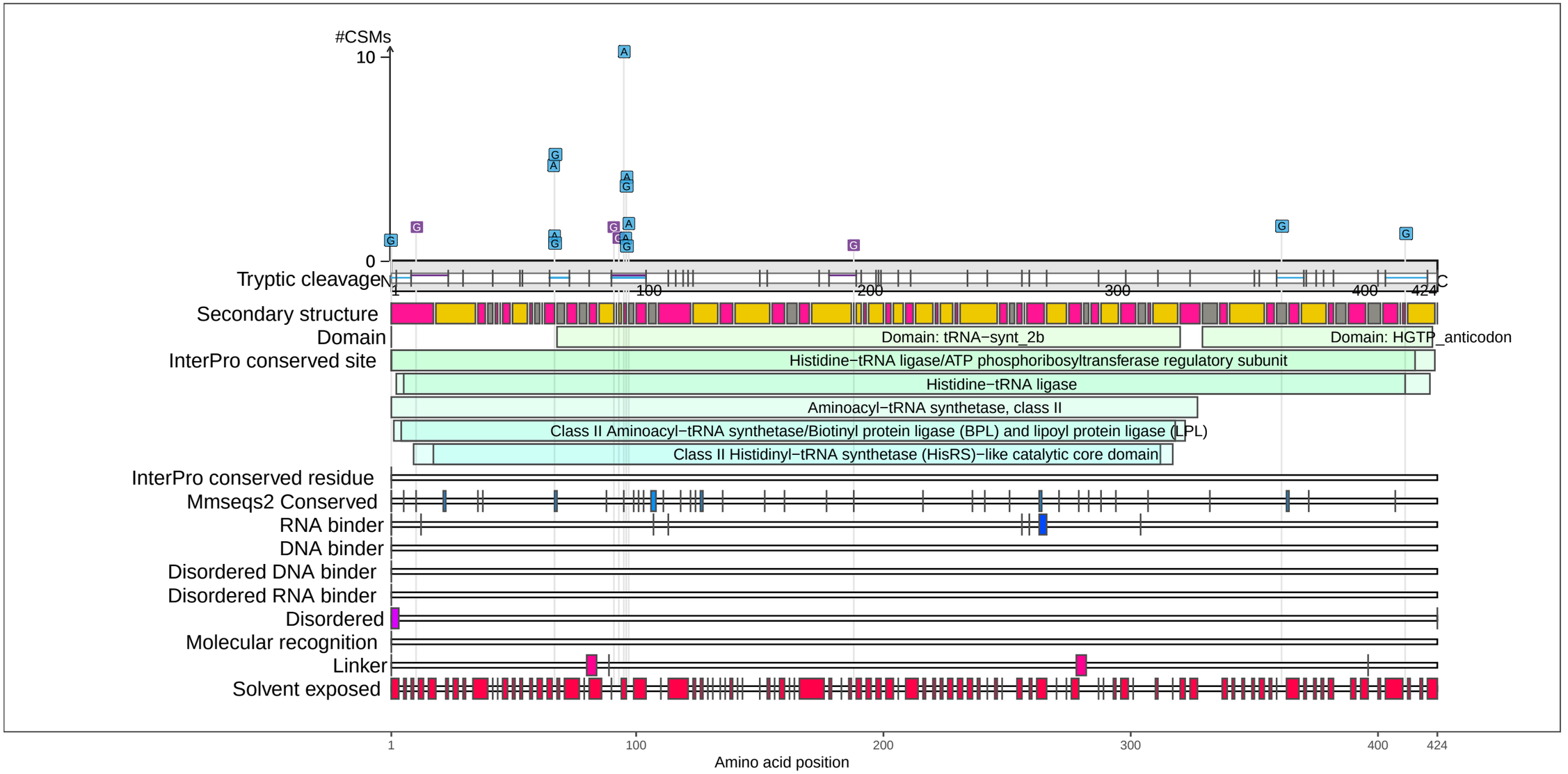
− RNA functions: not annotated



P60906
SYH_ECOLI Histidine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.35 (Q 95)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 2.7 (Q 90)

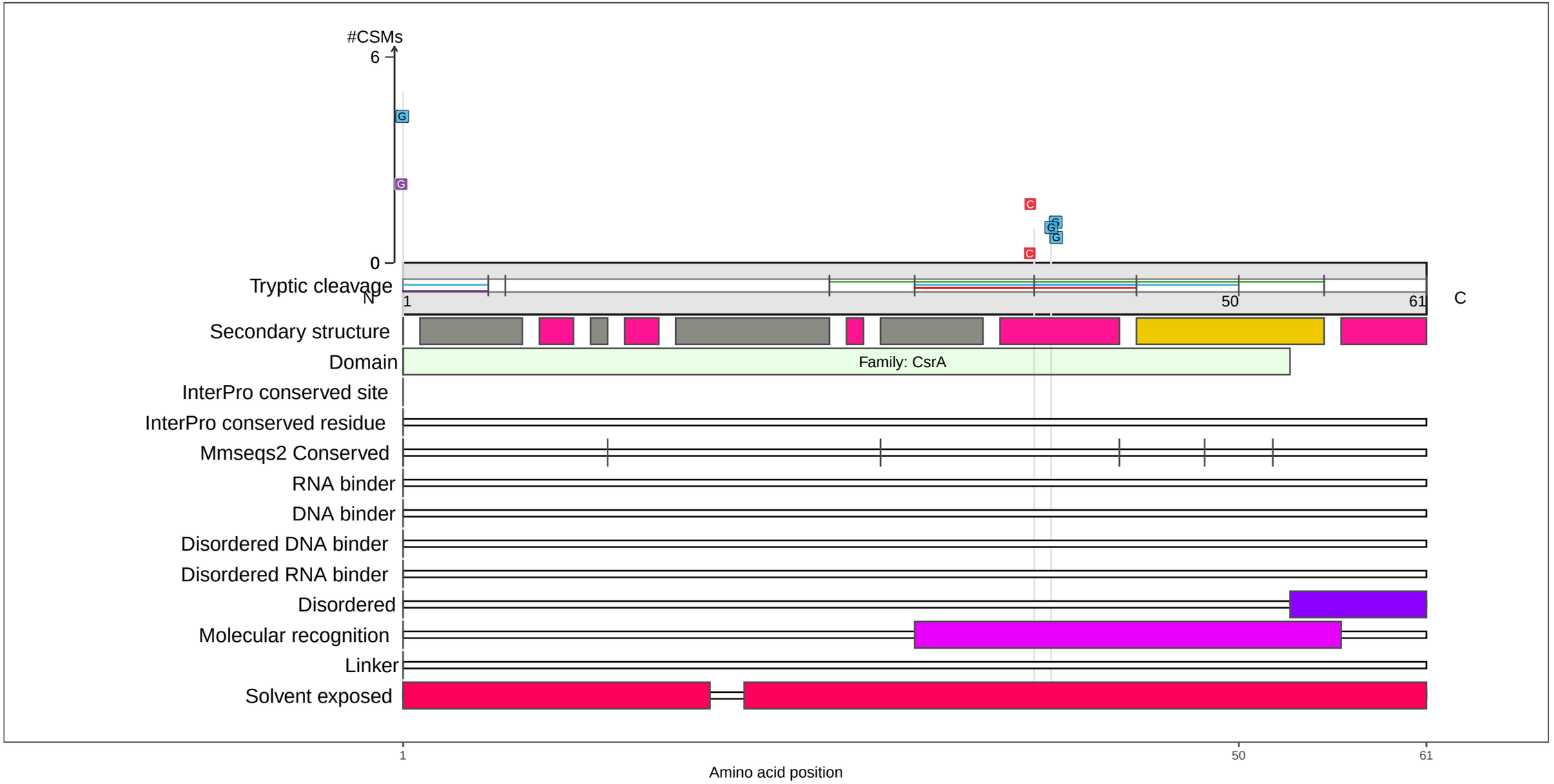
− RNA functions:
aminoacyl−tRNA ligase activity; histidine−tRNA ligase activity
histidyl−tRNA aminoacylation; Histidyl−tRNA synthetase; ncRNA metabolic process; RNA metabolic process
tRNA aminoacylation; tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetase class II core domain (G, H, P, S and T)



P69913
CSRA_ECOLI Carbon storage regulator

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 3.49 (Q 97)
PAXdb E.coli [ppm]: 3.33 (Q 98)

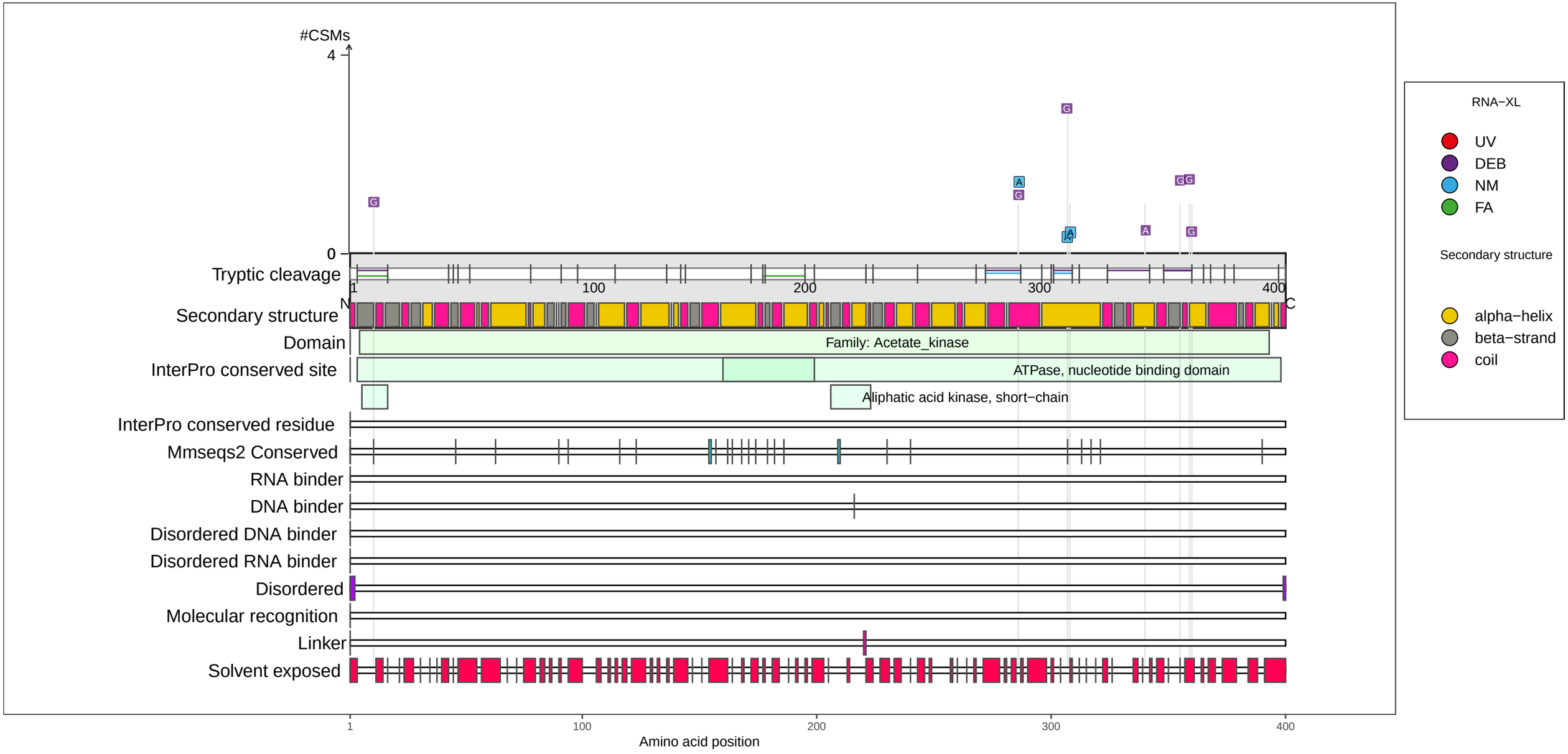
− RNA functions:
mRNA 5−UTR binding; mRNA binding; mRNA catabolic process; mRNA metabolic process
mRNA stabilization; RNA binding; RNA catabolic process; RNA metabolic process
RNA stabilization



P0A6A3
ACKA_ECOLI Acetate kinase

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 3.24 (Q 94)
PAXdb E.coli [ppm]: 2.99 (Q 94)

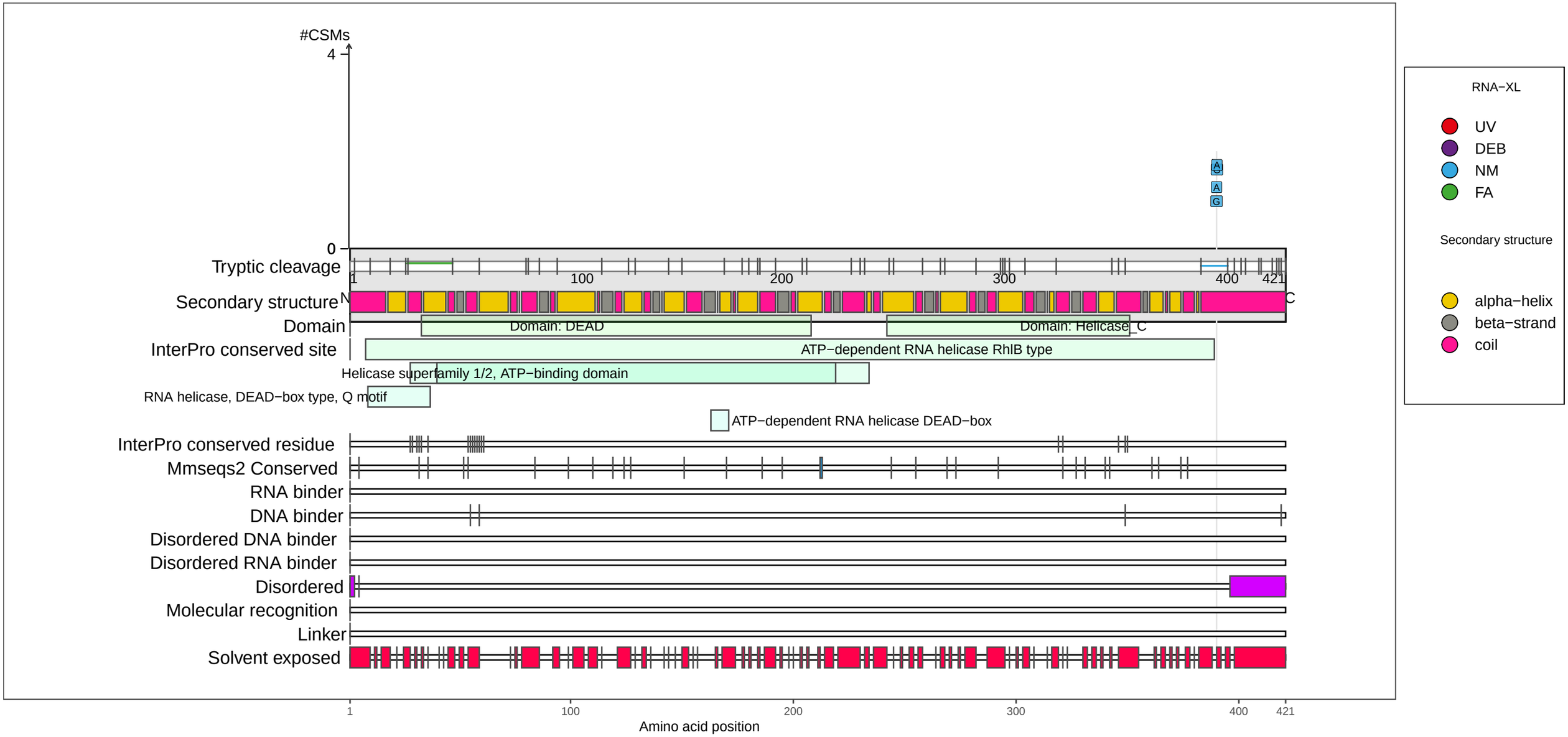
− RNA functions: not annotated



P0A8J8
RHLB_ECOLI ATP−dependent RNA helicase RhlB

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 2.41 (Q 83)

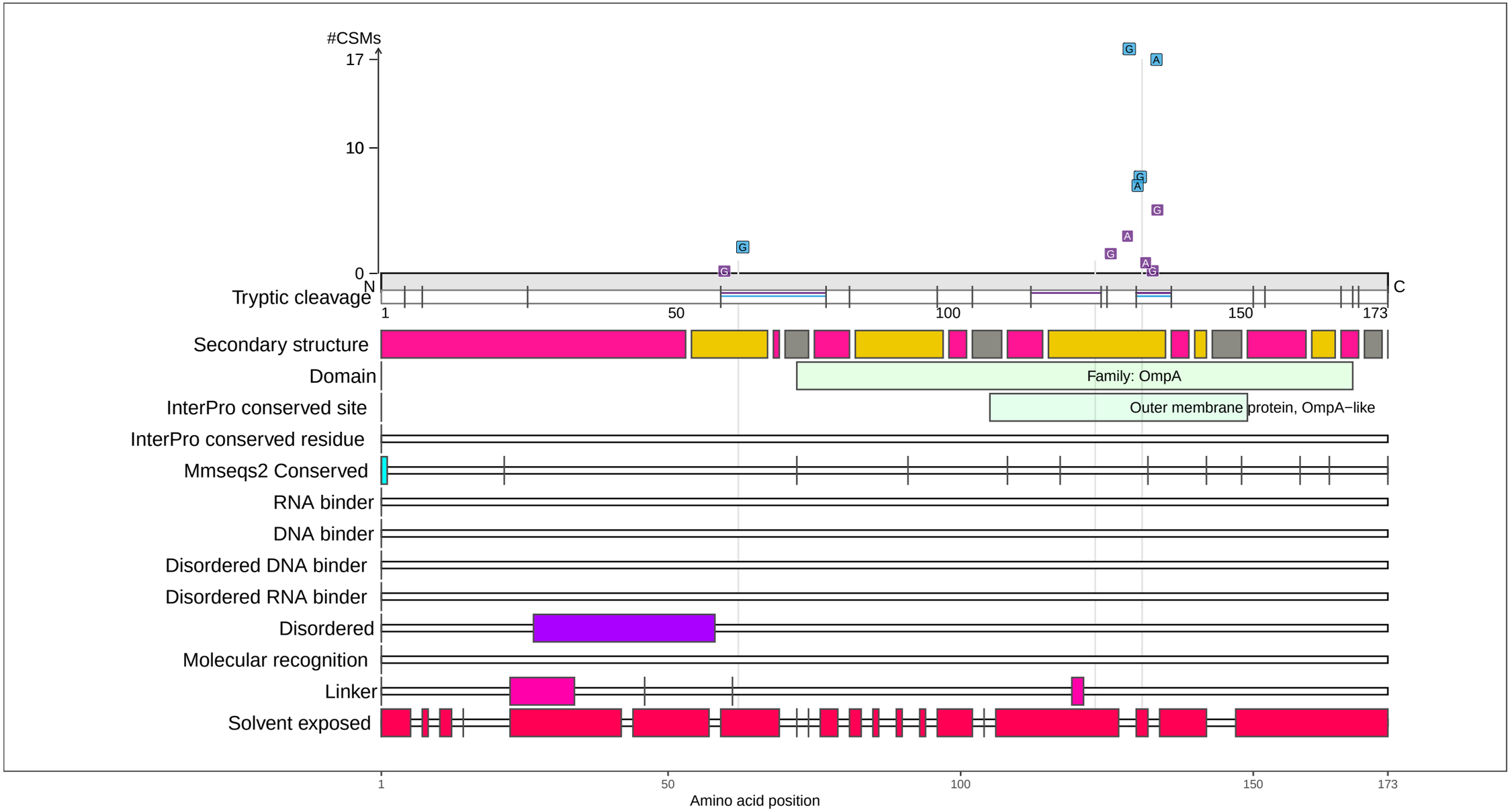
− RNA functions:
RNA binding; RNA catabolic process; RNA helicase activity; RNA metabolic process

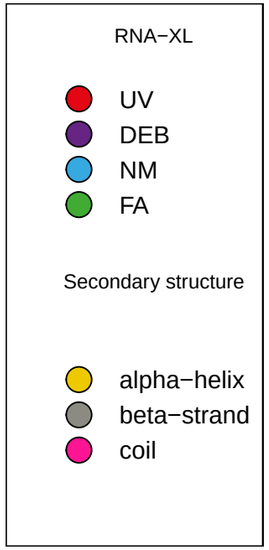


P0A912
PAL_ECOLI Peptidoglycan−associated lipoprotein

− Abundance:
tryptic [log10 Intensity]: 9.39 (Q 95)
PAXdb K12 strain [ppm]: 1.56 (Q 42)
PAXdb E.coli [ppm]: 2.56 (Q 87)

− RNA functions: not annotated

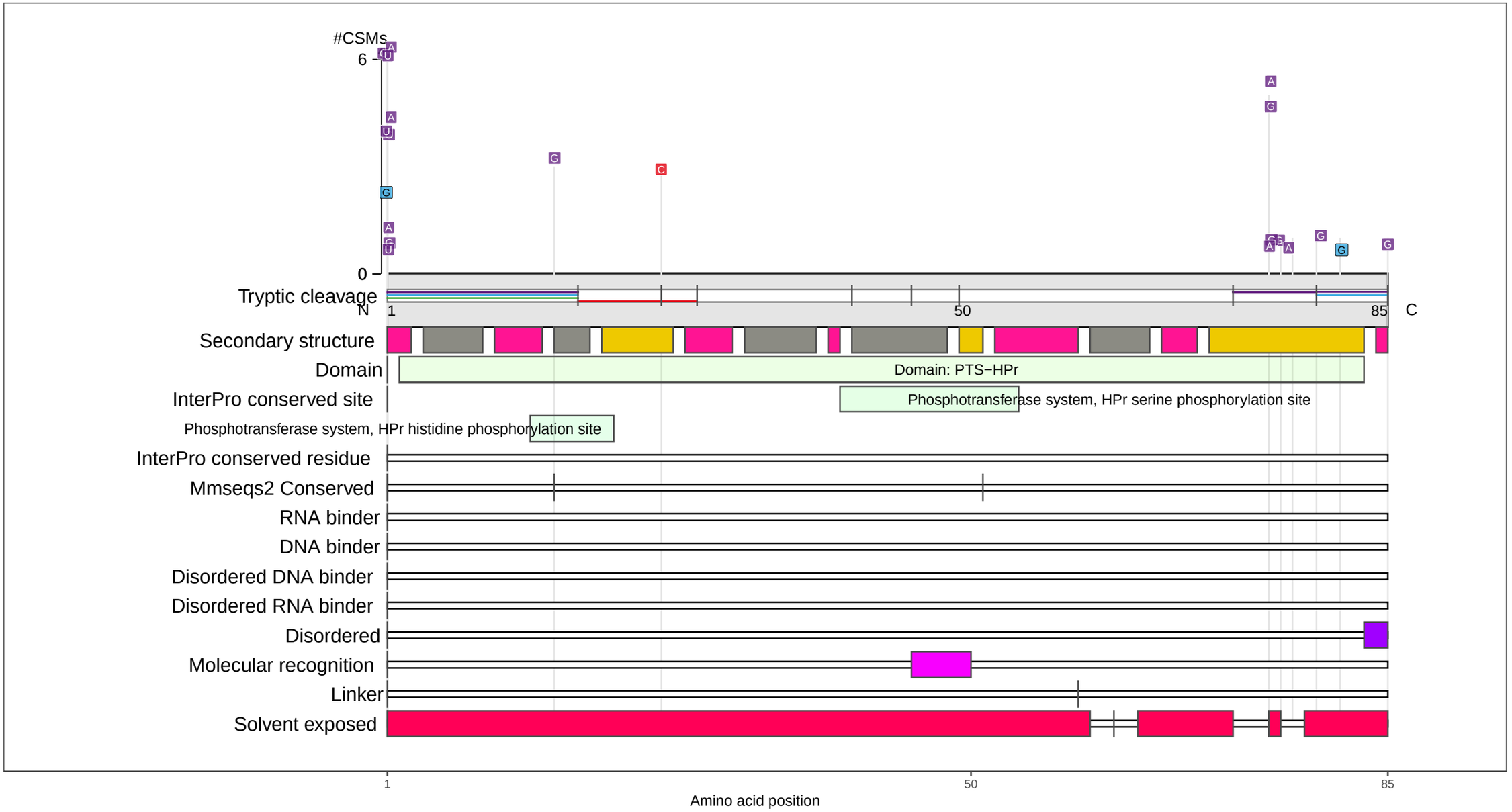




P0AA04
PTHP_ECOLI Phosphocarrier protein HPr

− Abundance:
tryptic [log10 Intensity]: 10.03 (Q 99)
PAXdb K12 strain [ppm]: 3.89 (Q 100)
PAXdb E.coli [ppm]: 3.19 (Q 96)

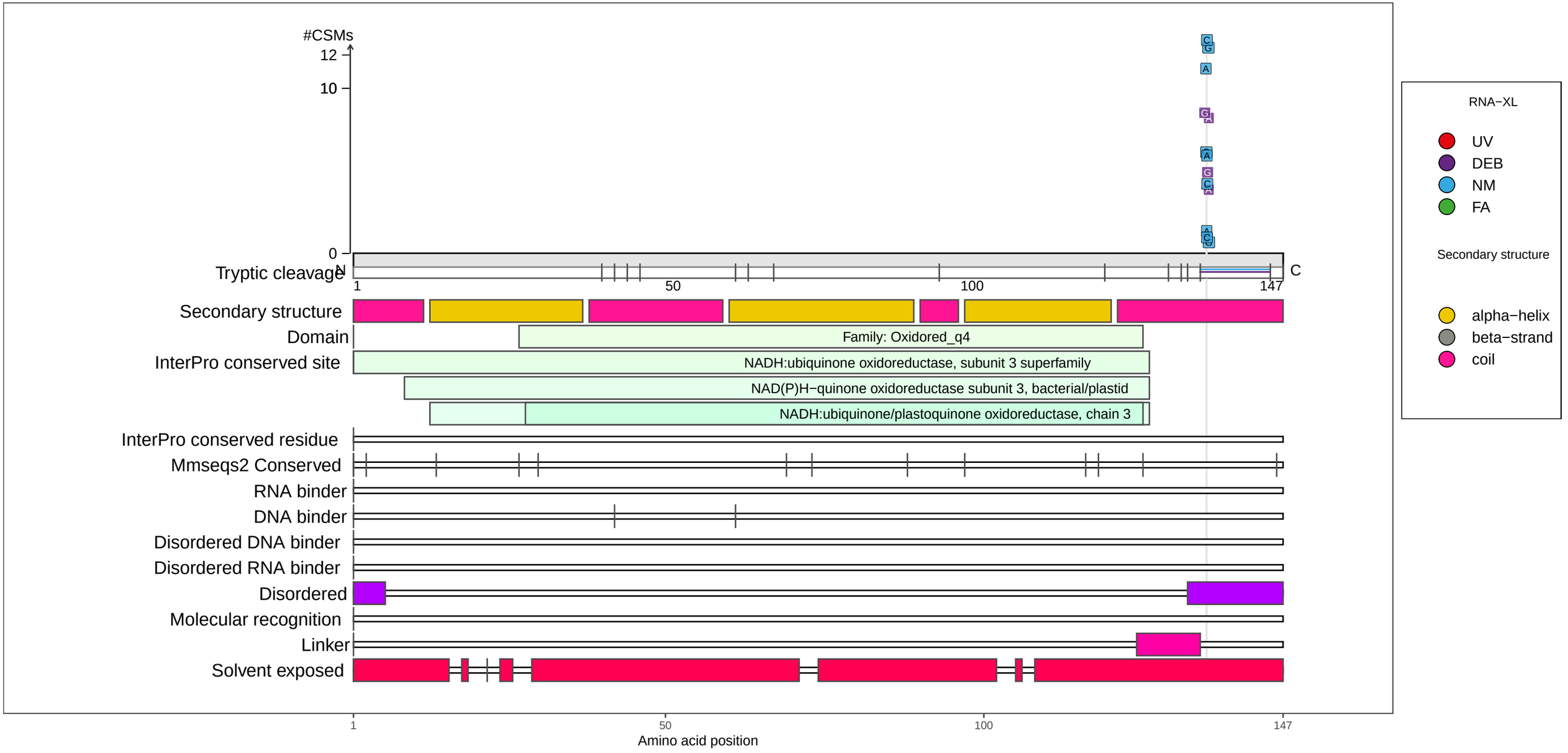
− RNA functions: not annotated



P0AFC3
NUOA_ECOLI NADH−quinone oxidoreductase subunit A

− Abundance:
tryptic [log10 Intensity]: 9.53 (Q 97)
PAXdb K12 strain [ppm]: 2.28 (Q 69)
PAXdb E.coli [ppm]: 2.56 (Q 87)

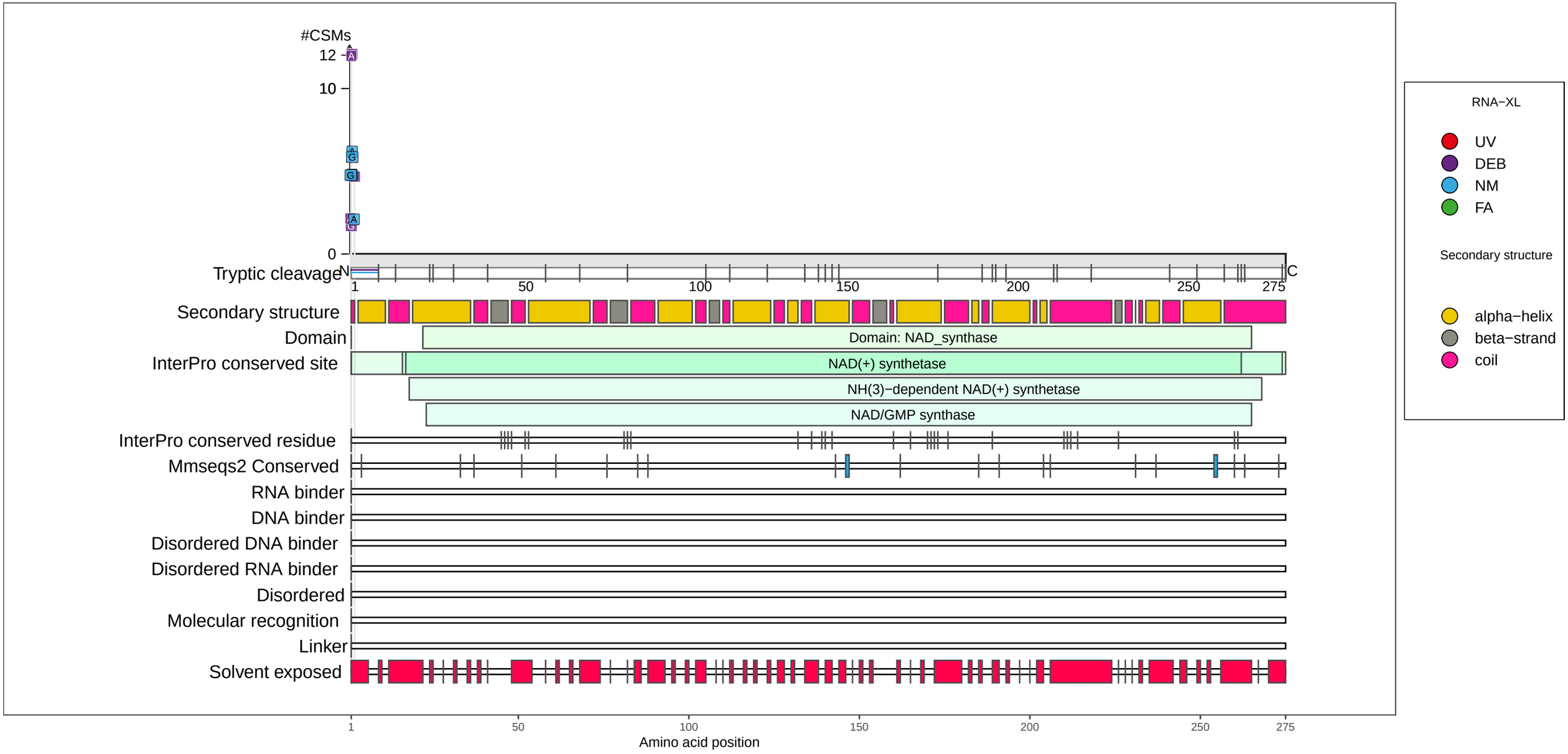
− RNA functions: not annotated



P18843
NADE_ECOLI NH(3)−dependent NAD(+) synthetase

− Abundance:
tryptic [log10 Intensity]: 8.56 (Q 77)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 2.68 (Q 89)

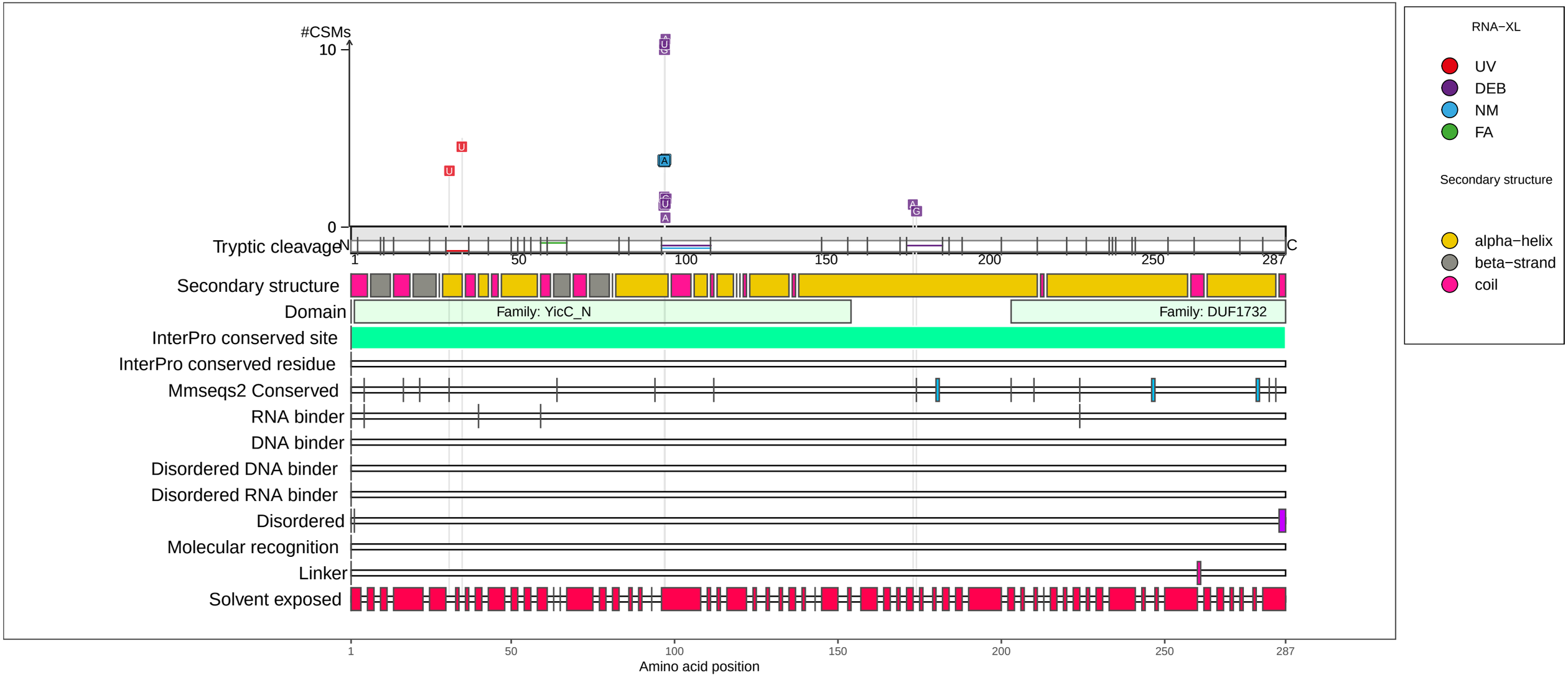
− RNA functions: not annotated



P23839
YICC_ECOLI UPF0701 protein YicC

− Abundance:
tryptic [log10 Intensity]: 8.35 (Q 71)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 2.27 (Q 79)

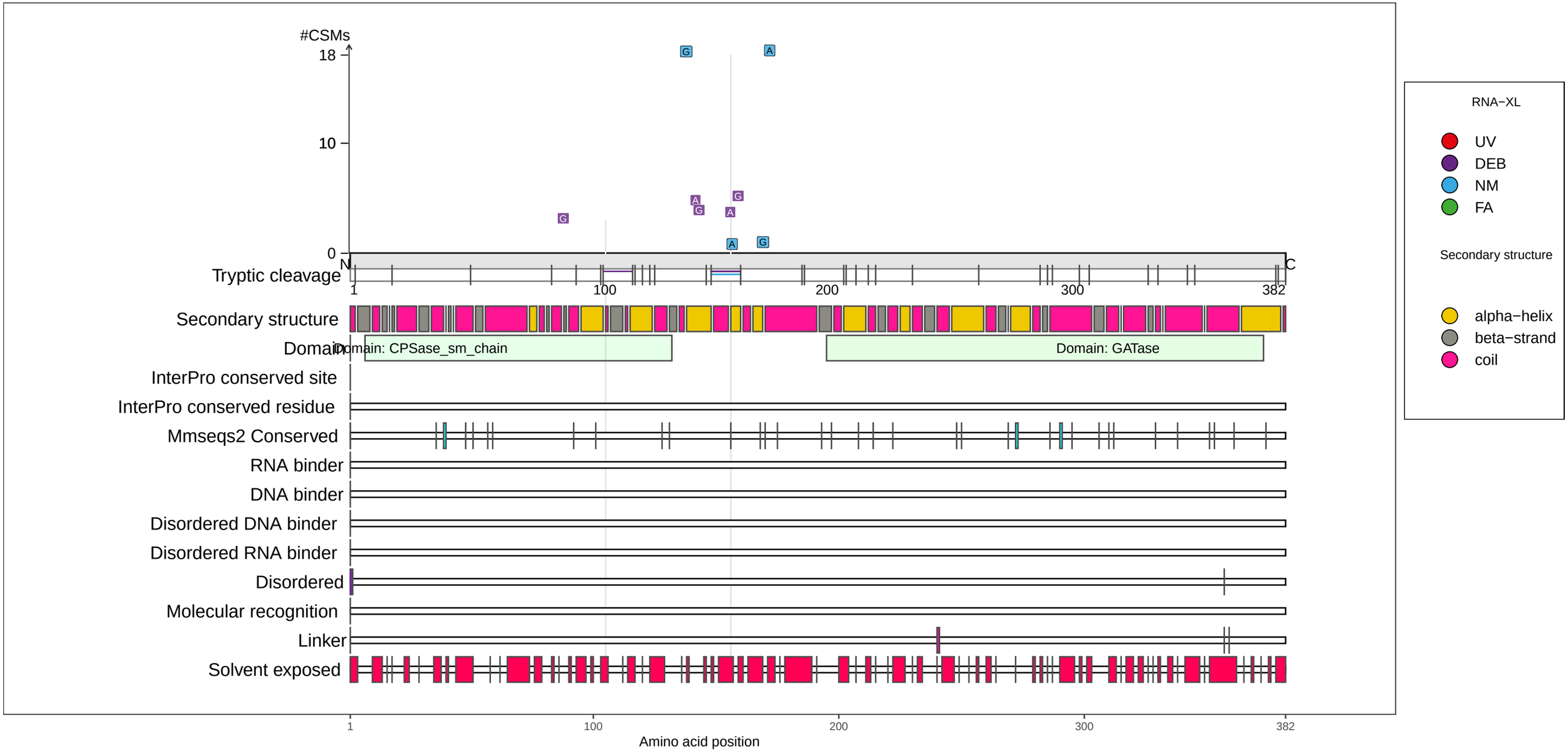
− RNA functions:
ncRNA catabolic process; ncRNA metabolic process; ncRNA processing; RNA binding
RNA catabolic process; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, exonucleolytic; RNA processing; rRNA catabolic process
rRNA metabolic process; rRNA processing; tRNA binding; tRNA metabolic process
tRNA nucleotidyltransferase activity; tRNA processing



P0A6F1
CARA_ECOLI Carbamoyl−phosphate synthase small chain

− Abundance:
tryptic [log10 Intensity]: 9.06 (Q 90)
PAXdb K12 strain [ppm]: 3.05 (Q 91)
PAXdb E.coli [ppm]: 3.1 (Q 96)

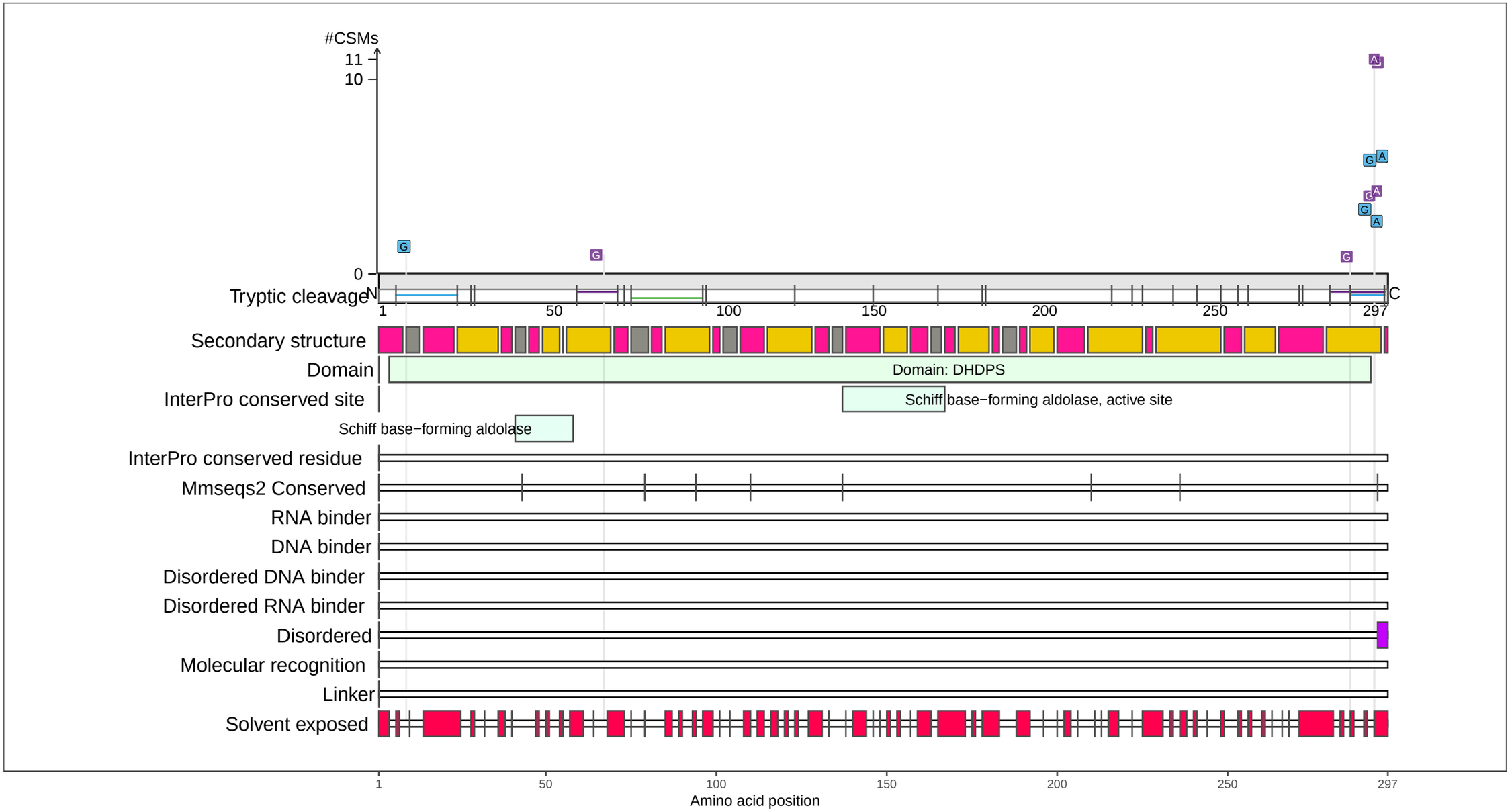
− RNA functions: not annotated



P0A6L4
NANA_ECOLI N−acetylneuraminate lyase

− Abundance:
tryptic [log10 Intensity]: 9.31 (Q 94)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.58 (Q 62)

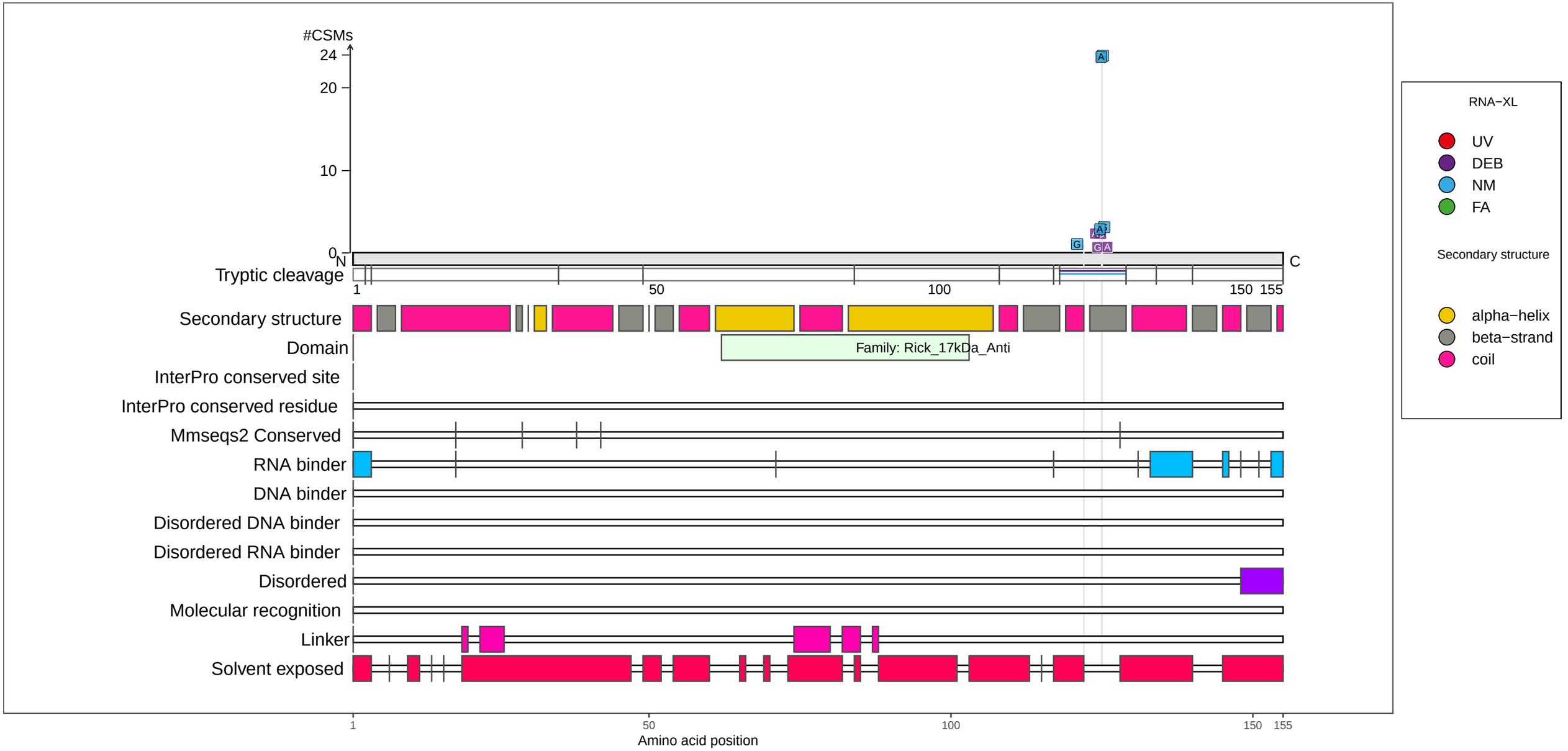
− RNA functions: not annotated



P0A905
SLYB_ECOLI Outer membrane lipoprotein SlyB

− Abundance:
tryptic [log10 Intensity]: 9.87 (Q 99)
PAXdb K12 strain [ppm]: 2.4 (Q 74)
PAXdb E.coli [ppm]: 3.01 (Q 95)

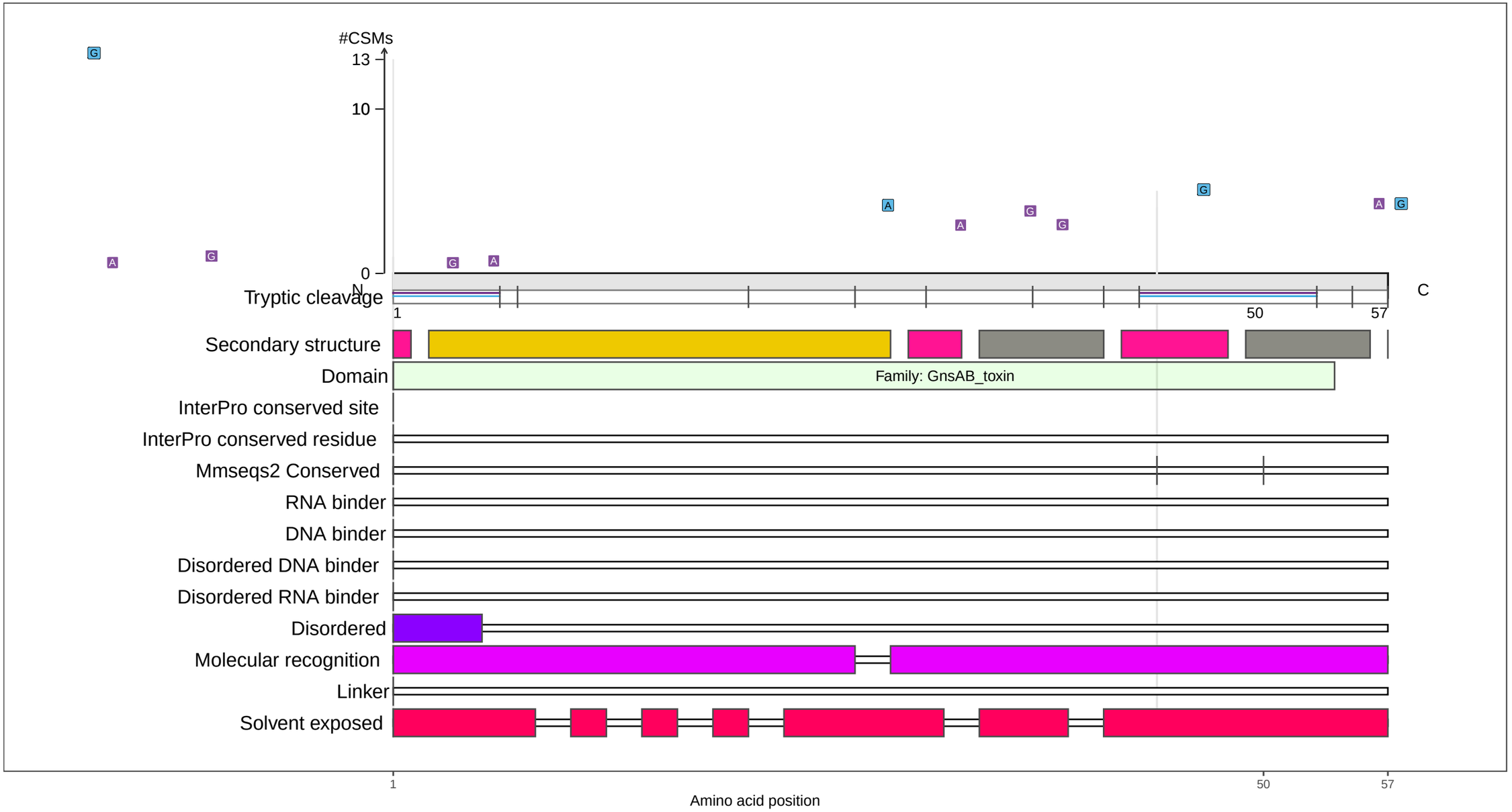
− RNA functions: not annotated

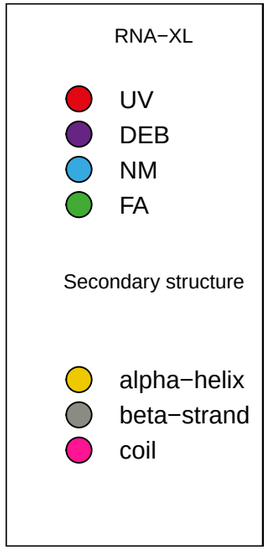


P0AC92
GNSA_ECOLI Protein GnsA

− Abundance:
tryptic [log10 Intensity]: 8.43 (Q 73)
PAXdb K12 strain [ppm]: 3.5 (Q 98)
PAXdb E.coli [ppm]: 2.08 (Q 74)

− RNA functions: not annotated

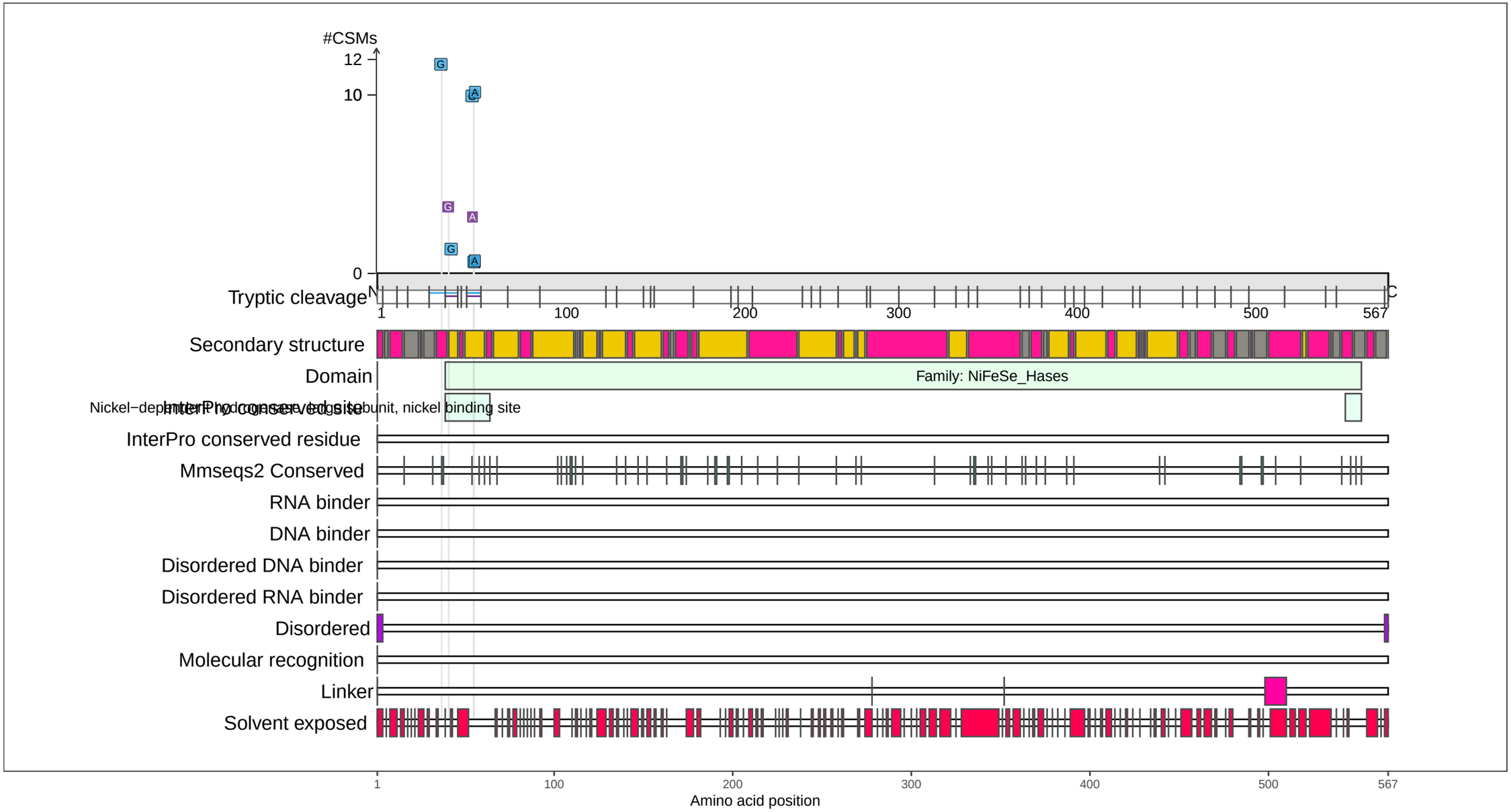


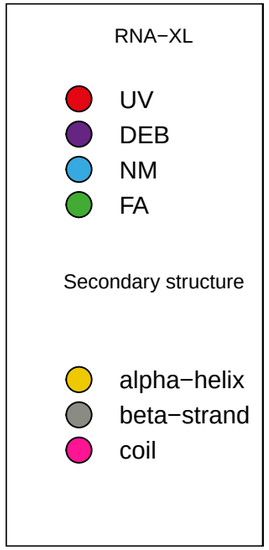


P0ACE0
MBHM_ECOLI Hydrogenase−2 large chain

− Abundance:
tryptic [log10 Intensity]: 8.59 (Q 78)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 1.74 (Q 65)

− RNA functions: not annotated

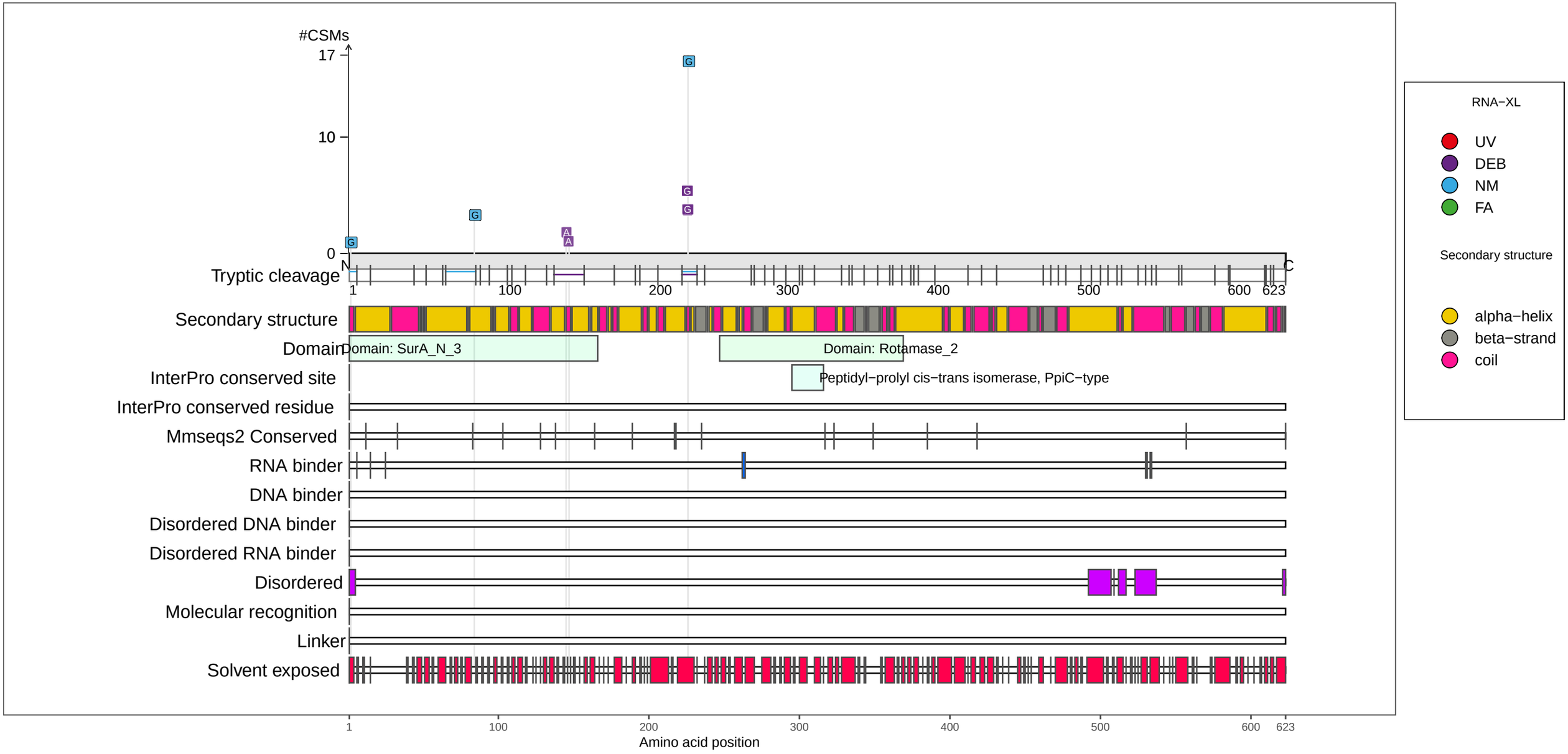




P0ADY1
PPID_ECOLI Periplasmic chaperone PpiD

− Abundance:
tryptic [log10 Intensity]: 8.66 (Q 80)
PAXdb K12 strain [ppm]: 2.53 (Q 78)
PAXdb E.coli [ppm]: 2.47 (Q 85)

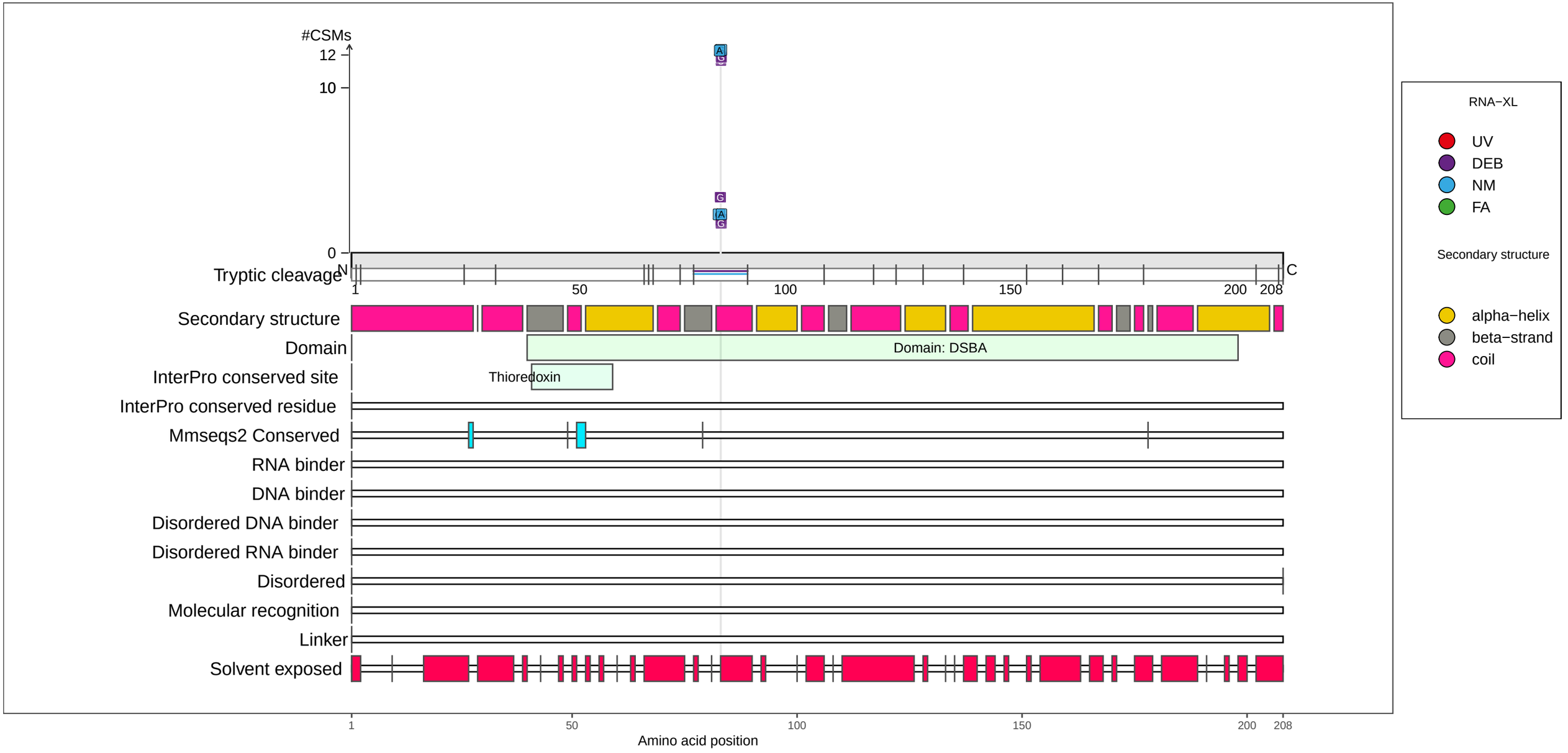
− RNA functions: not annotated



P0AEG4
DSBA_ECOLI Thiol:disulfide interchange protein DsbA

− Abundance:
tryptic [log10 Intensity]: 8.48 (Q 75)
PAXdb K12 strain [ppm]: 2.4 (Q 74)
PAXdb E.coli [ppm]: 2.61 (Q 88)

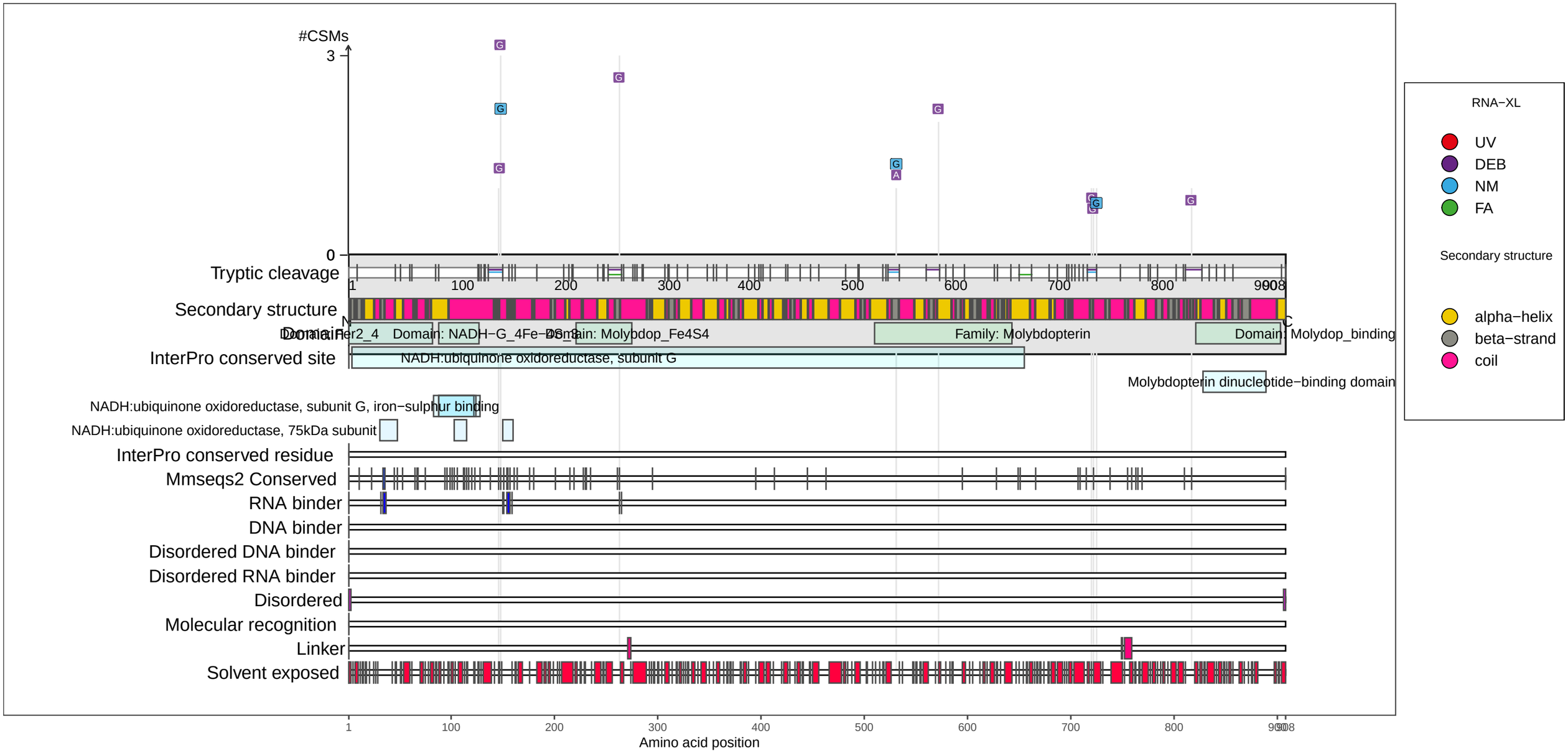
− RNA functions: not annotated



P33602
NUOG_ECOLI NADH−quinone oxidoreductase subunit G

− Abundance:
tryptic [log10 Intensity]: 9.64 (Q 97)
PAXdb K12 strain [ppm]: 2.5 (Q 78)
PAXdb E.coli [ppm]: 2.54 (Q 86)

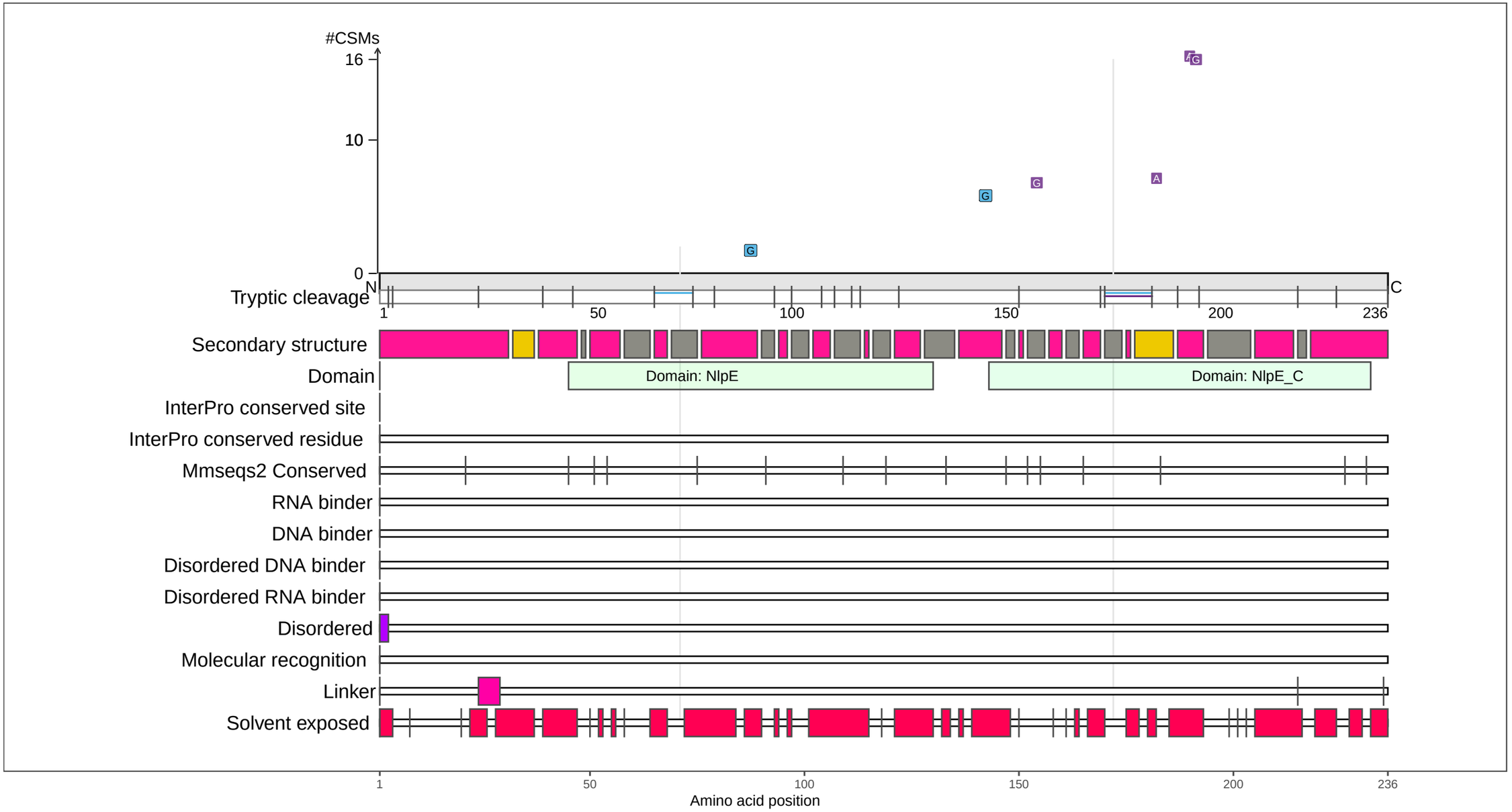
− RNA functions: not annotated

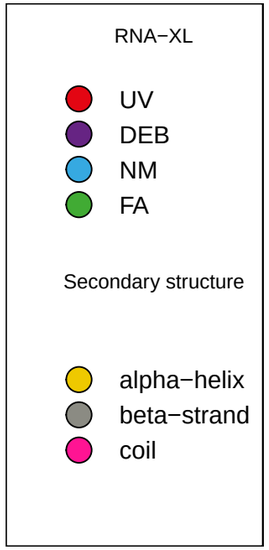


P40710
NLPE_ECOLI Lipoprotein NlpE

− Abundance:
tryptic [log10 Intensity]: 8.38 (Q 72)
PAXdb K12 strain [ppm]: 1.24 (Q 22)
PAXdb E.coli [ppm]: 1.04 (Q 48)

− RNA functions: not annotated

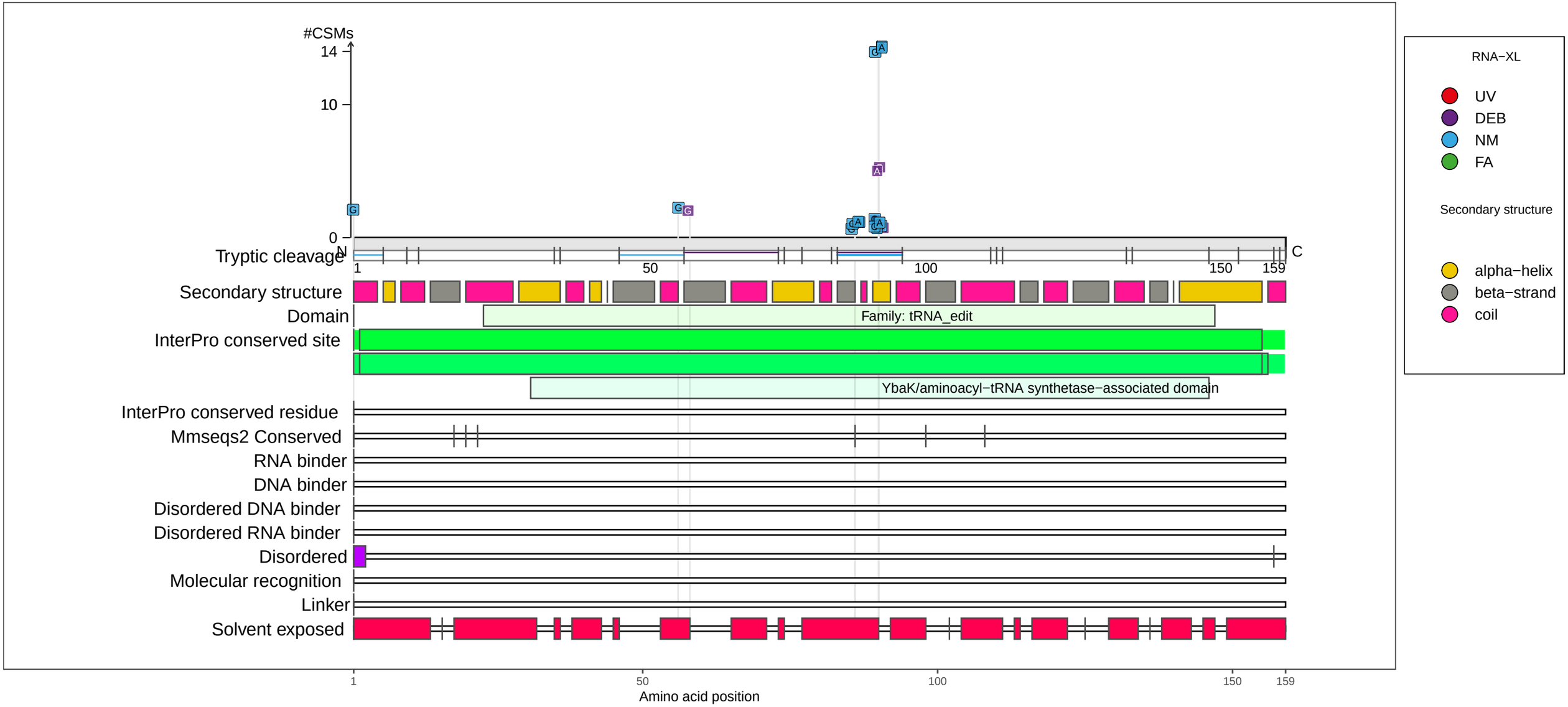




P0AAR3
YBAK_ECOLI Cys−tRNA(Pro)/Cys−tRNA(Cys) deacylase YbaK

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 2.84 (Q 87)
PAXdb E.coli [ppm]: 2.22 (Q 78)

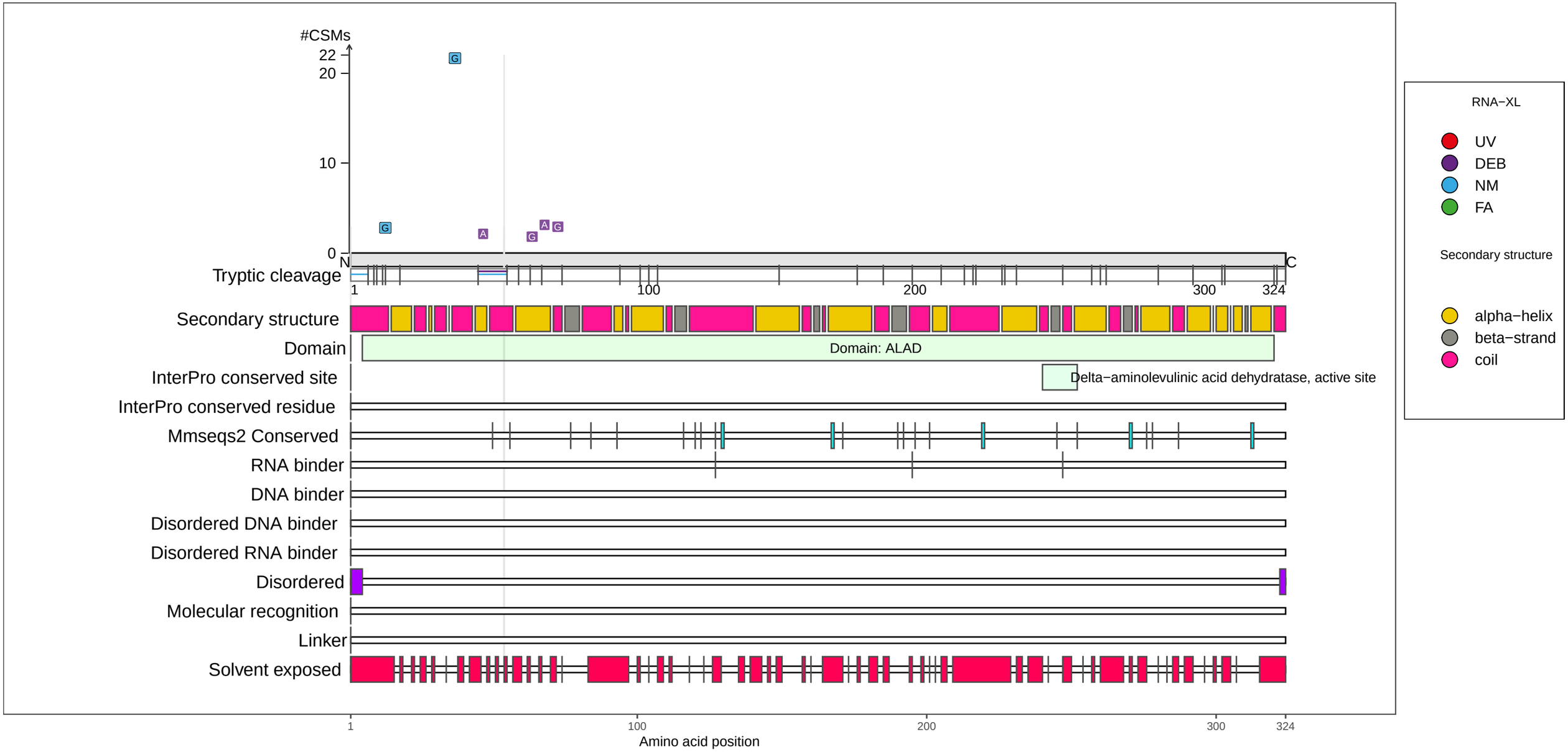
− RNA functions:
aminoacyl−tRNA editing activity; Aminoacyl−tRNA editing domain
aminoacyl−tRNA metabolism involved in translational fidelity; Cys−tRNA(Pro) hydrolase activity
ncRNA metabolic process; RNA metabolic process; tRNA metabolic process



P0ACB2
HEM2_ECOLI Delta−aminolevulinic acid dehydratase

− Abundance:
tryptic [log10 Intensity]: 9.6 (Q 97)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 2.1 (Q 75)

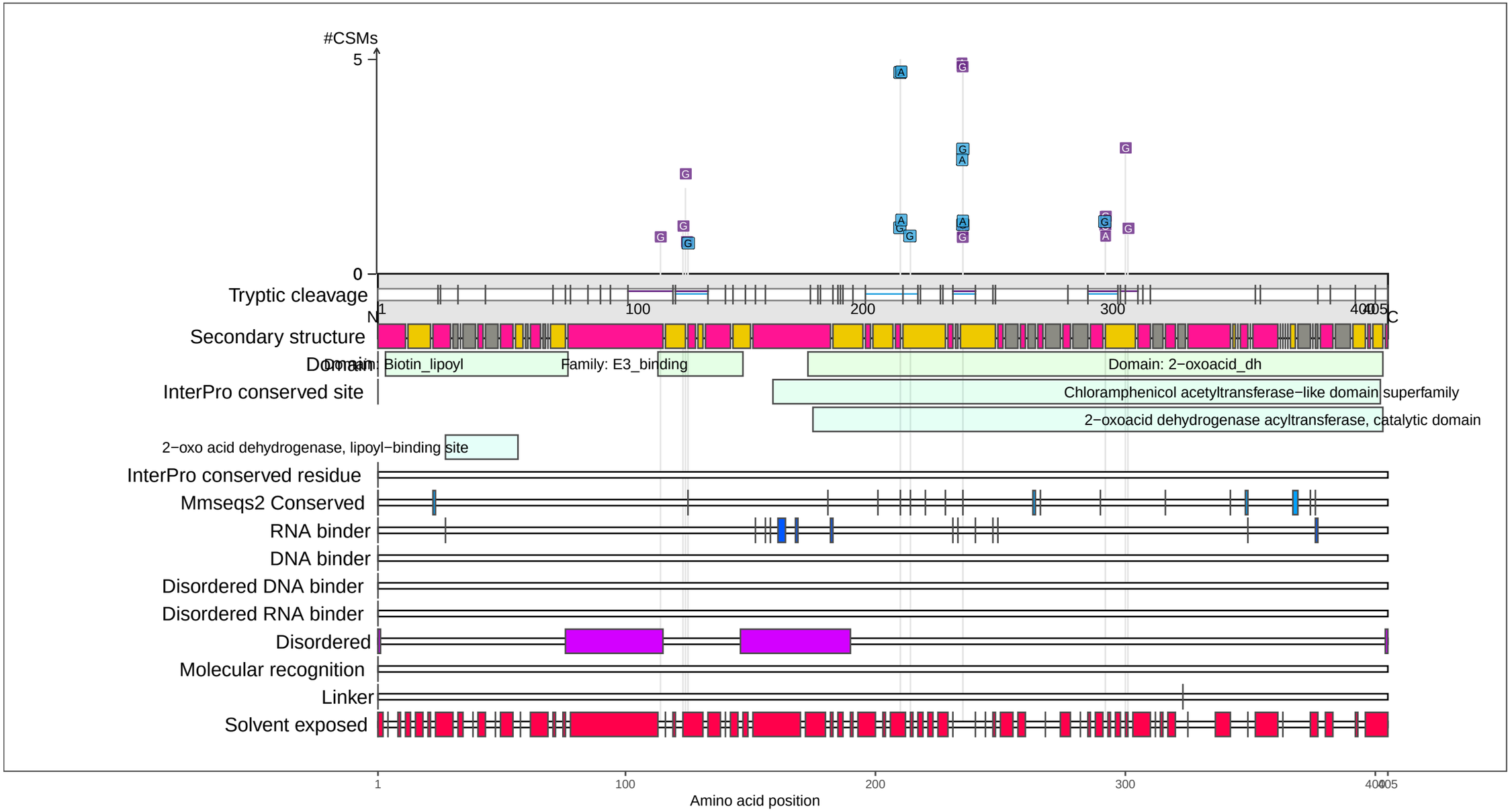
− RNA functions: not annotated

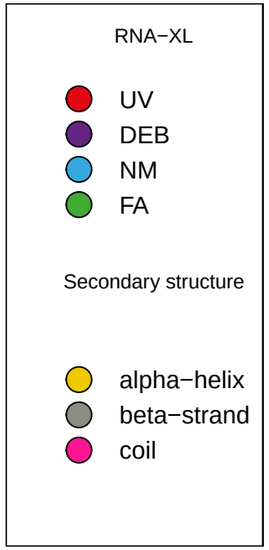


P0AFG6
ODO2_ECOLI Dihydrolipoyllysine−residue succinyltransferase component of 2−oxoglutarate dehydrogenase complex

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.71 (Q 99)
PAXdb E.coli [ppm]: 2.92 (Q 93)

− RNA functions: not annotated

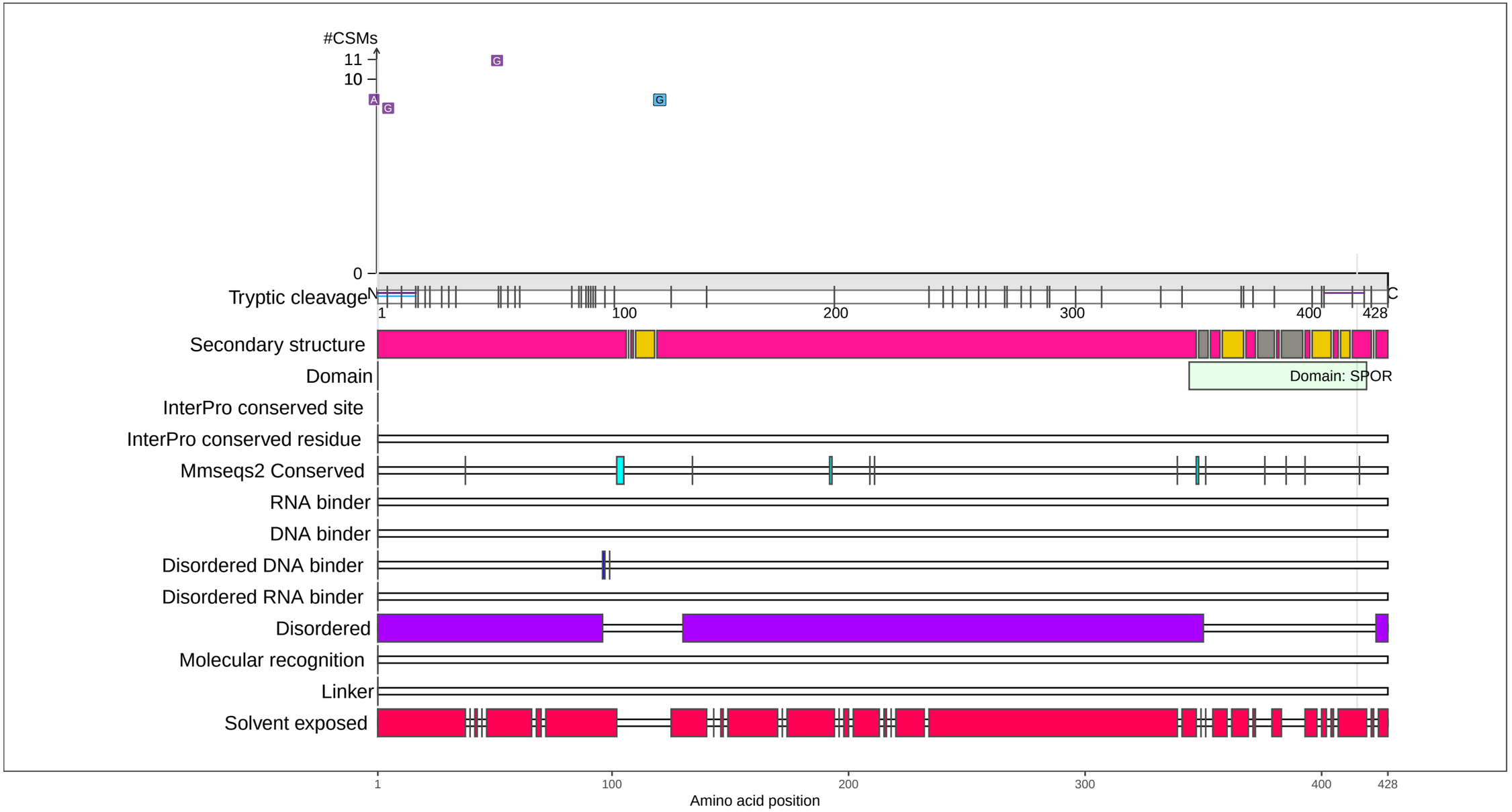


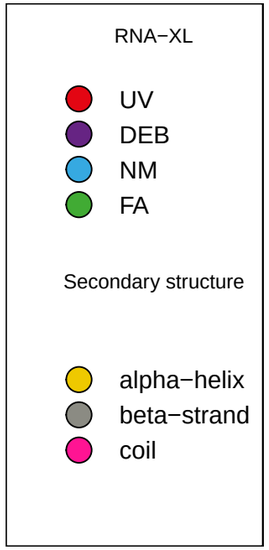


P11557
DAMX_ECOLI Cell division protein DamX

− Abundance:
tryptic [log10 Intensity]: 9.25 (Q 93)
PAXdb K12 strain [ppm]: 1.25 (Q 23)
PAXdb E.coli [ppm]: 2.24 (Q 78)

− RNA functions: not annotated

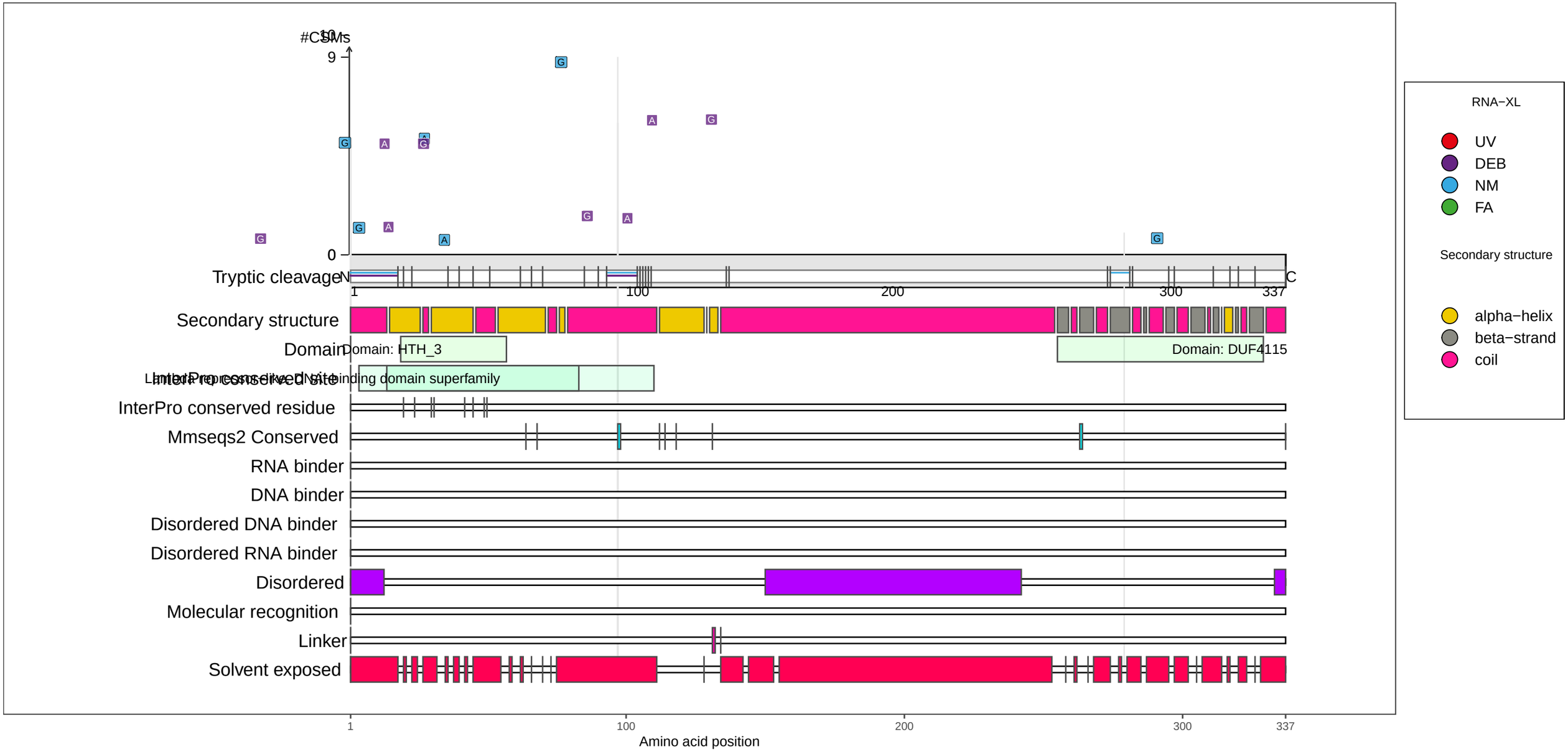




P27434
RODZ_ECOLI Cytoskeleton protein RodZ

− Abundance:
tryptic [log10 Intensity]: 8.31 (Q 70)
PAXdb K12 strain [ppm]: 2.54 (Q 78)
PAXdb E.coli [ppm]: 2.41 (Q 83)

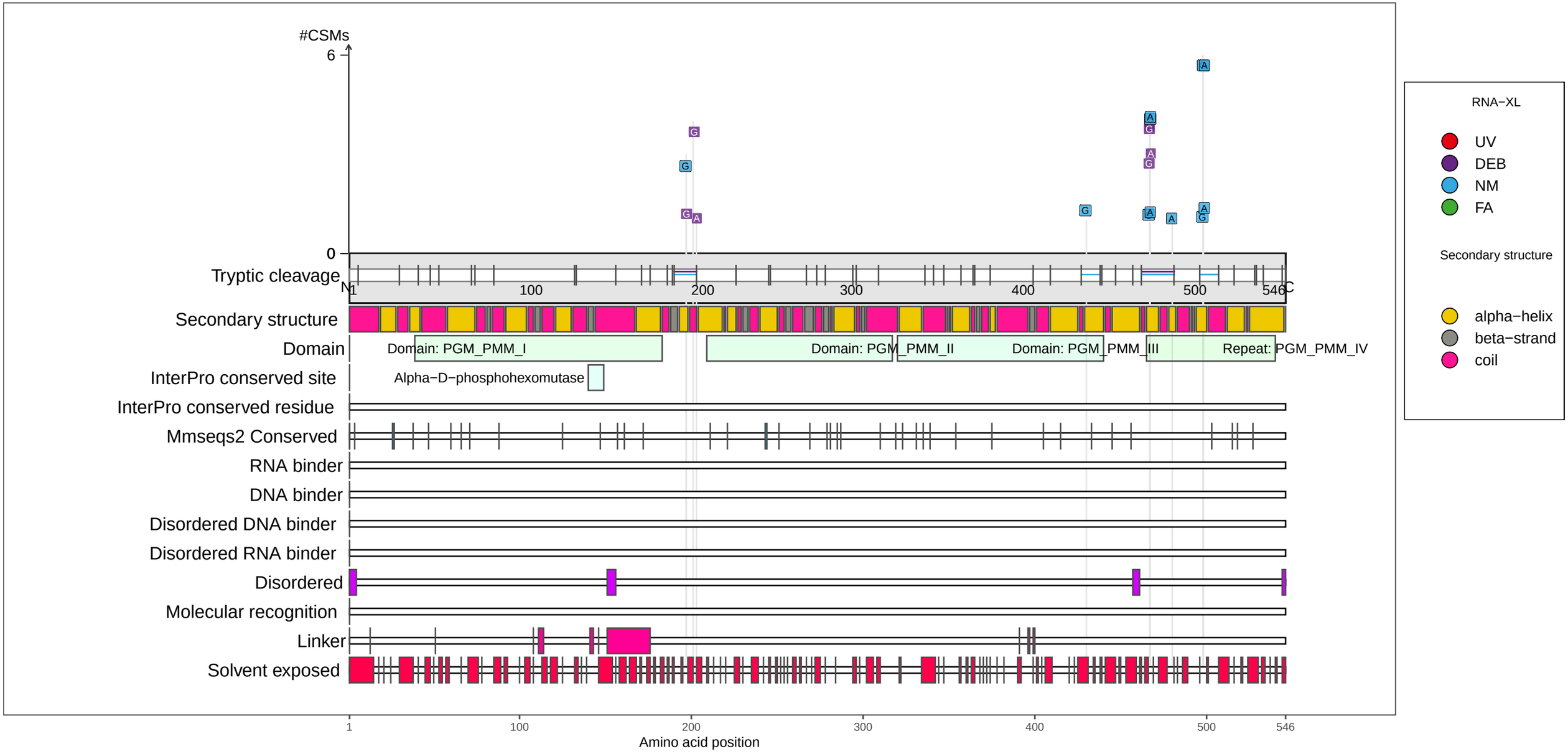
− RNA functions: not annotated



P36938
PGM_ECOLI Phosphoglucomutase

− Abundance:
tryptic [log10 Intensity]: 8.62 (Q 79)
PAXdb K12 strain [ppm]: 2.77 (Q 85)
PAXdb E.coli [ppm]: 2.8 (Q 92)

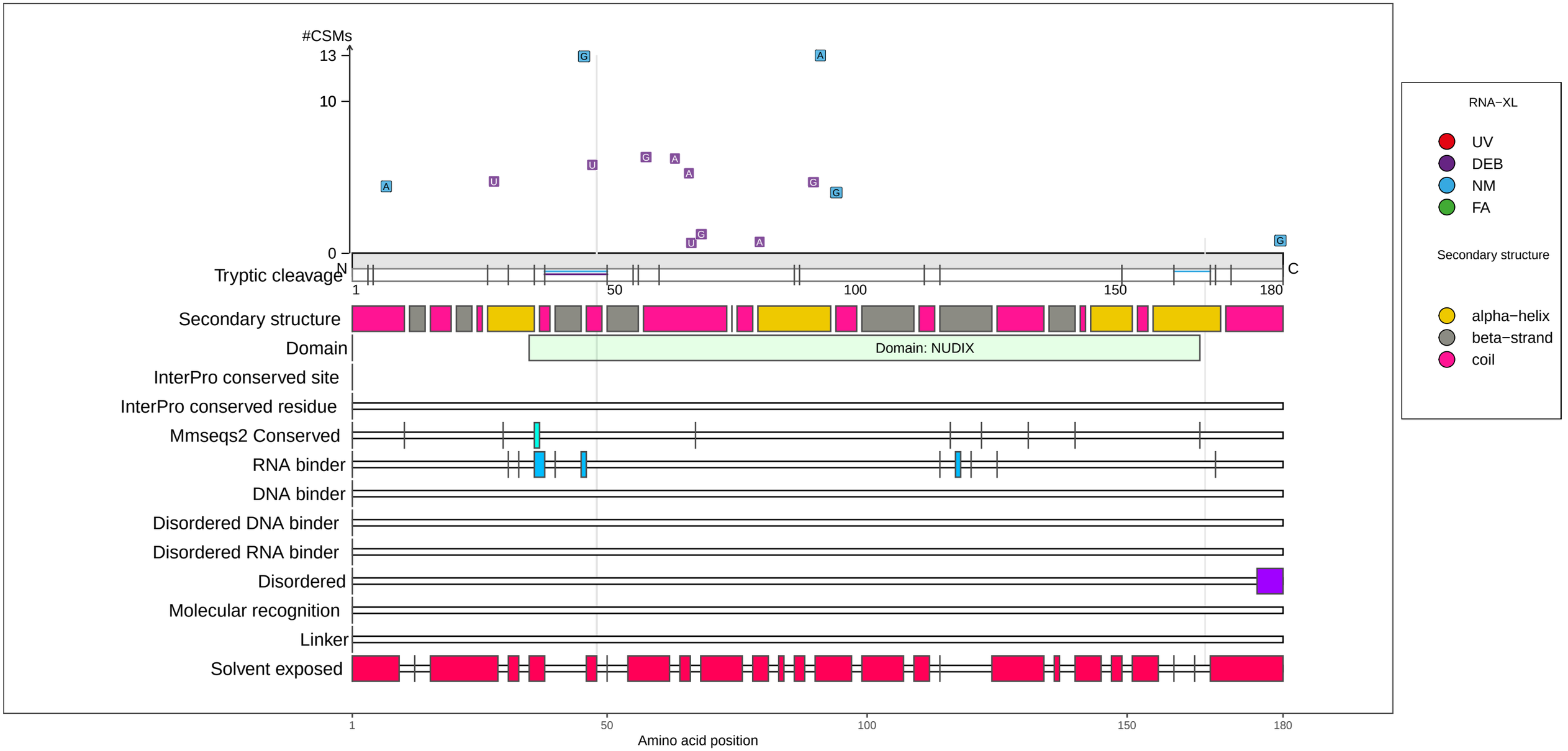
− RNA functions: not annotated



P65556
YFCD_ECOLI Uncharacterized Nudix hydrolase YfcD

− Abundance:
tryptic [log10 Intensity]: 8.39 (Q 72)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.39 (Q 83)

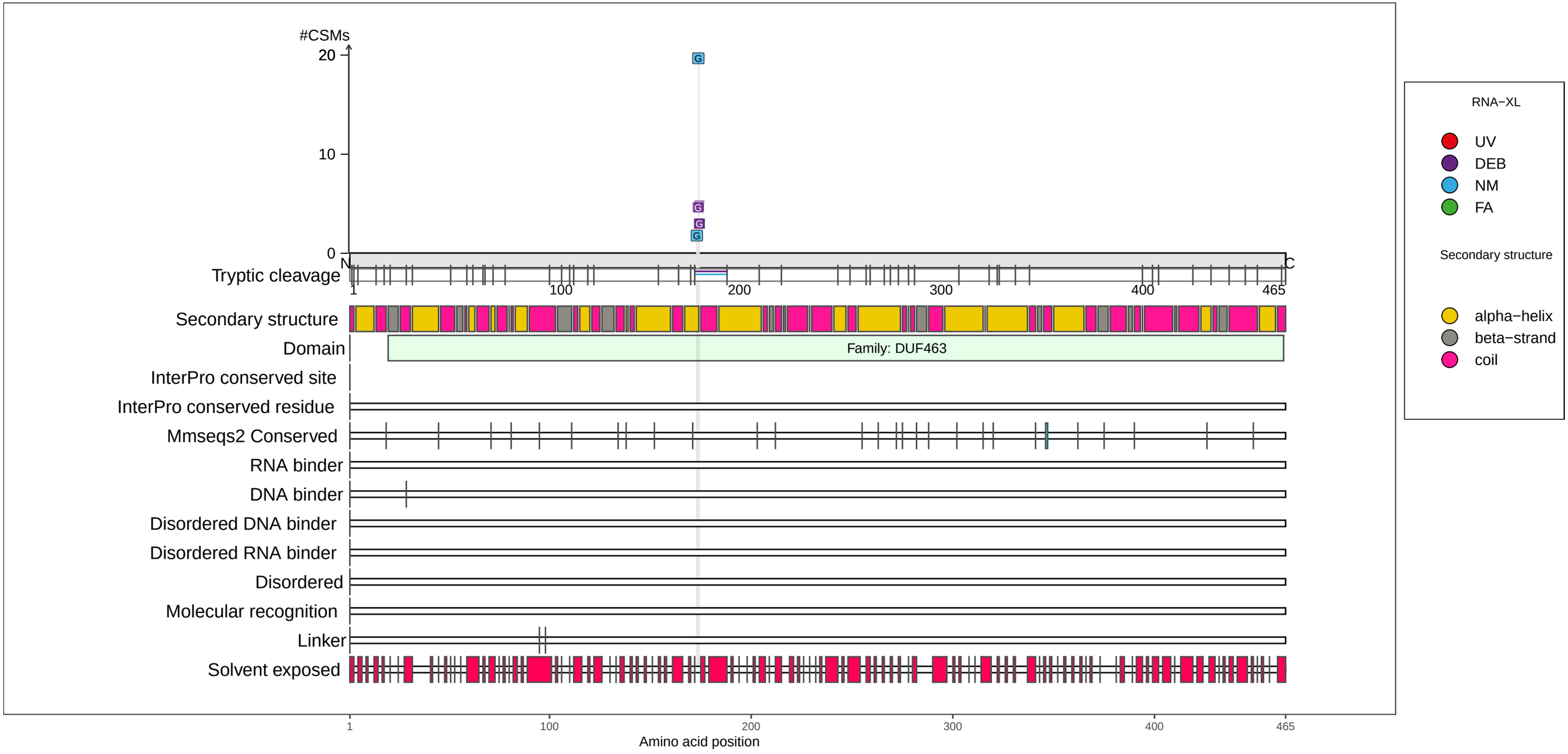
− RNA functions: not annotated



P76046
YCJX_ECOLI Uncharacterized protein YcjX

− Abundance:
tryptic [log10 Intensity]: 7.68 (Q 43)
PAXdb K12 strain [ppm]: 1.18 (Q 19)
PAXdb E.coli [ppm]: 1.26 (Q 54)

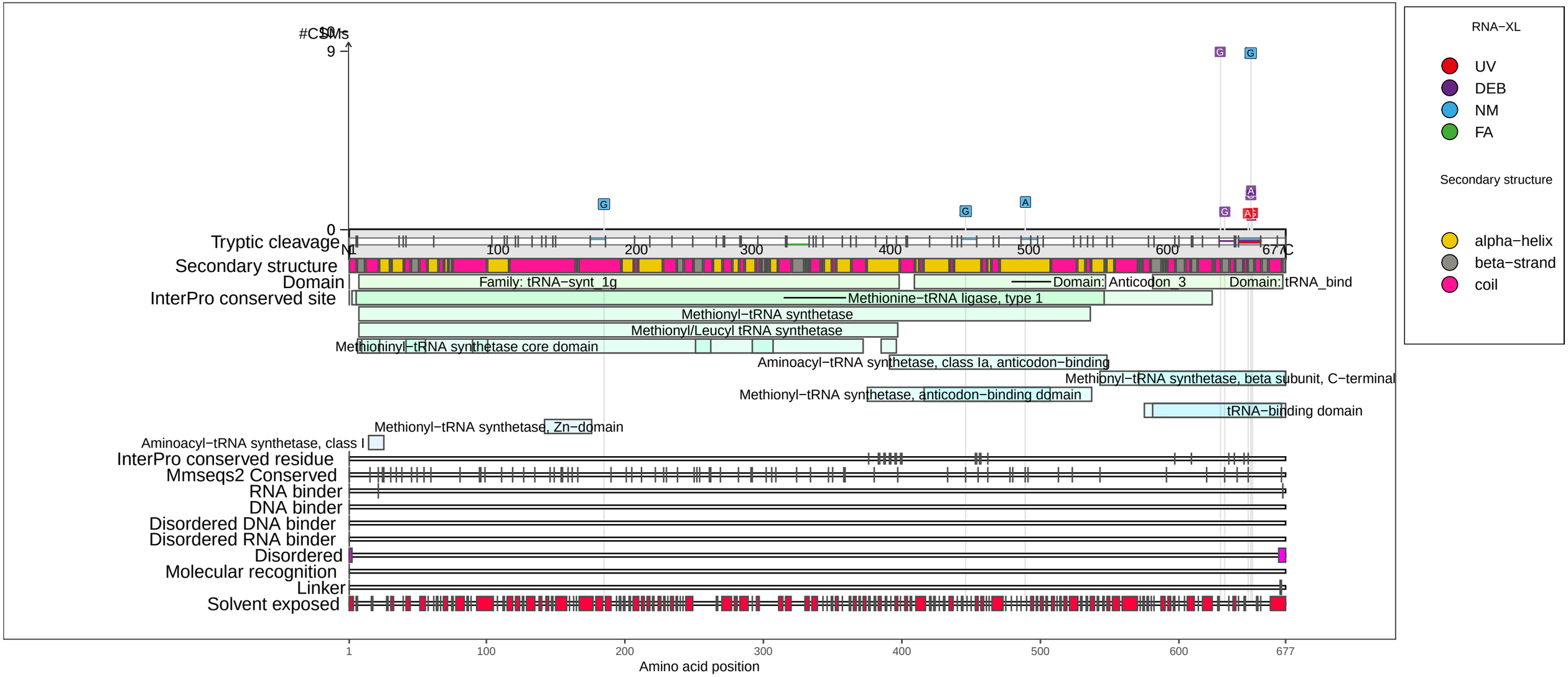
− RNA functions: not annotated



P00959
SYM_ECOLI Methionine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 8.96 (Q 87)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 2.68 (Q 89)

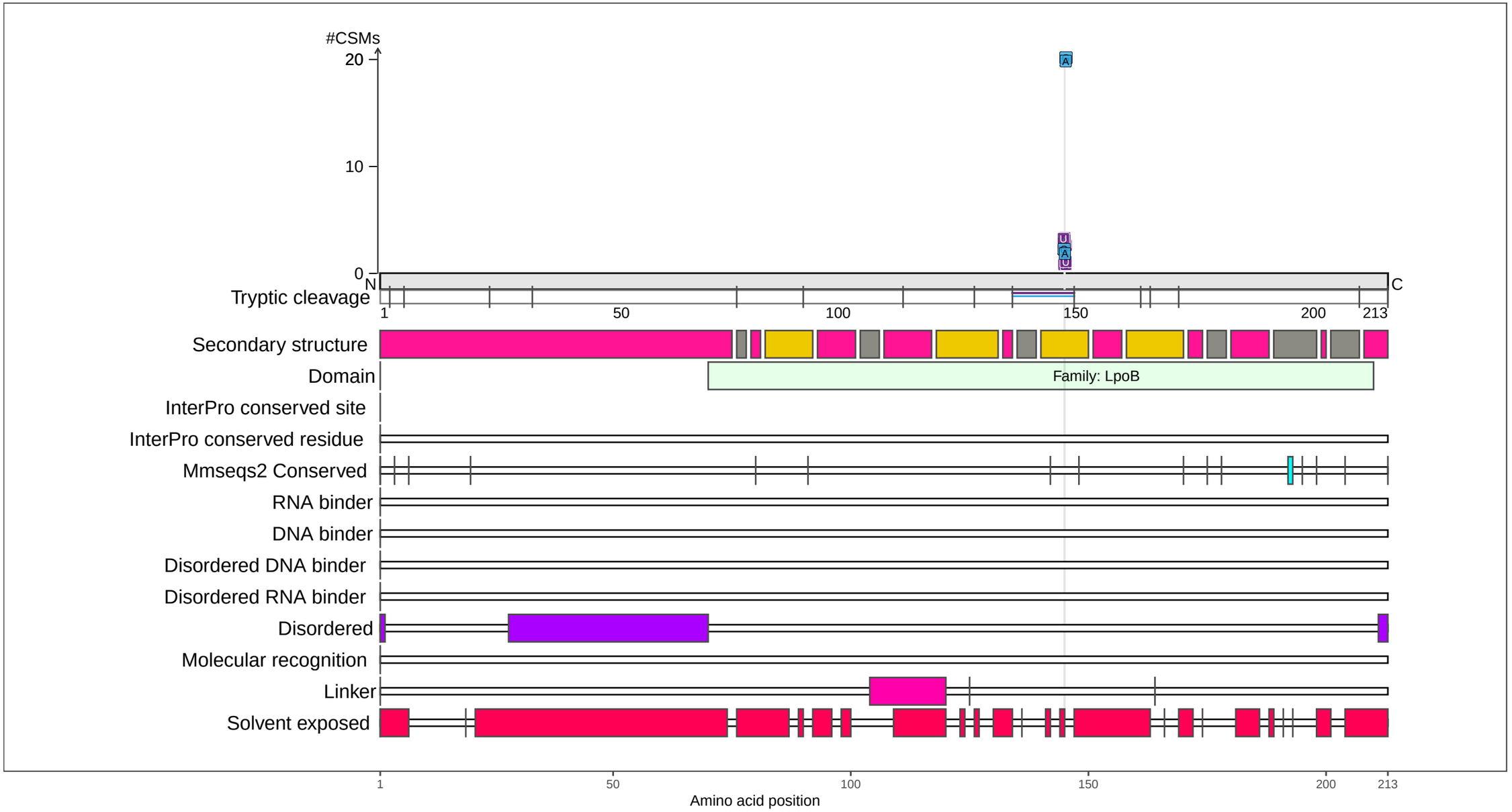
− RNA functions:
aminoacyl−tRNA ligase activity; methionine−tRNA ligase activity
methionyl−tRNA aminoacylation; ncRNA metabolic process; Putative tRNA binding domain; RNA binding
RNA metabolic process; tRNA aminoacylation; tRNA aminoacylation for protein translation
tRNA binding; tRNA metabolic process; tRNA synthetases class I (C) catalytic domain
tRNA synthetases class I (I, L, M and V); tRNA synthetases class I (M)

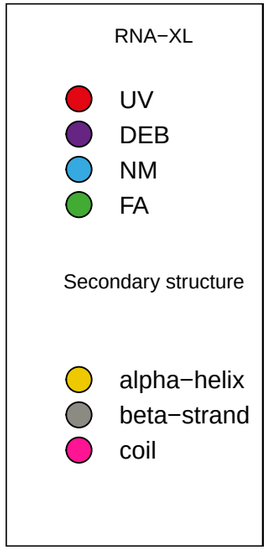


P0AB38
LPOB_ECOLI Penicillin−binding protein activator LpoB

− Abundance:
tryptic [log10 Intensity]: 8.2 (Q 65)
PAXdb K12 strain [ppm]: 2.16 (Q 65)
PAXdb E.coli [ppm]: 2.22 (Q 78)

− RNA functions: not annotated

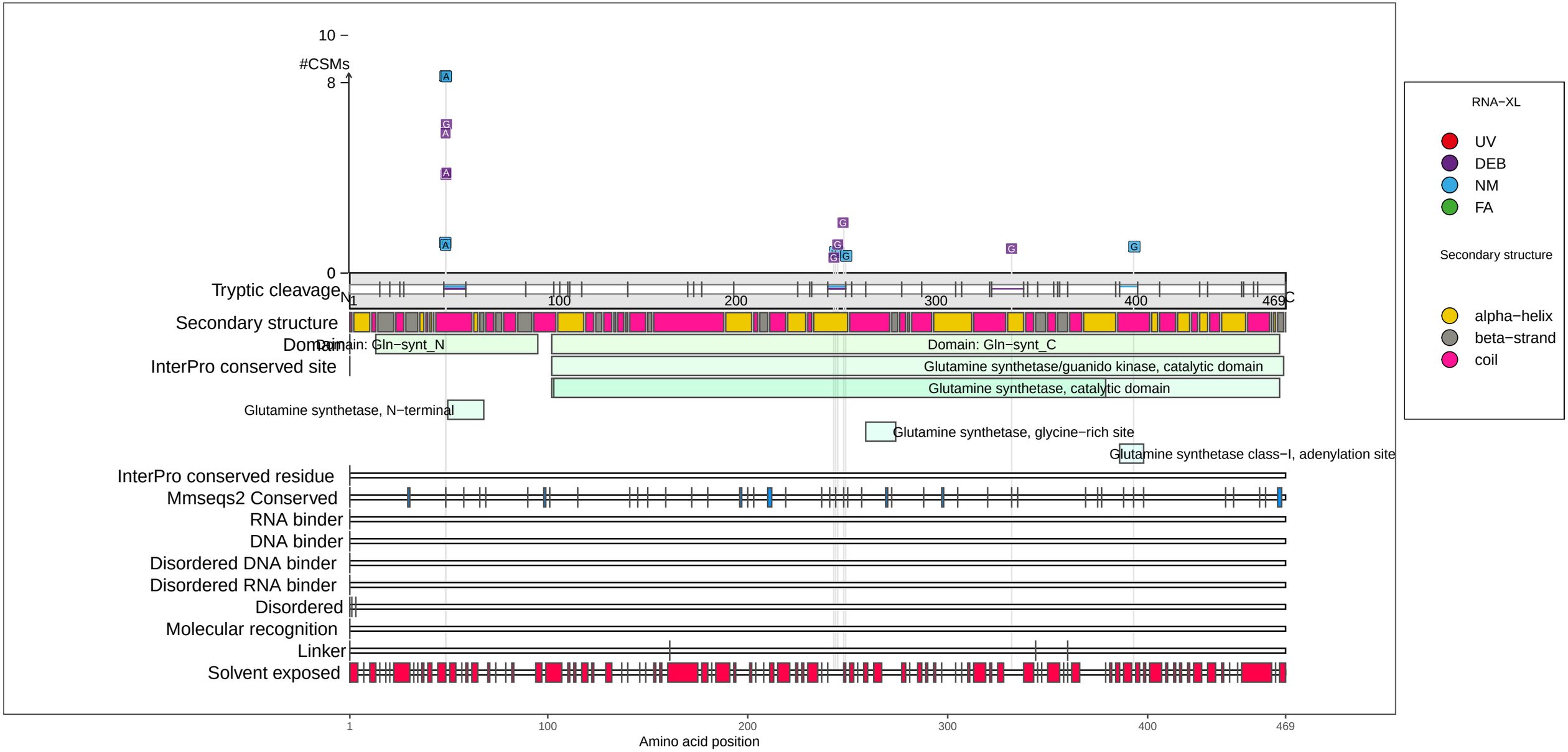




P0A9C5
GLN1B_ECOLI Glutamine synthetase

− Abundance:
tryptic [log10 Intensity]: 9.07 (Q 90)
PAXdb K12 strain [ppm]: 2.97 (Q 90)
PAXdb E.coli [ppm]: 2.89 (Q 93)

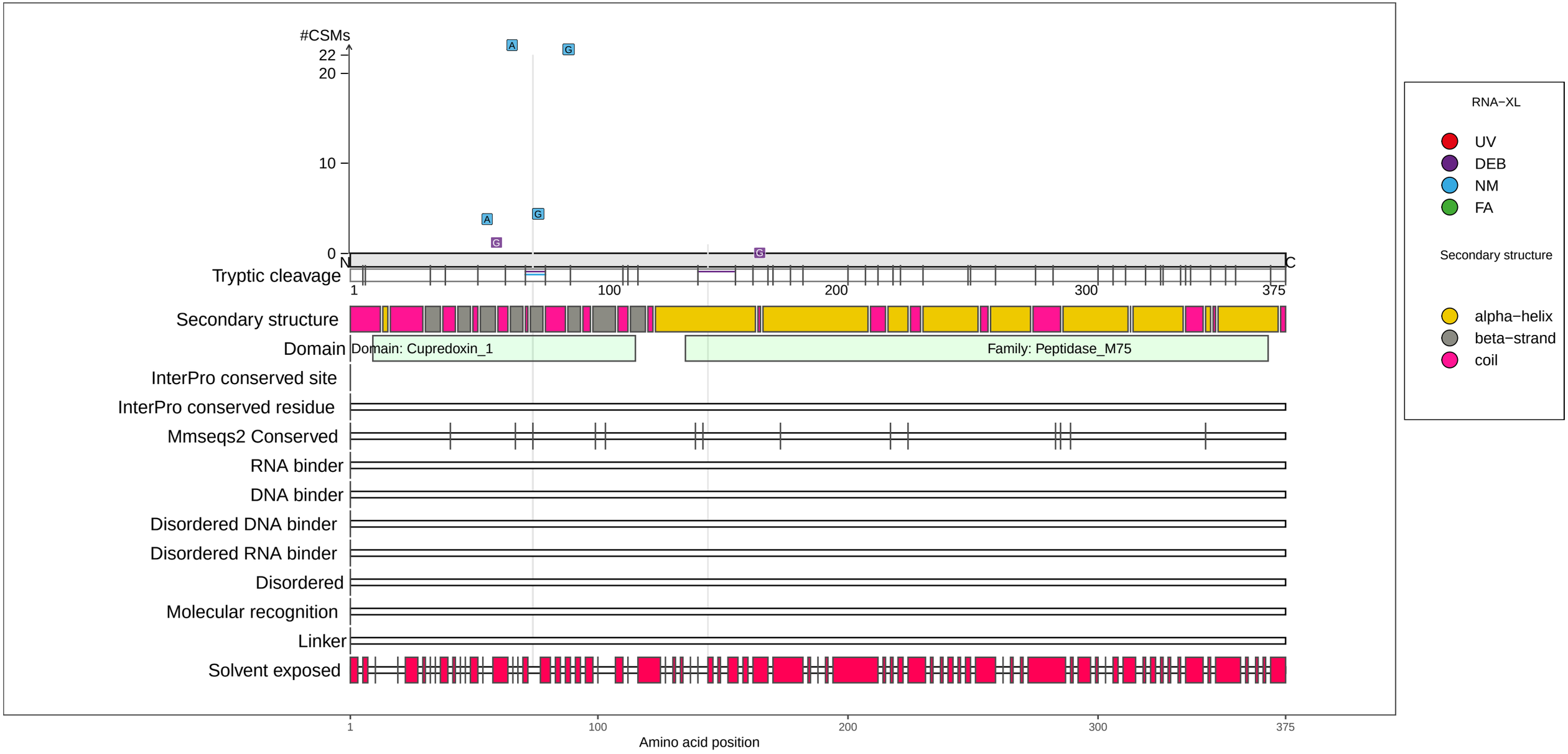
− RNA functions: not annotated



P0AB24
EFEO_ECOLI Iron uptake system component EfeO

− Abundance:
tryptic [log10 Intensity]: 8.44 (Q 73)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 2.09 (Q 74)

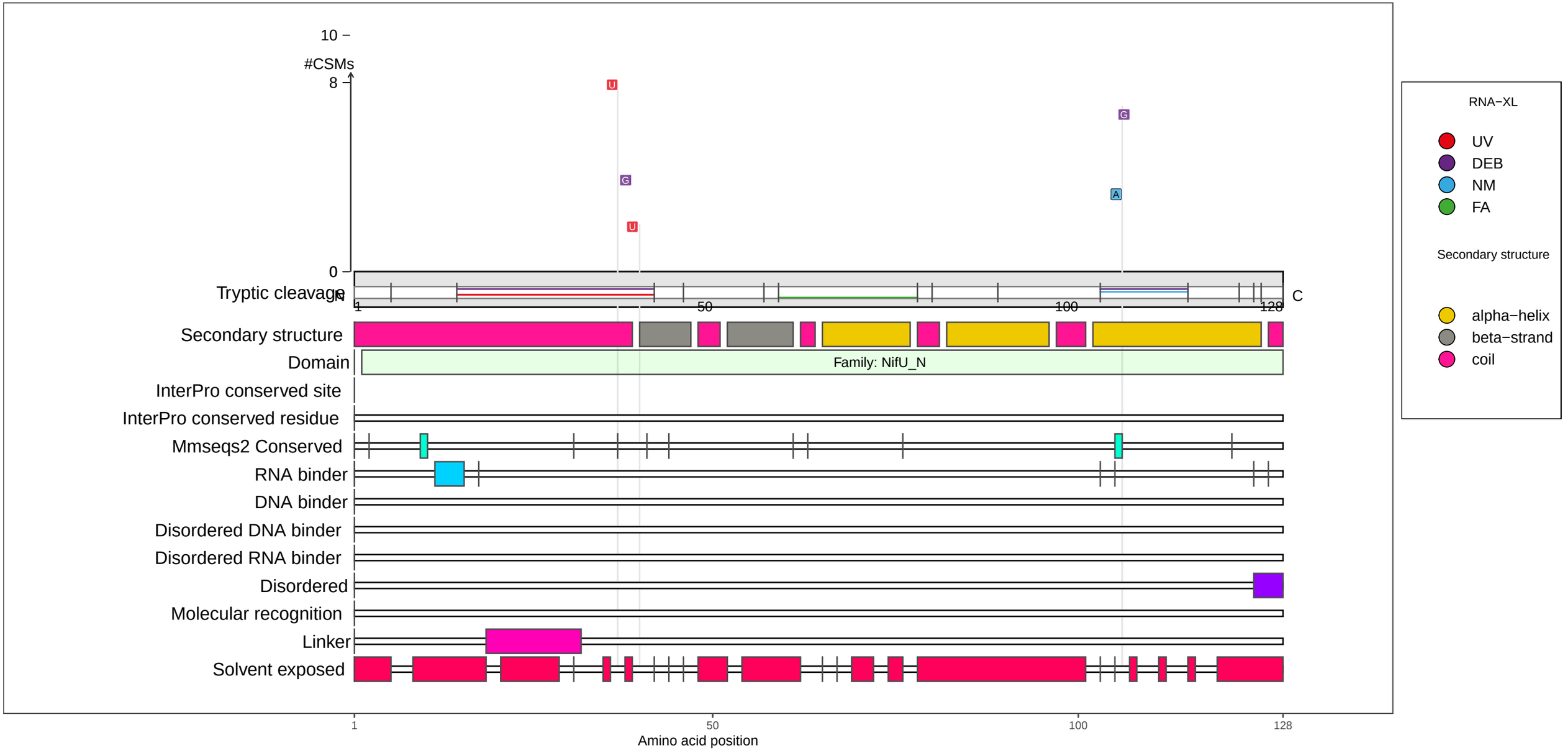
− RNA functions: not annotated



P0ACD4
ISCU_ECOLI Iron−sulfur cluster assembly scaffold protein IscU

− Abundance:
tryptic [log10 Intensity]: 8.15 (Q 63)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 3.27 (Q 97)

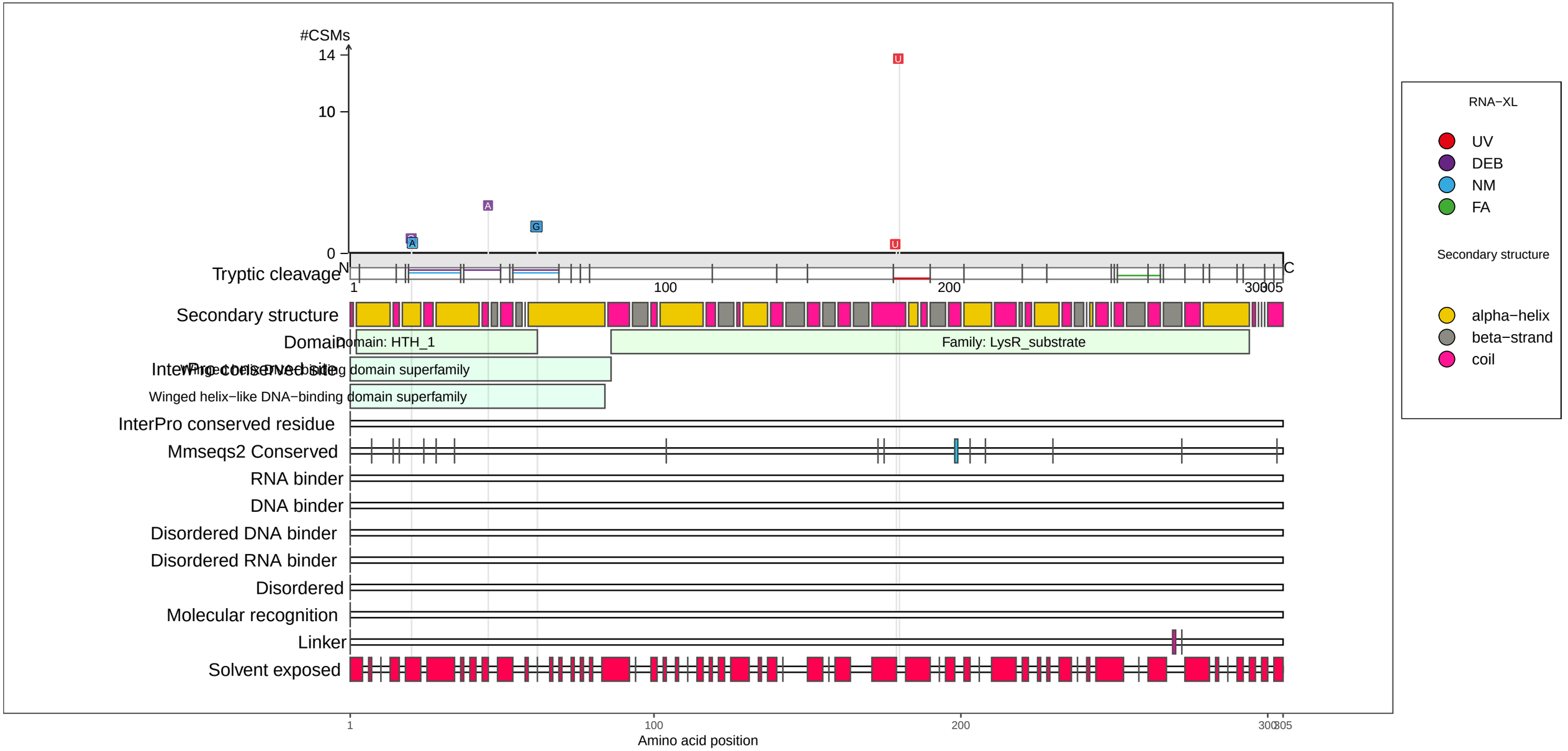
− RNA functions: not annotated



P0ACQ4
OXYR_ECOLI Hydrogen peroxide−inducible genes activator

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.38 (Q 83)

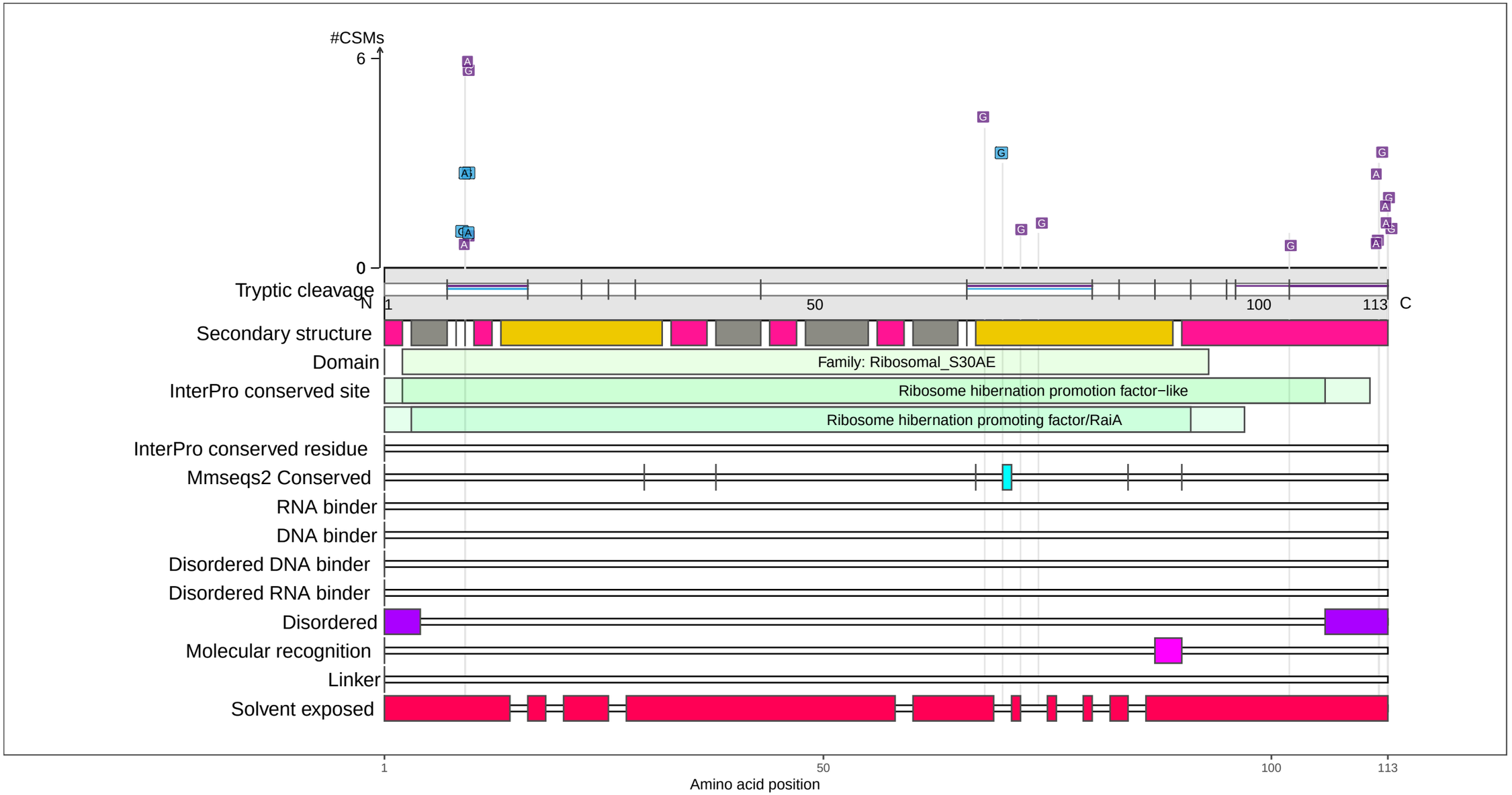
− RNA functions: not annotated



P0AD49
YFIA_ECOLI Ribosome−associated inhibitor A

− Abundance:
tryptic [log10 Intensity]: 8.69 (Q 81)
PAXdb K12 strain [ppm]: 2.9 (Q 88)
PAXdb E.coli [ppm]: 3.35 (Q 98)

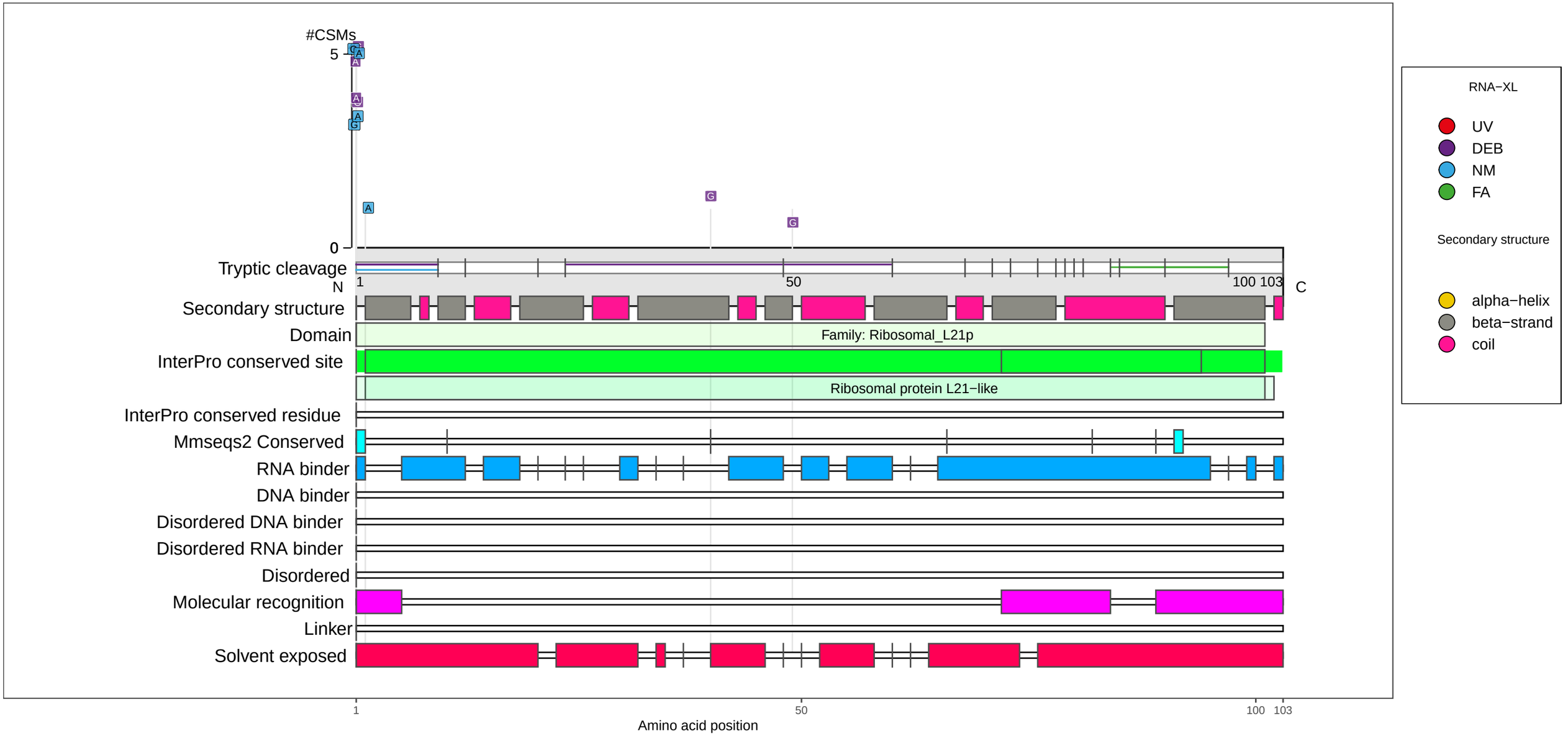
− RNA functions:
RNA binding; rRNA binding



P0AG48
RL21_ECOLI 50S ribosomal protein L21

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 3.52 (Q 98)
PAXdb E.coli [ppm]: 3.13 (Q 96)

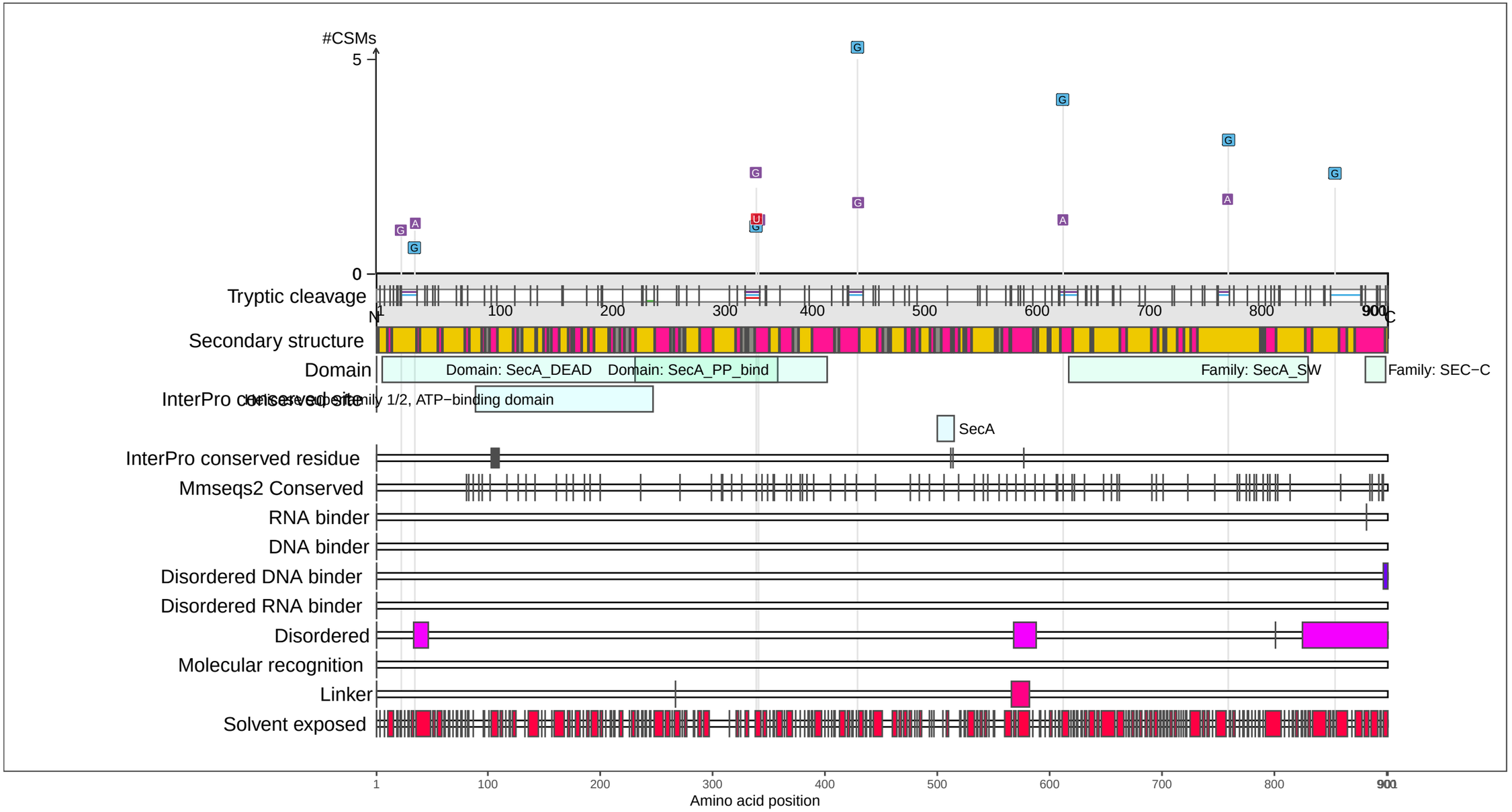
− RNA functions:
RNA binding; rRNA binding

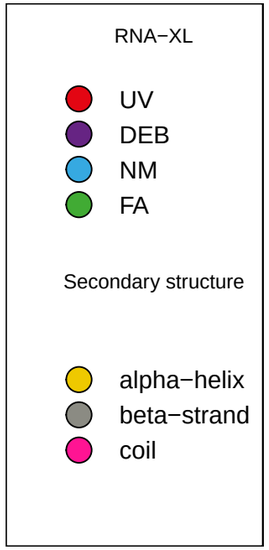


P10408
SECA_ECOLI Protein translocase subunit SecA

− Abundance:
tryptic [log10 Intensity]: 9.11 (Q 91)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 2.59 (Q 88)

− RNA functions: not annotated

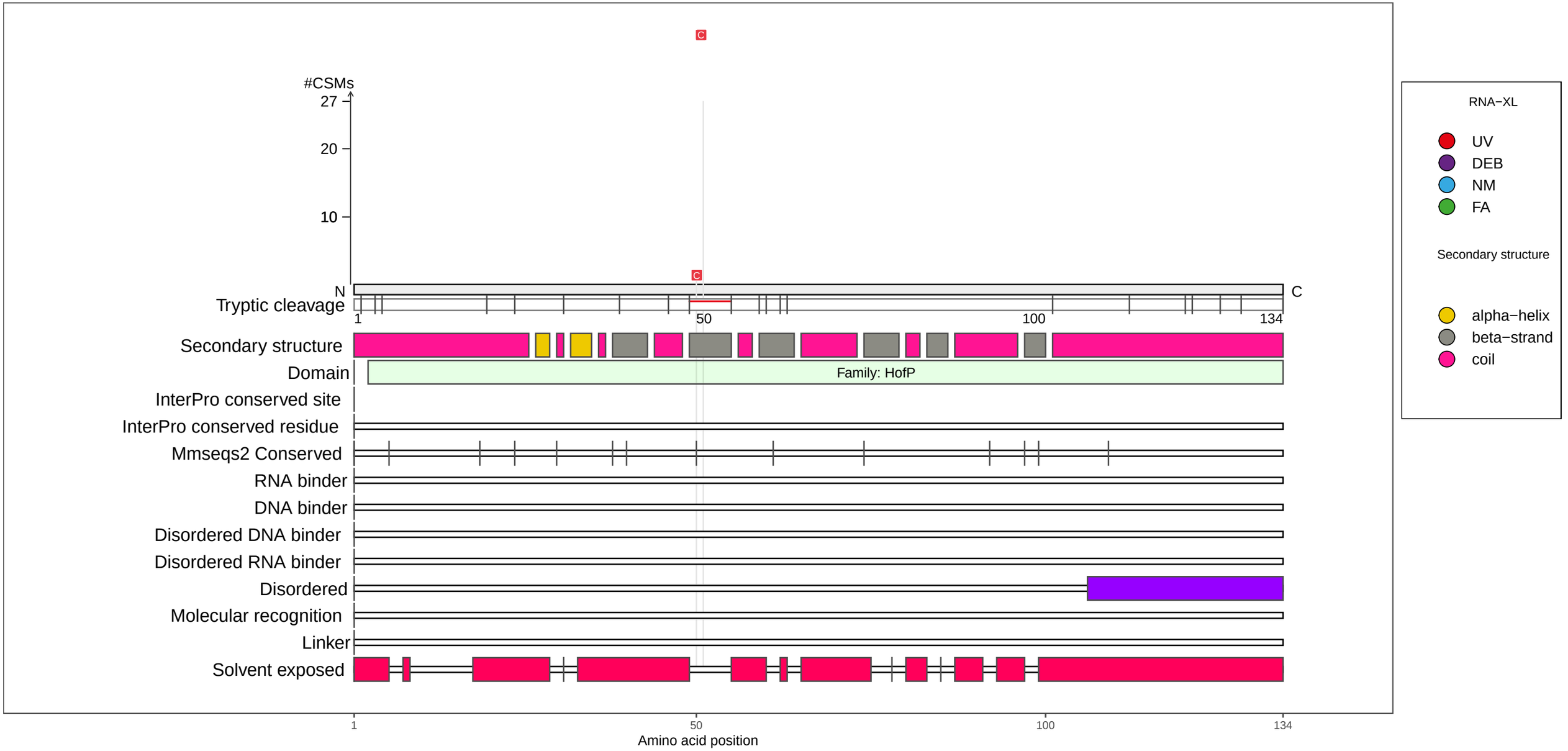




P45750
HOFP_ECOLI DNA utilization protein HofP

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.11 (Q 22)

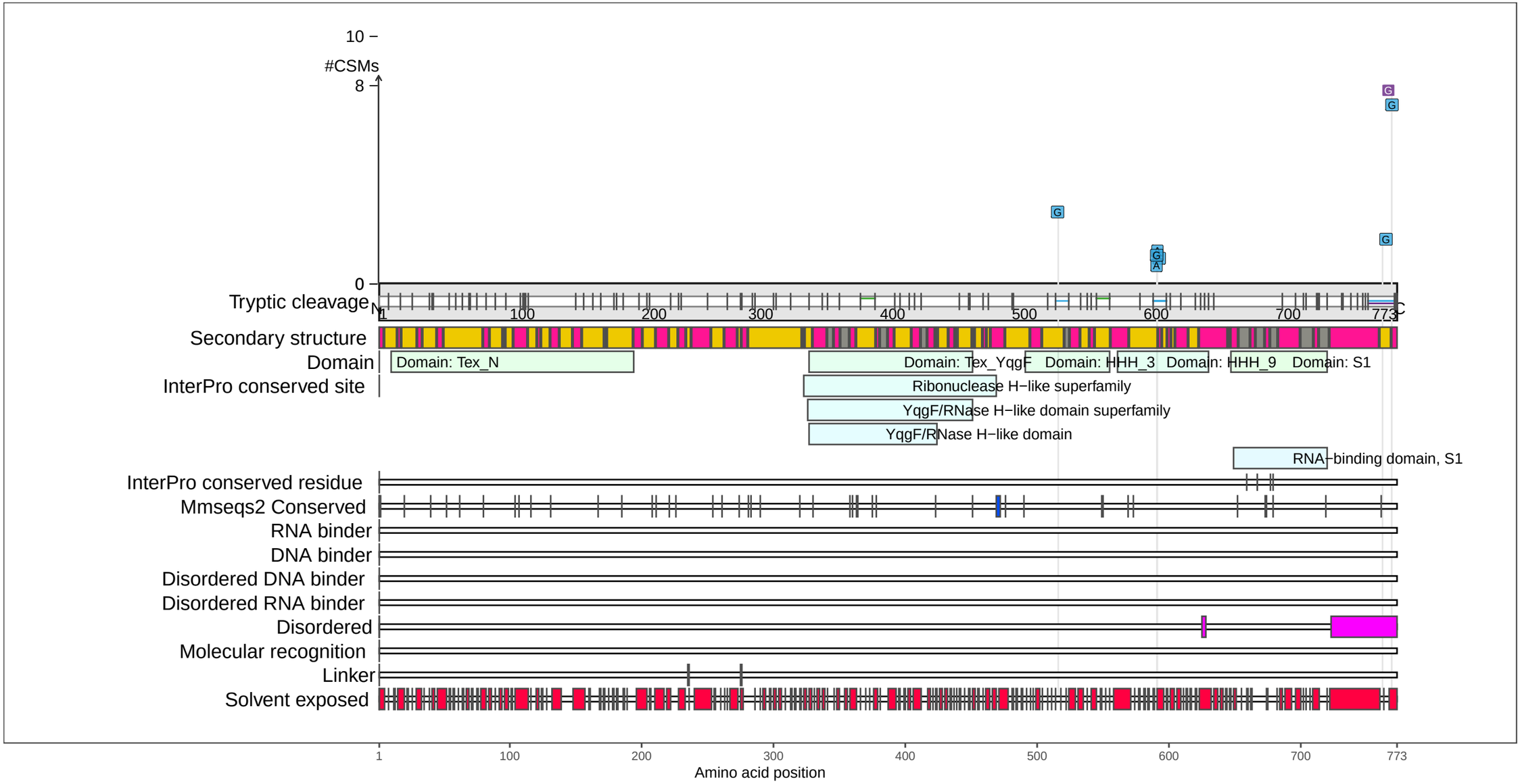
− RNA functions: not annotated

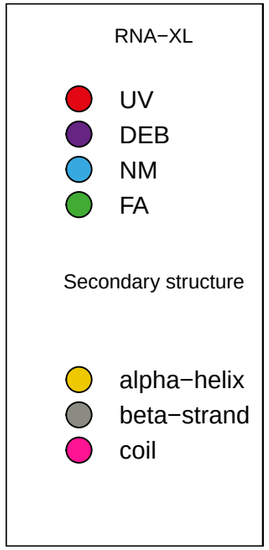


P46837
YHGF_ECOLI Protein YhgF

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 52)
PAXdb K12 strain [ppm]: 2.64 (Q 82)
PAXdb E.coli [ppm]: 1.89 (Q 69)

− RNA functions:
mRNA binding; Ribosomal protein S1−like RNA−binding domain; RNA binding
S1 RNA binding domain

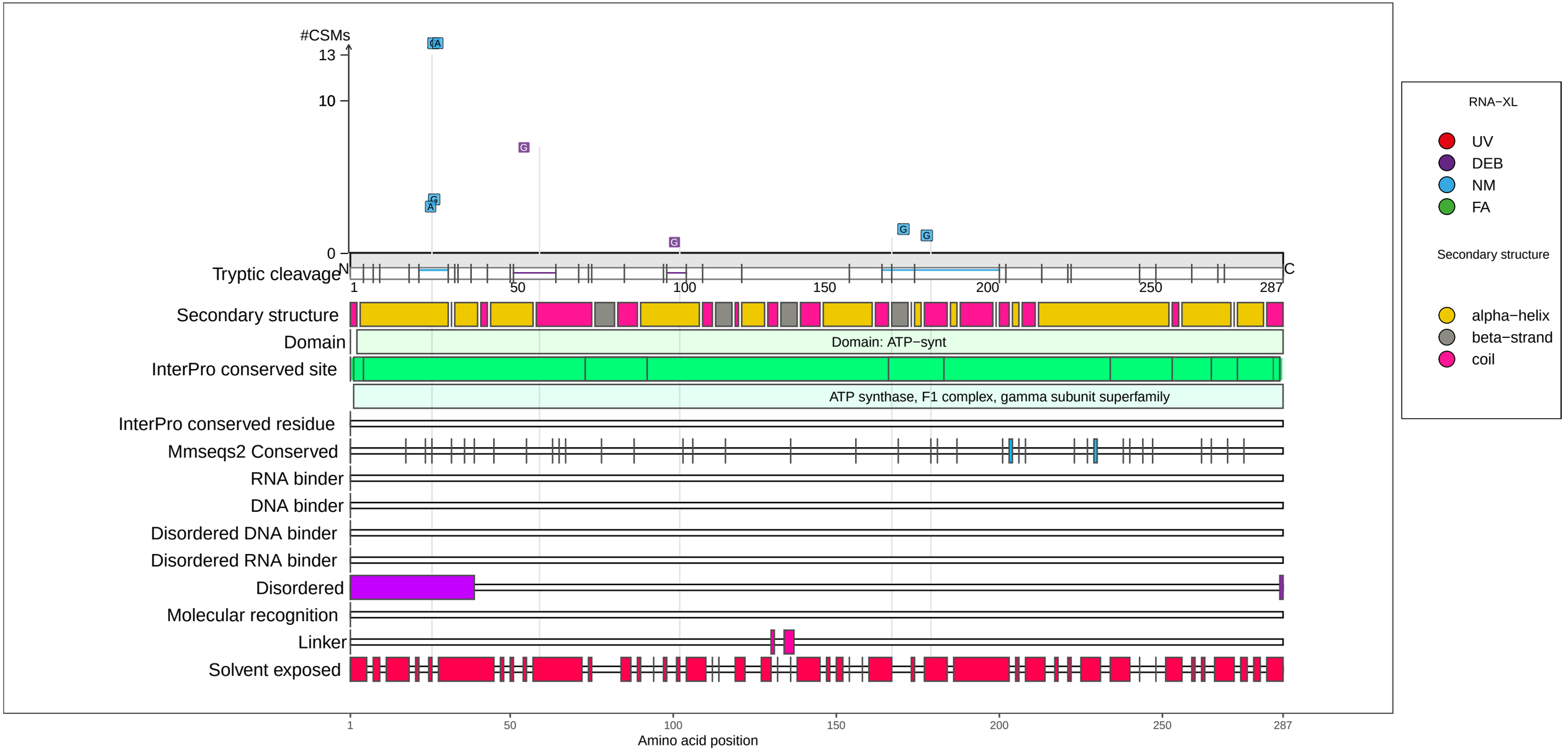




P0ABA6
ATPG_ECOLI ATP synthase gamma chain

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 77)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 3.04 (Q 95)

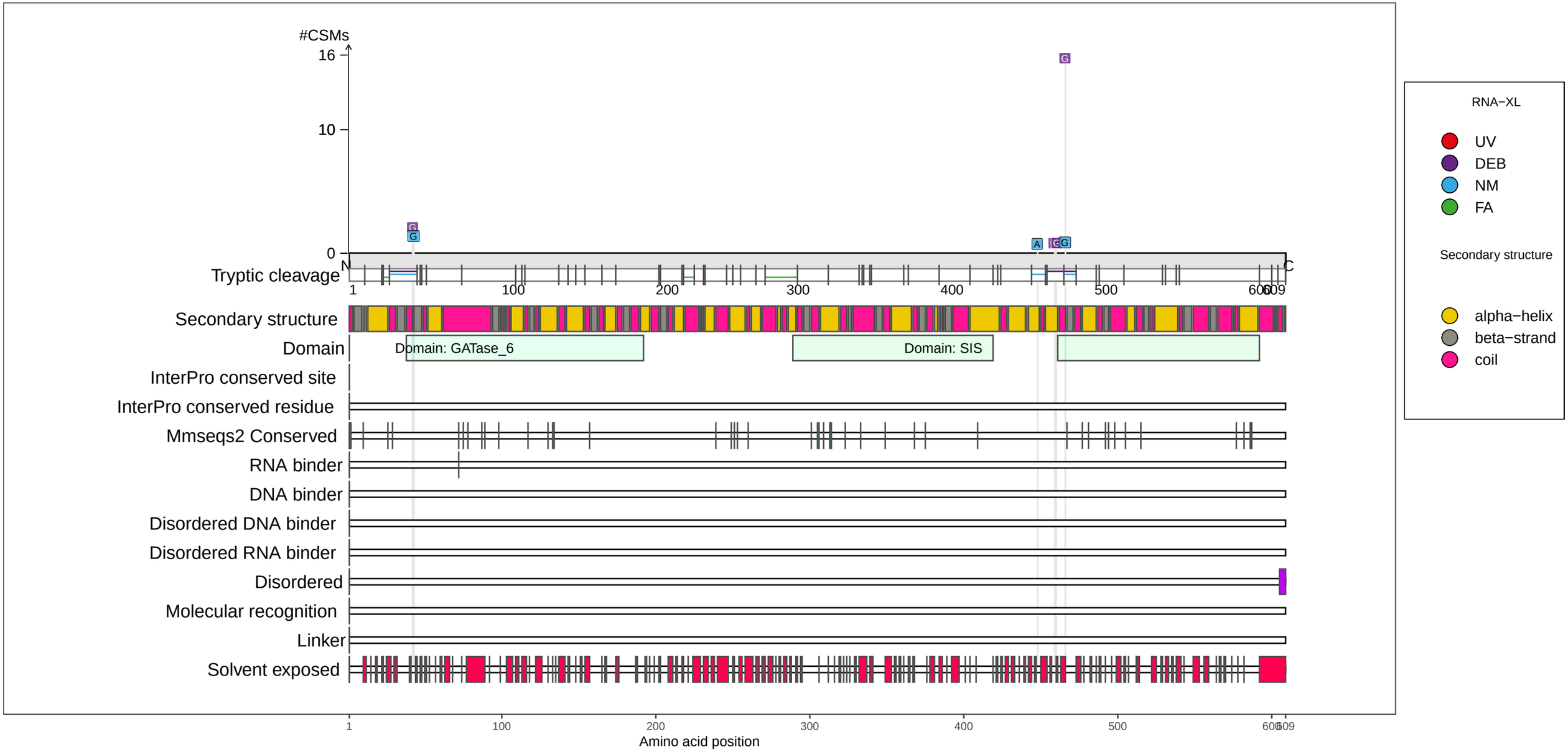
− RNA functions: not annotated



P17169
GLMS_ECOLI Glutamine−−fructose−6−phosphate aminotransferase [isomerizing]

− Abundance:
tryptic [log10 Intensity]: 9.69 (Q 98)
PAXdb K12 strain [ppm]: 3.12 (Q 93)
PAXdb E.coli [ppm]: 2.5 (Q 85)

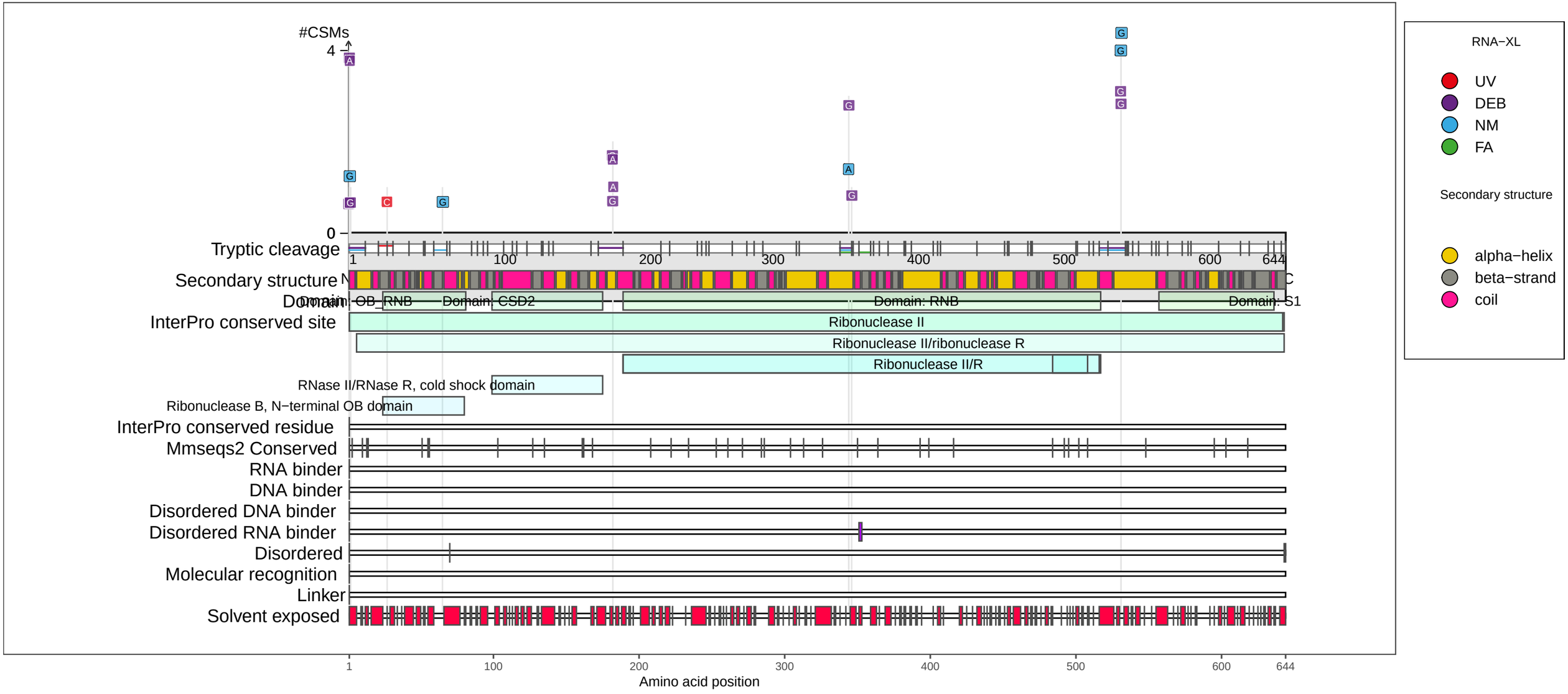
− RNA functions: not annotated



P30850
RNB_ECOLI Exoribonuclease 2

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 2.16 (Q 76)

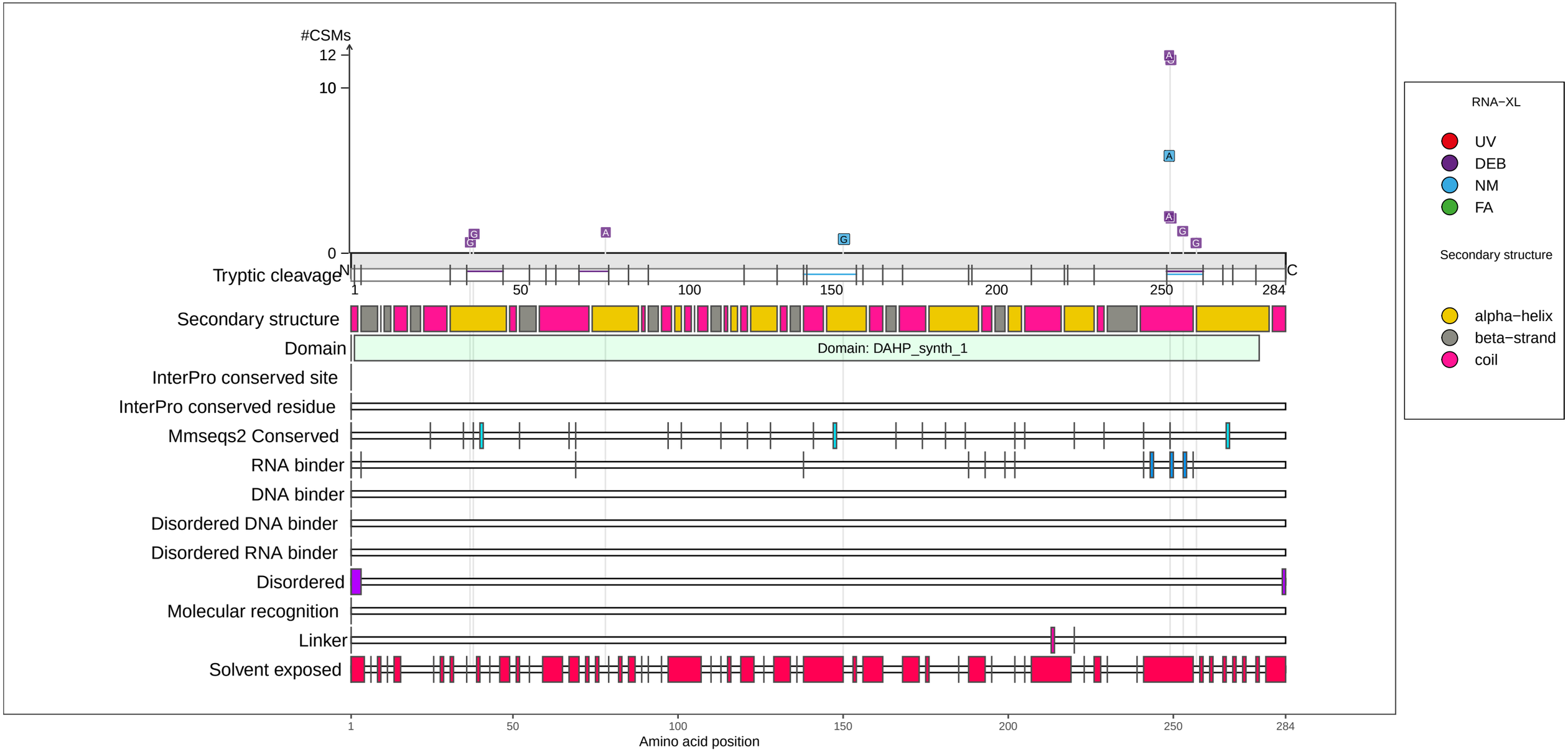
− RNA functions:
mRNA catabolic process; mRNA metabolic process
Ribosomal protein S1−like RNA−binding domain; RNA binding; RNA catabolic process; RNA metabolic process
RNA phosphodiester bond hydrolysis; RNA phosphodiester bond hydrolysis, exonucleolytic
S1 RNA binding domain



P0A715
KDSA_ECOLI 2−dehydro−3−deoxyphosphooctonate aldolase

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 3.45 (Q 97)
PAXdb E.coli [ppm]: 3.07 (Q 95)

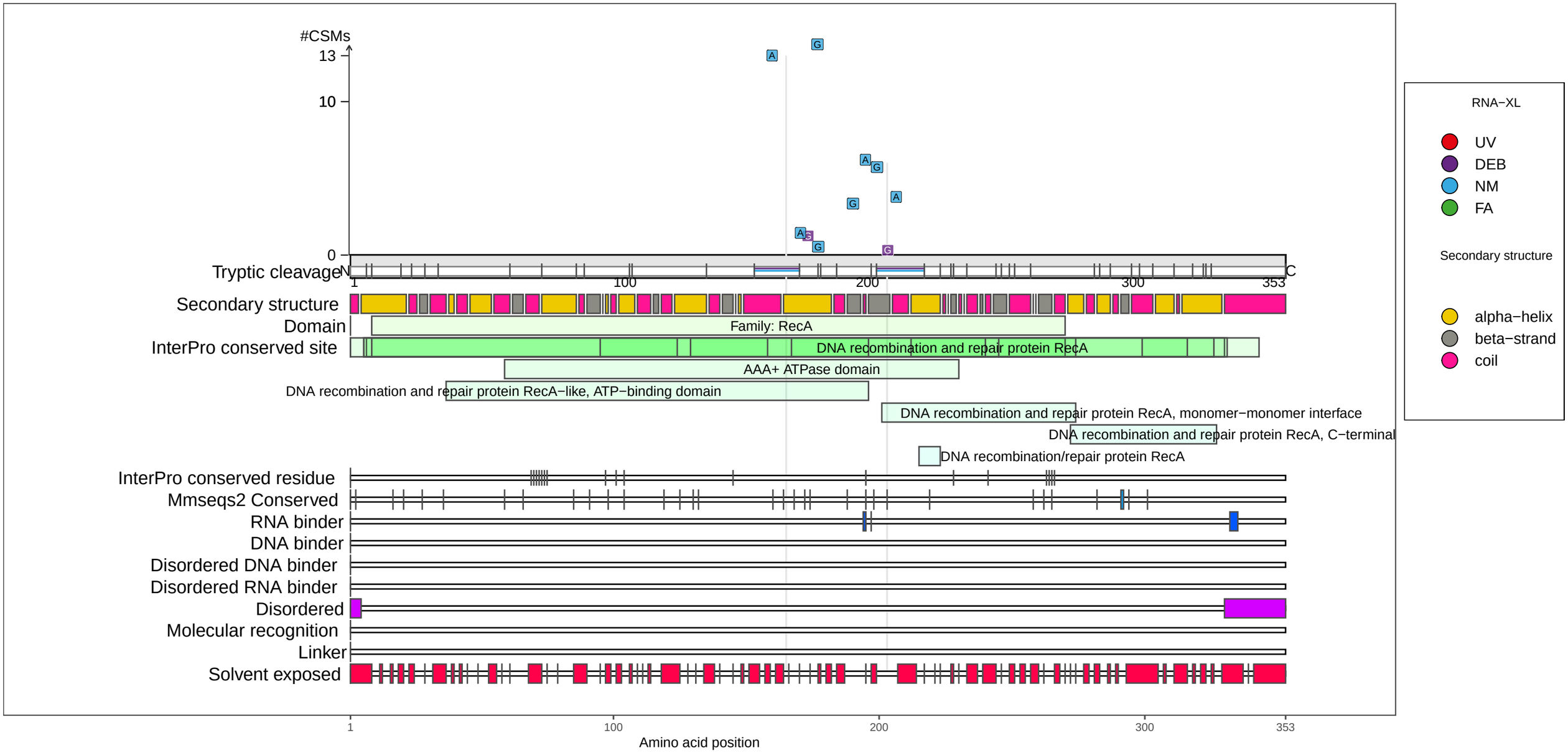
− RNA functions: not annotated



P0A7G6
RECA_ECOLI Protein RecA

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 2.86 (Q 88)
PAXdb E.coli [ppm]: 2.7 (Q 90)

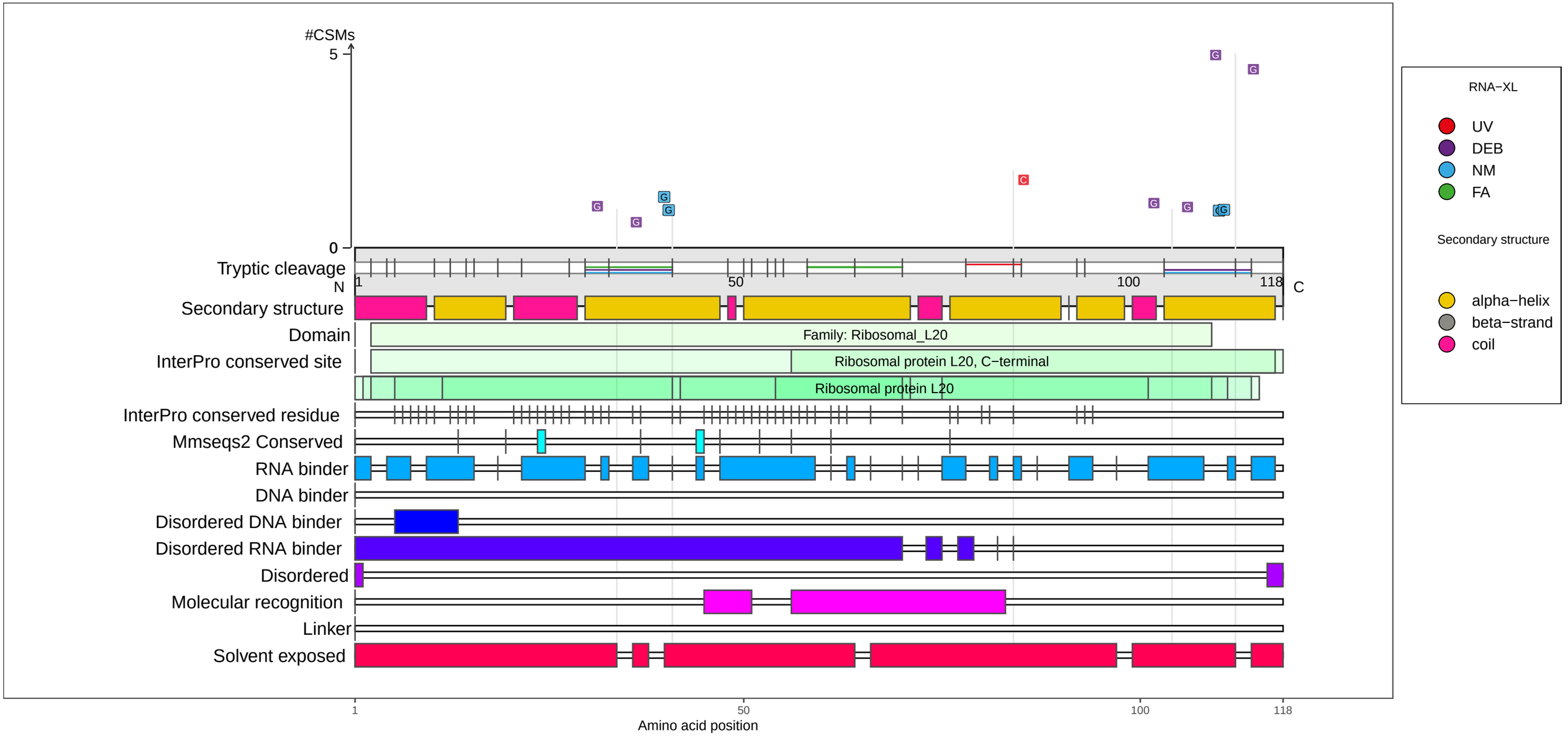
− RNA functions: not annotated



P0A7L3
RL20_ECOLI 50S ribosomal protein L20

− Abundance:
tryptic [log10 Intensity]: 9.04 (Q 89)
PAXdb K12 strain [ppm]: 3.02 (Q 91)
PAXdb E.coli [ppm]: 3.36 (Q 98)

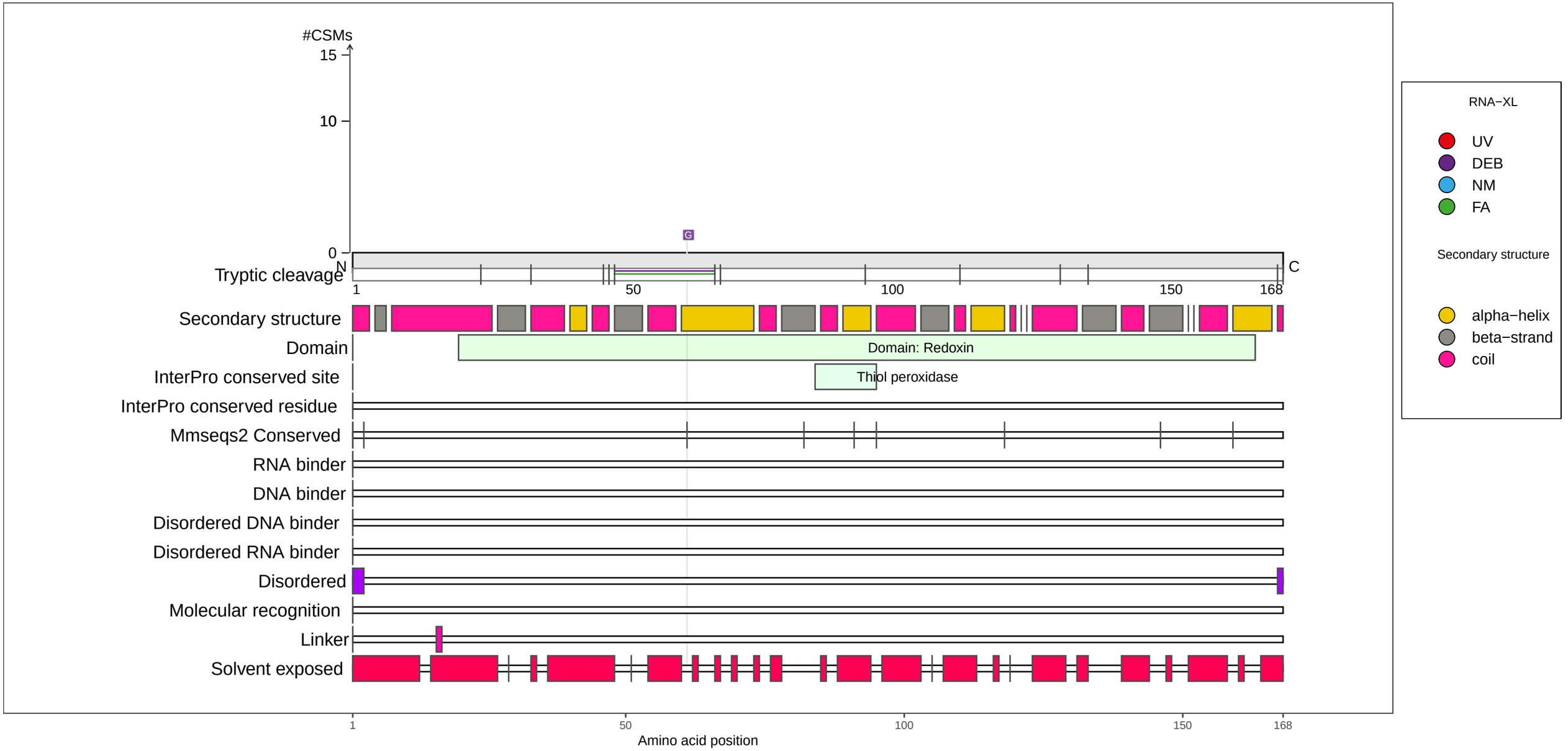
− RNA functions:
mRNA binding; RNA binding; rRNA binding



P0A862
TPX_ECOLI Thiol peroxidase

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.19 (Q 94)
PAXdb E.coli [ppm]: 3.39 (Q 98)

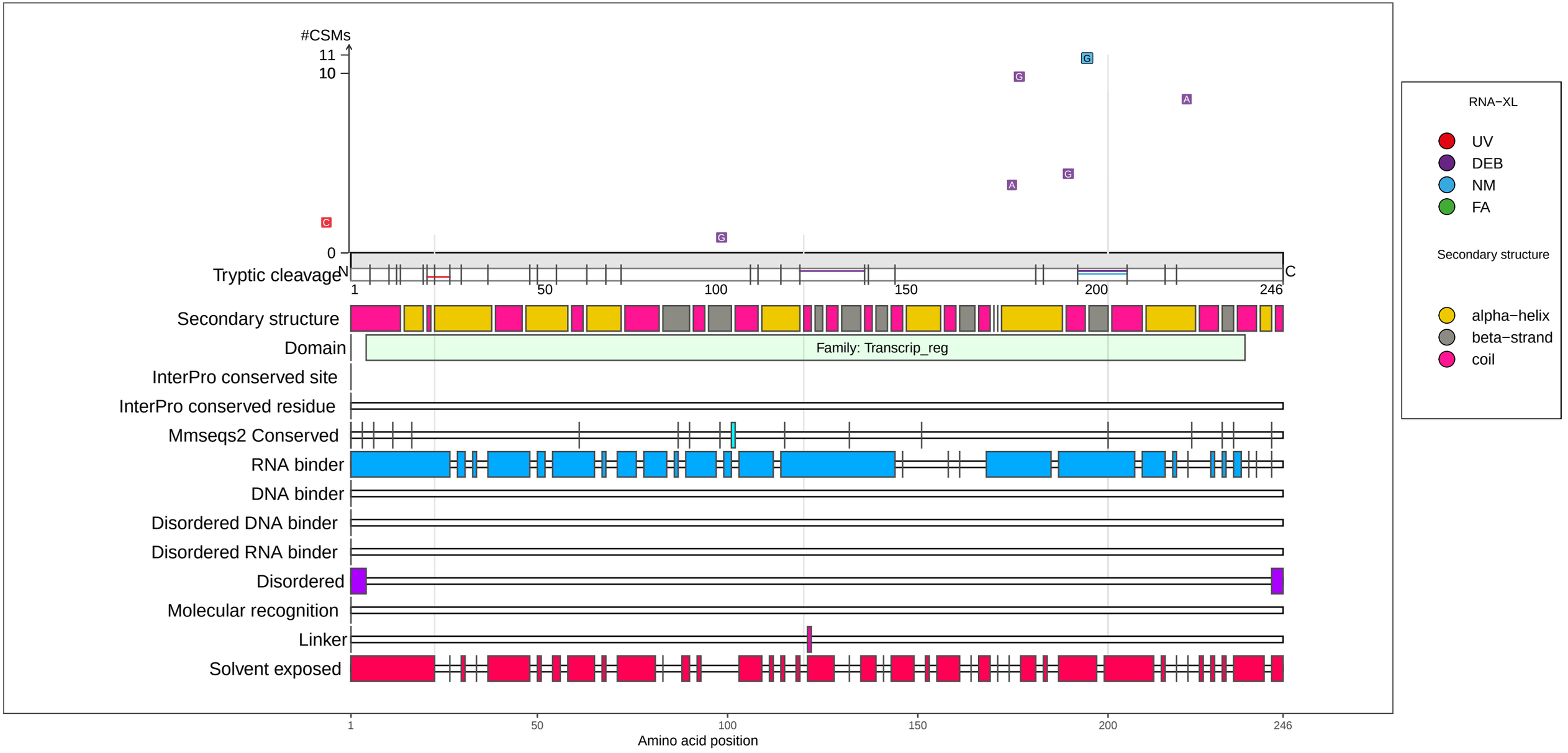
− RNA functions: not annotated



P0A8A0
YEBC_ECOLI Probable transcriptional regulatory protein YebC

− Abundance:
tryptic [log10 Intensity]: 7.94 (Q 56)
PAXdb K12 strain [ppm]: 2.95 (Q 89)
PAXdb E.coli [ppm]: 2.83 (Q 92)

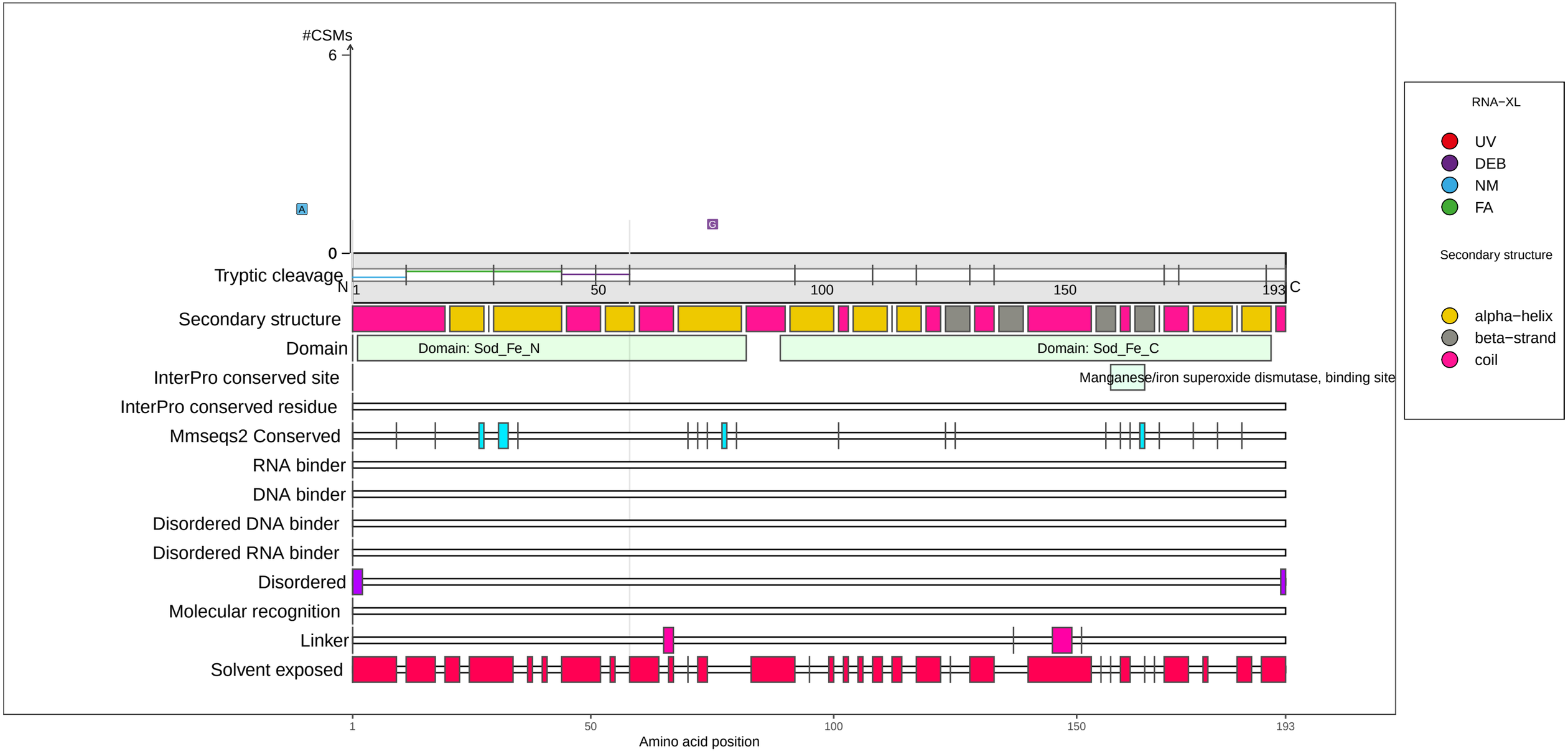
− RNA functions: not annotated



P0AGD3
SODF_ECOLI Superoxide dismutase [Fe]

− Abundance:
tryptic [log10 Intensity]: 9.9 (Q 99)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 2.92 (Q 94)

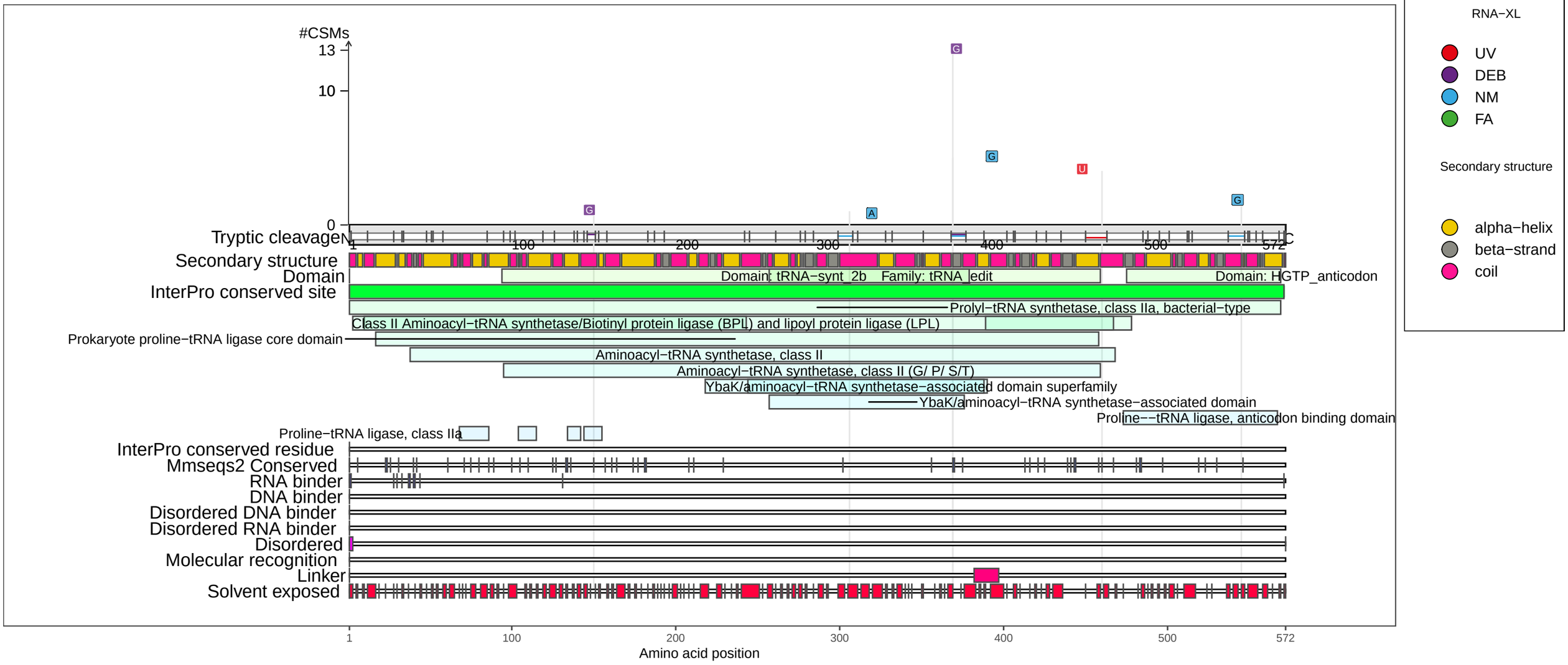
− RNA functions: not annotated



P16659
SYP_ECOLI Proline−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 2.99 (Q 90)
PAXdb E.coli [ppm]: 2.73 (Q 90)

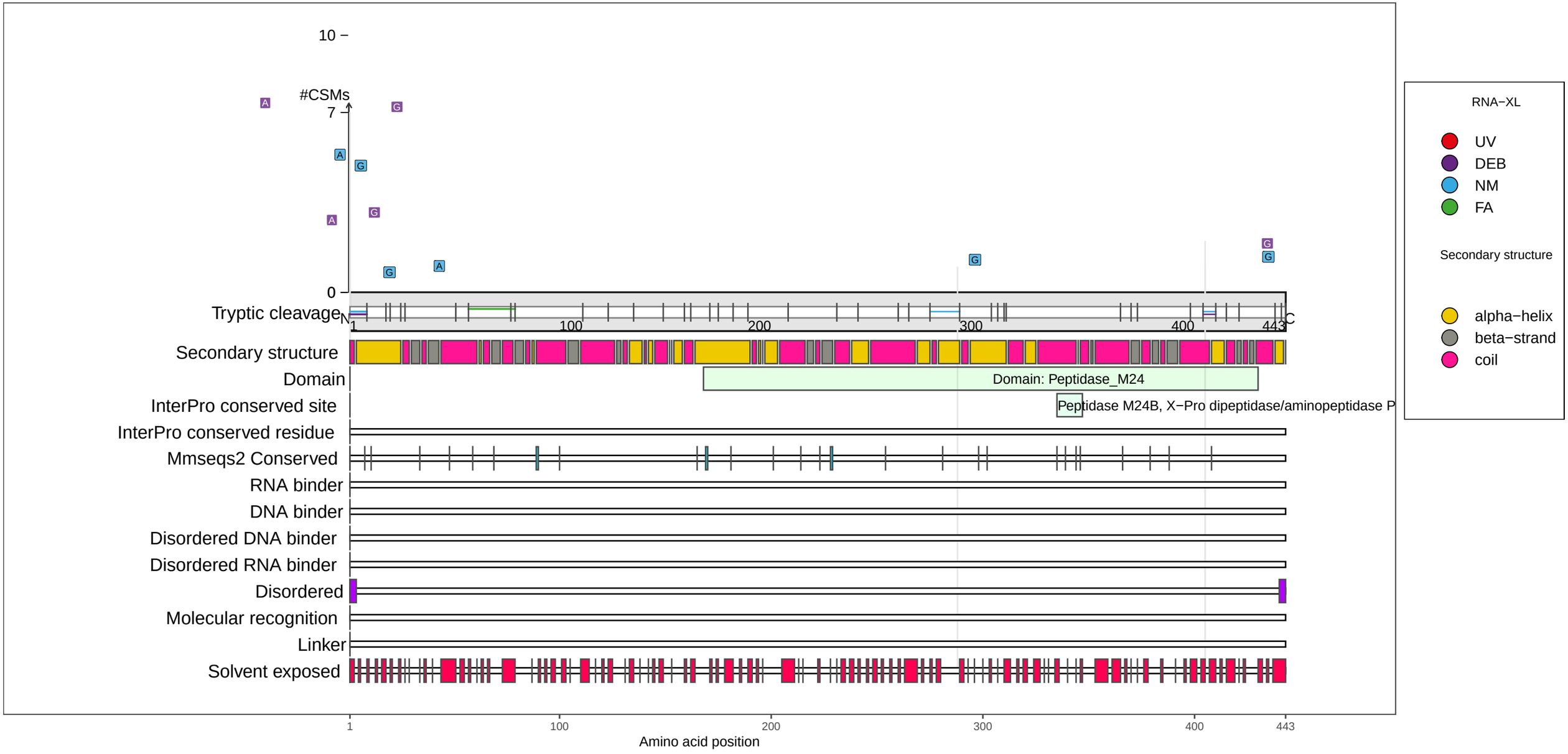
− RNA functions:
Ala−tRNA(Pro) hydrolase activity; aminoacyl−tRNA editing activity
Aminoacyl−tRNA editing domain; aminoacyl−tRNA ligase activity
aminoacyl−tRNA metabolism involved in translational fidelity; ncRNA metabolic process; proline−tRNA ligase activity
prolyl−tRNA aminoacylation; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process
tRNA synthetase class II core domain (G, H, P, S and T)



P21165
PEPQ_ECOLI Xaa−Pro dipeptidase

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 2.66 (Q 89)

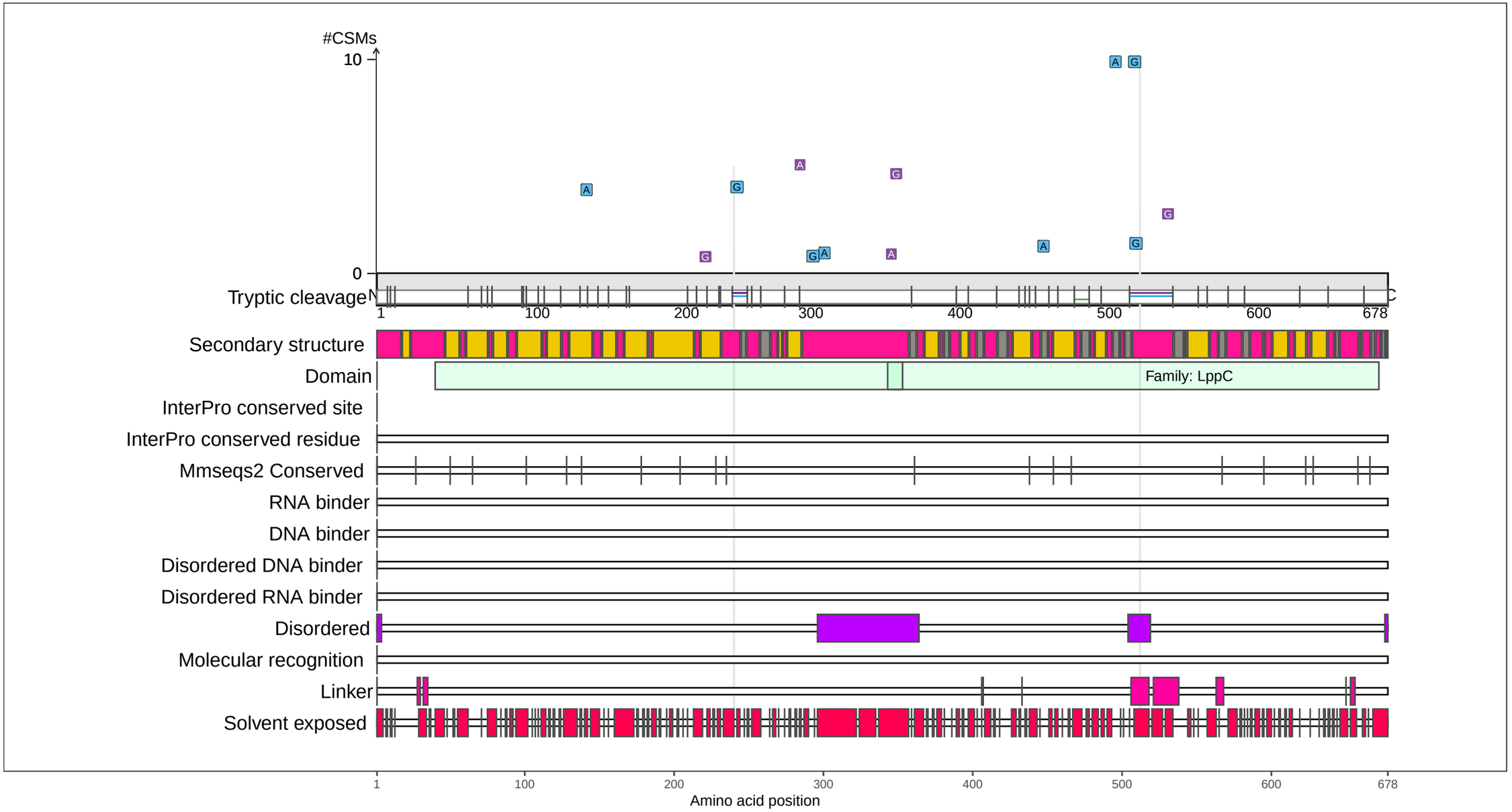
− RNA functions: not annotated

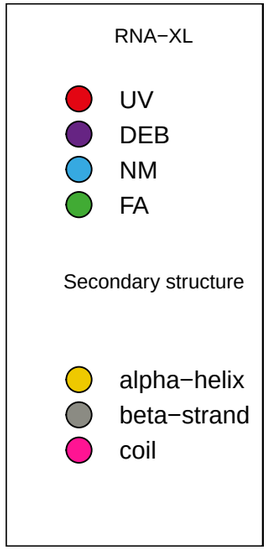


P45464
LPOA_ECOLI Penicillin−binding protein activator LpoA

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 1.24 (Q 23)
PAXdb E.coli [ppm]: 1.84 (Q 68)

− RNA functions: not annotated

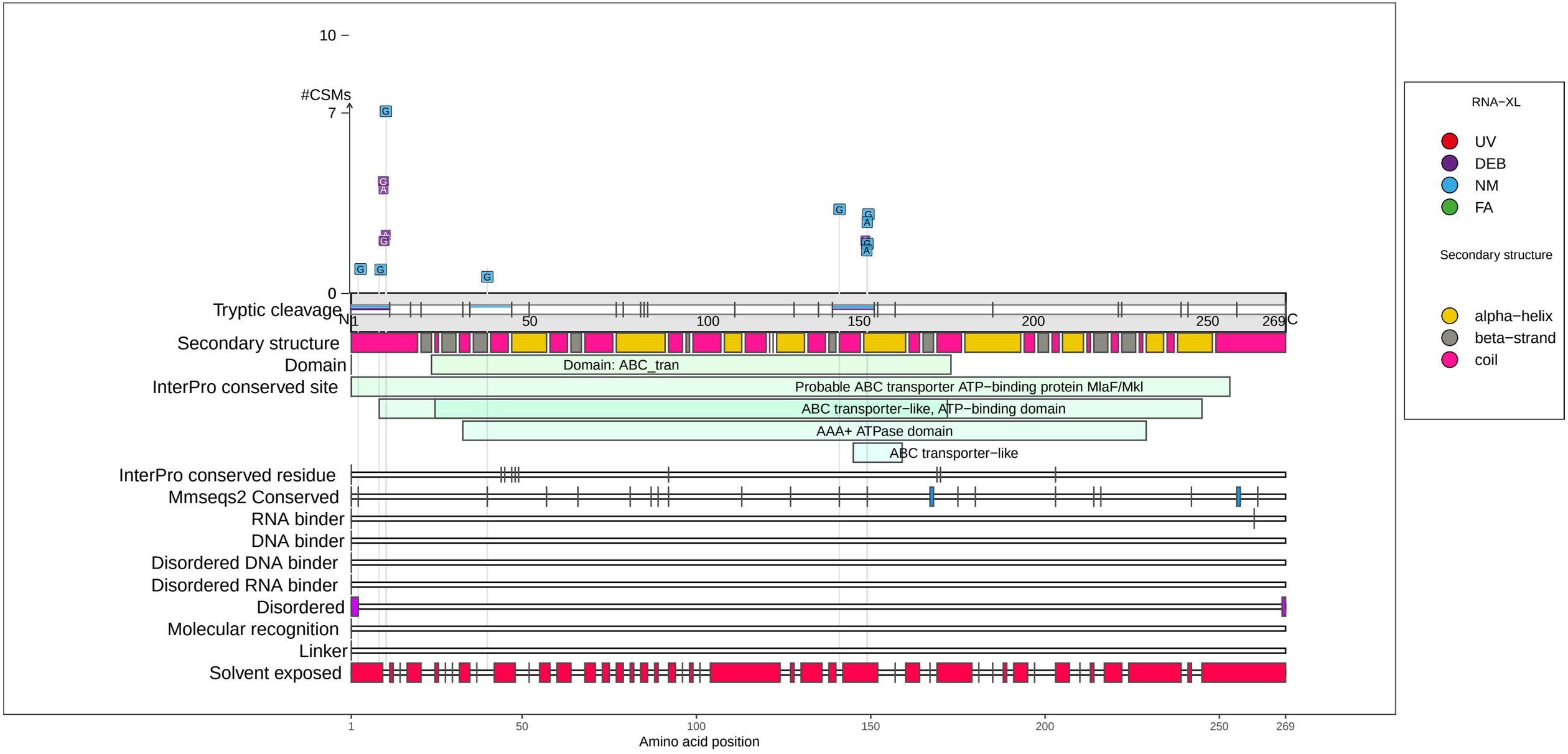




P63386
MLAF_ECOLI Intermembrane phospholipid transport system ATP−binding protein MlaF

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 25)
PAXdb K12 strain [ppm]: 1.72 (Q 50)
PAXdb E.coli [ppm]: 1.46 (Q 59)

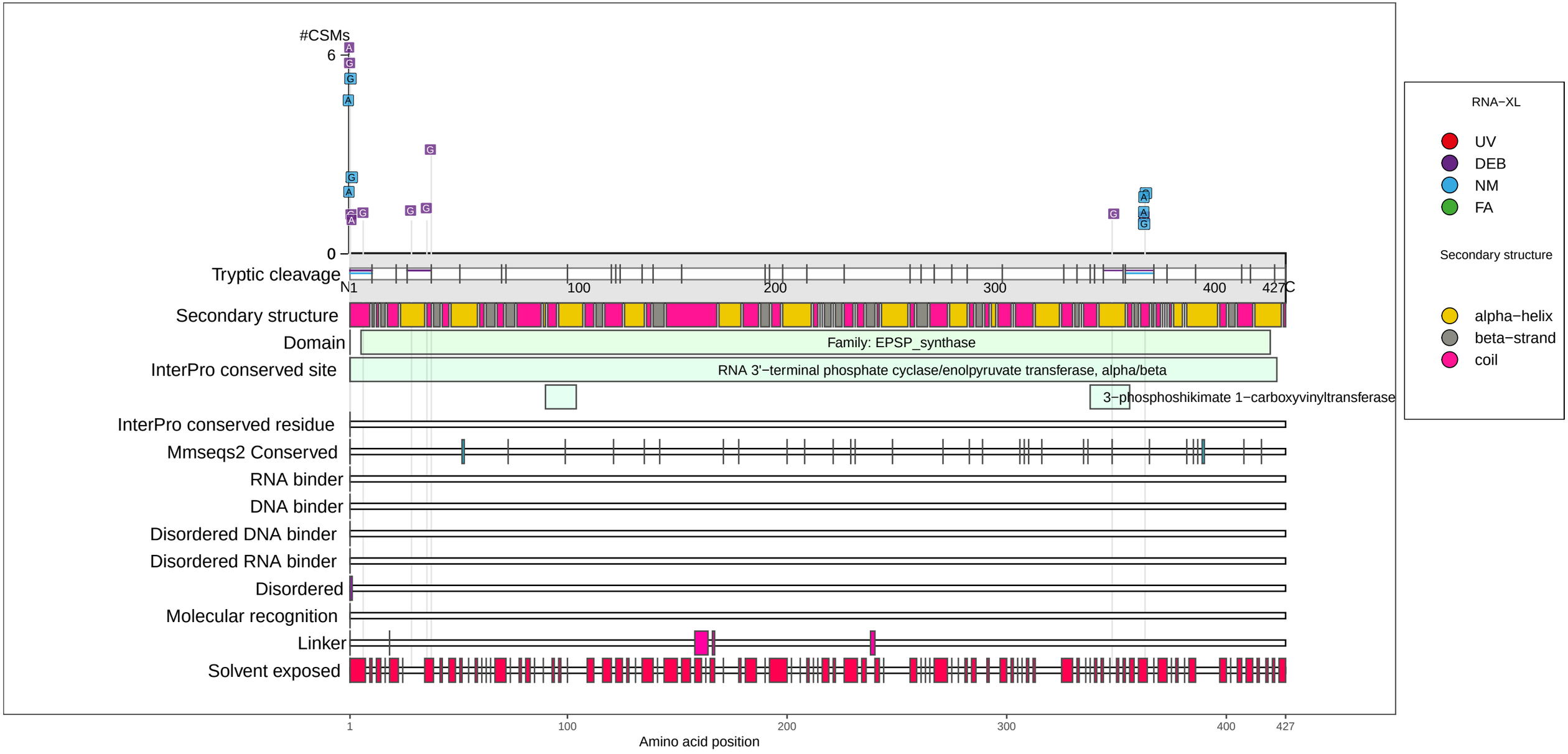
− RNA functions: not annotated



P0A6D3
AROA_ECOLI 3−phosphoshikimate 1−carboxyvinyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 2.04 (Q 62)
PAXdb E.coli [ppm]: 2.23 (Q 78)

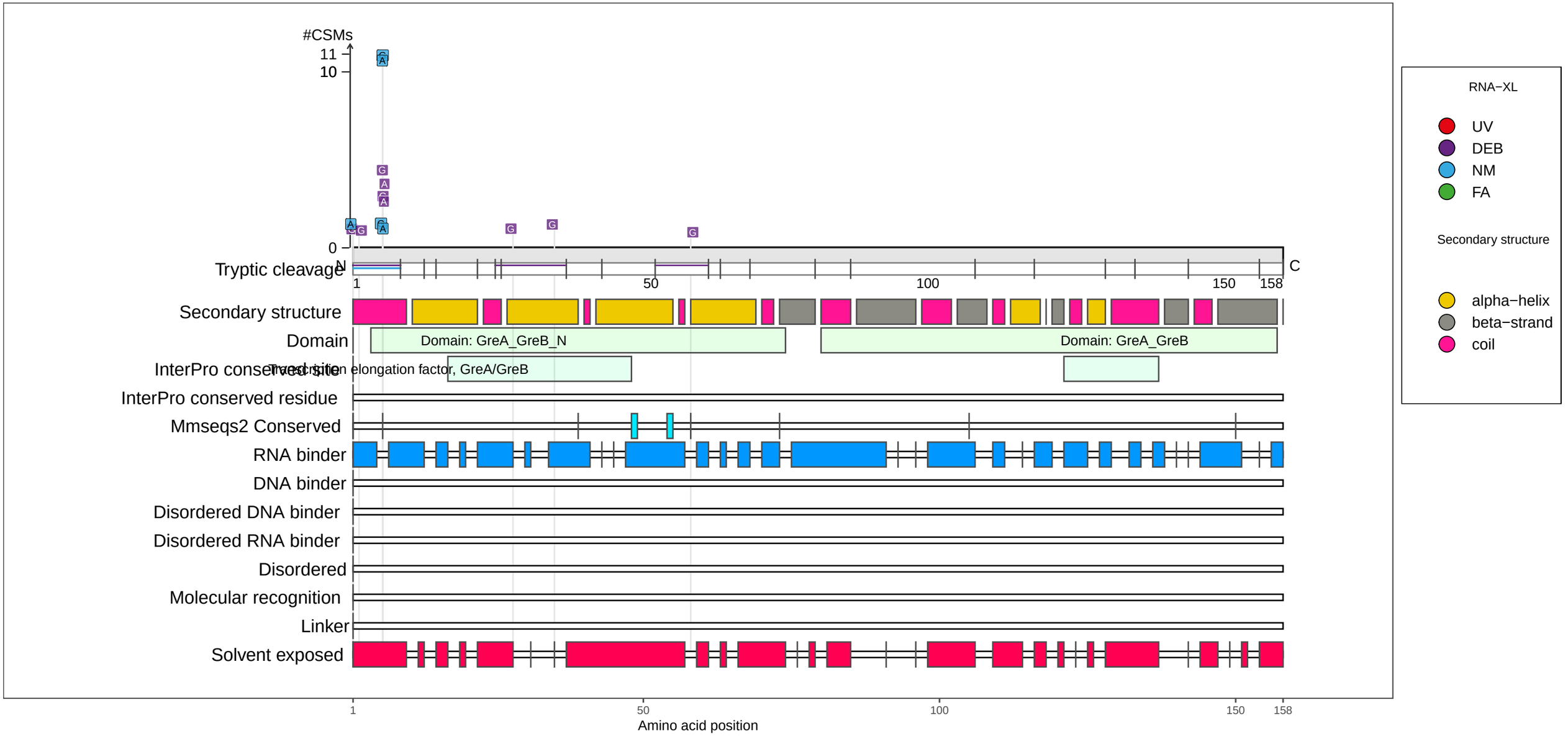
− RNA functions: not annotated



P0A6W5
GREA_ECOLI Transcription elongation factor GreA

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 3.31 (Q 95)
PAXdb E.coli [ppm]: 2.85 (Q 92)

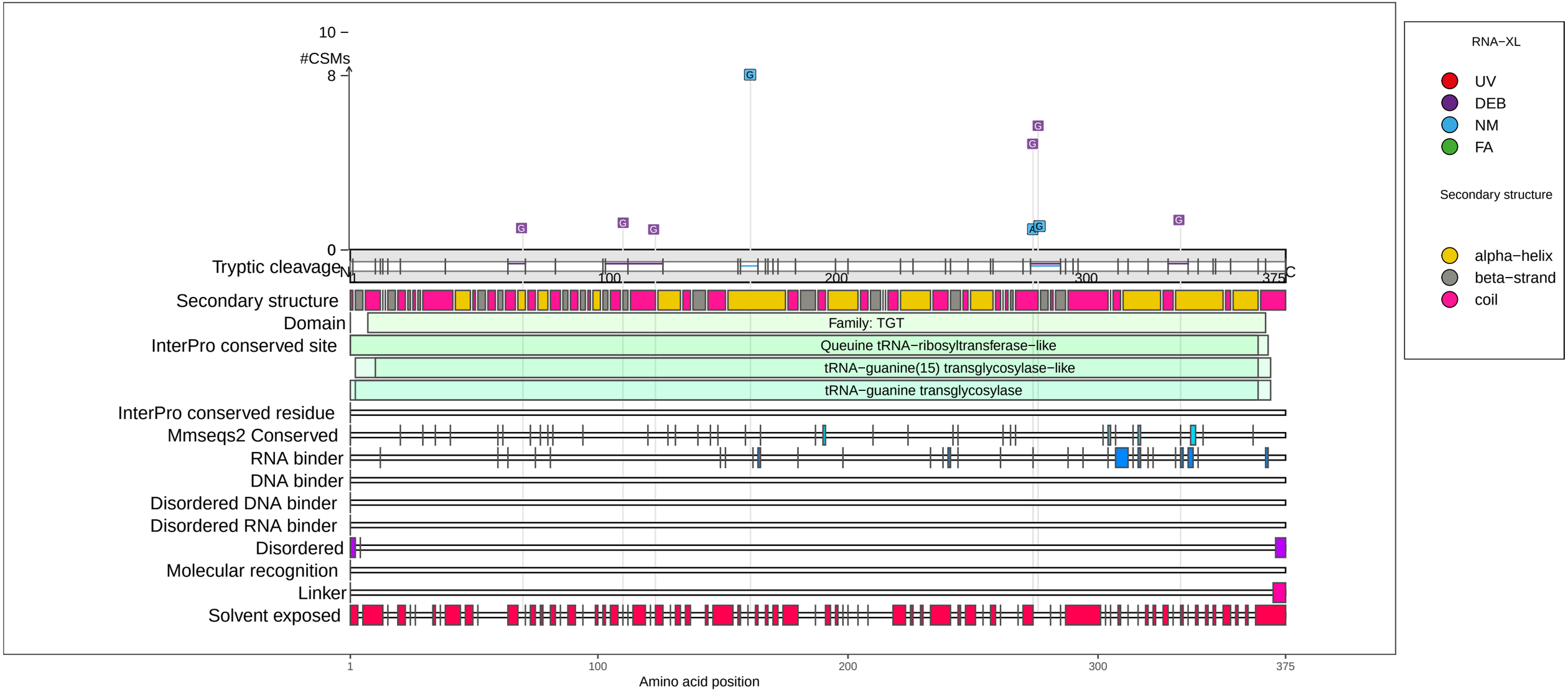
− RNA functions:
RNA biosynthetic process; RNA metabolic process; RNA polymerase binding



P0A847
TGT_ECOLI Queuine tRNA−ribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.01 (Q 58)
PAXdb K12 strain [ppm]: 2.08 (Q 63)
PAXdb E.coli [ppm]: 1.46 (Q 59)

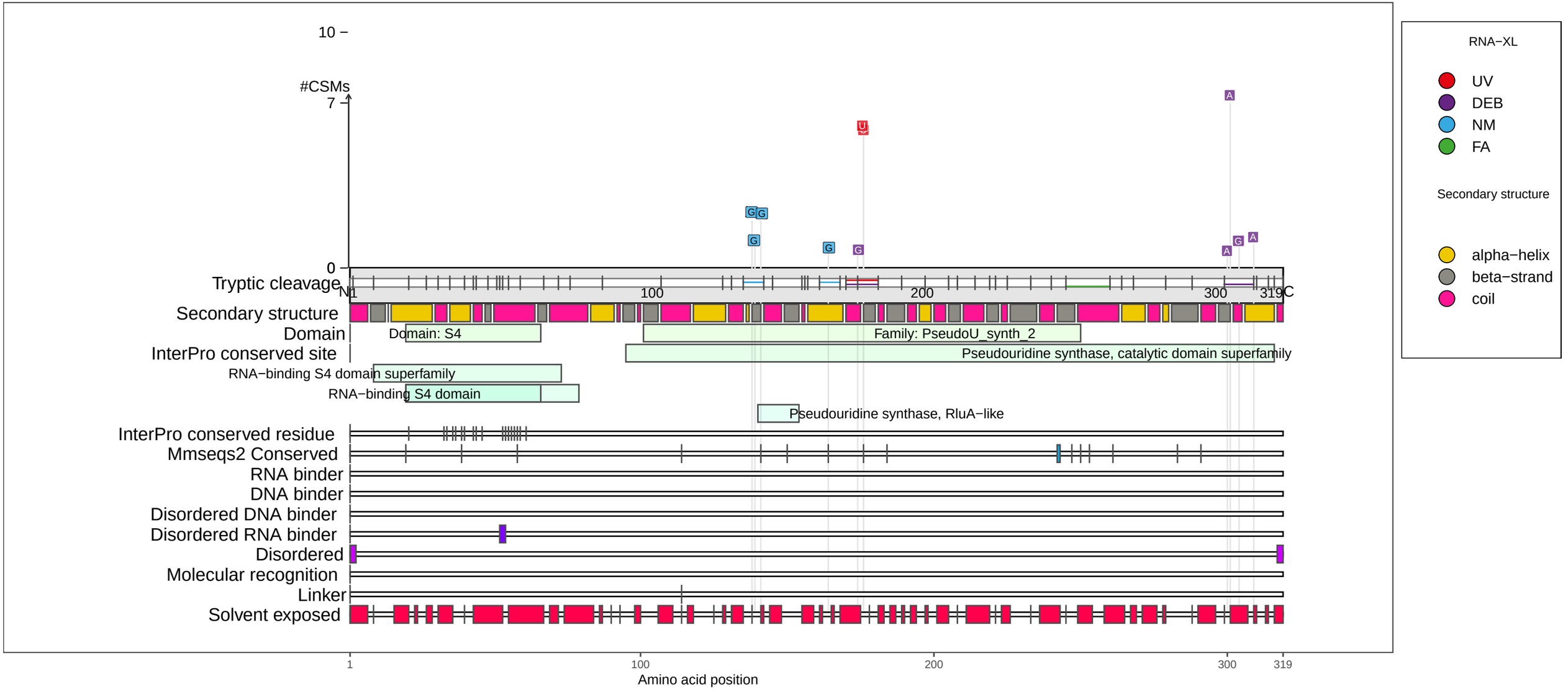
− RNA functions:
ncRNA metabolic process; ncRNA processing; Queuine tRNA−ribosyltransferase
RNA metabolic process; RNA modification; RNA processing; tRNA metabolic process; tRNA modification
tRNA processing; tRNA wobble base modification; tRNA wobble guanine modification
tRNA−guanine transglycosylation



P0AA39
RLUC_ECOLI Ribosomal large subunit pseudouridine synthase C

− Abundance:
tryptic [log10 Intensity]: 7.43 (Q 32)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 1.75 (Q 66)

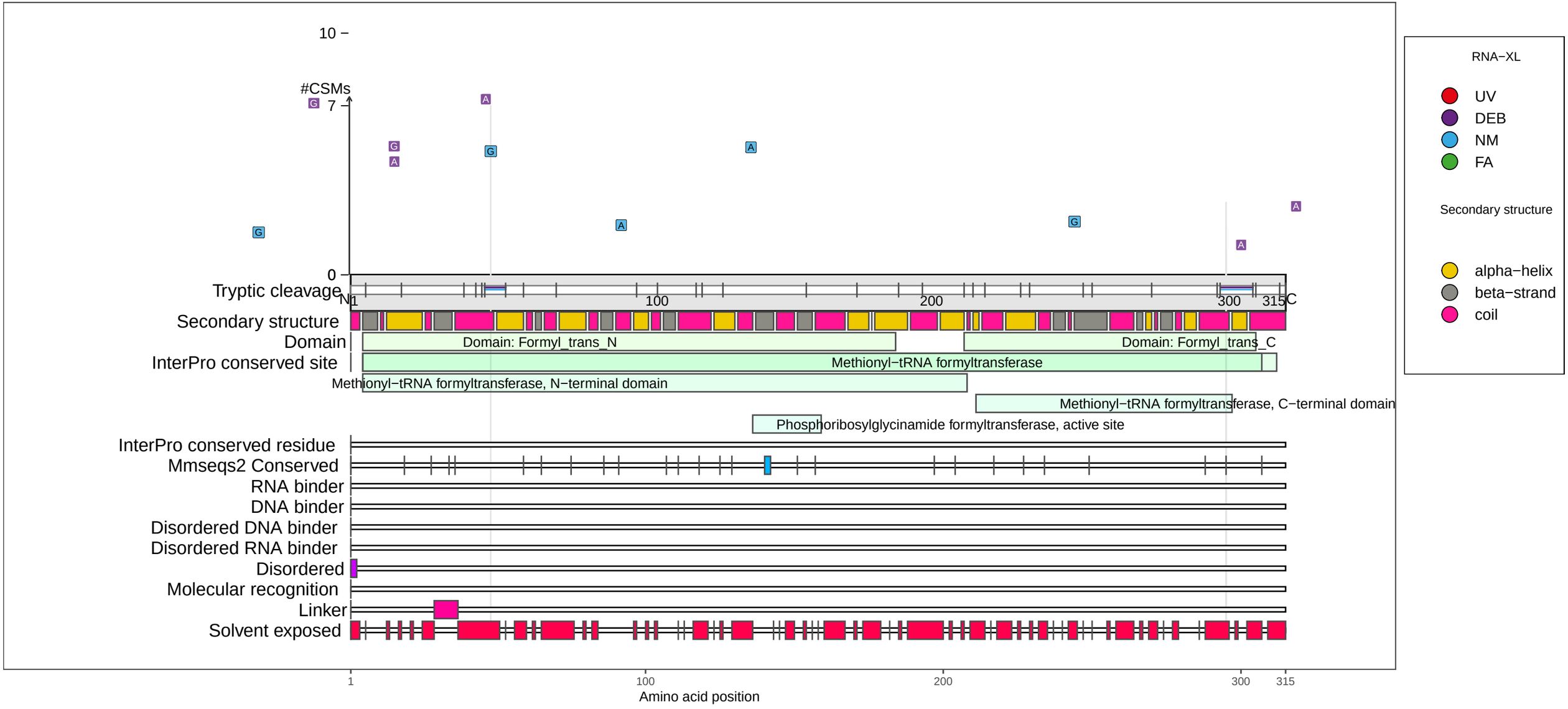
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; RNA pseudouridylate synthase; rRNA metabolic process
rRNA modification; rRNA processing; rRNA pseudouridine synthase activity
rRNA pseudouridine synthesis



P23882
FMT_ECOLI Methionyl−tRNA formyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 2.28 (Q 69)
PAXdb E.coli [ppm]: 2.34 (Q 82)

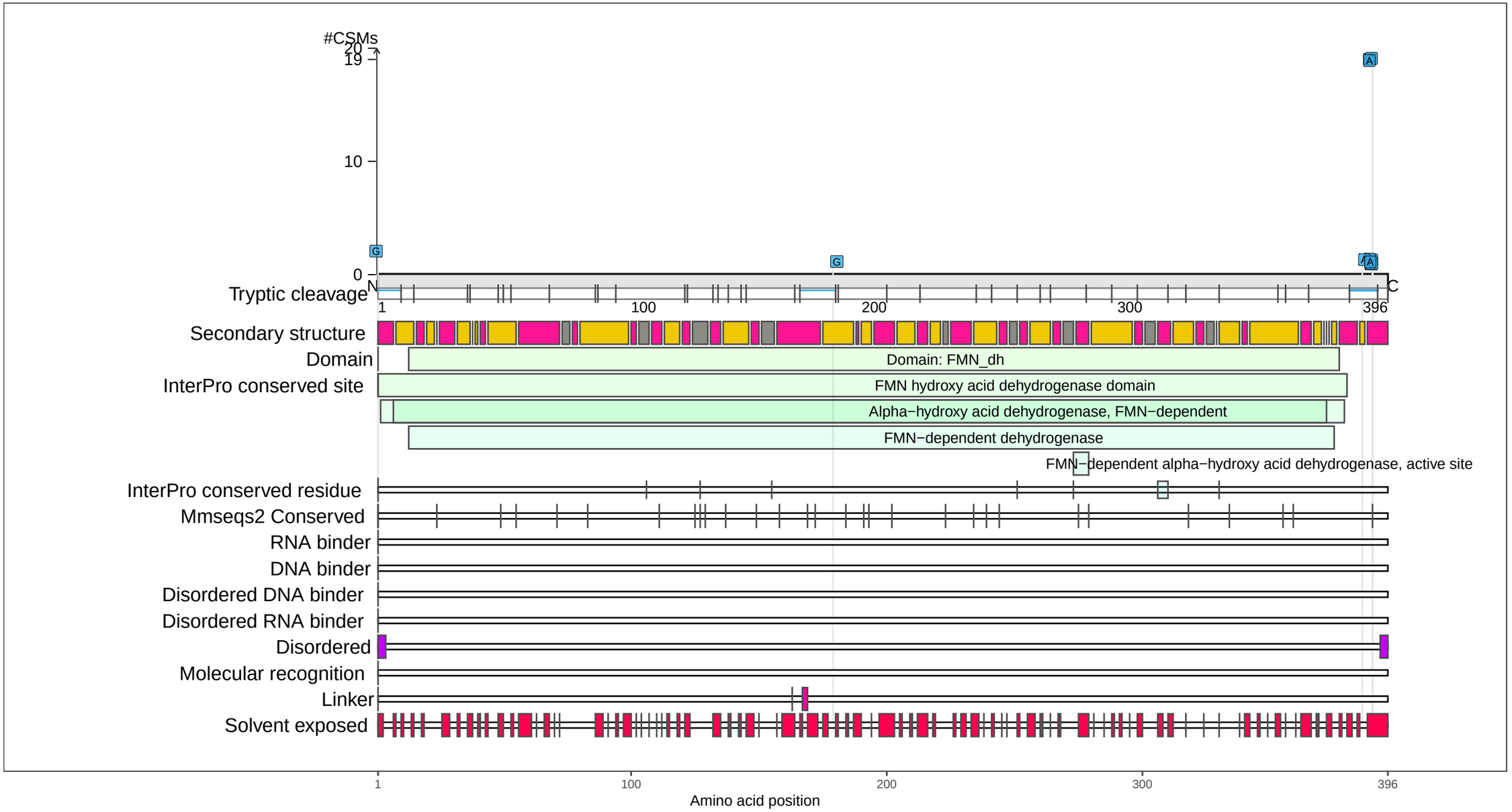
− RNA functions:
charged−tRNA amino acid modification; methionyl−tRNA formyltransferase activity
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing



P33232
LLDD_ECOLI L−lactate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 1.21 (Q 21)
PAXdb E.coli [ppm]: 1.91 (Q 70)

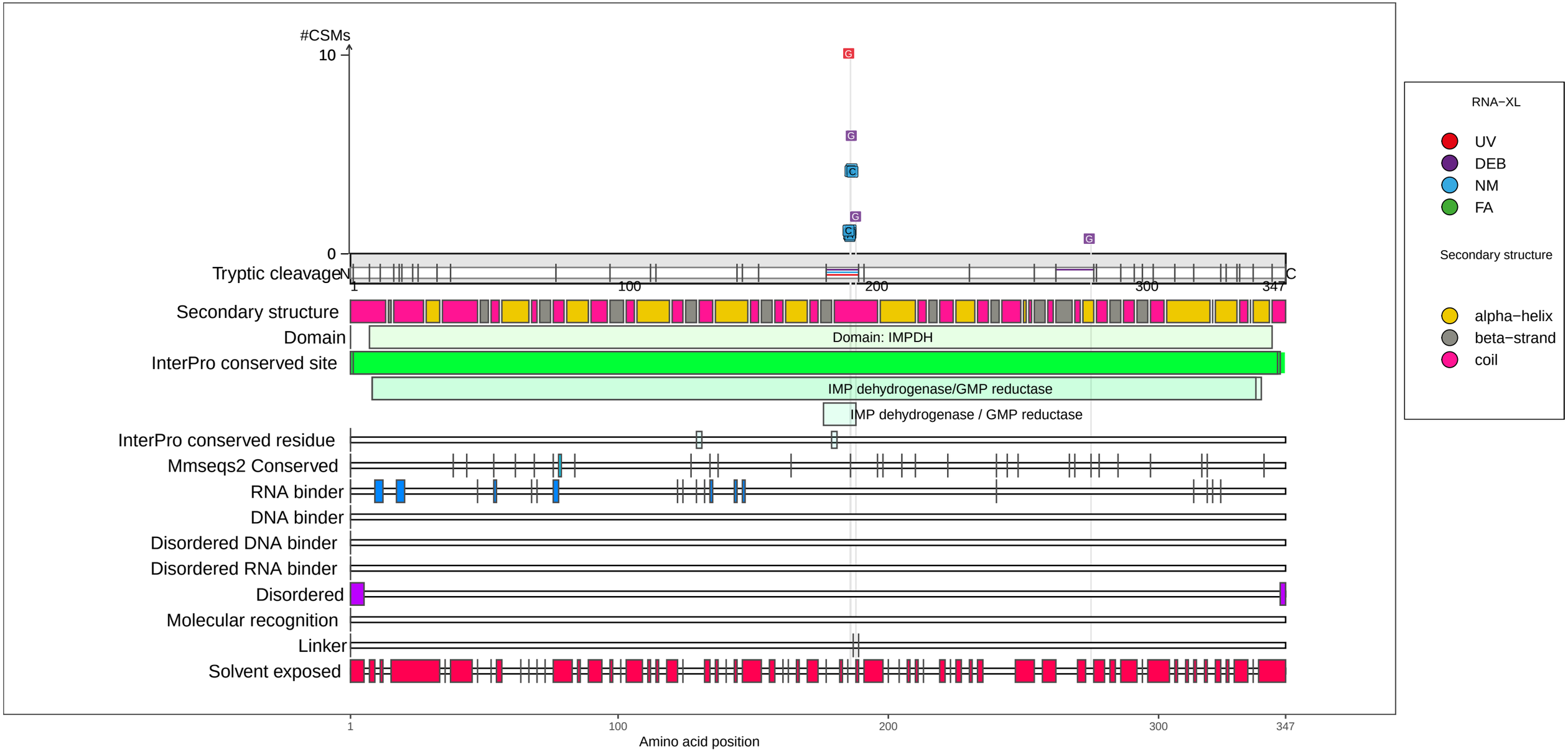
− RNA functions: not annotated



P60560
GUAC_ECOLI GMP reductase

− Abundance:
tryptic [log10 Intensity]: 8.34 (Q 71)
PAXdb K12 strain [ppm]: 1.19 (Q 19)
PAXdb E.coli [ppm]: 2.52 (Q 86)

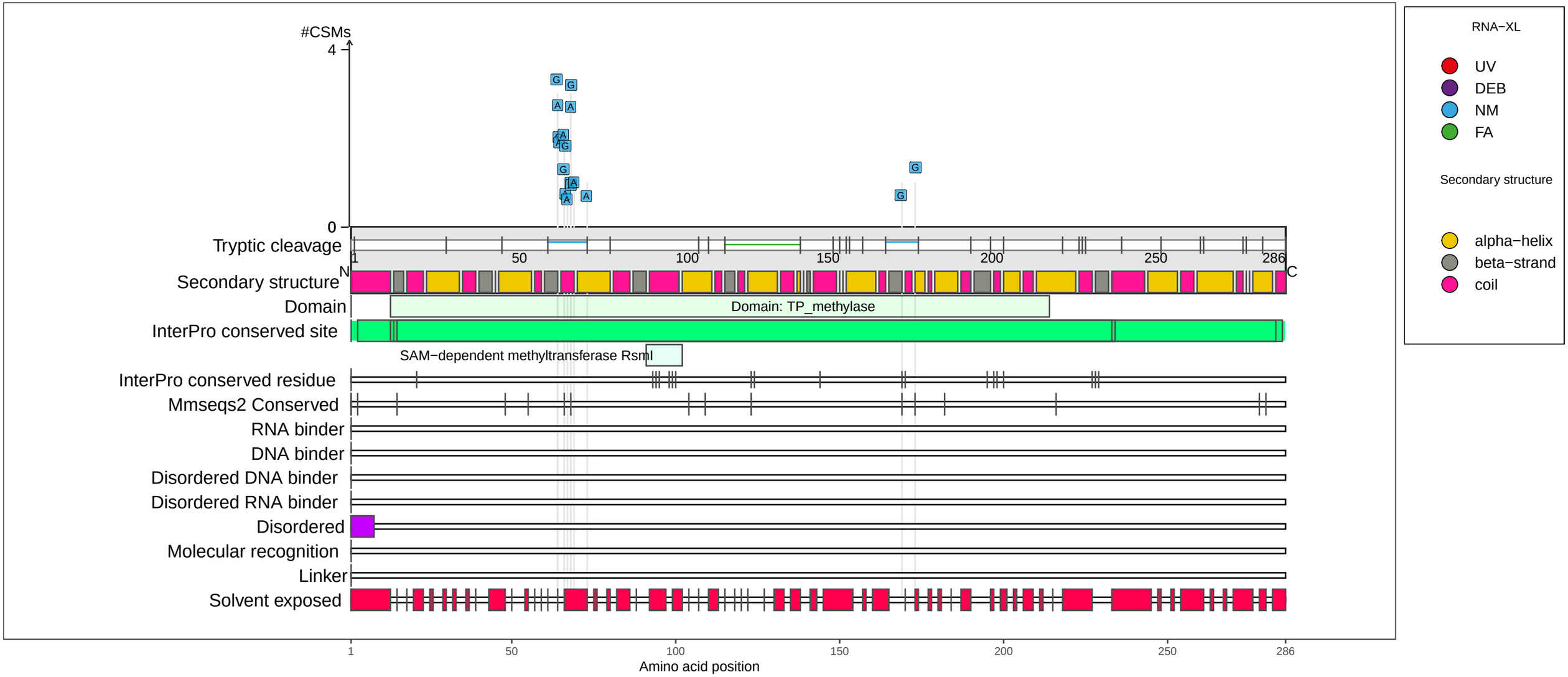
− RNA functions: not annotated



P67087
RSMI_ECOLI Ribosomal RNA small subunit methyltransferase I

− Abundance:
tryptic [log10 Intensity]: 6.89 (Q 9)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.02 (Q 73)

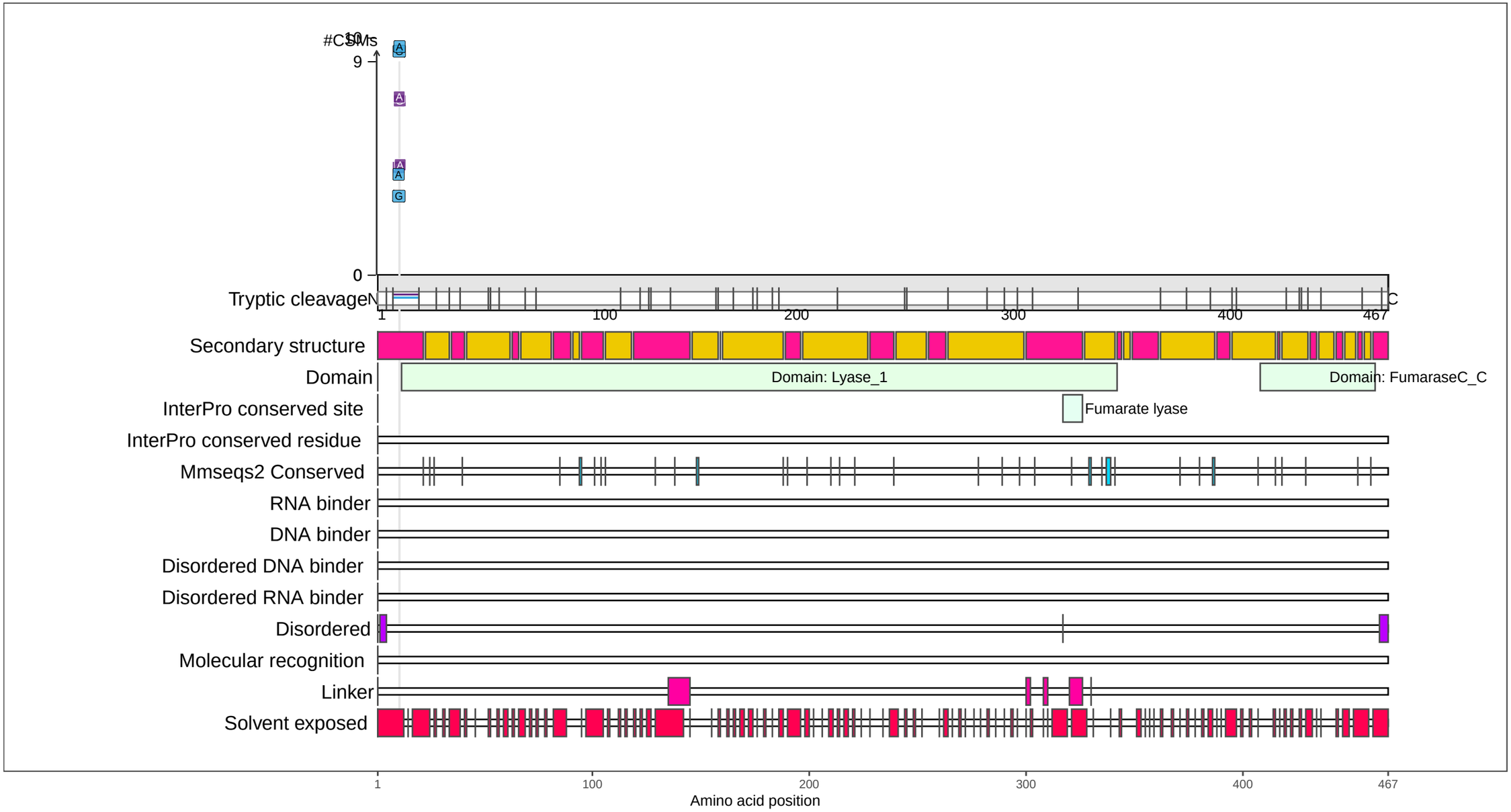
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification
RNA processing; rRNA (cytosine−2−O−)−methyltransferase activity
rRNA (cytosine) methyltransferase activity; rRNA 2−O−methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing

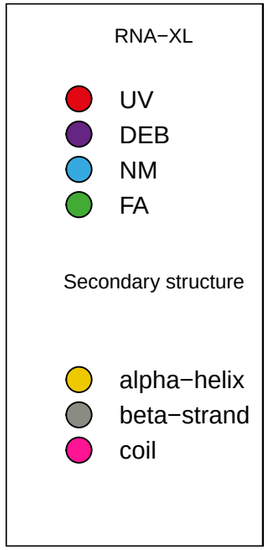


P05042
FUMC_ECOLI Fumarate hydratase class II

− Abundance:
tryptic [log10 Intensity]: 7.91 (Q 54)
PAXdb K12 strain [ppm]: 2.5 (Q 78)
PAXdb E.coli [ppm]: 2.81 (Q 92)

− RNA functions: not annotated

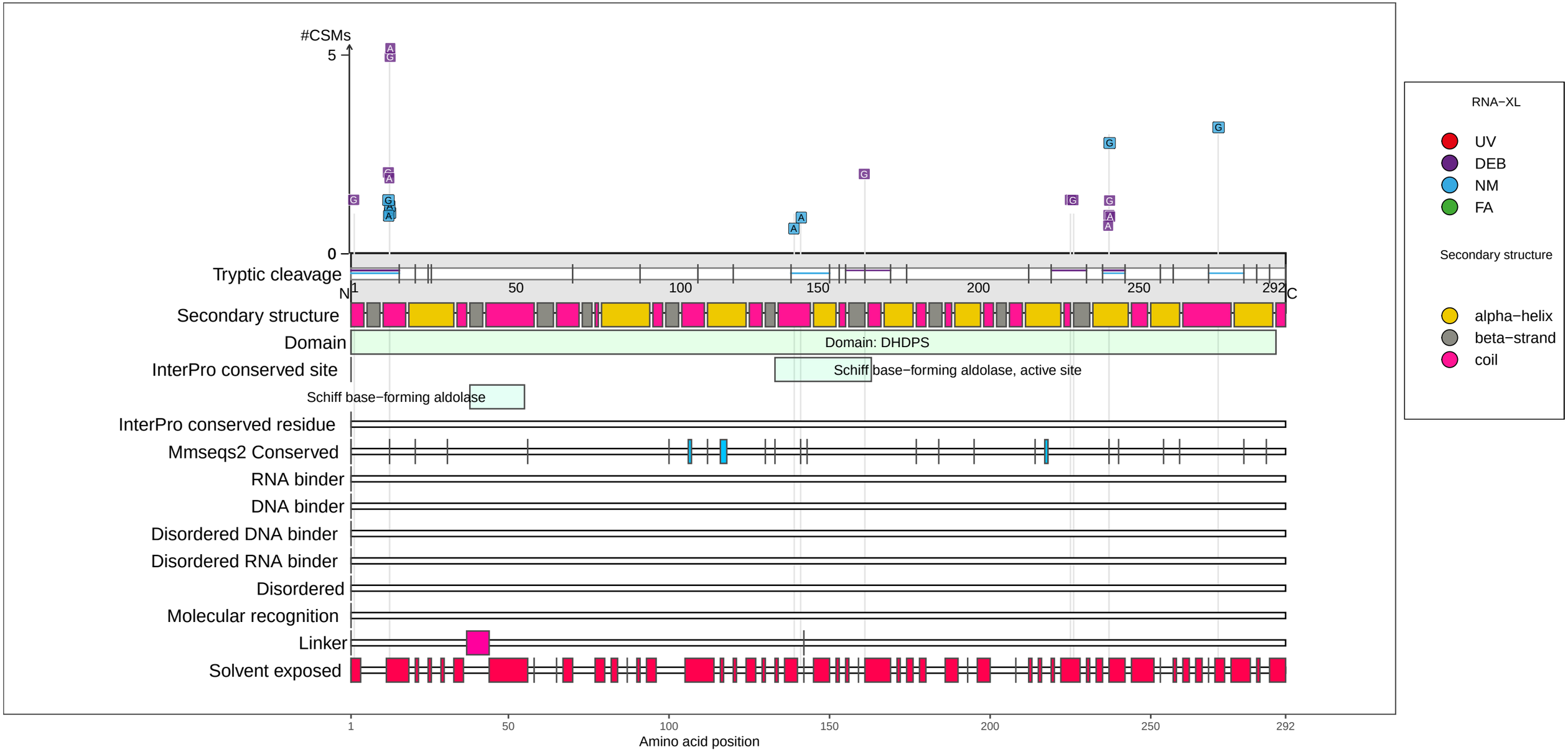




P0A6L2
DAPA_ECOLI 4−hydroxy−tetrahydrodipicolinate synthase

− Abundance:
tryptic [log10 Intensity]: 8.97 (Q 87)
PAXdb K12 strain [ppm]: 1.79 (Q 53)
PAXdb E.coli [ppm]: 2.42 (Q 83)

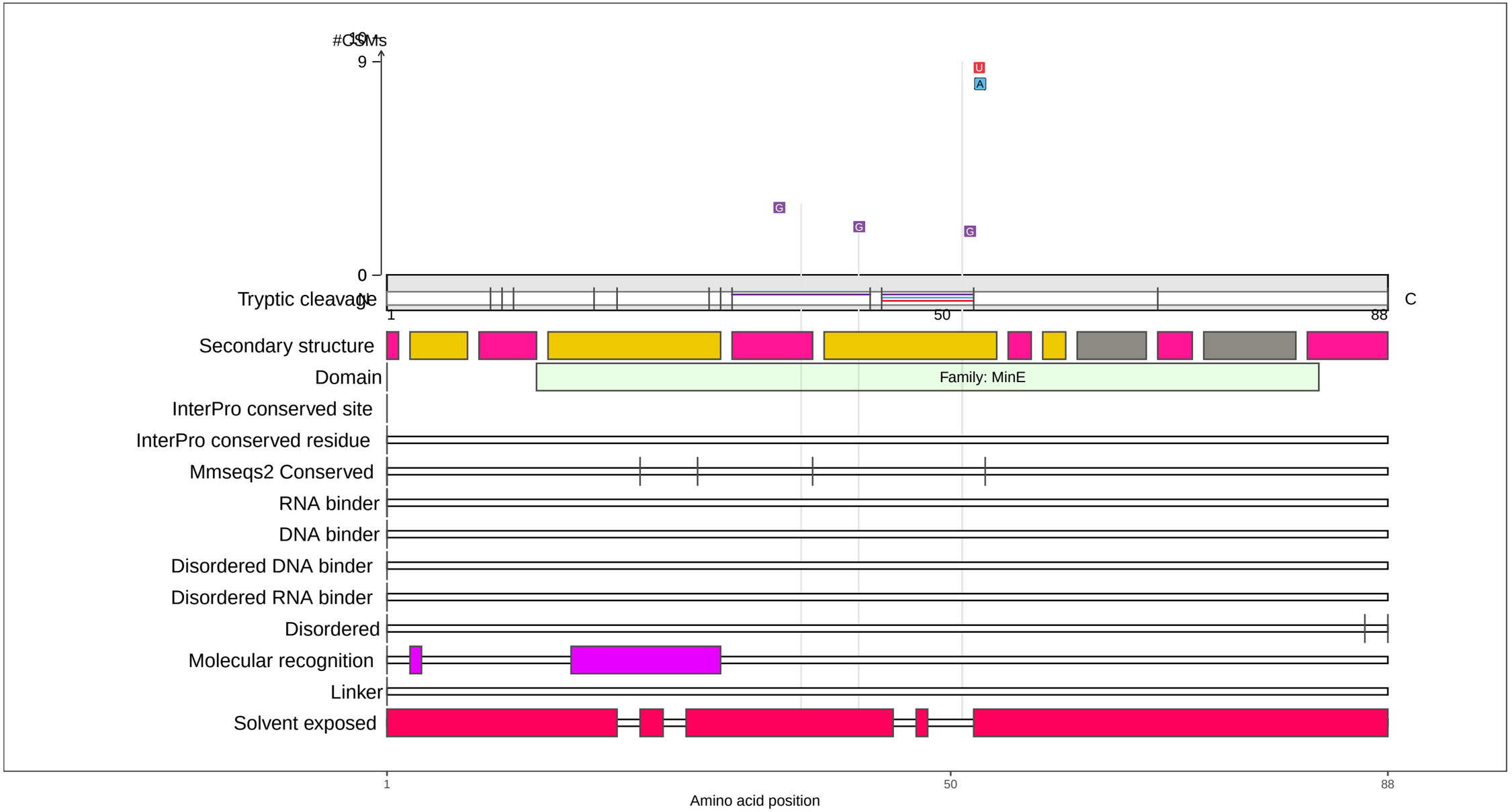
− RNA functions: not annotated

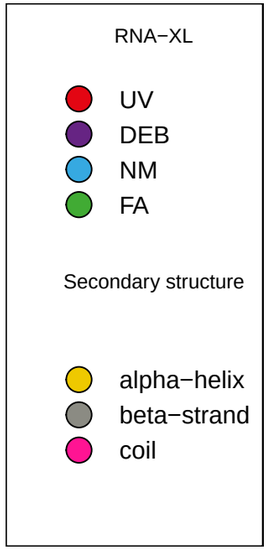


P0A734
MINE_ECOLI Cell division topological specificity factor

− Abundance:
tryptic [log10 Intensity]: 8.09 (Q 61)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.96 (Q 94)

− RNA functions: not annotated

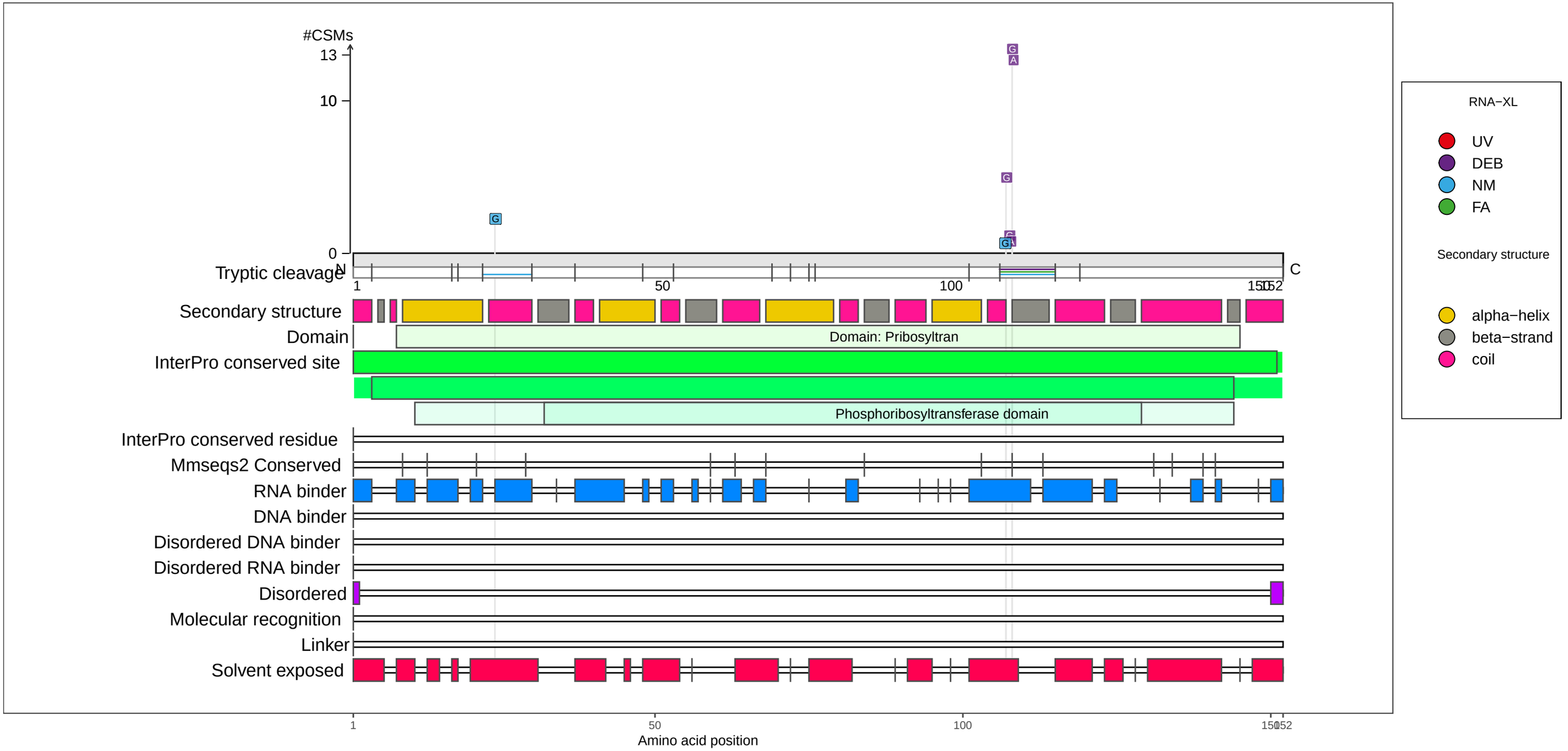




P0A9M5
XGPT_ECOLI Xanthine−guanine phosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.89 (Q 86)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: 2.11 (Q 75)

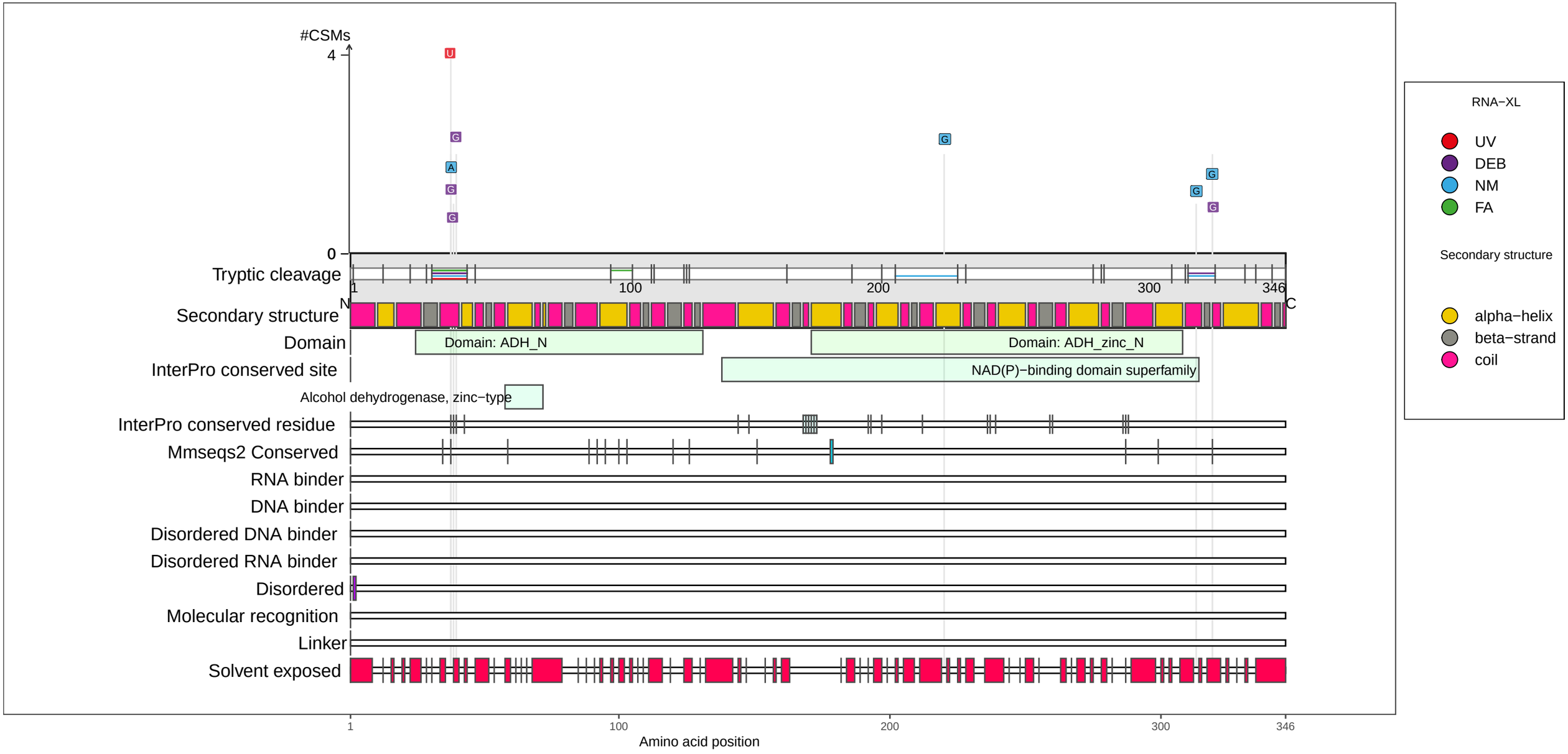
− RNA functions: not annotated



P0A9S3
GATD_ECOLI Galactitol 1−phosphate 5−dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.9 (Q 86)
PAXdb K12 strain [ppm]: 1.92 (Q 58)
PAXdb E.coli [ppm]: 2.81 (Q 92)

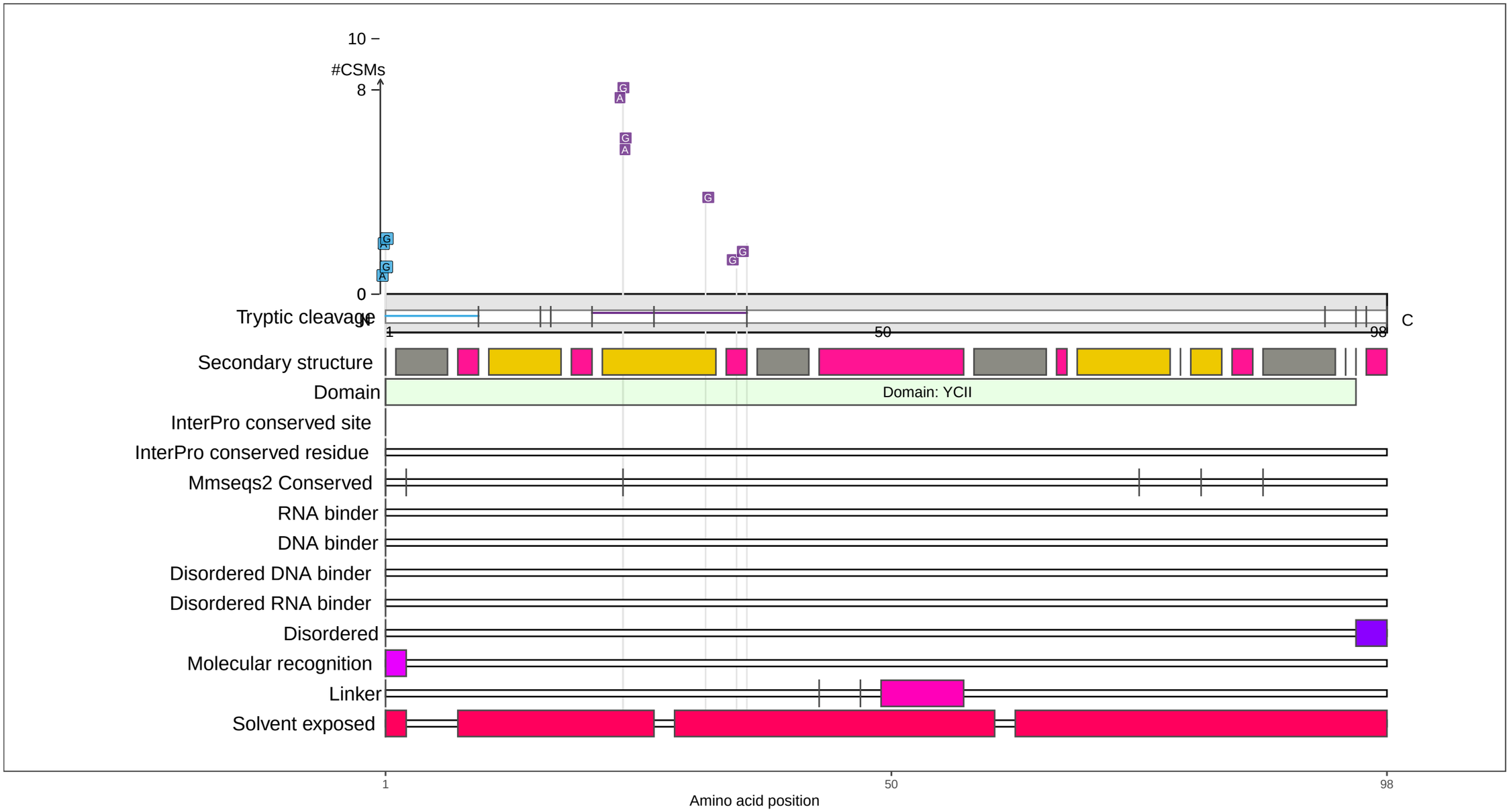
− RNA functions: not annotated

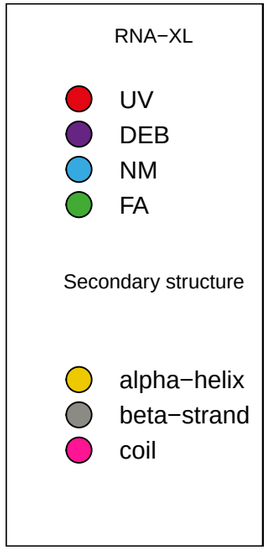


P0AB55
YCII_ECOLI Protein YciI

− Abundance:
tryptic [log10 Intensity]: 7.75 (Q 47)
PAXdb K12 strain [ppm]: 3.91 (Q 100)
PAXdb E.coli [ppm]: 2.97 (Q 94)

− RNA functions: not annotated

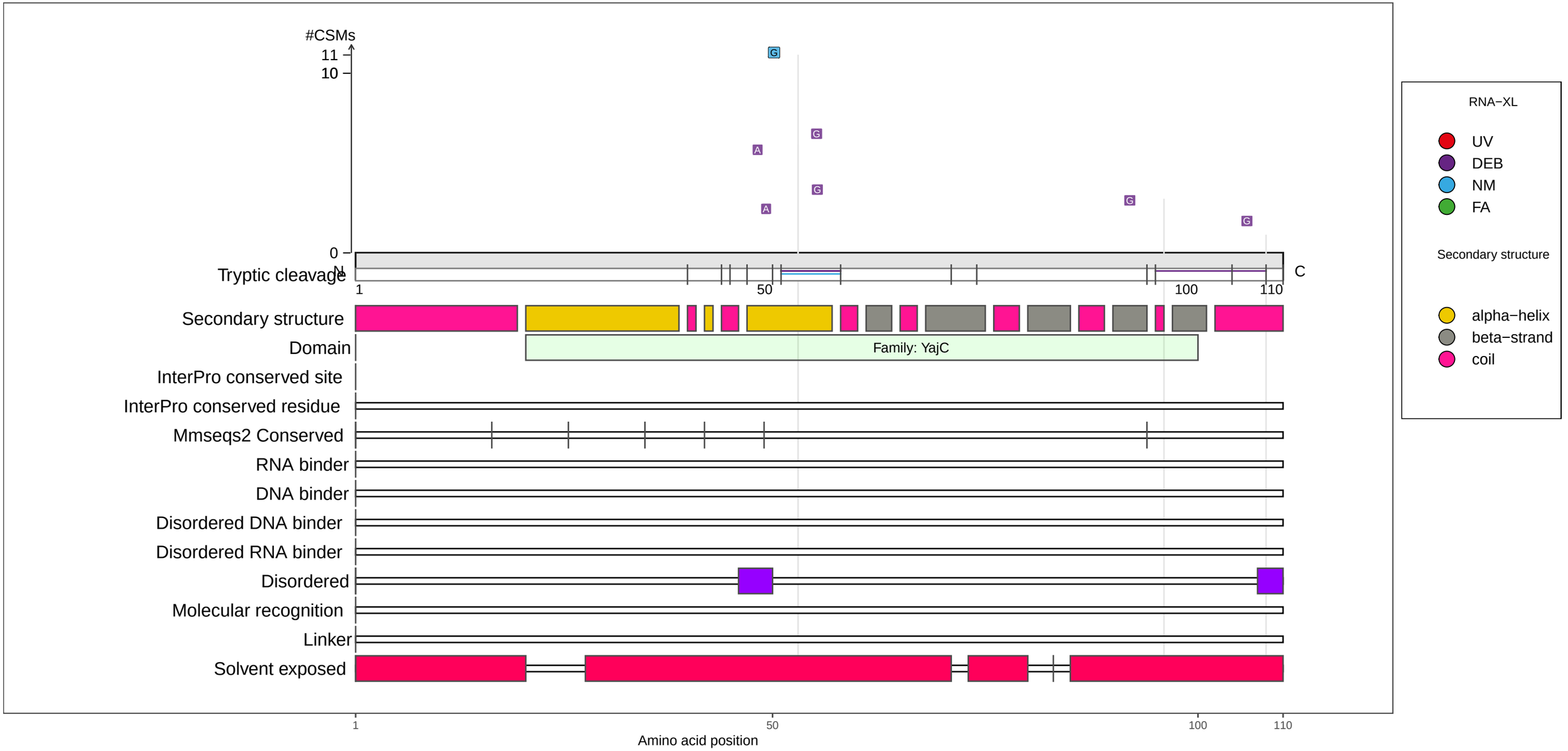




P0ADZ7
YAJC_ECOLI Sec translocon accessory complex subunit YajC

− Abundance:
tryptic [log10 Intensity]: 9.23 (Q 93)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 3.58 (Q 99)

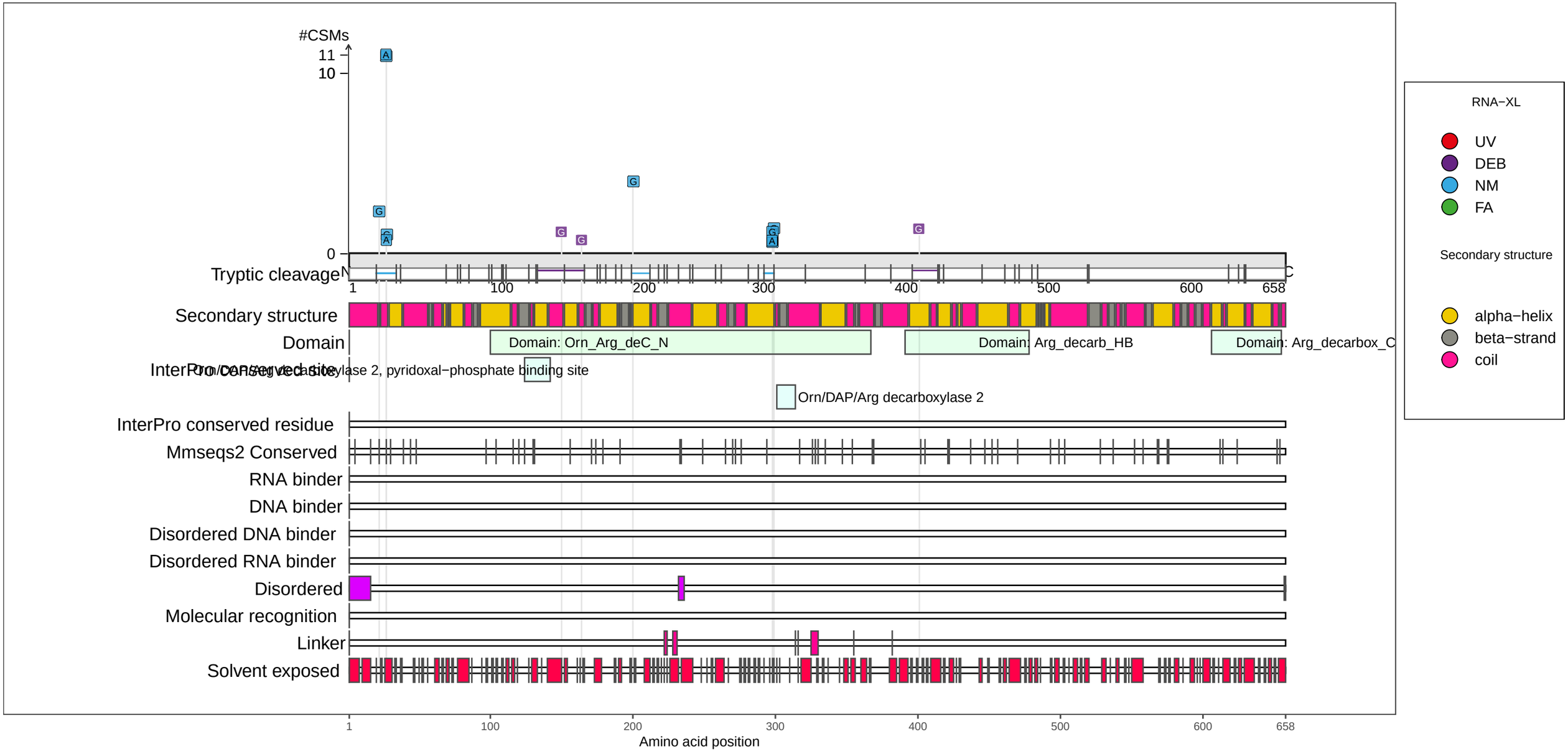
− RNA functions: not annotated



P21170
SPEA_ECOLI Biosynthetic arginine decarboxylase

− Abundance:
tryptic [log10 Intensity]: 8.9 (Q 86)
PAXdb K12 strain [ppm]: 2.87 (Q 88)
PAXdb E.coli [ppm]: 2.37 (Q 82)

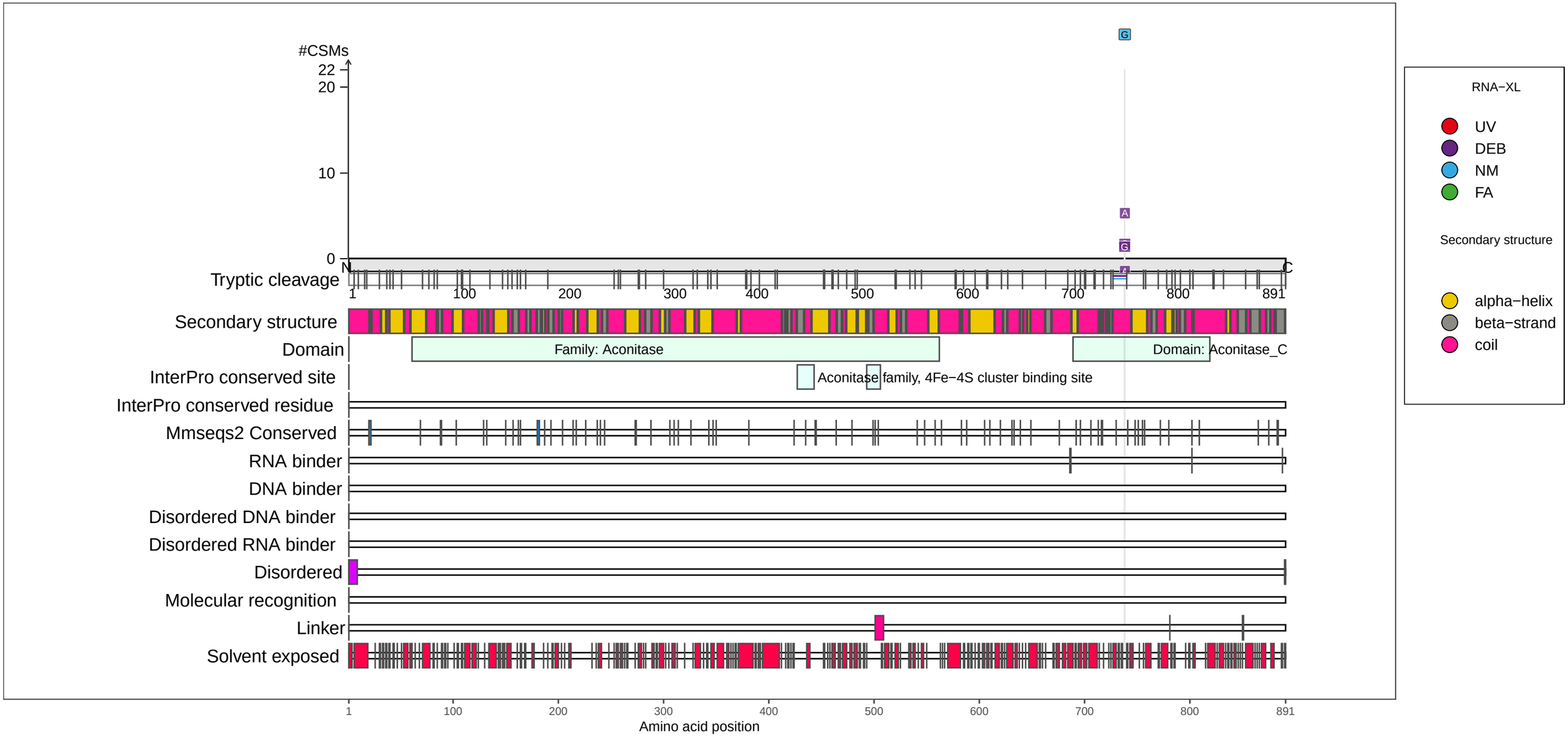
− RNA functions: not annotated



P25516
ACNA_ECOLI Aconitate hydratase A

− Abundance:
tryptic [log10 Intensity]: 8.48 (Q 75)
PAXdb K12 strain [ppm]: 2.9 (Q 88)
PAXdb E.coli [ppm]: 2.61 (Q 88)

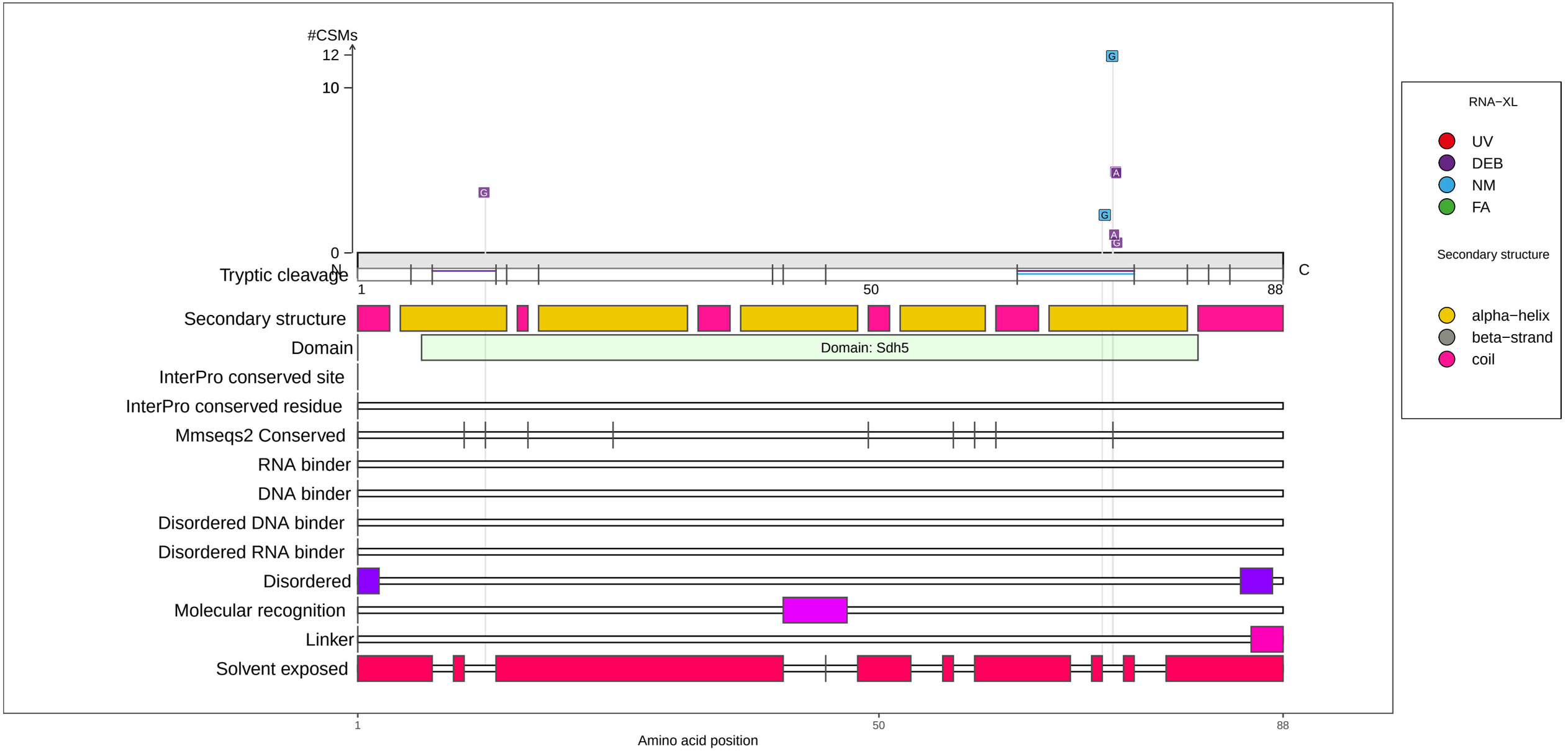
− RNA functions:
mRNA 3−UTR binding; mRNA binding; RNA binding



P64559
SDHE_ECOLI FAD assembly factor SdhE

− Abundance:
tryptic [log10 Intensity]: 8.63 (Q 79)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.88 (Q 69)

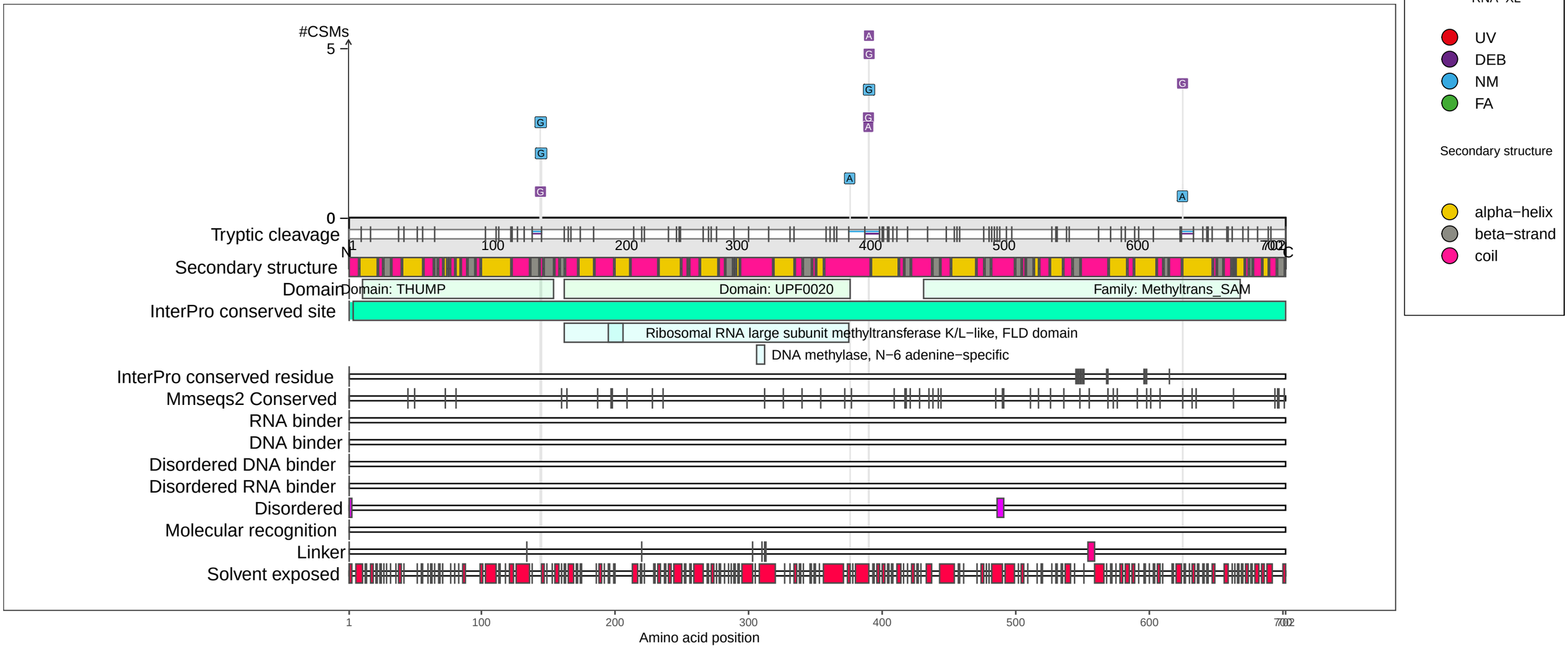
− RNA functions: not annotated



P75864
RLMKL_ECOLI Ribosomal RNA large subunit methyltransferase K/L

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 52)
PAXdb K12 strain [ppm]: 1.92 (Q 57)
PAXdb E.coli [ppm]: 1.3 (Q 54)

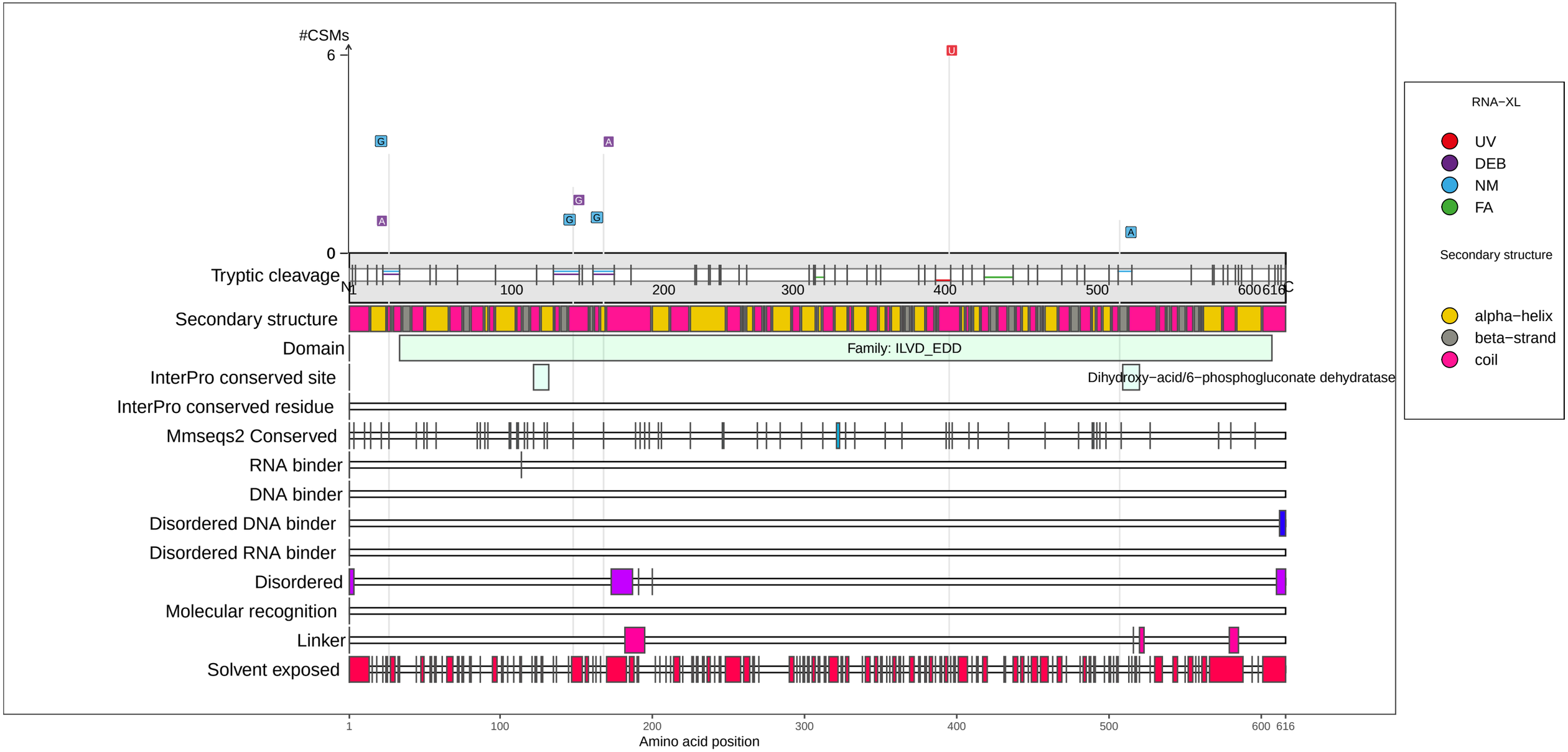
− RNA functions:
23S rRNA (guanine(2445)−N(2))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; Putative RNA methylase family UPF0020; RNA (guanine−N7)−methylation
RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (guanine−N2−)−methyltransferase activity
rRNA (guanine−N7−)−methyltransferase activity; rRNA (guanine−N7)−methylation
rRNA (guanine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P05791
ILVD_ECOLI Dihydroxy−acid dehydratase

− Abundance:
tryptic [log10 Intensity]: 8.97 (Q 87)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 1.99 (Q 72)

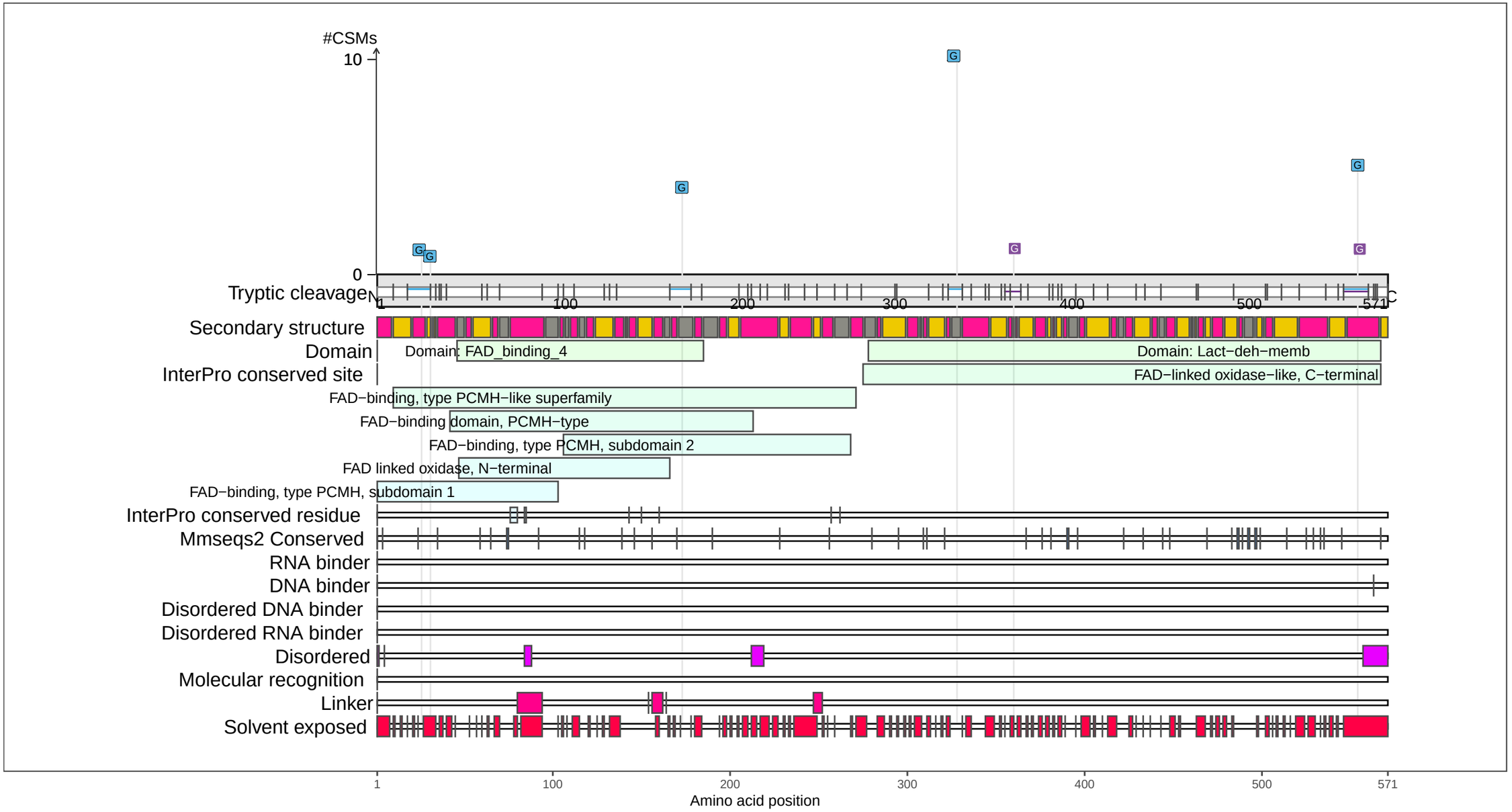
− RNA functions: not annotated



P06149
DLD_ECOLI Quinone−dependent D−lactate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.01 (Q 88)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 2.46 (Q 84)

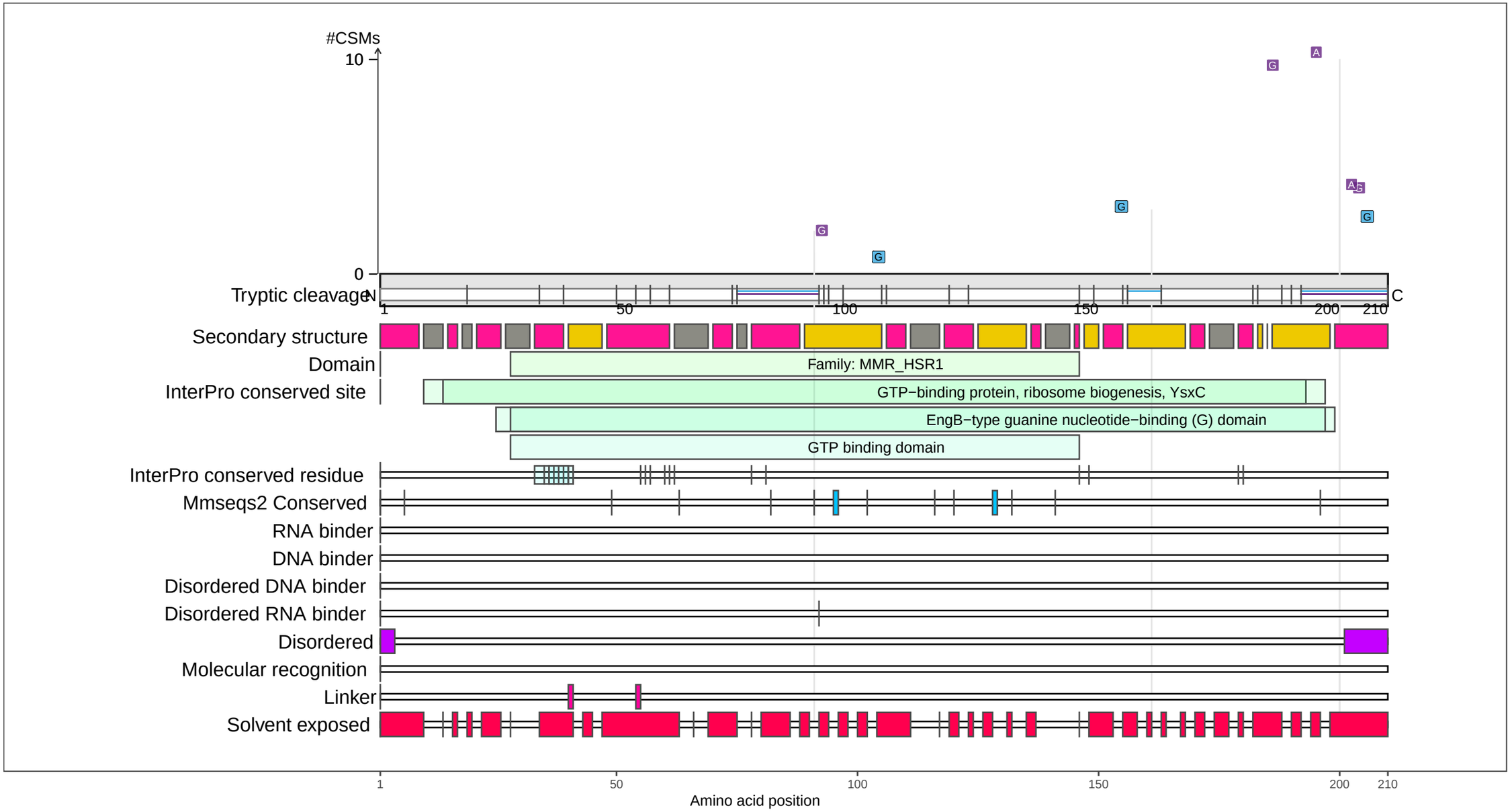
− RNA functions: not annotated



P0A6P7
ENGB_ECOLI Probable GTP−binding protein EngB

− Abundance:
tryptic [log10 Intensity]: 7.39 (Q 29)
PAXdb K12 strain [ppm]: 2.75 (Q 84)
PAXdb E.coli [ppm]: 2.2 (Q 77)

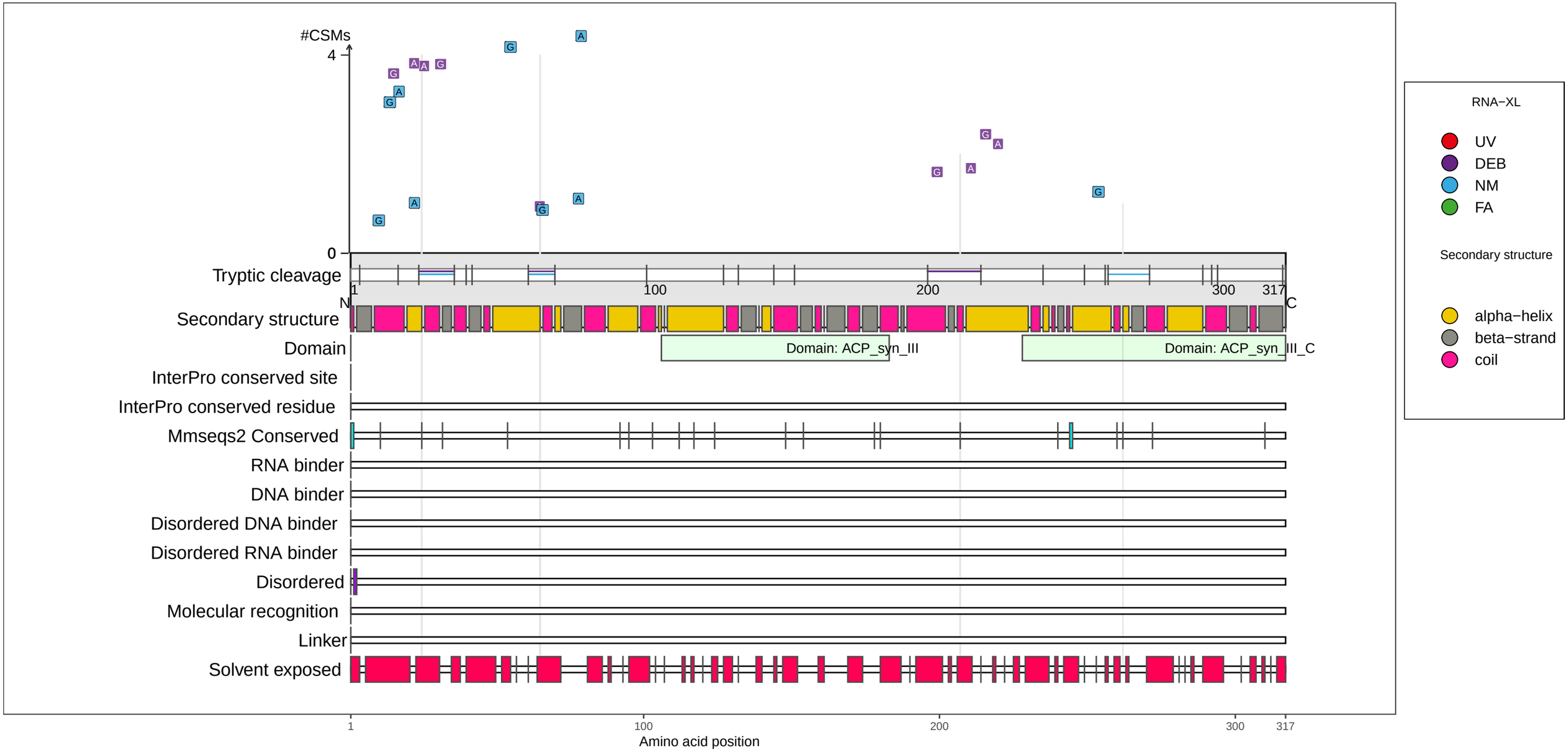
− RNA functions: not annotated



P0A6R0
FABH_ECOLI 3−oxoacyl−[acyl−carrier−protein] synthase 3

− Abundance:
tryptic [log10 Intensity]: 8.68 (Q 81)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 2.79 (Q 91)

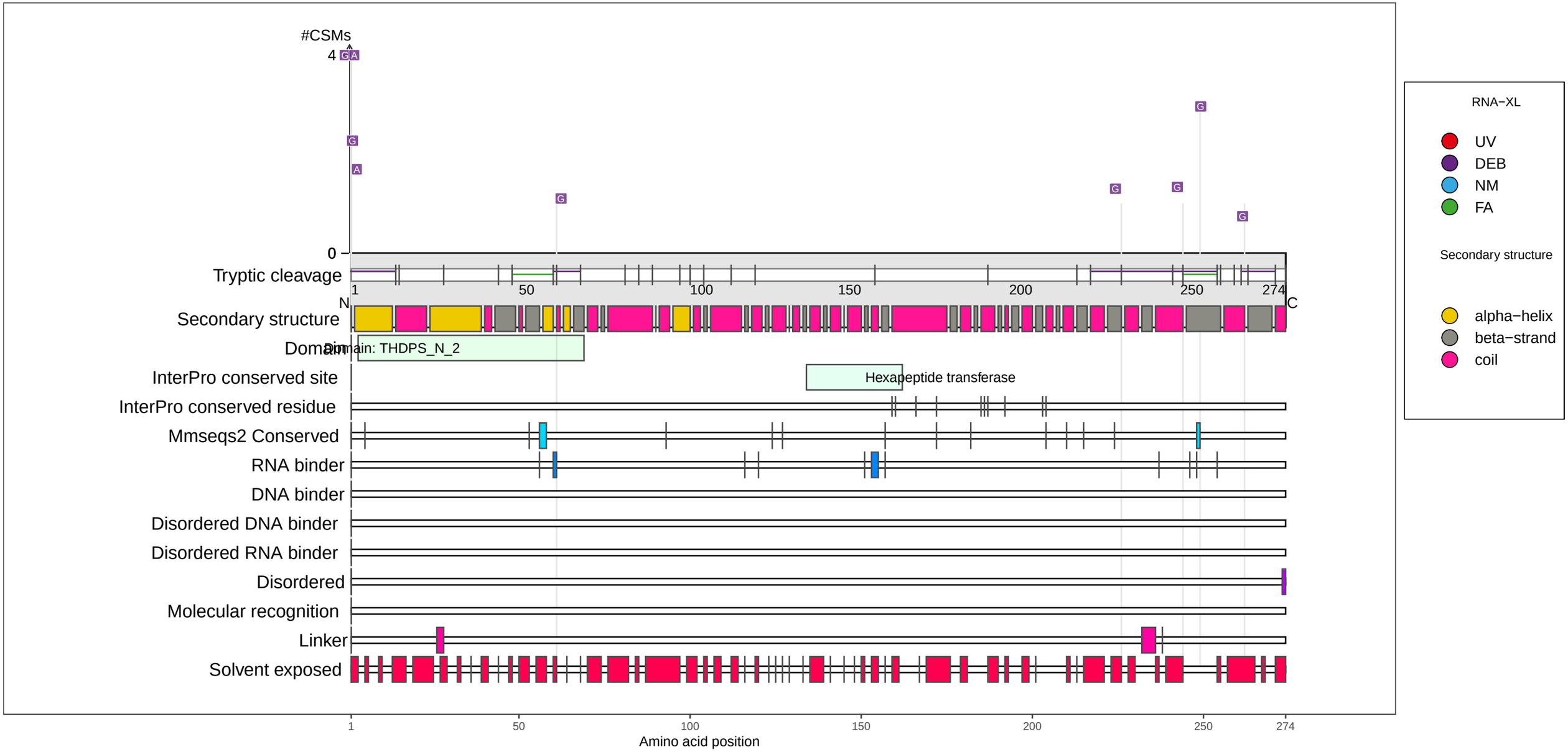
− RNA functions: not annotated



P0A9D8
DAPD_ECOLI 2,3,4,5−tetrahydropyridine−2,6−dicarboxylate N−succinyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 3.55 (Q 98)
PAXdb E.coli [ppm]: 2.99 (Q 94)

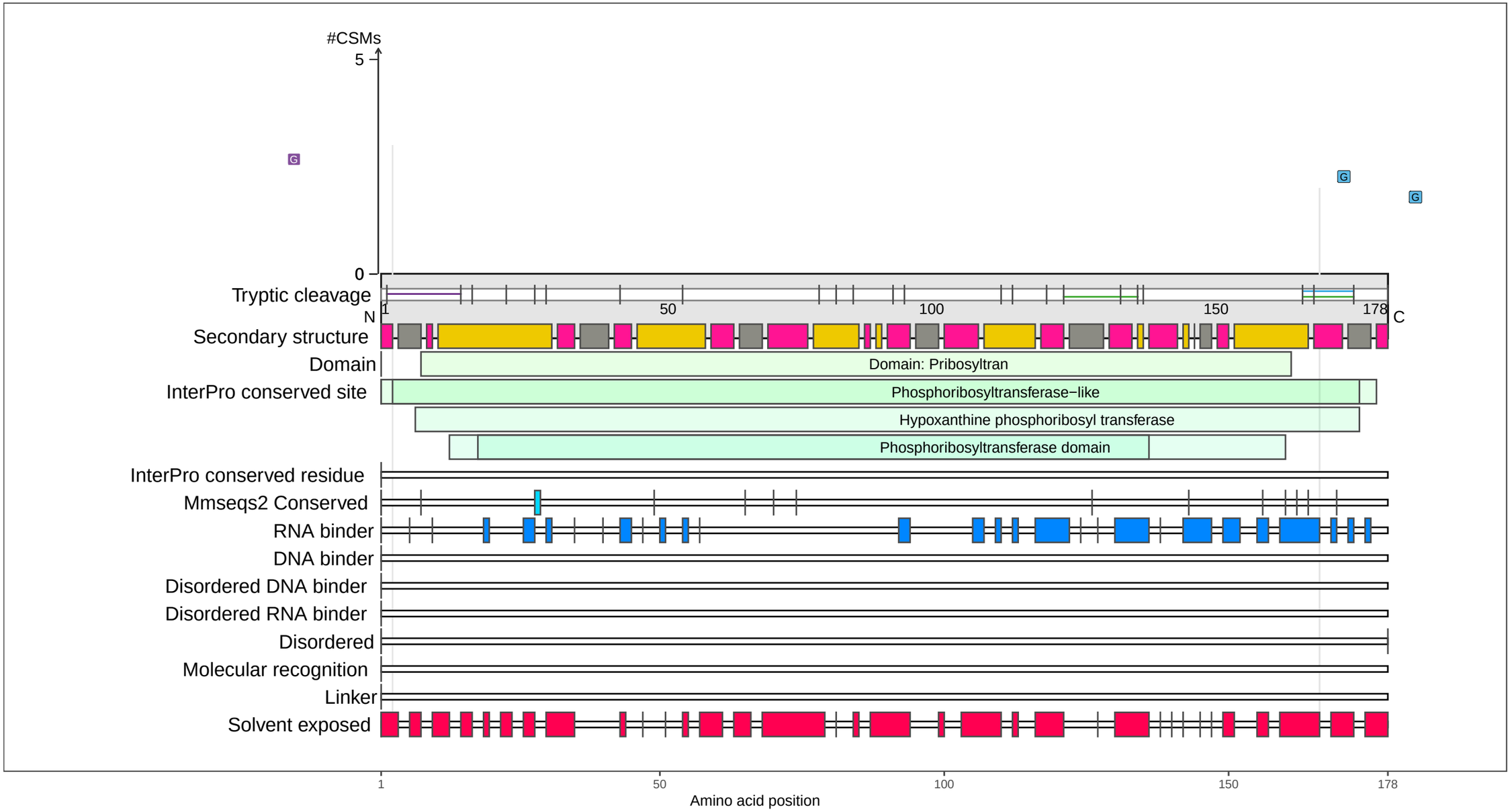
− RNA functions: not annotated



P0A9M2
HPRT_ECOLI Hypoxanthine phosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.15 (Q 92)
PAXdb K12 strain [ppm]: 3.34 (Q 96)
PAXdb E.coli [ppm]: 2.37 (Q 82)

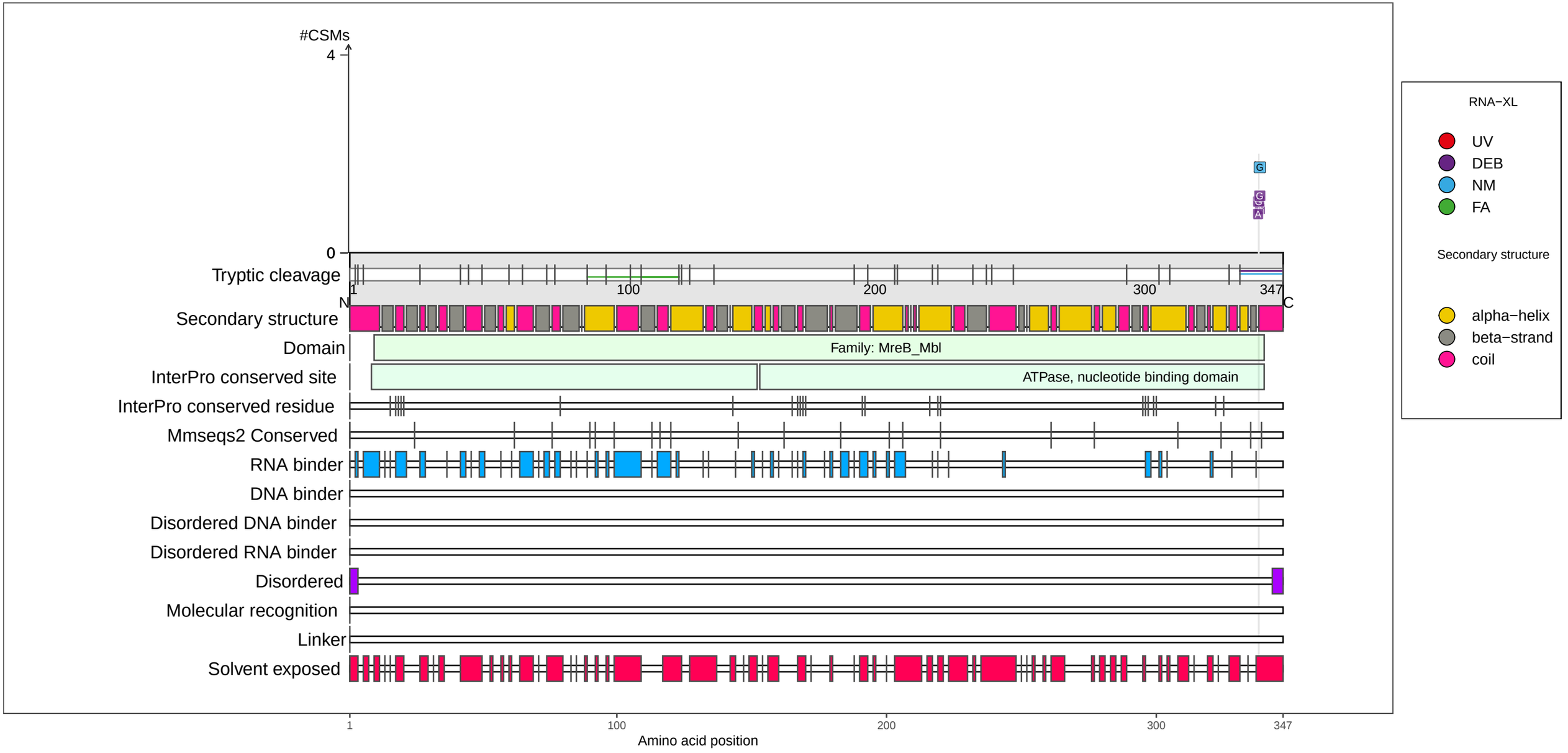
− RNA functions: not annotated



P0A9X4
MREB_ECOLI Cell shape−determining protein MreB

− Abundance:
tryptic [log10 Intensity]: 7.24 (Q 22)
PAXdb K12 strain [ppm]: 3.14 (Q 93)
PAXdb E.coli [ppm]: 2.99 (Q 95)

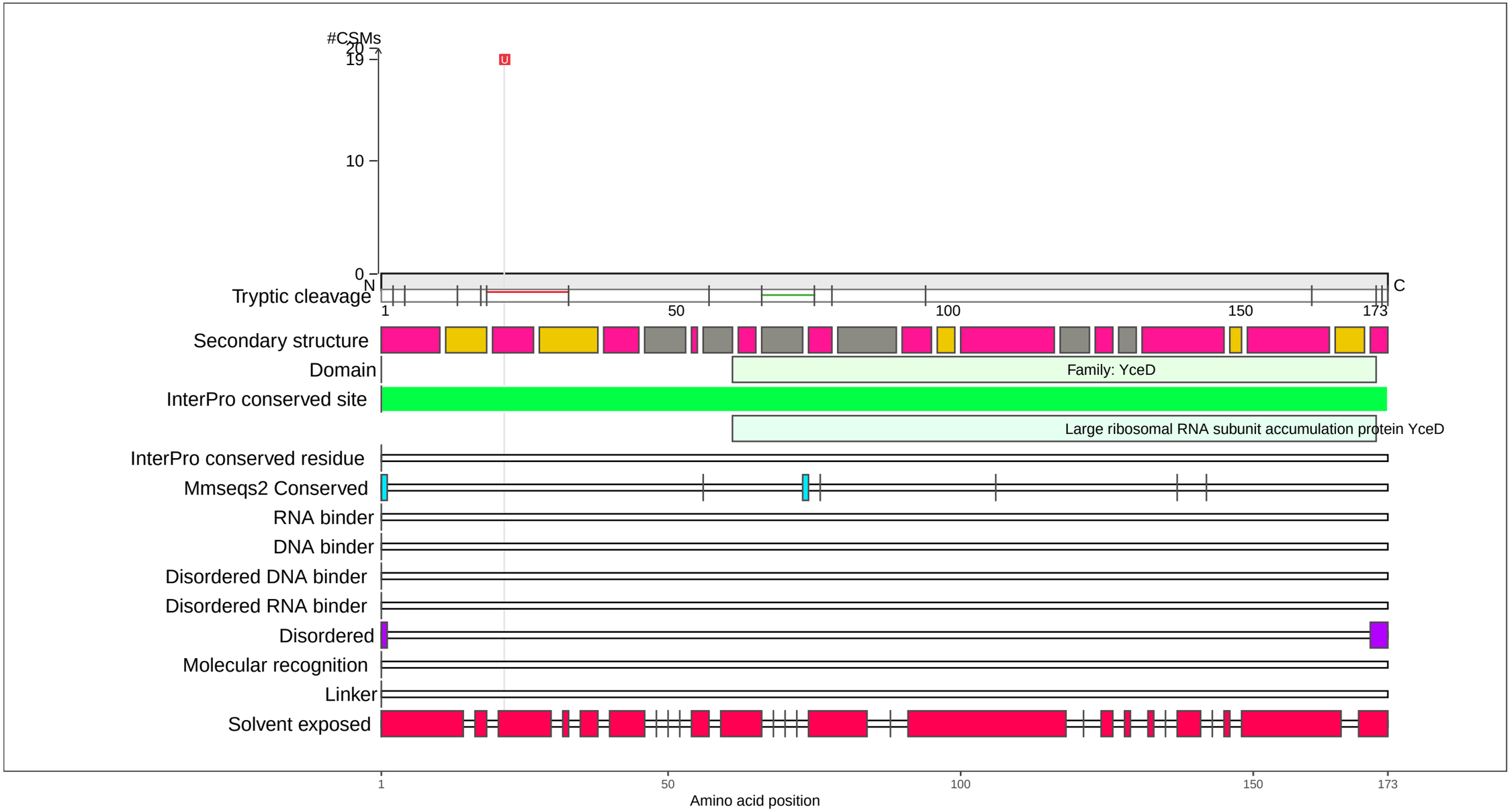
− RNA functions: not annotated



P0AB28
YCED_ECOLI Large ribosomal RNA subunit accumulation protein YceD

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: 2.16 (Q 65)
PAXdb E.coli [ppm]: 2.24 (Q 78)

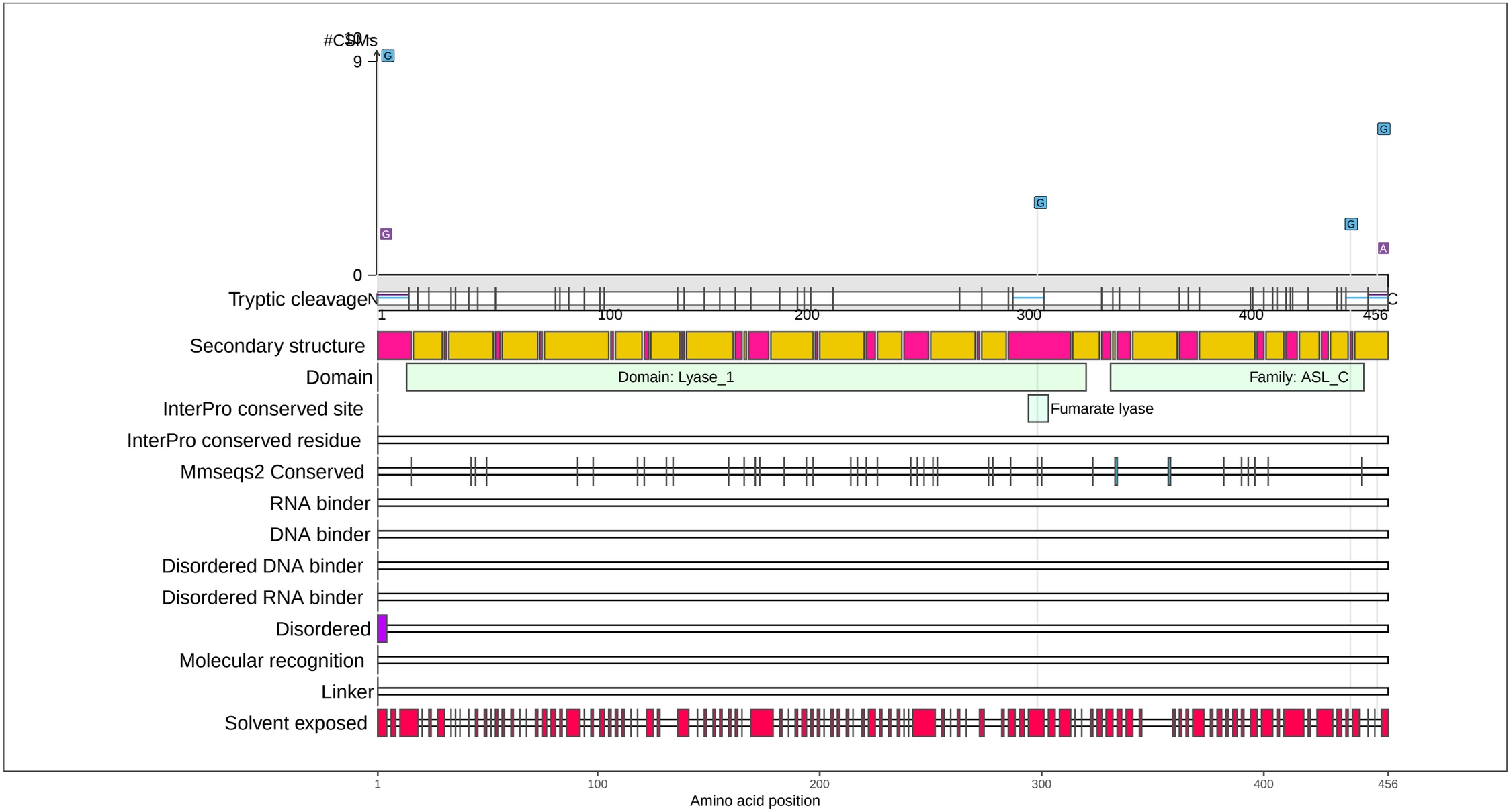
− RNA functions: not annotated



P0AB89
PUR8_ECOLI Adenylosuccinate lyase

− Abundance:
tryptic [log10 Intensity]: 8.75 (Q 82)
PAXdb K12 strain [ppm]: 3 (Q 91)
PAXdb E.coli [ppm]: 2.8 (Q 92)

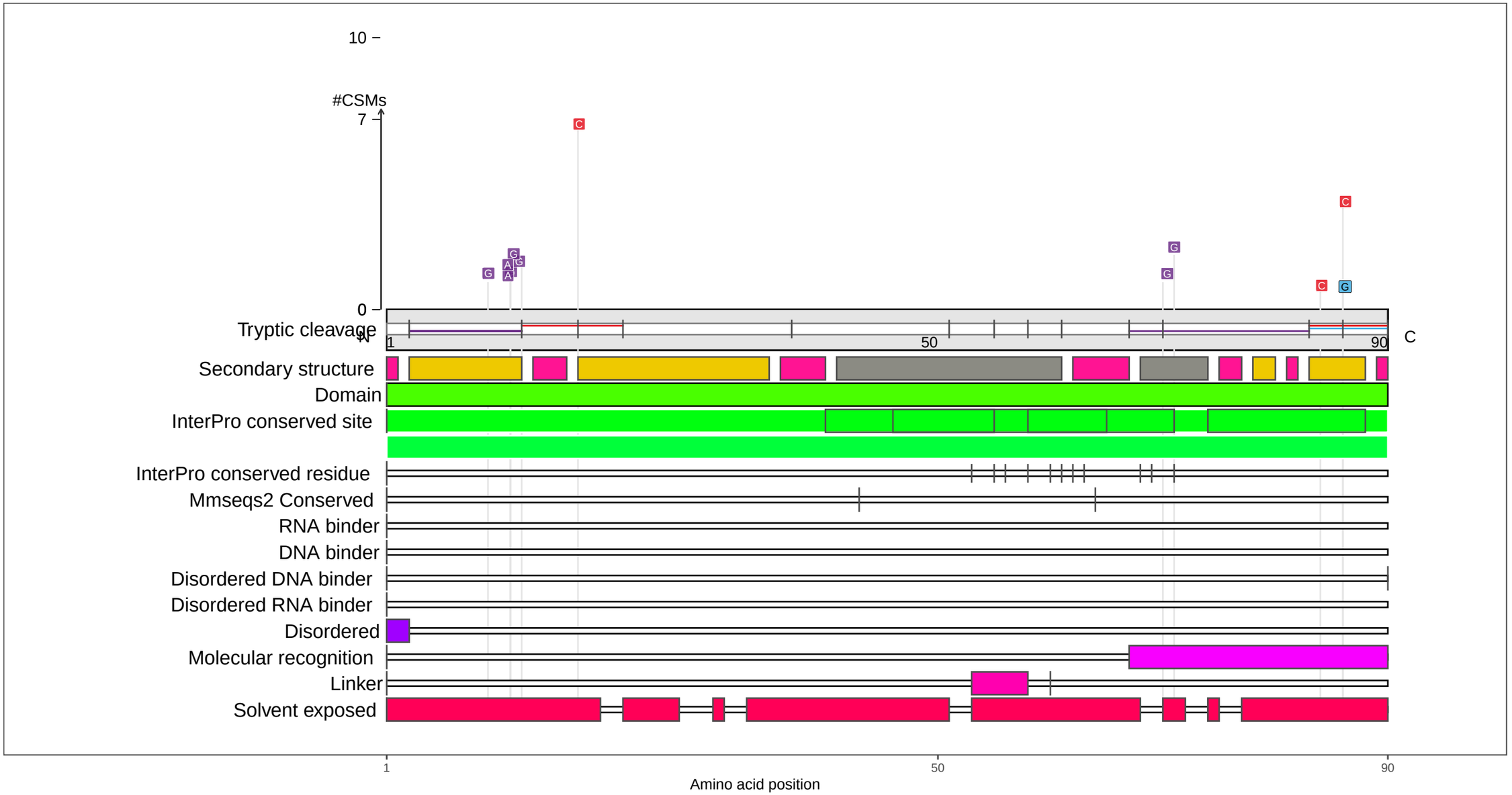
− RNA functions: not annotated



P0ACF0
DBHA_ECOLI DNA−binding protein HU−alpha

− Abundance:
tryptic [log10 Intensity]: 9.62 (Q 97)
PAXdb K12 strain [ppm]: 3.93 (Q 100)
PAXdb E.coli [ppm]: 3.67 (Q 100)

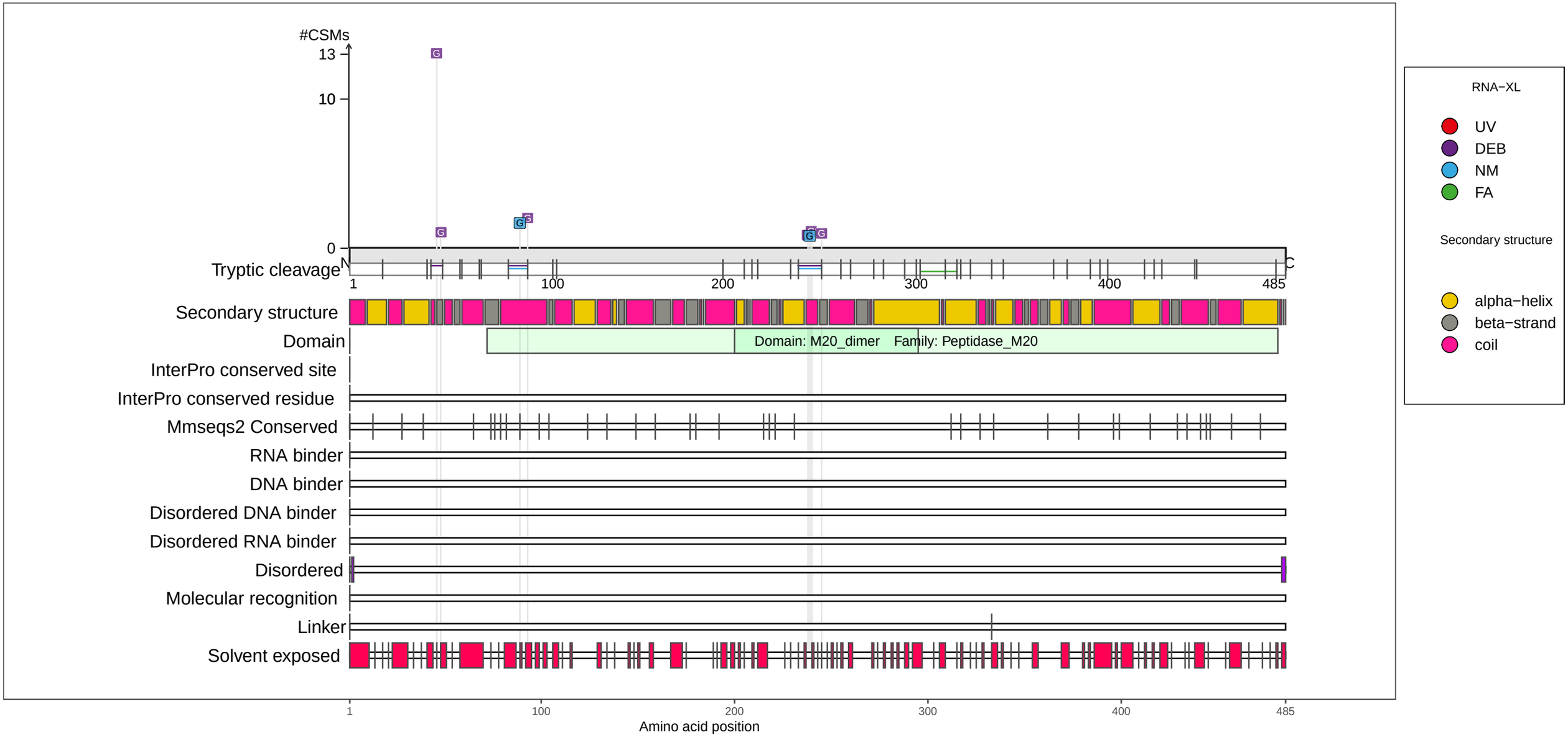
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P15288
PEPD_ECOLI Cytosol non−specific dipeptidase

− Abundance:
tryptic [log10 Intensity]: 9.28 (Q 94)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 2.99 (Q 94)

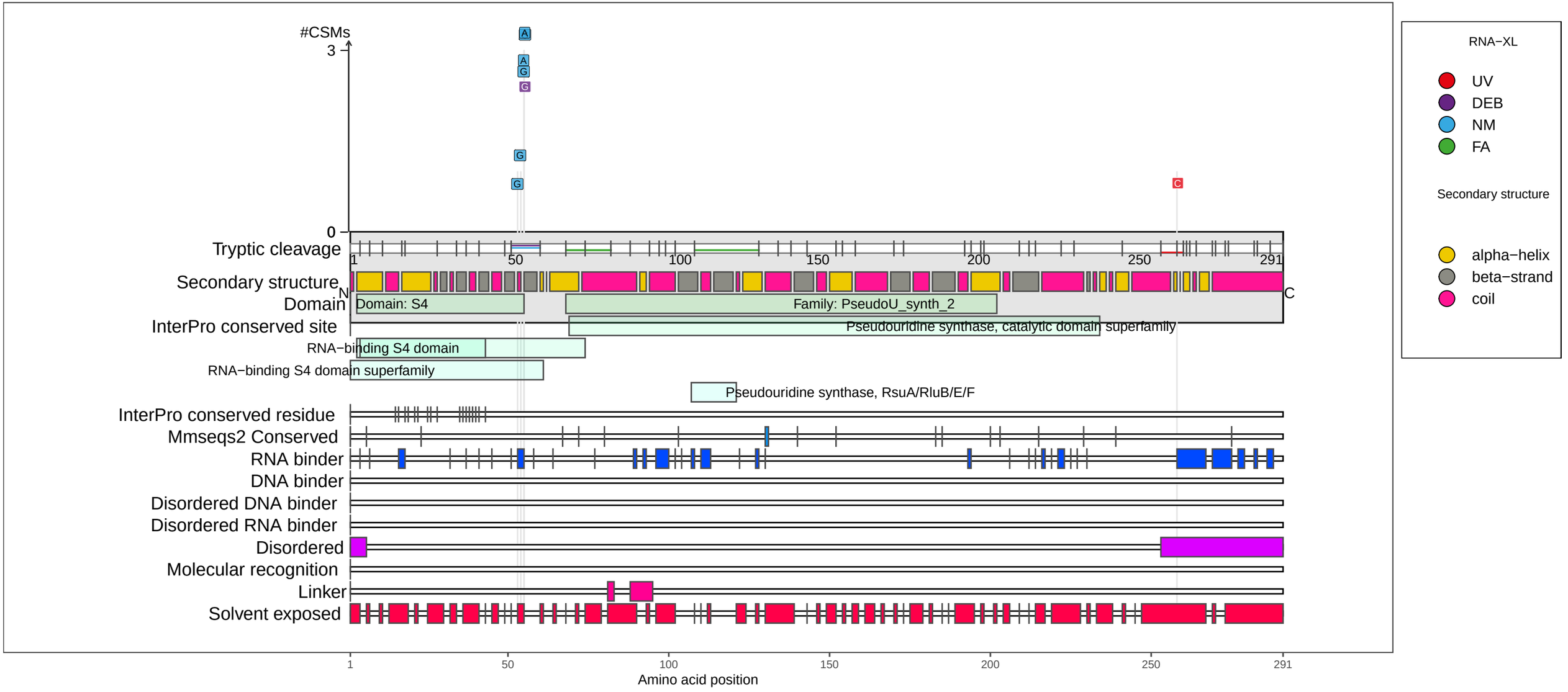
− RNA functions:
RNA binding; RNA ligase activity; RNA metabolic process; RNA processing



P37765
RLUB_ECOLI Ribosomal large subunit pseudouridine synthase B

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 2.2 (Q 77)

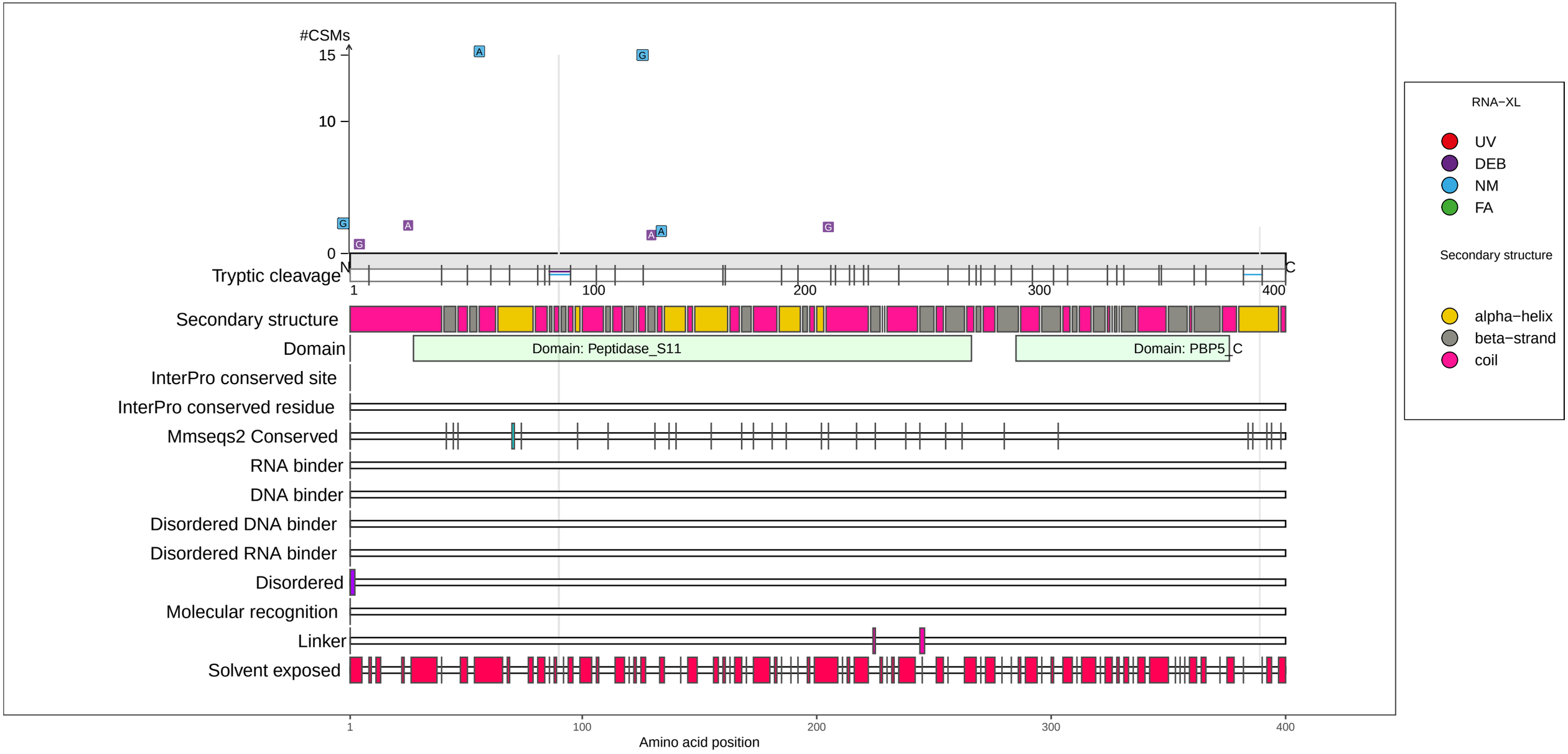
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; RNA pseudouridylate synthase; rRNA metabolic process
rRNA modification; rRNA processing; rRNA pseudouridine synthase activity
rRNA pseudouridine synthesis



P08506
DACC_ECOLI D−alanyl−D−alanine carboxypeptidase DacC

− Abundance:
tryptic [log10 Intensity]: 8.22 (Q 66)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 2.47 (Q 85)

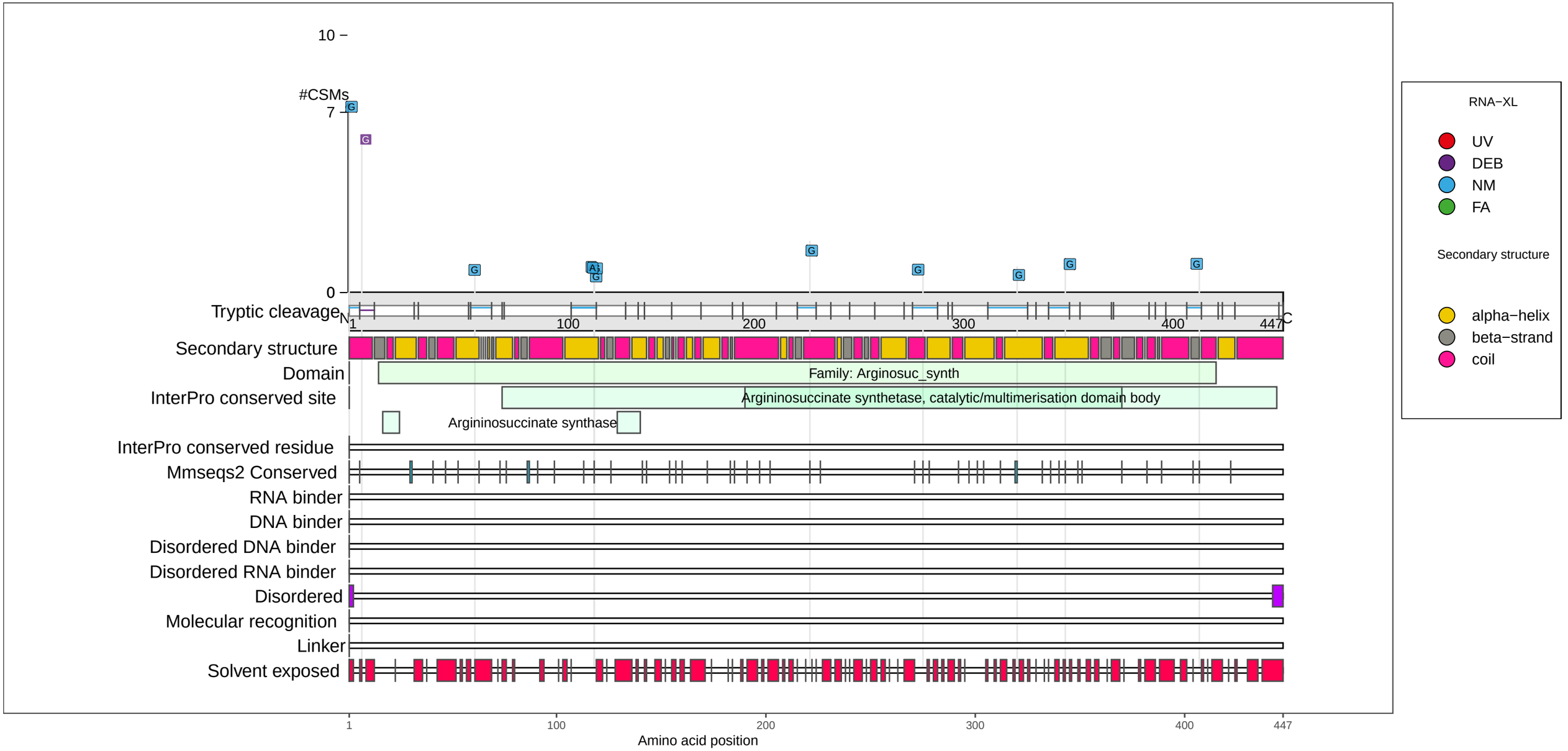
− RNA functions: not annotated



P0A6E4
ASSY_ECOLI Argininosuccinate synthase

− Abundance:
tryptic [log10 Intensity]: 9.02 (Q 89)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 2.74 (Q 91)

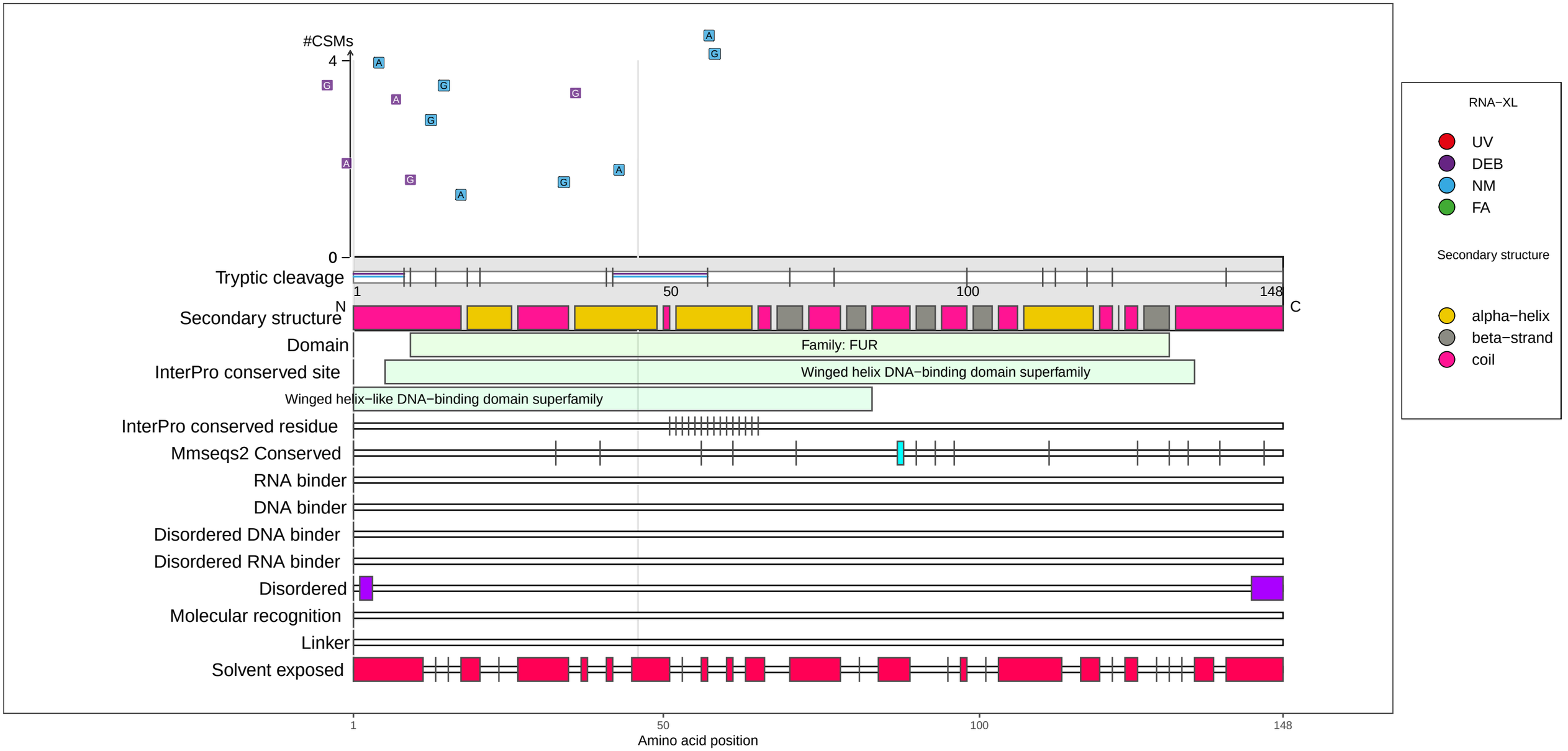
− RNA functions: not annotated



P0A9A9
FUR_ECOLI Ferric uptake regulation protein

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 3.15 (Q 93)
PAXdb E.coli [ppm]: 2.92 (Q 94)

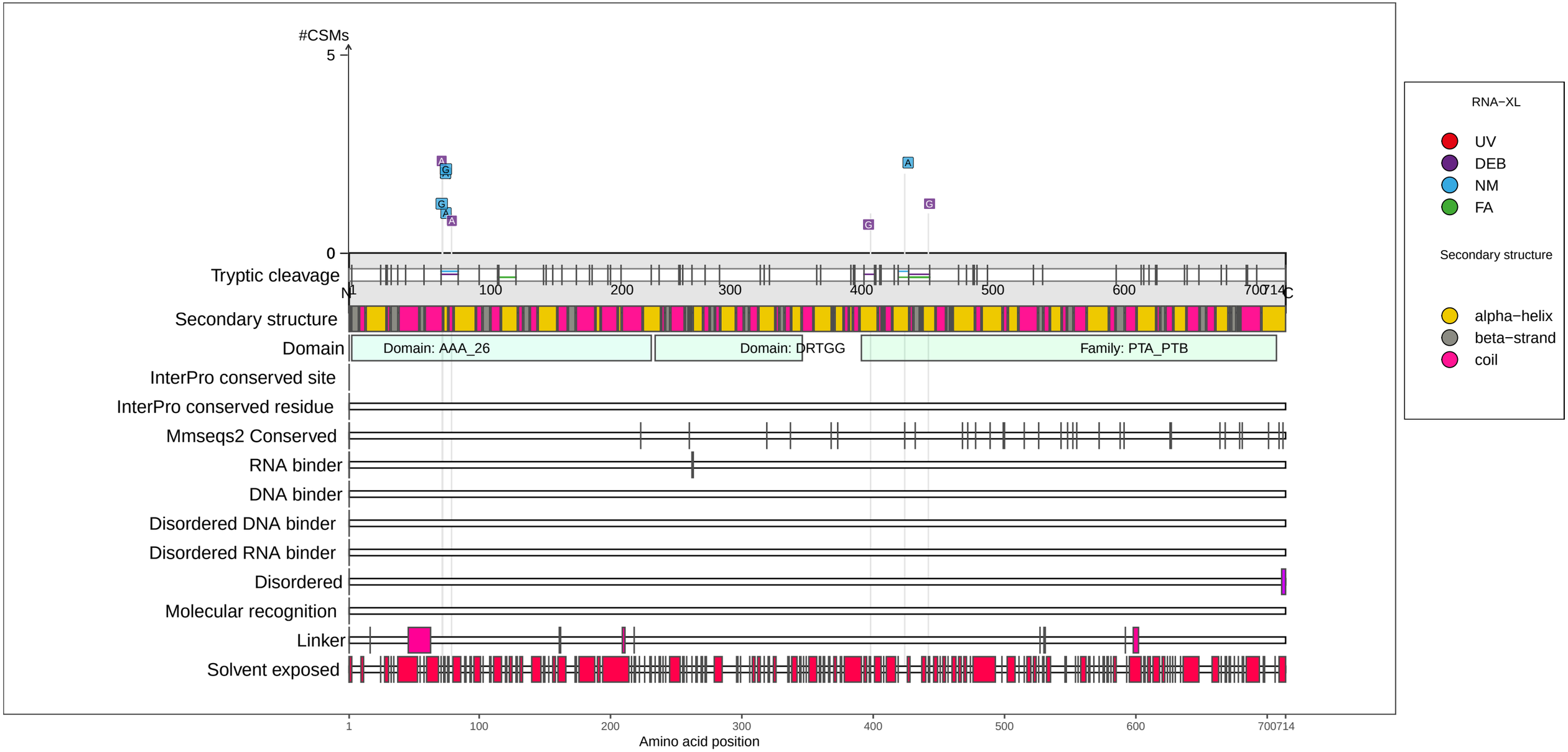
− RNA functions: not annotated



P0A9M8
PTA_ECOLI Phosphate acetyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 3.23 (Q 94)
PAXdb E.coli [ppm]: 2.88 (Q 93)

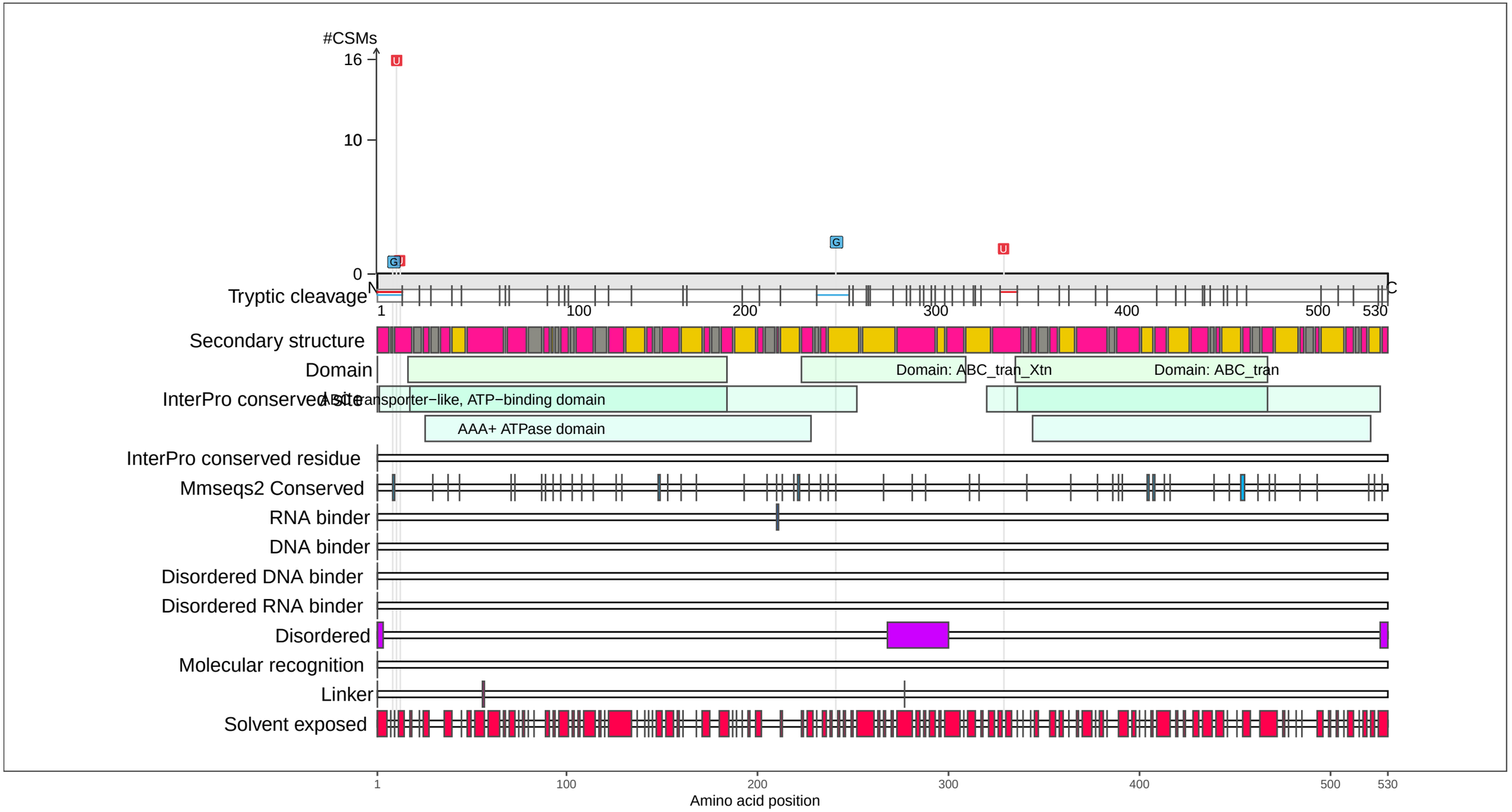
− RNA functions: not annotated

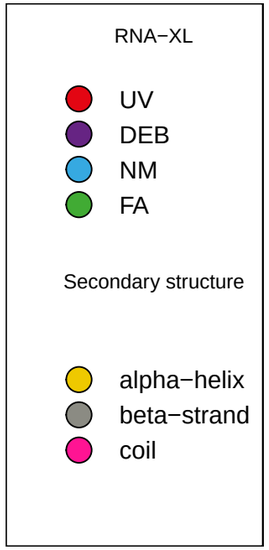


P0A9U3
YBIT_ECOLI Probable ATP−binding protein YbiT

− Abundance:
tryptic [log10 Intensity]: 9.15 (Q 92)
PAXdb K12 strain [ppm]: 2.44 (Q 75)
PAXdb E.coli [ppm]: 2.25 (Q 79)

− RNA functions: not annotated

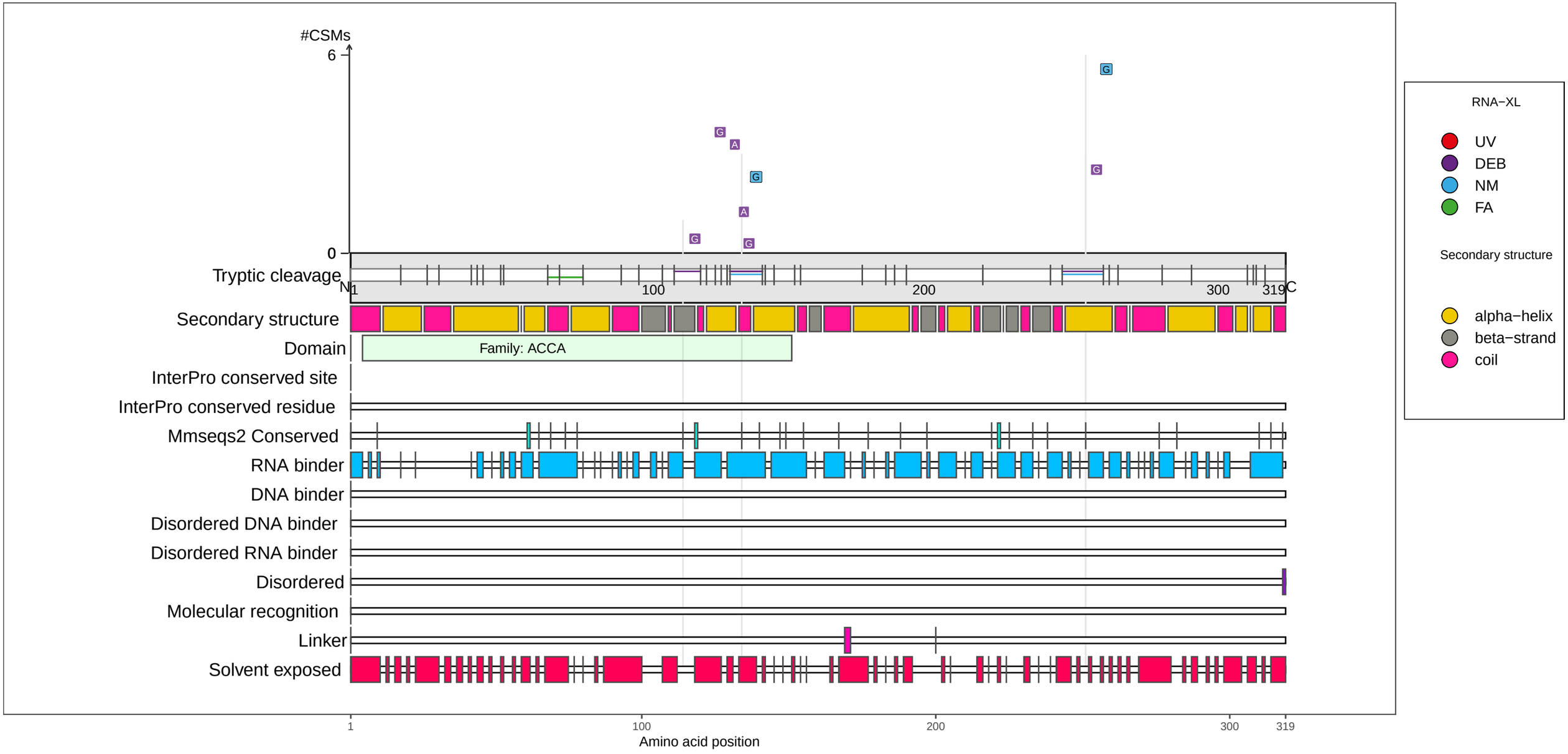




P0ABD5
ACCA_ECOLI Acetyl−coenzyme A carboxylase carboxyl transferase subunit alpha

− Abundance:
tryptic [log10 Intensity]: 8.48 (Q 75)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.88 (Q 93)

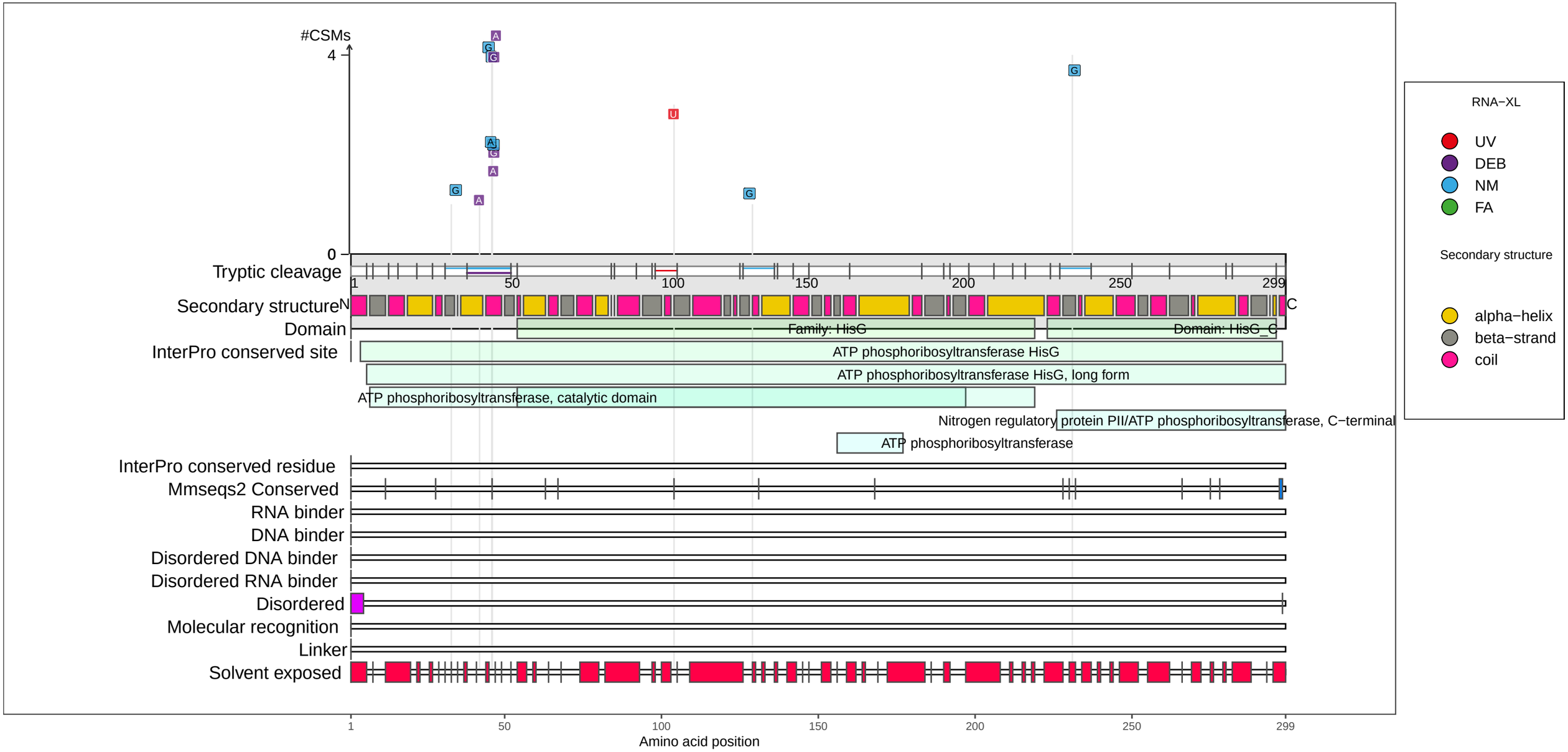
− RNA functions: not annotated



P60757
HIS1_ECOLI ATP phosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.14 (Q 63)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 2.52 (Q 86)

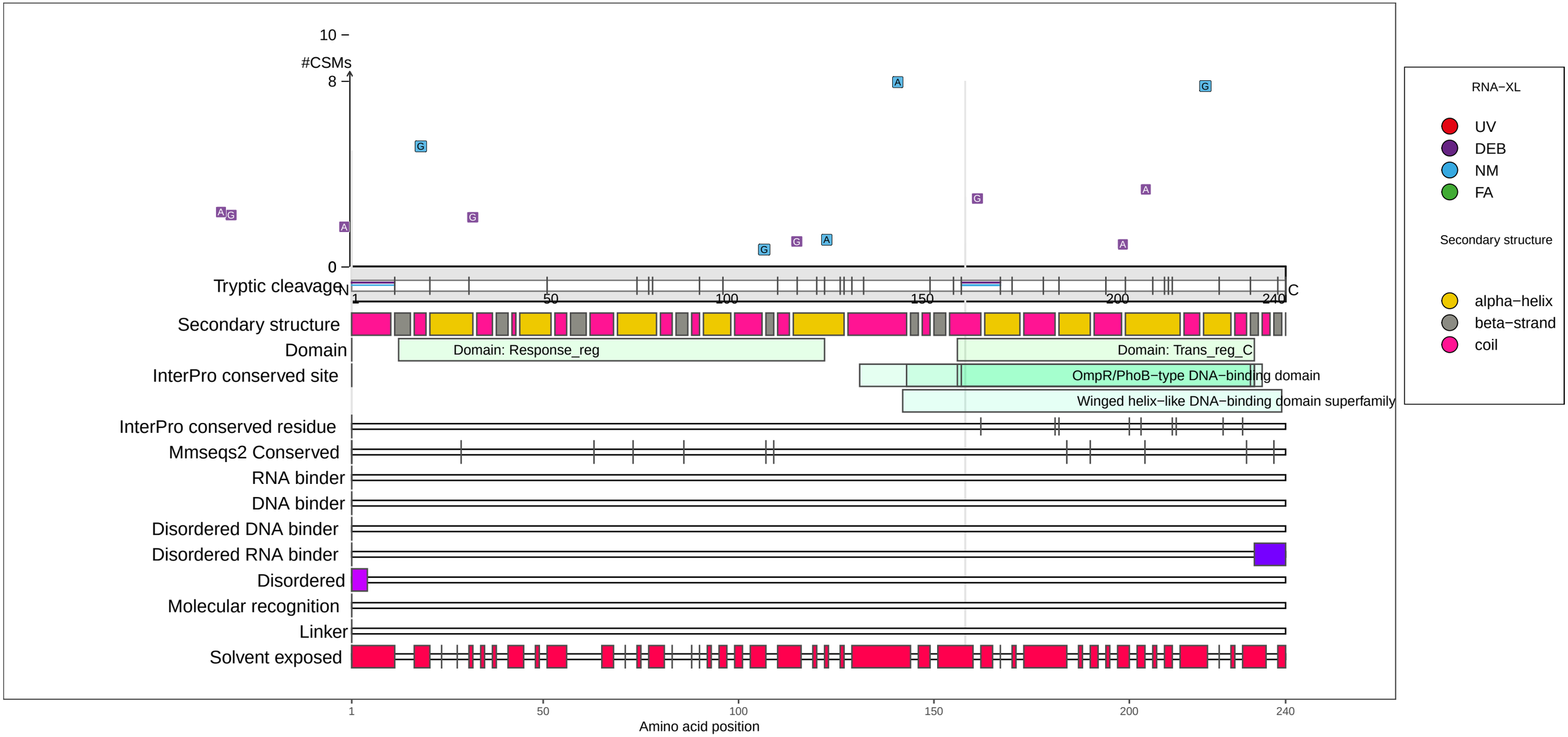
− RNA functions: not annotated



P69228
BAER_ECOLI Transcriptional regulatory protein BaeR

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: 1.55 (Q 41)
PAXdb E.coli [ppm]: 1.83 (Q 68)

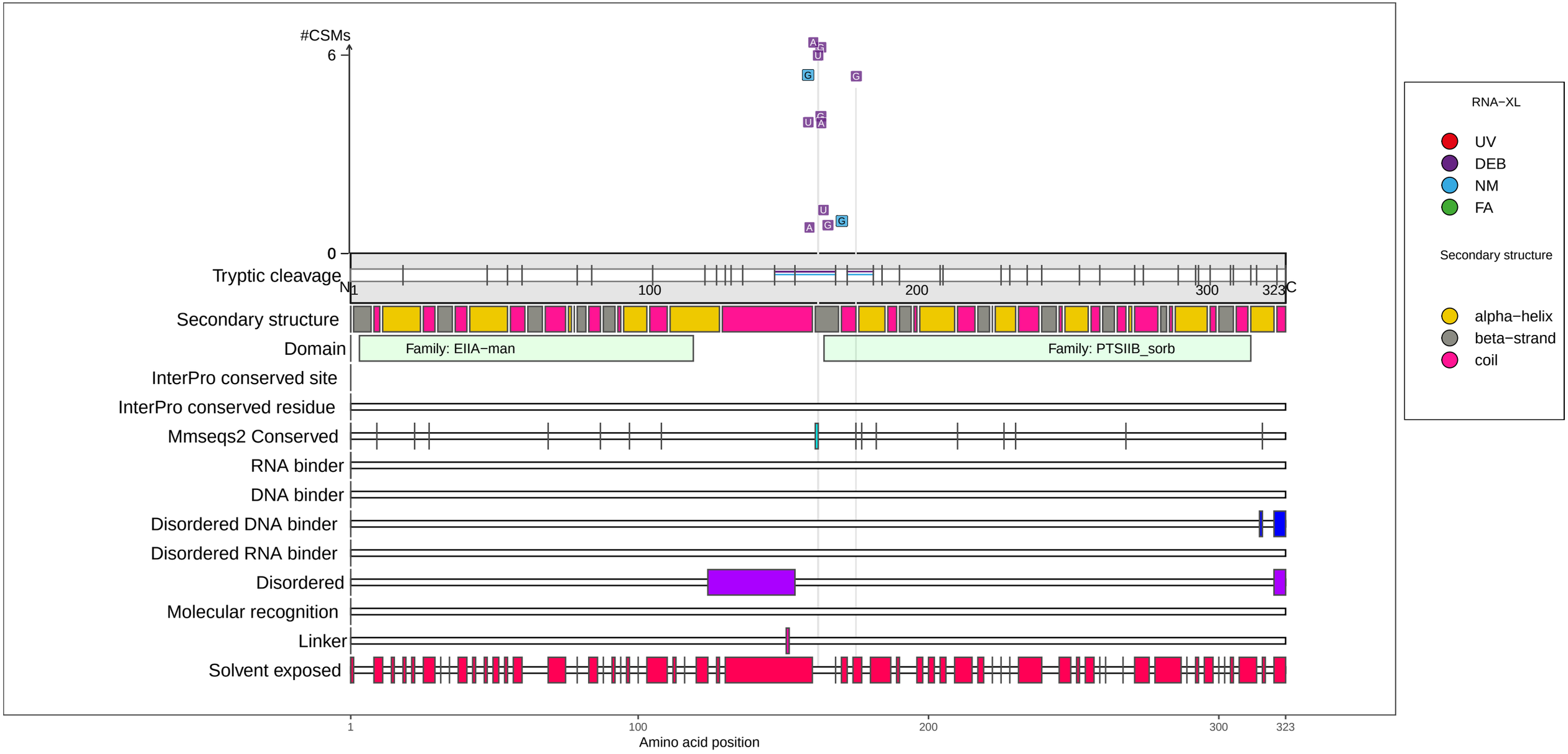
− RNA functions:
RNA biosynthetic process; RNA metabolic process



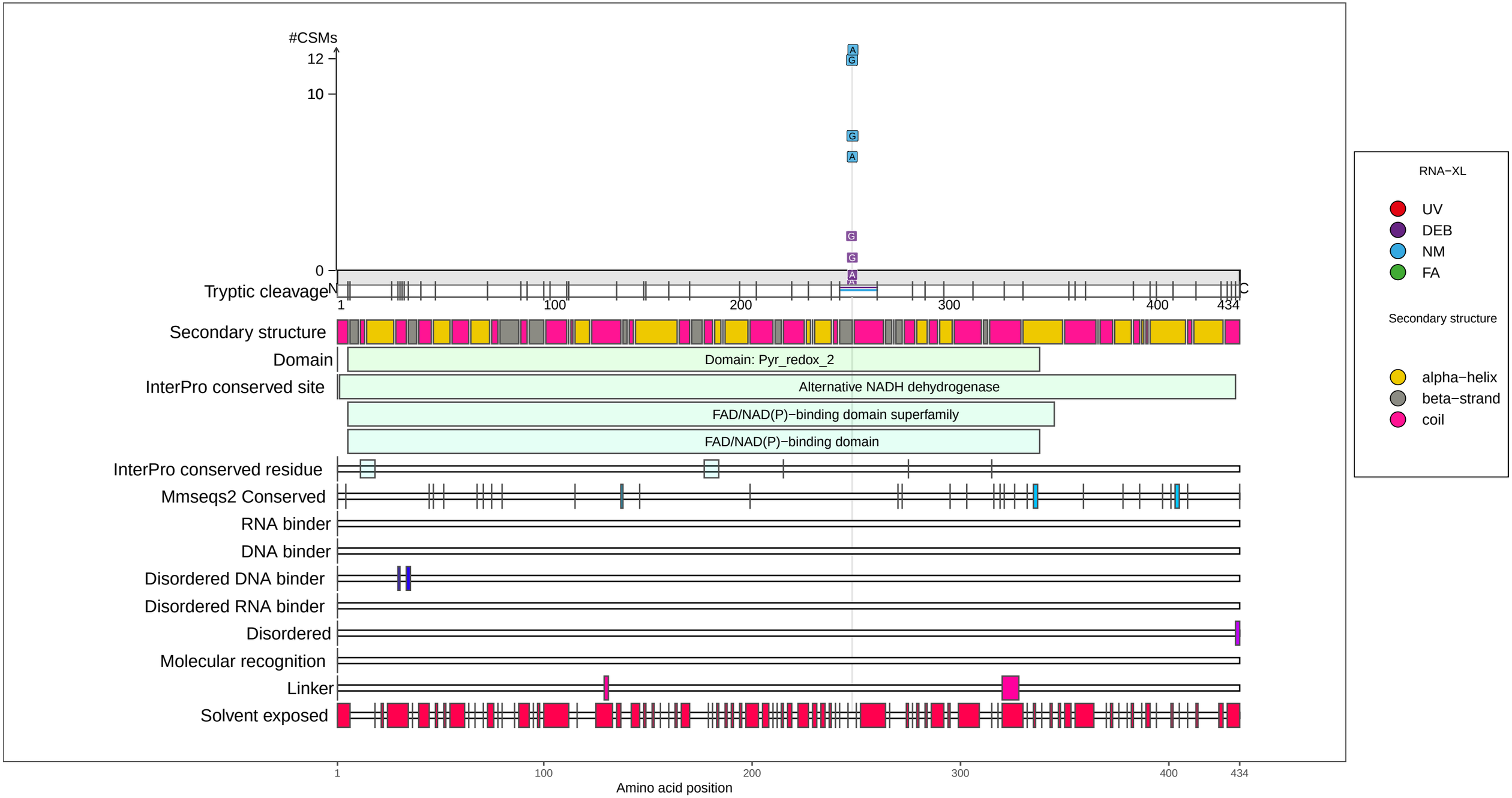
P69797
PTNAB_ECOLI PTS system mannose−specific EIIAB component

− Abundance:
tryptic [log10 Intensity]: 8.81 (Q 84)
PAXdb K12 strain [ppm]: 2.49 (Q 77)
PAXdb E.coli [ppm]: 3.21 (Q 97)

− RNA functions: not annotated



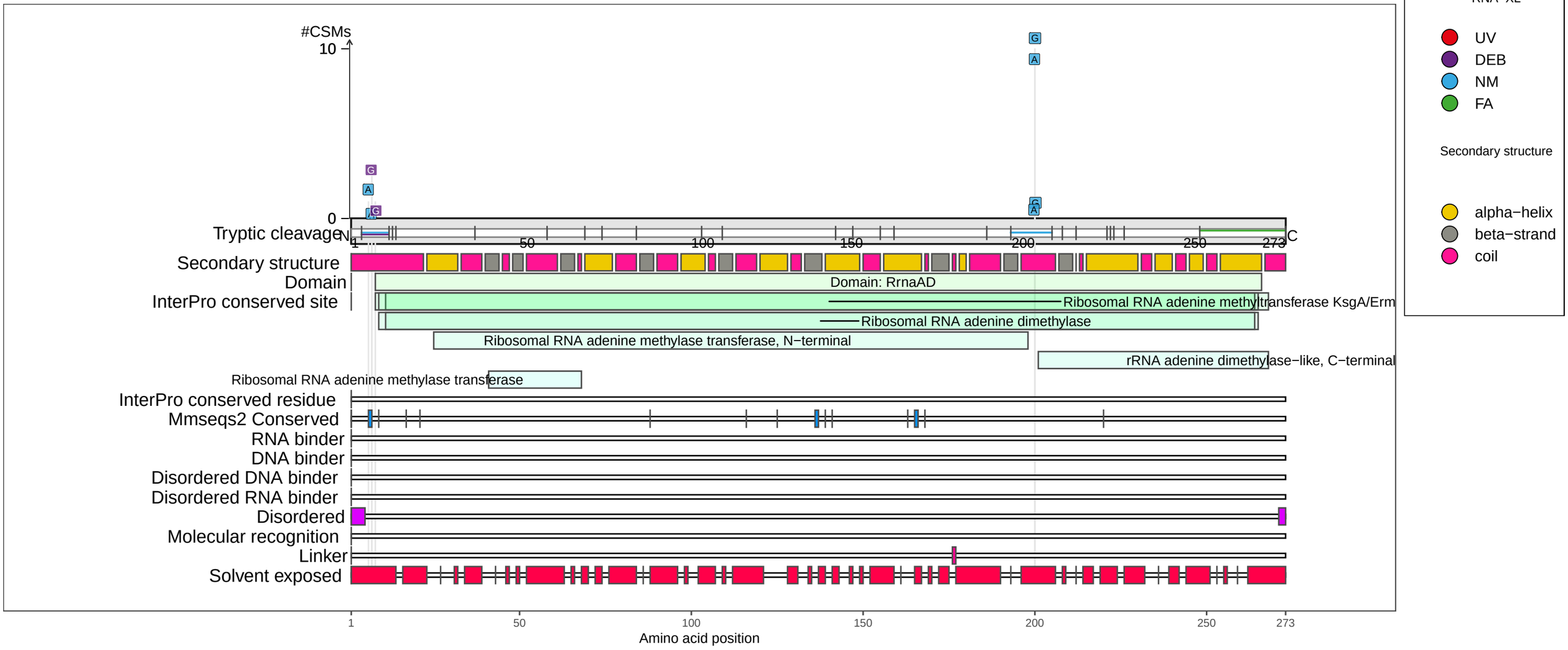
P00393
NDH_ECOLI Type II NADH:quinone oxidoreductase
− RNA functions: not annotated



P06992
RSMA_ECOLI Ribosomal RNA small subunit methyltransferase A

− Abundance:
tryptic [log10 Intensity]: 7.51 (Q 36)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 1.97 (Q 71)

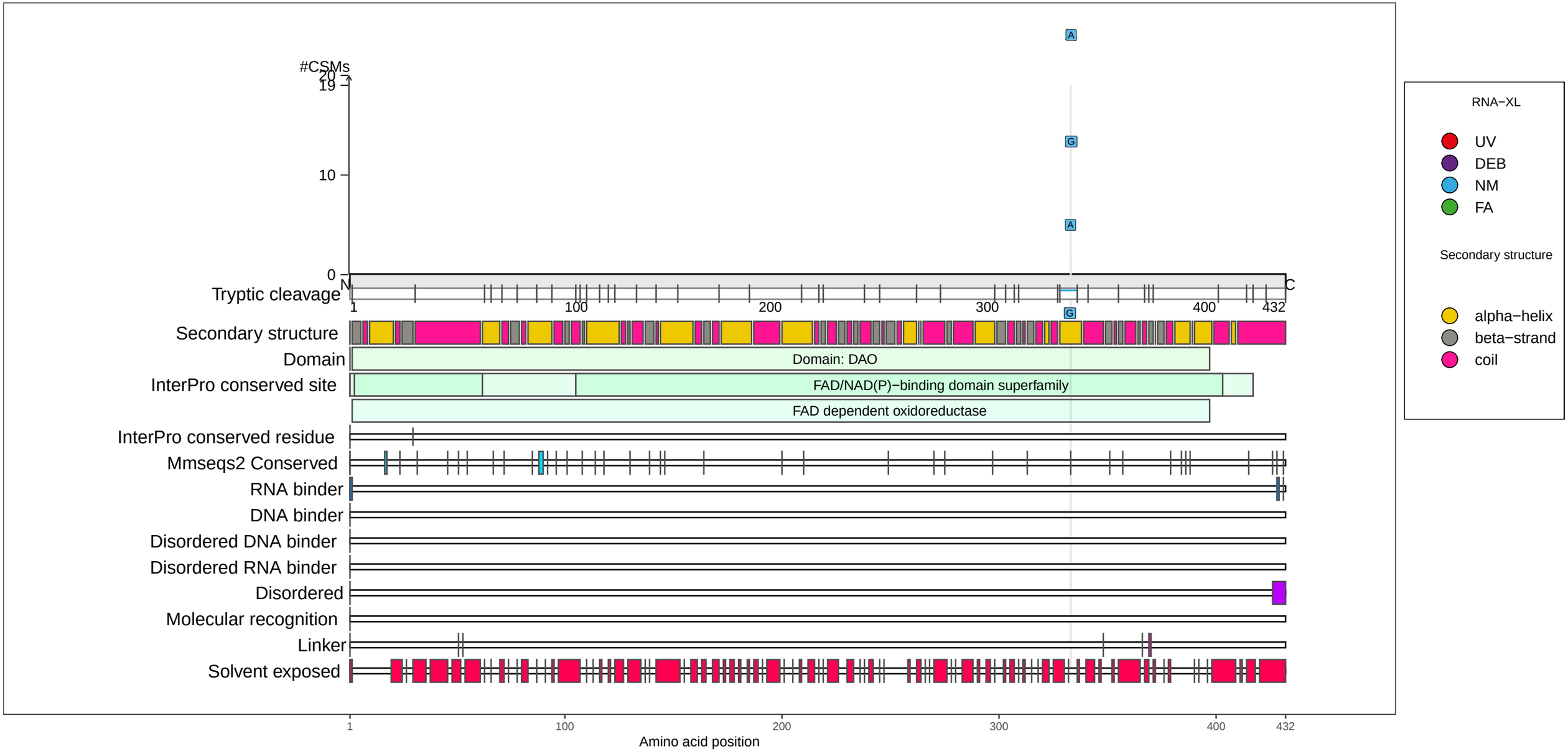
− RNA functions:
16S rRNA (adenine(1518)−N(6)/adenine(1519)−N(6))−dimethyltransferase activity
mRNA binding; ncRNA metabolic process; ncRNA processing
Ribosomal RNA adenine dimethylase; RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (adenine−N6−)−methyltransferase activity
rRNA (adenine−N6,N6−)−dimethyltransferase activity
rRNA (adenine) methyltransferase activity; rRNA base methylation; rRNA binding; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing



P0A6J5
DADA_ECOLI D−amino acid dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 7.33 (Q 26)
PAXdb K12 strain [ppm]: 1.96 (Q 59)
PAXdb E.coli [ppm]: 1.98 (Q 72)

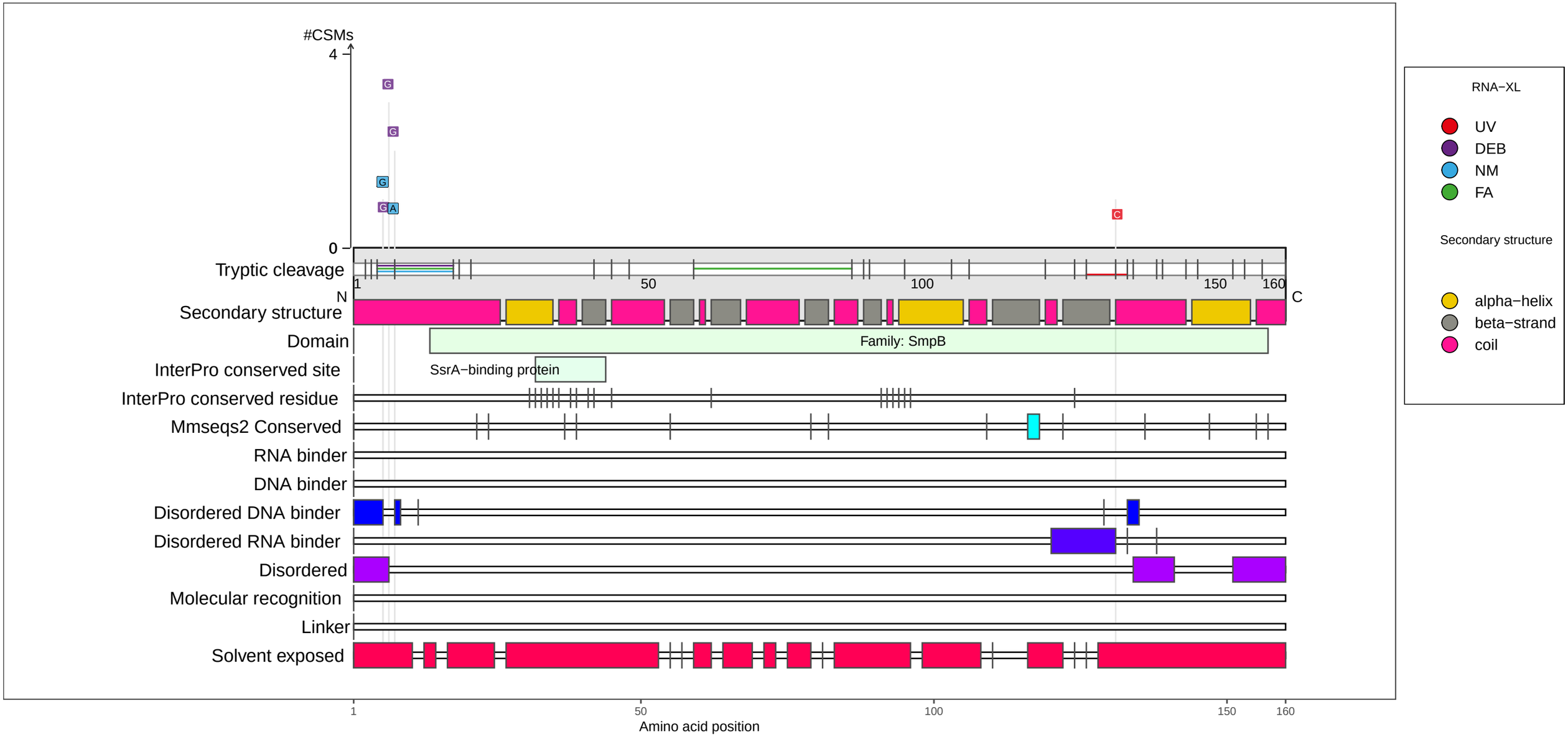
− RNA functions: not annotated



P0A832
SSRP_ECOLI SsrA−binding protein

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 1.9 (Q 70)

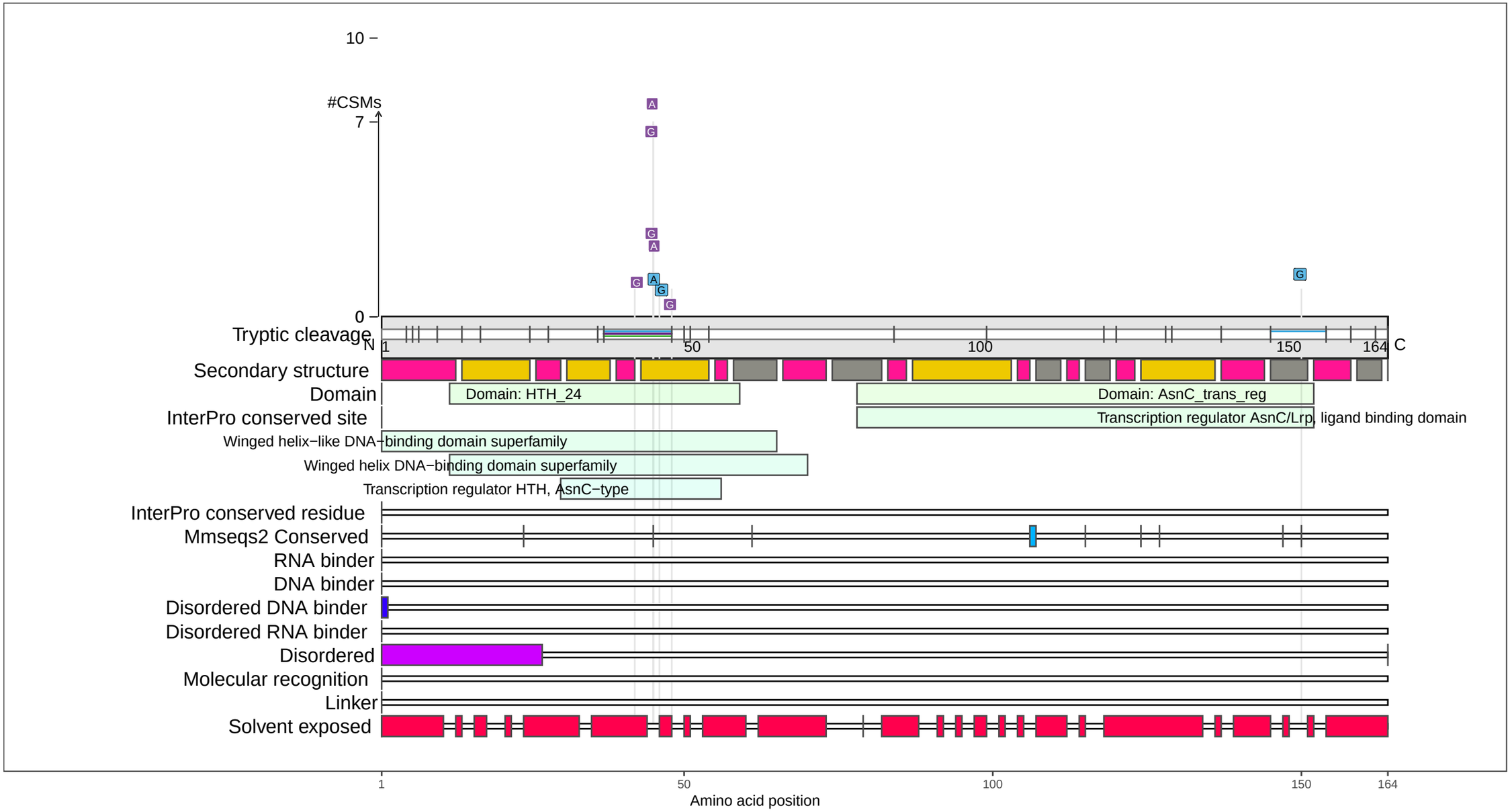
− RNA functions:
RNA binding

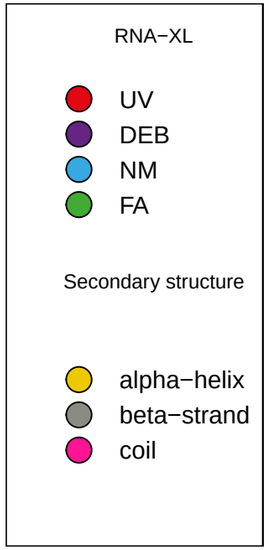


P0ACJ0
LRP_ECOLI Leucine−responsive regulatory protein

− Abundance:
tryptic [log10 Intensity]: 8.19 (Q 65)
PAXdb K12 strain [ppm]: 3.08 (Q 92)
PAXdb E.coli [ppm]: 3.05 (Q 95)

− RNA functions: not annotated

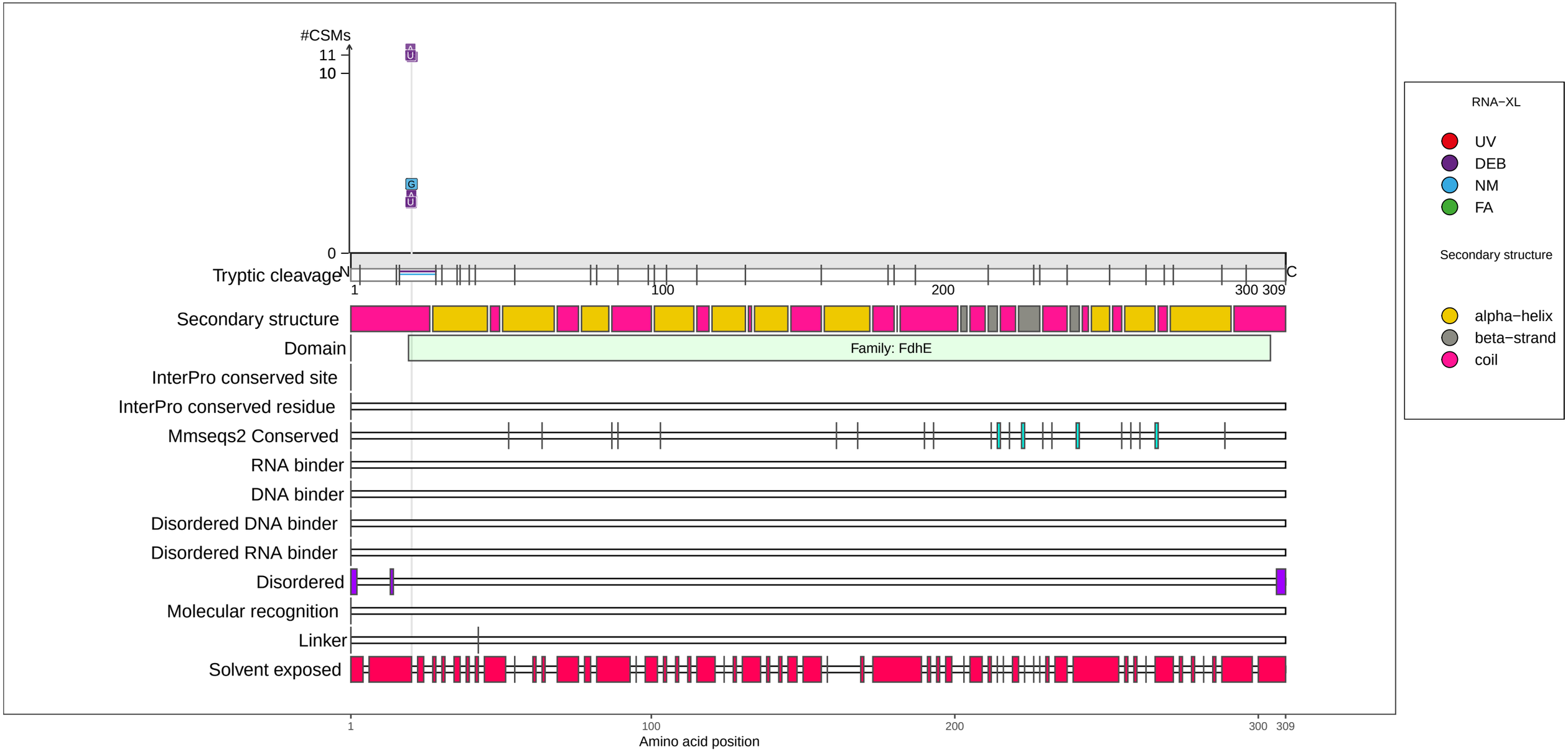




P13024
FDHE_ECOLI Protein FdhE

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 1.72 (Q 65)

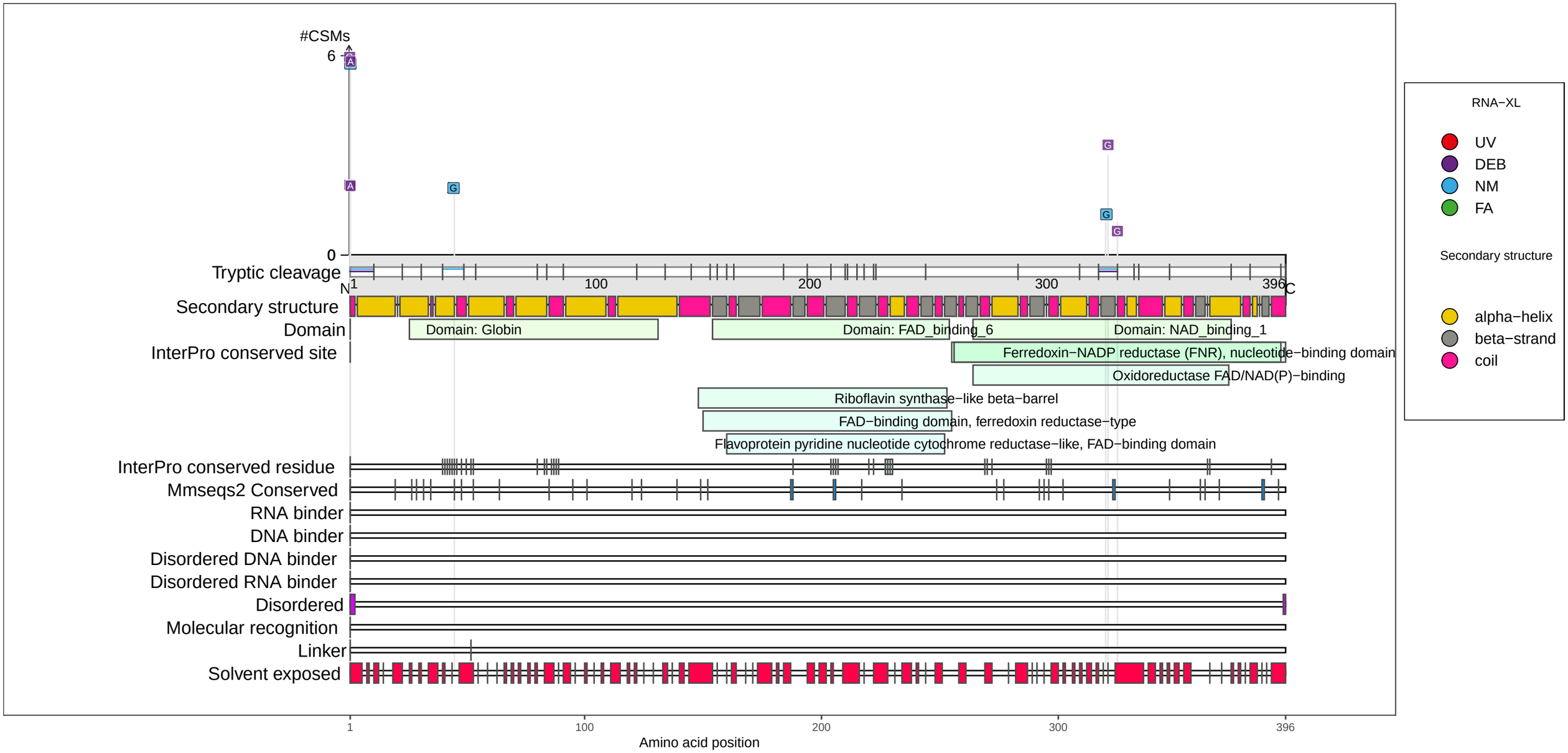
− RNA functions: not annotated



P24232
HMP_ECOLI Flavohemoprotein

− Abundance:
tryptic [log10 Intensity]: 8.14 (Q 63)
PAXdb K12 strain [ppm]: 1.52 (Q 39)
PAXdb E.coli [ppm]: 1.29 (Q 54)

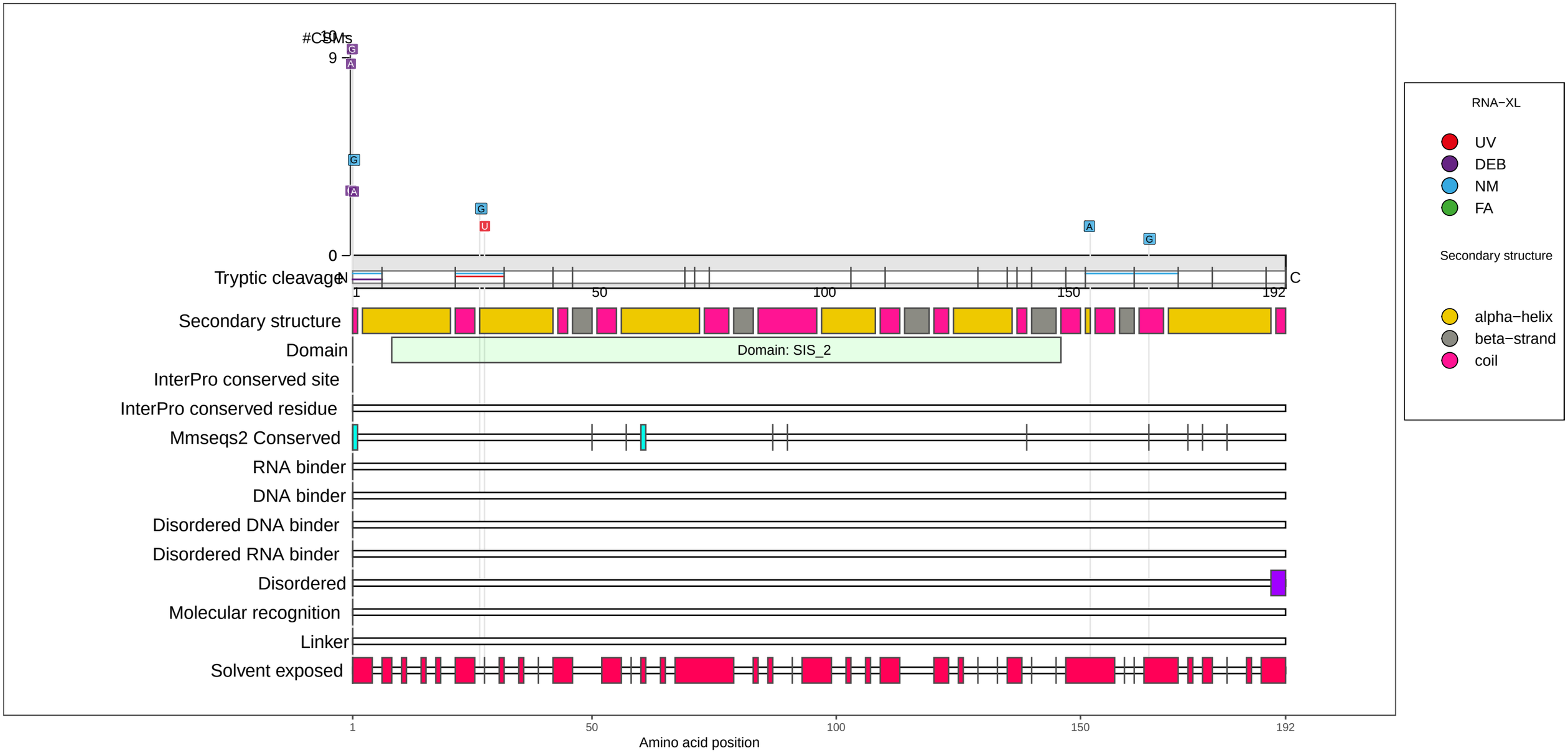
− RNA functions: not annotated



P63224
GMHA_ECOLI Phosphoheptose isomerase

− Abundance:
tryptic [log10 Intensity]: 9.17 (Q 92)
PAXdb K12 strain [ppm]: 2.45 (Q 76)
PAXdb E.coli [ppm]: 2.93 (Q 94)

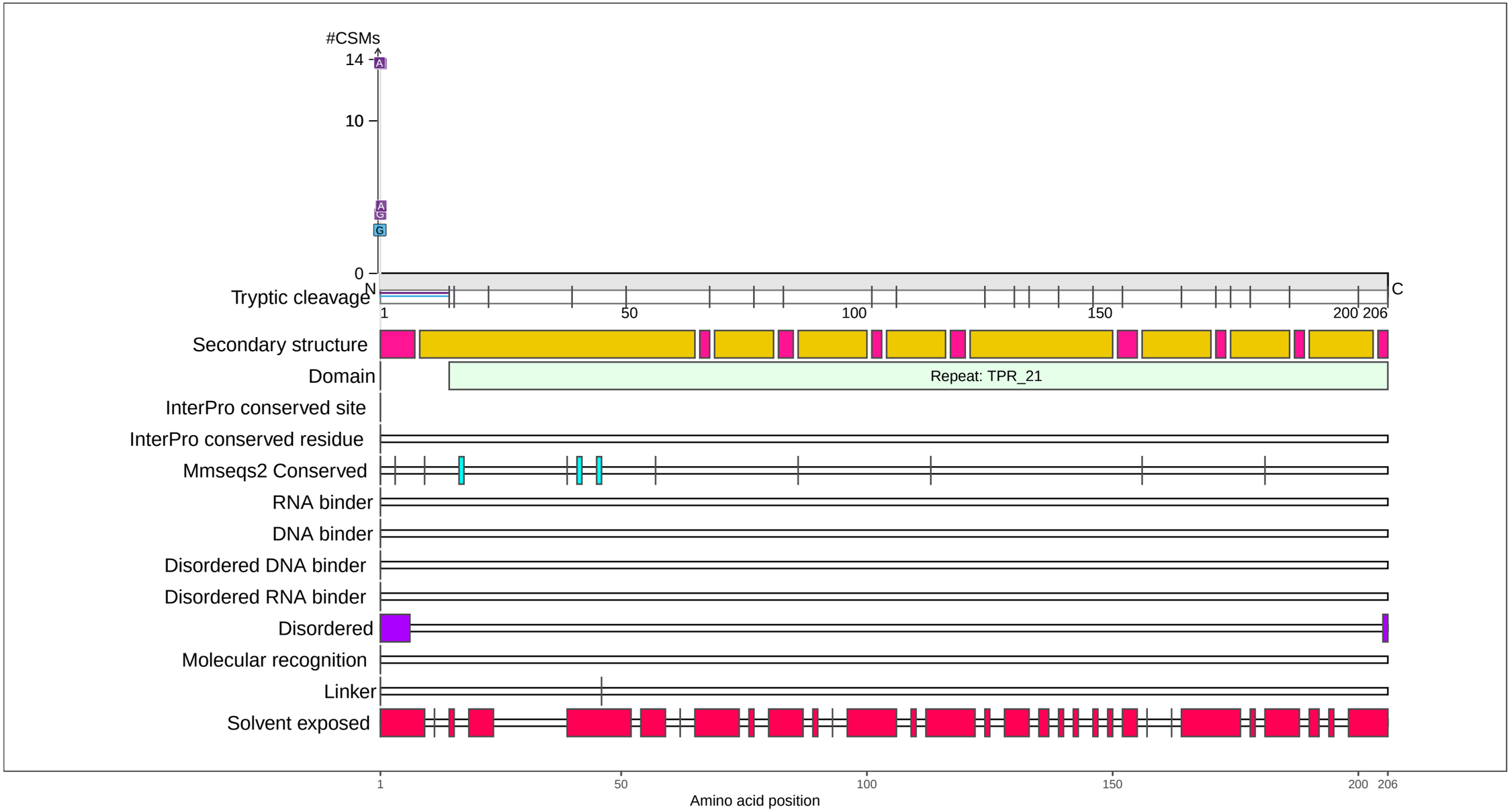
− RNA functions: not annotated

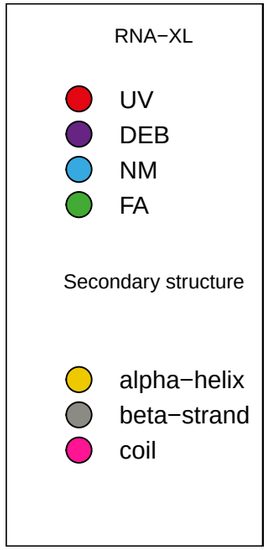


P76576
YFGM_ECOLI Ancillary SecYEG translocon subunit

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 1.9 (Q 57)
PAXdb E.coli [ppm]: 2.49 (Q 85)

− RNA functions: not annotated

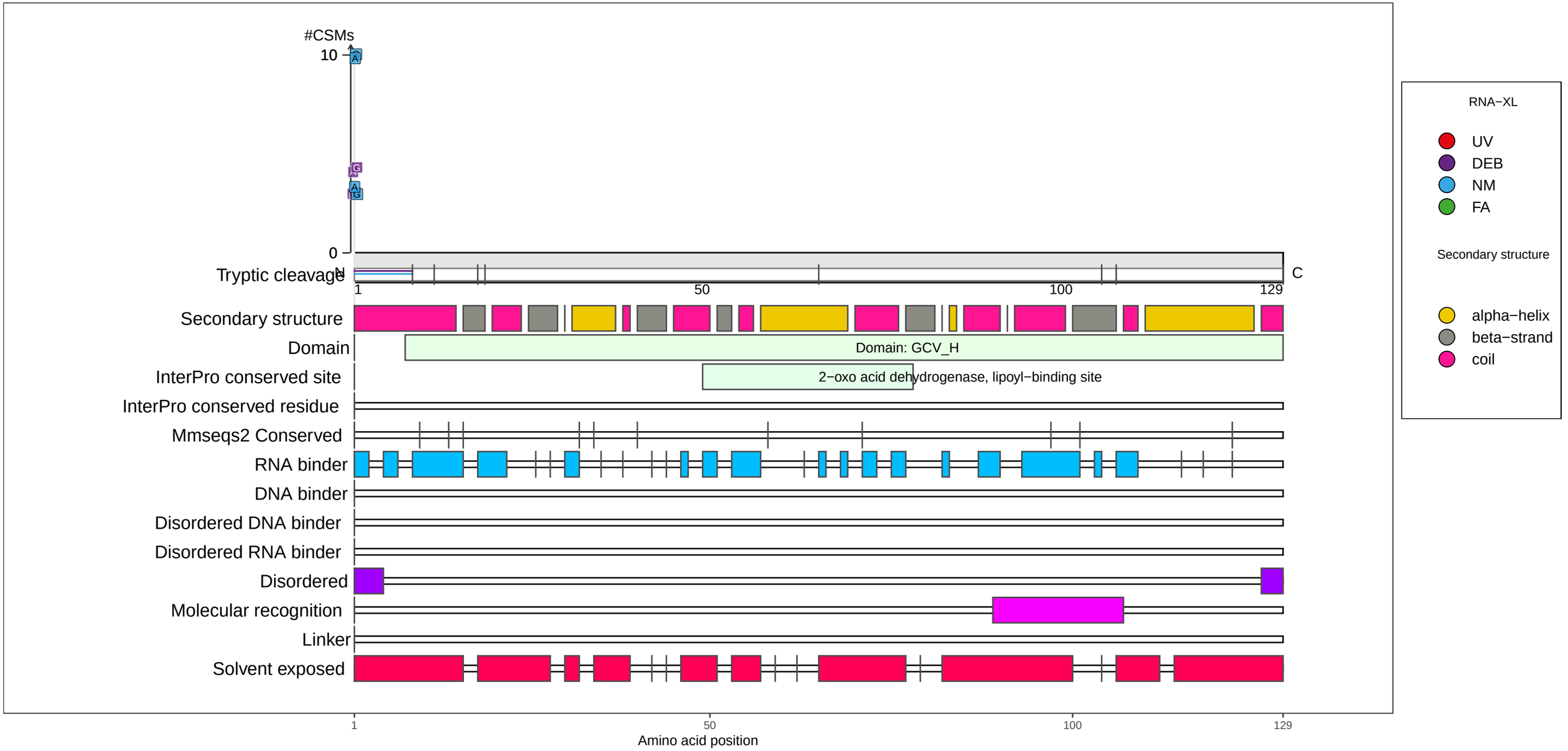




P0A6T9
GCSH_ECOLI Glycine cleavage system H protein

− Abundance:
tryptic [log10 Intensity]: 8.24 (Q 67)
PAXdb K12 strain [ppm]: 3.67 (Q 98)
PAXdb E.coli [ppm]: 2.59 (Q 88)

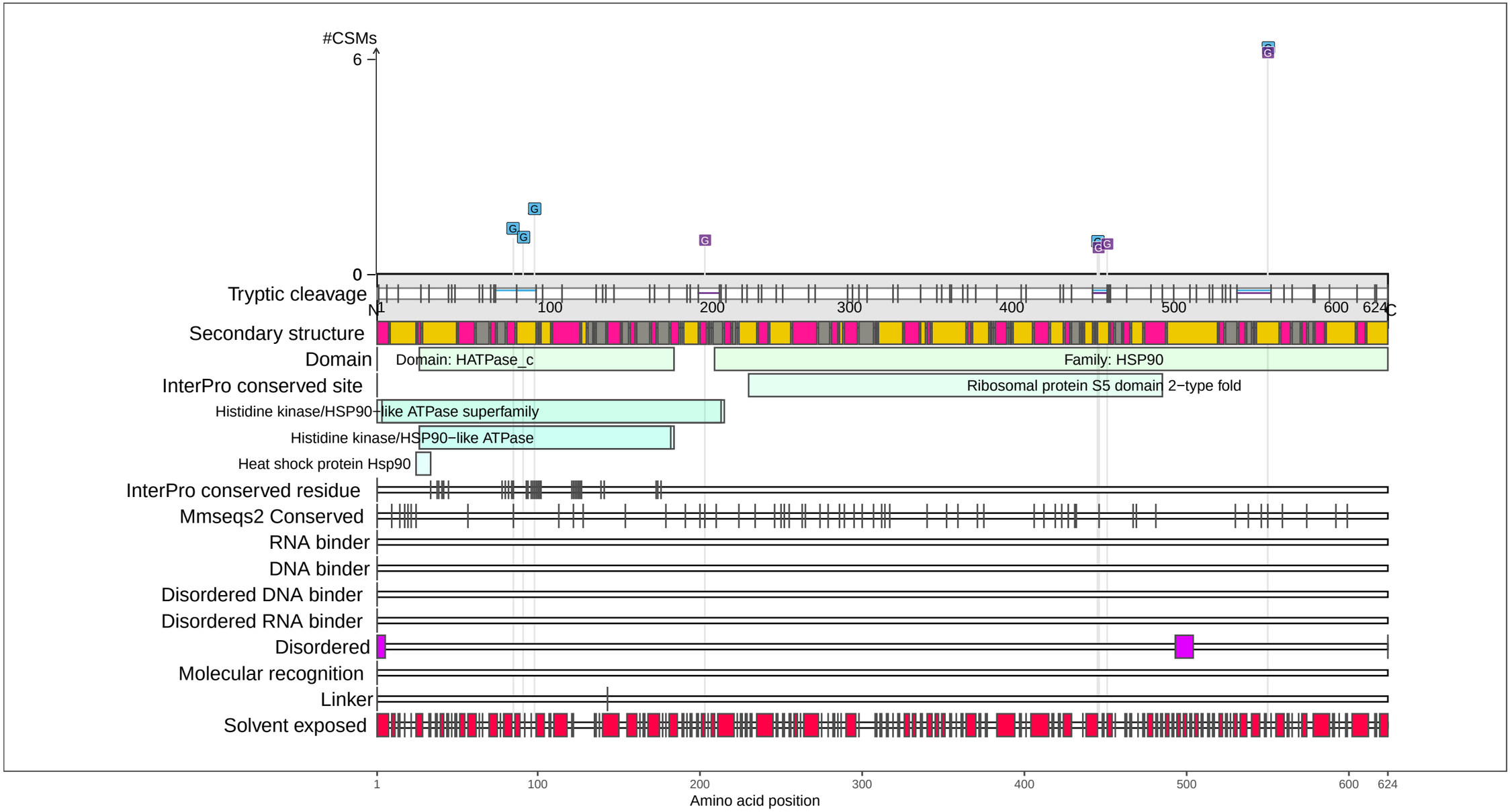
− RNA functions: not annotated



P0A6Z3
HTPG_ECOLI Chaperone protein HtpG

− Abundance:
tryptic [log10 Intensity]: 9.75 (Q 98)
PAXdb K12 strain [ppm]: 3.16 (Q 93)
PAXdb E.coli [ppm]: 2.67 (Q 89)

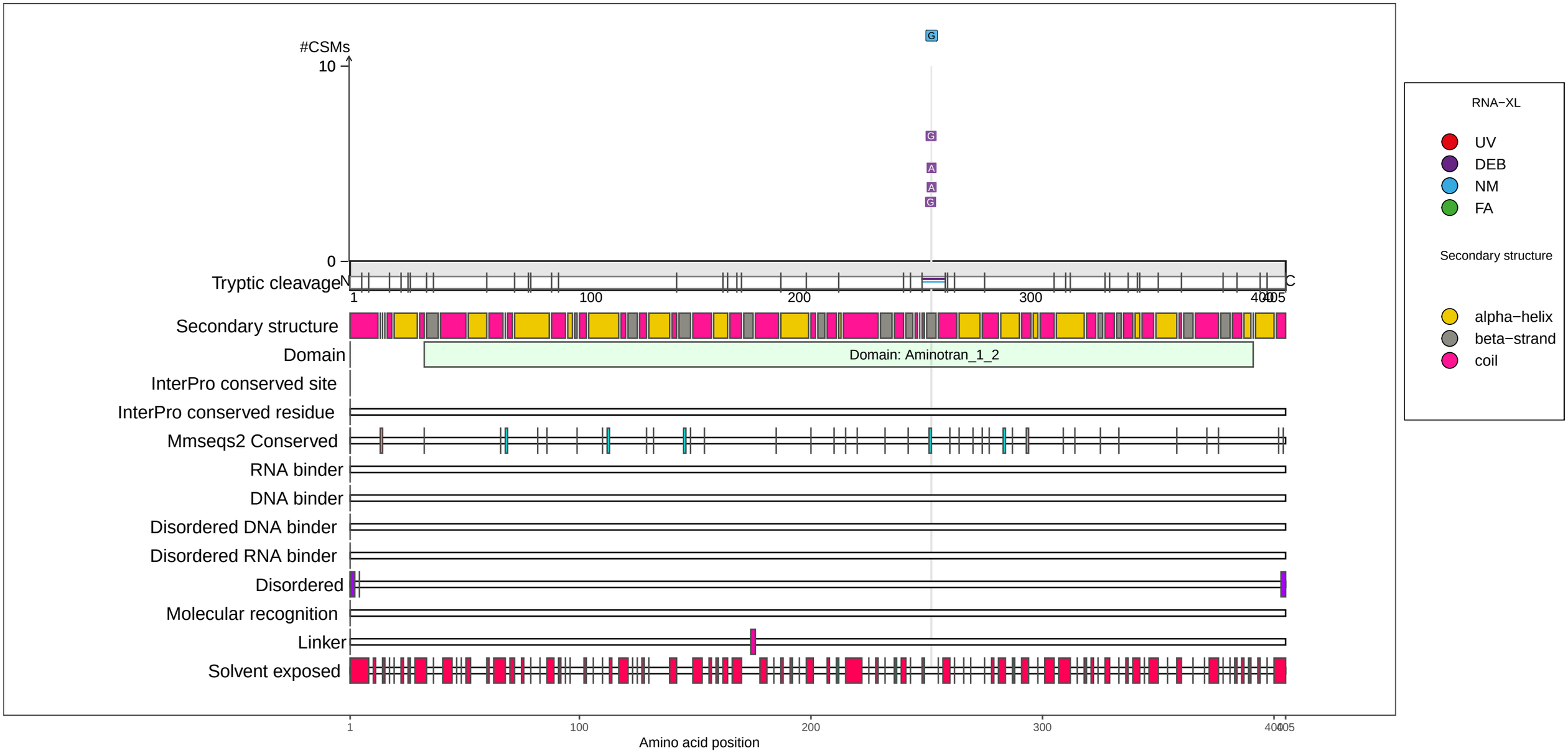
− RNA functions: not annotated



P0A959
ALAA_ECOLI Glutamate−pyruvate aminotransferase AlaA

− Abundance:
tryptic [log10 Intensity]: 7 (Q 13)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 2.04 (Q 73)

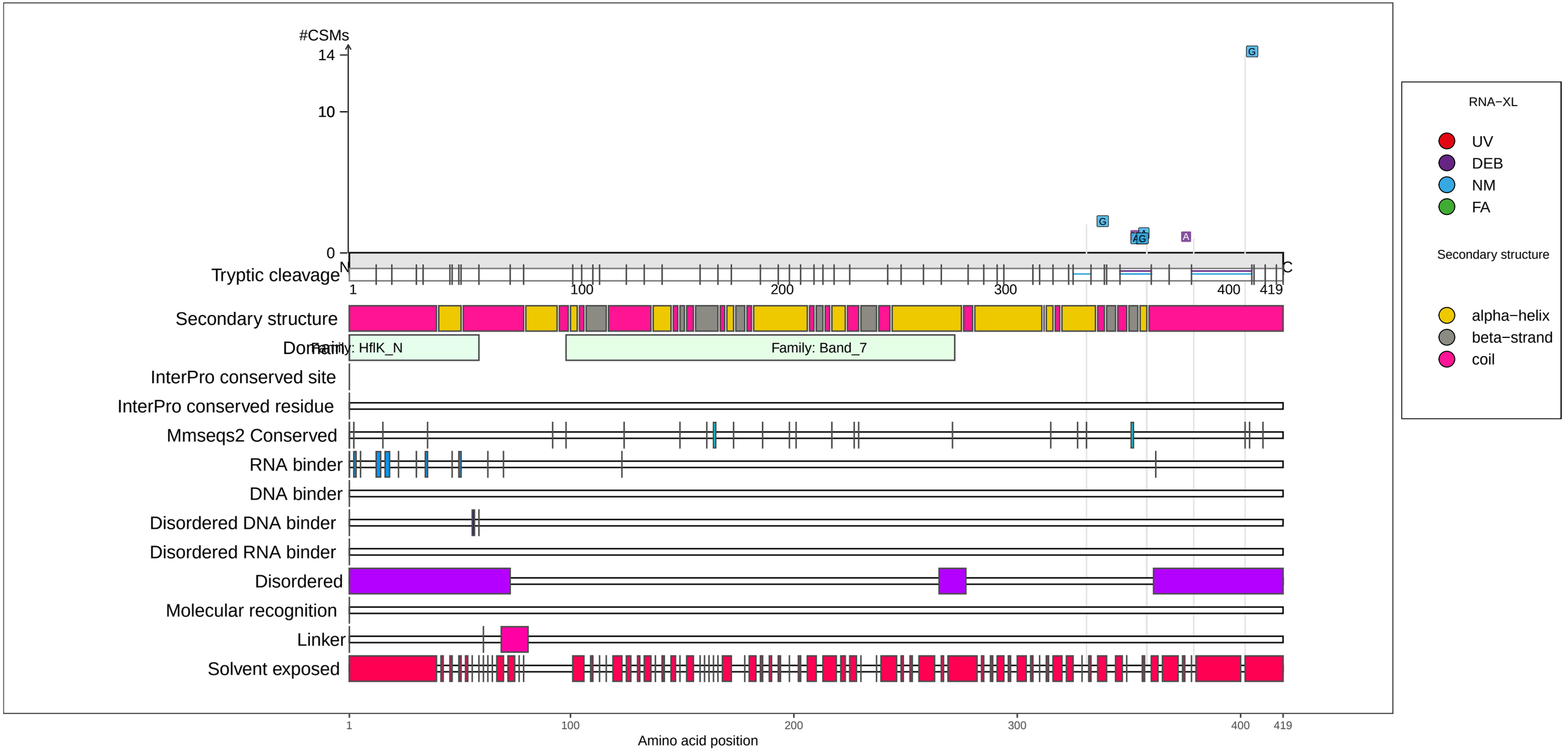
− RNA functions: not annotated



P0ABC7
HFLK_ECOLI Modulator of FtsH protease HflK

− Abundance:
tryptic [log10 Intensity]: 8.64 (Q 80)
PAXdb K12 strain [ppm]: 2.48 (Q 77)
PAXdb E.coli [ppm]: 2.59 (Q 88)

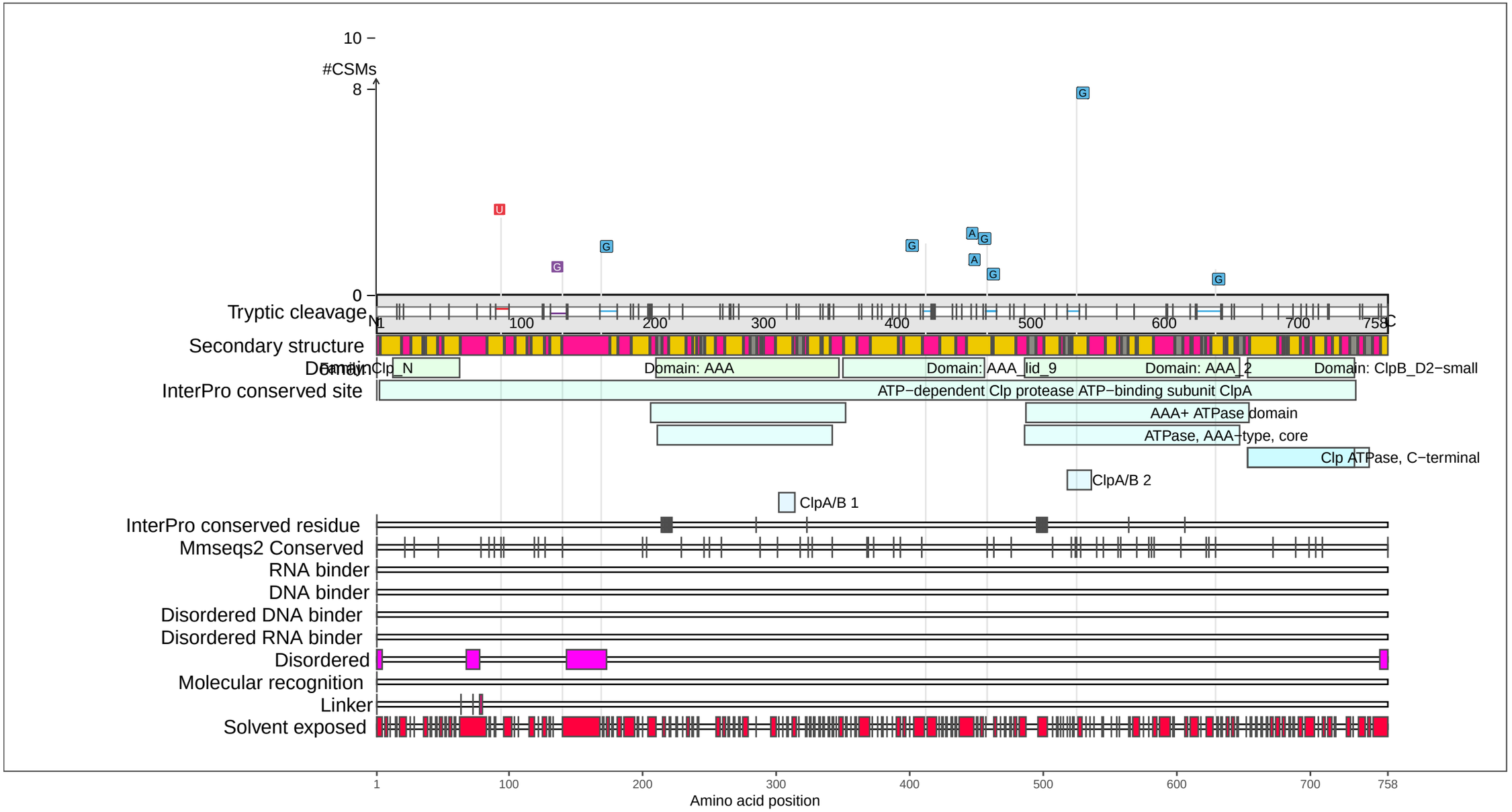
− RNA functions: not annotated



P0ABH9
CLPA_ECOLI ATP−dependent Clp protease ATP−binding subunit ClpA

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: 2.45 (Q 76)
PAXdb E.coli [ppm]: 2.72 (Q 90)

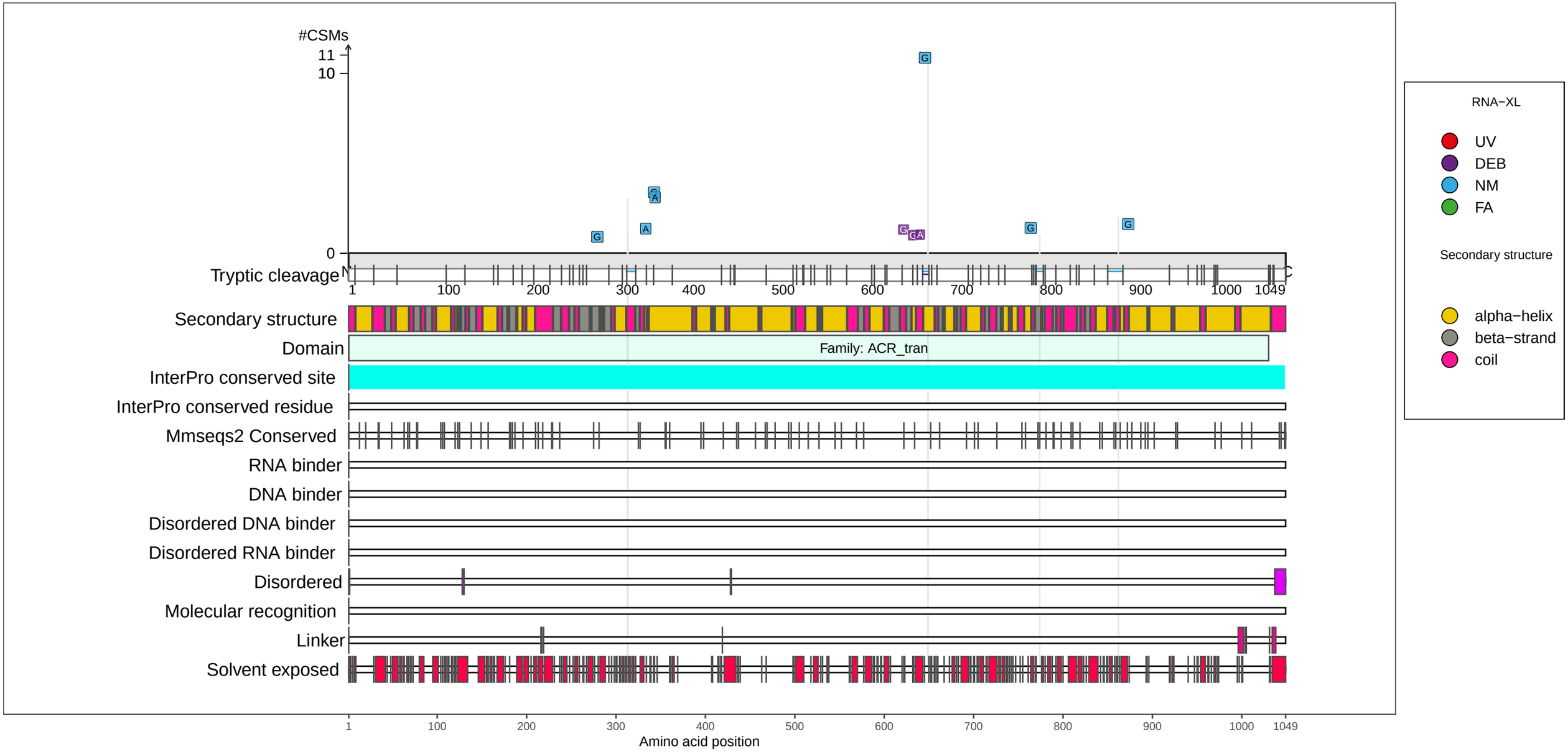
− RNA functions: not annotated



P31224
ACRB_ECOLI Multidrug efflux pump subunit AcrB

− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.72 (Q 65)

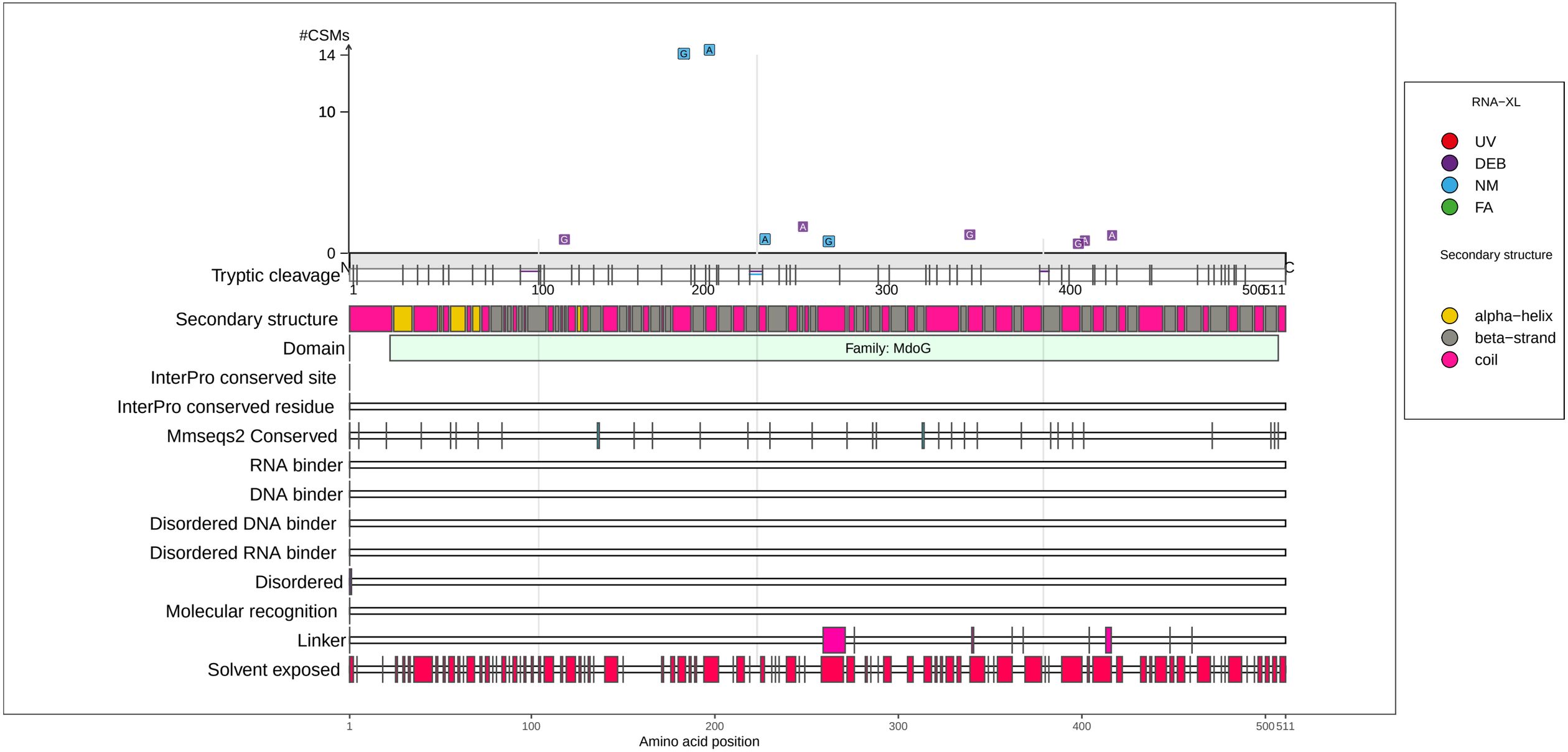
− RNA functions: not annotated



P33136
OPGG_ECOLI Glucans biosynthesis protein G

− Abundance:
tryptic [log10 Intensity]: 8.39 (Q 72)
PAXdb K12 strain [ppm]: 2.29 (Q 69)
PAXdb E.coli [ppm]: 2.43 (Q 84)

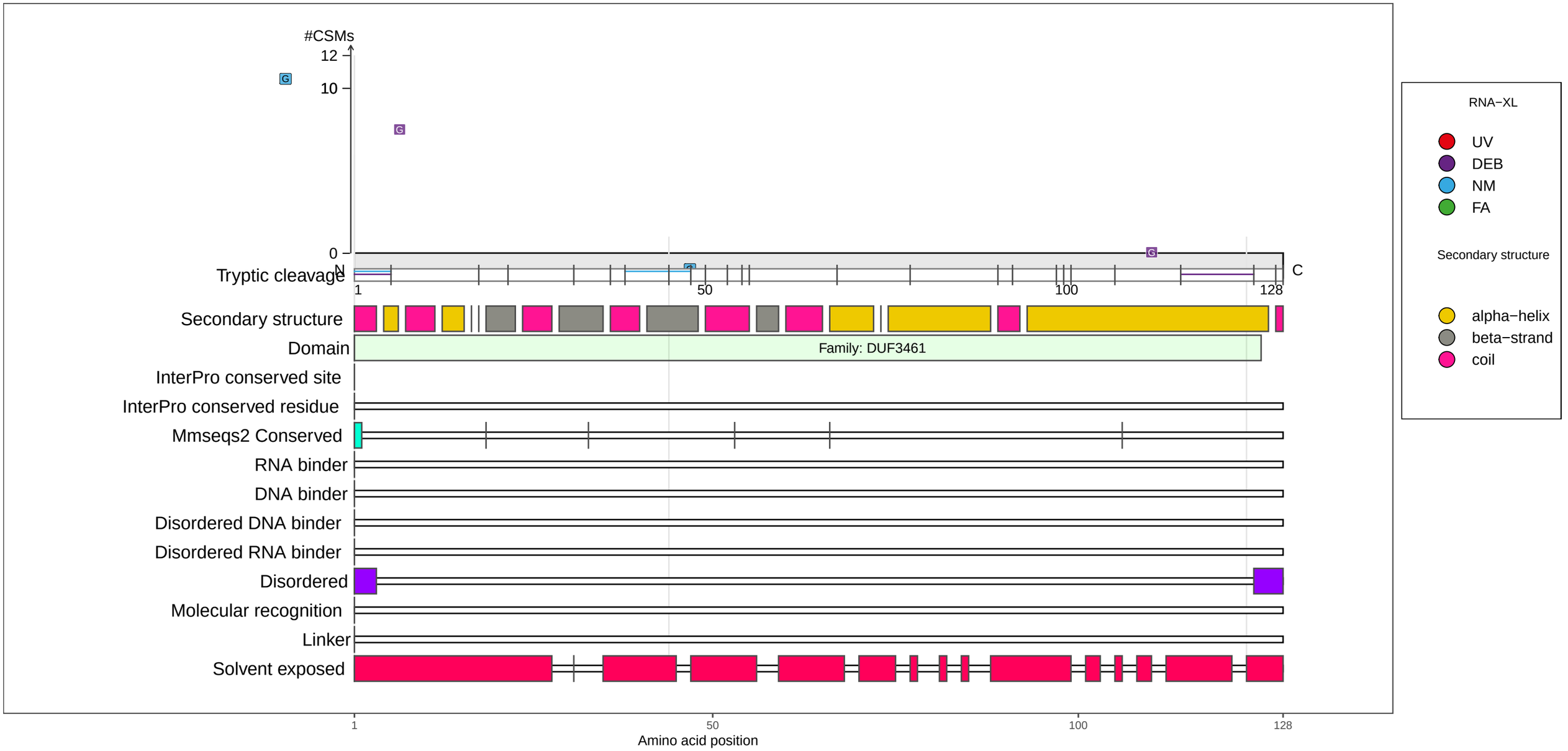
− RNA functions: not annotated



P62768
YAEH_ECOLI UPF0325 protein YaeH

− Abundance:
tryptic [log10 Intensity]: 7.67 (Q 43)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 3.13 (Q 96)

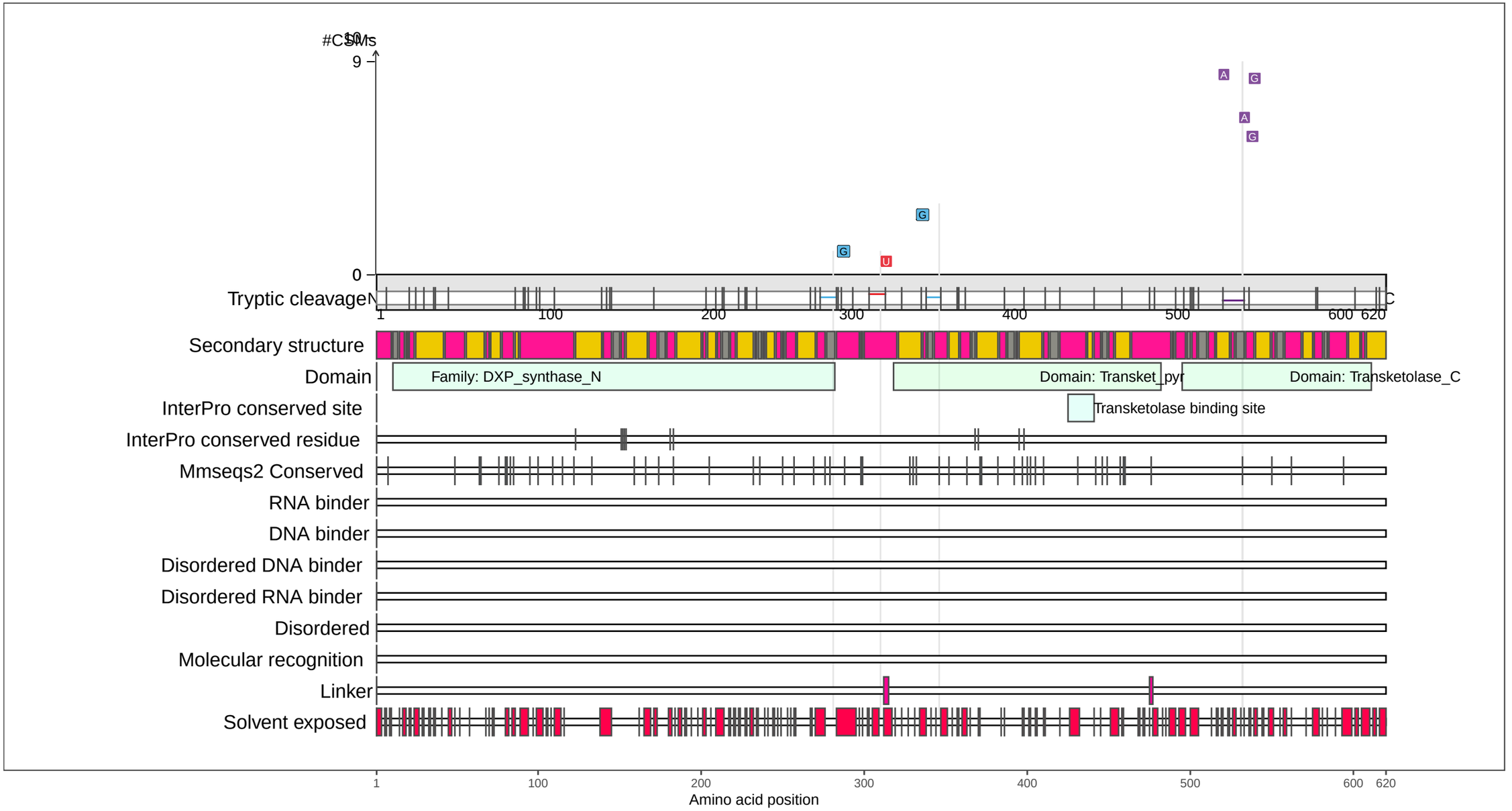
− RNA functions: not annotated

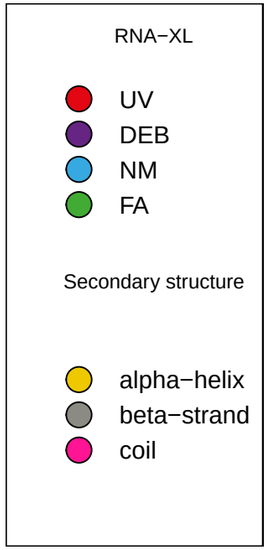


P77488
DXS_ECOLI 1−deoxy−D−xylulose−5−phosphate synthase

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 1.95 (Q 59)
PAXdb E.coli [ppm]: 2.25 (Q 79)

− RNA functions: not annotated

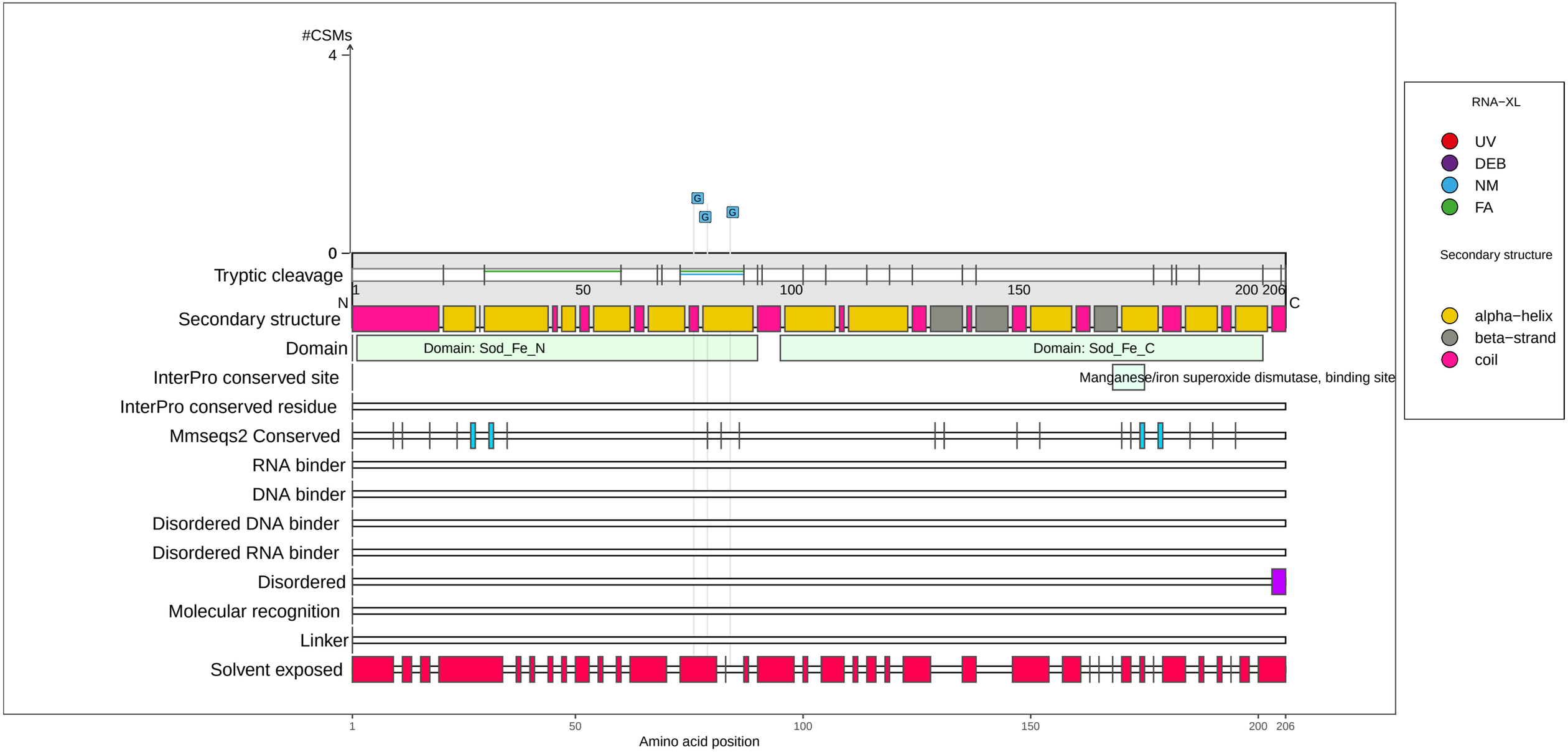




P00448
SODM_ECOLI Superoxide dismutase [Mn]

− Abundance:
tryptic [log10 Intensity]: 9.02 (Q 89)
PAXdb K12 strain [ppm]: 2.41 (Q 74)
PAXdb E.coli [ppm]: 3.73 (Q 100)

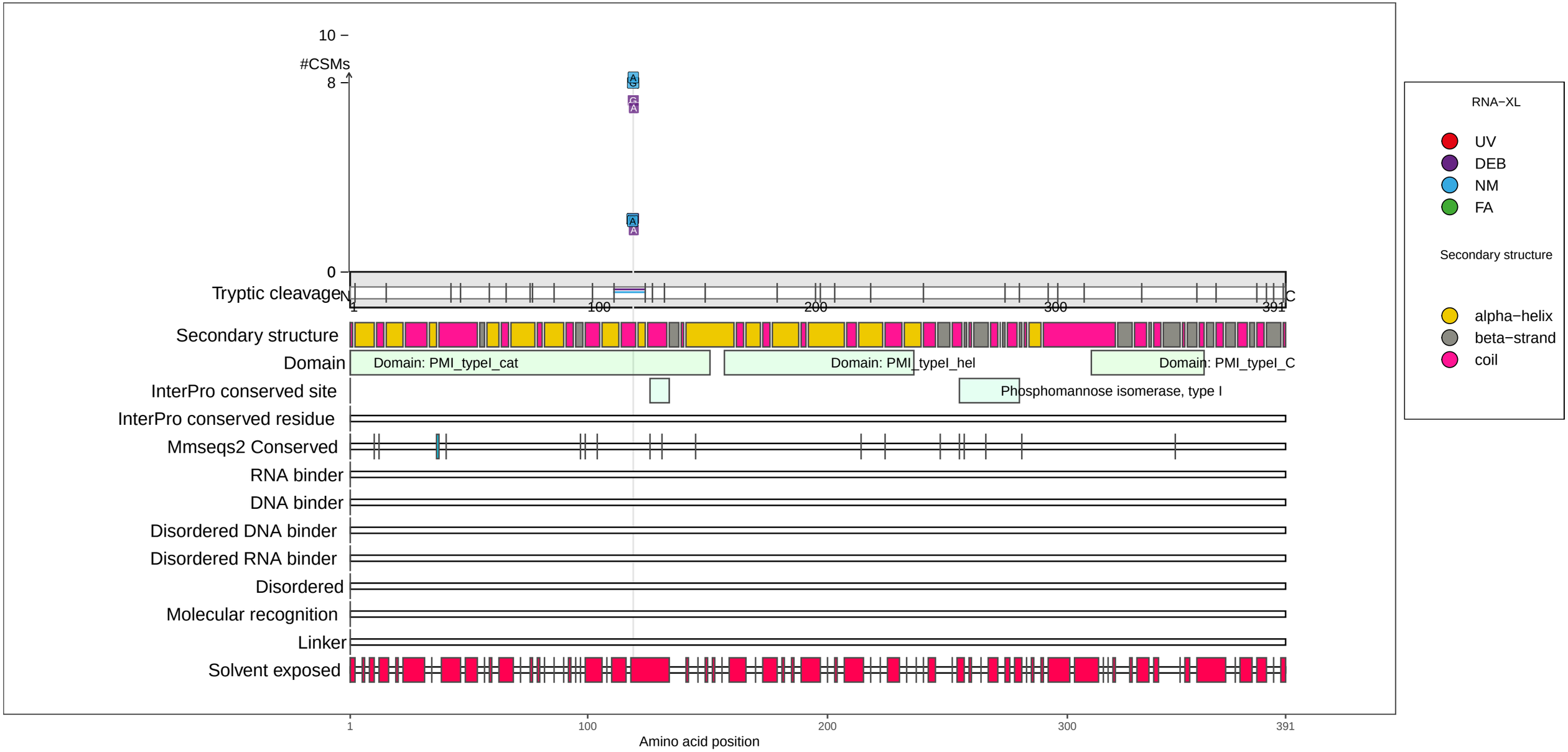
− RNA functions: not annotated



P00946
MANA_ECOLI Mannose−6−phosphate isomerase

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.56 (Q 87)

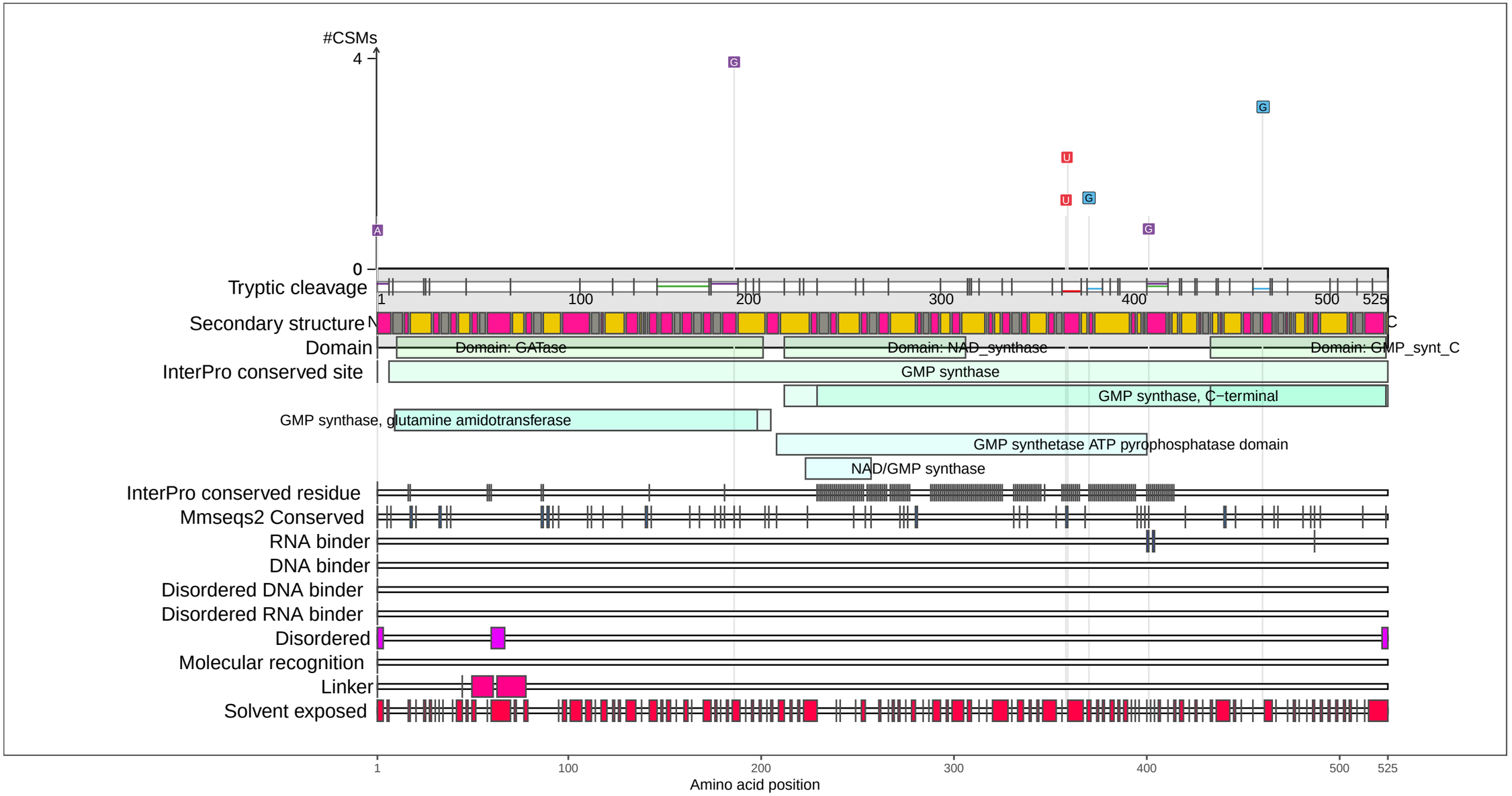
− RNA functions: not annotated

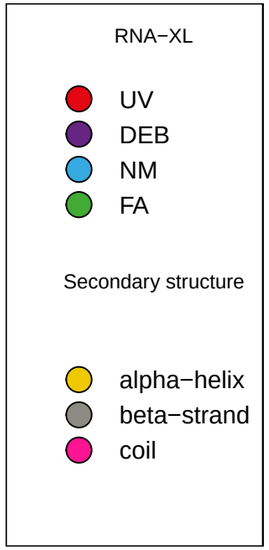


P04079
GUAA_ECOLI GMP synthase [glutamine−hydrolyzing]

− Abundance:
tryptic [log10 Intensity]: 9.46 (Q 96)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 3.05 (Q 95)

− RNA functions:
tRNA methyl transferase

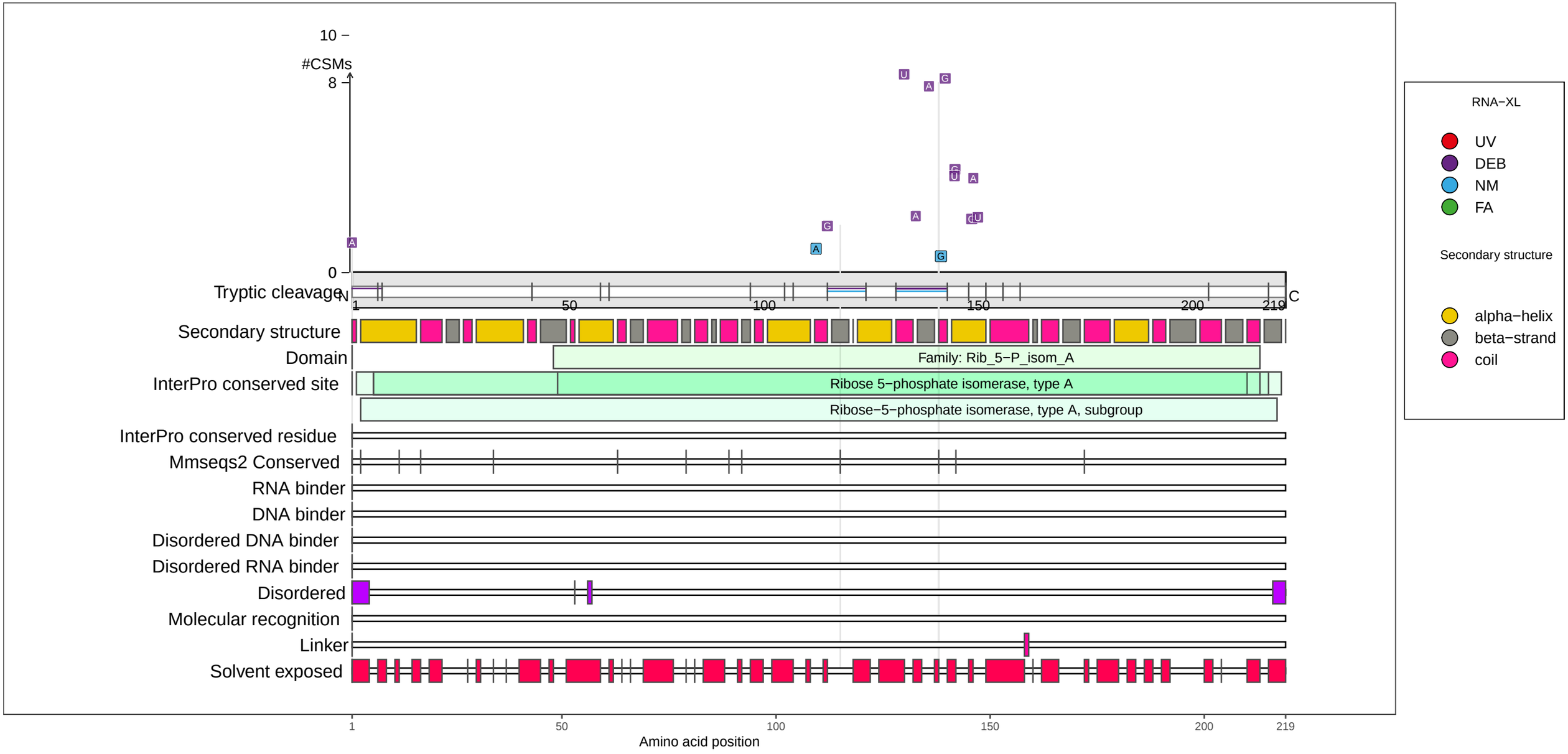




P0A7Z0
RPIA_ECOLI Ribose−5−phosphate isomerase A

− Abundance:
tryptic [log10 Intensity]: 8.6 (Q 79)
PAXdb K12 strain [ppm]: 3.49 (Q 97)
PAXdb E.coli [ppm]: 2.85 (Q 93)

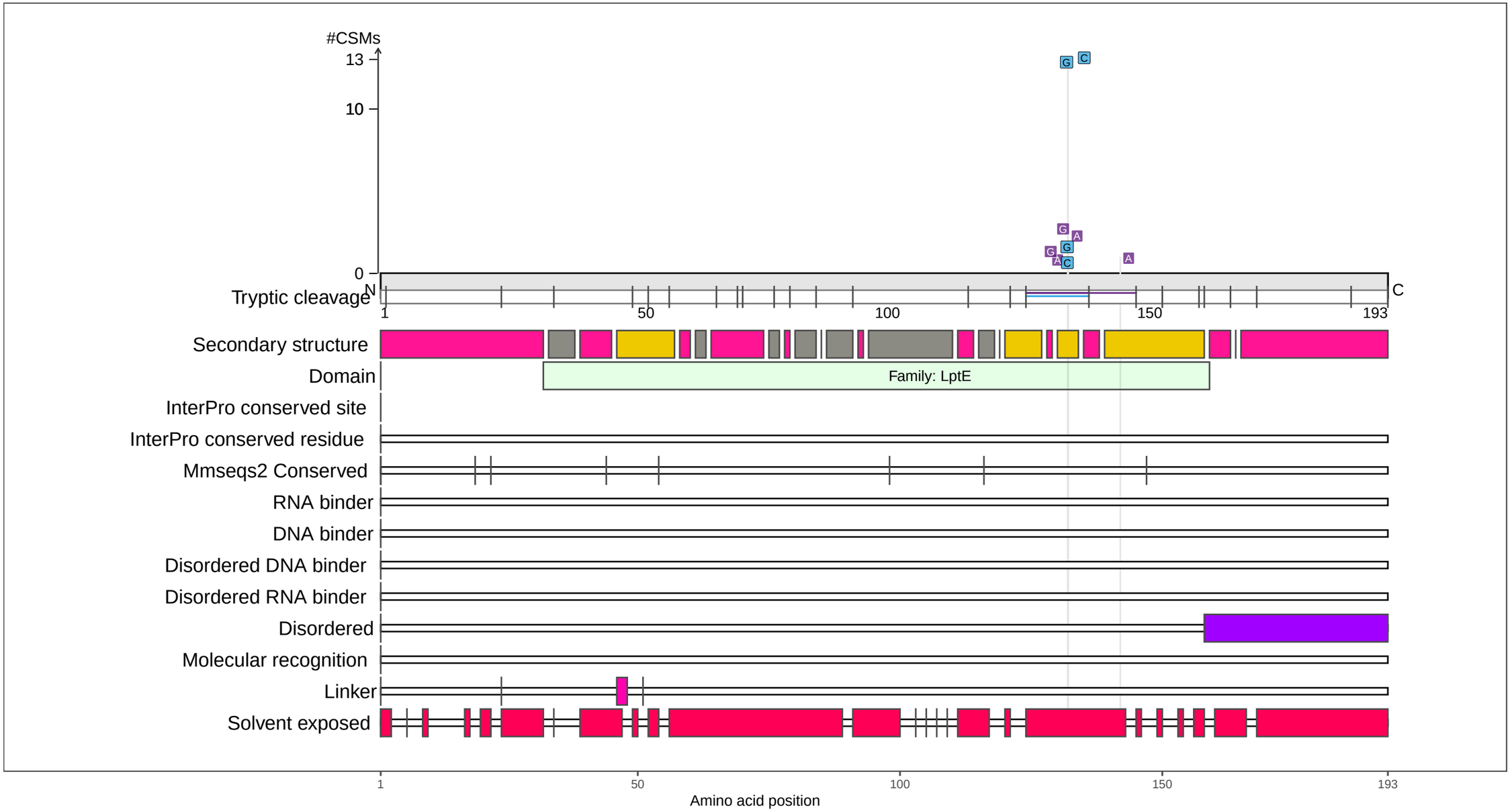
− RNA functions: not annotated

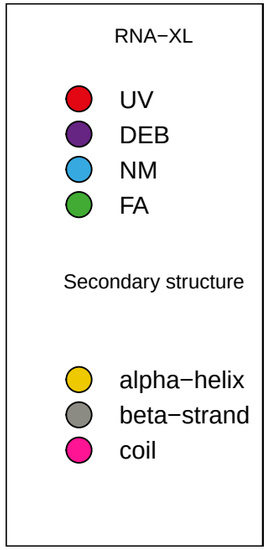


P0ADC1
LPTE_ECOLI LPS−assembly lipoprotein LptE

− Abundance:
tryptic [log10 Intensity]: 9.23 (Q 93)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 2.05 (Q 73)

− RNA functions: not annotated

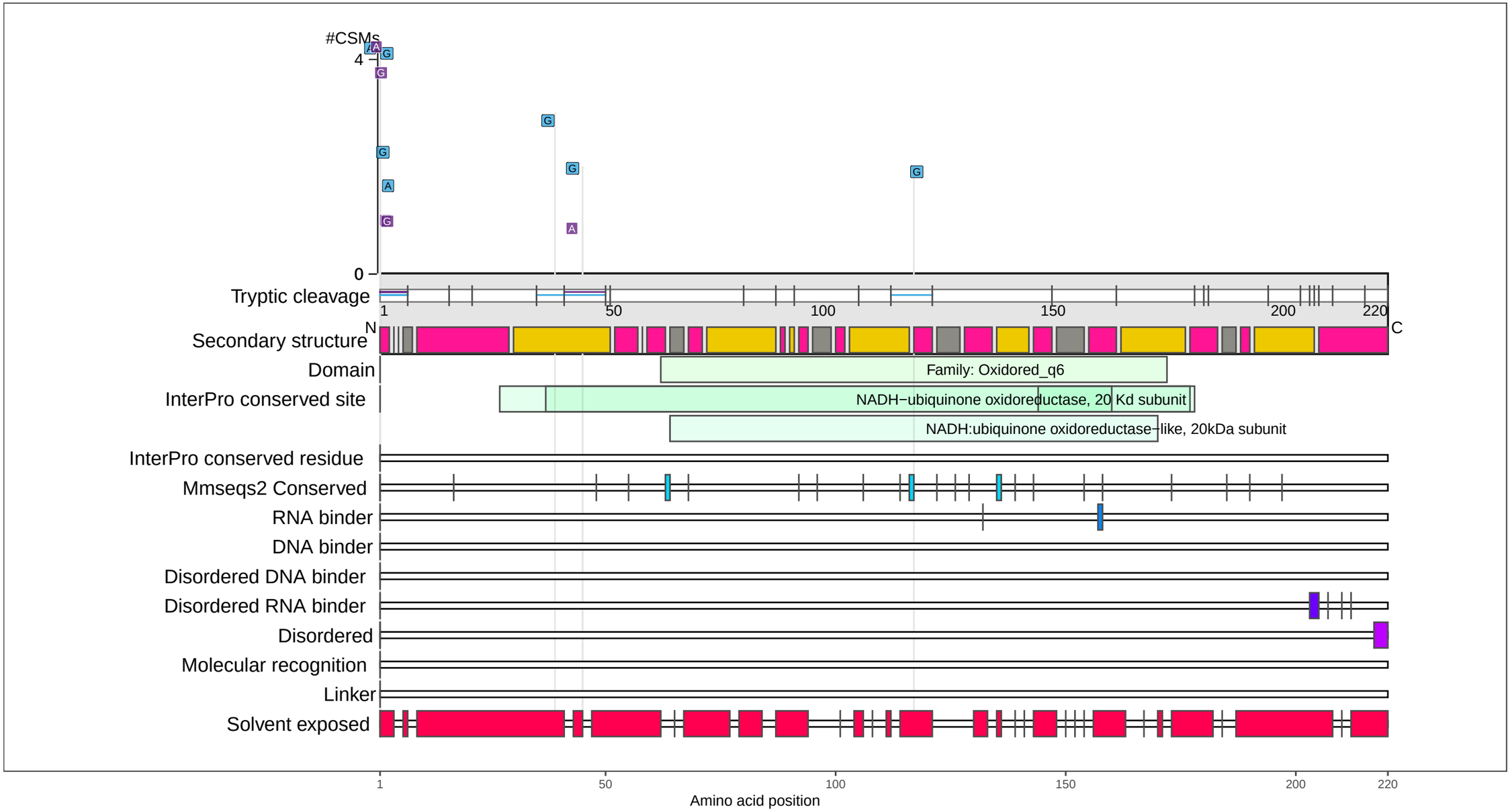




P0AFC7
NUOB_ECOLI NADH−quinone oxidoreductase subunit B

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 1.95 (Q 59)
PAXdb E.coli [ppm]: 2.59 (Q 88)

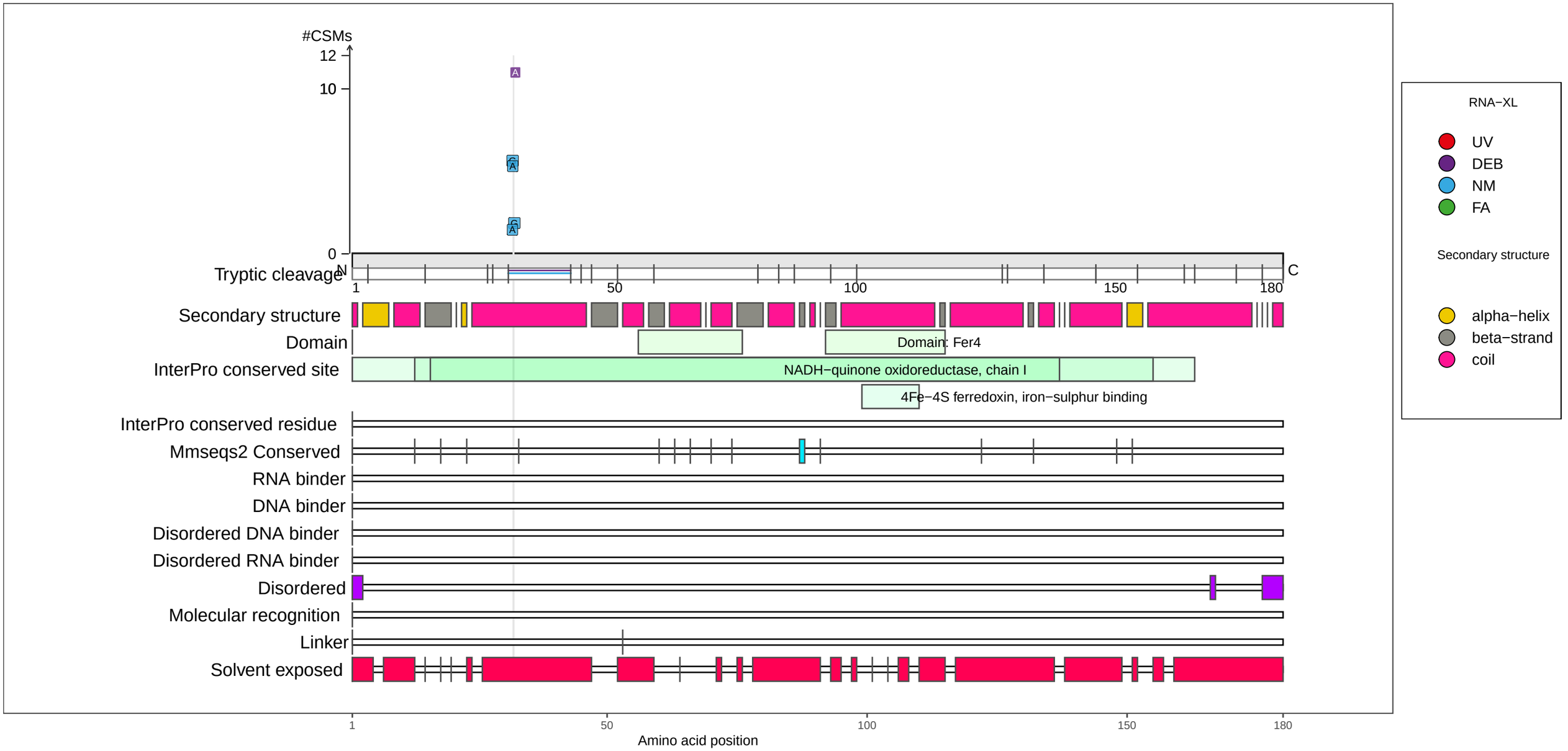
− RNA functions: not annotated



P0AFD6
NUOI_ECOLI NADH−quinone oxidoreductase subunit I

− Abundance:
tryptic [log10 Intensity]: 8.56 (Q 77)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 2.45 (Q 84)

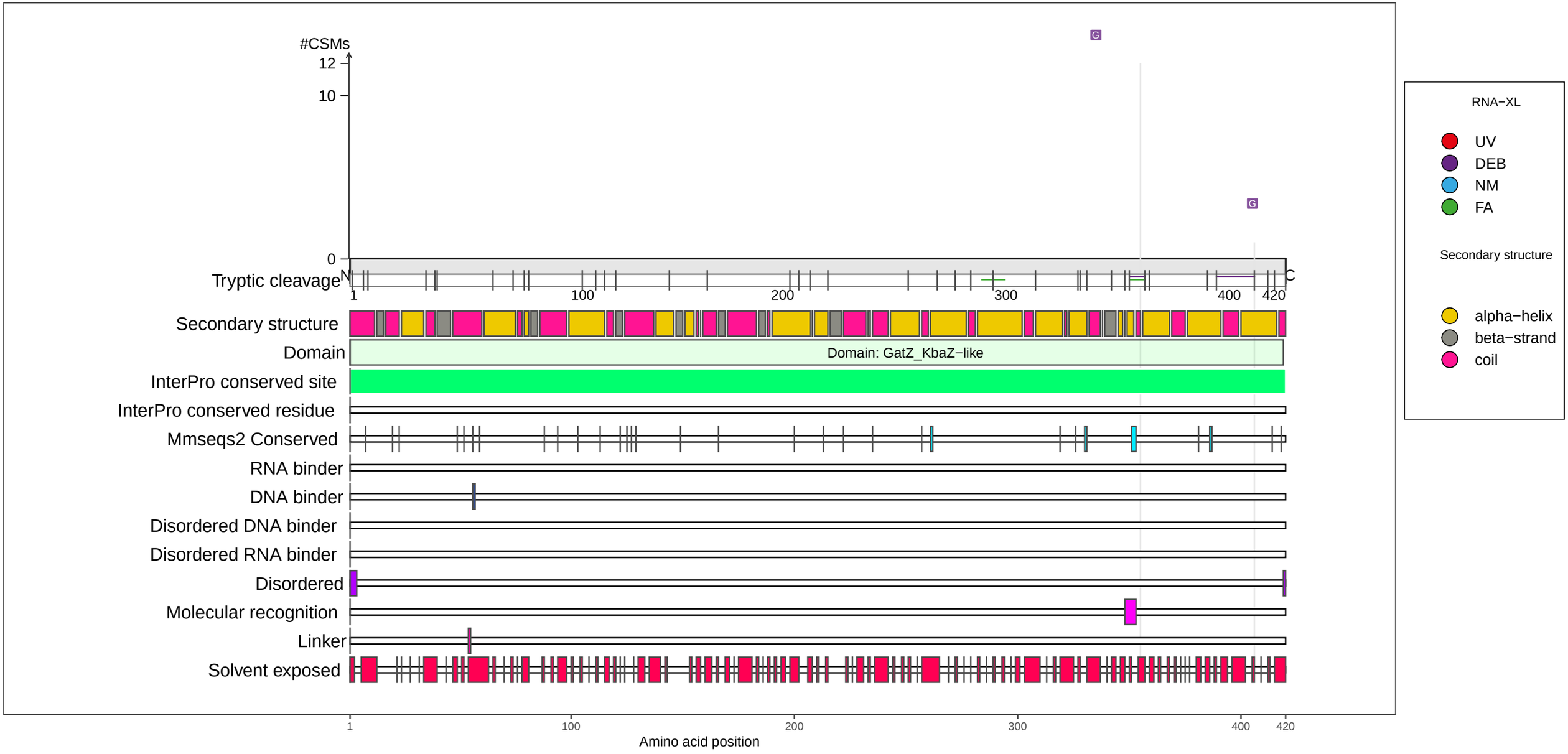
− RNA functions: not annotated



P0C8J8
GATZ_ECOLI D−tagatose−1,6−bisphosphate aldolase subunit GatZ

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 2.66 (Q 82)
PAXdb E.coli [ppm]: 3.48 (Q 99)

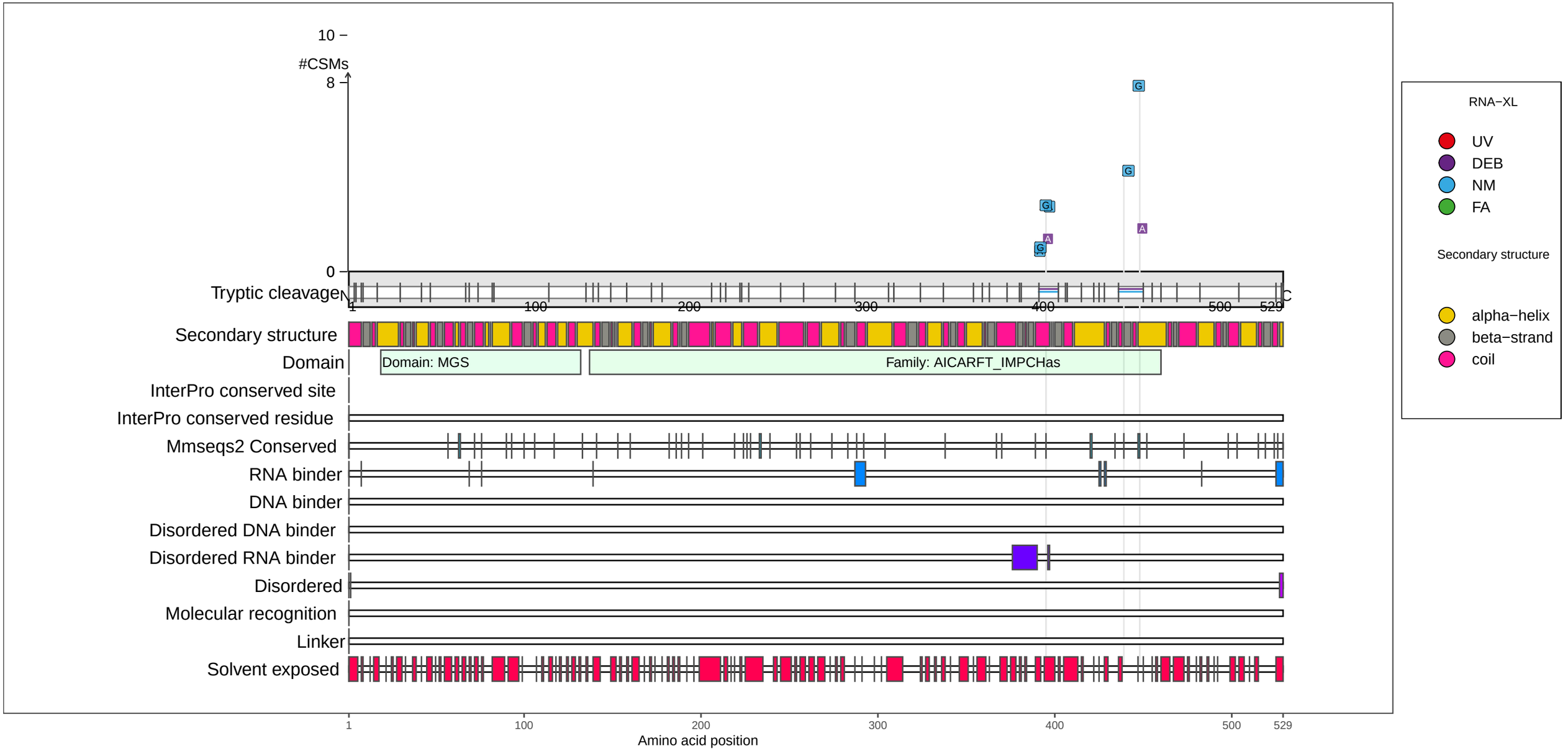
− RNA functions: not annotated



P15639
PUR9_ECOLI Bifunctional purine biosynthesis protein PurH

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 51)
PAXdb K12 strain [ppm]: 2.79 (Q 86)
PAXdb E.coli [ppm]: 2.55 (Q 87)

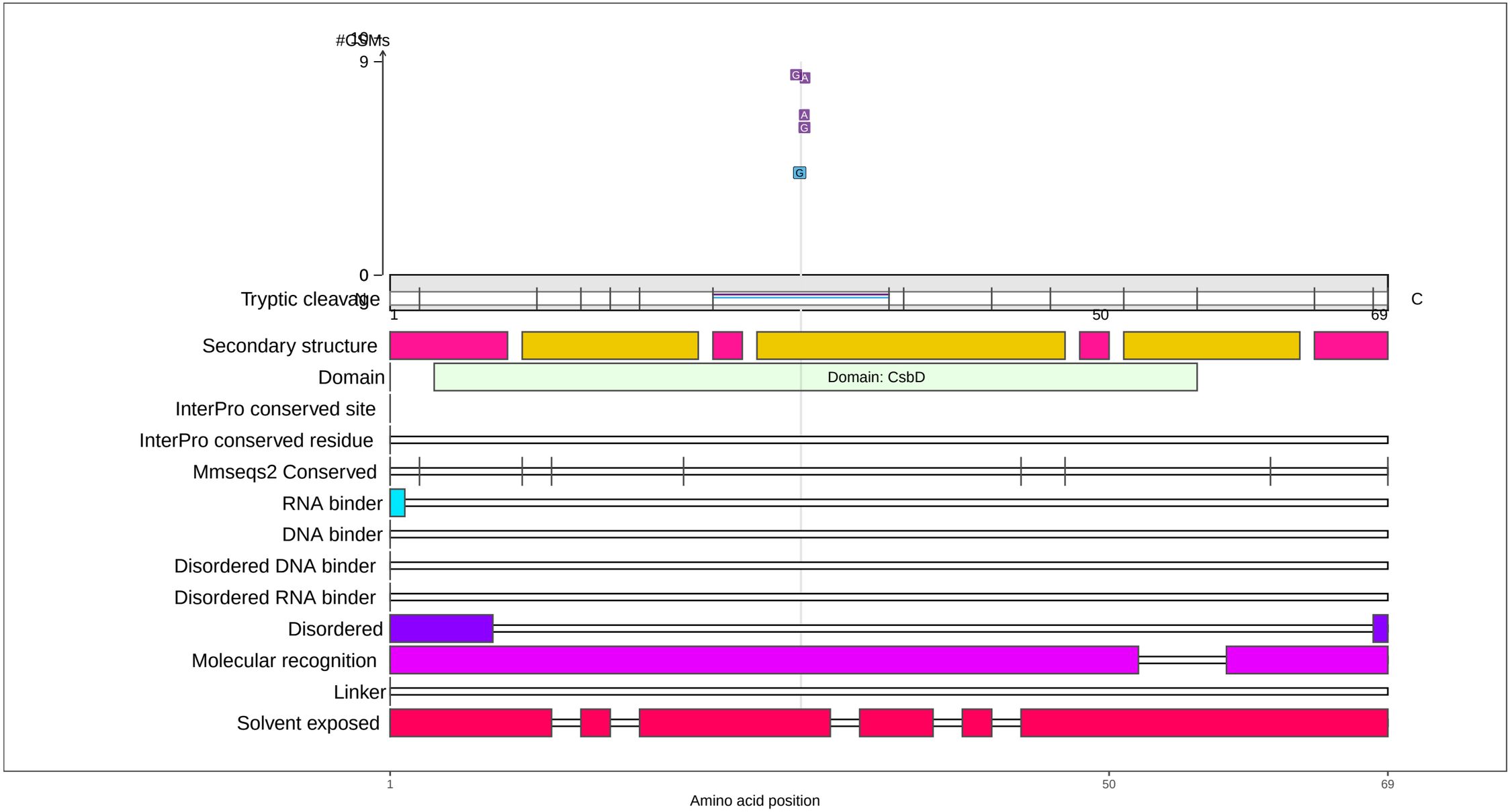
− RNA functions: not annotated

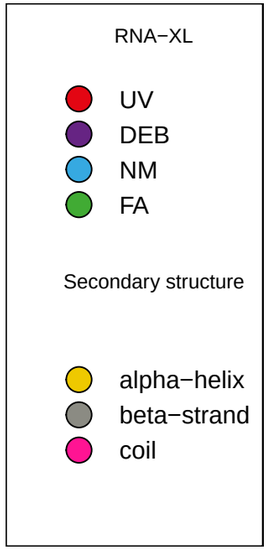


P68206
YJBJ_ECOLI UPF0337 protein YjbJ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 4.46 (Q 100)
PAXdb E.coli [ppm]: 3.07 (Q 96)

− RNA functions: not annotated

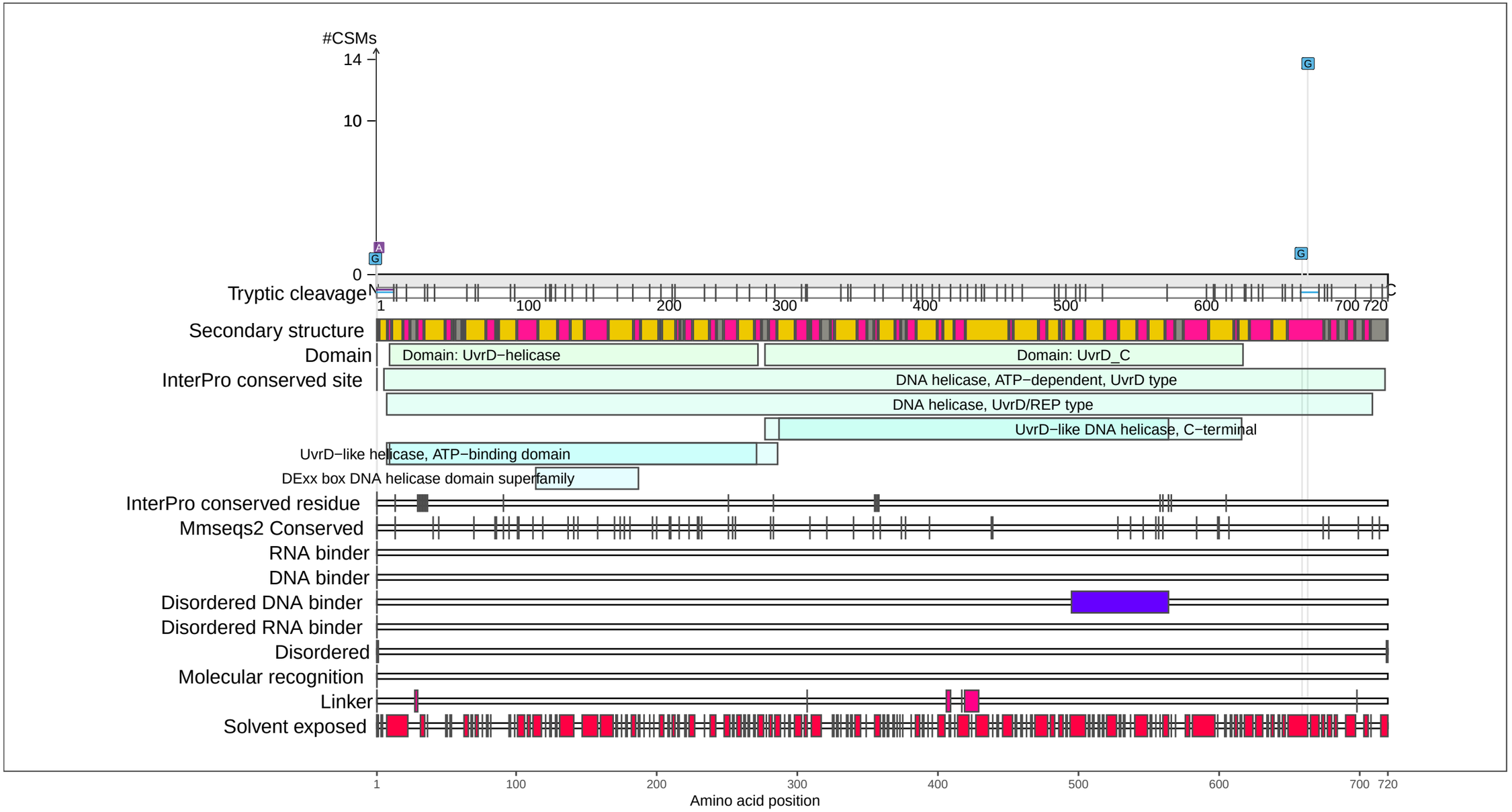


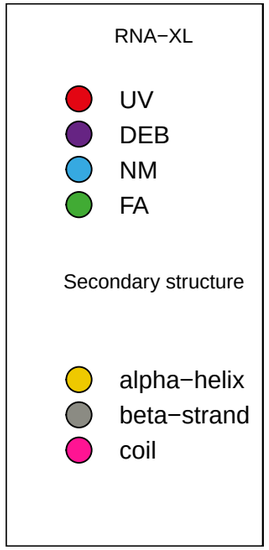


P03018
UVRD_ECOLI DNA helicase II

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: 1.83 (Q 54)
PAXdb E.coli [ppm]: 1.89 (Q 69)

− RNA functions: not annotated

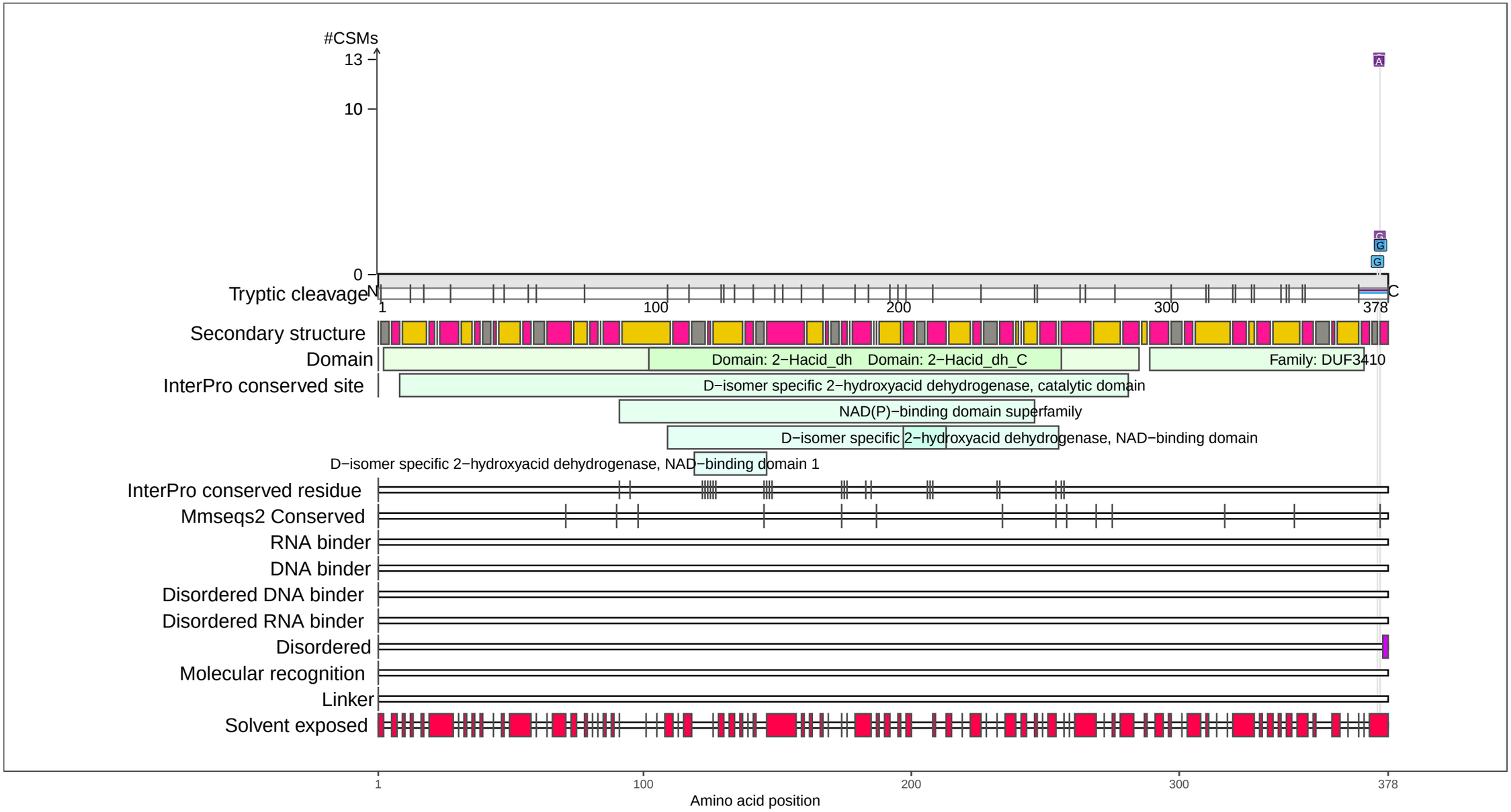


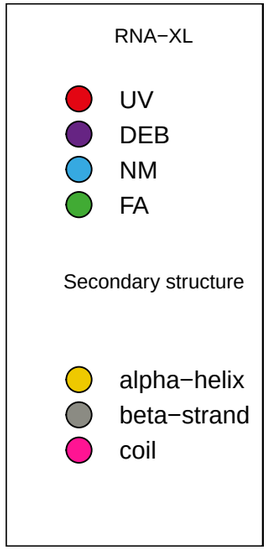


P05459
PDXB_ECOLI Erythronate−4−phosphate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.76 (Q 83)
PAXdb K12 strain [ppm]: 2.64 (Q 82)
PAXdb E.coli [ppm]: 2.33 (Q 81)

− RNA functions: not annotated

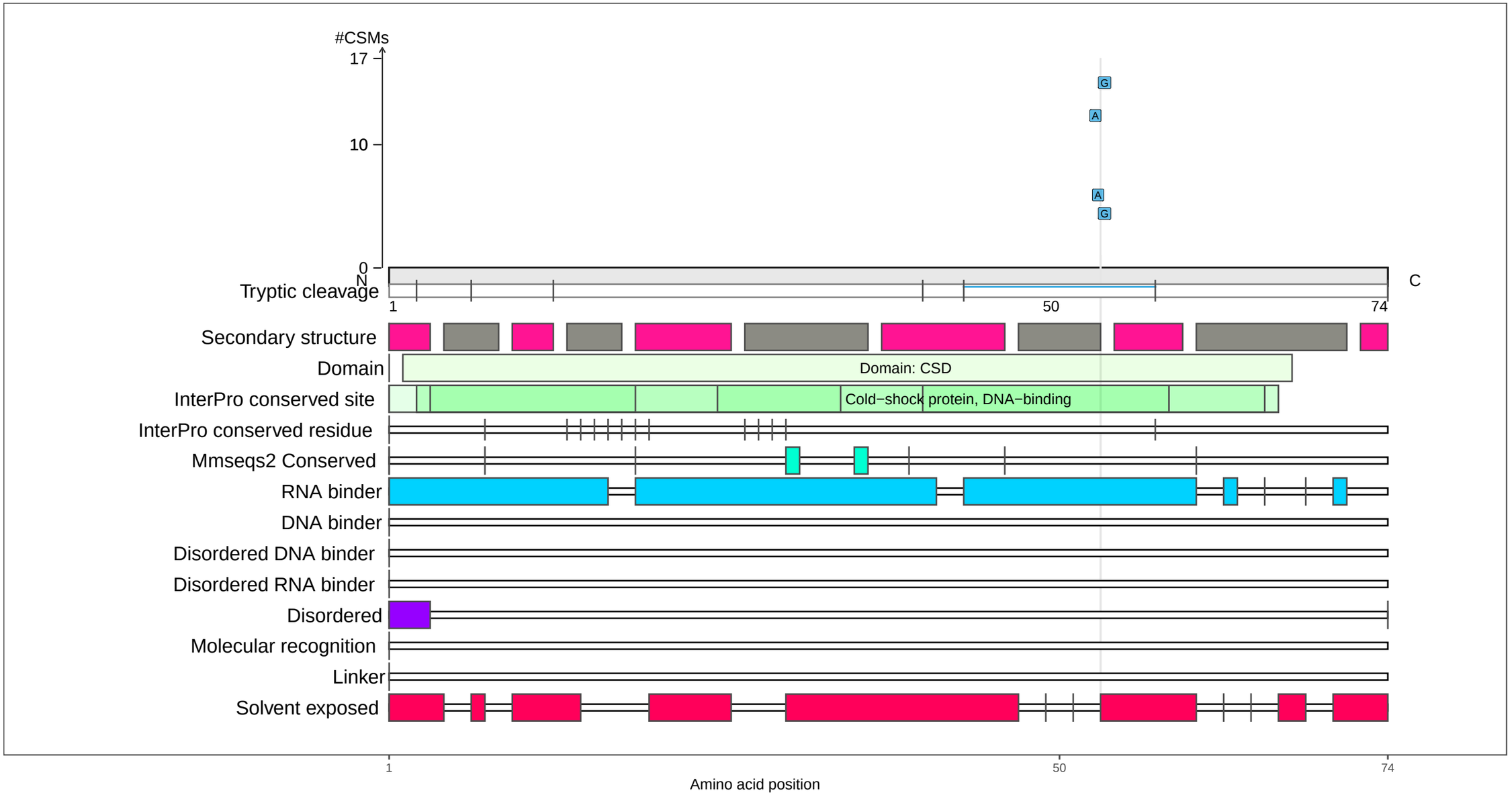




P0A968
CSPD_ECOLI Cold shock−like protein CspD

− Abundance:
tryptic [log10 Intensity]: 6.98 (Q 13)
PAXdb K12 strain [ppm]: 1.63 (Q 46)
PAXdb E.coli [ppm]: 2.87 (Q 93)

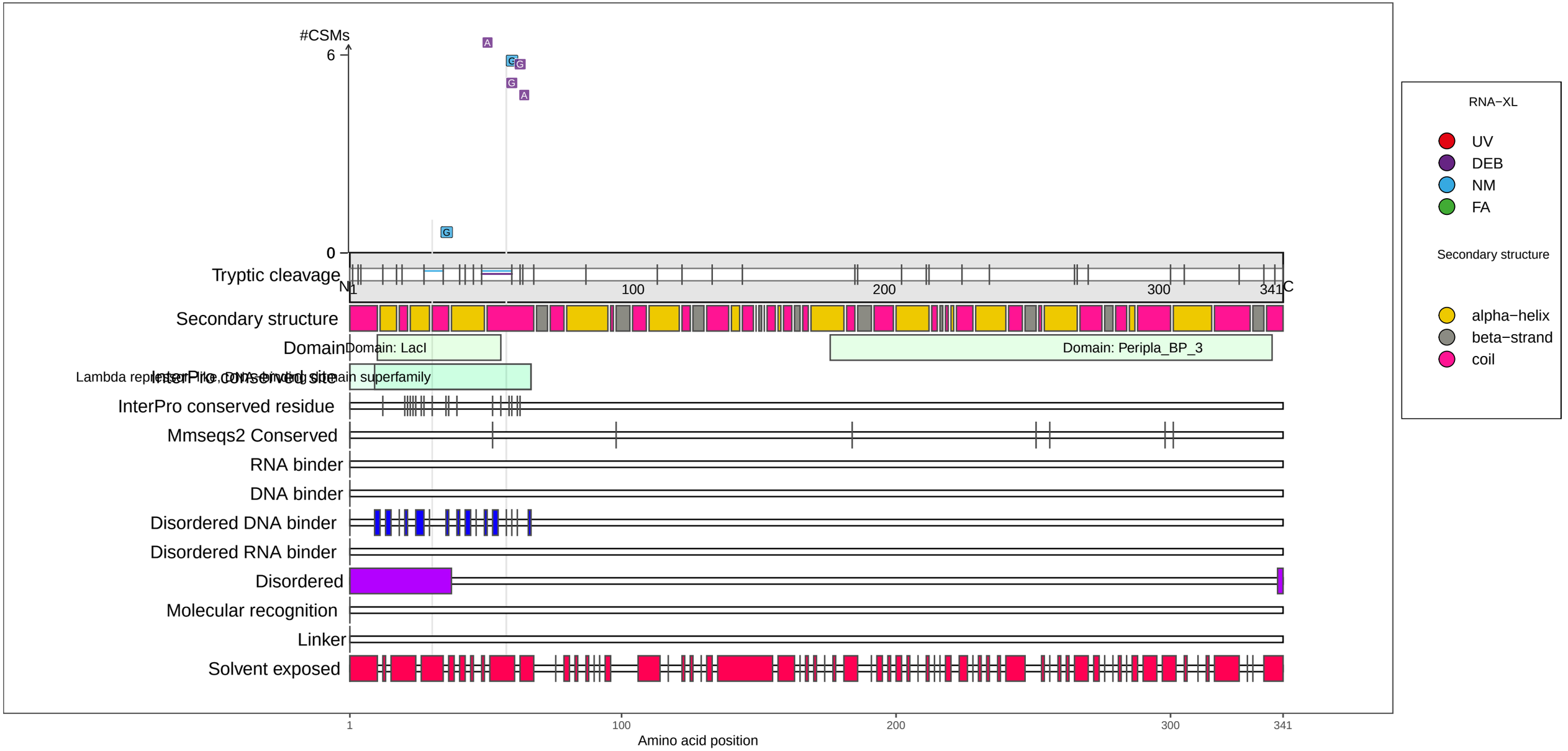
− RNA functions:
RNA binding



P0ACN7
CYTR_ECOLI HTH−type transcriptional repressor CytR

− Abundance:
tryptic [log10 Intensity]: 7.32 (Q 26)
PAXdb K12 strain [ppm]: 2.13 (Q 65)
PAXdb E.coli [ppm]: 0.42 (Q 34)

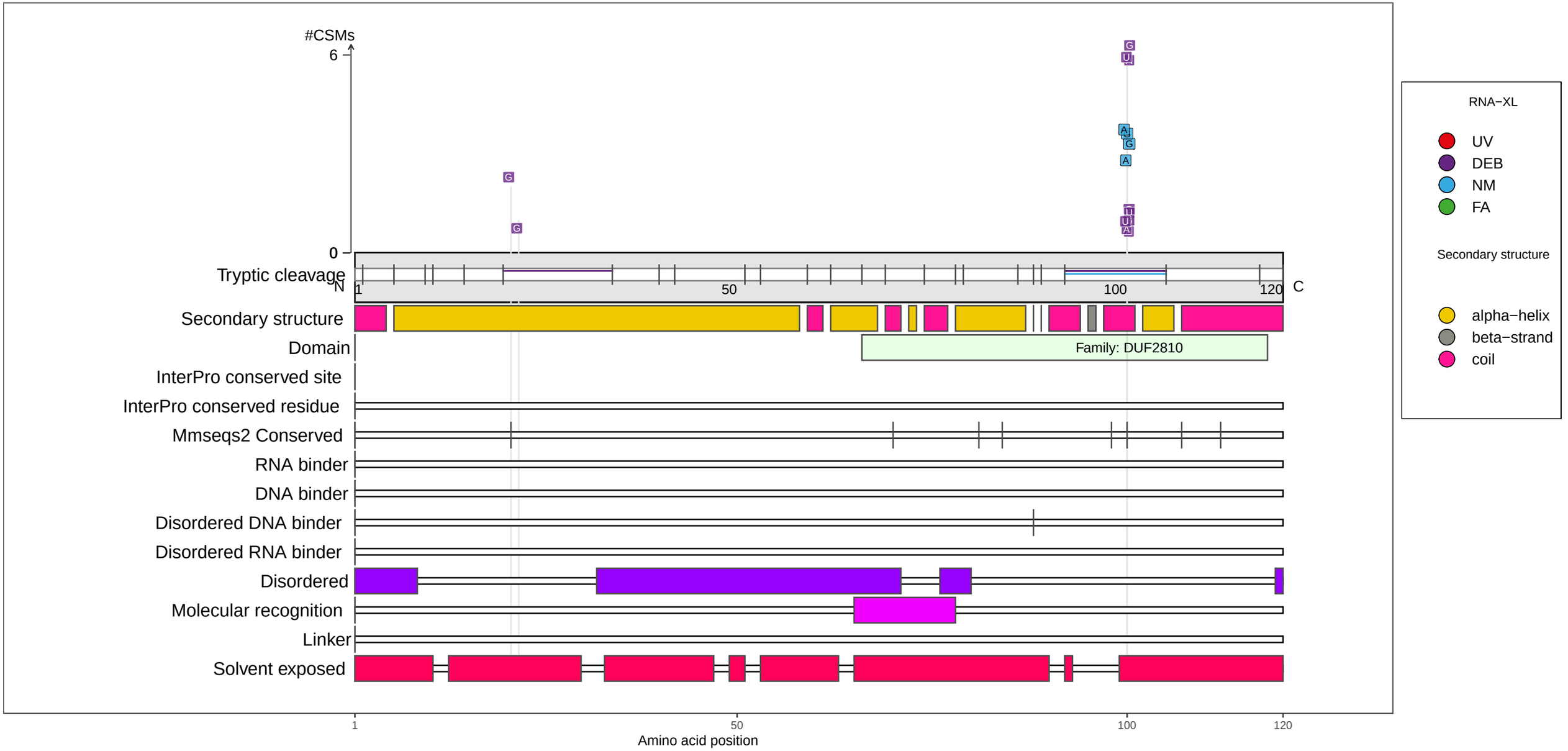
− RNA functions: not annotated



P0ADK8
YIBL_ECOLI Uncharacterized protein YibL

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 25)
PAXdb K12 strain [ppm]: 3.01 (Q 91)
PAXdb E.coli [ppm]: 2.38 (Q 83)

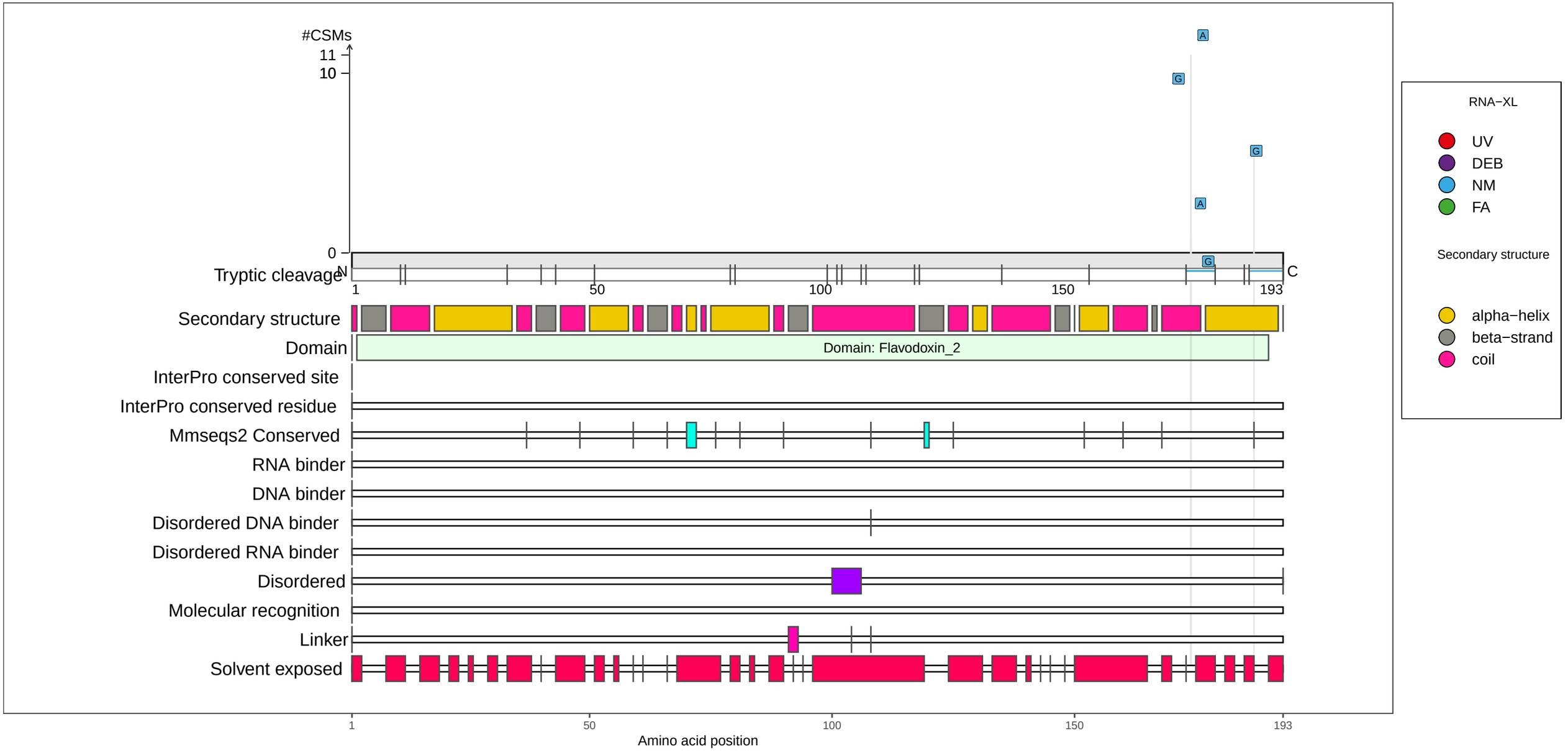
− RNA functions: not annotated



P0AEY5
MDAB_ECOLI NADPH:quinone oxidoreductase MdaB

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.12 (Q 75)

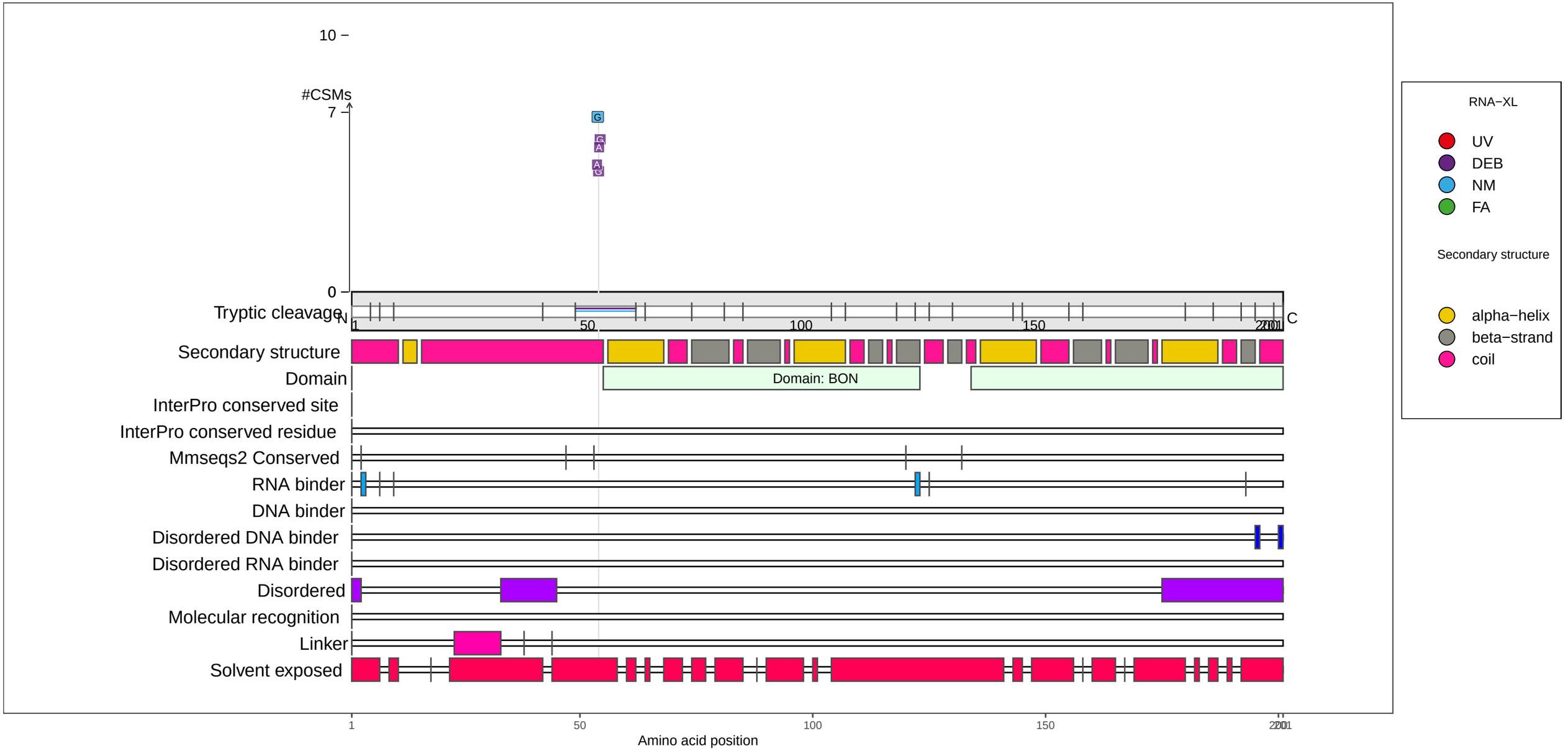
− RNA functions: not annotated



P0AFH8
OSMY_ECOLI Osmotically−inducible protein Y

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: 3.77 (Q 99)
PAXdb E.coli [ppm]: 2.85 (Q 92)

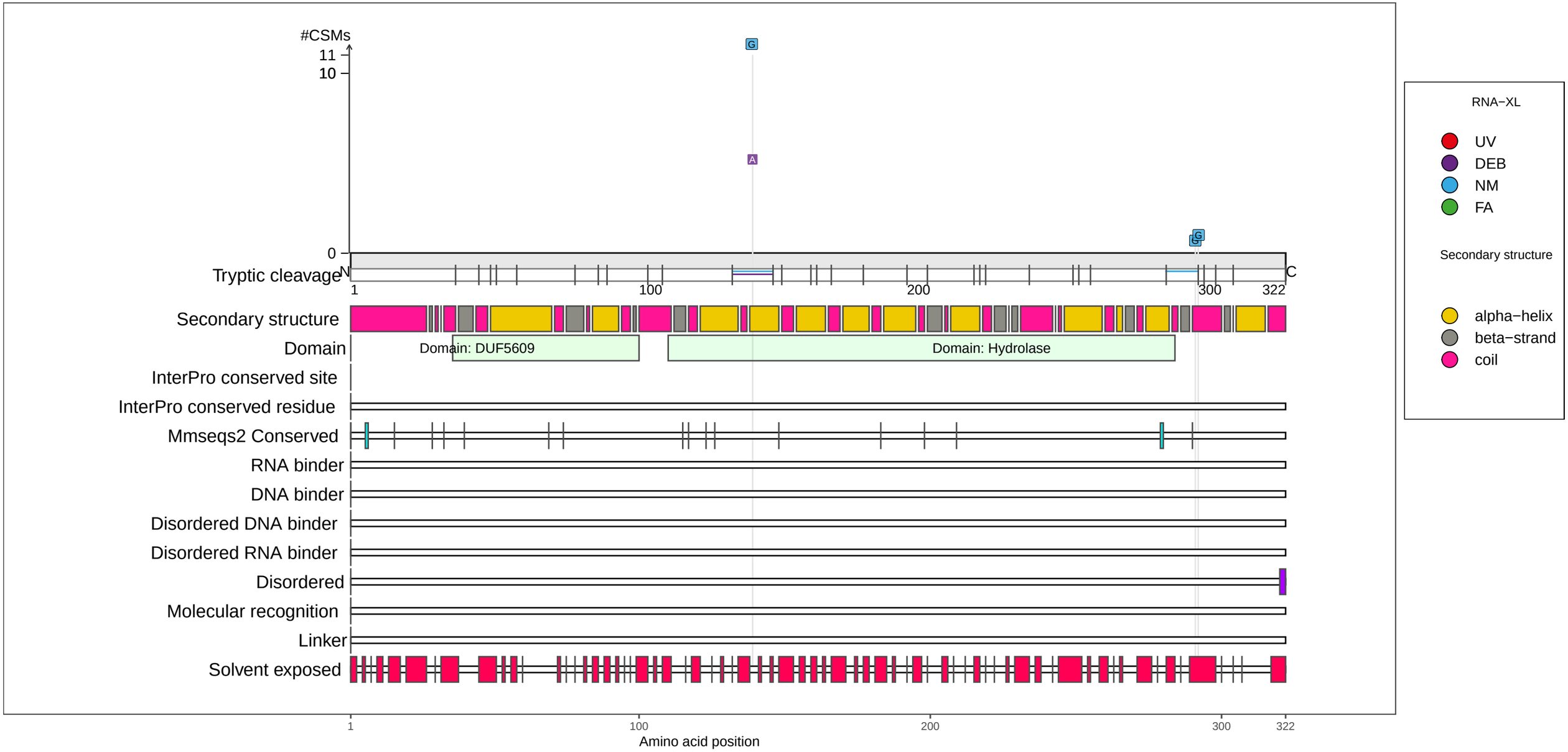
− RNA functions: not annotated



P0AGB0
SERB_ECOLI Phosphoserine phosphatase

− Abundance:
tryptic [log10 Intensity]: 8.79 (Q 83)
PAXdb K12 strain [ppm]: 1.45 (Q 35)
PAXdb E.coli [ppm]: 1.26 (Q 54)

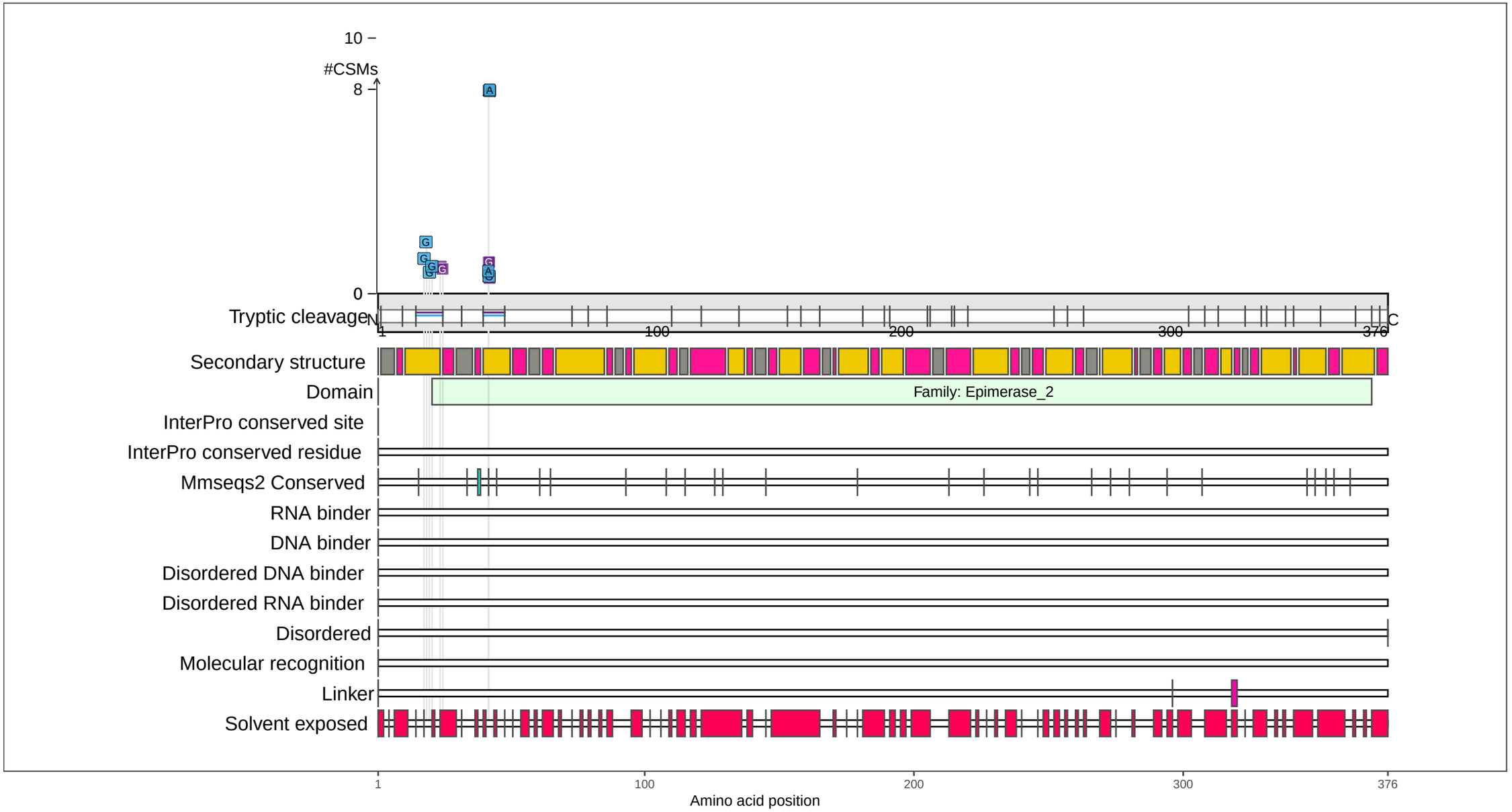
− RNA functions: not annotated



P27828
WECB_ECOLI UDP−N−acetylglucosamine 2−epimerase

− Abundance:
tryptic [log10 Intensity]: 8.07 (Q 60)
PAXdb K12 strain [ppm]: 1.02 (Q 12)
PAXdb E.coli [ppm]: 1.31 (Q 55)

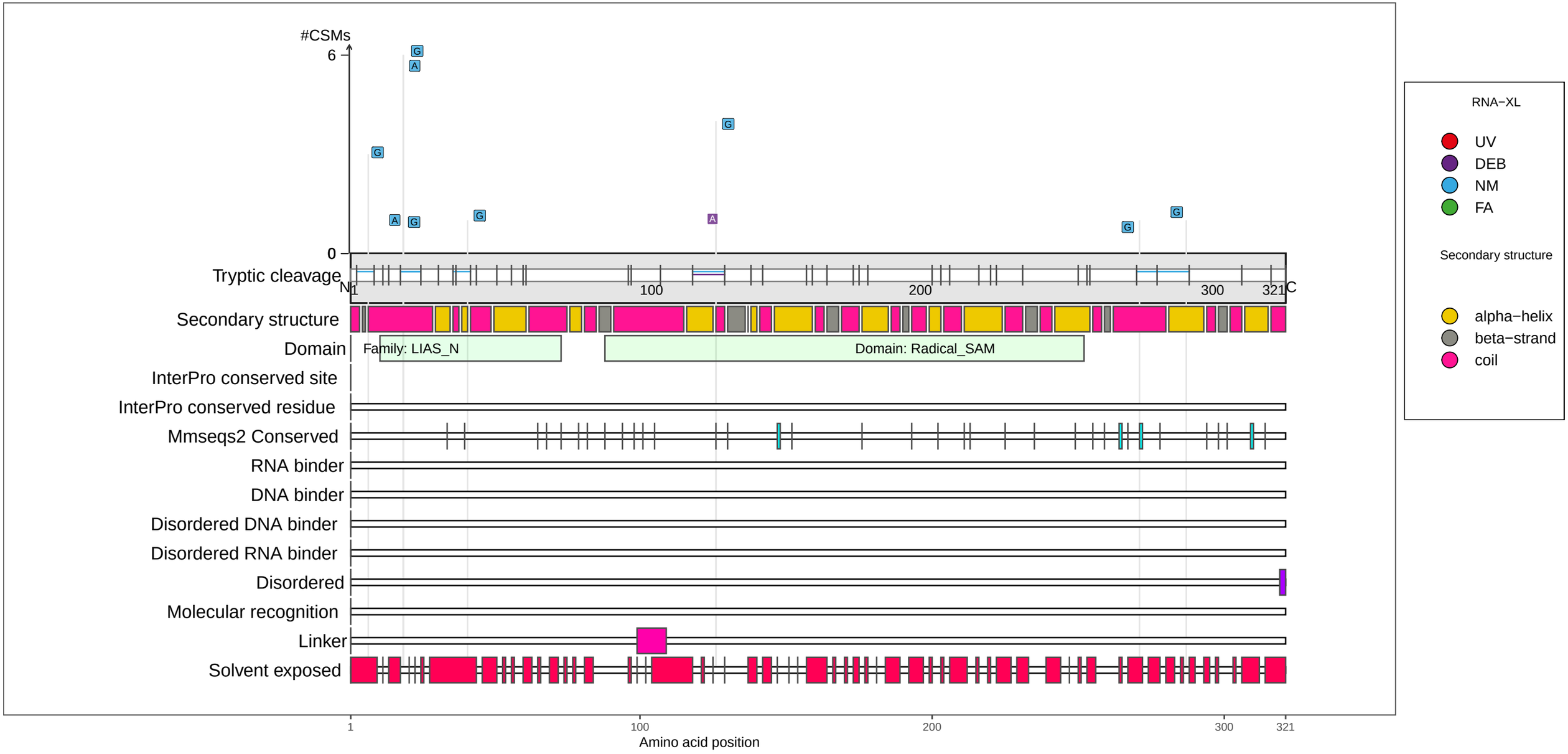
− RNA functions: not annotated



P60716
LIPA_ECOLI Lipoyl synthase

− Abundance:
tryptic [log10 Intensity]: 9.01 (Q 88)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 2.23 (Q 78)

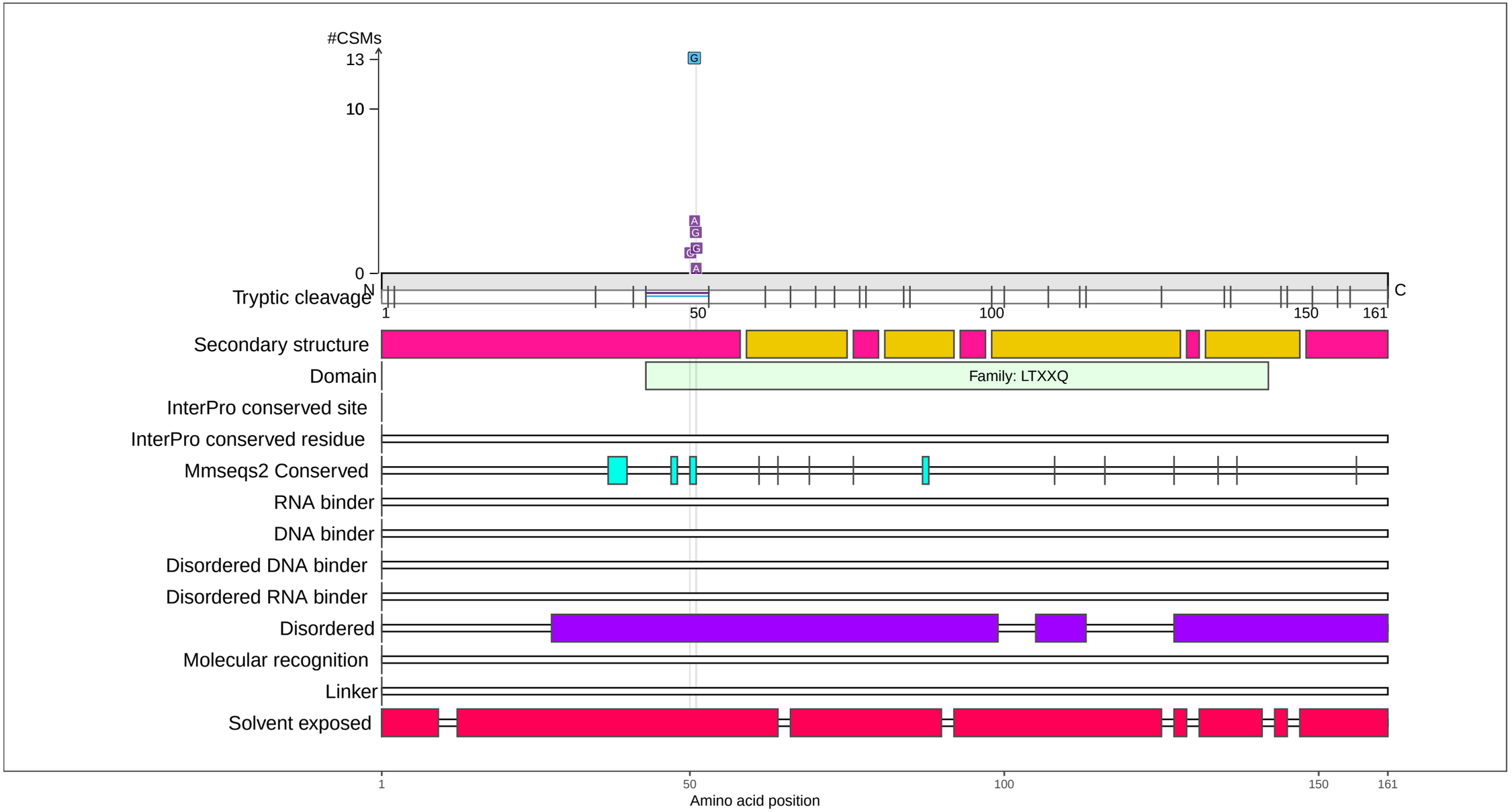
− RNA functions: not annotated

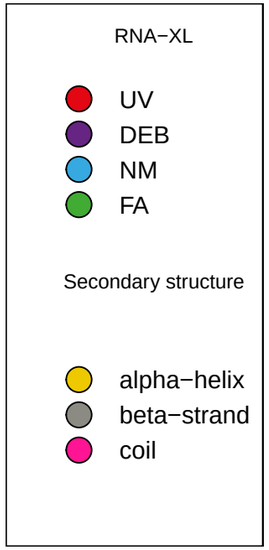


P77754
SPY_ECOLI Periplasmic chaperone Spy

− Abundance:
tryptic [log10 Intensity]: 6.7 (Q 5)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 2.56 (Q 87)

− RNA functions: not annotated

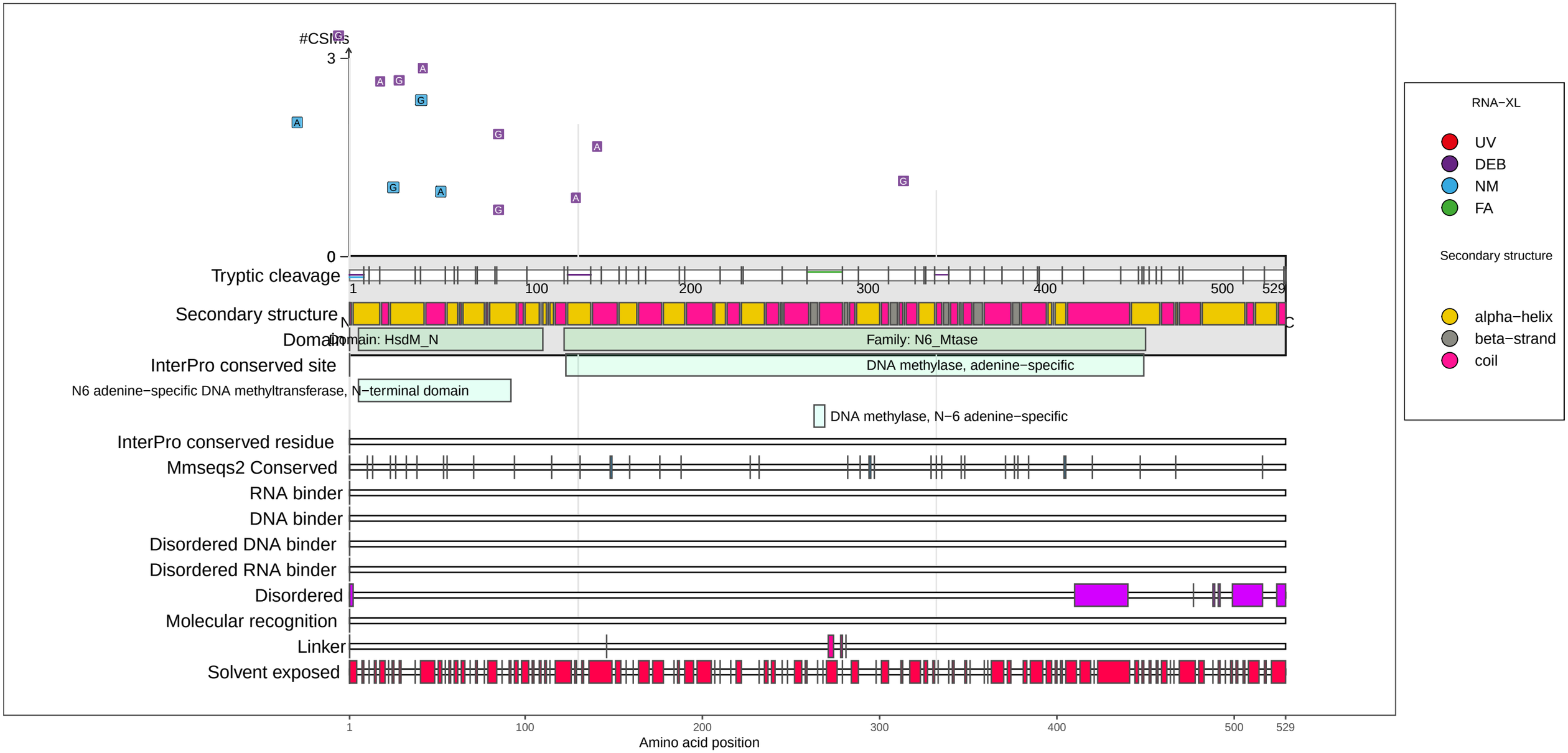




P08957
T1MK_ECOLI Type I restriction enzyme EcoKI methylase subunit

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: 2.13 (Q 65)
PAXdb E.coli [ppm]: 1.66 (Q 63)

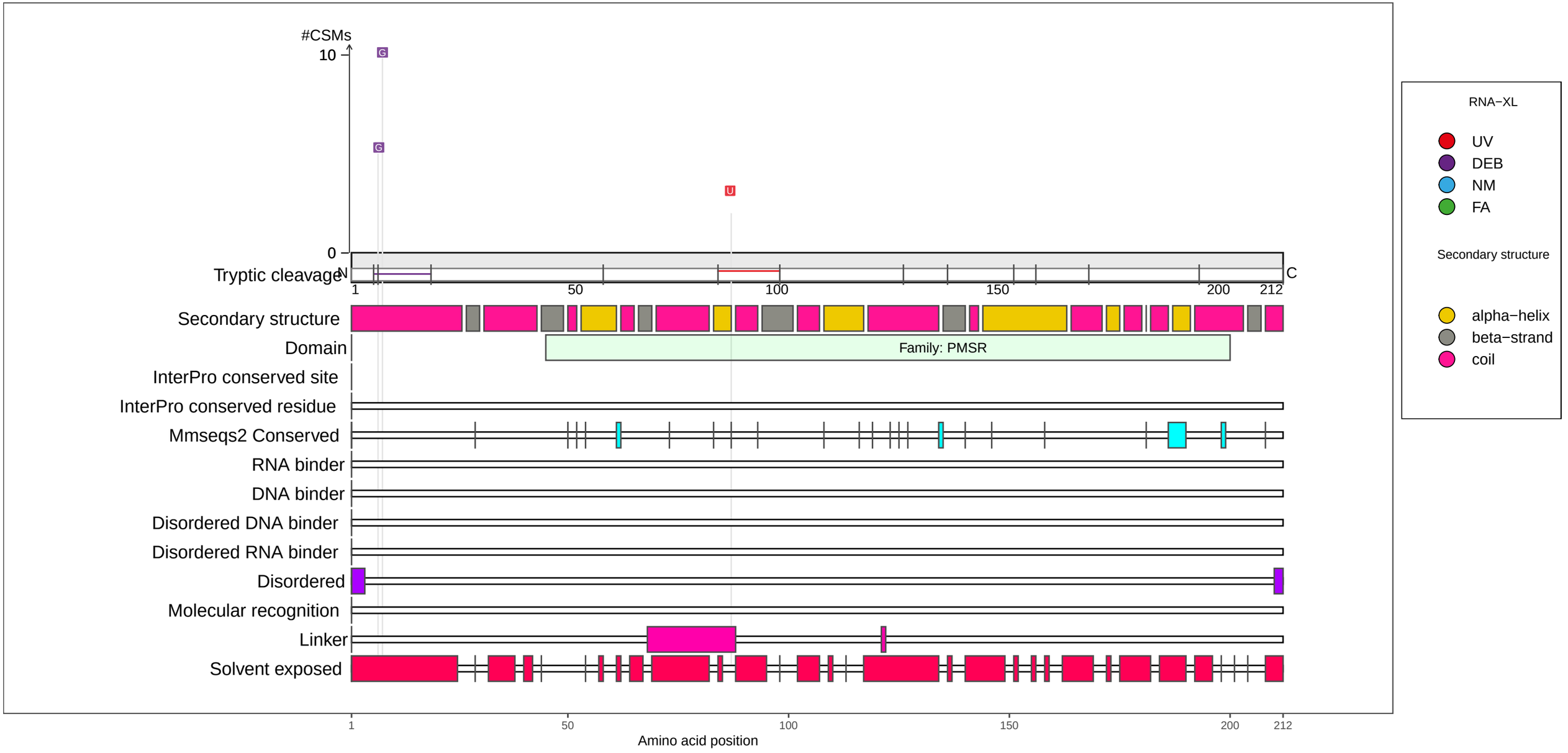
− RNA functions: not annotated



P0A744
MSRA_ECOLI Peptide methionine sulfoxide reductase MsrA

− Abundance:
tryptic [log10 Intensity]: 7.94 (Q 56)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.57 (Q 87)

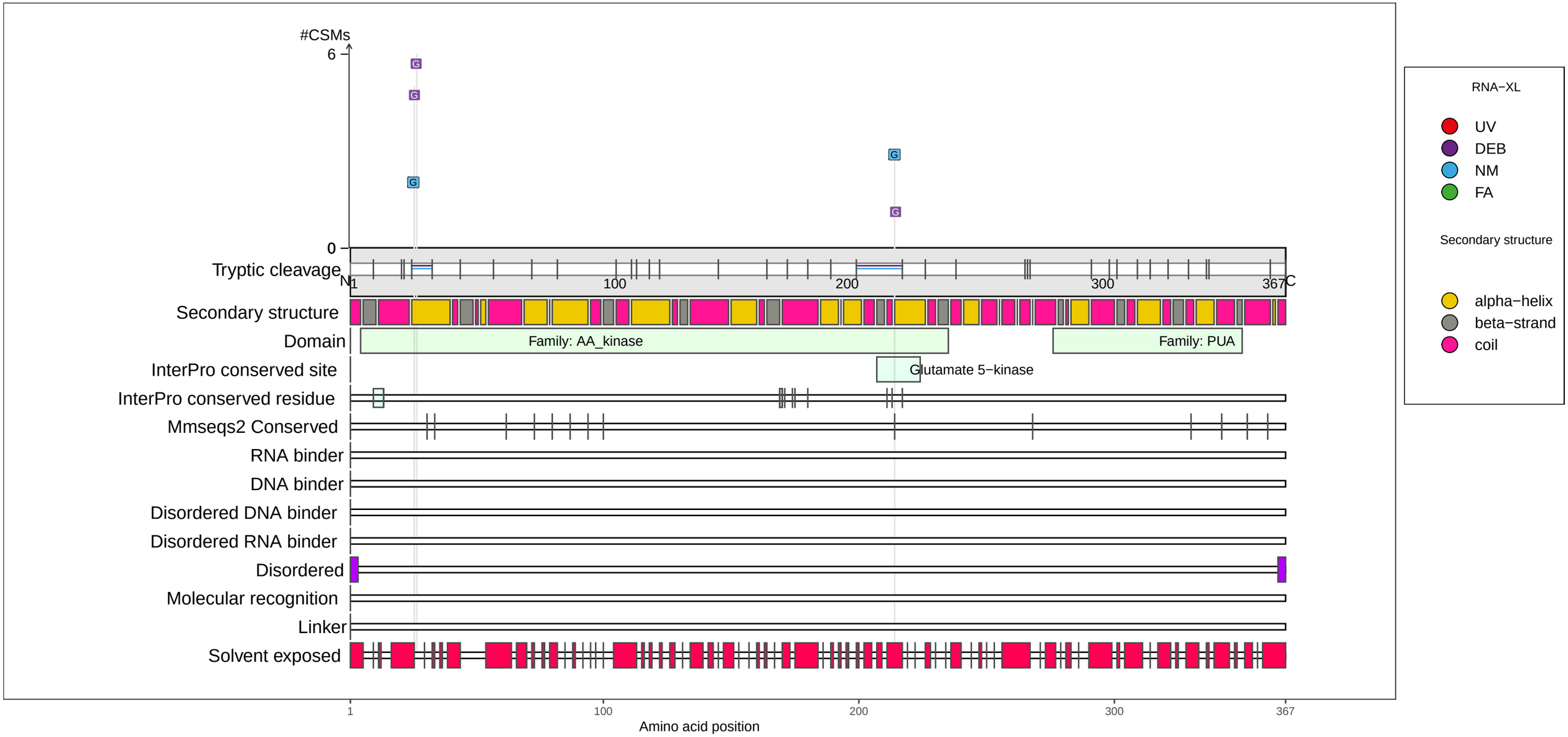
− RNA functions: not annotated



P0A7B5
PROB_ECOLI Glutamate 5−kinase

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 87)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.13 (Q 76)

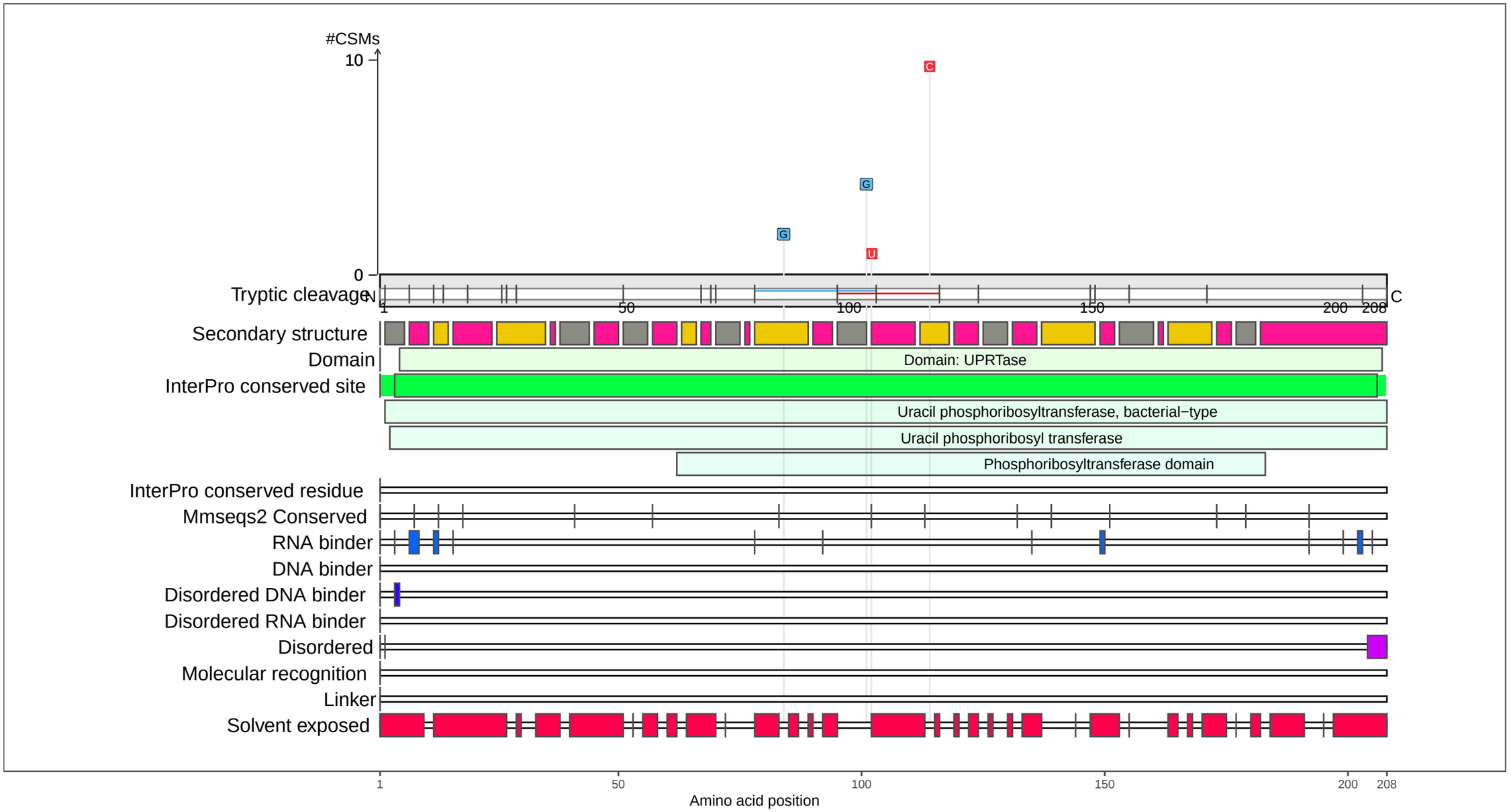
− RNA functions:
RNA binding



P0A8F0
UPP_ECOLI Uracil phosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 3.14 (Q 93)
PAXdb E.coli [ppm]: 3.07 (Q 95)

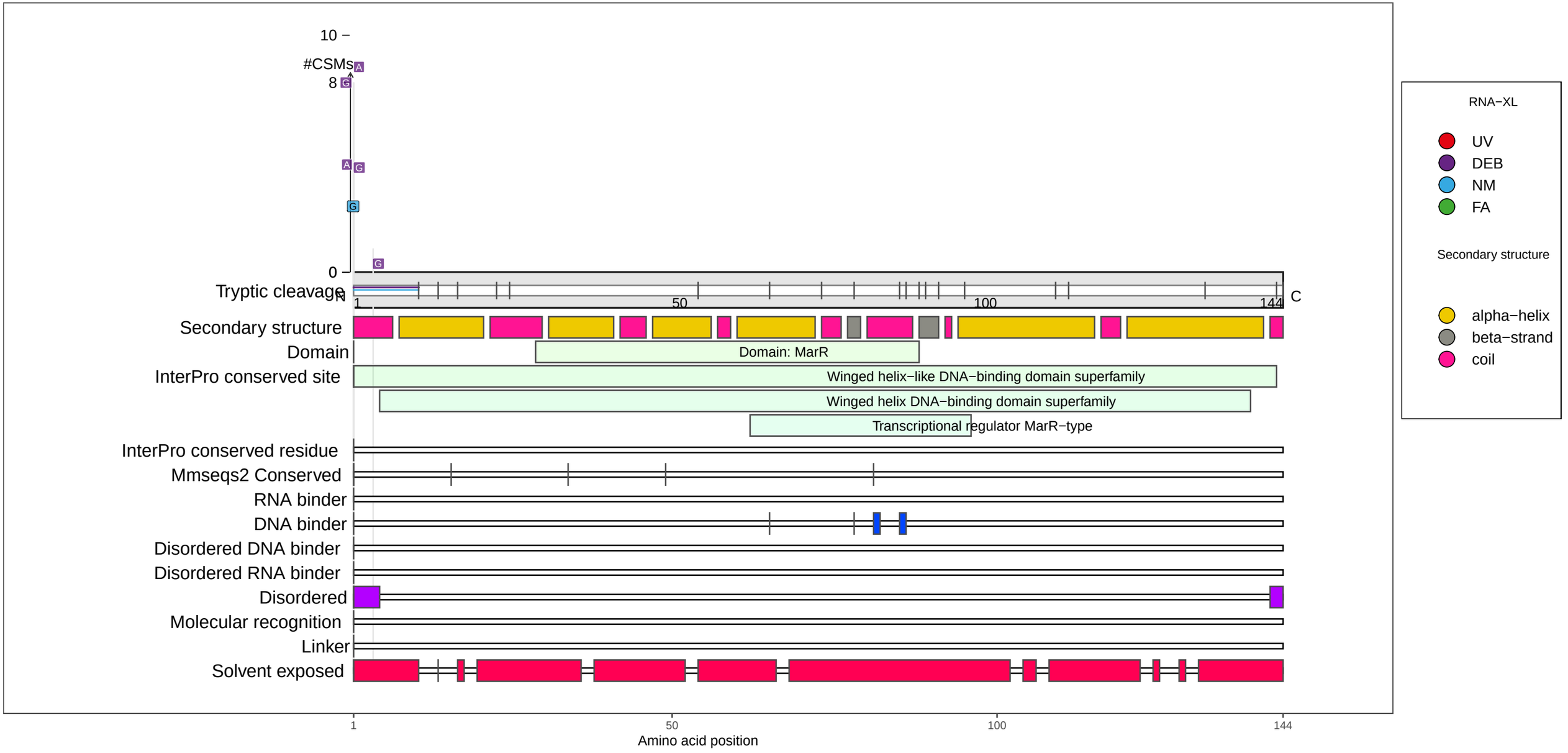
− RNA functions: not annotated



P0A8W2
SLYA_ECOLI Transcriptional regulator SlyA

− Abundance:
tryptic [log10 Intensity]: 7.36 (Q 27)
PAXdb K12 strain [ppm]: 2.24 (Q 68)
PAXdb E.coli [ppm]: 2.61 (Q 88)

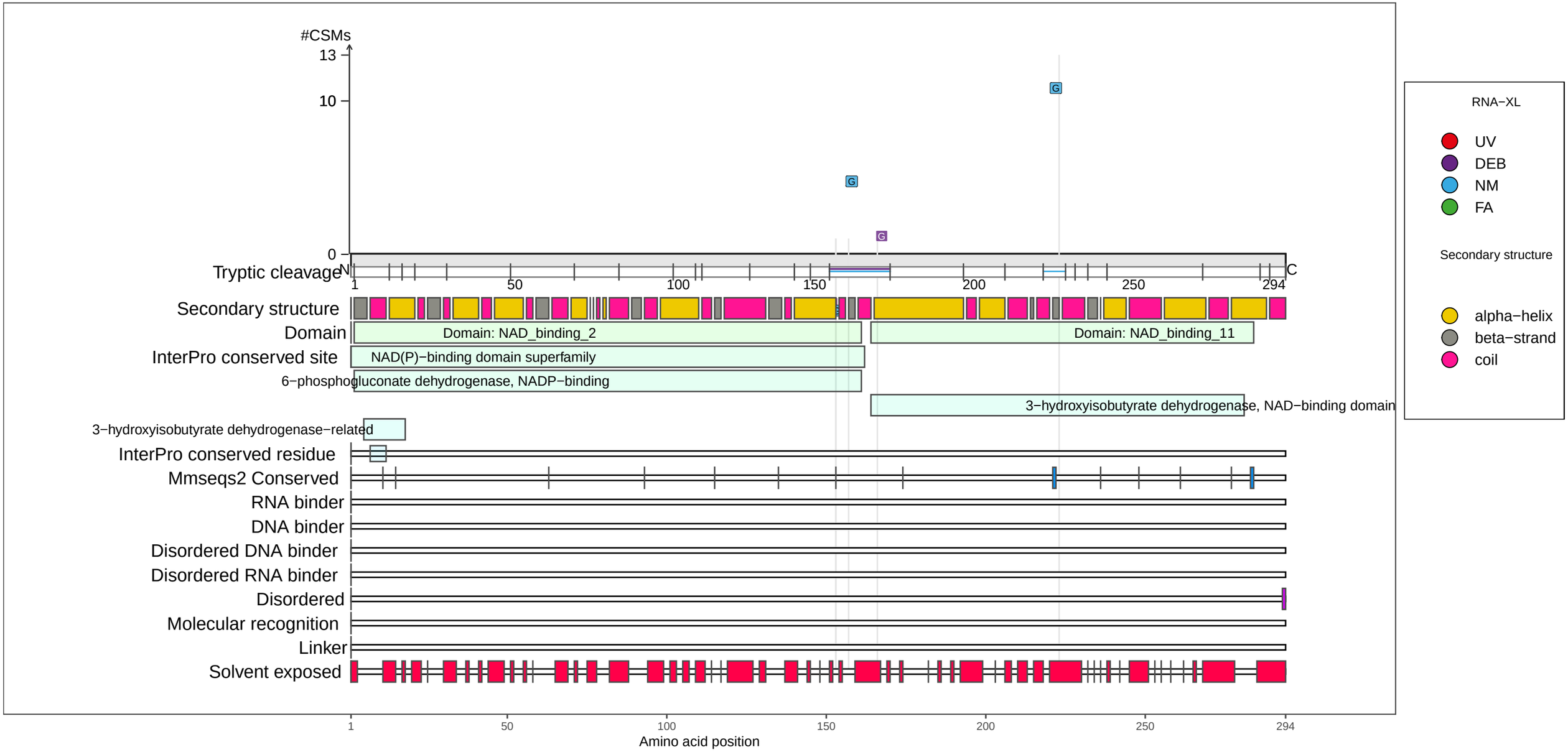
− RNA functions: not annotated



P0ABQ2
GARR_ECOLI 2−hydroxy−3−oxopropionate reductase

− Abundance:
tryptic [log10 Intensity]: 8.37 (Q 71)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 1.74 (Q 66)

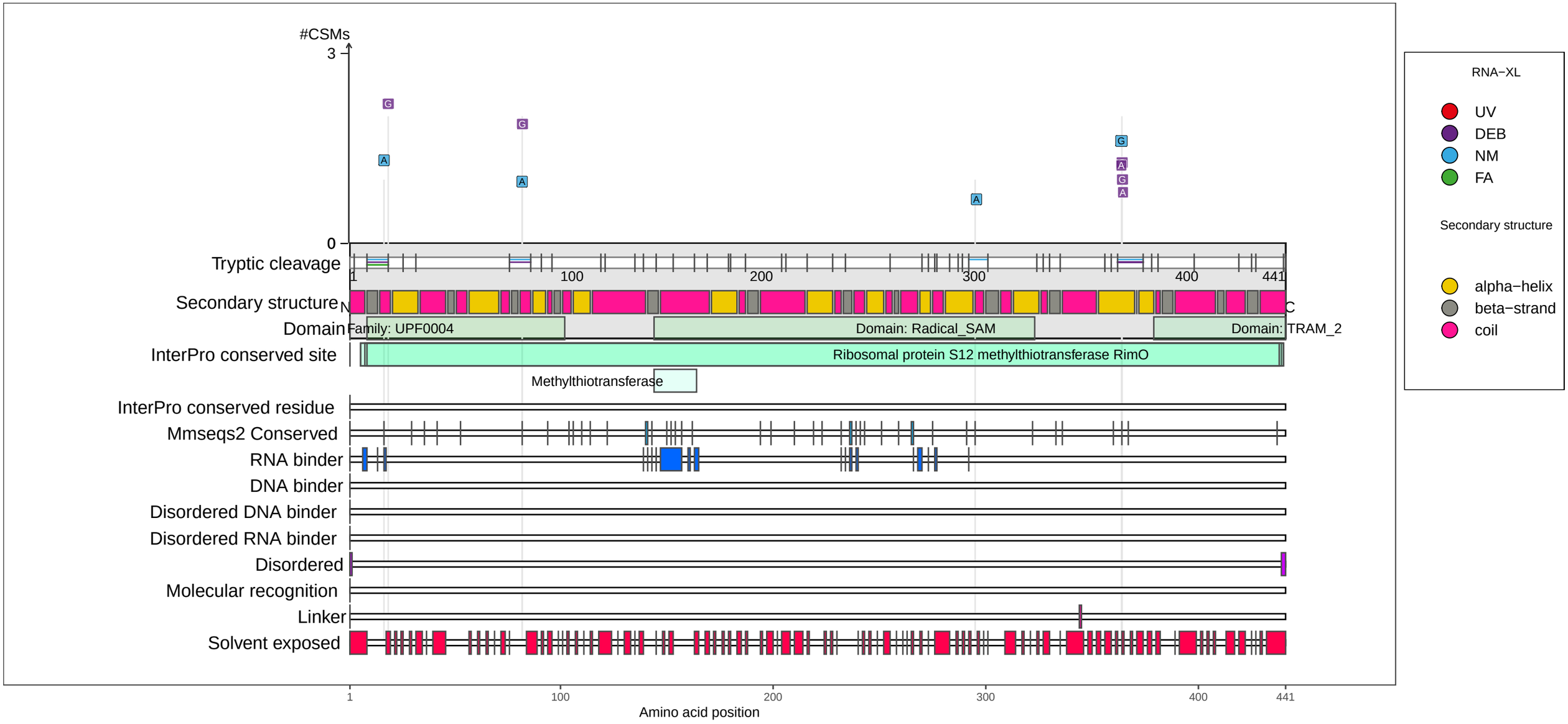
− RNA functions: not annotated



P0AEI4
RIMO_ECOLI Ribosomal protein S12 methylthiotransferase RimO

− Abundance:
tryptic [log10 Intensity]: 8.22 (Q 66)
PAXdb K12 strain [ppm]: 1.97 (Q 59)
PAXdb E.coli [ppm]: 1.3 (Q 55)

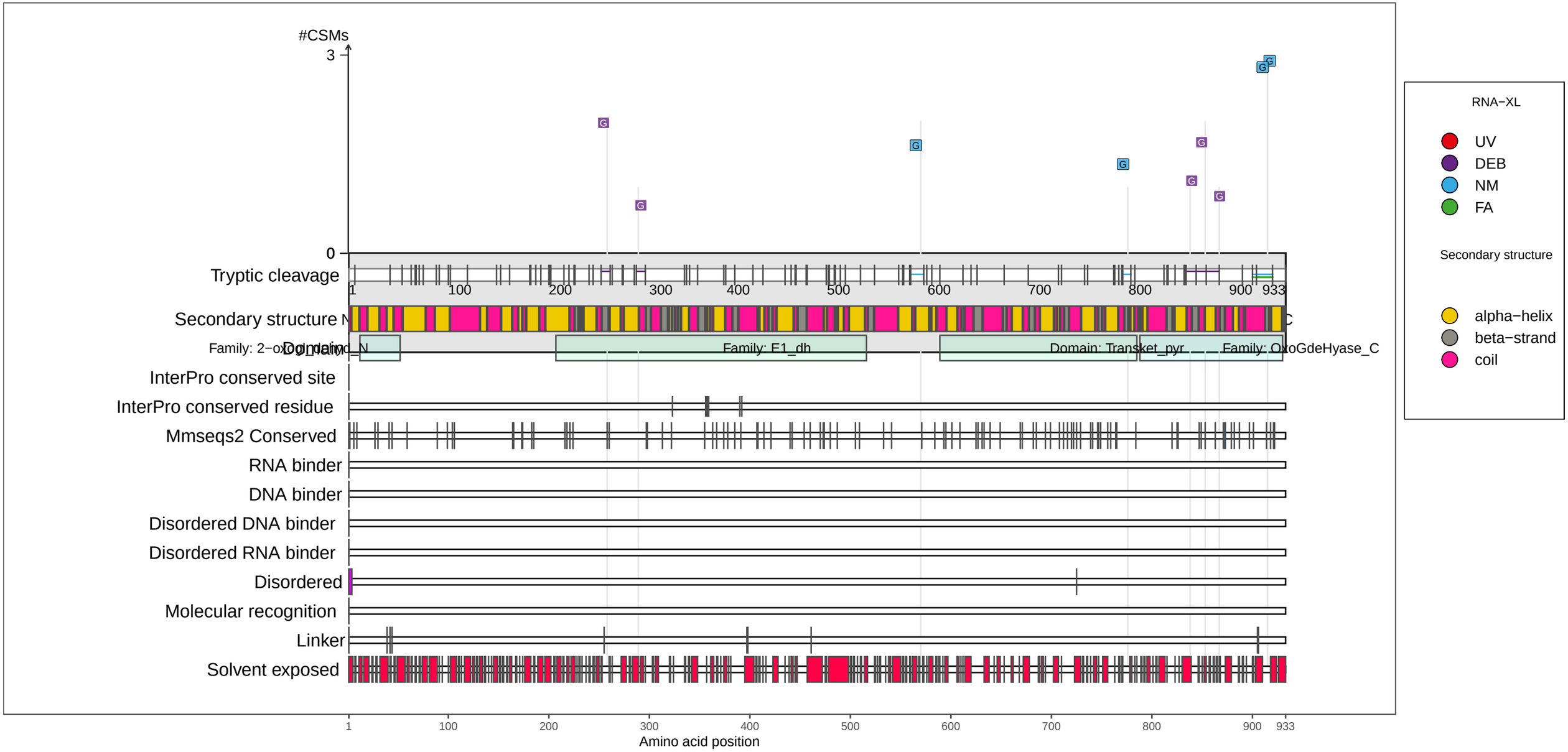
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing



P0AFG3
ODO1_ECOLI 2−oxoglutarate dehydrogenase E1 component

− Abundance:
tryptic [log10 Intensity]: 8.84 (Q 85)
PAXdb K12 strain [ppm]: 3.11 (Q 92)
PAXdb E.coli [ppm]: 2.91 (Q 93)

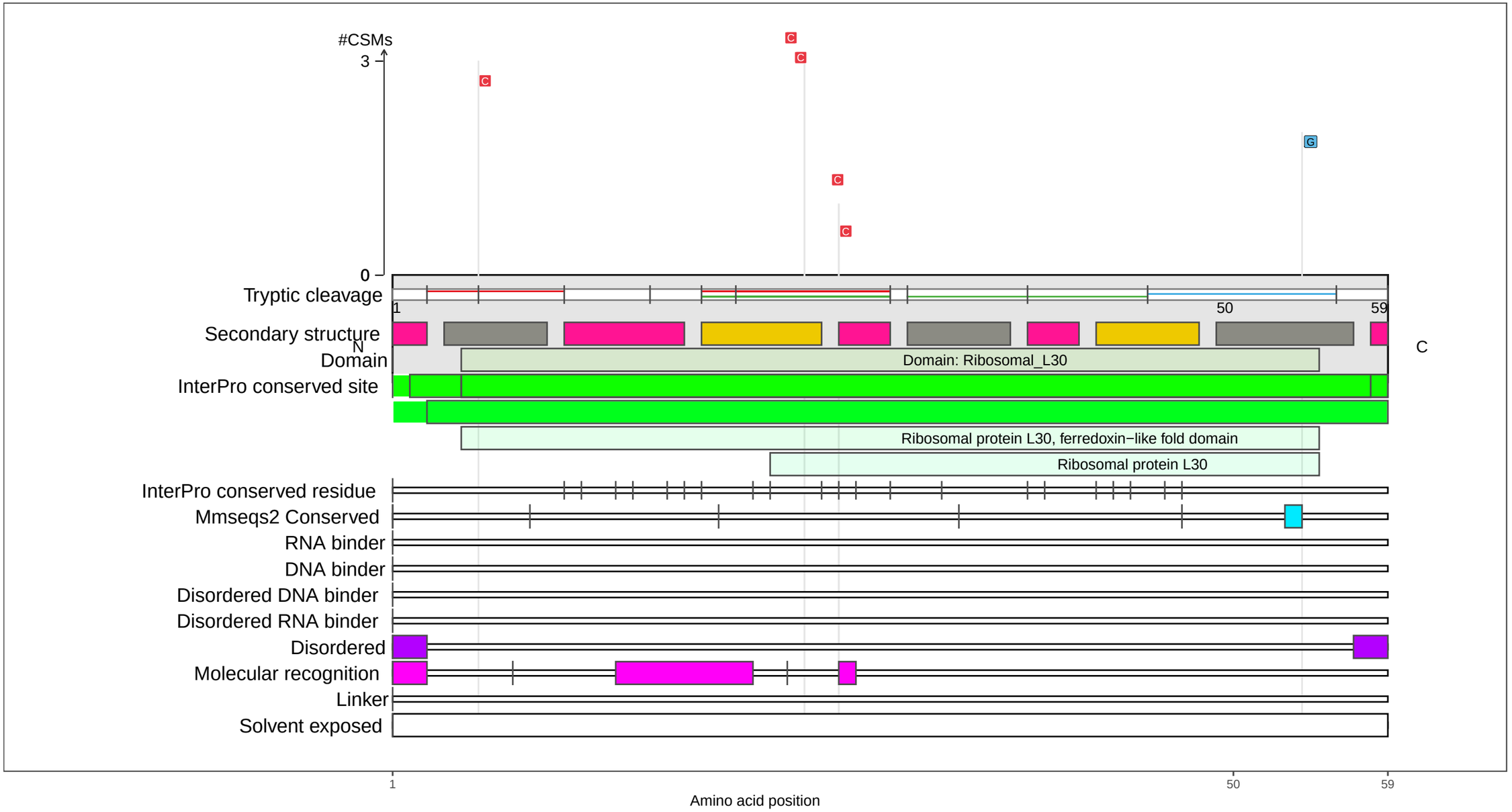
− RNA functions: not annotated



P0AG51
RL30_ECOLI 50S ribosomal protein L30

− Abundance:
tryptic [log10 Intensity]: 8.87 (Q 85)
PAXdb K12 strain [ppm]: 3.42 (Q 96)
PAXdb E.coli [ppm]: 3.46 (Q 99)

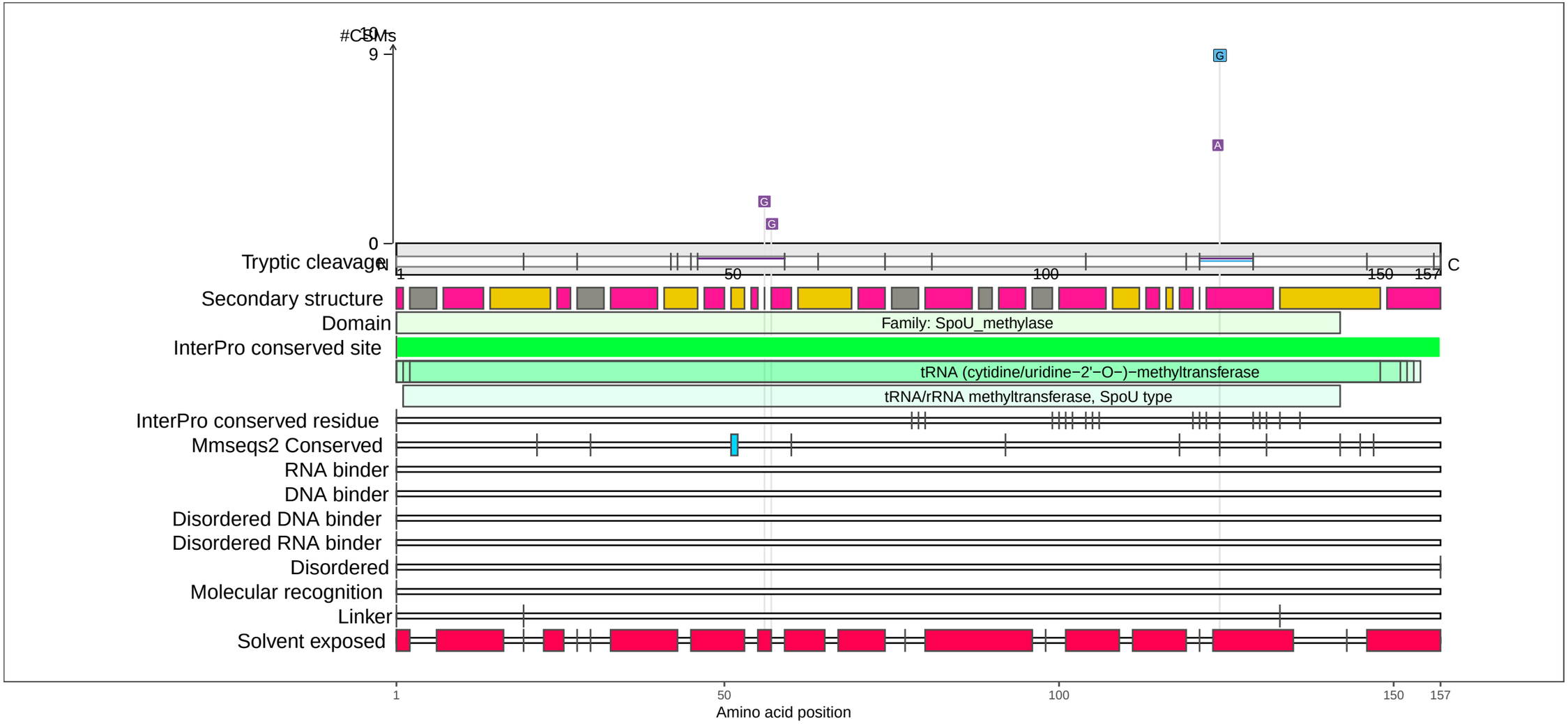
− RNA functions: not annotated

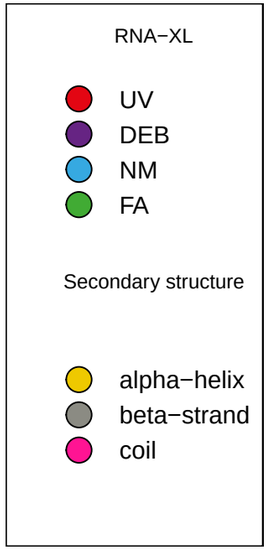


P0AGJ7
TRML_ECOLI tRNA (cytidine(34)−2'−O)−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.4 (Q 30)
PAXdb K12 strain [ppm]: 1.23 (Q 22)
PAXdb E.coli [ppm]: 1.16 (Q 51)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; SpoU rRNA Methylase family
tRNA (cytosine−2−O−)−methyltransferase activity; tRNA (cytosine) methyltransferase activity
tRNA (uracil−2−O−)−methyltransferase activity; tRNA (uracil) methyltransferase activity
tRNA 2−O−methyltransferase activity; tRNA metabolic process; tRNA methylation
tRNA methyltransferase activity; tRNA modification; tRNA nucleoside ribose methylation; tRNA processing

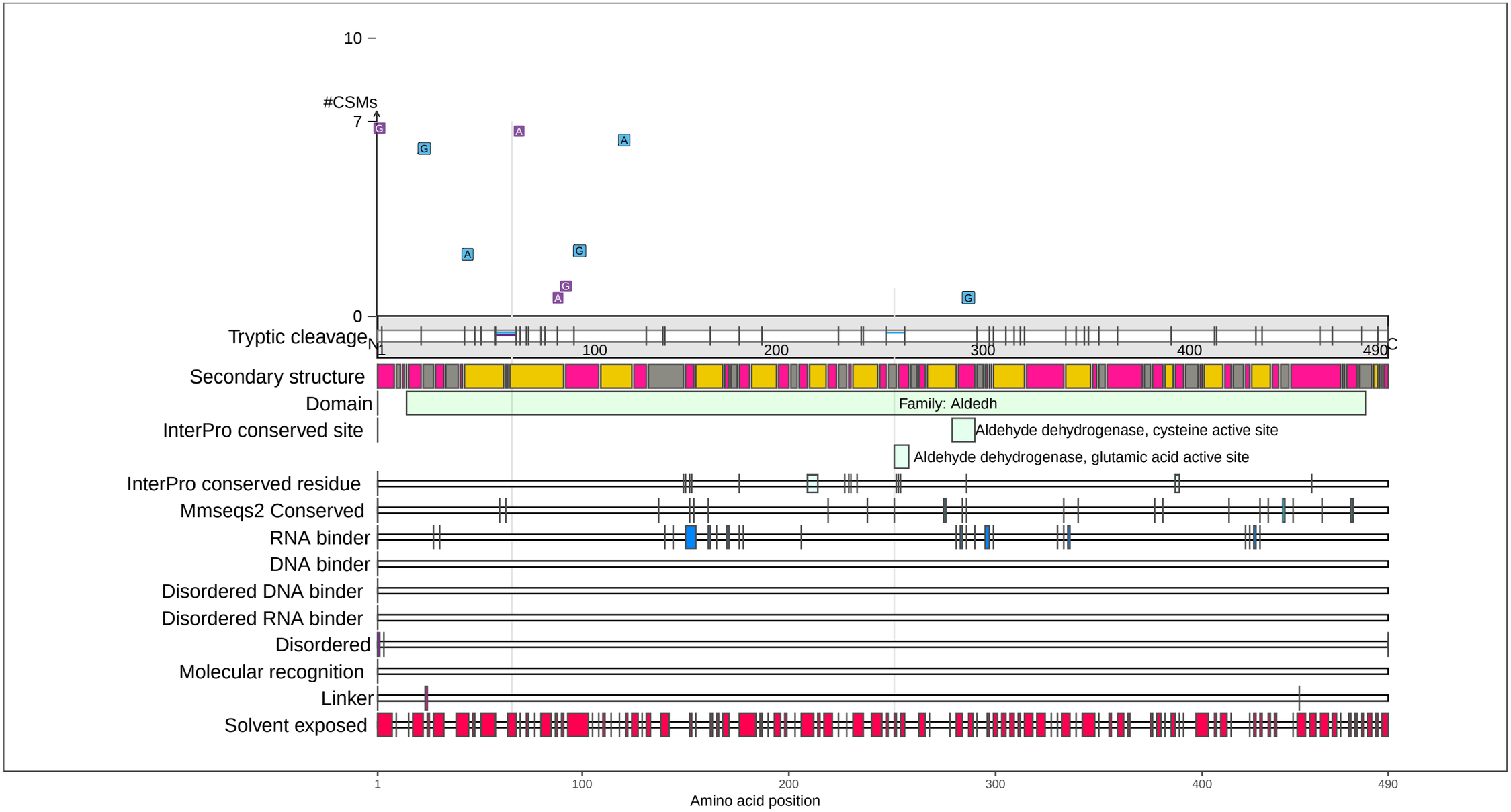


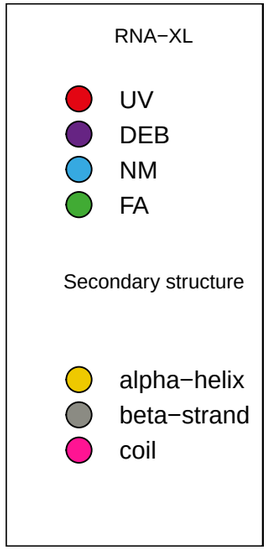


P17445
BETB_ECOLI Betaine aldehyde dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 7.79 (Q 49)
PAXdb K12 strain [ppm]: 1.53 (Q 40)
PAXdb E.coli [ppm]: 1.12 (Q 51)

− RNA functions: not annotated

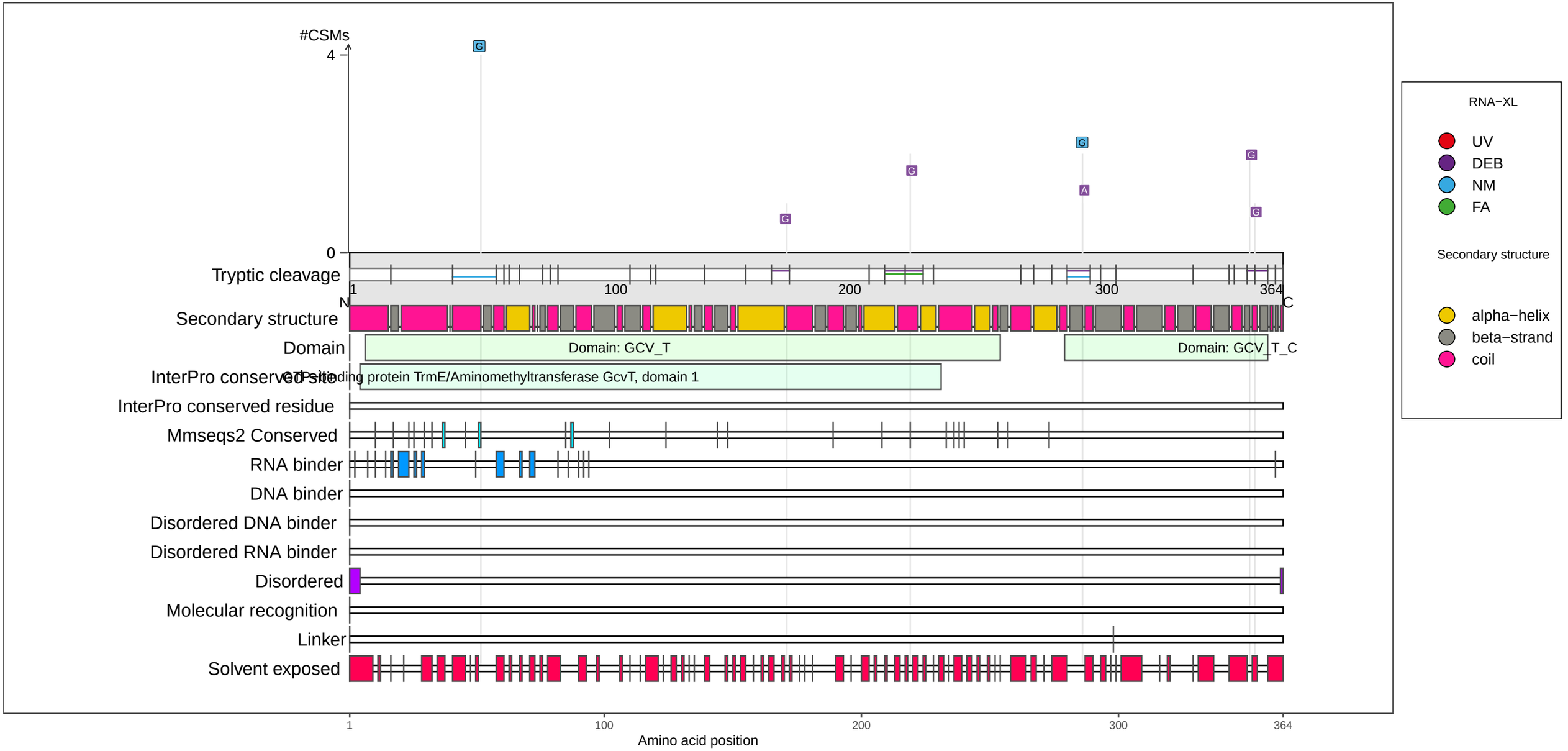




P27248
GCST_ECOLI Aminomethyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 3.2 (Q 94)
PAXdb E.coli [ppm]: 2.29 (Q 80)

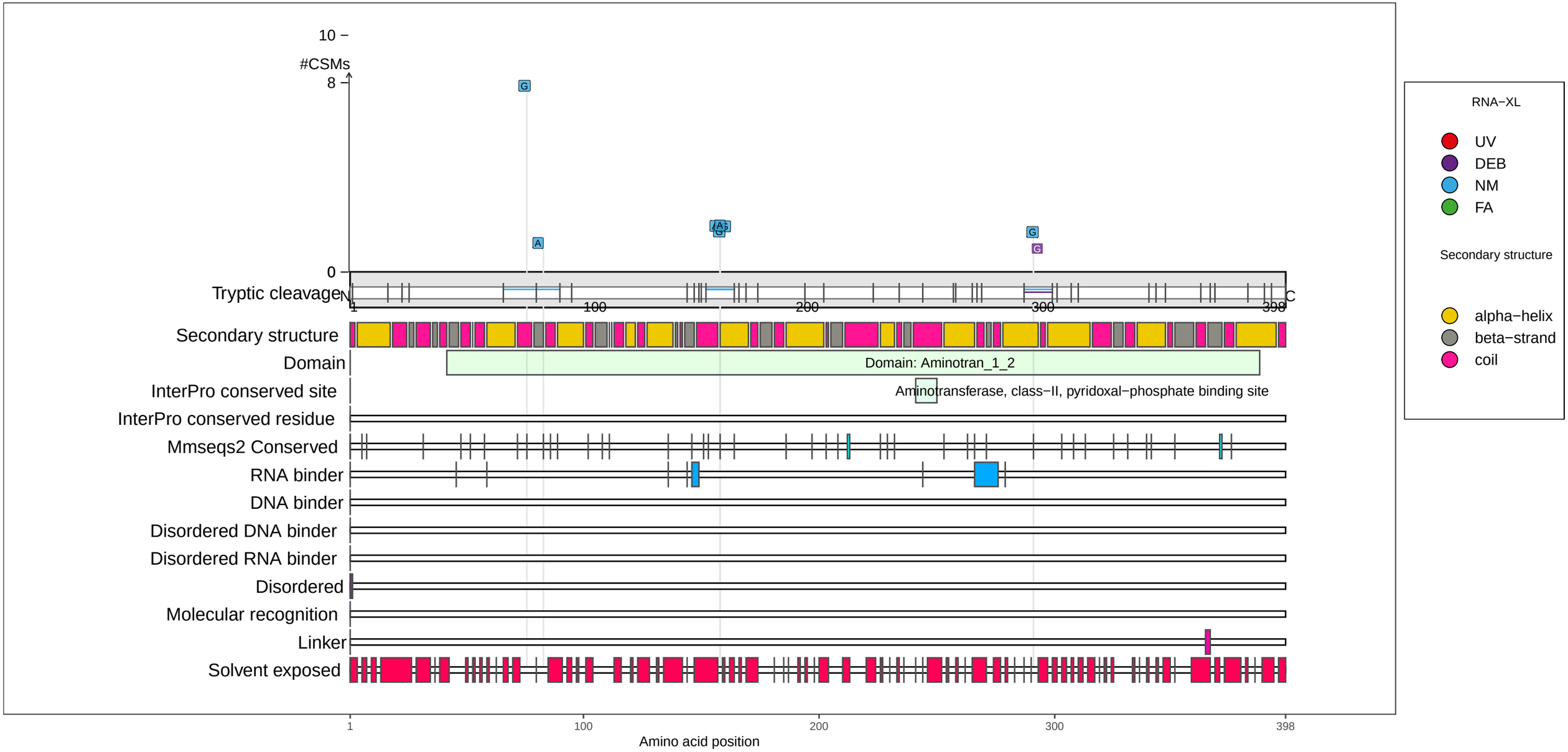
− RNA functions: not annotated



P0AB77
KBL_ECOLI 2−amino−3−ketobutyrate coenzyme A ligase

− Abundance:
tryptic [log10 Intensity]: 8.96 (Q 87)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 2.22 (Q 78)

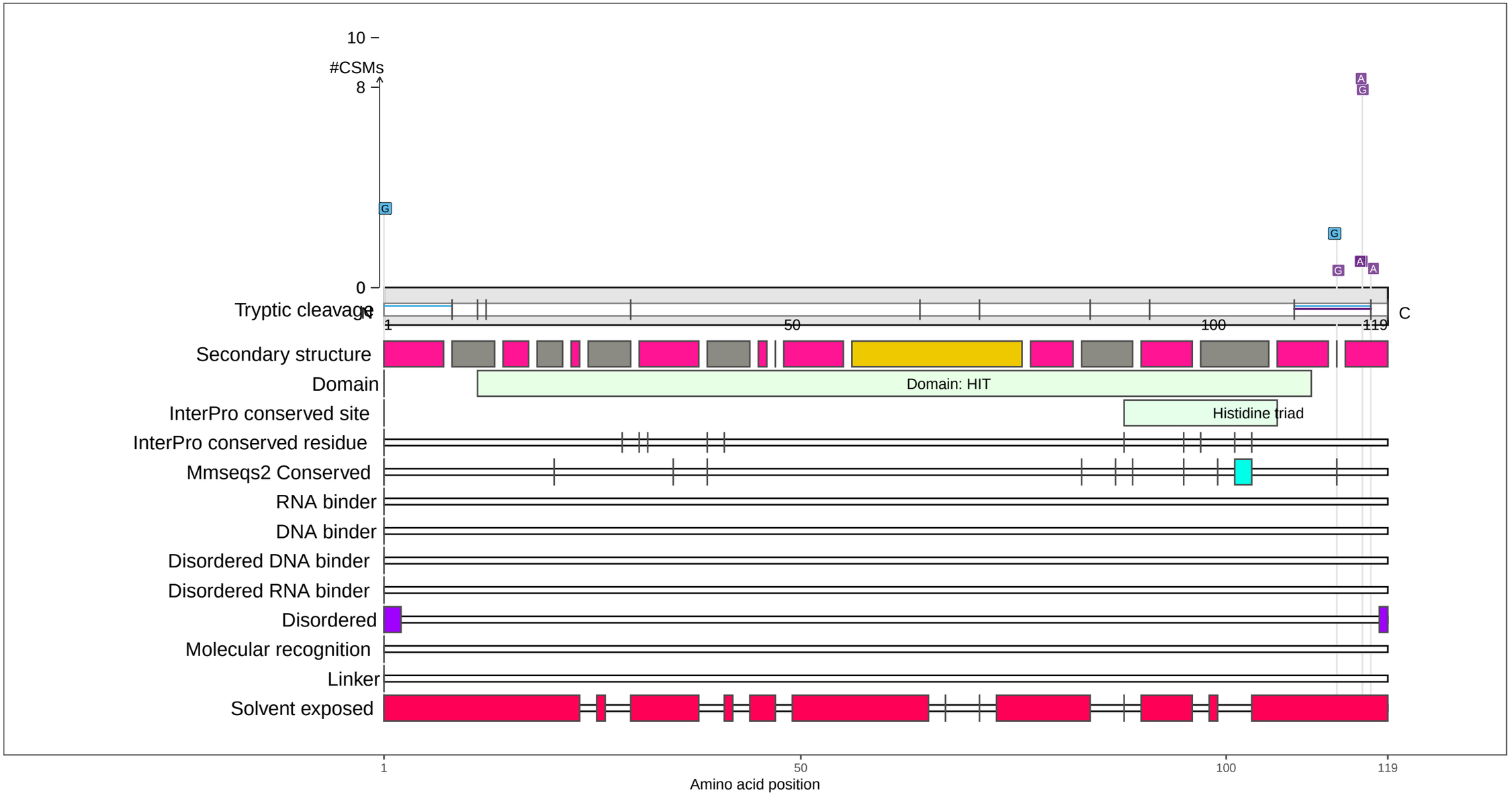
− RNA functions: not annotated



P0ACE7
HINT_ECOLI Purine nucleoside phosphoramidase

− Abundance:
tryptic [log10 Intensity]: 8.2 (Q 65)
PAXdb K12 strain [ppm]: 2.56 (Q 79)
PAXdb E.coli [ppm]: 3 (Q 95)

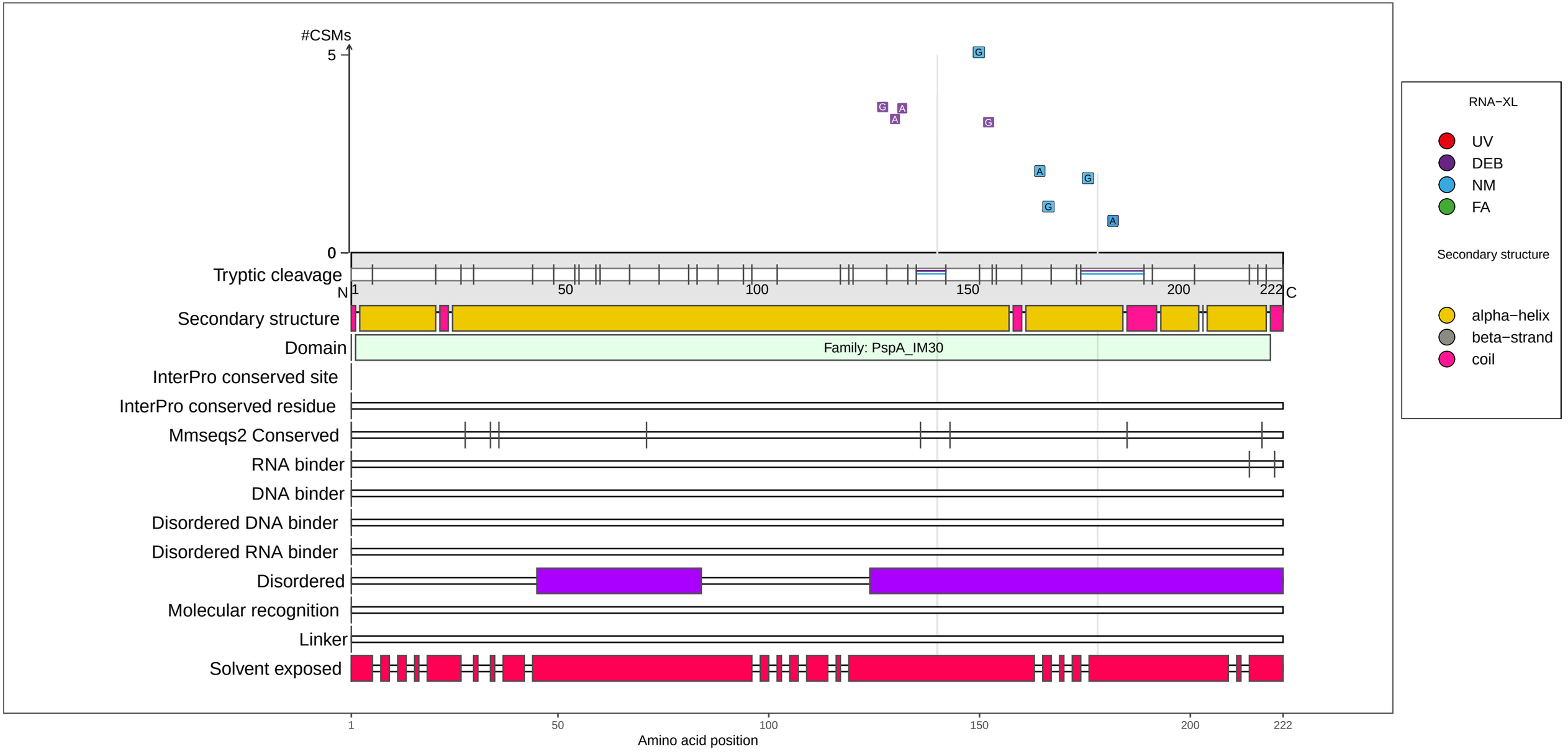
− RNA functions:
Scavenger mRNA decapping enzyme C−term binding



P0AFM6
PSPA_ECOLI Phage shock protein A

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 2.57 (Q 80)
PAXdb E.coli [ppm]: 2.73 (Q 90)

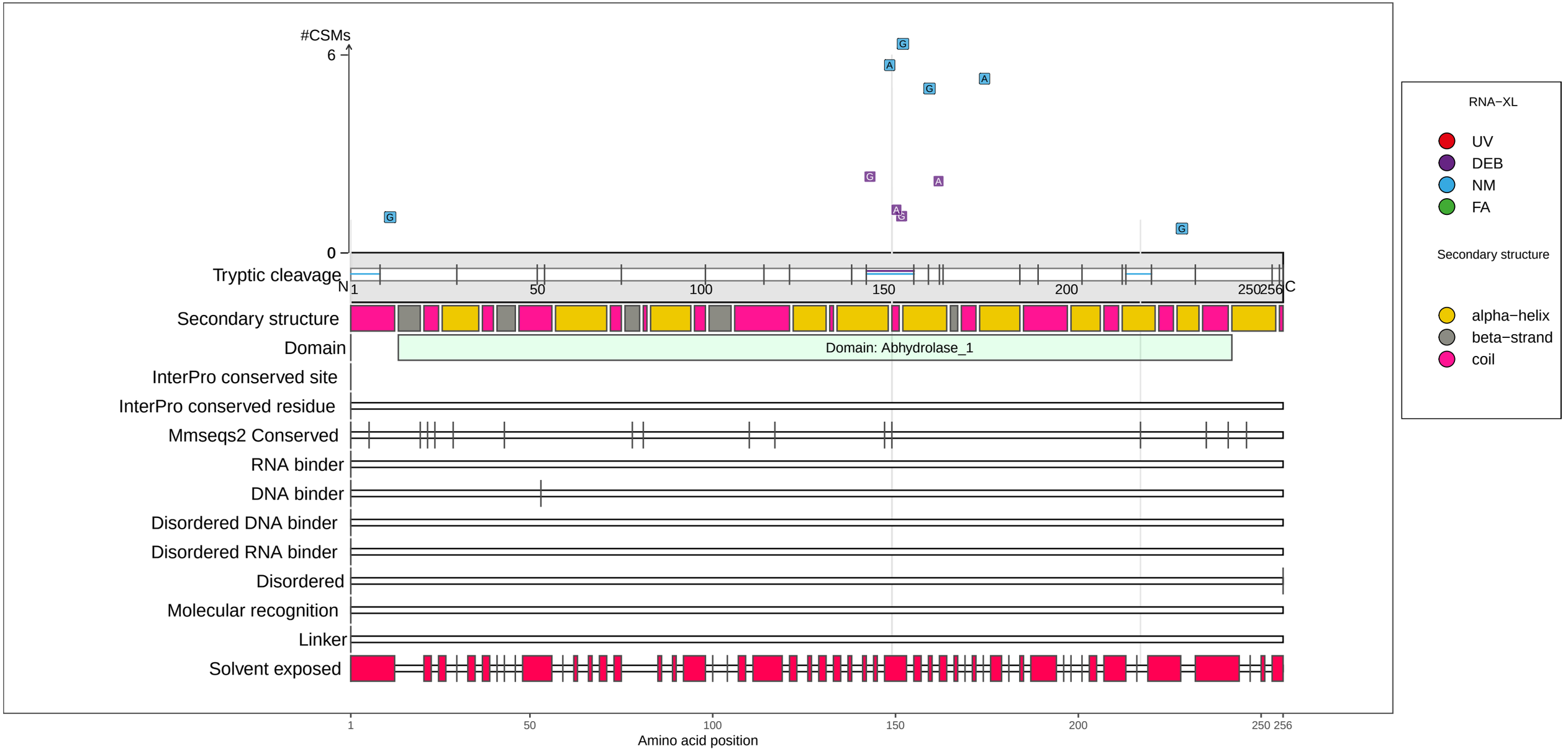
− RNA functions: not annotated



P13001
BIOH_ECOLI Pimeloyl−[acyl−carrier protein] methyl ester esterase

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.29 (Q 54)

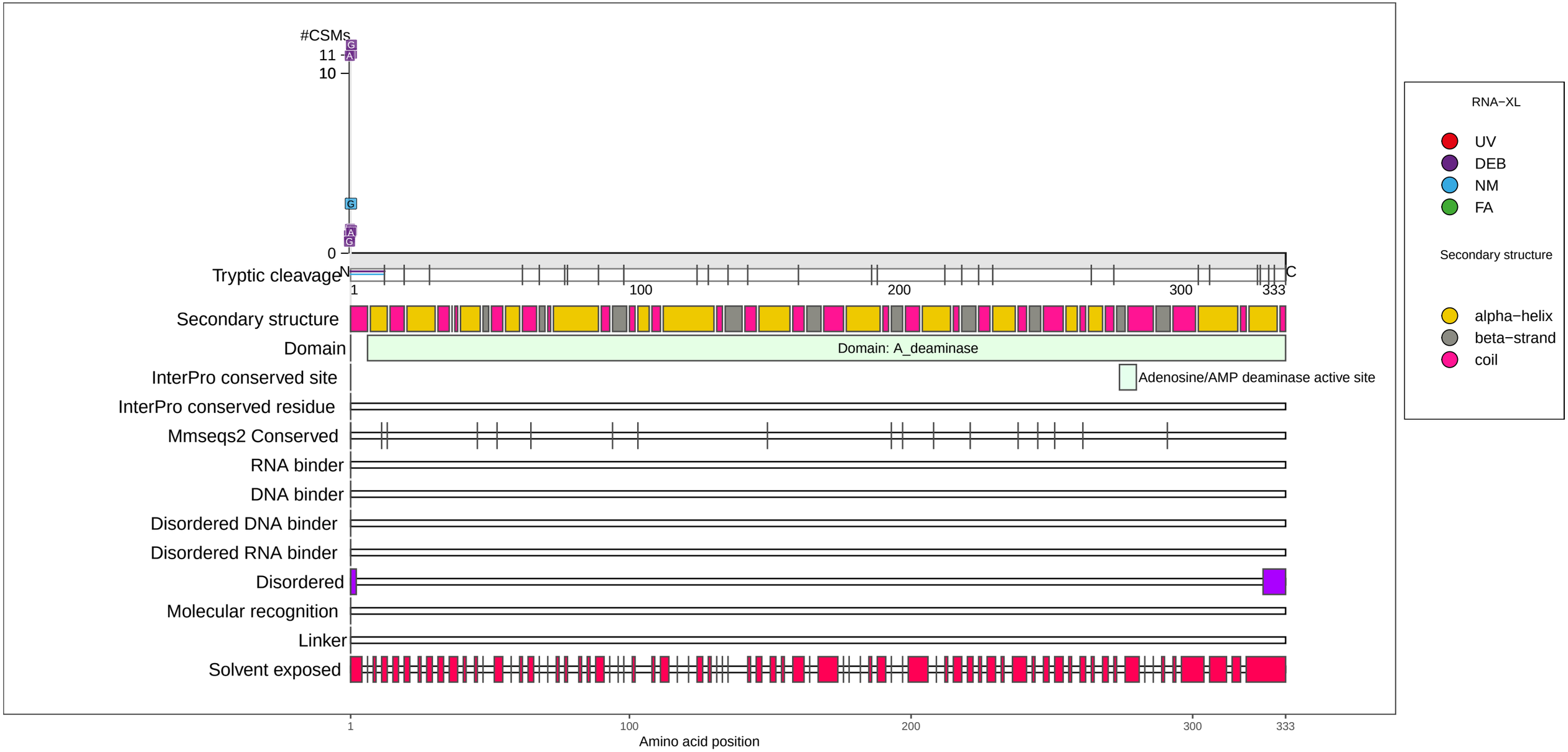
− RNA functions: not annotated



P22333
ADD_ECOLI Adenosine deaminase

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 2.25 (Q 68)
PAXdb E.coli [ppm]: 2.15 (Q 76)

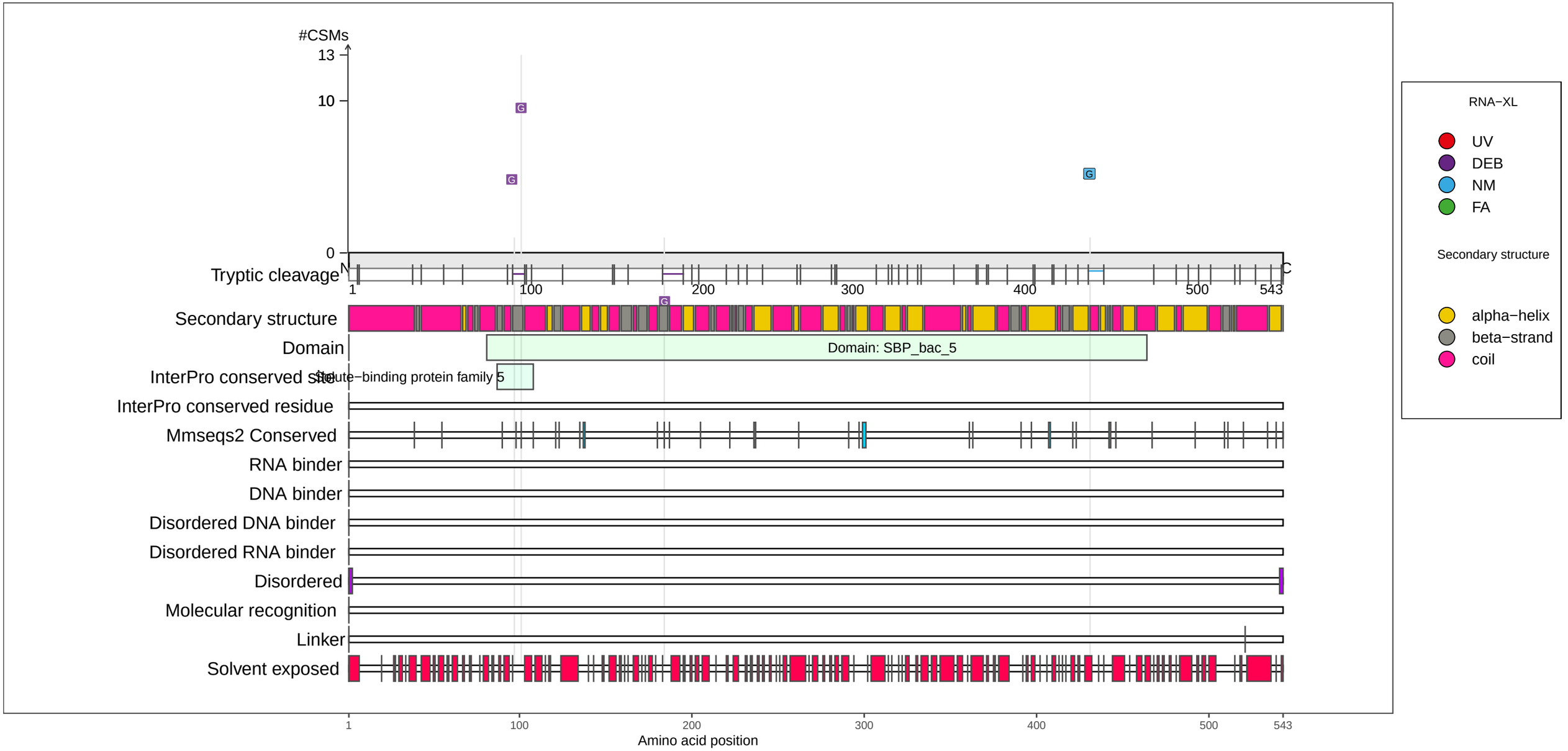
− RNA functions: not annotated



P23843
OPPA_ECOLI Periplasmic oligopeptide−binding protein

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 76)
PAXdb K12 strain [ppm]: 2.81 (Q 86)
PAXdb E.coli [ppm]: 3.15 (Q 96)

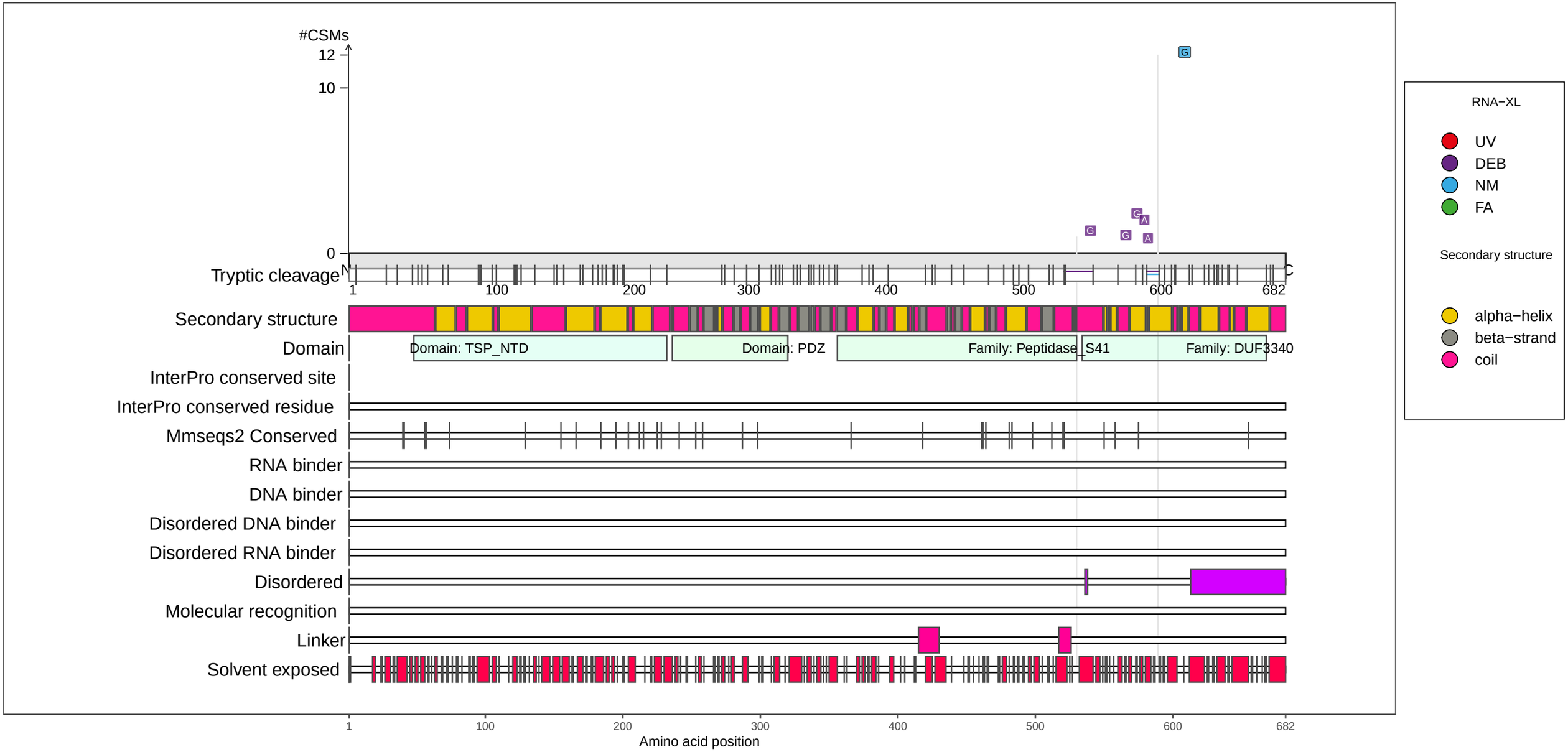
− RNA functions: not annotated



P23865
PRC_ECOLI Tail−specific protease

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: 1.59 (Q 44)
PAXdb E.coli [ppm]: 2.29 (Q 80)

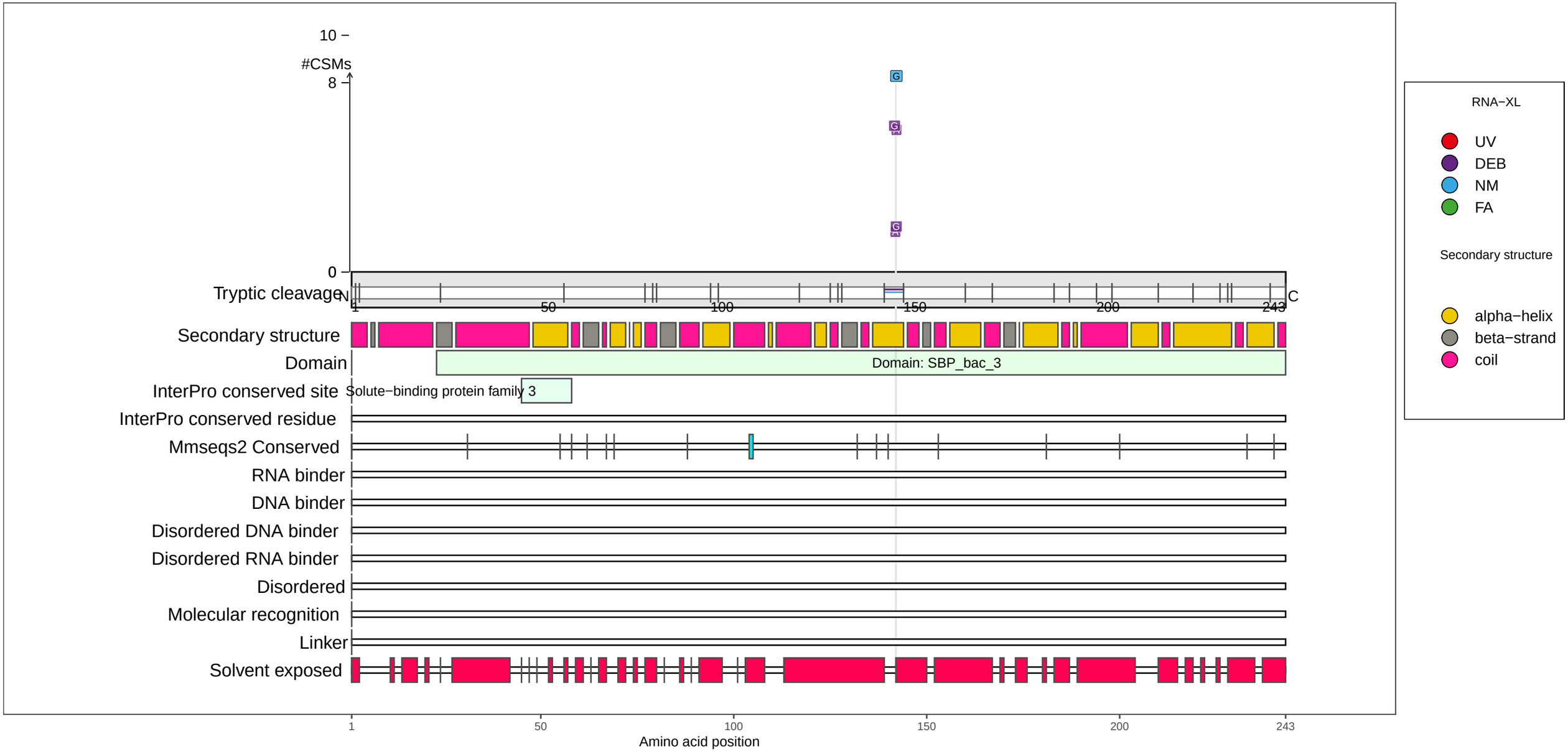
− RNA functions: not annotated



P30859
ARTI_ECOLI Putative ABC transporter arginine−binding protein 2

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 80)
PAXdb K12 strain [ppm]: 2.71 (Q 84)
PAXdb E.coli [ppm]: 2.94 (Q 94)

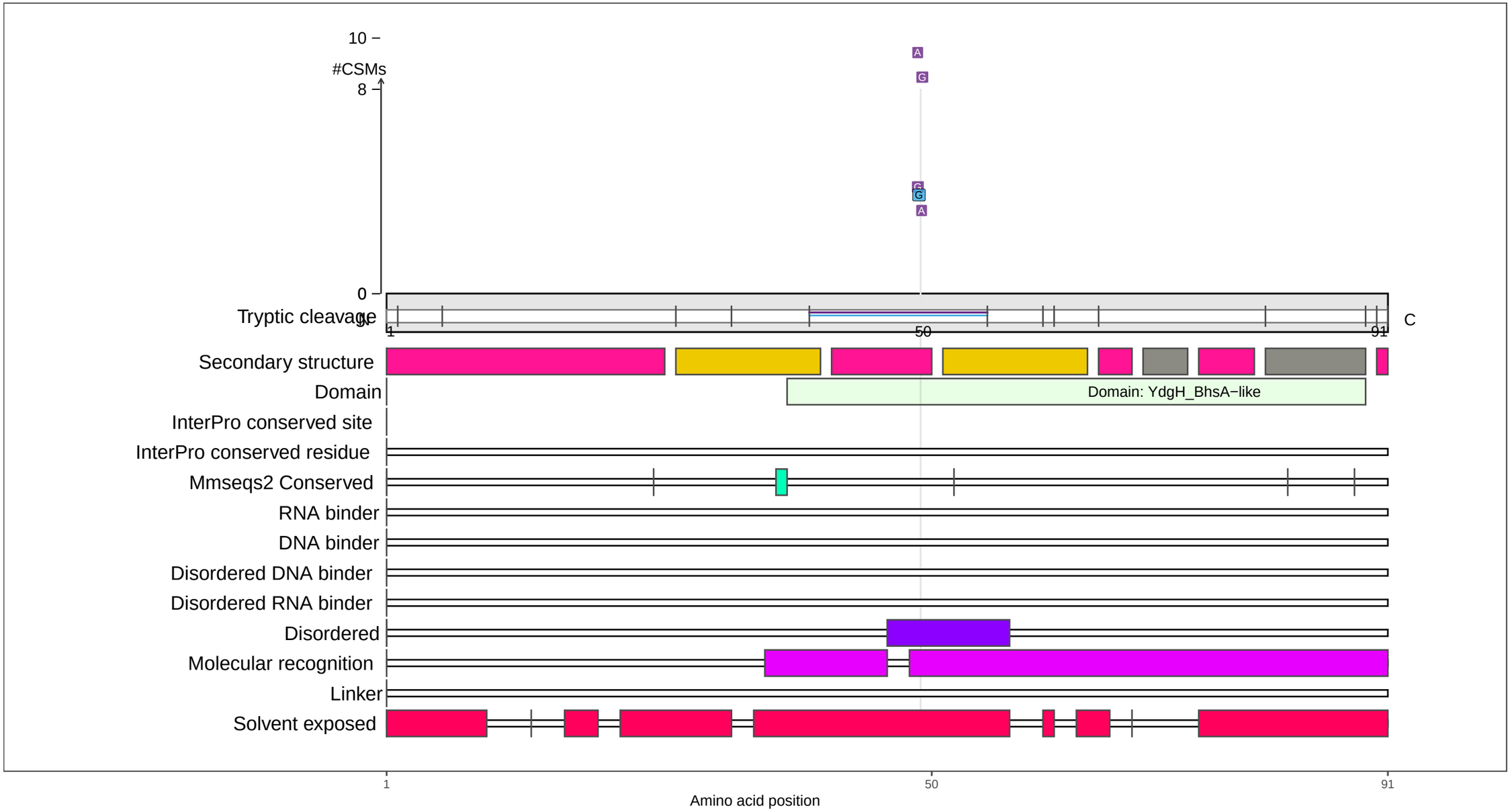
− RNA functions: not annotated

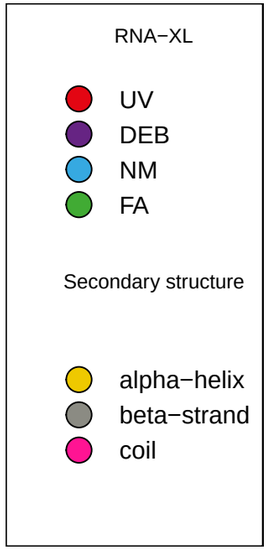


P75694
YAHO_ECOLI Uncharacterized protein YahO

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 3.17 (Q 96)

− RNA functions: not annotated

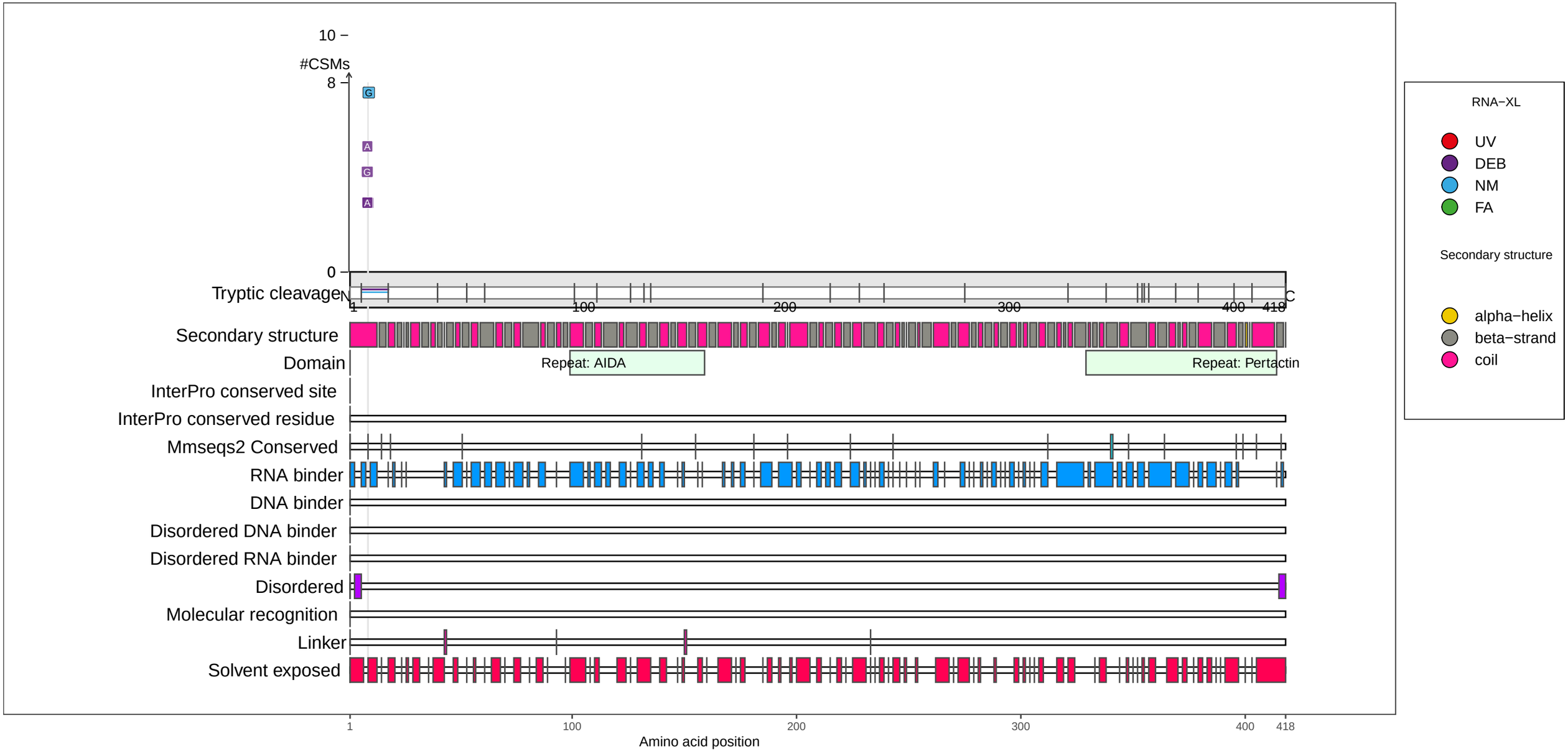




P77552
YDHQ_ECOLI Uncharacterized protein YdhQ

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 1.49 (Q 38)
PAXdb E.coli [ppm]: 0.68 (Q 40)

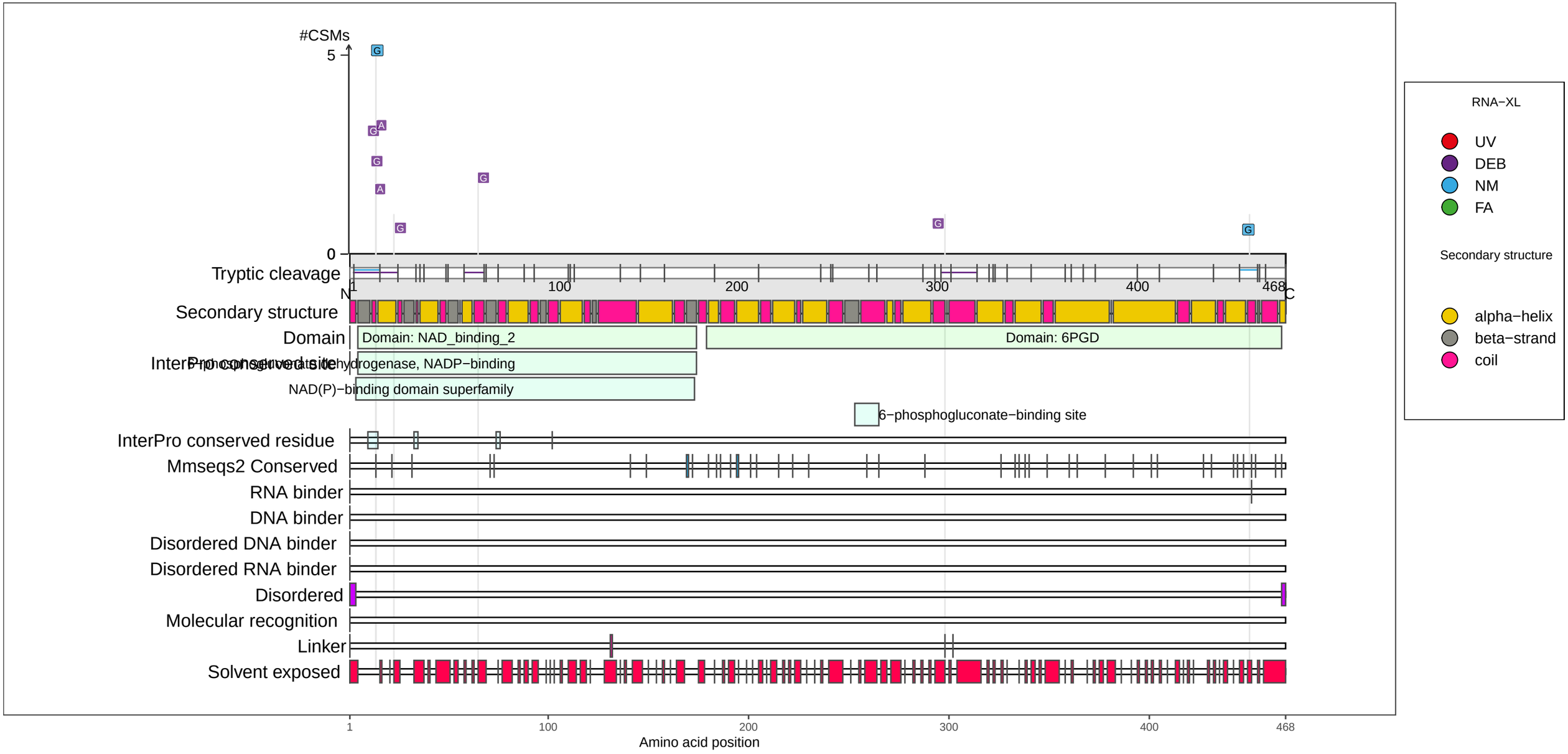
− RNA functions: not annotated



P00350
6PGD_ECOLI 6−phosphogluconate dehydrogenase, decarboxylating

− Abundance:
tryptic [log10 Intensity]: 9.41 (Q 95)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 3.18 (Q 96)

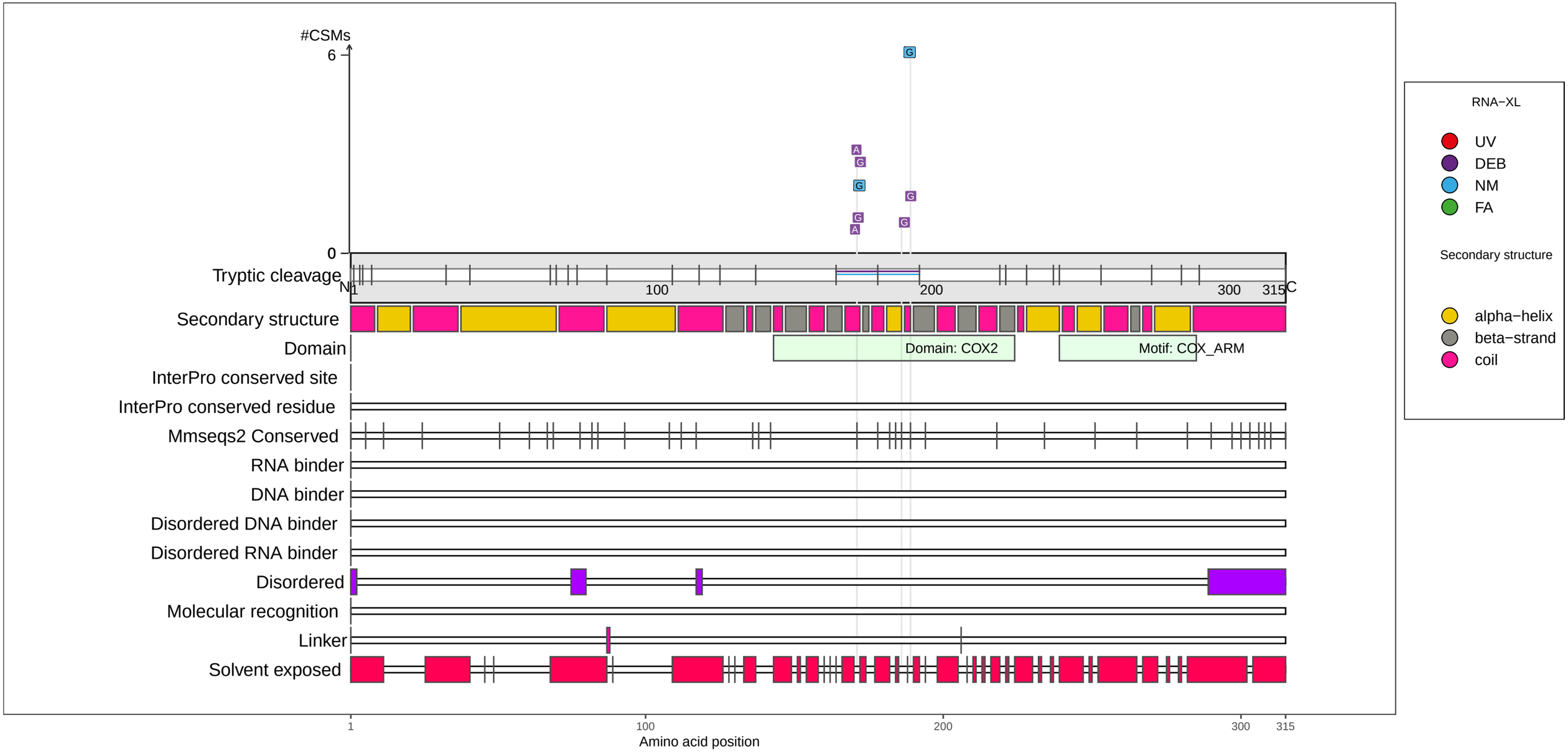
− RNA functions: not annotated



P0ABJ1
CYOA_ECOLI Cytochrome bo(3) ubiquinol oxidase subunit 2

− Abundance:
tryptic [log10 Intensity]: 9.75 (Q 98)
PAXdb K12 strain [ppm]: 2.08 (Q 63)
PAXdb E.coli [ppm]: 2.32 (Q 81)

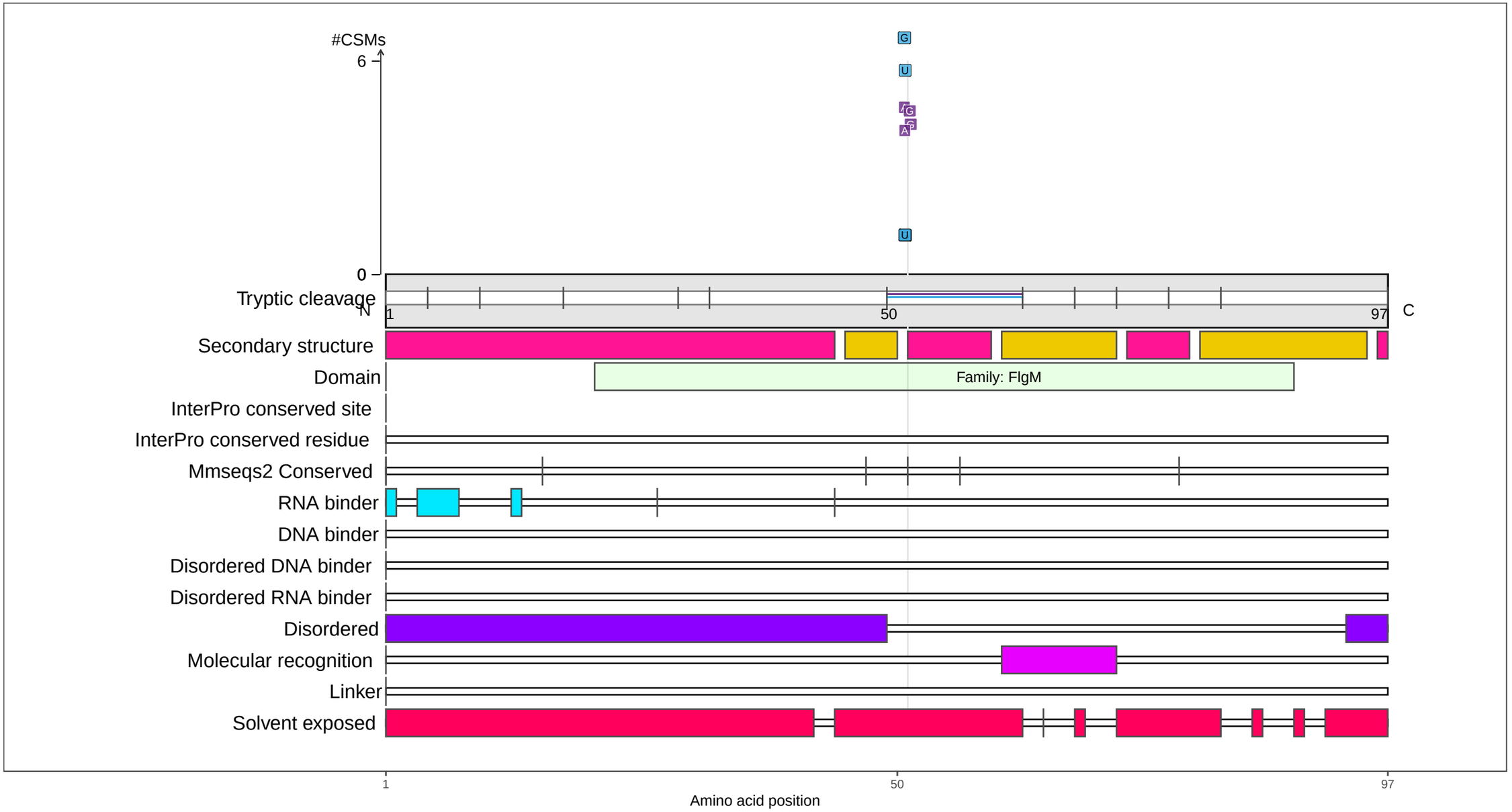
− RNA functions: not annotated



P0AEM4
FLGM_ECOLI Negative regulator of flagellin synthesis

− Abundance:
tryptic [log10 Intensity]: 7.56 (Q 38)
PAXdb K12 strain [ppm]: 3.09 (Q 92)
PAXdb E.coli [ppm]: 2.51 (Q 86)

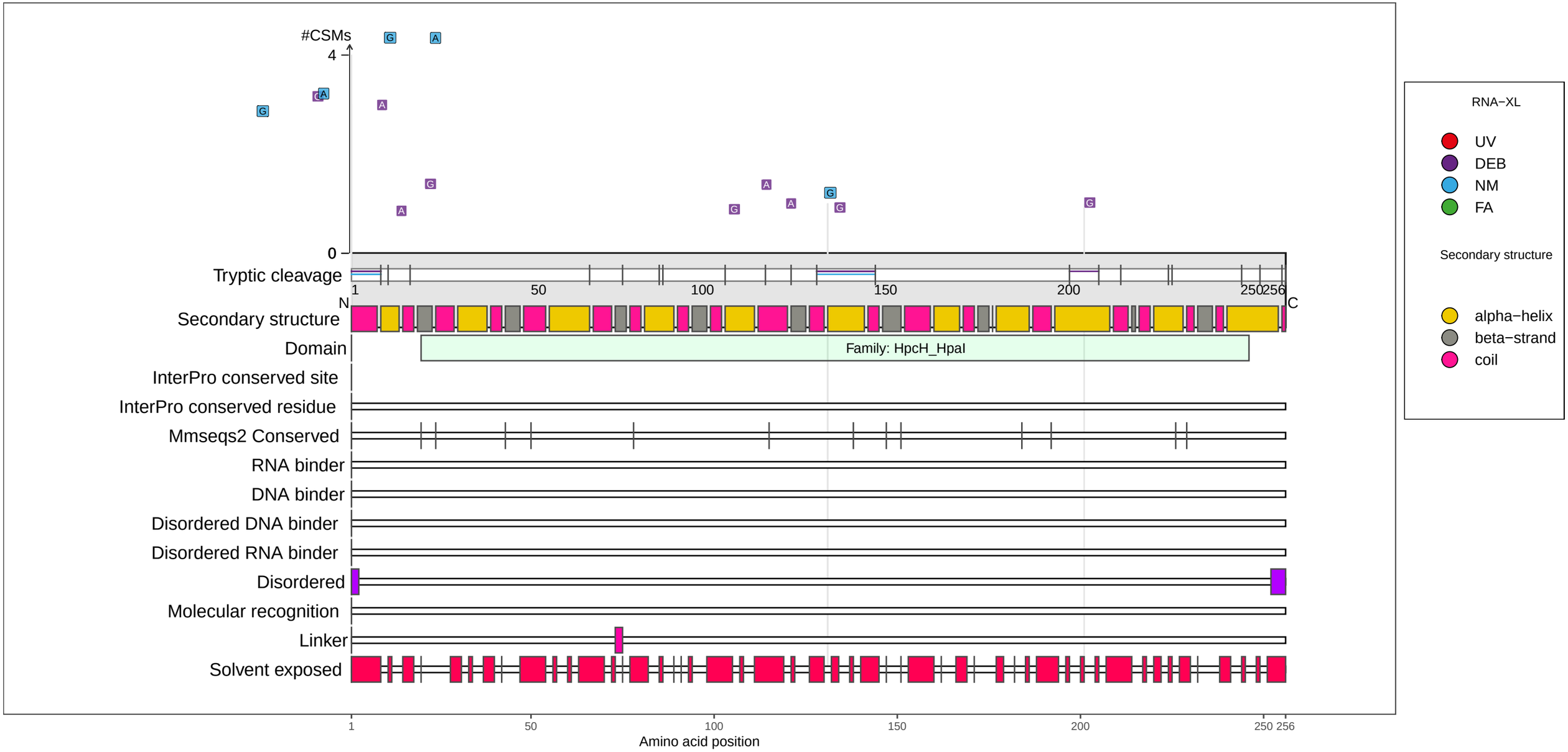
− RNA functions: not annotated



P23522
GARL_ECOLI 5−keto−4−deoxy−D−glucarate aldolase

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 45)
PAXdb K12 strain [ppm]: 1.38 (Q 31)
PAXdb E.coli [ppm]: 0.92 (Q 46)

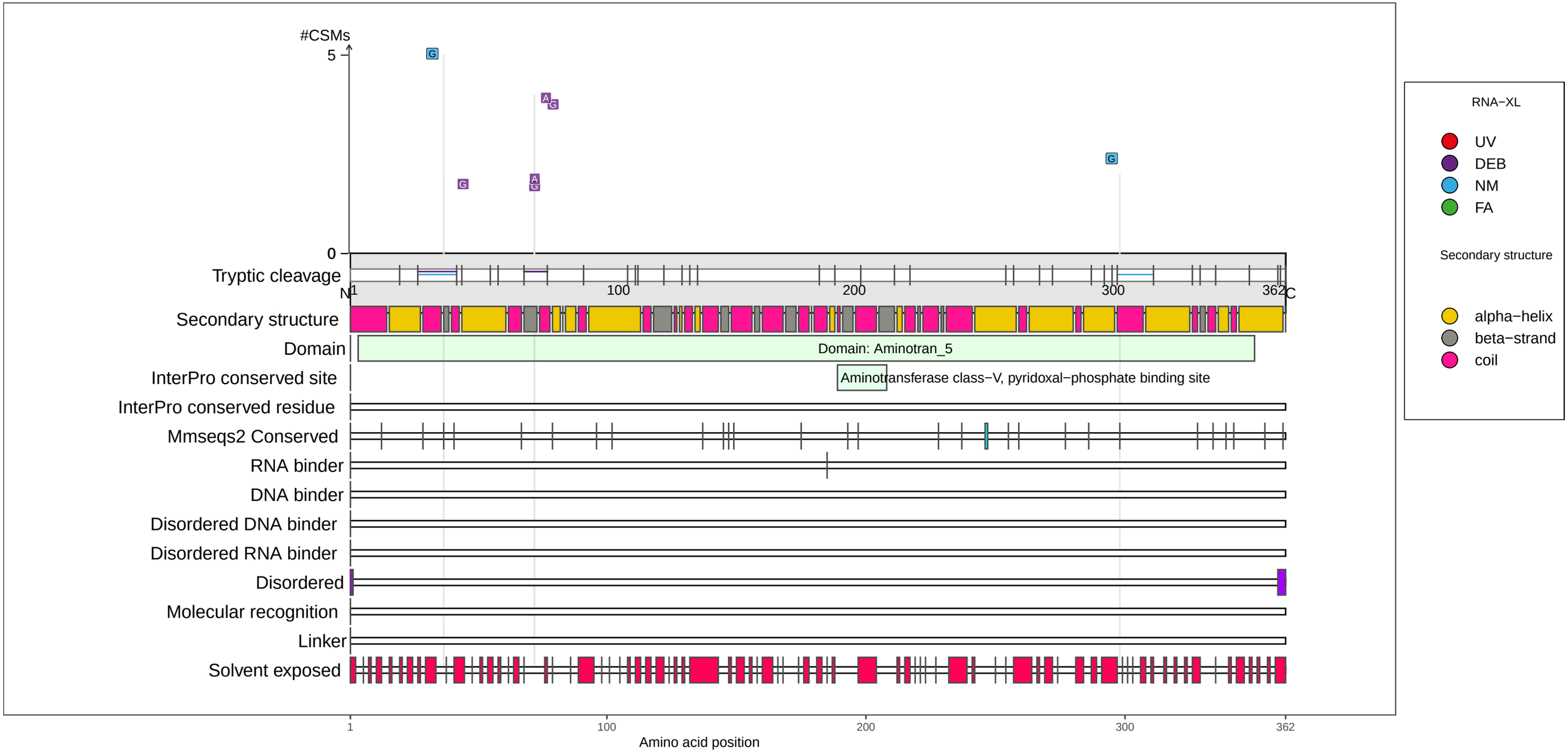
− RNA functions: not annotated



P23721
SERC_ECOLI Phosphoserine aminotransferase

− Abundance:
tryptic [log10 Intensity]: 8.99 (Q 88)
PAXdb K12 strain [ppm]: 2.42 (Q 75)
PAXdb E.coli [ppm]: 3.15 (Q 96)

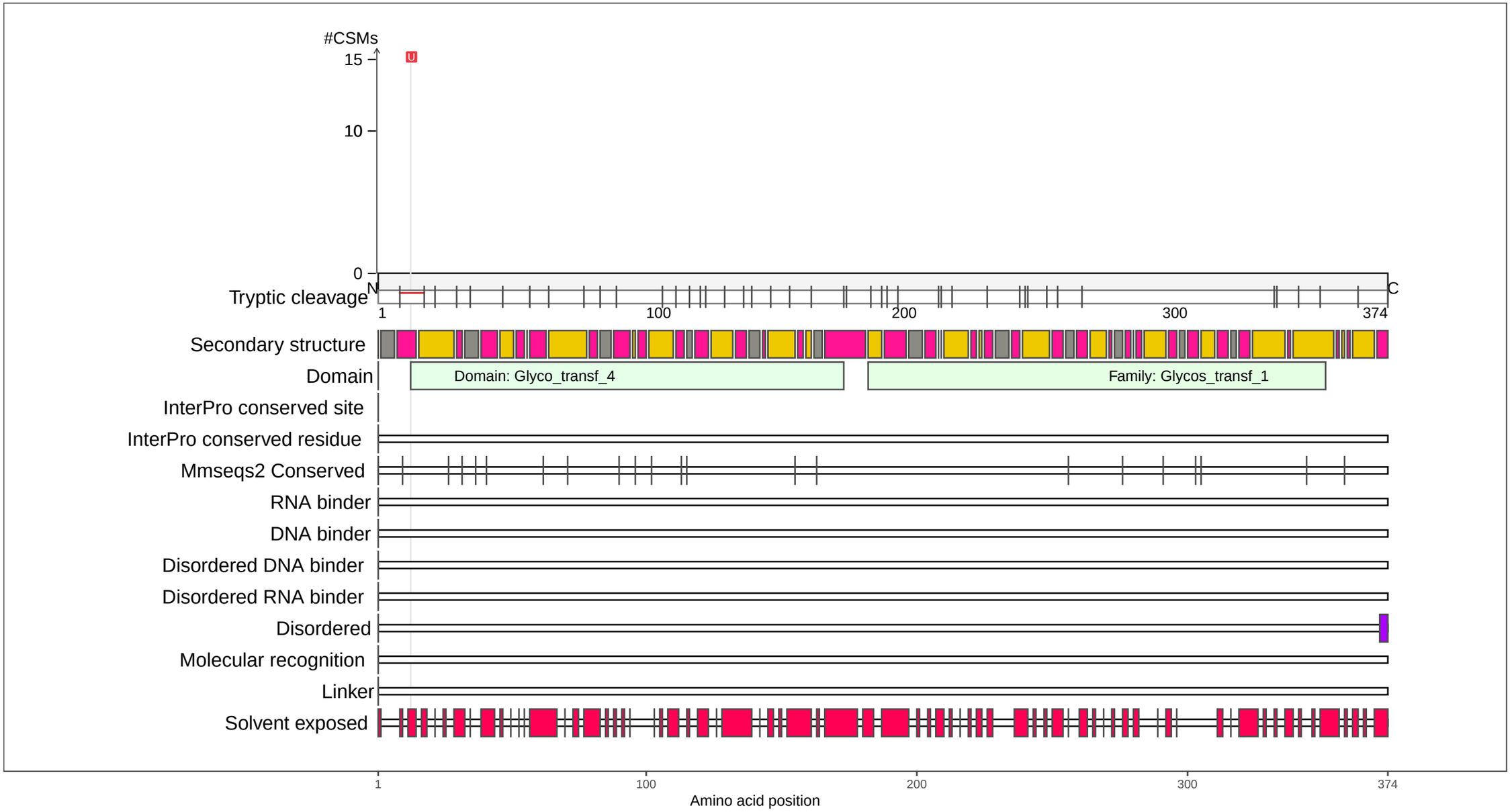
− RNA functions: not annotated



P25740
RFAG_ECOLI Lipopolysaccharide core biosynthesis protein RfaG

− Abundance:
tryptic [log10 Intensity]: 7.08 (Q 16)
PAXdb K12 strain [ppm]: 1.17 (Q 19)
PAXdb E.coli [ppm]: 0.48 (Q 36)

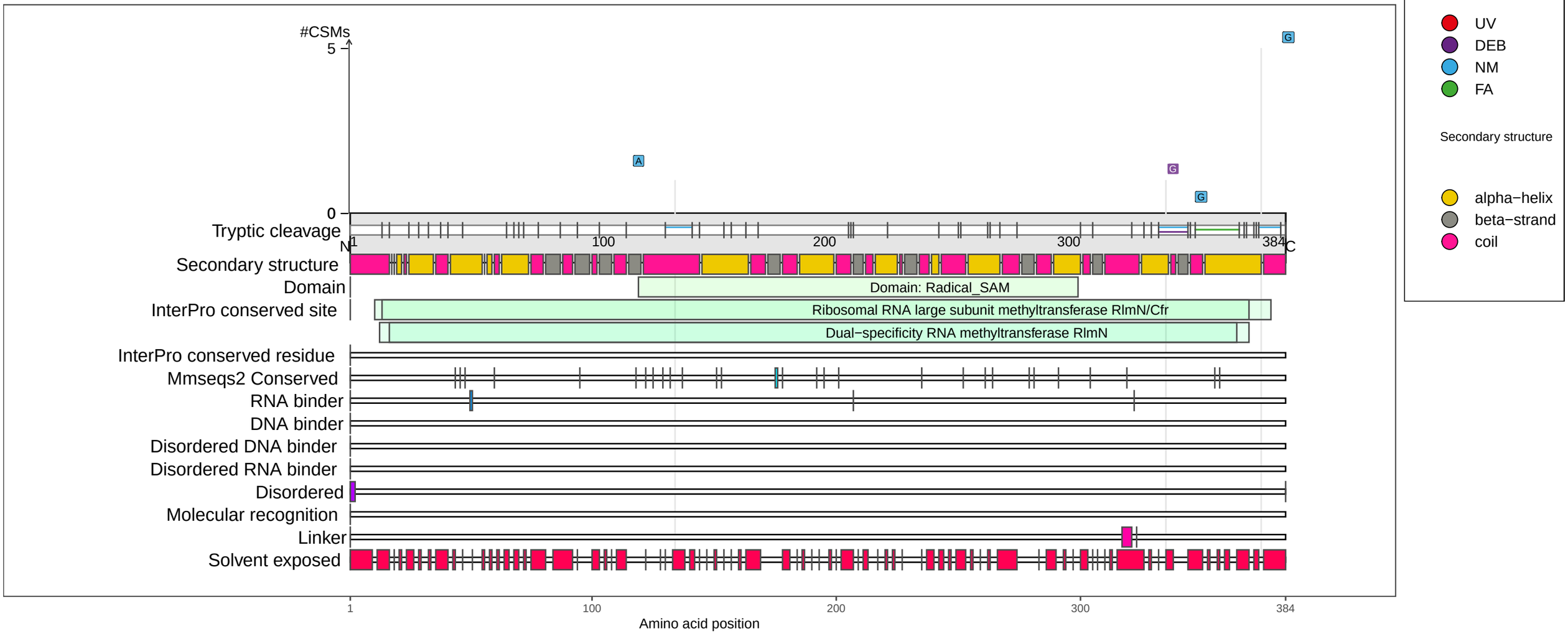
− RNA functions: not annotated



P36979
RLMN_ECOLI Dual−specificity RNA methyltransferase RlmN

− Abundance:
tryptic [log10 Intensity]: 7.66 (Q 43)
PAXdb K12 strain [ppm]: 1.17 (Q 19)
PAXdb E.coli [ppm]: 1.96 (Q 71)

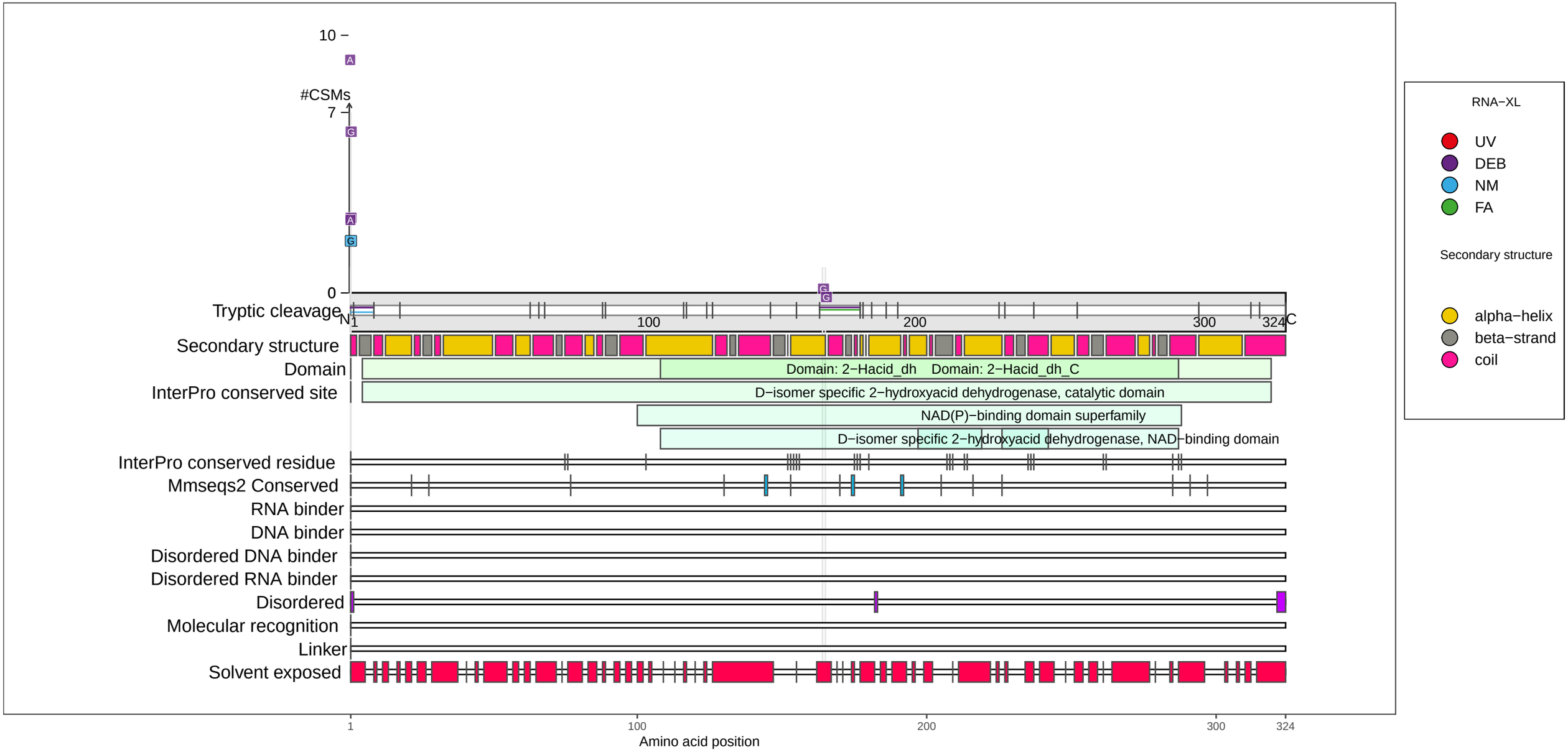
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA methylation; RNA methyltransferase activity; RNA modification; RNA processing
rRNA (adenine−C2−)−methyltransferase activity; rRNA (adenine) methyltransferase activity
rRNA base methylation; rRNA binding; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing
tRNA (adenine−C2−)−methyltransferase activity; tRNA (adenine) methyltransferase activity; tRNA binding
tRNA metabolic process; tRNA methylation; tRNA methyltransferase activity; tRNA modification
tRNA processing



P37666
GHRB_ECOLI Glyoxylate/hydroxypyruvate reductase B

− Abundance:
tryptic [log10 Intensity]: 8.41 (Q 73)
PAXdb K12 strain [ppm]: 2.61 (Q 81)
PAXdb E.coli [ppm]: 2.53 (Q 86)

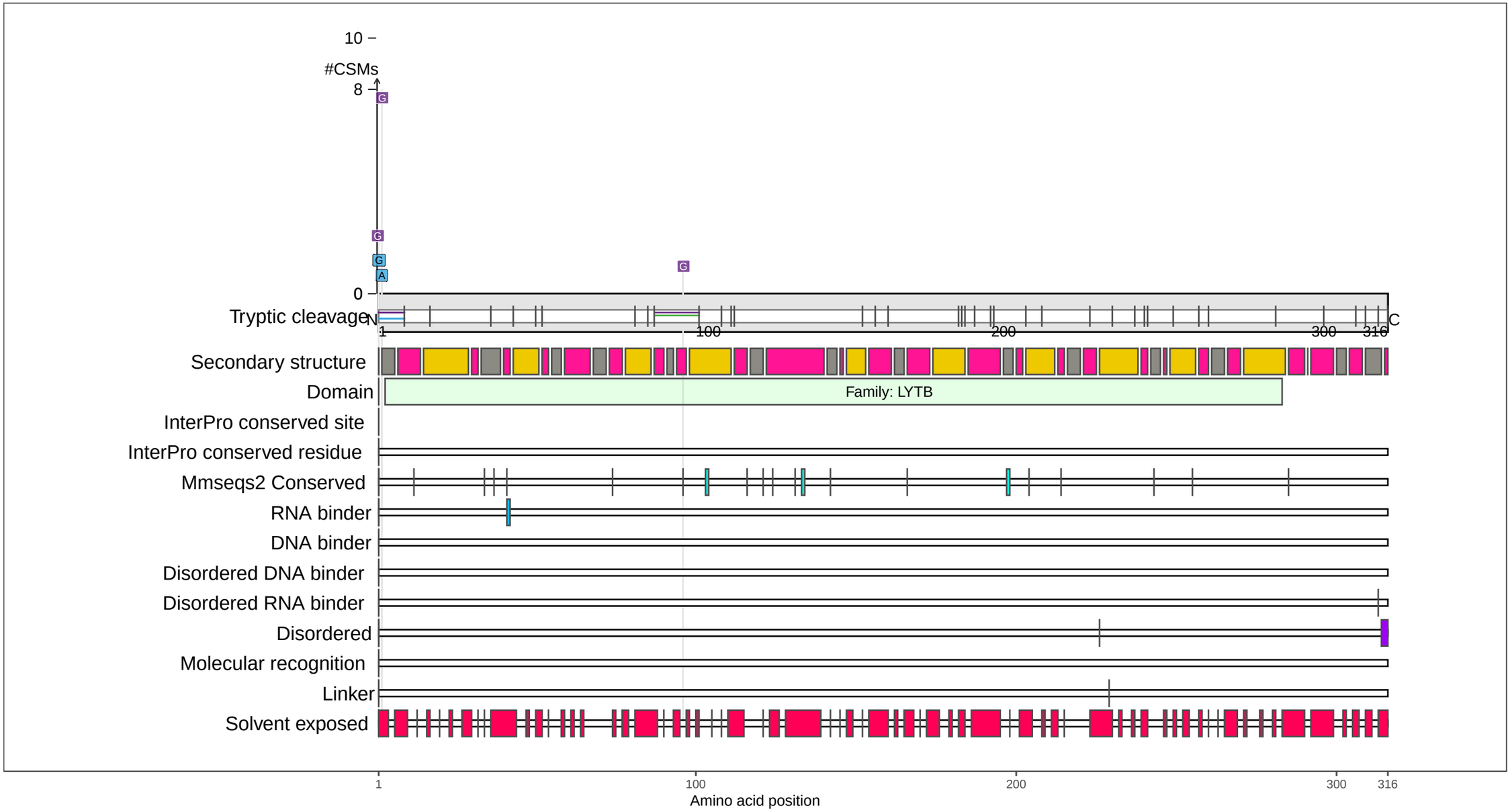
− RNA functions: not annotated

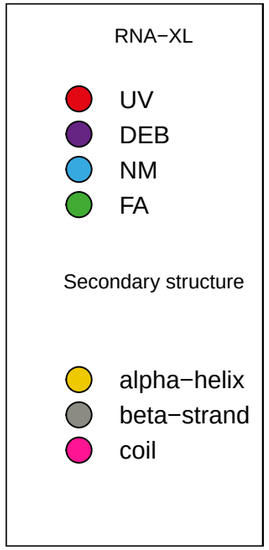


P62623
ISPH_ECOLI 4−hydroxy−3−methylbut−2−enyl diphosphate reductase

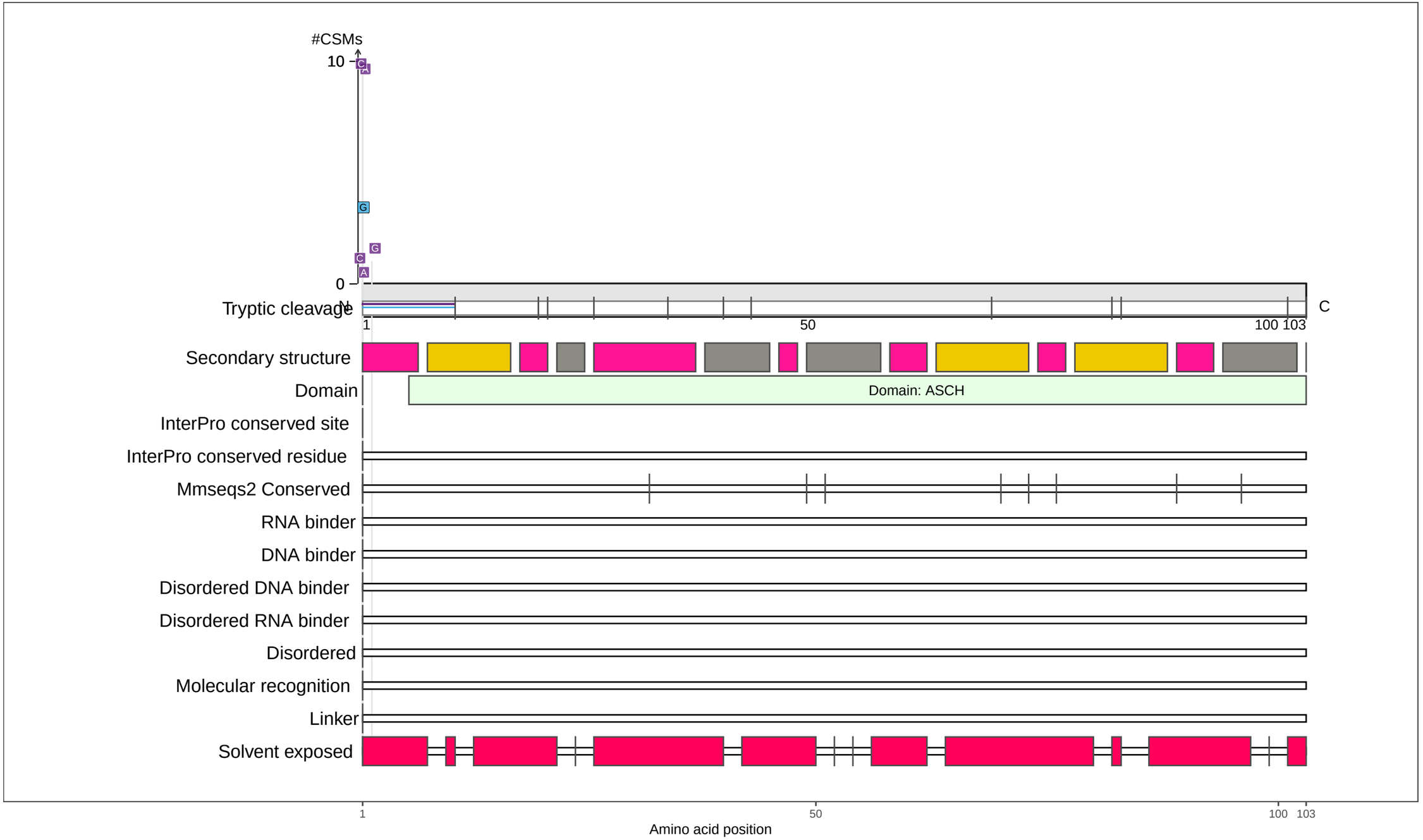
− Abundance:
tryptic [log10 Intensity]: 8.84 (Q 85)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.09 (Q 74)

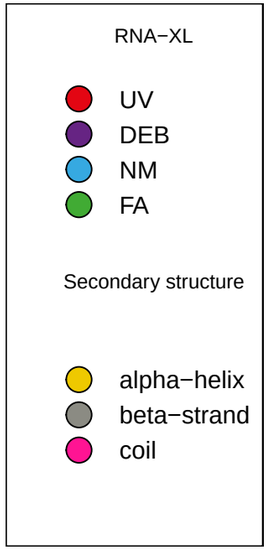
− RNA functions: not annotated





P67603
AC4CH_ECOLI N(4)−acetylcytidine amidohydrolase
− RNA functions: not annotated

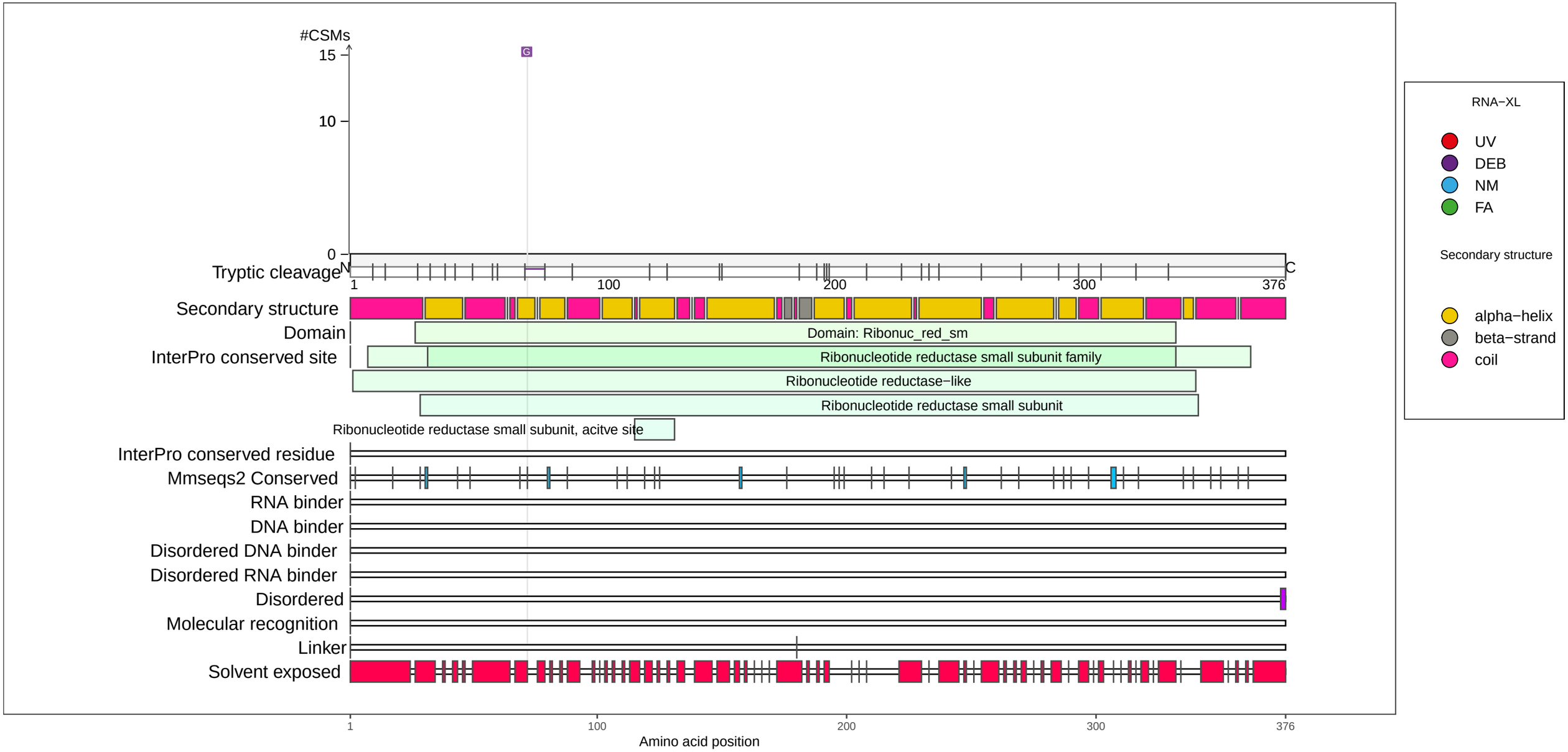




P69924
RIR2_ECOLI Ribonucleoside−diphosphate reductase 1 subunit beta

− Abundance:
tryptic [log10 Intensity]: 8.86 (Q 85)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 2.22 (Q 78)

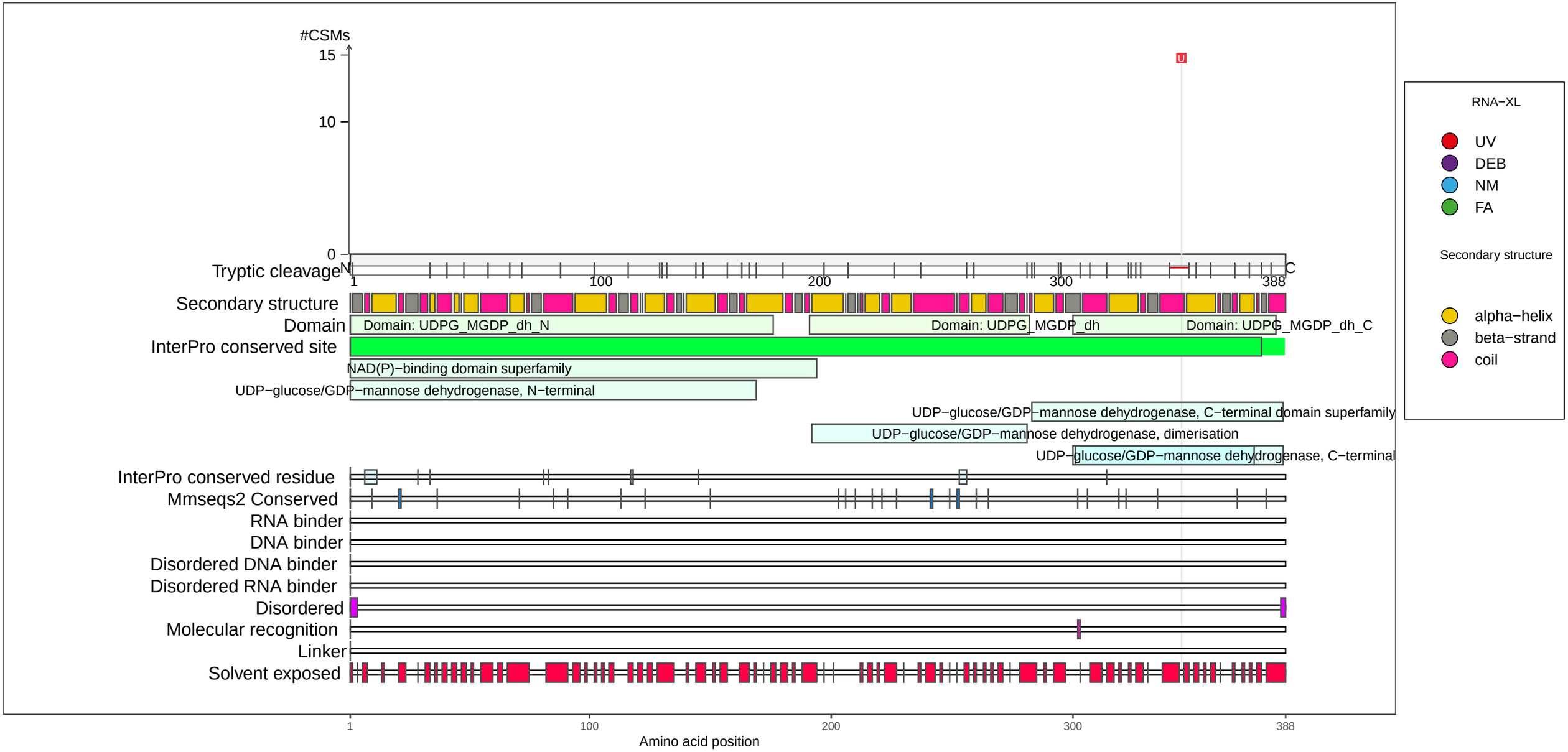
− RNA functions: not annotated



P76373
UDG_ECOLI UDP−glucose 6−dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 6.7 (Q 5)
PAXdb K12 strain [ppm]: 2.27 (Q 69)
PAXdb E.coli [ppm]: 1.15 (Q 51)

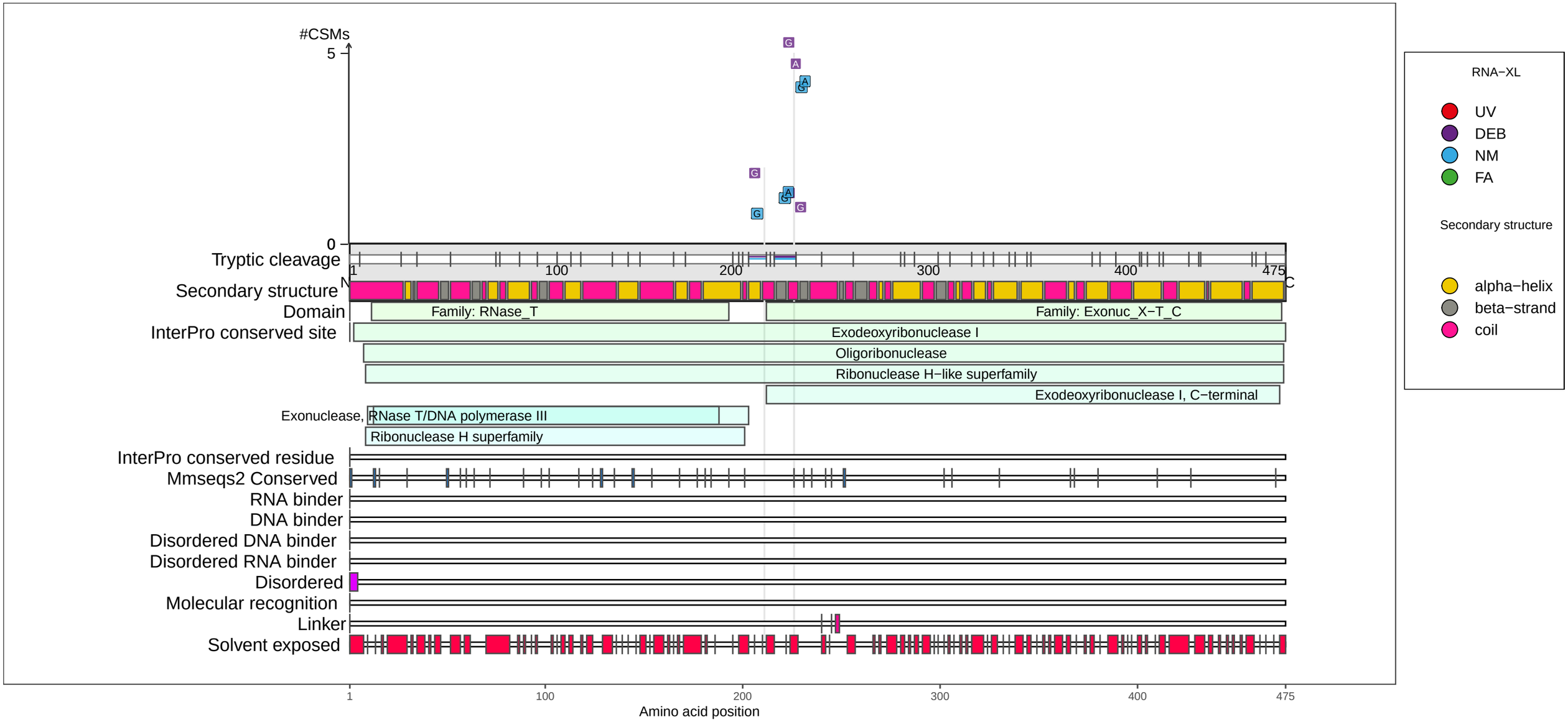
− RNA functions: not annotated



P04995
EX1_ECOLI Exodeoxyribonuclease I

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 1.26 (Q 24)
PAXdb E.coli [ppm]: 1.21 (Q 52)

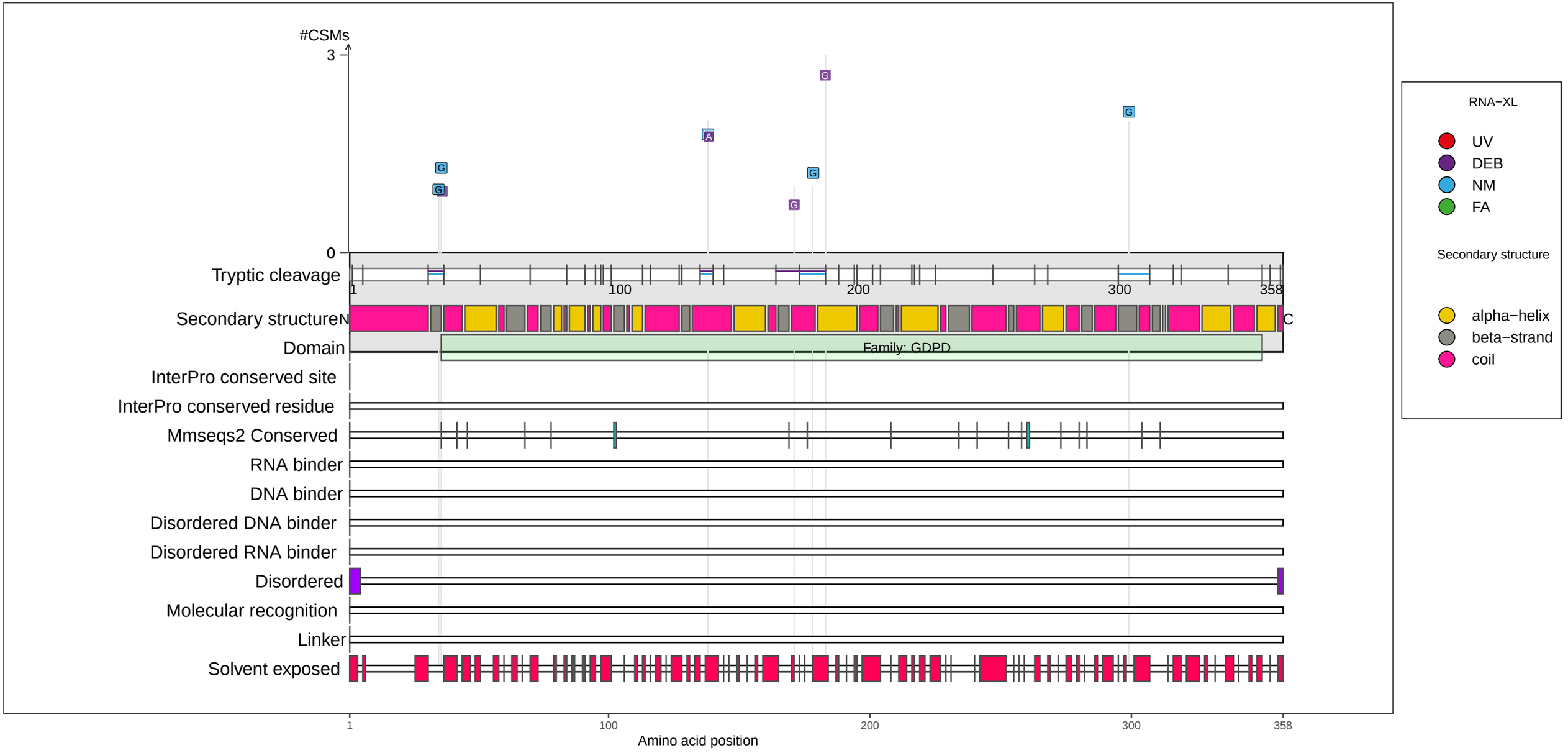
− RNA functions:
RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, exonucleolytic



P09394
GLPQ_ECOLI Glycerophosphodiester phosphodiesterase, periplasmic

− Abundance:
tryptic [log10 Intensity]: 9.44 (Q 96)
PAXdb K12 strain [ppm]: 2.86 (Q 87)
PAXdb E.coli [ppm]: 2.29 (Q 80)

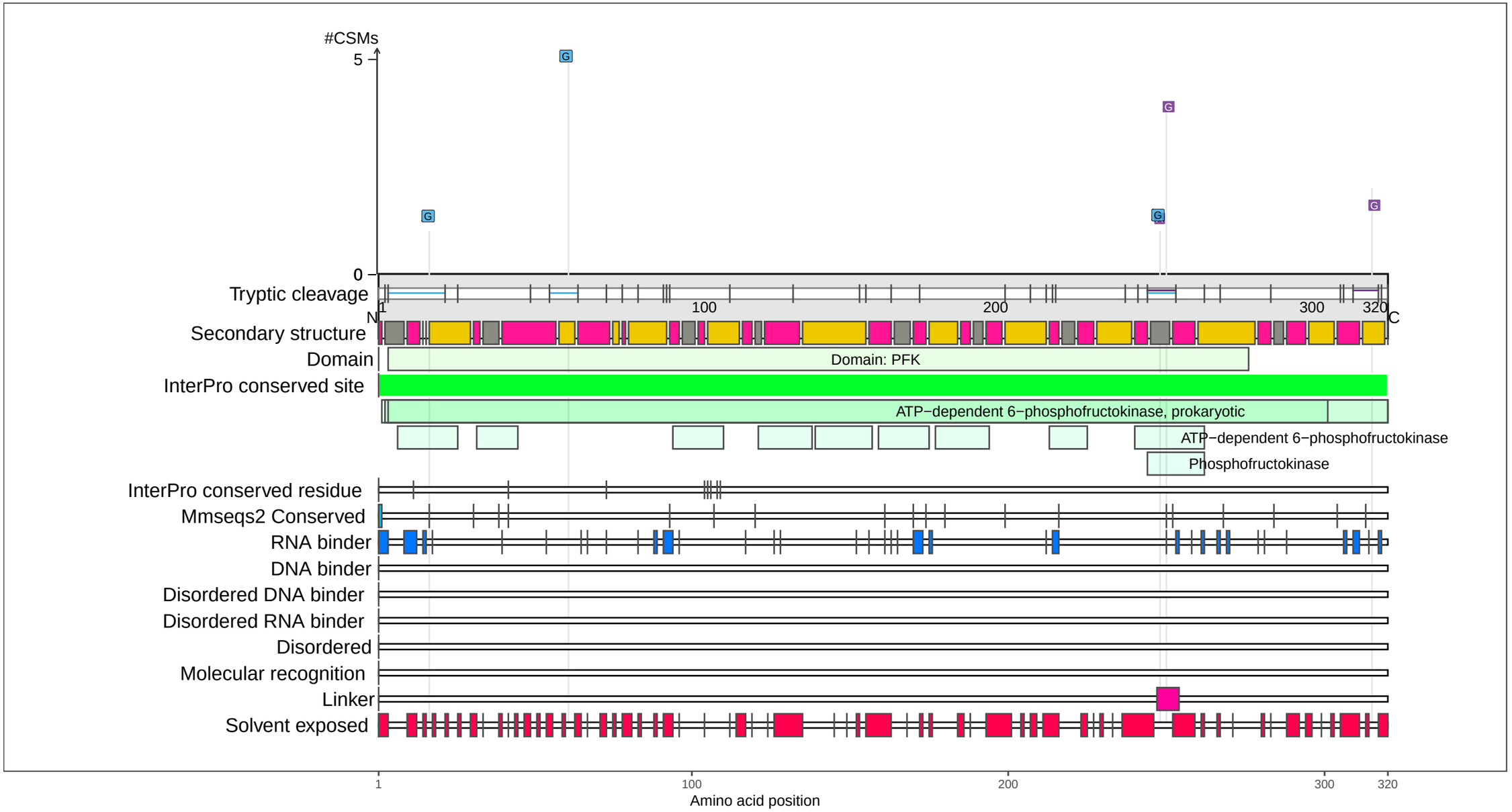
− RNA functions: not annotated

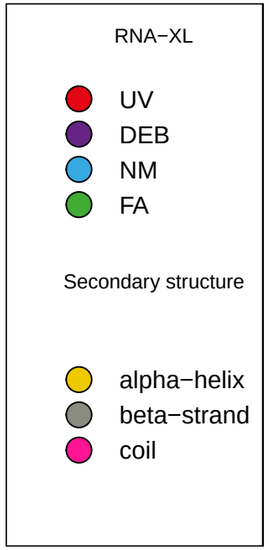


P0A796
PFKA_ECOLI ATP−dependent 6−phosphofructokinase isozyme 1

− Abundance:
tryptic [log10 Intensity]: 8.63 (Q 79)
PAXdb K12 strain [ppm]: 2.29 (Q 69)
PAXdb E.coli [ppm]: 2.9 (Q 93)

− RNA functions: not annotated

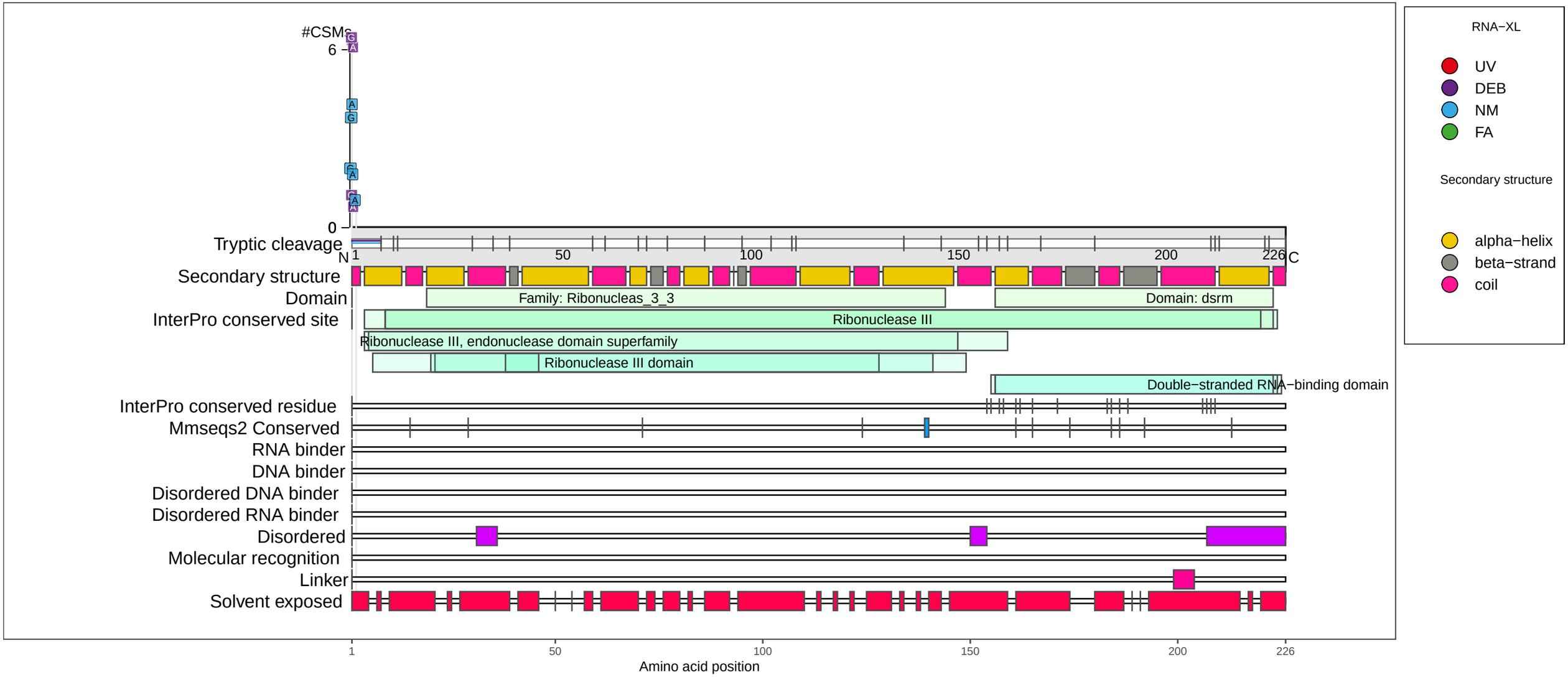




P0A7Y0
RNC_ECOLI Ribonuclease 3

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 2.43 (Q 84)

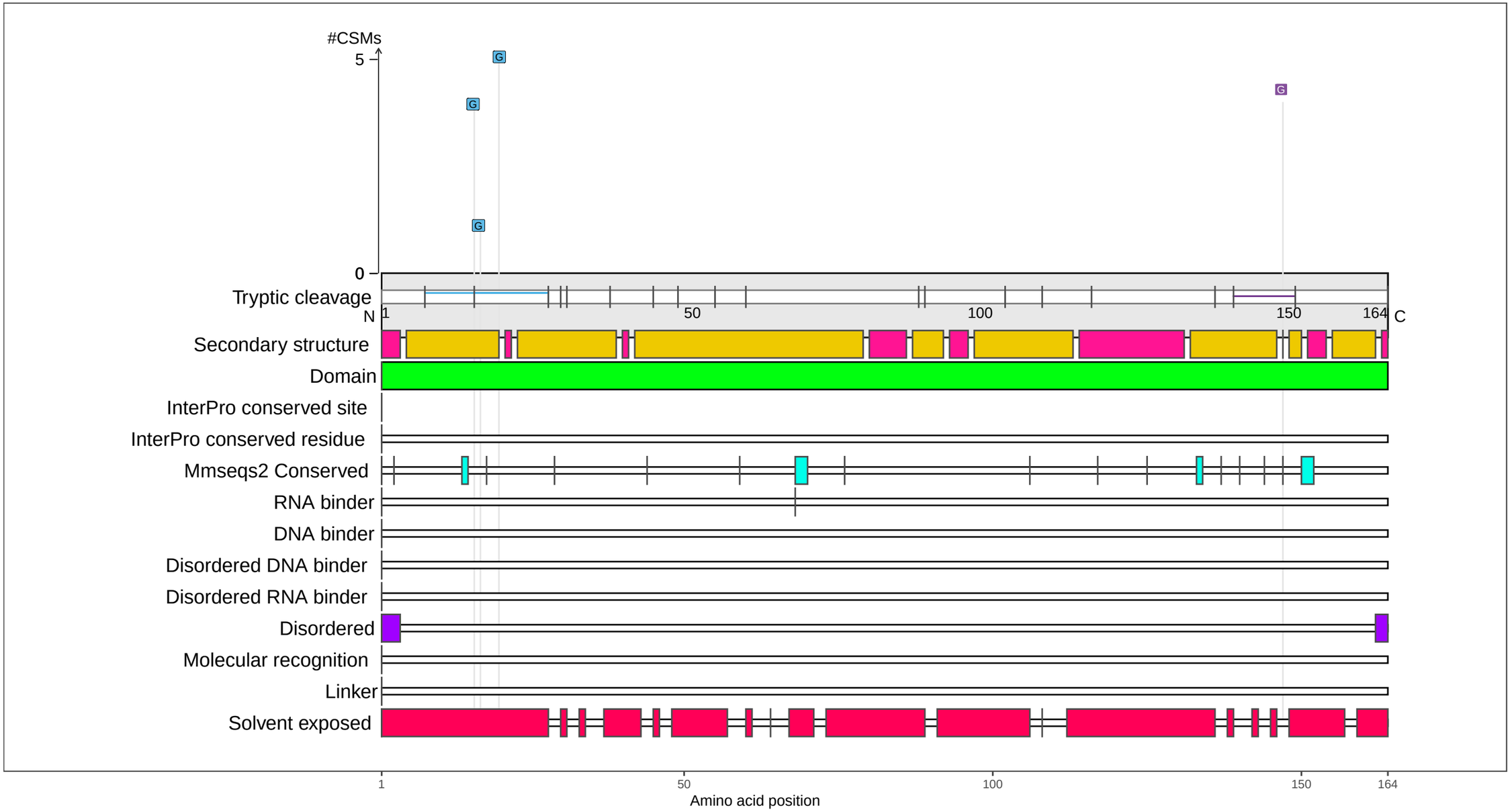
− RNA functions:
Double−stranded RNA binding motif; mRNA metabolic process; mRNA processing
ncRNA catabolic process; ncRNA metabolic process; ncRNA processing; RNA binding
RNA catabolic process; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic; RNA processing; rRNA binding; rRNA catabolic process
rRNA metabolic process; rRNA processing; tRNA metabolic process; tRNA processing



P0A8W8
YFBU_ECOLI UPF0304 protein YfbU

− Abundance:
tryptic [log10 Intensity]: 9.66 (Q 98)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 2.76 (Q 91)

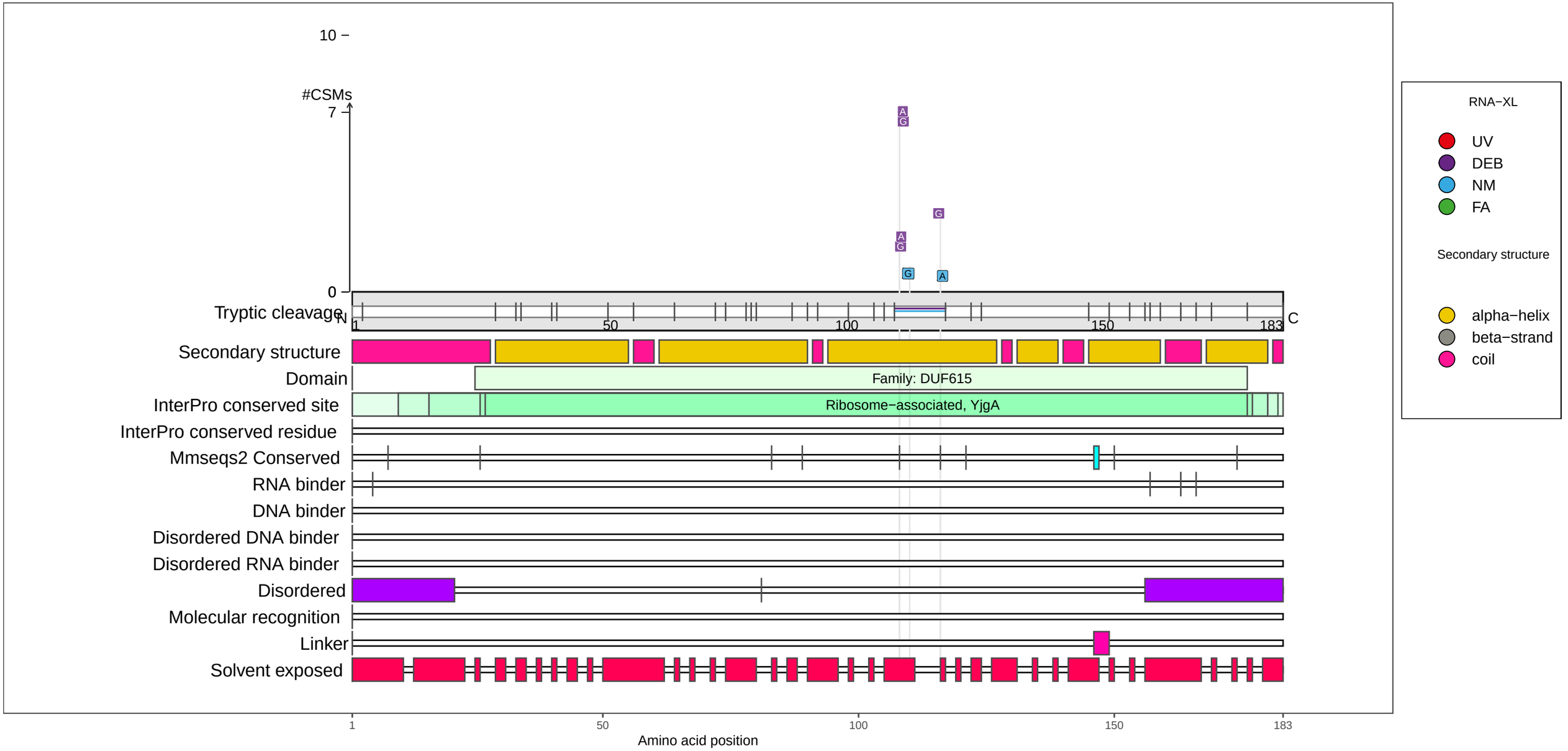
− RNA functions: not annotated



P0A8X0
YJGA_ECOLI UPF0307 protein YjgA

− Abundance:
tryptic [log10 Intensity]: 8.1 (Q 61)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 2.6 (Q 88)

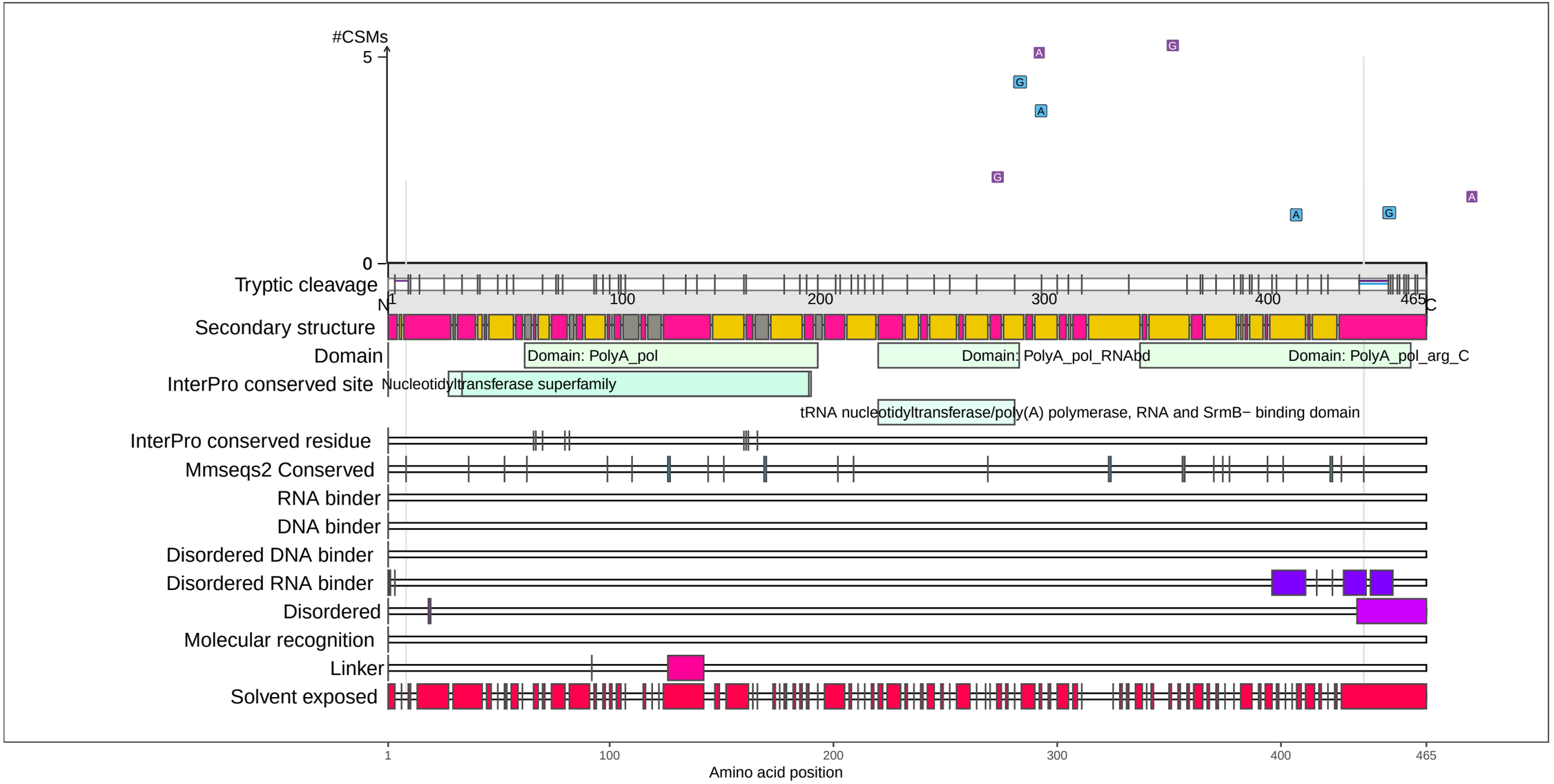
− RNA functions: not annotated

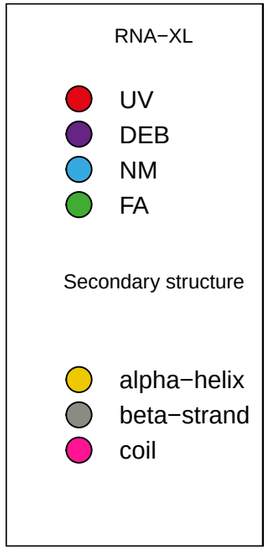


P0ABF1
PCNB_ECOLI Poly(A) polymerase I

− Abundance:
tryptic [log10 Intensity]: 7.56 (Q 38)
PAXdb K12 strain [ppm]: 1.95 (Q 59)
PAXdb E.coli [ppm]: 1.87 (Q 69)

− RNA functions:
mRNA 3−end processing; mRNA metabolic process; mRNA polyadenylation; mRNA processing
Probable RNA and SrmB− binding site of polymerase A; RNA 3−end processing; RNA binding
RNA metabolic process; RNA modification; RNA polyadenylation; RNA processing

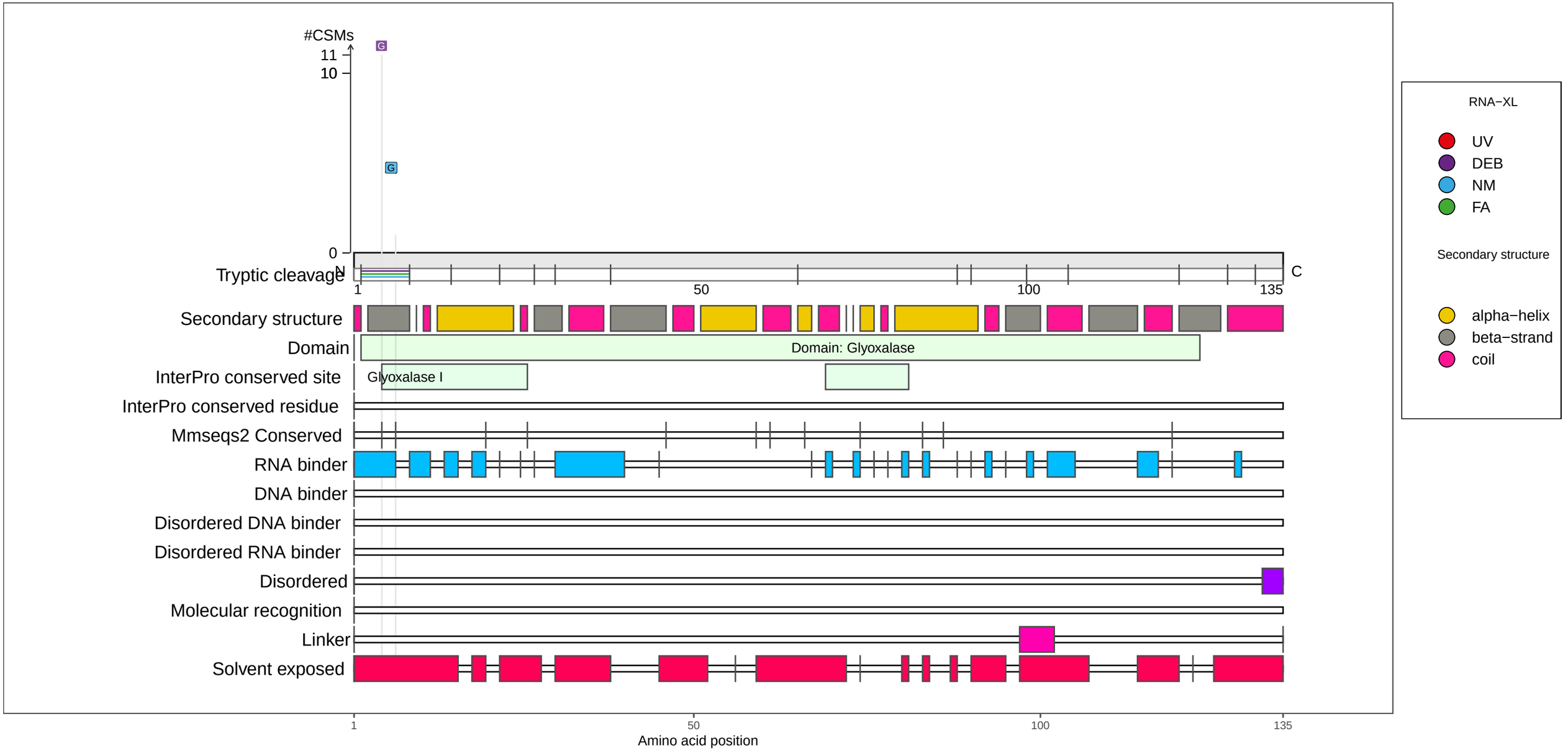




P0AC81
LGUL_ECOLI Lactoylglutathione lyase

− Abundance:
tryptic [log10 Intensity]: 7.98 (Q 57)
PAXdb K12 strain [ppm]: 1.69 (Q 49)
PAXdb E.coli [ppm]: 2.59 (Q 88)

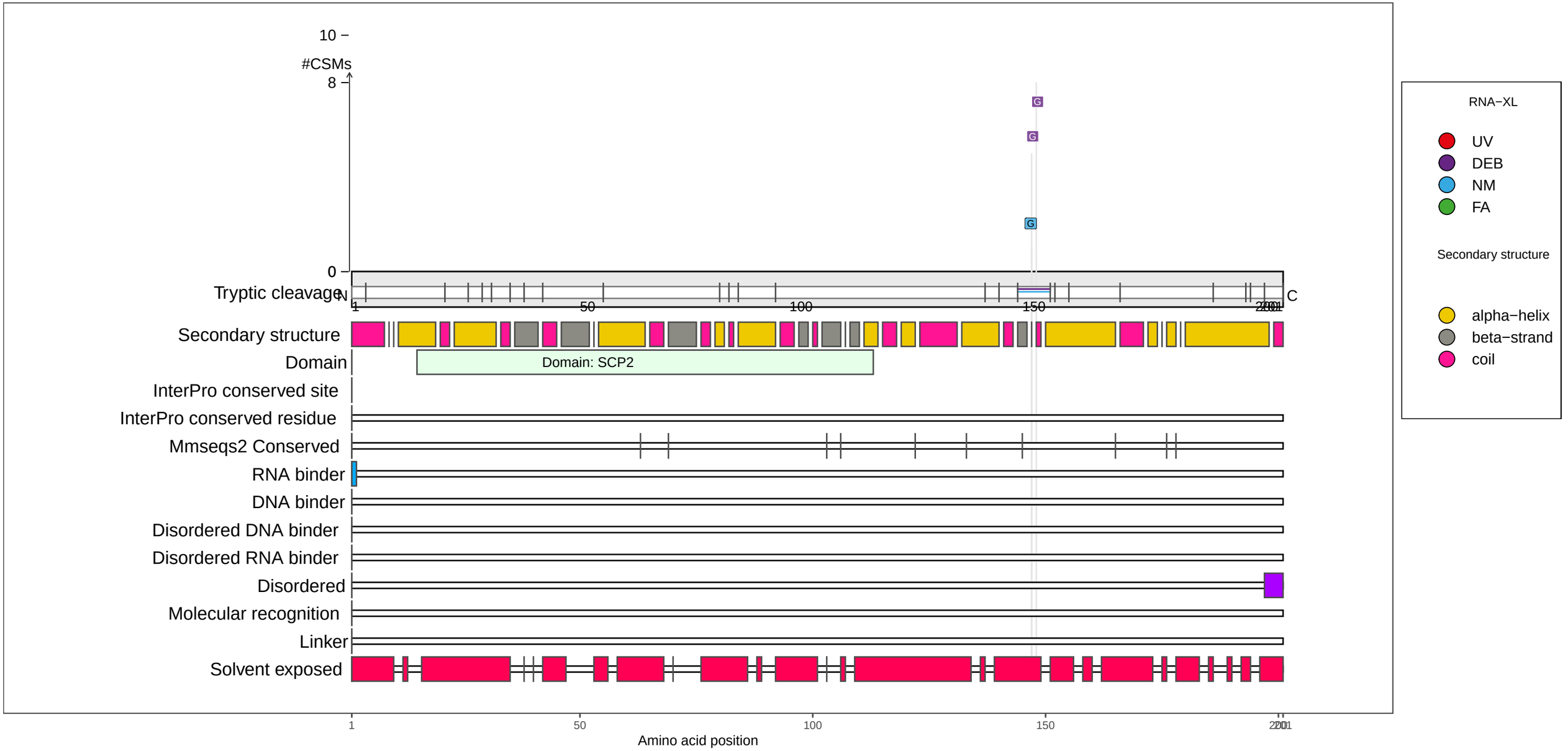
− RNA functions: not annotated



P0ADP7
UBIJ_ECOLI Ubiquinone biosynthesis accessor factor UbiJ

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 55)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.45 (Q 59)

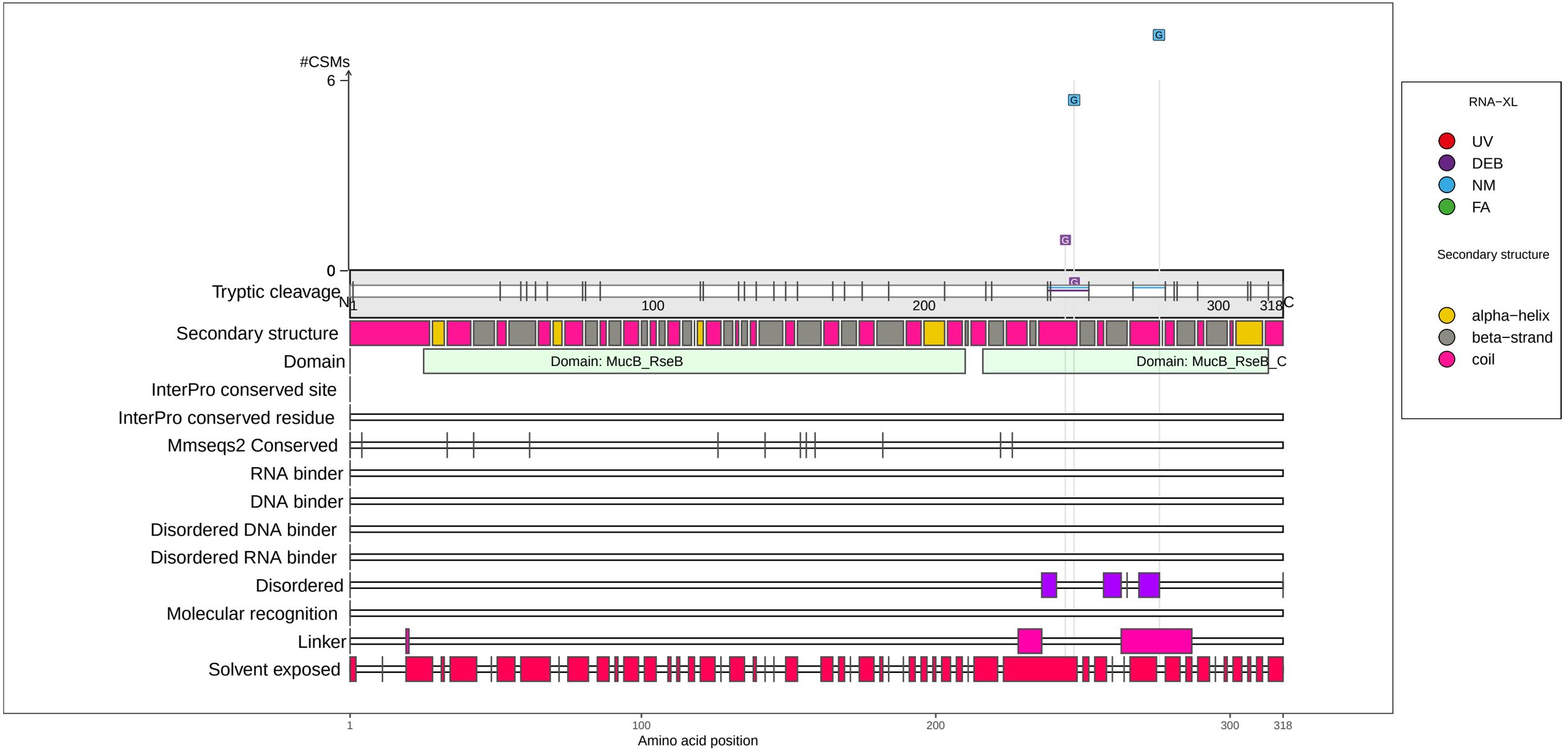
− RNA functions: not annotated



P0AFX9
RSEB_ECOLI Sigma−E factor regulatory protein RseB

− Abundance:
tryptic [log10 Intensity]: 8.26 (Q 68)
PAXdb K12 strain [ppm]: 2.5 (Q 78)
PAXdb E.coli [ppm]: 2.06 (Q 74)

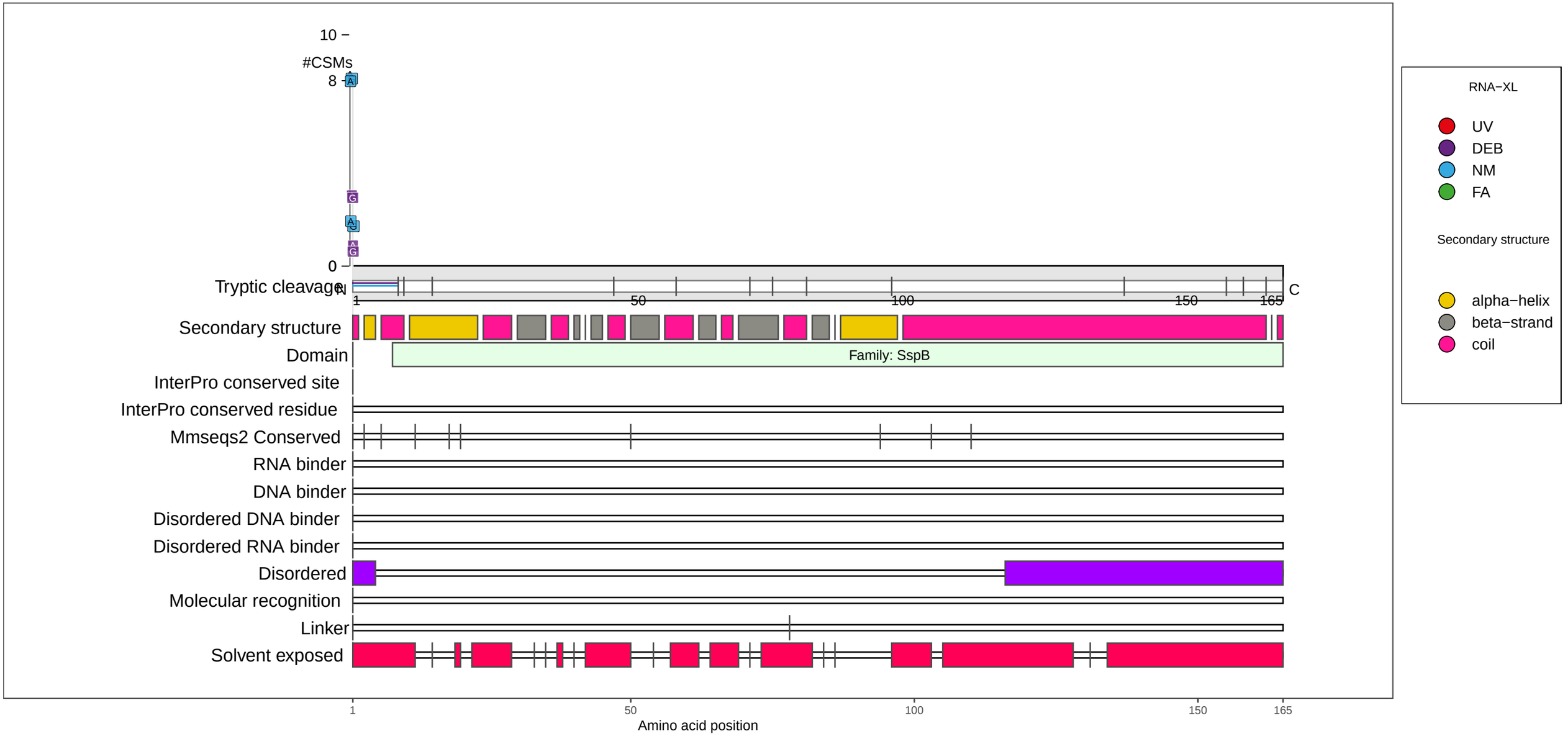
− RNA functions: not annotated



P0AFZ3
SSPB_ECOLI Stringent starvation protein B

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 51)
PAXdb K12 strain [ppm]: 1.66 (Q 48)
PAXdb E.coli [ppm]: 2.55 (Q 87)

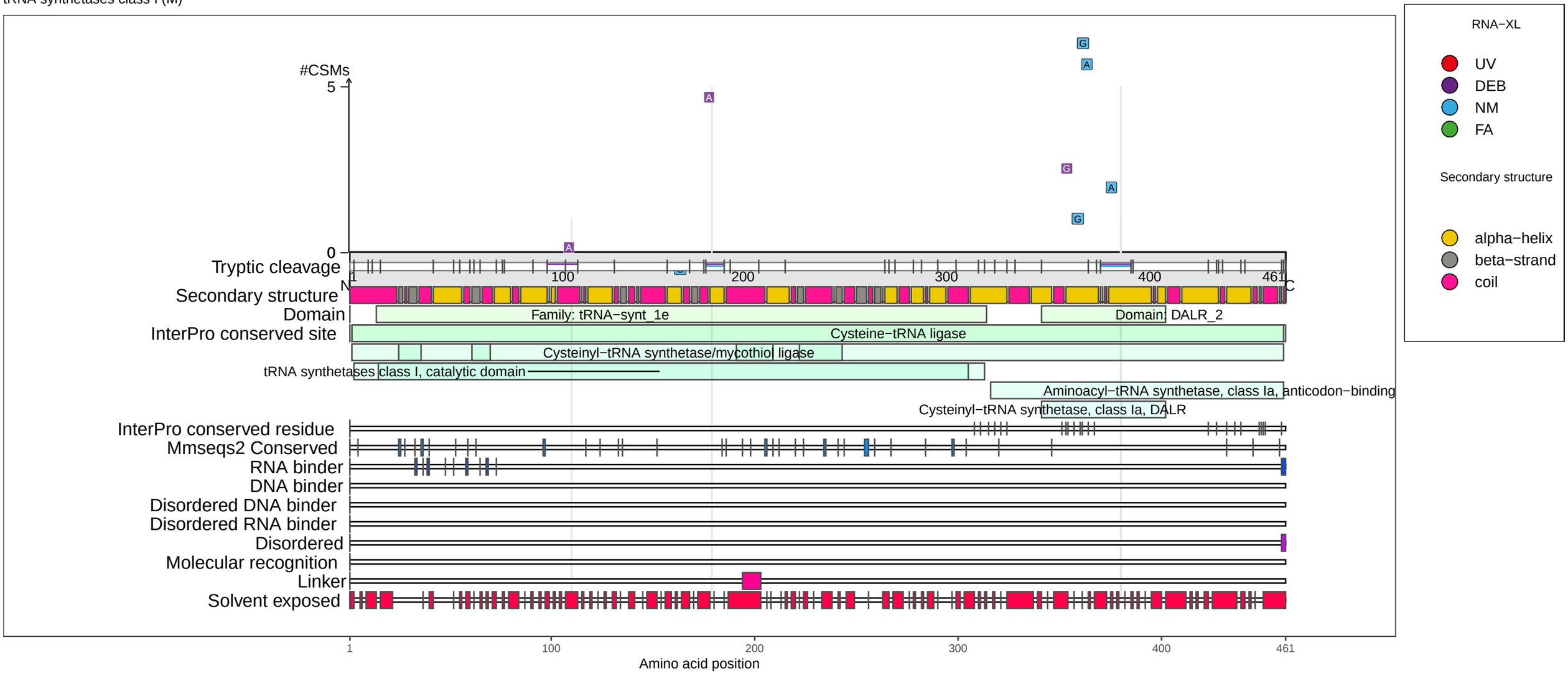
− RNA functions:
RNA binding



P21888
SYC_ECOLI Cysteine−−tRNA ligase

− Abundance:
tryptic [log10 Intensity]: 9.01 (Q 88)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 2.54 (Q 86)

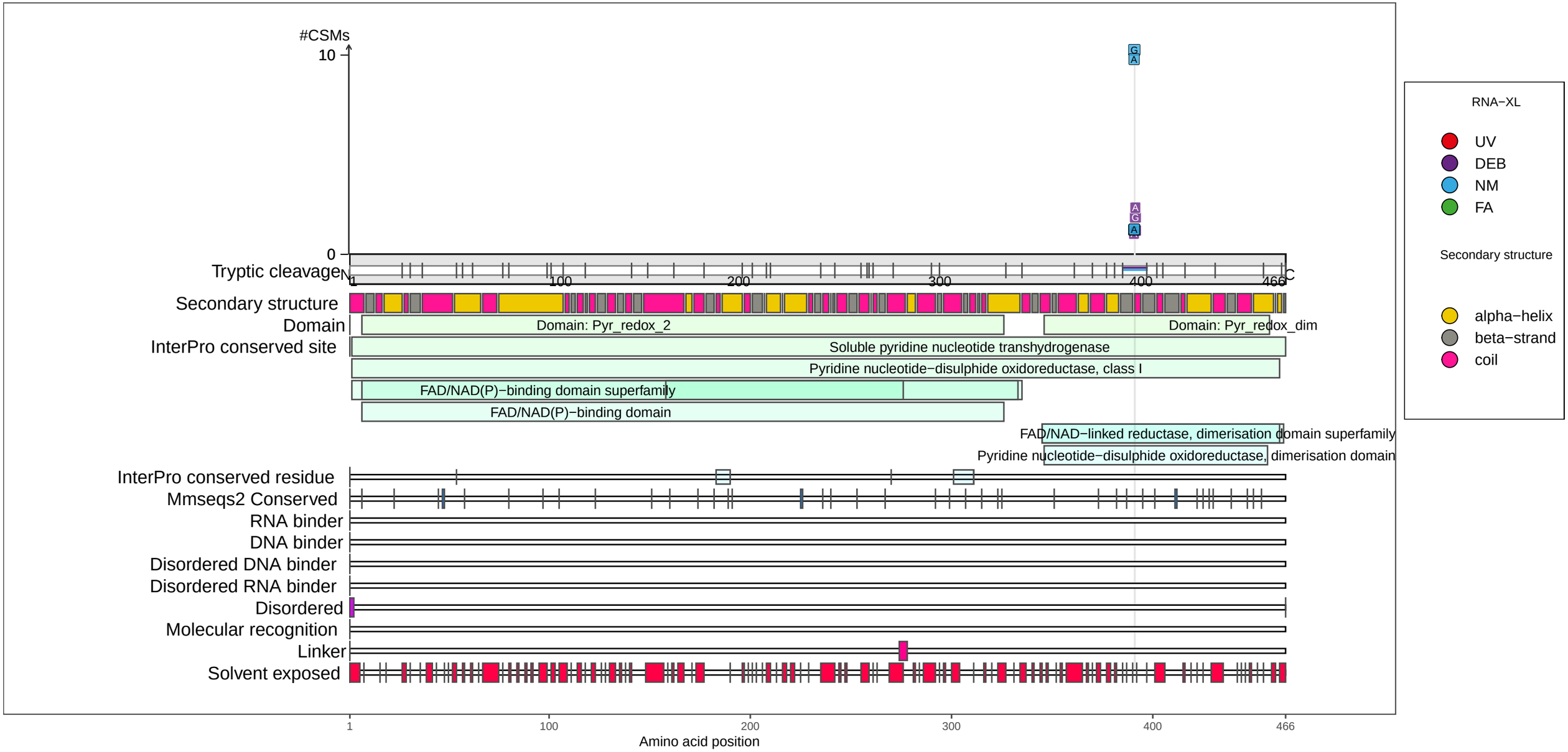
− RNA functions:
aminoacyl−tRNA ligase activity; cysteine−tRNA ligase activity
cysteinyl−tRNA aminoacylation; ncRNA metabolic process; RNA metabolic process
This DALR domain is found in cysteinyl−tRNA−synthetases.; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA metabolic process; tRNA synthetases class I (C) catalytic domain
tRNA synthetases class I (I, L, M and V); tRNA synthetases class I (K)
tRNA synthetases class I (M)



P27306
STHA_ECOLI Soluble pyridine nucleotide transhydrogenase

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 2.39 (Q 83)

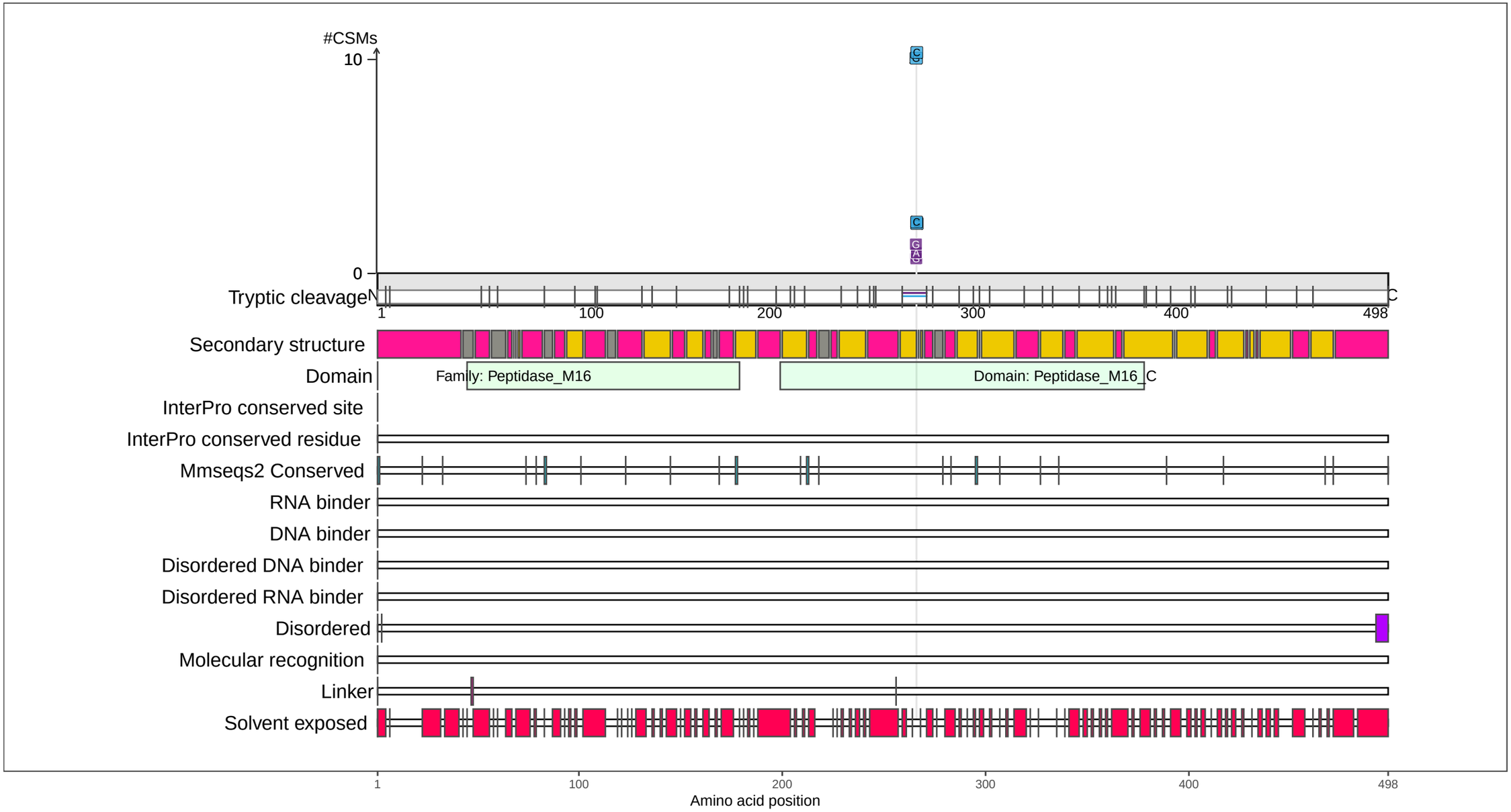
− RNA functions: not annotated



P37648
YHJJ_ECOLI Protein YhjJ

− Abundance:
tryptic [log10 Intensity]: 8.35 (Q 71)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 1.91 (Q 70)

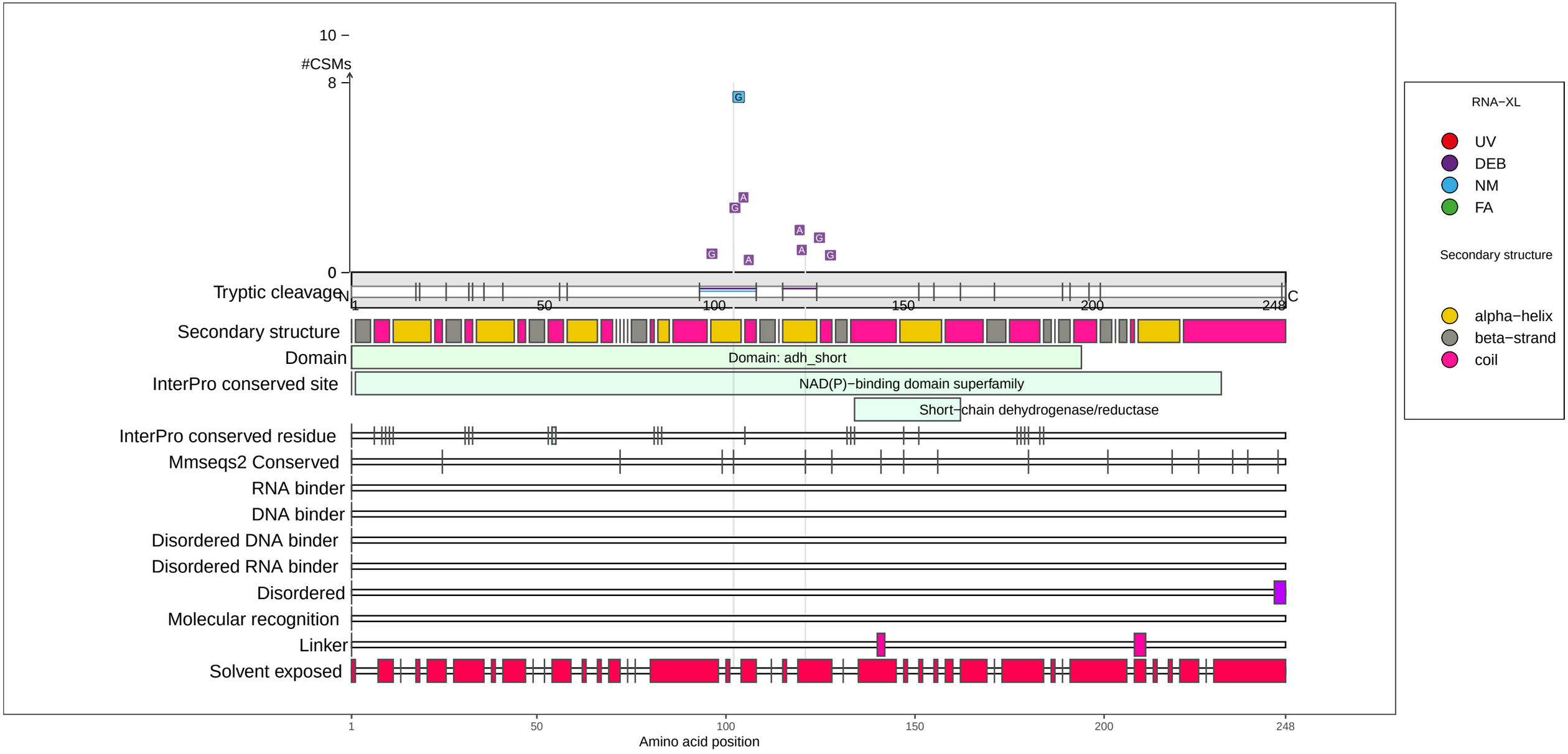
− RNA functions: not annotated



P39831
YDFG_ECOLI NADP−dependent 3−hydroxy acid dehydrogenase YdfG

− Abundance:
tryptic [log10 Intensity]: 8.36 (Q 71)
PAXdb K12 strain [ppm]: 3.02 (Q 91)
PAXdb E.coli [ppm]: 2.9 (Q 93)

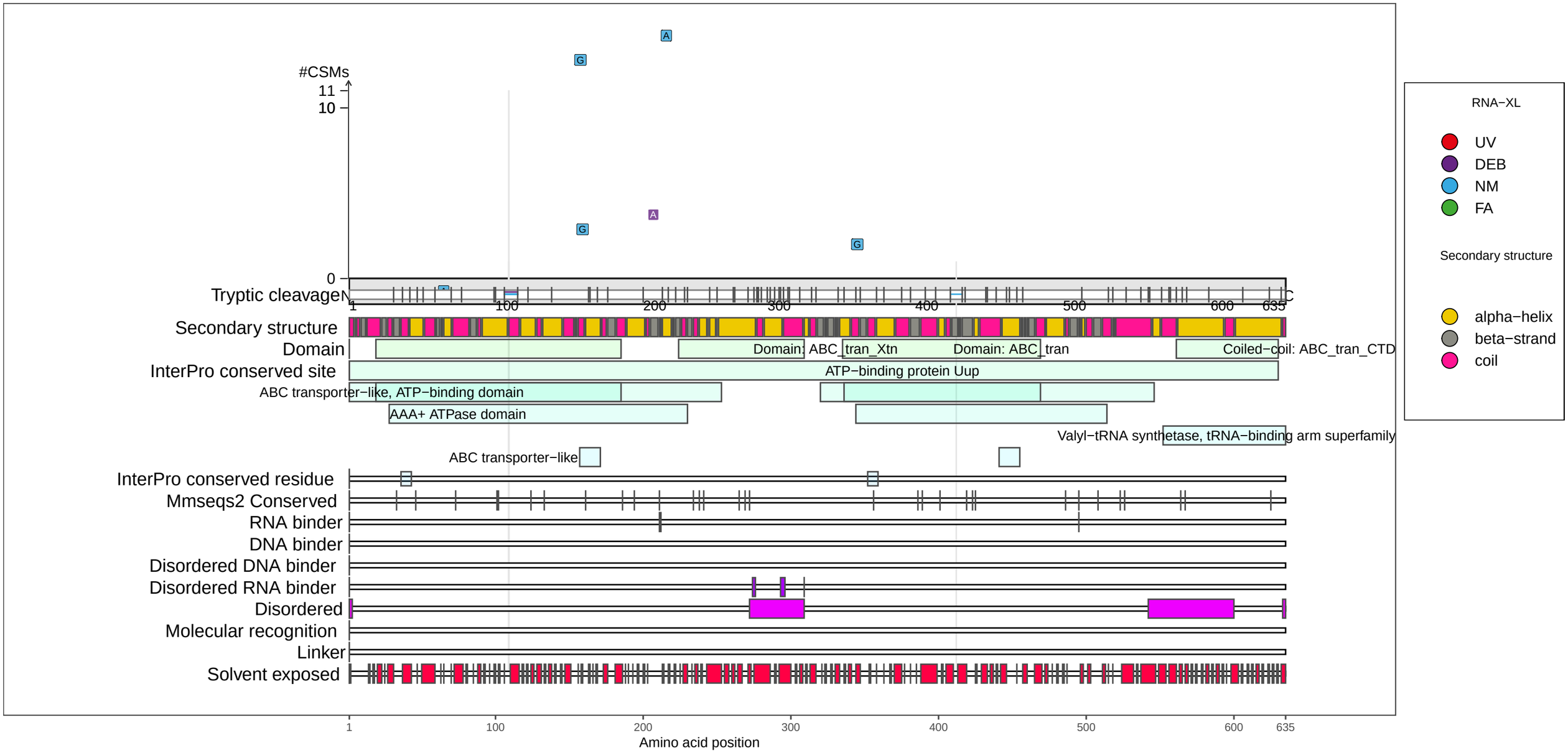
− RNA functions: not annotated



P43672
UUP_ECOLI ATP−binding protein Uup

− Abundance:
tryptic [log10 Intensity]: 8.77 (Q 83)
PAXdb K12 strain [ppm]: 1.32 (Q 28)
PAXdb E.coli [ppm]: 1.68 (Q 64)

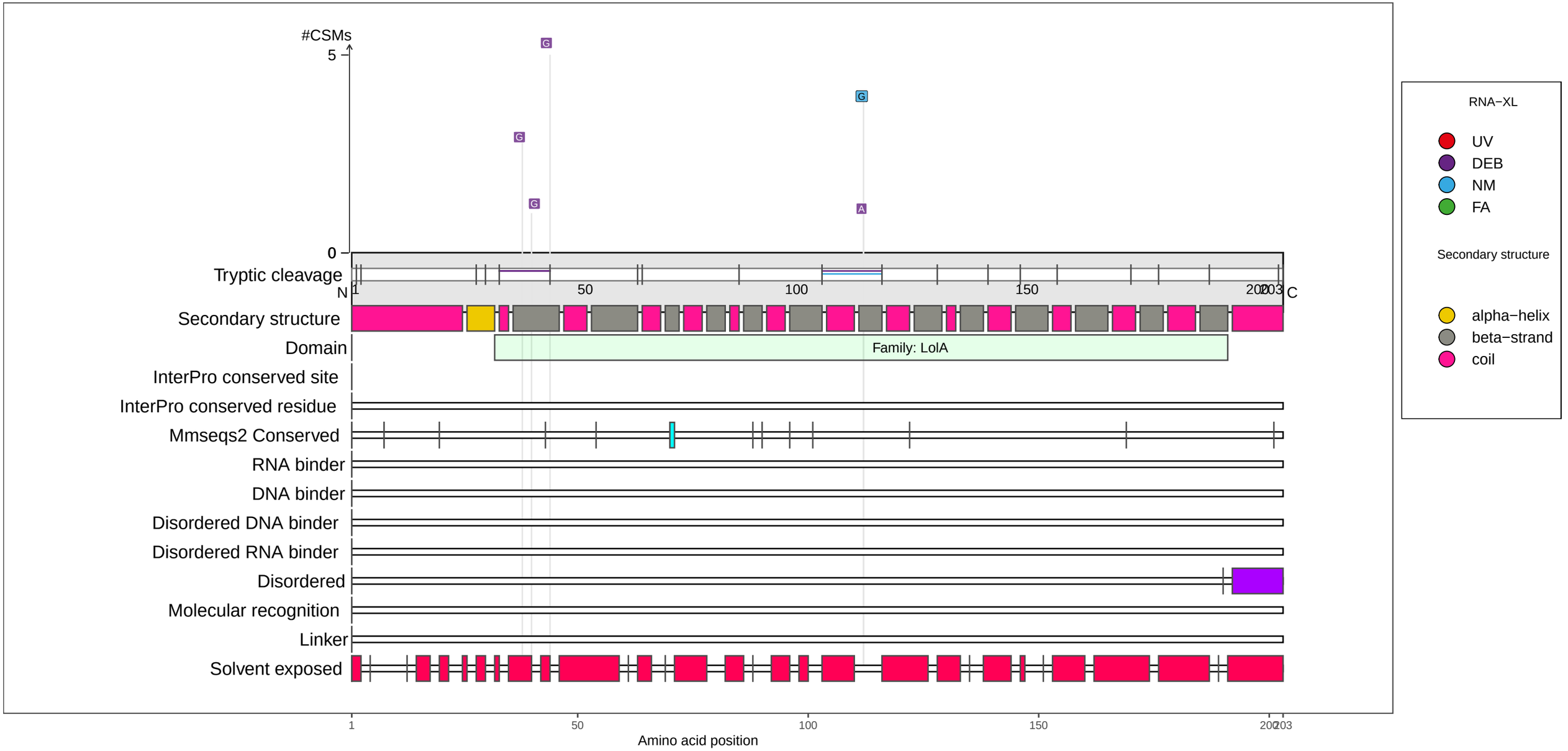
− RNA functions: not annotated



P61316
LOLA_ECOLI Outer−membrane lipoprotein carrier protein

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 2.56 (Q 87)

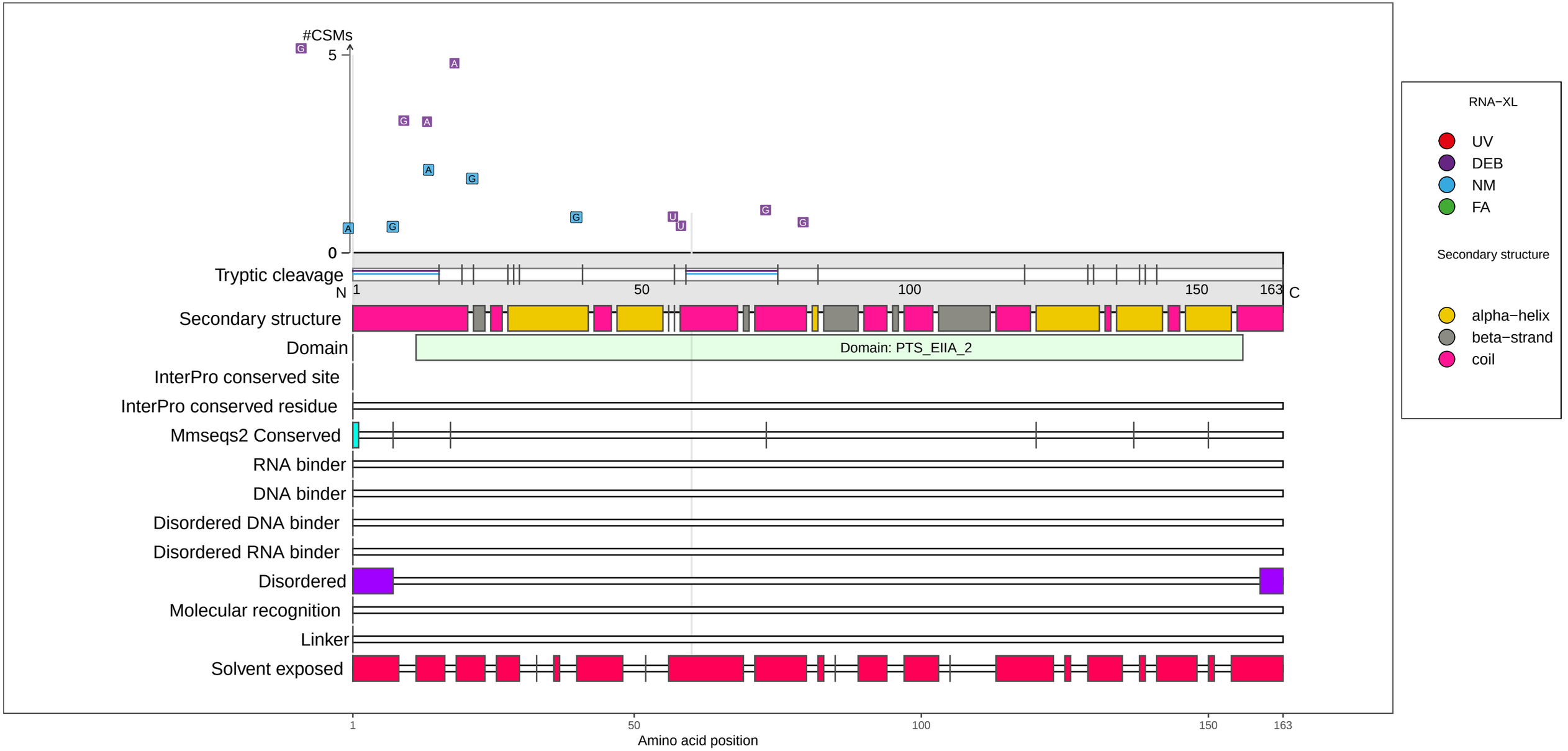
− RNA functions: not annotated



P69829
PTSN_ECOLI Nitrogen regulatory protein

− Abundance:
tryptic [log10 Intensity]: 8.01 (Q 58)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.57 (Q 87)

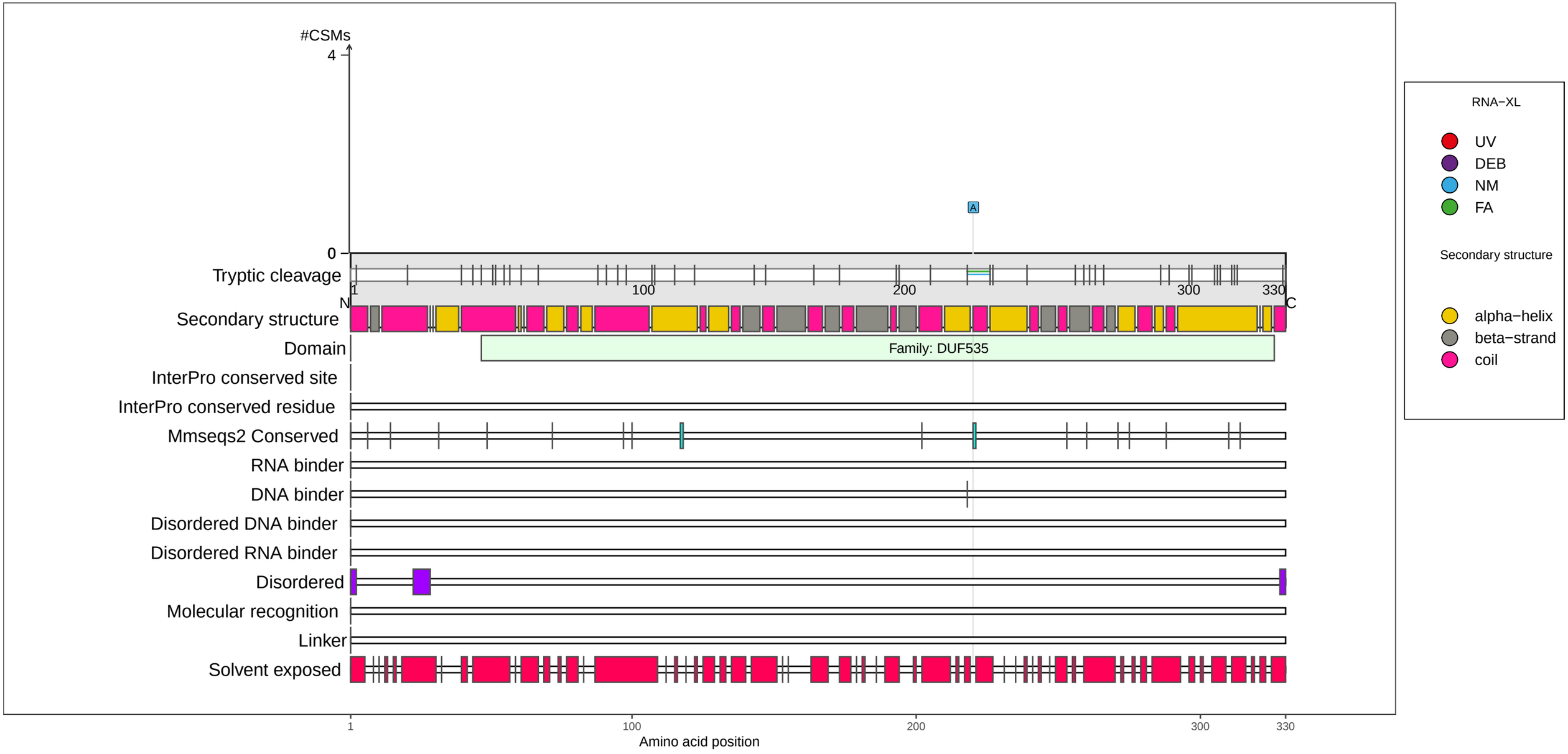
− RNA functions: not annotated



P75829
YBJX_ECOLI Uncharacterized protein YbjX

− Abundance:
tryptic [log10 Intensity]: 7.56 (Q 38)
PAXdb K12 strain [ppm]: 0.88 (Q 7)
PAXdb E.coli [ppm]: 1.35 (Q 56)

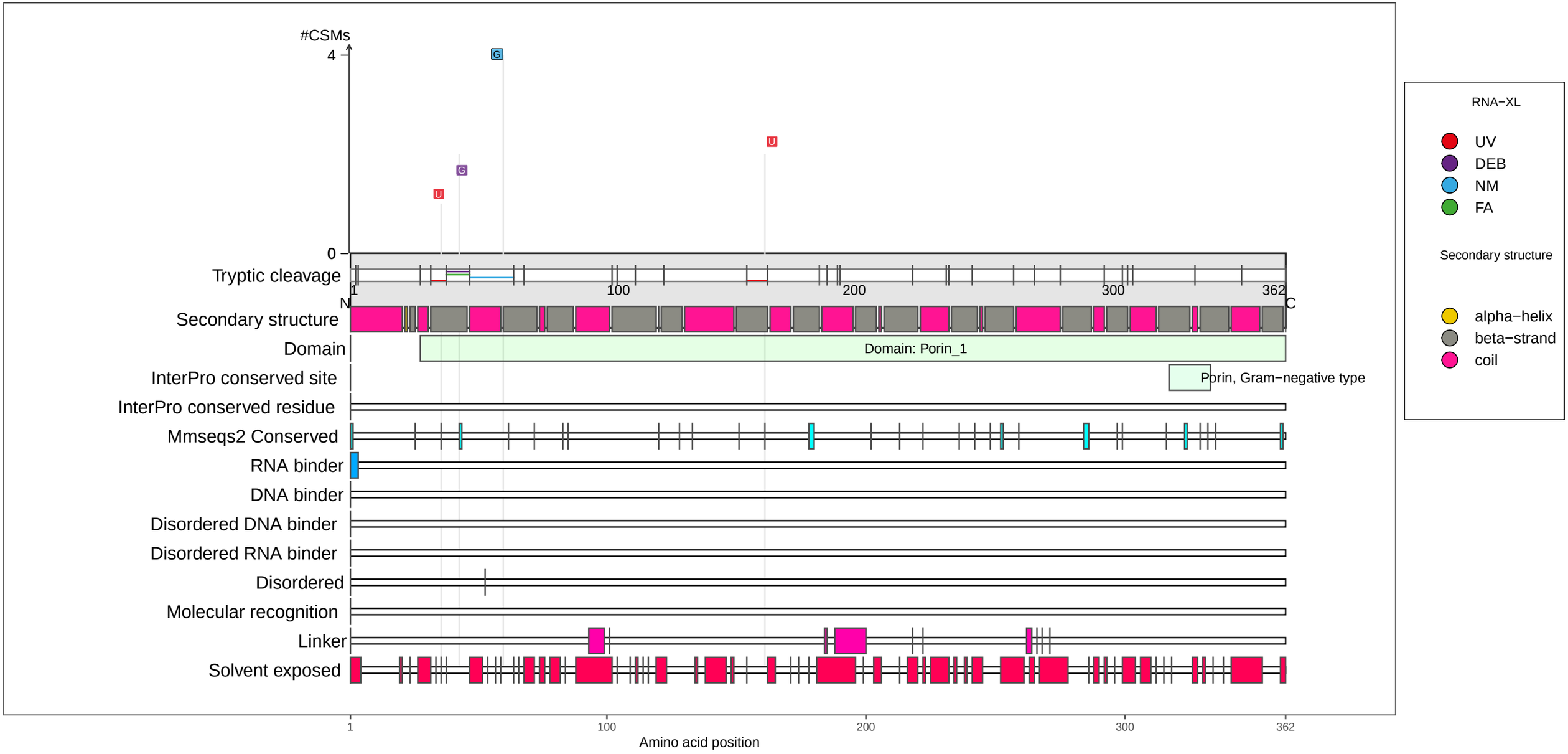
− RNA functions: not annotated



P02931
OMPF_ECOLI Outer membrane porin F

− Abundance:
tryptic [log10 Intensity]: 10.37 (Q 100)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.96 (Q 94)

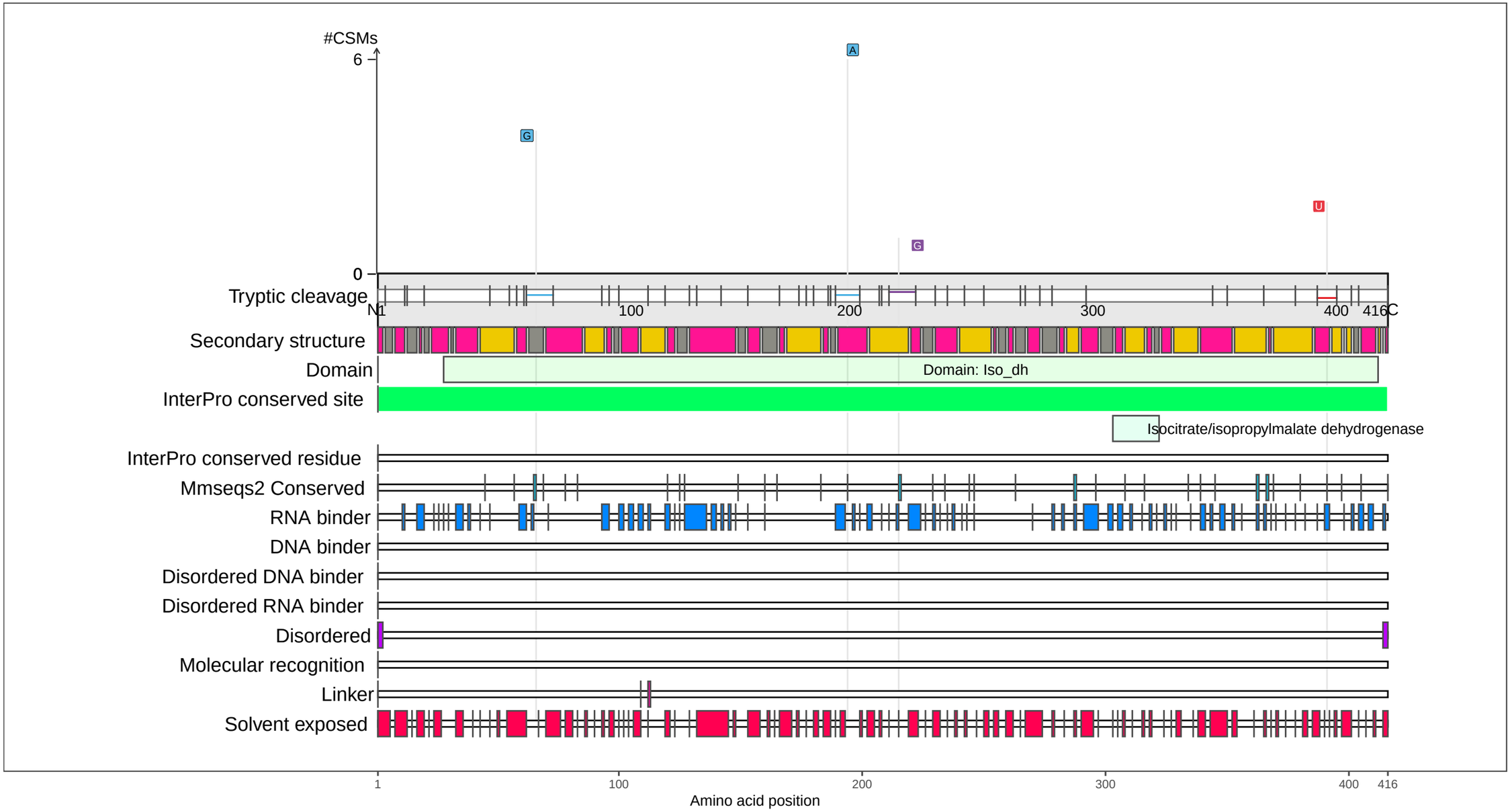
− RNA functions: not annotated



P08200
IDH_ECOLI Isocitrate dehydrogenase [NADP]

− Abundance:
tryptic [log10 Intensity]: 8.86 (Q 85)
PAXdb K12 strain [ppm]: 3.57 (Q 98)
PAXdb E.coli [ppm]: 3.47 (Q 99)

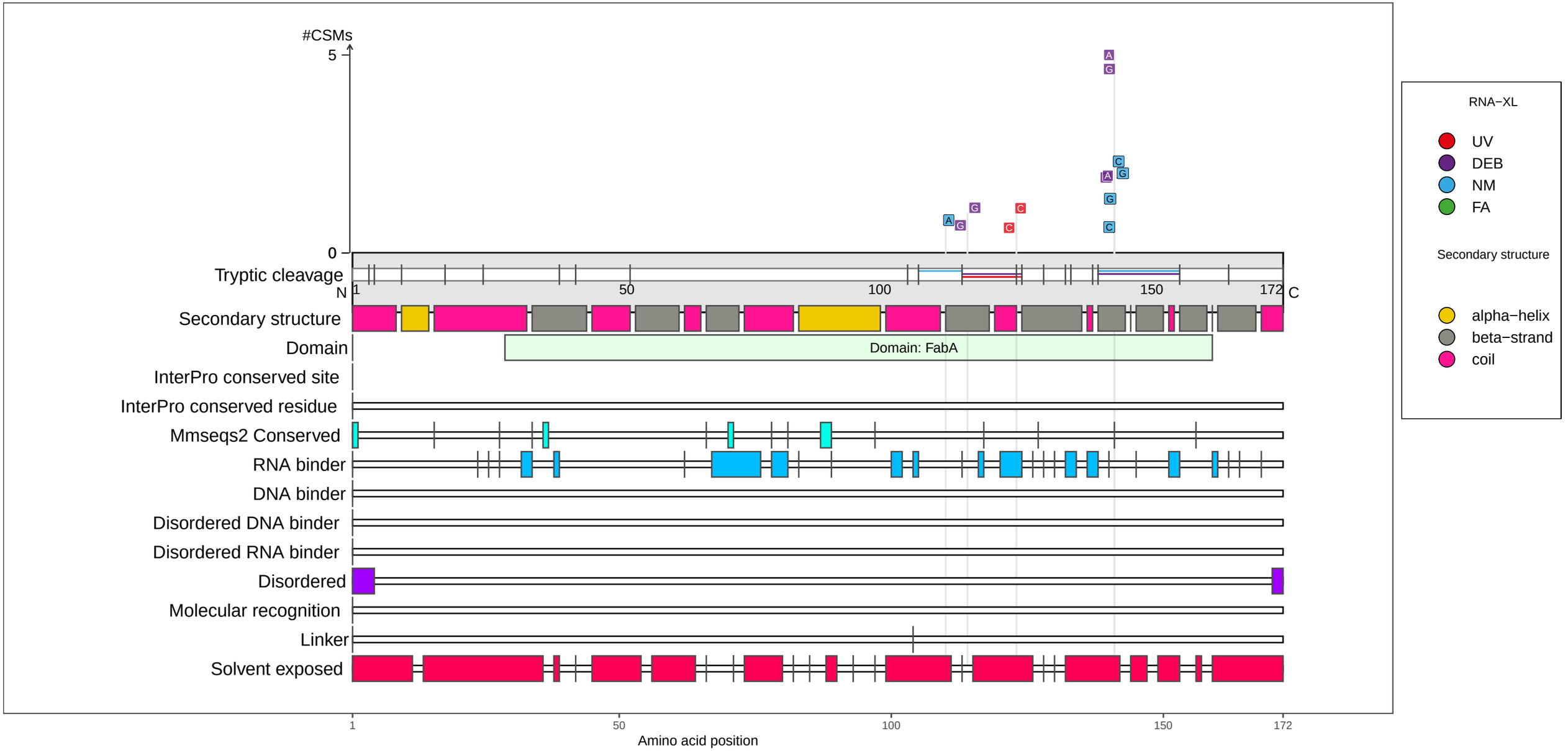
− RNA functions: not annotated



P0A6Q3
FABA_ECOLI 3−hydroxydecanoyl−[acyl−carrier−protein] dehydratase

− Abundance:
tryptic [log10 Intensity]: 9.63 (Q 97)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 3.31 (Q 98)

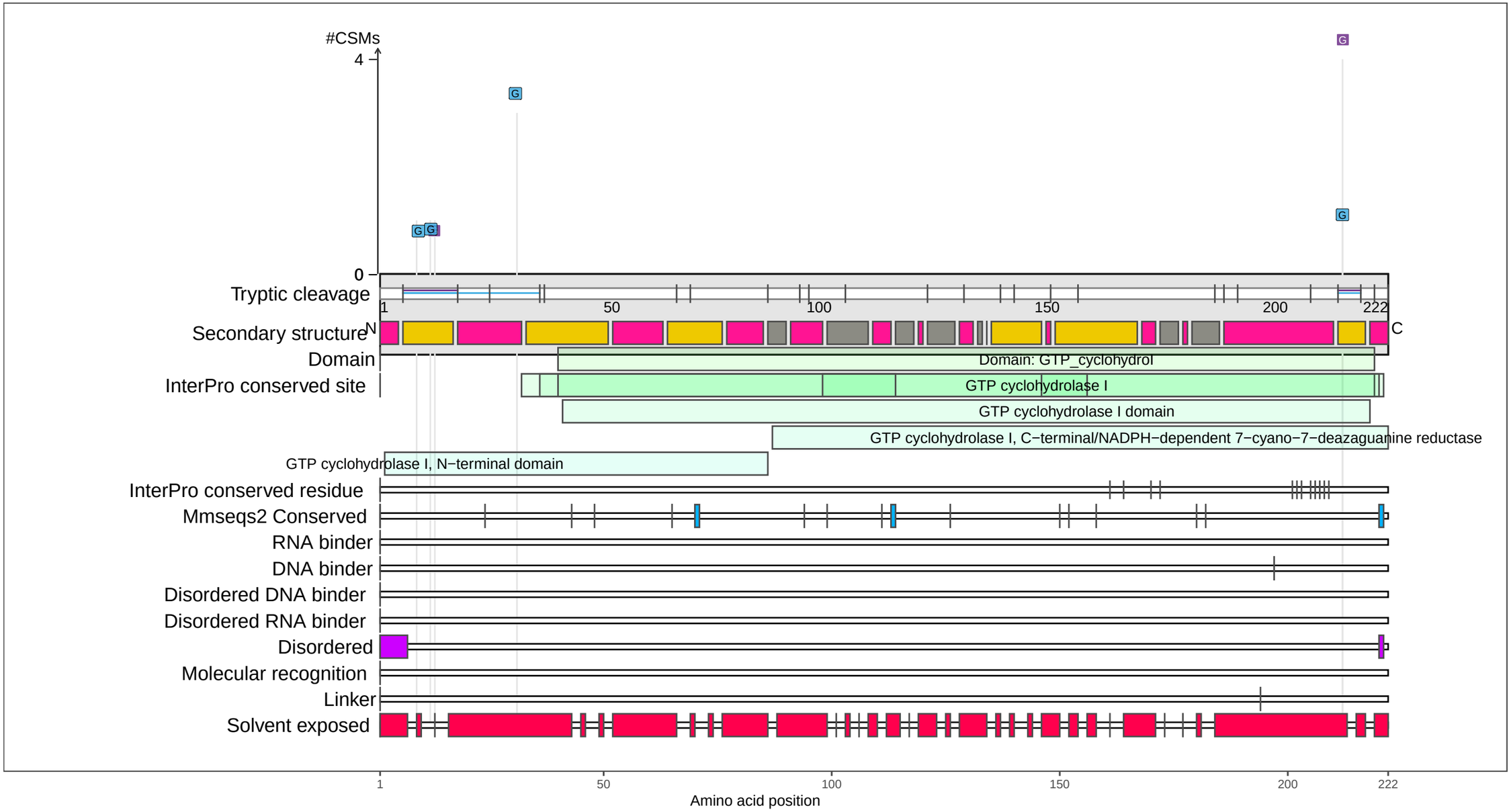
− RNA functions: not annotated



P0A6T5
GCH1_ECOLI GTP cyclohydrolase 1

− Abundance:
tryptic [log10 Intensity]: 9.2 (Q 93)
PAXdb K12 strain [ppm]: 1.34 (Q 29)
PAXdb E.coli [ppm]: 2.84 (Q 92)

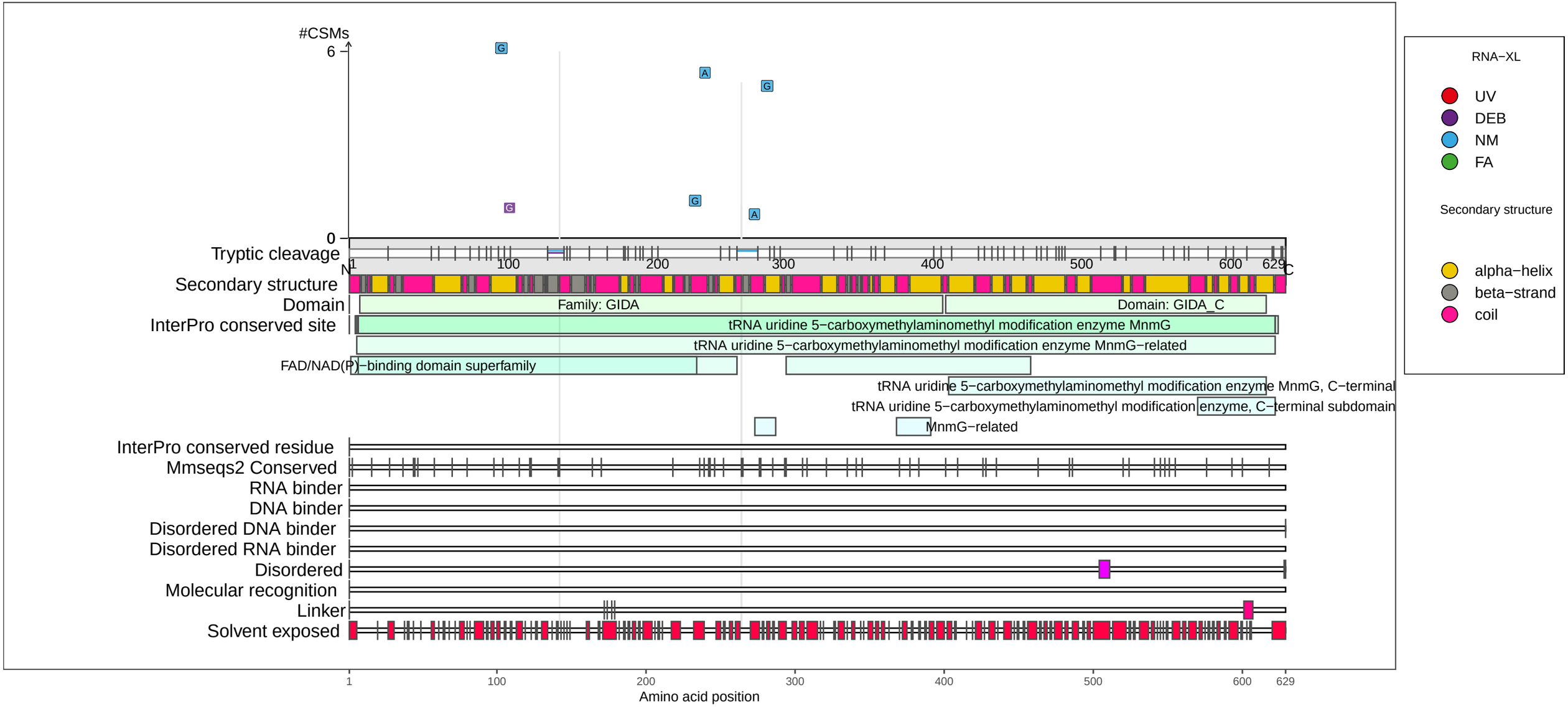
− RNA functions: not annotated



P0A6U3
MNMG_ECOLI tRNA uridine 5−carboxymethylaminomethyl modification enzyme MnmG

− Abundance:
tryptic [log10 Intensity]: 8.12 (Q 62)
PAXdb K12 strain [ppm]: 1.85 (Q 55)
PAXdb E.coli [ppm]: 1.42 (Q 57)

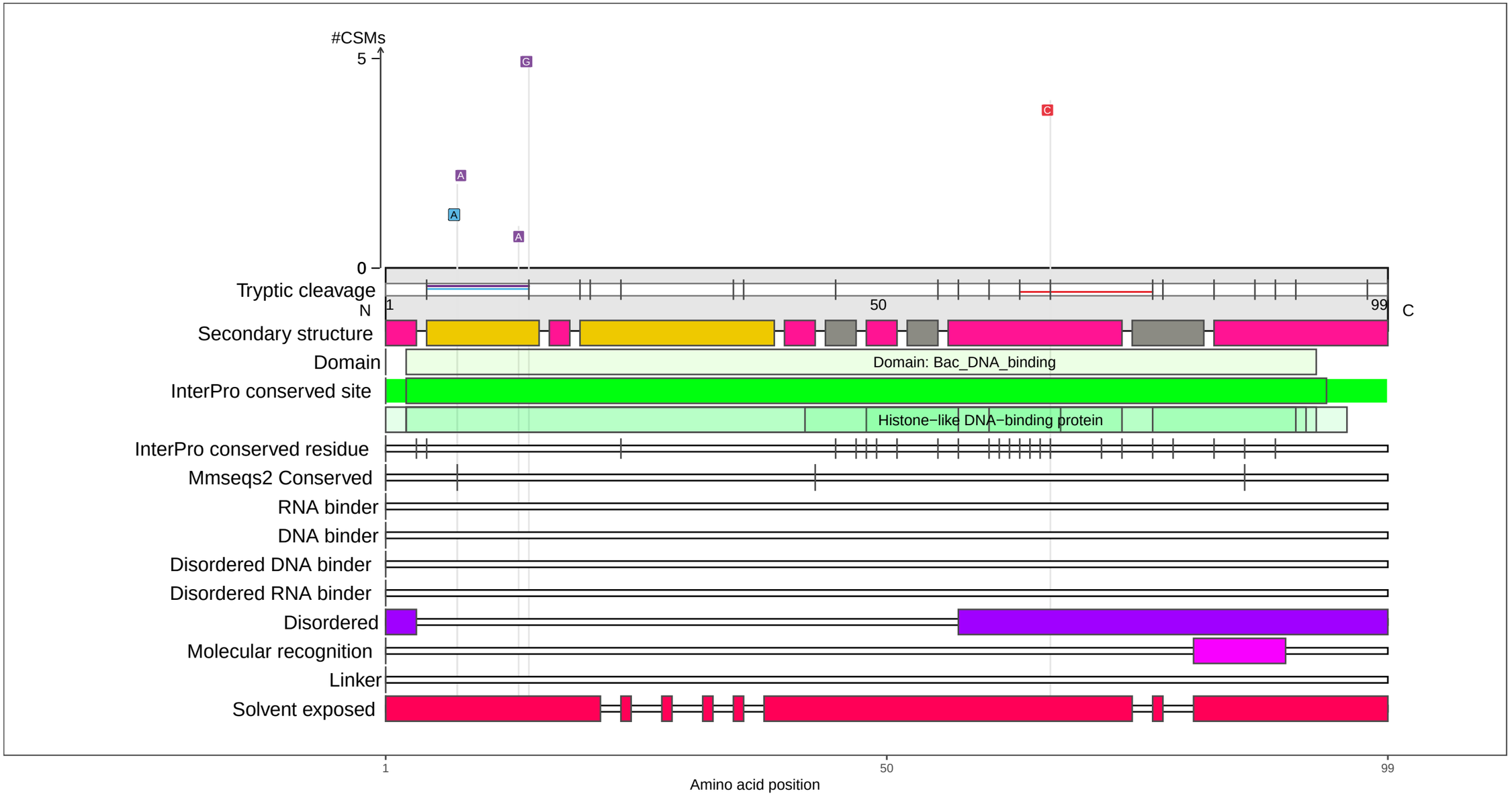
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA methylation
RNA modification; RNA processing; tRNA metabolic process; tRNA methylation; tRNA modification
tRNA processing; tRNA wobble base modification; tRNA wobble uridine modification



P0A6X7
IHFA_ECOLI Integration host factor subunit alpha

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 3.43 (Q 98)

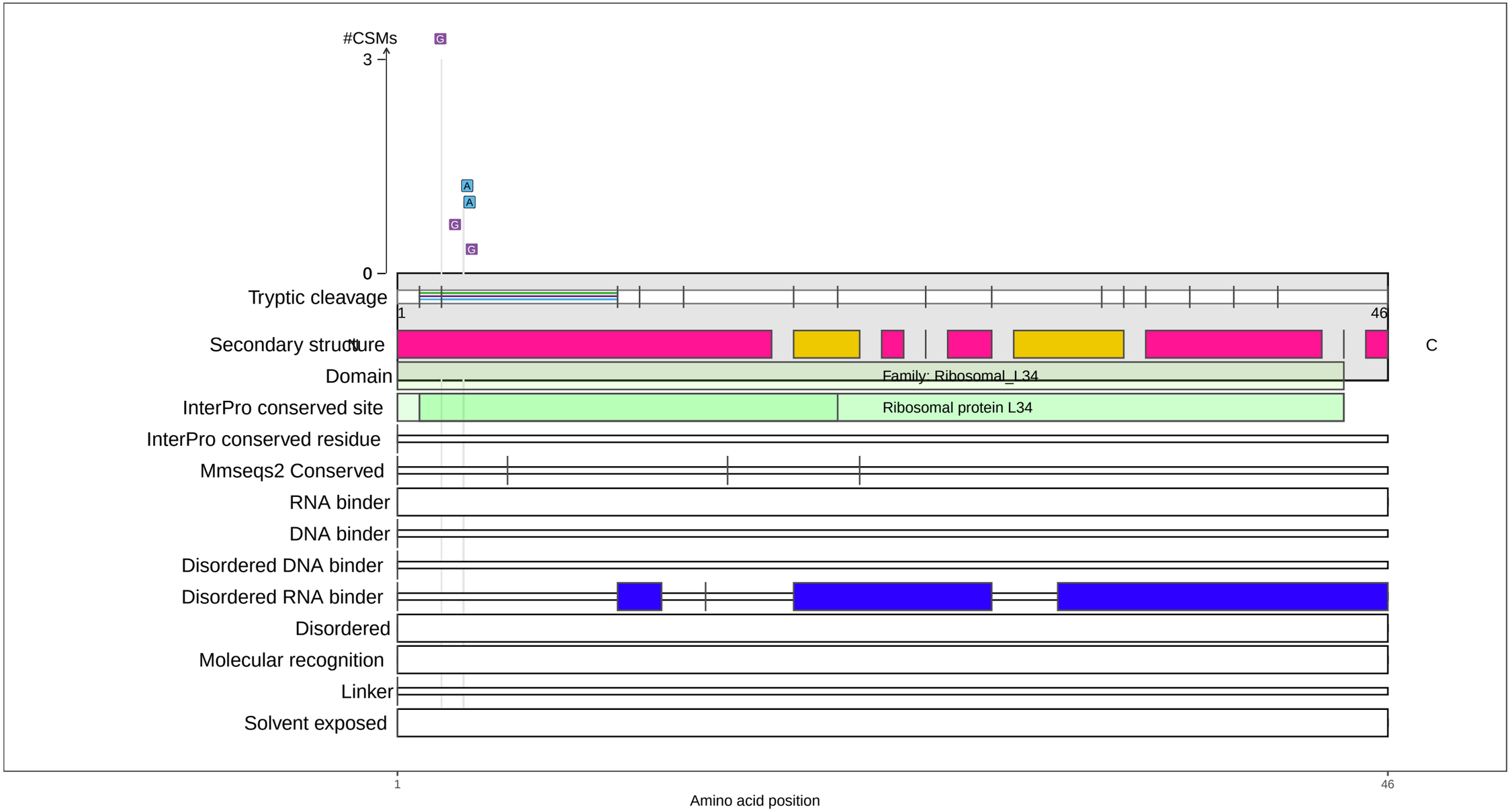
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0A7P5
RL34_ECOLI 50S ribosomal protein L34

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 3.48 (Q 97)
PAXdb E.coli [ppm]: 3.19 (Q 96)

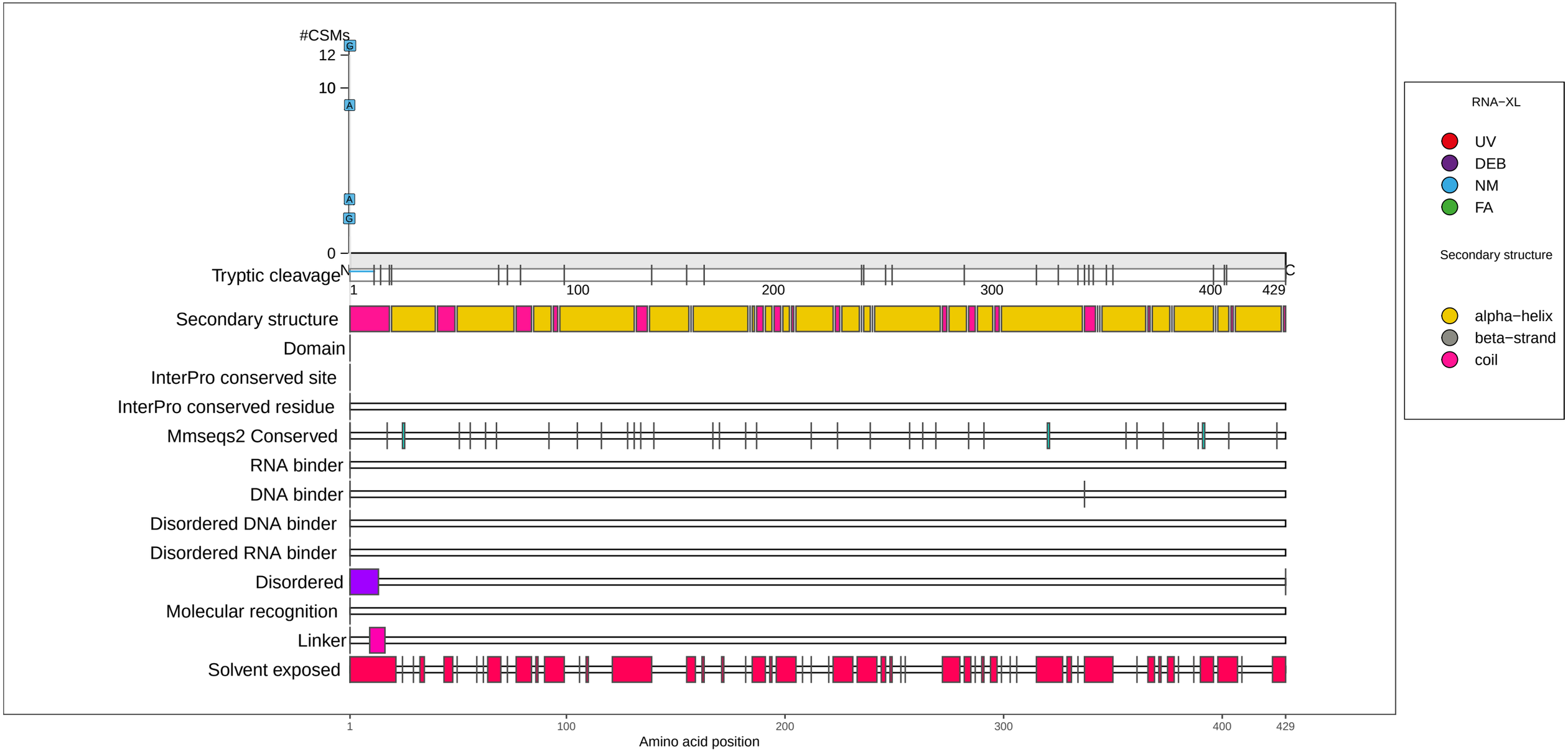
− RNA functions: not annotated



P0AAD6
SDAC_ECOLI Serine transporter SdaC

− Abundance:
tryptic [log10 Intensity]: 6.75 (Q 6)
PAXdb K12 strain [ppm]: 2.14 (Q 65)
PAXdb E.coli [ppm]: 1.99 (Q 72)

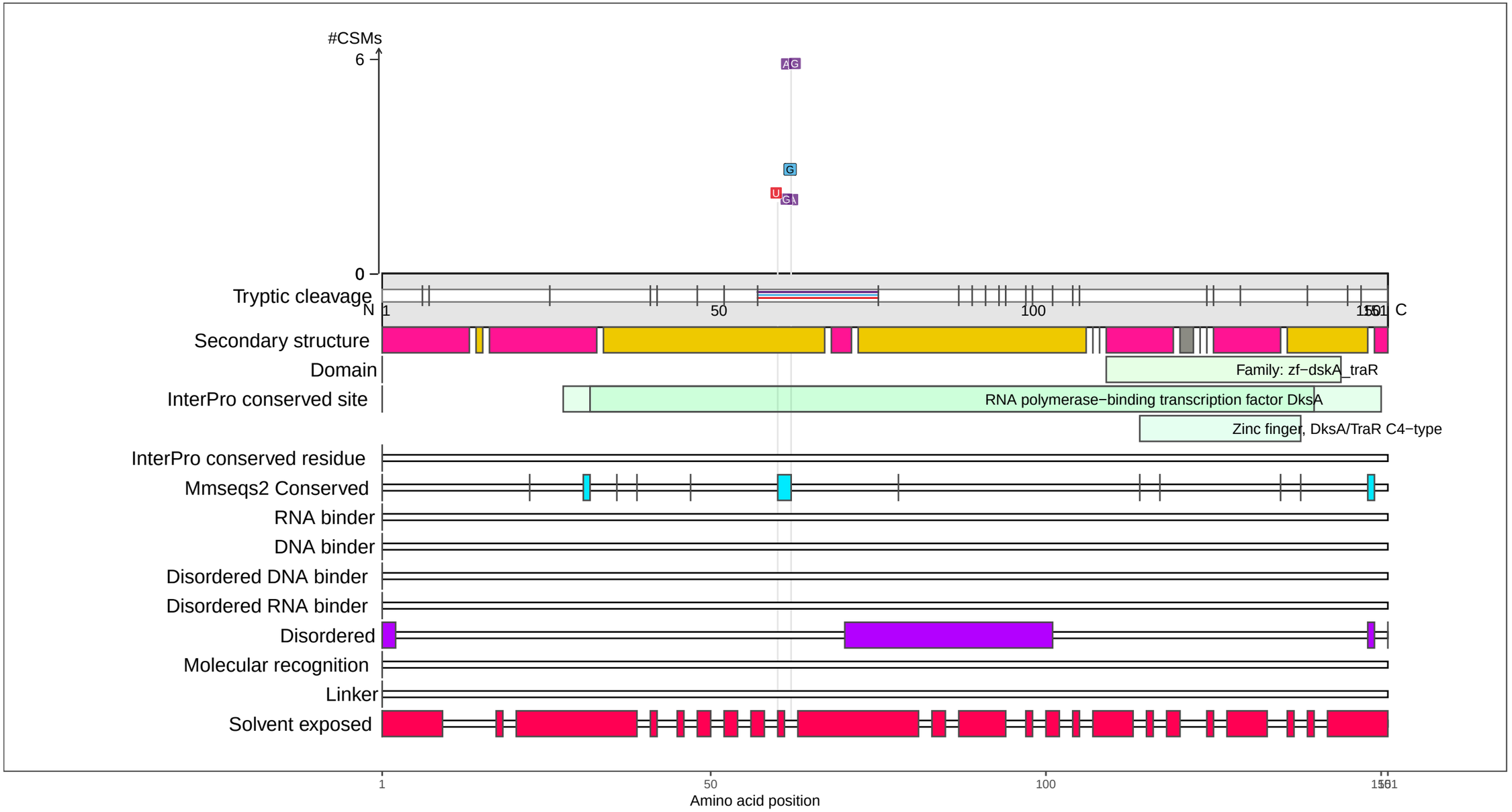
− RNA functions: not annotated

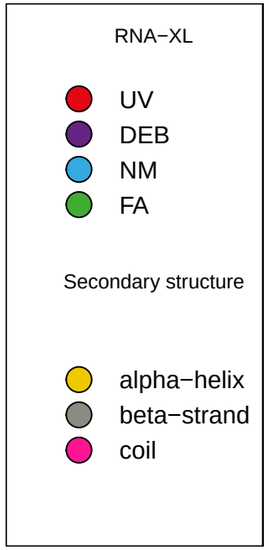


P0ABS1
DKSA_ECOLI RNA polymerase−binding transcription factor DksA

− Abundance:
tryptic [log10 Intensity]: 9.18 (Q 92)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.75 (Q 91)

− RNA functions: not annotated

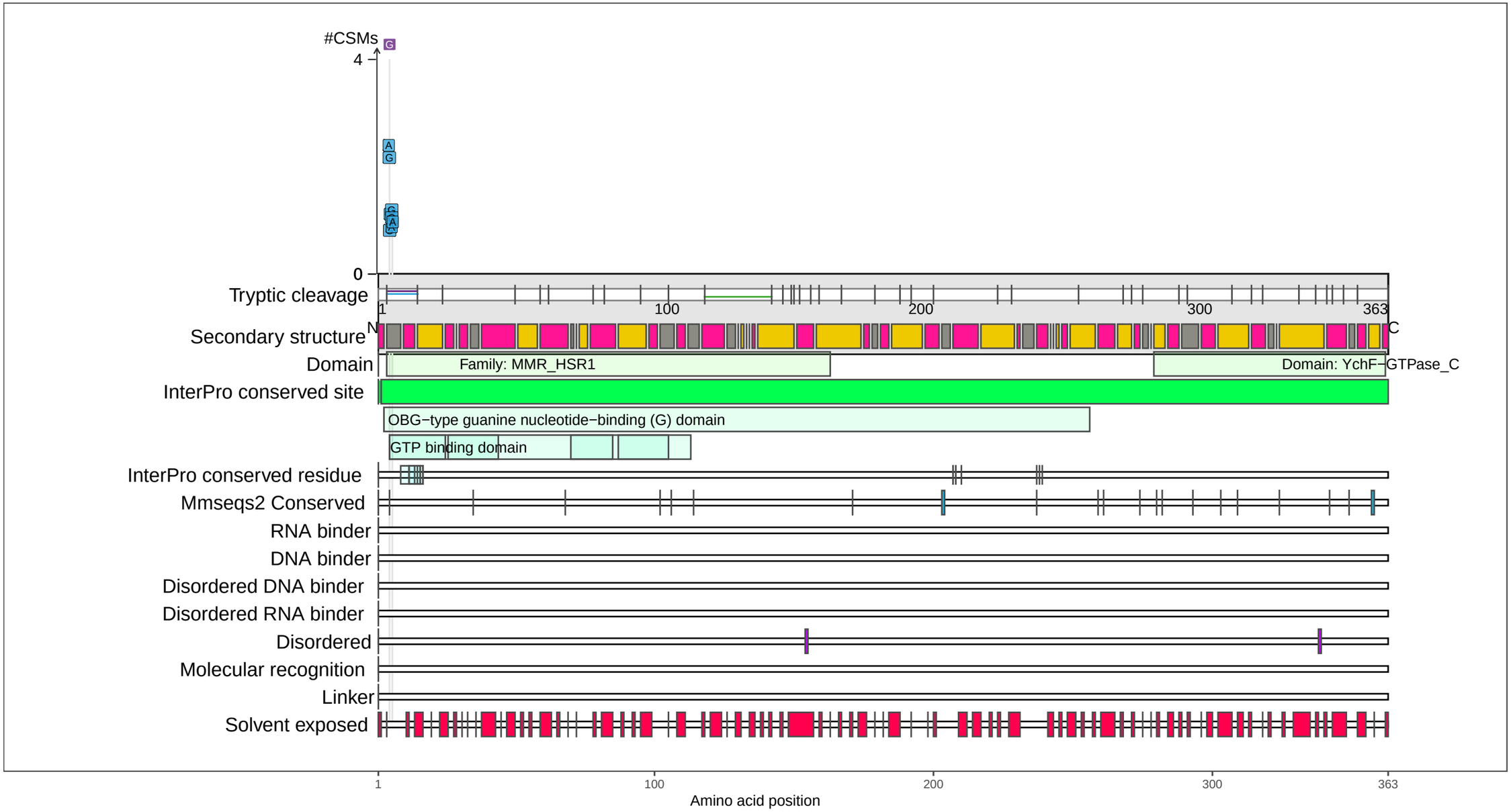




P0ABU2
YCHF_ECOLI Ribosome−binding ATPase YchF

− Abundance:
tryptic [log10 Intensity]: 8.42 (Q 73)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 2.42 (Q 83)

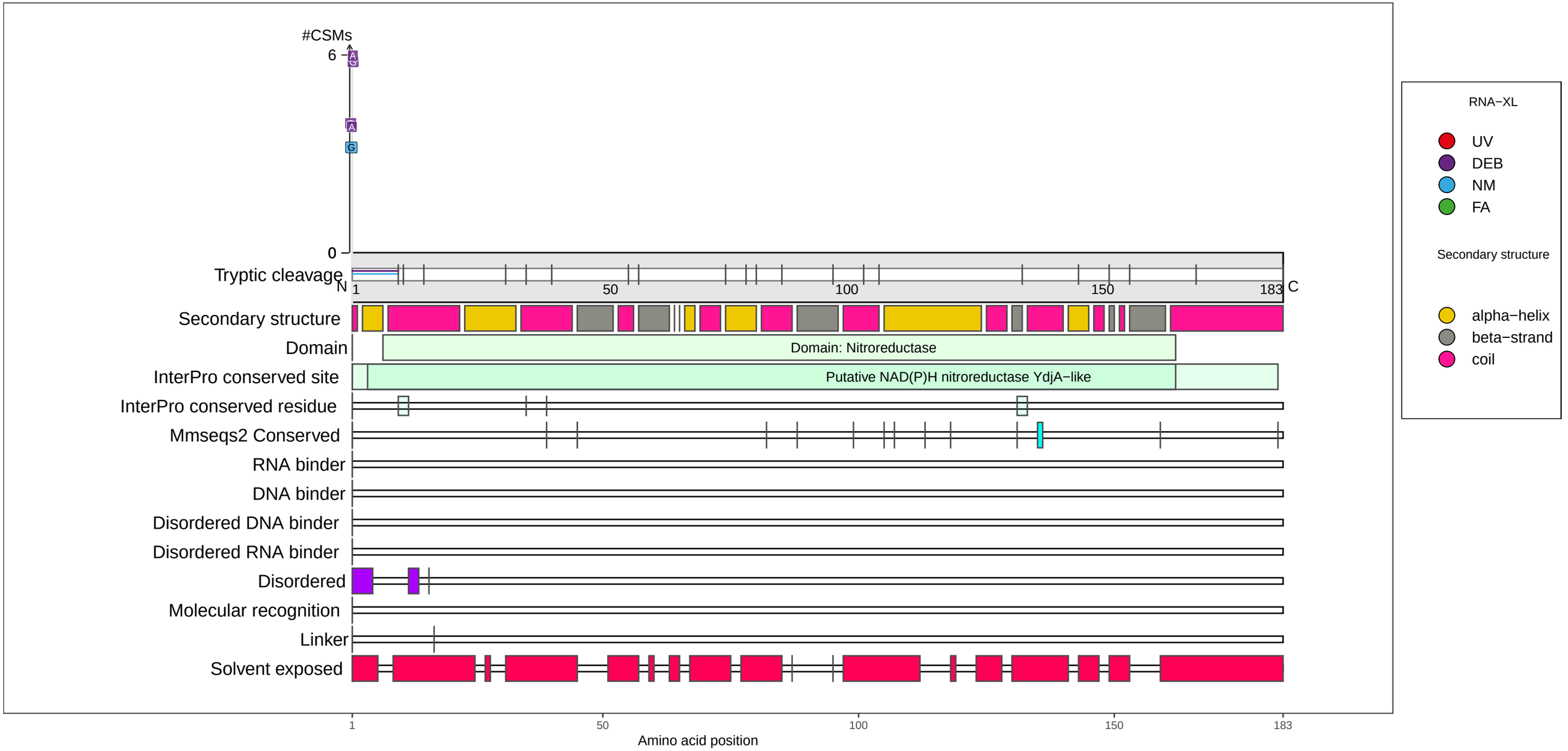
− RNA functions: not annotated



P0ACY1
YDJA_ECOLI Putative NAD(P)H nitroreductase YdjA

− Abundance:
tryptic [log10 Intensity]: 8.26 (Q 68)
PAXdb K12 strain [ppm]: 3.19 (Q 94)
PAXdb E.coli [ppm]: 2.61 (Q 88)

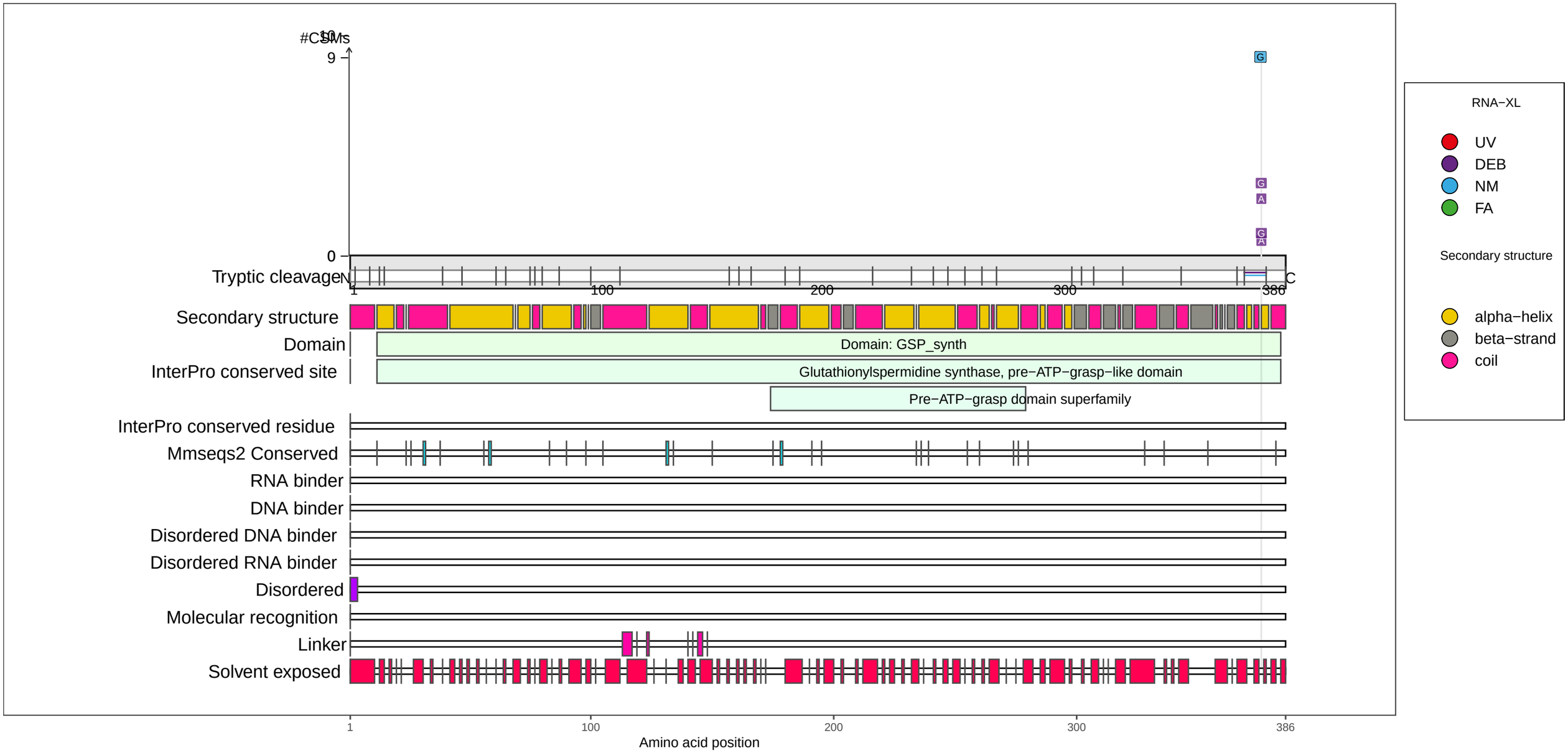
− RNA functions: not annotated



P0ADT5
YGIC_ECOLI Putative acid−−amine ligase YgiC

− Abundance:
tryptic [log10 Intensity]: 8.41 (Q 73)
PAXdb K12 strain [ppm]: 1.56 (Q 42)
PAXdb E.coli [ppm]: 1.3 (Q 55)

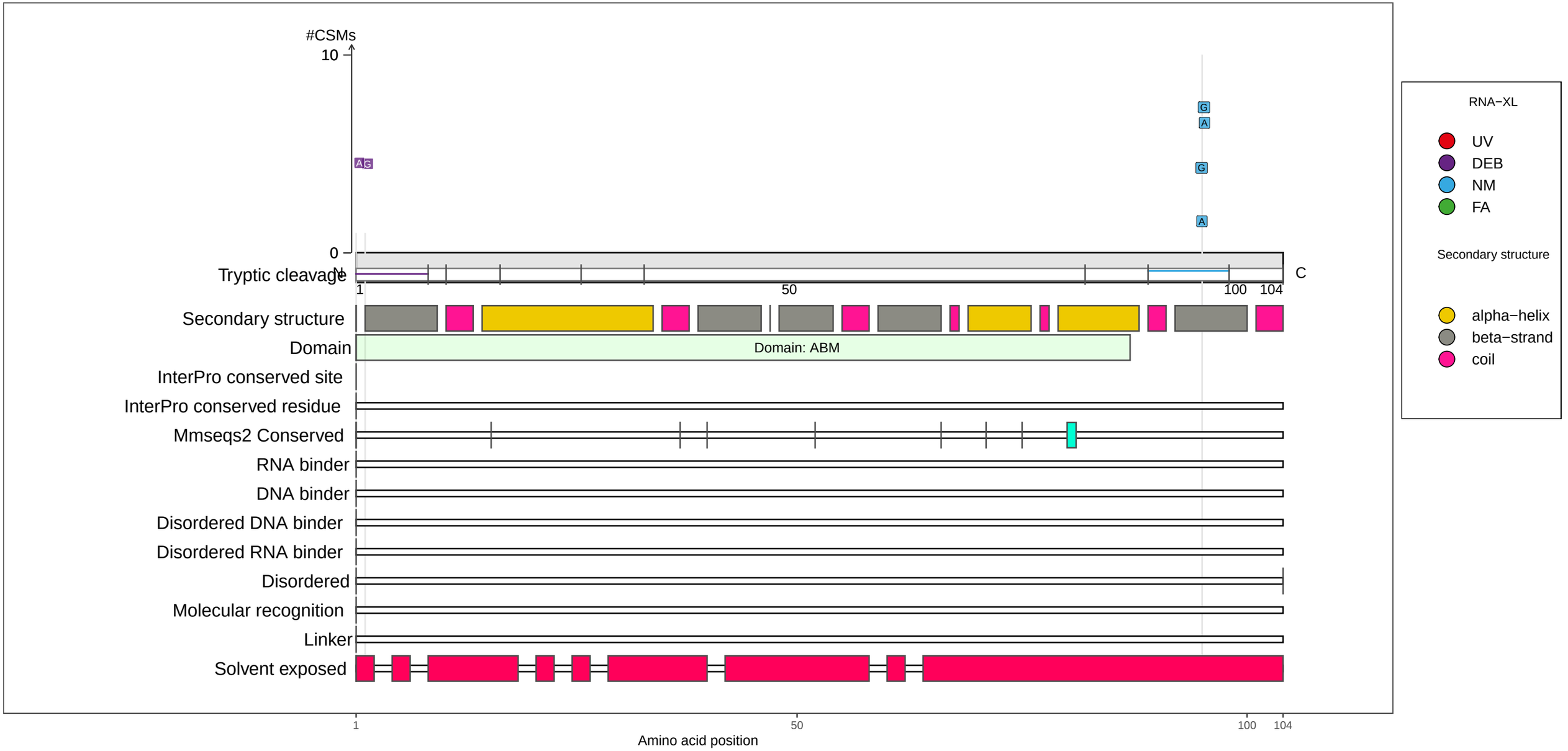
− RNA functions: not annotated



P0ADU2
YGIN_ECOLI Probable quinol monooxygenase YgiN

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 63)
PAXdb K12 strain [ppm]: 2.96 (Q 90)
PAXdb E.coli [ppm]: 2.71 (Q 90)

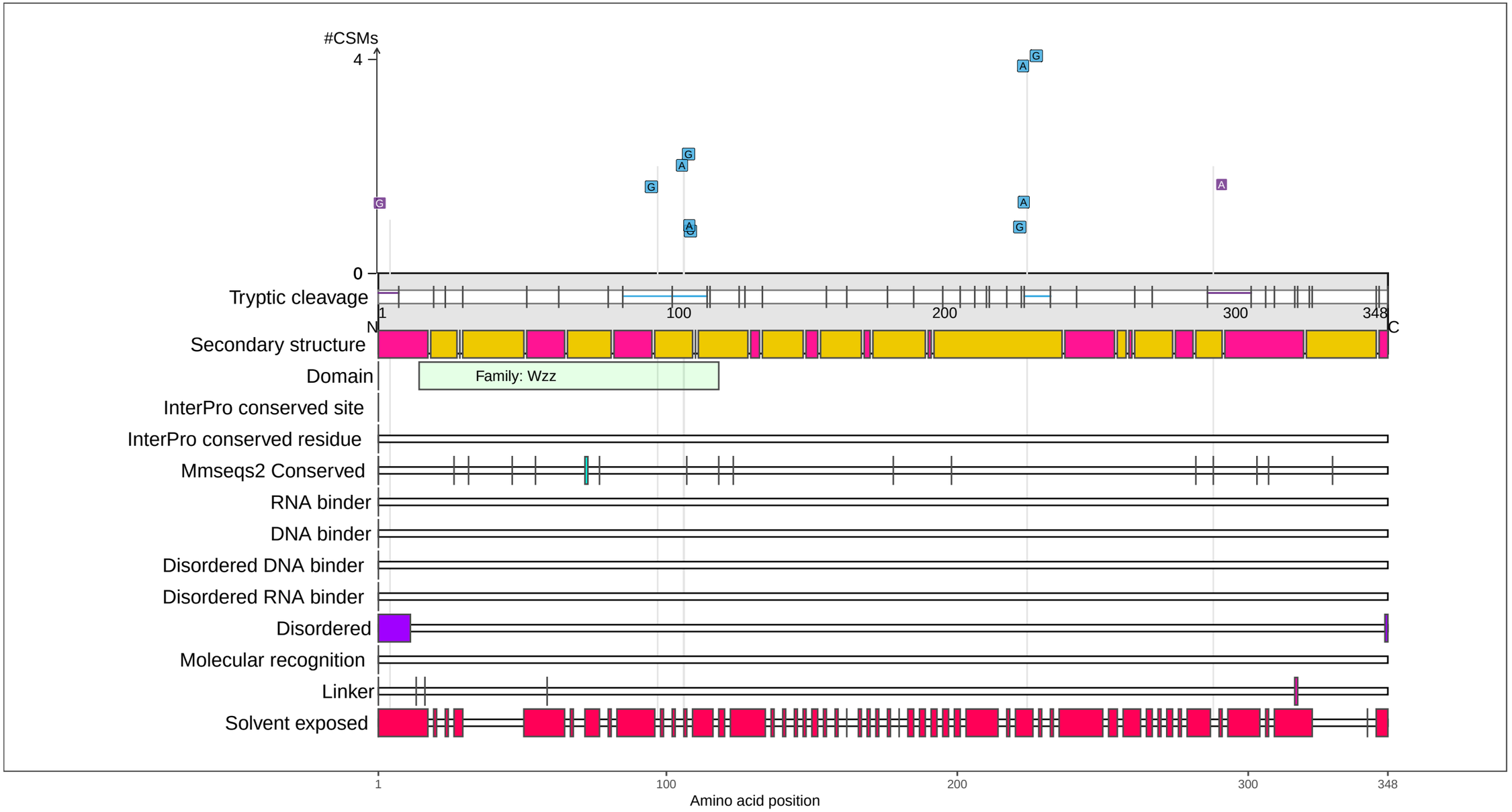
− RNA functions: not annotated



P0AG00
WZZE_ECOLI ECA polysaccharide chain length modulation protein

− Abundance:
tryptic [log10 Intensity]: 8.31 (Q 70)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.67 (Q 64)

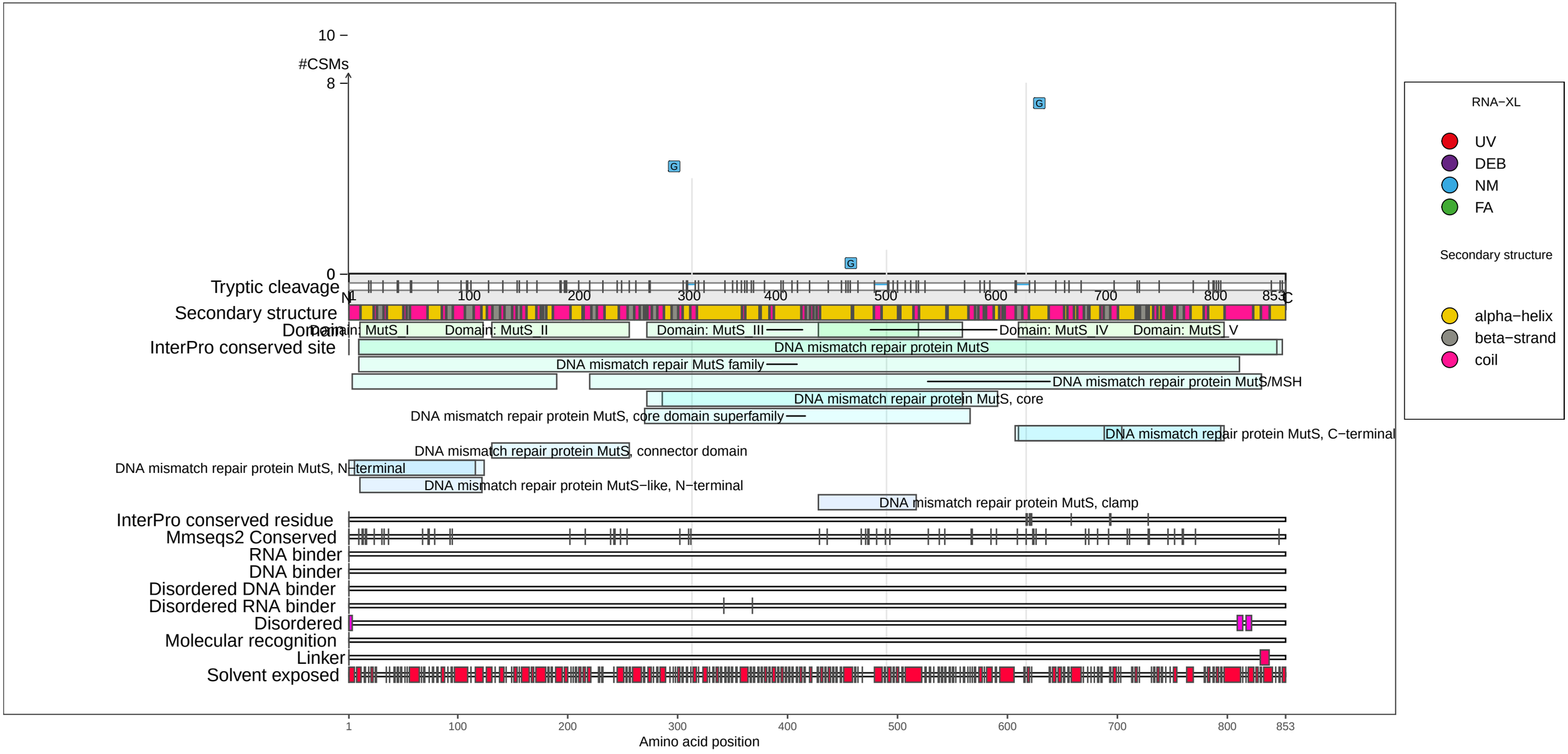
− RNA functions: not annotated



P23909
MUTS_ECOLI DNA mismatch repair protein MutS

− Abundance:
tryptic [log10 Intensity]: 6.63 (Q 4)
PAXdb K12 strain [ppm]: 1.57 (Q 43)
PAXdb E.coli [ppm]: 0.99 (Q 47)

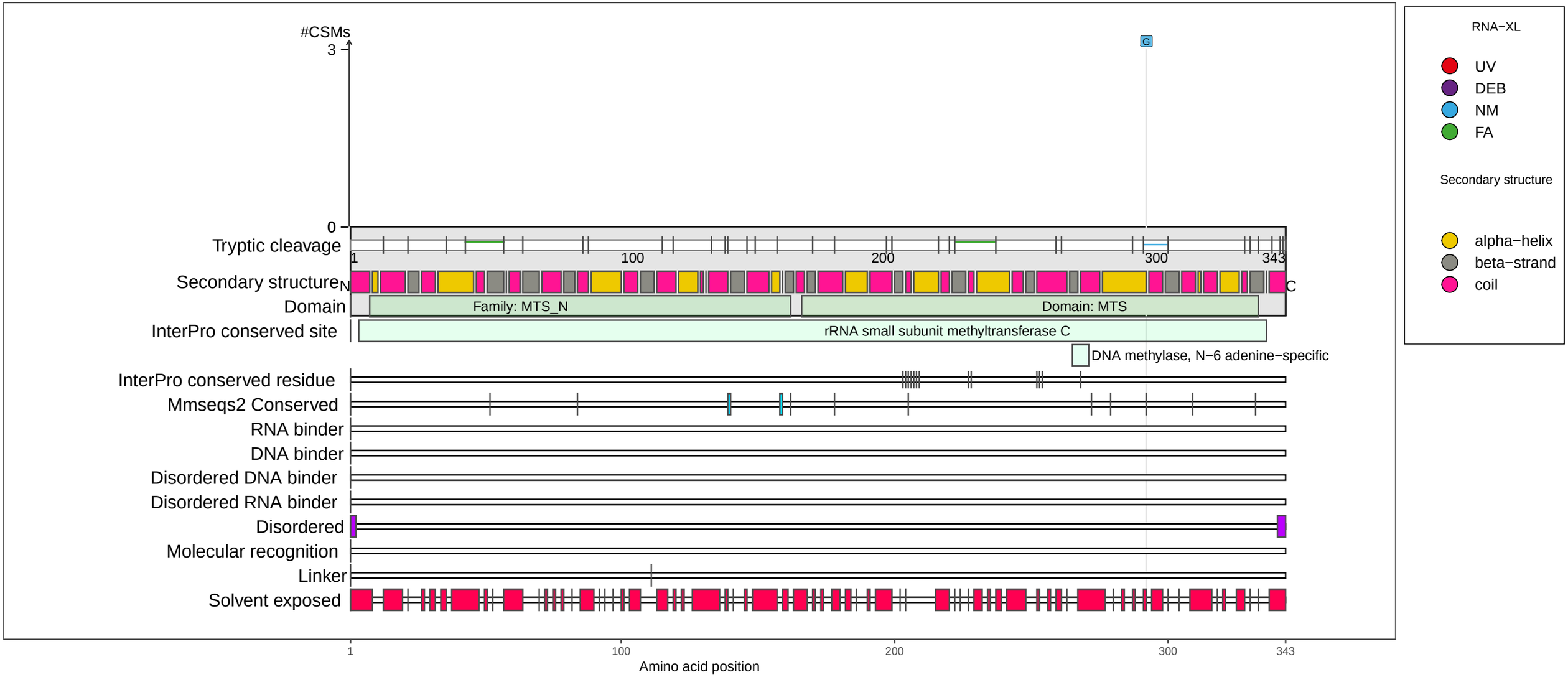
− RNA functions: not annotated



P39406
RSMC_ECOLI Ribosomal RNA small subunit methyltransferase C

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 1.71 (Q 64)

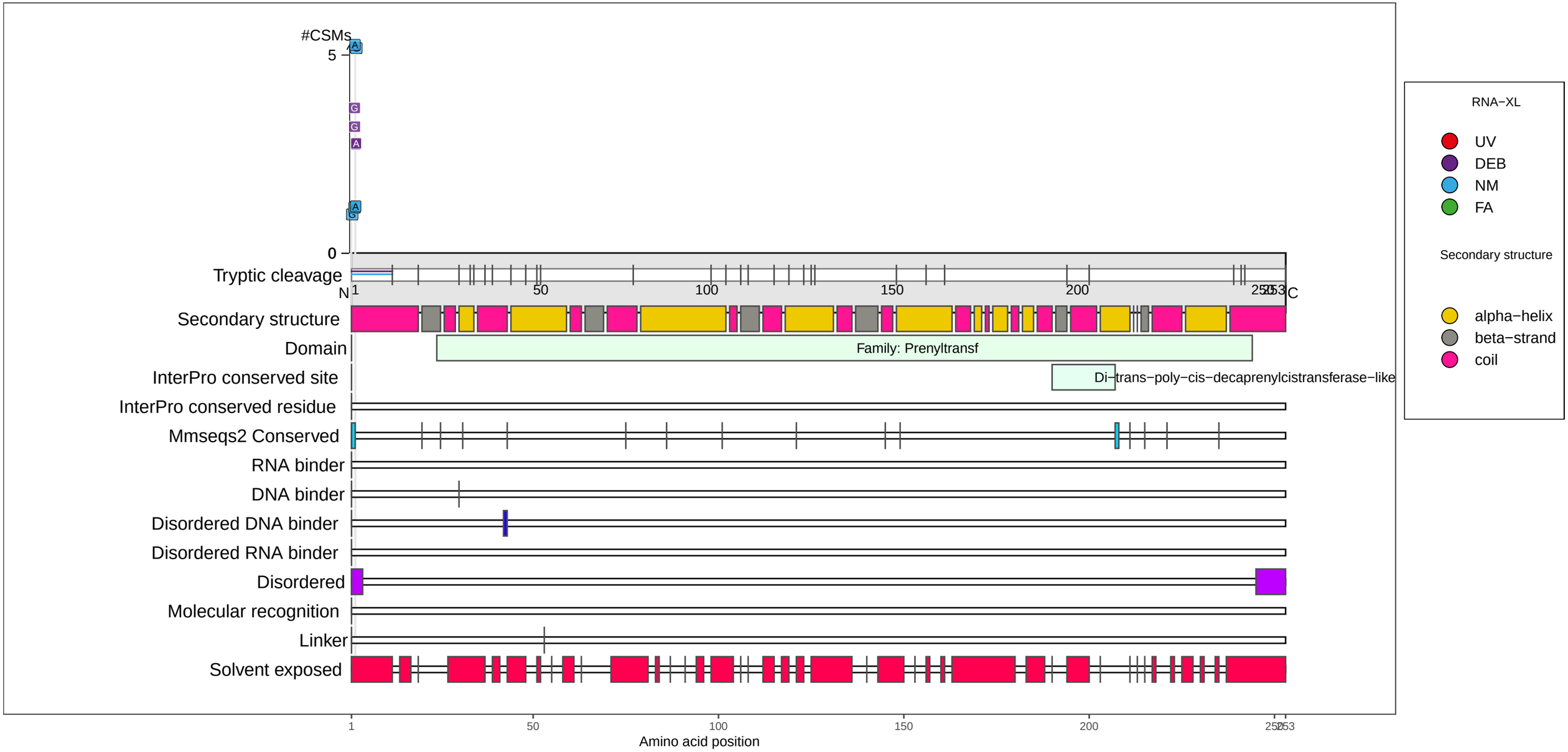
− RNA functions:
16S rRNA (guanine(1207)−N(2))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; RNA metabolic process; RNA methylation
RNA methyltransferase activity; RNA modification; RNA processing; rRNA (guanine−N2−)−methyltransferase activity
rRNA (guanine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P60472
UPPS_ECOLI Ditrans,polycis−undecaprenyl−diphosphate synthase ((2E,6E)−farnesyl−diphosphate specific)

− Abundance:
tryptic [log10 Intensity]: 6.74 (Q 6)
PAXdb K12 strain [ppm]: 1.87 (Q 56)
PAXdb E.coli [ppm]: 1.78 (Q 66)

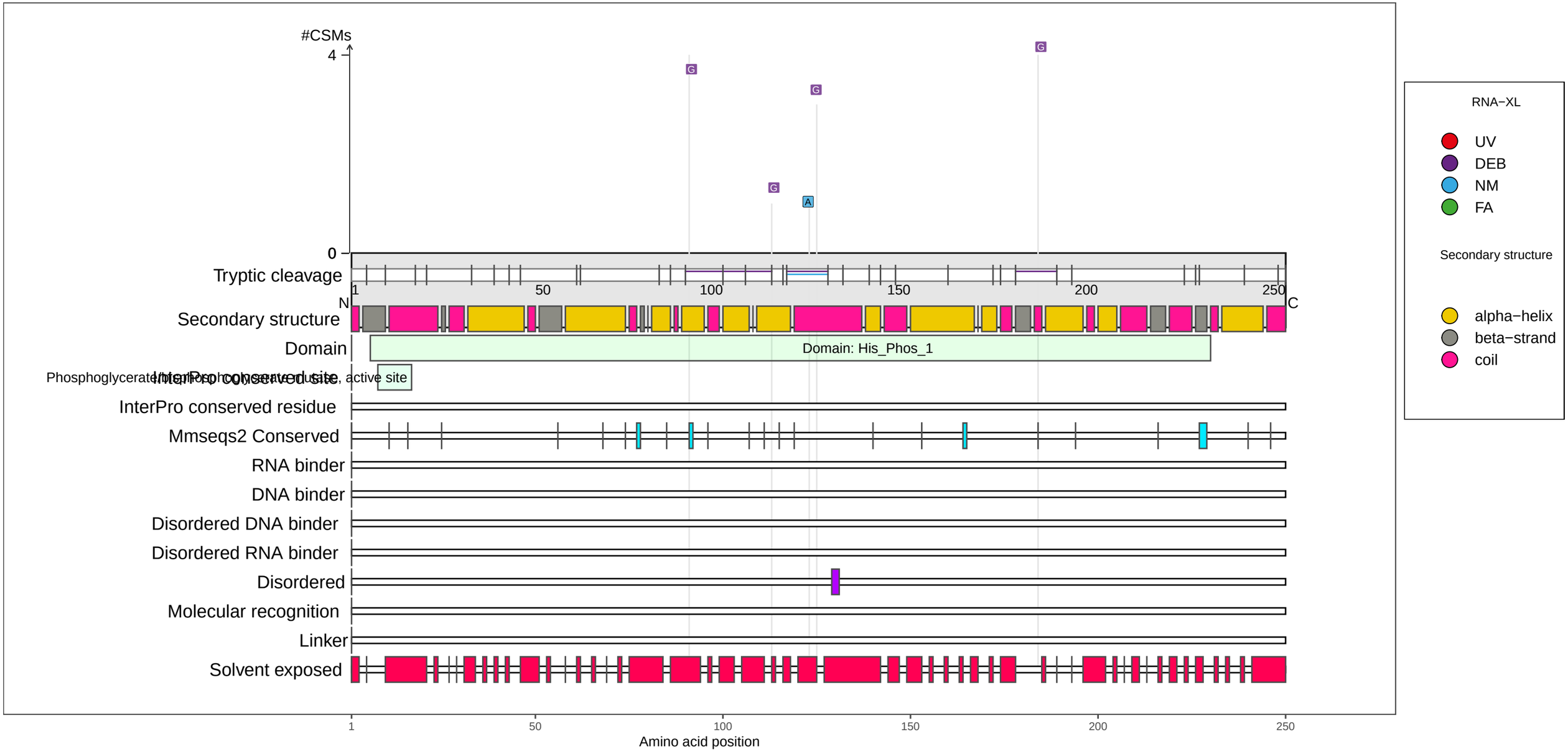
− RNA functions: not annotated



P62707
GPMA_ECOLI 2,3−bisphosphoglycerate−dependent phosphoglycerate mutase

− Abundance:
tryptic [log10 Intensity]: 9.1 (Q 91)
PAXdb K12 strain [ppm]: 3.61 (Q 98)
PAXdb E.coli [ppm]: 3.65 (Q 100)

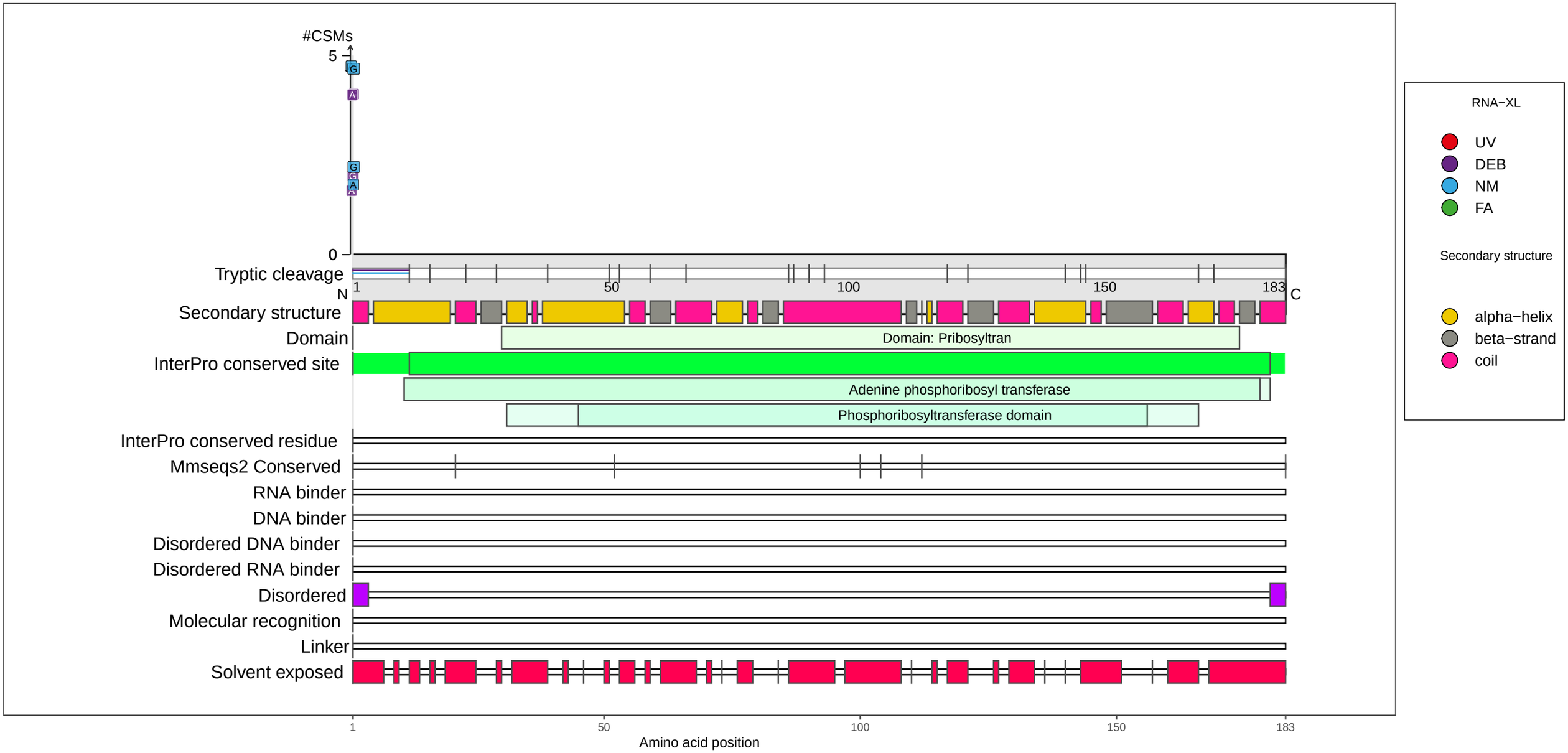
− RNA functions: not annotated



P69503
APT_ECOLI Adenine phosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 2.44 (Q 75)
PAXdb E.coli [ppm]: 2.42 (Q 84)

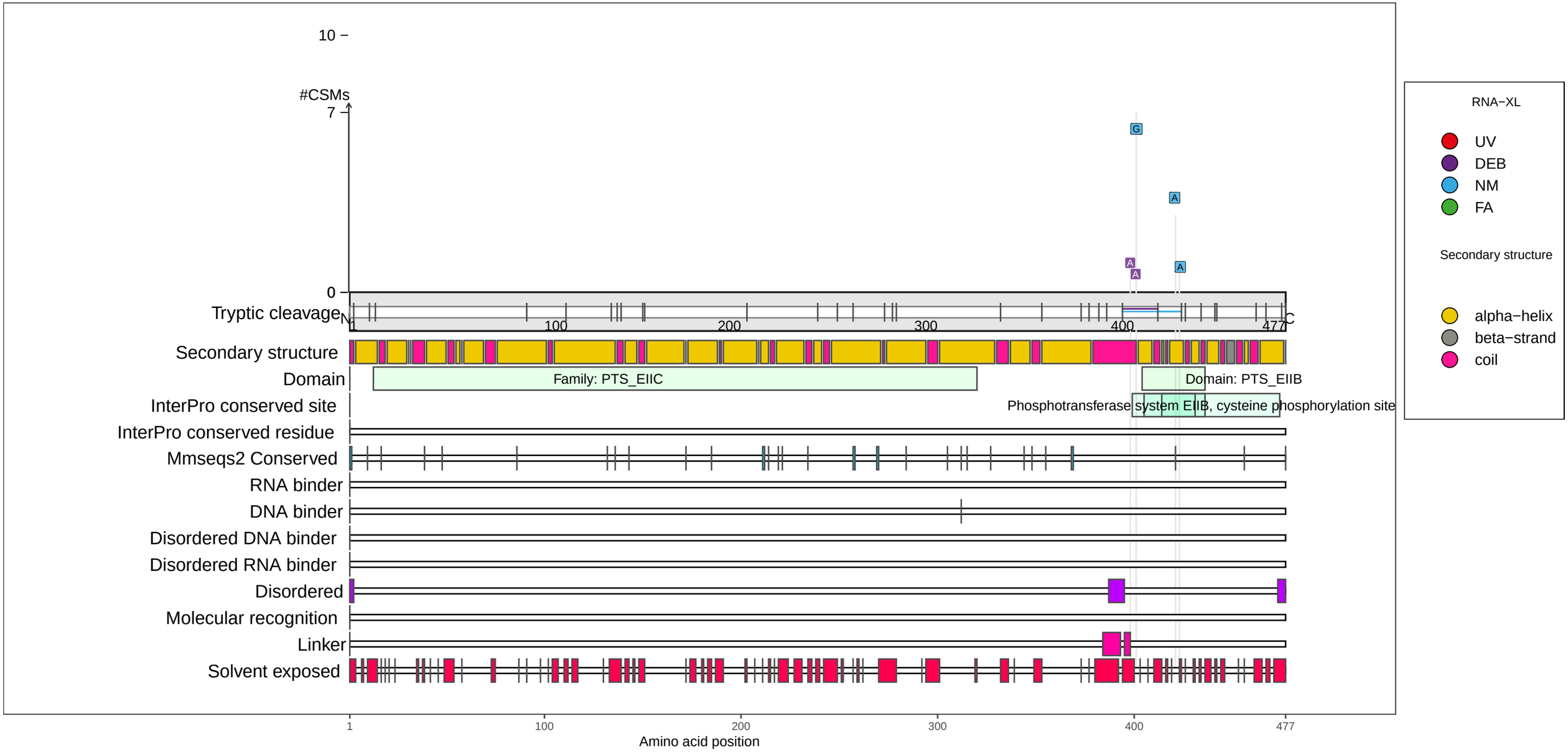
− RNA functions: not annotated



P69786
PTGCB_ECOLI PTS system glucose−specific EIICB component

− Abundance:
tryptic [log10 Intensity]: 9.43 (Q 96)
PAXdb K12 strain [ppm]: 2.05 (Q 62)
PAXdb E.coli [ppm]: 2.54 (Q 86)

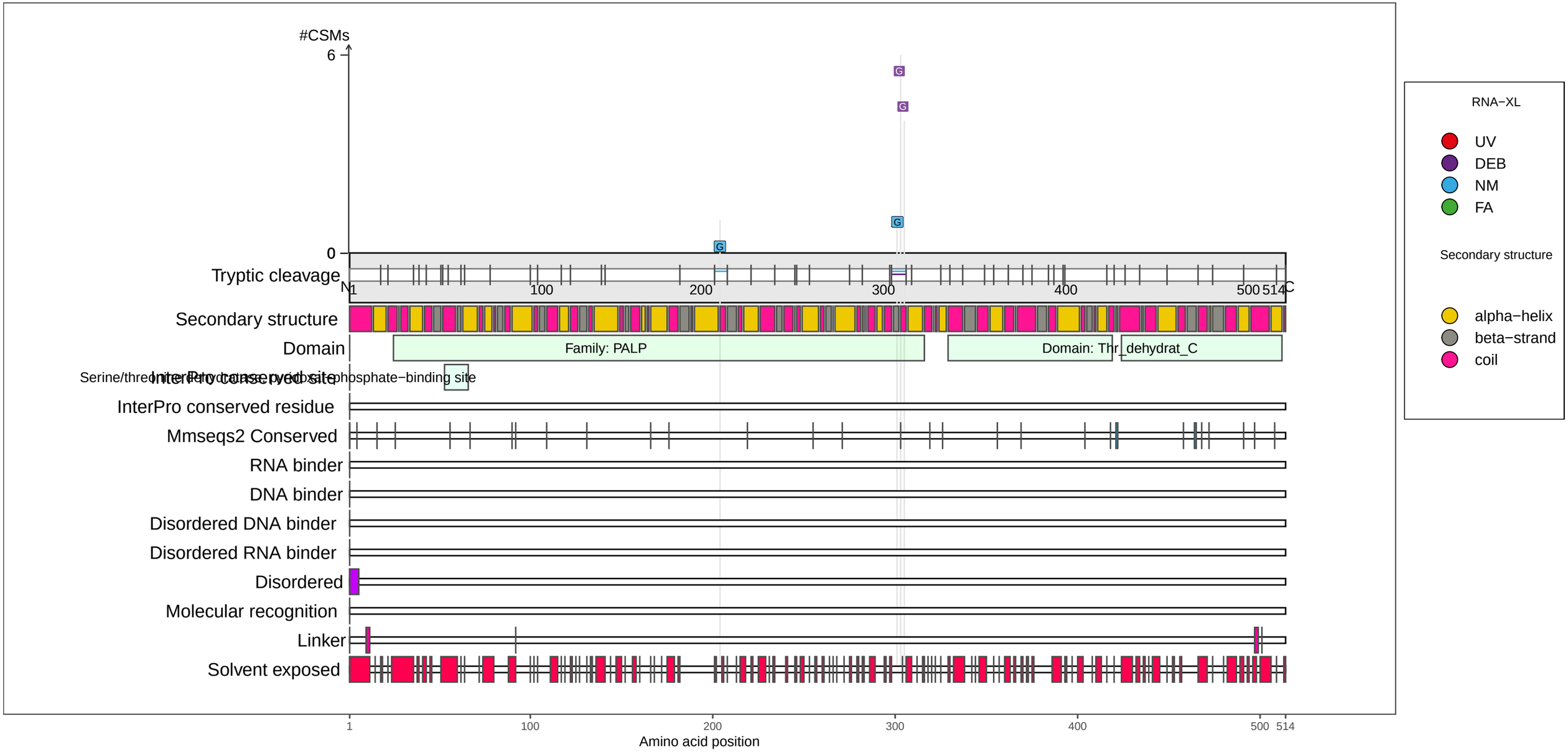
− RNA functions: not annotated



P04968
ILVA_ECOLI L−threonine dehydratase biosynthetic IlvA

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 1.5 (Q 38)
PAXdb E.coli [ppm]: 1.55 (Q 61)

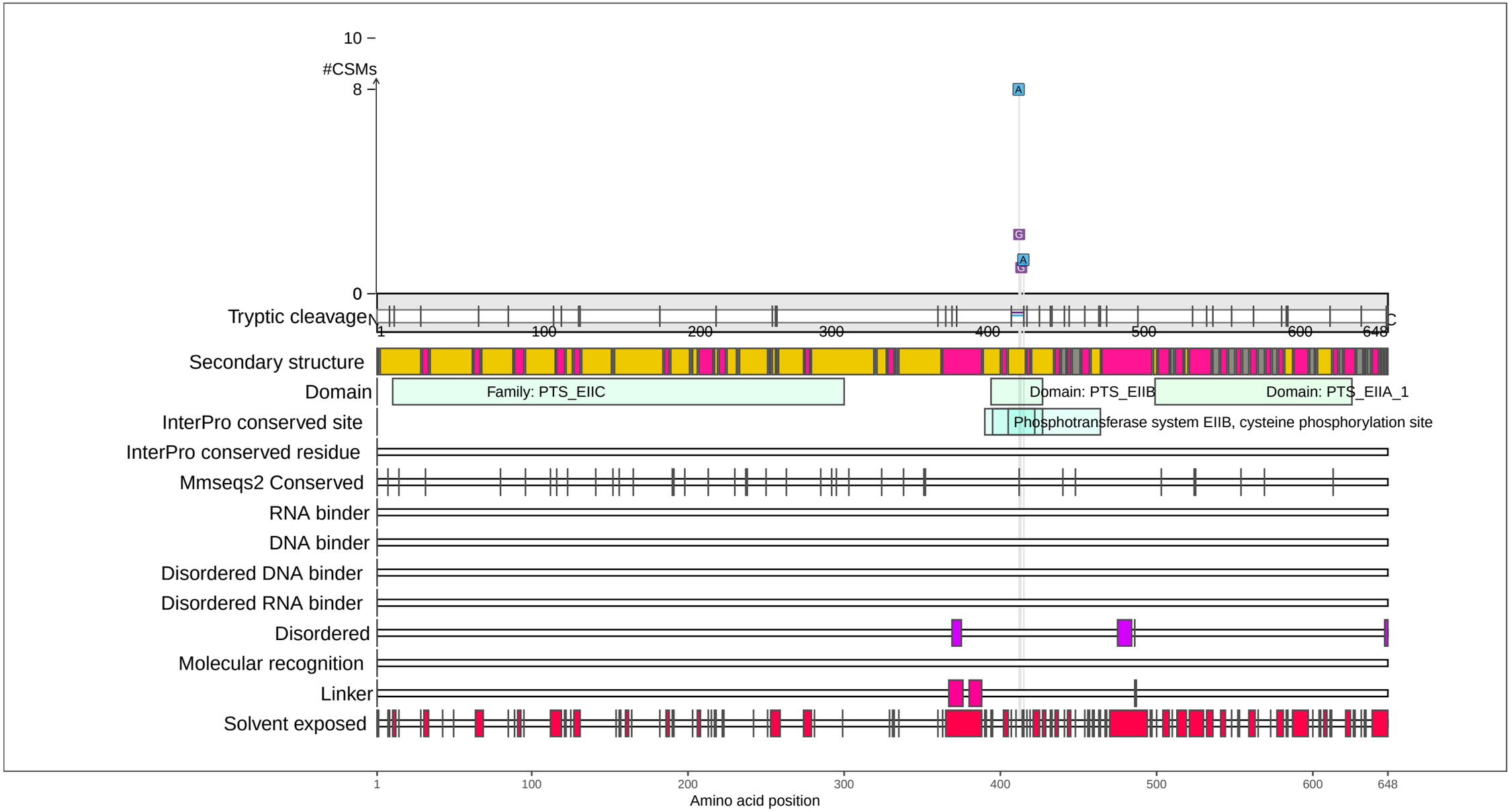
− RNA functions: not annotated



P09323
PTW3C_ECOLI PTS system N−acetylglucosamine−specific EIICBA component

− Abundance:
tryptic [log10 Intensity]: 8.72 (Q 81)
PAXdb K12 strain [ppm]: 1.42 (Q 34)
PAXdb E.coli [ppm]: 2.09 (Q 74)

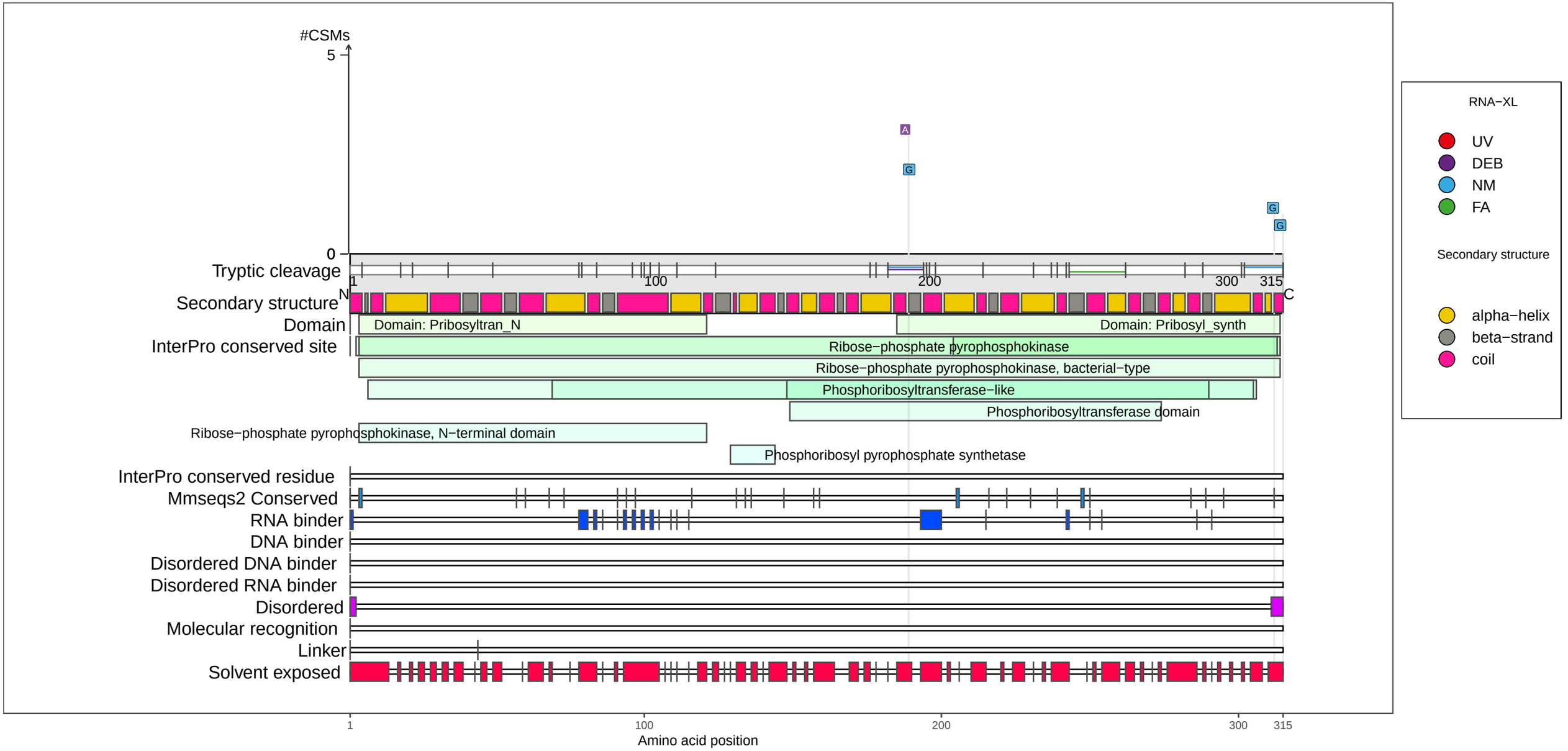
− RNA functions: not annotated



P0A717
KPRS_ECOLI Ribose−phosphate pyrophosphokinase

− Abundance:
tryptic [log10 Intensity]: 8.43 (Q 73)
PAXdb K12 strain [ppm]: 3.16 (Q 93)
PAXdb E.coli [ppm]: 3.07 (Q 96)

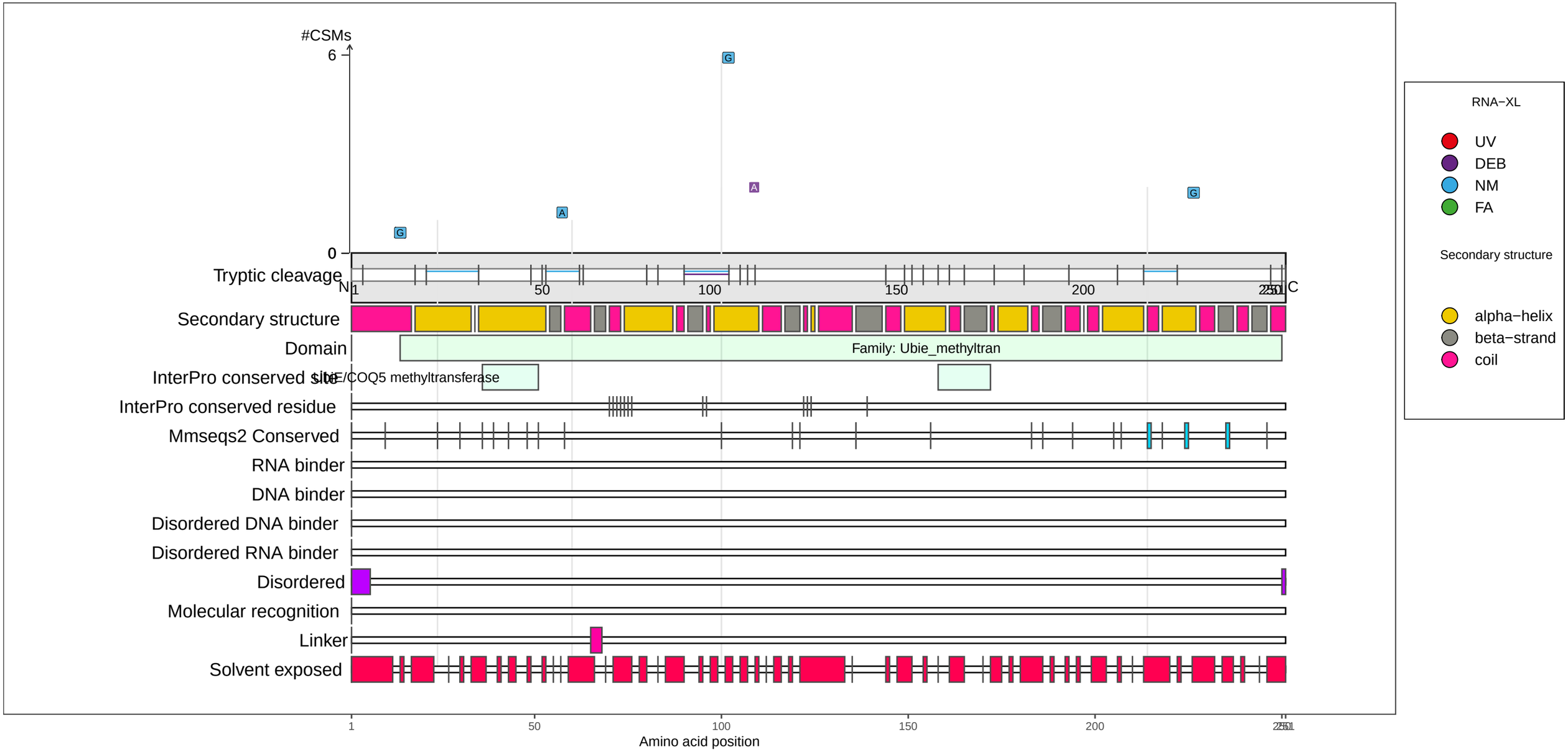
− RNA functions: not annotated



P0A887
UBIE_ECOLI Ubiquinone/menaquinone biosynthesis C−methyltransferase UbiE

− Abundance:
tryptic [log10 Intensity]: 7.21 (Q 21)
PAXdb K12 strain [ppm]: 2.72 (Q 84)
PAXdb E.coli [ppm]: 2.44 (Q 84)

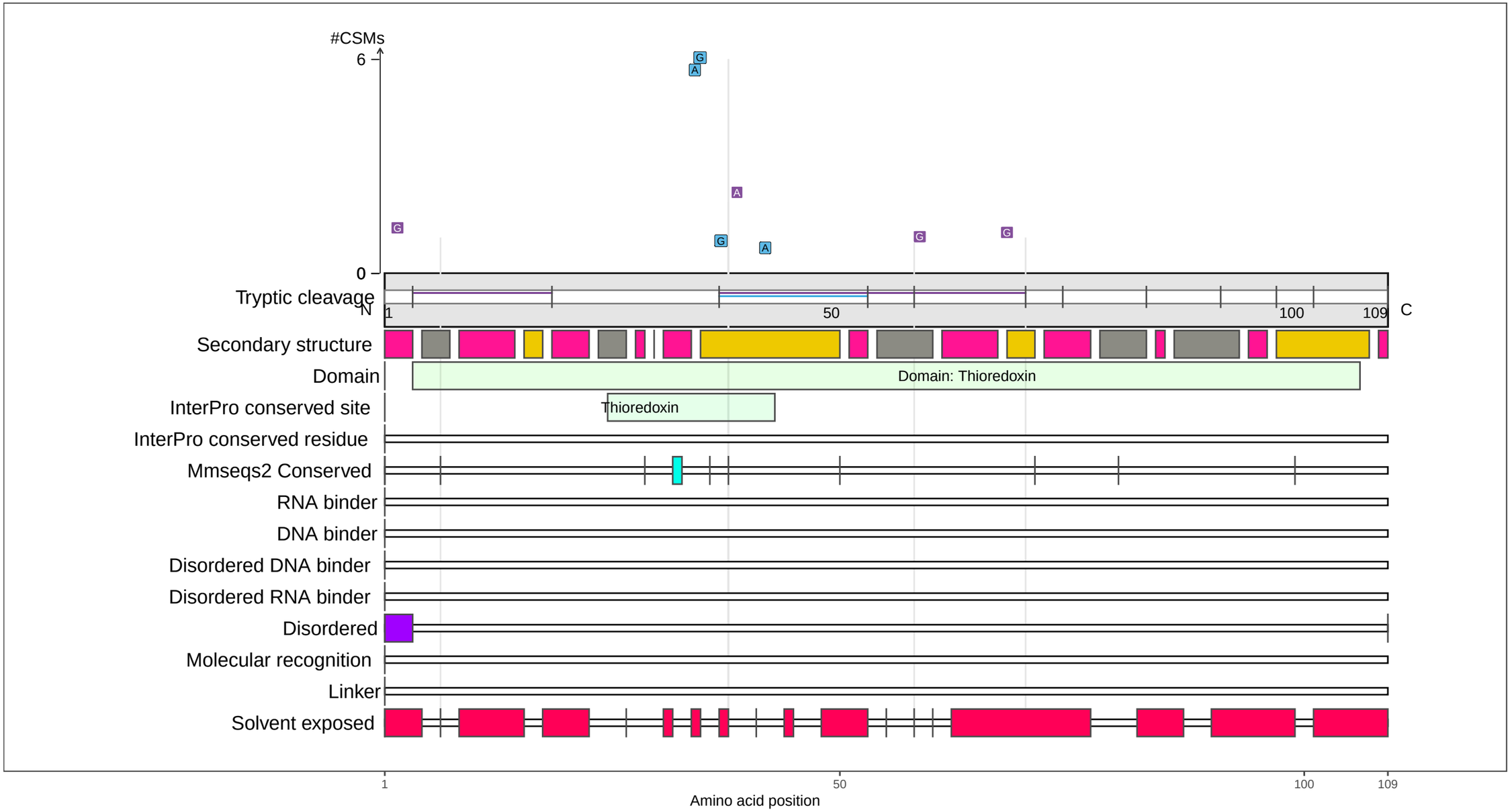
− RNA functions: not annotated



P0AA25
THIO_ECOLI Thioredoxin 1

− Abundance:
tryptic [log10 Intensity]: 9.11 (Q 91)
PAXdb K12 strain [ppm]: 3.17 (Q 94)
PAXdb E.coli [ppm]: 3.3 (Q 97)

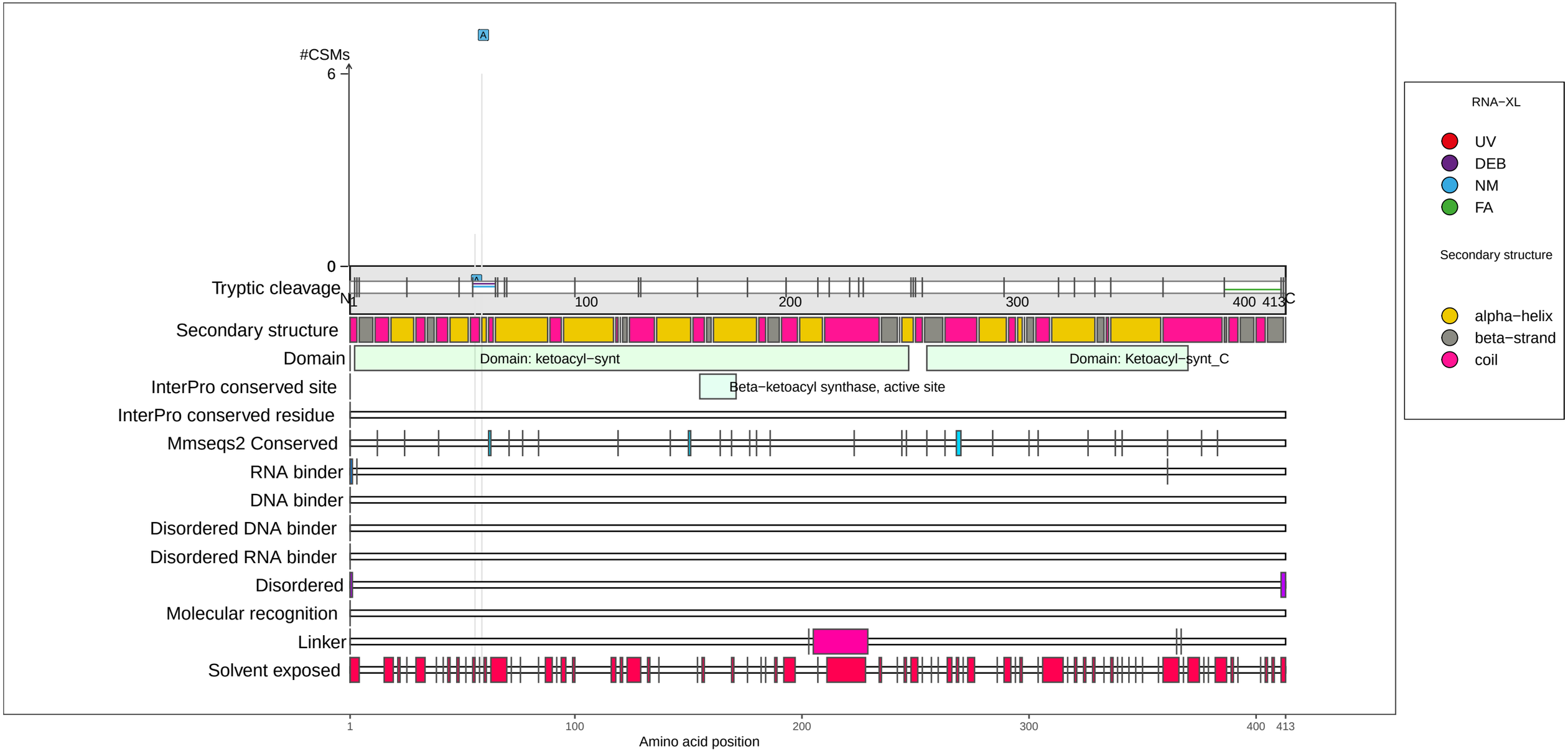
− RNA functions: not annotated



P0AAI5
FABF_ECOLI 3−oxoacyl−[acyl−carrier−protein] synthase 2

− Abundance:
tryptic [log10 Intensity]: 9.58 (Q 97)
PAXdb K12 strain [ppm]: 2.51 (Q 78)
PAXdb E.coli [ppm]: 2.59 (Q 88)

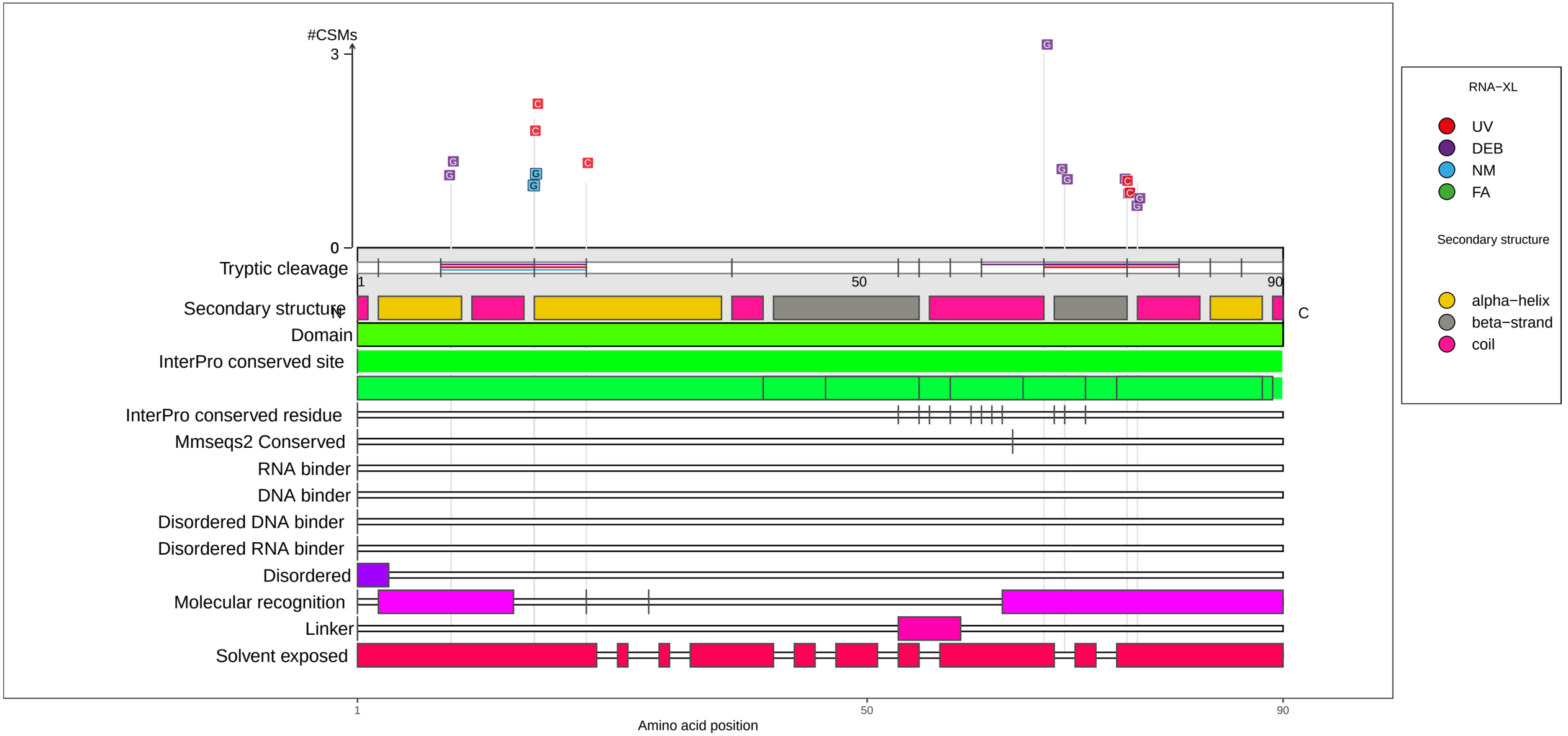
− RNA functions: not annotated



P0ACF4
DBHB_ECOLI DNA−binding protein HU−beta

− Abundance:
tryptic [log10 Intensity]: 9.53 (Q 97)
PAXdb K12 strain [ppm]: 3.83 (Q 100)
PAXdb E.coli [ppm]: 3.91 (Q 100)

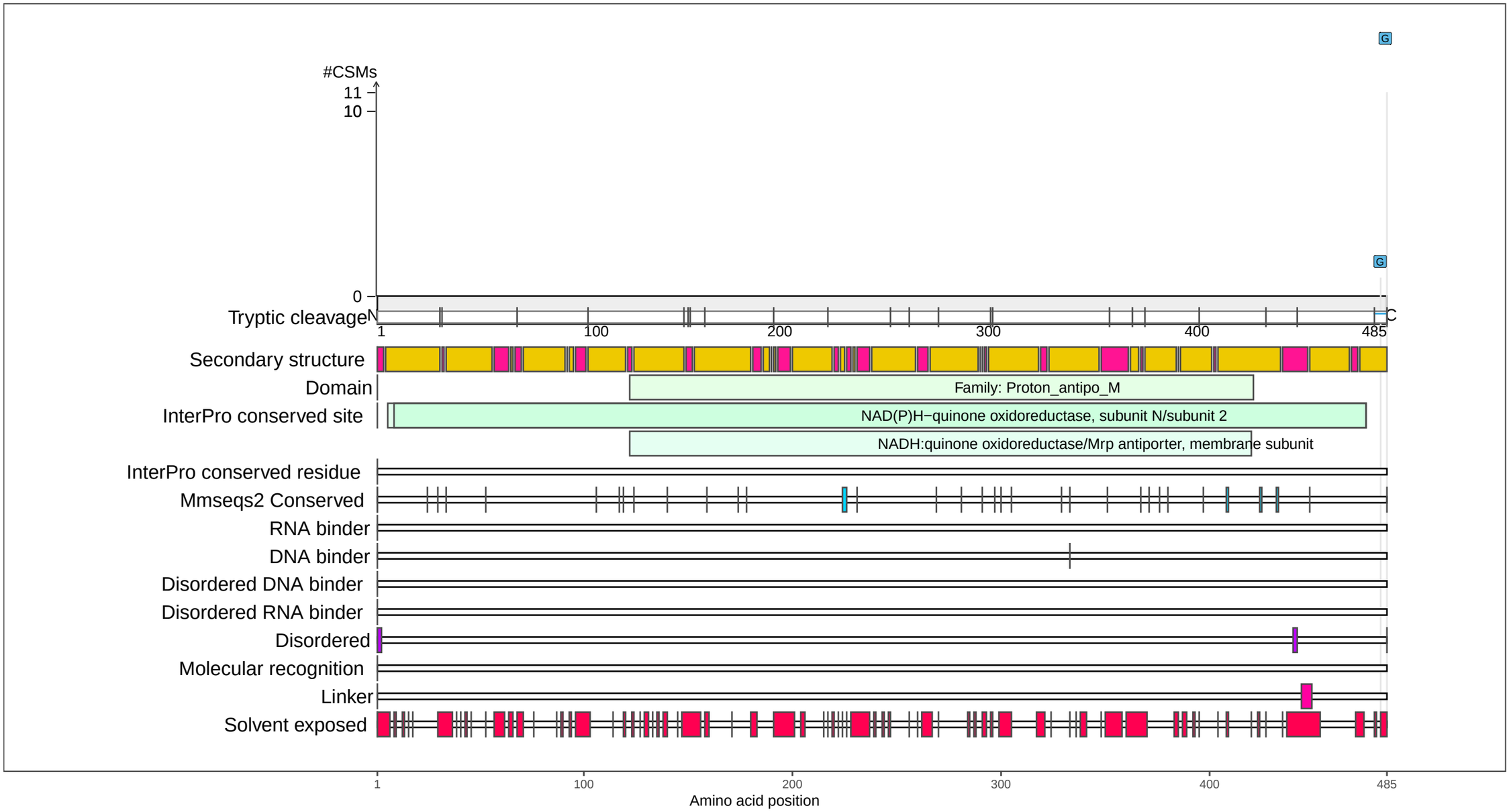
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0AFF0
NUON_ECOLI NADH−quinone oxidoreductase subunit N

− Abundance:
tryptic [log10 Intensity]: 8.81 (Q 84)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.04 (Q 48)

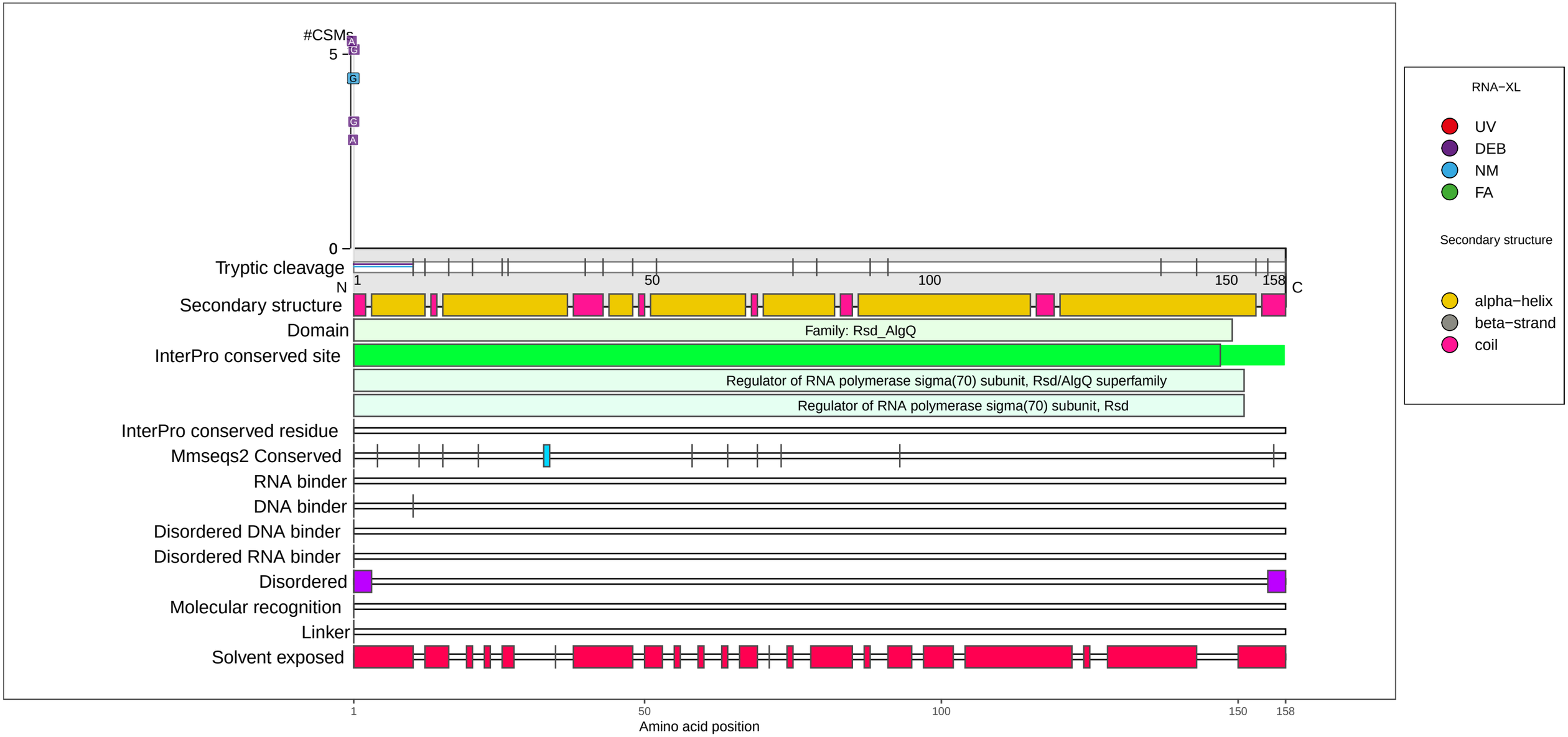
− RNA functions: not annotated



P0AFX4
RSD_ECOLI Regulator of sigma D

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: 2.51 (Q 86)

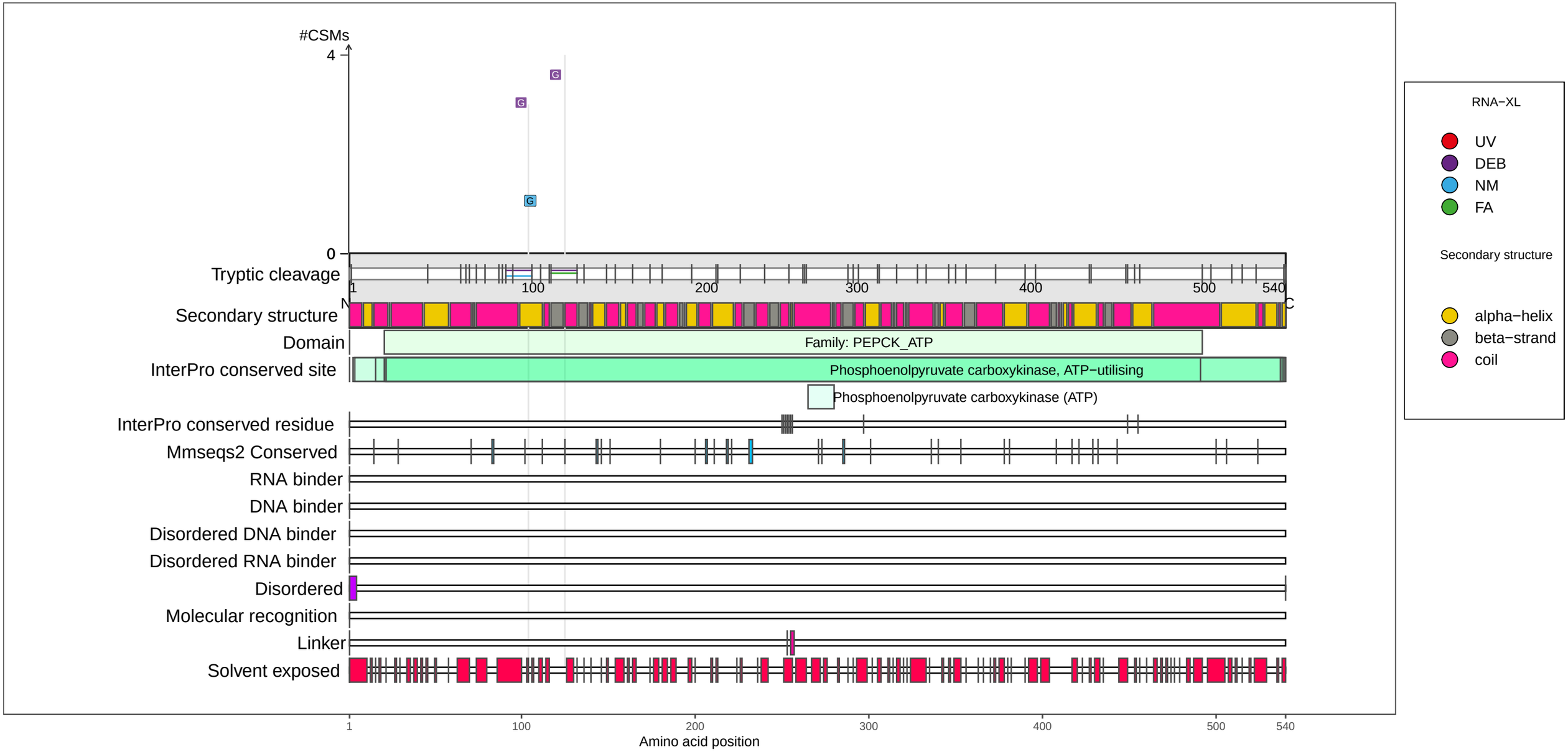
− RNA functions:
Regulator of RNA polymerase sigma(70) subunit, Rsd/AlgQ



P22259
PCKA_ECOLI Phosphoenolpyruvate carboxykinase (ATP)

− Abundance:
tryptic [log10 Intensity]: 9.21 (Q 93)
PAXdb K12 strain [ppm]: 2.66 (Q 82)
PAXdb E.coli [ppm]: 3.07 (Q 95)

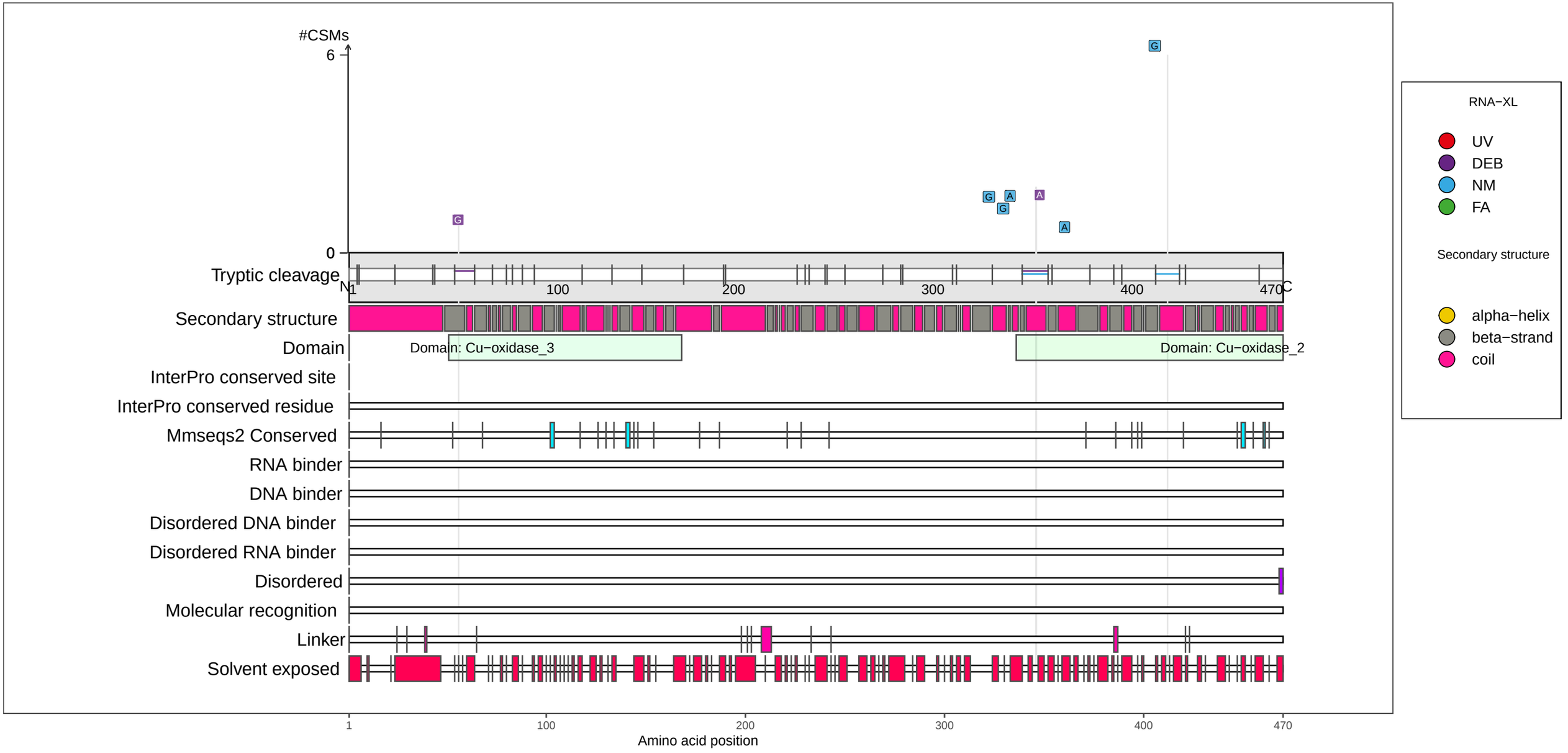
− RNA functions: not annotated



P26648
FTSP_ECOLI Cell division protein FtsP

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 56)
PAXdb K12 strain [ppm]: 1.66 (Q 48)
PAXdb E.coli [ppm]: 0.65 (Q 40)

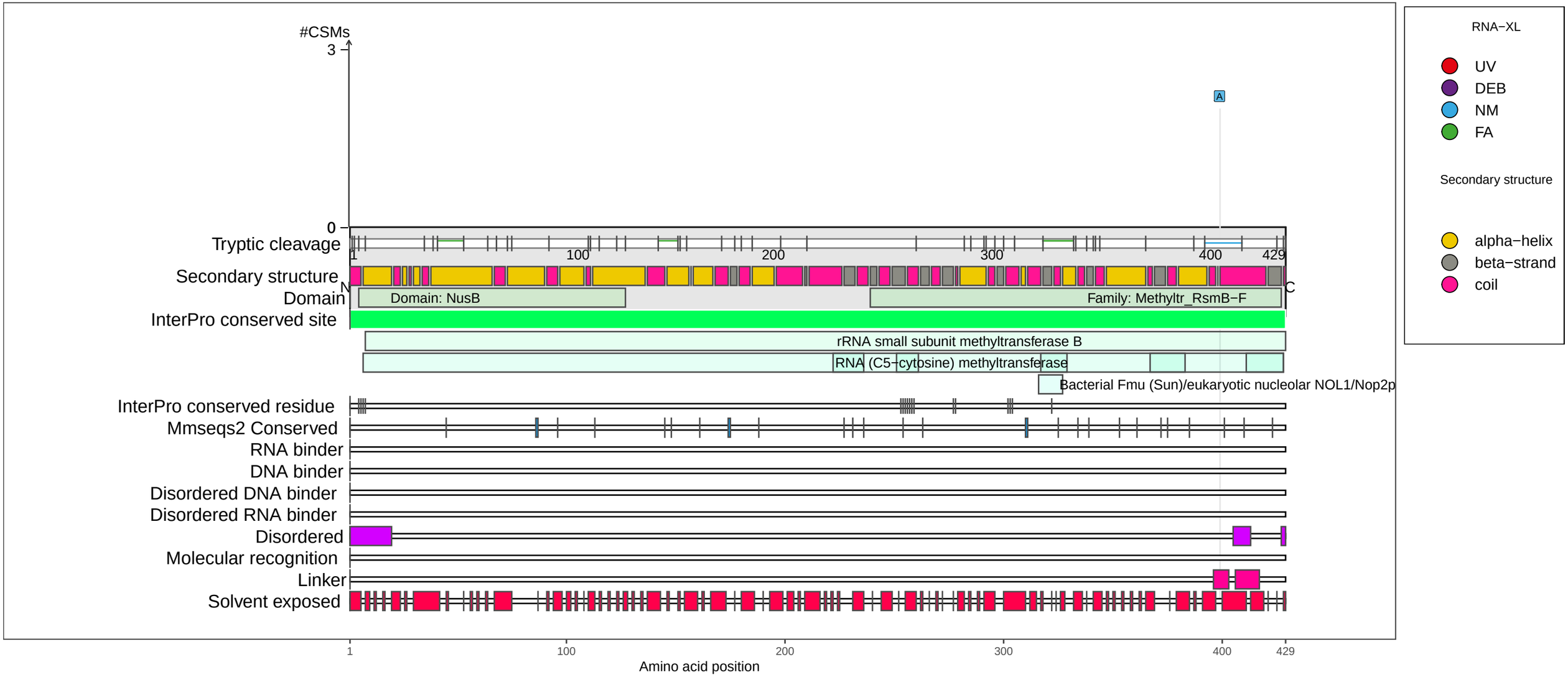
− RNA functions: not annotated



P36929
RSMB_ECOLI Ribosomal RNA small subunit methyltransferase B

− Abundance:
tryptic [log10 Intensity]: 7.98 (Q 57)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 1.56 (Q 61)

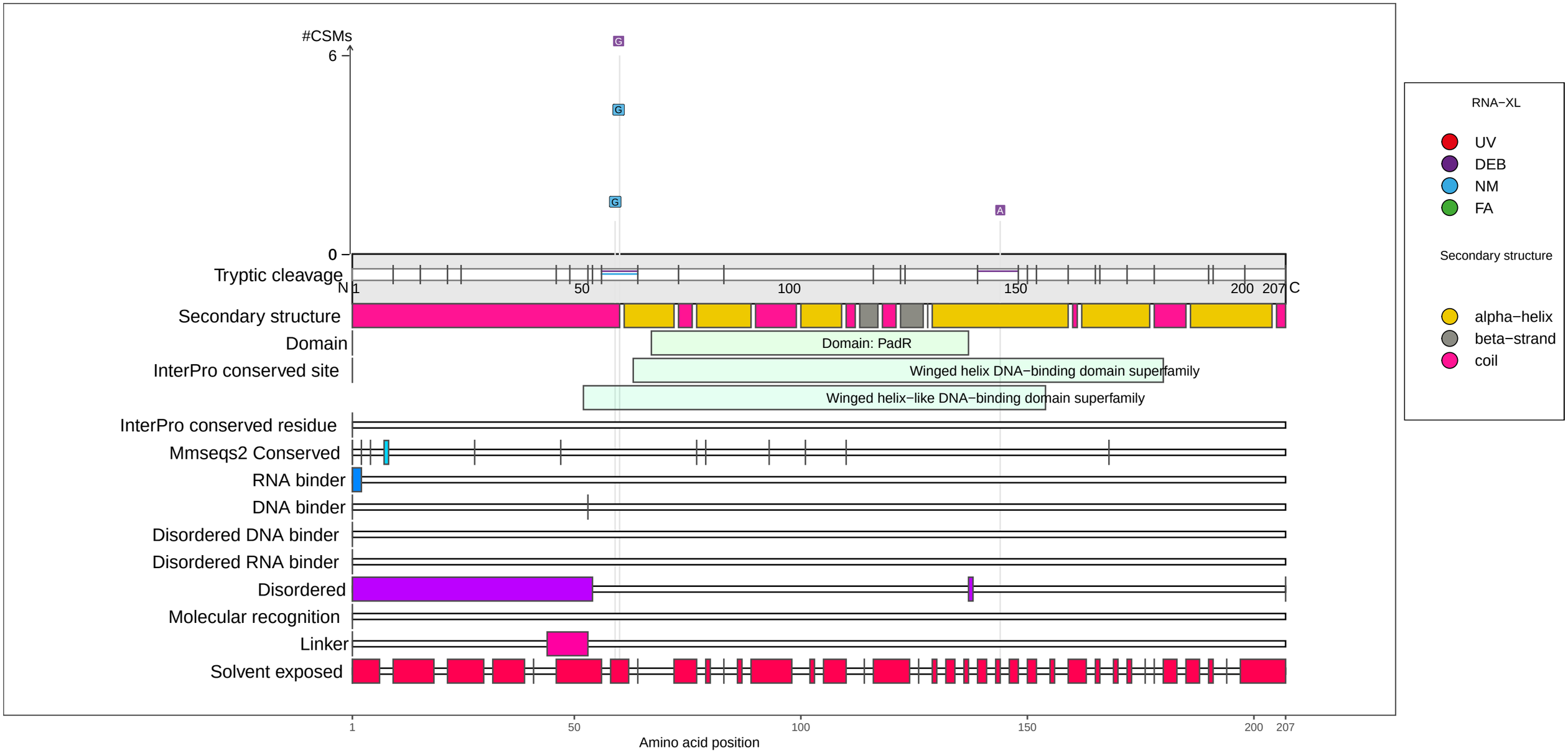
− RNA functions:
16S rRNA methyltransferase RsmB/F; ncRNA metabolic process; ncRNA processing
RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (cytosine−C5−)−methyltransferase activity
rRNA (cytosine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P64588
YQJI_ECOLI Transcriptional regulator YqjI

− Abundance:
tryptic [log10 Intensity]: 7.54 (Q 37)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.29 (Q 80)

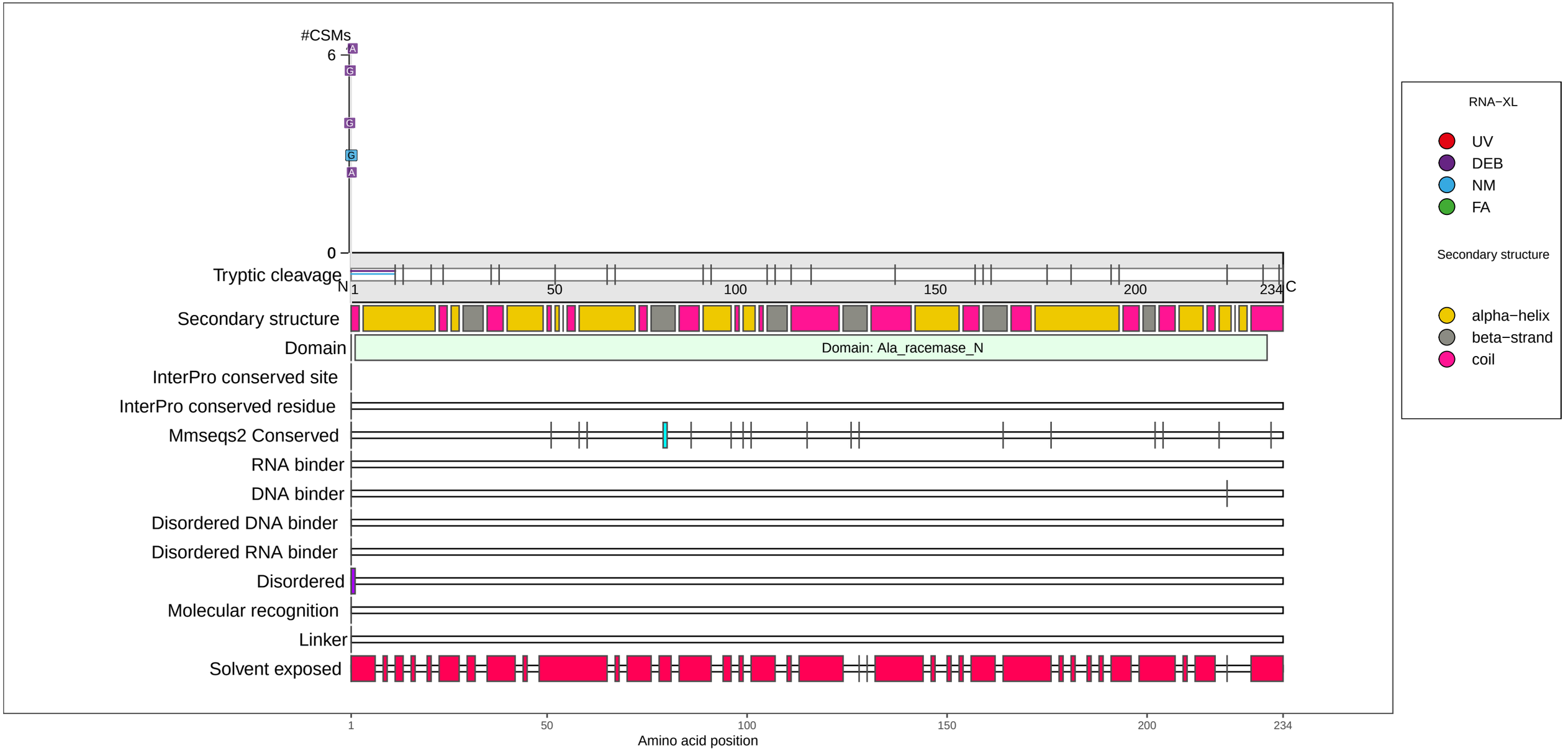
− RNA functions: not annotated



P67080
PLPHP_ECOLI Pyridoxal phosphate homeostasis protein

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 51)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.31 (Q 81)

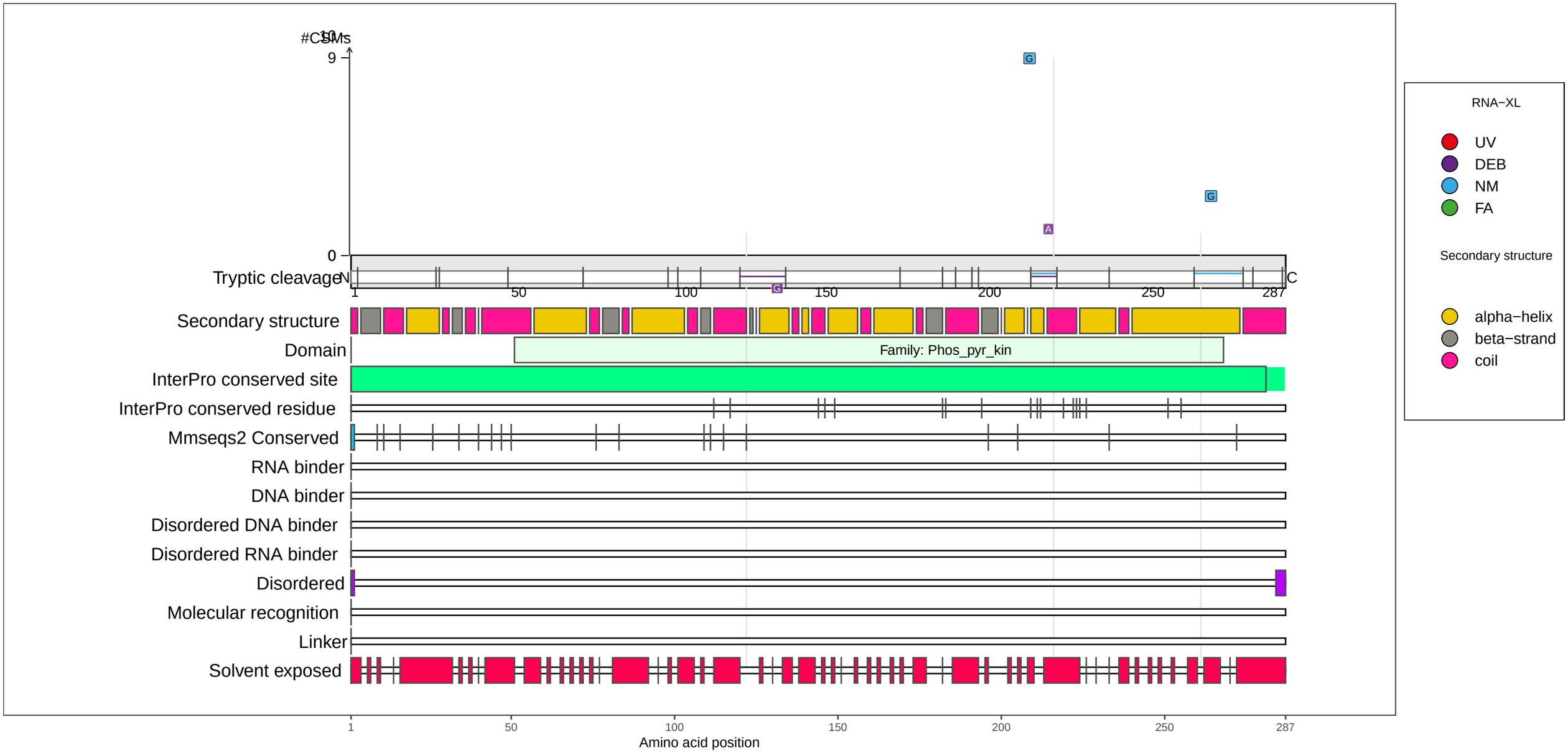
− RNA functions: not annotated



P77150
PDXY_ECOLI Pyridoxal kinase PdxY

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.55 (Q 61)

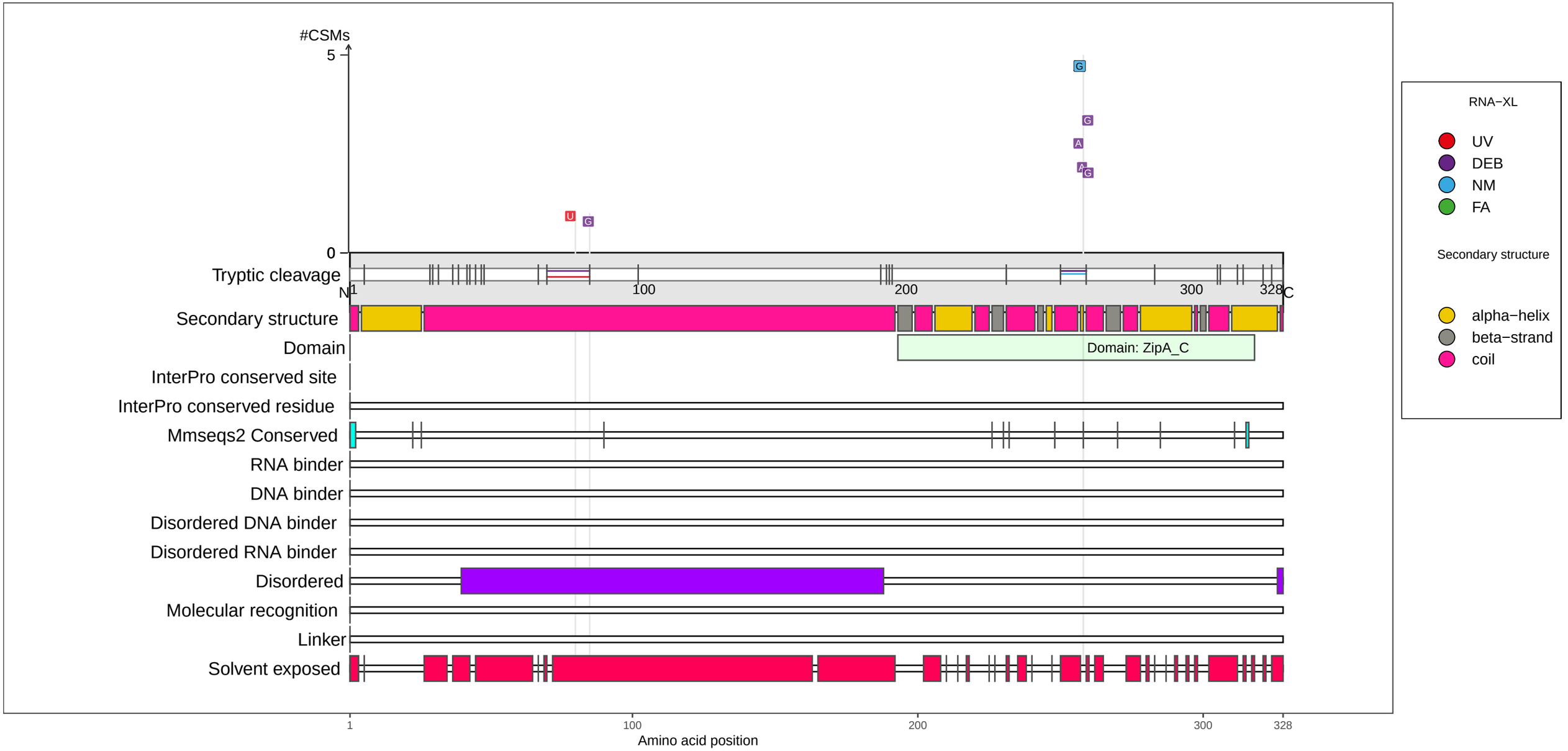
− RNA functions: not annotated



P77173
ZIPA_ECOLI Cell division protein ZipA

− Abundance:
tryptic [log10 Intensity]: 8.41 (Q 72)
PAXdb K12 strain [ppm]: 2.25 (Q 68)
PAXdb E.coli [ppm]: 1.74 (Q 66)

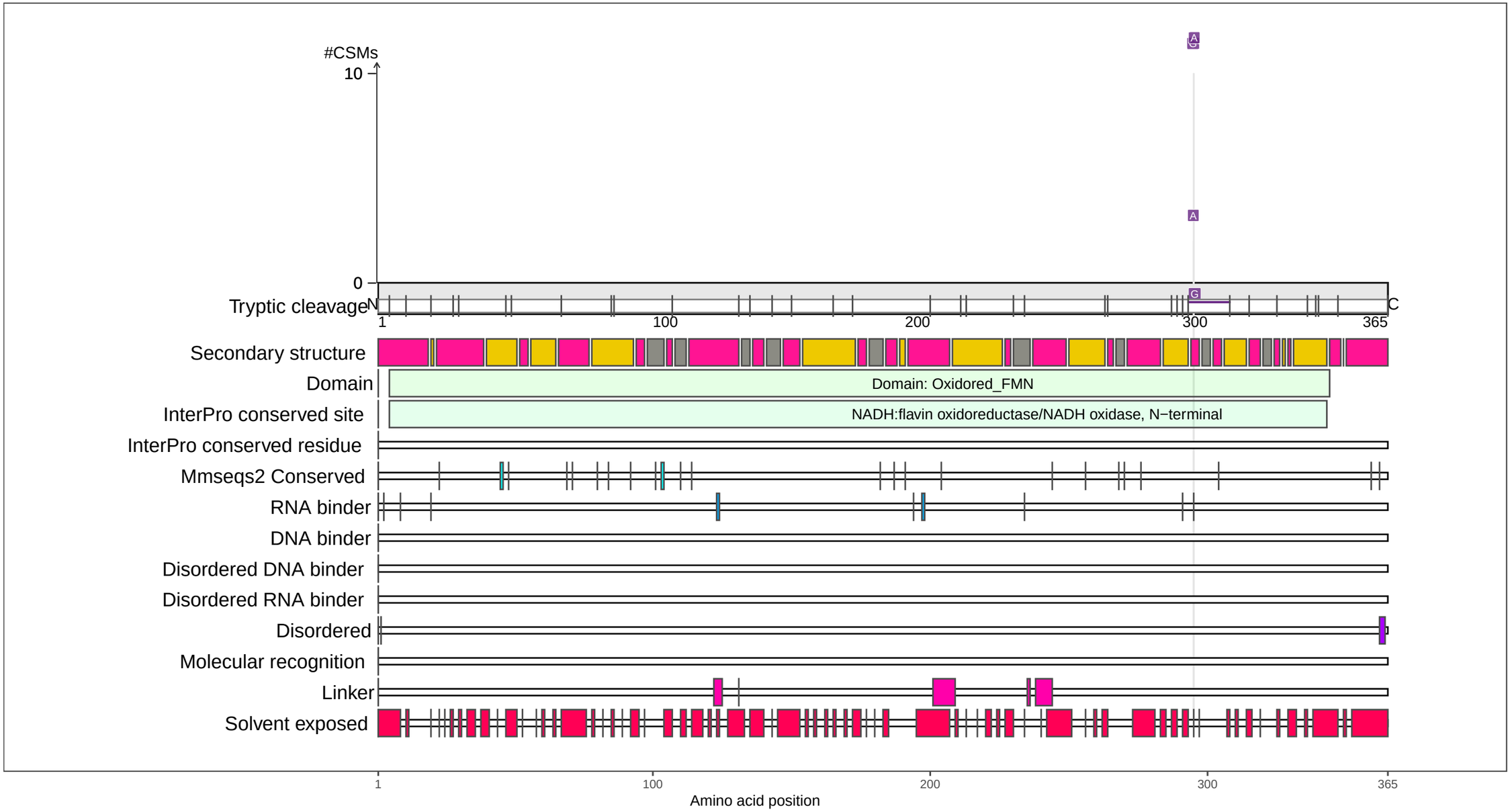
− RNA functions: not annotated



P77258
NEMA_ECOLI N−ethylmaleimide reductase

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 2.63 (Q 81)
PAXdb E.coli [ppm]: 1.27 (Q 54)

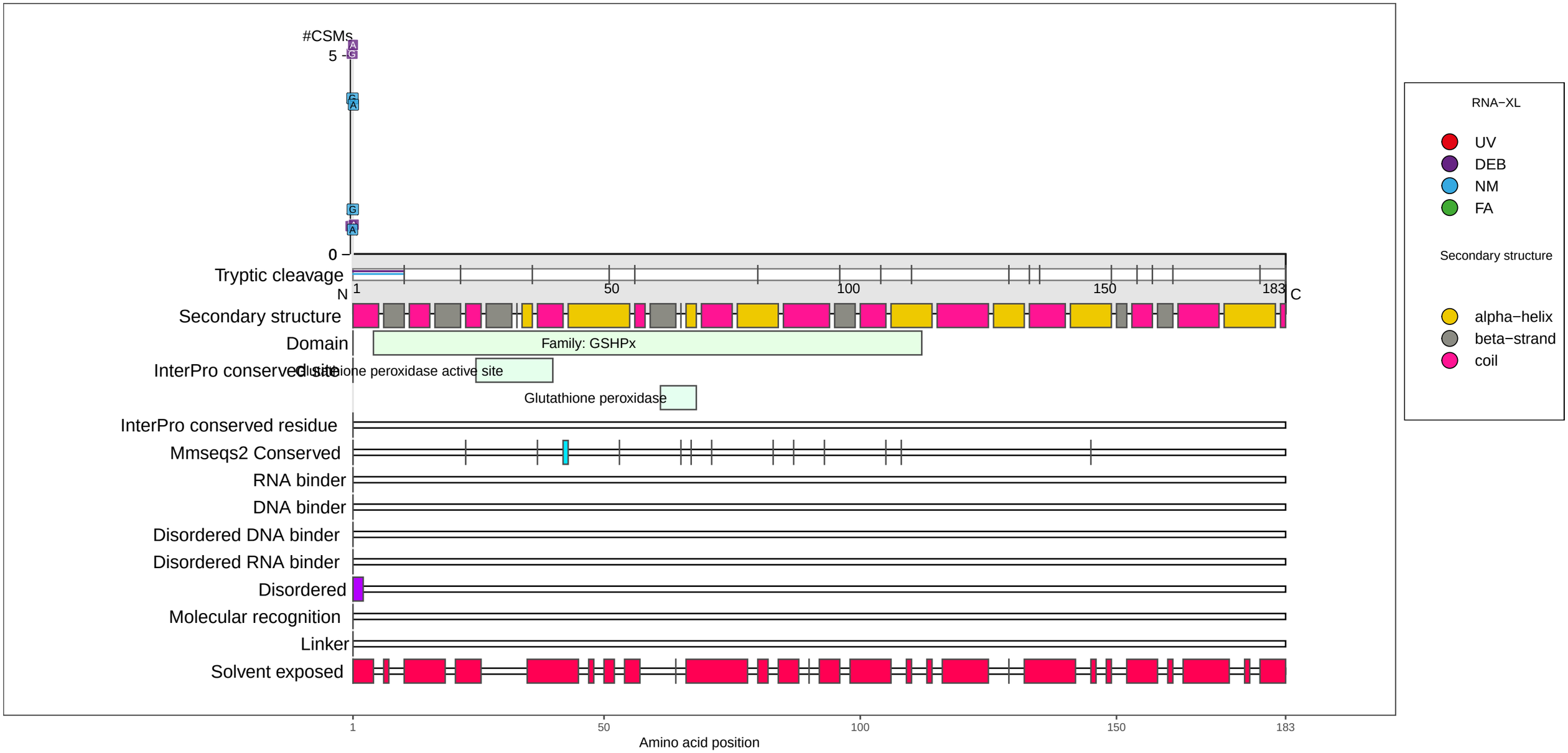
− RNA functions: not annotated



P06610
BTUE_ECOLI Thioredoxin/glutathione peroxidase BtuE

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 2.63 (Q 82)
PAXdb E.coli [ppm]: 2.77 (Q 91)

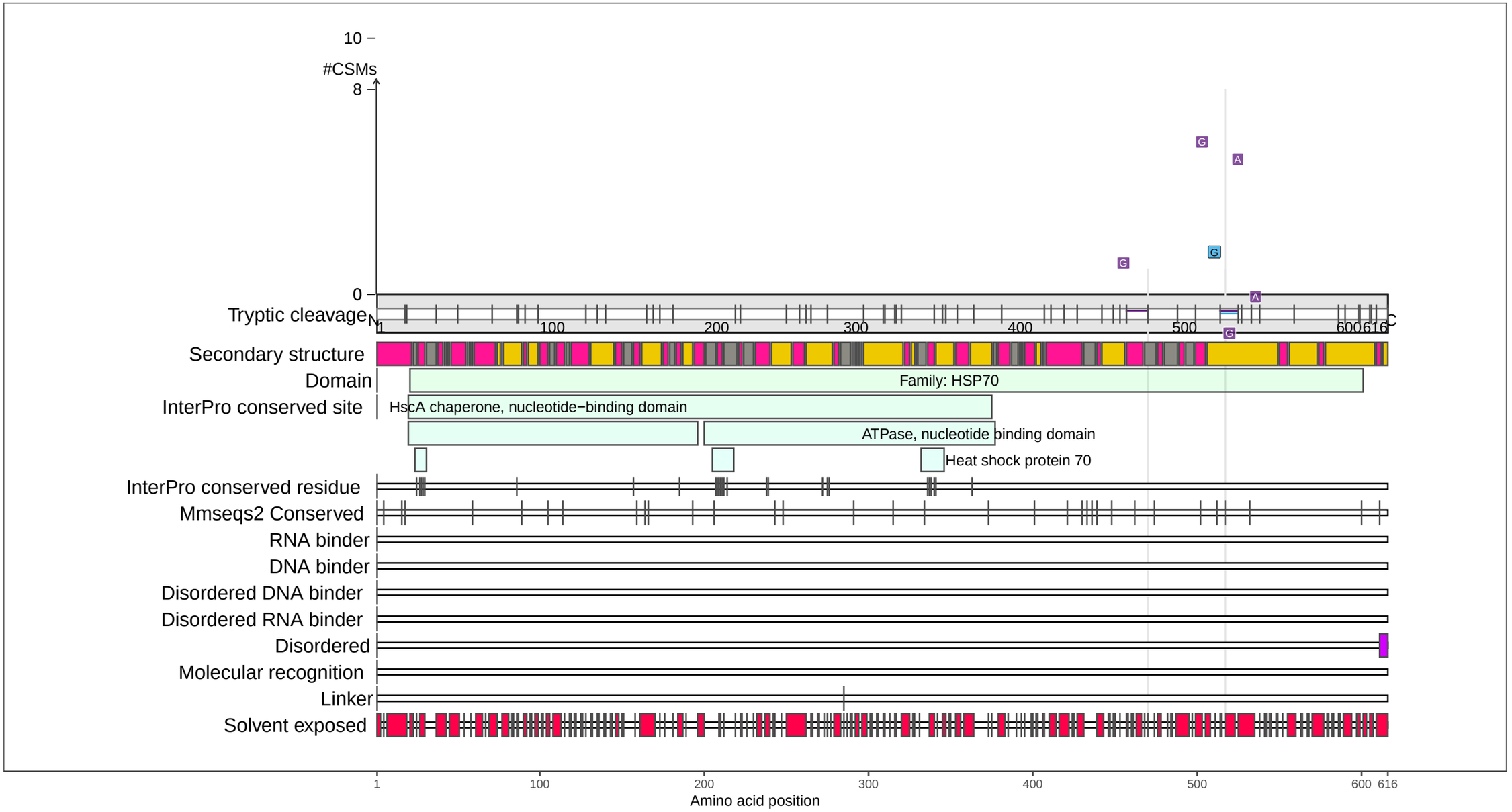
− RNA functions: not annotated



P0A6Z1
HSCA_ECOLI Chaperone protein HscA

− Abundance:
tryptic [log10 Intensity]: 8.64 (Q 80)
PAXdb K12 strain [ppm]: 2.42 (Q 75)
PAXdb E.coli [ppm]: 1.69 (Q 64)

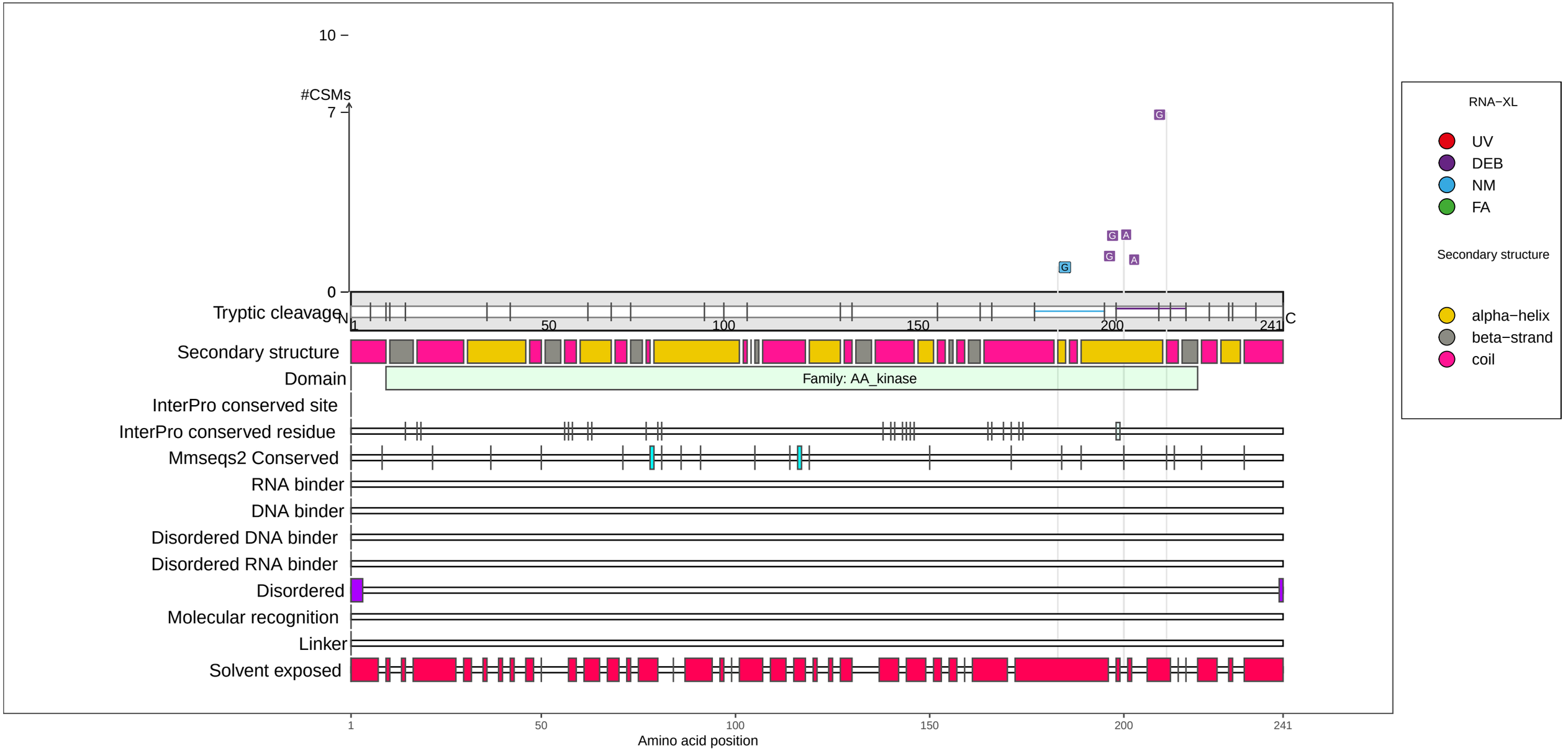
− RNA functions: not annotated



P0A7E9
PYRH_ECOLI Uridylate kinase

− Abundance:
tryptic [log10 Intensity]: 8.76 (Q 83)
PAXdb K12 strain [ppm]: 2.21 (Q 67)
PAXdb E.coli [ppm]: 2.66 (Q 89)

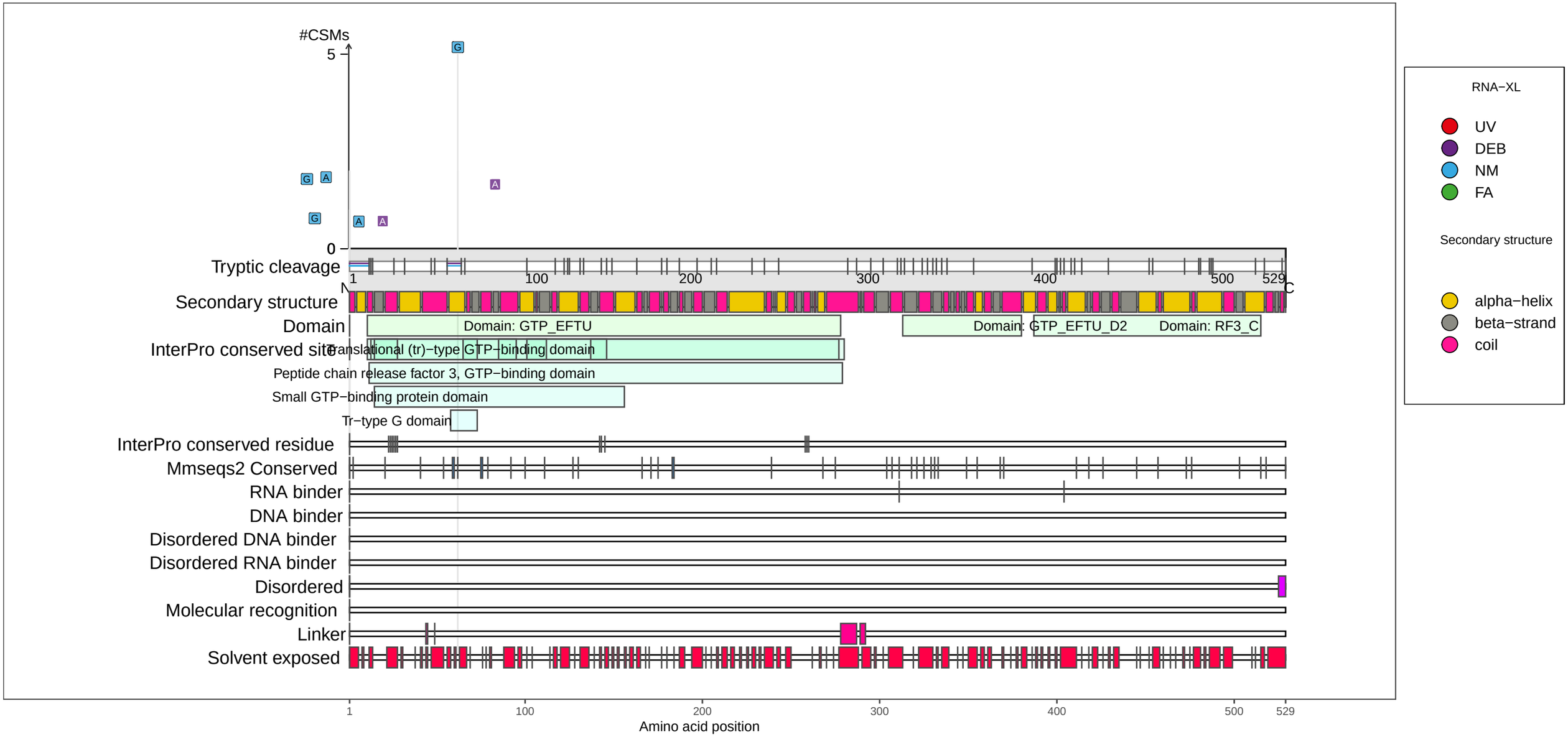
− RNA functions: not annotated



P0A7I4
RF3_ECOLI Peptide chain release factor RF3

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 2.17 (Q 77)

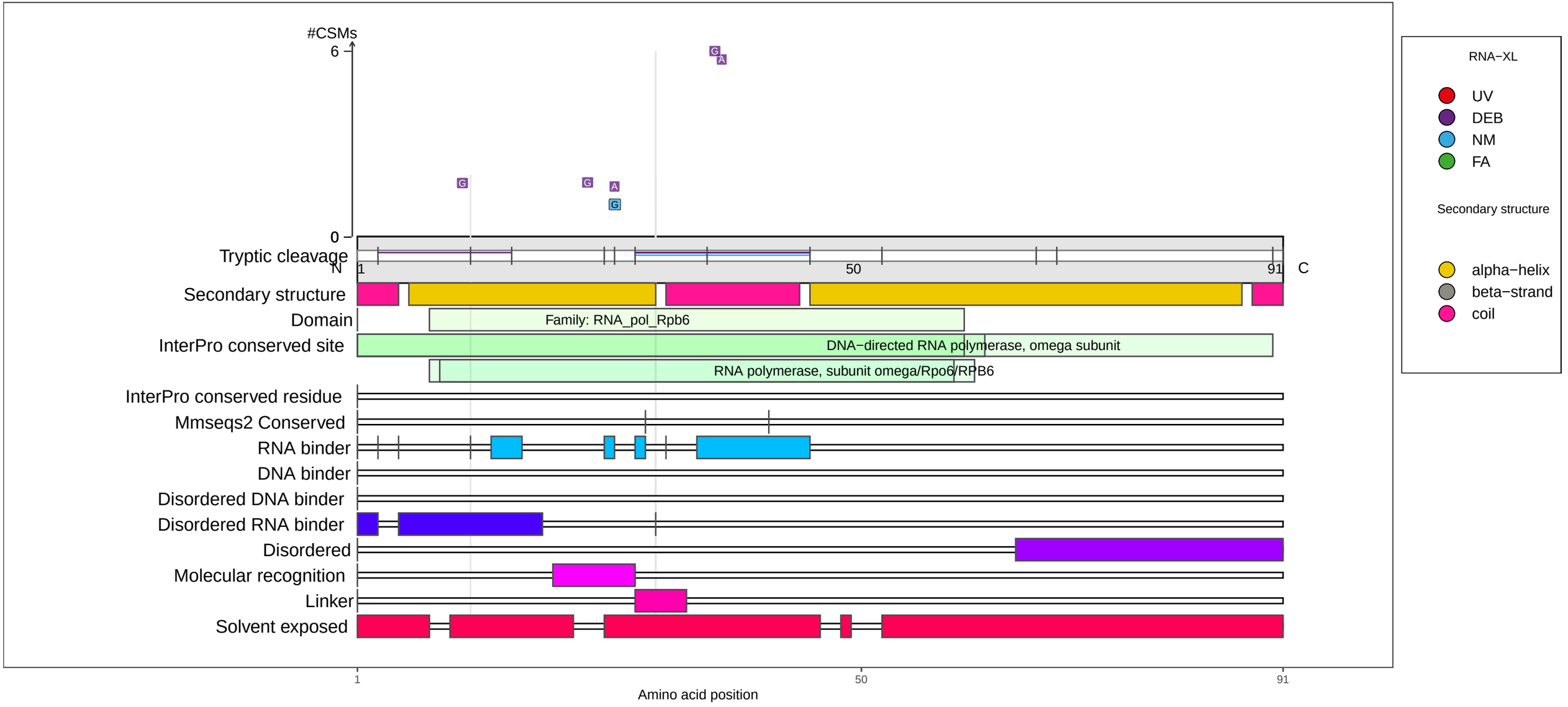
− RNA functions:
RNA binding



P0A800
RPOZ_ECOLI DNA−directed RNA polymerase subunit omega

− Abundance:
tryptic [log10 Intensity]: 8.84 (Q 84)
PAXdb K12 strain [ppm]: 3.56 (Q 98)
PAXdb E.coli [ppm]: 3.46 (Q 99)

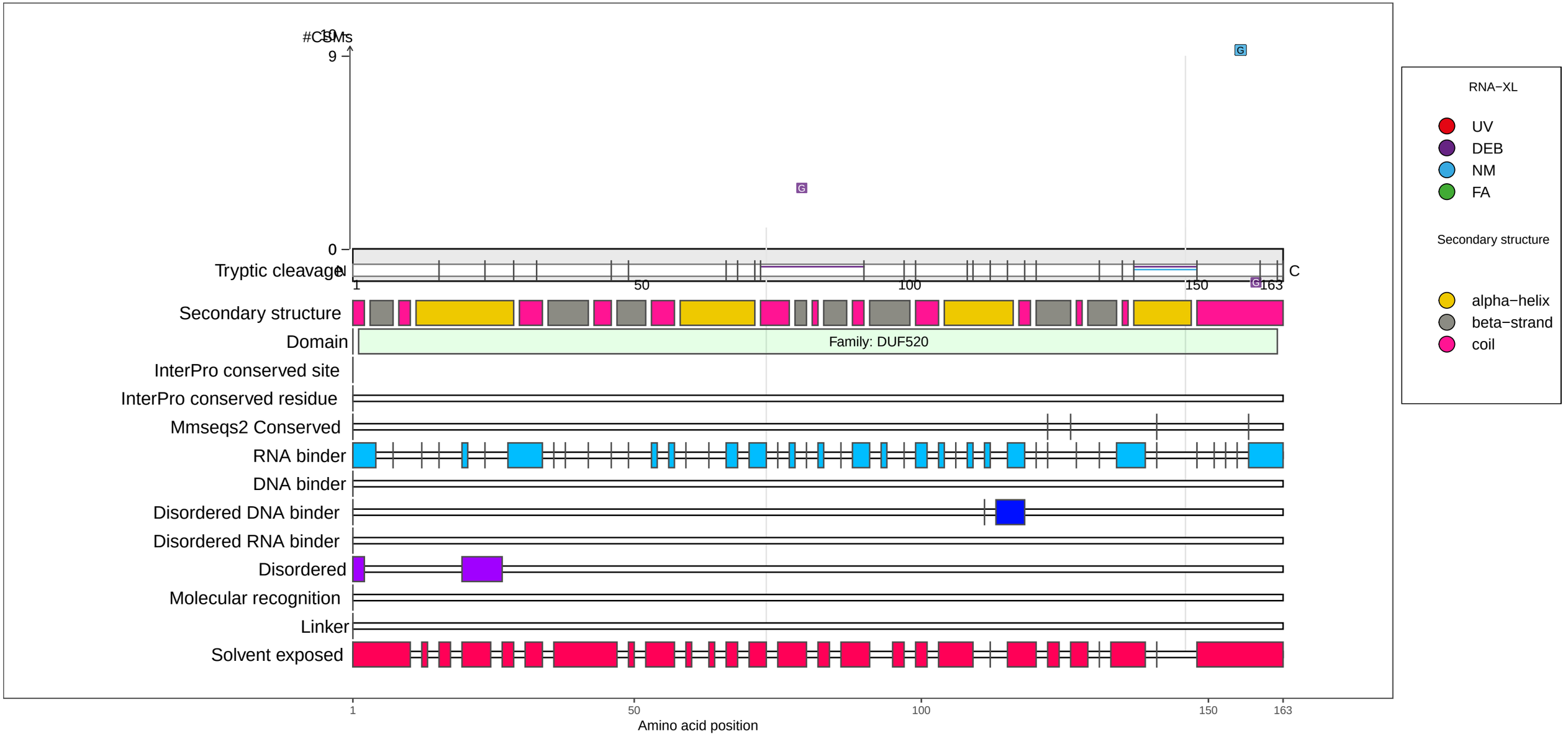
− RNA functions:
5−3 RNA polymerase activity; DNA−directed 5−3 RNA polymerase activity
RNA biosynthetic process; RNA metabolic process; RNA polymerase activity; RNA polymerase complex
RNA polymerase Rpb6



P0A8E7
YAJQ_ECOLI UPF0234 protein YajQ

− Abundance:
tryptic [log10 Intensity]: 8.6 (Q 79)
PAXdb K12 strain [ppm]: 3.31 (Q 95)
PAXdb E.coli [ppm]: 3.07 (Q 95)

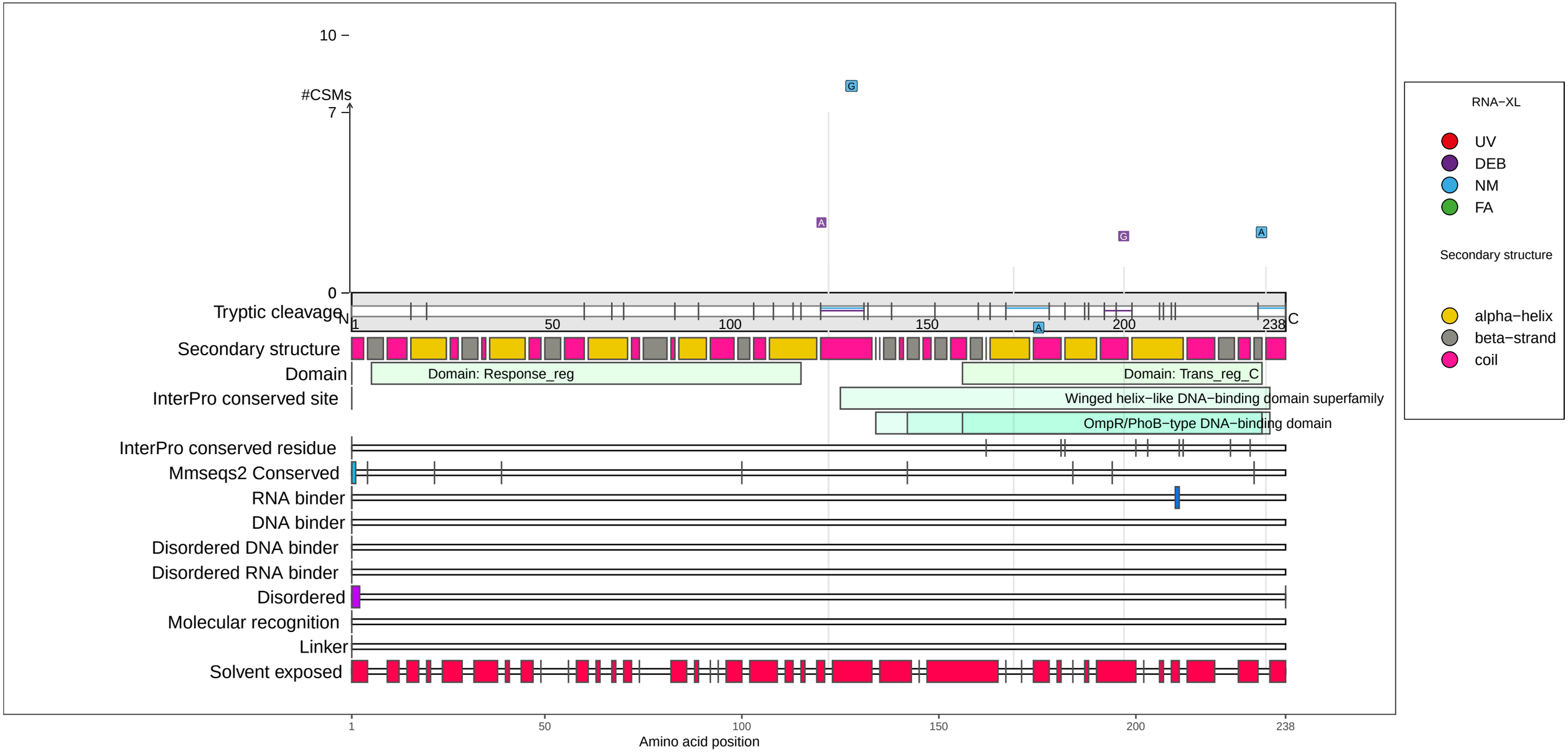
− RNA functions:
RNA binding; tRNA binding



P0A9Q1
ARCA_ECOLI Aerobic respiration control protein ArcA

− Abundance:
tryptic [log10 Intensity]: 8.07 (Q 60)
PAXdb K12 strain [ppm]: 3.13 (Q 93)
PAXdb E.coli [ppm]: 2.97 (Q 94)

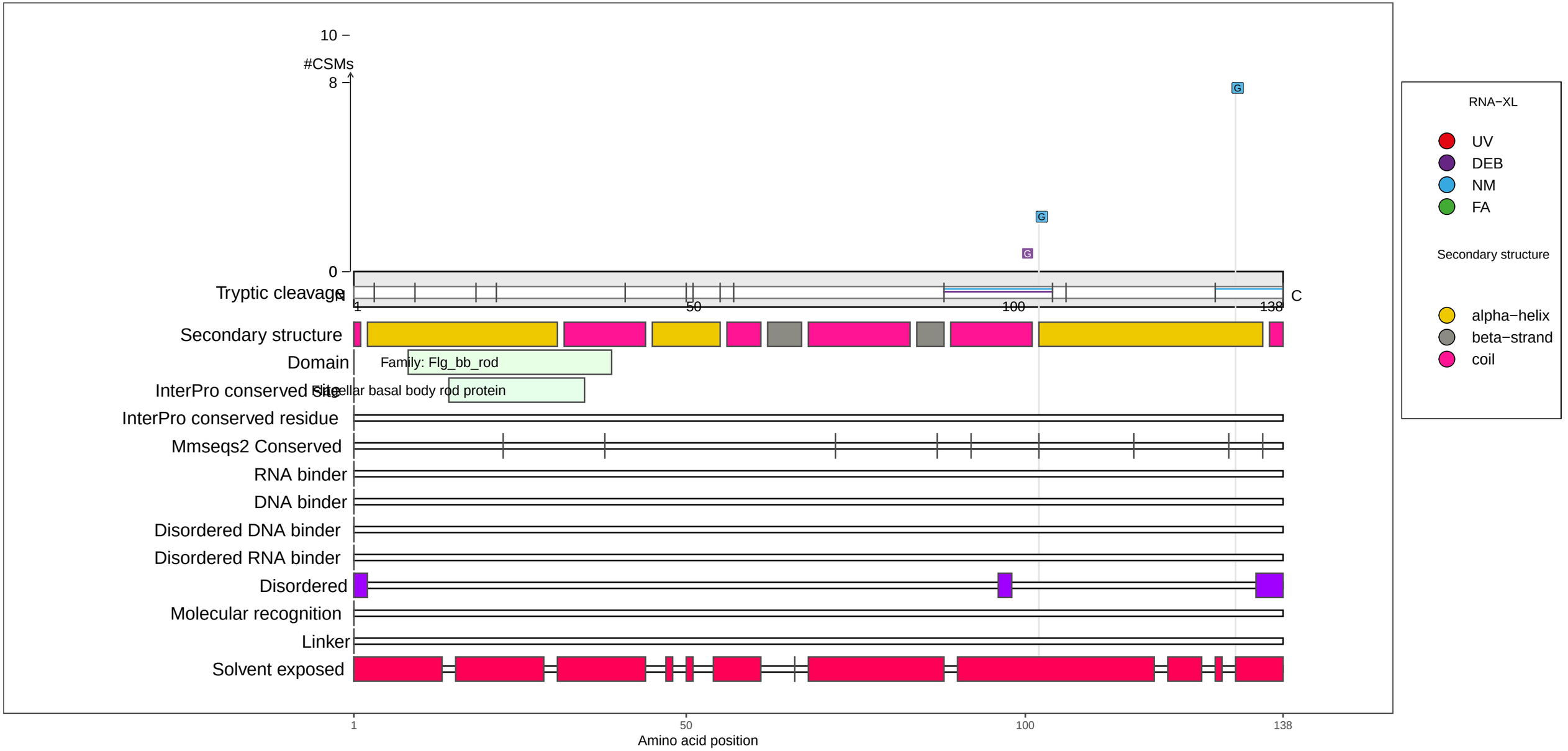
− RNA functions: not annotated



P0ABW9
FLGB_ECOLI Flagellar basal body rod protein FlgB

− Abundance:
tryptic [log10 Intensity]: 6.88 (Q 9)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.24 (Q 20)

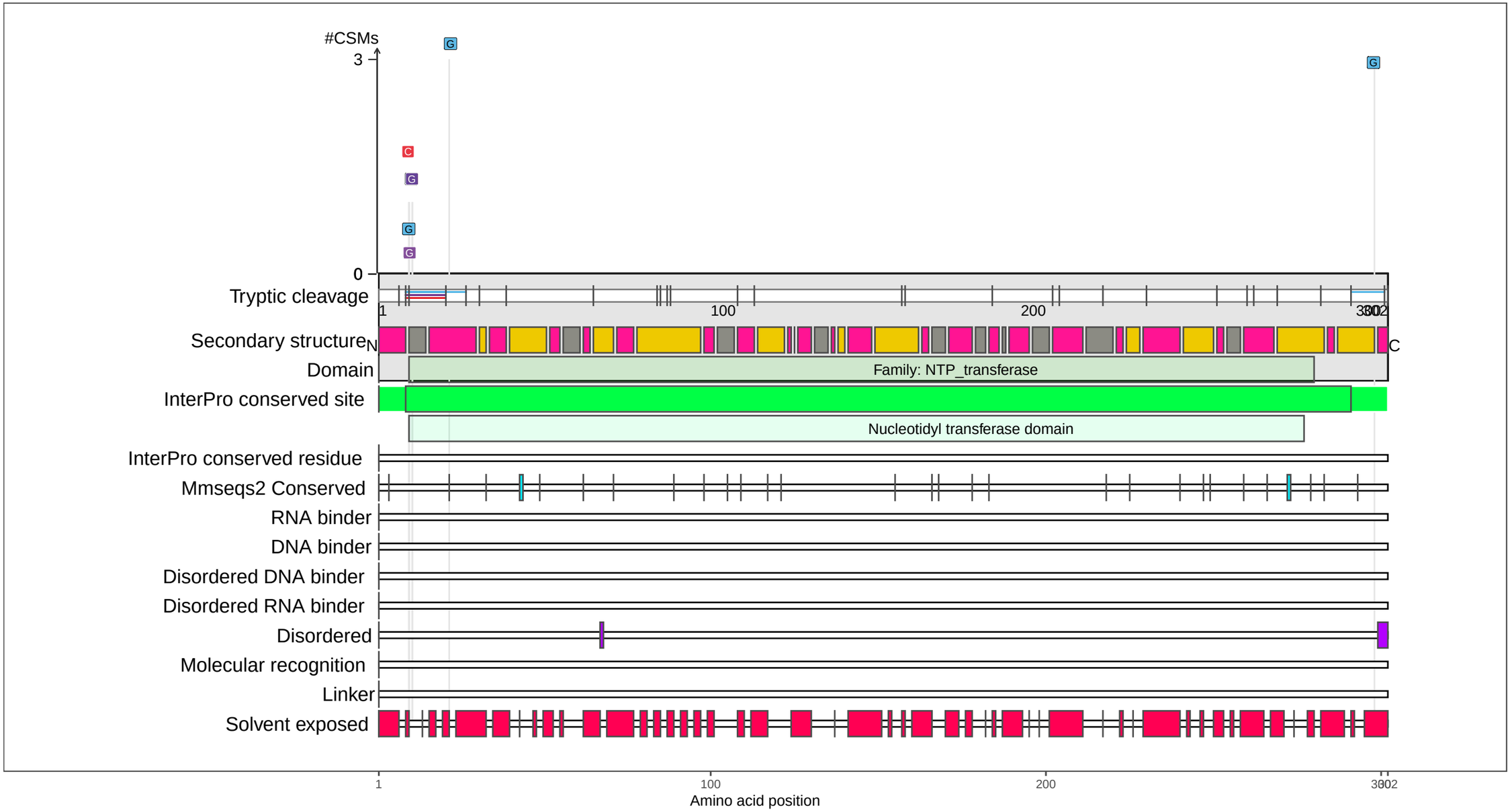
− RNA functions: not annotated



P0AEP3
GALU_ECOLI UTP−−glucose−1−phosphate uridylyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 2.72 (Q 84)
PAXdb E.coli [ppm]: 2.6 (Q 88)

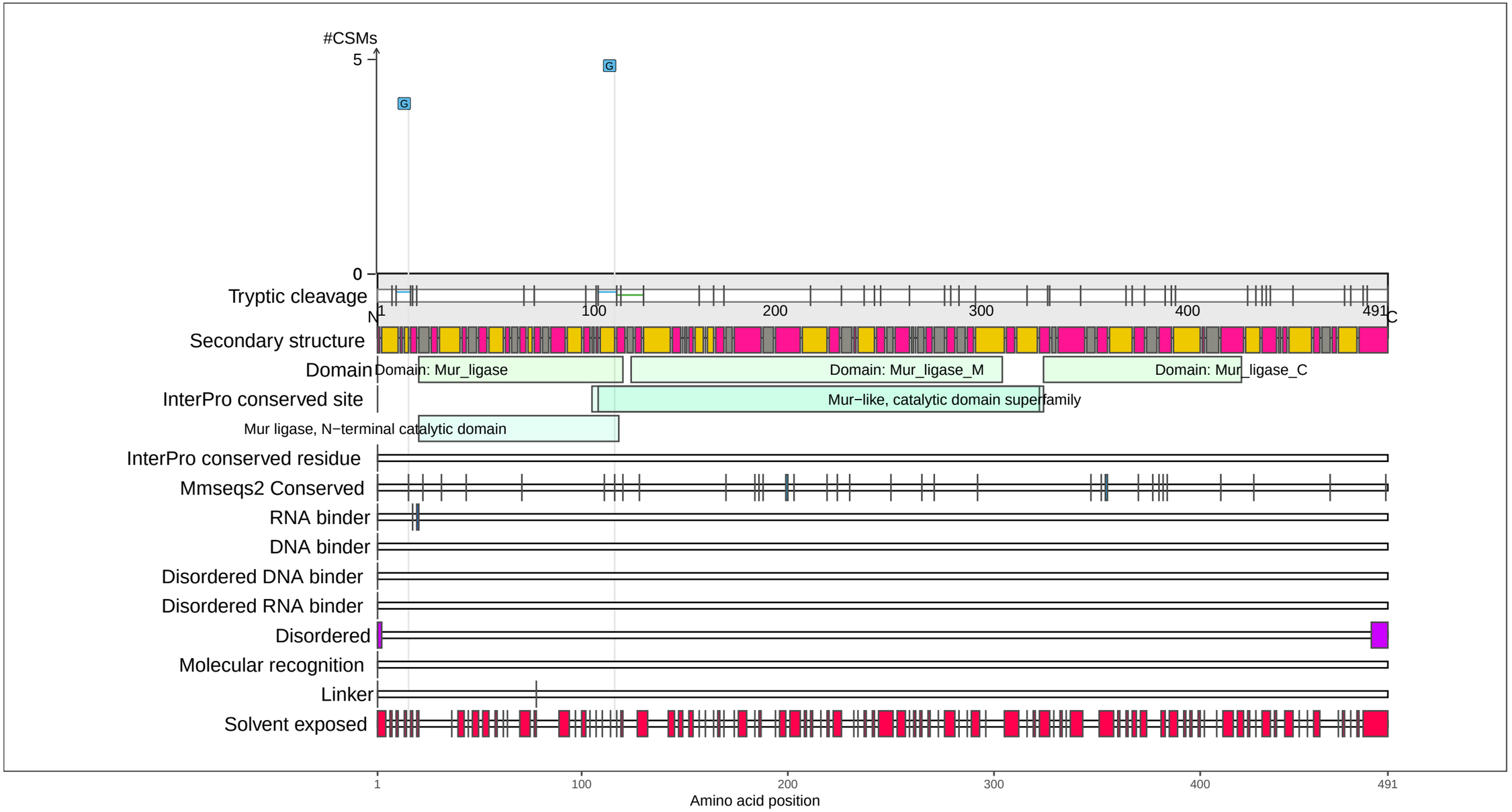
− RNA functions: not annotated



P17952
MURC_ECOLI UDP−N−acetylmuramate−−L−alanine ligase

− Abundance:
tryptic [log10 Intensity]: 8.2 (Q 65)
PAXdb K12 strain [ppm]: 1.91 (Q 57)
PAXdb E.coli [ppm]: 1.69 (Q 64)

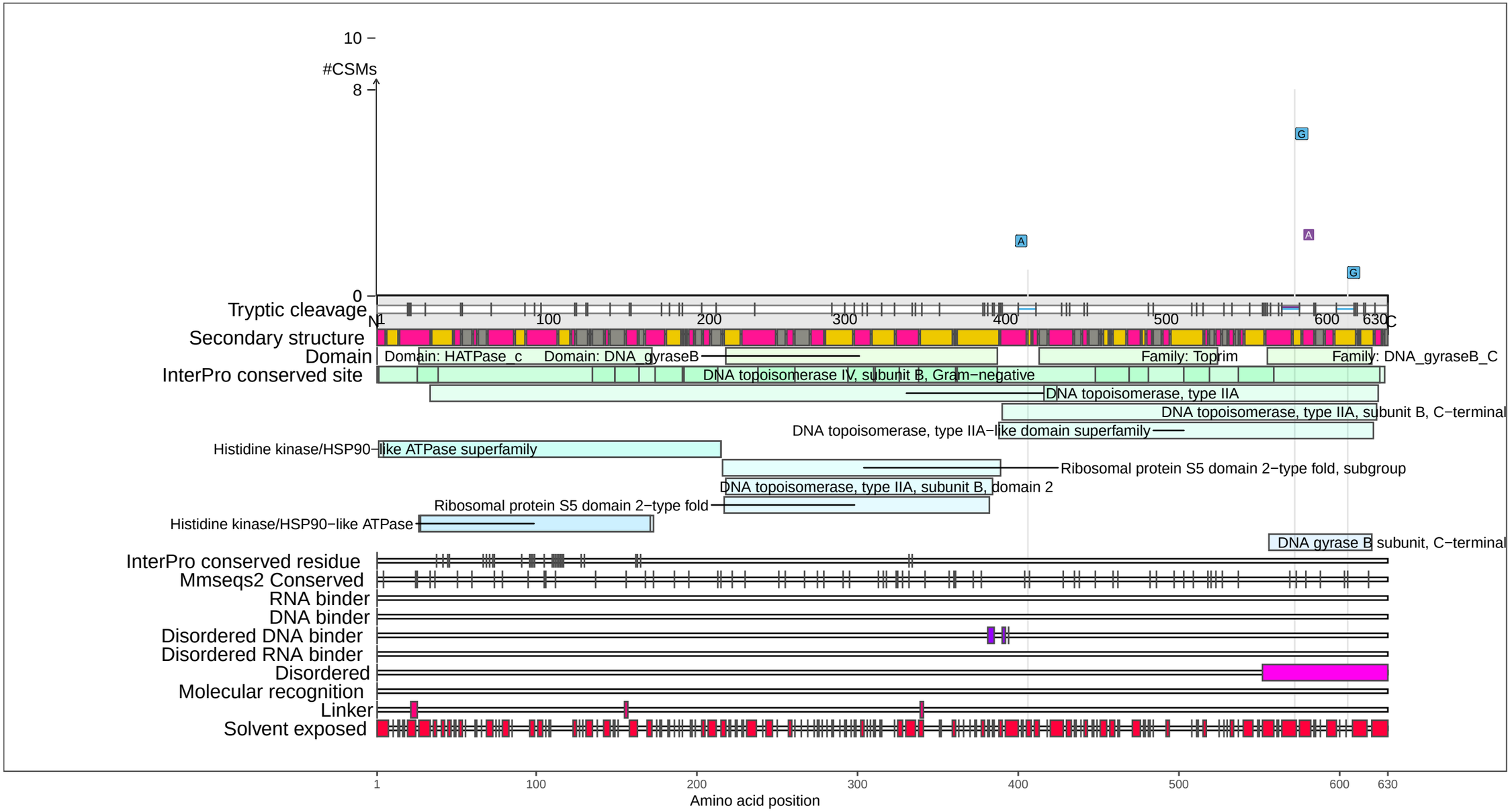
− RNA functions: not annotated



P20083
PARE_ECOLI DNA topoisomerase 4 subunit B

− Abundance:
tryptic [log10 Intensity]: 7.72 (Q 45)
PAXdb K12 strain [ppm]: 1.84 (Q 55)
PAXdb E.coli [ppm]: 1.39 (Q 57)

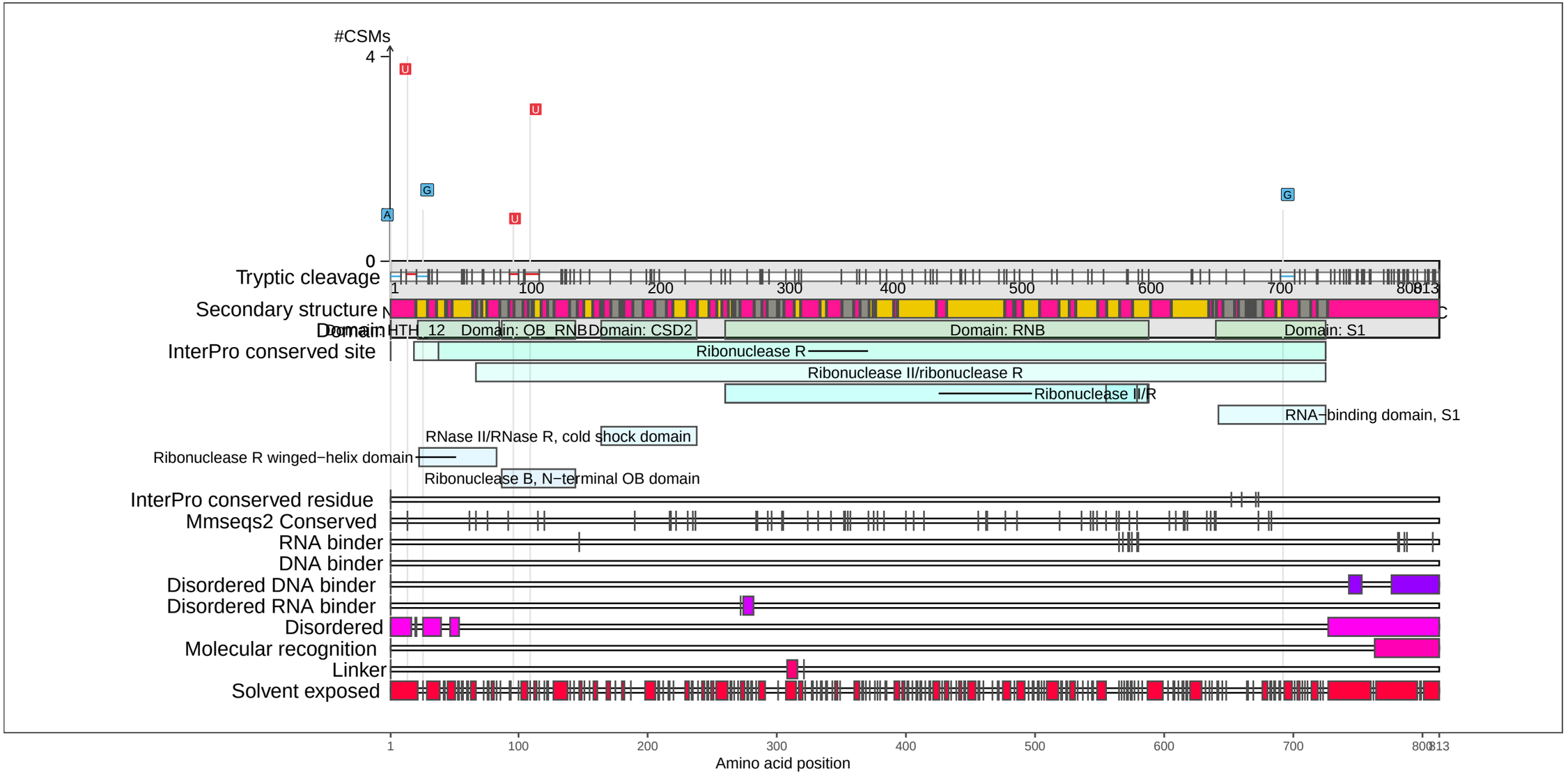
− RNA functions: not annotated

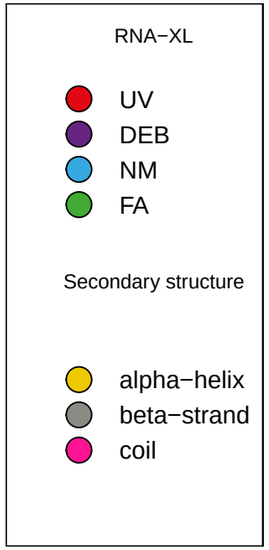


P21499
RNR_ECOLI Ribonuclease R

− Abundance:
tryptic [log10 Intensity]: 8.27 (Q 68)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 2.43 (Q 84)

− RNA functions:
3−5 RNA helicase activity; mRNA catabolic process; mRNA metabolic process
ncRNA metabolic process; ncRNA processing; RNA binding; RNA catabolic process
RNA helicase activity; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, exonucleolytic; RNA processing; S1 RNA binding domain

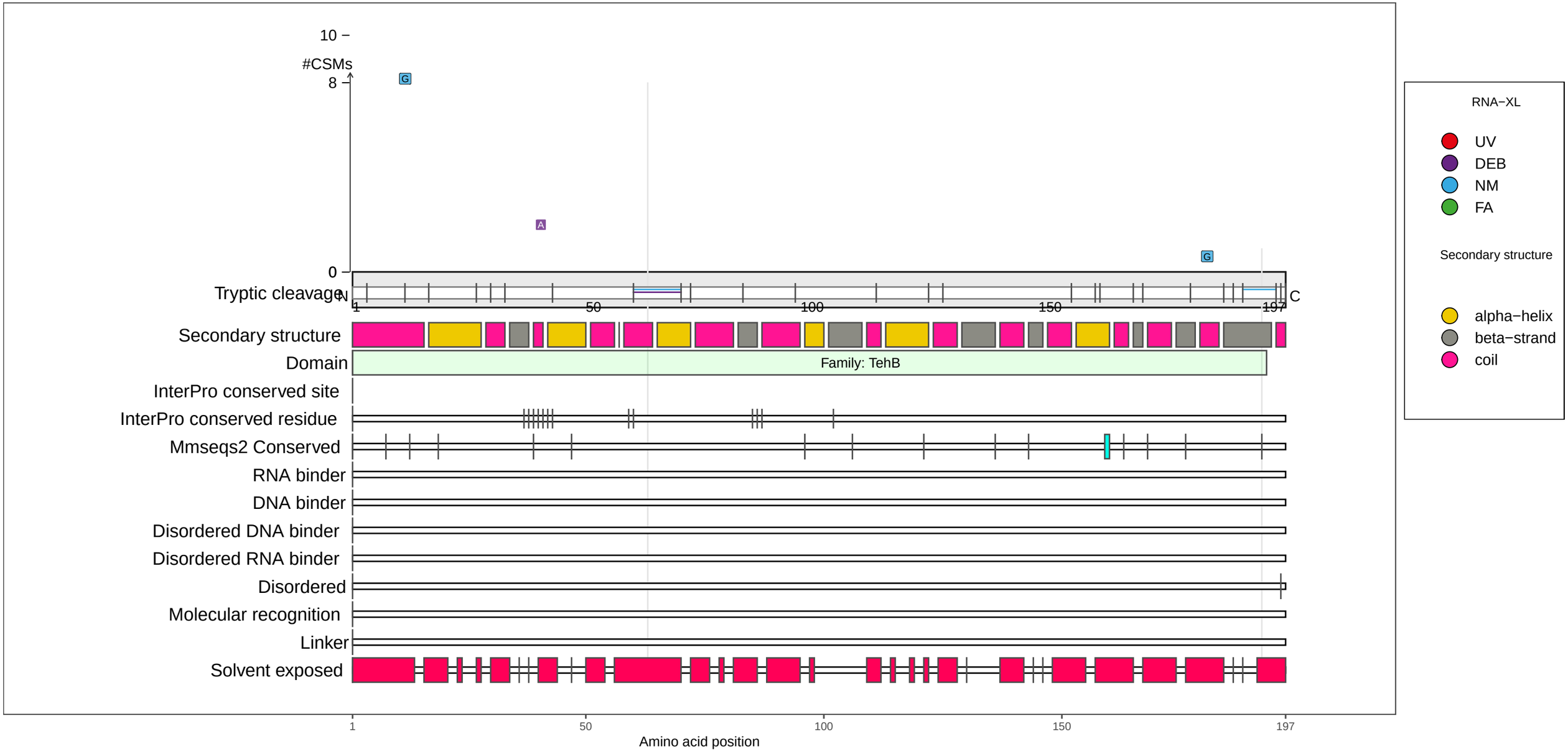




P25397
TEHB_ECOLI Tellurite methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.19 (Q 77)

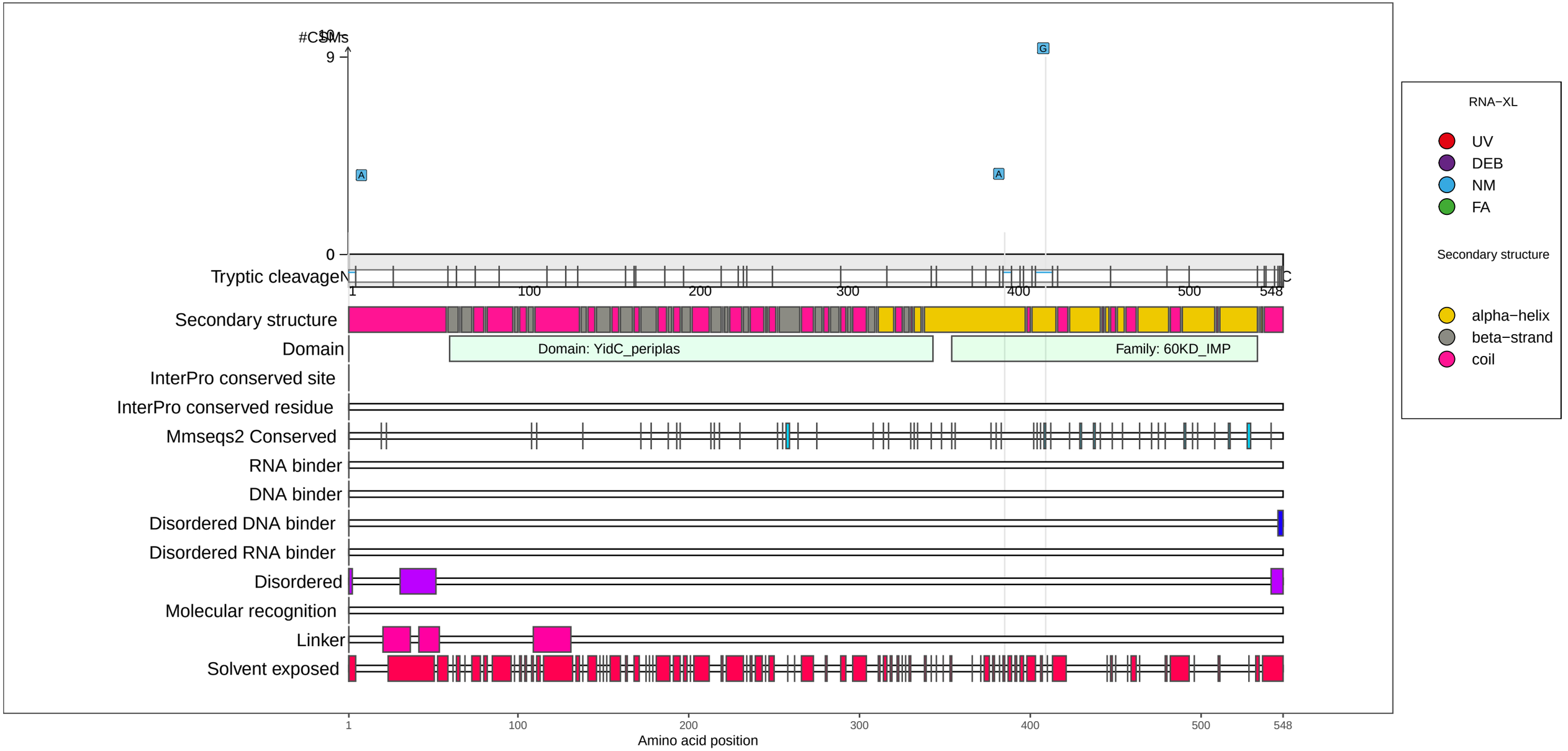
− RNA functions: not annotated



P25714
YIDC_ECOLI Membrane protein insertase YidC

− Abundance:
tryptic [log10 Intensity]: 7.59 (Q 39)
PAXdb K12 strain [ppm]: 2.01 (Q 61)
PAXdb E.coli [ppm]: 1.84 (Q 68)

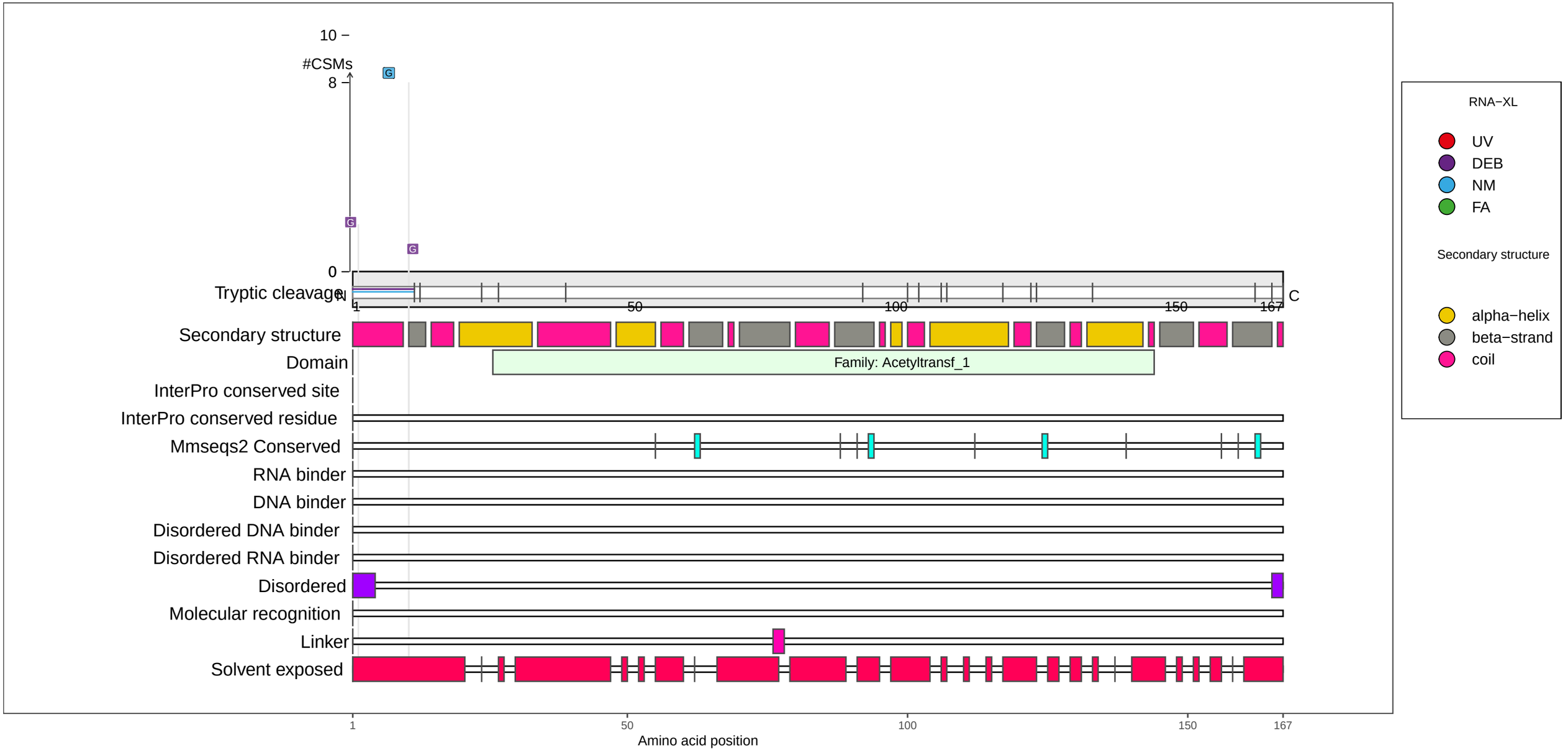
− RNA functions: not annotated



P39337
YJGM_ECOLI Uncharacterized N−acetyltransferase YjgM

− Abundance:
tryptic [log10 Intensity]: 7.14 (Q 18)
PAXdb K12 strain [ppm]: 2.11 (Q 64)
PAXdb E.coli [ppm]: 1.25 (Q 53)

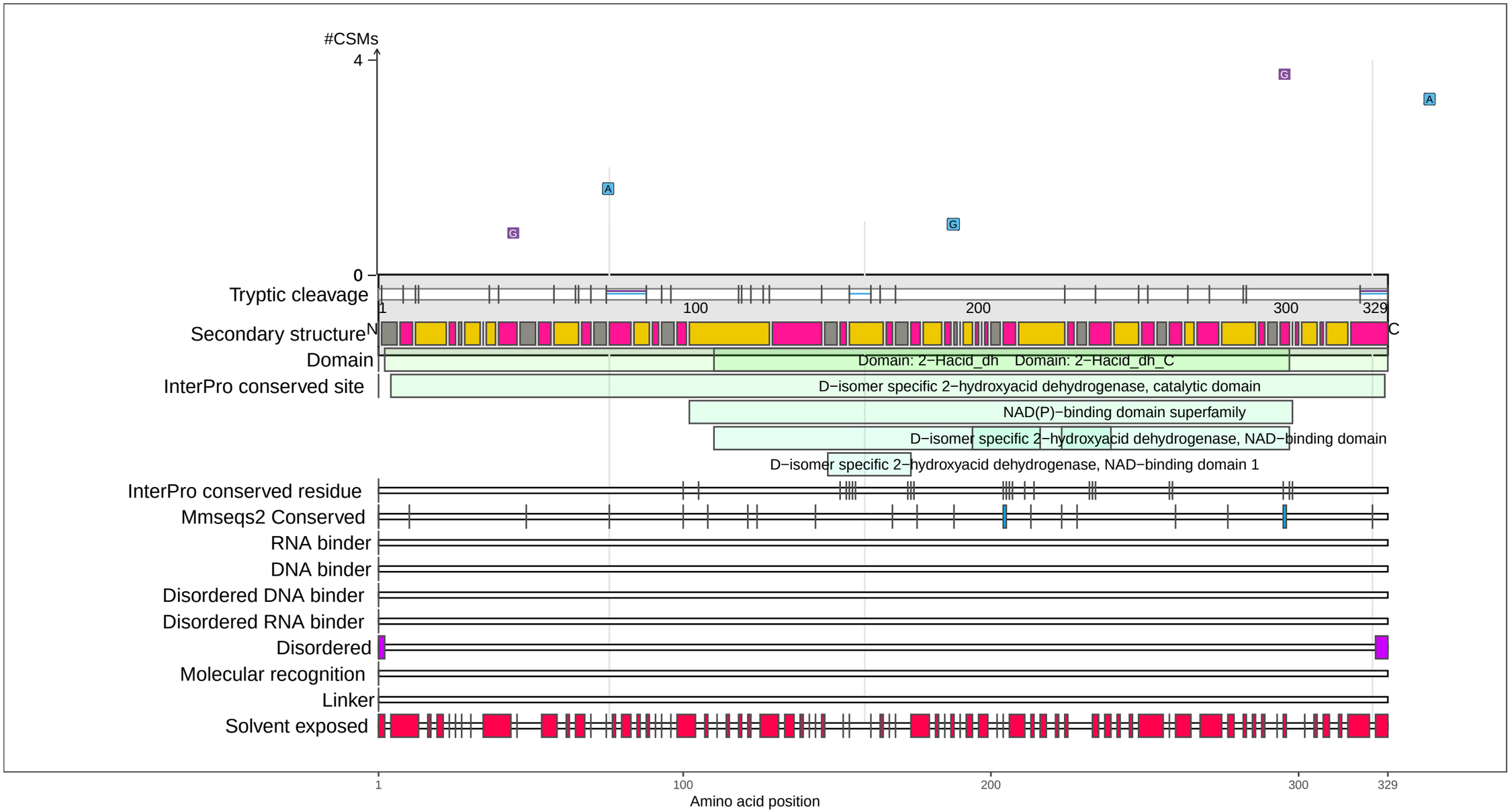
− RNA functions: not annotated

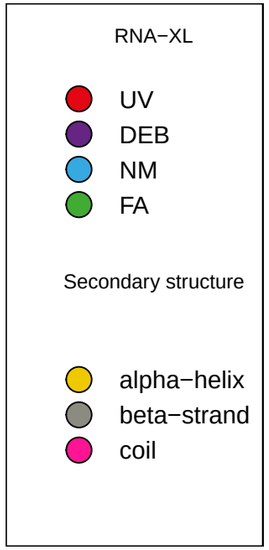


P52643
LDHD_ECOLI D−lactate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 69)
PAXdb K12 strain [ppm]: 2.87 (Q 88)
PAXdb E.coli [ppm]: 2.33 (Q 81)

− RNA functions: not annotated

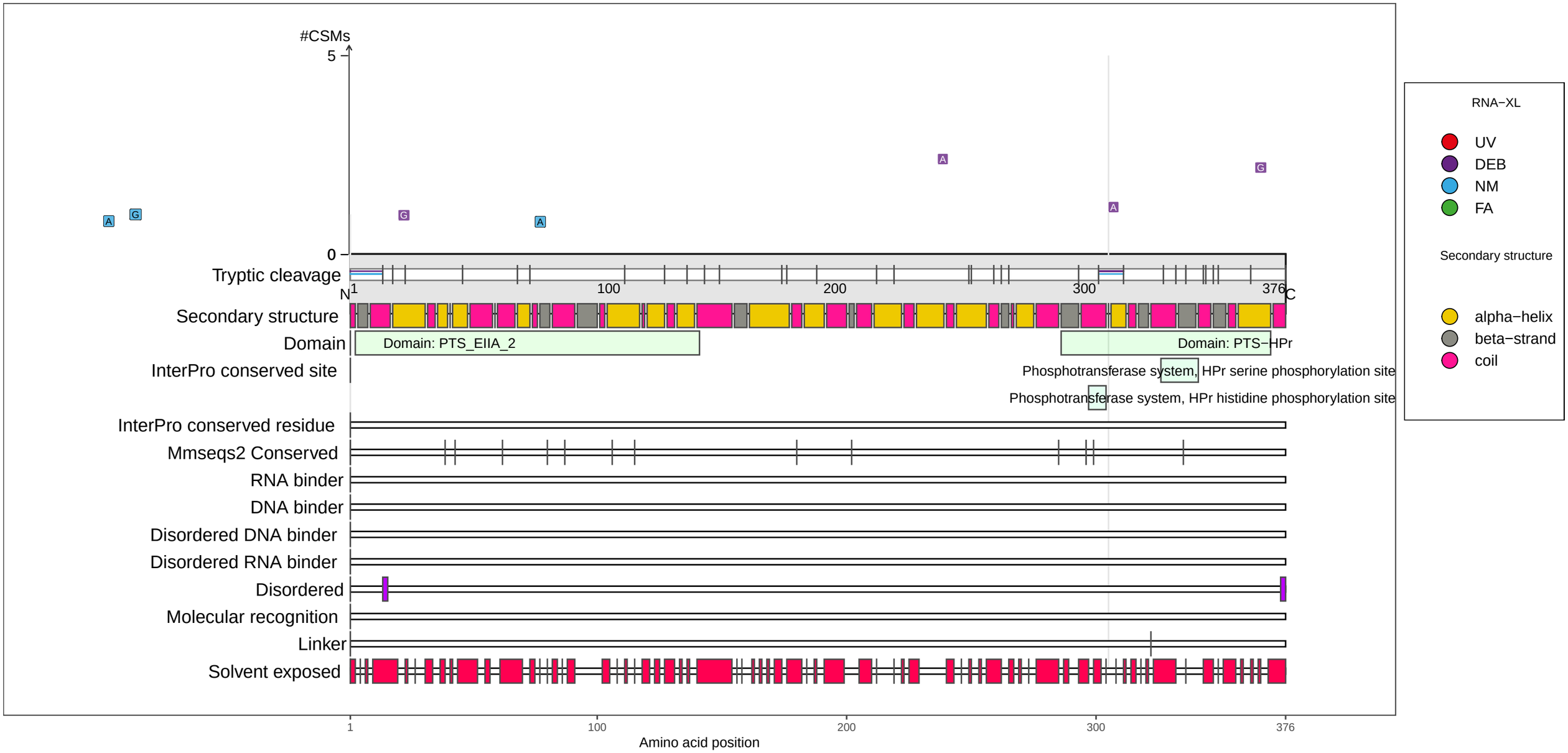




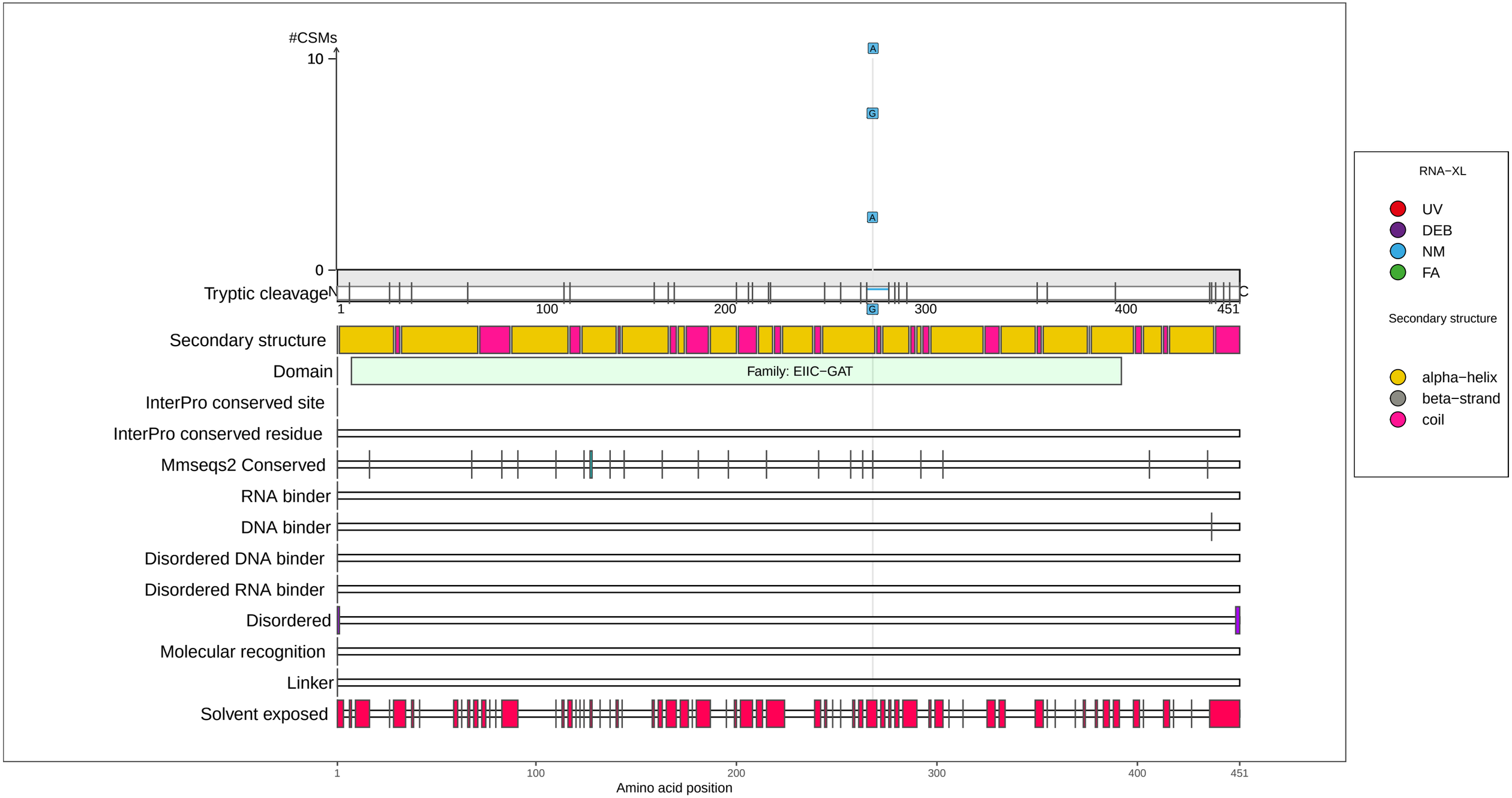
P69811
PTFAH_ECOLI Multiphosphoryl transfer protein

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 2.3 (Q 70)
PAXdb E.coli [ppm]: 2.06 (Q 74)

− RNA functions: not annotated



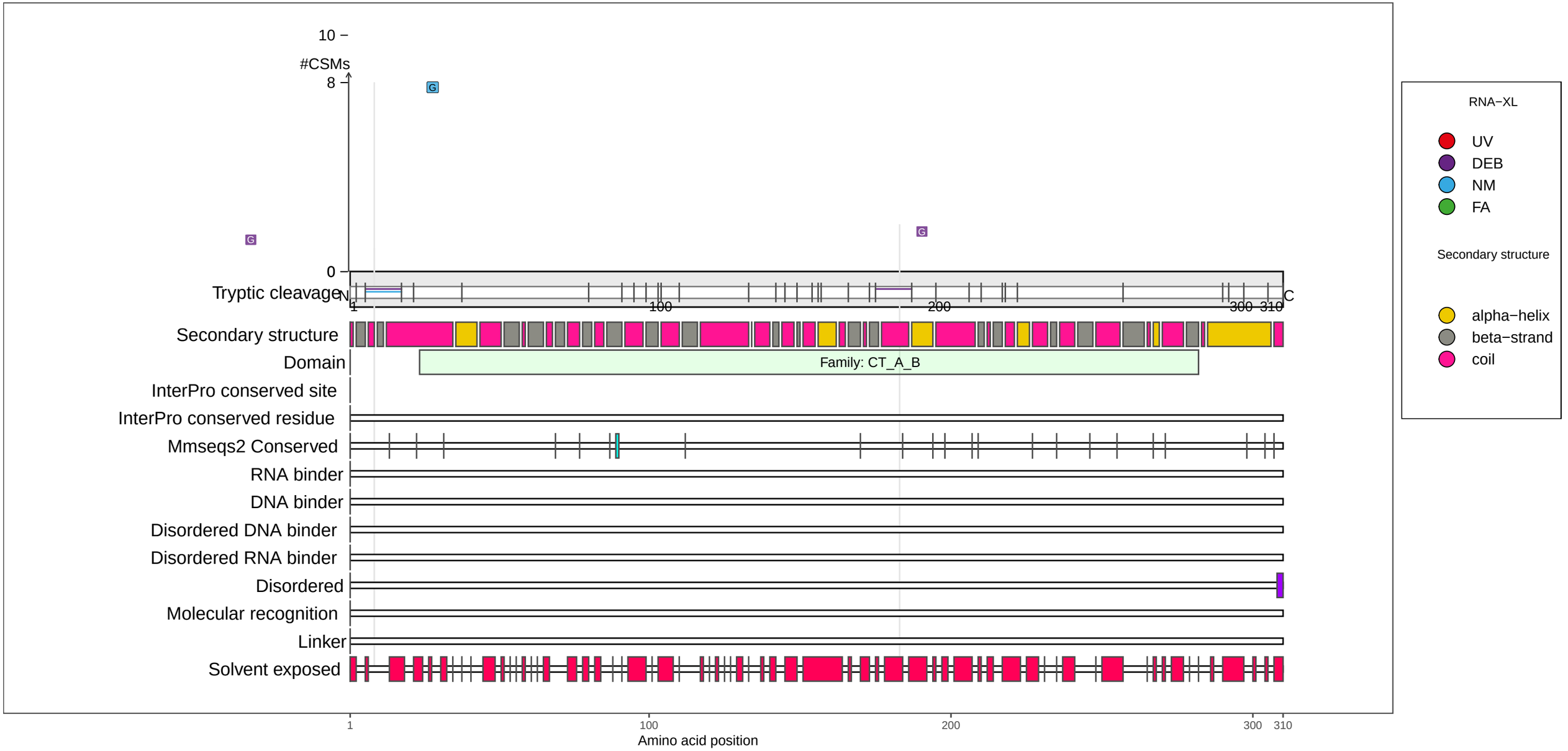
P69831
PTKC_ECOLI PTS system galactitol−specific EIIC component
− RNA functions: not annotated



P75745
PXPC_ECOLI 5−oxoprolinase subunit C

− Abundance:
tryptic [log10 Intensity]: 6.93 (Q 10)
PAXdb K12 strain [ppm]: 1.03 (Q 12)
PAXdb E.coli [ppm]: 1.83 (Q 68)

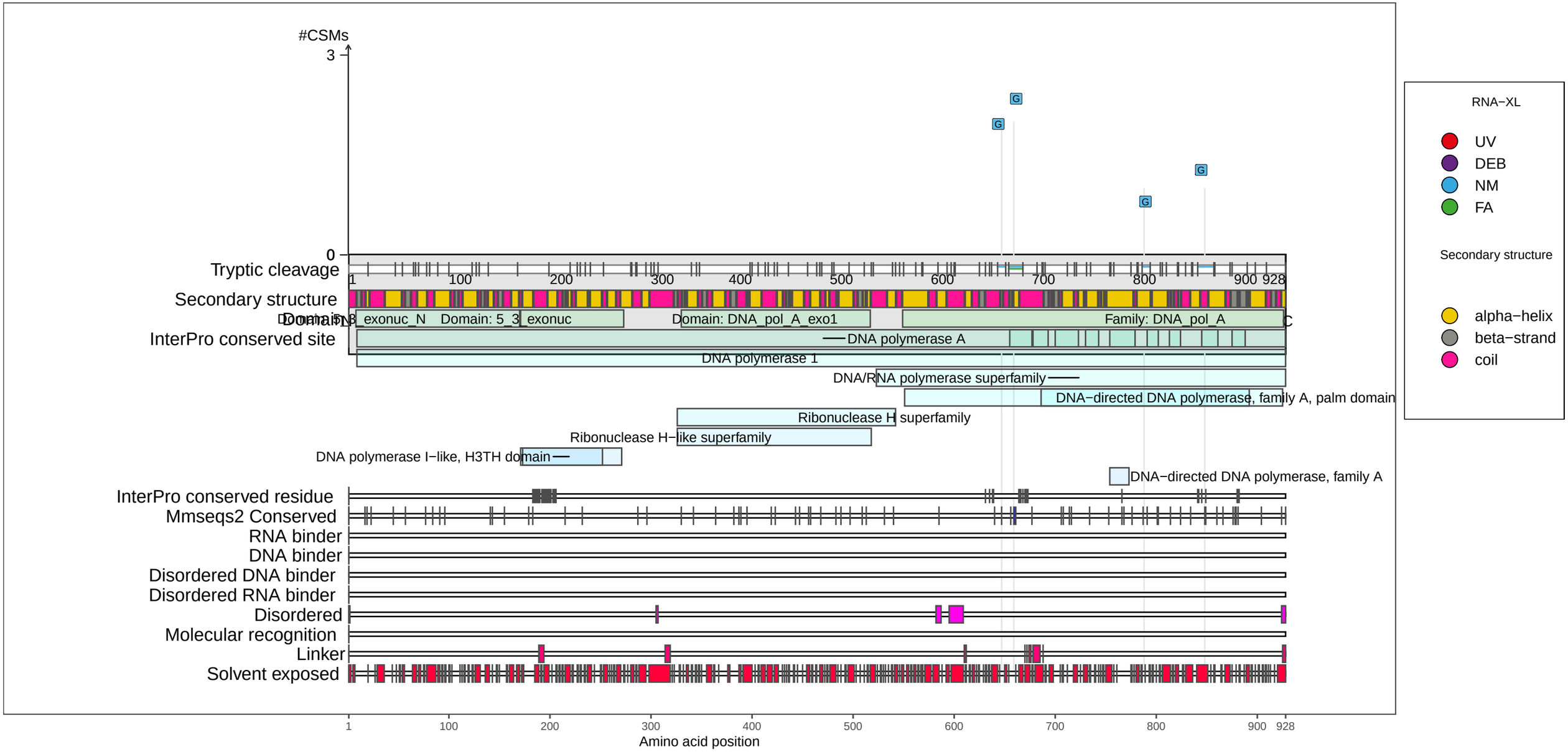
− RNA functions: not annotated



P00582
DPO1_ECOLI DNA polymerase I

− Abundance:
tryptic [log10 Intensity]: 8.85 (Q 85)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 2.47 (Q 85)

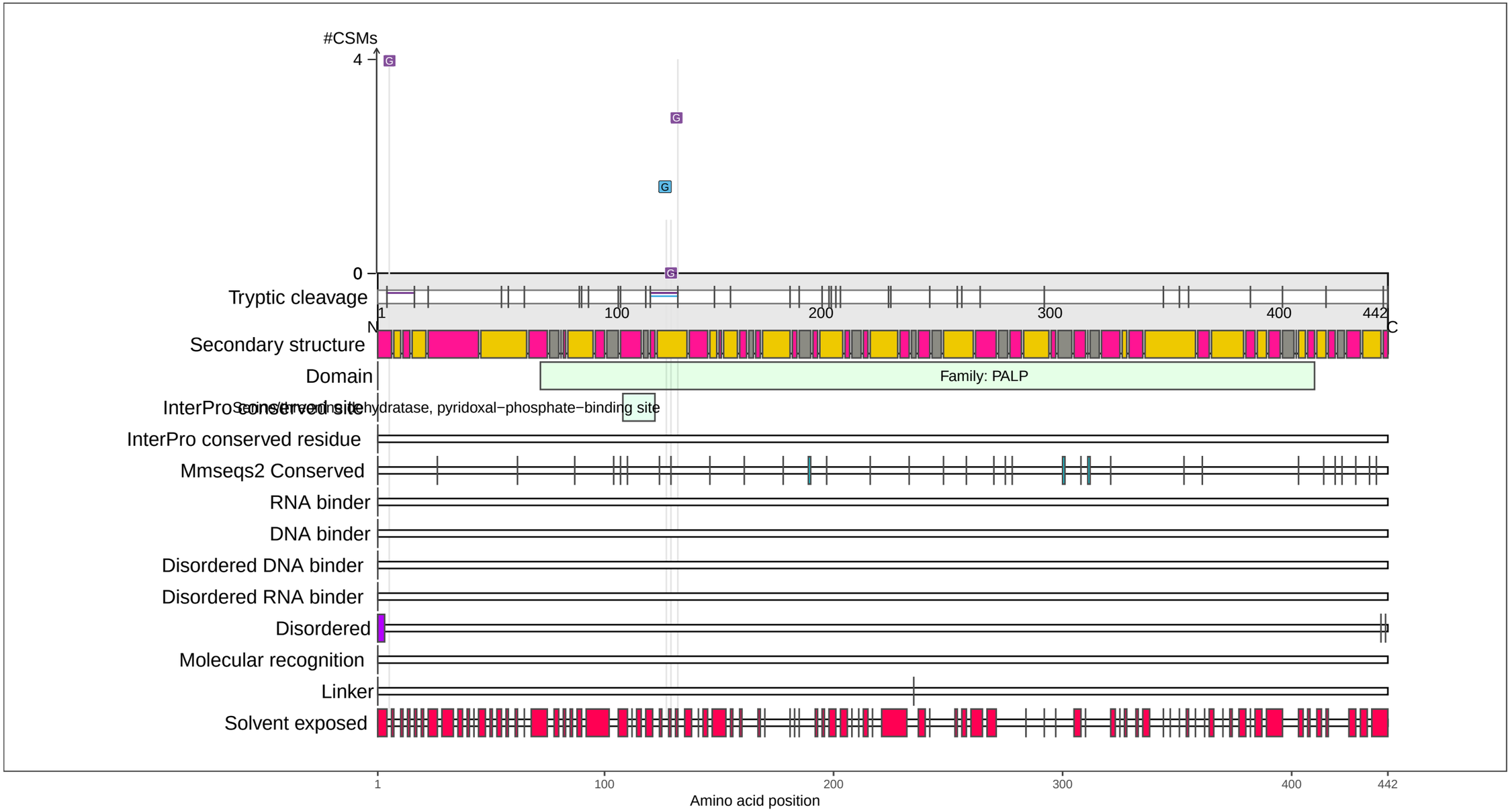
− RNA functions: not annotated

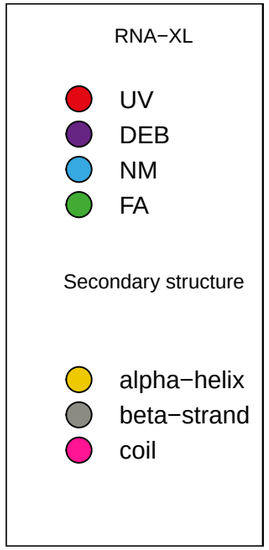


P00926
SDHD_ECOLI D−serine dehydratase

− Abundance:
tryptic [log10 Intensity]: 8.86 (Q 85)
PAXdb K12 strain [ppm]: 1.52 (Q 39)
PAXdb E.coli [ppm]: 1.16 (Q 51)

− RNA functions: not annotated

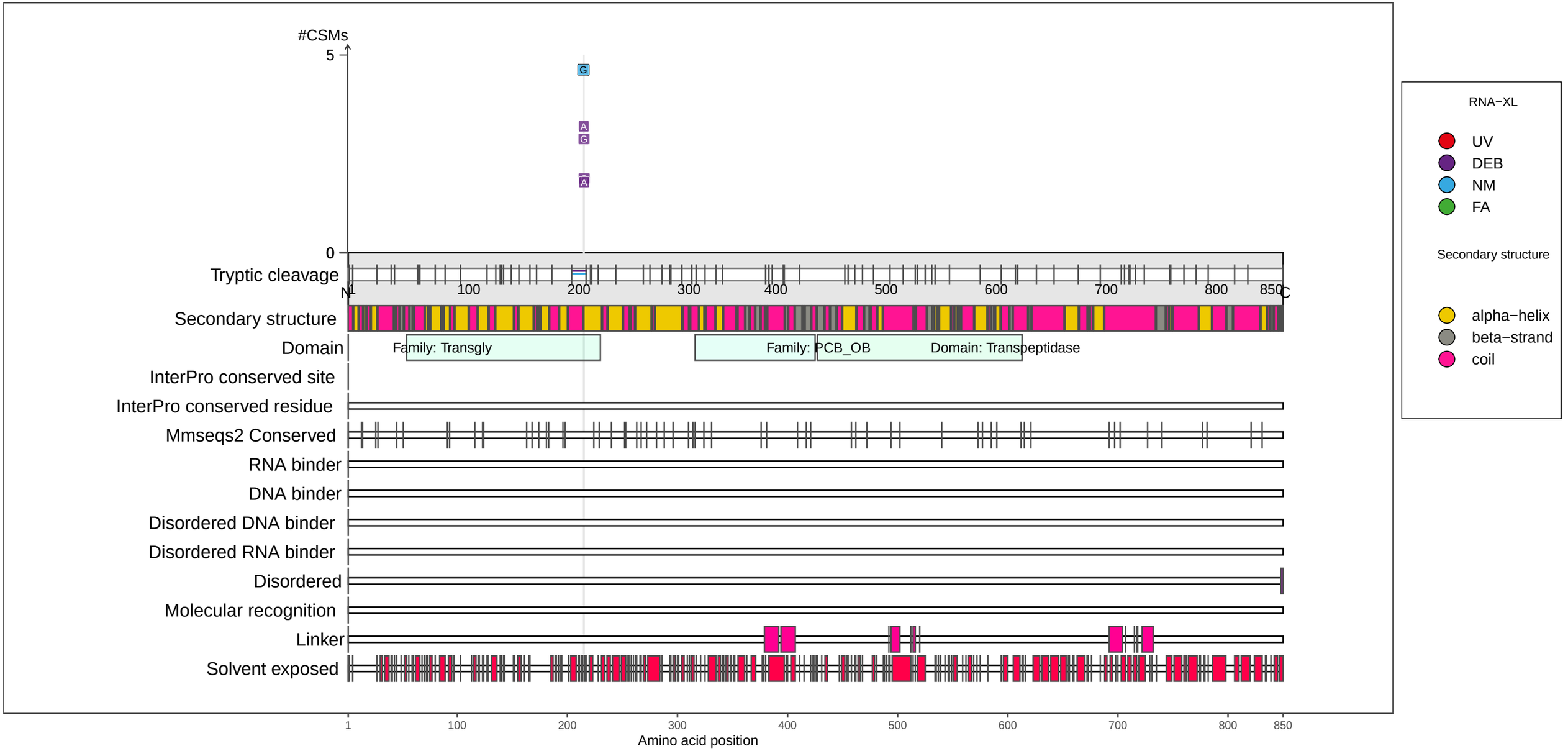




P02918
PBPA_ECOLI Penicillin−binding protein 1A

− Abundance:
tryptic [log10 Intensity]: 8.56 (Q 77)
PAXdb K12 strain [ppm]: 0.91 (Q 8)
PAXdb E.coli [ppm]: 0.94 (Q 46)

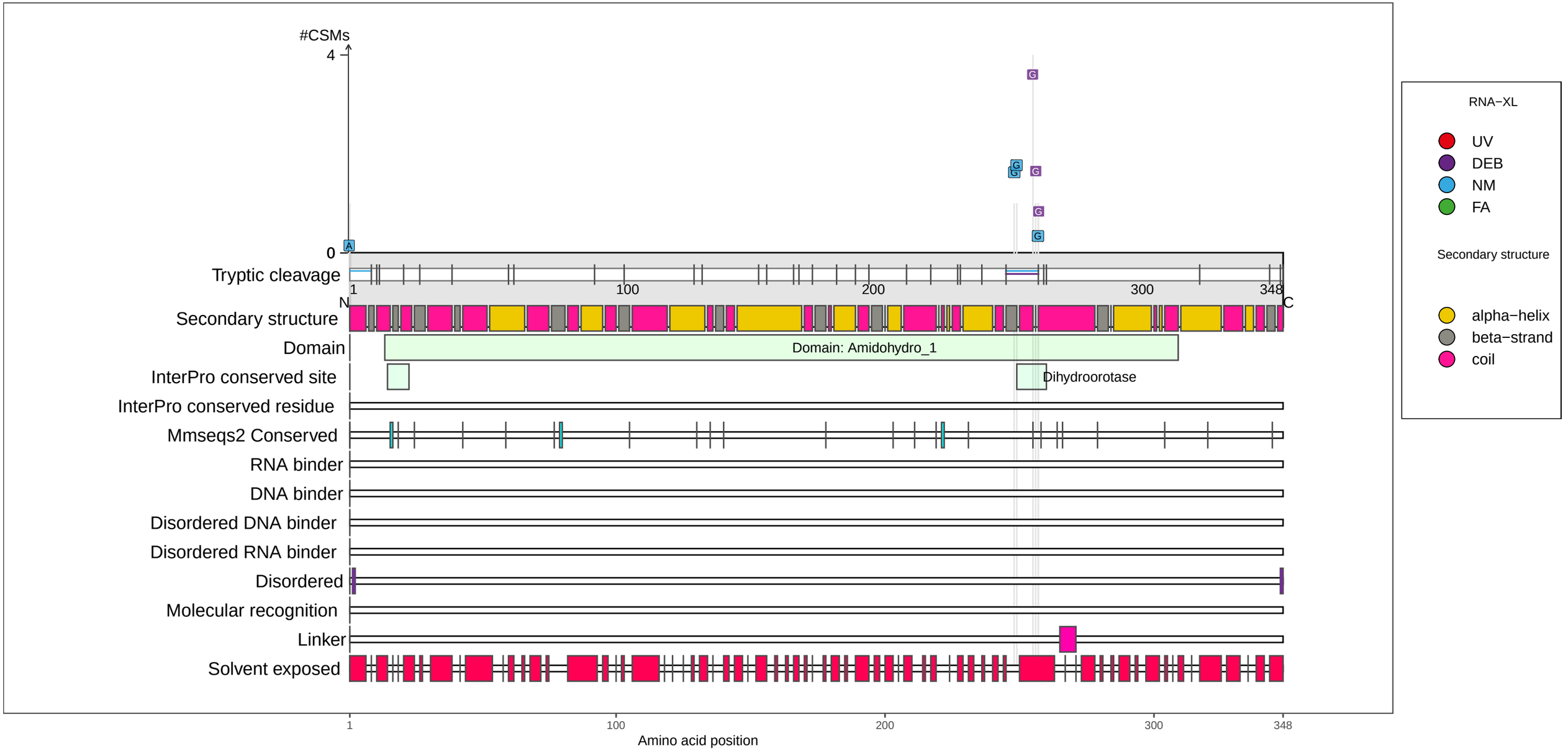
− RNA functions: not annotated



P05020
PYRC_ECOLI Dihydroorotase

− Abundance:
tryptic [log10 Intensity]: 7.37 (Q 28)
PAXdb K12 strain [ppm]: 1.65 (Q 47)
PAXdb E.coli [ppm]: 2.65 (Q 89)

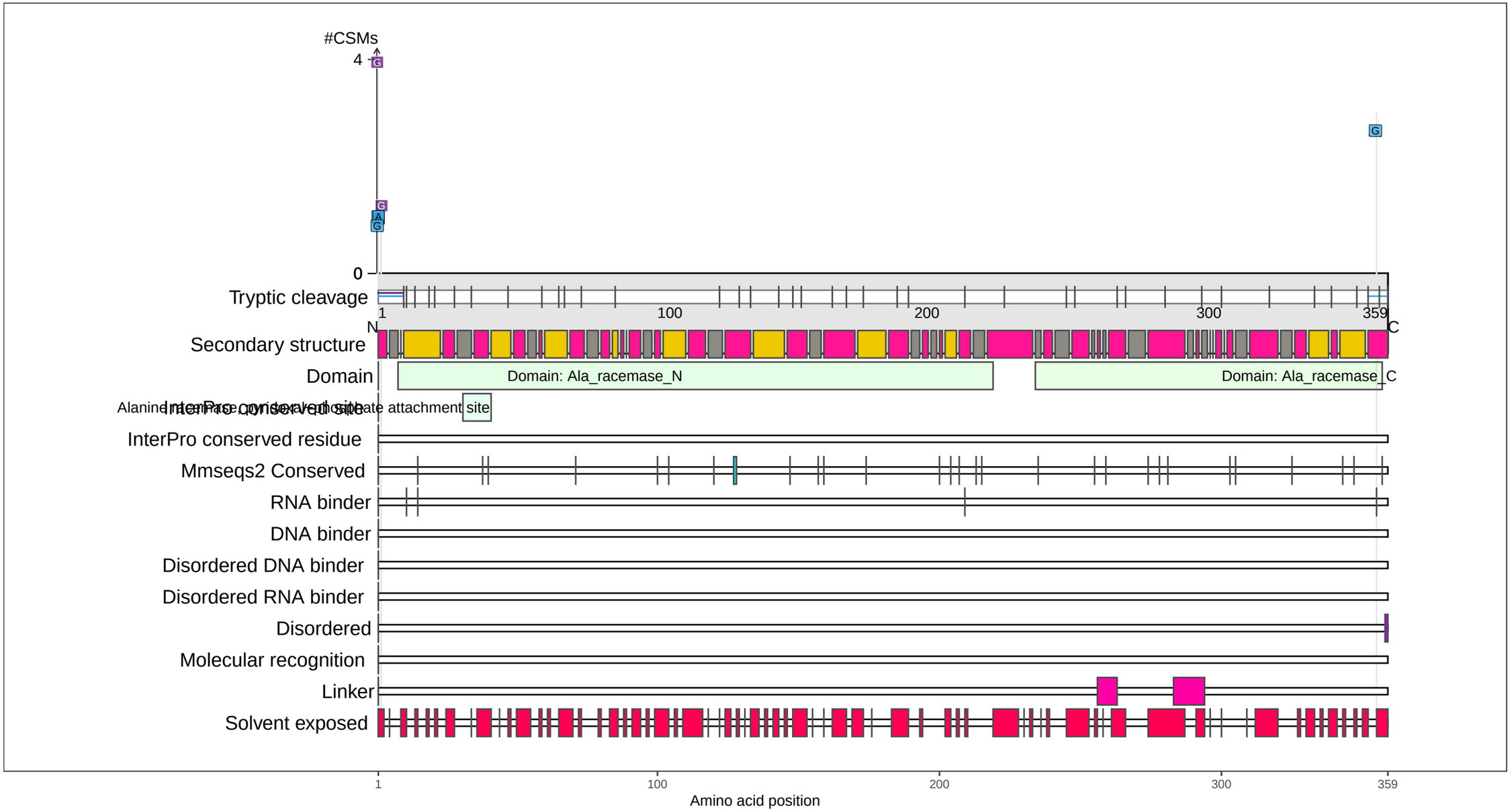
− RNA functions: not annotated



P0A6B4
ALR1_ECOLI Alanine racemase, biosynthetic

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 1.48 (Q 59)

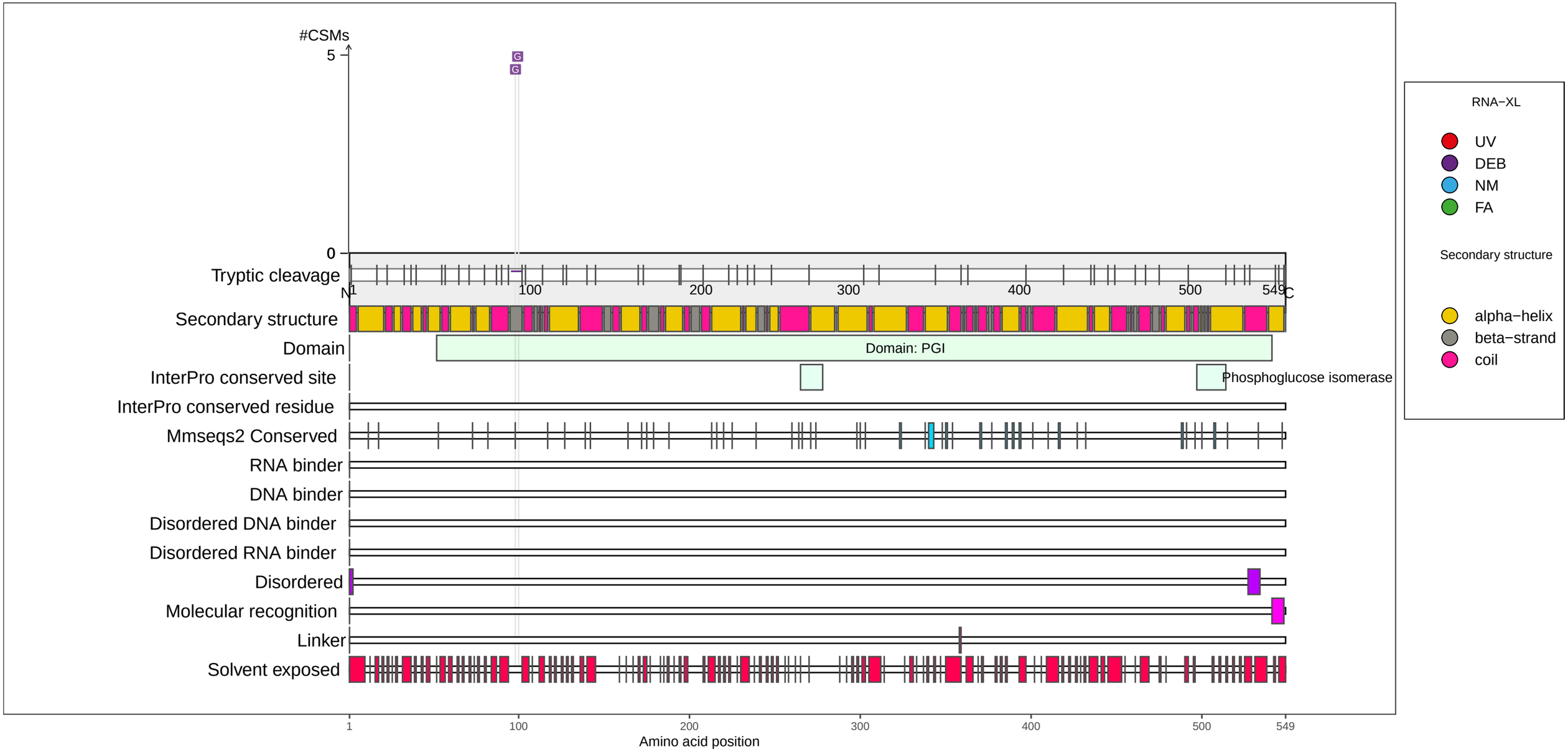
− RNA functions: not annotated



P0A6T1
G6PI_ECOLI Glucose−6−phosphate isomerase

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 2.63 (Q 82)
PAXdb E.coli [ppm]: 3.04 (Q 95)

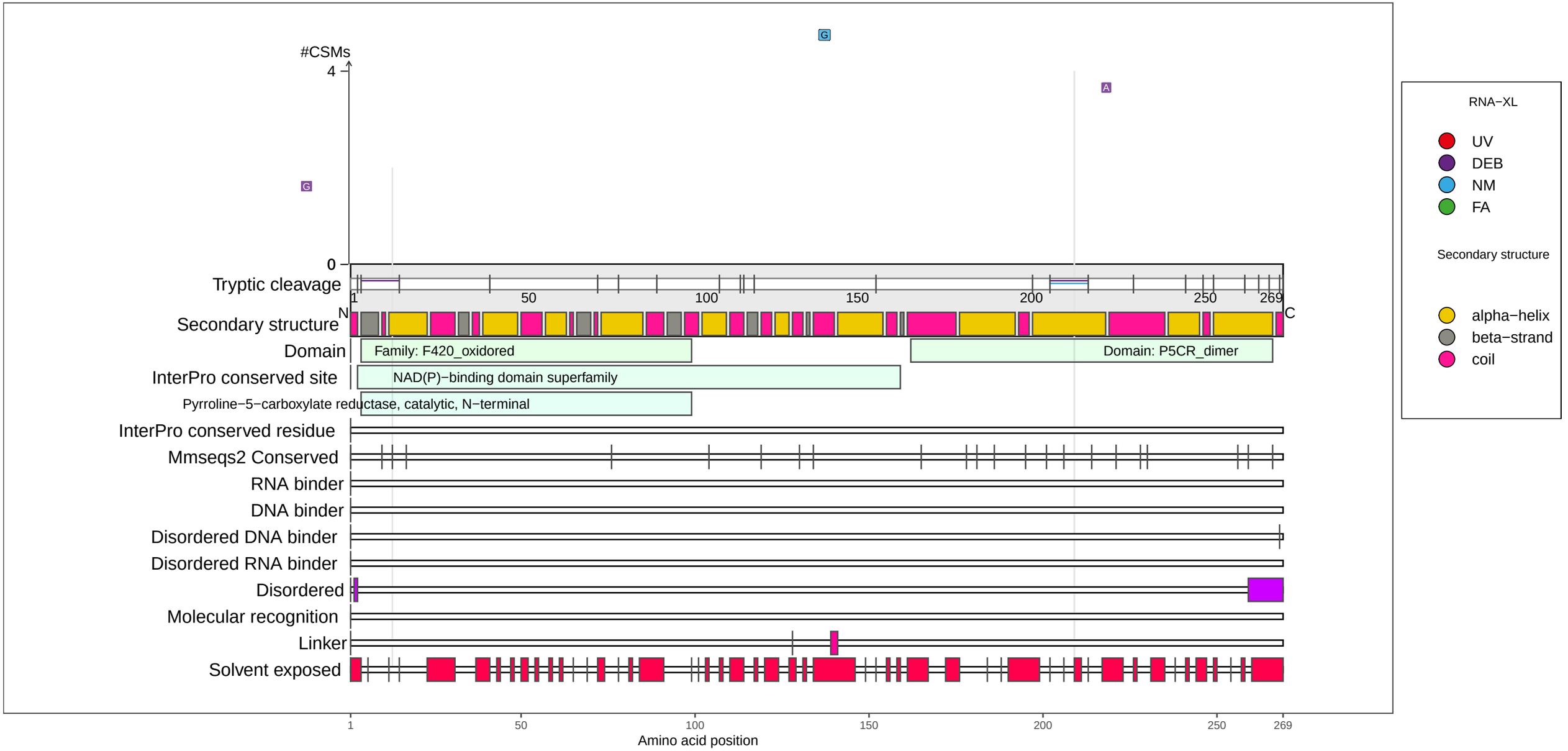
− RNA functions: not annotated



P0A9L8
P5CR_ECOLI Pyrroline−5−carboxylate reductase

− Abundance:
tryptic [log10 Intensity]: 8.62 (Q 79)
PAXdb K12 strain [ppm]: 2.38 (Q 73)
PAXdb E.coli [ppm]: 2.47 (Q 85)

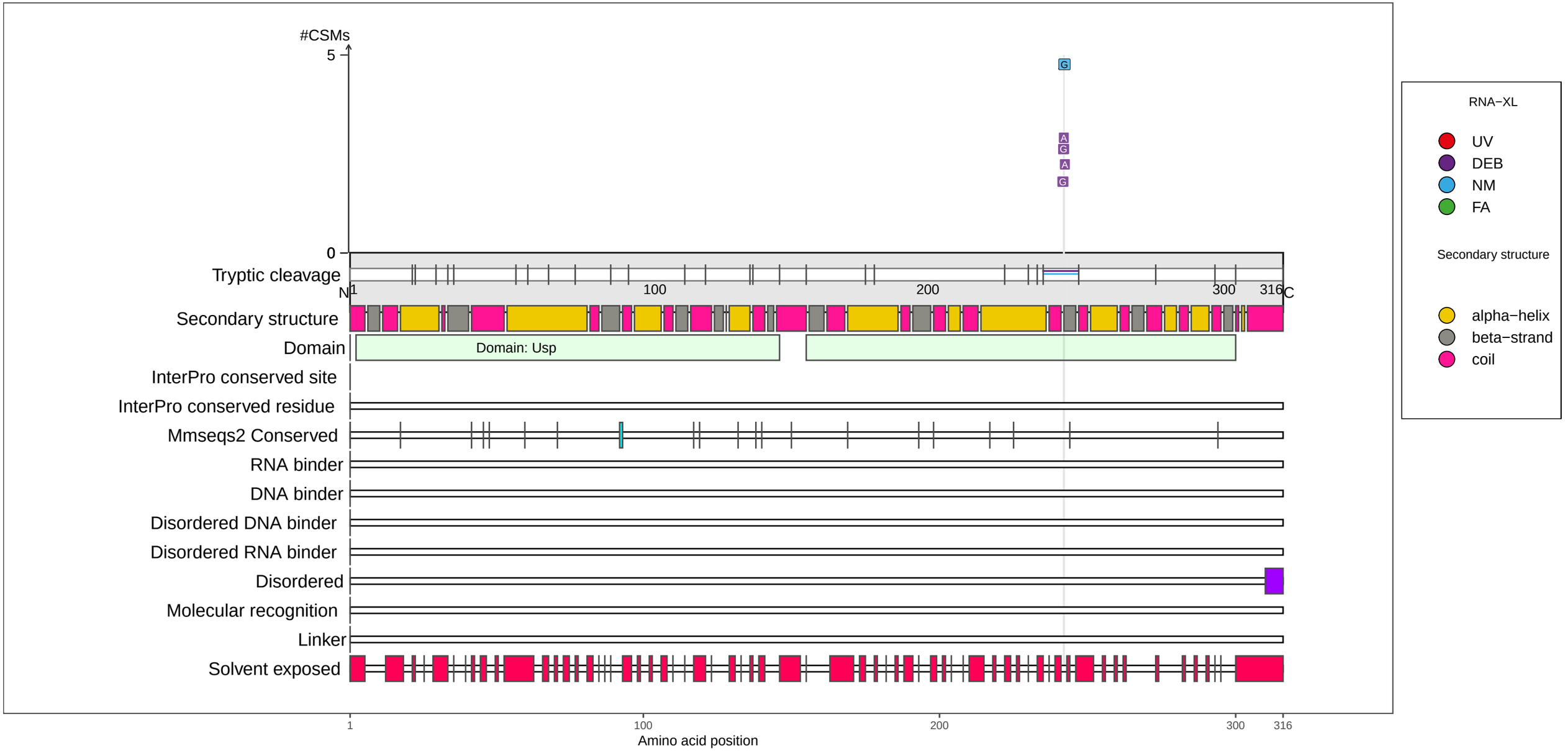
− RNA functions: not annotated



P0AAC0
USPE_ECOLI Universal stress protein E

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 2.08 (Q 63)
PAXdb E.coli [ppm]: 2.89 (Q 93)

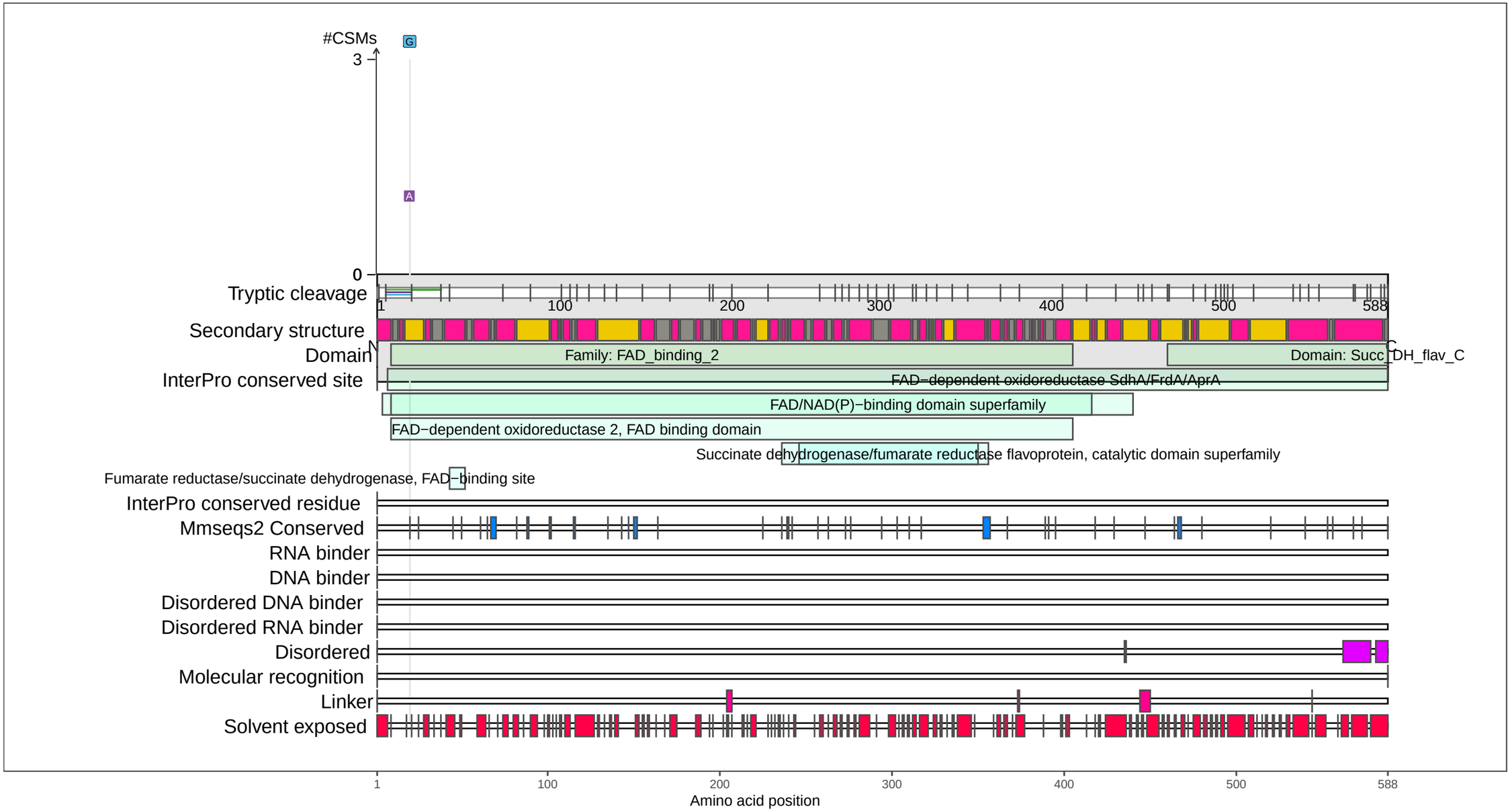
− RNA functions: not annotated



P0AC41
SDHA_ECOLI Succinate dehydrogenase flavoprotein subunit

− Abundance:
tryptic [log10 Intensity]: 8.79 (Q 83)
PAXdb K12 strain [ppm]: 2.28 (Q 69)
PAXdb E.coli [ppm]: 2.8 (Q 92)

− RNA functions: not annotated



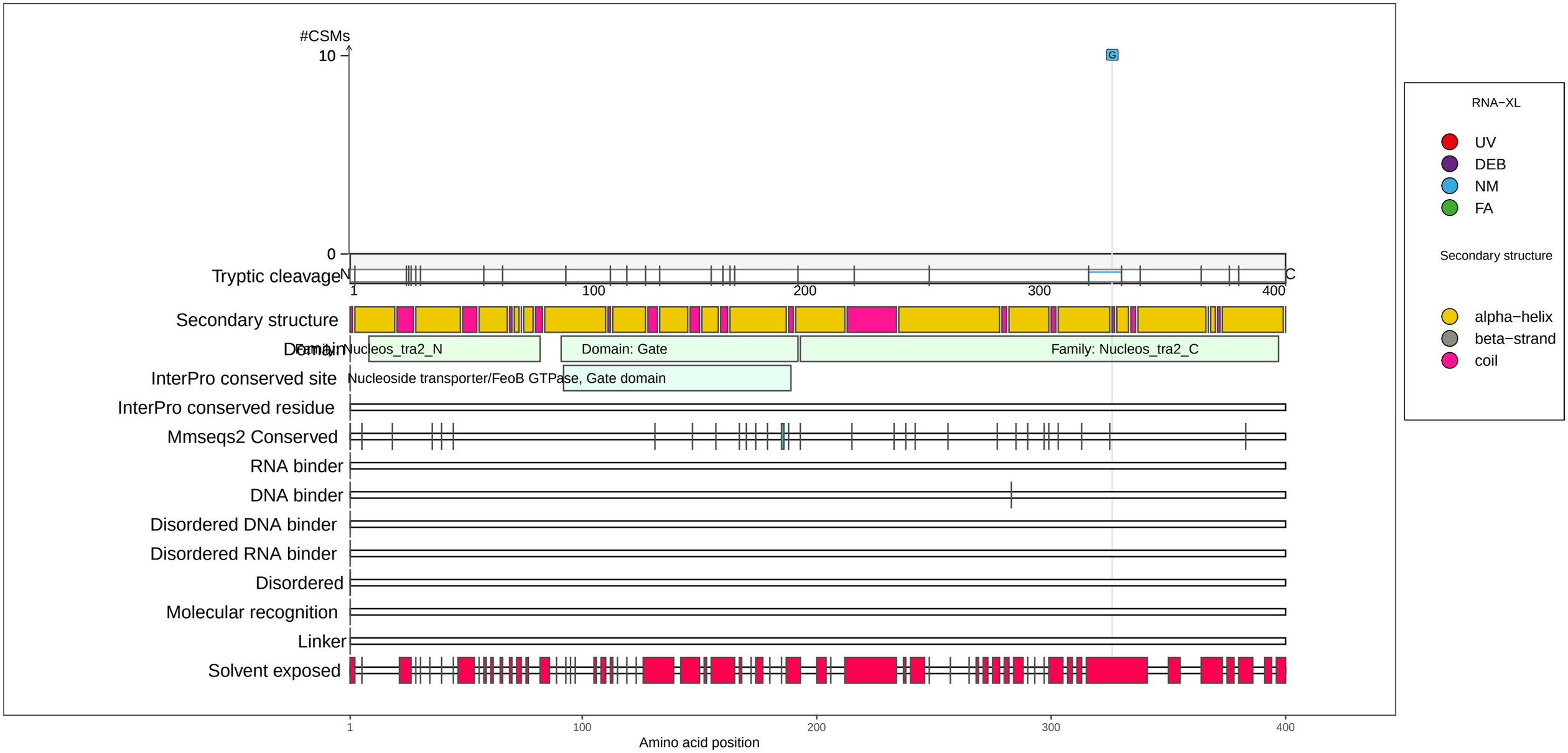
RNA−XL
UV
DEB
NM
FA

Secondary structure
alpha−helix
beta−strand
coil

P0AFF2
NUPC_ECOLI Nucleoside permease NupC

− Abundance:
tryptic [log10 Intensity]: 6.85 (Q 8)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.48 (Q 59)

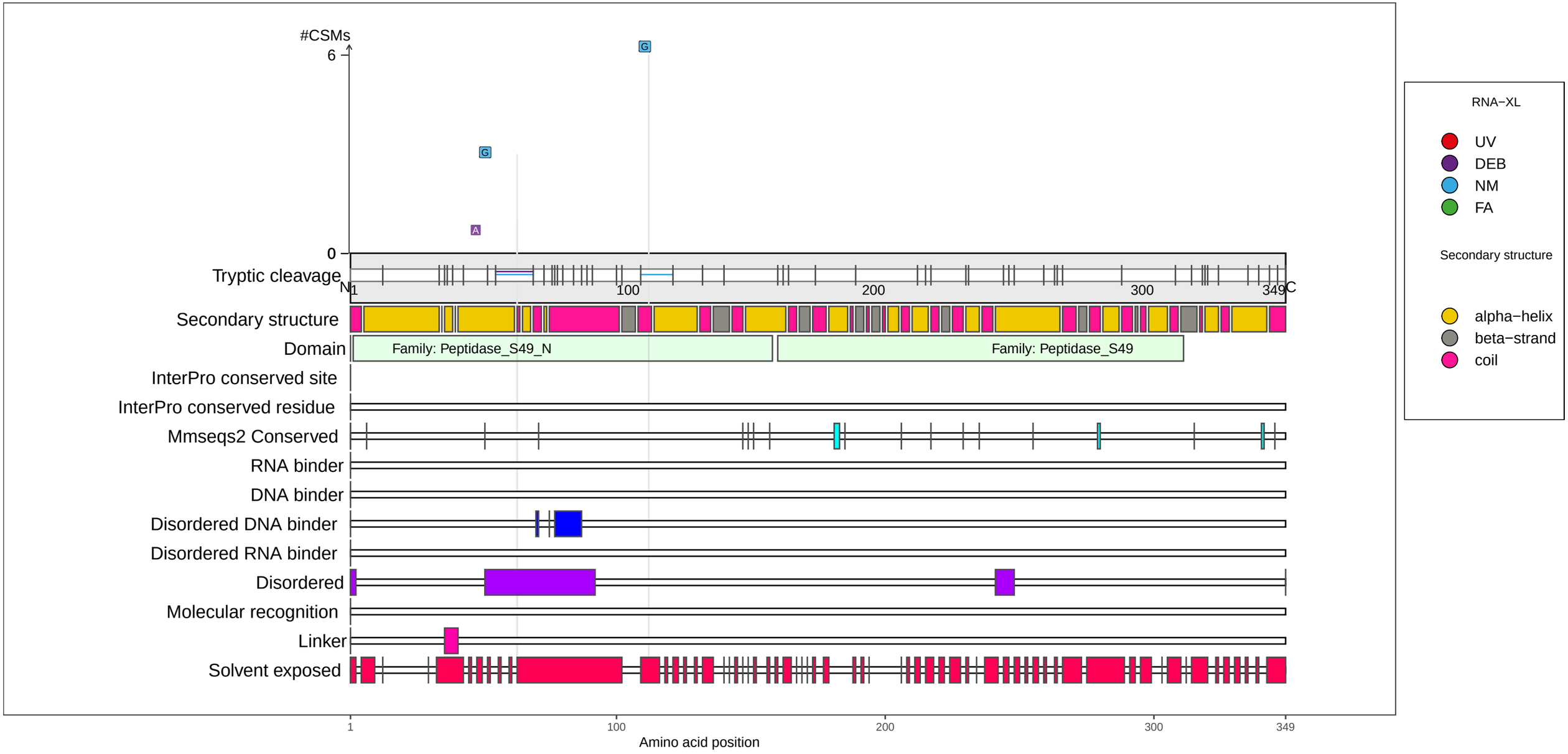
− RNA functions: not annotated



P0AG14
SOHB_ECOLI Probable protease SohB

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 2.24 (Q 79)

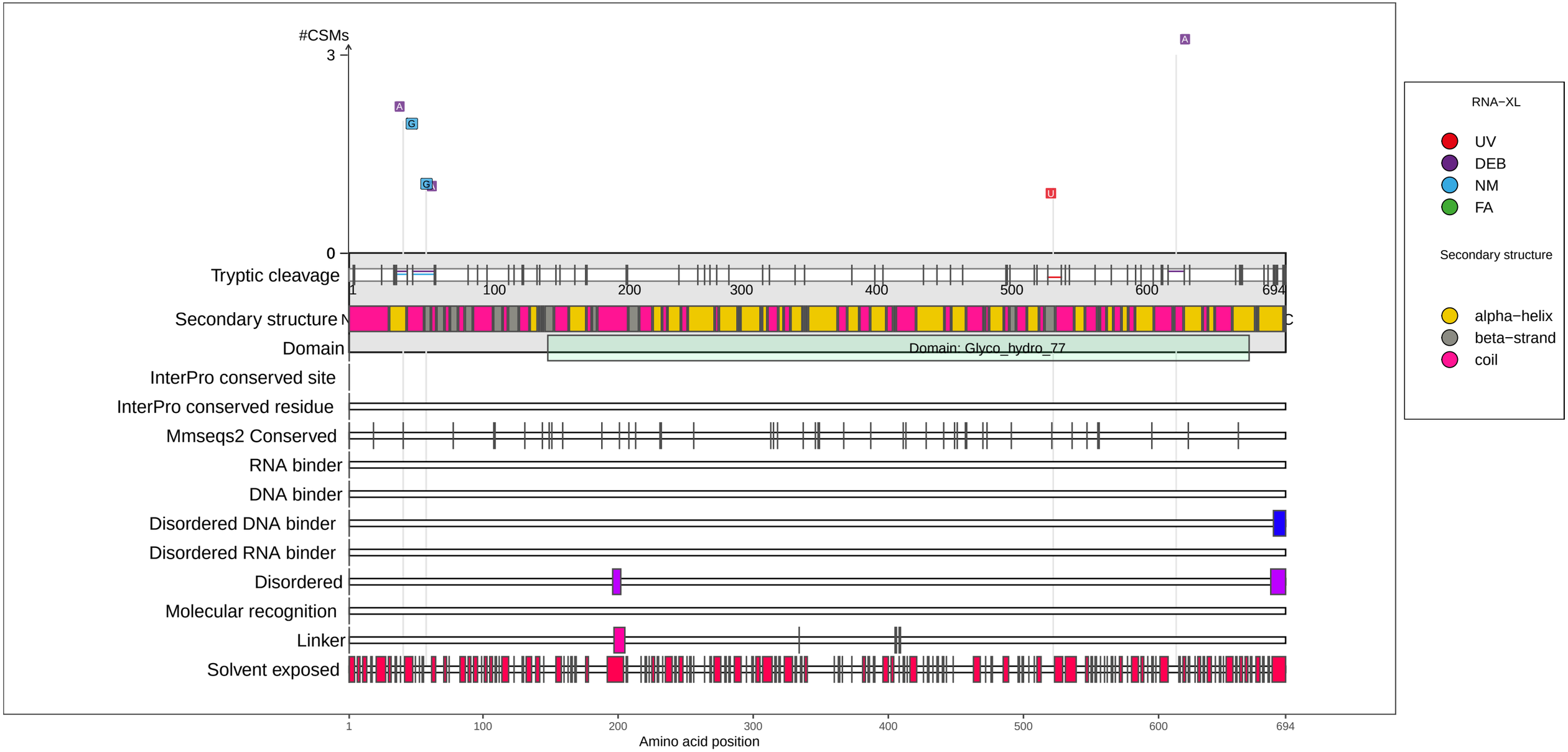
− RNA functions: not annotated



P15977
MALQ_ECOLI 4−alpha−glucanotransferase

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 68)
PAXdb K12 strain [ppm]: 2.64 (Q 82)
PAXdb E.coli [ppm]: 1.59 (Q 62)

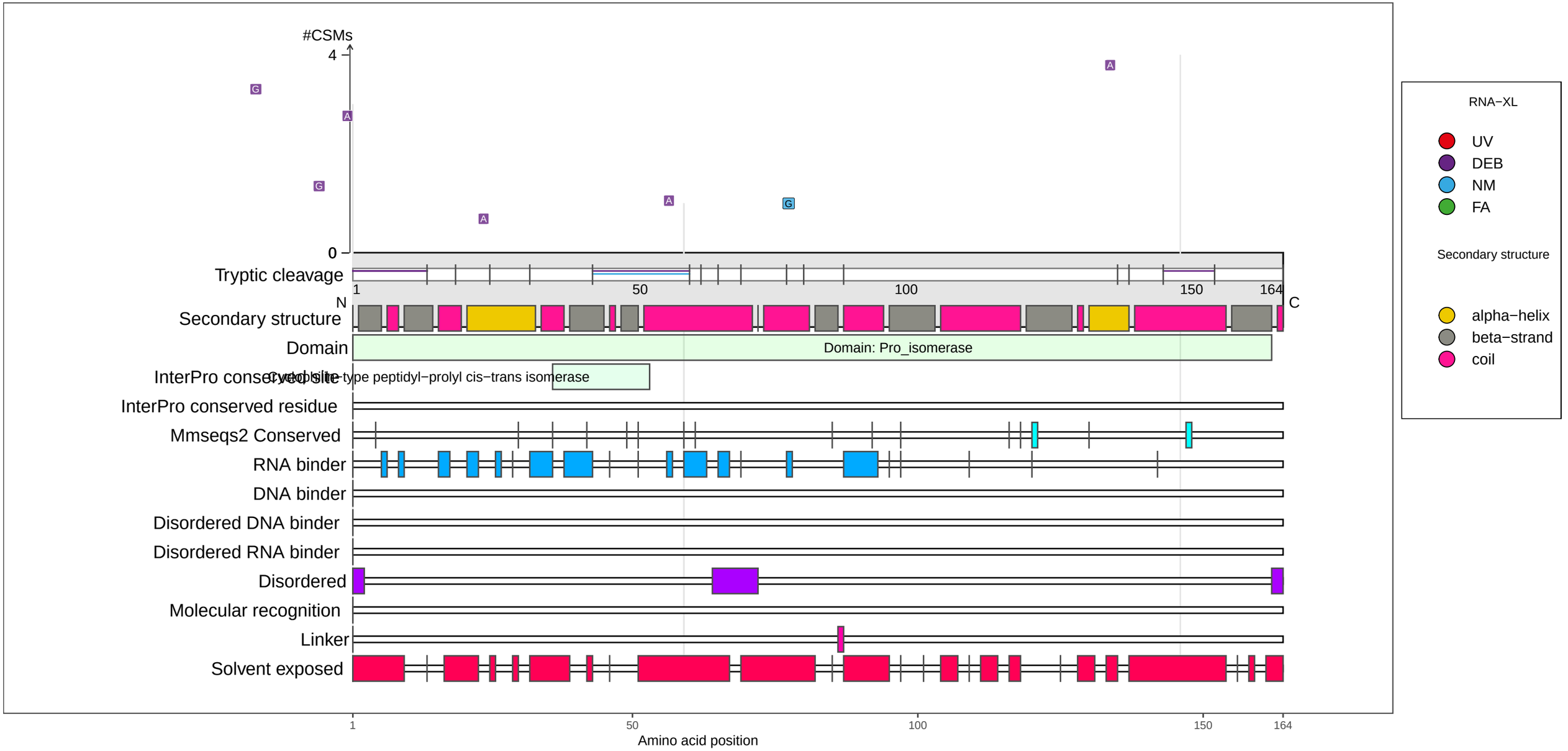
− RNA functions: not annotated



P23869
PPIB_ECOLI Peptidyl−prolyl cis−trans isomerase B

− Abundance:
tryptic [log10 Intensity]: 9.32 (Q 94)
PAXdb K12 strain [ppm]: 3.65 (Q 98)
PAXdb E.coli [ppm]: 3.21 (Q 97)

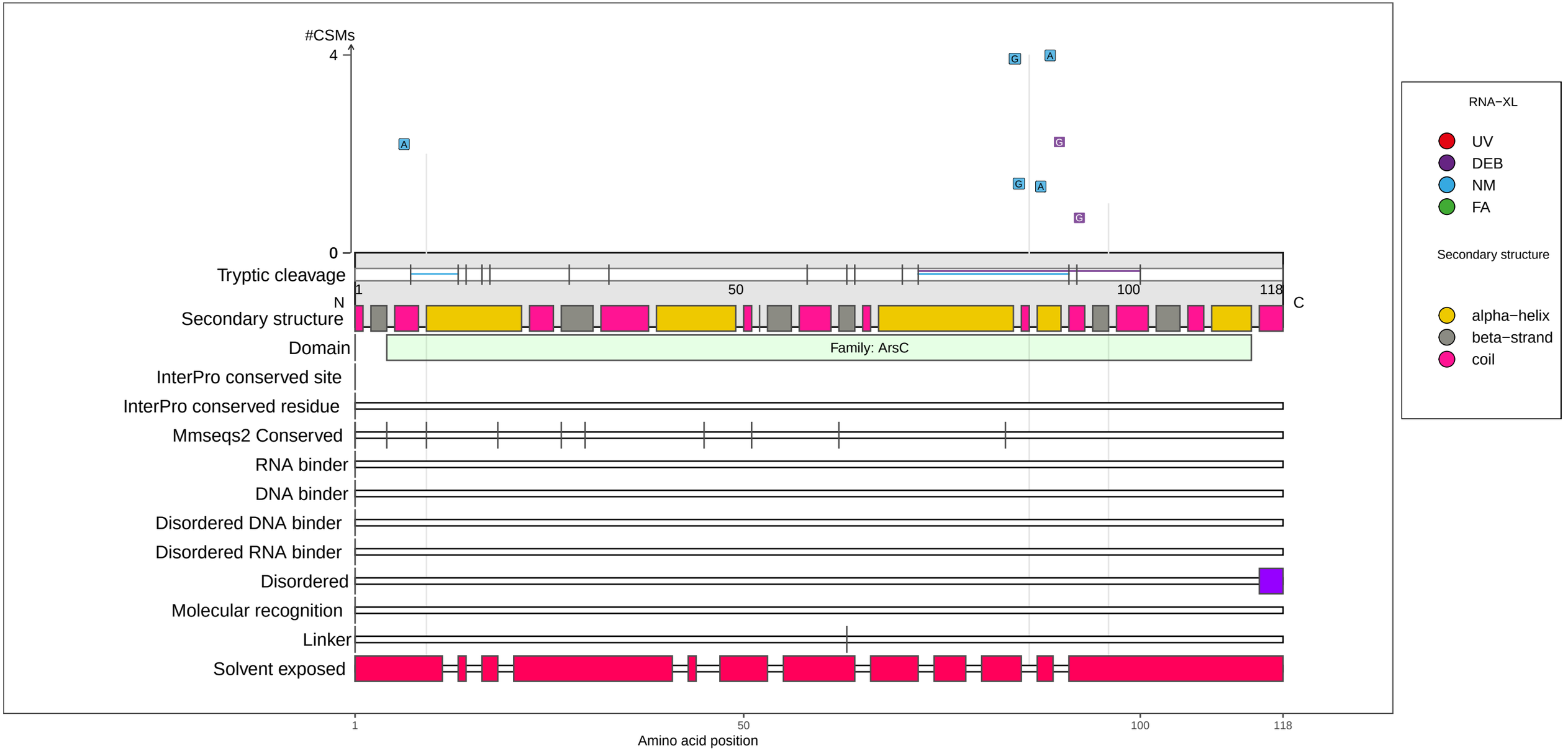
− RNA functions: not annotated



P24178
YFFB_ECOLI Protein YffB

− Abundance:
tryptic [log10 Intensity]: 7.55 (Q 37)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 2.25 (Q 79)

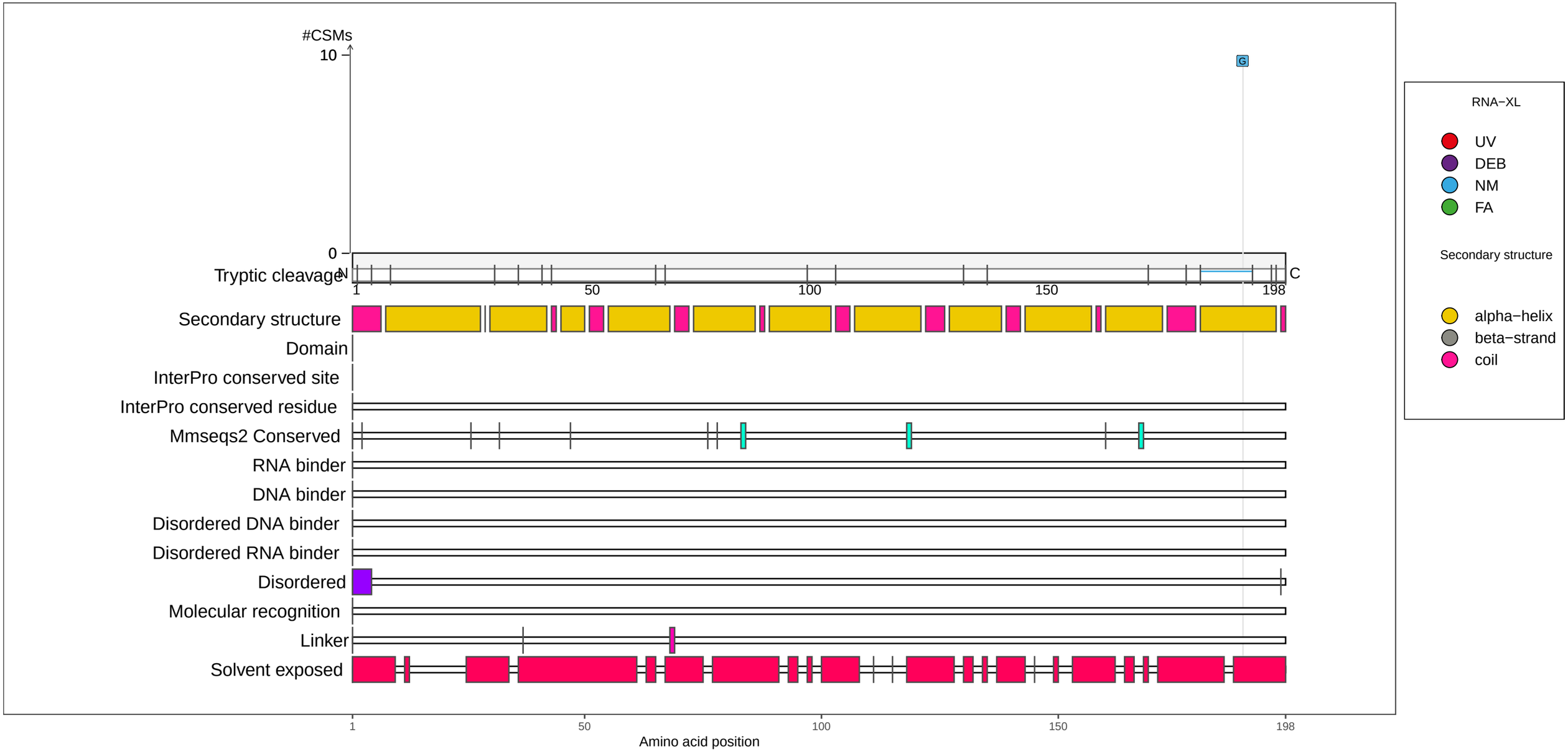
− RNA functions: not annotated



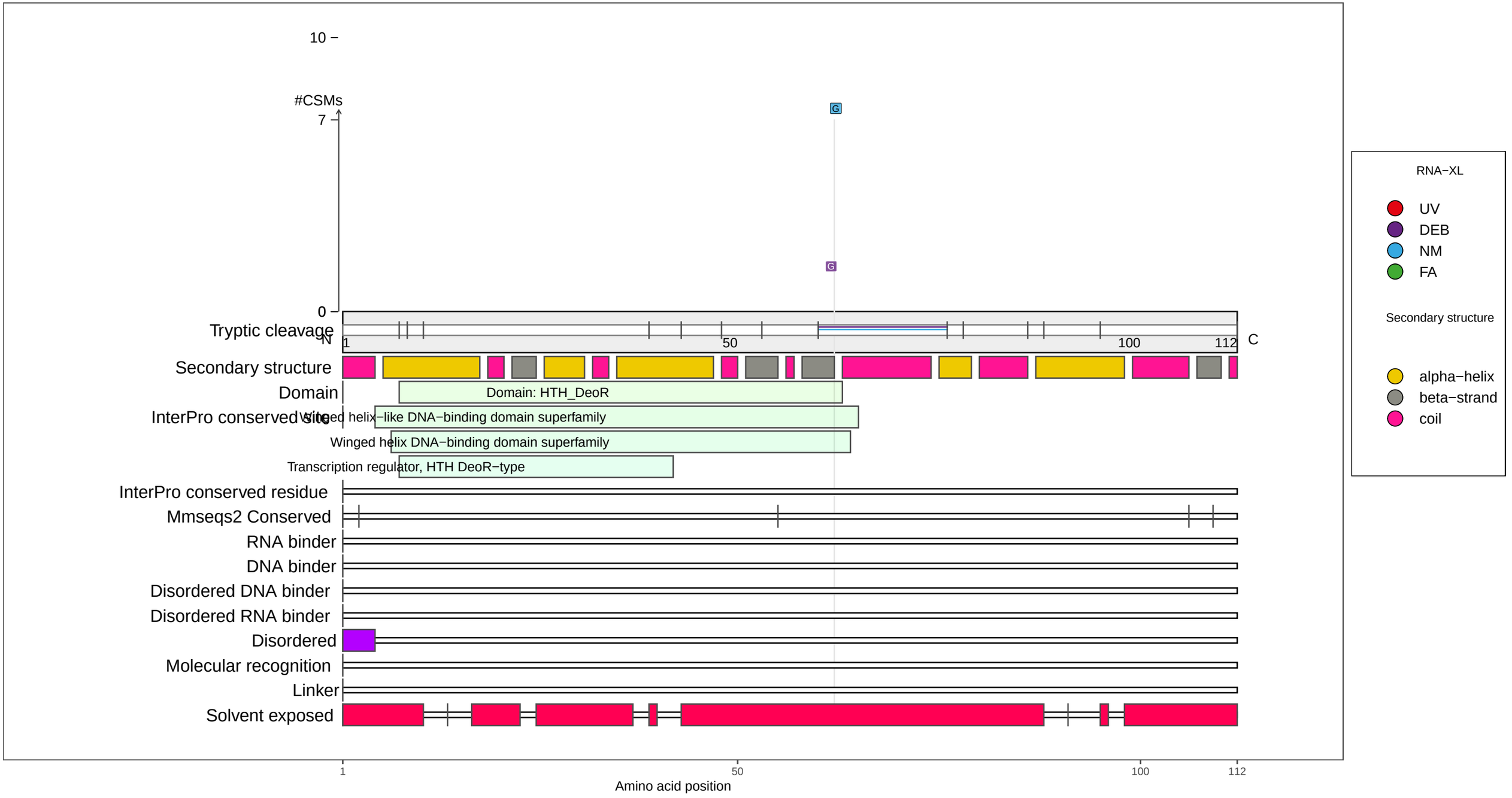
P32712
NRFG_ECOLI Formate−dependent nitrite reductase complex subunit NrfG

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

− RNA functions: not annotated



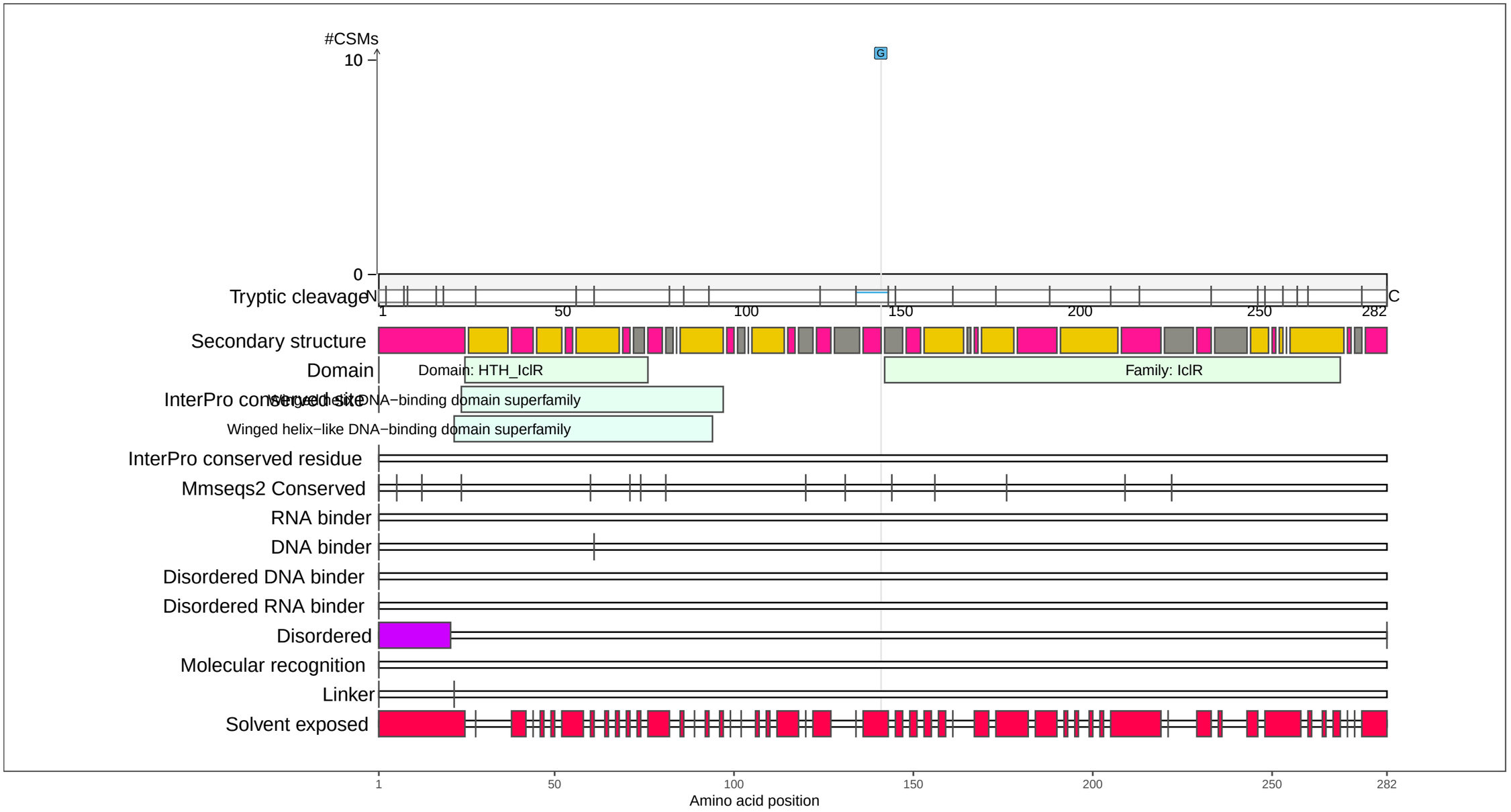
P36930
GATR_ECOLI Putative galactitol utilization operon repressor
− RNA functions: not annotated



P37671
YIAJ_ECOLI DNA−binding transcriptional repressor YiaJ

− Abundance:
tryptic [log10 Intensity]: 7.6 (Q 40)
PAXdb K12 strain [ppm]: 1.05 (Q 13)
PAXdb E.coli [ppm]: 1.74 (Q 66)

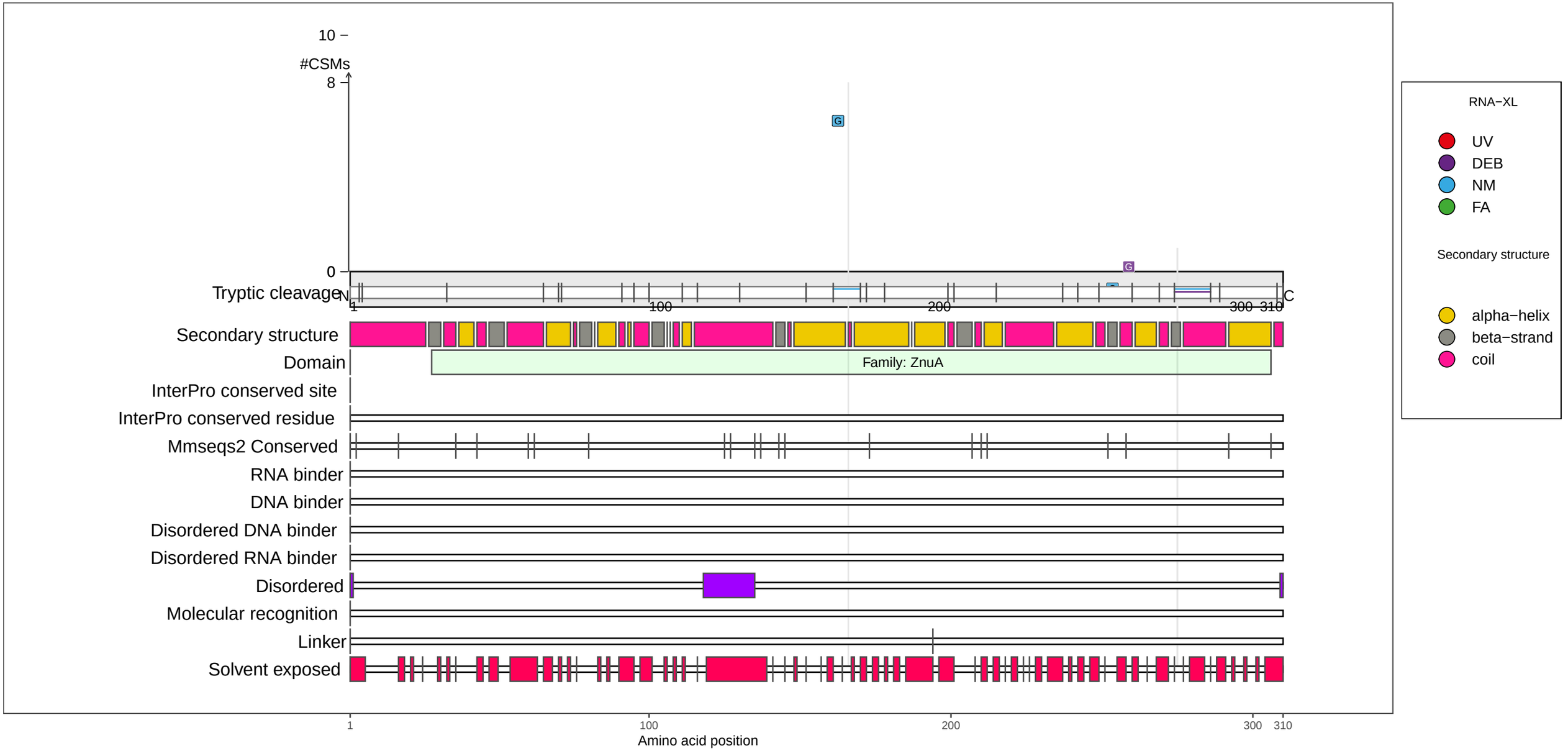
− RNA functions: not annotated



P39172
ZNUA_ECOLI High−affinity zinc uptake system protein ZnuA

− Abundance:
tryptic [log10 Intensity]: 8.23 (Q 67)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 2.99 (Q 95)

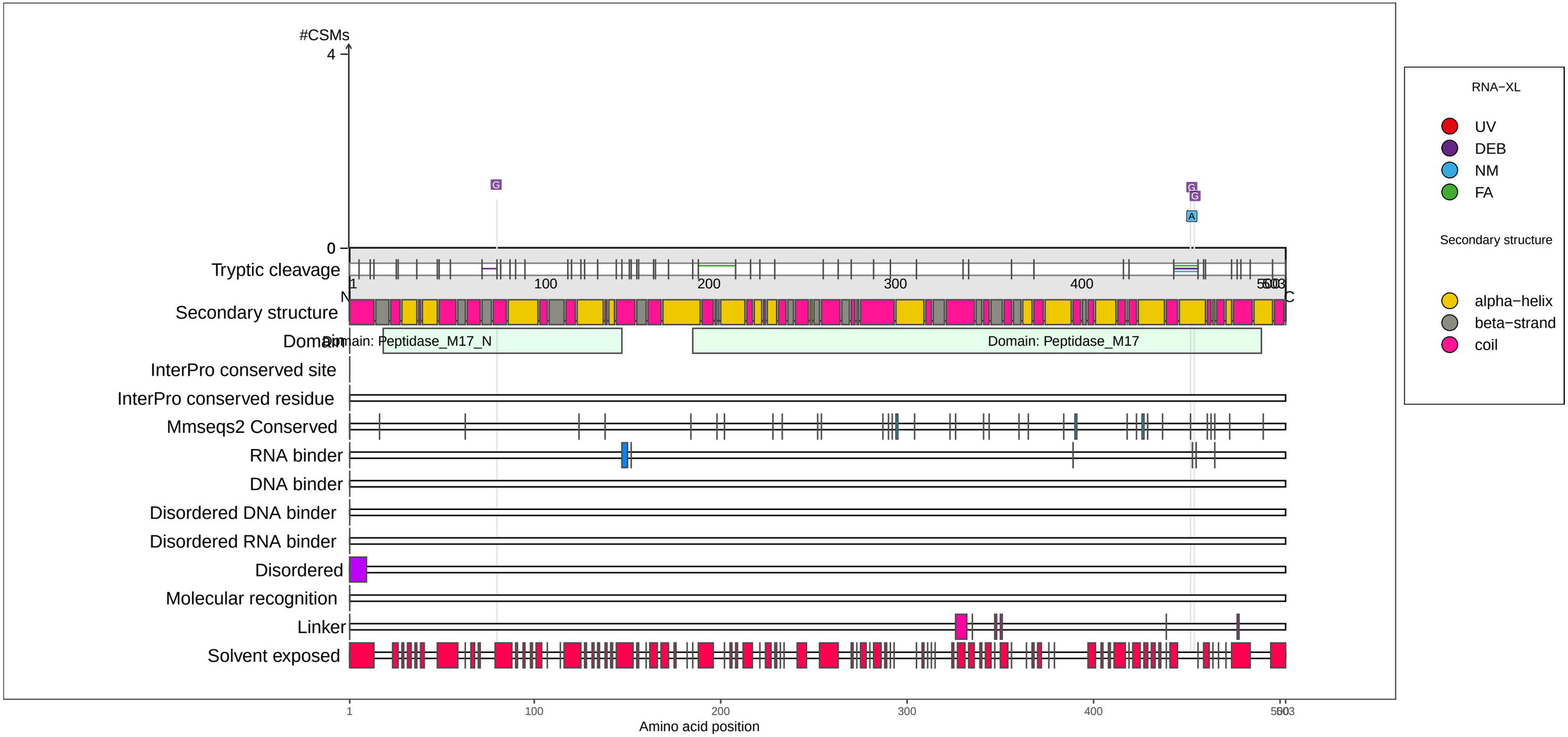
− RNA functions: not annotated



P68767
AMPA_ECOLI Cytosol aminopeptidase

− Abundance:
tryptic [log10 Intensity]: 8.14 (Q 63)
PAXdb K12 strain [ppm]: 1.63 (Q 46)
PAXdb E.coli [ppm]: 2.3 (Q 80)

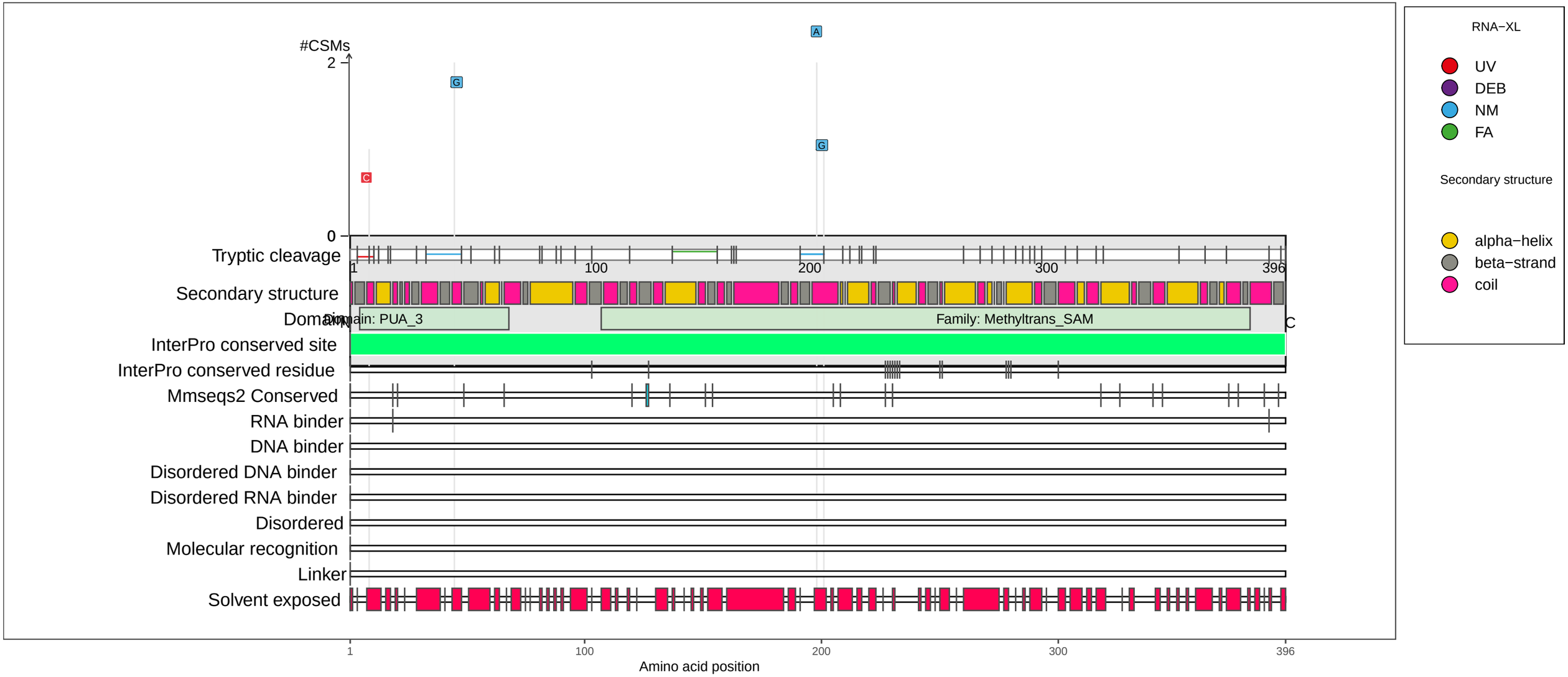
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P75876
RLMI_ECOLI Ribosomal RNA large subunit methyltransferase I

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.43 (Q 58)

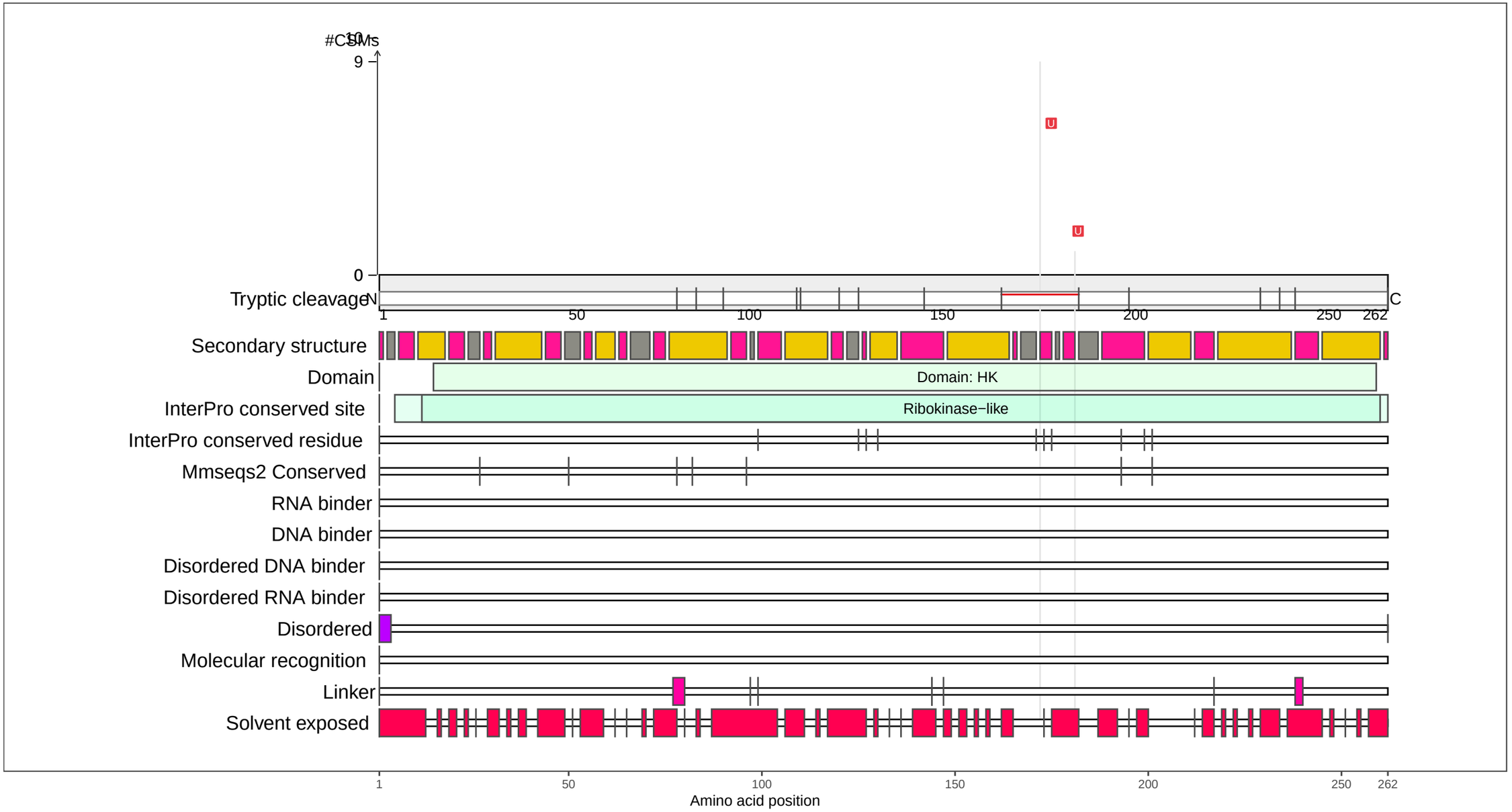
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA methylation; RNA methyltransferase activity; RNA modification; RNA processing
rRNA (cytosine−C5−)−methyltransferase activity; rRNA (cytosine) methyltransferase activity
rRNA base methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing

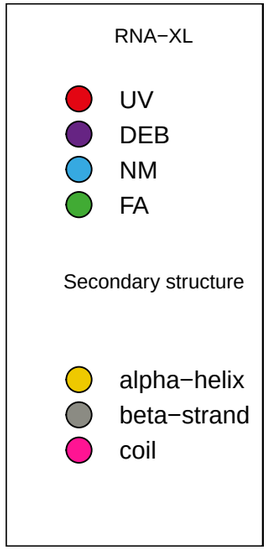


P76423
THIM_ECOLI Hydroxyethylthiazole kinase

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 1.9 (Q 57)
PAXdb E.coli [ppm]: 2.52 (Q 86)

− RNA functions: not annotated

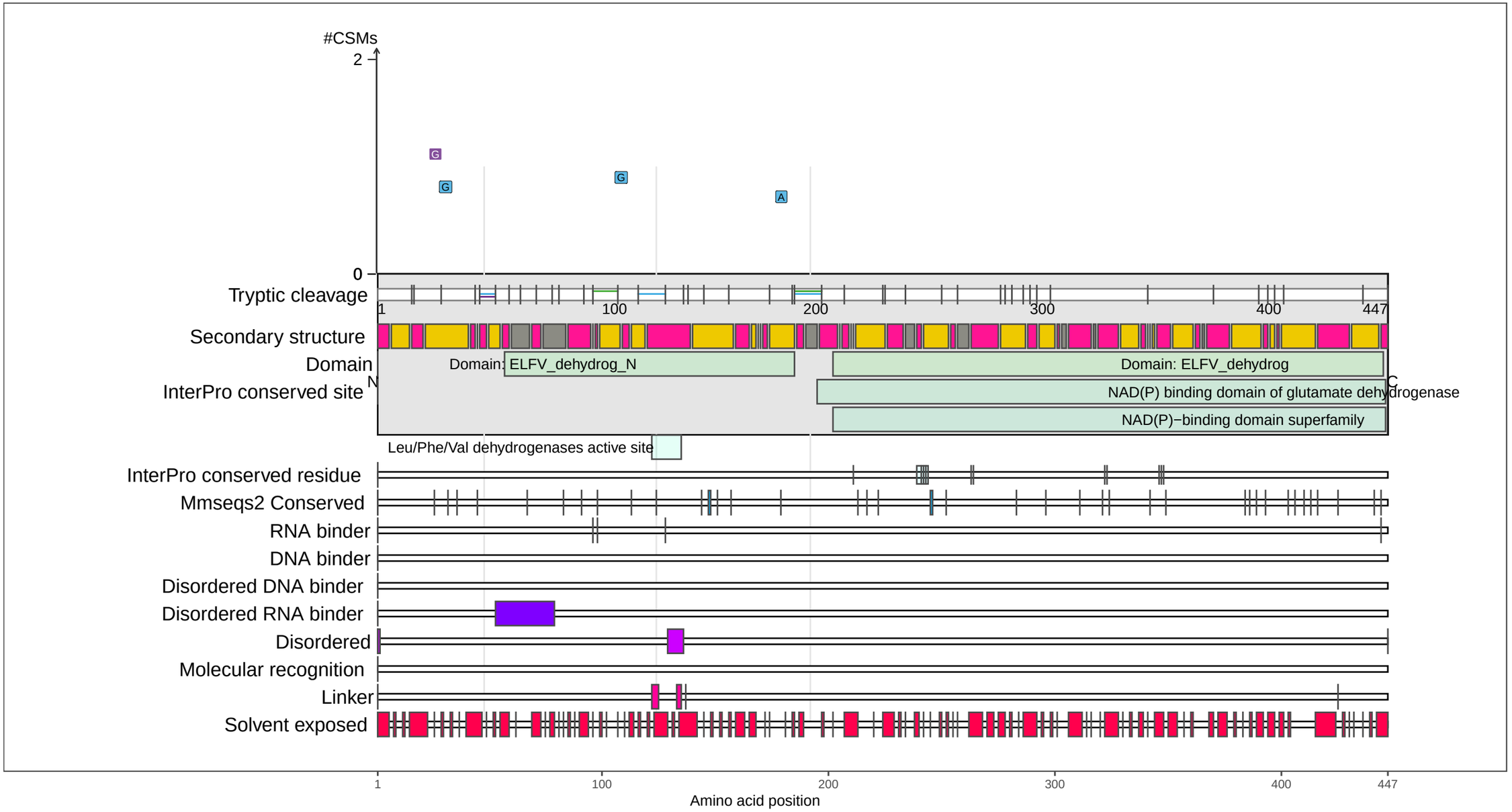


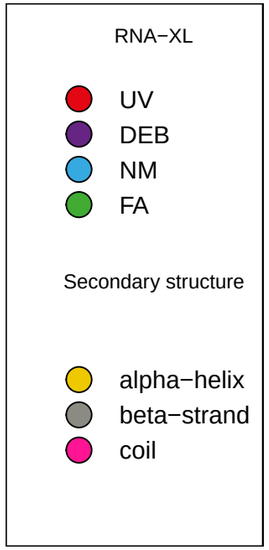


P00370
DHE4_ECOLI NADP−specific glutamate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.61 (Q 79)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 2.89 (Q 93)

− RNA functions: not annotated

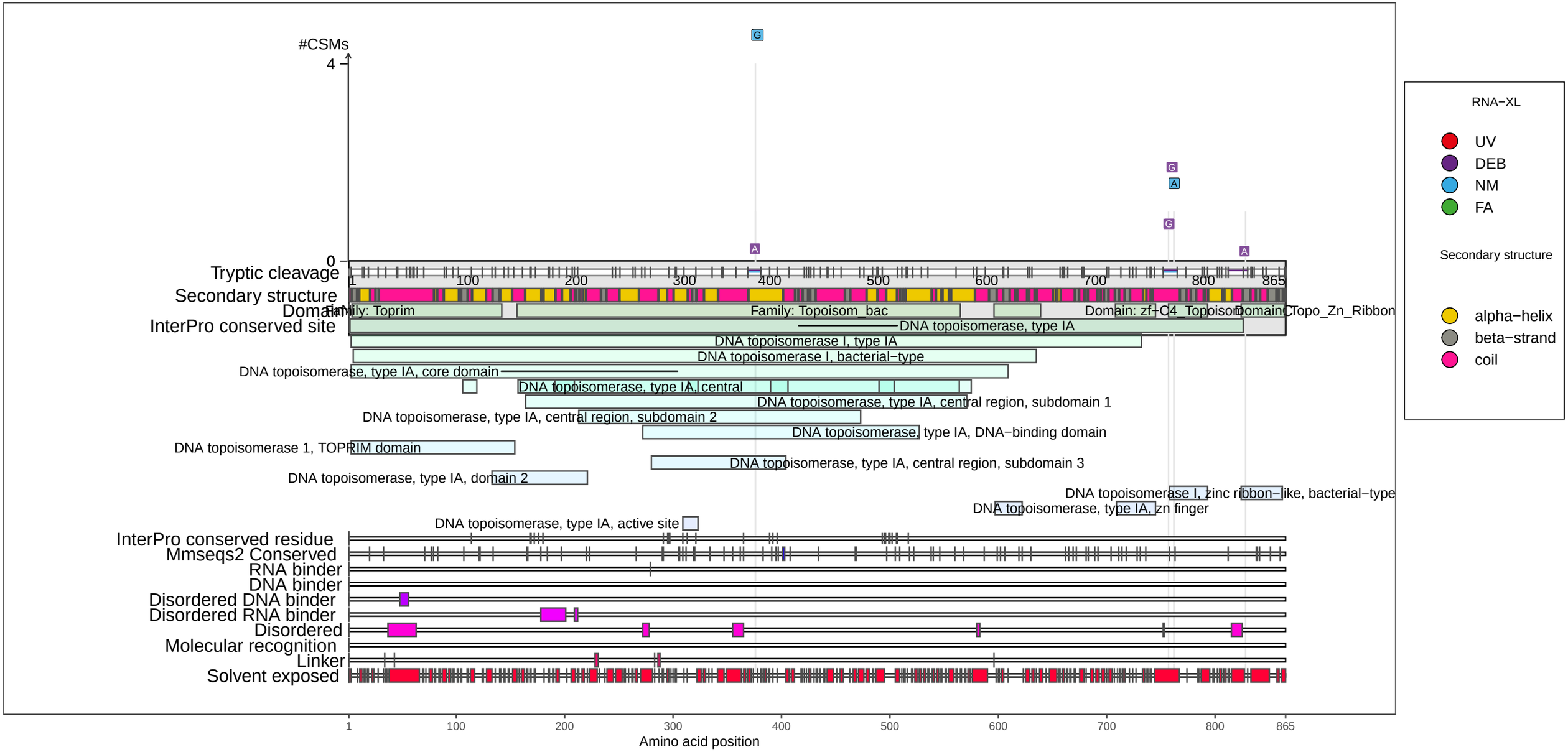




P06612
TOP1_ECOLI DNA topoisomerase 1

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 2.47 (Q 77)
PAXdb E.coli [ppm]: 2.36 (Q 82)

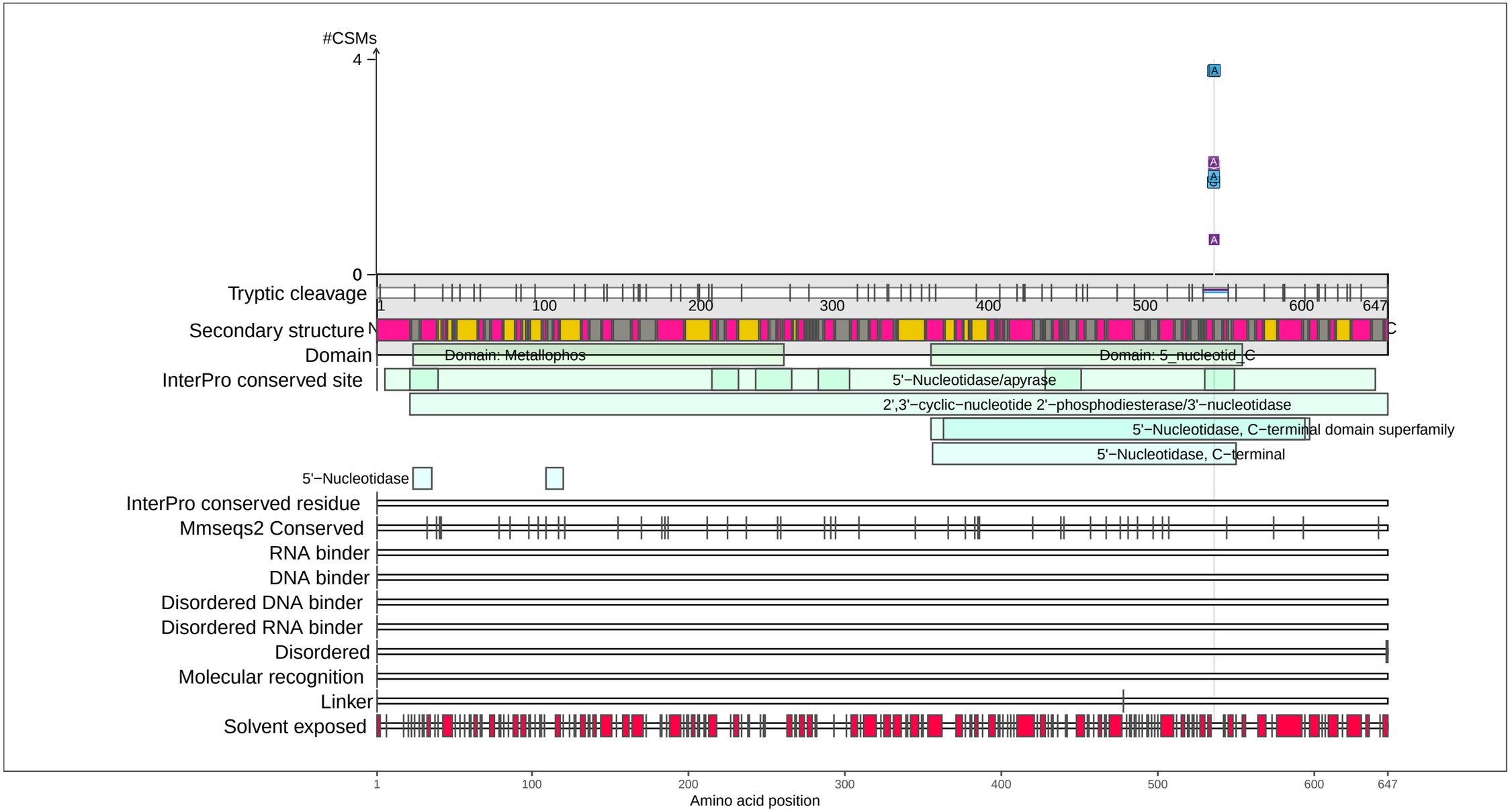
− RNA functions: not annotated



P08331
CPDB_ECOLI 2',3'−cyclic−nucleotide 2'−phosphodiesterase/3'−nucleotidase

− Abundance:
tryptic [log10 Intensity]: 8.56 (Q 77)
PAXdb K12 strain [ppm]: 1.6 (Q 44)
PAXdb E.coli [ppm]: 2.05 (Q 73)

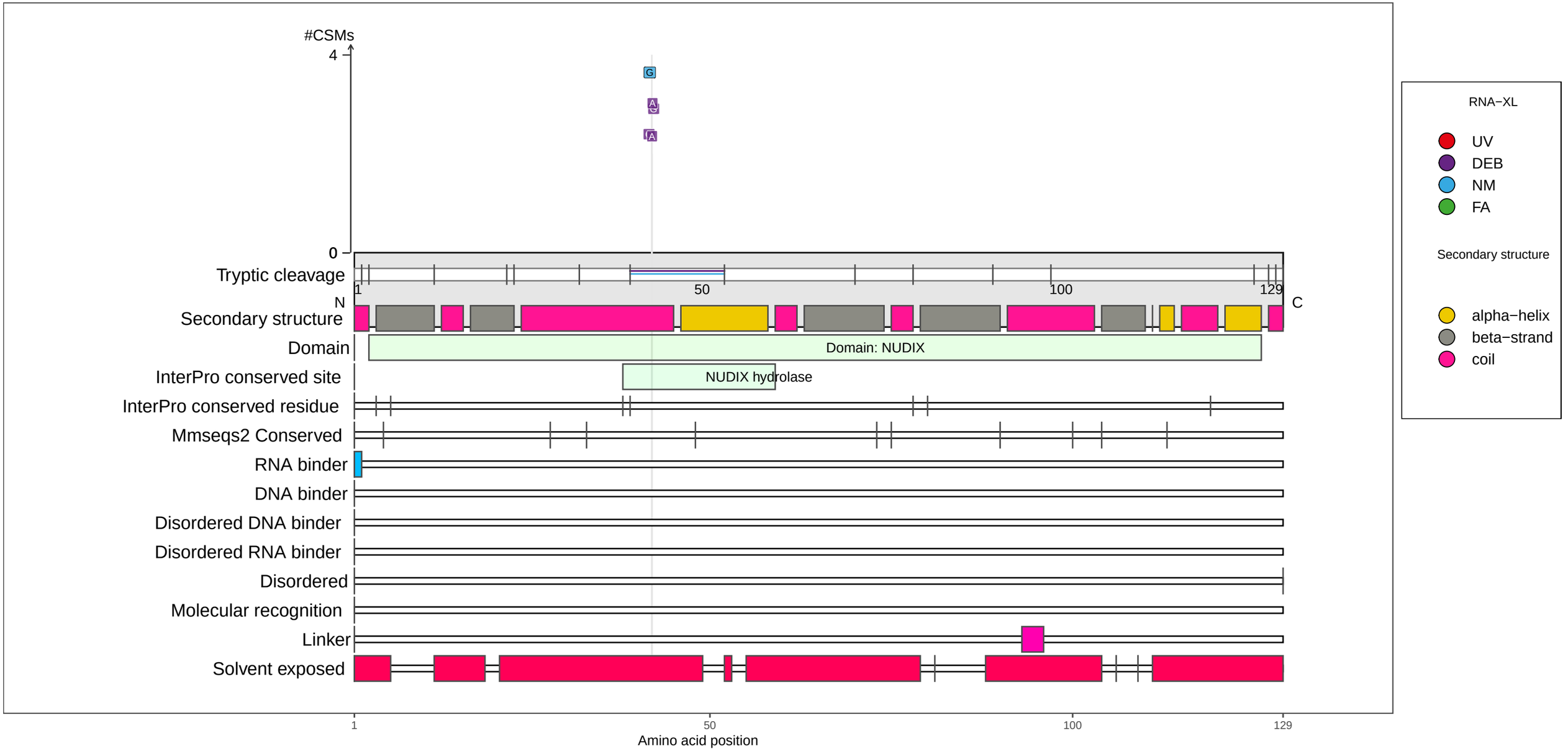
− RNA functions: not annotated



P08337
MUTT_ECOLI 8−oxo−dGTP diphosphatase

− Abundance:
tryptic [log10 Intensity]: 7.4 (Q 30)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.05 (Q 49)

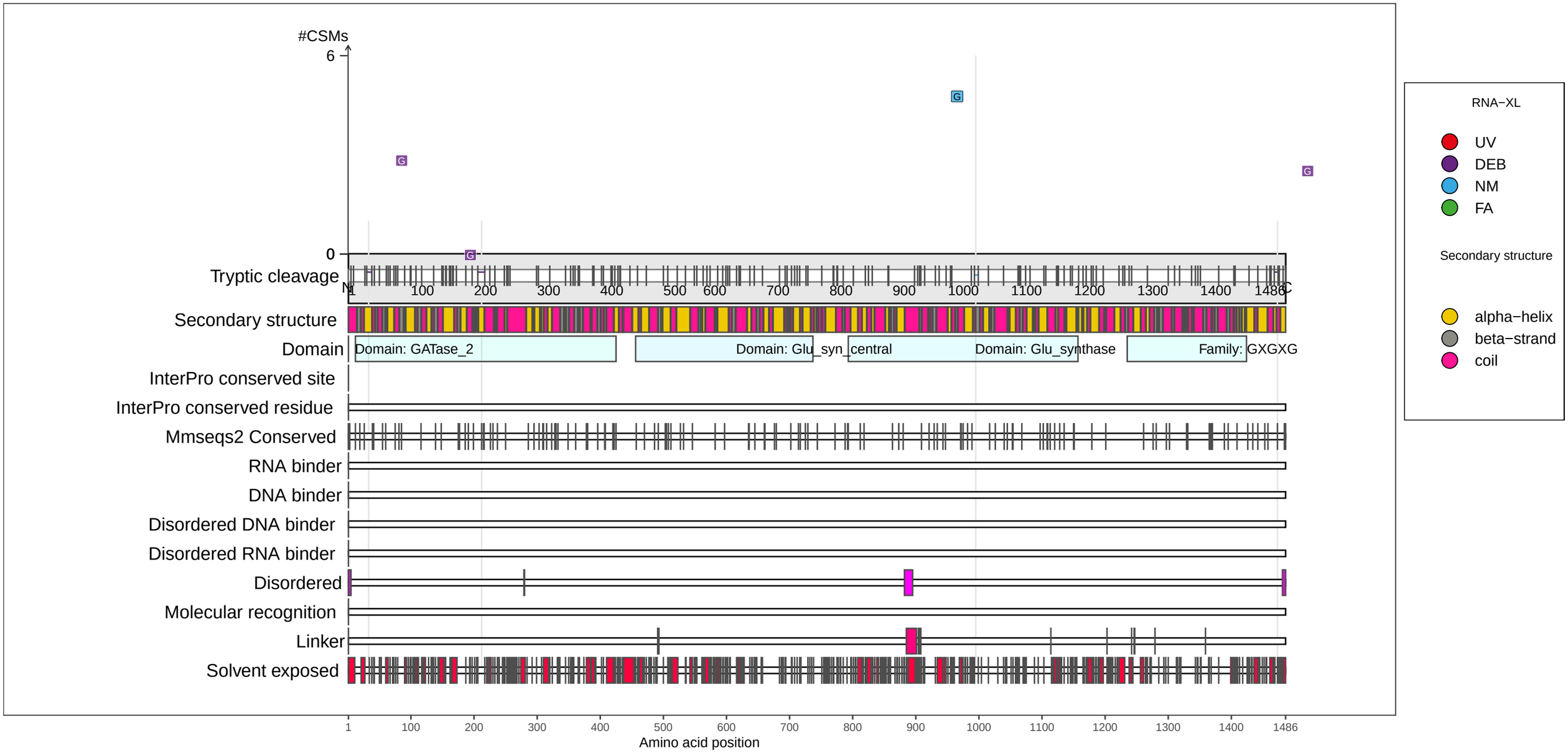
− RNA functions: not annotated



P09831
GLTB_ECOLI Glutamate synthase [NADPH] large chain

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 2.76 (Q 91)

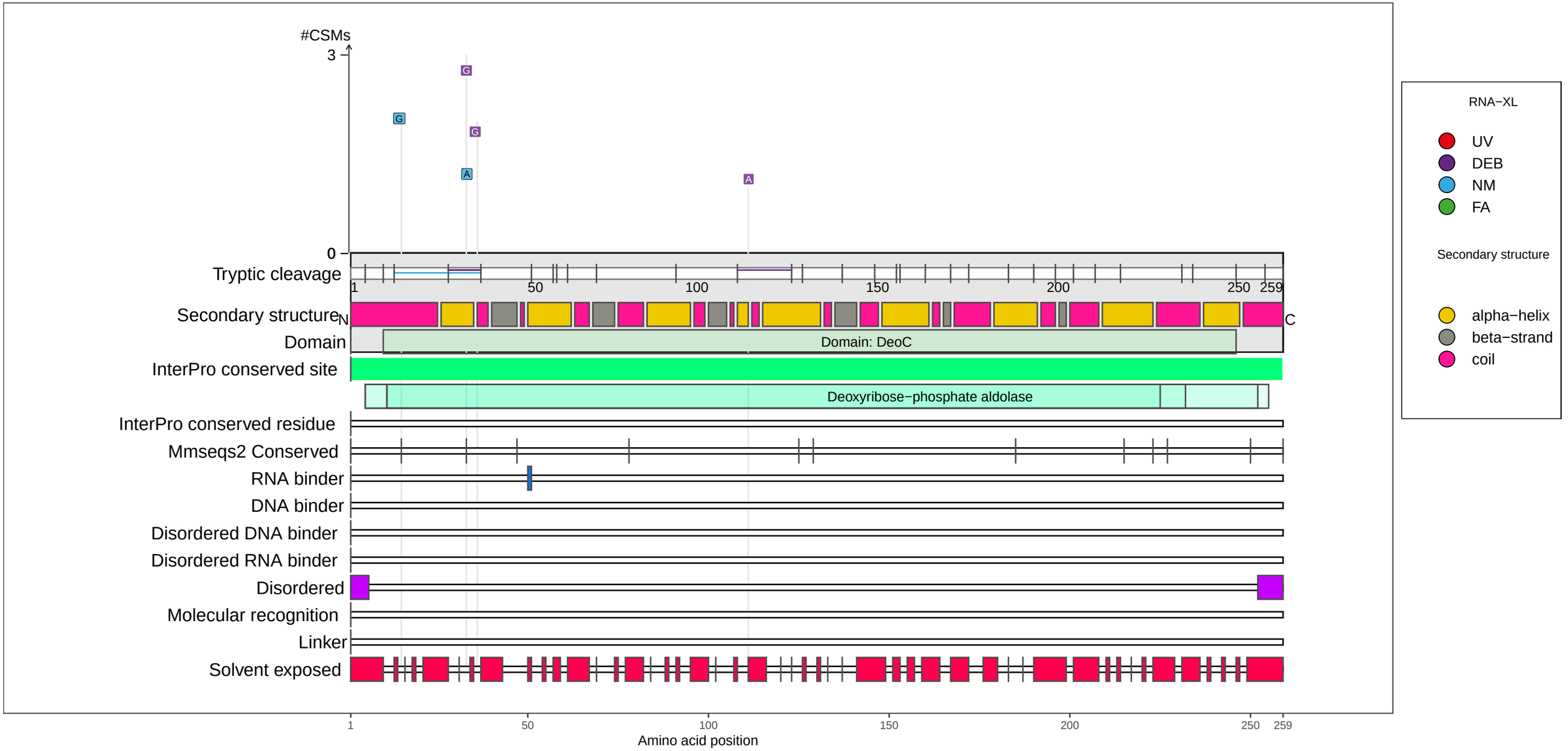
− RNA functions: not annotated



P0A6L0
DEOC_ECOLI Deoxyribose−phosphate aldolase

− Abundance:
tryptic [log10 Intensity]: 8.82 (Q 84)
PAXdb K12 strain [ppm]: 2.31 (Q 70)
PAXdb E.coli [ppm]: 2.67 (Q 89)

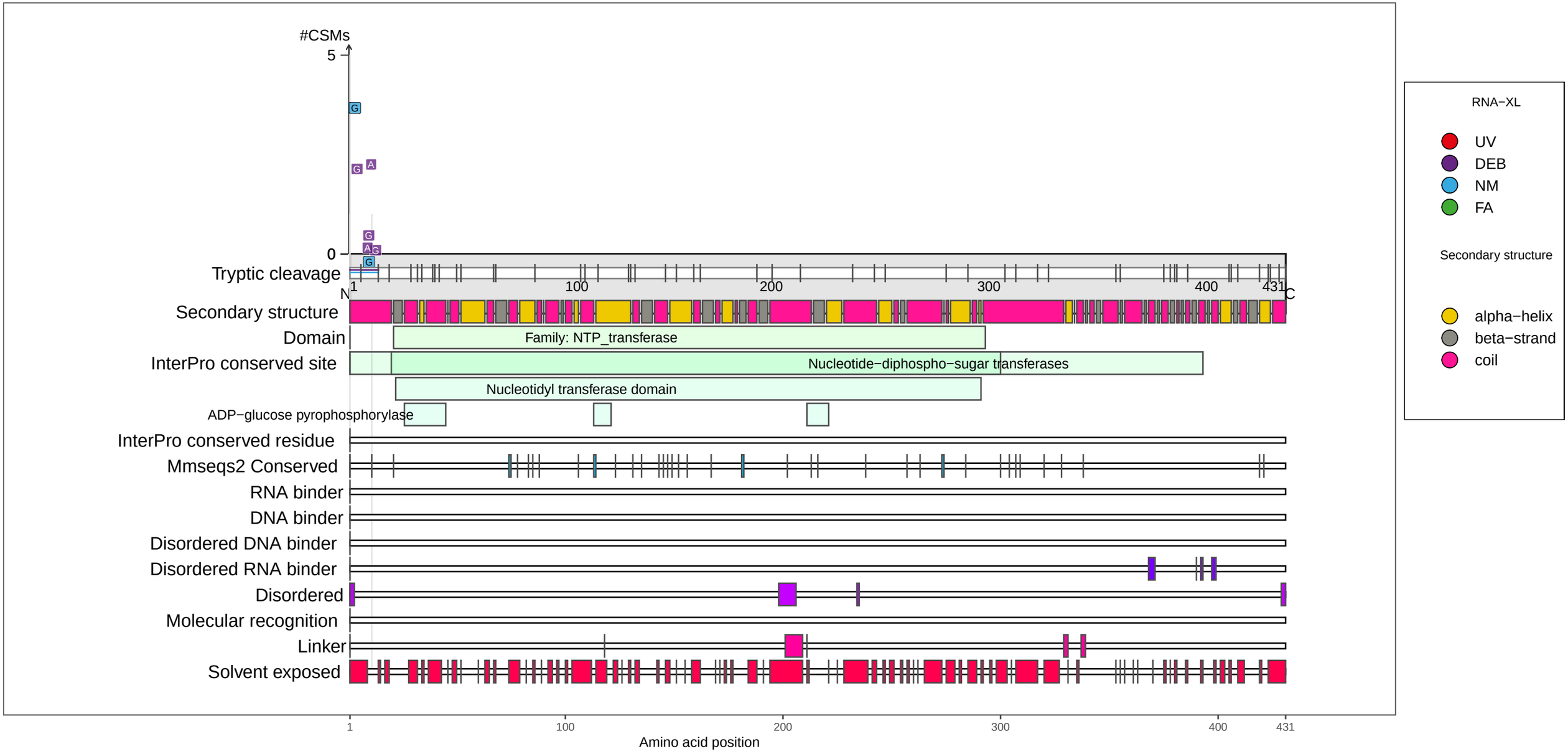
− RNA functions: not annotated



P0A6V1
GLGC_ECOLI Glucose−1−phosphate adenylyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: 1.84 (Q 55)
PAXdb E.coli [ppm]: 2.34 (Q 82)

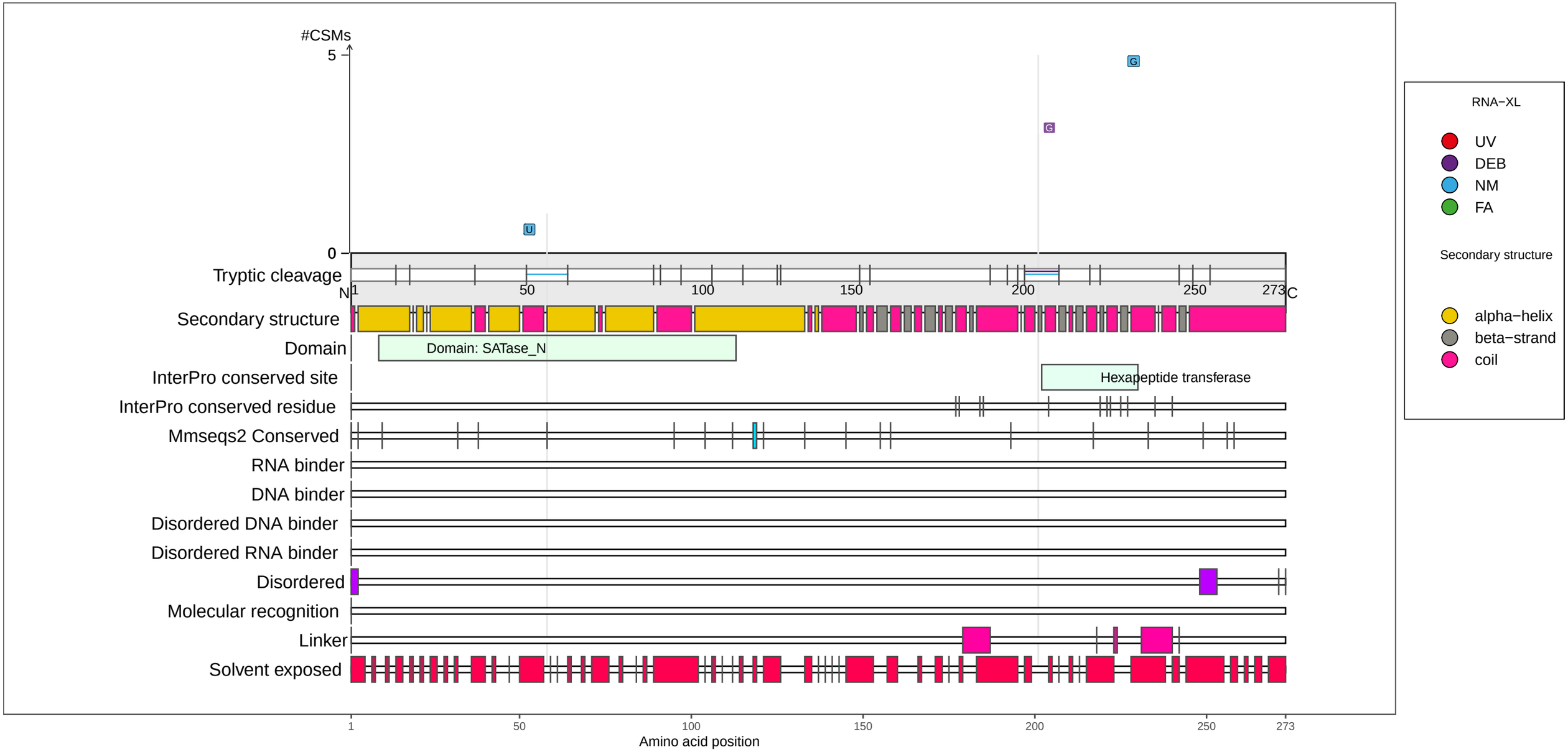
− RNA functions: not annotated



P0A9D4
CYSE_ECOLI Serine acetyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.61 (Q 79)
PAXdb K12 strain [ppm]: 2.45 (Q 76)
PAXdb E.coli [ppm]: 1.96 (Q 71)

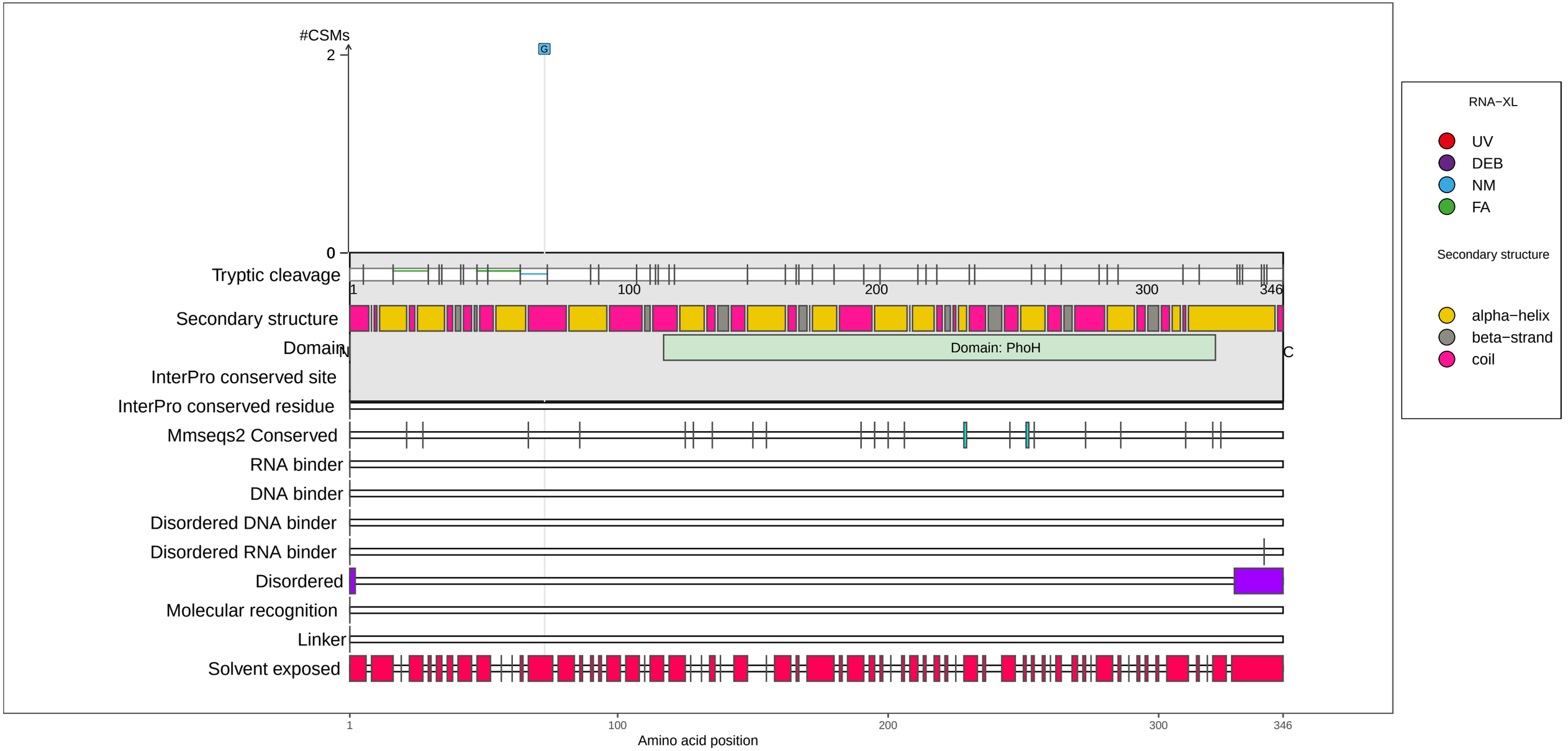
− RNA functions: not annotated



P0A9K3
PHOL_ECOLI PhoH−like protein

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 2.79 (Q 86)
PAXdb E.coli [ppm]: 2.56 (Q 87)

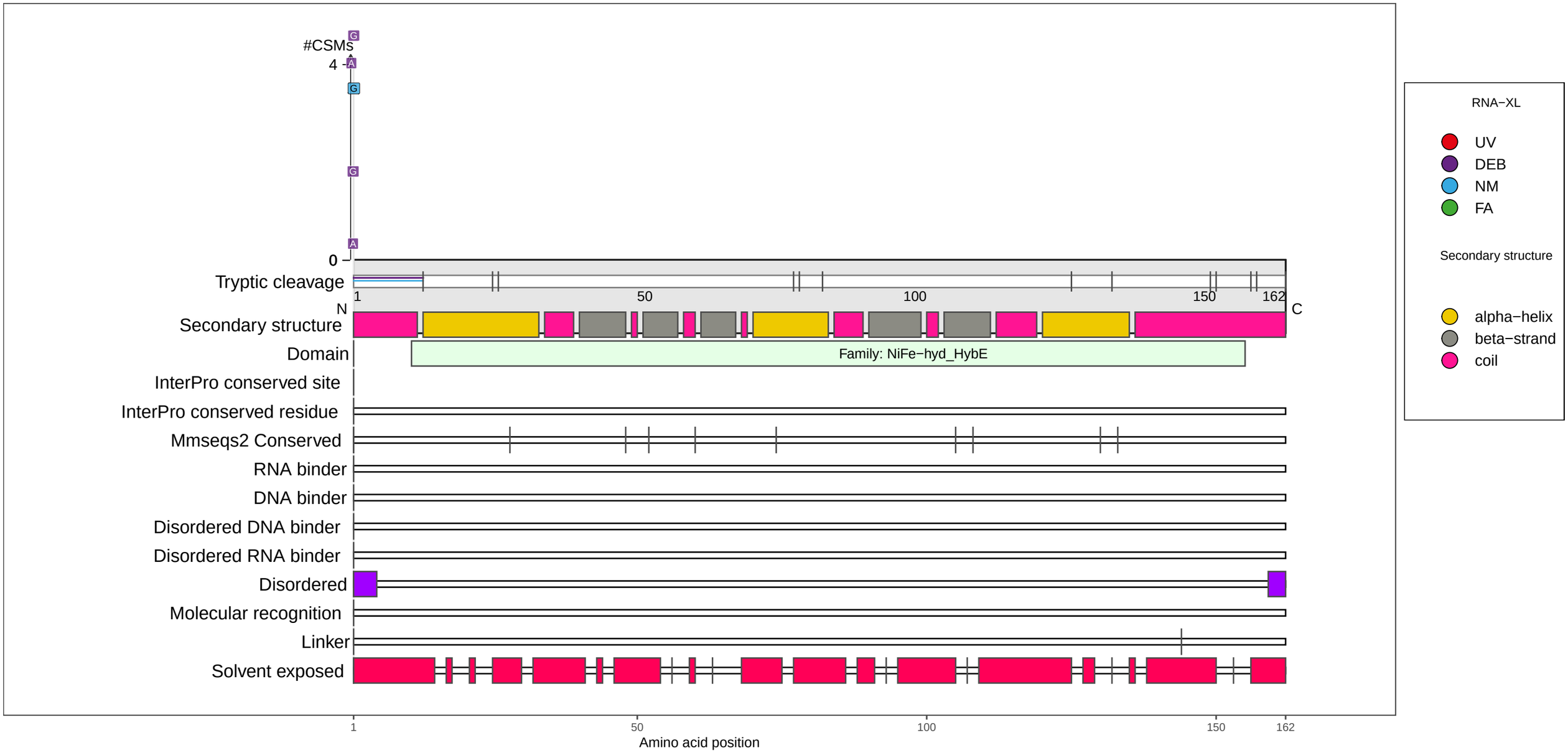
− RNA functions: not annotated



P0AAN1
HYBE_ECOLI Hydrogenase−2 operon protein HybE

− Abundance:
tryptic [log10 Intensity]: 7.45 (Q 32)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.19 (Q 21)

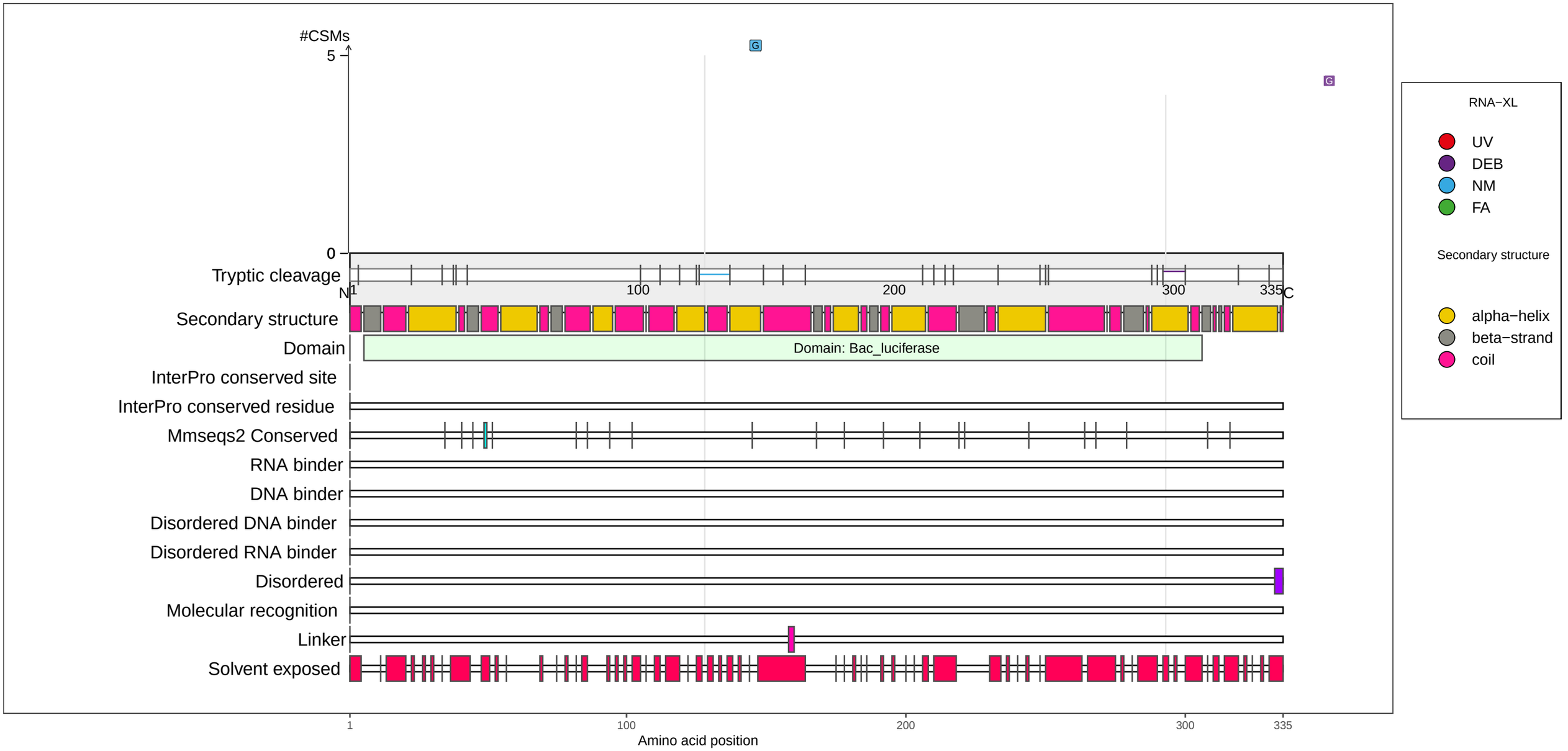
− RNA functions: not annotated



P0ADV5
YHBW_ECOLI Luciferase−like monooxygenase

− Abundance:
tryptic [log10 Intensity]: 8.13 (Q 63)
PAXdb K12 strain [ppm]: 2.82 (Q 87)
PAXdb E.coli [ppm]: 1.14 (Q 51)

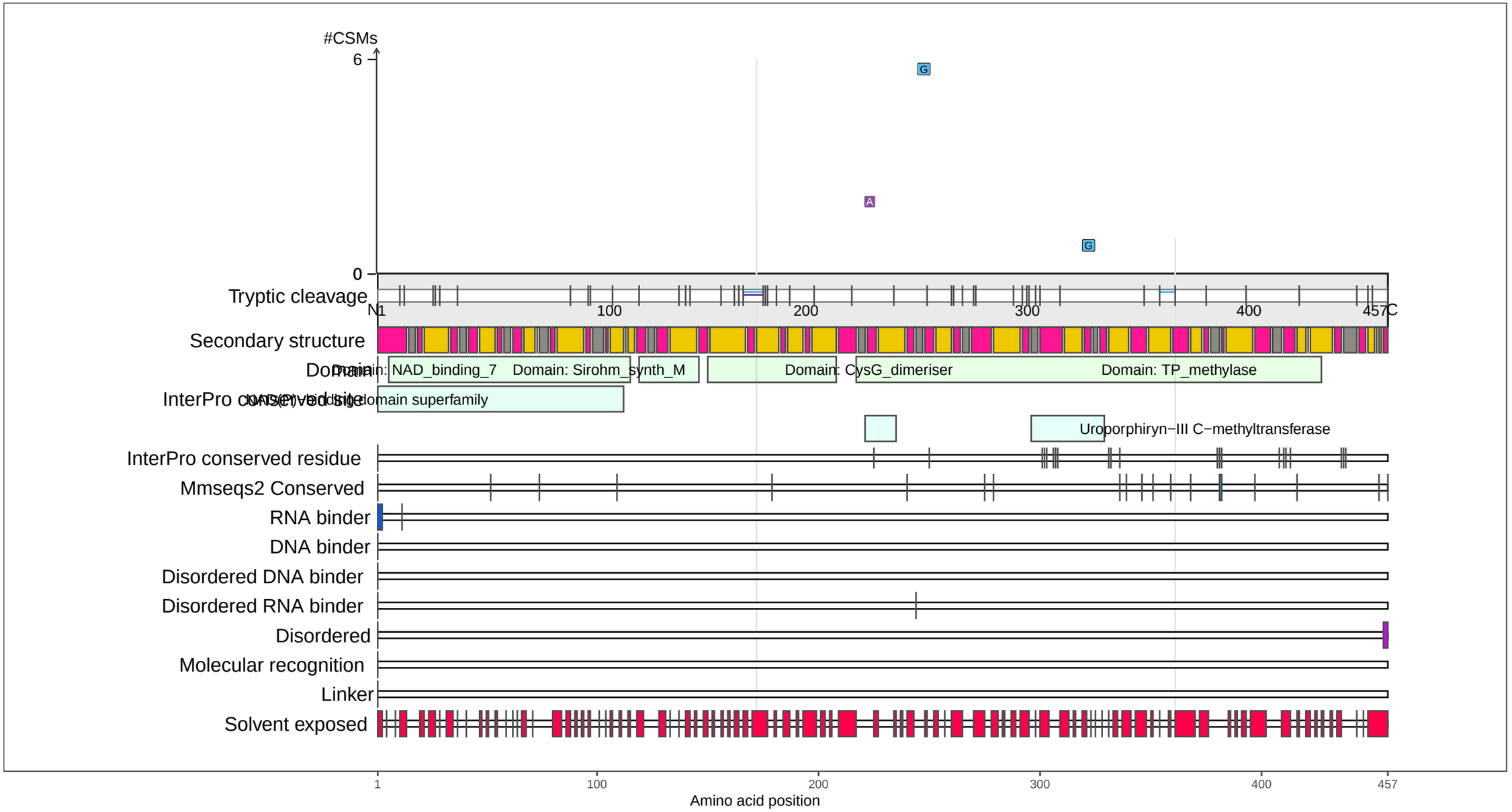
− RNA functions: not annotated



P0AEA8
CYSG_ECOLI Siroheme synthase

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 1.6 (Q 45)
PAXdb E.coli [ppm]: 0.99 (Q 47)

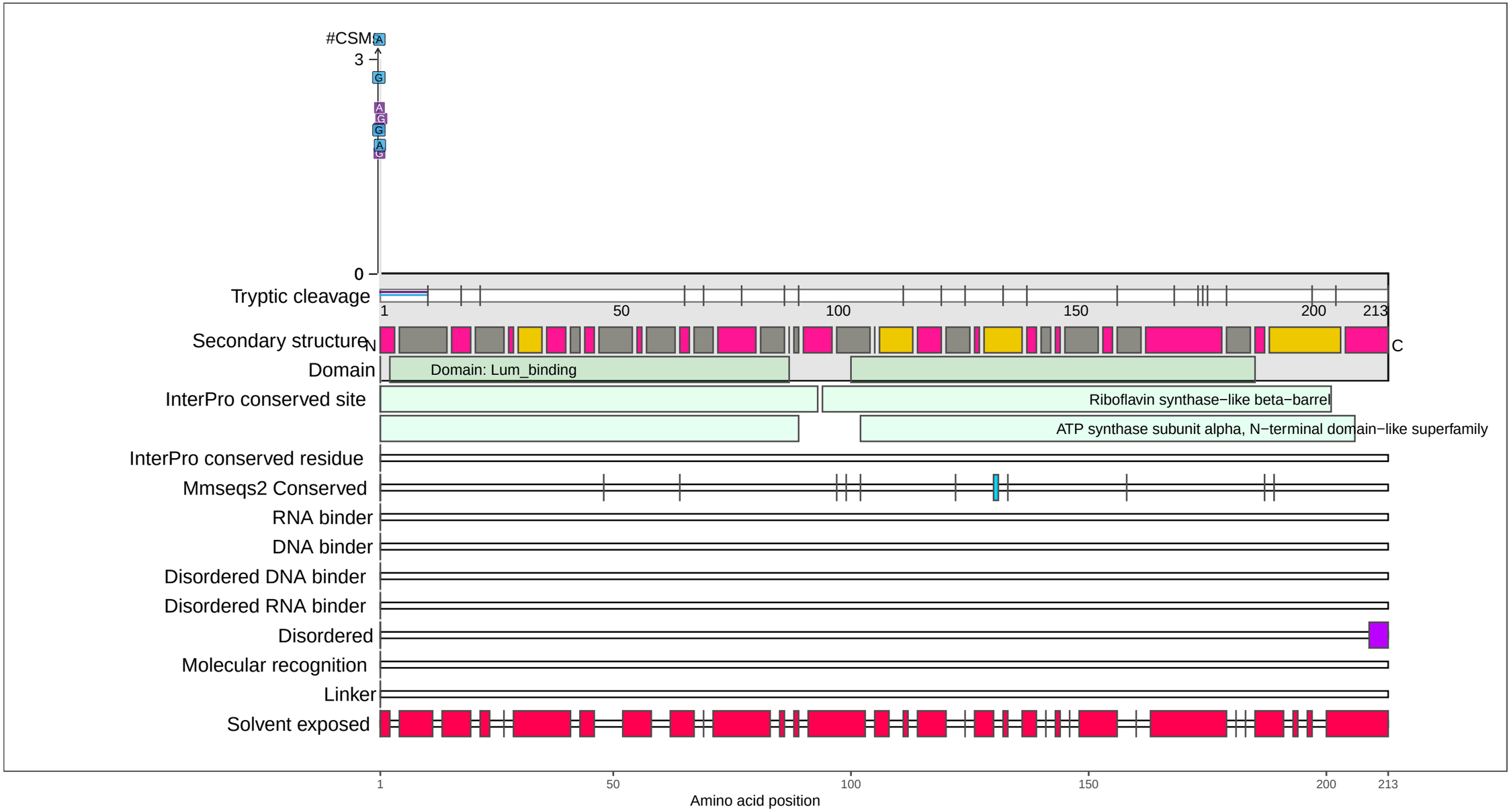
− RNA functions: not annotated

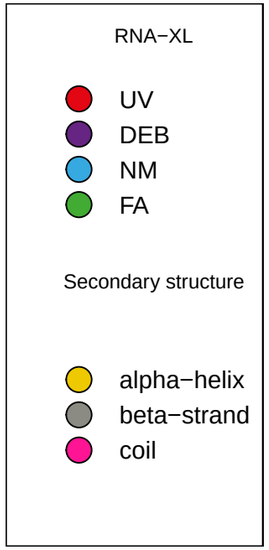


P0AFU8
RISA_ECOLI Riboflavin synthase

− Abundance:
tryptic [log10 Intensity]: 8.13 (Q 63)
PAXdb K12 strain [ppm]: 2.89 (Q 88)
PAXdb E.coli [ppm]: 2.32 (Q 81)

− RNA functions: not annotated

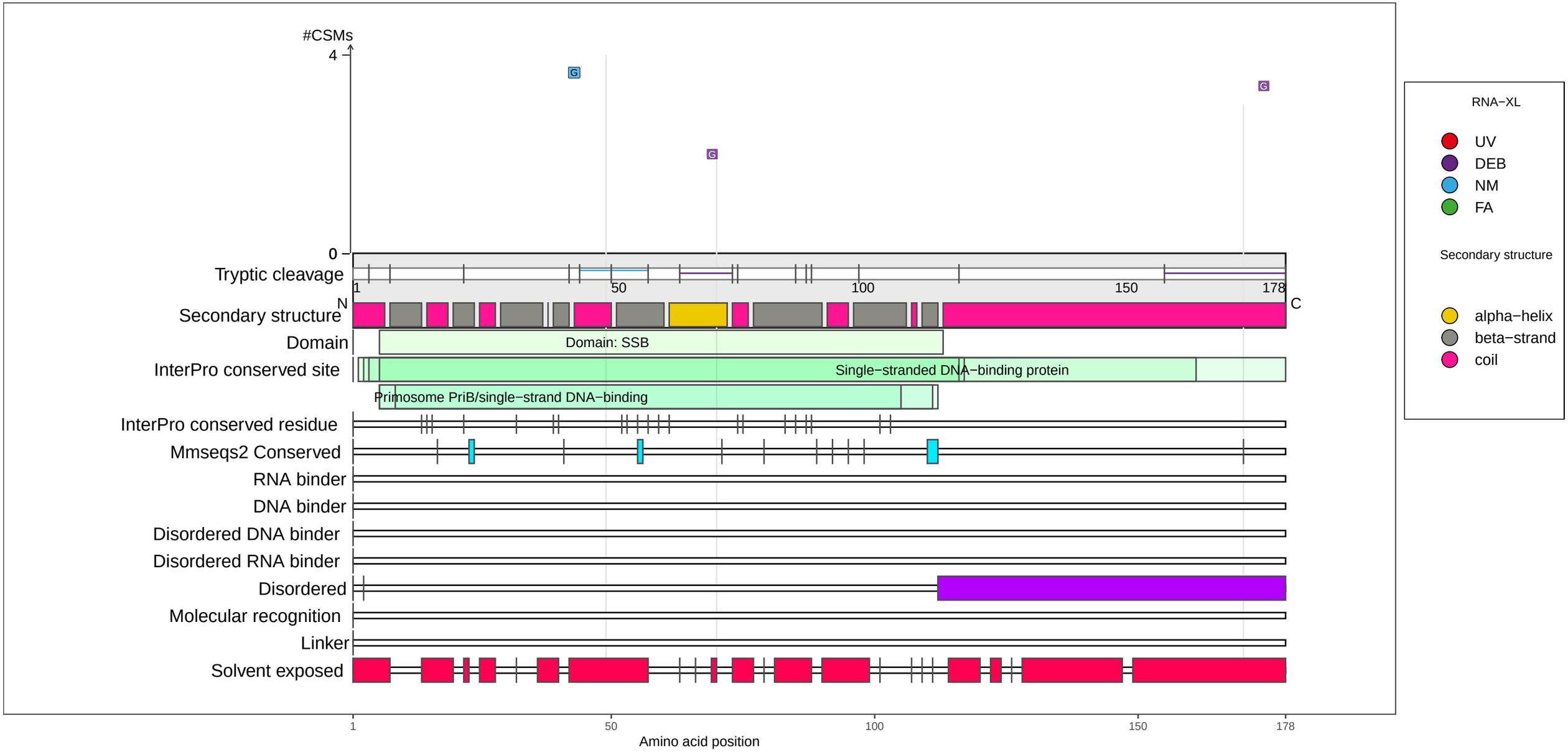




P0AGE0
SSB_ECOLI Single−stranded DNA−binding protein

− Abundance:
tryptic [log10 Intensity]: 9.32 (Q 94)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.7 (Q 90)

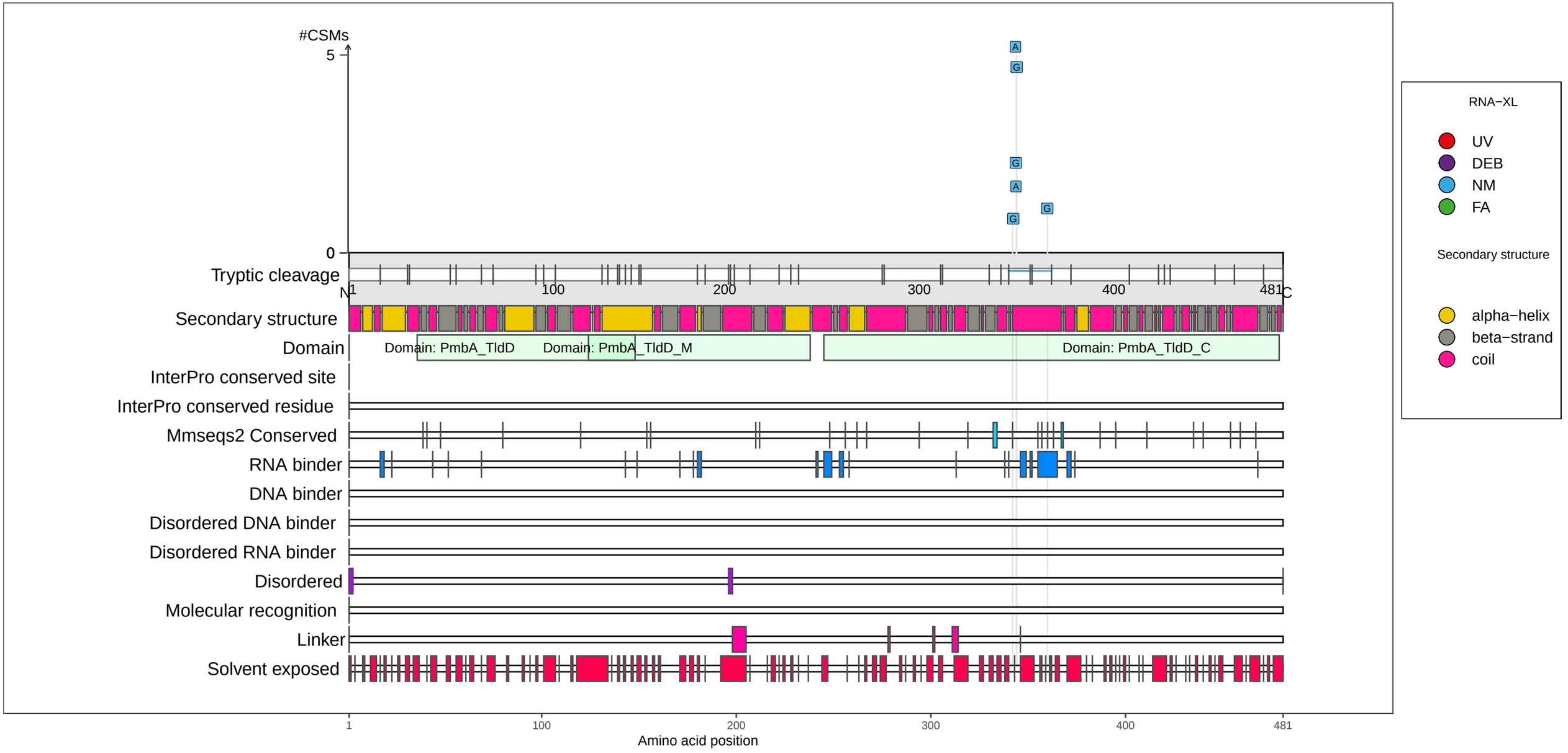
− RNA functions: not annotated



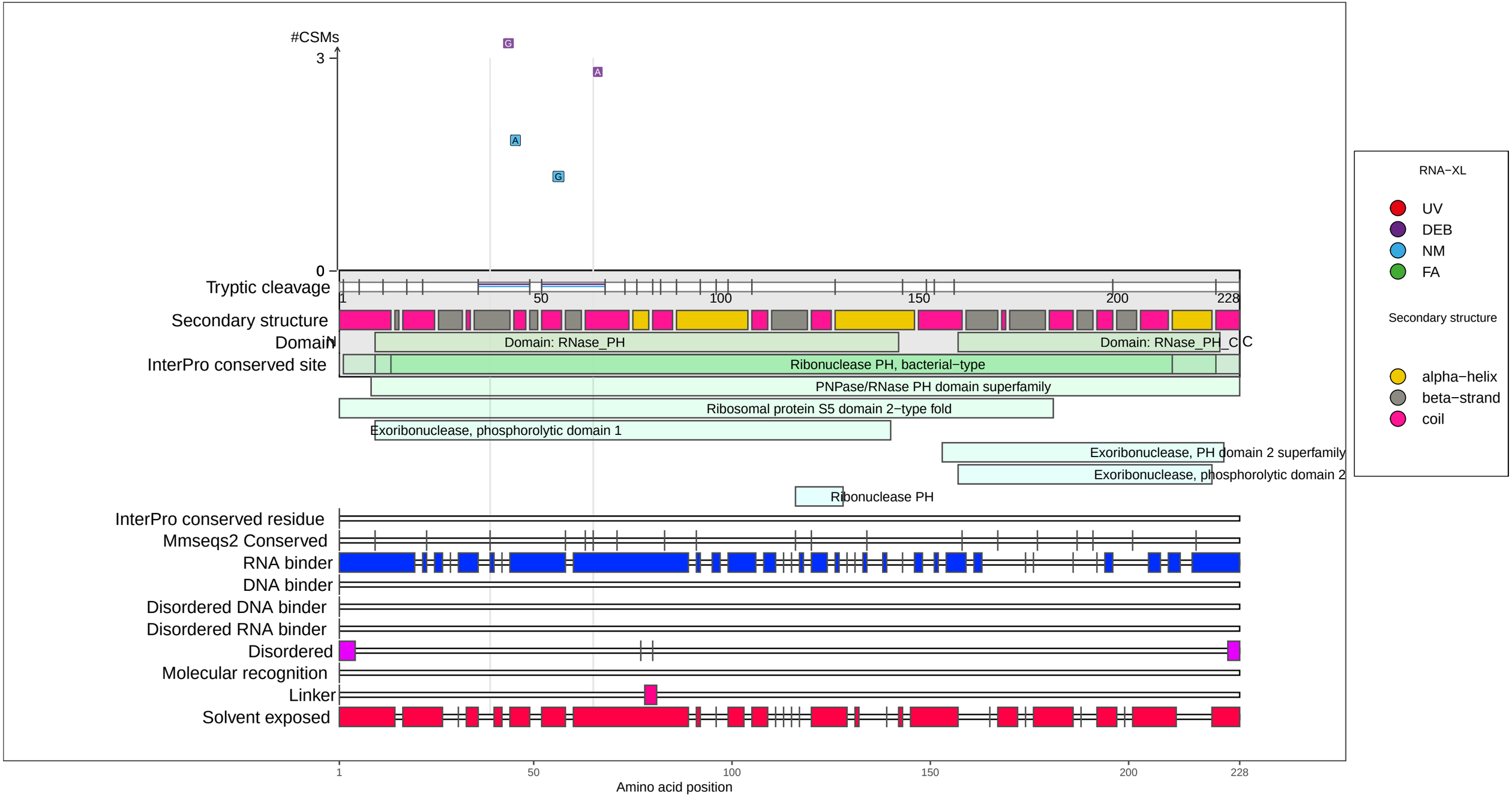
P0AGG8
TLDD_ECOLI Metalloprotease TldD

− Abundance:
tryptic [log10 Intensity]: 8.92 (Q 86)
PAXdb K12 strain [ppm]: 2.32 (Q 70)
PAXdb E.coli [ppm]: 2.44 (Q 84)

− RNA functions: not annotated



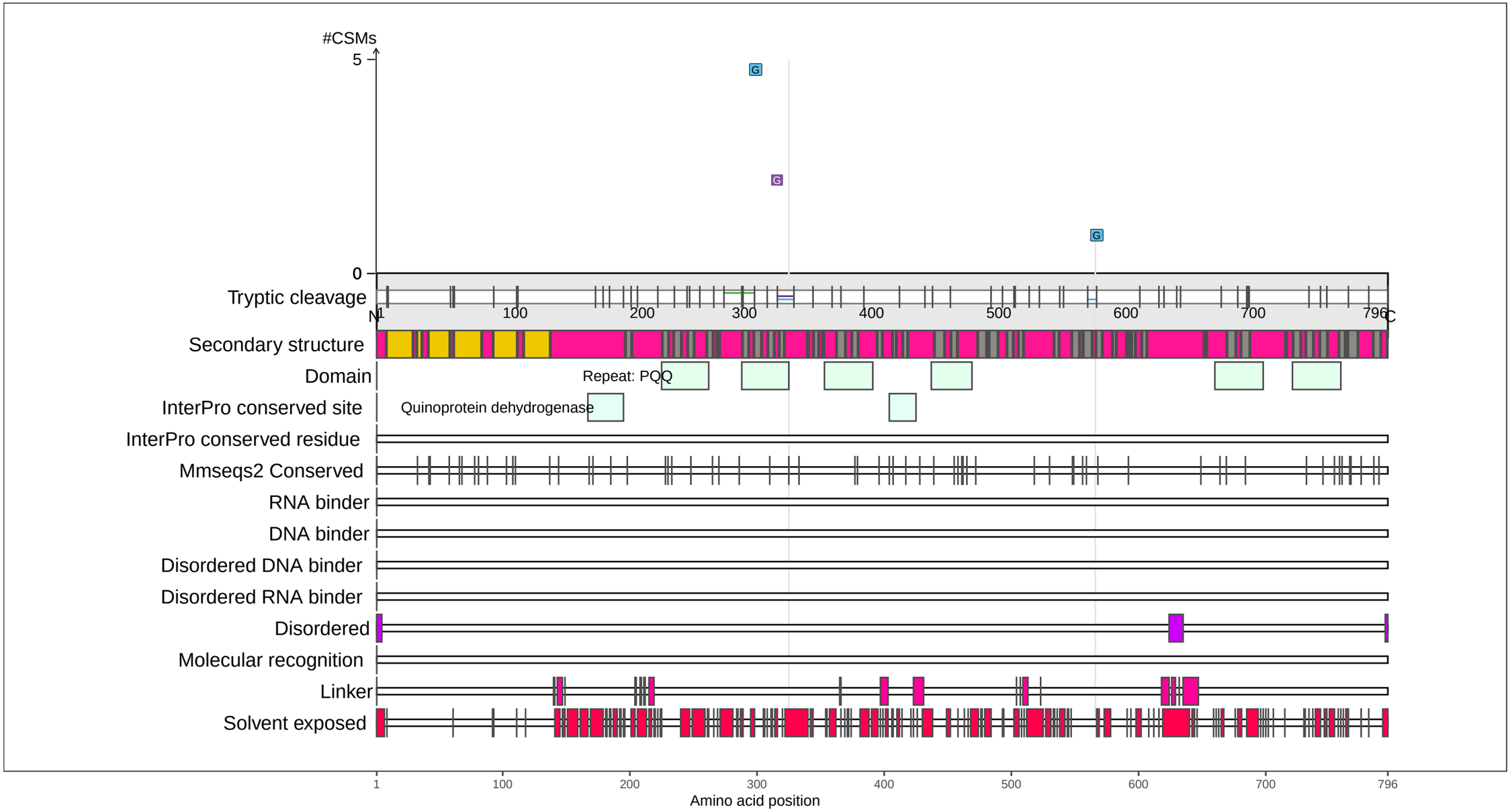
P0CG19
RNPH_ECOLI Truncated inactive ribonuclease PH
− RNA functions: not annotated

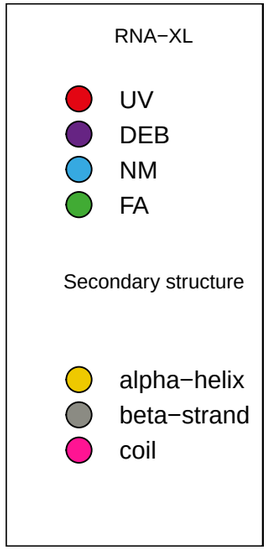


P15877
DHG_ECOLI Quinoprotein glucose dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.81 (Q 84)
PAXdb K12 strain [ppm]: 2.5 (Q 77)
PAXdb E.coli [ppm]: 1.74 (Q 65)

− RNA functions: not annotated

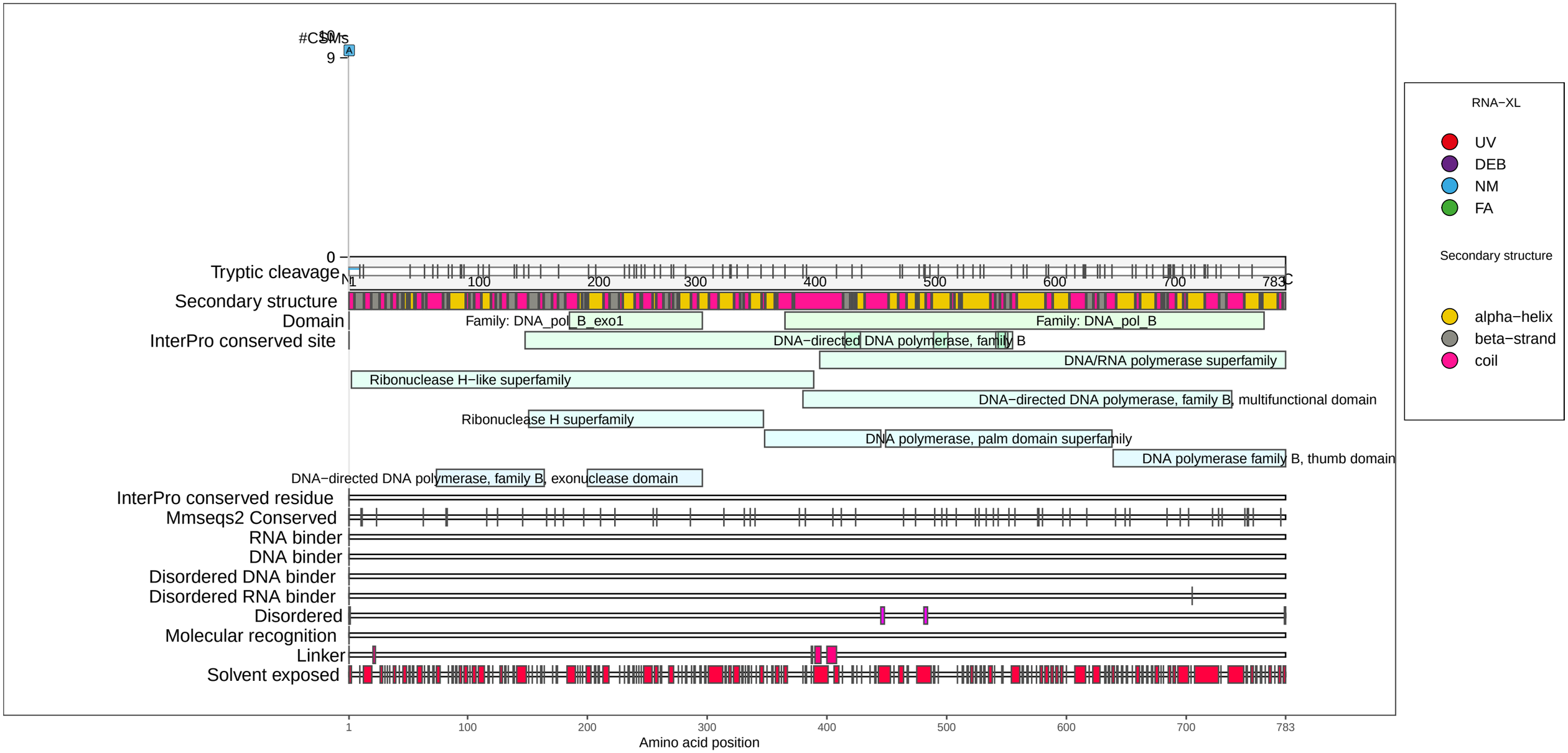




P21189
DPO2_ECOLI DNA polymerase II

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.62 (Q 46)
PAXdb E.coli [ppm]: −0.64 (Q 14)

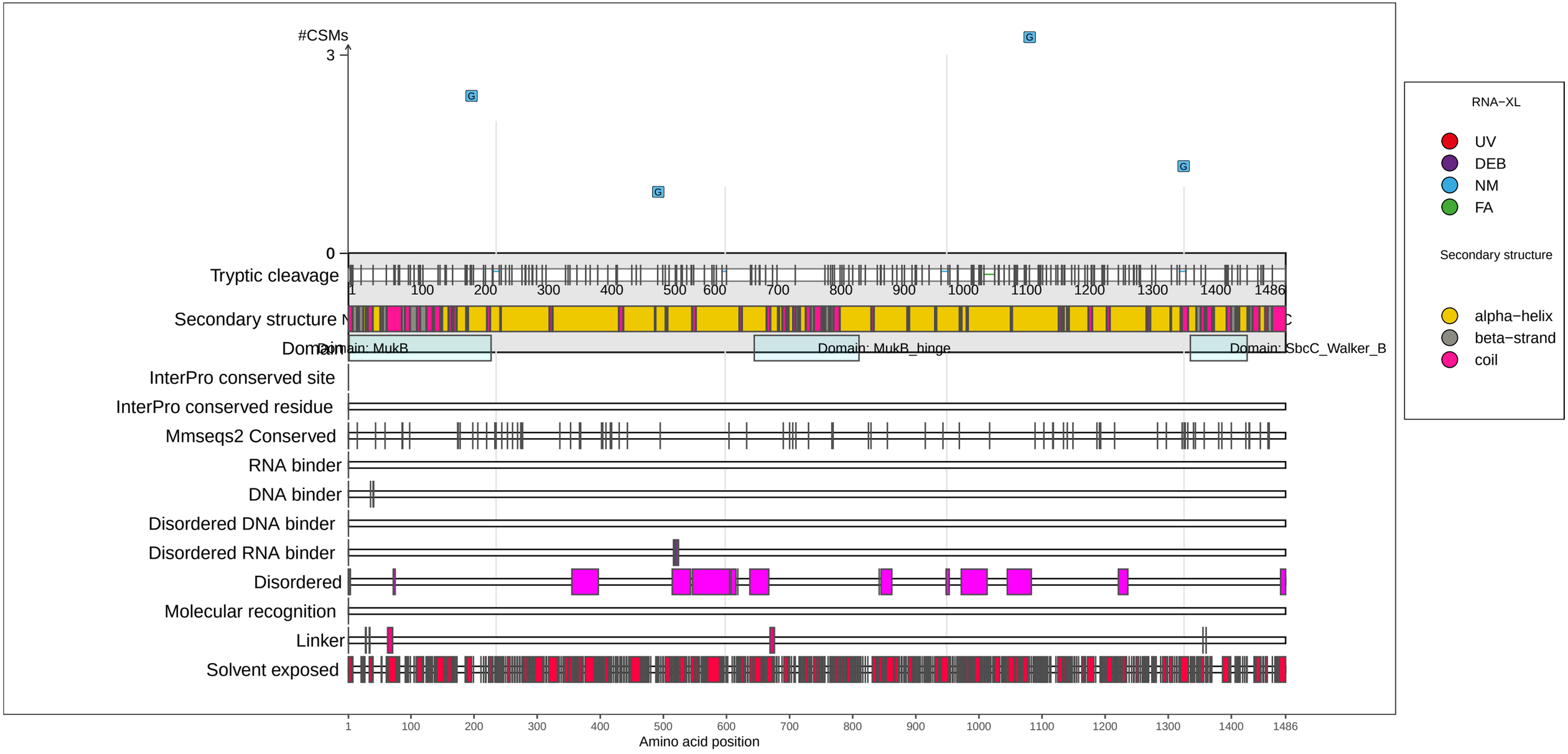
− RNA functions: not annotated



P22523
MUKB_ECOLI Chromosome partition protein MukB

− Abundance:
tryptic [log10 Intensity]: 7.24 (Q 22)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 2.09 (Q 74)

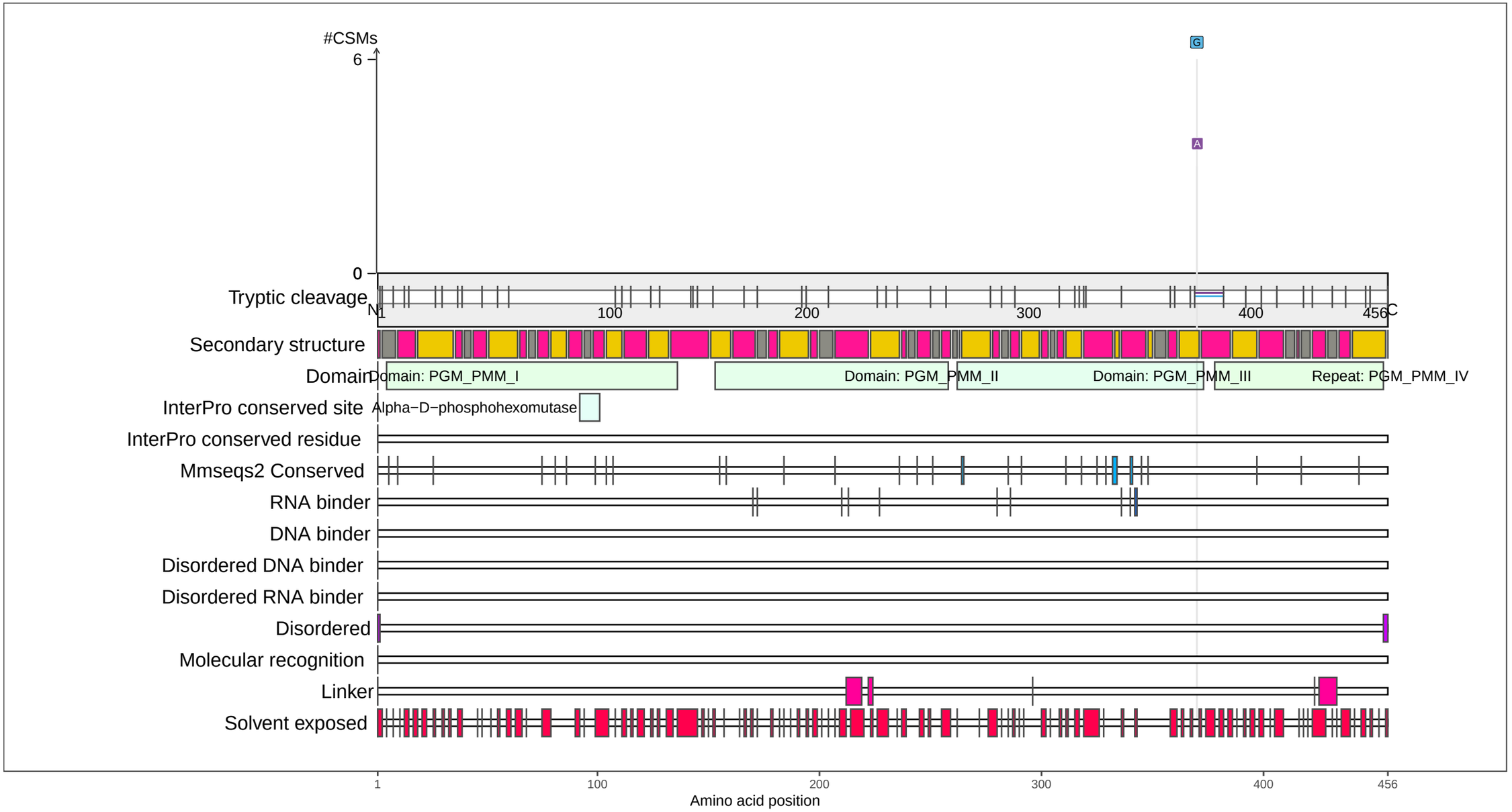
− RNA functions: not annotated



P24175
MANB_ECOLI Phosphomannomutase

− Abundance:
tryptic [log10 Intensity]: 7.26 (Q 23)
PAXdb K12 strain [ppm]: 1.26 (Q 24)
PAXdb E.coli [ppm]: 1.16 (Q 51)

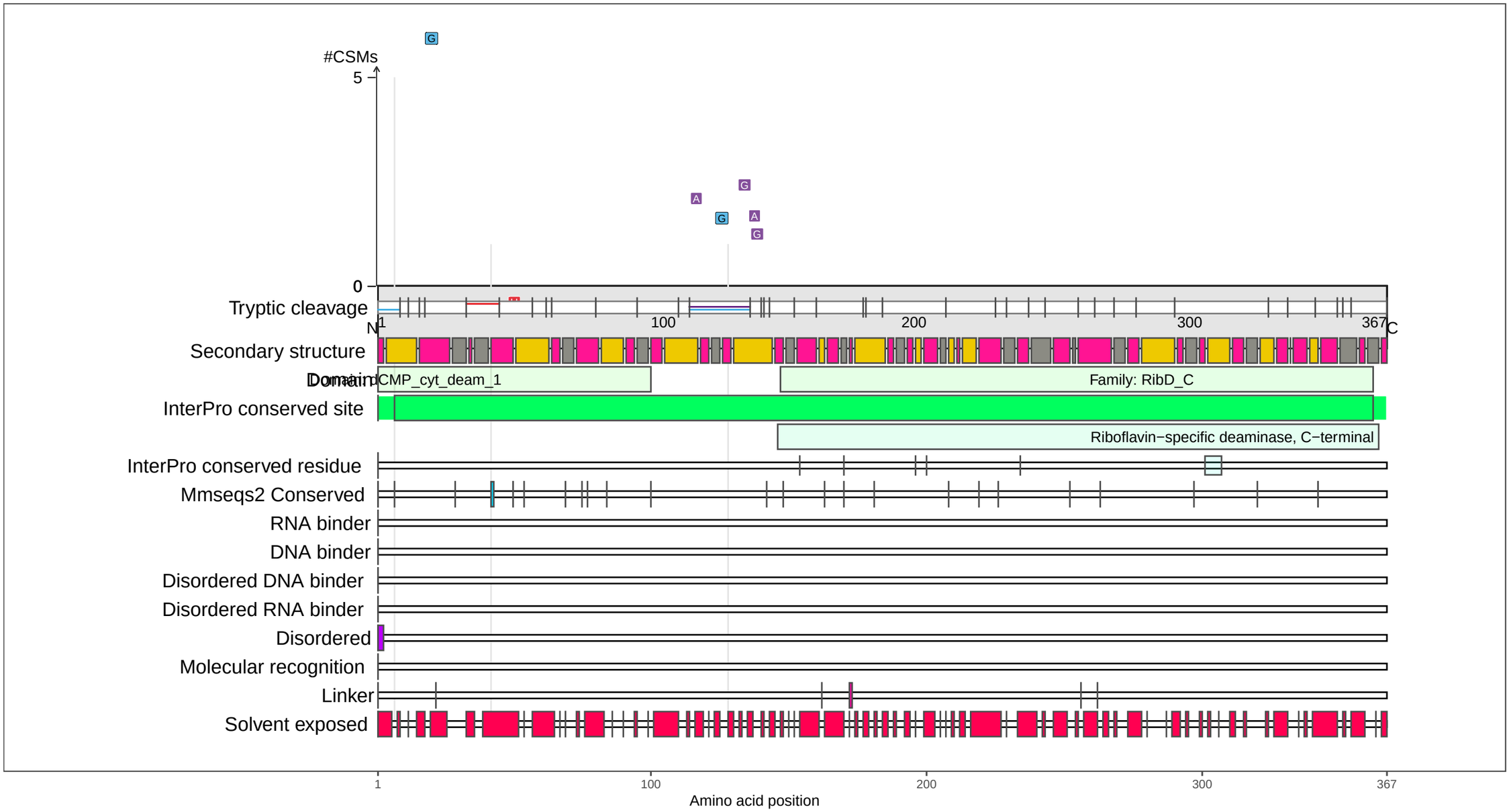
− RNA functions: not annotated

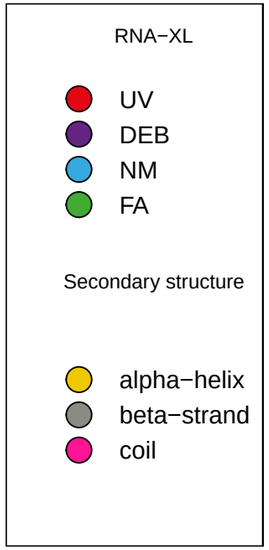


P25539
RIBD_ECOLI Riboflavin biosynthesis protein RibD

− Abundance:
tryptic [log10 Intensity]: 6.99 (Q 13)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 1.71 (Q 65)

− RNA functions: not annotated

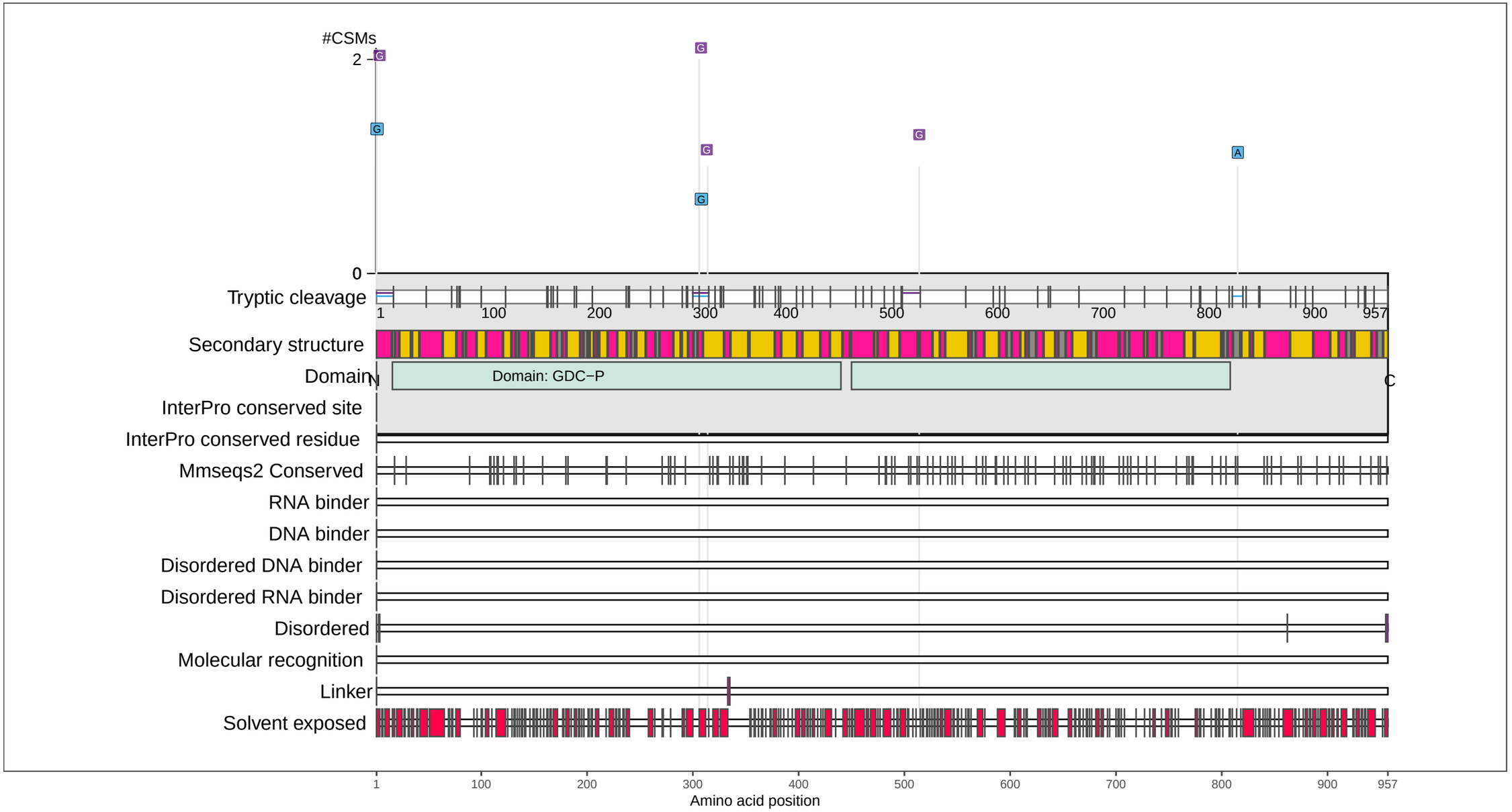




P33195
GCSP_ECOLI Glycine dehydrogenase (decarboxylating)

− Abundance:
tryptic [log10 Intensity]: 9.4 (Q 95)
PAXdb K12 strain [ppm]: 2.63 (Q 81)
PAXdb E.coli [ppm]: 2.51 (Q 86)

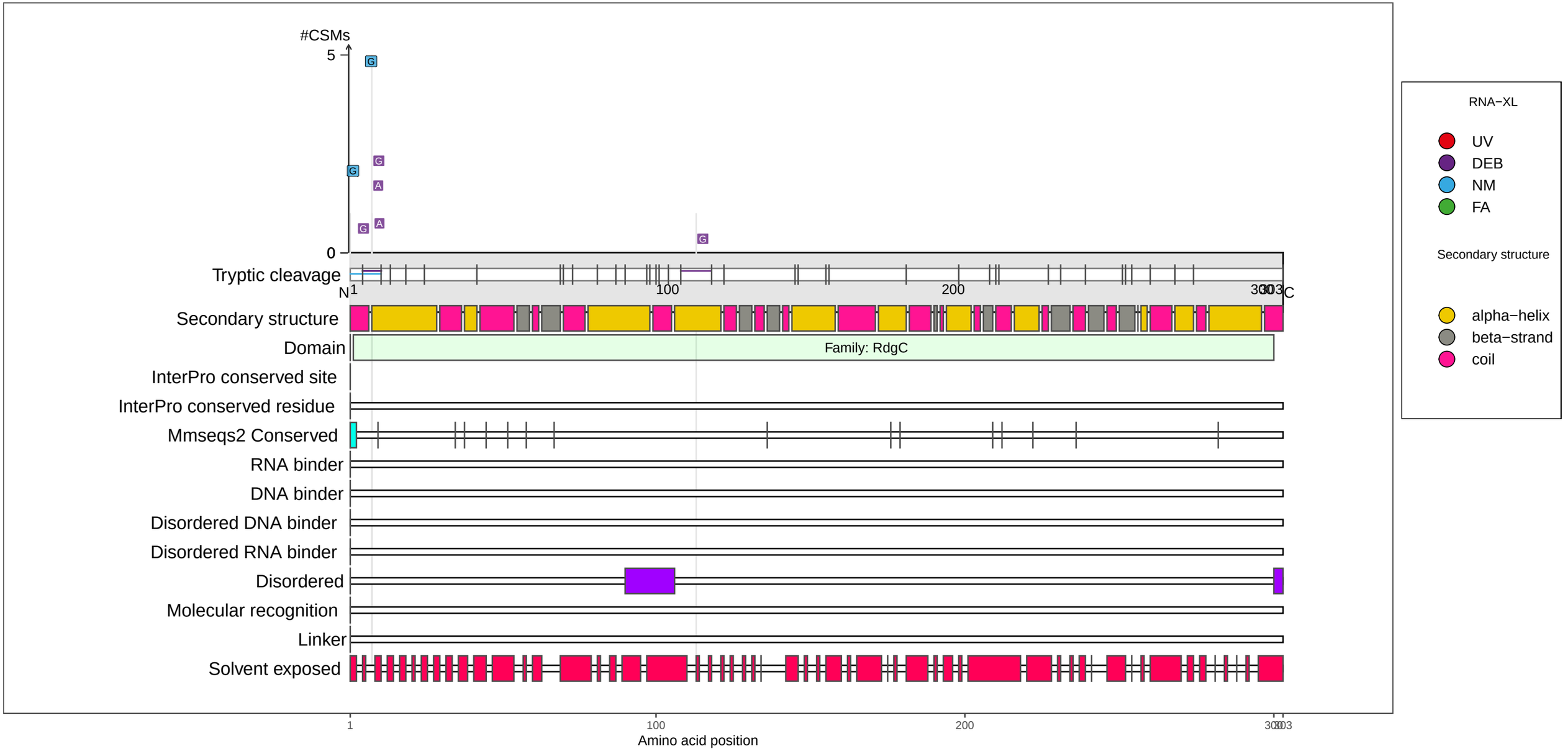
− RNA functions: not annotated



P36767
RDGC_ECOLI Recombination−associated protein RdgC

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 2.92 (Q 89)
PAXdb E.coli [ppm]: 2.04 (Q 73)

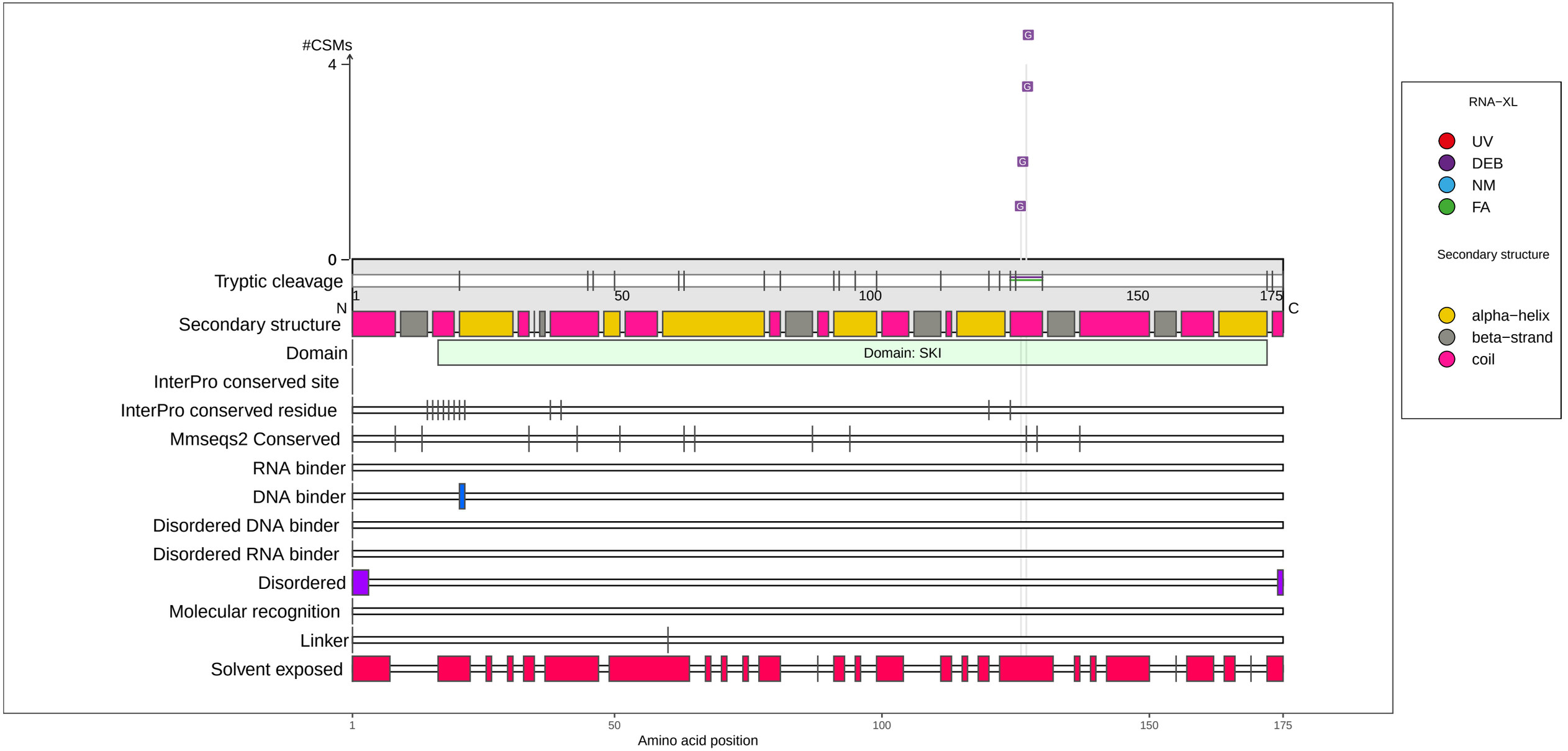
− RNA functions: not annotated



P46859
GNTK_ECOLI Thermoresistant gluconokinase

− Abundance:
tryptic [log10 Intensity]: 7.6 (Q 40)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 0.91 (Q 45)

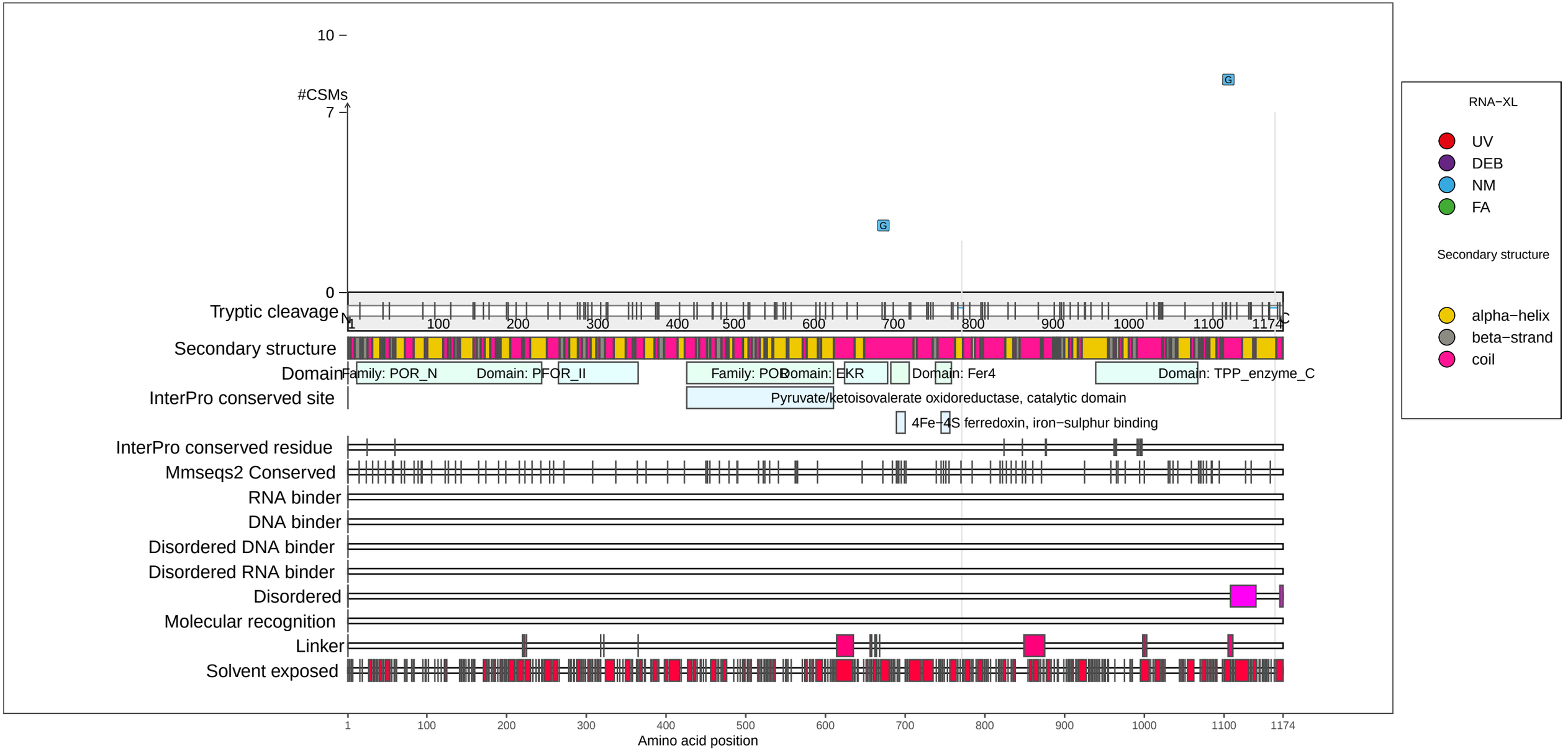
− RNA functions: not annotated



P52647
NIFJ_ECOLI Probable pyruvate−flavodoxin oxidoreductase

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: 2.22 (Q 68)
PAXdb E.coli [ppm]: 1.72 (Q 65)

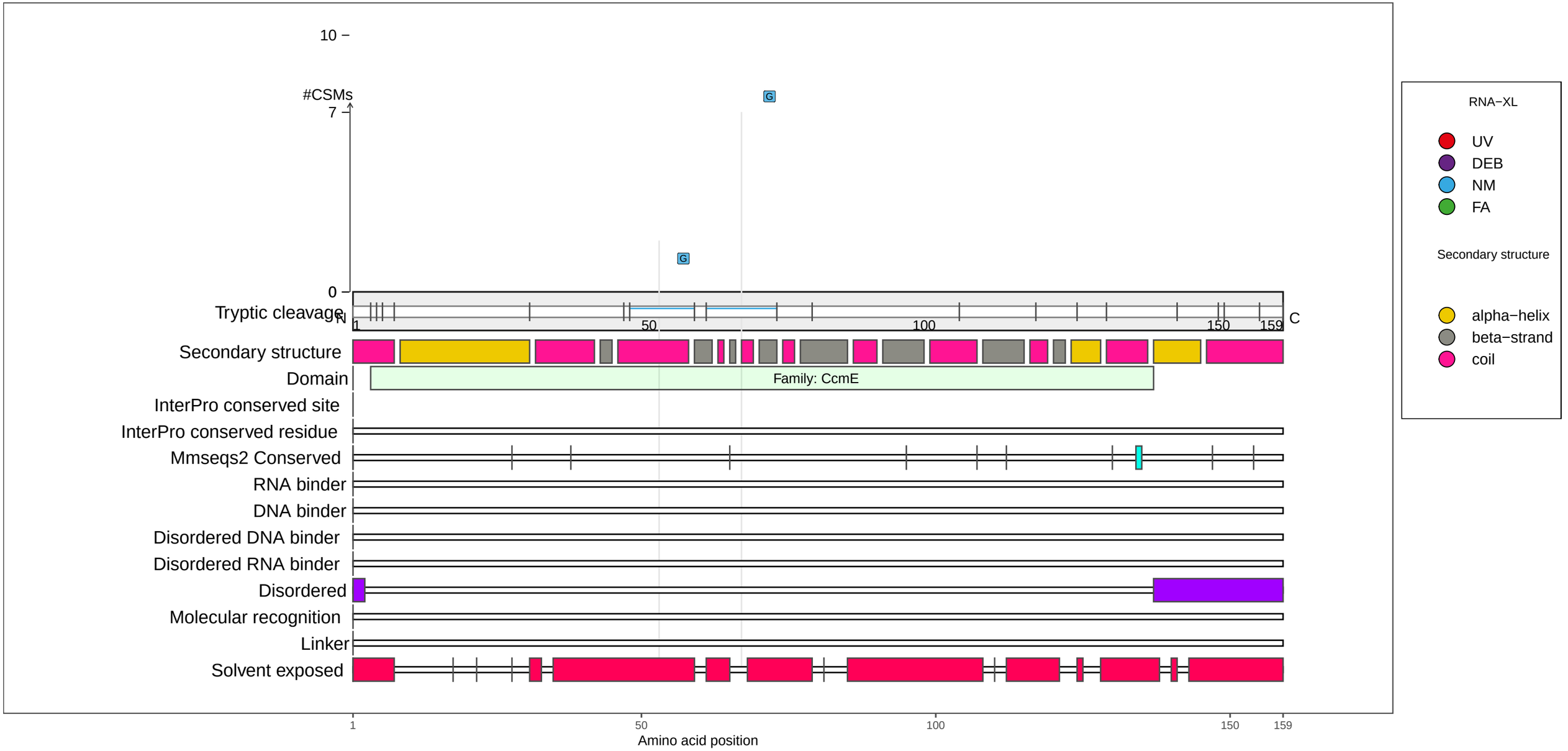
− RNA functions: not annotated



P69490
CCME_ECOLI Cytochrome c−type biogenesis protein CcmE

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 57)
PAXdb K12 strain [ppm]: 1.26 (Q 23)
PAXdb E.coli [ppm]: 0.18 (Q 29)

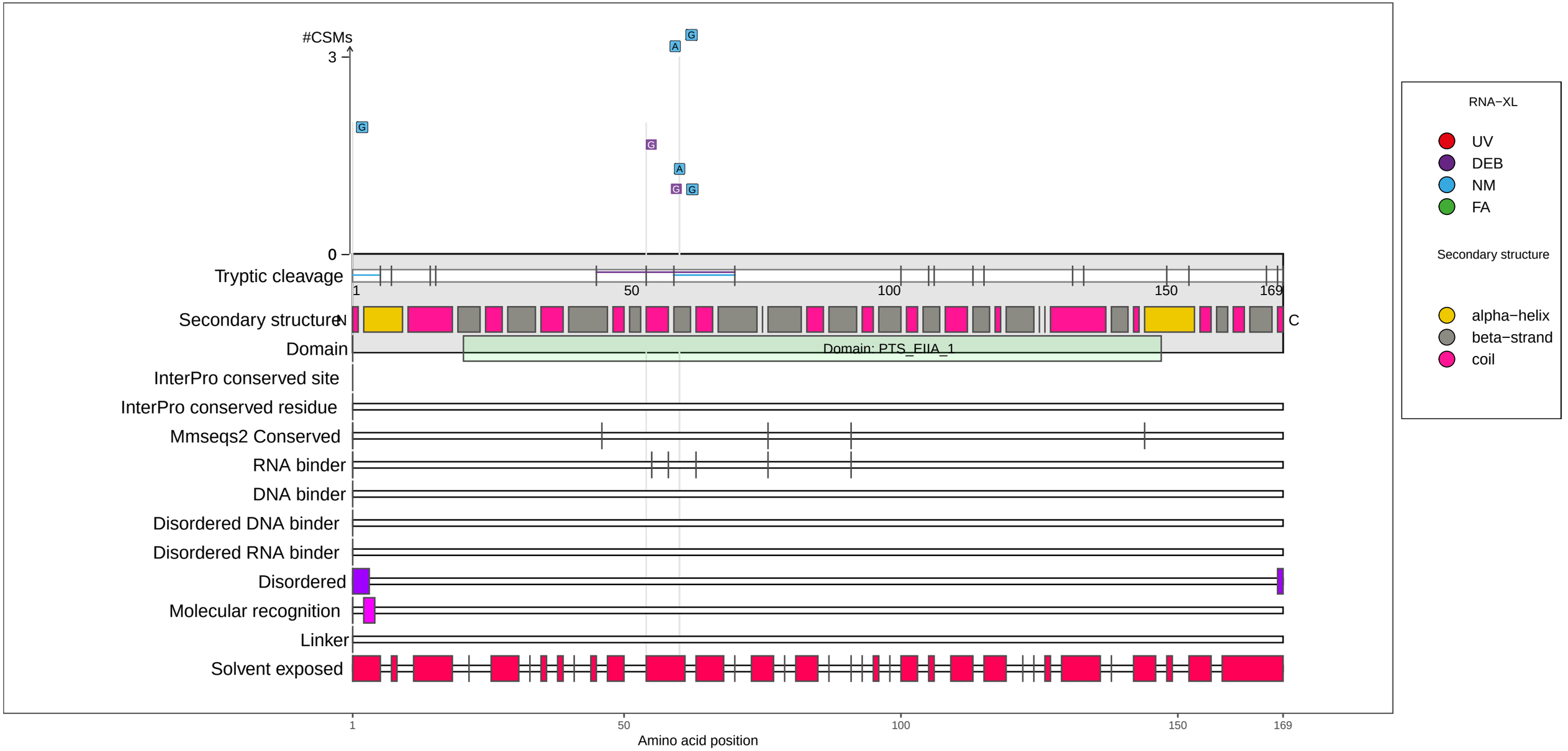
− RNA functions: not annotated



P69783
PTGA_ECOLI PTS system glucose−specific EIIA component

− Abundance:
tryptic [log10 Intensity]: 9.17 (Q 92)
PAXdb K12 strain [ppm]: 3.32 (Q 95)
PAXdb E.coli [ppm]: 3.5 (Q 99)

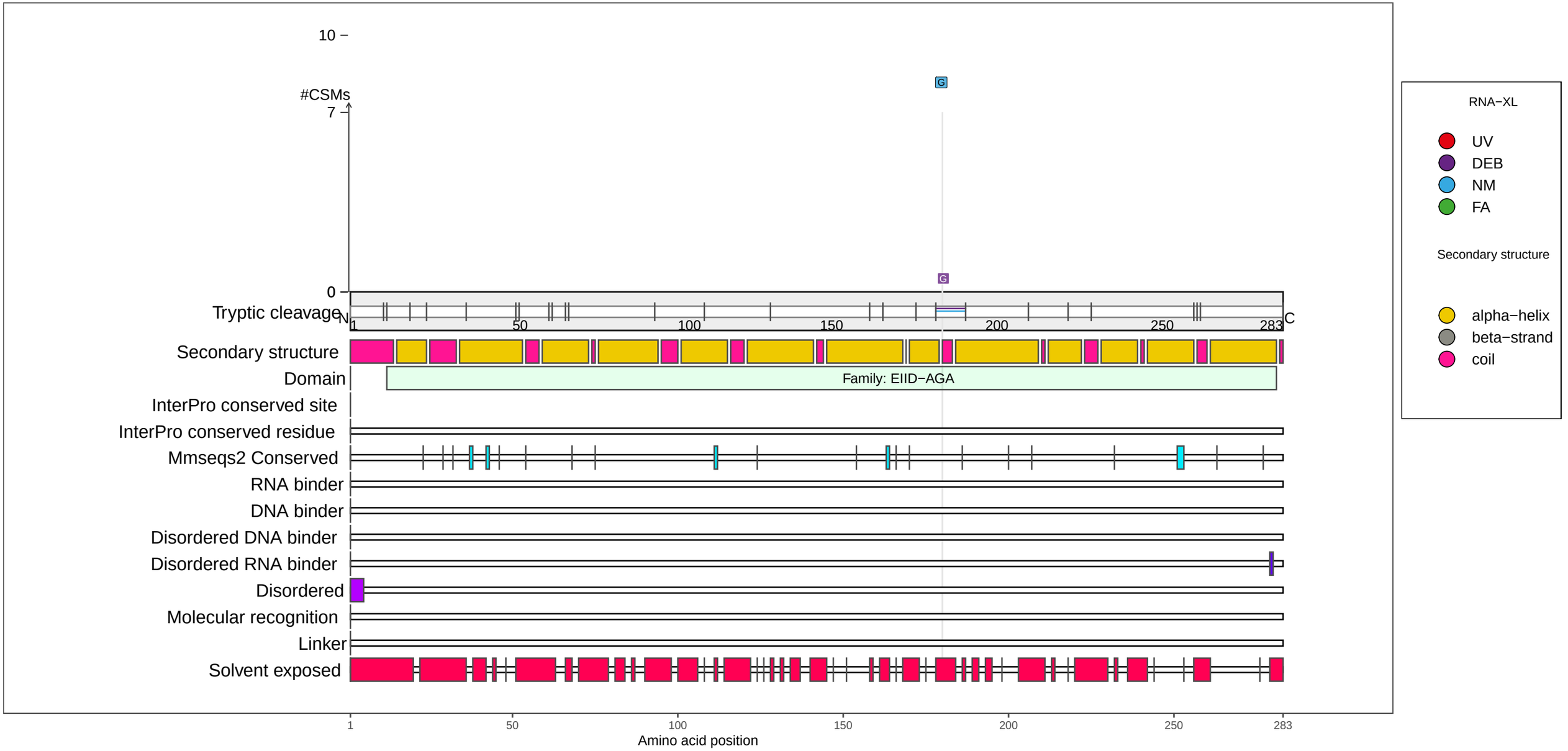
− RNA functions: not annotated



P69805
PTND_ECOLI PTS system mannose−specific EIID component

− Abundance:
tryptic [log10 Intensity]: 8.87 (Q 85)
PAXdb K12 strain [ppm]: 1.51 (Q 39)
PAXdb E.coli [ppm]: 2.58 (Q 88)

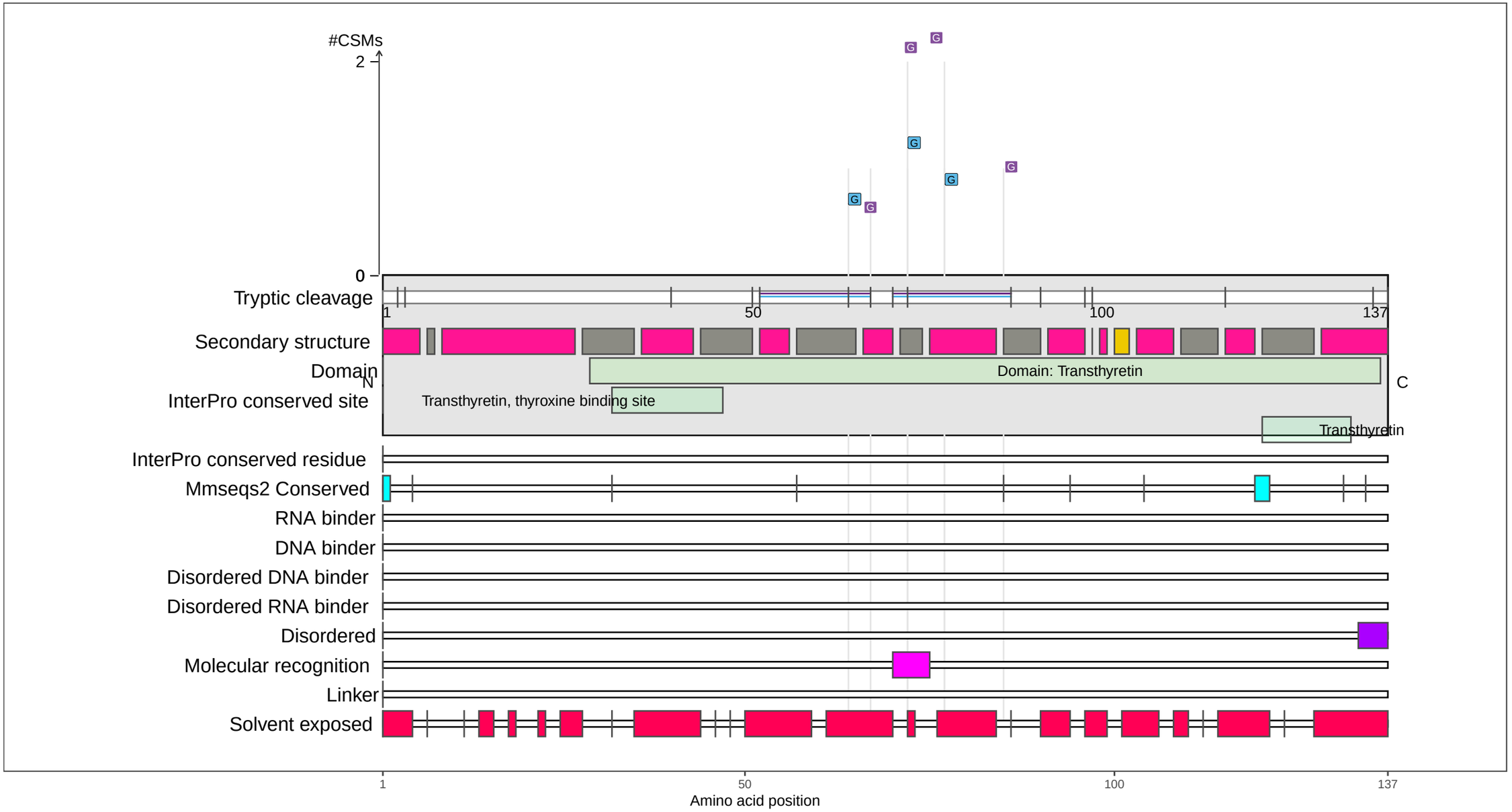
− RNA functions: not annotated



P76341
HIUH_ECOLI 5−hydroxyisourate hydrolase

− Abundance:
tryptic [log10 Intensity]: 7.33 (Q 26)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.95 (Q 47)

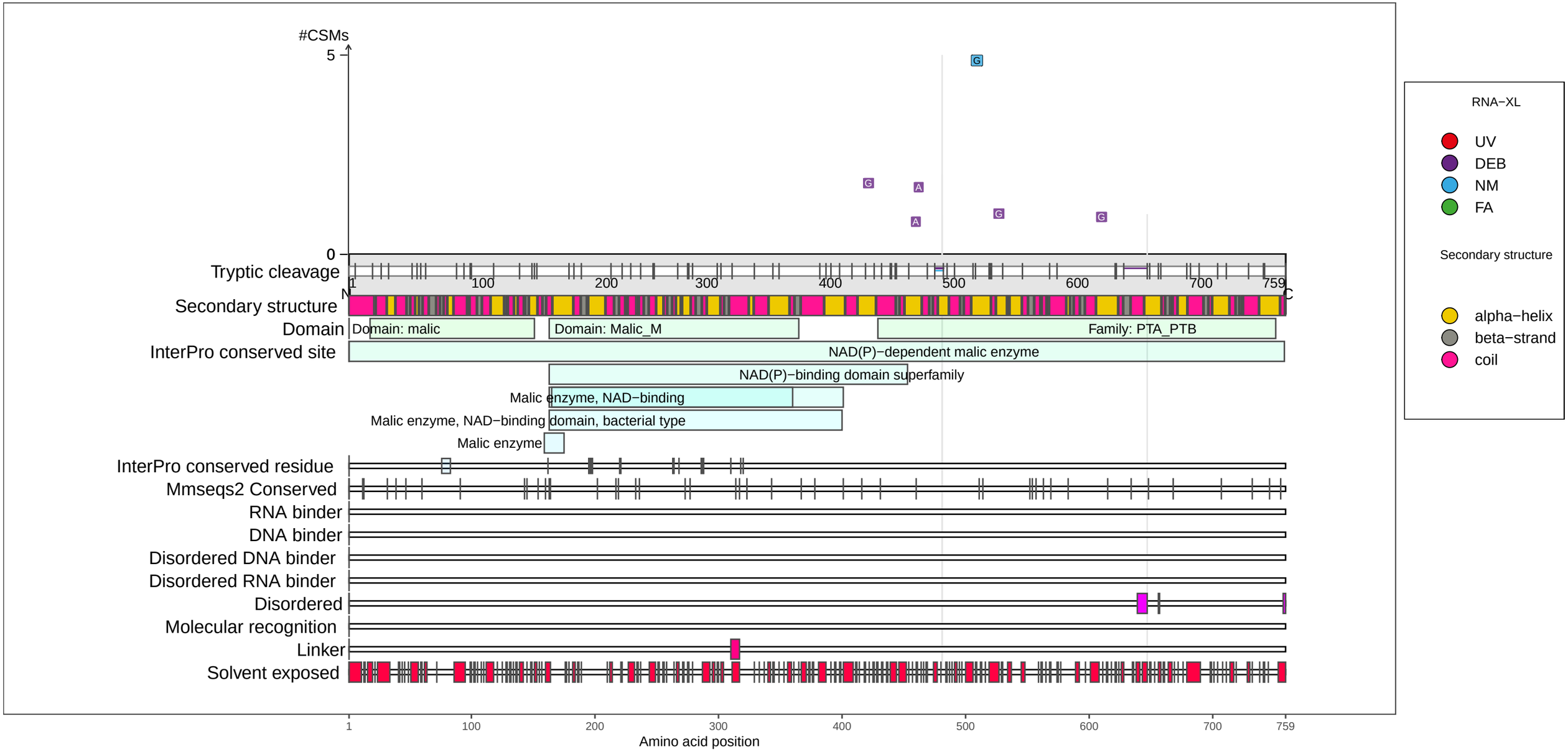
− RNA functions: not annotated



P76558
MAO2_ECOLI NADP−dependent malic enzyme

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 2.55 (Q 79)
PAXdb E.coli [ppm]: 2.83 (Q 92)

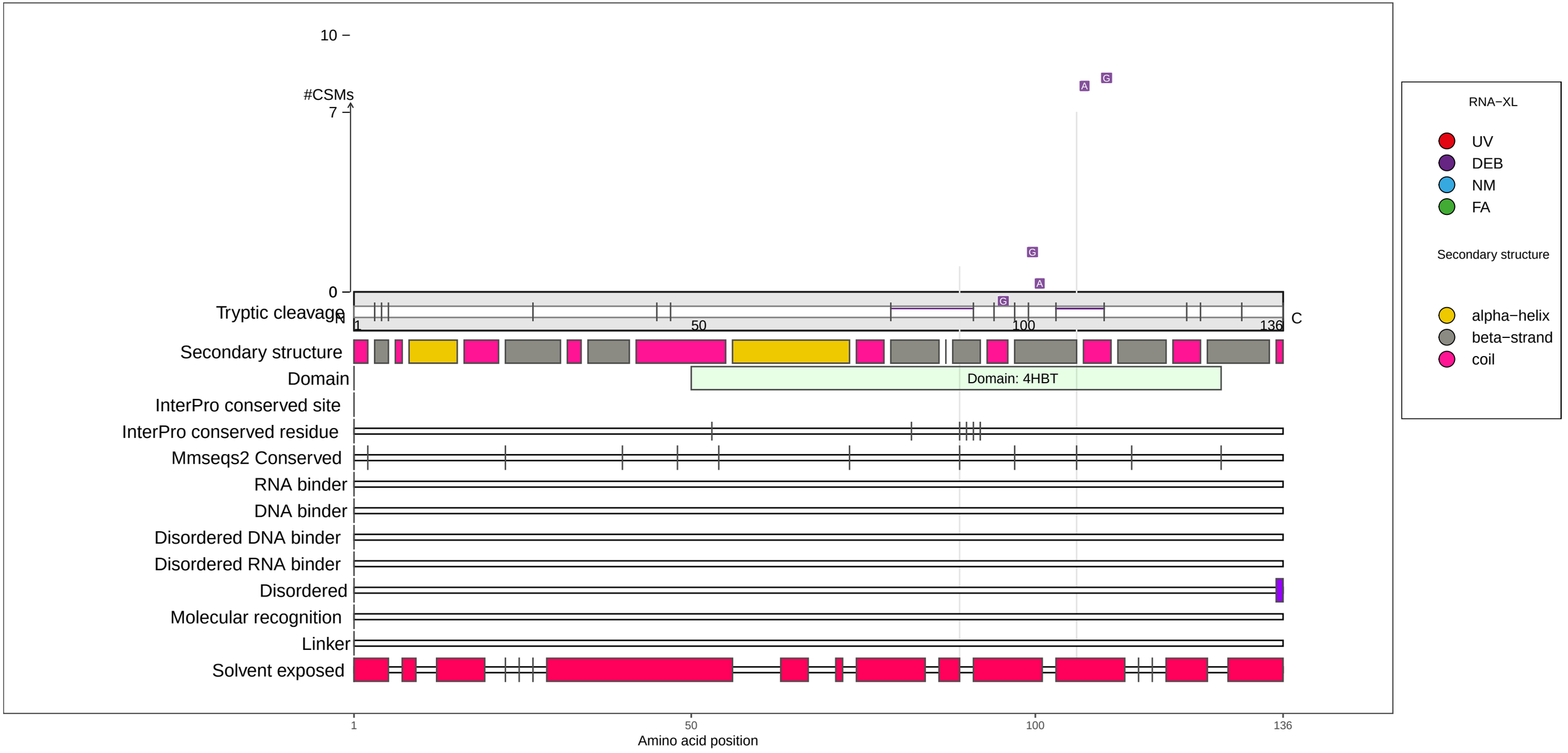
− RNA functions: not annotated



P77781
MENI_ECOLI 1,4−dihydroxy−2−naphthoyl−CoA hydrolase

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: 1.75 (Q 51)
PAXdb E.coli [ppm]: 1.51 (Q 60)

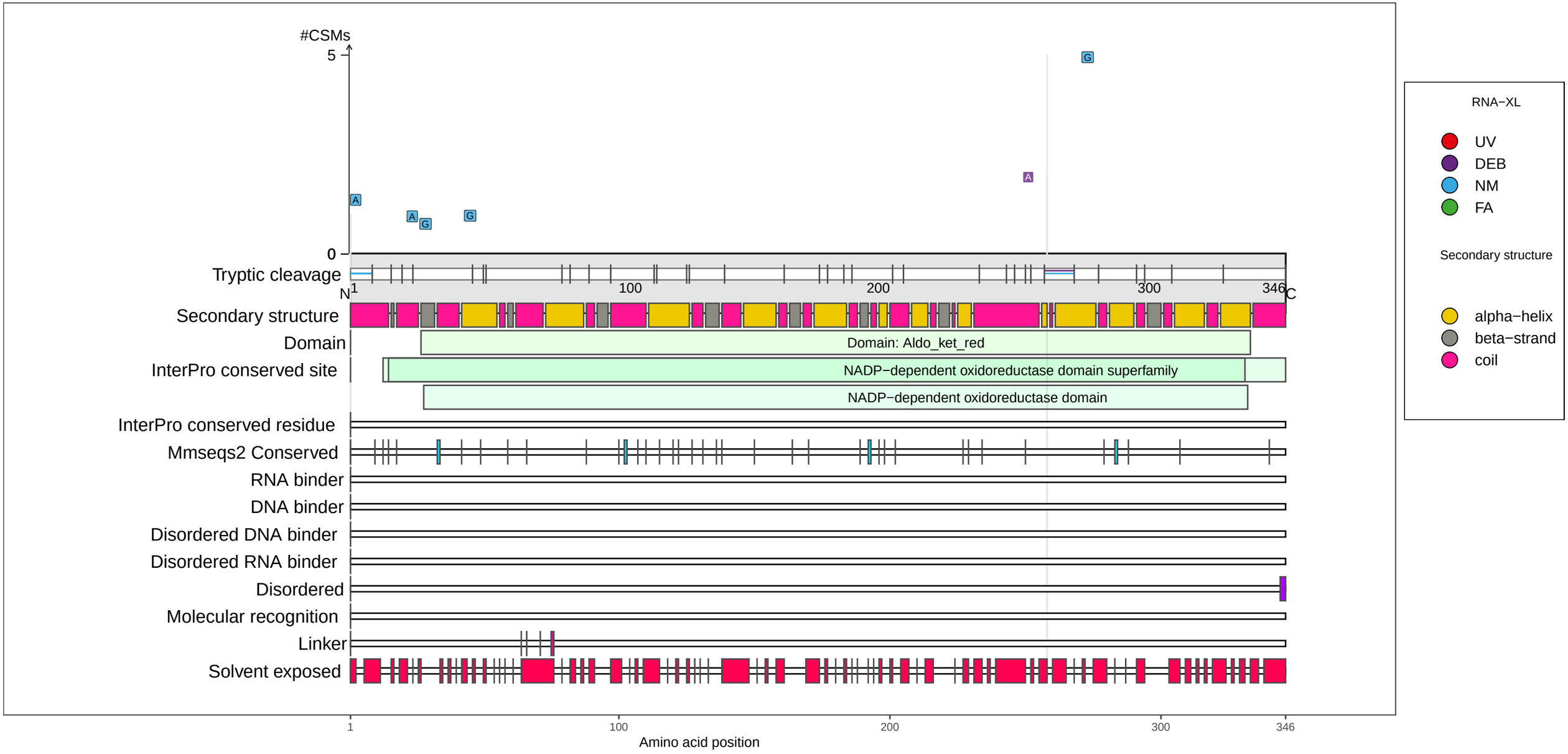
− RNA functions: not annotated



Q46851
GPR_ECOLI L−glyceraldehyde 3−phosphate reductase

− Abundance:
tryptic [log10 Intensity]: 8.07 (Q 60)
PAXdb K12 strain [ppm]: 2.54 (Q 78)
PAXdb E.coli [ppm]: 2.56 (Q 87)

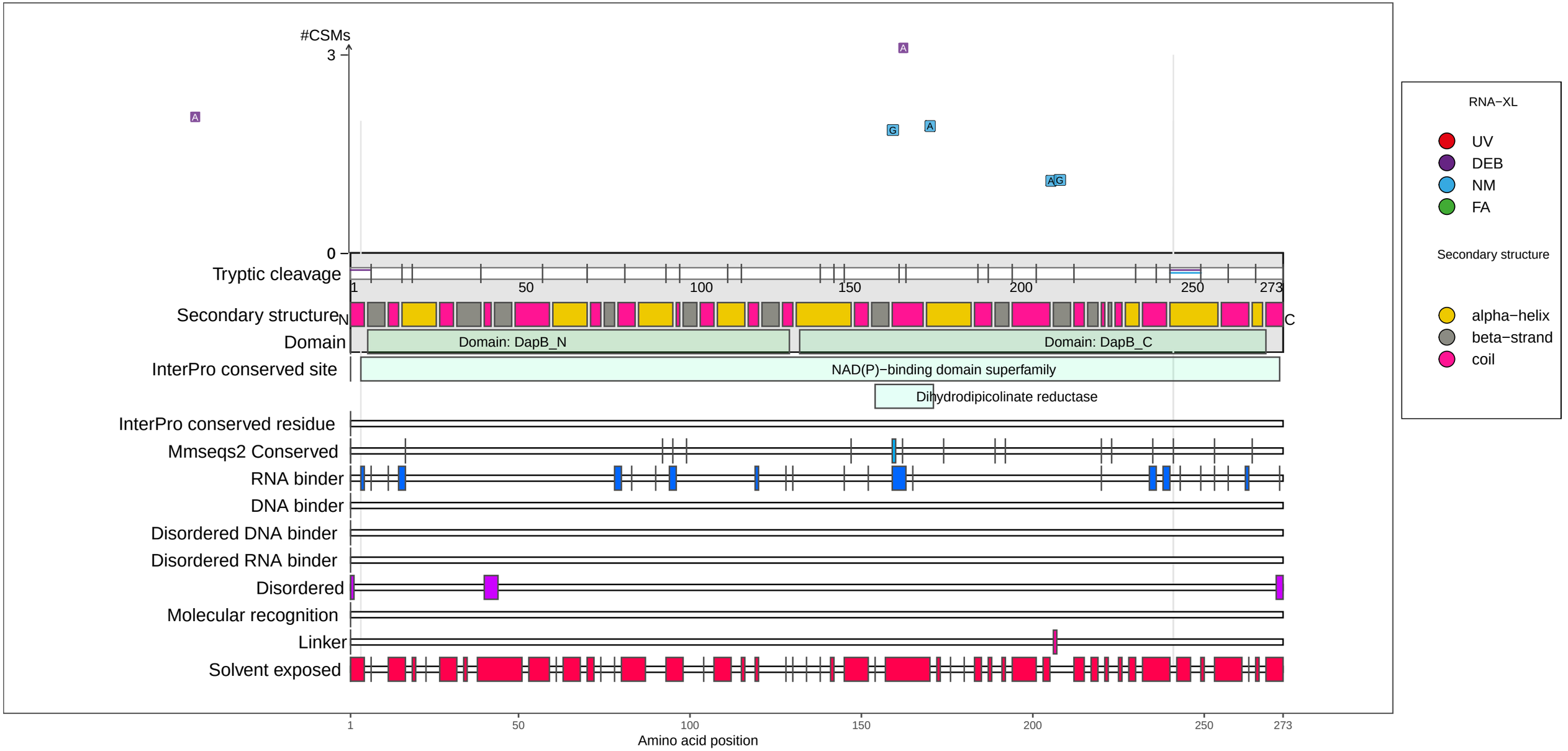
− RNA functions: not annotated



P04036
DAPB_ECOLI 4−hydroxy−tetrahydrodipicolinate reductase

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 50)
PAXdb K12 strain [ppm]: 1.96 (Q 59)
PAXdb E.coli [ppm]: 2.54 (Q 86)

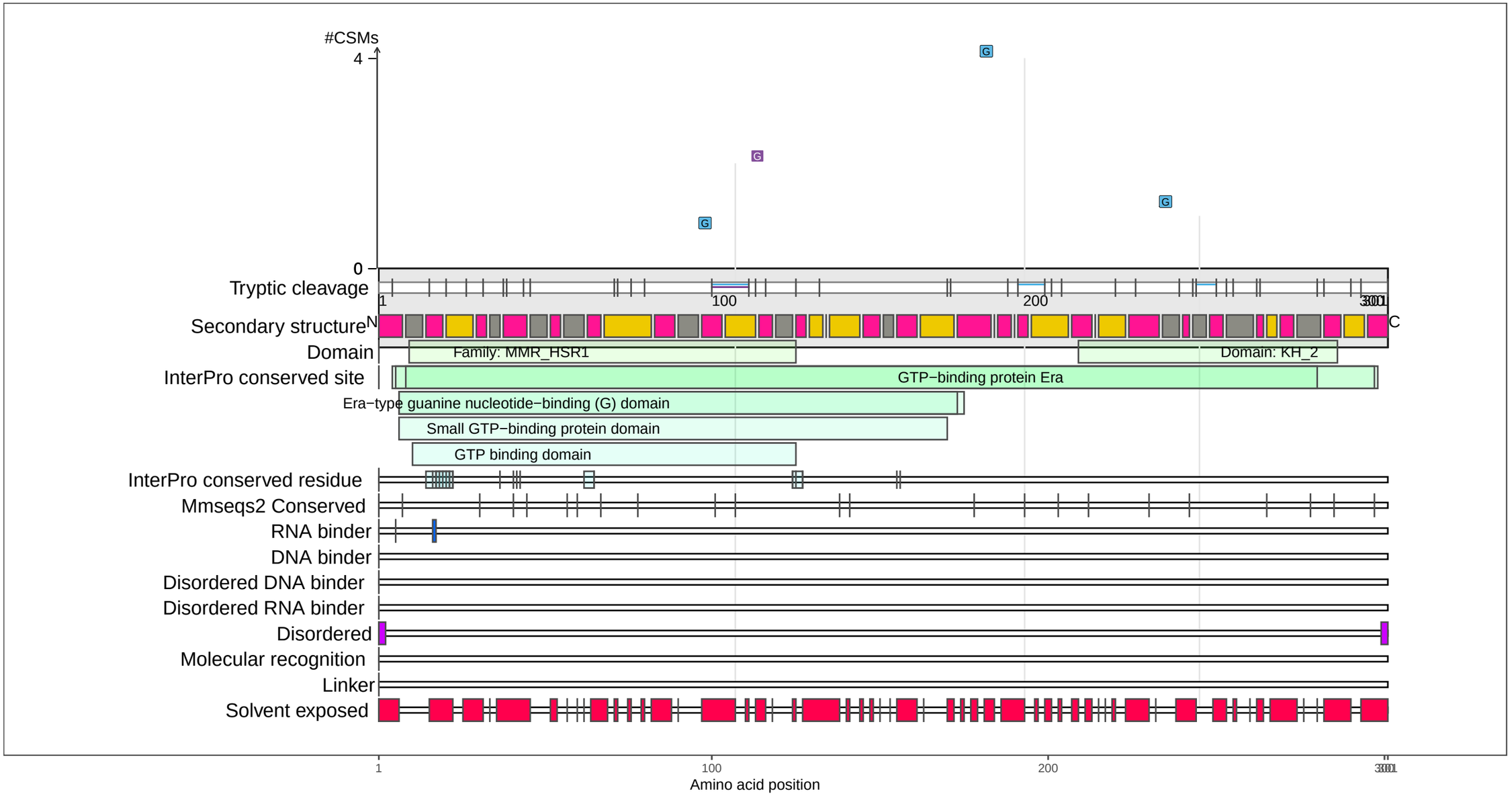
− RNA functions: not annotated



P06616
ERA_ECOLI GTPase Era

− Abundance:
tryptic [log10 Intensity]: 6.93 (Q 11)
PAXdb K12 strain [ppm]: 2.4 (Q 74)
PAXdb E.coli [ppm]: 1.59 (Q 62)

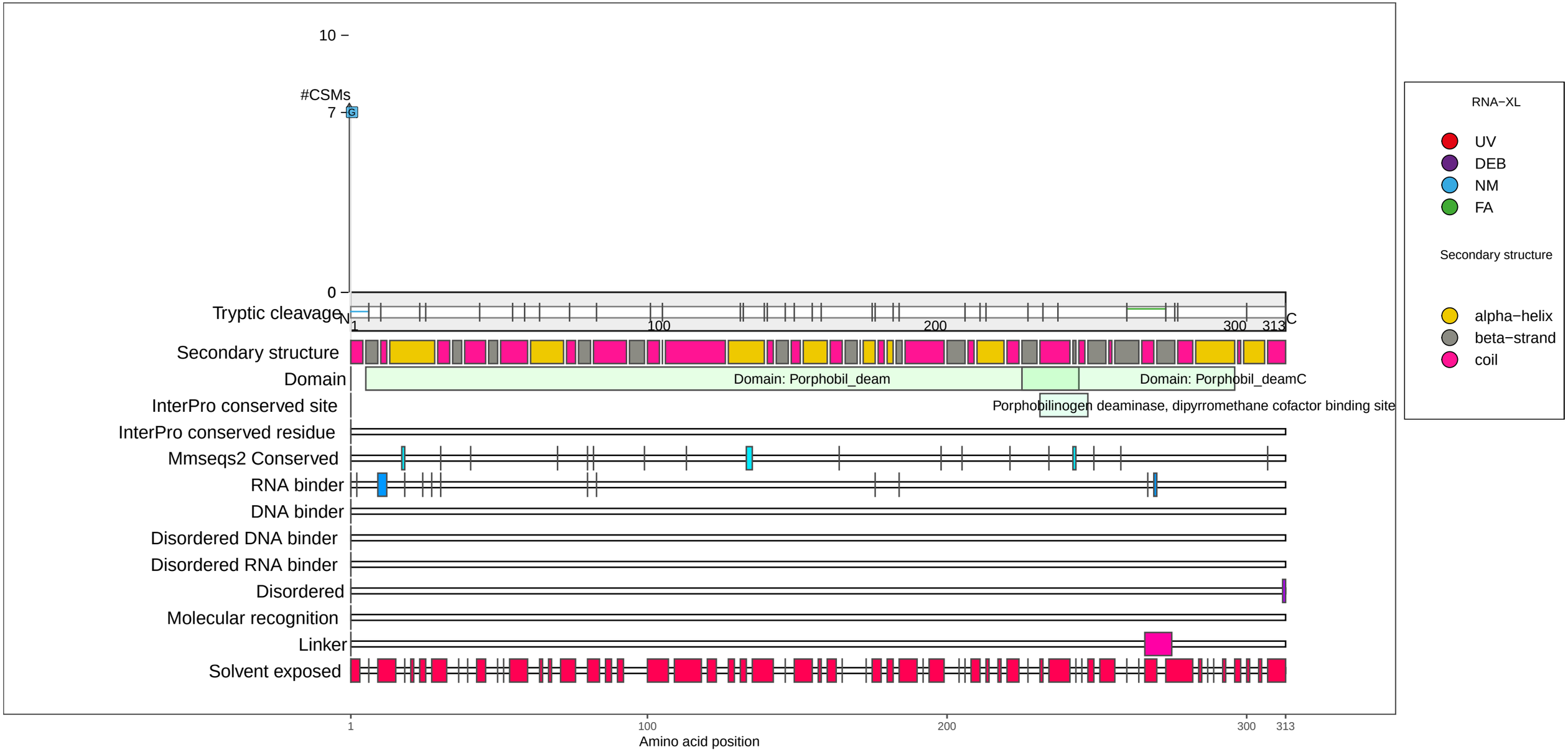
− RNA functions:
RNA binding; rRNA binding



P06983
HEM3_ECOLI Porphobilinogen deaminase

− Abundance:
tryptic [log10 Intensity]: 7.66 (Q 43)
PAXdb K12 strain [ppm]: 1.87 (Q 56)
PAXdb E.coli [ppm]: 1.19 (Q 52)

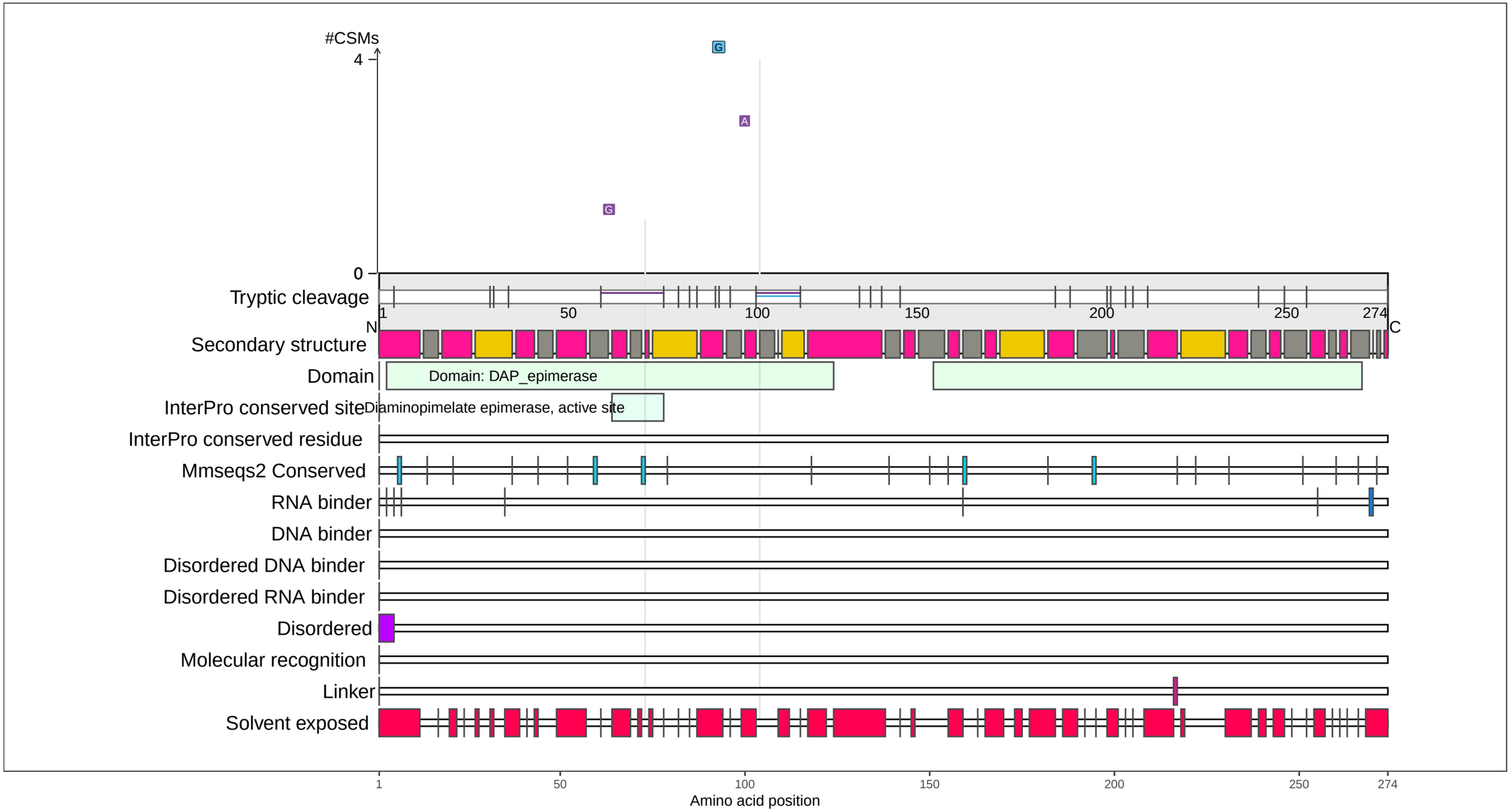
− RNA functions: not annotated

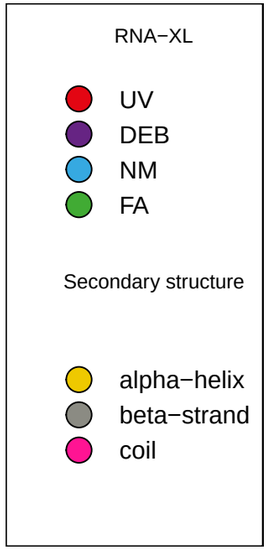


P0A6K1
DAPF_ECOLI Diaminopimelate epimerase

− Abundance:
tryptic [log10 Intensity]: 7.38 (Q 29)
PAXdb K12 strain [ppm]: 2.11 (Q 64)
PAXdb E.coli [ppm]: 2.11 (Q 75)

− RNA functions: not annotated

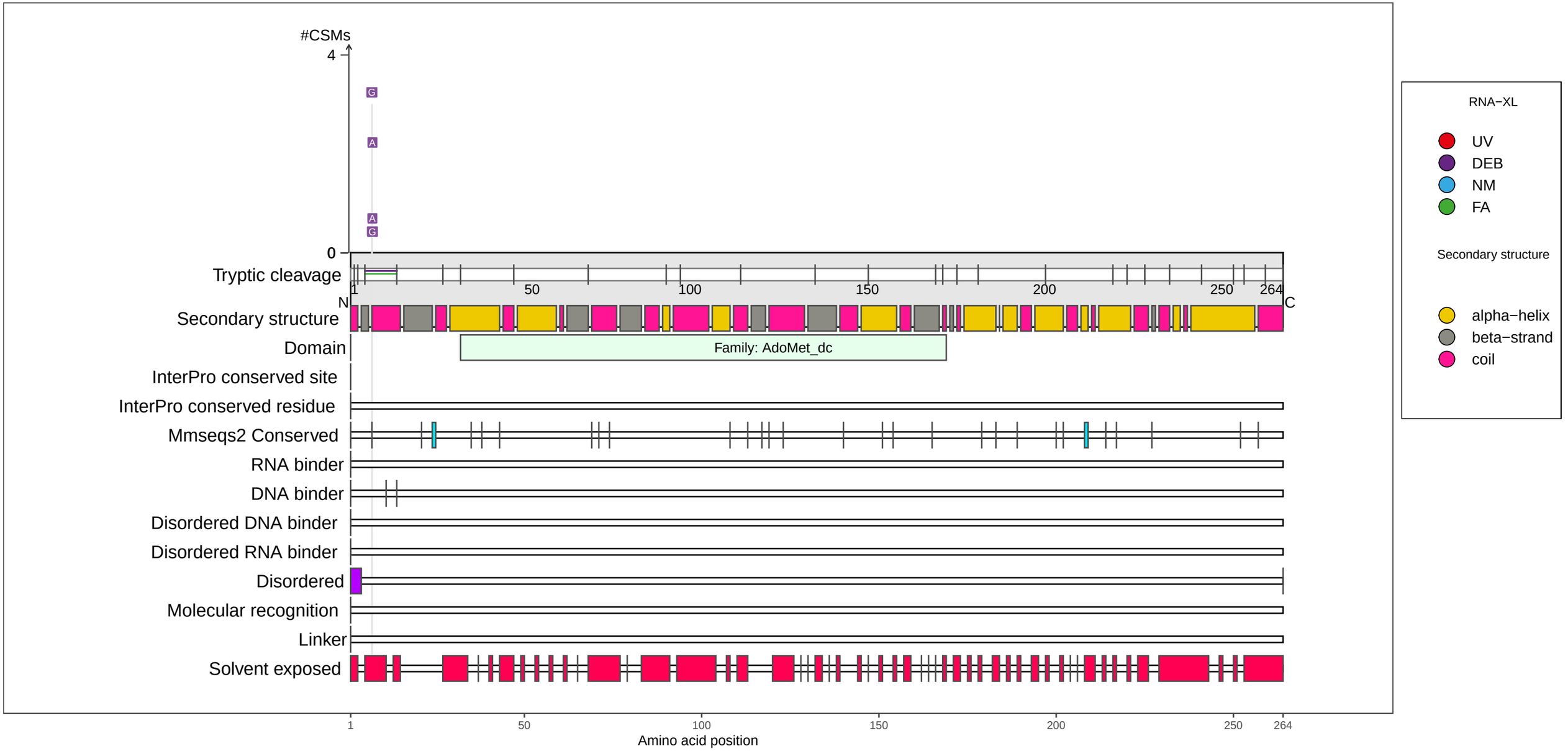




P0A7F6
SPED_ECOLI S−adenosylmethionine decarboxylase proenzyme

− Abundance:
tryptic [log10 Intensity]: 8.66 (Q 80)
PAXdb K12 strain [ppm]: 2.08 (Q 63)
PAXdb E.coli [ppm]: 2.18 (Q 77)

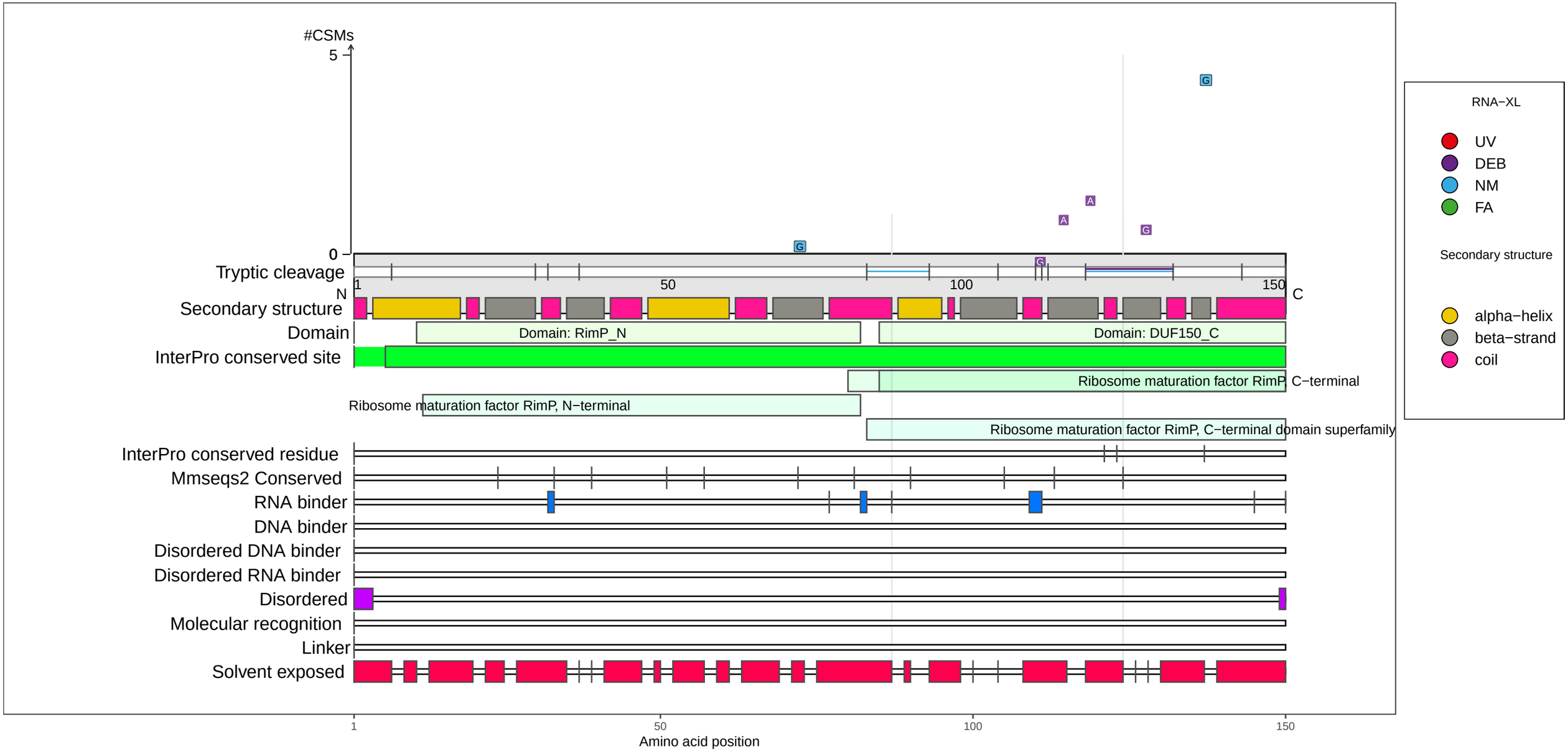
− RNA functions: not annotated



P0A8A8
RIMP_ECOLI Ribosome maturation factor RimP

− Abundance:
tryptic [log10 Intensity]: 9.48 (Q 96)
PAXdb K12 strain [ppm]: 2.21 (Q 67)
PAXdb E.coli [ppm]: 2.09 (Q 75)

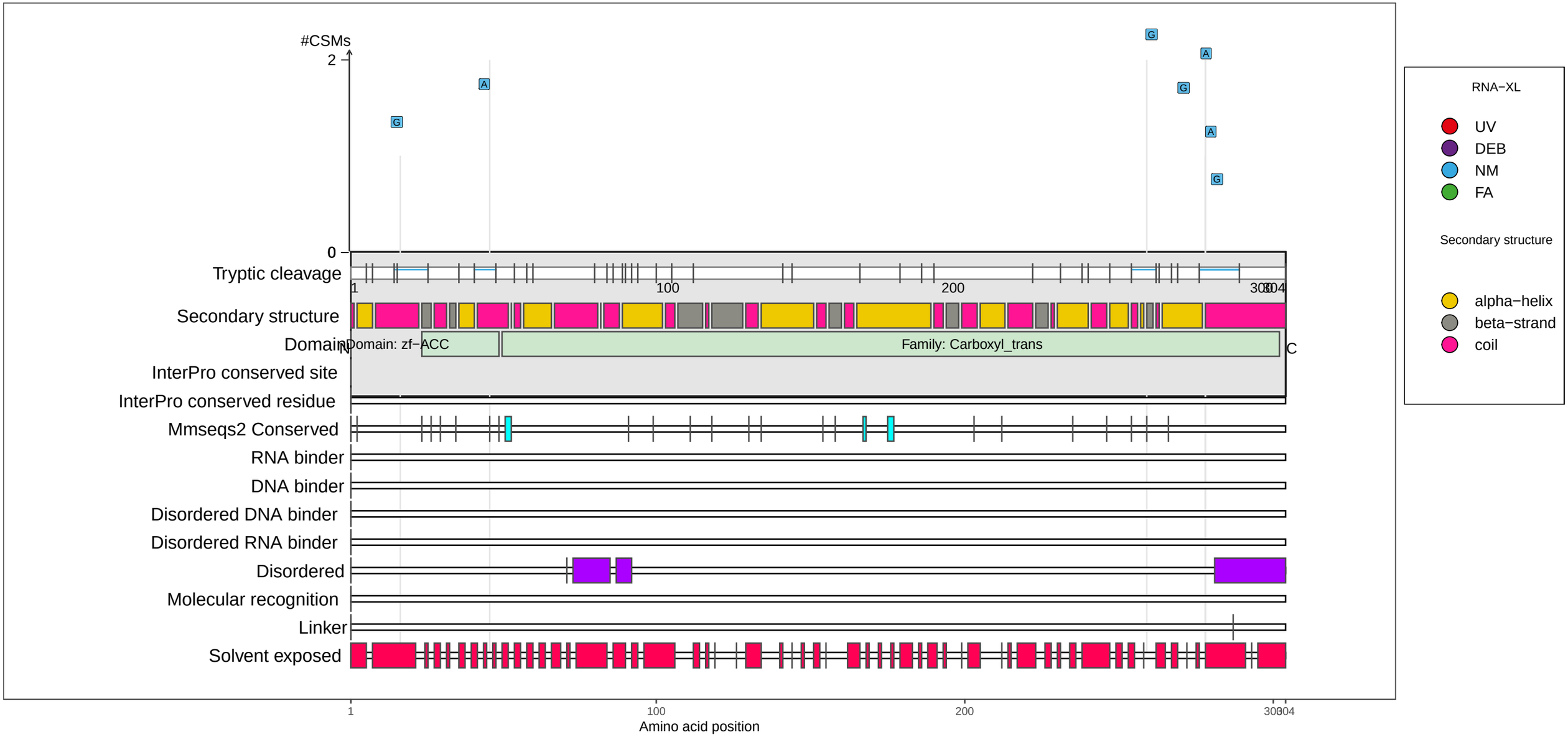
− RNA functions: not annotated



P0A9Q5
ACCD_ECOLI Acetyl−coenzyme A carboxylase carboxyl transferase subunit beta

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: 3.09 (Q 92)
PAXdb E.coli [ppm]: 2.58 (Q 87)

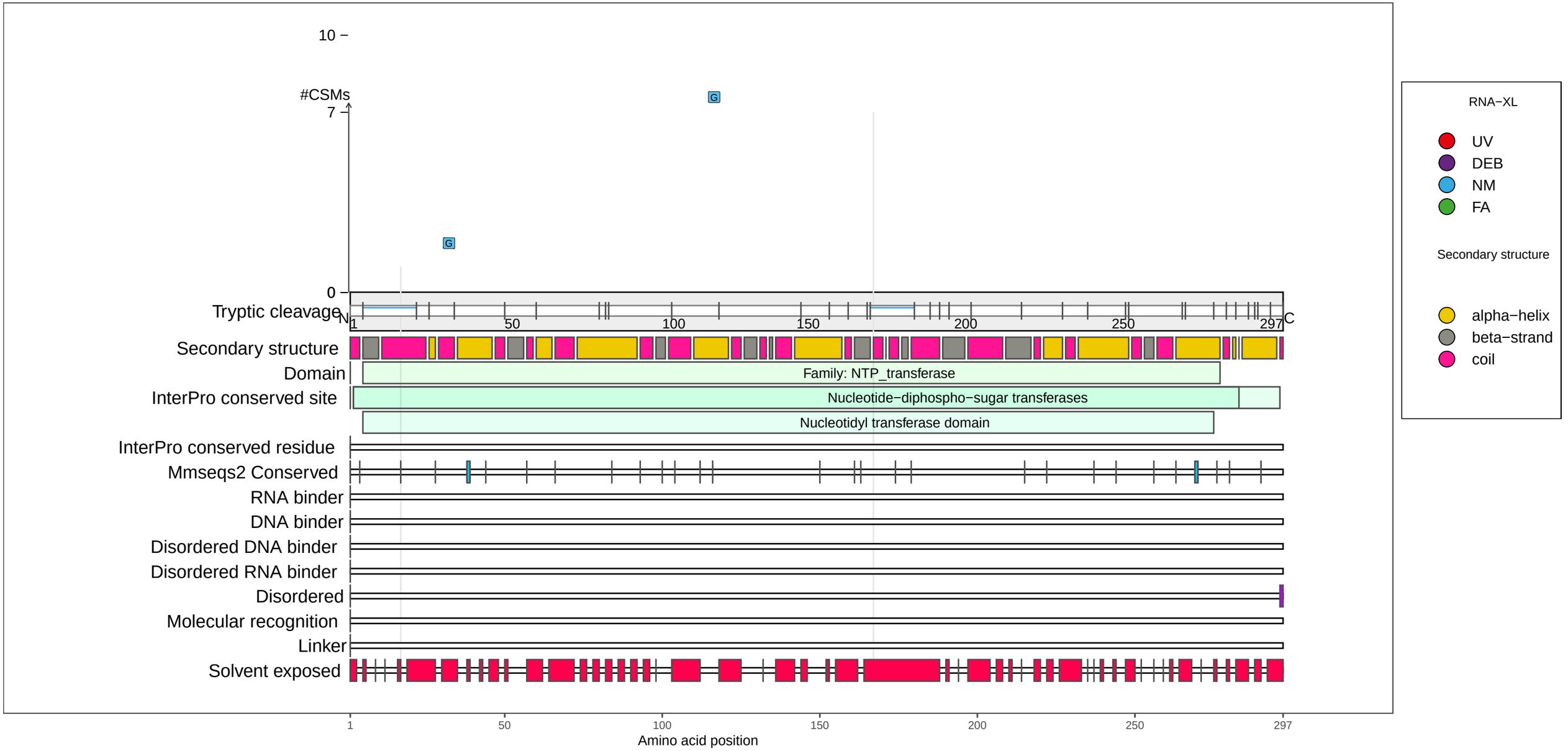
− RNA functions:
mRNA binding; RNA binding



P0AAB6
GALF_ECOLI UTP−−glucose−1−phosphate uridylyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 50)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.97 (Q 94)

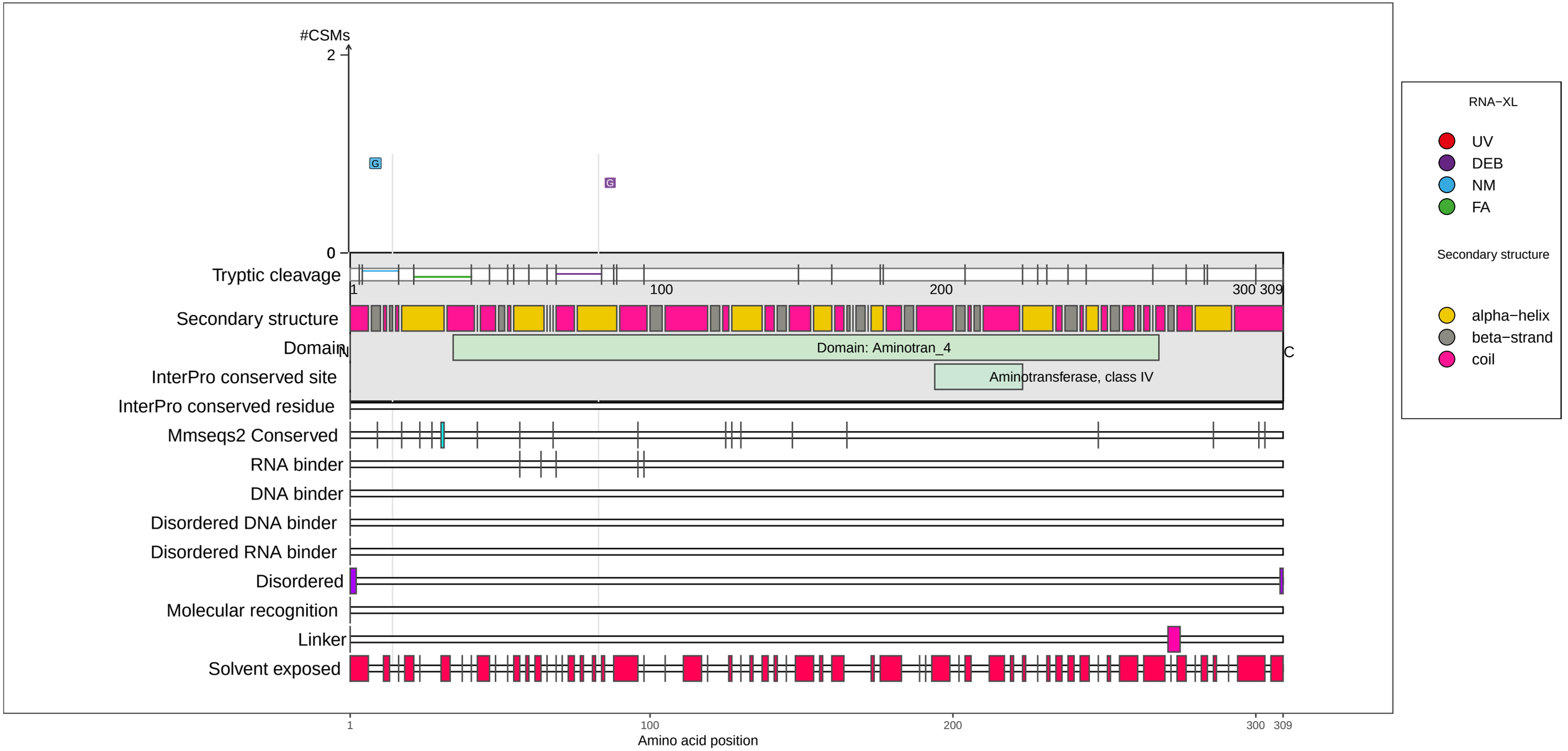
− RNA functions: not annotated



P0AB80
ILVE_ECOLI Branched−chain−amino−acid aminotransferase

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 2.75 (Q 85)
PAXdb E.coli [ppm]: 2.31 (Q 80)

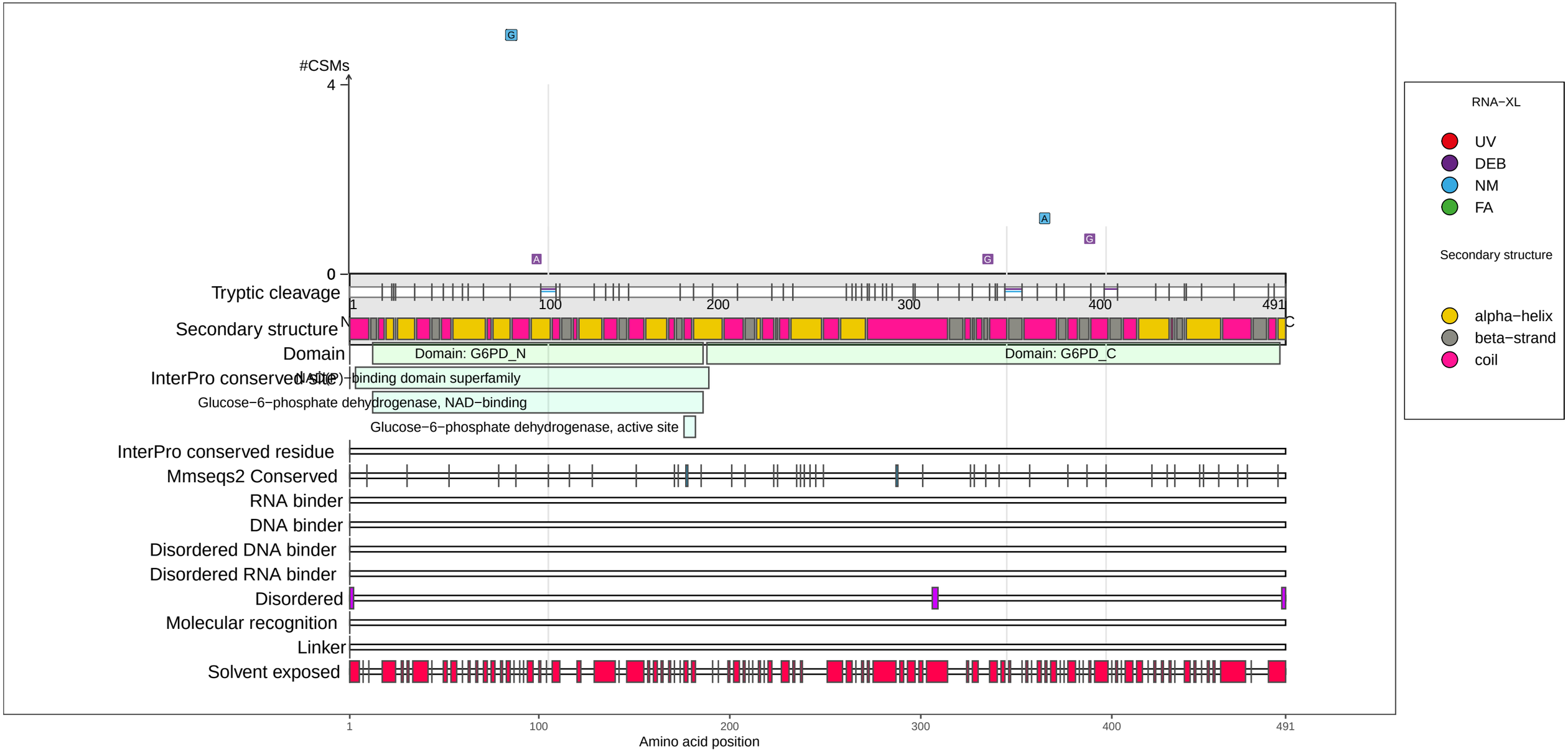
− RNA functions: not annotated



P0AC53
G6PD_ECOLI Glucose−6−phosphate 1−dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.95 (Q 87)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 2.76 (Q 91)

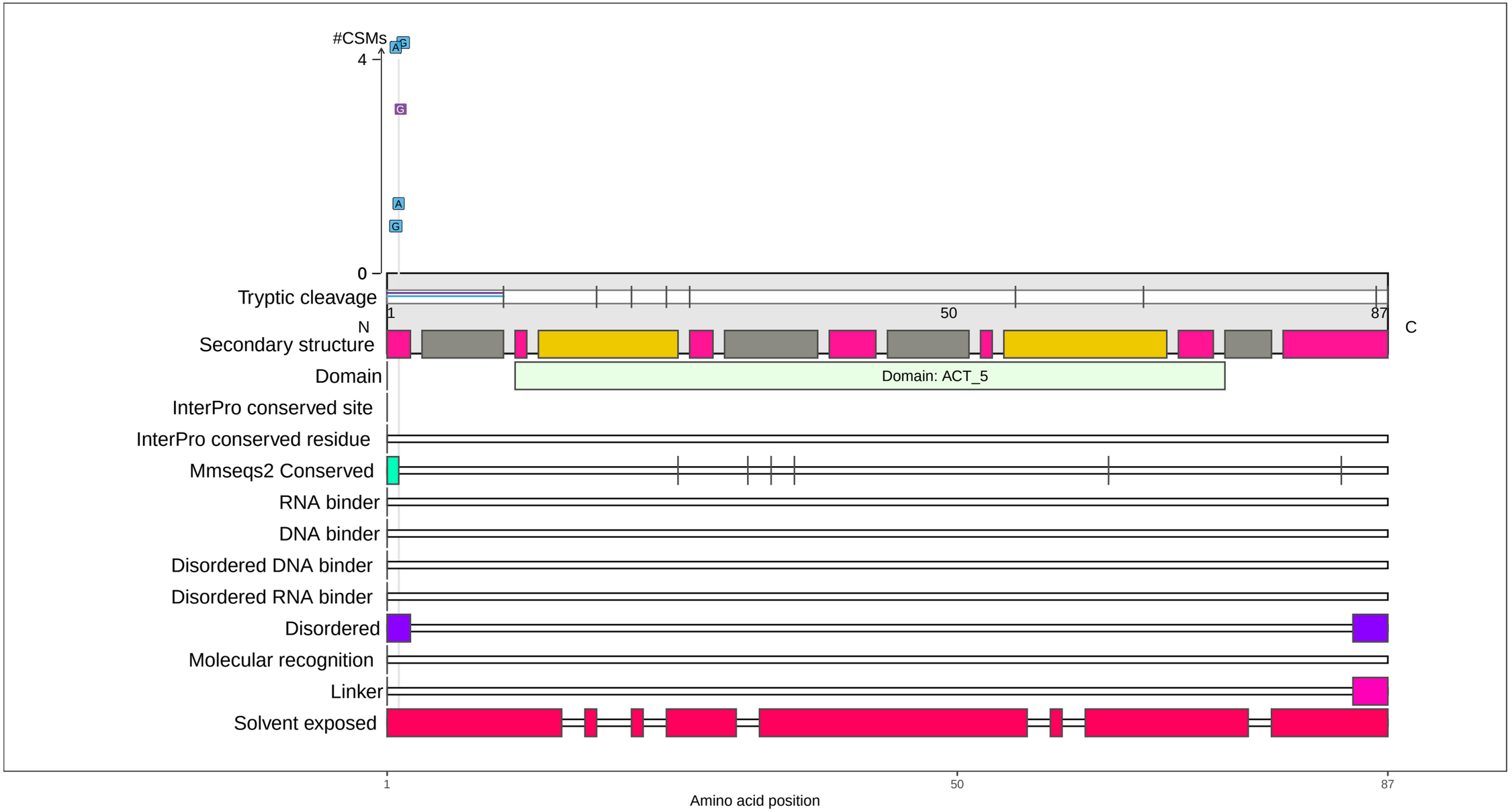
− RNA functions: not annotated

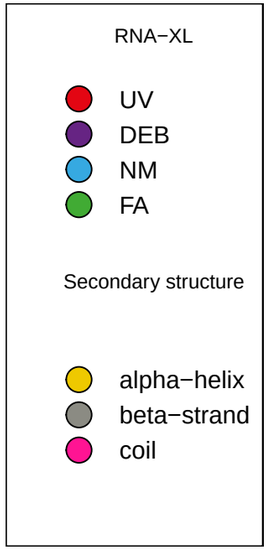


P0ADG1
ILVM_ECOLI Acetolactate synthase isozyme 2 small subunit

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

− RNA functions: not annotated

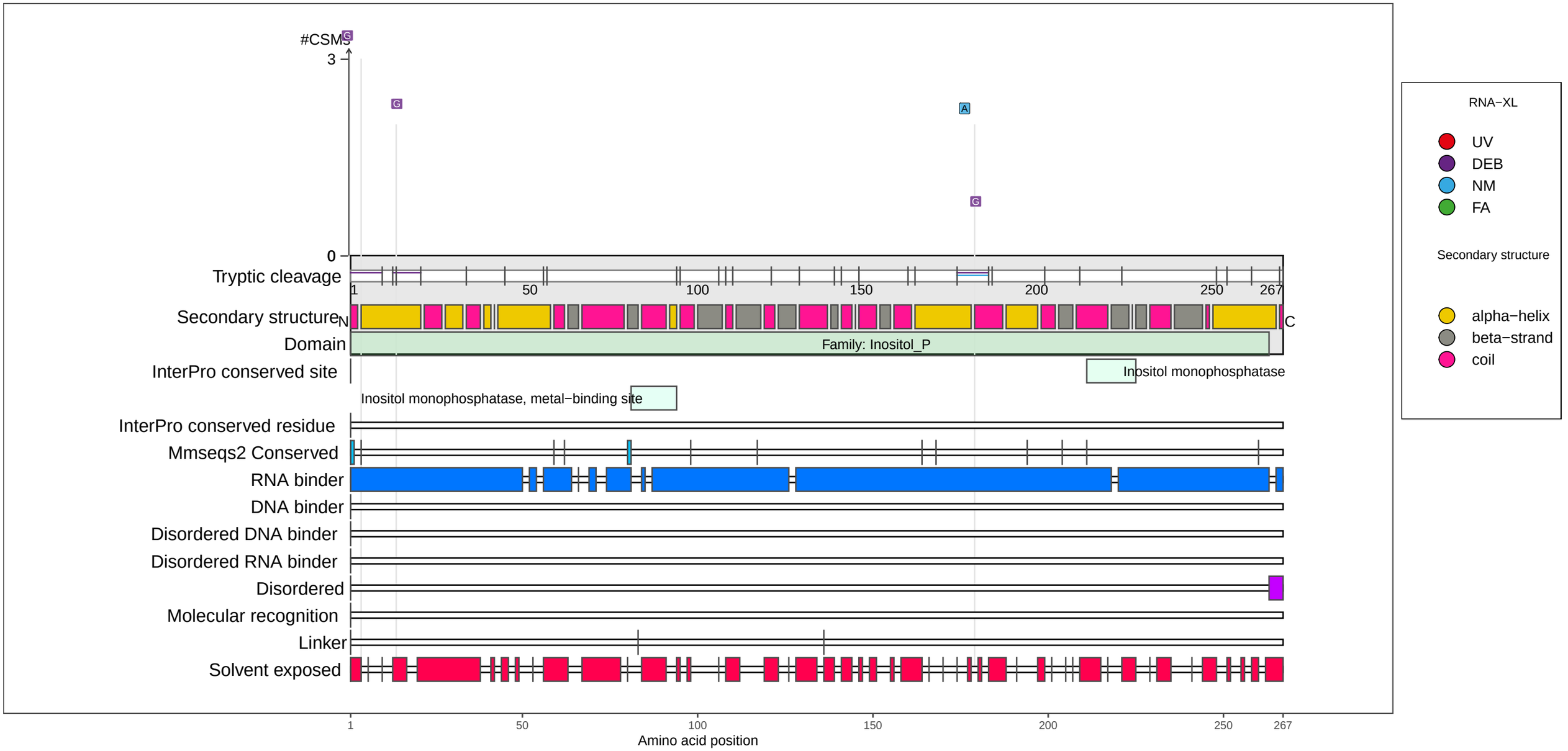




P0ADG4
SUHB_ECOLI Nus factor SuhB

− Abundance:
tryptic [log10 Intensity]: 9.28 (Q 94)
PAXdb K12 strain [ppm]: 2.31 (Q 70)
PAXdb E.coli [ppm]: 2.36 (Q 82)

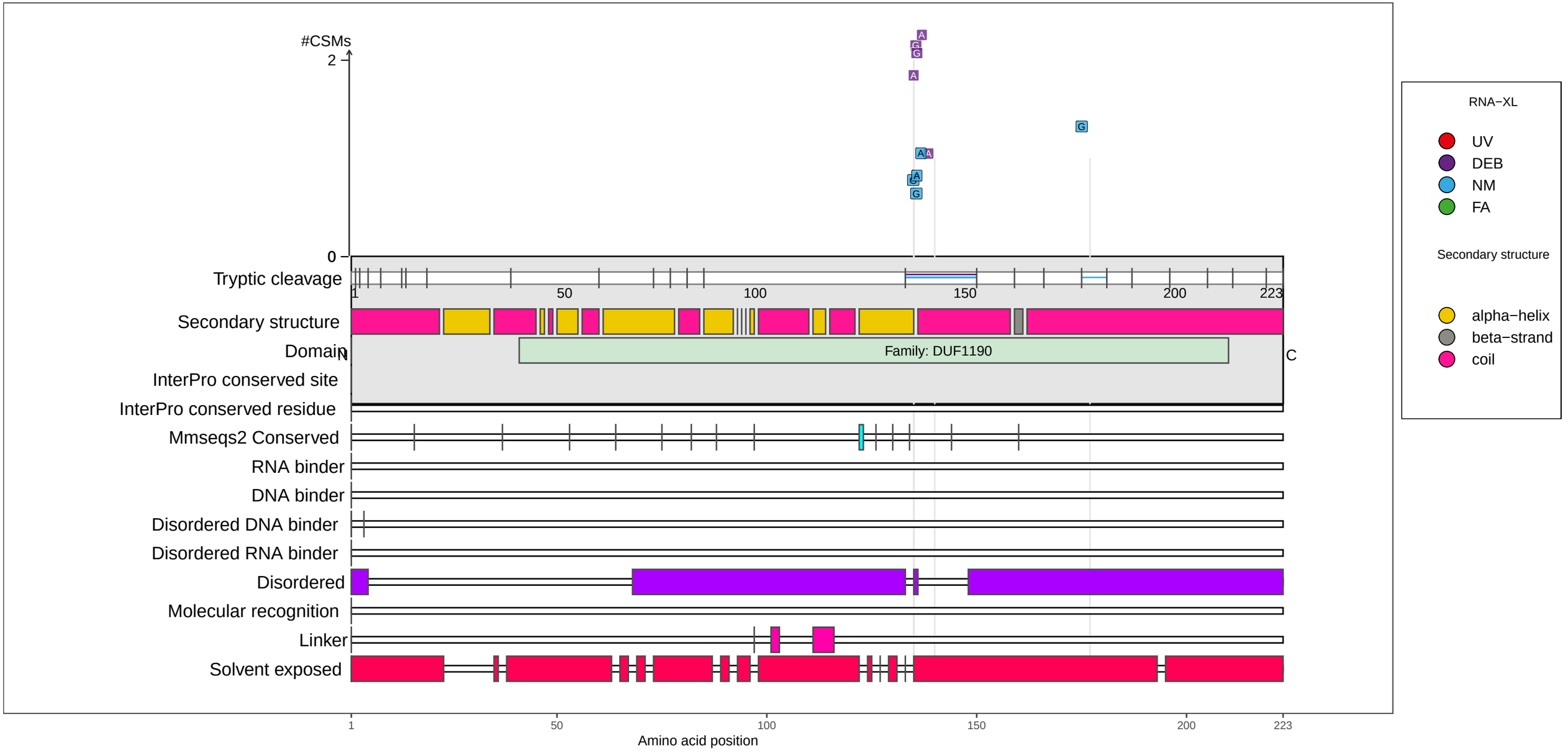
− RNA functions: not annotated



P0ADT2
YGIB_ECOLI UPF0441 protein YgiB

− Abundance:
tryptic [log10 Intensity]: 7.24 (Q 22)
PAXdb K12 strain [ppm]: 1.75 (Q 51)
PAXdb E.coli [ppm]: 1.85 (Q 68)

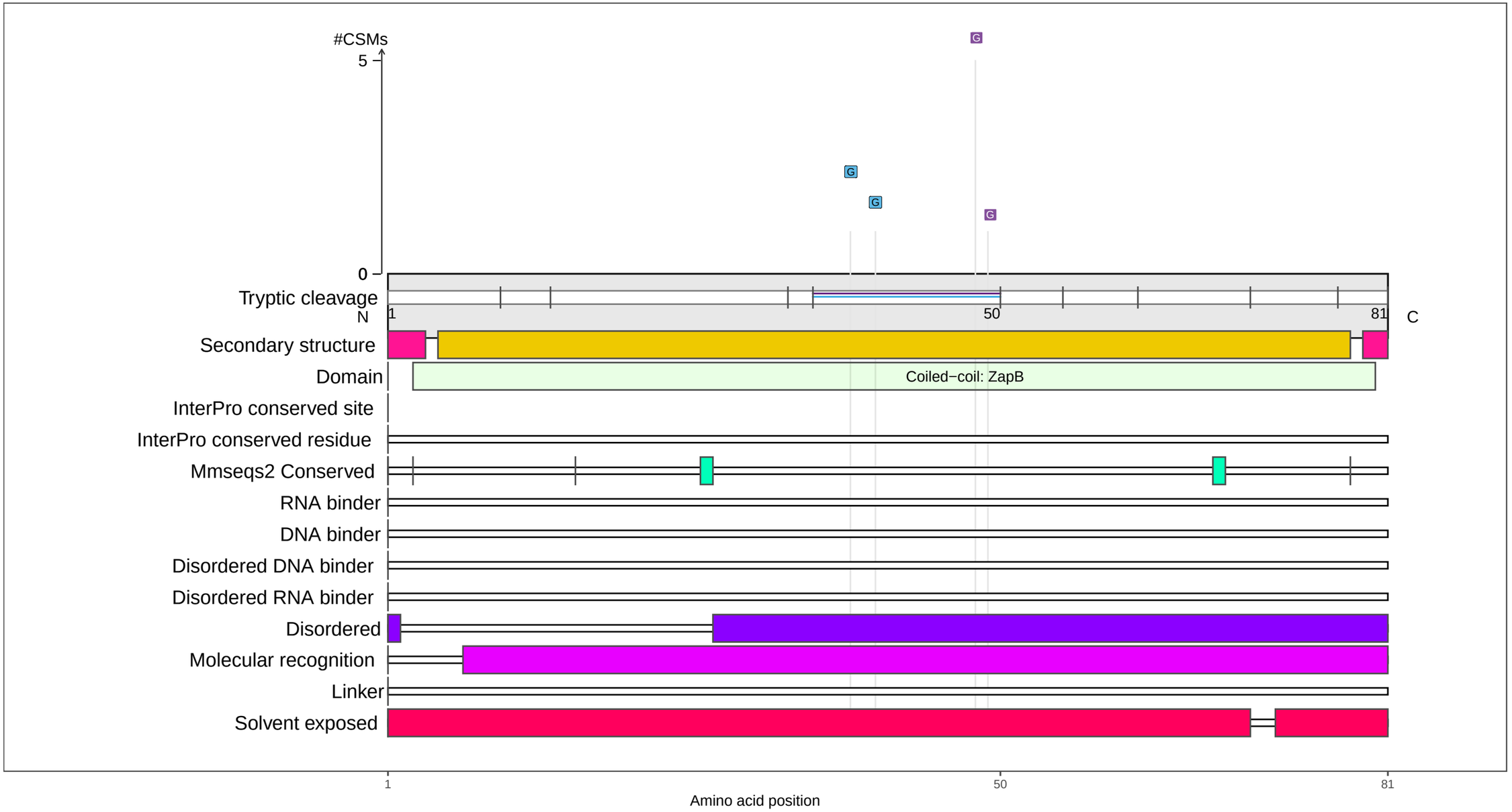
− RNA functions: not annotated



P0AF36
ZAPB_ECOLI Cell division protein ZapB

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: 3.37 (Q 96)
PAXdb E.coli [ppm]: 3.6 (Q 100)

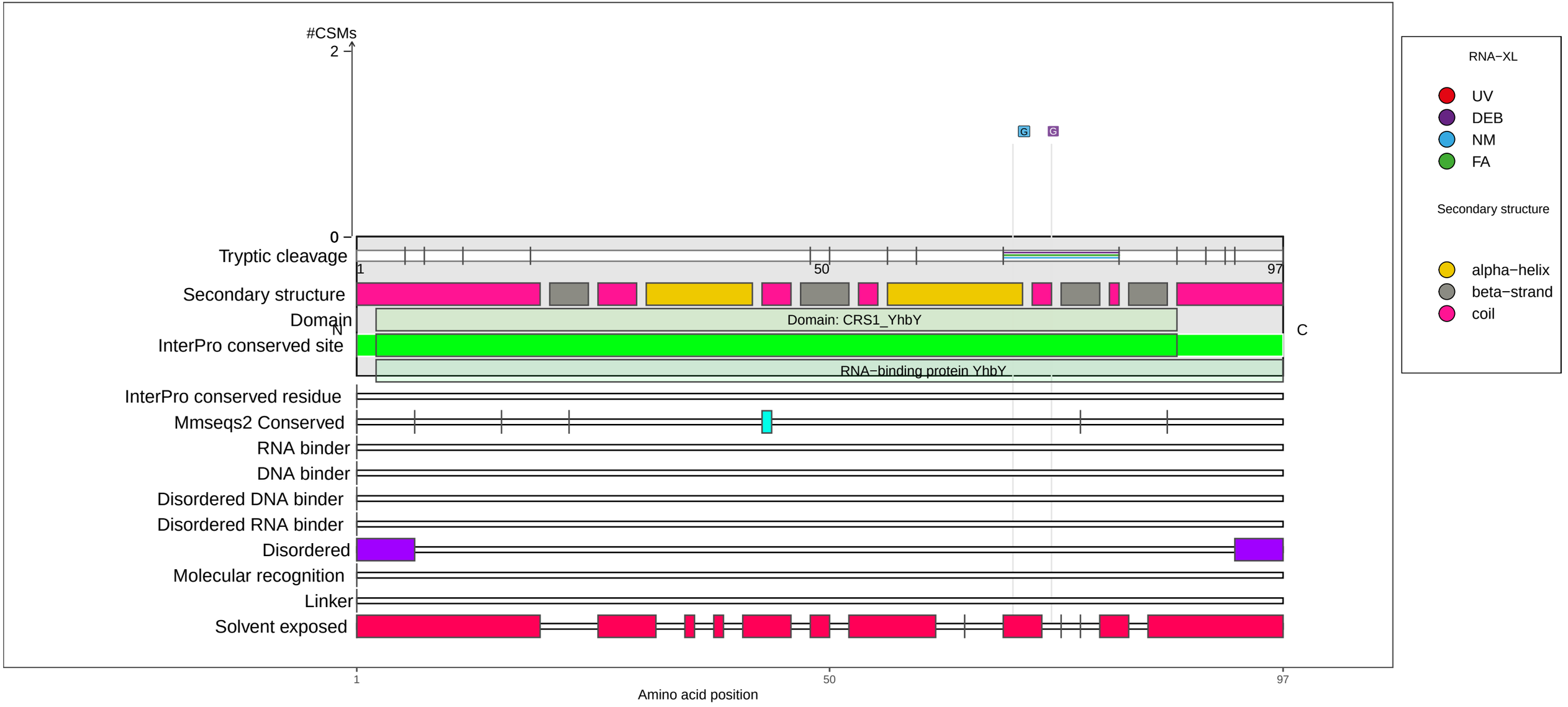
− RNA functions: not annotated



P0AGK4
YHBY_ECOLI RNA−binding protein YhbY

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 76)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 3.01 (Q 95)

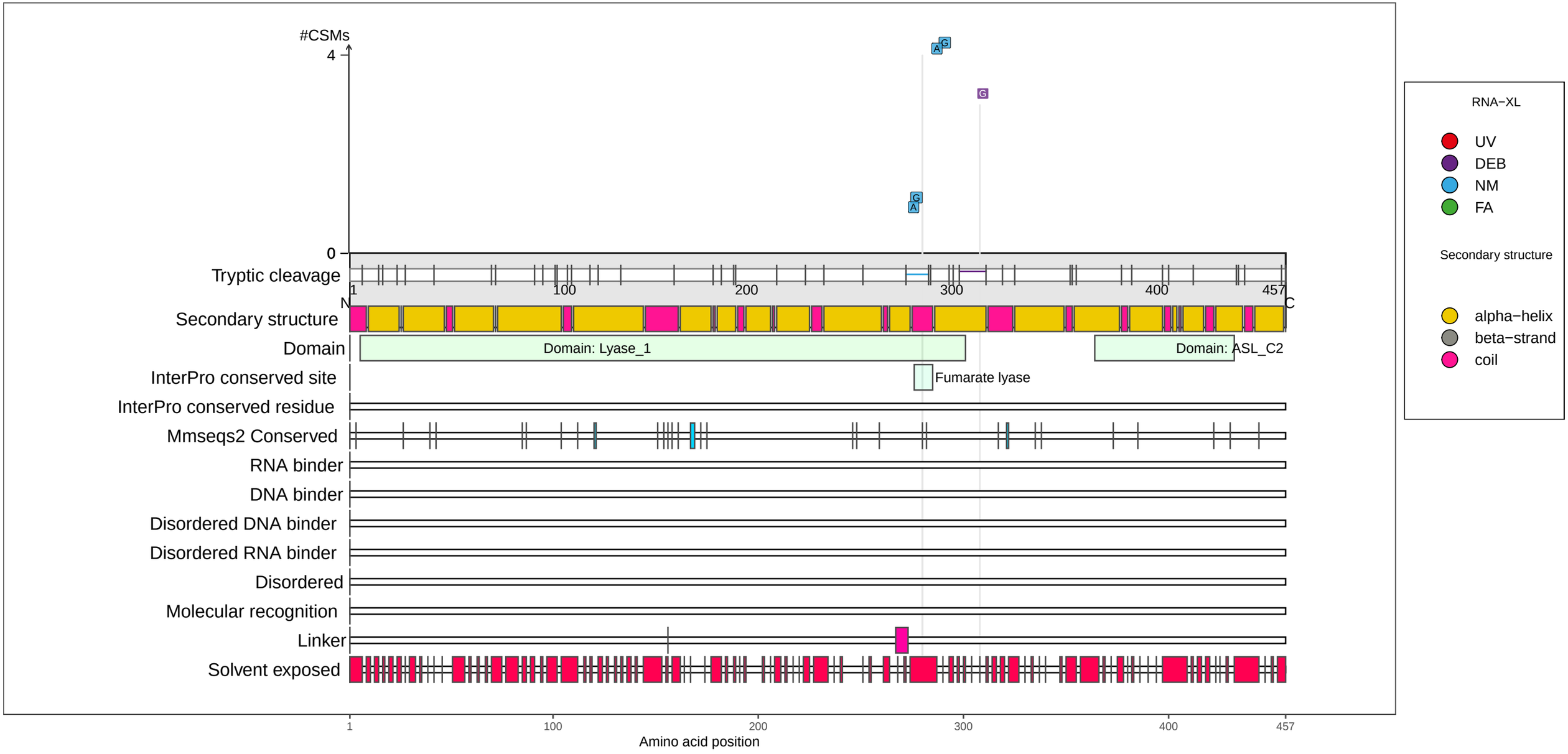
− RNA functions:
ncRNA 5−end processing; ncRNA metabolic process; ncRNA processing
RNA 5−end processing; RNA binding; RNA metabolic process; RNA processing; rRNA 5−end processing
rRNA metabolic process; rRNA processing



P11447
ARLY_ECOLI Argininosuccinate lyase

− Abundance:
tryptic [log10 Intensity]: 9.49 (Q 96)
PAXdb K12 strain [ppm]: 2.33 (Q 71)
PAXdb E.coli [ppm]: 2.15 (Q 76)

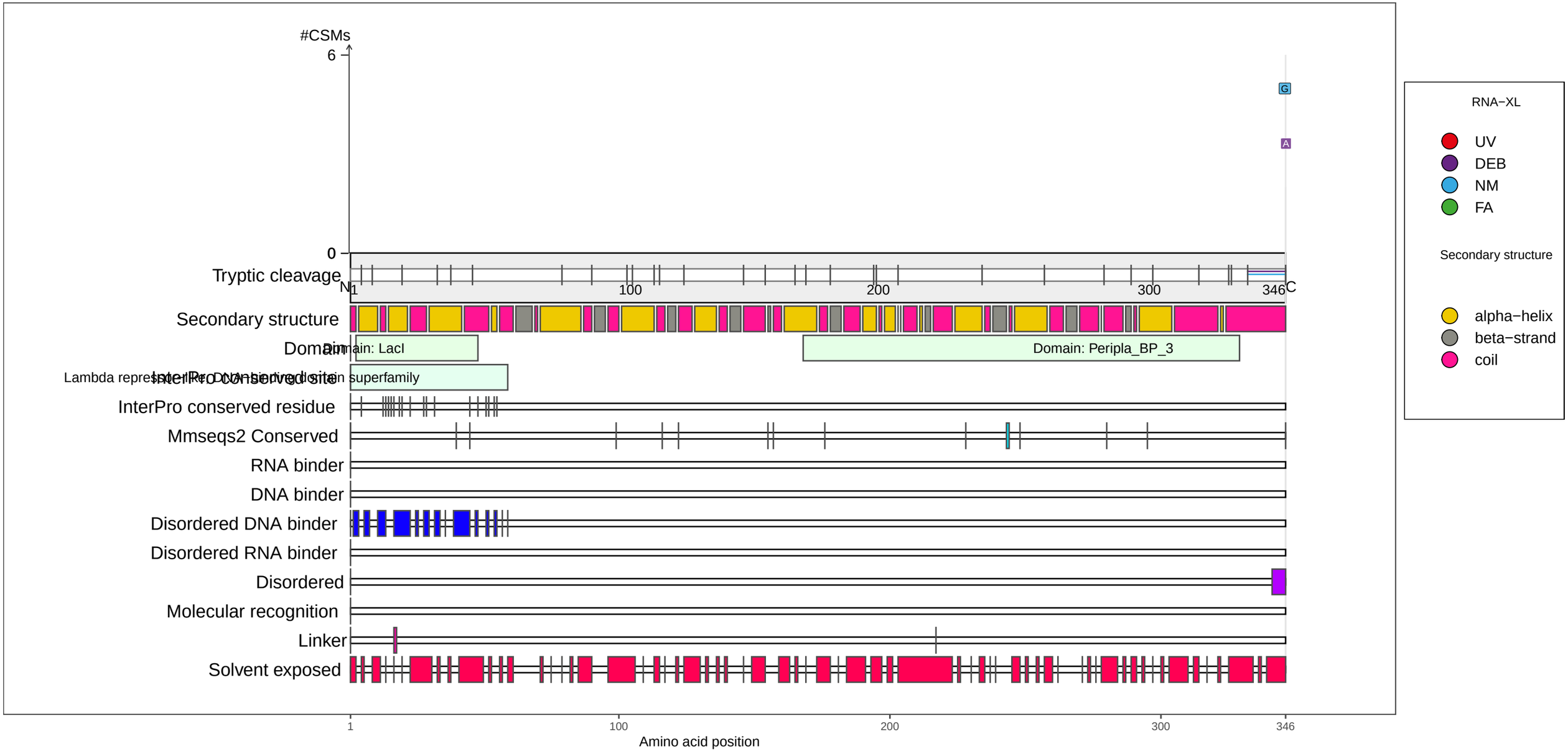
− RNA functions: not annotated



P25748
GALS_ECOLI HTH−type transcriptional regulator GalS

− Abundance:
tryptic [log10 Intensity]: 7.59 (Q 39)
PAXdb K12 strain [ppm]: 1.72 (Q 50)
PAXdb E.coli [ppm]: −0.15 (Q 21)

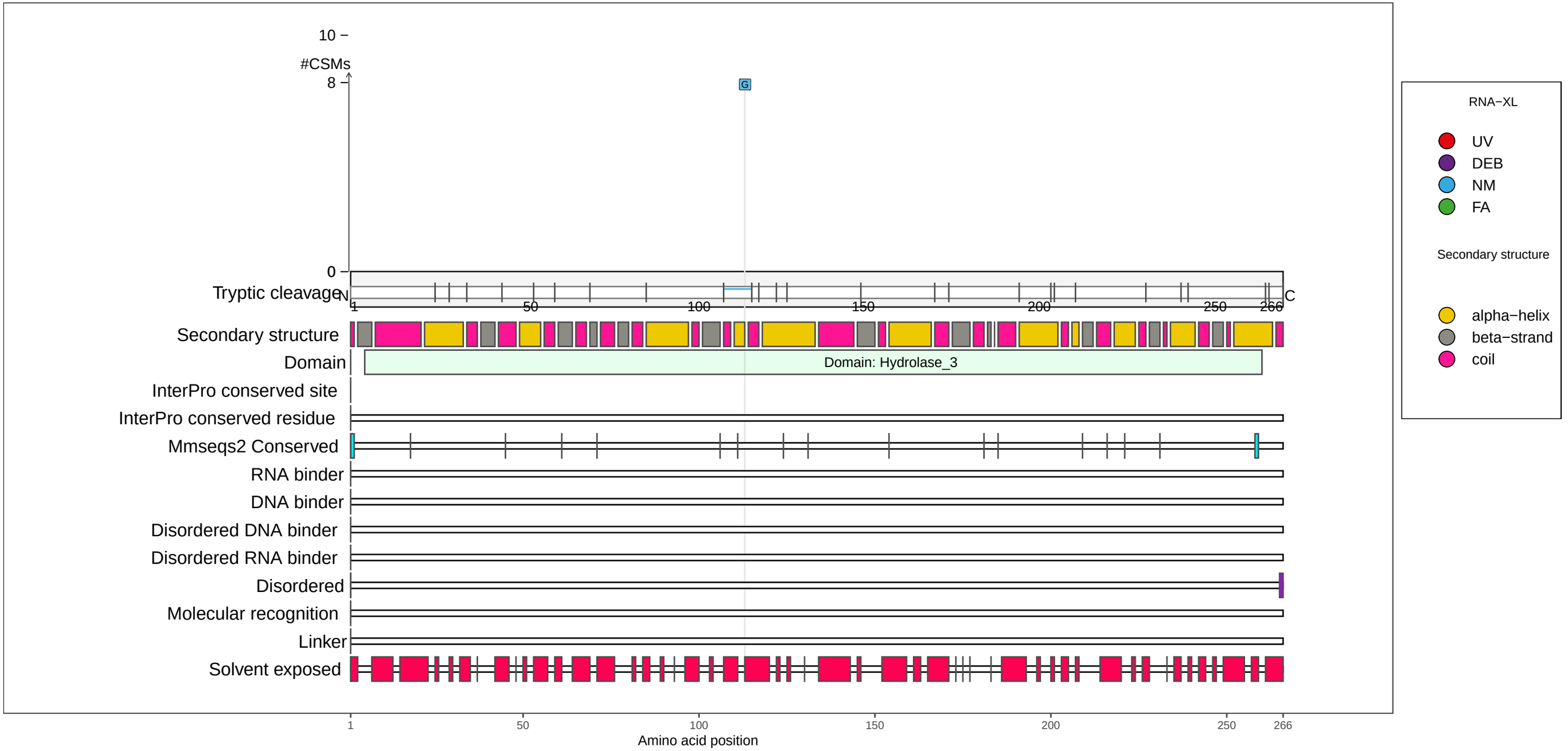
− RNA functions: not annotated



P27848
YIGL_ECOLI Pyridoxal phosphate phosphatase YigL

− Abundance:
tryptic [log10 Intensity]: 7.57 (Q 38)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 1.42 (Q 58)

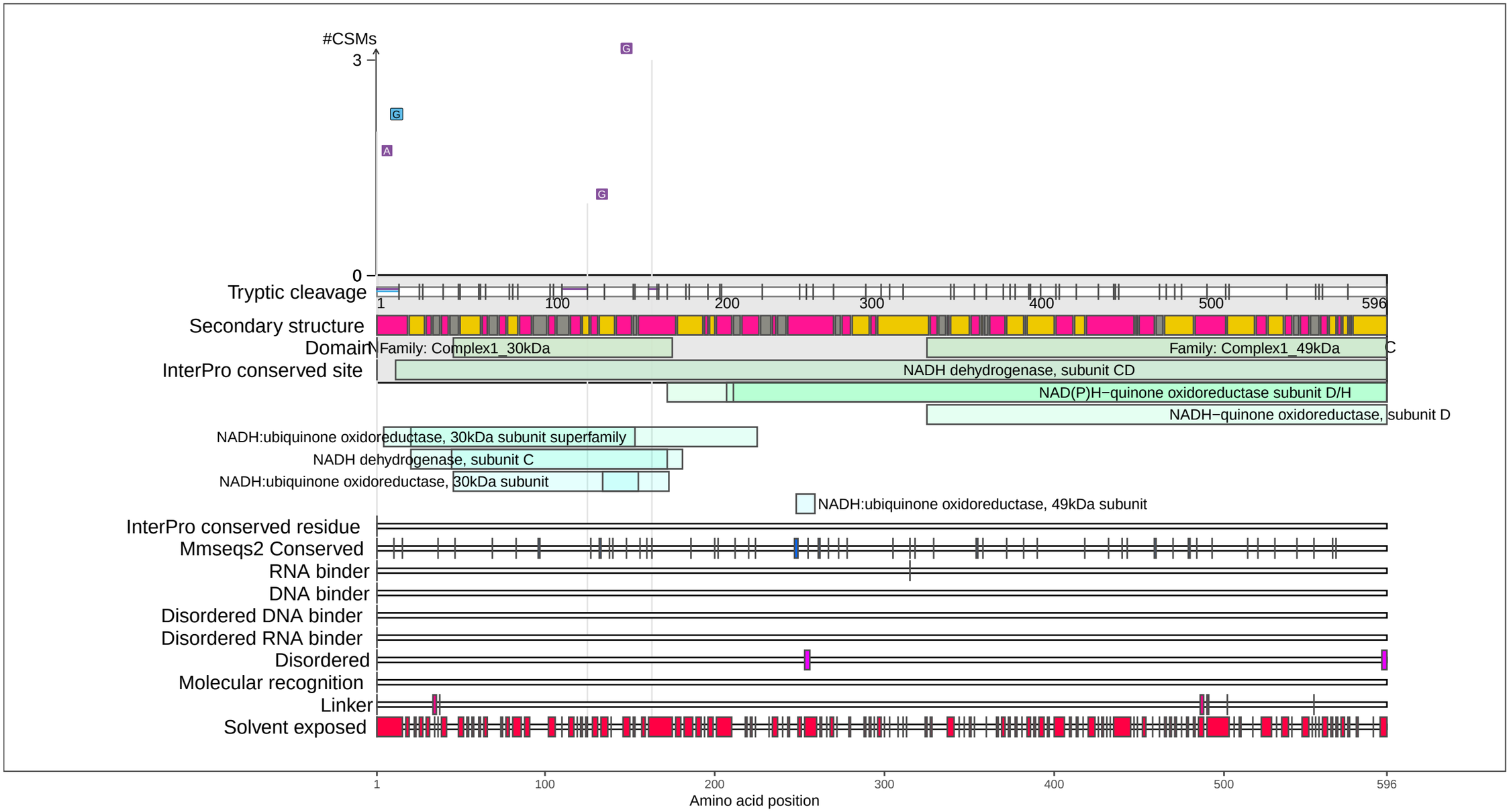
− RNA functions: not annotated

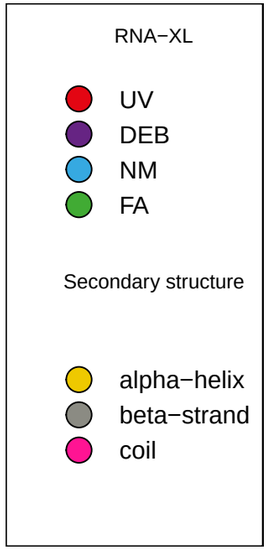


P33599
NUOCD_ECOLI NADH−quinone oxidoreductase subunit C/D

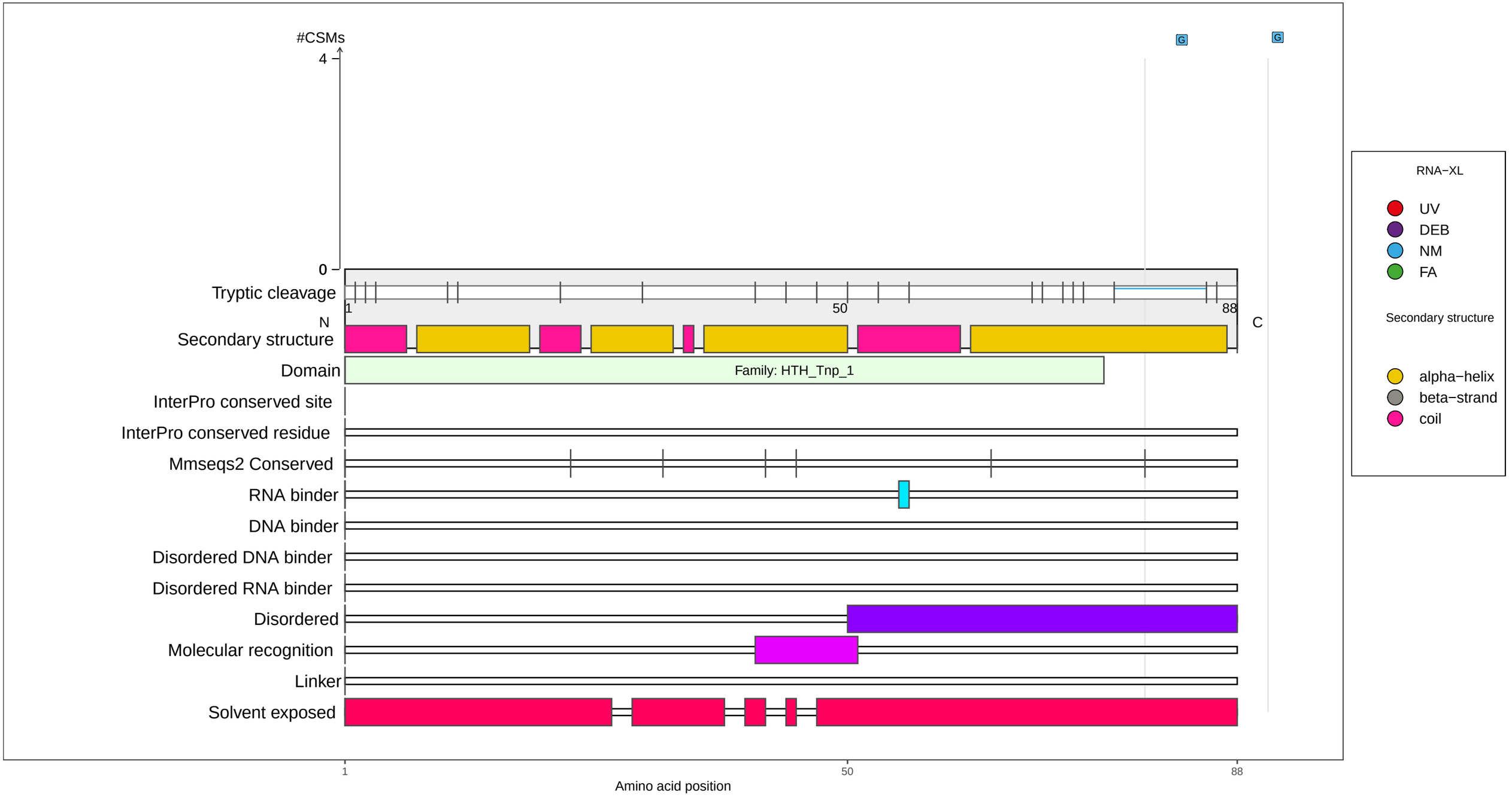
− Abundance:
tryptic [log10 Intensity]: 9.24 (Q 93)
PAXdb K12 strain [ppm]: 2.39 (Q 73)
PAXdb E.coli [ppm]: 2.58 (Q 88)

− RNA functions: not annotated





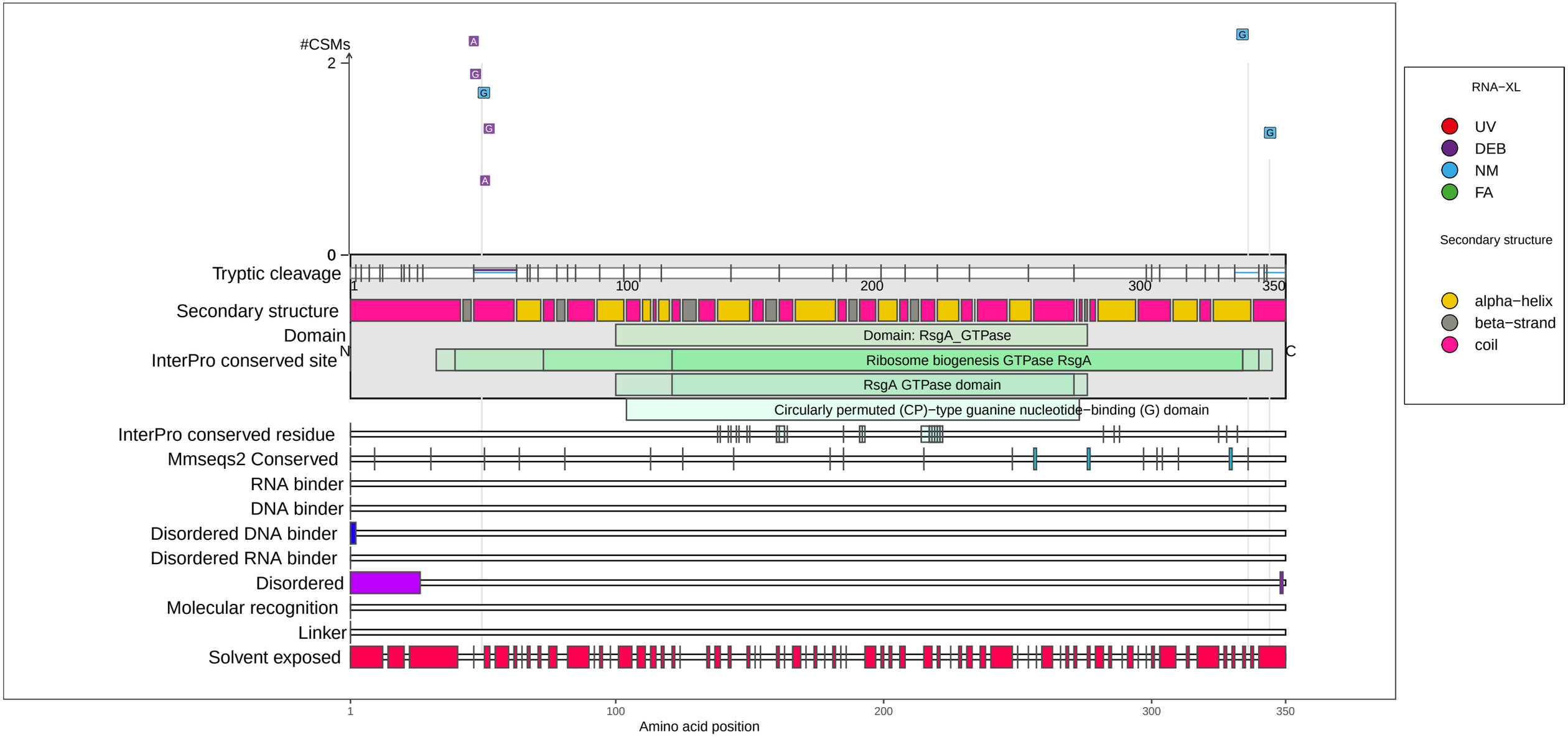
P39212
INSN2_ECOLI Putative transposase InsN for insertion sequence element IS911B
− RNA functions: not annotated



P39286
RSGA_ECOLI Small ribosomal subunit biogenesis GTPase RsgA

− Abundance:
tryptic [log10 Intensity]: 7.65 (Q 43)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 2.05 (Q 73)

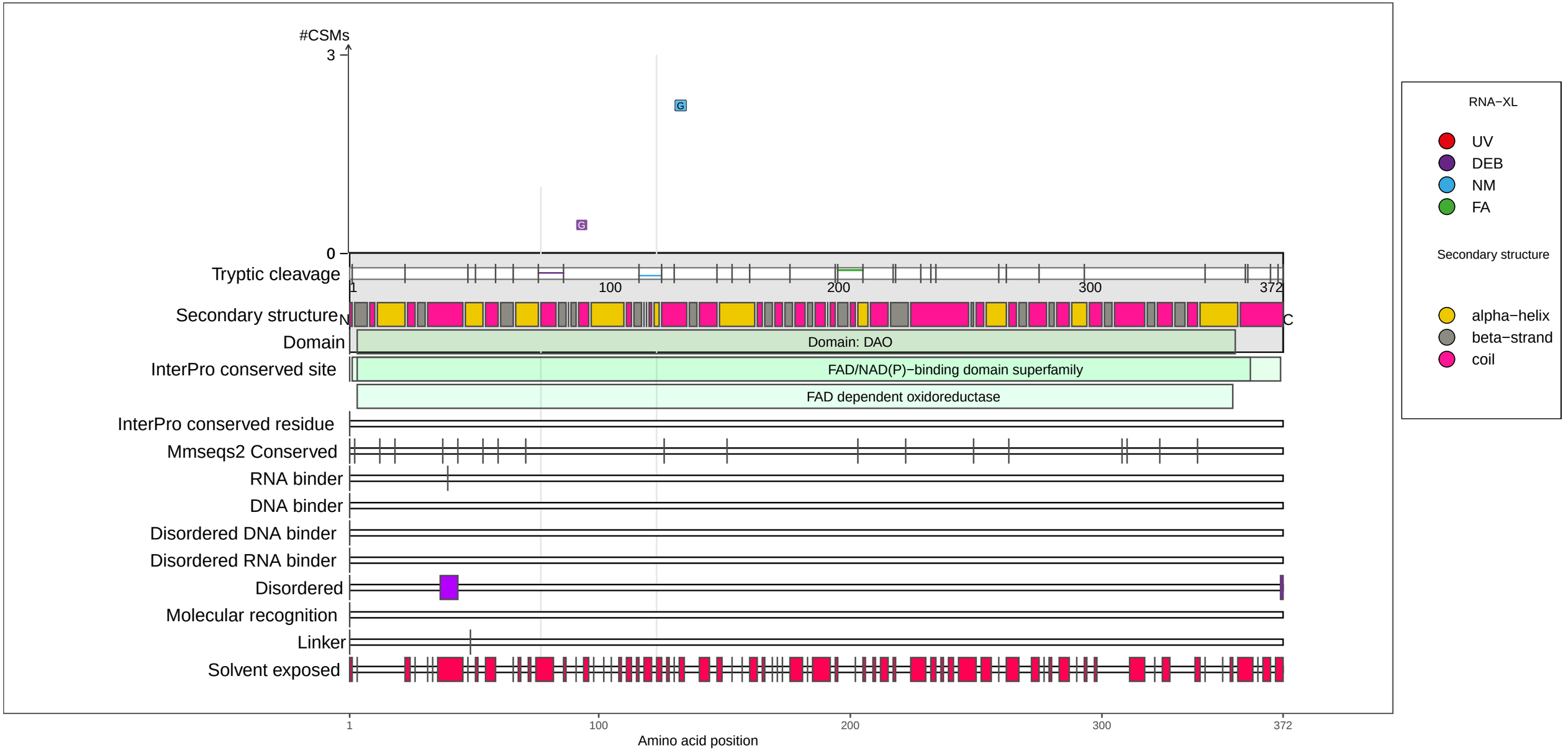
− RNA functions:
RNA binding; rRNA binding



P40874
MTOX_ECOLI N−methyl−L−tryptophan oxidase

− Abundance:
tryptic [log10 Intensity]: 8.31 (Q 70)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 1.9 (Q 70)

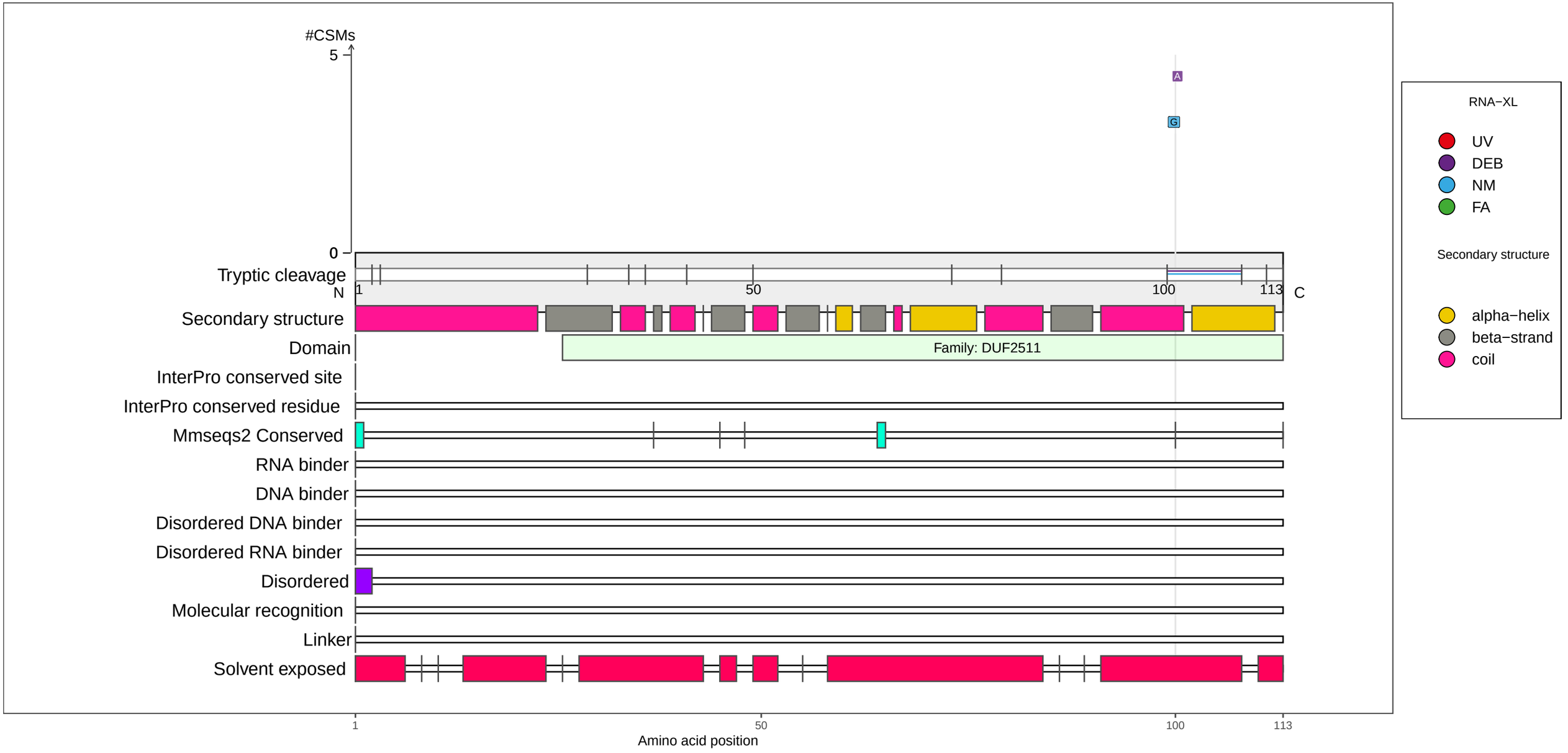
− RNA functions: not annotated



P64506
YEBY_ECOLI Uncharacterized protein YebY

− Abundance:
tryptic [log10 Intensity]: 7.99 (Q 57)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.55 (Q 61)

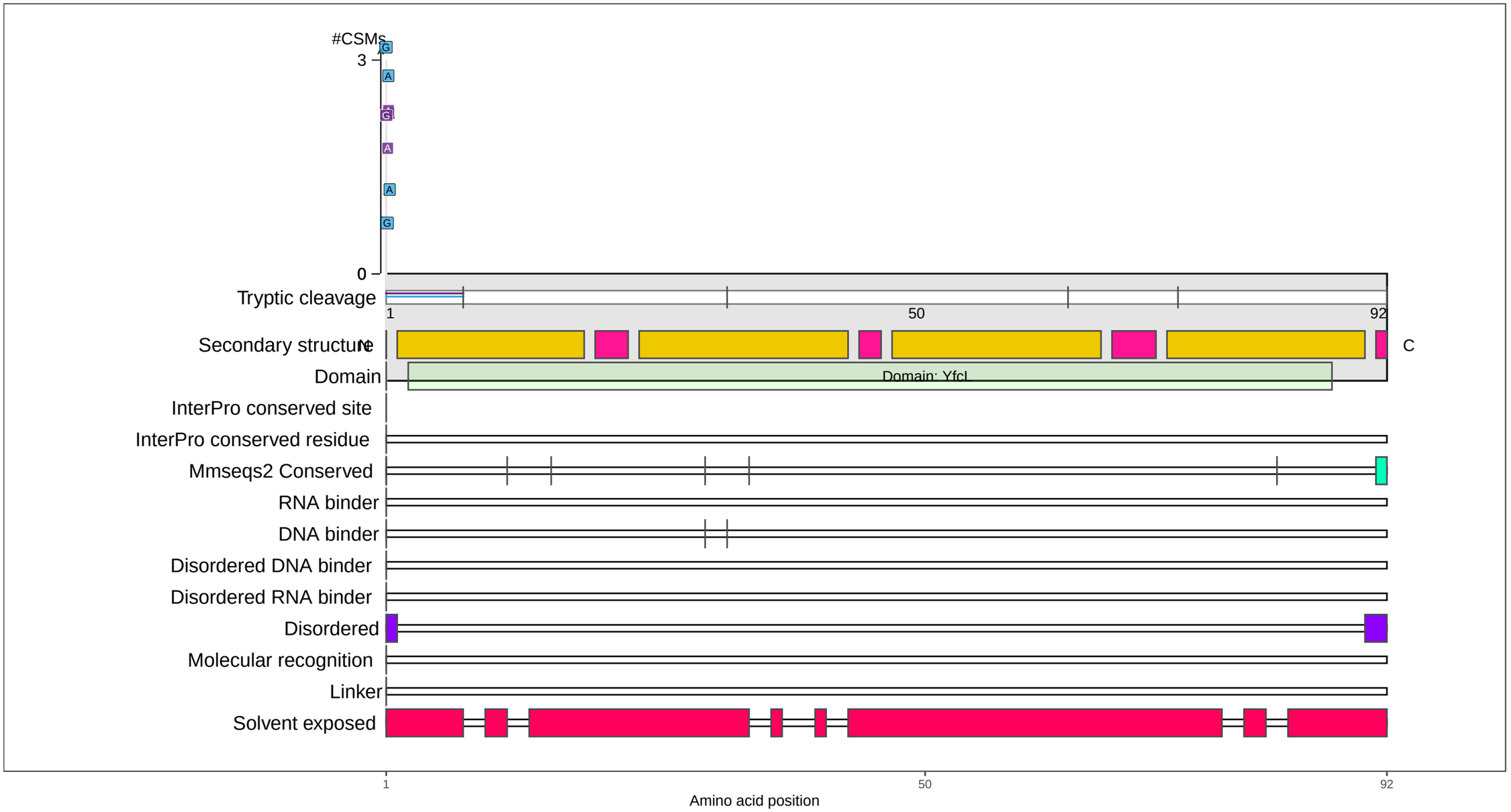
− RNA functions: not annotated

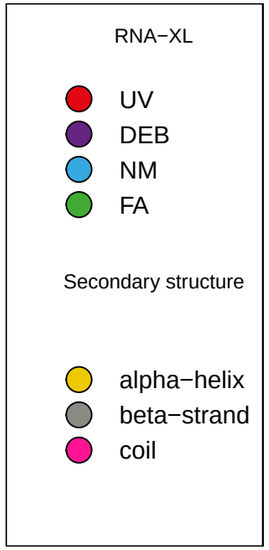


P64540
YFCL_ECOLI Uncharacterized protein YfcL

− Abundance:
tryptic [log10 Intensity]: 8.54 (Q 77)
PAXdb K12 strain [ppm]: 2.05 (Q 62)
PAXdb E.coli [ppm]: 1.79 (Q 67)

− RNA functions: not annotated

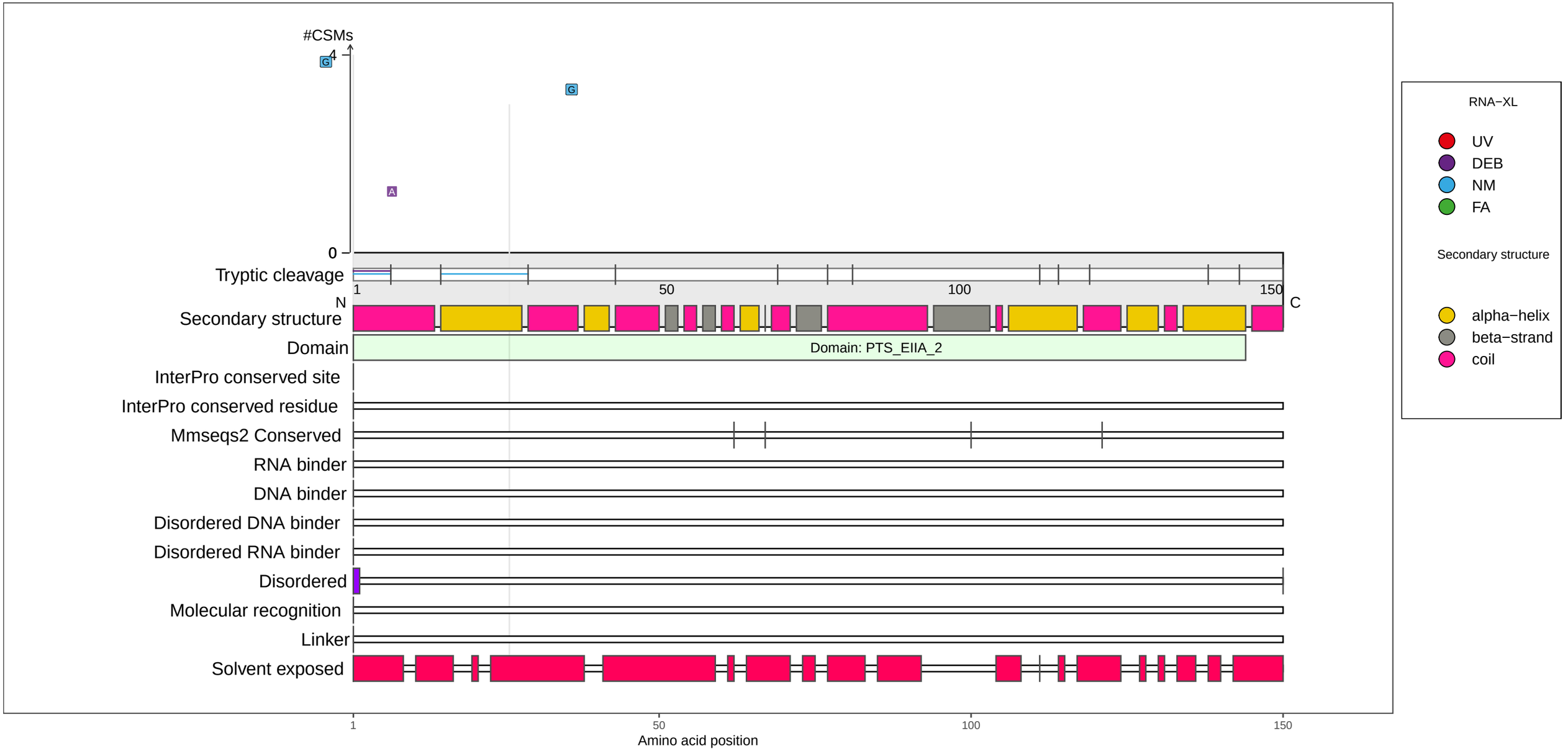




P69828
PTKA_ECOLI PTS system galactitol−specific EIIA component

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 3.36 (Q 98)

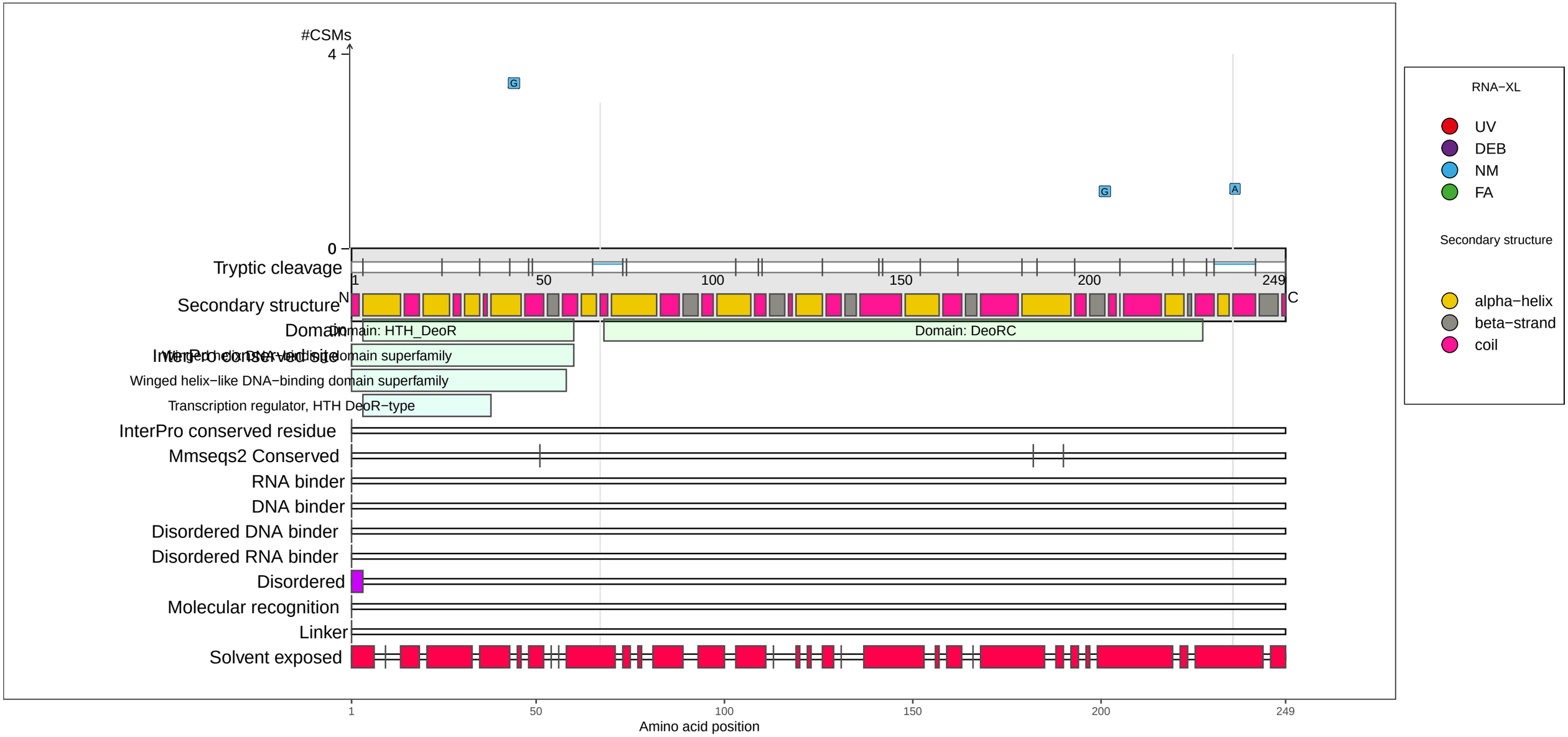
− RNA functions: not annotated



P76034
YCIT_ECOLI Uncharacterized HTH−type transcriptional regulator YciT

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 1.82 (Q 68)

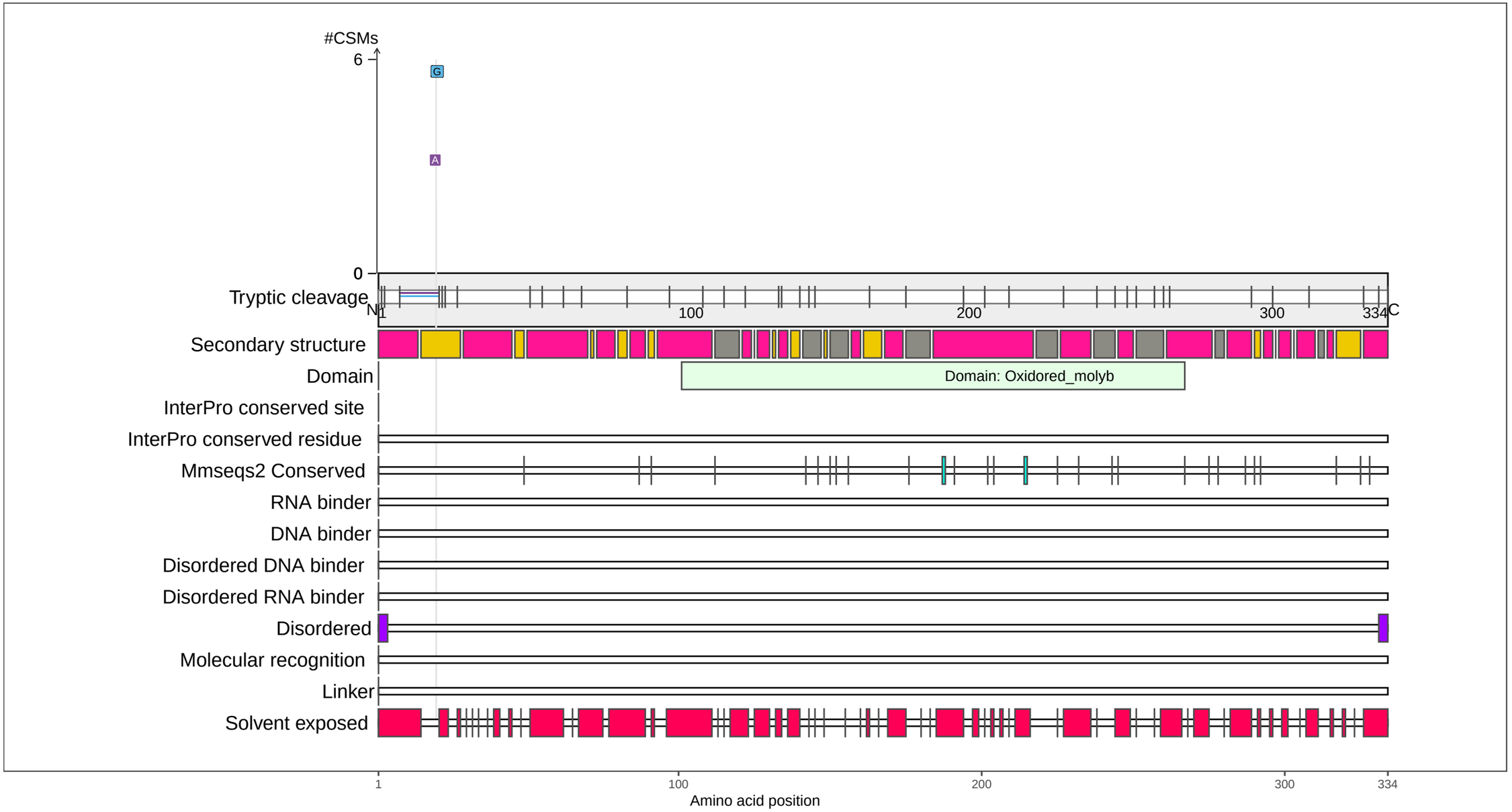
− RNA functions:
RNA biosynthetic process; RNA metabolic process

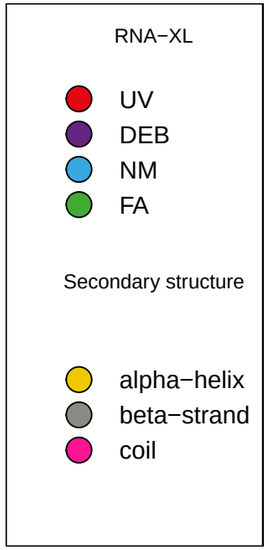


P76342
MSRP_ECOLI Protein−methionine−sulfoxide reductase catalytic subunit MsrP

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.16 (Q 18)
PAXdb E.coli [ppm]: 1.18 (Q 52)

− RNA functions: not annotated

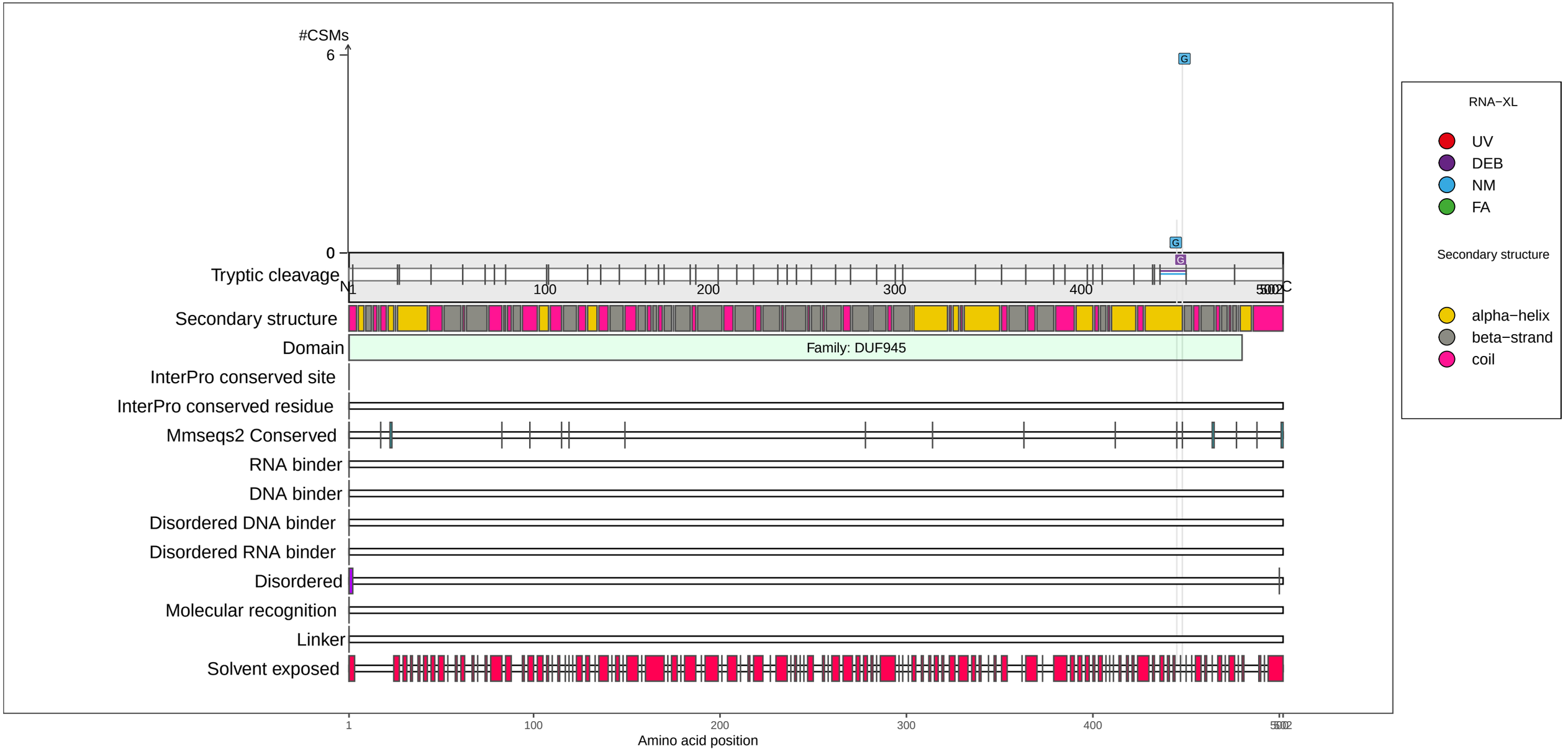




P77804
YDGA_ECOLI Protein YdgA

− Abundance:
tryptic [log10 Intensity]: 8.62 (Q 79)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: 2.66 (Q 89)

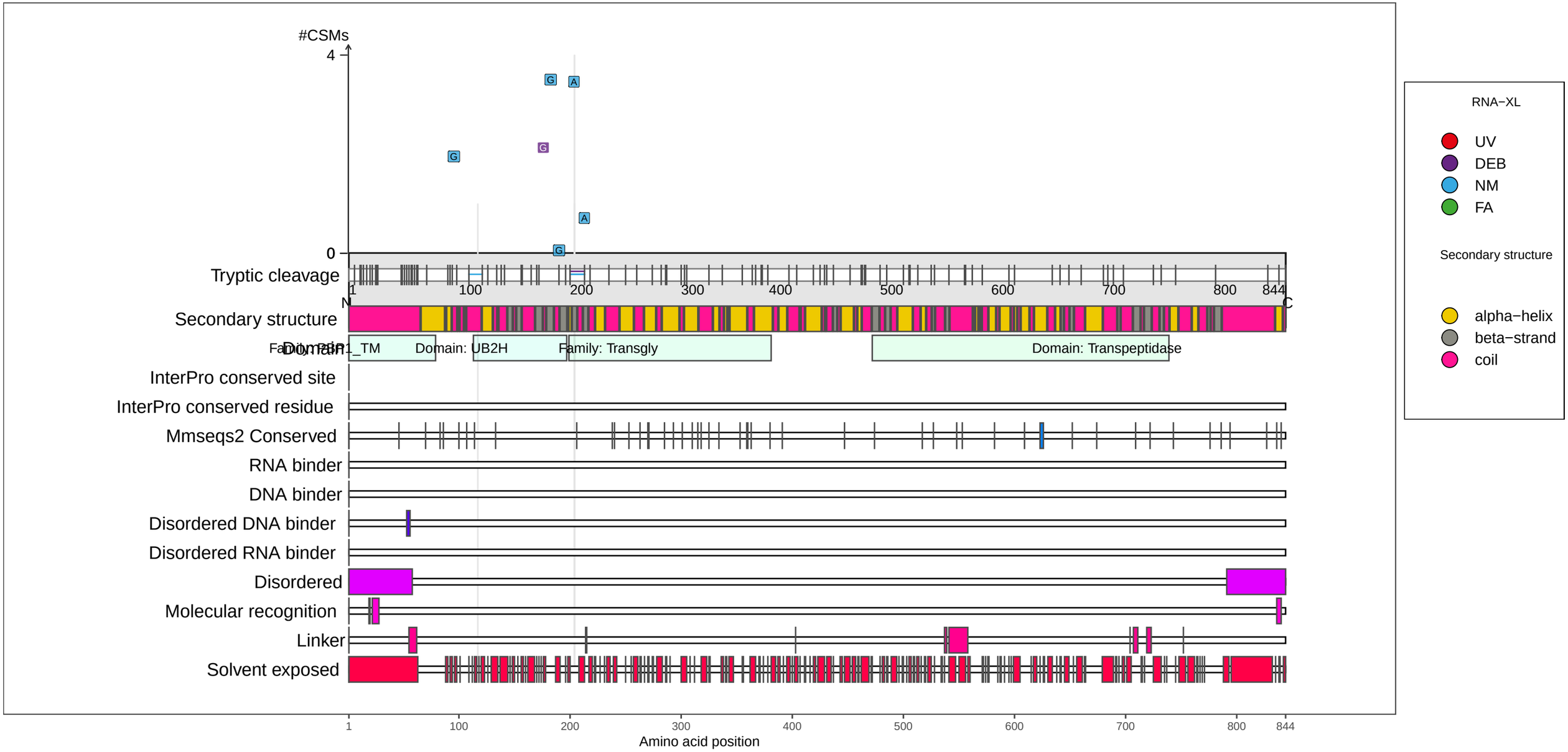
− RNA functions: not annotated



P02919
PBPB_ECOLI Penicillin−binding protein 1B

− Abundance:
tryptic [log10 Intensity]: 7.84 (Q 51)
PAXdb K12 strain [ppm]: 1.57 (Q 42)
PAXdb E.coli [ppm]: 1.31 (Q 55)

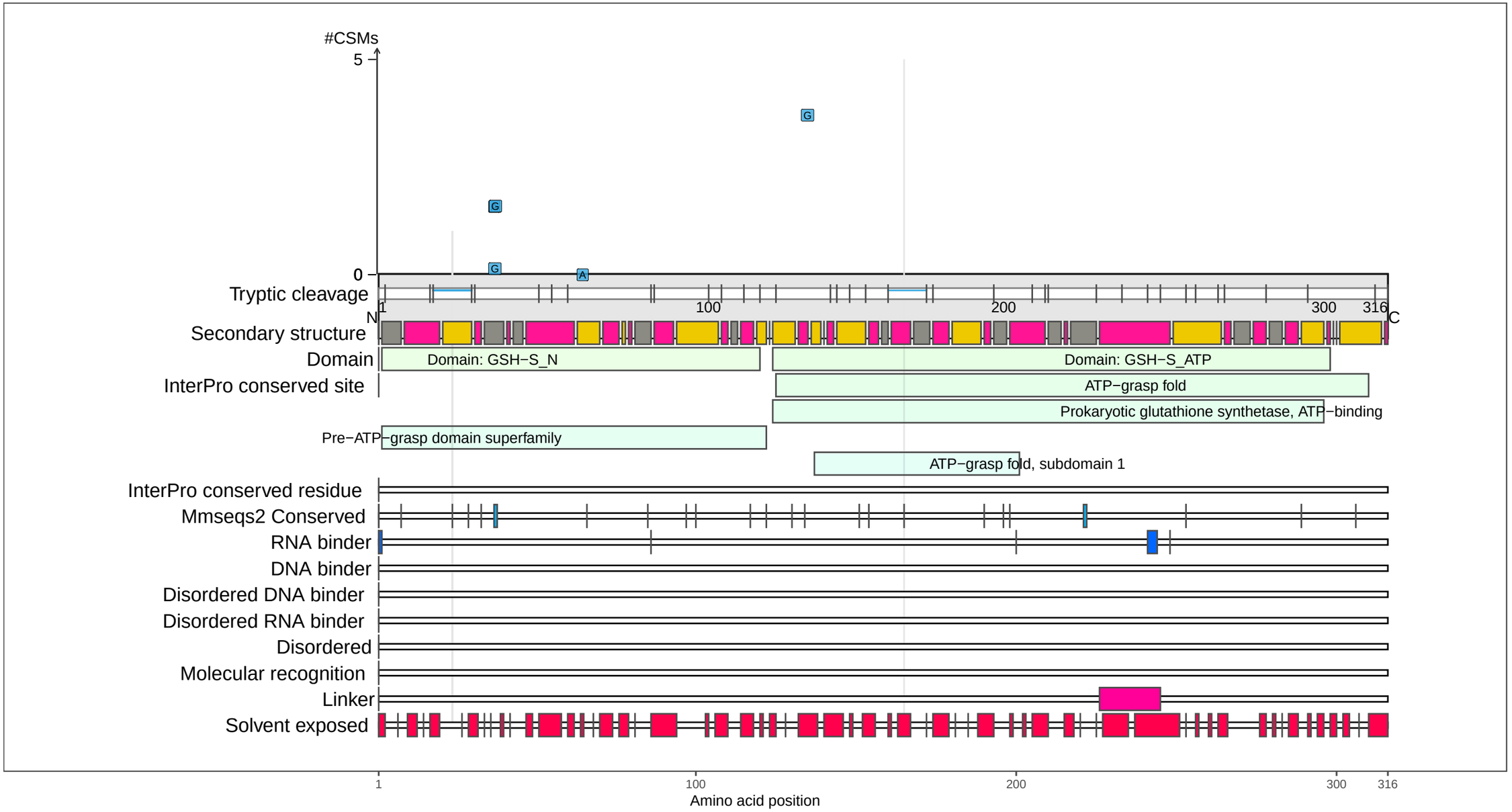
− RNA functions: not annotated



P04425
GSHB_ECOLI Glutathione synthetase

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 2.65 (Q 82)
PAXdb E.coli [ppm]: 2.25 (Q 79)

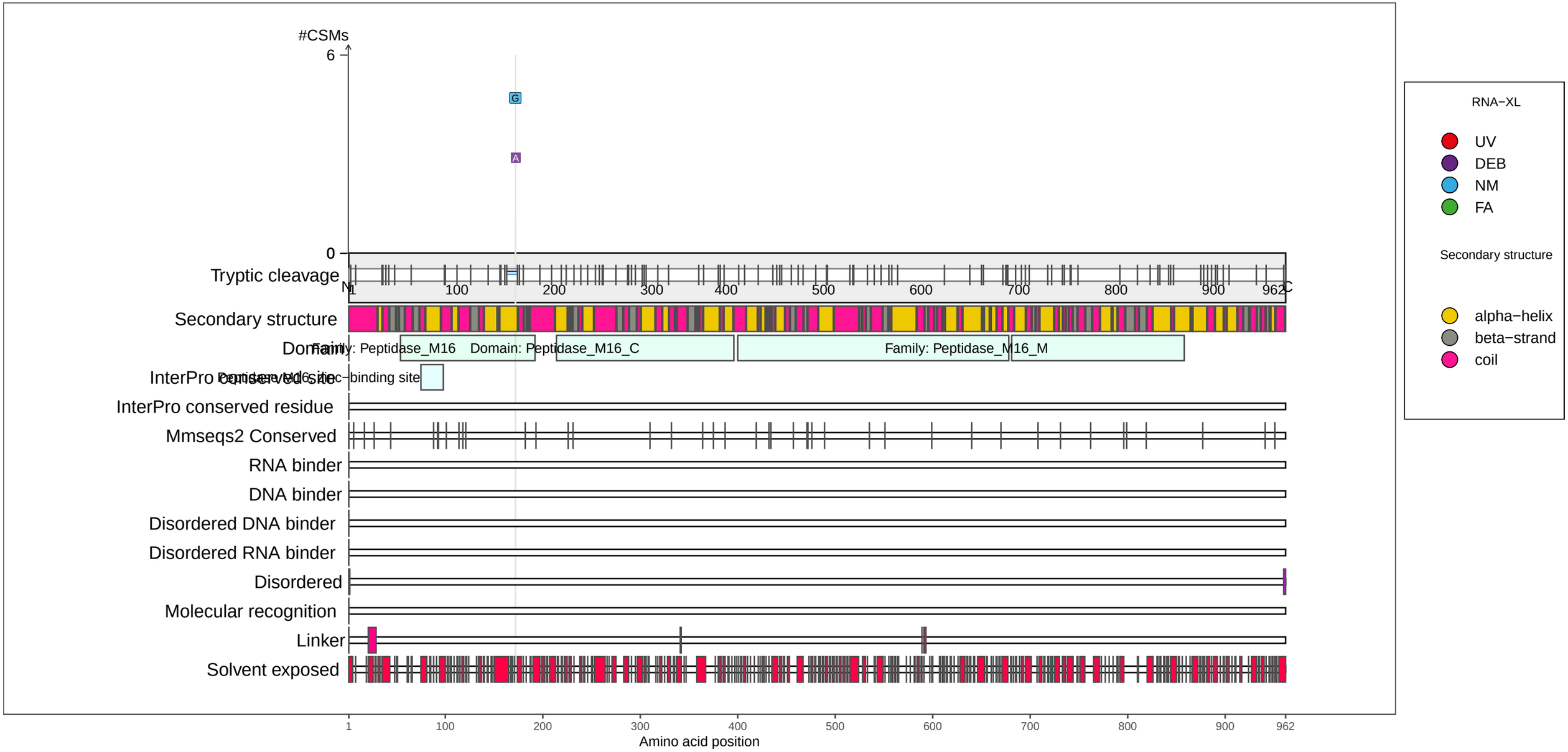
− RNA functions: not annotated



P05458
PTRA_ECOLI Protease 3

− Abundance:
tryptic [log10 Intensity]: 7.77 (Q 48)
PAXdb K12 strain [ppm]: 1.56 (Q 42)
PAXdb E.coli [ppm]: 1.05 (Q 49)

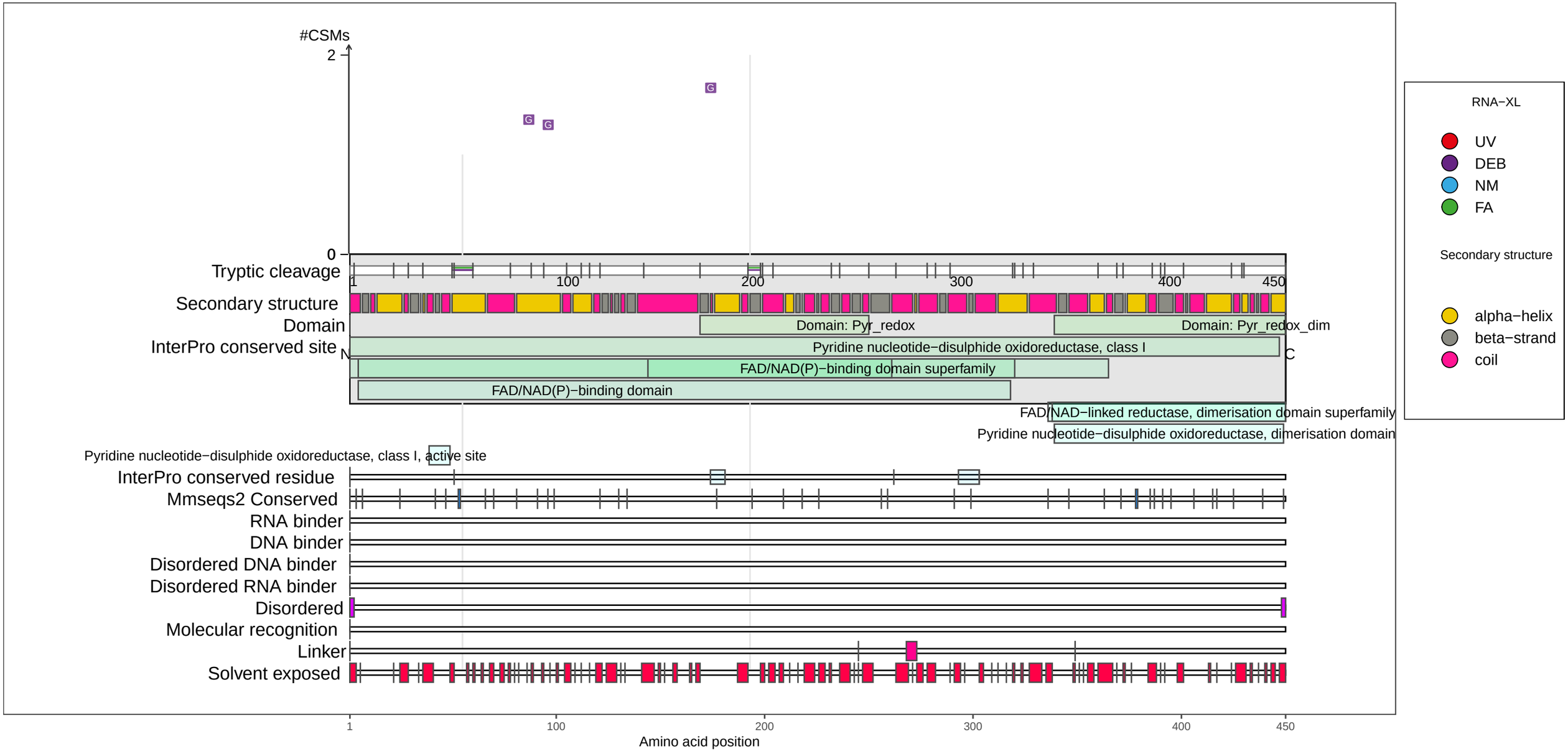
− RNA functions: not annotated



P06715
GSHR_ECOLI Glutathione reductase

− Abundance:
tryptic [log10 Intensity]: 9.13 (Q 91)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.06 (Q 74)

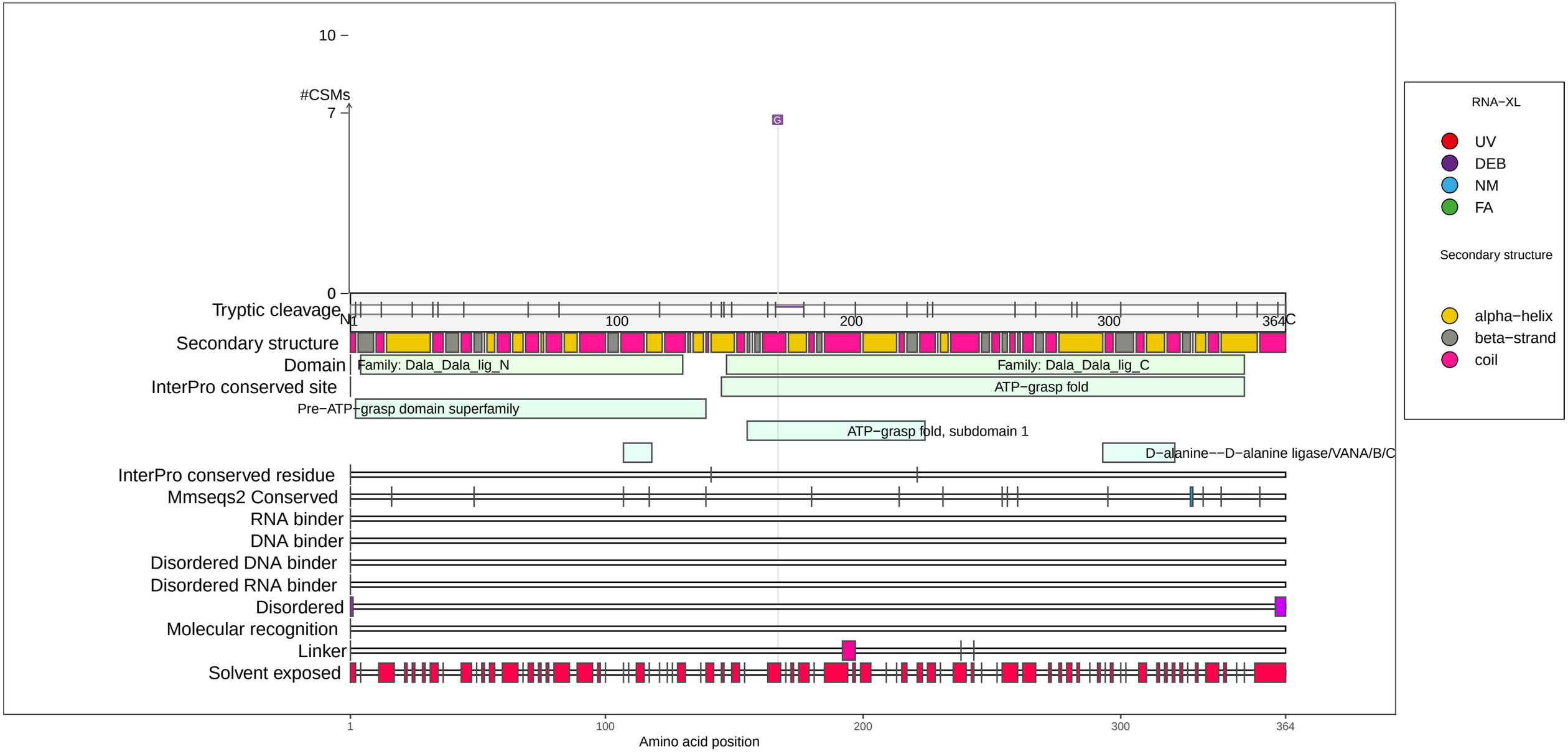
− RNA functions: not annotated



P0A6J8
DDLA_ECOLI D−alanine−−D−alanine ligase A

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 2.5 (Q 77)
PAXdb E.coli [ppm]: 2.11 (Q 75)

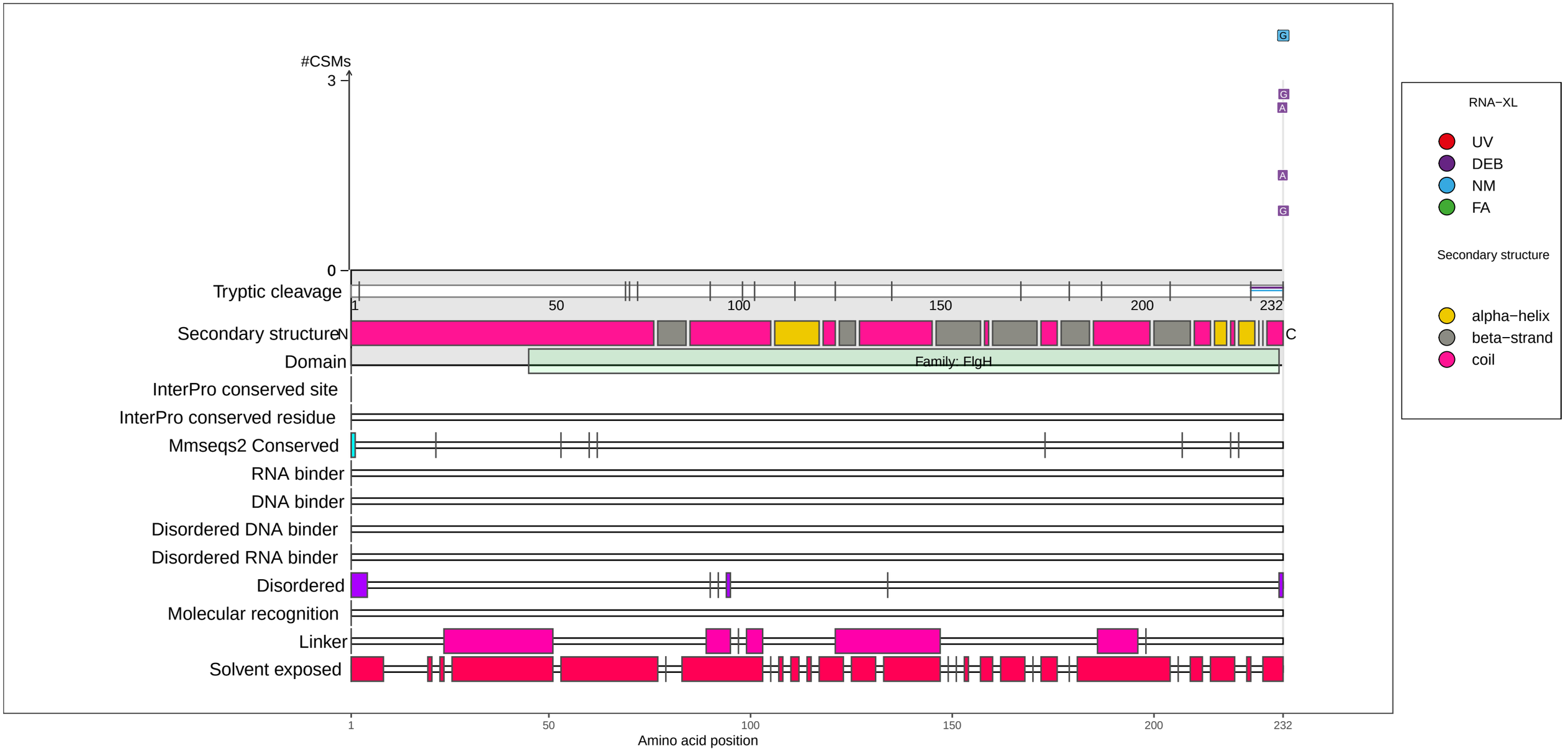
− RNA functions: not annotated



P0A6S0
FLGH_ECOLI Flagellar L−ring protein

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 1.9 (Q 70)

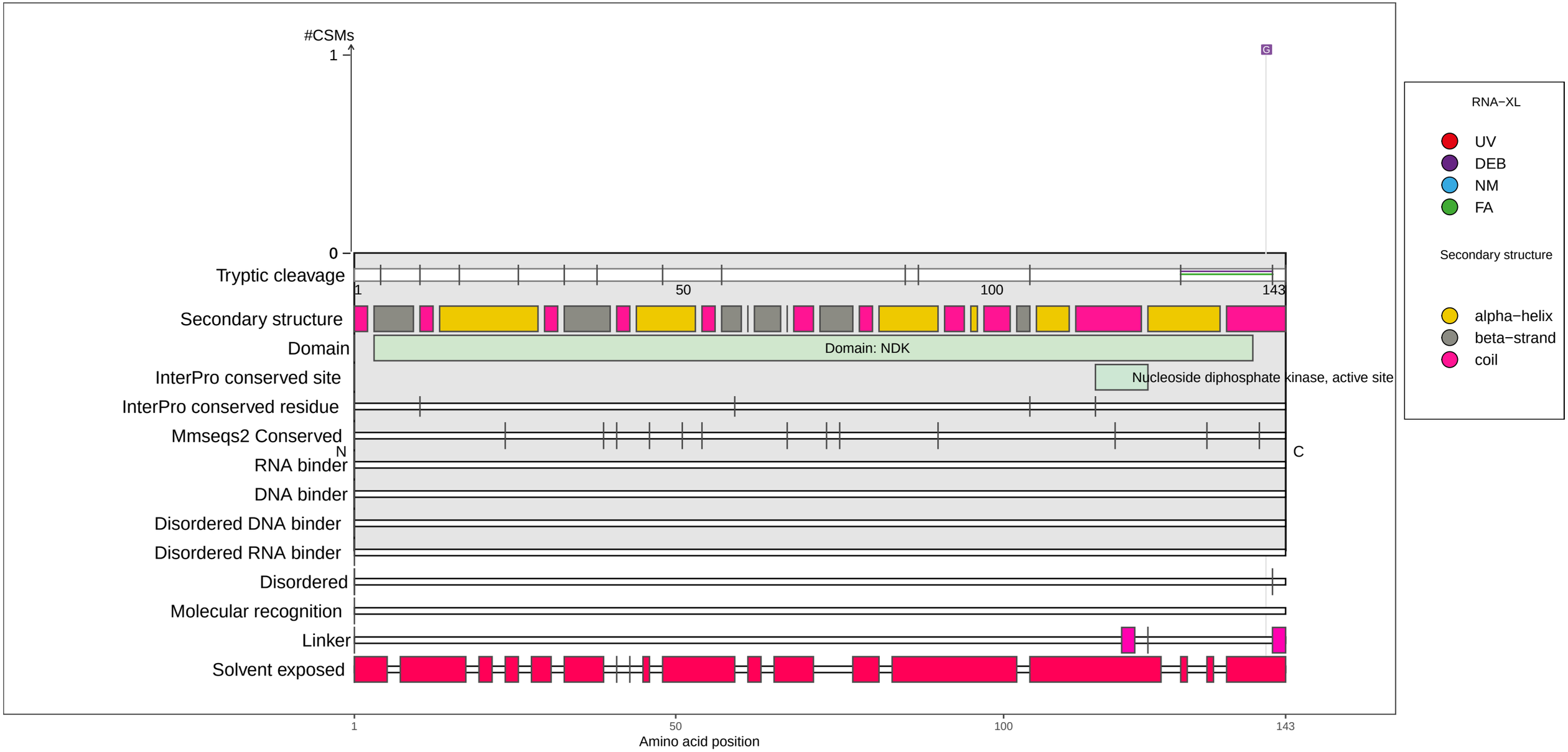
− RNA functions: not annotated



P0A763
NDK_ECOLI Nucleoside diphosphate kinase

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 3.56 (Q 98)
PAXdb E.coli [ppm]: 3.38 (Q 98)

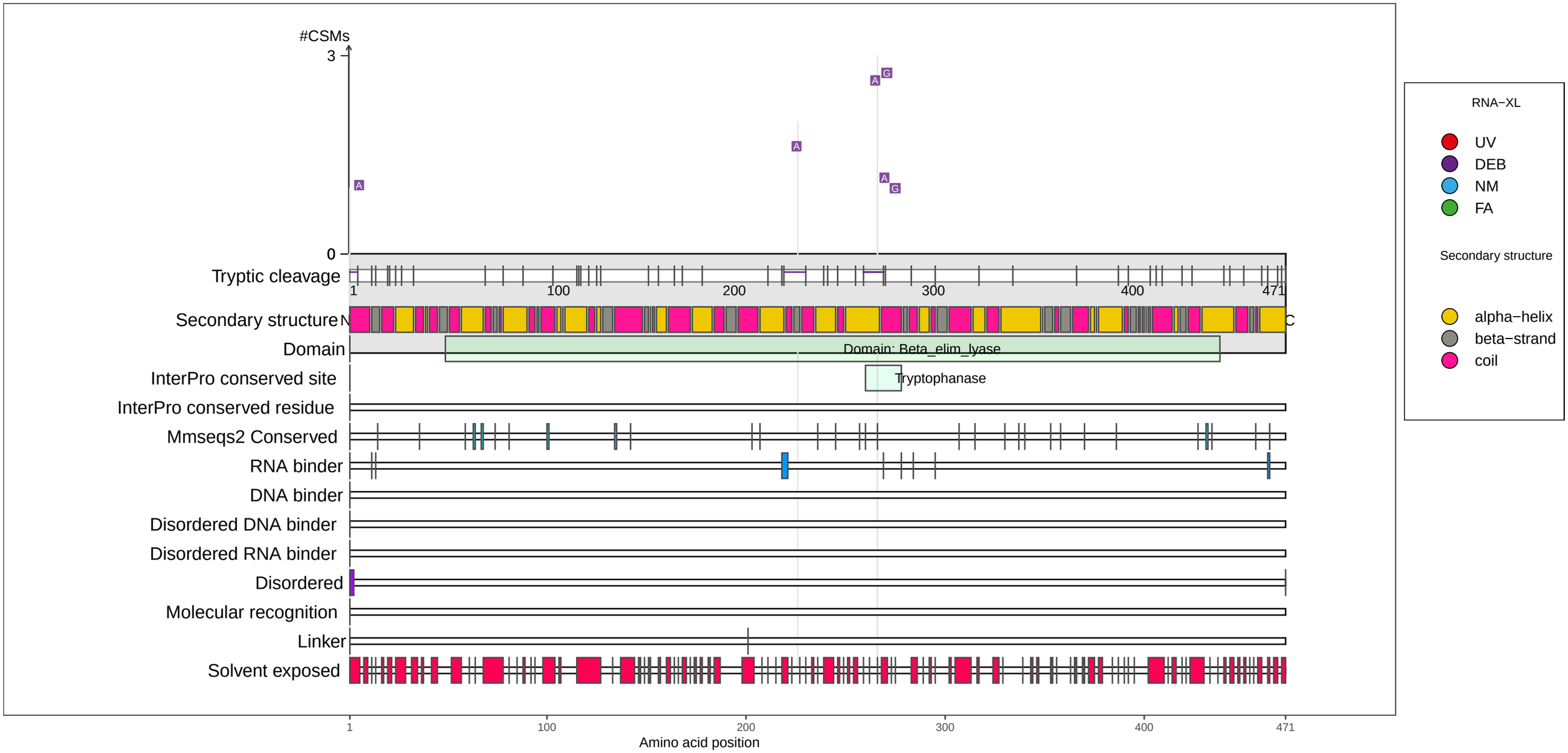
− RNA functions: not annotated



P0A853
TNAA_ECOLI Tryptophanase

− Abundance:
tryptic [log10 Intensity]: 8.36 (Q 71)
PAXdb K12 strain [ppm]: 3.68 (Q 99)
PAXdb E.coli [ppm]: 3.27 (Q 97)

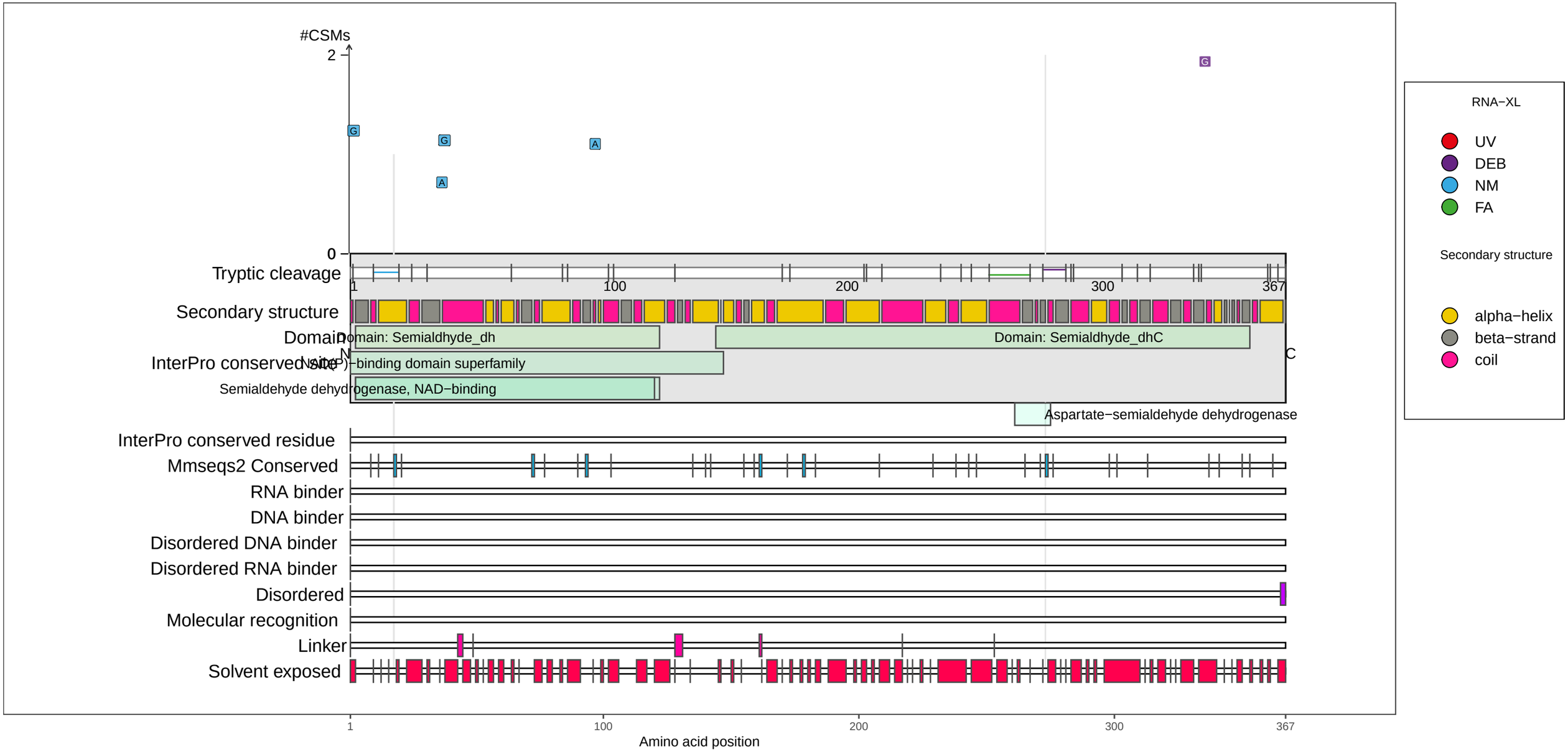
− RNA functions: not annotated



P0A9Q9
DHAS_ECOLI Aspartate−semialdehyde dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.85 (Q 85)
PAXdb K12 strain [ppm]: 2.56 (Q 79)
PAXdb E.coli [ppm]: 3.03 (Q 95)

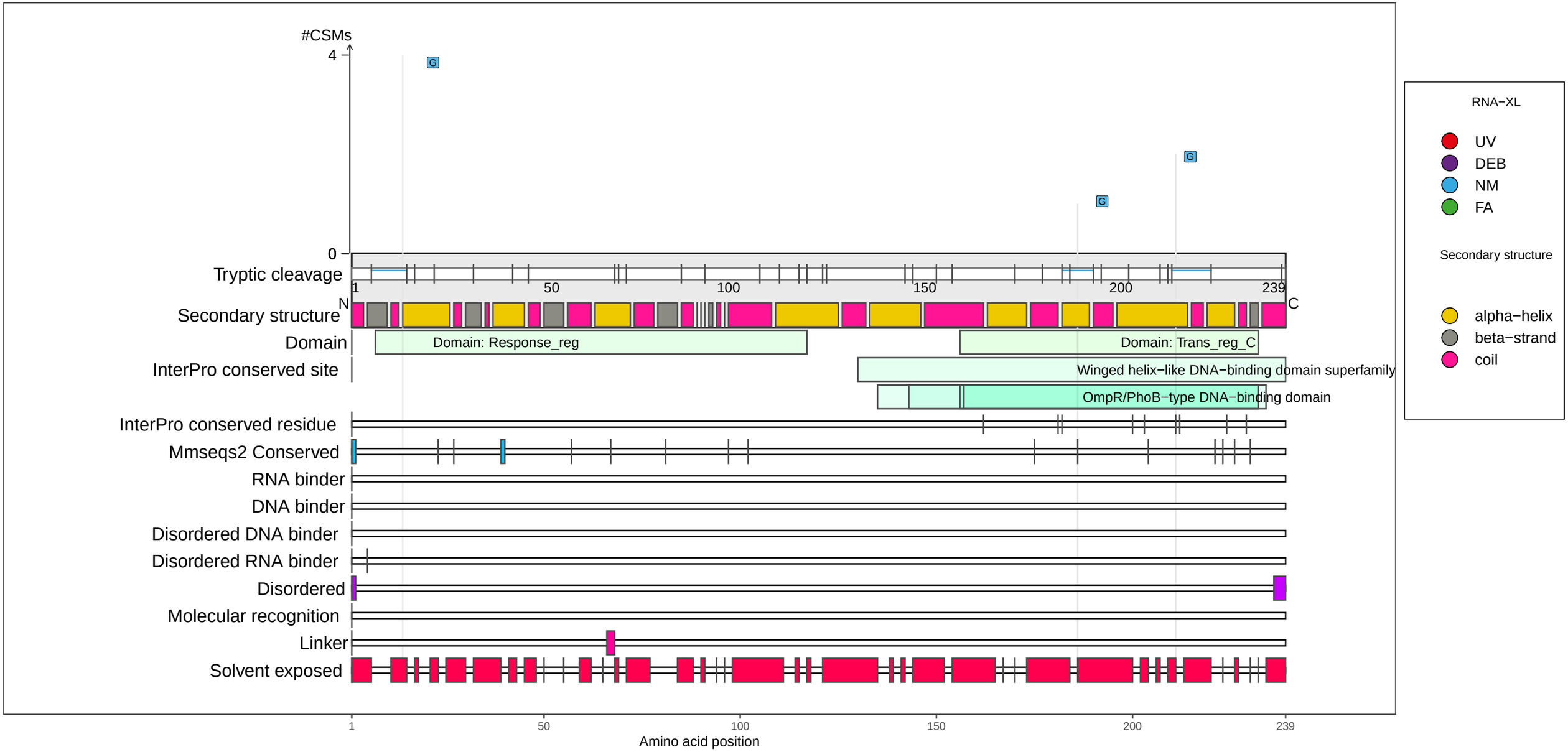
− RNA functions: not annotated



P0AA16
OMPR_ECOLI DNA−binding dual transcriptional regulator OmpR

− Abundance:
tryptic [log10 Intensity]: 6.76 (Q 6)
PAXdb K12 strain [ppm]: 2.65 (Q 82)
PAXdb E.coli [ppm]: 2.8 (Q 92)

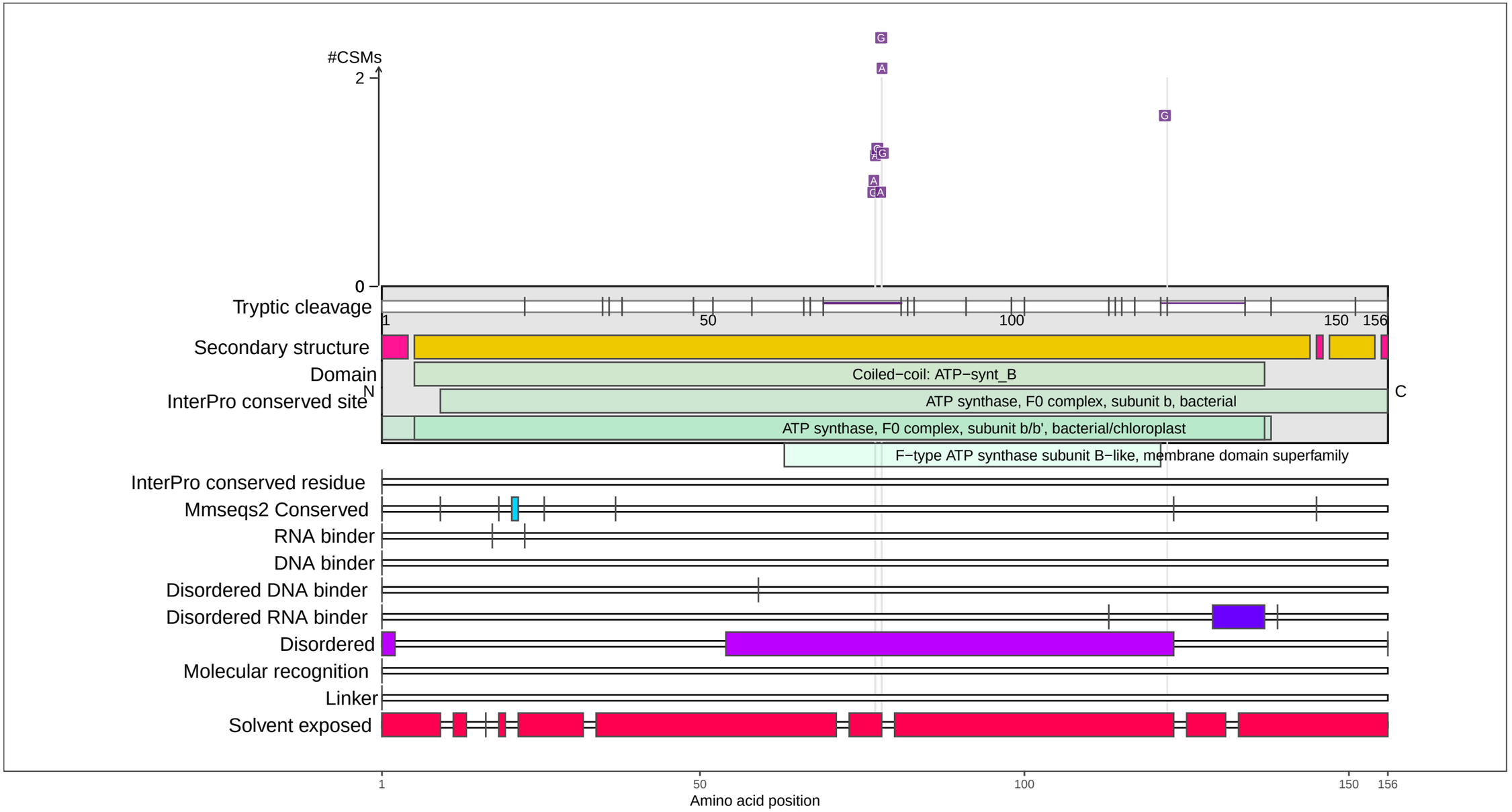
− RNA functions: not annotated



P0ABA0
ATPF_ECOLI ATP synthase subunit b

− Abundance:
tryptic [log10 Intensity]: 9 (Q 88)
PAXdb K12 strain [ppm]: 2.93 (Q 89)
PAXdb E.coli [ppm]: 2.93 (Q 94)

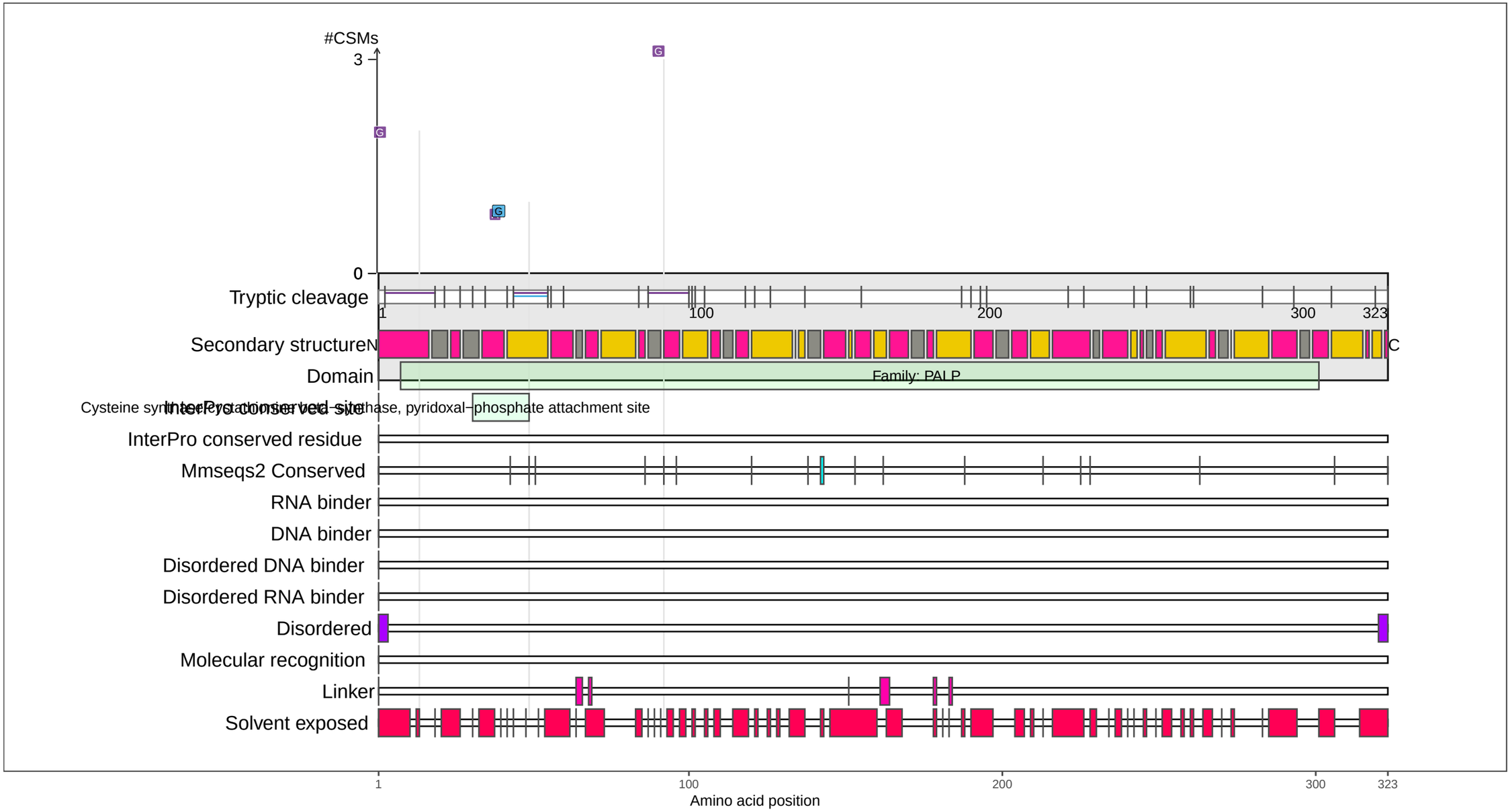
− RNA functions: not annotated

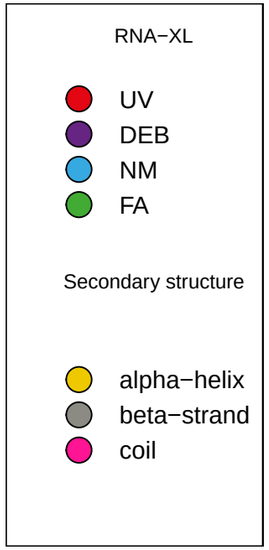


P0ABK5
CYSK_ECOLI Cysteine synthase A

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 2.98 (Q 90)
PAXdb E.coli [ppm]: 3.5 (Q 99)

− RNA functions: not annotated

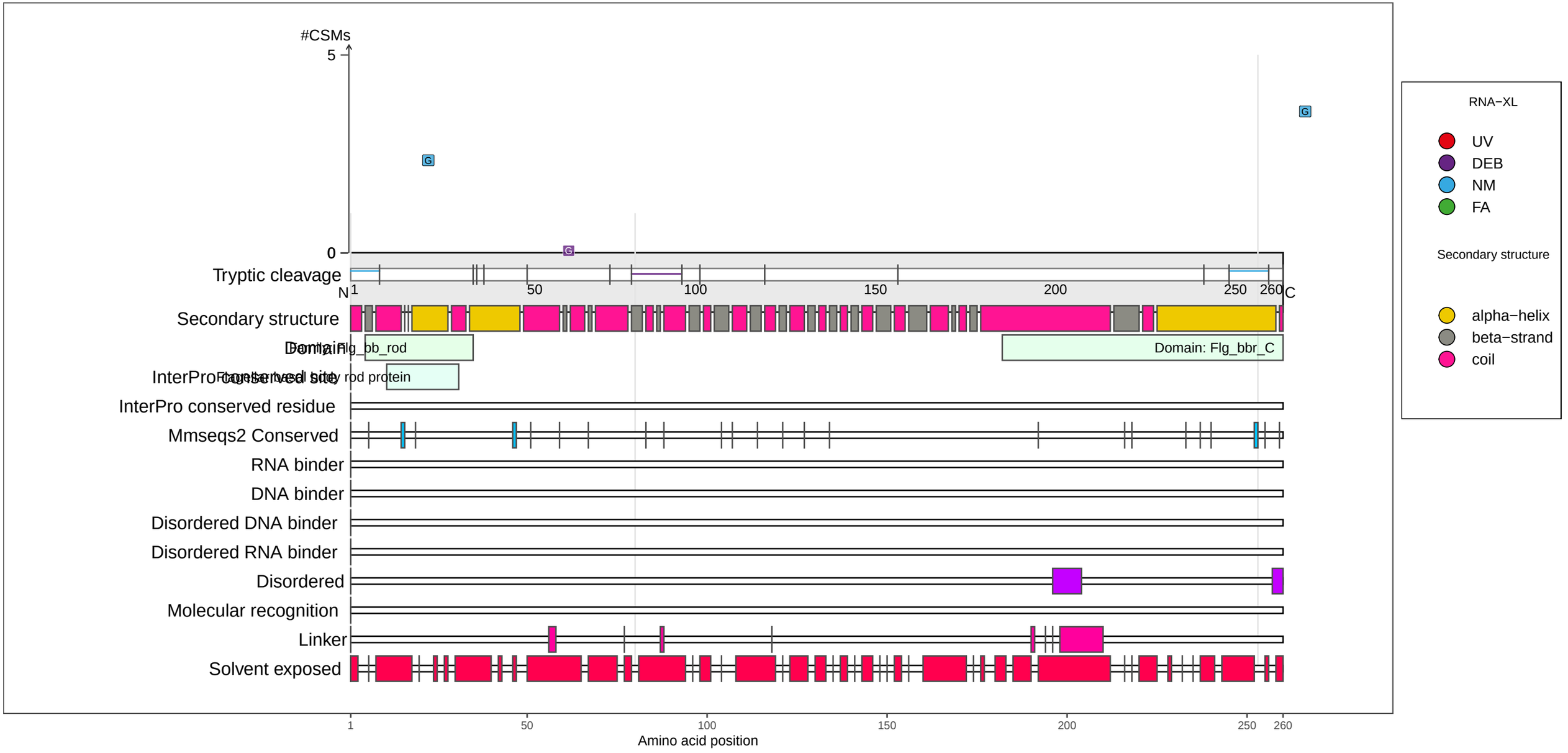




P0ABX5
FLGG_ECOLI Flagellar basal−body rod protein FlgG

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 1.77 (Q 52)
PAXdb E.coli [ppm]: 0.72 (Q 41)

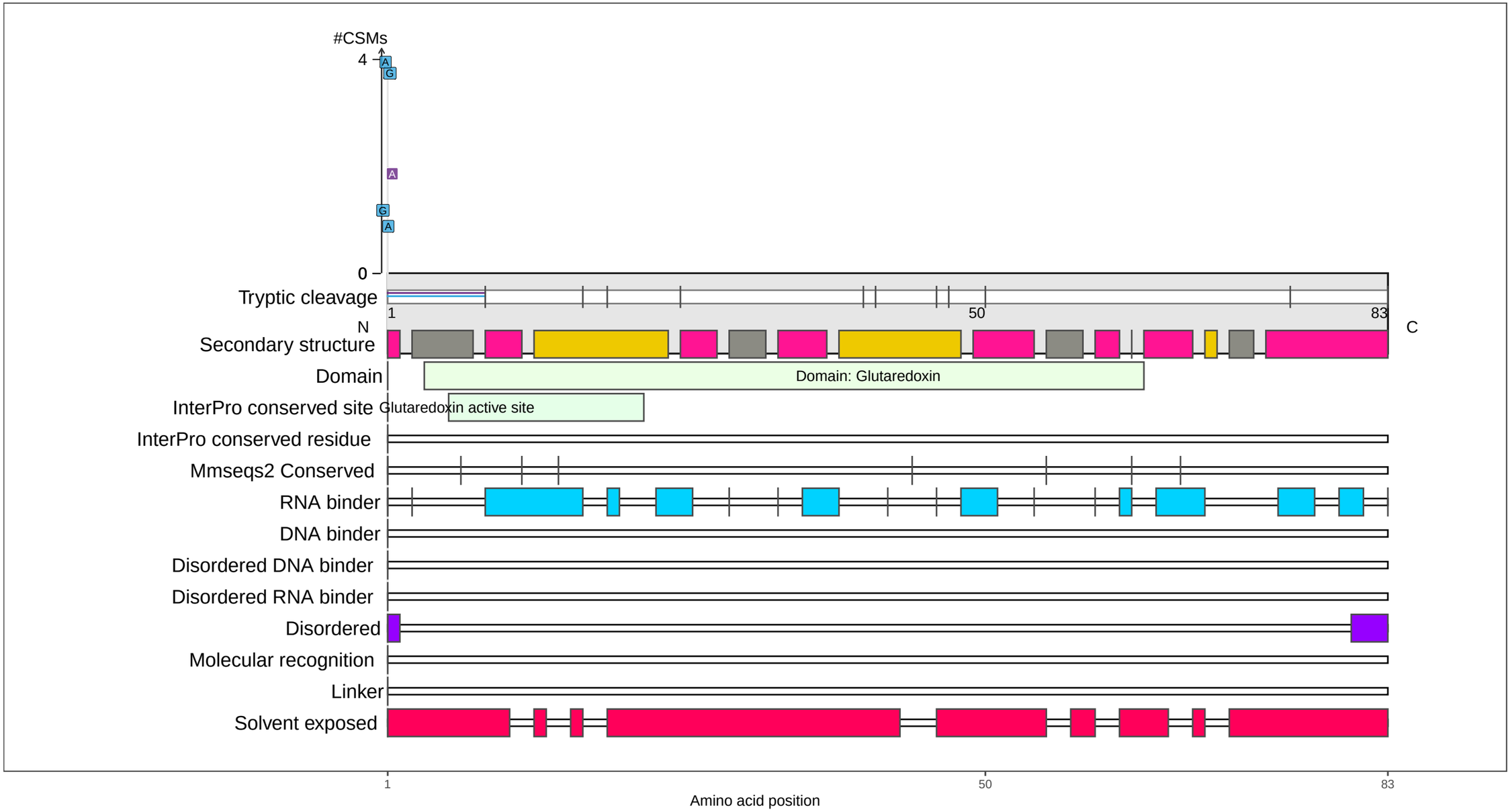
− RNA functions: not annotated



P0AC62
GLRX3_ECOLI Glutaredoxin 3

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 3.11 (Q 92)
PAXdb E.coli [ppm]: 2.8 (Q 92)

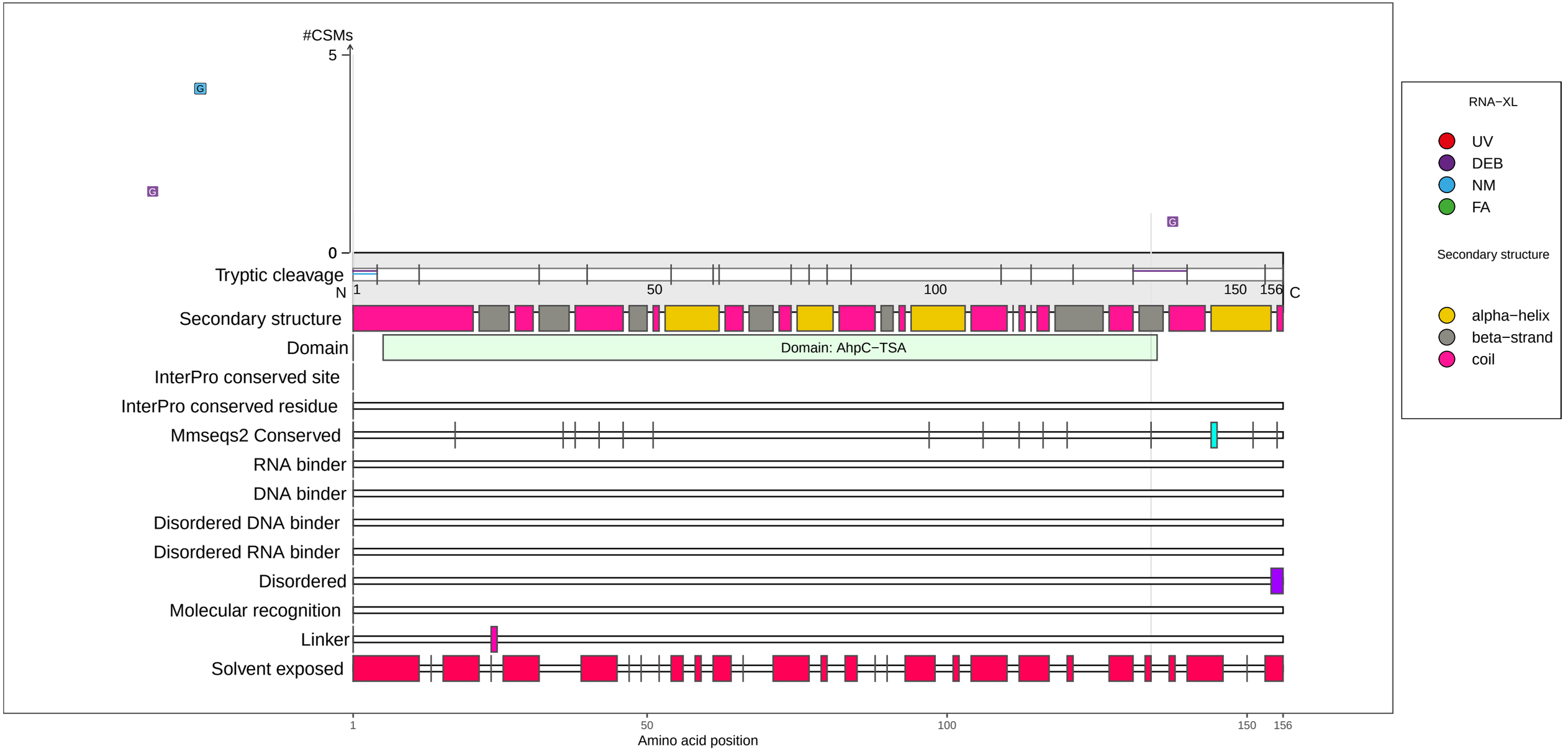
− RNA functions: not annotated



P0AE52
BCP_ECOLI Peroxiredoxin Bcp

− Abundance:
tryptic [log10 Intensity]: 8.78 (Q 83)
PAXdb K12 strain [ppm]: 3.45 (Q 97)
PAXdb E.coli [ppm]: 2.94 (Q 94)

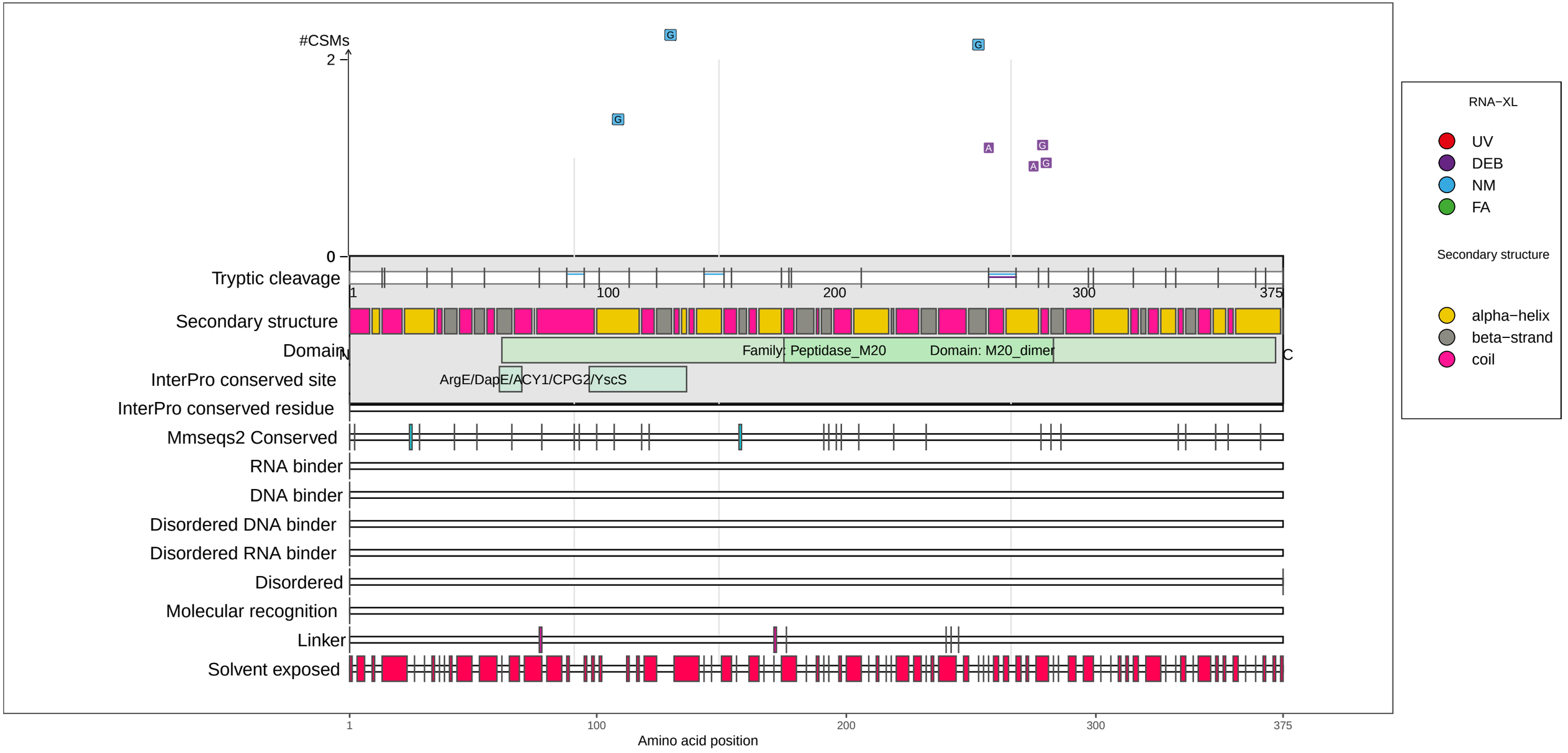
− RNA functions: not annotated



P0AED7
DAPE_ECOLI Succinyl−diaminopimelate desuccinylase

− Abundance:
tryptic [log10 Intensity]: 8.66 (Q 80)
PAXdb K12 strain [ppm]: 0.76 (Q 4)
PAXdb E.coli [ppm]: 1.46 (Q 59)

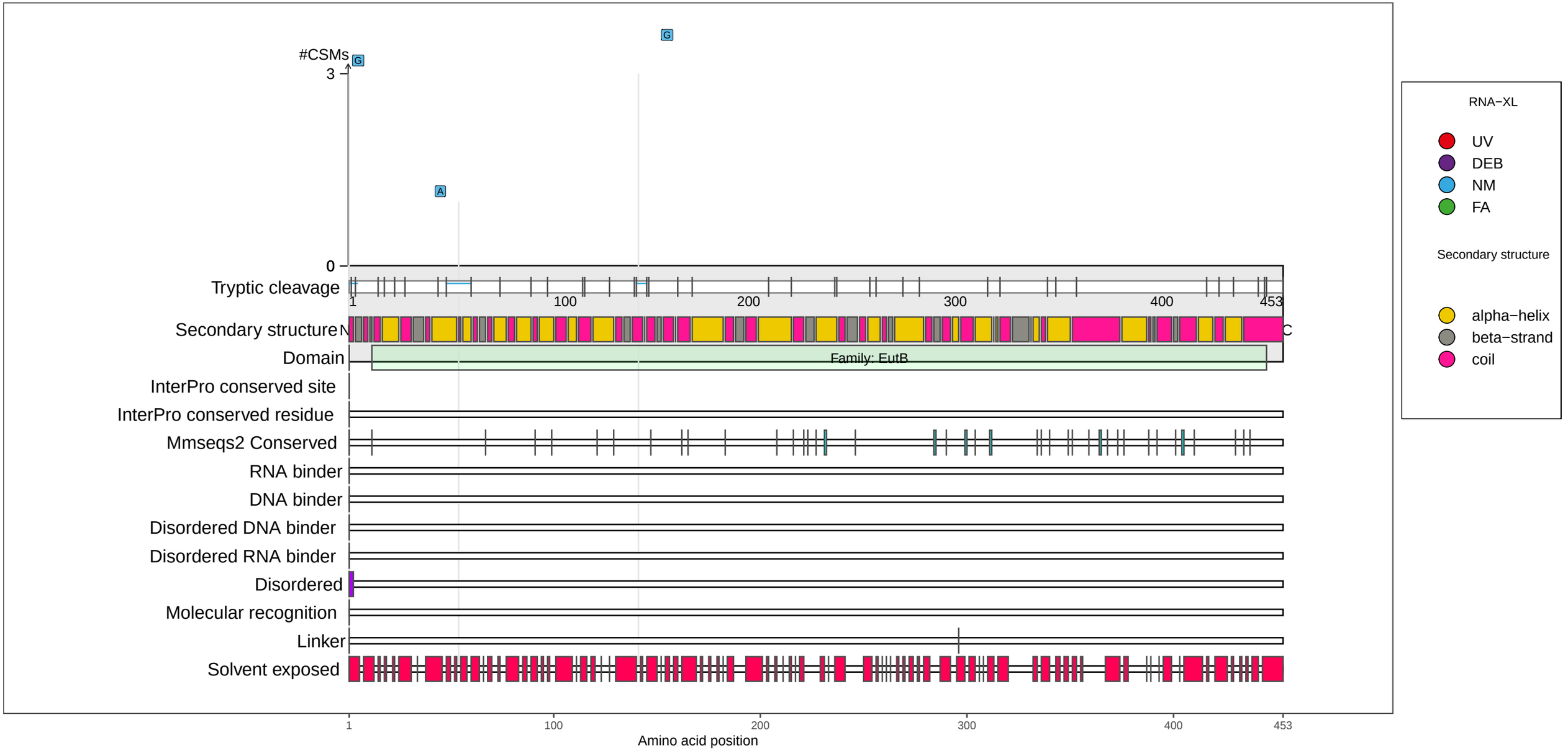
− RNA functions: not annotated



P0AEJ6
EUTB_ECOLI Ethanolamine ammonia−lyase large subunit

− Abundance:
tryptic [log10 Intensity]: 6.98 (Q 12)
PAXdb K12 strain [ppm]: 1.3 (Q 26)
PAXdb E.coli [ppm]: 1.31 (Q 55)

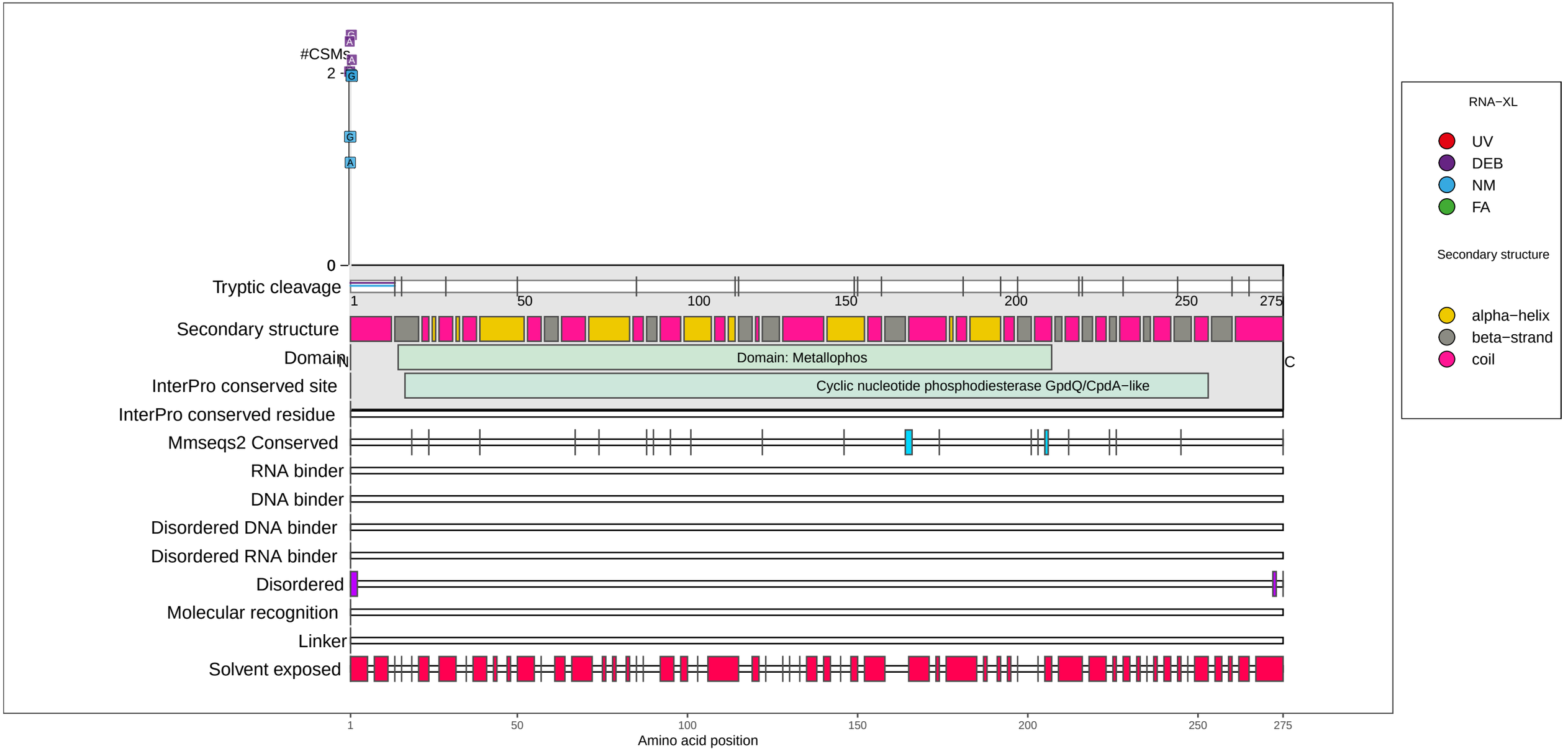
− RNA functions: not annotated



P0AEW4
CPDA_ECOLI 3',5'−cyclic adenosine monophosphate phosphodiesterase CpdA

− Abundance:
tryptic [log10 Intensity]: 7.63 (Q 41)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: 1.79 (Q 67)

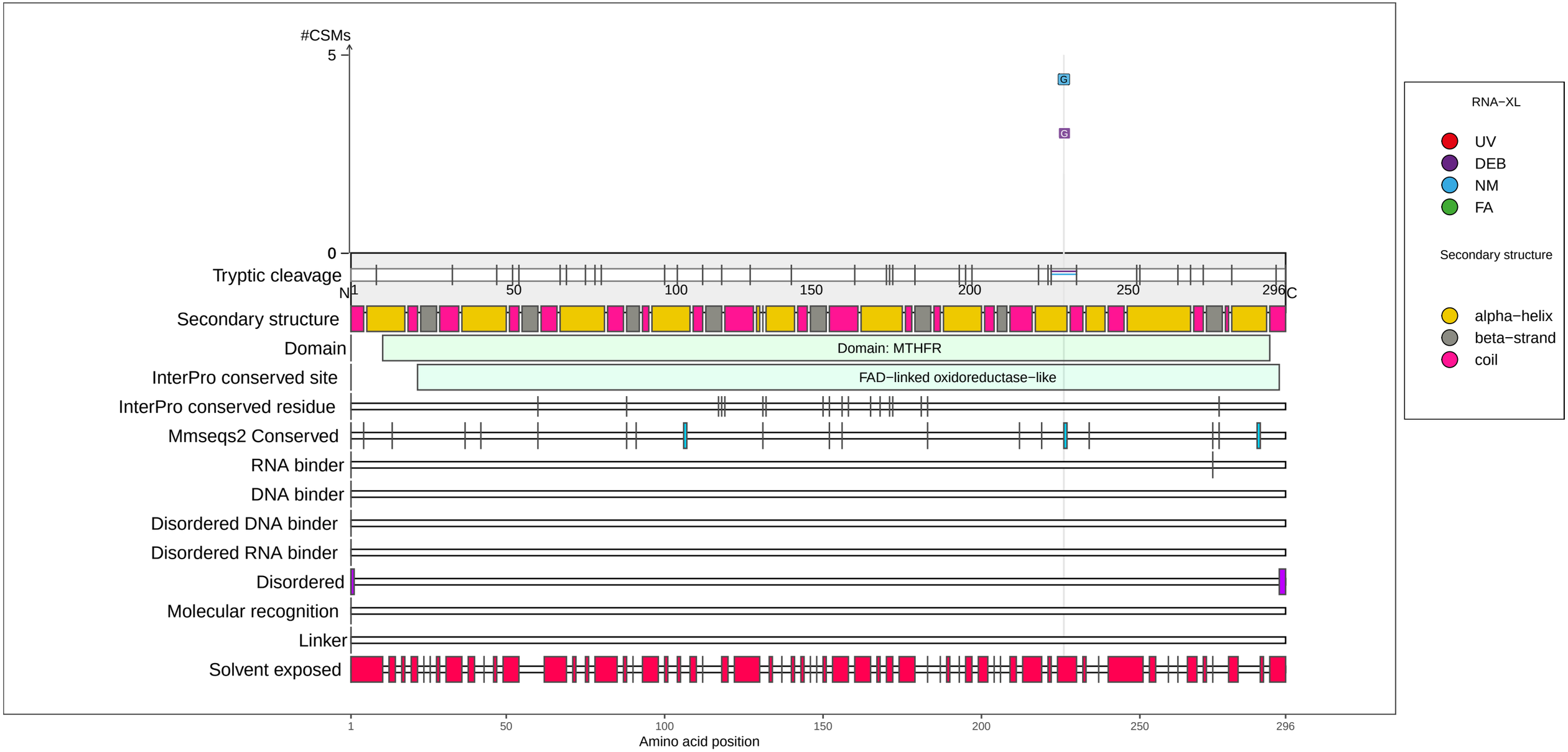
− RNA functions: not annotated



P0AEZ1
METF_ECOLI 5,10−methylenetetrahydrofolate reductase

− Abundance:
tryptic [log10 Intensity]: 7.32 (Q 26)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 2.47 (Q 85)

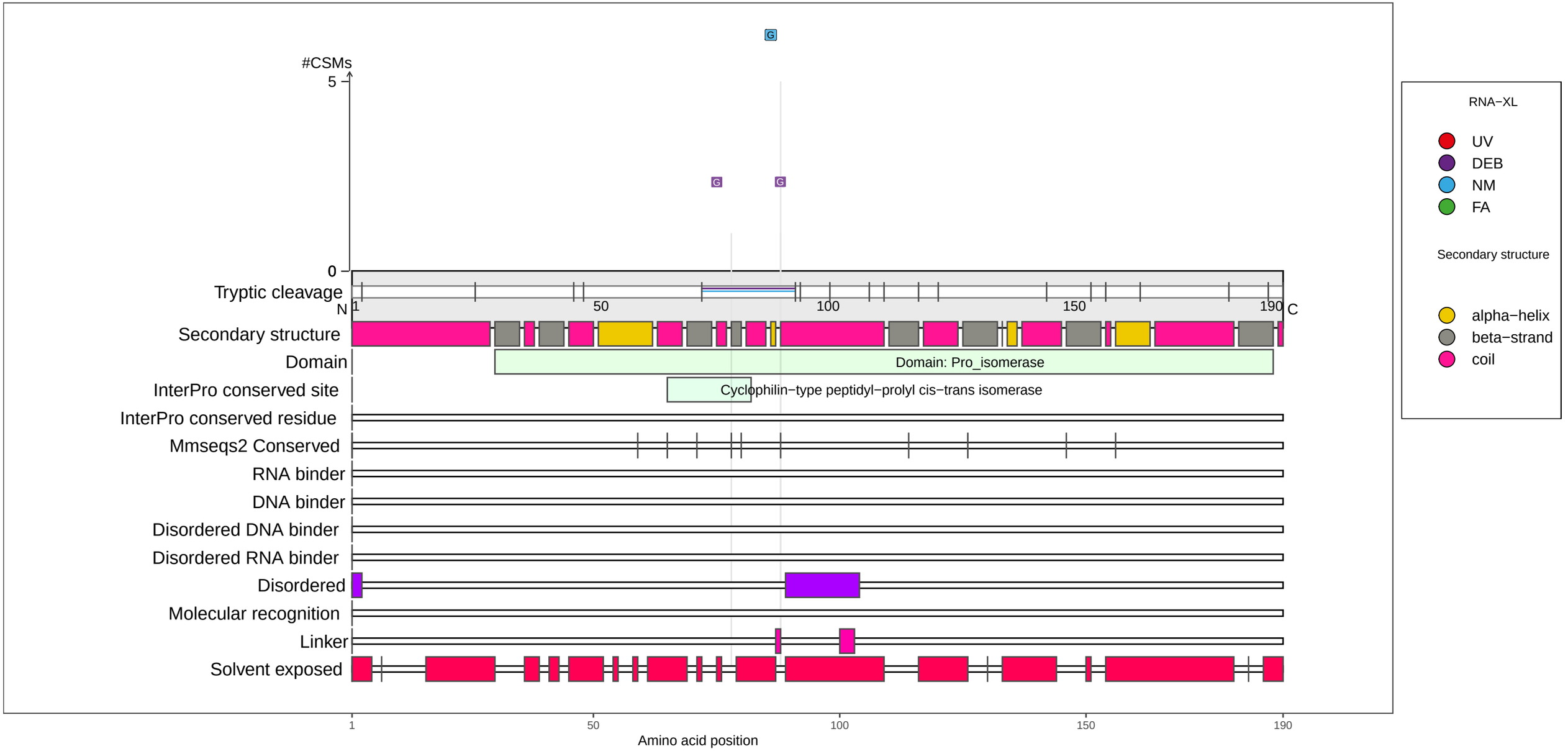
− RNA functions: not annotated



P0AFL3
PPIA_ECOLI Peptidyl−prolyl cis−trans isomerase A

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 87)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.53 (Q 86)

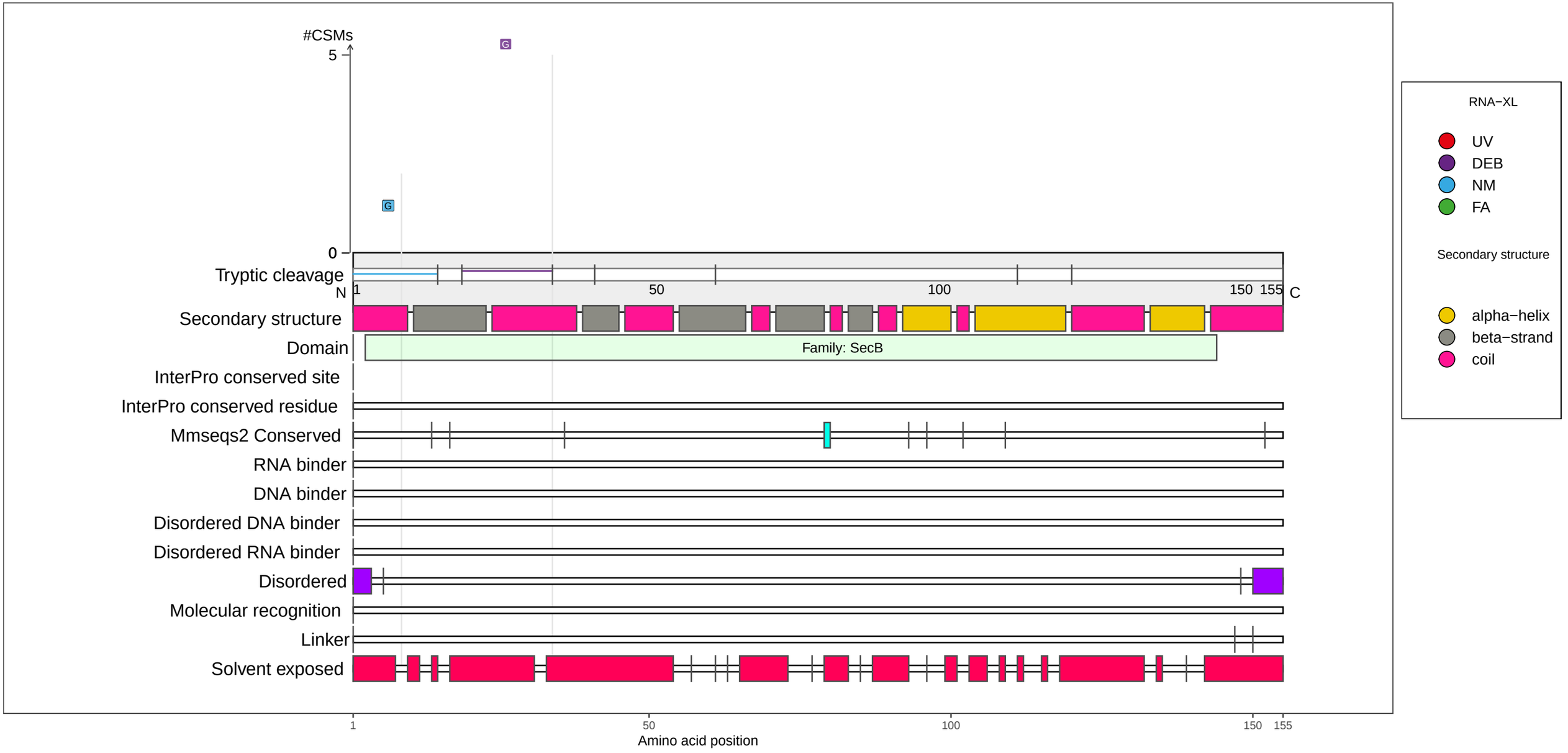
− RNA functions: not annotated



P0AG86
SECB_ECOLI Protein−export protein SecB

− Abundance:
tryptic [log10 Intensity]: 8.86 (Q 85)
PAXdb K12 strain [ppm]: 3.19 (Q 94)
PAXdb E.coli [ppm]: 3.42 (Q 98)

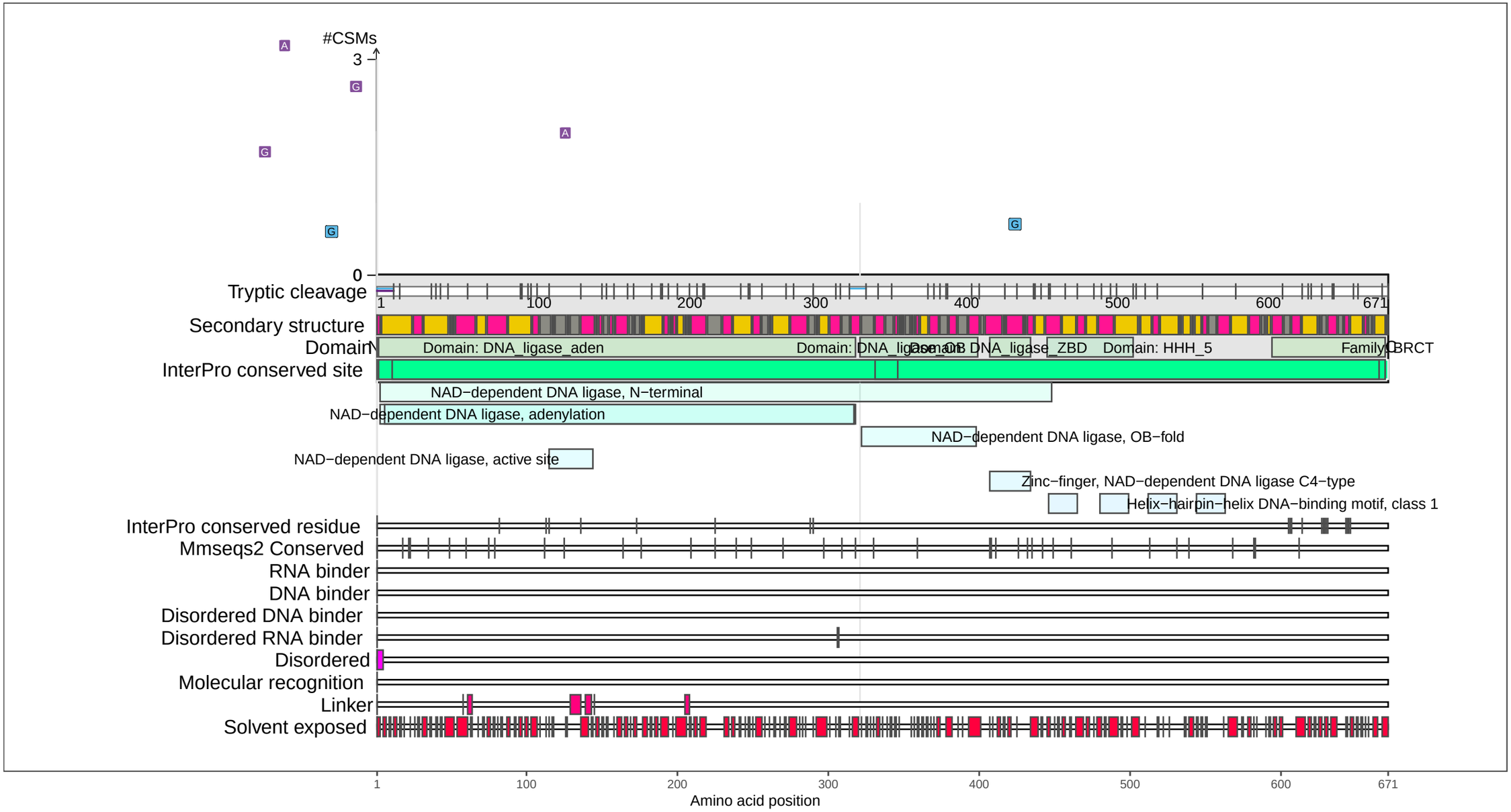
− RNA functions: not annotated

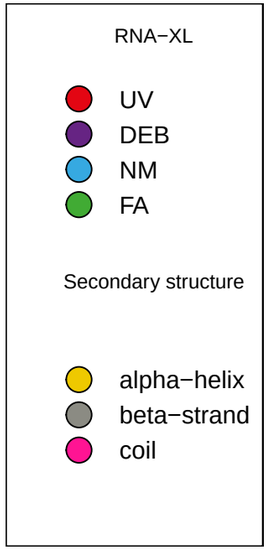


P15042
DNLJ_ECOLI DNA ligase

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 1.54 (Q 40)
PAXdb E.coli [ppm]: 1.91 (Q 70)

− RNA functions: not annotated

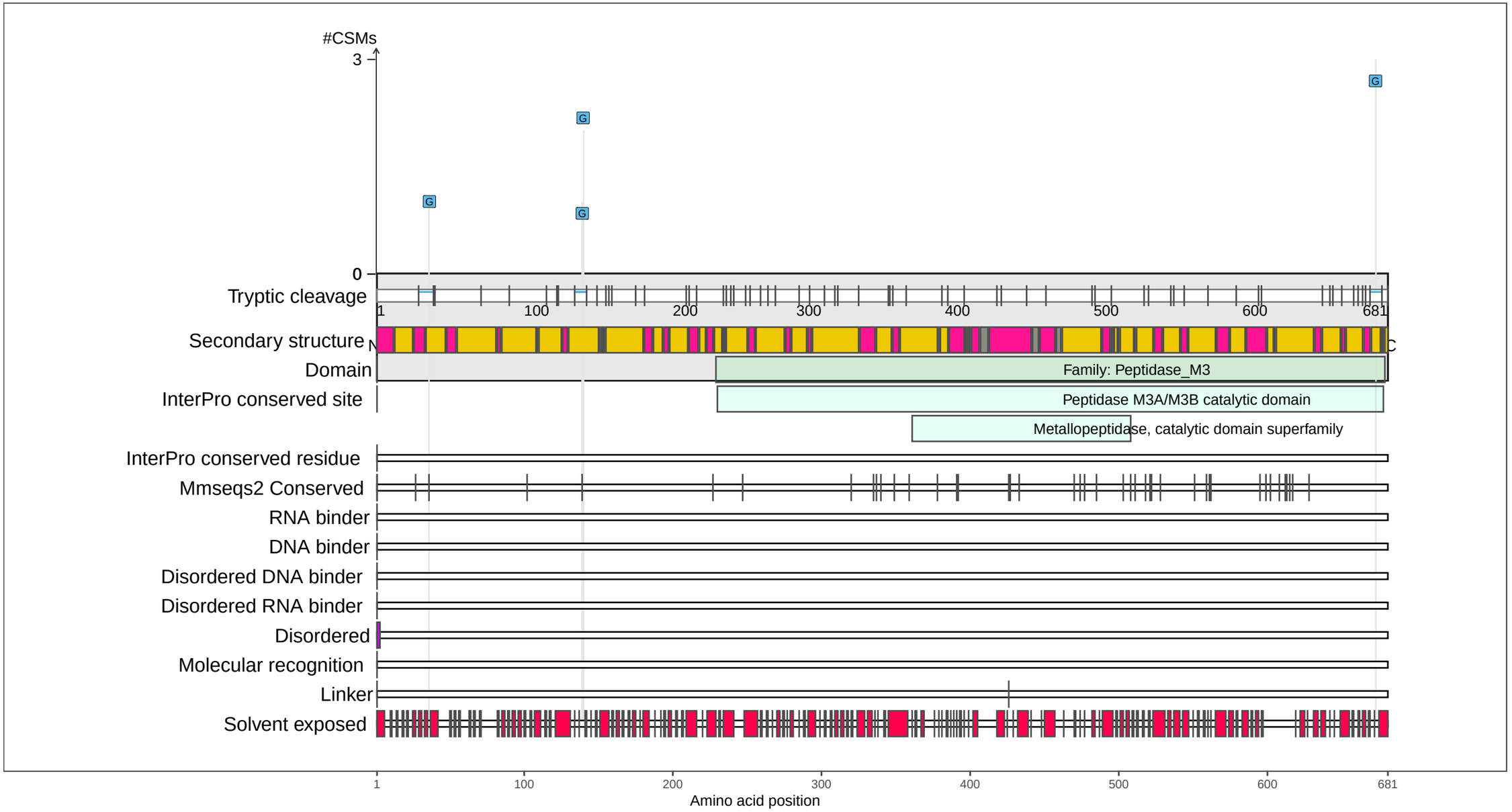


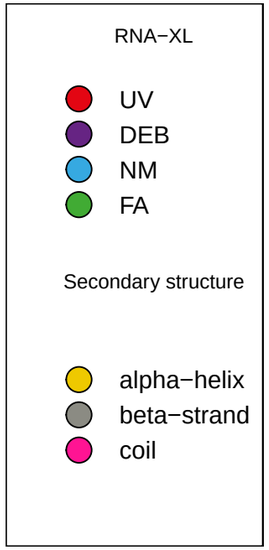


P24171
DCP_ECOLI Dipeptidyl carboxypeptidase

− Abundance:
tryptic [log10 Intensity]: 8.75 (Q 82)
PAXdb K12 strain [ppm]: 1.86 (Q 56)
PAXdb E.coli [ppm]: 2.41 (Q 83)

− RNA functions: not annotated

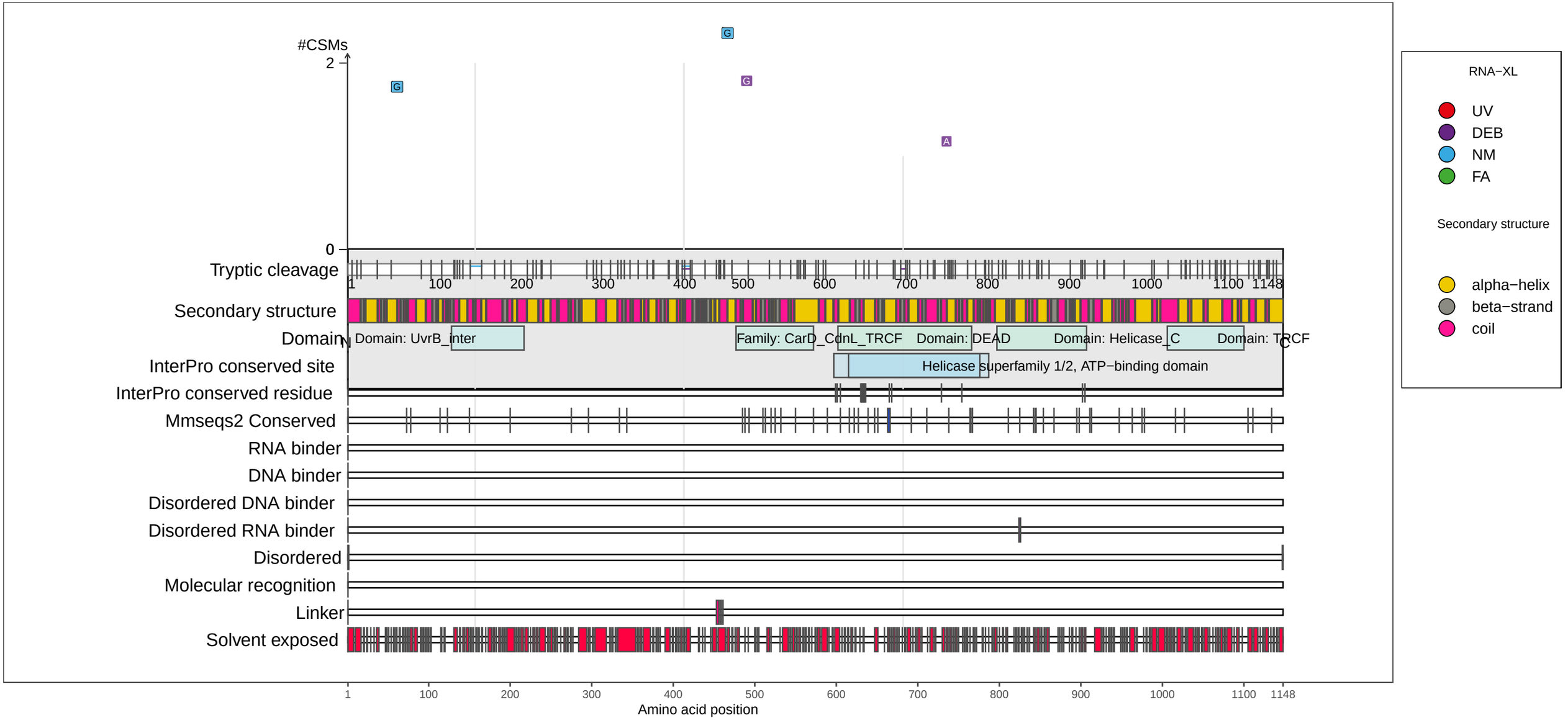




P30958
MFD_ECOLI Transcription−repair−coupling factor

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 54)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 1.74 (Q 66)

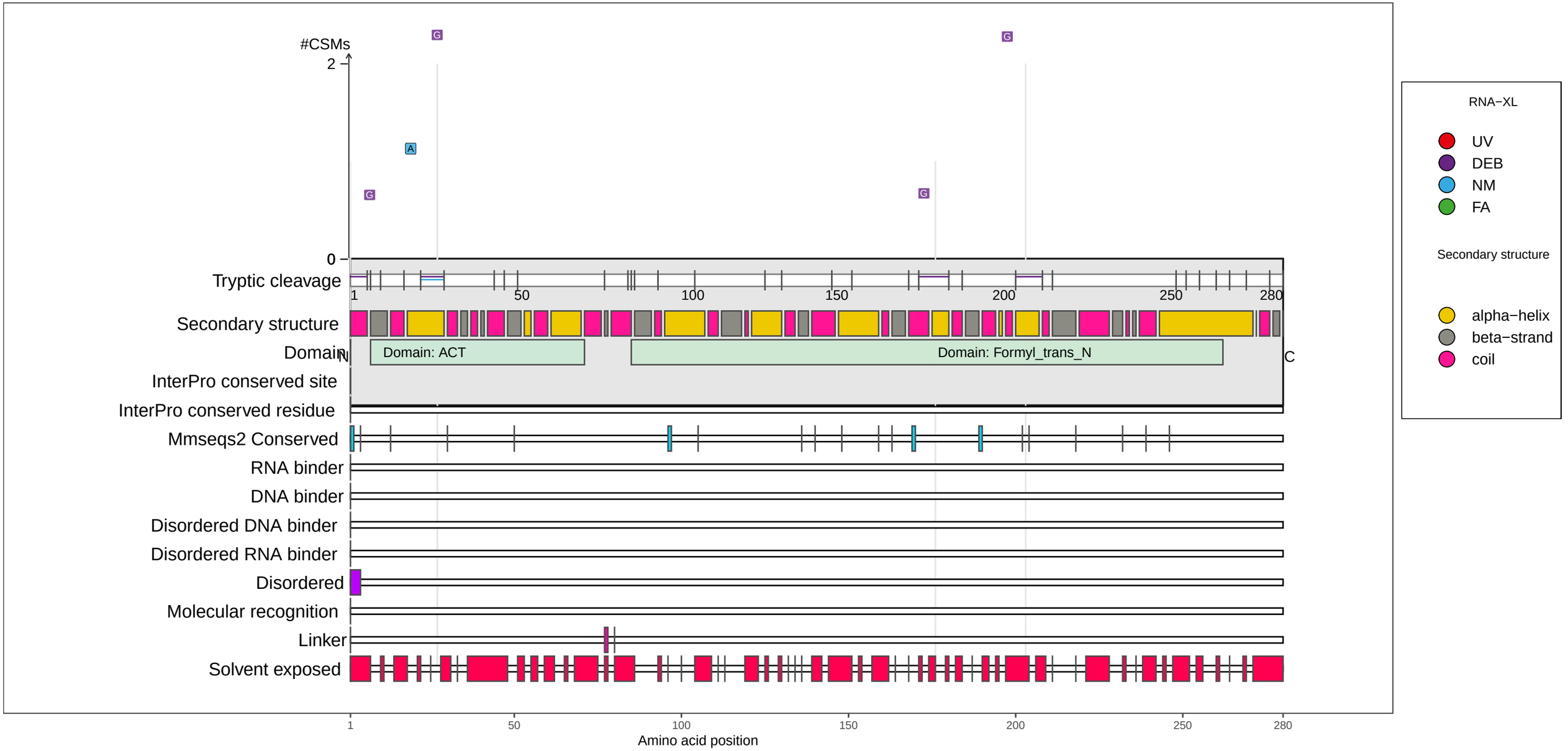
− RNA functions:
RNA polymerase binding; RNA polymerase core enzyme binding
This domain is found in proteins necessary for strand−specific repair in DNA such as TRCF in Escherichia coli. A lesion in the template strand blocks the RNA polymerase complex (RNAP). The RNAP−DNA−RNA complex is spec



P37051
PURU_ECOLI Formyltetrahydrofolate deformylase

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 92)
PAXdb K12 strain [ppm]: 2.24 (Q 68)
PAXdb E.coli [ppm]: 2.25 (Q 79)

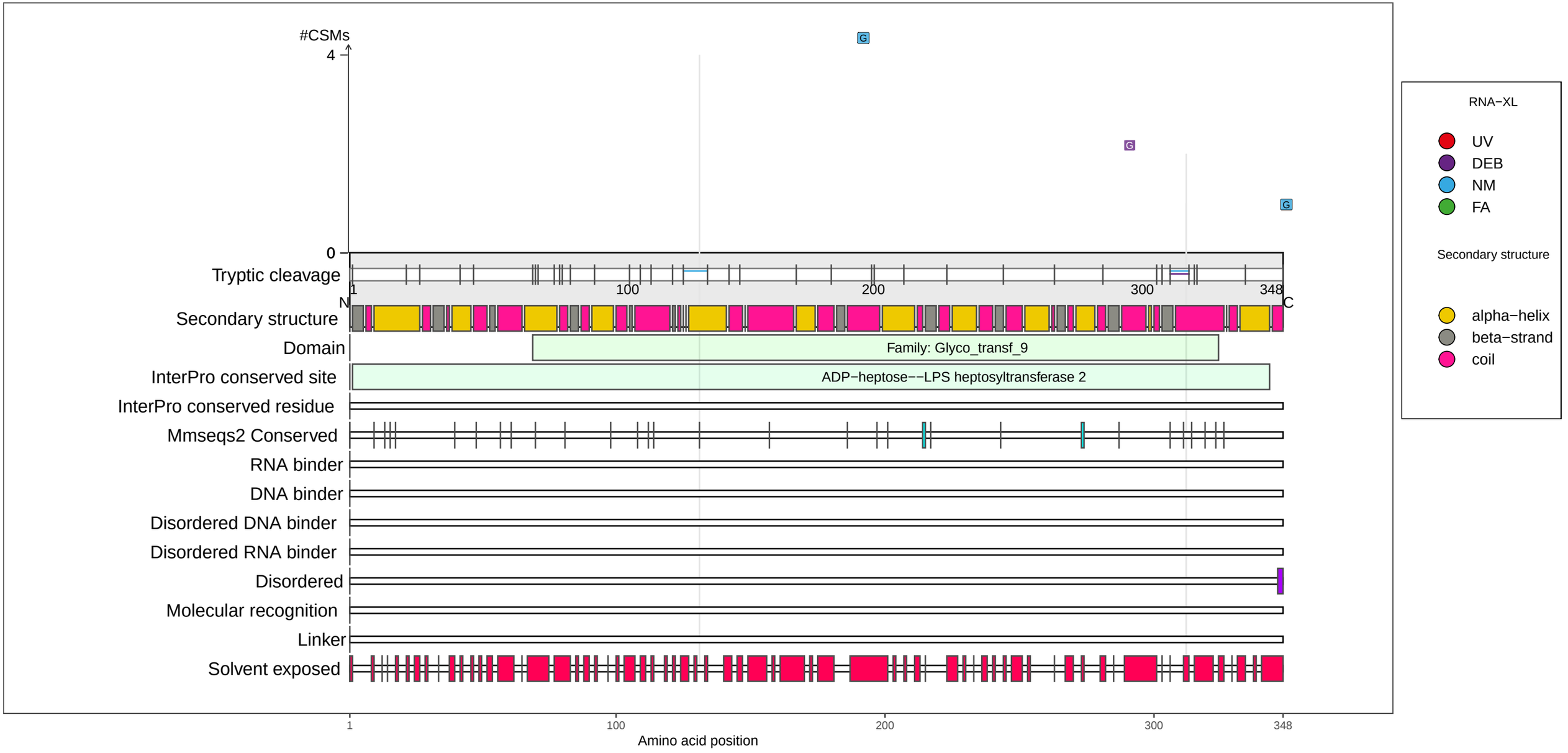
− RNA functions: not annotated



P37692
RFAF_ECOLI ADP−heptose−−LPS heptosyltransferase 2

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 1.83 (Q 54)
PAXdb E.coli [ppm]: 0.71 (Q 41)

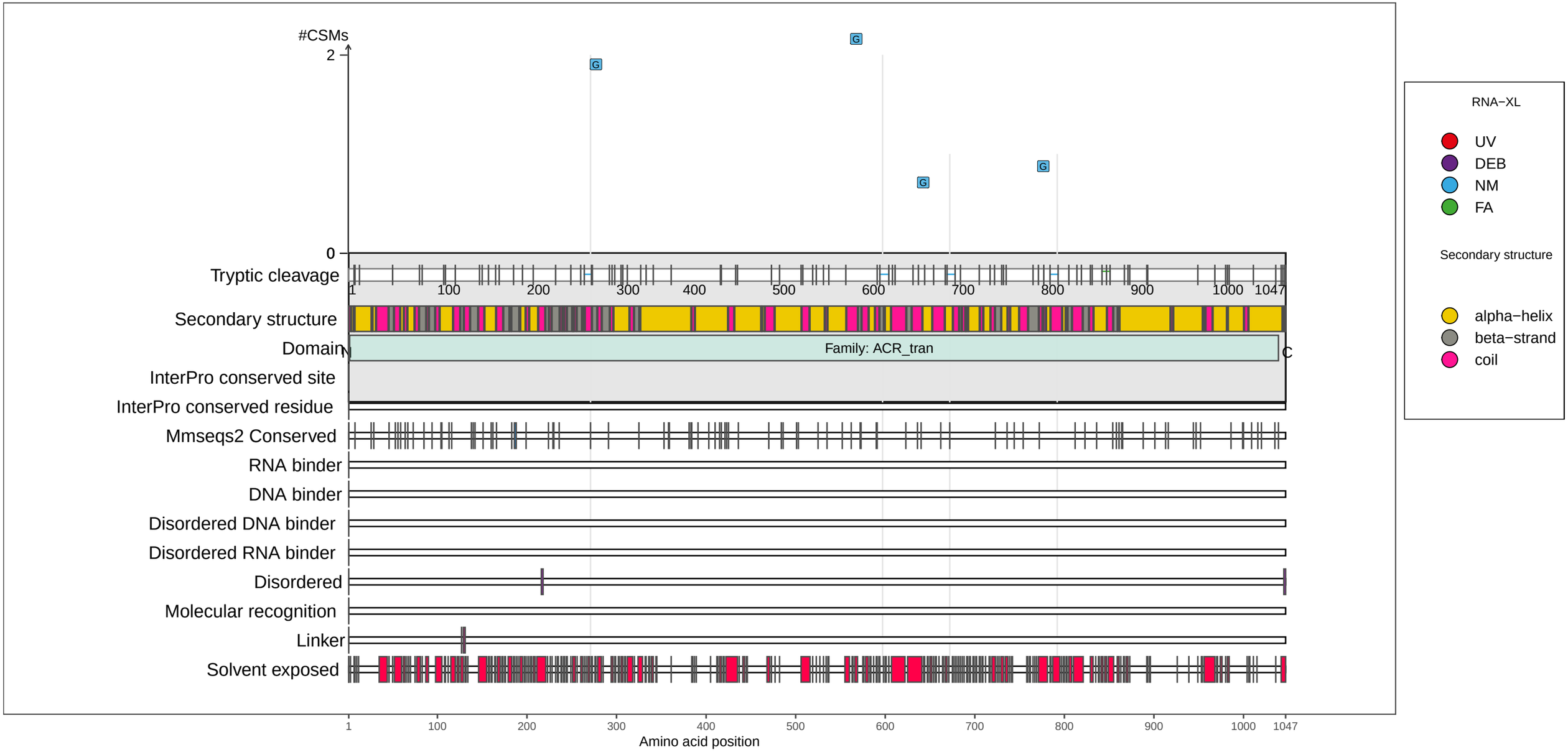
− RNA functions: not annotated



P38054
CUSA_ECOLI Cation efflux system protein CusA

− Abundance:
tryptic [log10 Intensity]: 7.11 (Q 17)
PAXdb K12 strain [ppm]: 1 (Q 11)
PAXdb E.coli [ppm]: 0.77 (Q 42)

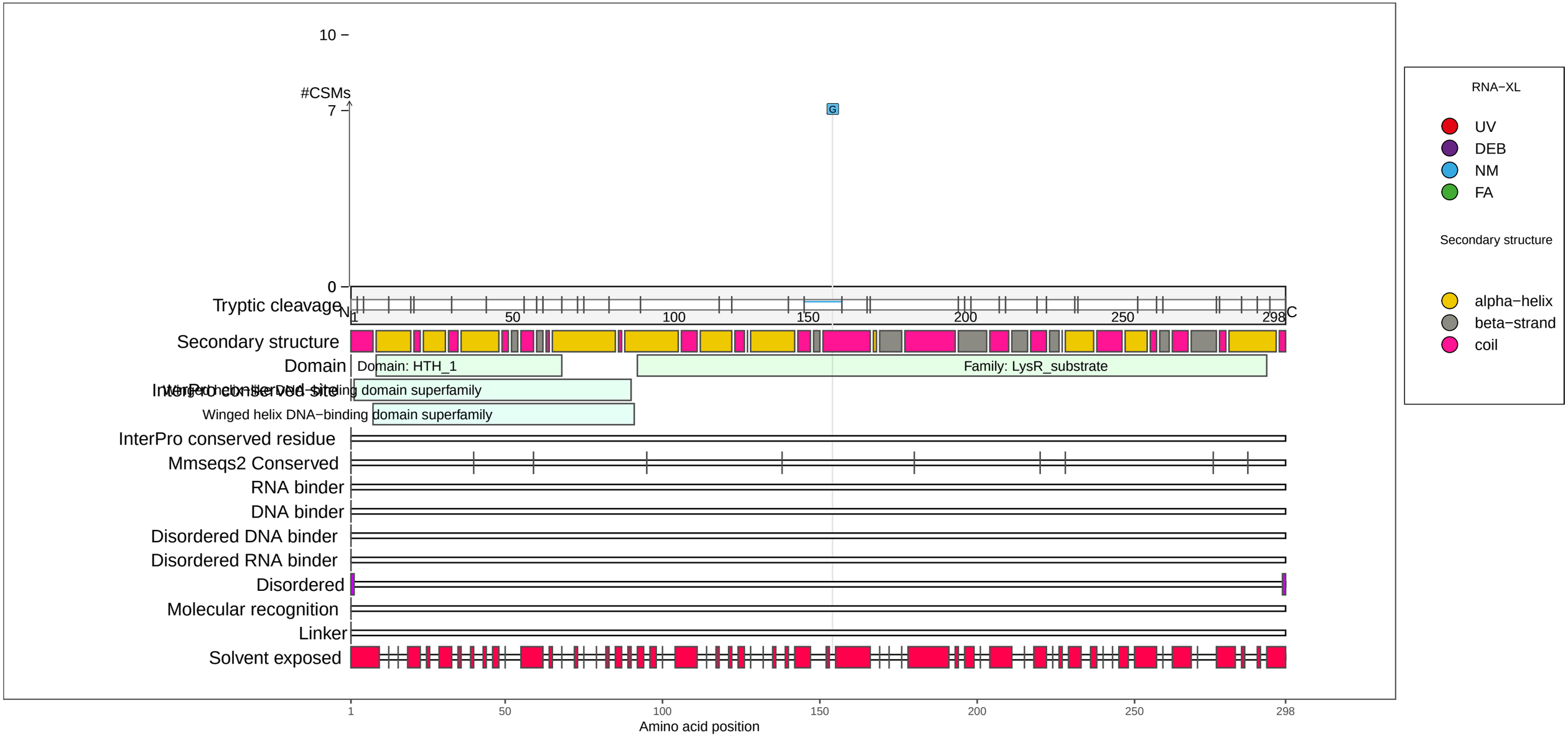
− RNA functions: not annotated



P67660
YHAJ_ECOLI Probable HTH−type transcriptional regulator YhaJ

− Abundance:
tryptic [log10 Intensity]: 7.08 (Q 16)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.87 (Q 69)

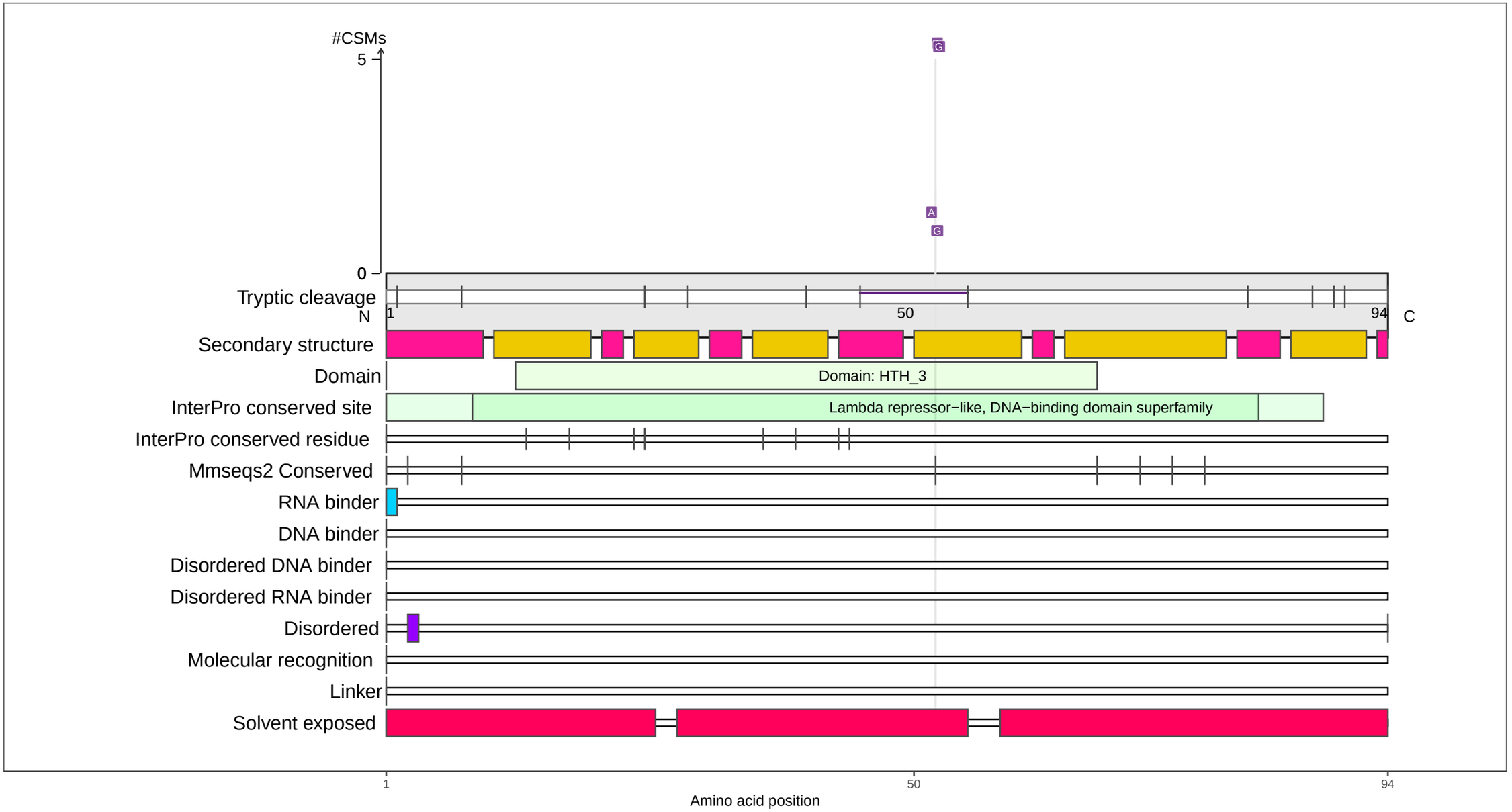
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P67699
YDDM_ECOLI Uncharacterized HTH−type transcriptional regulator YddM

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.38 (Q 17)

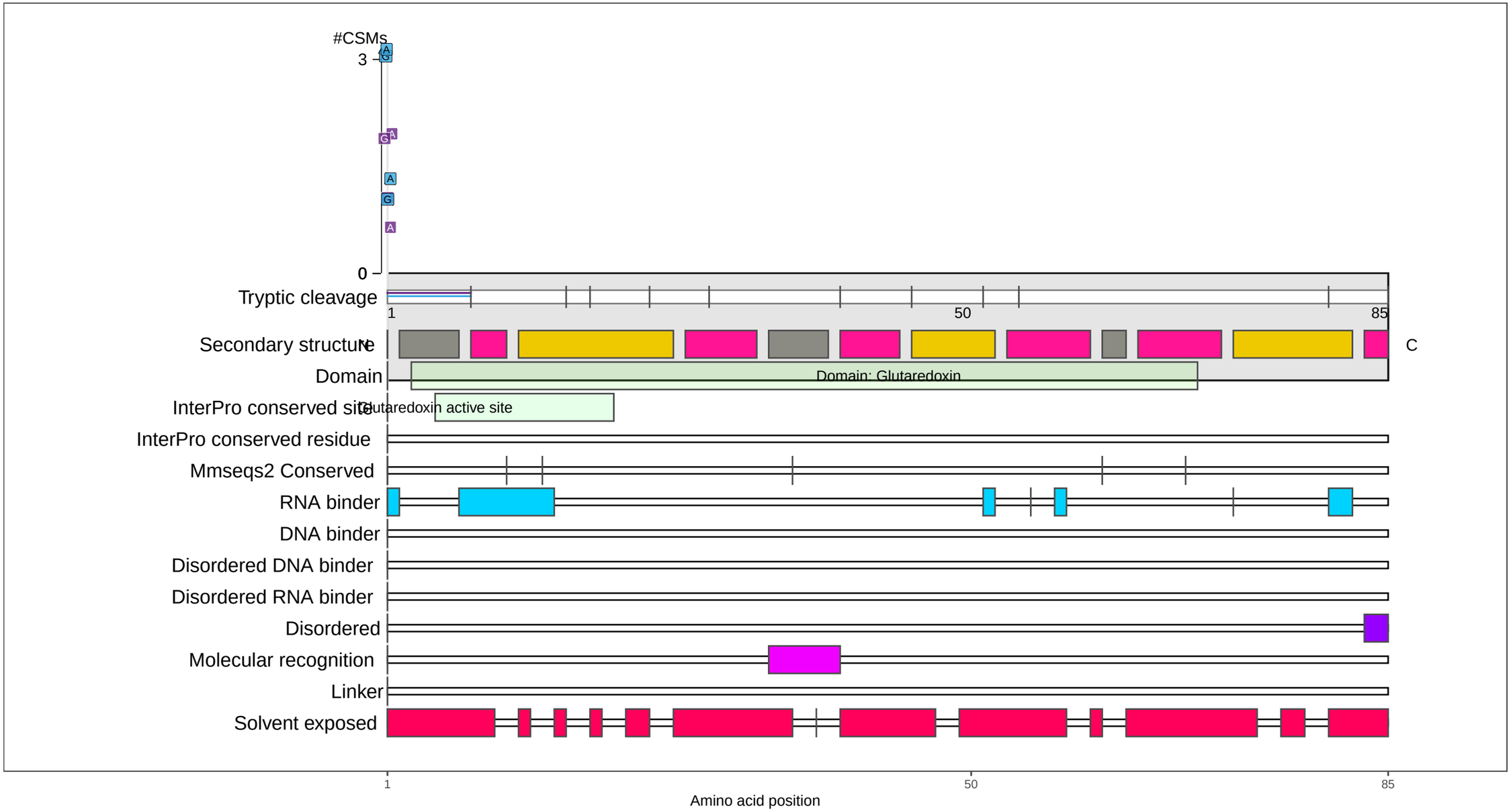
− RNA functions: not annotated

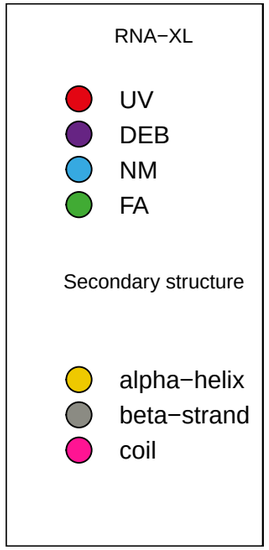


P68688
GLRX1_ECOLI Glutaredoxin 1

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 1.97 (Q 71)

− RNA functions: not annotated

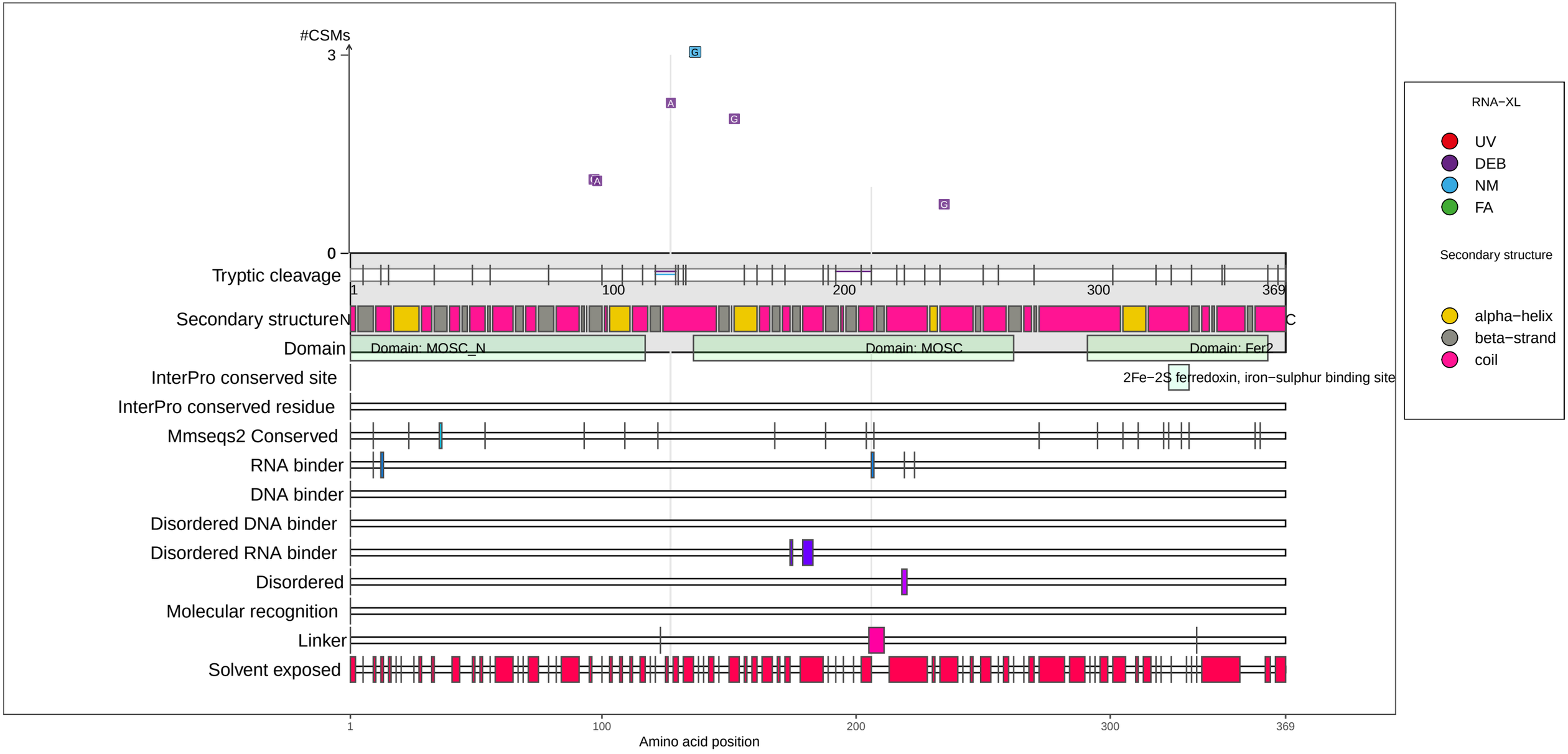




P75863
YCBX_ECOLI Uncharacterized protein YcbX

− Abundance:
tryptic [log10 Intensity]: 8.1 (Q 61)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 1.82 (Q 68)

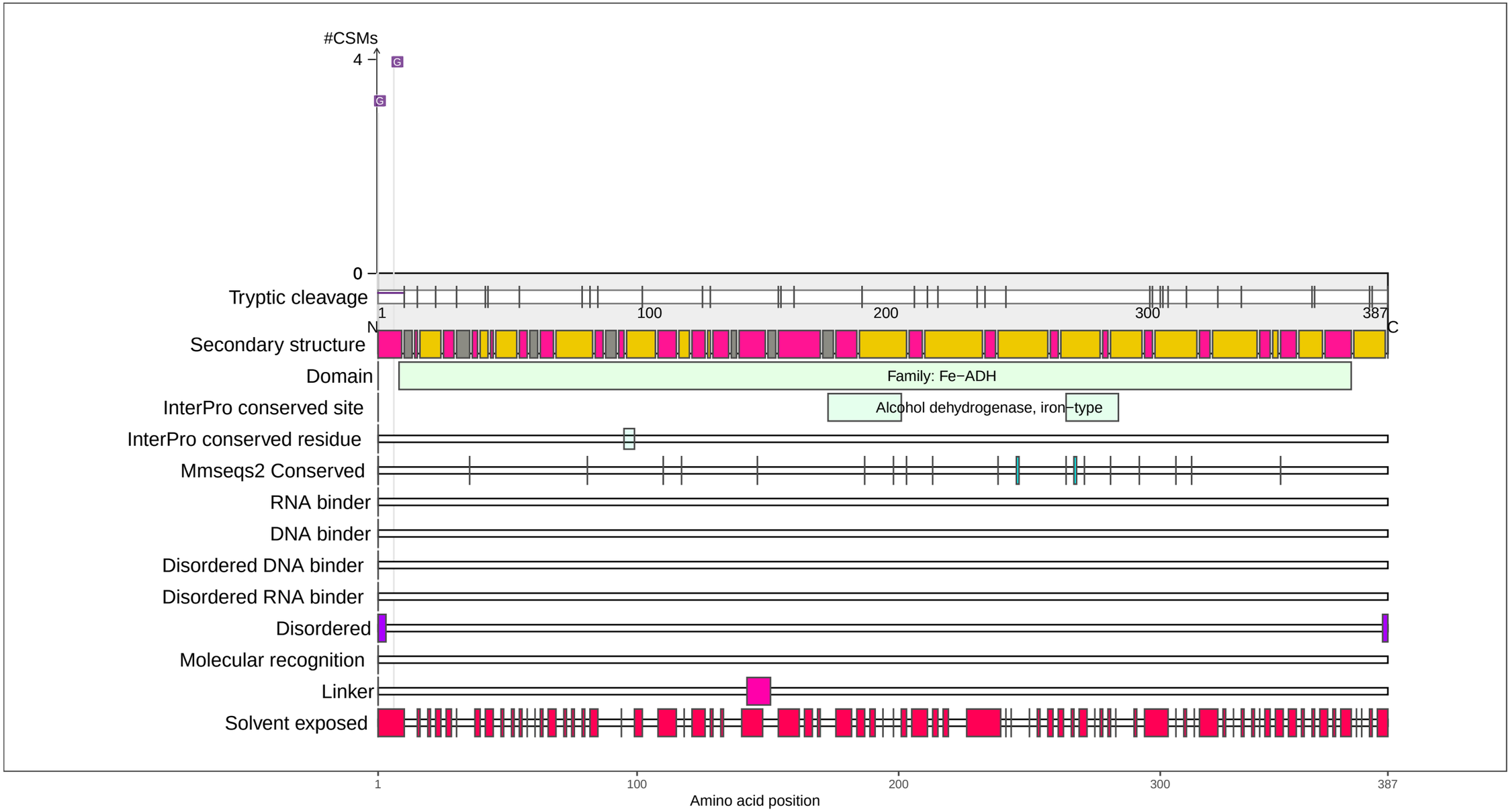
− RNA functions: not annotated



Q46856
YQHD_ECOLI Alcohol dehydrogenase YqhD

− Abundance:
tryptic [log10 Intensity]: 8.39 (Q 72)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 2.33 (Q 81)

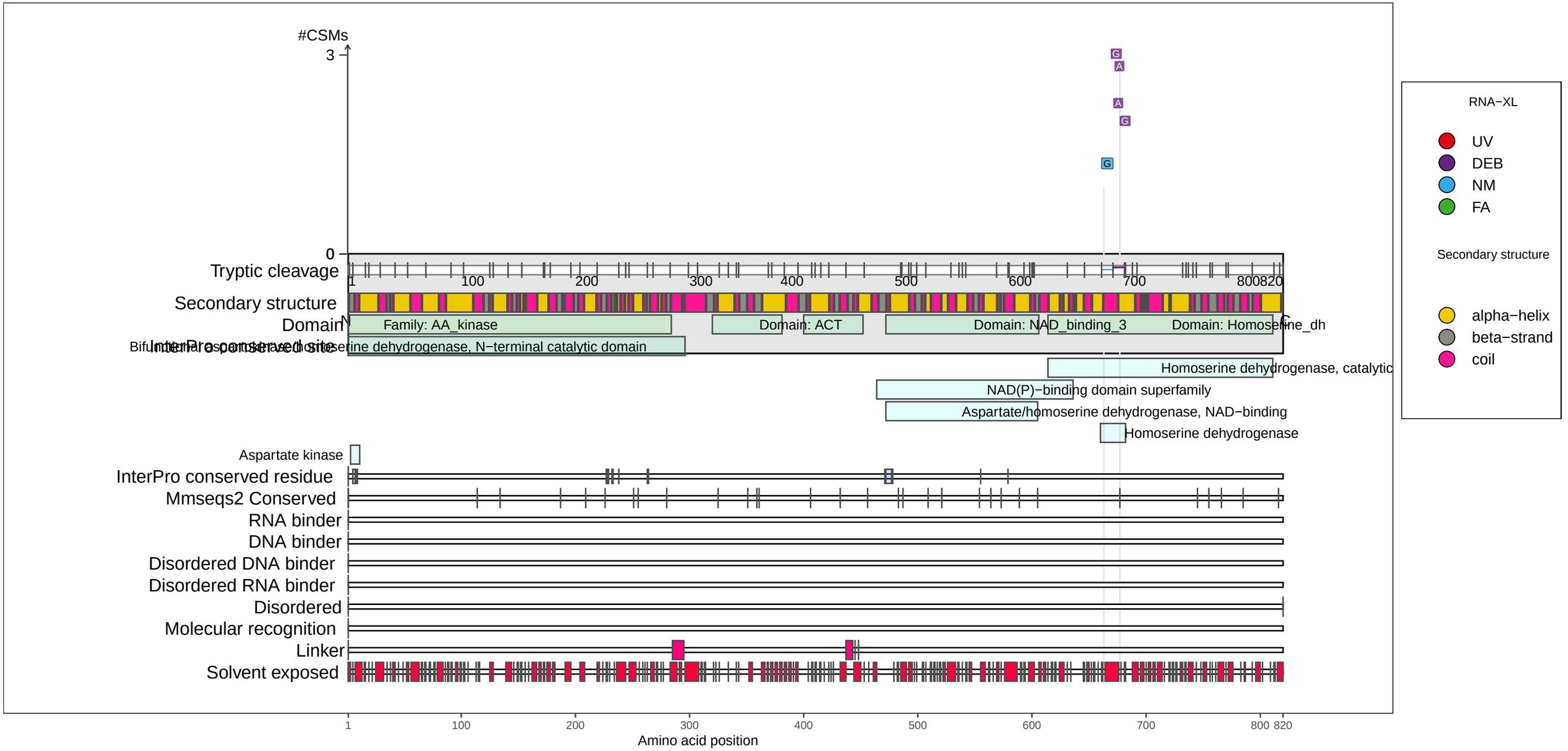
− RNA functions: not annotated



P00561
AK1H_ECOLI Bifunctional aspartokinase/homoserine dehydrogenase 1

− Abundance:
tryptic [log10 Intensity]: 7.13 (Q 18)
PAXdb K12 strain [ppm]: 2.32 (Q 70)
PAXdb E.coli [ppm]: 2.66 (Q 89)

− RNA functions: not annotated



P00962
SYQ_ECOLI Glutamine−−tRNA ligase

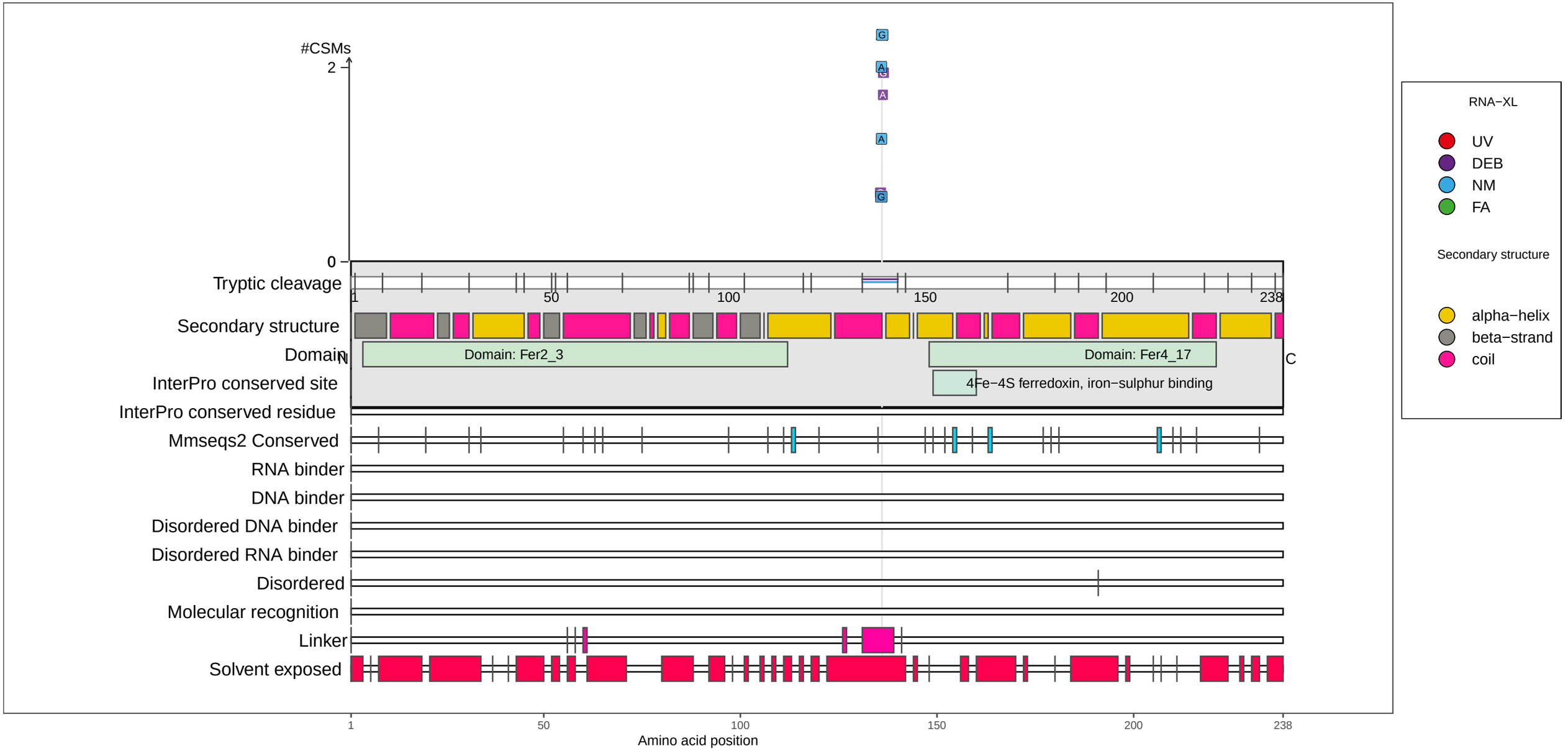
− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: 2.77 (Q 85)
PAXdb E.coli [ppm]: 2.68 (Q 89)

− RNA functions:
aminoacyl−tRNA ligase activity; glutamine−tRNA ligase activity
glutaminyl−tRNA aminoacylation; glutamyl−tRNA aminoacylation; ncRNA metabolic process
RNA metabolic process; tRNA aminoacylation; tRNA aminoacylation for protein translation
tRNA metabolic process; tRNA synthetases class I (E and Q), anti−codon binding domain
tRNA synthetases class I (E and Q), catalytic domain

P07014
SDHB_ECOLI Succinate dehydrogenase iron−sulfur subunit

− Abundance:
tryptic [log10 Intensity]: 8.66 (Q 80)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 2.82 (Q 92)

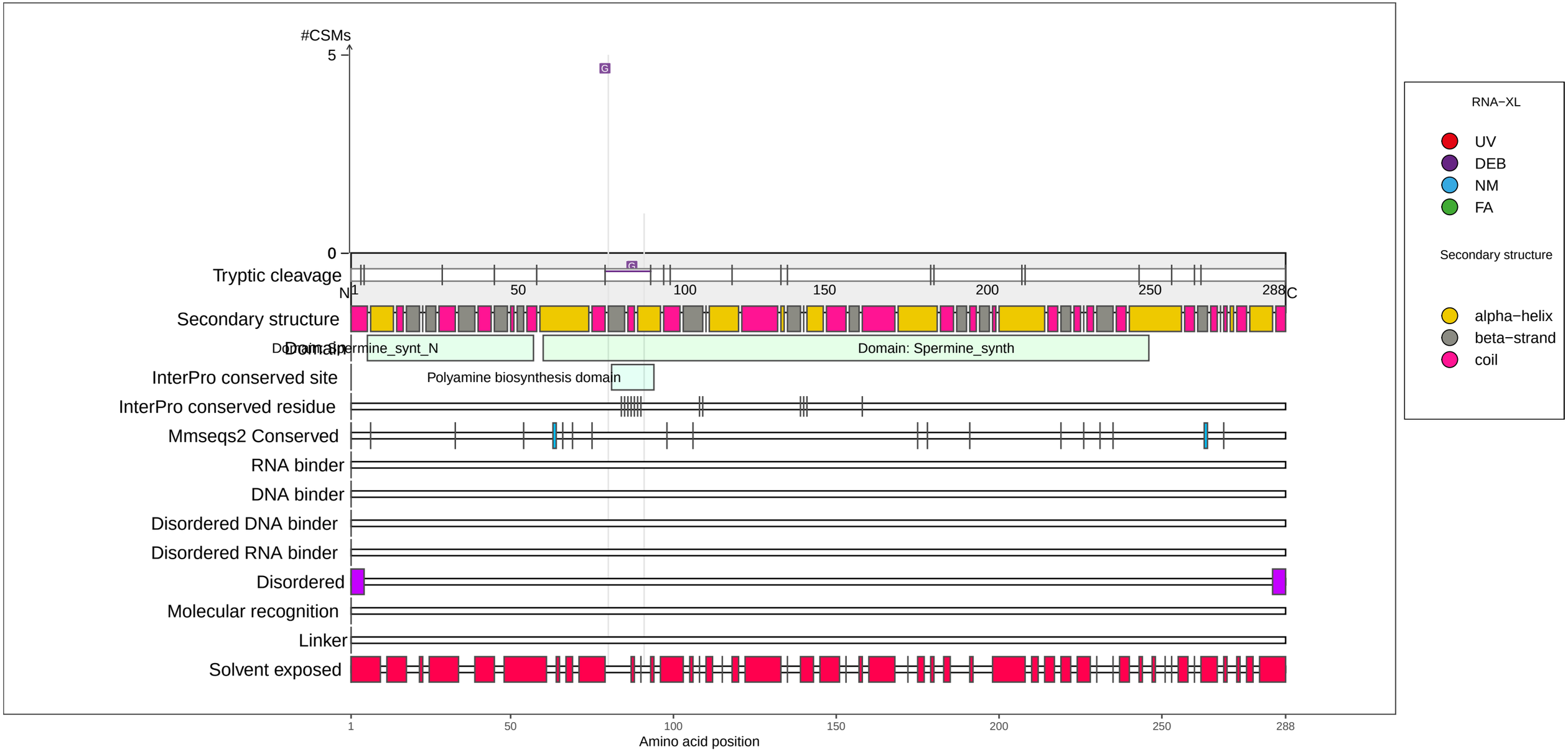
− RNA functions: not annotated



P09158
SPEE_ECOLI Polyamine aminopropyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.61 (Q 79)
PAXdb K12 strain [ppm]: 1.32 (Q 27)
PAXdb E.coli [ppm]: 2 (Q 72)

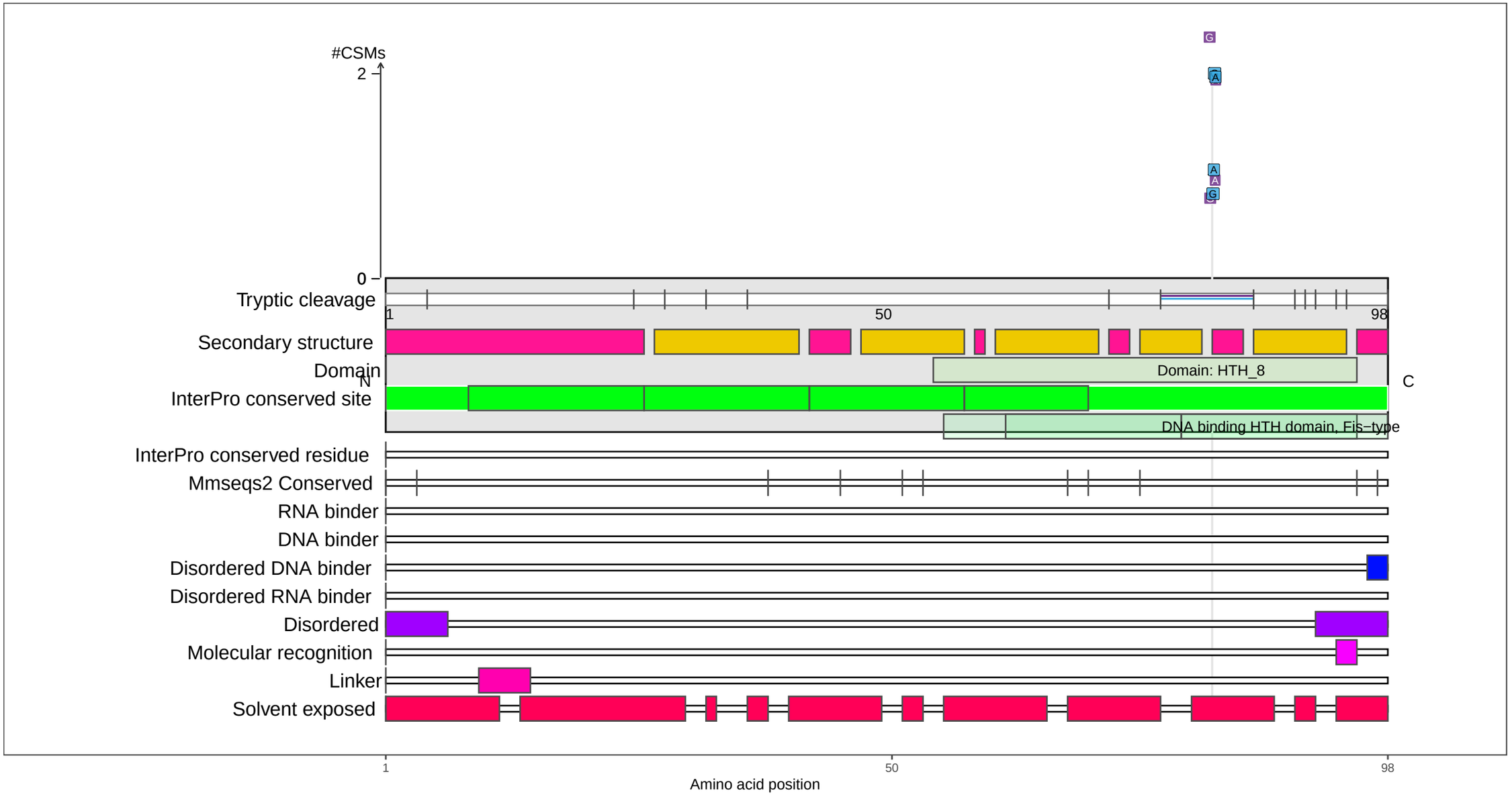
− RNA functions: not annotated



P0A6R3
FIS_ECOLI DNA−binding protein Fis

− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: 3.33 (Q 96)
PAXdb E.coli [ppm]: 2.39 (Q 83)

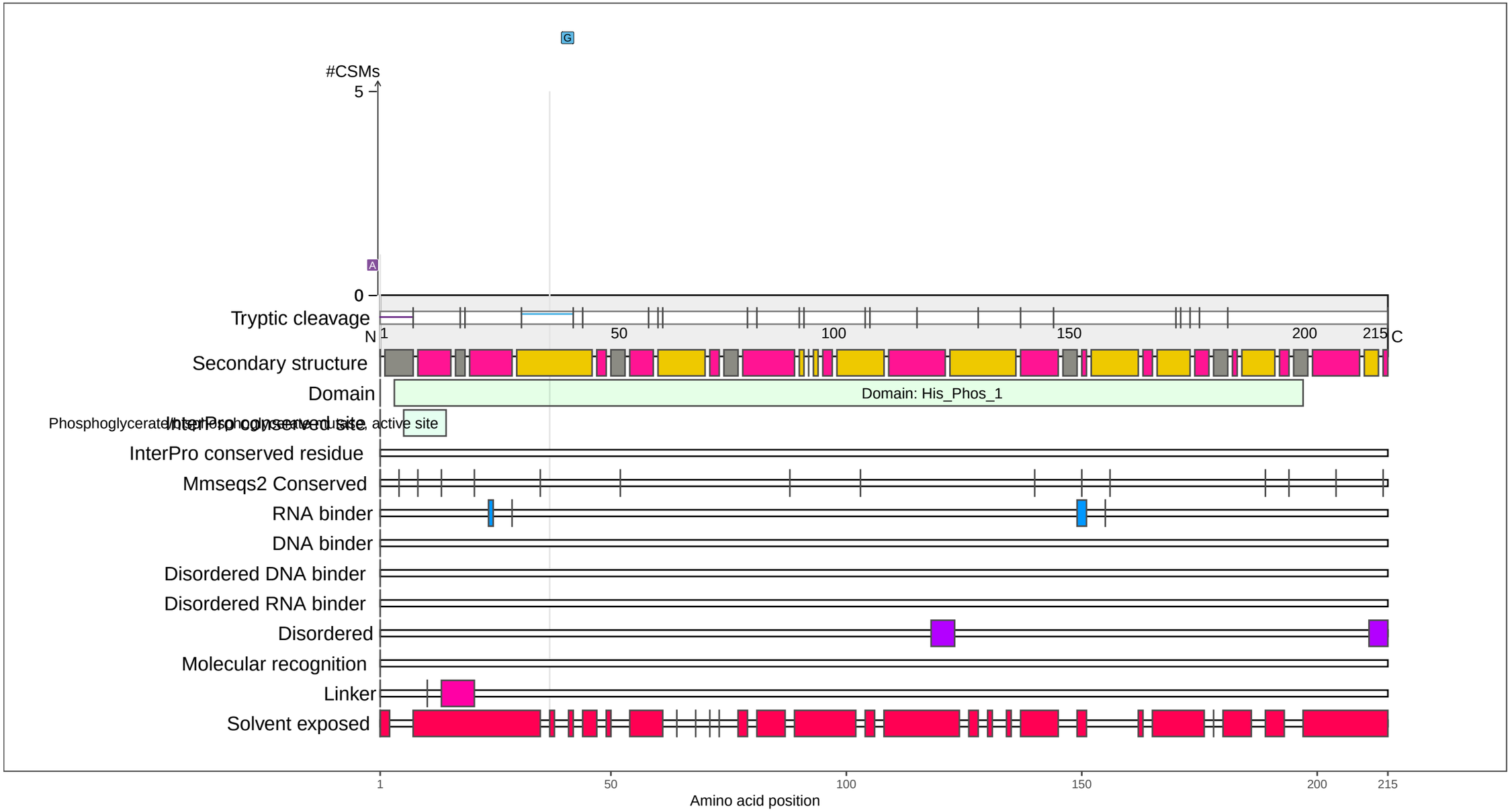
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0A7A2
GPMB_ECOLI Probable phosphoglycerate mutase GpmB

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 49)
PAXdb K12 strain [ppm]: 2.63 (Q 81)
PAXdb E.coli [ppm]: 1.92 (Q 70)

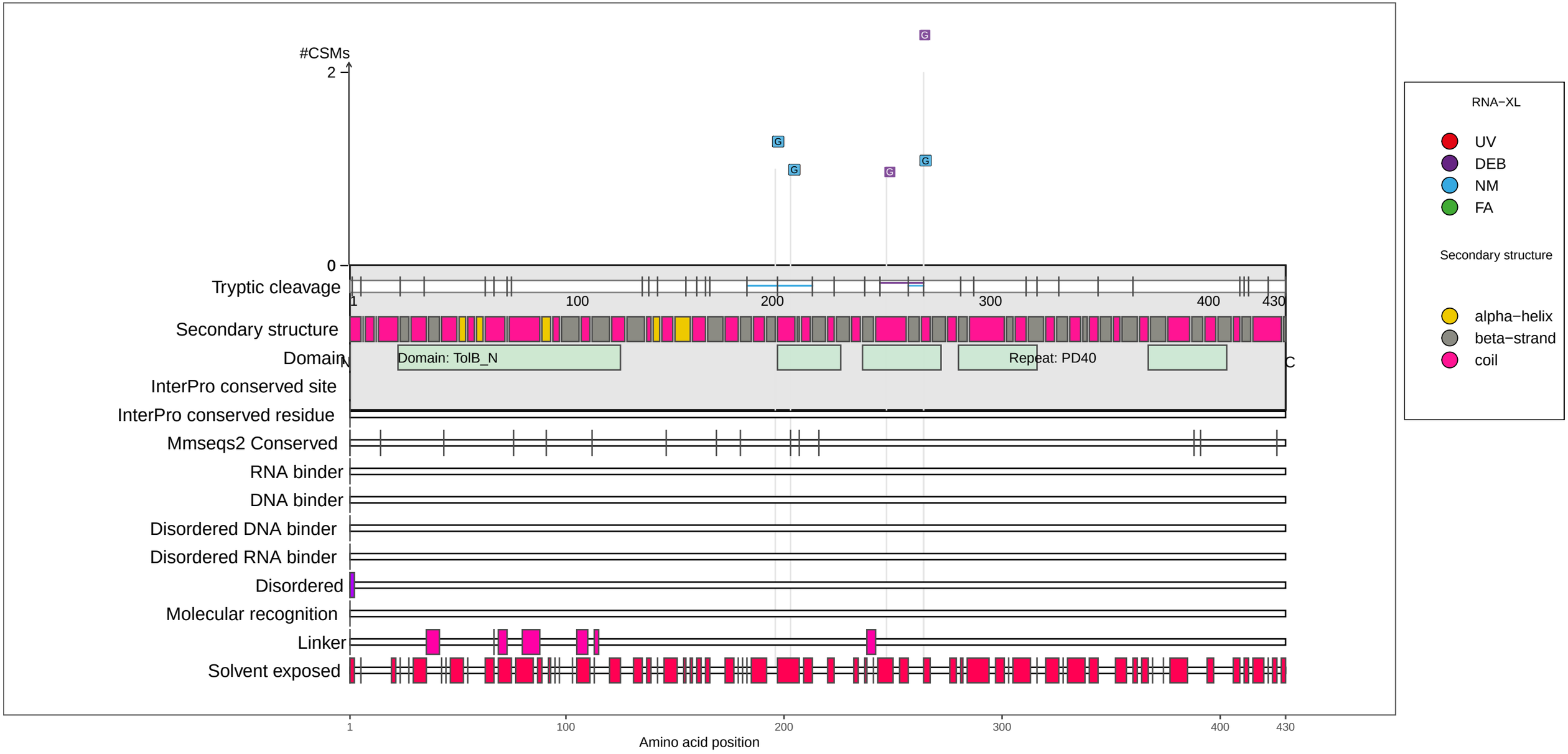
− RNA functions: not annotated



P0A855
TOLB_ECOLI Tol−Pal system protein TolB

− Abundance:
tryptic [log10 Intensity]: 8.72 (Q 82)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.75 (Q 91)

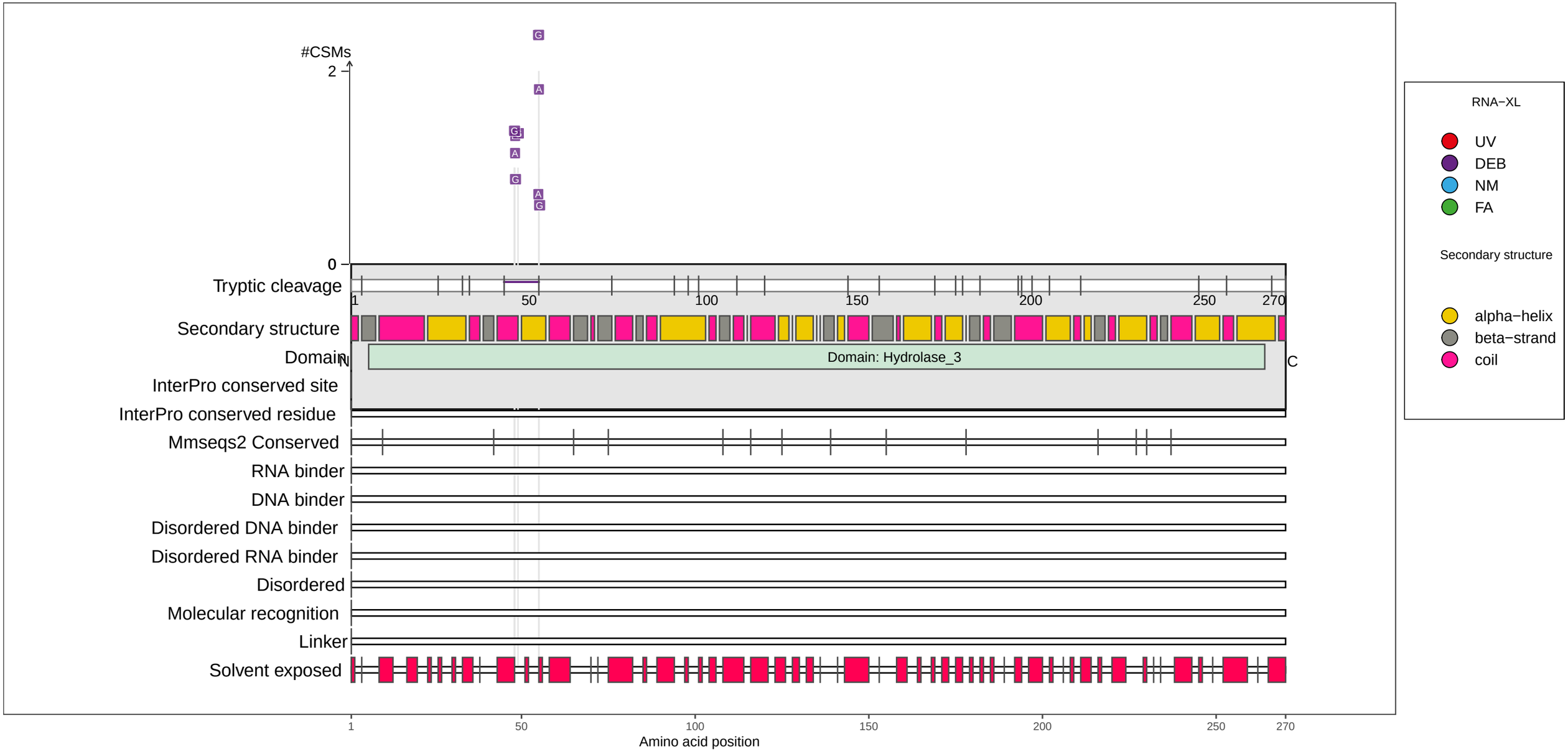
− RNA functions: not annotated



P0A8Y5
YIDA_ECOLI Sugar phosphatase YidA

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 3.15 (Q 93)
PAXdb E.coli [ppm]: 1.7 (Q 64)

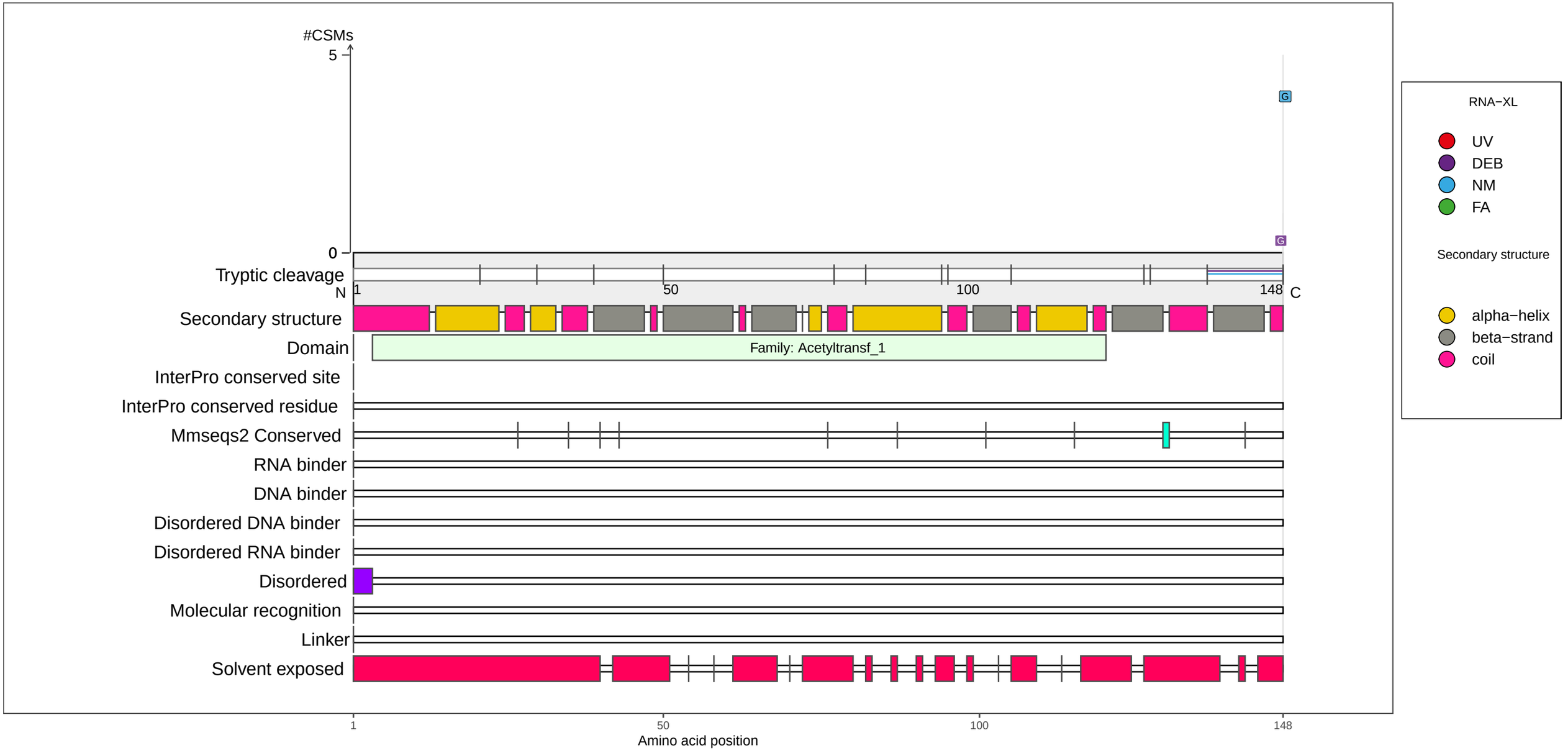
− RNA functions: not annotated



P0A944
RIMI_ECOLI [Ribosomal protein S18]−alanine N−acetyltransferase

− Abundance:
tryptic [log10 Intensity]: 6.67 (Q 5)
PAXdb K12 strain [ppm]: 1.21 (Q 21)
PAXdb E.coli [ppm]: 0.66 (Q 40)

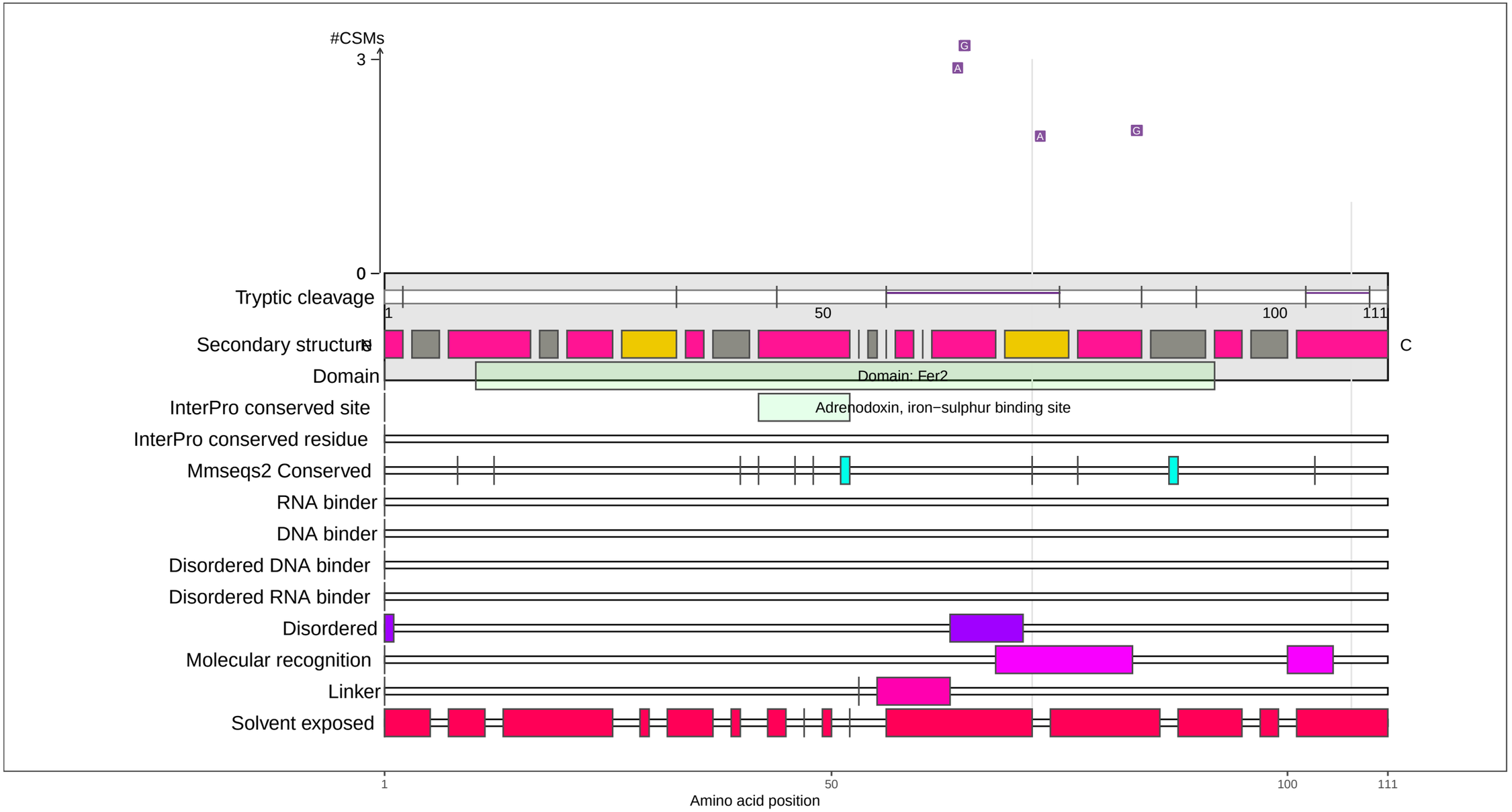
− RNA functions: not annotated



P0A9R4
FER_ECOLI 2Fe−2S ferredoxin

− Abundance:
tryptic [log10 Intensity]: 8 (Q 58)
PAXdb K12 strain [ppm]: 2.69 (Q 83)
PAXdb E.coli [ppm]: 2.59 (Q 88)

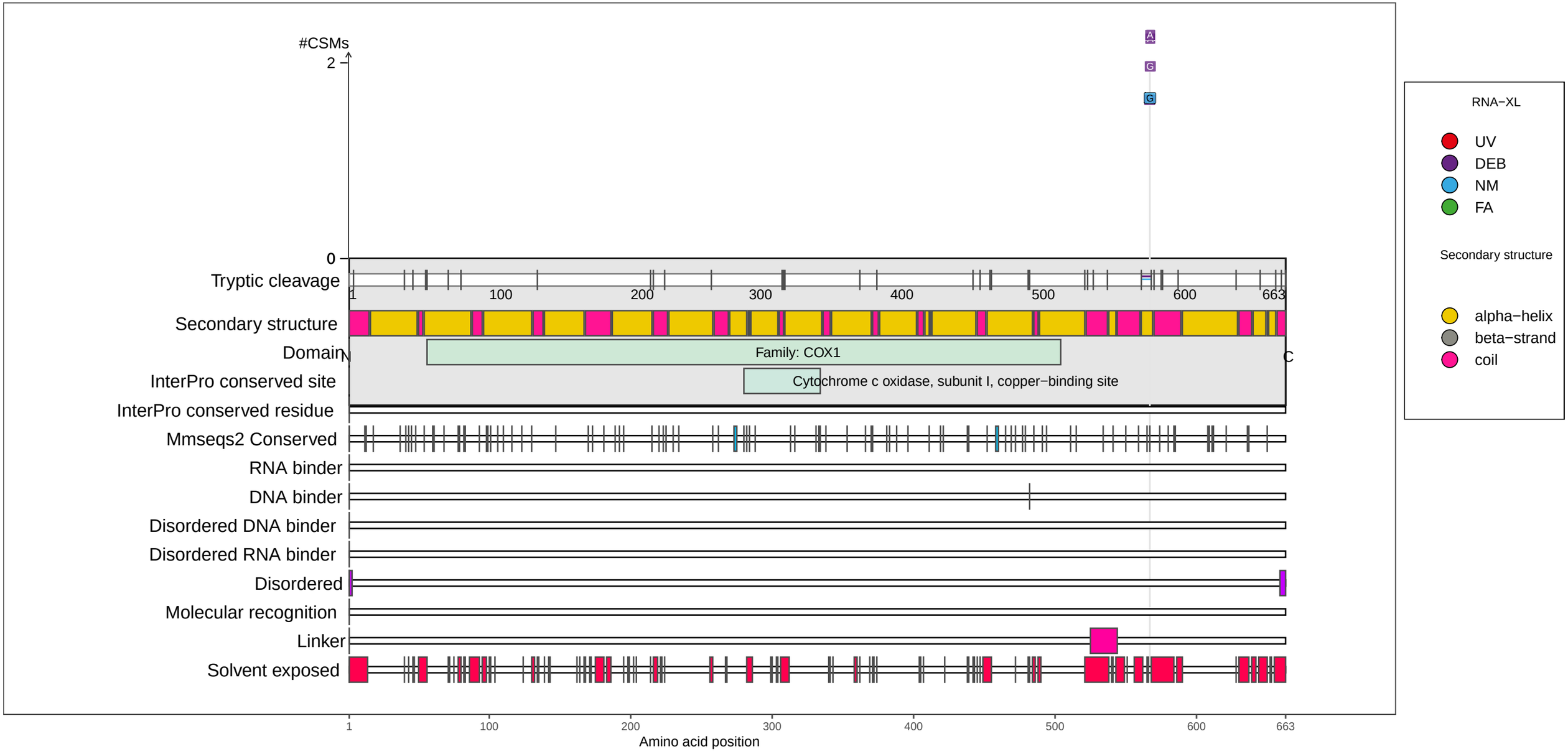
− RNA functions: not annotated



P0ABI8
CYOB_ECOLI Cytochrome bo(3) ubiquinol oxidase subunit 1

− Abundance:
tryptic [log10 Intensity]: 9.41 (Q 95)
PAXdb K12 strain [ppm]: 1.75 (Q 51)
PAXdb E.coli [ppm]: 1.8 (Q 67)

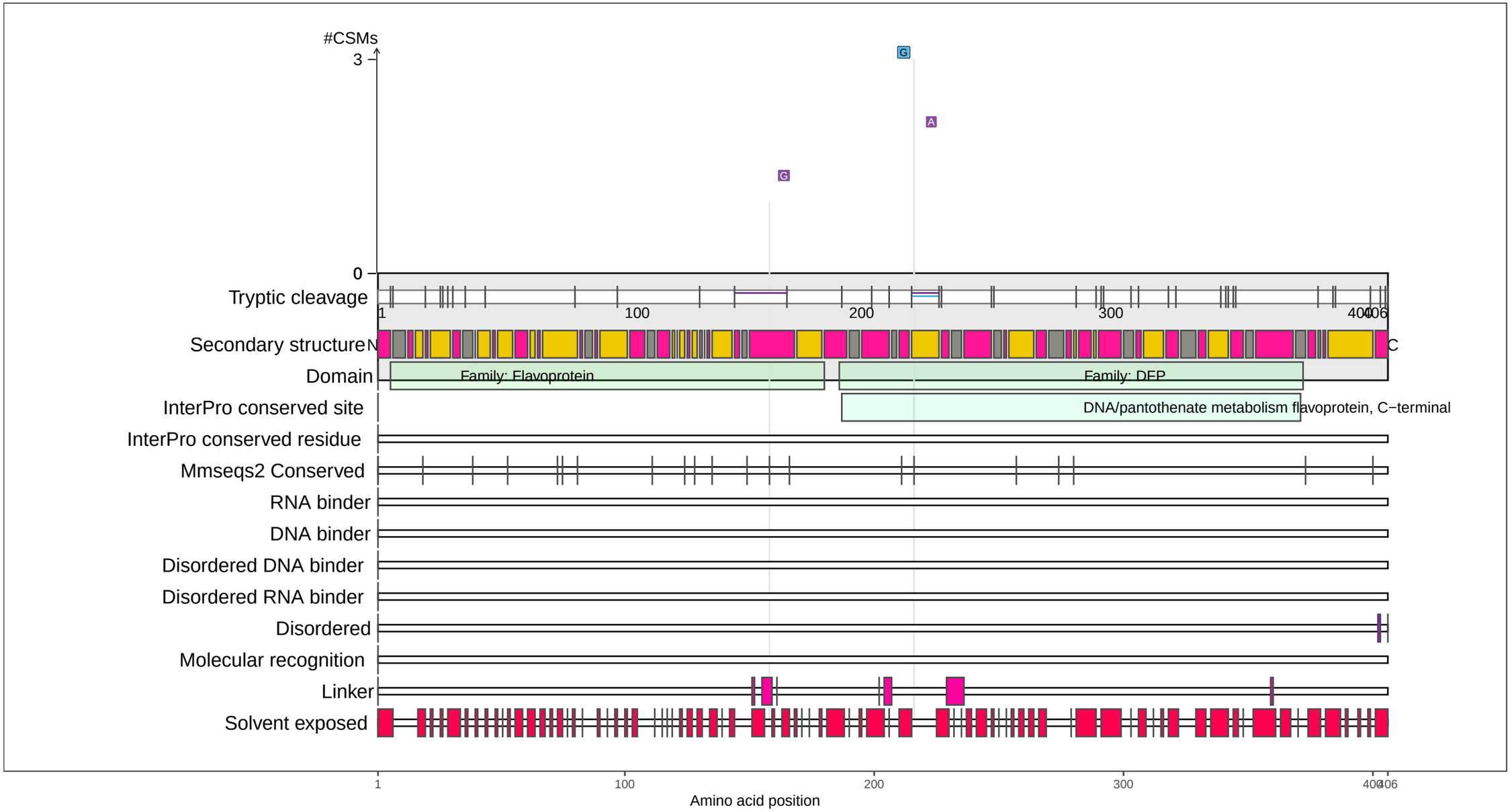
− RNA functions: not annotated

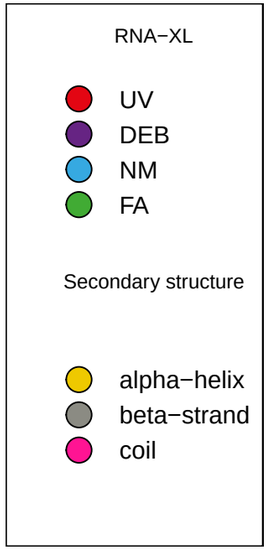


P0ABQ0
COABC_ECOLI Coenzyme A biosynthesis bifunctional protein CoaBC

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: 1.78 (Q 53)
PAXdb E.coli [ppm]: 2.15 (Q 76)

− RNA functions: not annotated

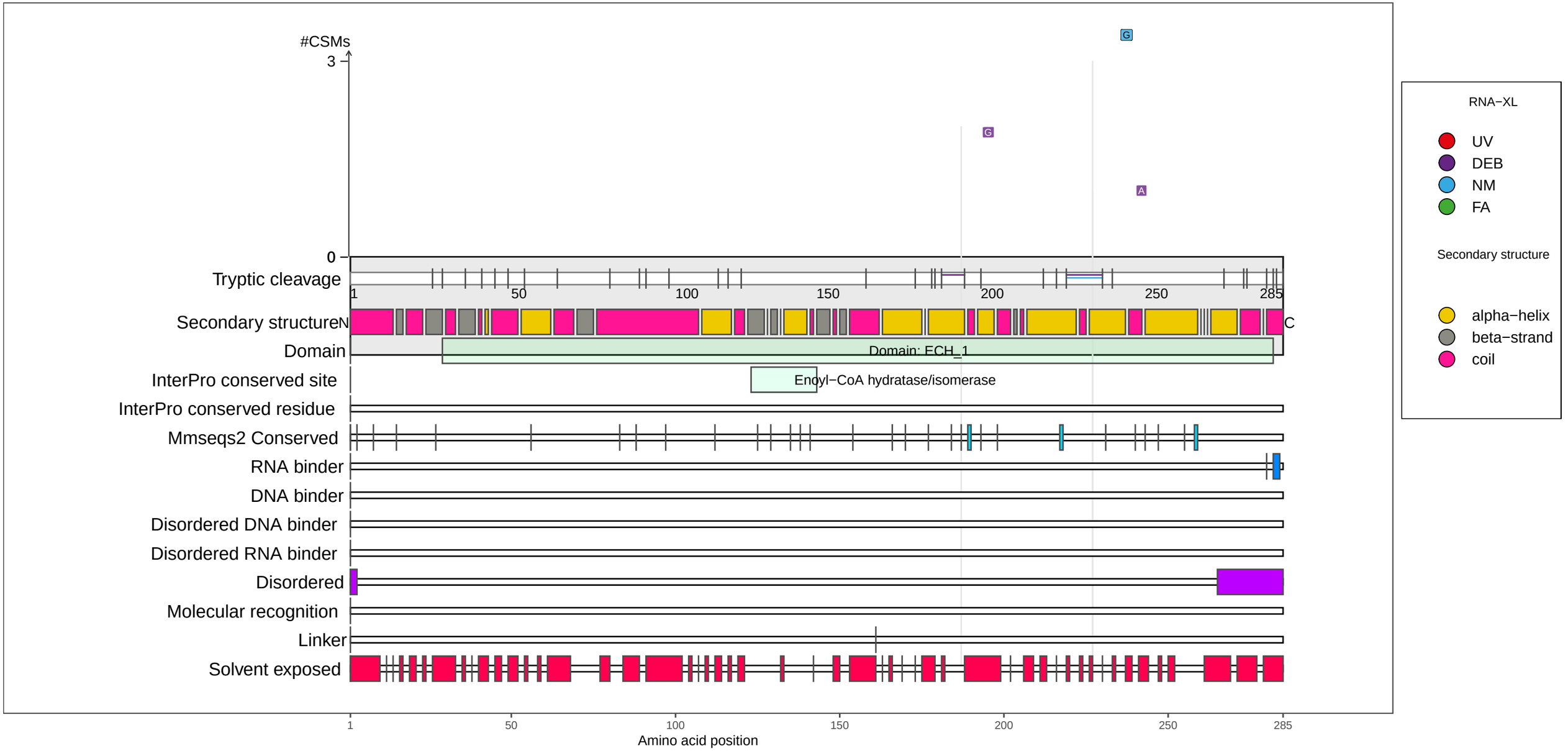




P0ABU0
MENB_ECOLI 1,4−dihydroxy−2−naphthoyl−CoA synthase

− Abundance:
tryptic [log10 Intensity]: 8.22 (Q 66)
PAXdb K12 strain [ppm]: 2.74 (Q 84)
PAXdb E.coli [ppm]: 2.45 (Q 84)

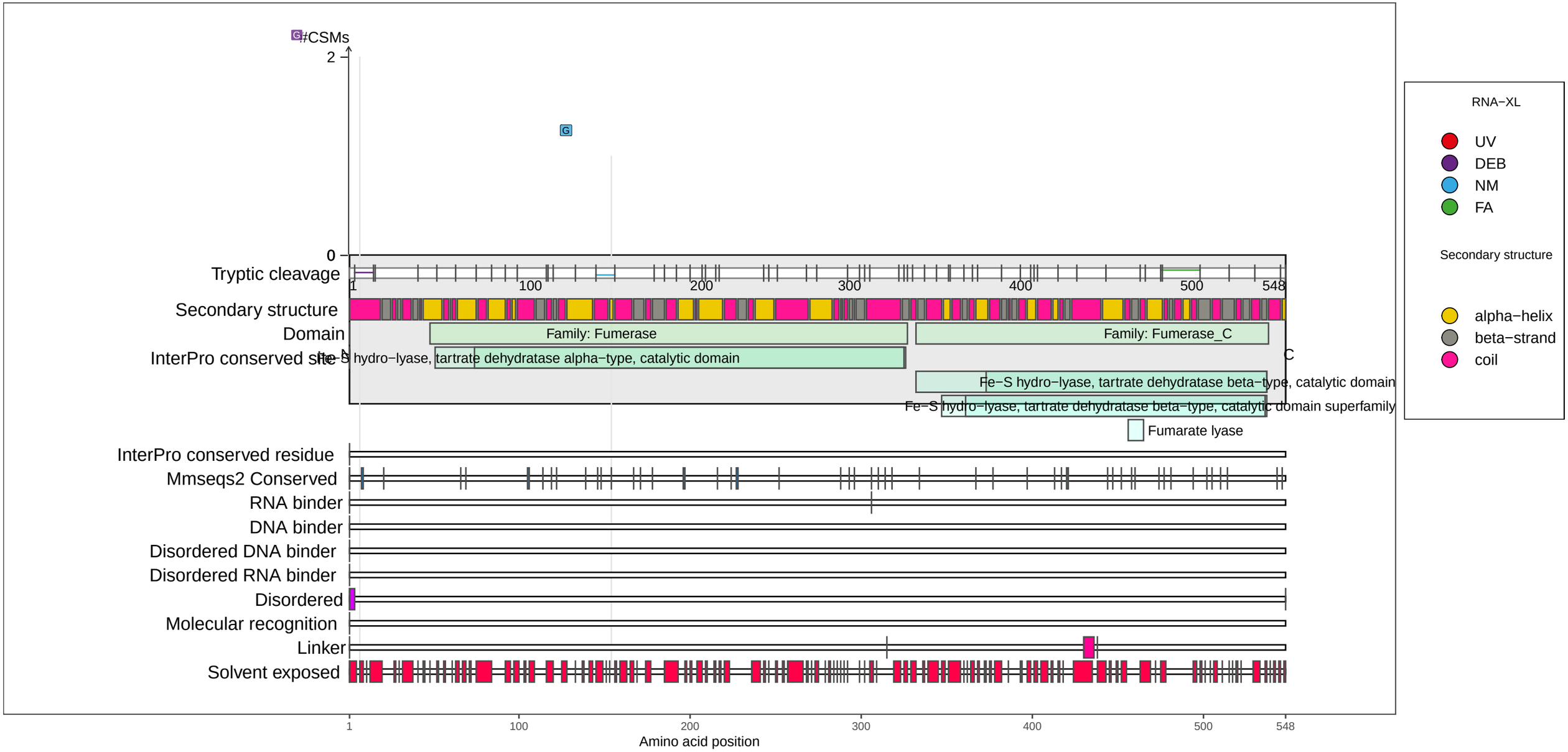
− RNA functions: not annotated



P0AC33
FUMA_ECOLI Fumarate hydratase class I, aerobic

− Abundance:
tryptic [log10 Intensity]: 8.54 (Q 77)
PAXdb K12 strain [ppm]: 2.58 (Q 80)
PAXdb E.coli [ppm]: 2.53 (Q 86)

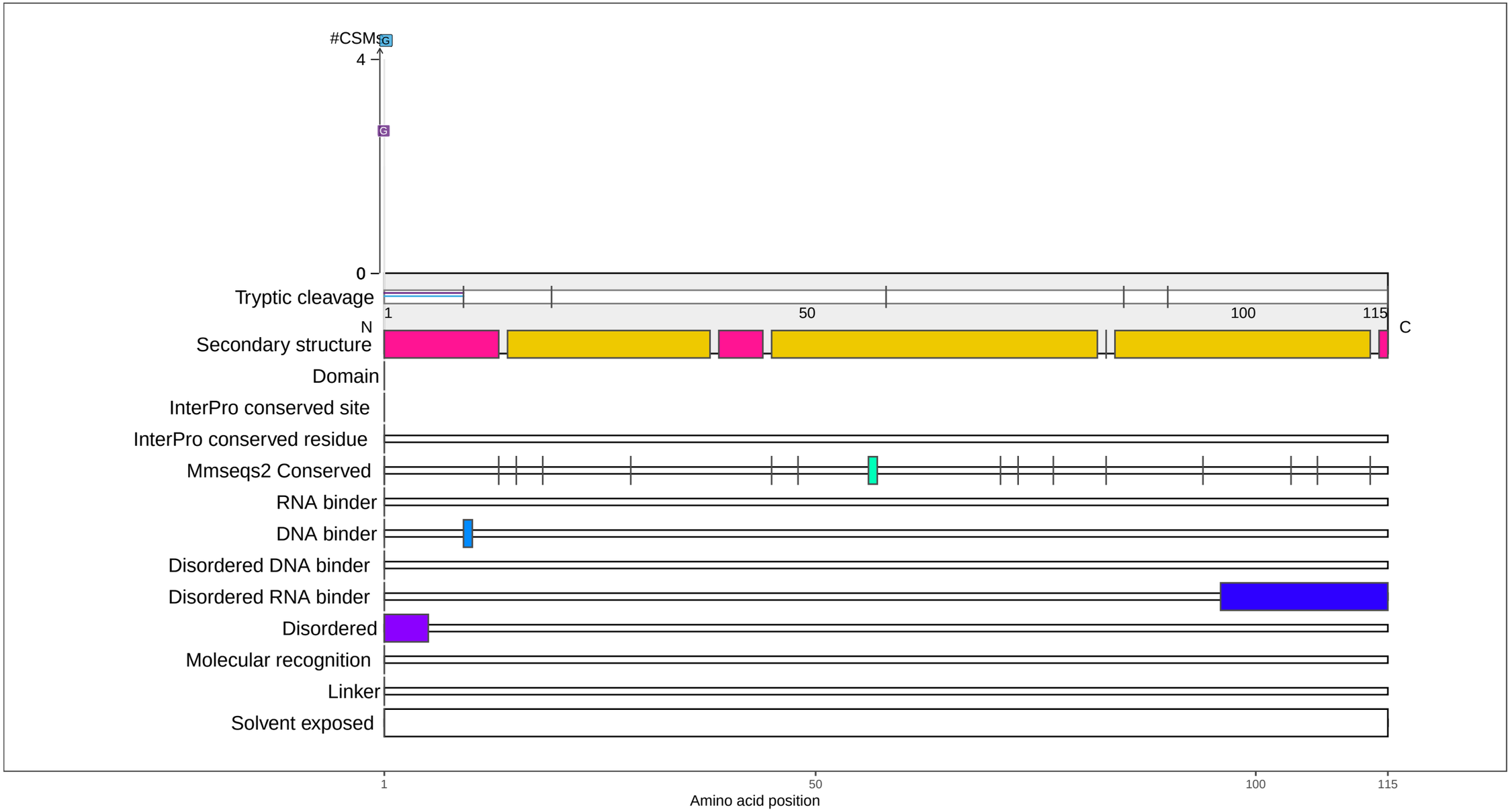
− RNA functions: not annotated

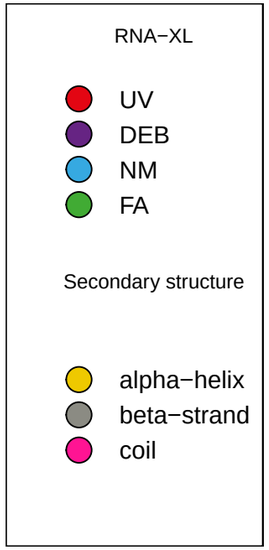


P0AC44
DHSD_ECOLI Succinate dehydrogenase hydrophobic membrane anchor subunit

− Abundance:
tryptic [log10 Intensity]: 8.34 (Q 71)
PAXdb K12 strain [ppm]: 2.14 (Q 65)
PAXdb E.coli [ppm]: 2.45 (Q 84)

− RNA functions: not annotated

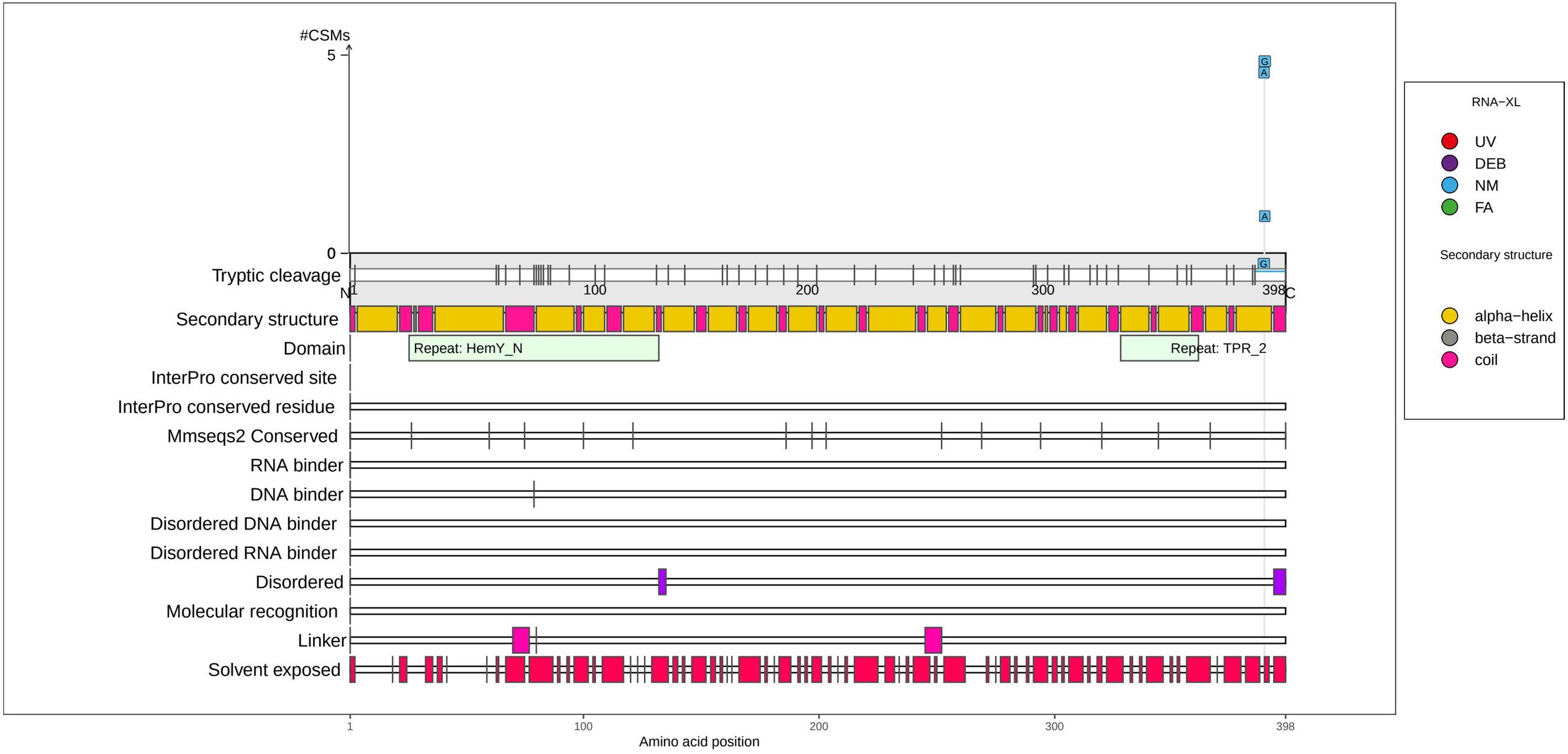




P0ACB7
HEMY_ECOLI Protein HemY

− Abundance:
tryptic [log10 Intensity]: 7.2 (Q 21)
PAXdb K12 strain [ppm]: 1.44 (Q 35)
PAXdb E.coli [ppm]: 1.95 (Q 71)

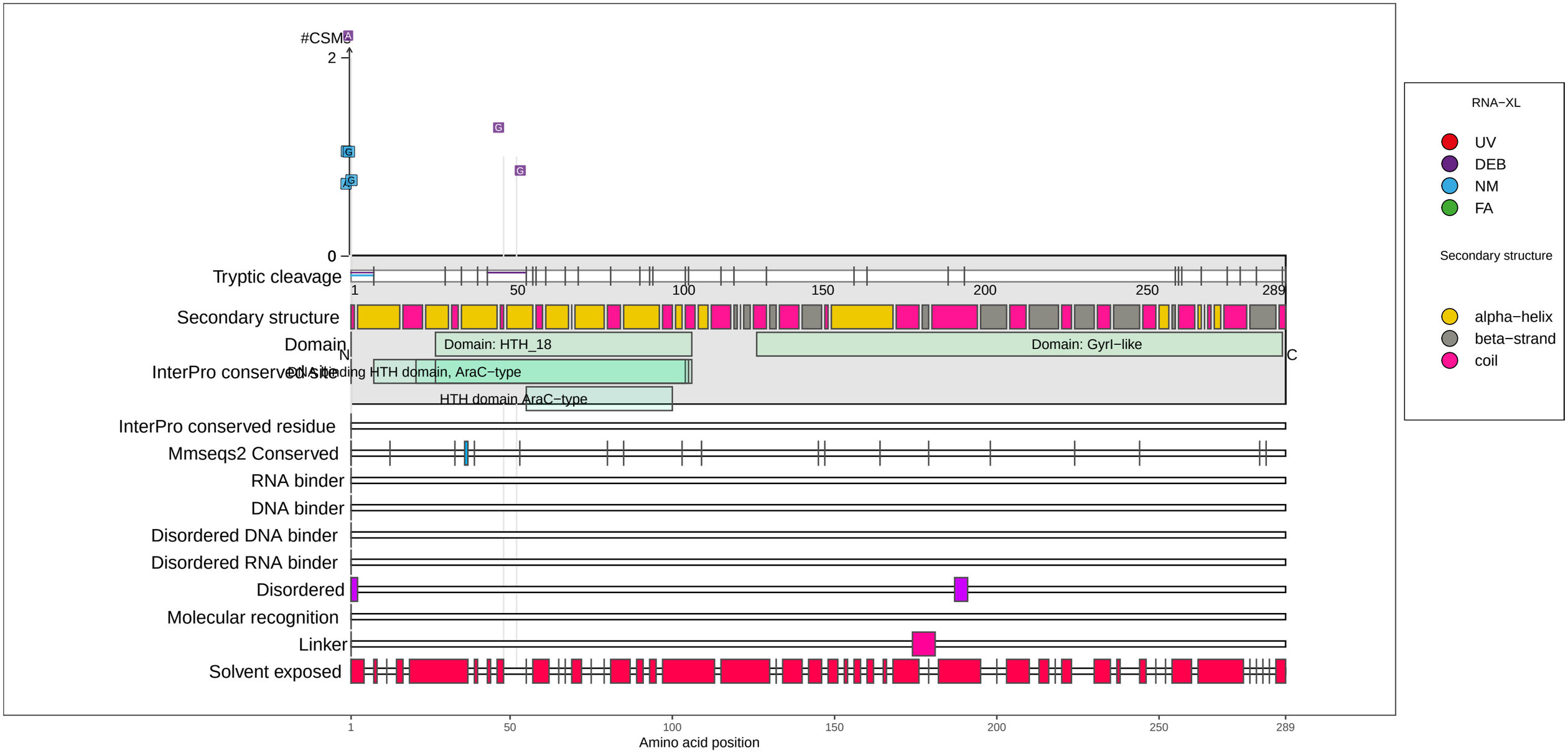
− RNA functions: not annotated



P0ACI0
ROB_ECOLI Right origin−binding protein

− Abundance:
tryptic [log10 Intensity]: 8 (Q 58)
PAXdb K12 strain [ppm]: 2.24 (Q 68)
PAXdb E.coli [ppm]: 2.17 (Q 77)

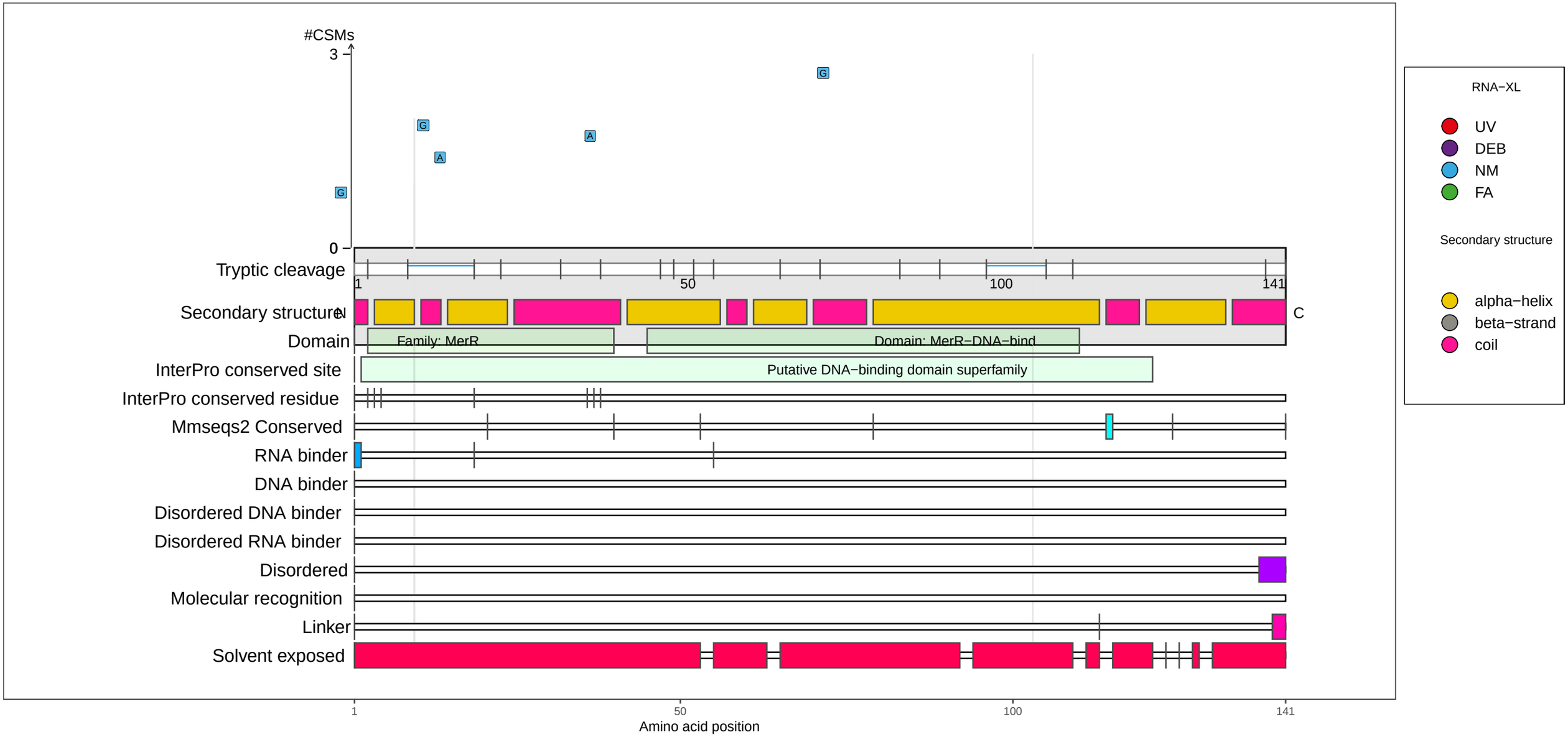
− RNA functions: not annotated



P0ACS5
ZNTR_ECOLI HTH−type transcriptional regulator ZntR

− Abundance:
tryptic [log10 Intensity]: 7.5 (Q 35)
PAXdb K12 strain [ppm]: 1.96 (Q 59)
PAXdb E.coli [ppm]: 0.92 (Q 46)

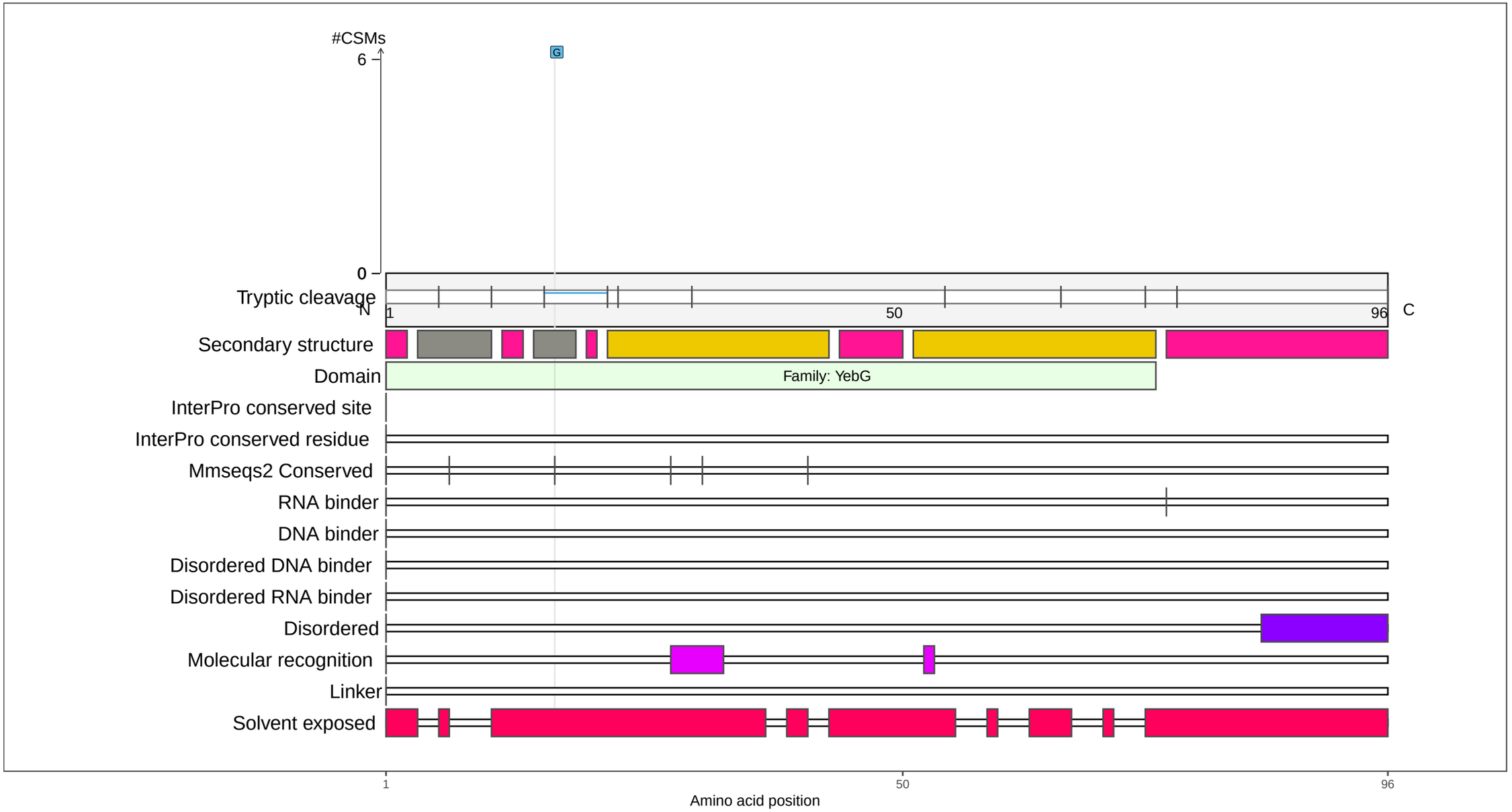
− RNA functions:
RNA biosynthetic process; RNA metabolic process

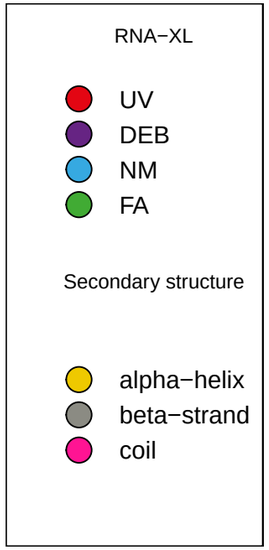


P0ACY9
YEBG_ECOLI Uncharacterized protein YebG

− Abundance:
tryptic [log10 Intensity]: 7.74 (Q 46)
PAXdb K12 strain [ppm]: 2.41 (Q 75)
PAXdb E.coli [ppm]: 2.28 (Q 80)

− RNA functions: not annotated

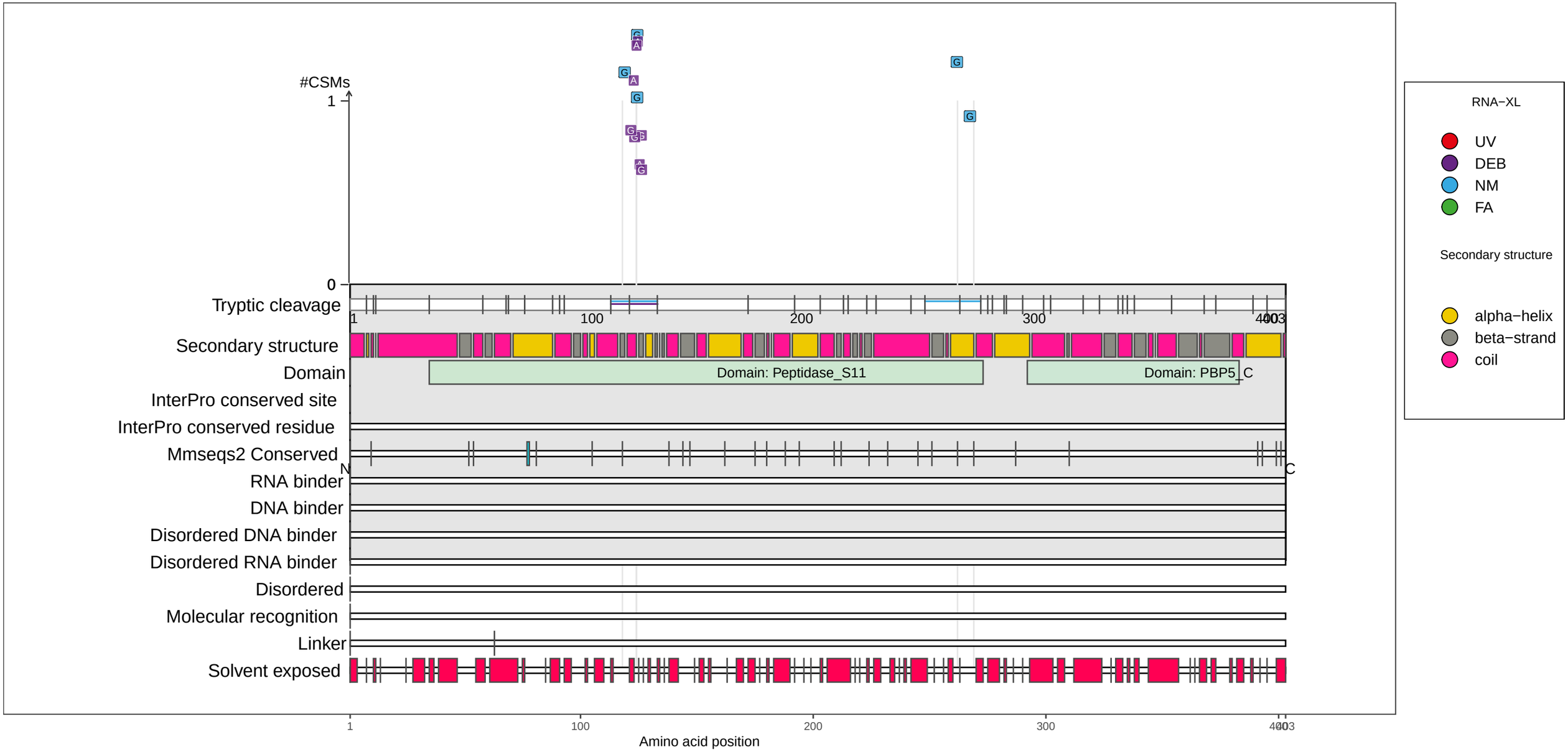




P0AEB2
DACA_ECOLI D−alanyl−D−alanine carboxypeptidase DacA

− Abundance:
tryptic [log10 Intensity]: 8.93 (Q 86)
PAXdb K12 strain [ppm]: 2.3 (Q 70)
PAXdb E.coli [ppm]: 2.36 (Q 82)

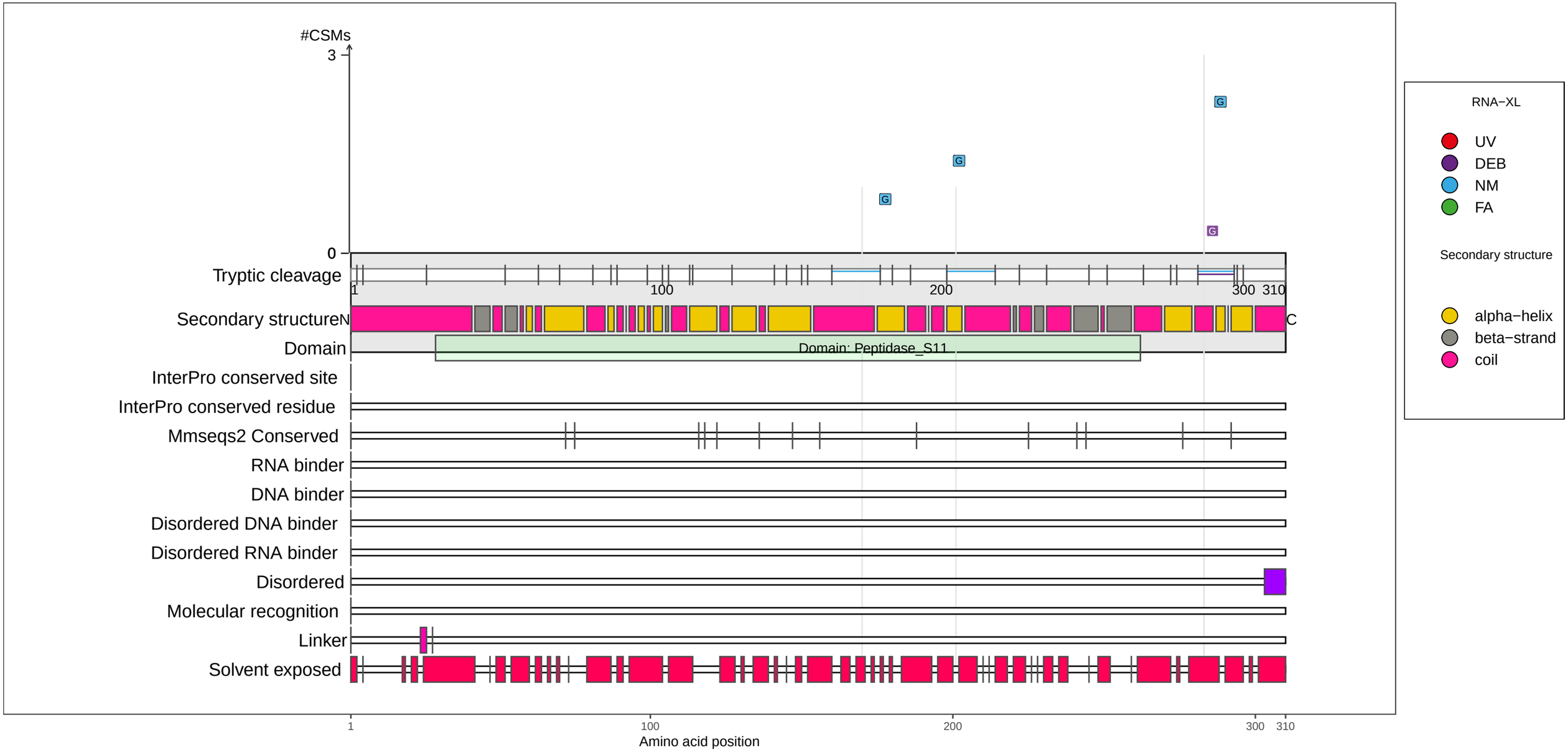
− RNA functions: not annotated



P0AFI5
PBP7_ECOLI D−alanyl−D−alanine endopeptidase

− Abundance:
tryptic [log10 Intensity]: 6.94 (Q 11)
PAXdb K12 strain [ppm]: 1.73 (Q 50)
PAXdb E.coli [ppm]: 0.76 (Q 42)

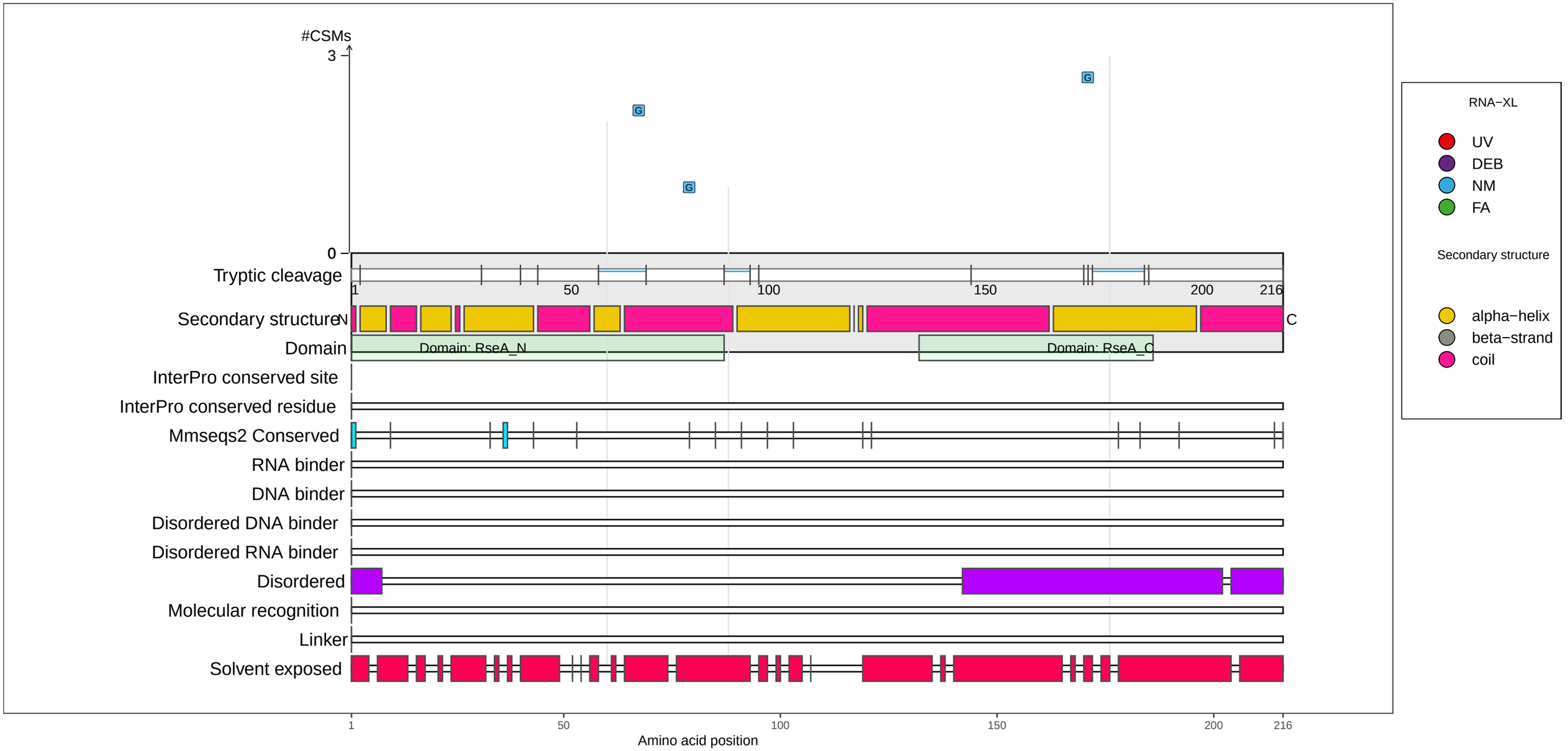
− RNA functions: not annotated



P0AFX7
RSEA_ECOLI Anti−sigma−E factor RseA

− Abundance:
tryptic [log10 Intensity]: 7.45 (Q 32)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.98 (Q 47)

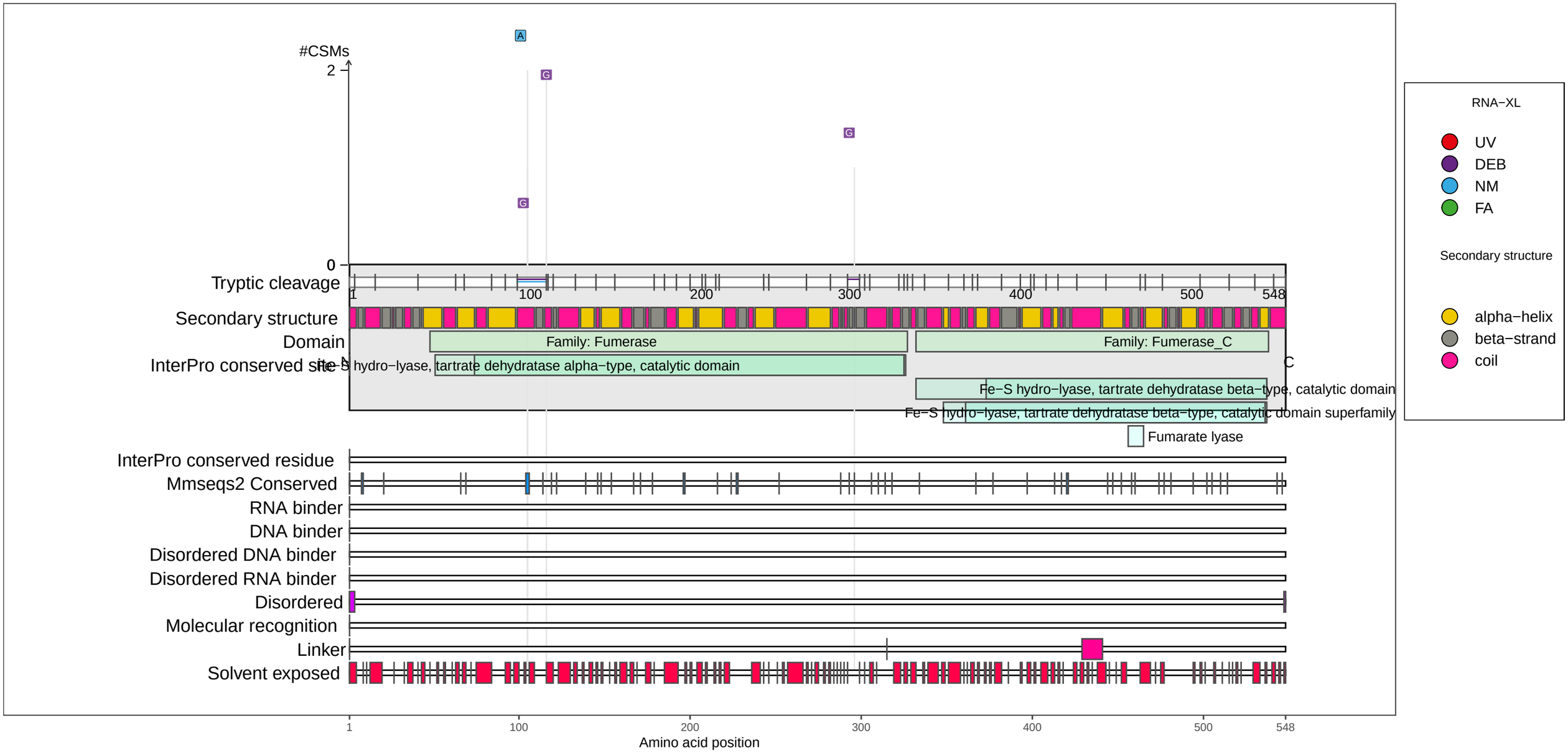
− RNA functions: not annotated



P14407
FUMB_ECOLI Fumarate hydratase class I, anaerobic

− Abundance:
tryptic [log10 Intensity]: 7.16 (Q 19)
PAXdb K12 strain [ppm]: 2.15 (Q 65)
PAXdb E.coli [ppm]: 1.72 (Q 65)

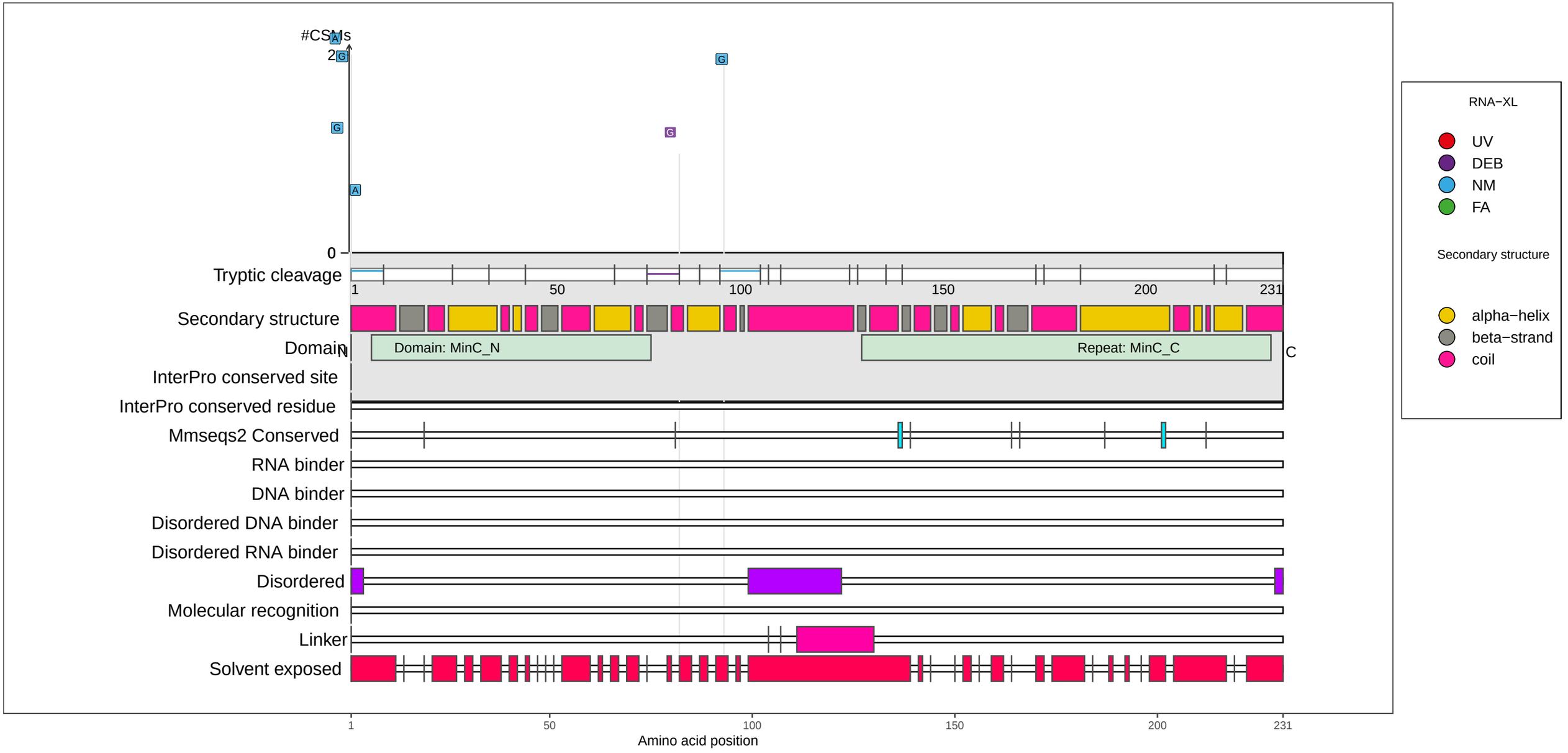
− RNA functions: not annotated



P18196
MINC_ECOLI Septum site−determining protein MinC

− Abundance:
tryptic [log10 Intensity]: 7.43 (Q 32)
PAXdb K12 strain [ppm]: 2.68 (Q 83)
PAXdb E.coli [ppm]: 1.55 (Q 61)

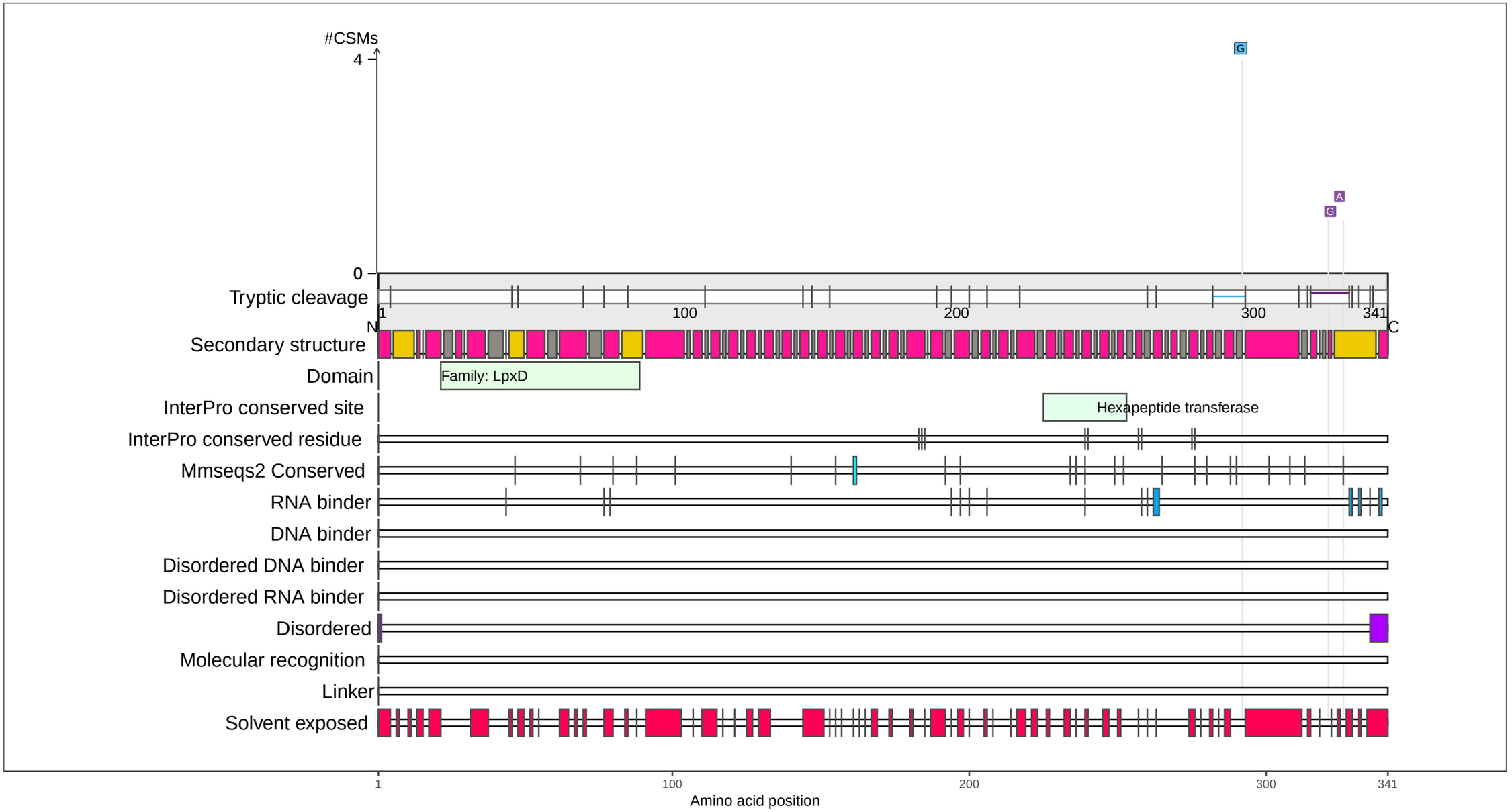
− RNA functions: not annotated



P21645
LPXD_ECOLI UDP−3−O−(3−hydroxymyristoyl)glucosamine N−acyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.31 (Q 25)
PAXdb K12 strain [ppm]: 2.09 (Q 63)
PAXdb E.coli [ppm]: 2.54 (Q 86)

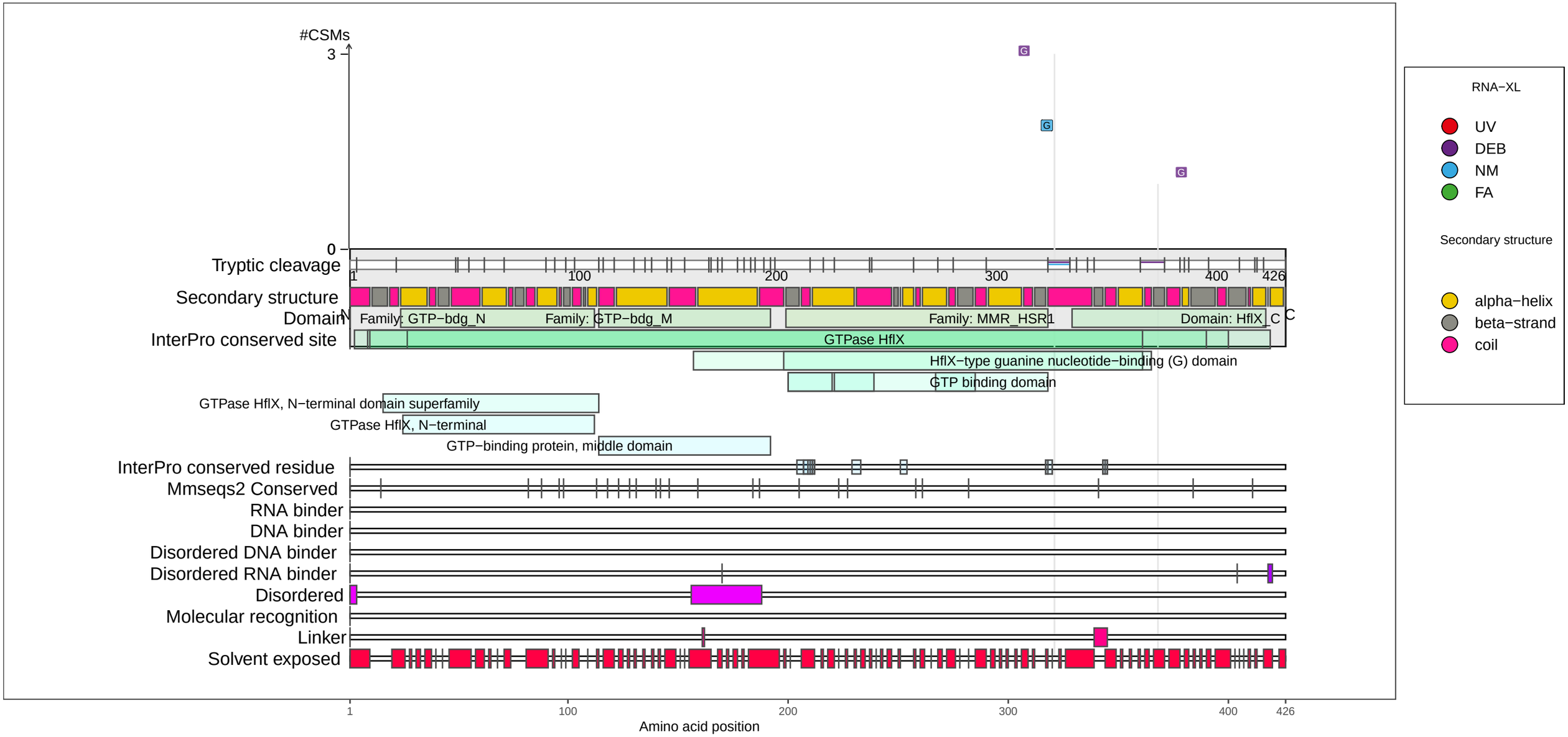
− RNA functions: not annotated



P25519
HFLX_ECOLI GTPase HflX

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 54)
PAXdb K12 strain [ppm]: 2.33 (Q 71)
PAXdb E.coli [ppm]: 1.9 (Q 69)

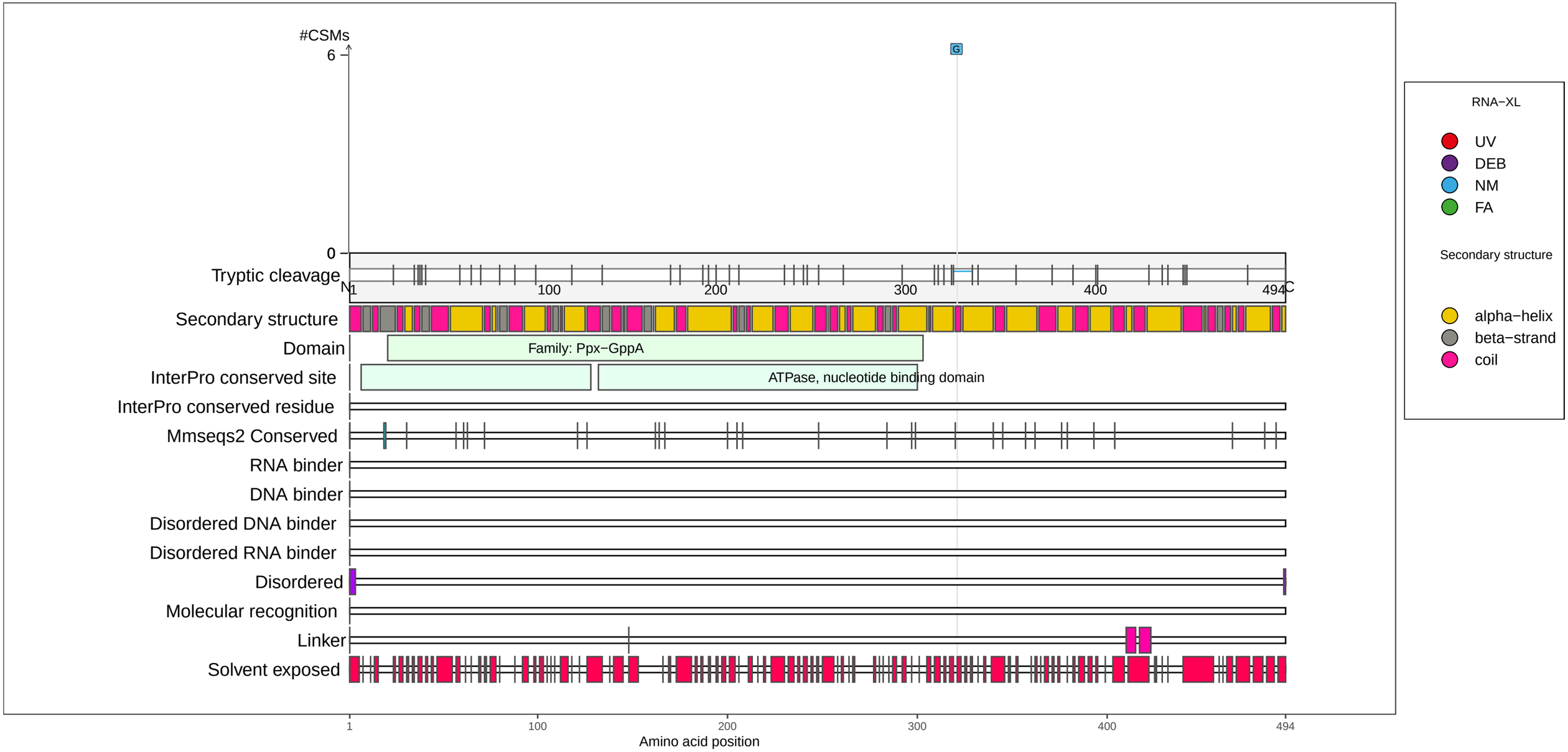
− RNA functions:
RNA binding; rRNA binding



P25552
GPPA_ECOLI Guanosine−5'−triphosphate,3'−diphosphate pyrophosphatase

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 0.78 (Q 4)
PAXdb E.coli [ppm]: 1.81 (Q 67)

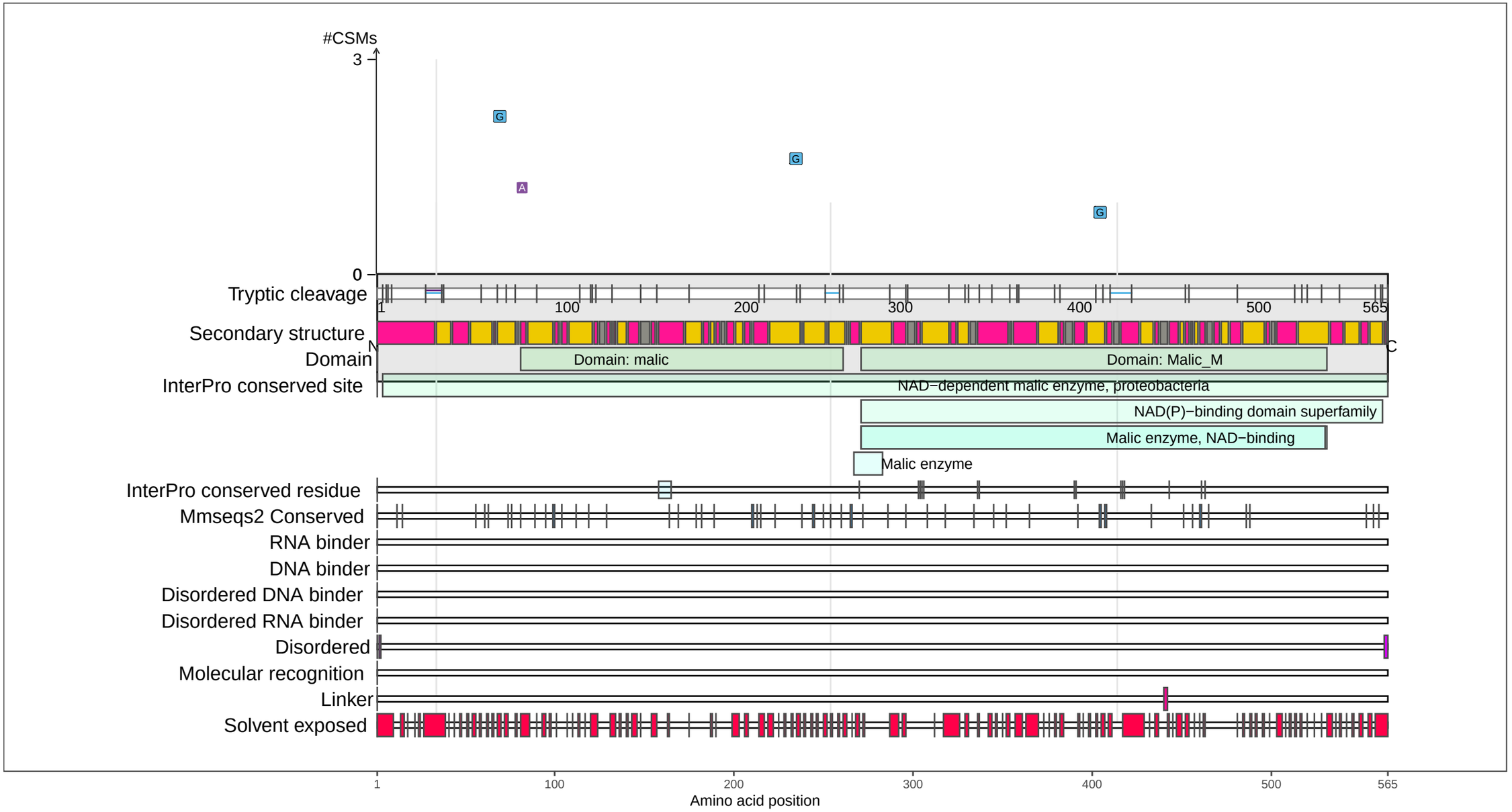
− RNA functions: not annotated

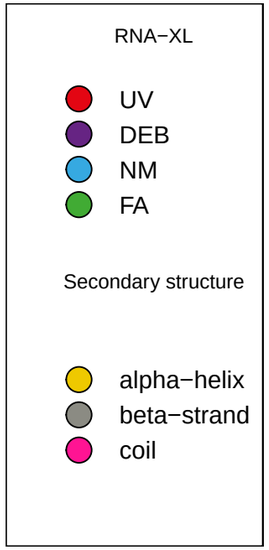


P26616
MAO1_ECOLI NAD−dependent malic enzyme

− Abundance:
tryptic [log10 Intensity]: 8.77 (Q 83)
PAXdb K12 strain [ppm]: 2.59 (Q 80)
PAXdb E.coli [ppm]: 2.47 (Q 85)

− RNA functions: not annotated

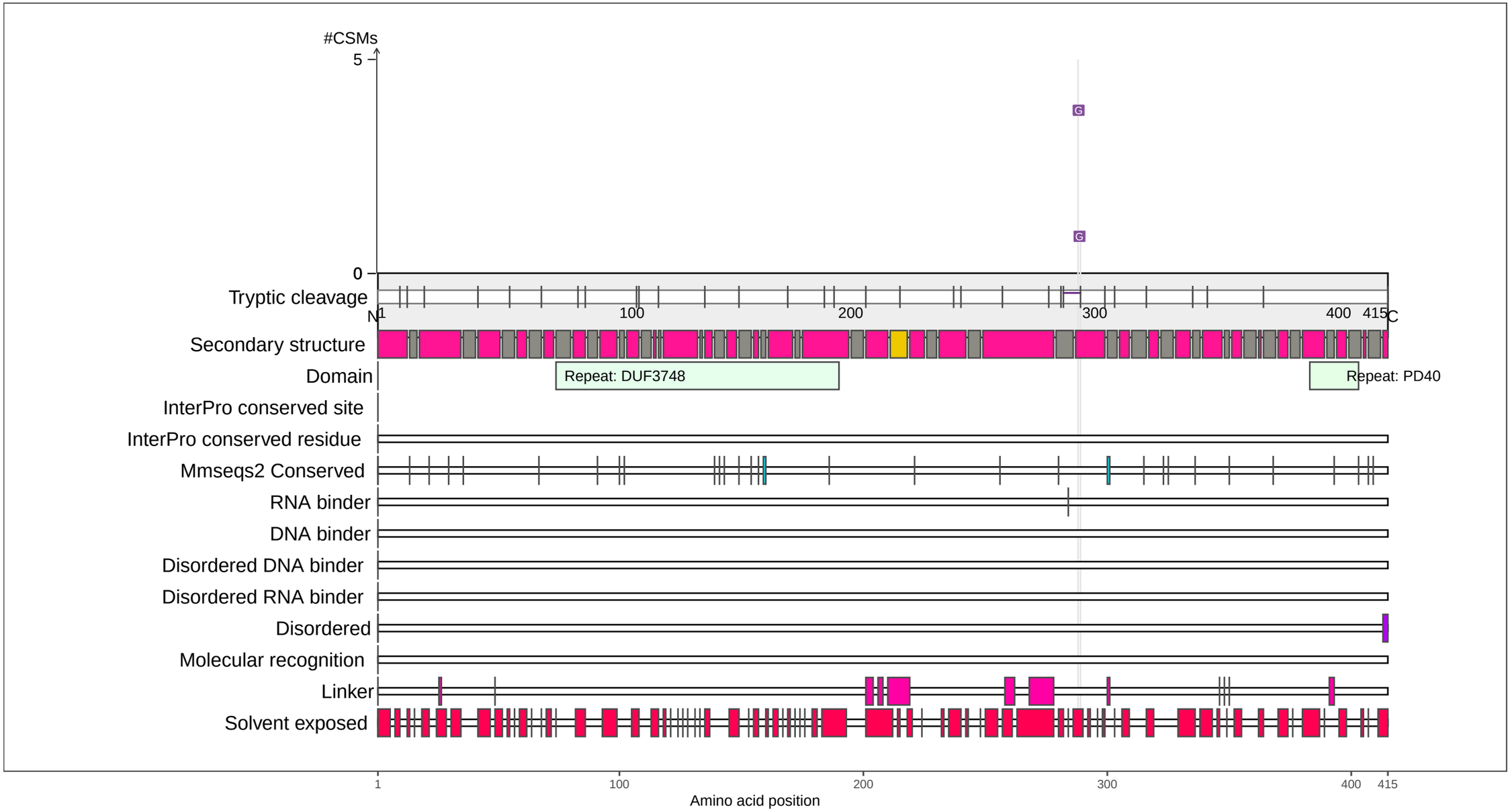


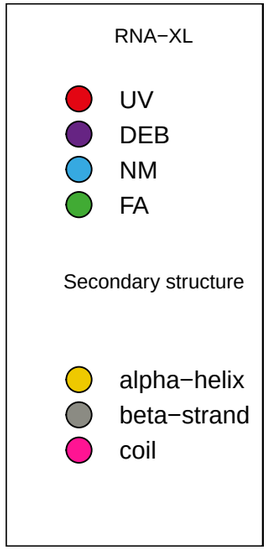


P31455
YIDR_ECOLI Uncharacterized protein YidR

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 1.49 (Q 59)

− RNA functions: not annotated

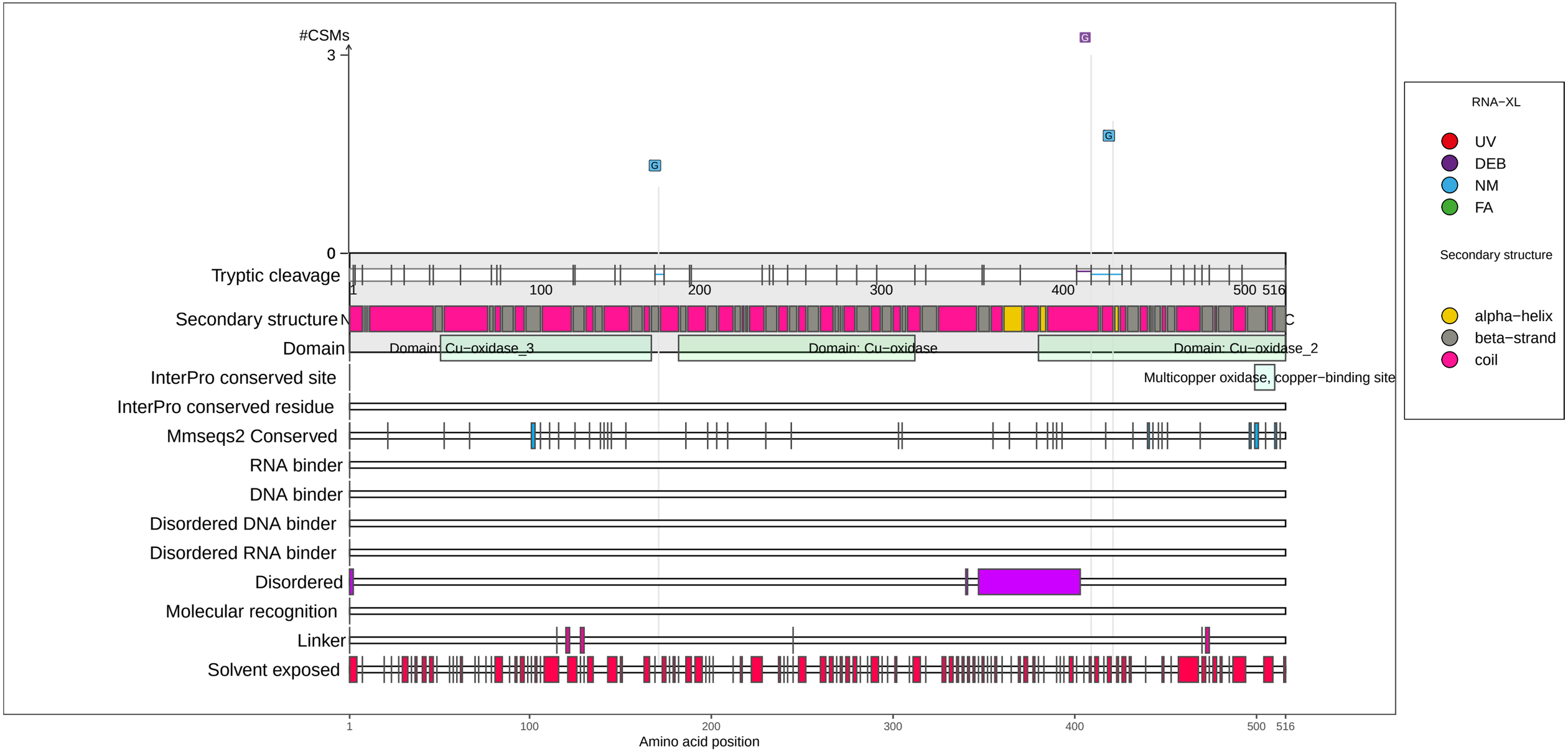




P36649
CUEO_ECOLI Blue copper oxidase CueO

− Abundance:
tryptic [log10 Intensity]: 7.93 (Q 55)
PAXdb K12 strain [ppm]: 1.01 (Q 11)
PAXdb E.coli [ppm]: 2 (Q 72)

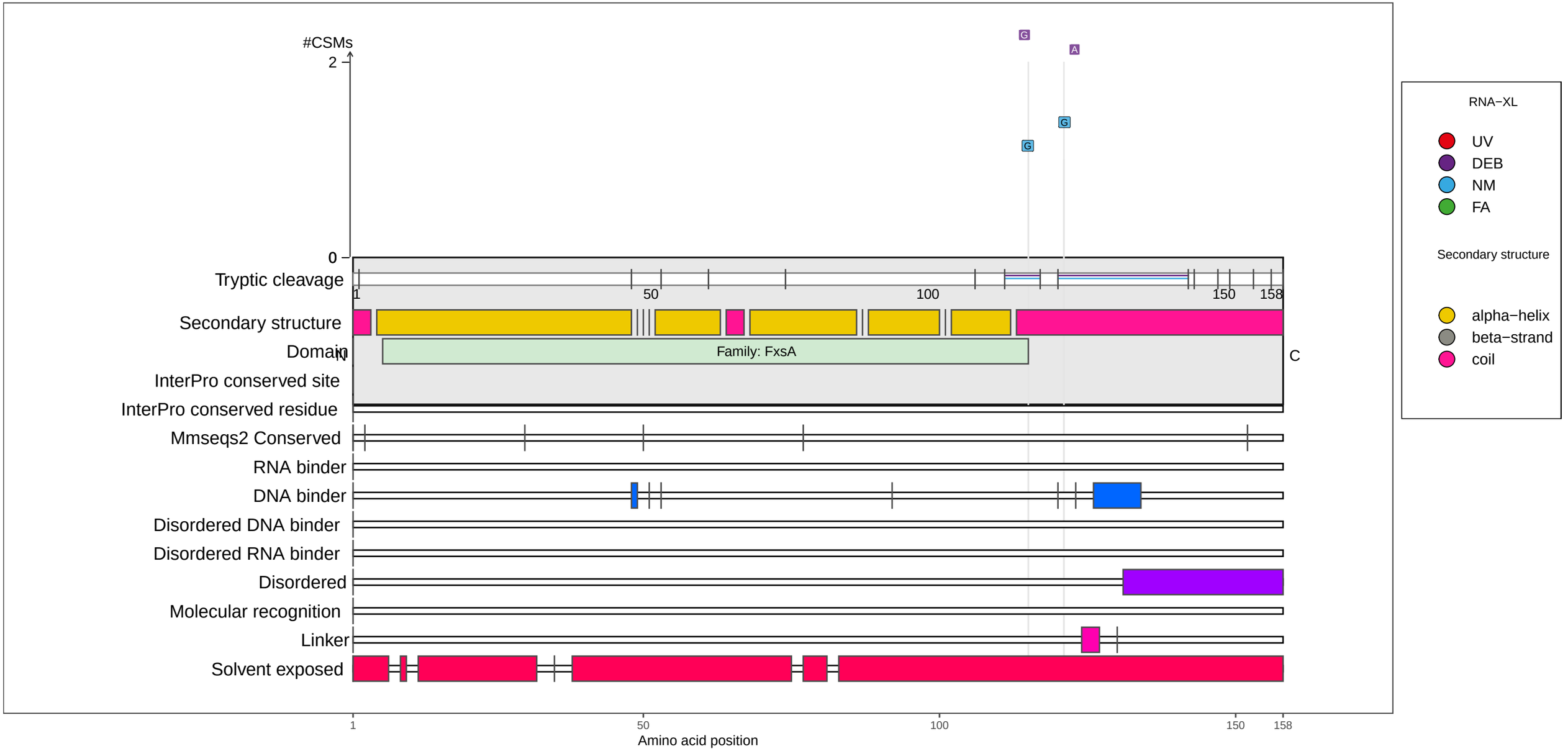
− RNA functions: not annotated



P37147
FXSA_ECOLI UPF0716 protein FxsA

− Abundance:
tryptic [log10 Intensity]: 8.02 (Q 58)
PAXdb K12 strain [ppm]: 2.05 (Q 62)
PAXdb E.coli [ppm]: 0.44 (Q 35)

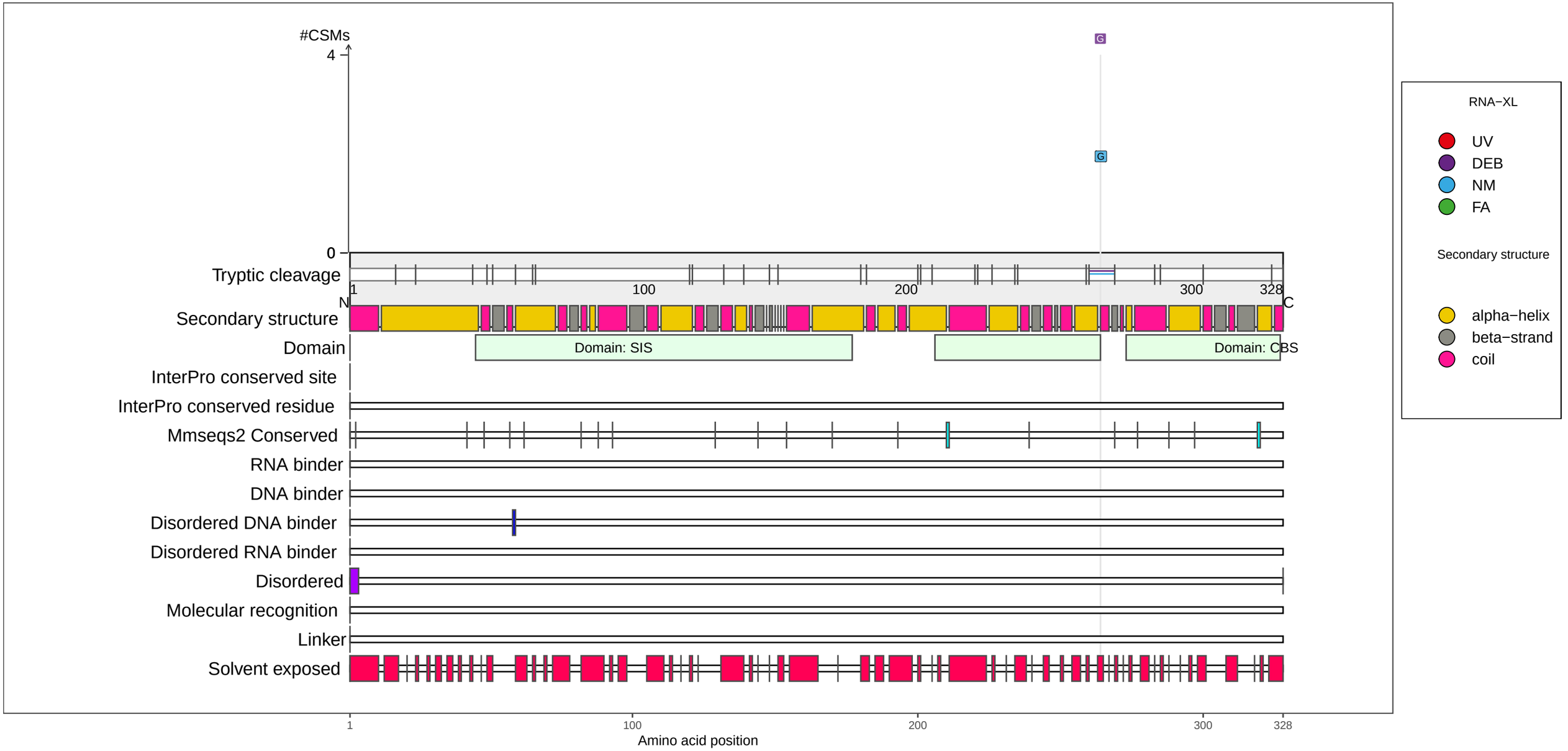
− RNA functions: not annotated



P45395
KDSD_ECOLI Arabinose 5−phosphate isomerase KdsD

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: 1.84 (Q 55)
PAXdb E.coli [ppm]: 2.1 (Q 75)

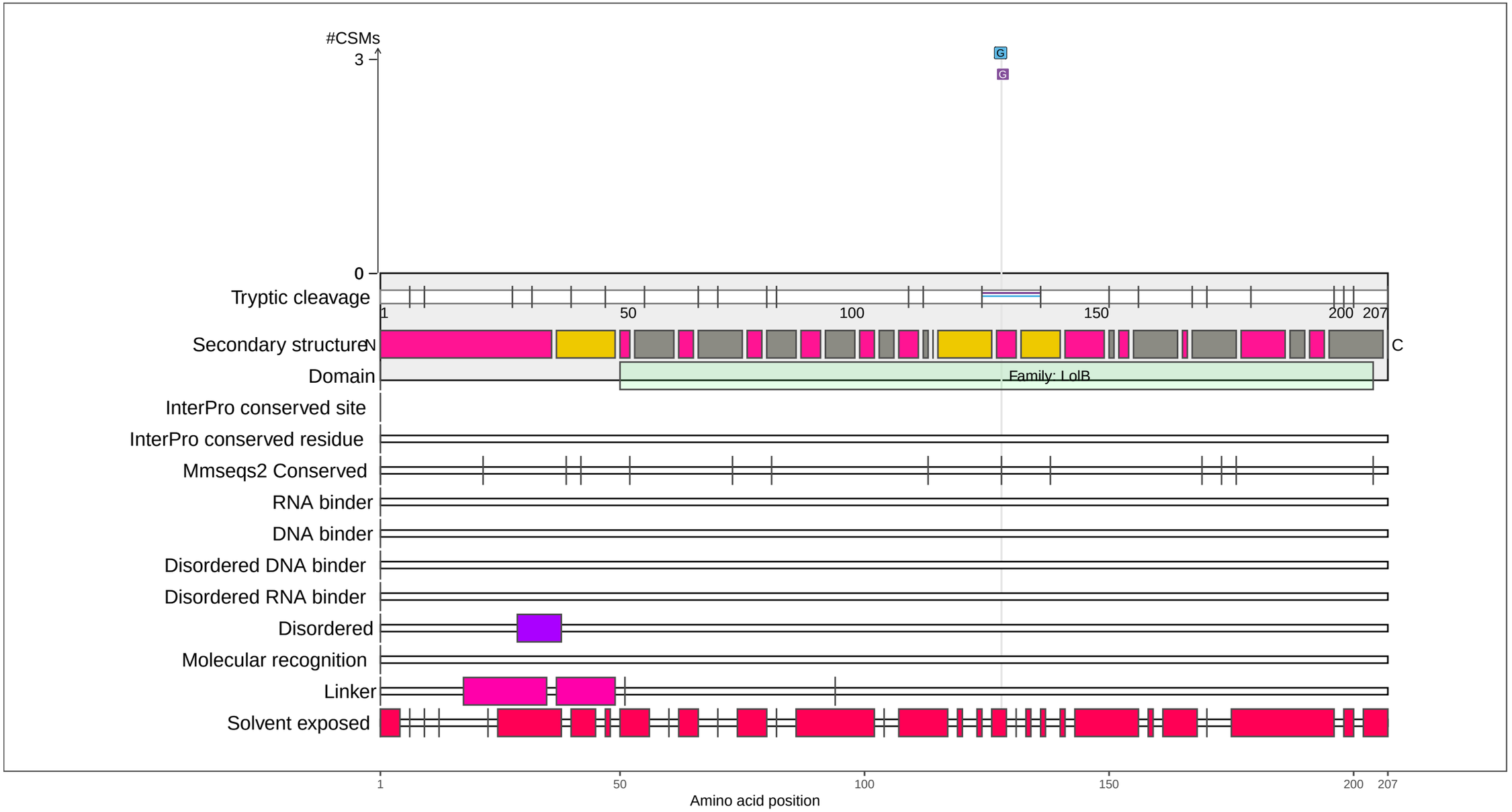
− RNA functions: not annotated



P61320
LOLB_ECOLI Outer−membrane lipoprotein LolB

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 1.41 (Q 33)
PAXdb E.coli [ppm]: 1.89 (Q 69)

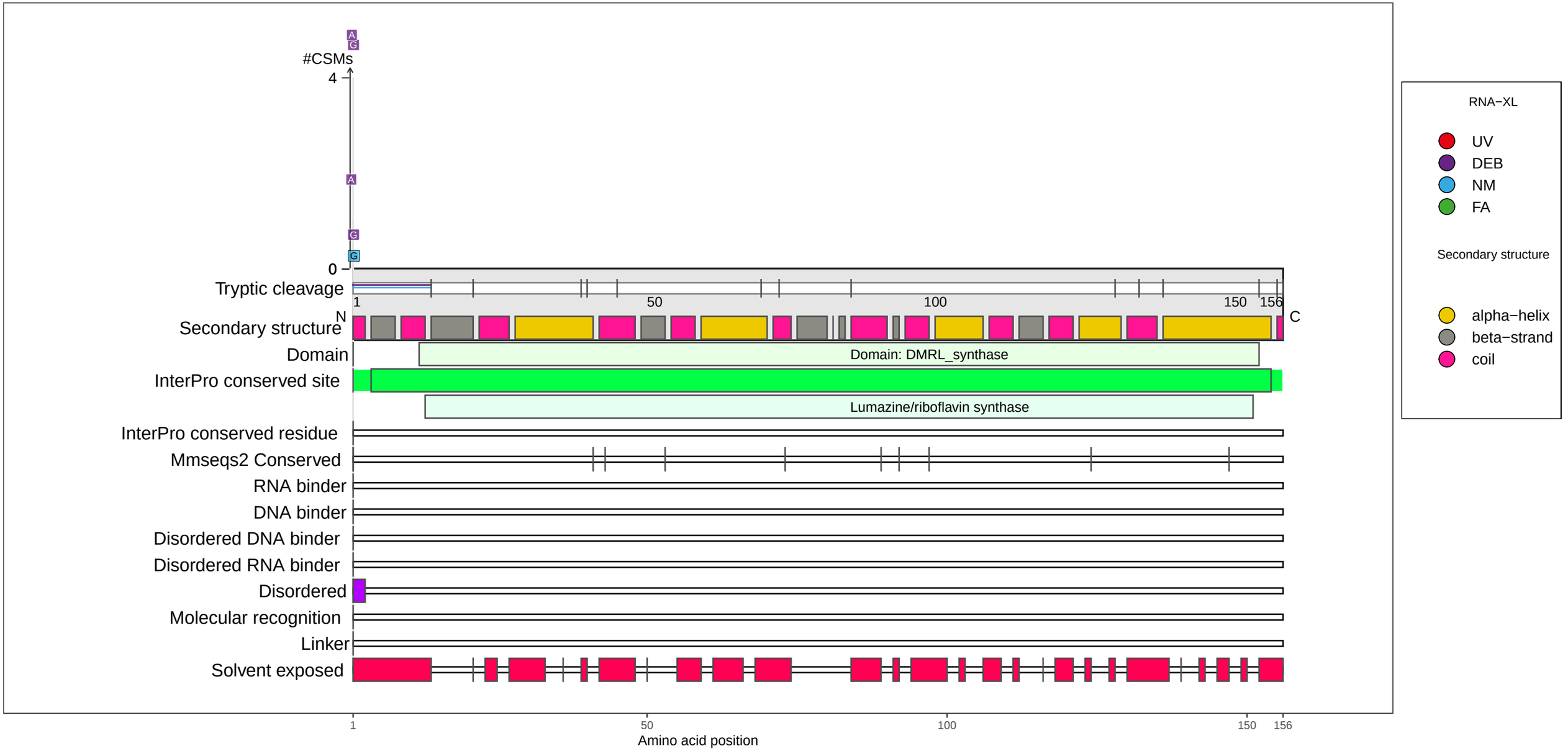
− RNA functions: not annotated



P61714
RISB_ECOLI 6,7−dimethyl−8−ribityllumazine synthase

− Abundance:
tryptic [log10 Intensity]: 9.19 (Q 93)
PAXdb K12 strain [ppm]: 3.13 (Q 93)
PAXdb E.coli [ppm]: 3.19 (Q 96)

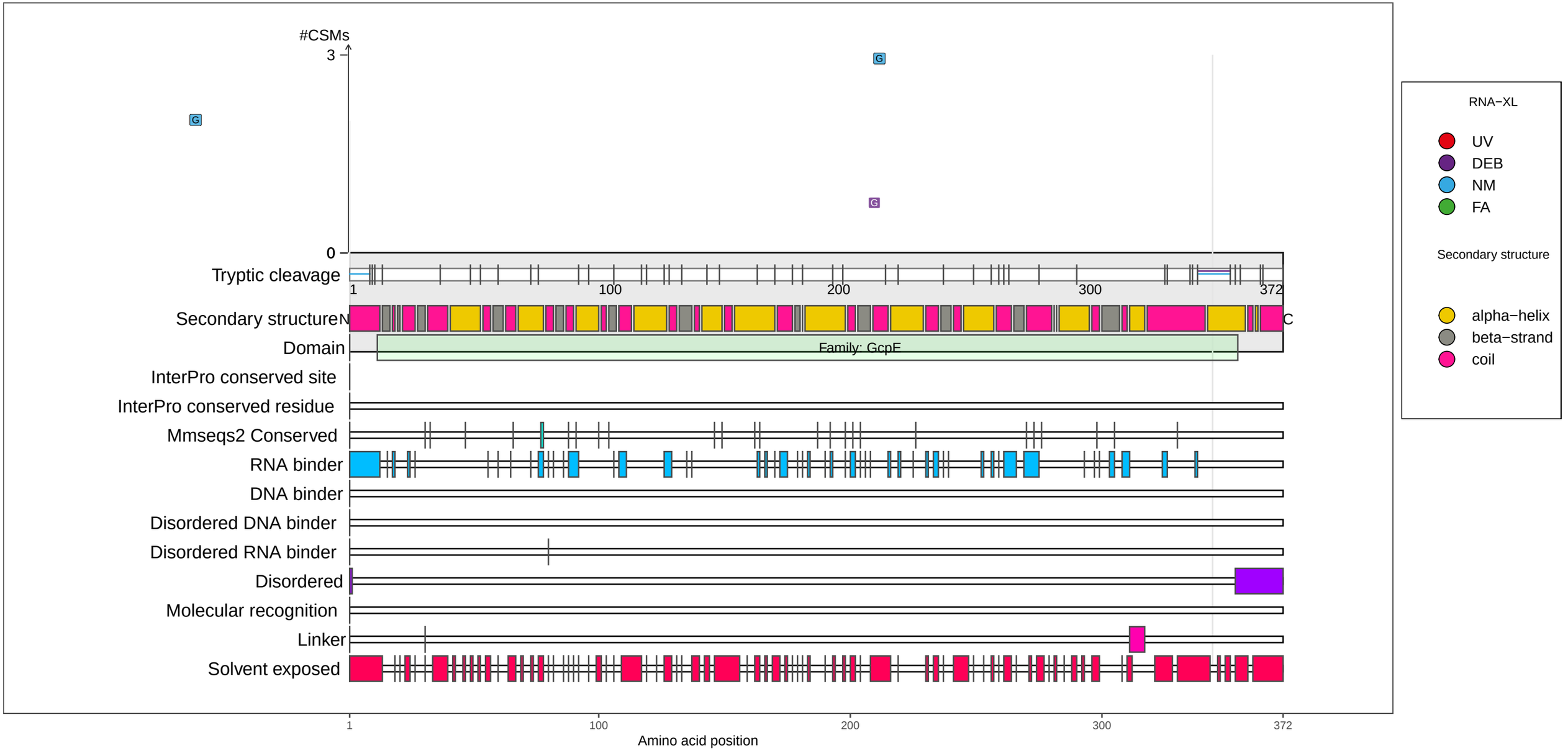
− RNA functions: not annotated



P62620
ISPG_ECOLI 4−hydroxy−3−methylbut−2−en−1−yl diphosphate synthase (flavodoxin)

− Abundance:
tryptic [log10 Intensity]: 8.62 (Q 79)
PAXdb K12 strain [ppm]: 2.72 (Q 84)
PAXdb E.coli [ppm]: 2.44 (Q 84)

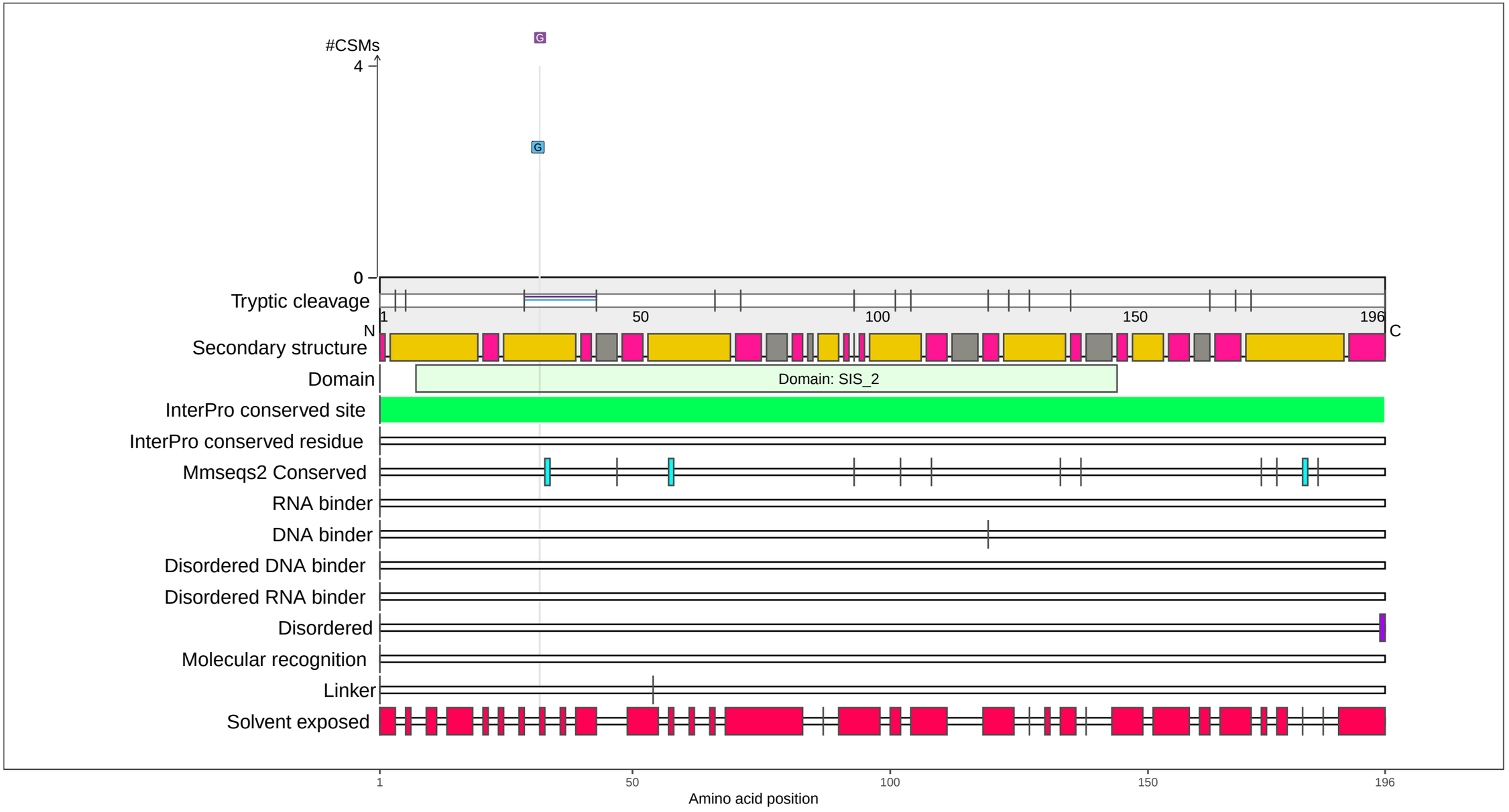
− RNA functions: not annotated

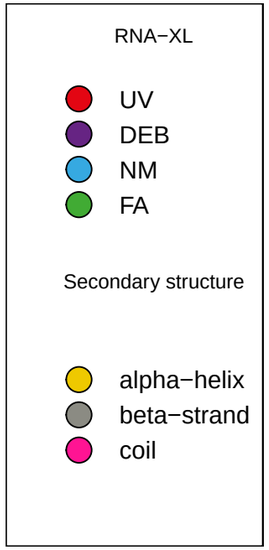


P66817
DIAA_ECOLI DnaA initiator−associating protein DiaA

− Abundance:
tryptic [log10 Intensity]: 7.27 (Q 24)
PAXdb K12 strain [ppm]: 1.43 (Q 34)
PAXdb E.coli [ppm]: 1.47 (Q 59)

− RNA functions: not annotated

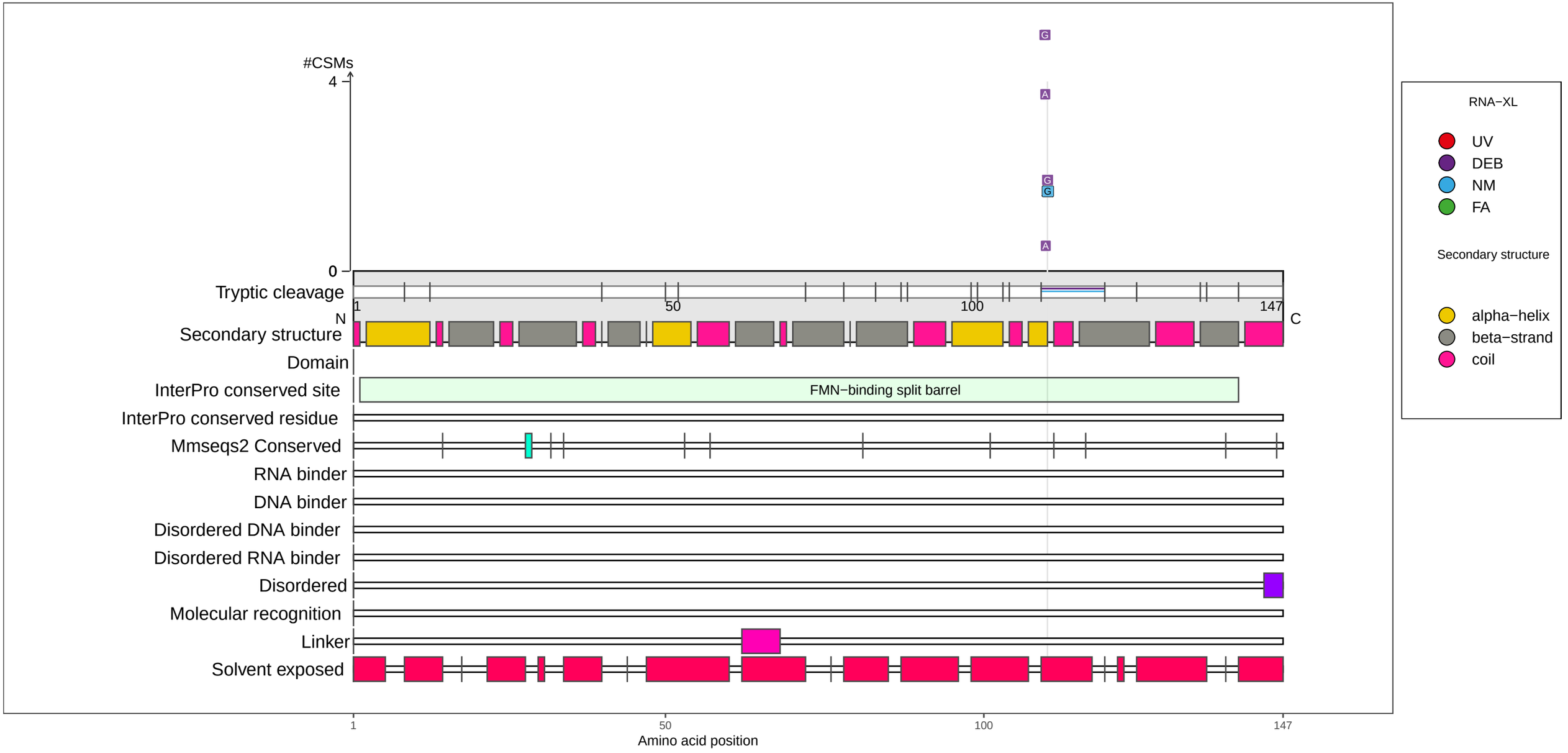




P67762
YHBP_ECOLI UPF0306 protein YhbP

− Abundance:
tryptic [log10 Intensity]: 6.76 (Q 6)
PAXdb K12 strain [ppm]: 2.12 (Q 65)
PAXdb E.coli [ppm]: 0.41 (Q 34)

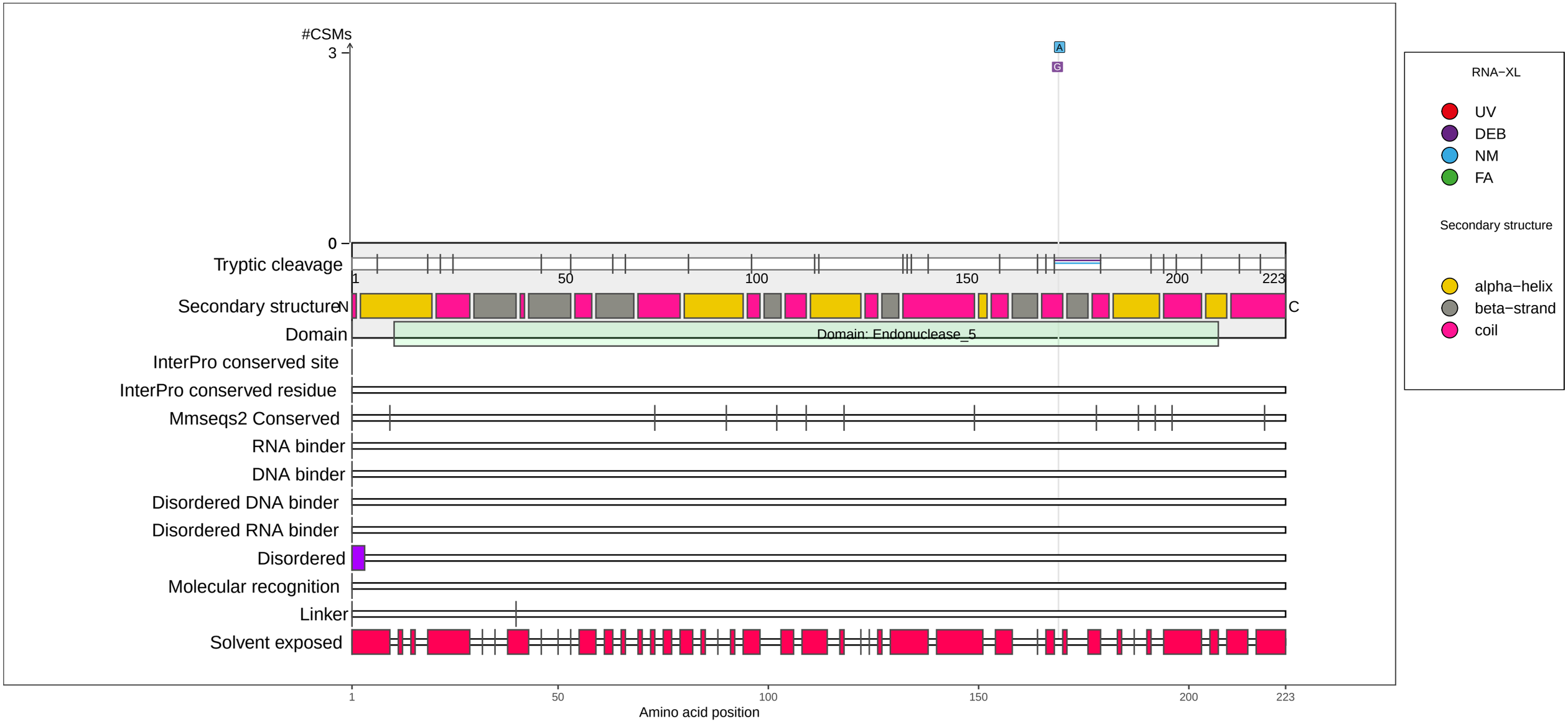
− RNA functions: not annotated



P68739
NFI_ECOLI Endonuclease V

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 1.21 (Q 21)
PAXdb E.coli [ppm]: 1.4 (Q 57)

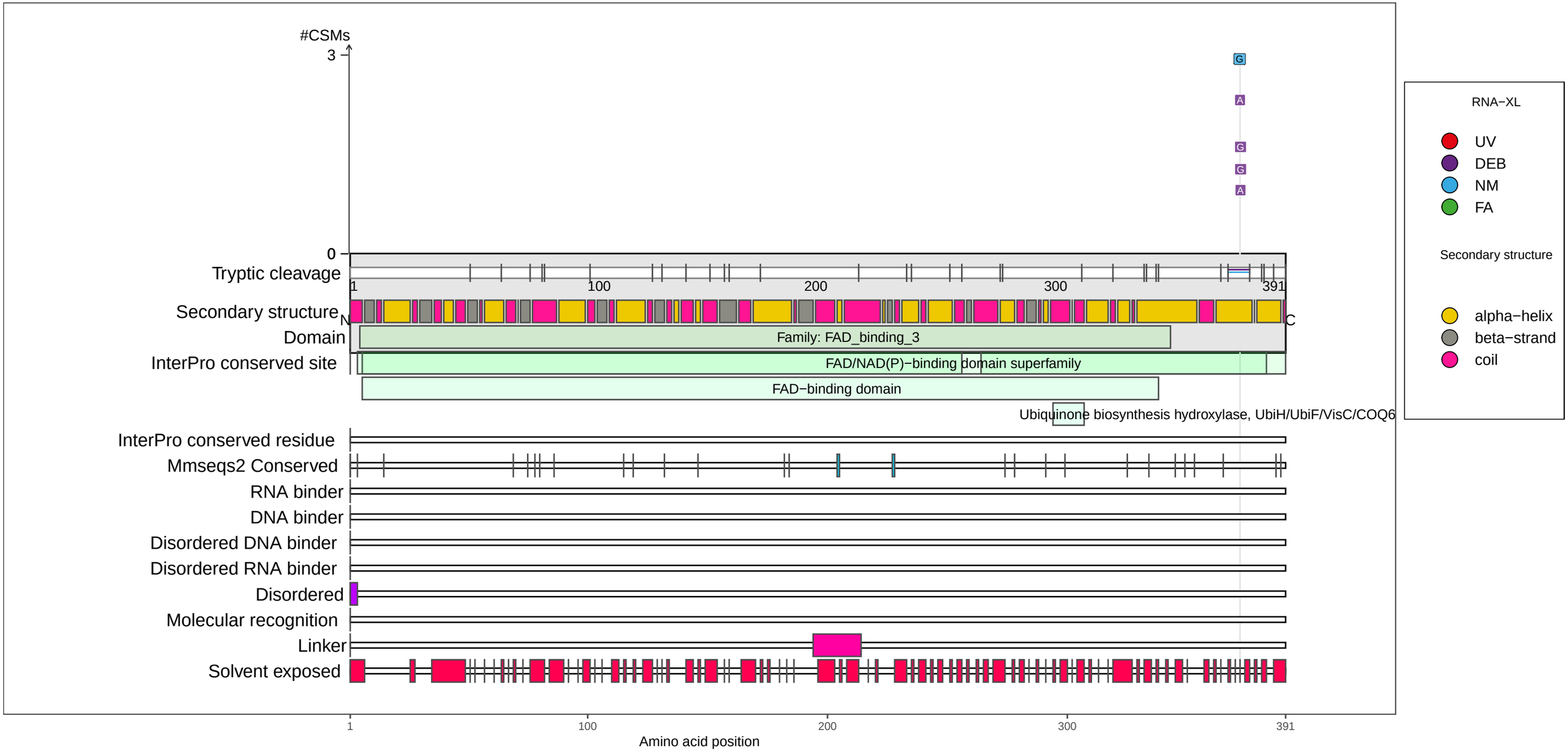
− RNA functions:
RNA binding; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic



P75728
UBIF_ECOLI 3−demethoxyubiquinol 3−hydroxylase

− Abundance:
tryptic [log10 Intensity]: 7.73 (Q 46)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 1.96 (Q 71)

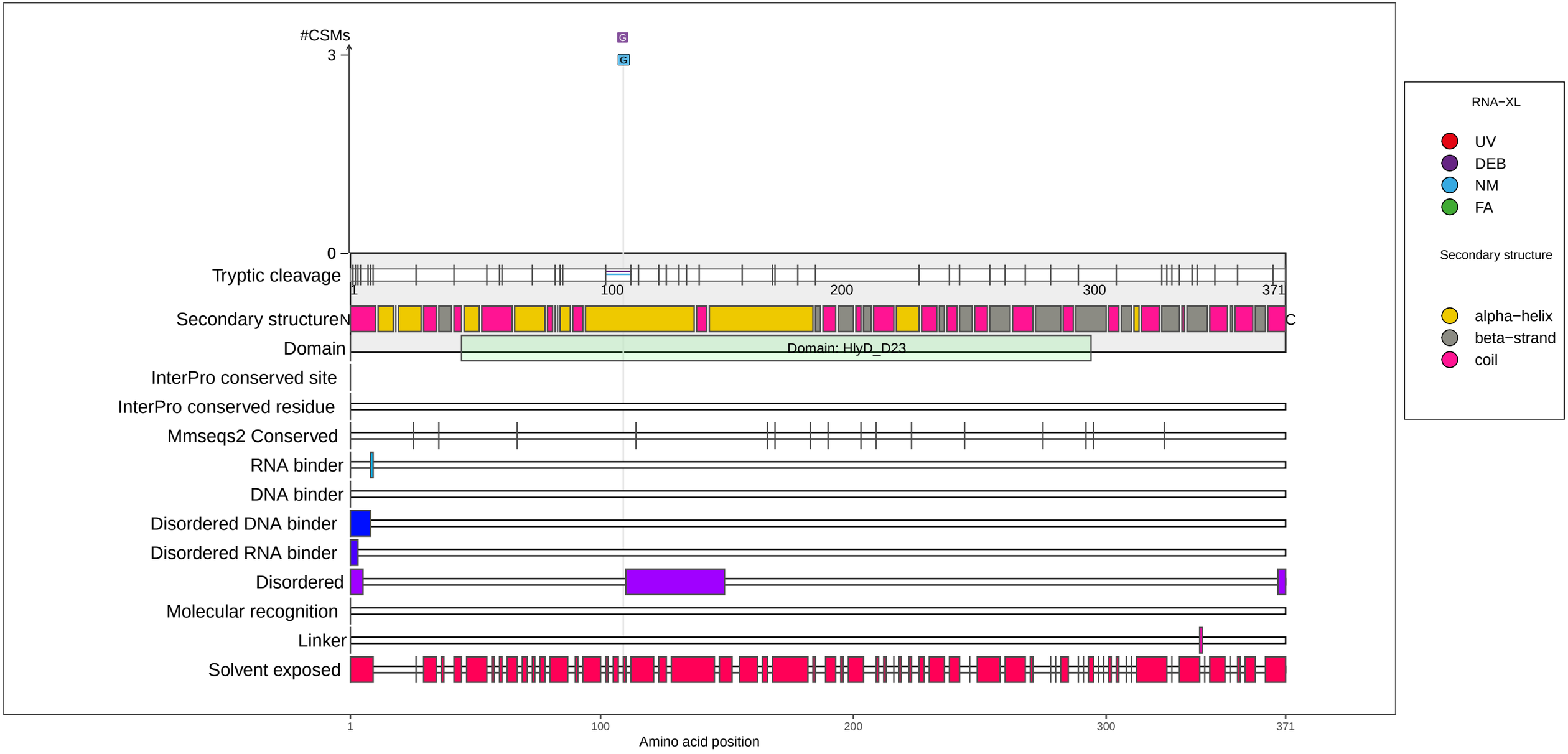
− RNA functions: not annotated



P75830
MACA_ECOLI Macrolide export protein MacA

− Abundance:
tryptic [log10 Intensity]: 7.53 (Q 36)
PAXdb K12 strain [ppm]: 1.24 (Q 22)
PAXdb E.coli [ppm]: 1.2 (Q 52)

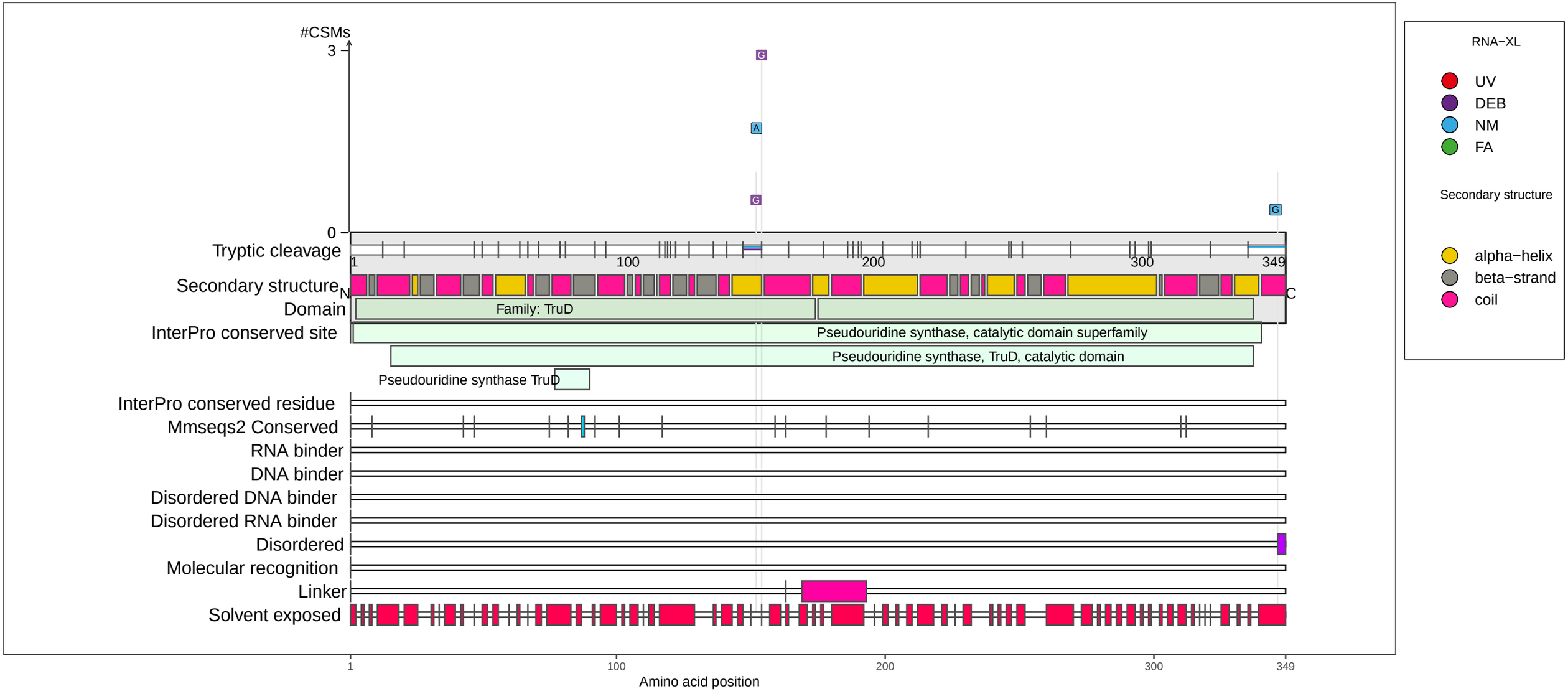
− RNA functions: not annotated



Q57261
TRUD_ECOLI tRNA pseudouridine synthase D

− Abundance:
tryptic [log10 Intensity]: 8.39 (Q 72)
PAXdb K12 strain [ppm]: 2.3 (Q 70)
PAXdb E.coli [ppm]: 1.7 (Q 64)

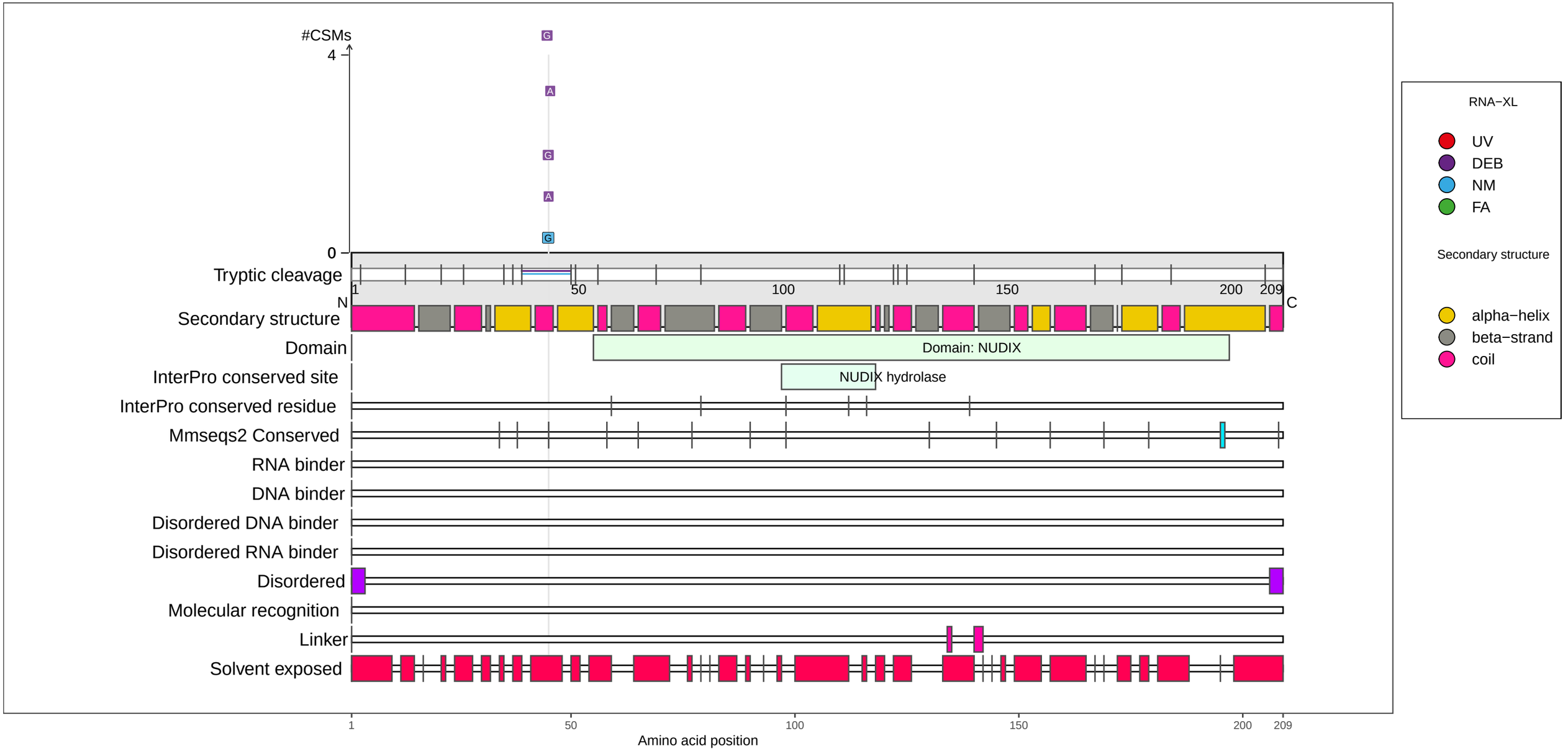
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA pseudouridine synthase activity; tRNA pseudouridine synthase D (TruD)
tRNA pseudouridine synthesis



Q93K97
ADPP_ECOLI ADP−ribose pyrophosphatase

− Abundance:
tryptic [log10 Intensity]: 8.38 (Q 72)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.83 (Q 68)

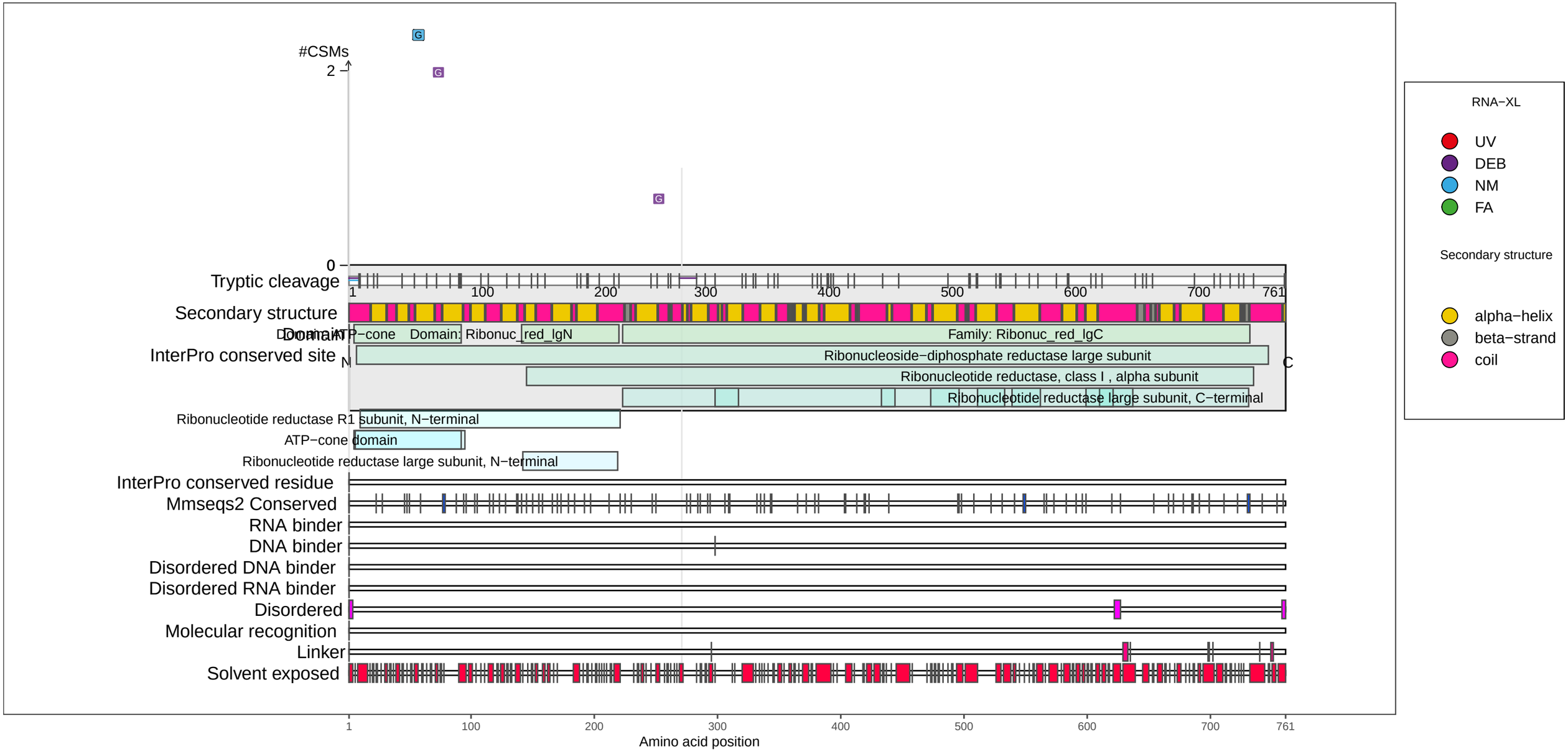
− RNA functions: not annotated



P00452
RIR1_ECOLI Ribonucleoside−diphosphate reductase 1 subunit alpha

− Abundance:
tryptic [log10 Intensity]: 9.14 (Q 91)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 2.89 (Q 93)

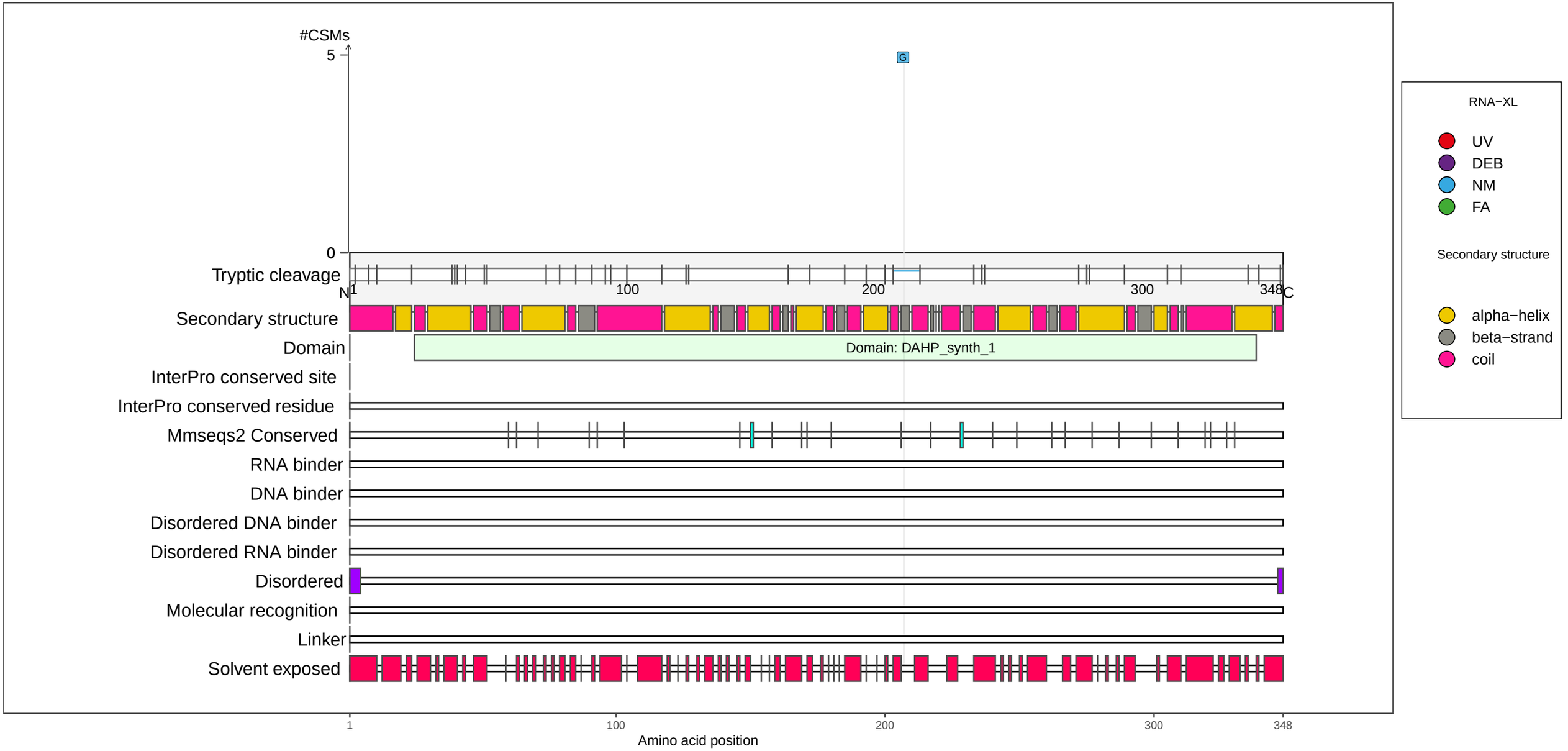
− RNA functions: not annotated



P00887
AROH_ECOLI Phospho−2−dehydro−3−deoxyheptonate aldolase, Trp−sensitive

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 1.45 (Q 35)
PAXdb E.coli [ppm]: 1.42 (Q 58)

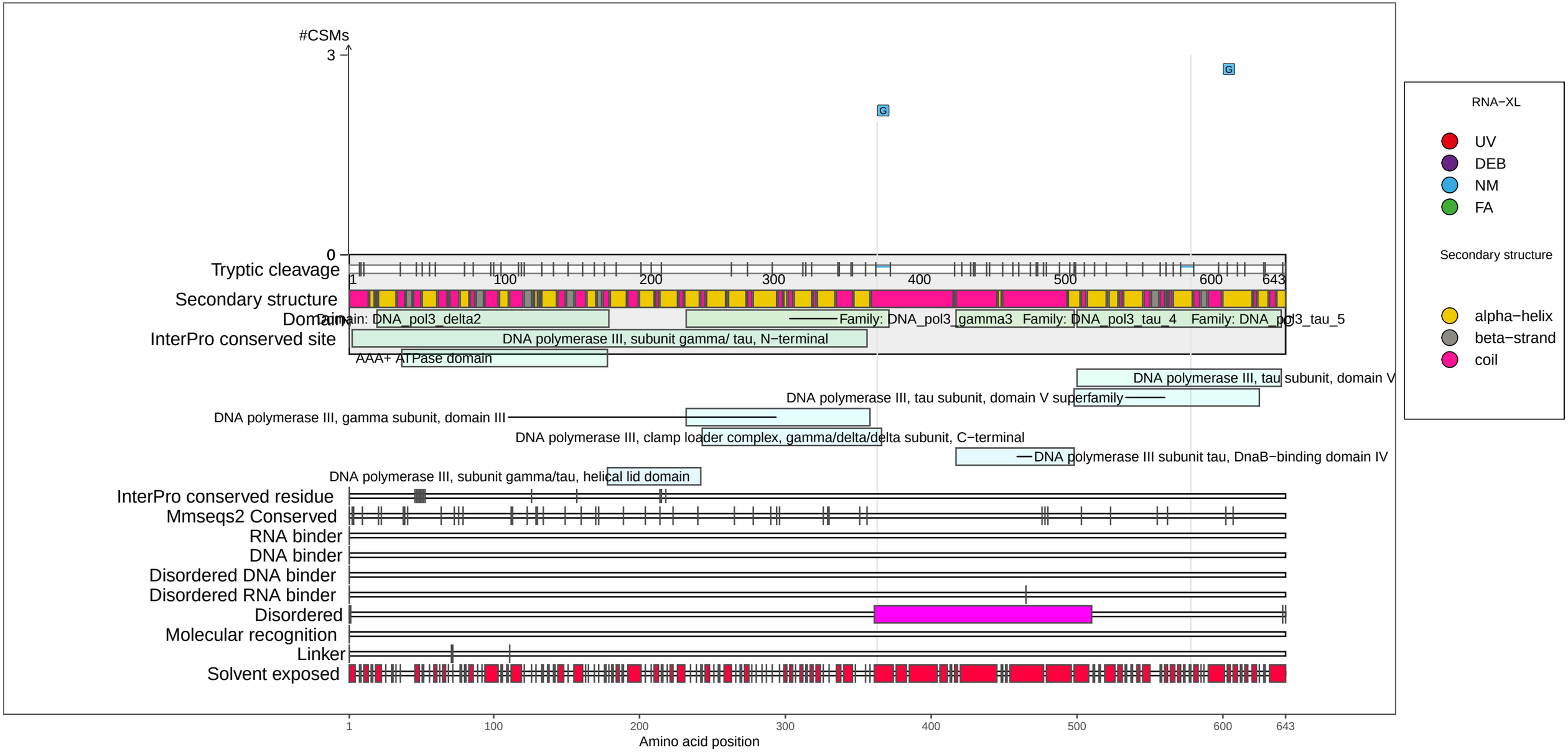
− RNA functions: not annotated



P06710
DPO3X_ECOLI DNA polymerase III subunit tau

− Abundance:
tryptic [log10 Intensity]: 7.06 (Q 15)
PAXdb K12 strain [ppm]: 1.77 (Q 52)
PAXdb E.coli [ppm]: 1.59 (Q 62)

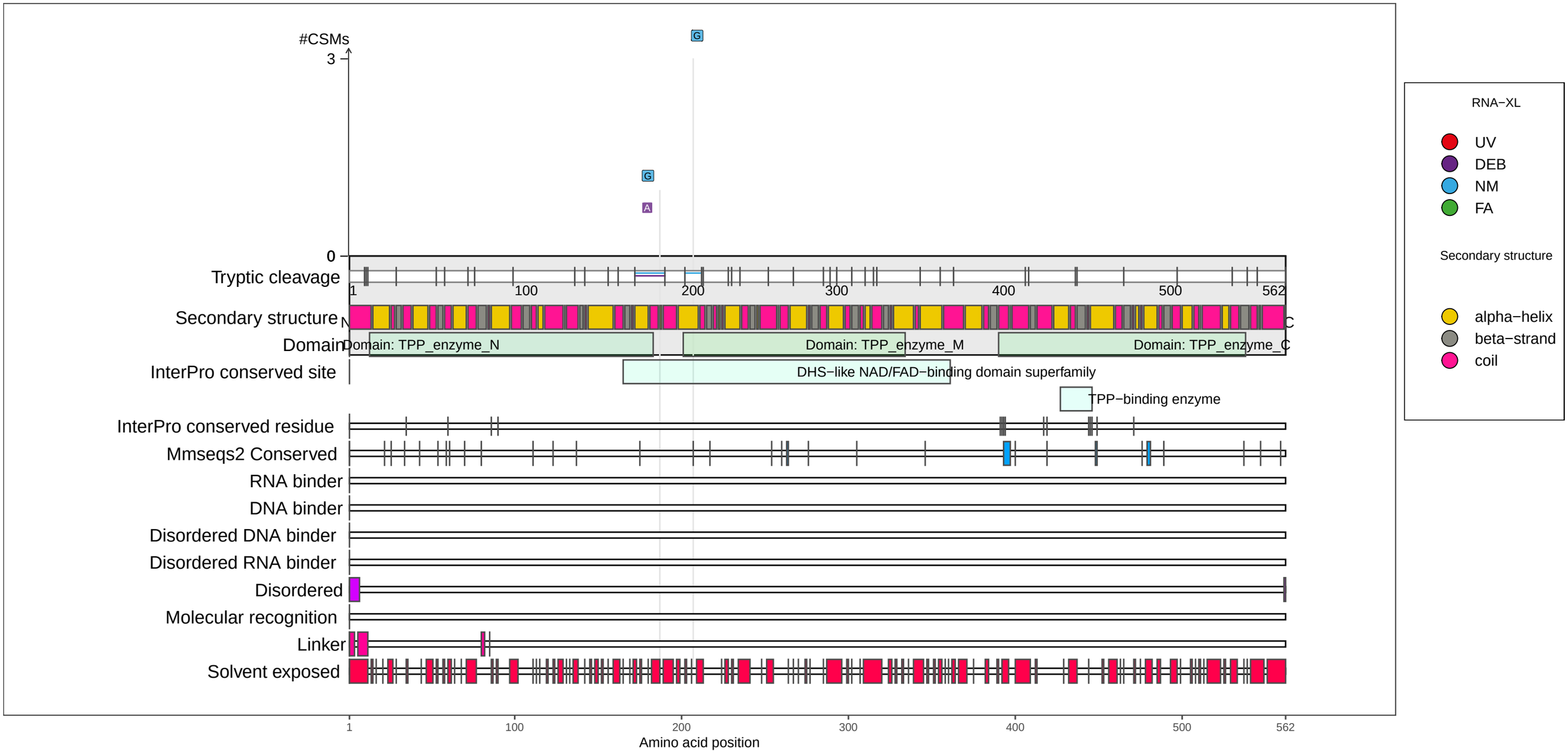
− RNA functions: not annotated



P08142
ILVB_ECOLI Acetolactate synthase isozyme 1 large subunit

− Abundance:
tryptic [log10 Intensity]: 6.44 (Q 2)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.59 (Q 88)

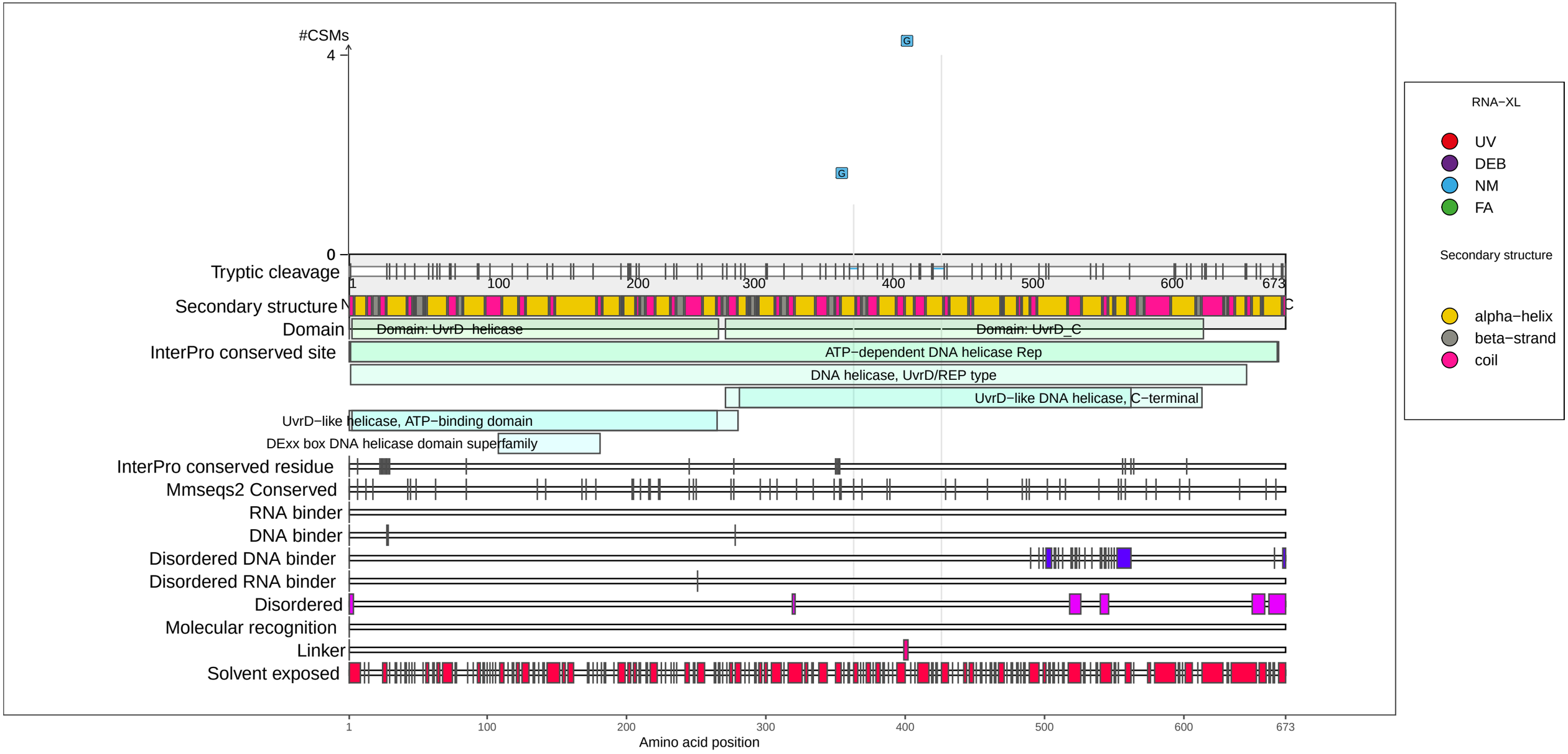
− RNA functions: not annotated



P09980
REP_ECOLI ATP−dependent DNA helicase Rep

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.8 (Q 5)
PAXdb E.coli [ppm]: 1 (Q 48)

− RNA functions: not annotated



P0A698
UVRA_ECOLI UvrABC system protein A

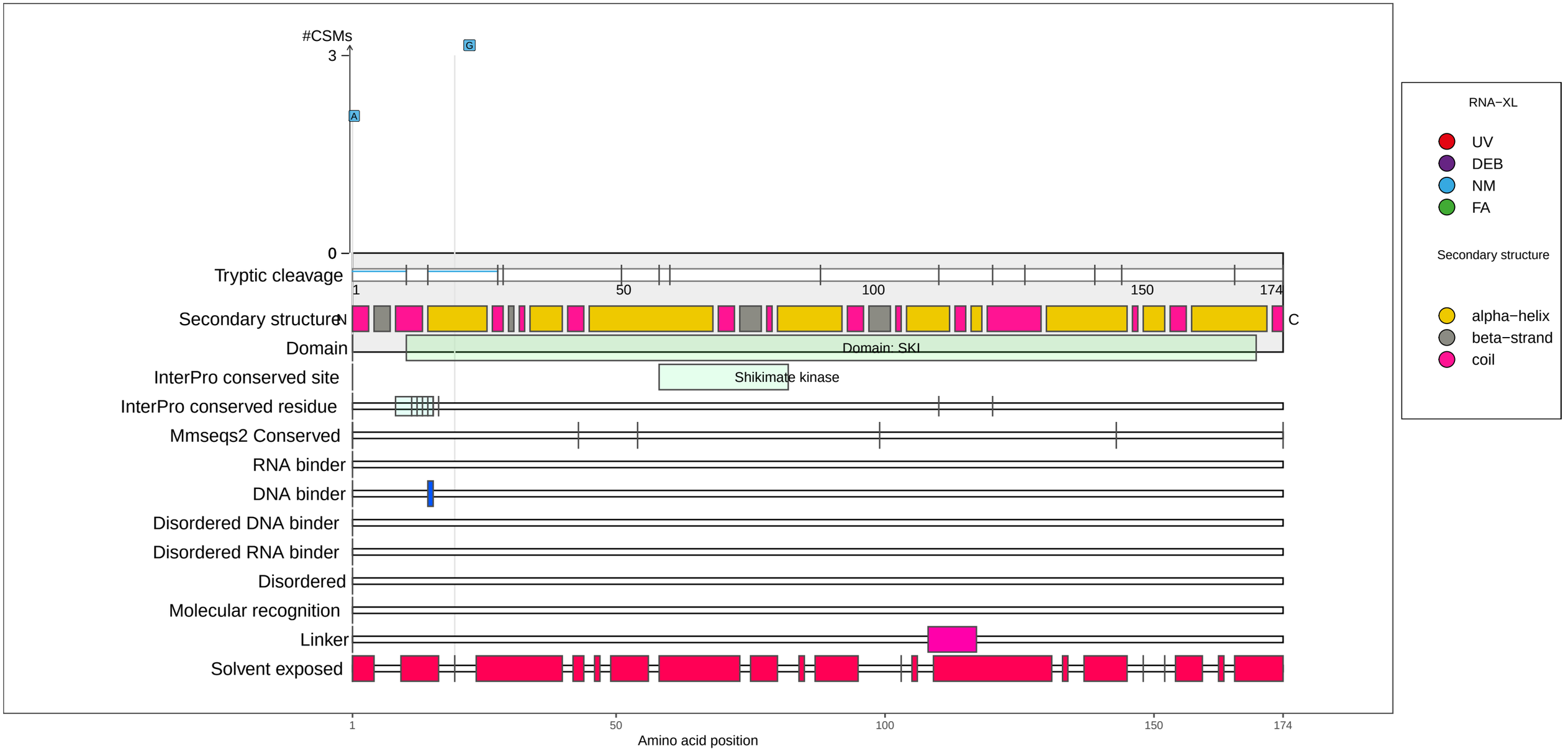
− Abundance:
tryptic [log10 Intensity]: 8.97 (Q 87)
PAXdb K12 strain [ppm]: 2.35 (Q 72)
PAXdb E.coli [ppm]: 1.92 (Q 70)

− RNA functions: not annotated

P0A6E1
AROL_ECOLI Shikimate kinase 2

− Abundance:
tryptic [log10 Intensity]: 7.7 (Q 44)
PAXdb K12 strain [ppm]: 1.47 (Q 36)
PAXdb E.coli [ppm]: 1.8 (Q 67)

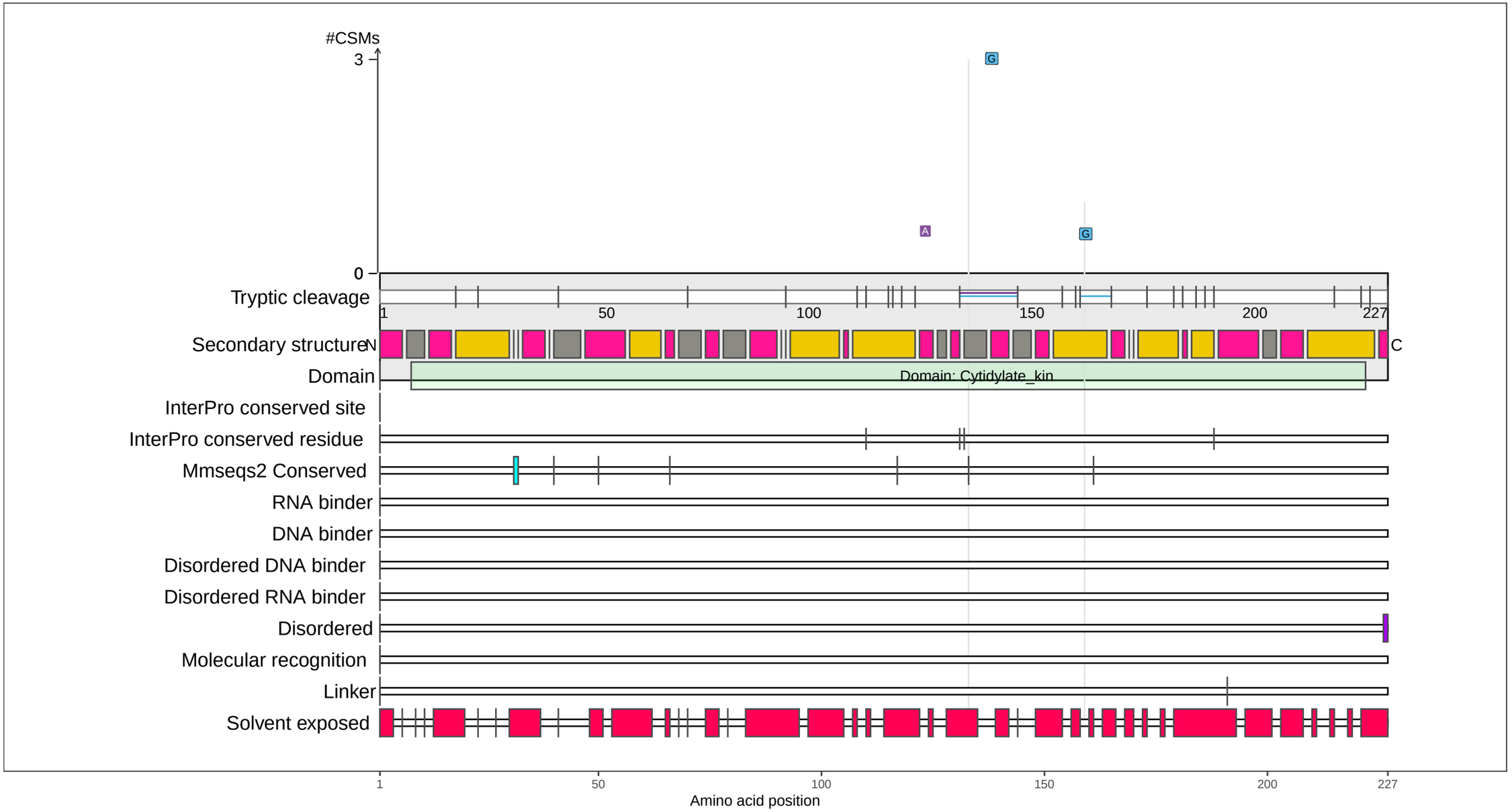
− RNA functions: not annotated

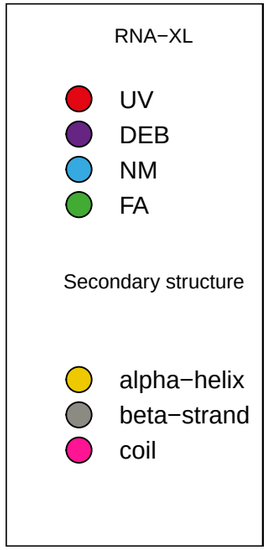


P0A6I0
KCY_ECOLI Cytidylate kinase

− Abundance:
tryptic [log10 Intensity]: 8.09 (Q 61)
PAXdb K12 strain [ppm]: 1.98 (Q 60)
PAXdb E.coli [ppm]: 2.31 (Q 81)

− RNA functions: not annotated

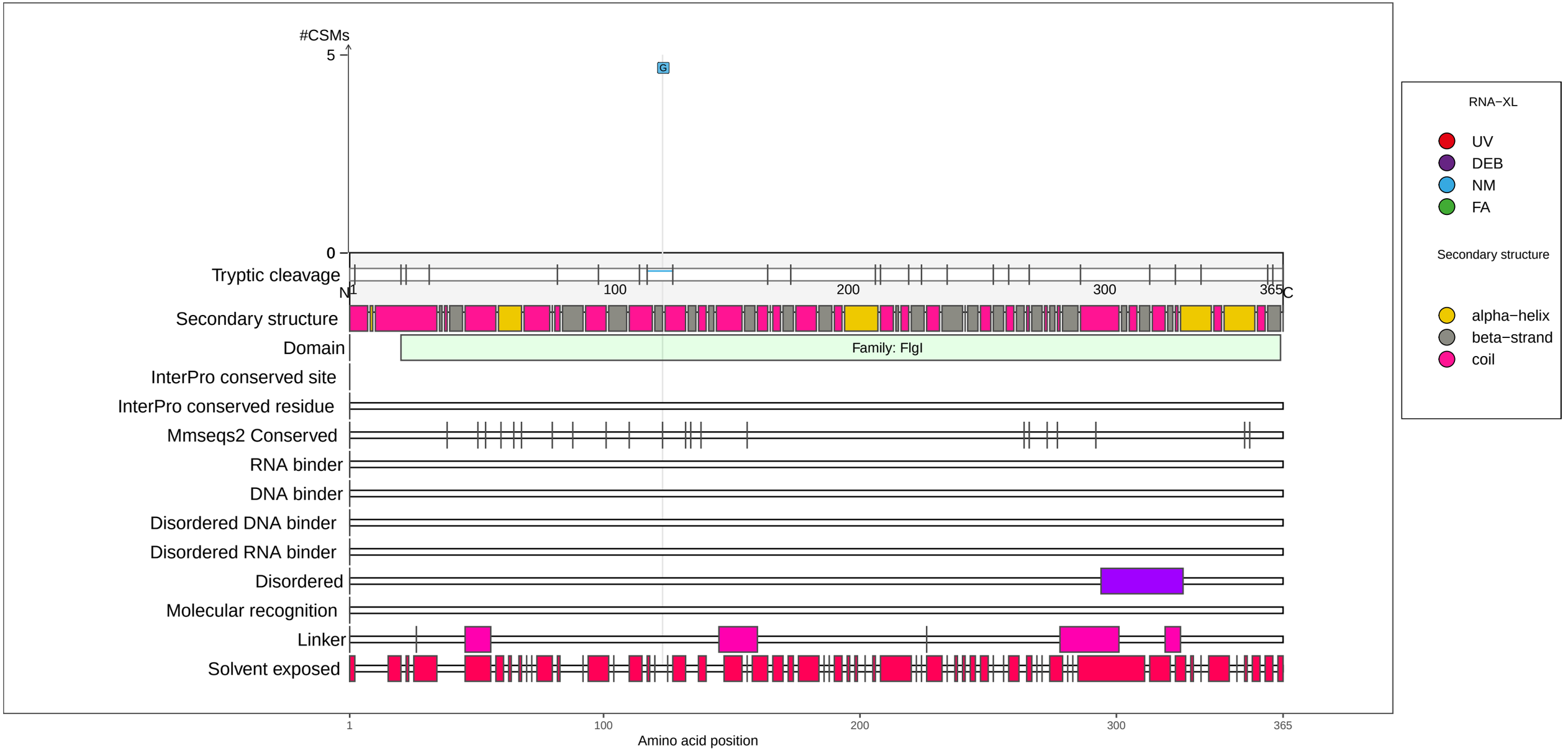




P0A6S3
FLGI_ECOLI Flagellar P−ring protein

− Abundance:
tryptic [log10 Intensity]: 6.7 (Q 5)
PAXdb K12 strain [ppm]: 1.81 (Q 54)
PAXdb E.coli [ppm]: −0.09 (Q 23)

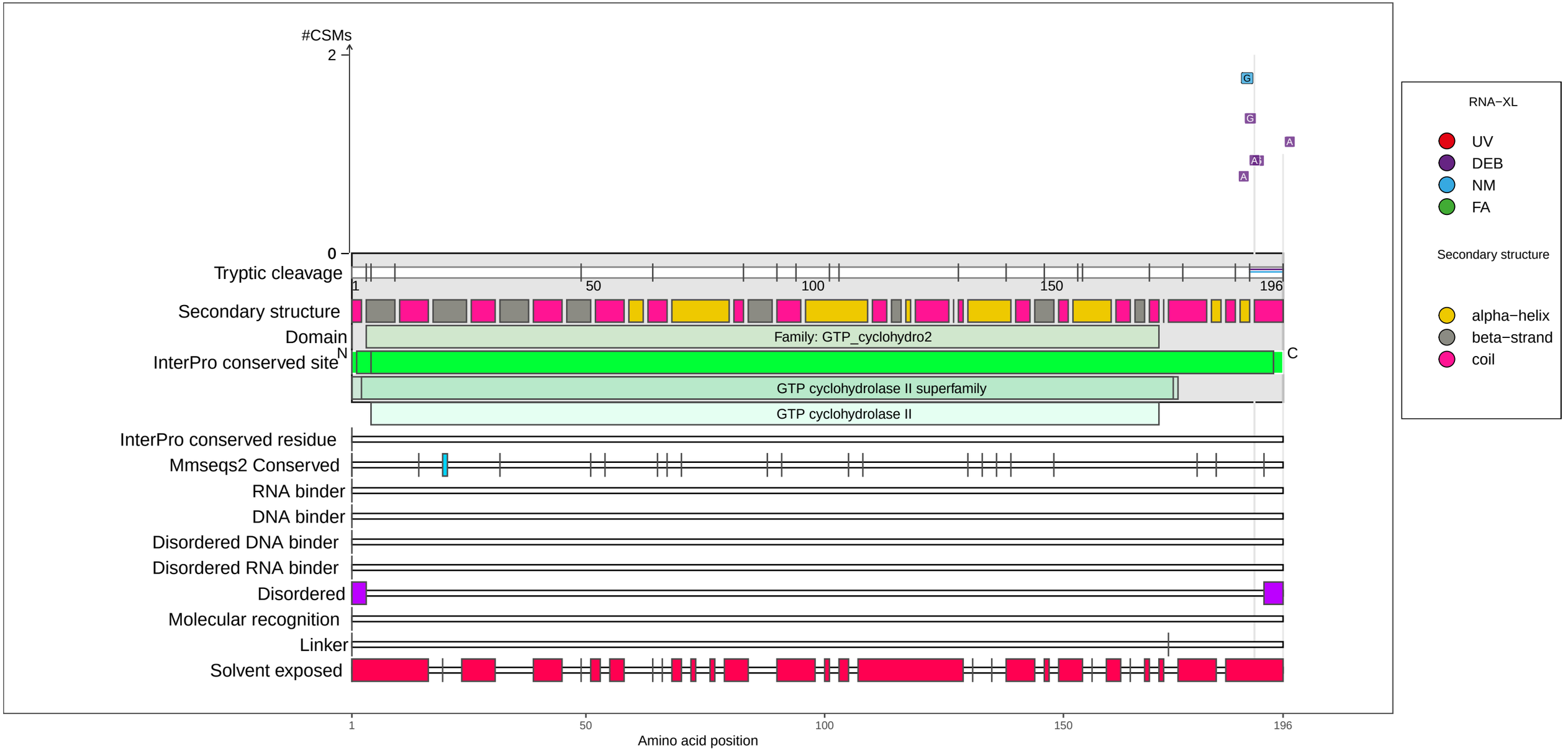
− RNA functions: not annotated



P0A7I7
RIBA_ECOLI GTP cyclohydrolase−2

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 1.35 (Q 29)
PAXdb E.coli [ppm]: 1.74 (Q 66)

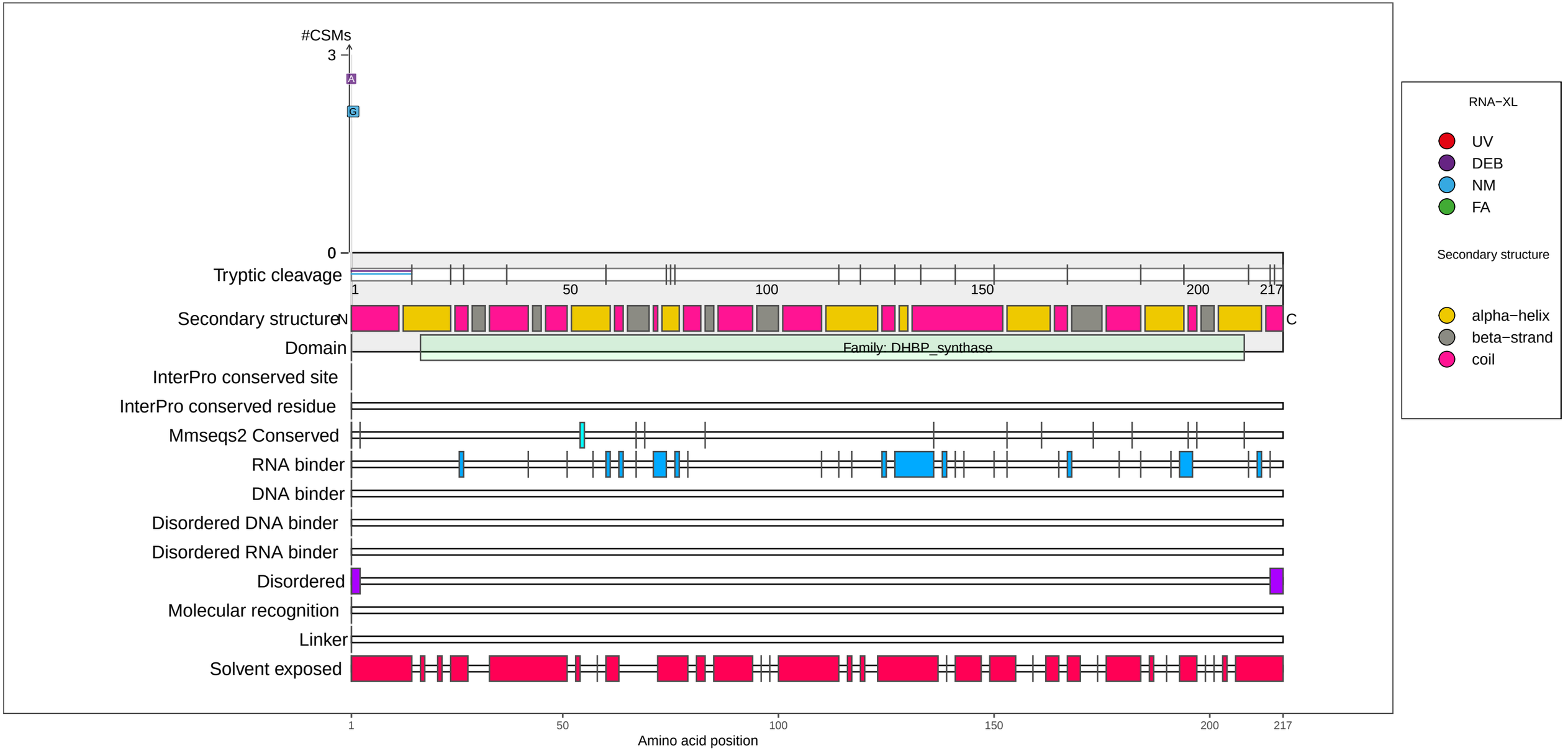
− RNA functions: not annotated



P0A7J0
RIBB_ECOLI 3,4−dihydroxy−2−butanone 4−phosphate synthase

− Abundance:
tryptic [log10 Intensity]: 8.4 (Q 72)
PAXdb K12 strain [ppm]: 2.81 (Q 86)
PAXdb E.coli [ppm]: 2.62 (Q 89)

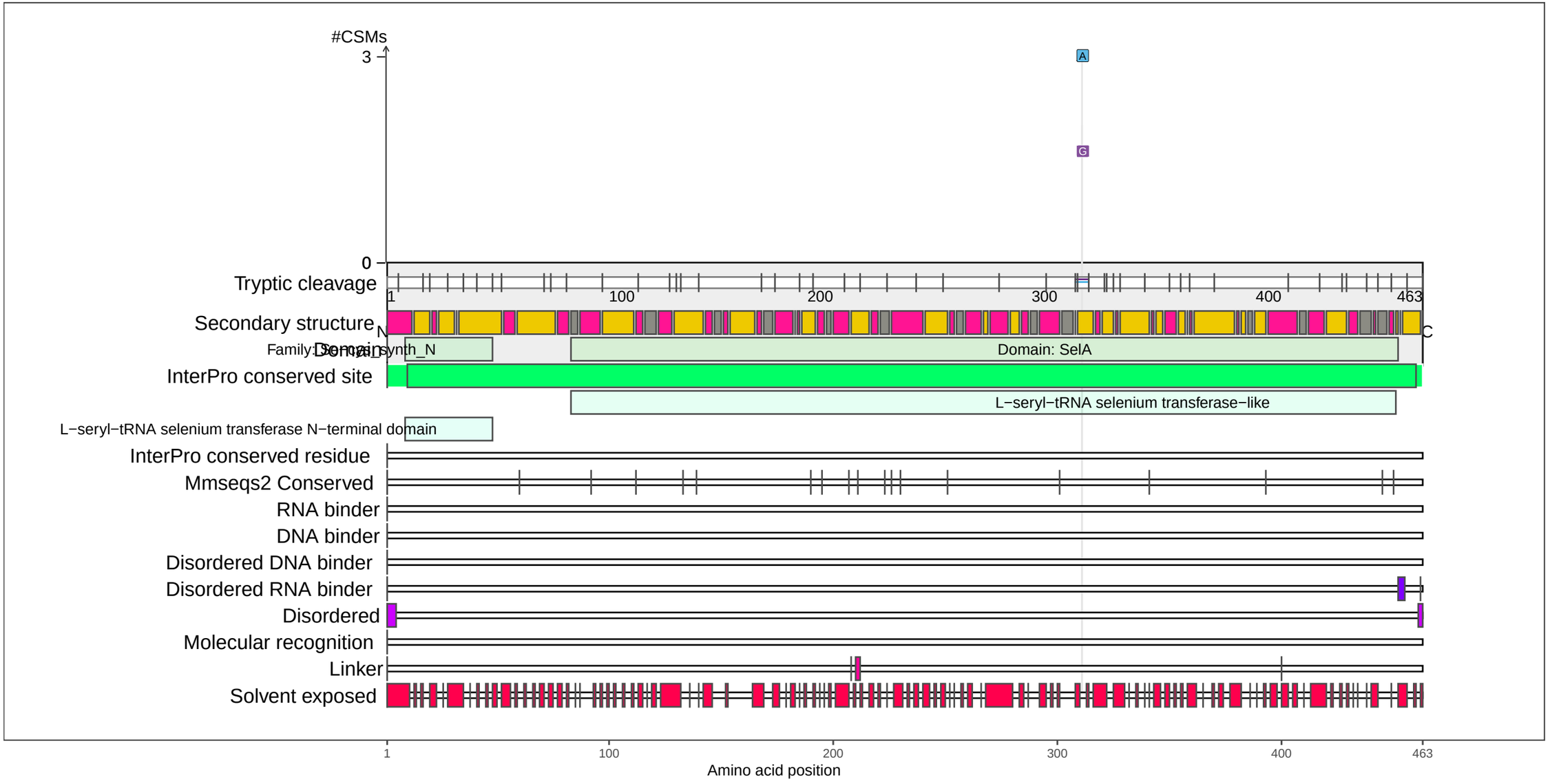
− RNA functions: not annotated

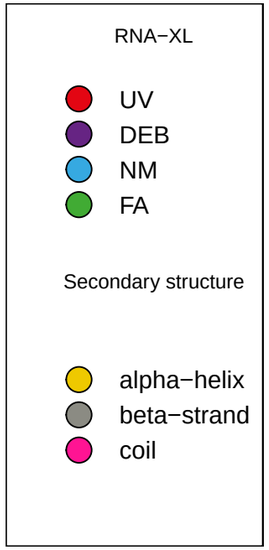


P0A821
SELA_ECOLI L−seryl−tRNA(Sec) selenium transferase

− Abundance:
tryptic [log10 Intensity]: 7.63 (Q 41)
PAXdb K12 strain [ppm]: 1.05 (Q 13)
PAXdb E.coli [ppm]: 0.98 (Q 47)

− RNA functions:
L−seryl−tRNA selenium transferase; L−seryl−tRNASec selenium transferase activity
ncRNA metabolic process; RNA biosynthetic process; RNA metabolic process
selenocysteinyl−tRNA(Sec) biosynthetic process; tRNA metabolic process

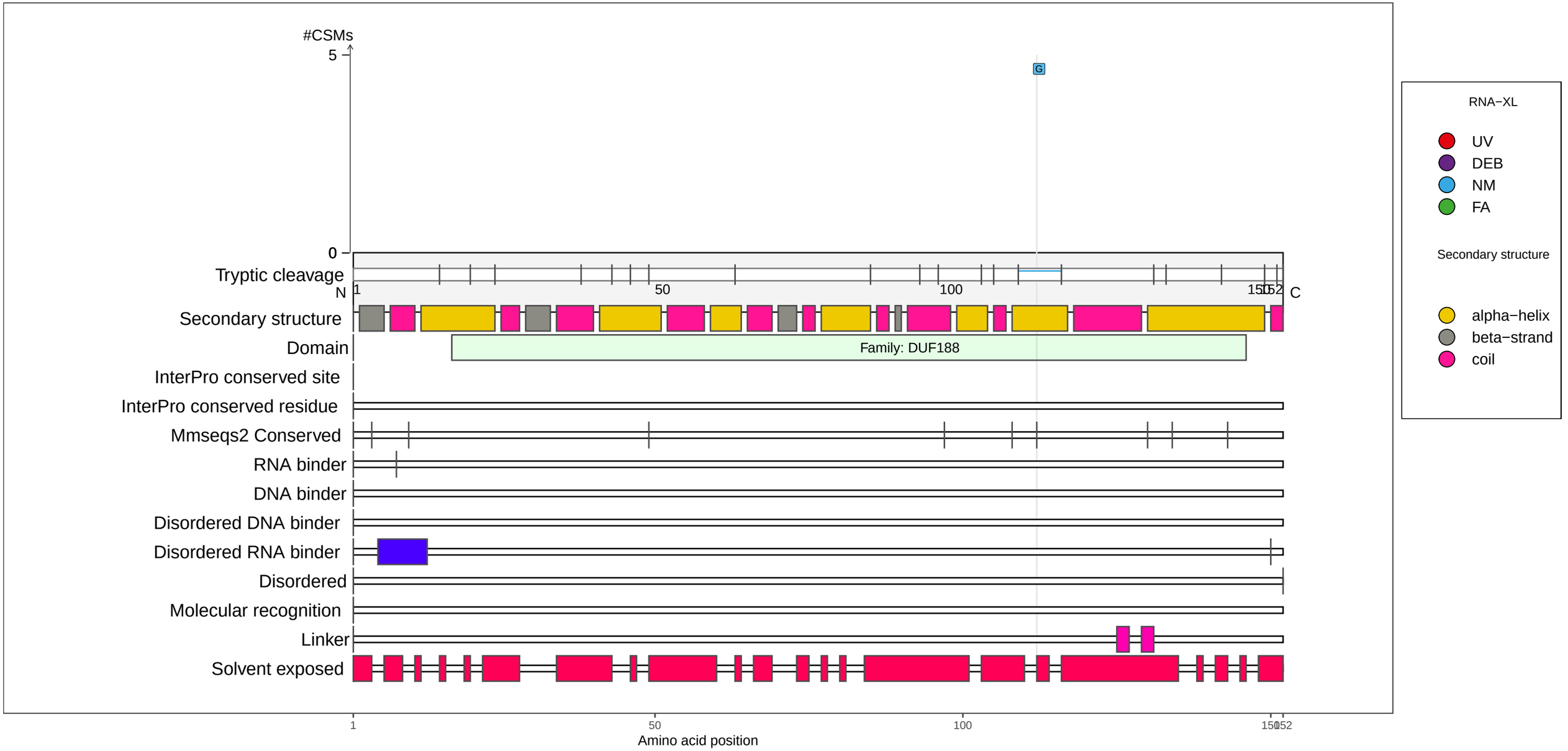




P0A8D3
YAII_ECOLI UPF0178 protein YaiI

− Abundance:
tryptic [log10 Intensity]: 7.64 (Q 42)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 1.3 (Q 55)

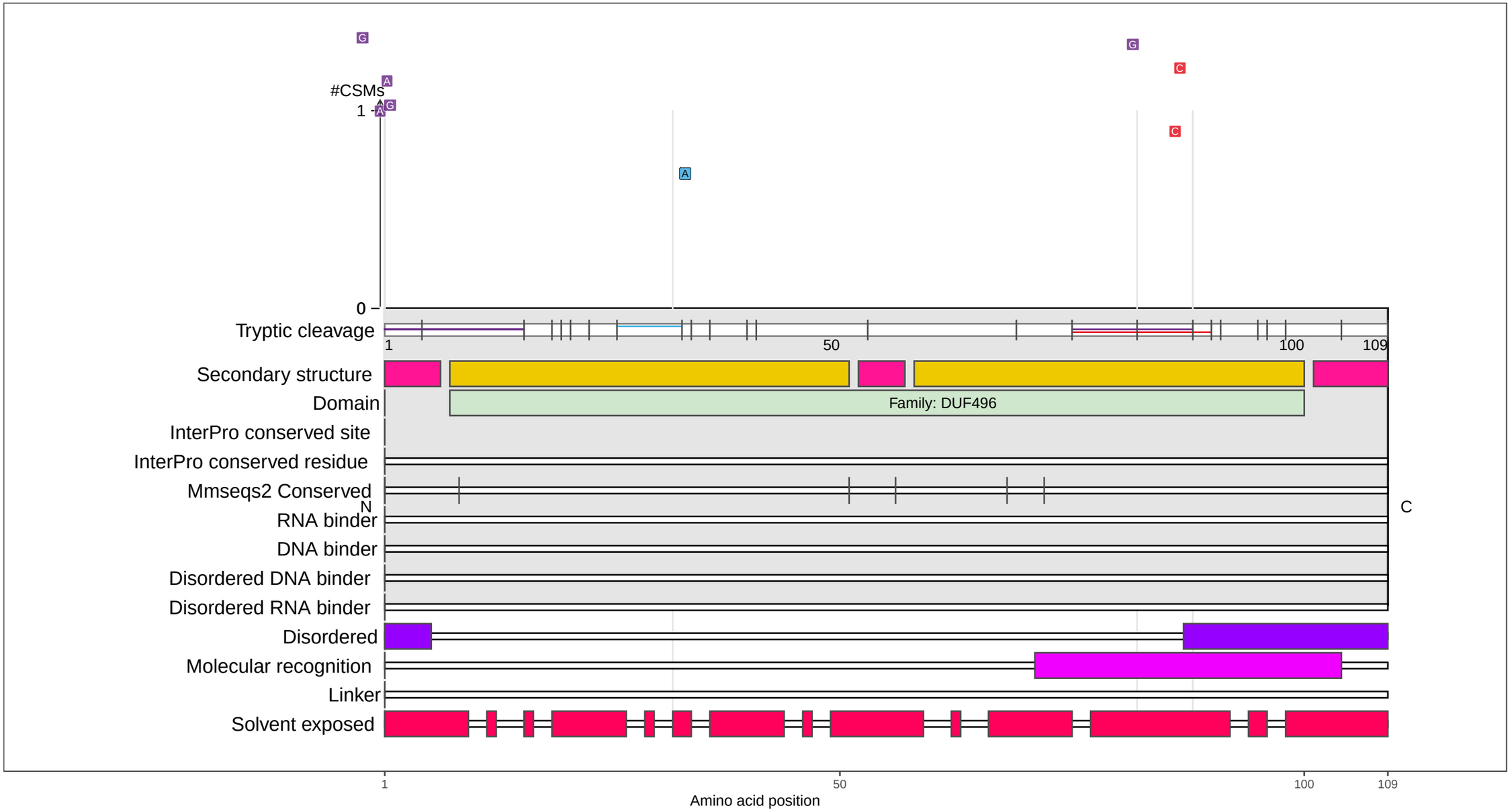
− RNA functions: not annotated



P0A8M6
YEEX_ECOLI UPF0265 protein YeeX

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 69)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 3.29 (Q 97)

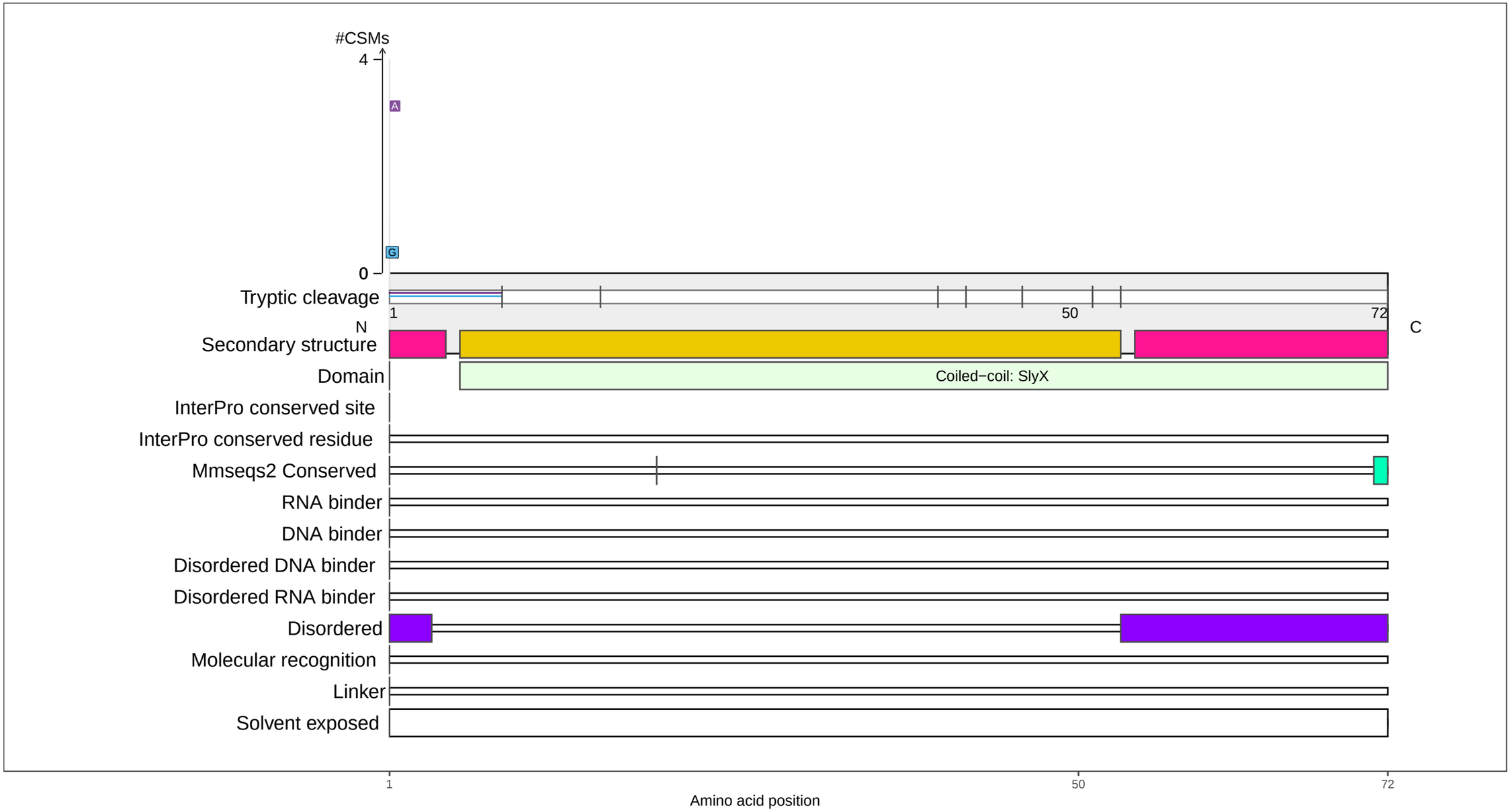
− RNA functions: not annotated

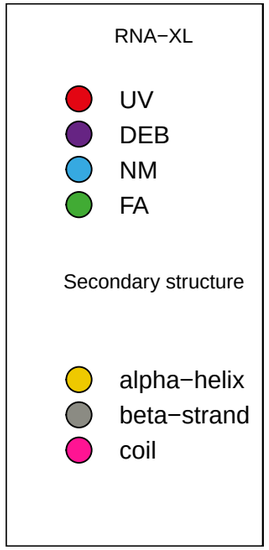


P0A8R4
SLYX_ECOLI Protein SlyX

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.36 (Q 73)
PAXdb E.coli [ppm]: 1.88 (Q 69)

− RNA functions: not annotated

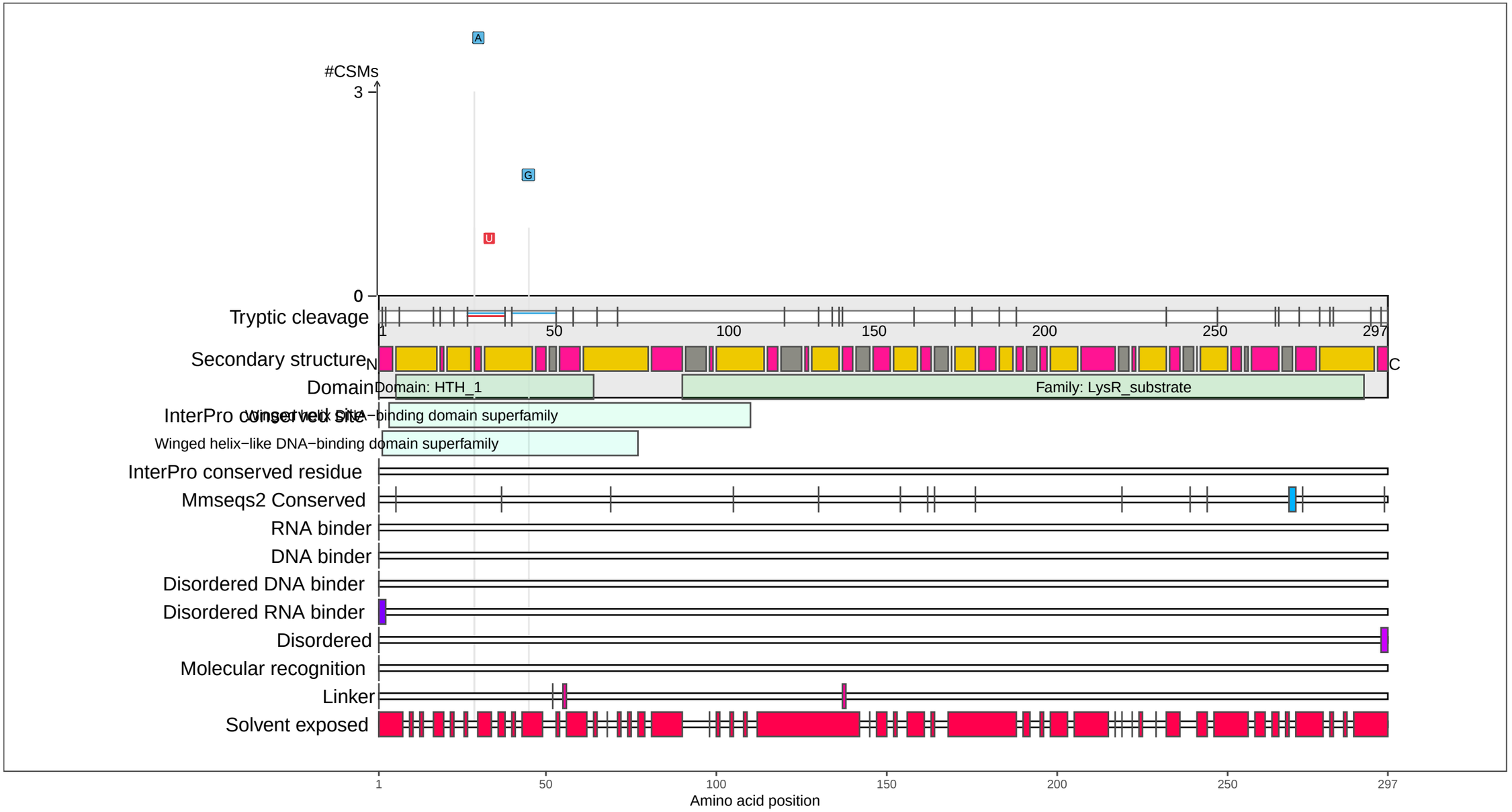


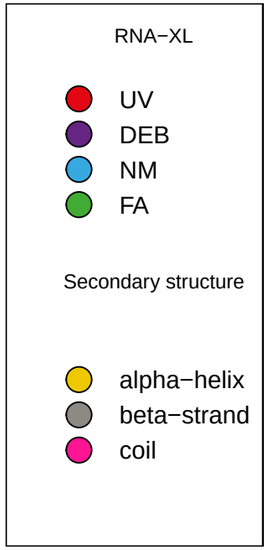


P0A8S1
ARGP_ECOLI HTH−type transcriptional regulator ArgP

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.08 (Q 63)
PAXdb E.coli [ppm]: 2.34 (Q 82)

− RNA functions: not annotated

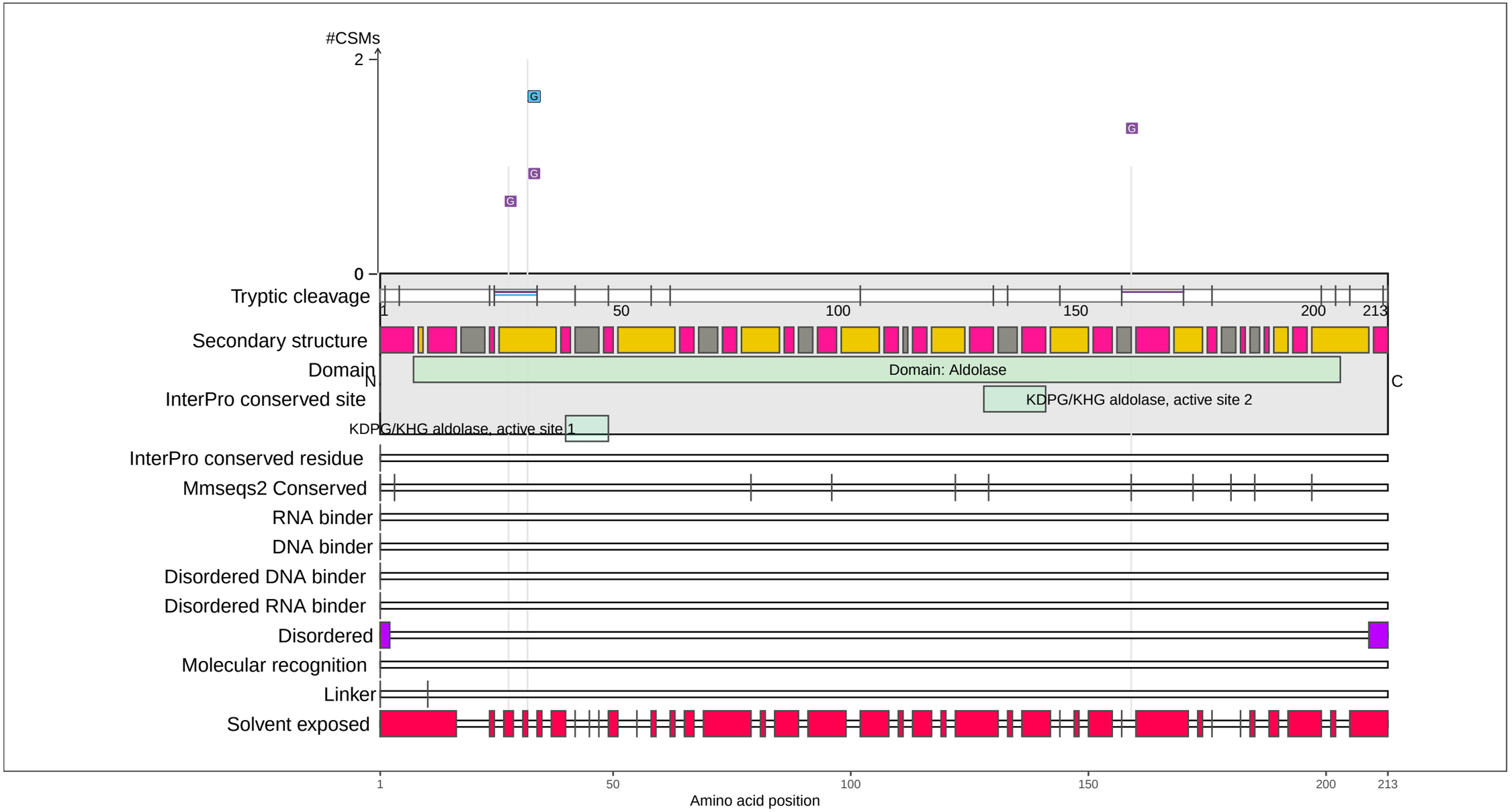




P0A955
ALKH_ECOLI KHG/KDPG aldolase

− Abundance:
tryptic [log10 Intensity]: 8.95 (Q 87)
PAXdb K12 strain [ppm]: 3.15 (Q 93)
PAXdb E.coli [ppm]: 2.93 (Q 94)

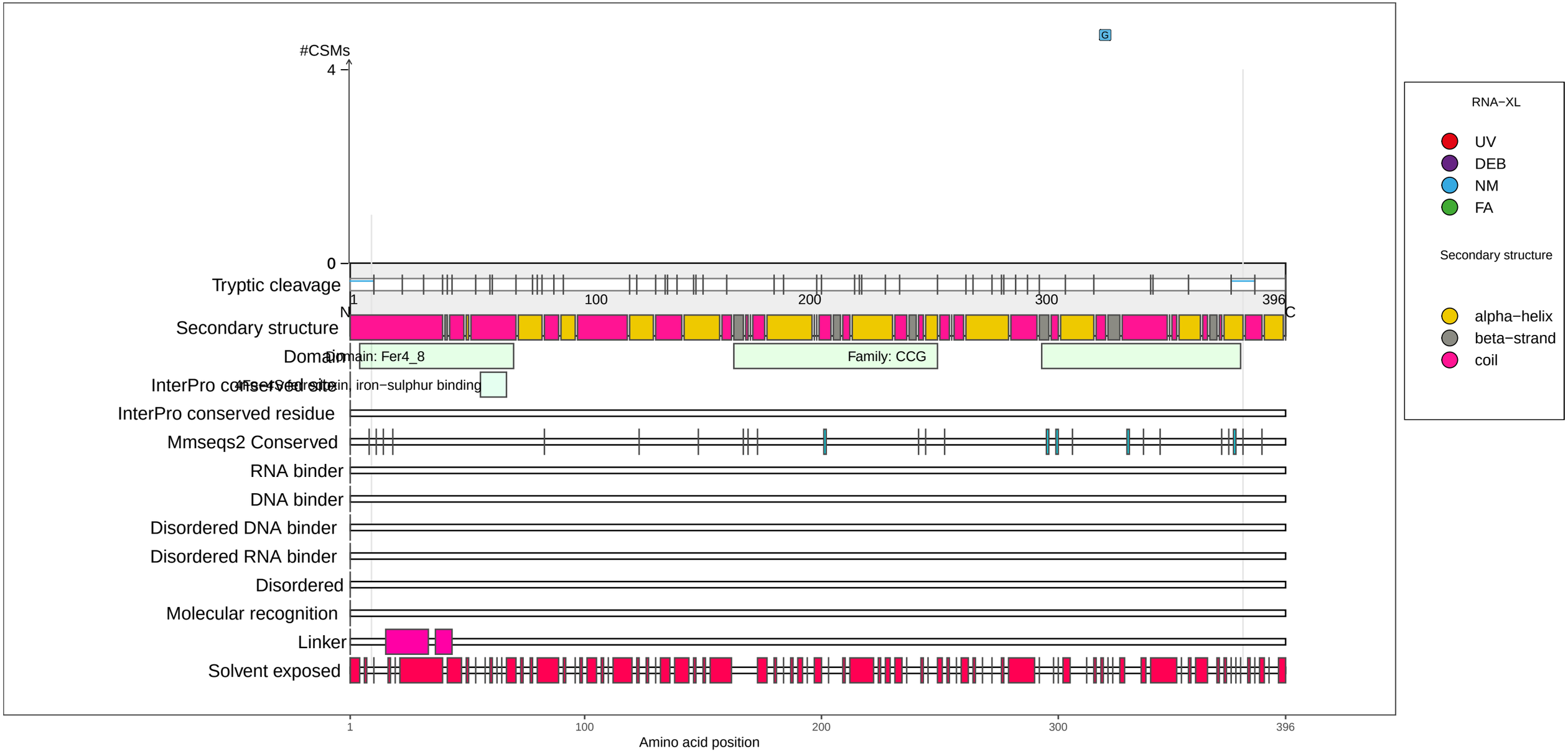
− RNA functions: not annotated



P0A996
GLPC_ECOLI Anaerobic glycerol−3−phosphate dehydrogenase subunit C

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: 0.74 (Q 3)
PAXdb E.coli [ppm]: 1.56 (Q 61)

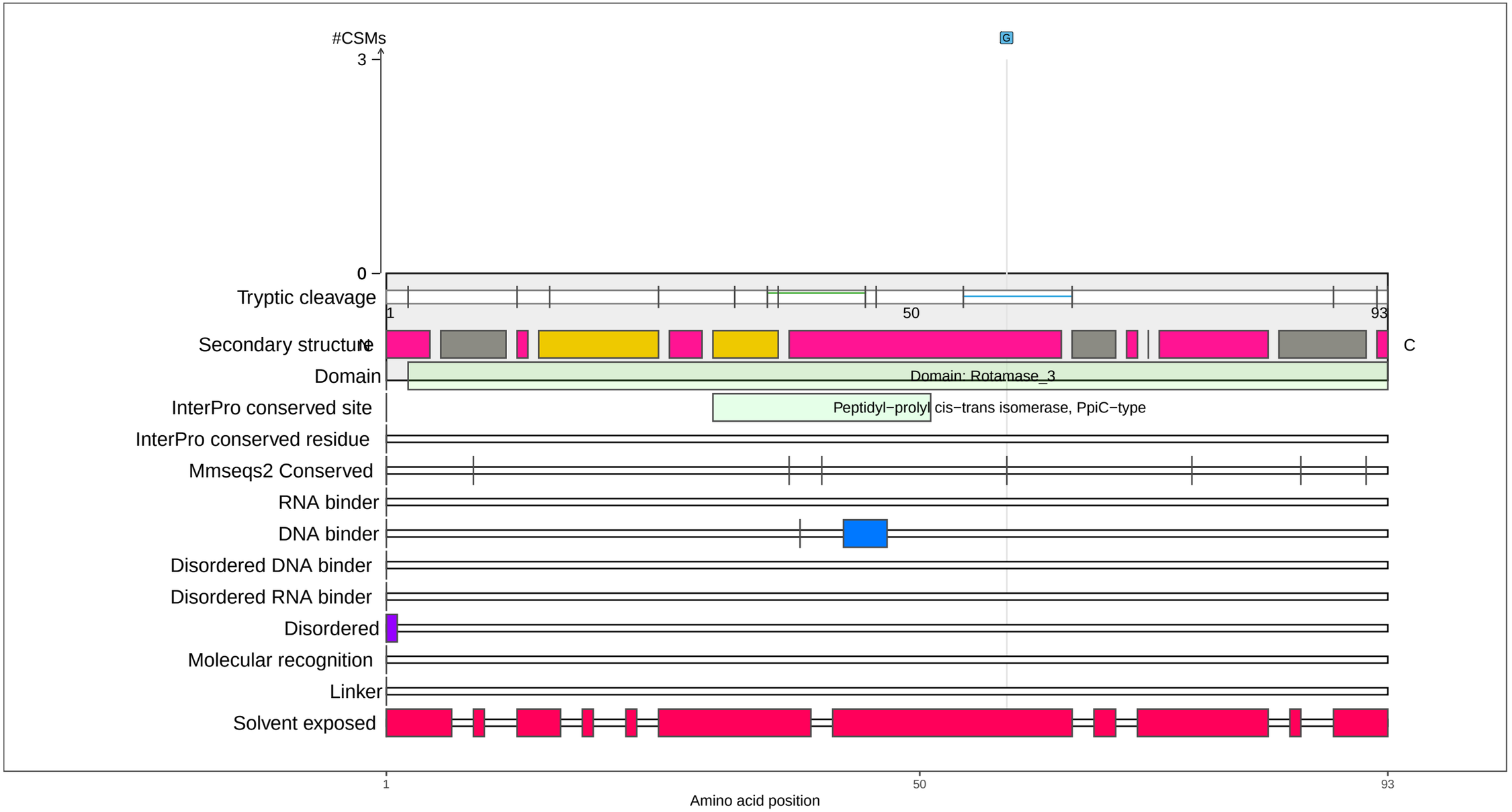
− RNA functions: not annotated

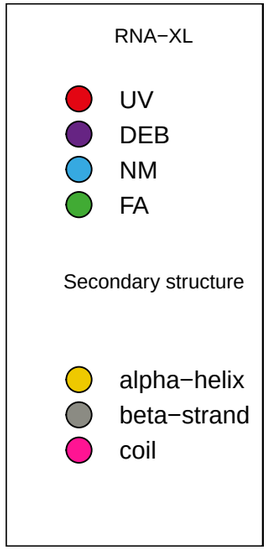


P0A9L5
PPIC_ECOLI Peptidyl−prolyl cis−trans isomerase C

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.59 (Q 88)

− RNA functions: not annotated

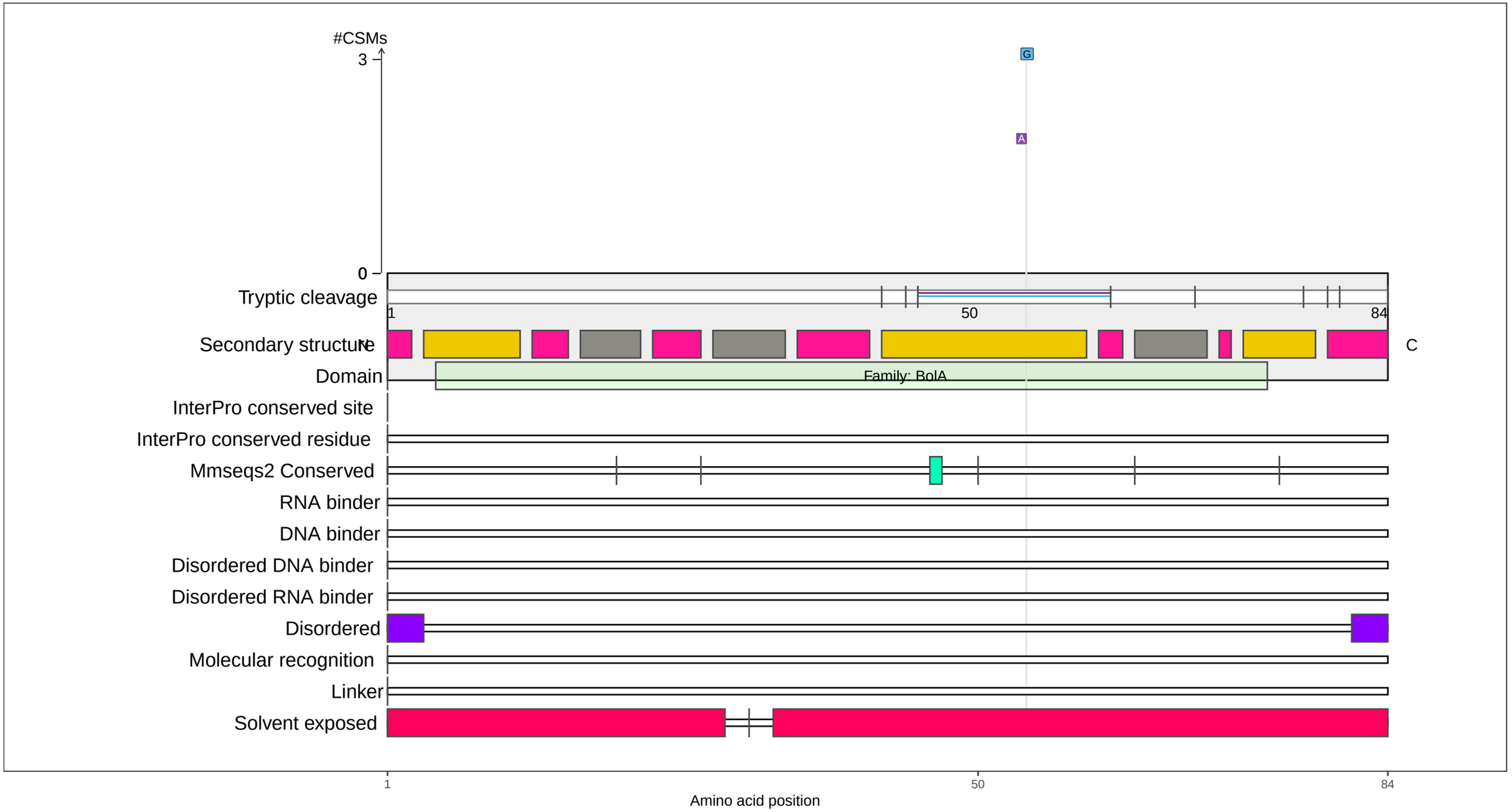


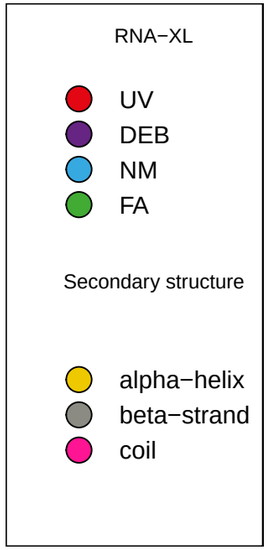


P0A9W6
IBAG_ECOLI Acid stress protein IbaG

− Abundance:
tryptic [log10 Intensity]: 8.09 (Q 61)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 2.62 (Q 88)

− RNA functions: not annotated

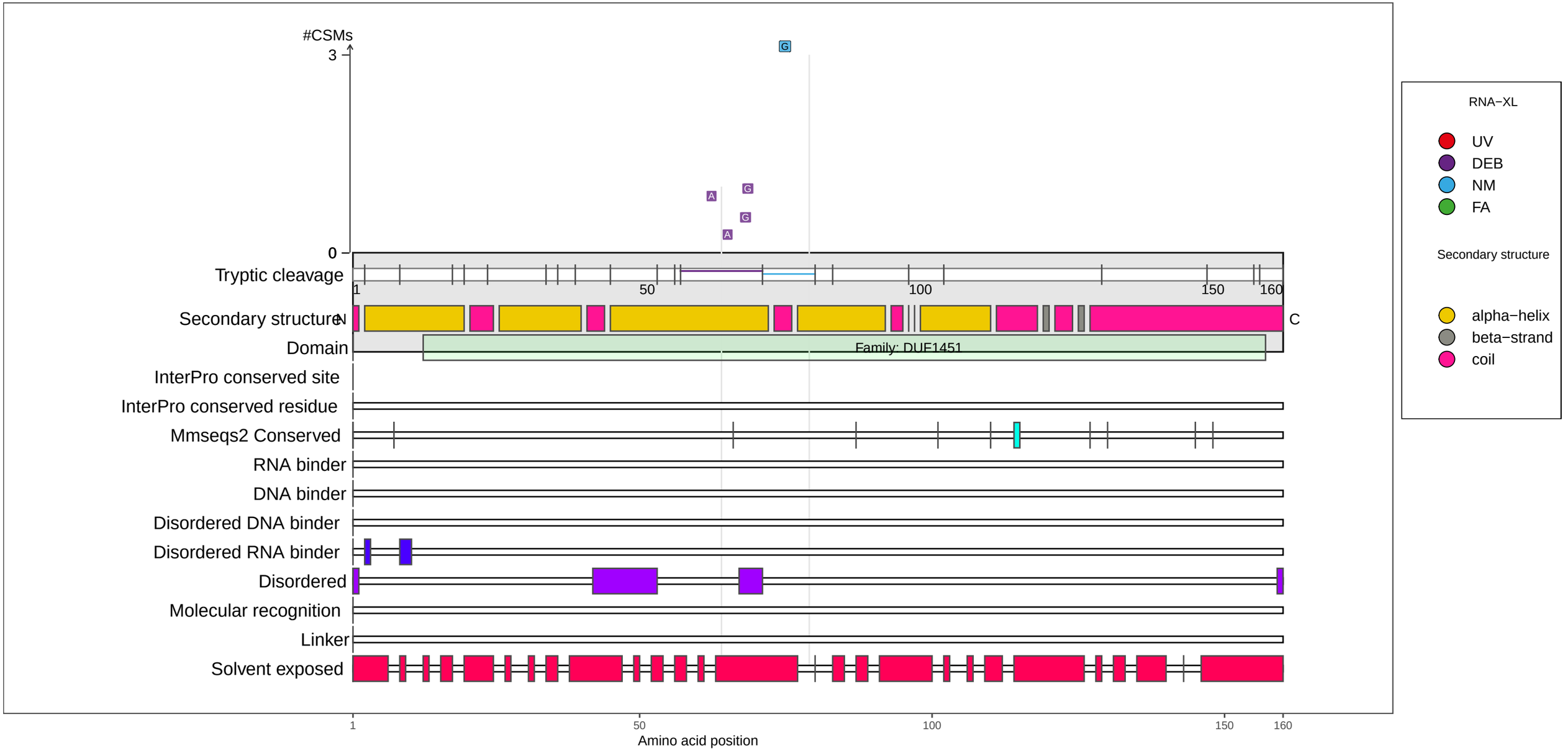




P0AAT9
YBEL_ECOLI Uncharacterized protein YbeL

− Abundance:
tryptic [log10 Intensity]: 7.7 (Q 44)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 2.86 (Q 93)

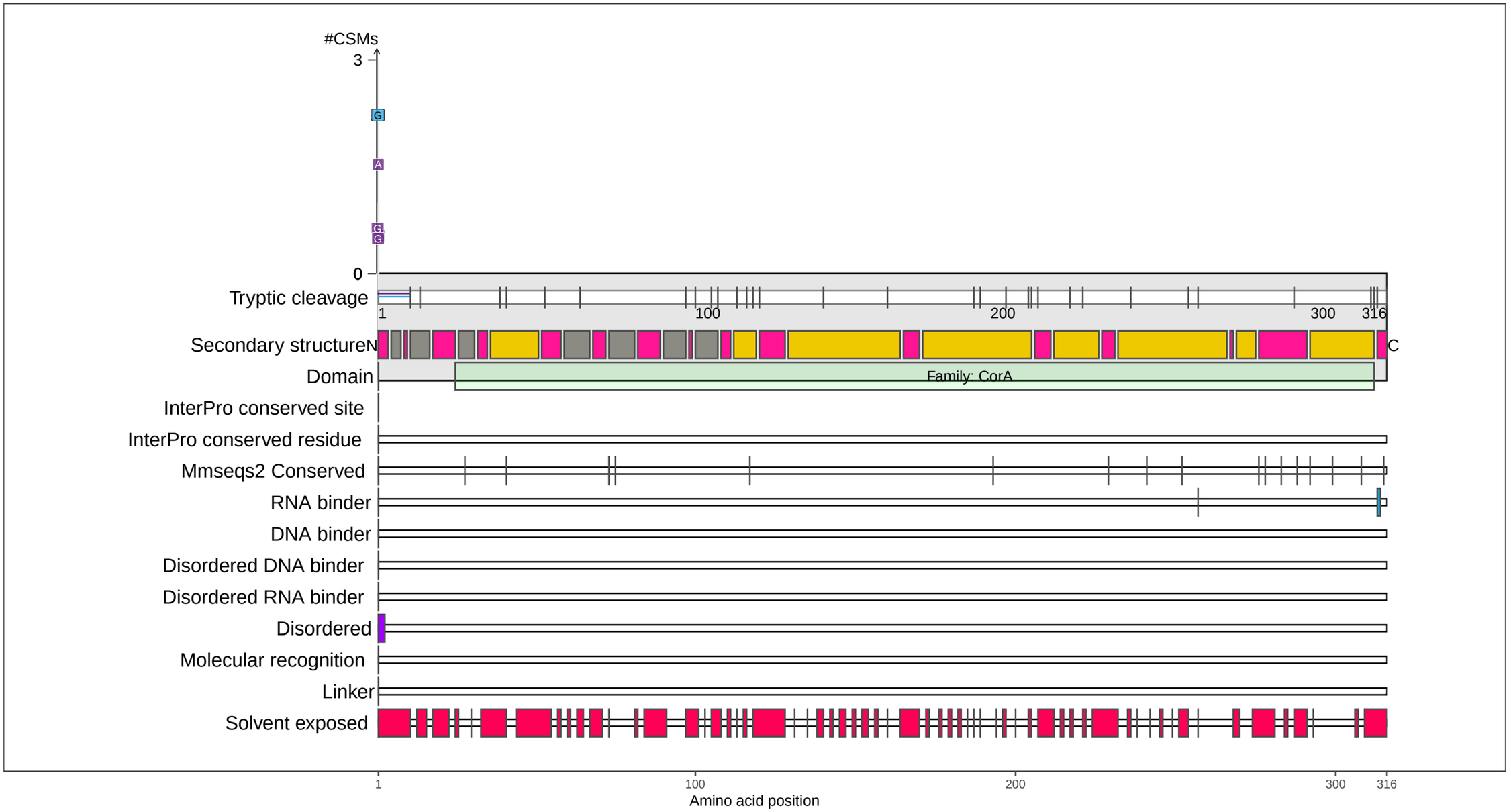
− RNA functions: not annotated



P0ABI4
CORA_ECOLI Magnesium transport protein CorA

− Abundance:
tryptic [log10 Intensity]: 7.13 (Q 18)
PAXdb K12 strain [ppm]: 2.21 (Q 67)
PAXdb E.coli [ppm]: 2.2 (Q 78)

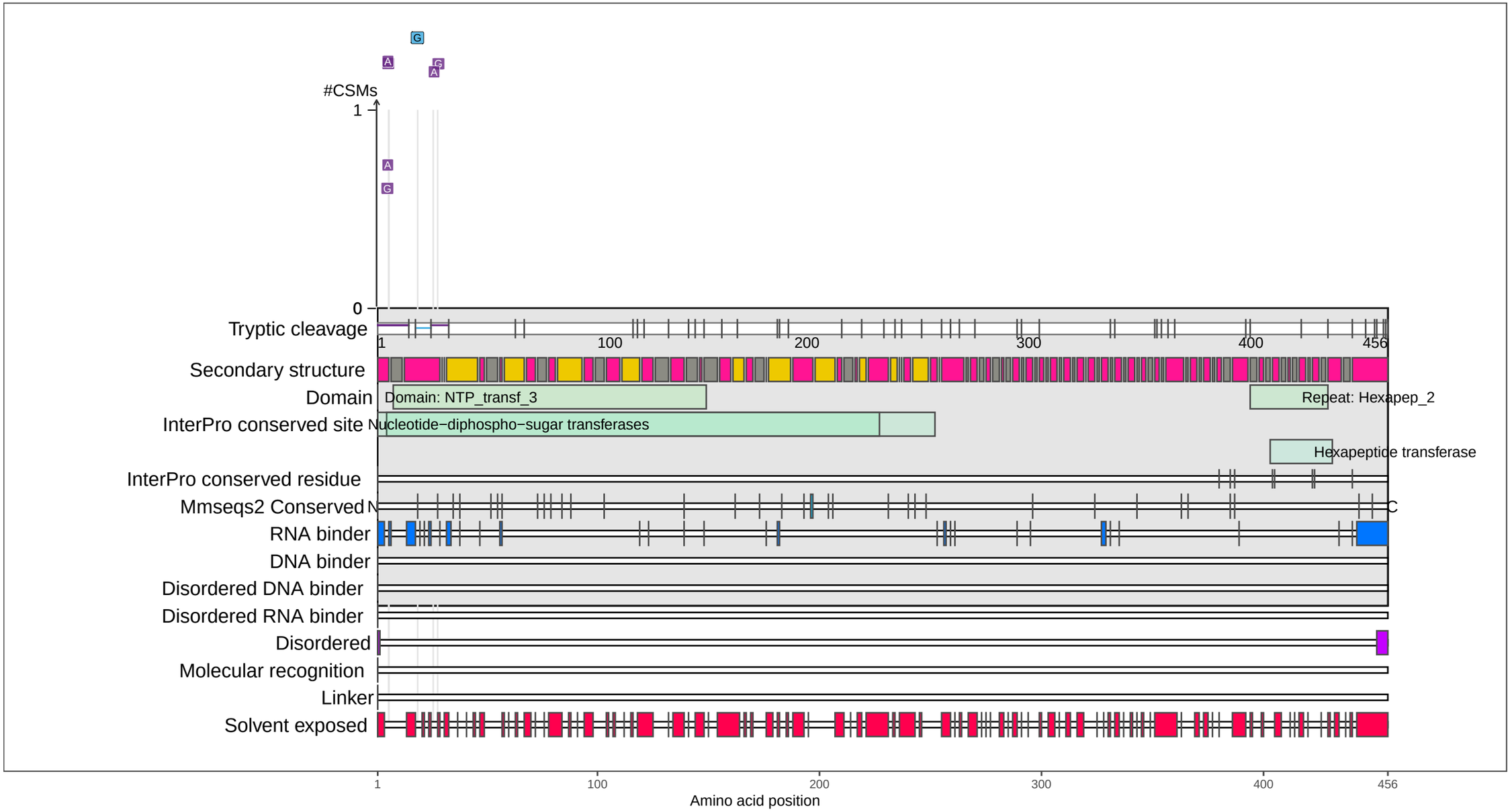
− RNA functions: not annotated



P0ACC7
GLMU_ECOLI Bifunctional protein GlmU

− Abundance:
tryptic [log10 Intensity]: 8.64 (Q 80)
PAXdb K12 strain [ppm]: 1.91 (Q 57)
PAXdb E.coli [ppm]: 2.25 (Q 79)

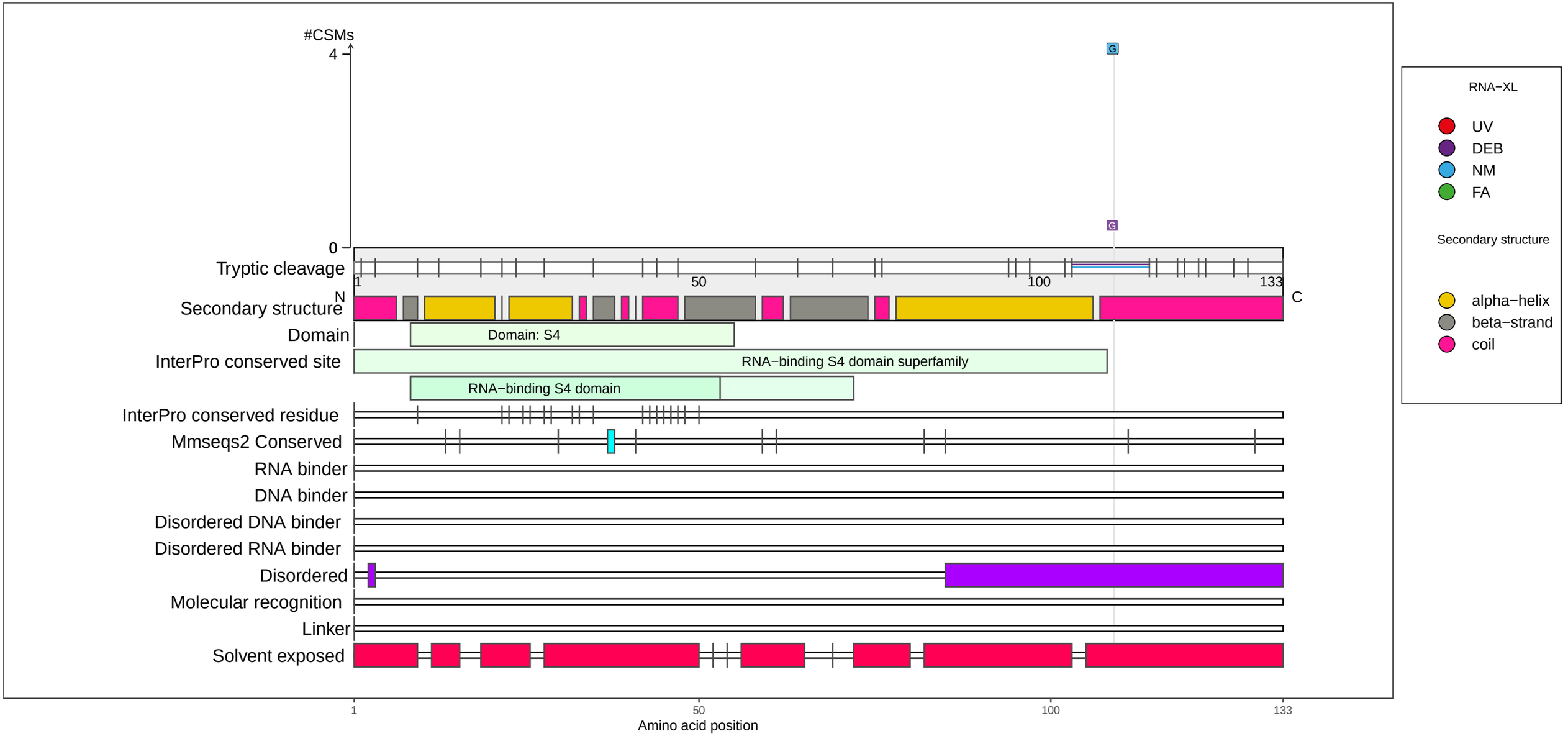
− RNA functions: not annotated



P0ACG8
HSLR_ECOLI Heat shock protein 15

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.82 (Q 68)

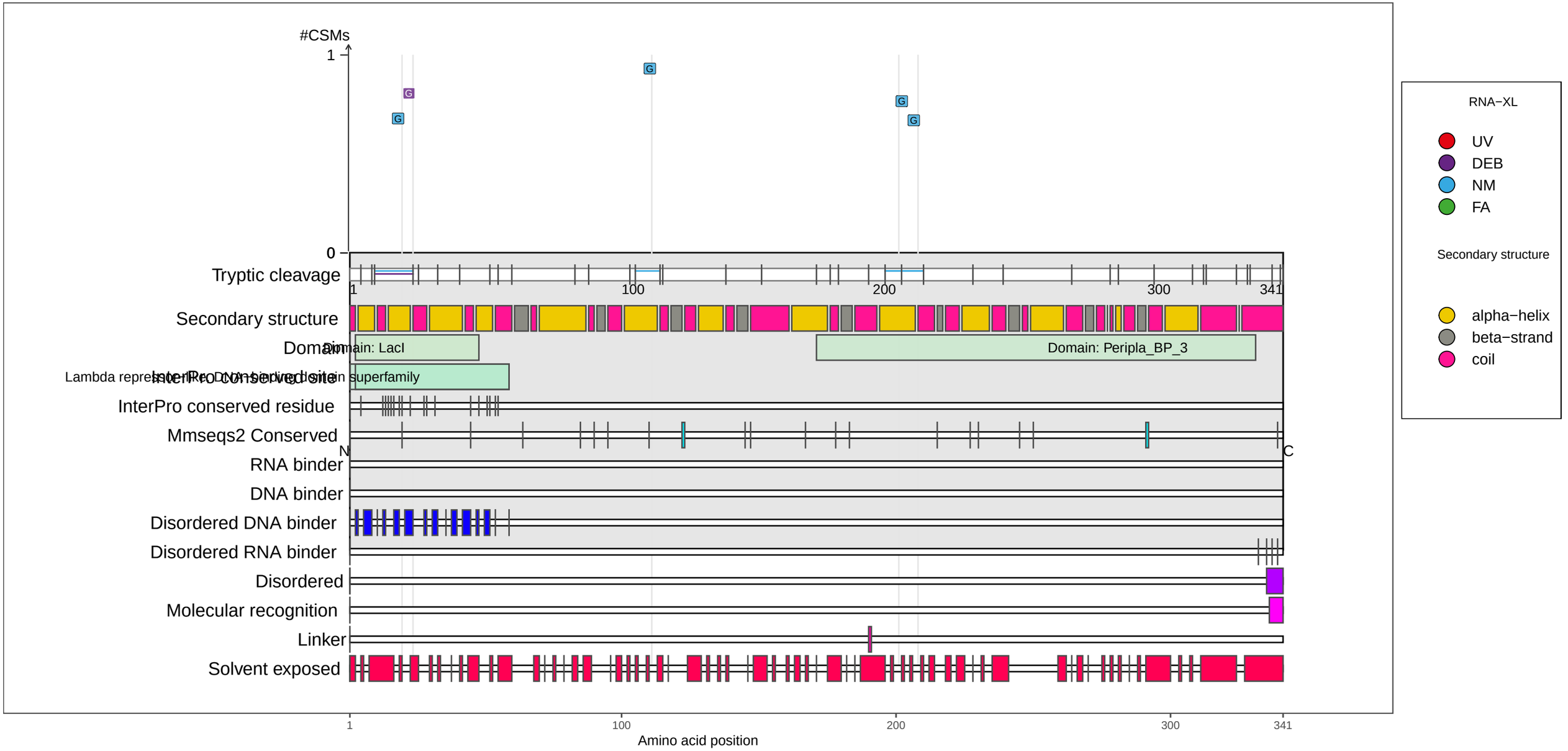
− RNA functions:
RNA binding



P0ACP7
PURR_ECOLI HTH−type transcriptional repressor PurR

− Abundance:
tryptic [log10 Intensity]: 8.03 (Q 59)
PAXdb K12 strain [ppm]: 1.63 (Q 46)
PAXdb E.coli [ppm]: 2.42 (Q 83)

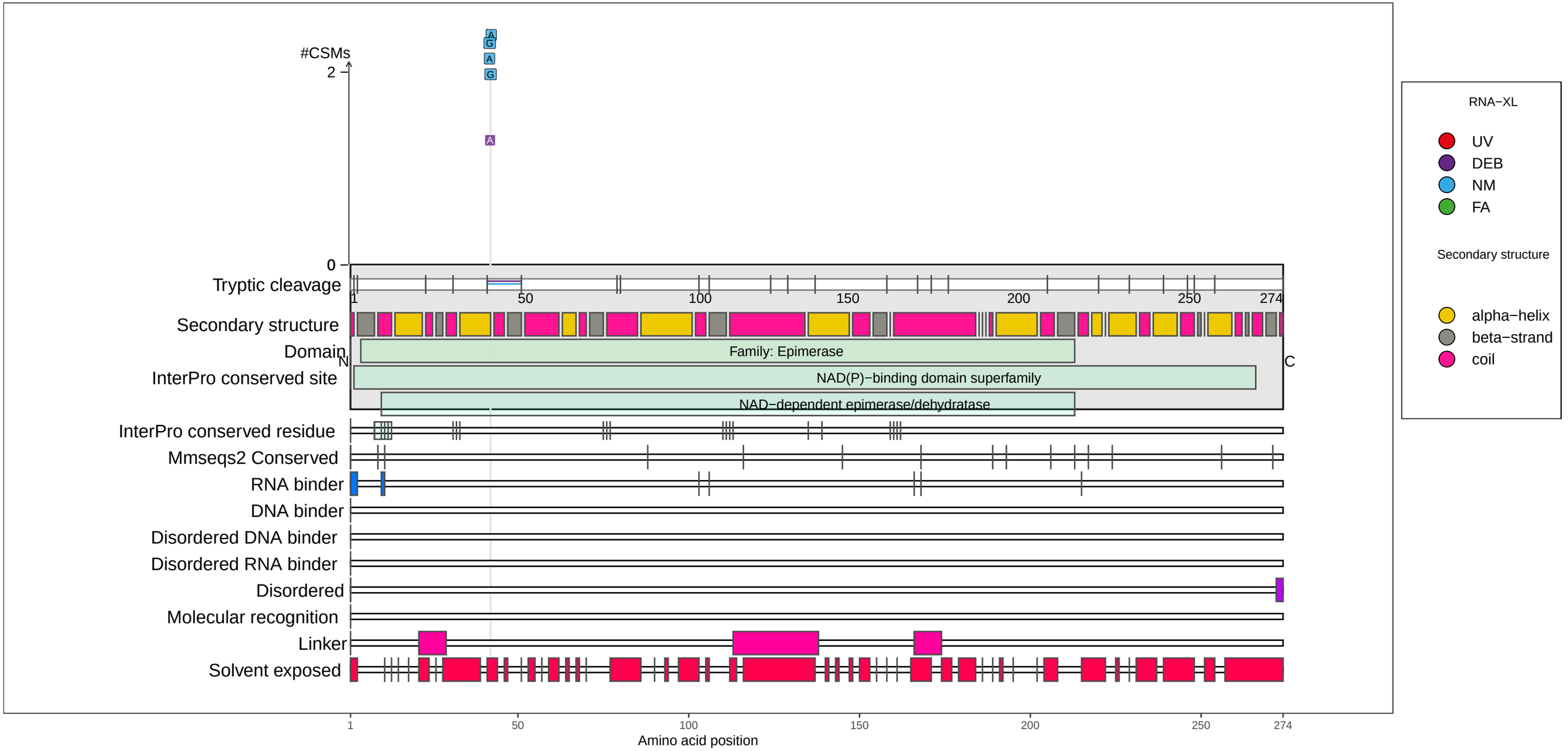
− RNA functions: not annotated



P0AD12
YEEZ_ECOLI Protein YeeZ

− Abundance:
tryptic [log10 Intensity]: 7.32 (Q 26)
PAXdb K12 strain [ppm]: 2.33 (Q 71)
PAXdb E.coli [ppm]: 2.27 (Q 79)

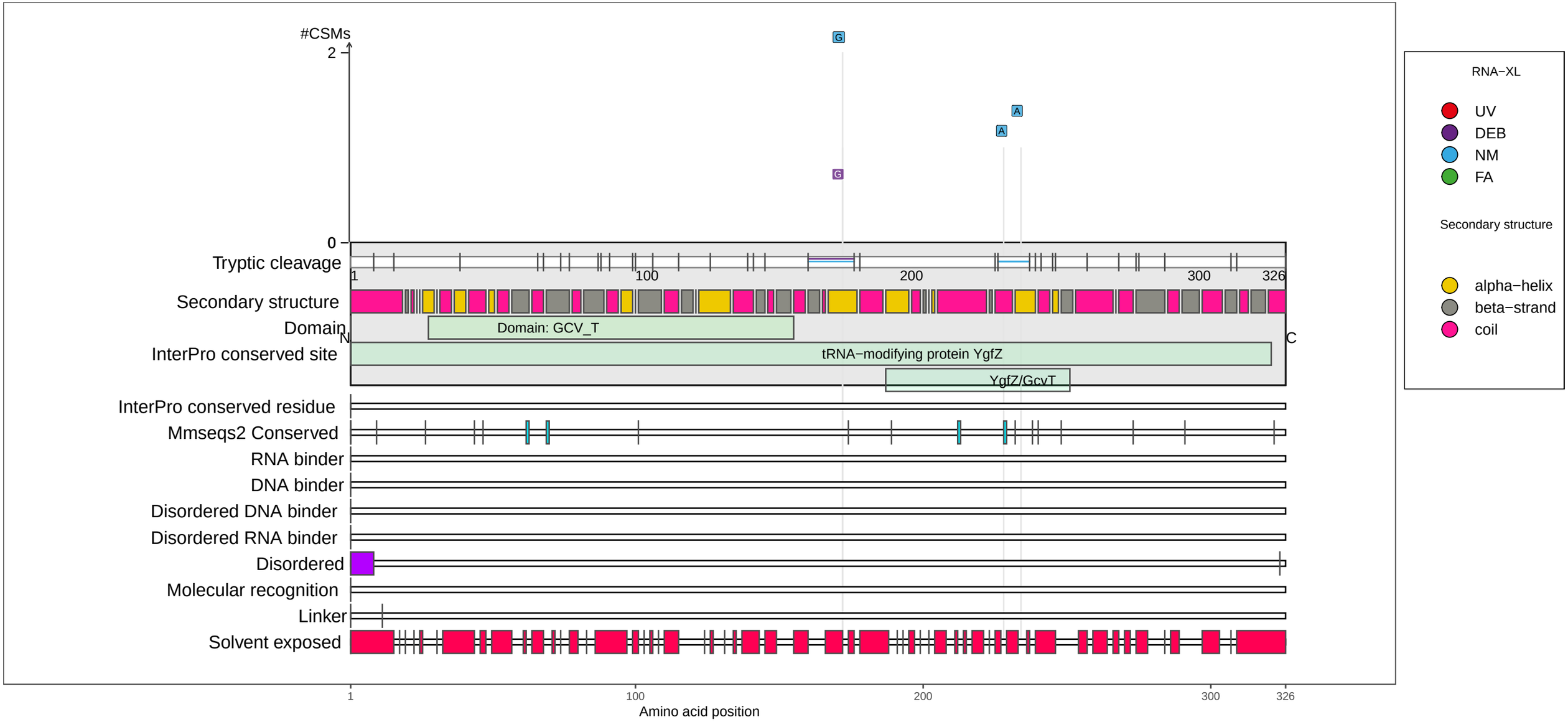
− RNA functions: not annotated



P0ADE8
YGFZ_ECOLI tRNA−modifying protein YgfZ

− Abundance:
tryptic [log10 Intensity]: 8.78 (Q 83)
PAXdb K12 strain [ppm]: 3.19 (Q 94)
PAXdb E.coli [ppm]: 2.64 (Q 89)

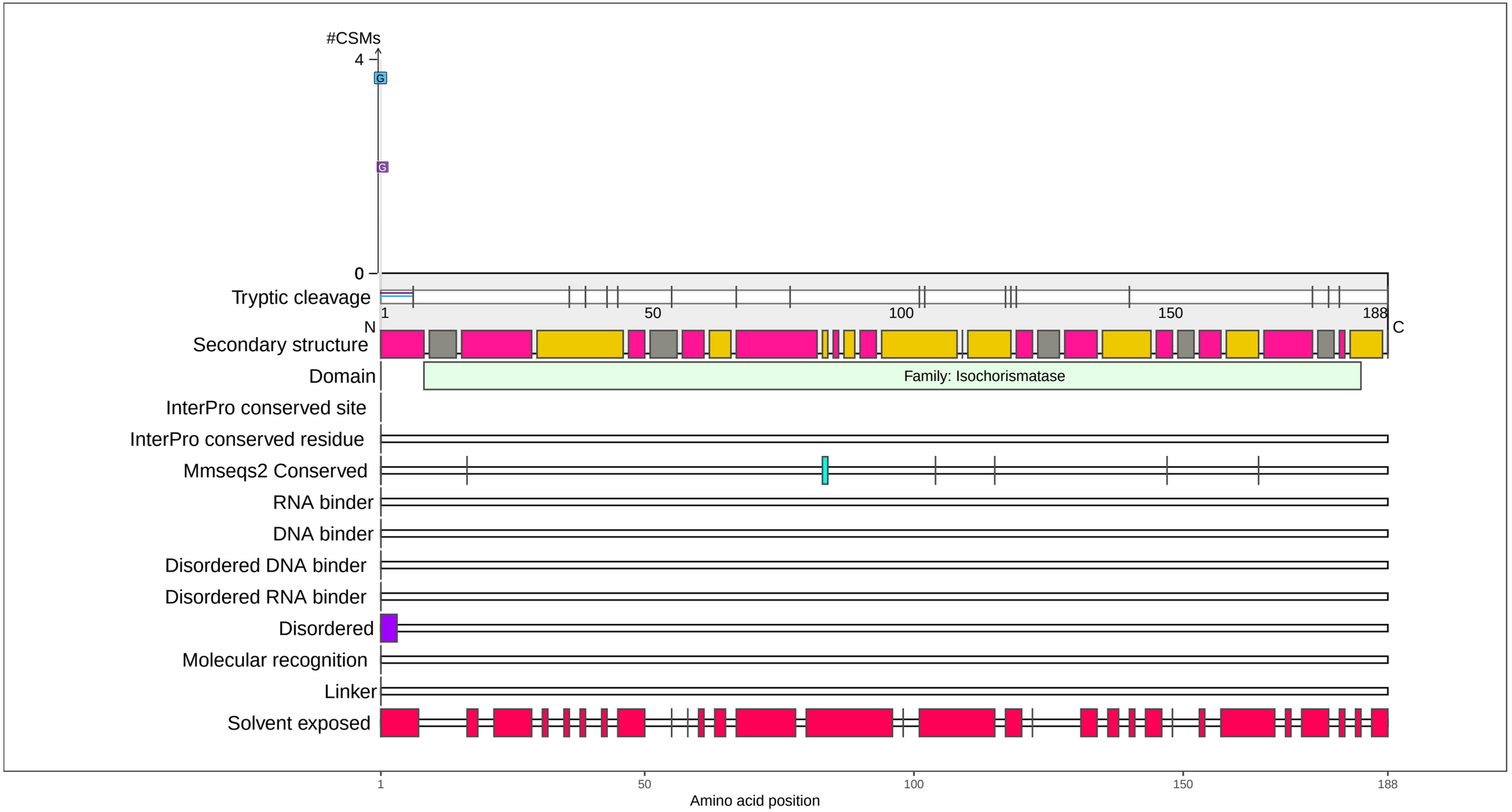
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA processing

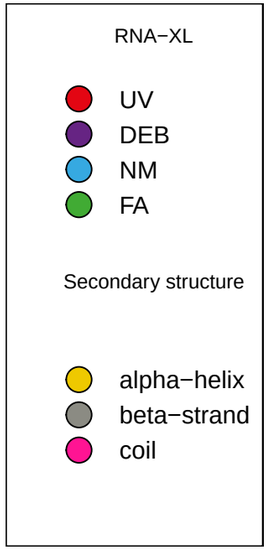


P0ADI7
YECD_ECOLI Isochorismatase family protein YecD

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 51)
PAXdb K12 strain [ppm]: 2.23 (Q 68)
PAXdb E.coli [ppm]: 2.09 (Q 74)

− RNA functions: not annotated

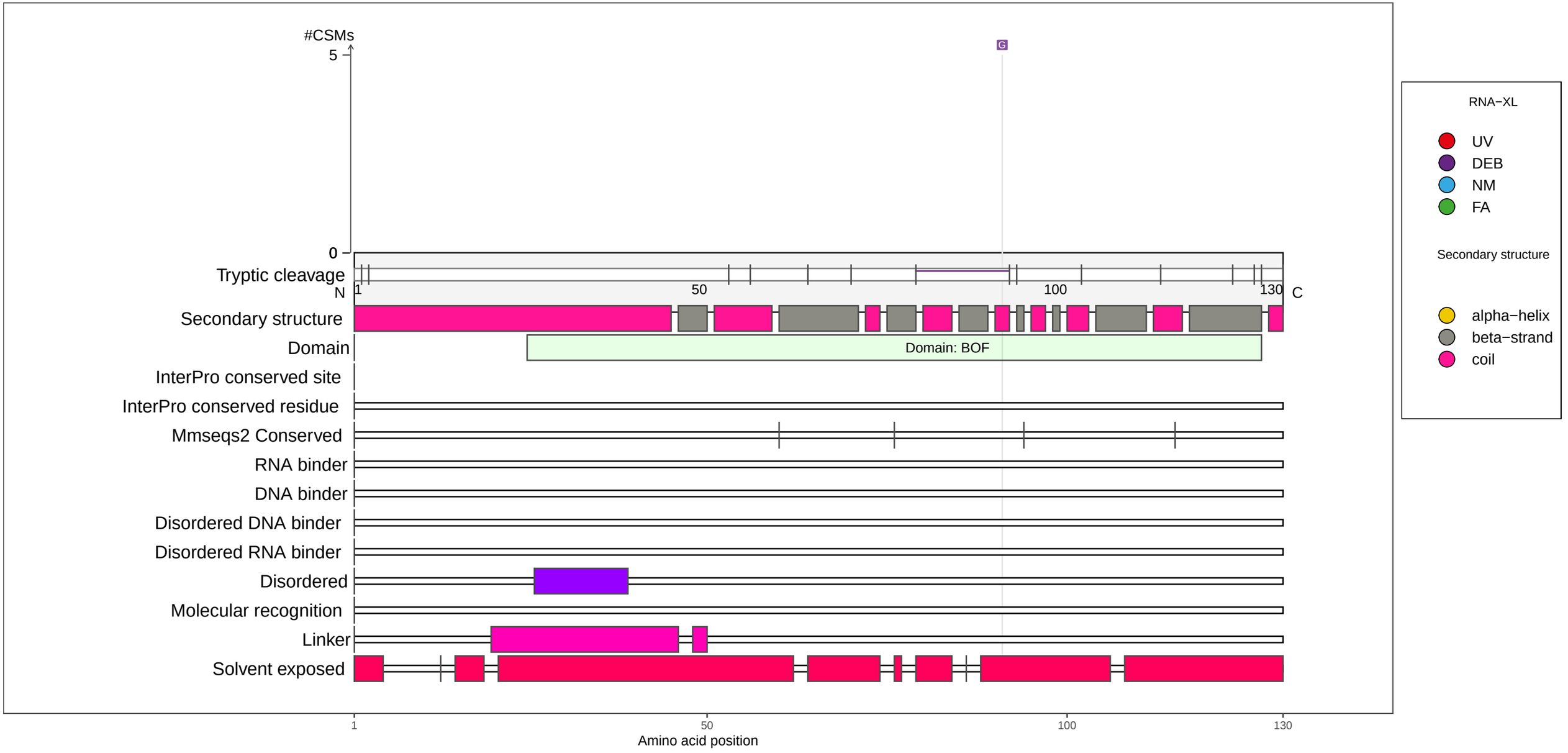




P0ADU5
YGIW_ECOLI Protein YgiW

− Abundance:
tryptic [log10 Intensity]: 8.64 (Q 80)
PAXdb K12 strain [ppm]: 3.41 (Q 96)
PAXdb E.coli [ppm]: 2.83 (Q 92)

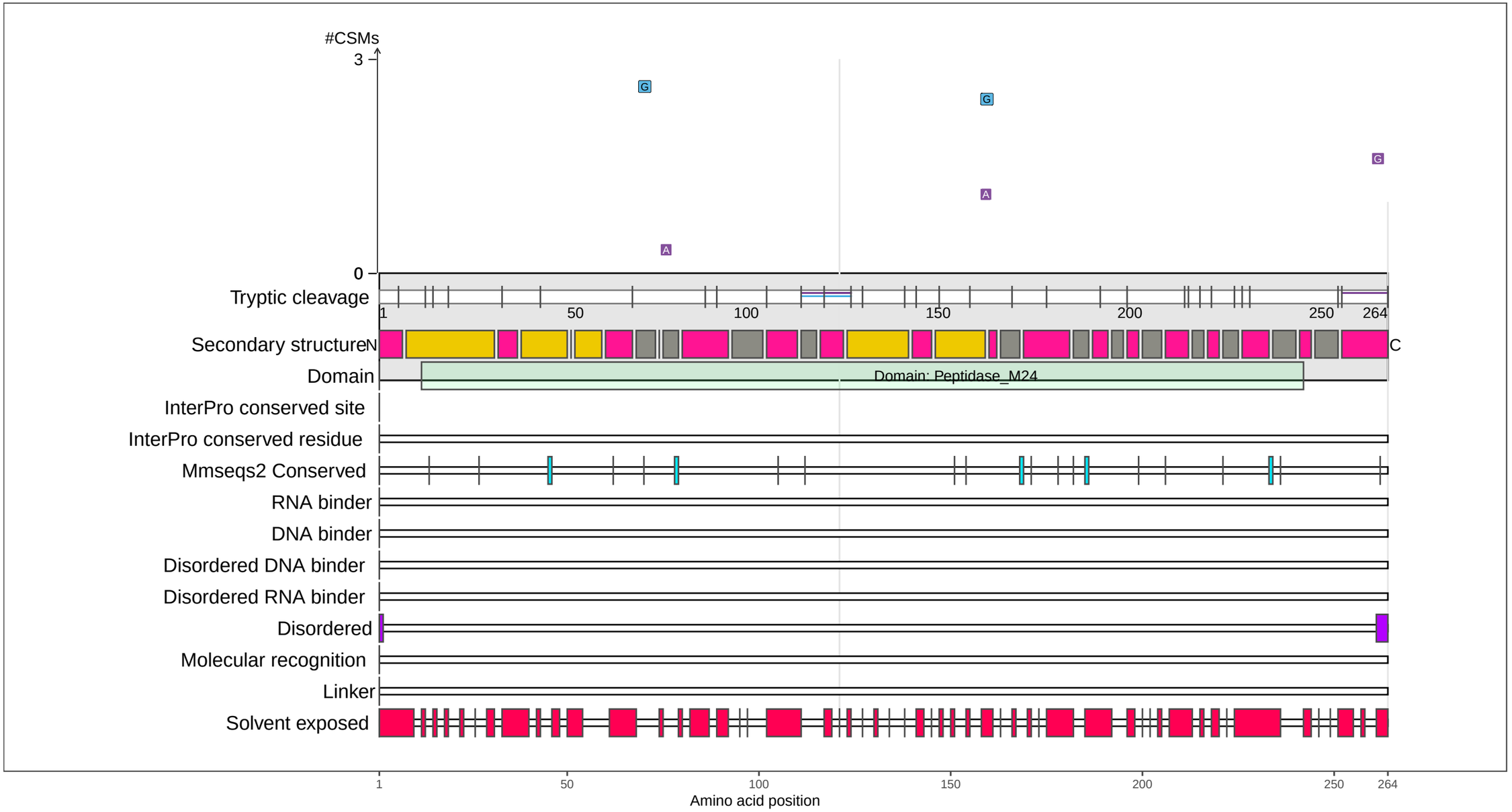
− RNA functions: not annotated



P0AE18
MAP1_ECOLI Methionine aminopeptidase

− Abundance:
tryptic [log10 Intensity]: 9.13 (Q 91)
PAXdb K12 strain [ppm]: 3.18 (Q 94)
PAXdb E.coli [ppm]: 2.71 (Q 90)

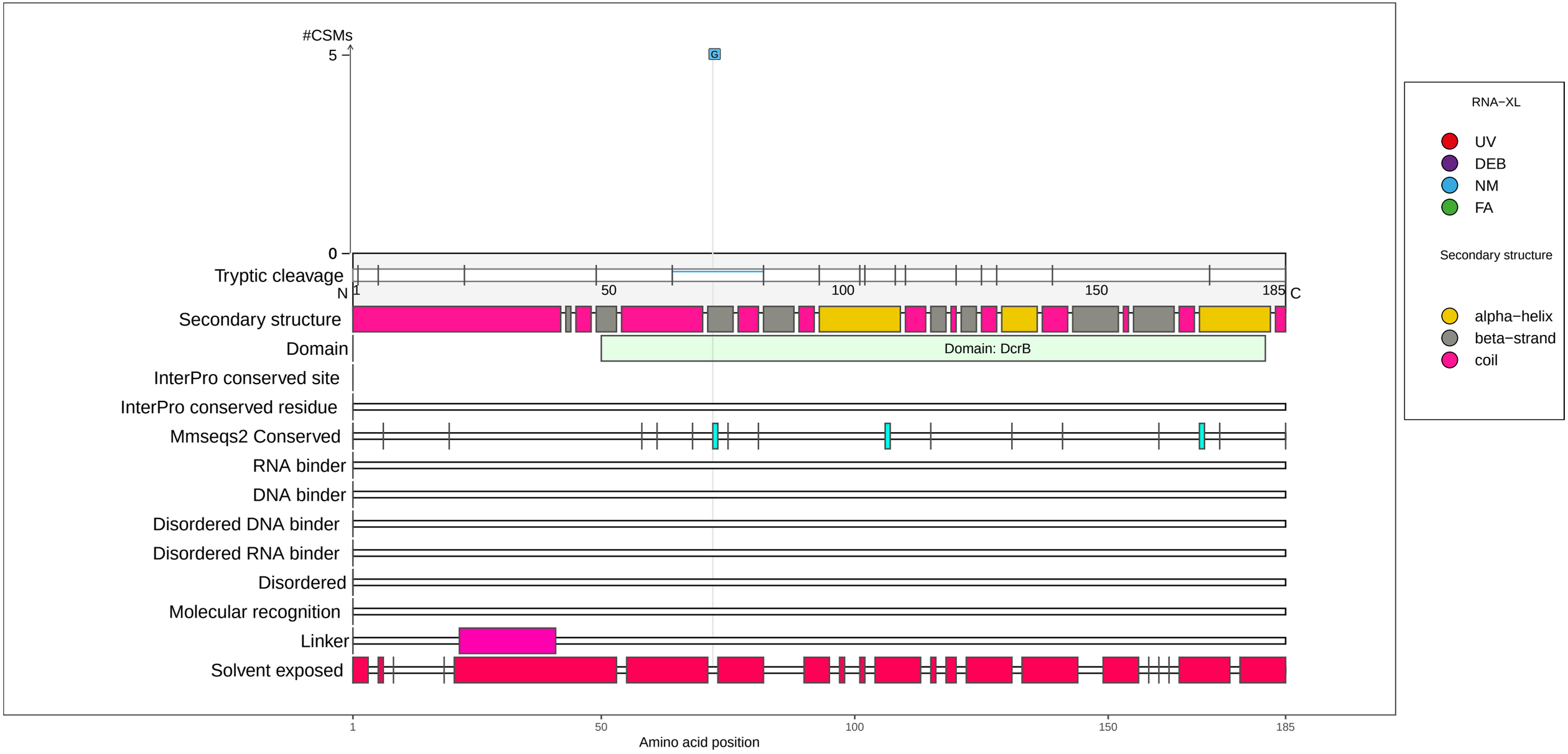
− RNA functions: not annotated



P0AEE1
DCRB_ECOLI Inner membrane lipoprotein DcrB

− Abundance:
tryptic [log10 Intensity]: 8.45 (Q 74)
PAXdb K12 strain [ppm]: 2.5 (Q 78)
PAXdb E.coli [ppm]: 2.44 (Q 84)

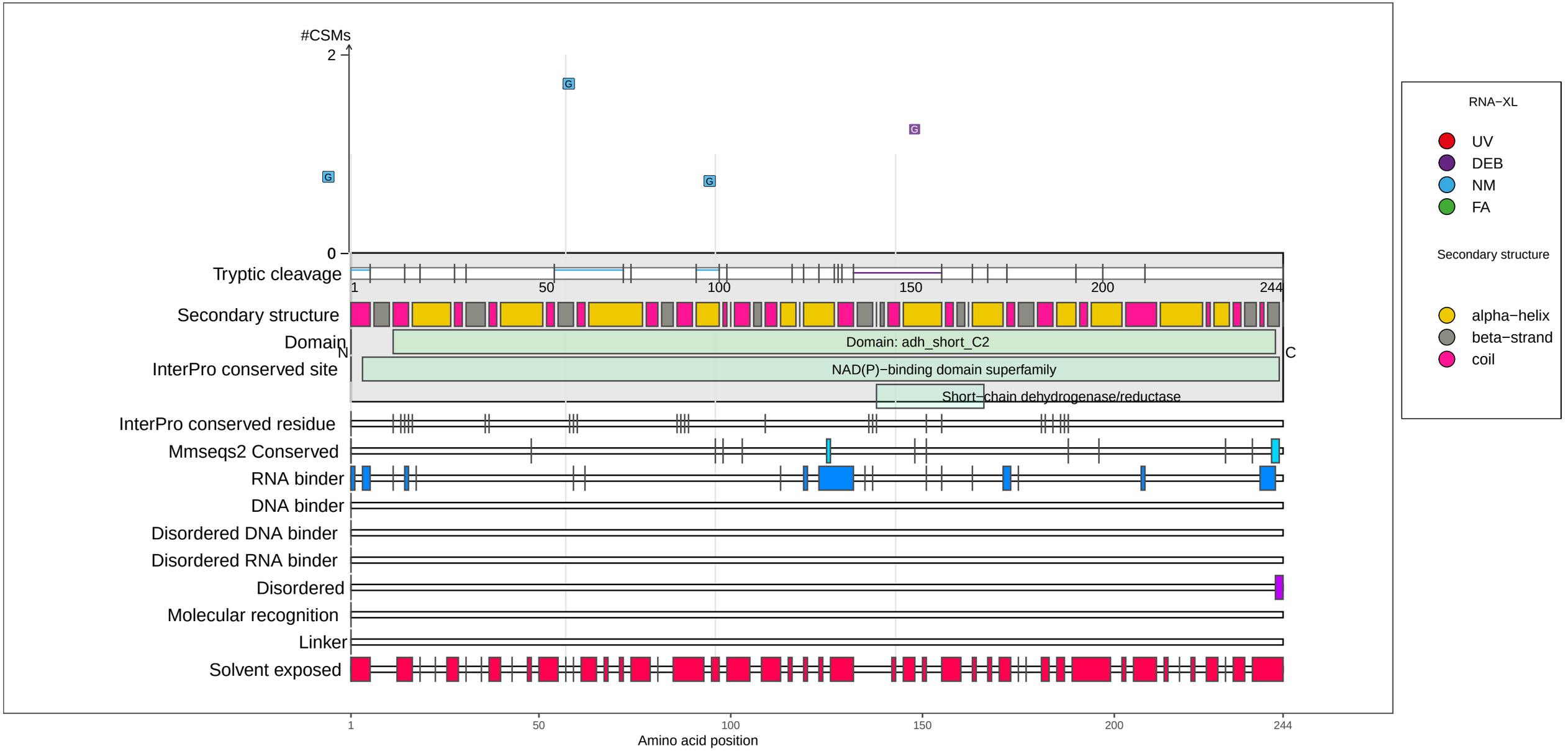
− RNA functions: not annotated



P0AEK2
FABG_ECOLI 3−oxoacyl−[acyl−carrier−protein] reductase FabG

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 3.12 (Q 93)
PAXdb E.coli [ppm]: 3.07 (Q 95)

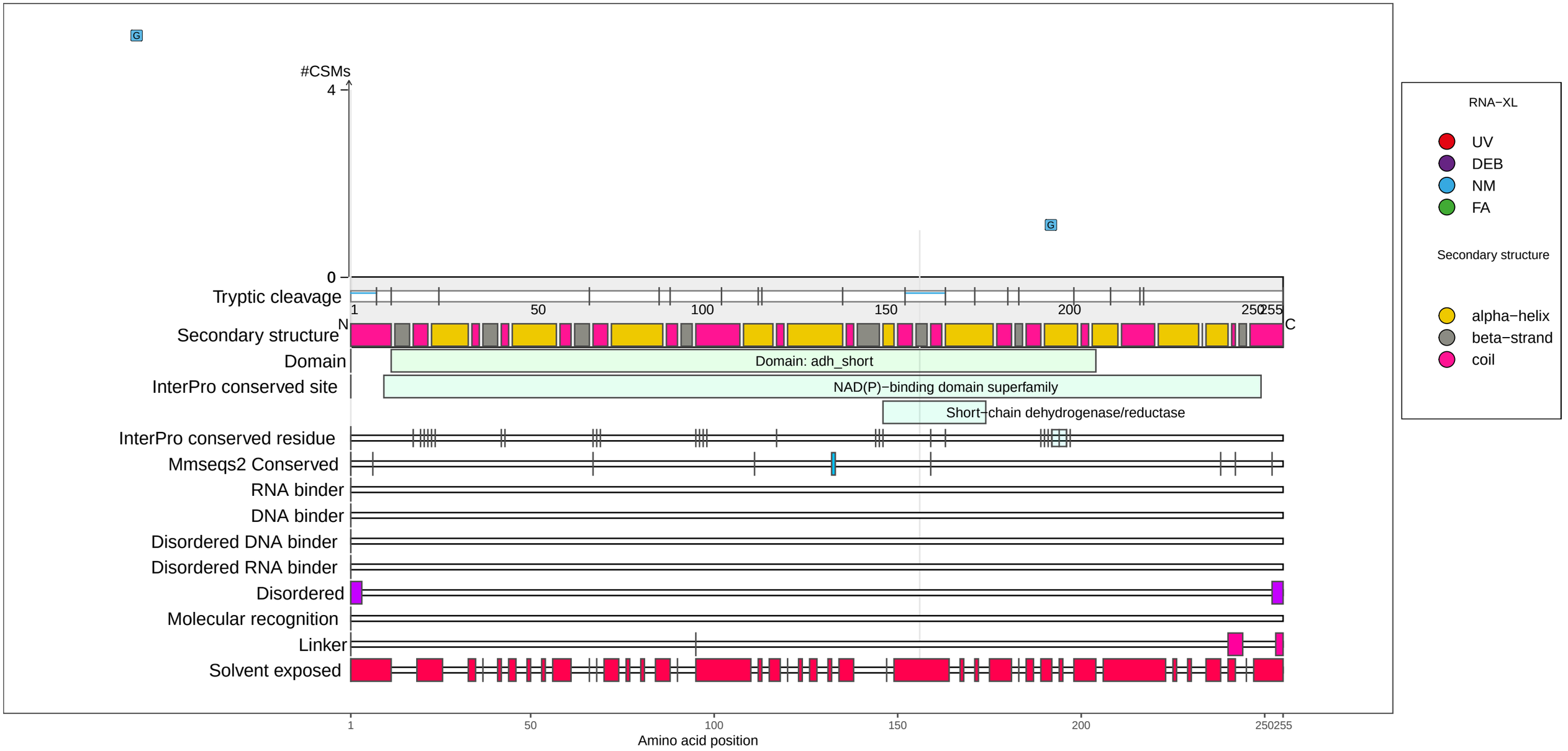
− RNA functions: not annotated



P0AET8
HDHA_ECOLI 7alpha−hydroxysteroid dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 7.35 (Q 27)
PAXdb K12 strain [ppm]: 2.72 (Q 84)
PAXdb E.coli [ppm]: 2.55 (Q 87)

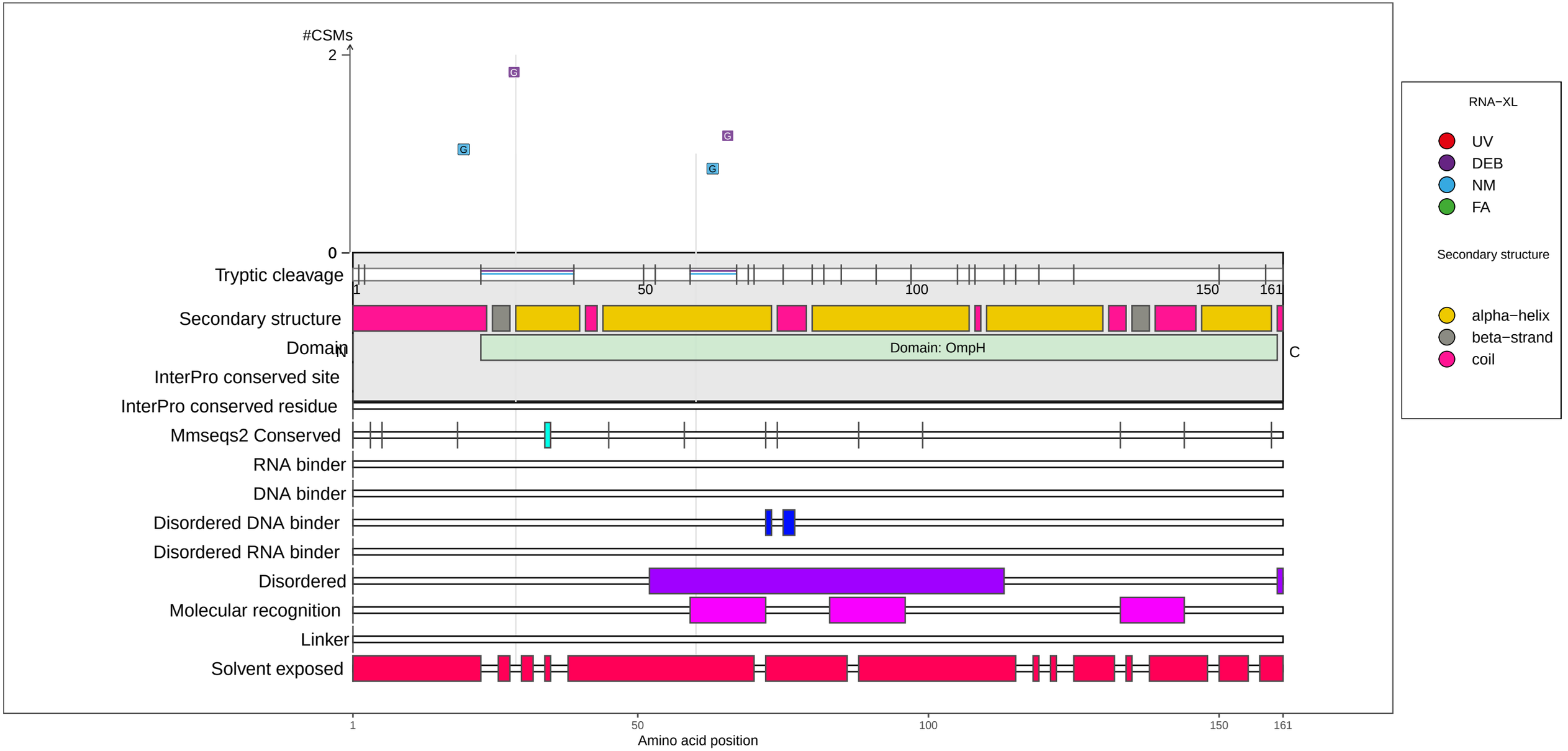
− RNA functions: not annotated



P0AEU7
SKP_ECOLI Chaperone protein Skp

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 3.35 (Q 96)
PAXdb E.coli [ppm]: 3.07 (Q 95)

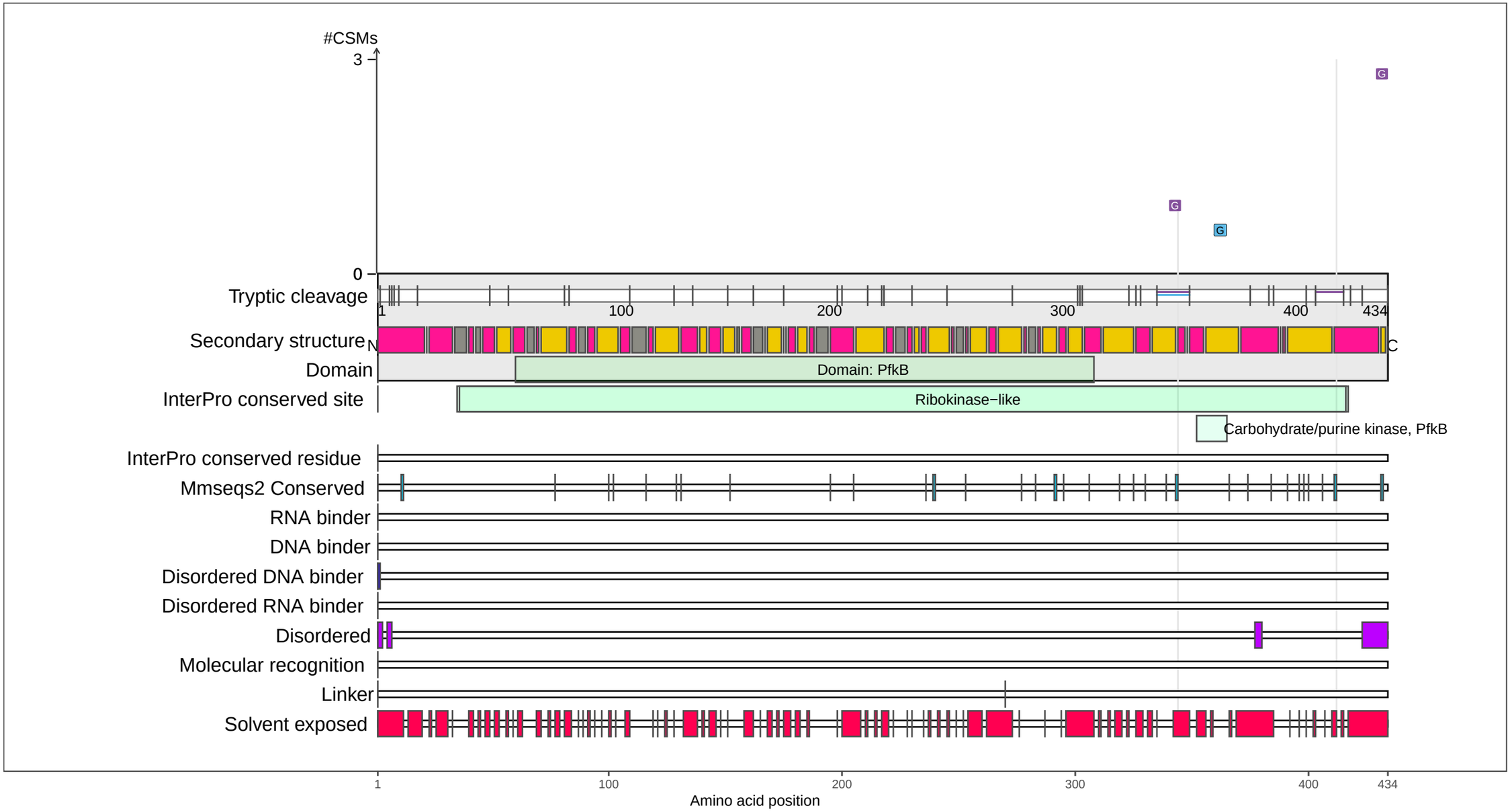
− RNA functions: not annotated

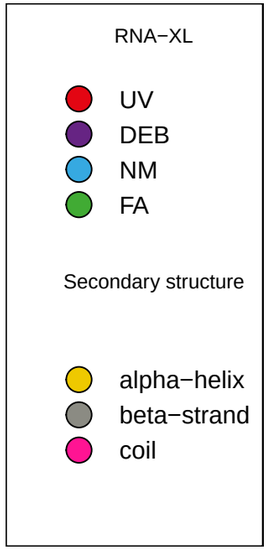


P0AEW6
INGK_ECOLI Guanosine−inosine kinase

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 2.22 (Q 67)
PAXdb E.coli [ppm]: 0.99 (Q 47)

− RNA functions: not annotated

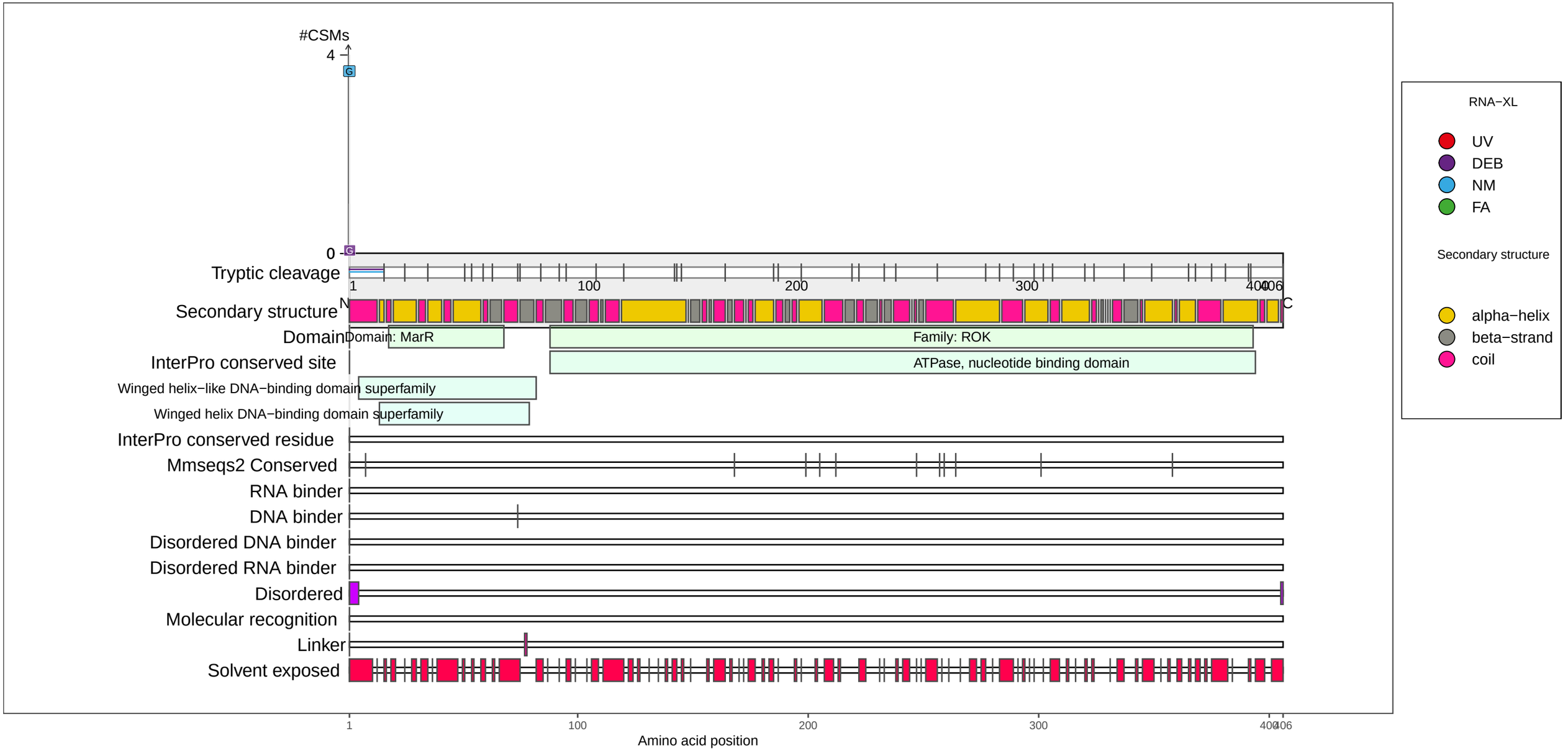




P0AF20
NAGC_ECOLI N−acetylglucosamine repressor

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 2.08 (Q 74)

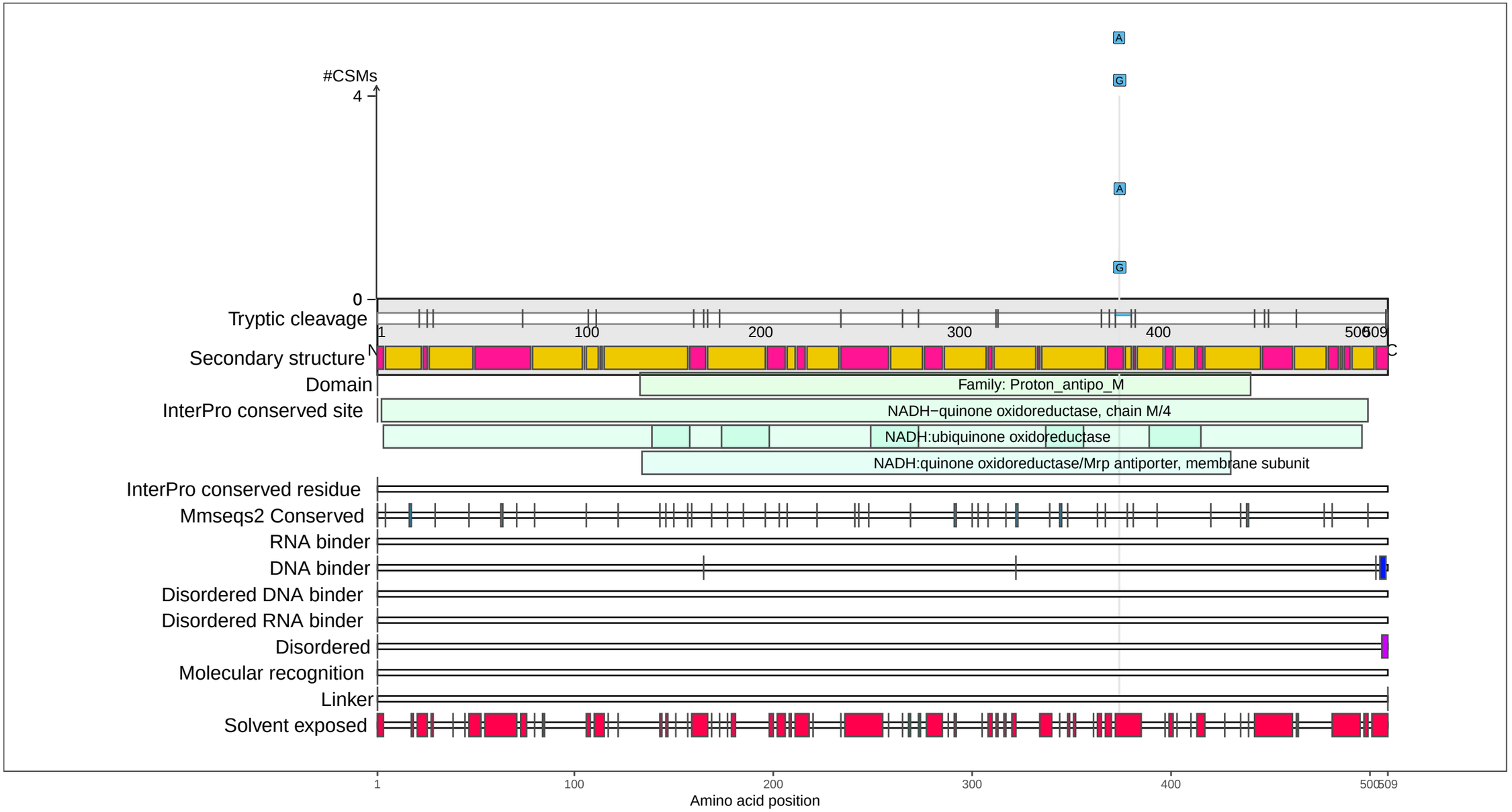
− RNA functions: not annotated



P0AFE8
NUOM_ECOLI NADH−quinone oxidoreductase subunit M

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.46 (Q 35)

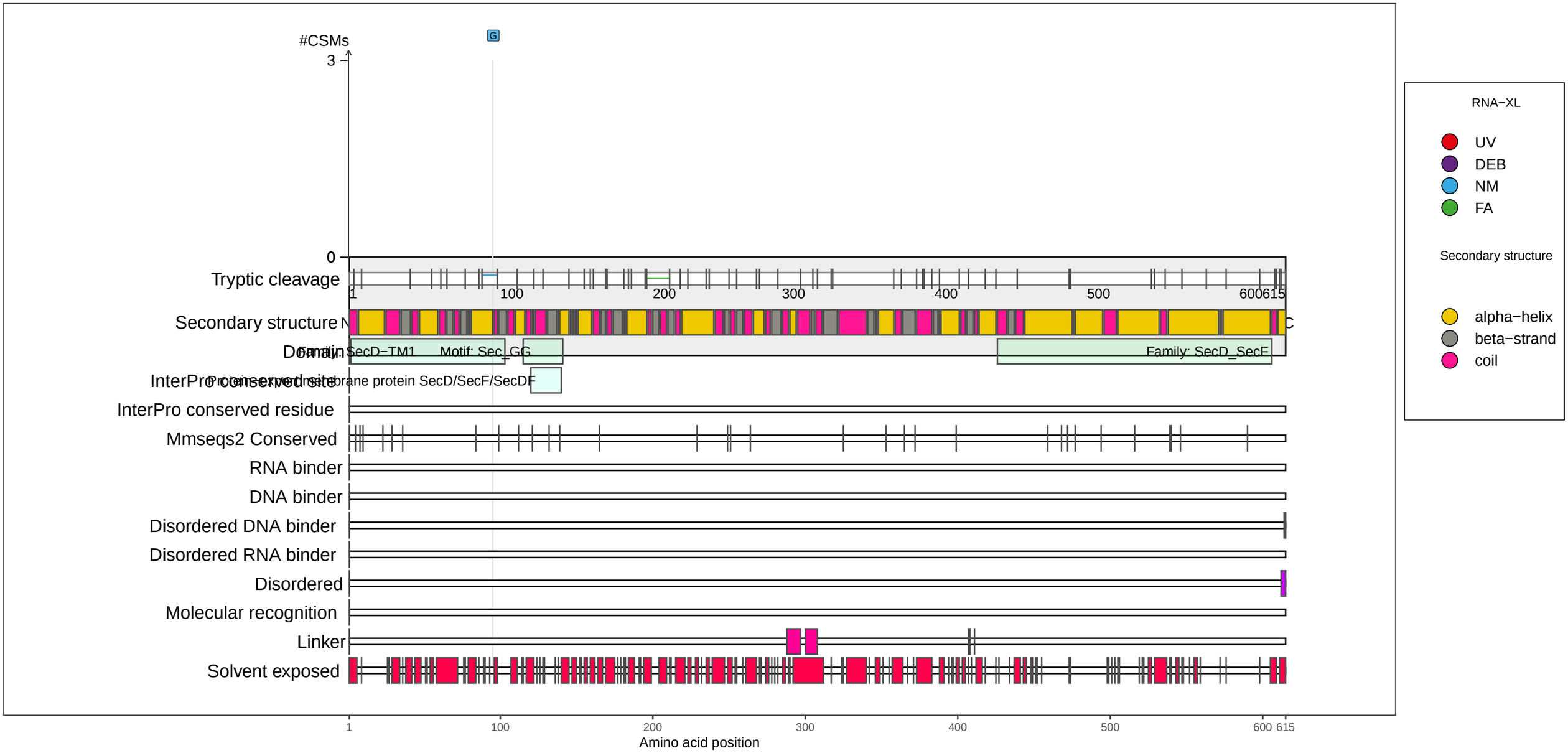
− RNA functions: not annotated



P0AG90
SECD_ECOLI Protein translocase subunit SecD

− Abundance:
tryptic [log10 Intensity]: 7.42 (Q 31)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 2 (Q 72)

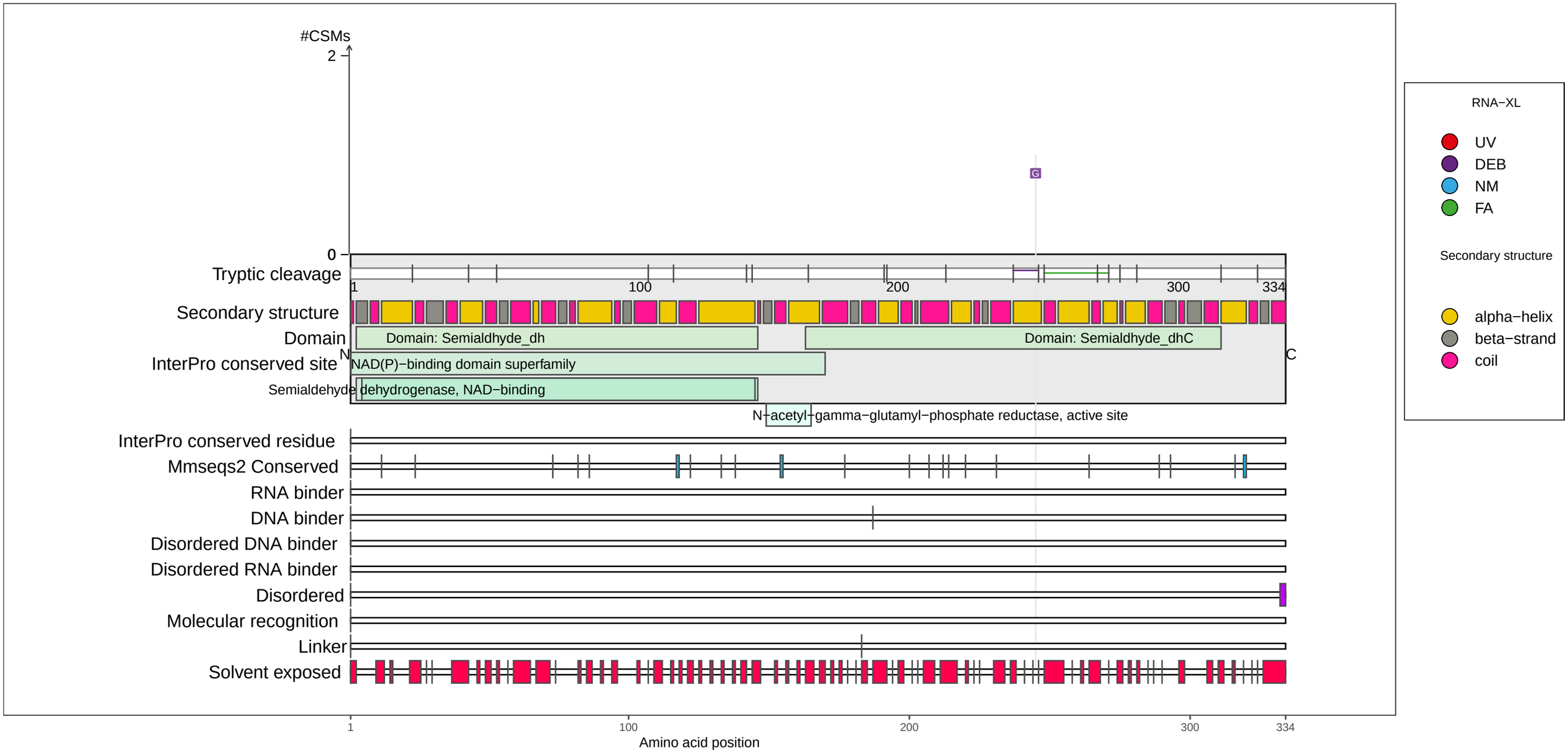
− RNA functions: not annotated



P11446
ARGC_ECOLI N−acetyl−gamma−glutamyl−phosphate reductase

− Abundance:
tryptic [log10 Intensity]: 8.32 (Q 70)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.27 (Q 54)

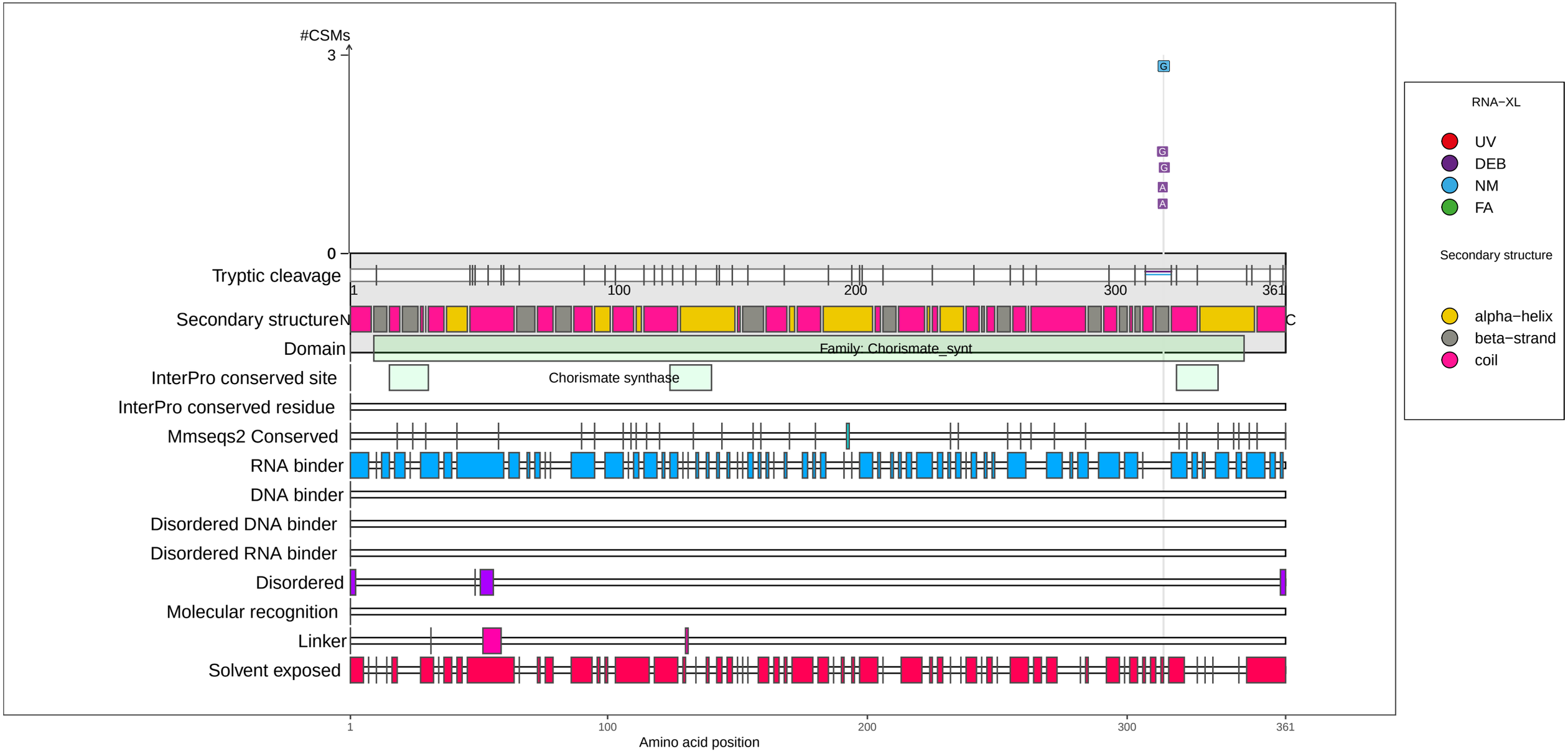
− RNA functions: not annotated



P12008
AROC_ECOLI Chorismate synthase

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: 2.17 (Q 66)
PAXdb E.coli [ppm]: 1.98 (Q 72)

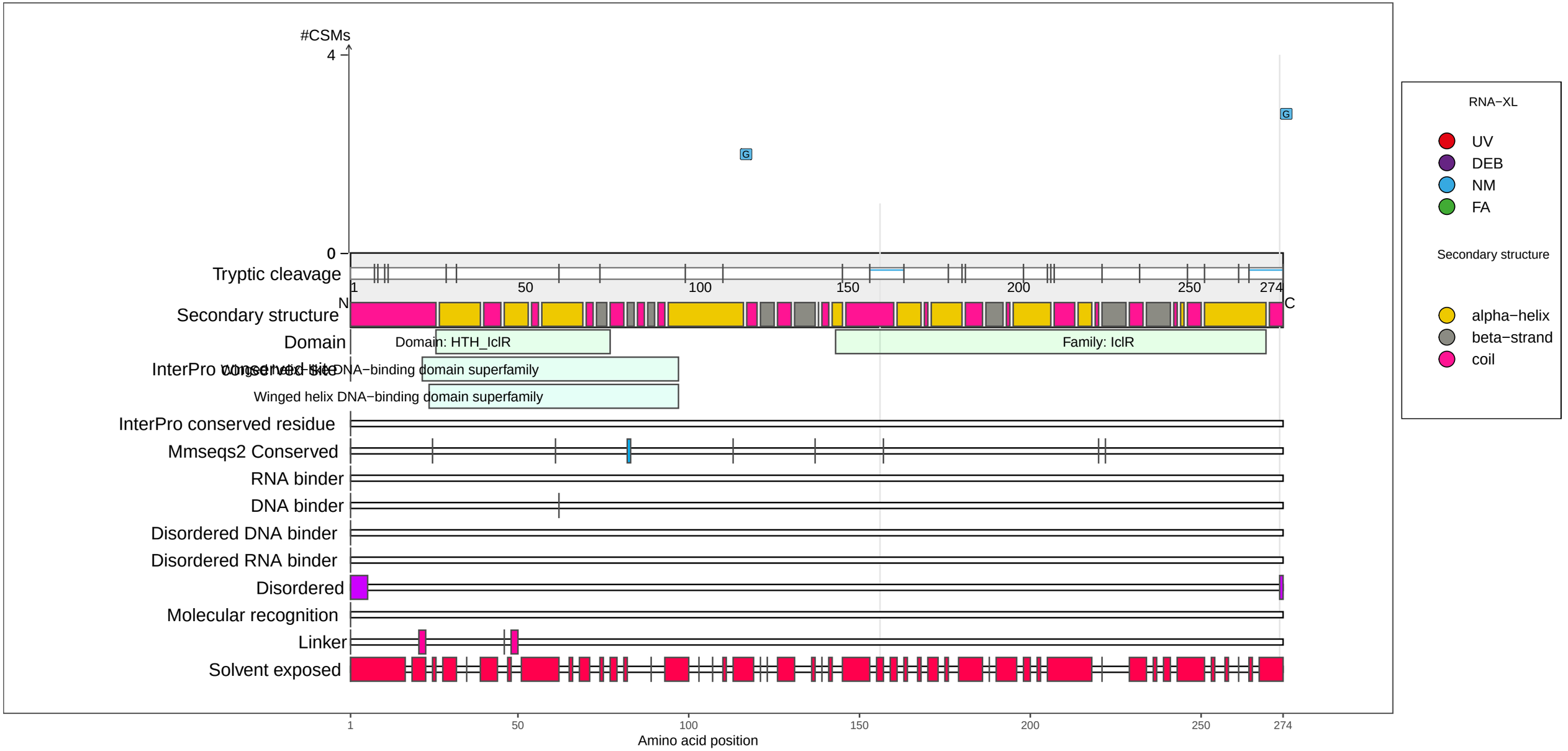
− RNA functions: not annotated



P16528
ICLR_ECOLI Transcriptional repressor IclR

− Abundance:
tryptic [log10 Intensity]: 7.45 (Q 33)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.33 (Q 32)

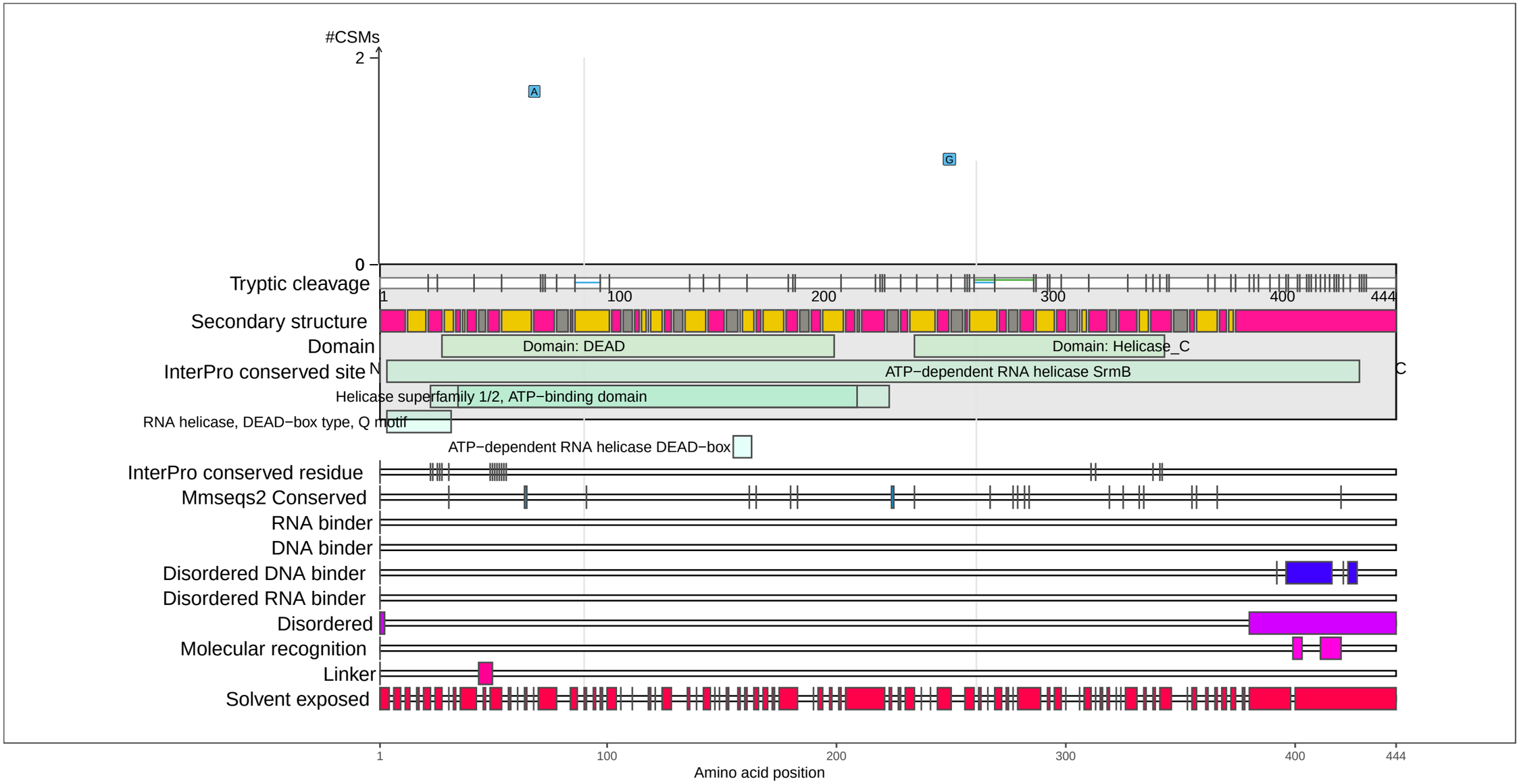
− RNA functions: not annotated

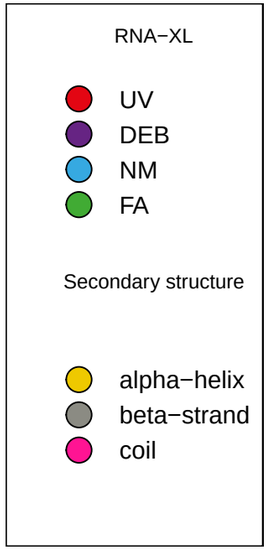


P21507
SRMB_ECOLI ATP−dependent RNA helicase SrmB

− Abundance:
tryptic [log10 Intensity]: 7.75 (Q 46)
PAXdb K12 strain [ppm]: 2.34 (Q 71)
PAXdb E.coli [ppm]: 2.02 (Q 73)

− RNA functions:
RNA binding; RNA helicase activity; RNA strand annealing activity
RNA−dependent ATPase activity

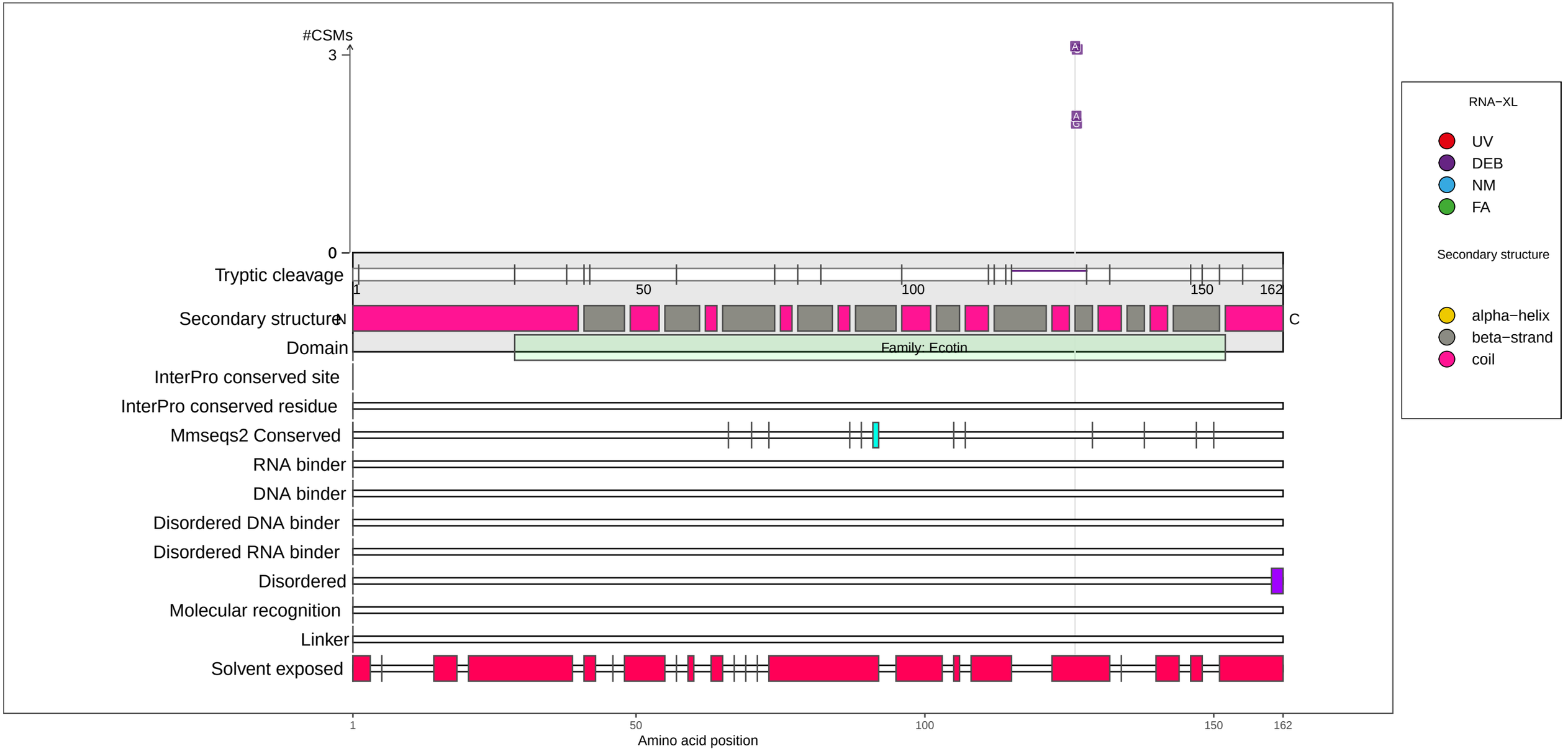




P23827
ECOT_ECOLI Ecotin

− Abundance:
tryptic [log10 Intensity]: 8.19 (Q 65)
PAXdb K12 strain [ppm]: 2.58 (Q 80)
PAXdb E.coli [ppm]: 1.57 (Q 61)

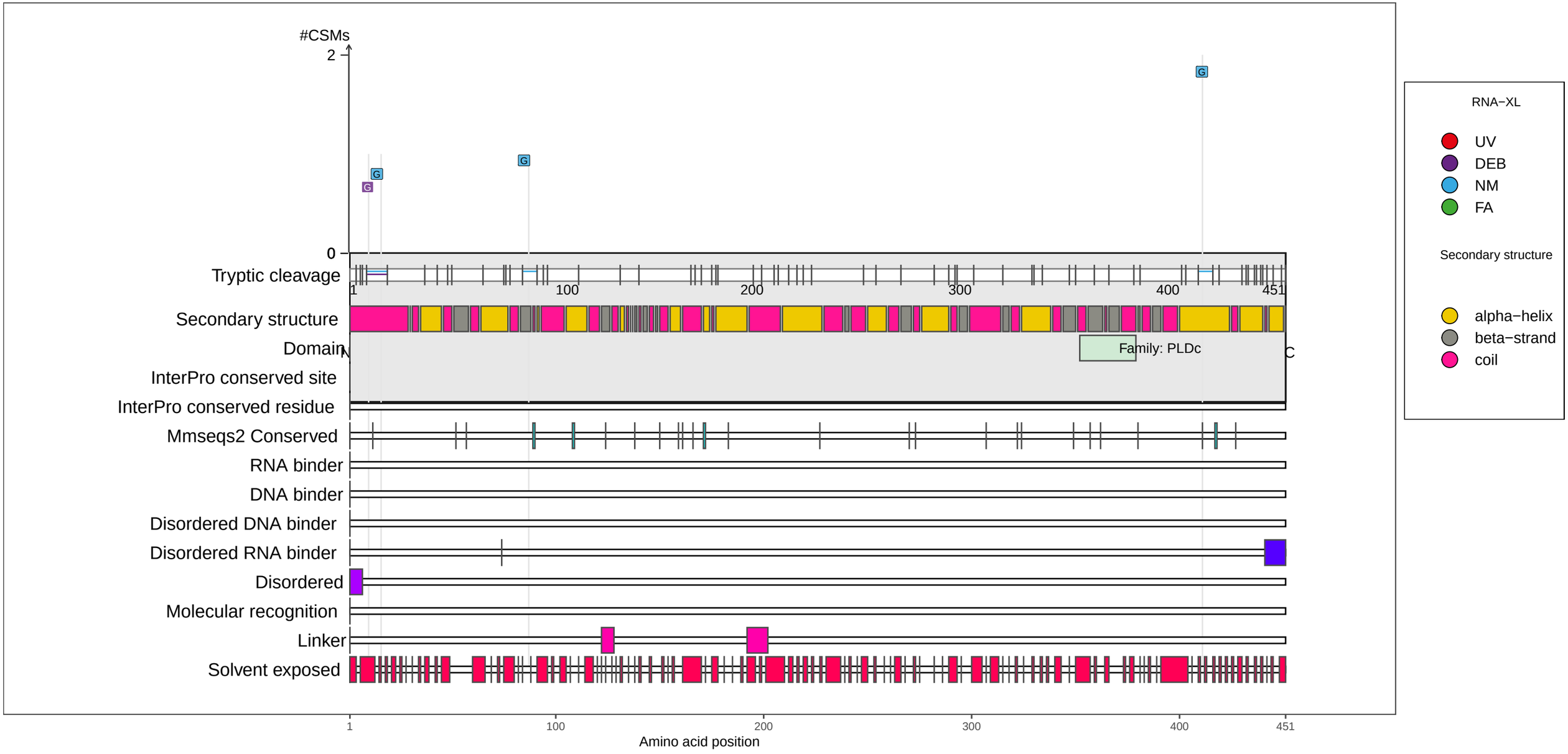
− RNA functions: not annotated



P23830
PSS_ECOLI CDP−diacylglycerol−−serine O−phosphatidyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.25 (Q 67)
PAXdb K12 strain [ppm]: 1.86 (Q 56)
PAXdb E.coli [ppm]: 2.68 (Q 90)

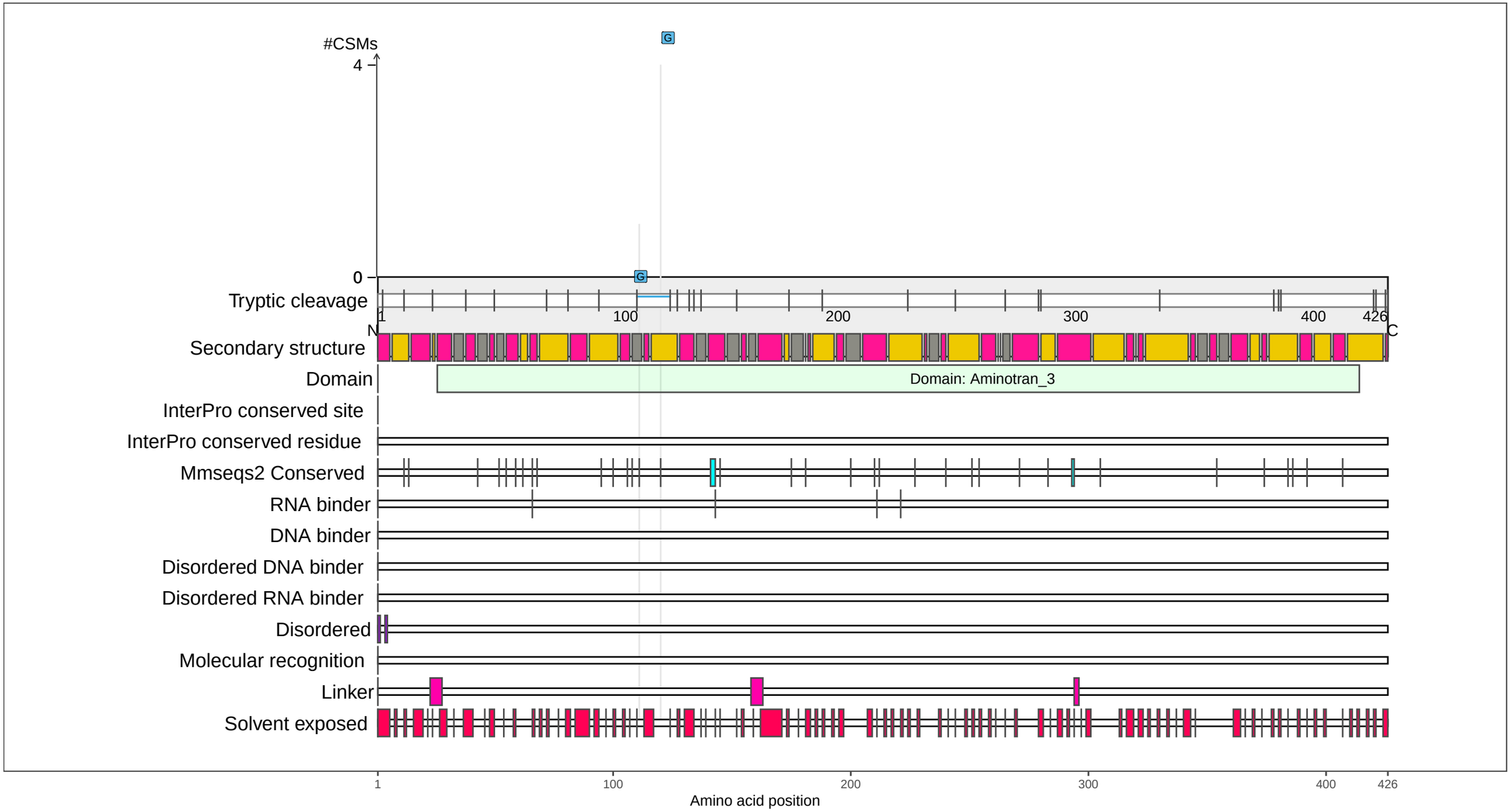
− RNA functions: not annotated

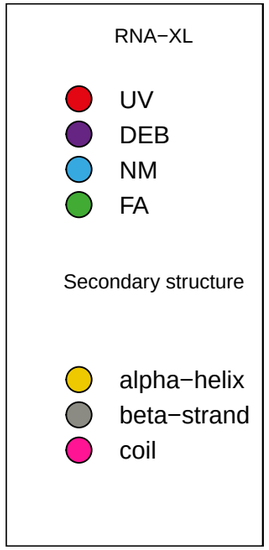


P23893
GSA_ECOLI Glutamate−1−semialdehyde 2,1−aminomutase

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 3 (Q 91)
PAXdb E.coli [ppm]: 2.46 (Q 85)

− RNA functions: not annotated

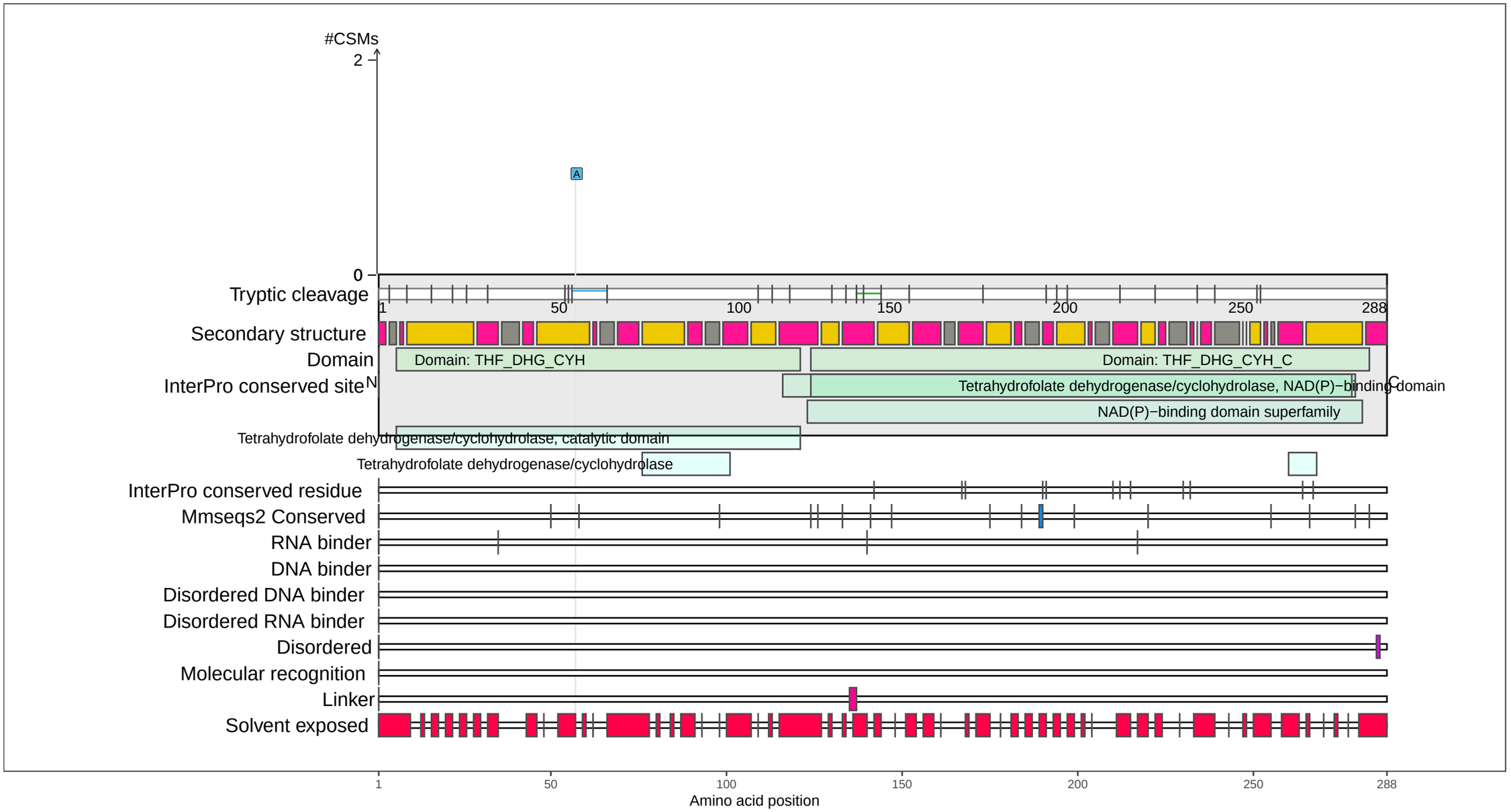


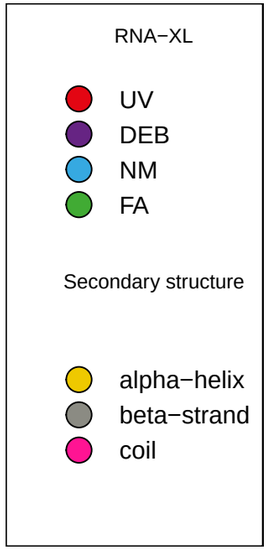


P24186
FOLD_ECOLI Bifunctional protein FolD

− Abundance:
tryptic [log10 Intensity]: 9.05 (Q 89)
PAXdb K12 strain [ppm]: 2.53 (Q 78)
PAXdb E.coli [ppm]: 2.01 (Q 72)

− RNA functions: not annotated

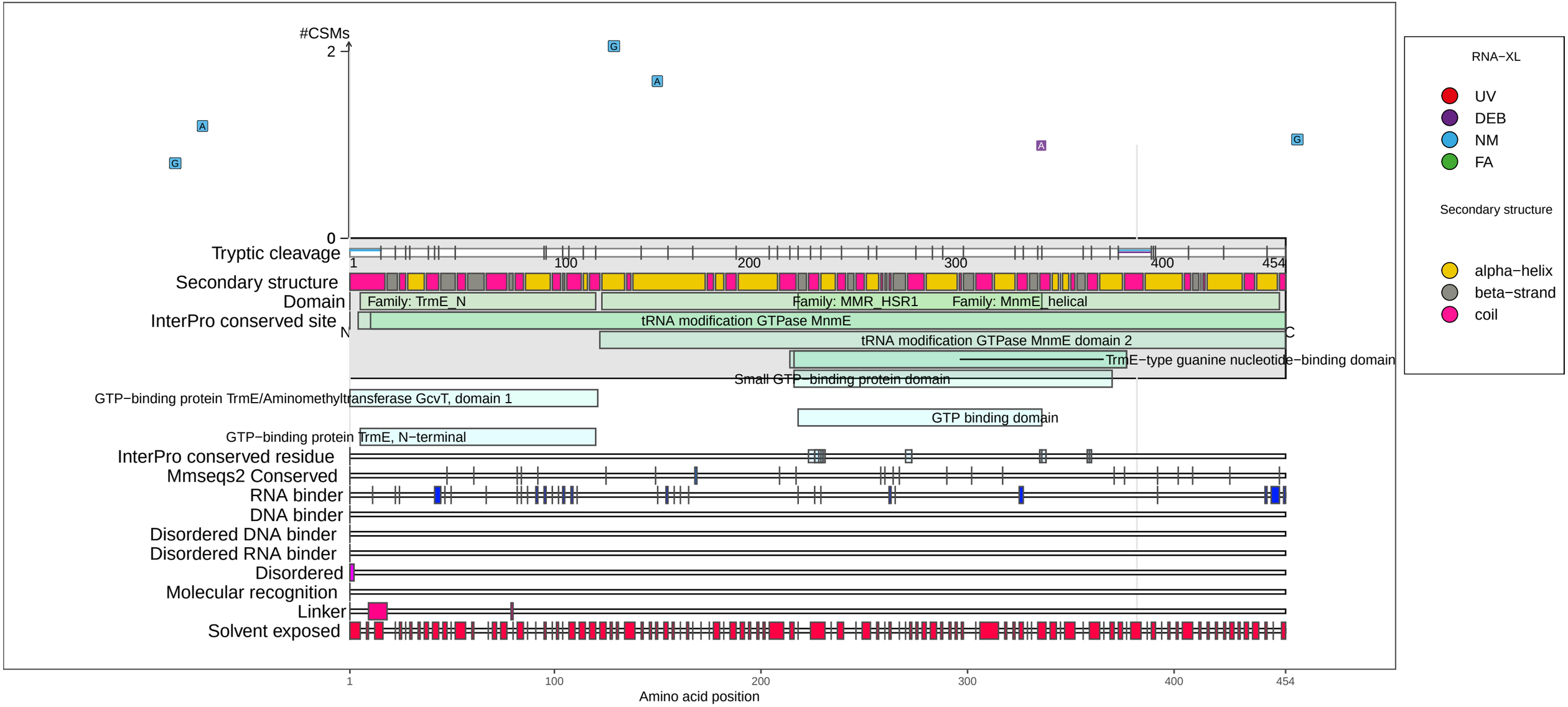




P25522
MNME_ECOLI tRNA modification GTPase MnmE

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.15 (Q 65)
PAXdb E.coli [ppm]: 2.6 (Q 88)

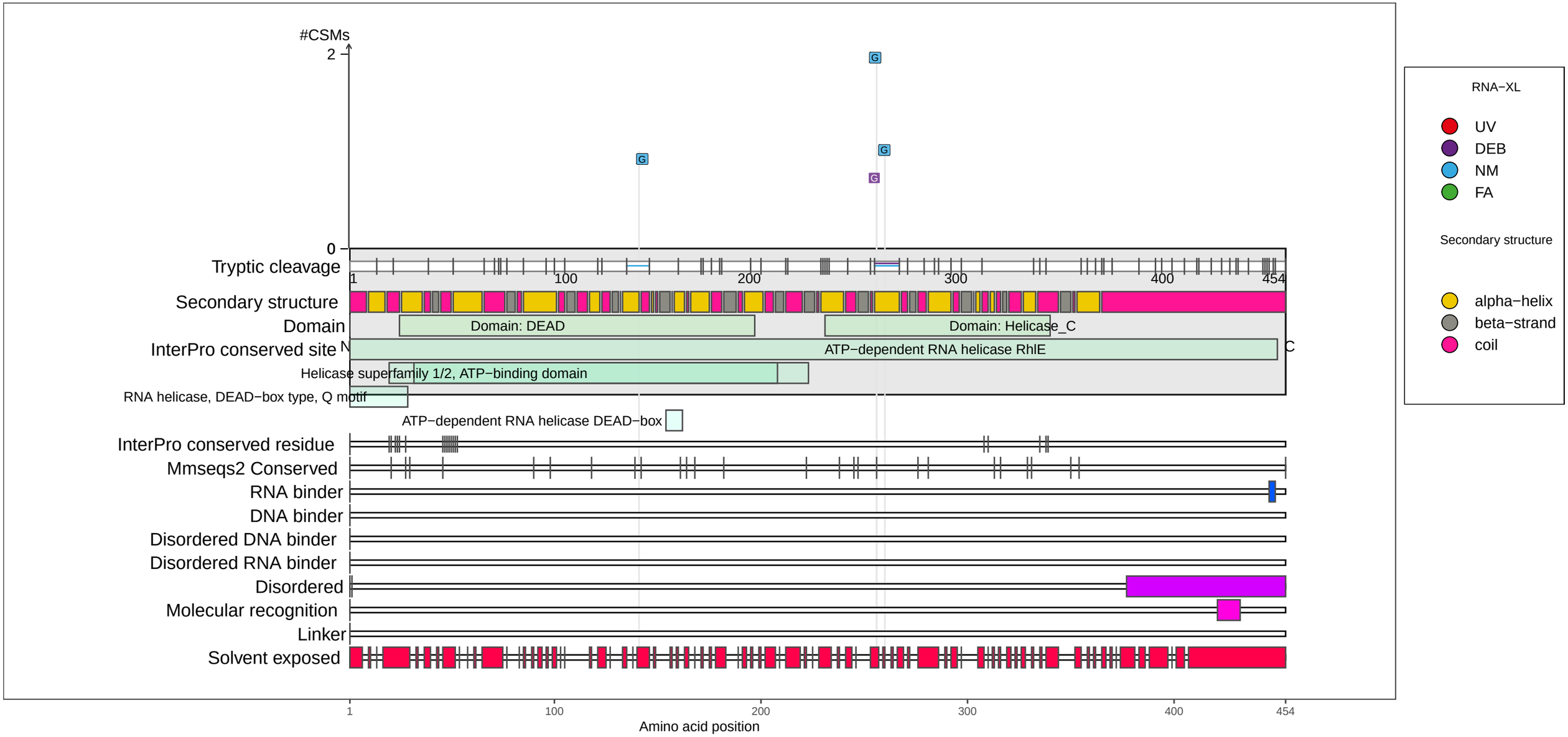
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA methylation
RNA modification; RNA processing; tRNA metabolic process; tRNA methylation; tRNA modification
tRNA processing; tRNA wobble base modification; tRNA wobble uridine modification



P25888
RHLE_ECOLI ATP−dependent RNA helicase RhlE

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 2.41 (Q 74)
PAXdb E.coli [ppm]: 1.01 (Q 48)

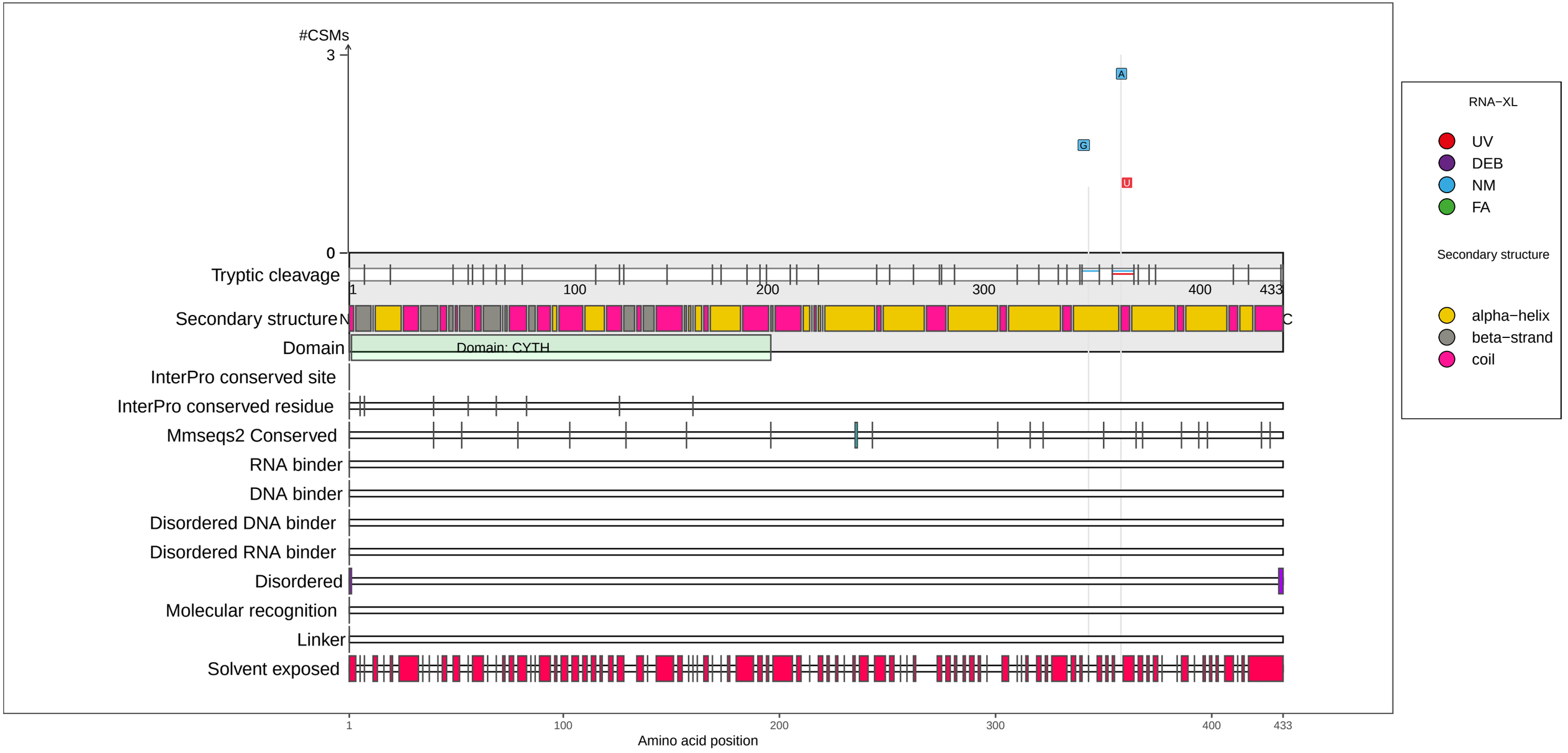
− RNA functions:
RNA binding; RNA helicase activity



P30871
3PASE_ECOLI Inorganic triphosphatase

− Abundance:
tryptic [log10 Intensity]: 6.83 (Q 8)
PAXdb K12 strain [ppm]: 2.41 (Q 75)
PAXdb E.coli [ppm]: 1.94 (Q 70)

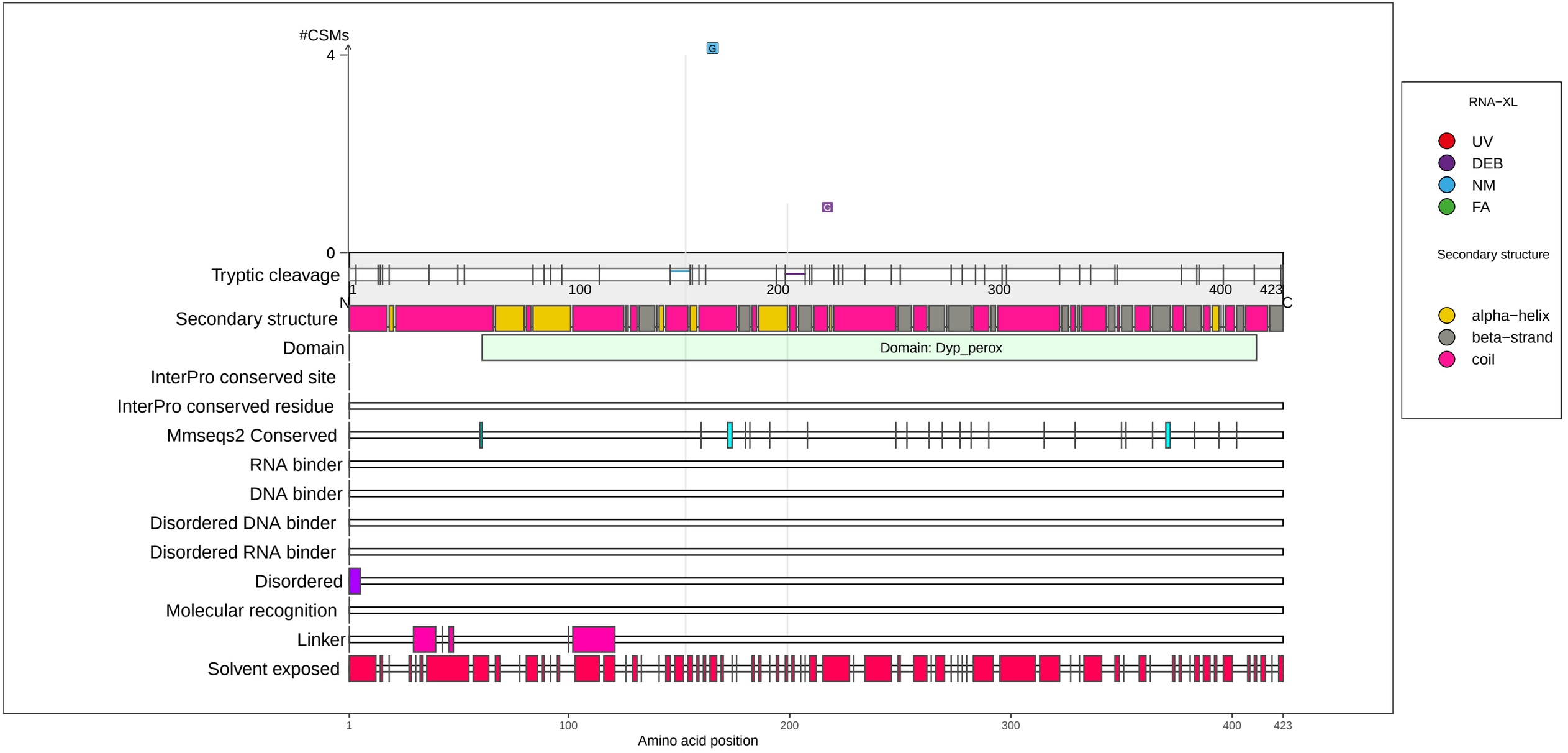
− RNA functions: not annotated



P31545
EFEB_ECOLI Deferrochelatase/peroxidase EfeB

− Abundance:
tryptic [log10 Intensity]: 7.54 (Q 37)
PAXdb K12 strain [ppm]: 1.69 (Q 49)
PAXdb E.coli [ppm]: −0.26 (Q 19)

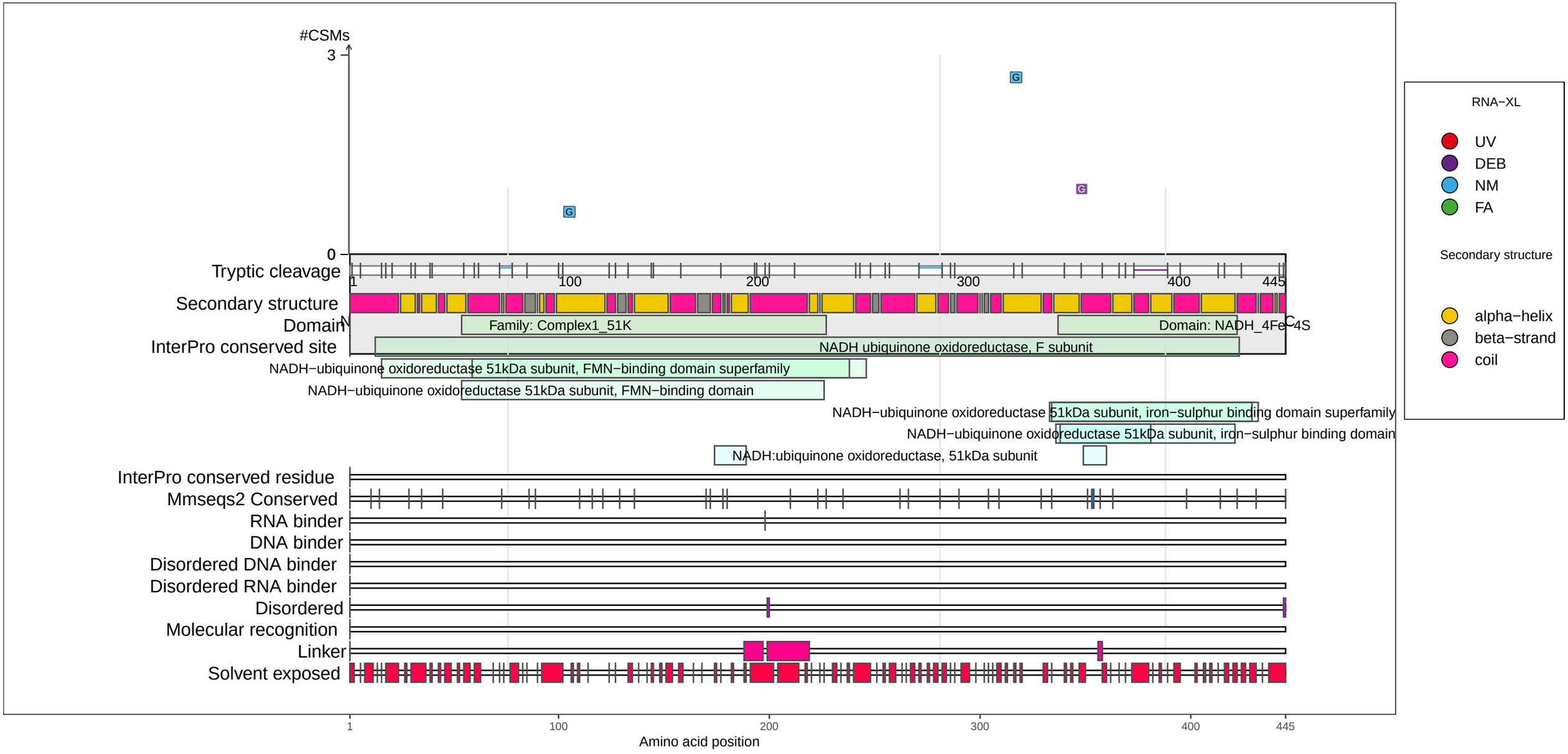
− RNA functions: not annotated



P31979
NUOF_ECOLI NADH−quinone oxidoreductase subunit F

− Abundance:
tryptic [log10 Intensity]: 9.23 (Q 93)
PAXdb K12 strain [ppm]: 2.85 (Q 87)
PAXdb E.coli [ppm]: 2.27 (Q 80)

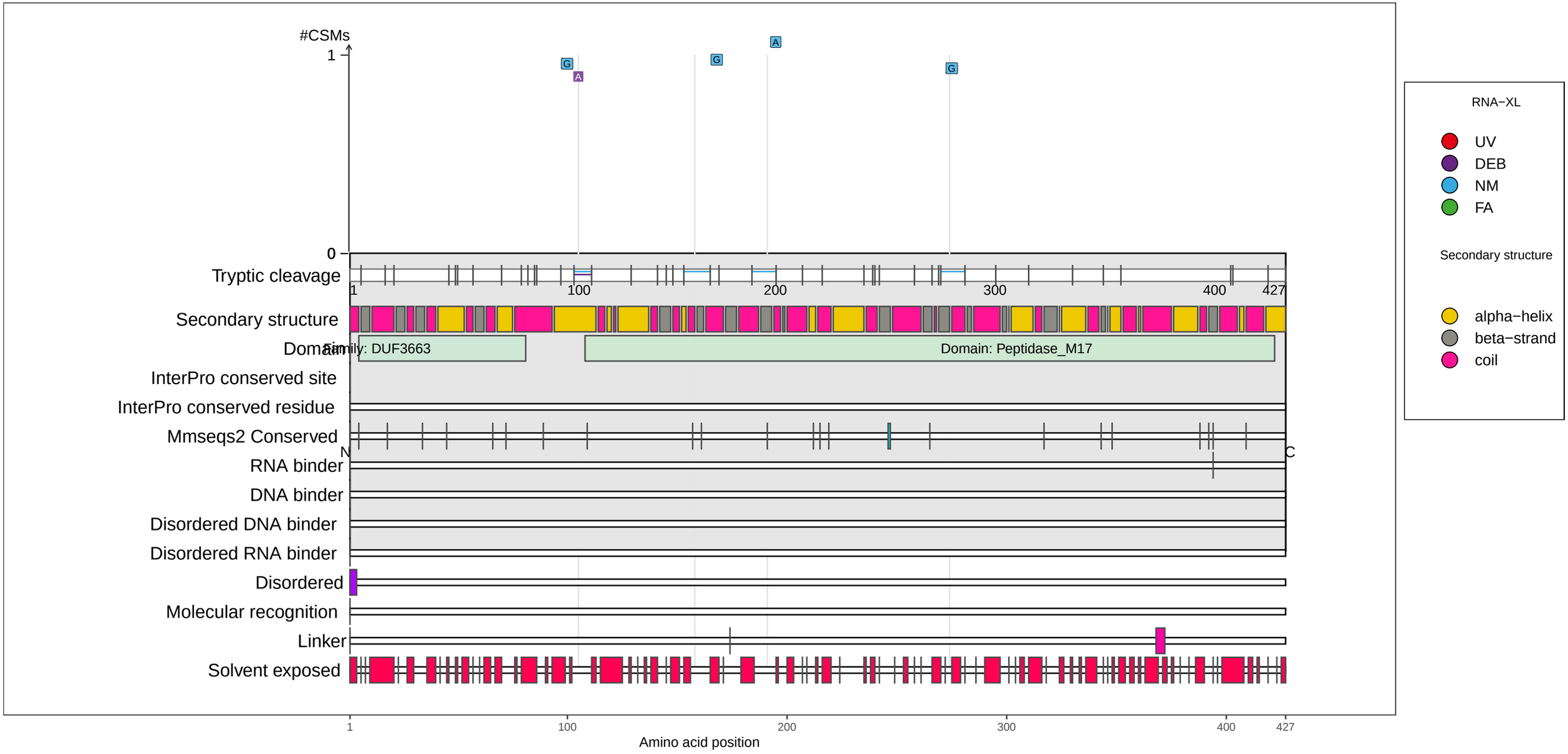
− RNA functions: not annotated



P37095
PEPB_ECOLI Peptidase B

− Abundance:
tryptic [log10 Intensity]: 8.41 (Q 73)
PAXdb K12 strain [ppm]: 2.48 (Q 77)
PAXdb E.coli [ppm]: 2.82 (Q 92)

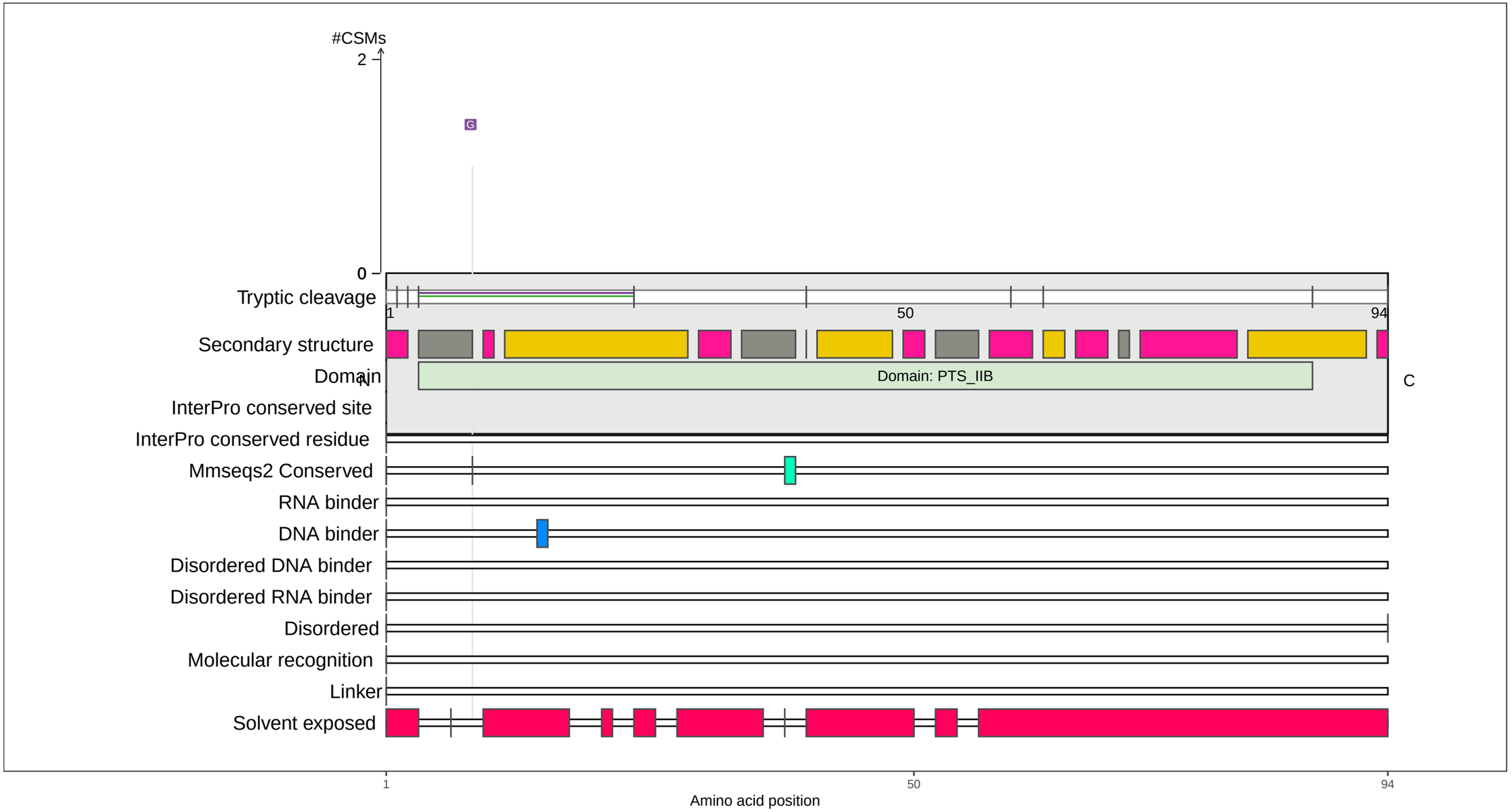
− RNA functions: not annotated

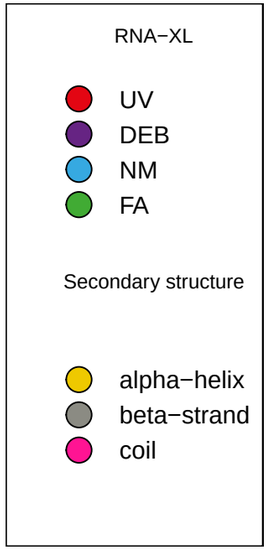


P37188
PTKB_ECOLI PTS system galactitol−specific EIIB component

− Abundance:
tryptic [log10 Intensity]: 8.48 (Q 75)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 3.79 (Q 100)

− RNA functions: not annotated

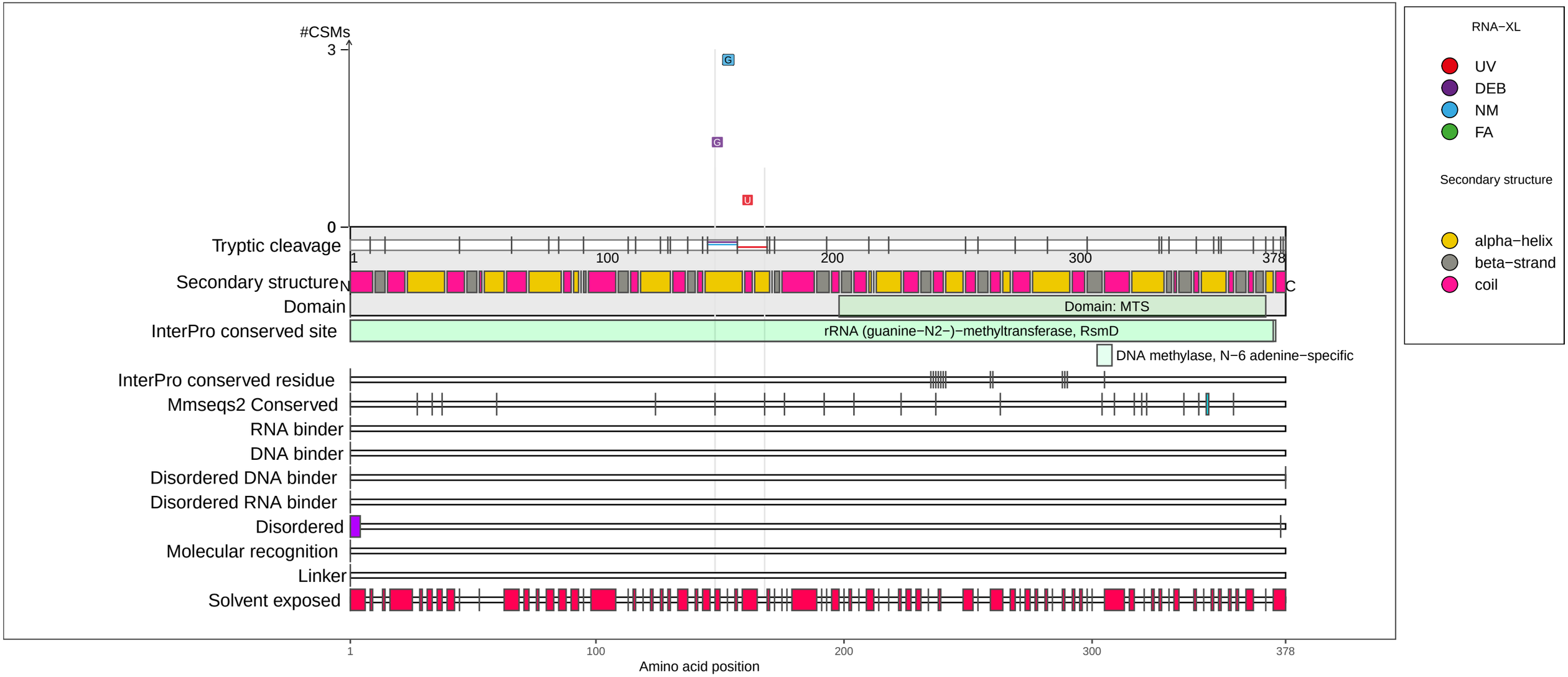




P42596
RLMG_ECOLI Ribosomal RNA large subunit methyltransferase G

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: 1.42 (Q 34)
PAXdb E.coli [ppm]: 0.2 (Q 29)

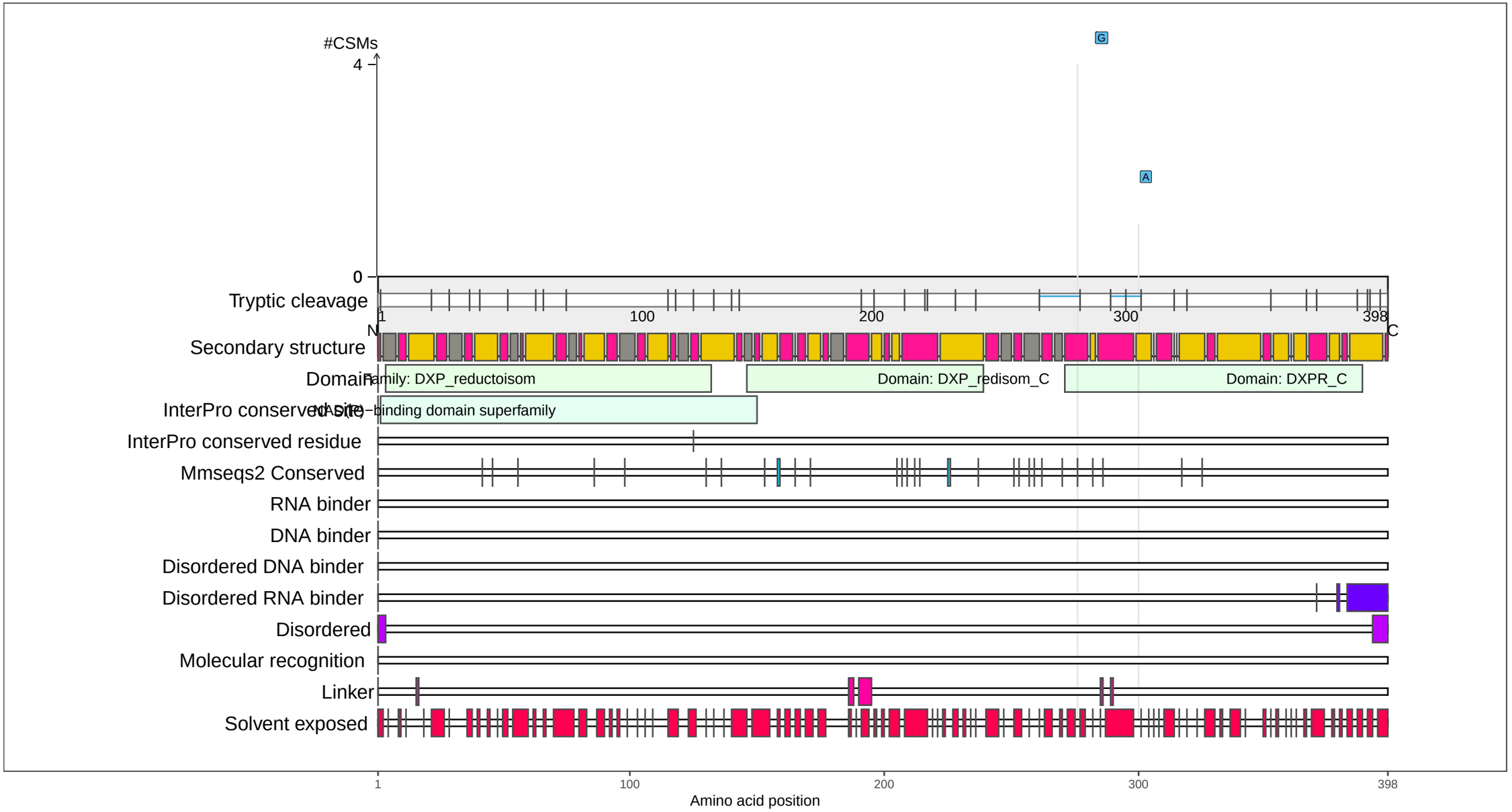
− RNA functions:
23S rRNA (guanine(1835)−N(2))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; RNA metabolic process; RNA methylation
RNA methyltransferase activity; RNA modification; RNA processing; rRNA (guanine−N2−)−methyltransferase activity
rRNA (guanine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P45568
DXR_ECOLI 1−deoxy−D−xylulose 5−phosphate reductoisomerase

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 1.43 (Q 34)
PAXdb E.coli [ppm]: 0.31 (Q 32)

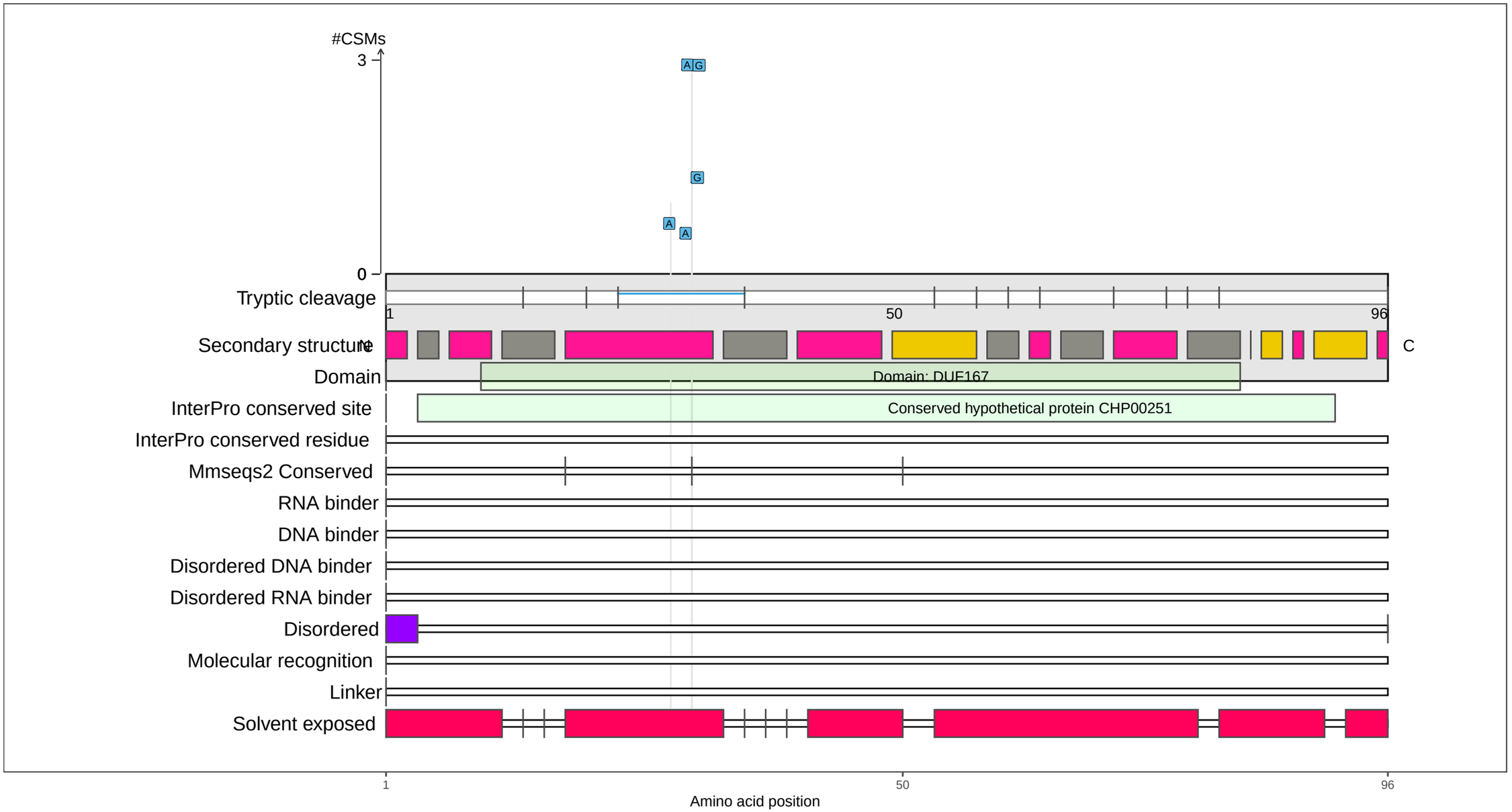
− RNA functions: not annotated



P52060
YGGU_ECOLI UPF0235 protein YggU

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 16)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.95 (Q 47)

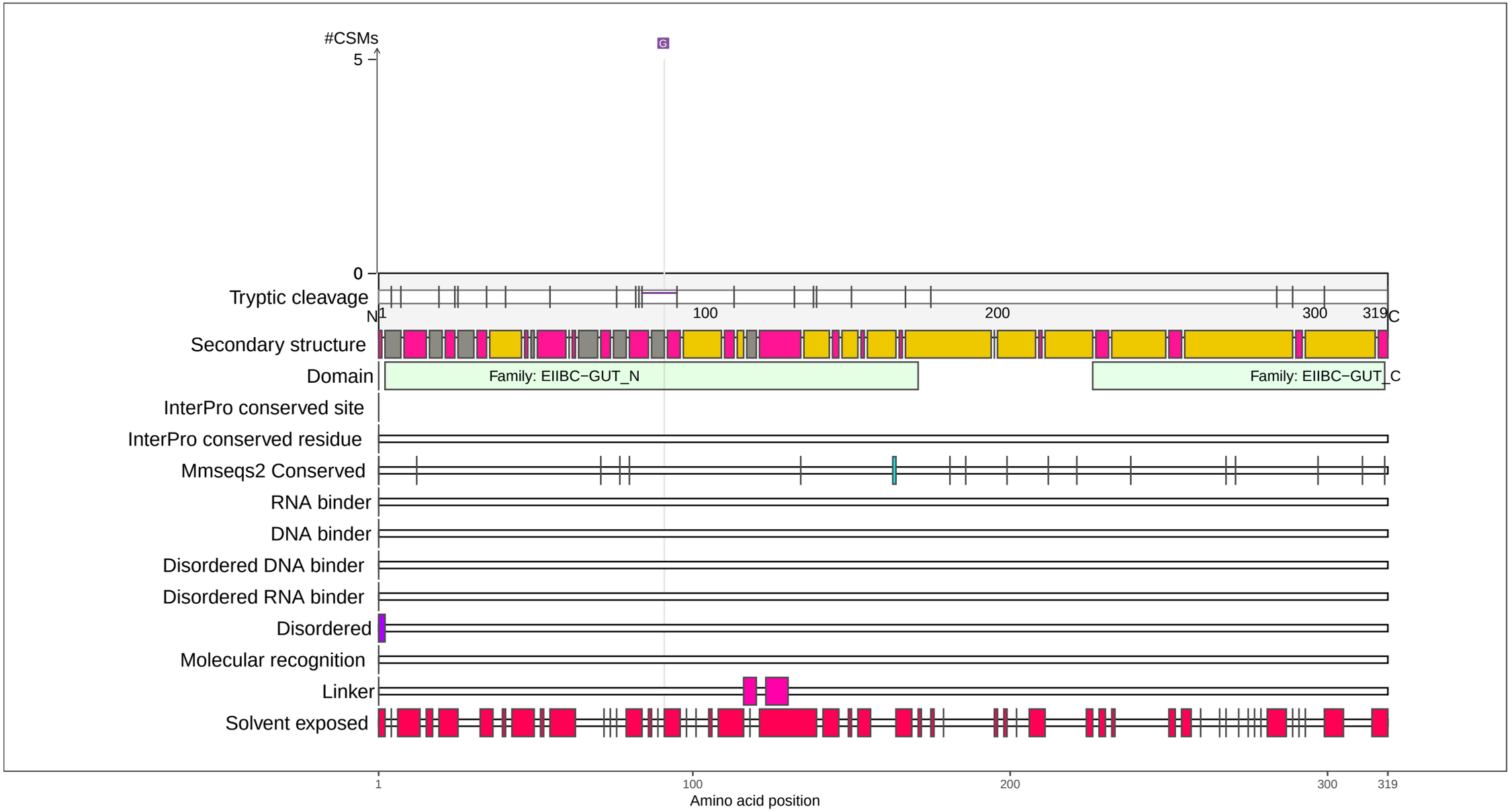
− RNA functions: not annotated

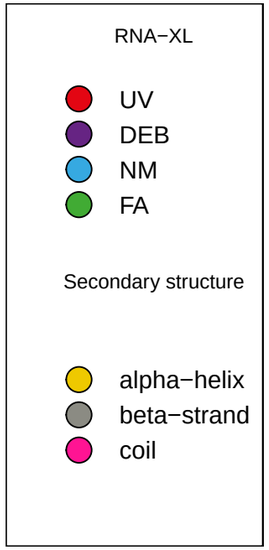


P56580
PTHB_ECOLI PTS system glucitol/sorbitol−specific EIIB component

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 56)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.15 (Q 28)

− RNA functions: not annotated

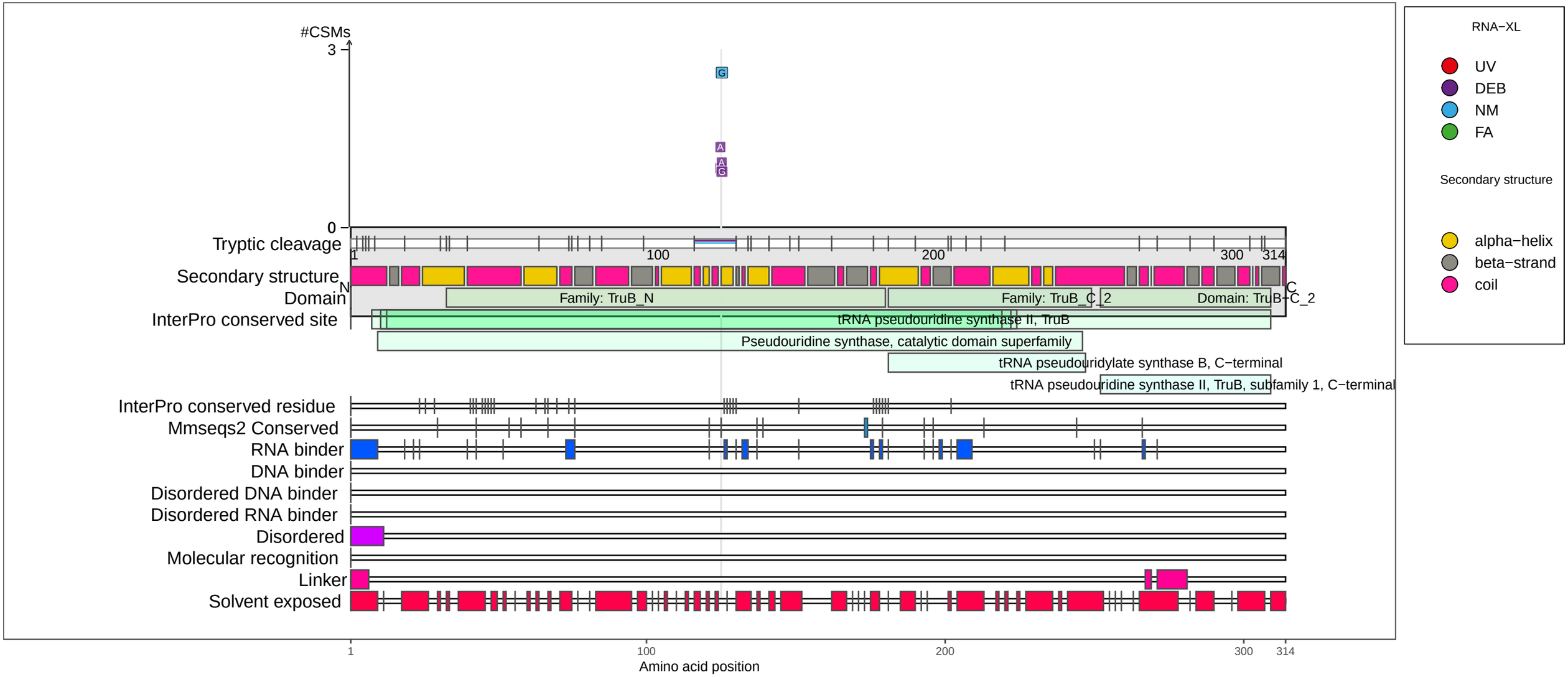




P60340
TRUB_ECOLI tRNA pseudouridine synthase B

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 2.05 (Q 62)
PAXdb E.coli [ppm]: 0.93 (Q 46)

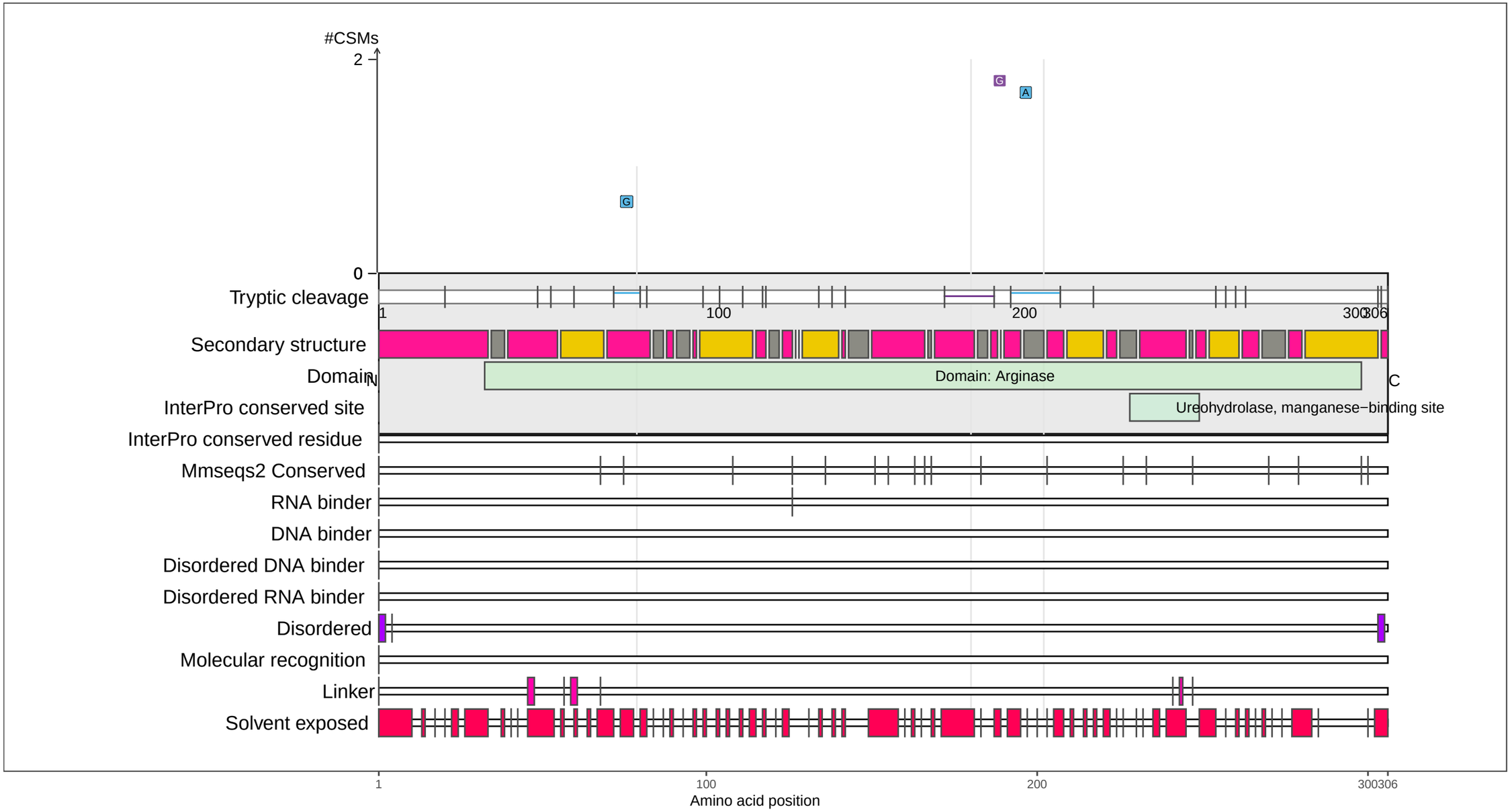
− RNA functions:
mRNA metabolic process; mRNA modification; mRNA pseudouridine synthesis
ncRNA metabolic process; ncRNA processing; RNA binding; RNA folding; RNA metabolic process
RNA modification; RNA processing; tRNA binding; tRNA folding; tRNA metabolic process
tRNA modification; tRNA processing; tRNA pseudouridine synthase activity
tRNA pseudouridine synthesis; tRNA pseudouridylate synthase B C−terminal domain

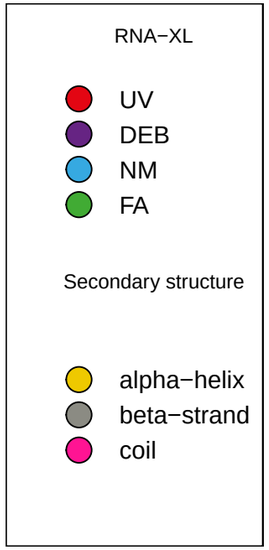


P60651
SPEB_ECOLI Agmatinase

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.42 (Q 84)

− RNA functions: not annotated

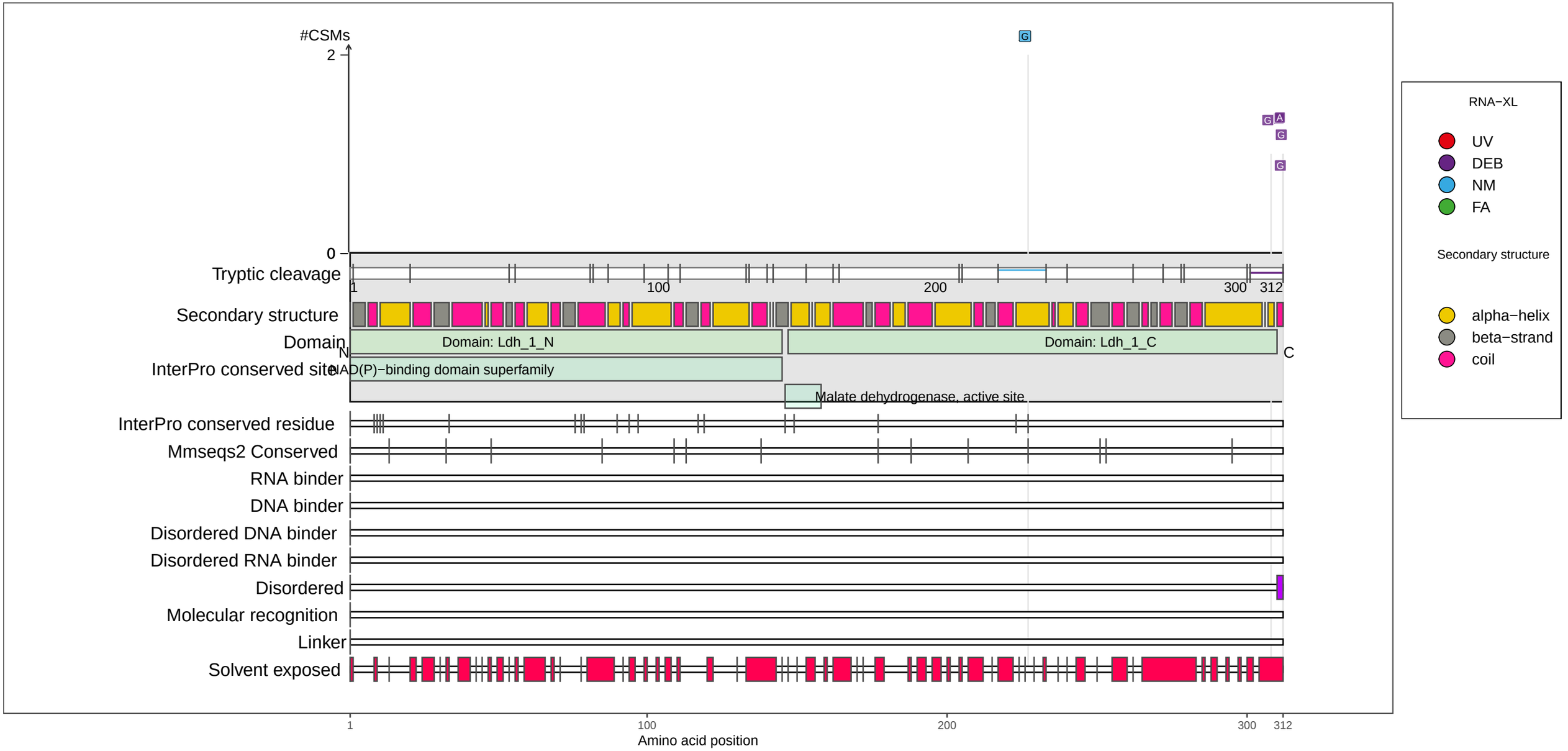




P61889
MDH_ECOLI Malate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 3.25 (Q 95)
PAXdb E.coli [ppm]: 3.77 (Q 100)

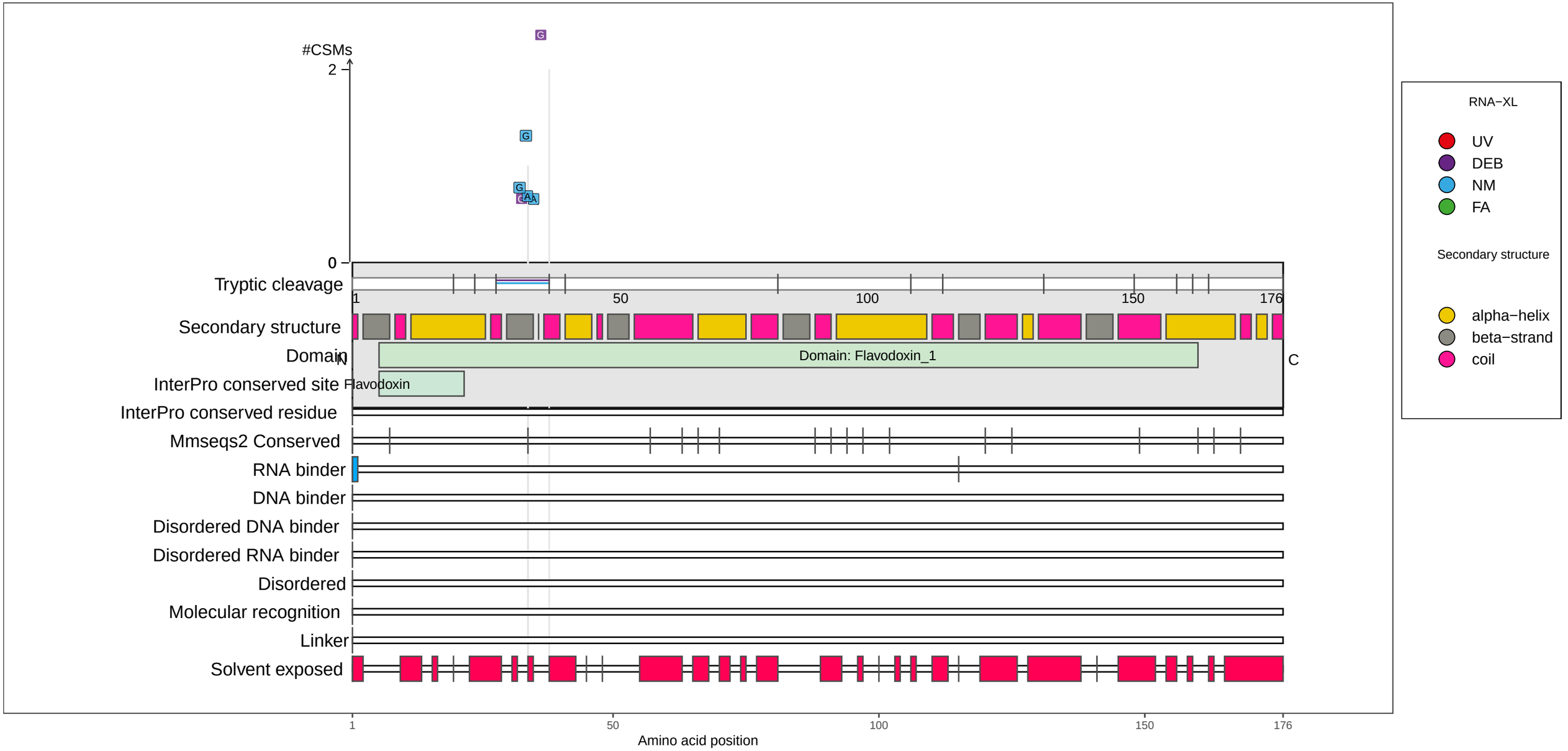
− RNA functions: not annotated



P61949
FLAV_ECOLI Flavodoxin 1

− Abundance:
tryptic [log10 Intensity]: 10.45 (Q 100)
PAXdb K12 strain [ppm]: 2.52 (Q 78)
PAXdb E.coli [ppm]: 3.03 (Q 95)

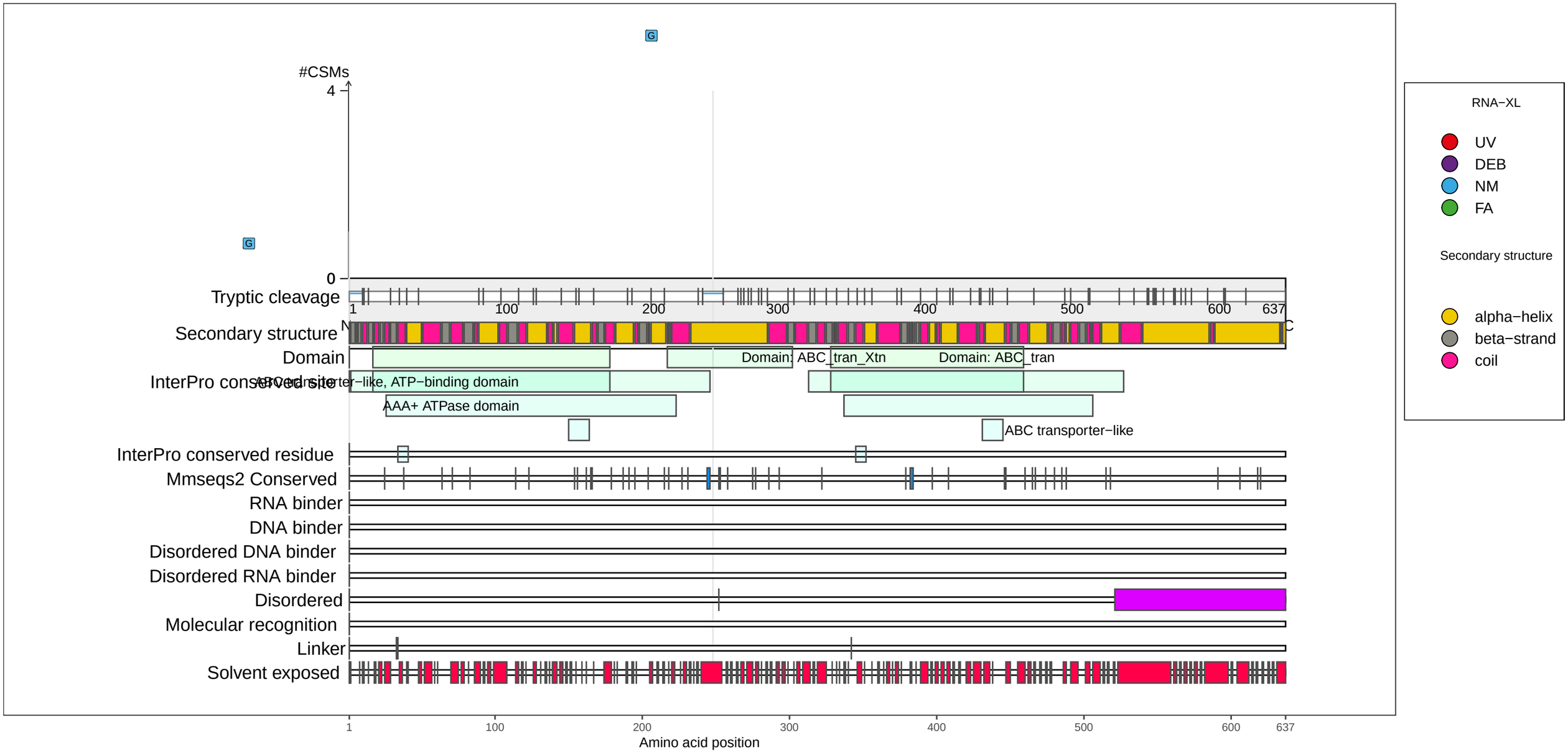
− RNA functions: not annotated



P63389
YHES_ECOLI Probable ATP−binding protein YheS

− Abundance:
tryptic [log10 Intensity]: 8.5 (Q 76)
PAXdb K12 strain [ppm]: 2.12 (Q 65)
PAXdb E.coli [ppm]: 1.17 (Q 52)

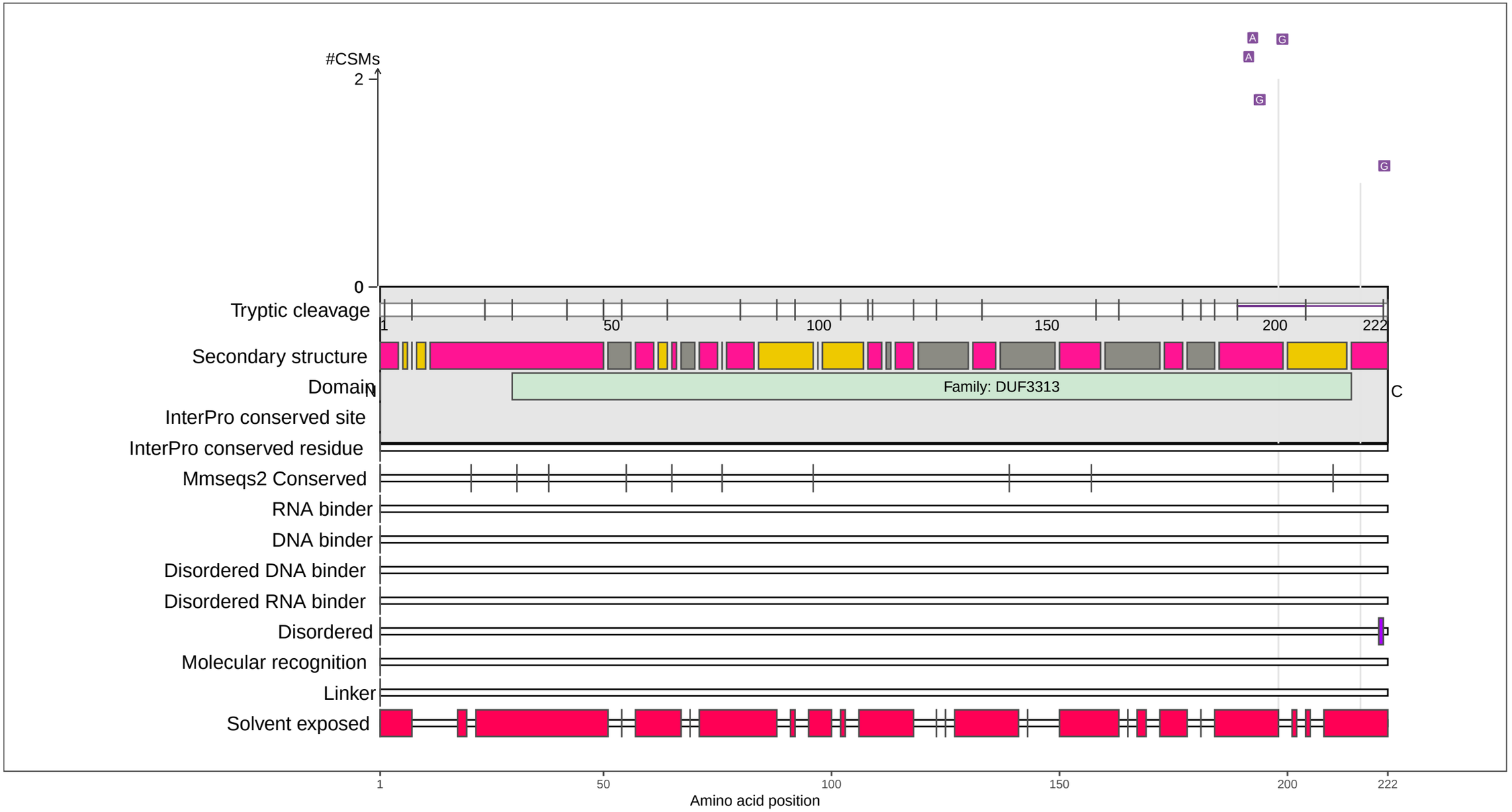
− RNA functions: not annotated

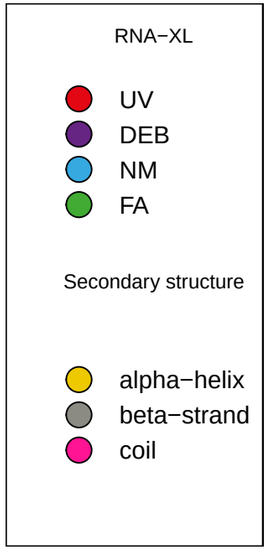


P64451
YDCL_ECOLI Uncharacterized lipoprotein YdcL

− Abundance:
tryptic [log10 Intensity]: 7.54 (Q 37)
PAXdb K12 strain [ppm]: 1.49 (Q 38)
PAXdb E.coli [ppm]: 2.86 (Q 93)

− RNA functions: not annotated

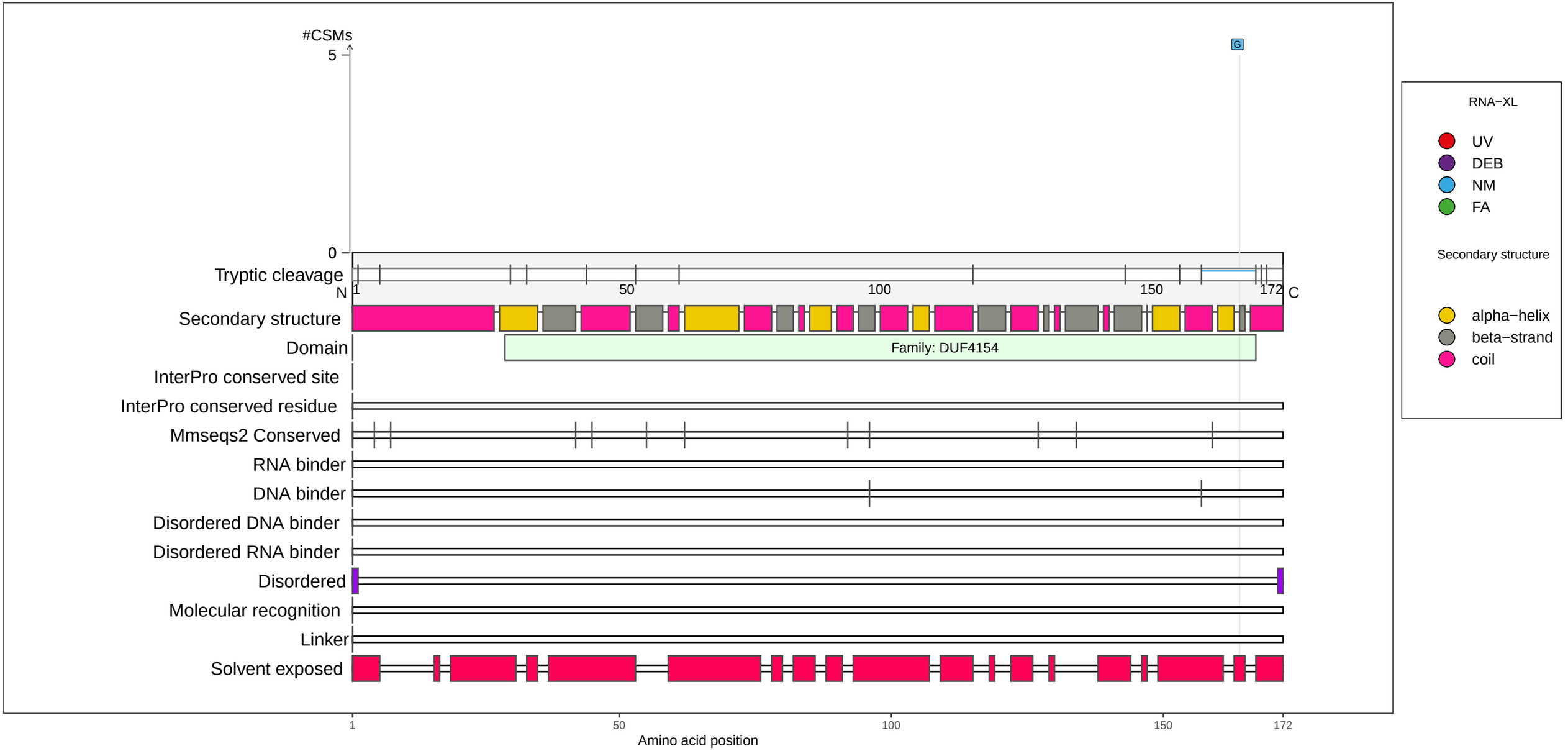




P64548
YFIR_ECOLI Protein YfiR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.03 (Q 62)
PAXdb E.coli [ppm]: −0.08 (Q 23)

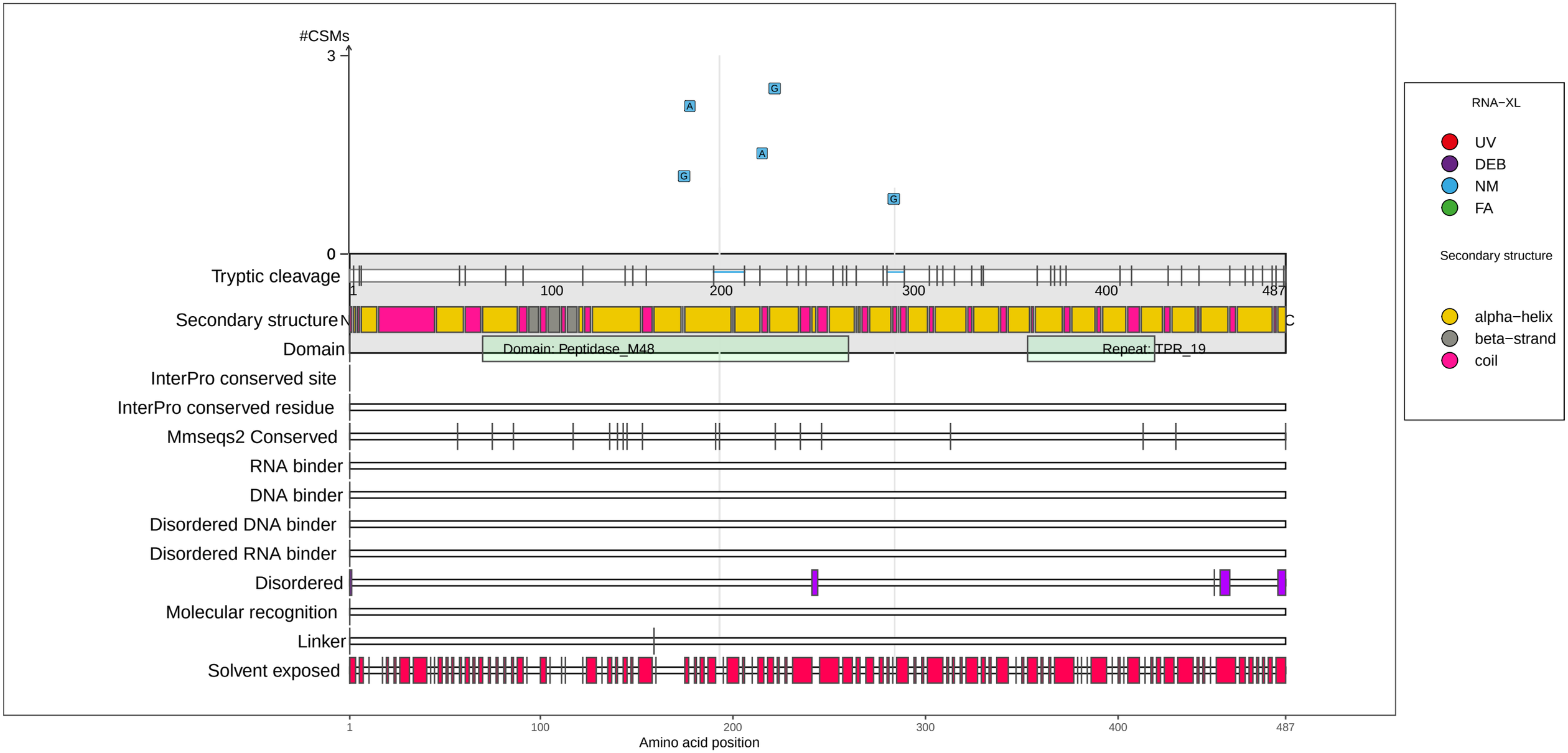
− RNA functions: not annotated



P66948
BEPA_ECOLI Beta−barrel assembly−enhancing protease

− Abundance:
tryptic [log10 Intensity]: 8.42 (Q 73)
PAXdb K12 strain [ppm]: 1.42 (Q 34)
PAXdb E.coli [ppm]: 1.88 (Q 69)

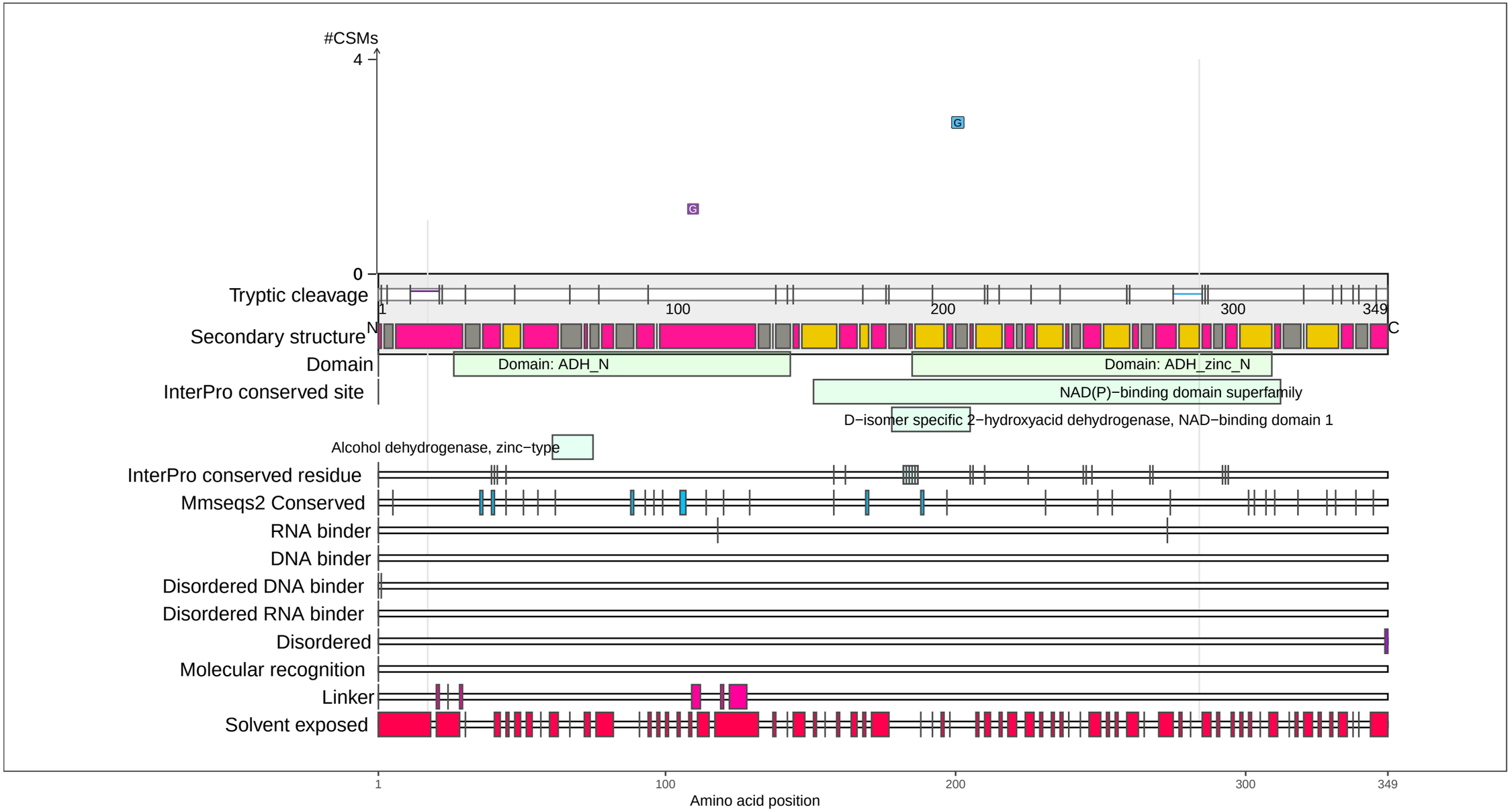
− RNA functions: not annotated



P75691
YAHK_ECOLI Aldehyde reductase YahK

− Abundance:
tryptic [log10 Intensity]: 7.2 (Q 21)
PAXdb K12 strain [ppm]: 0.83 (Q 6)
PAXdb E.coli [ppm]: 3.07 (Q 95)

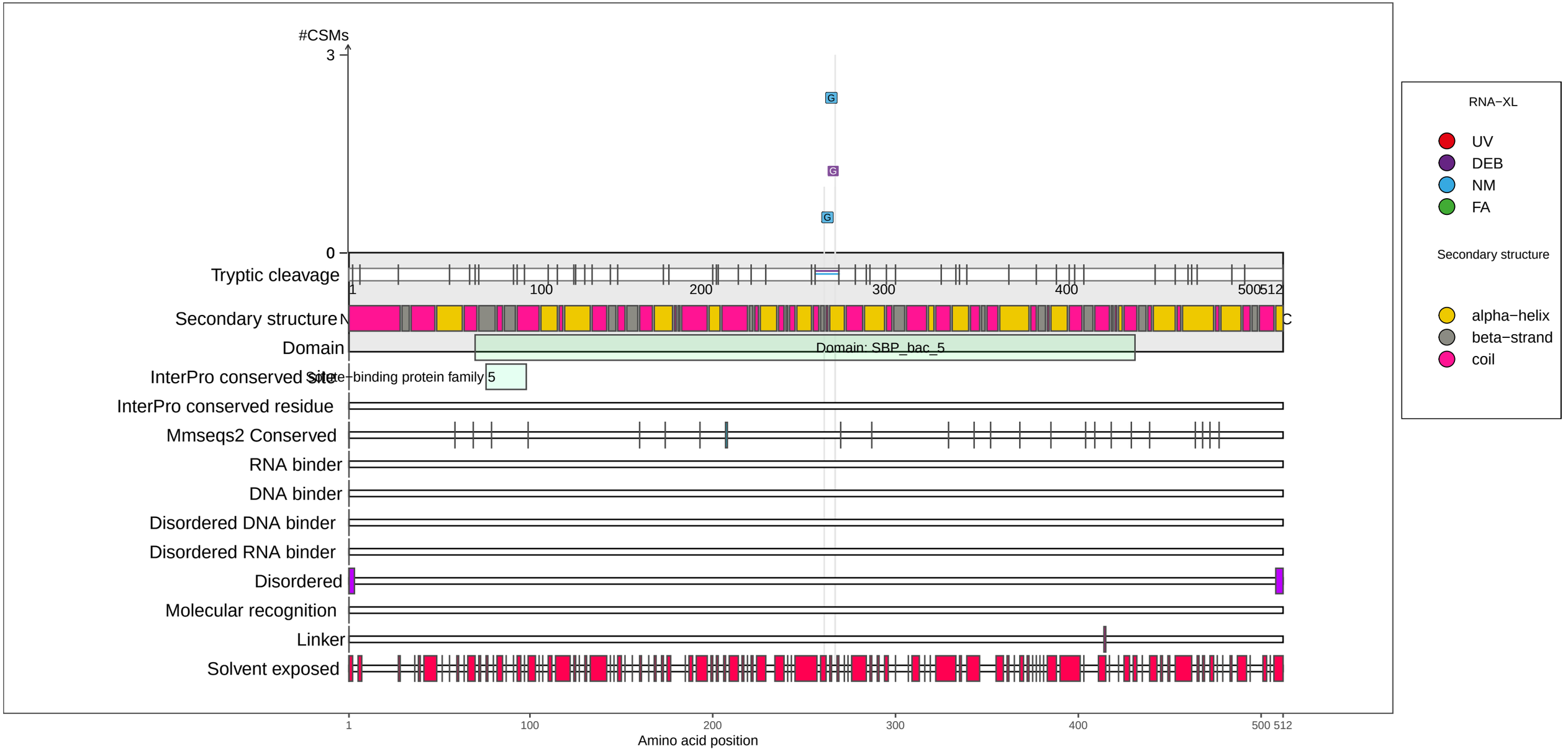
− RNA functions: not annotated



P75797
GSIB_ECOLI Glutathione−binding protein GsiB

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 2.4 (Q 83)

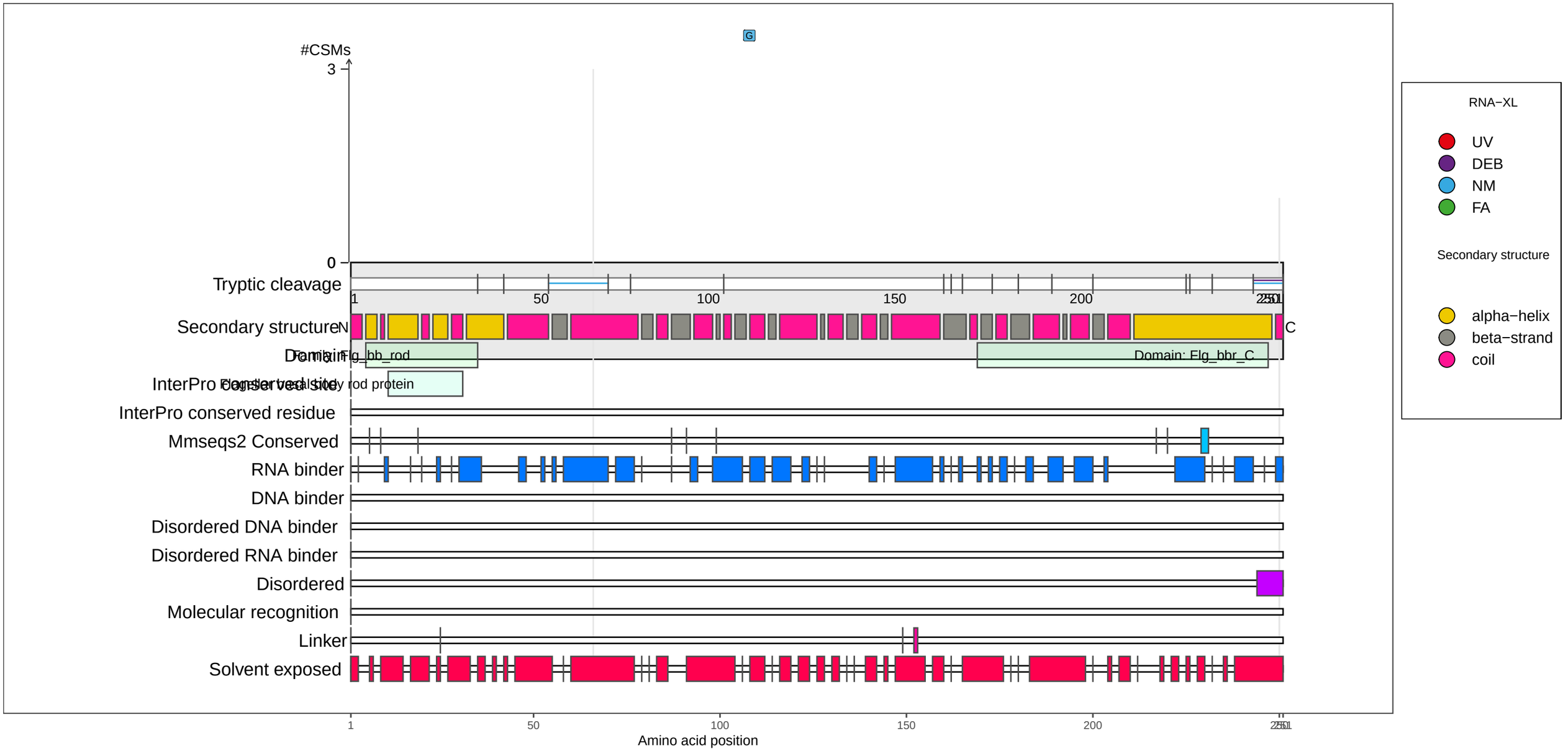
− RNA functions: not annotated



P75938
FLGF_ECOLI Flagellar basal−body rod protein FlgF

− Abundance:
tryptic [log10 Intensity]: 7.14 (Q 18)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.35 (Q 32)

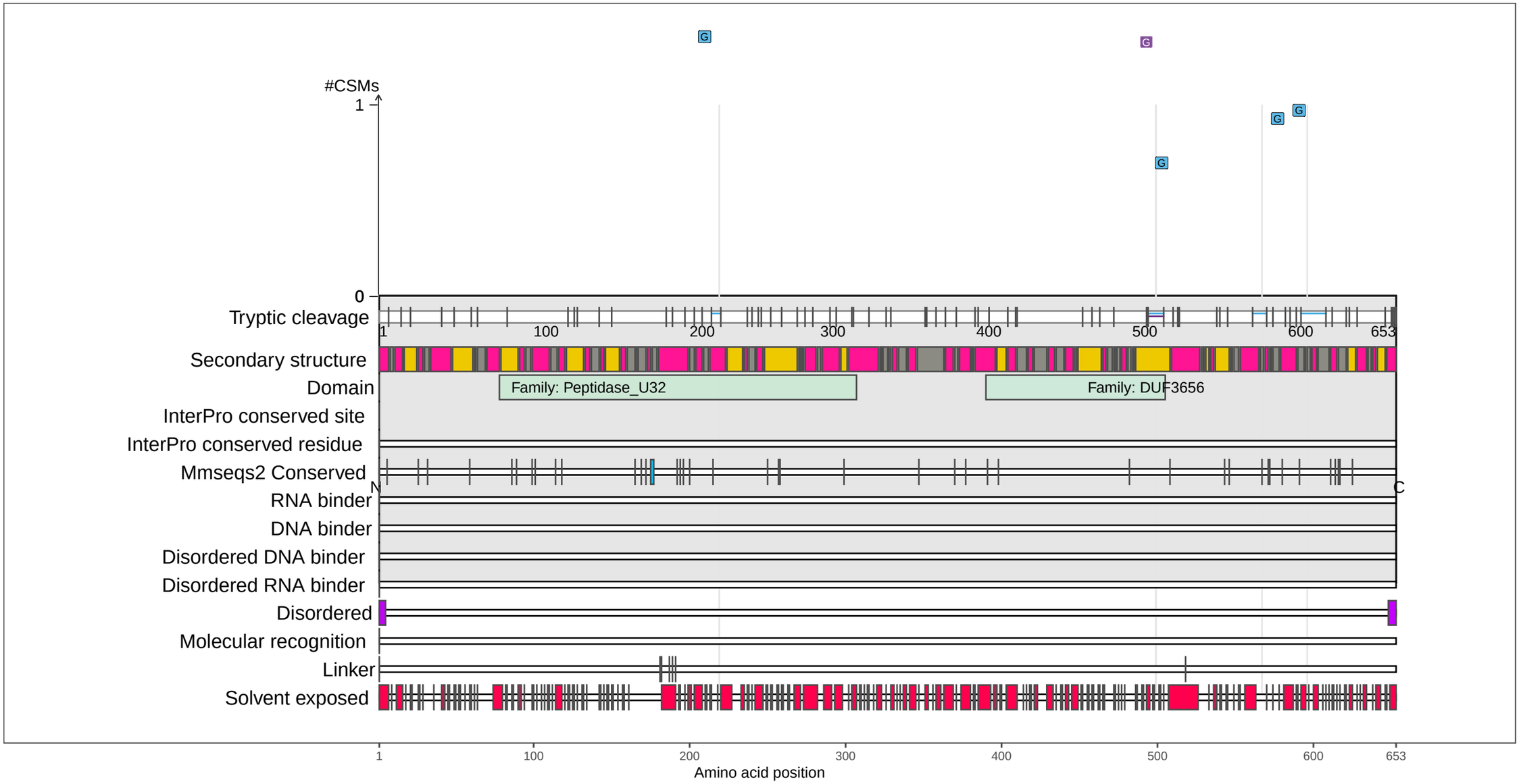
− RNA functions: not annotated



P76104
RLHA_ECOLI 23S rRNA 5−hydroxycytidine C2501 synthase

− Abundance:
tryptic [log10 Intensity]: 6.91 (Q 10)
PAXdb K12 strain [ppm]: 0.69 (Q 3)
PAXdb E.coli [ppm]: 1.41 (Q 57)

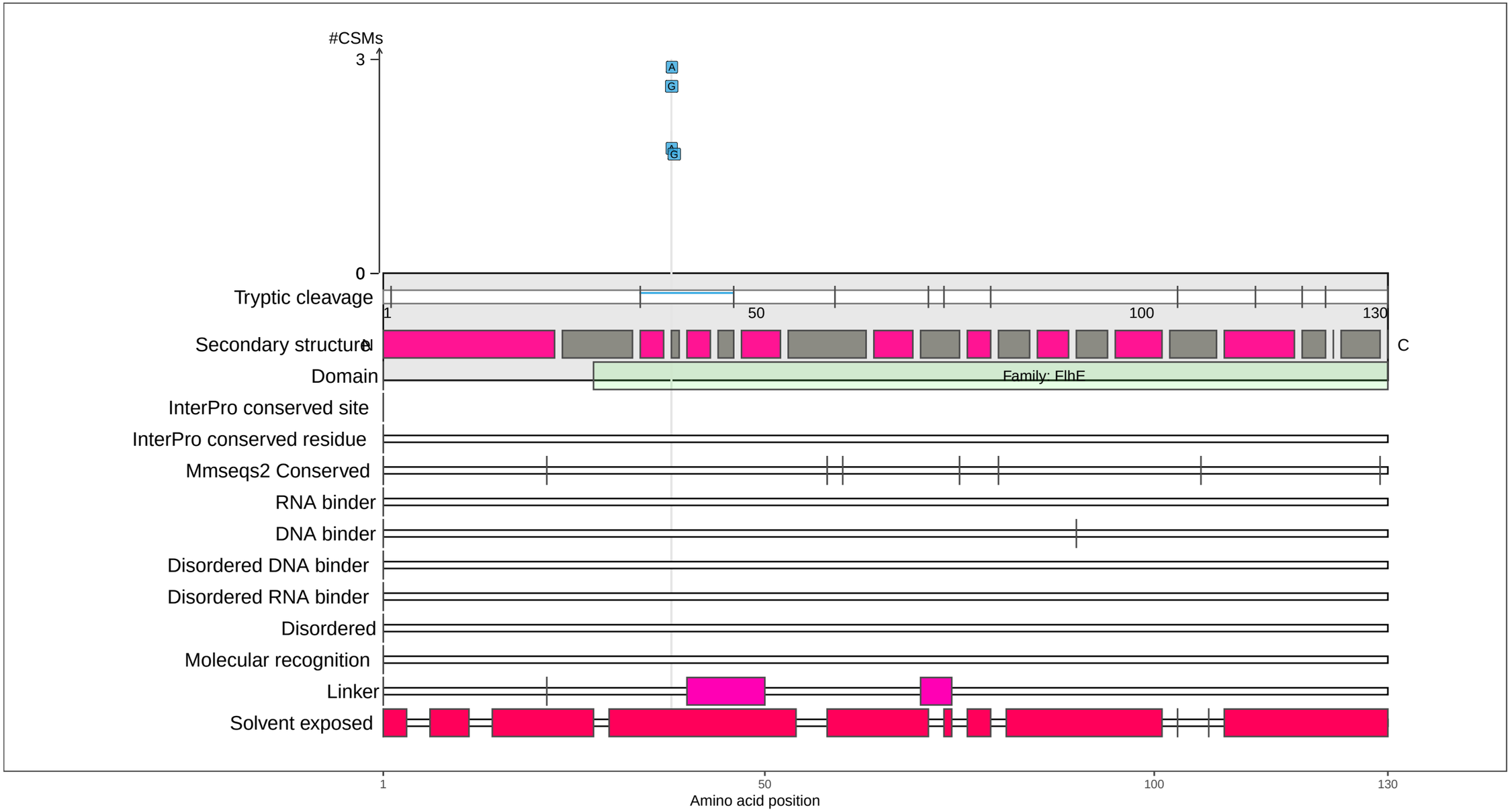
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; rRNA metabolic process; rRNA modification; rRNA processing

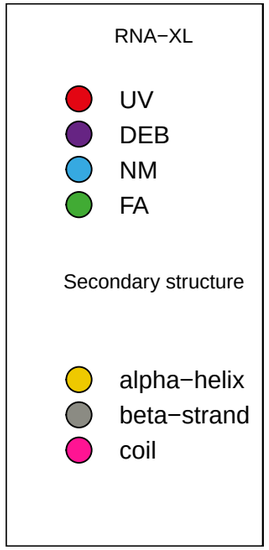


P76297
FLHE_ECOLI Flagellar protein FlhE

− Abundance:
tryptic [log10 Intensity]: 7.9 (Q 54)
PAXdb K12 strain [ppm]: 1.71 (Q 50)
PAXdb E.coli [ppm]: 0.24 (Q 30)

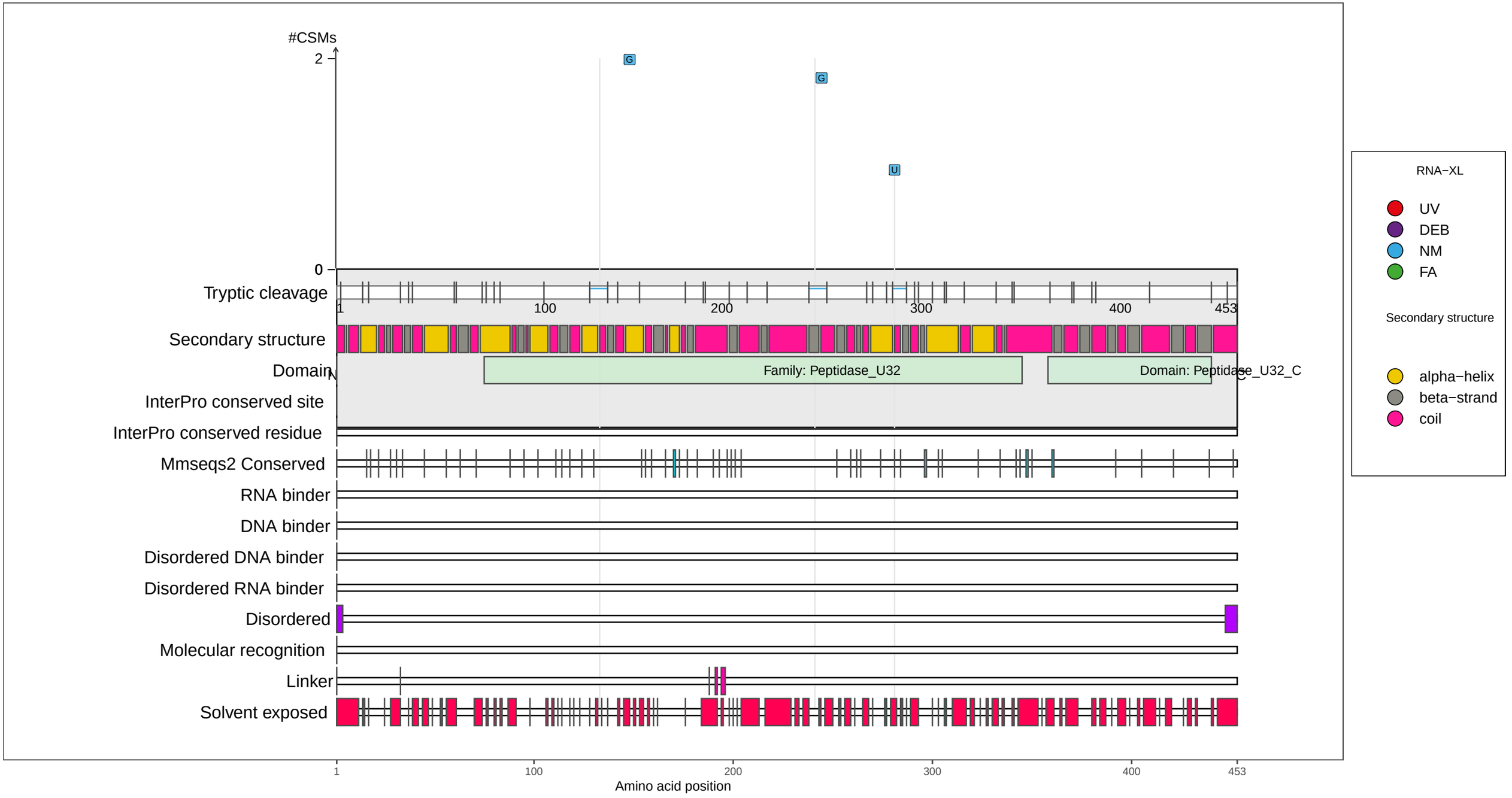
− RNA functions: not annotated





P76403
TRHP_ECOLI tRNA hydroxylation protein P

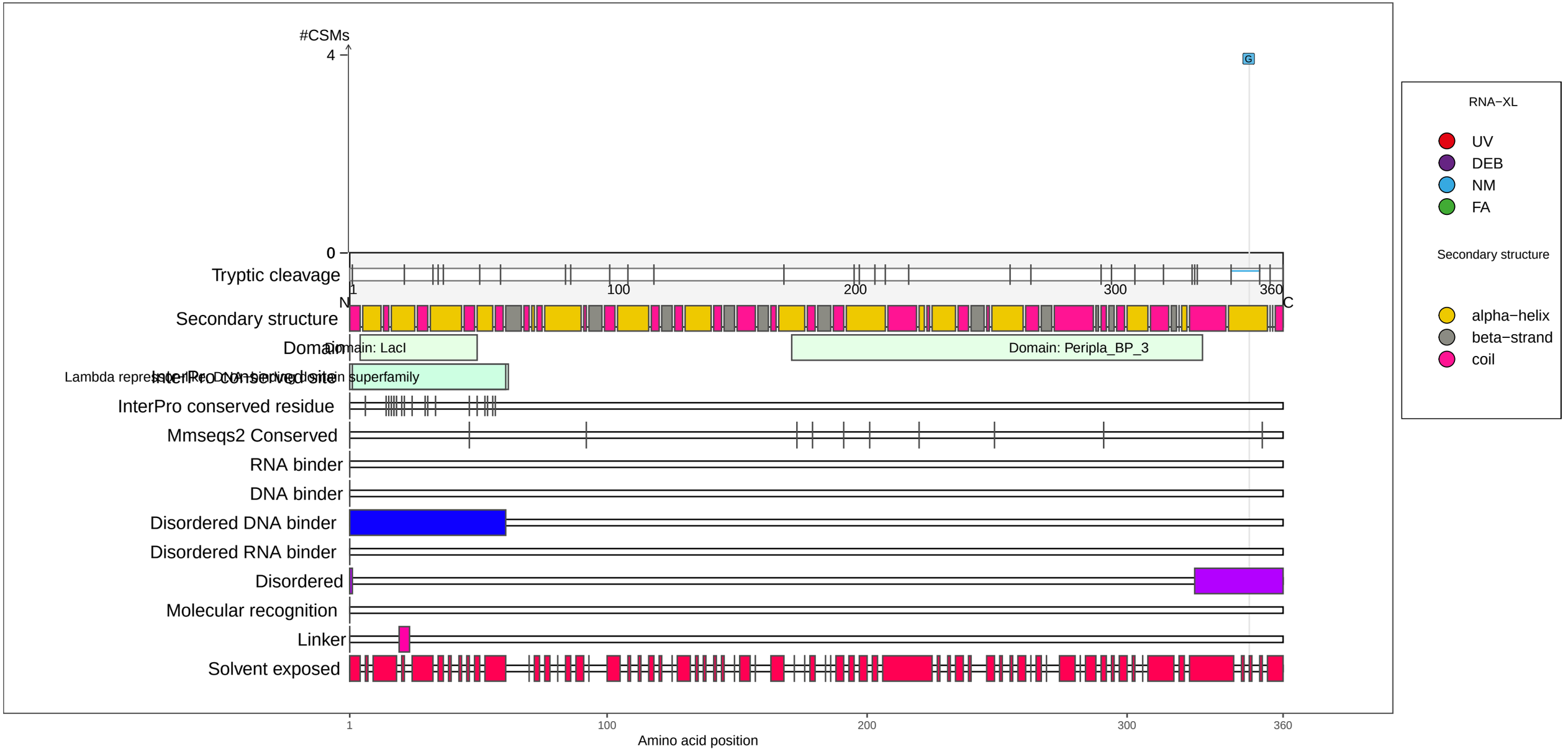
− RNA functions: not annotated



P03023
LACI_ECOLI Lactose operon repressor

− Abundance:
tryptic [log10 Intensity]: 7.7 (Q 44)
PAXdb K12 strain [ppm]: 2.67 (Q 82)
PAXdb E.coli [ppm]: 1.28 (Q 54)

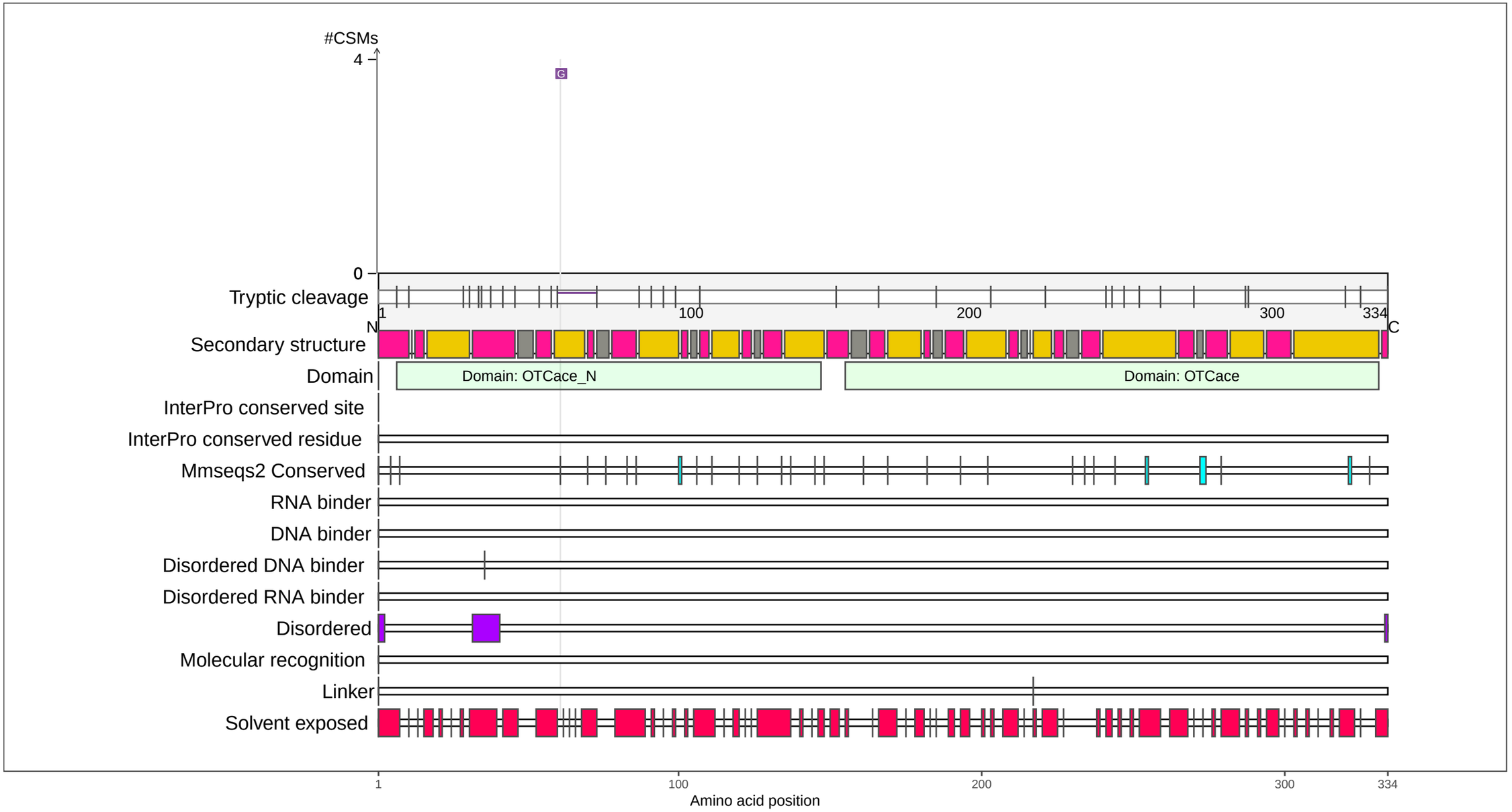
− RNA functions: not annotated

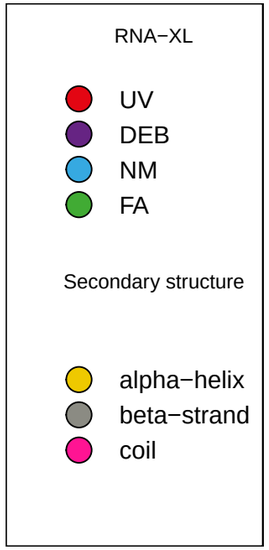


P04391
OTC1_ECOLI Ornithine carbamoyltransferase subunit I

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 0.43 (Q 1)
PAXdb E.coli [ppm]: 2.36 (Q 82)

− RNA functions: not annotated

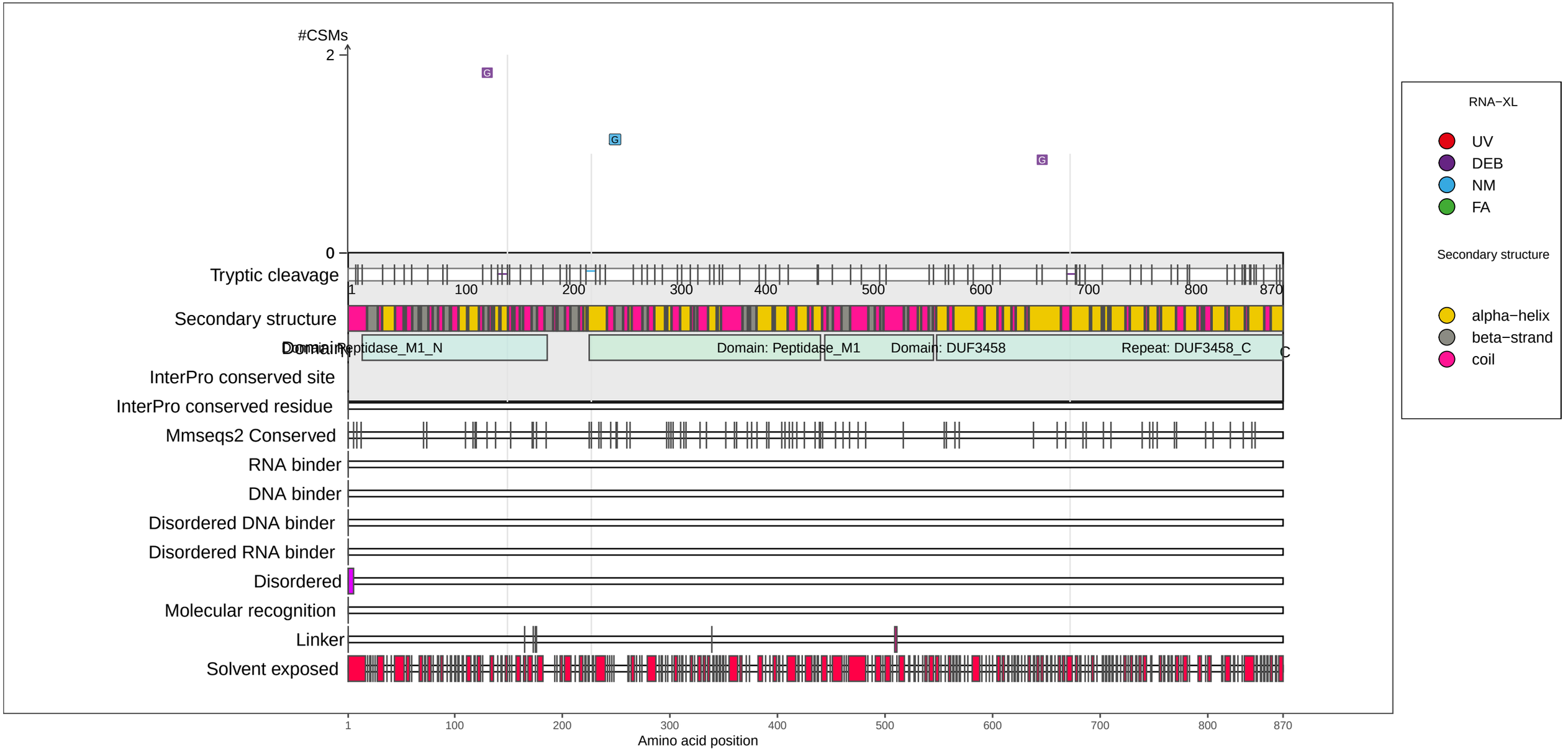




P04825
AMPN_ECOLI Aminopeptidase N

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 2.82 (Q 86)
PAXdb E.coli [ppm]: 2.72 (Q 90)

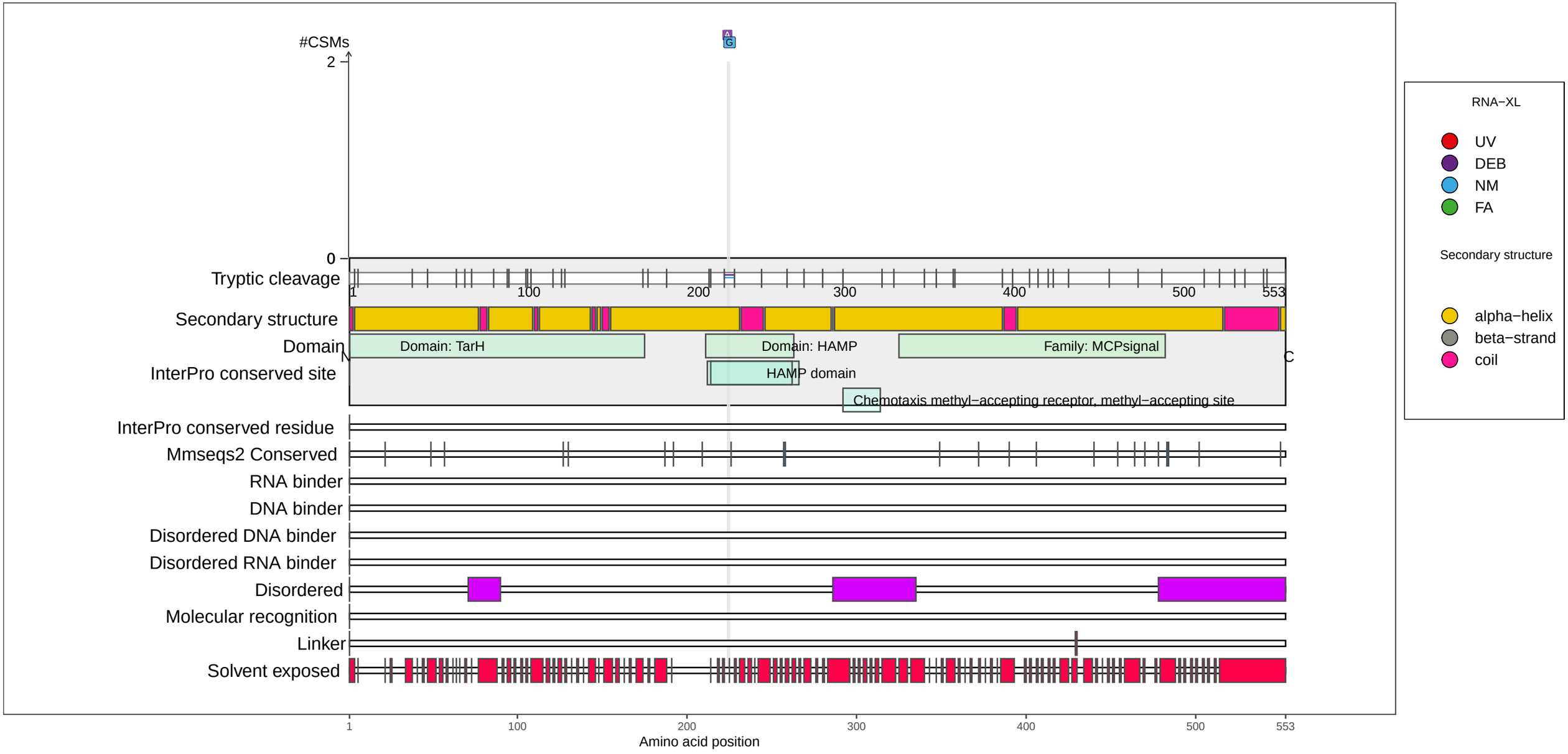
− RNA functions: not annotated



P07017
MCP2_ECOLI Methyl−accepting chemotaxis protein II

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.23 (Q 22)
PAXdb E.coli [ppm]: 2.57 (Q 87)

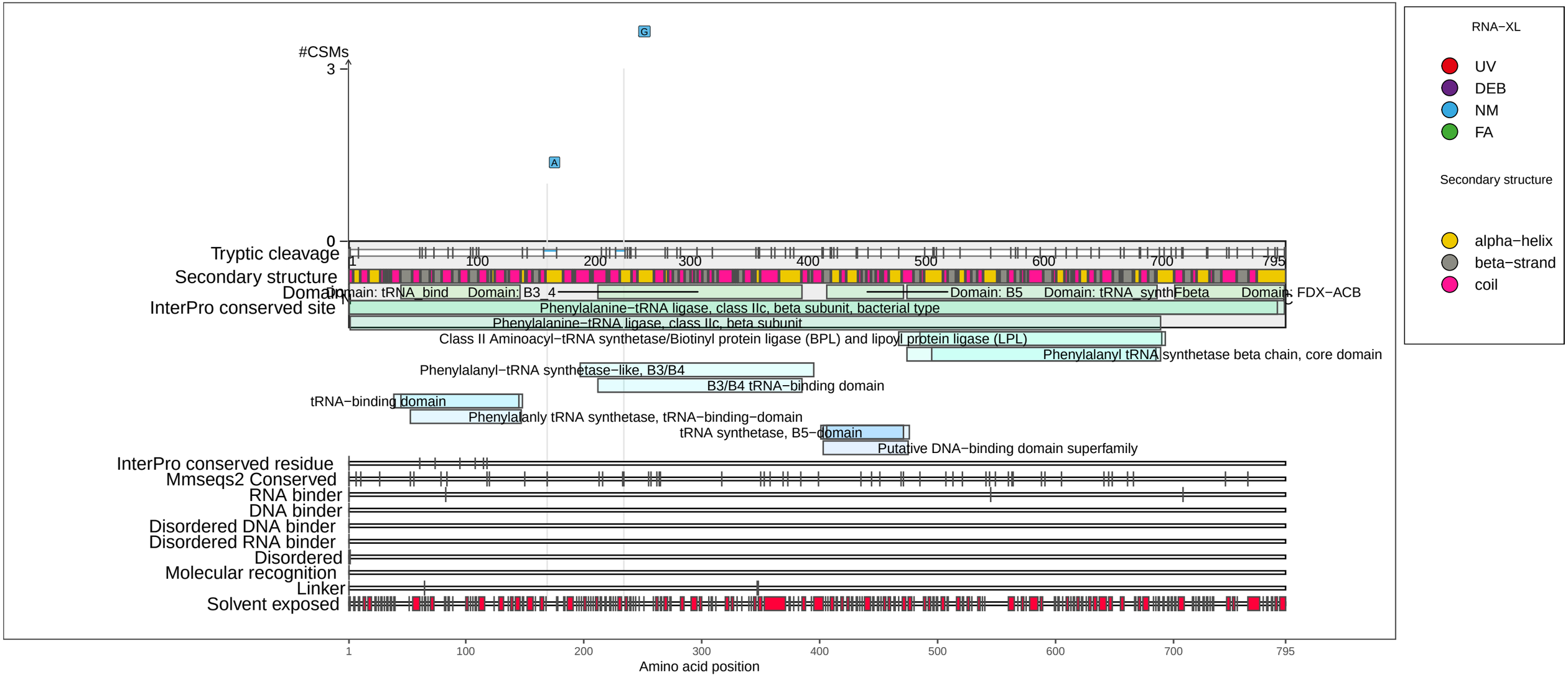
− RNA functions: not annotated



P07395
SYFB_ECOLI Phenylalanine−−tRNA ligase beta subunit

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 2.87 (Q 88)
PAXdb E.coli [ppm]: 2.42 (Q 83)

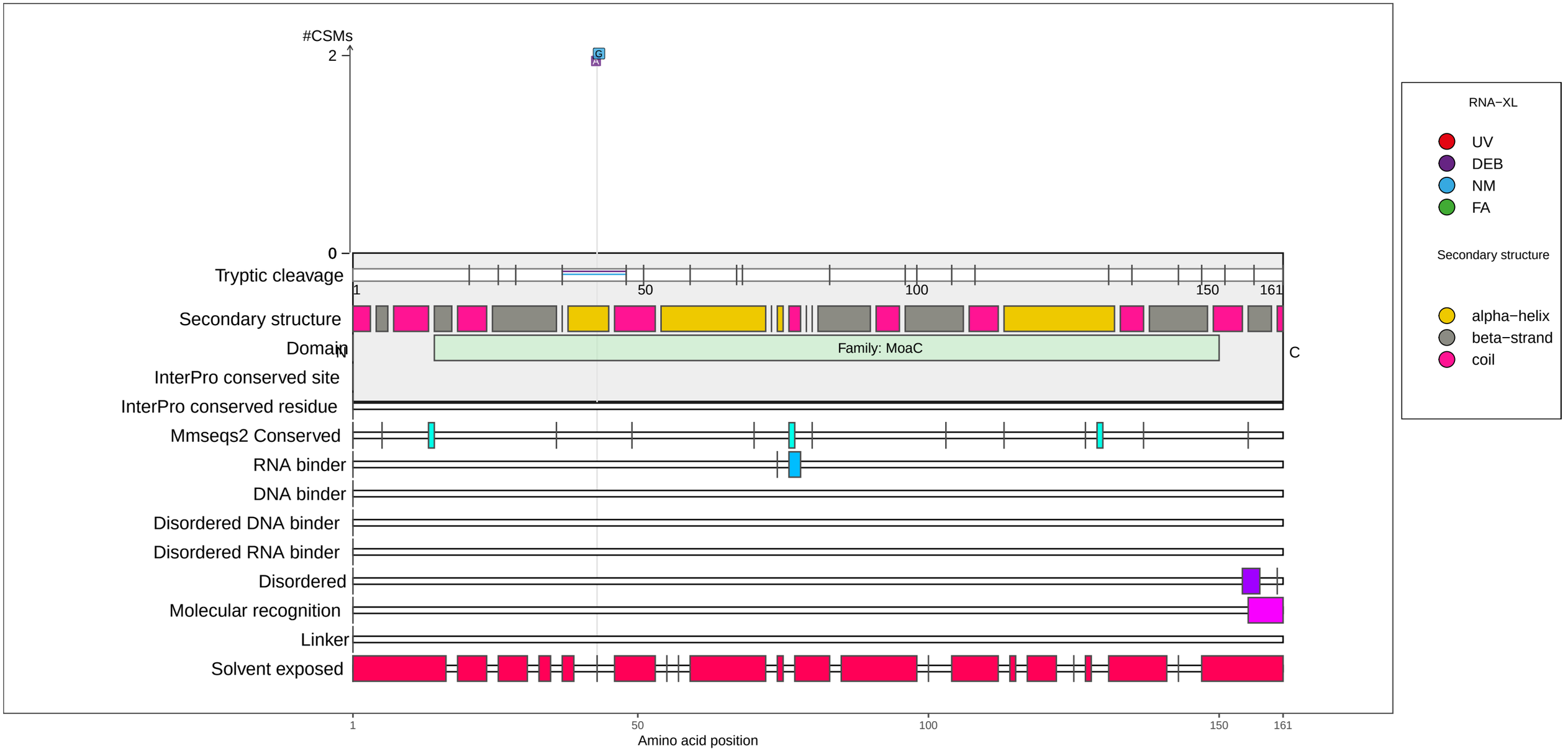
− RNA functions:
aminoacyl−tRNA ligase activity; ncRNA metabolic process
phenylalanine−tRNA ligase activity; phenylalanine−tRNA ligase complex; phenylalanyl−tRNA aminoacylation
Putative tRNA binding domain; RNA binding; RNA metabolic process; tRNA aminoacylation
tRNA aminoacylation for protein translation; tRNA binding; tRNA metabolic process
tRNA synthetase B5 domain



P0A738
MOAC_ECOLI Cyclic pyranopterin monophosphate synthase

− Abundance:
tryptic [log10 Intensity]: 7.68 (Q 44)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.12 (Q 75)

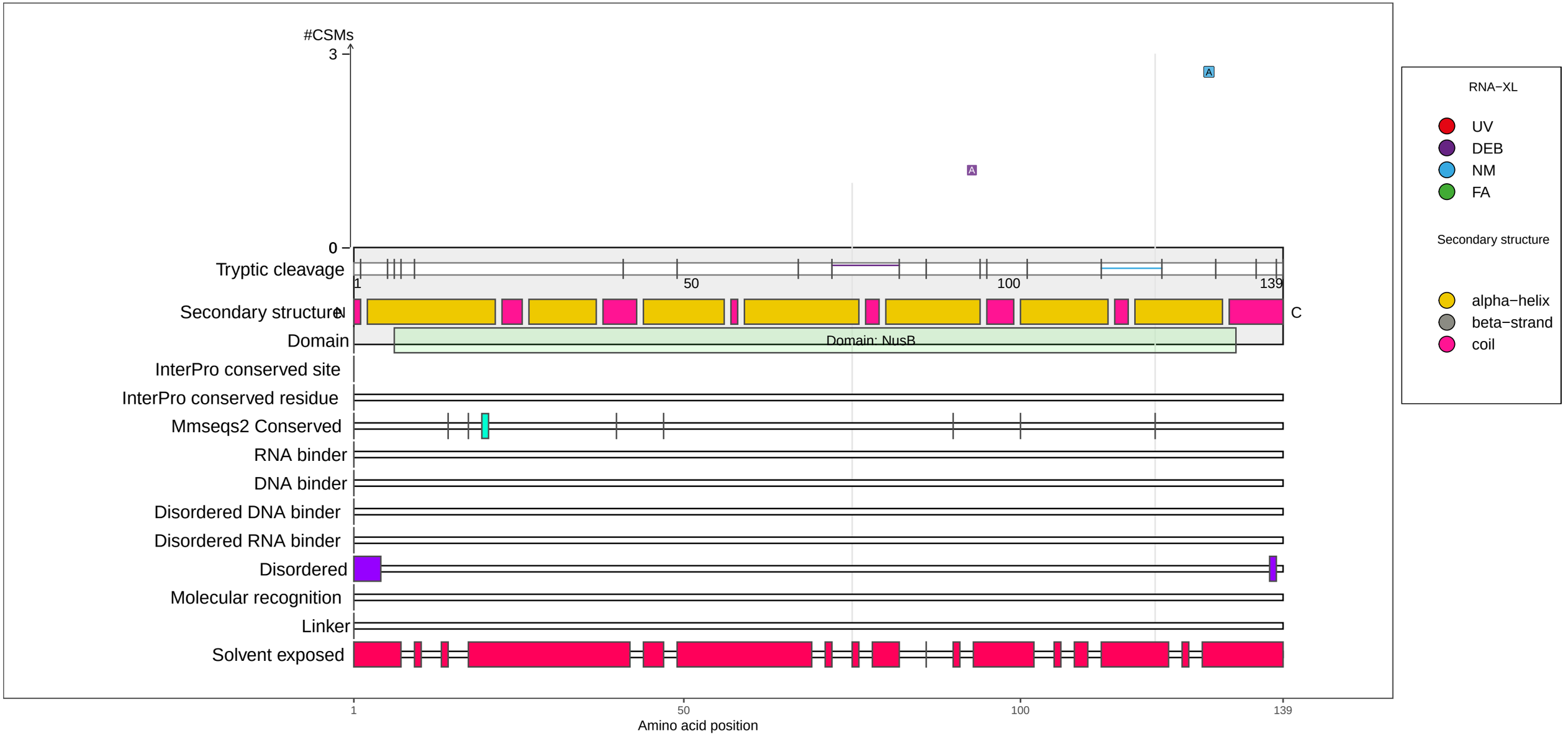
− RNA functions: not annotated



P0A780
NUSB_ECOLI Transcription antitermination protein NusB

− Abundance:
tryptic [log10 Intensity]: 8.94 (Q 87)
PAXdb K12 strain [ppm]: 2.45 (Q 76)
PAXdb E.coli [ppm]: 2.28 (Q 80)

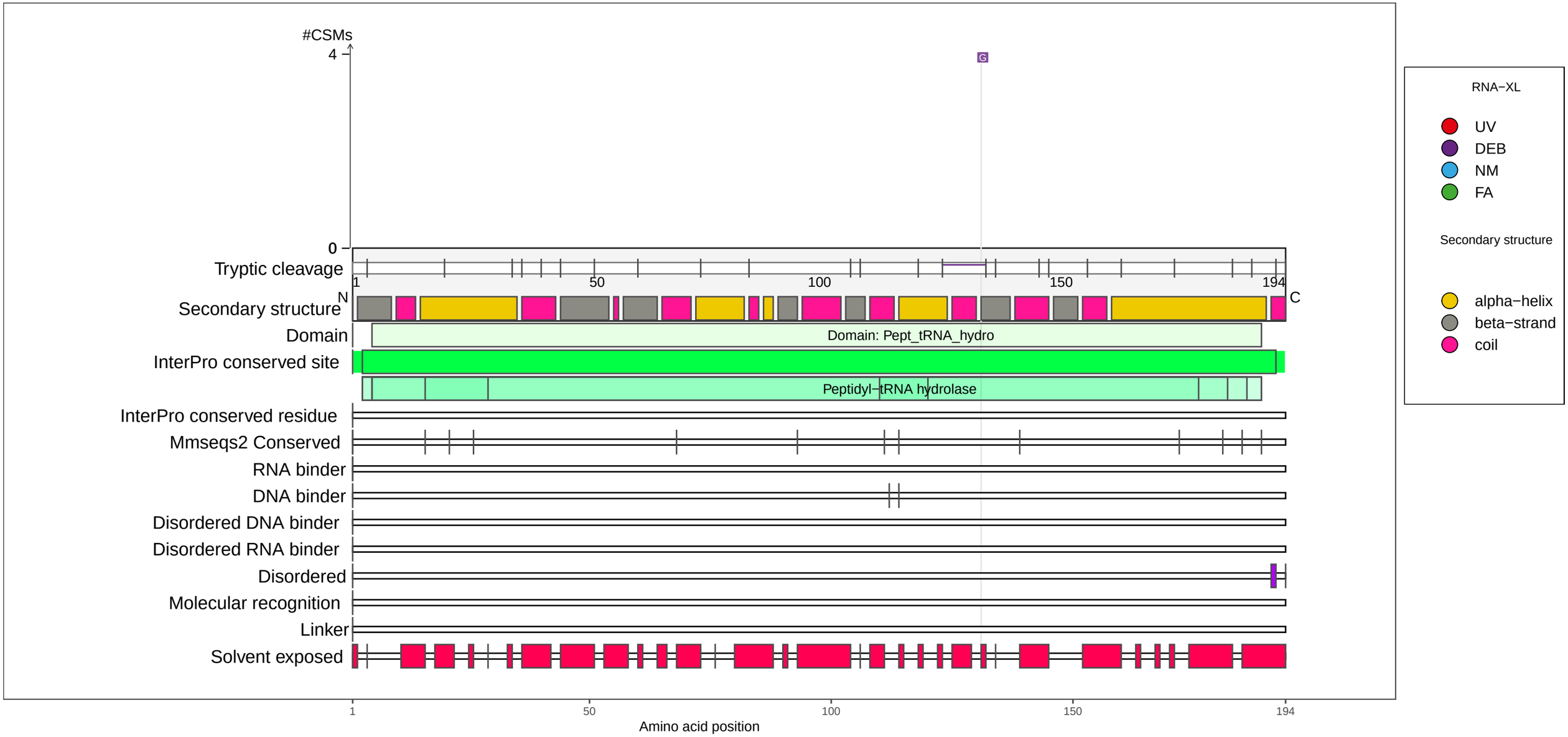
− RNA functions:
RNA binding; RNA biosynthetic process; RNA metabolic process



P0A7D1
PTH_ECOLI Peptidyl−tRNA hydrolase

− Abundance:
tryptic [log10 Intensity]: 7.65 (Q 43)
PAXdb K12 strain [ppm]: 1.88 (Q 56)
PAXdb E.coli [ppm]: 1.95 (Q 71)

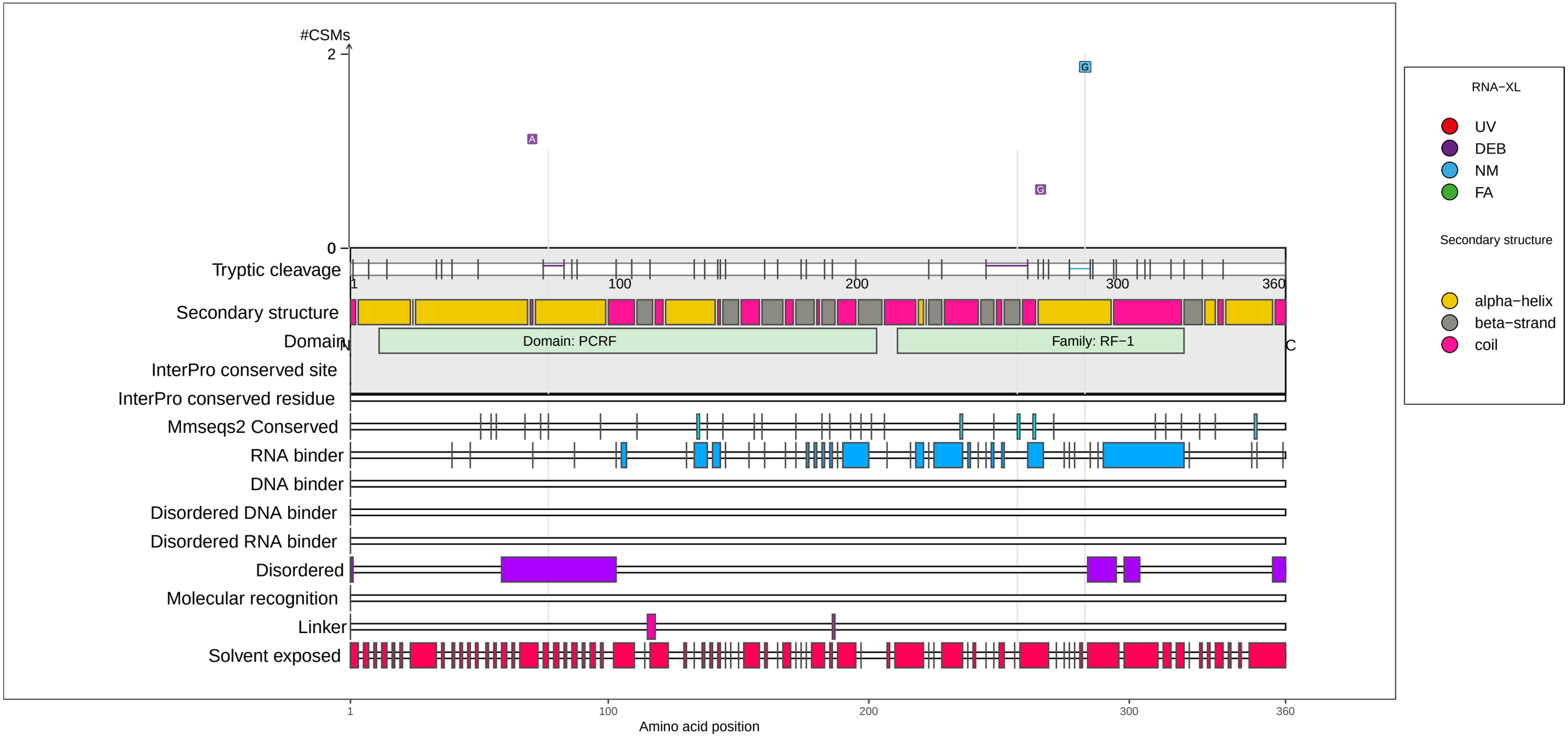
− RNA functions:
aminoacyl−tRNA hydrolase activity; Peptidyl−tRNA hydrolase



P0A7I0
RF1_ECOLI Peptide chain release factor RF1

− Abundance:
tryptic [log10 Intensity]: 7.99 (Q 57)
PAXdb K12 strain [ppm]: 2.29 (Q 70)
PAXdb E.coli [ppm]: 1.84 (Q 68)

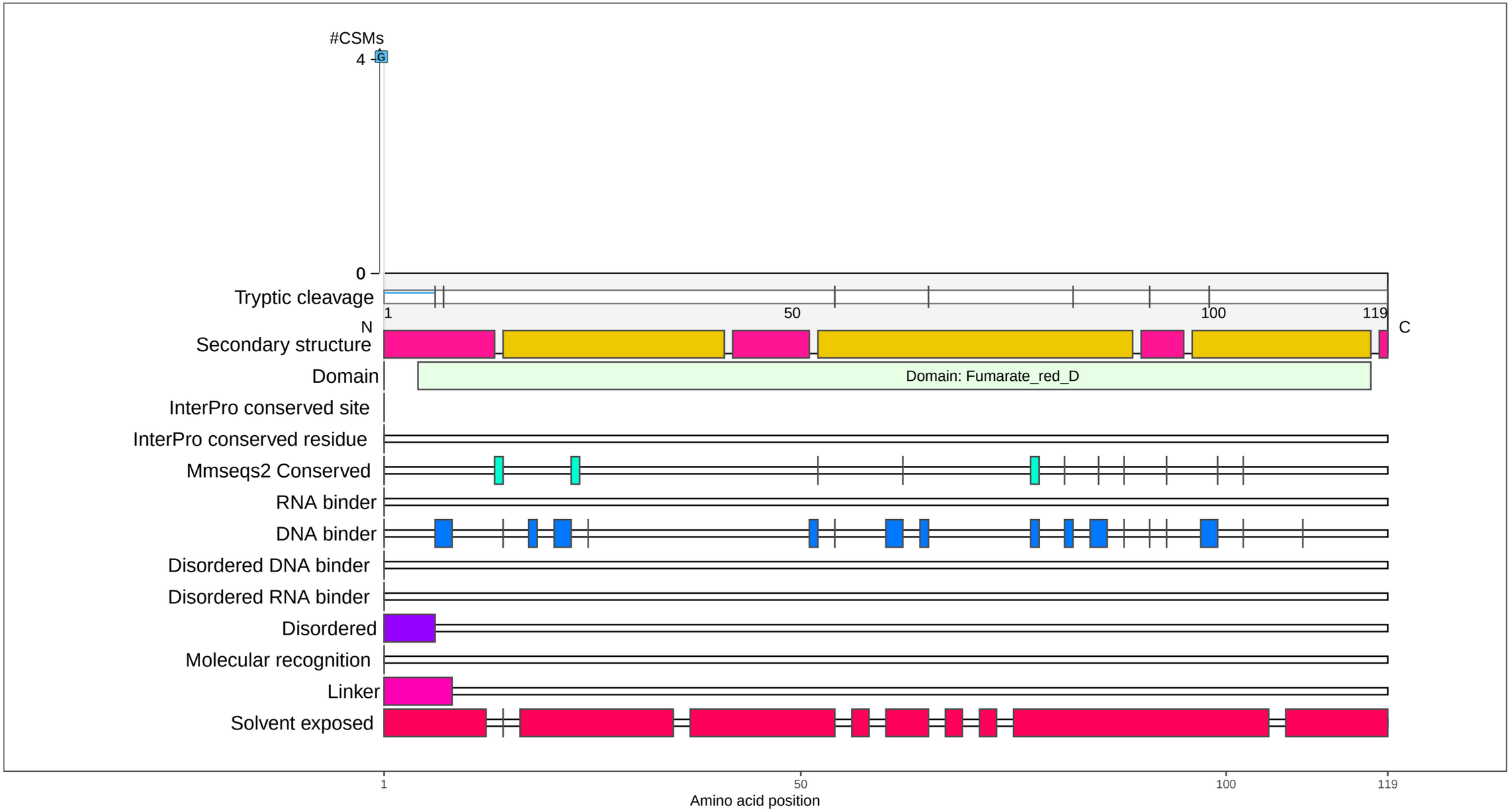
− RNA functions:
RNA binding

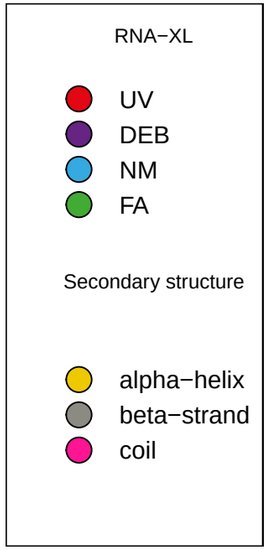


P0A8Q3
FRDD_ECOLI Fumarate reductase subunit D

− Abundance:
tryptic [log10 Intensity]: 7.2 (Q 21)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.37 (Q 33)

− RNA functions: not annotated

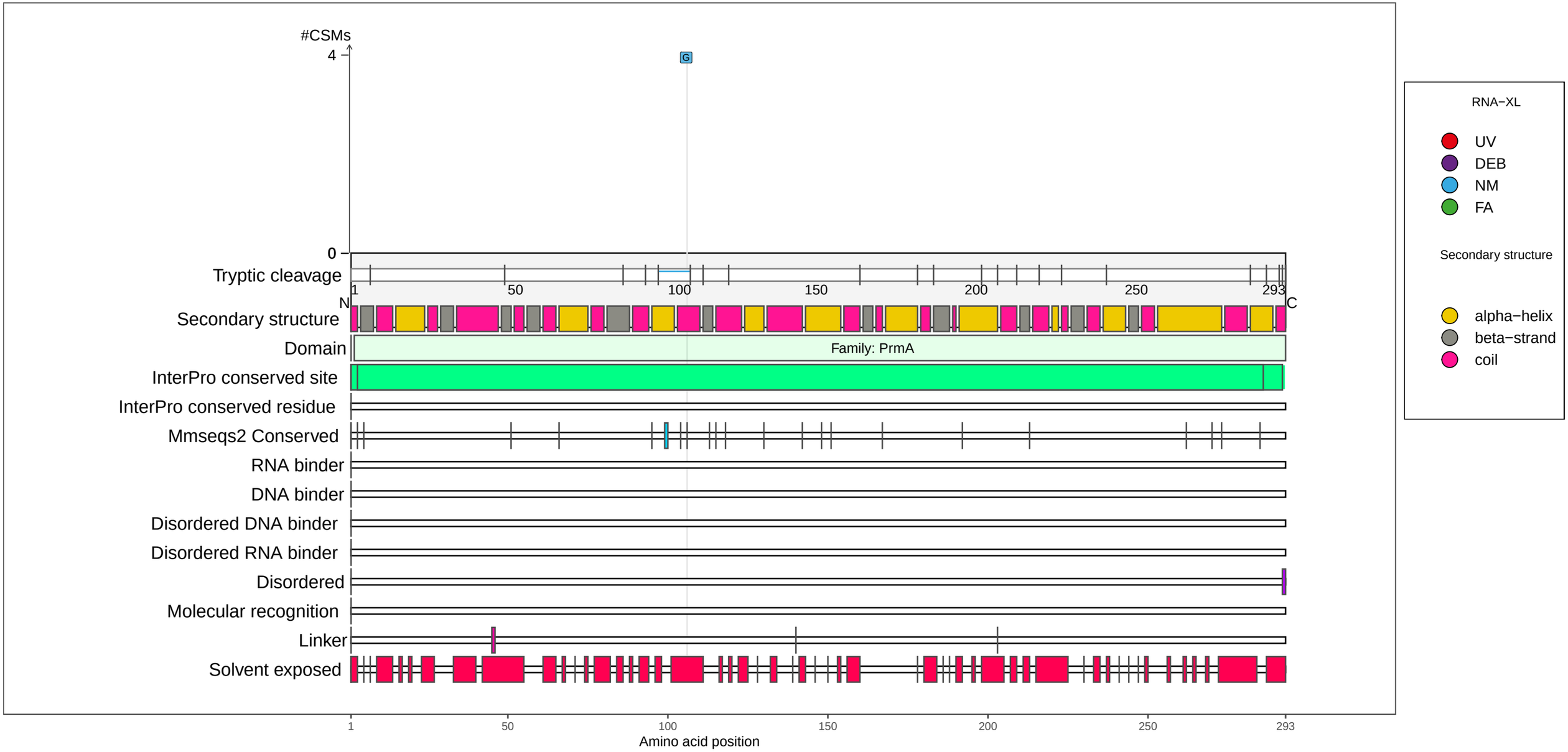




P0A8T1
PRMA_ECOLI Ribosomal protein L11 methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 2.26 (Q 69)
PAXdb E.coli [ppm]: 2.15 (Q 76)

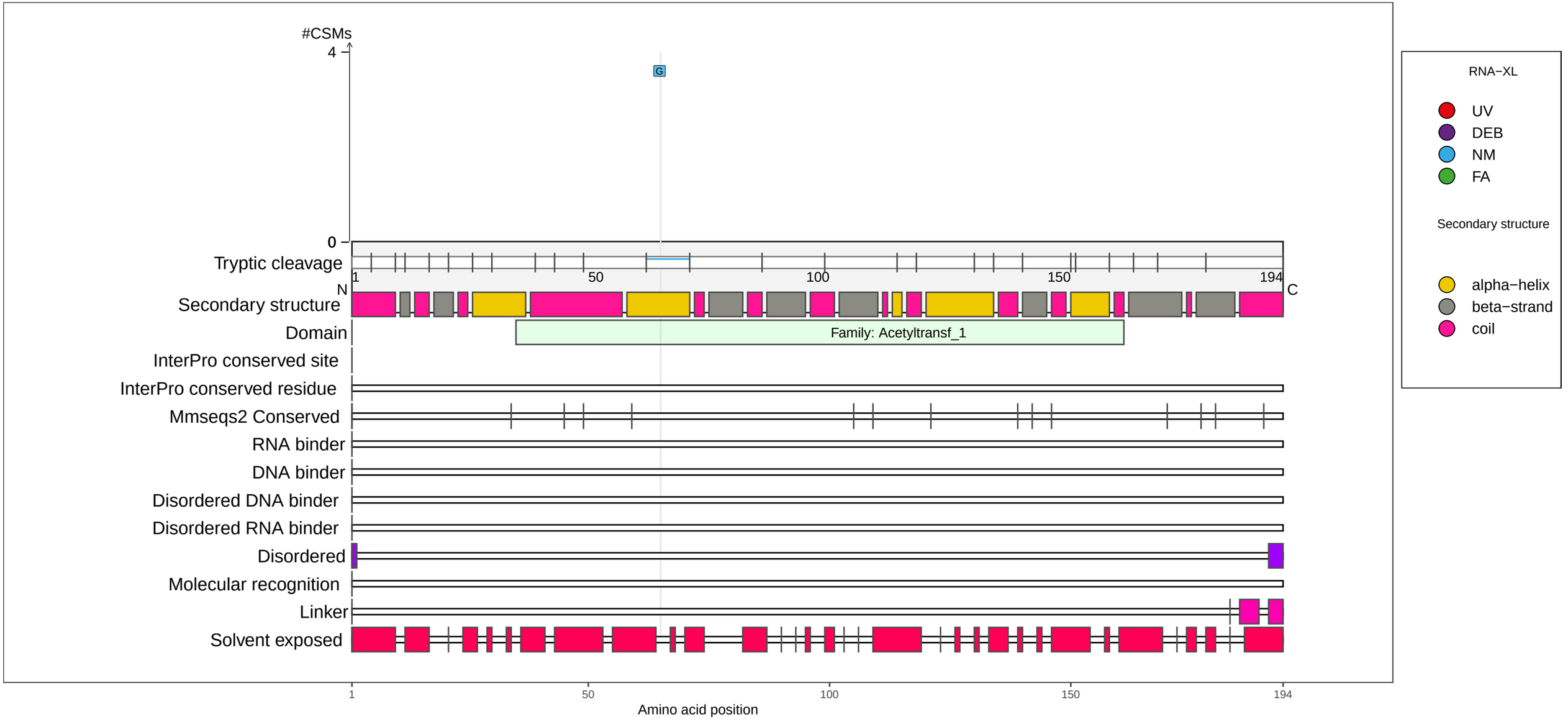
− RNA functions: not annotated



P0A948
RIMJ_ECOLI [Ribosomal protein S5]−alanine N−acetyltransferase

− Abundance:
tryptic [log10 Intensity]: 6.95 (Q 12)
PAXdb K12 strain [ppm]: 1.37 (Q 30)
PAXdb E.coli [ppm]: 1.28 (Q 54)

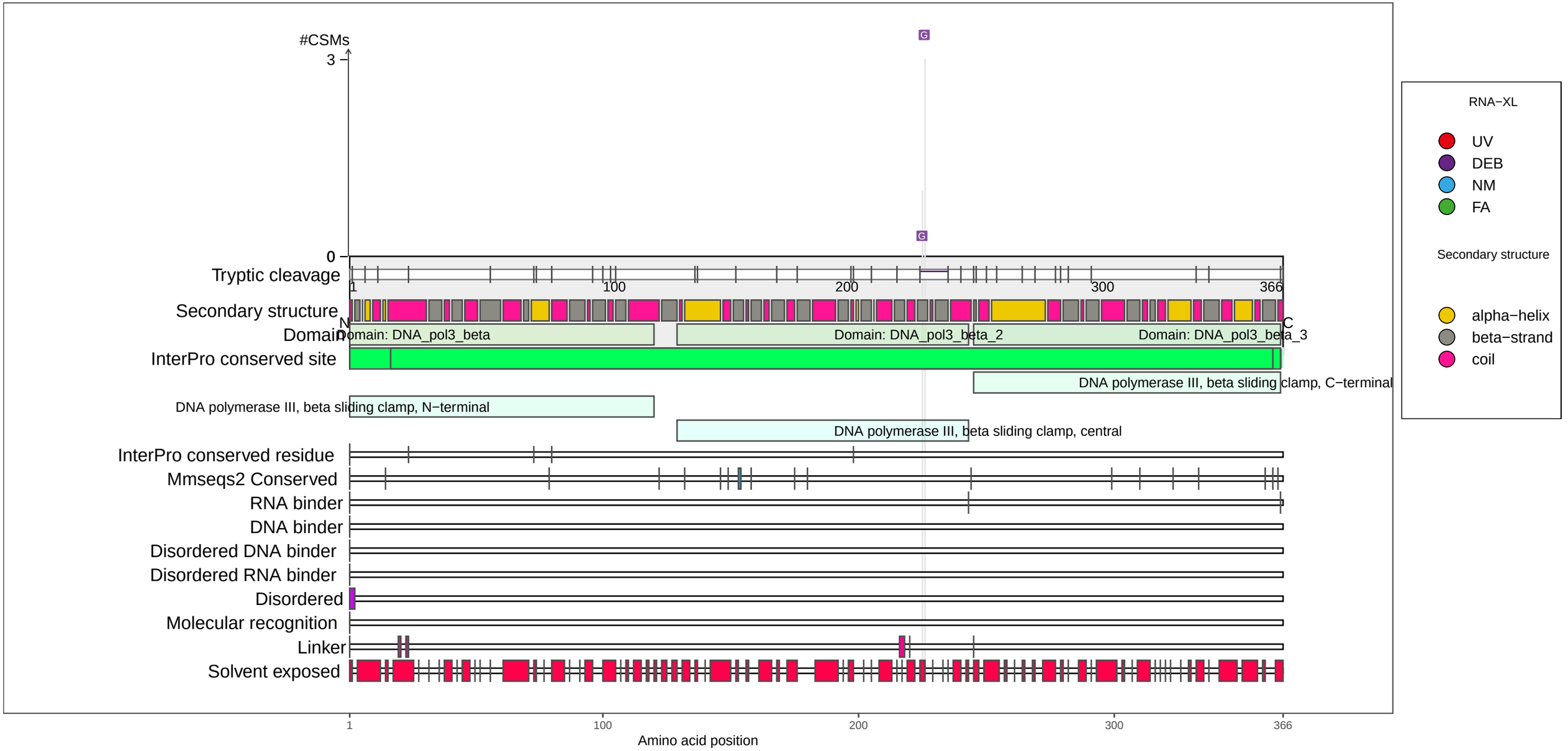
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA processing
rRNA metabolic process; rRNA processing



P0A988
DPO3B_ECOLI Beta sliding clamp

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 2.27 (Q 69)
PAXdb E.coli [ppm]: 2.18 (Q 77)

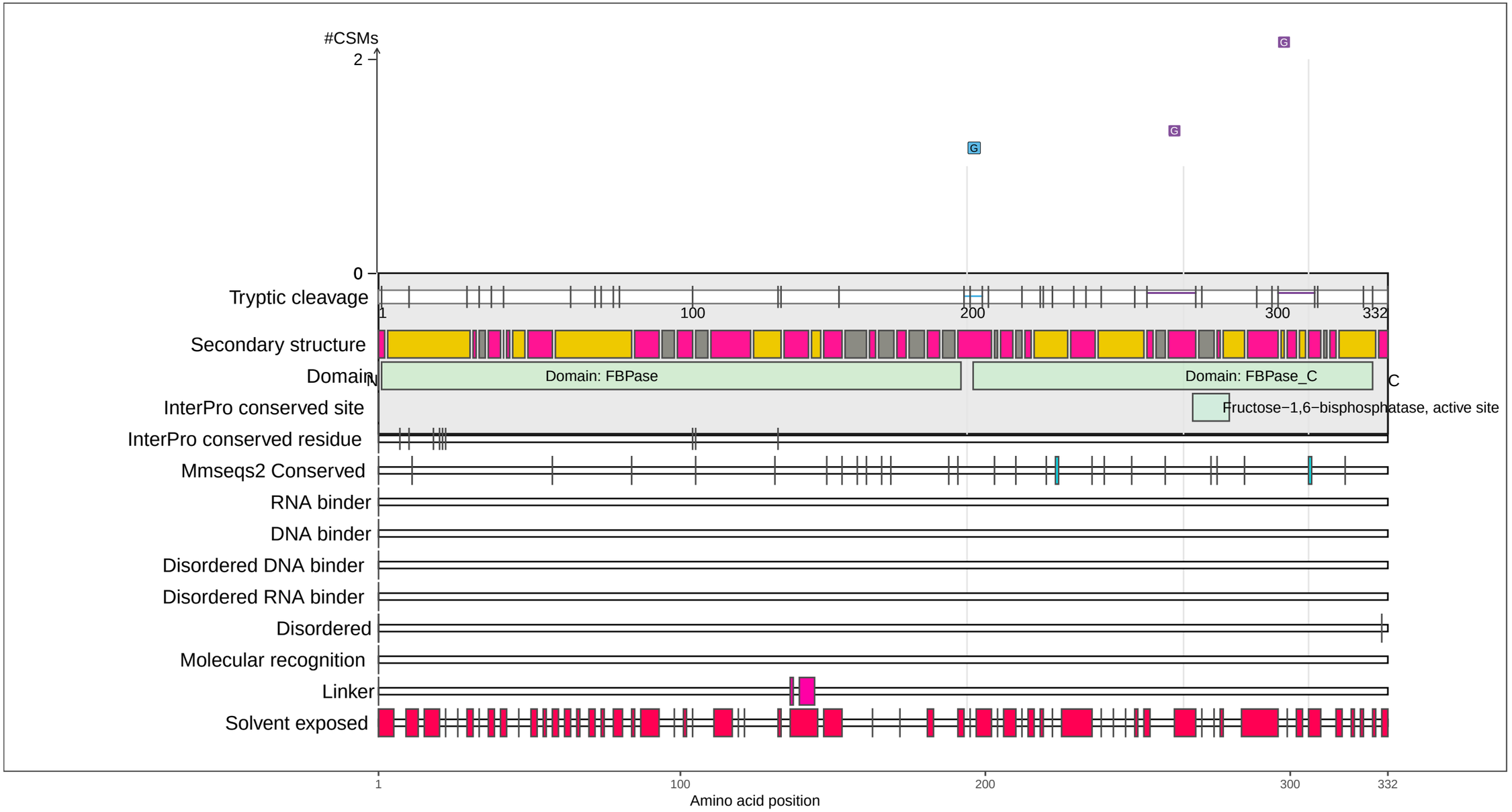
− RNA functions: not annotated



P0A993
F16PA_ECOLI Fructose−1,6−bisphosphatase class 1

− Abundance:
tryptic [log10 Intensity]: 8.38 (Q 72)
PAXdb K12 strain [ppm]: 2.74 (Q 84)
PAXdb E.coli [ppm]: 2.31 (Q 80)

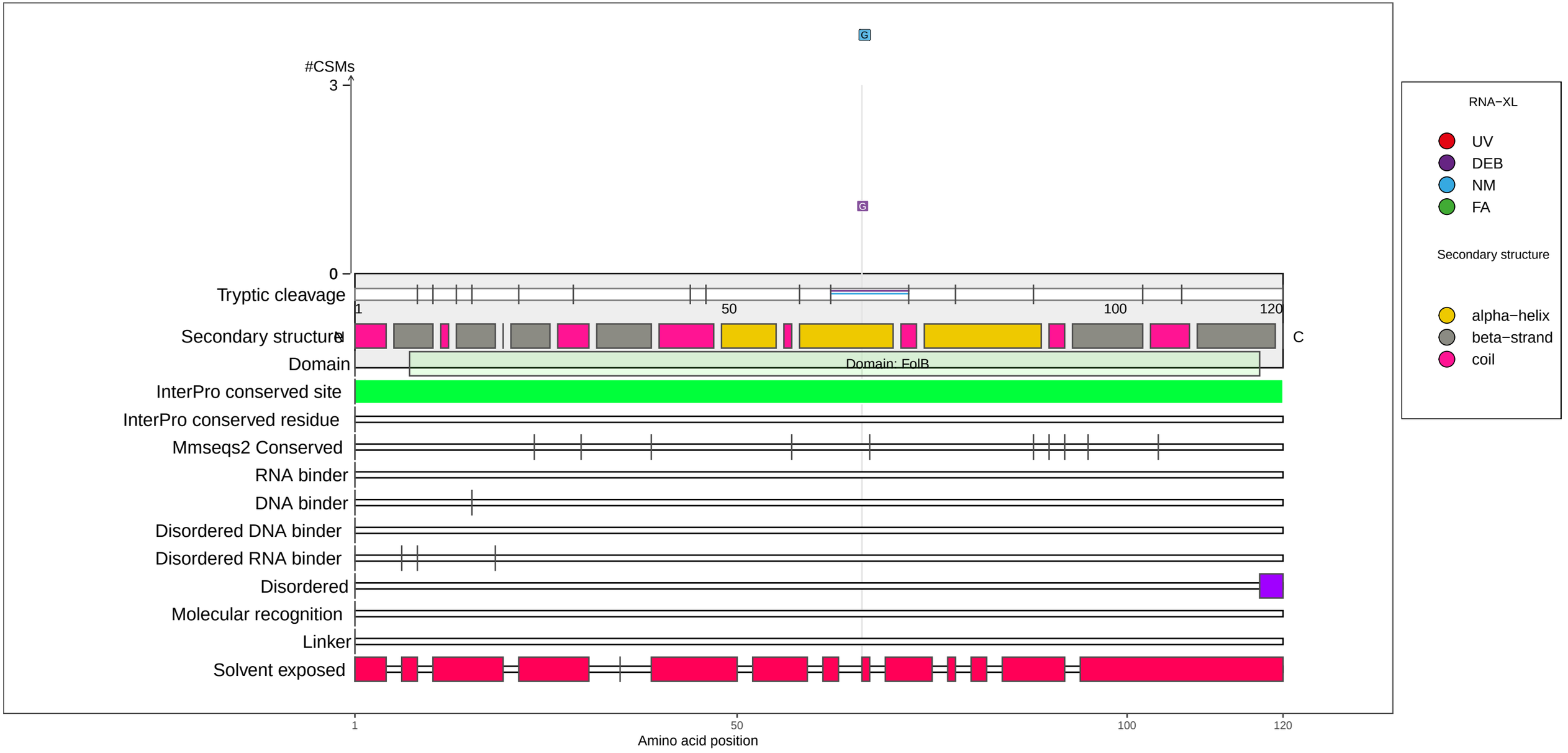
− RNA functions: not annotated



P0AC19
FOLX_ECOLI Dihydroneopterin triphosphate 2'−epimerase

− Abundance:
tryptic [log10 Intensity]: 8.82 (Q 84)
PAXdb K12 strain [ppm]: 2.2 (Q 67)
PAXdb E.coli [ppm]: 2.24 (Q 78)

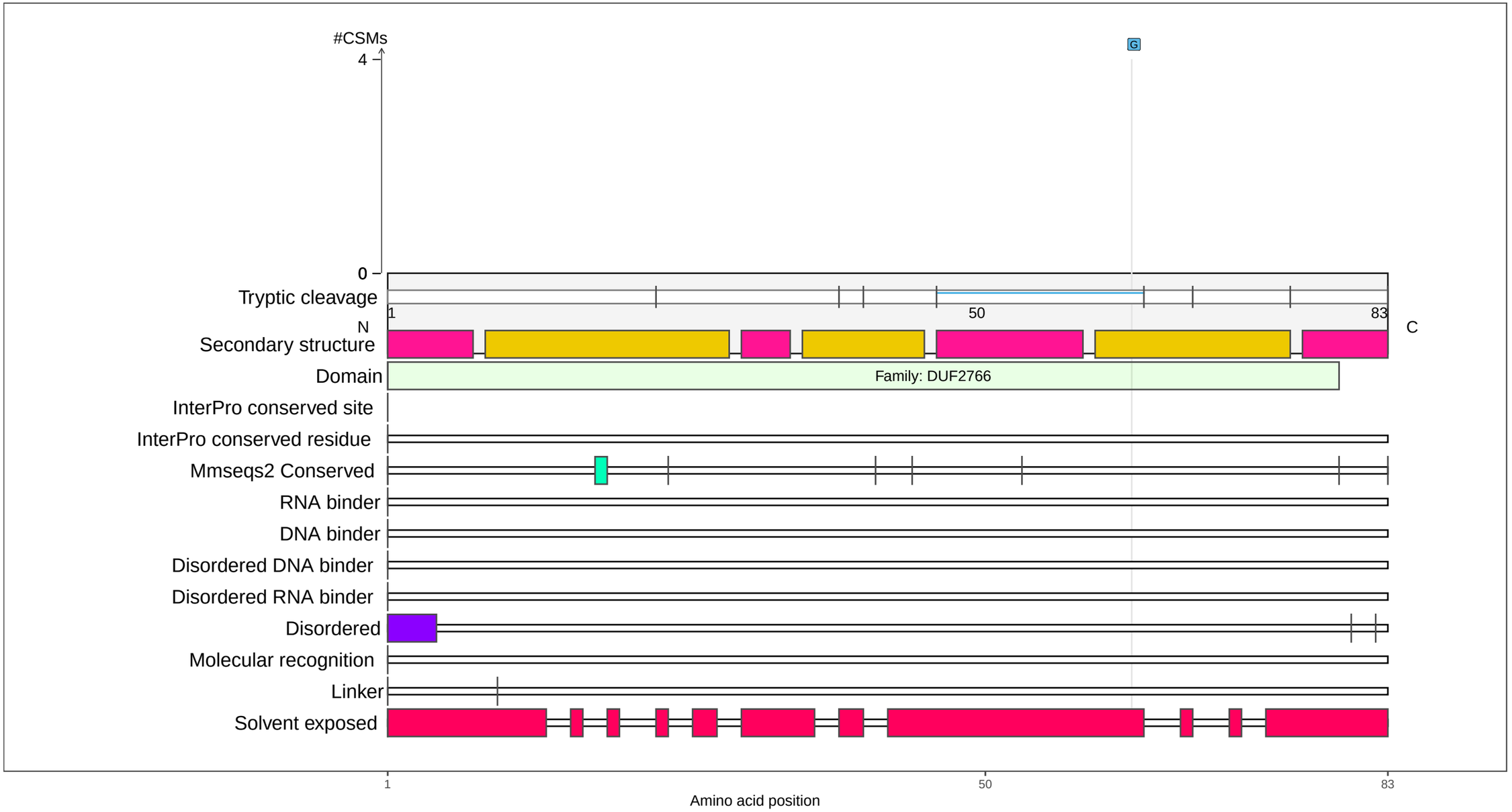
− RNA functions: not annotated

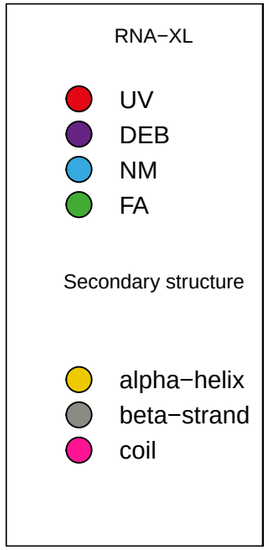


P0AD10
YECJ_ECOLI Uncharacterized protein YecJ

− Abundance:
tryptic [log10 Intensity]: 7.43 (Q 32)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.11 (Q 75)

− RNA functions: not annotated

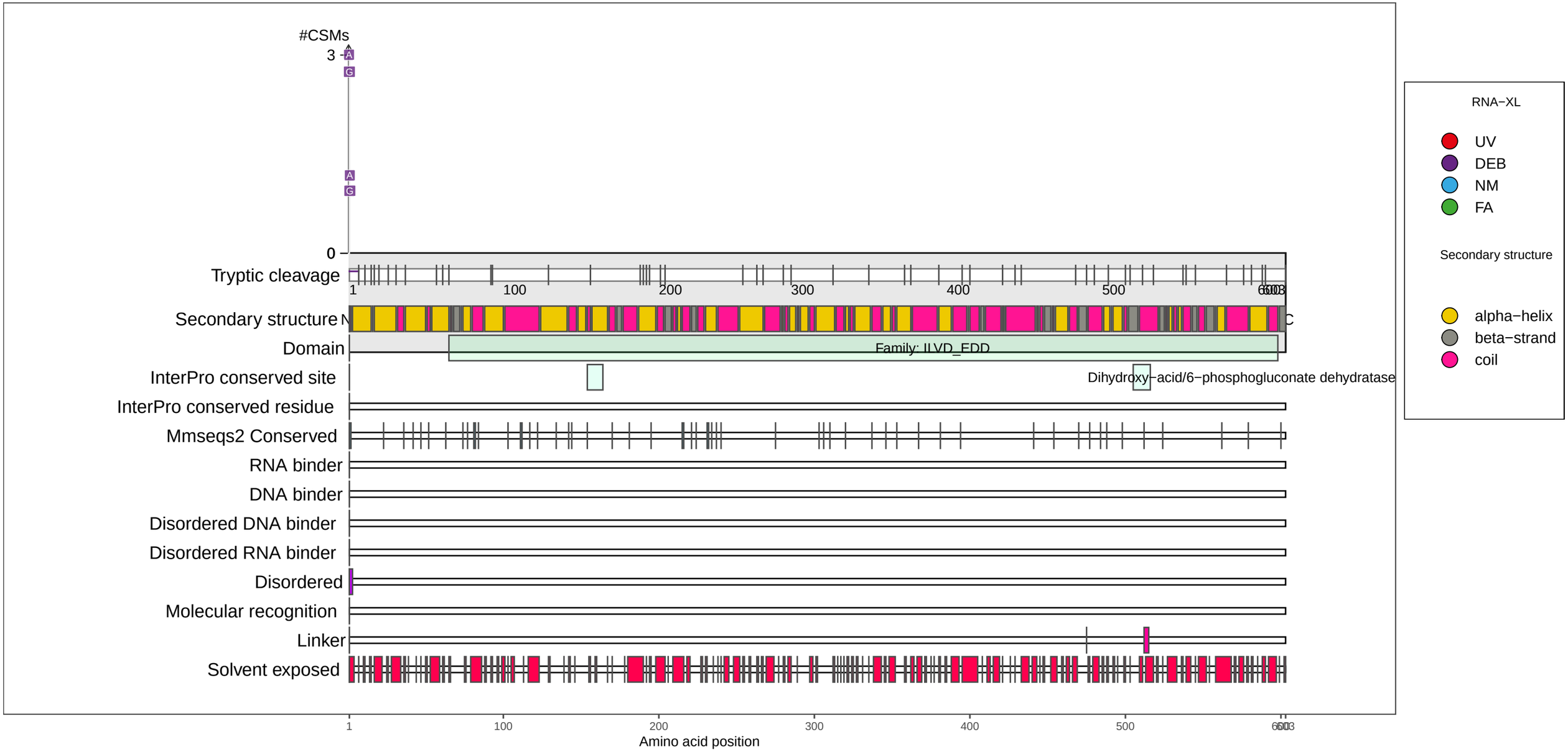




P0ADF6
EDD_ECOLI Phosphogluconate dehydratase

− Abundance:
tryptic [log10 Intensity]: 8.09 (Q 61)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 1.61 (Q 63)

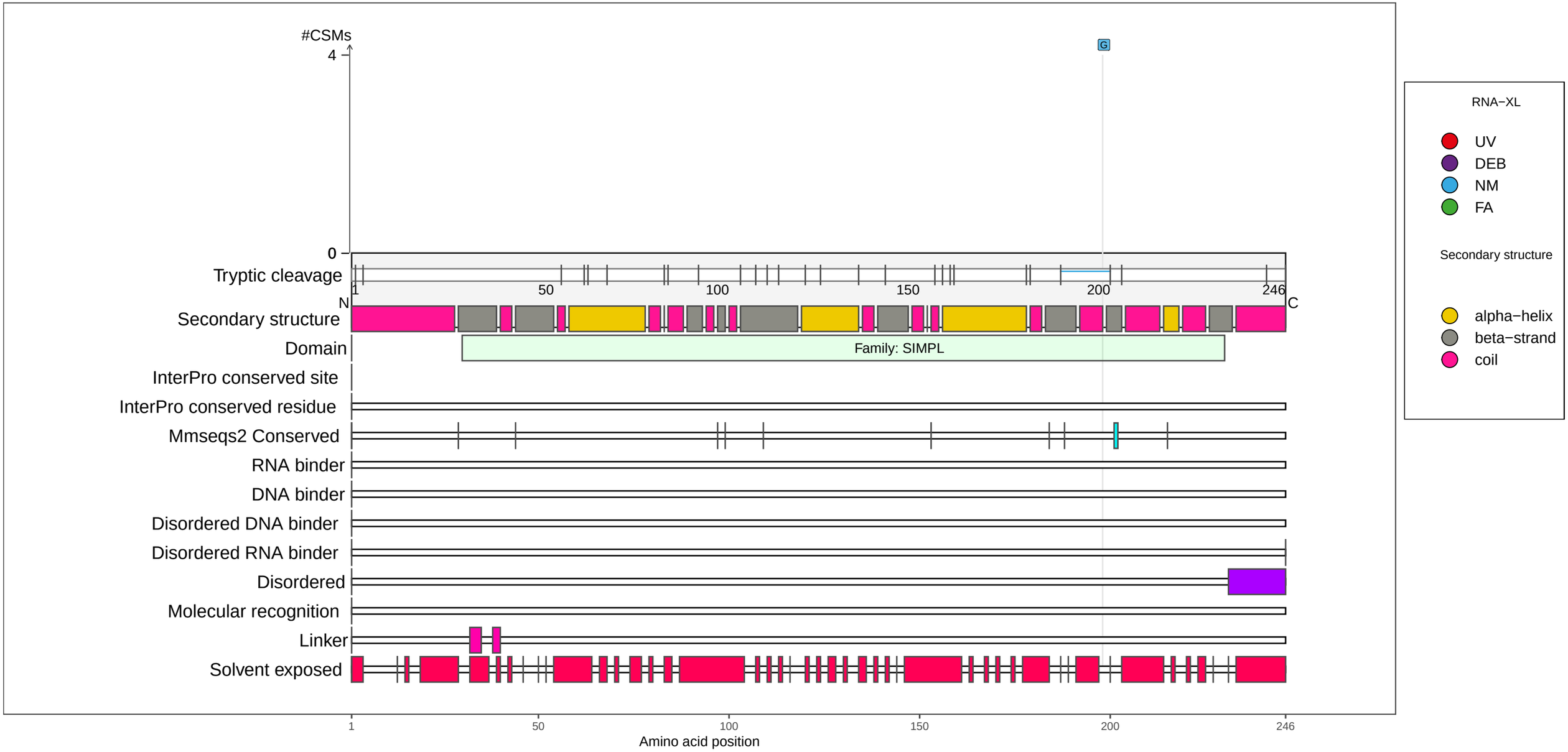
− RNA functions: not annotated



P0ADS6
YGGE_ECOLI Uncharacterized protein YggE

− Abundance:
tryptic [log10 Intensity]: 8.44 (Q 73)
PAXdb K12 strain [ppm]: 1.62 (Q 45)
PAXdb E.coli [ppm]: 2.67 (Q 89)

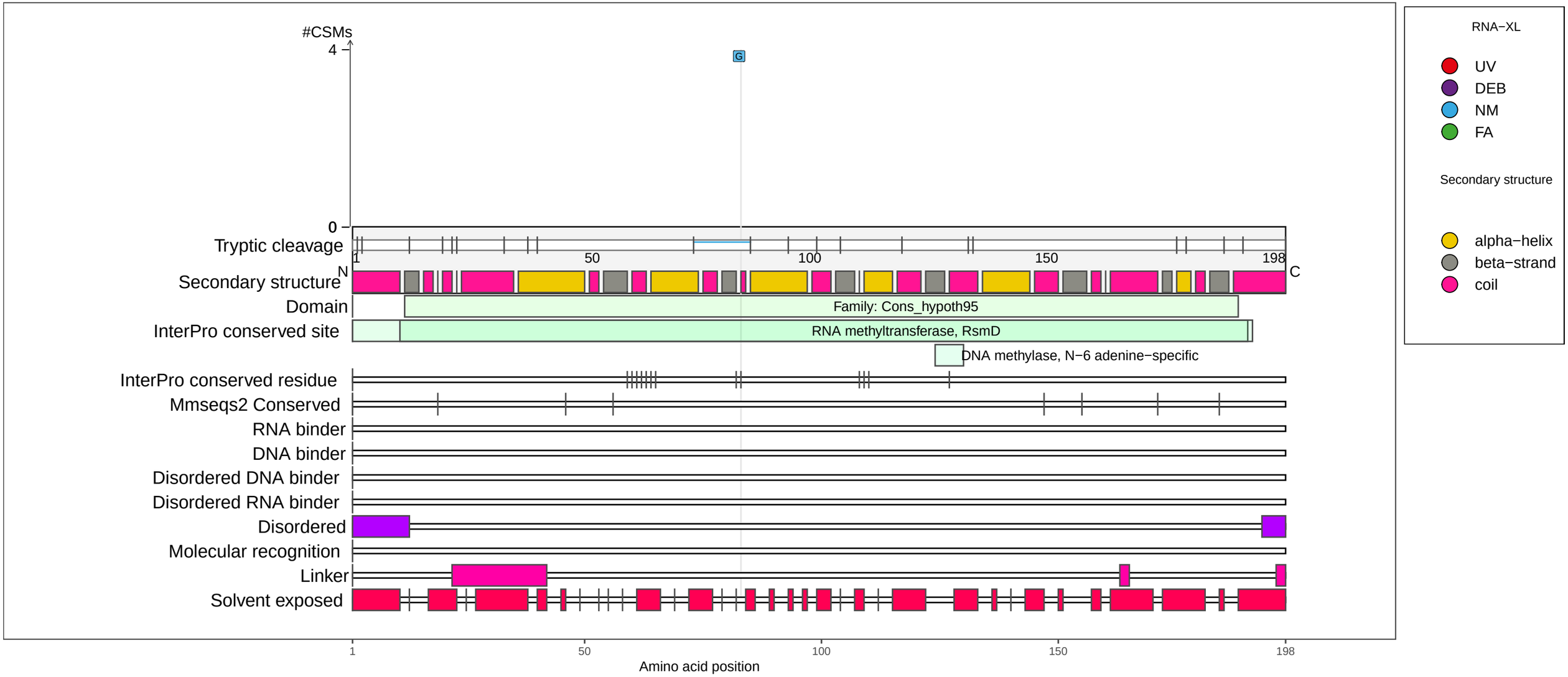
− RNA functions: not annotated



P0ADX9
RSMD_ECOLI Ribosomal RNA small subunit methyltransferase D

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.4 (Q 33)
PAXdb E.coli [ppm]: 1.55 (Q 61)

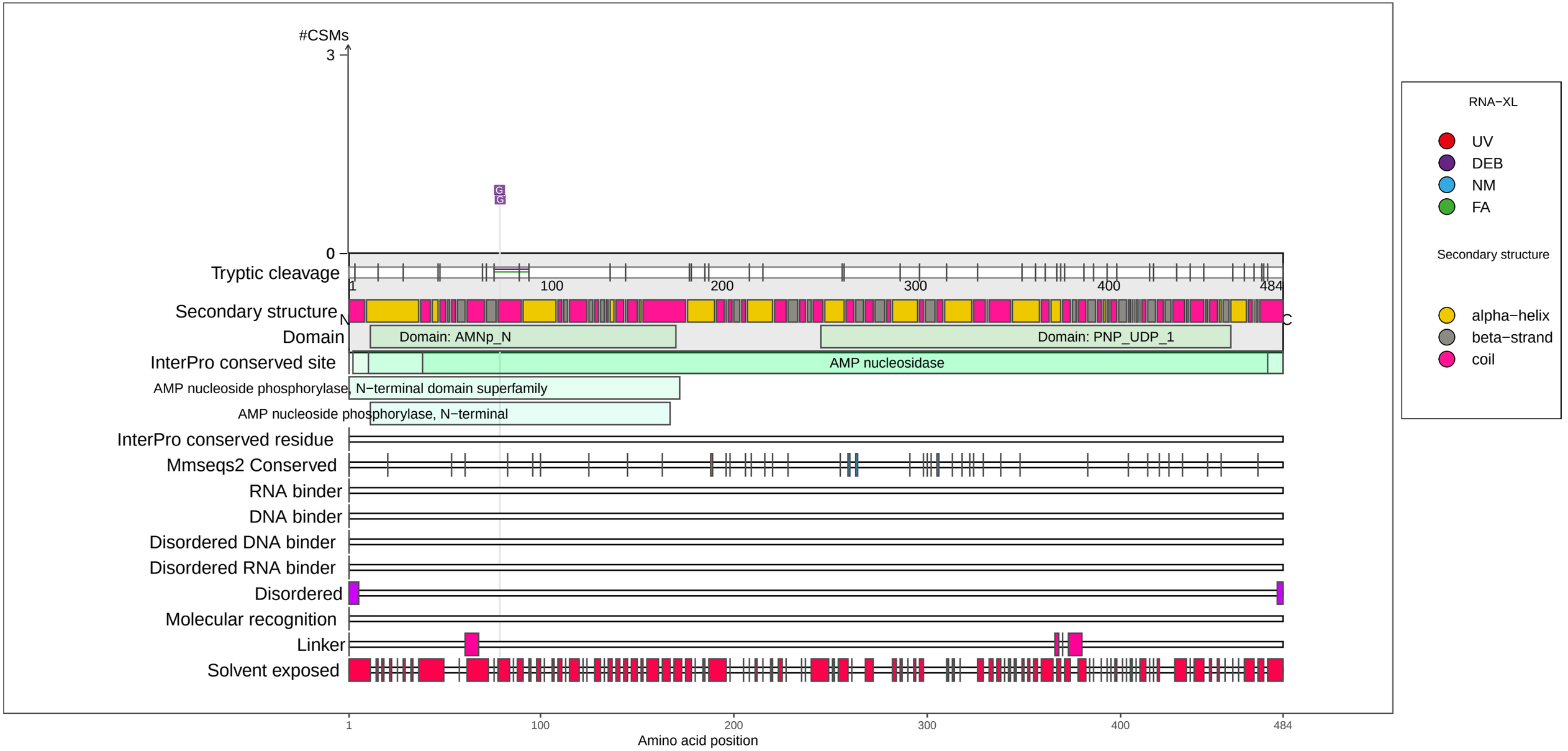
− RNA functions:
16S rRNA (guanine(966)−N(2))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (guanine−N2−)−methyltransferase activity
rRNA (guanine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P0AE12
AMN_ECOLI AMP nucleosidase

− Abundance:
tryptic [log10 Intensity]: 8.4 (Q 72)
PAXdb K12 strain [ppm]: 2.1 (Q 64)
PAXdb E.coli [ppm]: 1.7 (Q 64)

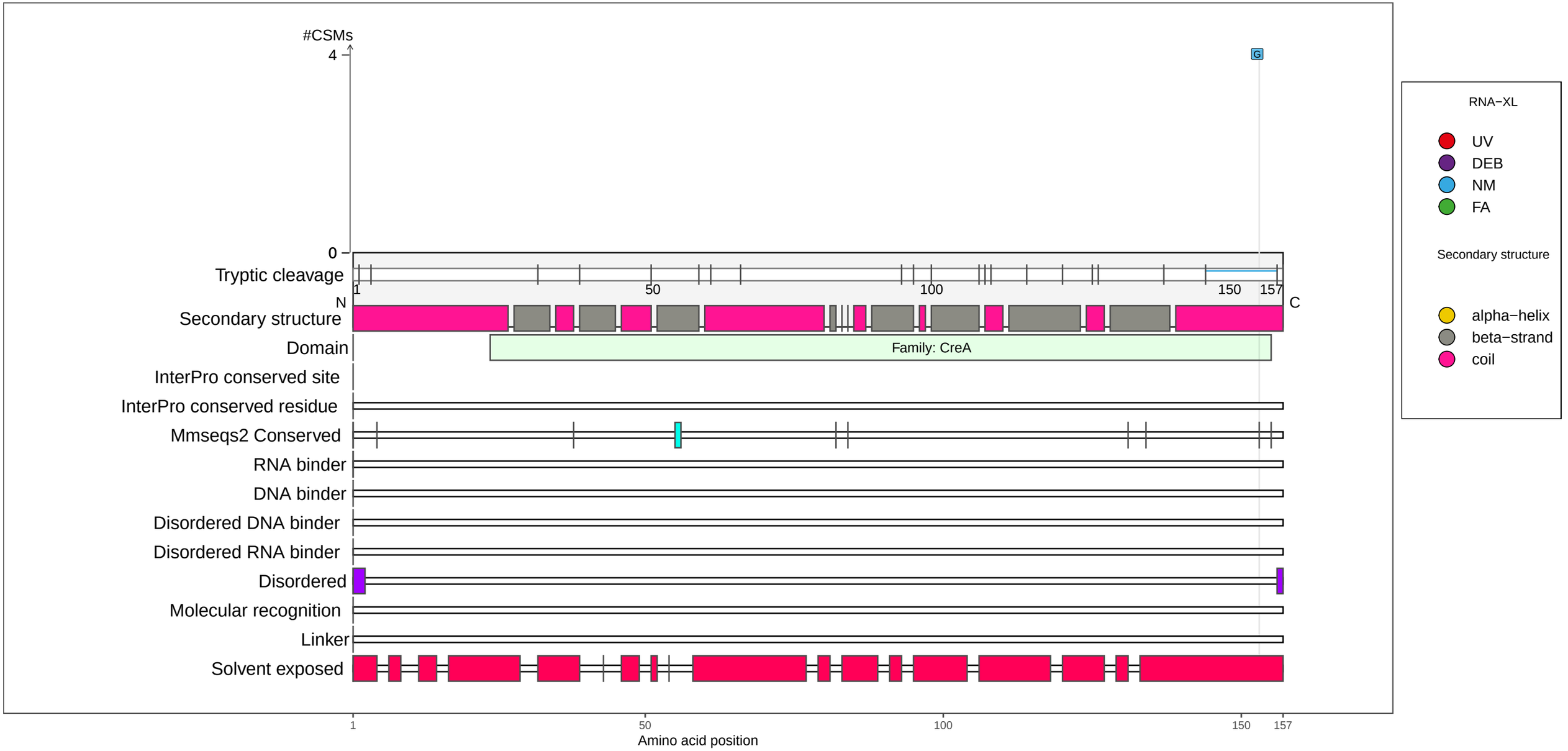
− RNA functions: not annotated



P0AE91
CREA_ECOLI Protein CreA

− Abundance:
tryptic [log10 Intensity]: 7.98 (Q 57)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 1.77 (Q 66)

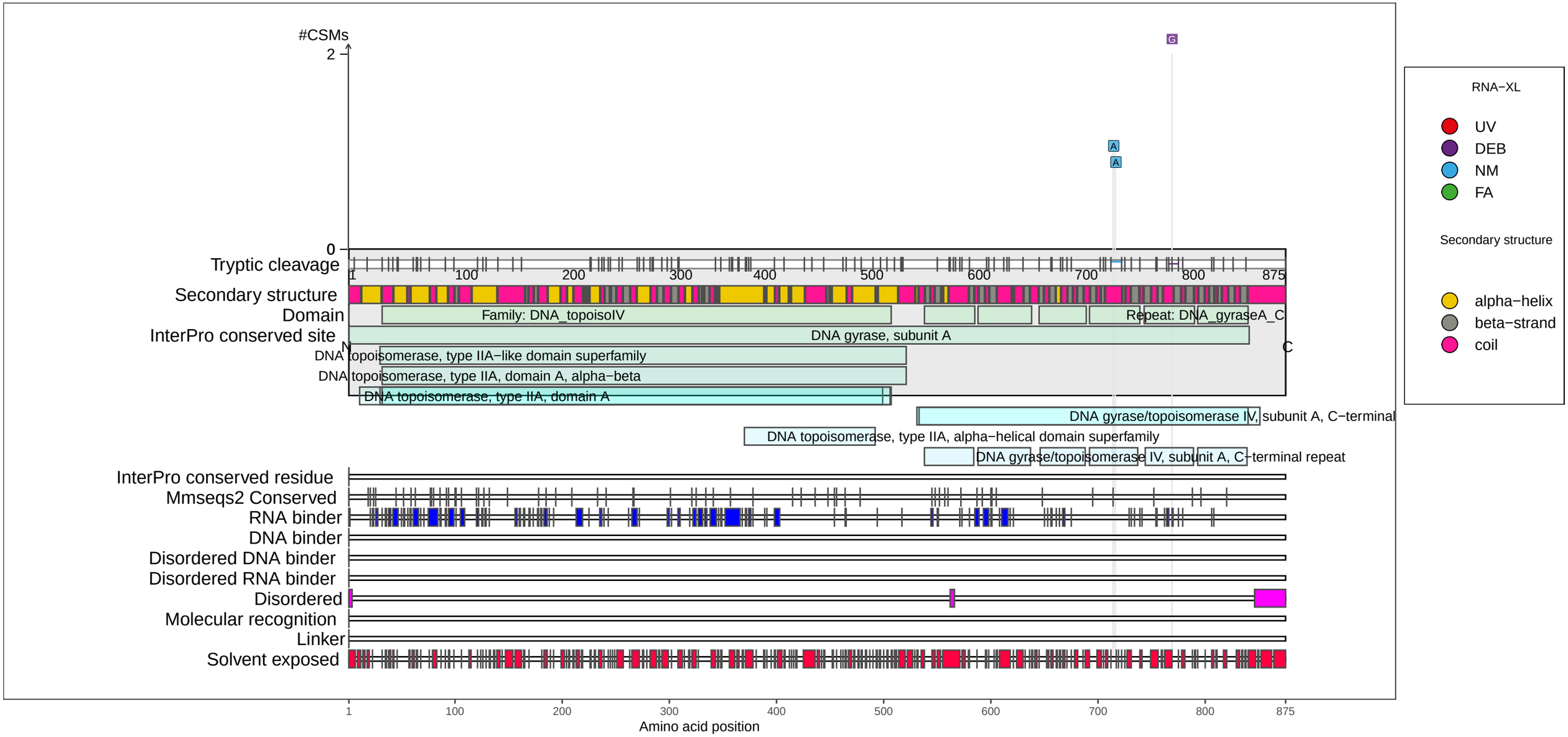
− RNA functions: not annotated



P0AES4
GYRA_ECOLI DNA gyrase subunit A

− Abundance:
tryptic [log10 Intensity]: 8.85 (Q 85)
PAXdb K12 strain [ppm]: 2.71 (Q 84)
PAXdb E.coli [ppm]: 2.67 (Q 89)

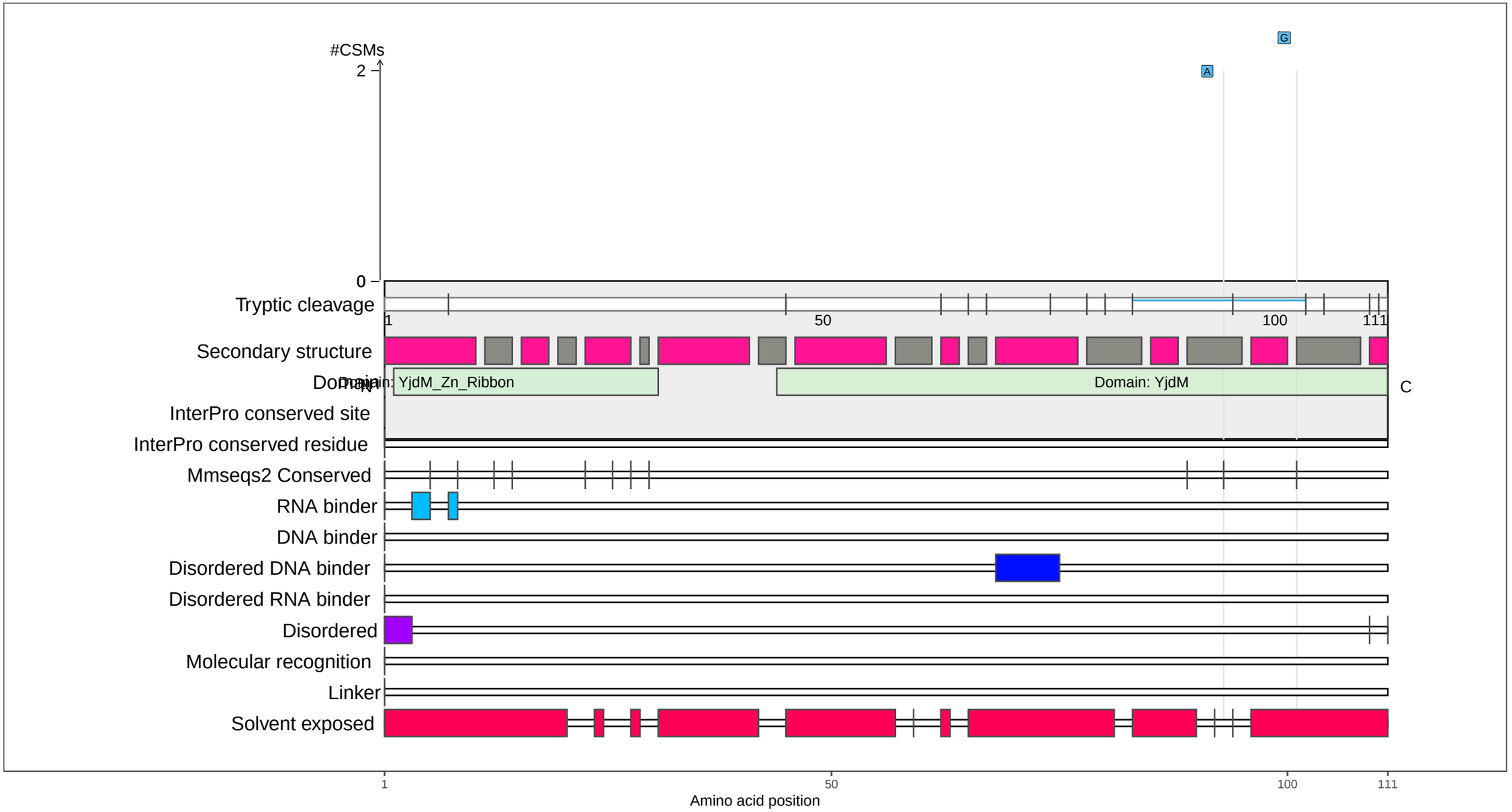
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0AFJ1
YJDM_ECOLI Protein YjdM

− Abundance:
tryptic [log10 Intensity]: 7.53 (Q 37)
PAXdb K12 strain [ppm]: 3.5 (Q 97)
PAXdb E.coli [ppm]: 2.3 (Q 80)

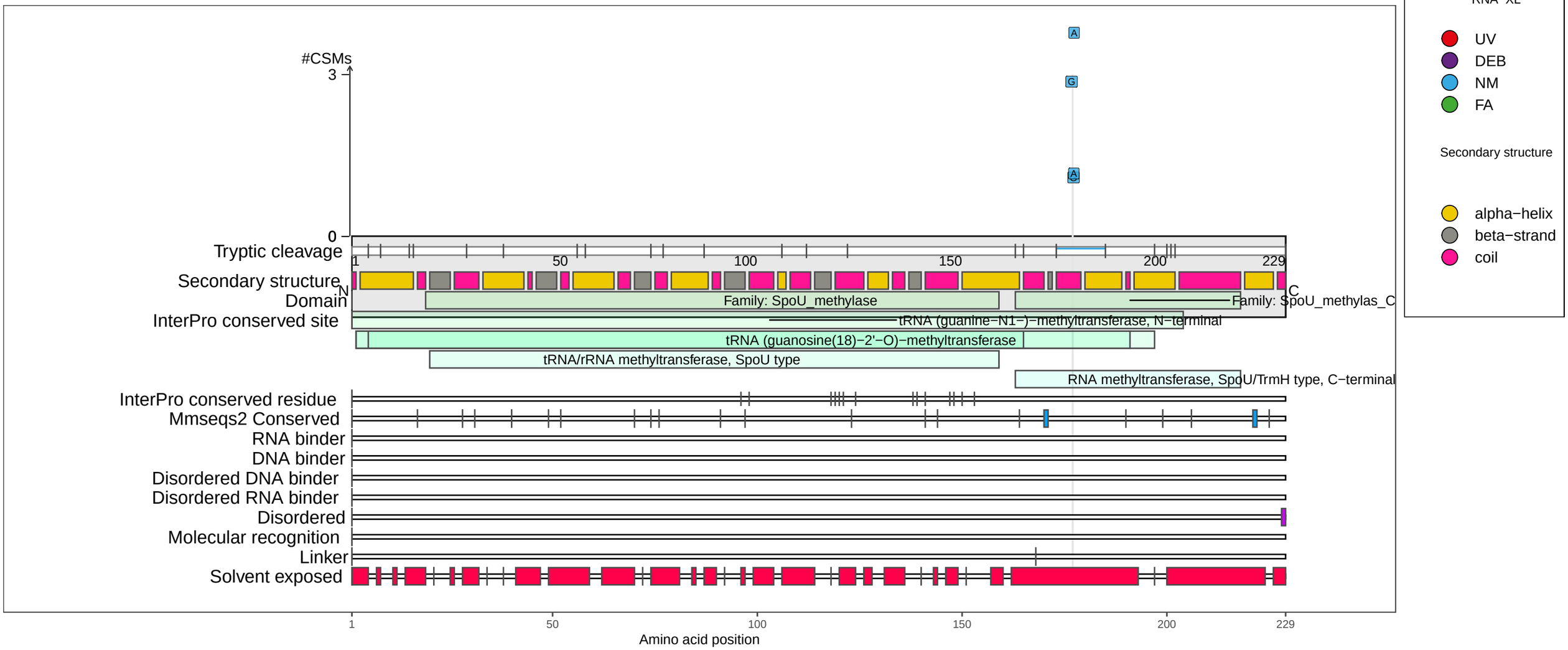
− RNA functions: not annotated



P0AGJ2
TRMH_ECOLI tRNA (guanosine(18)−2'−O)−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 2.33 (Q 71)
PAXdb E.coli [ppm]: 1.02 (Q 48)

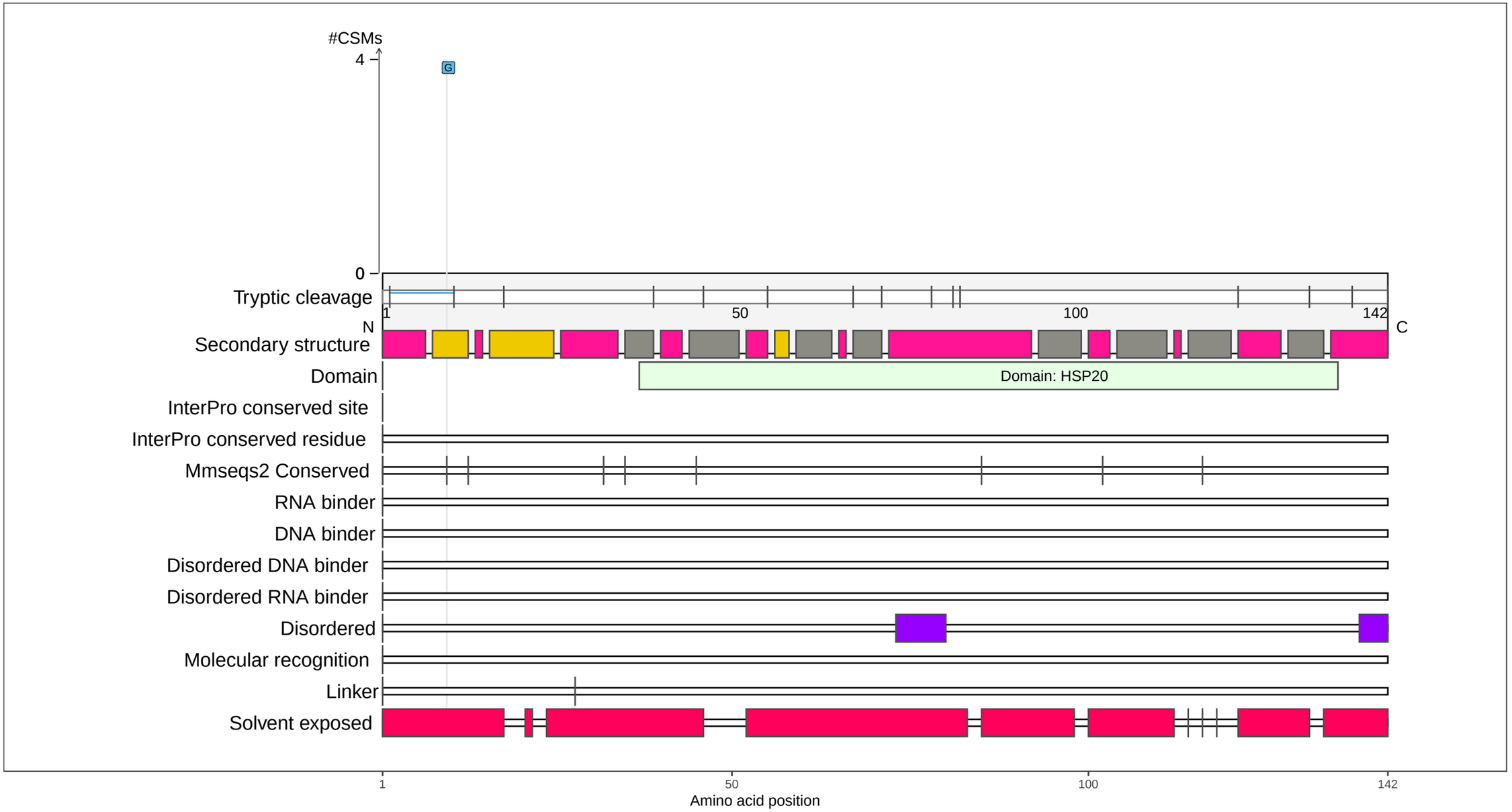
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; SpoU rRNA Methylase family; SpoU, rRNA methylase, C−terminal
tRNA (guanine) methyltransferase activity
tRNA (guanosine−2−O−)−methyltransferase activity; tRNA 2−O−methyltransferase activity; tRNA binding
tRNA guanine ribose methylation; tRNA metabolic process; tRNA methylation; tRNA methyltransferase activity
tRNA modification; tRNA nucleoside ribose methylation; tRNA processing

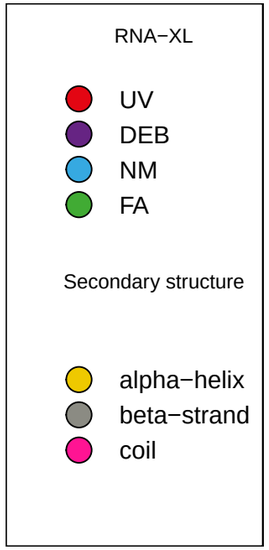


P0C058
IBPB_ECOLI Small heat shock protein IbpB

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 55)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.99 (Q 72)

− RNA functions: not annotated

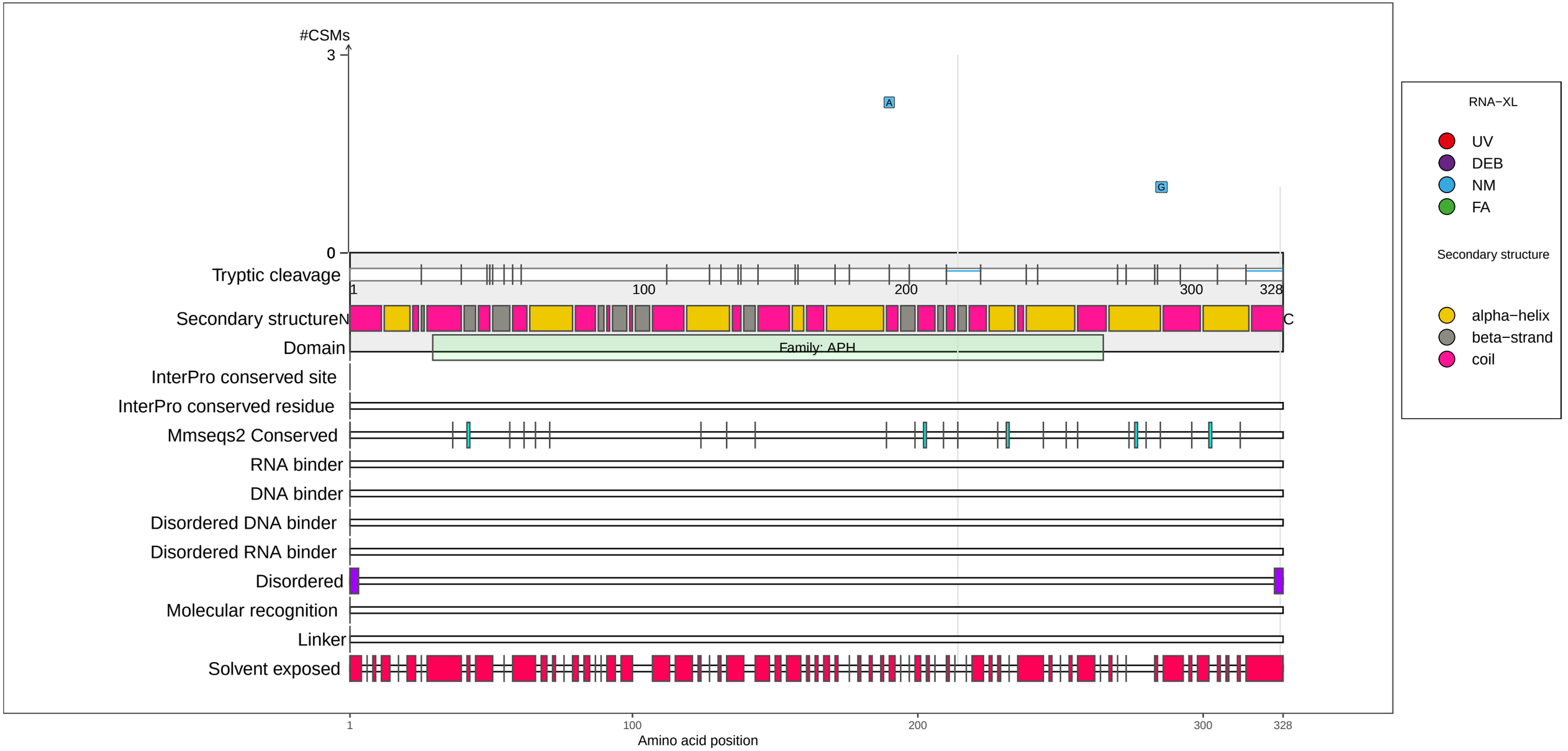




P0C0K3
SRKA_ECOLI Stress response kinase A

− Abundance:
tryptic [log10 Intensity]: 7.13 (Q 18)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.24 (Q 30)

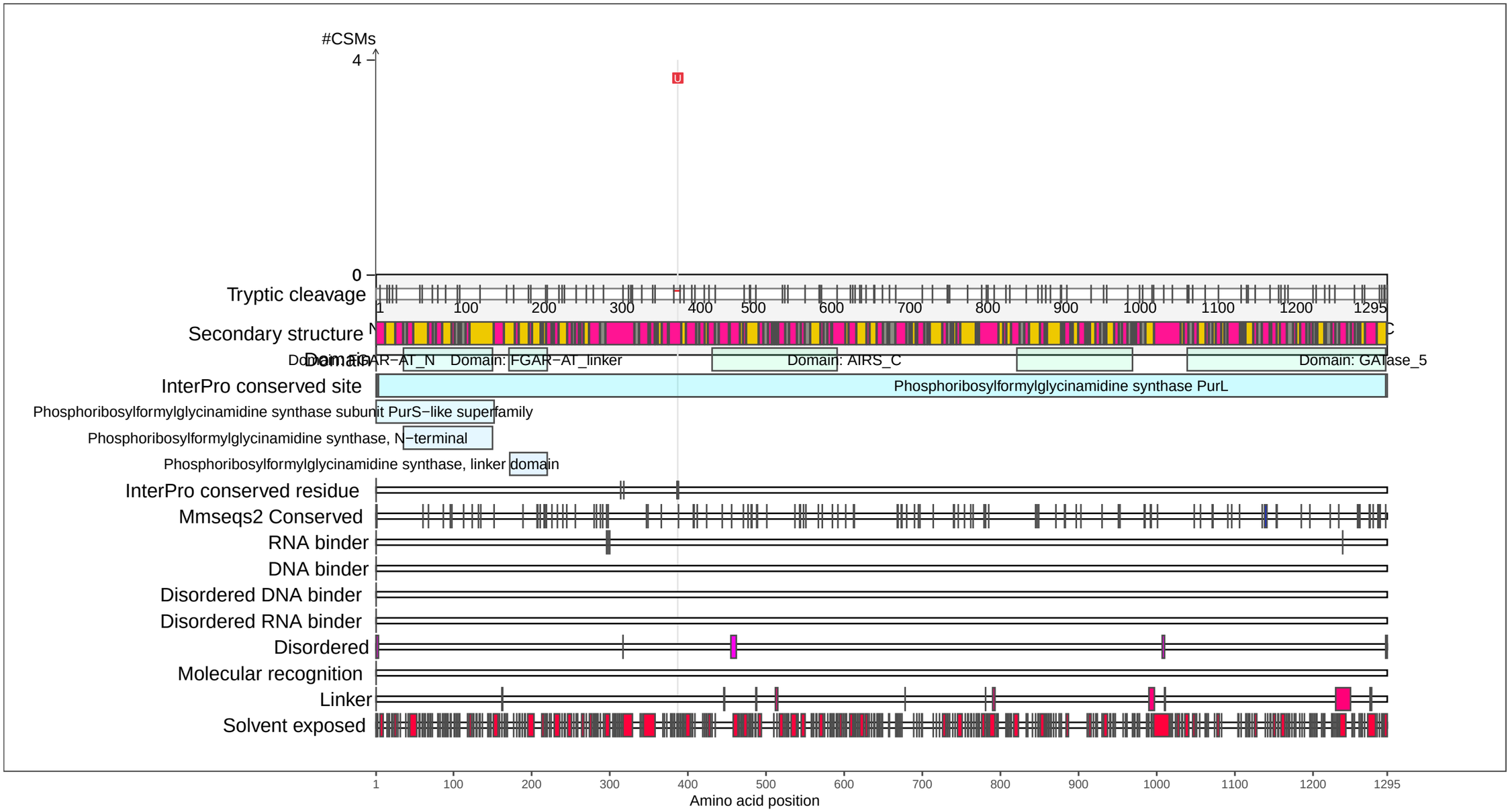
− RNA functions: not annotated

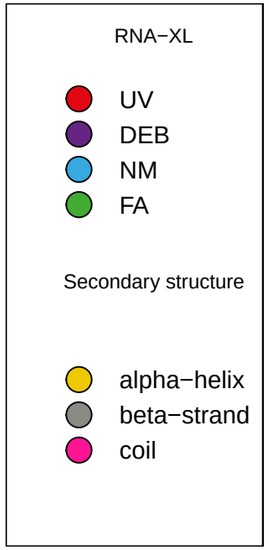


P15254
PUR4_ECOLI Phosphoribosylformylglycinamidine synthase

− Abundance:
tryptic [log10 Intensity]: 8.63 (Q 80)
PAXdb K12 strain [ppm]: 2.7 (Q 83)
PAXdb E.coli [ppm]: 2.57 (Q 87)

− RNA functions: not annotated

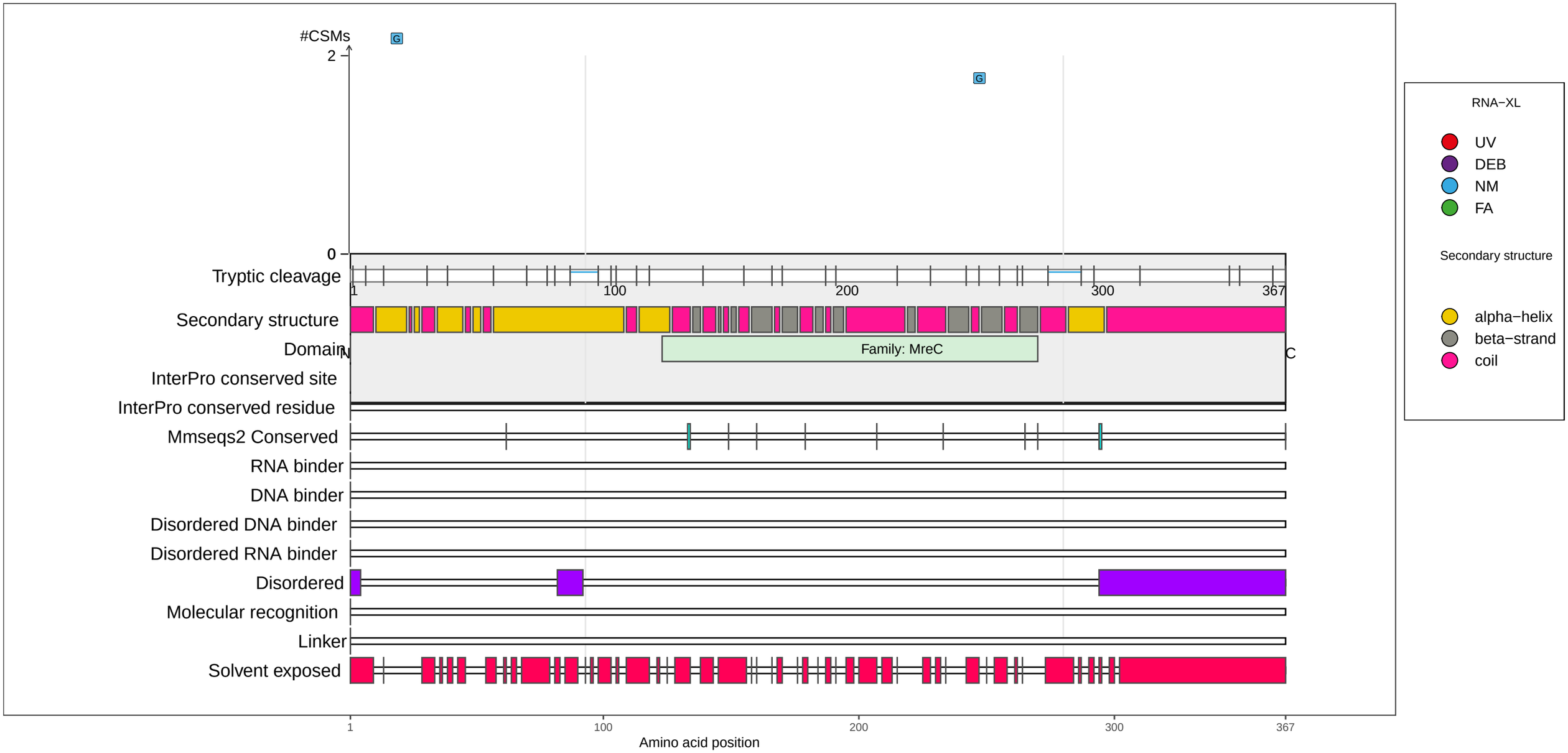




P16926
MREC_ECOLI Cell shape−determining protein MreC

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 1.1 (Q 50)

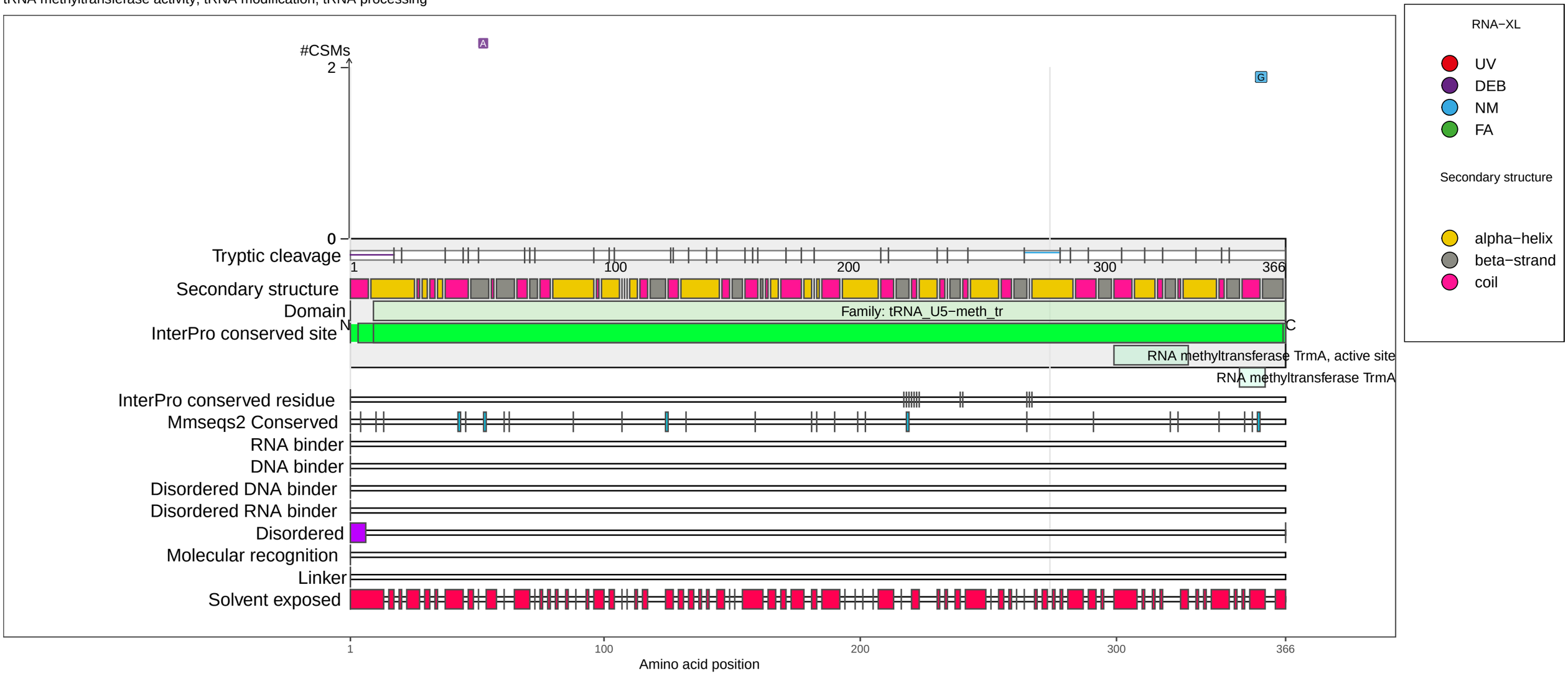
− RNA functions: not annotated



P23003
TRMA_ECOLI tRNA/tmRNA (uracil−C(5))−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 51)
PAXdb K12 strain [ppm]: 0.69 (Q 3)
PAXdb E.coli [ppm]: 1.89 (Q 69)

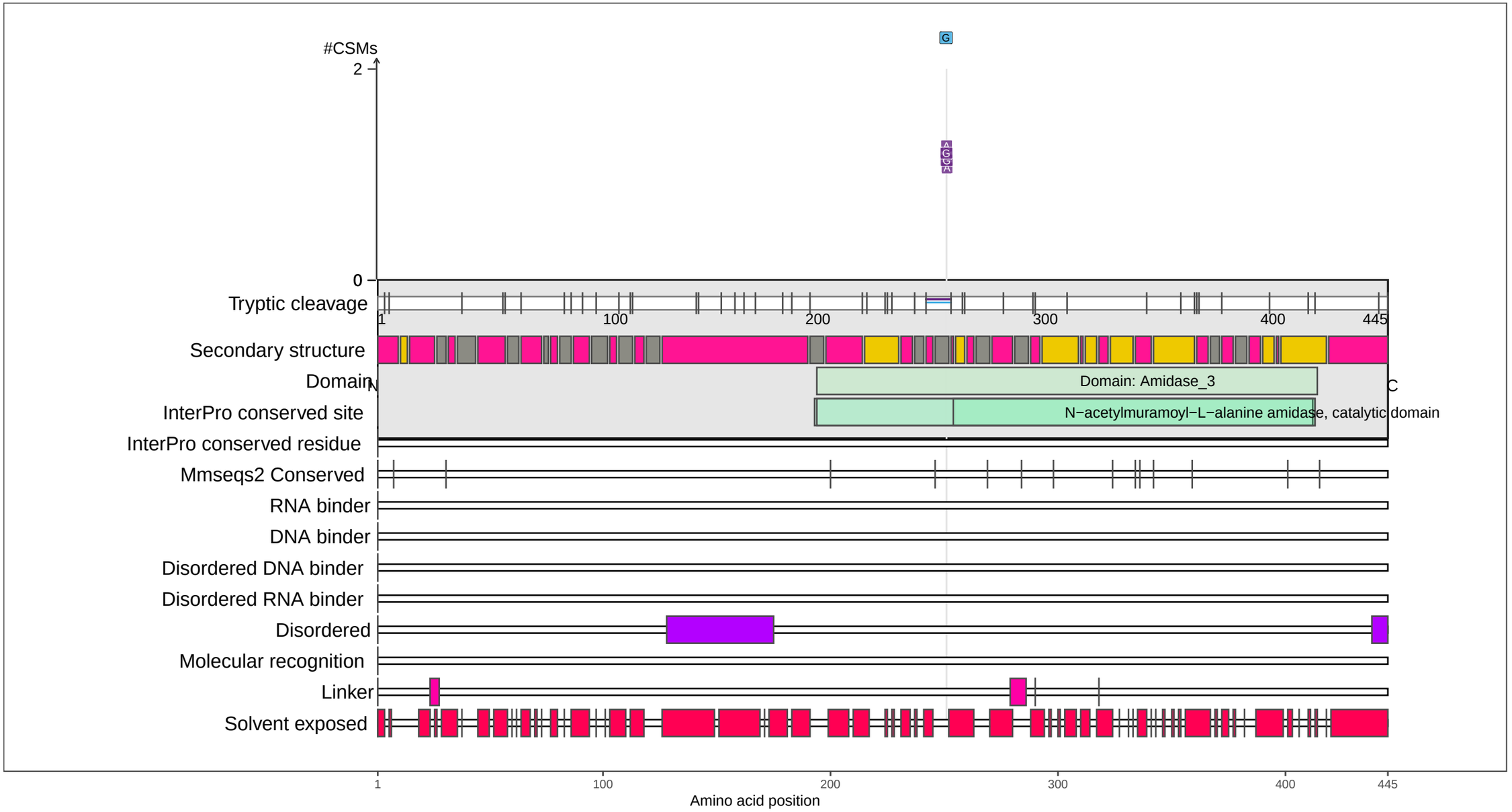
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA methylation; RNA methyltransferase activity; RNA modification; RNA processing; rRNA binding
S−adenosylmethionine−dependent tRNA (m5U54) methyltransferase activity
tRNA (m5U54) methyltransferase activity; tRNA (Uracil−5−)−methyltransferase
tRNA (uracil) methyltransferase activity; tRNA binding; tRNA metabolic process; tRNA methylation
tRNA methyltransferase activity; tRNA modification; tRNA processing

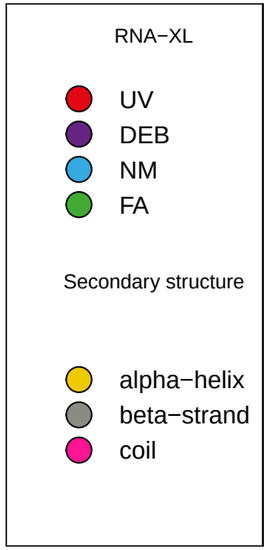


P26365
AMIB_ECOLI N−acetylmuramoyl−L−alanine amidase AmiB

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.44 (Q 35)

− RNA functions: not annotated

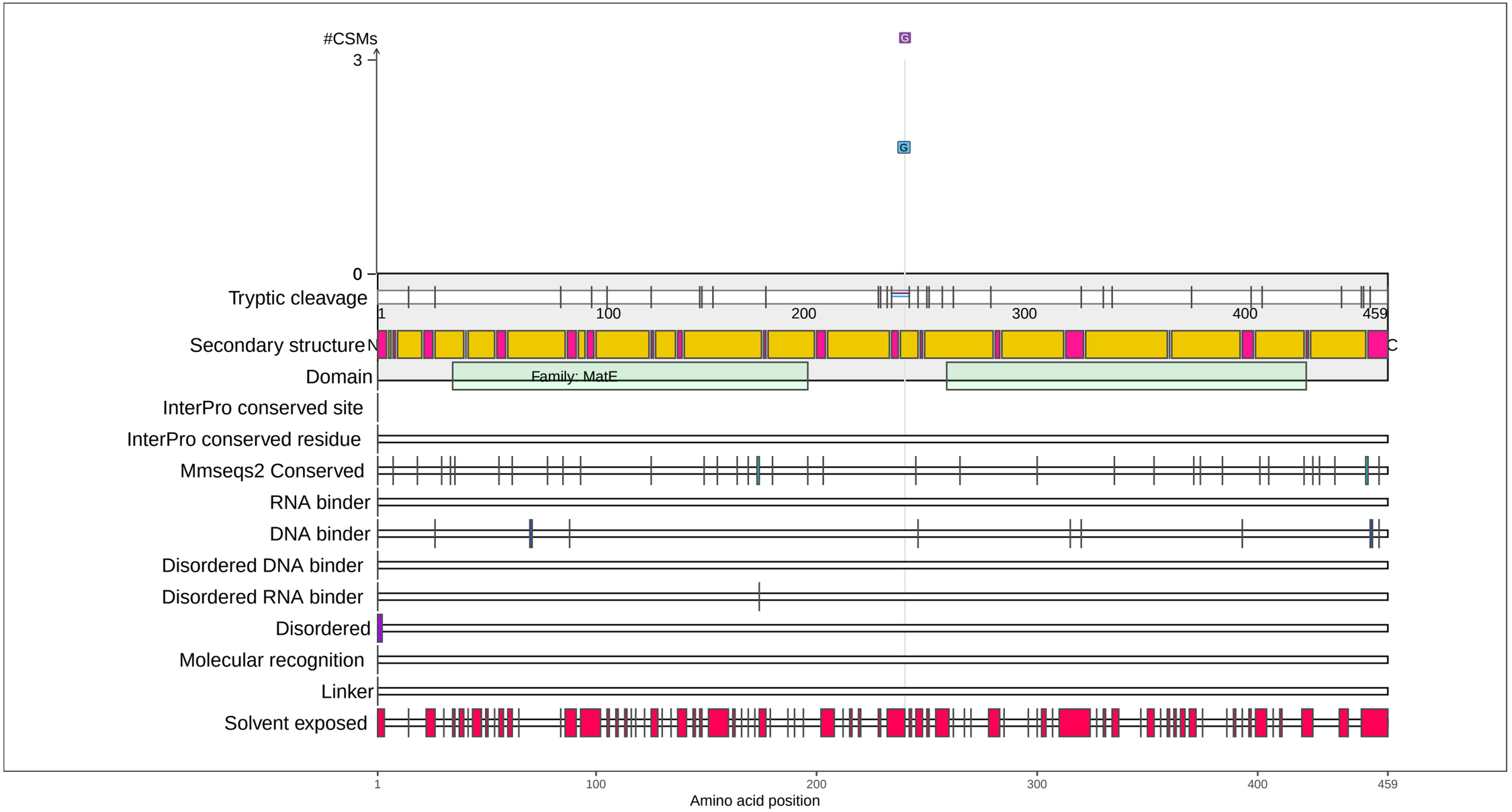




P28303
DINF_ECOLI DNA damage−inducible protein F

− Abundance:
tryptic [log10 Intensity]: 7.28 (Q 24)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.06 (Q 26)

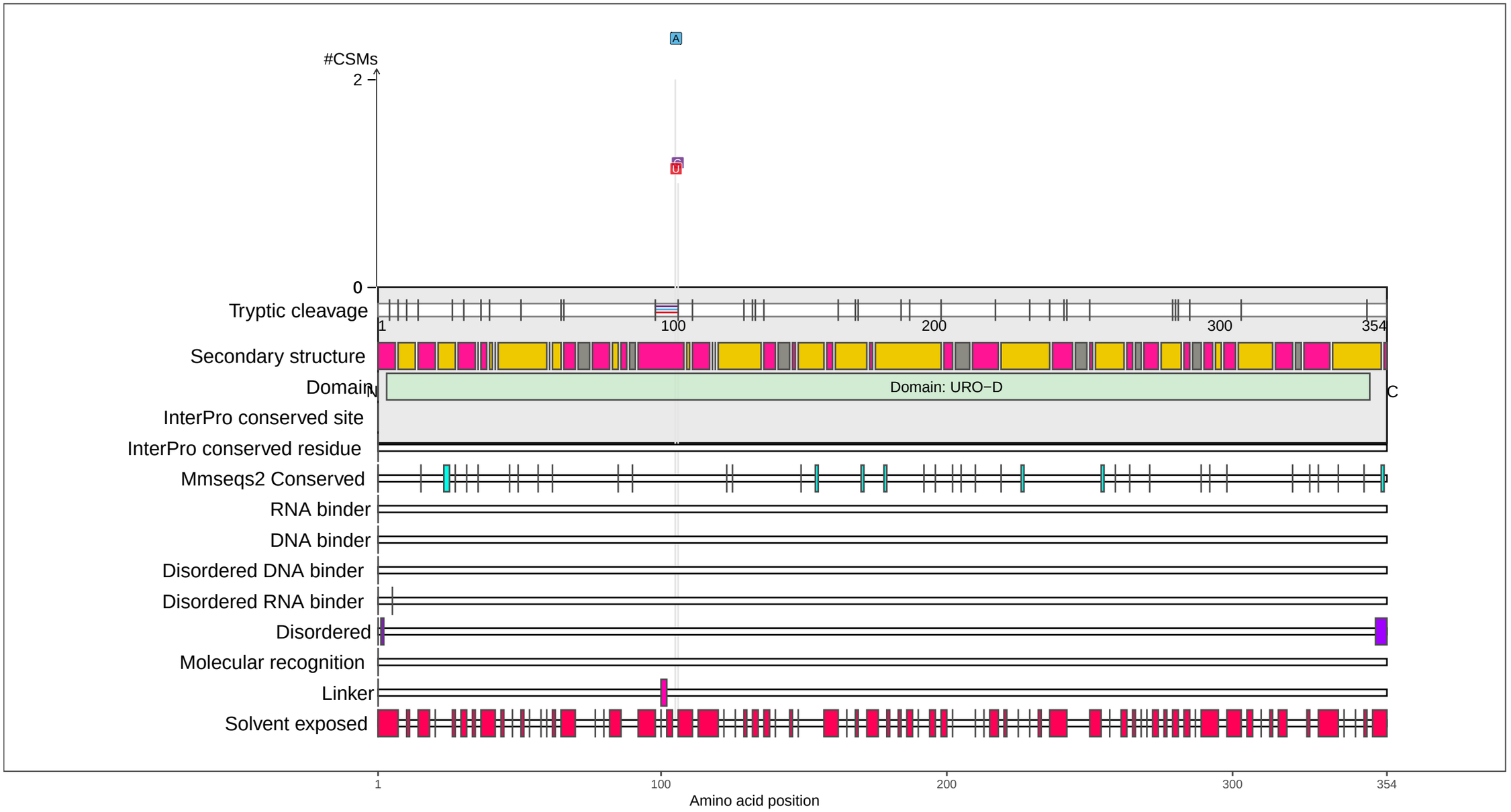
− RNA functions: not annotated



P29680
DCUP_ECOLI Uroporphyrinogen decarboxylase

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 1.9 (Q 57)
PAXdb E.coli [ppm]: 2.18 (Q 77)

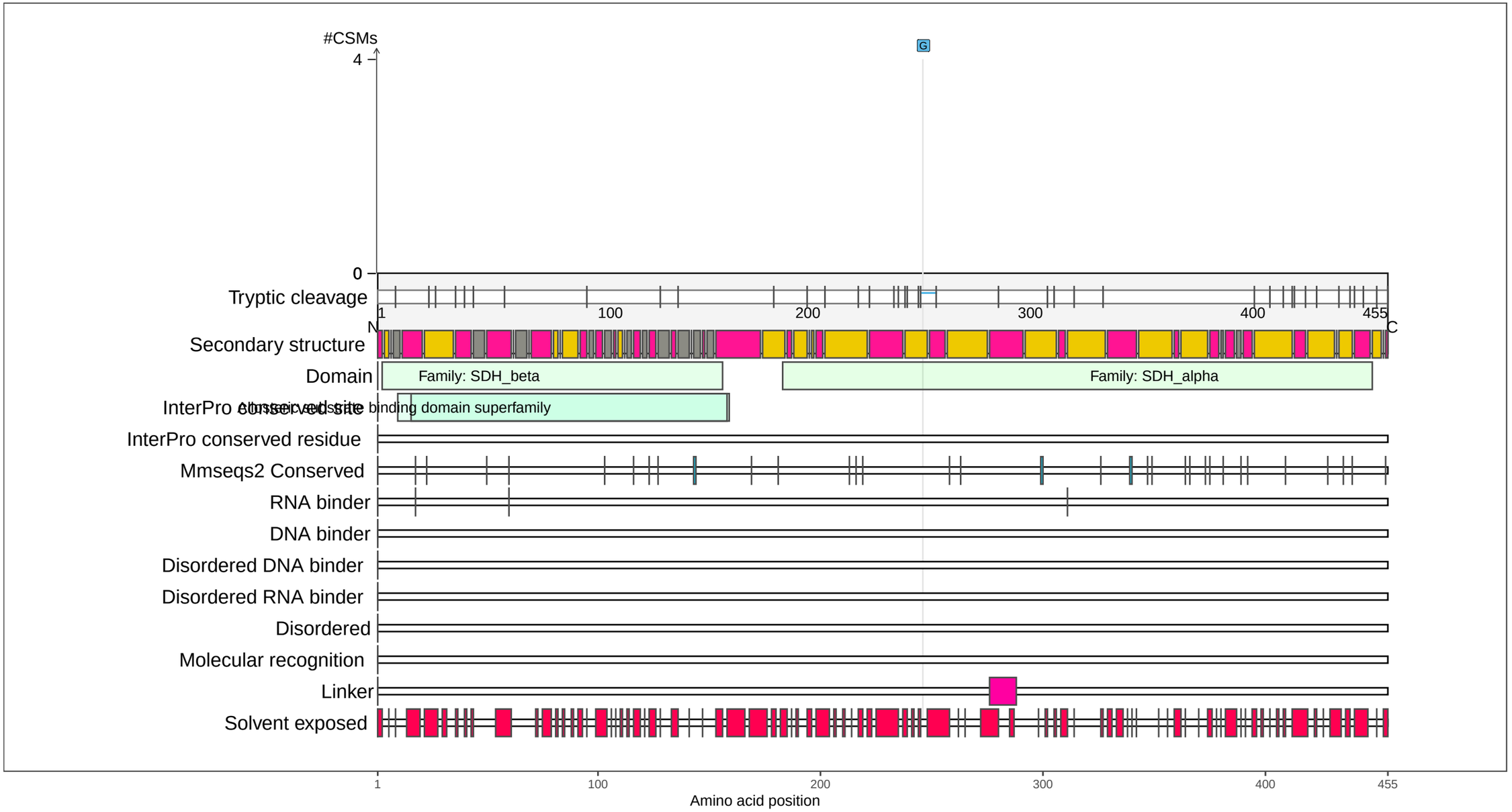
− RNA functions: not annotated

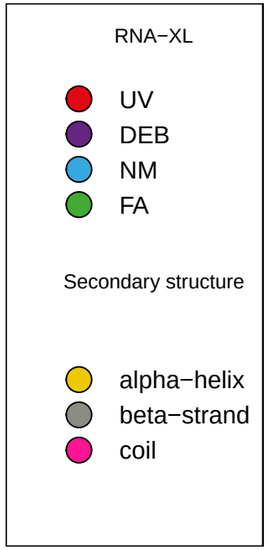


P30744
SDHM_ECOLI L−serine dehydratase 2

− Abundance:
tryptic [log10 Intensity]: 7.59 (Q 40)
PAXdb K12 strain [ppm]: 1.45 (Q 36)
PAXdb E.coli [ppm]: 0.78 (Q 43)

− RNA functions: not annotated

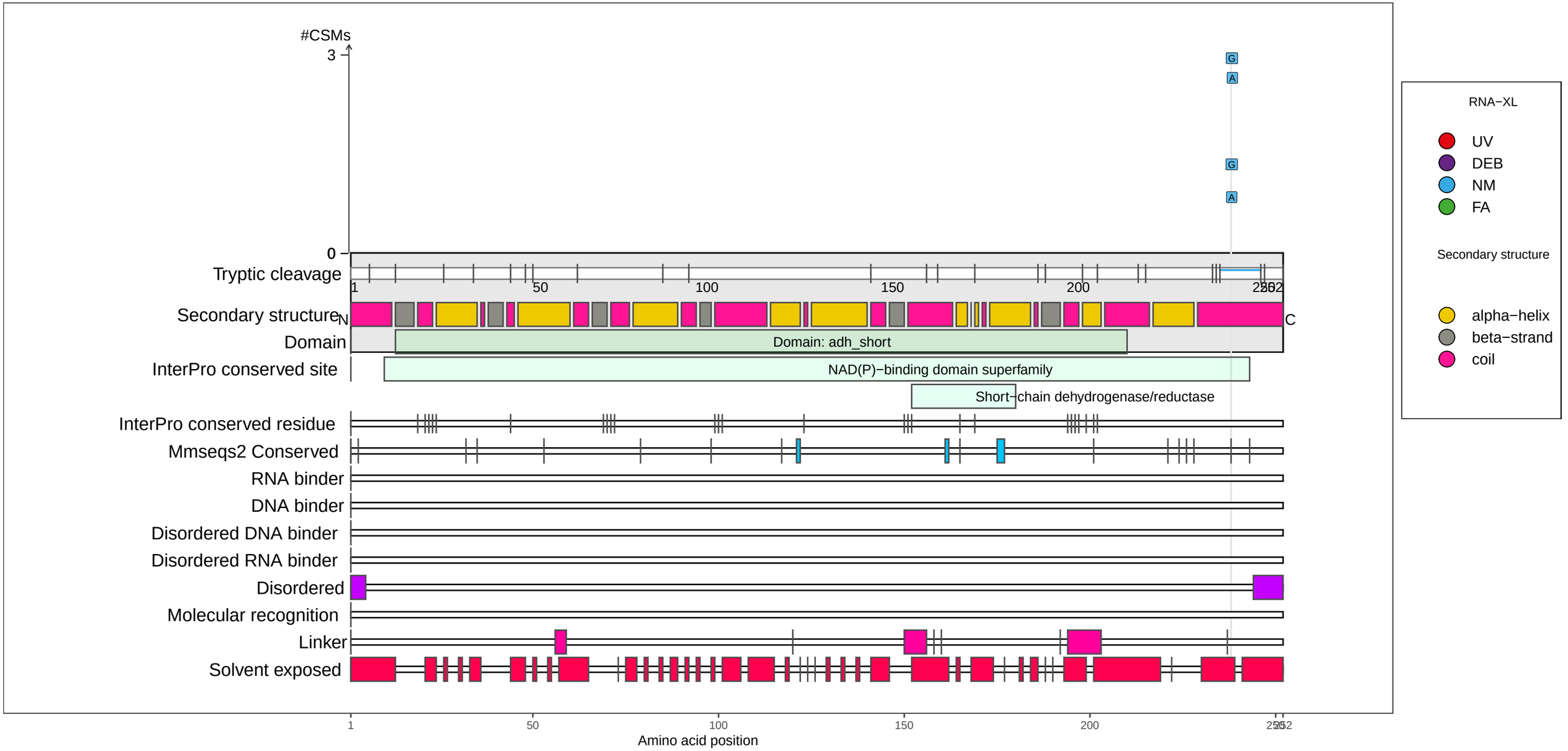




P31808
YCIK_ECOLI Uncharacterized oxidoreductase YciK

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 17)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 1.42 (Q 57)

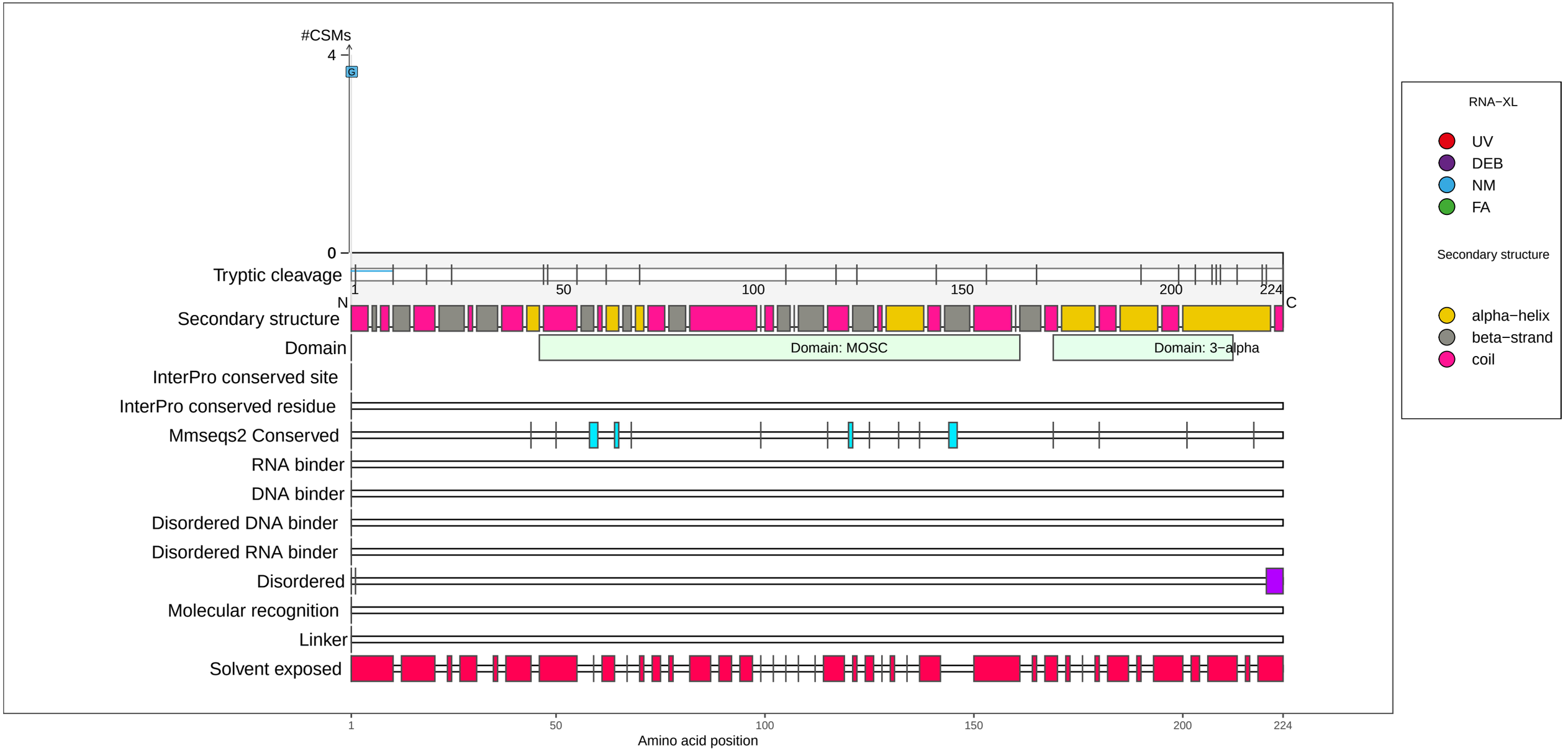
− RNA functions: not annotated



P32157
YIIM_ECOLI Protein YiiM

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: 2.31 (Q 70)
PAXdb E.coli [ppm]: 2.11 (Q 75)

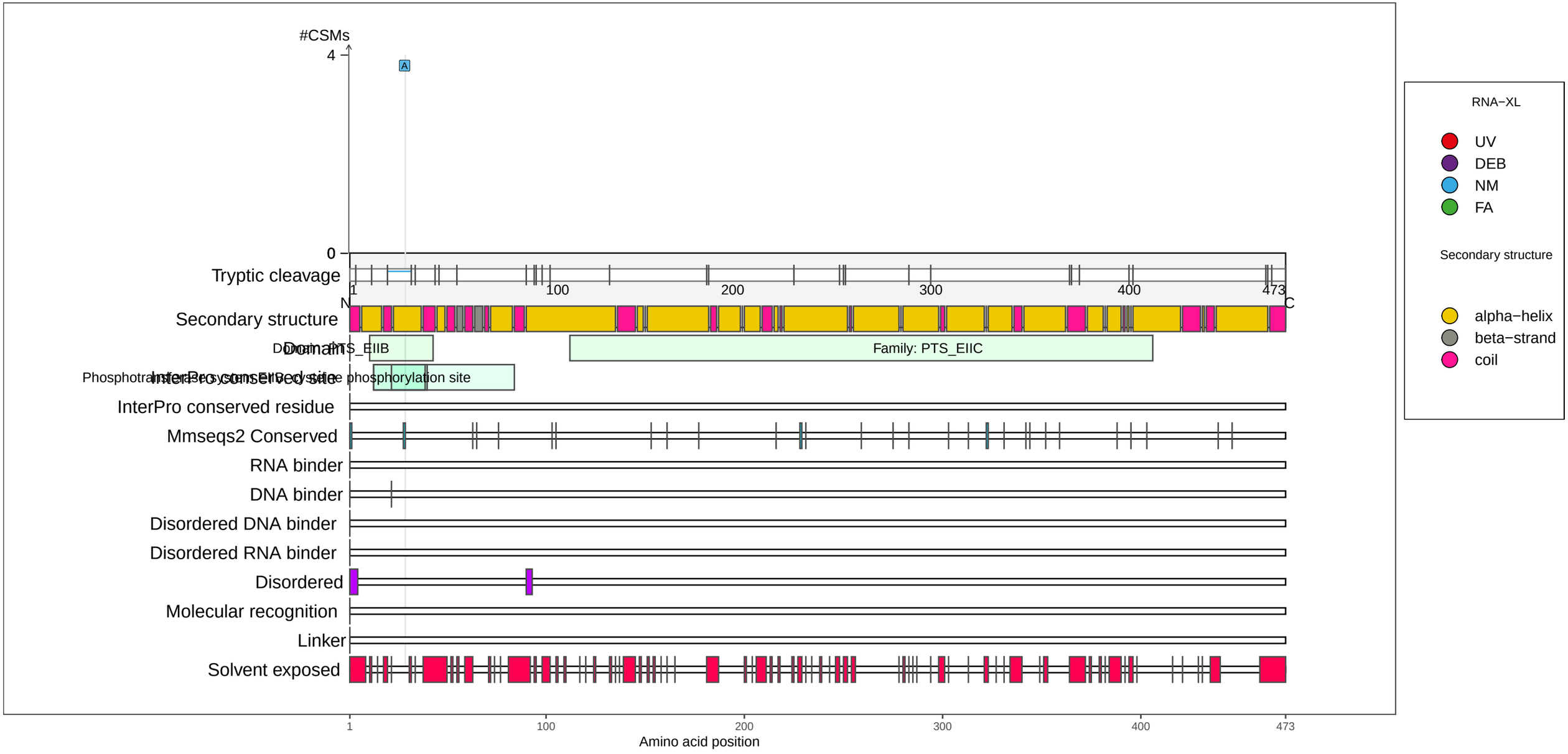
− RNA functions: not annotated



P36672
PTTBC_ECOLI PTS system trehalose−specific EIIBC component

− Abundance:
tryptic [log10 Intensity]: 8.46 (Q 74)
PAXdb K12 strain [ppm]: 1.52 (Q 39)
PAXdb E.coli [ppm]: 1.07 (Q 49)

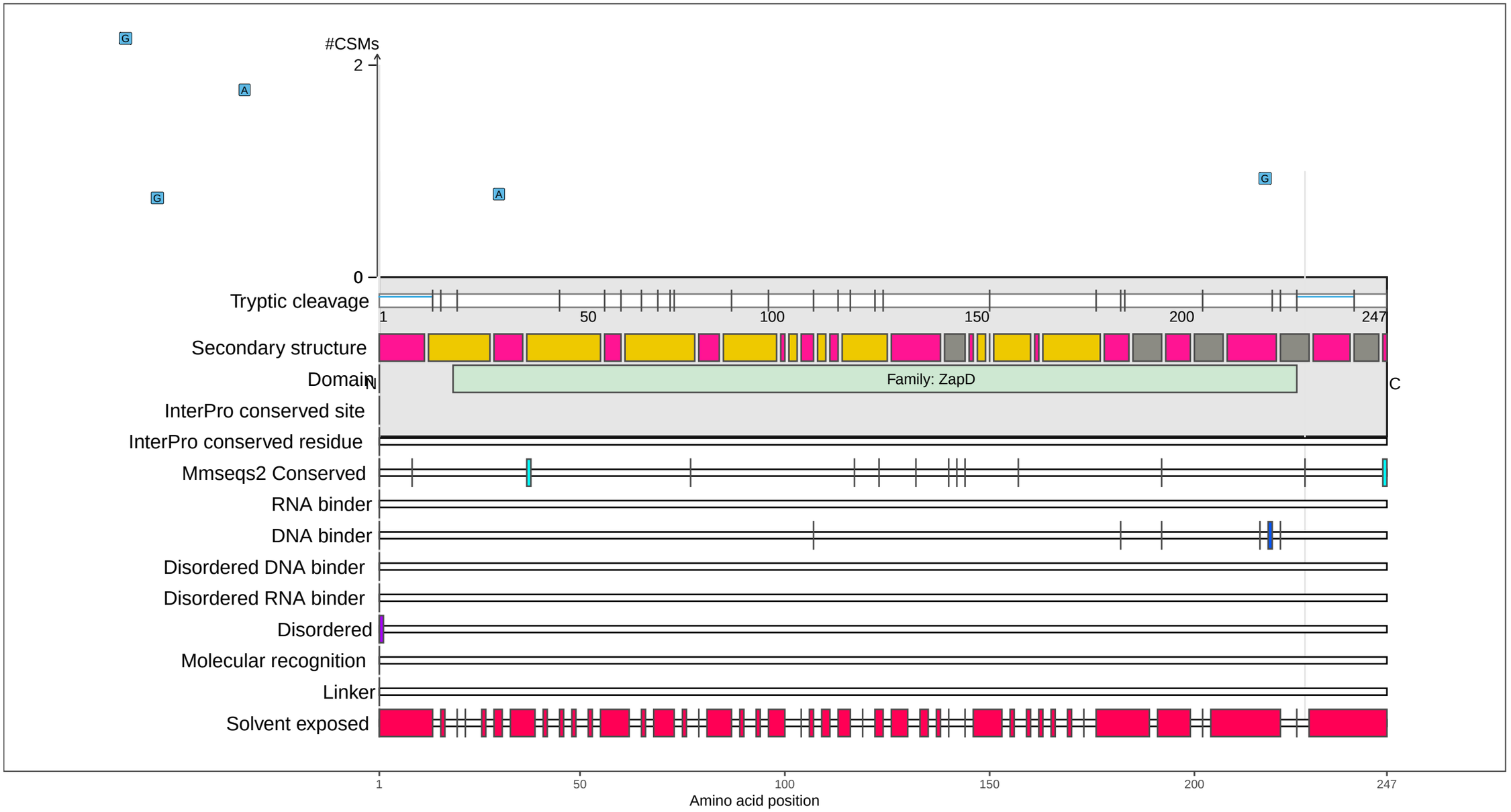
− RNA functions: not annotated

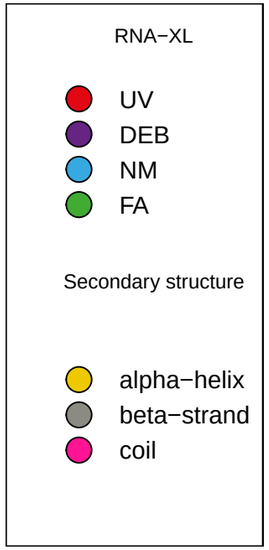


P36680
ZAPD_ECOLI Cell division protein ZapD

− Abundance:
tryptic [log10 Intensity]: 8.68 (Q 81)
PAXdb K12 strain [ppm]: 1.74 (Q 51)
PAXdb E.coli [ppm]: 1.82 (Q 67)

− RNA functions: not annotated

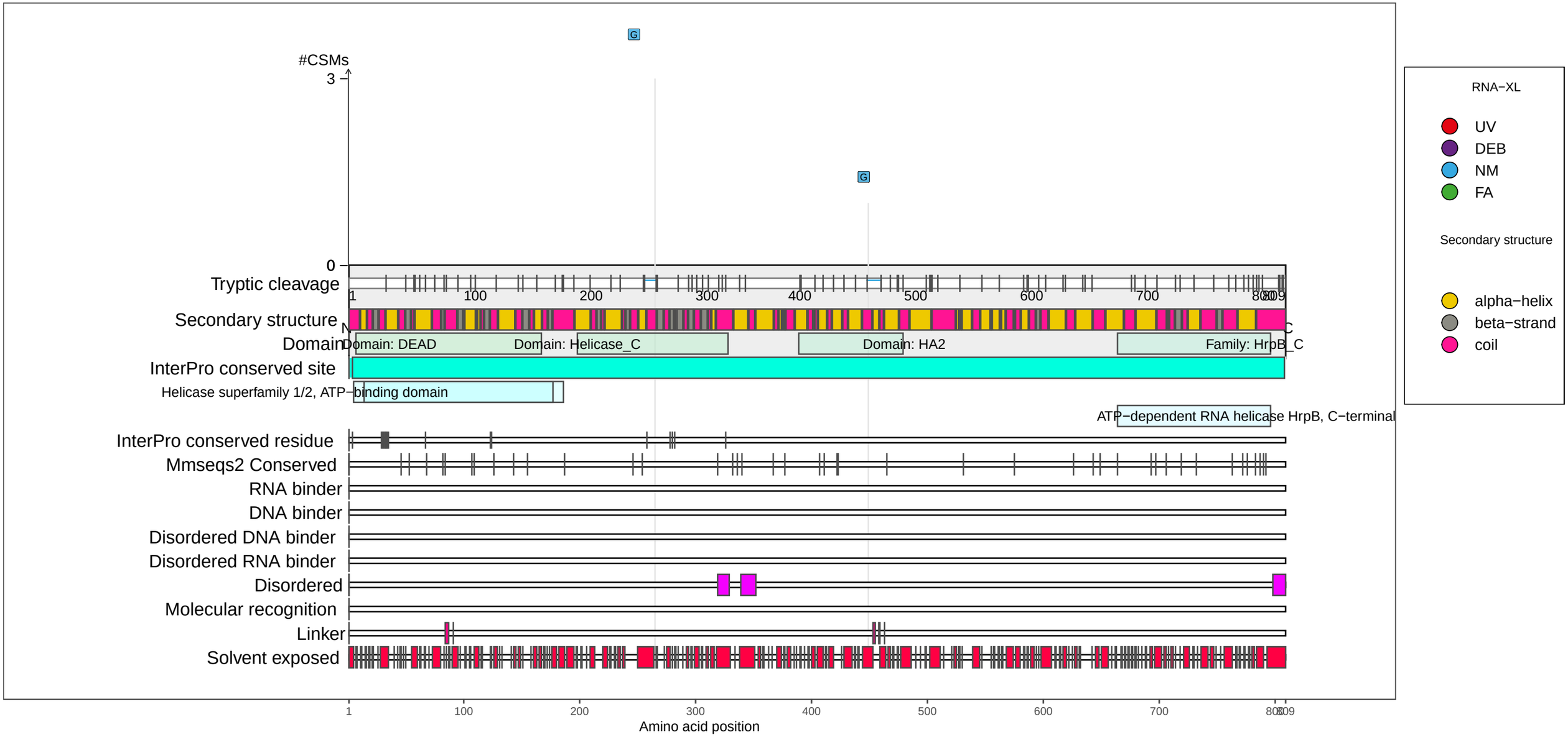




P37024
HRPB_ECOLI ATP−dependent RNA helicase HrpB

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: 1.18 (Q 19)
PAXdb E.coli [ppm]: −0.04 (Q 24)

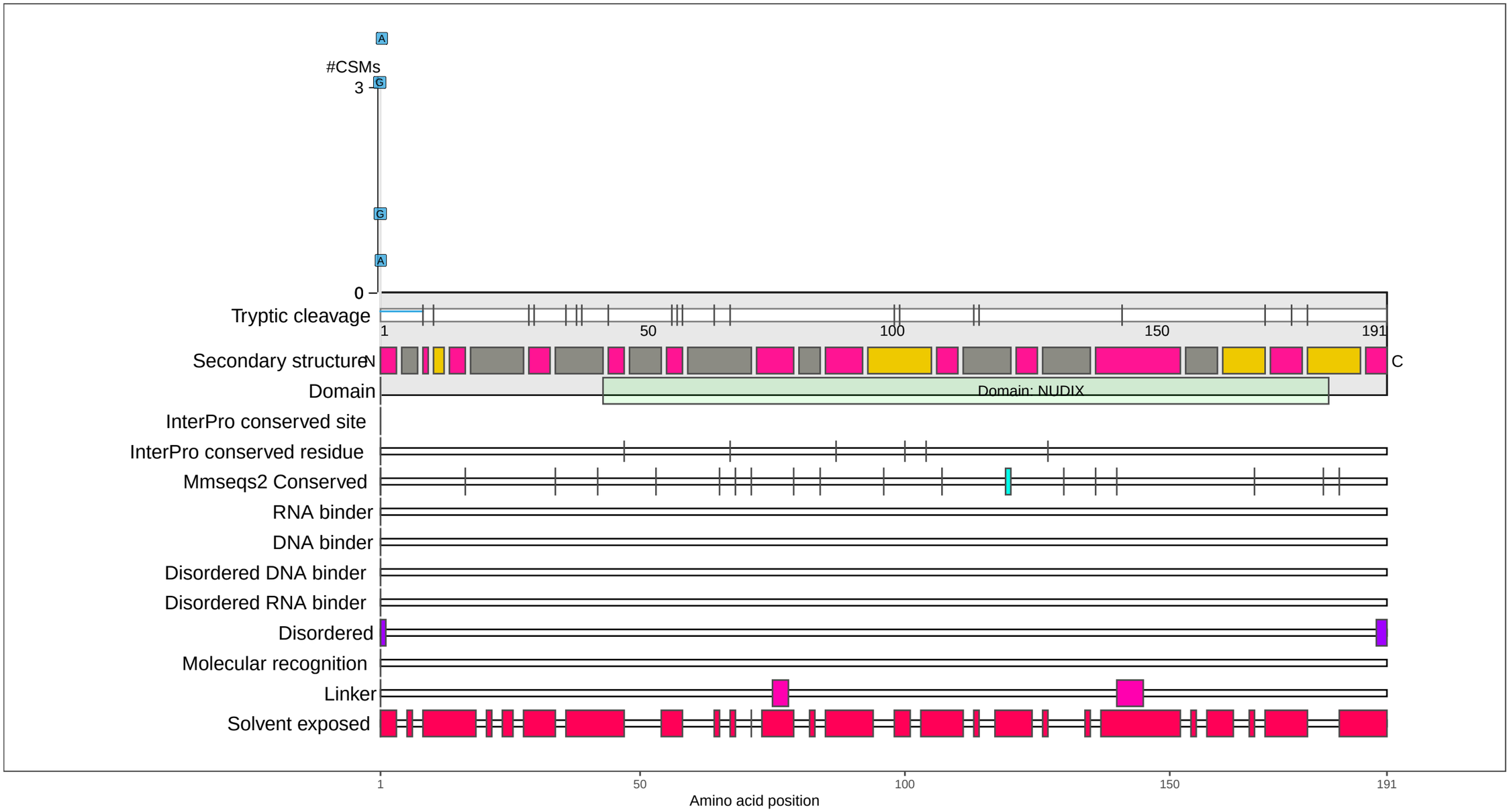
− RNA functions:
RNA helicase activity

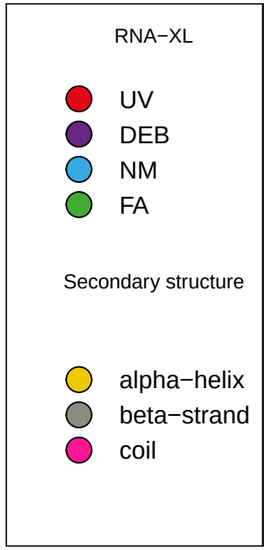


P37128
NUDK_ECOLI GDP−mannose pyrophosphatase

− Abundance:
tryptic [log10 Intensity]: 7.97 (Q 57)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 1.63 (Q 63)

− RNA functions: not annotated

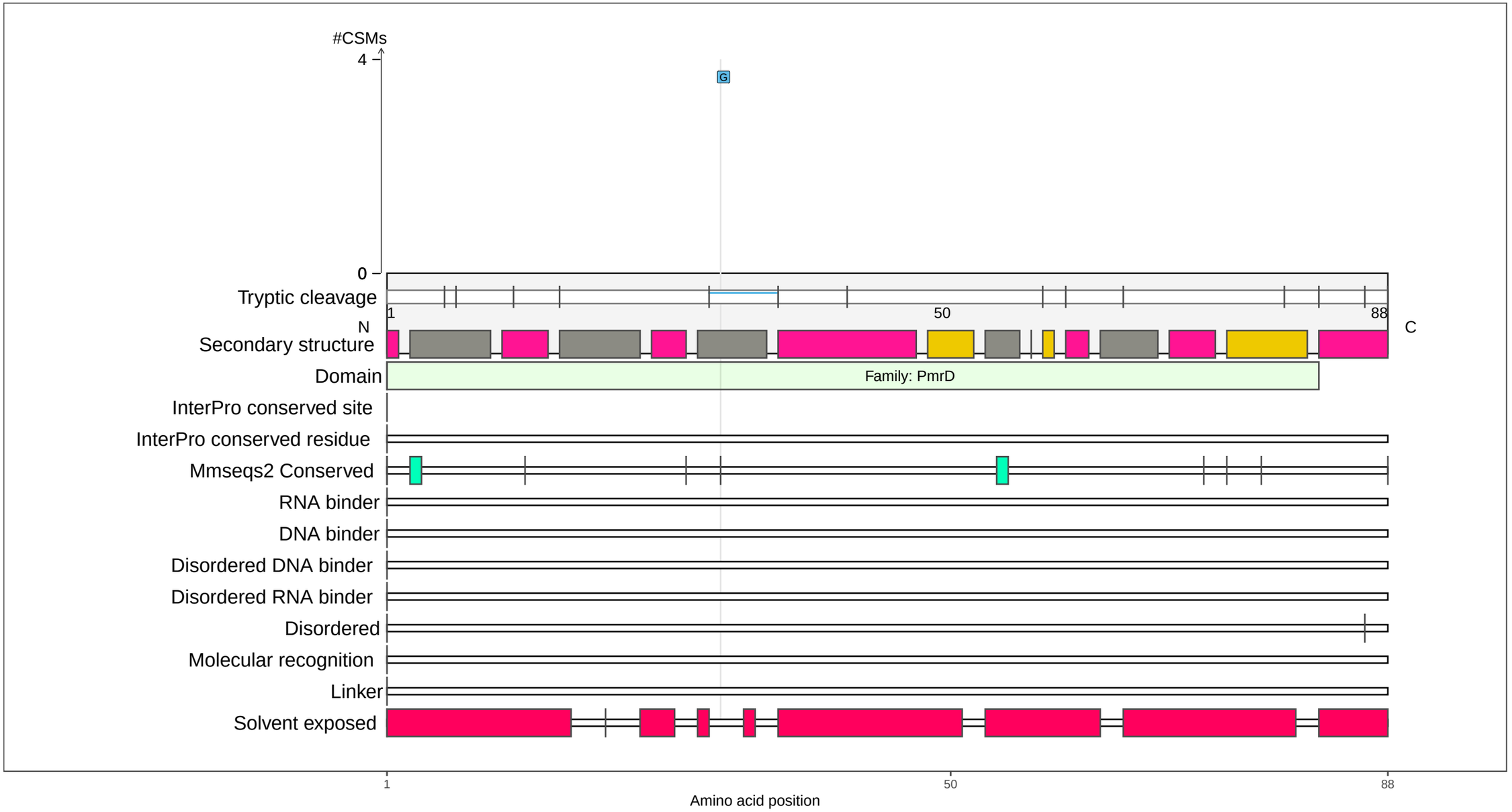




P37590
PMRD_ECOLI Signal transduction protein PmrD

− Abundance:
tryptic [log10 Intensity]: 7.44 (Q 32)
PAXdb K12 strain [ppm]: 2.01 (Q 61)
PAXdb E.coli [ppm]: 1.75 (Q 66)

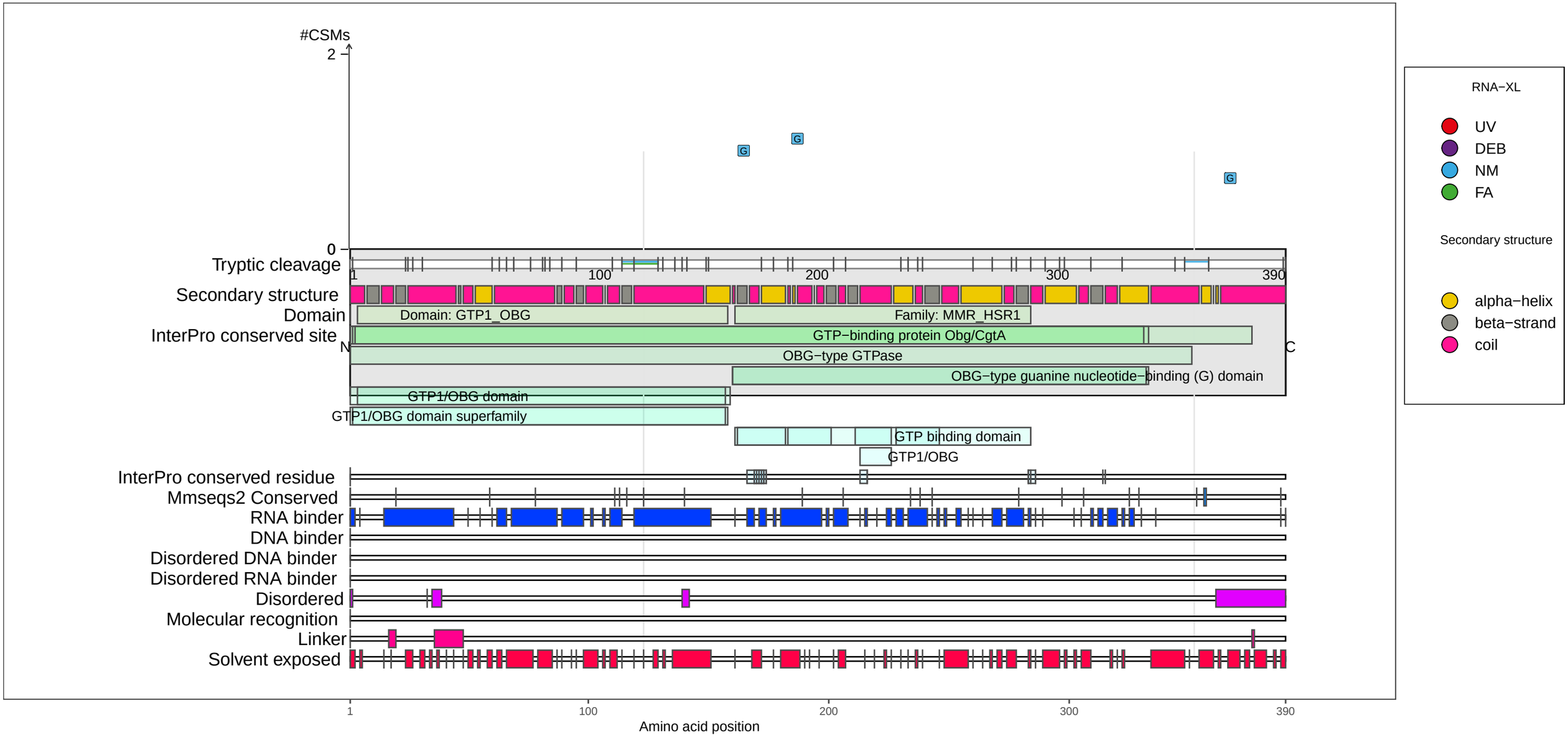
− RNA functions: not annotated



P42641
OBG_ECOLI GTPase ObgE/CgtA

− Abundance:
tryptic [log10 Intensity]: 7.74 (Q 46)
PAXdb K12 strain [ppm]: 1.25 (Q 23)
PAXdb E.coli [ppm]: 2.5 (Q 85)

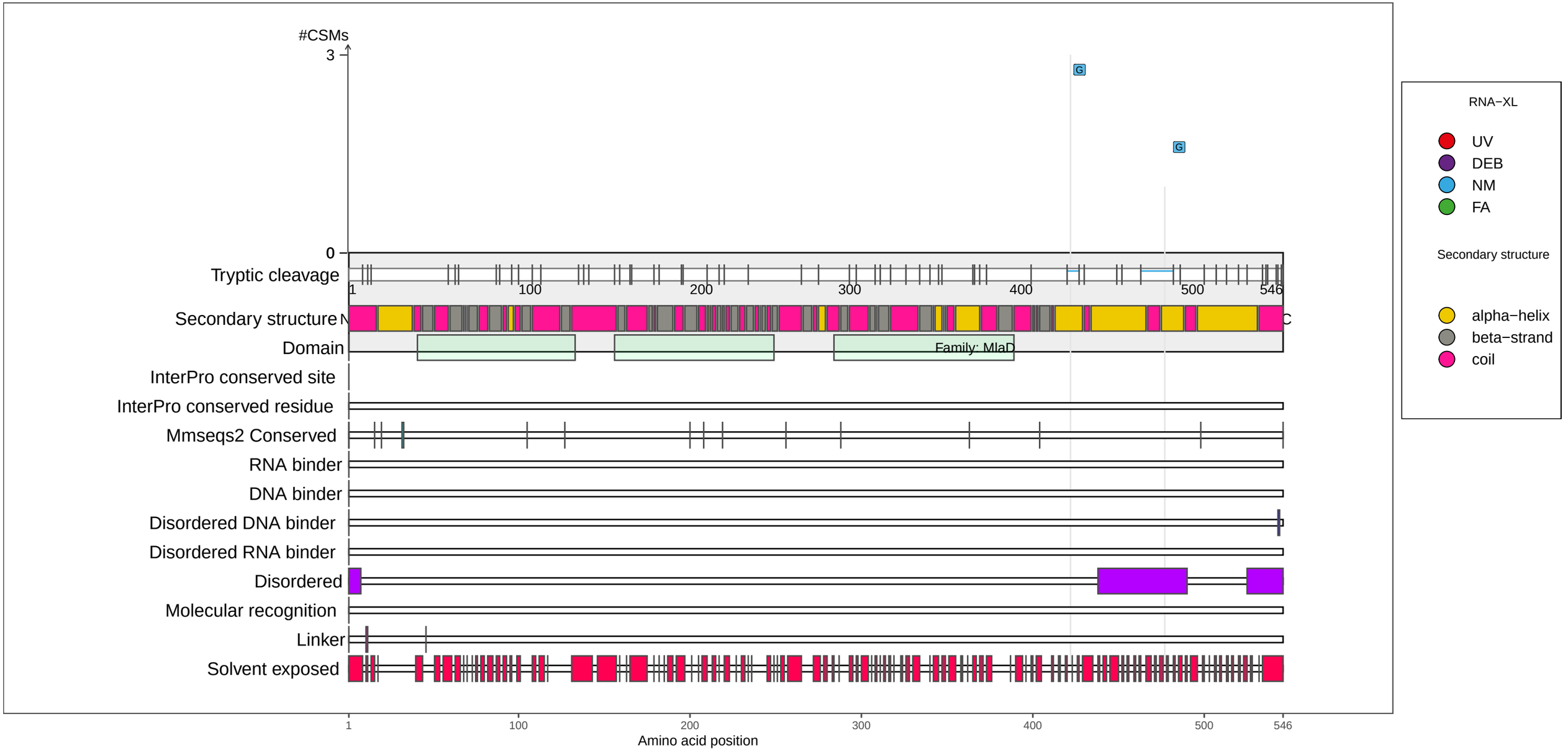
− RNA functions:
RNA binding; rRNA binding



P43671
PQIB_ECOLI Intermembrane transport protein PqiB

− Abundance:
tryptic [log10 Intensity]: 7.72 (Q 45)
PAXdb K12 strain [ppm]: 1.23 (Q 22)
PAXdb E.coli [ppm]: 1.25 (Q 53)

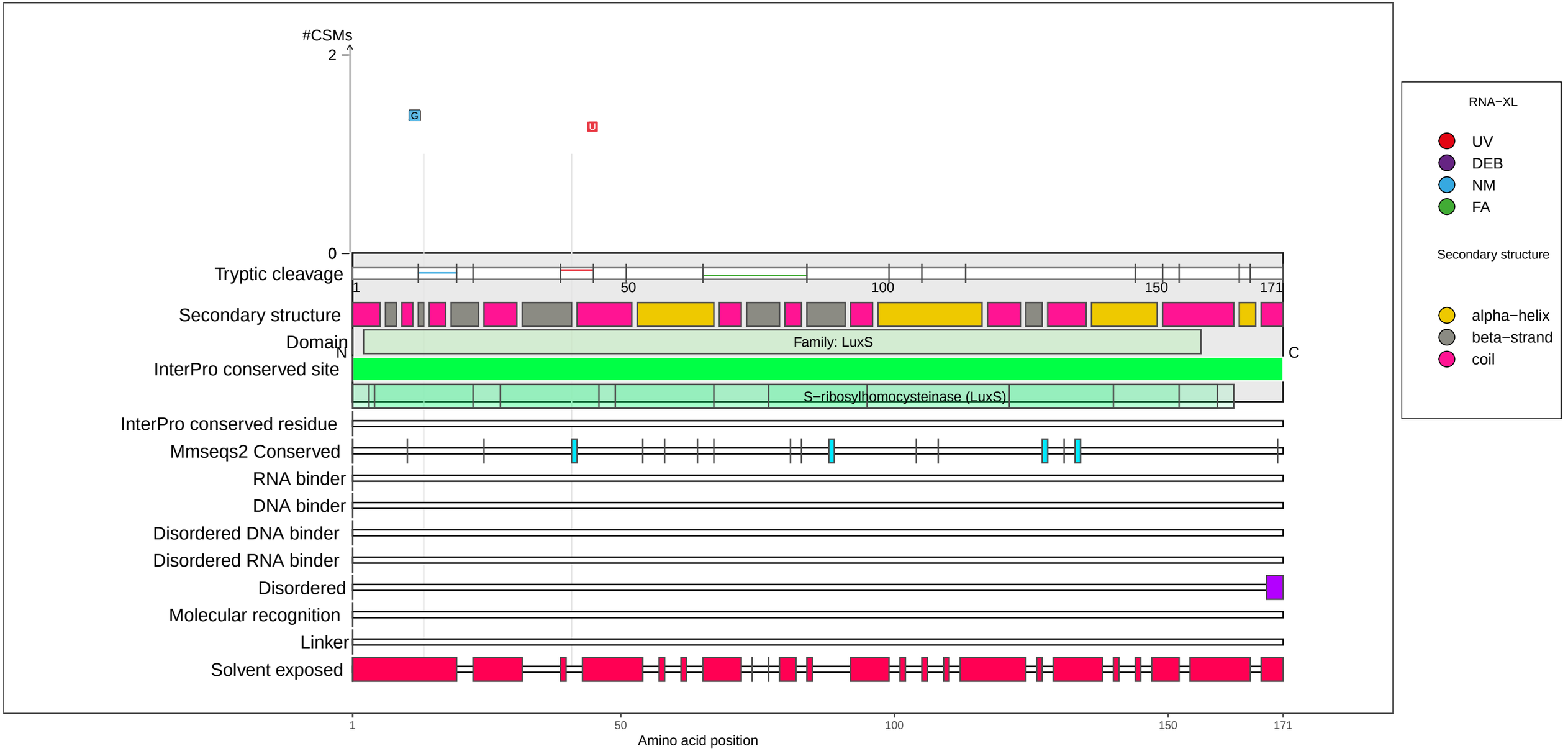
− RNA functions: not annotated



P45578
LUXS_ECOLI S−ribosylhomocysteine lyase

− Abundance:
tryptic [log10 Intensity]: 8.44 (Q 73)
PAXdb K12 strain [ppm]: 3.38 (Q 96)
PAXdb E.coli [ppm]: 3.11 (Q 96)

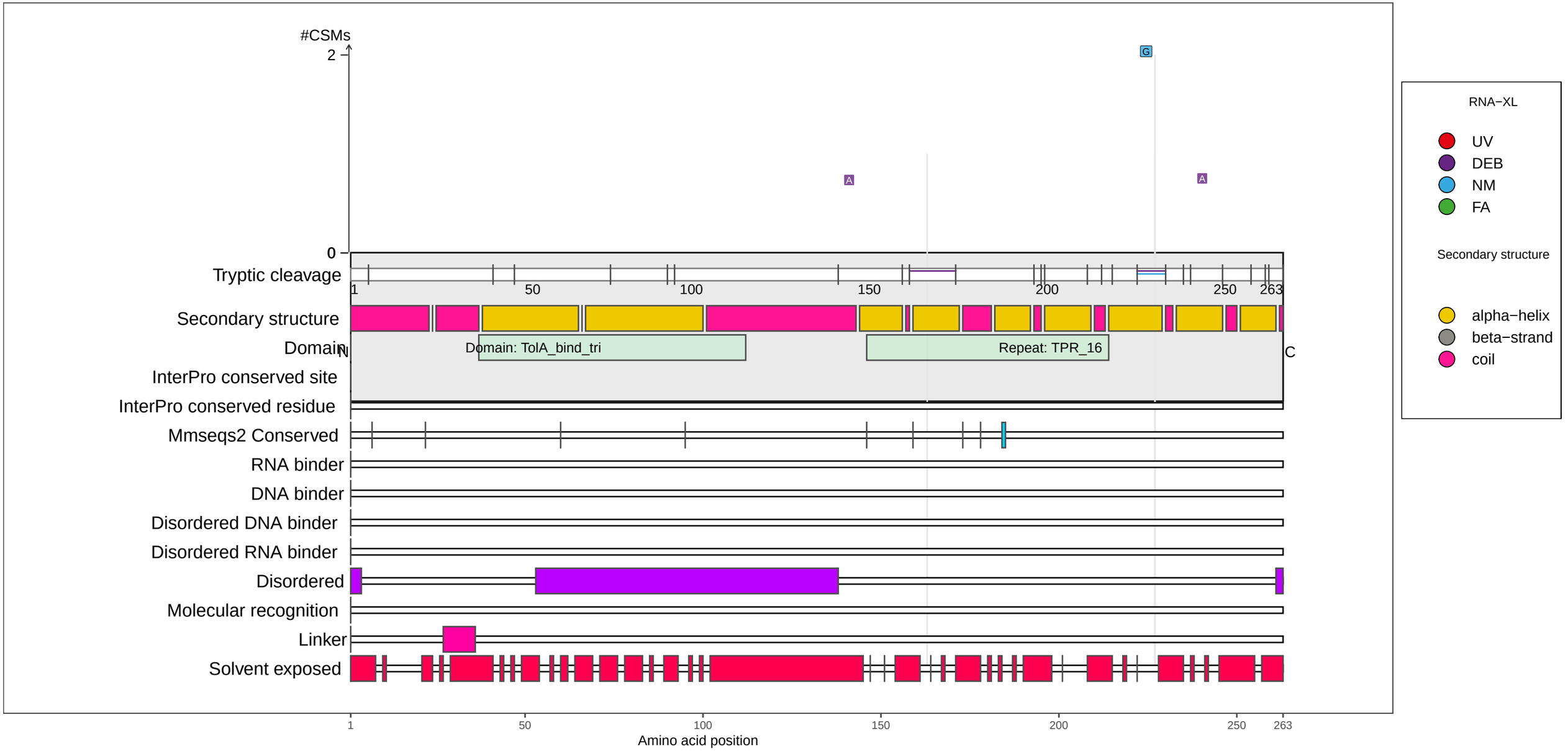
− RNA functions: not annotated



P45955
CPOB_ECOLI Cell division coordinator CpoB

− Abundance:
tryptic [log10 Intensity]: 8.29 (Q 69)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 2.25 (Q 79)

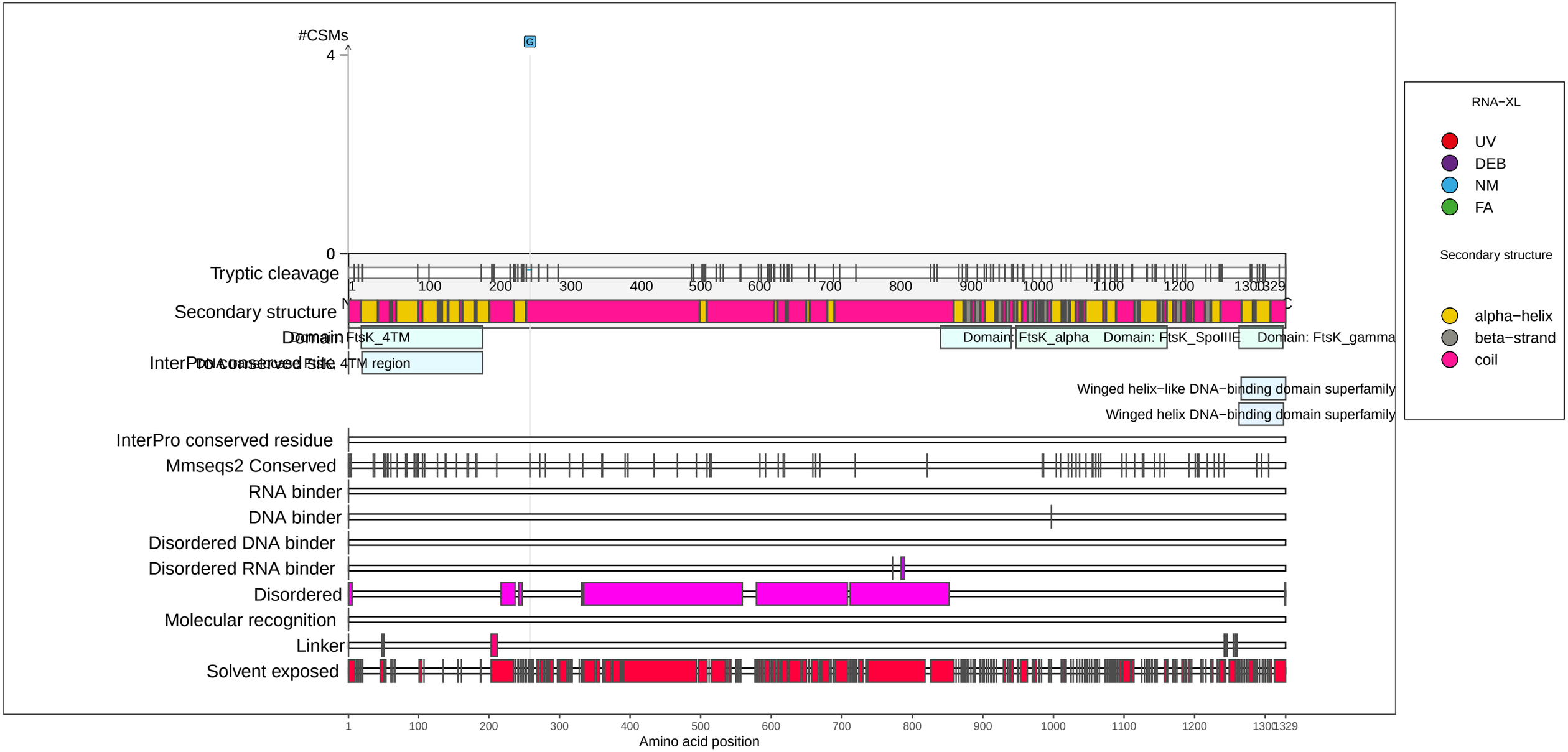
− RNA functions: not annotated



P46889
FTSK_ECOLI DNA translocase FtsK

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: 1.6 (Q 45)
PAXdb E.coli [ppm]: 1.28 (Q 54)

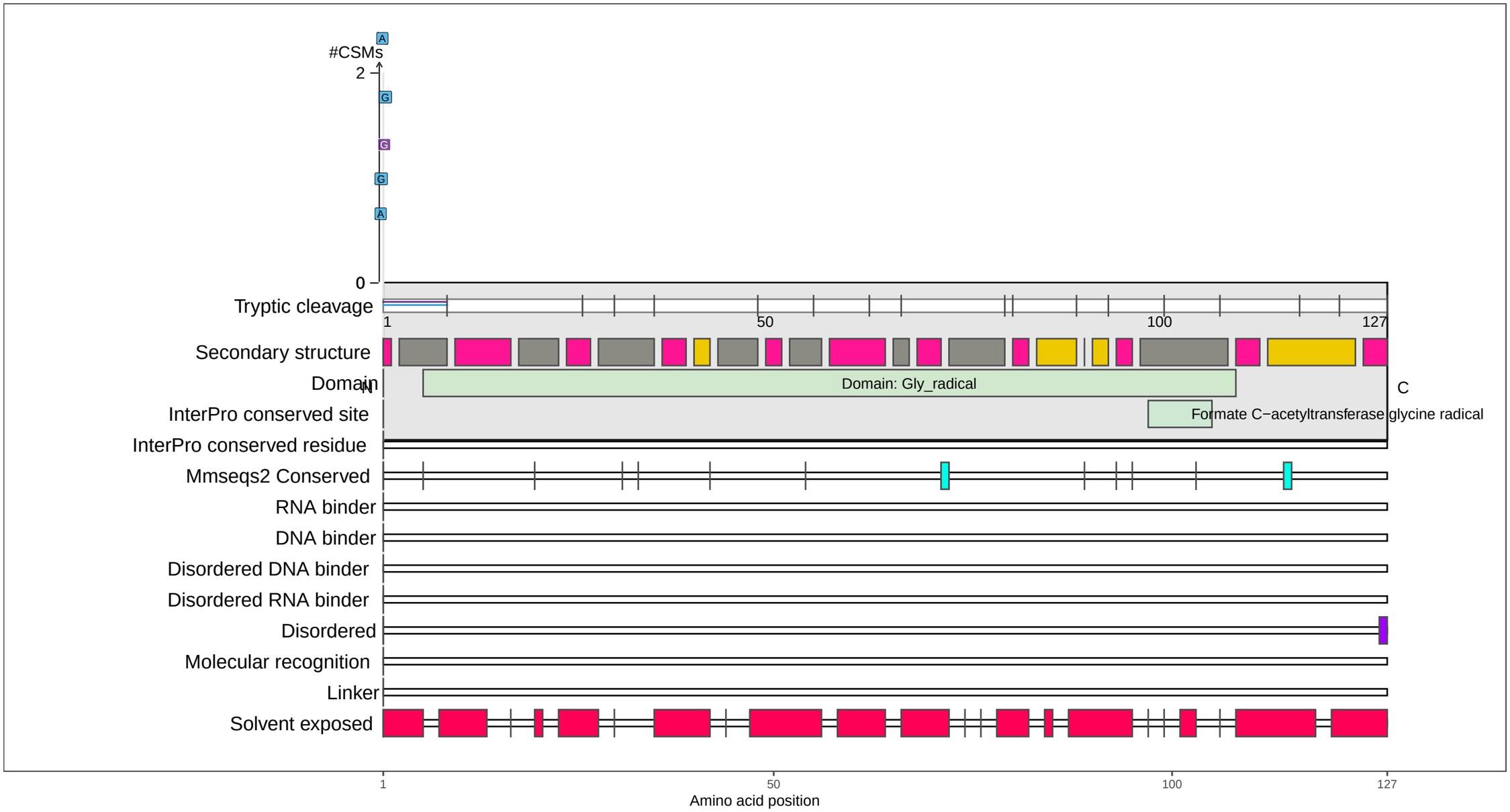
− RNA functions: not annotated

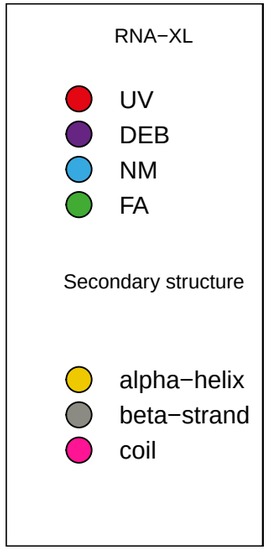


P68066
GRCA_ECOLI Autonomous glycyl radical cofactor

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 16)
PAXdb K12 strain [ppm]: 2.89 (Q 88)
PAXdb E.coli [ppm]: 3.24 (Q 97)

− RNA functions: not annotated

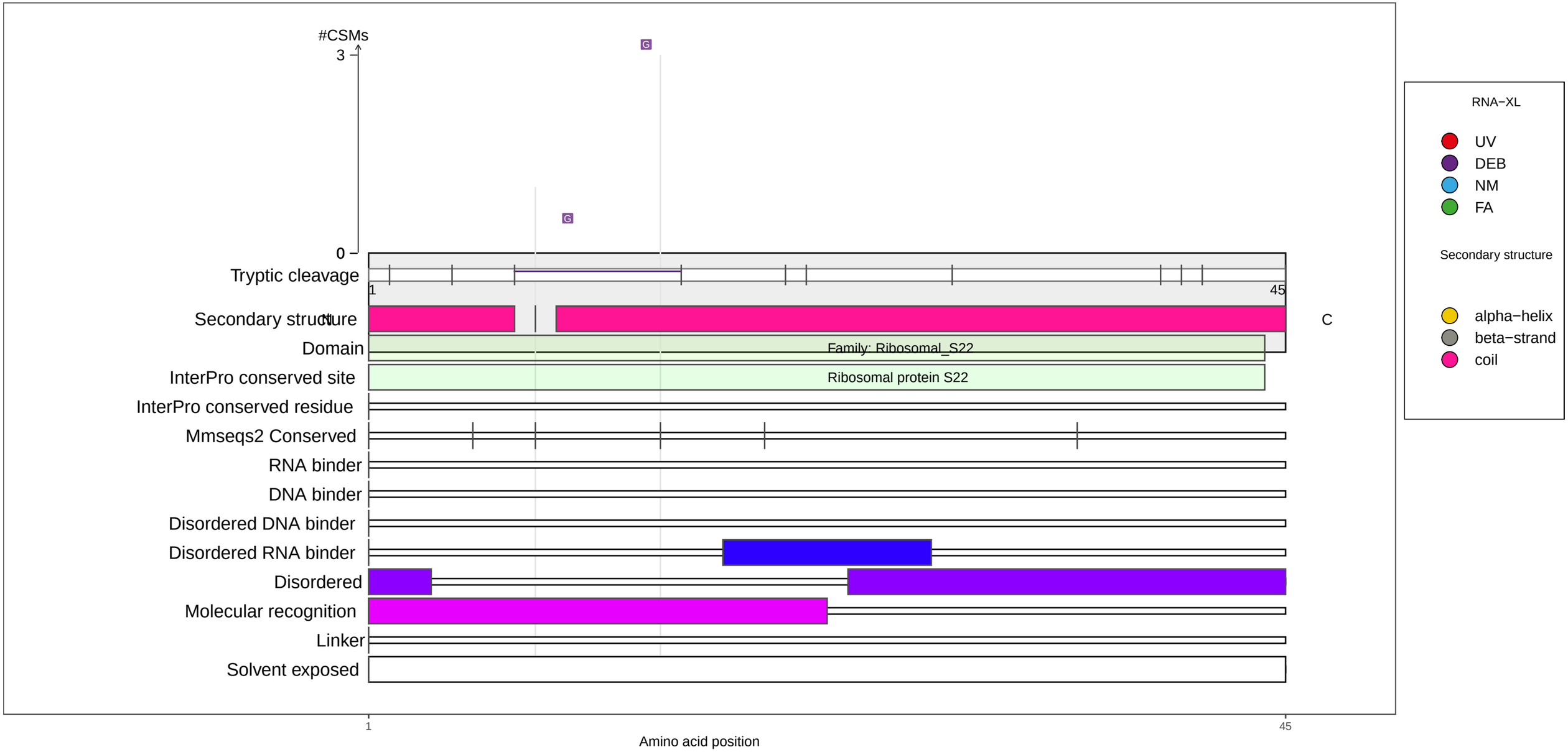




P68191
SRA_ECOLI Stationary−phase−induced ribosome−associated protein

− Abundance:
tryptic [log10 Intensity]: 7.17 (Q 20)
PAXdb K12 strain [ppm]: 2.91 (Q 88)
PAXdb E.coli [ppm]: 3.9 (Q 100)

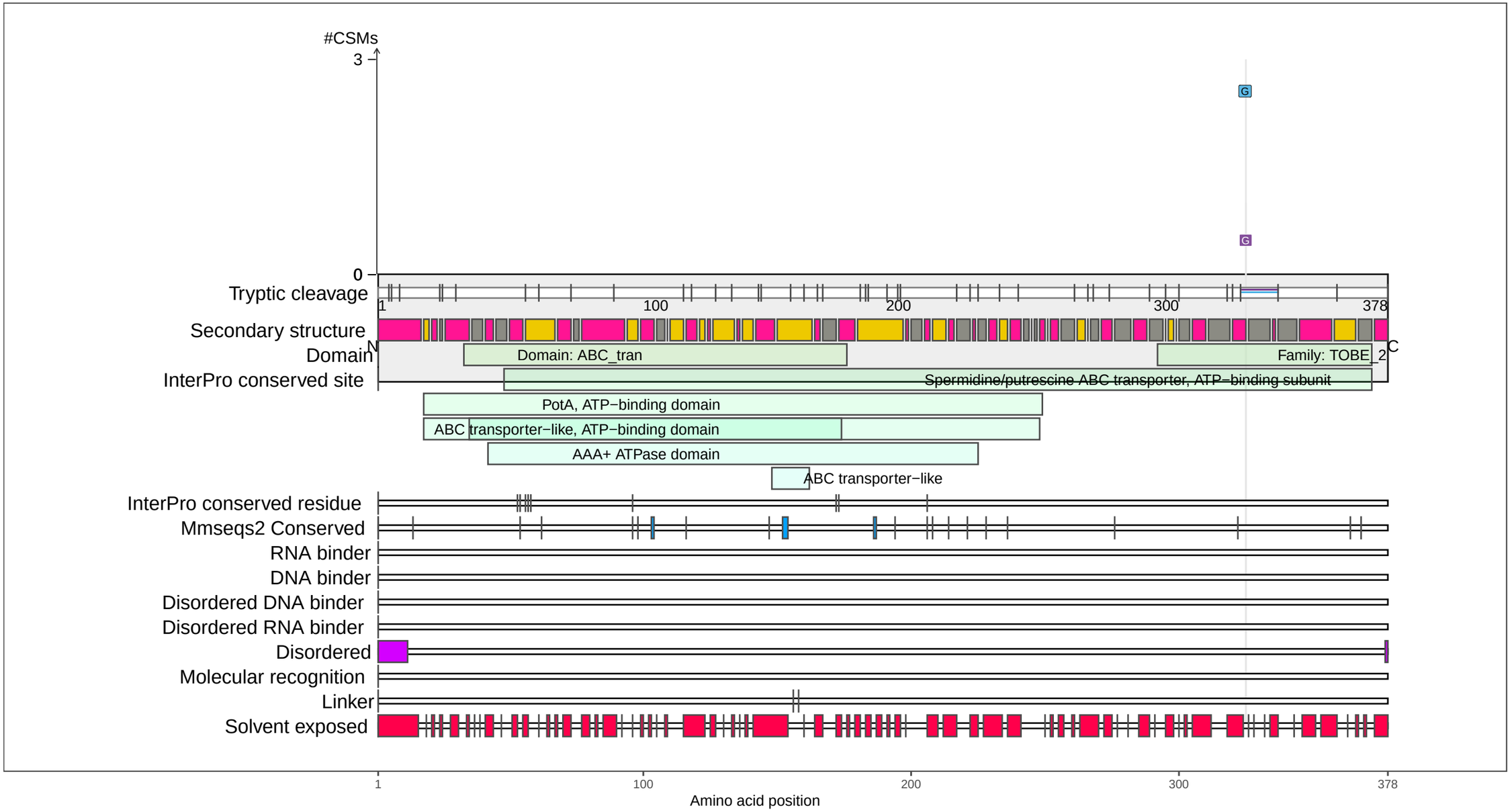
− RNA functions: not annotated



P69874
POTA_ECOLI Spermidine/putrescine import ATP−binding protein PotA

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: 1.65 (Q 47)
PAXdb E.coli [ppm]: 1.82 (Q 68)

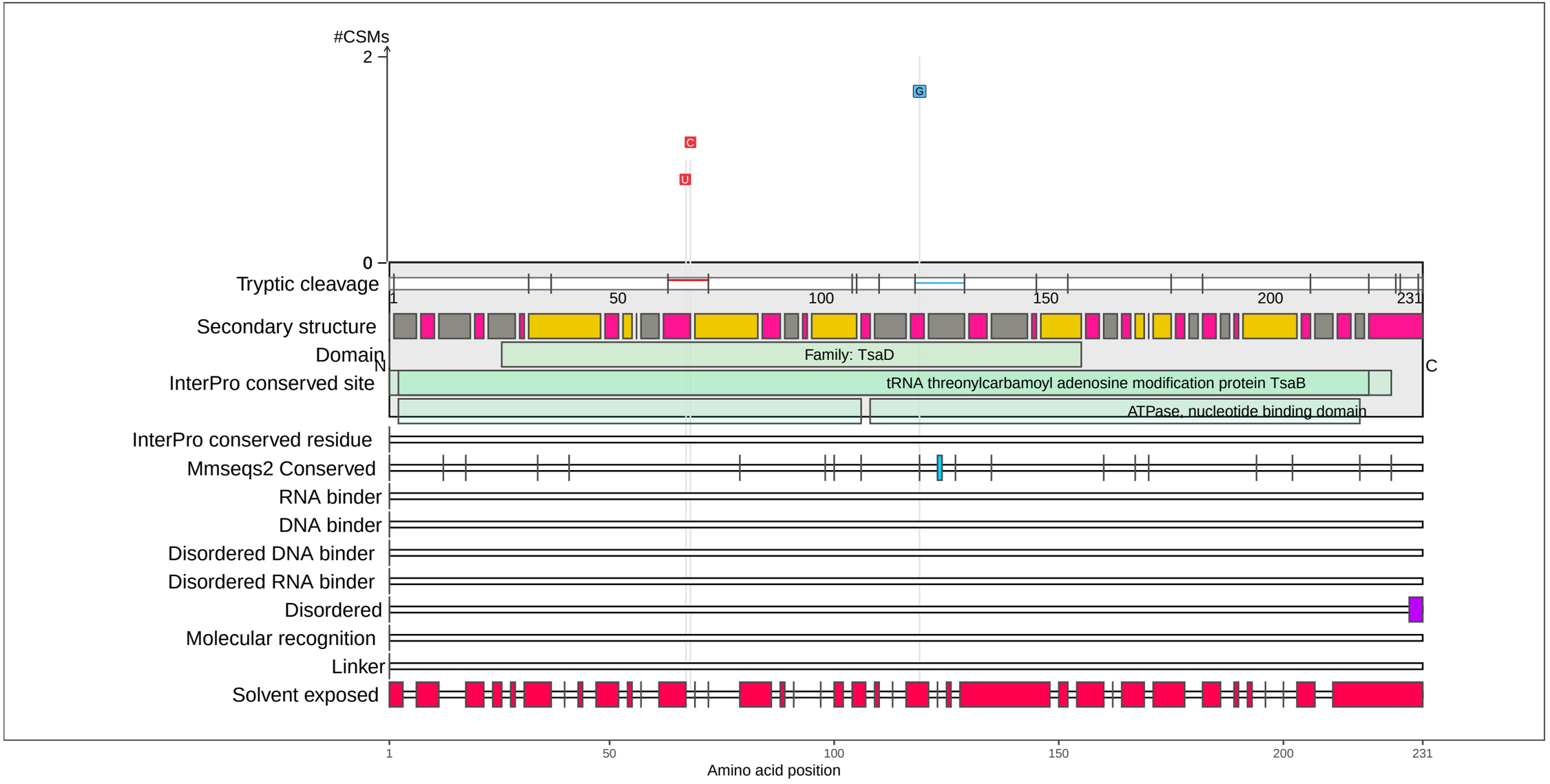
− RNA functions: not annotated

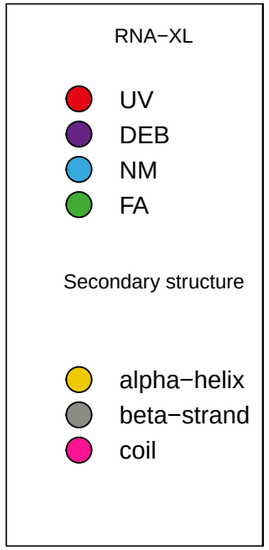


P76256
TSAB_ECOLI tRNA threonylcarbamoyladenosine biosynthesis protein TsaB

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 2.17 (Q 66)
PAXdb E.coli [ppm]: 1.31 (Q 55)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA threonylcarbamoyladenosine metabolic process; tRNA threonylcarbamoyladenosine modification

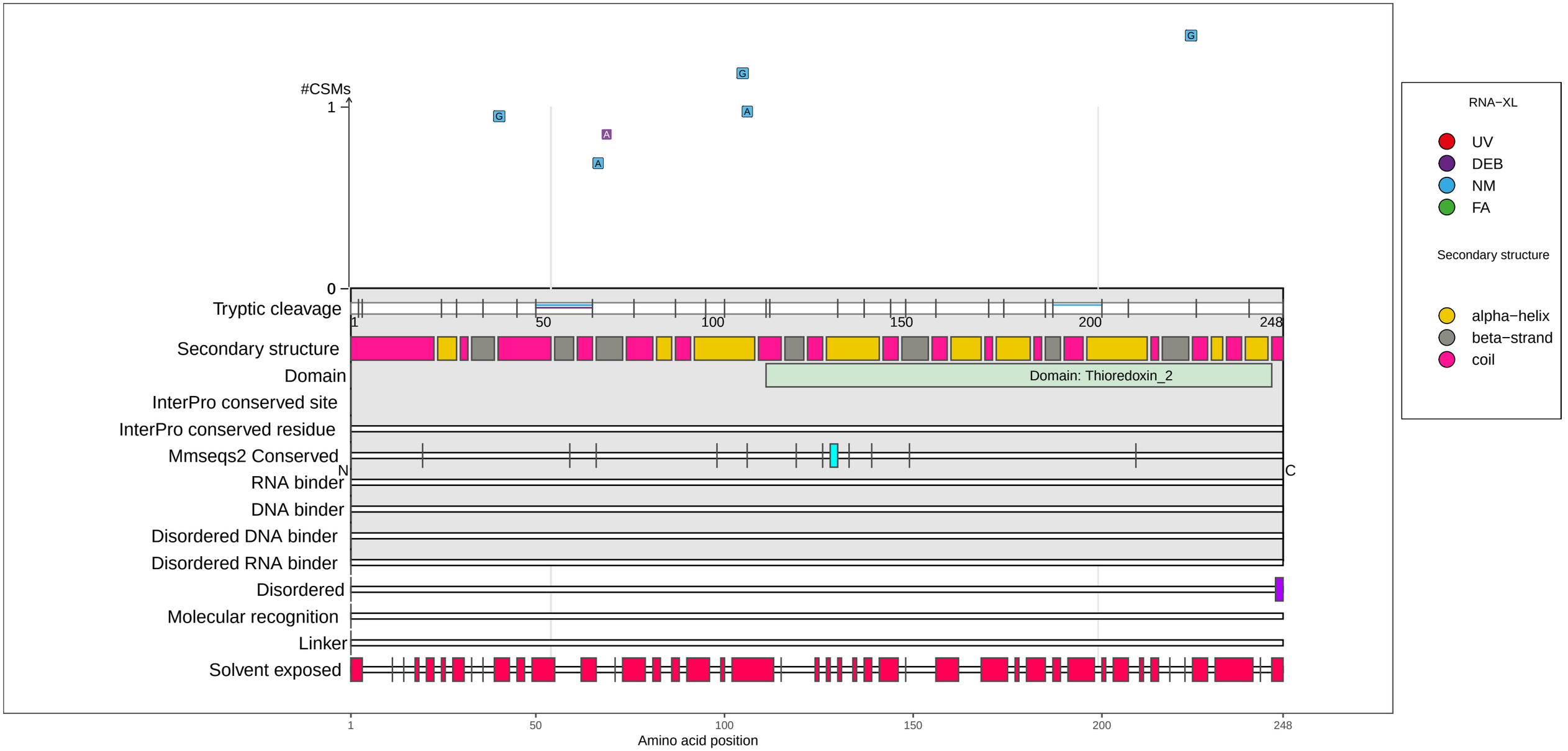




P77202
DSBG_ECOLI Thiol:disulfide interchange protein DsbG

− Abundance:
tryptic [log10 Intensity]: 7.26 (Q 23)
PAXdb K12 strain [ppm]: 0.98 (Q 10)
PAXdb E.coli [ppm]: 1.73 (Q 65)

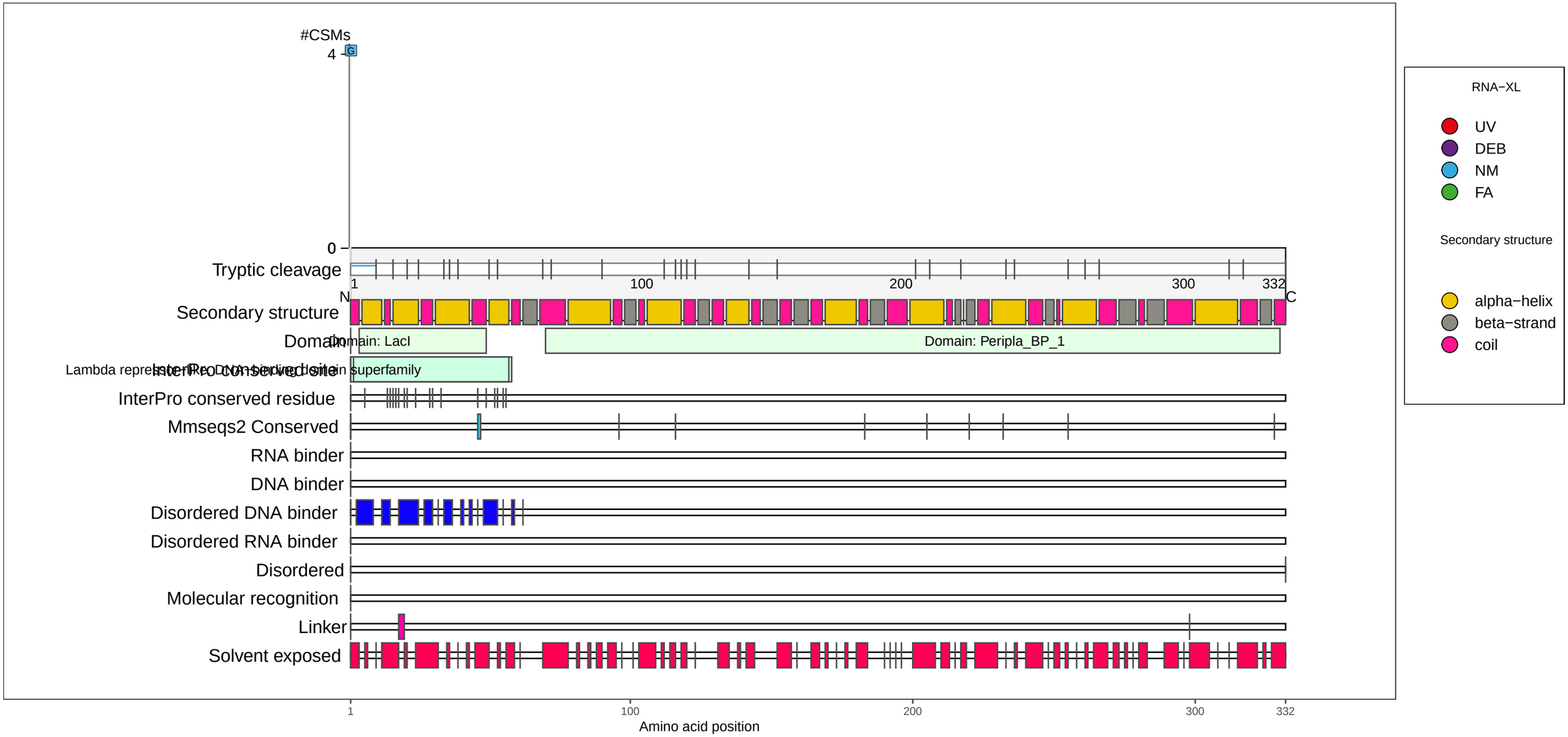
− RNA functions: not annotated



P77615
YCJW_ECOLI Uncharacterized HTH−type transcriptional regulator YcjW

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 45)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 0.54 (Q 37)

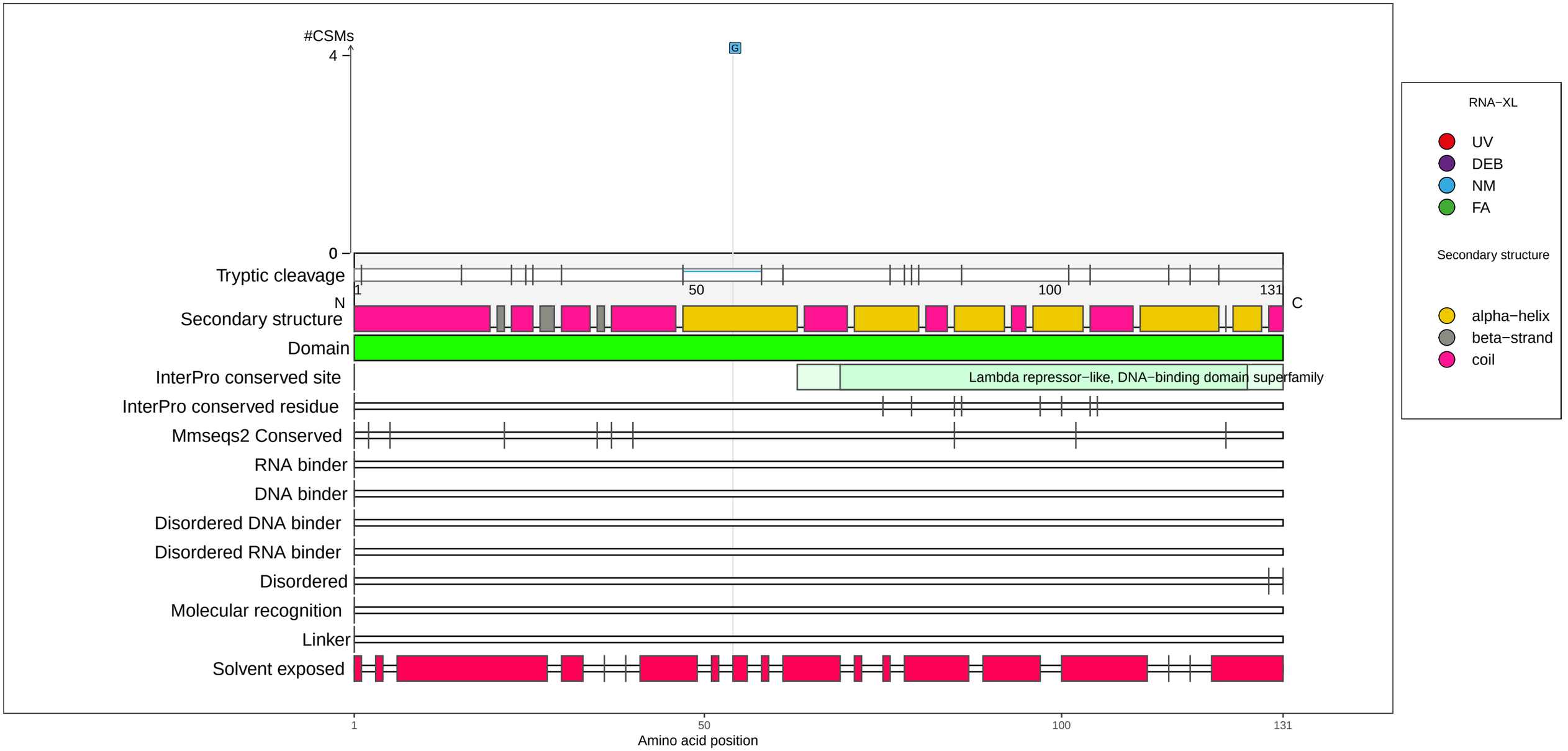
− RNA functions:
RNA biosynthetic process; RNA metabolic process



Q46864
MQSA_ECOLI Antitoxin MqsA

− Abundance:
tryptic [log10 Intensity]: 6.51 (Q 3)
PAXdb K12 strain [ppm]: 1.54 (Q 40)
PAXdb E.coli [ppm]: 0.65 (Q 40)

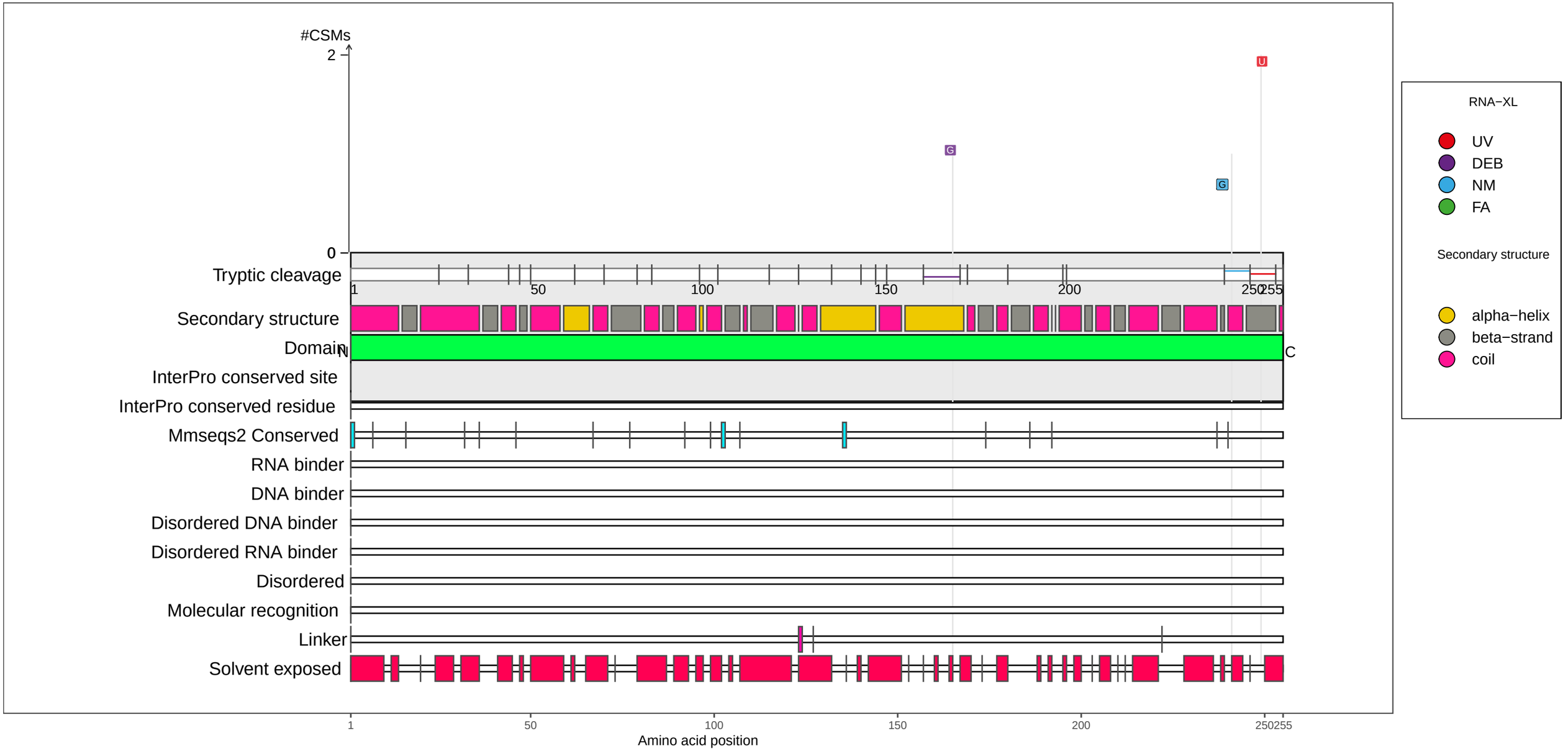
− RNA functions: not annotated



Q47147
YAFJ_ECOLI Putative glutamine amidotransferase YafJ

− Abundance:
tryptic [log10 Intensity]: 8.23 (Q 67)
PAXdb K12 strain [ppm]: 1.77 (Q 52)
PAXdb E.coli [ppm]: 1.05 (Q 49)

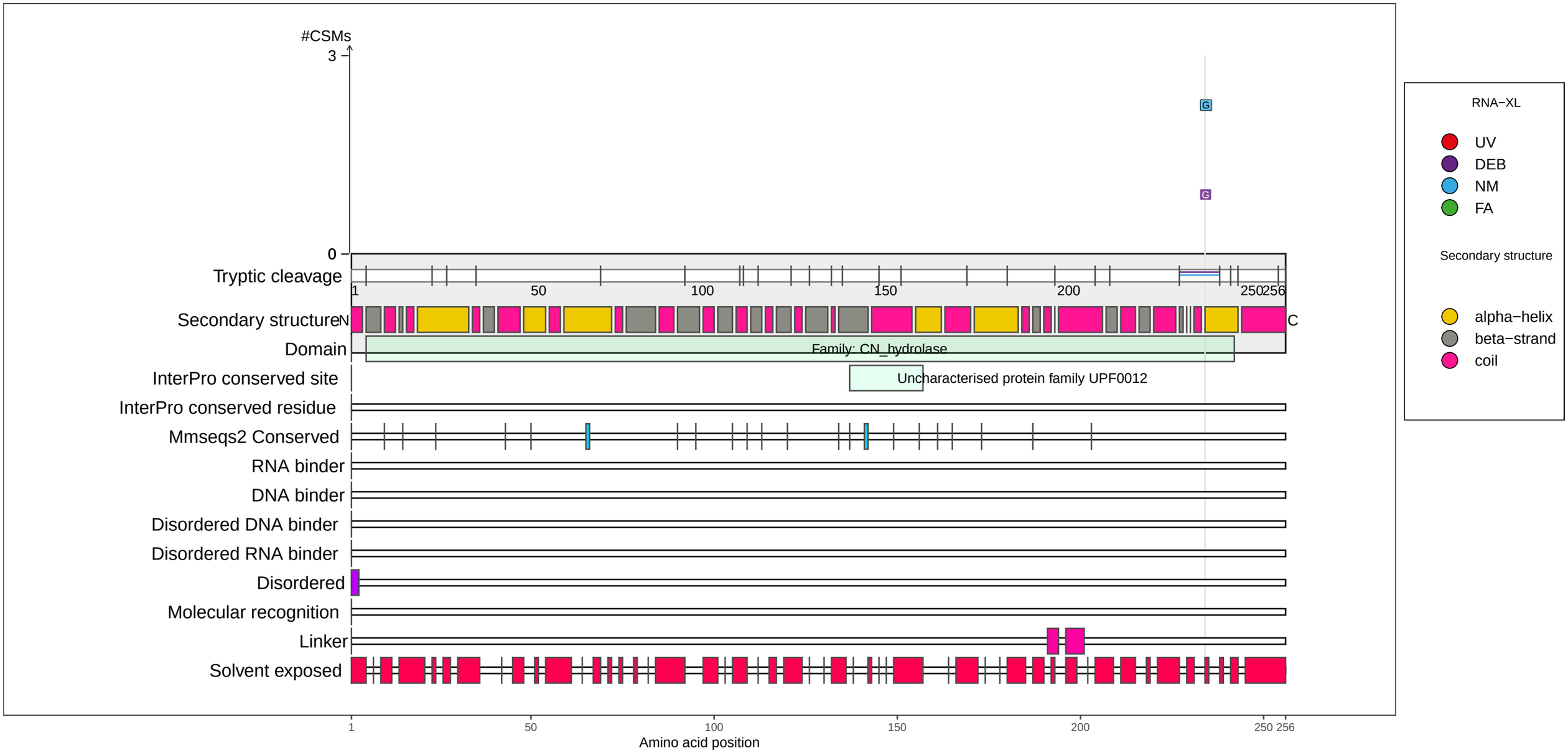
− RNA functions: not annotated



Q47679
YAFV_ECOLI Omega−amidase YafV

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 24)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.76 (Q 66)

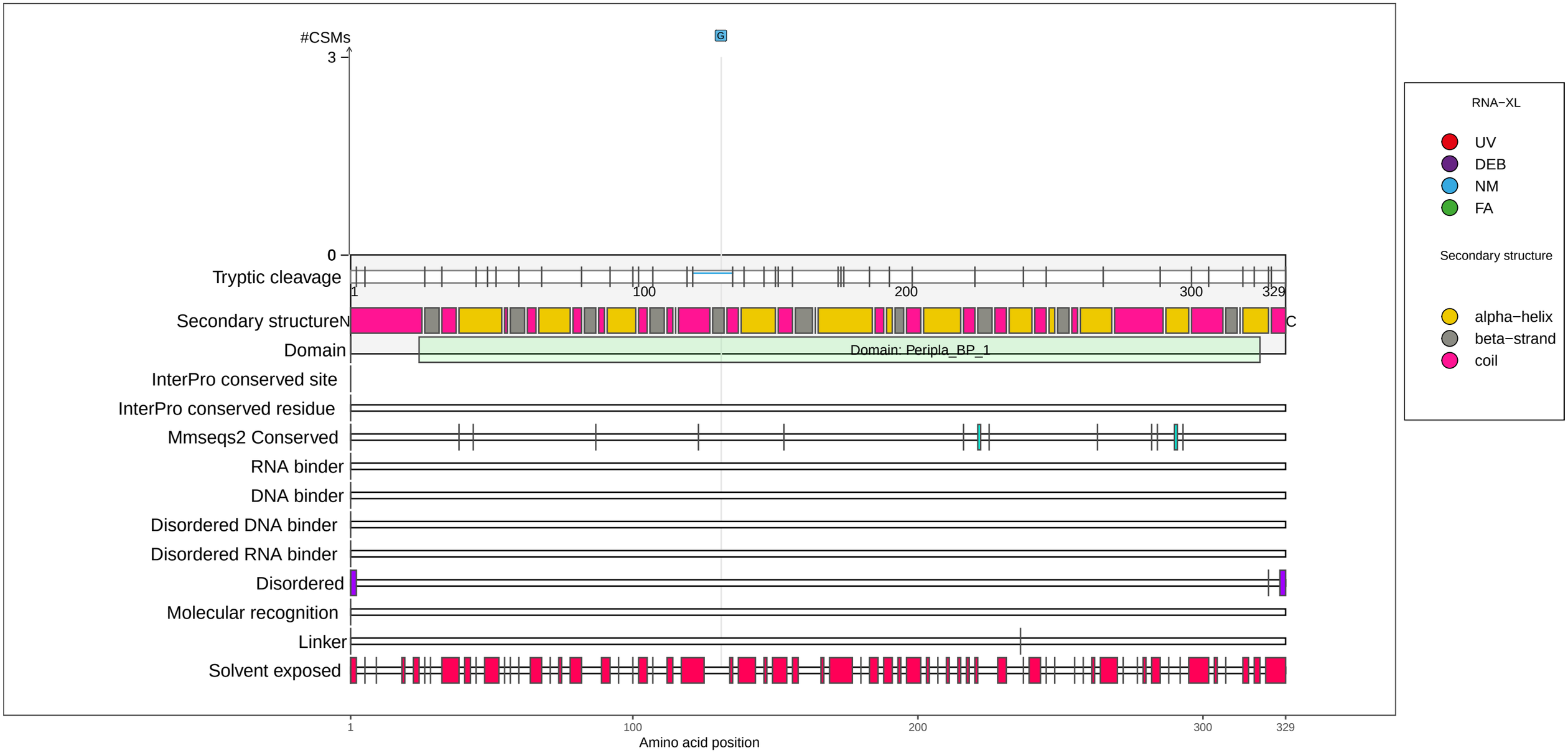
− RNA functions: not annotated



P02924
ARAF_ECOLI L−arabinose−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.15 (Q 19)
PAXdb K12 strain [ppm]: 1.67 (Q 48)
PAXdb E.coli [ppm]: 2.54 (Q 86)

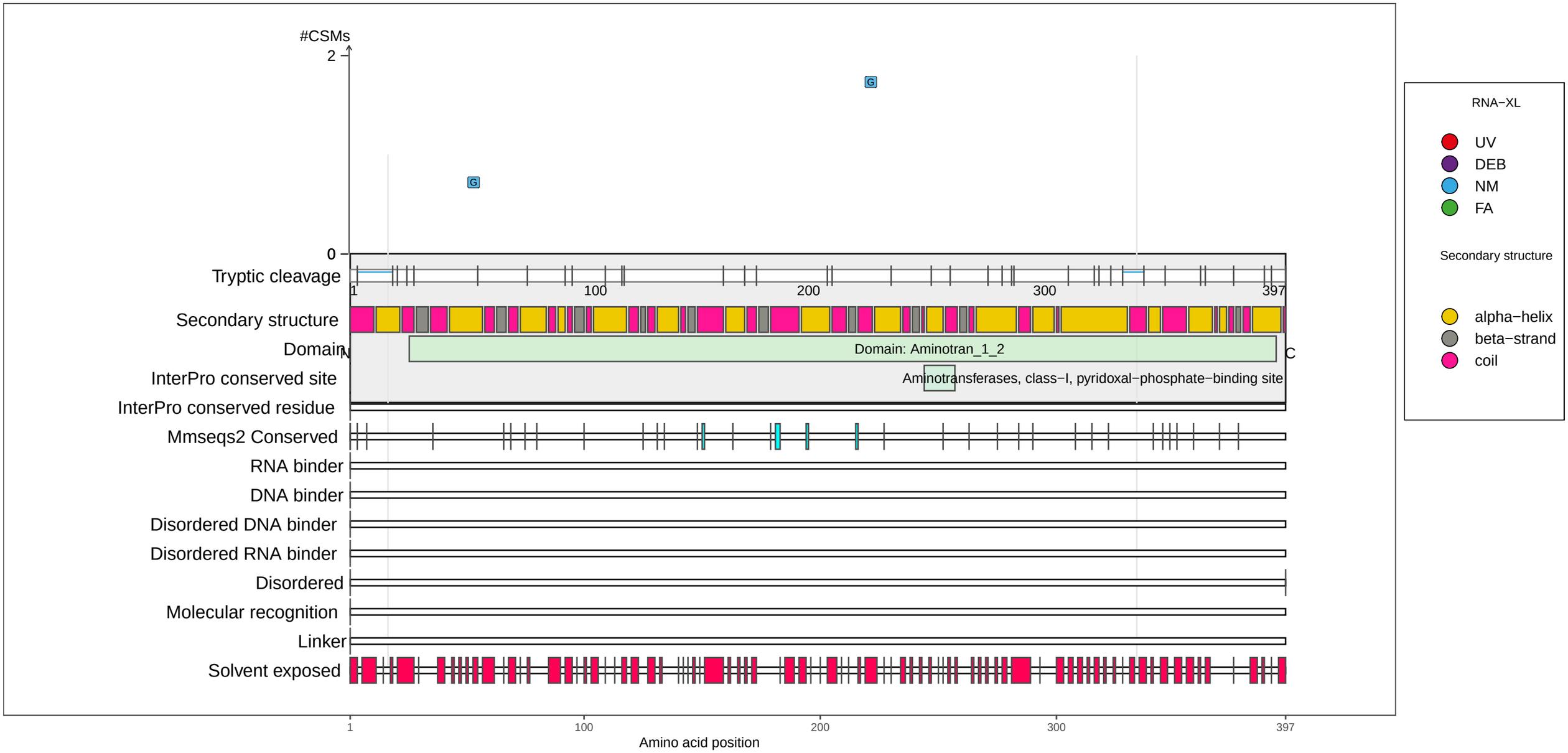
− RNA functions: not annotated



P04693
TYRB_ECOLI Aromatic−amino−acid aminotransferase

− Abundance:
tryptic [log10 Intensity]: 8.34 (Q 71)
PAXdb K12 strain [ppm]: 2.82 (Q 87)
PAXdb E.coli [ppm]: 2.39 (Q 83)

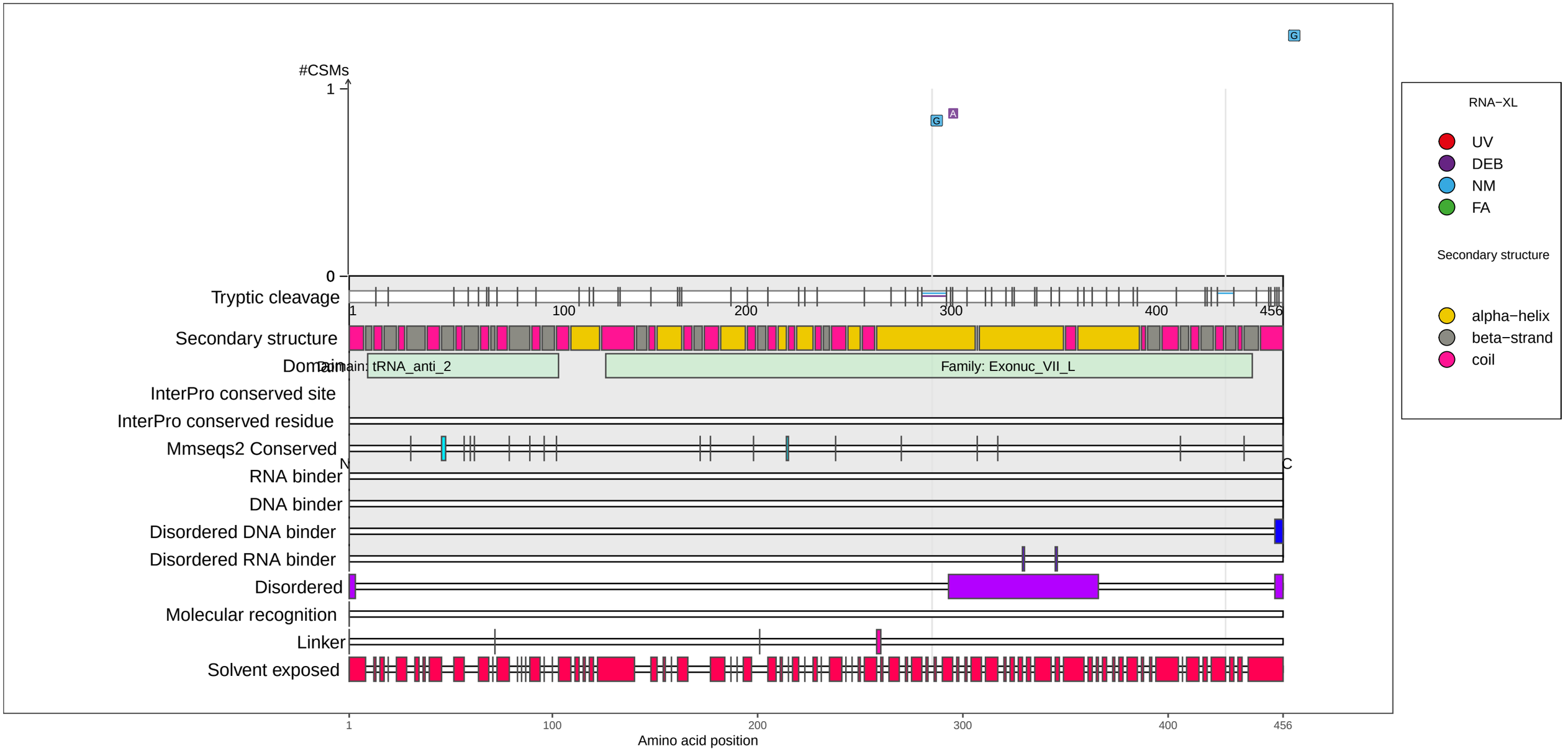
− RNA functions: not annotated



P04994
EX7L_ECOLI Exodeoxyribonuclease 7 large subunit

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 64)
PAXdb K12 strain [ppm]: 1.28 (Q 25)
PAXdb E.coli [ppm]: 0.33 (Q 32)

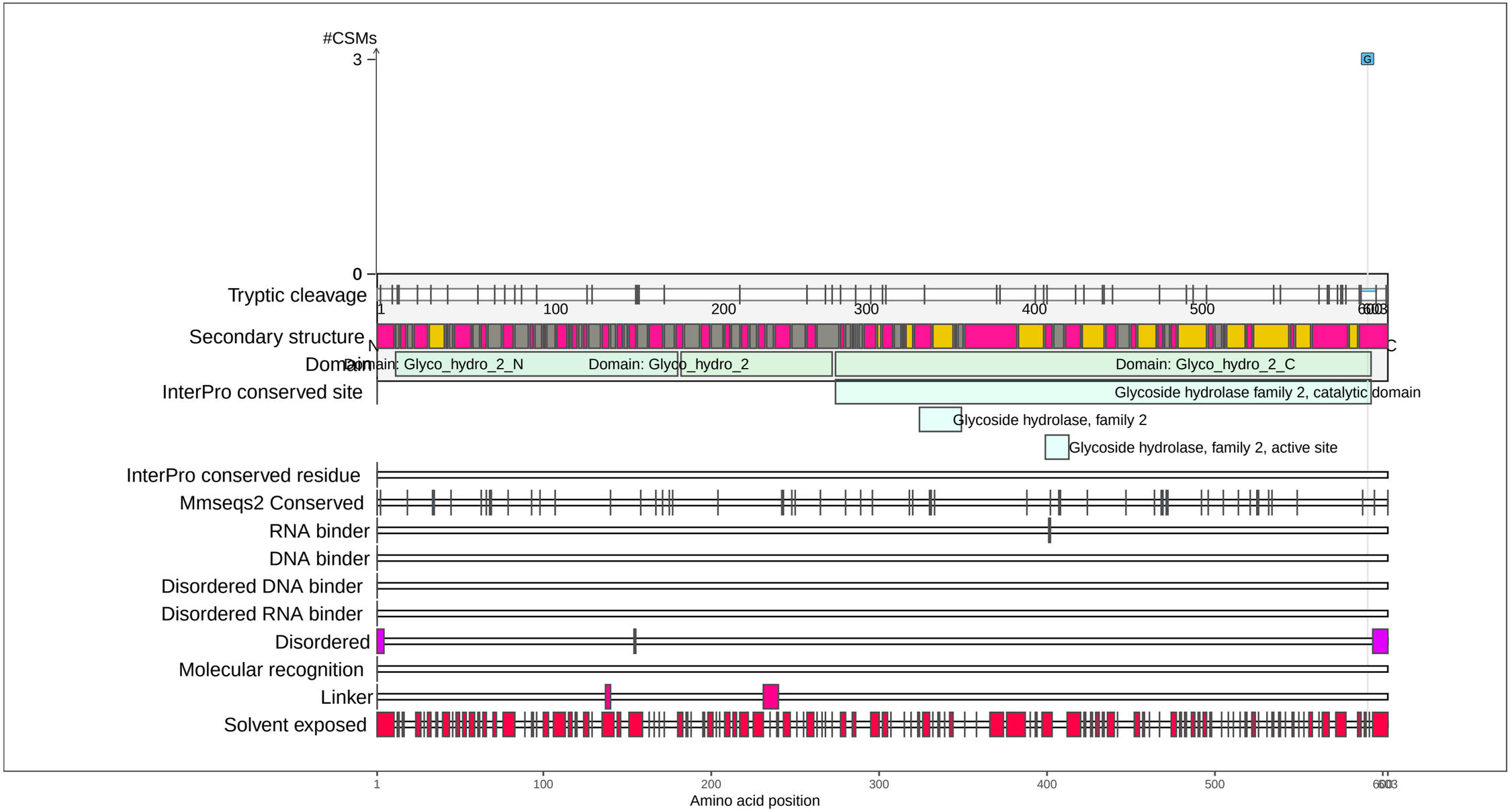
− RNA functions: not annotated

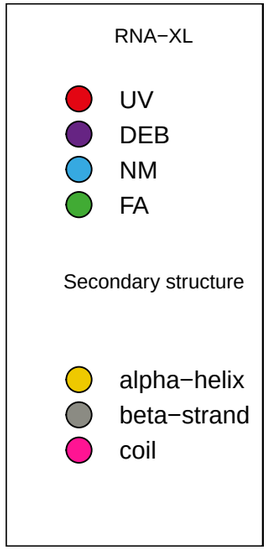


P05804
BGLR_ECOLI Beta−glucuronidase

− Abundance:
tryptic [log10 Intensity]: 7.1 (Q 17)
PAXdb K12 strain [ppm]: 1.76 (Q 52)
PAXdb E.coli [ppm]: 0.55 (Q 37)

− RNA functions: not annotated

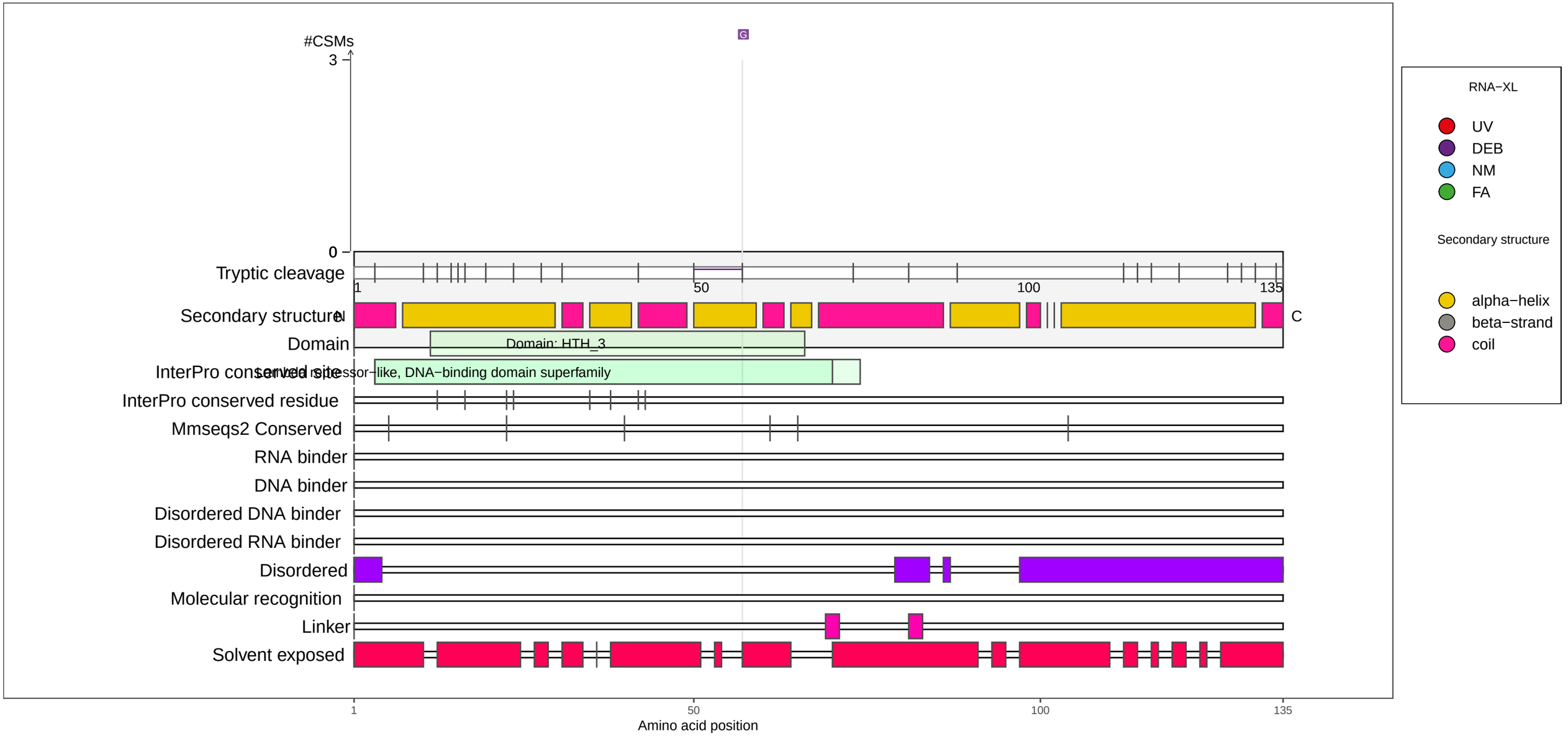




P06966
DICA_ECOLI HTH−type transcriptional regulator DicA

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.37 (Q 30)
PAXdb E.coli [ppm]: 1.59 (Q 62)

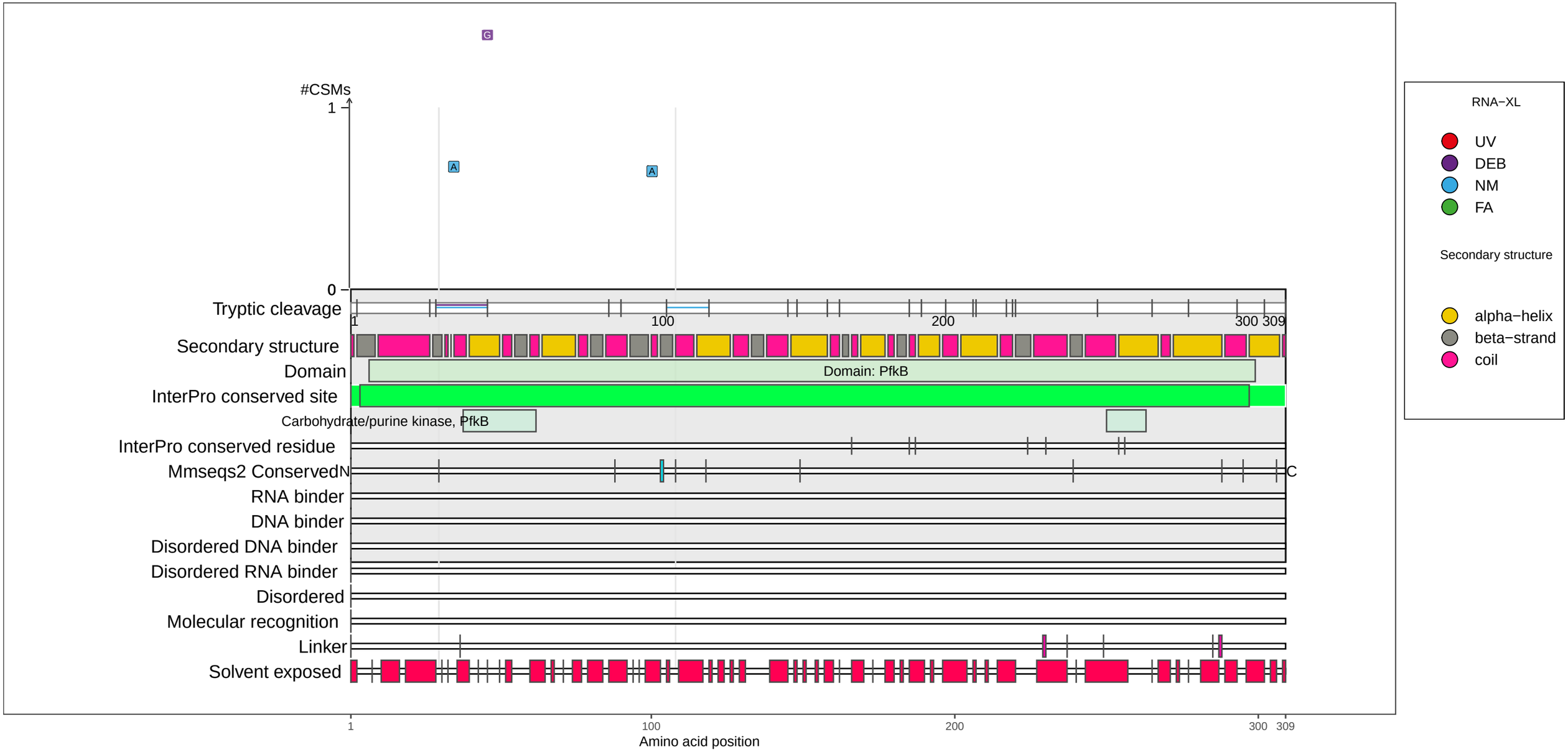
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P06999
PFKB_ECOLI ATP−dependent 6−phosphofructokinase isozyme 2

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 2.99 (Q 91)
PAXdb E.coli [ppm]: 2.47 (Q 85)

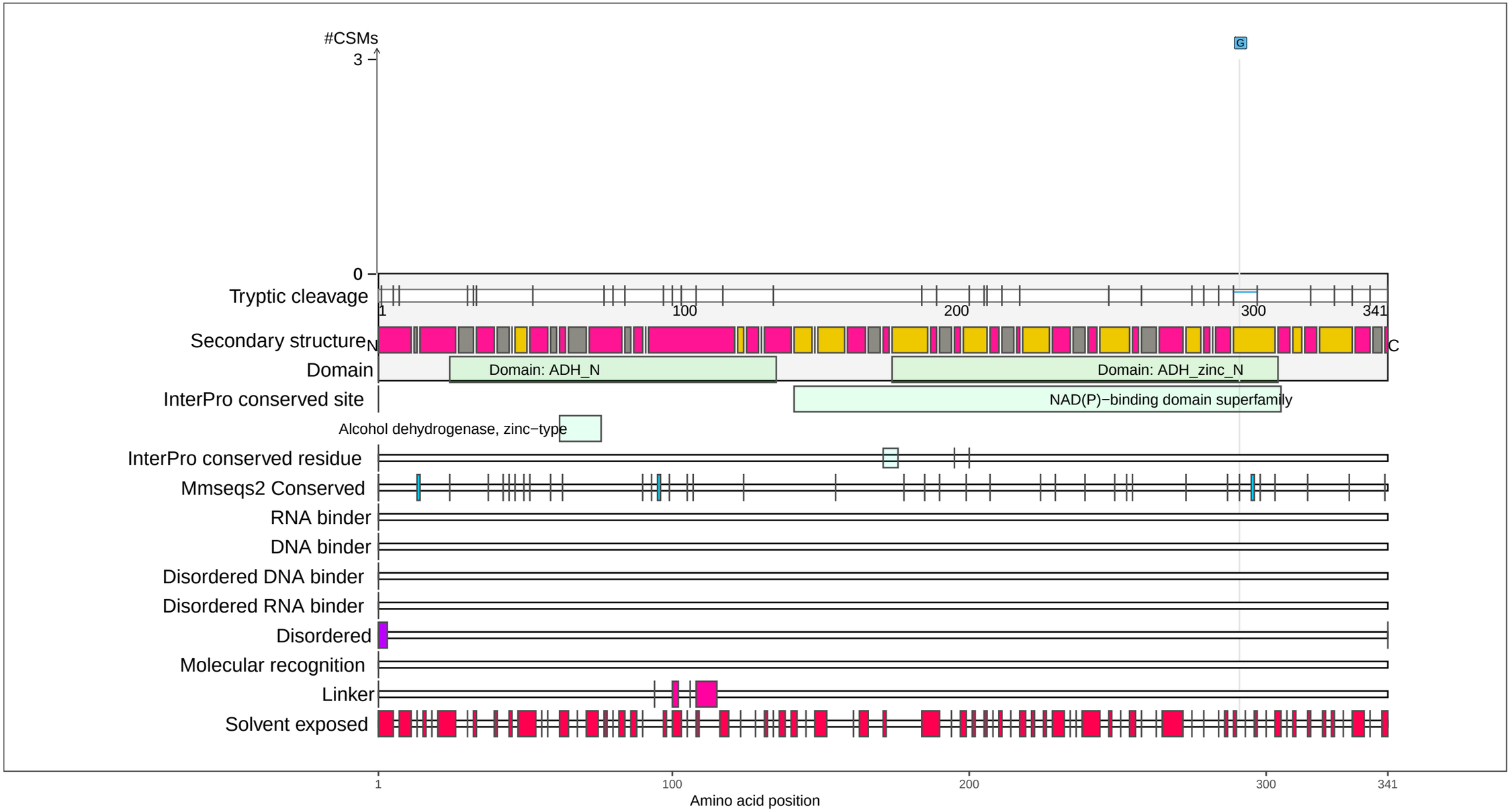
− RNA functions: not annotated



P07913
TDH_ECOLI L−threonine 3−dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.3 (Q 94)
PAXdb K12 strain [ppm]: 2.69 (Q 83)
PAXdb E.coli [ppm]: 1.95 (Q 71)

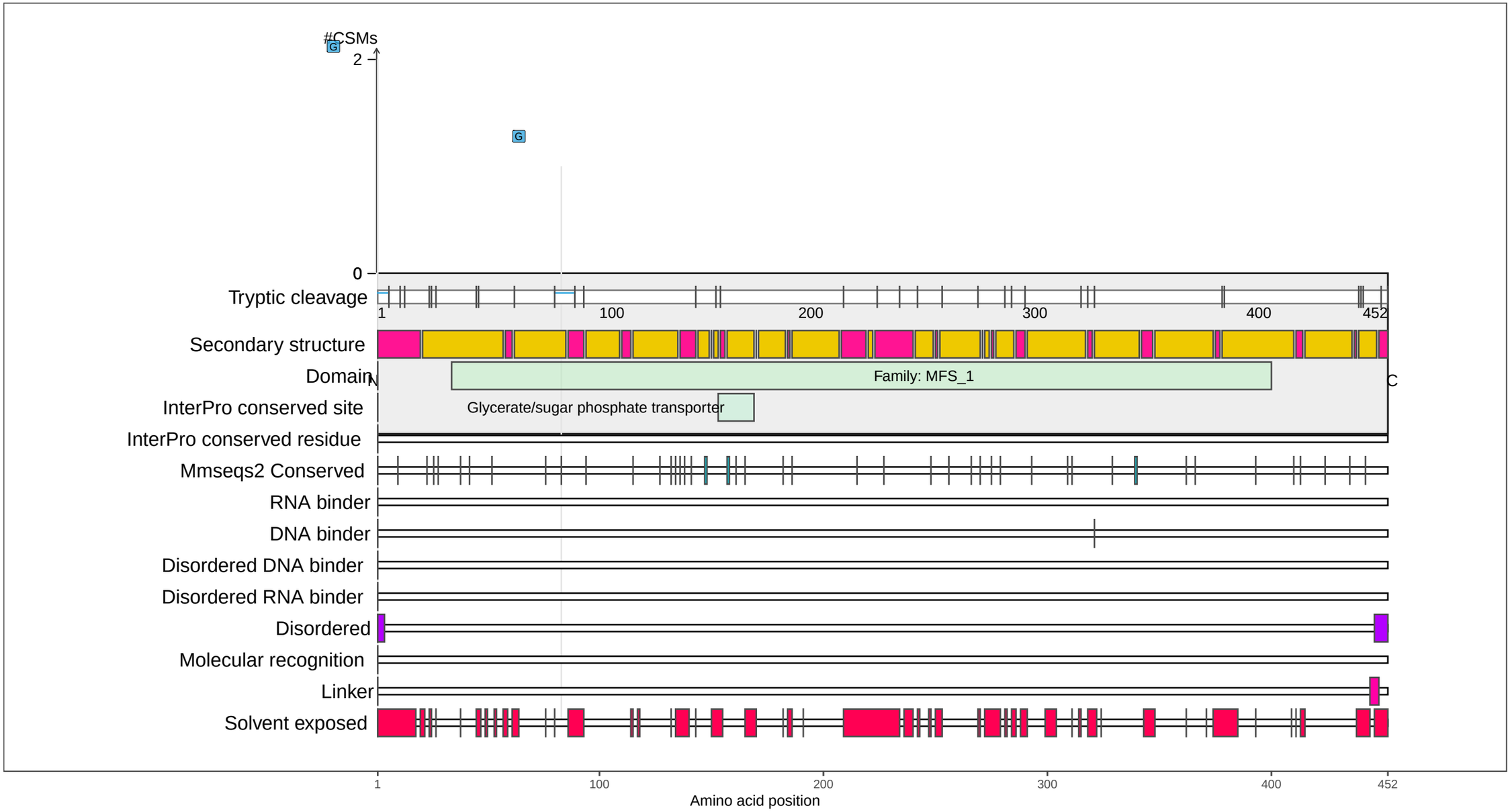
− RNA functions: not annotated



P08194
GLPT_ECOLI Glycerol−3−phosphate transporter

− Abundance:
tryptic [log10 Intensity]: 9.34 (Q 95)
PAXdb K12 strain [ppm]: 2.47 (Q 76)
PAXdb E.coli [ppm]: 1.61 (Q 63)

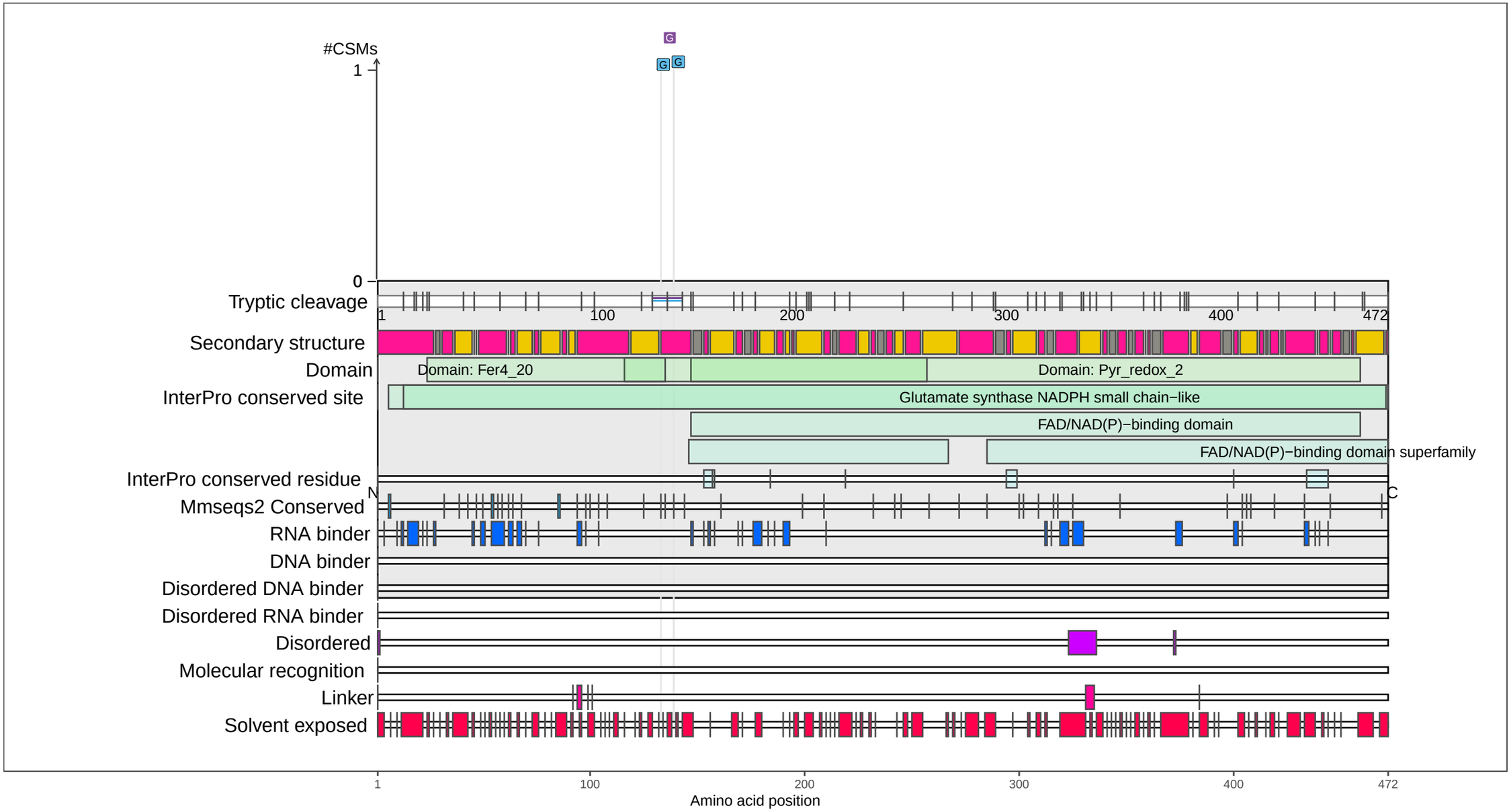
− RNA functions: not annotated



P09832
GLTD_ECOLI Glutamate synthase [NADPH] small chain

− Abundance:
tryptic [log10 Intensity]: 7.65 (Q 43)
PAXdb K12 strain [ppm]: 2.66 (Q 82)
PAXdb E.coli [ppm]: 2.92 (Q 94)

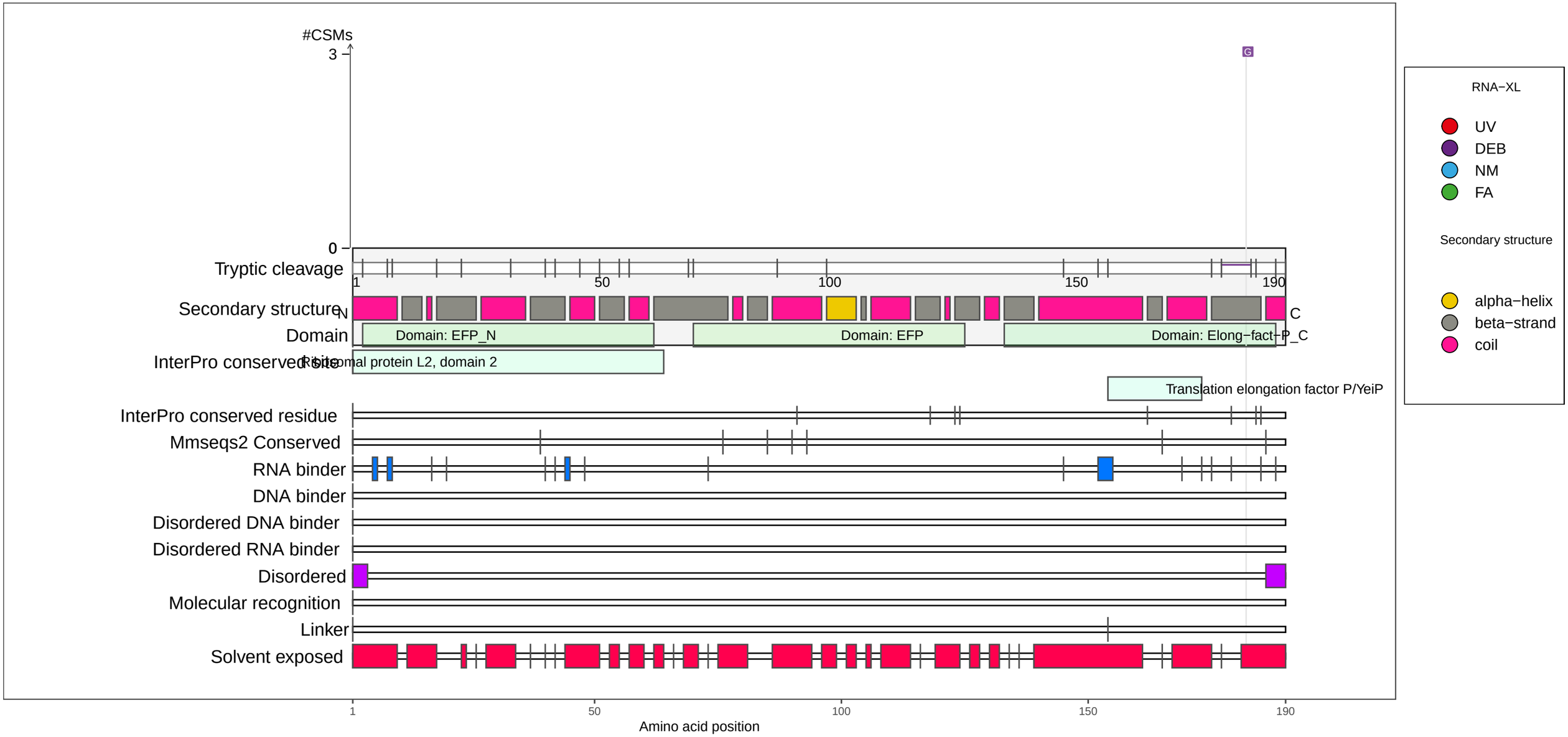
− RNA functions: not annotated



P0A6N8
EFPL_ECOLI Elongation factor P−like protein

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: 3.03 (Q 91)
PAXdb E.coli [ppm]: 2.72 (Q 90)

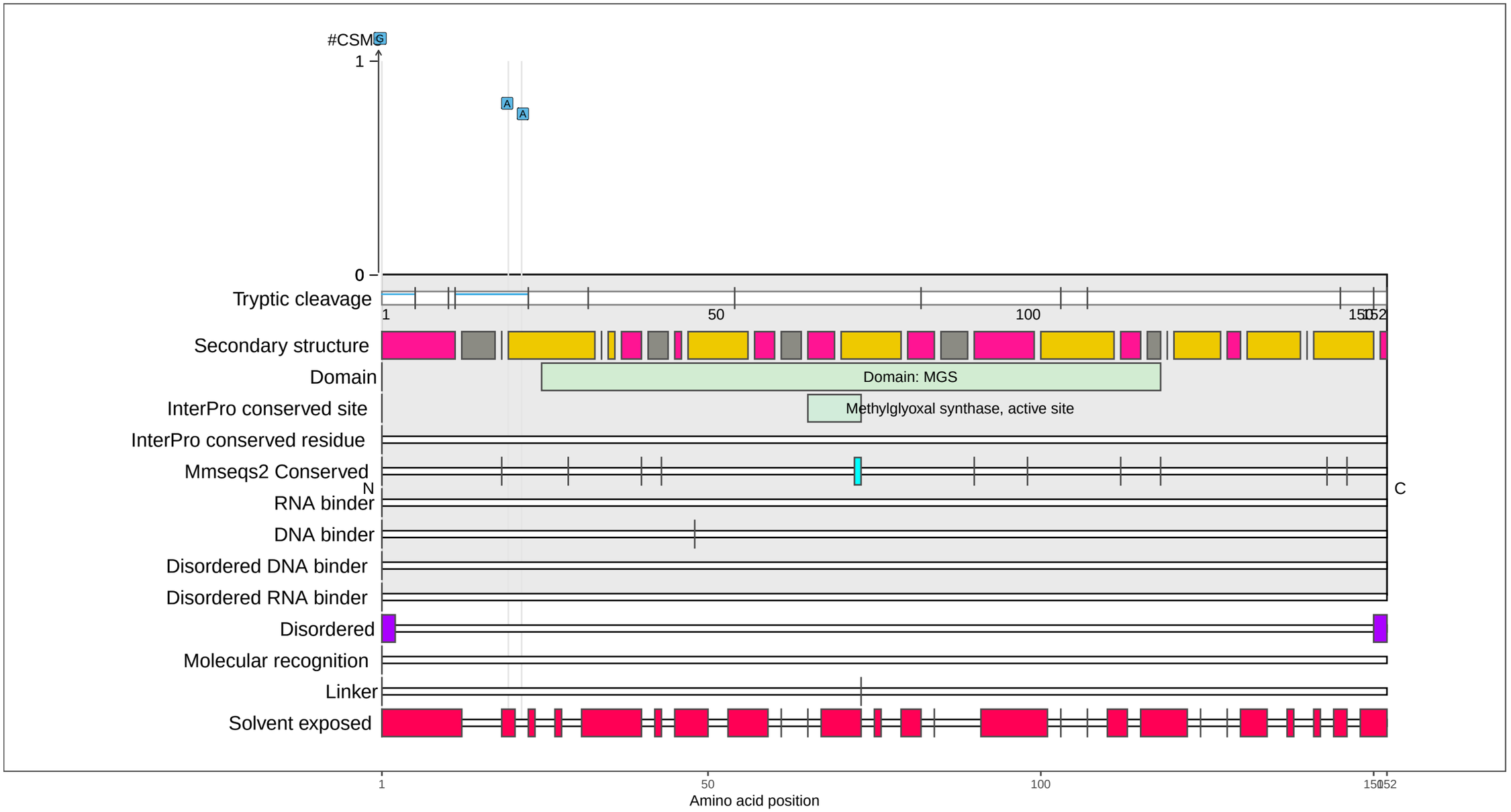
− RNA functions:
RNA binding



P0A731
MGSA_ECOLI Methylglyoxal synthase

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.39 (Q 83)

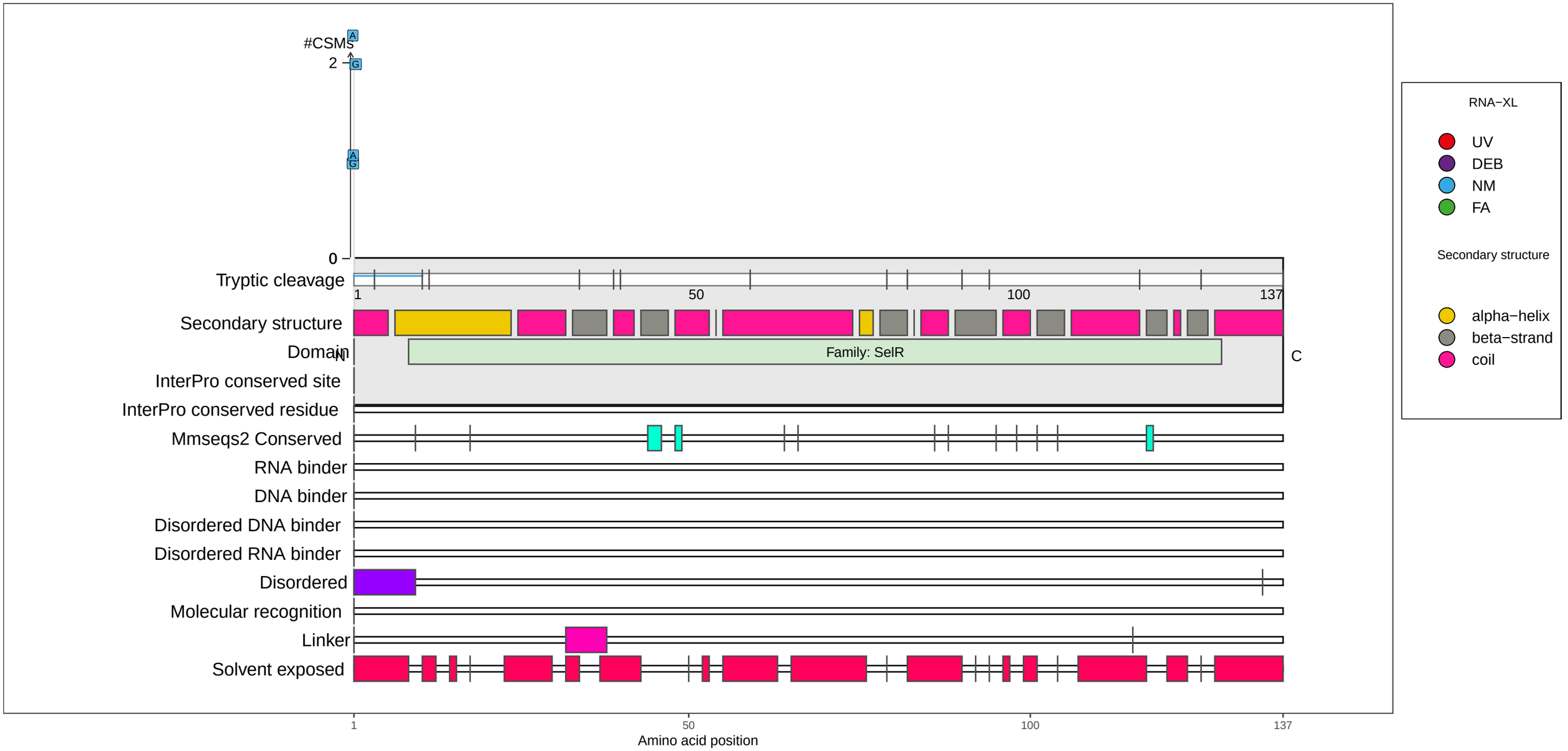
− RNA functions: not annotated



P0A746
MSRB_ECOLI Peptide methionine sulfoxide reductase MsrB

− Abundance:
tryptic [log10 Intensity]: 7.57 (Q 38)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 2.7 (Q 90)

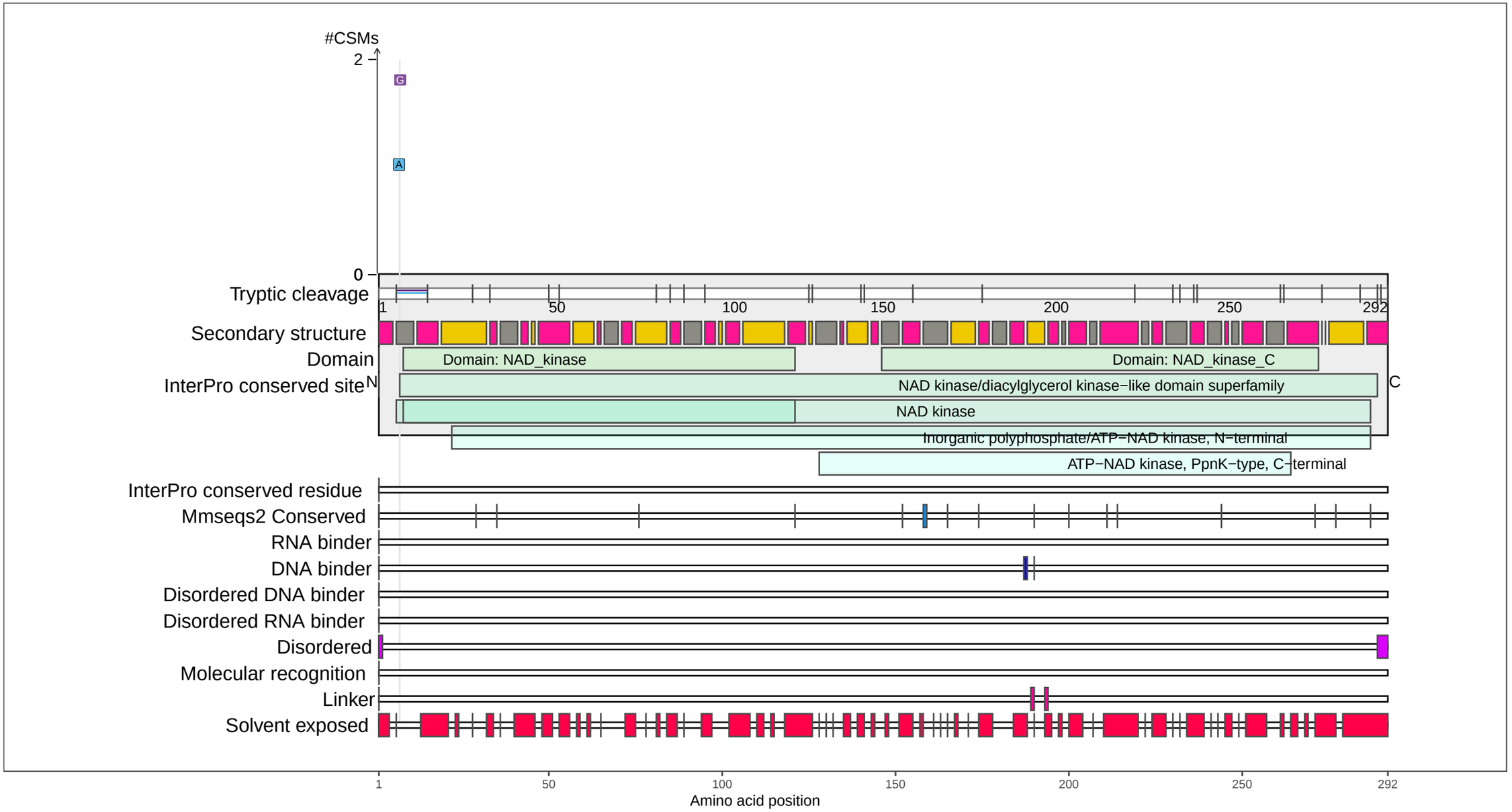
− RNA functions: not annotated

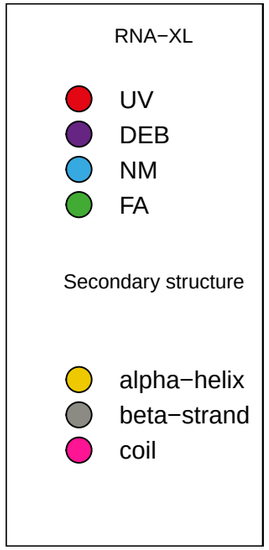


P0A7B3
NADK_ECOLI NAD kinase

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 1.04 (Q 13)
PAXdb E.coli [ppm]: 1.62 (Q 63)

− RNA functions: not annotated

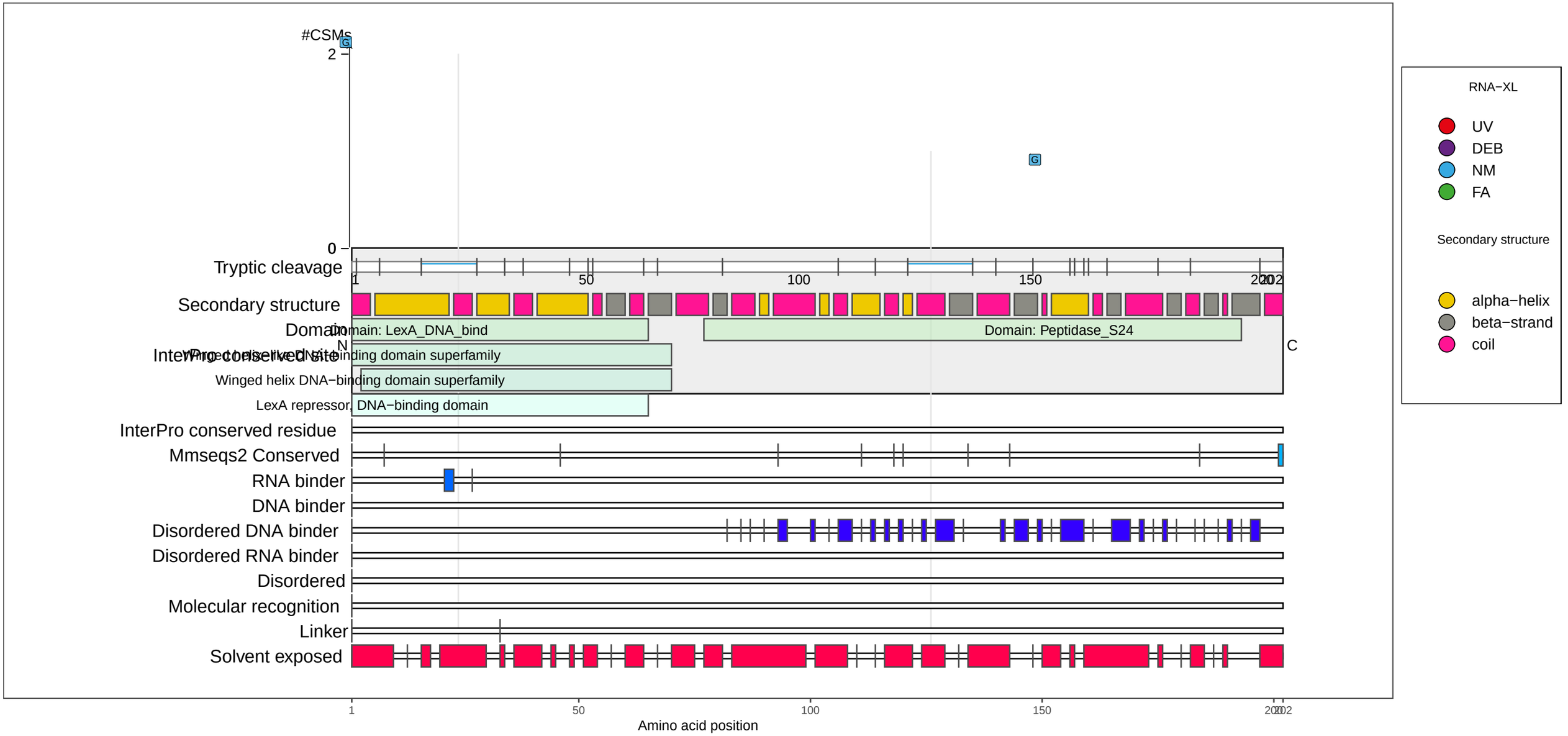




P0A7C2
LEXA_ECOLI LexA repressor

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: 2.32 (Q 70)
PAXdb E.coli [ppm]: 1.82 (Q 67)

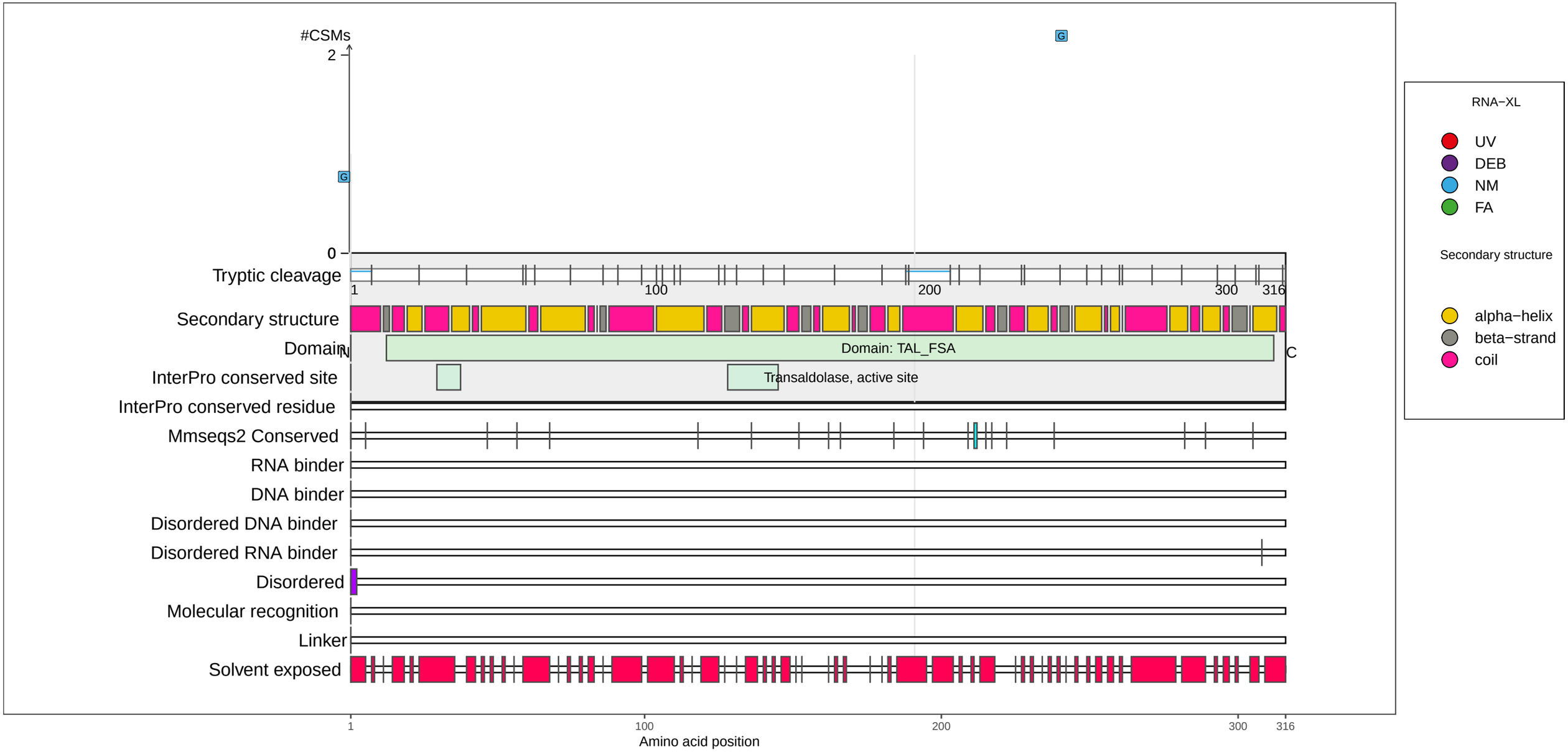
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0A867
TALA_ECOLI Transaldolase A

− Abundance:
tryptic [log10 Intensity]: 7.51 (Q 35)
PAXdb K12 strain [ppm]: 2.73 (Q 84)
PAXdb E.coli [ppm]: 3.1 (Q 96)

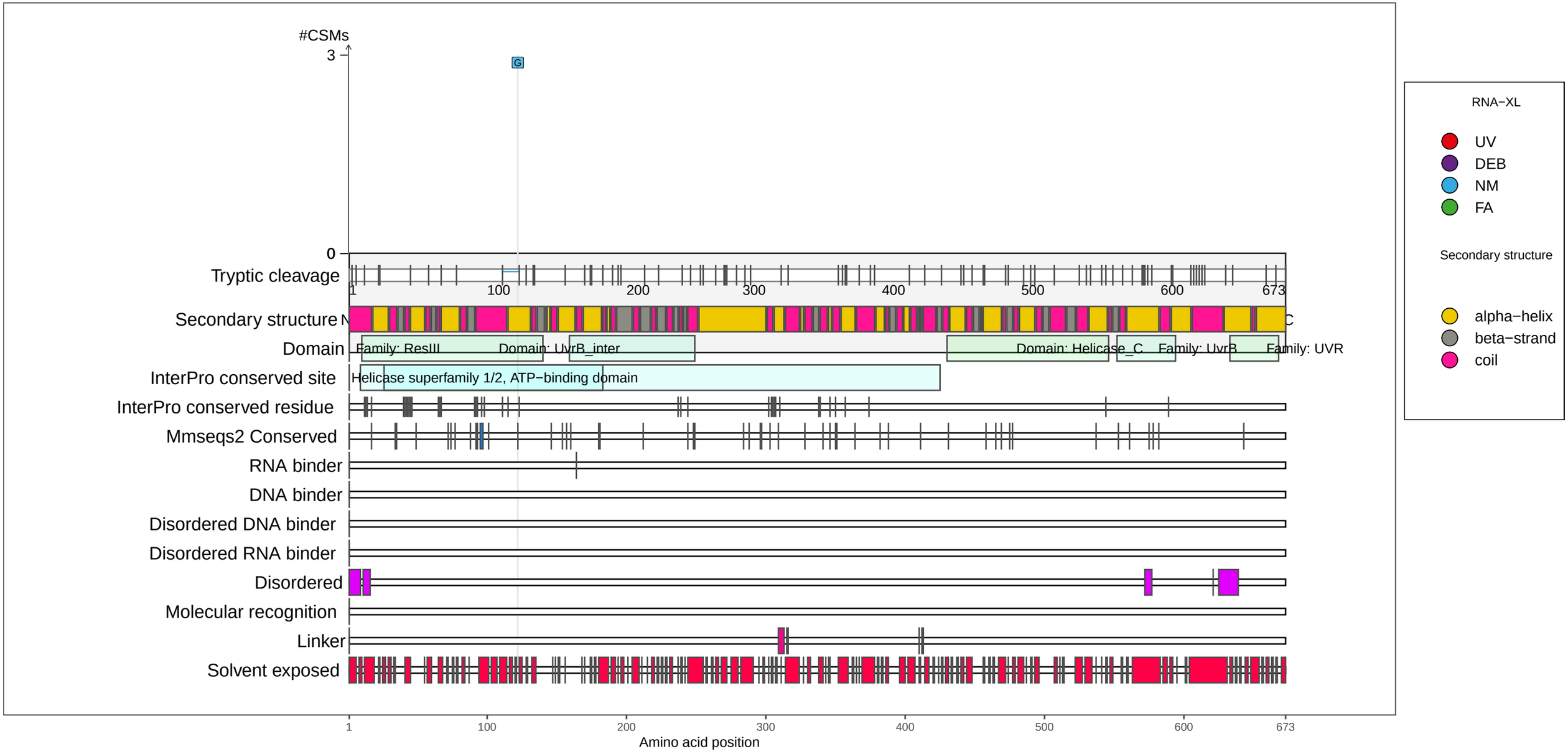
− RNA functions: not annotated



P0A8F8
UVRB_ECOLI UvrABC system protein B

− Abundance:
tryptic [log10 Intensity]: 8.22 (Q 66)
PAXdb K12 strain [ppm]: 2.26 (Q 68)
PAXdb E.coli [ppm]: 1.77 (Q 66)

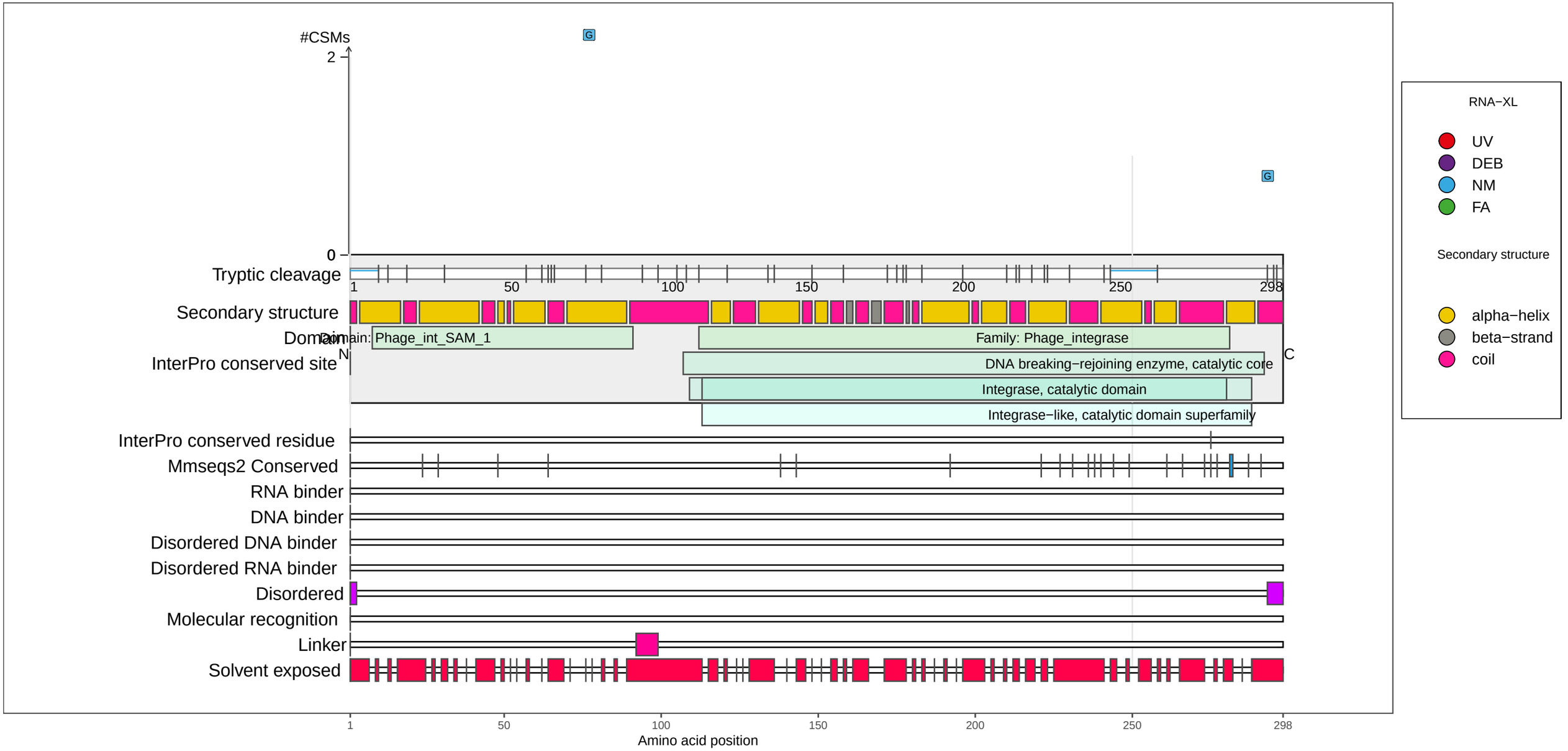
− RNA functions: not annotated



P0A8P6
XERC_ECOLI Tyrosine recombinase XerC

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.47 (Q 37)
PAXdb E.coli [ppm]: 0.46 (Q 35)

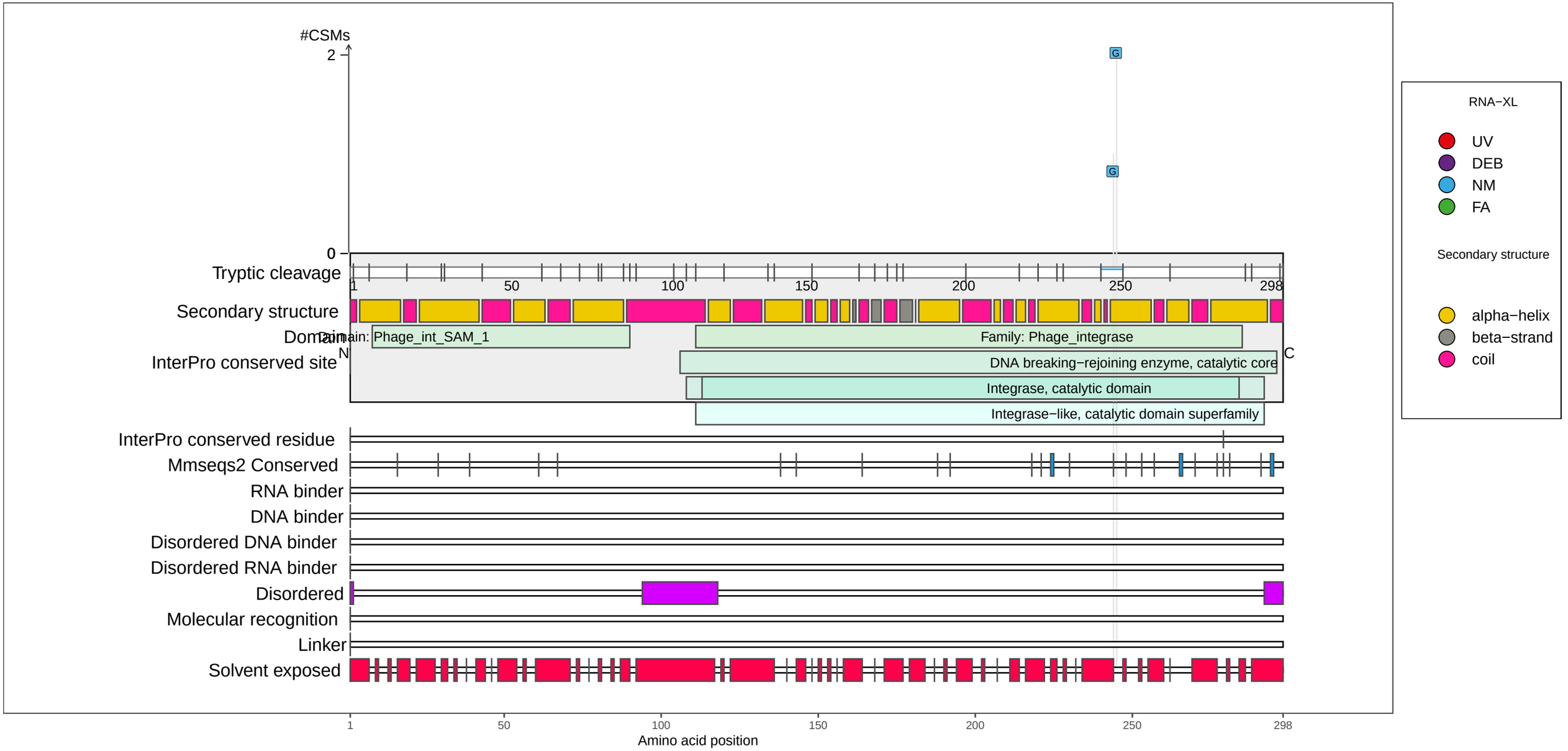
− RNA functions: not annotated



P0A8P8
XERD_ECOLI Tyrosine recombinase XerD

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.92 (Q 8)
PAXdb E.coli [ppm]: 0.26 (Q 31)

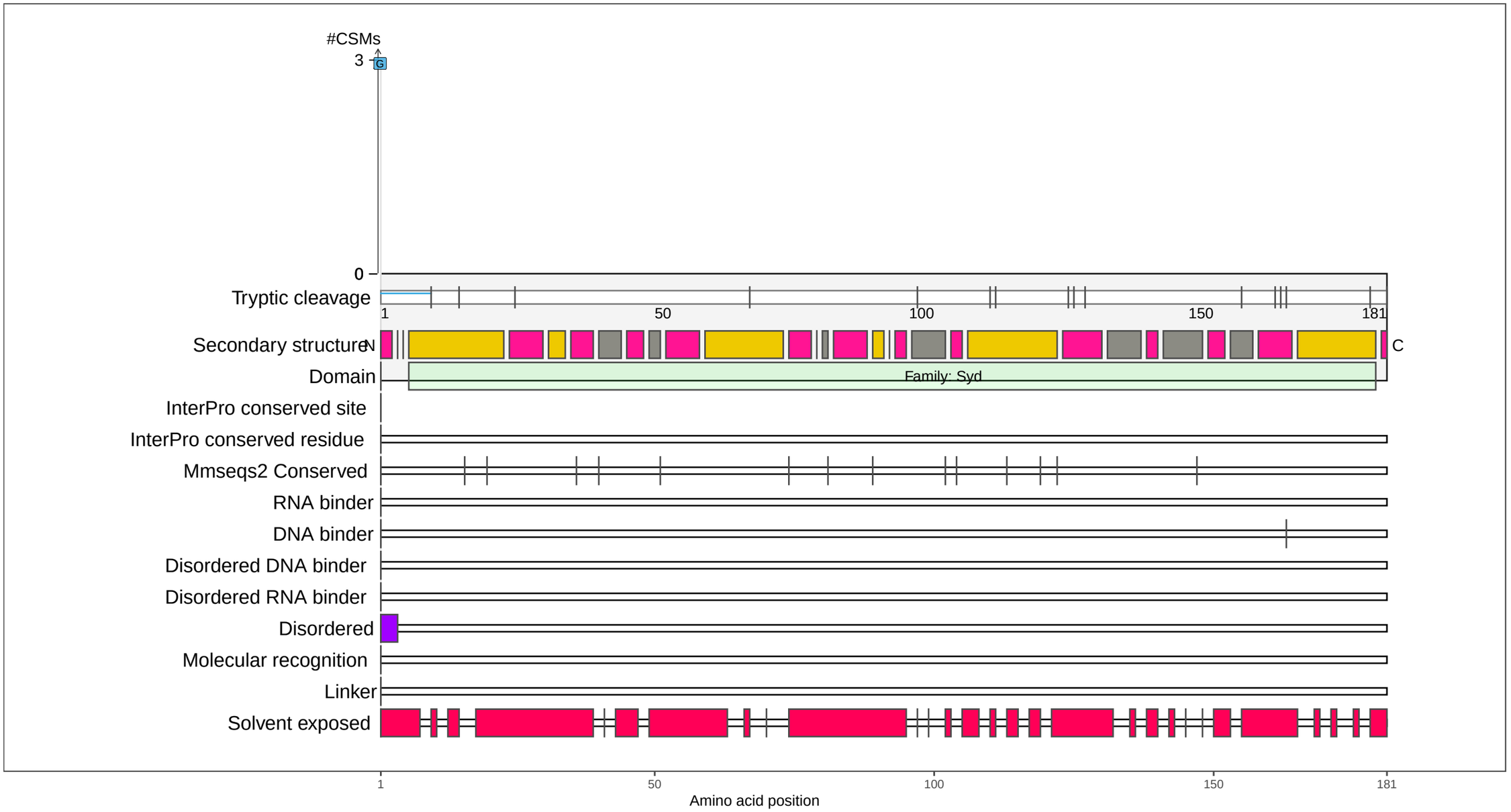
− RNA functions: not annotated

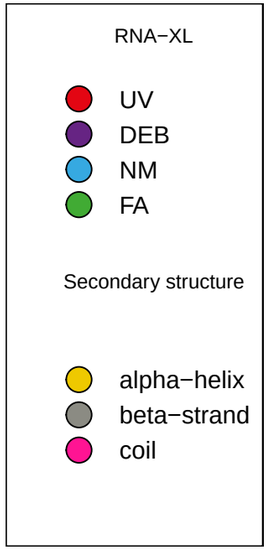


P0A8U0
SYDP_ECOLI Protein Syd

− Abundance:
tryptic [log10 Intensity]: 7.91 (Q 54)
PAXdb K12 strain [ppm]: 2.31 (Q 70)
PAXdb E.coli [ppm]: 1.55 (Q 61)

− RNA functions: not annotated

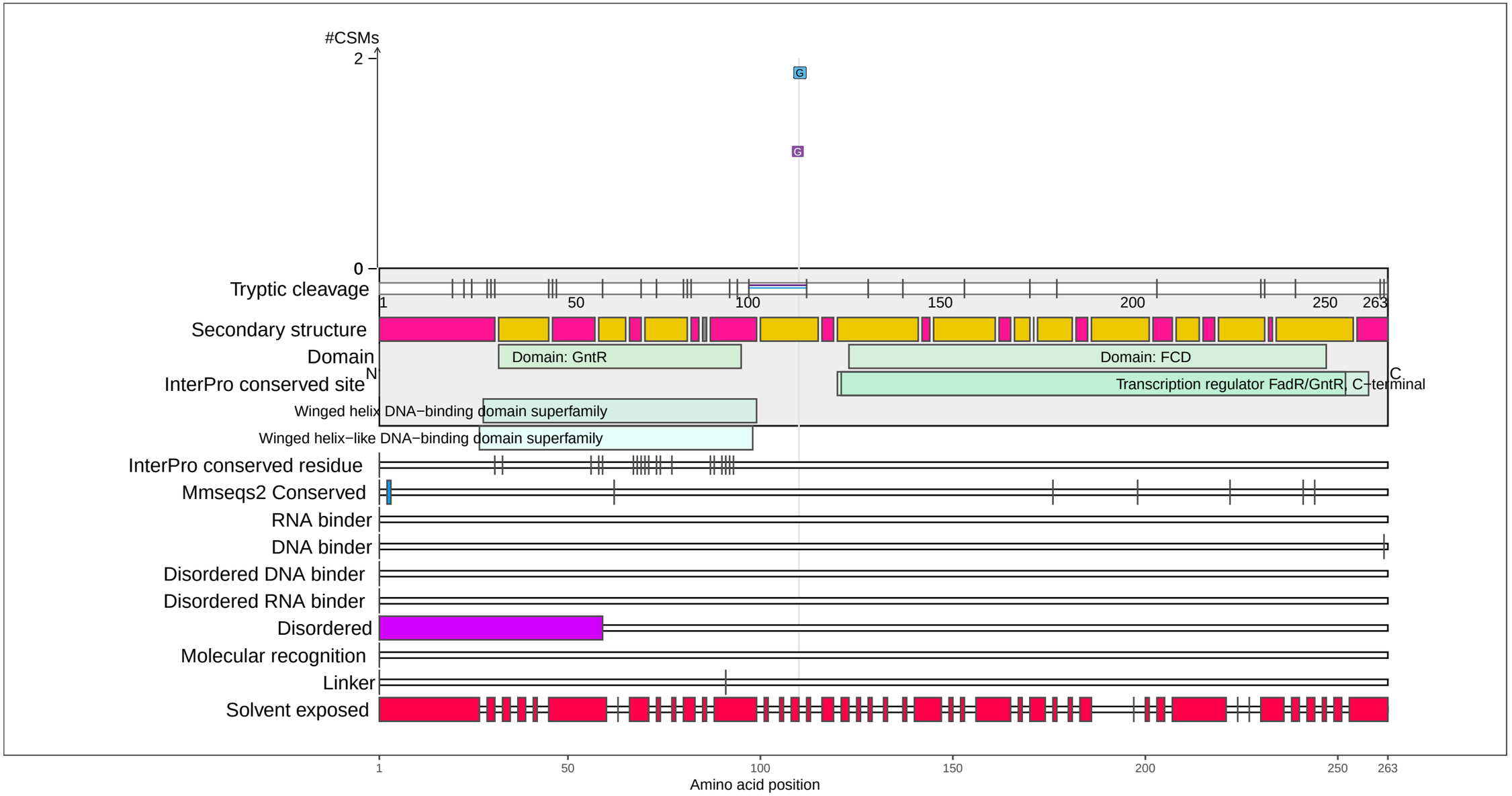




P0A8W0
NANR_ECOLI HTH−type transcriptional repressor NanR

− Abundance:
tryptic [log10 Intensity]: 8.2 (Q 65)
PAXdb K12 strain [ppm]: 1.78 (Q 53)
PAXdb E.coli [ppm]: 1.17 (Q 52)

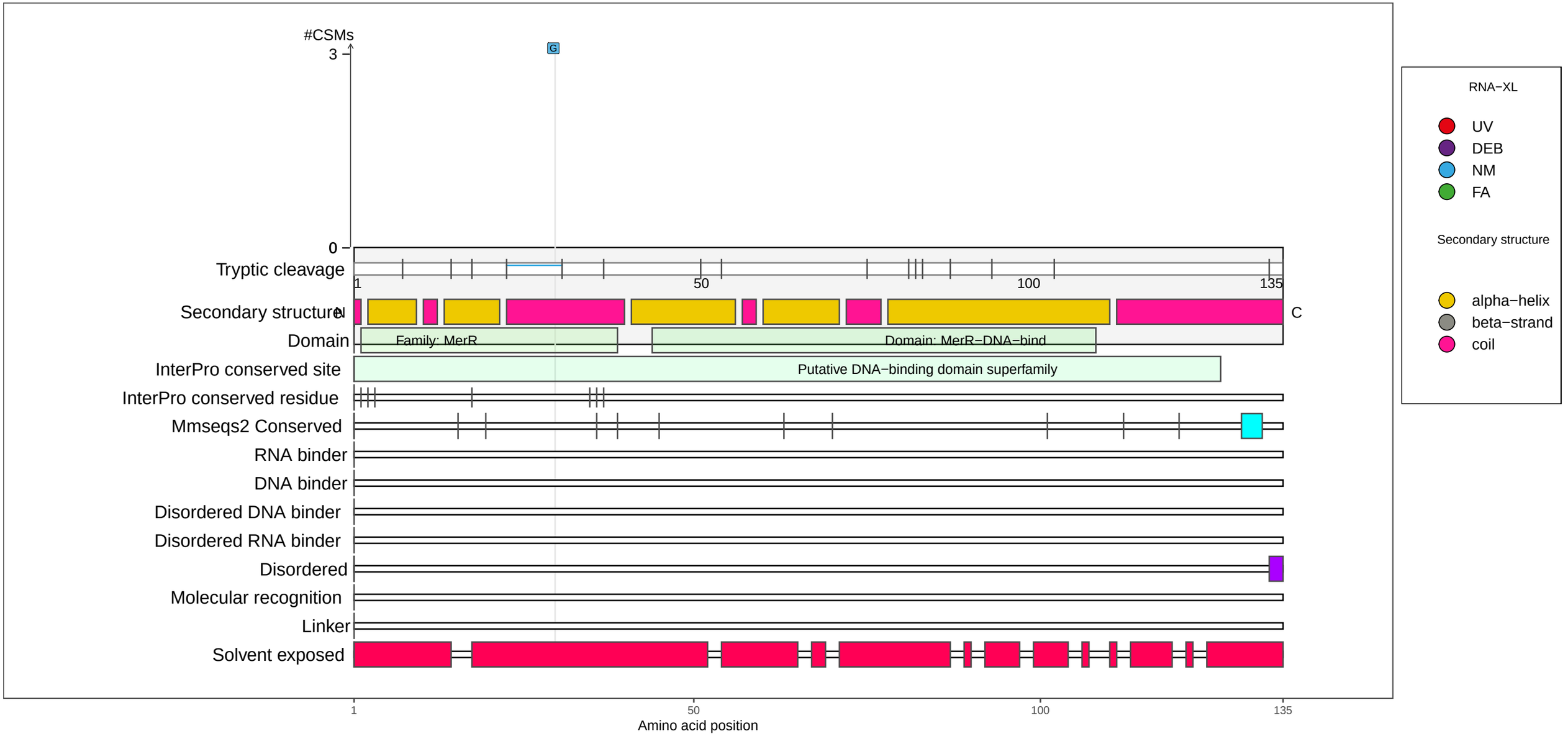
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0A9G4
CUER_ECOLI HTH−type transcriptional regulator CueR

− Abundance:
tryptic [log10 Intensity]: 7.02 (Q 14)
PAXdb K12 strain [ppm]: 1.51 (Q 39)
PAXdb E.coli [ppm]: 0.84 (Q 44)

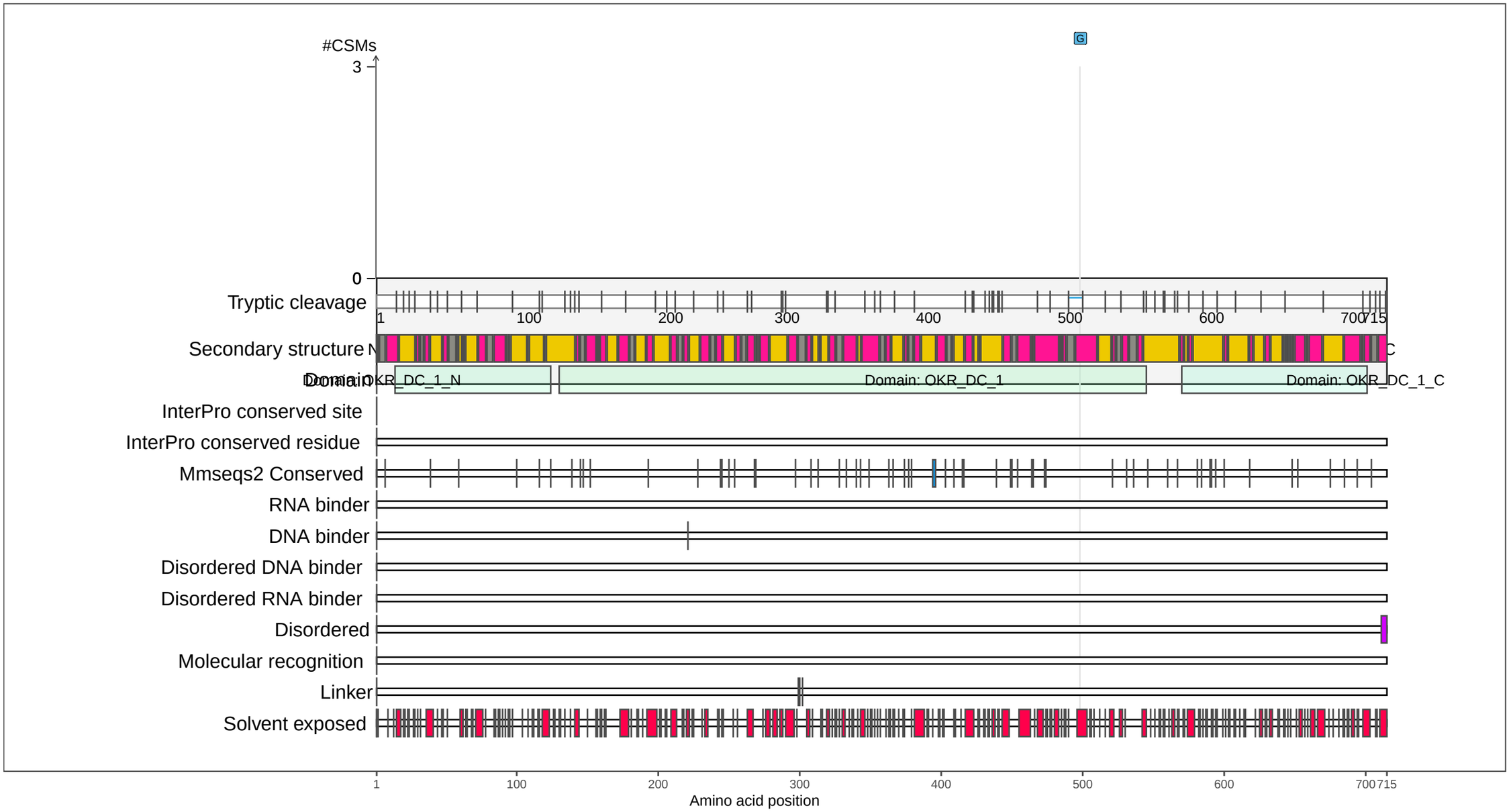
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0A9H3
LDCI_ECOLI Inducible lysine decarboxylase

− Abundance:
tryptic [log10 Intensity]: 8.12 (Q 62)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.25 (Q 53)

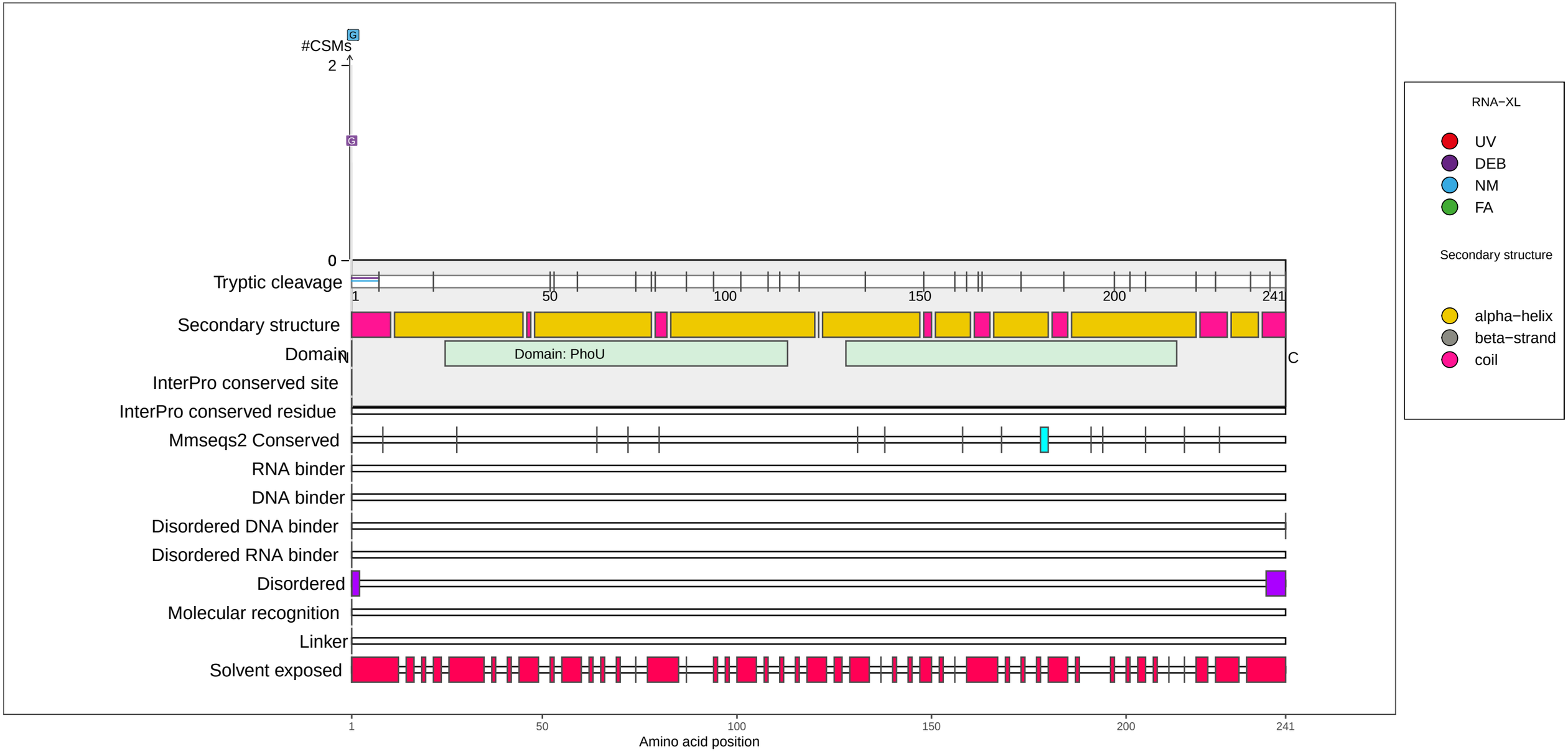
− RNA functions: not annotated



P0A9K7
PHOU_ECOLI Phosphate−specific transport system accessory protein PhoU

− Abundance:
tryptic [log10 Intensity]: 8.45 (Q 73)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 1.89 (Q 69)

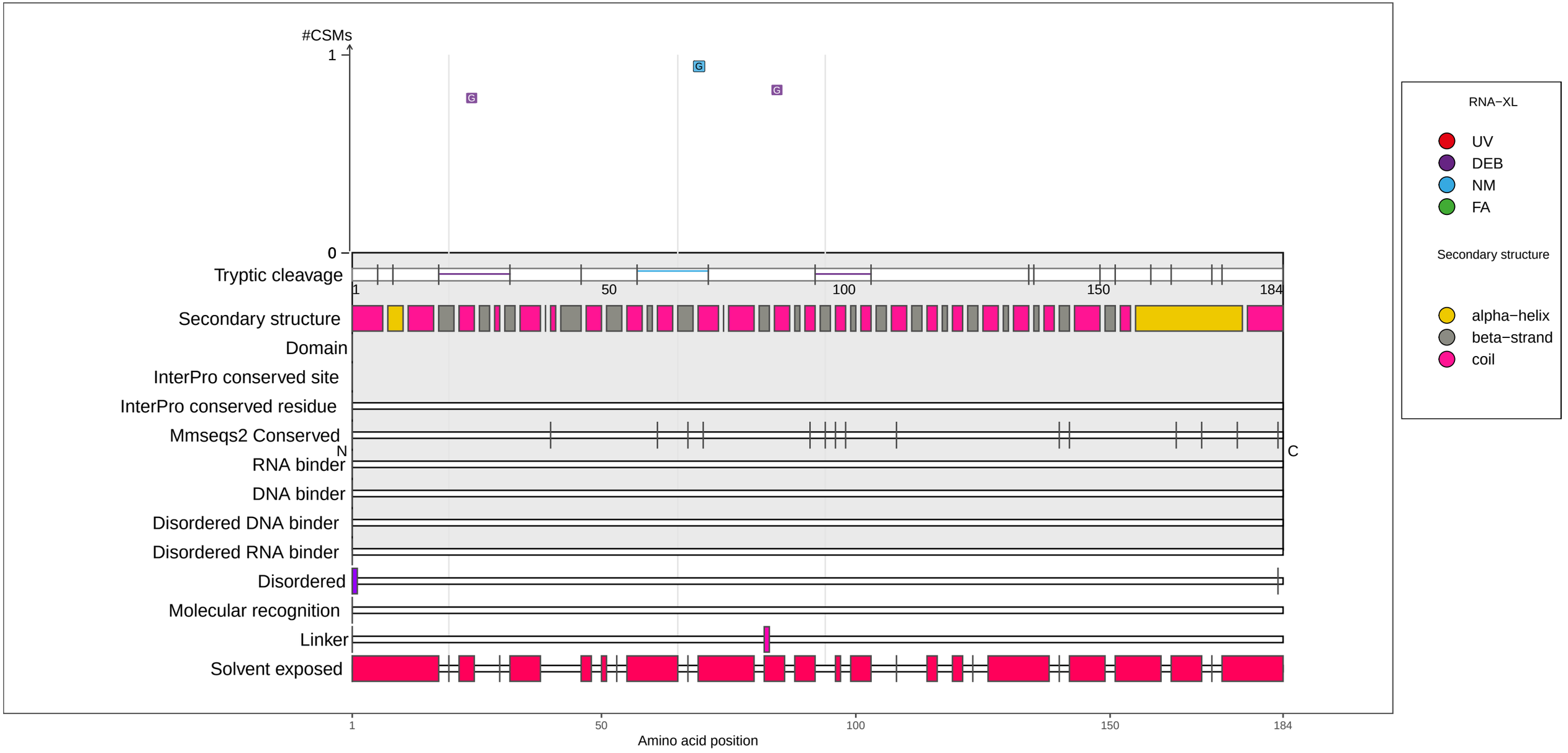
− RNA functions: not annotated



P0A9W9
YRDA_ECOLI Protein YrdA

− Abundance:
tryptic [log10 Intensity]: 8.59 (Q 78)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.53 (Q 86)

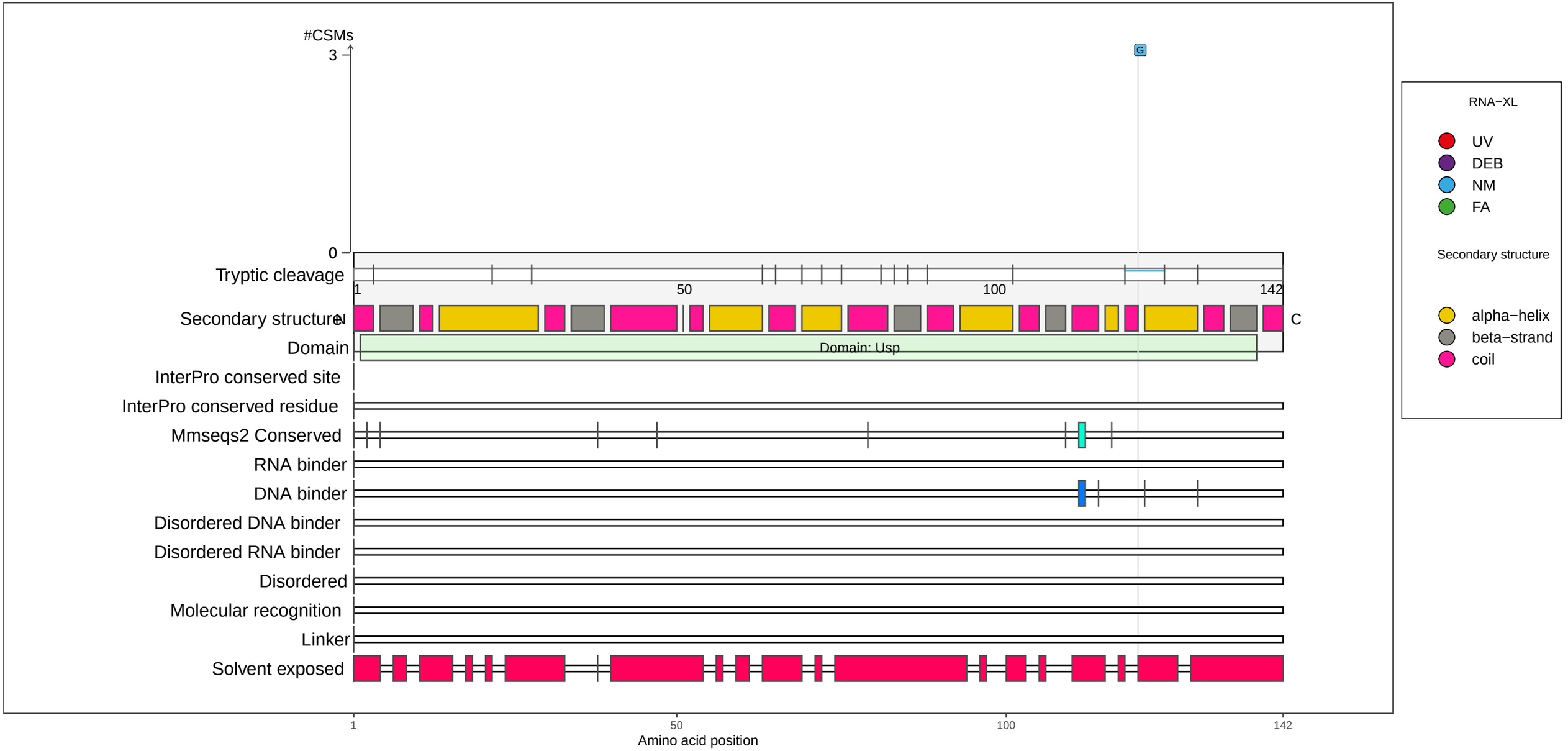
− RNA functions: not annotated



P0AAB8
USPD_ECOLI Universal stress protein D

− Abundance:
tryptic [log10 Intensity]: 8 (Q 58)
PAXdb K12 strain [ppm]: 2.68 (Q 83)
PAXdb E.coli [ppm]: 2.23 (Q 78)

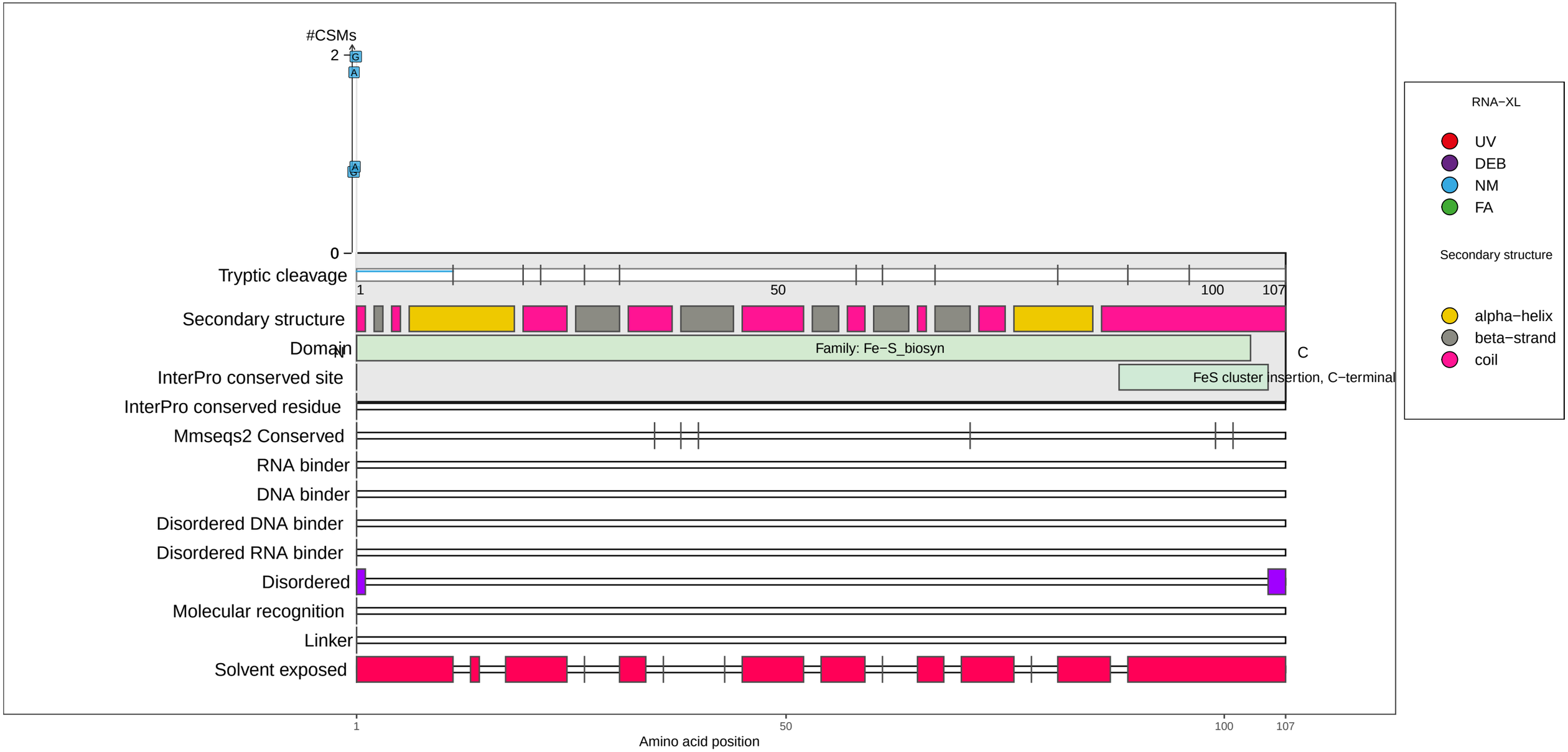
− RNA functions: not annotated



P0AAC8
ISCA_ECOLI Iron−binding protein IscA

− Abundance:
tryptic [log10 Intensity]: 7.88 (Q 53)
PAXdb K12 strain [ppm]: 2.24 (Q 68)
PAXdb E.coli [ppm]: 1.81 (Q 67)

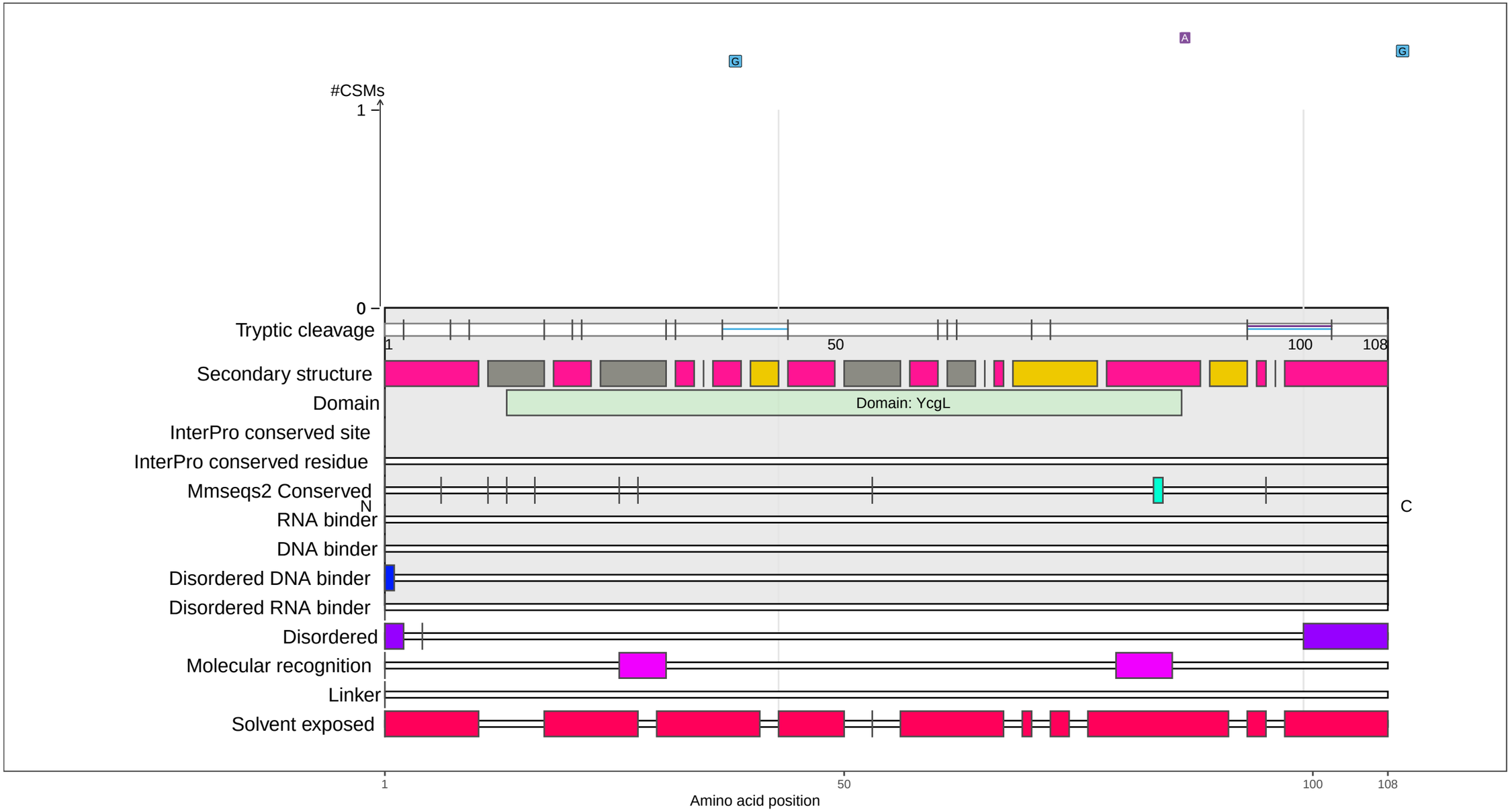
− RNA functions: not annotated



P0AB43
YCGL_ECOLI Protein YcgL

− Abundance:
tryptic [log10 Intensity]: 8.05 (Q 59)
PAXdb K12 strain [ppm]: 2.95 (Q 90)
PAXdb E.coli [ppm]: 2 (Q 72)

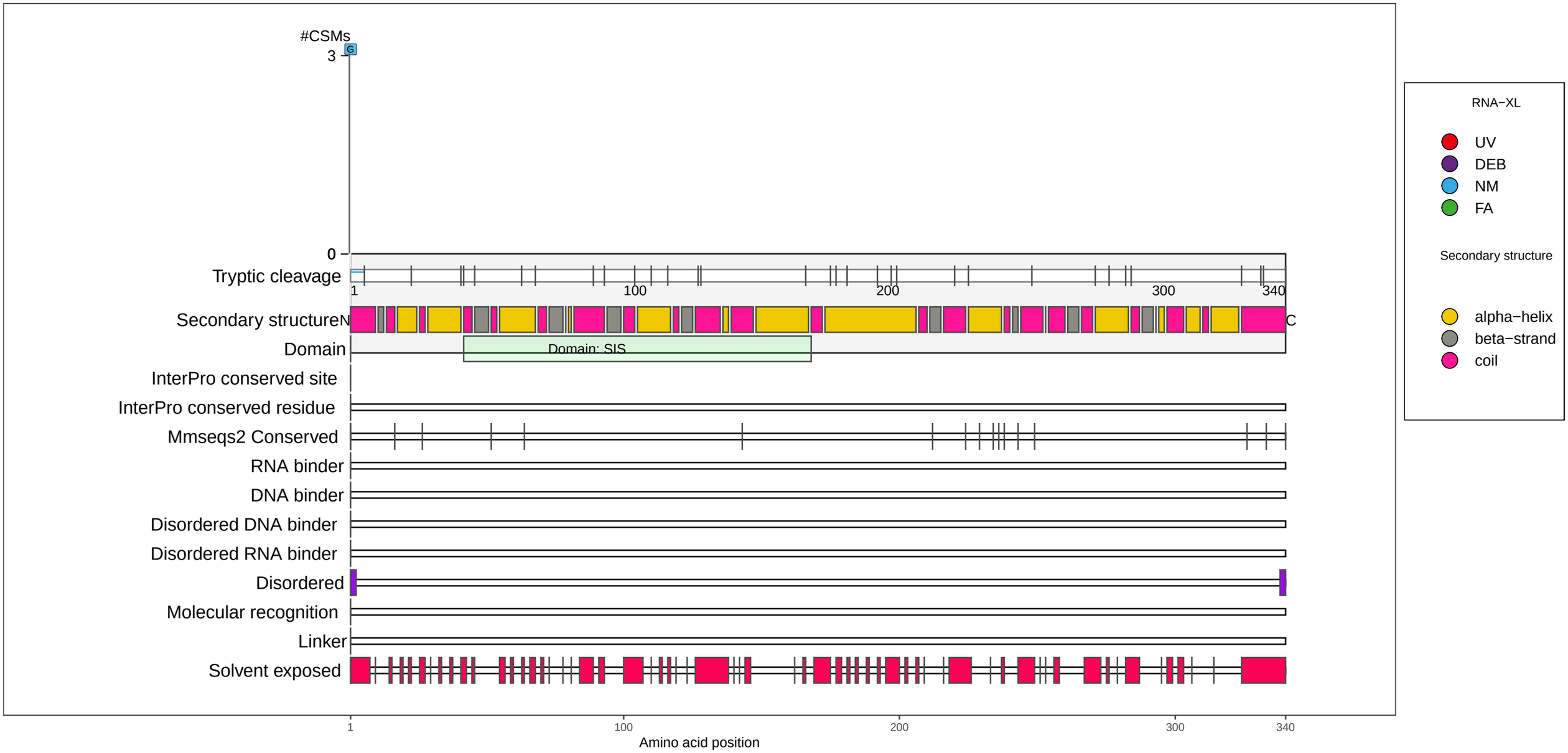
− RNA functions: not annotated



P0AC00
FRLB_ECOLI Fructoselysine 6−phosphate deglycase

− Abundance:
tryptic [log10 Intensity]: 7.6 (Q 40)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −2.1 (Q 1)

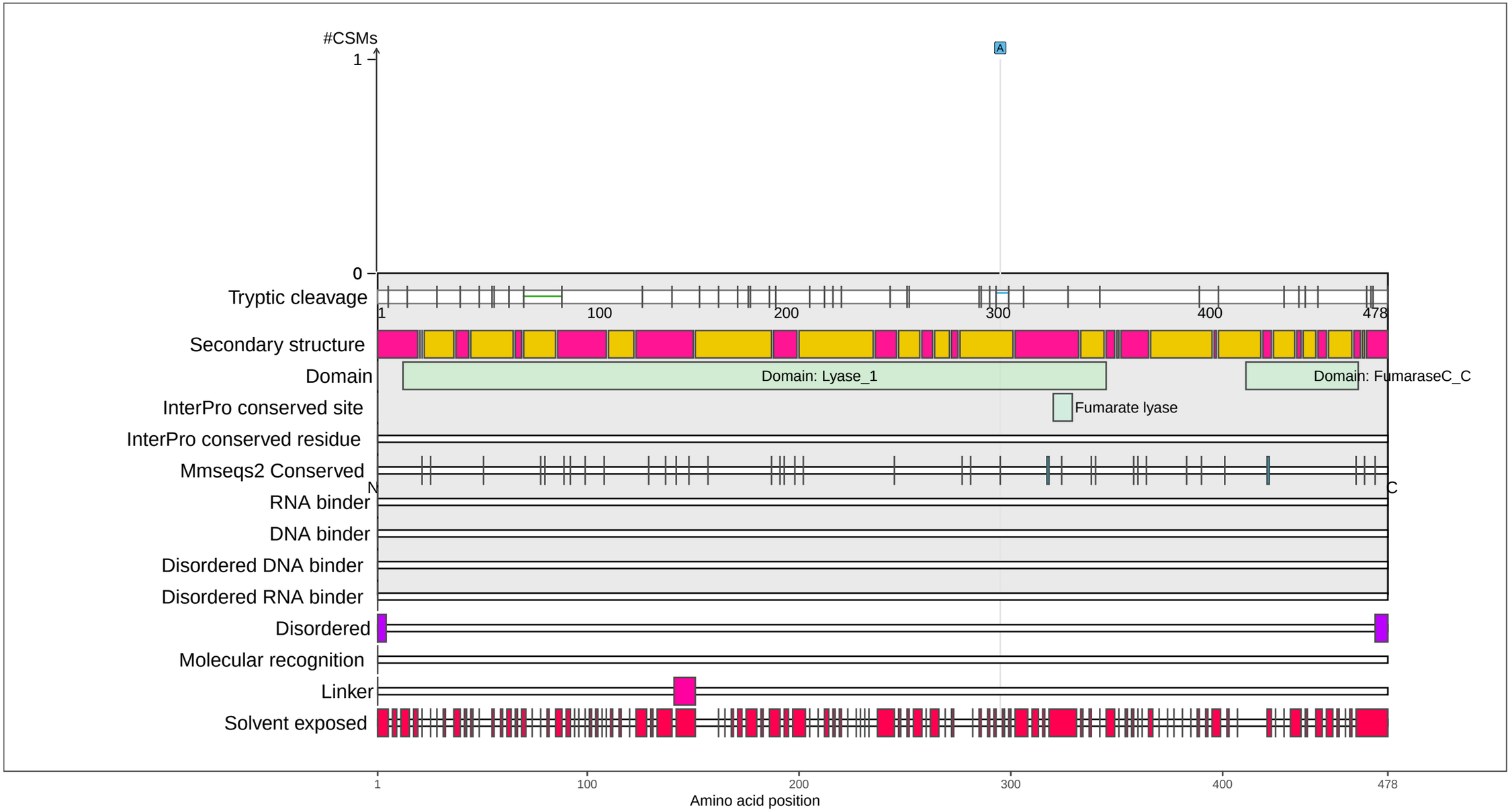
− RNA functions: not annotated

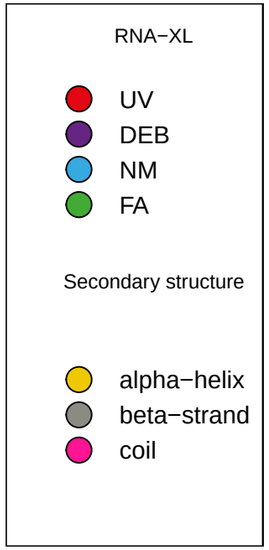


P0AC38
ASPA_ECOLI Aspartate ammonia−lyase

− Abundance:
tryptic [log10 Intensity]: 9.32 (Q 94)
PAXdb K12 strain [ppm]: 2.97 (Q 90)
PAXdb E.coli [ppm]: 2.9 (Q 93)

− RNA functions: not annotated

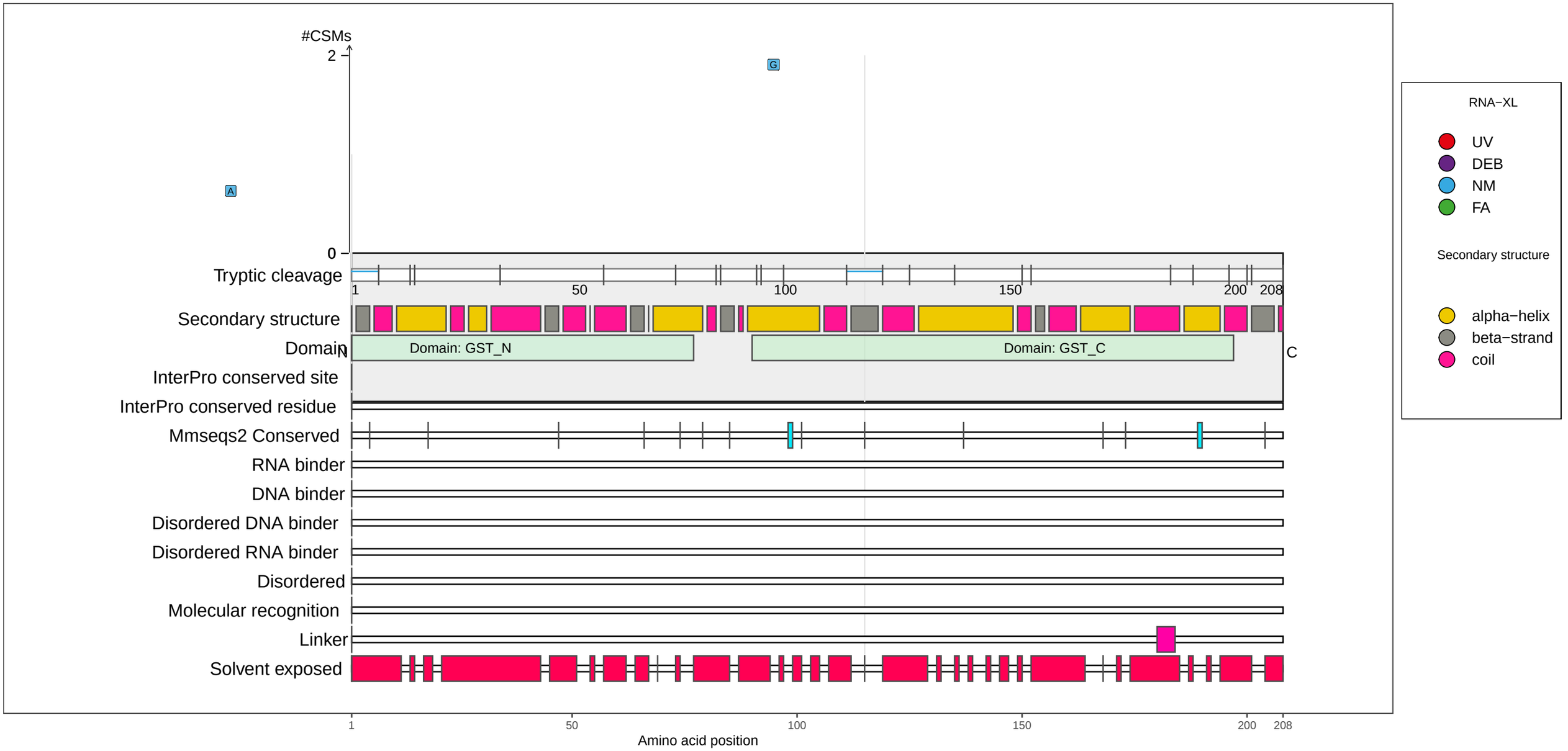




P0ACA7
GSTB_ECOLI Glutathione S−transferase GstB

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 61)
PAXdb K12 strain [ppm]: 2.27 (Q 69)
PAXdb E.coli [ppm]: 2.92 (Q 93)

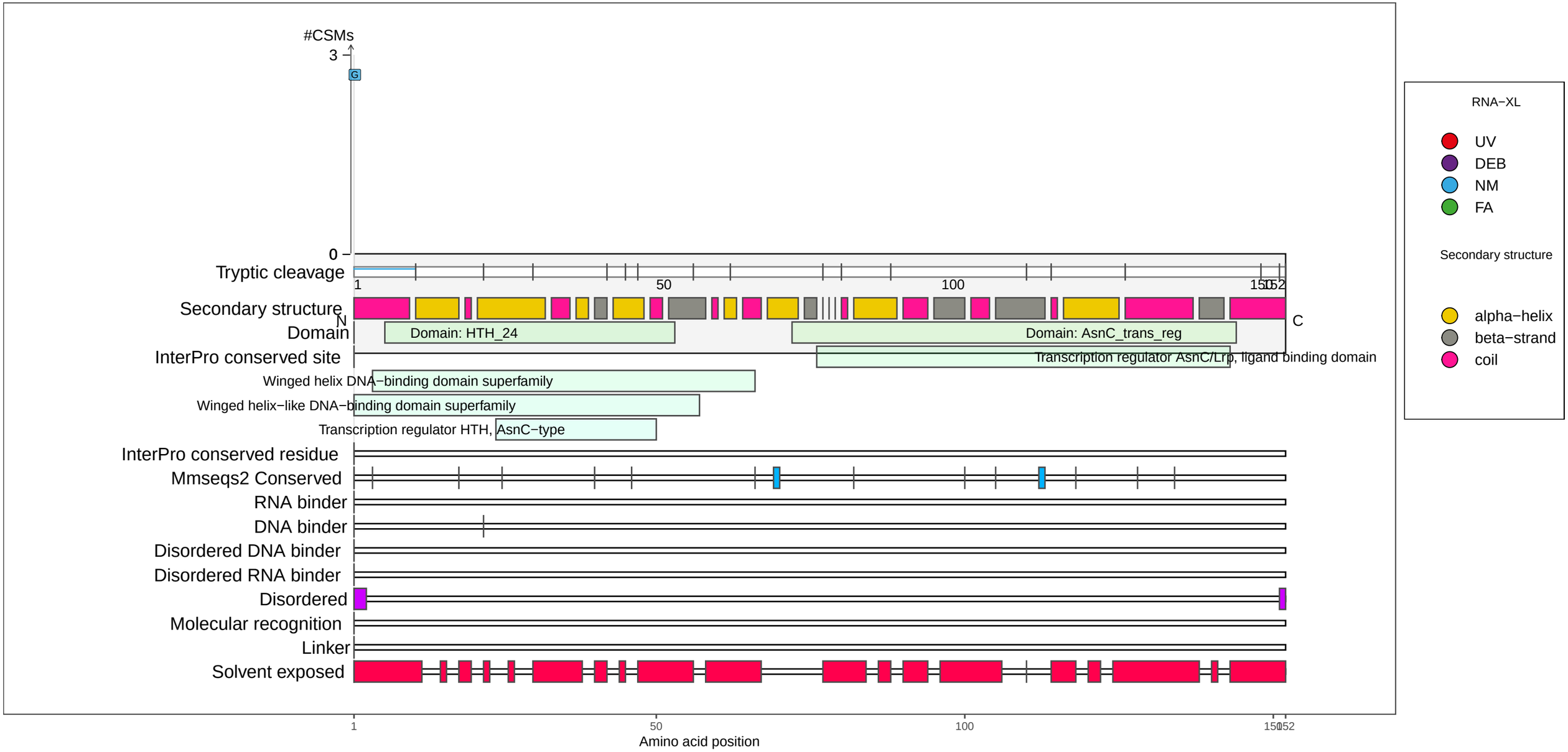
− RNA functions: not annotated



P0ACI6
ASNC_ECOLI Regulatory protein AsnC

− Abundance:
tryptic [log10 Intensity]: 6.81 (Q 7)
PAXdb K12 strain [ppm]: 2.76 (Q 85)
PAXdb E.coli [ppm]: 2.26 (Q 79)

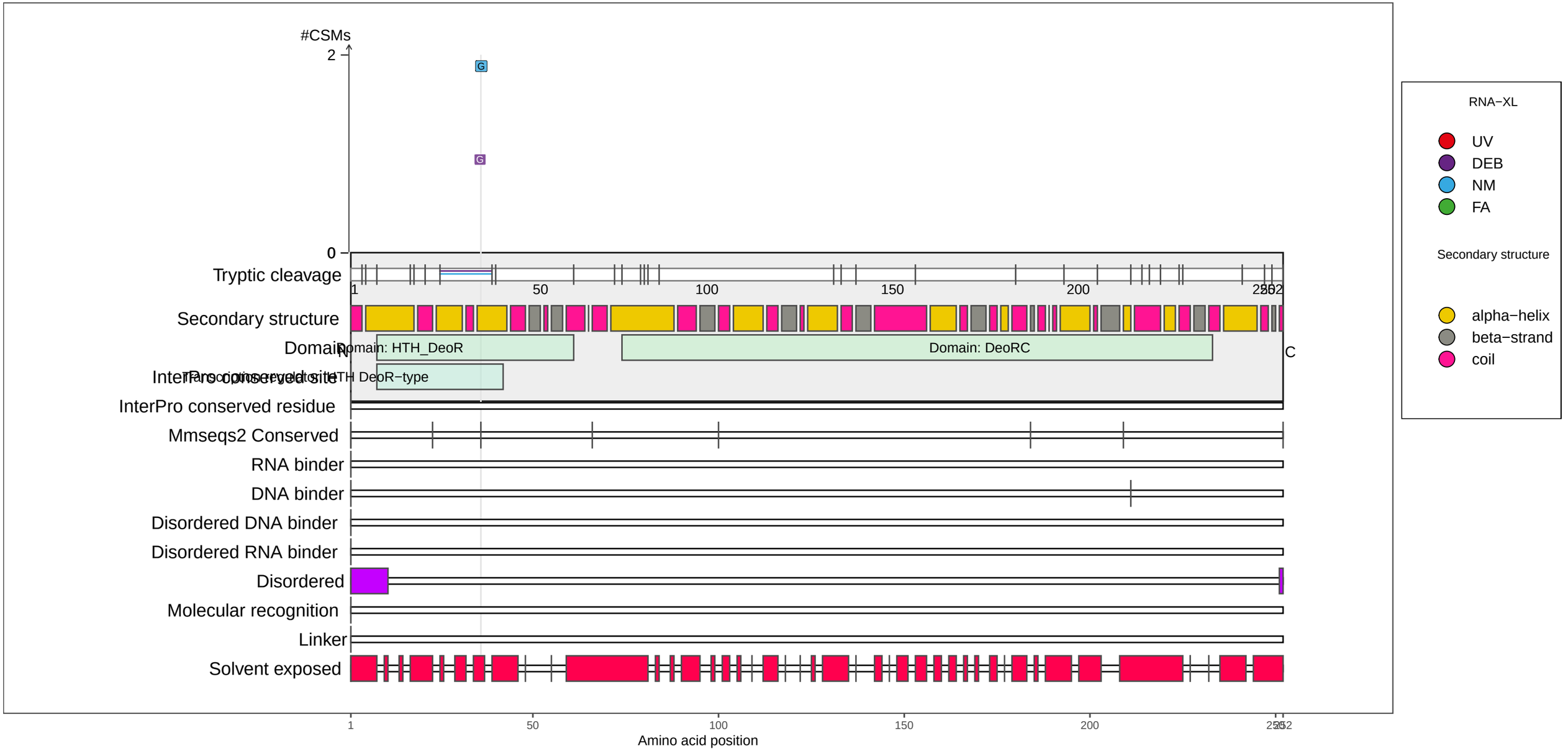
− RNA functions: not annotated



P0ACK5
DEOR_ECOLI Deoxyribose operon repressor

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 0.45 (Q 35)

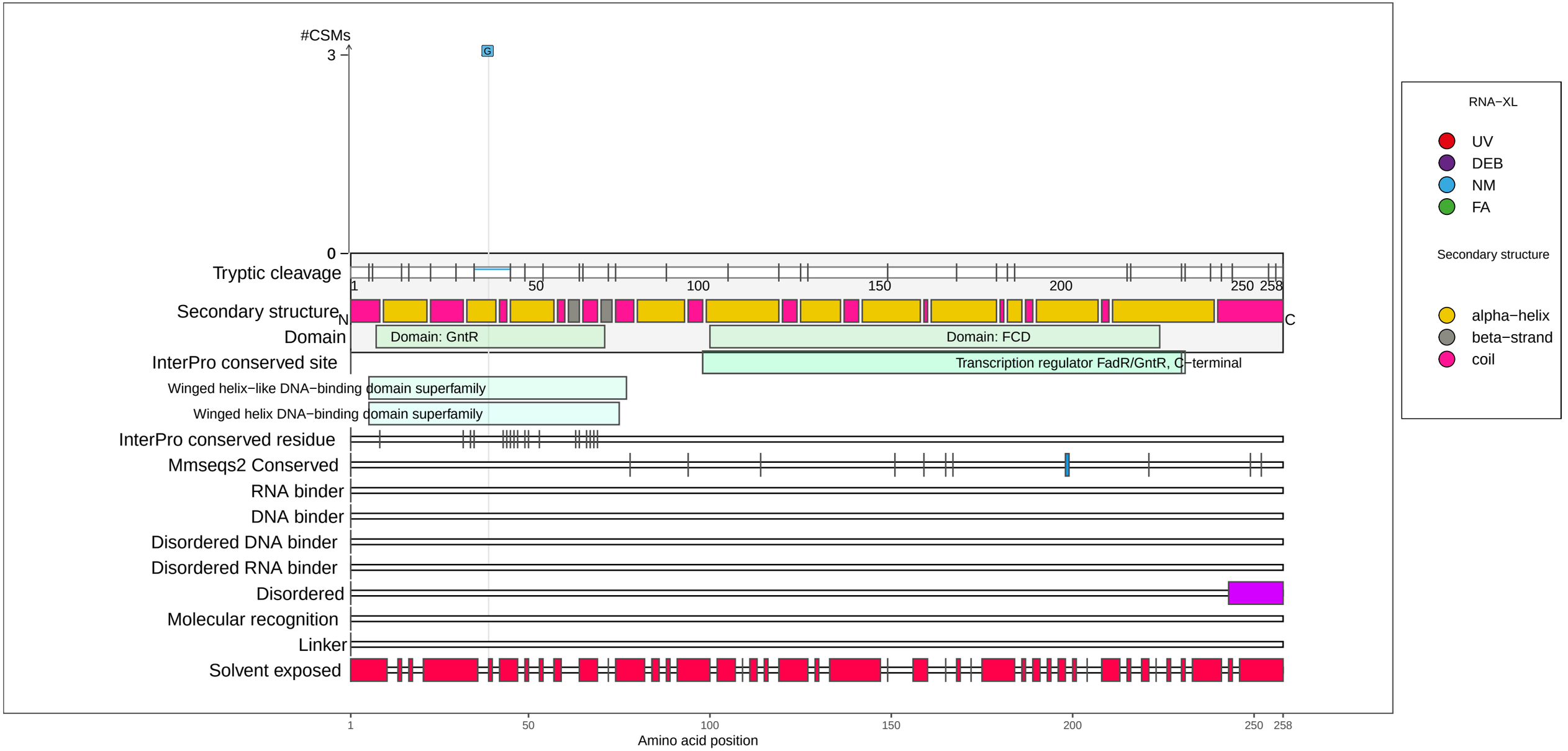
− RNA functions: not annotated



P0ACL7
LLDR_ECOLI Putative L−lactate dehydrogenase operon regulatory protein

− Abundance:
tryptic [log10 Intensity]: 7.16 (Q 19)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: −0.98 (Q 9)

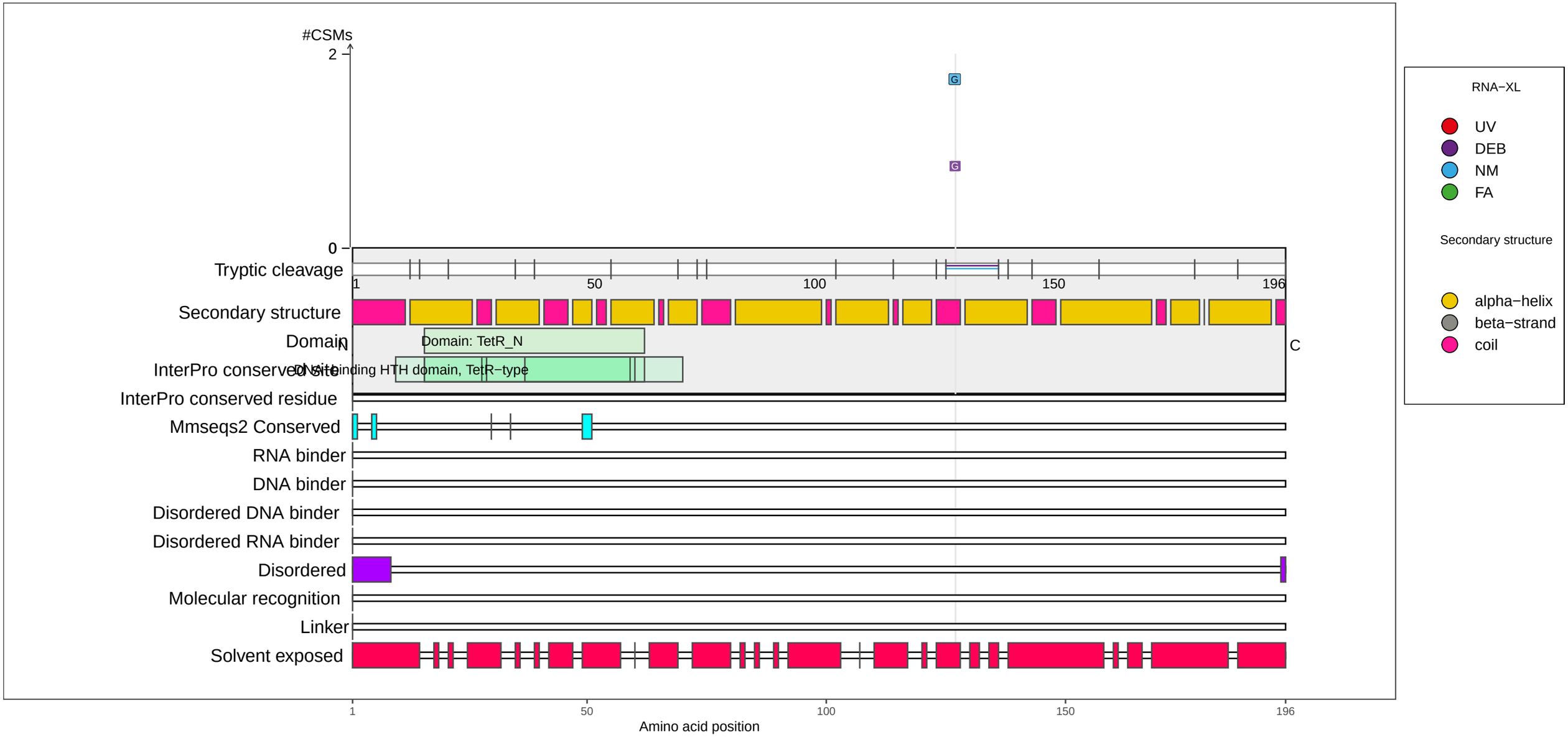
− RNA functions: not annotated



P0ACT6
UIDR_ECOLI HTH−type transcriptional regulator UidR

− Abundance:
tryptic [log10 Intensity]: 6.94 (Q 11)
PAXdb K12 strain [ppm]: 0.93 (Q 8)
PAXdb E.coli [ppm]: 0.74 (Q 42)

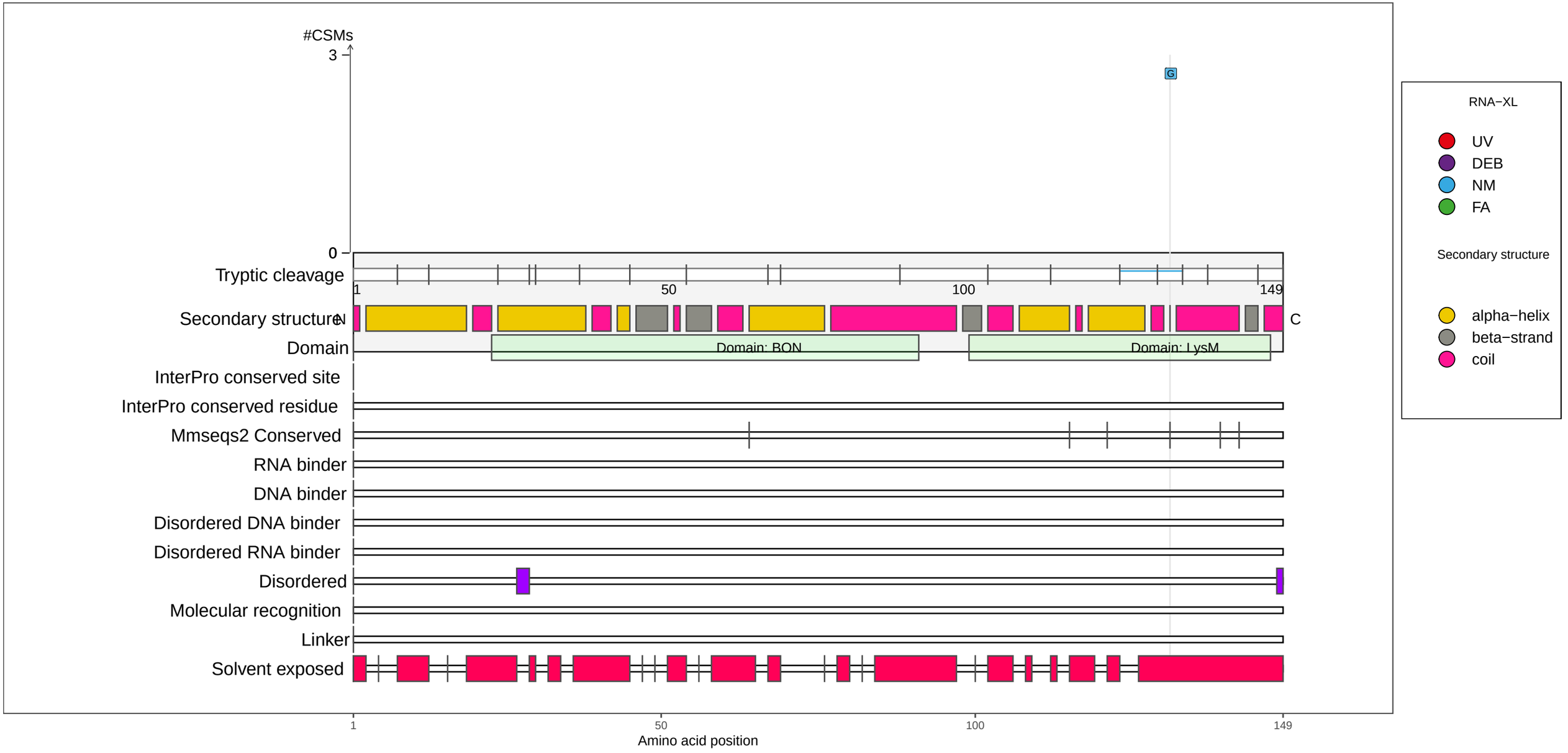
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0ADE6
KBP_ECOLI Potassium binding protein Kbp

− Abundance:
tryptic [log10 Intensity]: 7.13 (Q 18)
PAXdb K12 strain [ppm]: 2.2 (Q 67)
PAXdb E.coli [ppm]: 3.64 (Q 100)

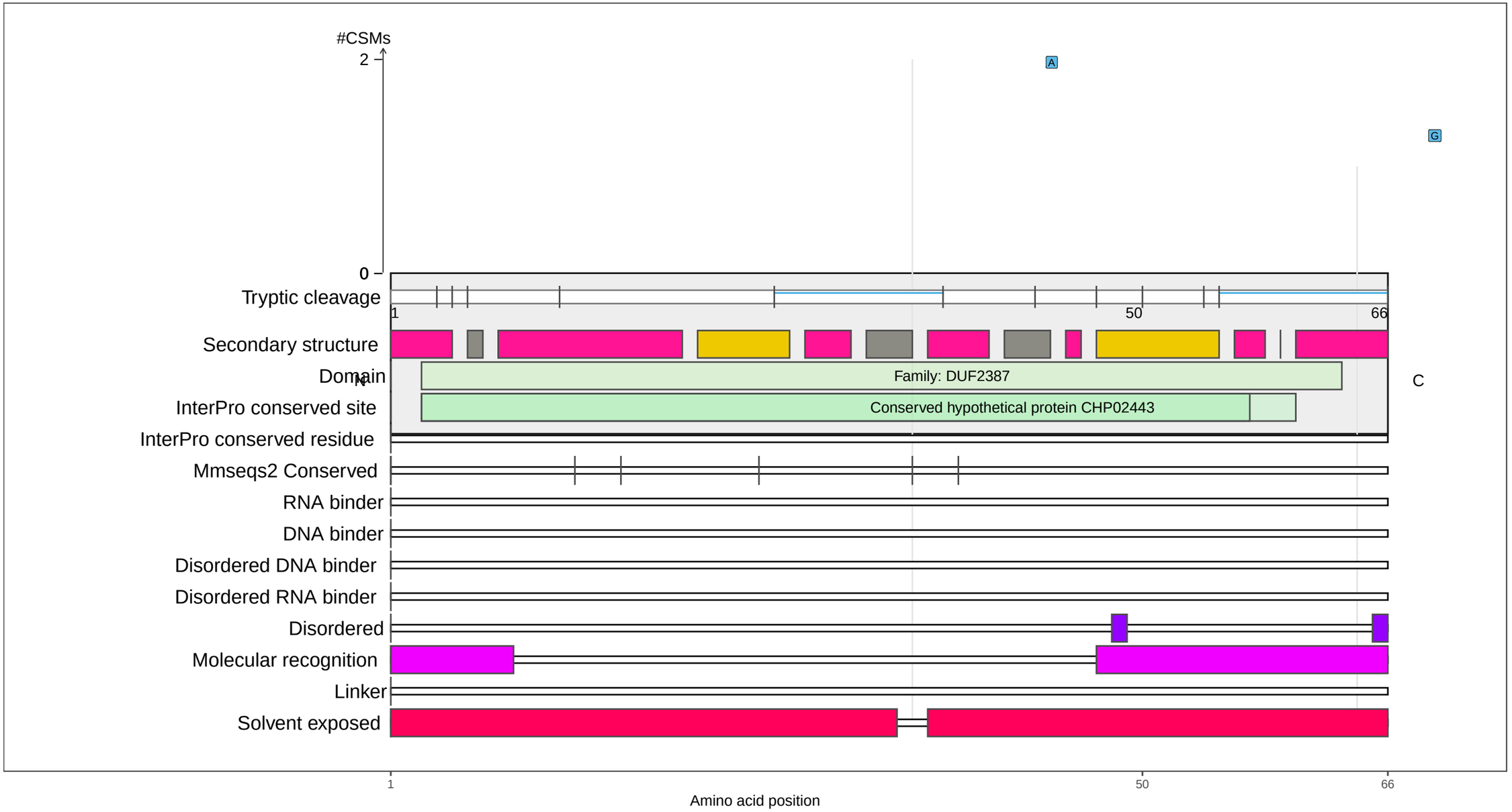
− RNA functions: not annotated

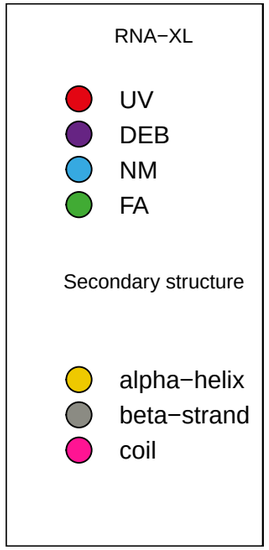


P0ADW8
YHEV_ECOLI Uncharacterized protein YheV

− Abundance:
tryptic [log10 Intensity]: 8.02 (Q 58)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 1.31 (Q 55)

− RNA functions: not annotated

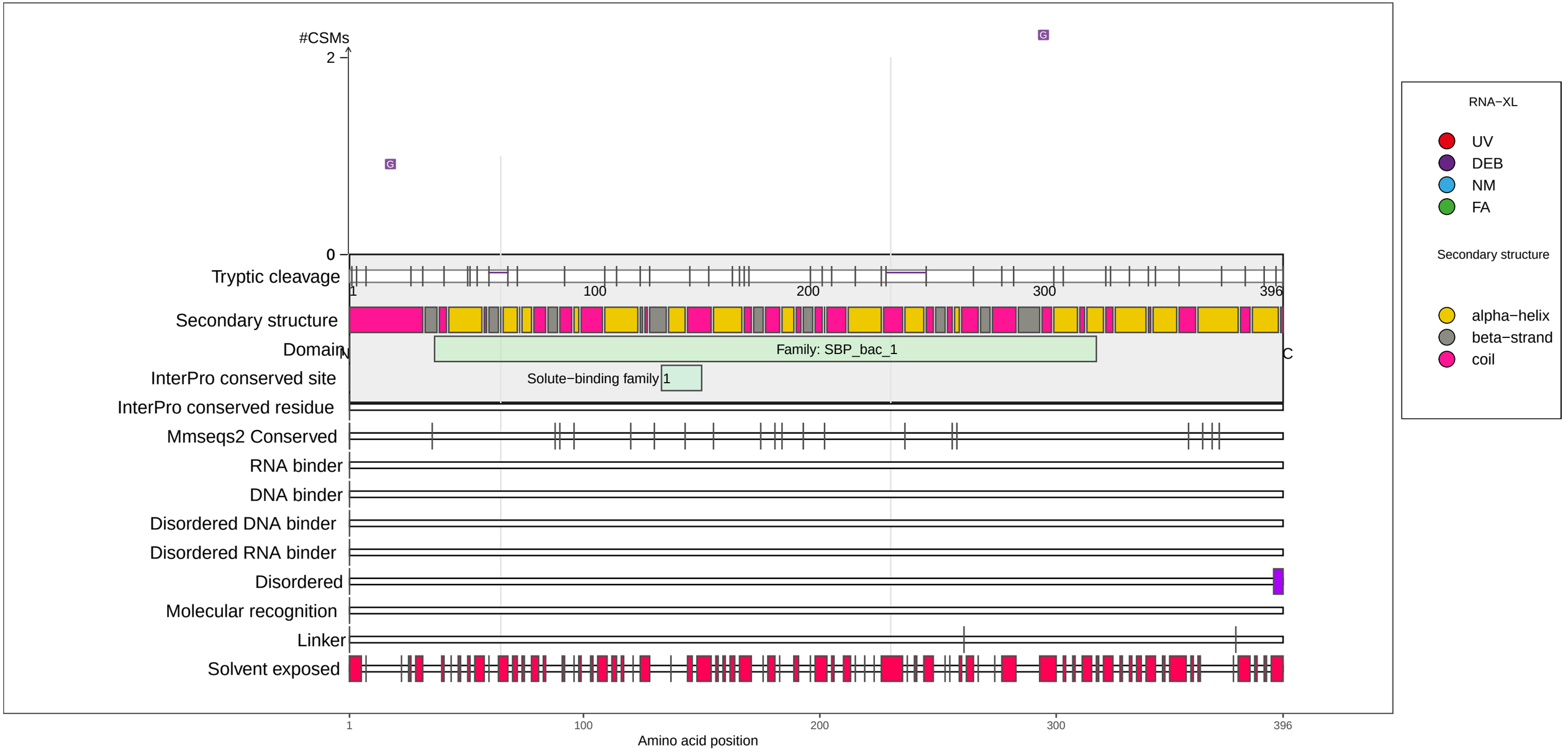




P0AEX9
MALE_ECOLI Maltose/maltodextrin−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 8.94 (Q 87)
PAXdb K12 strain [ppm]: 2.7 (Q 83)
PAXdb E.coli [ppm]: 3.25 (Q 97)

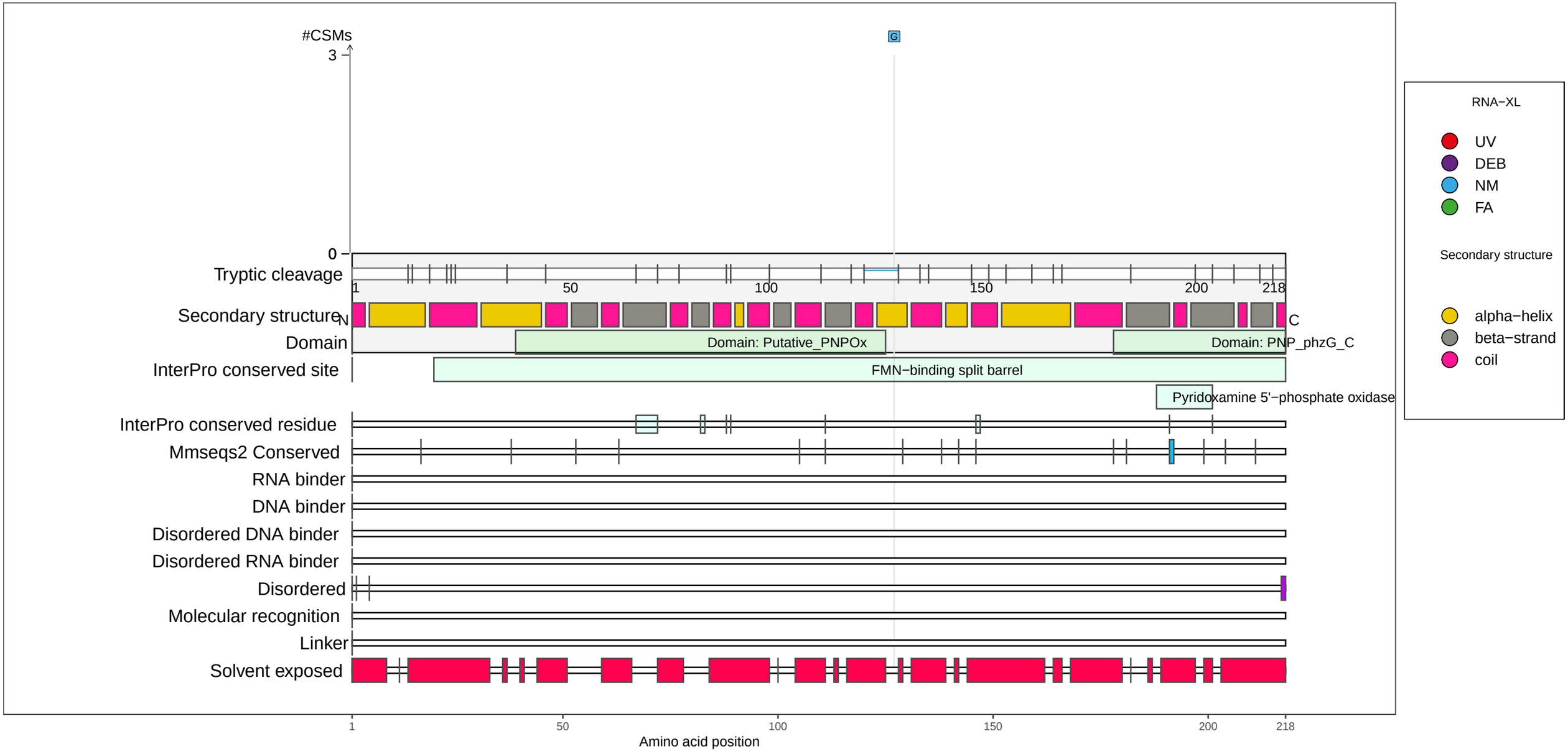
− RNA functions: not annotated



P0AFI7
PDXH_ECOLI Pyridoxine/pyridoxamine 5'−phosphate oxidase

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 61)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 2.48 (Q 85)

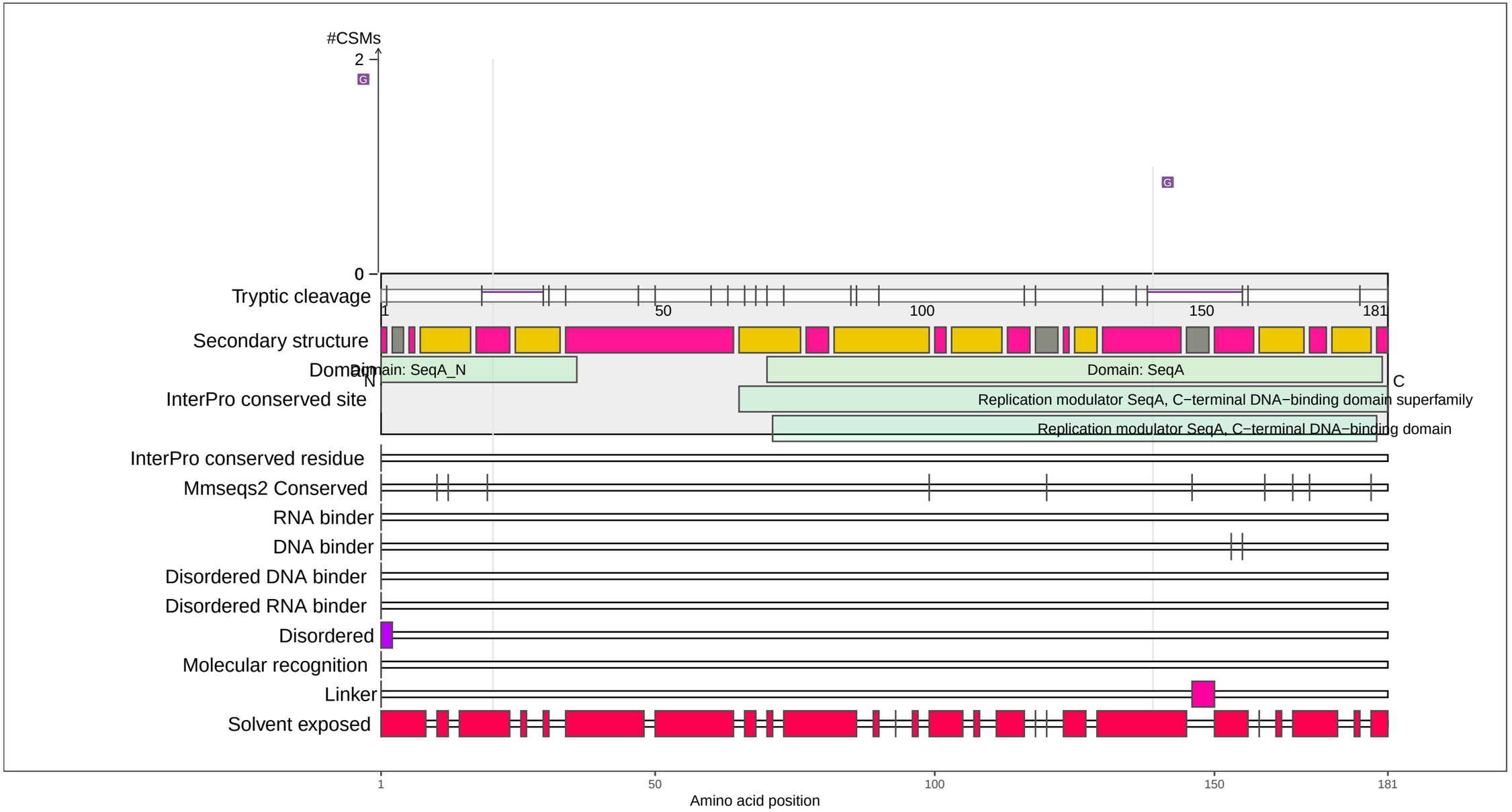
− RNA functions: not annotated

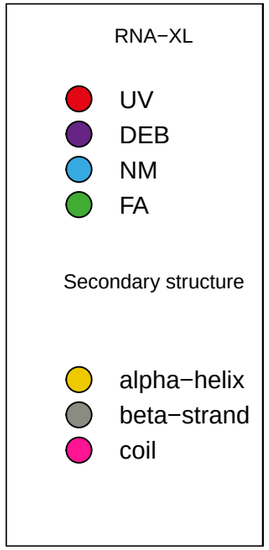


P0AFY8
SEQA_ECOLI Negative modulator of initiation of replication

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: 2.74 (Q 84)
PAXdb E.coli [ppm]: 2.34 (Q 82)

− RNA functions: not annotated

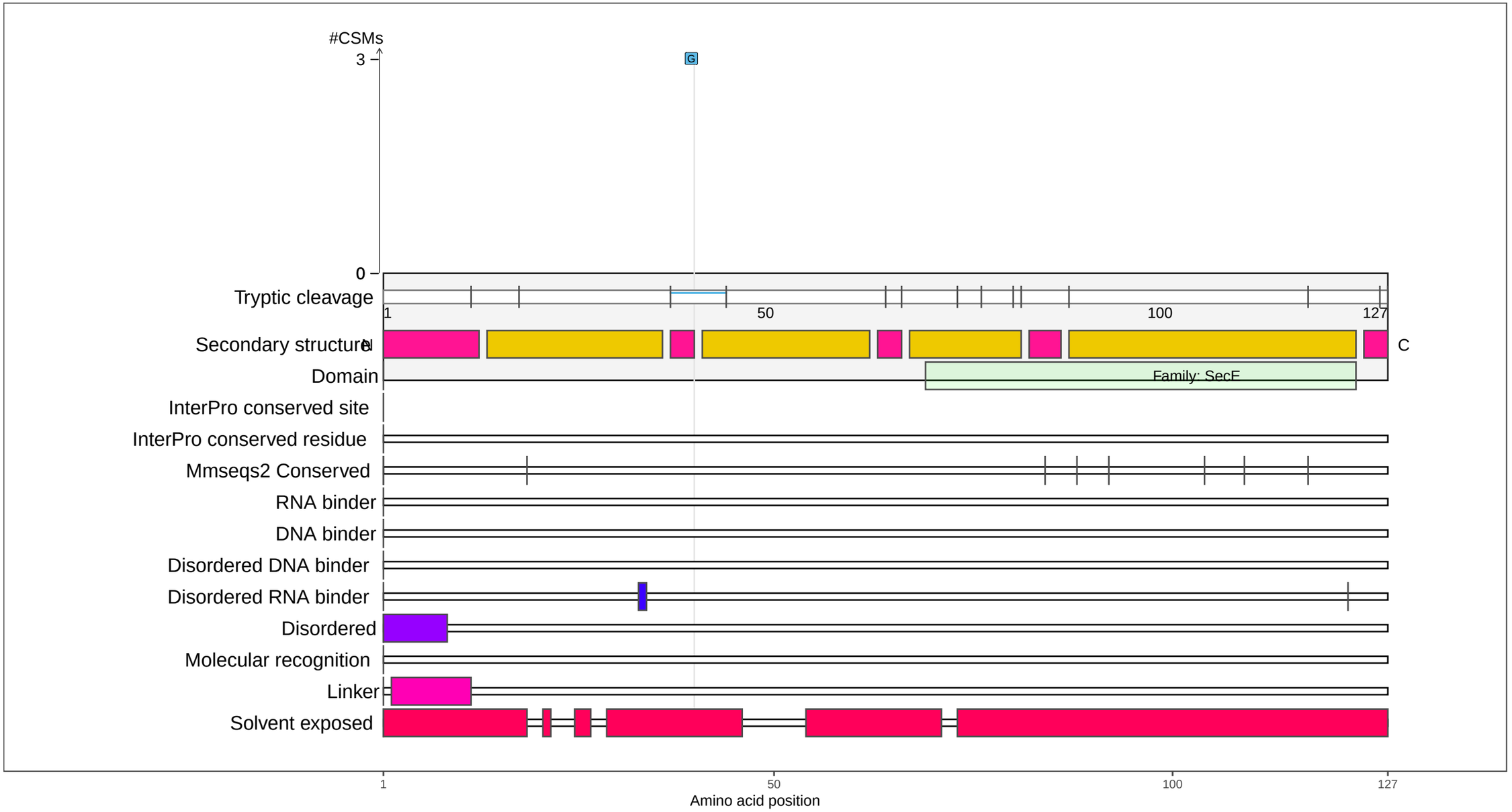


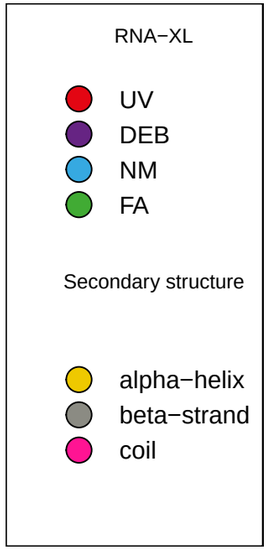


P0AG96
SECE_ECOLI Protein translocase subunit SecE

− Abundance:
tryptic [log10 Intensity]: 8.6 (Q 79)
PAXdb K12 strain [ppm]: 1.62 (Q 45)
PAXdb E.coli [ppm]: 1.56 (Q 61)

− RNA functions: not annotated

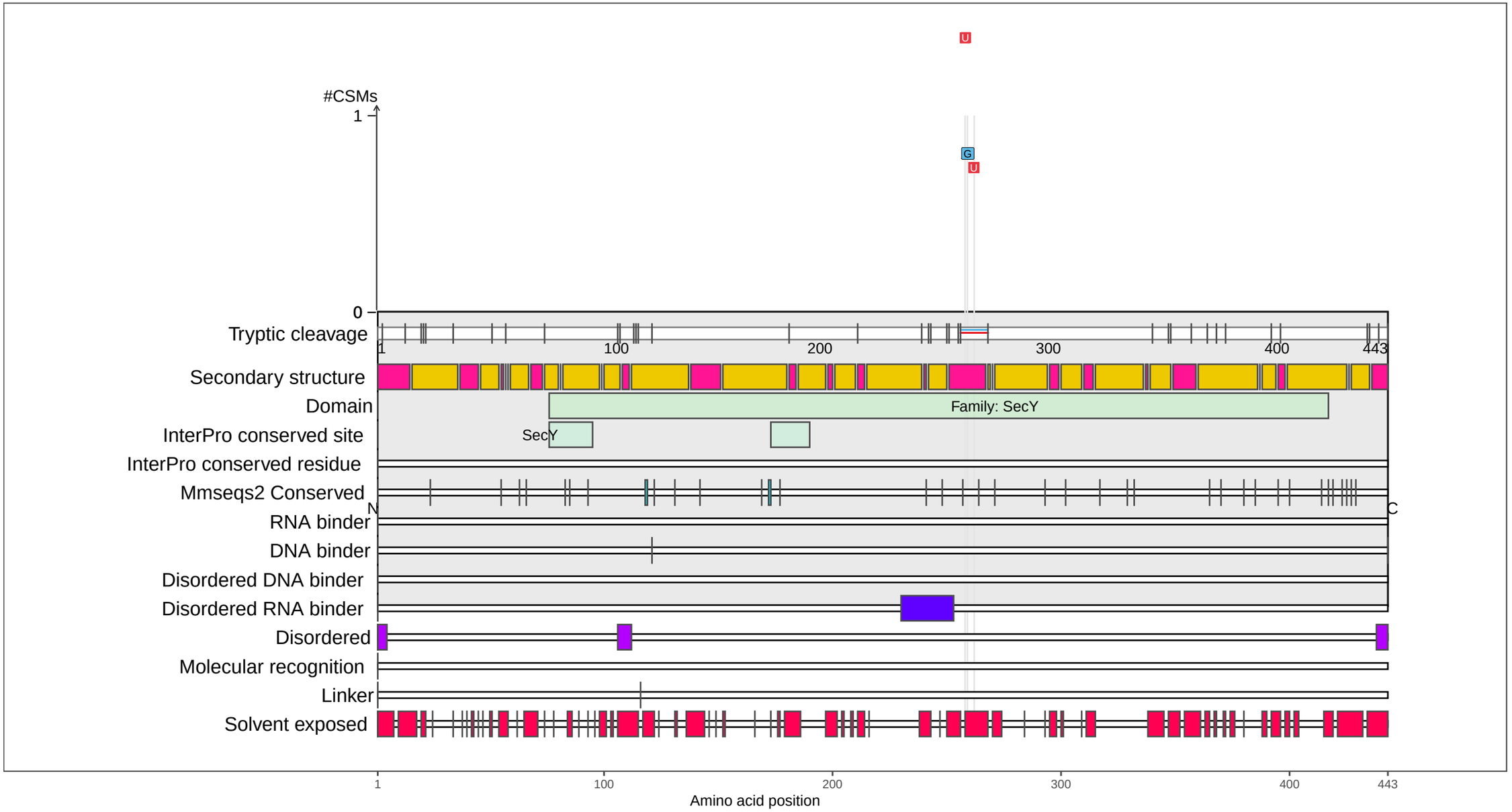




P0AGA2
SECY_ECOLI Protein translocase subunit SecY

− Abundance:
tryptic [log10 Intensity]: 7.41 (Q 30)
PAXdb K12 strain [ppm]: 2.11 (Q 64)
PAXdb E.coli [ppm]: 1.96 (Q 71)

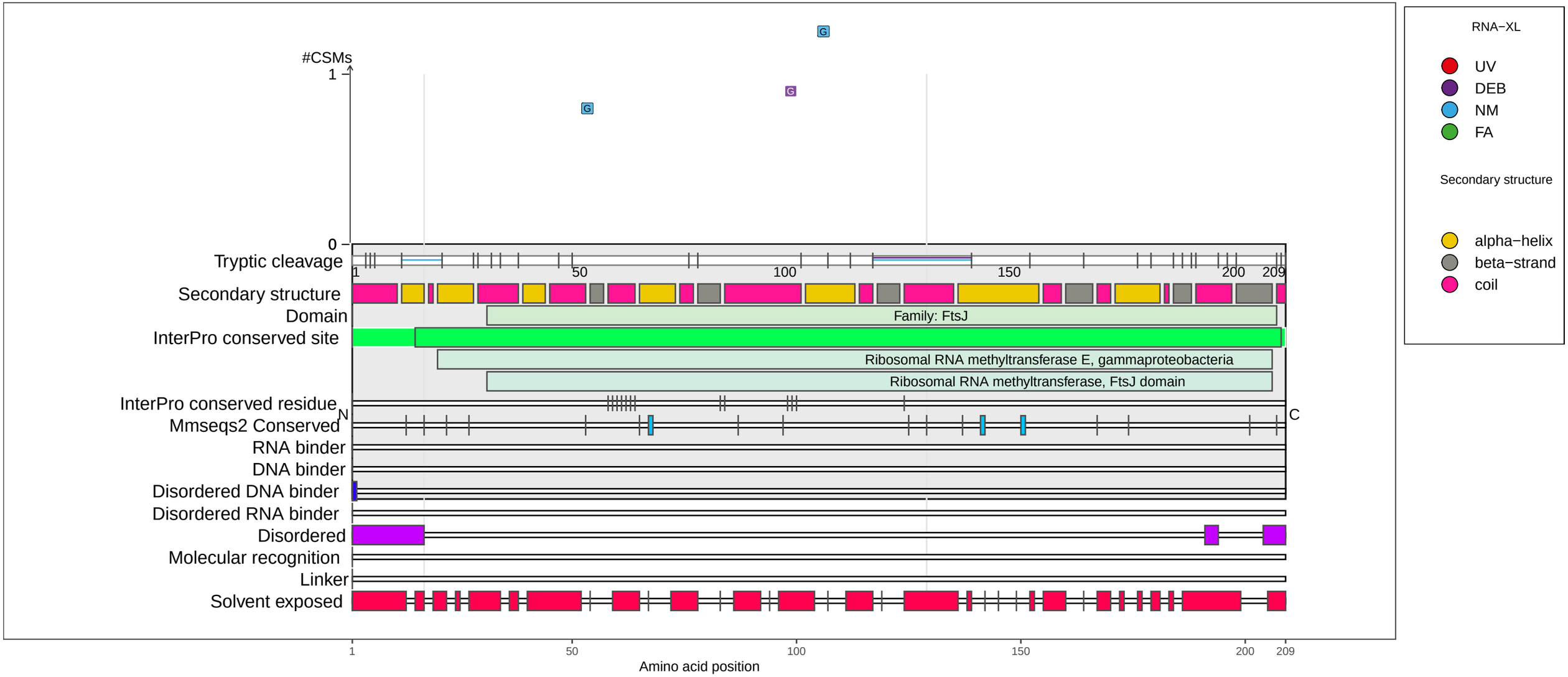
− RNA functions: not annotated



P0C0R7
RLME_ECOLI Ribosomal RNA large subunit methyltransferase E

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 17)
PAXdb K12 strain [ppm]: 2.49 (Q 77)
PAXdb E.coli [ppm]: 1.73 (Q 65)

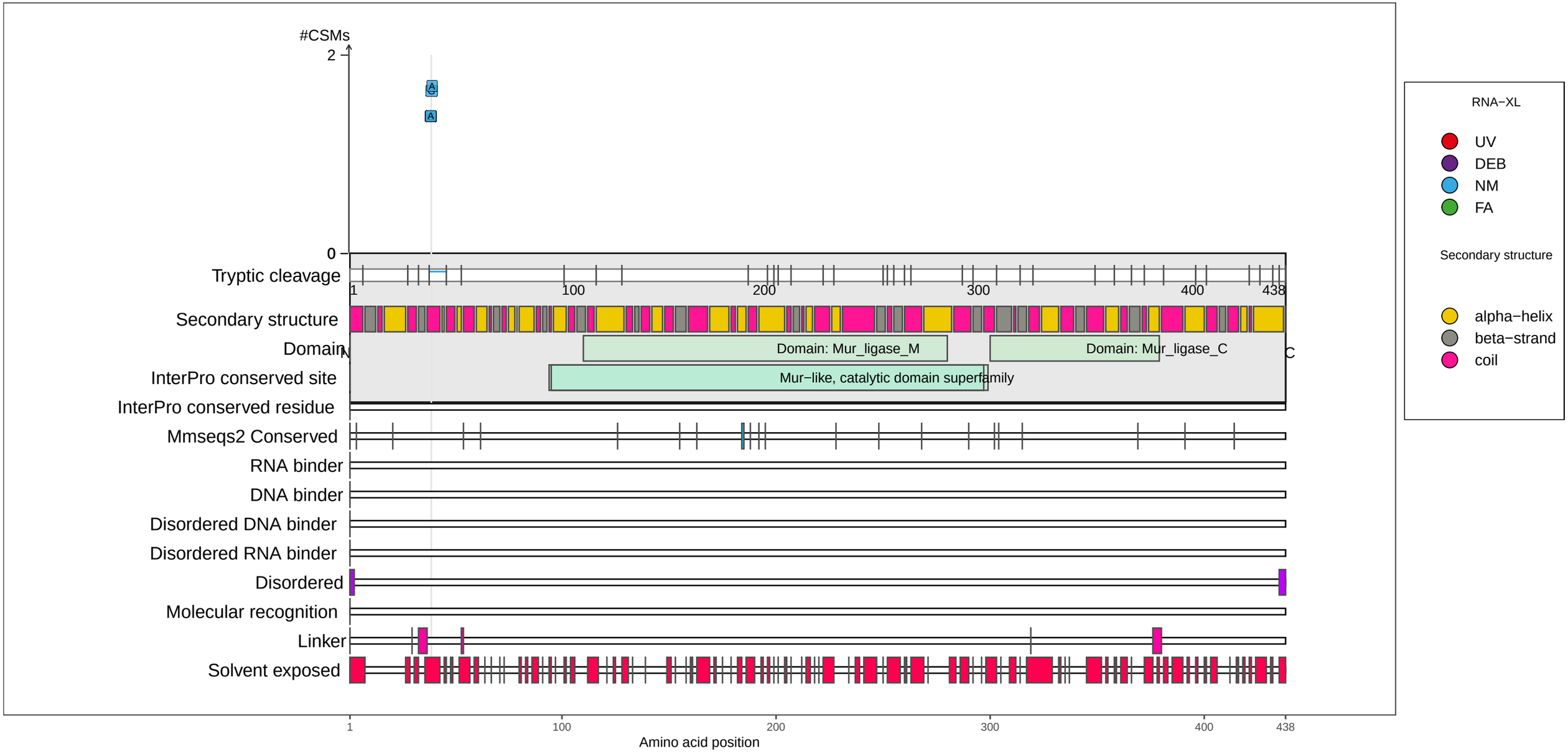
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification
RNA processing; rRNA (uridine−2−O−)−methyltransferase activity
rRNA (uridine) methyltransferase activity; rRNA 2−O−methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing



P14900
MURD_ECOLI UDP−N−acetylmuramoylalanine−−D−glutamate ligase

− Abundance:
tryptic [log10 Intensity]: 8.27 (Q 68)
PAXdb K12 strain [ppm]: 1.71 (Q 49)
PAXdb E.coli [ppm]: 1.74 (Q 65)

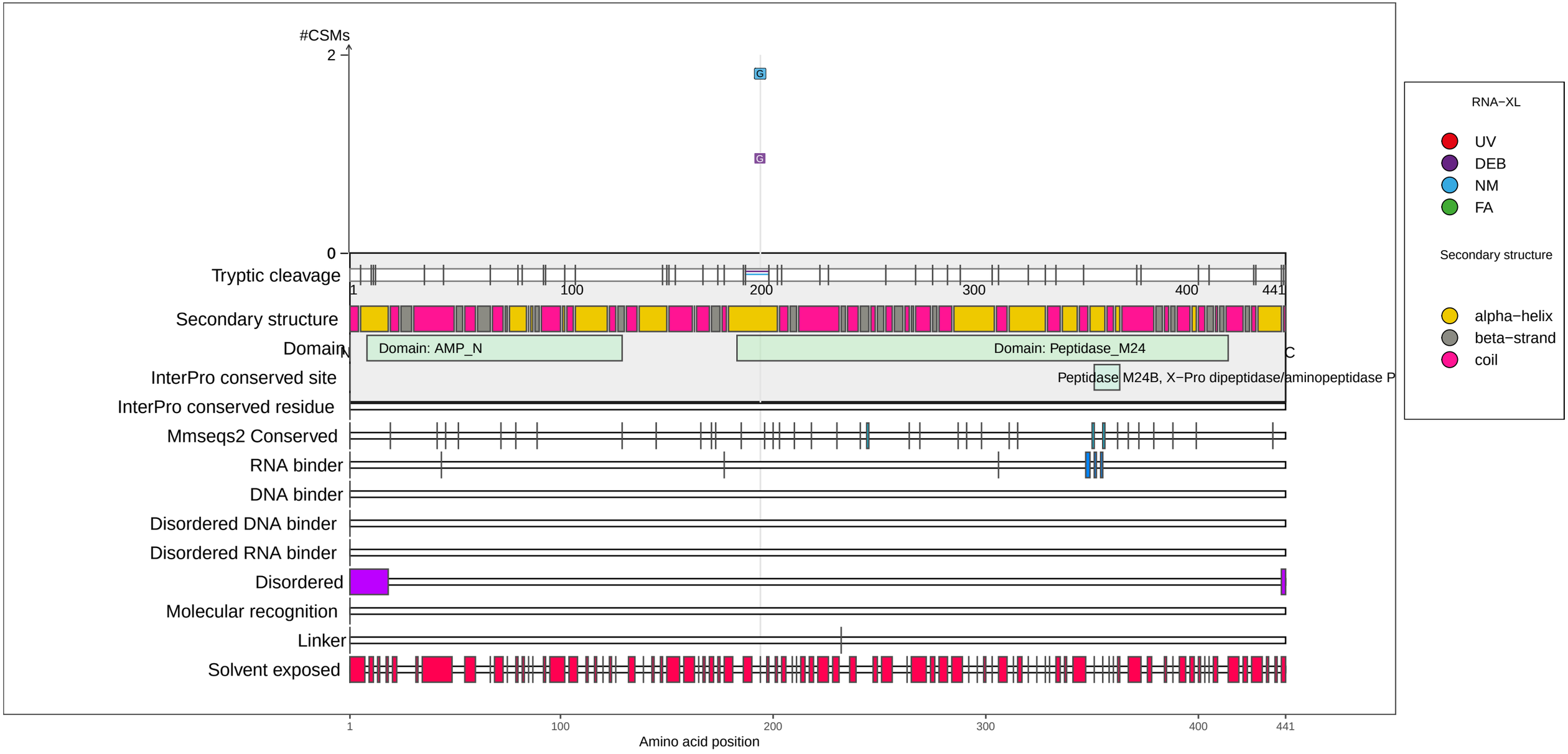
− RNA functions: not annotated



P15034
AMPP_ECOLI Xaa−Pro aminopeptidase

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 2.51 (Q 78)
PAXdb E.coli [ppm]: 2.74 (Q 91)

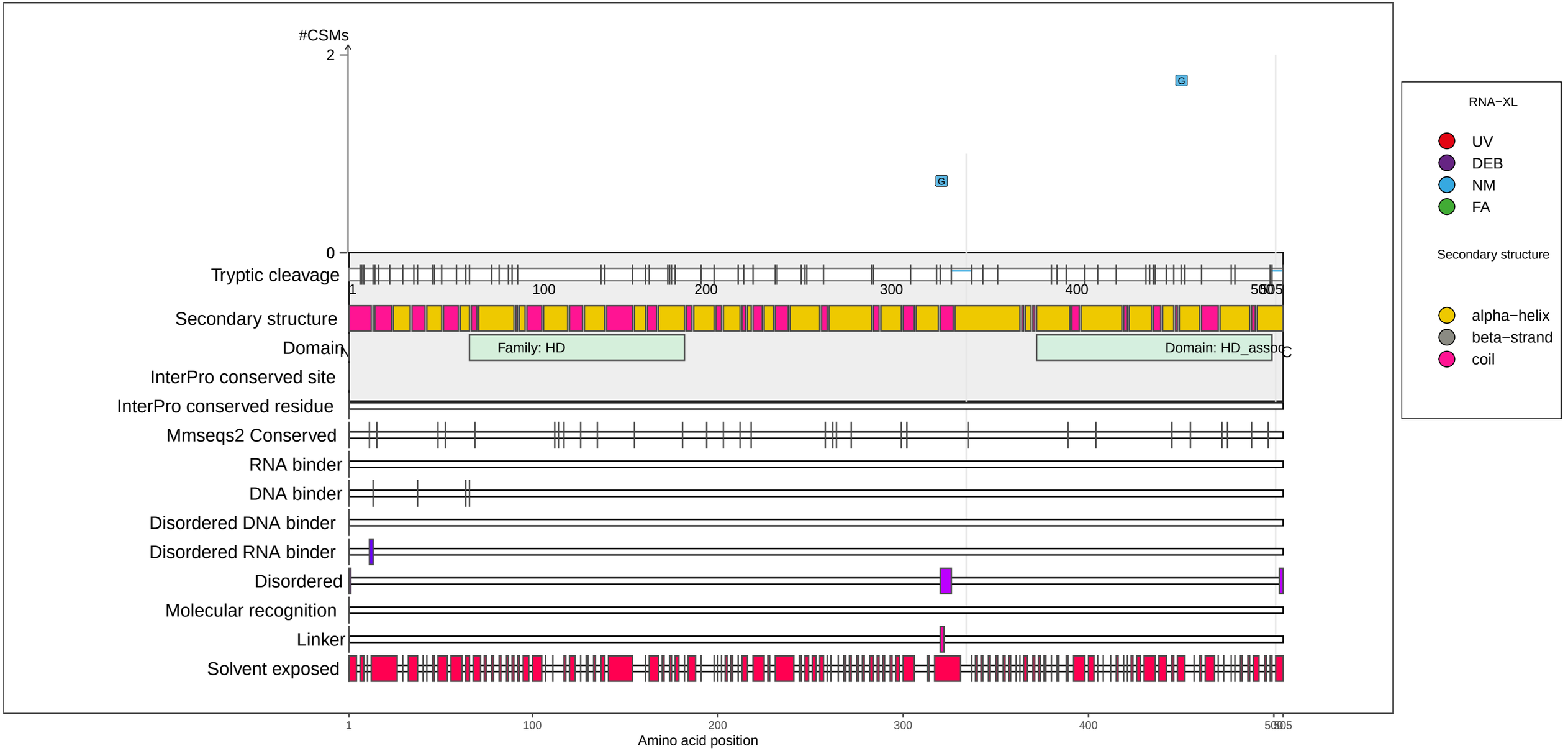
− RNA functions: not annotated



P15723
DGTP_ECOLI Deoxyguanosinetriphosphate triphosphohydrolase

− Abundance:
tryptic [log10 Intensity]: 7.34 (Q 27)
PAXdb K12 strain [ppm]: 0.9 (Q 8)
PAXdb E.coli [ppm]: 0.59 (Q 38)

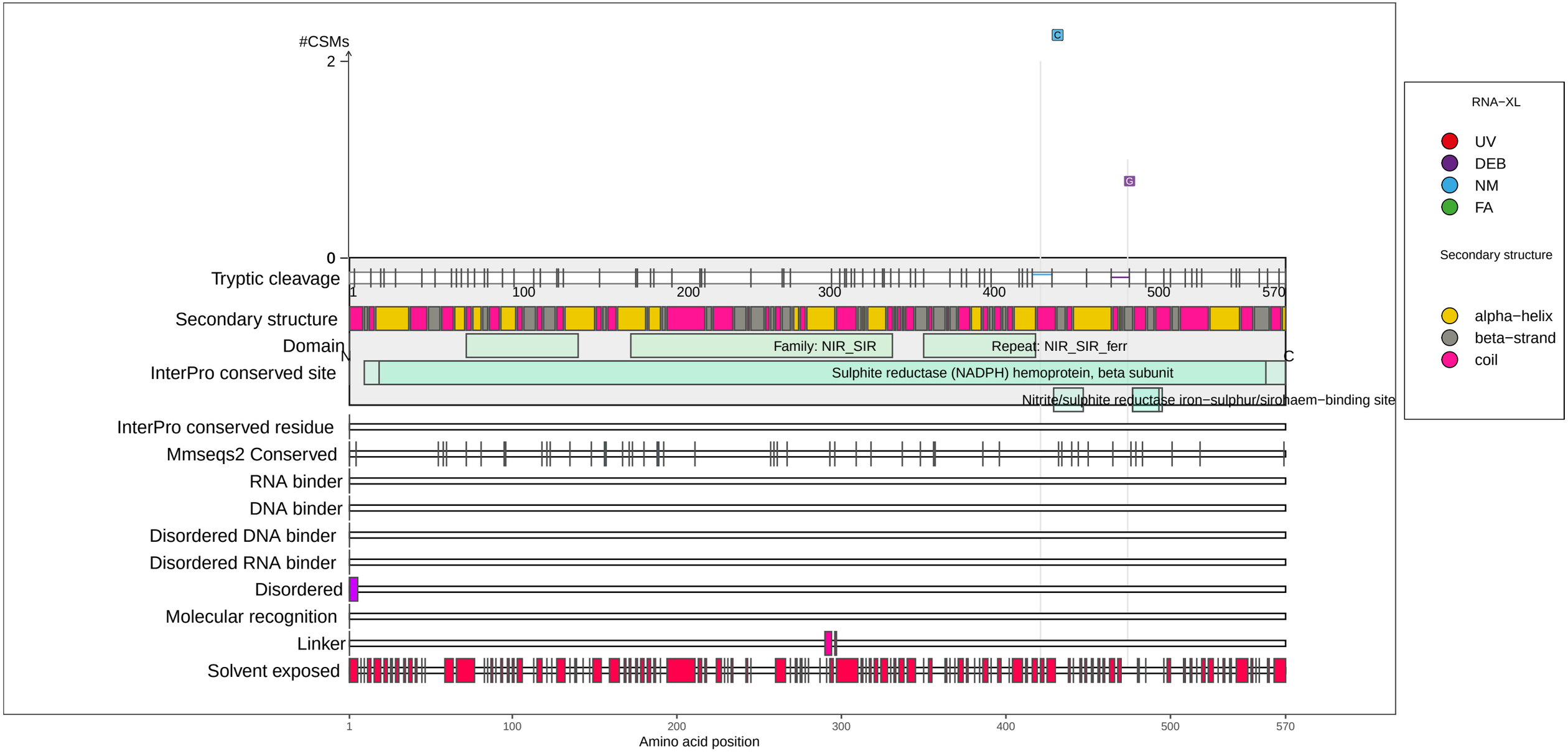
− RNA functions: not annotated



P17846
CYSI_ECOLI Sulfite reductase [NADPH] hemoprotein beta−component

− Abundance:
tryptic [log10 Intensity]: 7 (Q 13)
PAXdb K12 strain [ppm]: 2.81 (Q 86)
PAXdb E.coli [ppm]: 2.56 (Q 87)

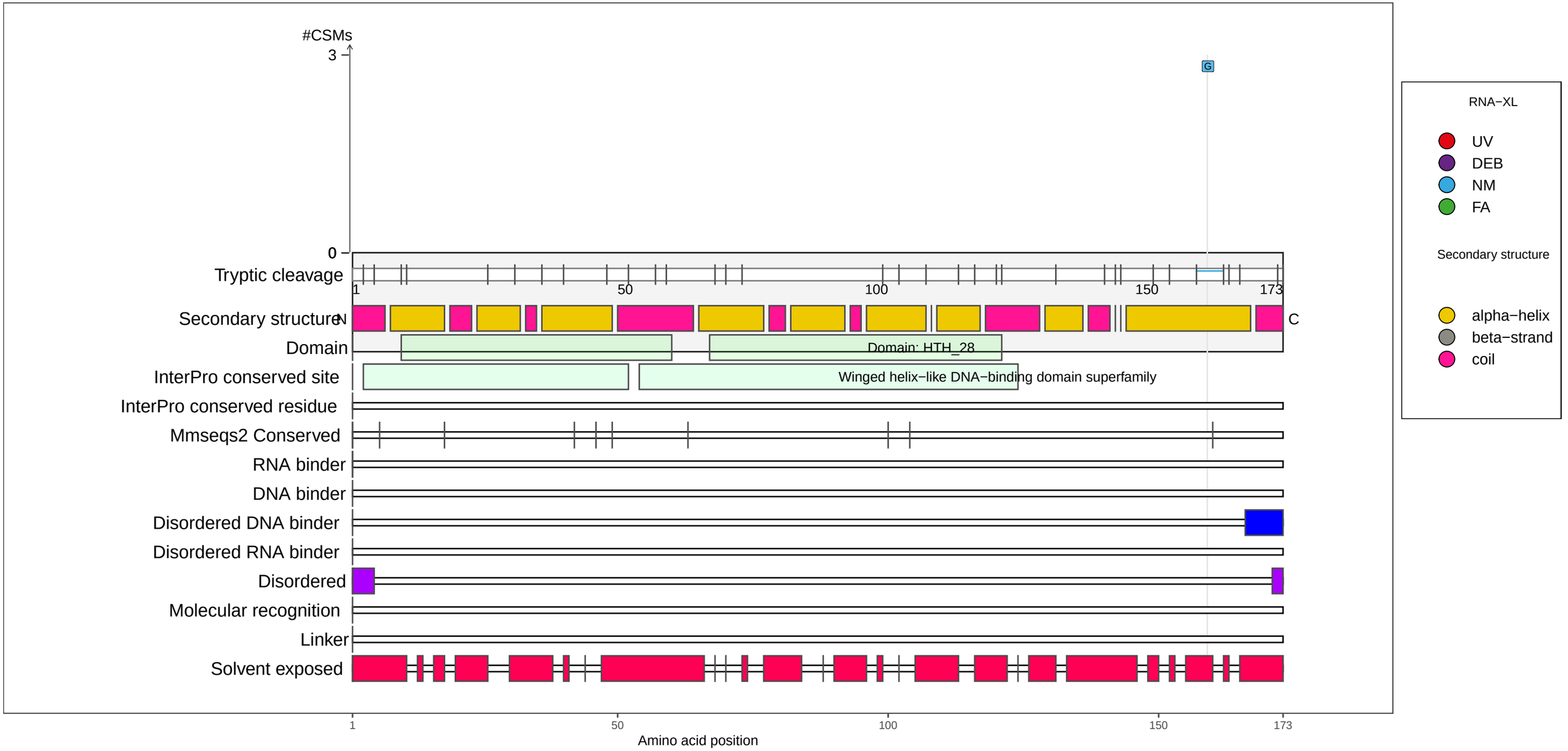
− RNA functions: not annotated



P19768
INSJ_ECOLI Insertion element IS150 protein InsJ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

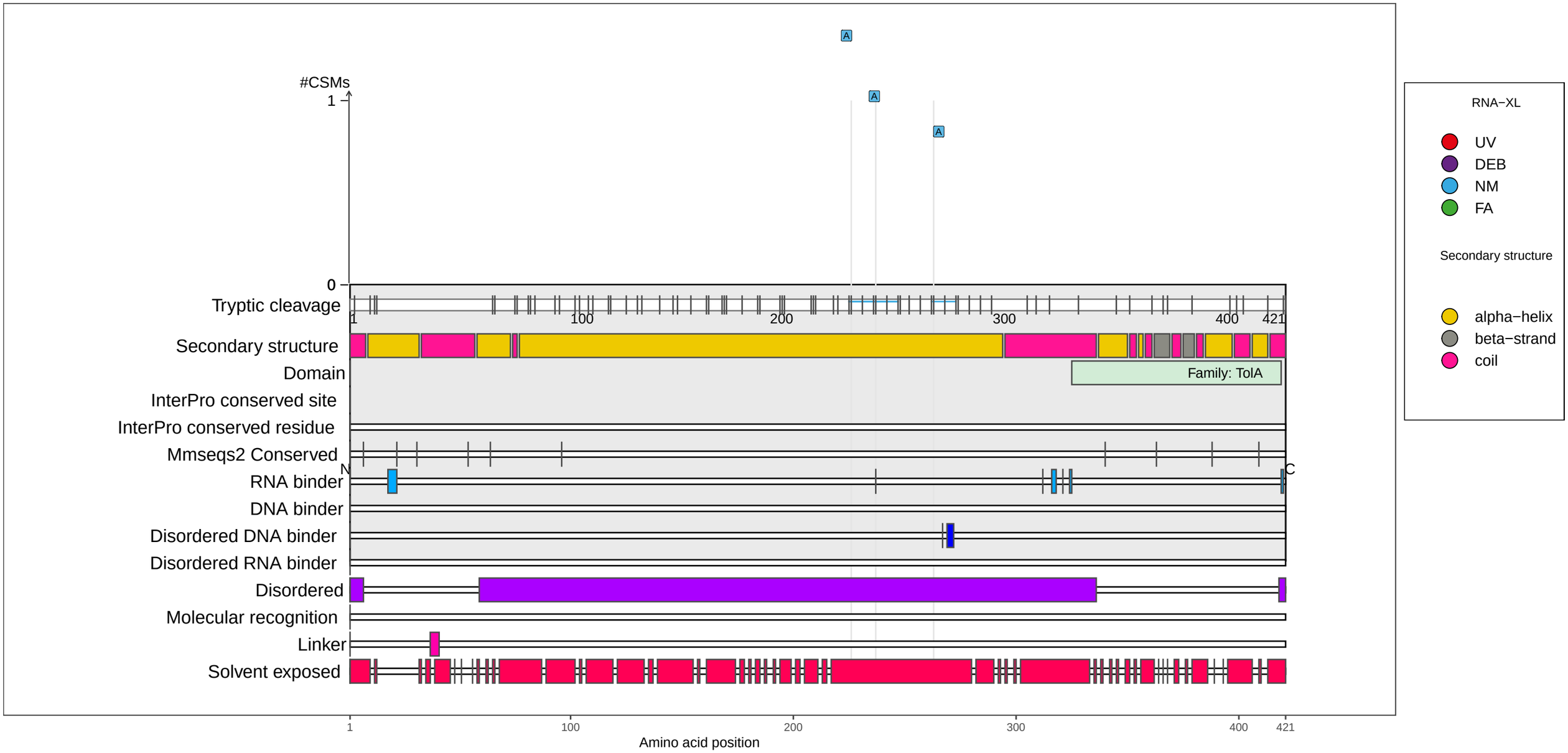
− RNA functions: not annotated



P19934
TOLA_ECOLI Tol−Pal system protein TolA

− Abundance:
tryptic [log10 Intensity]: 7.45 (Q 33)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 1.25 (Q 53)

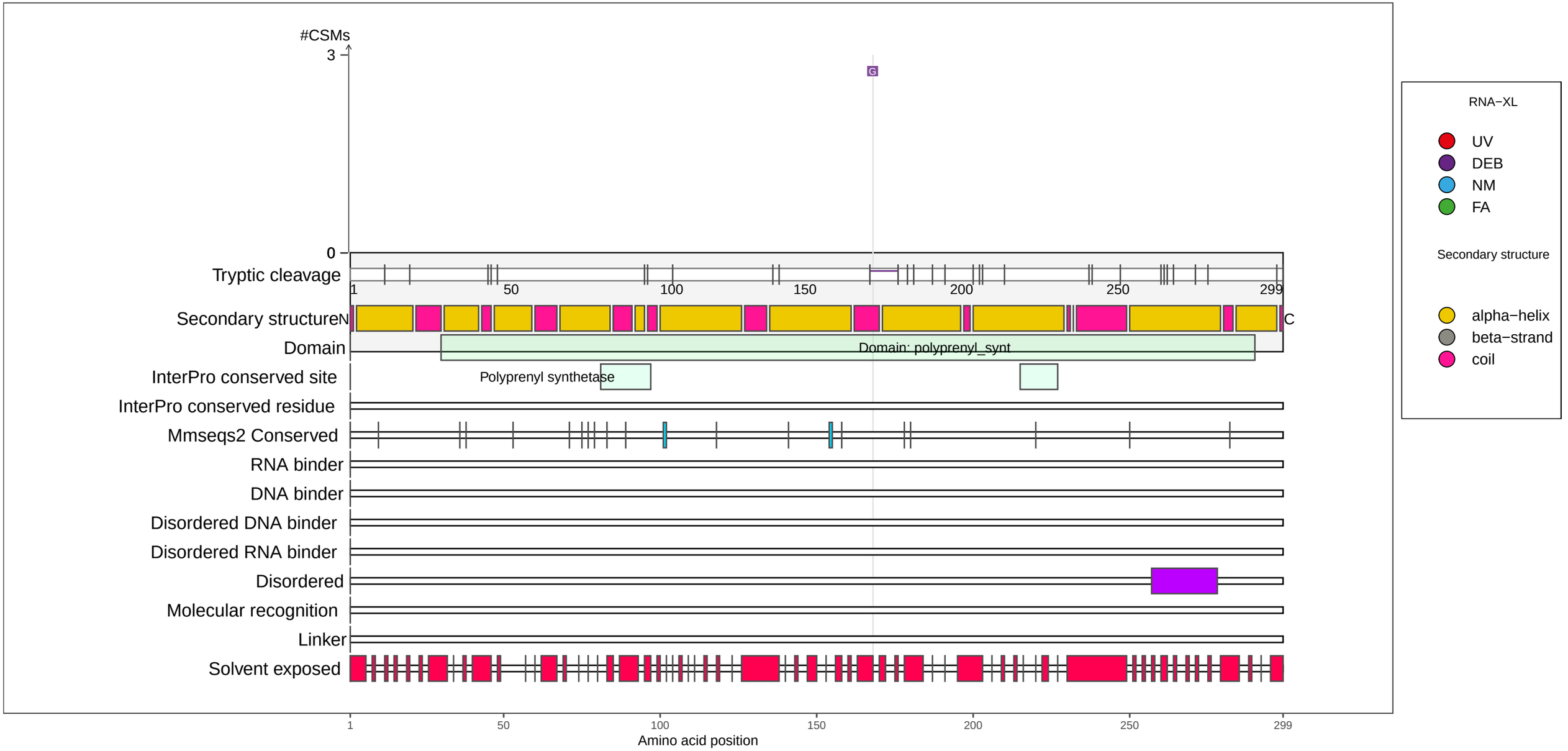
− RNA functions: not annotated



P22939
ISPA_ECOLI Farnesyl diphosphate synthase

− Abundance:
tryptic [log10 Intensity]: 7.17 (Q 20)
PAXdb K12 strain [ppm]: 2.4 (Q 74)
PAXdb E.coli [ppm]: 1.95 (Q 71)

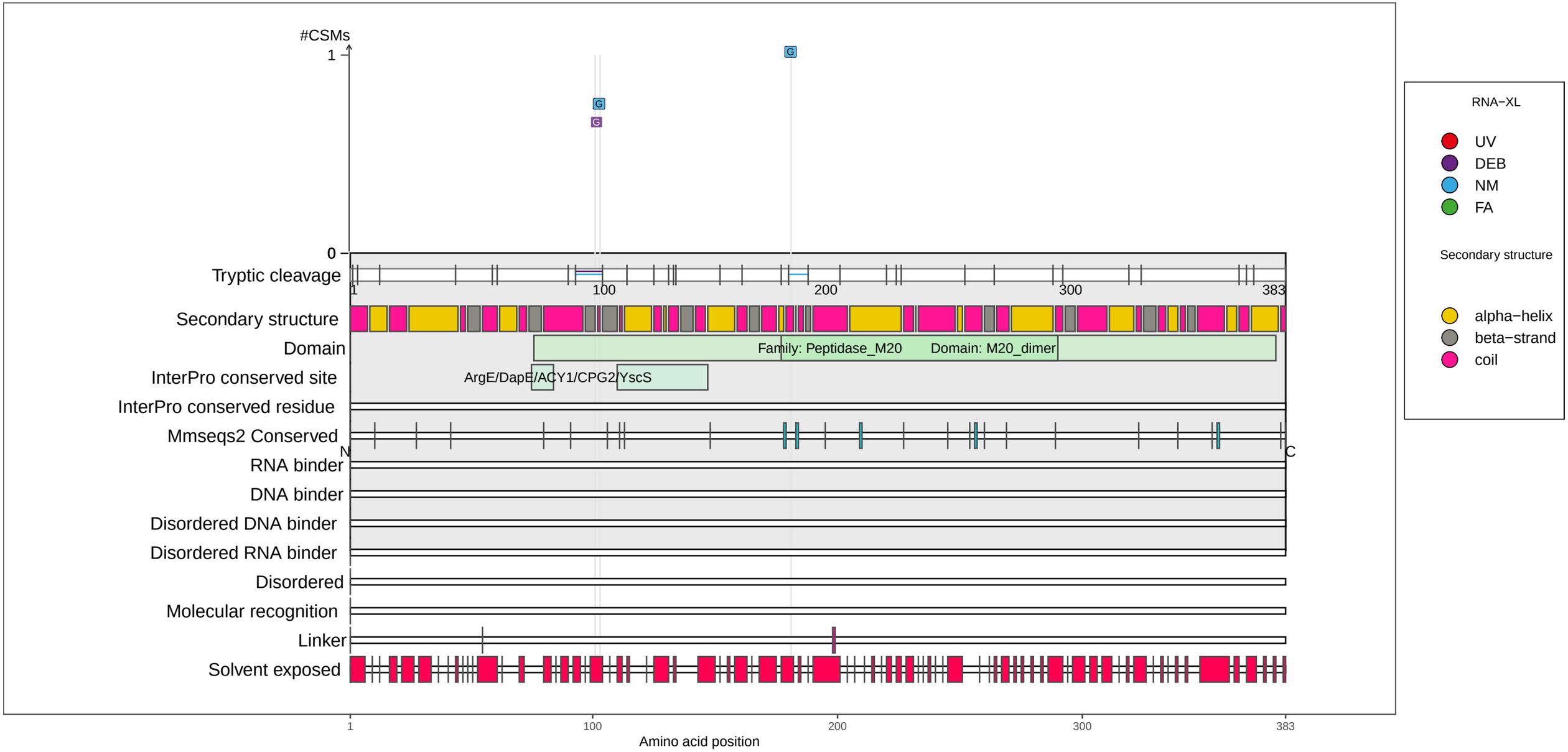
− RNA functions: not annotated



P23908
ARGE_ECOLI Acetylornithine deacetylase

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: 1.03 (Q 12)
PAXdb E.coli [ppm]: 2.13 (Q 76)

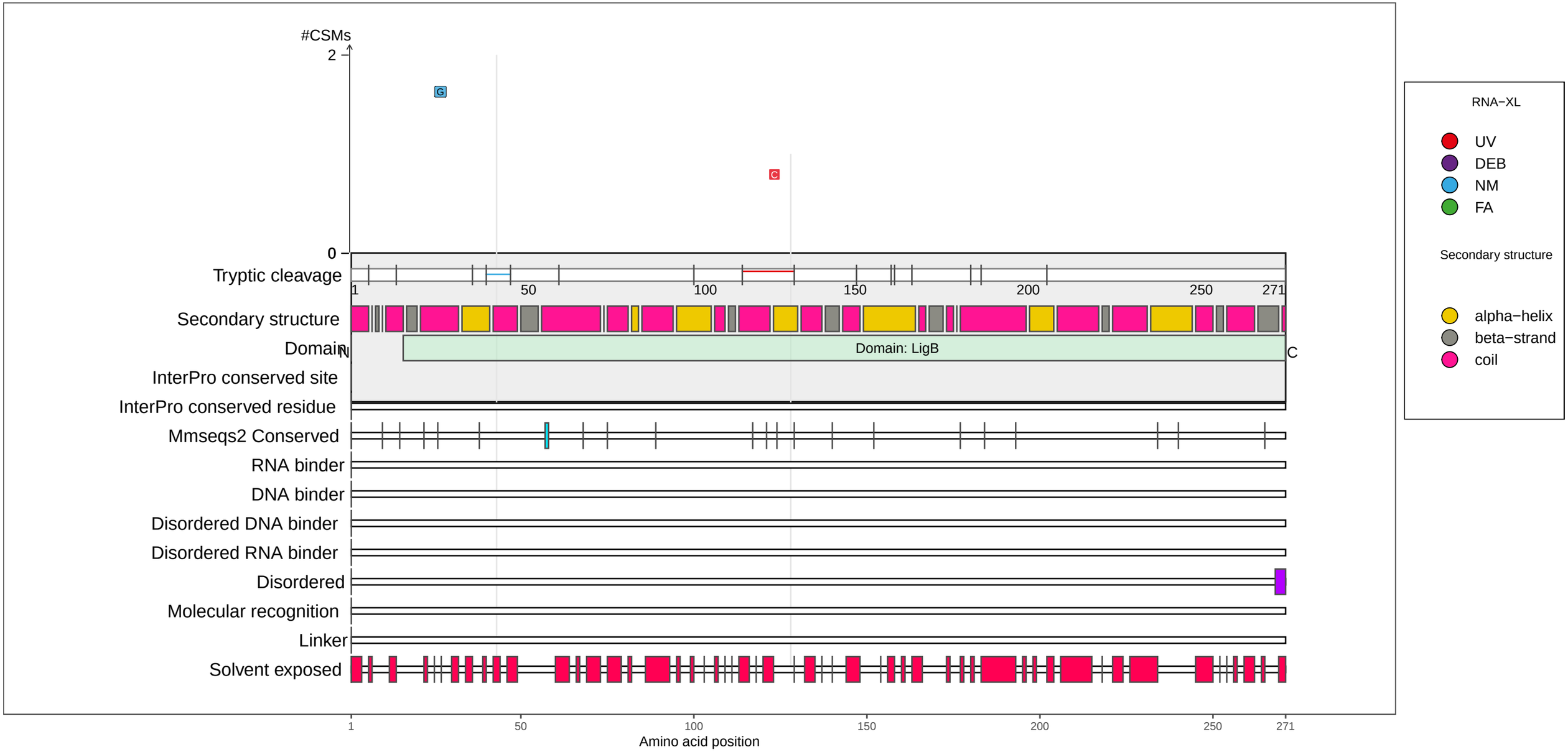
− RNA functions: not annotated



P24197
YGID_ECOLI 4,5−DOPA dioxygenase extradiol

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.1 (Q 27)

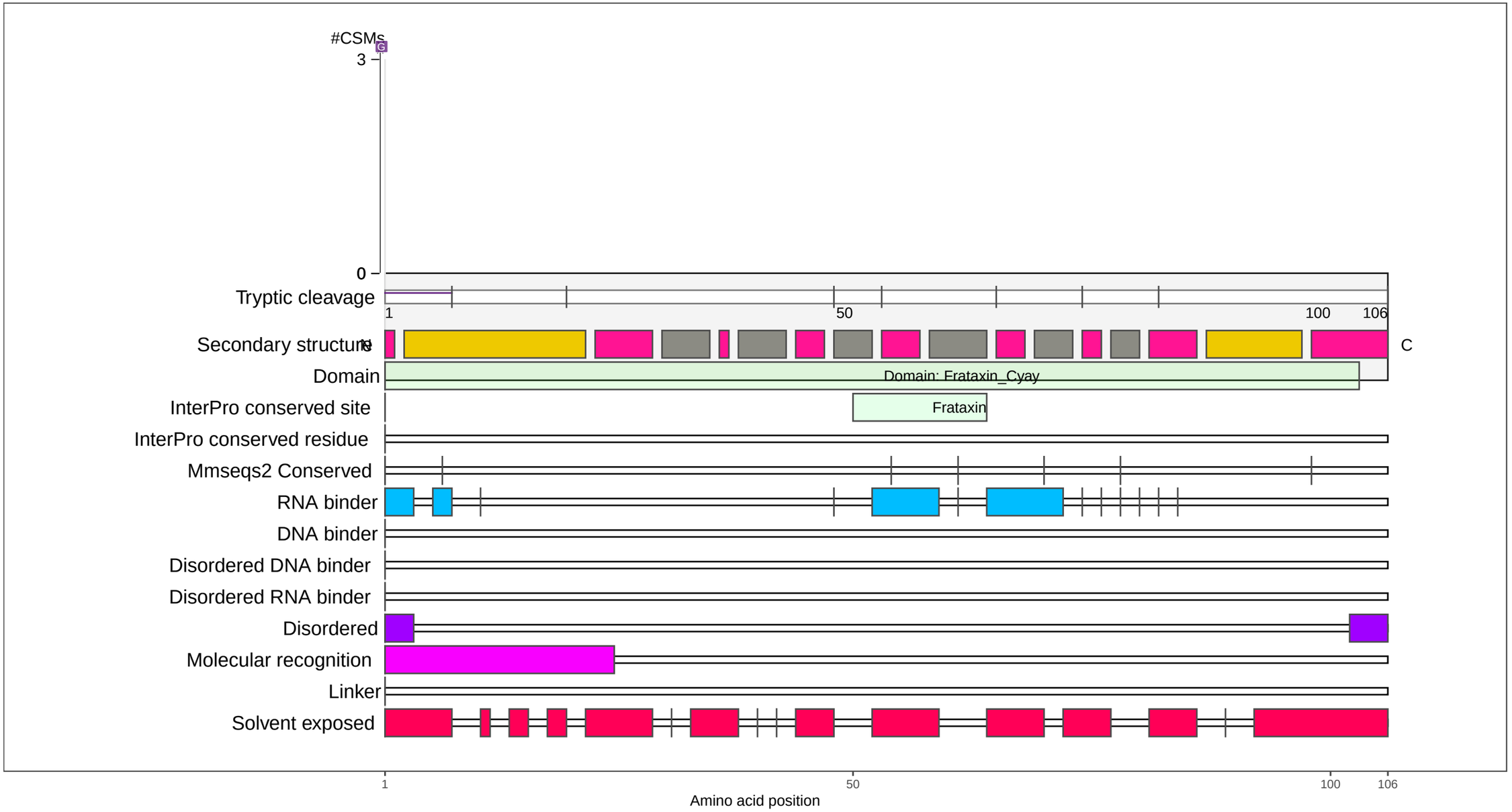
− RNA functions: not annotated



P27838
CYAY_ECOLI Iron−sulfur cluster assembly protein CyaY

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 55)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.33 (Q 81)

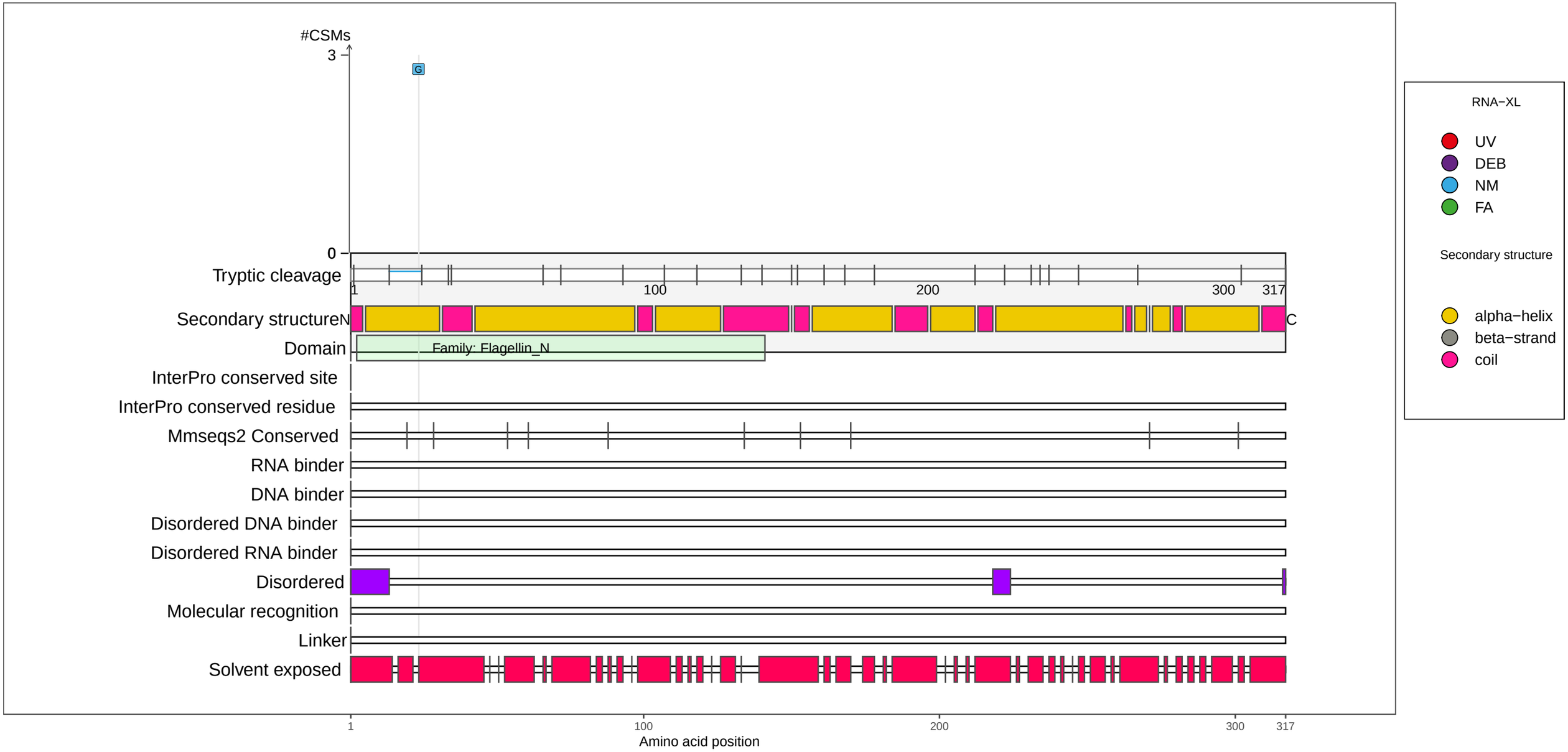
− RNA functions: not annotated



P29744
FLGL_ECOLI Flagellar hook−associated protein 3

− Abundance:
tryptic [log10 Intensity]: 7.2 (Q 21)
PAXdb K12 strain [ppm]: 1.74 (Q 51)
PAXdb E.coli [ppm]: 1.92 (Q 70)

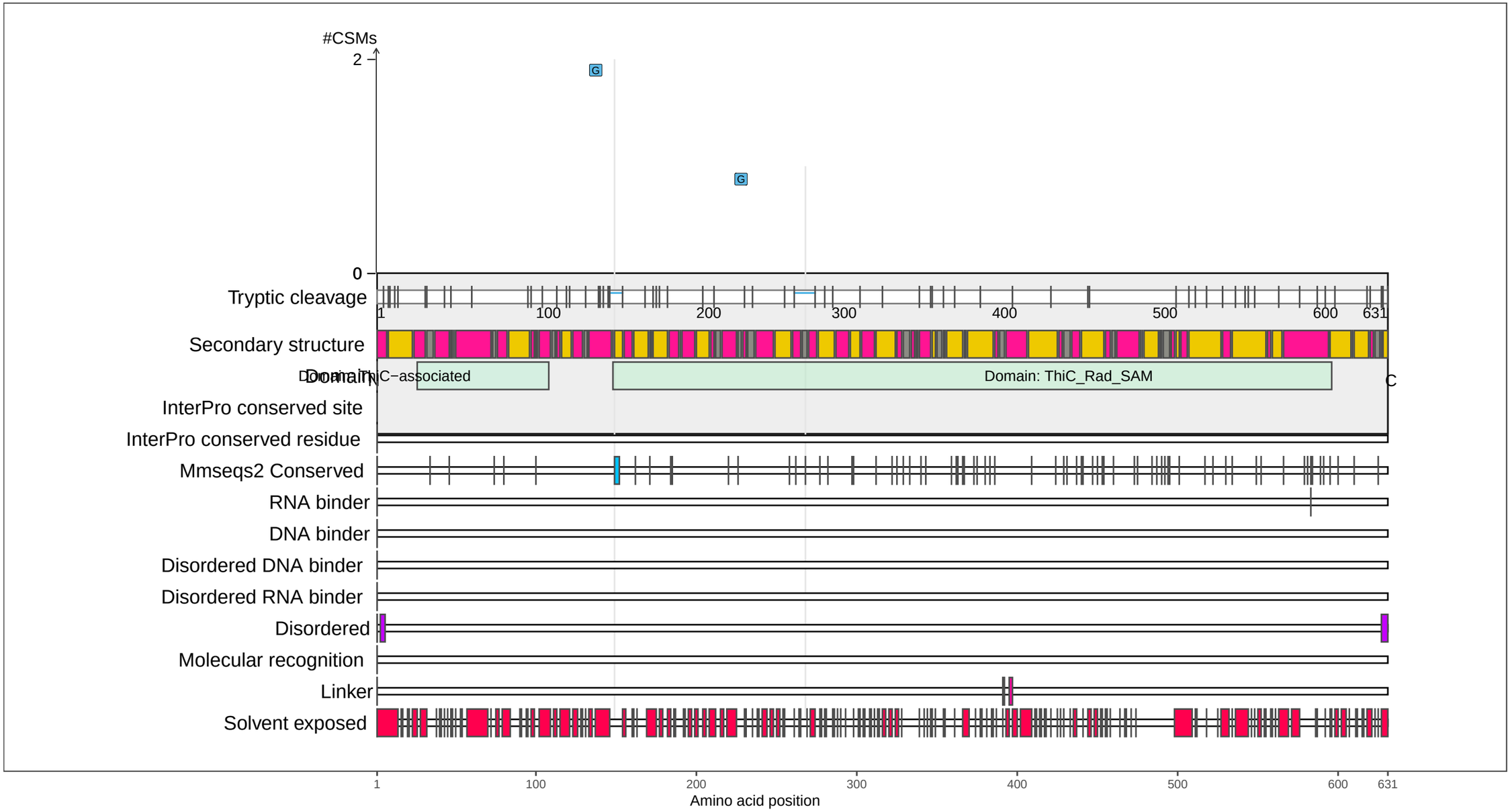
− RNA functions: not annotated

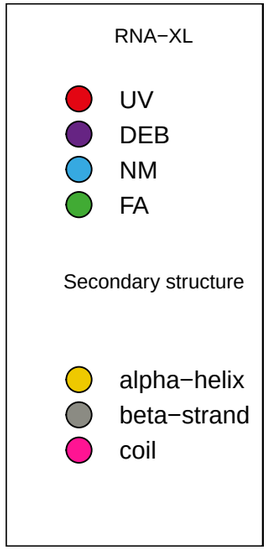


P30136
THIC_ECOLI Phosphomethylpyrimidine synthase

− Abundance:
tryptic [log10 Intensity]: 7.17 (Q 20)
PAXdb K12 strain [ppm]: 0.58 (Q 1)
PAXdb E.coli [ppm]: 1.98 (Q 72)

− RNA functions: not annotated

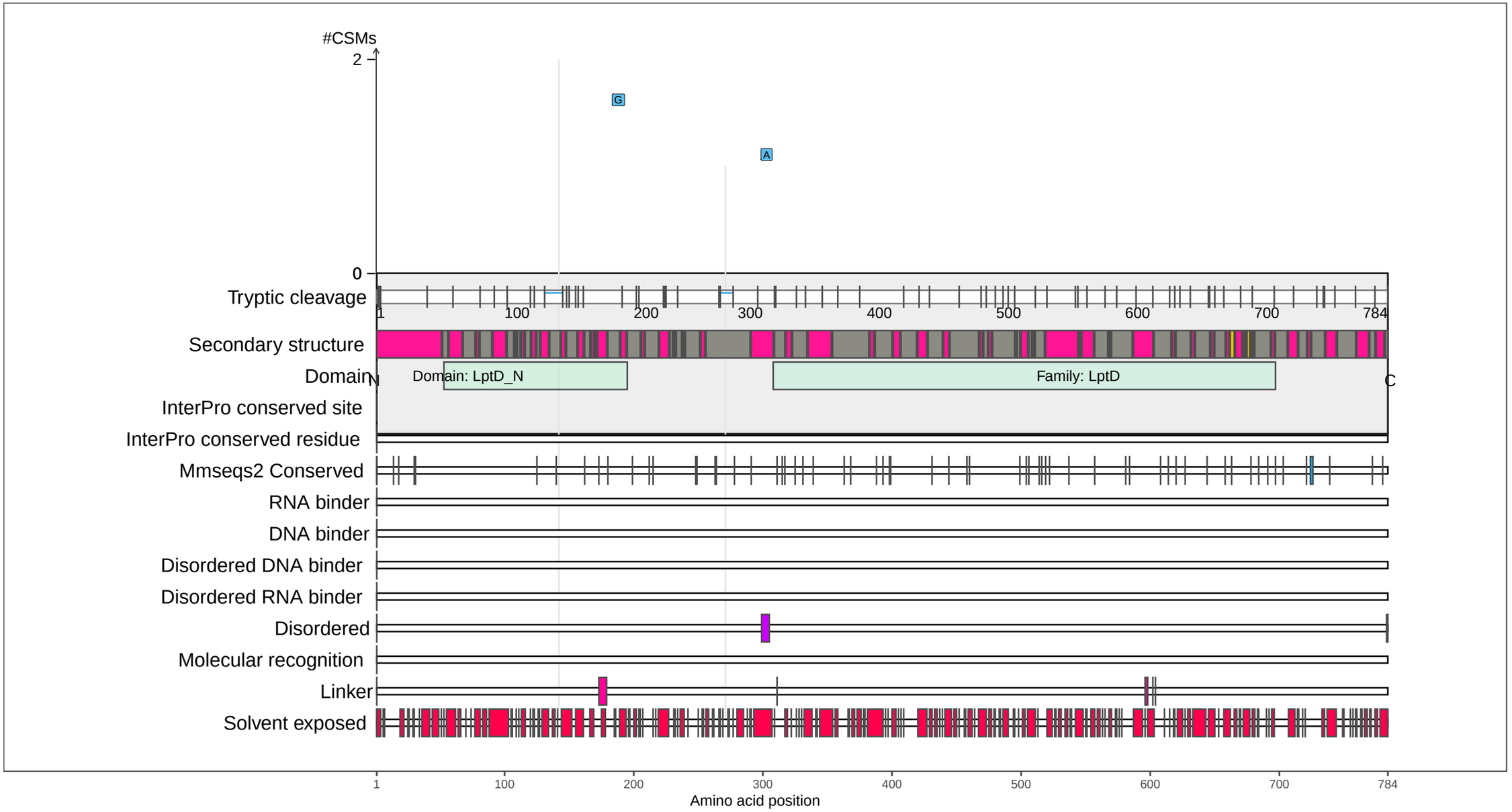




P31554
LPTD_ECOLI LPS−assembly protein LptD

− Abundance:
tryptic [log10 Intensity]: 9.51 (Q 97)
PAXdb K12 strain [ppm]: 0.75 (Q 4)
PAXdb E.coli [ppm]: 1.78 (Q 66)

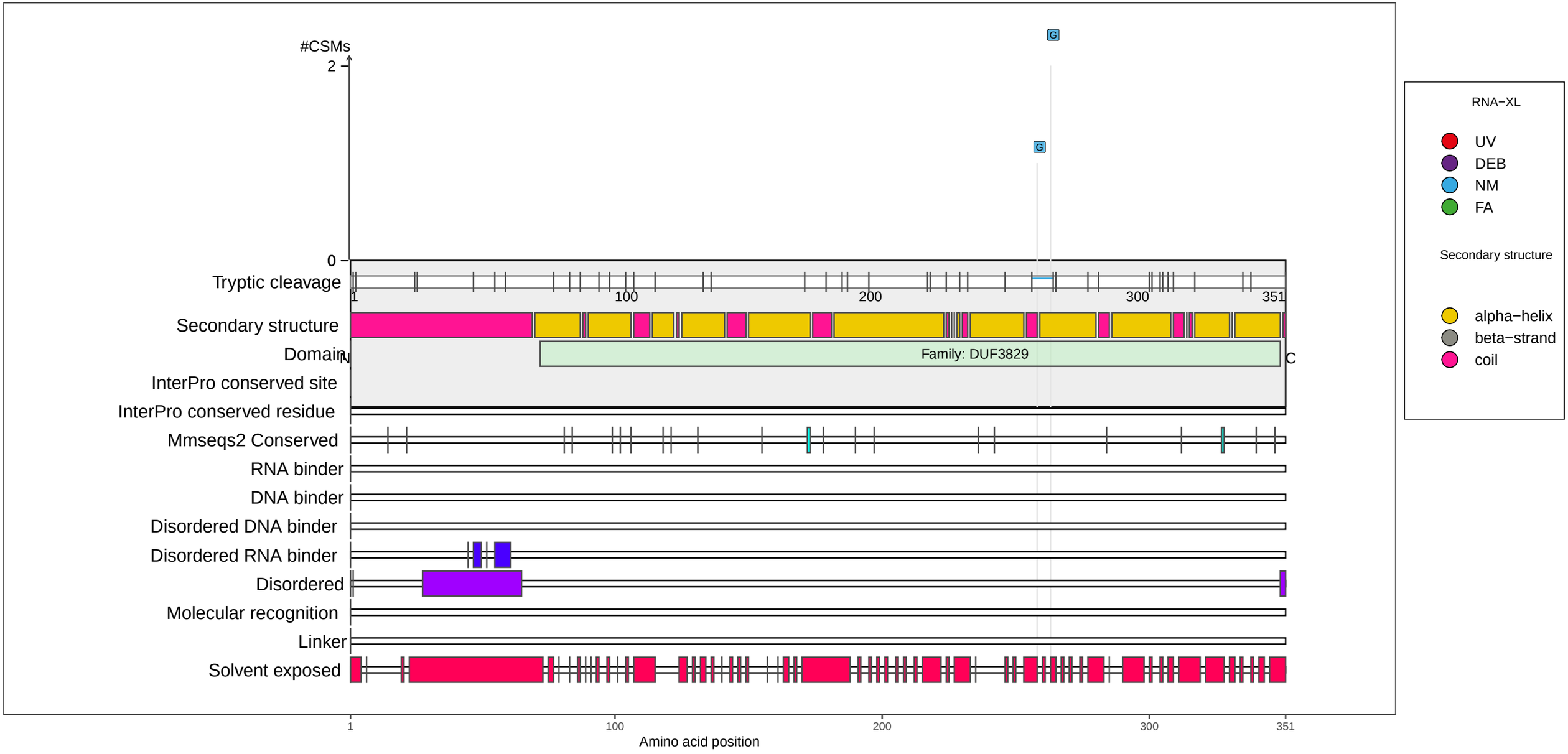
− RNA functions: not annotated



P32151
YIIG_ECOLI Uncharacterized protein YiiG

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.21 (Q 21)
PAXdb E.coli [ppm]: −0.31 (Q 19)

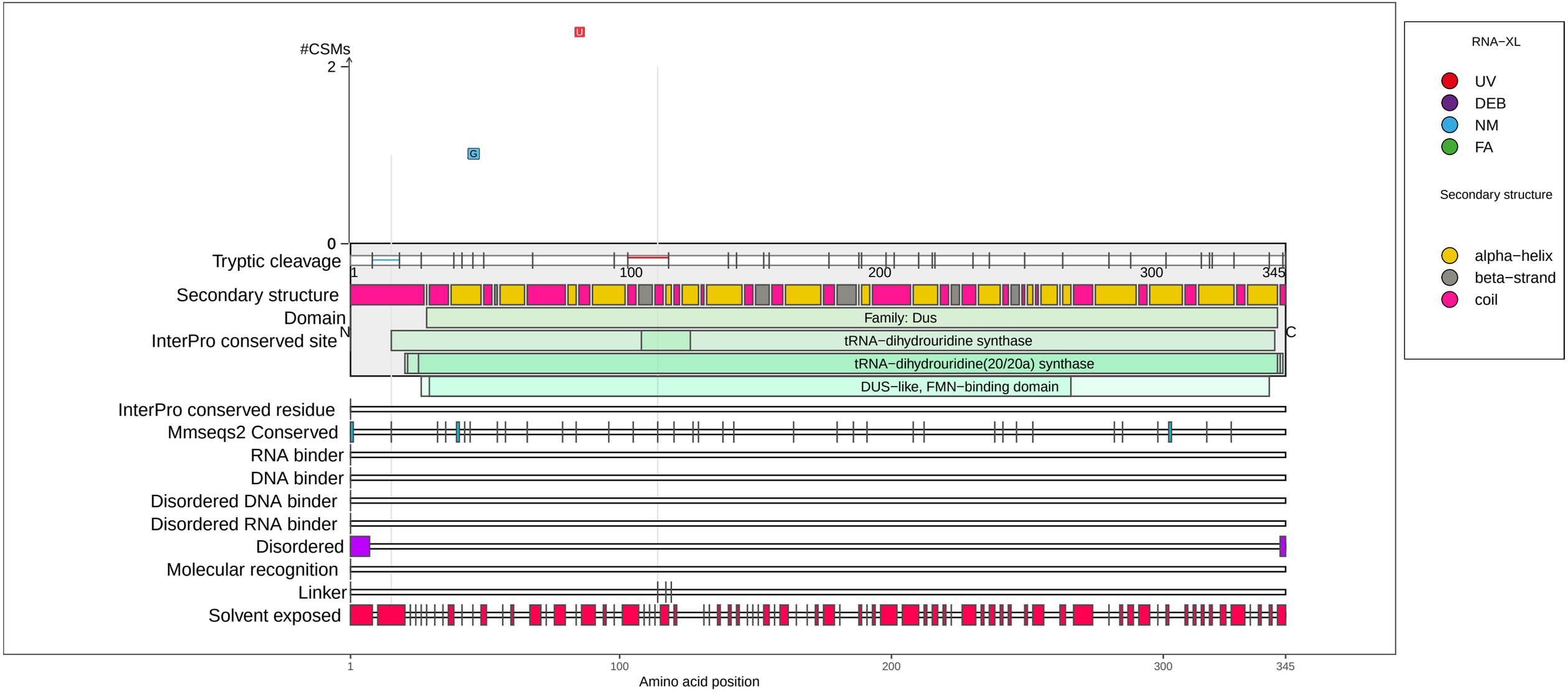
− RNA functions: not annotated



P32695
DUSA_ECOLI tRNA−dihydrouridine(20/20a) synthase

− Abundance:
tryptic [log10 Intensity]: 7.89 (Q 53)
PAXdb K12 strain [ppm]: 0.83 (Q 6)
PAXdb E.coli [ppm]: 1.6 (Q 62)

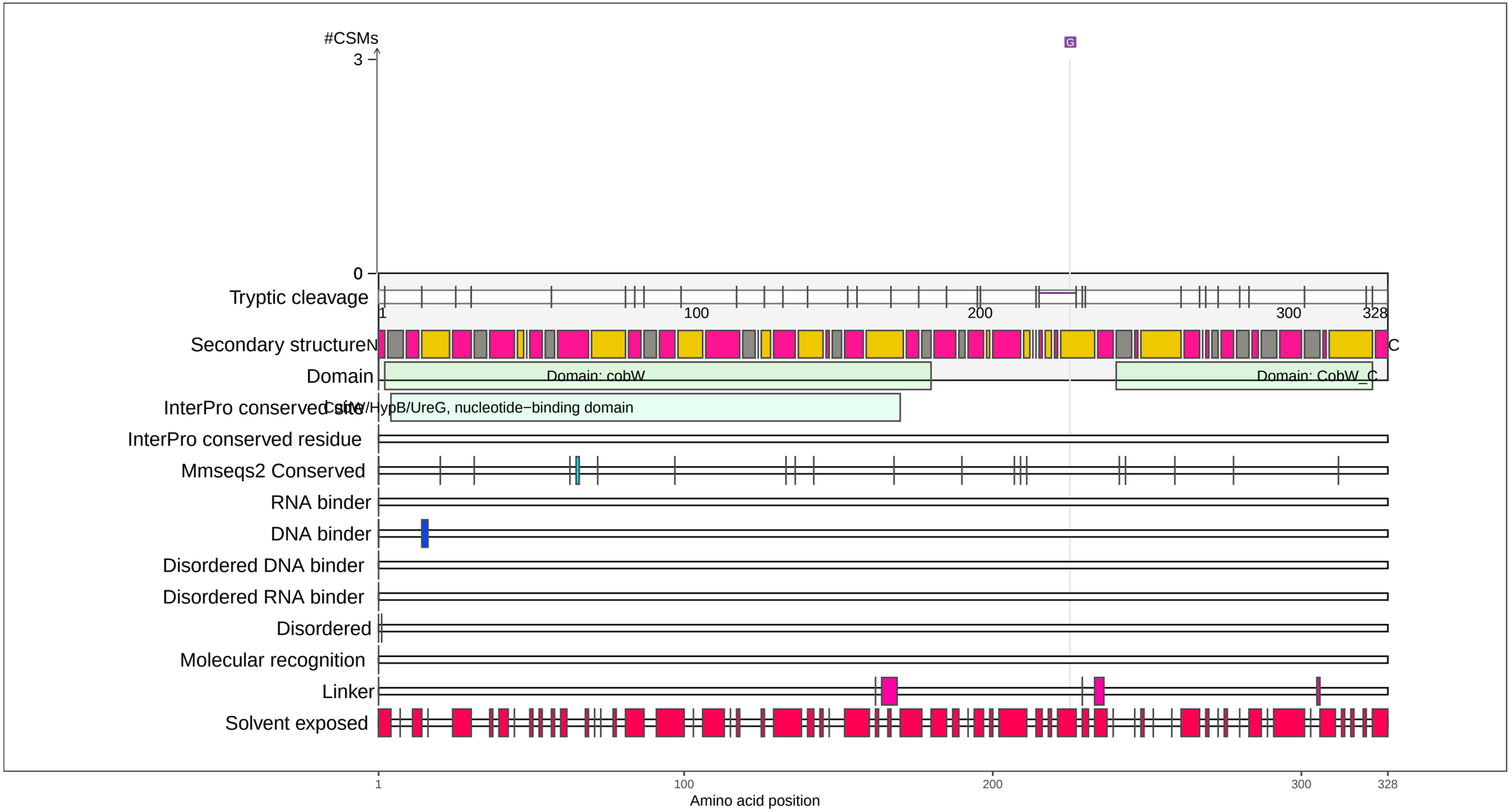
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; tRNA binding; tRNA dihydrouridine synthase activity
tRNA dihydrouridine synthesis; tRNA metabolic process; tRNA modification; tRNA processing
tRNA−dihydrouridine20 synthase activity

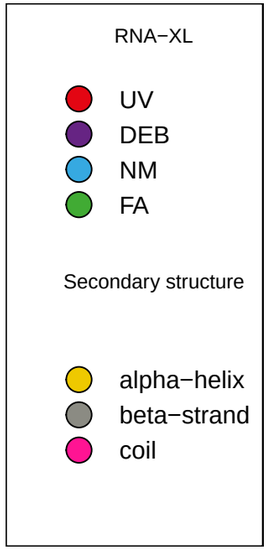


P33030
YEIR_ECOLI Zinc−binding GTPase YeiR

− Abundance:
tryptic [log10 Intensity]: 7.83 (Q 50)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 0.59 (Q 38)

− RNA functions: not annotated

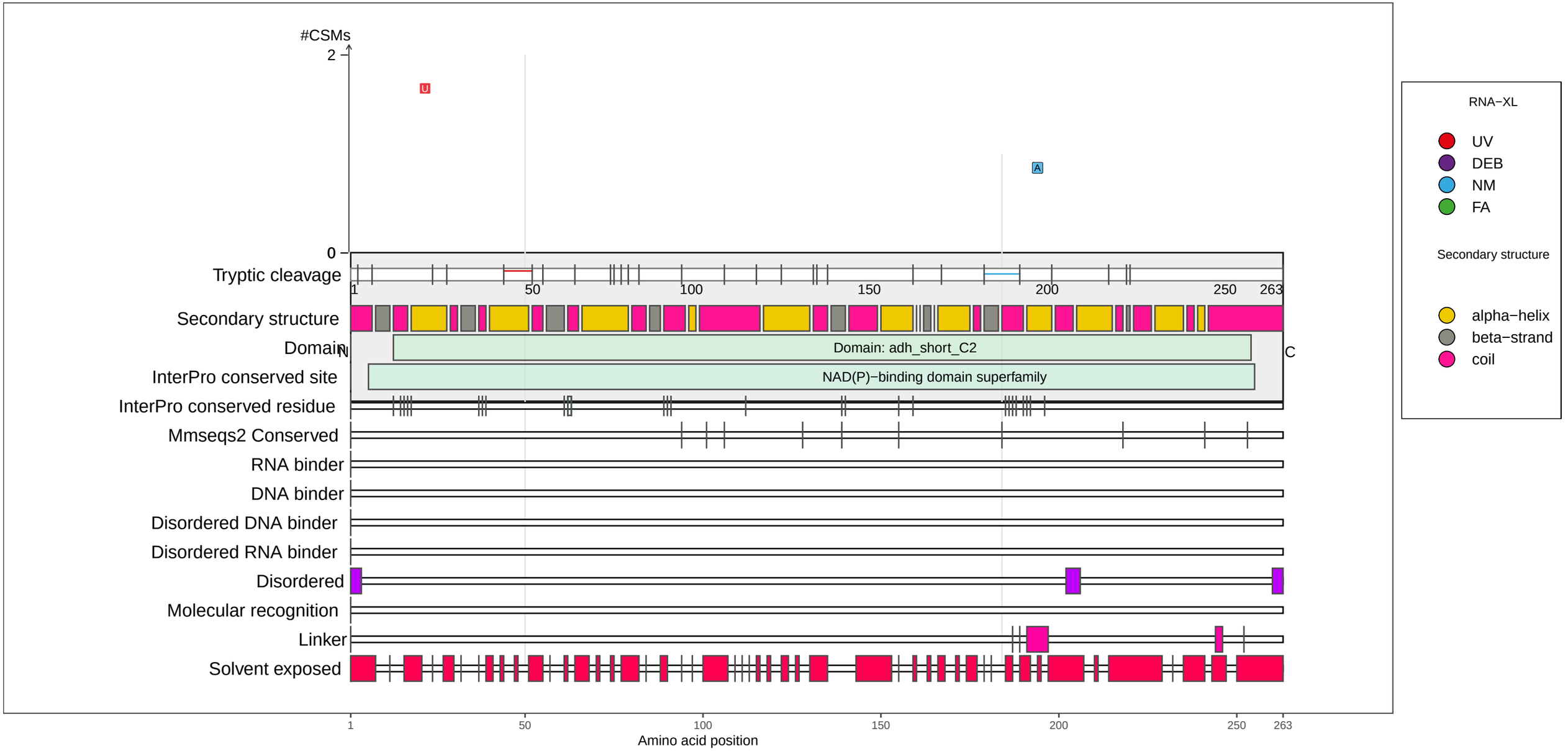




P37440
UCPA_ECOLI Oxidoreductase UcpA

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 2.47 (Q 76)
PAXdb E.coli [ppm]: 2.32 (Q 81)

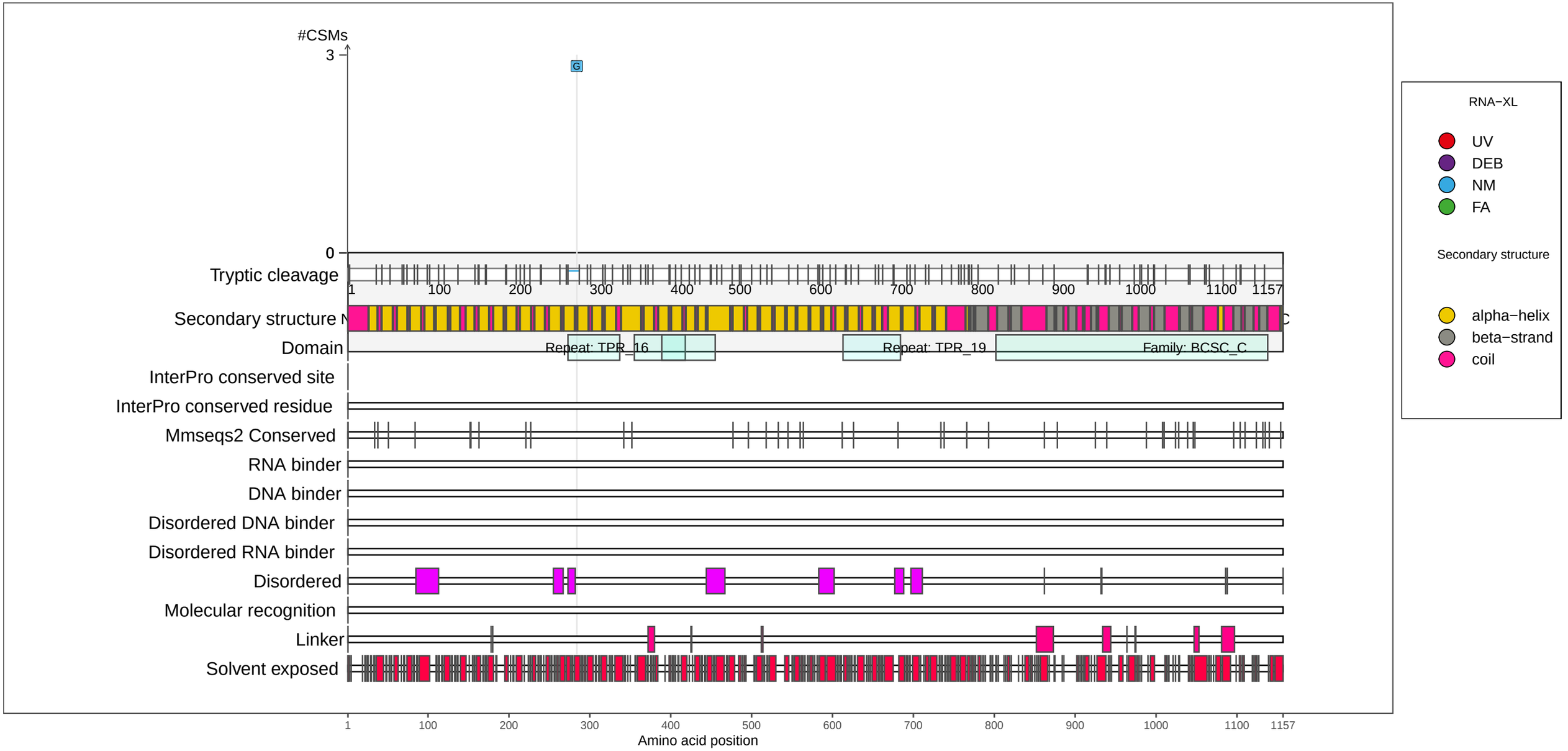
− RNA functions: not annotated



P37650
BCSC_ECOLI Cellulose synthase operon protein C

− Abundance:
tryptic [log10 Intensity]: 7.59 (Q 39)
PAXdb K12 strain [ppm]: 1.01 (Q 11)
PAXdb E.coli [ppm]: 0.81 (Q 43)

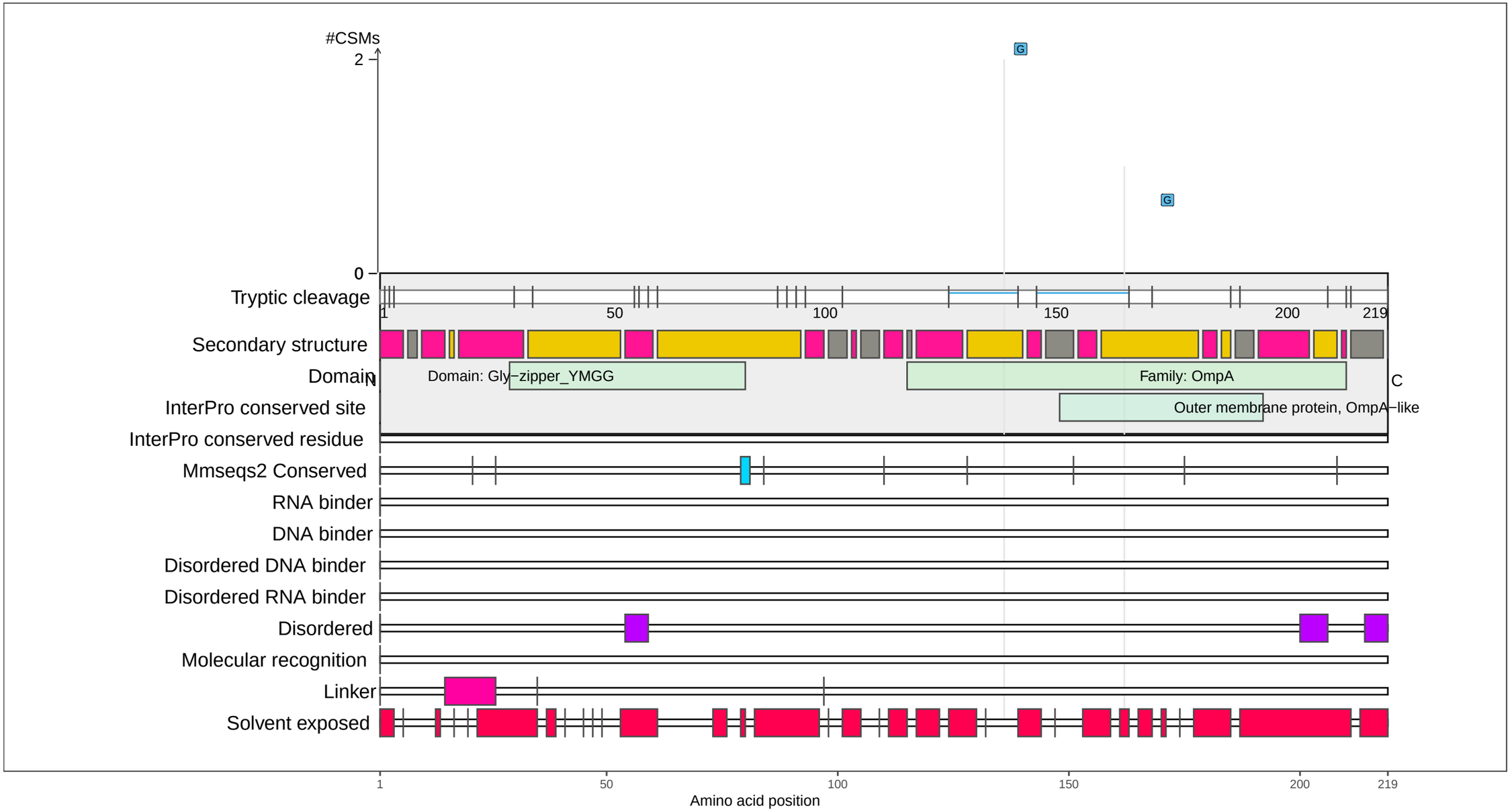
− RNA functions: not annotated

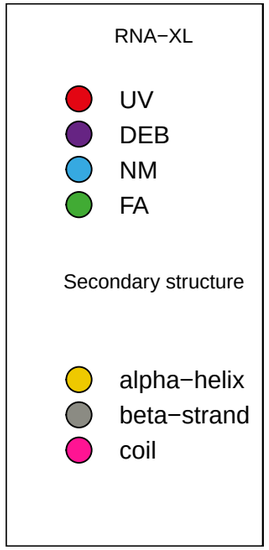


P37665
YIAD_ECOLI Probable lipoprotein YiaD

− Abundance:
tryptic [log10 Intensity]: 9.4 (Q 95)
PAXdb K12 strain [ppm]: 1.97 (Q 59)
PAXdb E.coli [ppm]: 1.6 (Q 62)

− RNA functions: not annotated

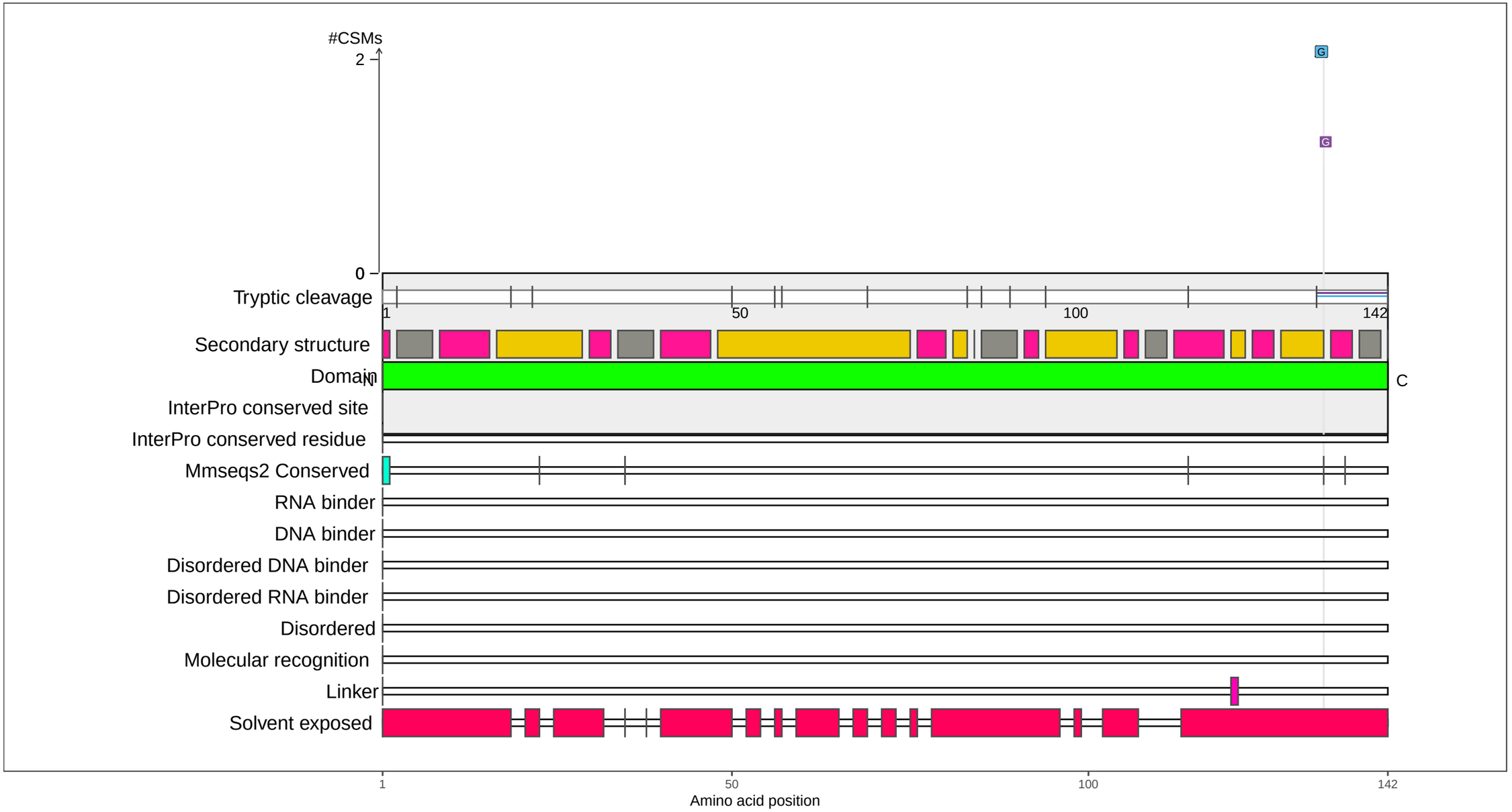




P39177
USPG_ECOLI Universal stress protein UP12

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 64)
PAXdb K12 strain [ppm]: 2 (Q 60)
PAXdb E.coli [ppm]: 3.16 (Q 96)

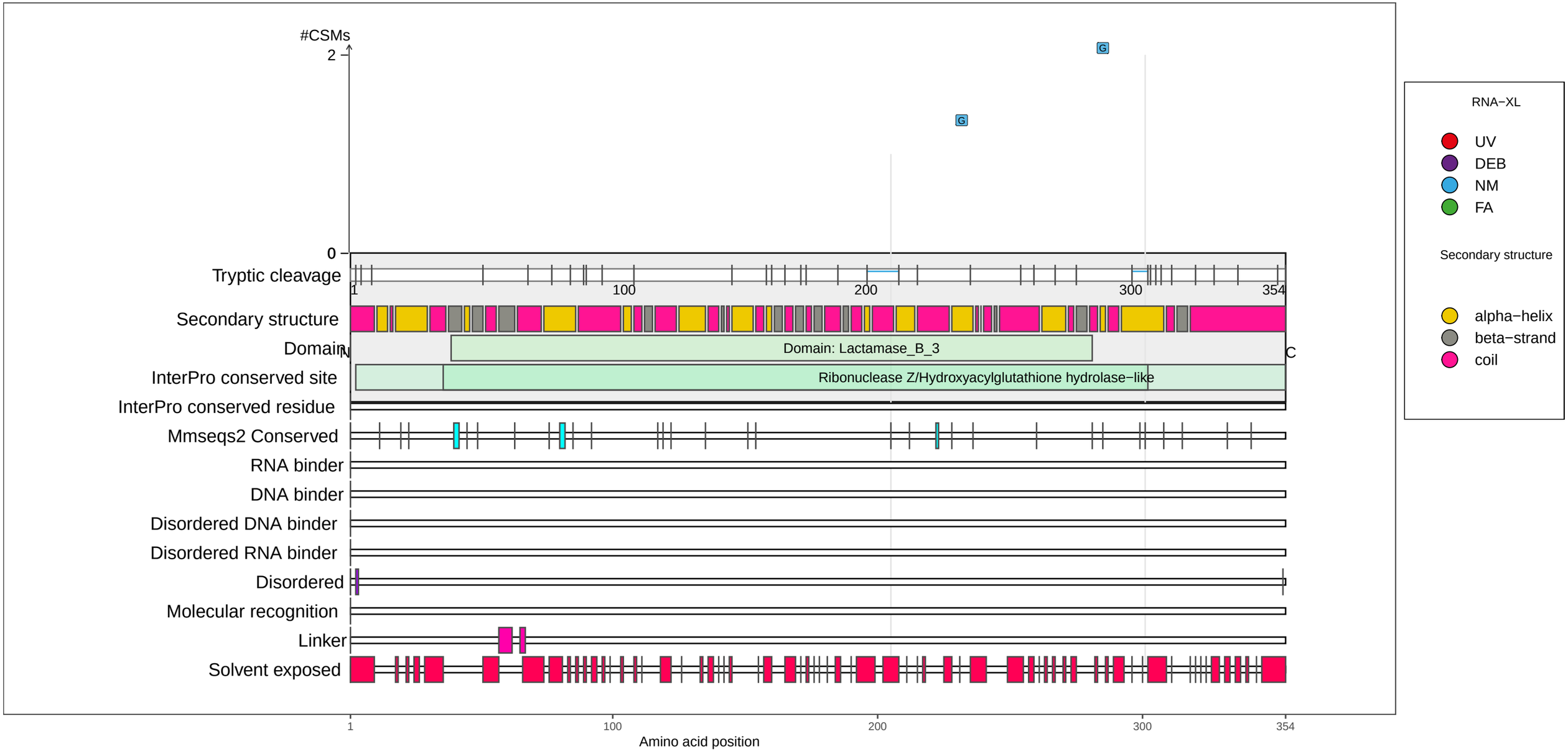
− RNA functions: not annotated



P39300
ULAG_ECOLI Probable L−ascorbate−6−phosphate lactonase UlaG

− Abundance:
tryptic [log10 Intensity]: 7.38 (Q 29)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 1.3 (Q 54)

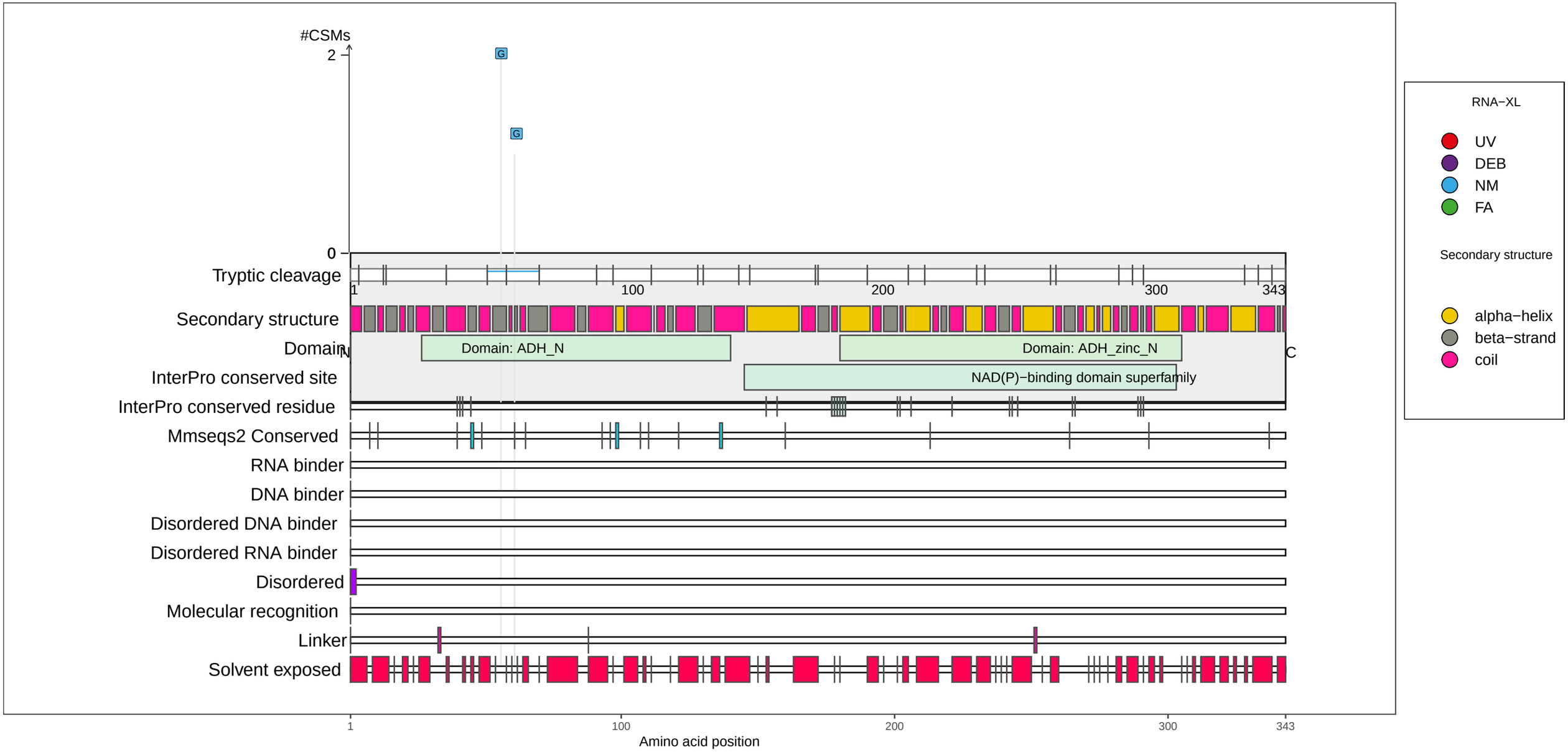
− RNA functions: not annotated



P39346
IDND_ECOLI L−idonate 5−dehydrogenase (NAD(P)(+))

− Abundance:
tryptic [log10 Intensity]: 8.57 (Q 78)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.4 (Q 5)

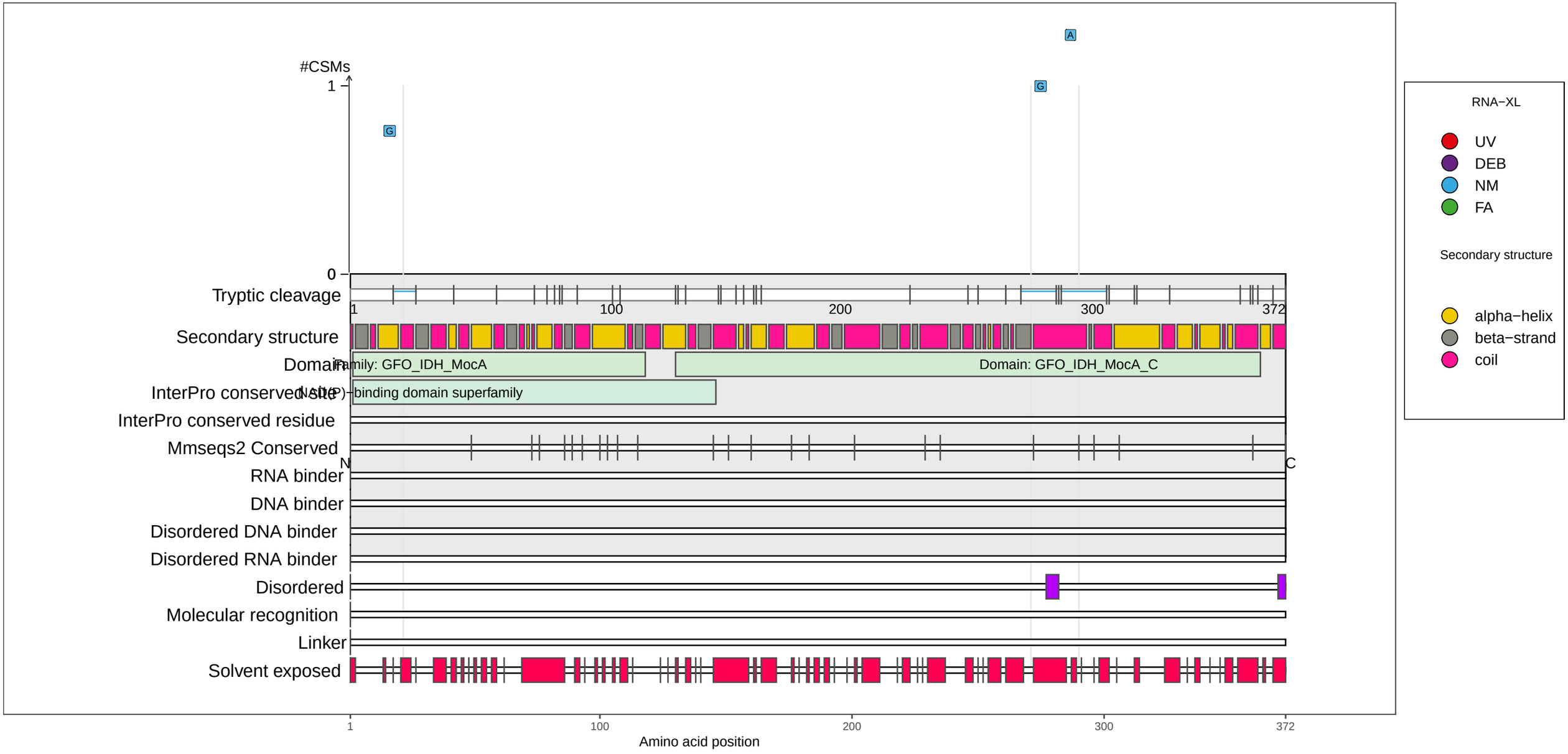
− RNA functions: not annotated



P39353
YJHC_ECOLI Uncharacterized oxidoreductase YjhC

− Abundance:
tryptic [log10 Intensity]: 8.05 (Q 59)
PAXdb K12 strain [ppm]: 1.08 (Q 15)
PAXdb E.coli [ppm]: 0.81 (Q 43)

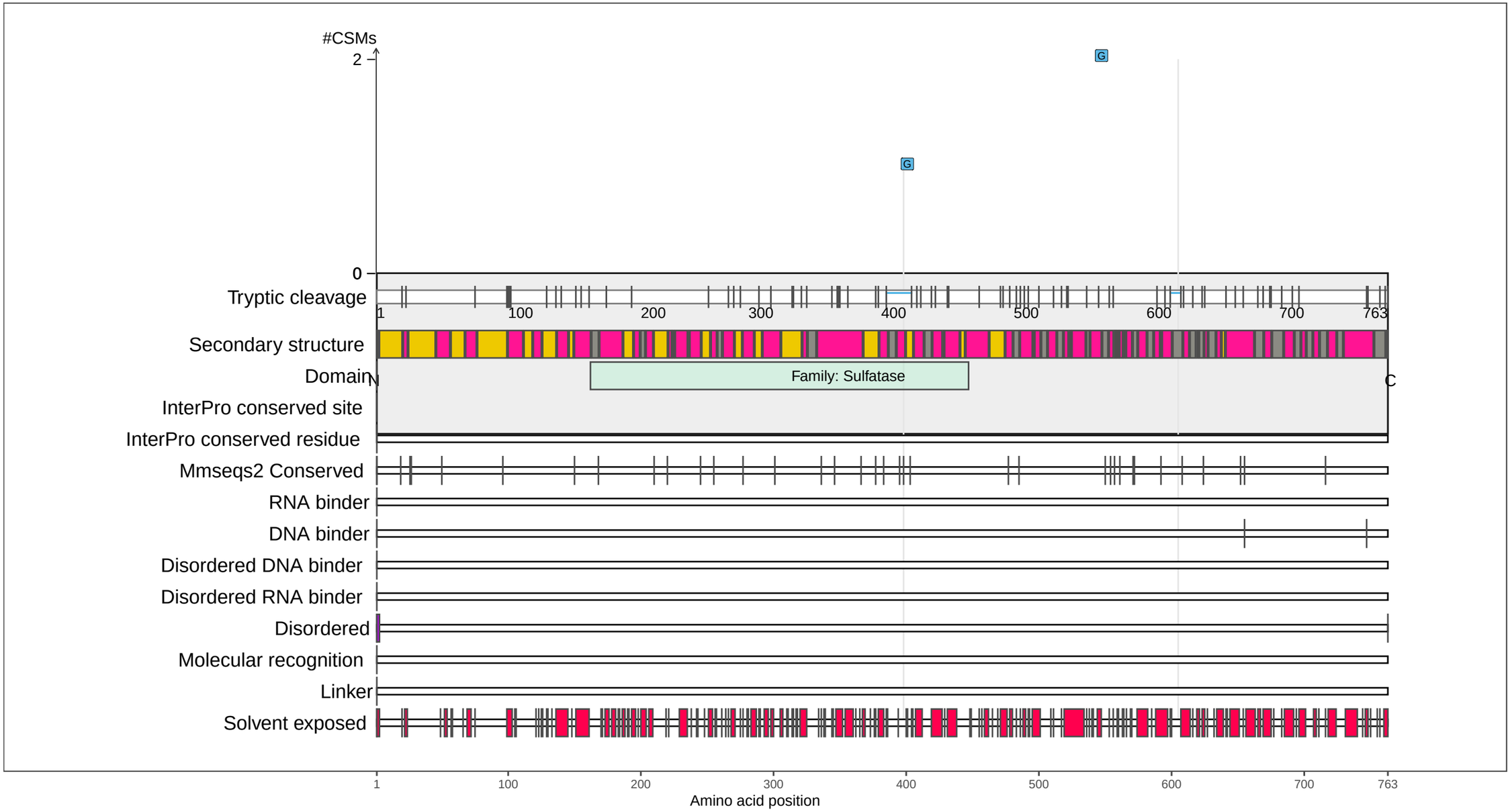
− RNA functions: not annotated

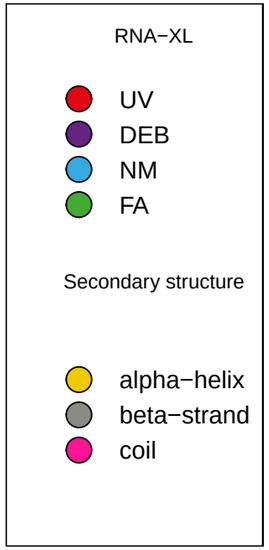


P39401
OPGB_ECOLI Phosphoglycerol transferase I

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 64)
PAXdb K12 strain [ppm]: 1.55 (Q 41)
PAXdb E.coli [ppm]: 0.3 (Q 32)

− RNA functions: not annotated

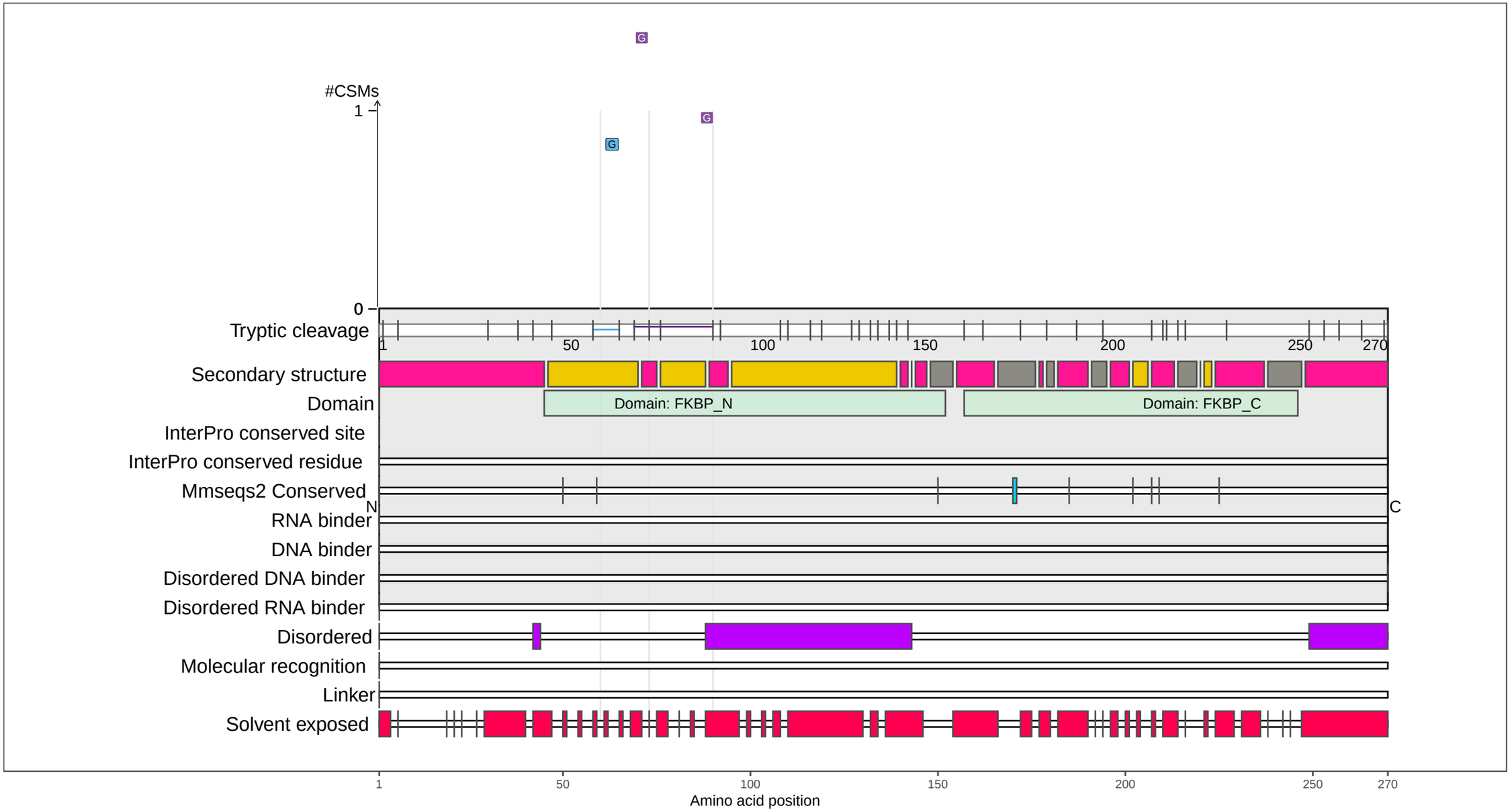




P45523
FKBA_ECOLI FKBP−type peptidyl−prolyl cis−trans isomerase FkpA

− Abundance:
tryptic [log10 Intensity]: 9.51 (Q 97)
PAXdb K12 strain [ppm]: 3.49 (Q 97)
PAXdb E.coli [ppm]: 2.71 (Q 90)

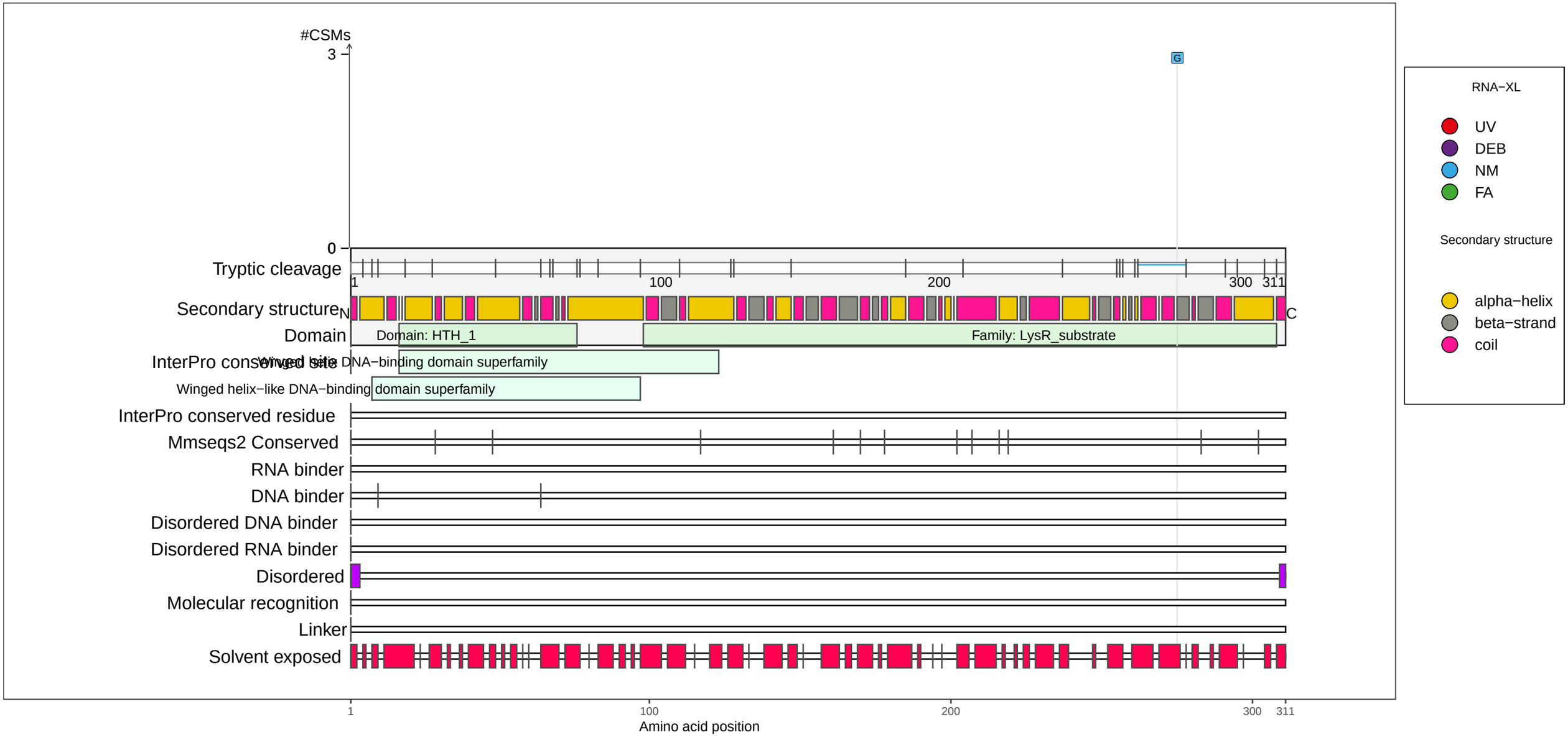
− RNA functions: not annotated



P46068
DSDC_ECOLI HTH−type transcriptional regulator DsdC

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.94 (Q 10)

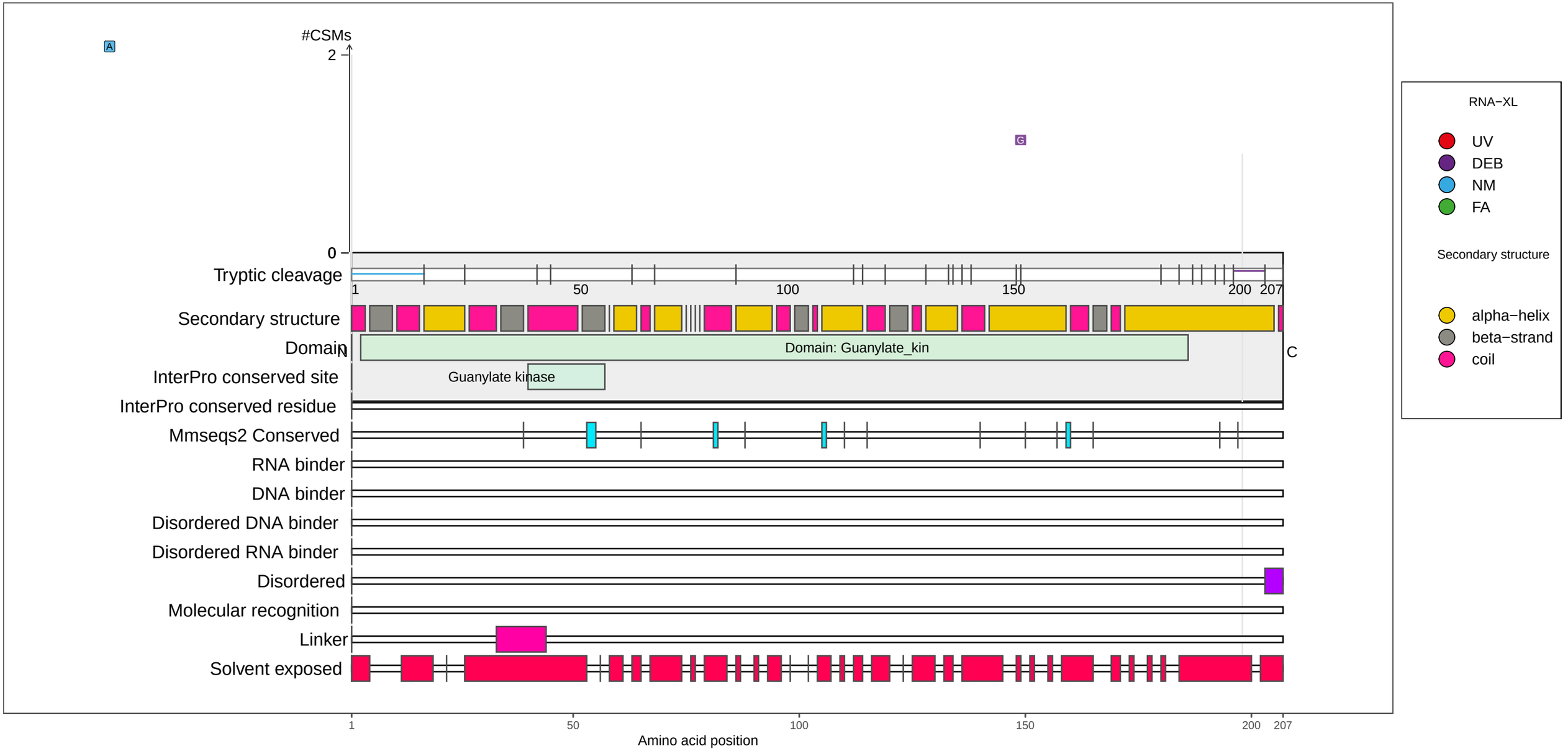
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P60546
KGUA_ECOLI Guanylate kinase

− Abundance:
tryptic [log10 Intensity]: 9.1 (Q 91)
PAXdb K12 strain [ppm]: 2.9 (Q 88)
PAXdb E.coli [ppm]: 2.18 (Q 77)

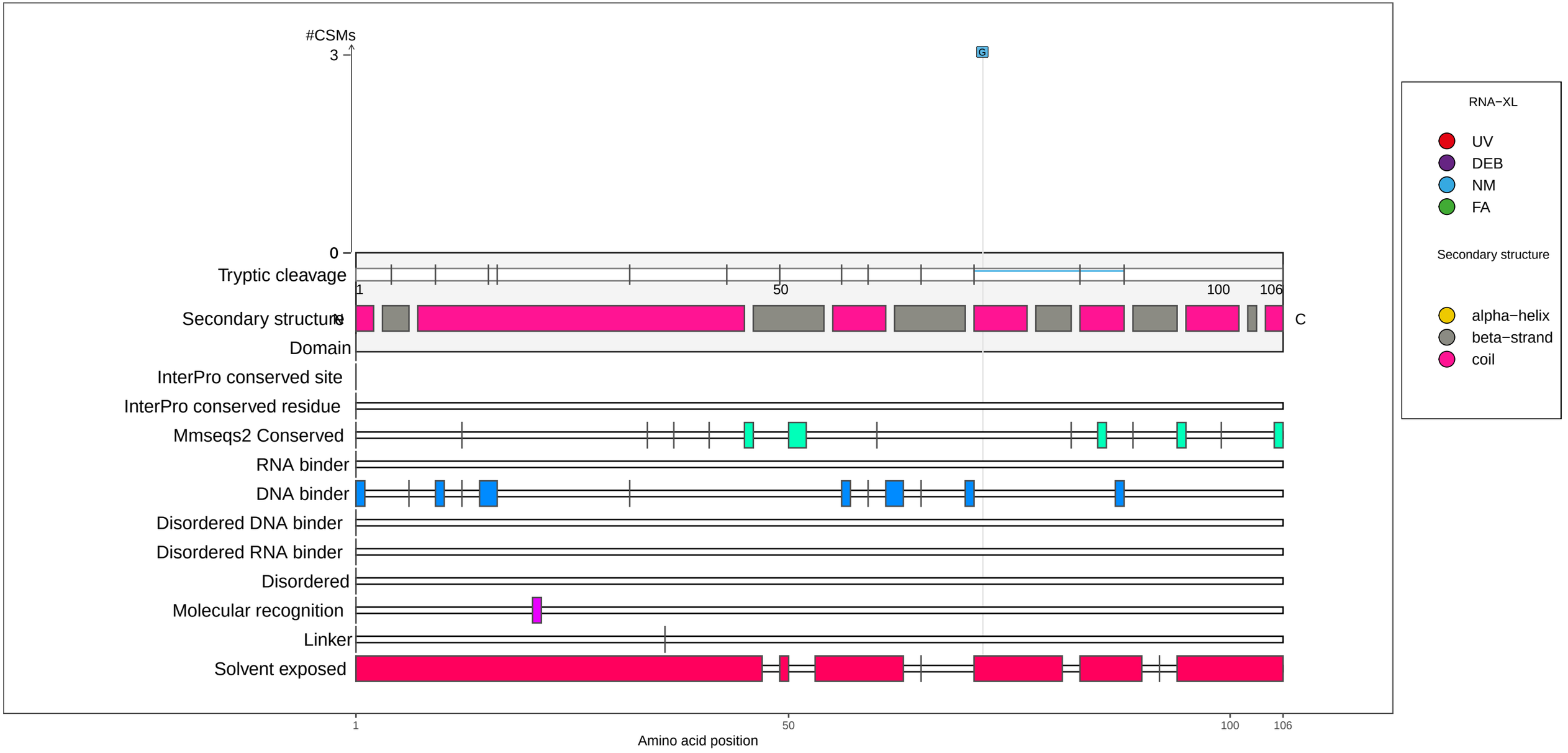
− RNA functions: not annotated



P62066
YCEQ_ECOLI Uncharacterized protein YceQ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.56 (Q 42)
PAXdb E.coli [ppm]: −1.2 (Q 7)

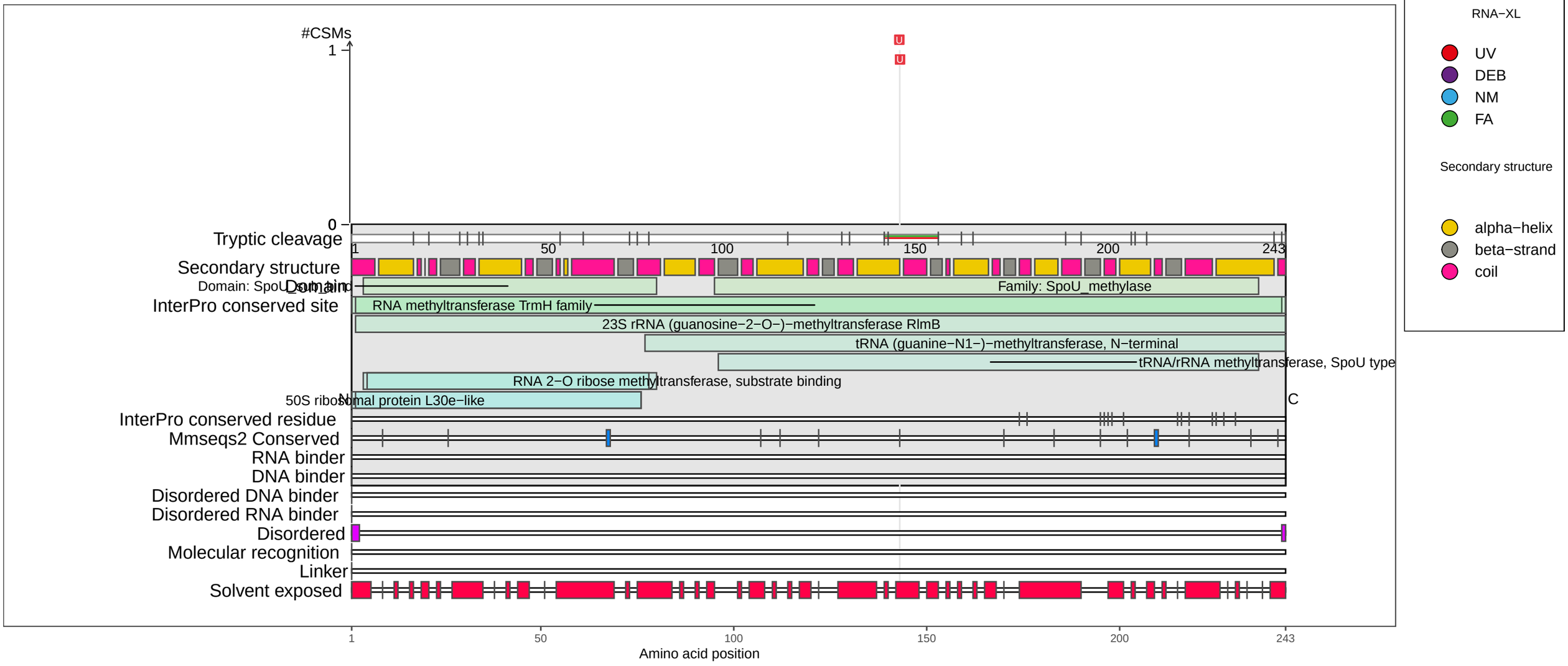
− RNA functions: not annotated



P63177
RLMB_ECOLI 23S rRNA (guanosine−2'−O−)−methyltransferase RlmB

− Abundance:
tryptic [log10 Intensity]: 7.57 (Q 38)
PAXdb K12 strain [ppm]: 2.69 (Q 83)
PAXdb E.coli [ppm]: 1.94 (Q 71)

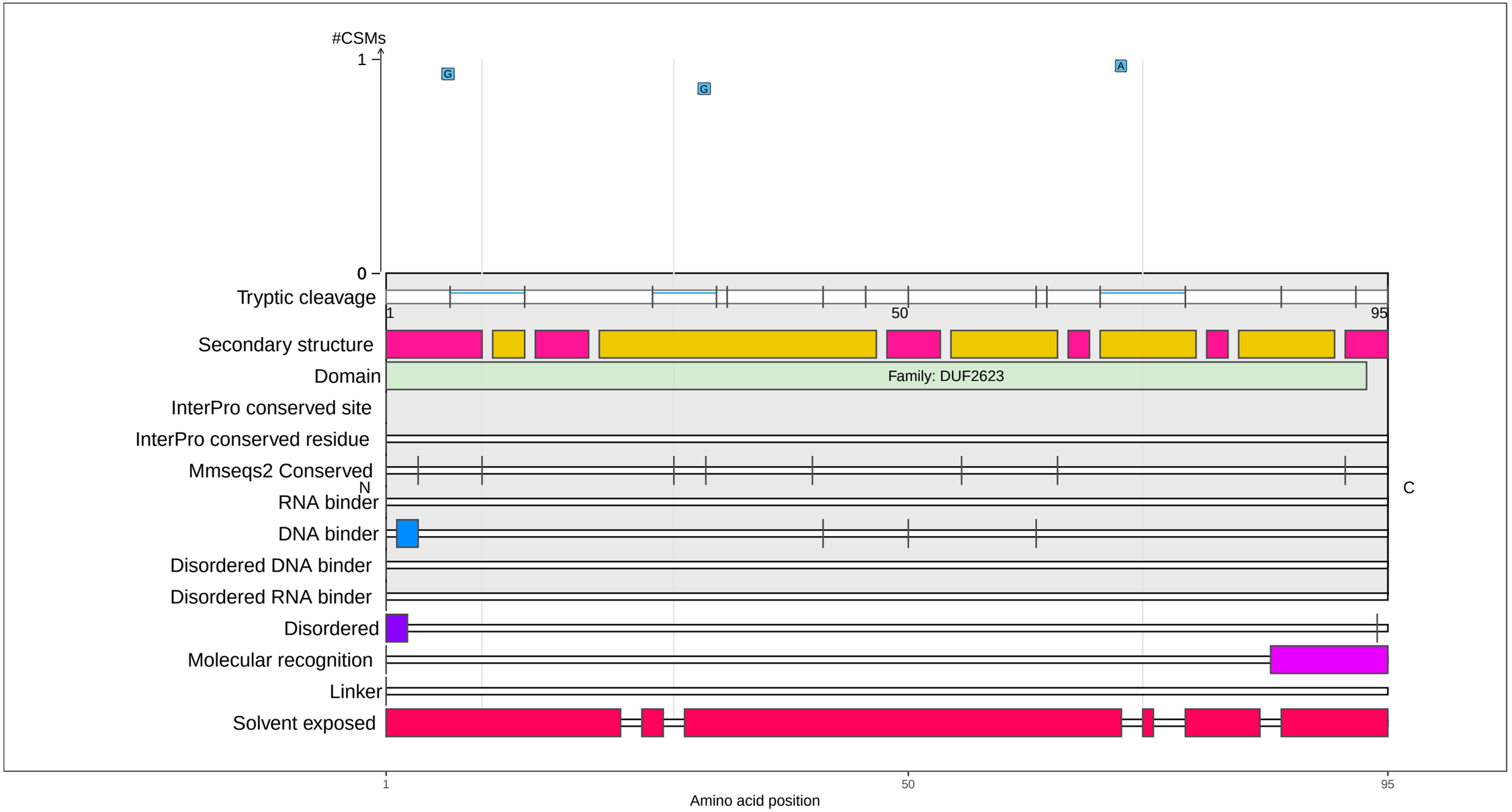
− RNA functions:
ncRNA metabolic process; ncRNA processing
RNA 2−O ribose methyltransferase substrate binding; RNA 2−O−methyltransferase activity; RNA binding; RNA metabolic process
RNA methylation; RNA methyltransferase activity; RNA modification; RNA processing
rRNA (guanine) methyltransferase activity; rRNA (guanosine−2−O−)−methyltransferase activity
rRNA 2−O−methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing; SpoU rRNA Methylase family



P64574
YGHW_ECOLI Uncharacterized protein YghW

− Abundance:
tryptic [log10 Intensity]: 6.93 (Q 11)
PAXdb K12 strain [ppm]: 1.95 (Q 59)
PAXdb E.coli [ppm]: 0.9 (Q 45)

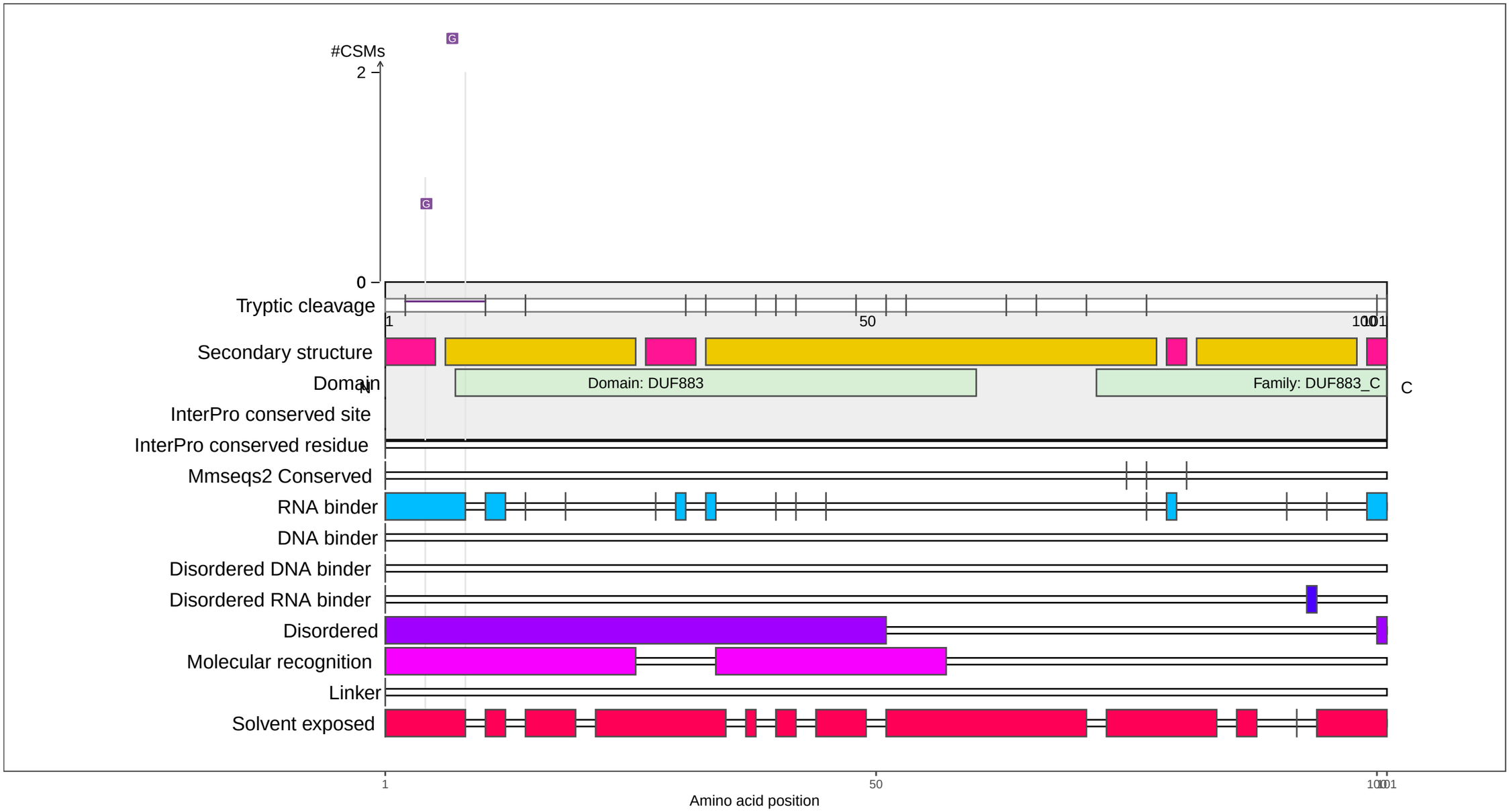
− RNA functions: not annotated

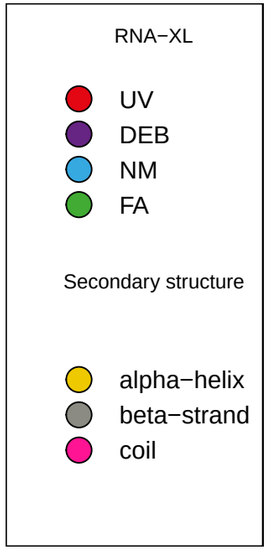


P64581
YQJD_ECOLI Uncharacterized protein YqjD

− Abundance:
tryptic [log10 Intensity]: 8.91 (Q 86)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 3.37 (Q 98)

− RNA functions: not annotated

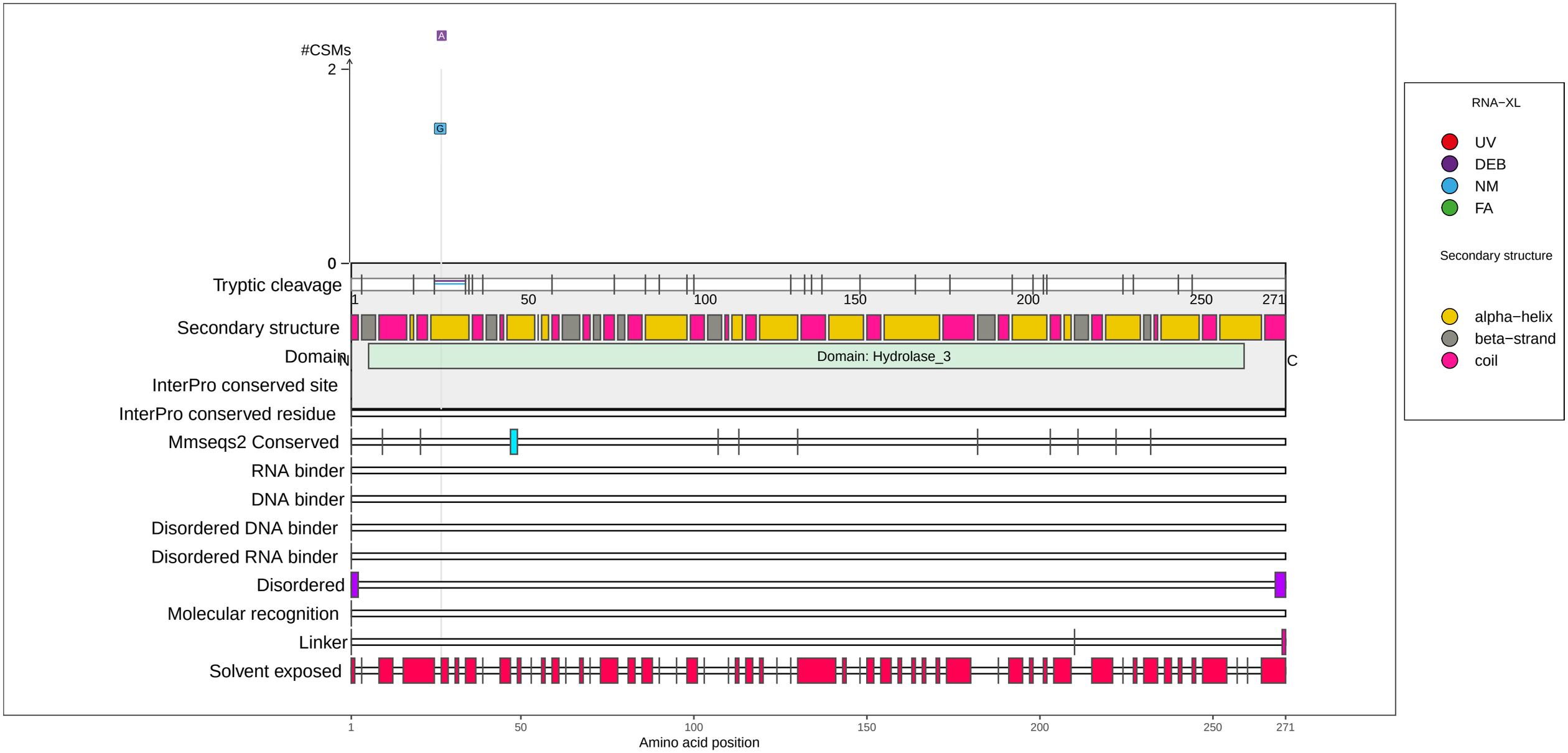




P75792
SUPH_ECOLI Sugar phosphatase YbiV

− Abundance:
tryptic [log10 Intensity]: 7.41 (Q 30)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 1.65 (Q 63)

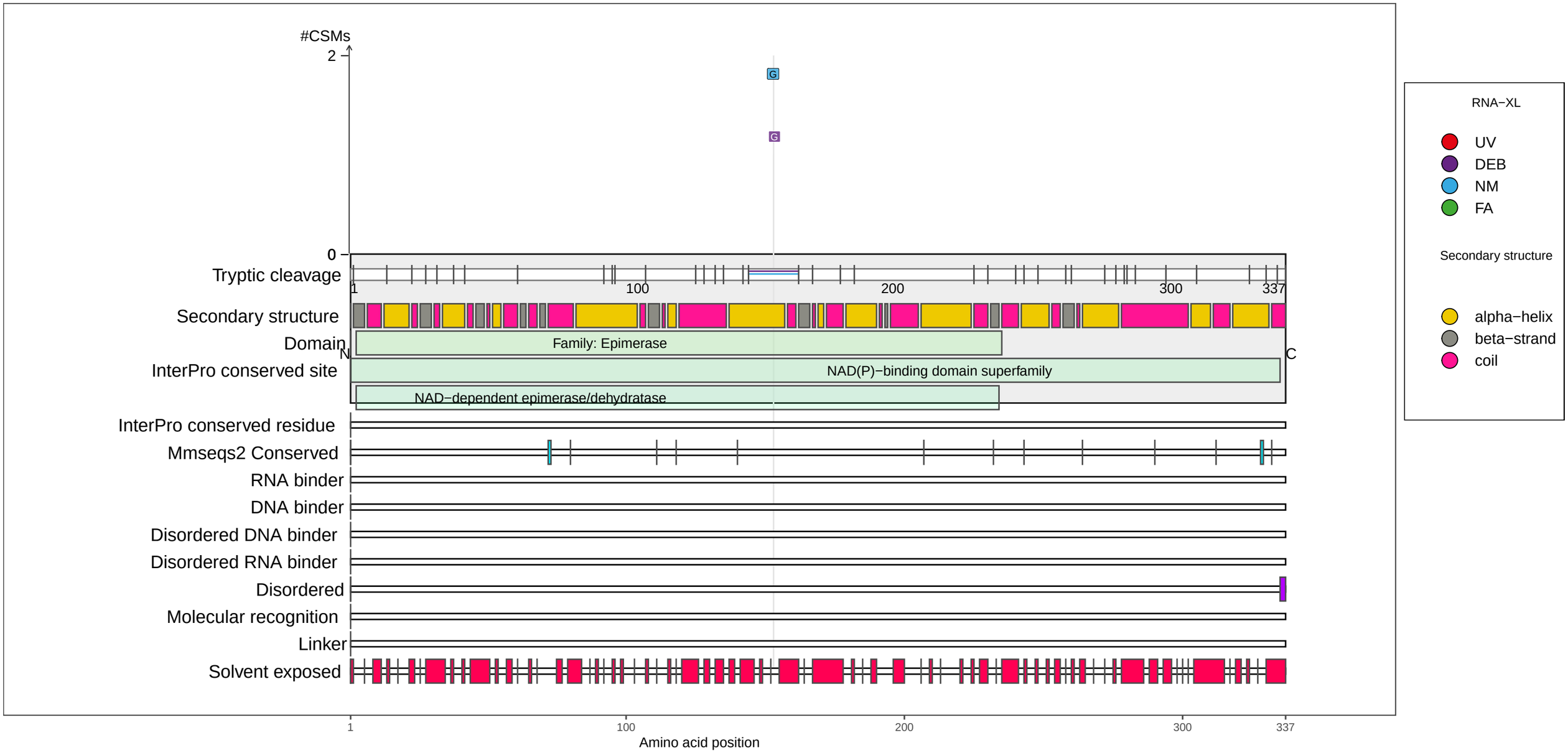
− RNA functions: not annotated



P75821
YBJS_ECOLI Uncharacterized protein YbjS

− Abundance:
tryptic [log10 Intensity]: 6.89 (Q 9)
PAXdb K12 strain [ppm]: 1.35 (Q 29)
PAXdb E.coli [ppm]: 0.62 (Q 39)

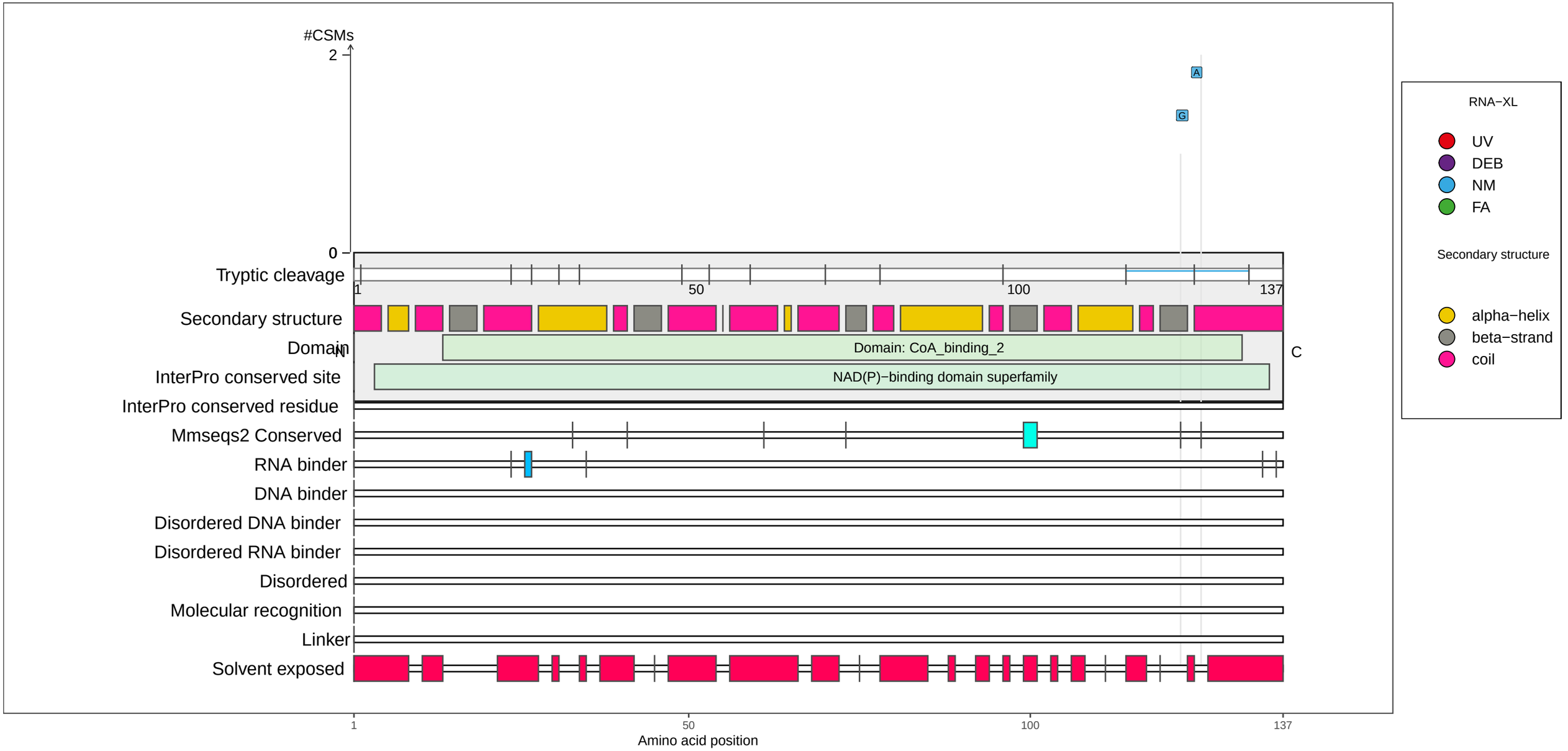
− RNA functions: not annotated



P75874
YCCU_ECOLI Uncharacterized protein YccU

− Abundance:
tryptic [log10 Intensity]: 7.8 (Q 49)
PAXdb K12 strain [ppm]: 2.88 (Q 88)
PAXdb E.coli [ppm]: 2.75 (Q 91)

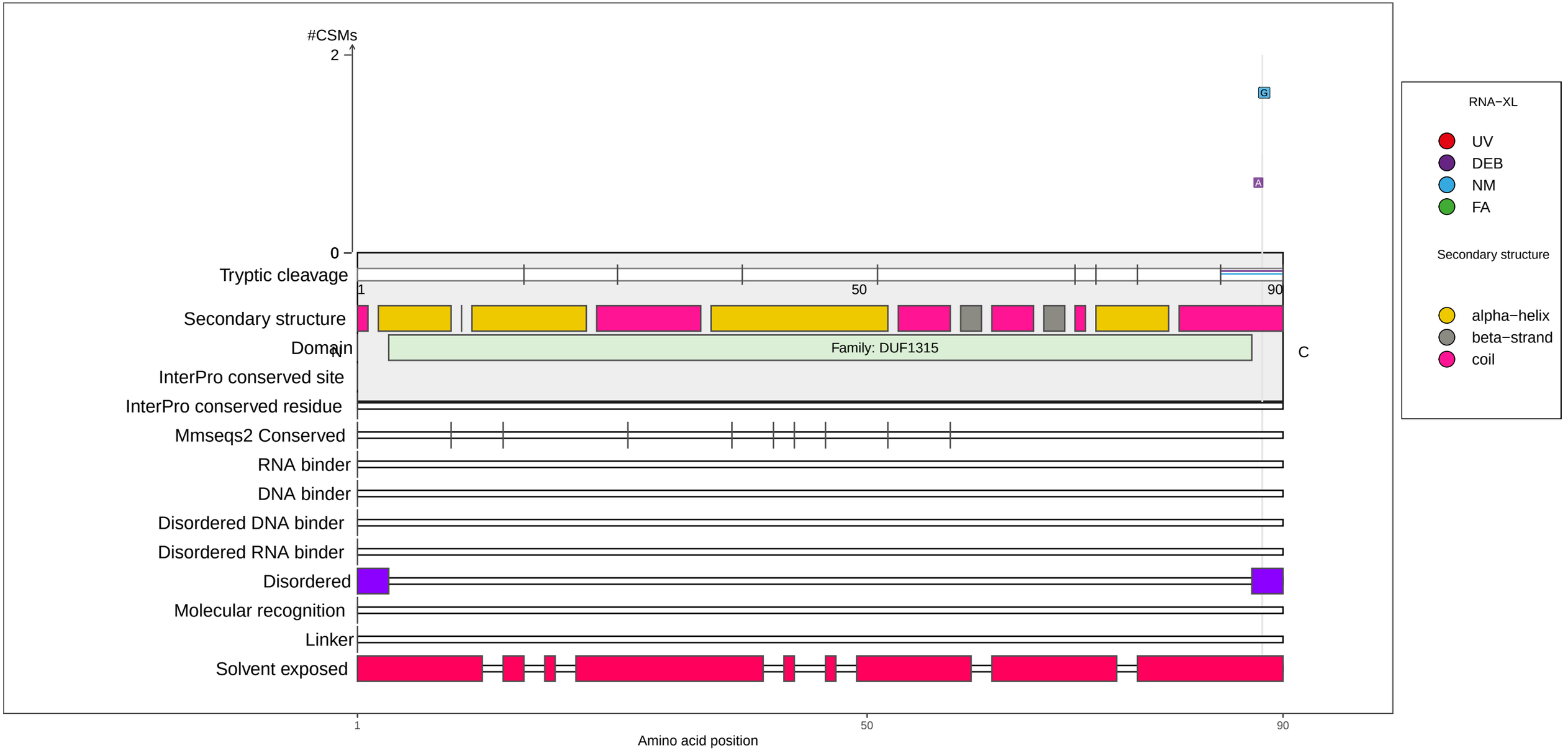
− RNA functions: not annotated



P76231
YEAC_ECOLI Uncharacterized protein YeaC

− Abundance:
tryptic [log10 Intensity]: 7.53 (Q 36)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.68 (Q 64)

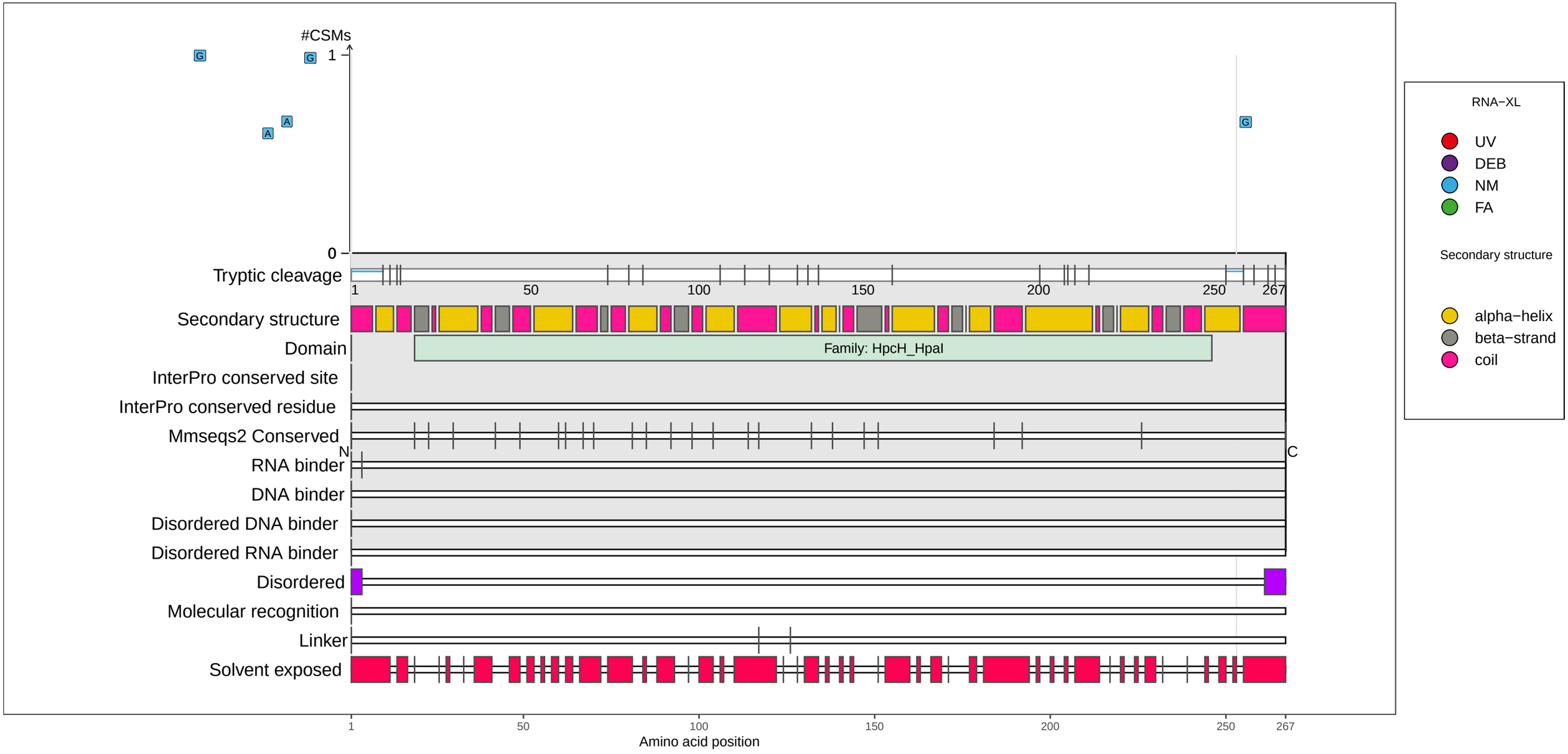
− RNA functions: not annotated



P76469
RHMA_ECOLI 2−keto−3−deoxy−L−rhamnonate aldolase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.1 (Q 27)

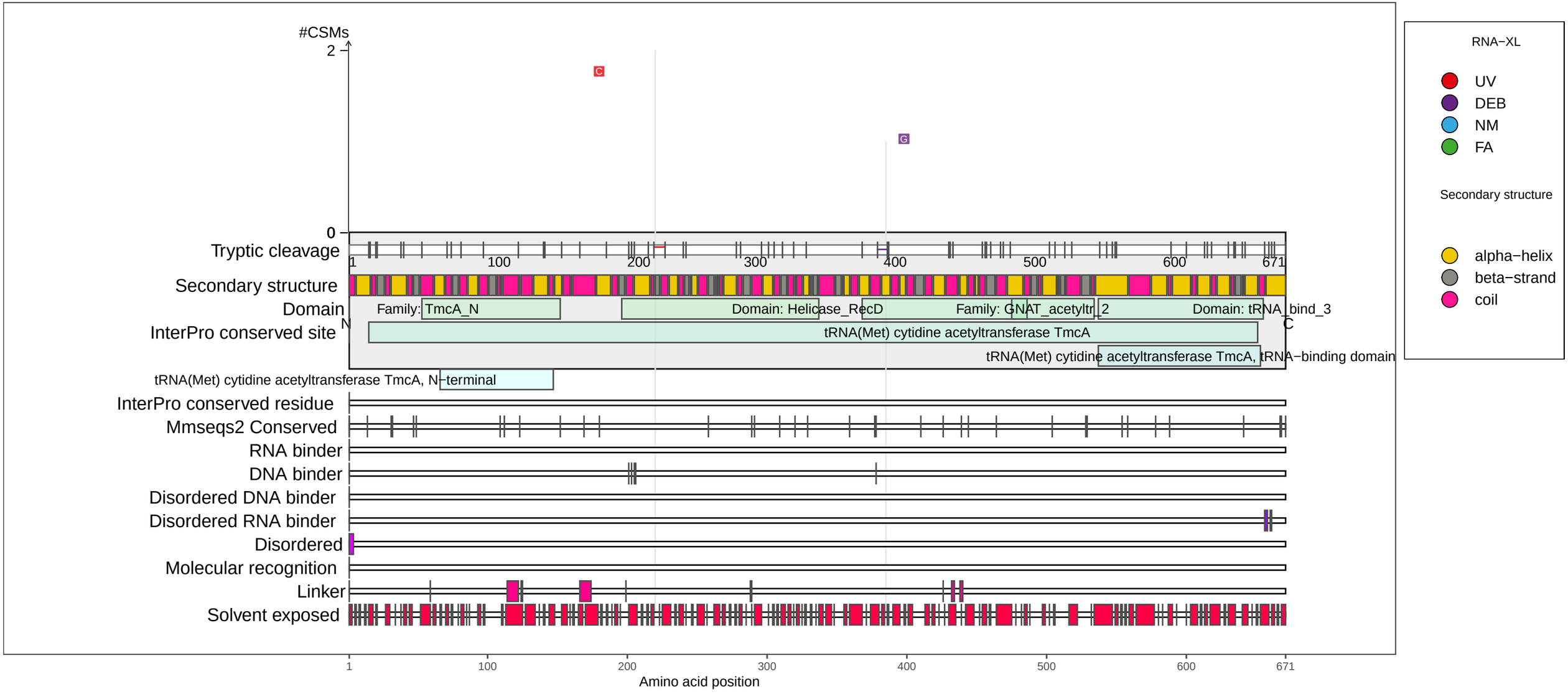
− RNA functions: not annotated



P76562
TMCA_ECOLI tRNA(Met) cytidine acetyltransferase TmcA

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 16)
PAXdb K12 strain [ppm]: 1.76 (Q 52)
PAXdb E.coli [ppm]: 0.76 (Q 42)

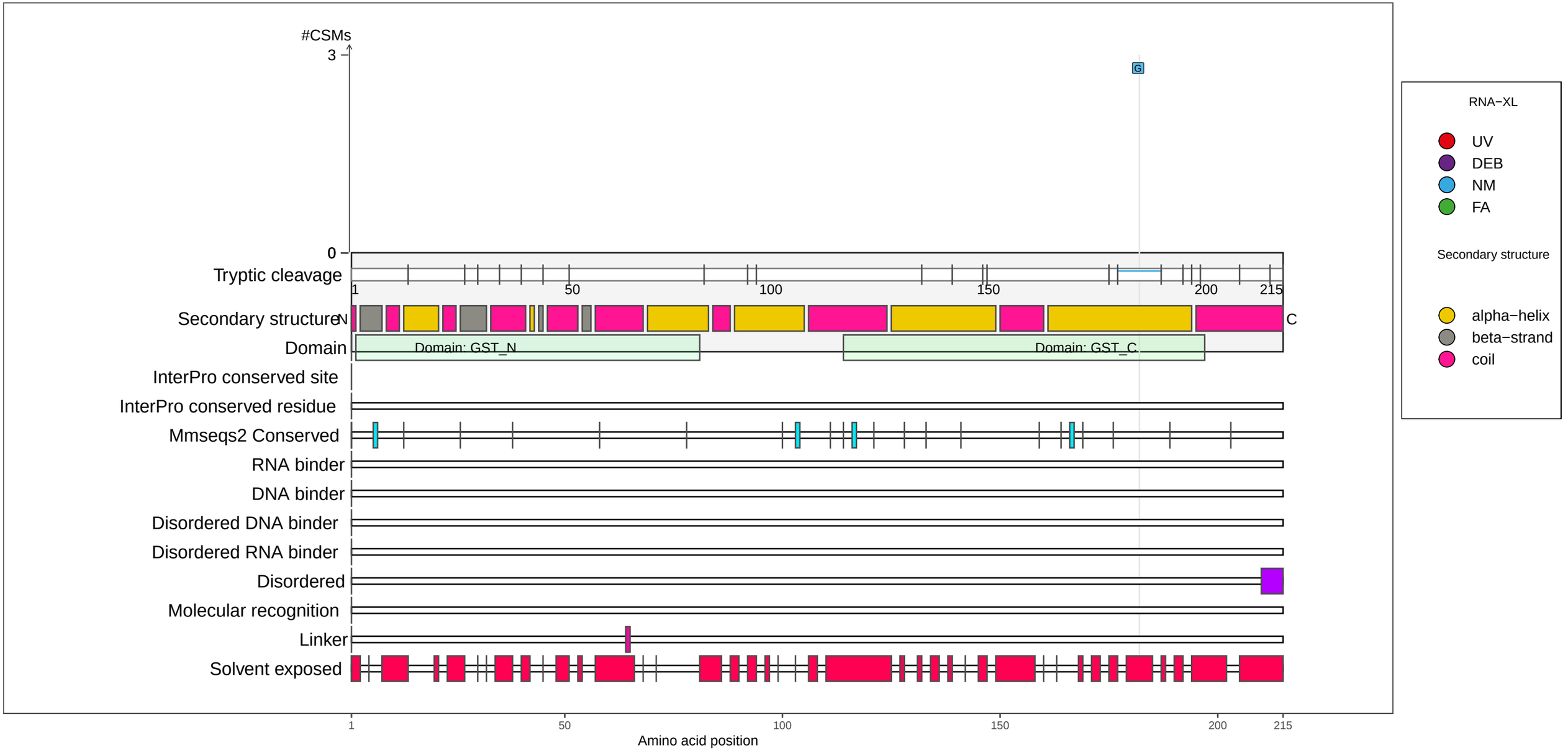
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA acetylation; RNA binding
RNA metabolic process; RNA modification; RNA processing; tRNA acetylation; tRNA binding
tRNA metabolic process; tRNA modification; tRNA N−acetyltransferase activity; tRNA processing
tRNA wobble base modification; tRNA wobble cytosine modification; tRNA−binding domain



P77526
YFCG_ECOLI Disulfide−bond oxidoreductase YfcG

− Abundance:
tryptic [log10 Intensity]: 6.6 (Q 3)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 1.81 (Q 67)

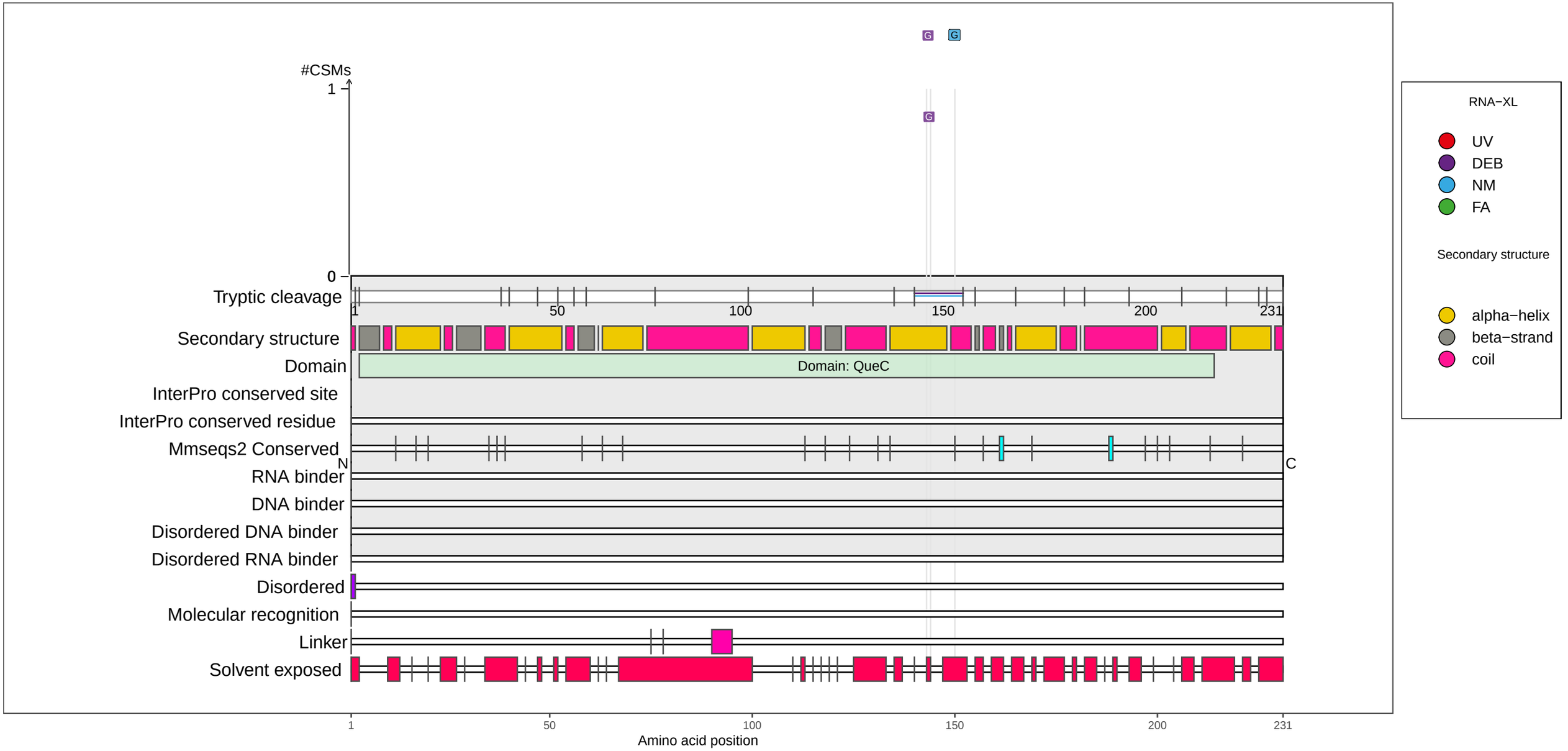
− RNA functions: not annotated



P77756
QUEC_ECOLI 7−cyano−7−deazaguanine synthase

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 55)
PAXdb K12 strain [ppm]: 2.11 (Q 64)
PAXdb E.coli [ppm]: 1.93 (Q 70)

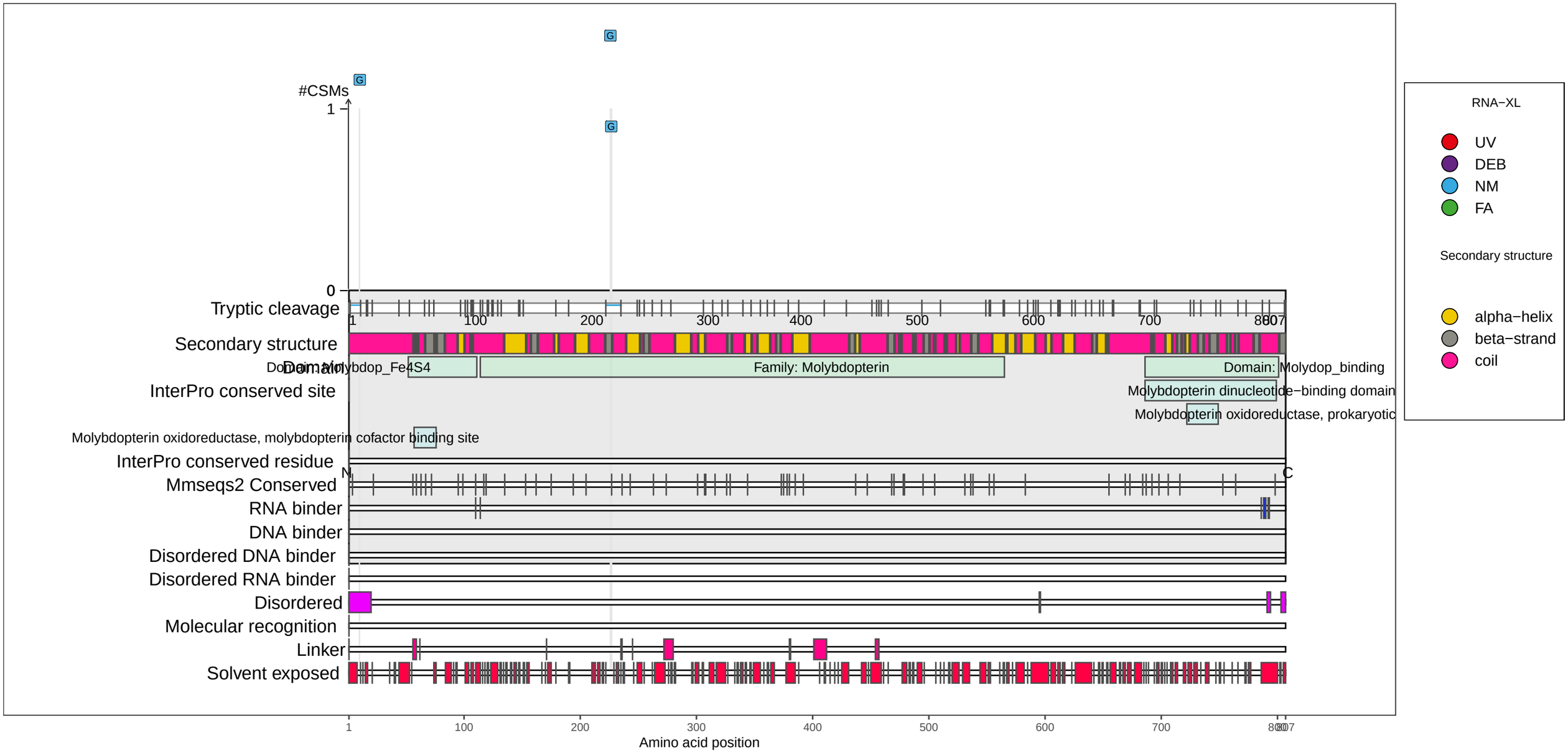
− RNA functions: not annotated



P77783
YNFF_ECOLI Probable dimethyl sulfoxide reductase chain YnfF

− Abundance:
tryptic [log10 Intensity]: 7.79 (Q 48)
PAXdb K12 strain [ppm]: 0.68 (Q 2)
PAXdb E.coli [ppm]: −0.01 (Q 25)

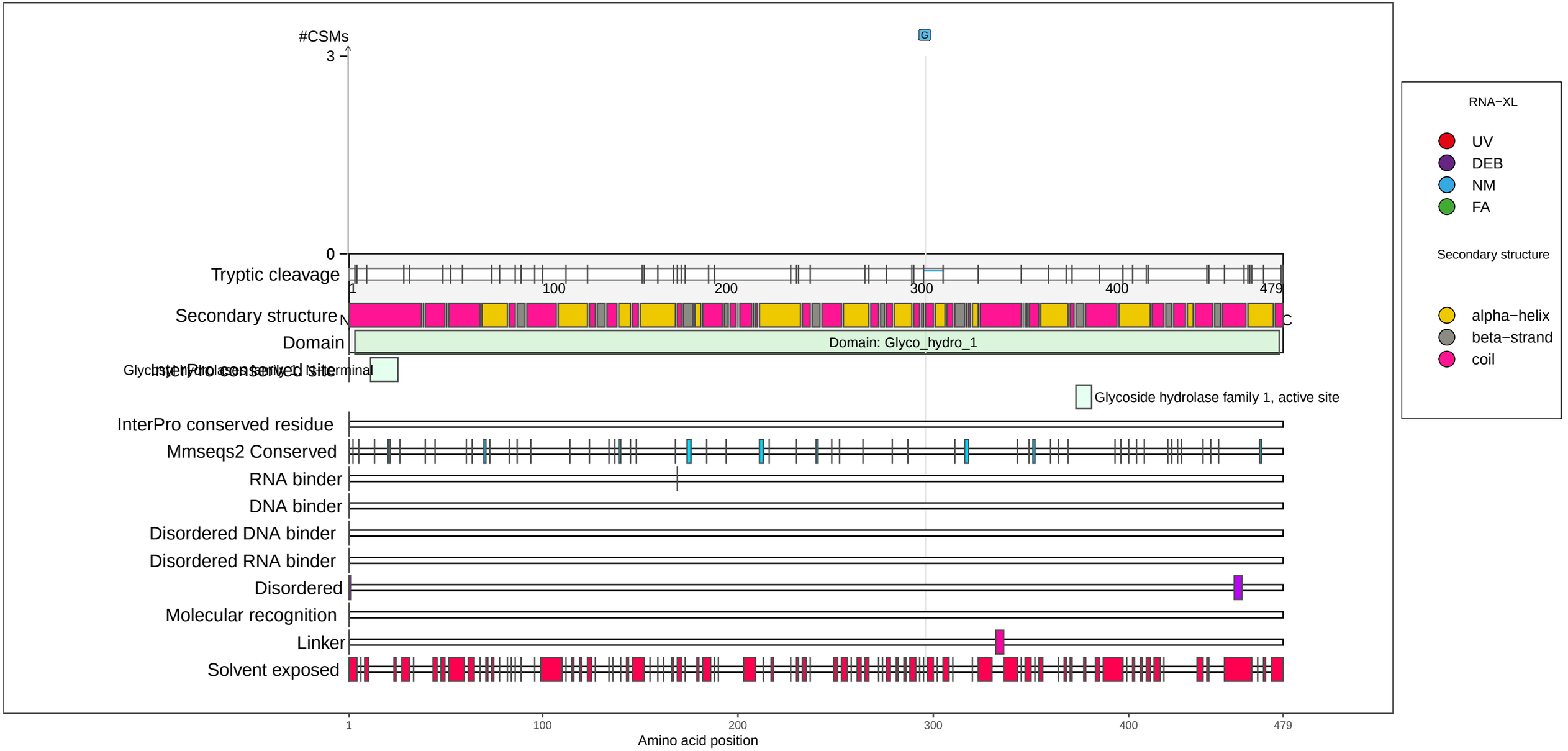
− RNA functions: not annotated



Q46829
BGLA_ECOLI 6−phospho−beta−glucosidase BglA

− Abundance:
tryptic [log10 Intensity]: 9.04 (Q 89)
PAXdb K12 strain [ppm]: 1.68 (Q 48)
PAXdb E.coli [ppm]: 2.3 (Q 80)

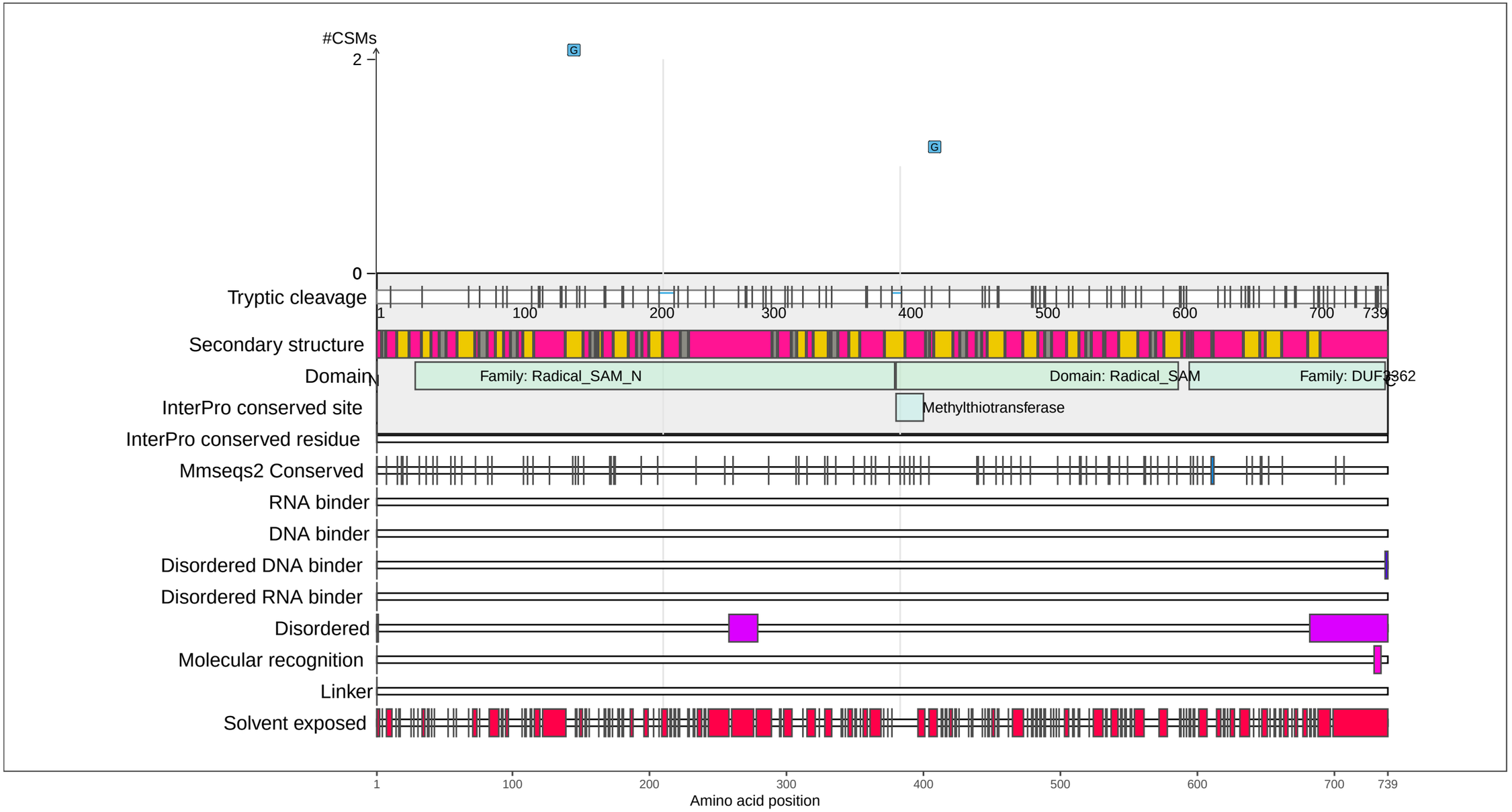
− RNA functions: not annotated

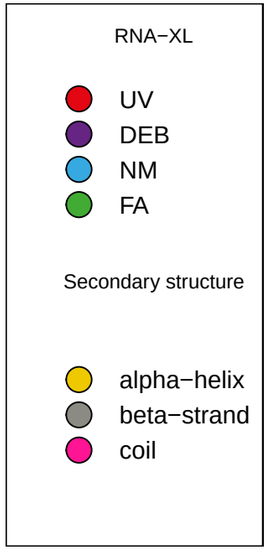


Q46861
YGIQ_ECOLI UPF0313 protein YgiQ

− Abundance:
tryptic [log10 Intensity]: 6.61 (Q 4)
PAXdb K12 strain [ppm]: 0.83 (Q 6)
PAXdb E.coli [ppm]: 0.16 (Q 28)

− RNA functions: not annotated

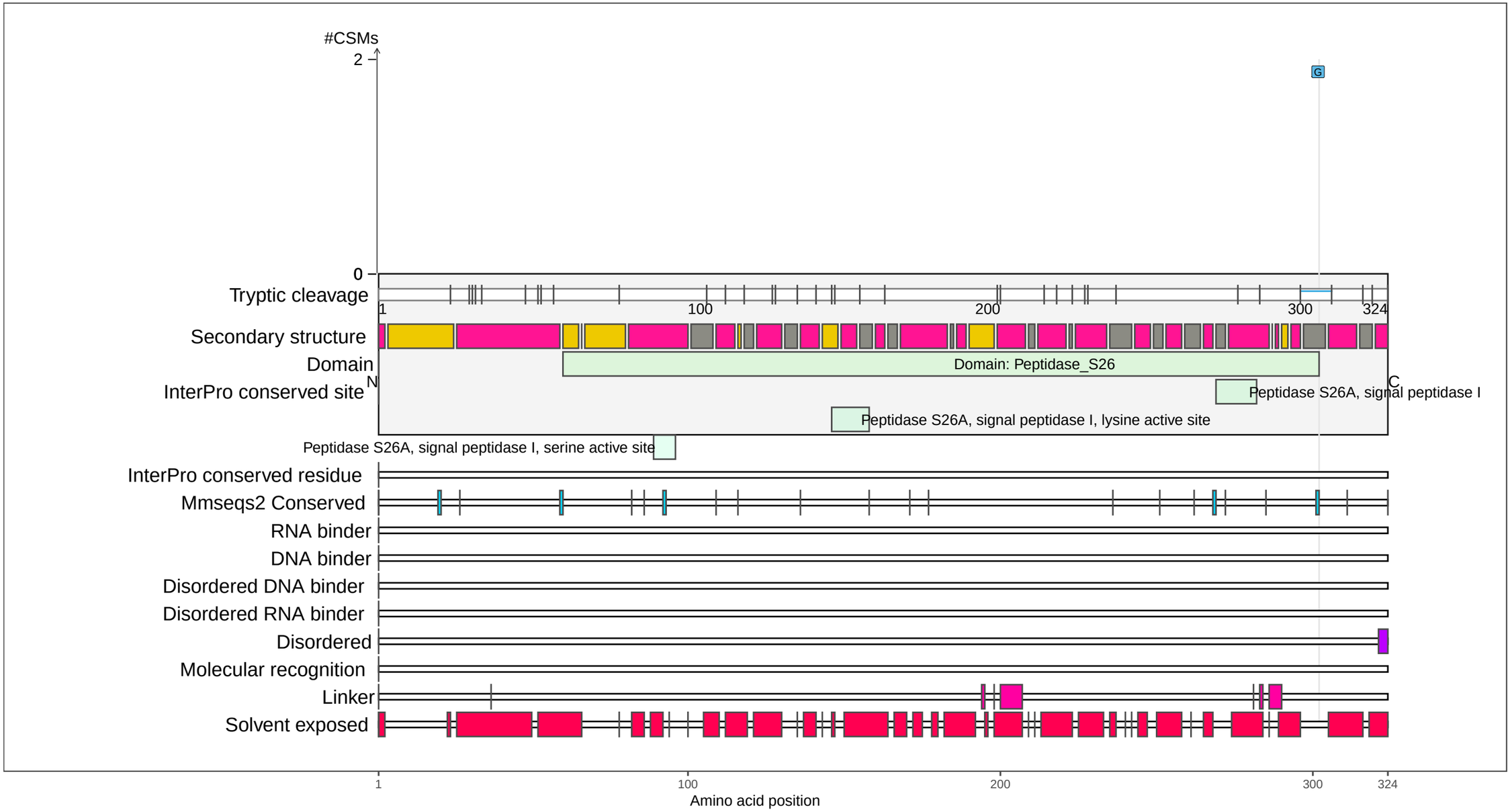




P00803
LEP_ECOLI Signal peptidase I

− Abundance:
tryptic [log10 Intensity]: 8.27 (Q 68)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.85 (Q 68)

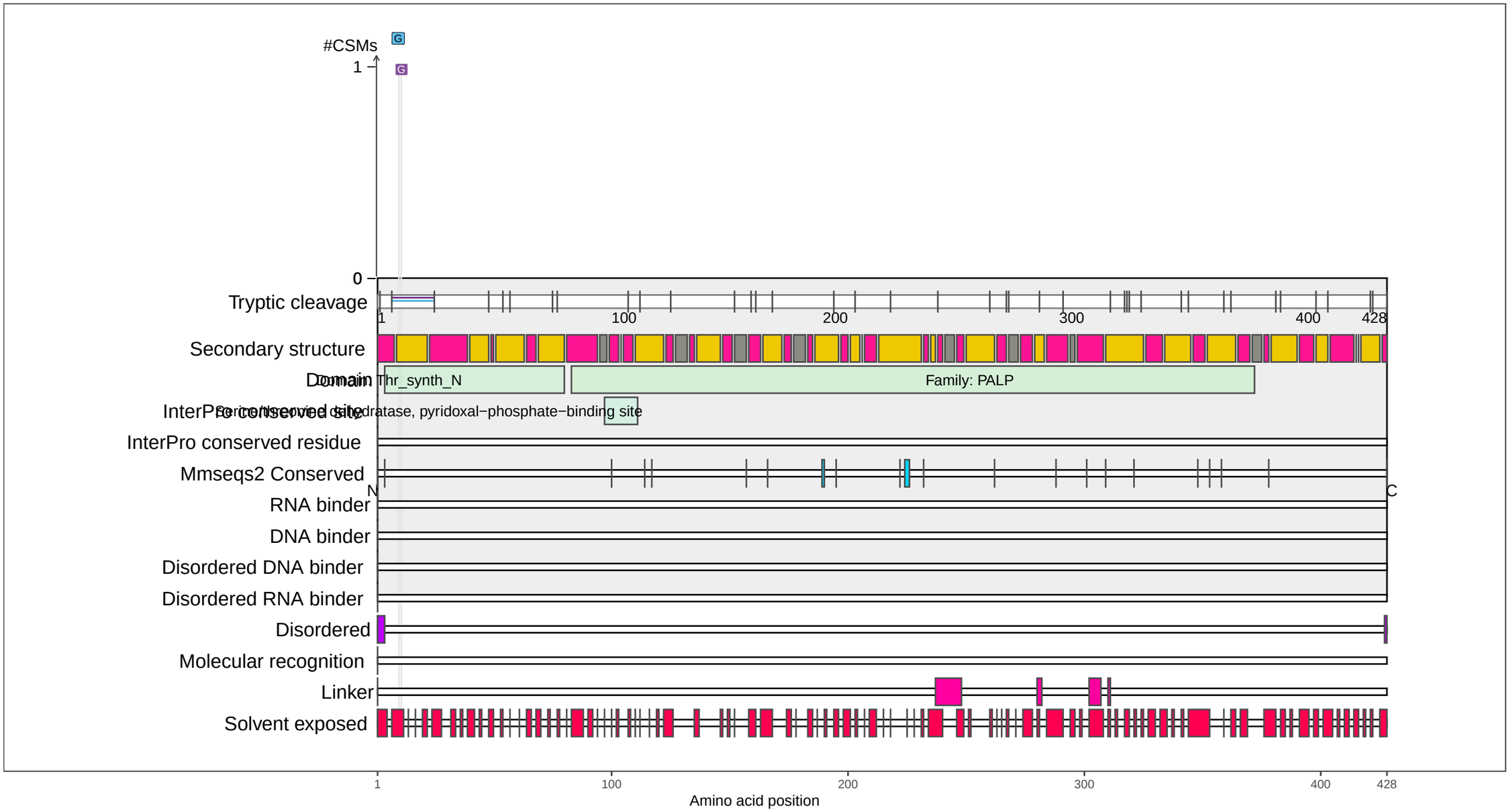
− RNA functions: not annotated



P00934
THRC_ECOLI Threonine synthase

− Abundance:
tryptic [log10 Intensity]: 7.99 (Q 57)
PAXdb K12 strain [ppm]: 2.56 (Q 79)
PAXdb E.coli [ppm]: 2.9 (Q 93)

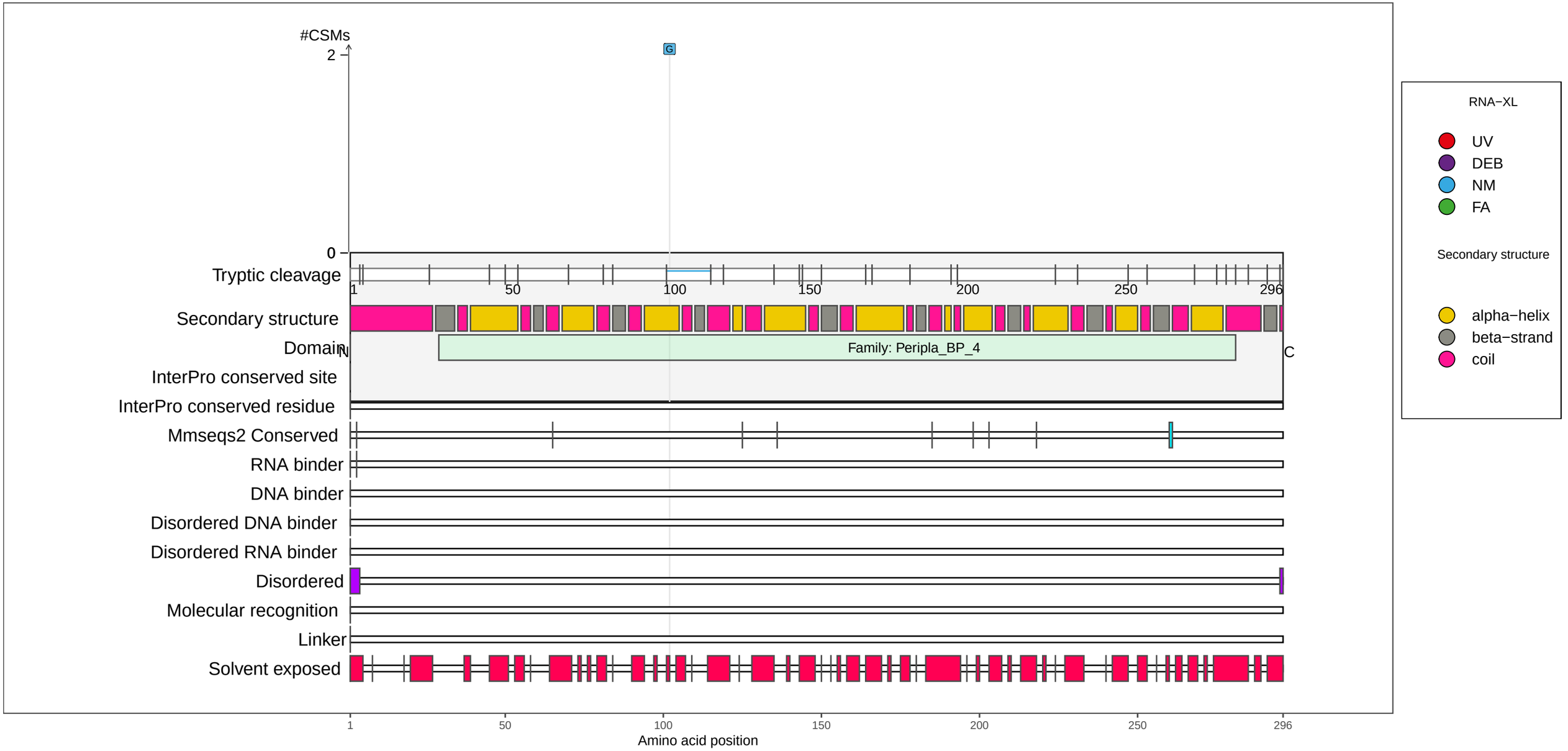
− RNA functions: not annotated



P02925
RBSB_ECOLI Ribose import binding protein RbsB

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 71)
PAXdb K12 strain [ppm]: 3.16 (Q 93)
PAXdb E.coli [ppm]: 3.26 (Q 97)

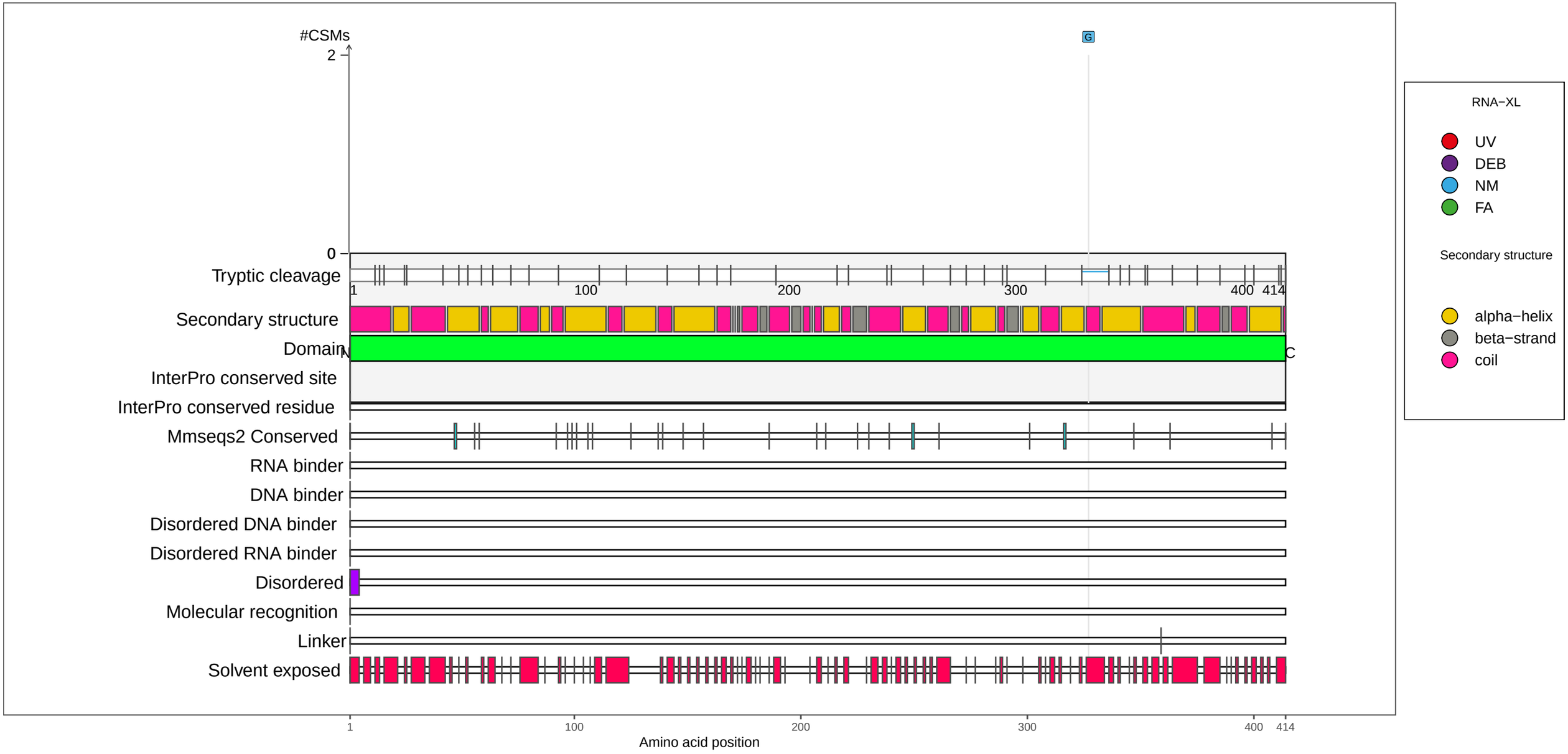
− RNA functions: not annotated



P04335
FRSA_ECOLI Esterase FrsA

− Abundance:
tryptic [log10 Intensity]: 8.73 (Q 82)
PAXdb K12 strain [ppm]: 2.24 (Q 68)
PAXdb E.coli [ppm]: 1.63 (Q 63)

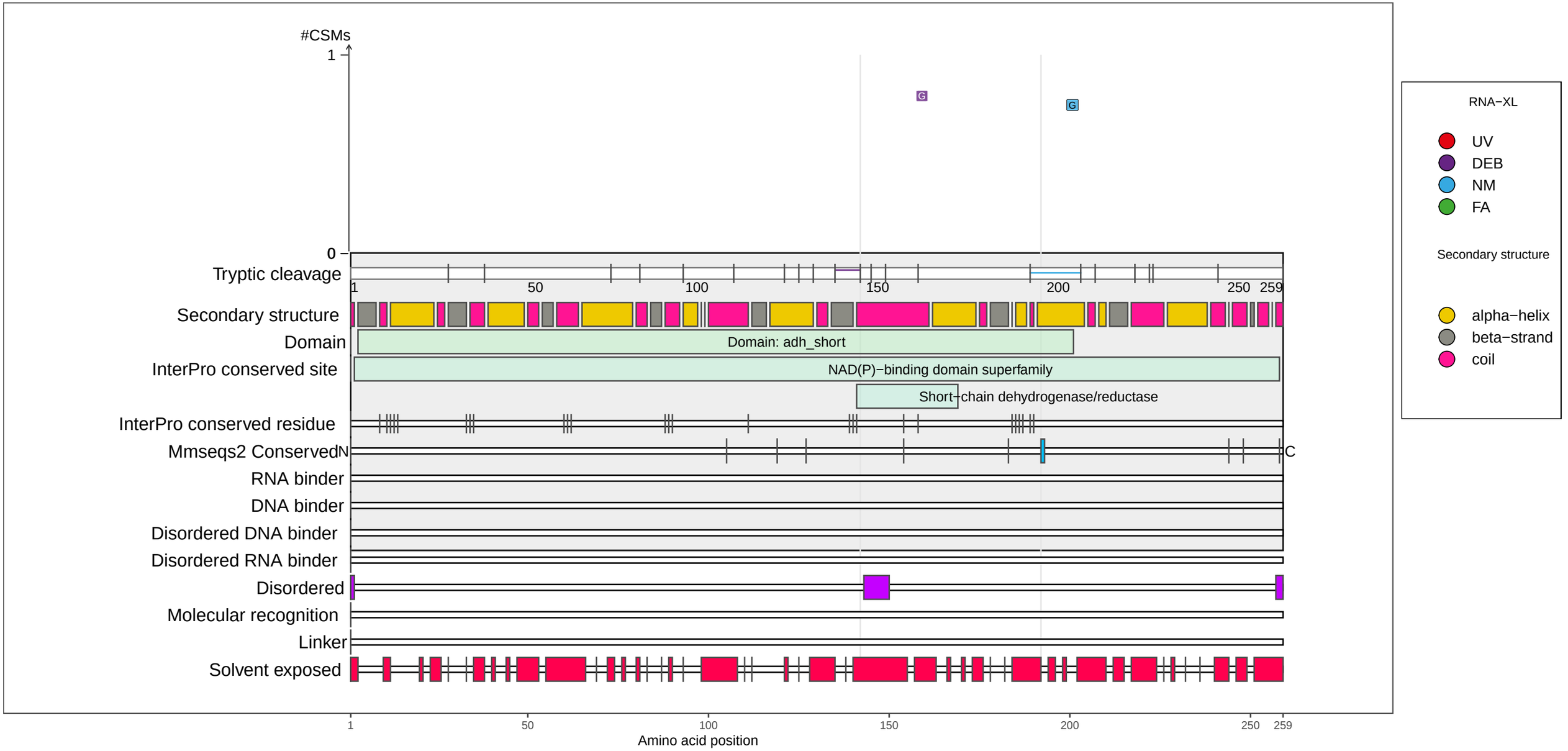
− RNA functions: not annotated



P05707
SRLD_ECOLI Sorbitol−6−phosphate 2−dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 9.06 (Q 90)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.05 (Q 26)

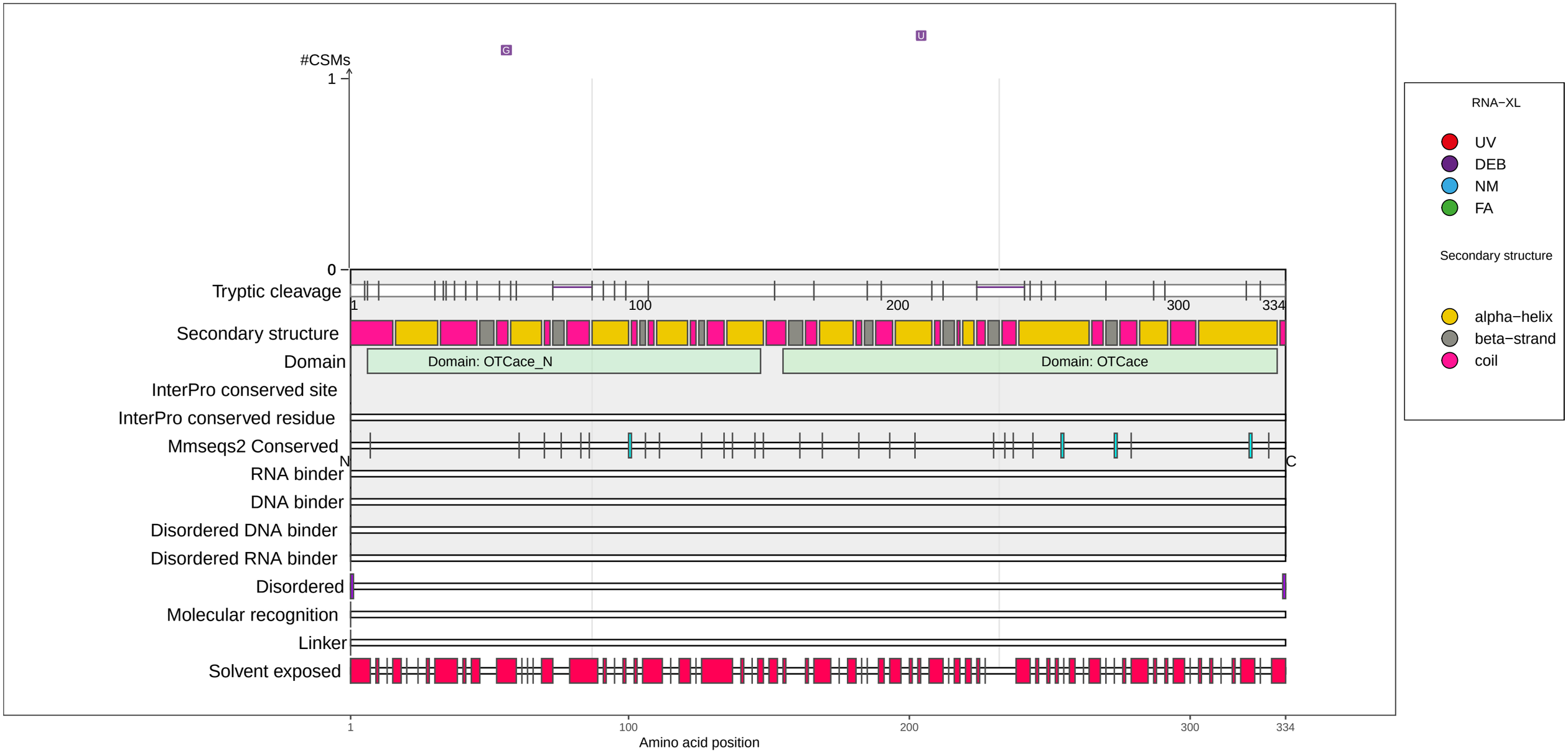
− RNA functions: not annotated



P06960
OTC2_ECOLI Ornithine carbamoyltransferase subunit F

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.43 (Q 1)
PAXdb E.coli [ppm]: 1.41 (Q 57)

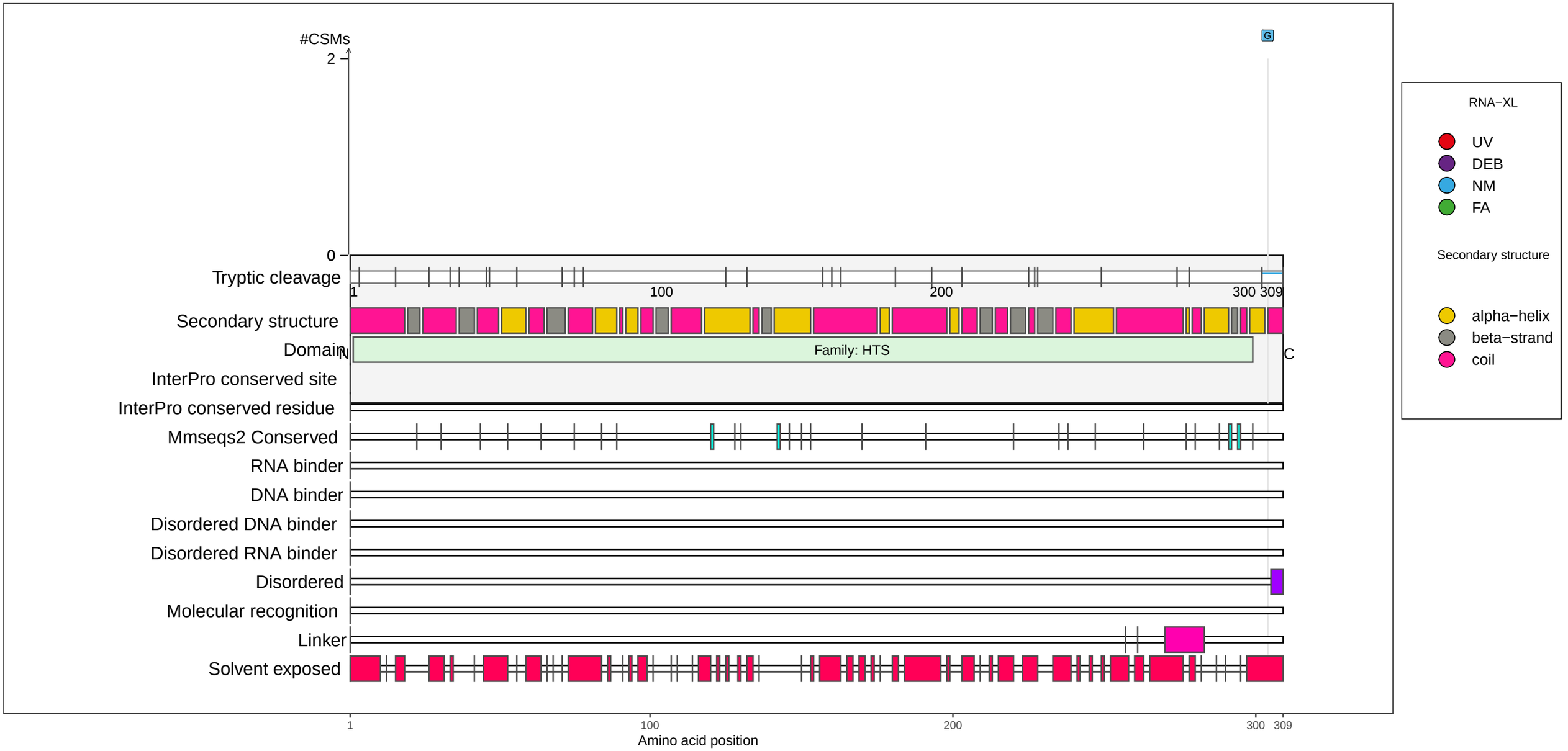
− RNA functions: not annotated



P07623
METAS_ECOLI Homoserine O−succinyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.6 (Q 40)
PAXdb K12 strain [ppm]: 2.12 (Q 65)
PAXdb E.coli [ppm]: 2.19 (Q 77)

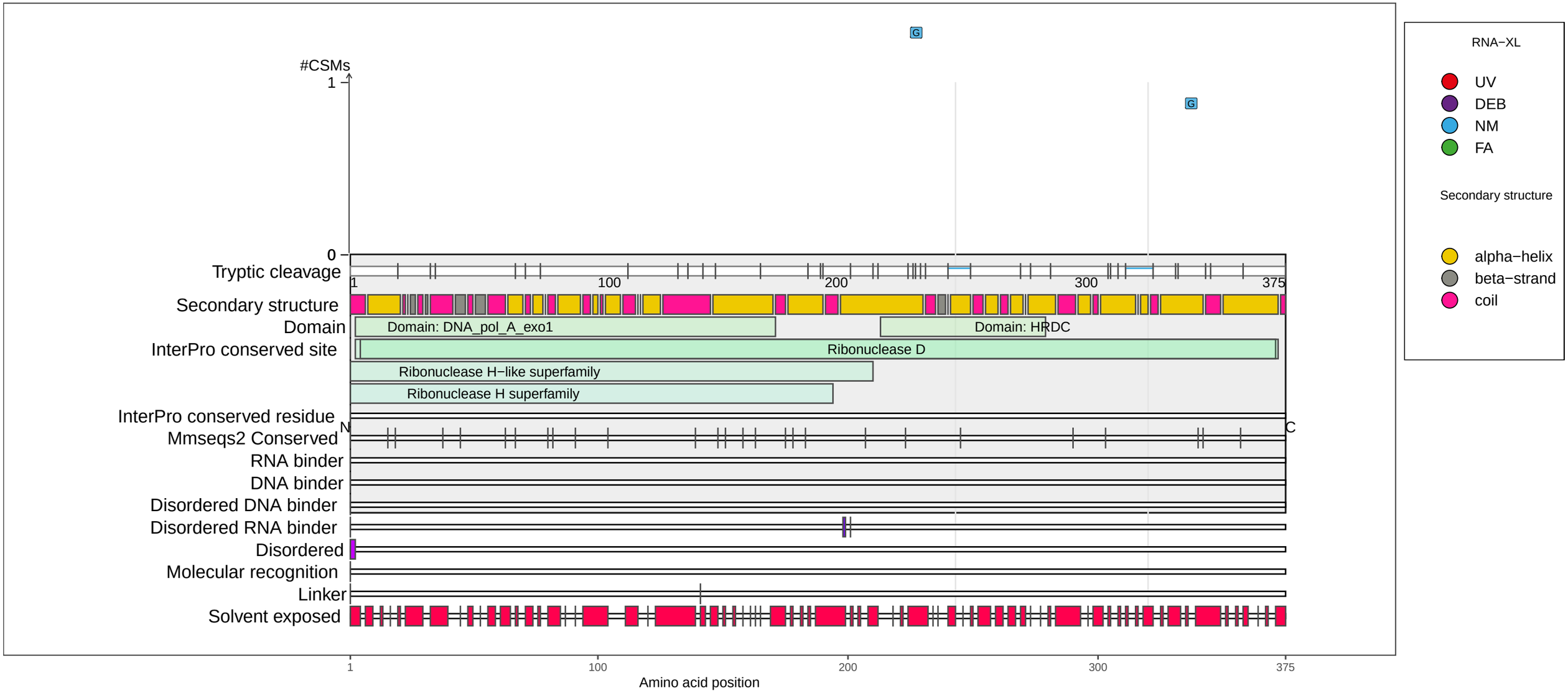
− RNA functions: not annotated



P09155
RND_ECOLI Ribonuclease D

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.92 (Q 58)
PAXdb E.coli [ppm]: 1.09 (Q 50)

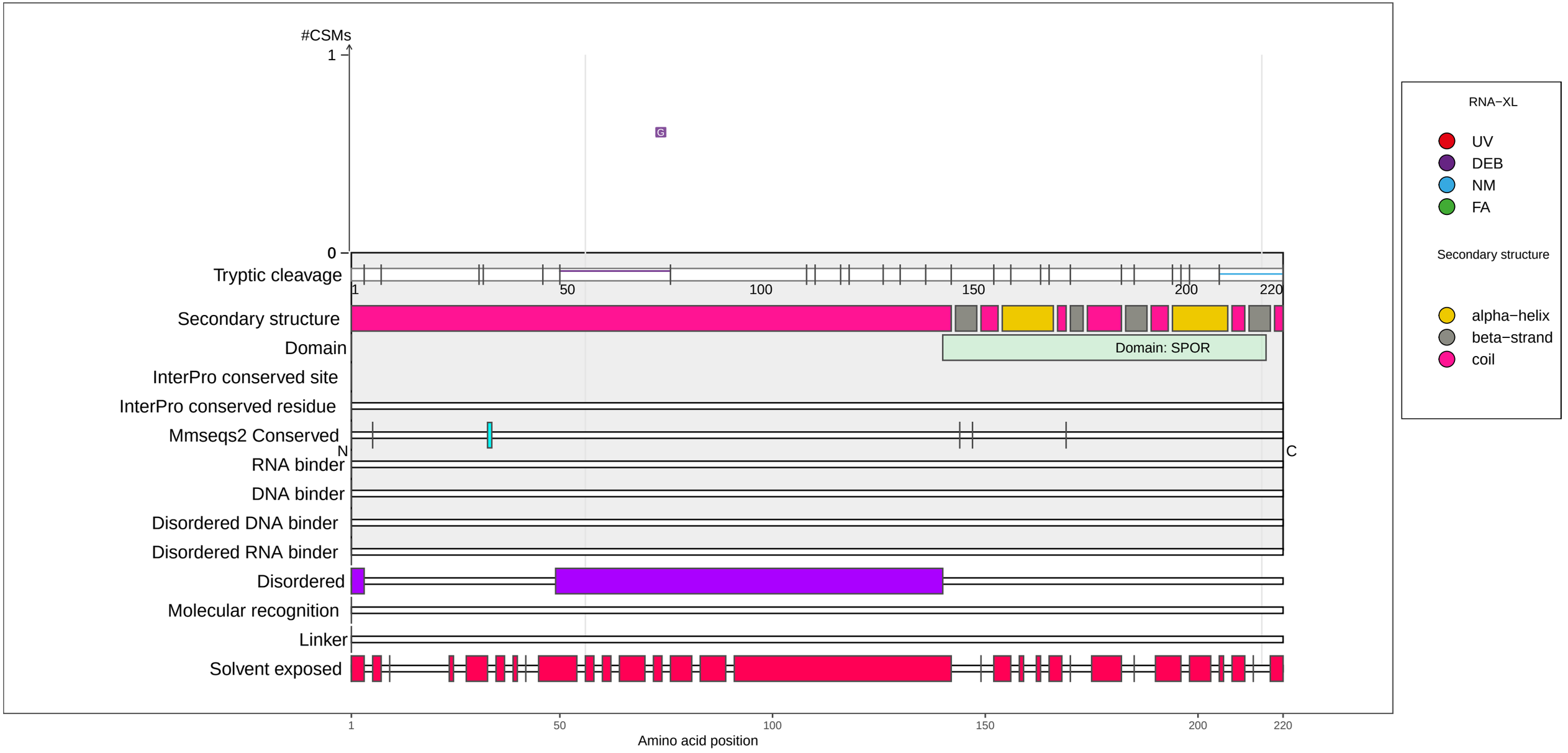
− RNA functions:
ncRNA 3−end processing; ncRNA metabolic process; ncRNA processing
RNA 3−end processing; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, exonucleolytic; RNA processing; tRNA 3−end processing
tRNA metabolic process; tRNA processing



P09549
DEDD_ECOLI Cell division protein DedD

− Abundance:
tryptic [log10 Intensity]: 7.42 (Q 31)
PAXdb K12 strain [ppm]: 2.61 (Q 81)
PAXdb E.coli [ppm]: 1.35 (Q 56)

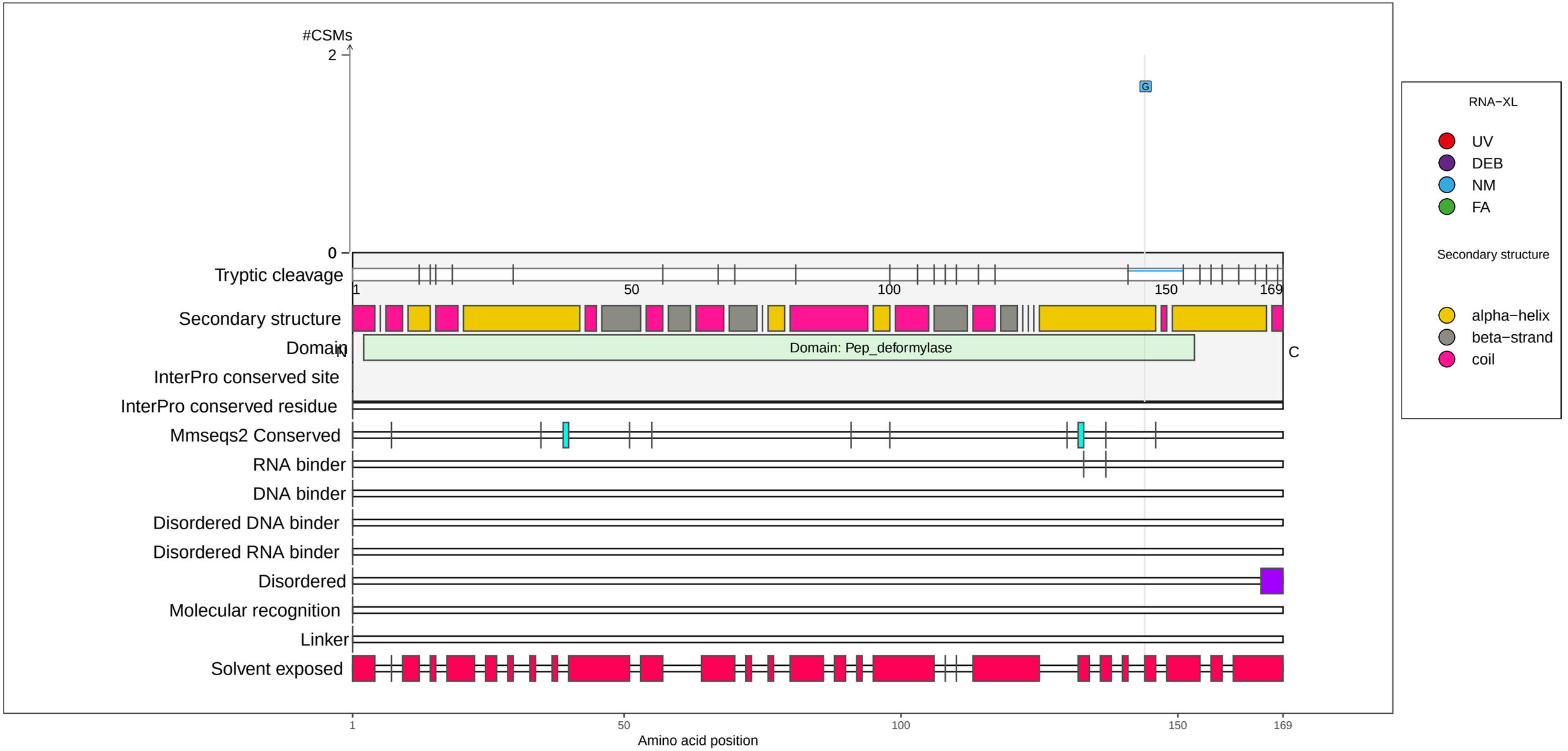
− RNA functions: not annotated



P0A6K3
DEF_ECOLI Peptide deformylase

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 3.14 (Q 93)
PAXdb E.coli [ppm]: 2.55 (Q 87)

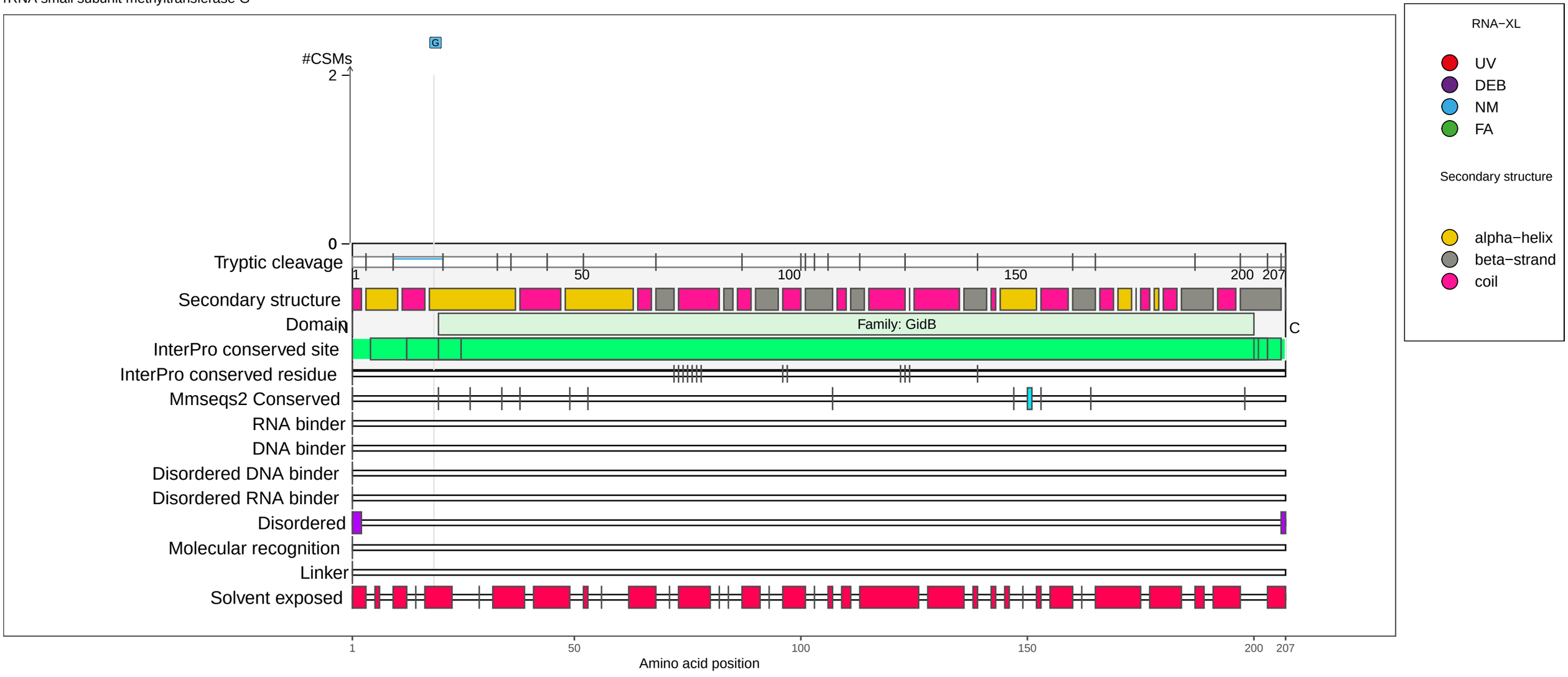
− RNA functions: not annotated



P0A6U5
RSMG_ECOLI Ribosomal RNA small subunit methyltransferase G

− Abundance:
tryptic [log10 Intensity]: 7.73 (Q 46)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.63 (Q 63)

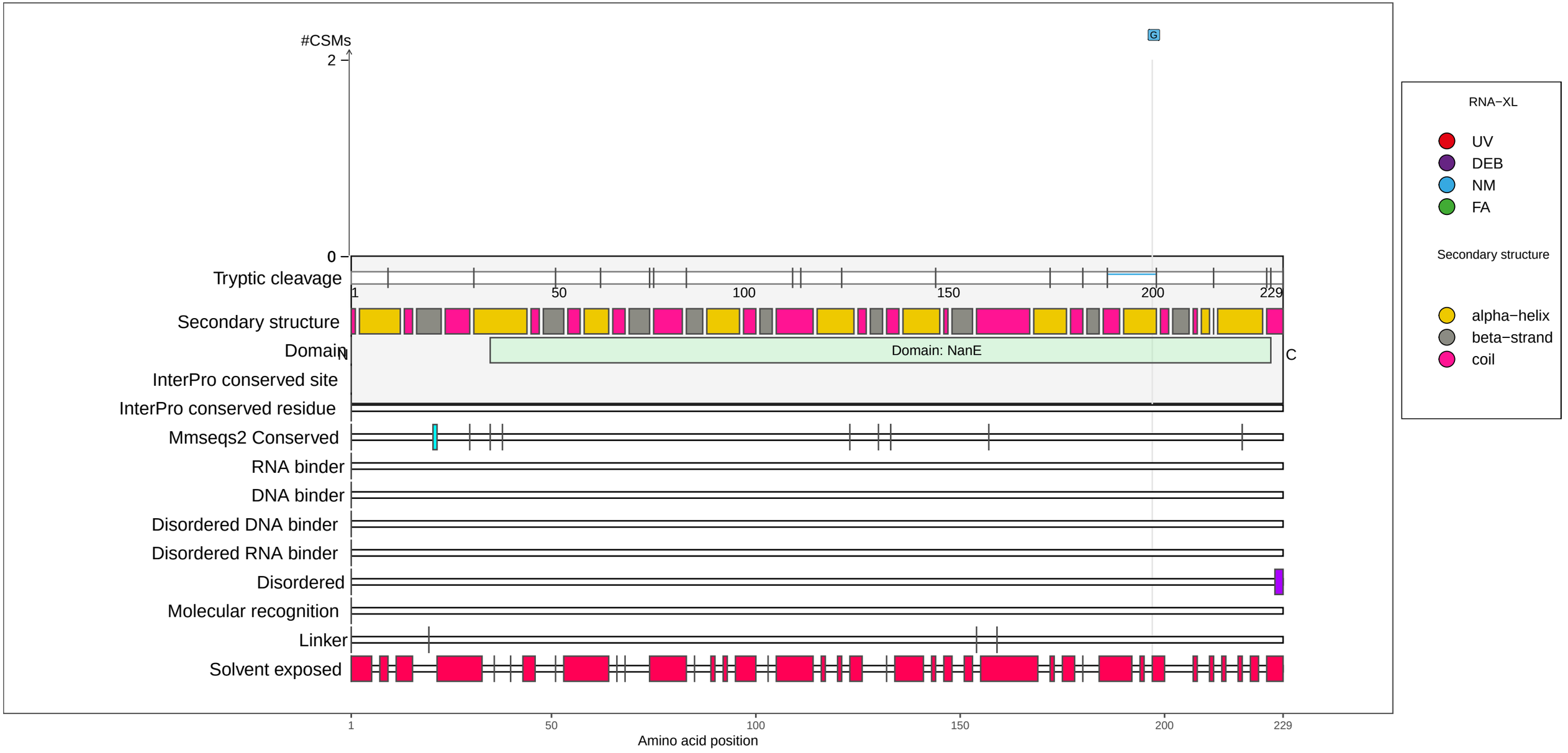
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA (guanine−N7)−methylation
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification
RNA processing; rRNA (guanine−N7−)−methyltransferase activity; rRNA (guanine−N7)−methylation
rRNA (guanine) methyltransferase activity; rRNA base methylation
rRNA metabolic process; rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing
rRNA small subunit methyltransferase G



P0A761
NANE_ECOLI Putative N−acetylmannosamine−6−phosphate 2−epimerase

− Abundance:
tryptic [log10 Intensity]: 8.42 (Q 73)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 1.43 (Q 58)

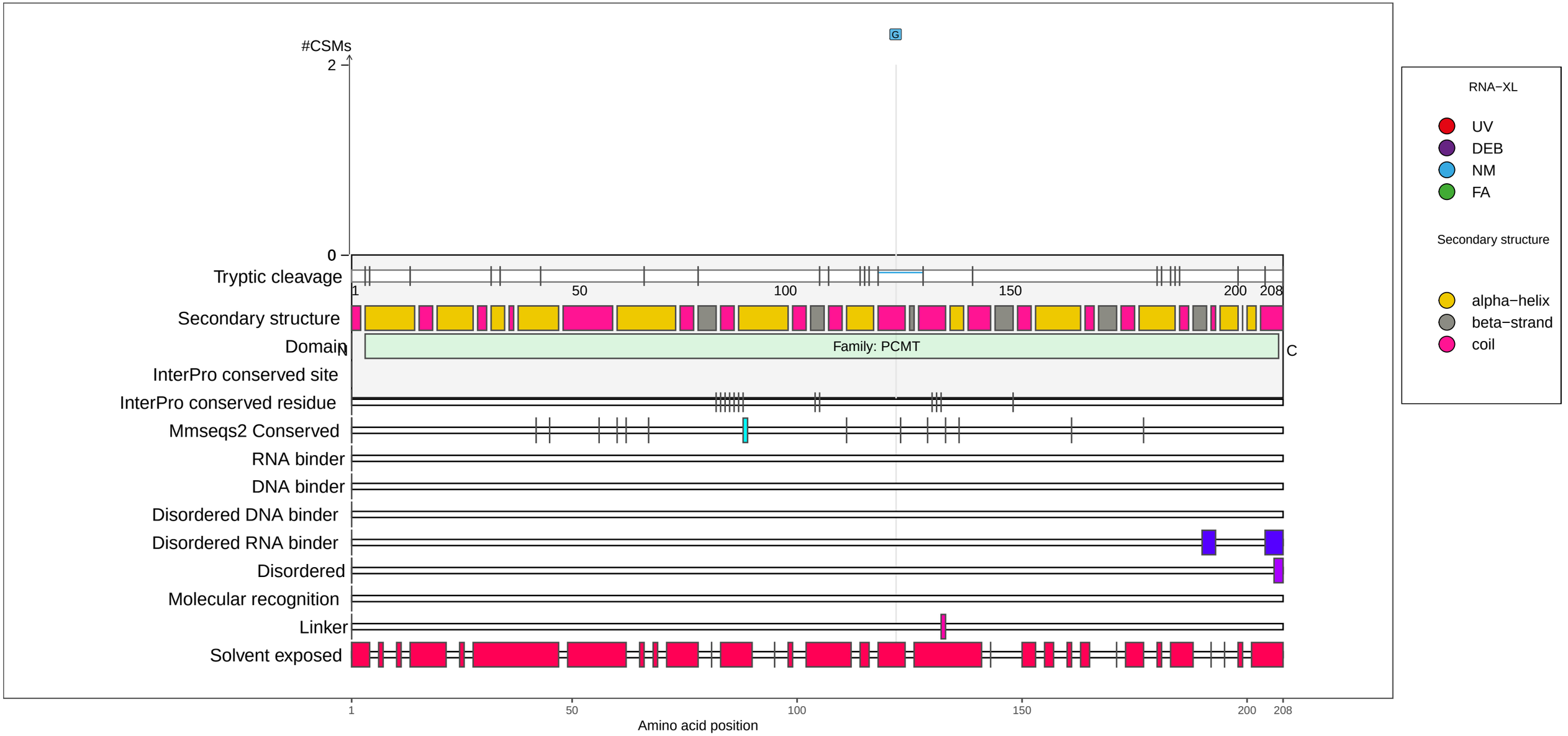
− RNA functions: not annotated



P0A7A5
PIMT_ECOLI Protein−L−isoaspartate O−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.38 (Q 28)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 1.38 (Q 56)

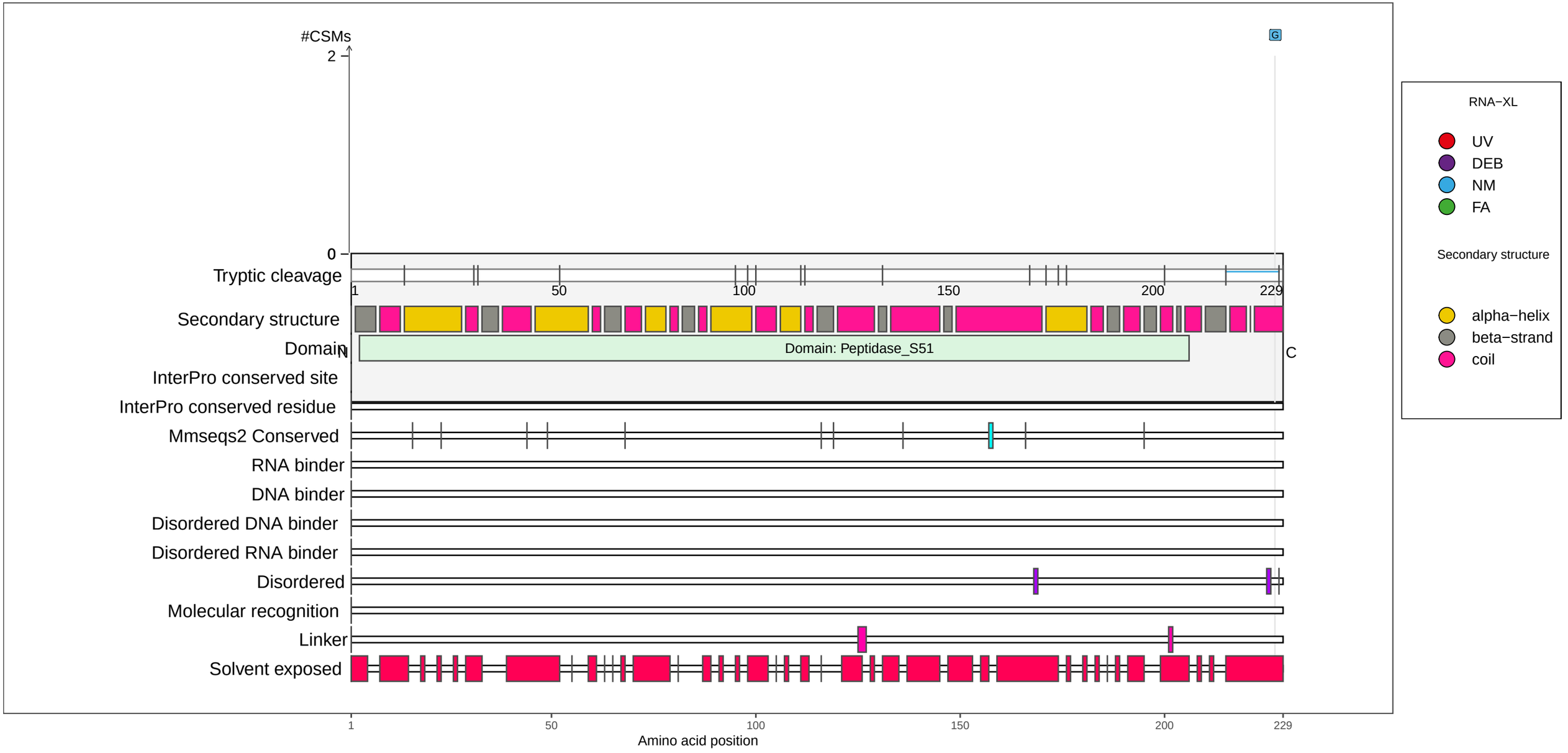
− RNA functions:
Ribosomal RNA adenine dimethylase



P0A7C6
PEPE_ECOLI Peptidase E

− Abundance:
tryptic [log10 Intensity]: 6.99 (Q 13)
PAXdb K12 strain [ppm]: 1.83 (Q 54)
PAXdb E.coli [ppm]: 2.12 (Q 75)

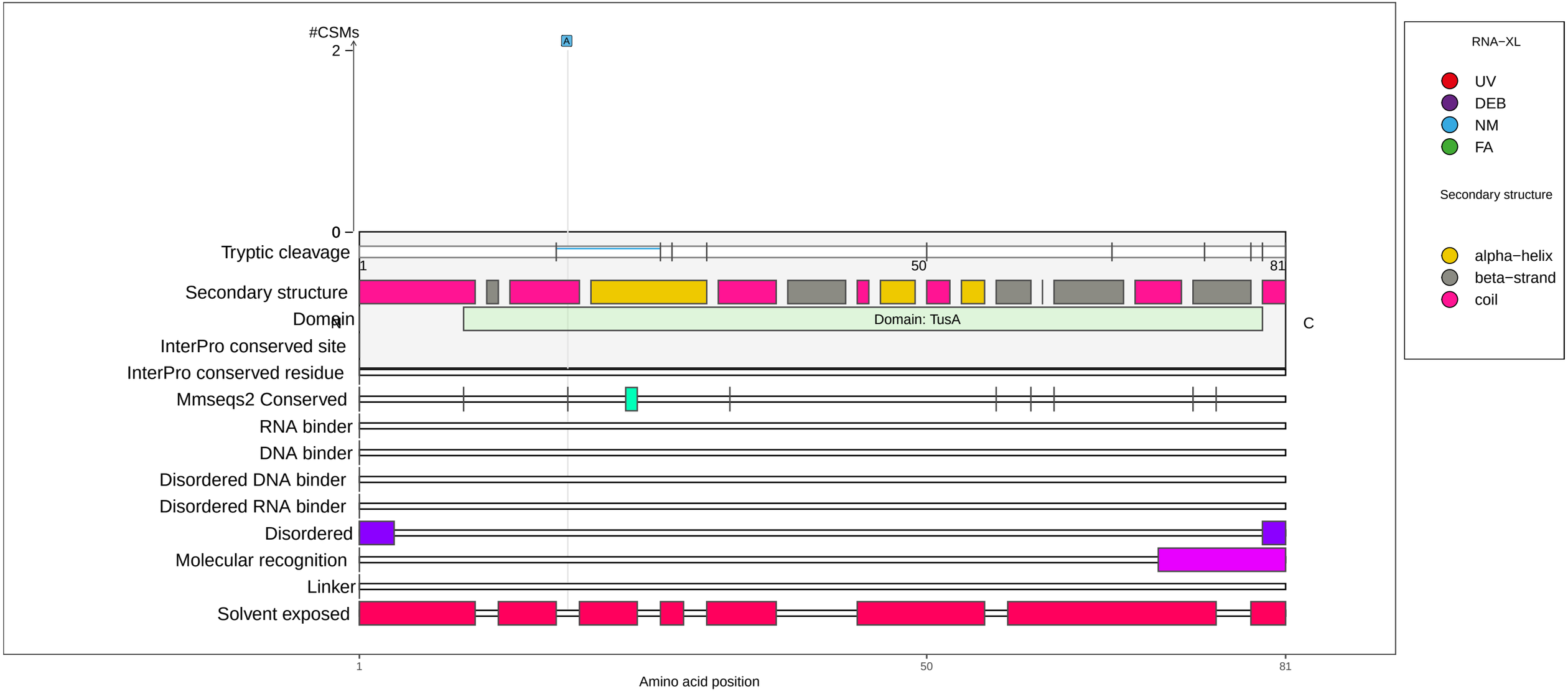
− RNA functions: not annotated



P0A890
TUSA_ECOLI Sulfur carrier protein TusA

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 2.64 (Q 82)
PAXdb E.coli [ppm]: 1.8 (Q 67)

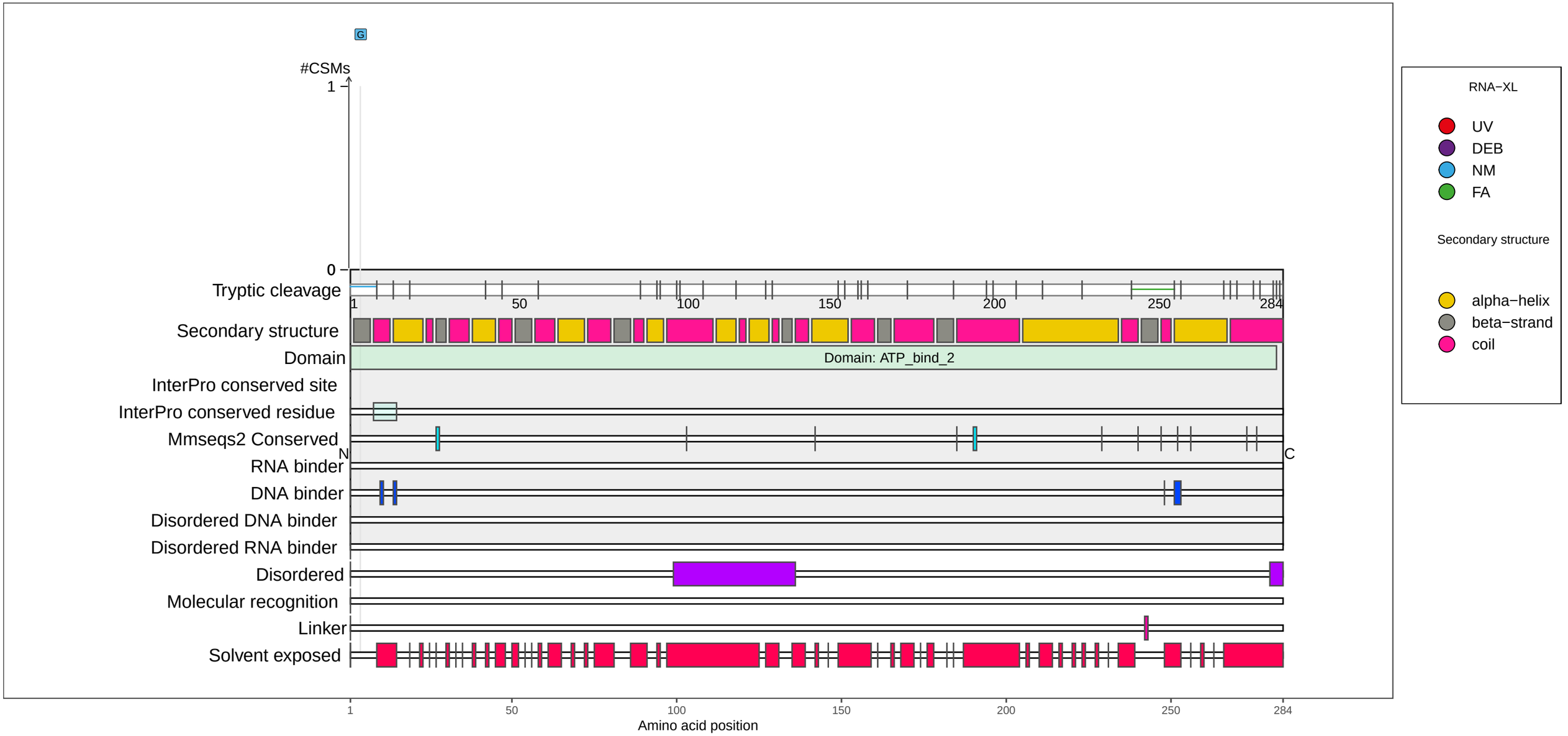
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA thio−modification; tRNA wobble base modification; tRNA wobble position uridine thiolation
tRNA wobble uridine modification



P0A894
RAPZ_ECOLI RNase adapter protein RapZ

− Abundance:
tryptic [log10 Intensity]: 8.15 (Q 63)
PAXdb K12 strain [ppm]: 1.92 (Q 57)
PAXdb E.coli [ppm]: 2.14 (Q 76)

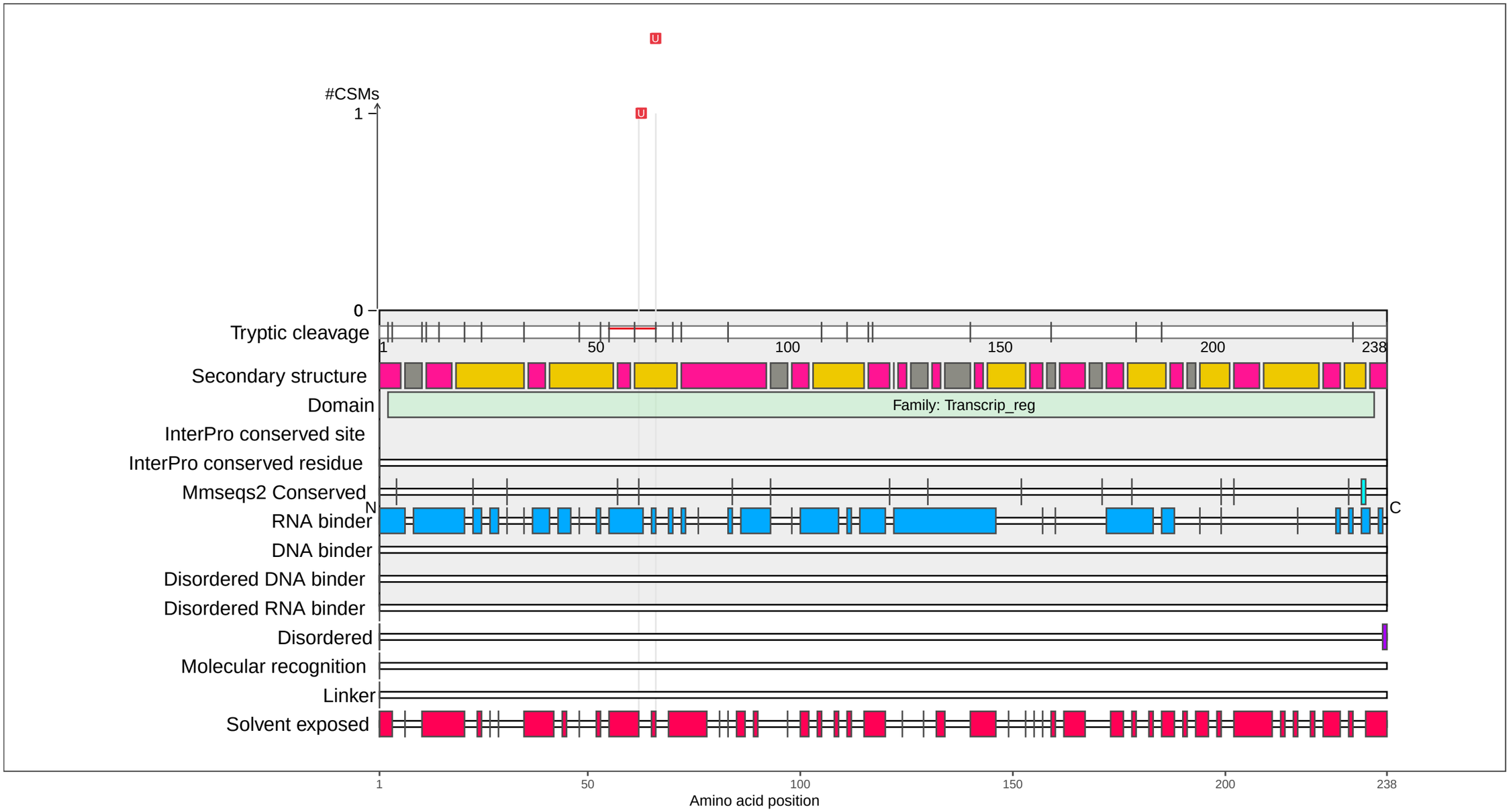
− RNA functions:
RNA binding; RNA destabilization



P0A8A2
YEEN_ECOLI Probable transcriptional regulatory protein YeeN

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 2.63 (Q 81)
PAXdb E.coli [ppm]: 2.33 (Q 81)

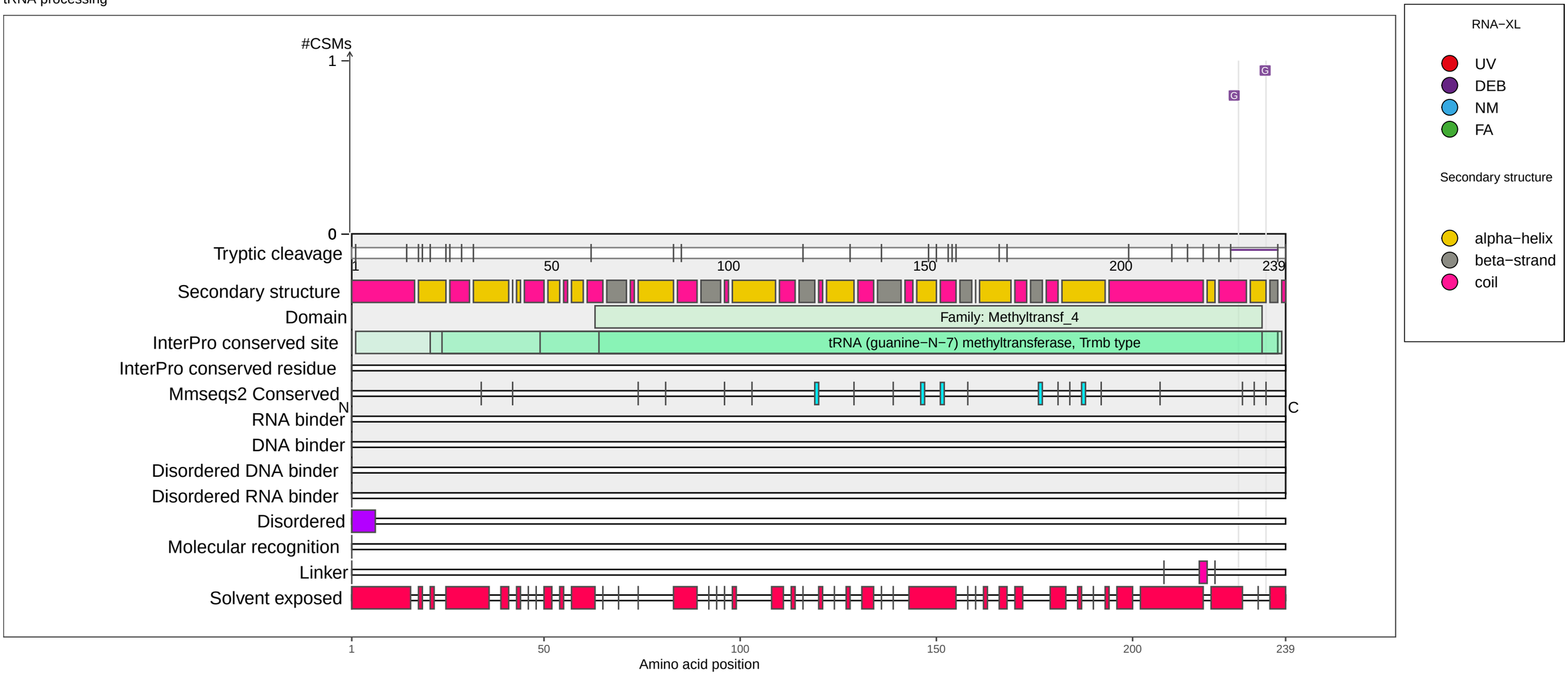
− RNA functions: not annotated



P0A8I5
TRMB_ECOLI tRNA (guanine−N(7)−)−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.28 (Q 80)

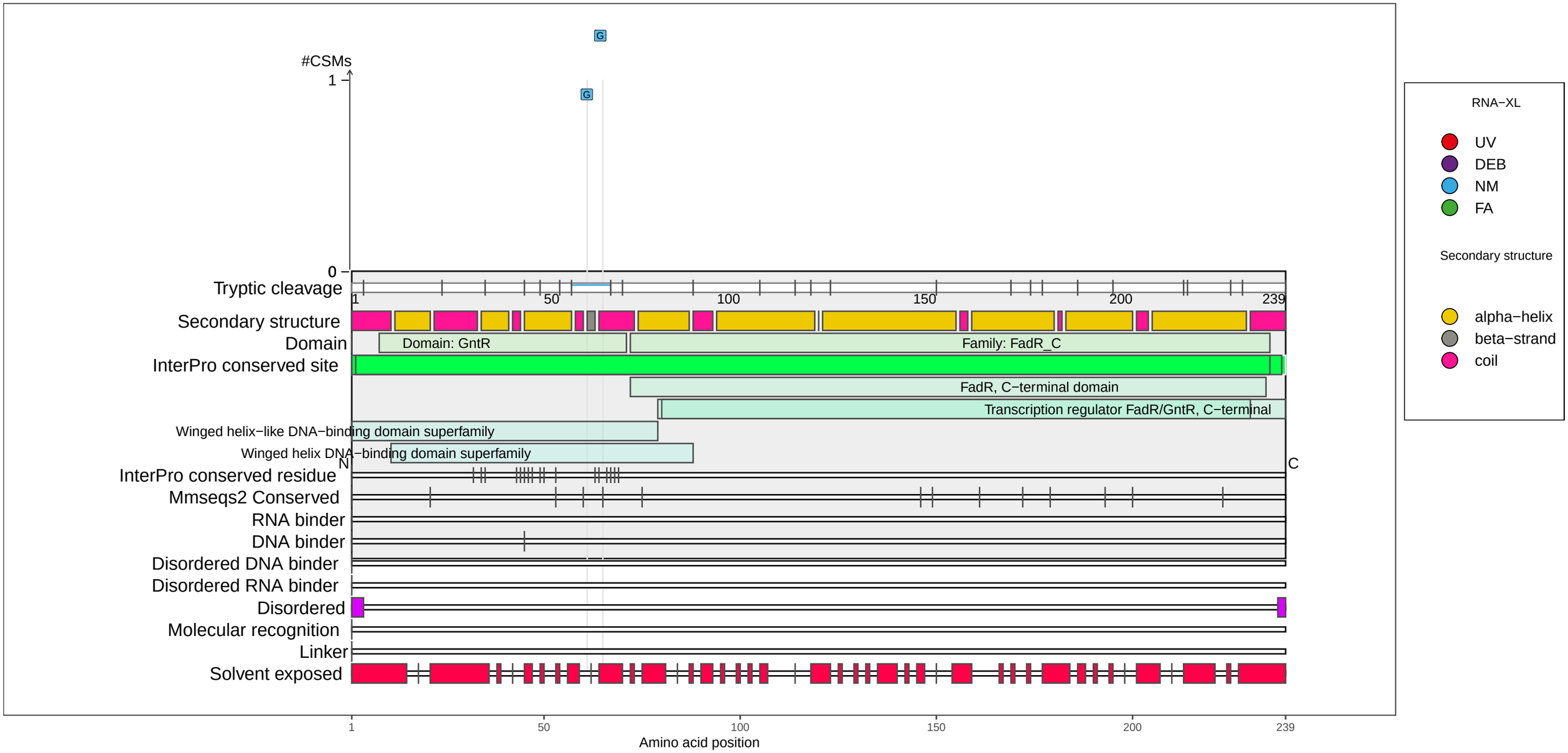
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA (guanine−N7)−methylation
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification
RNA processing; tRNA (guanine−N7−)−methyltransferase activity; tRNA (guanine−N7)−methylation
tRNA (guanine) methyltransferase activity; tRNA metabolic process; tRNA methylation
tRNA methyltransferase activity; tRNA methyltransferase complex; tRNA modification
tRNA processing



P0A8V6
FADR_ECOLI Fatty acid metabolism regulator protein

− Abundance:
tryptic [log10 Intensity]: 8.02 (Q 58)
PAXdb K12 strain [ppm]: 1.51 (Q 39)
PAXdb E.coli [ppm]: 2.32 (Q 81)

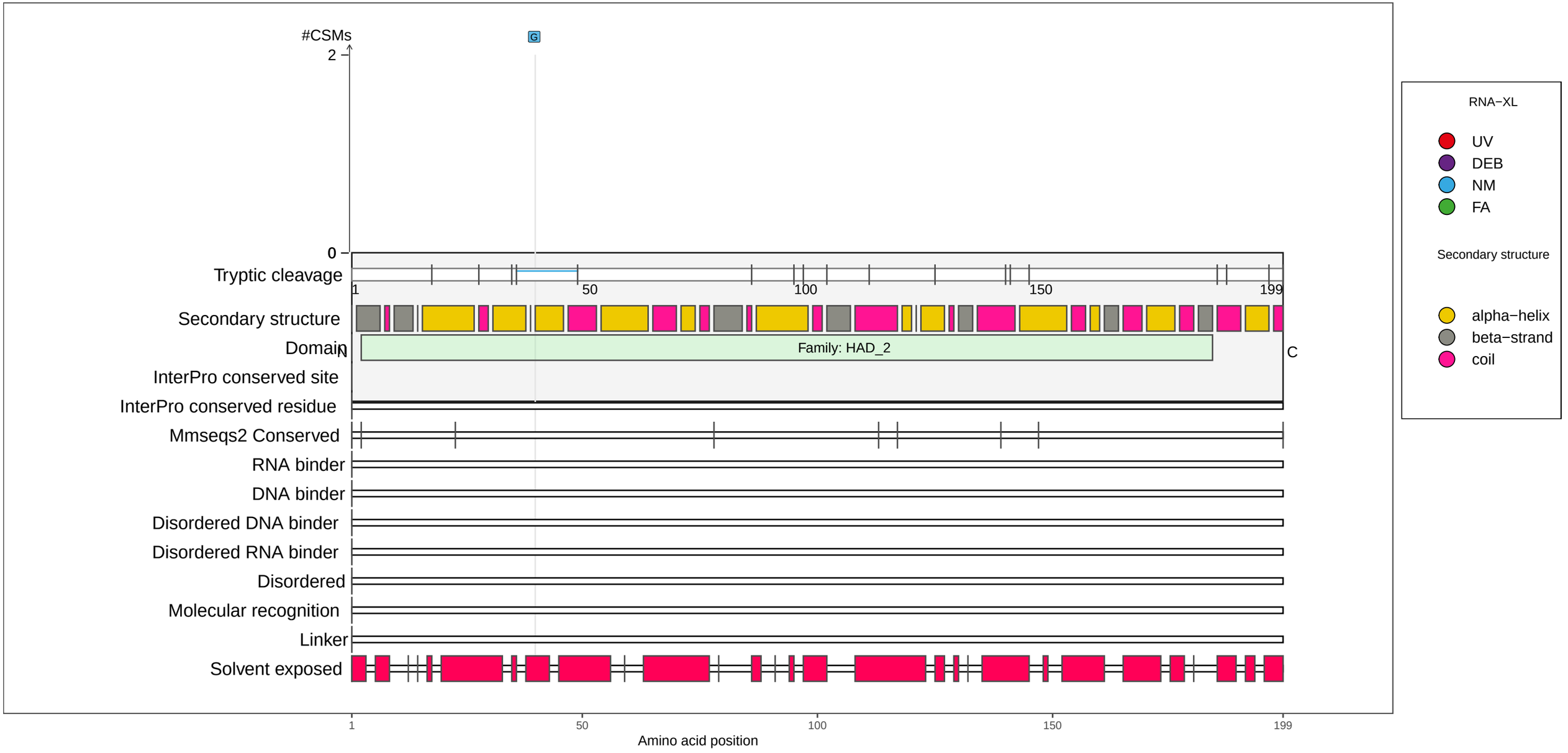
− RNA functions: not annotated



P0A8Y3
YIHX_ECOLI Alpha−D−glucose 1−phosphate phosphatase YihX

− Abundance:
tryptic [log10 Intensity]: 7.93 (Q 55)
PAXdb K12 strain [ppm]: 1.1 (Q 16)
PAXdb E.coli [ppm]: 2.23 (Q 78)

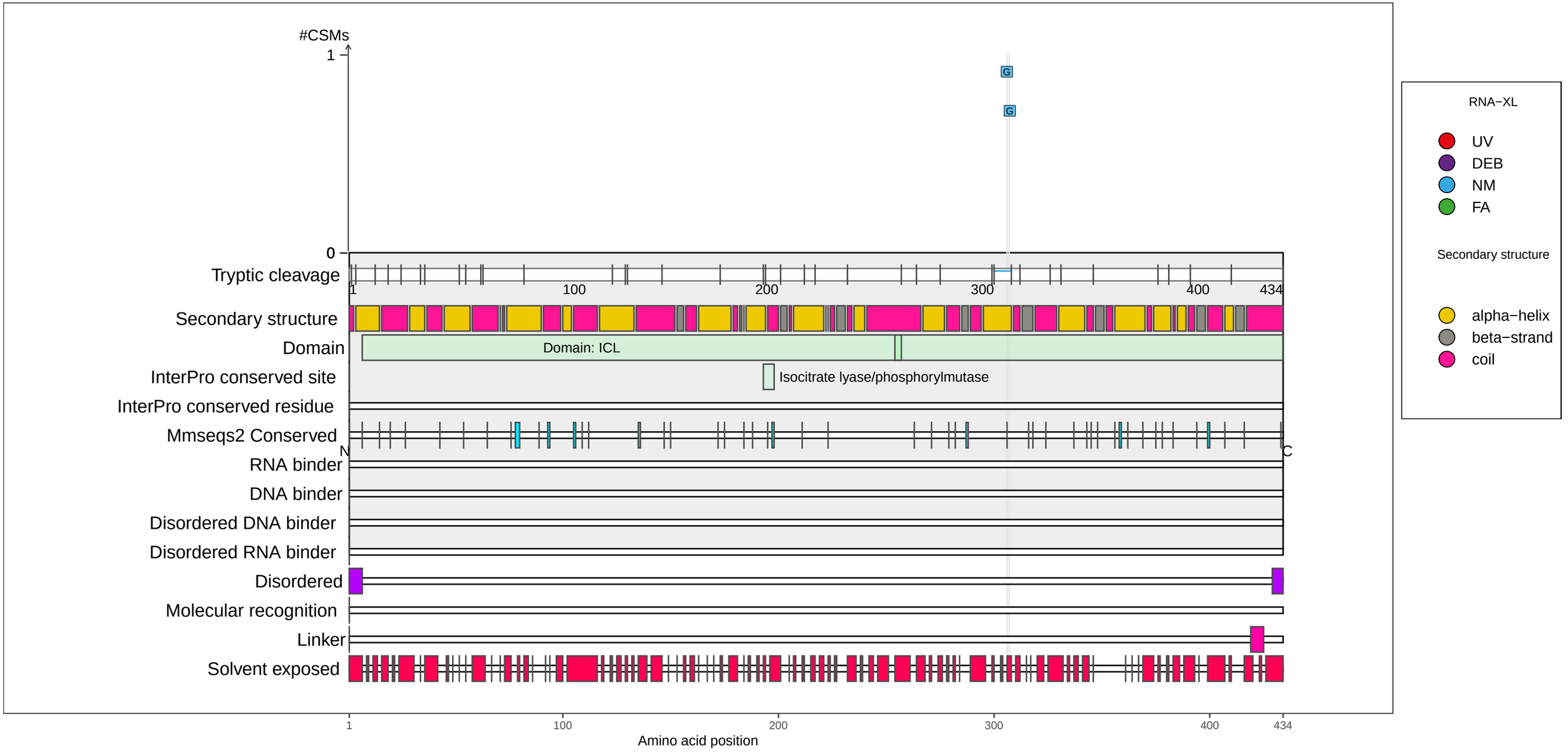
− RNA functions: not annotated



P0A9G6
ACEA_ECOLI Isocitrate lyase

− Abundance:
tryptic [log10 Intensity]: 8.27 (Q 68)
PAXdb K12 strain [ppm]: 2.72 (Q 84)
PAXdb E.coli [ppm]: 3.73 (Q 100)

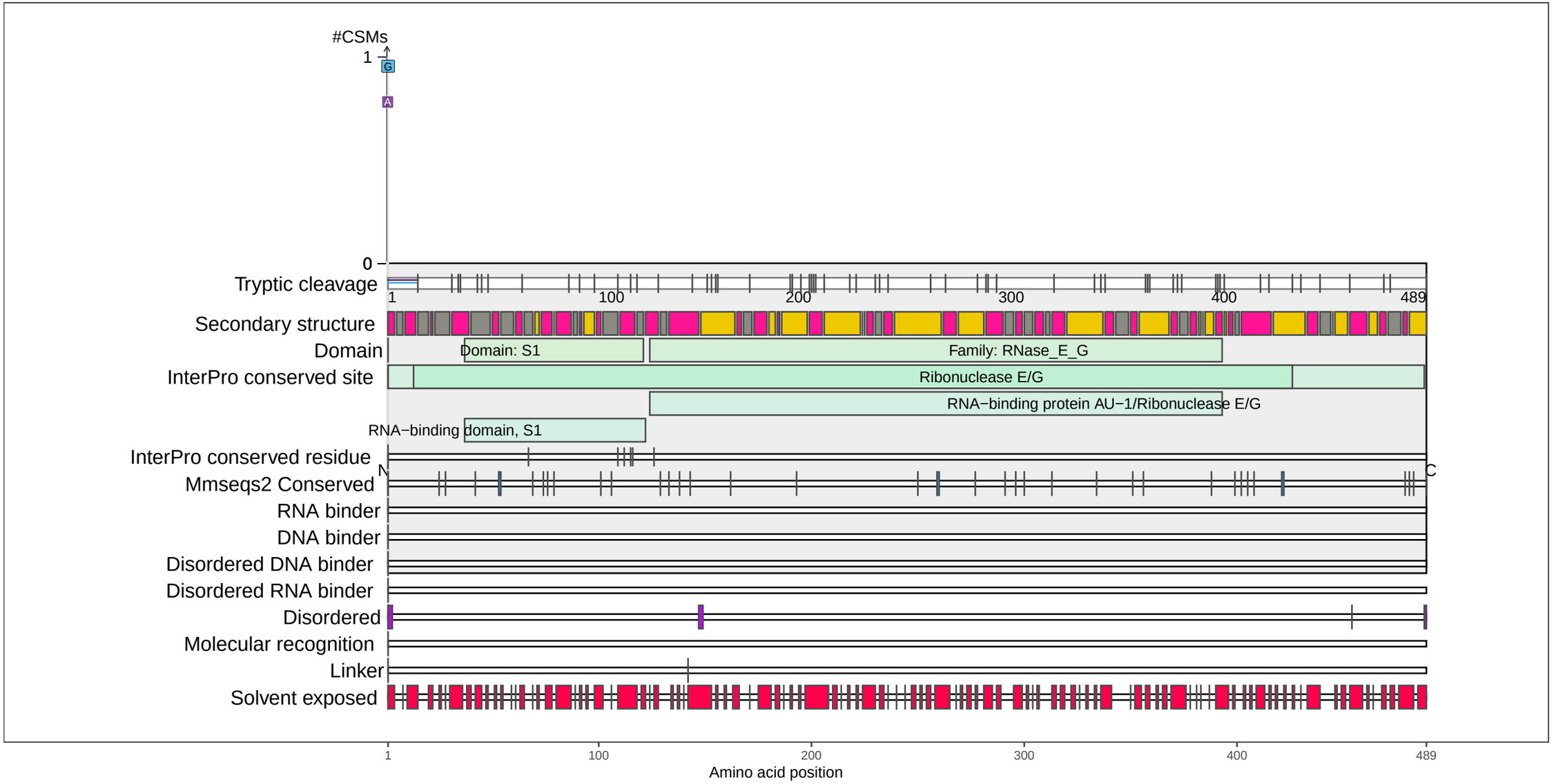
− RNA functions: not annotated



P0A9J0
RNG_ECOLI Ribonuclease G

− Abundance:
tryptic [log10 Intensity]: 8.04 (Q 59)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 1.19 (Q 52)

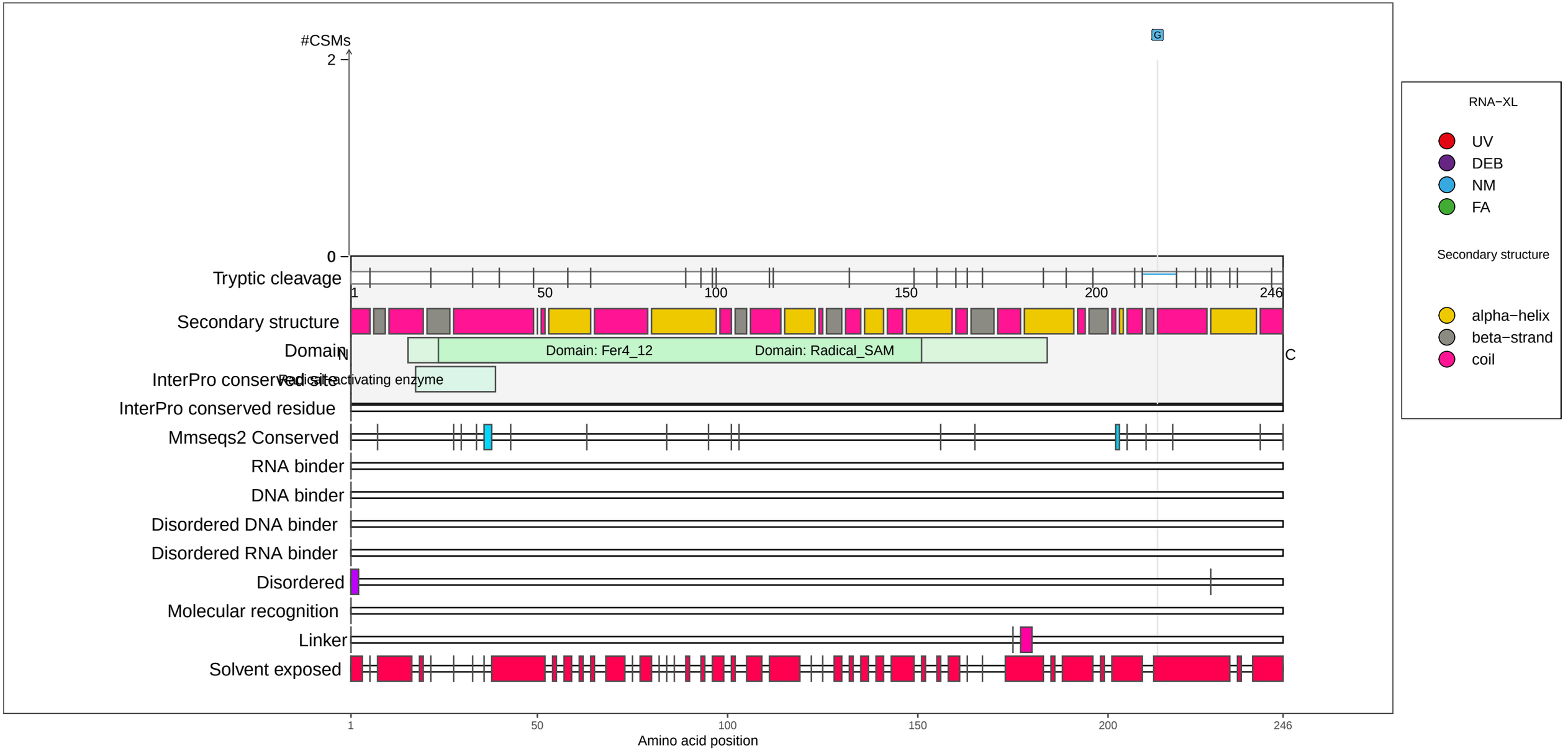
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA phosphodiester bond hydrolysis; RNA processing; rRNA metabolic process; rRNA processing
S1 RNA binding domain



P0A9N4
PFLA_ECOLI Pyruvate formate−lyase 1−activating enzyme

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 68)
PAXdb K12 strain [ppm]: 2.68 (Q 83)
PAXdb E.coli [ppm]: 1.91 (Q 70)

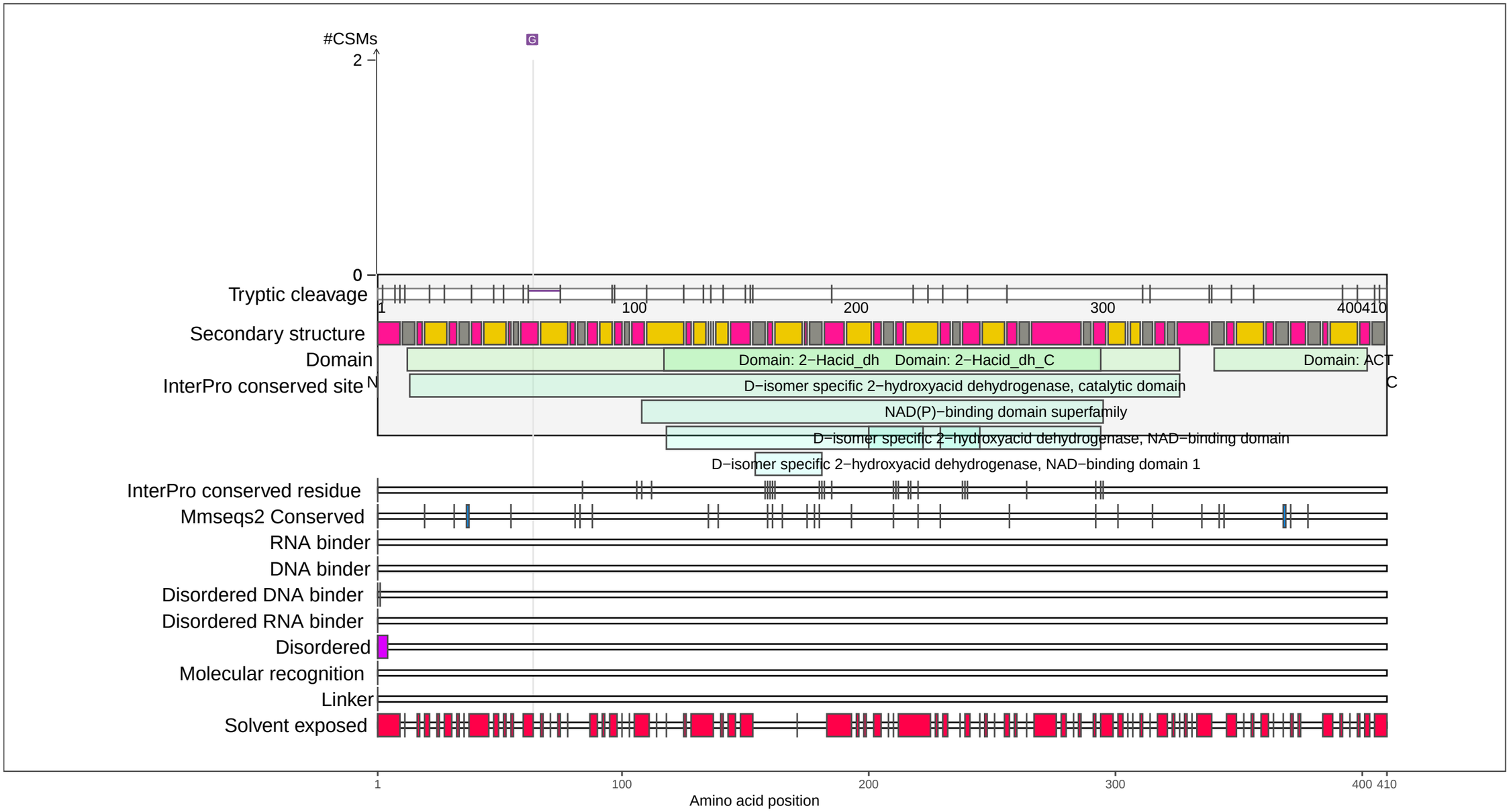
− RNA functions: not annotated



P0A9T0
SERA_ECOLI D−3−phosphoglycerate dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 3.34 (Q 96)
PAXdb E.coli [ppm]: 3.04 (Q 95)

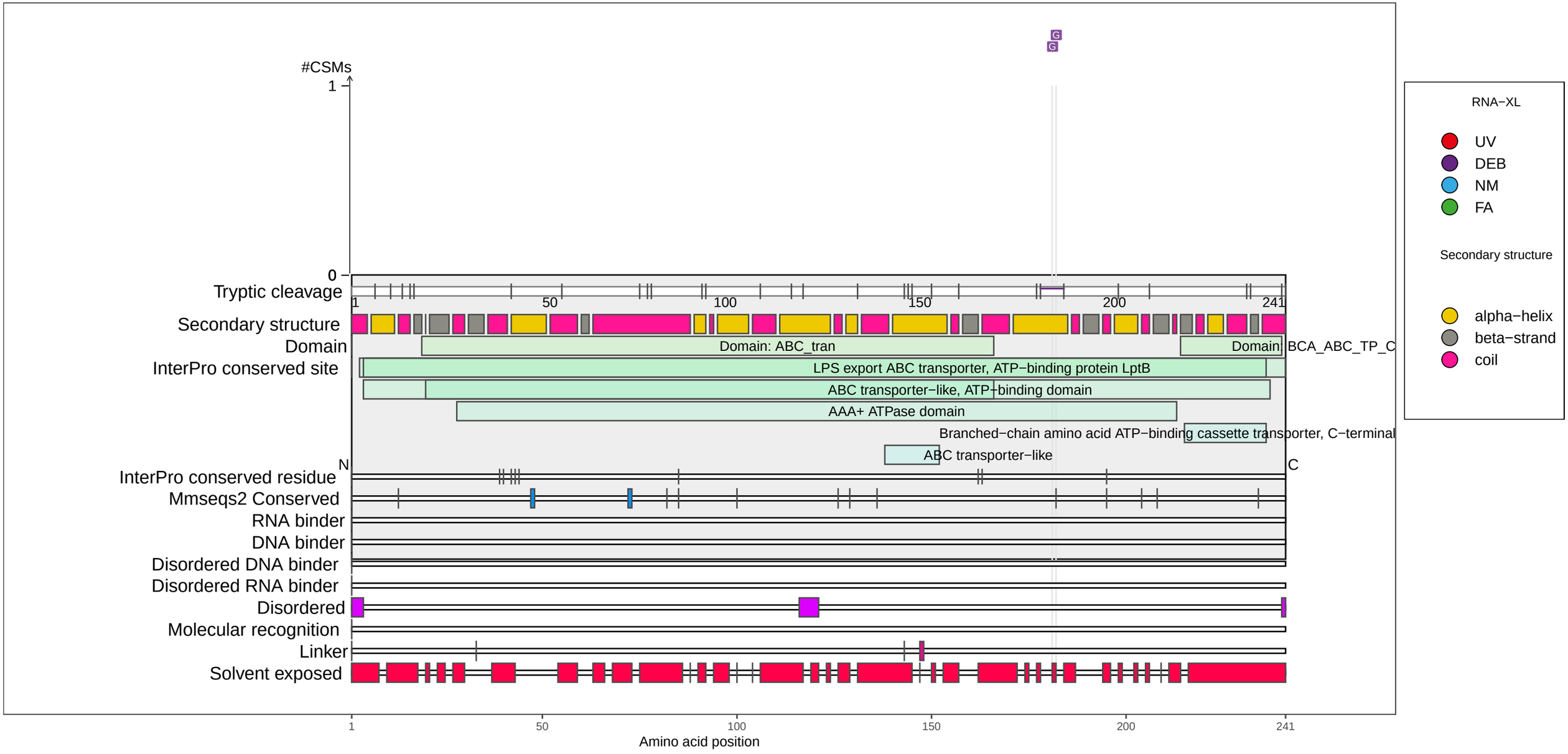
− RNA functions: not annotated



P0A9V1
LPTB_ECOLI Lipopolysaccharide export system ATP−binding protein LptB

− Abundance:
tryptic [log10 Intensity]: 7.87 (Q 52)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.35 (Q 82)

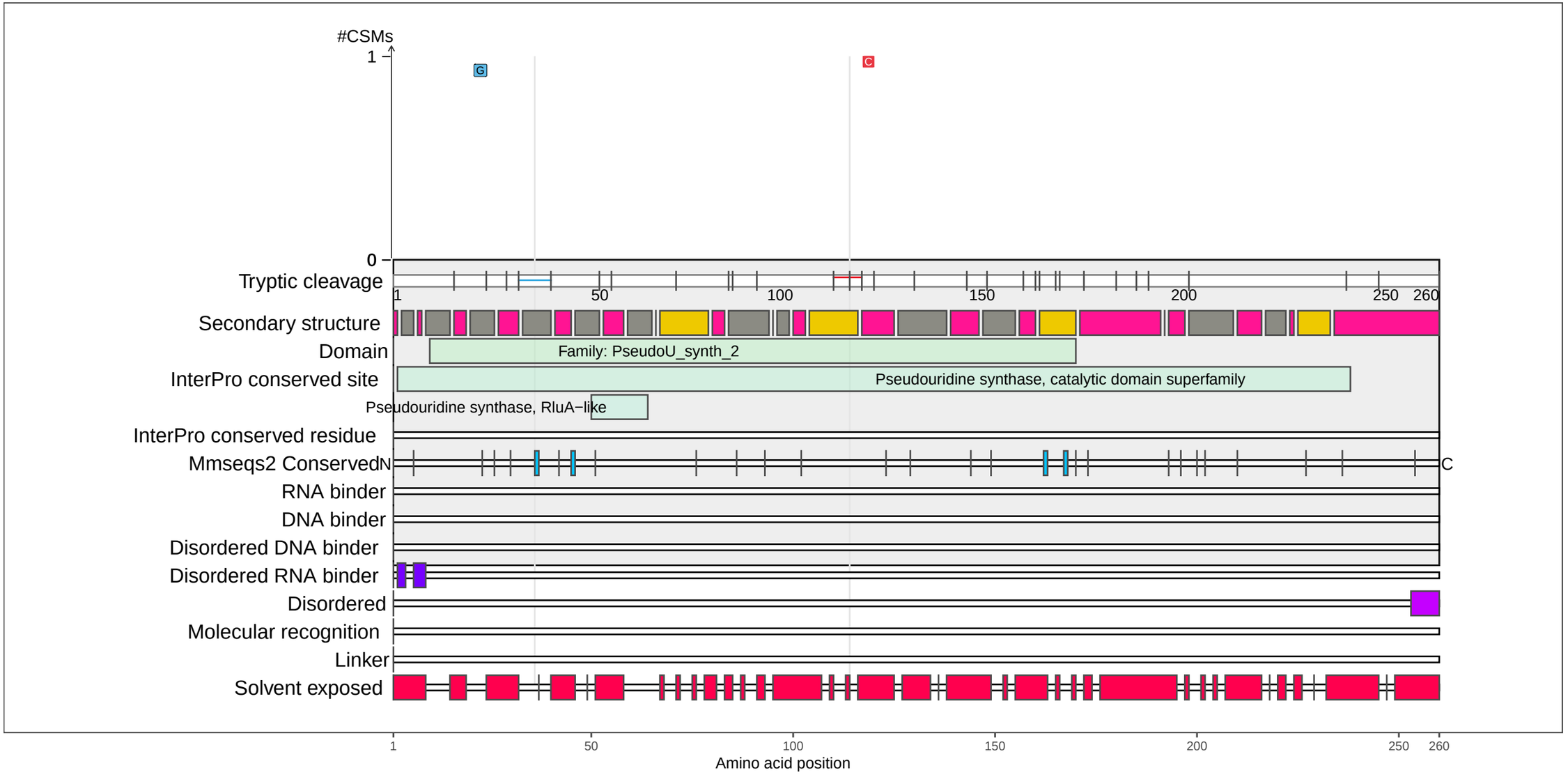
− RNA functions: not annotated

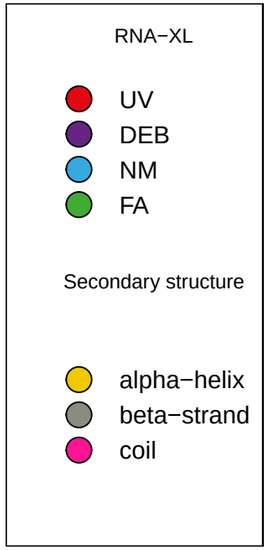


P0AA41
TRUC_ECOLI tRNA pseudouridine synthase C

− Abundance:
tryptic [log10 Intensity]: 6.95 (Q 11)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.1 (Q 27)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; RNA pseudouridylate synthase; tRNA metabolic process
tRNA modification; tRNA processing; tRNA pseudouridine synthase activity
tRNA pseudouridine synthesis

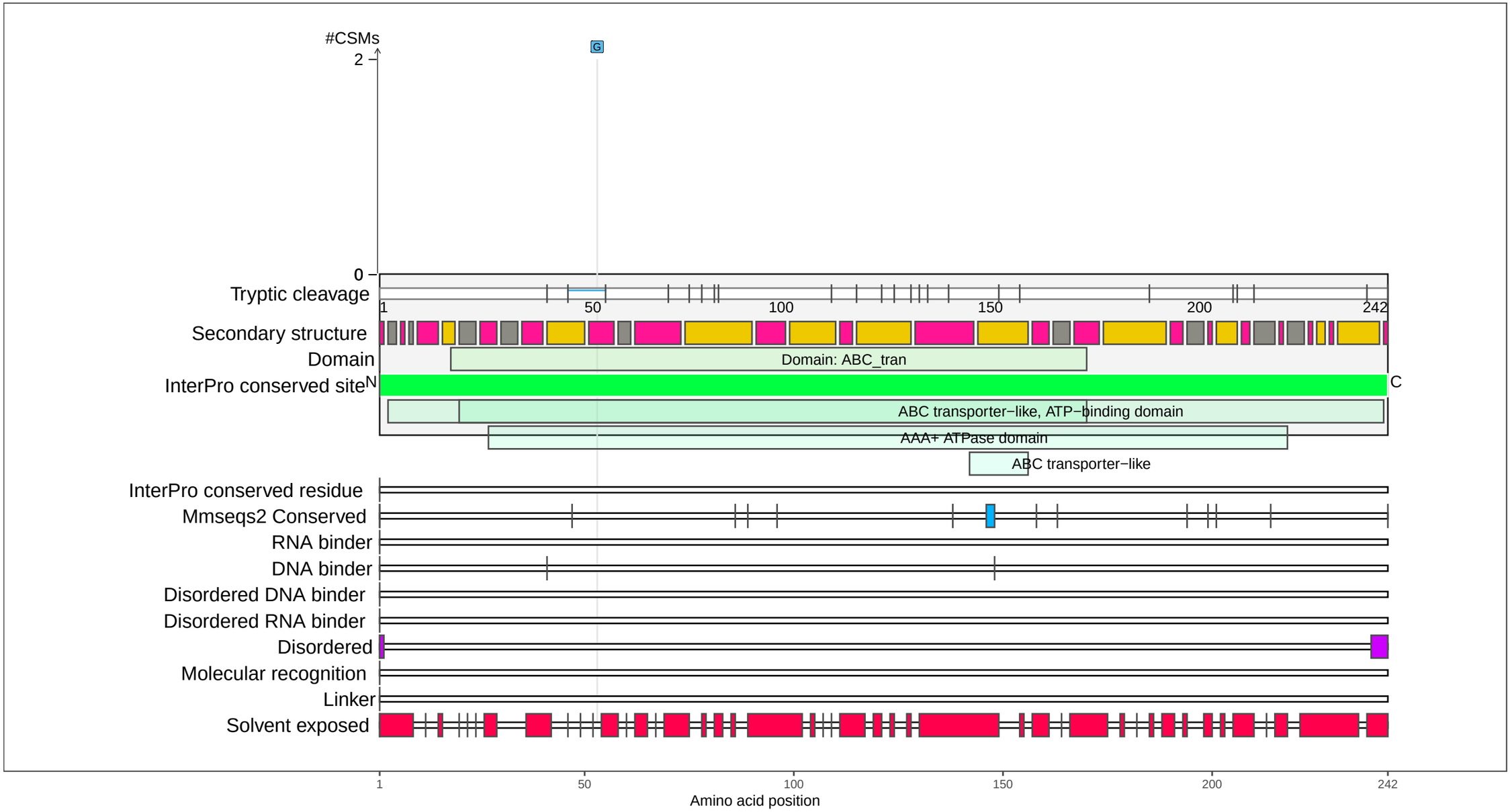


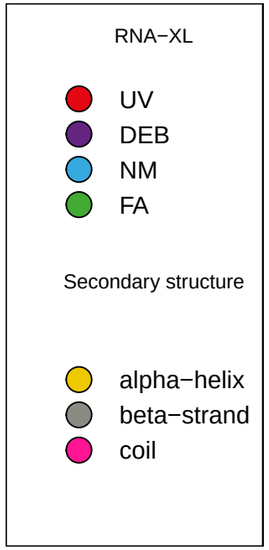


P0AAF6
ARTP_ECOLI Arginine transport ATP−binding protein ArtP

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 45)
PAXdb K12 strain [ppm]: 2.37 (Q 73)
PAXdb E.coli [ppm]: 2.3 (Q 80)

− RNA functions: not annotated

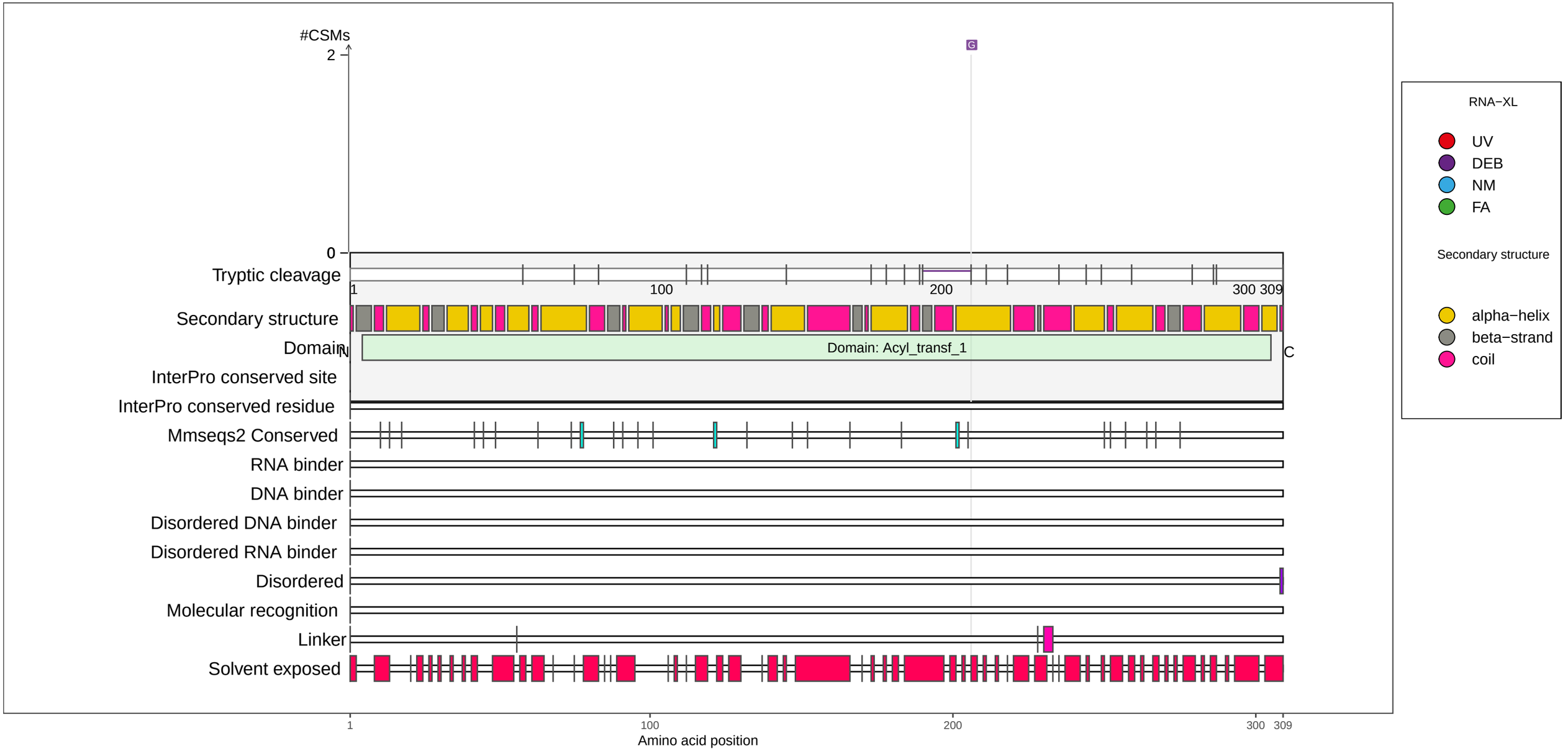




P0AAI9
FABD_ECOLI Malonyl CoA−acyl carrier protein transacylase

− Abundance:
tryptic [log10 Intensity]: 8.55 (Q 77)
PAXdb K12 strain [ppm]: 2.61 (Q 80)
PAXdb E.coli [ppm]: 2.94 (Q 94)

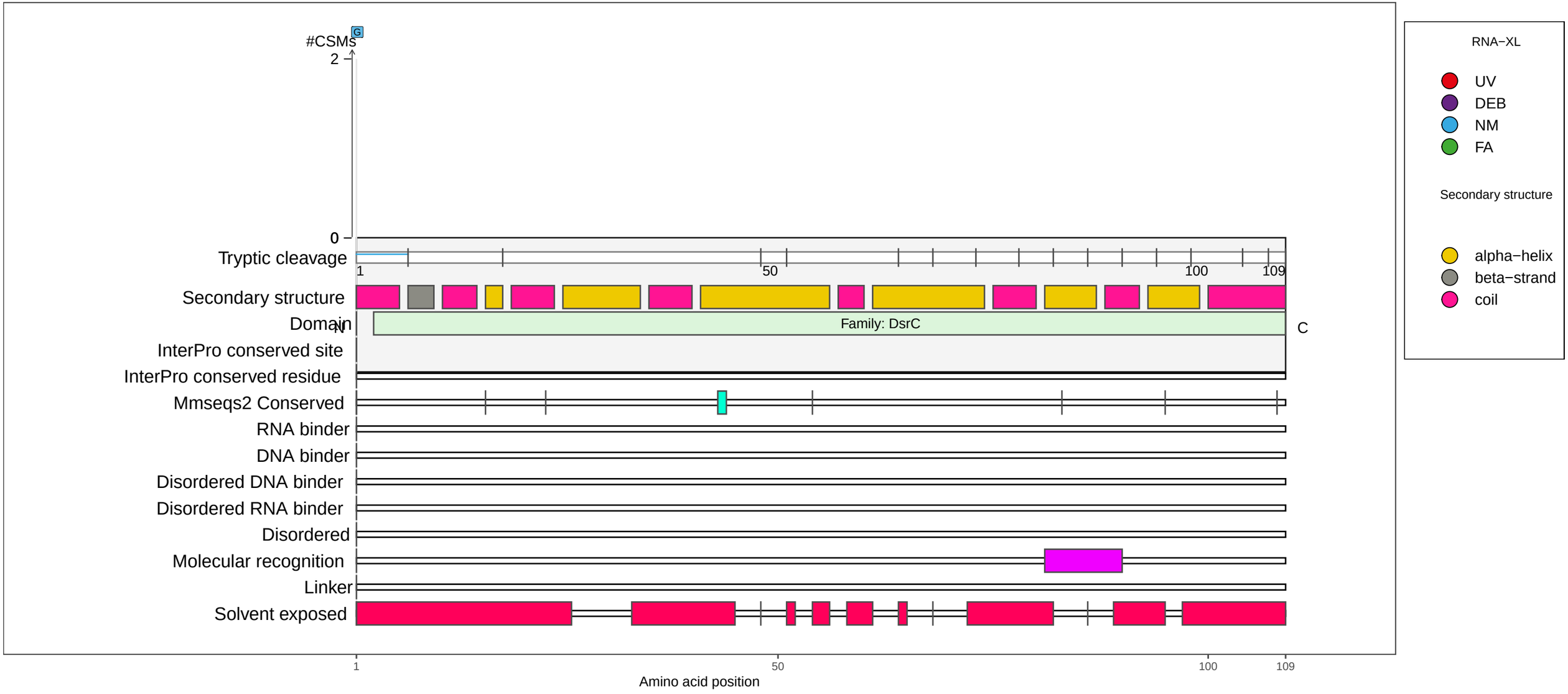
− RNA functions: not annotated



P0AB18
TUSE_ECOLI Sulfurtransferase TusE

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 61)
PAXdb K12 strain [ppm]: 1.81 (Q 54)
PAXdb E.coli [ppm]: 1.51 (Q 60)

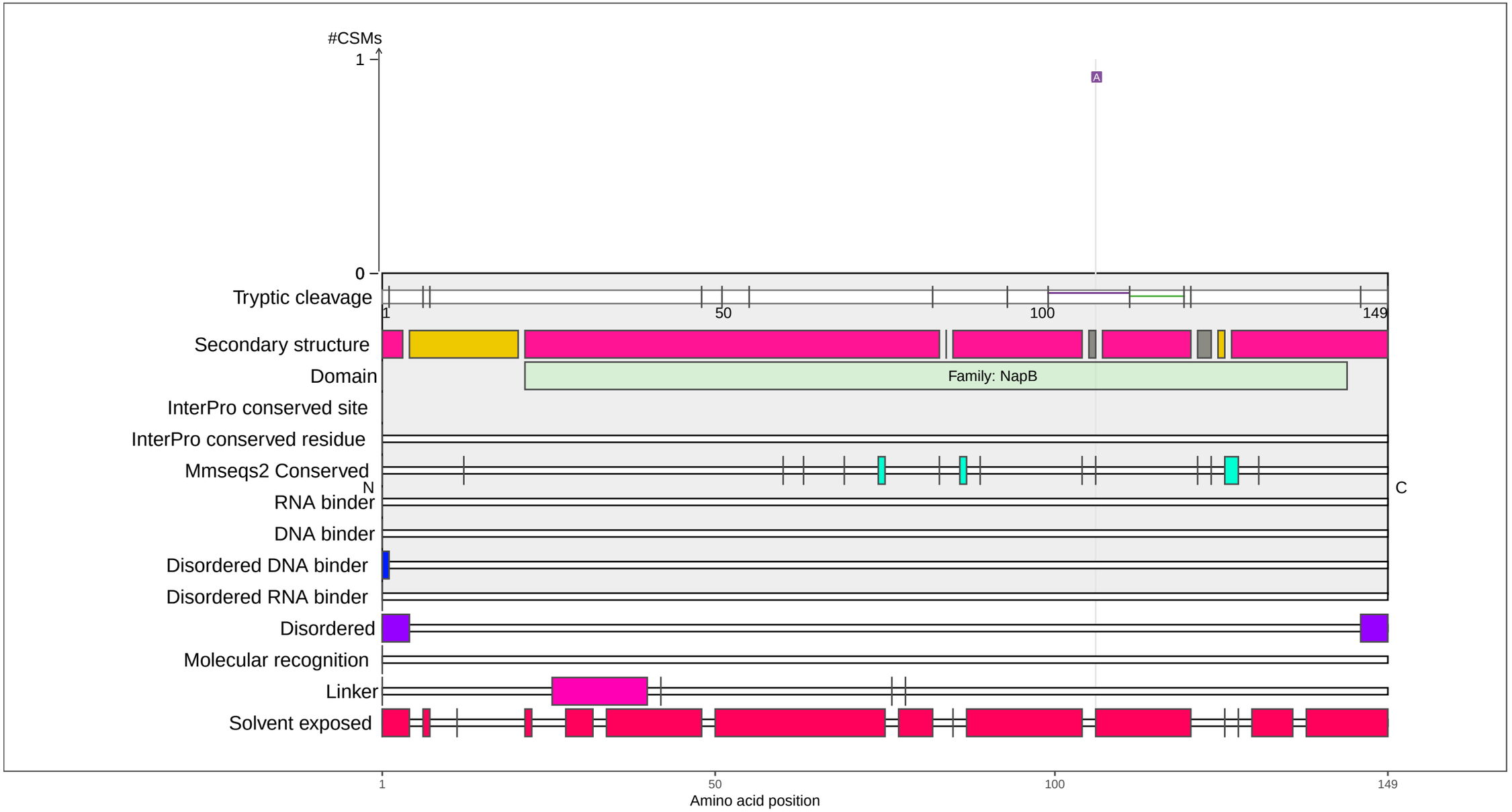
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA thio−modification; tRNA wobble base modification; tRNA wobble position uridine thiolation
tRNA wobble uridine modification



P0ABL3
NAPB_ECOLI Periplasmic nitrate reductase, electron transfer subunit

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.36 (Q 18)

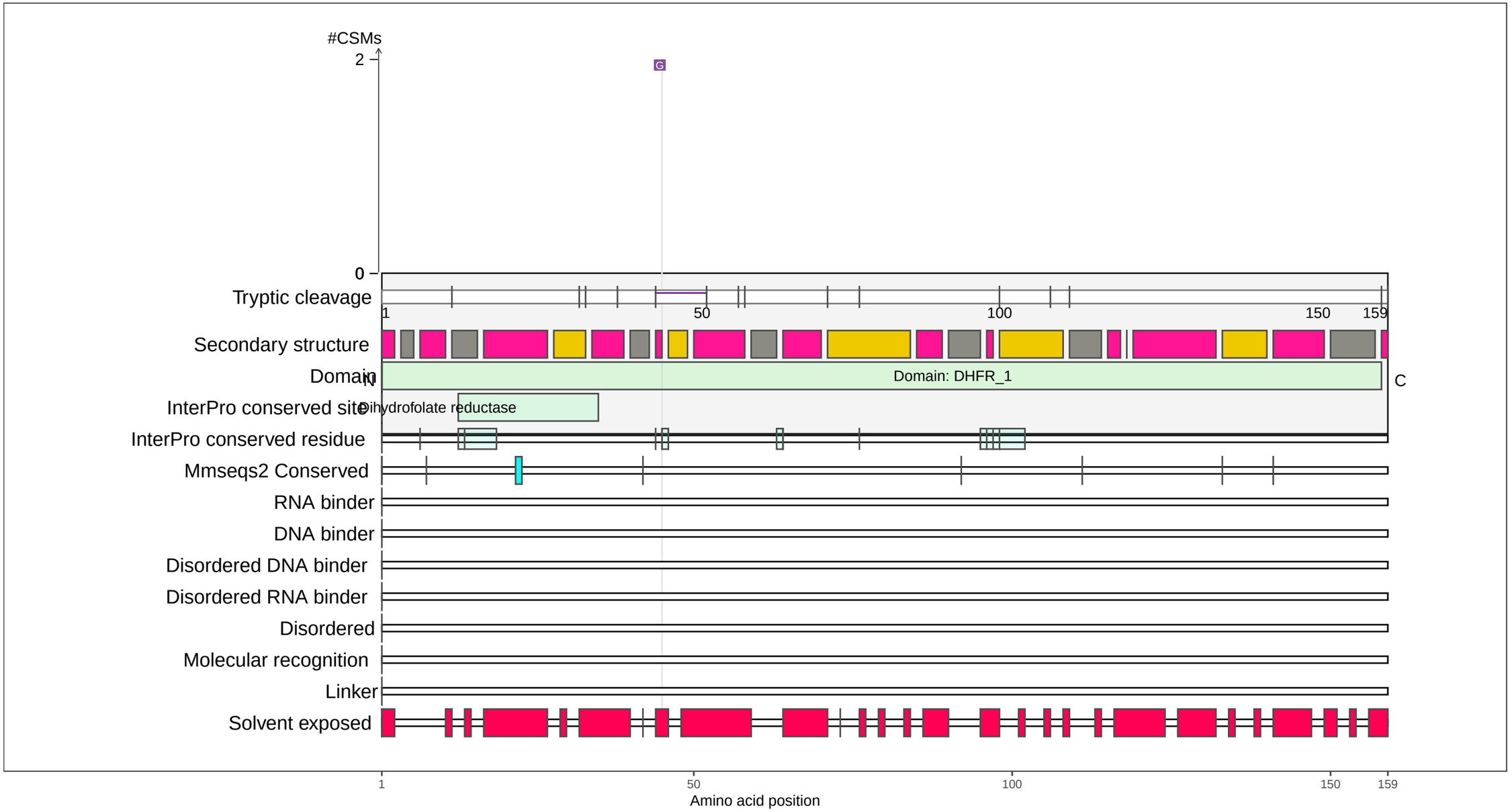
− RNA functions: not annotated



P0ABQ4
DYR_ECOLI Dihydrofolate reductase

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 17)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.13 (Q 76)

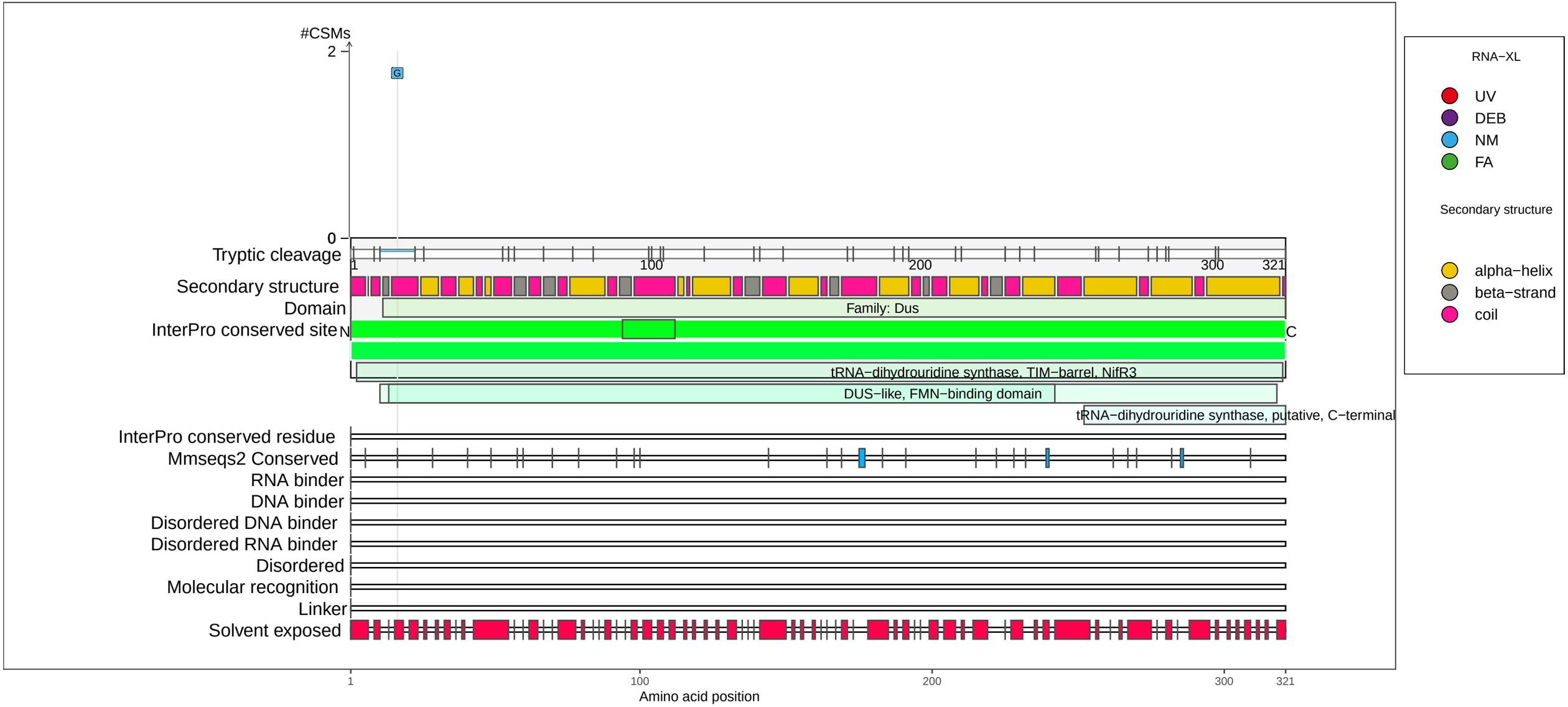
− RNA functions: not annotated



P0ABT5
DUSB_ECOLI tRNA−dihydrouridine synthase B

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.11 (Q 22)

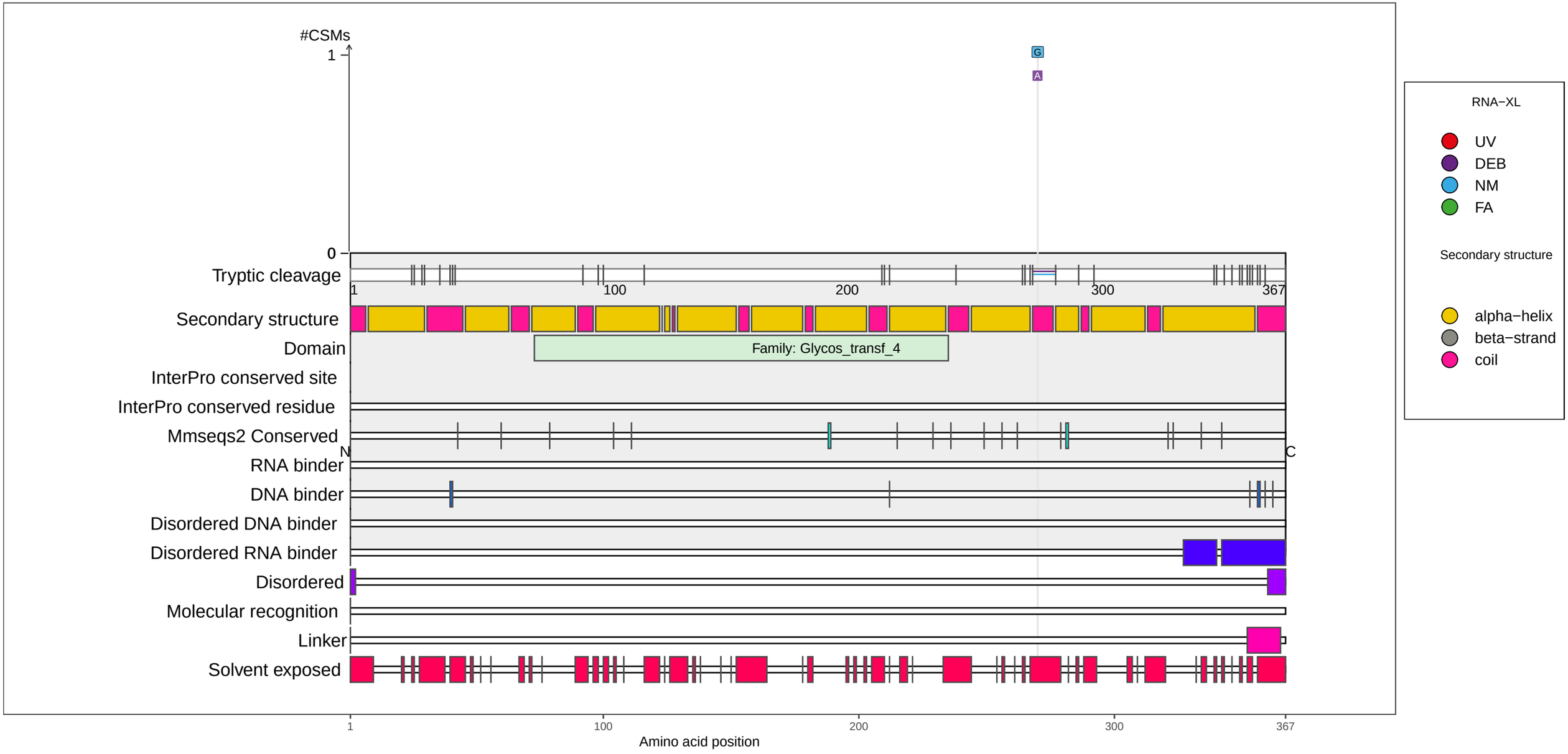
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; tRNA binding; tRNA dihydrouridine synthase activity
tRNA dihydrouridine synthesis; tRNA metabolic process; tRNA modification; tRNA processing



P0AC78
WECA_ECOLI Undecaprenyl−phosphate alpha−N−acetylglucosaminyl 1−phosphate transferase

− Abundance:
tryptic [log10 Intensity]: 6.96 (Q 12)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.52 (Q 15)

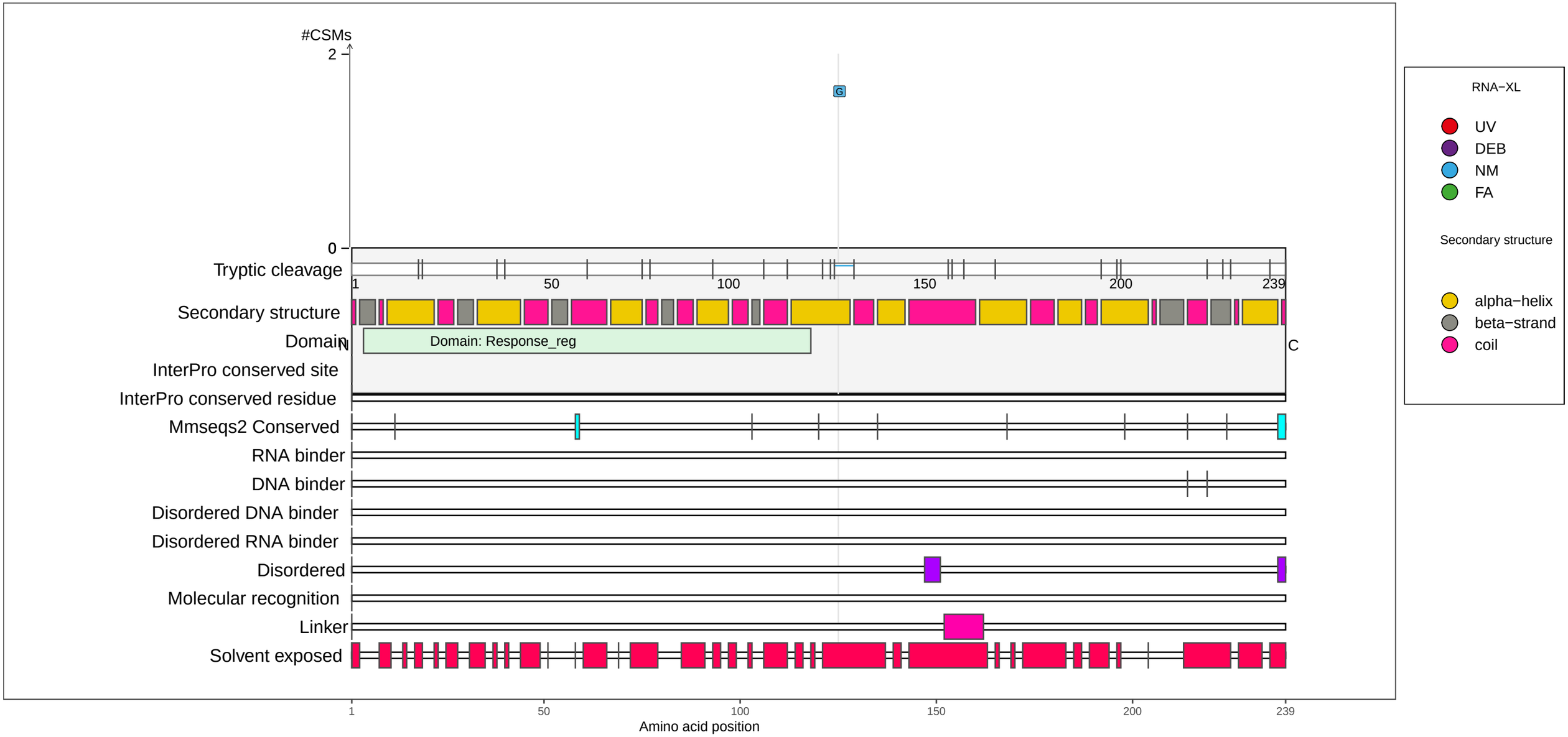
− RNA functions: not annotated



P0AD01
DCUR_ECOLI Transcriptional regulatory protein DcuR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.86 (Q 44)

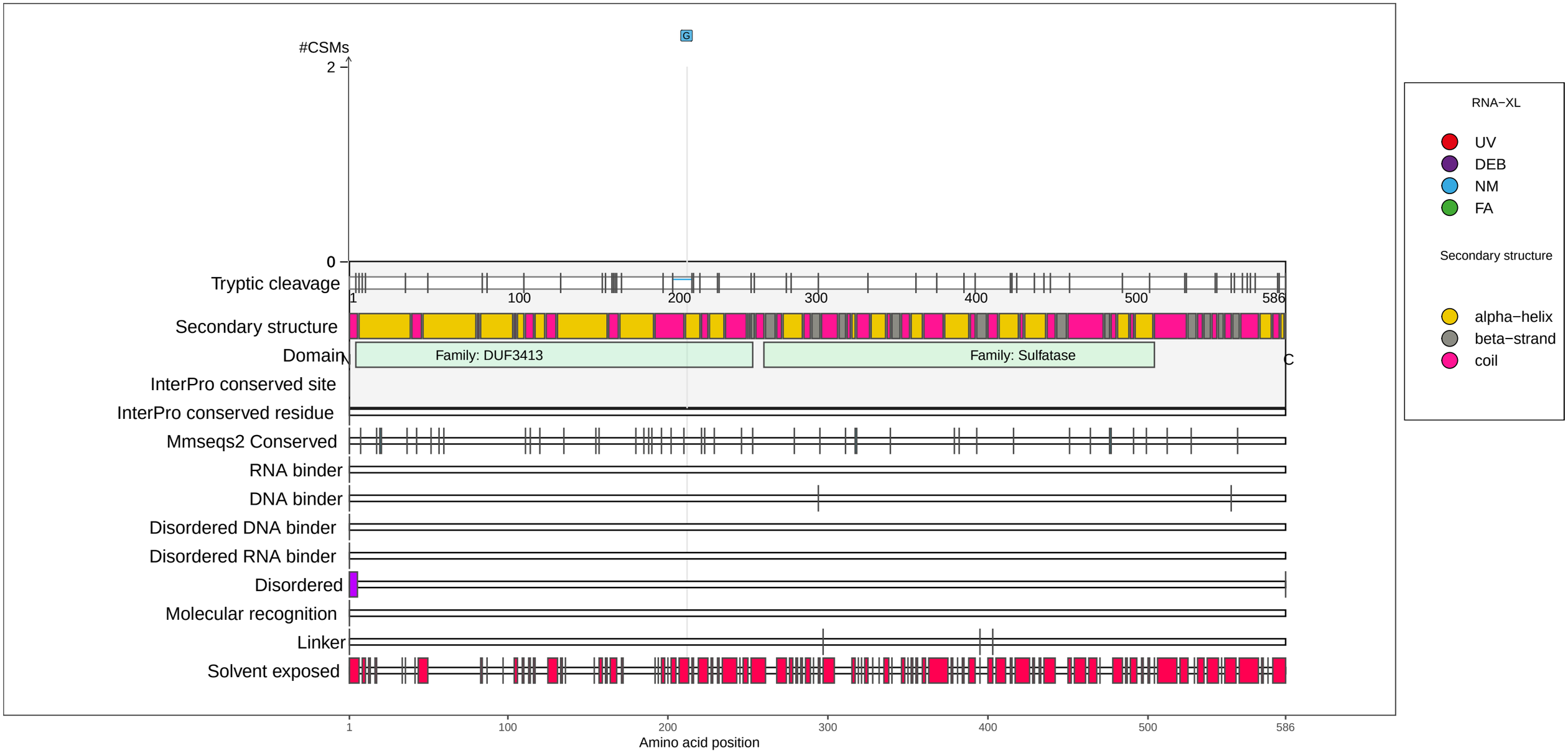
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0AD27
YEJM_ECOLI Inner membrane protein YejM

− Abundance:
tryptic [log10 Intensity]: 6.94 (Q 11)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.52 (Q 36)

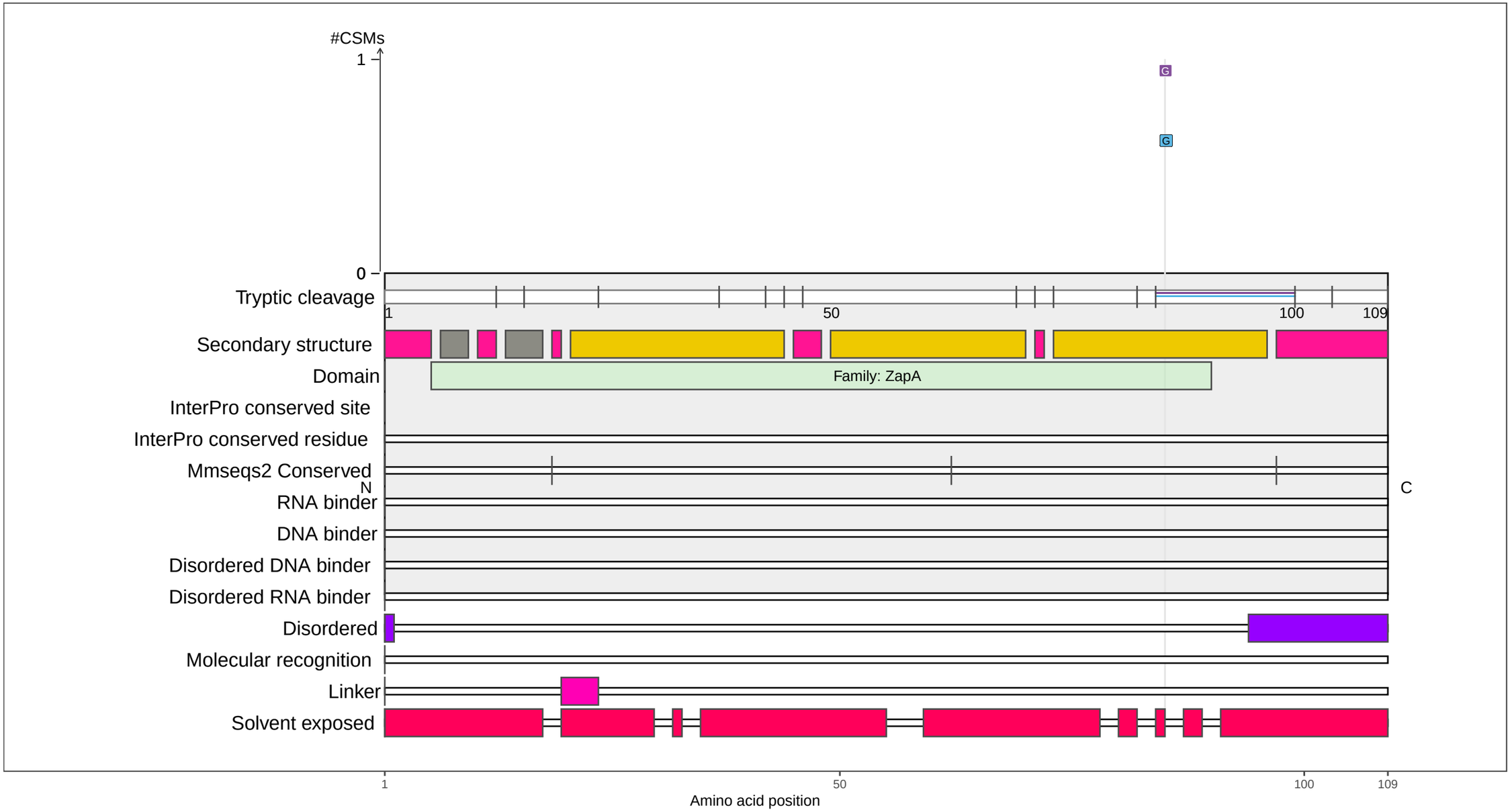
− RNA functions: not annotated



P0ADS2
ZAPA_ECOLI Cell division protein ZapA

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: 2.48 (Q 77)
PAXdb E.coli [ppm]: 2.24 (Q 78)

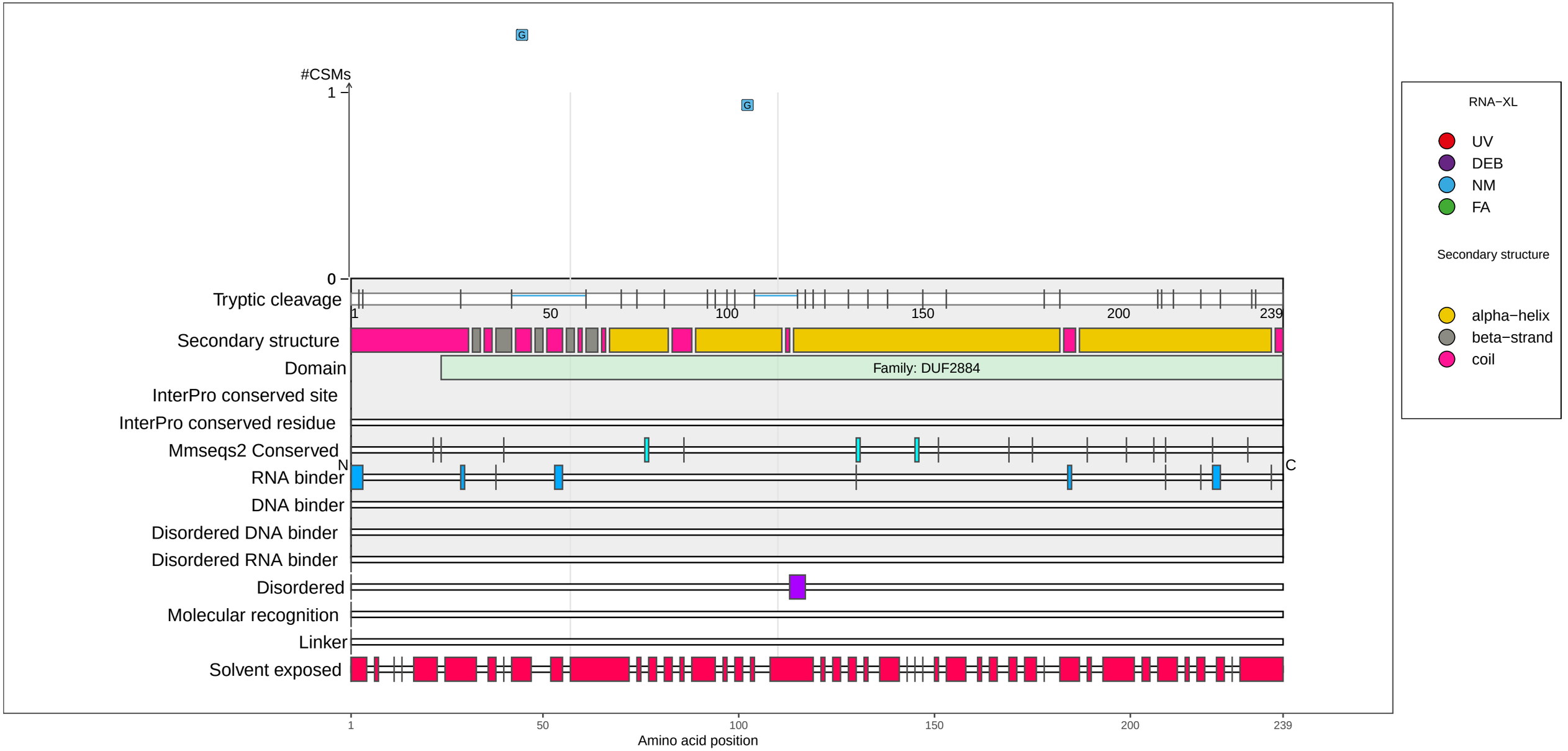
− RNA functions: not annotated



P0ADS9
YGGN_ECOLI Uncharacterized protein YggN

− Abundance:
tryptic [log10 Intensity]: 6.81 (Q 7)
PAXdb K12 strain [ppm]: 1.88 (Q 56)
PAXdb E.coli [ppm]: 2.23 (Q 78)

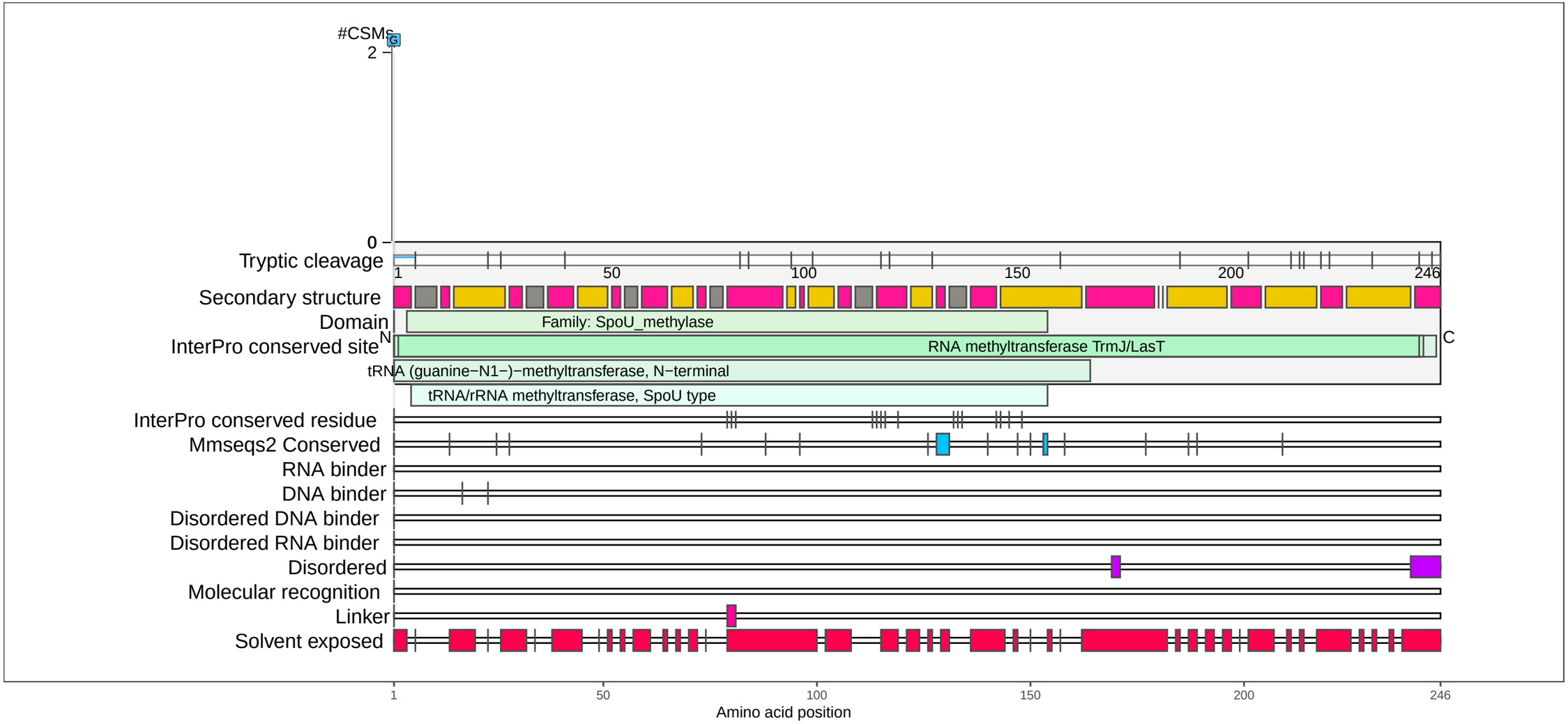
− RNA functions: not annotated



P0AE01
TRMJ_ECOLI tRNA (cytidine/uridine−2'−O−)−methyltransferase TrmJ

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 1.91 (Q 70)

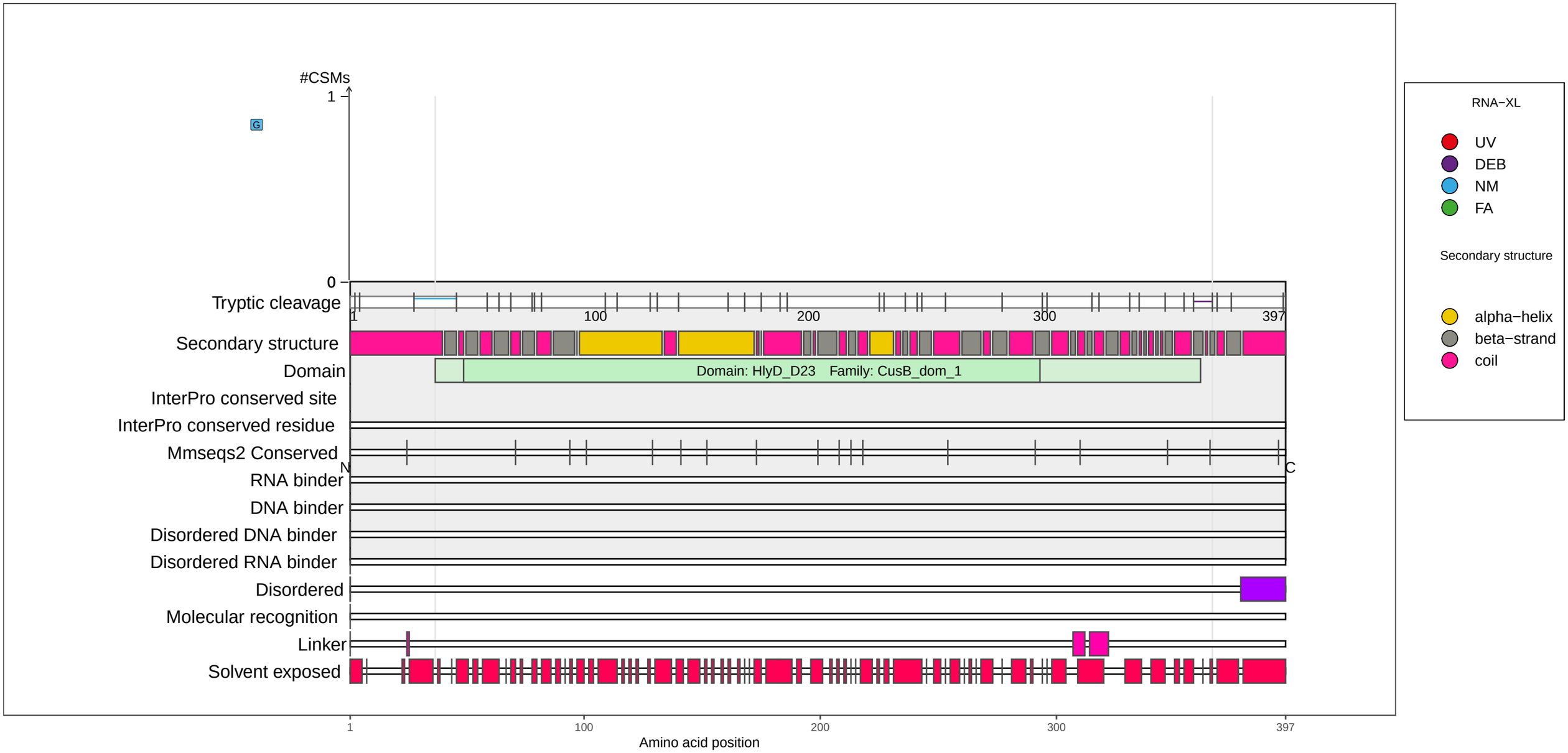
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA binding; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; SpoU rRNA Methylase family
tRNA (cytosine−2−O−)−methyltransferase activity; tRNA (cytosine) methyltransferase activity
tRNA (uracil−2−O−)−methyltransferase activity; tRNA (uracil) methyltransferase activity
tRNA 2−O−methyltransferase activity; tRNA metabolic process; tRNA methylation
tRNA methyltransferase activity; tRNA modification; tRNA nucleoside ribose methylation; tRNA processing



P0AE06
ACRA_ECOLI Multidrug efflux pump subunit AcrA

− Abundance:
tryptic [log10 Intensity]: 8.84 (Q 84)
PAXdb K12 strain [ppm]: 2.26 (Q 69)
PAXdb E.coli [ppm]: 2.44 (Q 84)

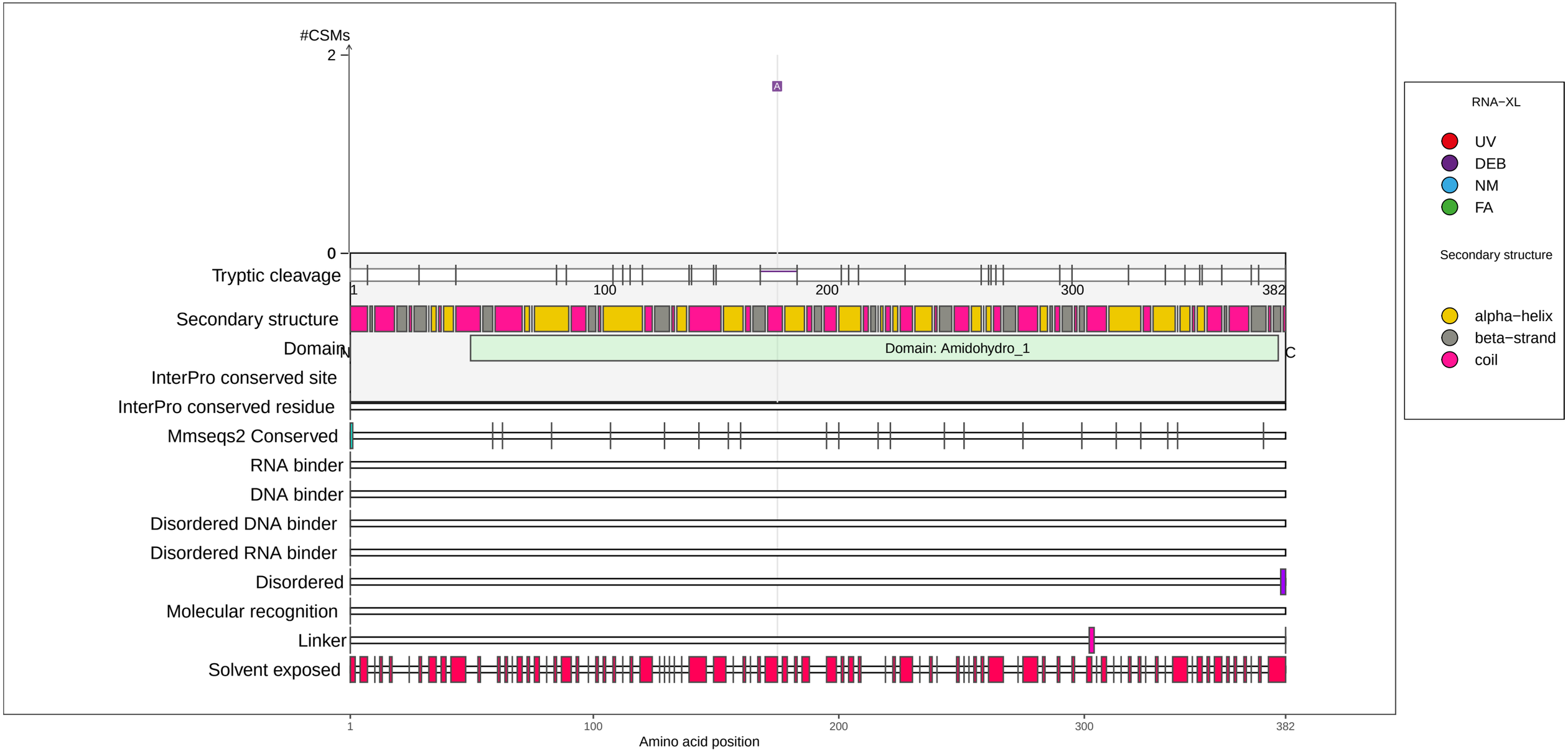
− RNA functions: not annotated



P0AF18
NAGA_ECOLI N−acetylglucosamine−6−phosphate deacetylase

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 2.73 (Q 84)
PAXdb E.coli [ppm]: 2.13 (Q 76)

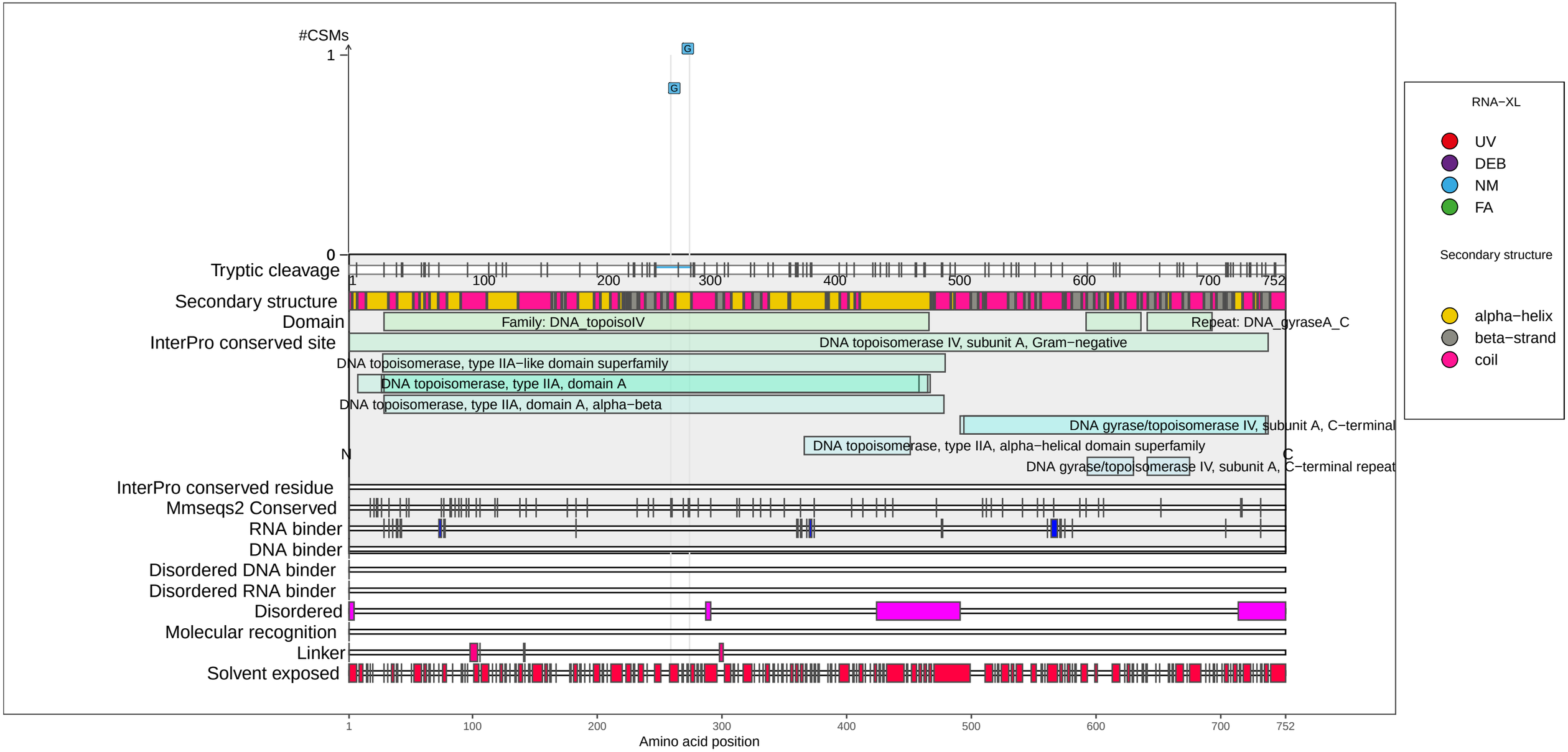
− RNA functions: not annotated



P0AFI2
PARC_ECOLI DNA topoisomerase 4 subunit A

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 1.81 (Q 54)
PAXdb E.coli [ppm]: 1.95 (Q 71)

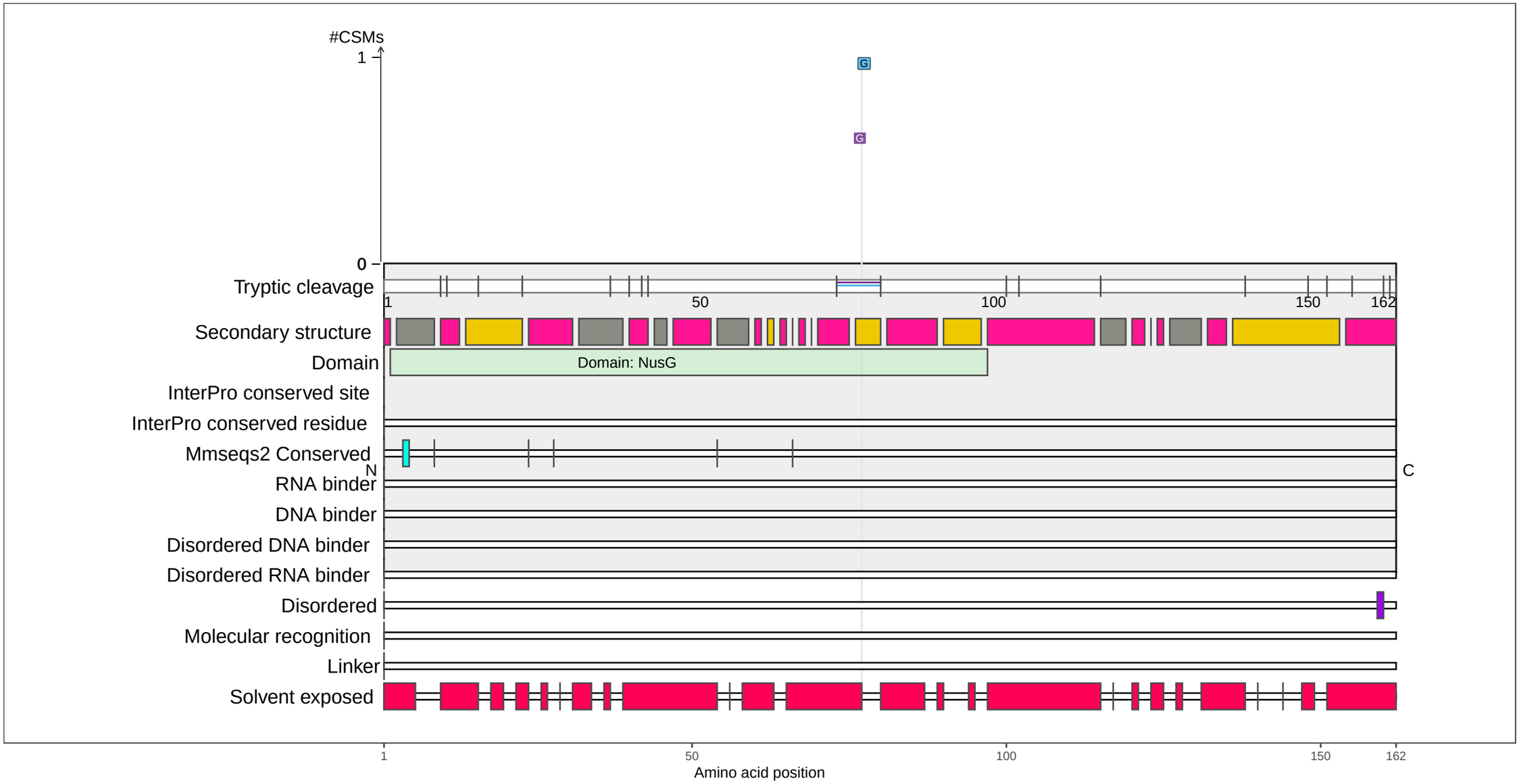
− RNA functions: not annotated

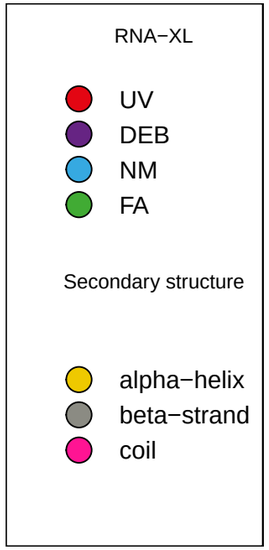


P0AFW0
RFAH_ECOLI Transcription antitermination protein RfaH

− Abundance:
tryptic [log10 Intensity]: 6.22 (Q 1)
PAXdb K12 strain [ppm]: 1.76 (Q 52)
PAXdb E.coli [ppm]: 1.12 (Q 51)

− RNA functions:
RNA biosynthetic process; RNA metabolic process; RNA polymerase binding
RNA polymerase core enzyme binding

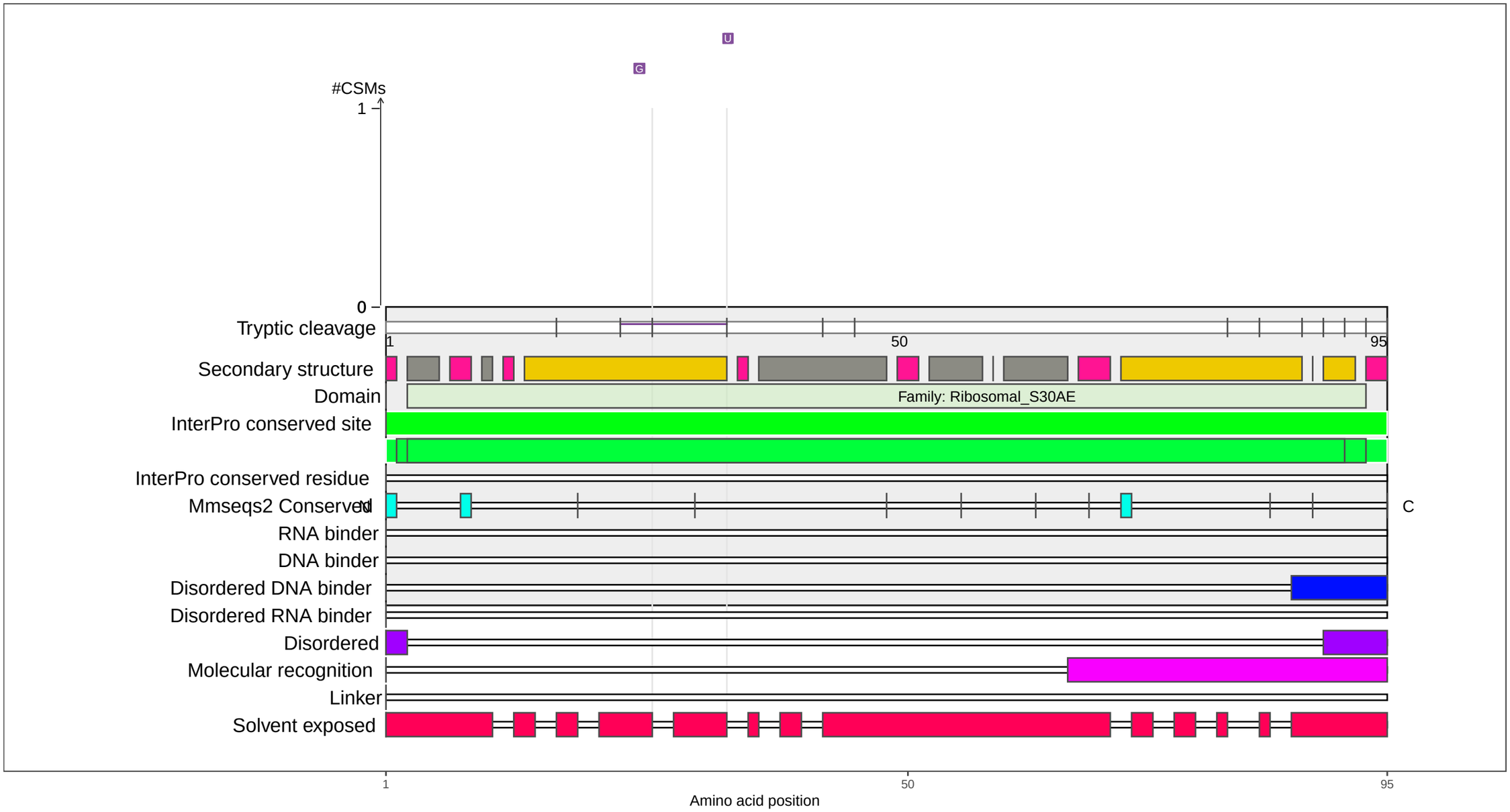




P0AFX0
HPF_ECOLI Ribosome hibernation promoting factor

− Abundance:
tryptic [log10 Intensity]: 8.88 (Q 85)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 3.29 (Q 97)

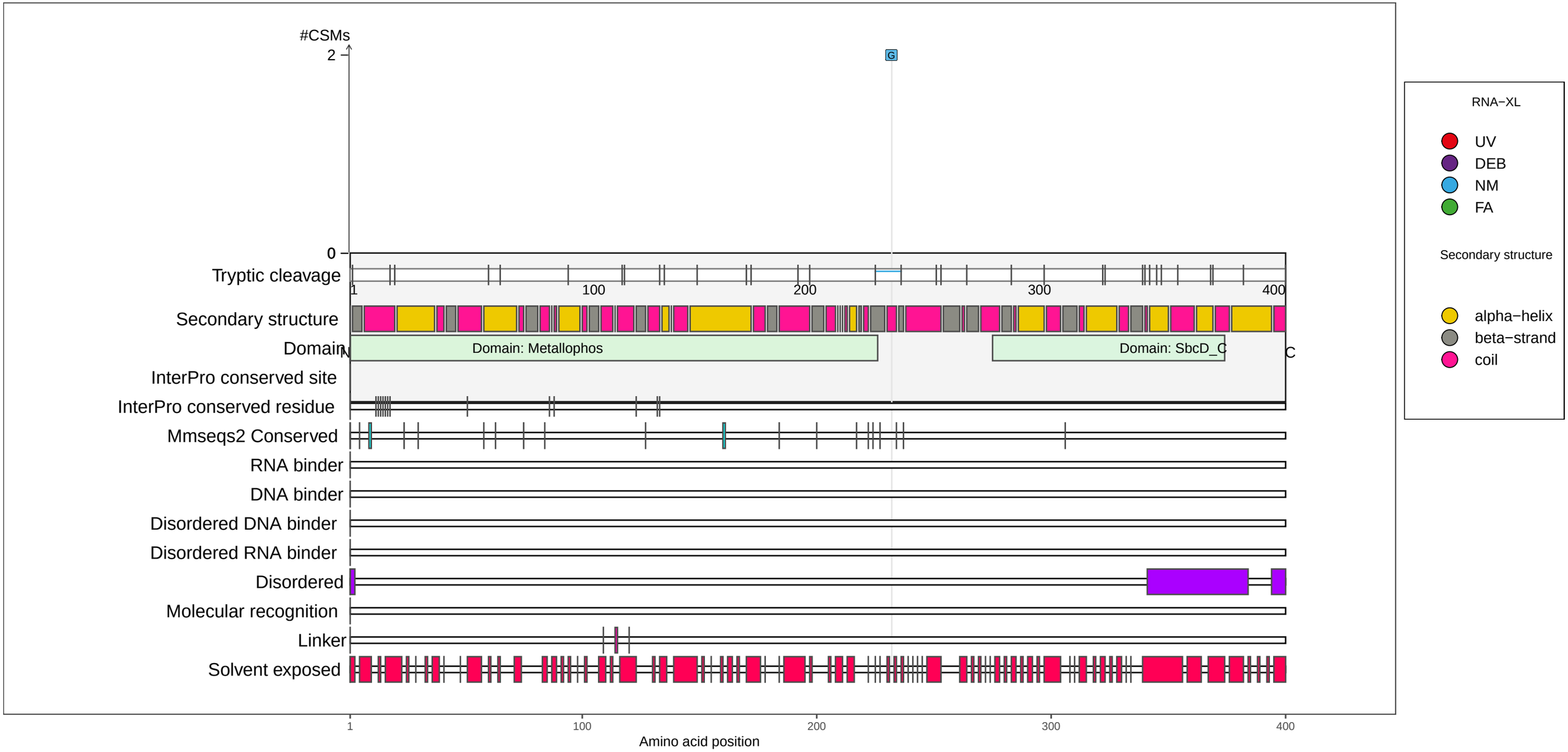
− RNA functions: not annotated



P0AG76
SBCD_ECOLI Nuclease SbcCD subunit D

− Abundance:
tryptic [log10 Intensity]: 7.24 (Q 23)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.01 (Q 9)

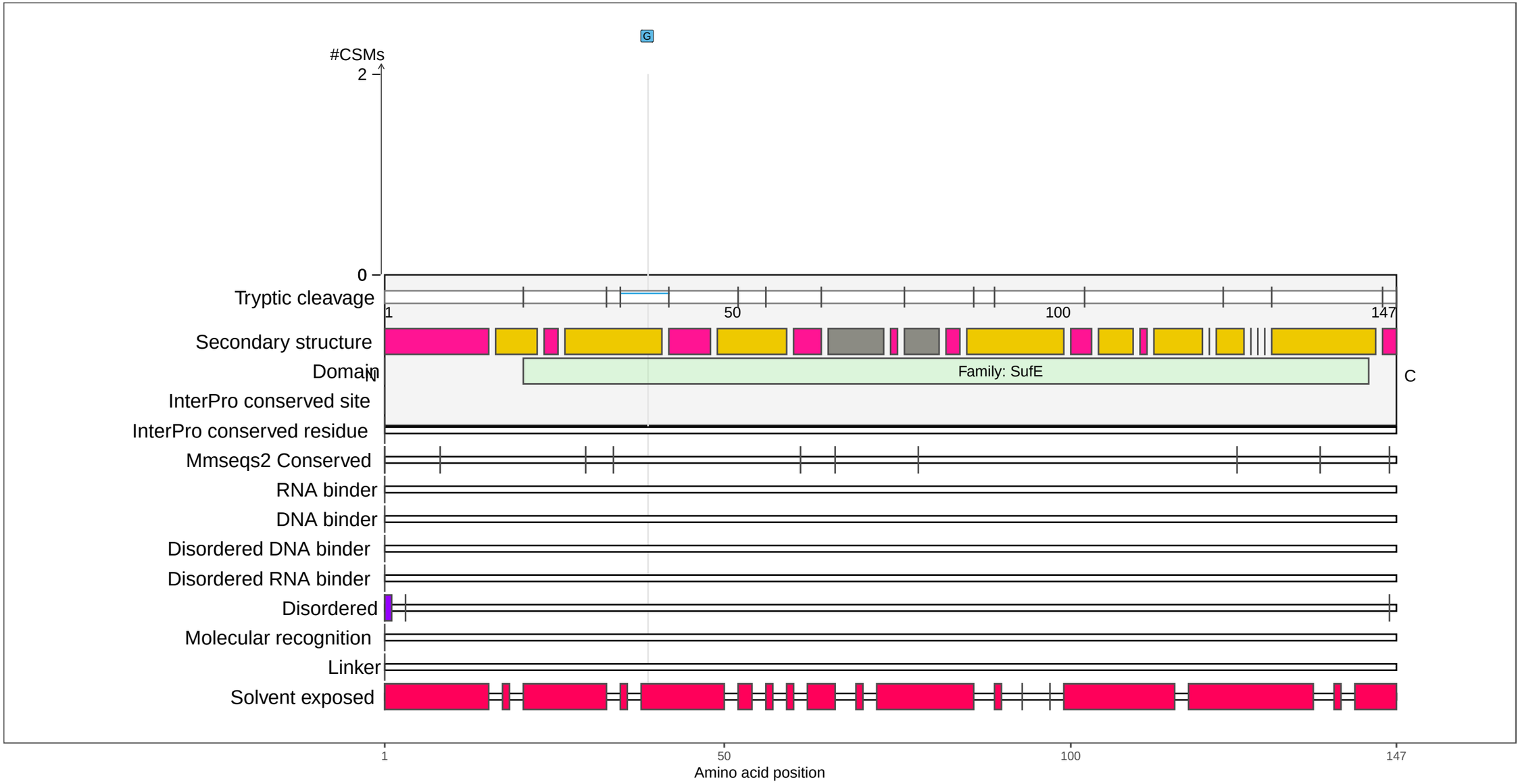
− RNA functions: not annotated

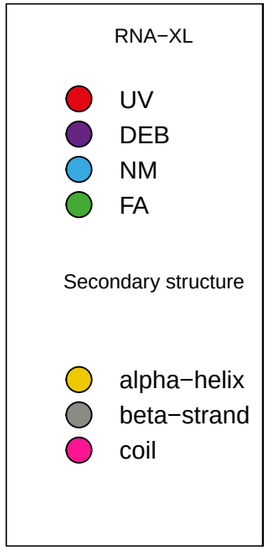


P0AGF2
CSDE_ECOLI Sulfur acceptor protein CsdE

− Abundance:
tryptic [log10 Intensity]: 7.7 (Q 44)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 1.73 (Q 65)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing

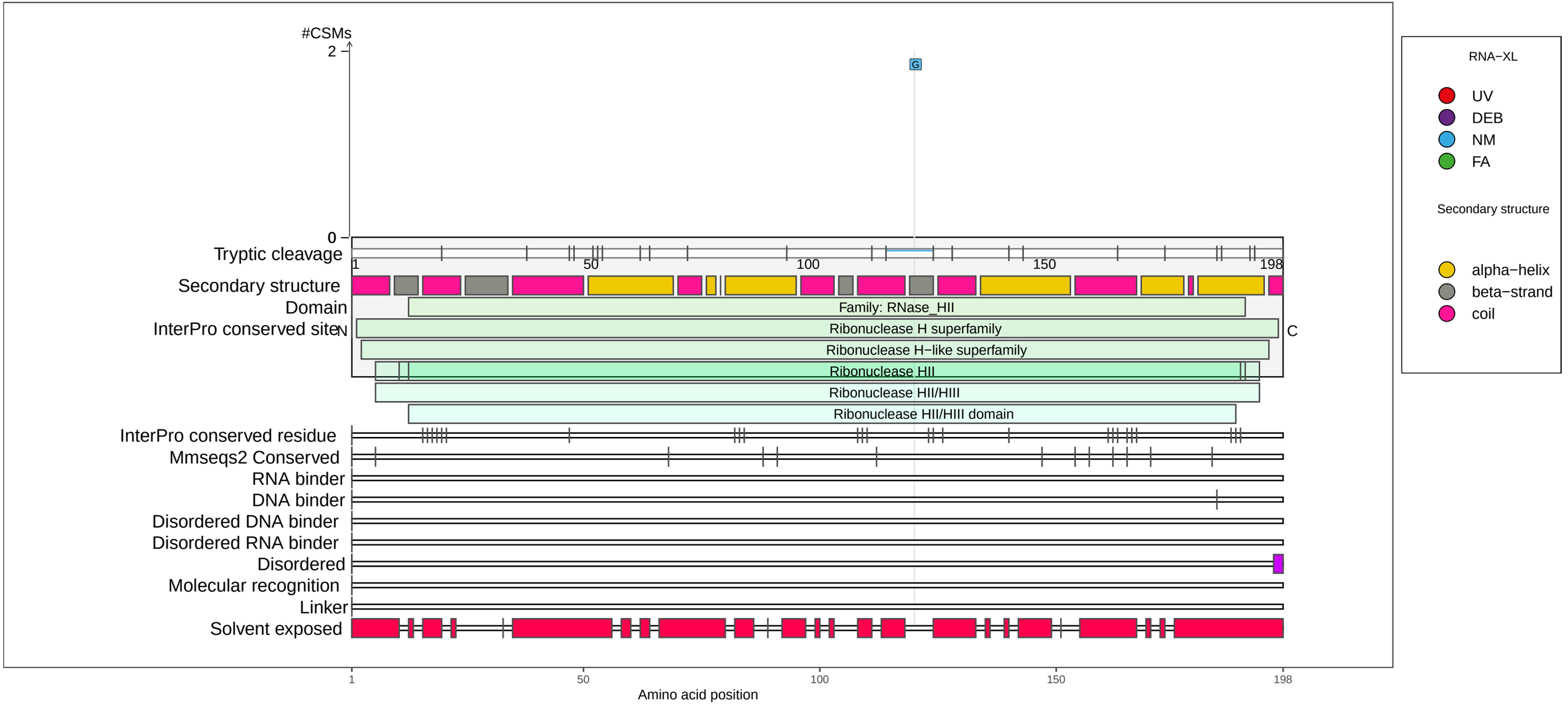




P10442
RNH2_ECOLI Ribonuclease HII

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.36 (Q 56)

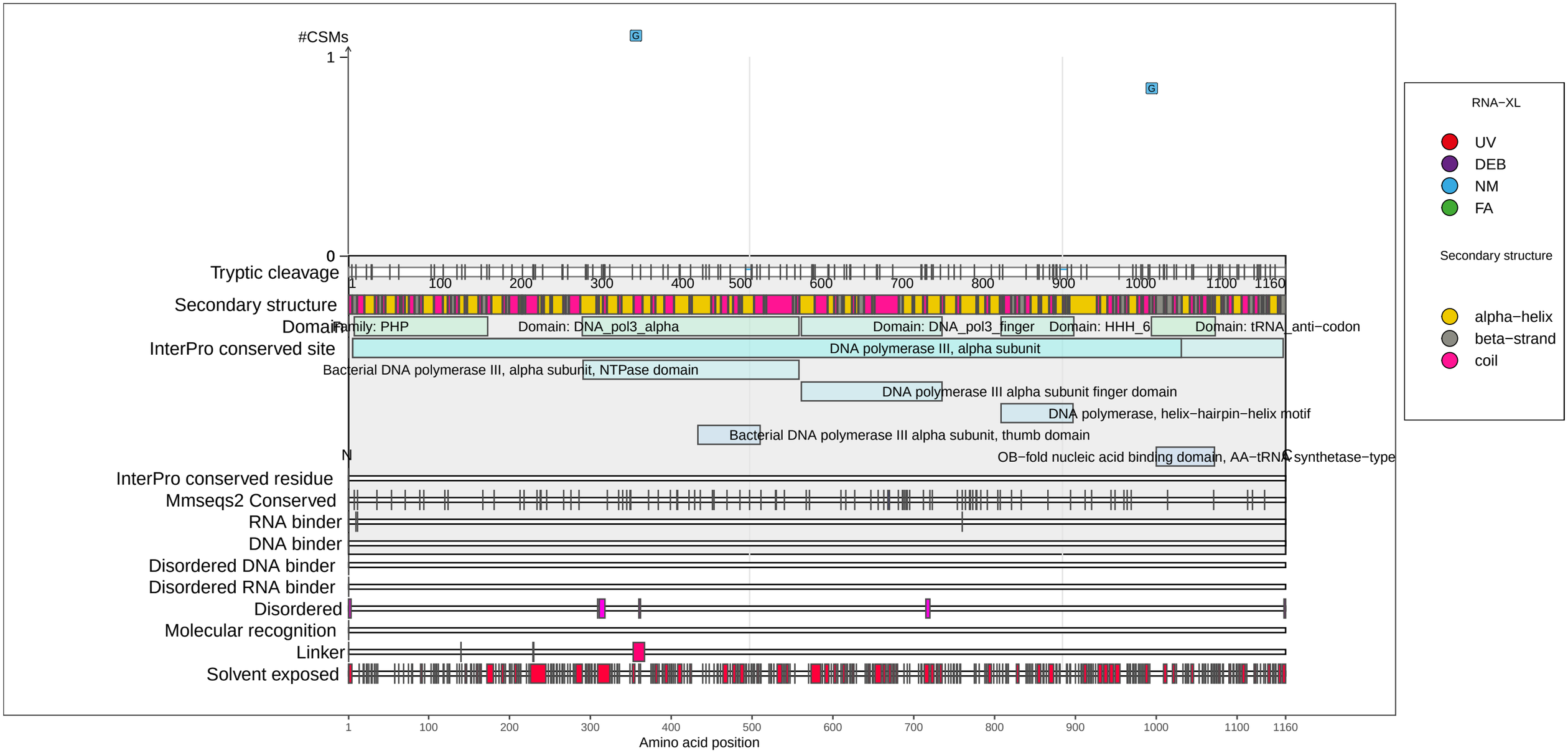
− RNA functions:
DNA replication, removal of RNA primer; RNA binding; RNA catabolic process
RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic; RNA−DNA hybrid ribonuclease activity



P10443
DPO3A_ECOLI DNA polymerase III subunit alpha

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1 (Q 11)
PAXdb E.coli [ppm]: 1.26 (Q 54)

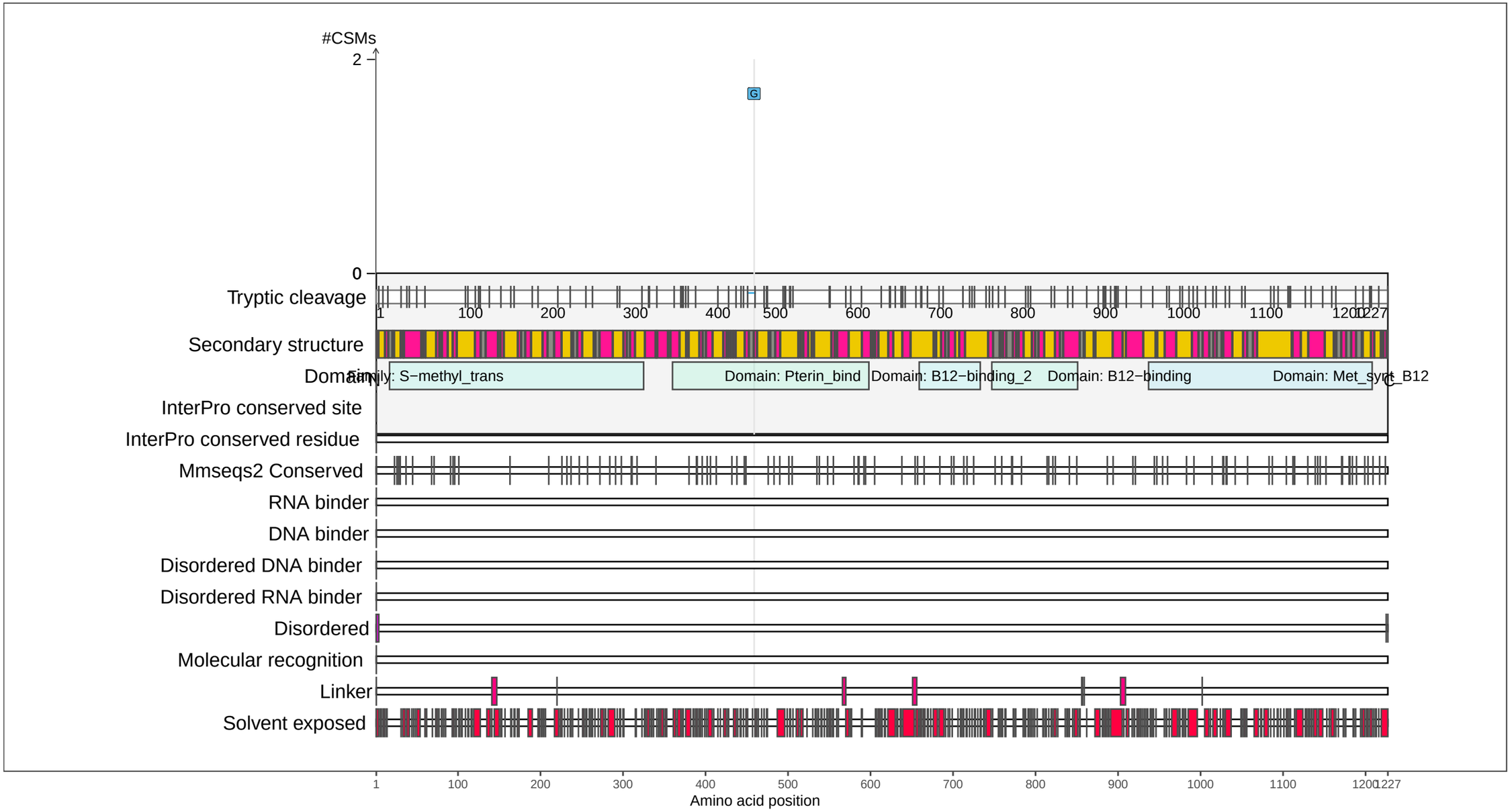
− RNA functions: not annotated



P13009
METH_ECOLI Methionine synthase

− Abundance:
tryptic [log10 Intensity]: 8.34 (Q 71)
PAXdb K12 strain [ppm]: 2.33 (Q 71)
PAXdb E.coli [ppm]: 1.81 (Q 67)

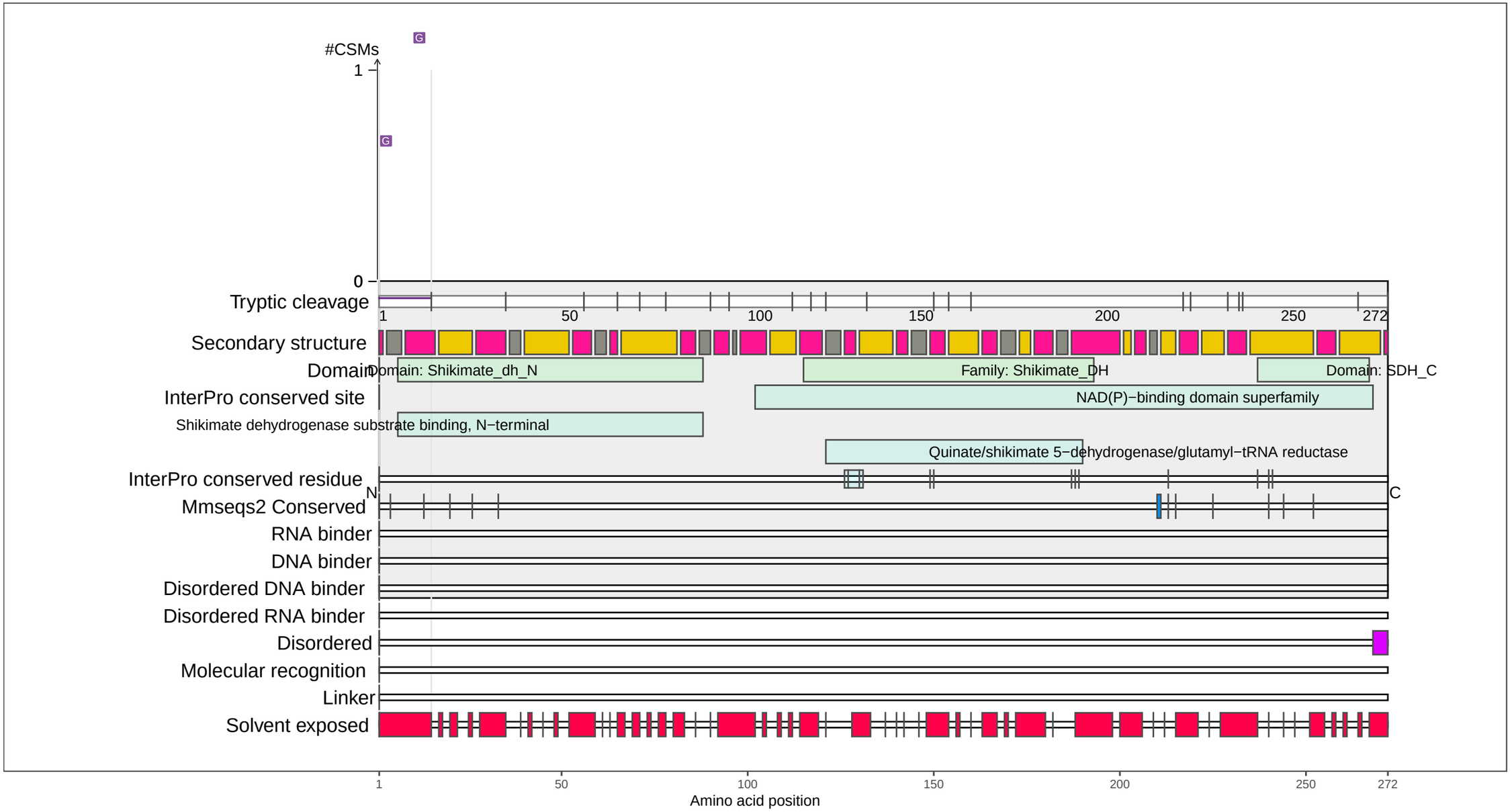
− RNA functions: not annotated

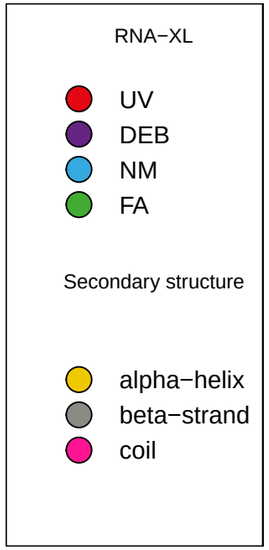


P15770
AROE_ECOLI Shikimate dehydrogenase (NADP(+))

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.86 (Q 69)

− RNA functions: not annotated

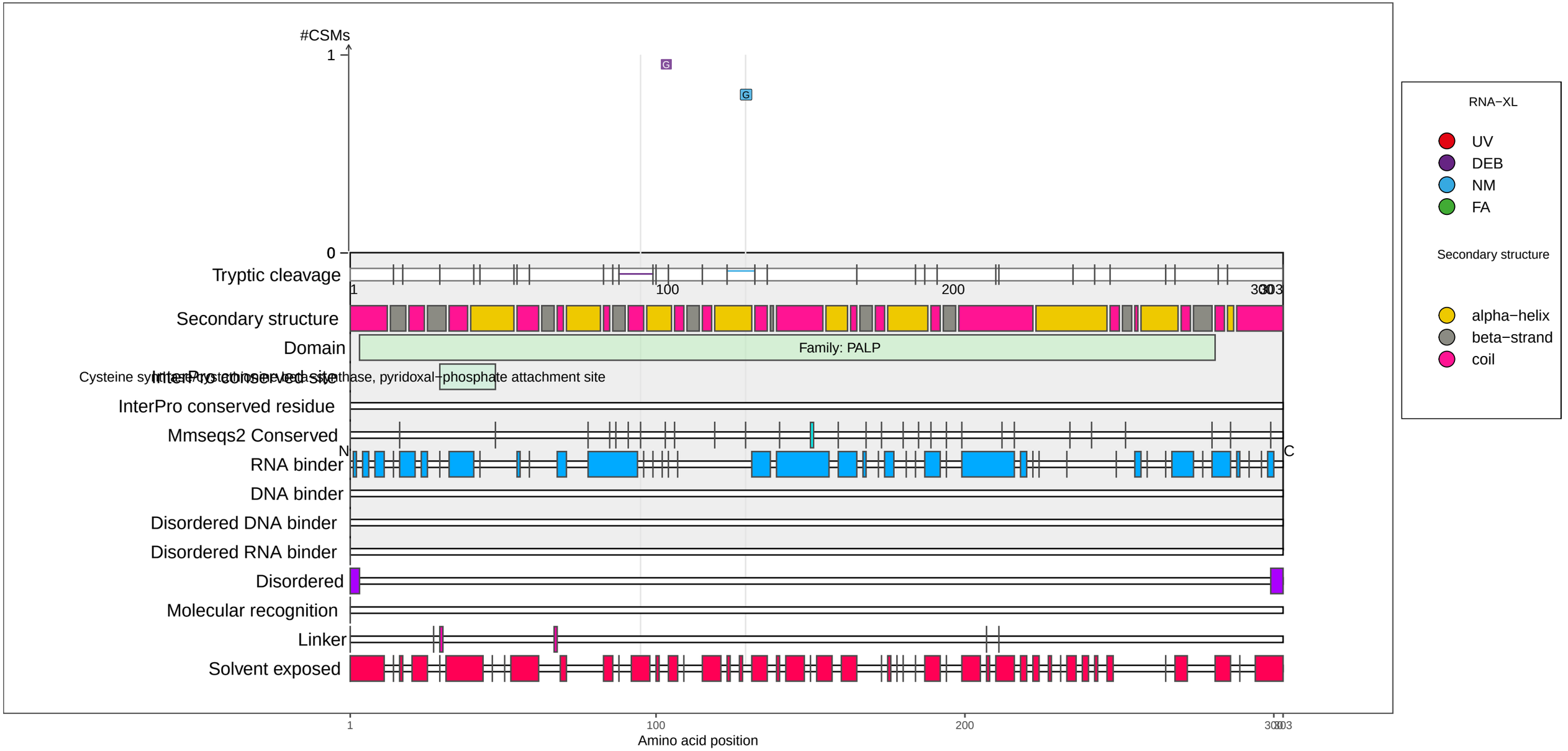




P16703
CYSM_ECOLI Cysteine synthase B

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.1 (Q 75)

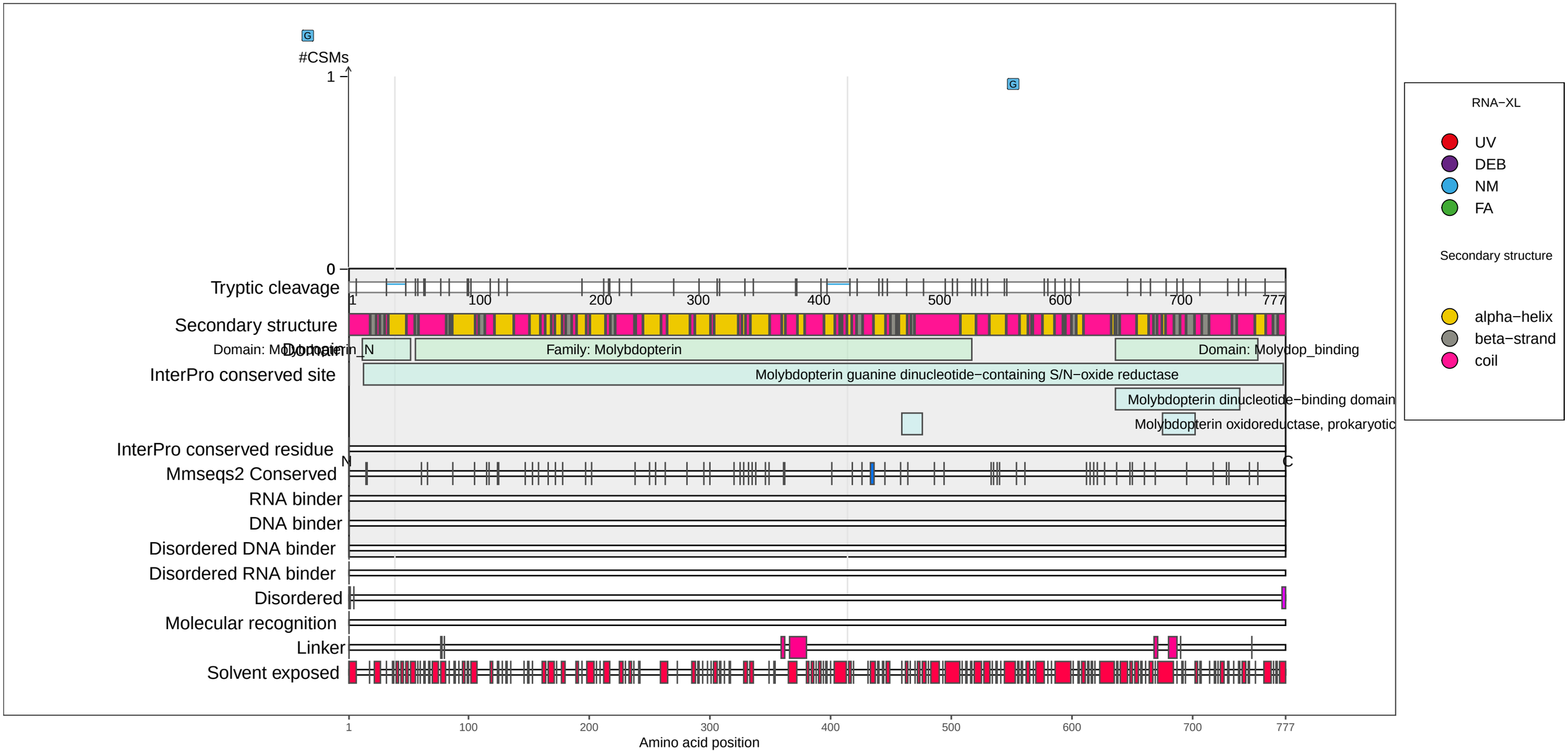
− RNA functions: not annotated



P20099
BISC_ECOLI Biotin sulfoxide reductase

− Abundance:
tryptic [log10 Intensity]: 6.8 (Q 7)
PAXdb K12 strain [ppm]: 1 (Q 11)
PAXdb E.coli [ppm]: 1.2 (Q 52)

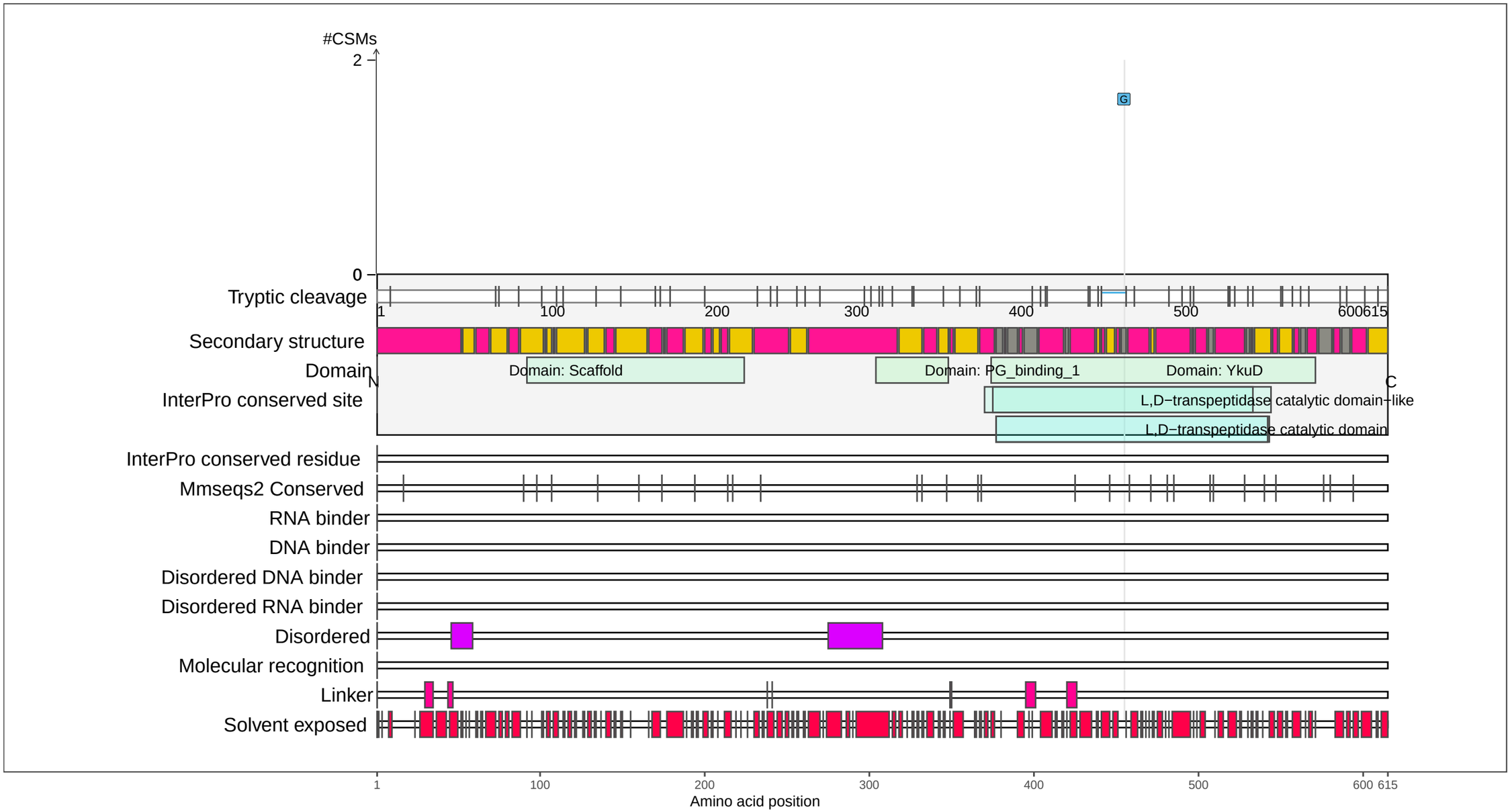
− RNA functions: not annotated

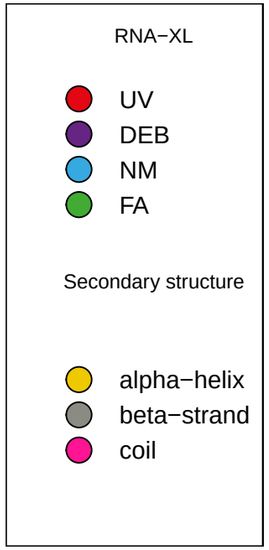


P22525
YCBB_ECOLI Probable L,D−transpeptidase YcbB

− Abundance:
tryptic [log10 Intensity]: 7.12 (Q 17)
PAXdb K12 strain [ppm]: 0.58 (Q 1)
PAXdb E.coli [ppm]: 1.09 (Q 50)

− RNA functions: not annotated

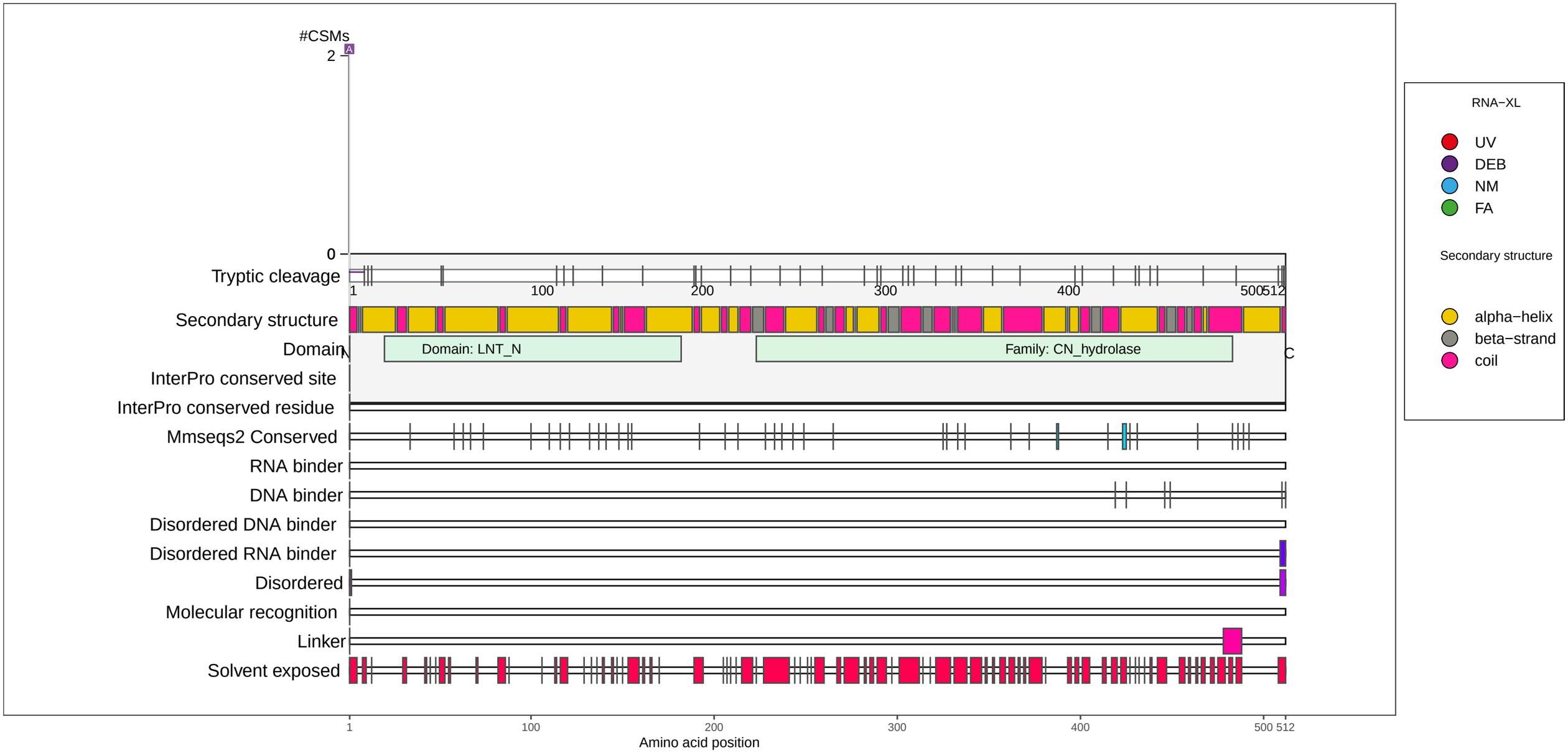




P23930
LNT_ECOLI Apolipoprotein N−acyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.12 (Q 62)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.6 (Q 38)

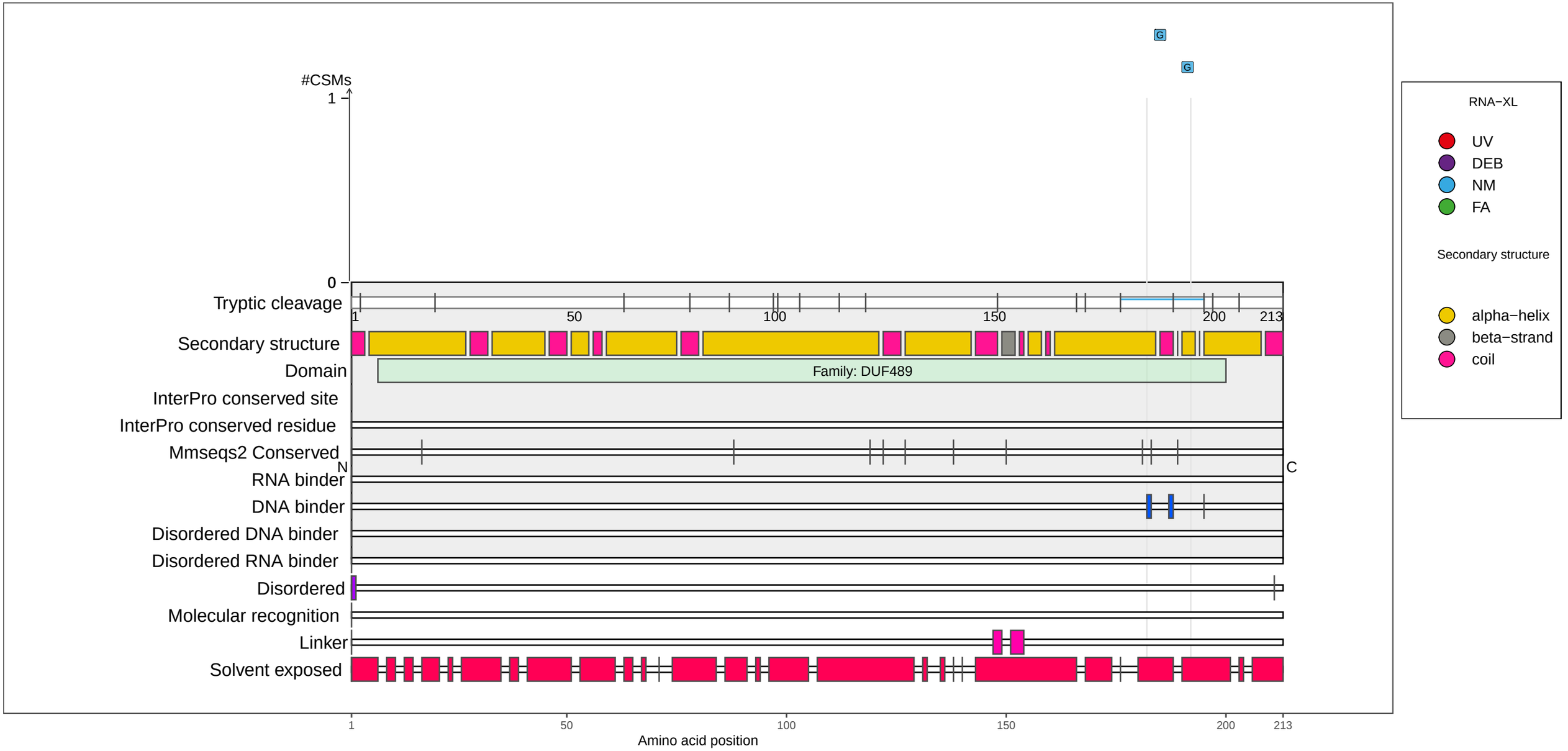
− RNA functions: not annotated



P25746
HFLD_ECOLI High frequency lysogenization protein HflD

− Abundance:
tryptic [log10 Intensity]: 6.84 (Q 8)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.63 (Q 63)

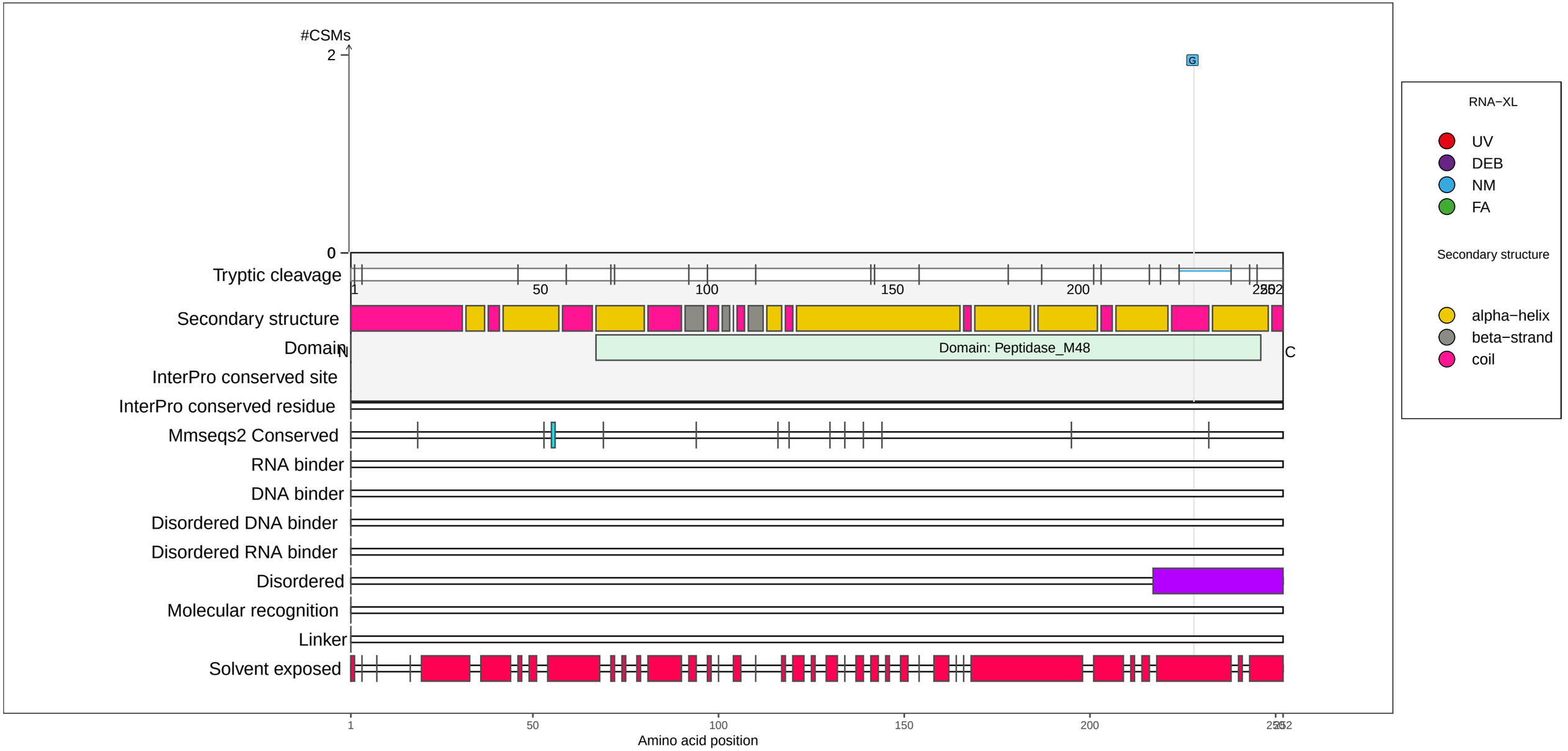
− RNA functions: not annotated



P25894
LOIP_ECOLI Metalloprotease LoiP

− Abundance:
tryptic [log10 Intensity]: 7.53 (Q 36)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 1.75 (Q 66)

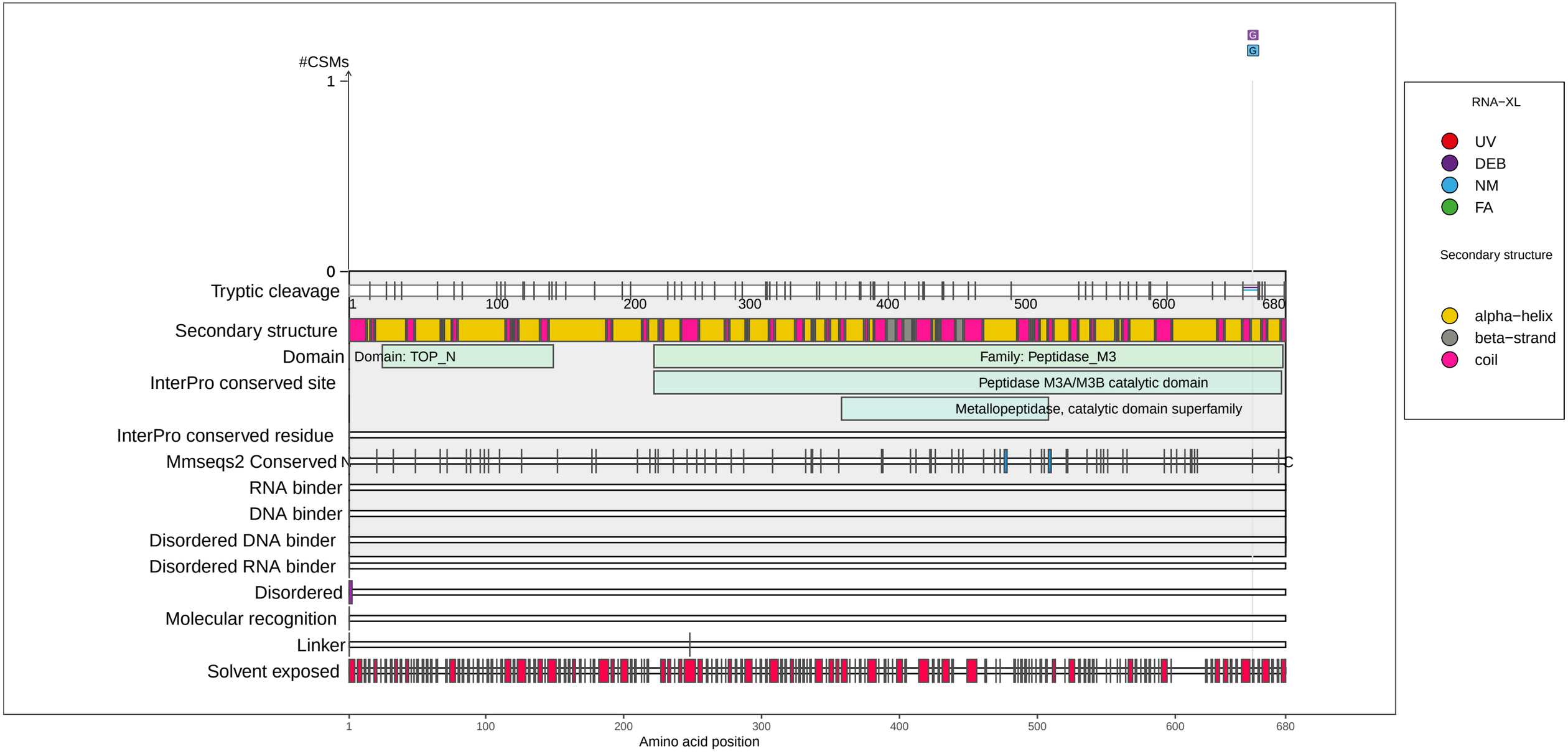
− RNA functions: not annotated



P27298
OPDA_ECOLI Oligopeptidase A

− Abundance:
tryptic [log10 Intensity]: 9.08 (Q 90)
PAXdb K12 strain [ppm]: 2.89 (Q 88)
PAXdb E.coli [ppm]: 2.52 (Q 86)

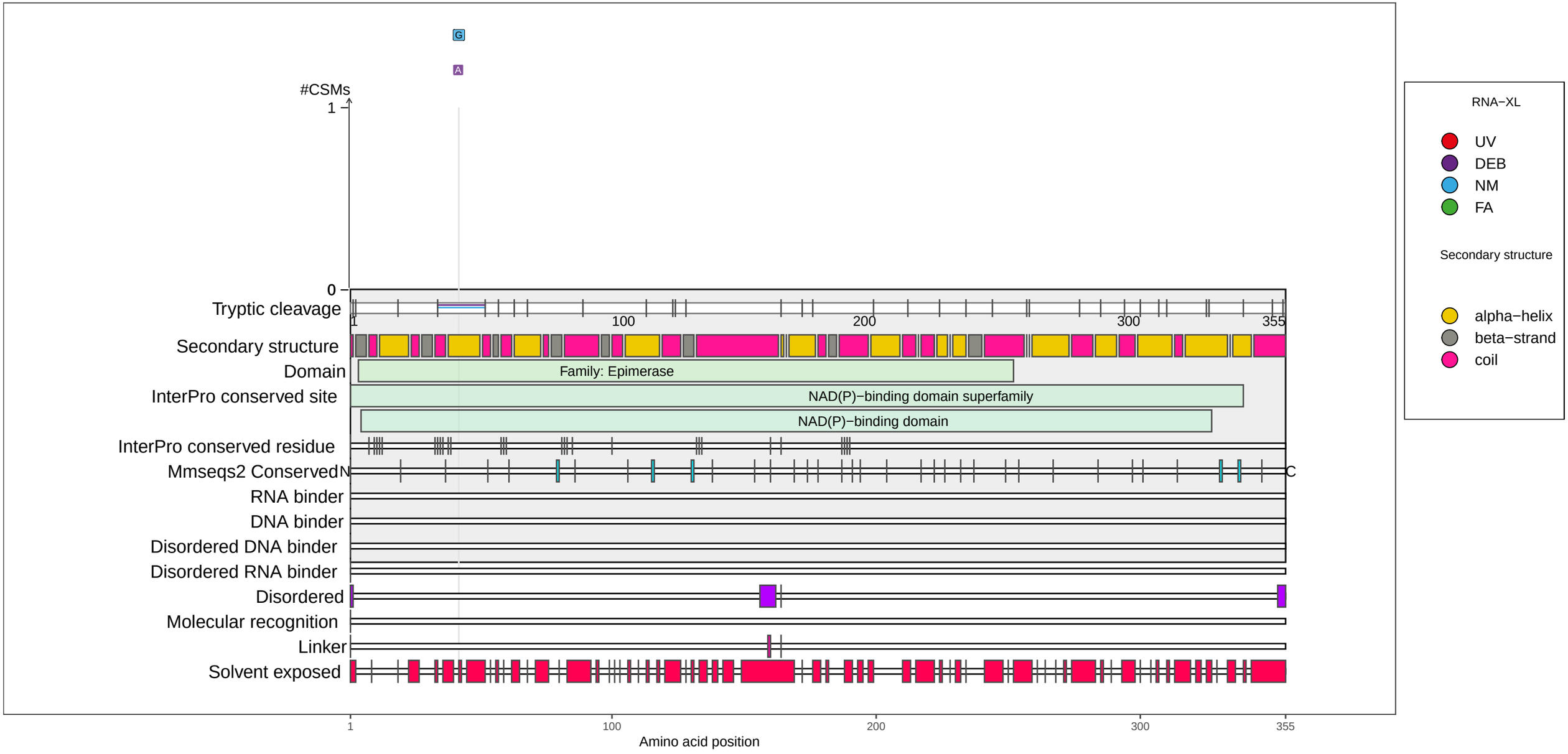
− RNA functions: not annotated



P27830
RMLB2_ECOLI dTDP−glucose 4,6−dehydratase 2

− Abundance:
tryptic [log10 Intensity]: 8.72 (Q 82)
PAXdb K12 strain [ppm]: 0.6 (Q 1)
PAXdb E.coli [ppm]: 0.73 (Q 41)

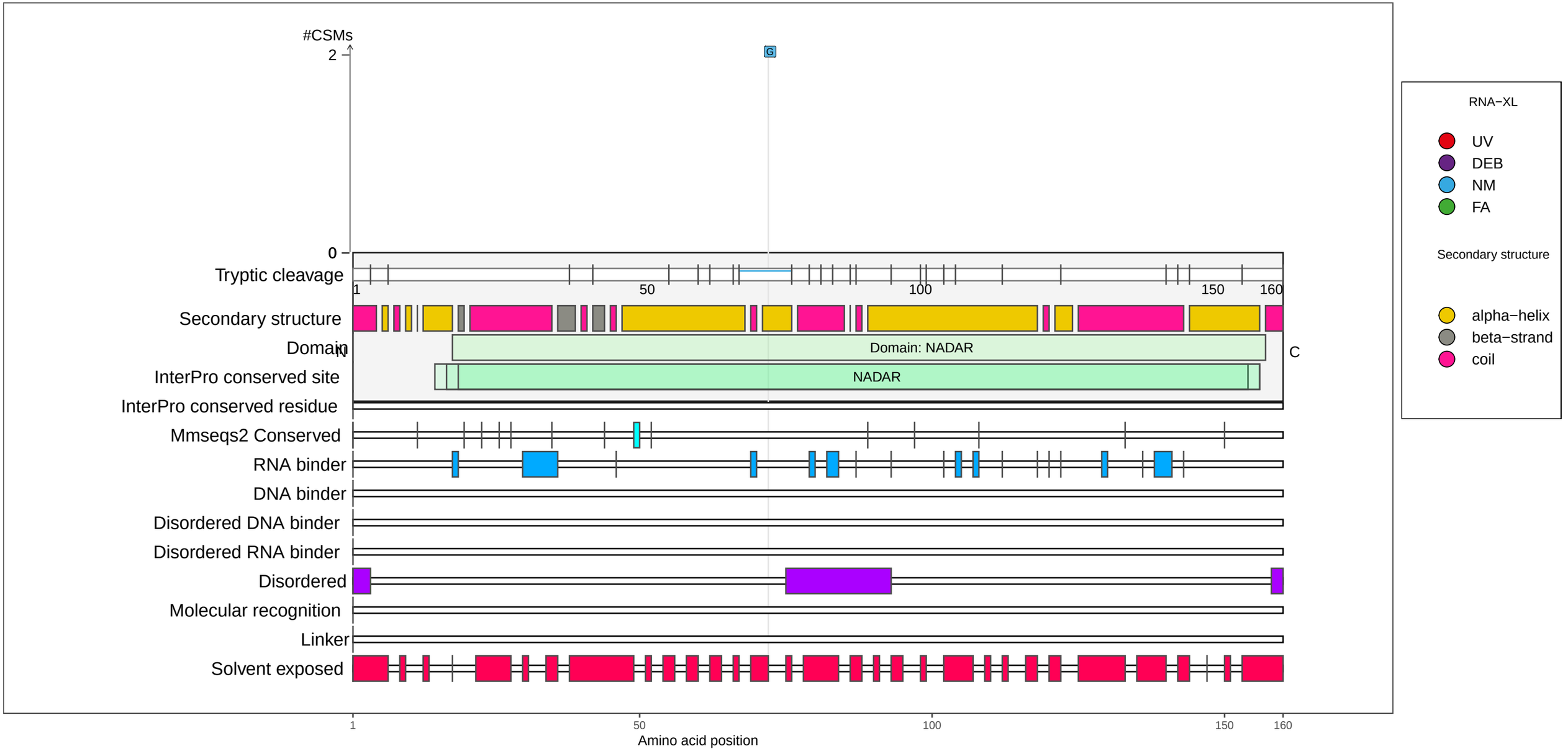
− RNA functions: not annotated



P30176
RIBX_ECOLI N−glycosidase YbiA

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.27 (Q 24)
PAXdb E.coli [ppm]: −0.13 (Q 22)

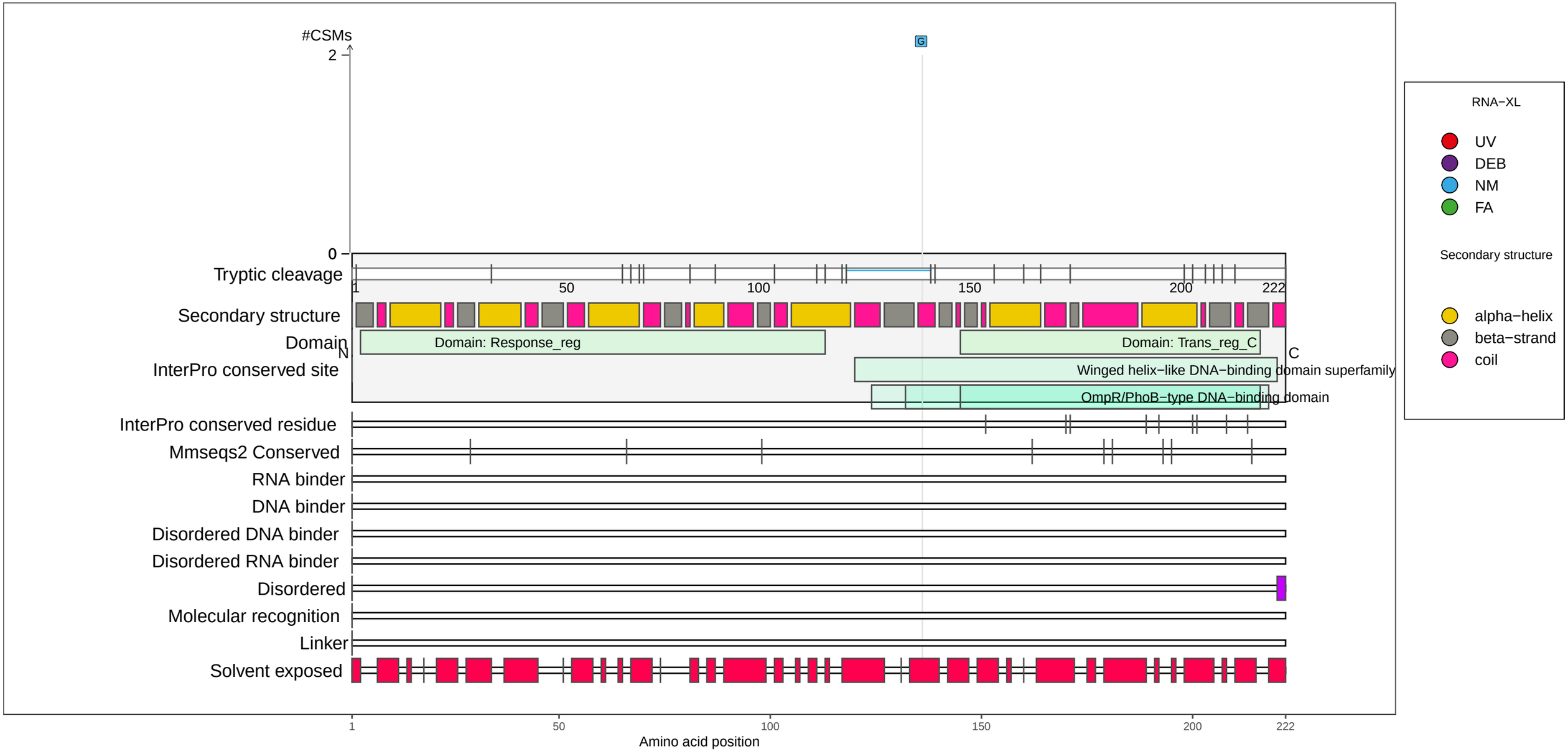
− RNA functions: not annotated



P30843
BASR_ECOLI Transcriptional regulatory protein BasR

− Abundance:
tryptic [log10 Intensity]: 8.74 (Q 82)
PAXdb K12 strain [ppm]: 2.18 (Q 66)
PAXdb E.coli [ppm]: 2.25 (Q 79)

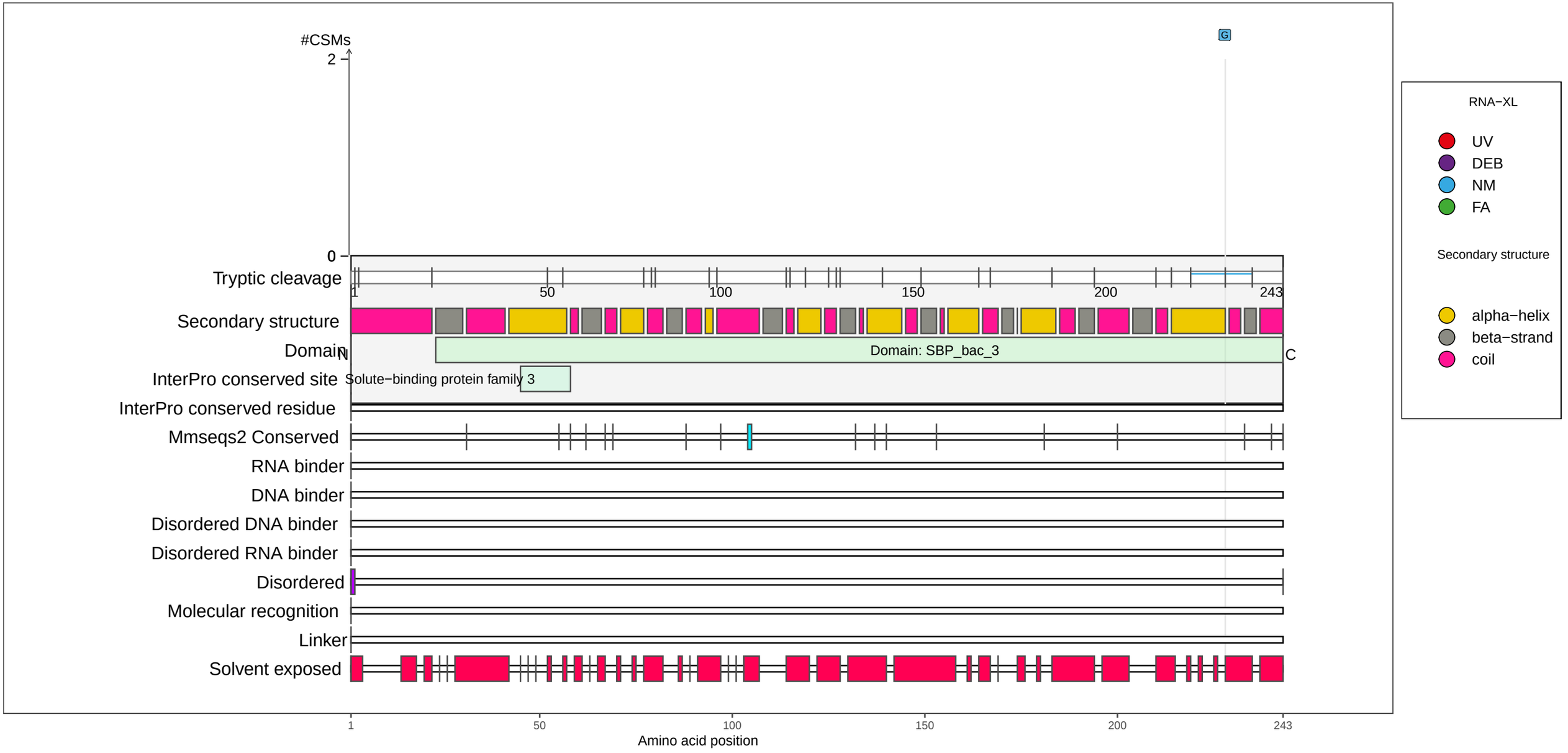
− RNA functions: not annotated



P30860
ARTJ_ECOLI ABC transporter arginine−binding protein 1

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 65)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: 2.67 (Q 89)

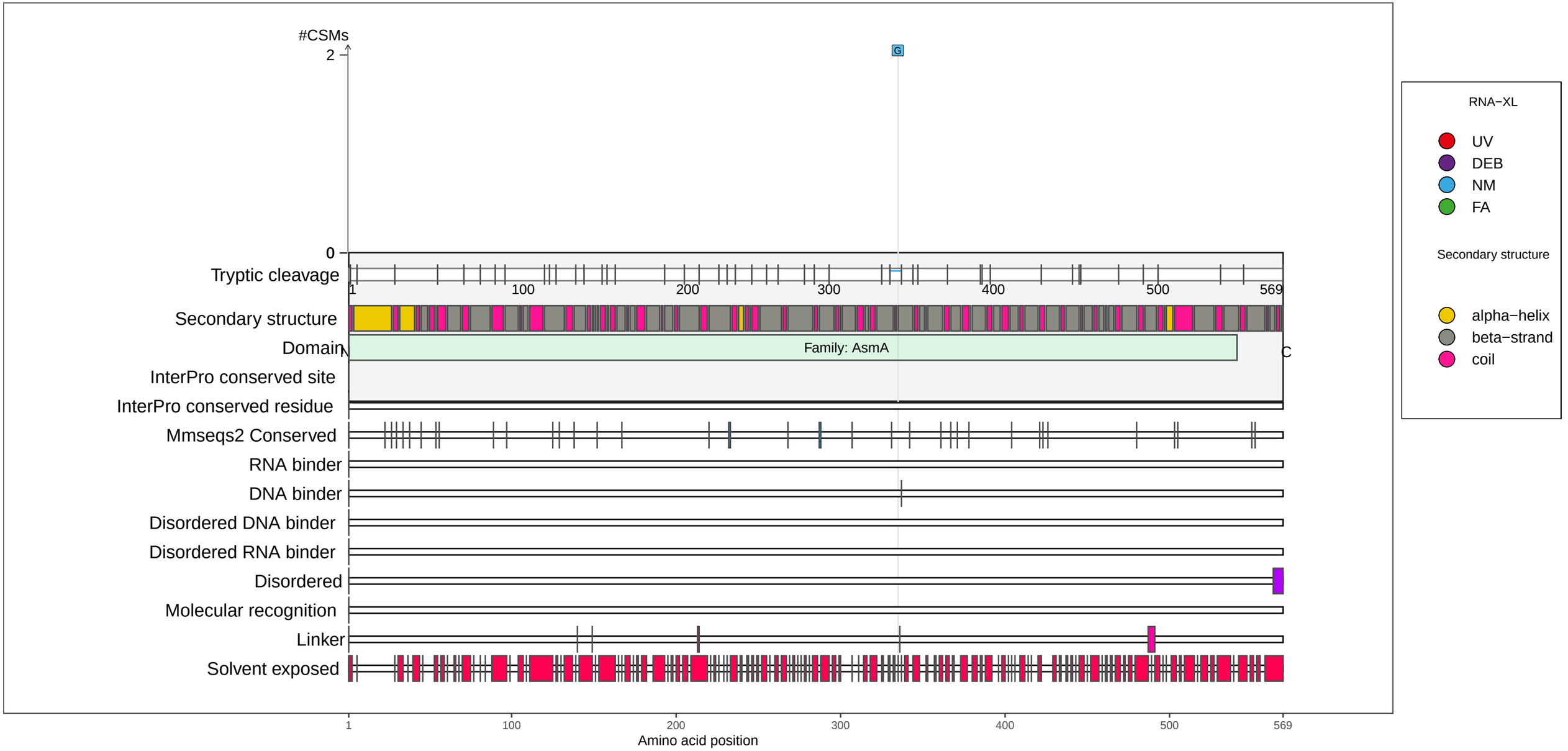
− RNA functions: not annotated



P31433
YICH_ECOLI AsmA family protein YicH

− Abundance:
tryptic [log10 Intensity]: 8.05 (Q 60)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.37 (Q 56)

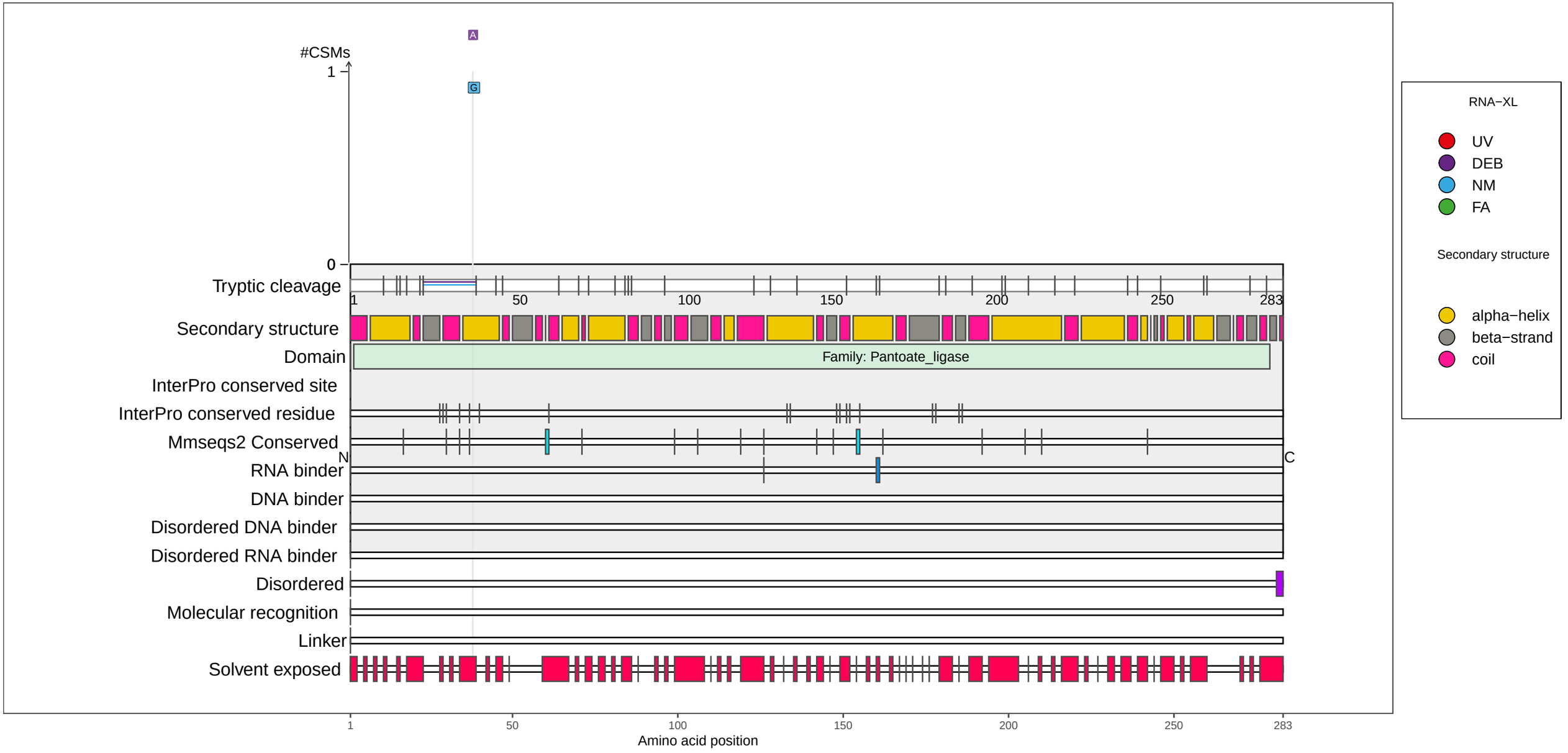
− RNA functions: not annotated



P31663
PANC_ECOLI Pantothenate synthetase

− Abundance:
tryptic [log10 Intensity]: 8.67 (Q 81)
PAXdb K12 strain [ppm]: 2.4 (Q 74)
PAXdb E.coli [ppm]: 2.78 (Q 91)

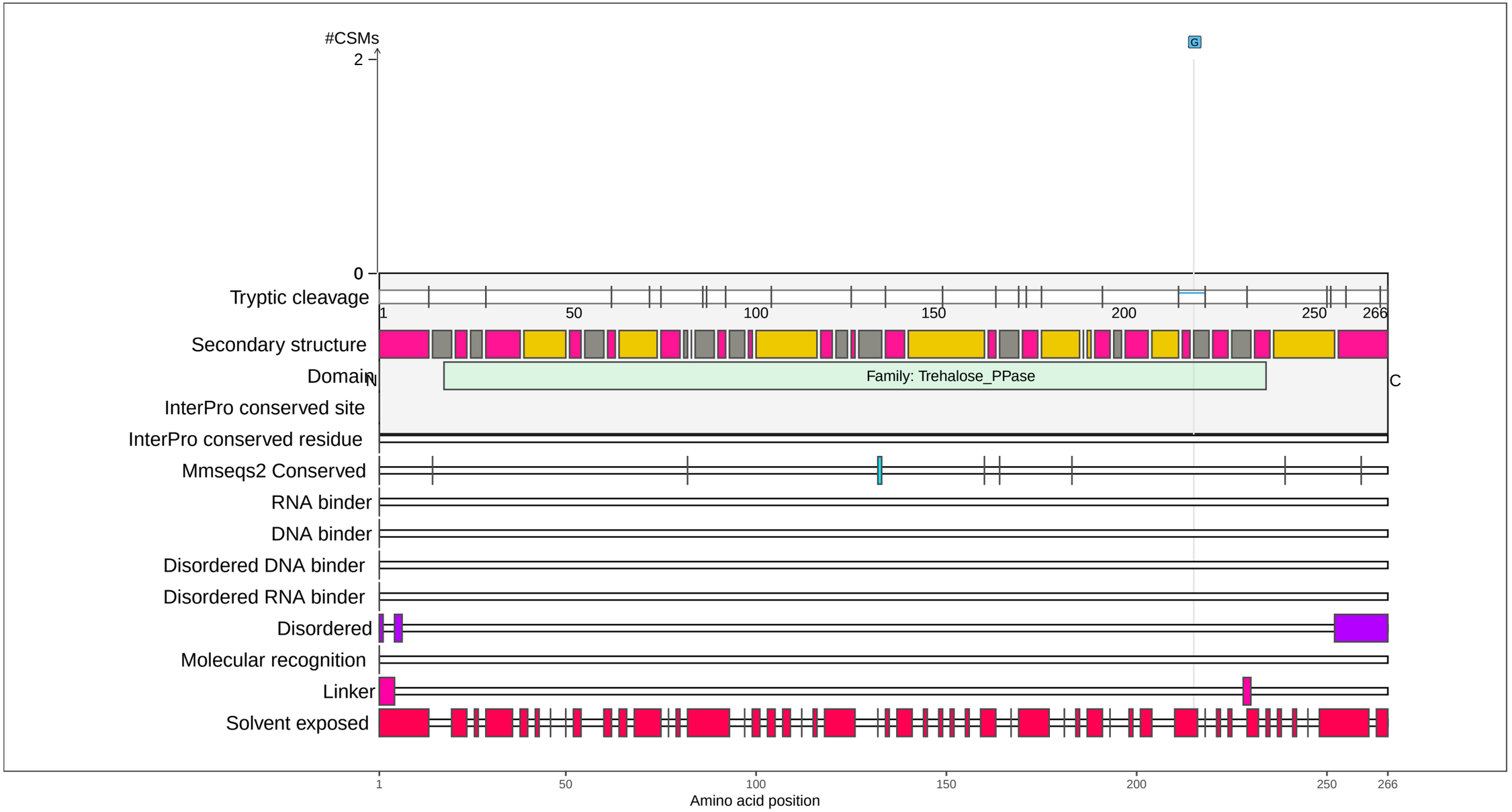
− RNA functions: not annotated



P31678
OTSB_ECOLI Trehalose−6−phosphate phosphatase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.5 (Q 60)

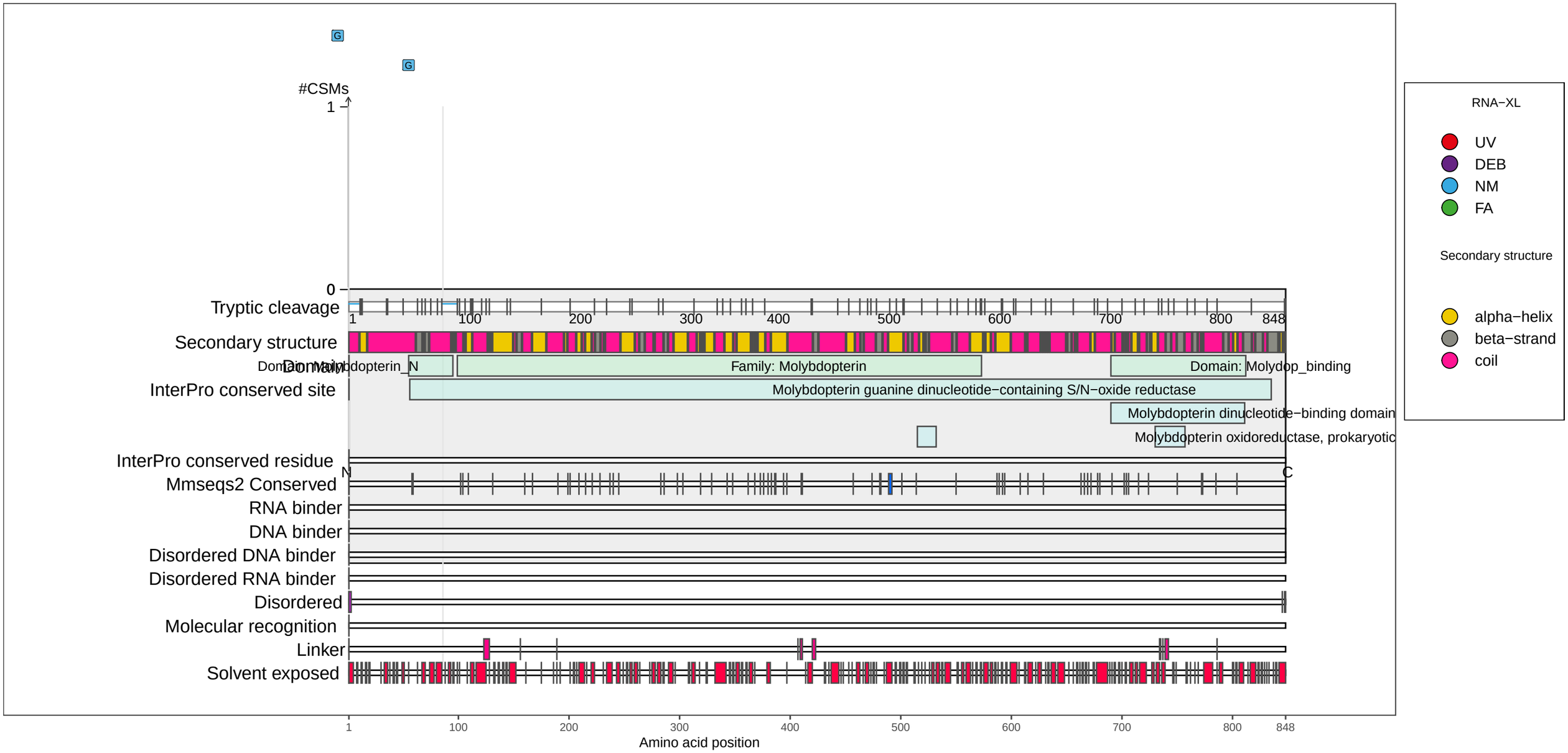
− RNA functions: not annotated



P33225
TORA_ECOLI Trimethylamine−N−oxide reductase 1

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.88 (Q 7)
PAXdb E.coli [ppm]: 0.25 (Q 30)

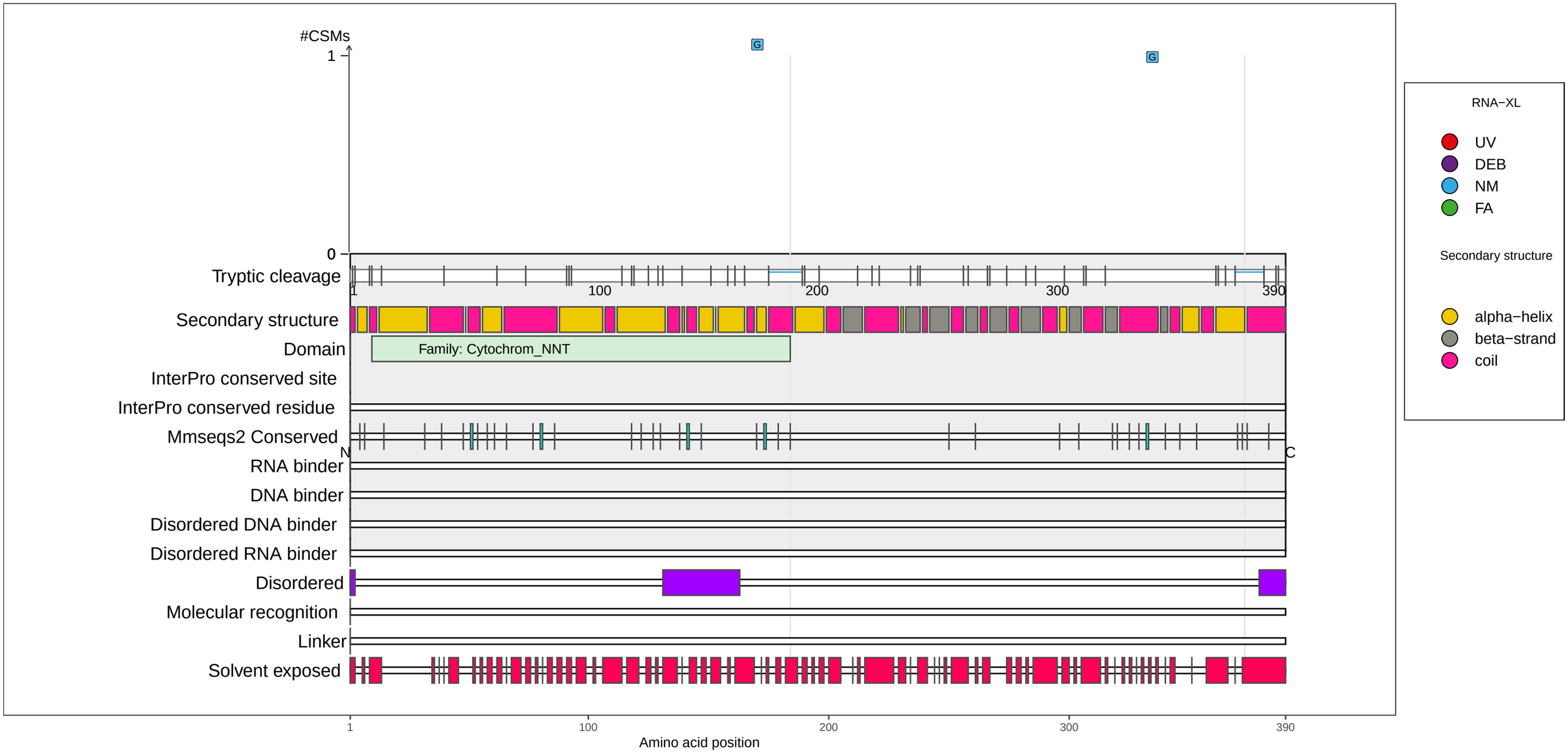
− RNA functions: not annotated



P33226
TORC_ECOLI Cytochrome c−type protein TorC

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.74 (Q 51)
PAXdb E.coli [ppm]: −0.57 (Q 15)

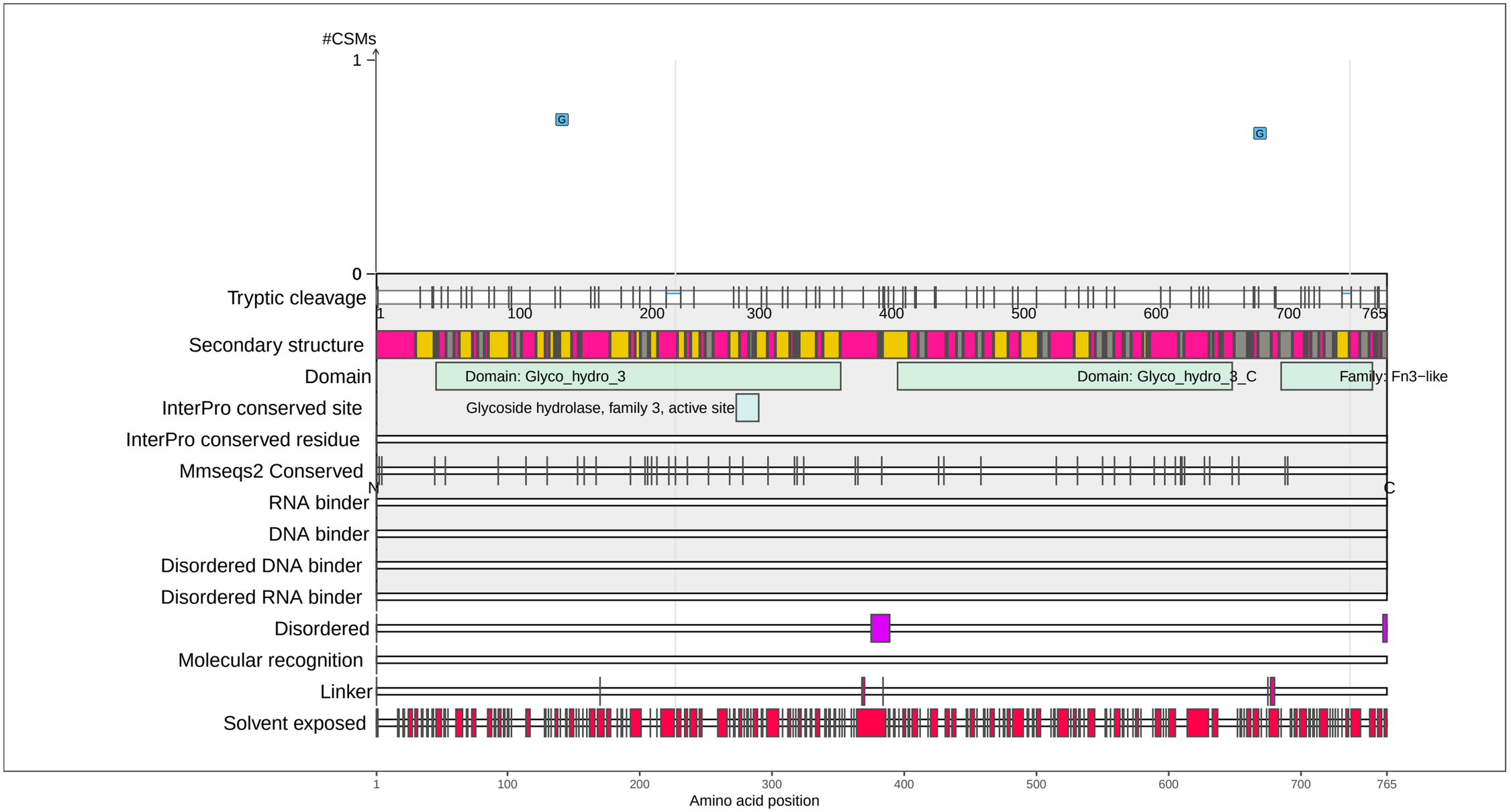
− RNA functions: not annotated



P33363
BGLX_ECOLI Periplasmic beta−glucosidase

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 1.73 (Q 50)
PAXdb E.coli [ppm]: 1.71 (Q 64)

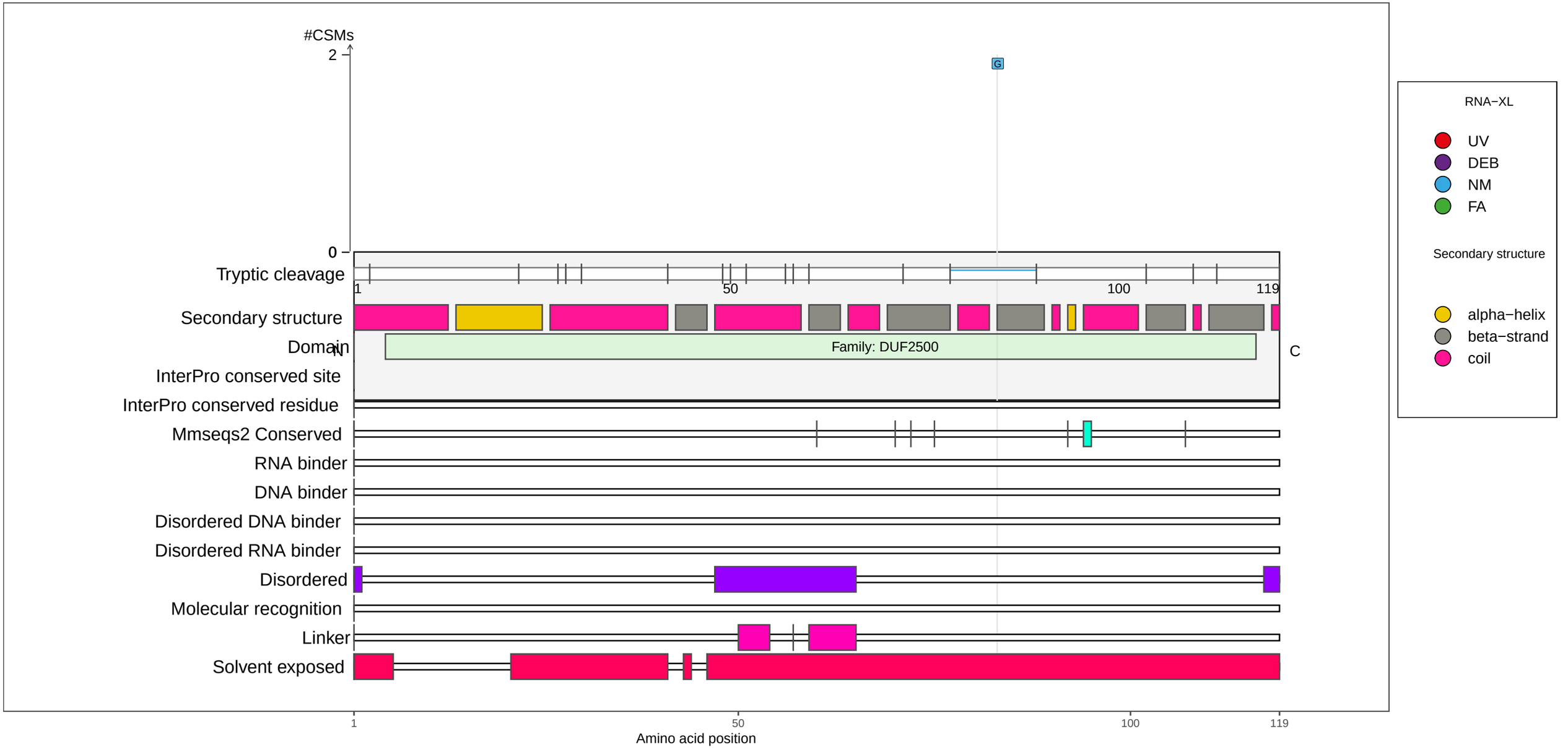
− RNA functions: not annotated



P37615
YHHM_ECOLI Uncharacterized protein YhhM

− Abundance:
tryptic [log10 Intensity]: 8.32 (Q 70)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.07 (Q 49)

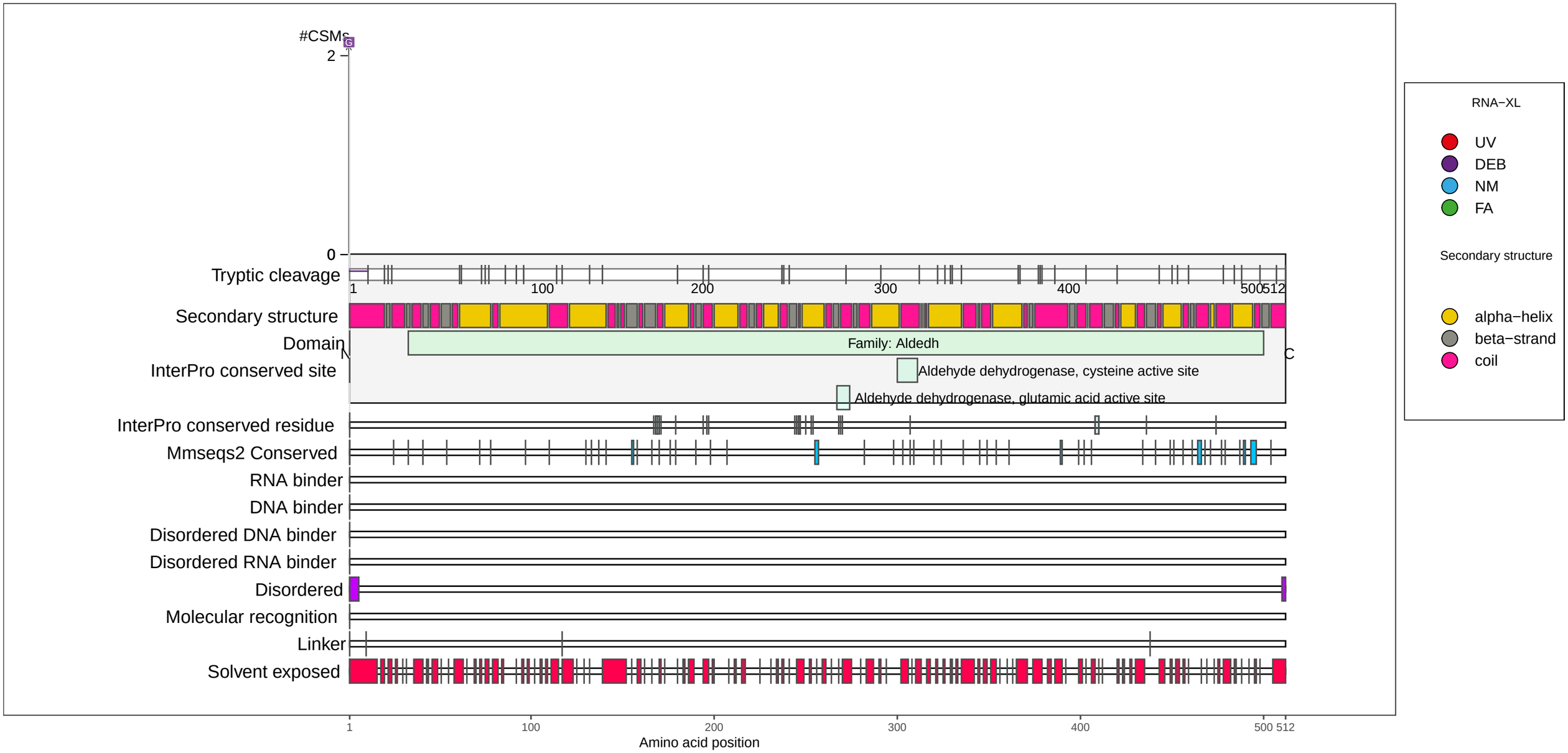
− RNA functions: not annotated



P37685
ALDB_ECOLI Aldehyde dehydrogenase B

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.3 (Q 70)
PAXdb E.coli [ppm]: 2.95 (Q 94)

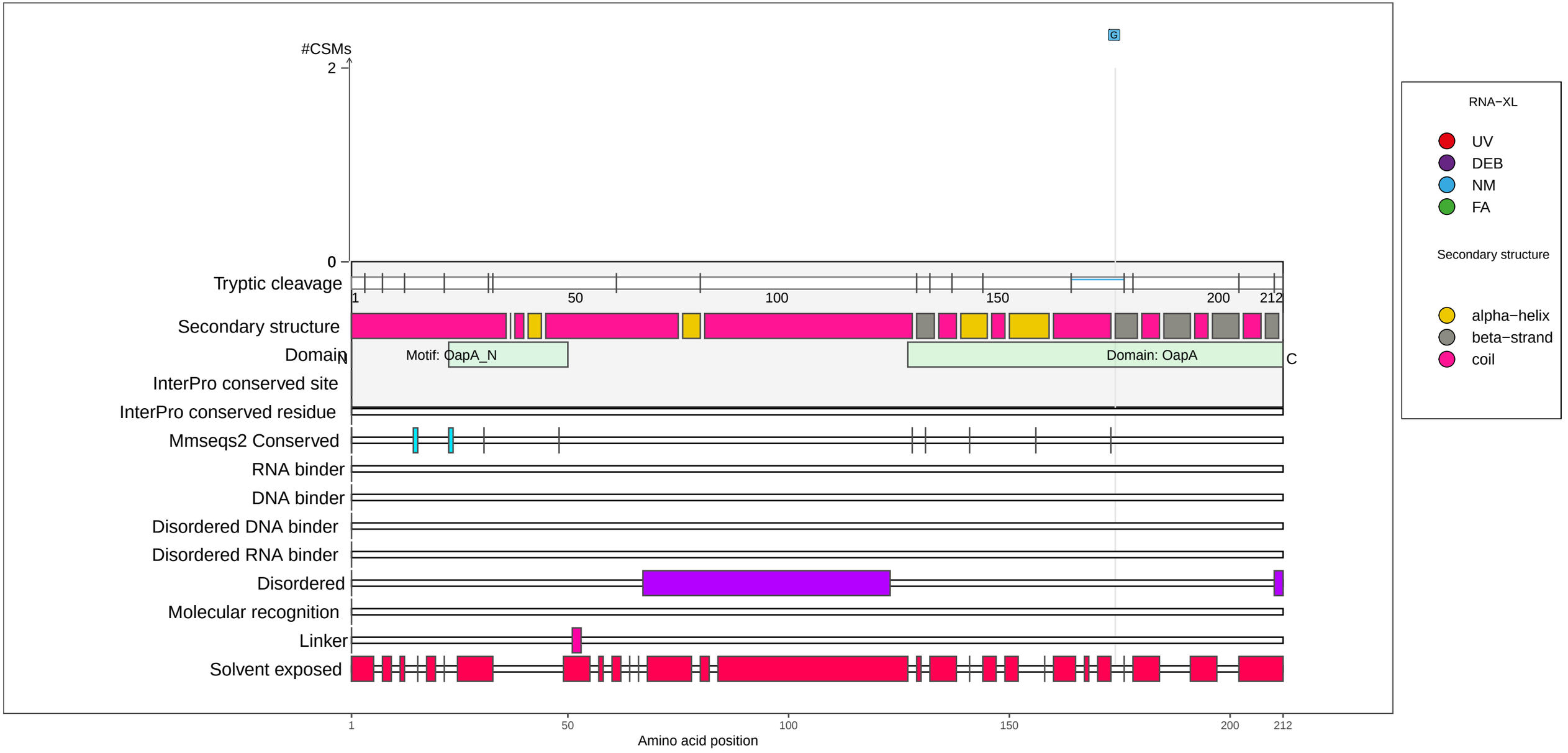
− RNA functions: not annotated



P39310
YTFB_ECOLI Cell division protein YtfB

− Abundance:
tryptic [log10 Intensity]: 7.51 (Q 35)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.91 (Q 70)

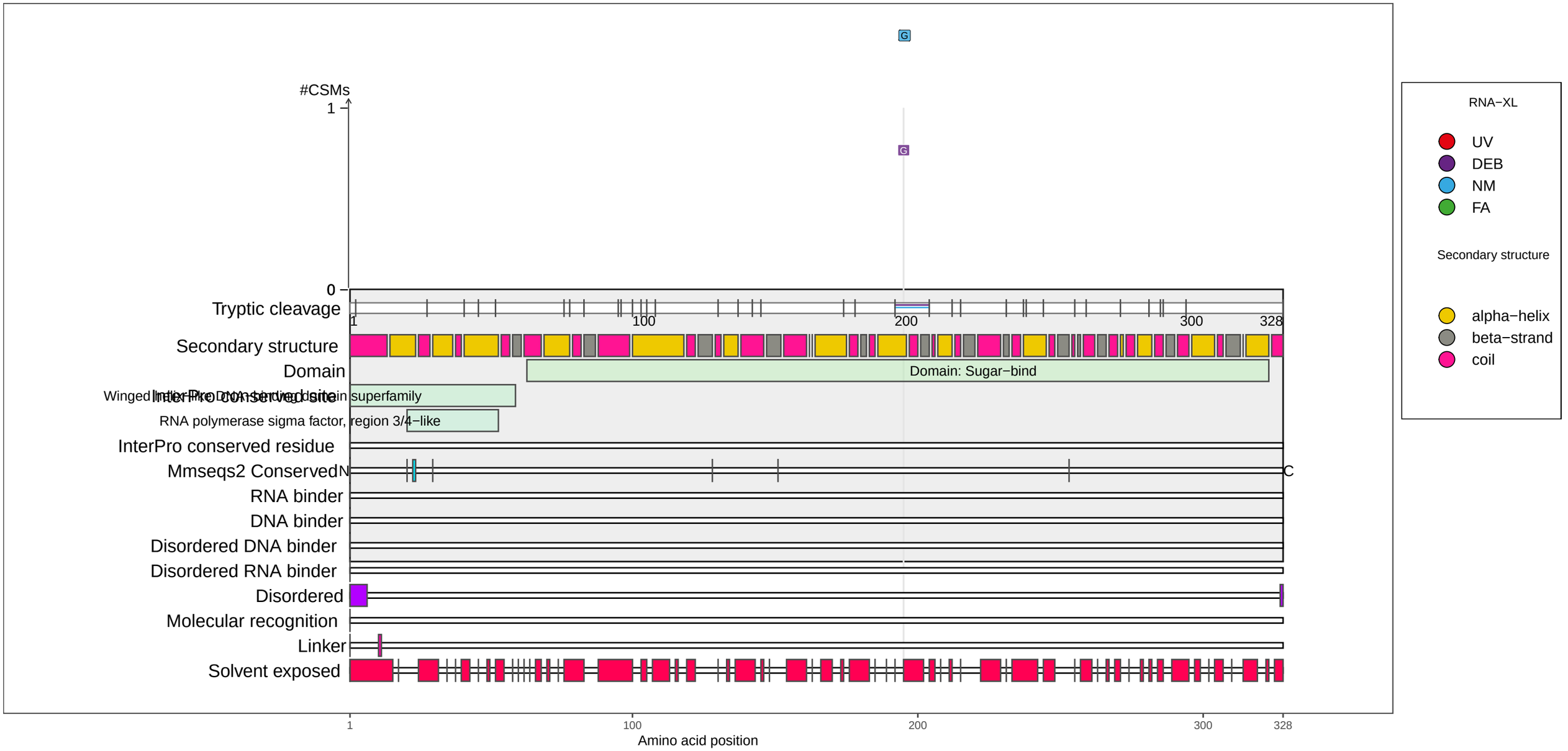
− RNA functions: not annotated



P39356
YJHU_ECOLI Uncharacterized transcriptional regulator YjhU

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.76 (Q 66)

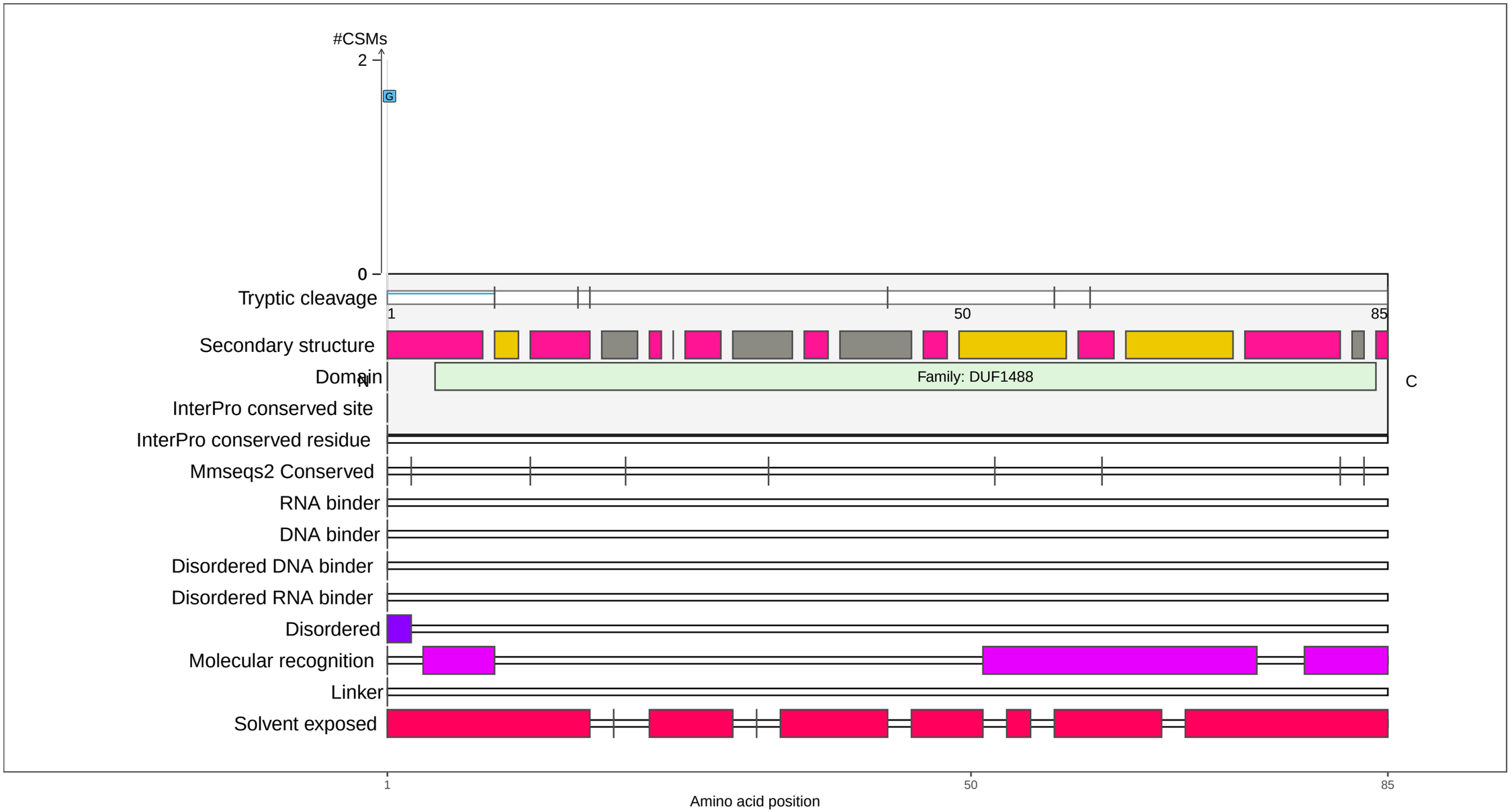
− RNA functions: not annotated

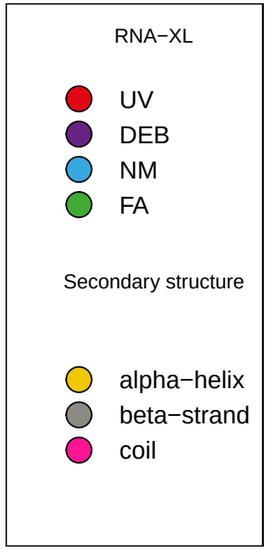


P45795
YRDB_ECOLI Uncharacterized protein YrdB

− Abundance:
tryptic [log10 Intensity]: 7.42 (Q 31)
PAXdb K12 strain [ppm]: 1.53 (Q 40)
PAXdb E.coli [ppm]: 0.77 (Q 42)

− RNA functions: not annotated

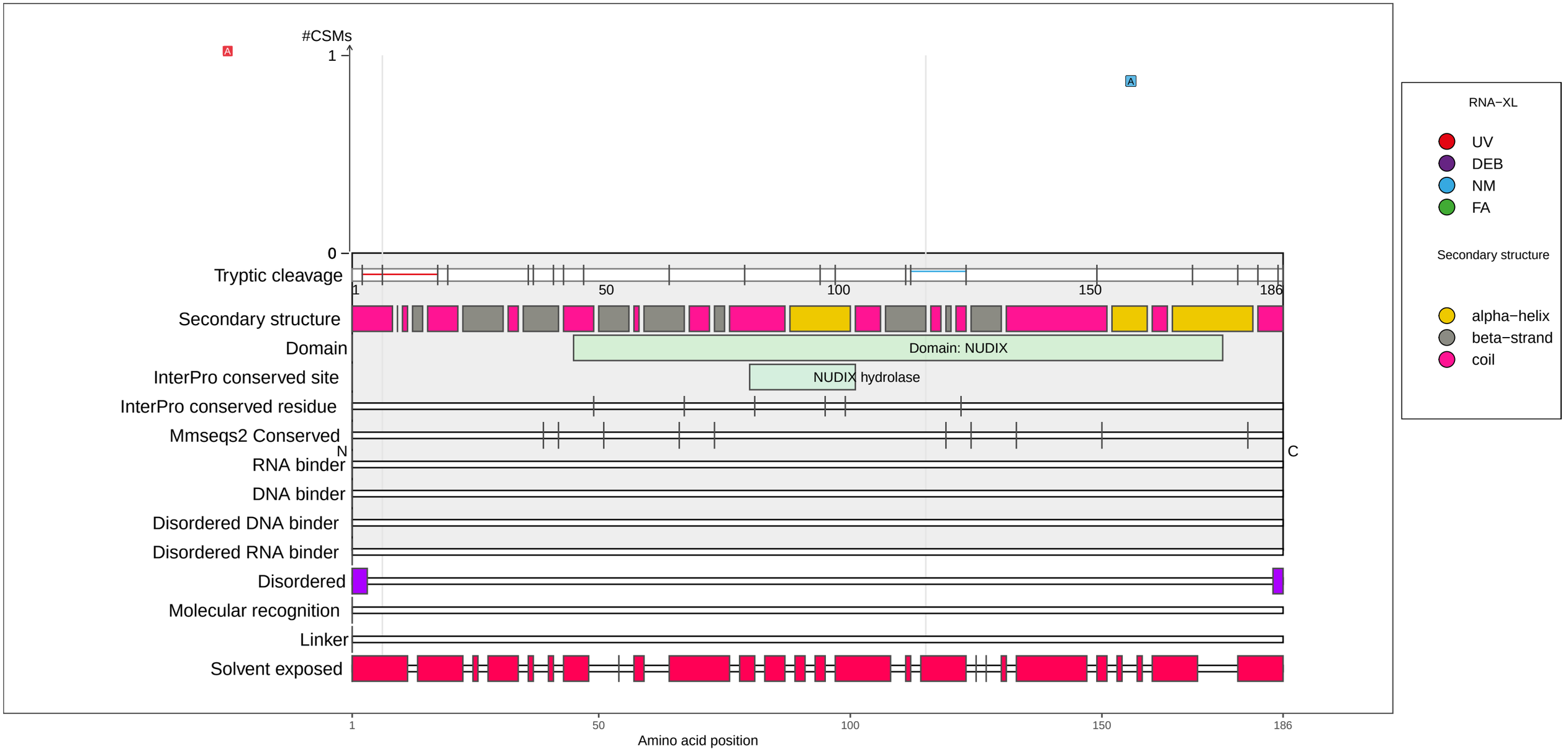




P45799
NUDE_ECOLI ADP compounds hydrolase NudE

− Abundance:
tryptic [log10 Intensity]: 8.23 (Q 67)
PAXdb K12 strain [ppm]: 2.36 (Q 72)
PAXdb E.coli [ppm]: 1.57 (Q 62)

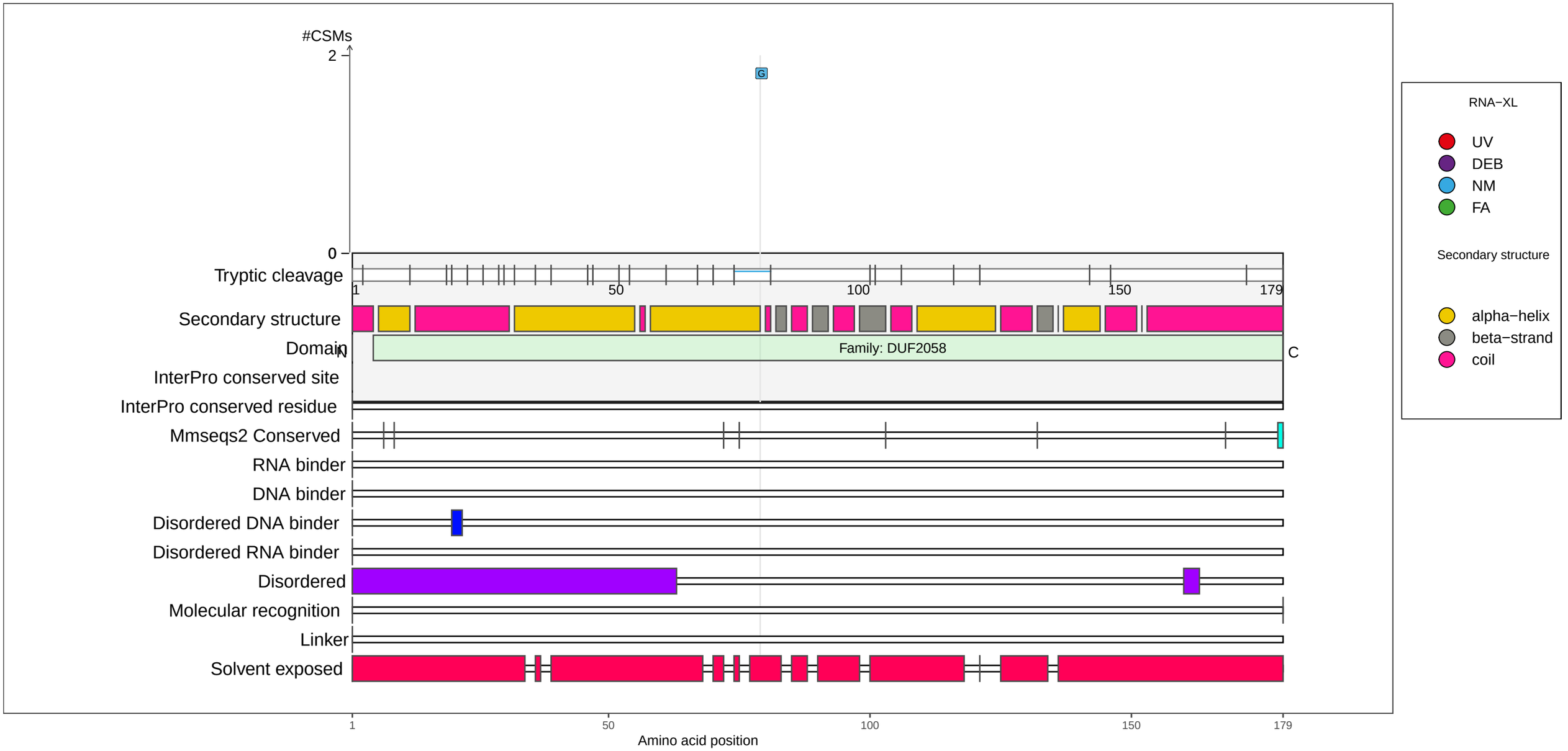
− RNA functions: not annotated



P51024
YAIL_ECOLI Uncharacterized protein YaiL

− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 2.39 (Q 73)
PAXdb E.coli [ppm]: 1.7 (Q 64)

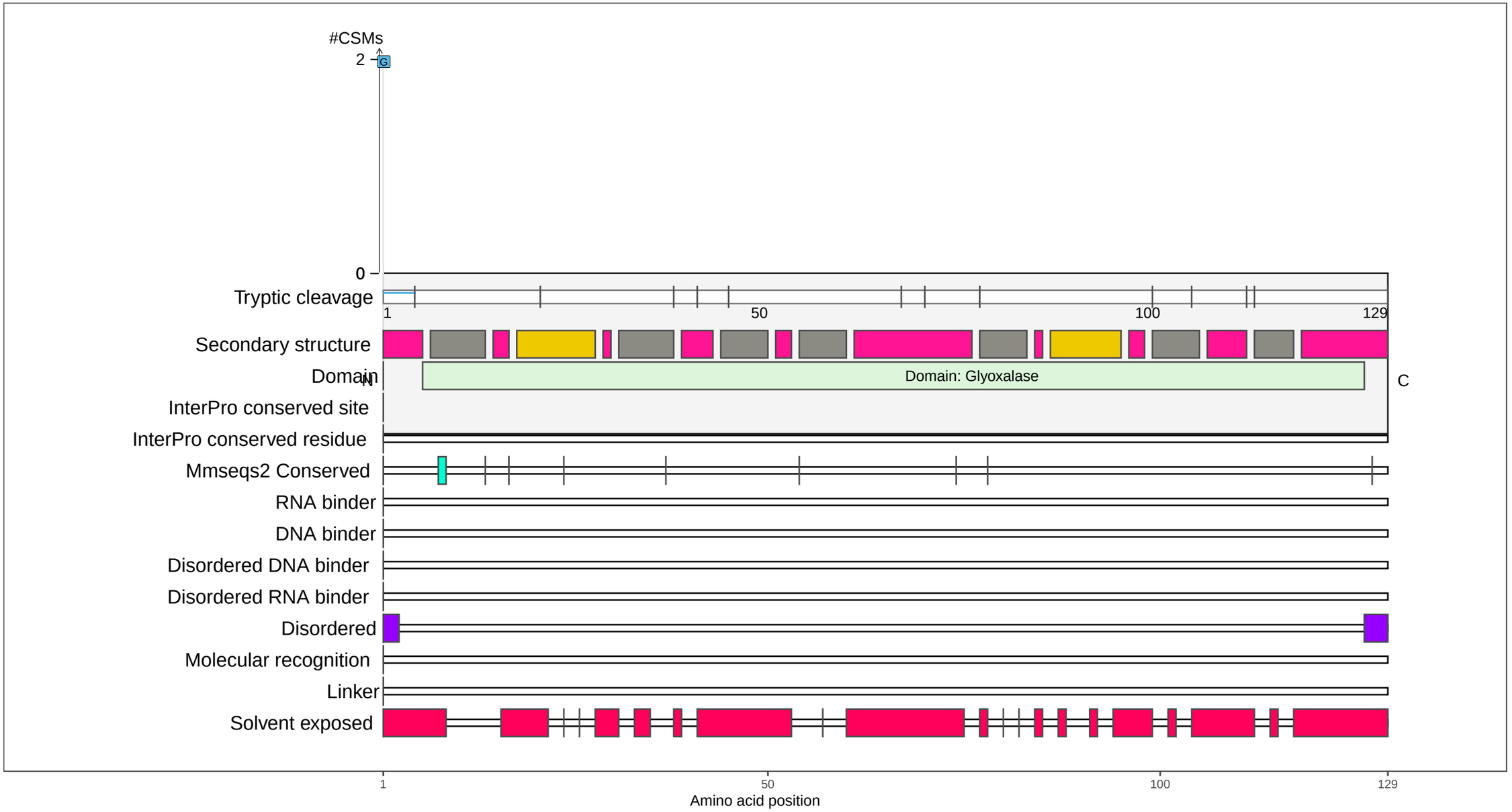
− RNA functions: not annotated

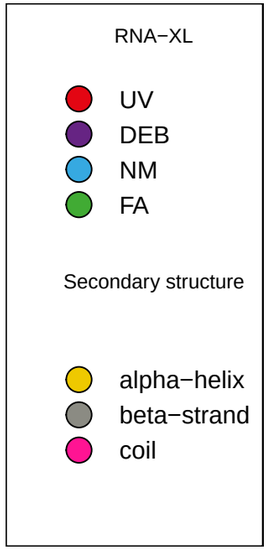


P52096
YAER_ECOLI Uncharacterized protein YaeR

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.05 (Q 73)

− RNA functions: not annotated

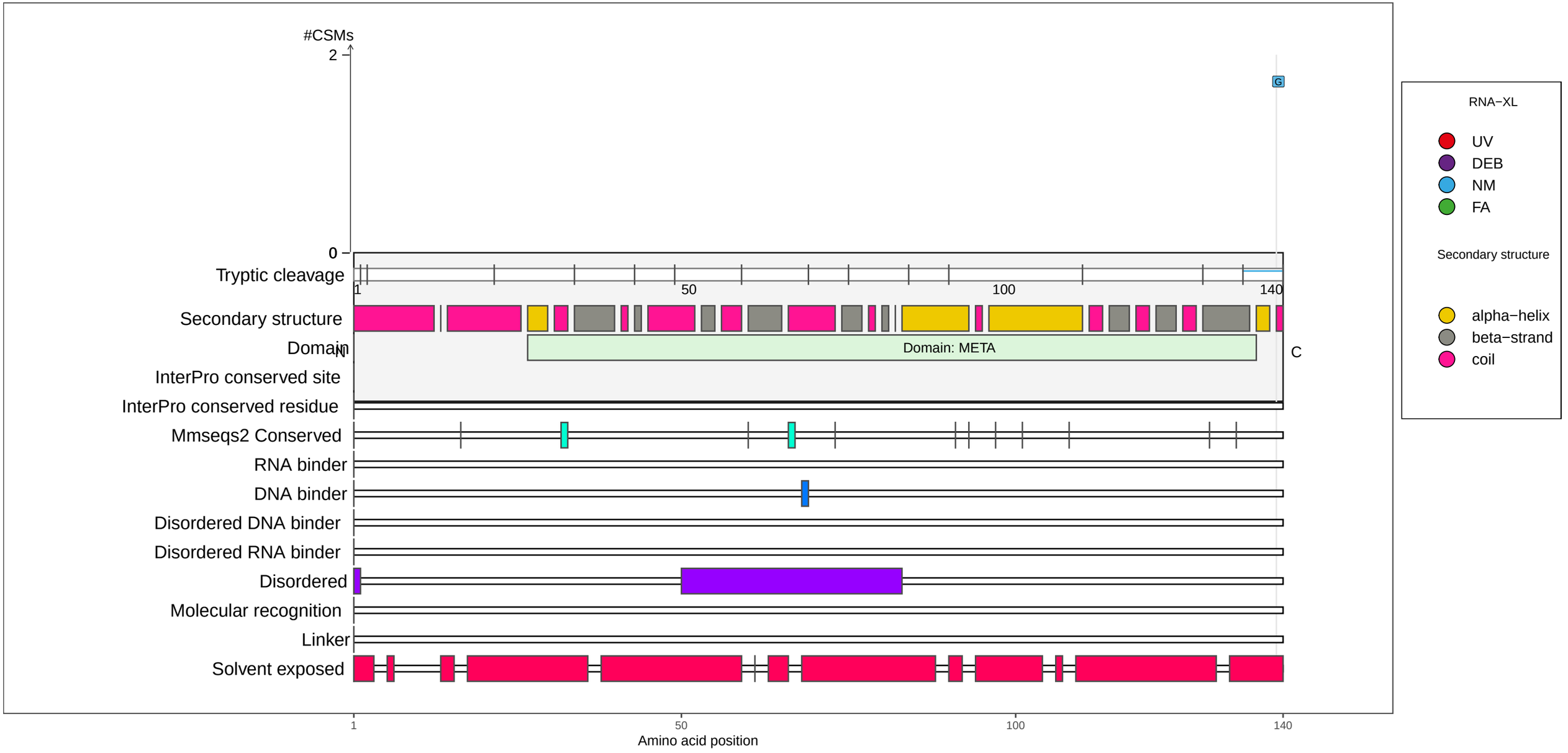




P52644
HSLJ_ECOLI Heat shock protein HslJ

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: 1.48 (Q 37)
PAXdb E.coli [ppm]: 1.34 (Q 56)

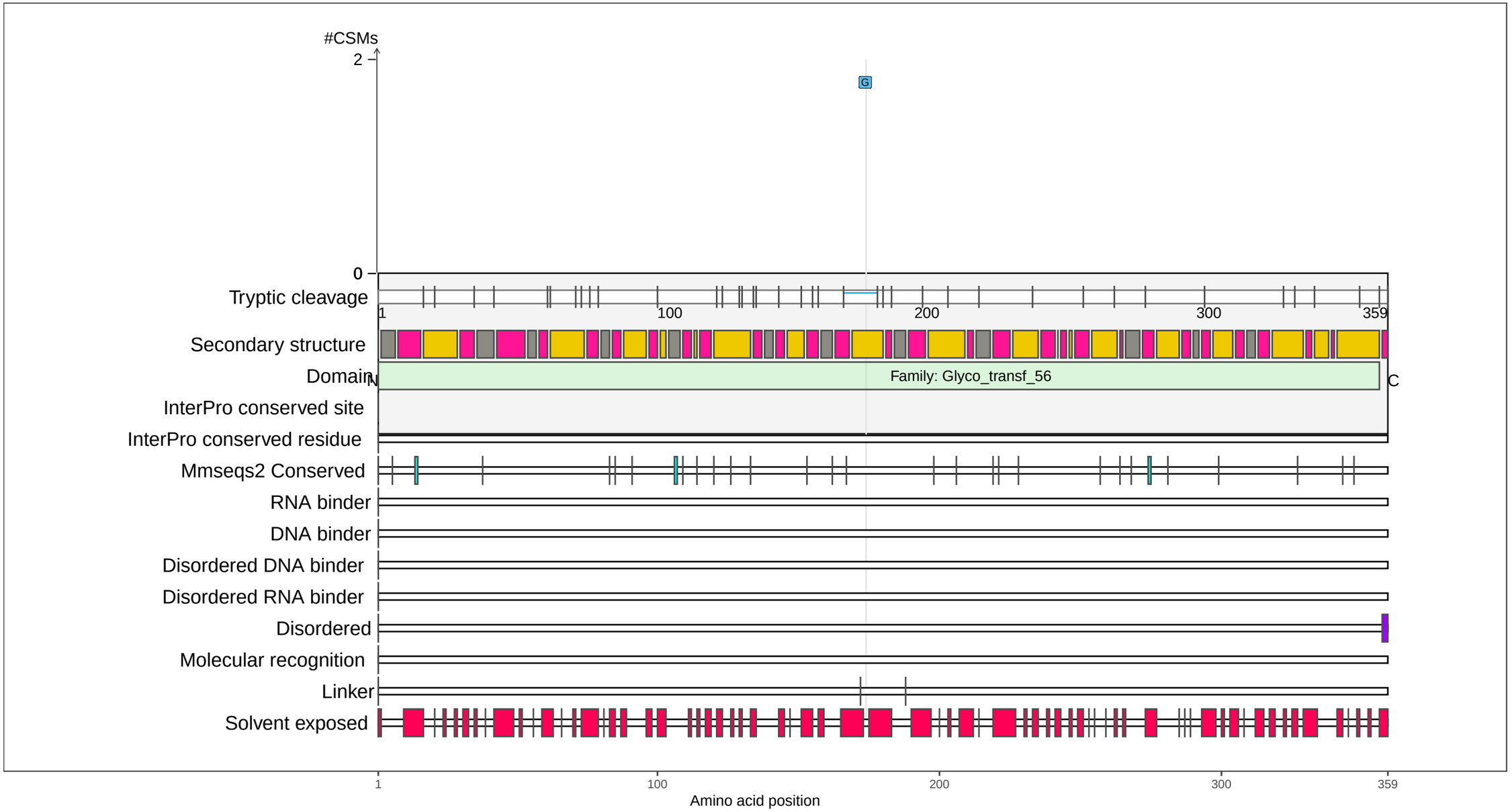
− RNA functions: not annotated



P56258
WECF_ECOLI TDP−N−acetylfucosamine:lipid II N−acetylfucosaminyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.25 (Q 23)
PAXdb K12 strain [ppm]: 1.2 (Q 20)
PAXdb E.coli [ppm]: −0.15 (Q 21)

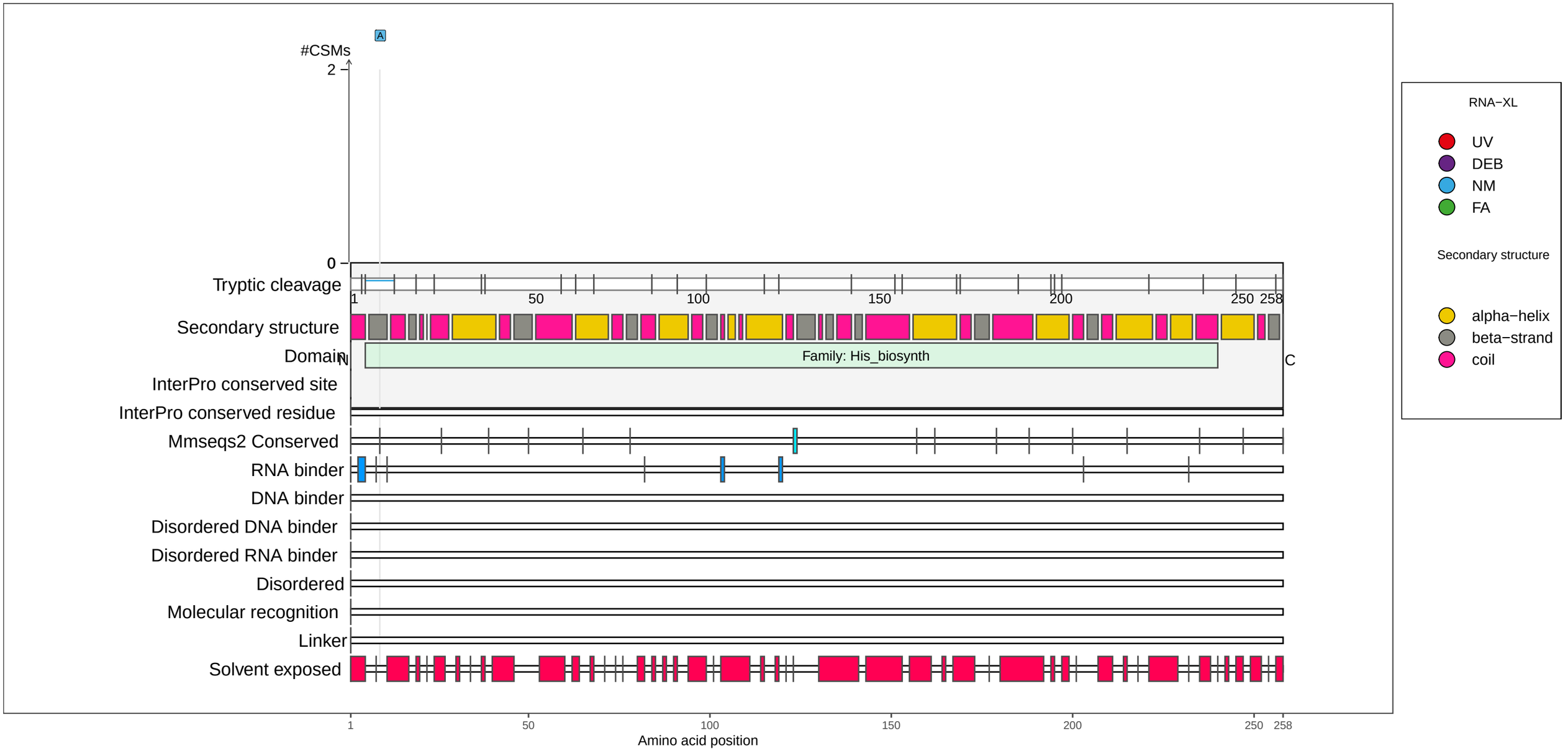
− RNA functions: not annotated



P60664
HIS6_ECOLI Imidazole glycerol phosphate synthase subunit HisF

− Abundance:
tryptic [log10 Intensity]: 8.54 (Q 77)
PAXdb K12 strain [ppm]: 1.5 (Q 38)
PAXdb E.coli [ppm]: 2.12 (Q 75)

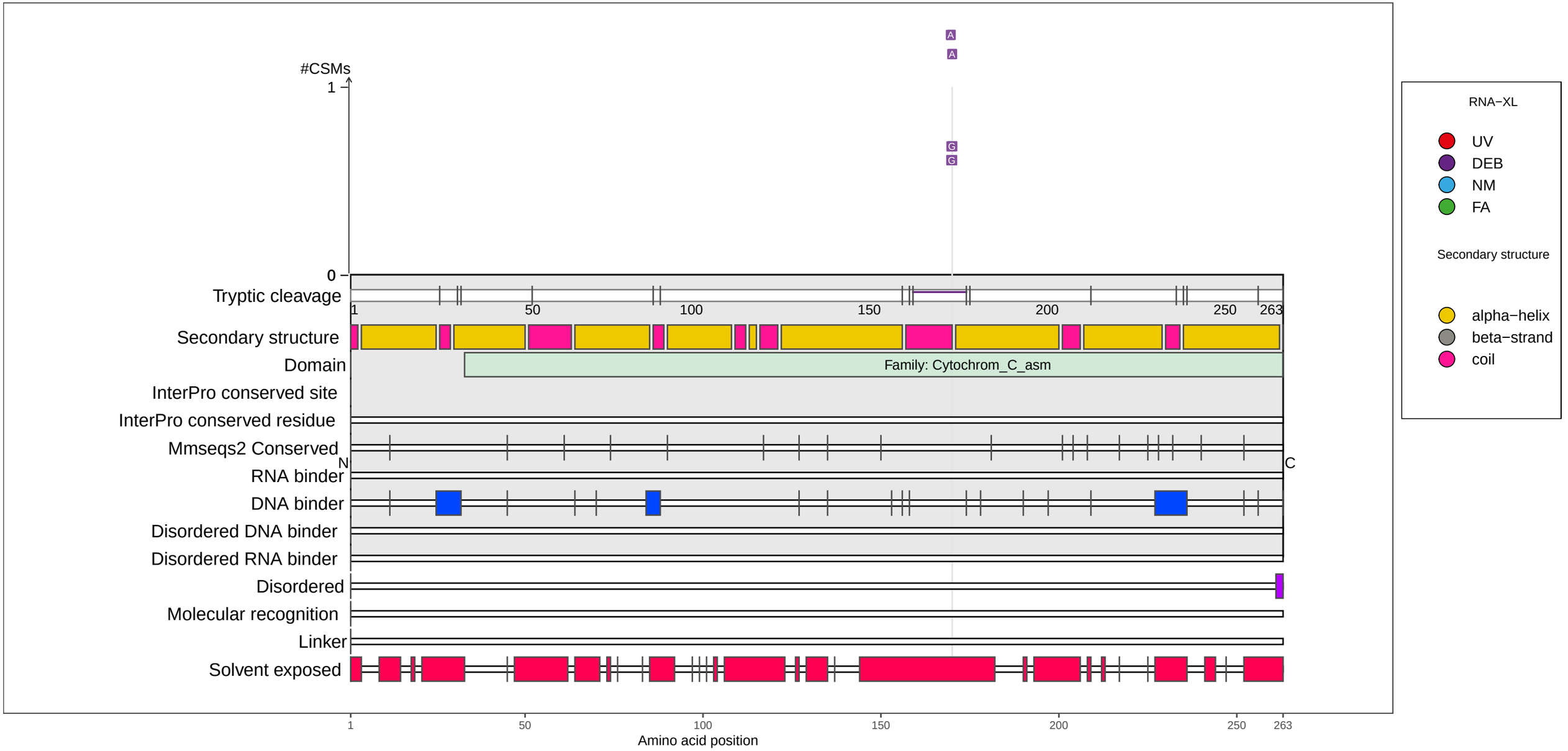
− RNA functions: not annotated



P64432
YPJD_ECOLI Inner membrane protein YpjD

− Abundance:
tryptic [log10 Intensity]: 7.19 (Q 20)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.48 (Q 36)

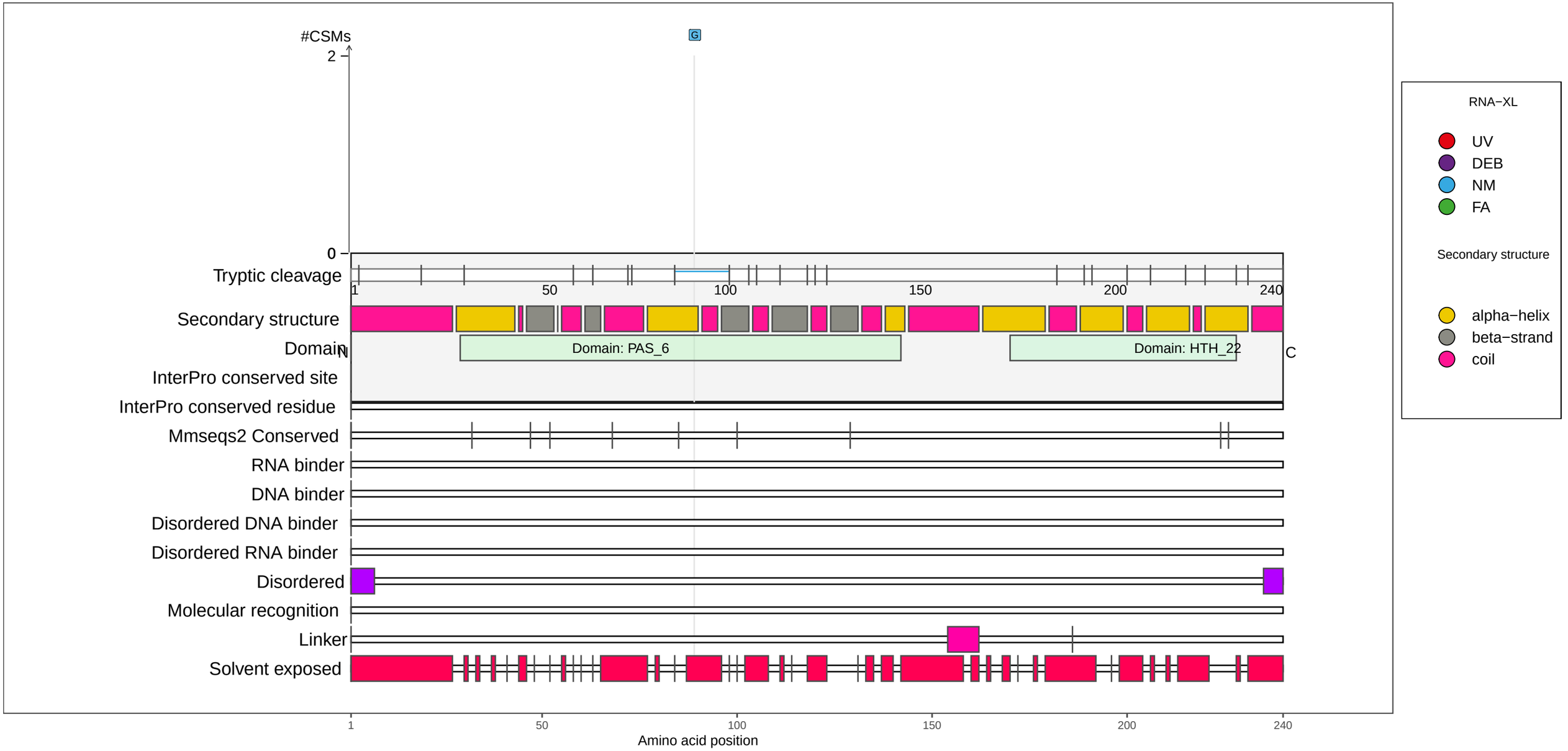
− RNA functions: not annotated



P64624
YHEO_ECOLI Uncharacterized protein YheO

− Abundance:
tryptic [log10 Intensity]: 7.61 (Q 40)
PAXdb K12 strain [ppm]: 2.6 (Q 80)
PAXdb E.coli [ppm]: 2.01 (Q 72)

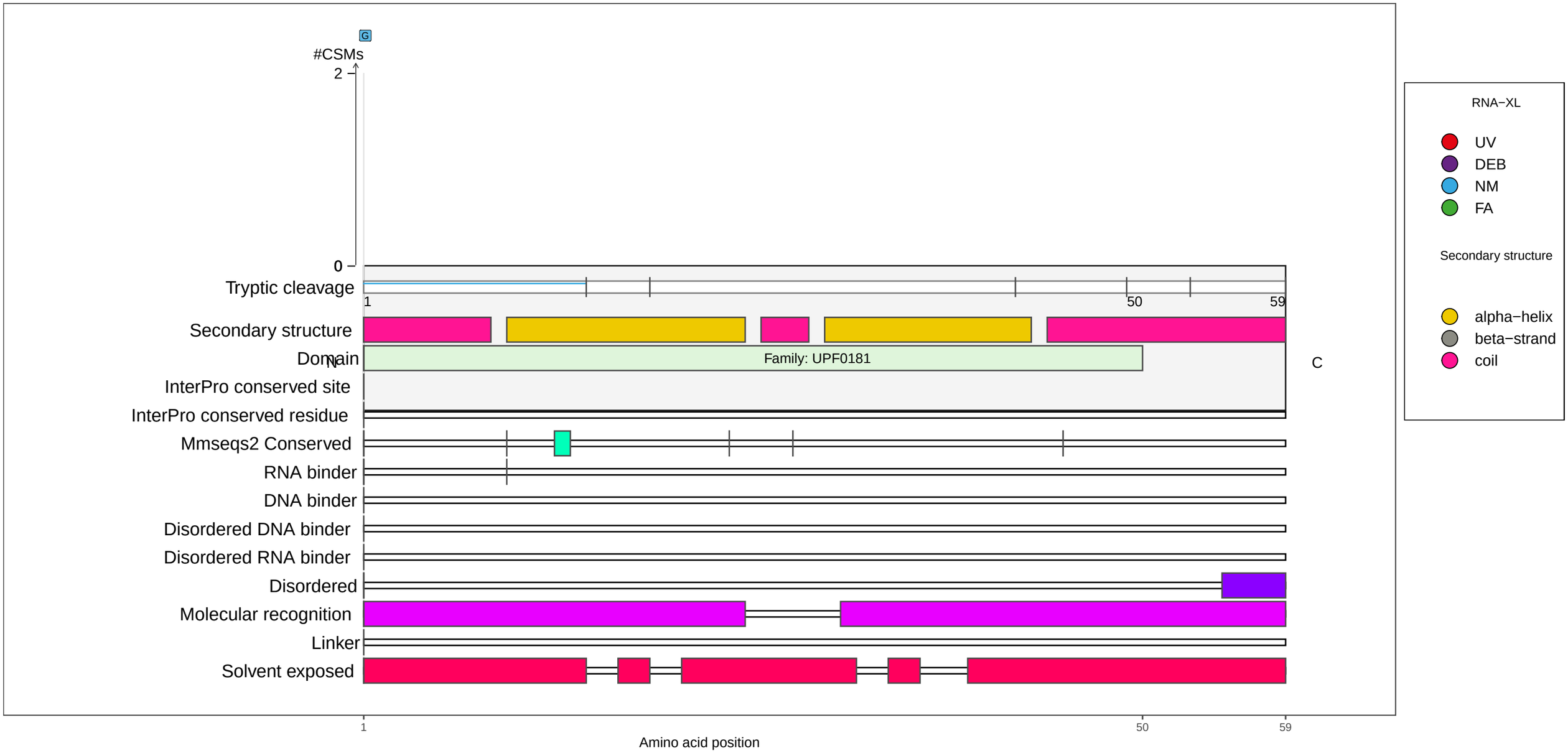
− RNA functions: not annotated



P67338
YOAH_ECOLI UPF0181 protein YoaH

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.12 (Q 22)

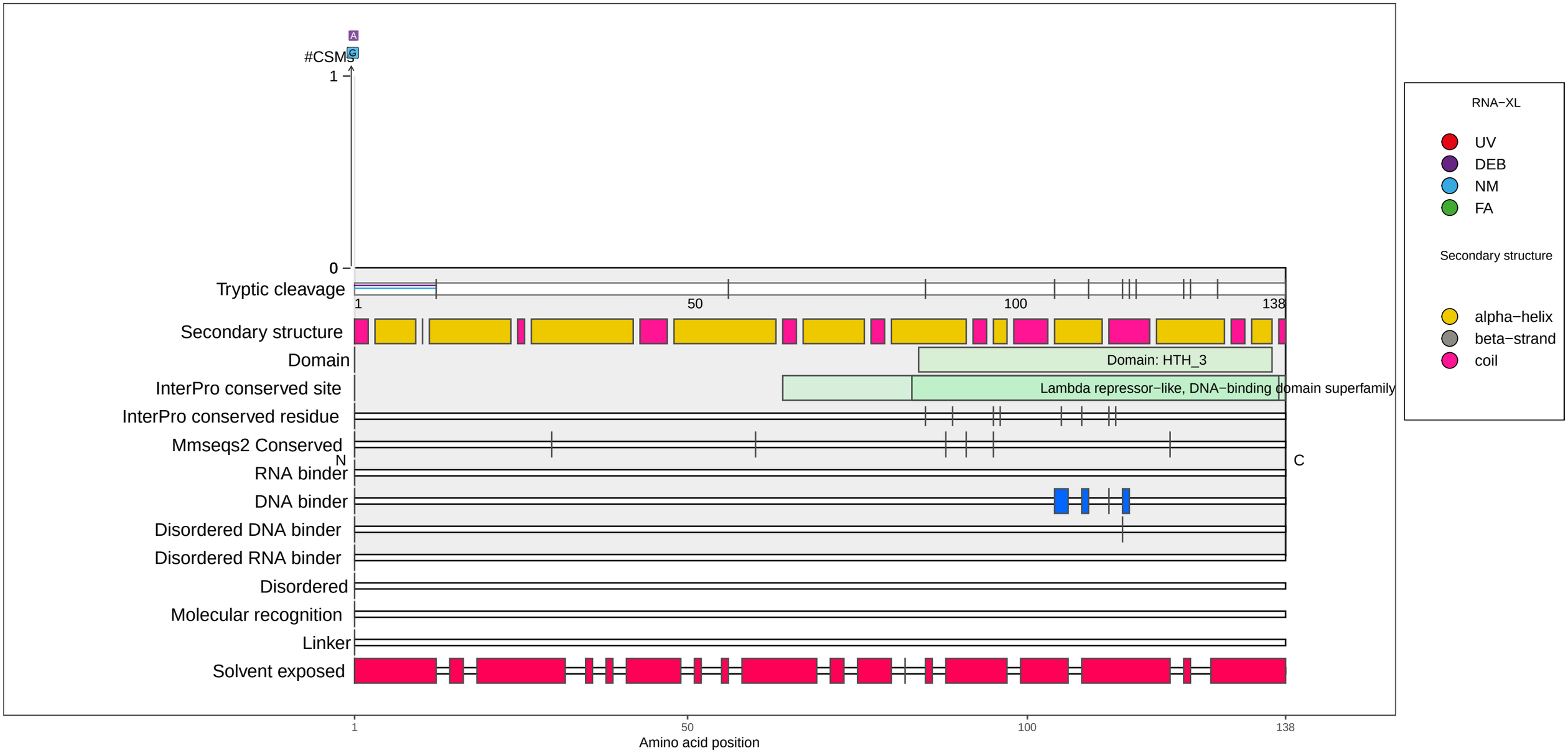
− RNA functions: not annotated



P67701
HIGA_ECOLI Antitoxin HigA

− Abundance:
tryptic [log10 Intensity]: 6.83 (Q 8)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.67 (Q 40)

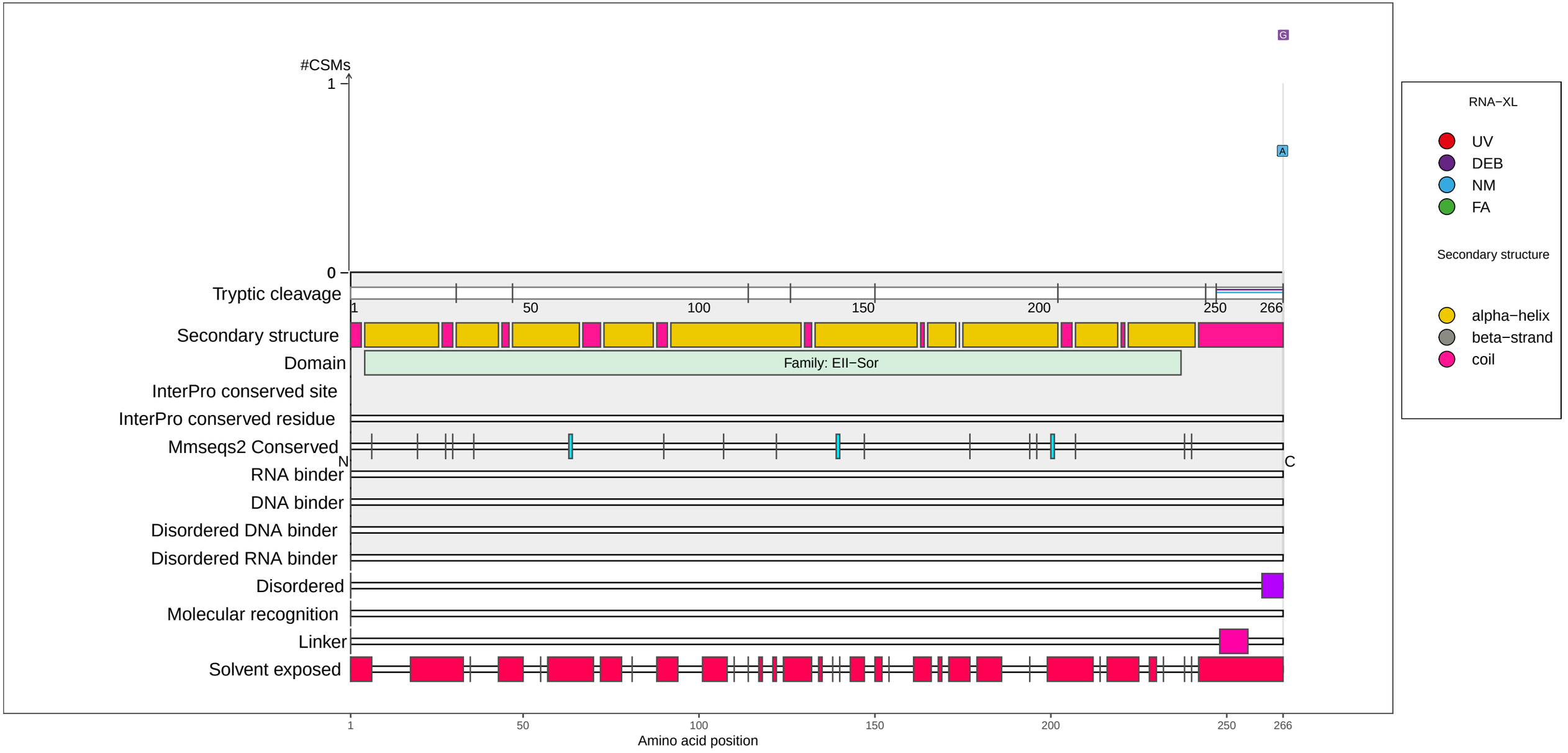
− RNA functions: not annotated



P69801
PTNC_ECOLI PTS system mannose−specific EIIC component

− Abundance:
tryptic [log10 Intensity]: 8.91 (Q 86)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.77 (Q 91)

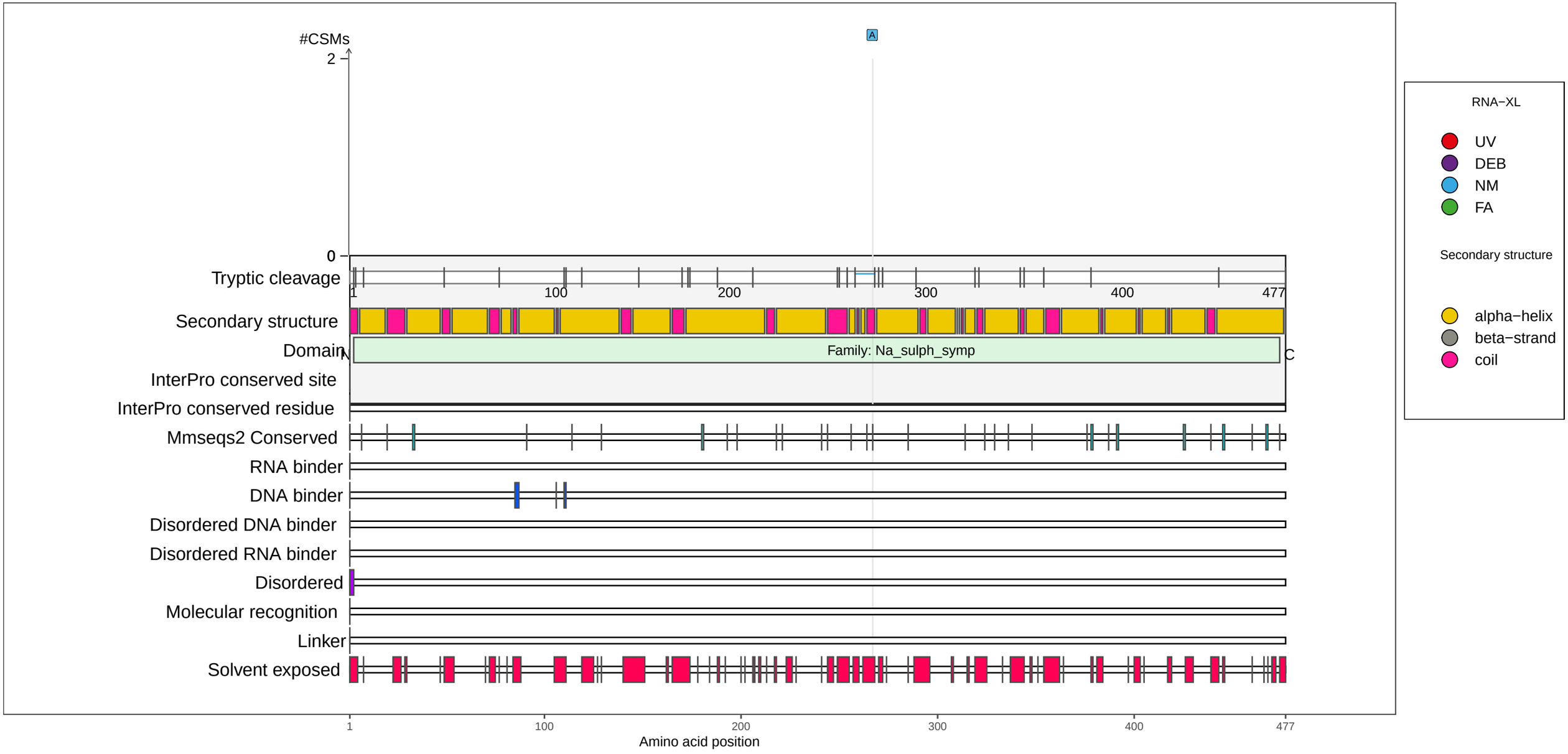
− RNA functions: not annotated



P75763
YBHI_ECOLI Inner membrane protein YbhI

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.38 (Q 17)

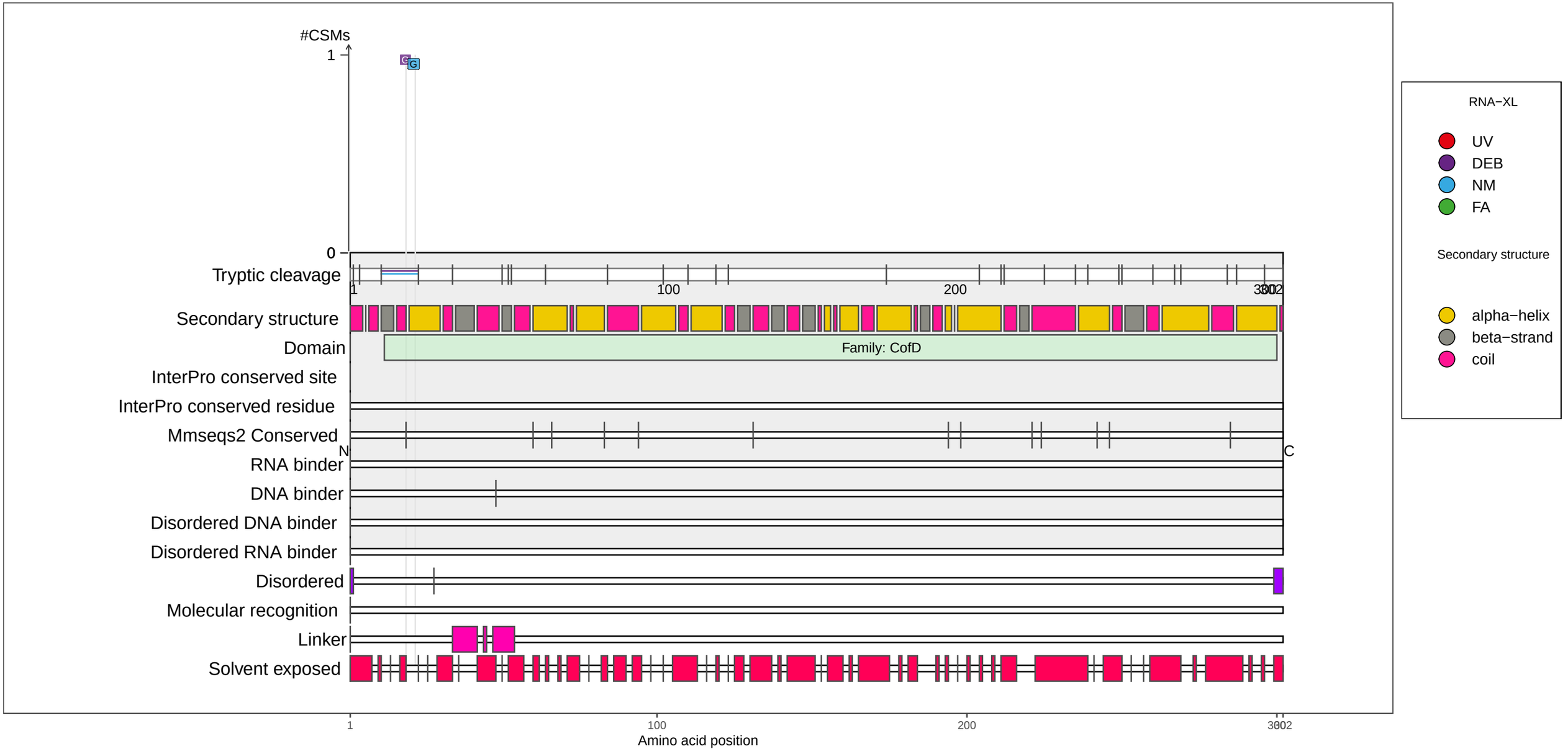
− RNA functions: not annotated



P75767
GNGF_ECOLI Putative gluconeogenesis factor

− Abundance:
tryptic [log10 Intensity]: 6.99 (Q 13)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.35 (Q 32)

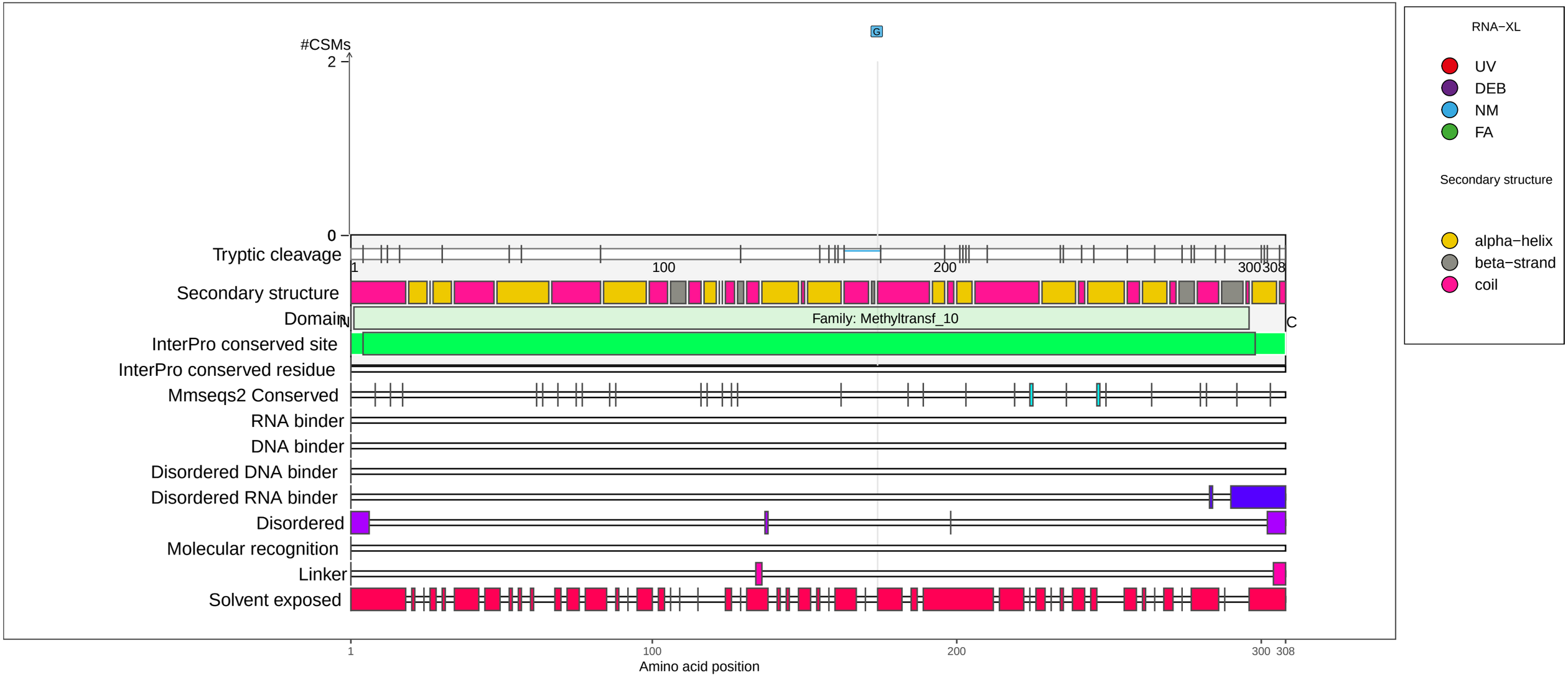
− RNA functions: not annotated



P75782
RLMF_ECOLI Ribosomal RNA large subunit methyltransferase F

− Abundance:
tryptic [log10 Intensity]: 6.58 (Q 3)
PAXdb K12 strain [ppm]: 1.49 (Q 38)
PAXdb E.coli [ppm]: 1.71 (Q 65)

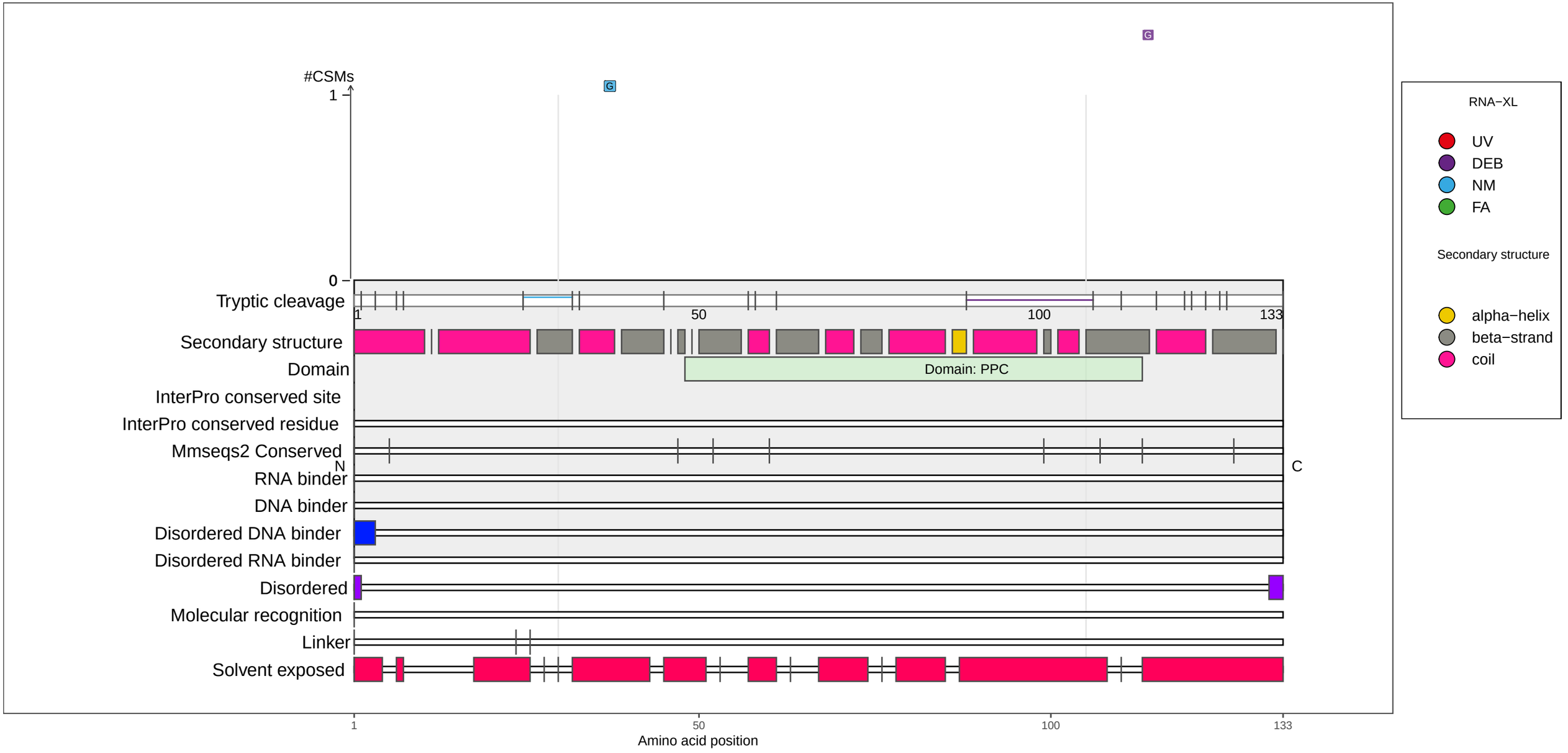
− RNA functions:
23S rRNA (adenine(1618)−N(6))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; RNA metabolic process; RNA methylation
RNA methyltransferase activity; RNA modification; RNA processing; rRNA (adenine−N6−)−methyltransferase activity
rRNA (adenine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P76002
PLIG_ECOLI Inhibitor of g−type lysozyme

− Abundance:
tryptic [log10 Intensity]: 8.1 (Q 61)
PAXdb K12 strain [ppm]: 2.32 (Q 70)
PAXdb E.coli [ppm]: 2.05 (Q 73)

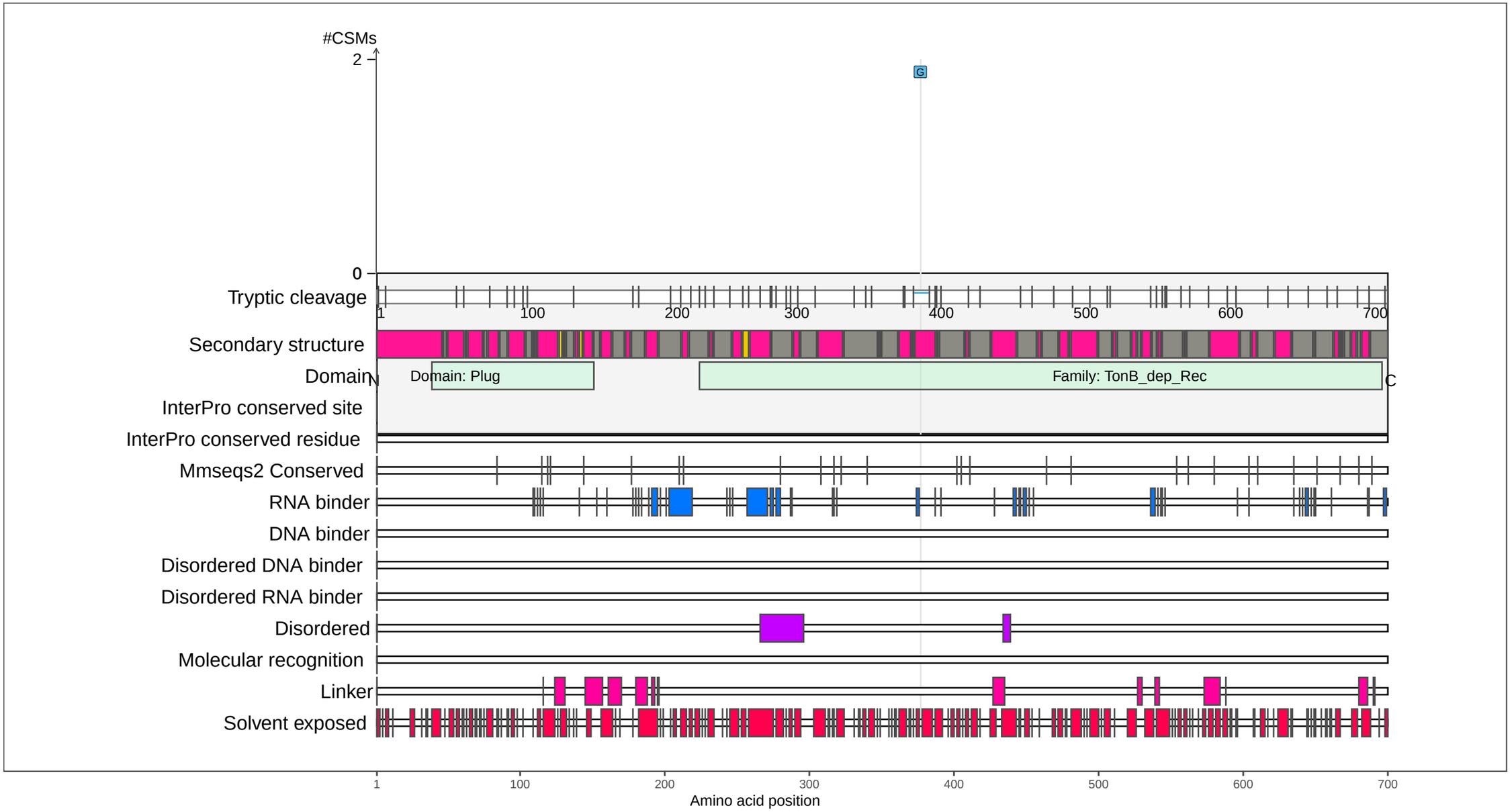
− RNA functions: not annotated

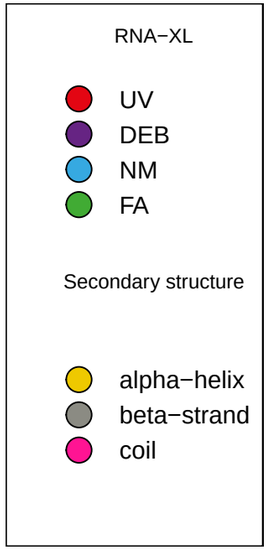


P76115
YNCD_ECOLI Probable TonB−dependent receptor YncD

− Abundance:
tryptic [log10 Intensity]: 8.97 (Q 87)
PAXdb K12 strain [ppm]: 0.88 (Q 7)
PAXdb E.coli [ppm]: 0.09 (Q 27)

− RNA functions: not annotated

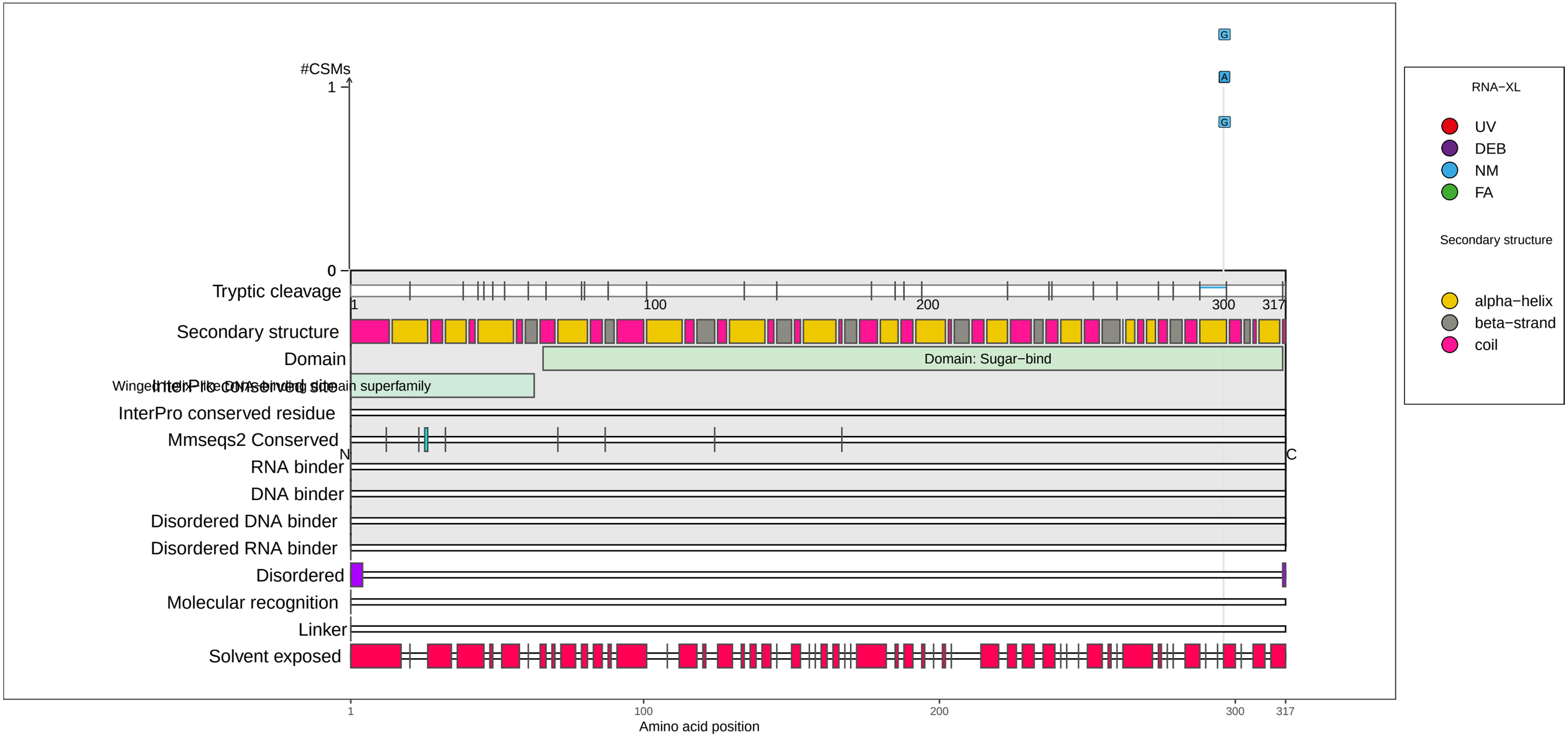




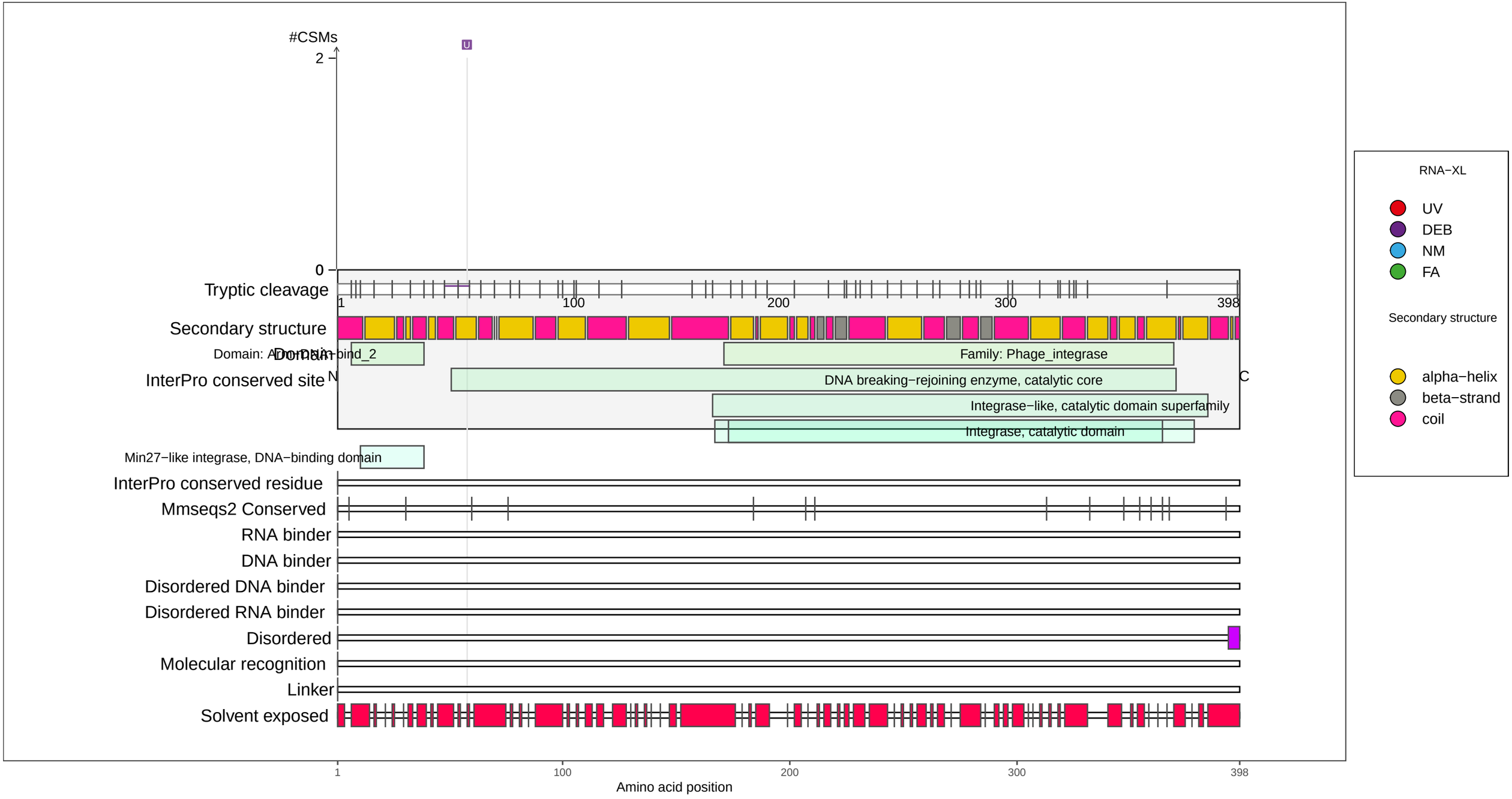
P76141
LSRR_ECOLI Transcriptional regulator LsrR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.2 (Q 20)
PAXdb E.coli [ppm]: 1.15 (Q 51)

− RNA functions:
RNA biosynthetic process; RNA metabolic process



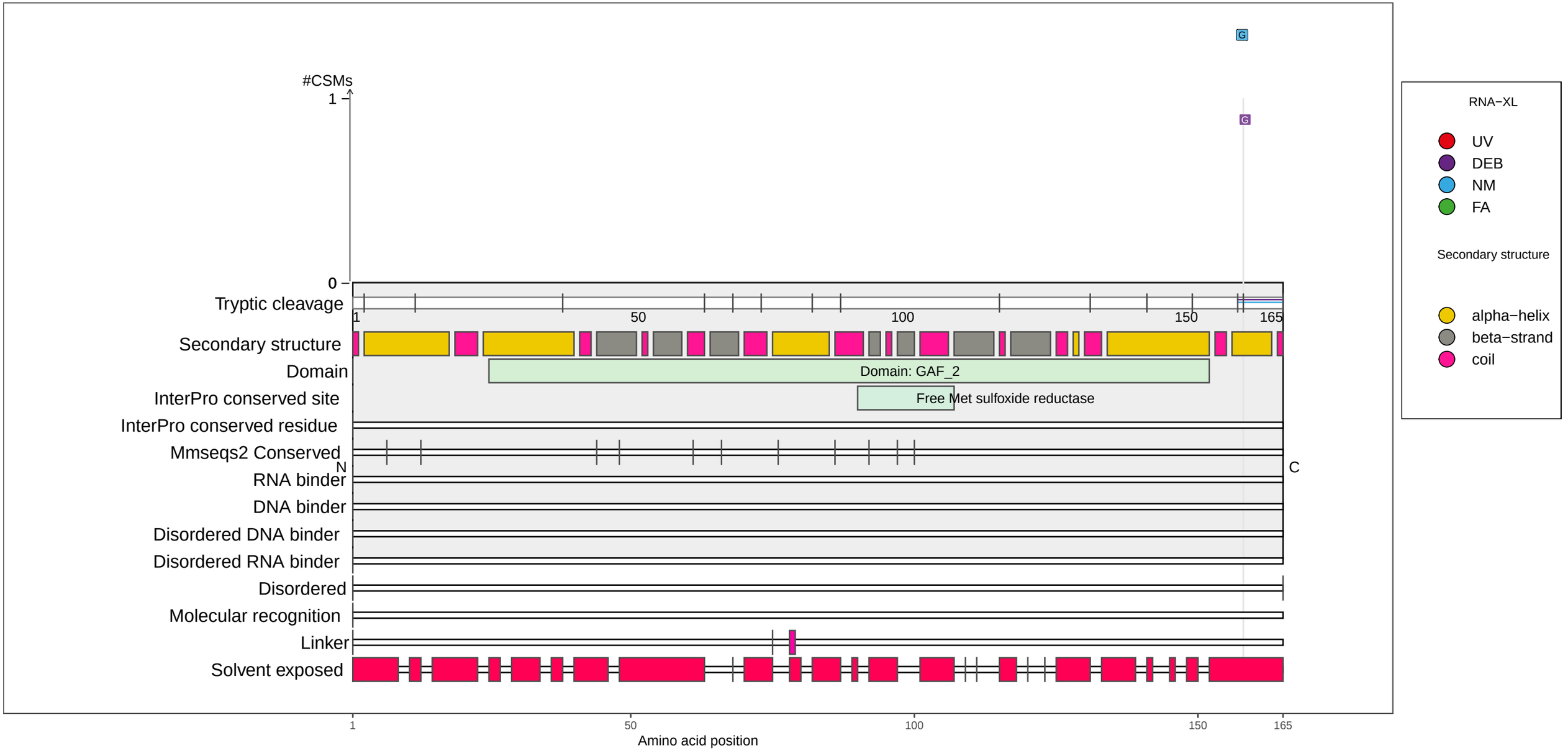
P76168
INTQ_ECOLI Putative defective protein IntQ
− RNA functions: not annotated



P76270
MSRC_ECOLI Free methionine−R−sulfoxide reductase

− Abundance:
tryptic [log10 Intensity]: 8.39 (Q 72)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 2.31 (Q 81)

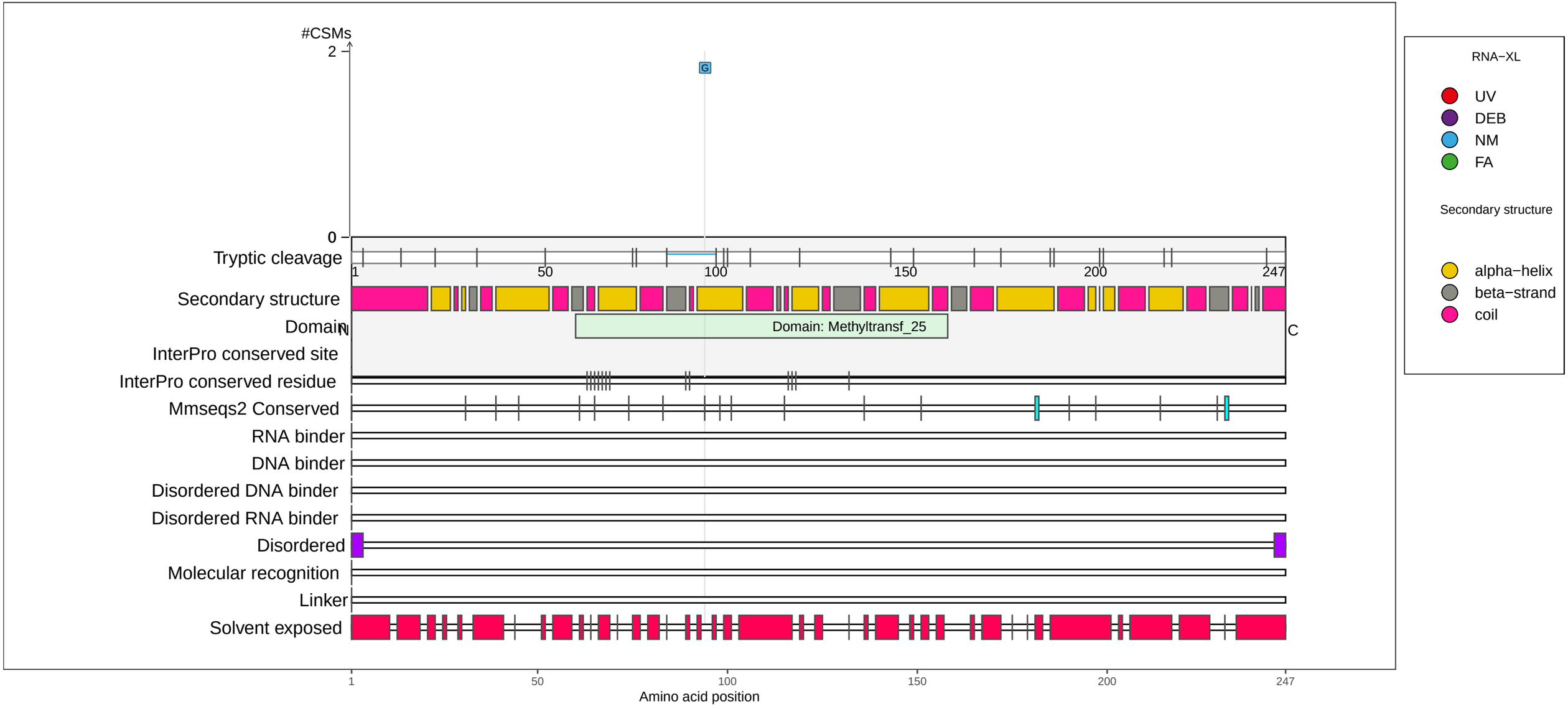
− RNA functions: not annotated



P76290
CMOA_ECOLI Carboxy−S−adenosyl−L−methionine synthase

− Abundance:
tryptic [log10 Intensity]: 7.55 (Q 37)
PAXdb K12 strain [ppm]: 1.7 (Q 49)
PAXdb E.coli [ppm]: 1.66 (Q 63)

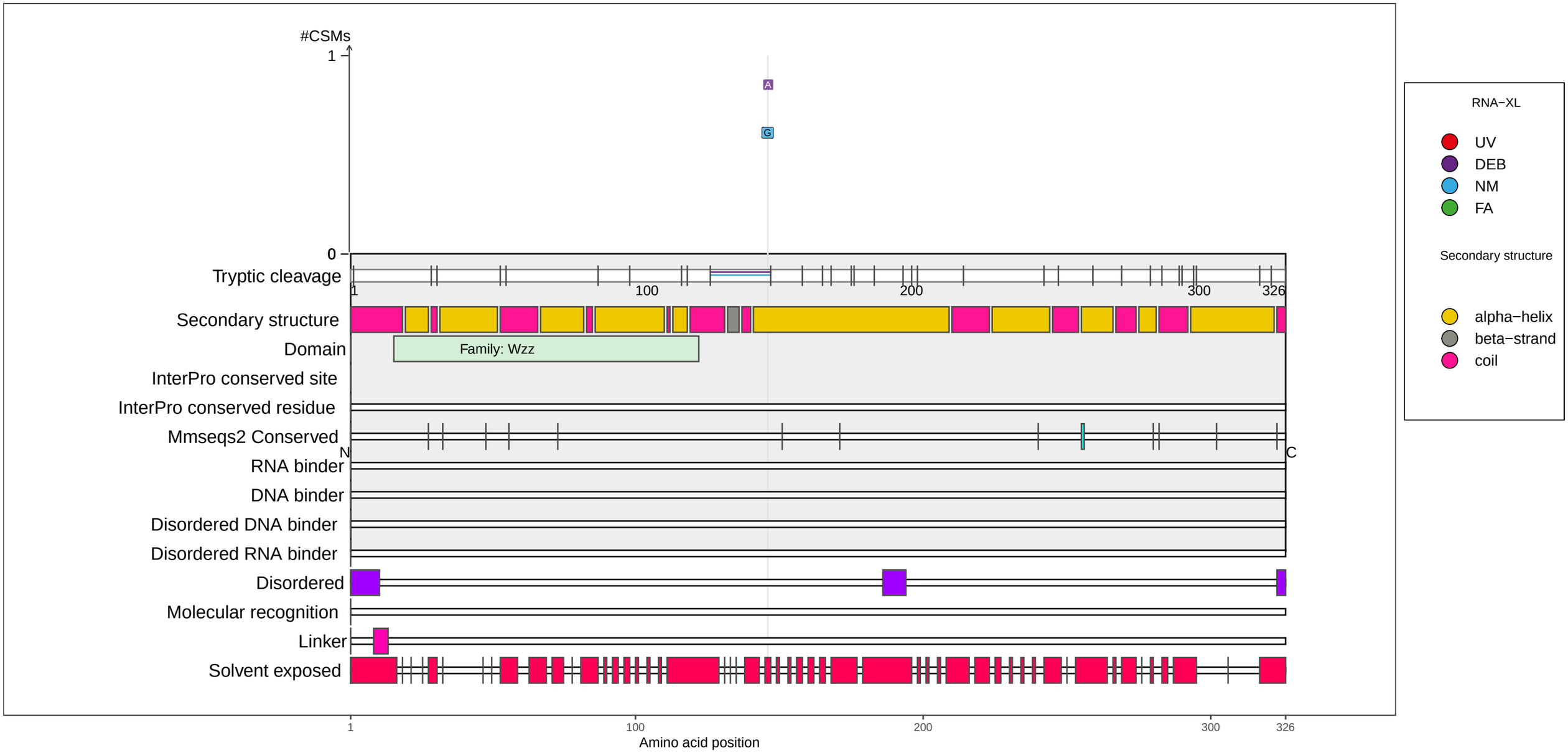
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA wobble base modification; tRNA wobble uridine modification



P76372
WZZB_ECOLI Chain length determinant protein

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 1.46 (Q 36)
PAXdb E.coli [ppm]: 2.42 (Q 84)

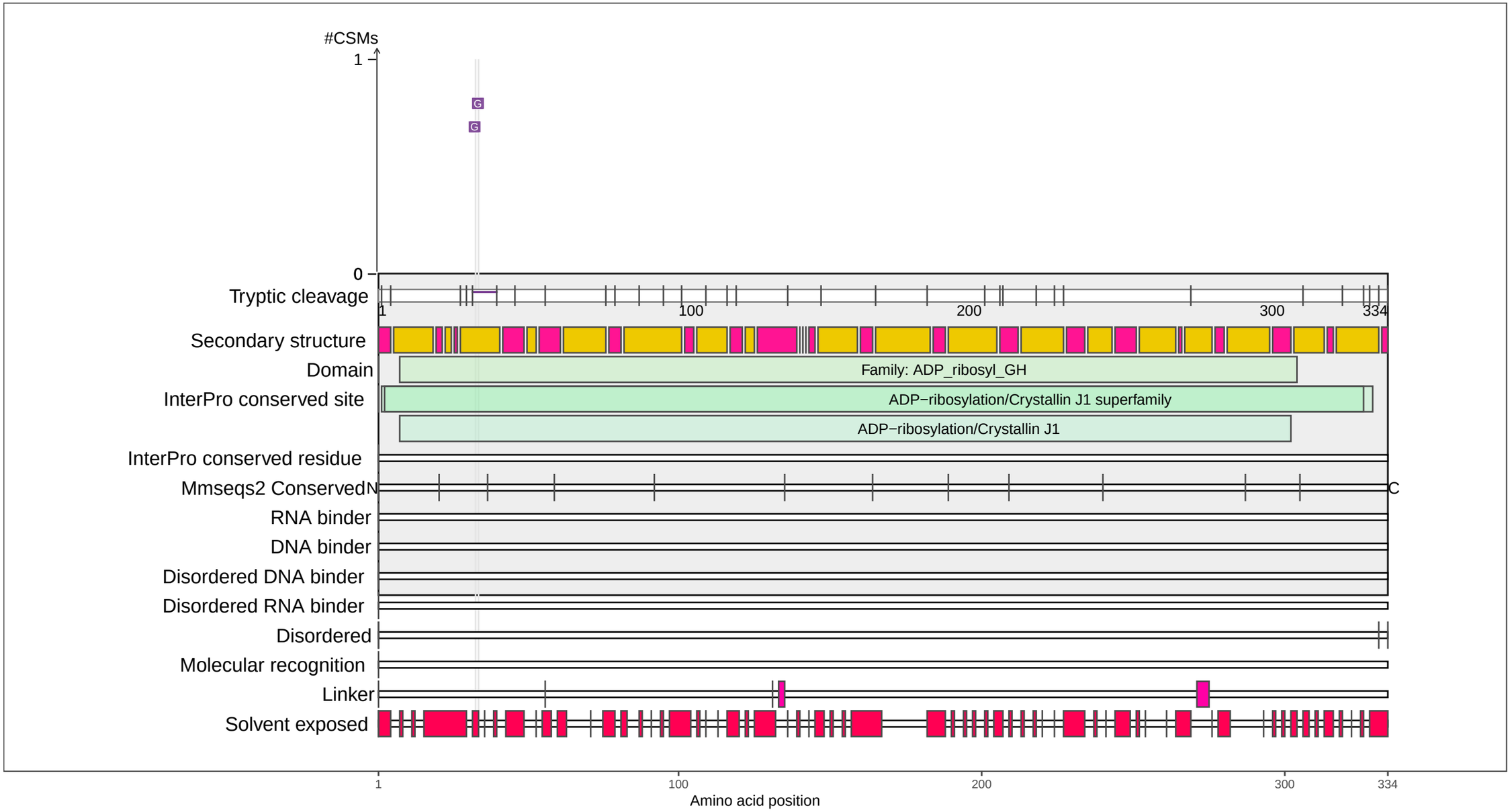
− RNA functions: not annotated

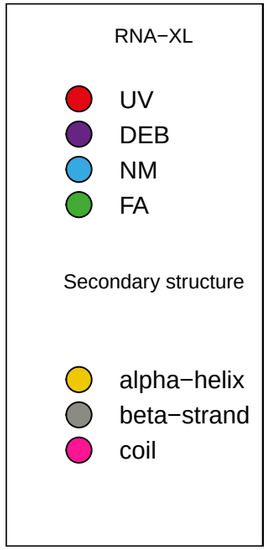


P76418
YEGU_ECOLI Uncharacterized protein YegU

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 63)
PAXdb K12 strain [ppm]: 0.77 (Q 4)
PAXdb E.coli [ppm]: 1.14 (Q 51)

− RNA functions: not annotated

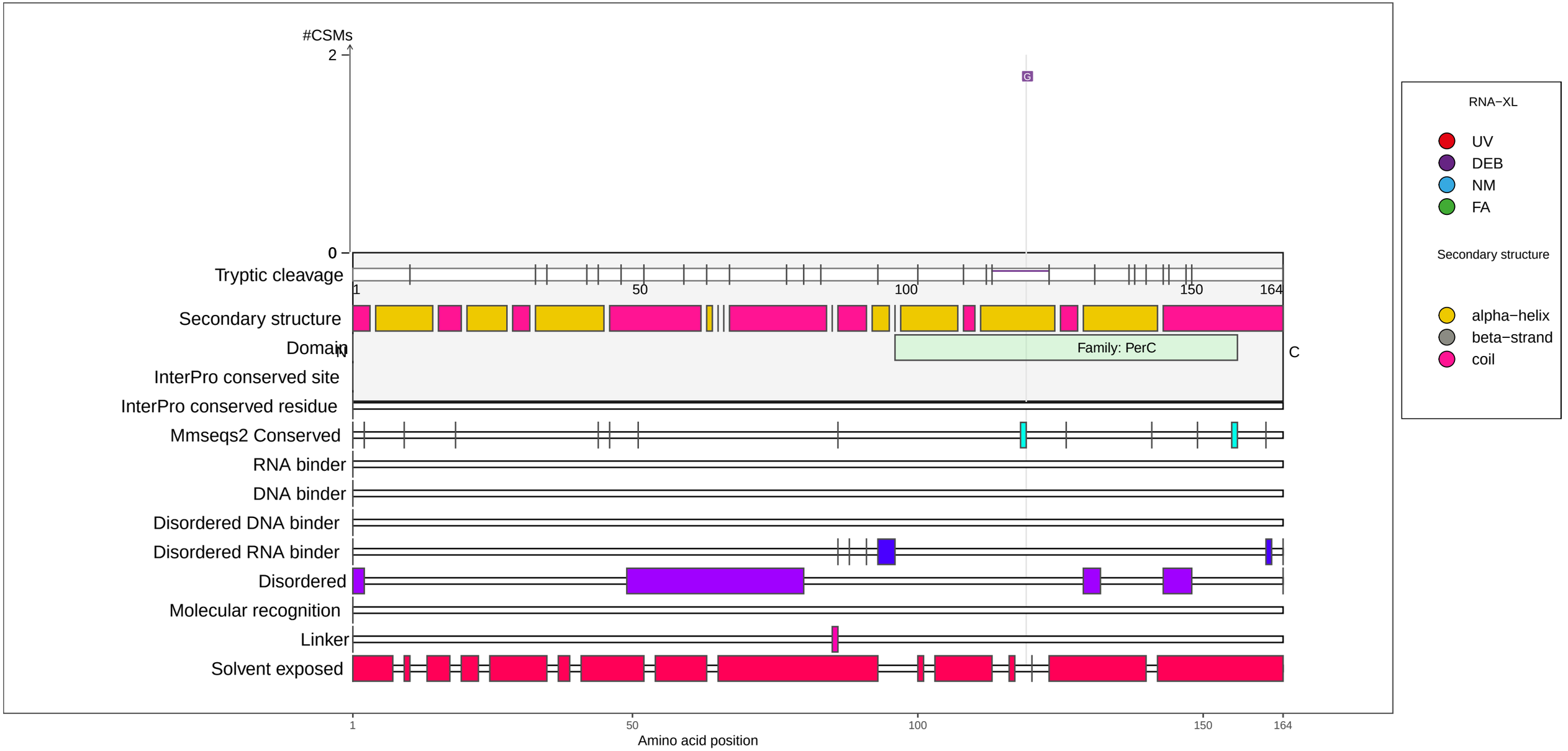




P76510
YFDN_ECOLI Uncharacterized protein YfdN

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.99 (Q 60)
PAXdb E.coli [ppm]: −0.78 (Q 12)

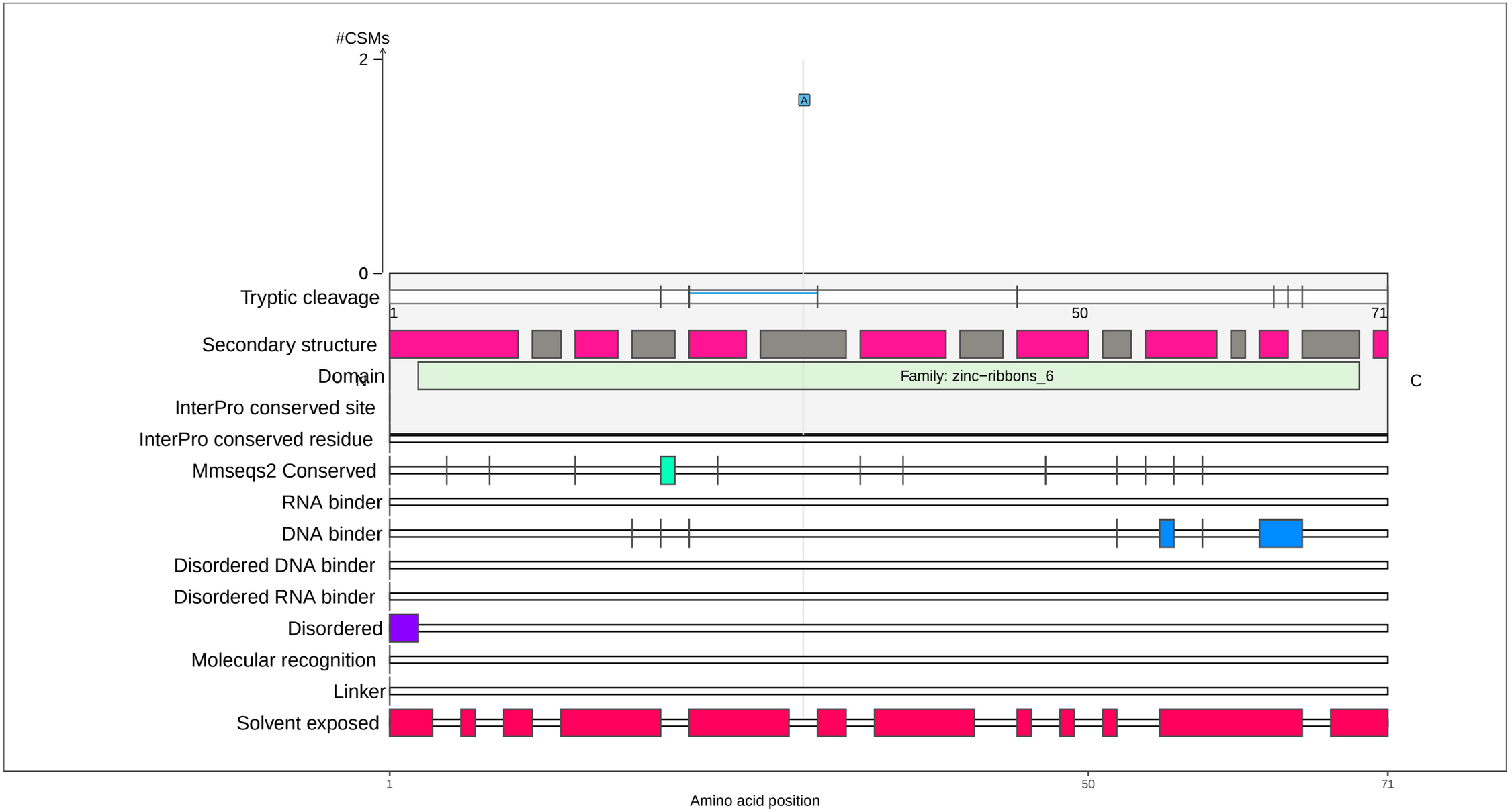
− RNA functions: not annotated

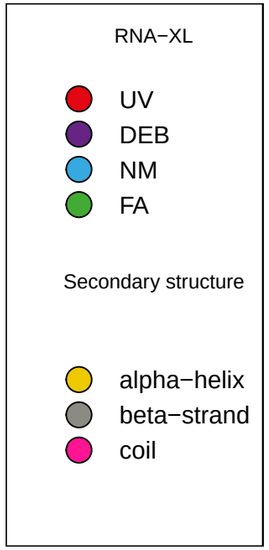


P76575
YFGJ_ECOLI Uncharacterized protein YfgJ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.7 (Q 41)

− RNA functions: not annotated

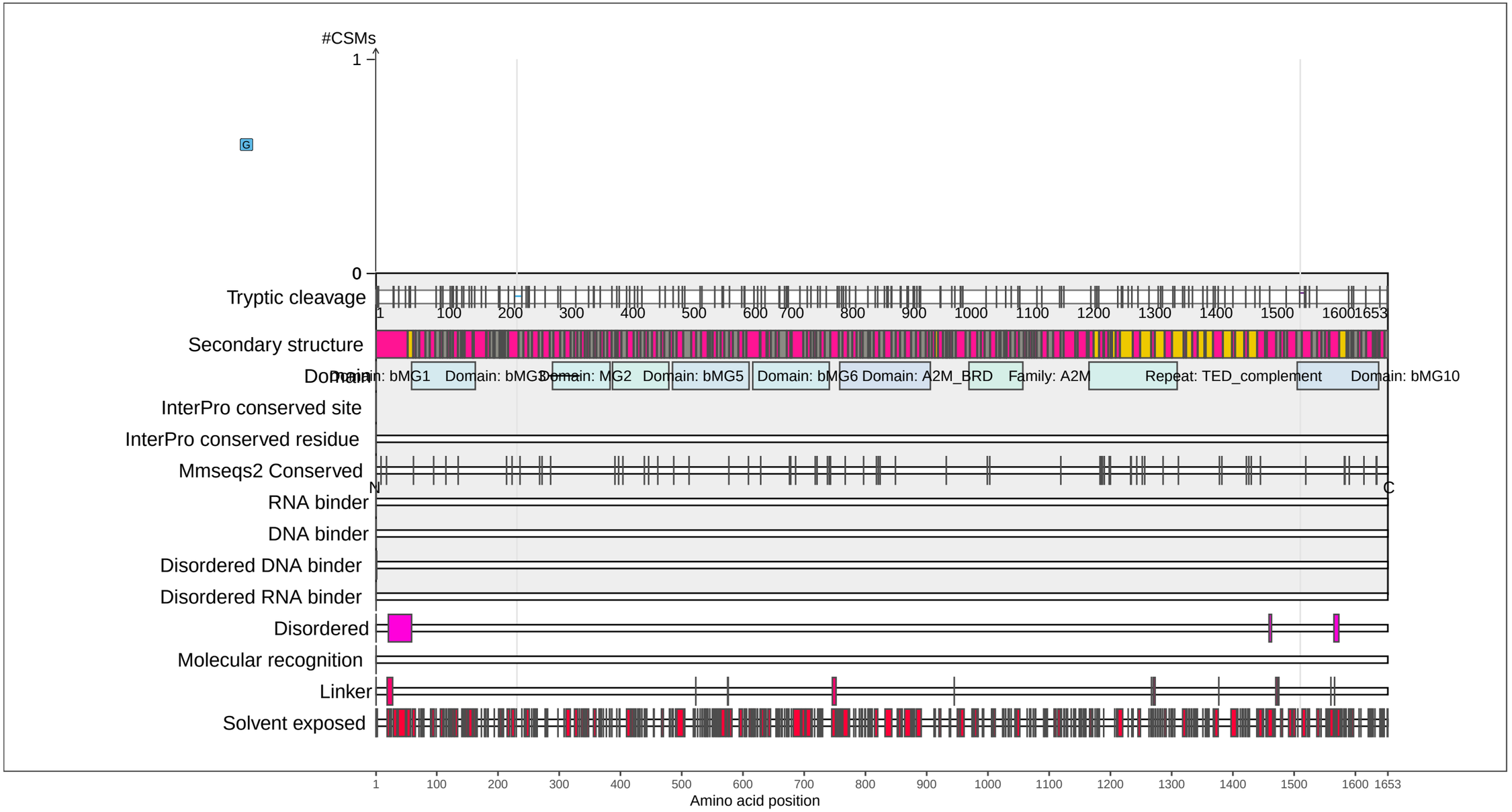




P76578
A2MG_ECOLI Alpha−2−macroglobulin

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 51)
PAXdb K12 strain [ppm]: 1.09 (Q 15)
PAXdb E.coli [ppm]: 1.21 (Q 53)

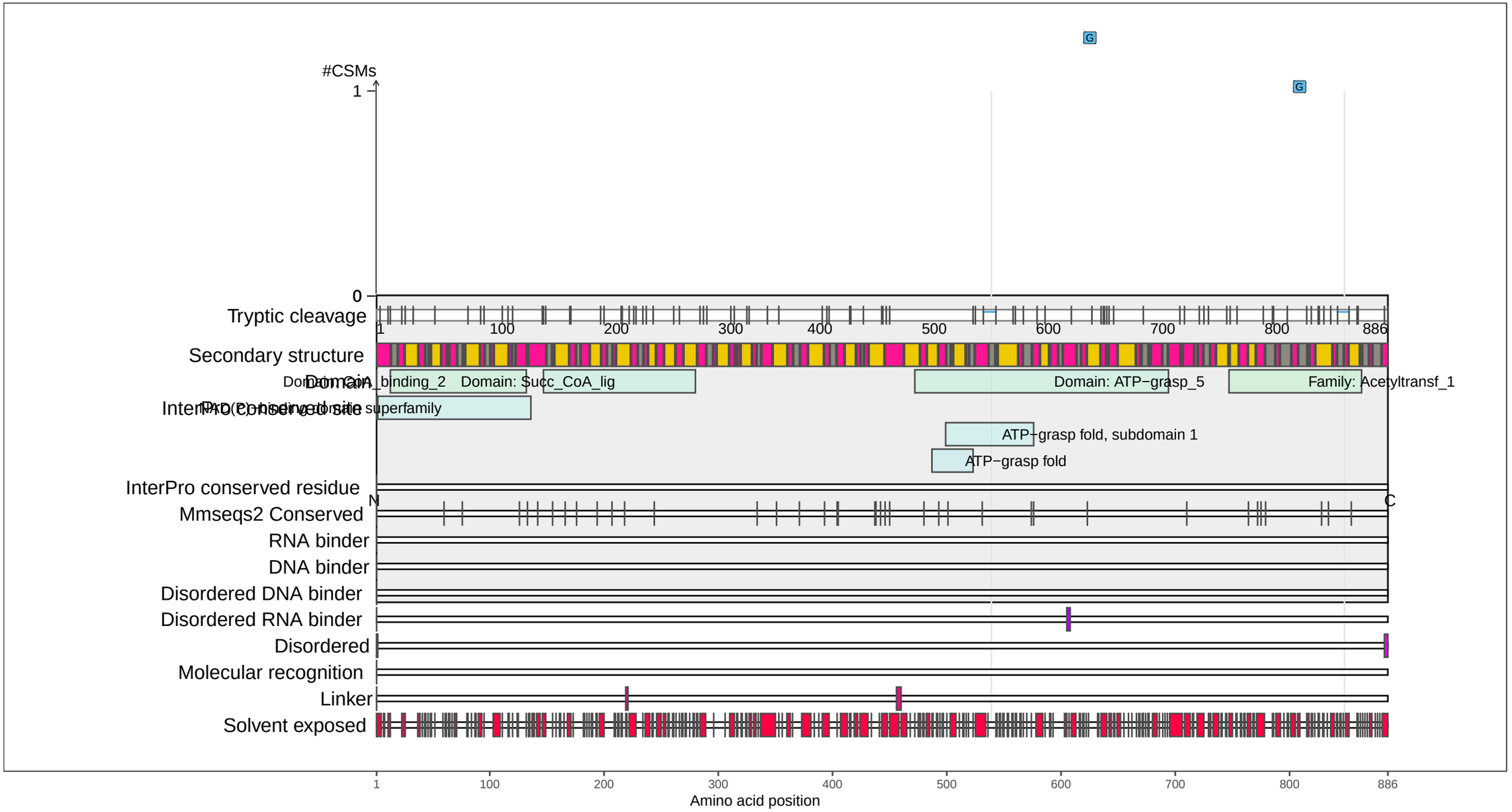
− RNA functions: not annotated



P76594
LYSAC_ECOLI Peptidyl−lysine N−acetyltransferase PatZ

− Abundance:
tryptic [log10 Intensity]: 7.44 (Q 32)
PAXdb K12 strain [ppm]: 1.5 (Q 38)
PAXdb E.coli [ppm]: 1.81 (Q 67)

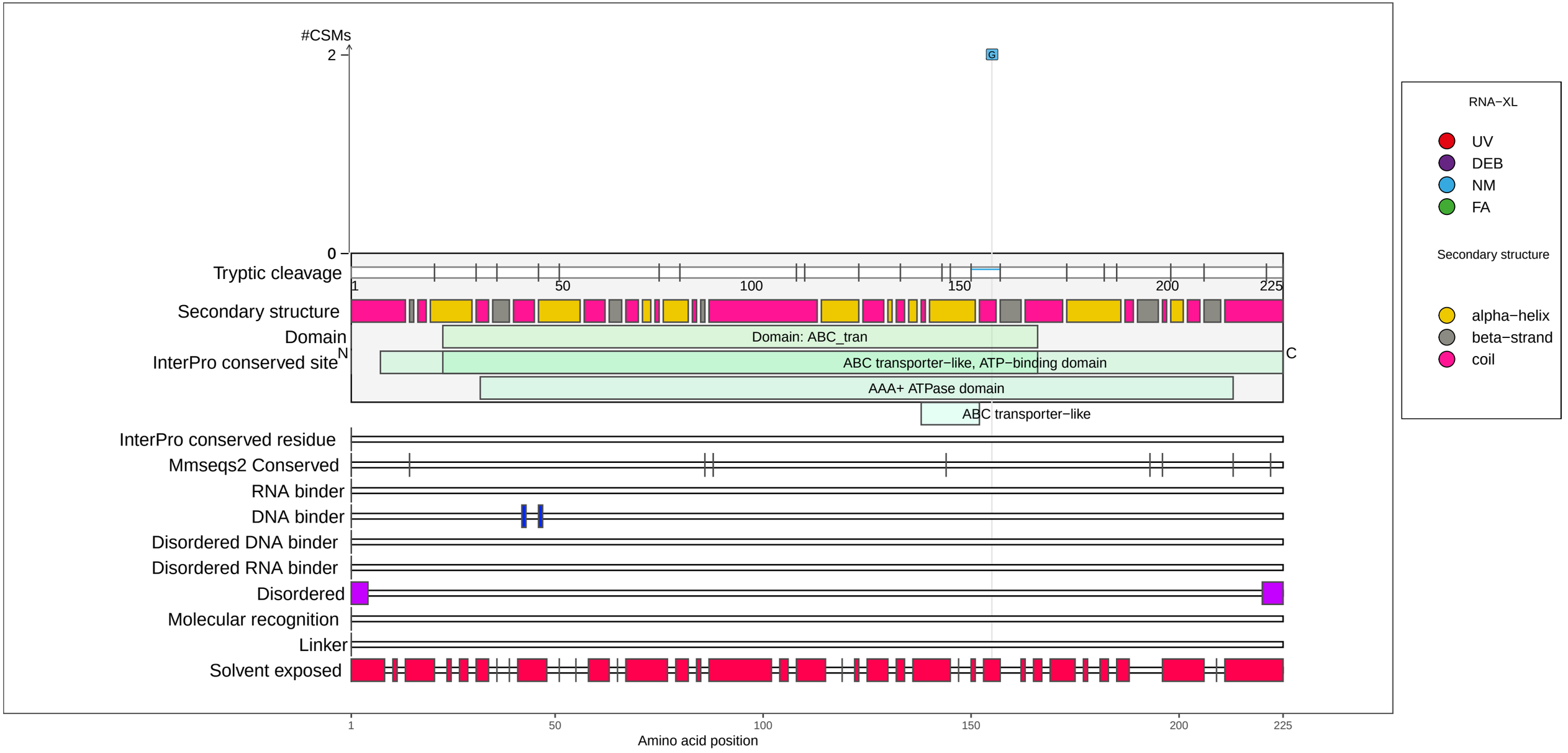
− RNA functions: not annotated



P77279
FETA_ECOLI Probable iron export ATP−binding protein FetA

− Abundance:
tryptic [log10 Intensity]: 7.01 (Q 13)
PAXdb K12 strain [ppm]: 1.62 (Q 46)
PAXdb E.coli [ppm]: 0.93 (Q 46)

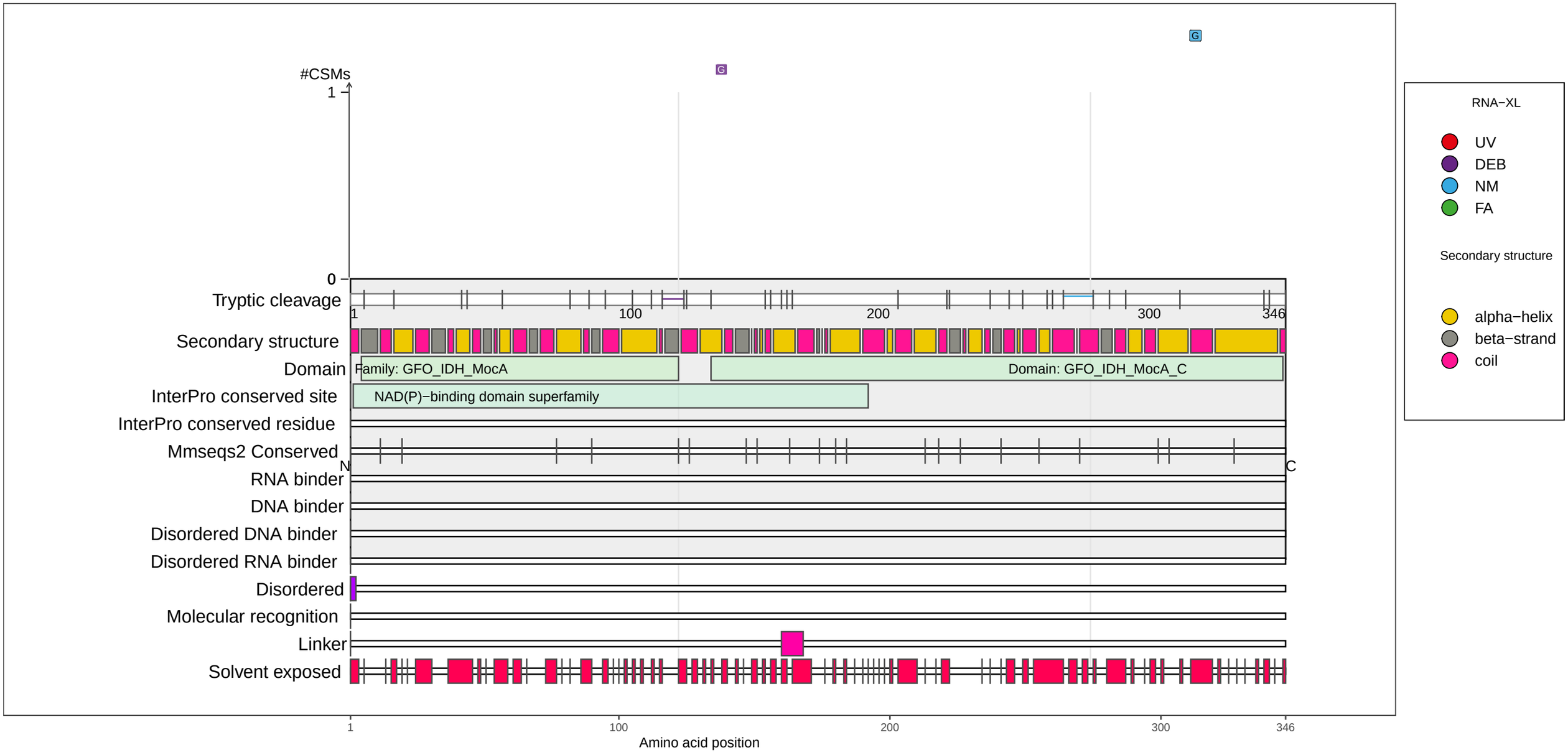
− RNA functions: not annotated



P77376
YDGJ_ECOLI Uncharacterized oxidoreductase YdgJ

− Abundance:
tryptic [log10 Intensity]: 7.89 (Q 53)
PAXdb K12 strain [ppm]: 1.38 (Q 31)
PAXdb E.coli [ppm]: 2.04 (Q 73)

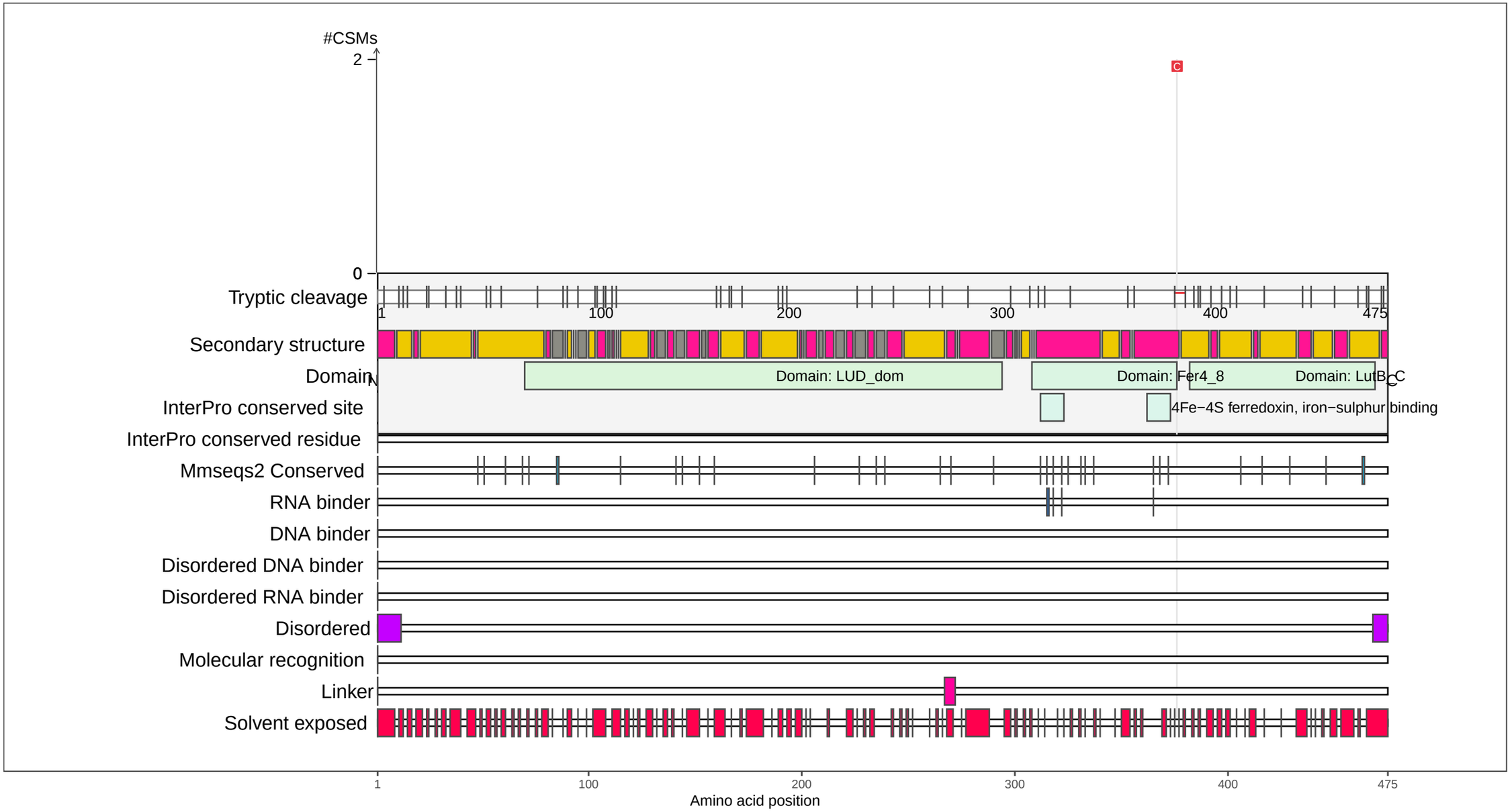
− RNA functions: not annotated



P77536
YKGF_ECOLI Uncharacterized electron transport protein YkgF

− Abundance:
tryptic [log10 Intensity]: 7.39 (Q 29)
PAXdb K12 strain [ppm]: 1.32 (Q 28)
PAXdb E.coli [ppm]: 0.67 (Q 40)

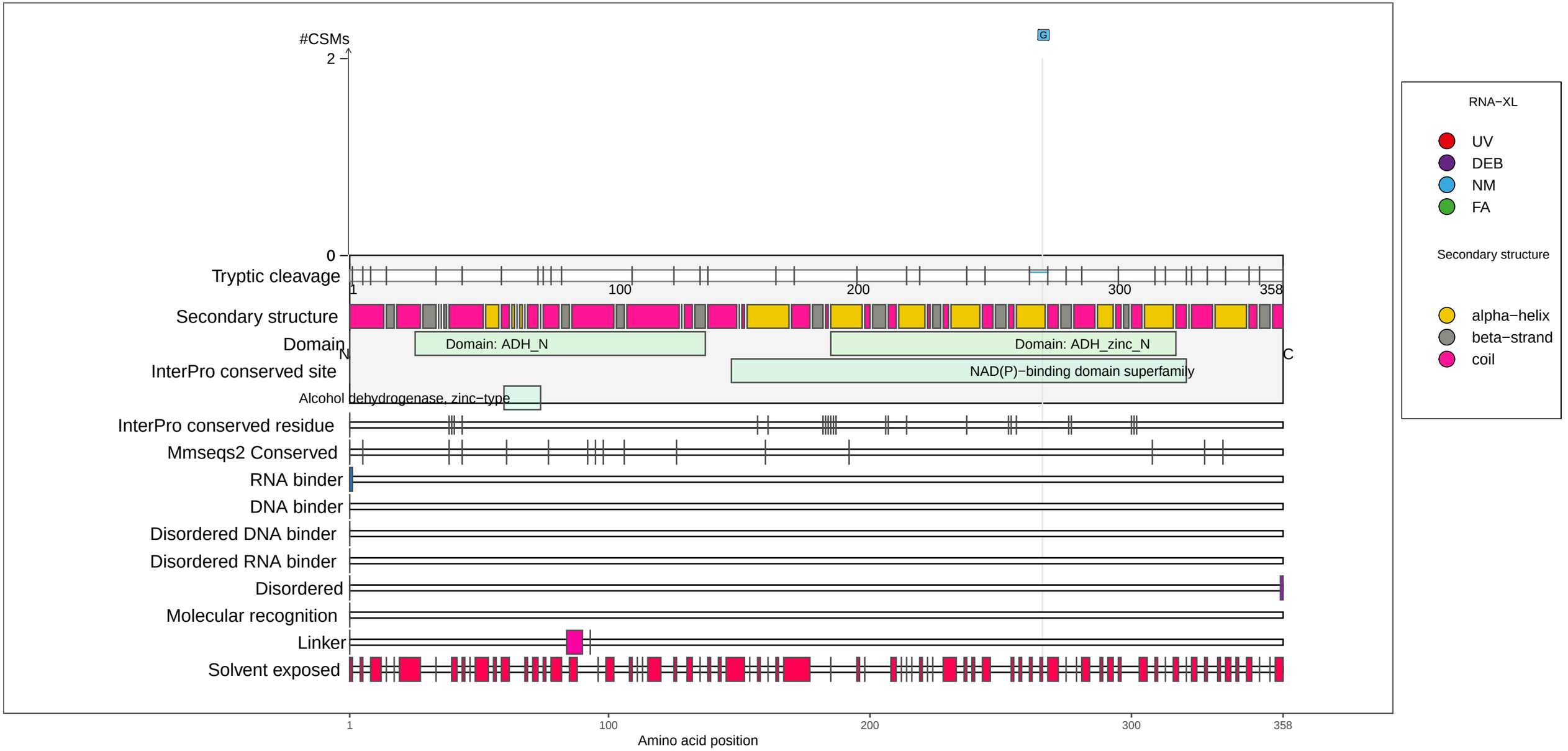
− RNA functions: not annotated



P77539
YDJL_ECOLI Uncharacterized zinc−type alcohol dehydrogenase−like protein YdjL

− Abundance:
tryptic [log10 Intensity]: 6.85 (Q 8)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.37 (Q 33)

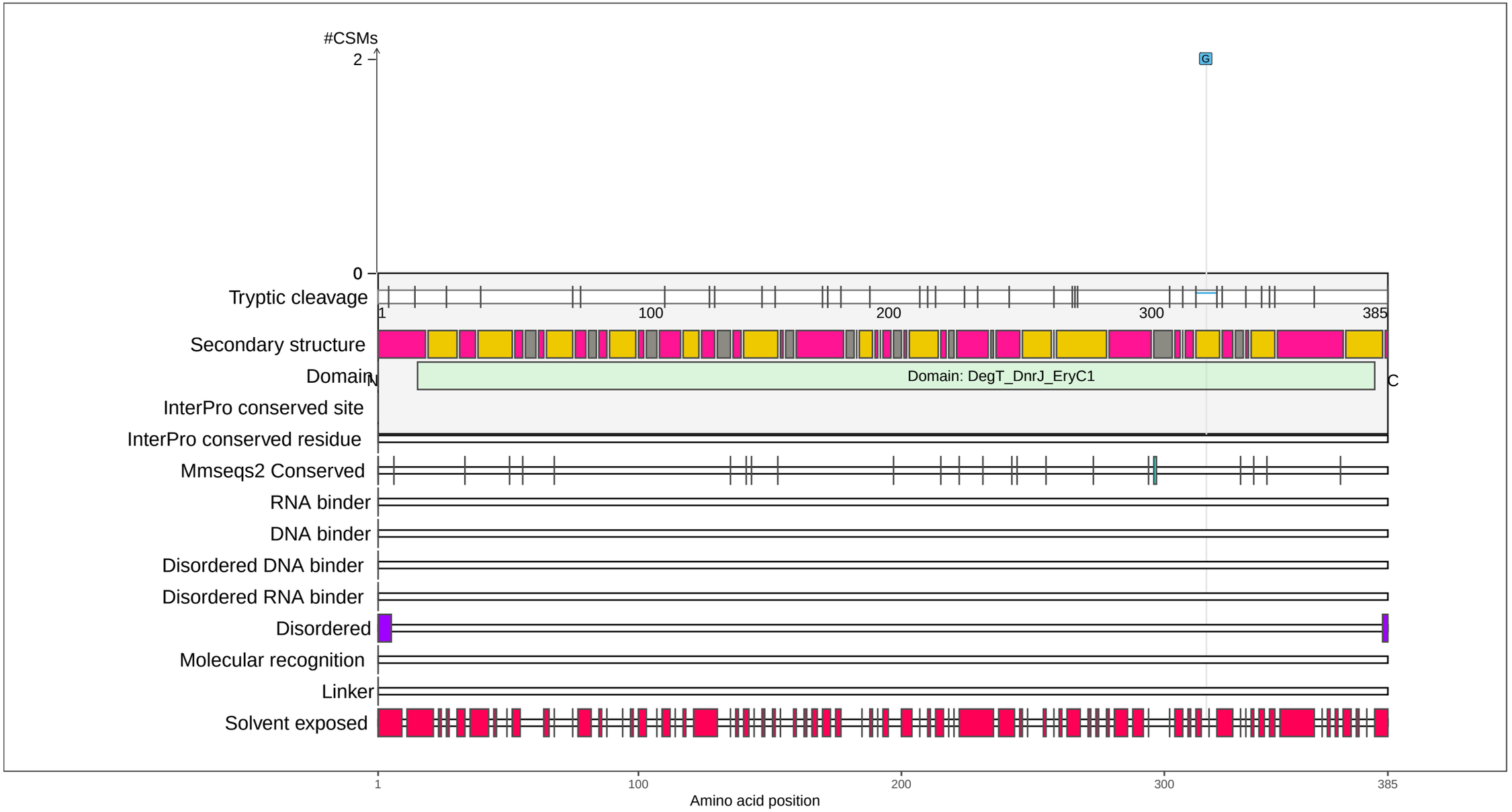
− RNA functions: not annotated



P77690
ARNB_ECOLI UDP−4−amino−4−deoxy−L−arabinose−−oxoglutarate aminotransferase

− Abundance:
tryptic [log10 Intensity]: 8.52 (Q 76)
PAXdb K12 strain [ppm]: 2.22 (Q 67)
PAXdb E.coli [ppm]: 2.07 (Q 74)

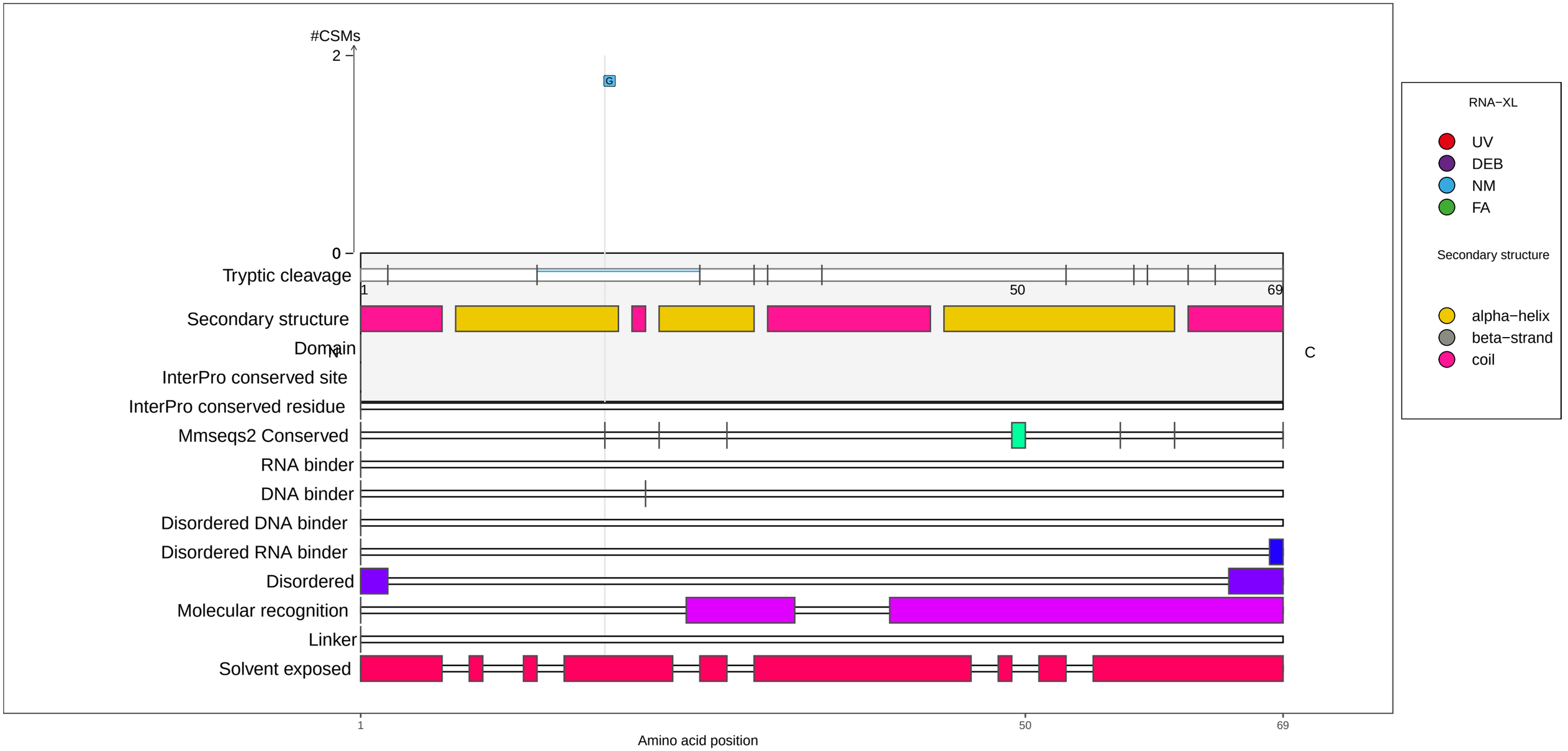
− RNA functions: not annotated



Q2M7R5
YIBT_ECOLI Uncharacterized protein YibT

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.22 (Q 78)

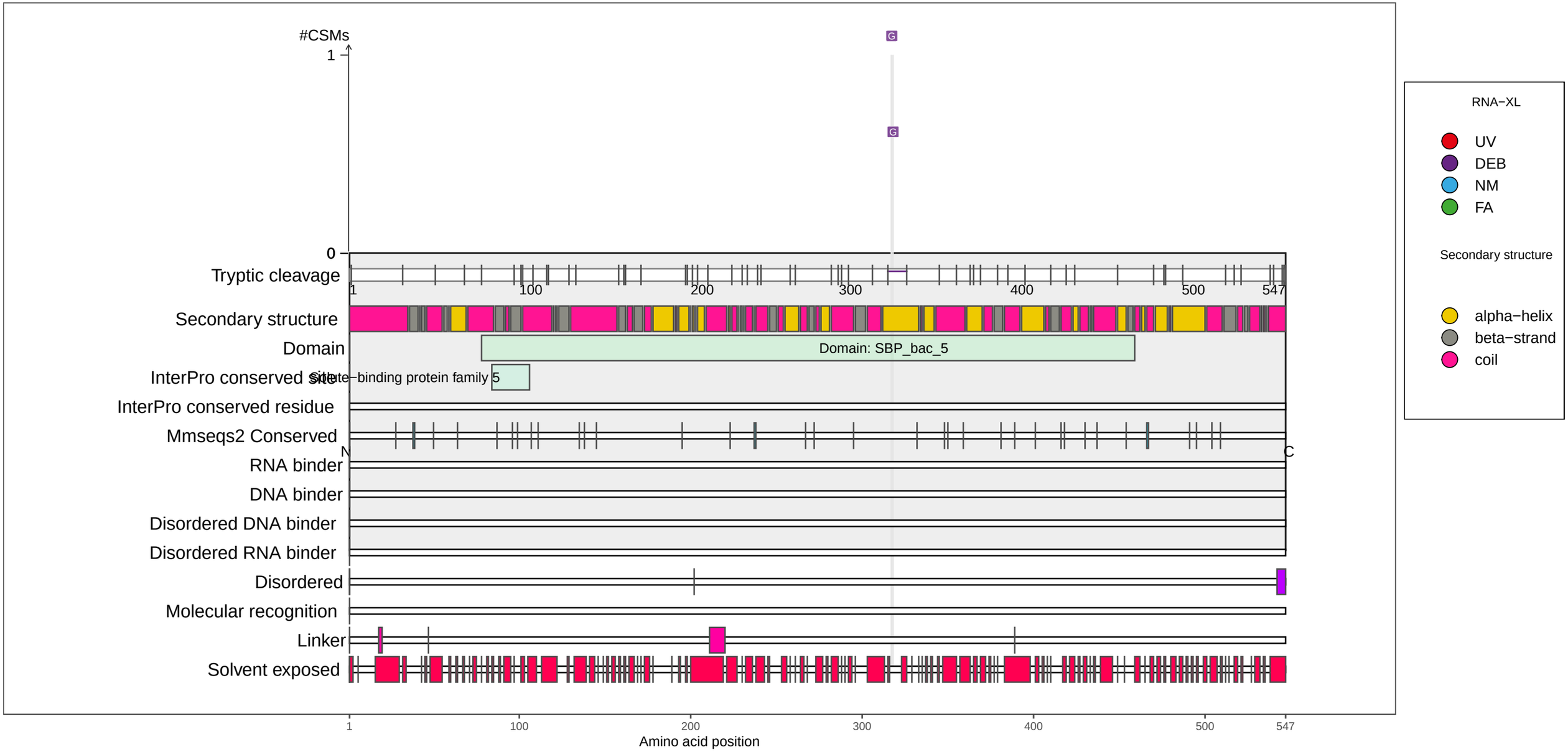
− RNA functions: not annotated



Q47622
SAPA_ECOLI Probable ABC transporter periplasmic−binding protein SapA

− Abundance:
tryptic [log10 Intensity]: 7.32 (Q 26)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 1.05 (Q 49)

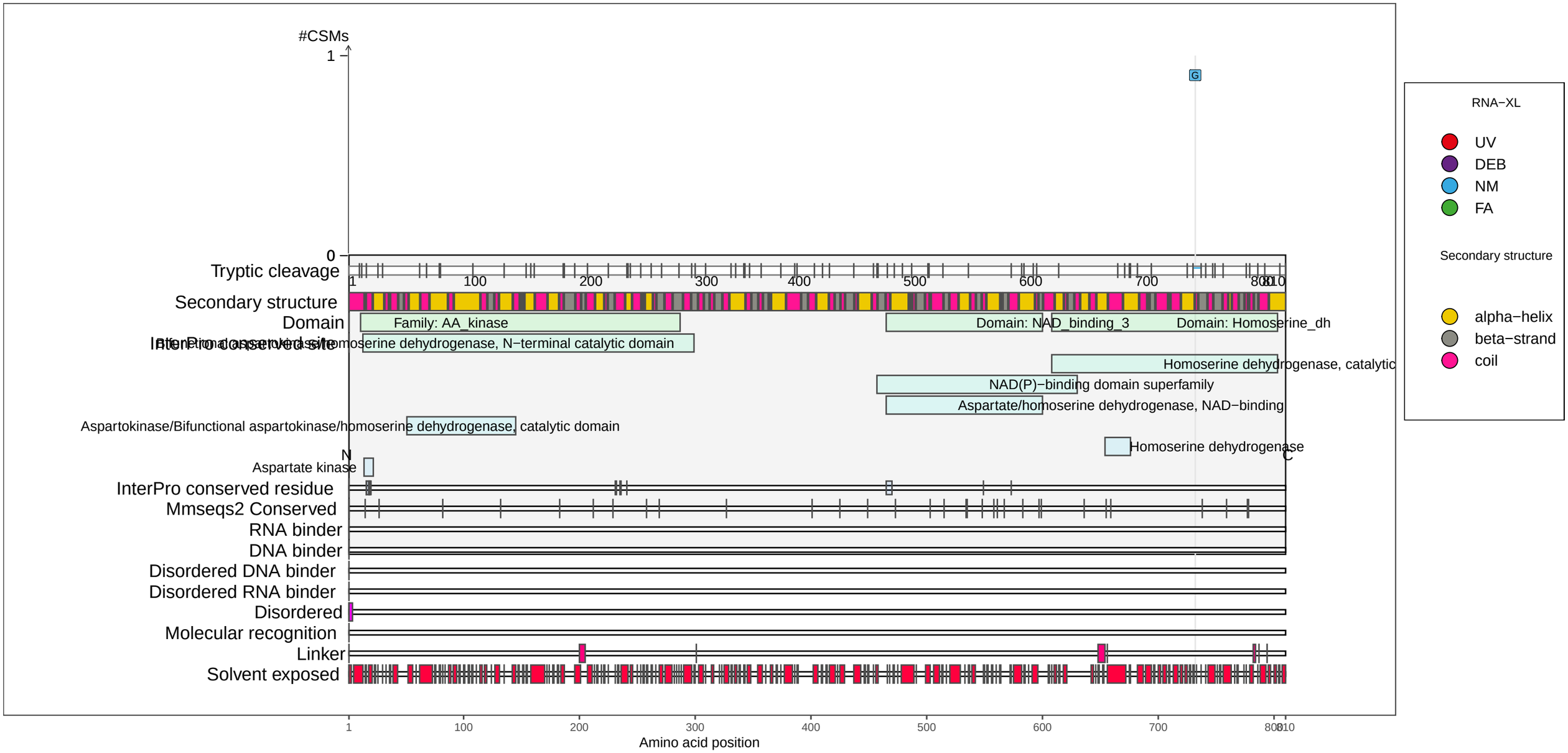
− RNA functions: not annotated



P00562
AK2H_ECOLI Bifunctional aspartokinase/homoserine dehydrogenase 2

− Abundance:
tryptic [log10 Intensity]: 7.5 (Q 35)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 2.15 (Q 76)

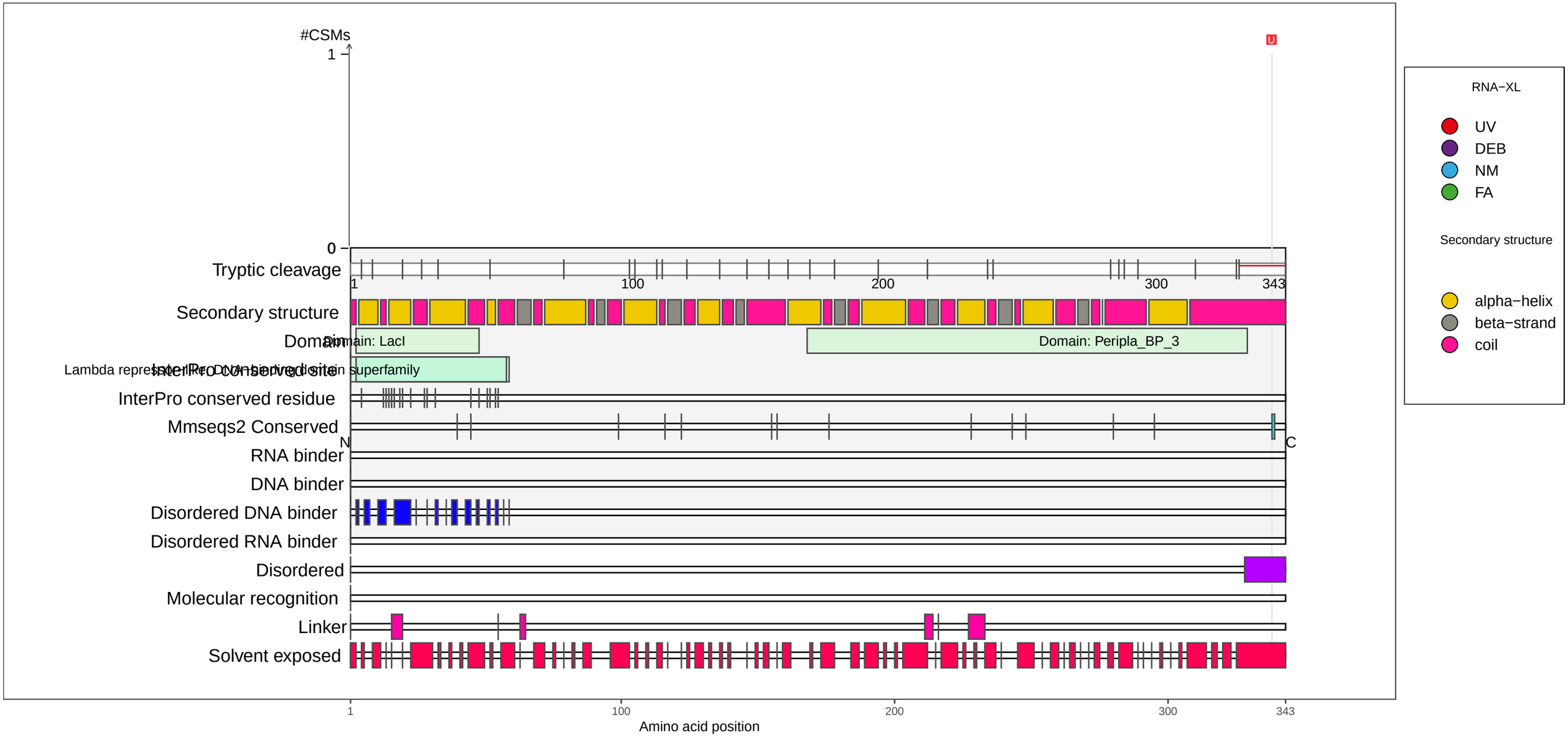
− RNA functions: not annotated



P03024
GALR_ECOLI HTH−type transcriptional regulator GalR

− Abundance:
tryptic [log10 Intensity]: 8.16 (Q 63)
PAXdb K12 strain [ppm]: 1.28 (Q 25)
PAXdb E.coli [ppm]: 0.28 (Q 31)

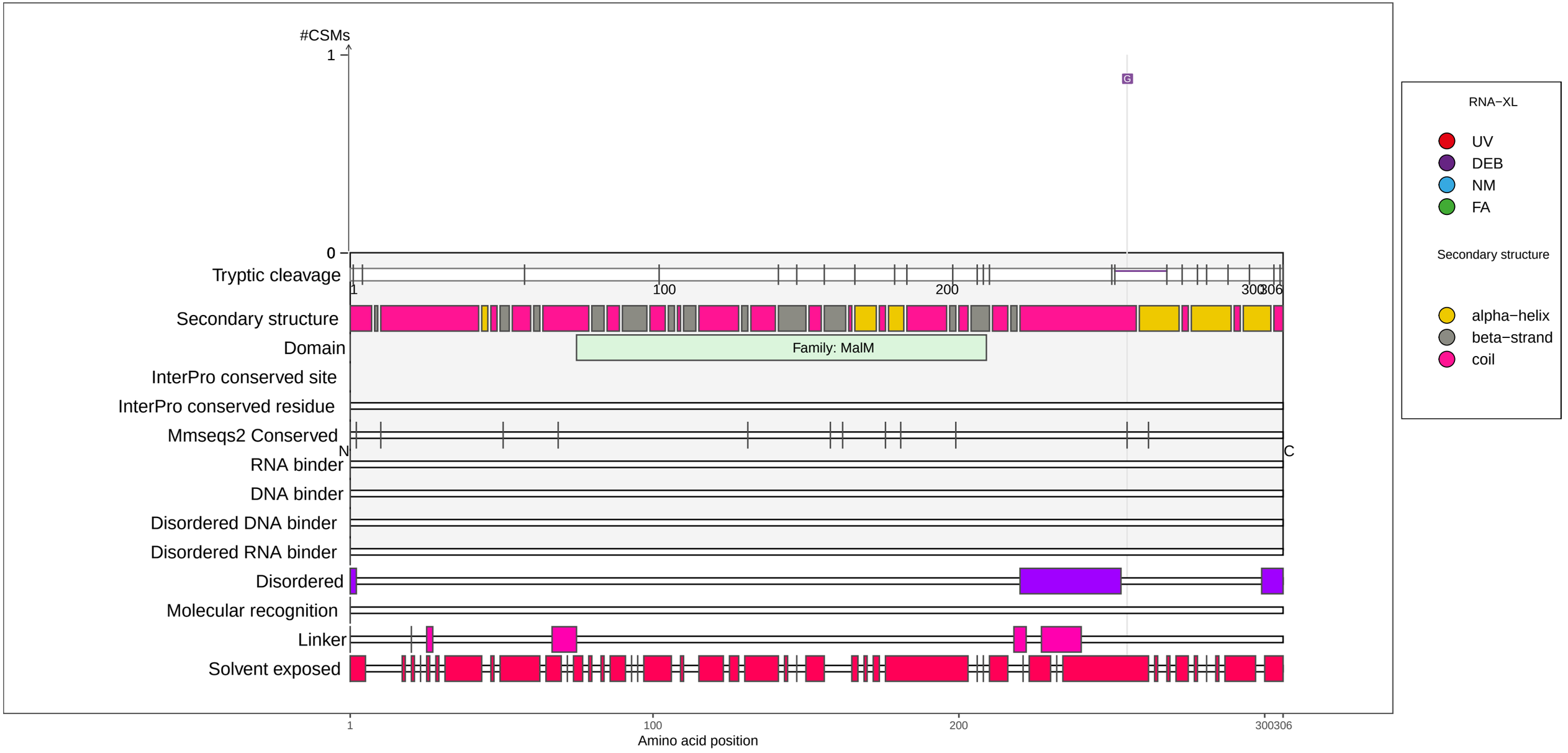
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P03841
MALM_ECOLI Maltose operon periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.64 (Q 42)
PAXdb K12 strain [ppm]: 3.06 (Q 92)
PAXdb E.coli [ppm]: 2.45 (Q 84)

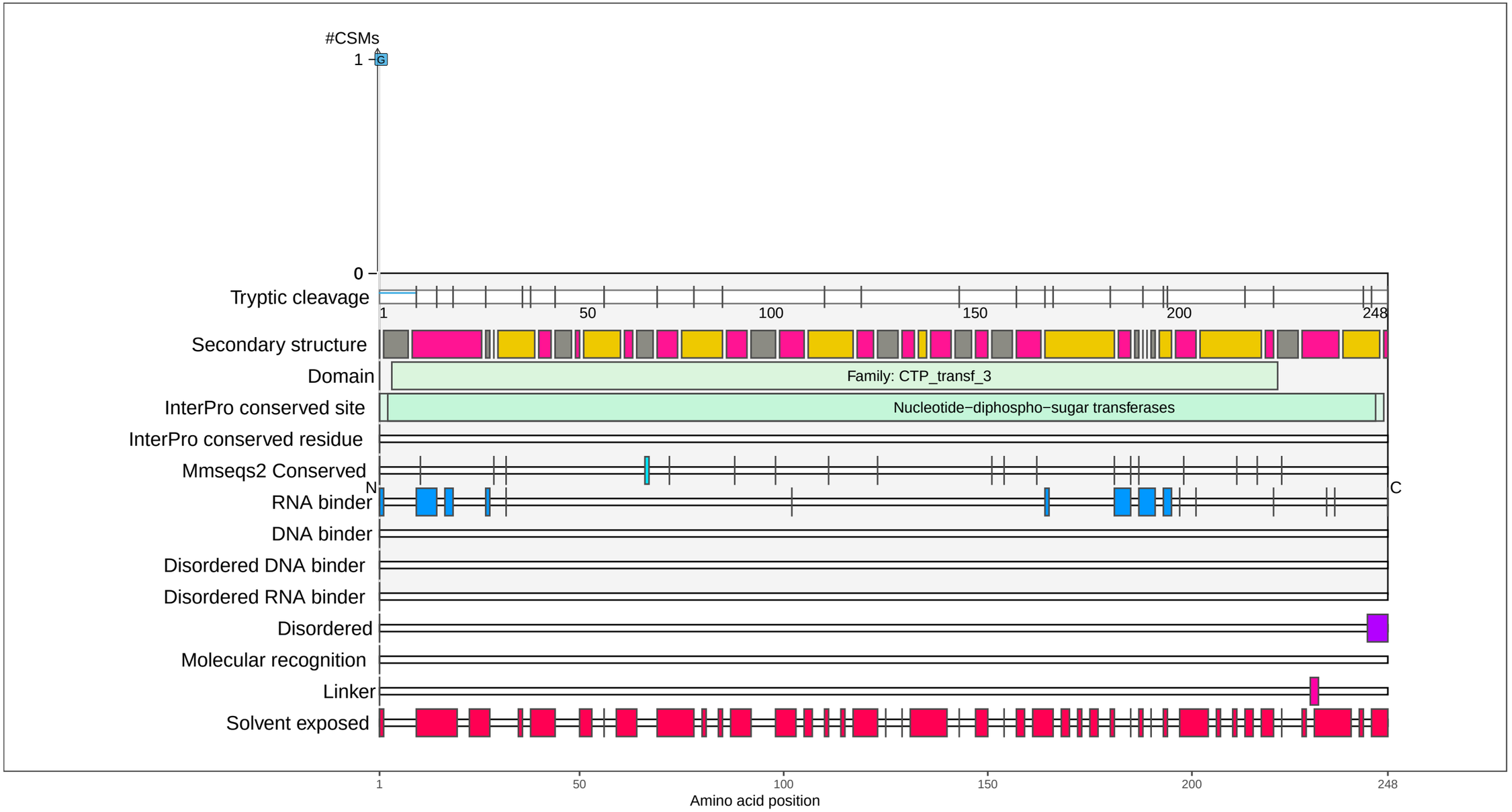
− RNA functions: not annotated



P04951
KDSB_ECOLI 3−deoxy−manno−octulosonate cytidylyltransferase

− Abundance:
tryptic [log10 Intensity]: 8.84 (Q 84)
PAXdb K12 strain [ppm]: 1.9 (Q 57)
PAXdb E.coli [ppm]: 2.45 (Q 84)

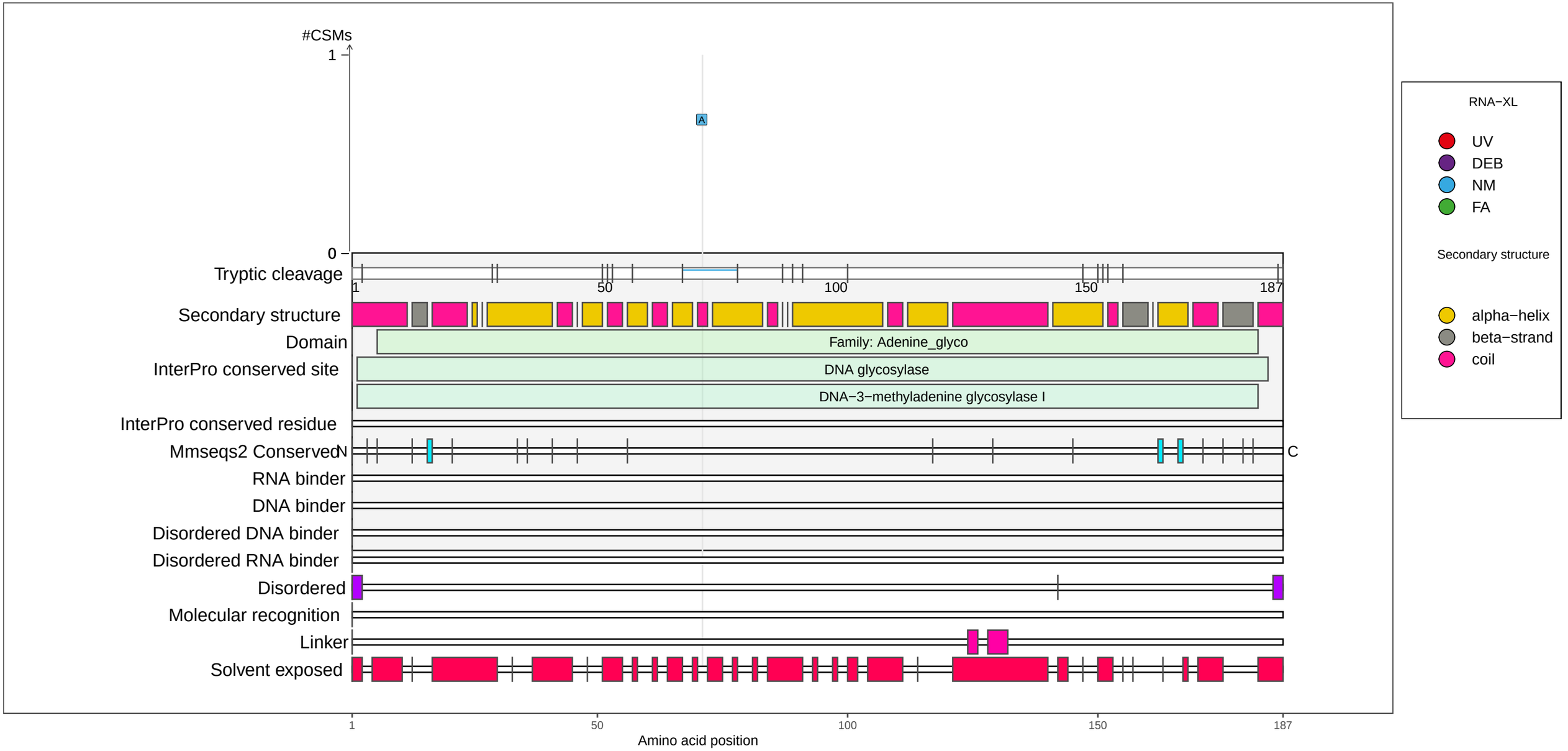
− RNA functions: not annotated



P05100
3MG1_ECOLI DNA−3−methyladenine glycosylase 1

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.61 (Q 39)

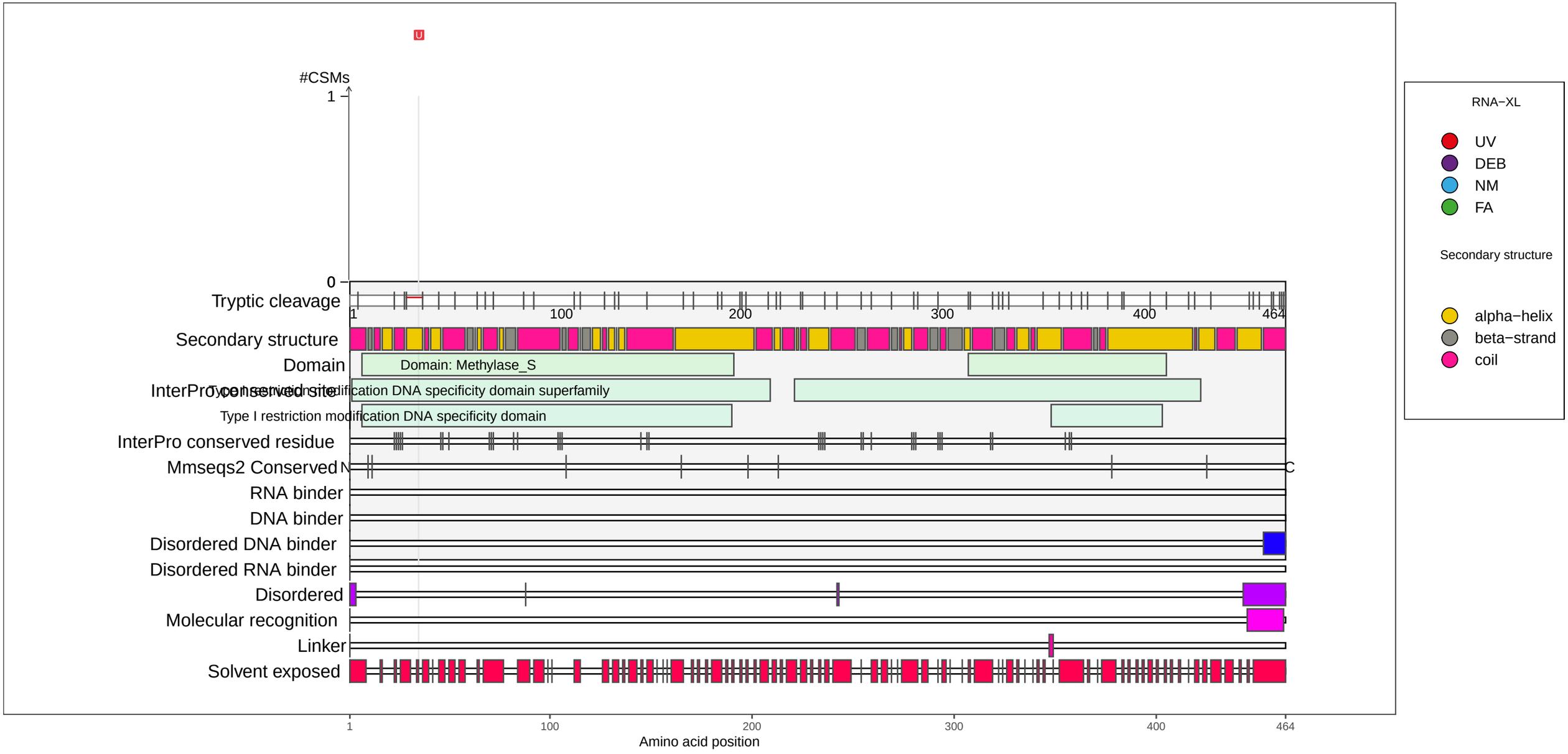
− RNA functions: not annotated



P05719
T1SK_ECOLI Type I restriction enzyme EcoKI specificity subunit

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.18 (Q 19)
PAXdb E.coli [ppm]: 0.8 (Q 43)

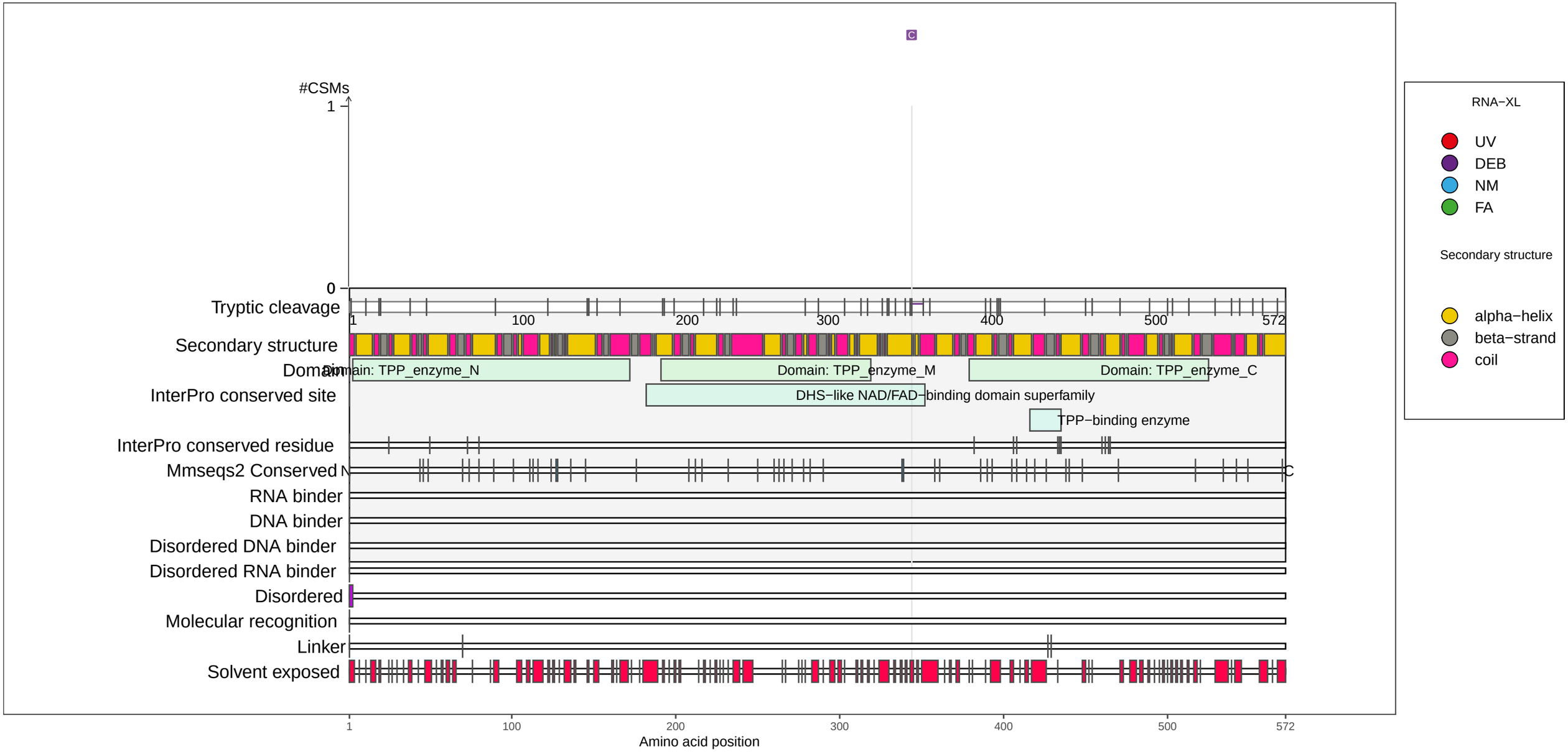
− RNA functions: not annotated



P07003
POXB_ECOLI Pyruvate dehydrogenase [ubiquinone]

− Abundance:
tryptic [log10 Intensity]: 7.16 (Q 19)
PAXdb K12 strain [ppm]: 2.91 (Q 89)
PAXdb E.coli [ppm]: 2.59 (Q 88)

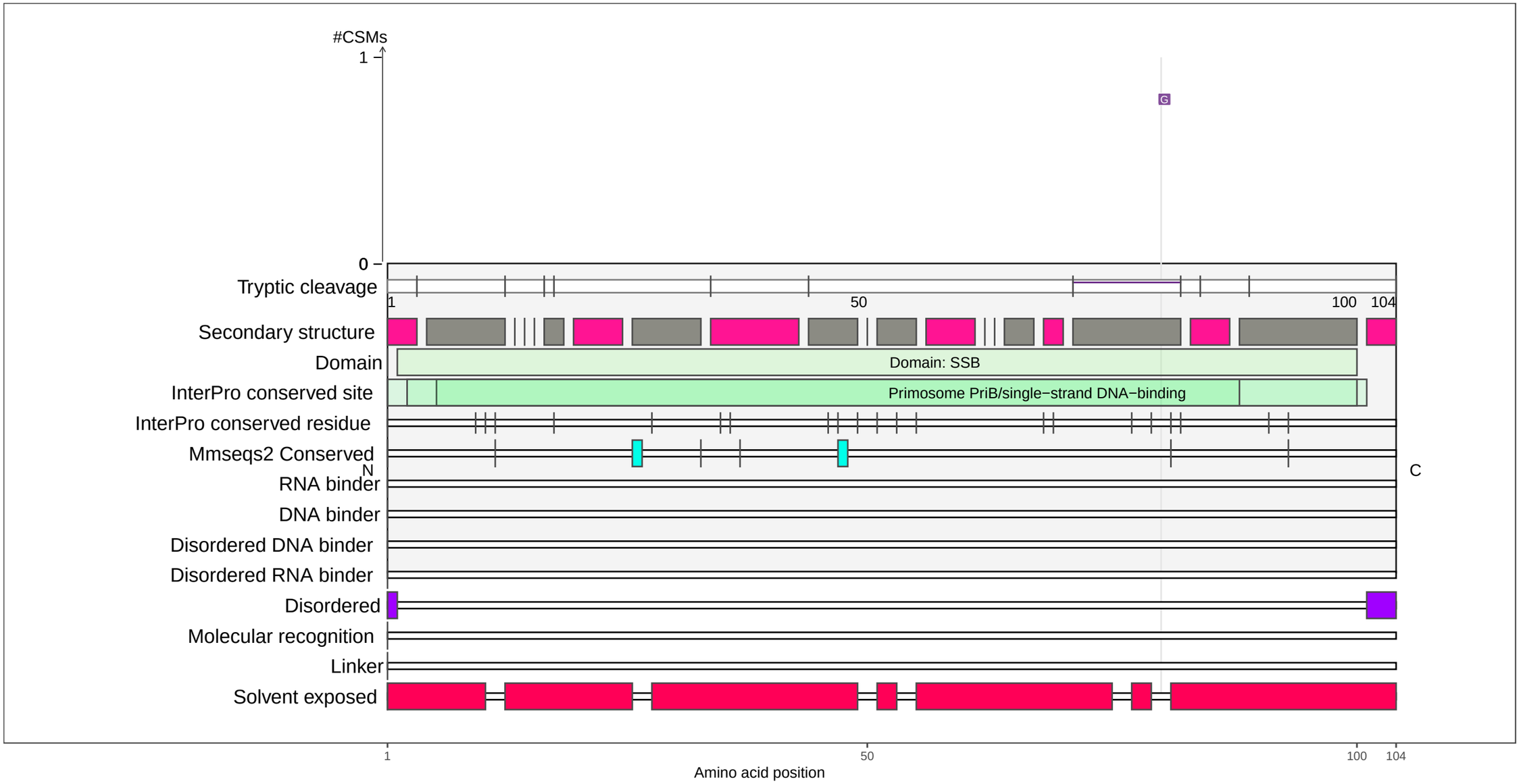
− RNA functions: not annotated

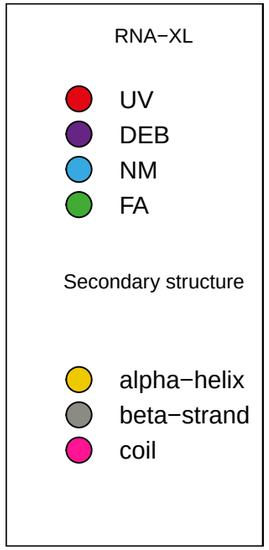


P07013
PRIB_ECOLI Primosomal replication protein N

− Abundance:
tryptic [log10 Intensity]: 7.68 (Q 44)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.31 (Q 32)

− RNA functions:
DNA replication, synthesis of RNA primer; RNA biosynthetic process
RNA metabolic process

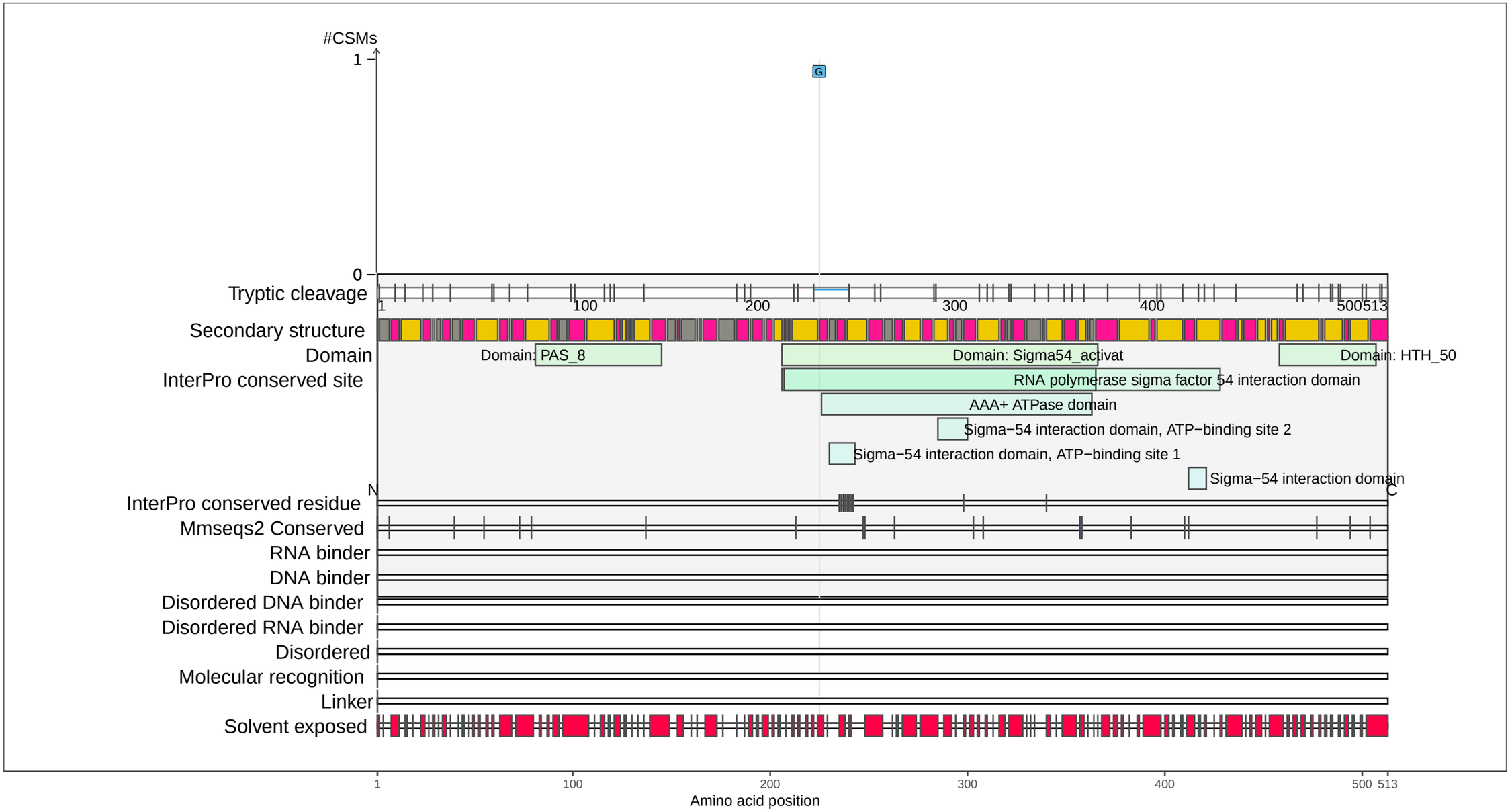


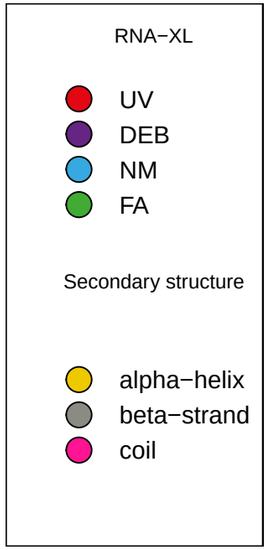


P07604
TYRR_ECOLI HTH−type transcriptional regulatory protein TyrR

− Abundance:
tryptic [log10 Intensity]: 6.43 (Q 2)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.78 (Q 66)

− RNA functions: not annotated

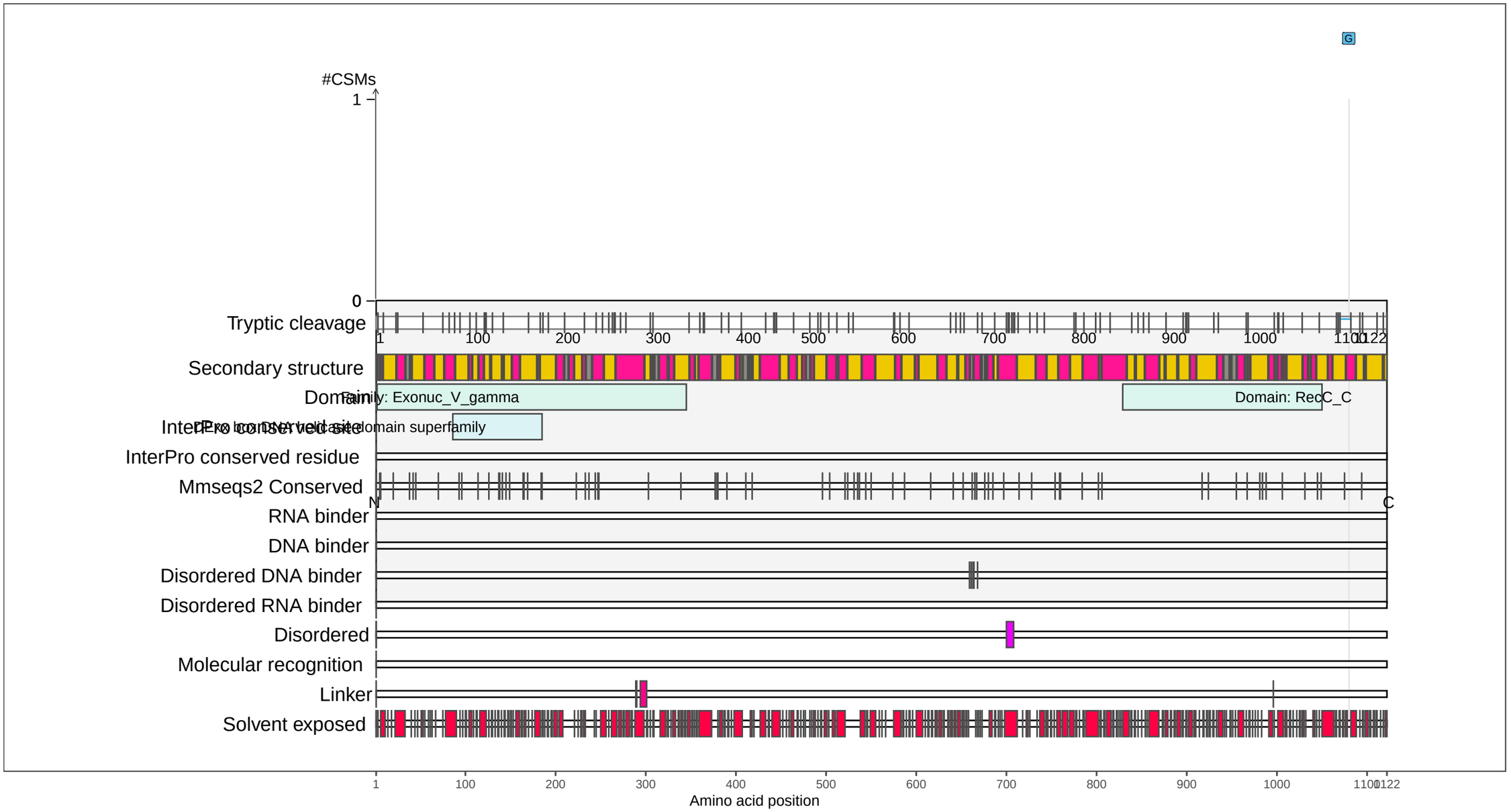




P07648
RECC_ECOLI RecBCD enzyme subunit RecC

− Abundance:
tryptic [log10 Intensity]: 7.06 (Q 15)
PAXdb K12 strain [ppm]: 1.16 (Q 18)
PAXdb E.coli [ppm]: 0.39 (Q 33)

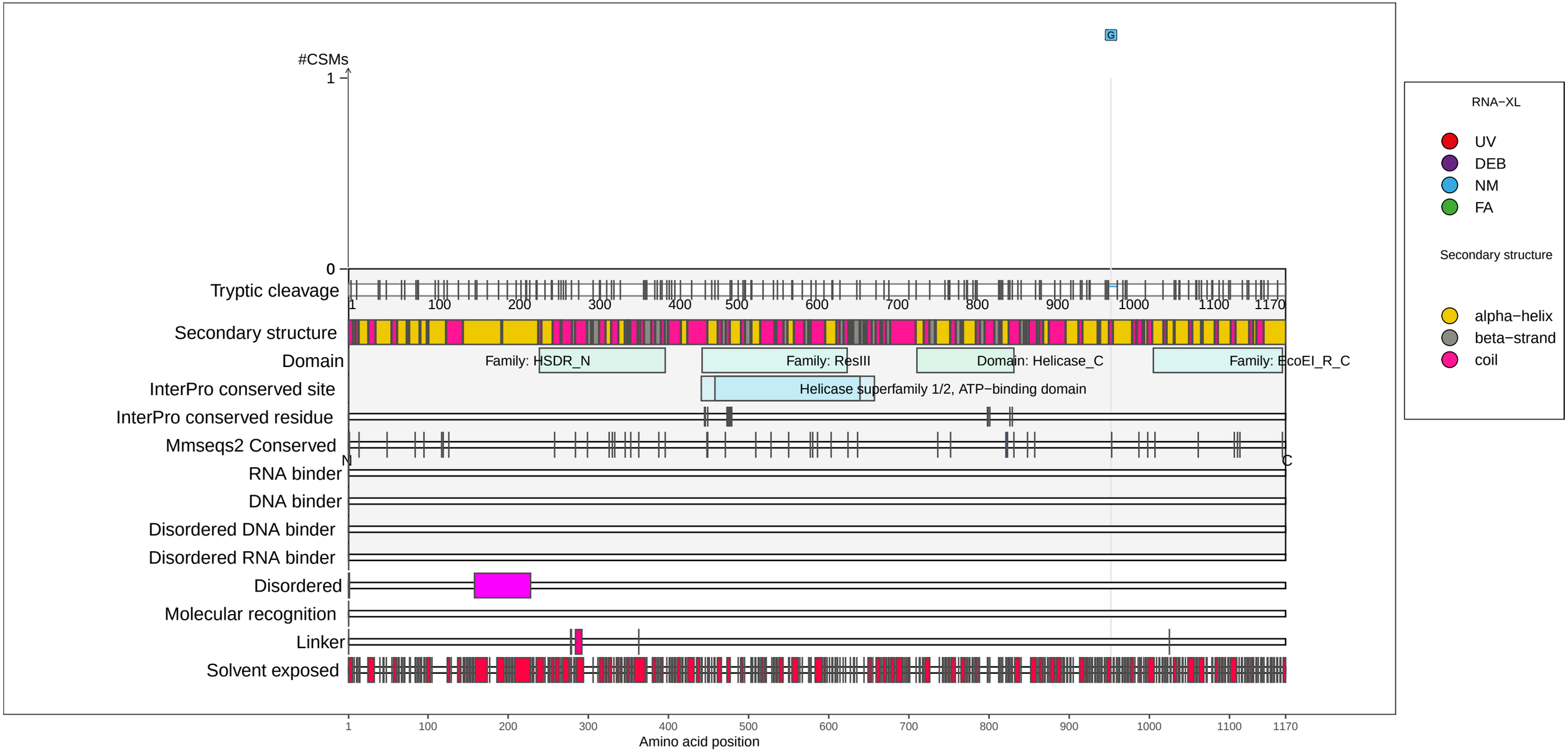
− RNA functions: not annotated



P08956
T1RK_ECOLI Type I restriction enzyme EcoKI endonuclease subunit

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 1.14 (Q 17)
PAXdb E.coli [ppm]: 1.16 (Q 51)

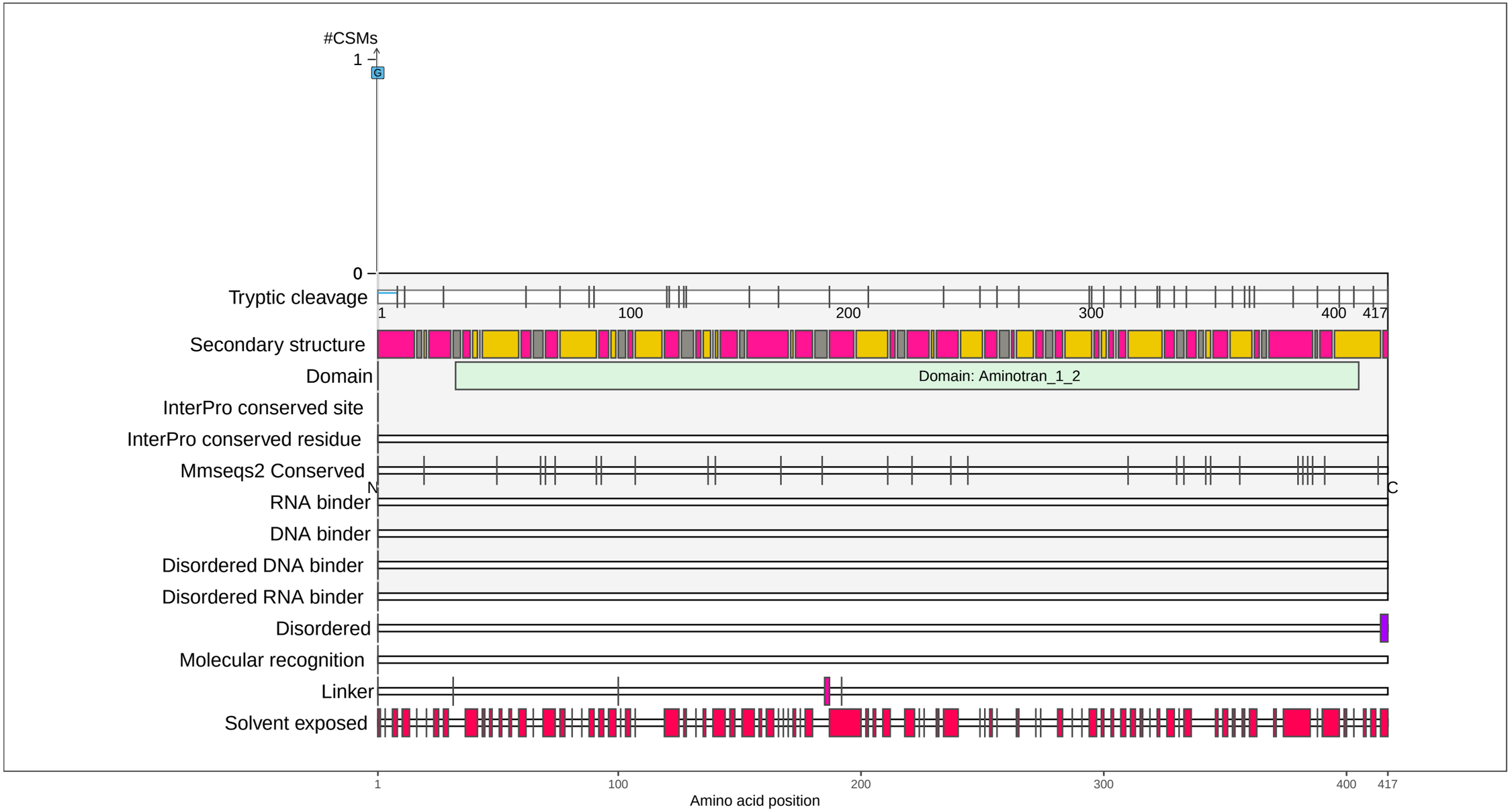
− RNA functions: not annotated



P09053
AVTA_ECOLI Valine−−pyruvate aminotransferase

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 69)
PAXdb K12 strain [ppm]: 1.93 (Q 58)
PAXdb E.coli [ppm]: 1.52 (Q 60)

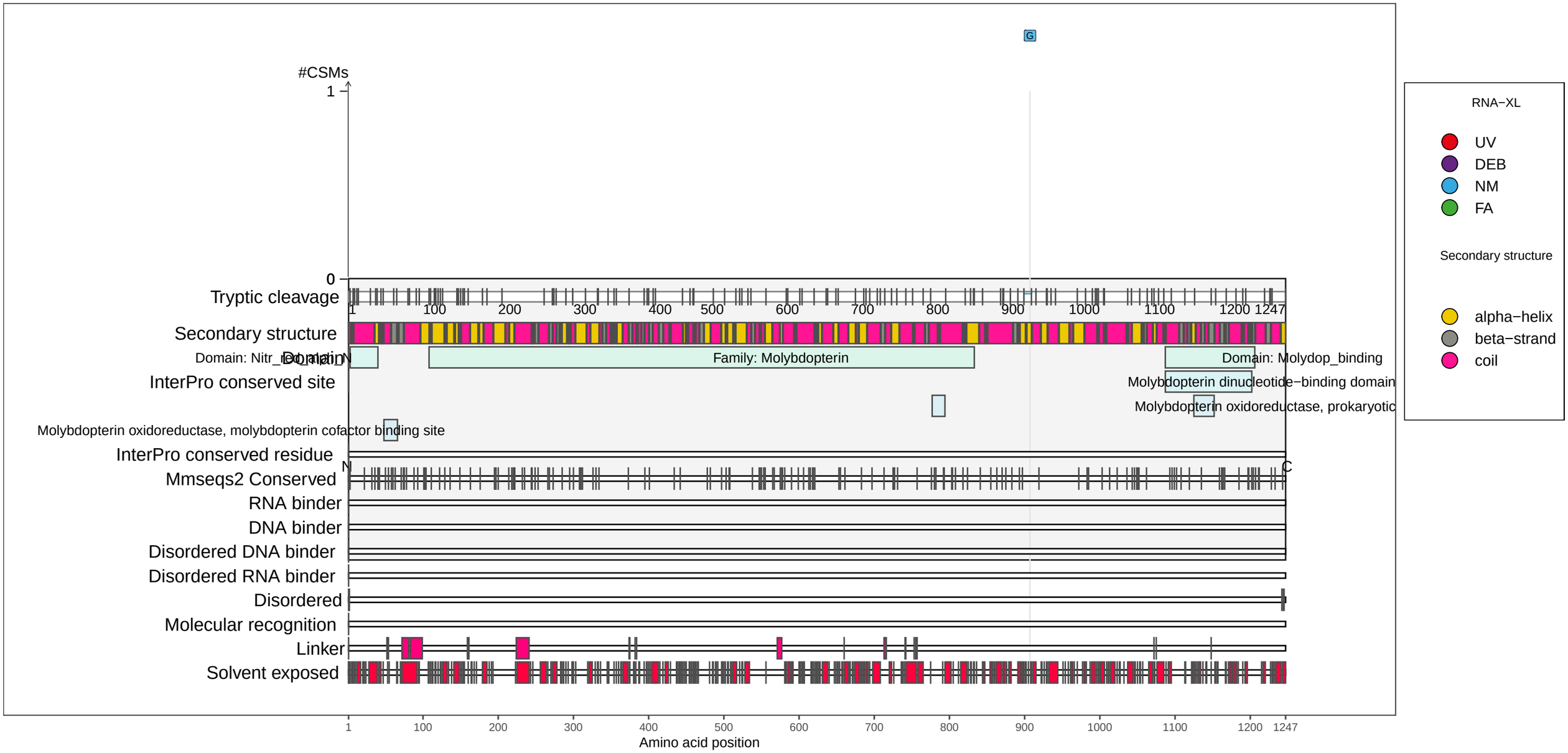
− RNA functions: not annotated



P09152
NARG_ECOLI Respiratory nitrate reductase 1 alpha chain

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.96 (Q 9)
PAXdb E.coli [ppm]: 1.46 (Q 59)

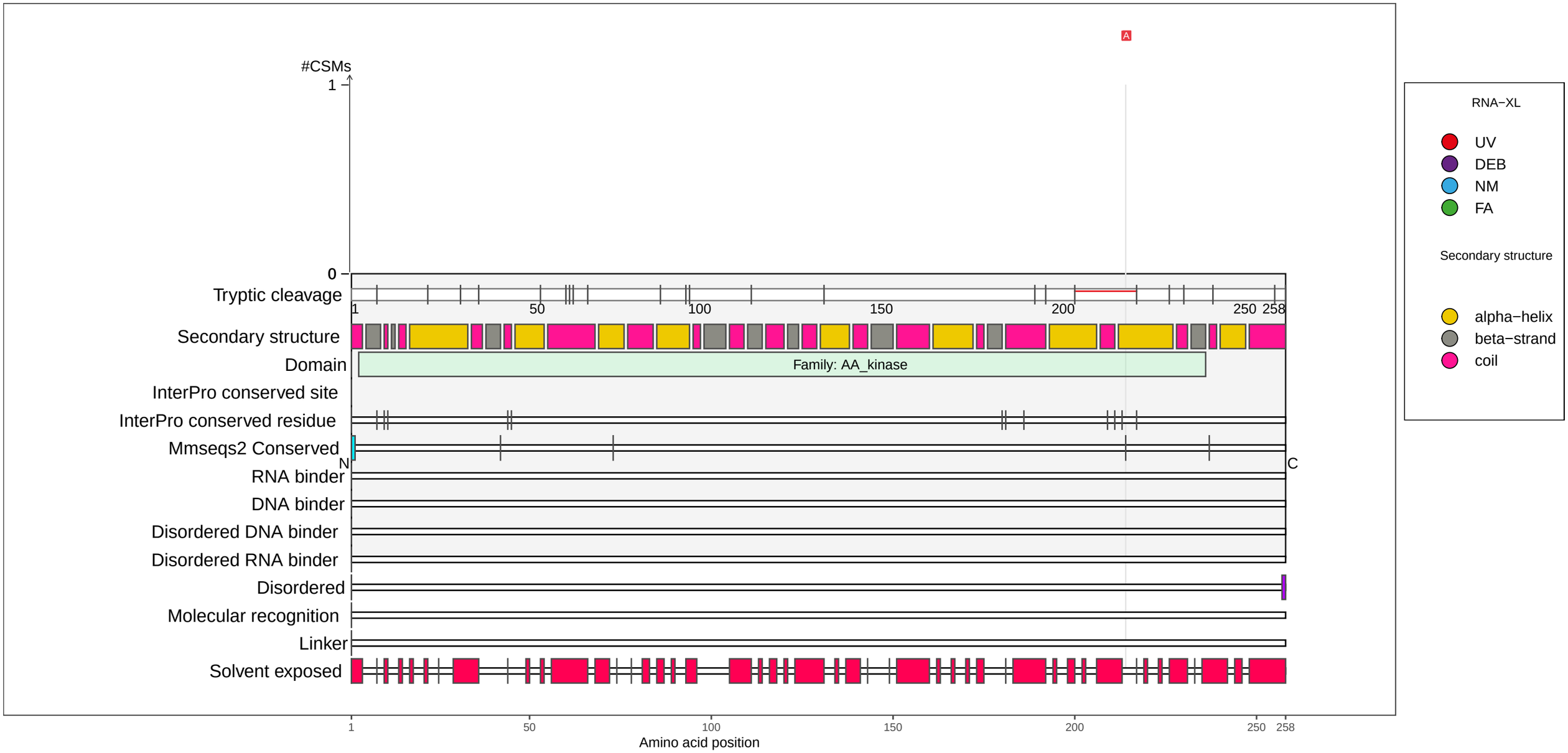
− RNA functions: not annotated



P0A6C8
ARGB_ECOLI Acetylglutamate kinase

− Abundance:
tryptic [log10 Intensity]: 8.78 (Q 83)
PAXdb K12 strain [ppm]: 2.83 (Q 87)
PAXdb E.coli [ppm]: 2.26 (Q 79)

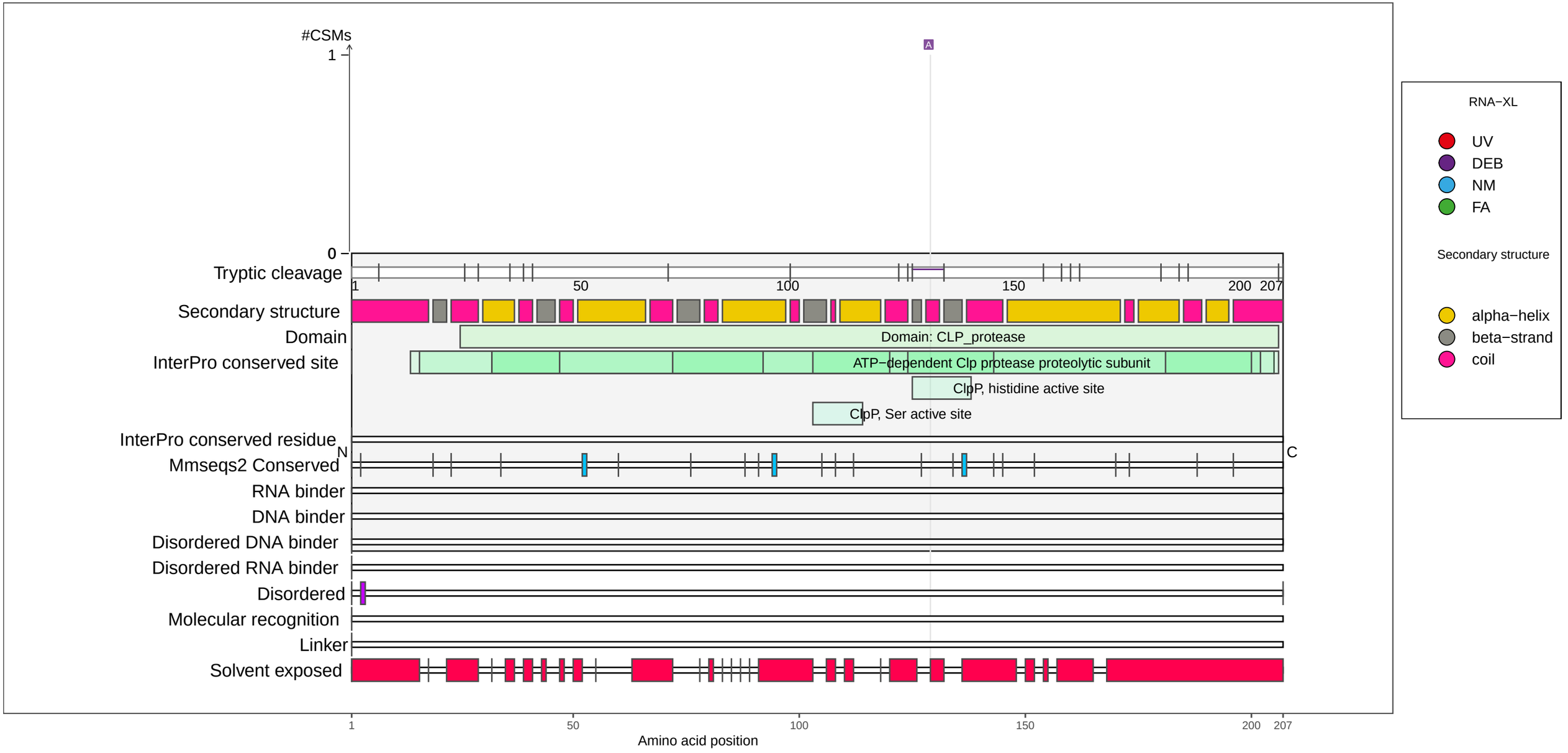
− RNA functions: not annotated



P0A6G7
CLPP_ECOLI ATP−dependent Clp protease proteolytic subunit

− Abundance:
tryptic [log10 Intensity]: 8.94 (Q 87)
PAXdb K12 strain [ppm]: 2.79 (Q 86)
PAXdb E.coli [ppm]: 3.17 (Q 96)

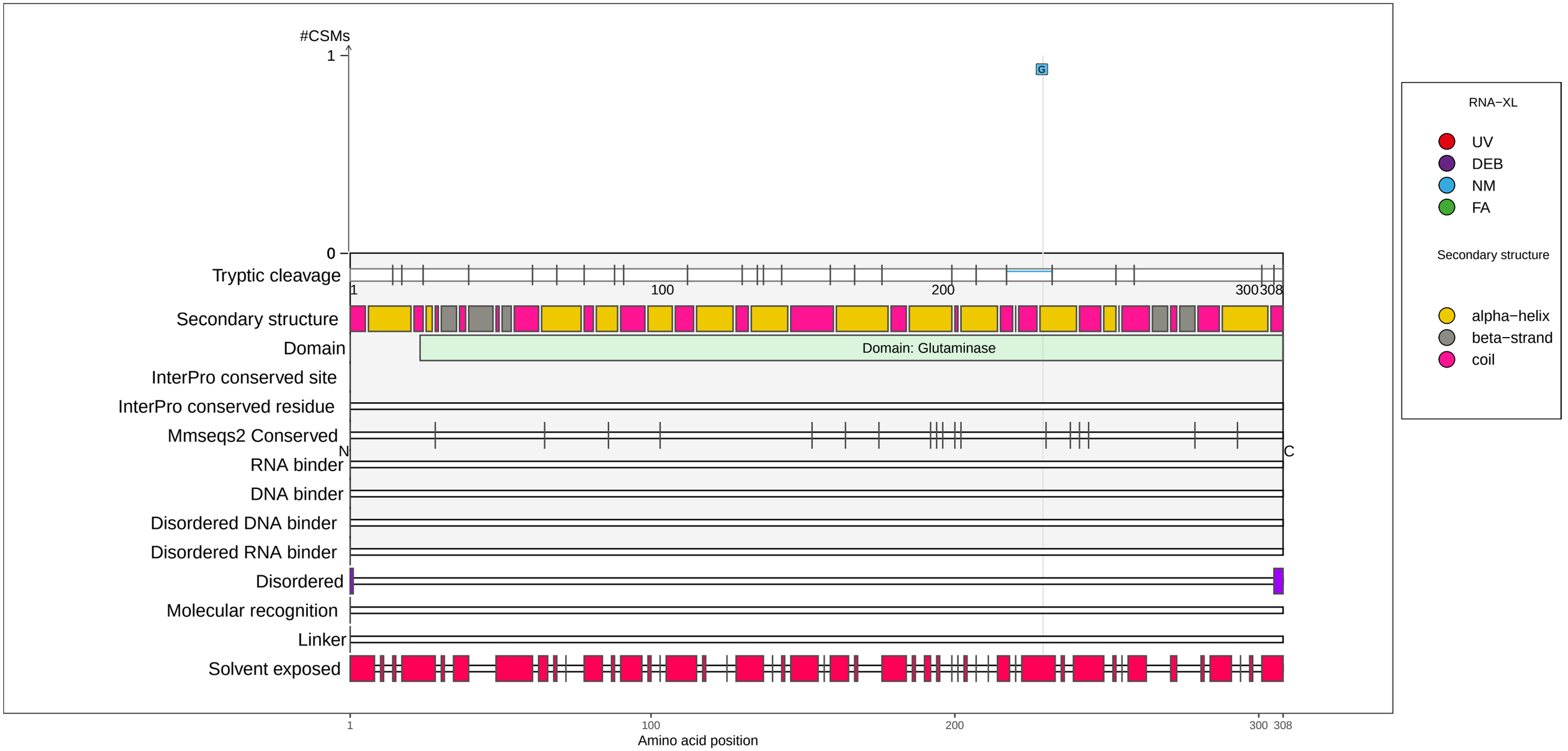
− RNA functions: not annotated



P0A6W0
GLSA2_ECOLI Glutaminase 2

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: 1.69 (Q 49)
PAXdb E.coli [ppm]: 0.29 (Q 31)

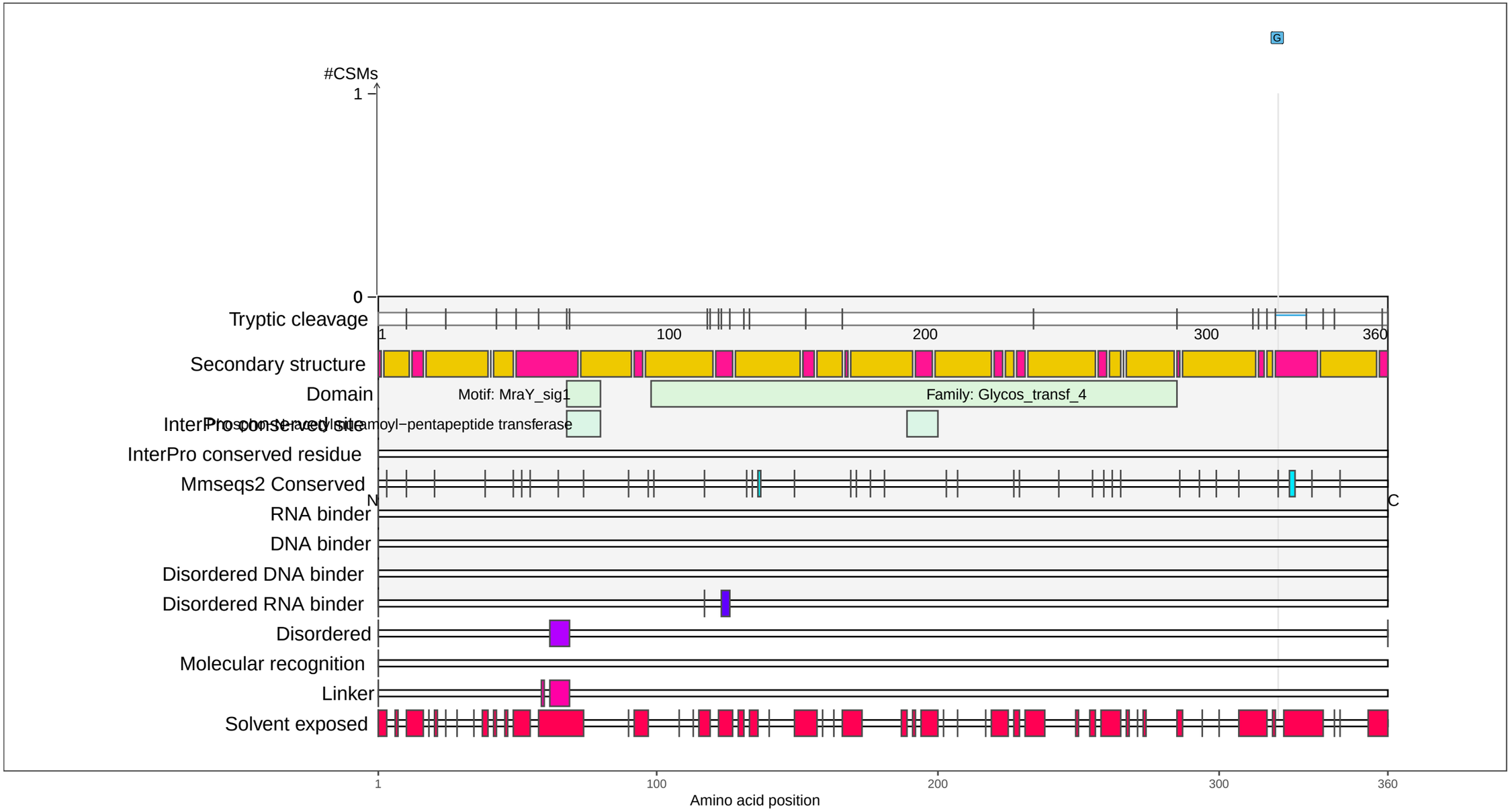
− RNA functions: not annotated



P0A6W3
MRAY_ECOLI Phospho−N−acetylmuramoyl−pentapeptide−transferase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.87 (Q 45)

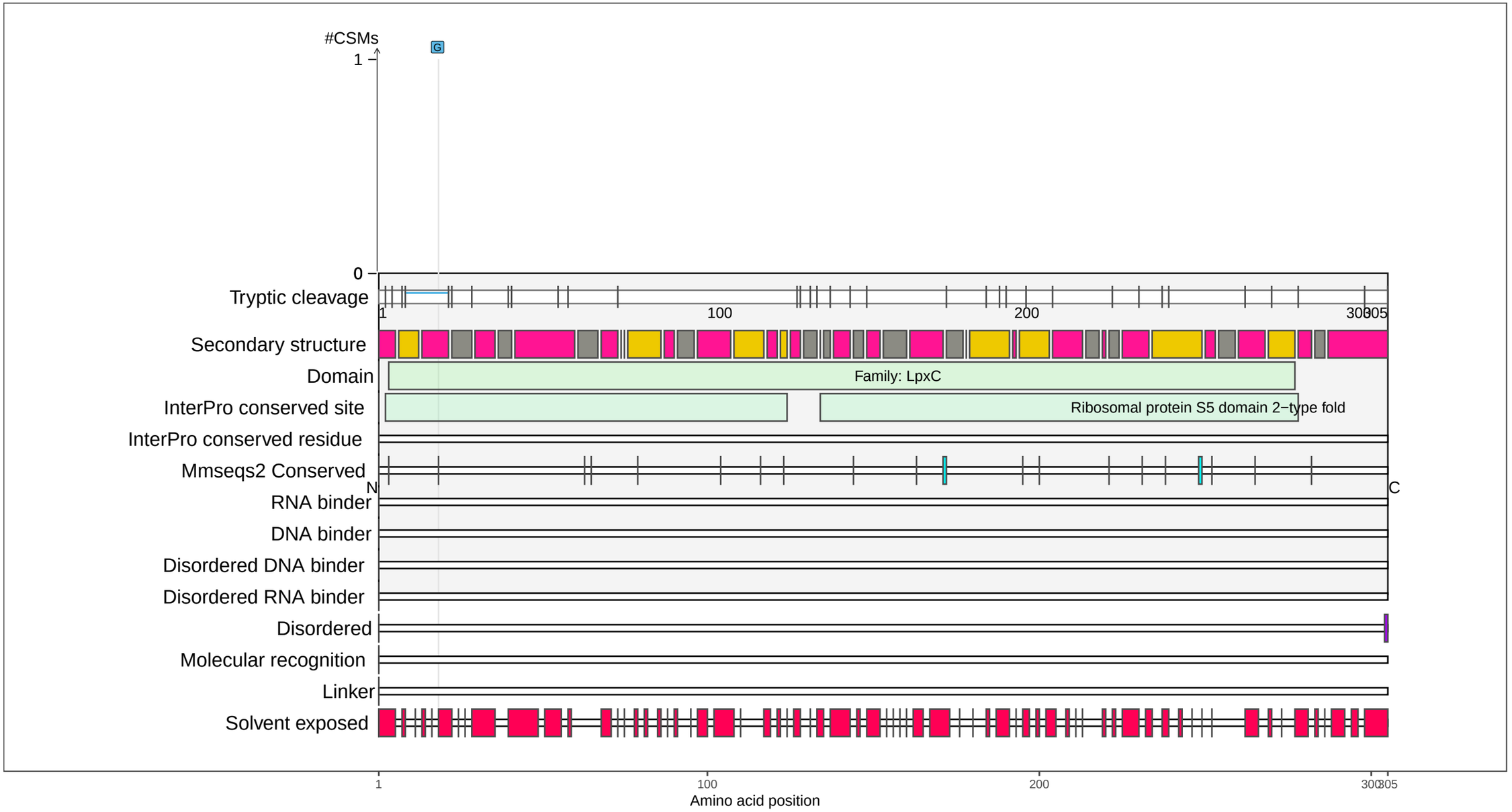
− RNA functions: not annotated



P0A725
LPXC_ECOLI UDP−3−O−acyl−N−acetylglucosamine deacetylase

− Abundance:
tryptic [log10 Intensity]: 7.4 (Q 30)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.55 (Q 61)

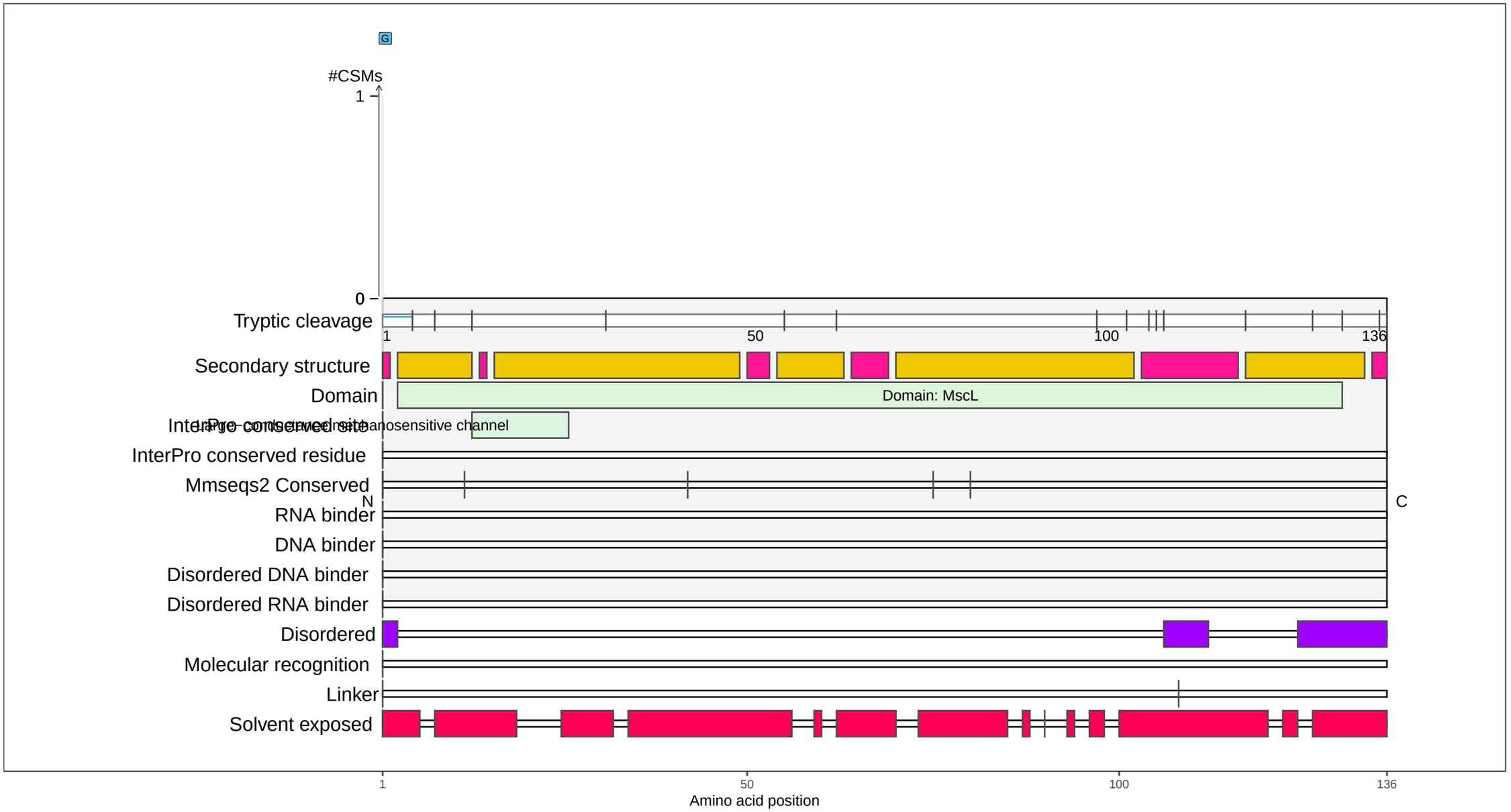
− RNA functions: not annotated

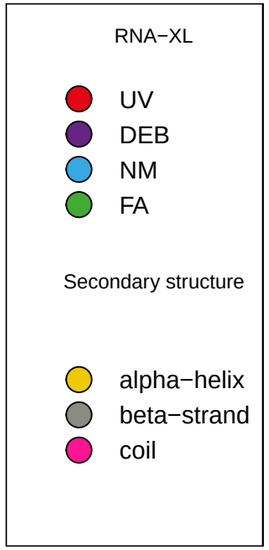


P0A742
MSCL_ECOLI Large−conductance mechanosensitive channel

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 61)
PAXdb K12 strain [ppm]: 1.87 (Q 56)
PAXdb E.coli [ppm]: 2.23 (Q 78)

− RNA functions: not annotated

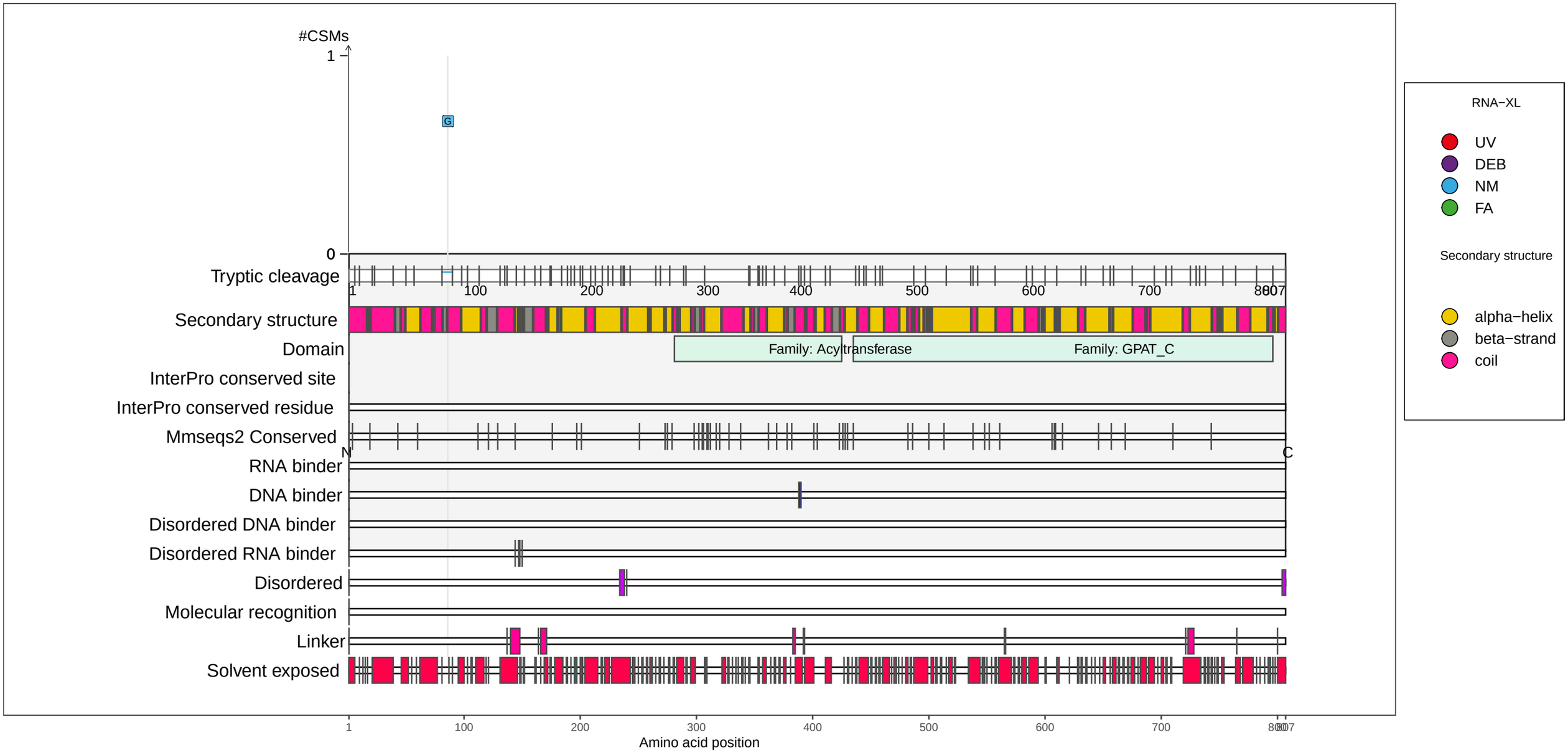




P0A7A7
PLSB_ECOLI Glycerol−3−phosphate acyltransferase

− Abundance:
tryptic [log10 Intensity]: 6.89 (Q 9)
PAXdb K12 strain [ppm]: 0.93 (Q 8)
PAXdb E.coli [ppm]: 2.3 (Q 80)

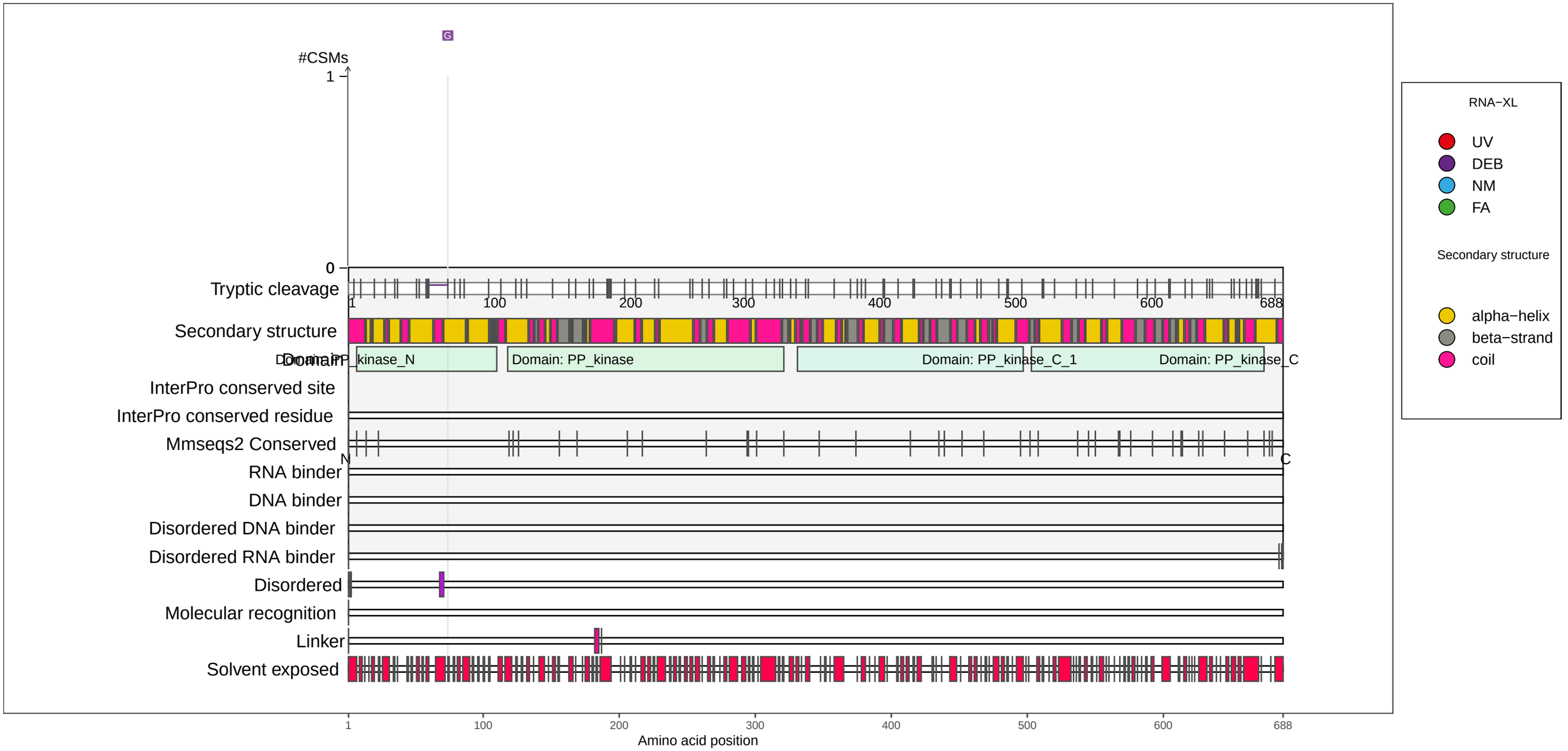
− RNA functions: not annotated



P0A7B1
PPK1_ECOLI Polyphosphate kinase

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 56)
PAXdb K12 strain [ppm]: 2.17 (Q 66)
PAXdb E.coli [ppm]: 1.98 (Q 72)

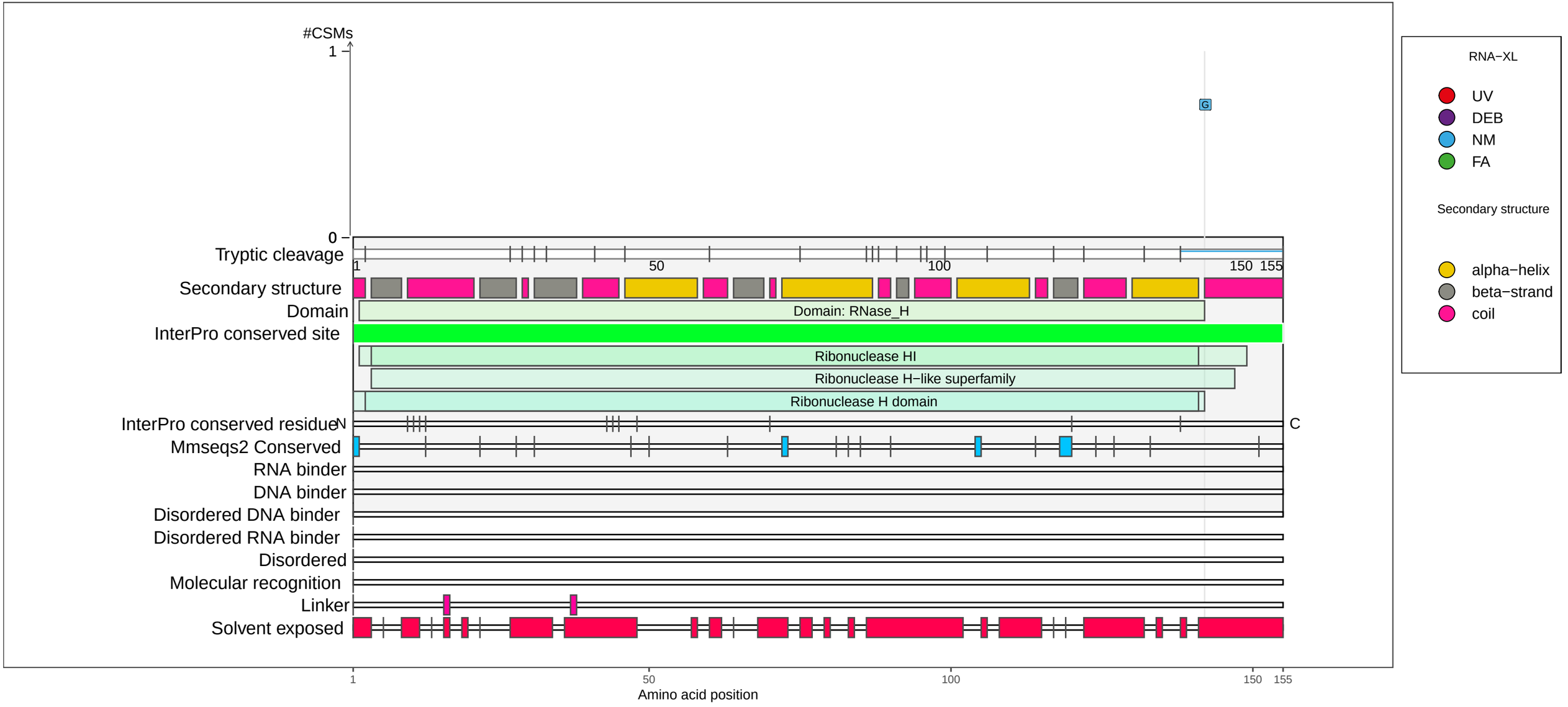
− RNA functions: not annotated



P0A7Y4
RNH_ECOLI Ribonuclease HI

− Abundance:
tryptic [log10 Intensity]: 7.73 (Q 46)
PAXdb K12 strain [ppm]: 1.33 (Q 28)
PAXdb E.coli [ppm]: 0.66 (Q 40)

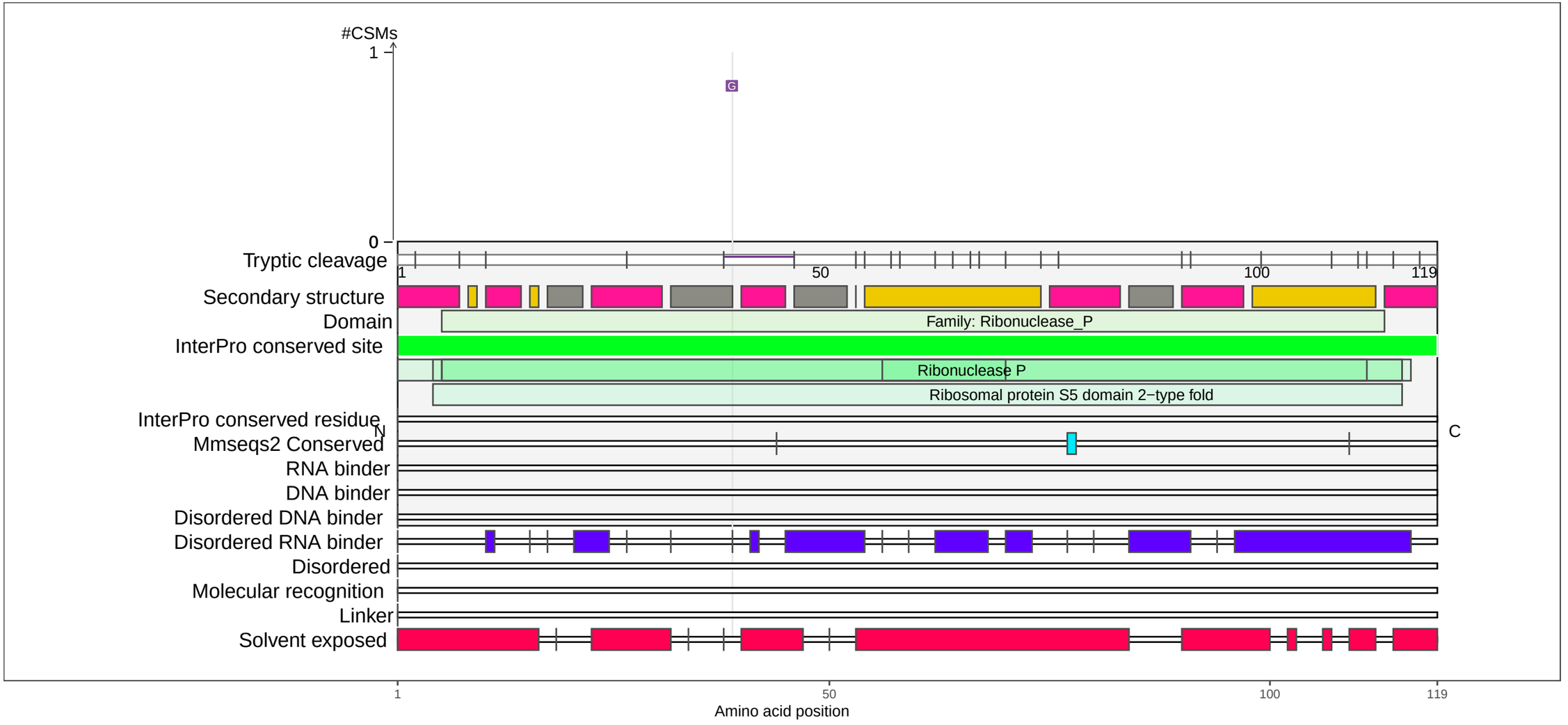
− RNA functions:
DNA replication, removal of RNA primer; RNA catabolic process; RNA metabolic process
RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic; RNA−DNA hybrid ribonuclease activity

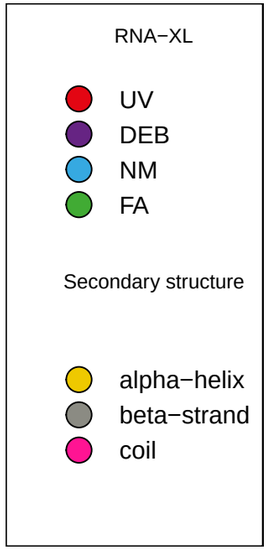


P0A7Y8
RNPA_ECOLI Ribonuclease P protein component

− Abundance:
tryptic [log10 Intensity]: 7.26 (Q 23)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.92 (Q 70)

− RNA functions:
3−tRNA processing endoribonuclease activity; ncRNA 3−end processing
ncRNA 5−end processing; ncRNA metabolic process; ncRNA processing; RNA 3−end processing
RNA 5−end processing; RNA binding; RNA metabolic process; RNA phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis, endonucleolytic; RNA processing; tRNA 3−end processing
tRNA 3−trailer cleavage; tRNA 3−trailer cleavage, endonucleolytic
tRNA 5−end processing; tRNA 5−leader removal; tRNA binding; tRNA metabolic process; tRNA processing
tRNA−specific ribonuclease activity

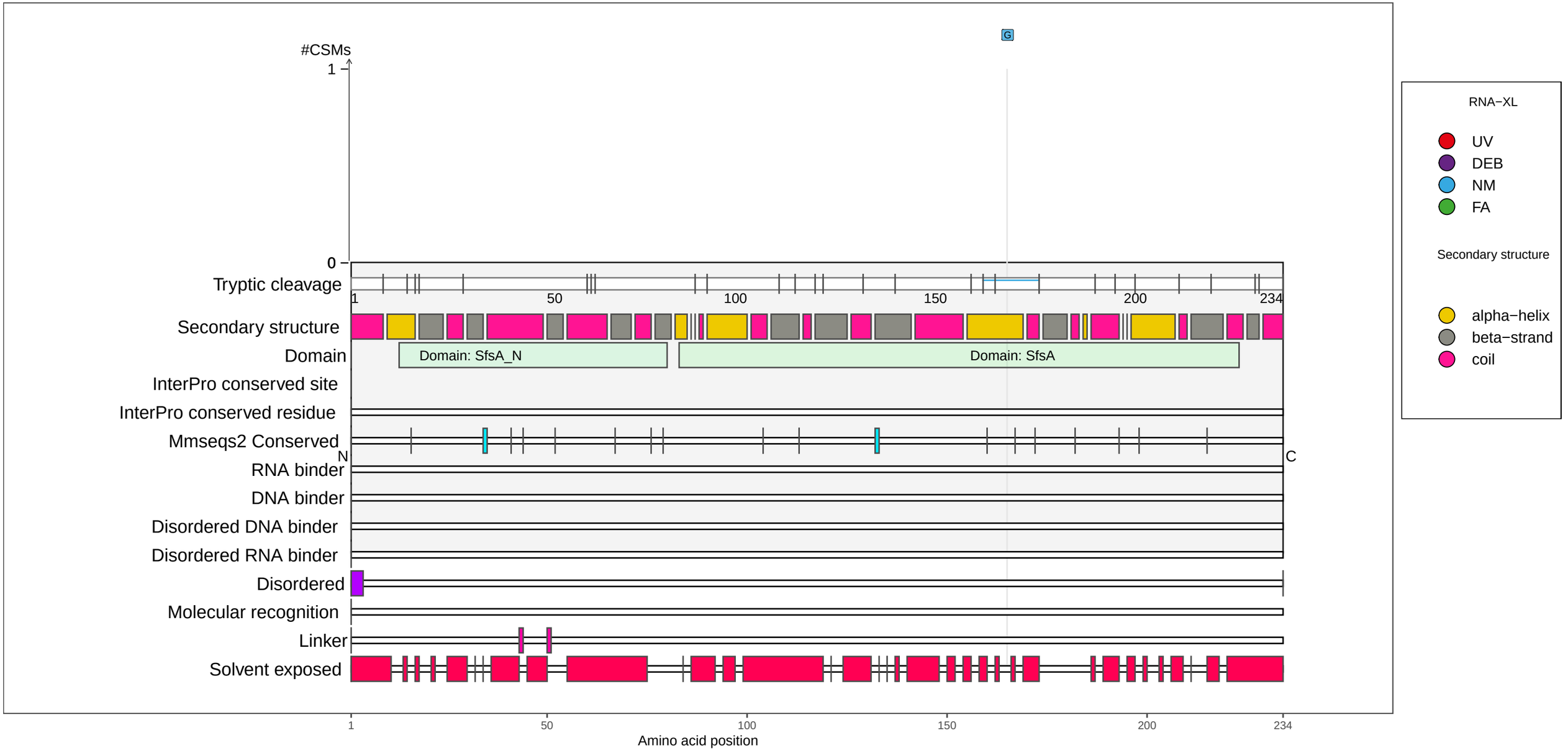




P0A823
SFSA_ECOLI Sugar fermentation stimulation protein A

− Abundance:
tryptic [log10 Intensity]: 7.54 (Q 37)
PAXdb K12 strain [ppm]: 1.41 (Q 33)
PAXdb E.coli [ppm]: 0.31 (Q 32)

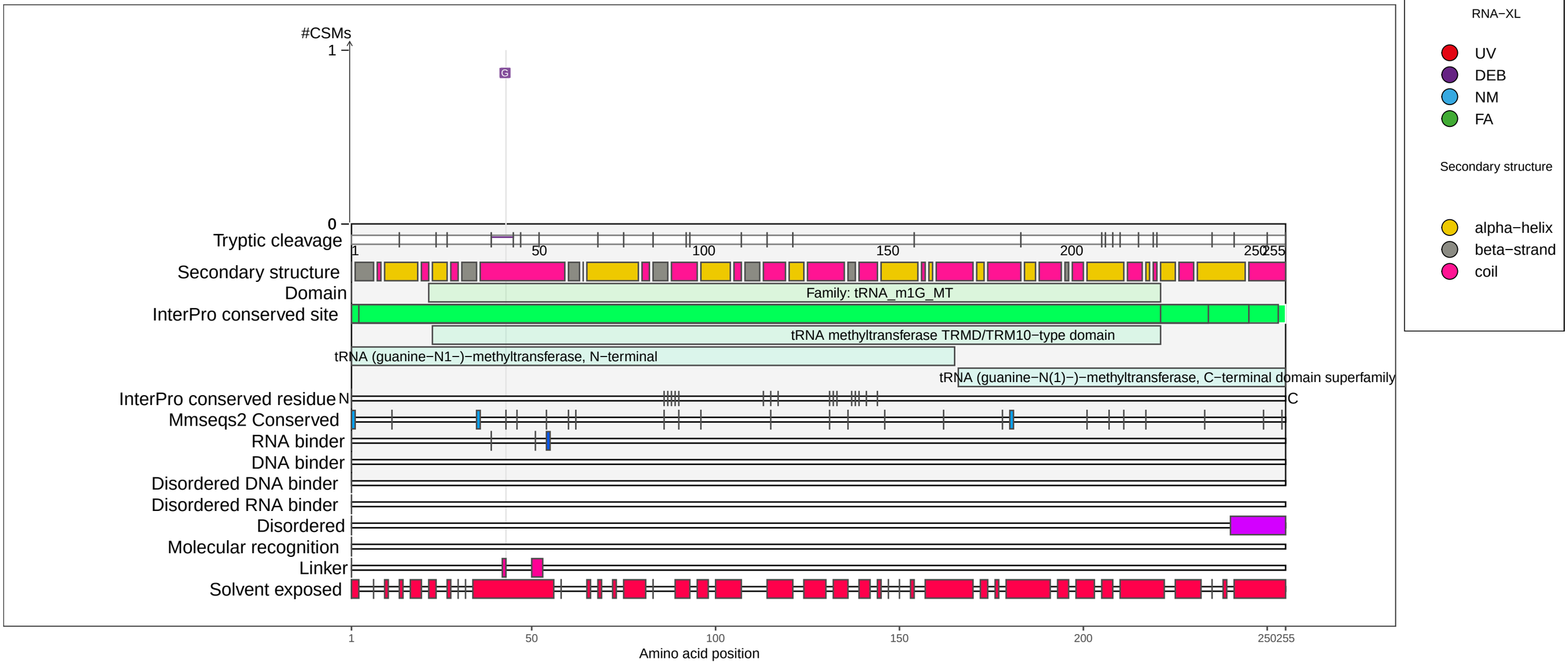
− RNA functions: not annotated



P0A873
TRMD_ECOLI tRNA (guanine−N(1)−)−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.77 (Q 48)
PAXdb K12 strain [ppm]: 1.81 (Q 54)
PAXdb E.coli [ppm]: 1.21 (Q 52)

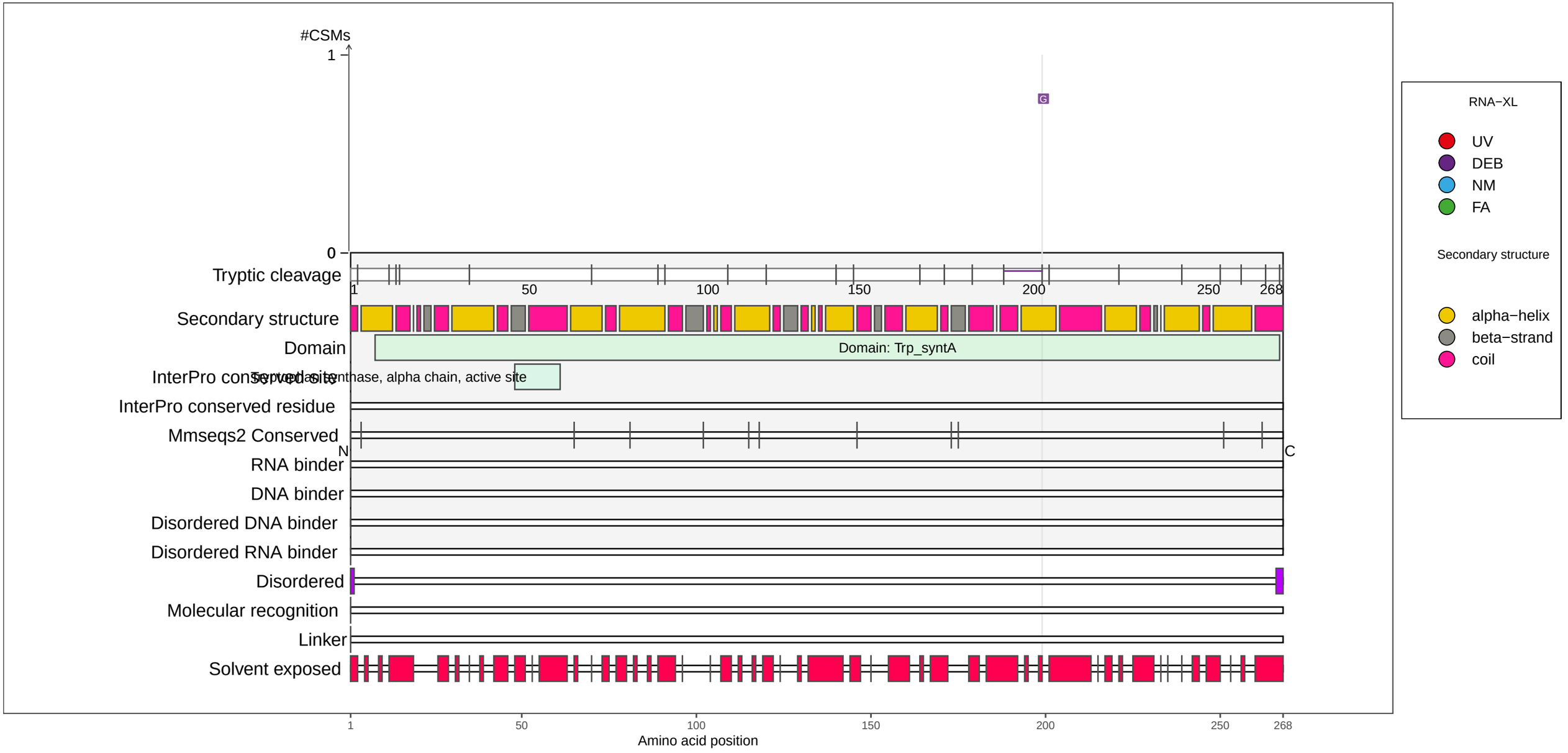
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA methylation
RNA methyltransferase activity; RNA modification; RNA processing
tRNA (Guanine−1)−methyltransferase; tRNA (guanine−N1−)−methyltransferase activity
tRNA (guanine(37)−N(1))−methyltransferase activity; tRNA (guanine) methyltransferase activity
tRNA metabolic process; tRNA methylation; tRNA methyltransferase activity; tRNA modification
tRNA N1−guanine methylation; tRNA processing



P0A877
TRPA_ECOLI Tryptophan synthase alpha chain

− Abundance:
tryptic [log10 Intensity]: 7.22 (Q 22)
PAXdb K12 strain [ppm]: 2.19 (Q 66)
PAXdb E.coli [ppm]: 2.82 (Q 92)

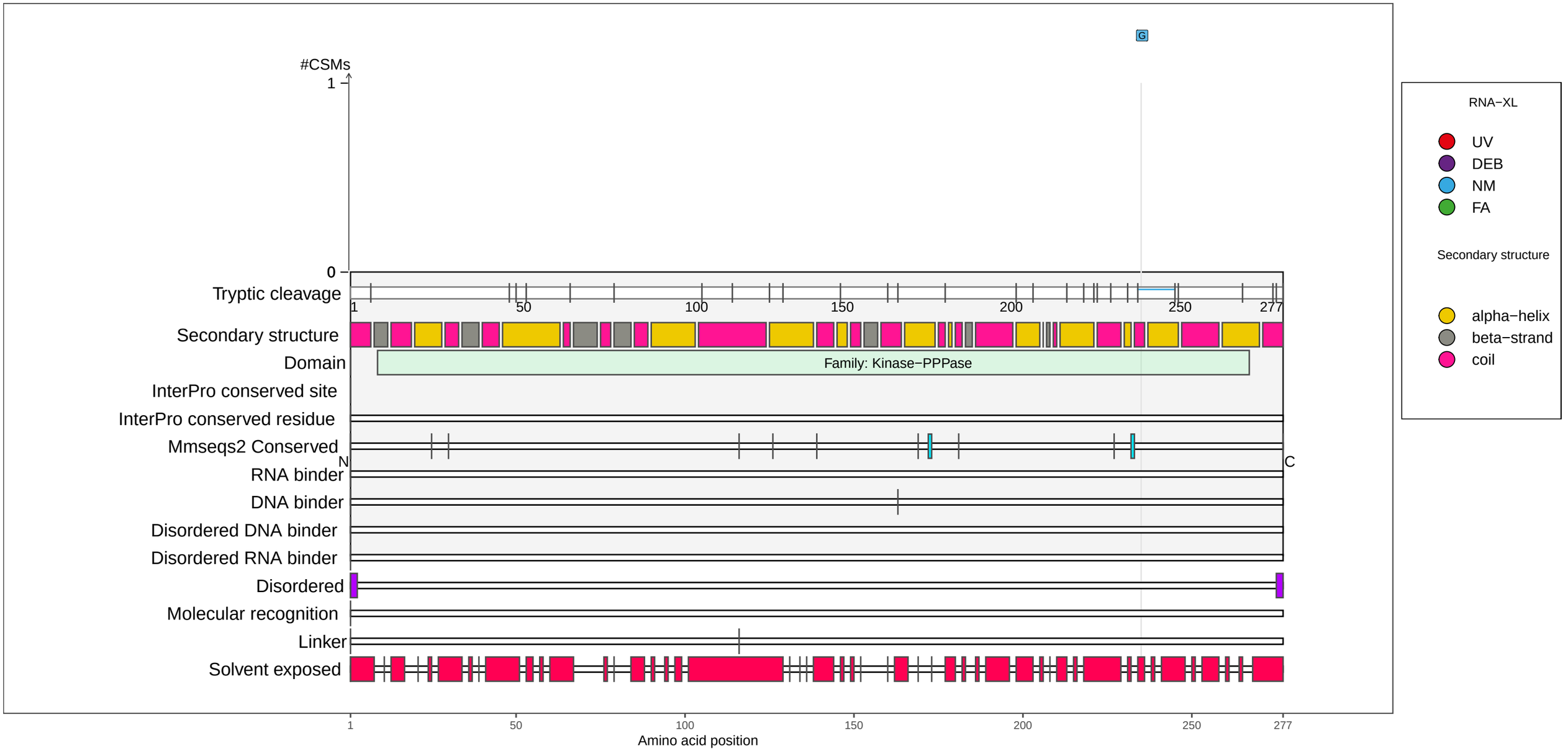
− RNA functions: not annotated



P0A8A4
PSRP_ECOLI Phosphoenolpyruvate synthase regulatory protein

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.98 (Q 72)

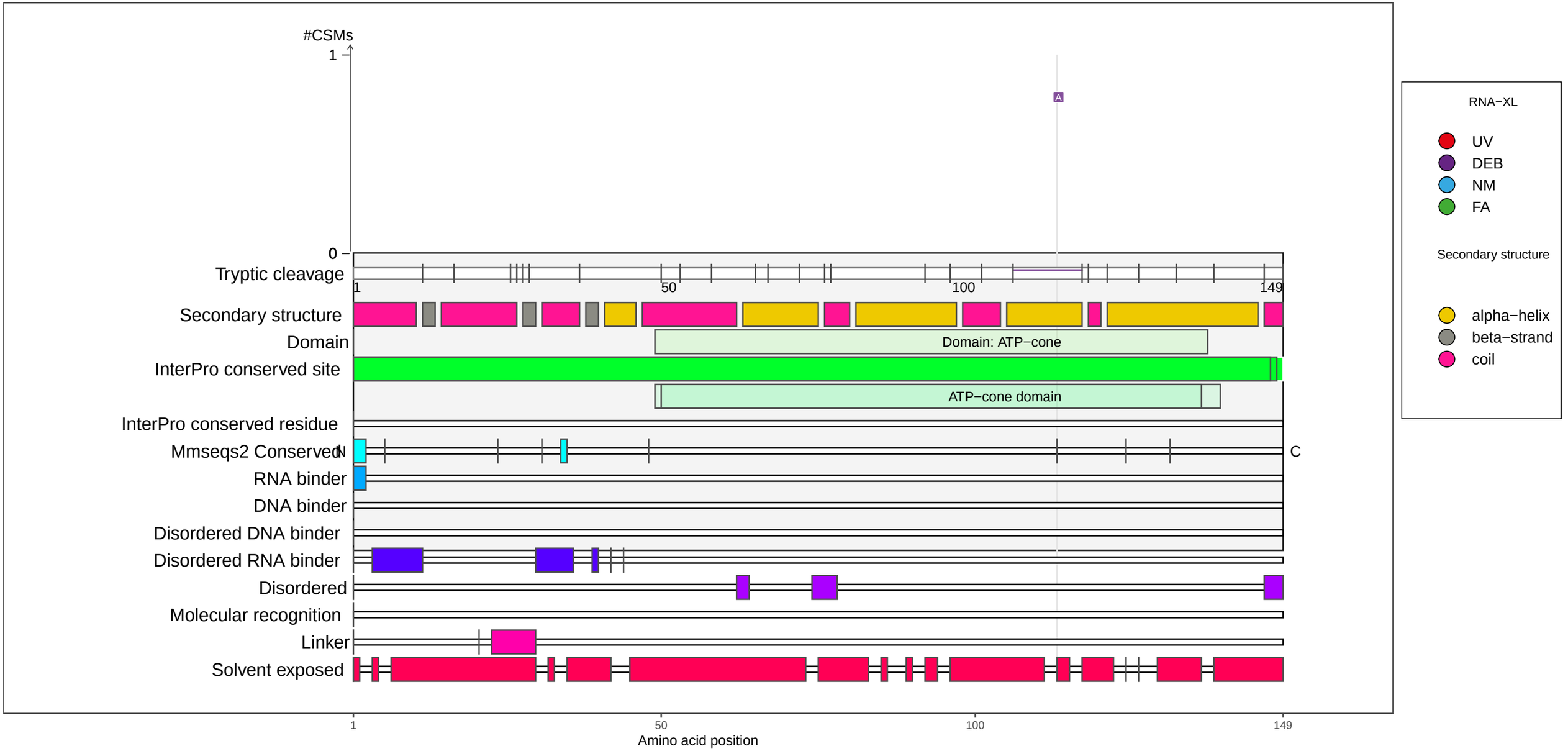
− RNA functions: not annotated



P0A8D0
NRDR_ECOLI Transcriptional repressor NrdR

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: 2.5 (Q 77)
PAXdb E.coli [ppm]: 2.01 (Q 72)

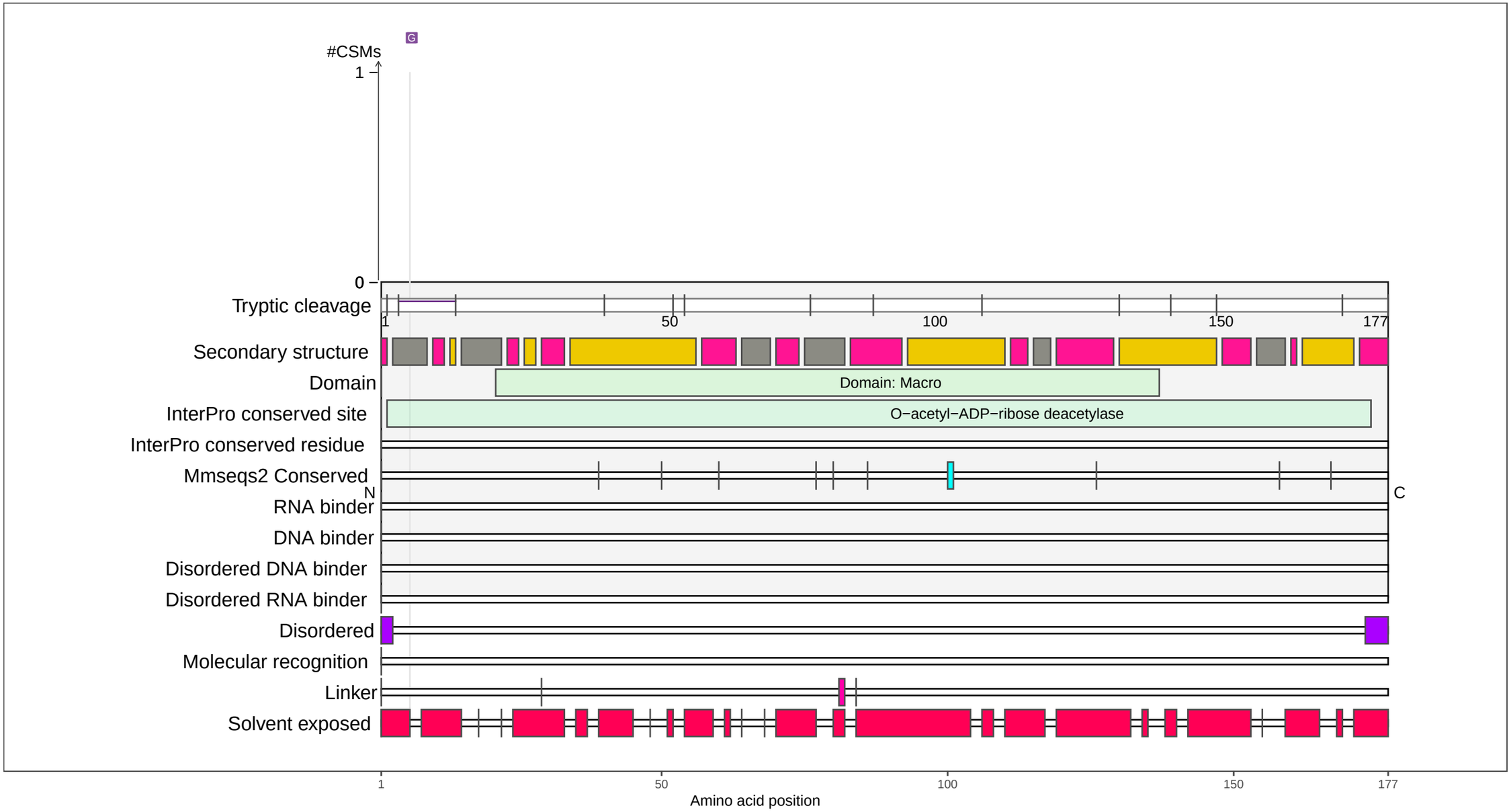
− RNA functions: not annotated



P0A8D6
YMDB_ECOLI O−acetyl−ADP−ribose deacetylase

− Abundance:
tryptic [log10 Intensity]: 6.87 (Q 9)
PAXdb K12 strain [ppm]: 1.85 (Q 55)
PAXdb E.coli [ppm]: 2.18 (Q 77)

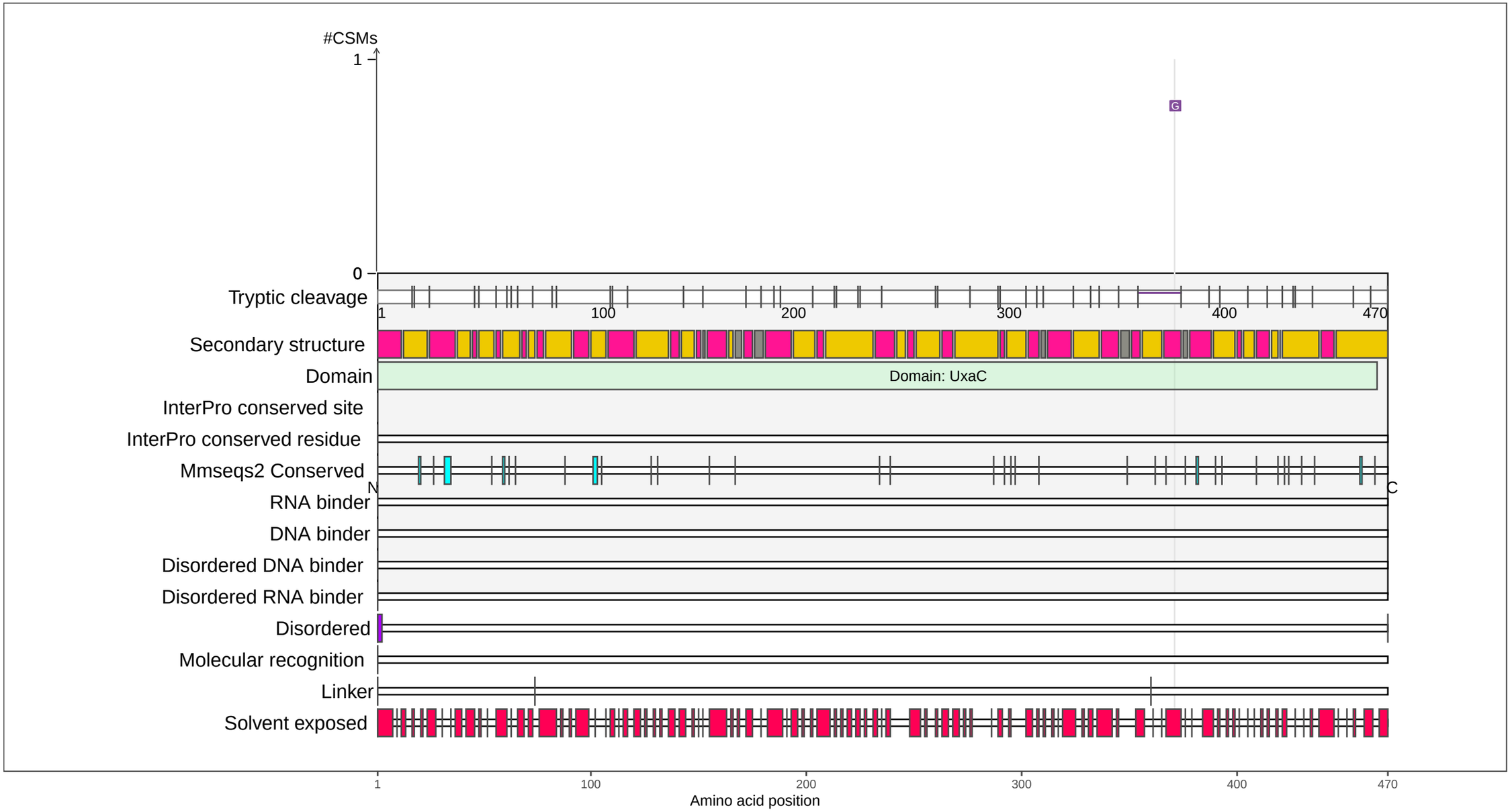
− RNA functions: not annotated

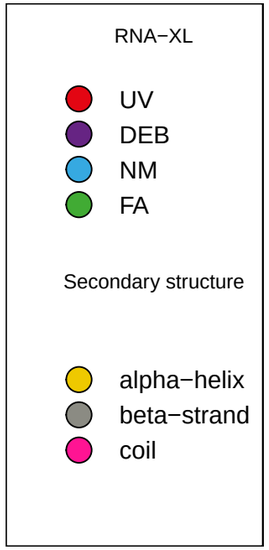


P0A8G3
UXAC_ECOLI Uronate isomerase

− Abundance:
tryptic [log10 Intensity]: 8.21 (Q 66)
PAXdb K12 strain [ppm]: 1.71 (Q 49)
PAXdb E.coli [ppm]: 2.11 (Q 75)

− RNA functions: not annotated

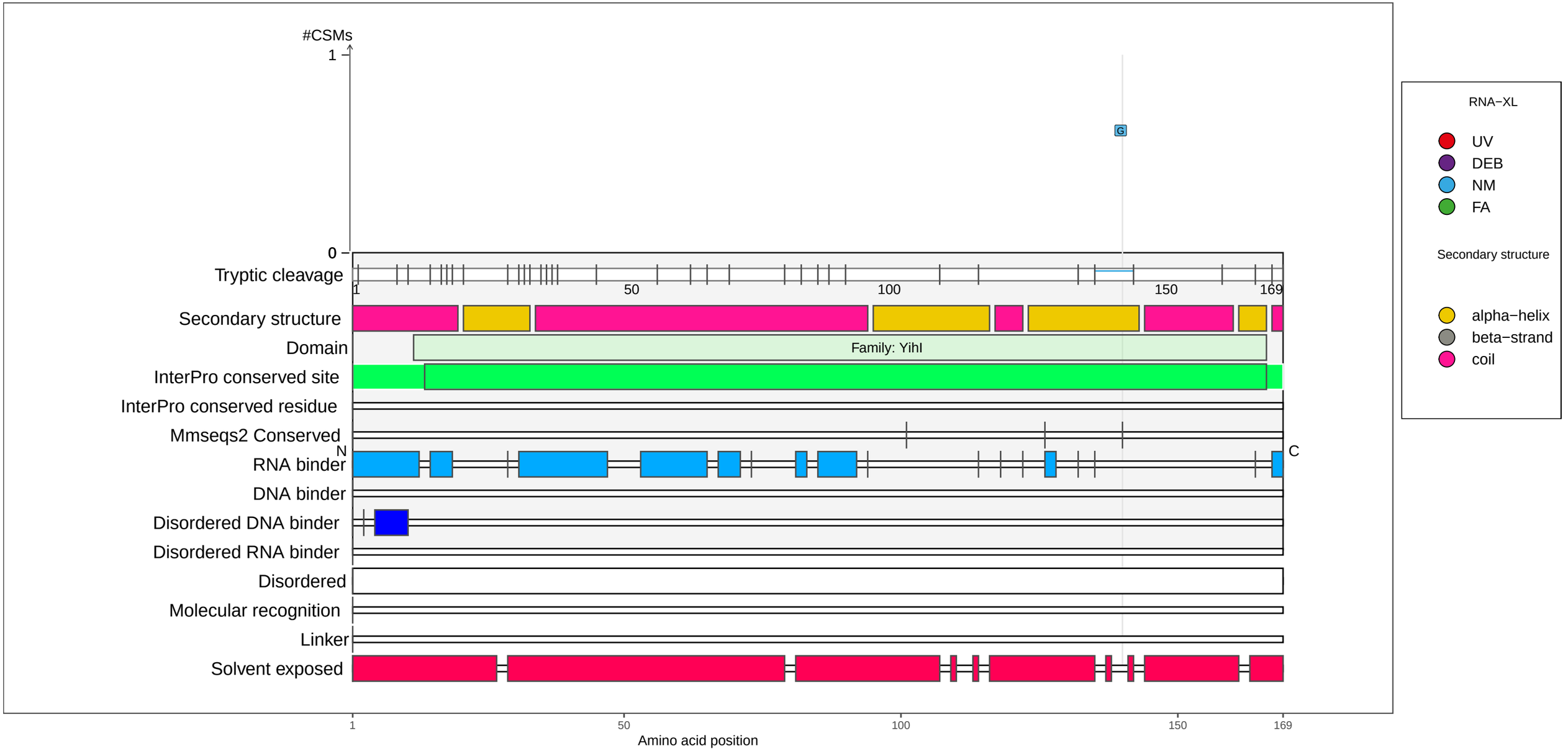




P0A8H6
YIHI_ECOLI Der GTPase−activating protein YihI

− Abundance:
tryptic [log10 Intensity]: 7.98 (Q 57)
PAXdb K12 strain [ppm]: 2.29 (Q 70)
PAXdb E.coli [ppm]: 2.58 (Q 88)

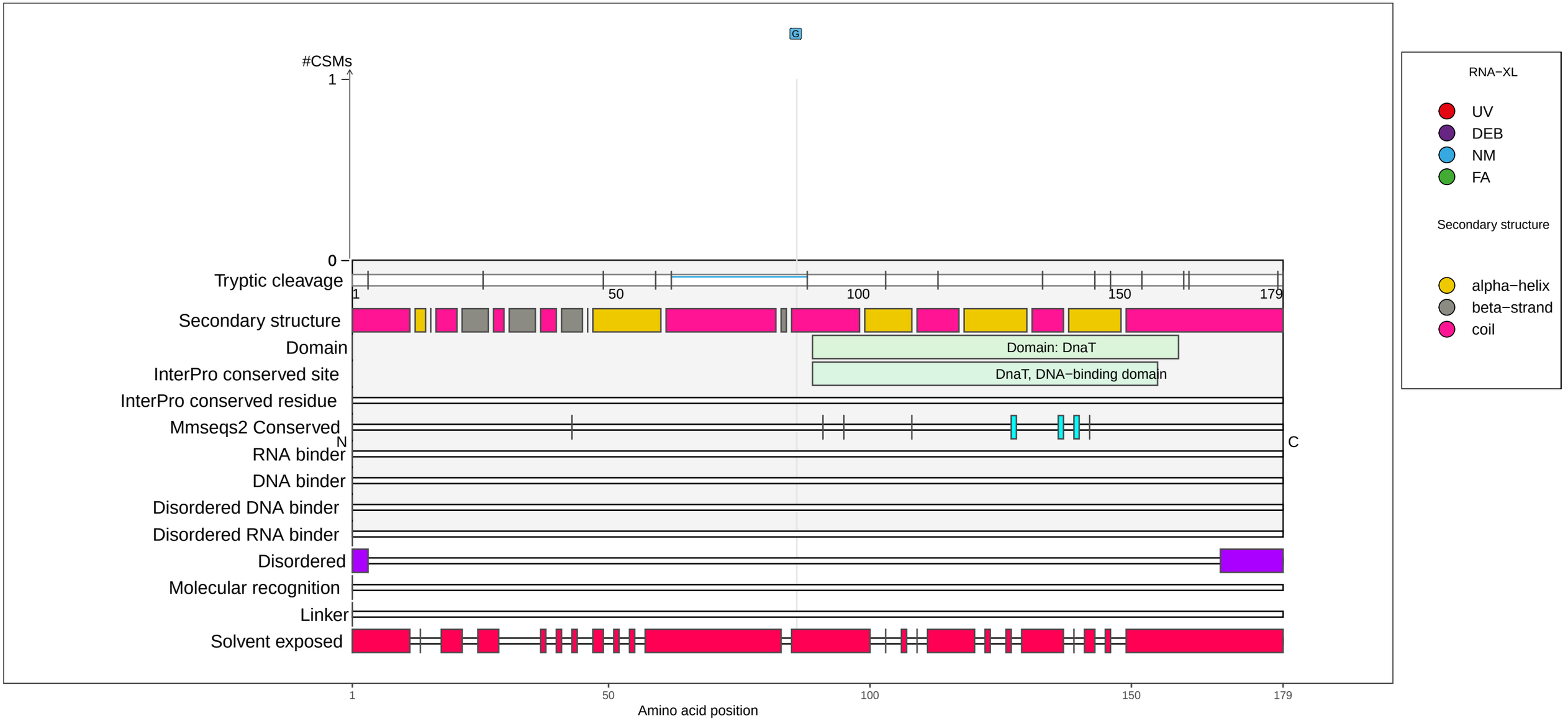
− RNA functions: not annotated



P0A8J2
DNAT_ECOLI Primosomal protein 1

− Abundance:
tryptic [log10 Intensity]: 7.47 (Q 33)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.56 (Q 61)

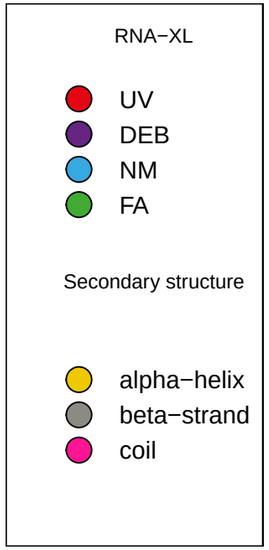
− RNA functions:
DNA replication, synthesis of RNA primer; RNA biosynthetic process
RNA metabolic process



P0A8L7
YCIU_ECOLI UPF0263 protein YciU

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.66 (Q 63)

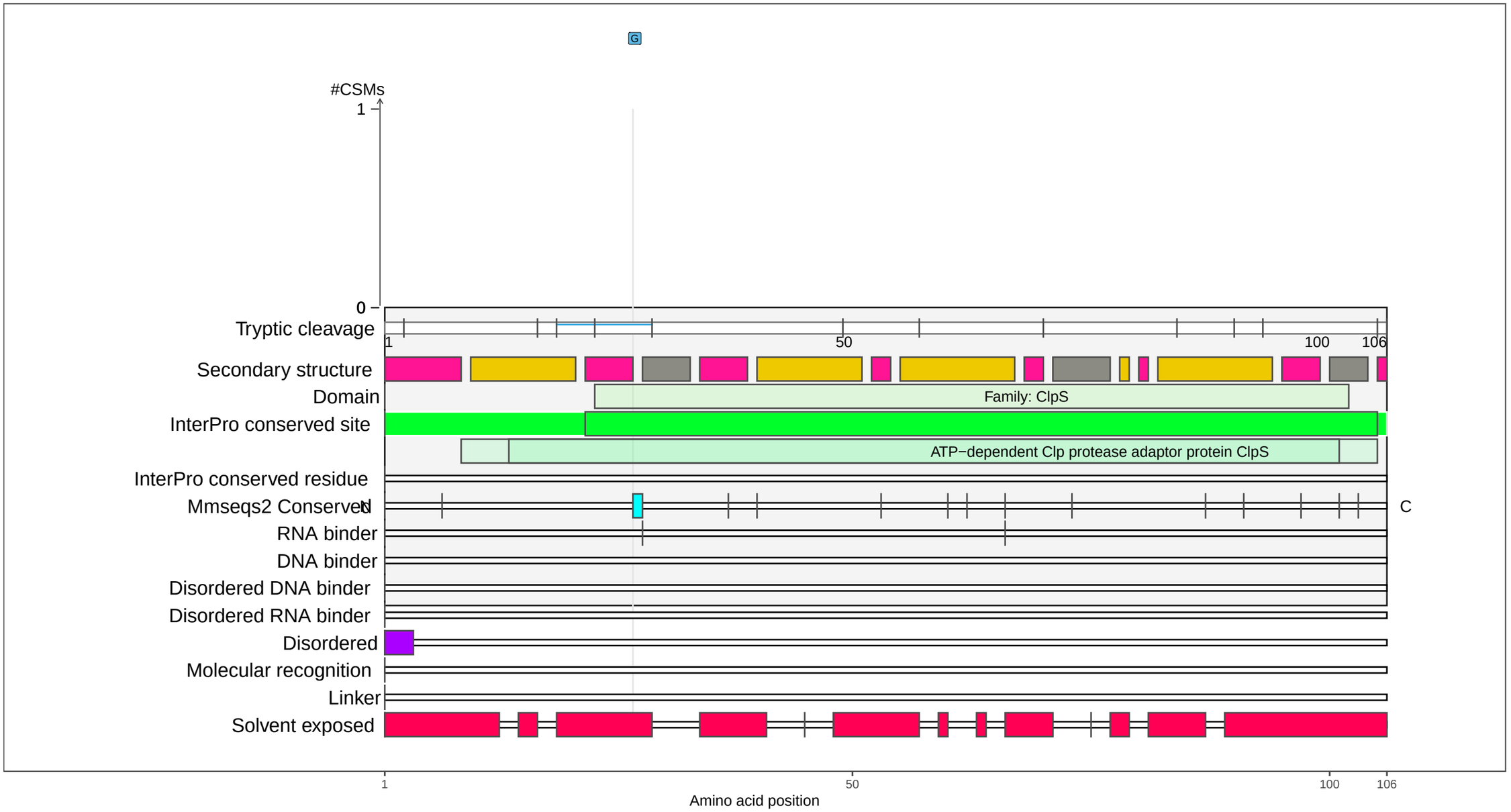
− RNA functions: not annotated



P0A8Q6
CLPS_ECOLI ATP−dependent Clp protease adapter protein ClpS

− Abundance:
tryptic [log10 Intensity]: 7.44 (Q 32)
PAXdb K12 strain [ppm]: 1.46 (Q 36)
PAXdb E.coli [ppm]: 0.9 (Q 45)

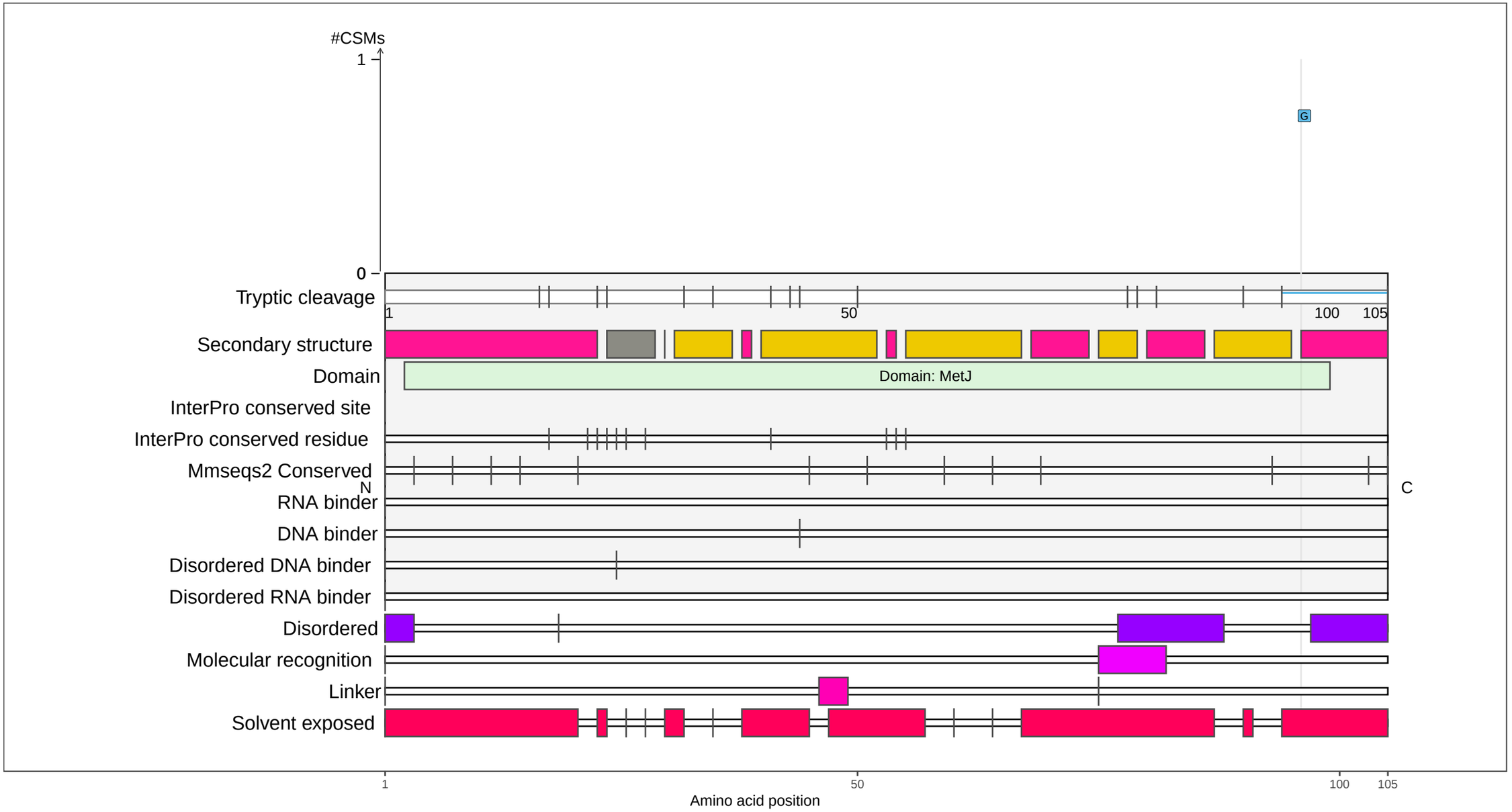
− RNA functions: not annotated



P0A8U6
METJ_ECOLI Met repressor

− Abundance:
tryptic [log10 Intensity]: 7.89 (Q 53)
PAXdb K12 strain [ppm]: 3.24 (Q 94)
PAXdb E.coli [ppm]: 2.86 (Q 93)

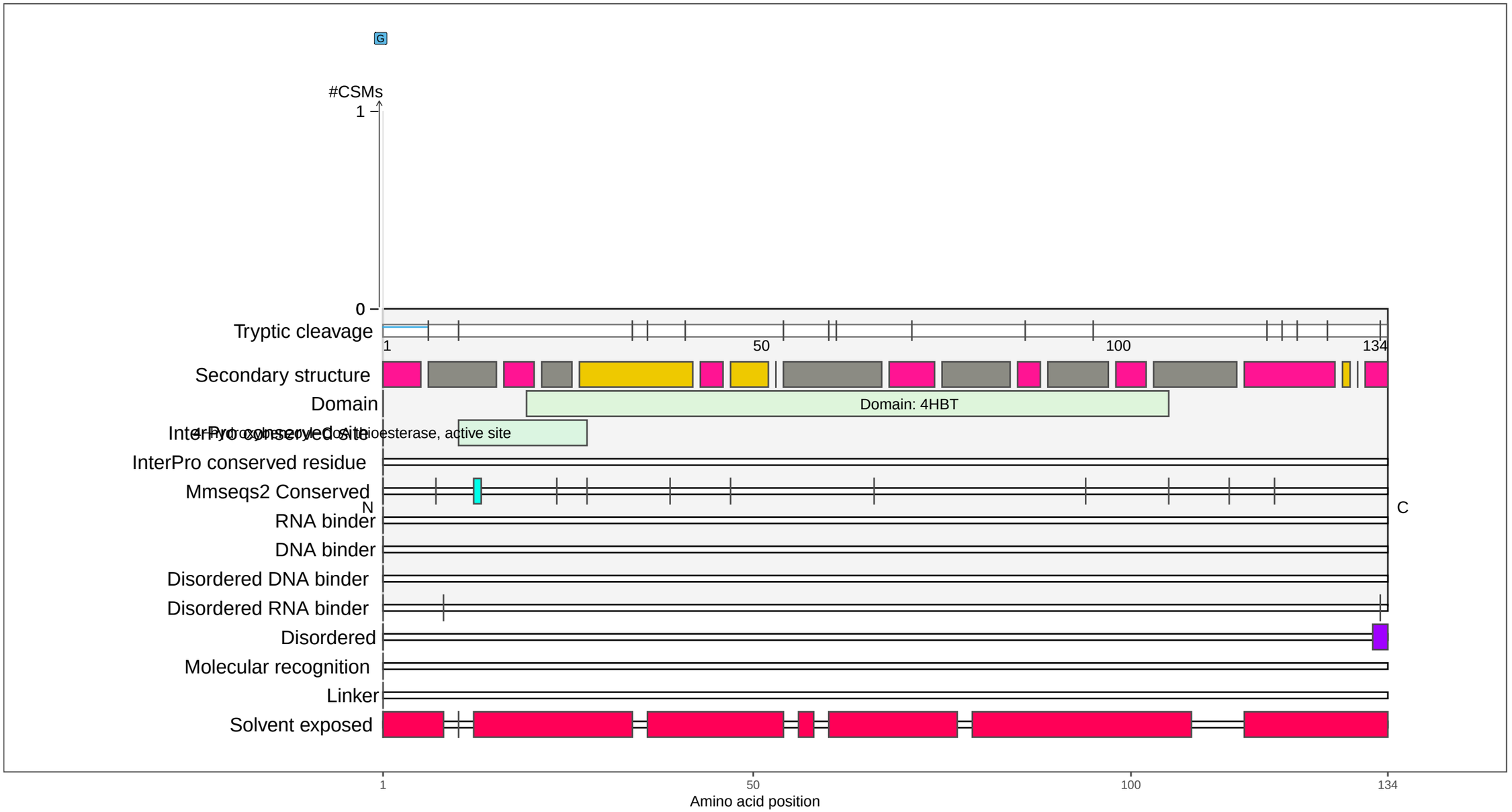
− RNA functions: not annotated

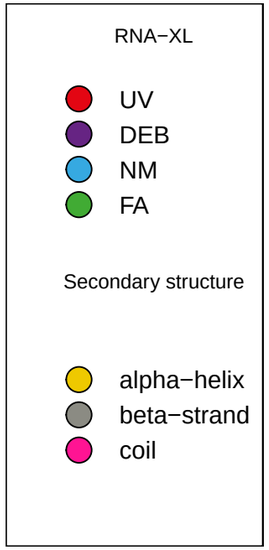


P0A8Z3
YBGC_ECOLI Acyl−CoA thioester hydrolase YbgC

− Abundance:
tryptic [log10 Intensity]: 7.56 (Q 38)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.93 (Q 70)

− RNA functions: not annotated

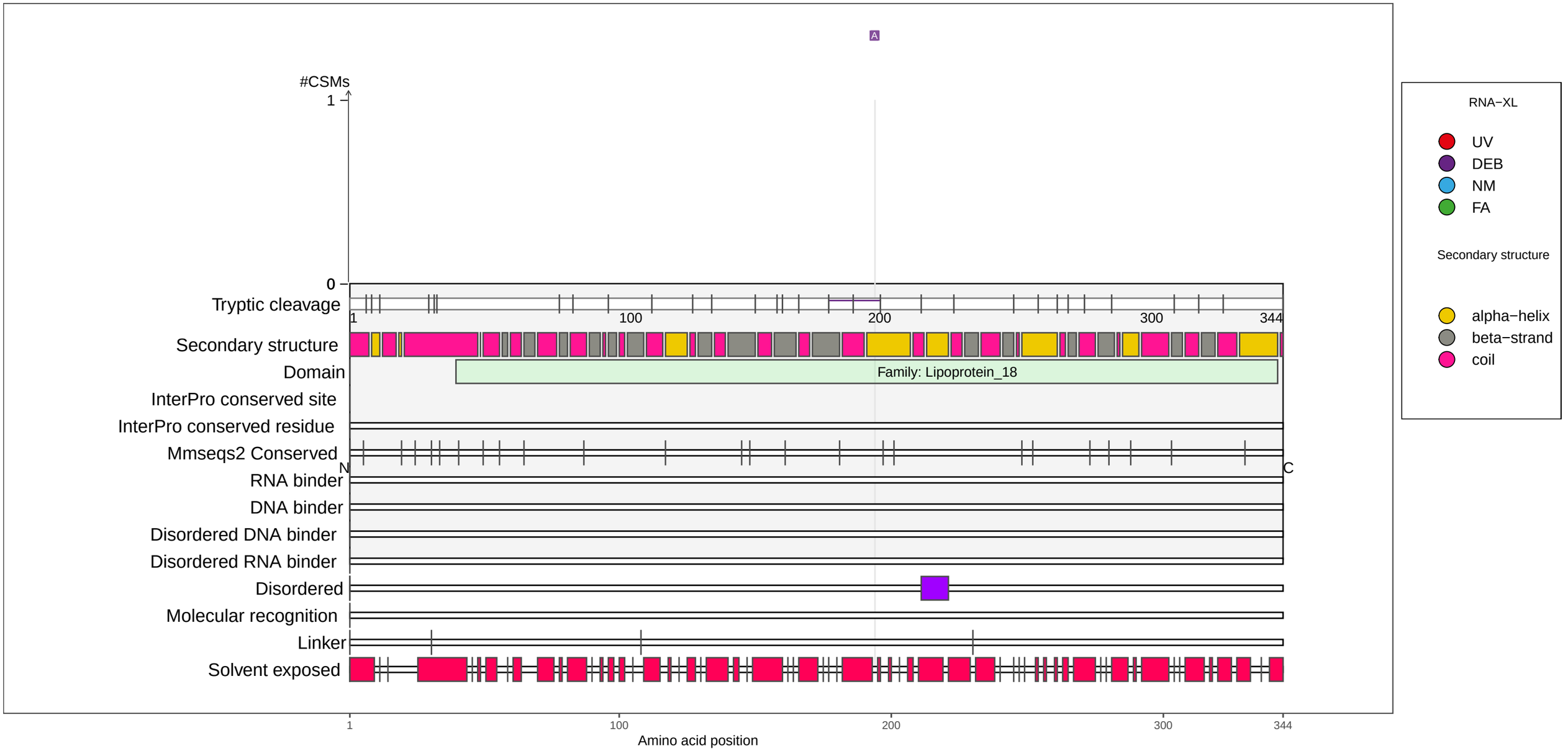




P0A903
BAMC_ECOLI Outer membrane protein assembly factor BamC

− Abundance:
tryptic [log10 Intensity]: 8.77 (Q 83)
PAXdb K12 strain [ppm]: 2.02 (Q 61)
PAXdb E.coli [ppm]: 2.45 (Q 84)

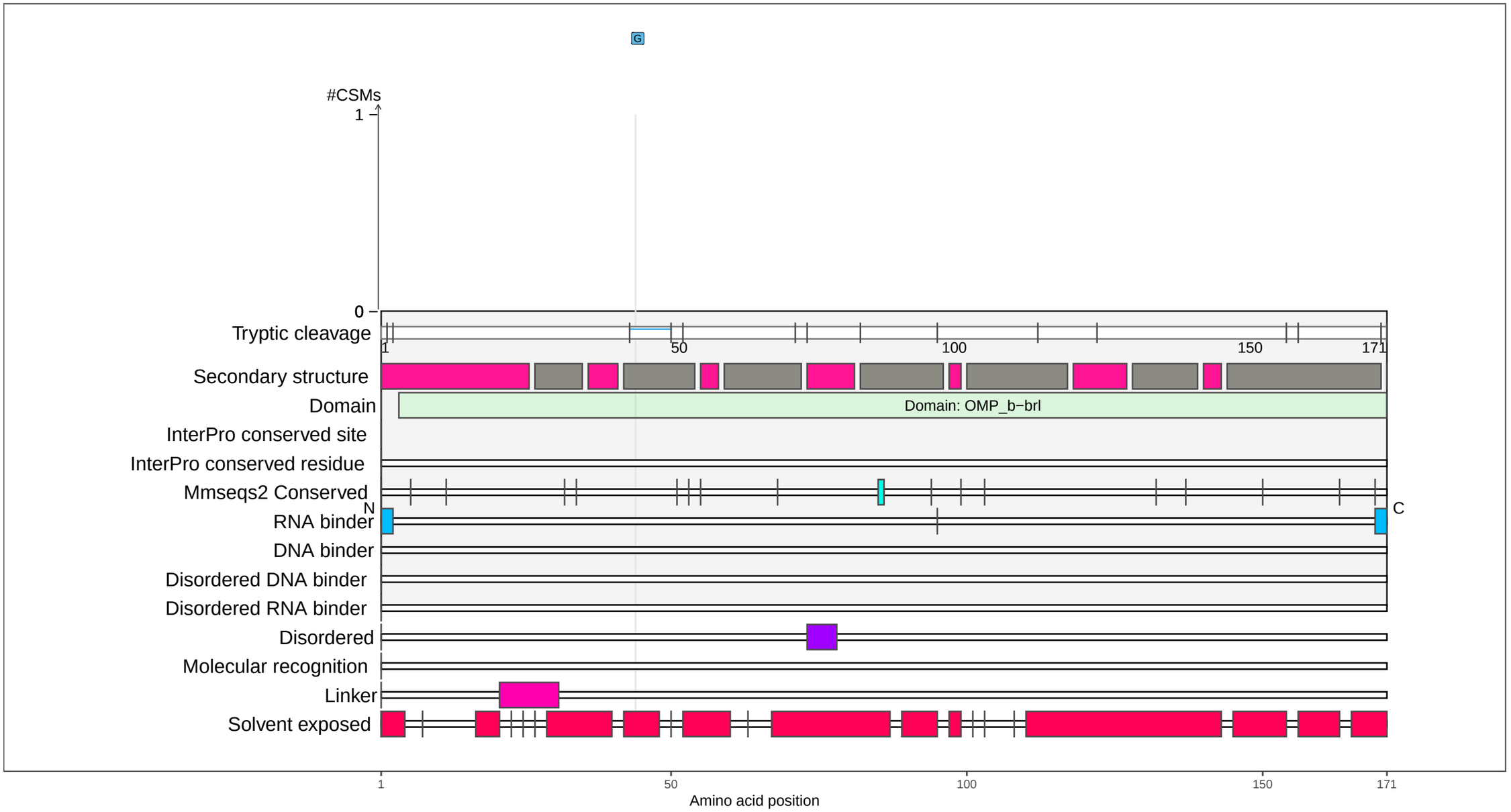
− RNA functions: not annotated

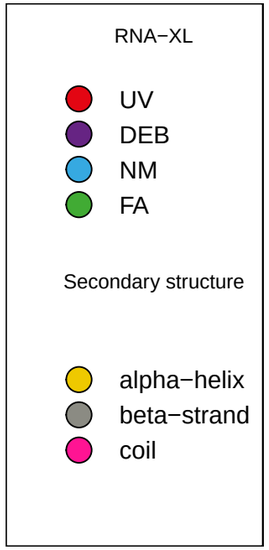


P0A917
OMPX_ECOLI Outer membrane protein X

− Abundance:
tryptic [log10 Intensity]: 9.6 (Q 97)
PAXdb K12 strain [ppm]: 1.54 (Q 40)
PAXdb E.coli [ppm]: 2.73 (Q 90)

− RNA functions: not annotated

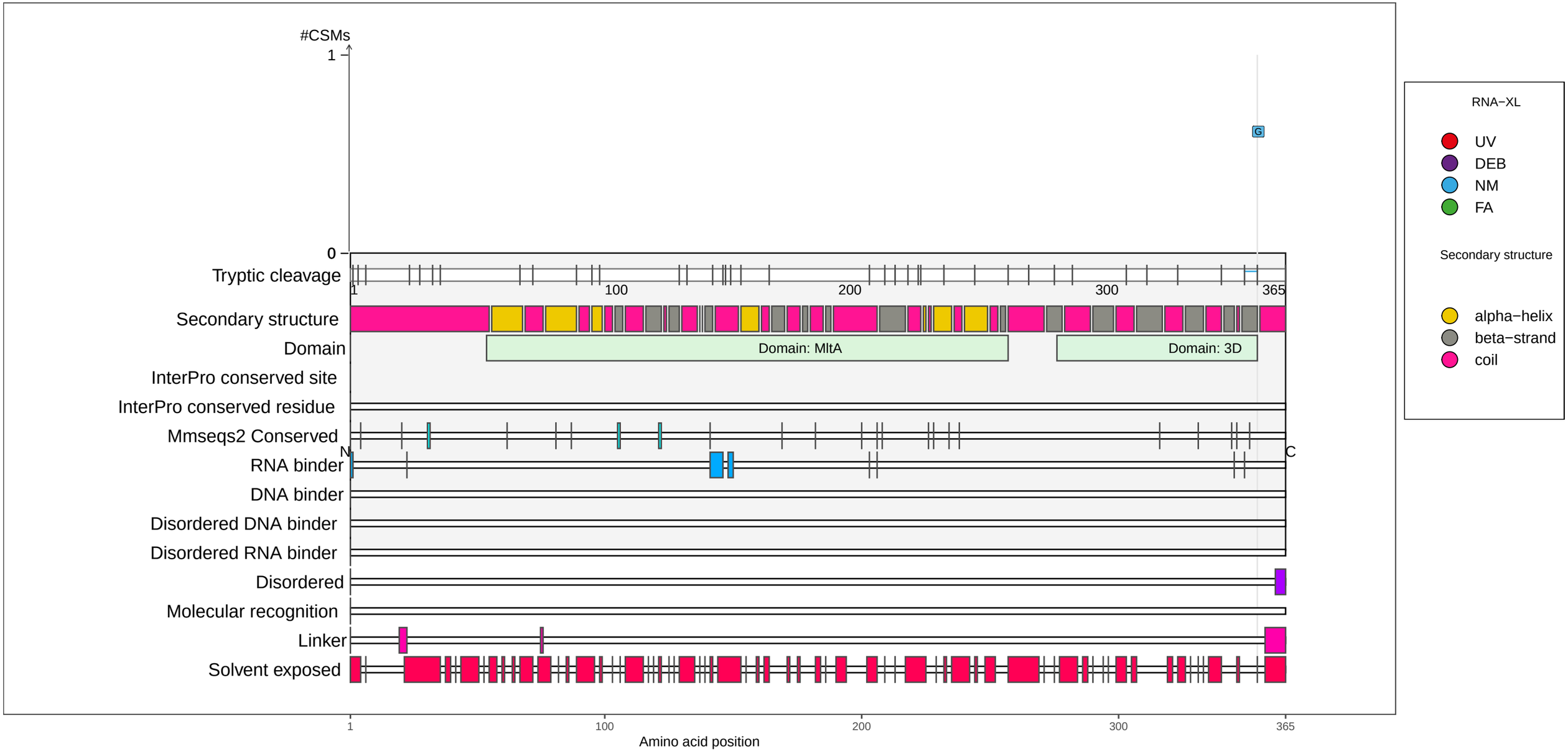




P0A935
MLTA_ECOLI Membrane−bound lytic murein transglycosylase A

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 0.85 (Q 6)
PAXdb E.coli [ppm]: 1.1 (Q 50)

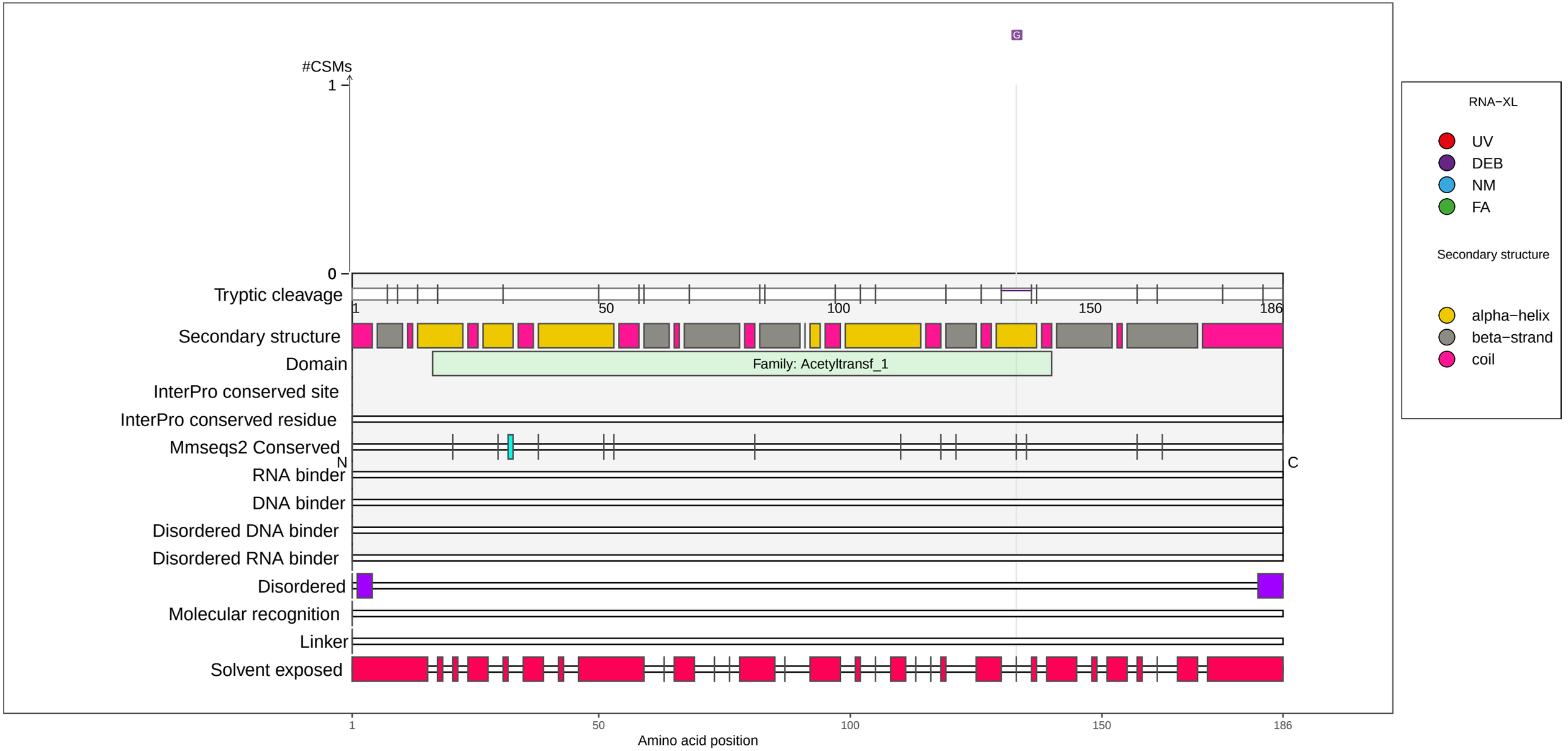
− RNA functions: not annotated



P0A951
ATDA_ECOLI Spermidine N(1)−acetyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.93 (Q 55)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.6 (Q 62)

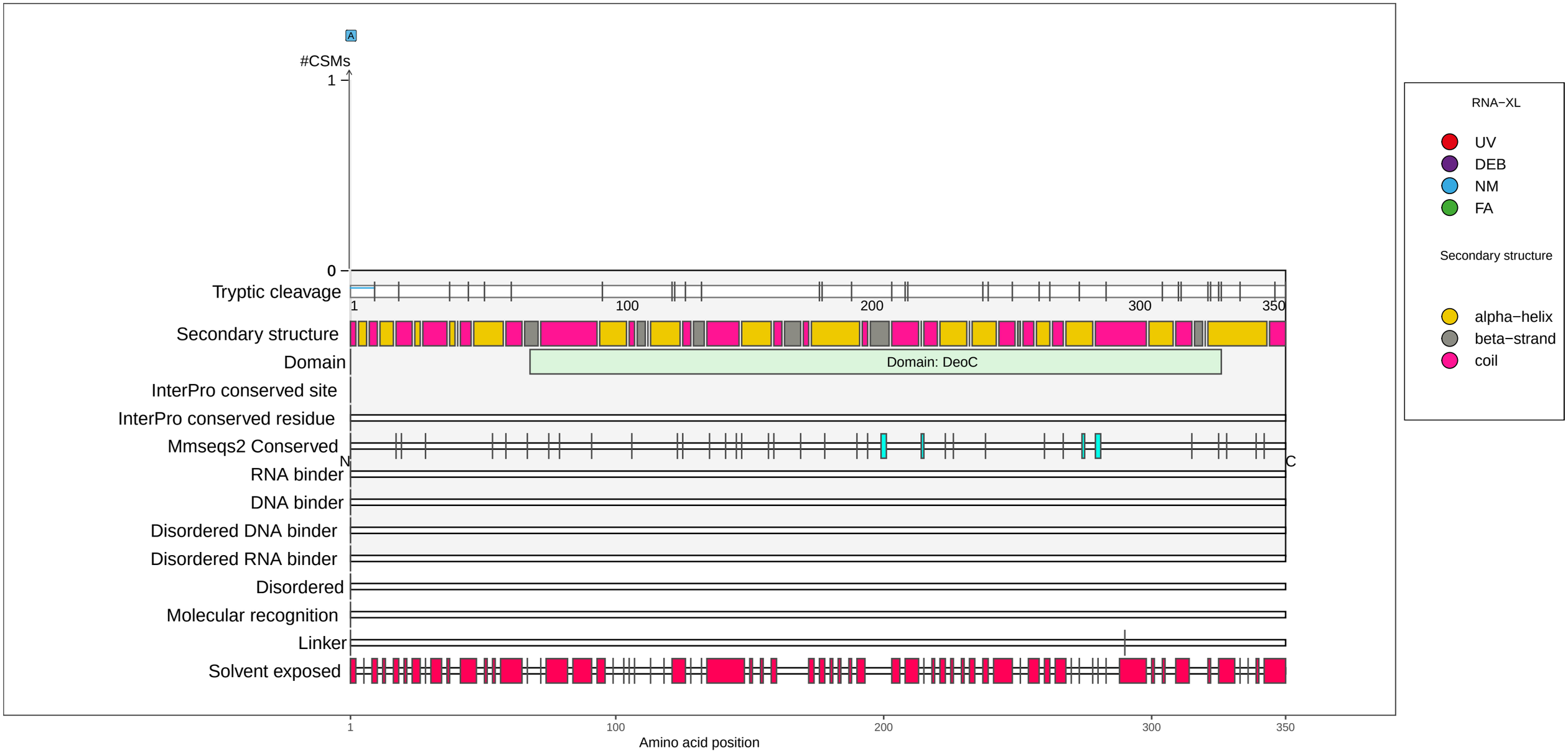
− RNA functions: not annotated



P0A991
ALF1_ECOLI Fructose−bisphosphate aldolase class 1

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 2.83 (Q 87)
PAXdb E.coli [ppm]: 2.92 (Q 94)

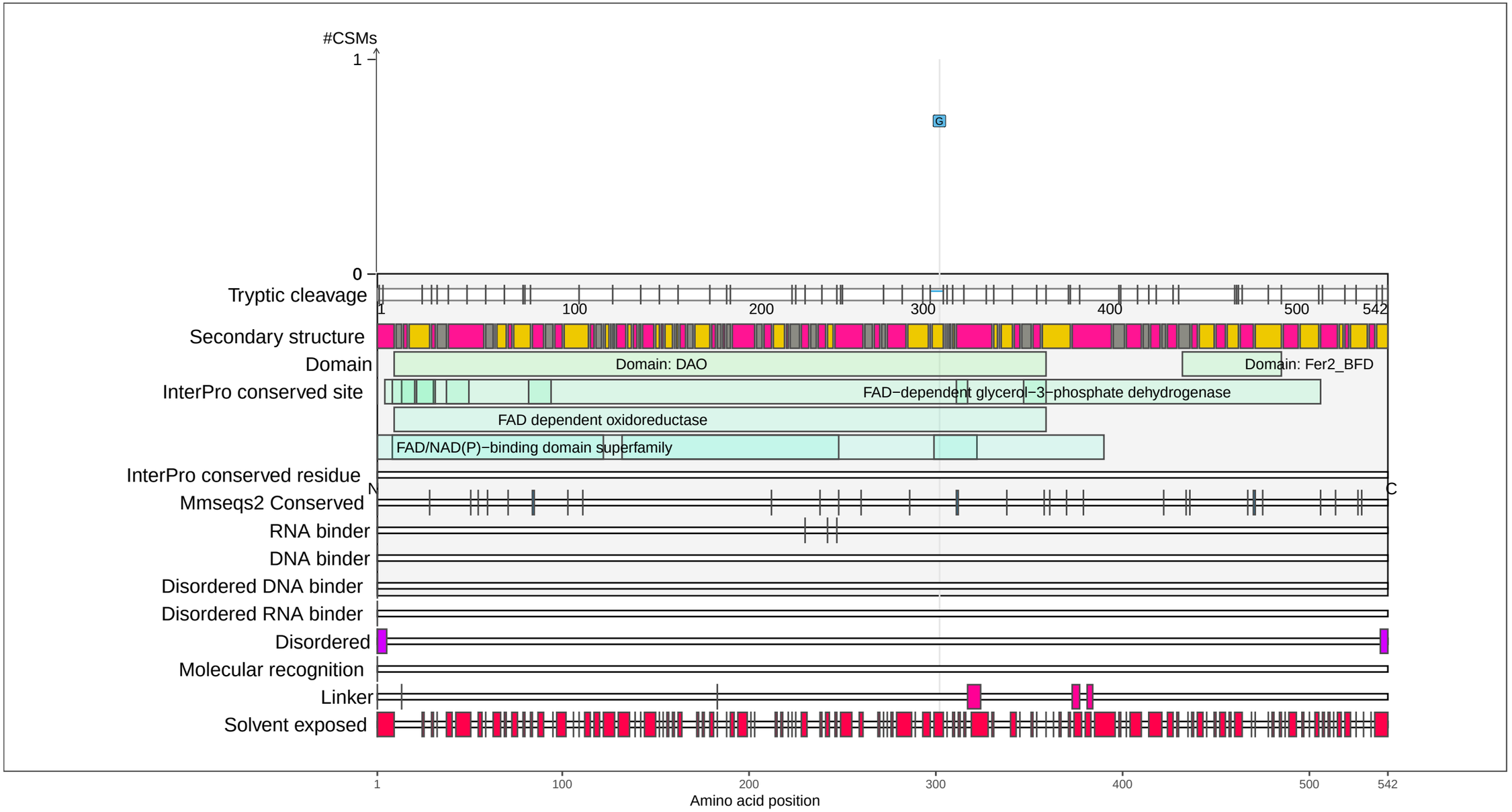
− RNA functions: not annotated



P0A9C0
GLPA_ECOLI Anaerobic glycerol−3−phosphate dehydrogenase subunit A

− Abundance:
tryptic [log10 Intensity]: 8.49 (Q 75)
PAXdb K12 strain [ppm]: 2.46 (Q 76)
PAXdb E.coli [ppm]: 2.04 (Q 73)

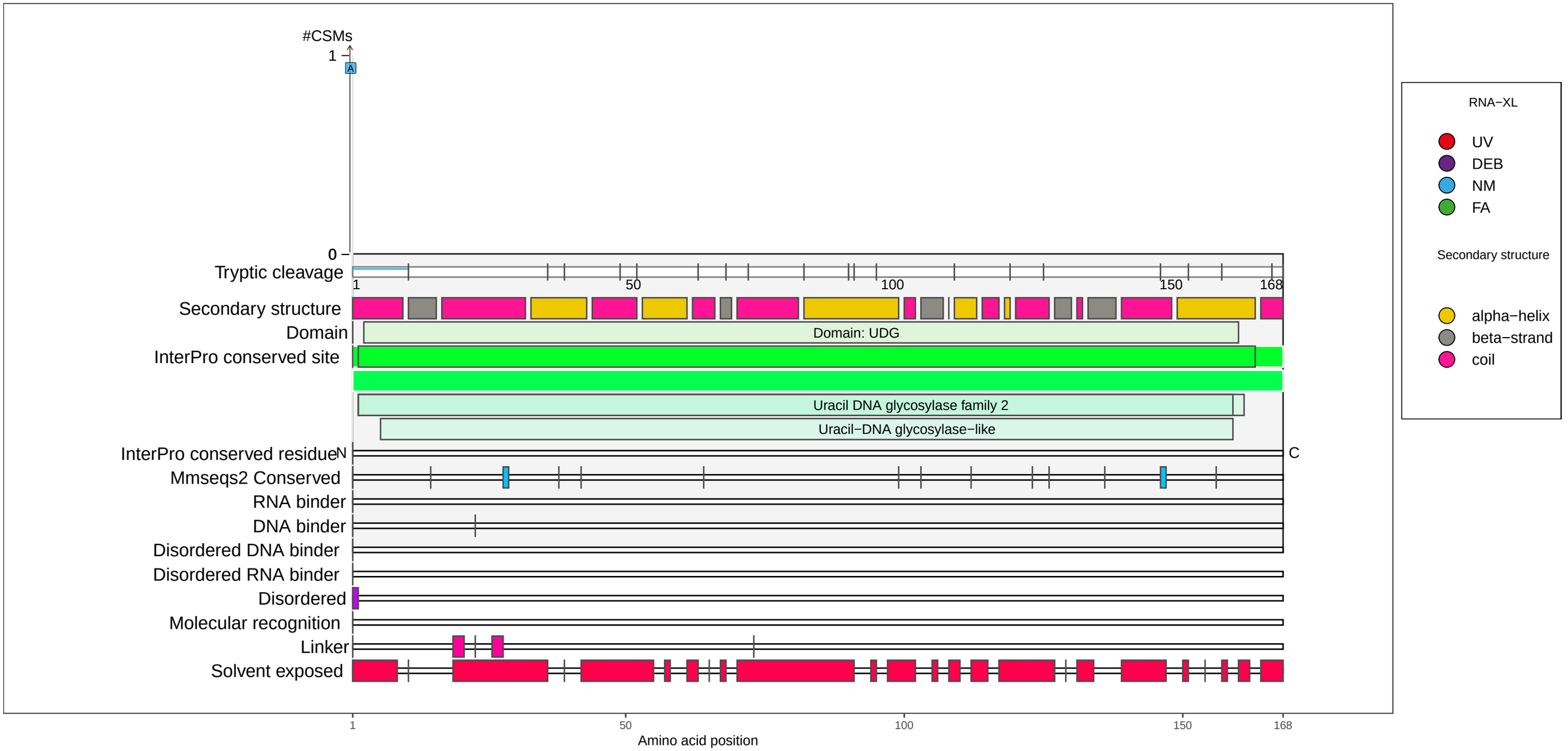
− RNA functions: not annotated



P0A9H1
MUG_ECOLI G/U mismatch−specific DNA glycosylase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.62 (Q 81)
PAXdb E.coli [ppm]: 2.03 (Q 73)

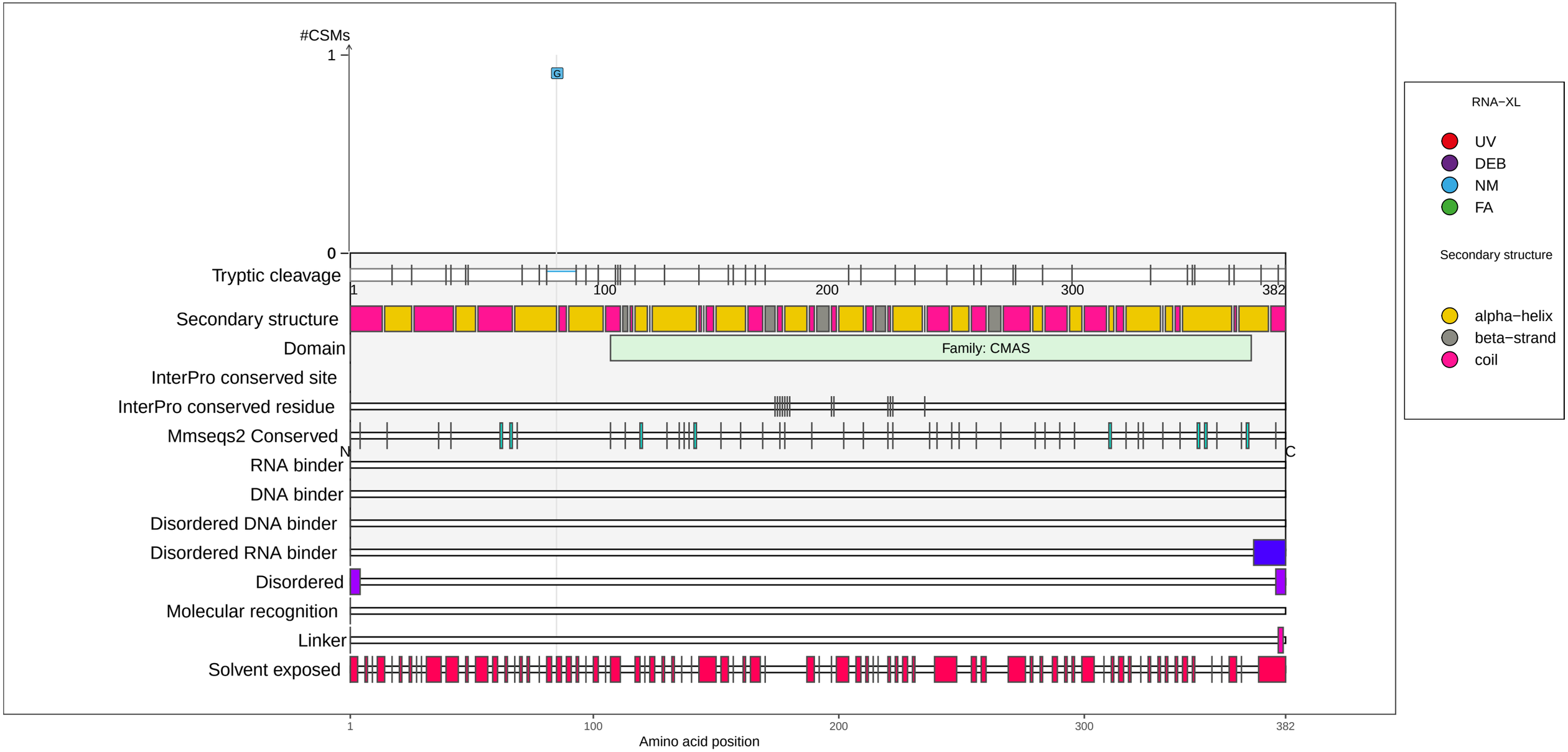
− RNA functions: not annotated



P0A9H7
CFA_ECOLI Cyclopropane−fatty−acyl−phospholipid synthase

− Abundance:
tryptic [log10 Intensity]: 8.66 (Q 80)
PAXdb K12 strain [ppm]: 2.12 (Q 65)
PAXdb E.coli [ppm]: 1.91 (Q 70)

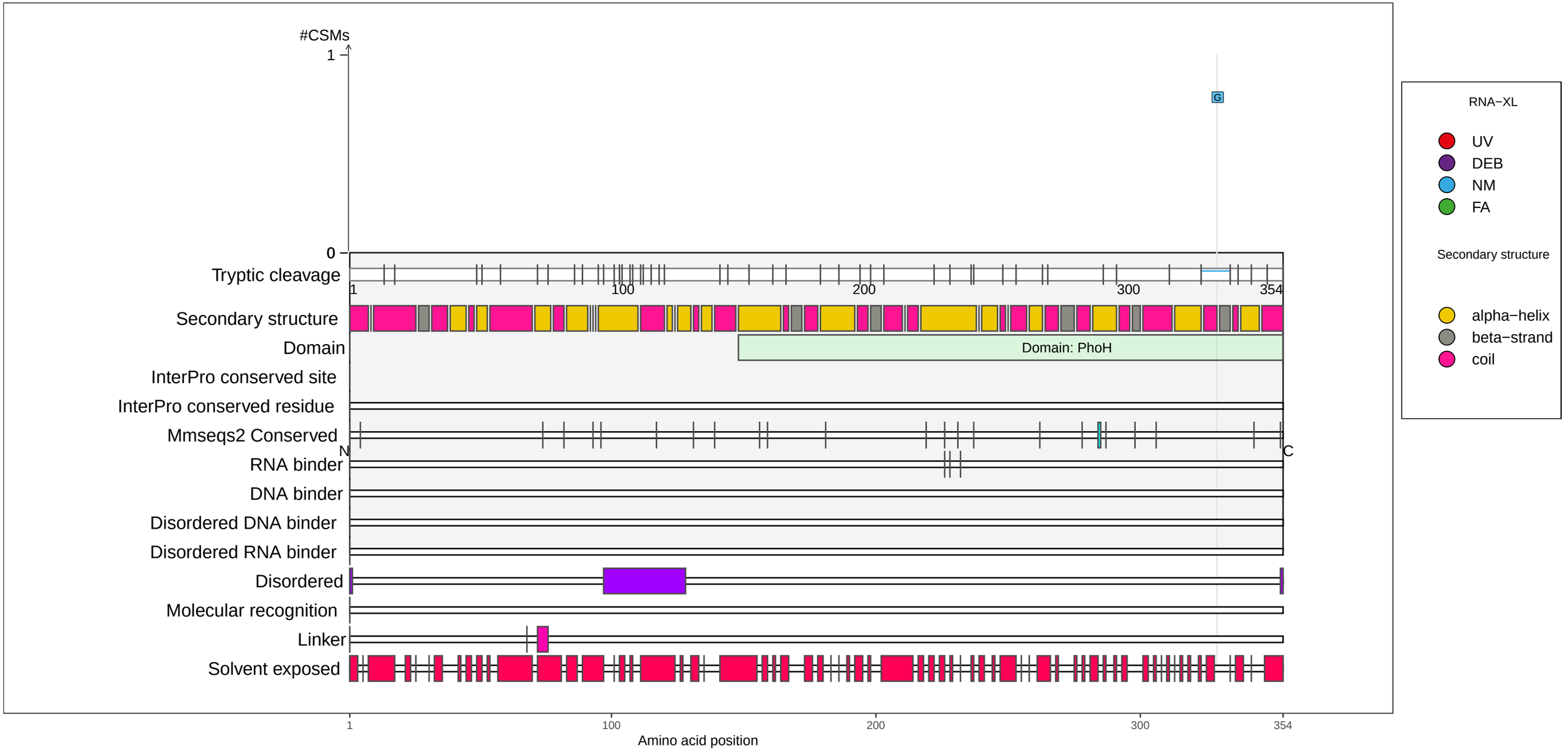
− RNA functions: not annotated



P0A9K1
PHOH_ECOLI Protein PhoH

− Abundance:
tryptic [log10 Intensity]: 6.72 (Q 6)
PAXdb K12 strain [ppm]: 0.81 (Q 5)
PAXdb E.coli [ppm]: 1.48 (Q 59)

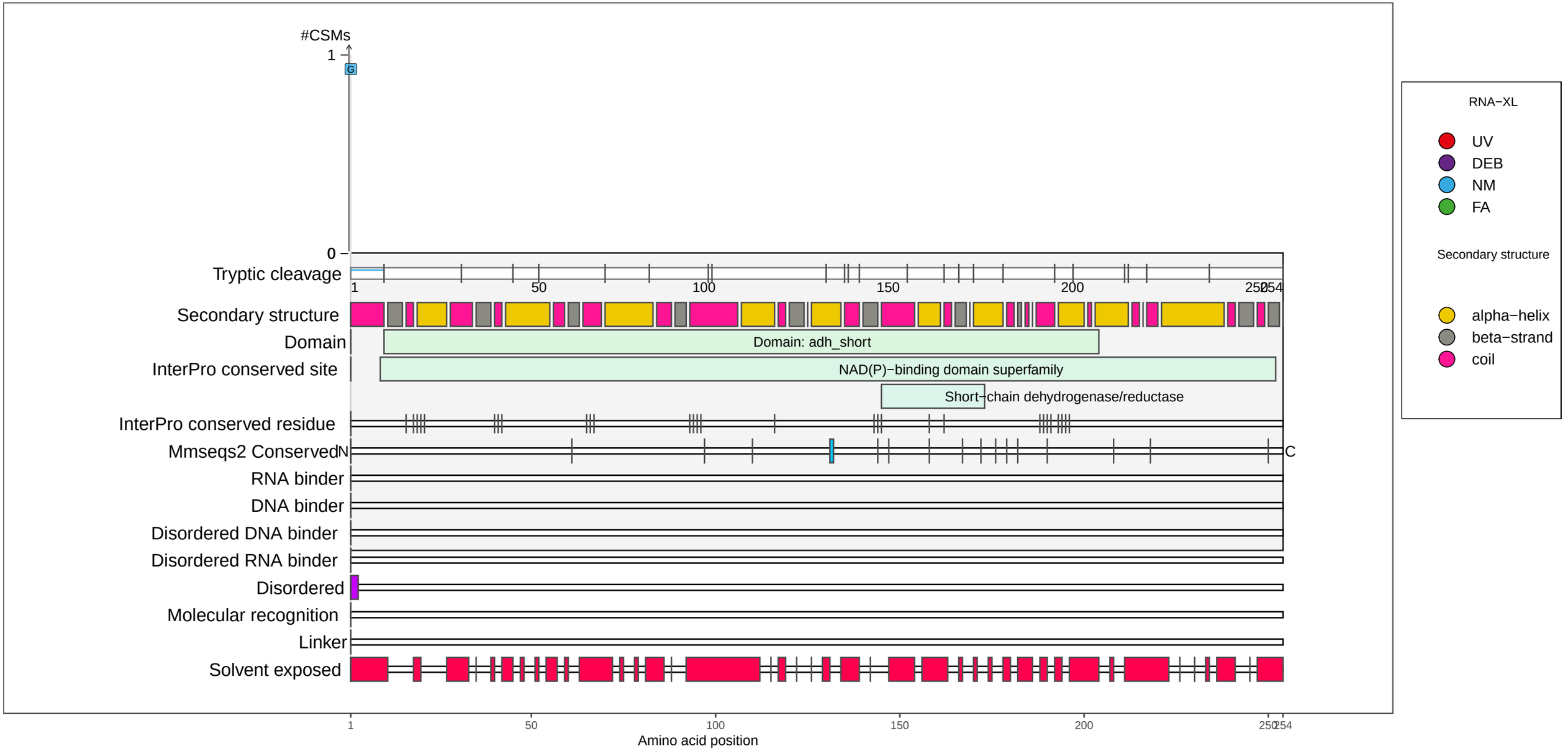
− RNA functions: not annotated



P0A9P9
IDNO_ECOLI 5−keto−D−gluconate 5−reductase

− Abundance:
tryptic [log10 Intensity]: 6.5 (Q 2)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.02 (Q 48)

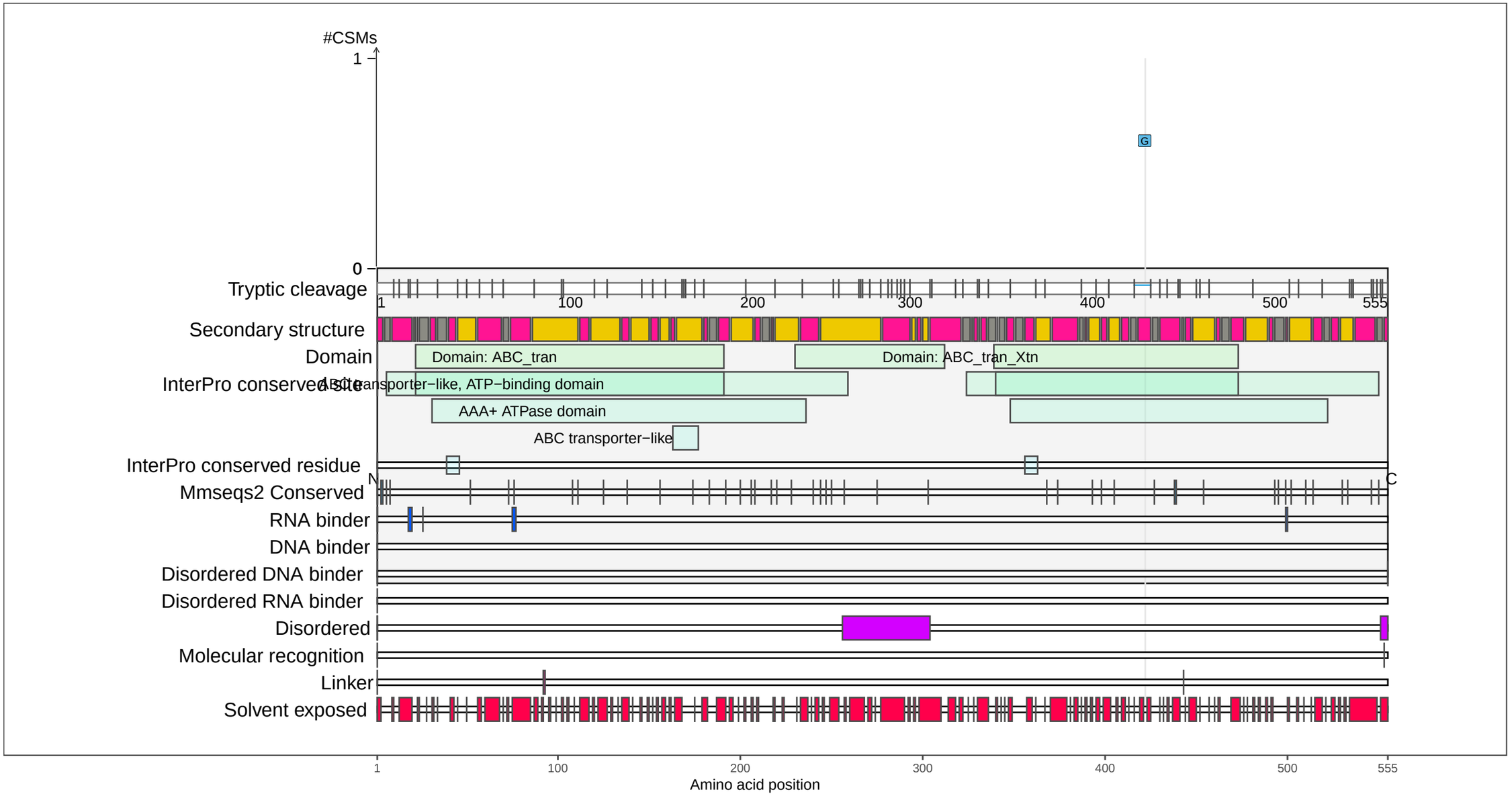
− RNA functions: not annotated

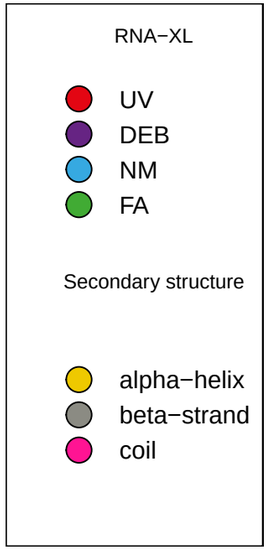


P0A9W3
ETTA_ECOLI Energy−dependent translational throttle protein EttA

− Abundance:
tryptic [log10 Intensity]: 8.58 (Q 78)
PAXdb K12 strain [ppm]: 2.79 (Q 86)
PAXdb E.coli [ppm]: 2.74 (Q 91)

− RNA functions:
RNA binding; rRNA binding; tRNA binding

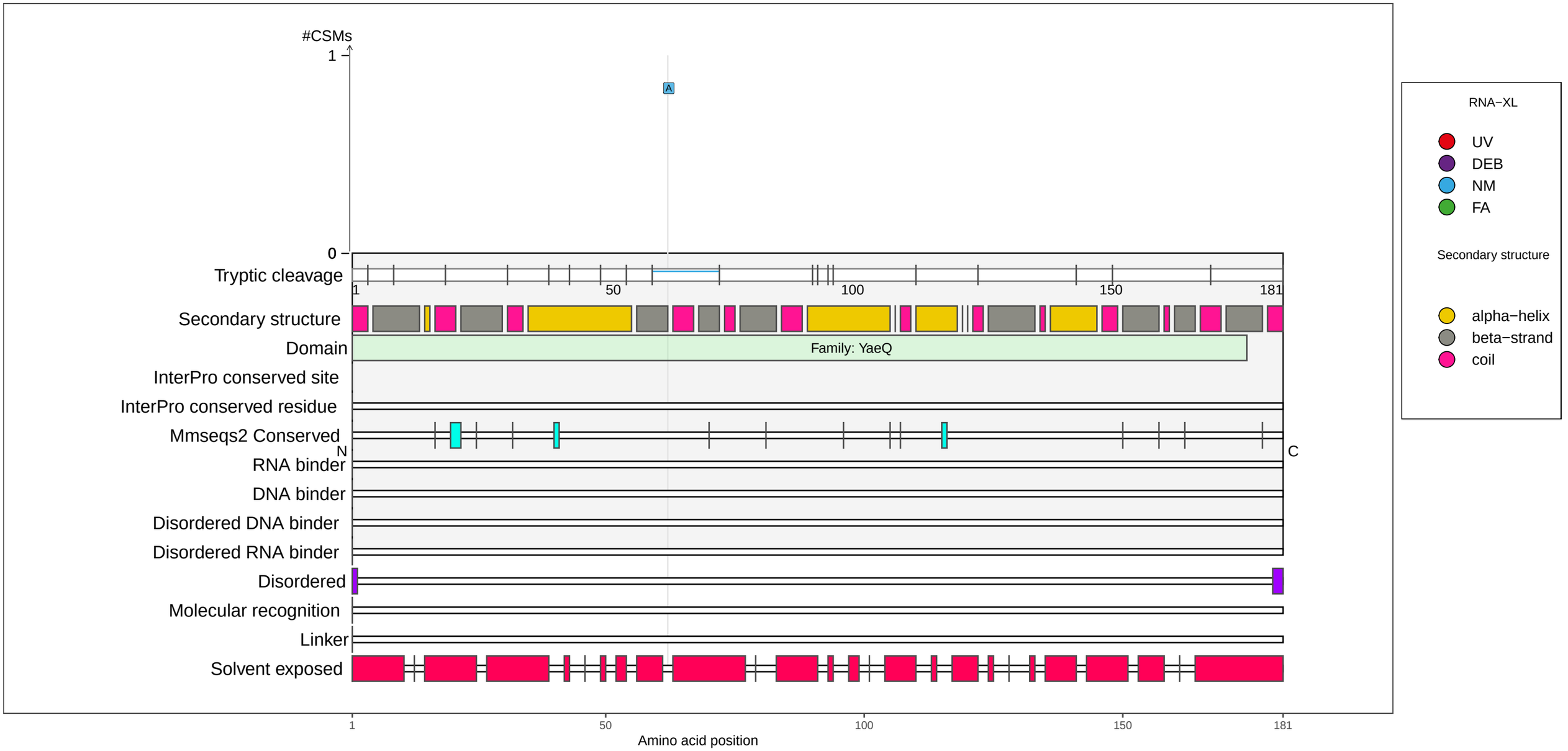




P0AA97
YAEQ_ECOLI Uncharacterized protein YaeQ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.36 (Q 30)
PAXdb E.coli [ppm]: 1.33 (Q 55)

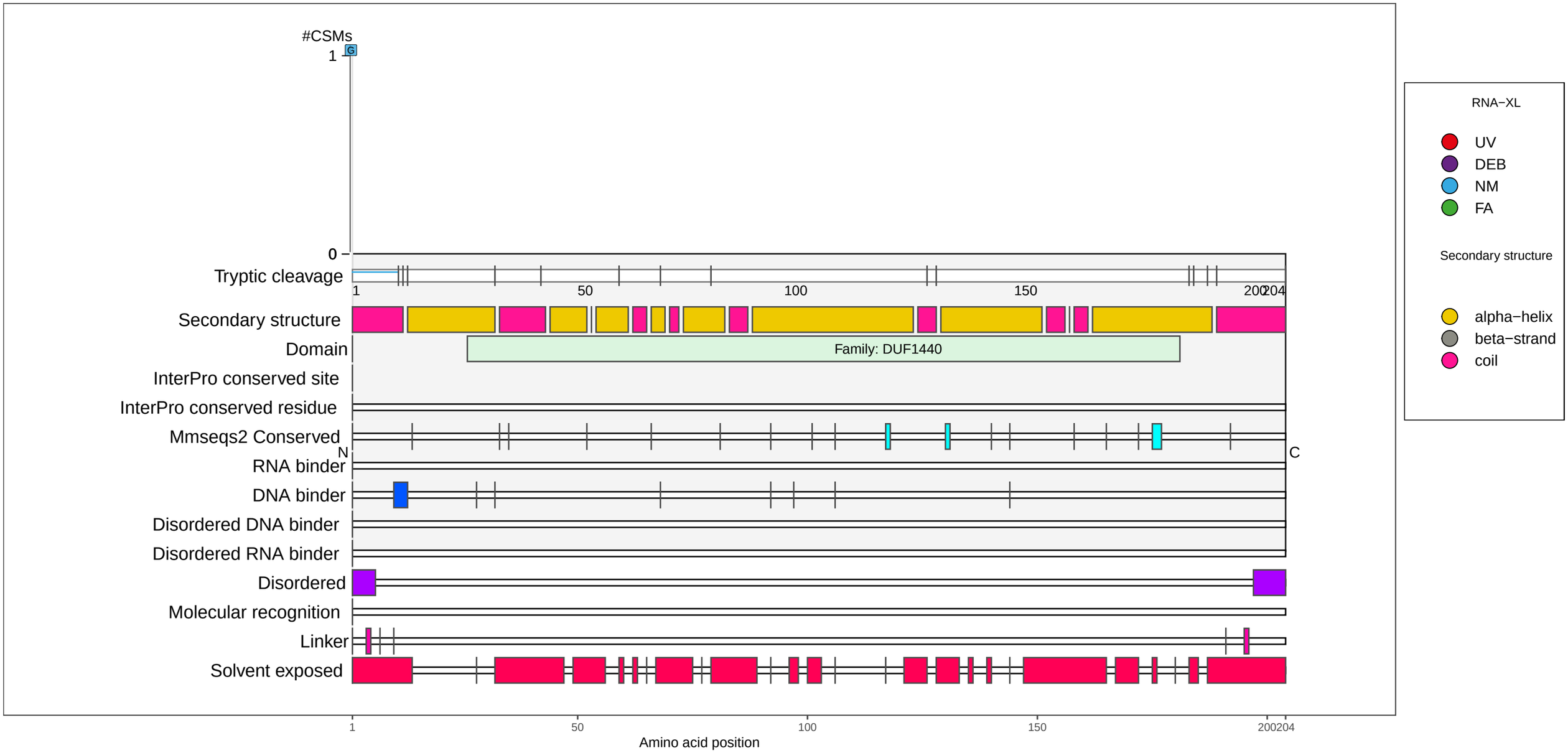
− RNA functions: not annotated



P0AAA1
YAGU_ECOLI Inner membrane protein YagU

− Abundance:
tryptic [log10 Intensity]: 7.9 (Q 54)
PAXdb K12 strain [ppm]: 1.18 (Q 19)
PAXdb E.coli [ppm]: 2.09 (Q 75)

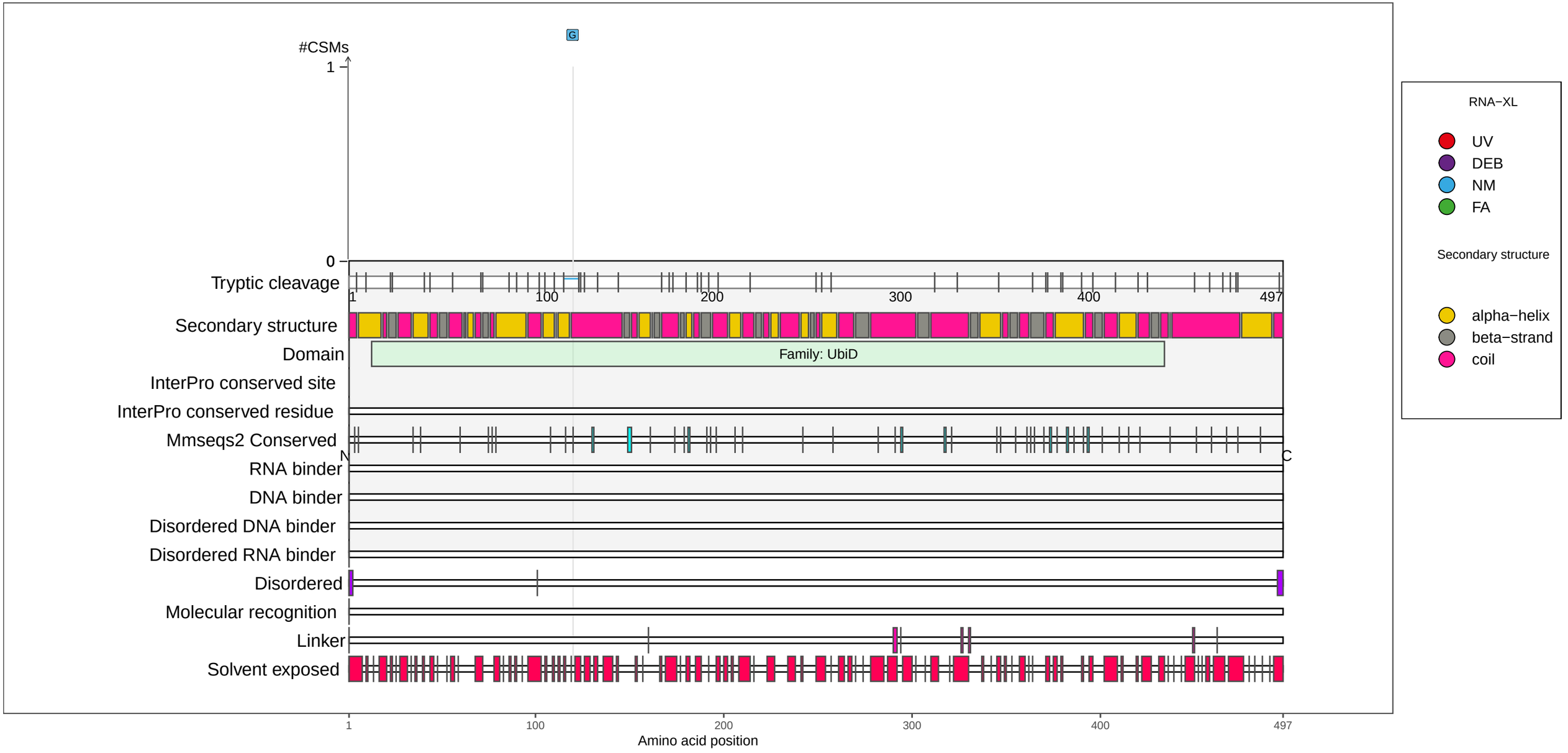
− RNA functions: not annotated



P0AAB4
UBID_ECOLI 3−octaprenyl−4−hydroxybenzoate carboxy−lyase

− Abundance:
tryptic [log10 Intensity]: 8.28 (Q 68)
PAXdb K12 strain [ppm]: 1.76 (Q 52)
PAXdb E.coli [ppm]: 1.7 (Q 64)

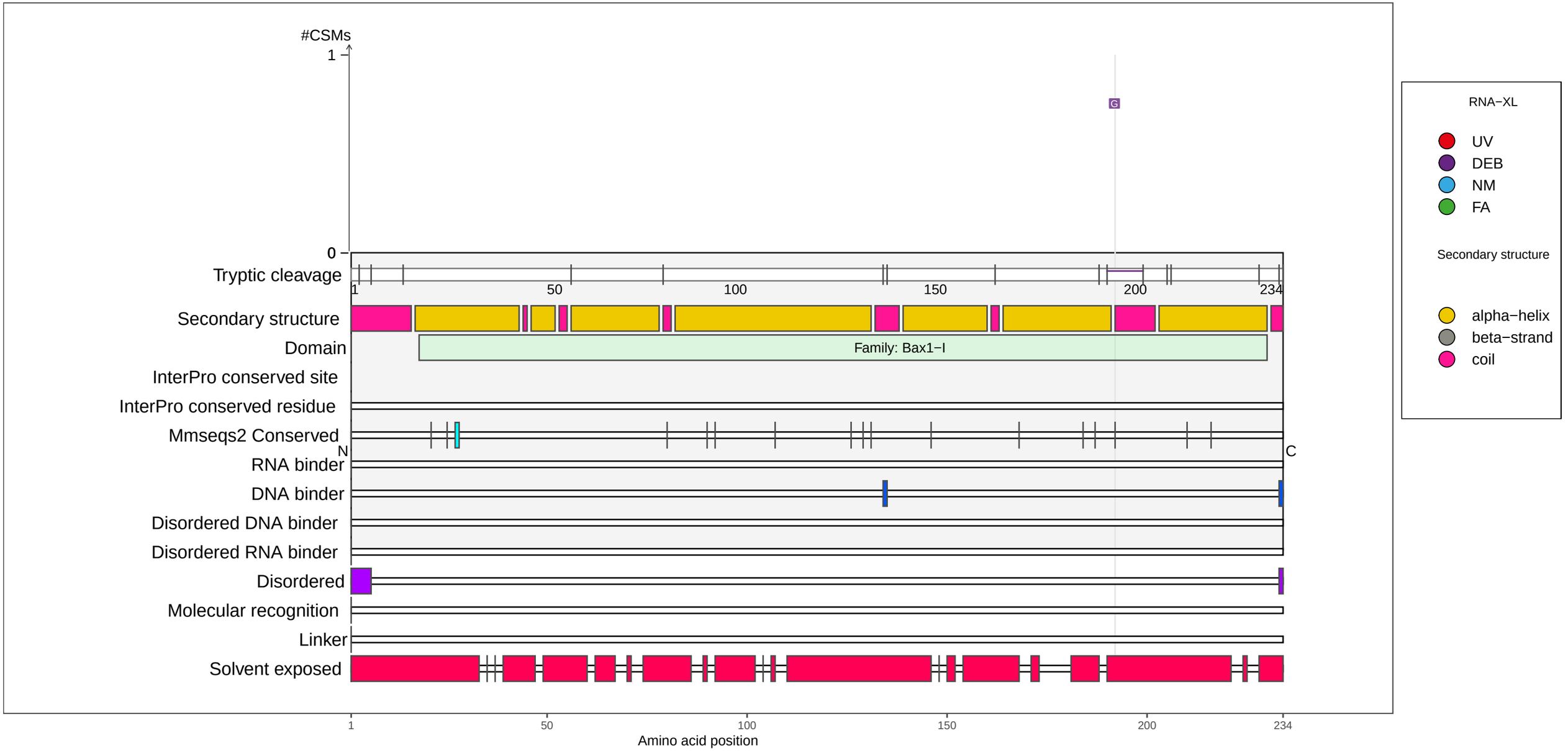
− RNA functions: not annotated



P0AAC4
YBHL_ECOLI Inner membrane protein YbhL

− Abundance:
tryptic [log10 Intensity]: 8.35 (Q 71)
PAXdb K12 strain [ppm]: 2.02 (Q 61)
PAXdb E.coli [ppm]: 0.57 (Q 38)

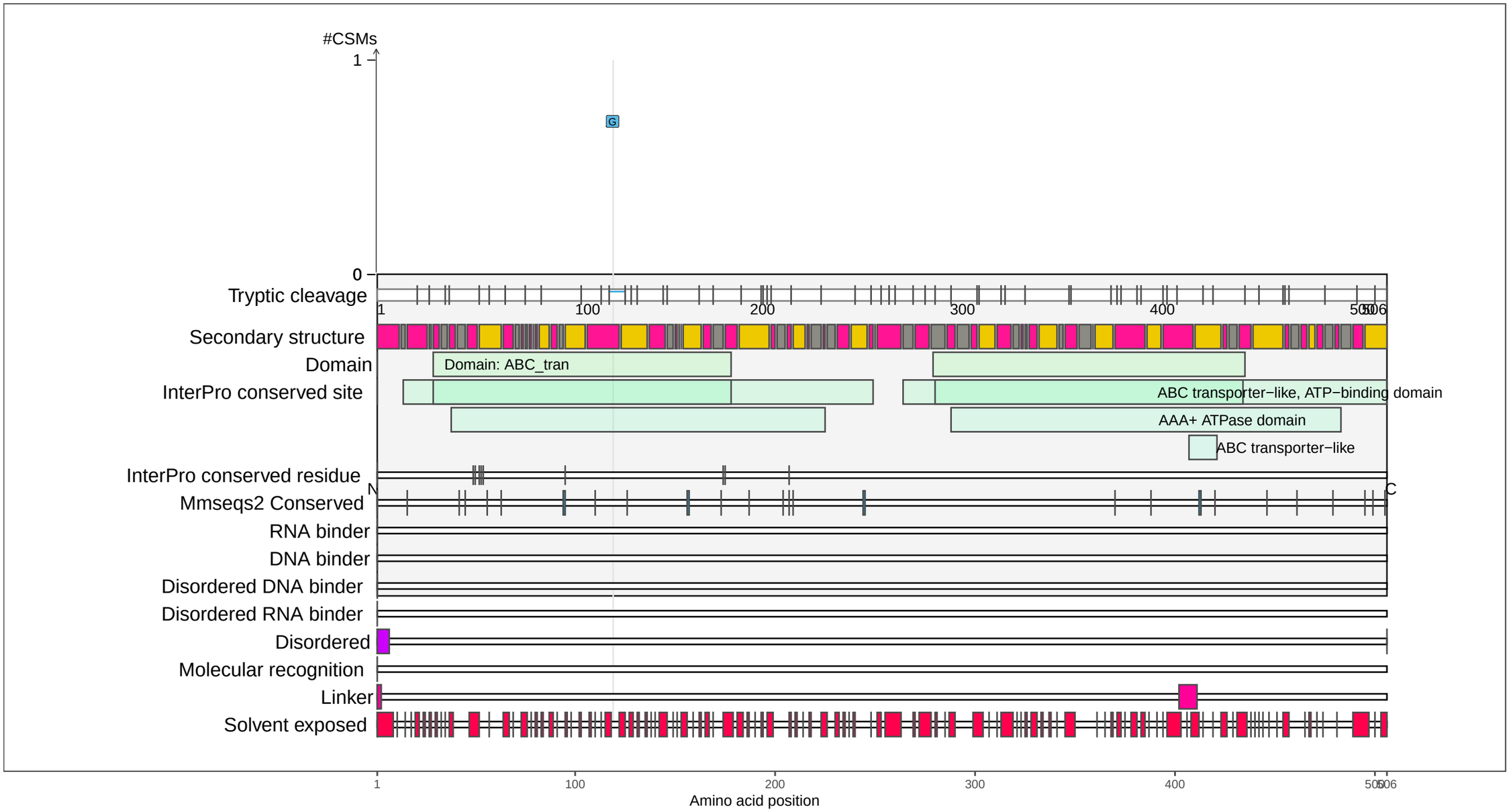
− RNA functions: not annotated



P0AAG8
MGLA_ECOLI Galactose/methyl galactoside import ATP−binding protein MglA

− Abundance:
tryptic [log10 Intensity]: 6.79 (Q 7)
PAXdb K12 strain [ppm]: 1.49 (Q 37)
PAXdb E.coli [ppm]: 2.17 (Q 77)

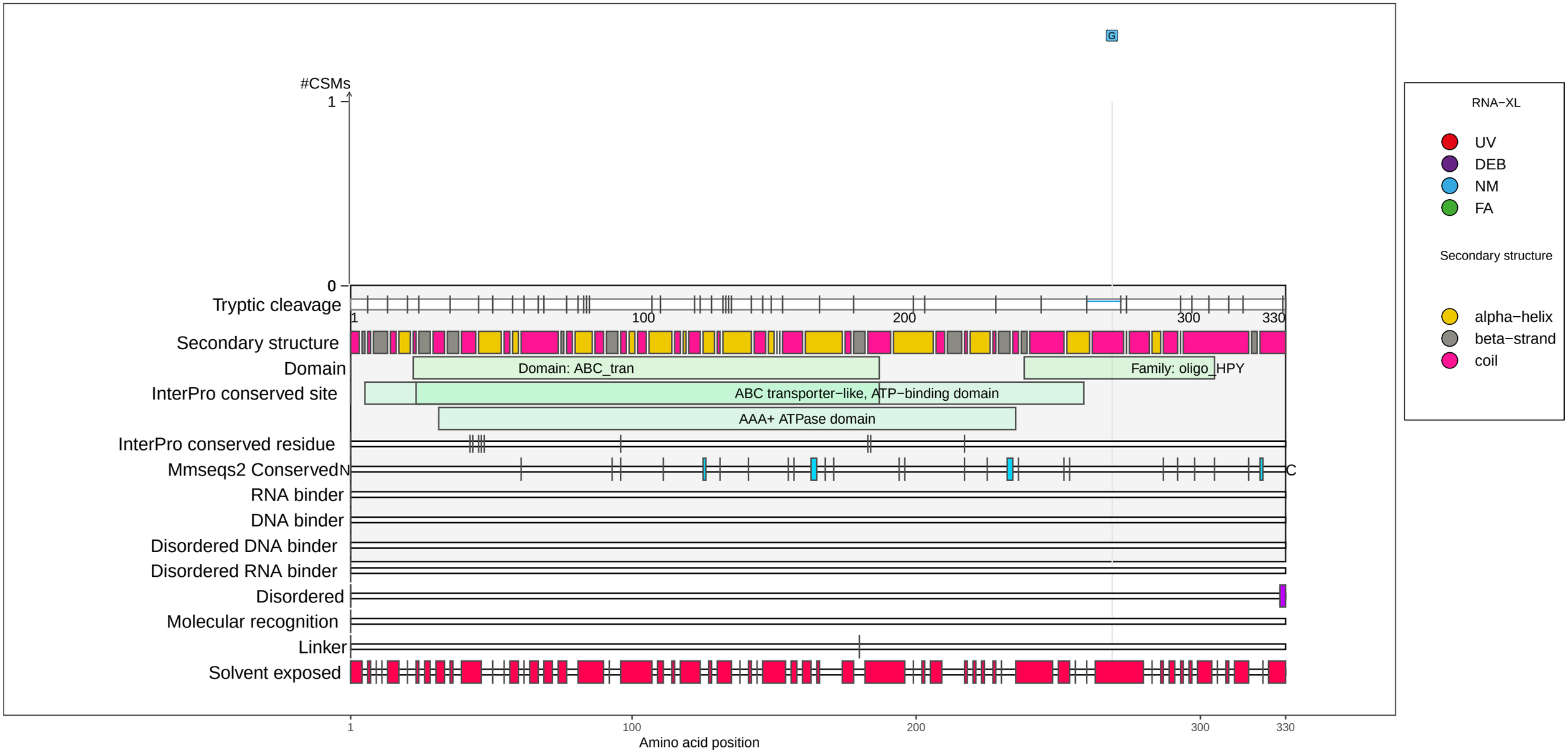
− RNA functions: not annotated



P0AAH4
SAPD_ECOLI Putrescine export system ATP−binding protein SapD

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.68 (Q 48)
PAXdb E.coli [ppm]: −0.02 (Q 24)

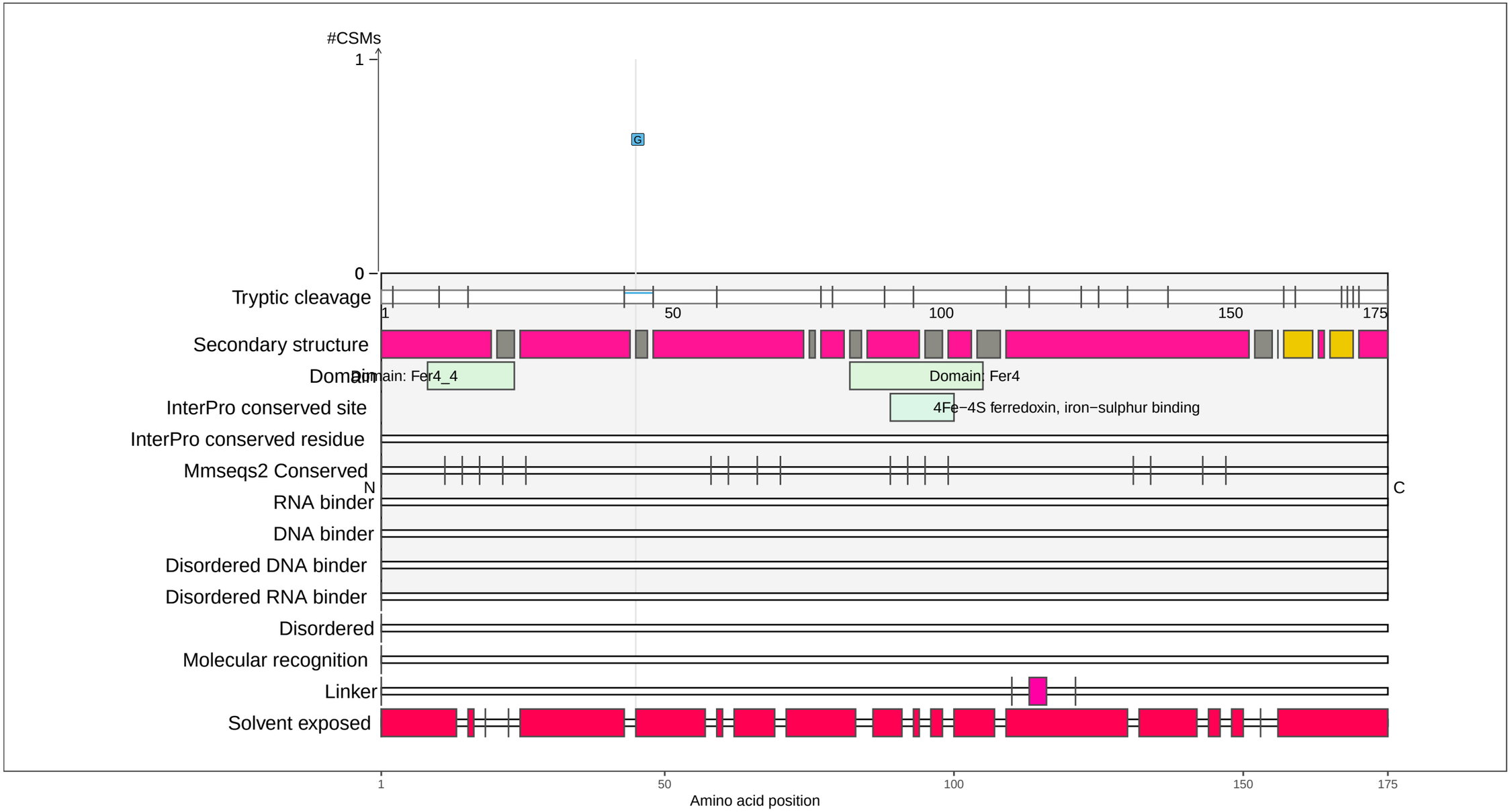
− RNA functions: not annotated



P0AAK4
HYDN_ECOLI Electron transport protein HydN

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −2.7 (Q 1)

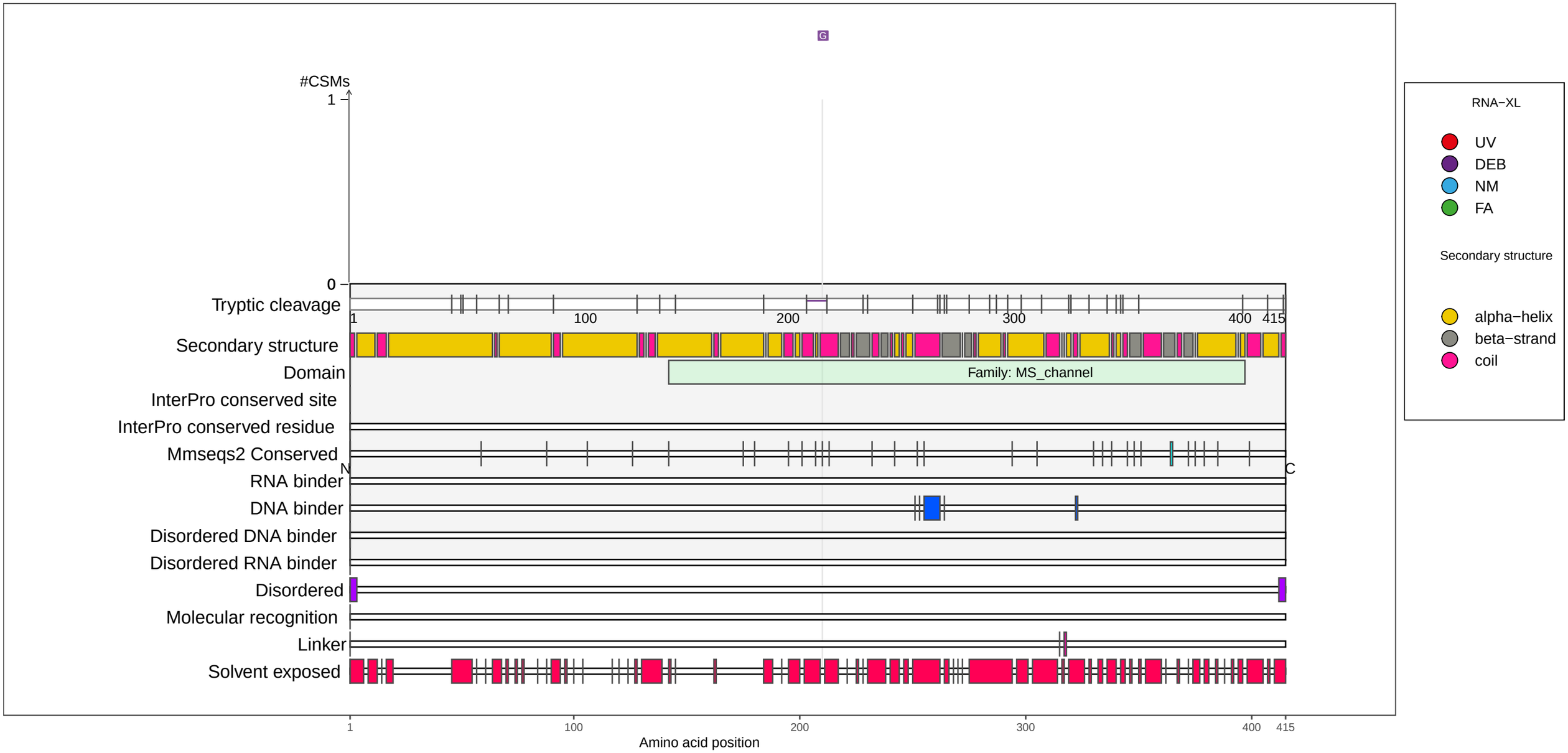
− RNA functions: not annotated



P0AAT4
YBDG_ECOLI Miniconductance mechanosensitive channel YbdG

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.35 (Q 56)

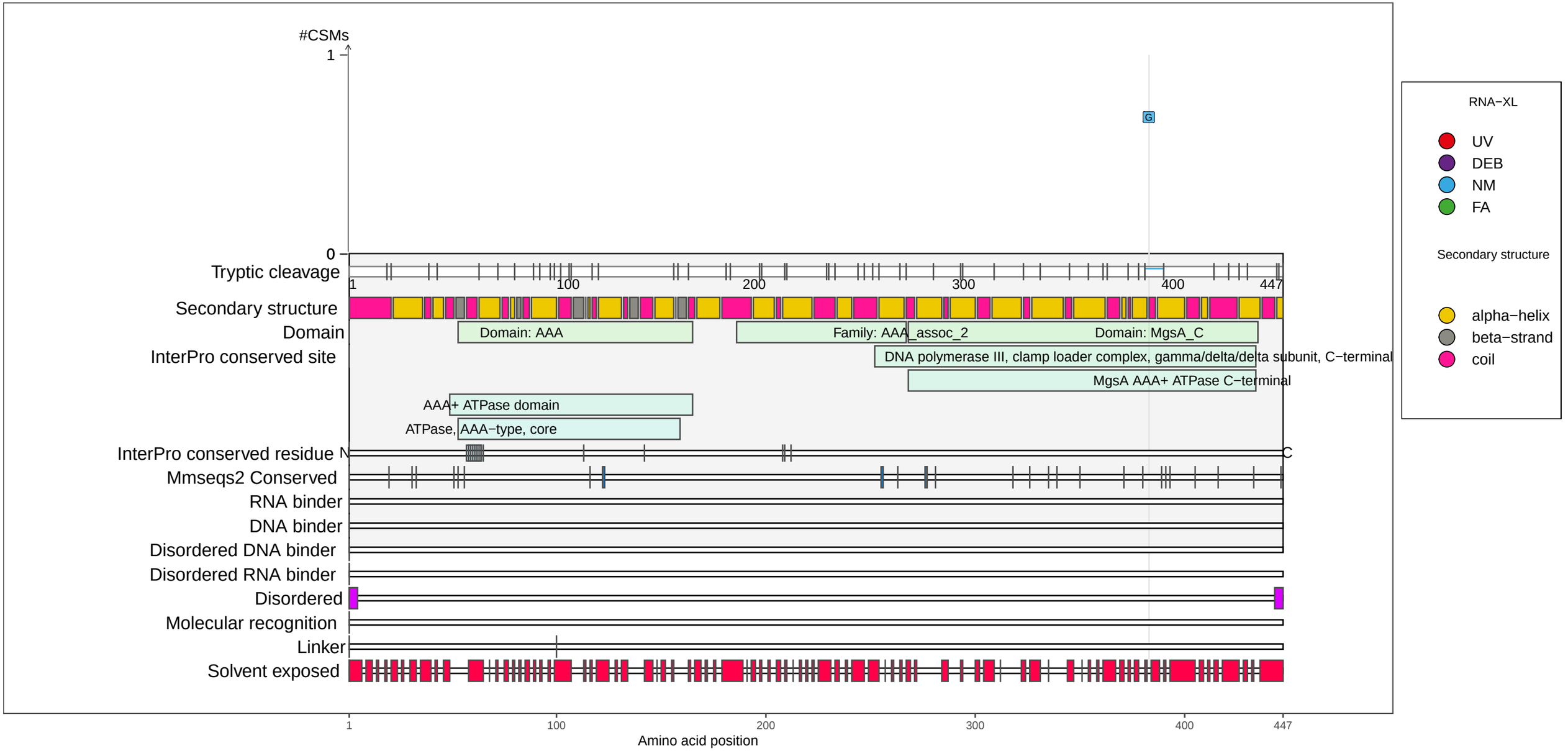
− RNA functions: not annotated



P0AAZ4
RARA_ECOLI Replication−associated recombination protein A

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.79 (Q 53)
PAXdb E.coli [ppm]: 1.37 (Q 56)

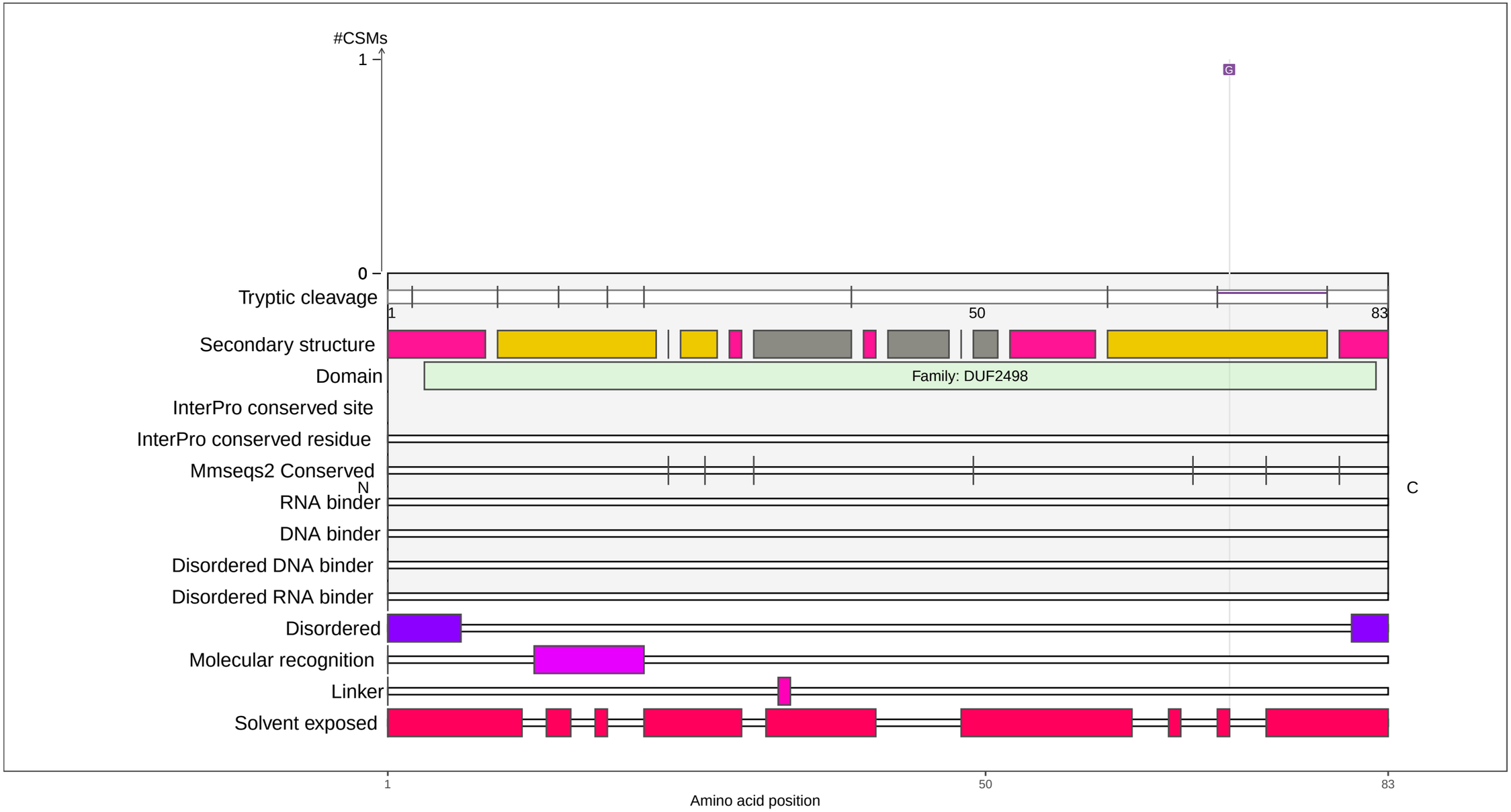
− RNA functions: not annotated



P0AB61
YCIN_ECOLI Protein YciN

− Abundance:
tryptic [log10 Intensity]: 8.44 (Q 73)
PAXdb K12 strain [ppm]: 3.41 (Q 96)
PAXdb E.coli [ppm]: 2.67 (Q 89)

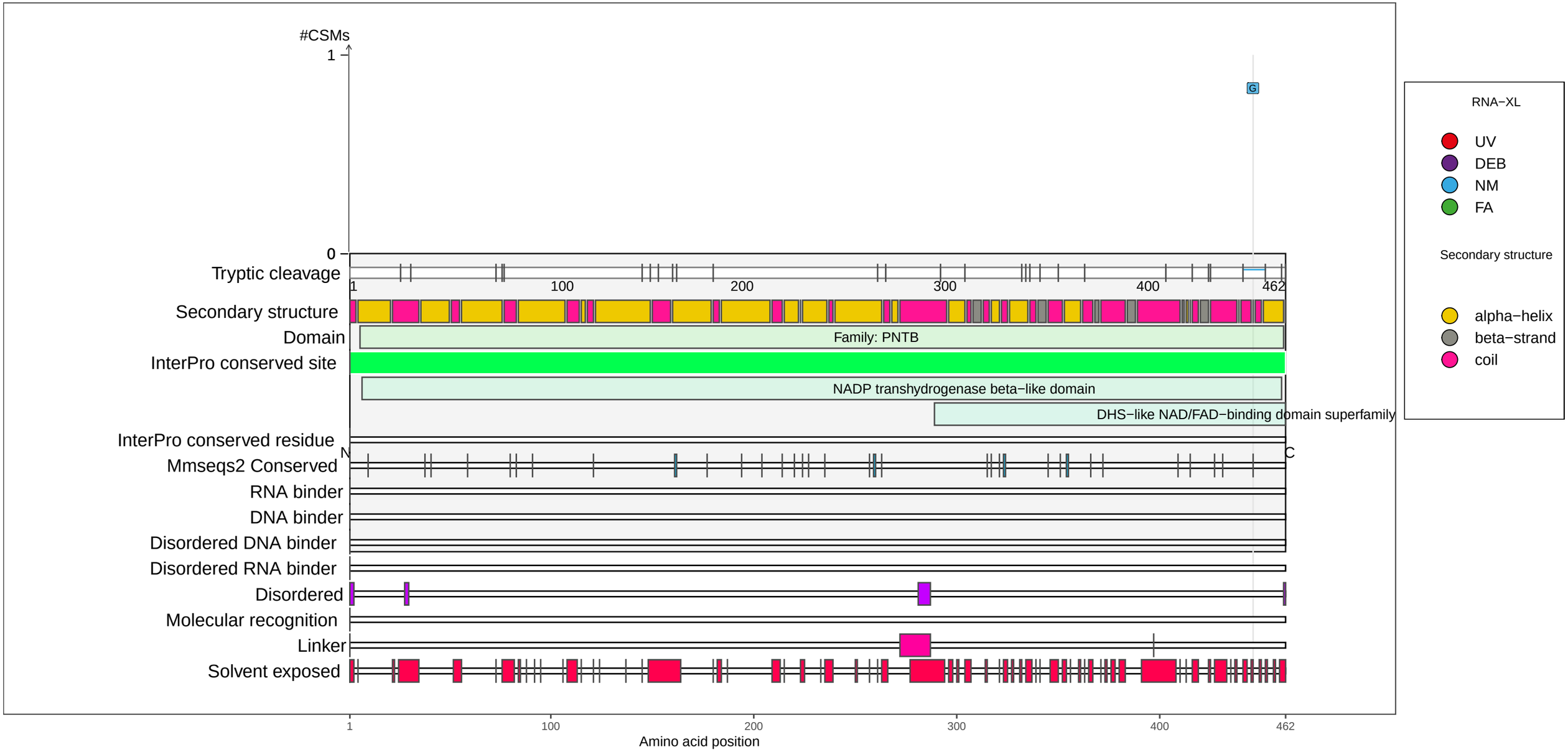
− RNA functions: not annotated



P0AB67
PNTB_ECOLI NAD(P) transhydrogenase subunit beta

− Abundance:
tryptic [log10 Intensity]: 7.34 (Q 27)
PAXdb K12 strain [ppm]: 1.97 (Q 59)
PAXdb E.coli [ppm]: 2.49 (Q 85)

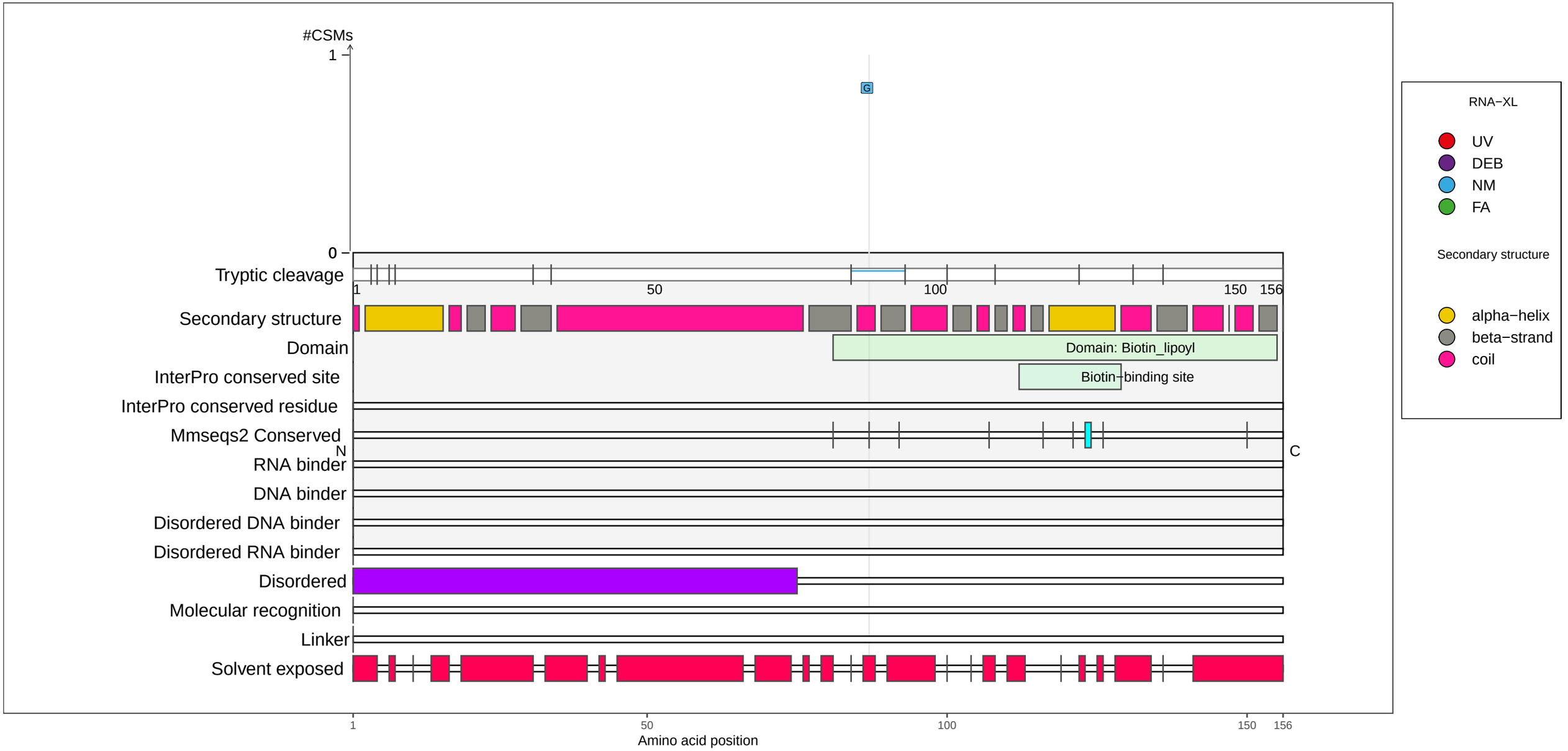
− RNA functions: not annotated



P0ABD8
BCCP_ECOLI Biotin carboxyl carrier protein of acetyl−CoA carboxylase

− Abundance:
tryptic [log10 Intensity]: 8.61 (Q 79)
PAXdb K12 strain [ppm]: 2.16 (Q 66)
PAXdb E.coli [ppm]: 2.47 (Q 85)

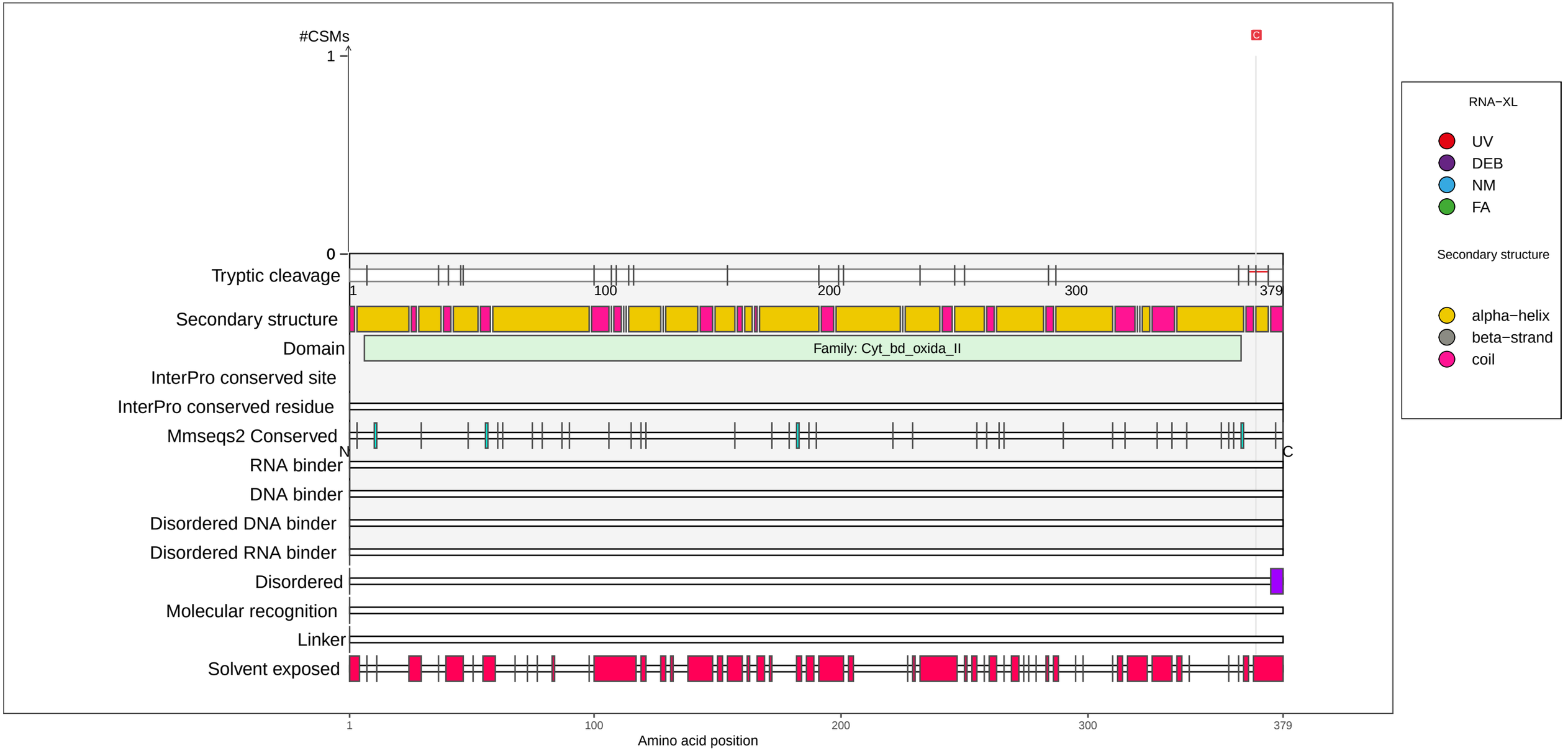
− RNA functions: not annotated



P0ABK2
CYDB_ECOLI Cytochrome bd−I ubiquinol oxidase subunit 2

− Abundance:
tryptic [log10 Intensity]: 9.89 (Q 99)
PAXdb K12 strain [ppm]: 2.65 (Q 82)
PAXdb E.coli [ppm]: 2.36 (Q 82)

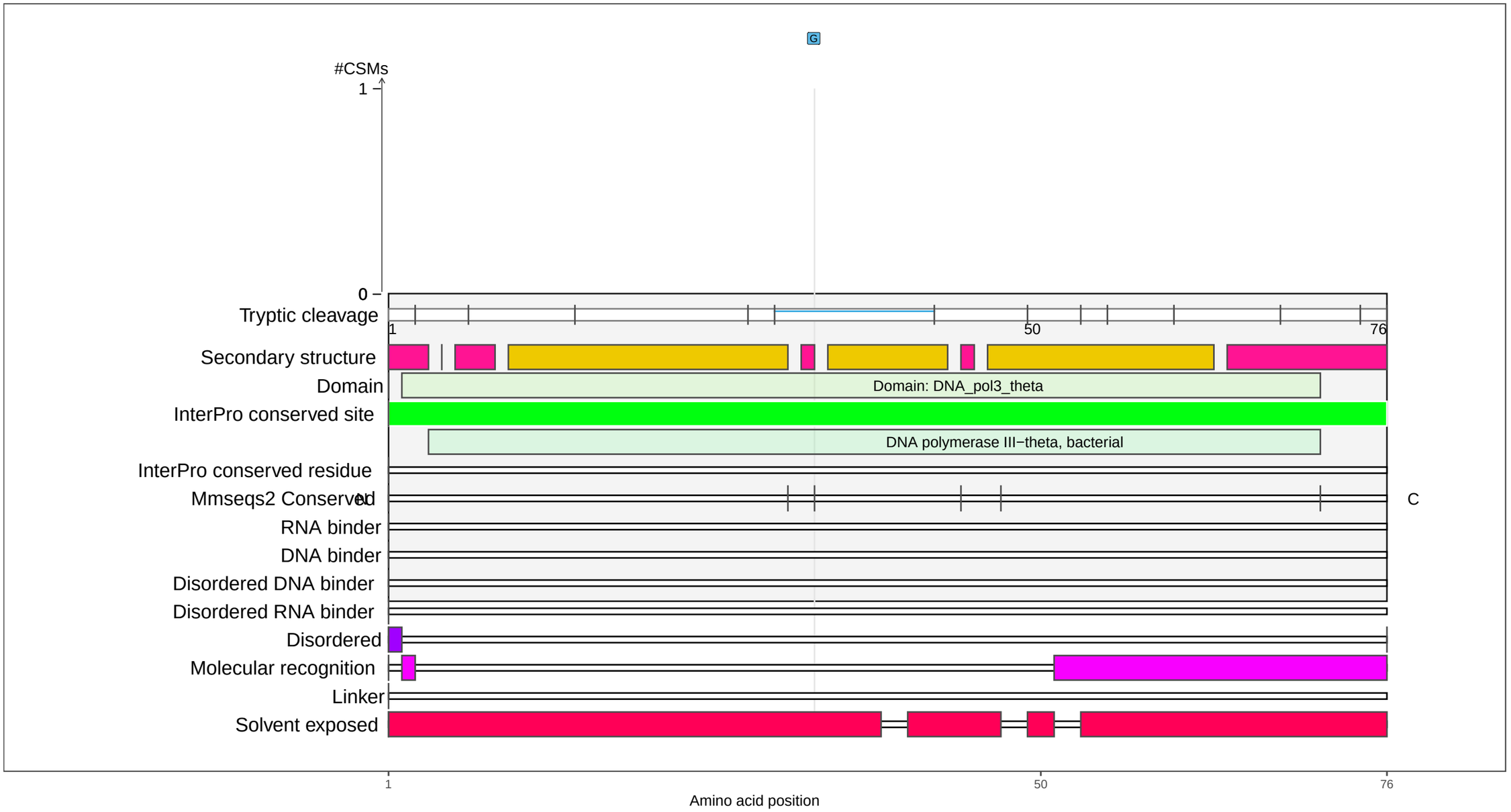
− RNA functions: not annotated



P0ABS8
HOLE_ECOLI DNA polymerase III subunit theta

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.76 (Q 52)
PAXdb E.coli [ppm]: 1.04 (Q 49)

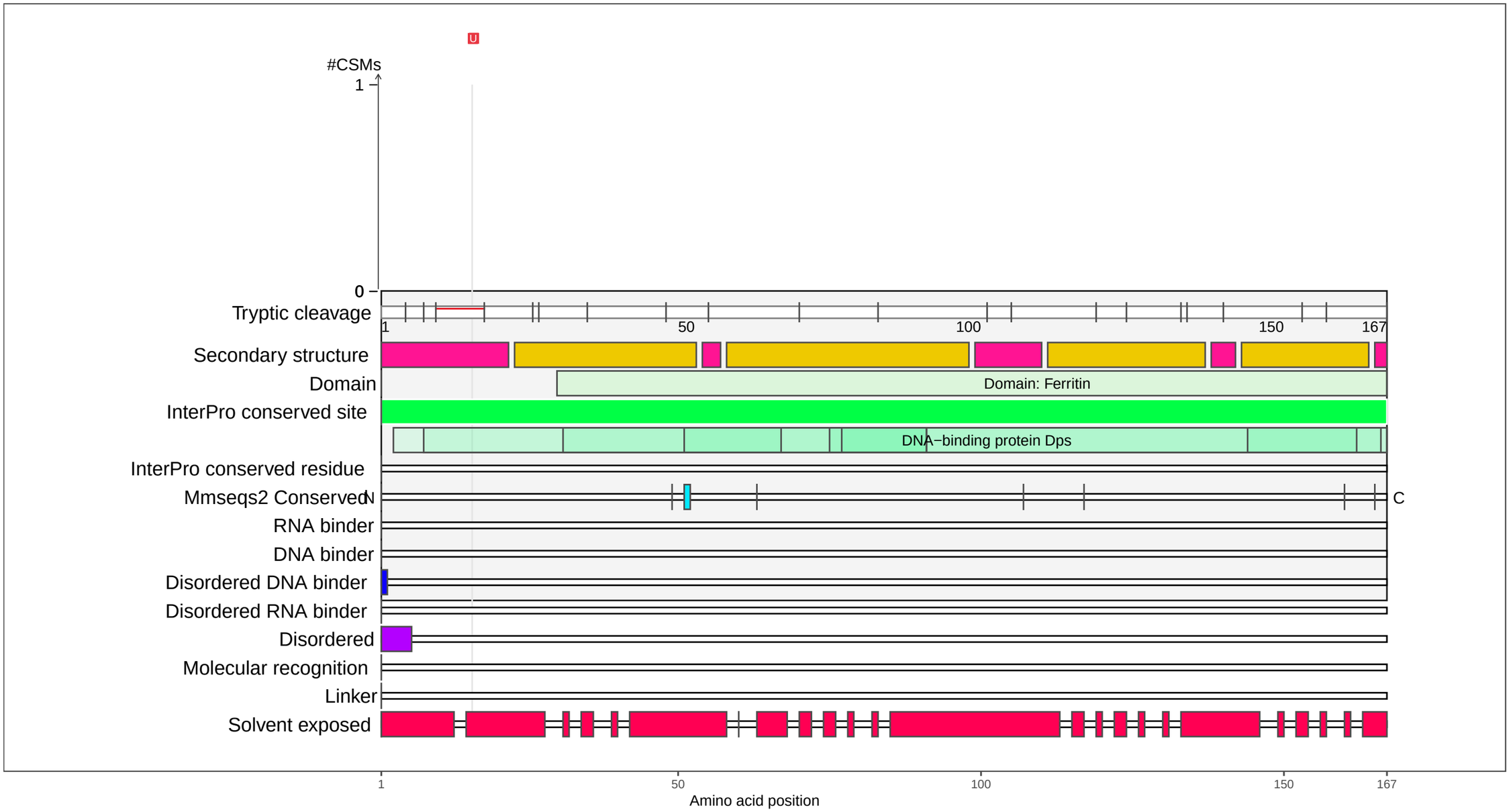
− RNA functions: not annotated



P0ABT2
DPS_ECOLI DNA protection during starvation protein

− Abundance:
tryptic [log10 Intensity]: 8.03 (Q 59)
PAXdb K12 strain [ppm]: 2.34 (Q 71)
PAXdb E.coli [ppm]: 3.49 (Q 99)

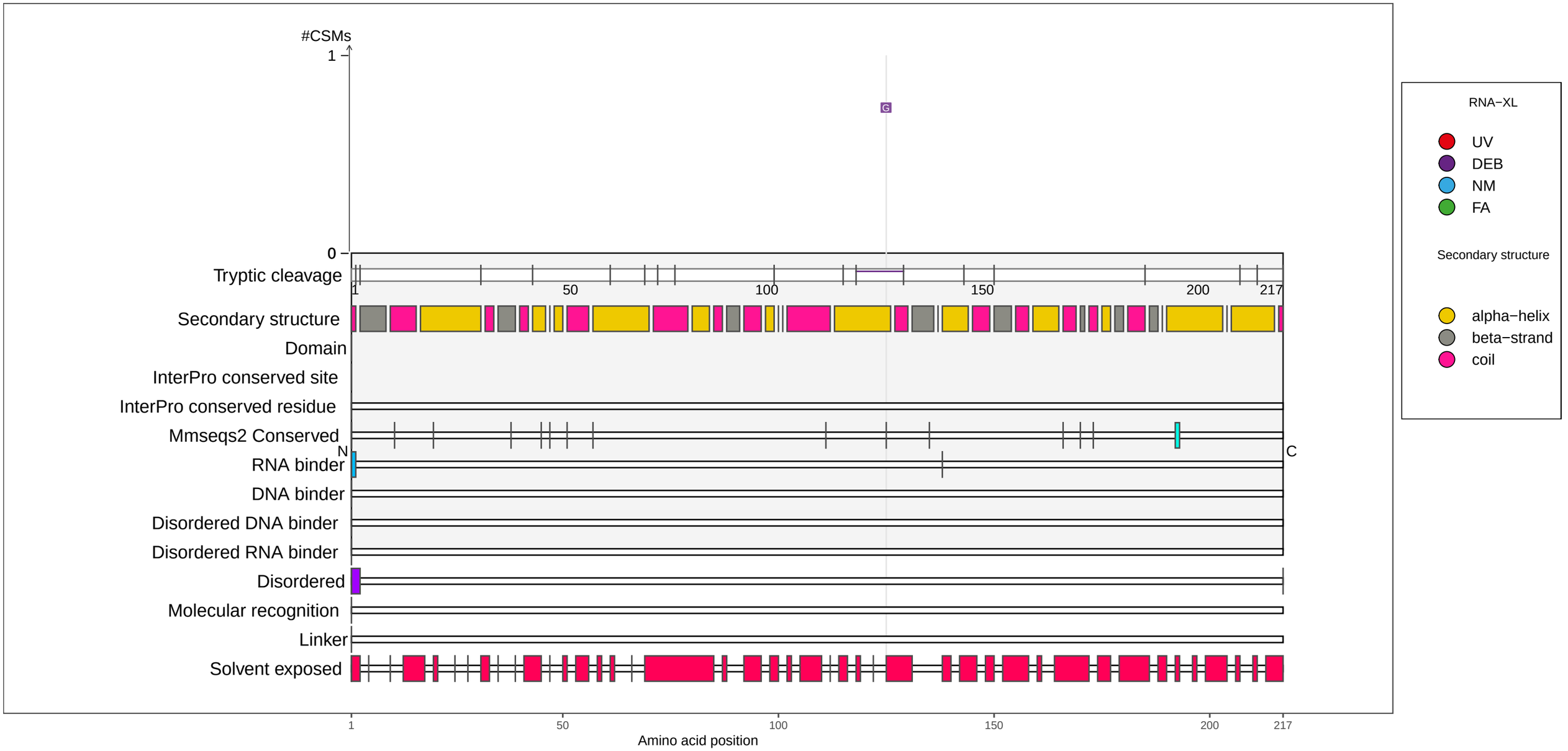
− RNA functions: not annotated



P0ABU5
ELBB_ECOLI Glyoxalase ElbB

− Abundance:
tryptic [log10 Intensity]: 8.08 (Q 60)
PAXdb K12 strain [ppm]: 1.72 (Q 50)
PAXdb E.coli [ppm]: 2.52 (Q 86)

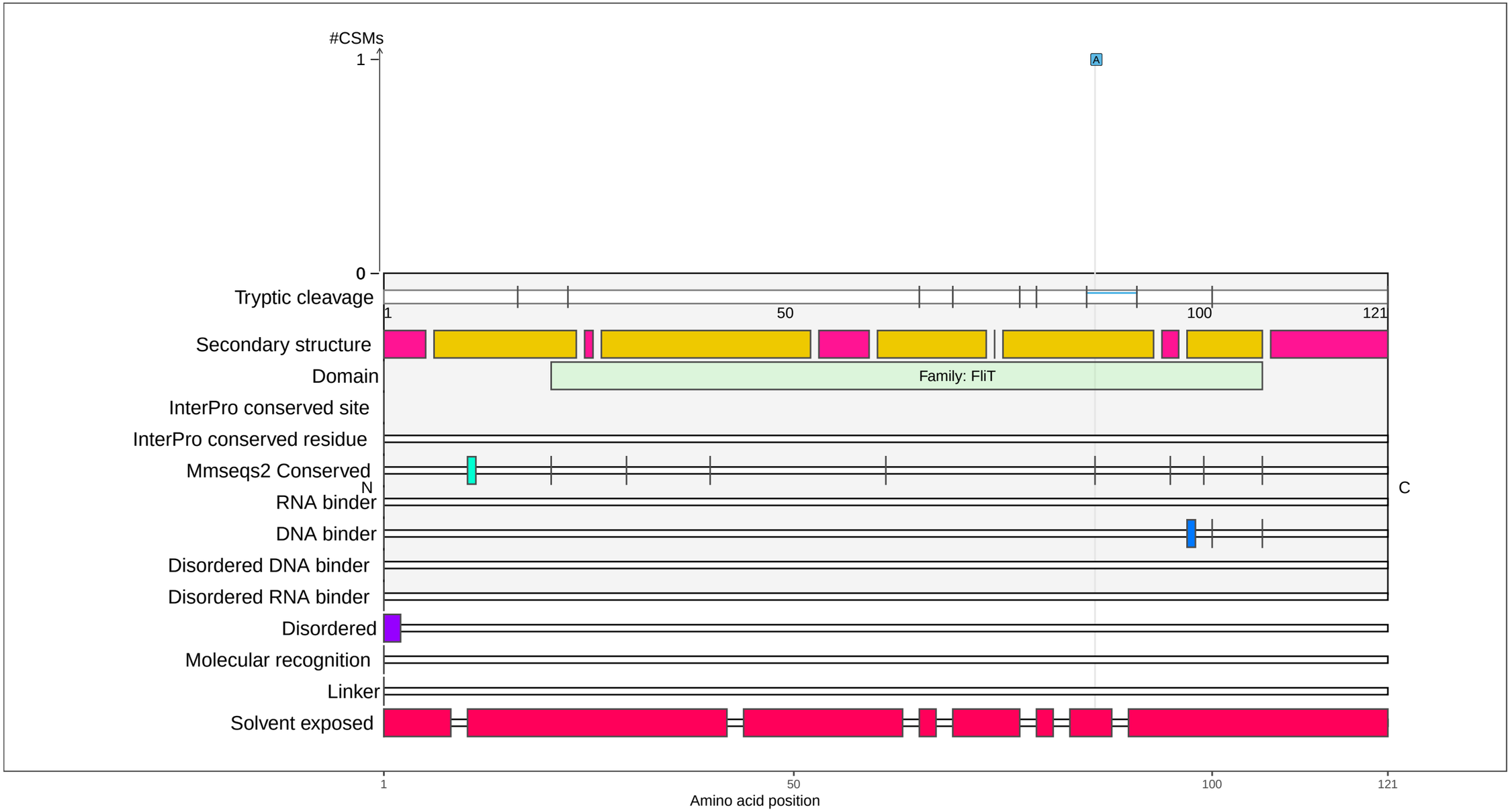
− RNA functions: not annotated



P0ABY2
FLIT_ECOLI Flagellar protein FliT

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

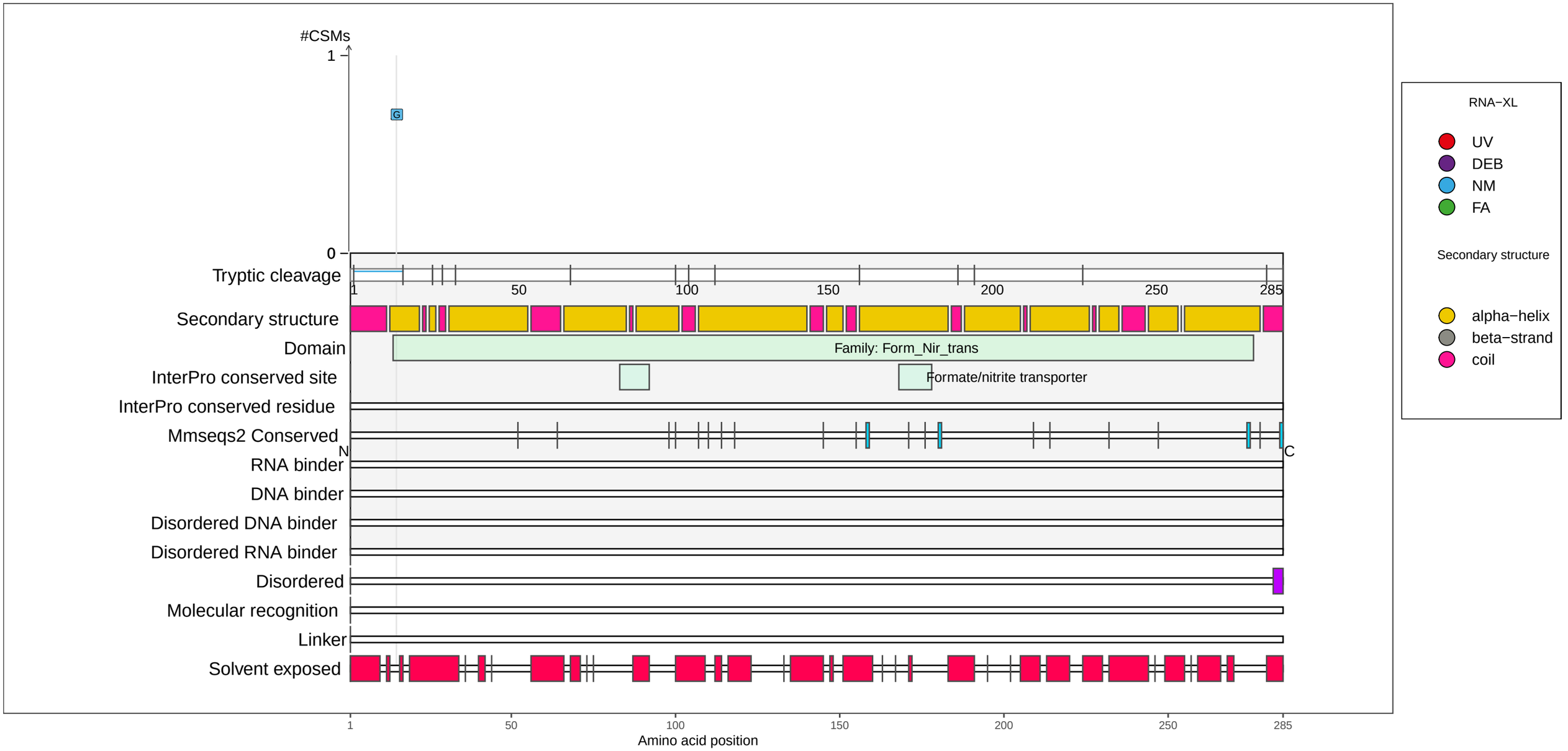
− RNA functions: not annotated



P0AC23
FOCA_ECOLI Probable formate transporter 1

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 1.68 (Q 64)

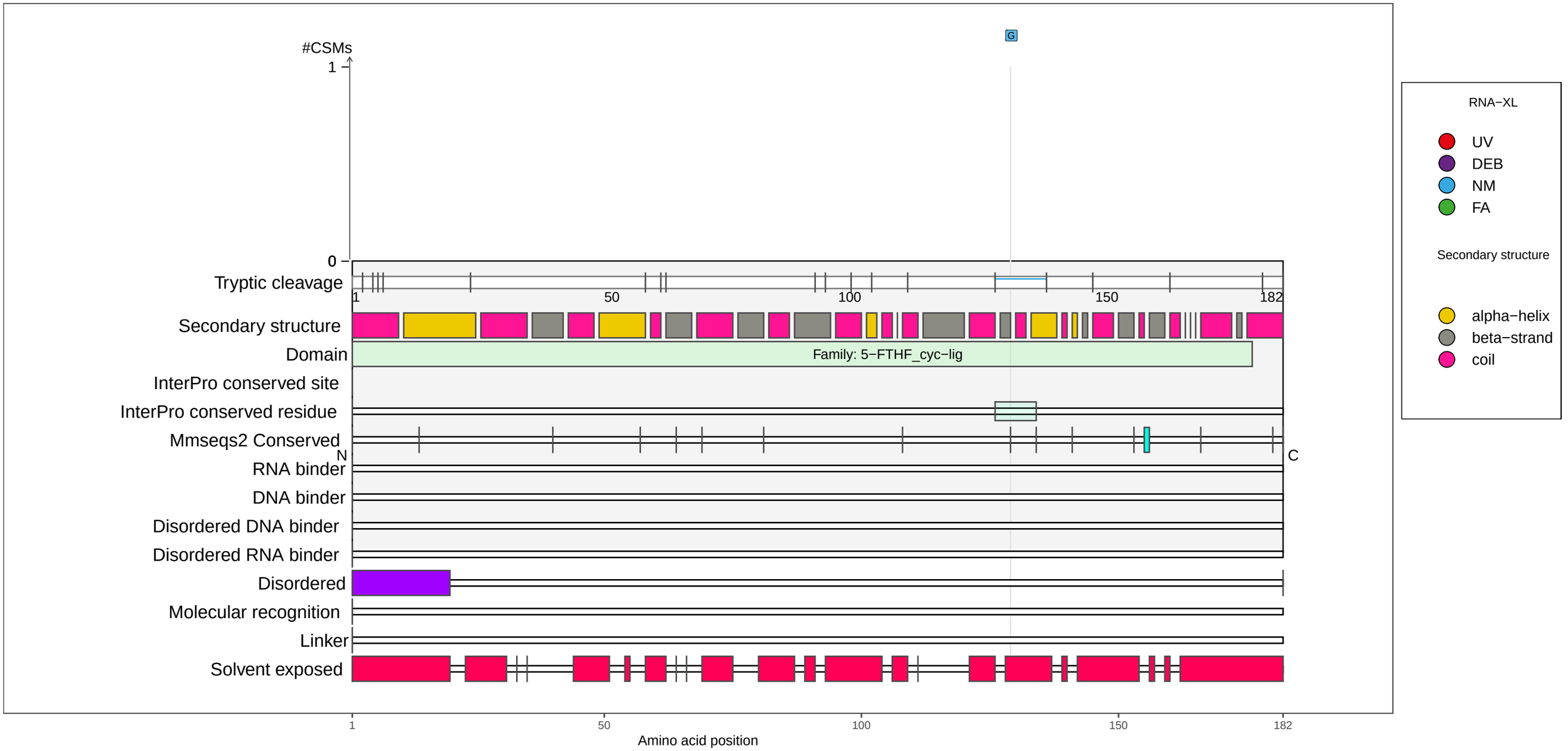
− RNA functions: not annotated



P0AC28
5FCL_ECOLI 5−formyltetrahydrofolate cyclo−ligase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.05 (Q 49)

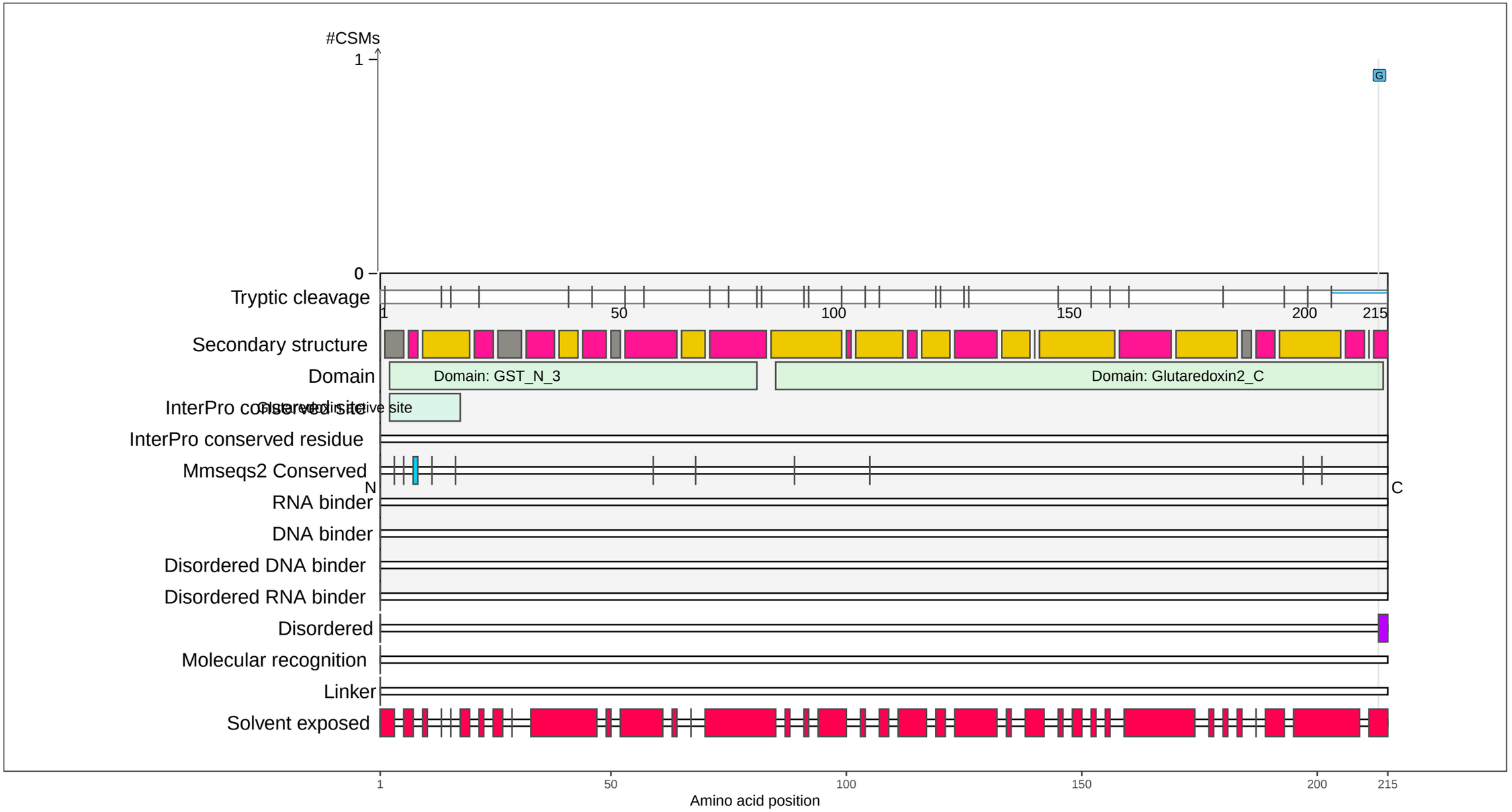
− RNA functions: not annotated



P0AC59
GLRX2_ECOLI Glutaredoxin 2

− Abundance:
tryptic [log10 Intensity]: 7.14 (Q 18)
PAXdb K12 strain [ppm]: 2.57 (Q 79)
PAXdb E.coli [ppm]: 2.69 (Q 90)

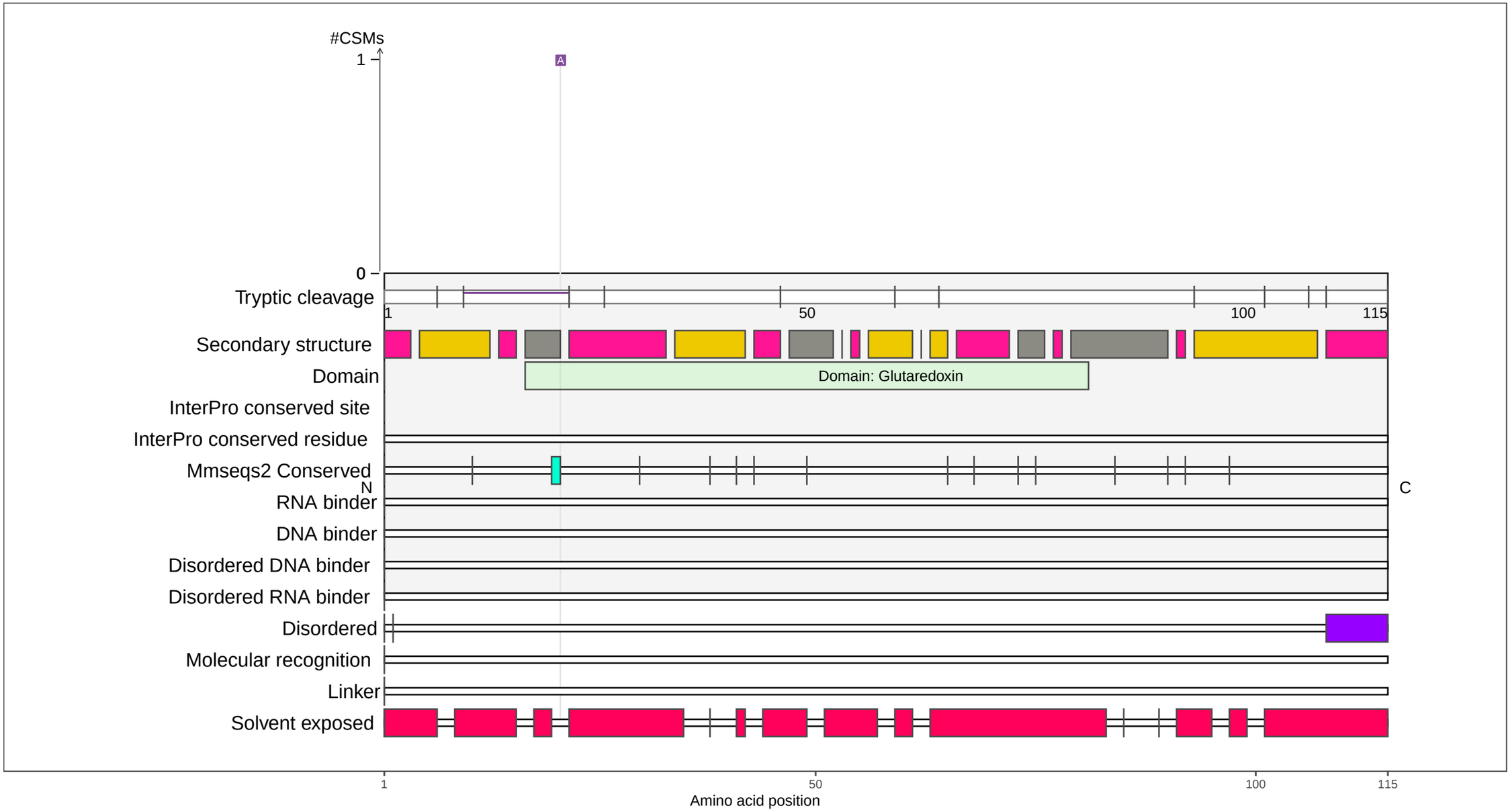
− RNA functions: not annotated

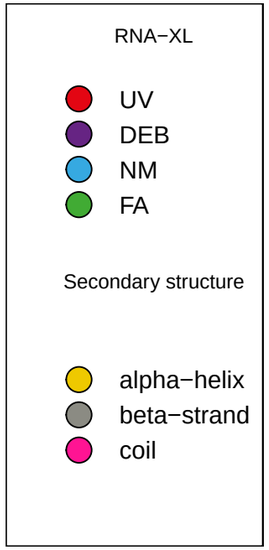


P0AC69
GLRX4_ECOLI Glutaredoxin 4

− Abundance:
tryptic [log10 Intensity]: 9.33 (Q 94)
PAXdb K12 strain [ppm]: 3.09 (Q 92)
PAXdb E.coli [ppm]: 3.21 (Q 97)

− RNA functions: not annotated

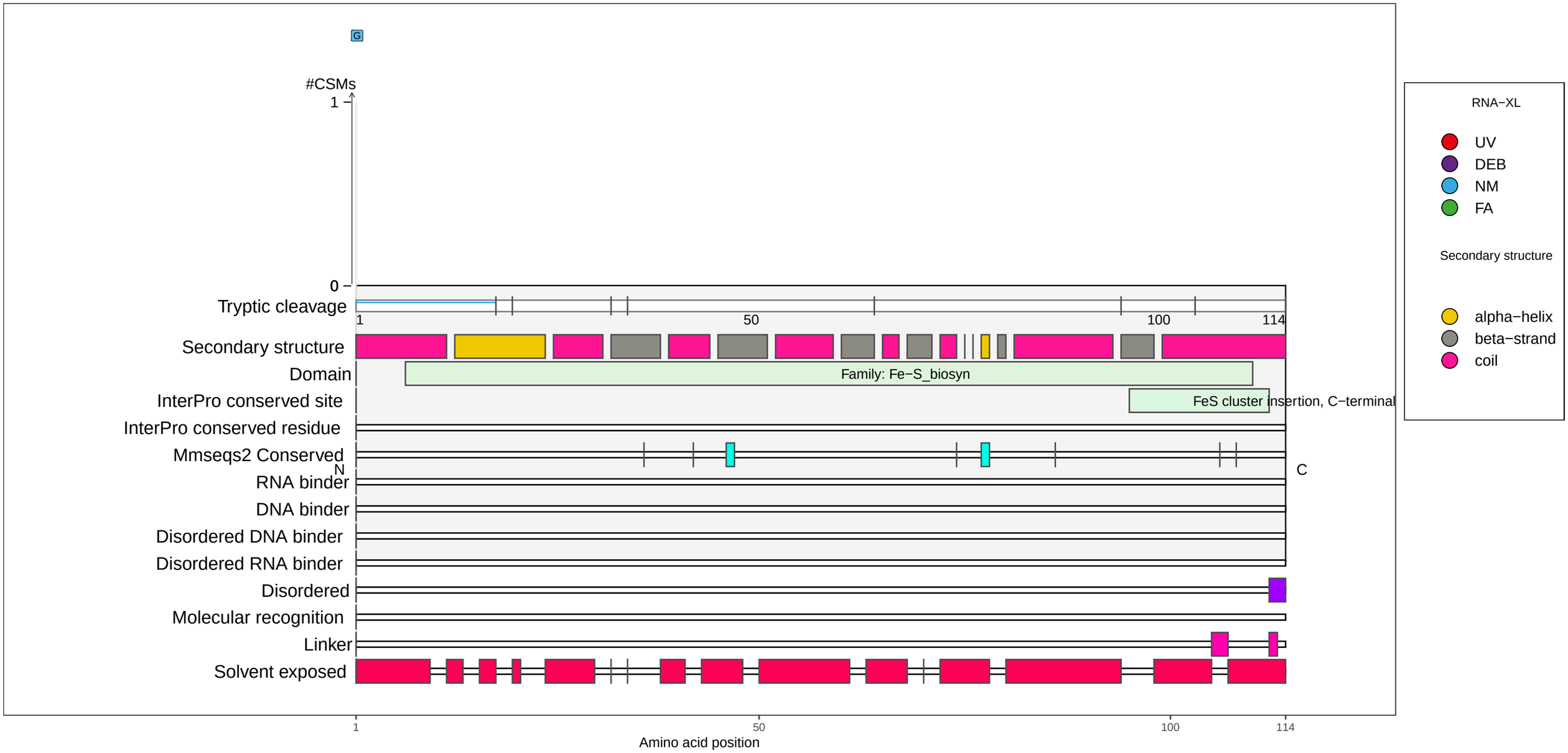




P0ACC3
ERPA_ECOLI Iron−sulfur cluster insertion protein ErpA

− Abundance:
tryptic [log10 Intensity]: 8.42 (Q 73)
PAXdb K12 strain [ppm]: 3.35 (Q 96)
PAXdb E.coli [ppm]: 2.79 (Q 91)

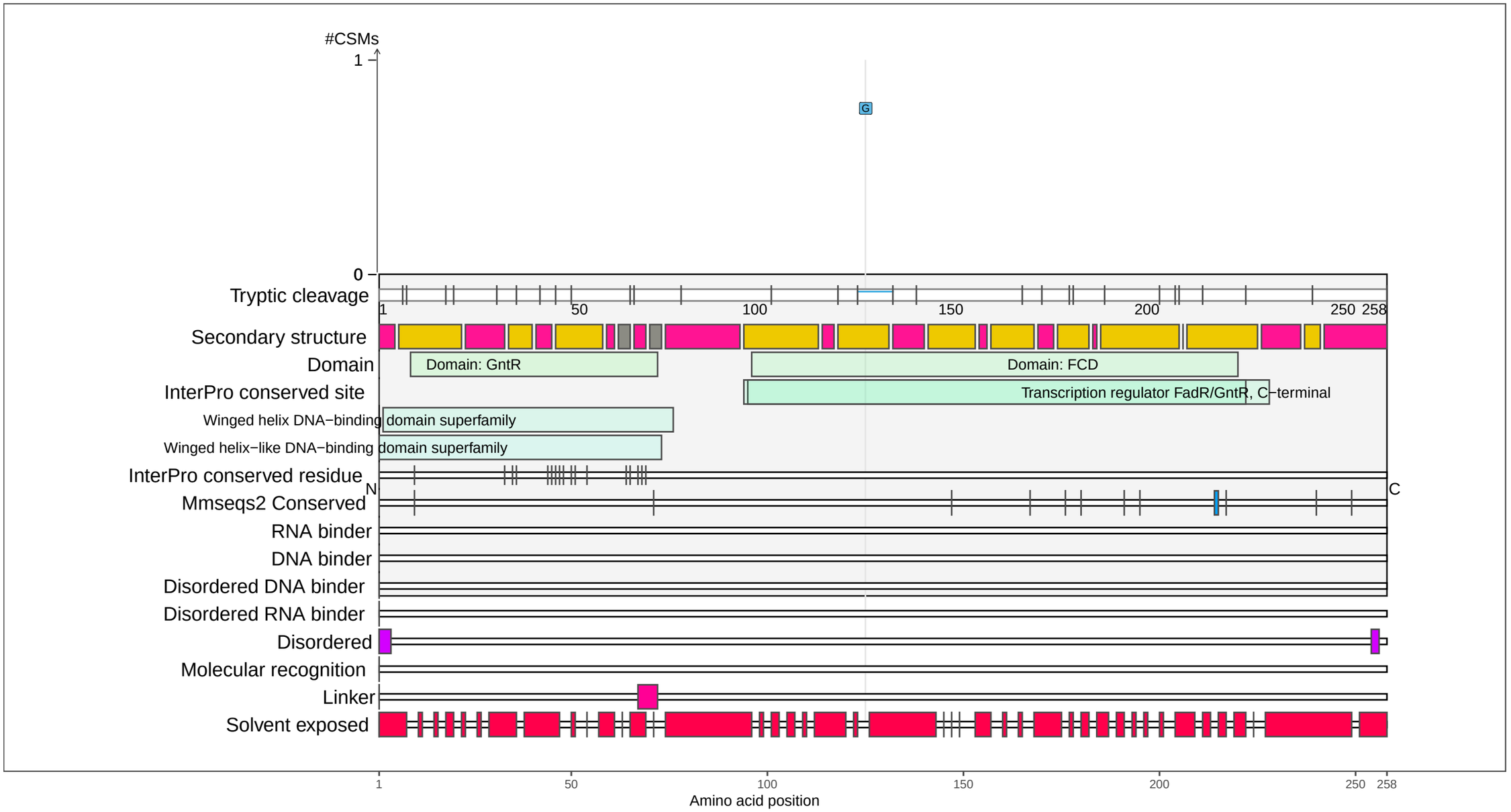
− RNA functions: not annotated



P0ACL2
EXUR_ECOLI Exu regulon transcriptional regulator

− Abundance:
tryptic [log10 Intensity]: 7.48 (Q 34)
PAXdb K12 strain [ppm]: 1.38 (Q 31)
PAXdb E.coli [ppm]: 1.43 (Q 58)

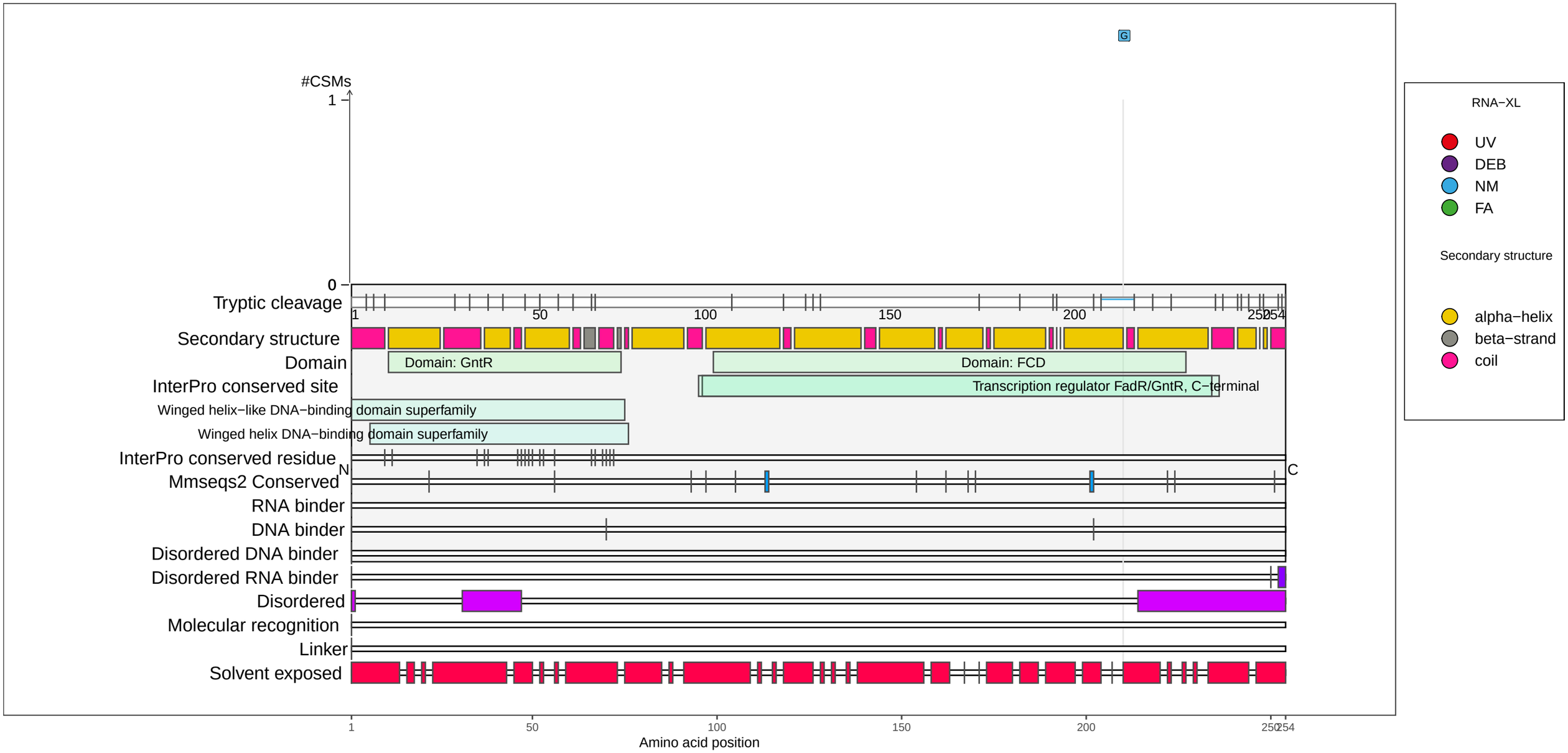
− RNA functions: not annotated



P0ACL9
PDHR_ECOLI Pyruvate dehydrogenase complex repressor

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.19 (Q 52)

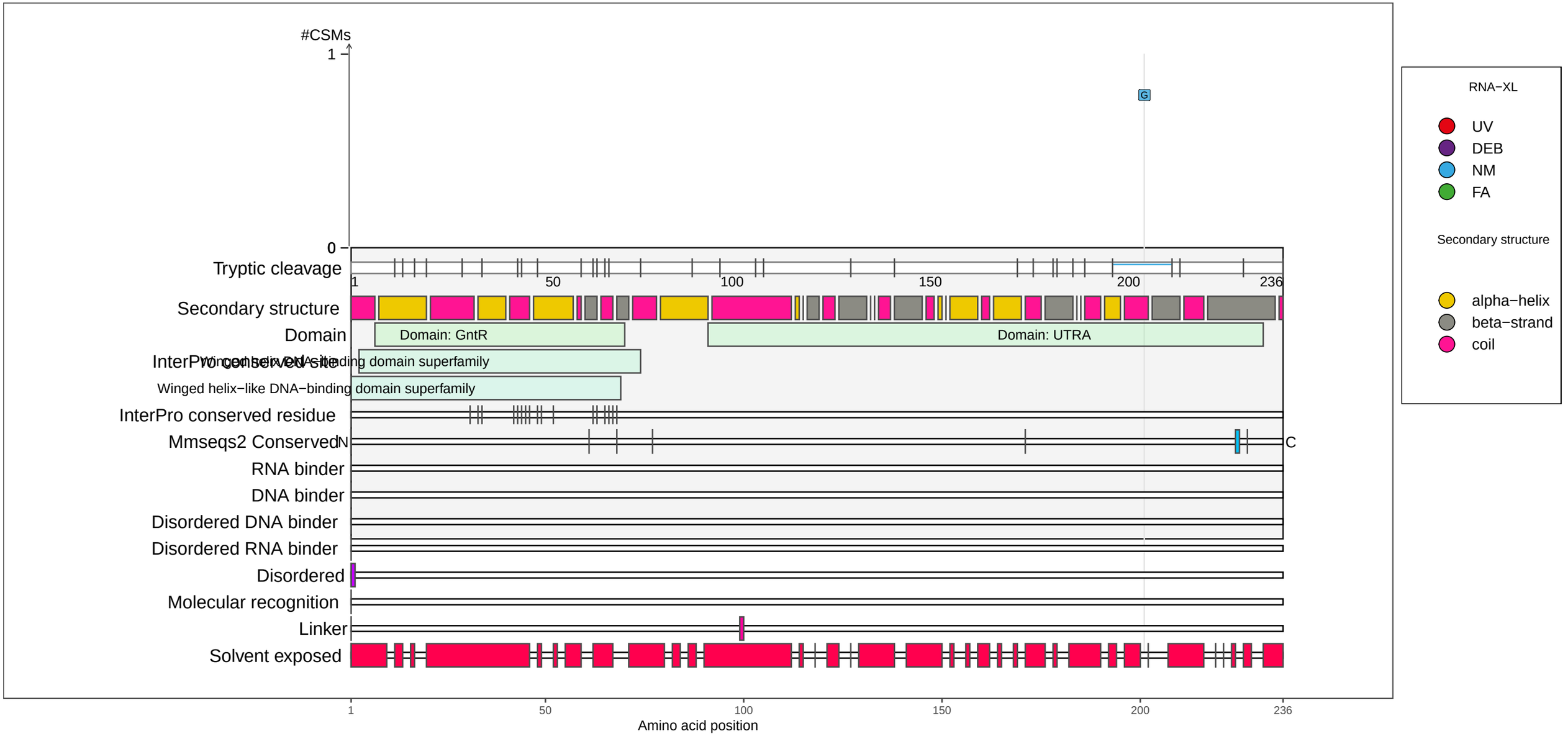
− RNA functions: not annotated



P0ACM9
YIHL_ECOLI Uncharacterized HTH−type transcriptional regulator YihL

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 0.17 (Q 28)

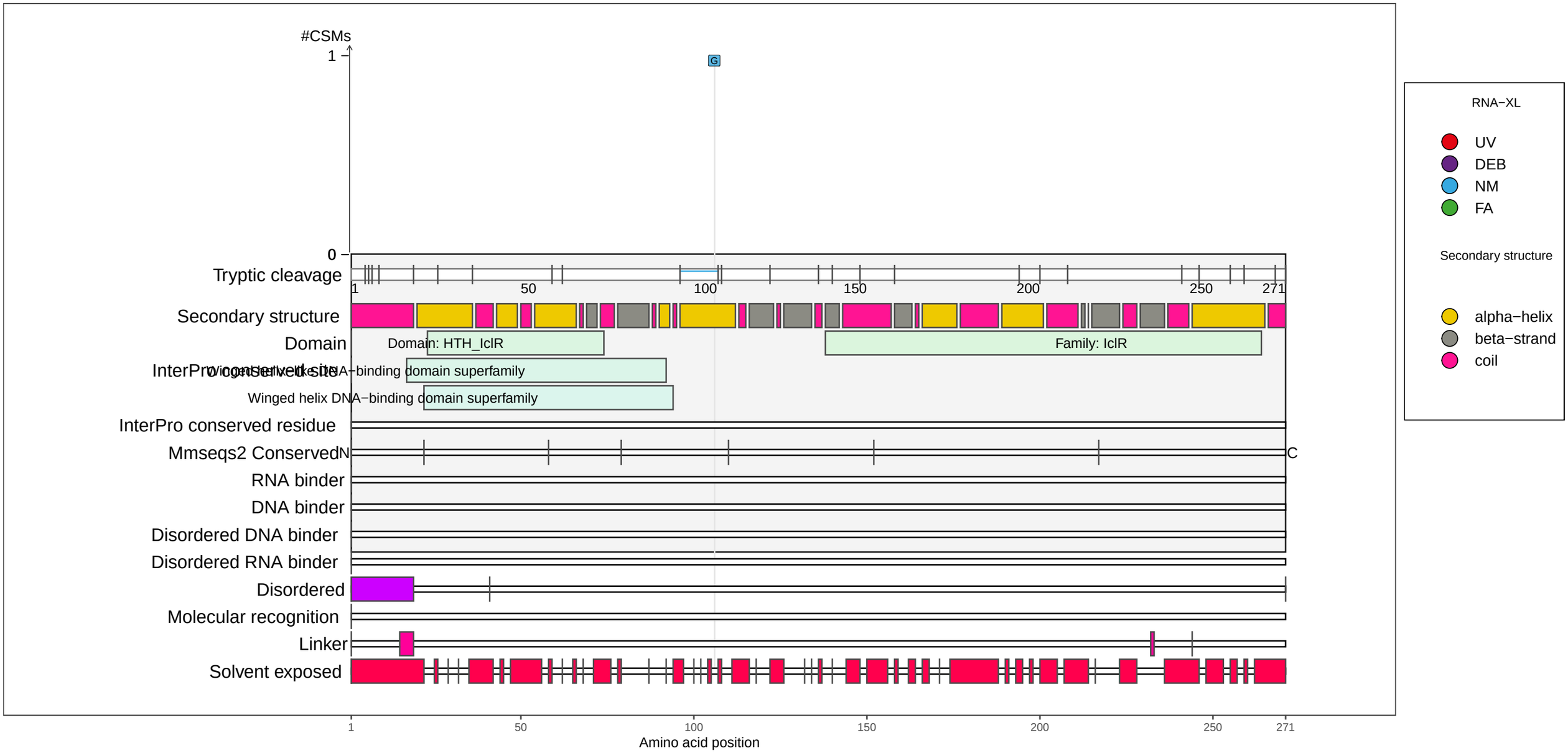
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P0ACN4
ALLR_ECOLI HTH−type transcriptional repressor AllR

− Abundance:
tryptic [log10 Intensity]: 8.31 (Q 70)
PAXdb K12 strain [ppm]: 2.47 (Q 77)
PAXdb E.coli [ppm]: 1.78 (Q 66)

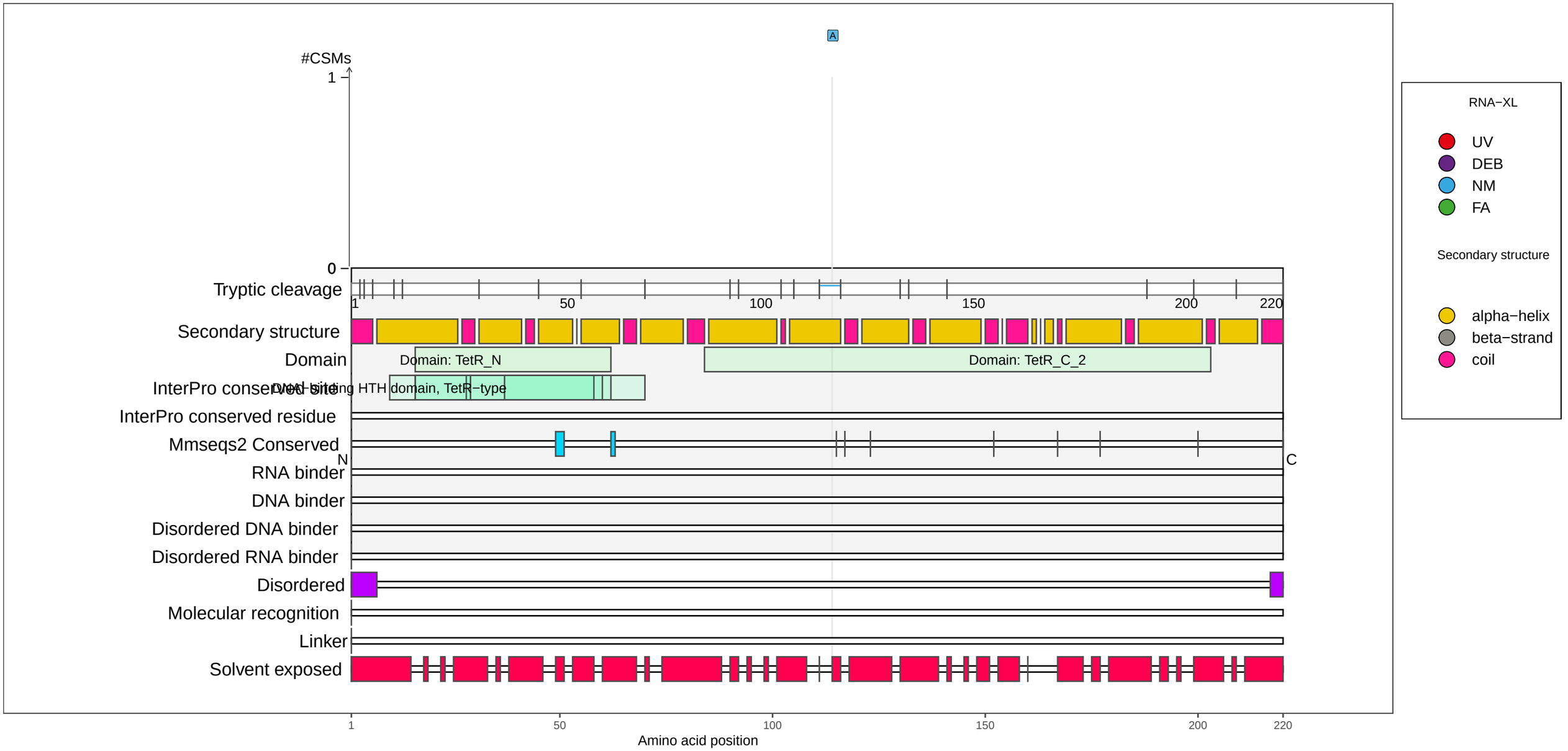
− RNA functions: not annotated



P0ACT2
ENVR_ECOLI Probable acrEF/envCD operon repressor

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.8 (Q 2)

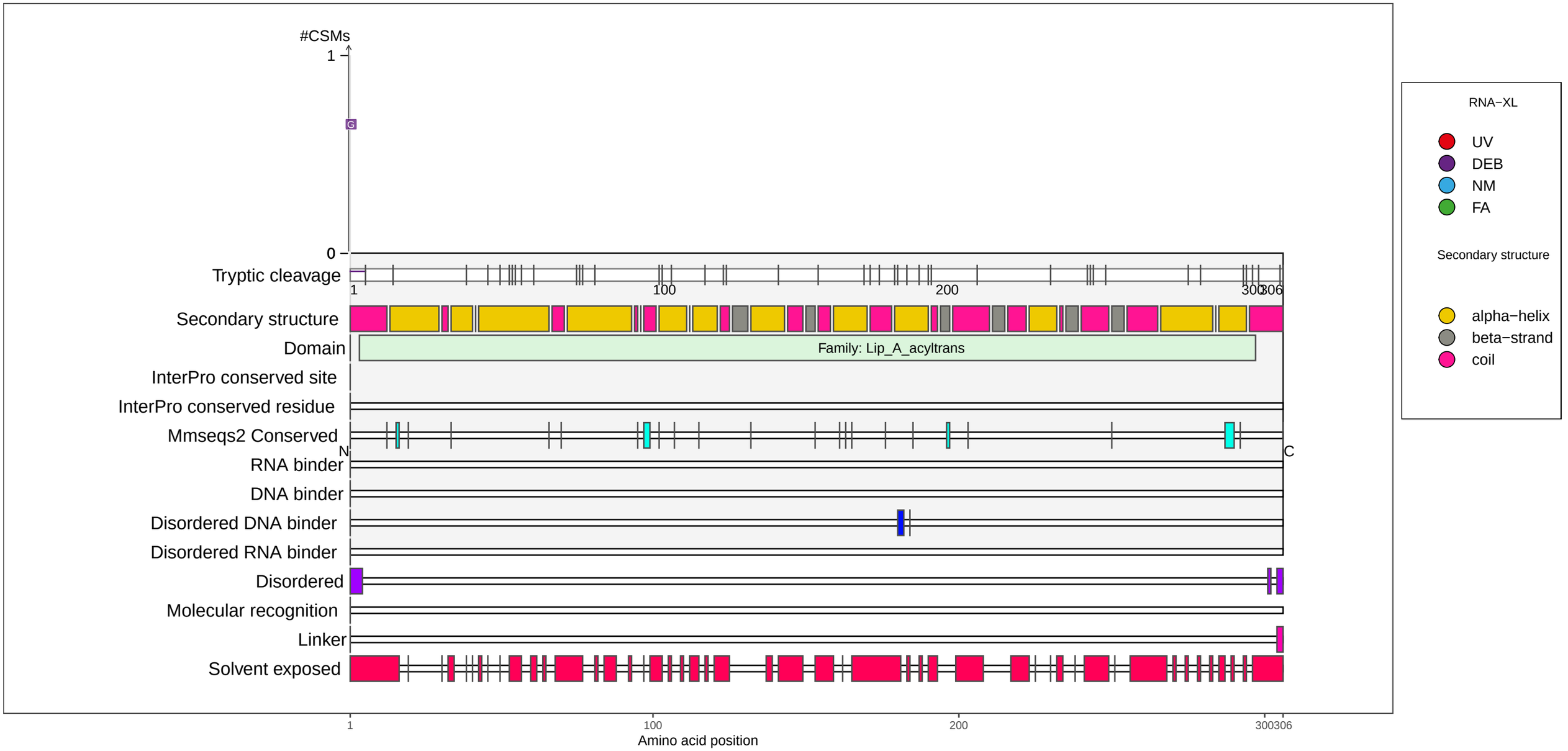
− RNA functions: not annotated



P0ACV0
LPXL_ECOLI Lipid A biosynthesis lauroyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 0.99 (Q 10)
PAXdb E.coli [ppm]: 0.04 (Q 25)

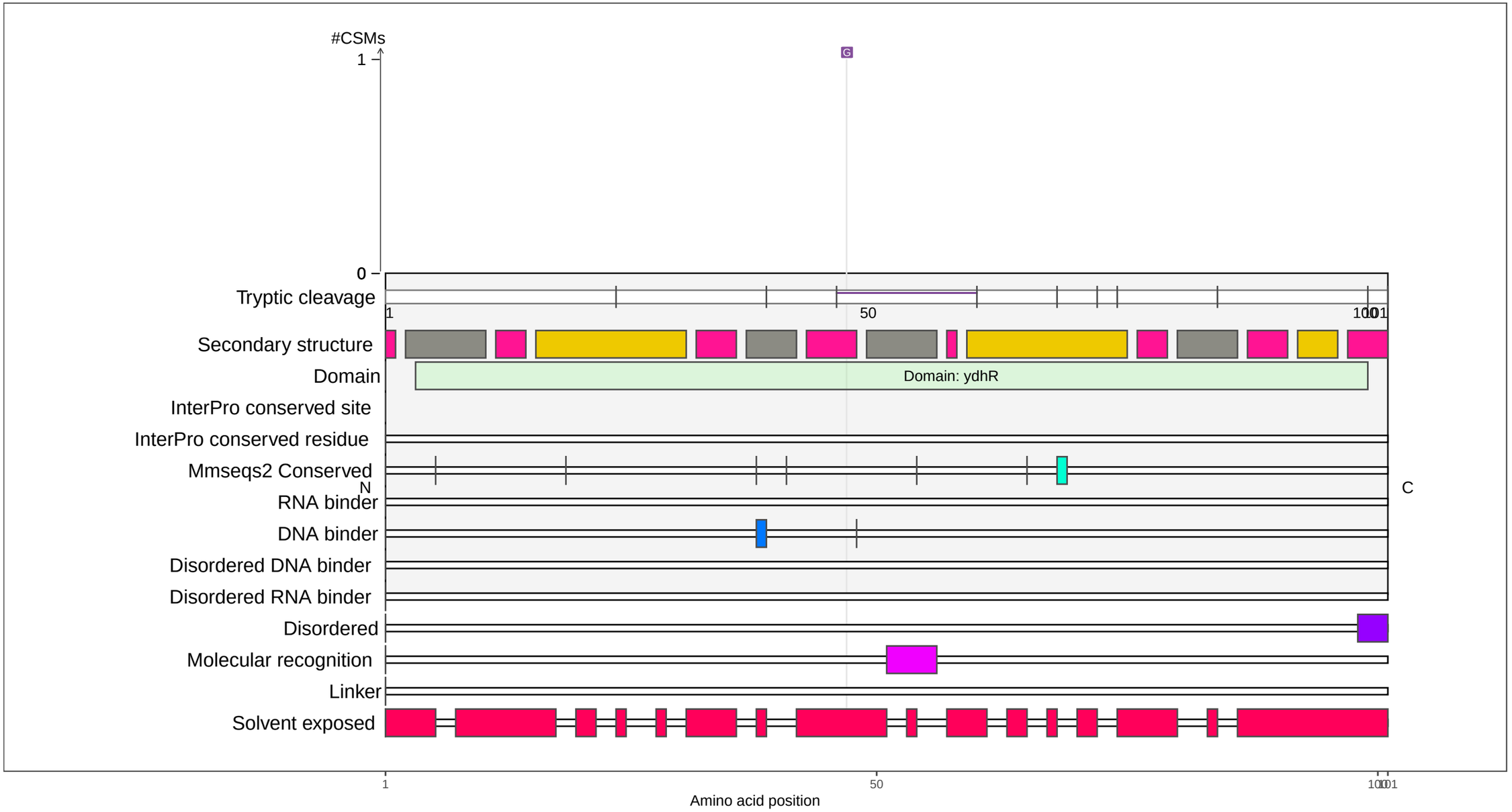
− RNA functions: not annotated



P0ACX3
YDHR_ECOLI Putative monooxygenase YdhR

− Abundance:
tryptic [log10 Intensity]: 8.45 (Q 73)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 2.85 (Q 93)

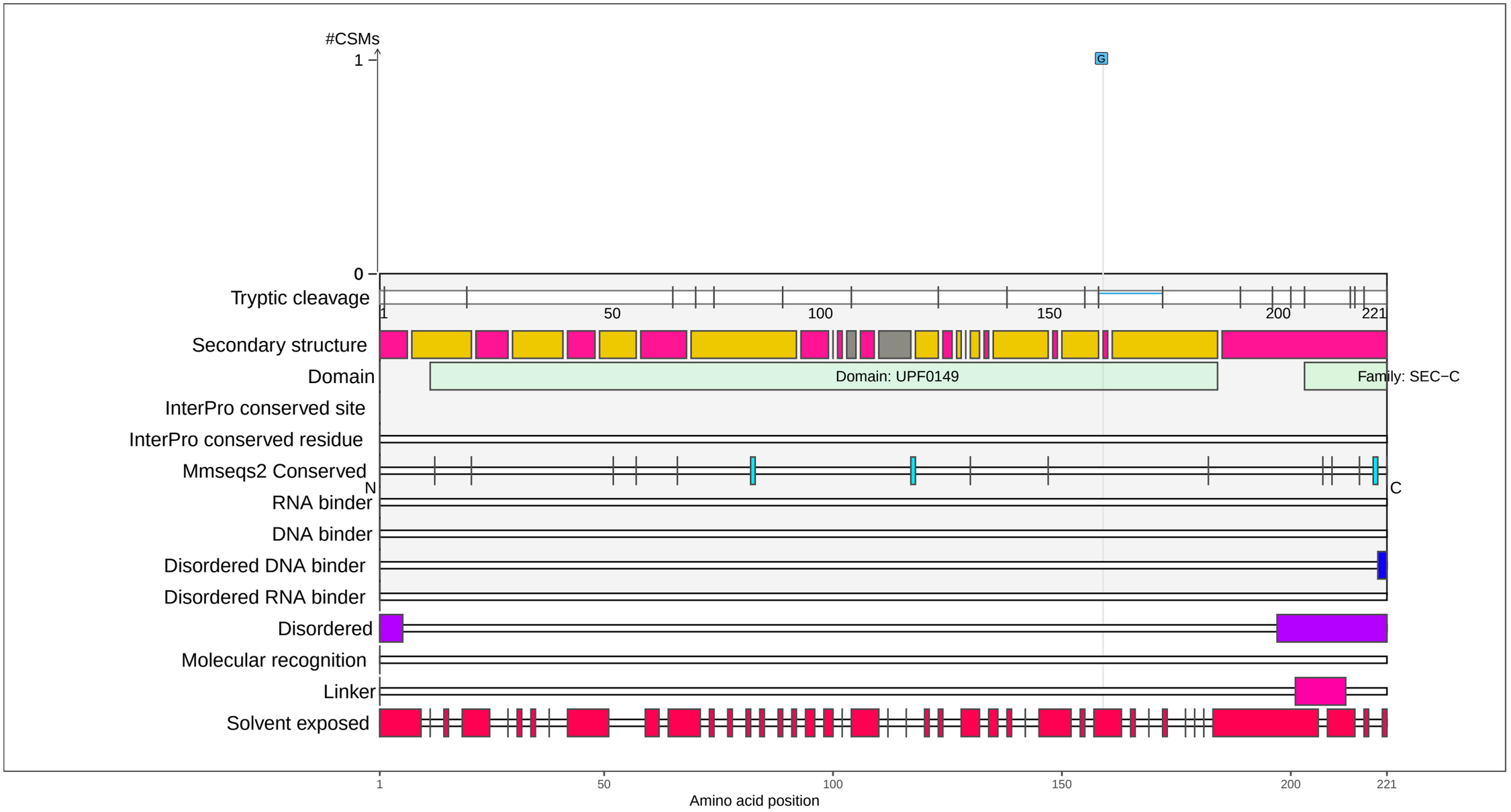
− RNA functions: not annotated



P0AD05
YECA_ECOLI Uncharacterized protein YecA

− Abundance:
tryptic [log10 Intensity]: 6.82 (Q 8)
PAXdb K12 strain [ppm]: 1.8 (Q 53)
PAXdb E.coli [ppm]: 2.45 (Q 84)

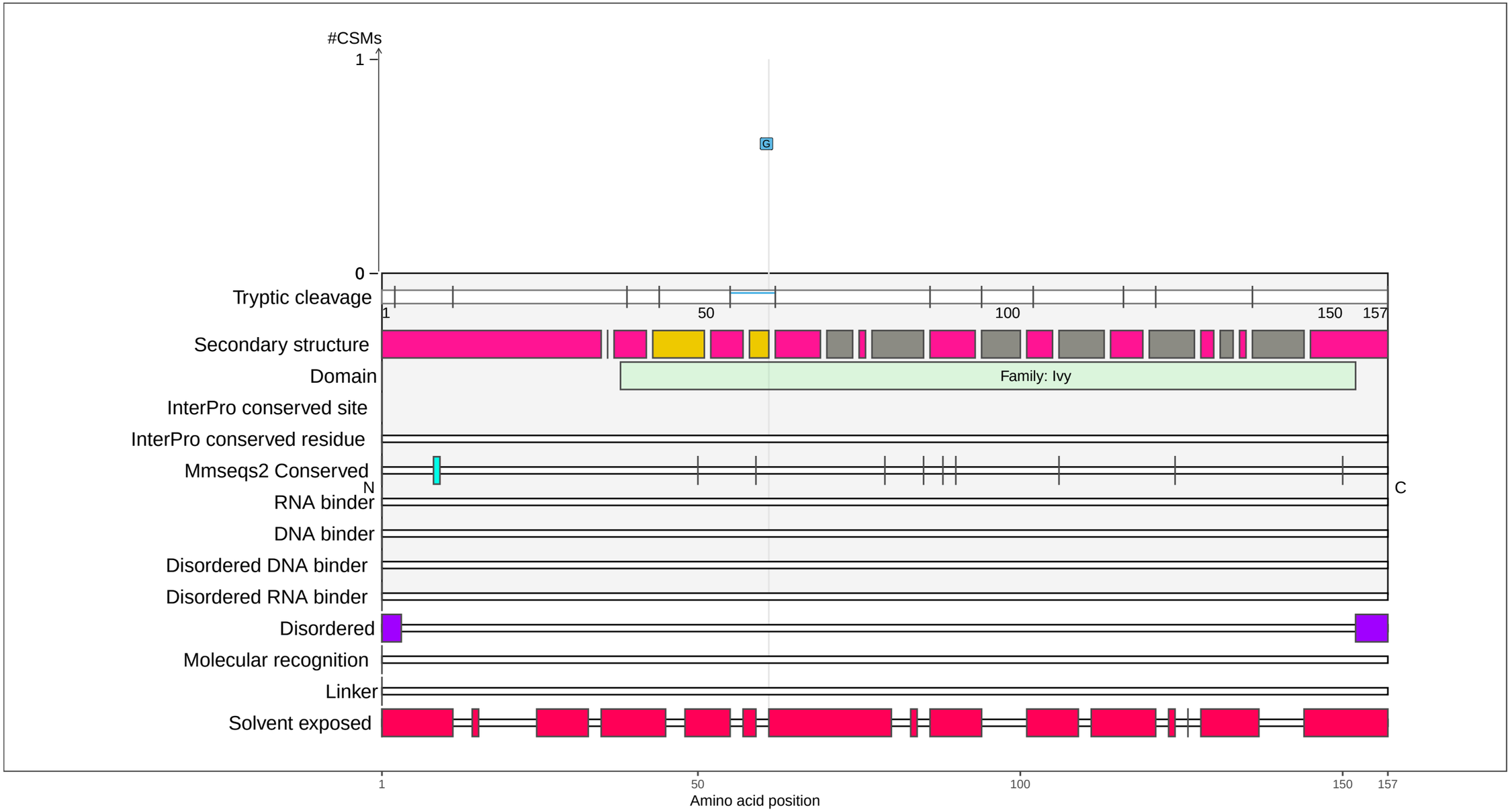
− RNA functions: not annotated



P0AD59
IVY_ECOLI Inhibitor of vertebrate lysozyme

− Abundance:
tryptic [log10 Intensity]: 7.75 (Q 47)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 2.81 (Q 92)

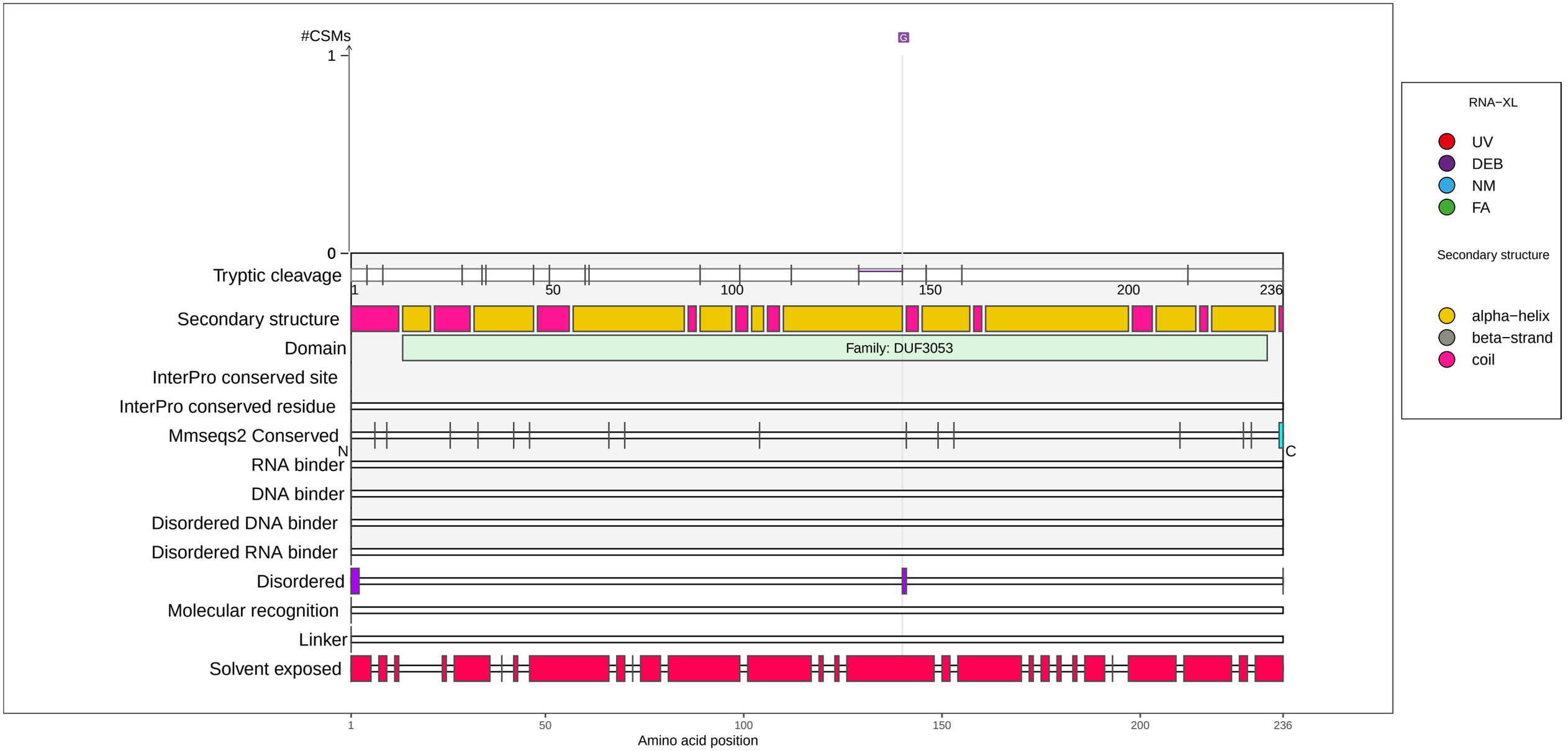
− RNA functions: not annotated



P0ADK0
YIAF_ECOLI Uncharacterized protein YiaF

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 1.37 (Q 31)
PAXdb E.coli [ppm]: 2.57 (Q 87)

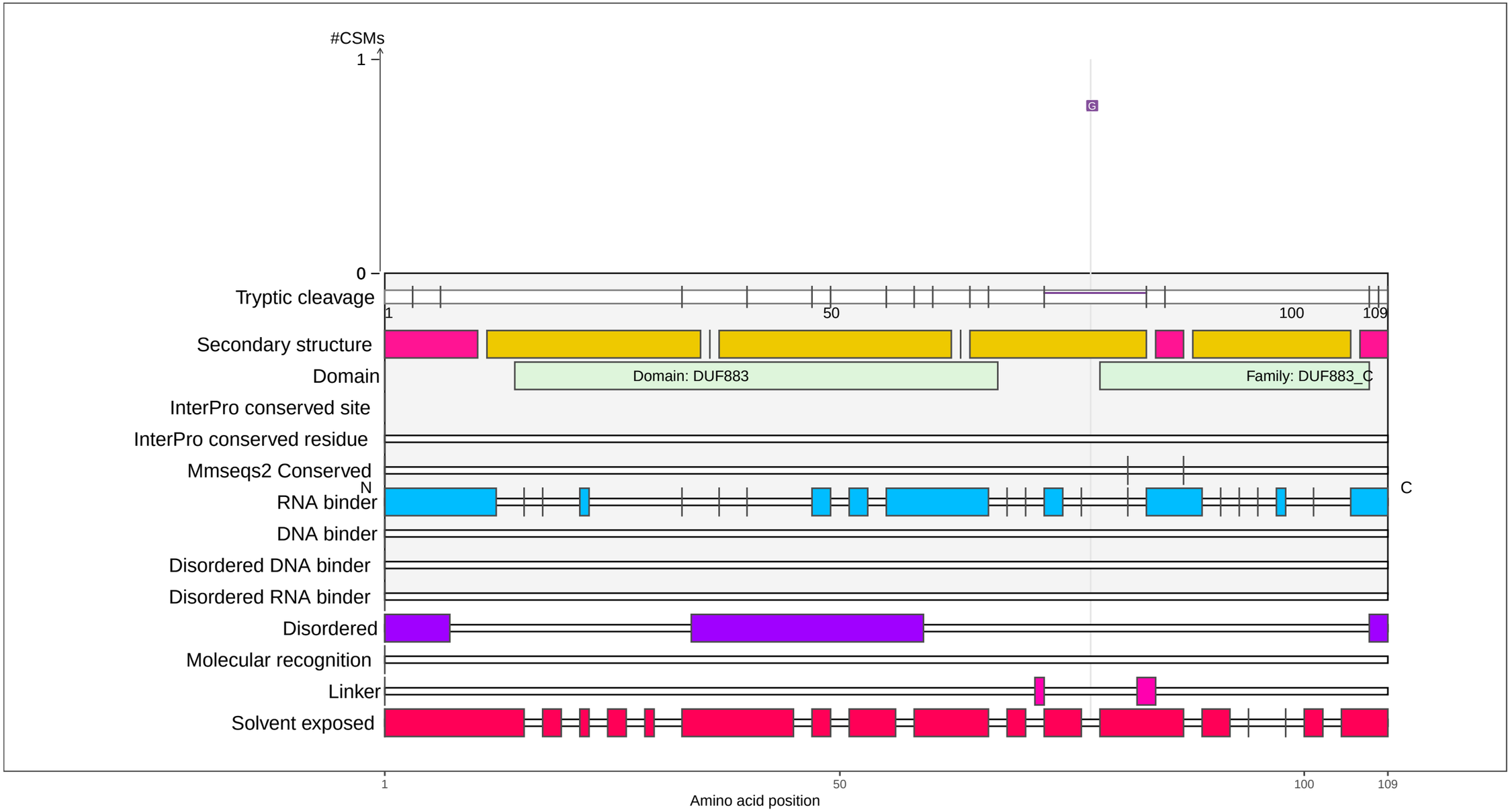
− RNA functions: not annotated



P0ADQ7
YGAM_ECOLI Uncharacterized protein YgaM

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.52 (Q 78)
PAXdb E.coli [ppm]: 2.41 (Q 83)

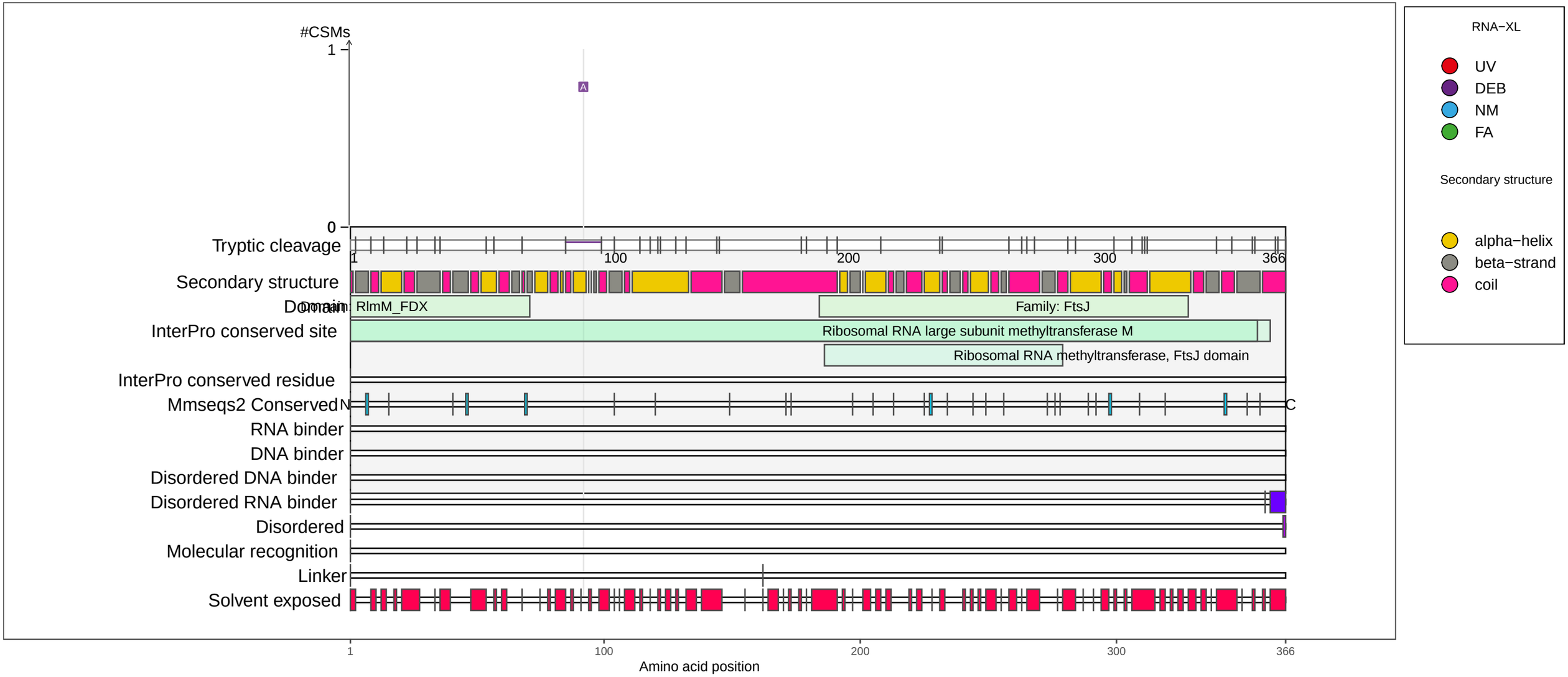
− RNA functions: not annotated



P0ADR6
RLMM_ECOLI Ribosomal RNA large subunit methyltransferase M

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 52)
PAXdb K12 strain [ppm]: 1.29 (Q 26)
PAXdb E.coli [ppm]: 1.18 (Q 52)

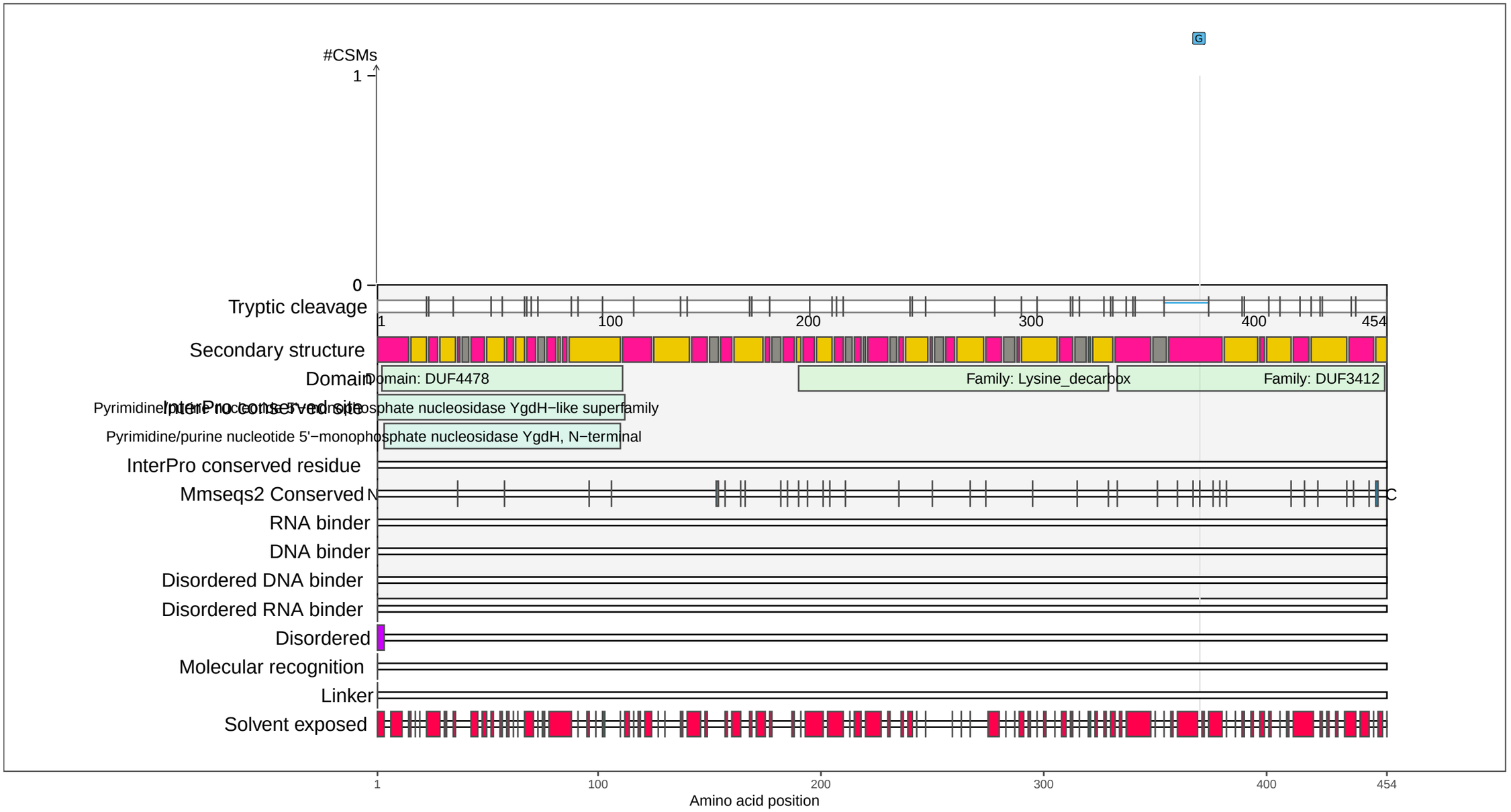
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA 2−O−methyltransferase activity
RNA metabolic process; RNA methylation; RNA methyltransferase activity; RNA modification
RNA processing; rRNA (cytosine−2−O−)−methyltransferase activity
rRNA (cytosine) methyltransferase activity; rRNA 2−O−methylation; rRNA metabolic process; rRNA methylation
rRNA methyltransferase activity; rRNA modification; rRNA processing



P0ADR8
PPNN_ECOLI Pyrimidine/purine nucleotide 5'−monophosphate nucleosidase

− Abundance:
tryptic [log10 Intensity]: 8.63 (Q 79)
PAXdb K12 strain [ppm]: 2.42 (Q 75)
PAXdb E.coli [ppm]: 1.7 (Q 64)

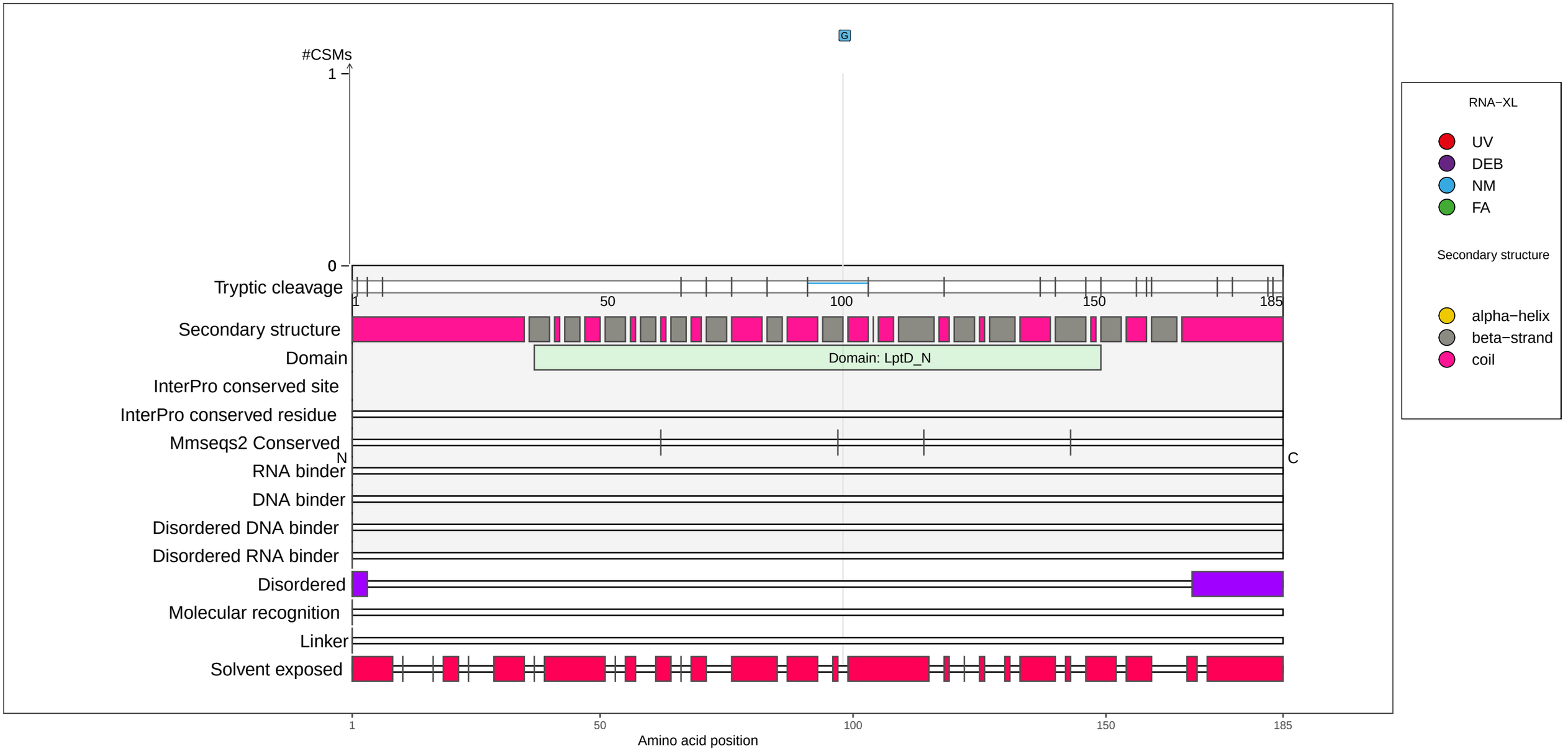
− RNA functions: not annotated



P0ADV1
LPTA_ECOLI Lipopolysaccharide export system protein LptA

− Abundance:
tryptic [log10 Intensity]: 8.17 (Q 64)
PAXdb K12 strain [ppm]: 2.58 (Q 80)
PAXdb E.coli [ppm]: 2.04 (Q 73)

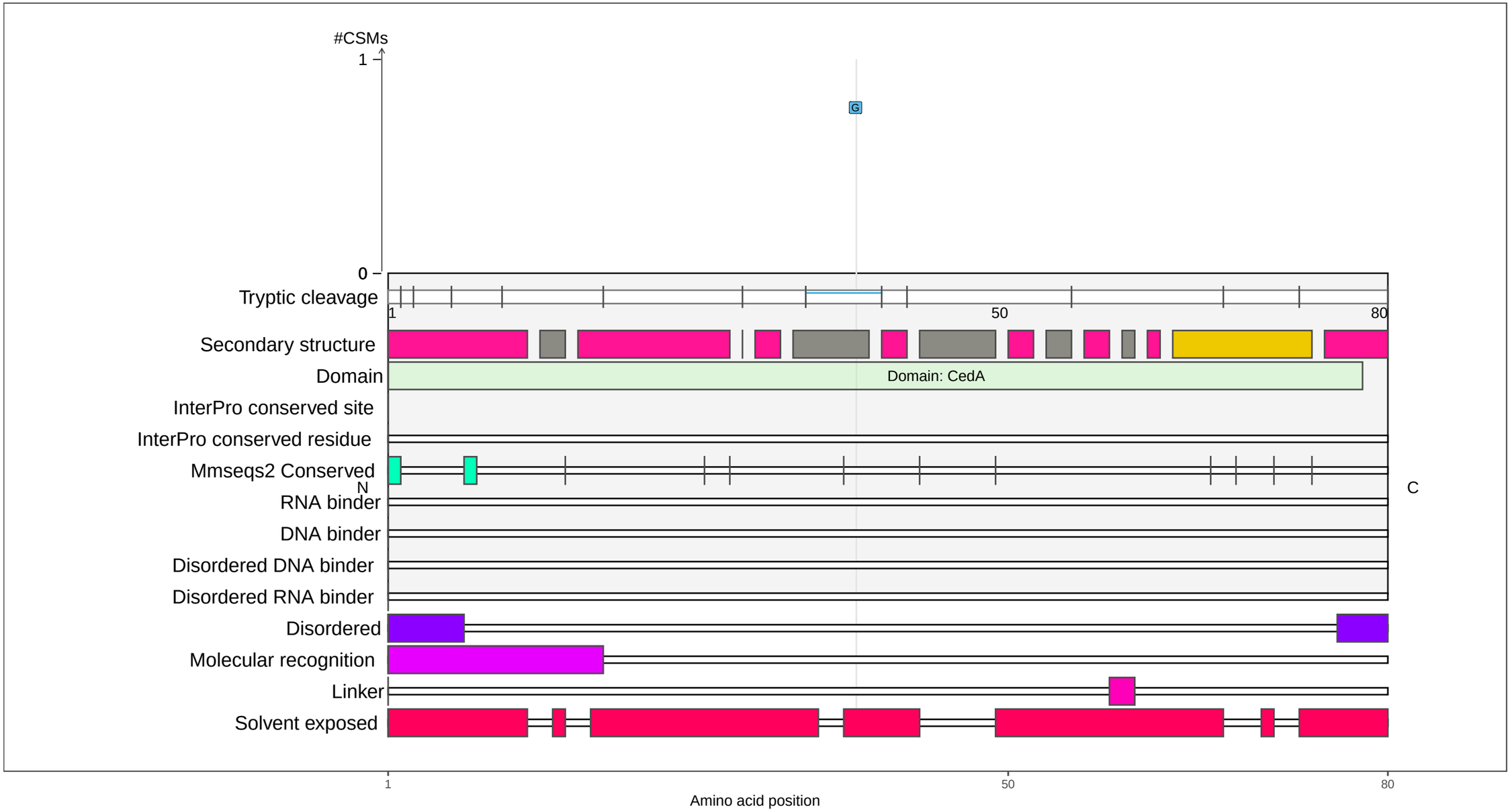
− RNA functions: not annotated



P0AE60
CEDA_ECOLI Cell division activator CedA

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 16)
PAXdb K12 strain [ppm]: 1.84 (Q 55)
PAXdb E.coli [ppm]: 1.4 (Q 57)

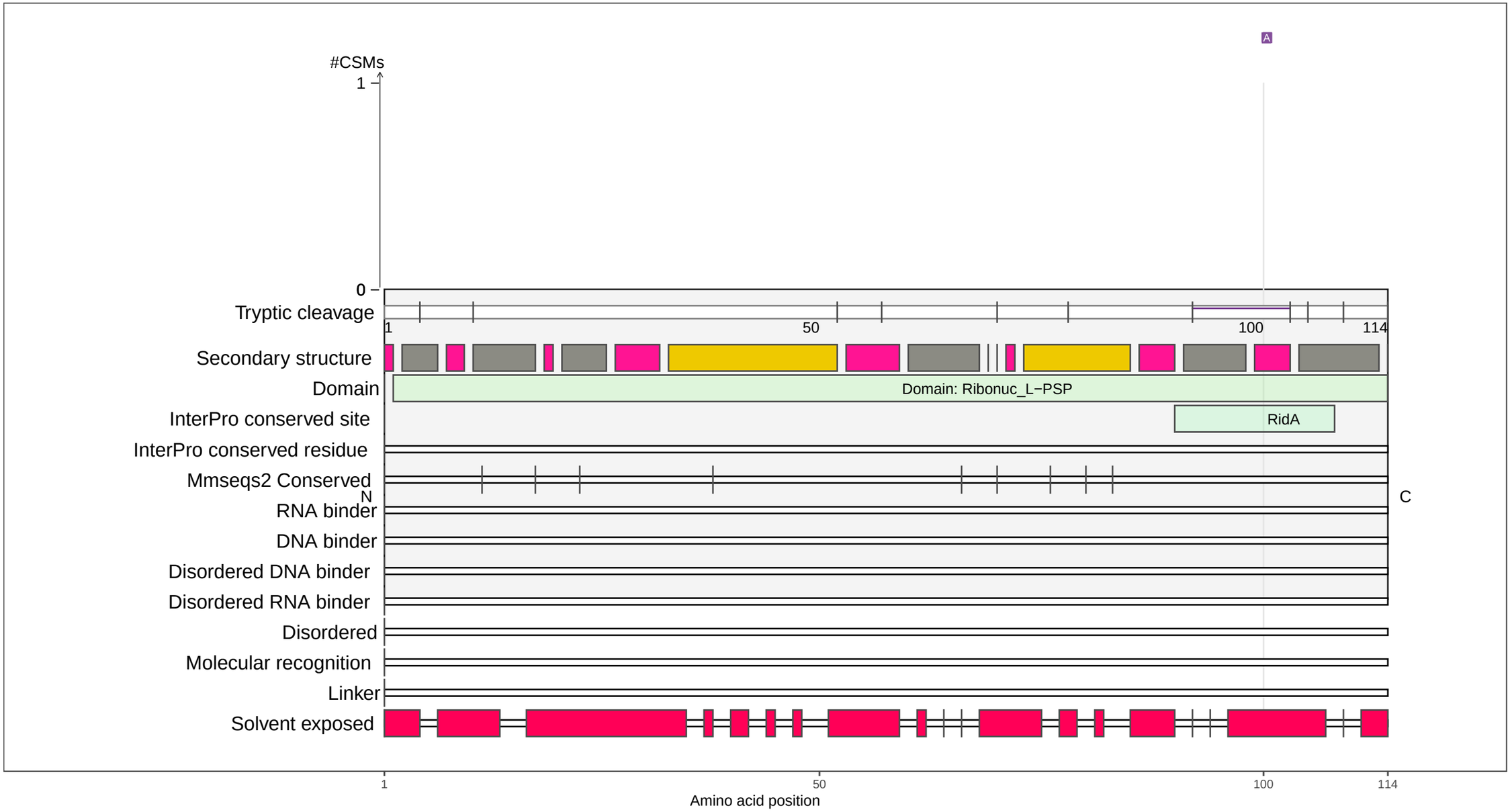
− RNA functions: not annotated



P0AEB7
YOAB_ECOLI RutC family protein YoaB

− Abundance:
tryptic [log10 Intensity]: 8.98 (Q 88)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.71 (Q 90)

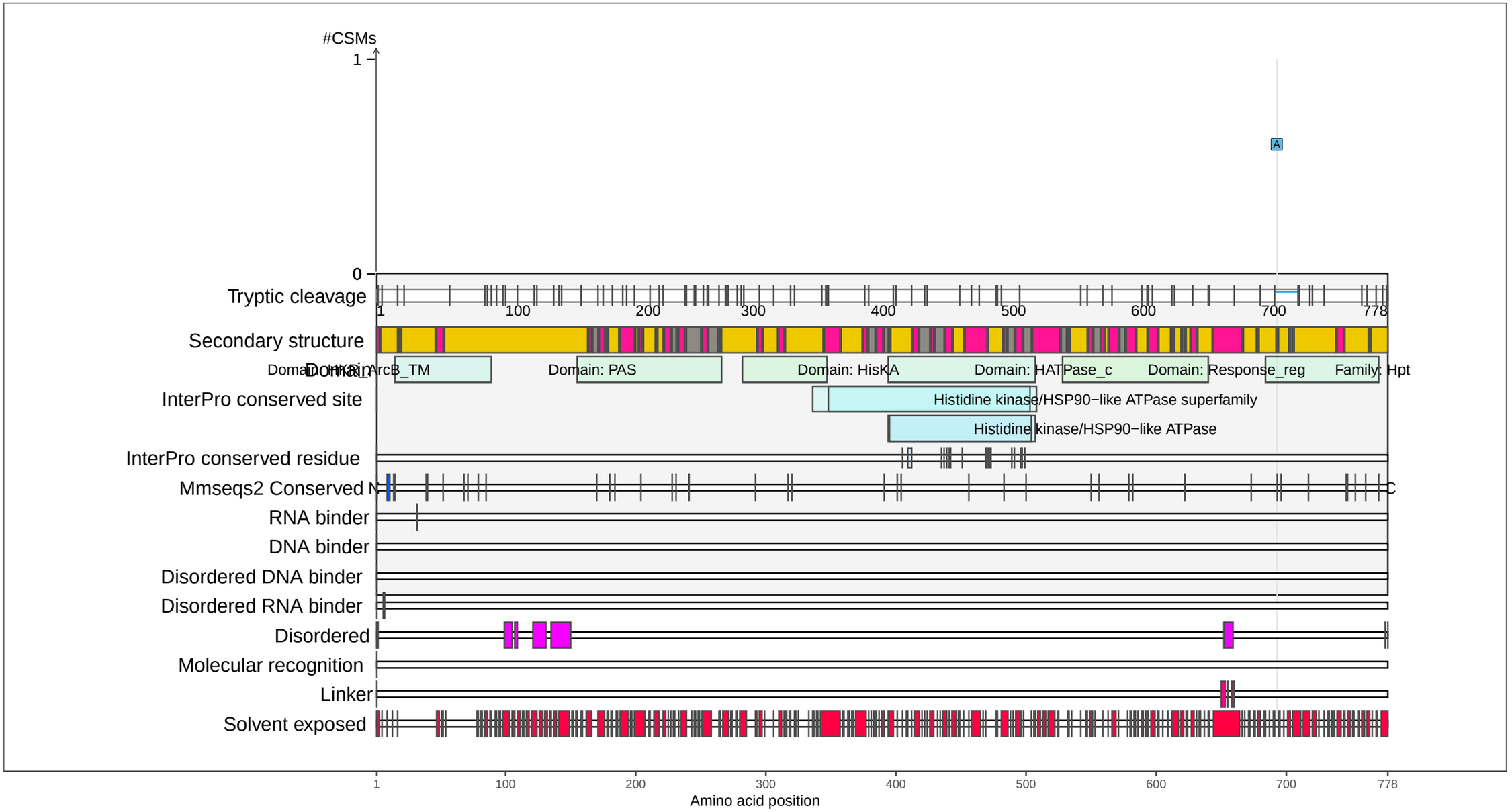
− RNA functions: not annotated

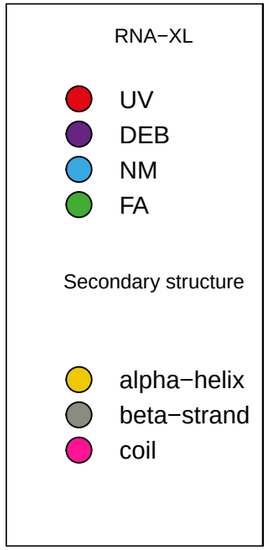


P0AEC3
ARCB_ECOLI Aerobic respiration control sensor protein ArcB

− Abundance:
tryptic [log10 Intensity]: 7.09 (Q 16)
PAXdb K12 strain [ppm]: 2.03 (Q 61)
PAXdb E.coli [ppm]: 2.18 (Q 77)

− RNA functions: not annotated

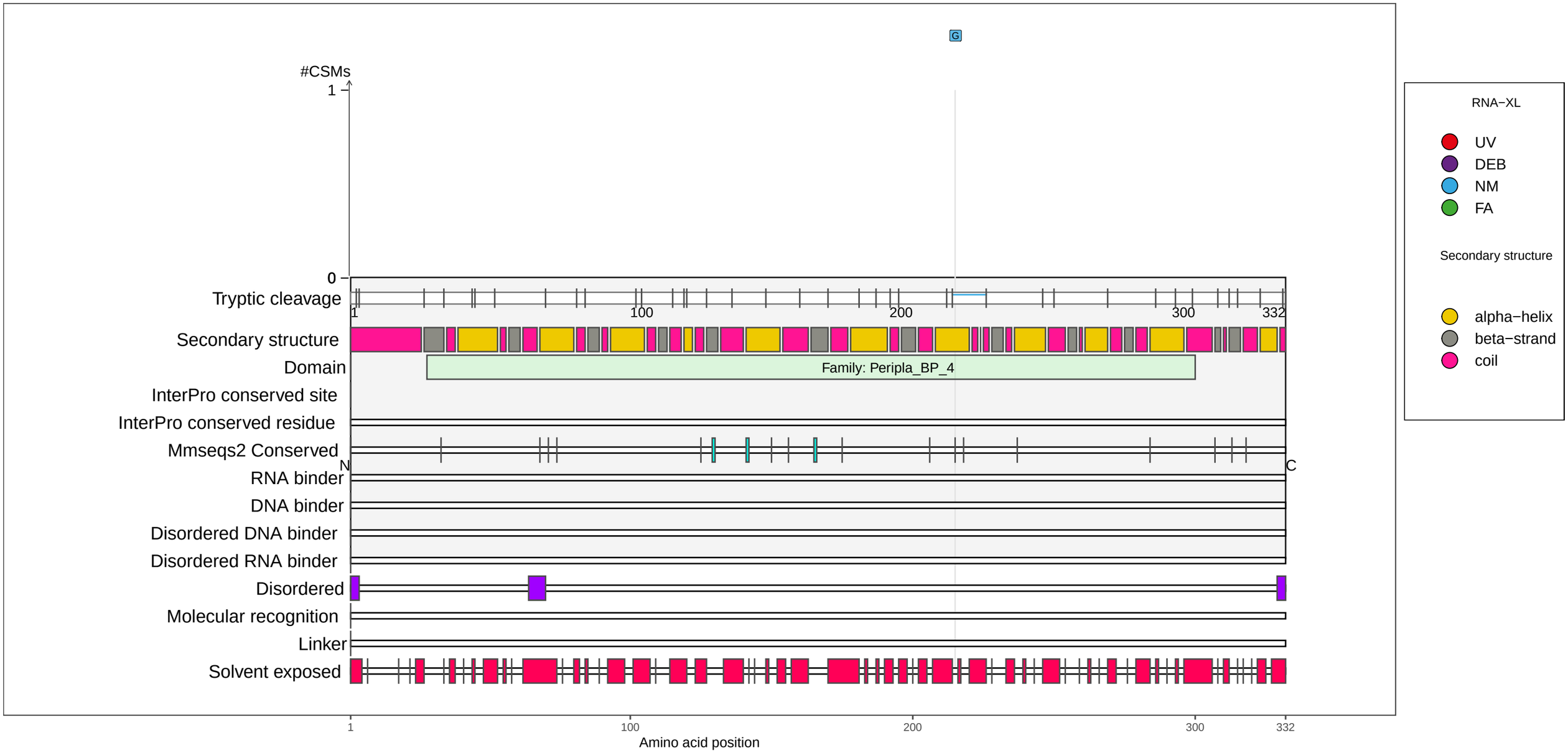




P0AEE5
DGAL_ECOLI D−galactose−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.18 (Q 20)
PAXdb K12 strain [ppm]: 3.02 (Q 91)
PAXdb E.coli [ppm]: 3.5 (Q 99)

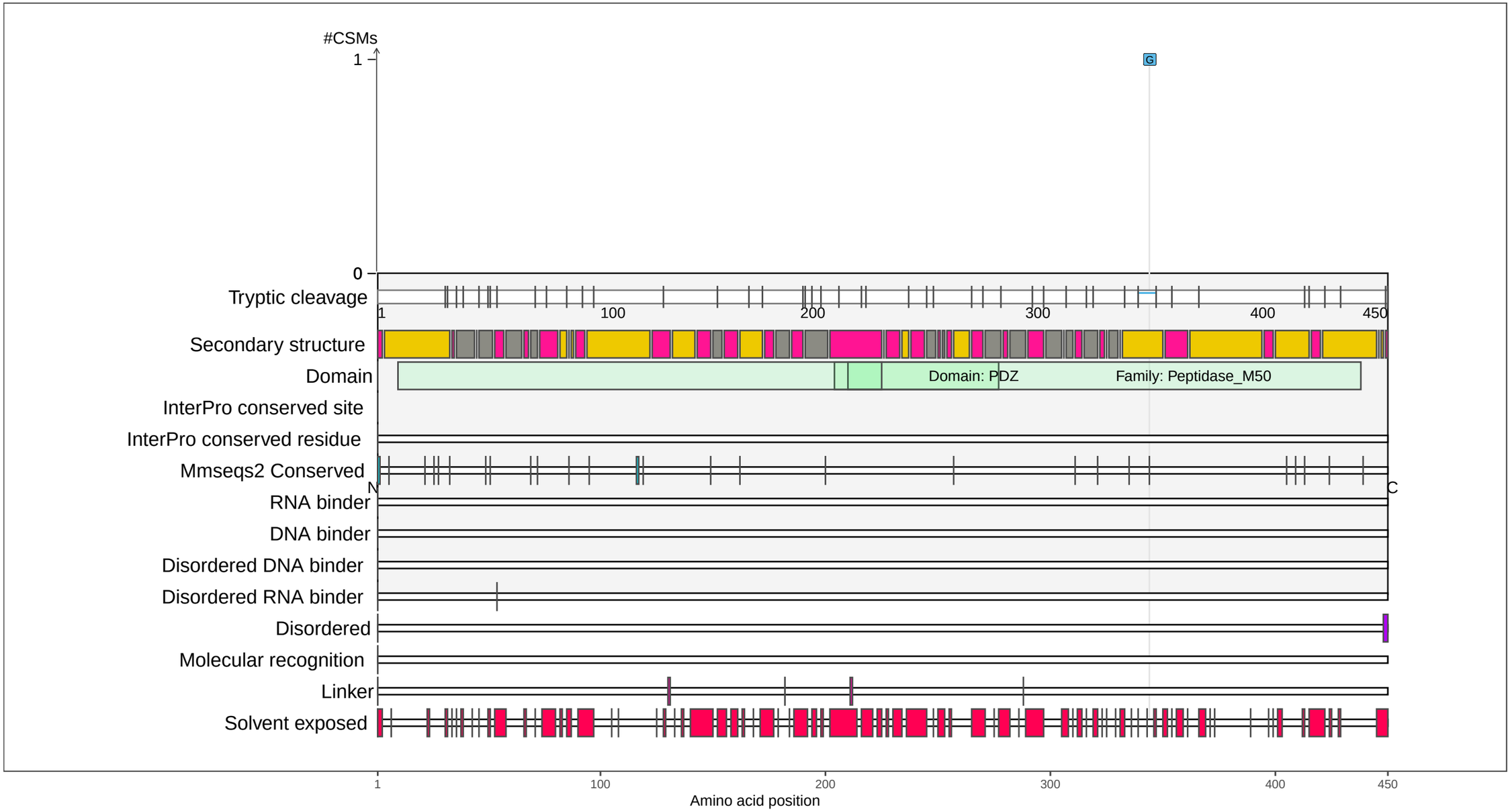
− RNA functions: not annotated

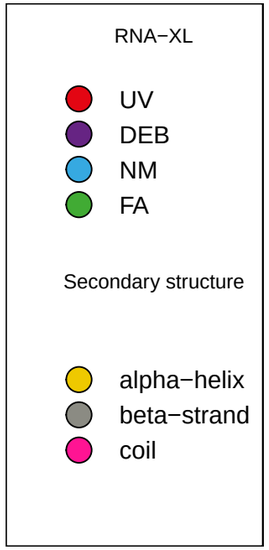


P0AEH1
RSEP_ECOLI Regulator of sigma−E protease RseP

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.73 (Q 41)

− RNA functions: not annotated

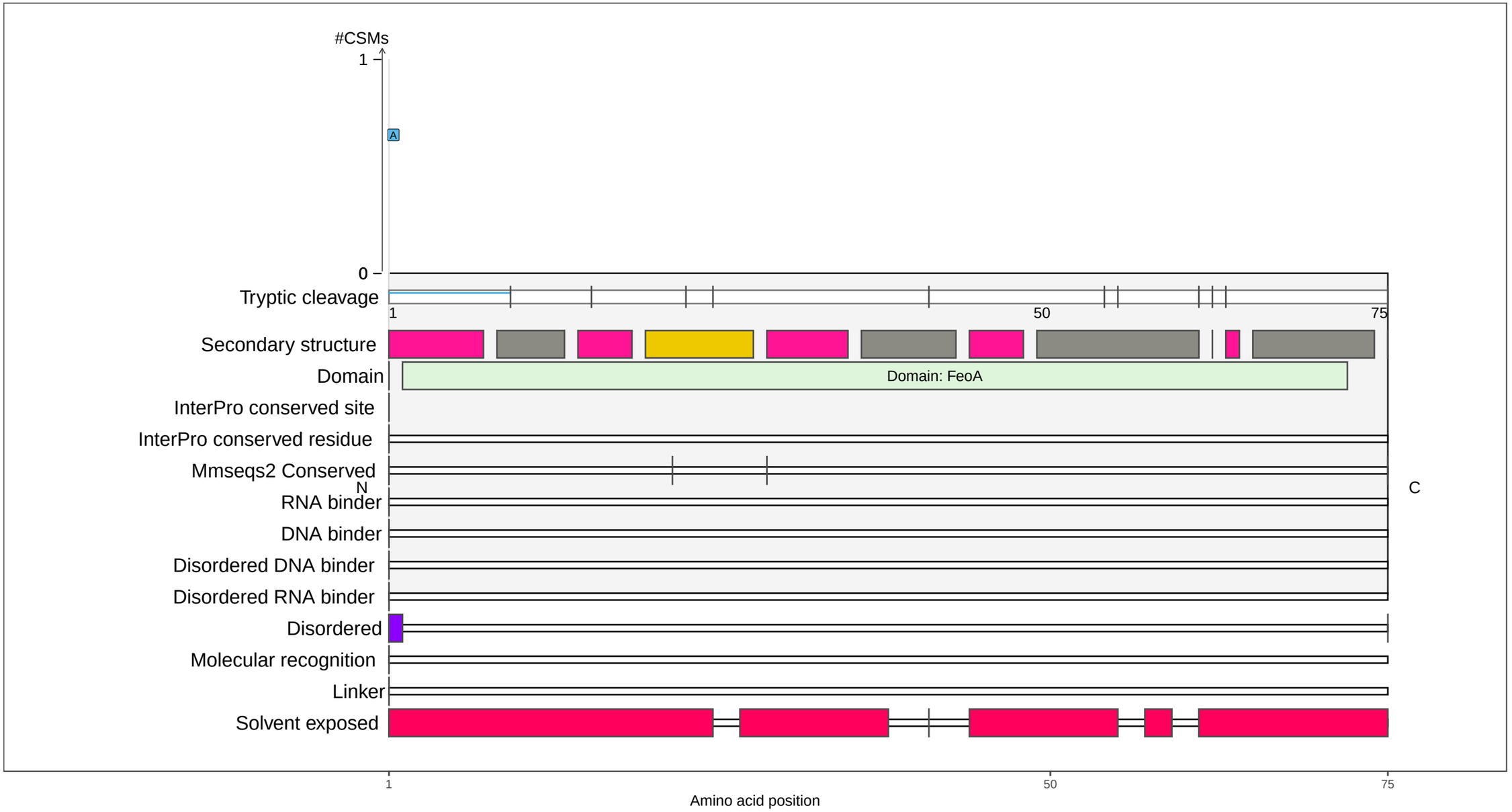


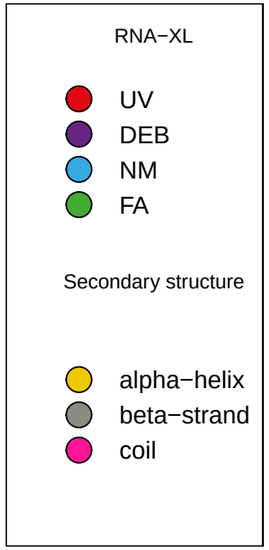


P0AEL3
FEOA_ECOLI Fe(2+) transport protein A

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.56 (Q 87)

− RNA functions: not annotated

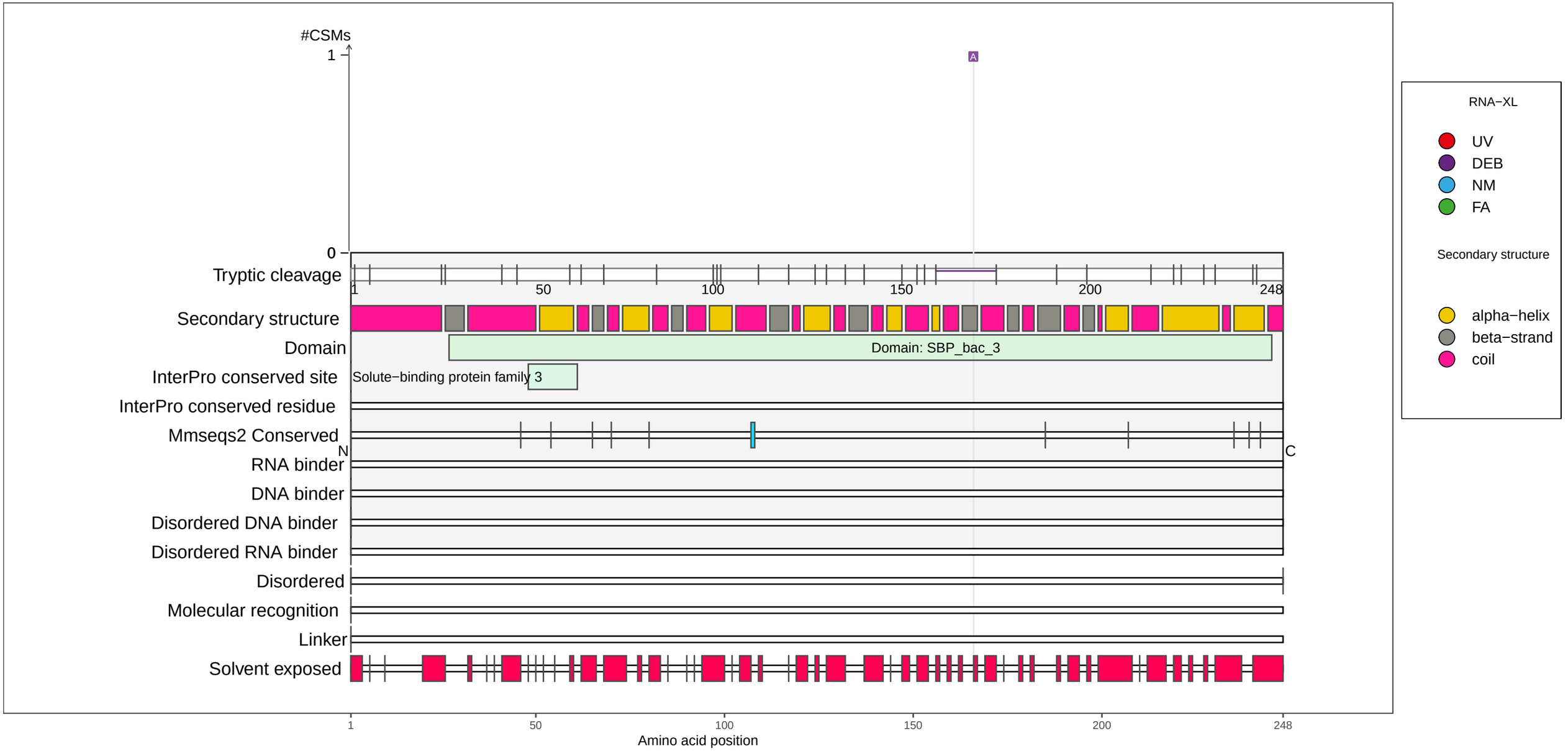




P0AEQ3
GLNH_ECOLI Glutamine−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 55)
PAXdb K12 strain [ppm]: 2.88 (Q 88)
PAXdb E.coli [ppm]: 3.47 (Q 99)

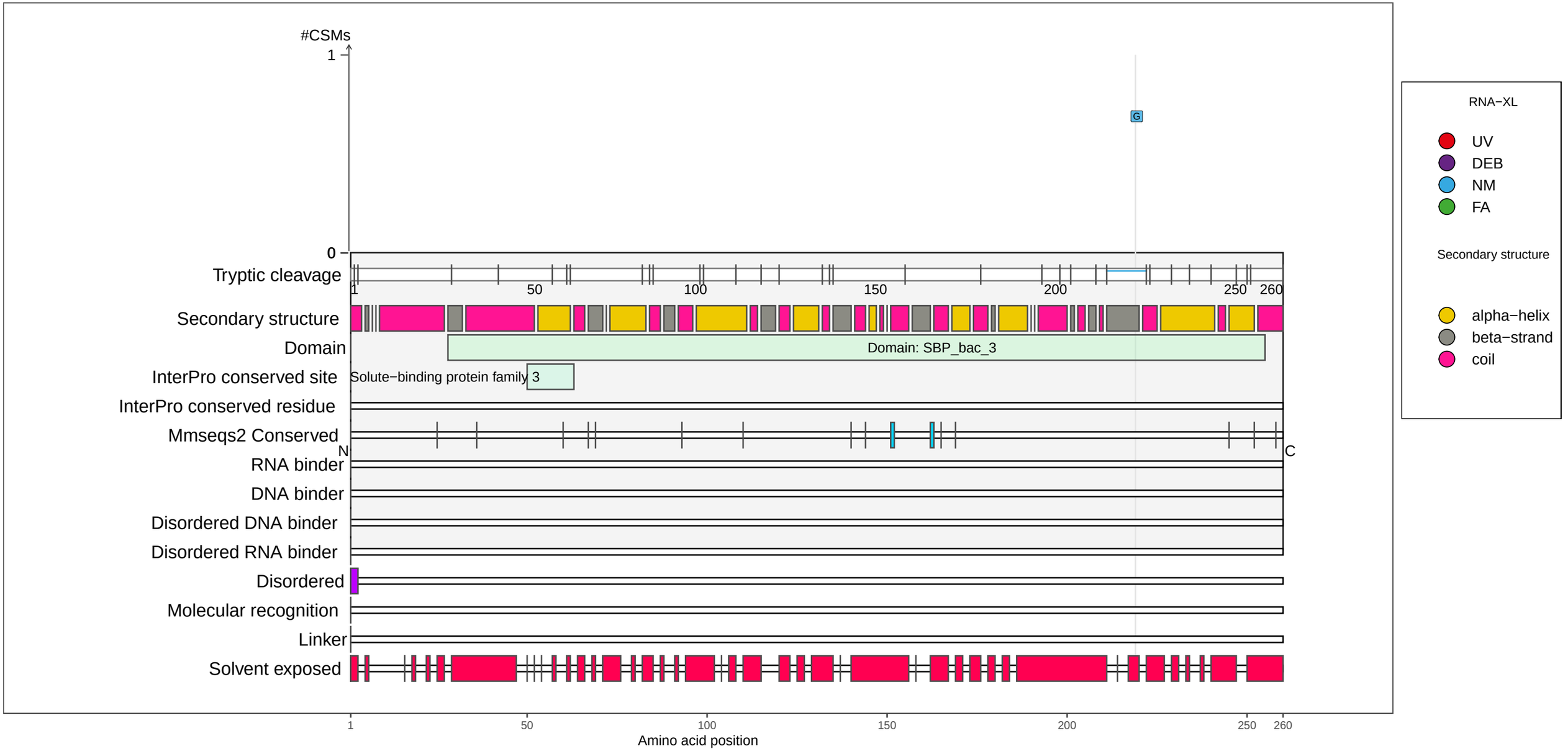
− RNA functions: not annotated



P0AEU0
HISJ_ECOLI Histidine−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 9.68 (Q 98)
PAXdb K12 strain [ppm]: 2.97 (Q 90)
PAXdb E.coli [ppm]: 2.97 (Q 94)

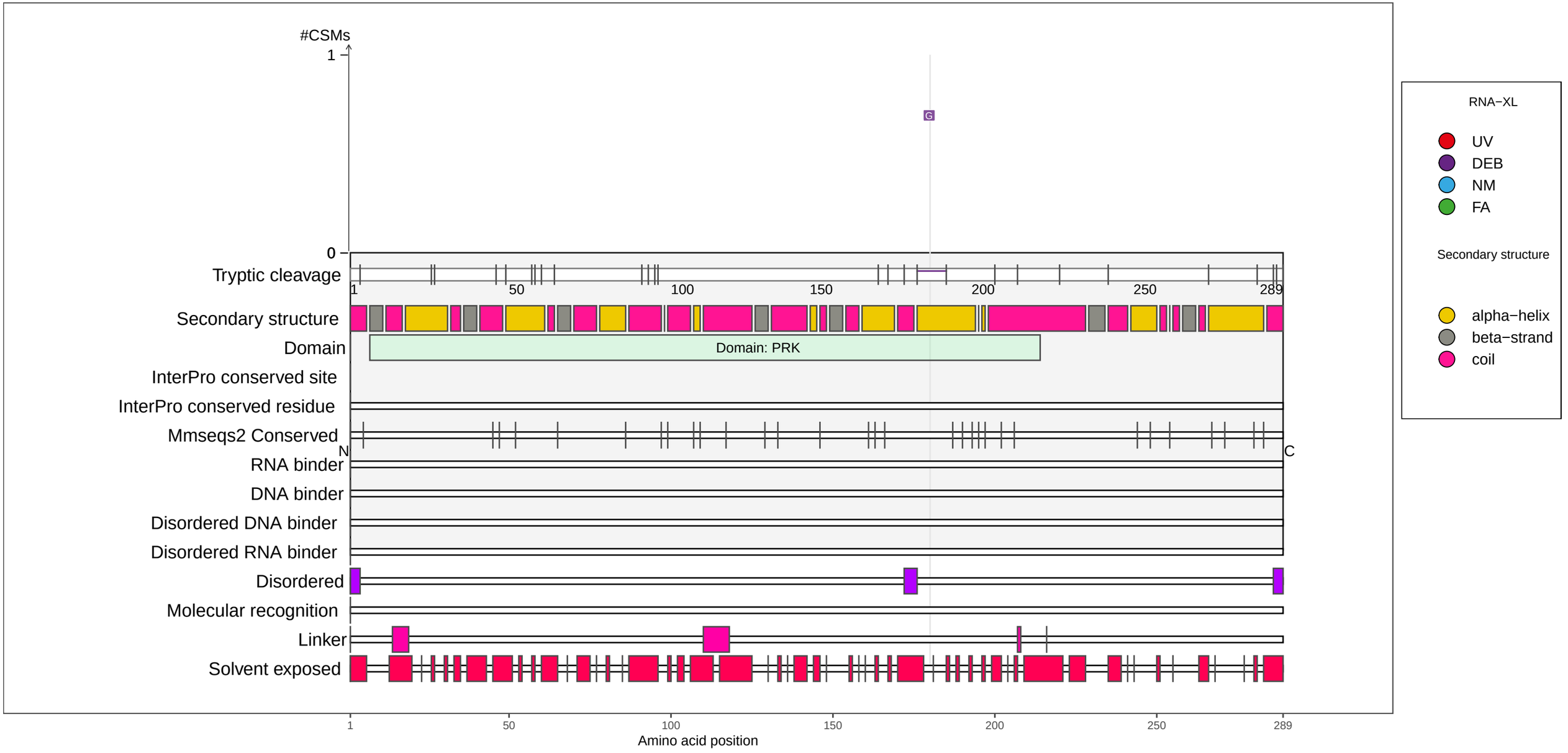
− RNA functions: not annotated



P0AEX5
KPPR_ECOLI Probable phosphoribulokinase

− Abundance:
tryptic [log10 Intensity]: 8.24 (Q 67)
PAXdb K12 strain [ppm]: 1.76 (Q 51)
PAXdb E.coli [ppm]: 1.85 (Q 68)

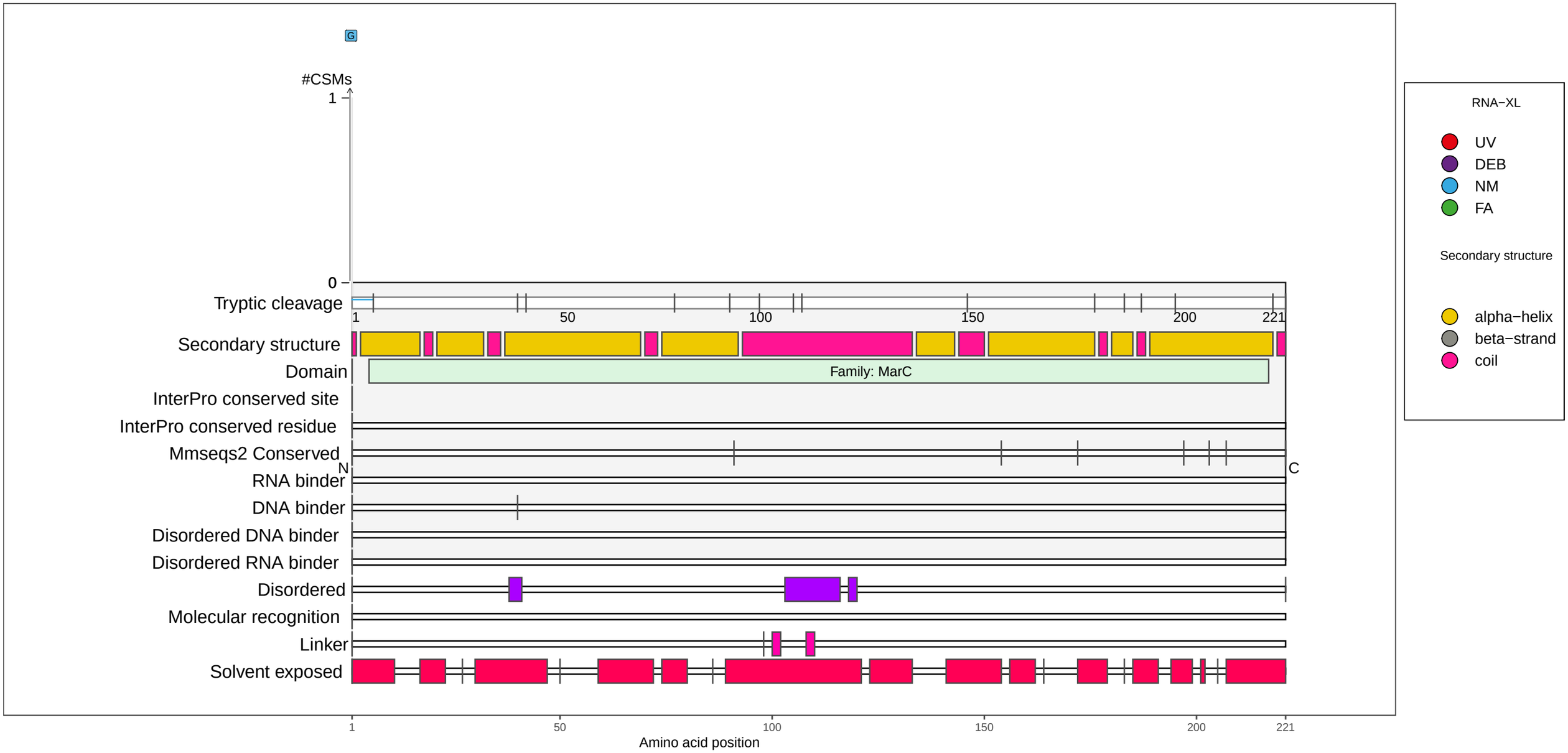
− RNA functions: not annotated



P0AEY1
MARC_ECOLI UPF0056 inner membrane protein MarC

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.12 (Q 22)

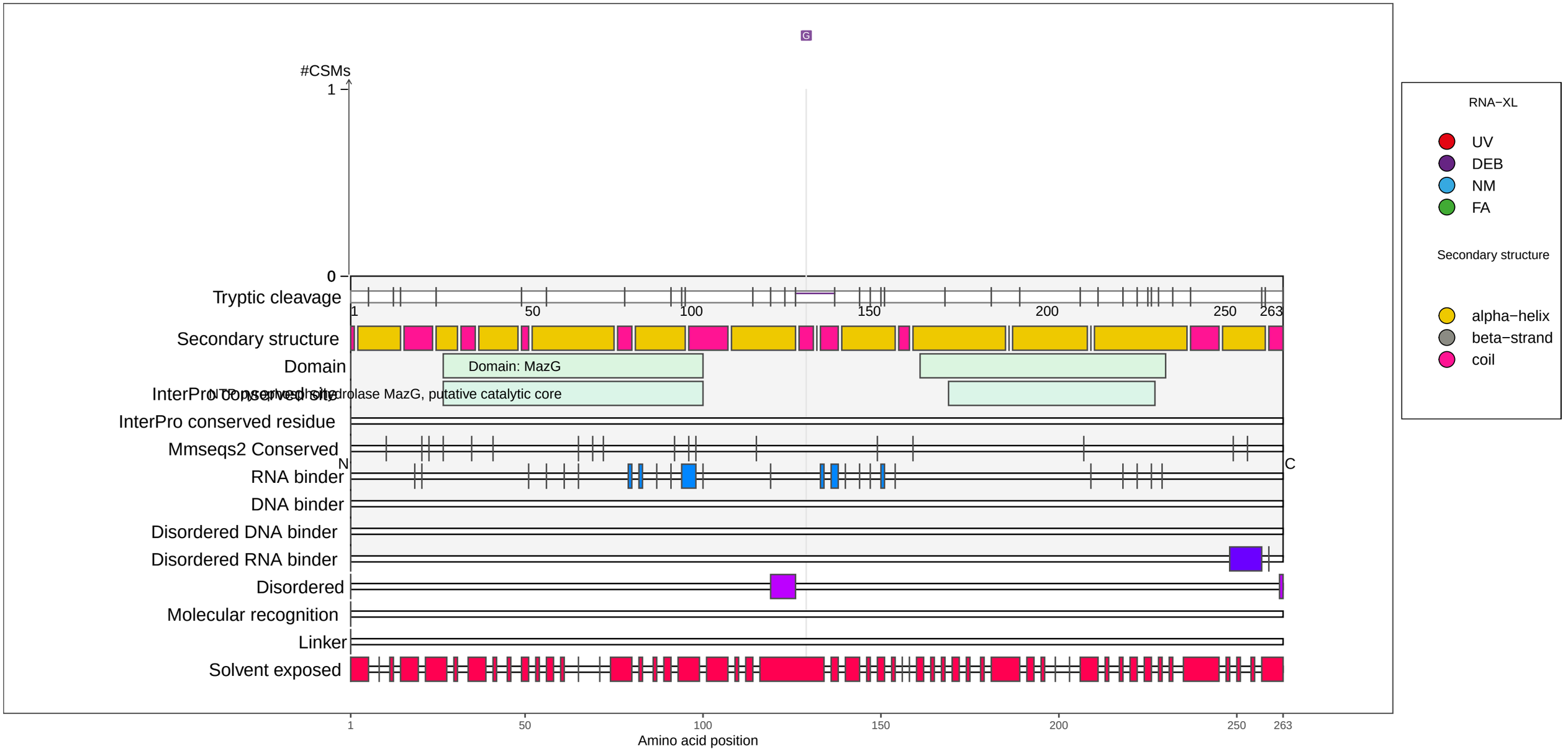
− RNA functions: not annotated



P0AEY3
MAZG_ECOLI Nucleoside triphosphate pyrophosphohydrolase

− Abundance:
tryptic [log10 Intensity]: 8.26 (Q 68)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.68 (Q 40)

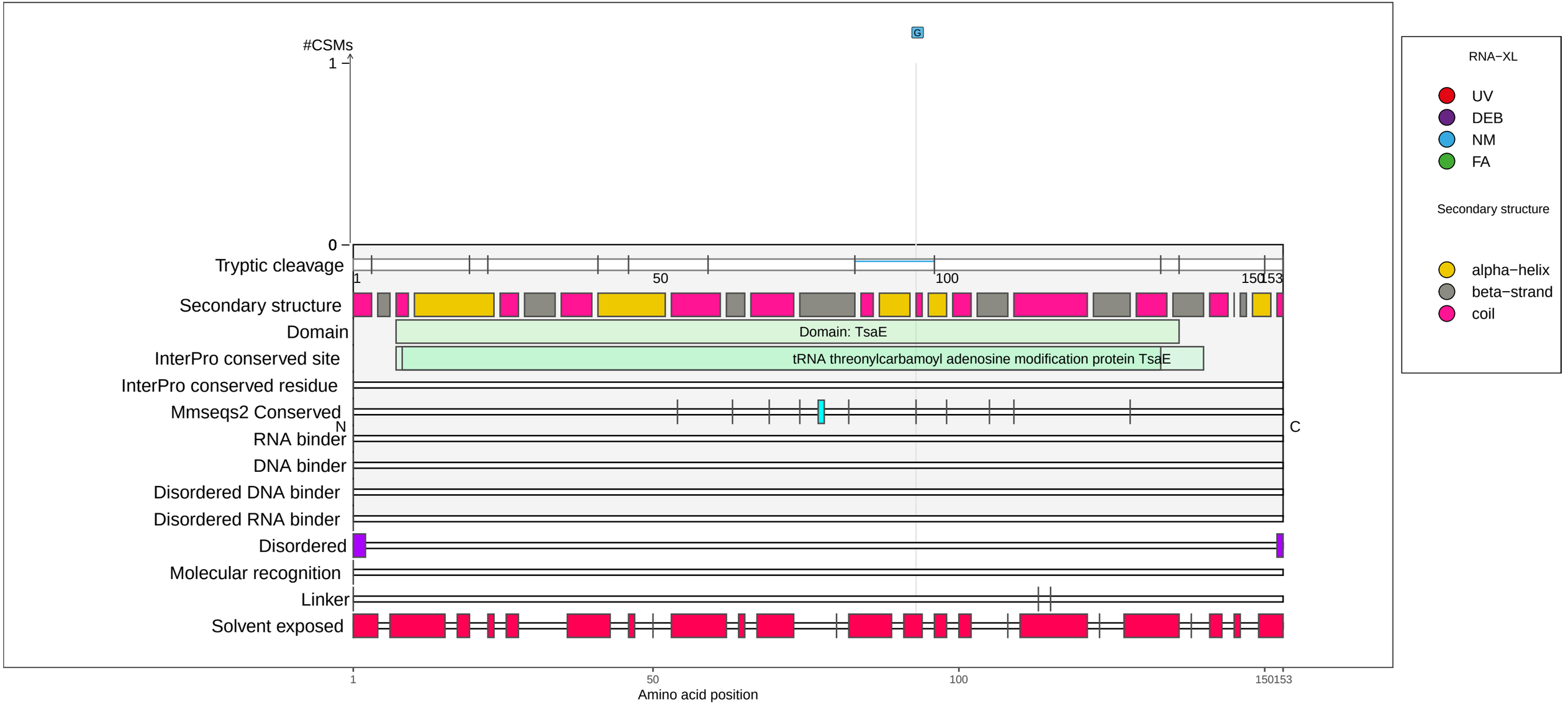
− RNA functions: not annotated



P0AF67
TSAE_ECOLI tRNA threonylcarbamoyladenosine biosynthesis protein TsaE

− Abundance:
tryptic [log10 Intensity]: 7.52 (Q 36)
PAXdb K12 strain [ppm]: 2.39 (Q 74)
PAXdb E.coli [ppm]: 2.07 (Q 74)

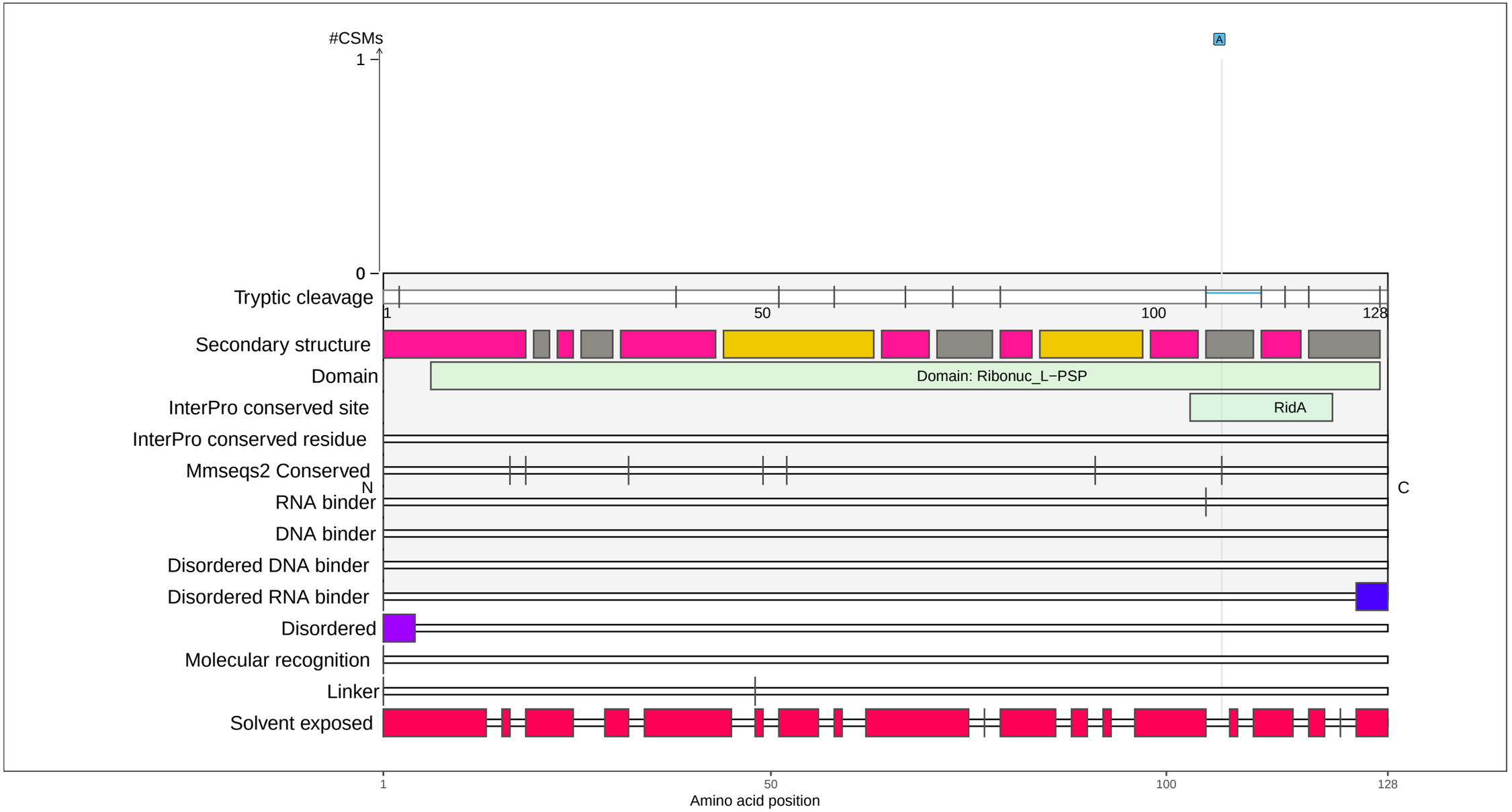
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA threonylcarbamoyladenosine metabolic process; tRNA threonylcarbamoyladenosine modification



P0AF93
RIDA_ECOLI 2−iminobutanoate/2−iminopropanoate deaminase

− Abundance:
tryptic [log10 Intensity]: 8.31 (Q 70)
PAXdb K12 strain [ppm]: 2.92 (Q 89)
PAXdb E.coli [ppm]: 3.64 (Q 100)

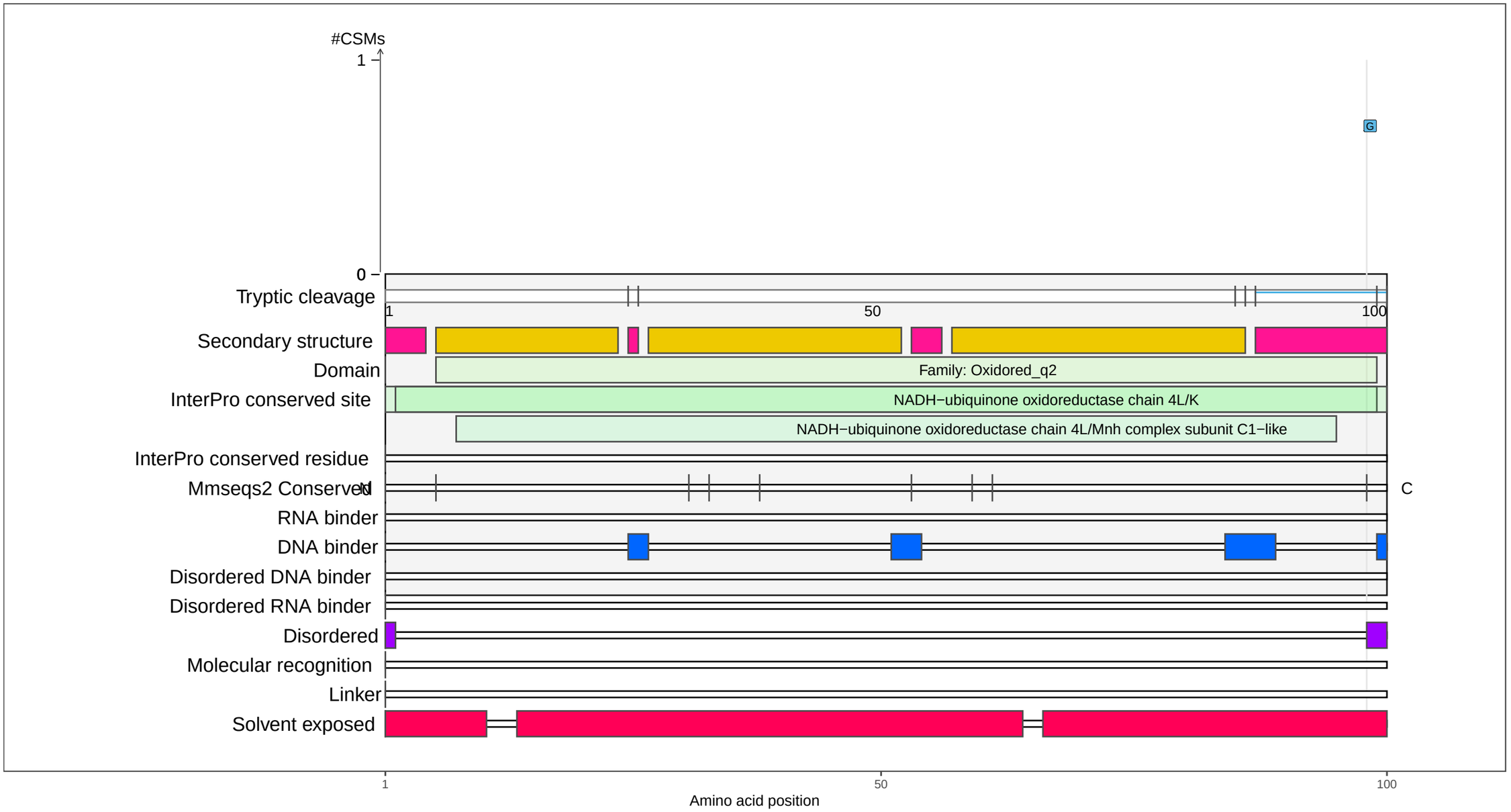
− RNA functions: not annotated



P0AFE4
NUOK_ECOLI NADH−quinone oxidoreductase subunit K

− Abundance:
tryptic [log10 Intensity]: 9.03 (Q 89)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.98 (Q 72)

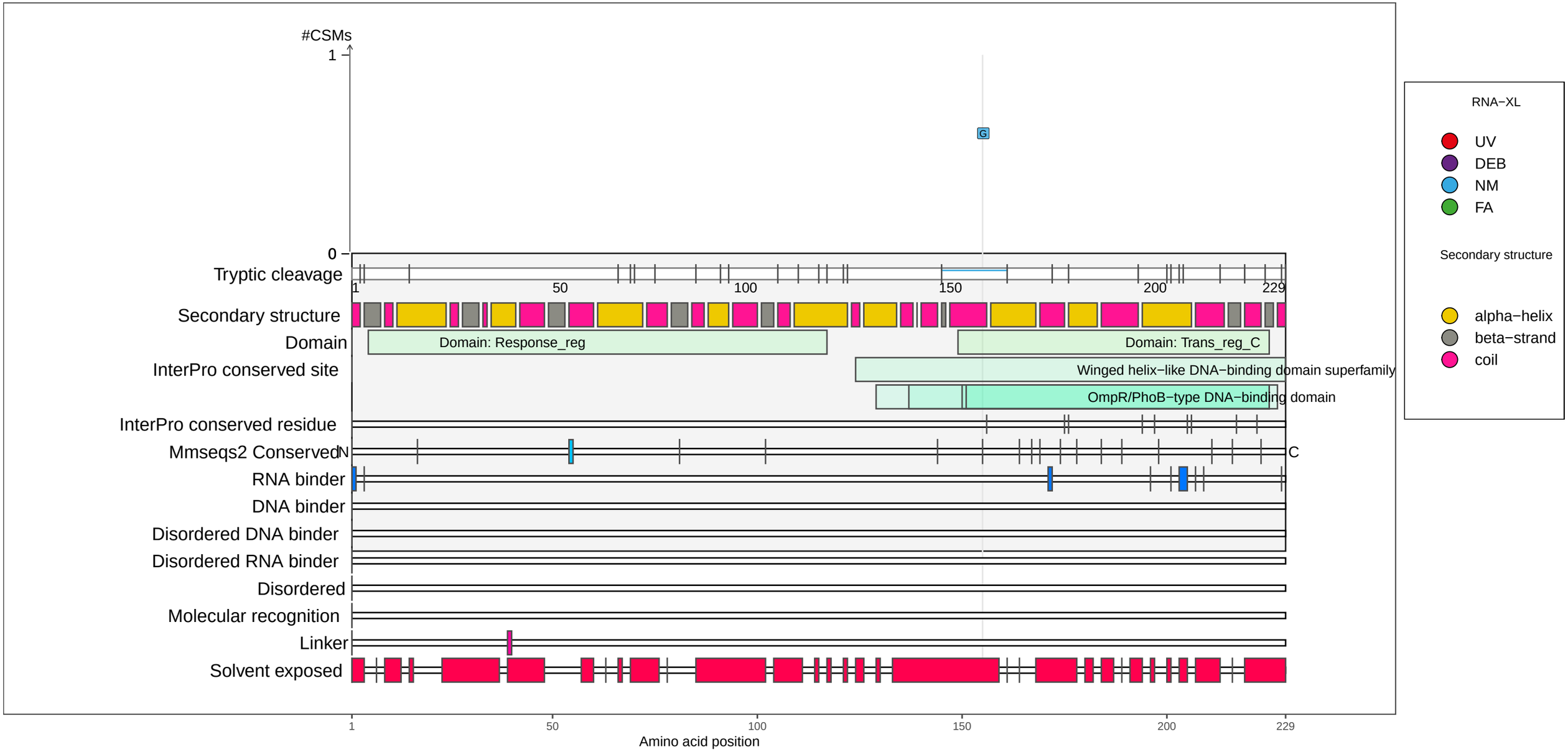
− RNA functions: not annotated



P0AFJ5
PHOB_ECOLI Phosphate regulon transcriptional regulatory protein PhoB

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 45)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.01 (Q 48)

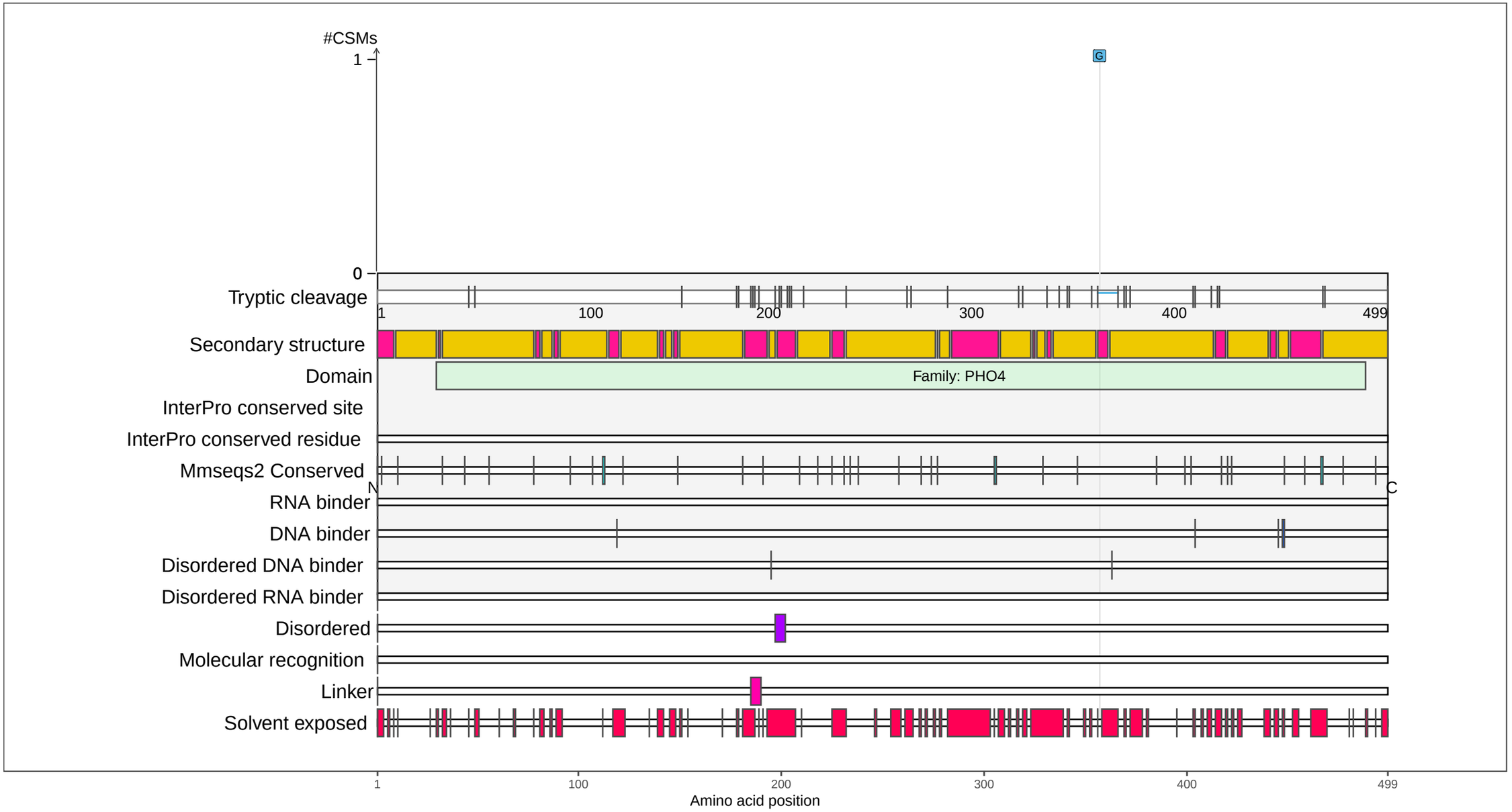
− RNA functions: not annotated



P0AFJ7
PITA_ECOLI Low−affinity inorganic phosphate transporter 1

− Abundance:
tryptic [log10 Intensity]: 6.78 (Q 7)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.46 (Q 59)

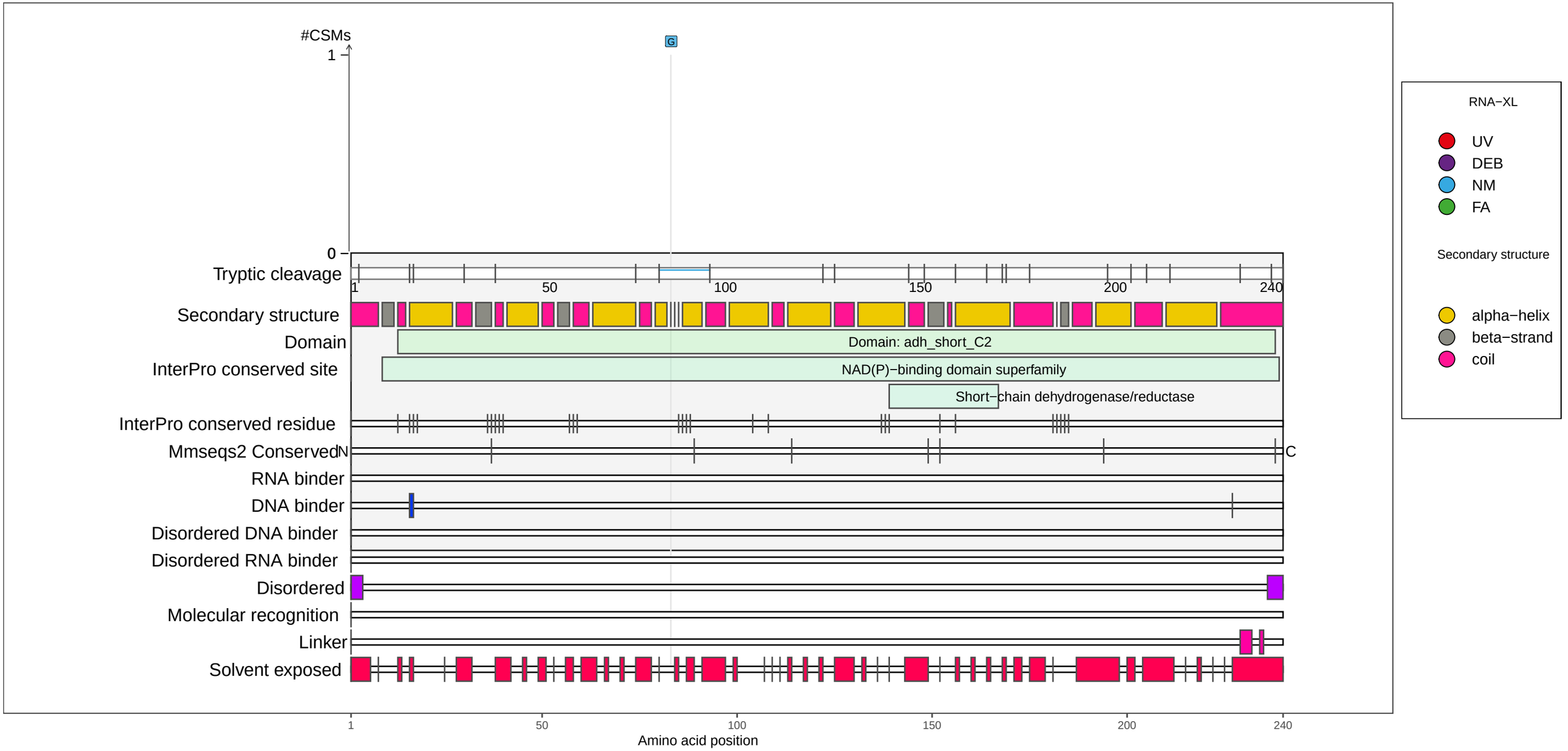
− RNA functions: not annotated



P0AFS3
FOLM_ECOLI Dihydromonapterin reductase

− Abundance:
tryptic [log10 Intensity]: 7.32 (Q 26)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.12 (Q 22)

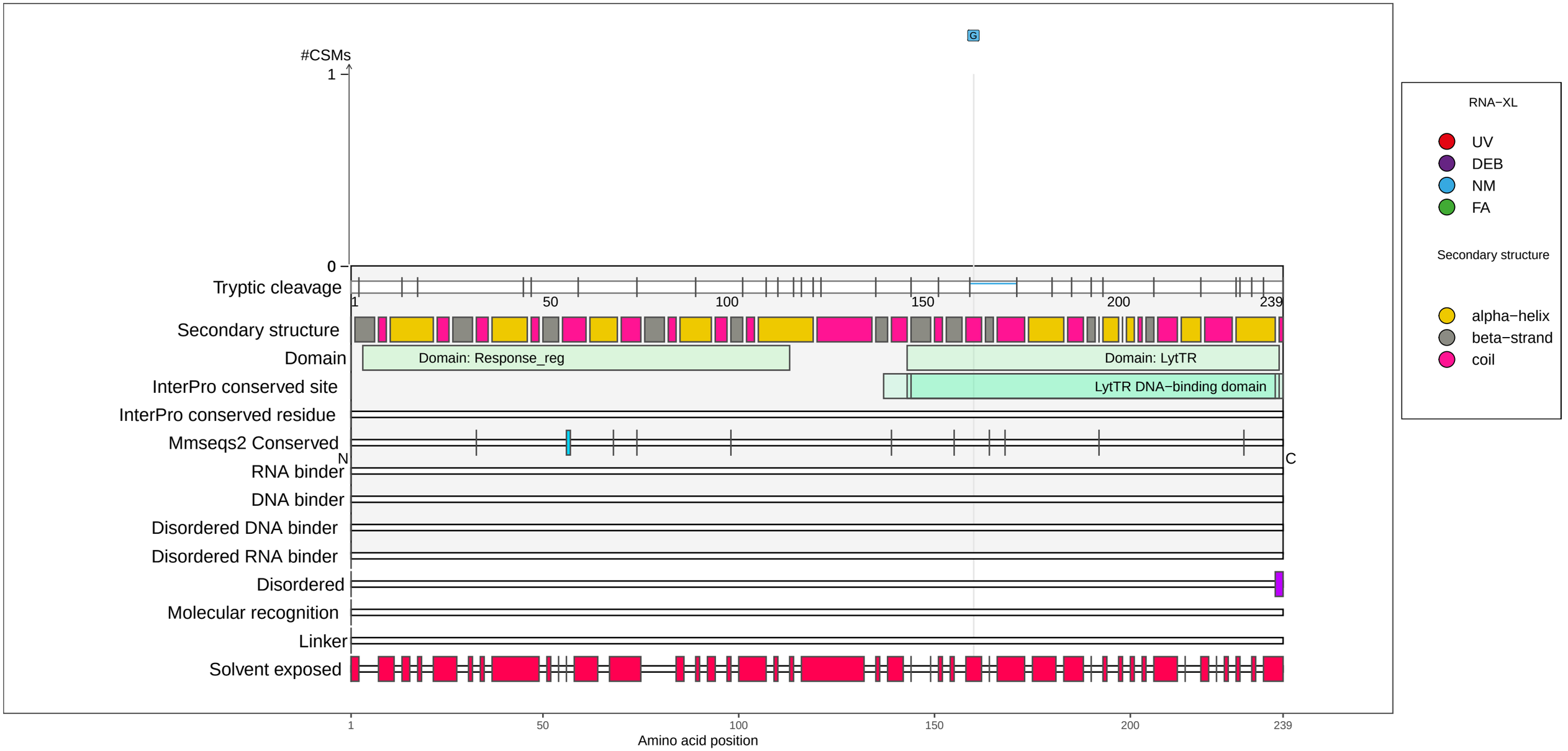
− RNA functions: not annotated



P0AFT5
BTSR_ECOLI Transcriptional regulatory protein BtsR

− Abundance:
tryptic [log10 Intensity]: 7.28 (Q 24)
PAXdb K12 strain [ppm]: 1.57 (Q 43)
PAXdb E.coli [ppm]: 0.82 (Q 43)

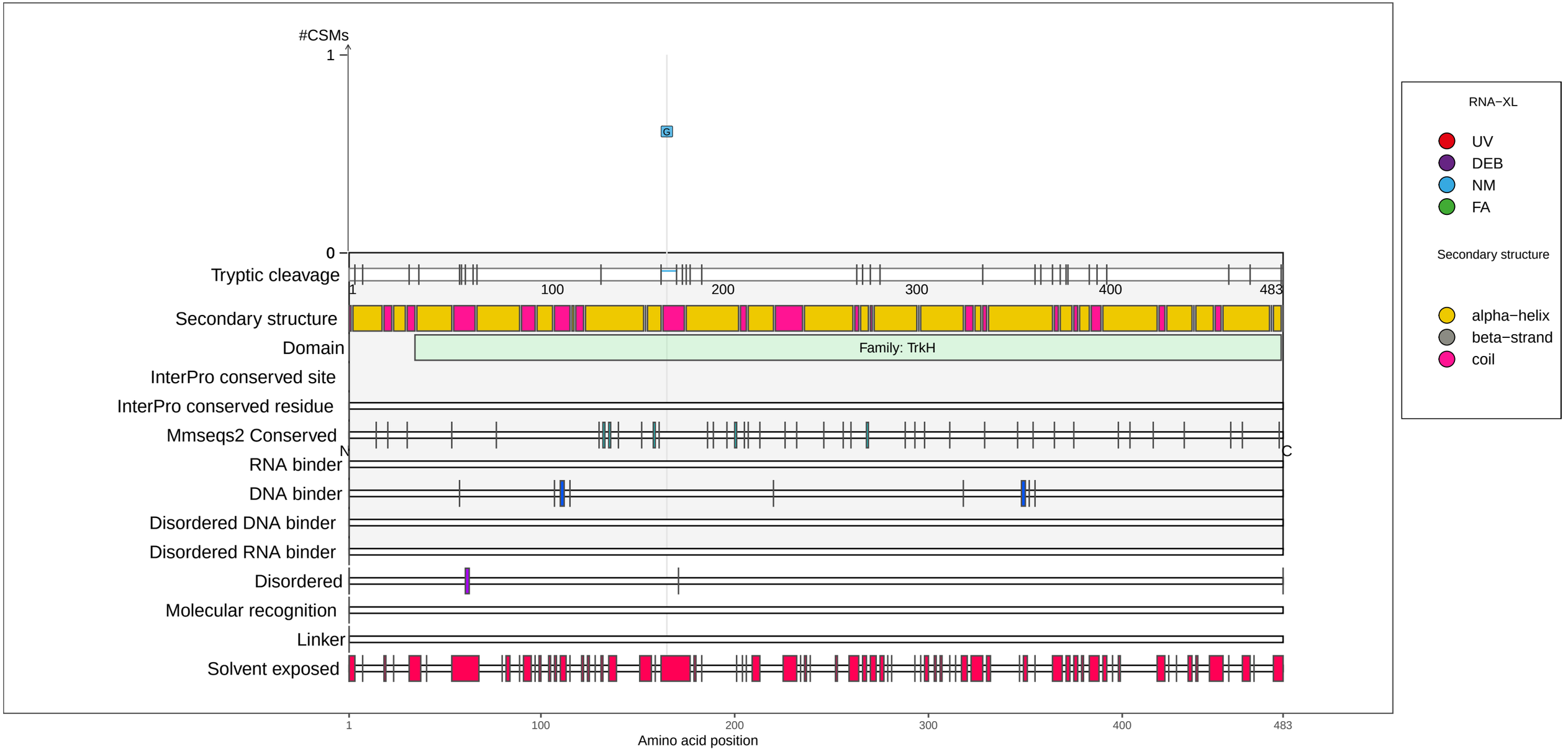
− RNA functions: not annotated



P0AFZ7
TRKH_ECOLI Trk system potassium uptake protein TrkH

− Abundance:
tryptic [log10 Intensity]: 6.36 (Q 1)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.59 (Q 3)

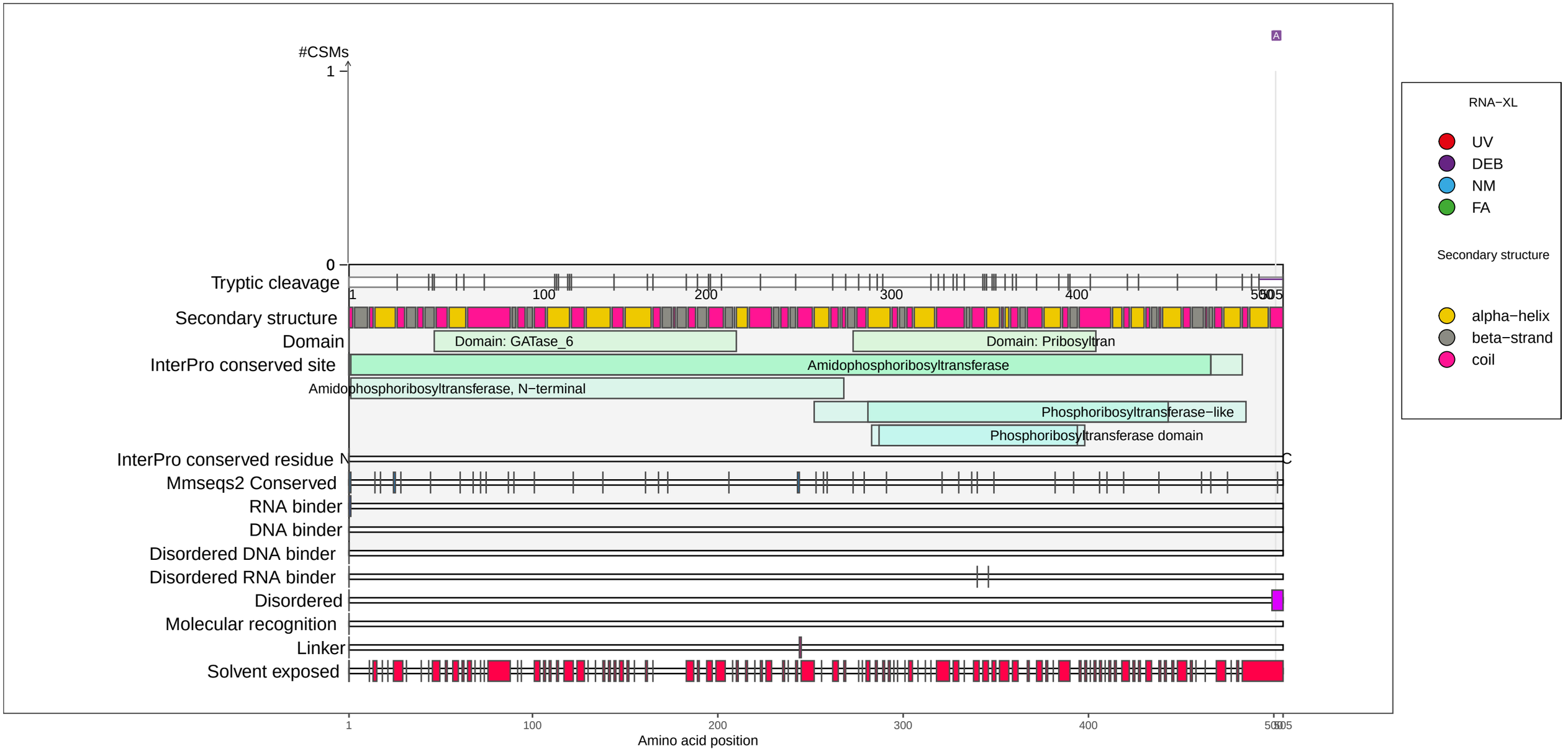
− RNA functions: not annotated



P0AG16
PUR1_ECOLI Amidophosphoribosyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: 2.22 (Q 68)
PAXdb E.coli [ppm]: 2.04 (Q 73)

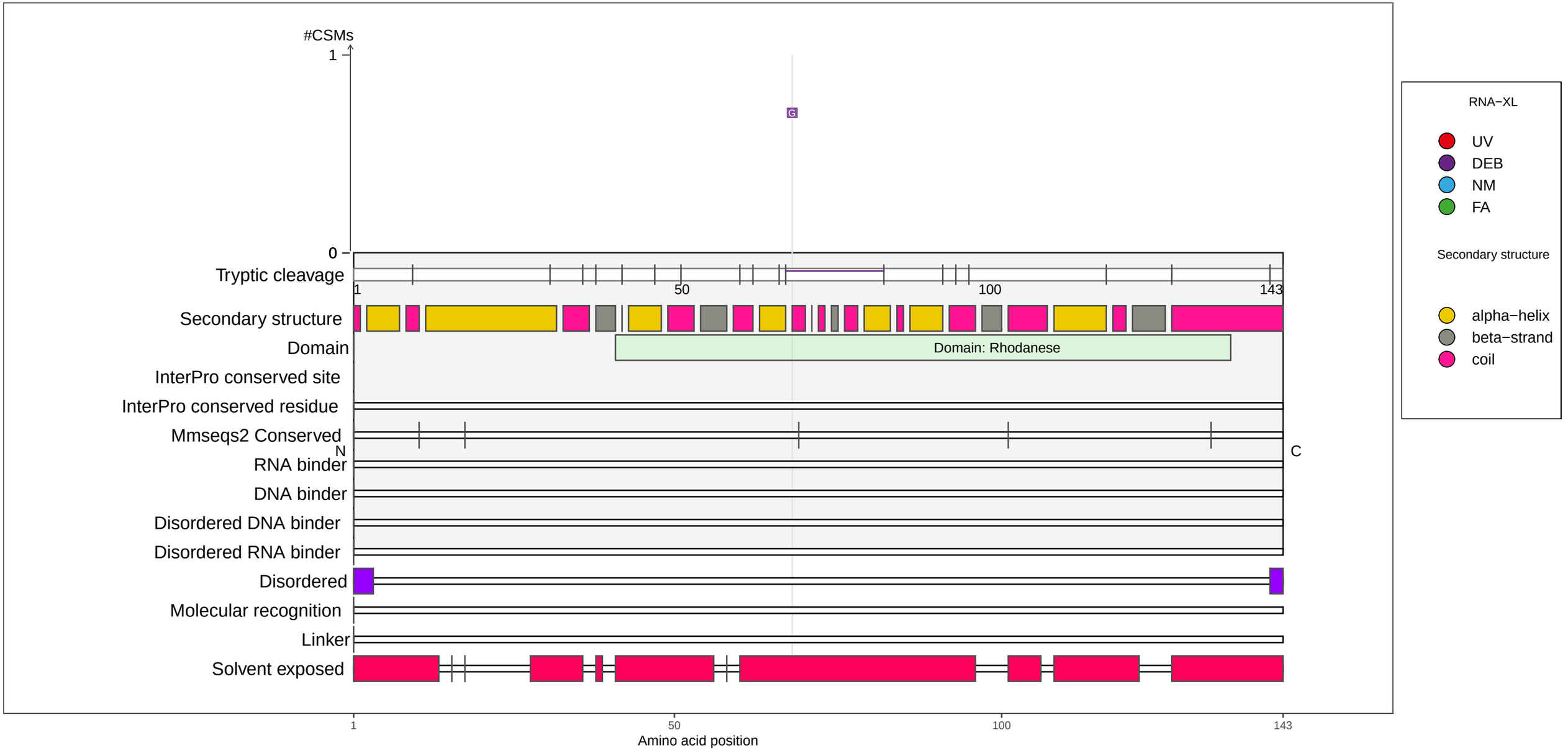
− RNA functions: not annotated



P0AG27
YIBN_ECOLI Uncharacterized protein YibN

− Abundance:
tryptic [log10 Intensity]: 8.42 (Q 73)
PAXdb K12 strain [ppm]: 2.35 (Q 72)
PAXdb E.coli [ppm]: 2.45 (Q 84)

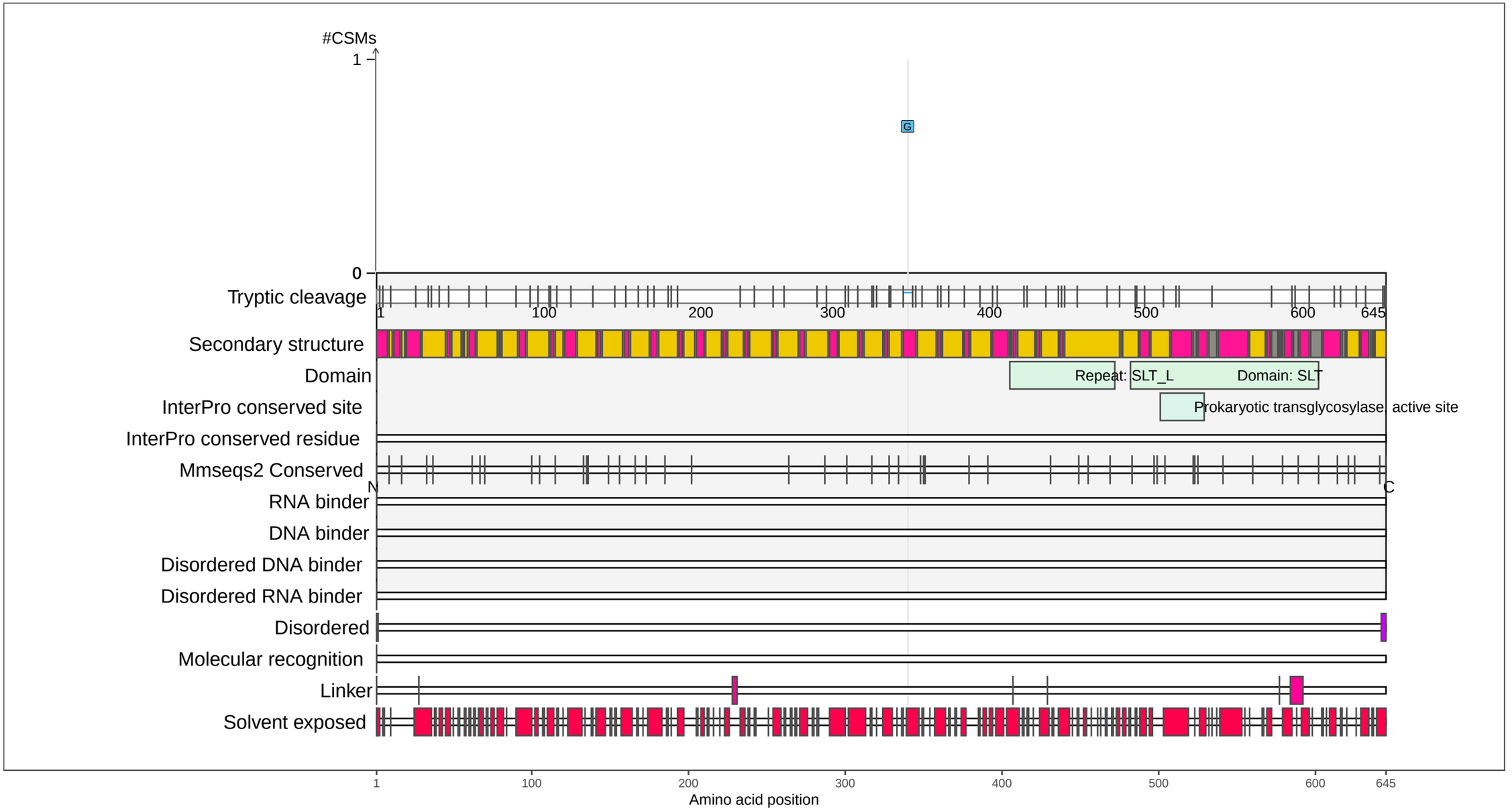
− RNA functions: not annotated

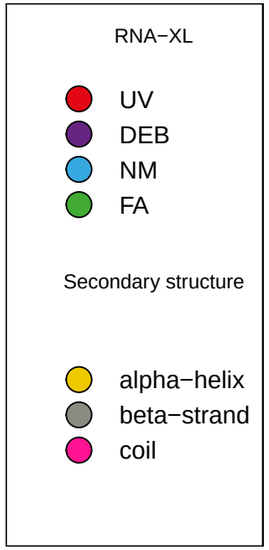


P0AGC3
SLT_ECOLI Soluble lytic murein transglycosylase

− Abundance:
tryptic [log10 Intensity]: 7.14 (Q 18)
PAXdb K12 strain [ppm]: 1.57 (Q 42)
PAXdb E.coli [ppm]: 1.89 (Q 69)

− RNA functions: not annotated

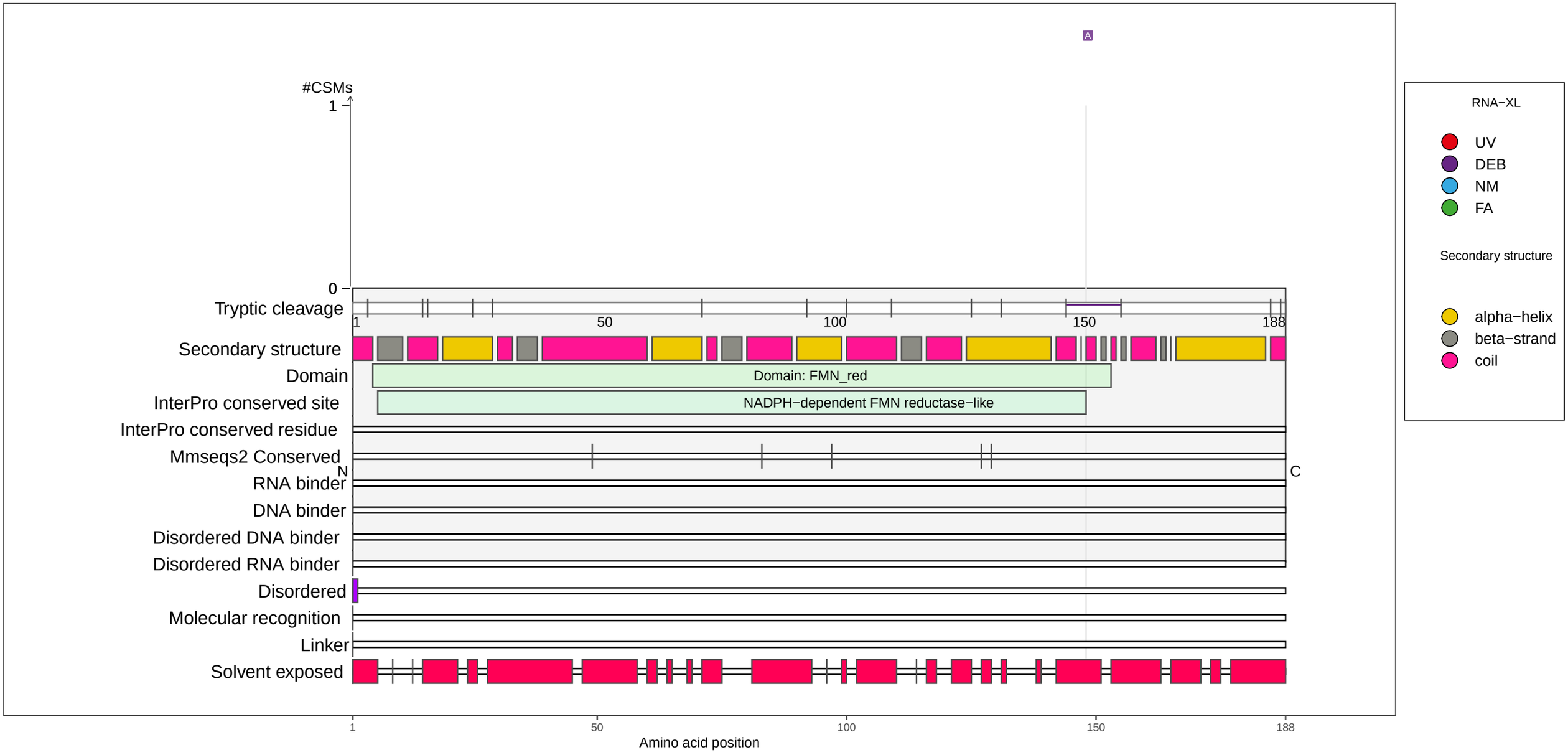




P0AGE6
CHRR_ECOLI Quinone reductase

− Abundance:
tryptic [log10 Intensity]: 8.05 (Q 59)
PAXdb K12 strain [ppm]: 1.37 (Q 31)
PAXdb E.coli [ppm]: 2.85 (Q 92)

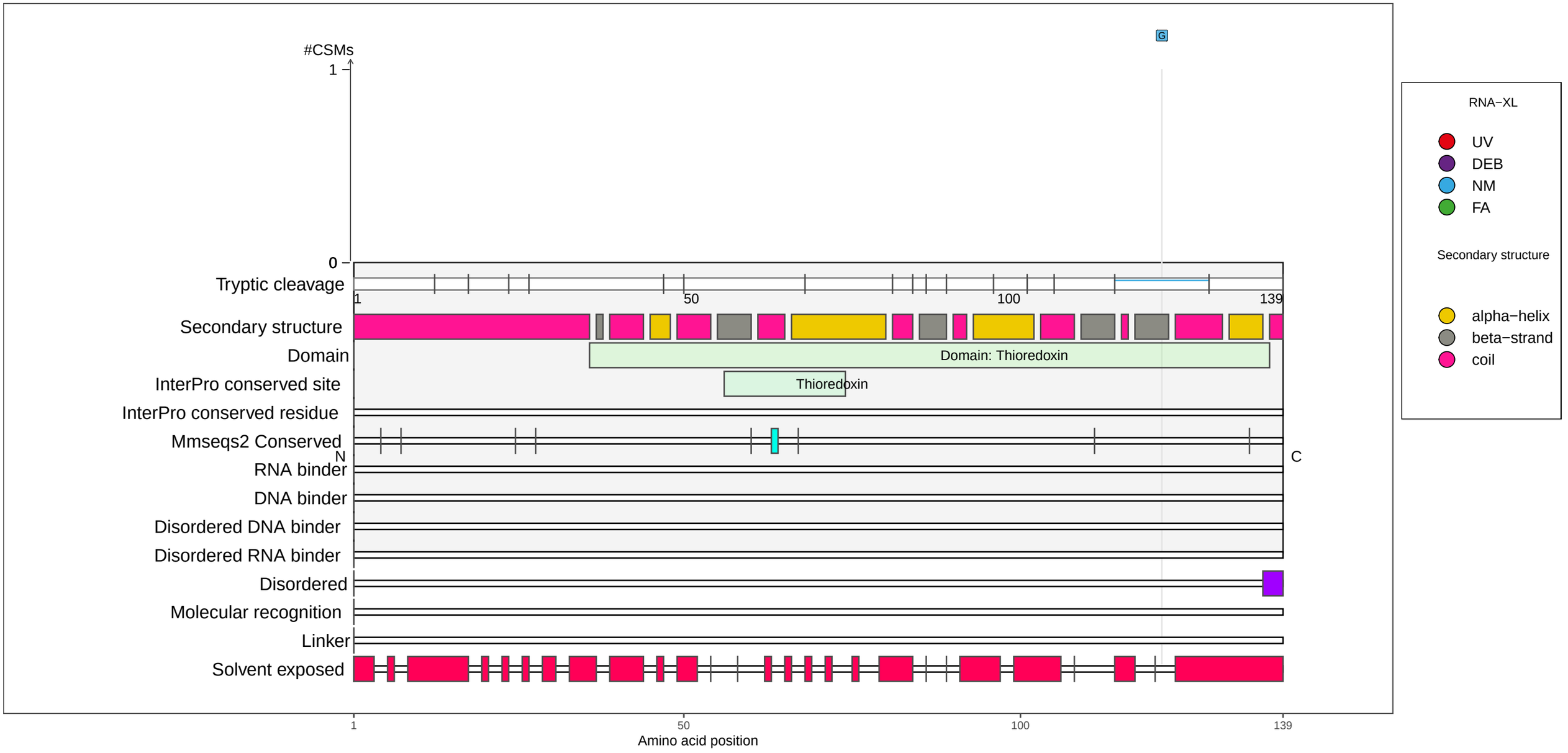
− RNA functions: not annotated



P0AGG4
THIO2_ECOLI Thioredoxin 2

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 54)
PAXdb K12 strain [ppm]: 2.8 (Q 86)
PAXdb E.coli [ppm]: 1.27 (Q 54)

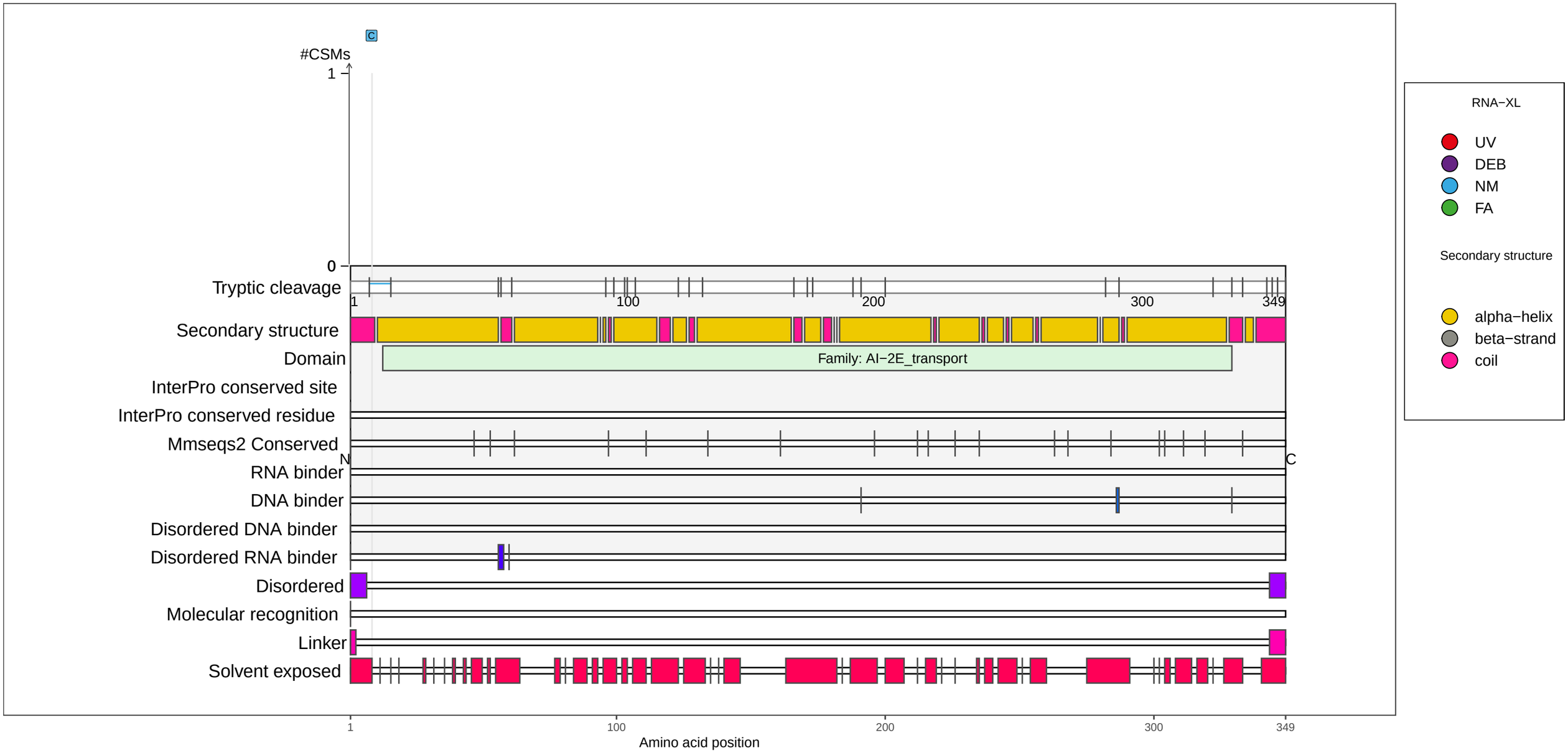
− RNA functions: not annotated



P0AGM0
YHHT_ECOLI Putative transport protein YhhT

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.94 (Q 10)

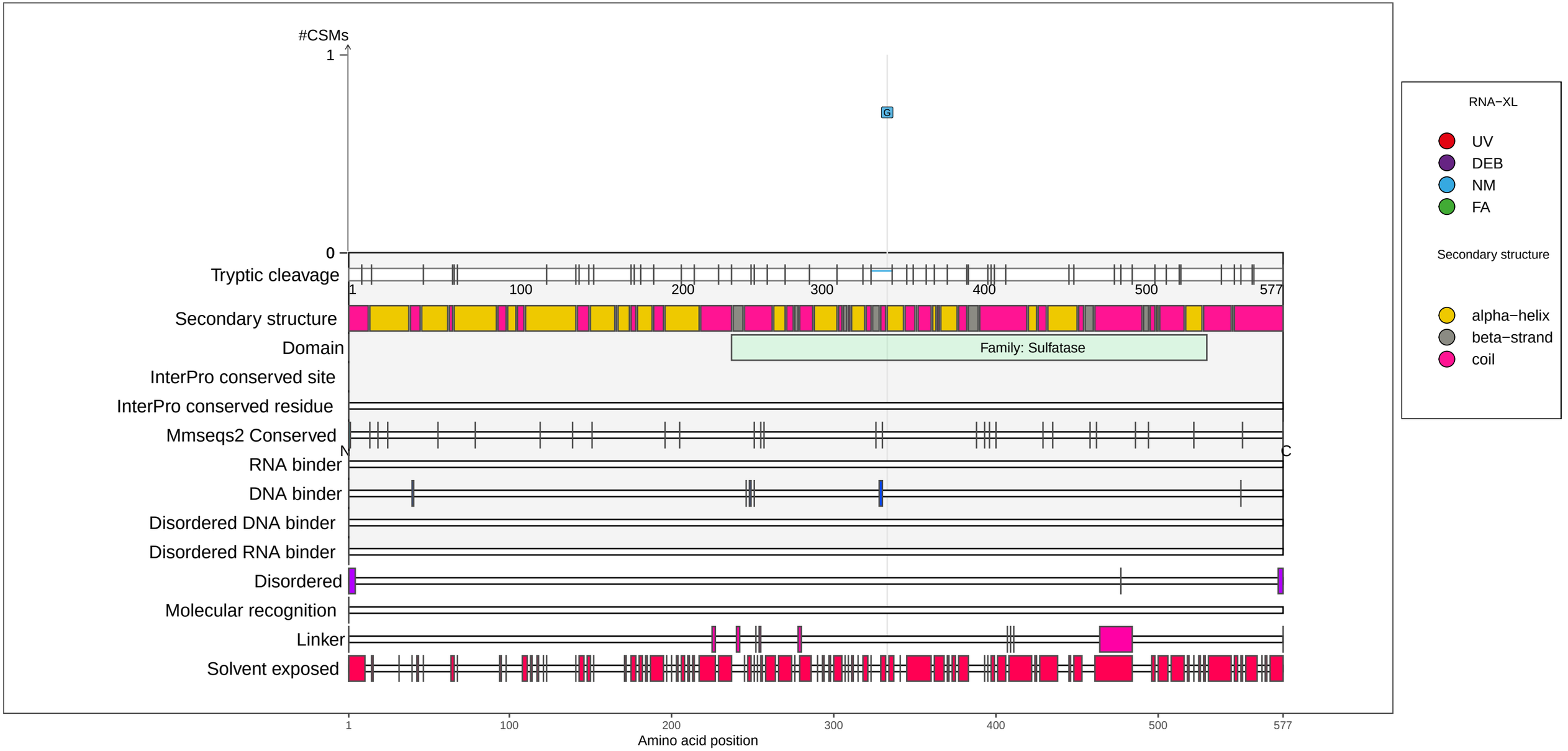
− RNA functions: not annotated



P0CB39
EPTC_ECOLI Phosphoethanolamine transferase EptC

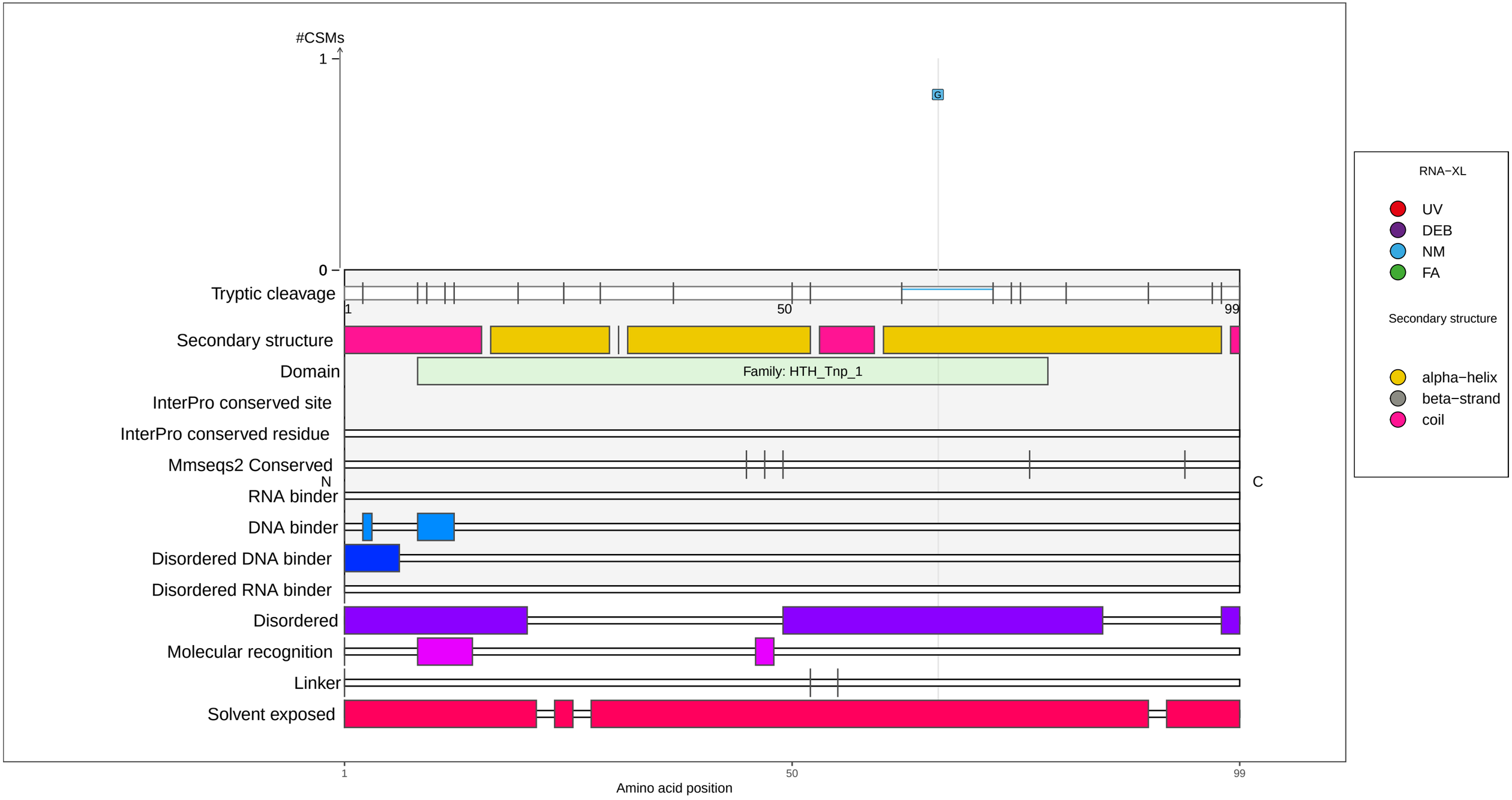
− Abundance:
tryptic [log10 Intensity]: 7.82 (Q 50)
PAXdb K12 strain [ppm]: 2.16 (Q 66)
PAXdb E.coli [ppm]: 1.08 (Q 50)

− RNA functions: not annotated

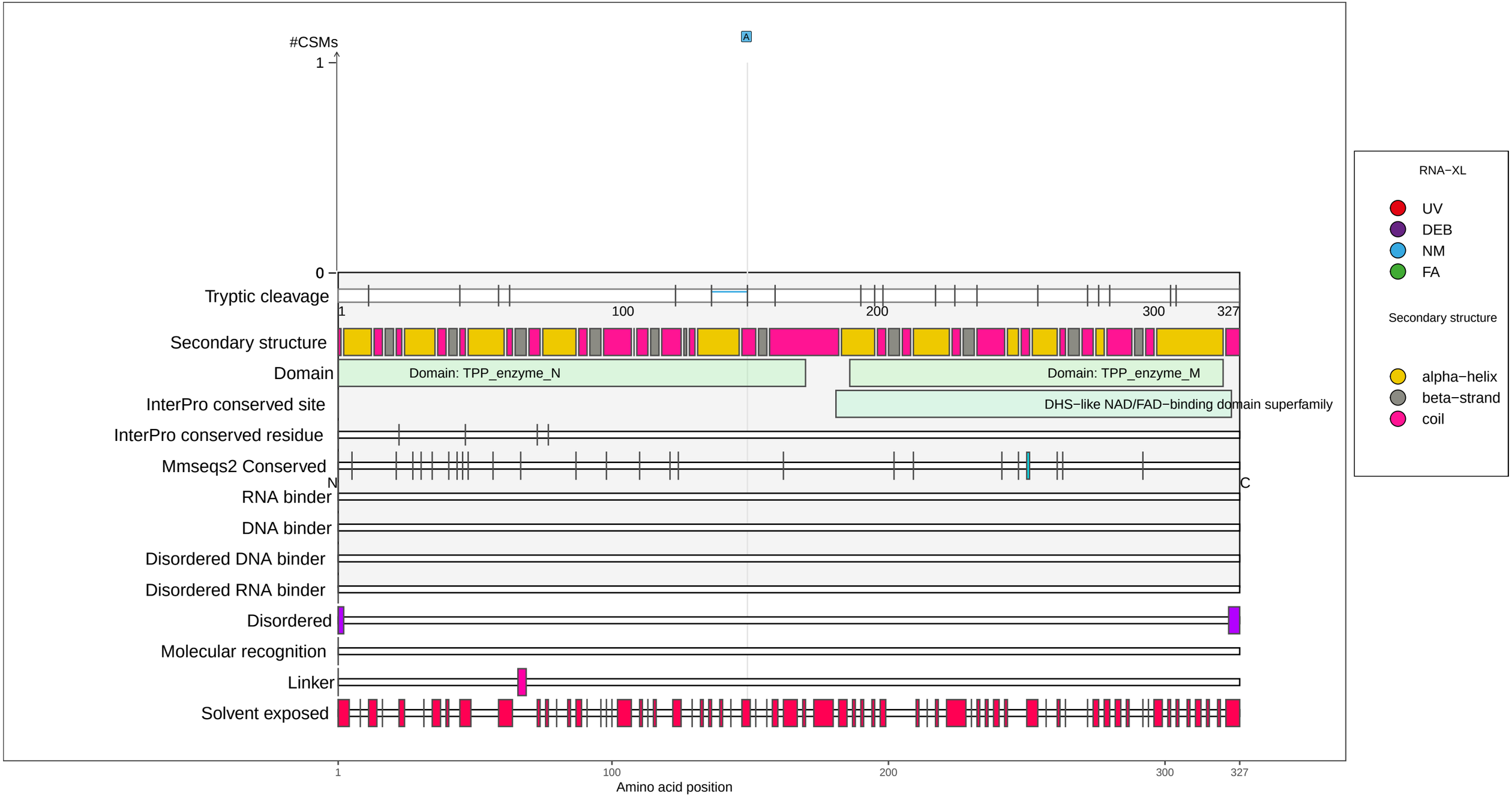


P0CF67
INSE2_ECOLI Transposase InsE for insertion sequence IS3B

− RNA functions: not annotated



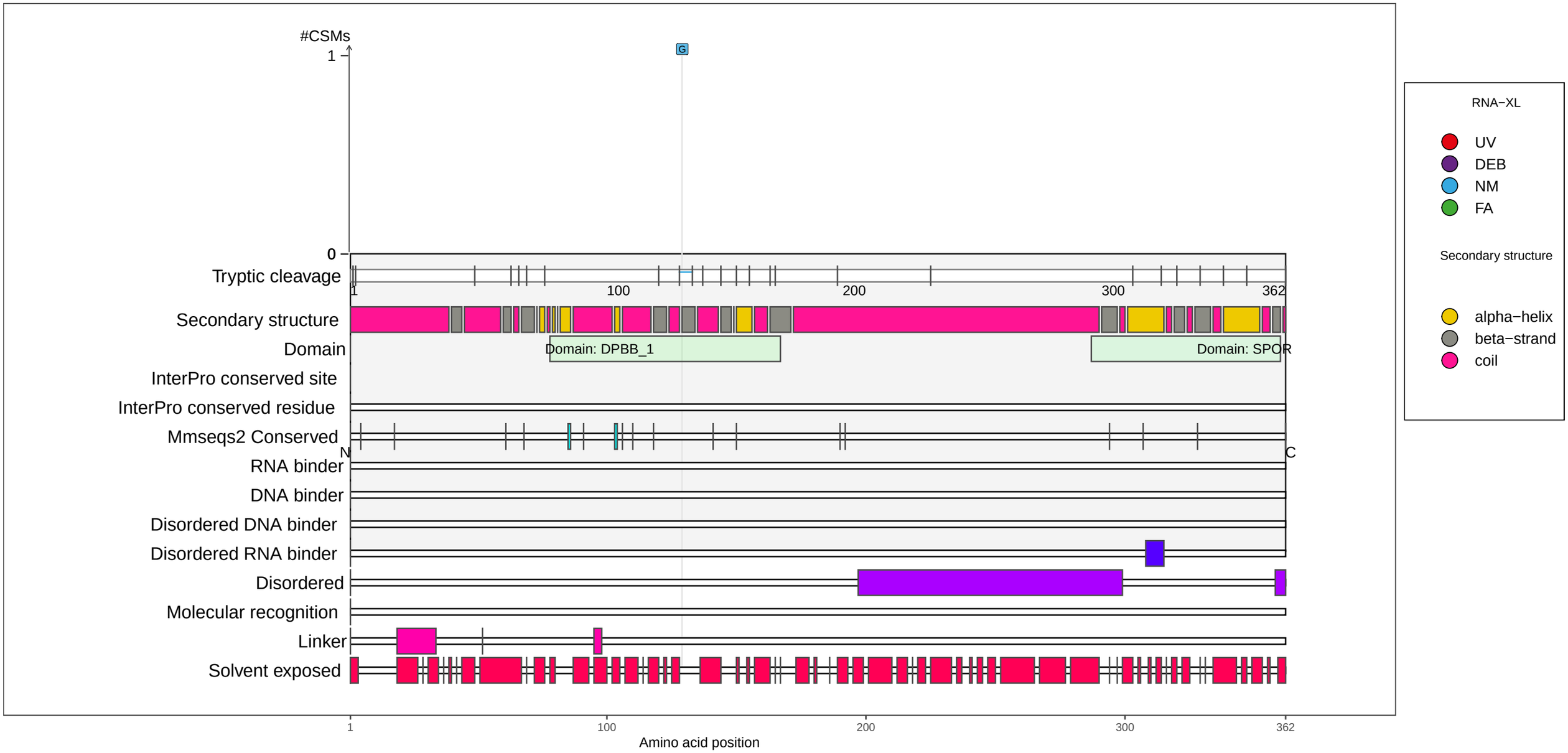
P0DP89
ILVGP_ECOLI Putative acetolactate synthase isozyme 2 large subunit
− RNA functions: not annotated



P10100
RLPA_ECOLI Endolytic peptidoglycan transglycosylase RlpA

− Abundance:
tryptic [log10 Intensity]: 7.7 (Q 44)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.58 (Q 62)

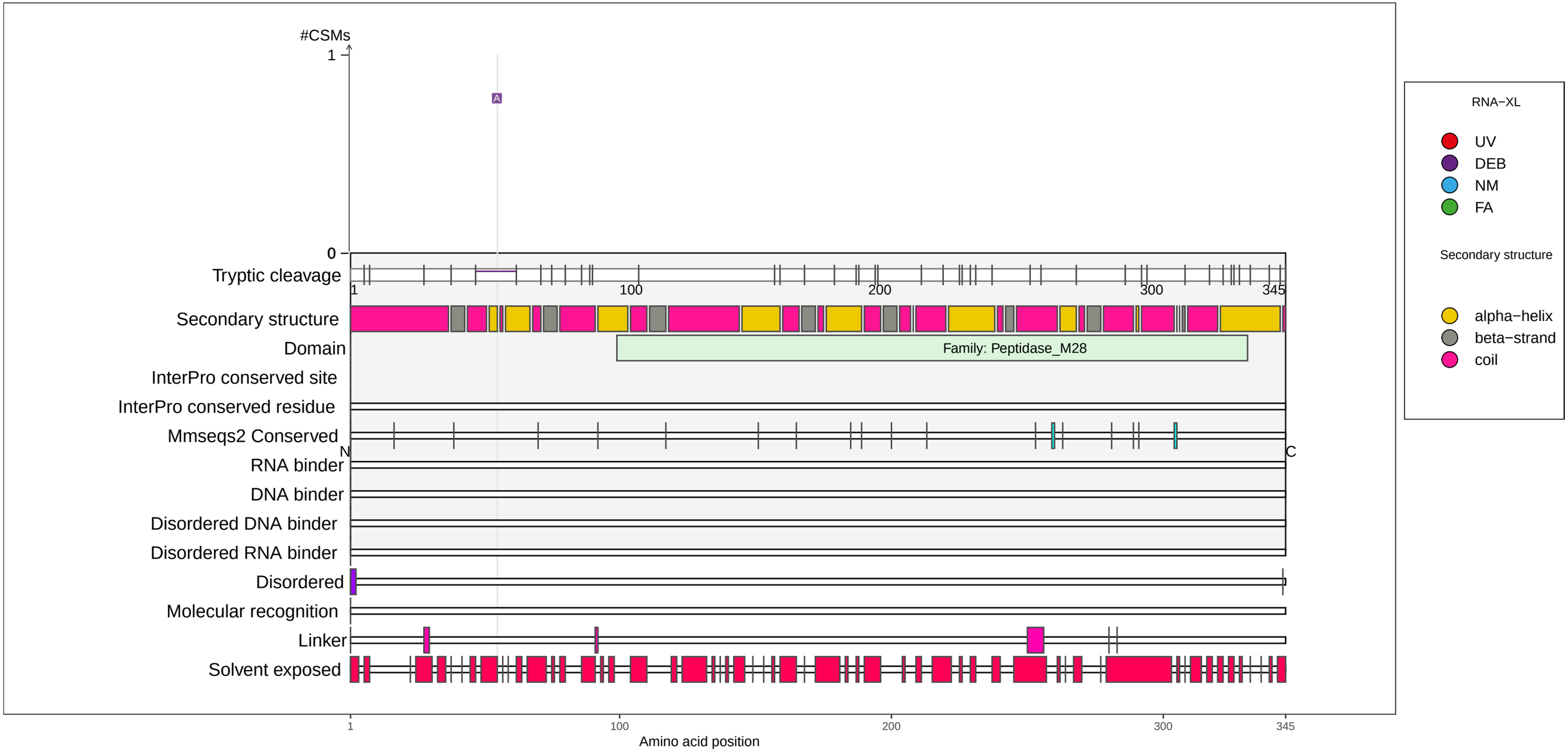
− RNA functions: not annotated



P10423
IAP_ECOLI Alkaline phosphatase isozyme conversion protein

− Abundance:
tryptic [log10 Intensity]: 8.83 (Q 84)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 0.05 (Q 26)

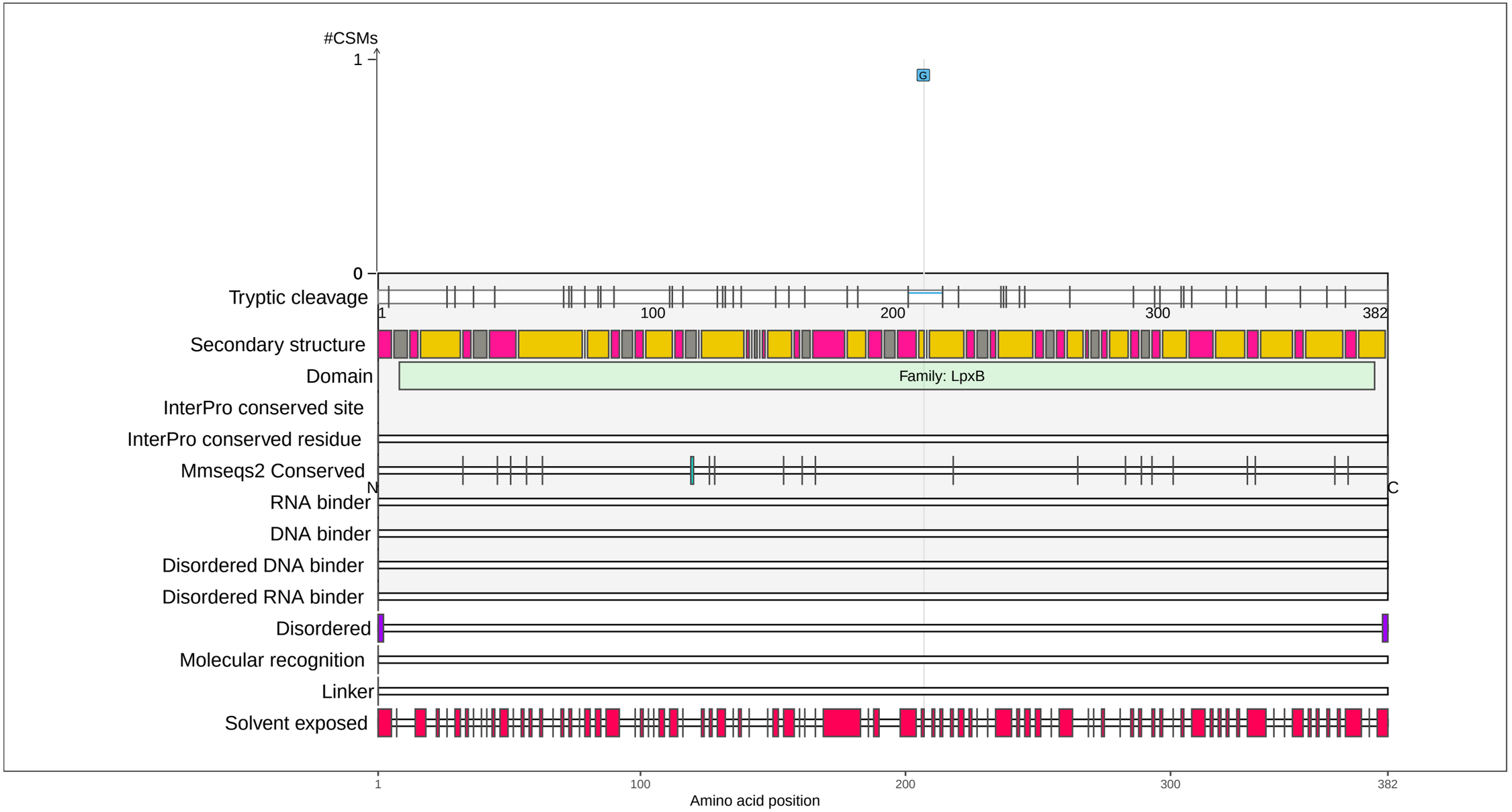
− RNA functions: not annotated



P10441
LPXB_ECOLI Lipid−A−disaccharide synthase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.79 (Q 5)
PAXdb E.coli [ppm]: 1.86 (Q 69)

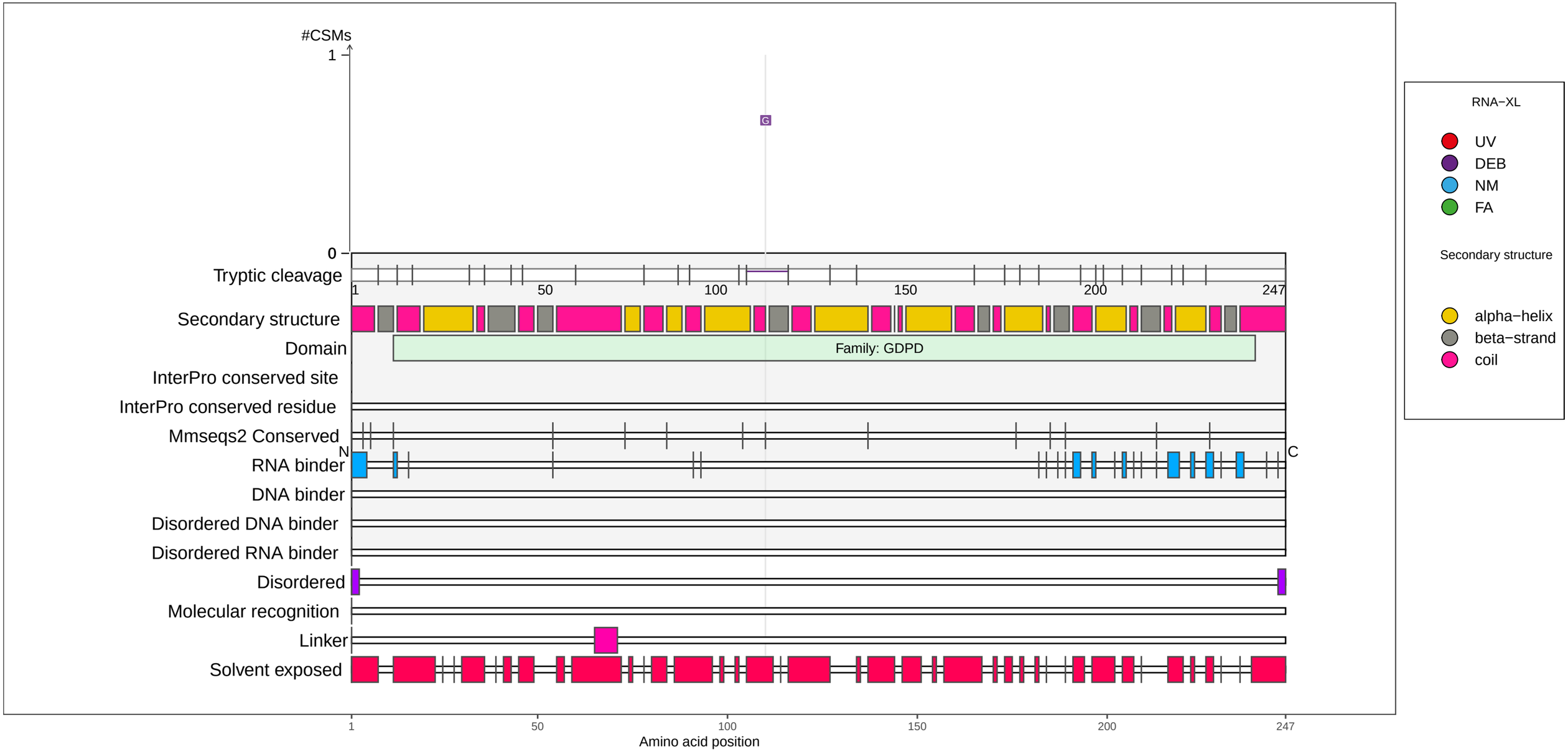
− RNA functions: not annotated



P10908
UGPQ_ECOLI Glycerophosphodiester phosphodiesterase, cytoplasmic

− Abundance:
tryptic [log10 Intensity]: 7.65 (Q 42)
PAXdb K12 strain [ppm]: 1.55 (Q 41)
PAXdb E.coli [ppm]: 1.53 (Q 60)

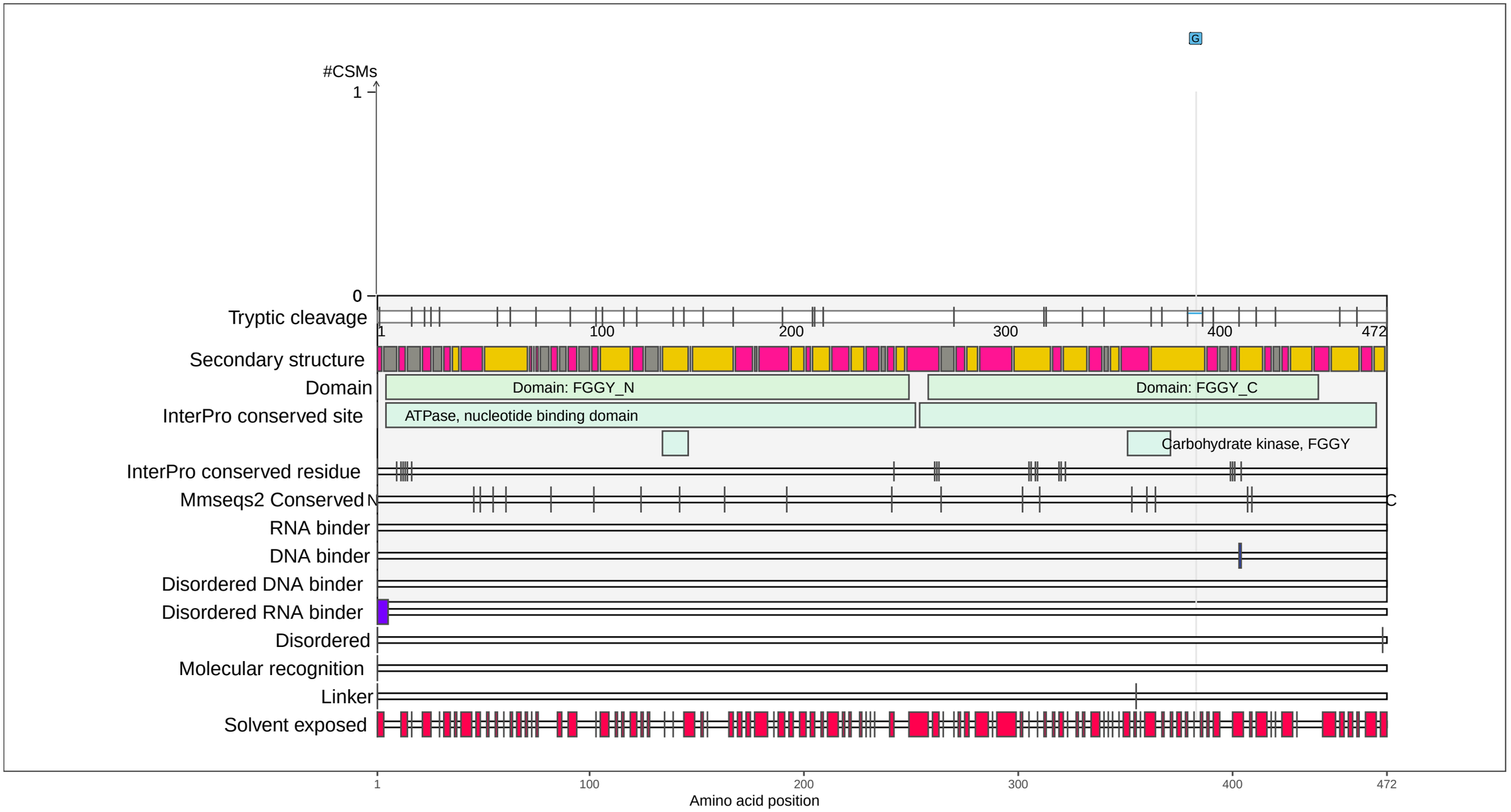
− RNA functions: not annotated



P11553
FUCK_ECOLI L−fuculokinase

− Abundance:
tryptic [log10 Intensity]: 7.71 (Q 45)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 1.41 (Q 57)

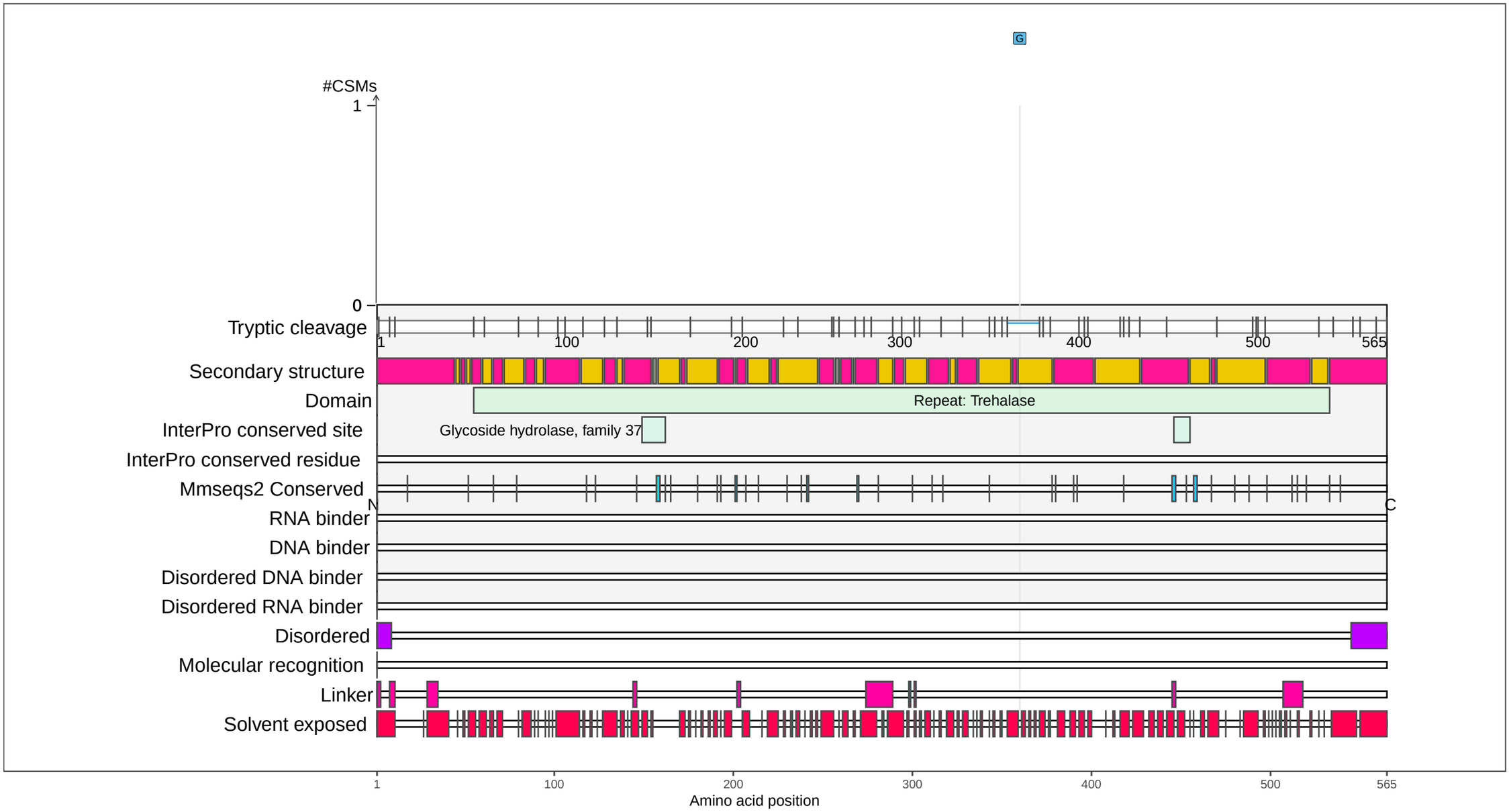
− RNA functions: not annotated



P13482
TREA_ECOLI Periplasmic trehalase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.62 (Q 46)
PAXdb E.coli [ppm]: 2.55 (Q 87)

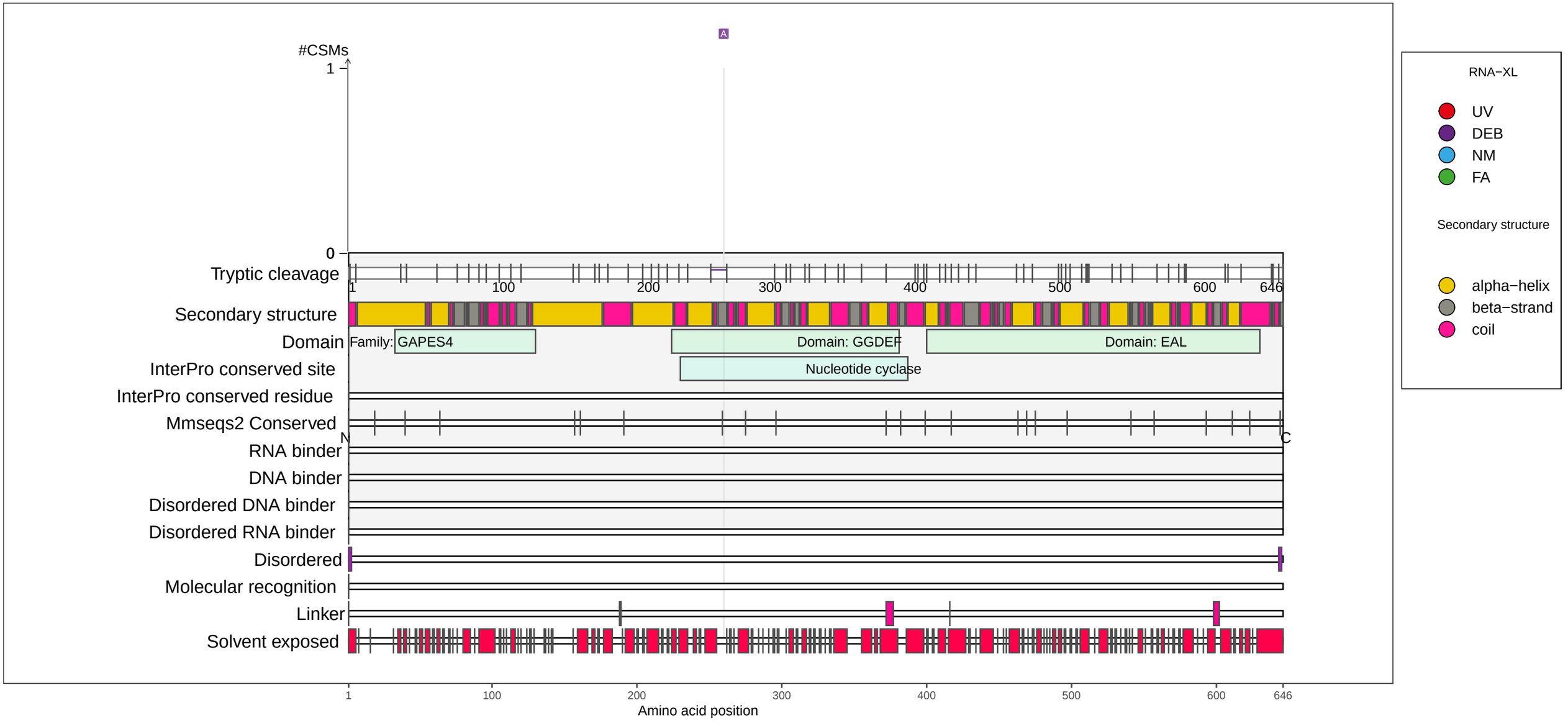
− RNA functions: not annotated



P13518
CSRD_ECOLI RNase E specificity factor CsrD

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.73 (Q 3)
PAXdb E.coli [ppm]: 1.27 (Q 54)

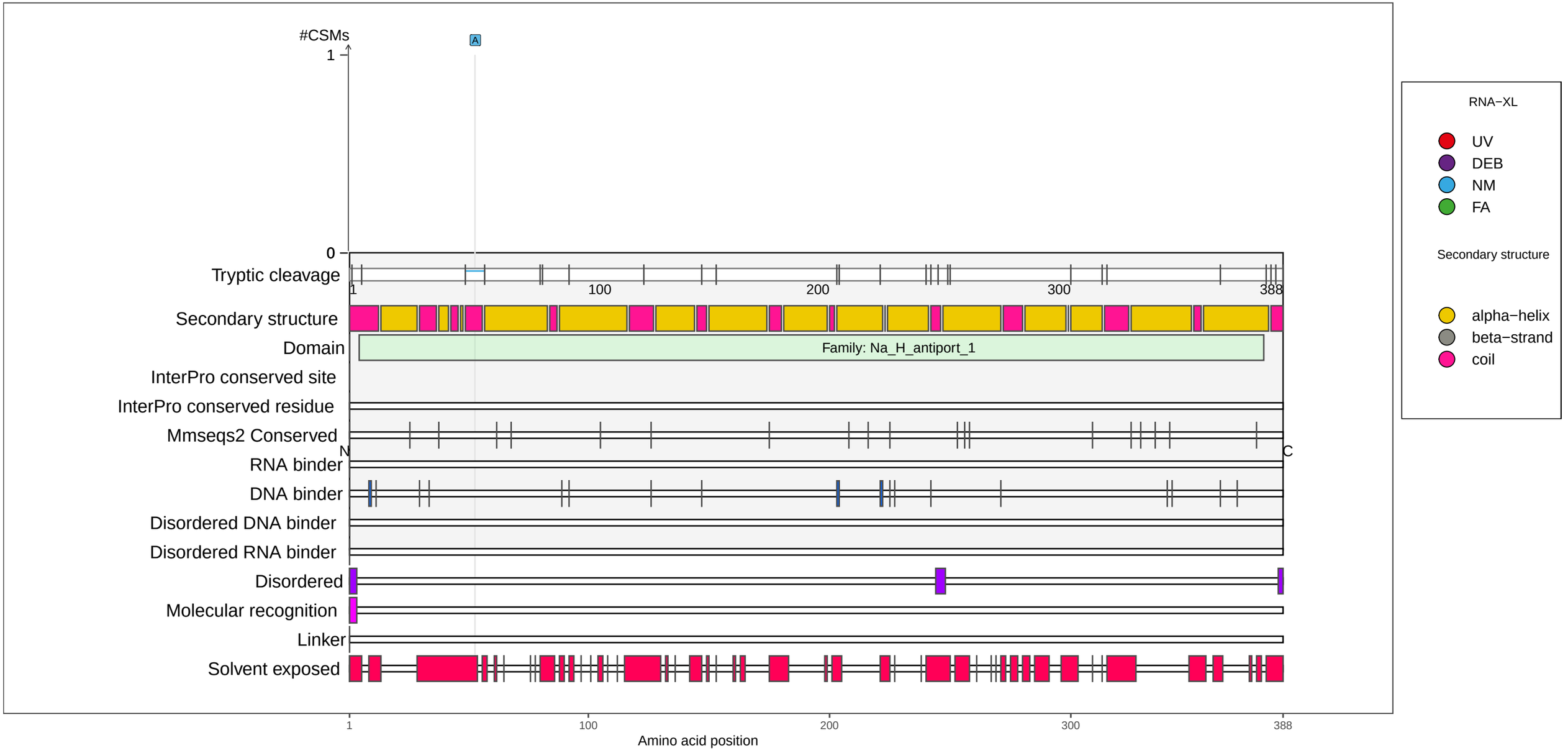
− RNA functions:
ncRNA catabolic process; ncRNA metabolic process; RNA catabolic process
RNA metabolic process



P13738
NHAA_ECOLI Na(+)/H(+) antiporter NhaA

− Abundance:
tryptic [log10 Intensity]: 7.27 (Q 24)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.72 (Q 41)

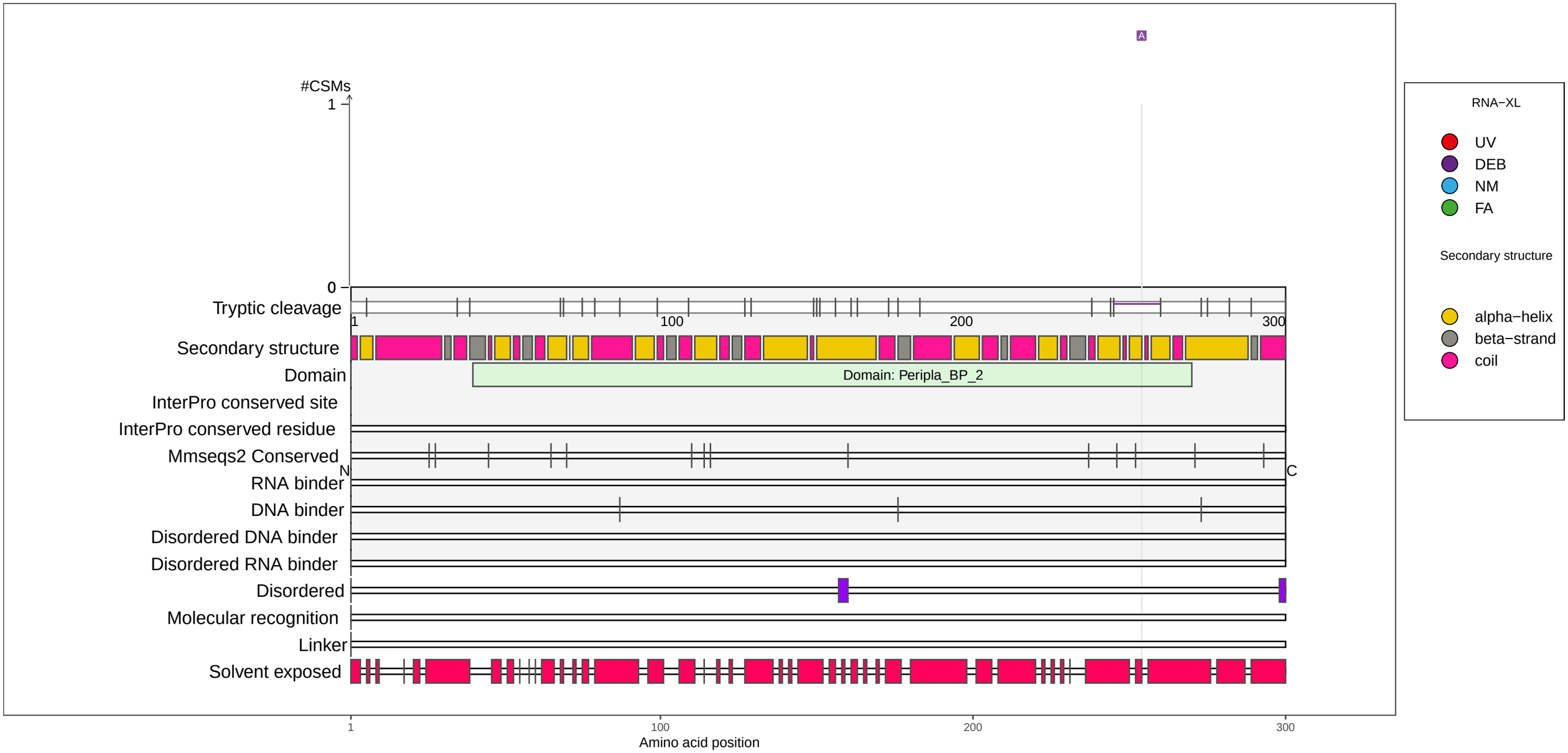
− RNA functions: not annotated



P15028
FECB_ECOLI Fe(3+) dicitrate−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.37 (Q 28)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.03 (Q 24)

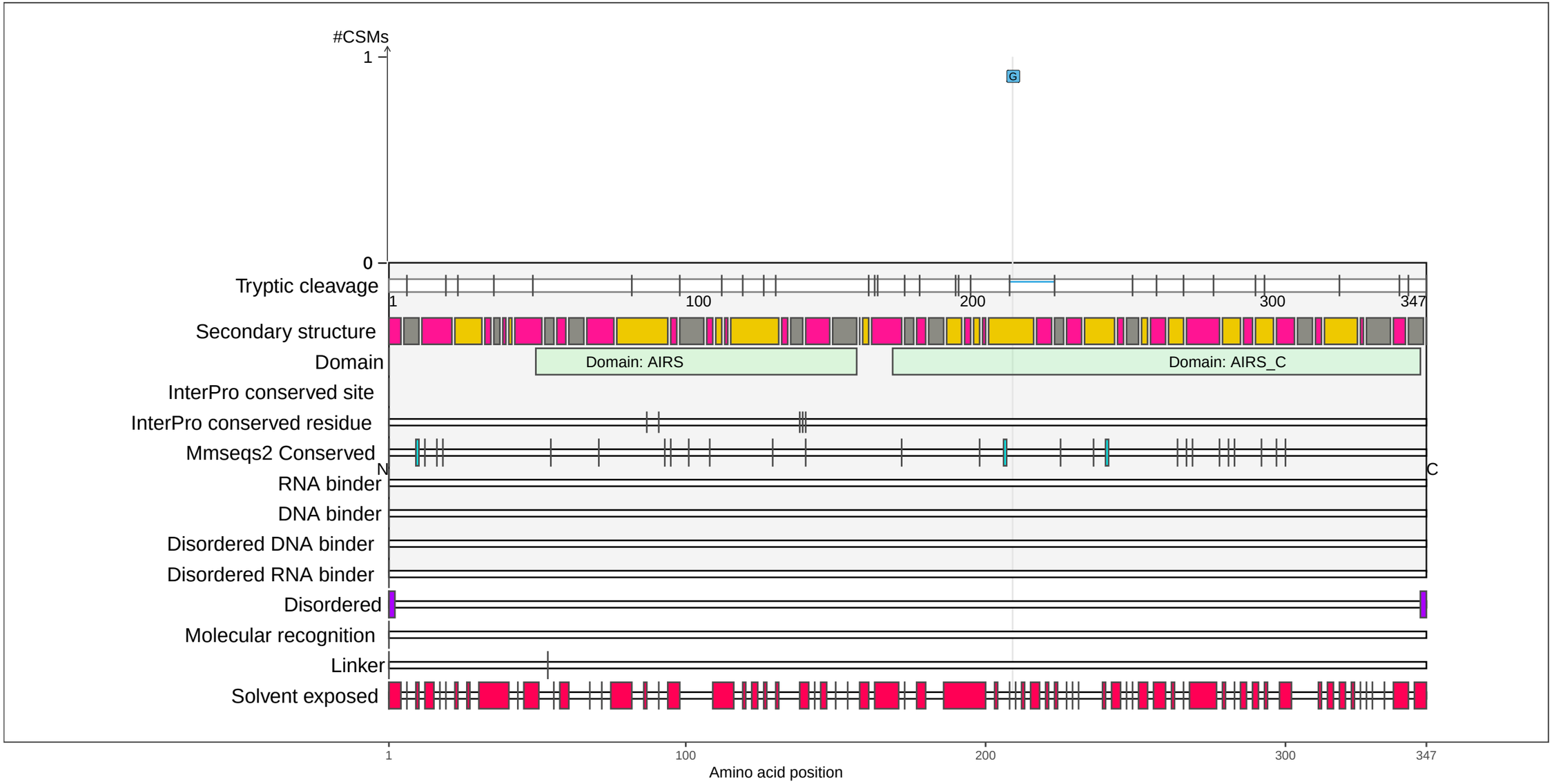
− RNA functions: not annotated

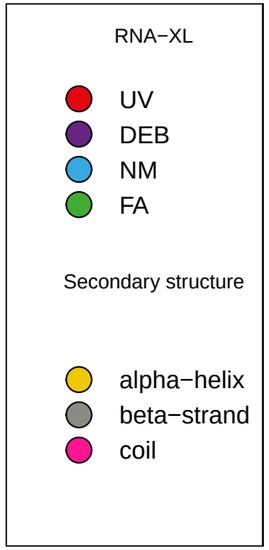


P16456
SELD_ECOLI Selenide, water dikinase

− Abundance:
tryptic [log10 Intensity]: 8.14 (Q 63)
PAXdb K12 strain [ppm]: 2.71 (Q 84)
PAXdb E.coli [ppm]: 2.37 (Q 82)

− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA seleno−modification

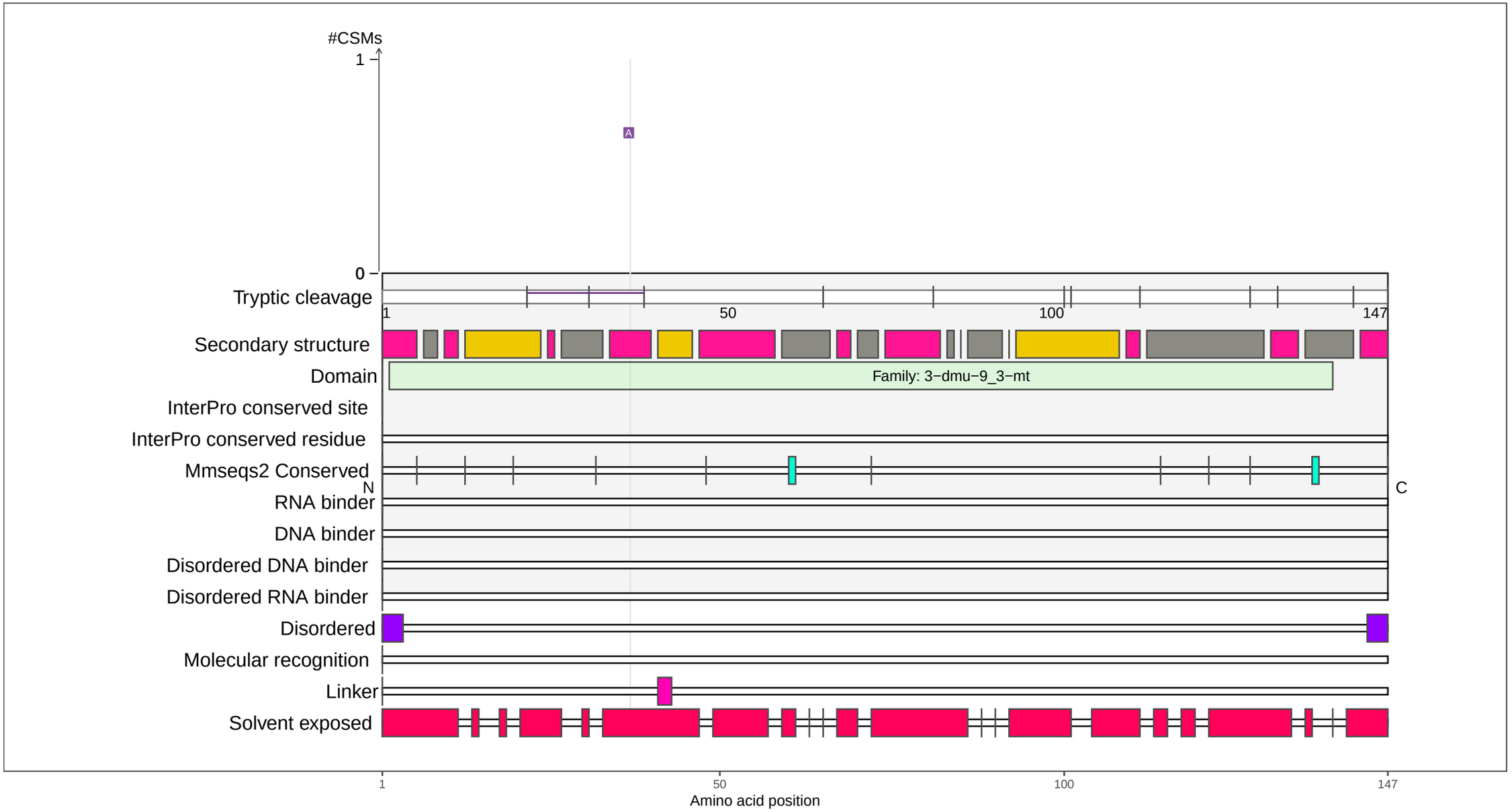




P16681
YJDN_ECOLI Protein YjdN

− Abundance:
tryptic [log10 Intensity]: 6.91 (Q 10)
PAXdb K12 strain [ppm]: 1.83 (Q 54)
PAXdb E.coli [ppm]: 2.53 (Q 86)

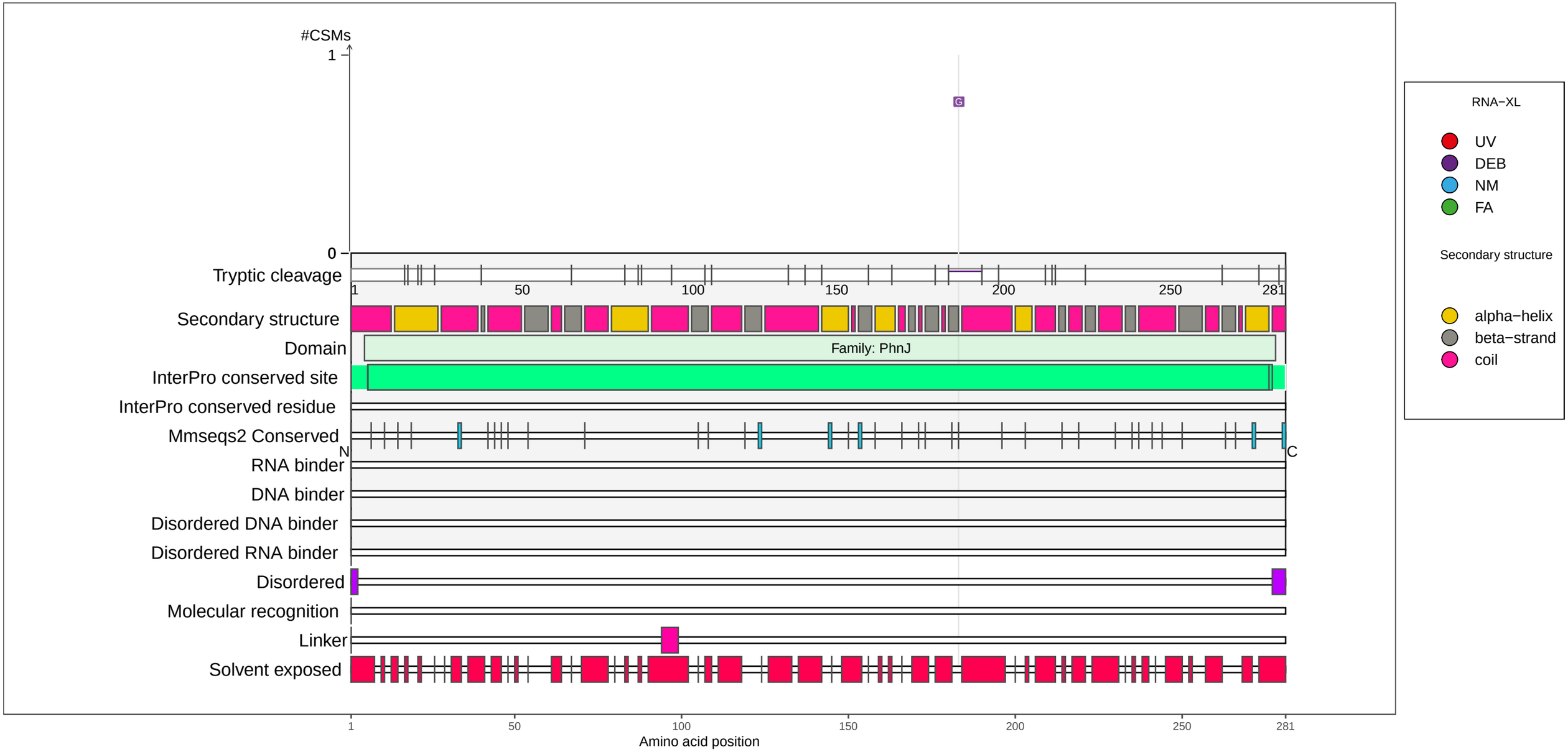
− RNA functions: not annotated



P16688
PHNJ_ECOLI Alpha−D−ribose 1−methylphosphonate 5−phosphate C−P lyase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.59 (Q 62)

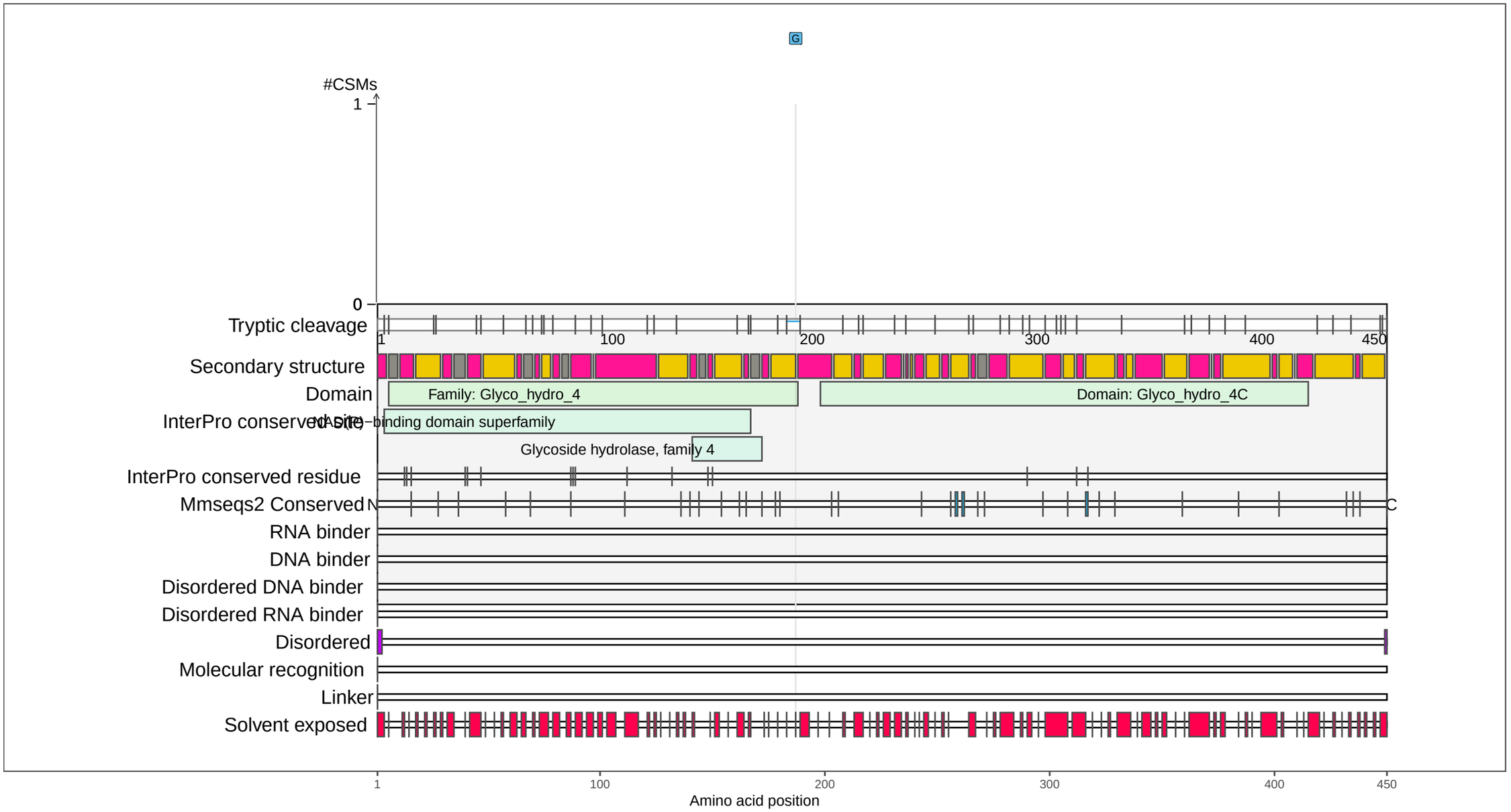
− RNA functions: not annotated



P17411
CHBF_ECOLI 6−phospho−beta−glucosidase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.25 (Q 23)
PAXdb E.coli [ppm]: −0.72 (Q 12)

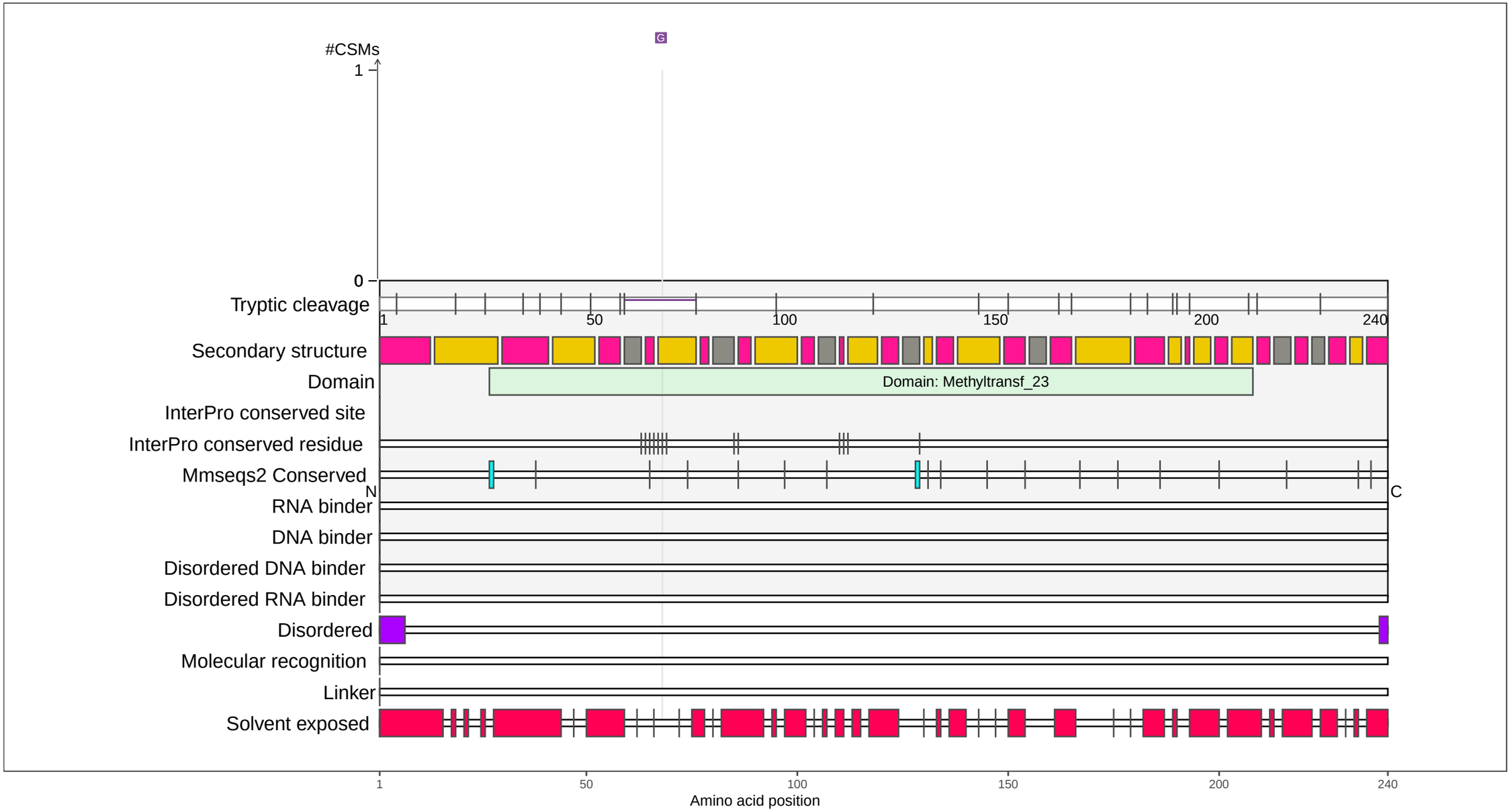
− RNA functions: not annotated



P17993
UBIG_ECOLI Ubiquinone biosynthesis O−methyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.72 (Q 45)
PAXdb K12 strain [ppm]: 2.52 (Q 78)
PAXdb E.coli [ppm]: 2.06 (Q 74)

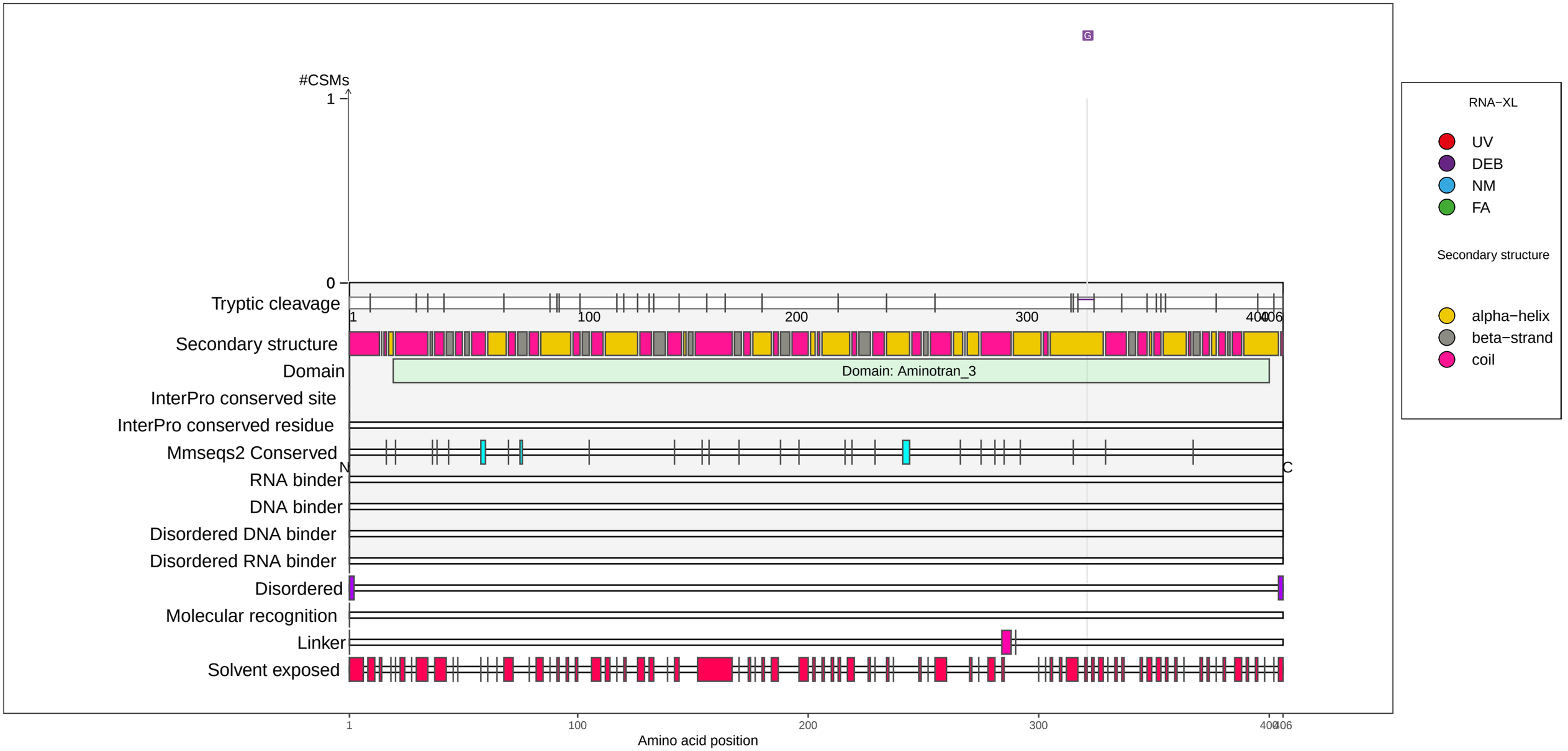
− RNA functions: not annotated



P18335
ARGD_ECOLI Acetylornithine/succinyldiaminopimelate aminotransferase

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 77)
PAXdb K12 strain [ppm]: 2.74 (Q 84)
PAXdb E.coli [ppm]: 2.51 (Q 86)

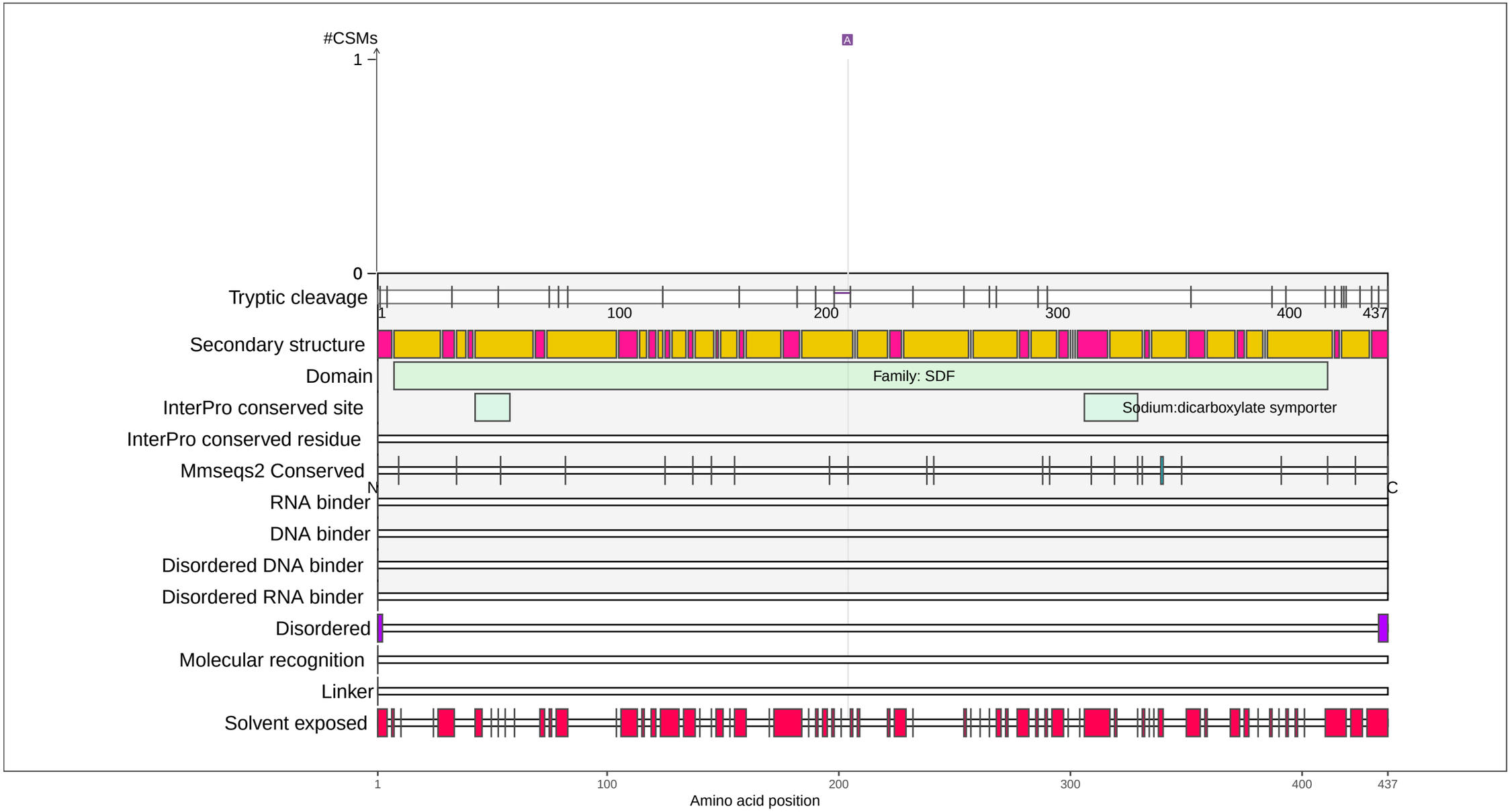
− RNA functions: not annotated

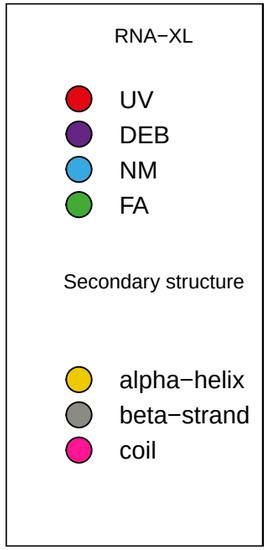


P21345
GLTP_ECOLI Proton/glutamate−aspartate symporter

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.58 (Q 38)

− RNA functions: not annotated

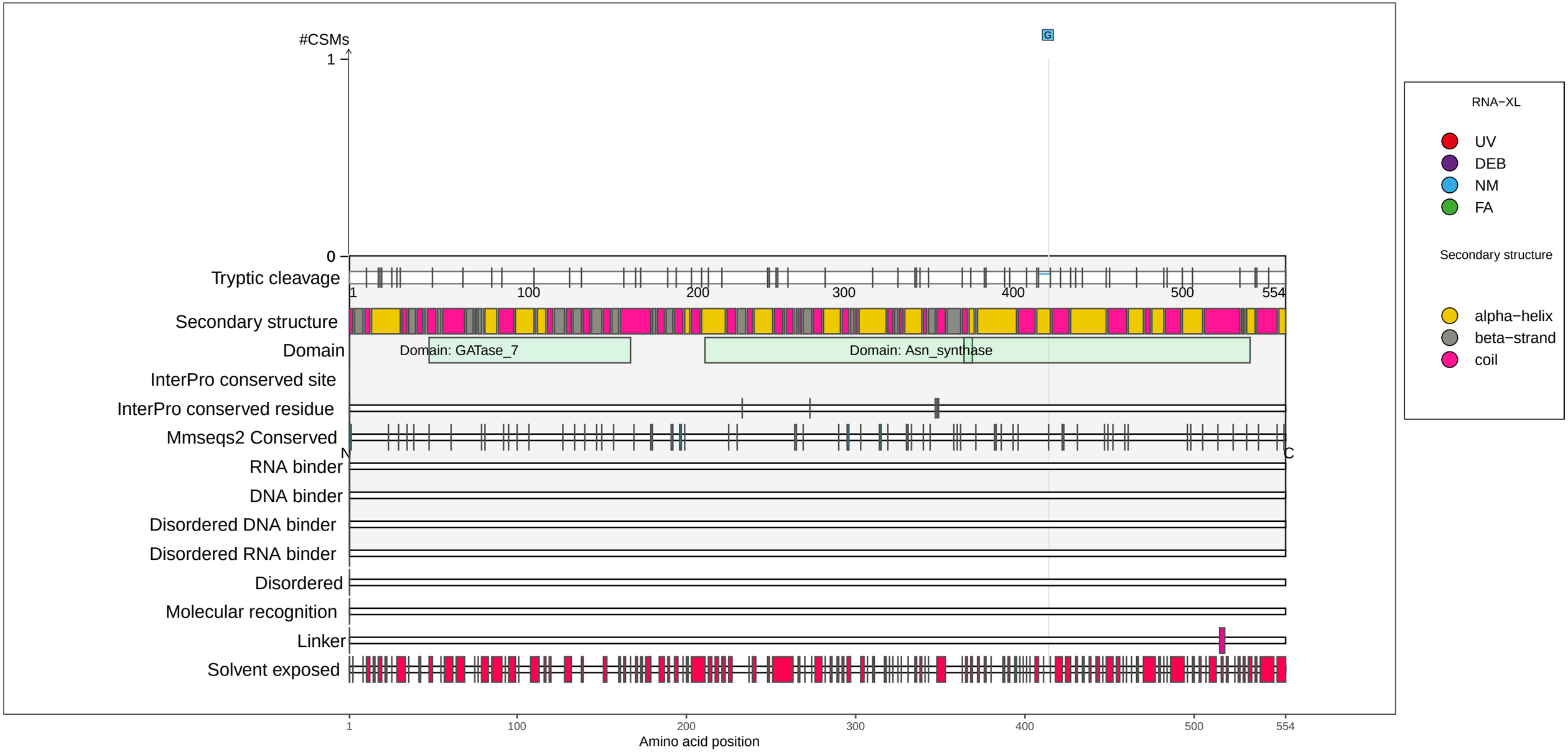




P22106
ASNB_ECOLI Asparagine synthetase B [glutamine−hydrolyzing]

− Abundance:
tryptic [log10 Intensity]: 8.19 (Q 65)
PAXdb K12 strain [ppm]: 2.44 (Q 76)
PAXdb E.coli [ppm]: 2.29 (Q 80)

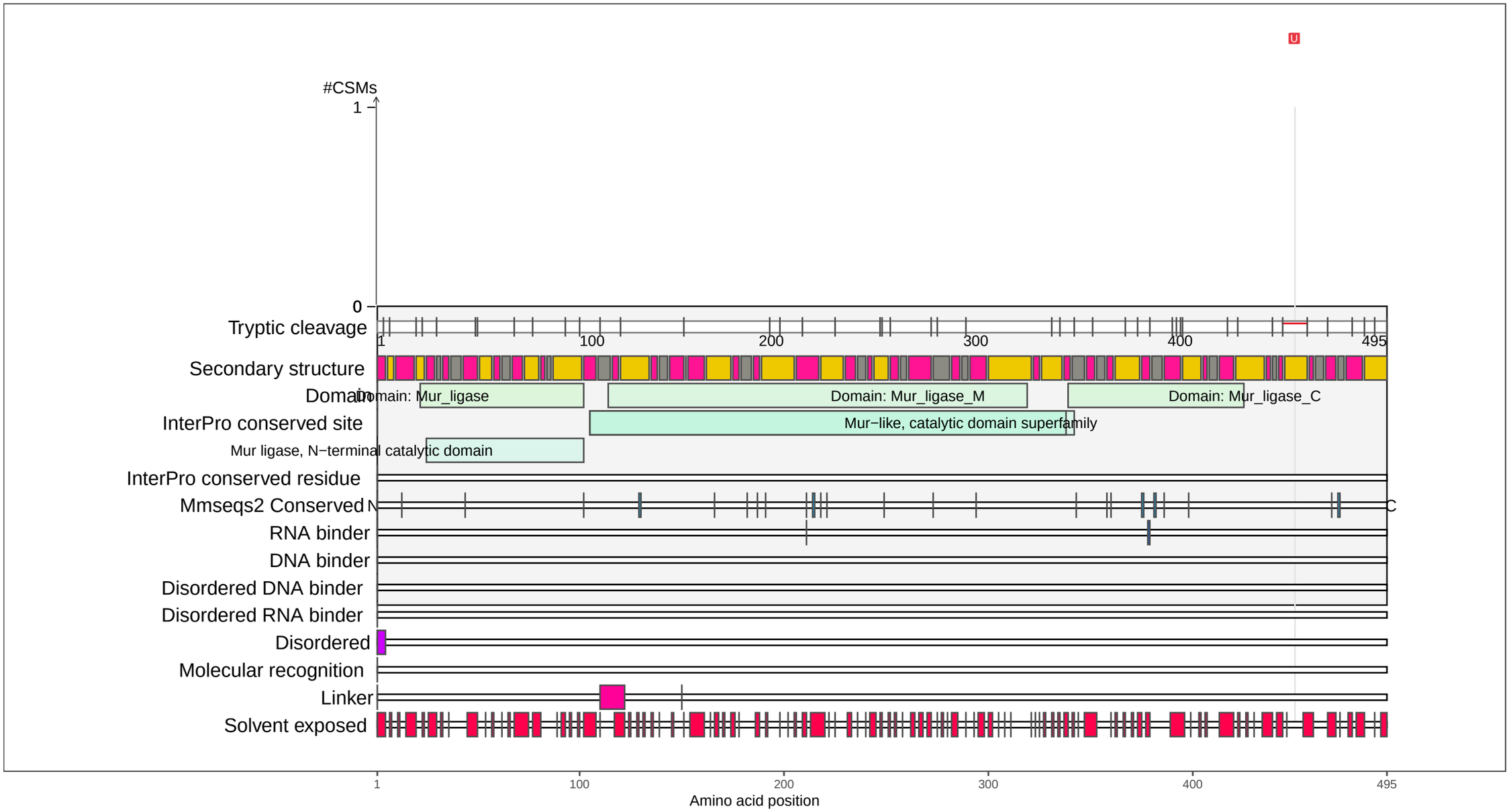
− RNA functions: not annotated



P22188
MURE_ECOLI UDP−N−acetylmuramoyl−L−alanyl−D−glutamate−−2,6−diaminopimelate ligase

− Abundance:
tryptic [log10 Intensity]: 8.53 (Q 76)
PAXdb K12 strain [ppm]: 1.94 (Q 58)
PAXdb E.coli [ppm]: 2.14 (Q 76)

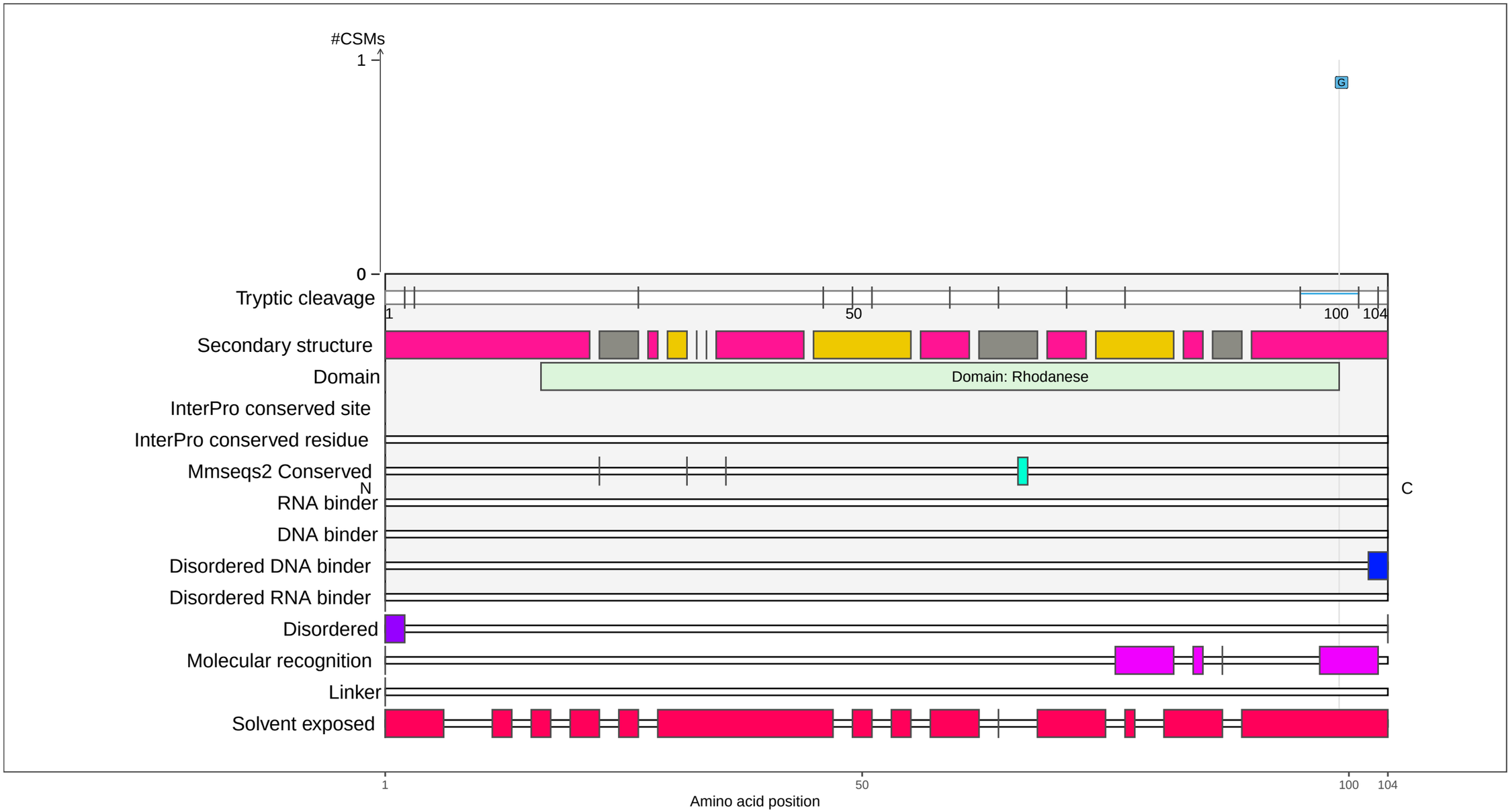
− RNA functions: not annotated



P23857
PSPE_ECOLI Thiosulfate sulfurtransferase PspE

− Abundance:
tryptic [log10 Intensity]: 9.21 (Q 93)
PAXdb K12 strain [ppm]: 2.94 (Q 89)
PAXdb E.coli [ppm]: 2.43 (Q 84)

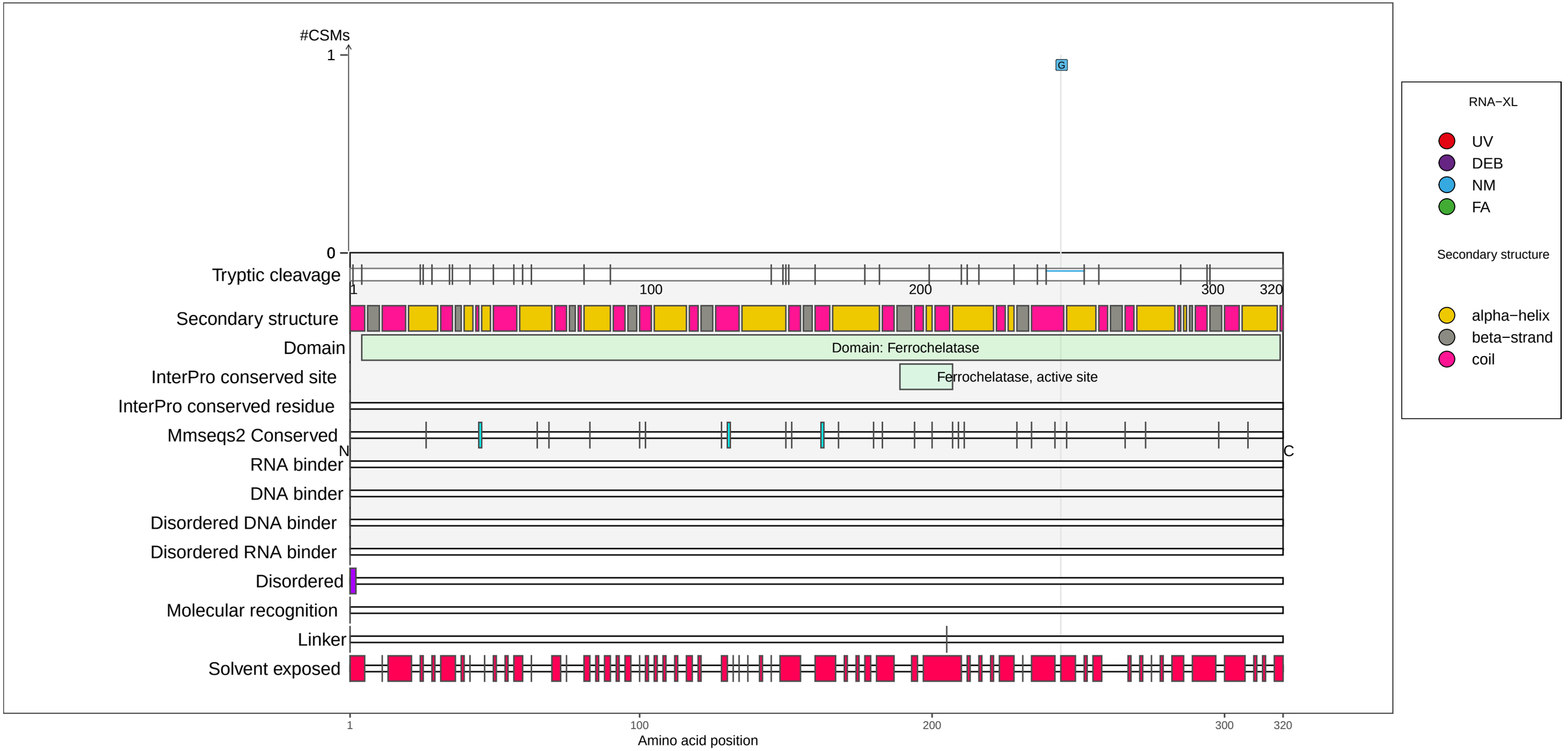
− RNA functions: not annotated



P23871
HEMH_ECOLI Ferrochelatase

− Abundance:
tryptic [log10 Intensity]: 7.02 (Q 14)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.71 (Q 41)

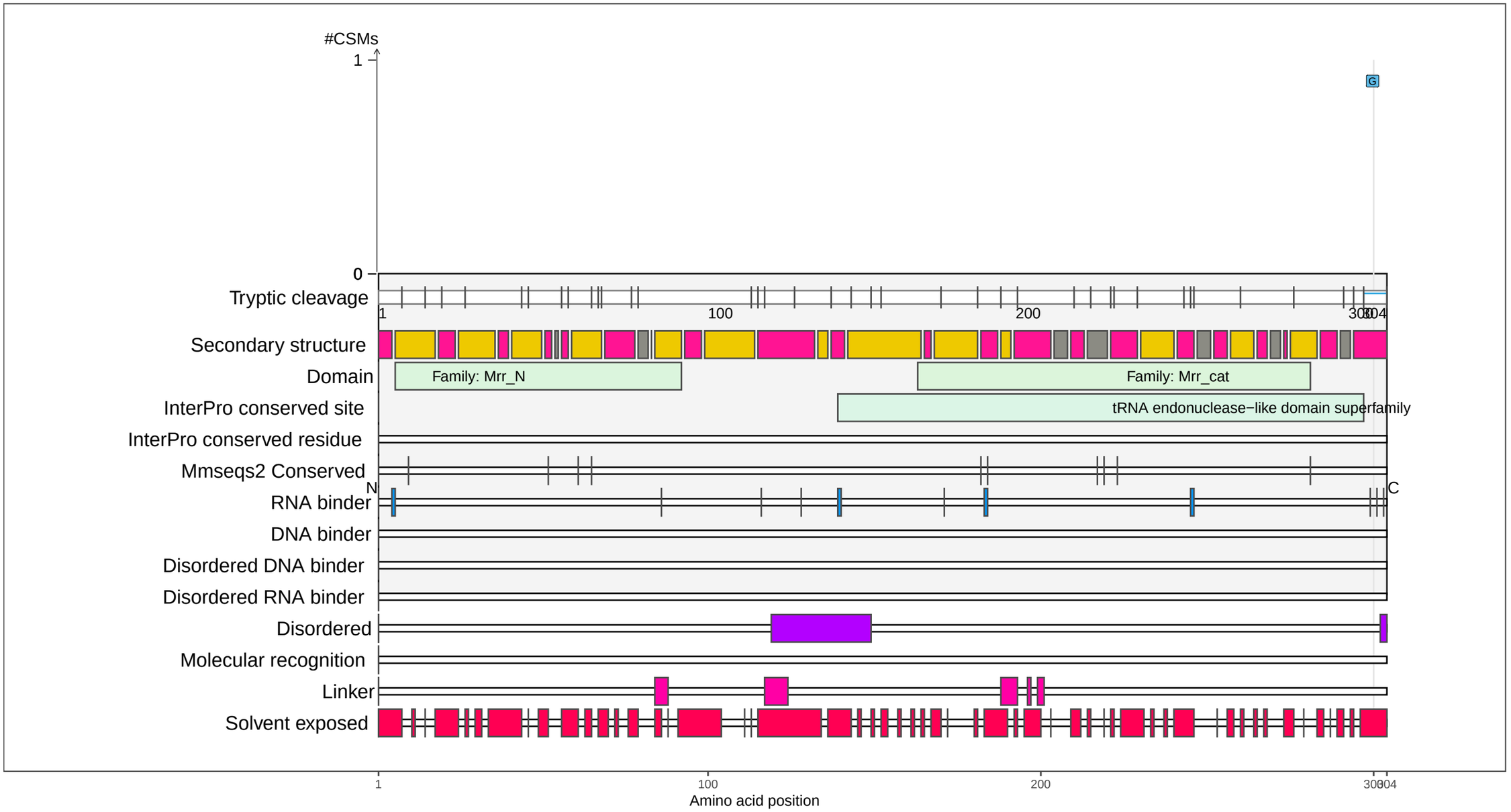
− RNA functions: not annotated



P24202
MRR_ECOLI Type IV methyl−directed restriction enzyme EcoKMrr

− Abundance:
tryptic [log10 Intensity]: 8.06 (Q 60)
PAXdb K12 strain [ppm]: 1.47 (Q 36)
PAXdb E.coli [ppm]: 1.24 (Q 53)

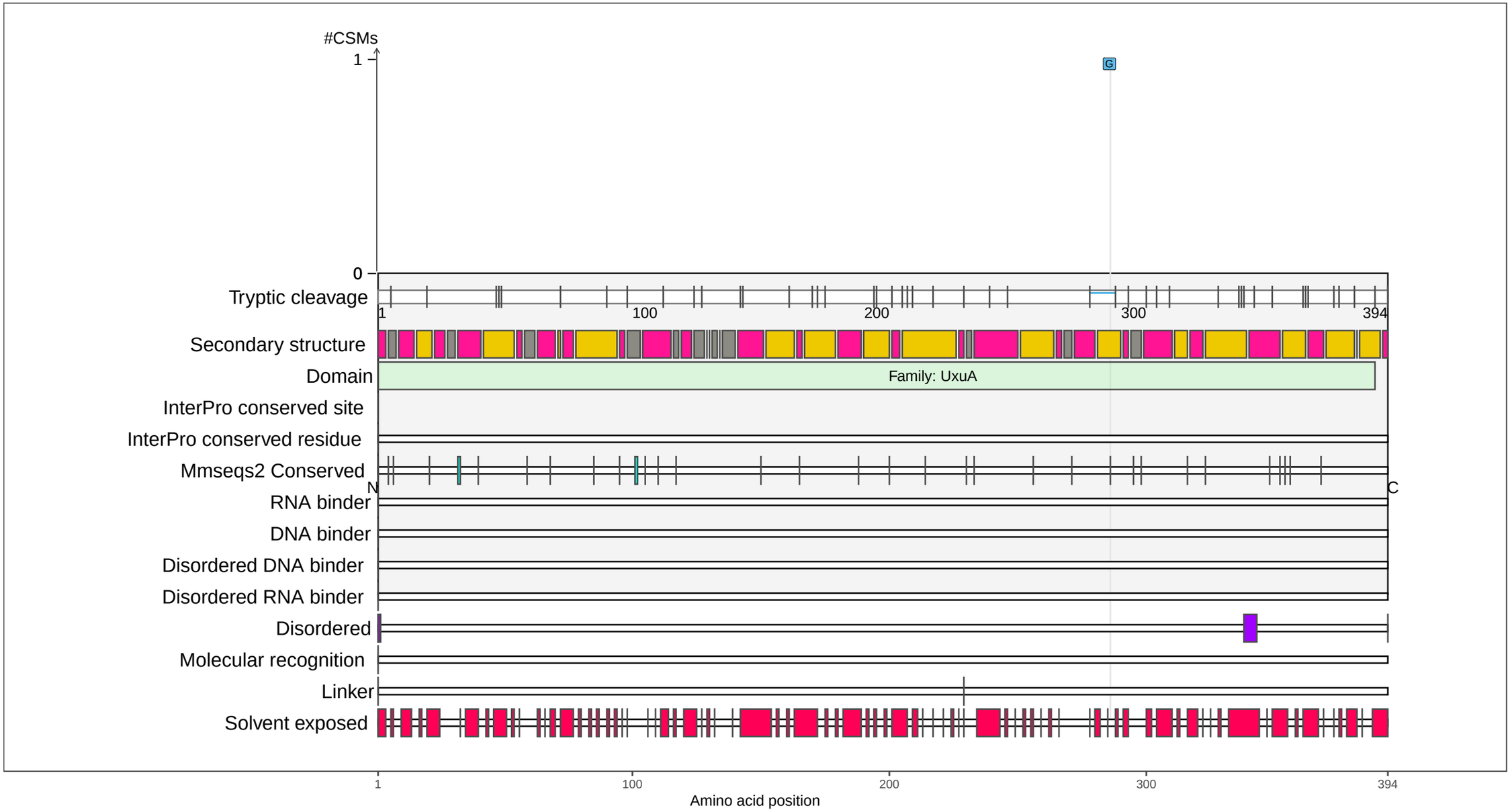
− RNA functions: not annotated



P24215
UXUA_ECOLI Mannonate dehydratase

− Abundance:
tryptic [log10 Intensity]: 7.69 (Q 44)
PAXdb K12 strain [ppm]: 2.21 (Q 67)
PAXdb E.coli [ppm]: 2.17 (Q 77)

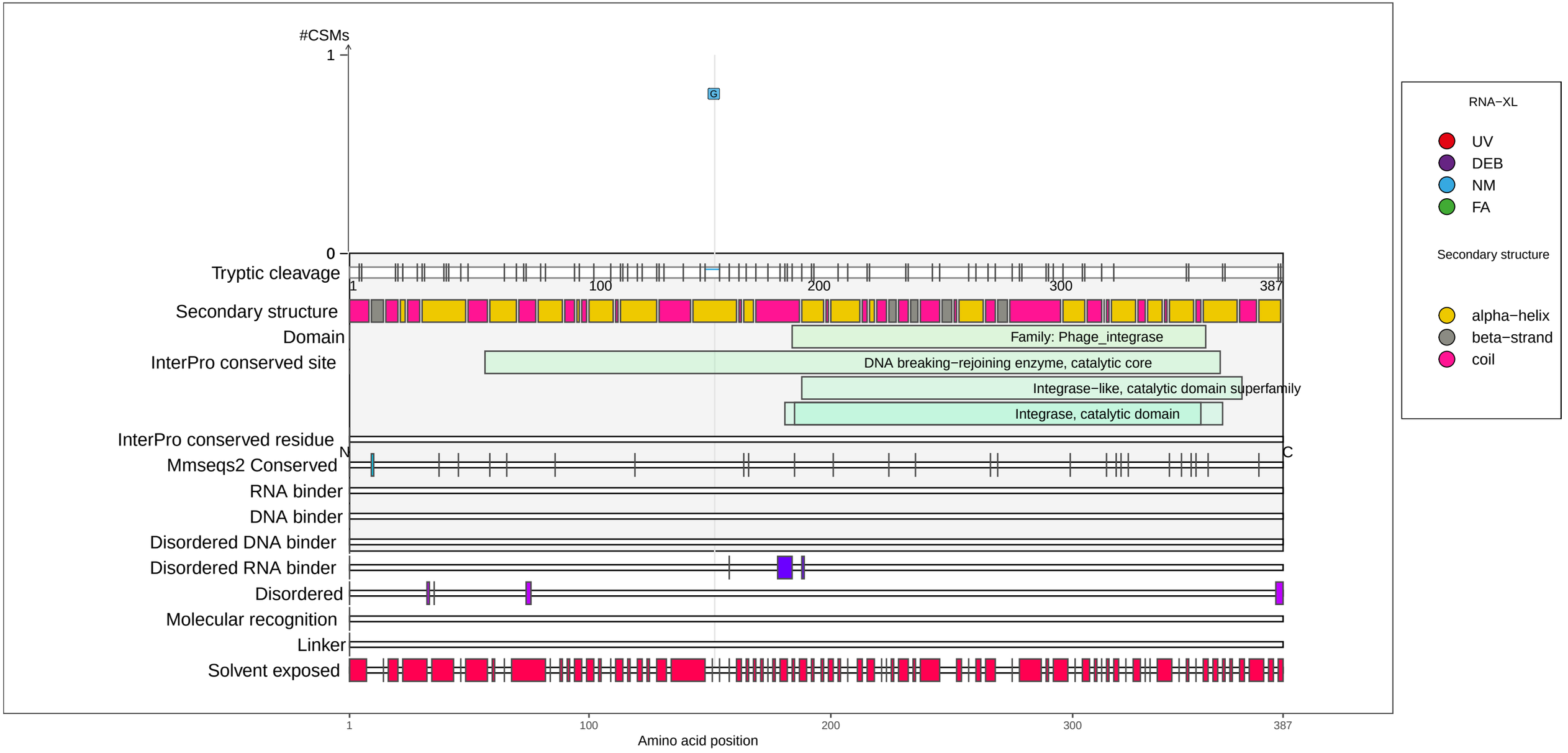
− RNA functions: not annotated



P24218
INTD_ECOLI Prophage integrase IntD

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.75 (Q 42)

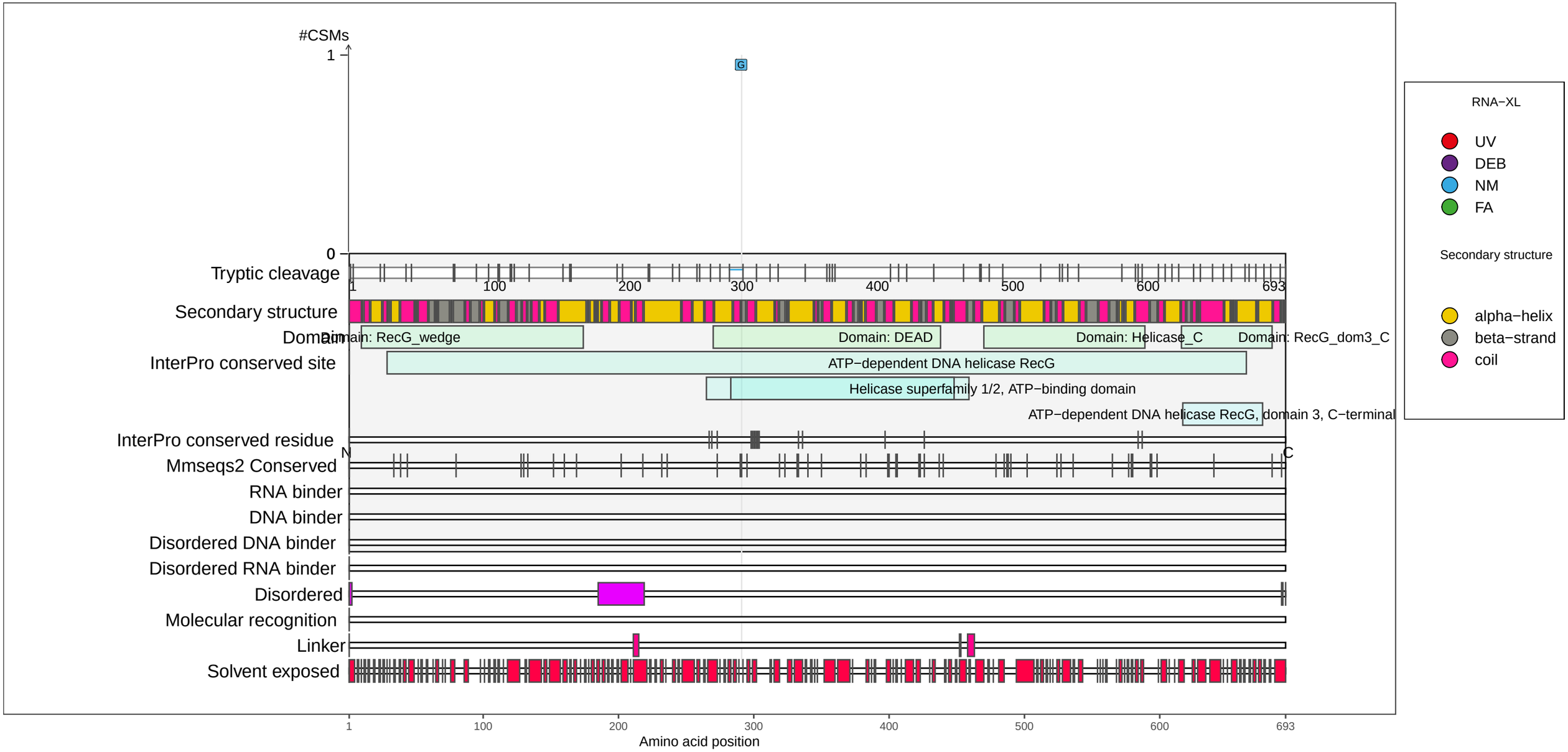
− RNA functions: not annotated



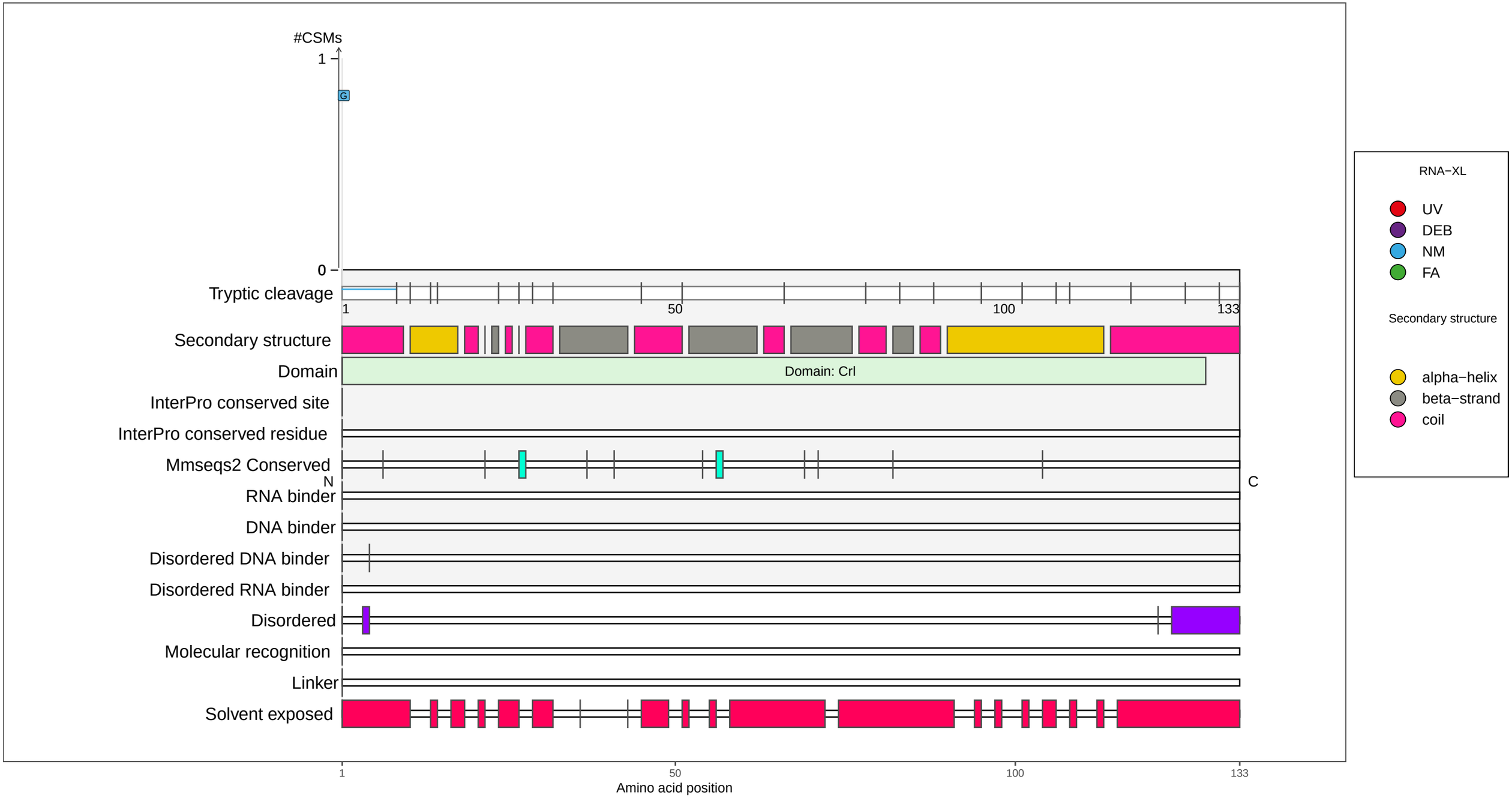
P24230
RECG_ECOLI ATP−dependent DNA helicase RecG

− Abundance:
tryptic [log10 Intensity]: 6.79 (Q 7)
PAXdb K12 strain [ppm]: 1.24 (Q 22)
PAXdb E.coli [ppm]: 1.23 (Q 53)

− RNA functions: not annotated



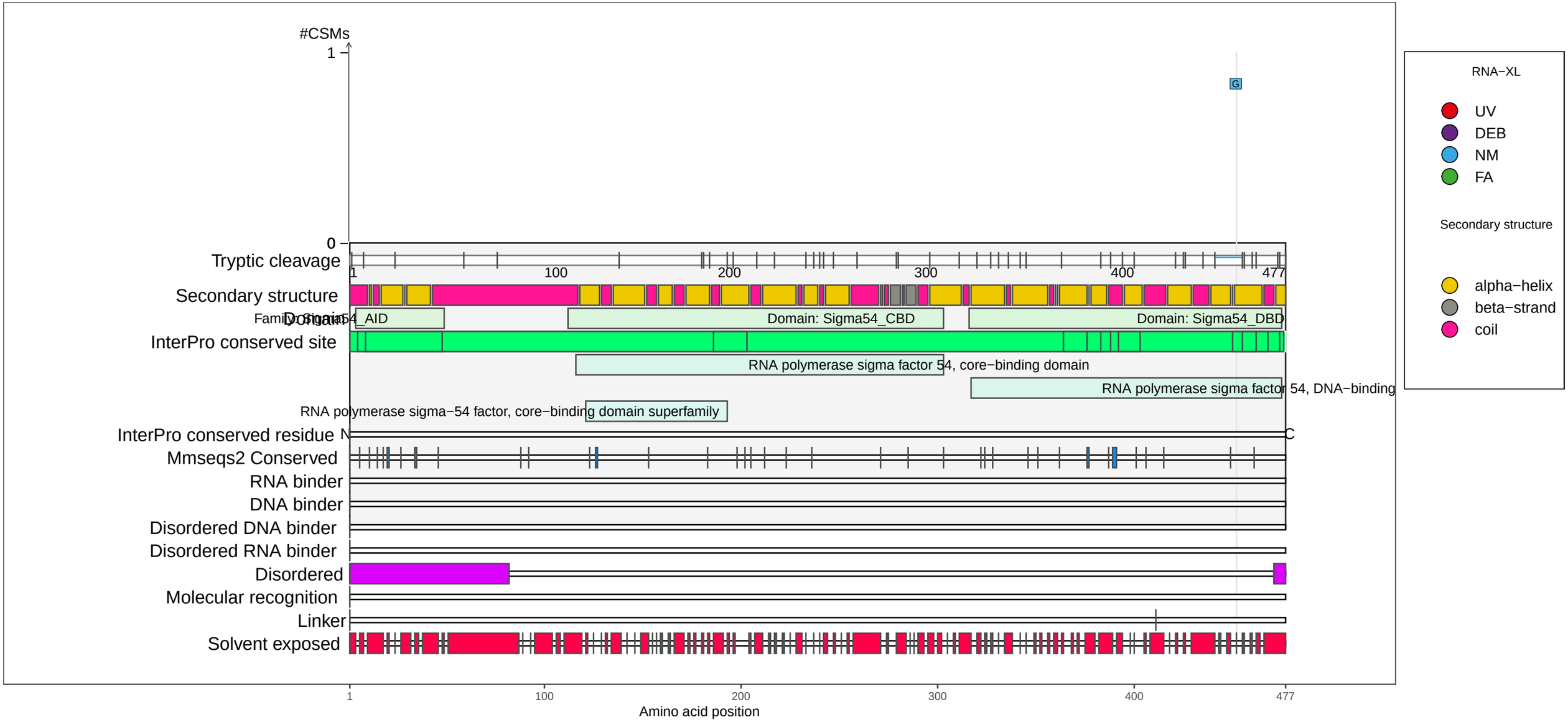
P24251
CRL_ECOLI Sigma factor−binding protein Crl
− RNA functions: not annotated



P24255
RP54_ECOLI RNA polymerase sigma−54 factor

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 2.06 (Q 74)

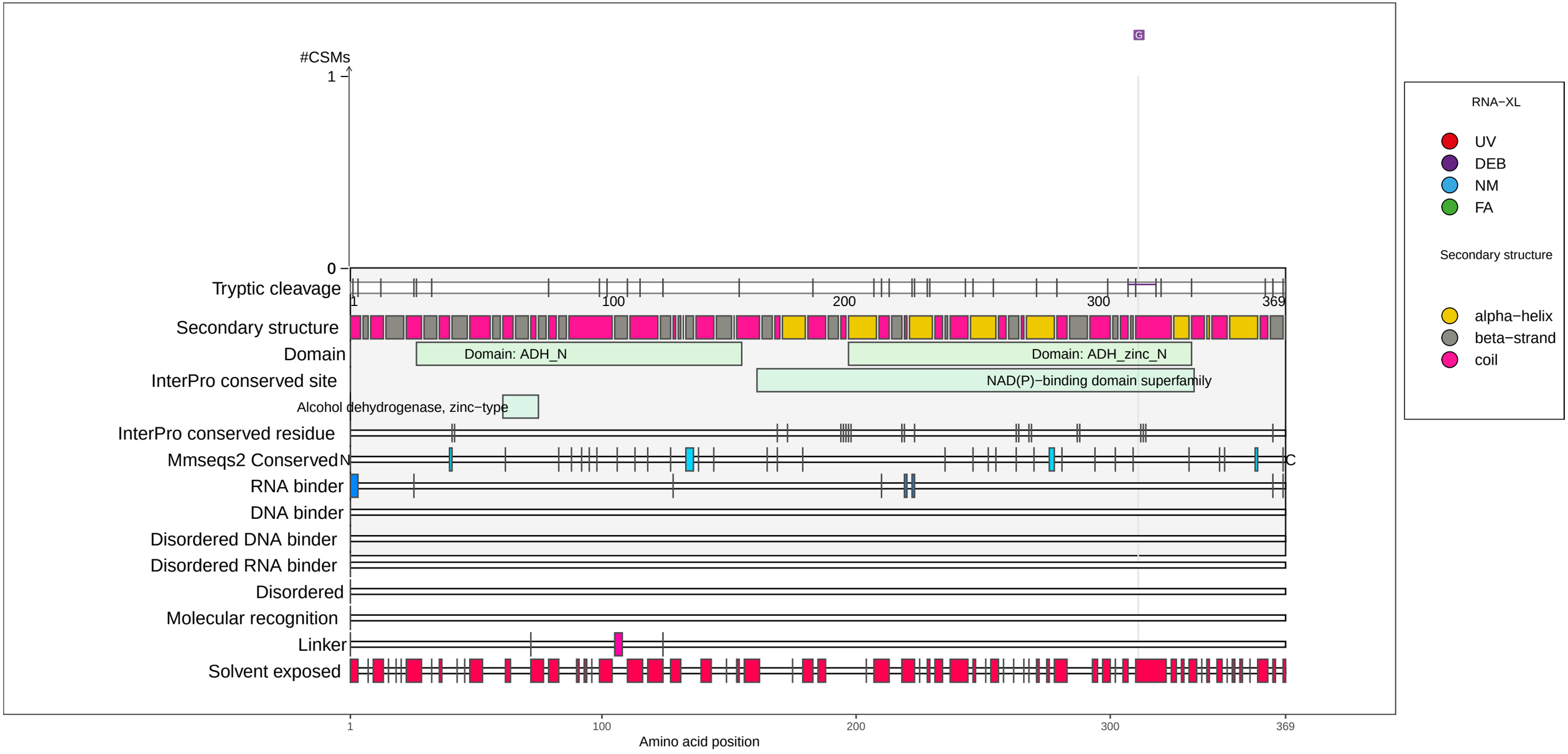
− RNA functions:
5−3 RNA polymerase activity; DNA−directed 5−3 RNA polymerase activity
RNA biosynthetic process; RNA metabolic process; RNA polymerase activity



P25437
FRMA_ECOLI S−(hydroxymethyl)glutathione dehydrogenase

− Abundance:
tryptic [log10 Intensity]: 7.85 (Q 51)
PAXdb K12 strain [ppm]: 2.3 (Q 70)
PAXdb E.coli [ppm]: 2.25 (Q 79)

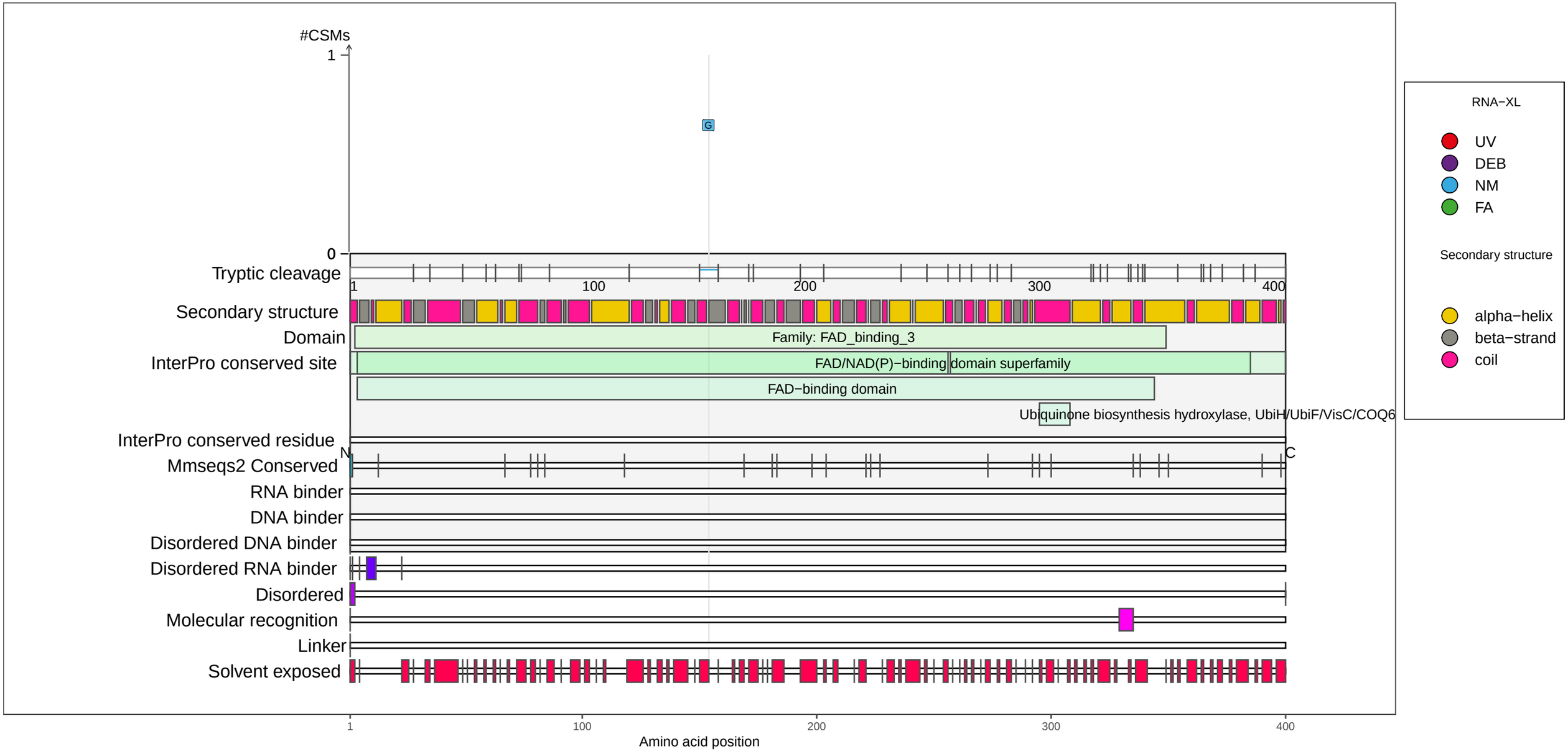
− RNA functions: not annotated



P25535
UBII_ECOLI 2−octaprenylphenol hydroxylase

− Abundance:
tryptic [log10 Intensity]: 7.67 (Q 43)
PAXdb K12 strain [ppm]: 1.67 (Q 48)
PAXdb E.coli [ppm]: 1.81 (Q 67)

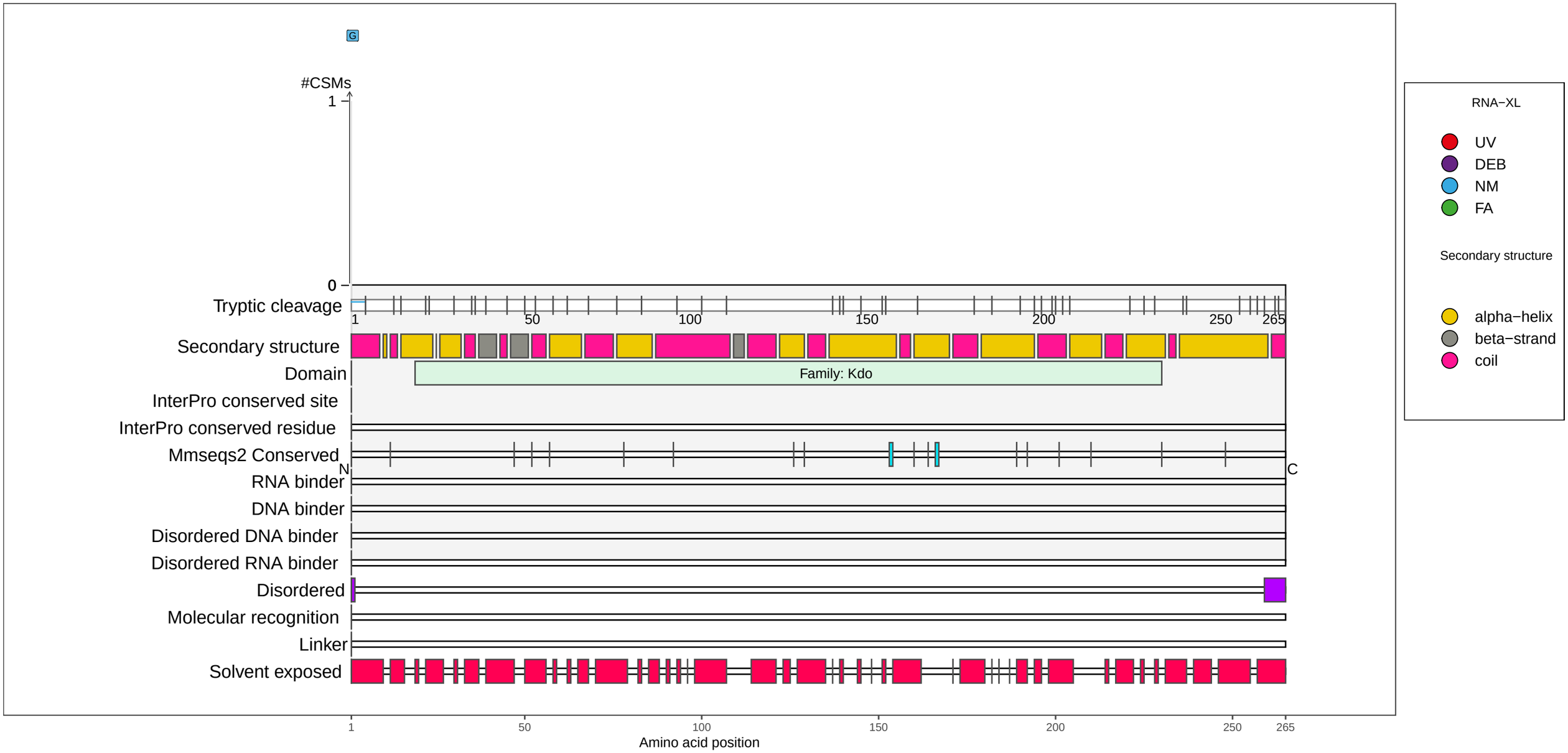
− RNA functions: not annotated



P25741
RFAP_ECOLI Lipopolysaccharide core heptose(I) kinase RfaP

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.66 (Q 48)
PAXdb E.coli [ppm]: 0.8 (Q 43)

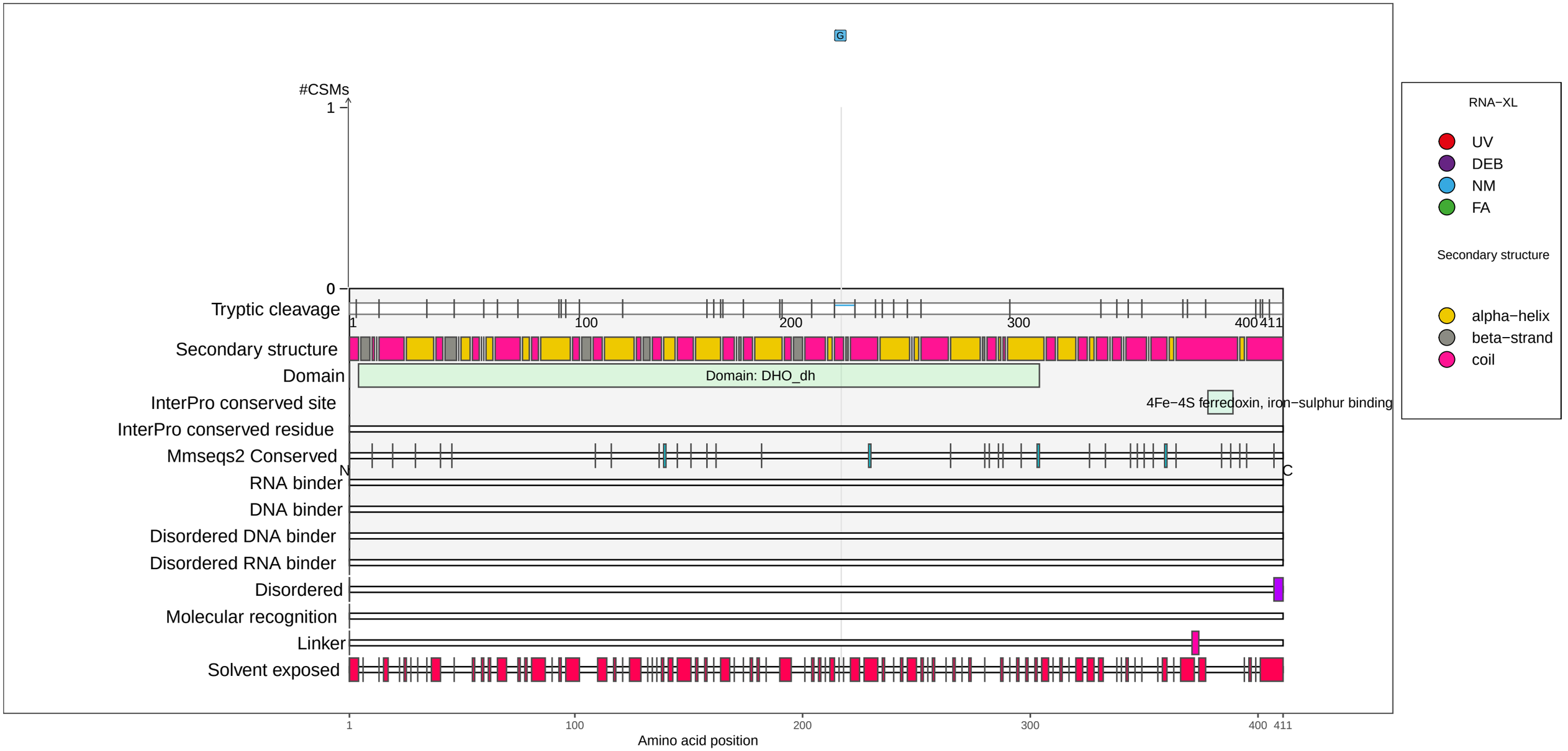
− RNA functions: not annotated



P25889
PREA_ECOLI NAD−dependent dihydropyrimidine dehydrogenase subunit PreA

− Abundance:
tryptic [log10 Intensity]: 7.86 (Q 52)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.57 (Q 62)

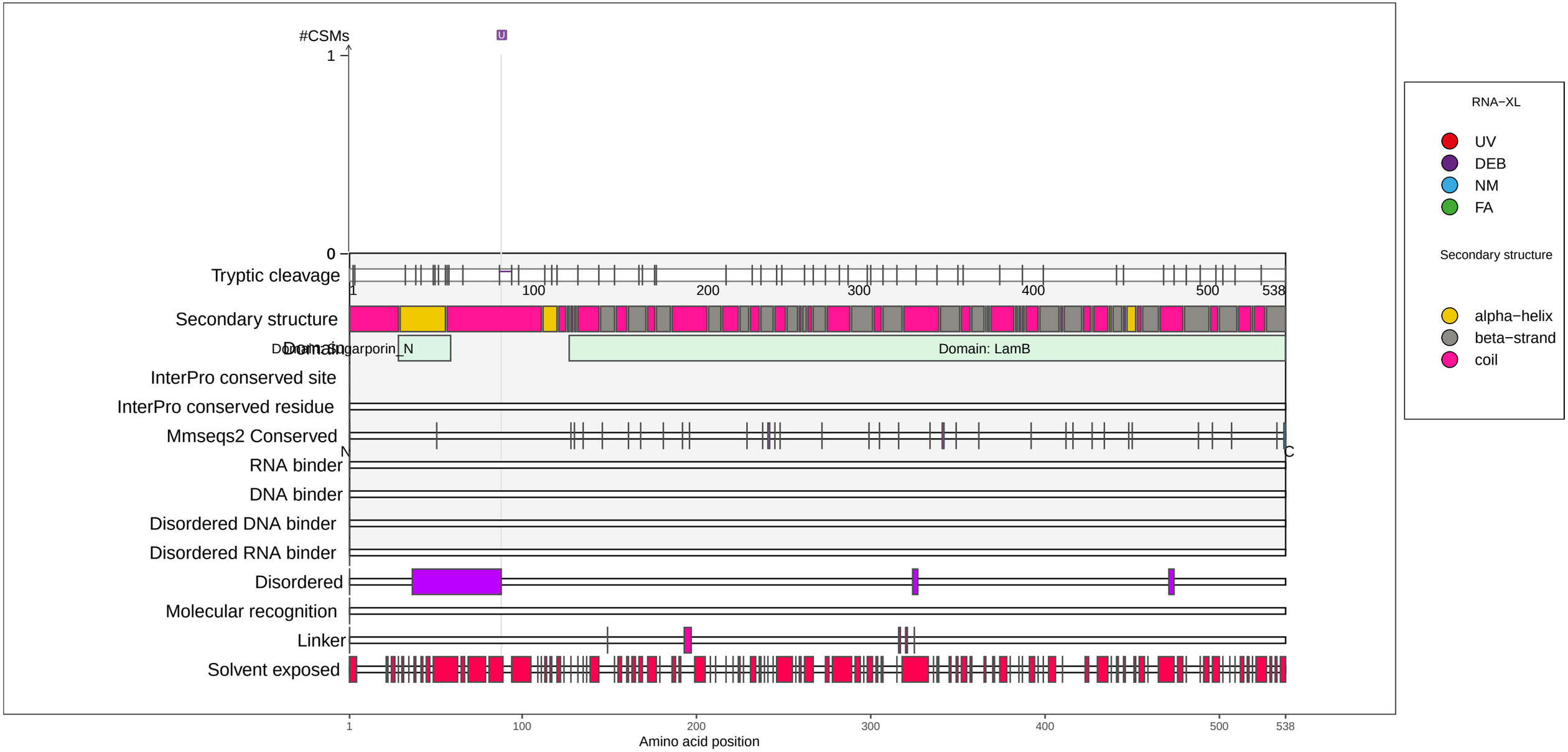
− RNA functions: not annotated



P26218
BGLH_ECOLI Cryptic outer membrane porin BglH

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −2 (Q 1)

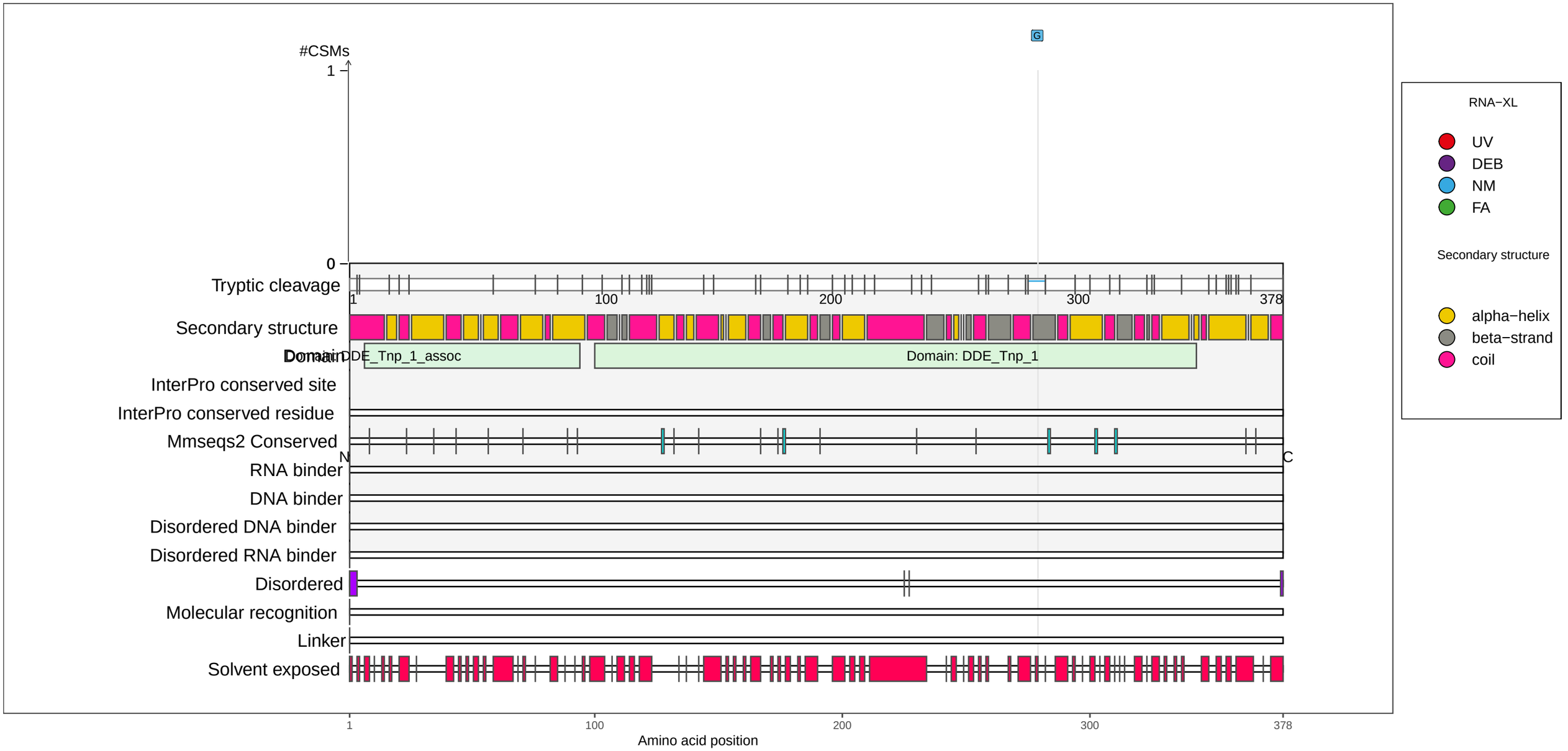
− RNA functions: not annotated



P28917
YDCC_ECOLI H repeat−associated putative transposase YdcC

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.28 (Q 19)

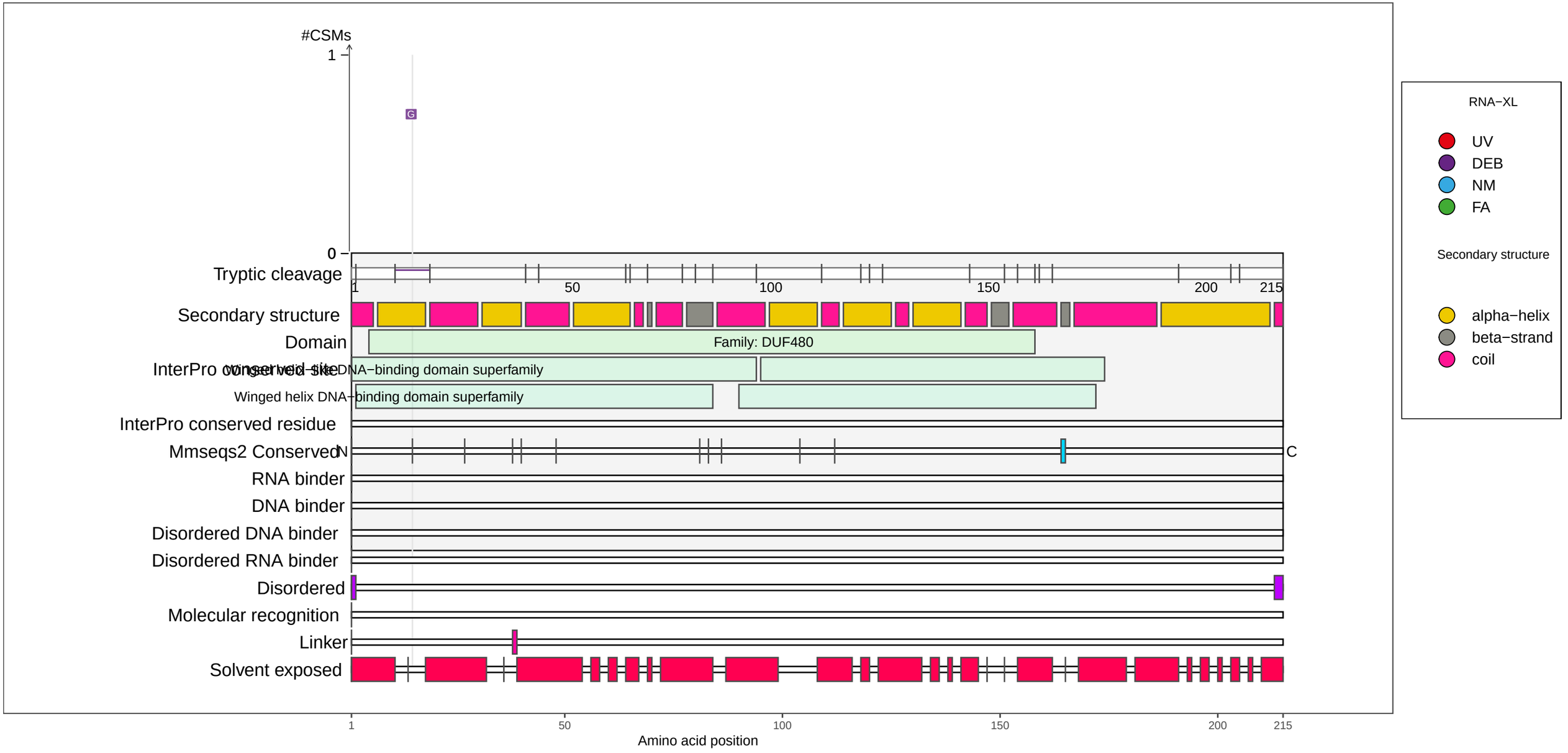
− RNA functions: not annotated



P29217
YCEH_ECOLI UPF0502 protein YceH

− Abundance:
tryptic [log10 Intensity]: 8 (Q 58)
PAXdb K12 strain [ppm]: 2.04 (Q 62)
PAXdb E.coli [ppm]: 2.46 (Q 85)

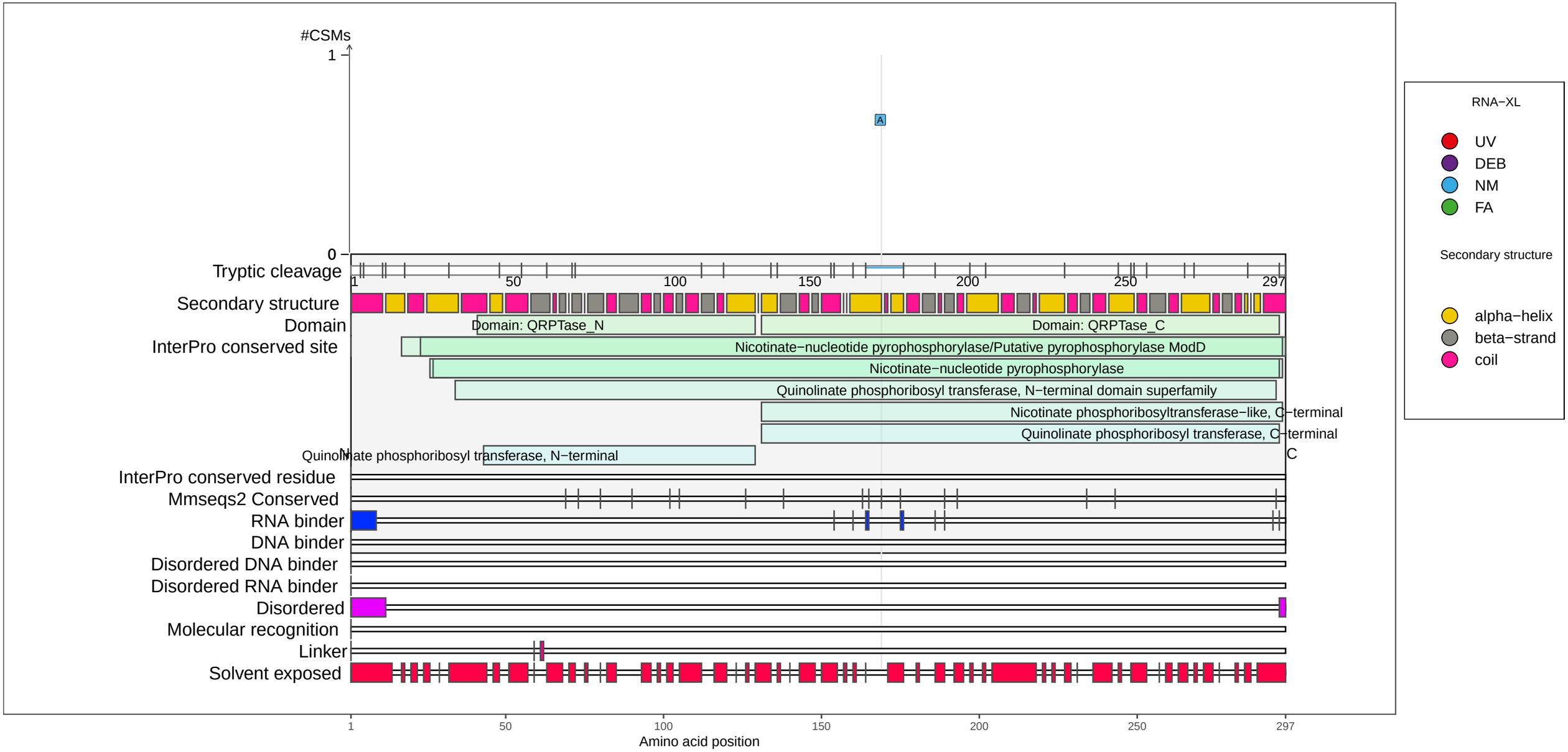
− RNA functions: not annotated



P30011
NADC_ECOLI Nicotinate−nucleotide pyrophosphorylase [carboxylating]

− Abundance:
tryptic [log10 Intensity]: 8.5 (Q 75)
PAXdb K12 strain [ppm]: 2 (Q 60)
PAXdb E.coli [ppm]: 2.37 (Q 82)

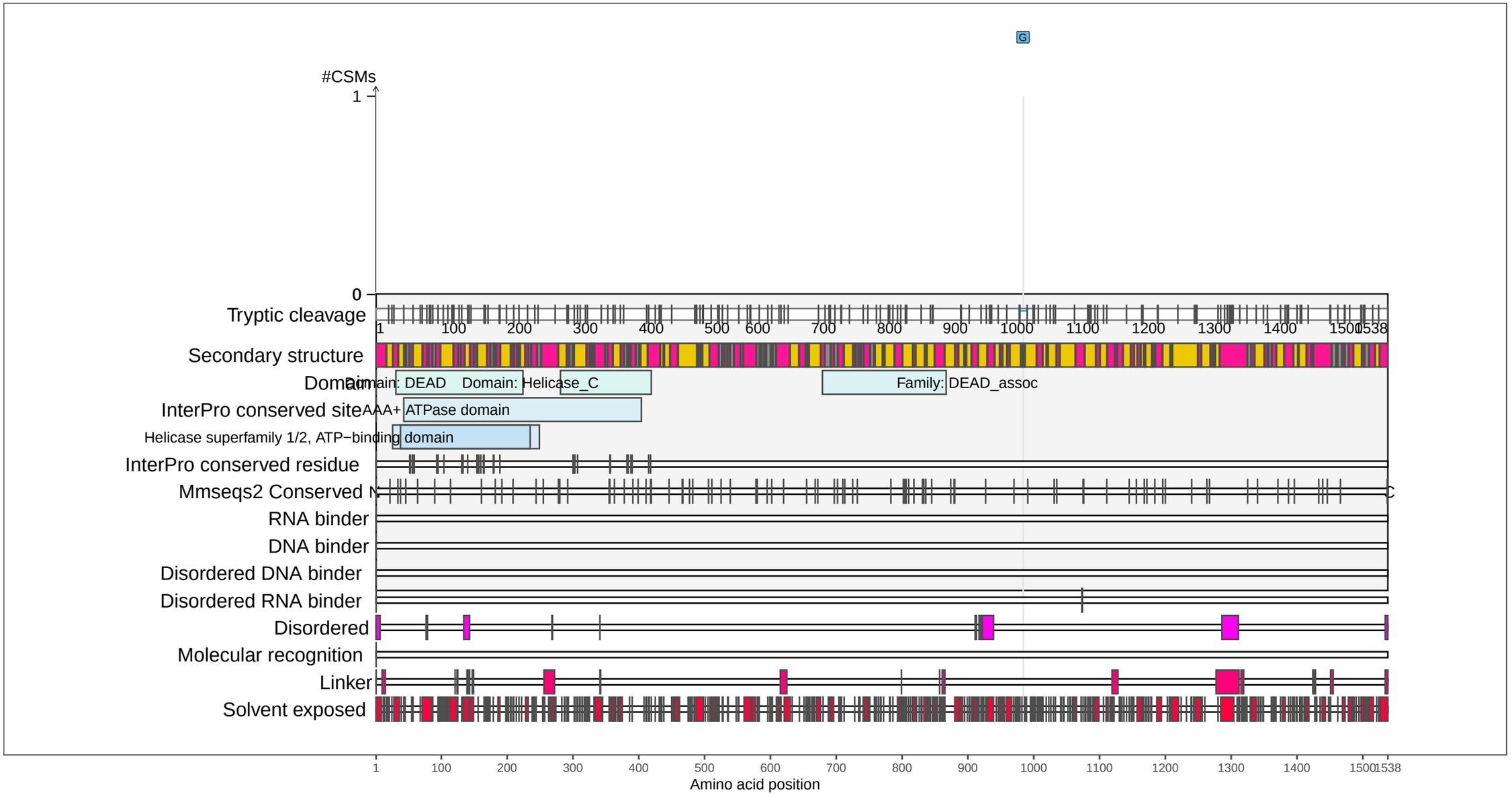
− RNA functions: not annotated



P30015
LHR_ECOLI Probable ATP−dependent helicase lhr

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.51 (Q 39)
PAXdb E.coli [ppm]: 0.96 (Q 47)

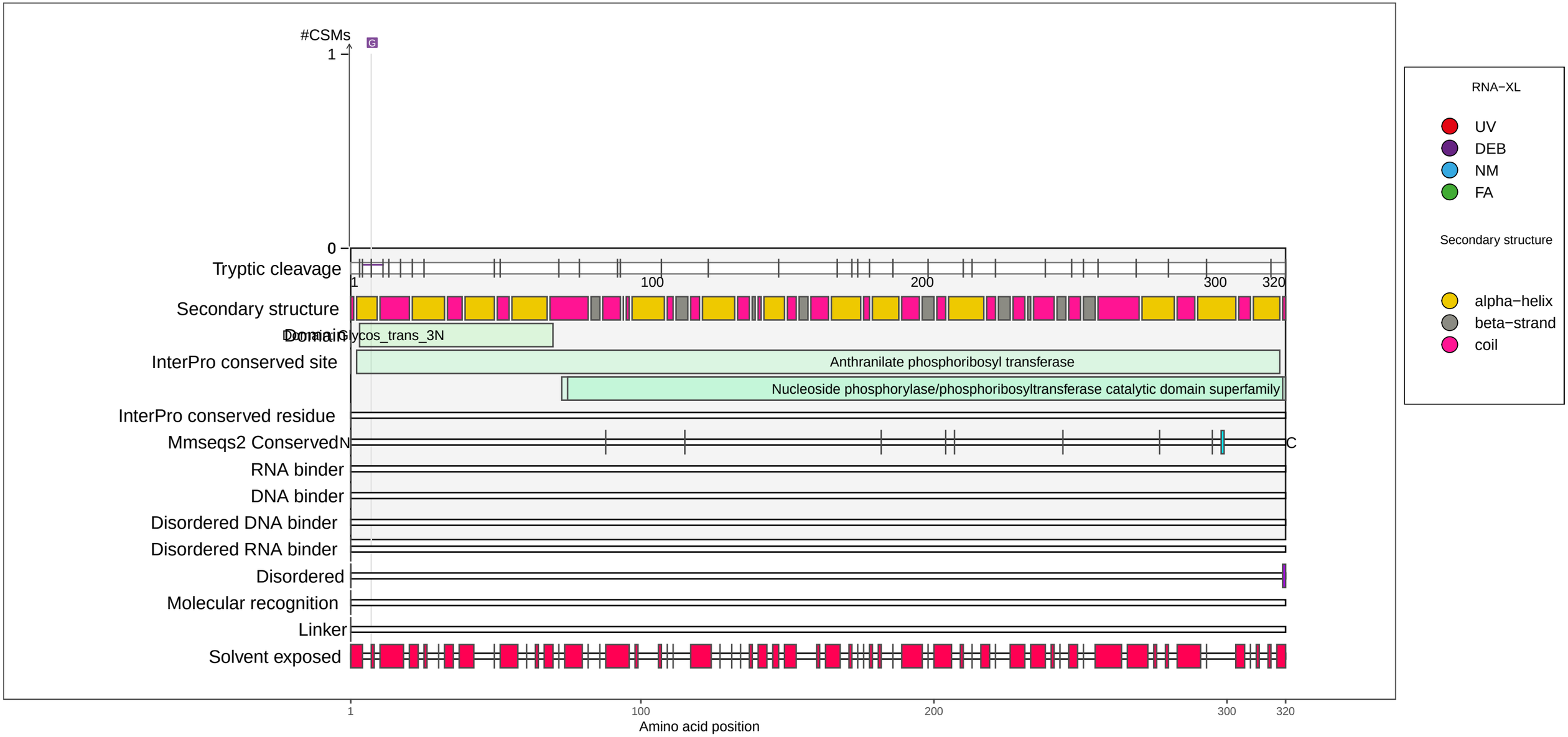
− RNA functions:
RNA binding; RNA helicase activity



P30177
YBIB_ECOLI Uncharacterized protein YbiB

− Abundance:
tryptic [log10 Intensity]: 8.15 (Q 63)
PAXdb K12 strain [ppm]: 2.2 (Q 67)
PAXdb E.coli [ppm]: 2.48 (Q 85)

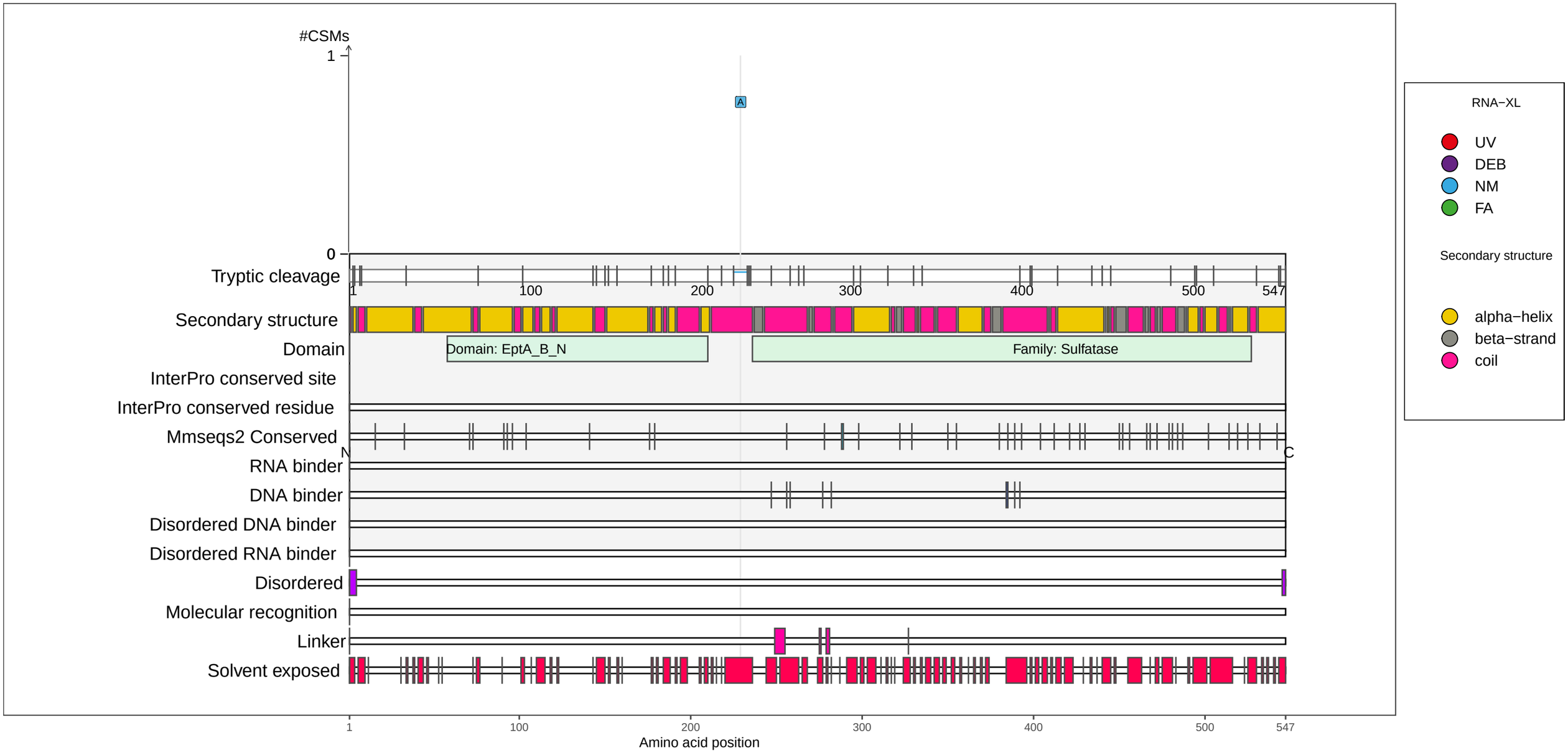
− RNA functions:
RNA binding



P30845
EPTA_ECOLI Phosphoethanolamine transferase EptA

− Abundance:
tryptic [log10 Intensity]: 8.2 (Q 65)
PAXdb K12 strain [ppm]: 1.91 (Q 57)
PAXdb E.coli [ppm]: −0.21 (Q 20)

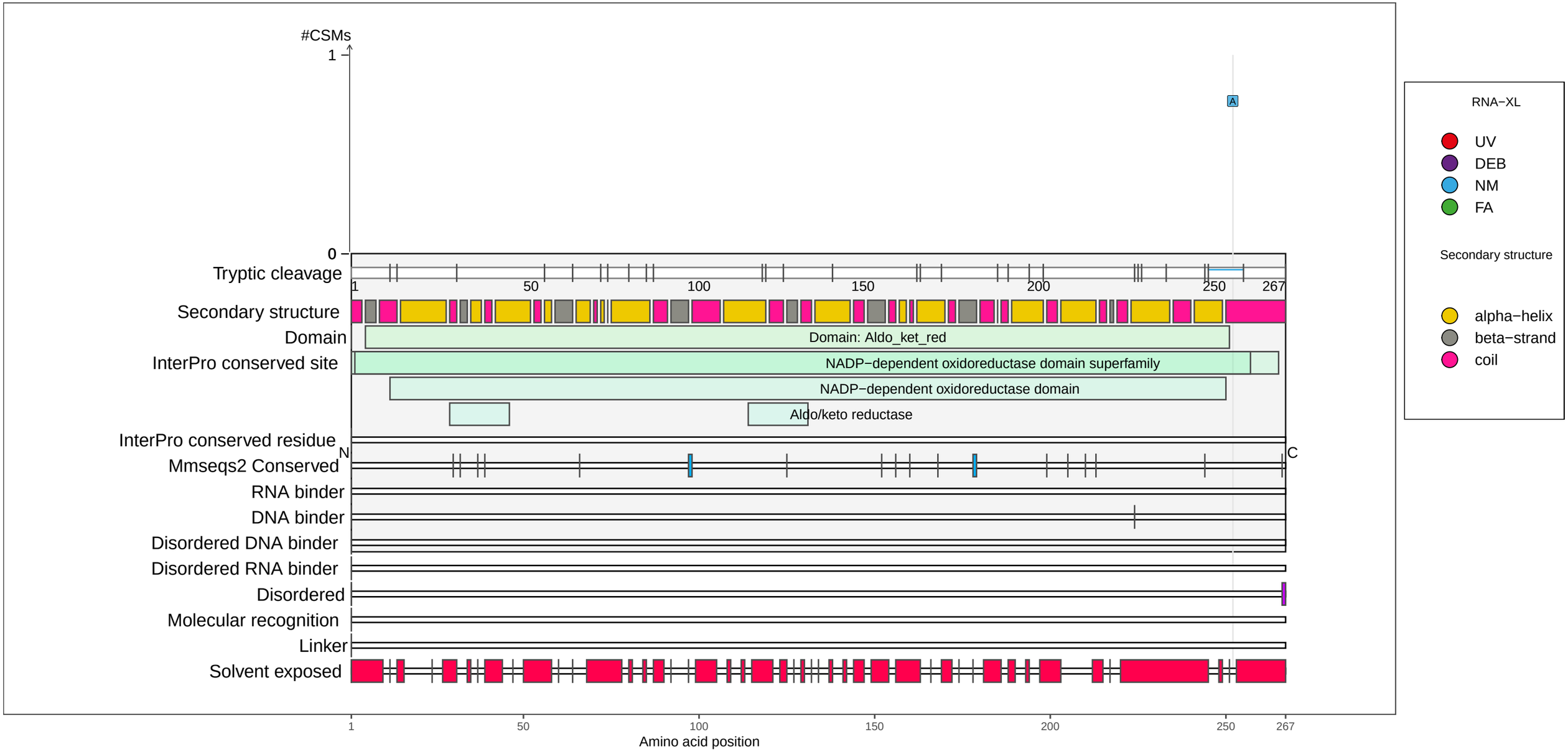
− RNA functions: not annotated



P30863
DKGB_ECOLI 2,5−diketo−D−gluconic acid reductase B

− Abundance:
tryptic [log10 Intensity]: 7.57 (Q 38)
PAXdb K12 strain [ppm]: 2.15 (Q 65)
PAXdb E.coli [ppm]: 1.88 (Q 69)

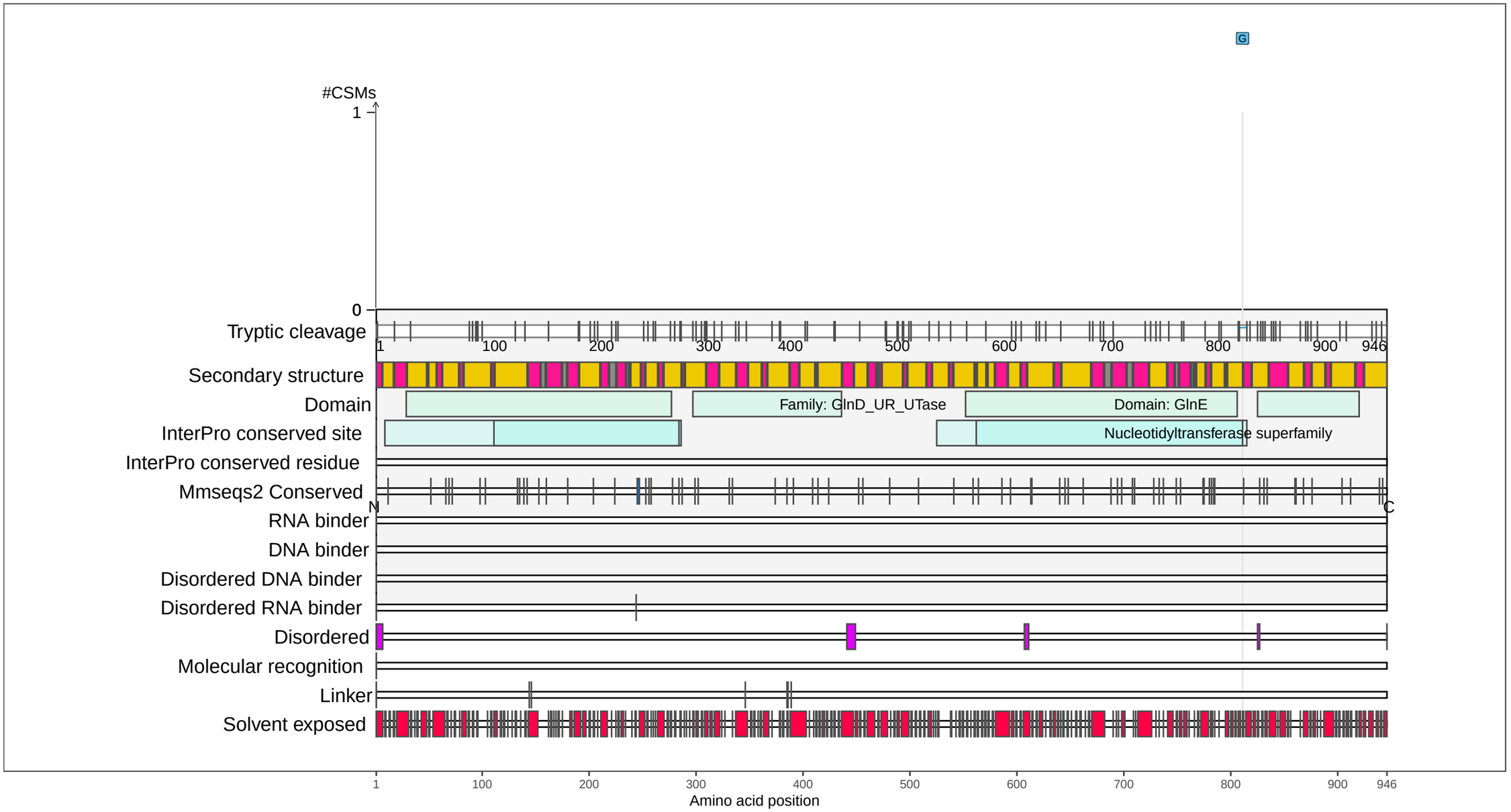
− RNA functions: not annotated



P30870
GLNE_ECOLI Bifunctional glutamine synthetase adenylyltransferase/adenylyl−removing enzyme

− Abundance:
tryptic [log10 Intensity]: 6.68 (Q 5)
PAXdb K12 strain [ppm]: 1.61 (Q 45)
PAXdb E.coli [ppm]: 1.66 (Q 63)

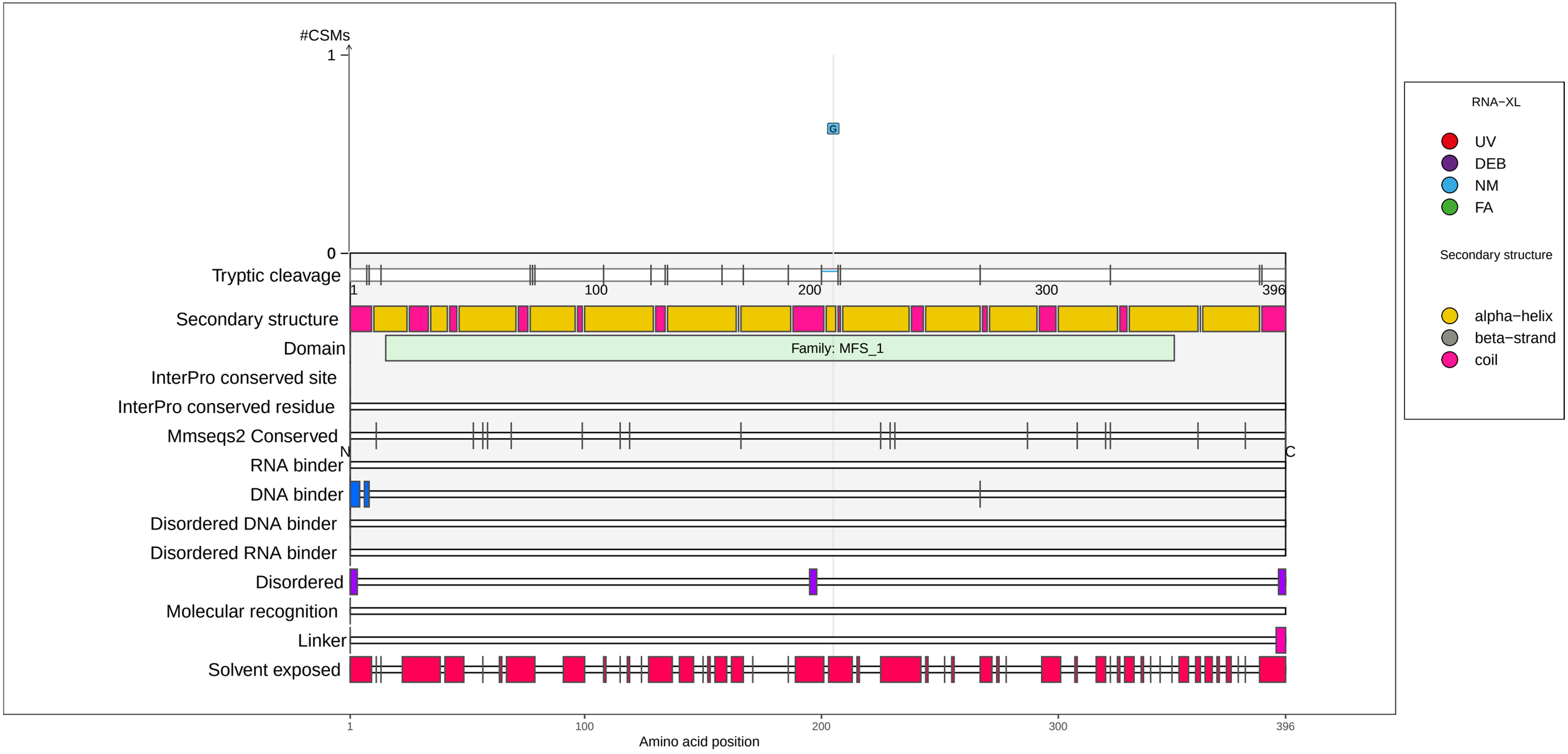
− RNA functions: not annotated



P31122
SOTB_ECOLI Sugar efflux transporter

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.39 (Q 5)

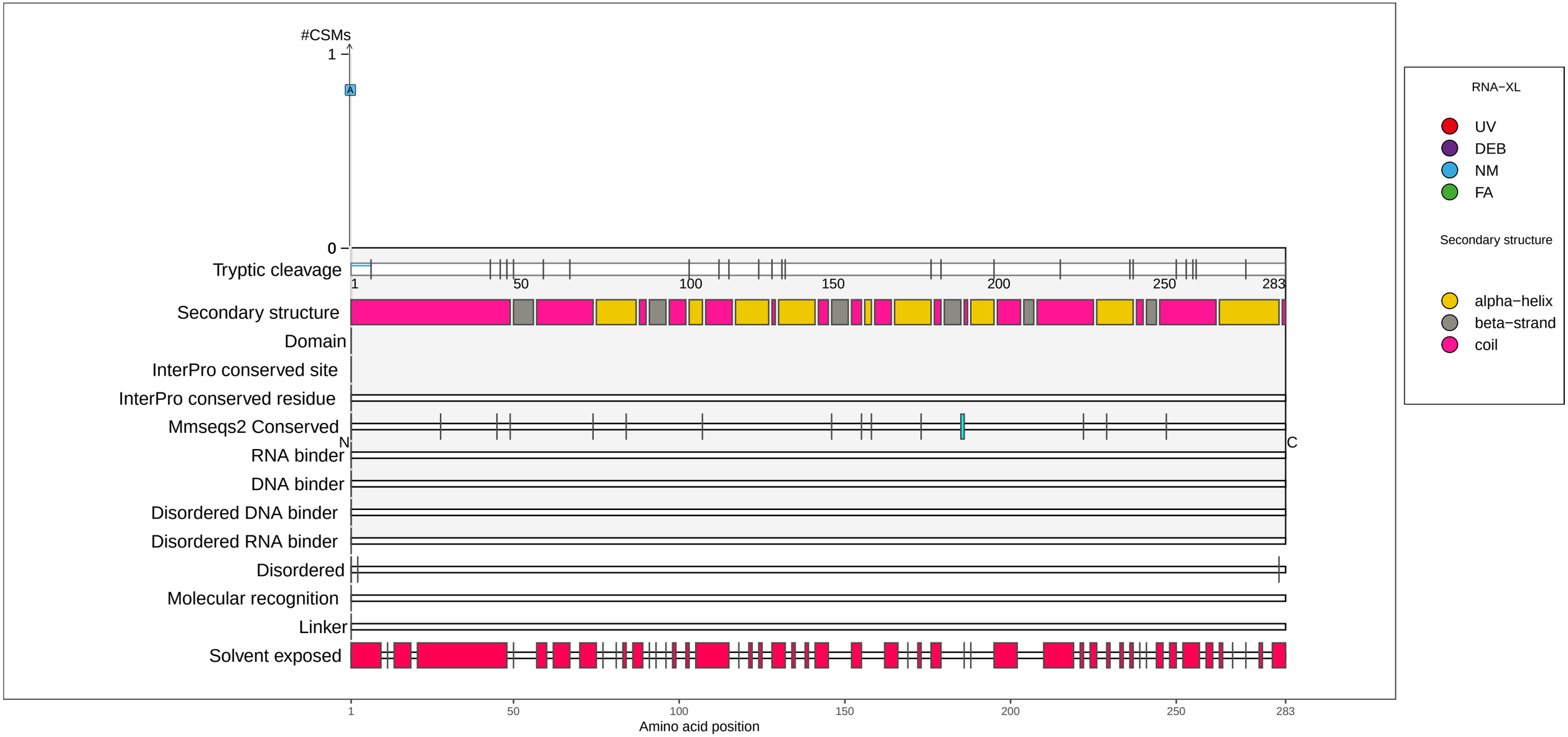
− RNA functions: not annotated



P31658
HCHA_ECOLI Protein/nucleic acid deglycase 1

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 2.78 (Q 85)
PAXdb E.coli [ppm]: 2.75 (Q 91)

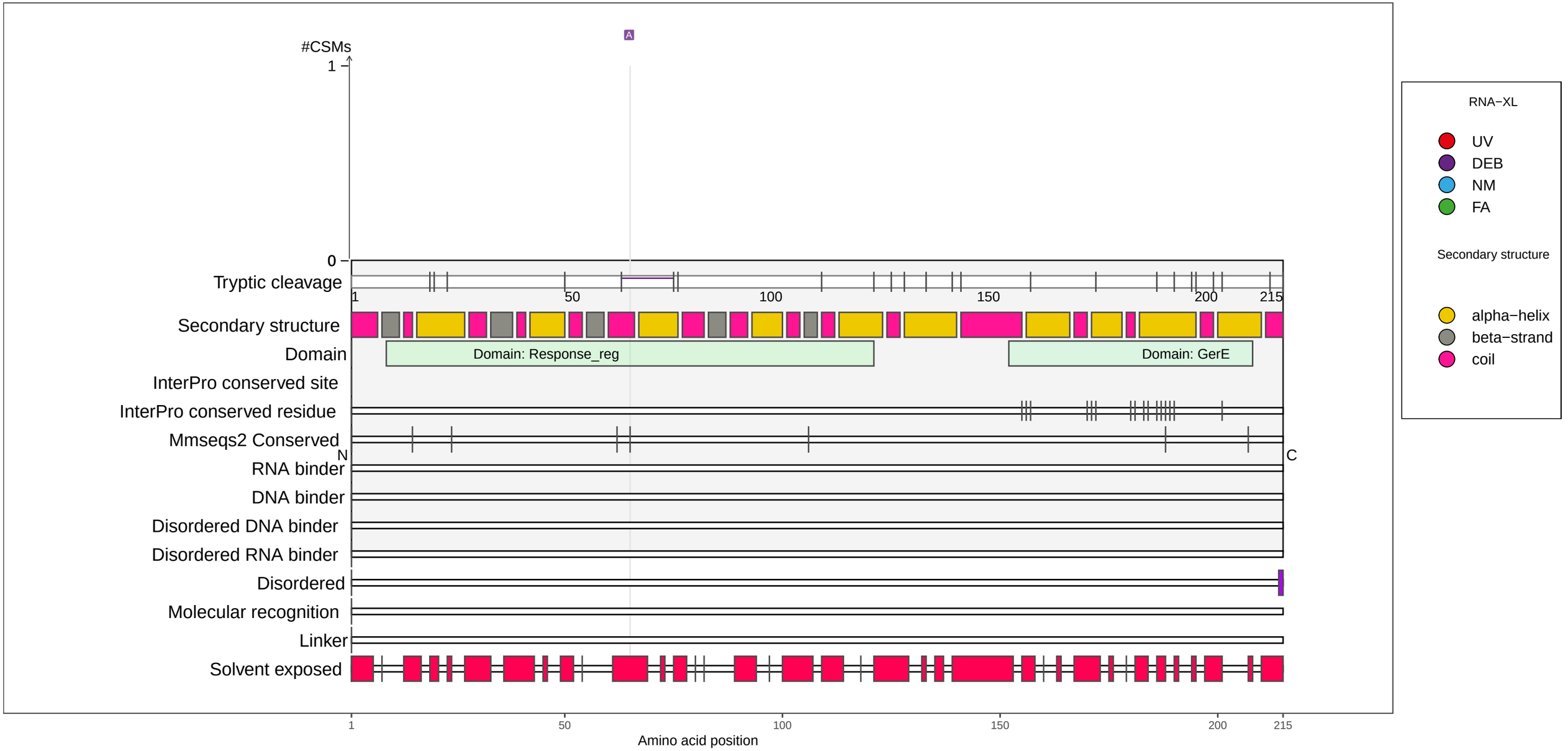
− RNA functions:
RNA metabolic process; RNA repair



P31802
NARP_ECOLI Nitrate/nitrite response regulator protein NarP

− Abundance:
tryptic [log10 Intensity]: 7.84 (Q 51)
PAXdb K12 strain [ppm]: 1.35 (Q 30)
PAXdb E.coli [ppm]: 1.66 (Q 63)

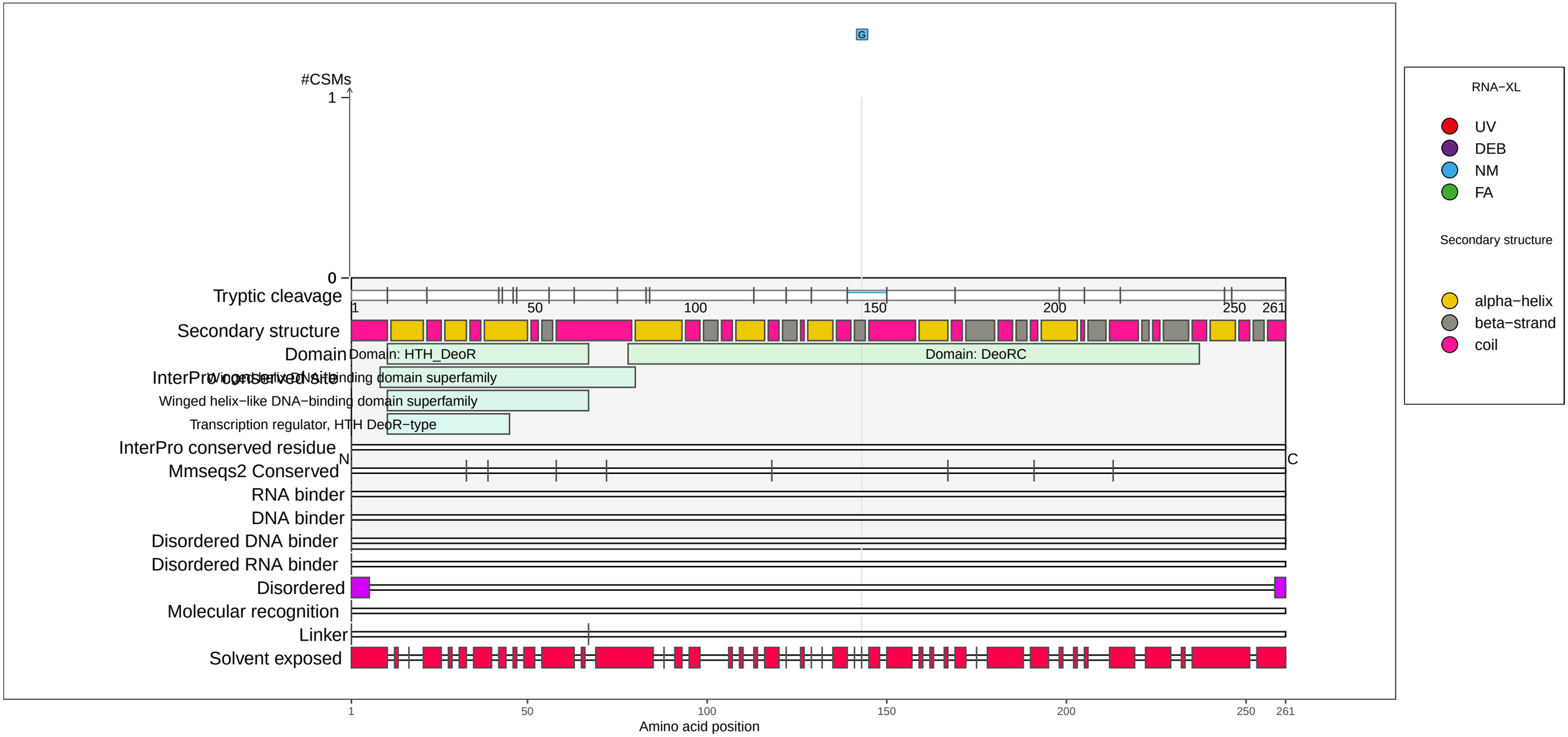
− RNA functions: not annotated



P32144
CSQR_ECOLI HTH−type transcriptional repressor CsqR

− Abundance:
tryptic [log10 Intensity]: 7.97 (Q 57)
PAXdb K12 strain [ppm]: 1.42 (Q 34)
PAXdb E.coli [ppm]: 1.69 (Q 64)

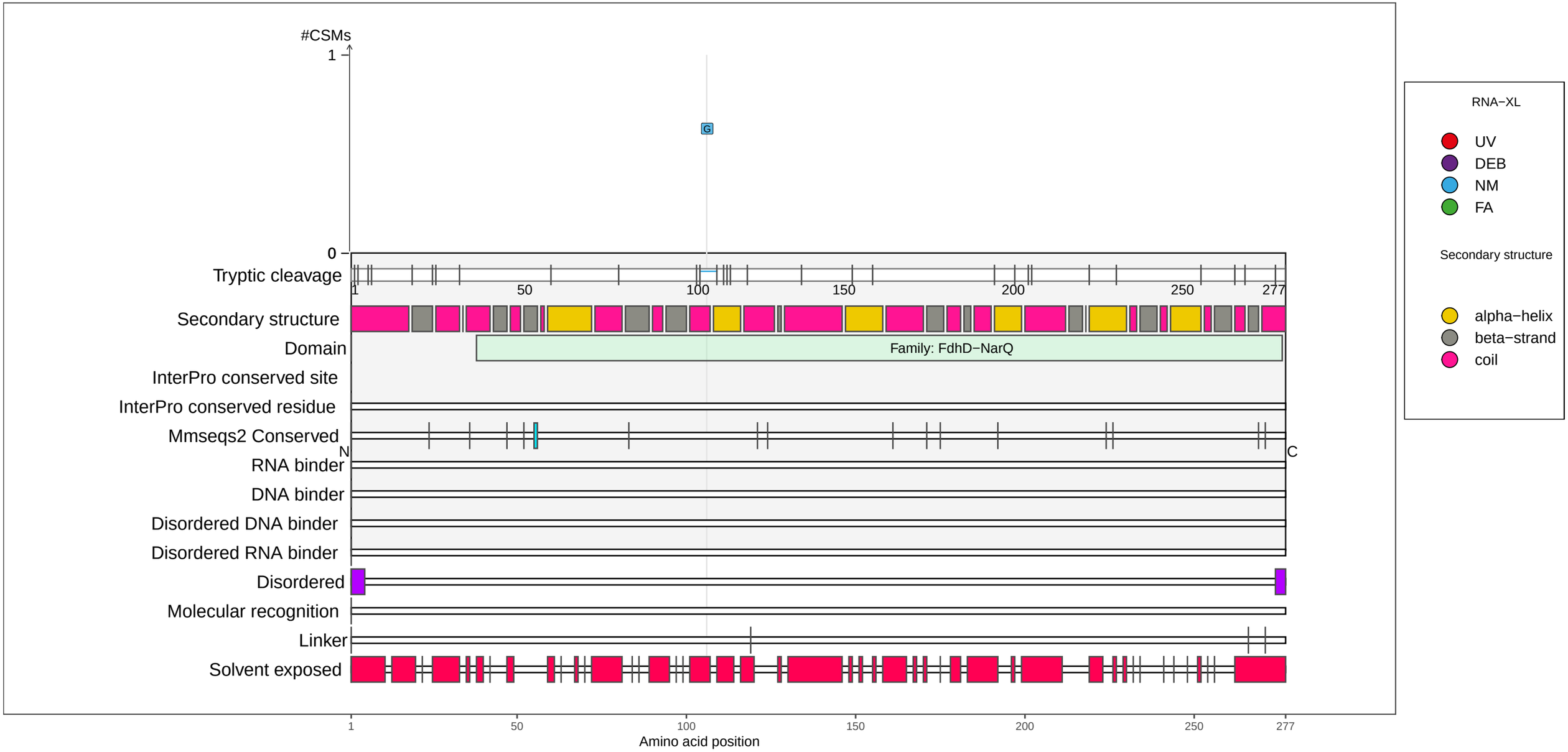
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P32177
FDHD_ECOLI Sulfur carrier protein FdhD

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 25)
PAXdb K12 strain [ppm]: 1.59 (Q 44)
PAXdb E.coli [ppm]: 1.09 (Q 50)

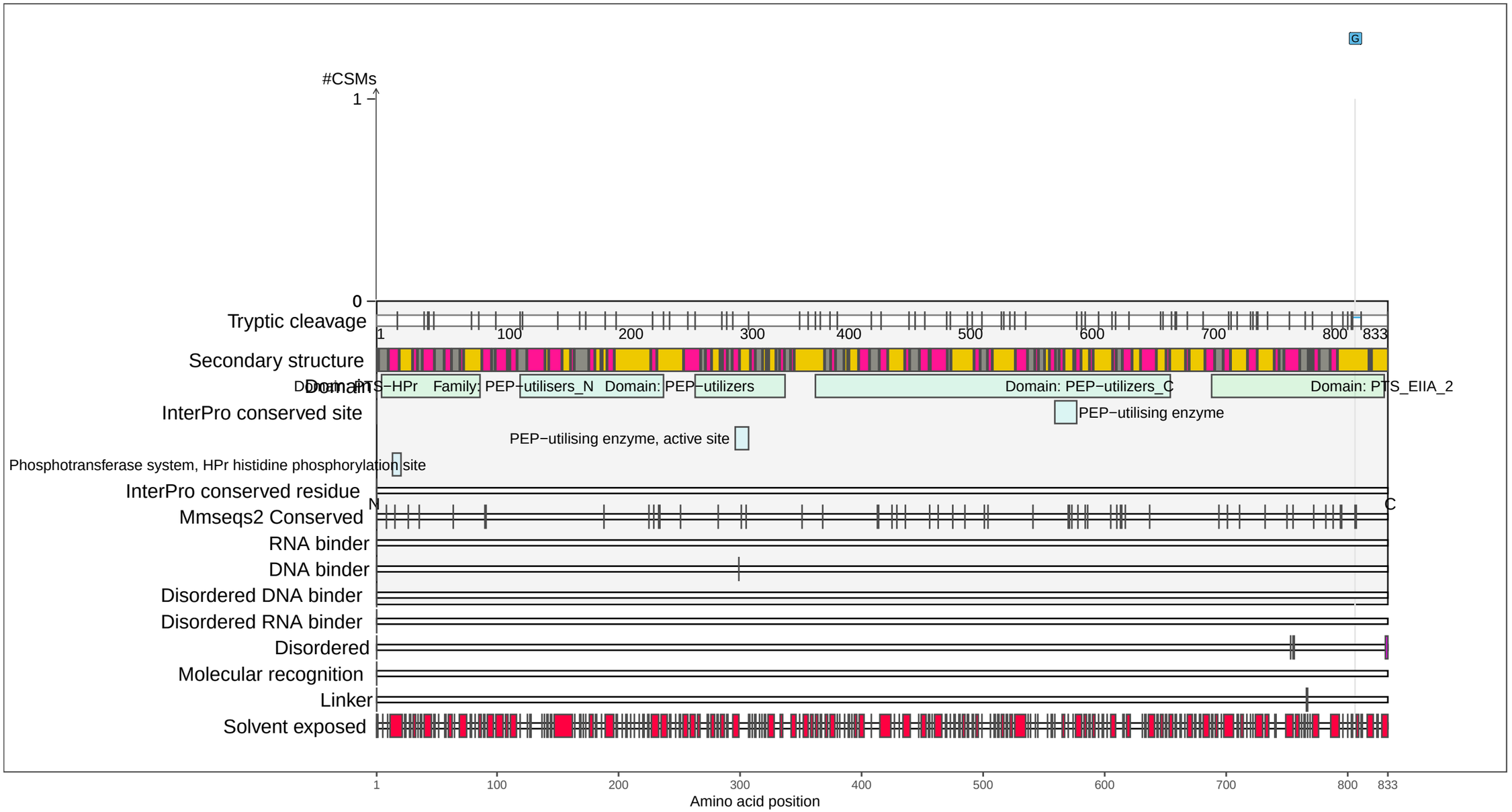
− RNA functions: not annotated



P32670
PTFX2_ECOLI Multiphosphoryl transfer protein 2

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 24)
PAXdb K12 strain [ppm]: 1.43 (Q 34)
PAXdb E.coli [ppm]: 0.11 (Q 27)

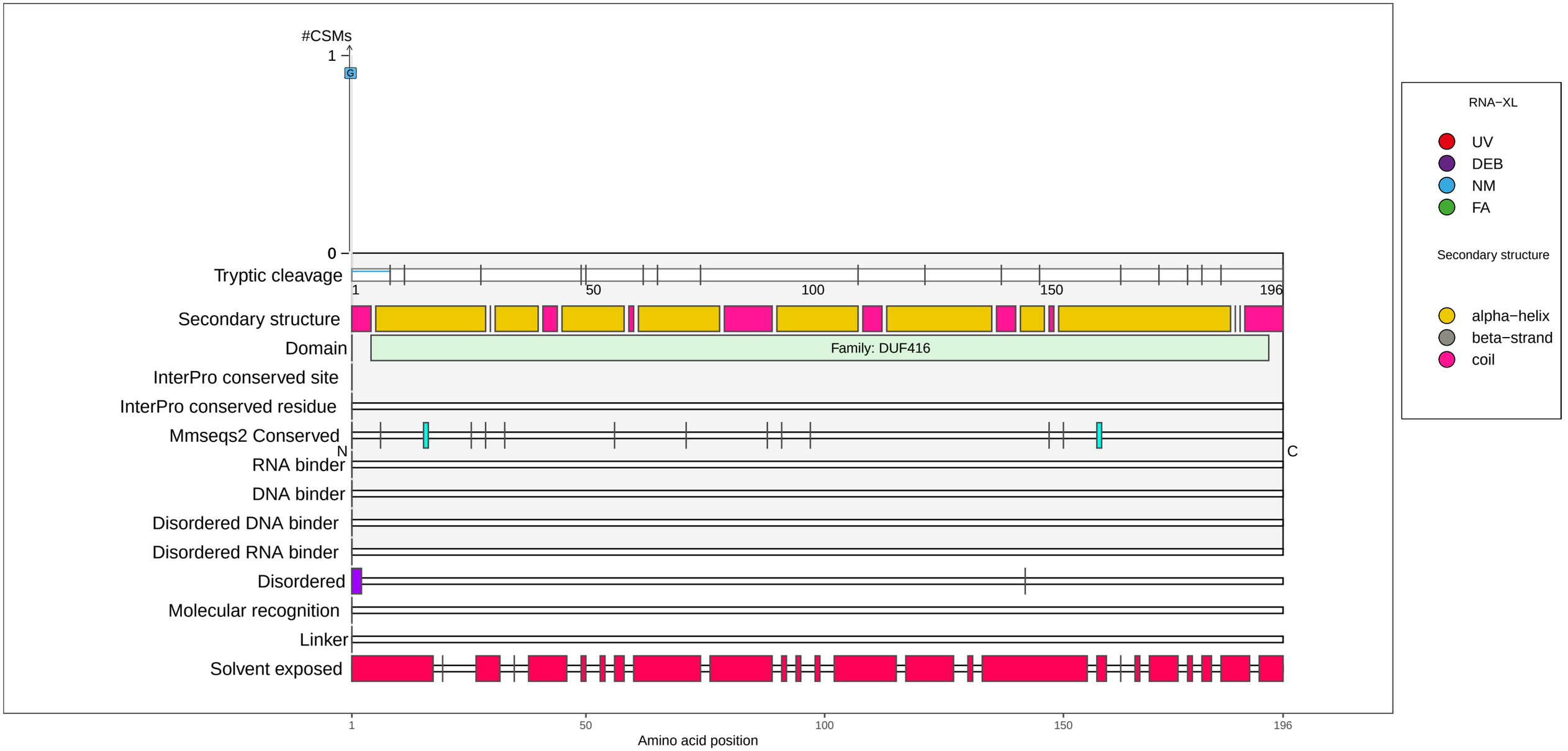
− RNA functions: not annotated



P32680
YJAG_ECOLI Uncharacterized protein YjaG

− Abundance:
tryptic [log10 Intensity]: 7.78 (Q 48)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.11 (Q 75)

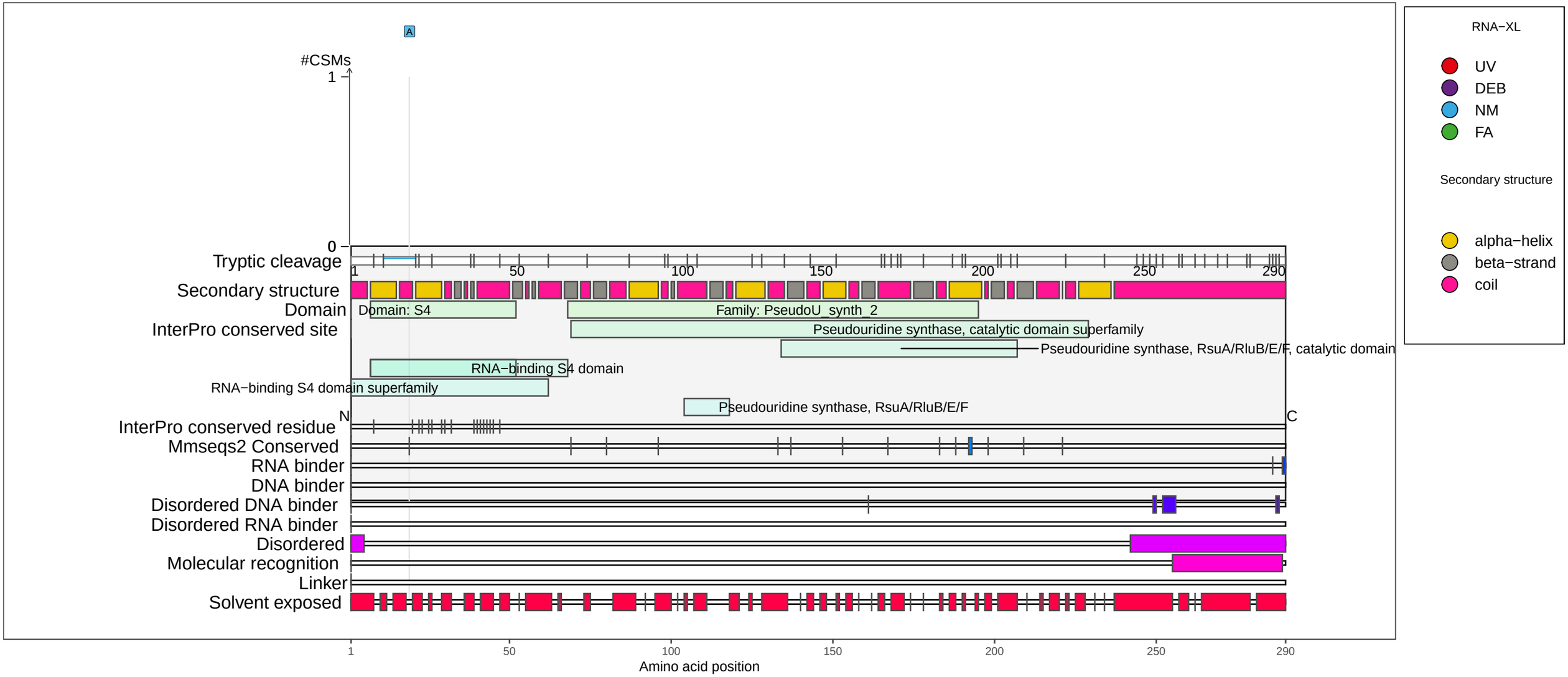
− RNA functions: not annotated



P32684
RLUF_ECOLI Dual−specificity RNA pseudouridine synthase RluF

− Abundance:
tryptic [log10 Intensity]: 7.76 (Q 47)
PAXdb K12 strain [ppm]: 0.83 (Q 6)
PAXdb E.coli [ppm]: 0.99 (Q 47)

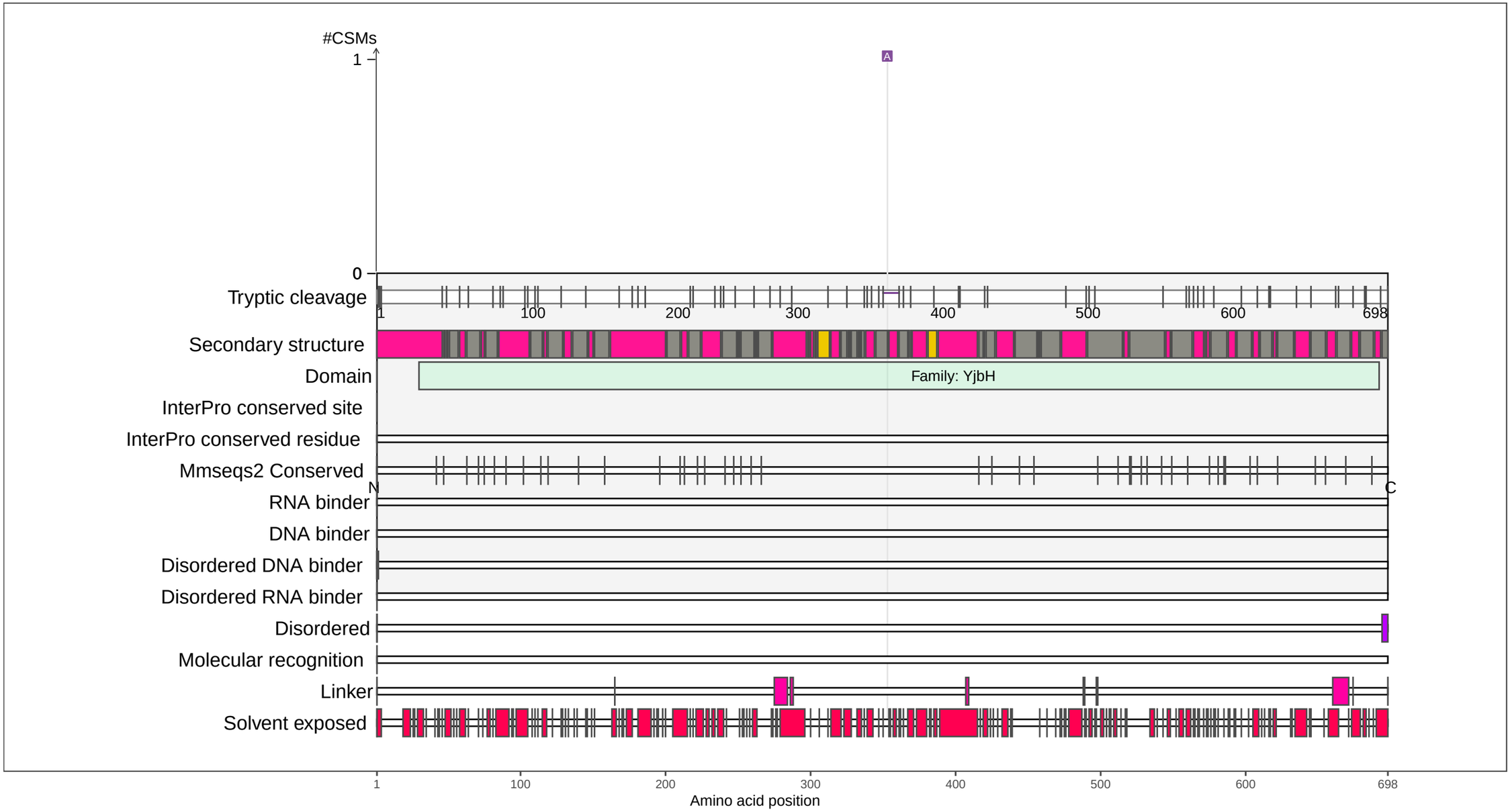
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; RNA pseudouridylate synthase; rRNA metabolic process
rRNA modification; rRNA processing; rRNA pseudouridine synthase activity
rRNA pseudouridine synthesis; tRNA metabolic process; tRNA modification; tRNA processing
tRNA pseudouridine synthesis



P32689
YJBH_ECOLI Uncharacterized lipoprotein YjbH

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.83 (Q 6)
PAXdb E.coli [ppm]: −1.85 (Q 2)

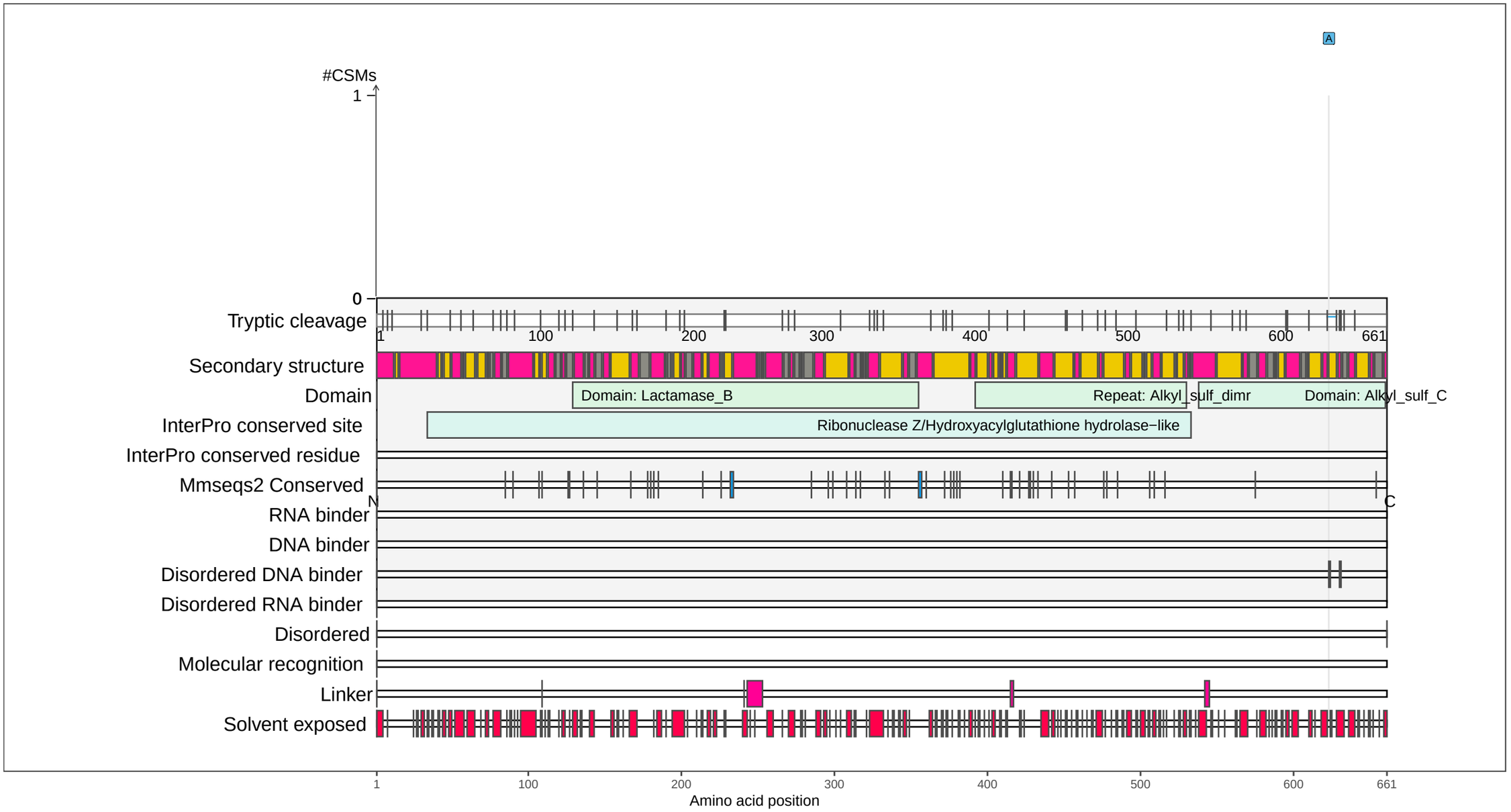
− RNA functions: not annotated



P32717
YJCS_ECOLI Putative alkyl/aryl−sulfatase YjcS

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.74 (Q 12)

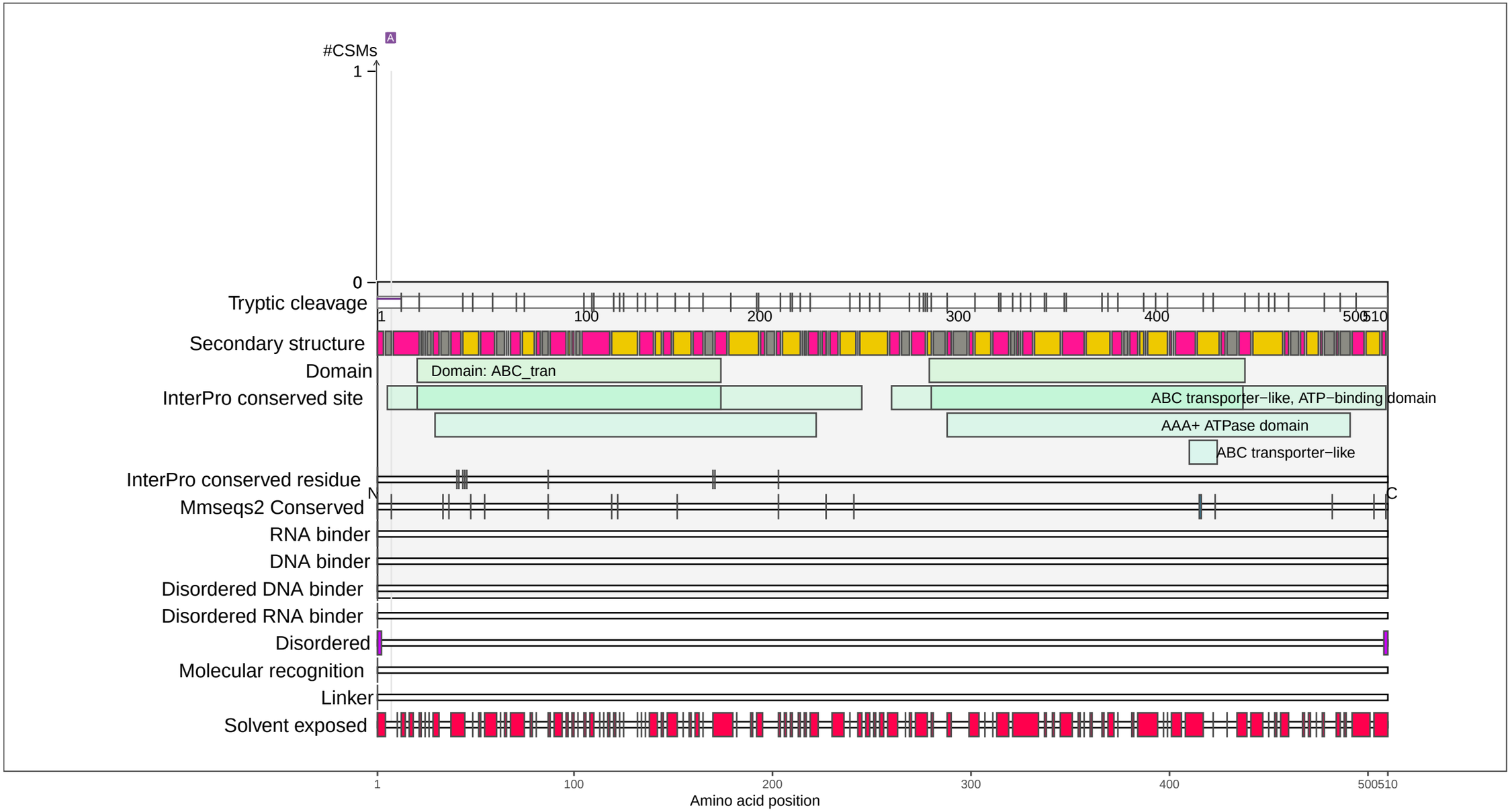
− RNA functions: not annotated

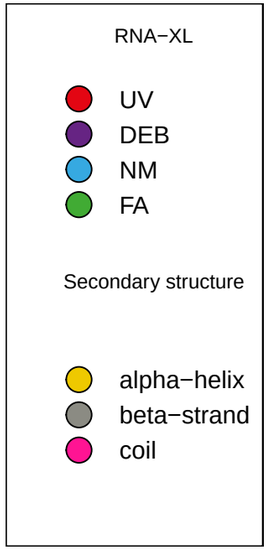


P32721
ALSA_ECOLI D−allose import ATP−binding protein AlsA

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.64 (Q 46)
PAXdb E.coli [ppm]: 0.45 (Q 35)

− RNA functions: not annotated

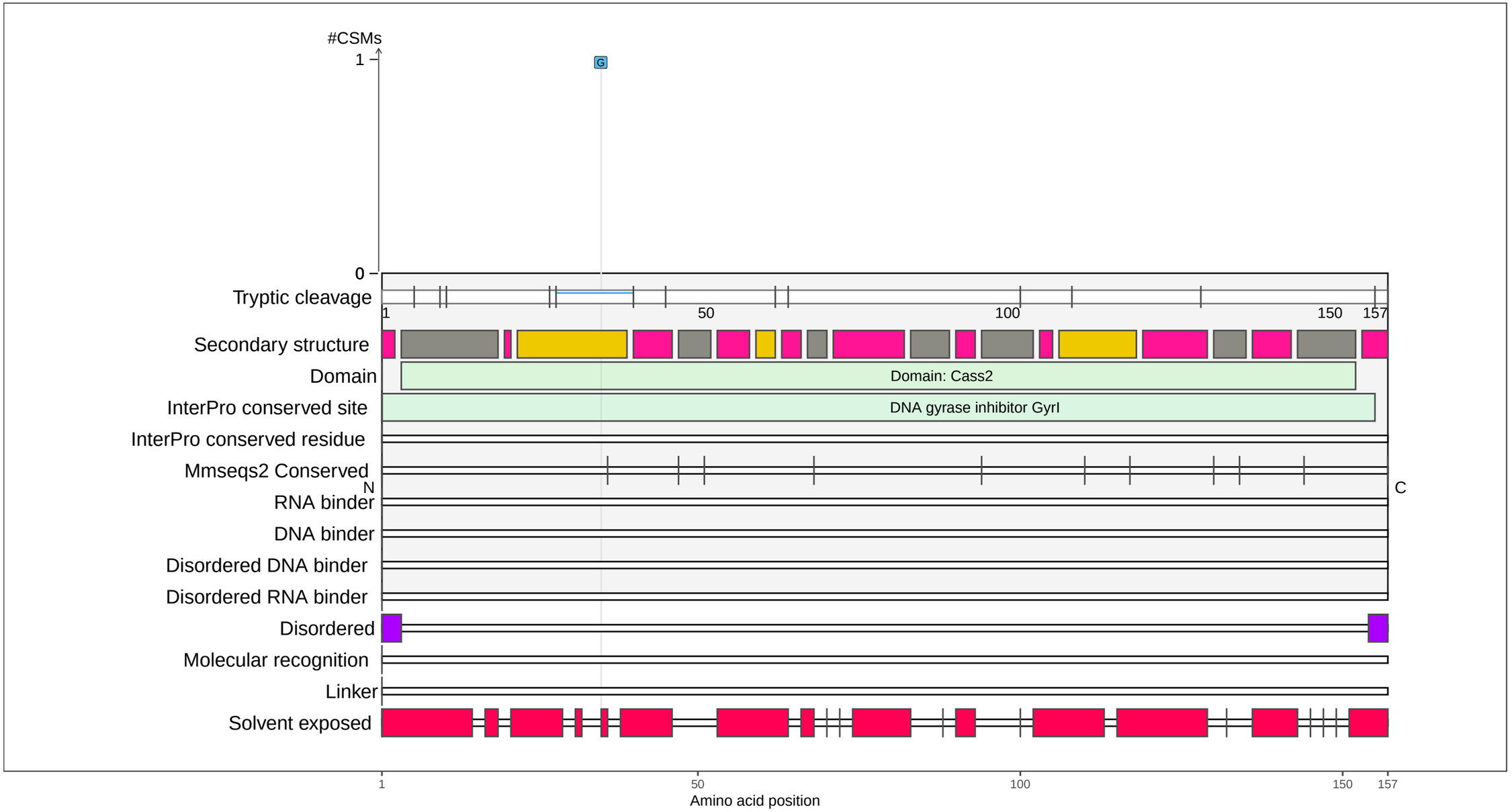


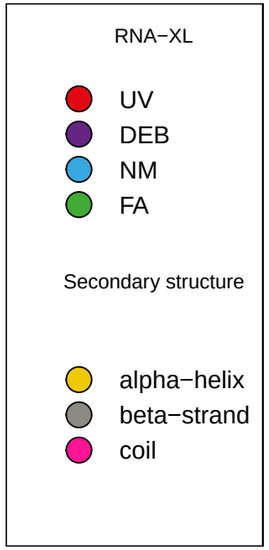


P33012
SBMC_ECOLI DNA gyrase inhibitor

− Abundance:
tryptic [log10 Intensity]: 8.12 (Q 62)
PAXdb K12 strain [ppm]: 1.37 (Q 31)
PAXdb E.coli [ppm]: 2.14 (Q 76)

− RNA functions: not annotated

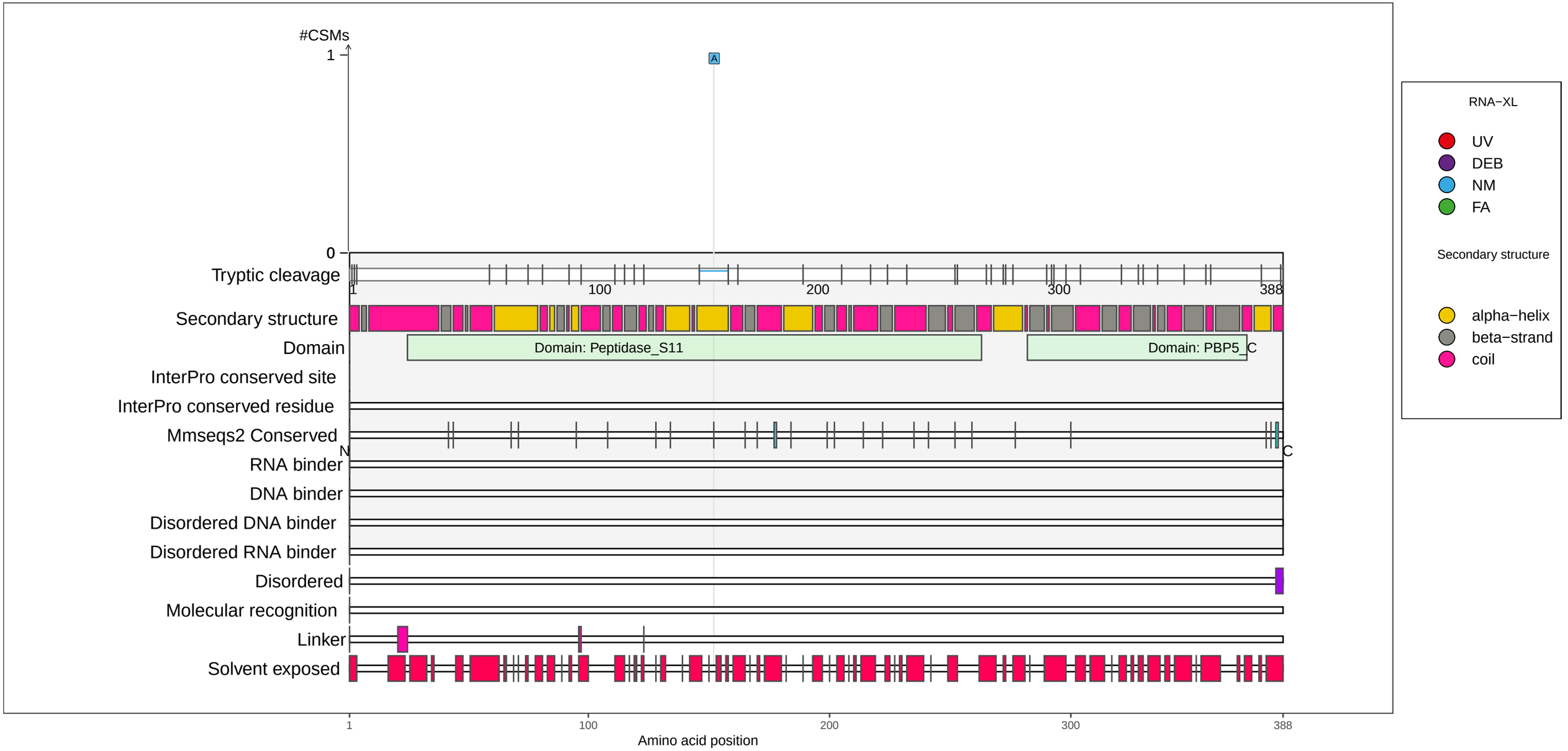




P33013
DACD_ECOLI D−alanyl−D−alanine carboxypeptidase DacD

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.63 (Q 14)

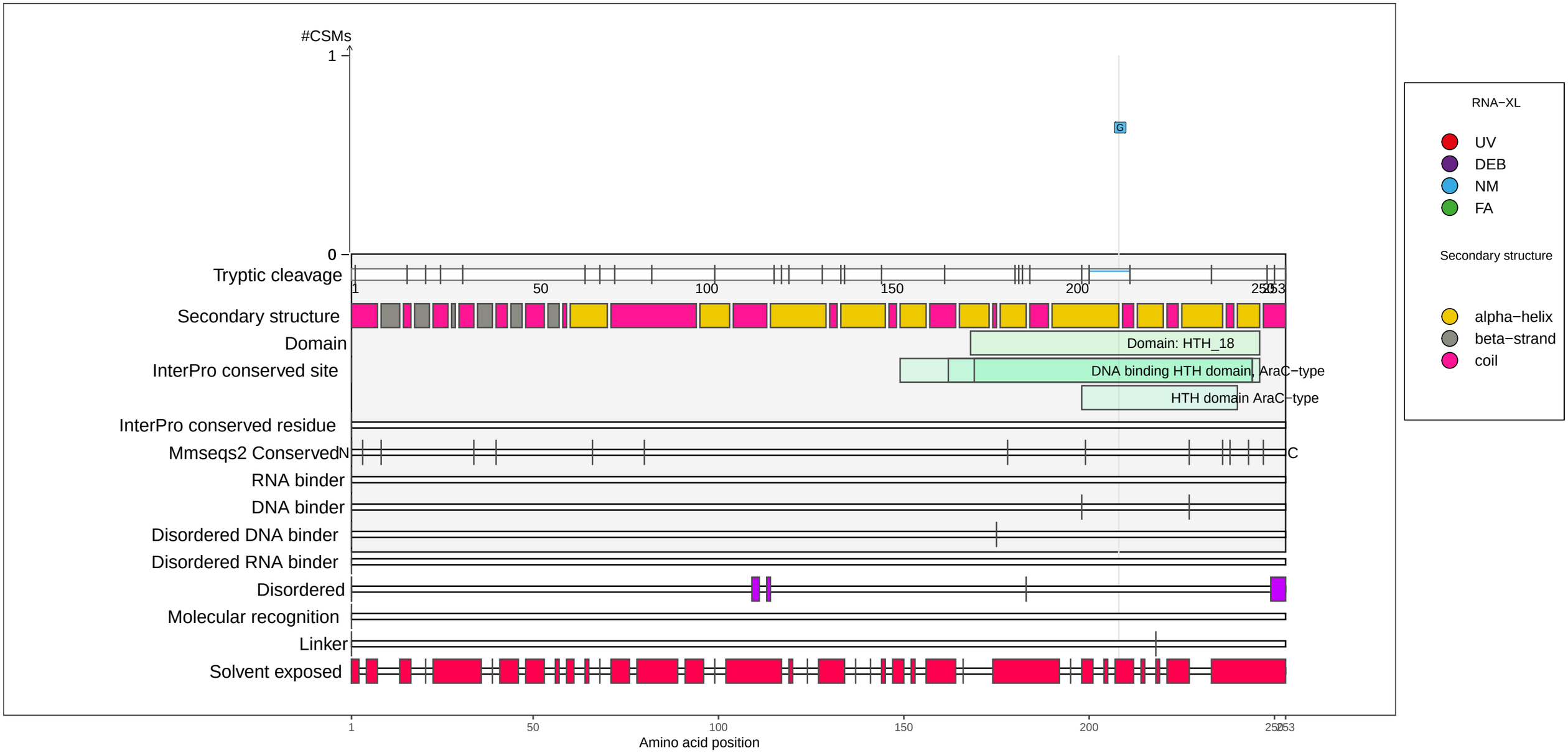
− RNA functions: not annotated



P33234
ADIY_ECOLI HTH−type transcriptional regulator AdiY

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.7 (Q 2)

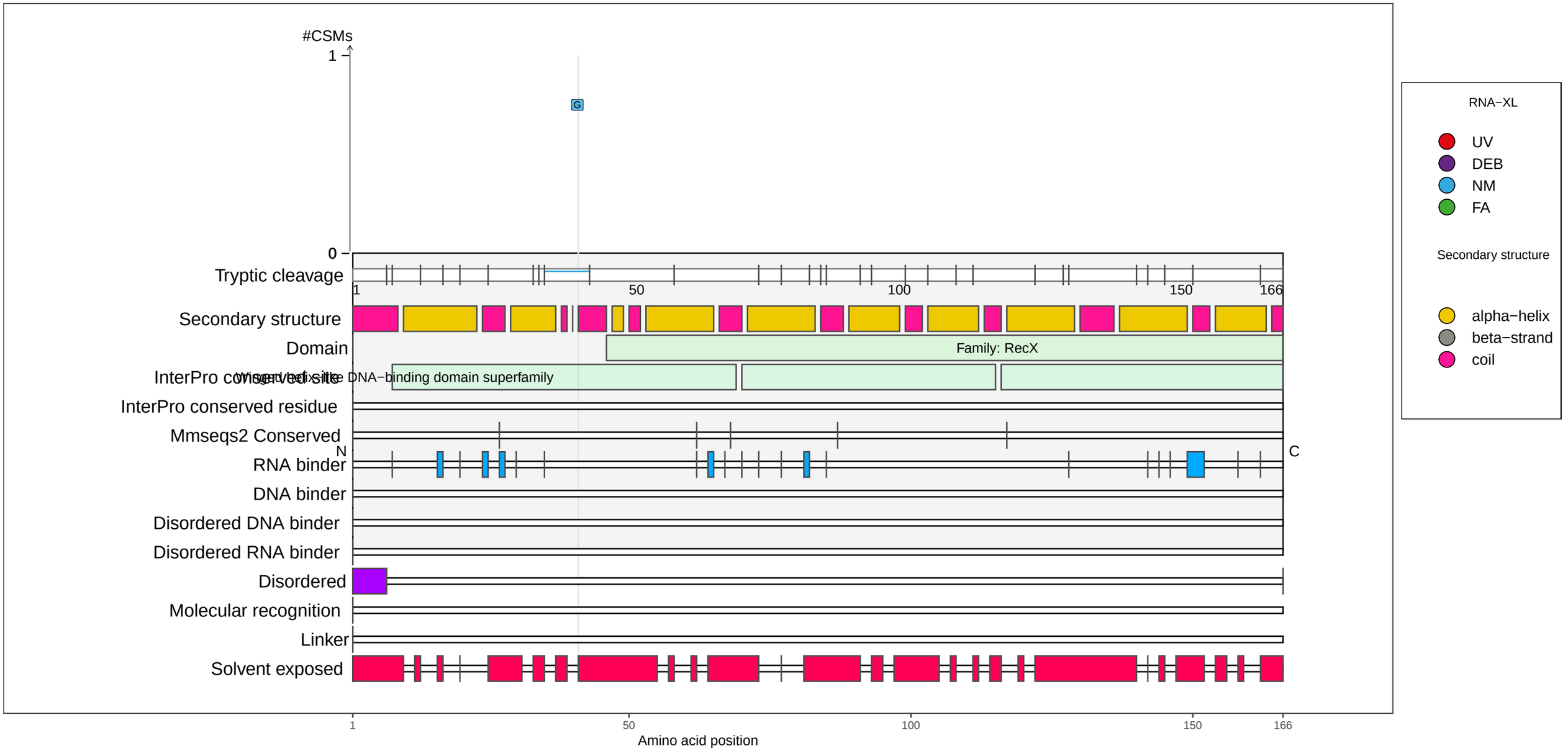
− RNA functions: not annotated



P33596
RECX_ECOLI Regulatory protein RecX

− Abundance:
tryptic [log10 Intensity]: 6.4 (Q 2)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.43 (Q 34)

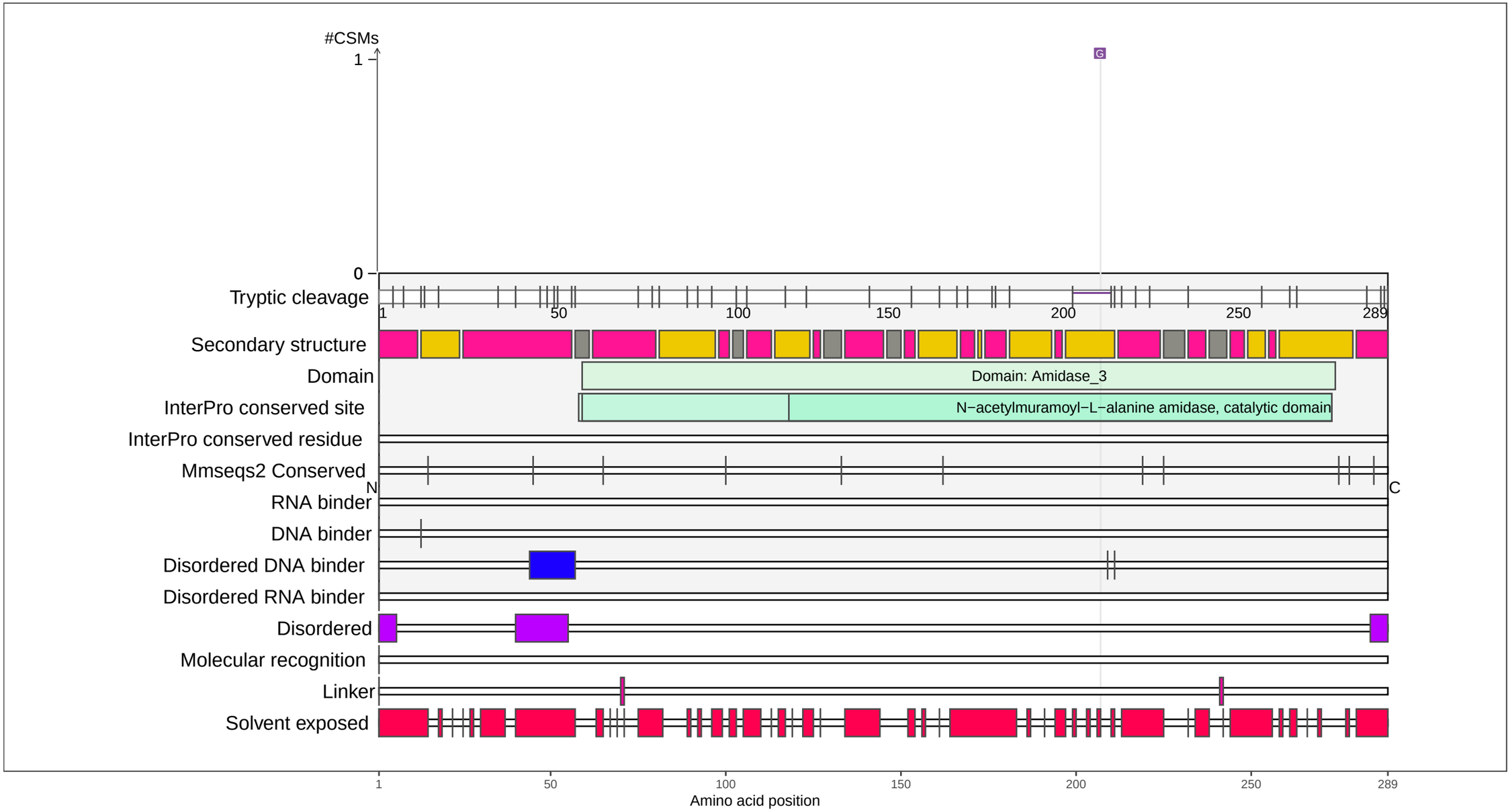
− RNA functions: not annotated



P36548
AMIA_ECOLI N−acetylmuramoyl−L−alanine amidase AmiA

− Abundance:
tryptic [log10 Intensity]: 7.17 (Q 20)
PAXdb K12 strain [ppm]: 1.15 (Q 18)
PAXdb E.coli [ppm]: 0.64 (Q 39)

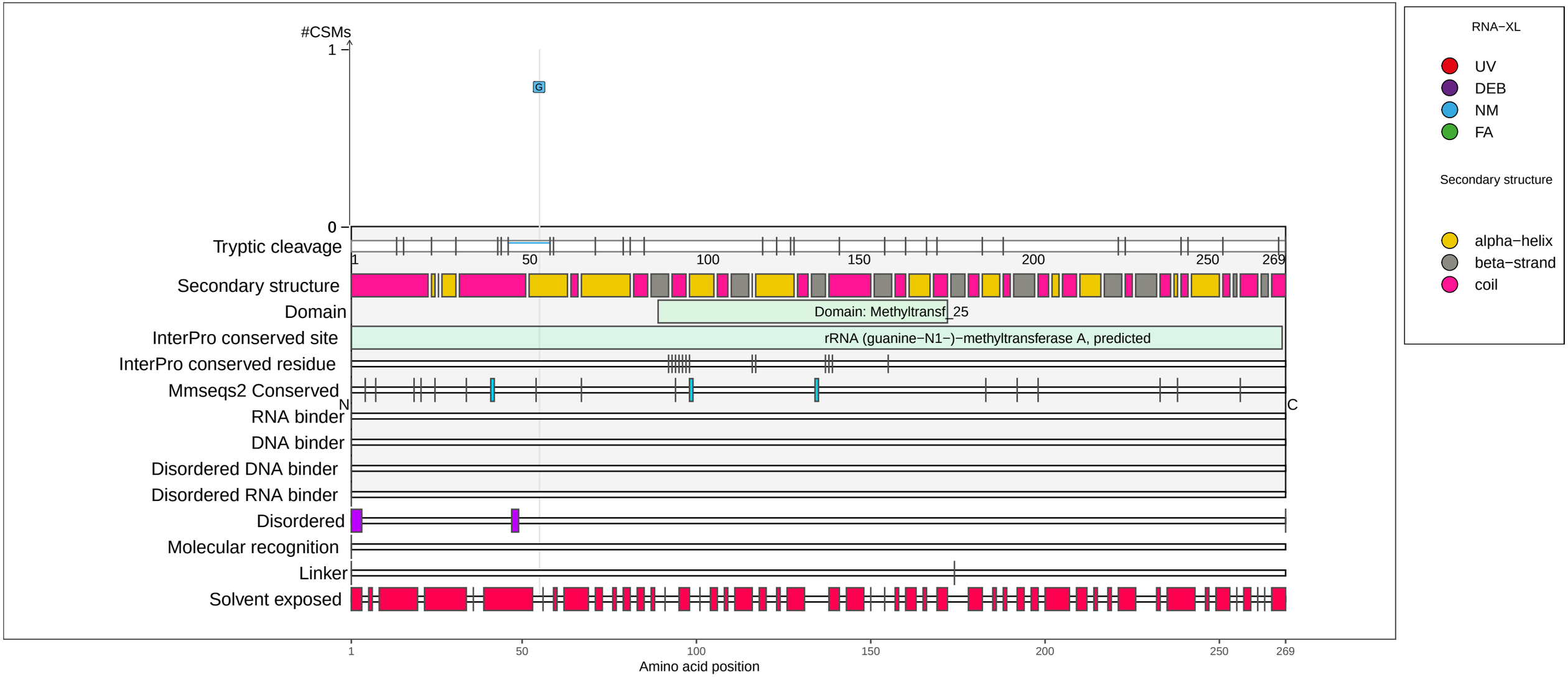
− RNA functions: not annotated



P36999
RLMA_ECOLI 23S rRNA (guanine(745)−N(1))−methyltransferase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.85 (Q 44)

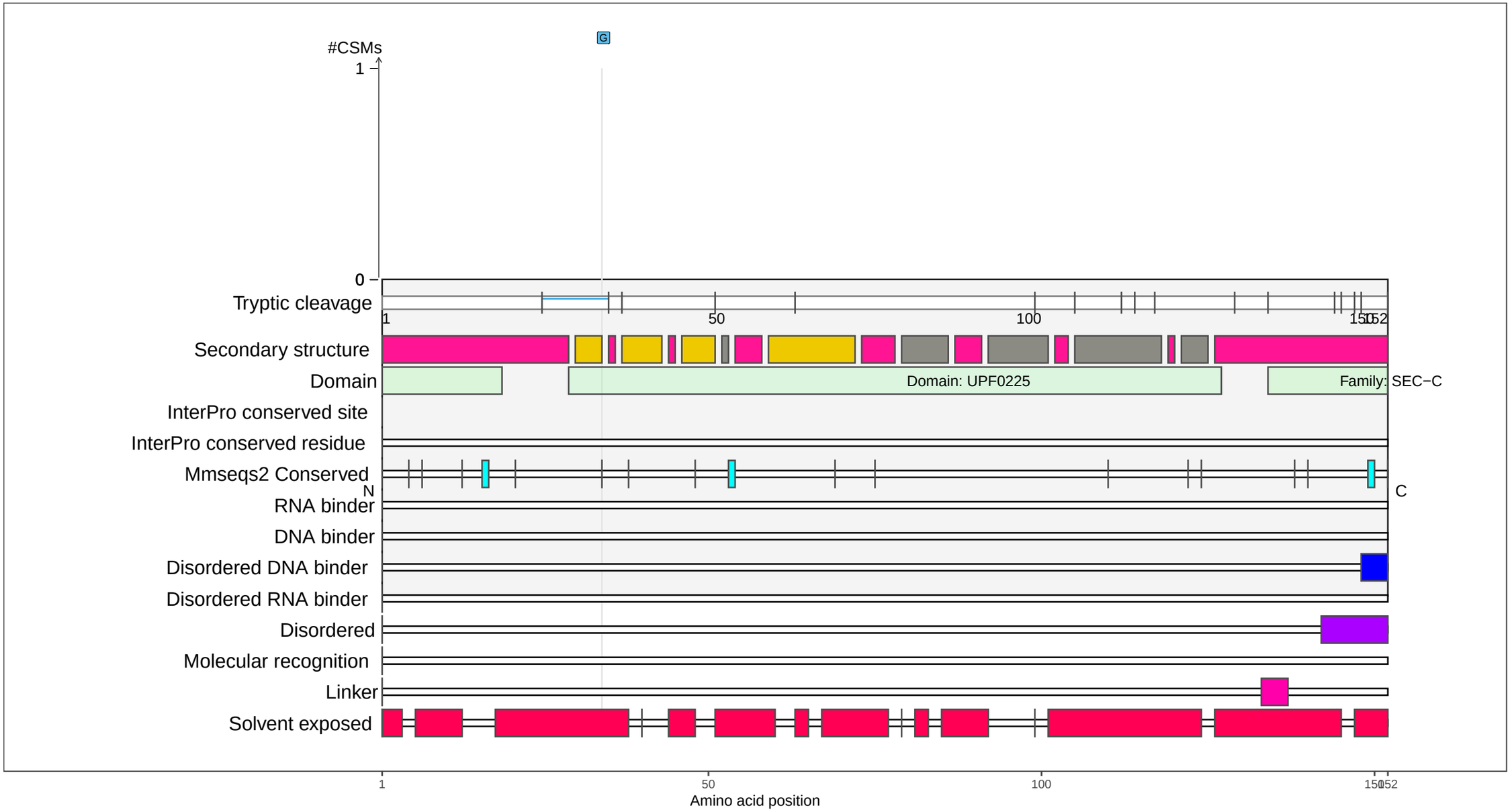
− RNA functions:
23S rRNA (guanine(745)−N(1))−methyltransferase activity; ncRNA metabolic process
ncRNA processing; RNA metabolic process; RNA methylation; RNA methyltransferase activity
RNA modification; RNA processing; rRNA (guanine−N1−)−methyltransferase activity
rRNA (guanine) methyltransferase activity; rRNA base methylation; rRNA metabolic process
rRNA methylation; rRNA methyltransferase activity; rRNA modification; rRNA processing



P37052
YCHJ_ECOLI UPF0225 protein YchJ

− Abundance:
tryptic [log10 Intensity]: 7.81 (Q 49)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.45 (Q 58)

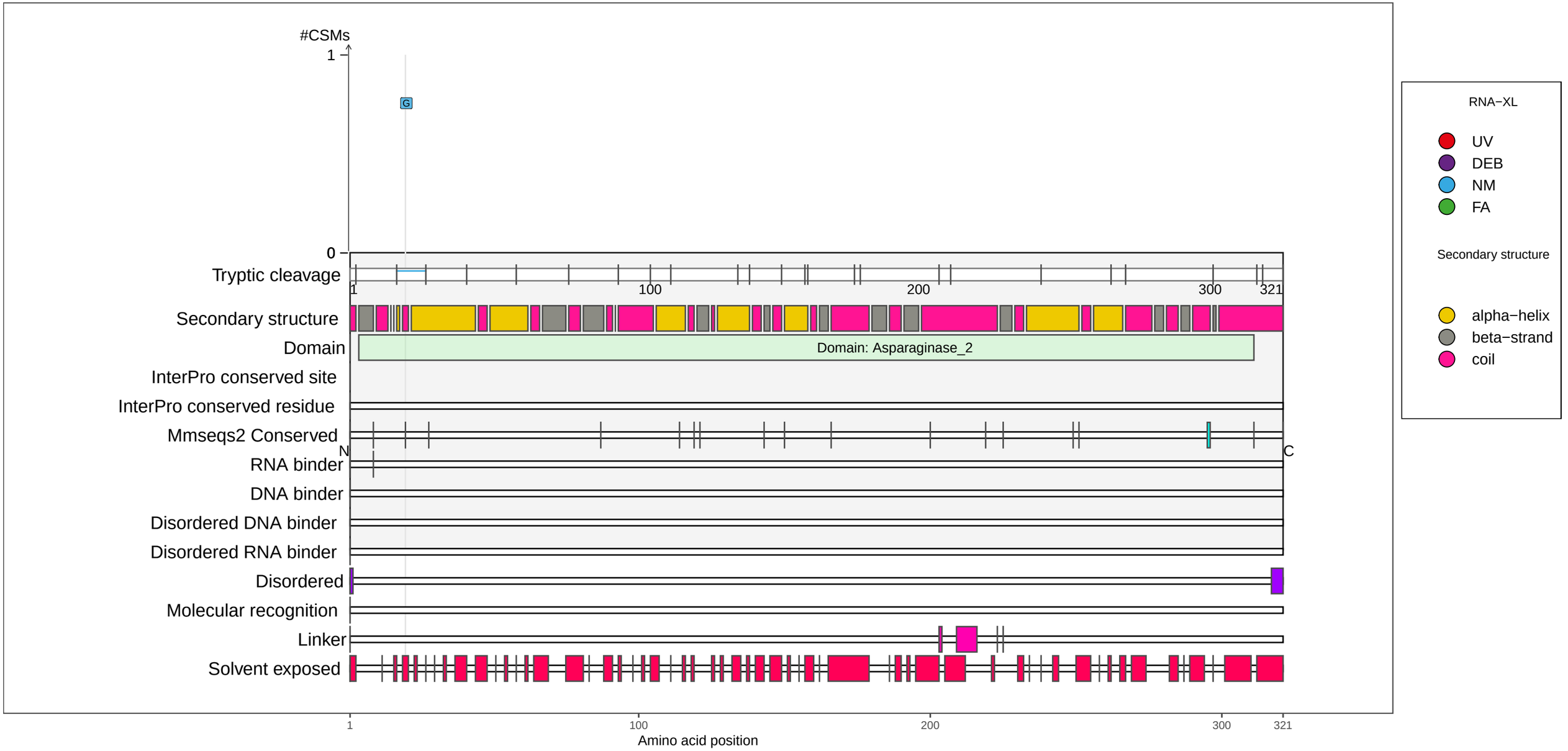
− RNA functions: not annotated



P37595
IAAA_ECOLI Isoaspartyl peptidase

− Abundance:
tryptic [log10 Intensity]: 7.74 (Q 46)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.97 (Q 47)

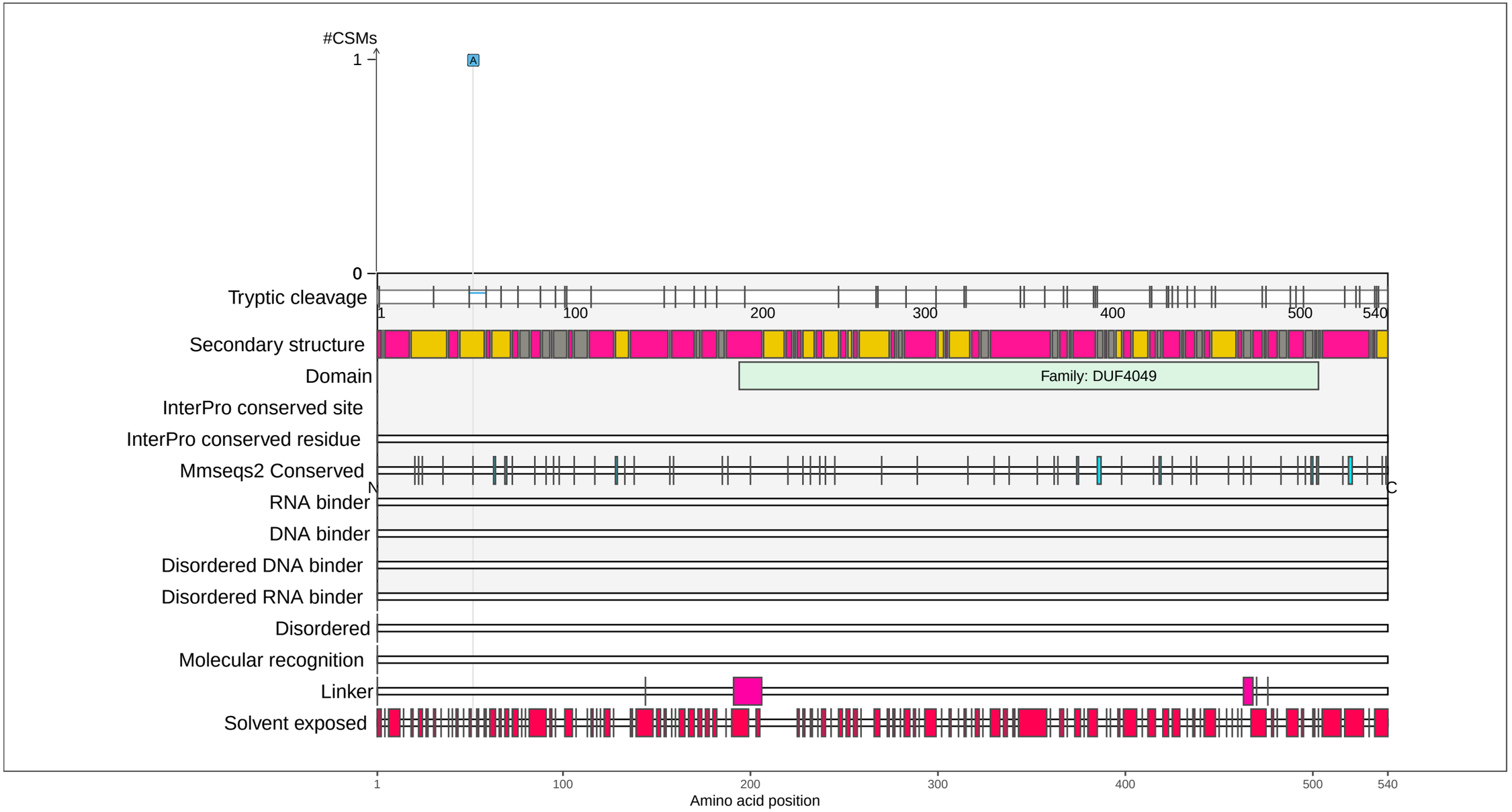
− RNA functions: not annotated



P37627
YHIJ_ECOLI Uncharacterized protein YhiJ

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.24 (Q 30)

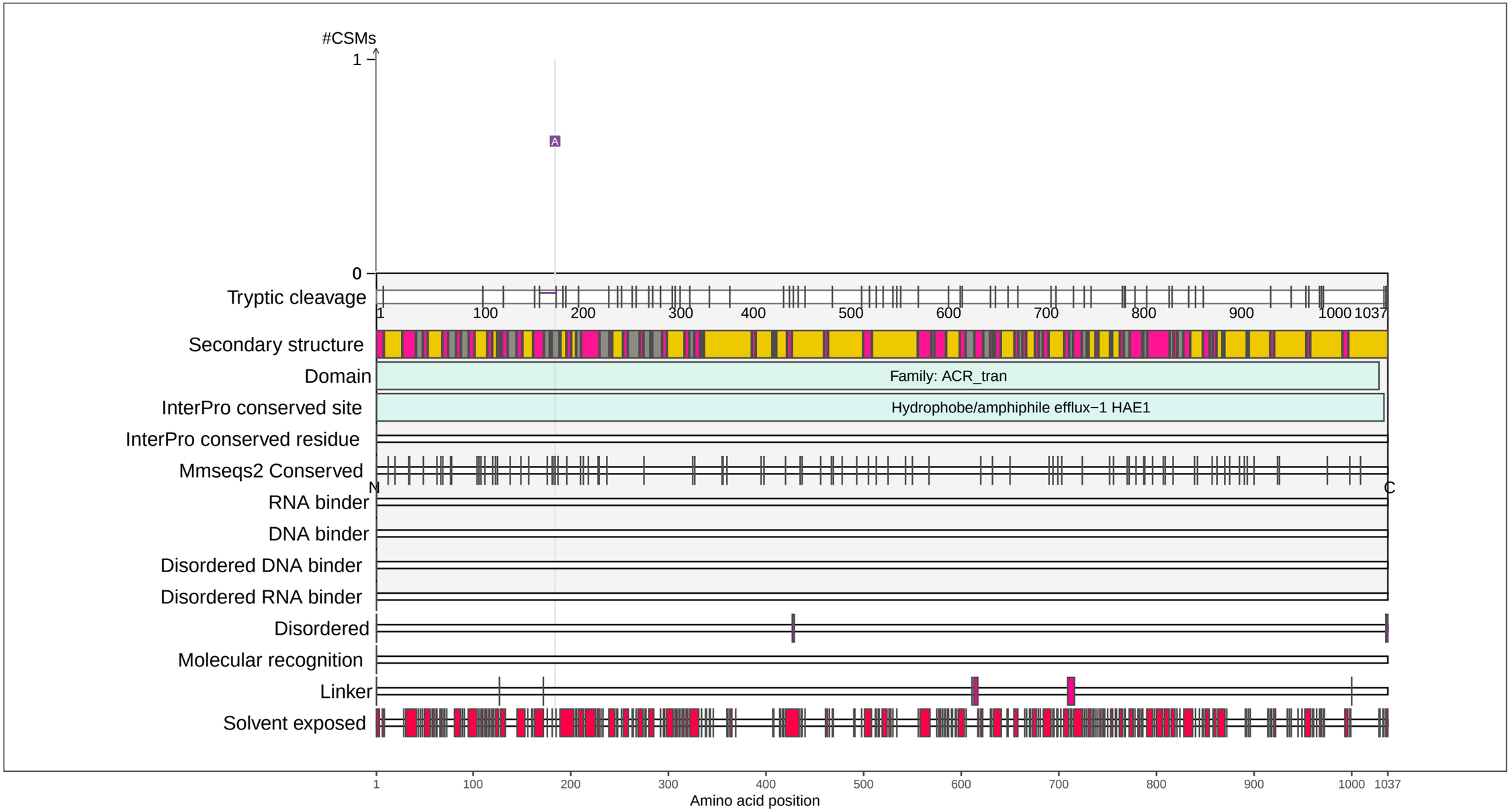
− RNA functions: not annotated



P37637
MDTF_ECOLI Multidrug resistance protein MdtF

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.57 (Q 43)
PAXdb E.coli [ppm]: 0.65 (Q 40)

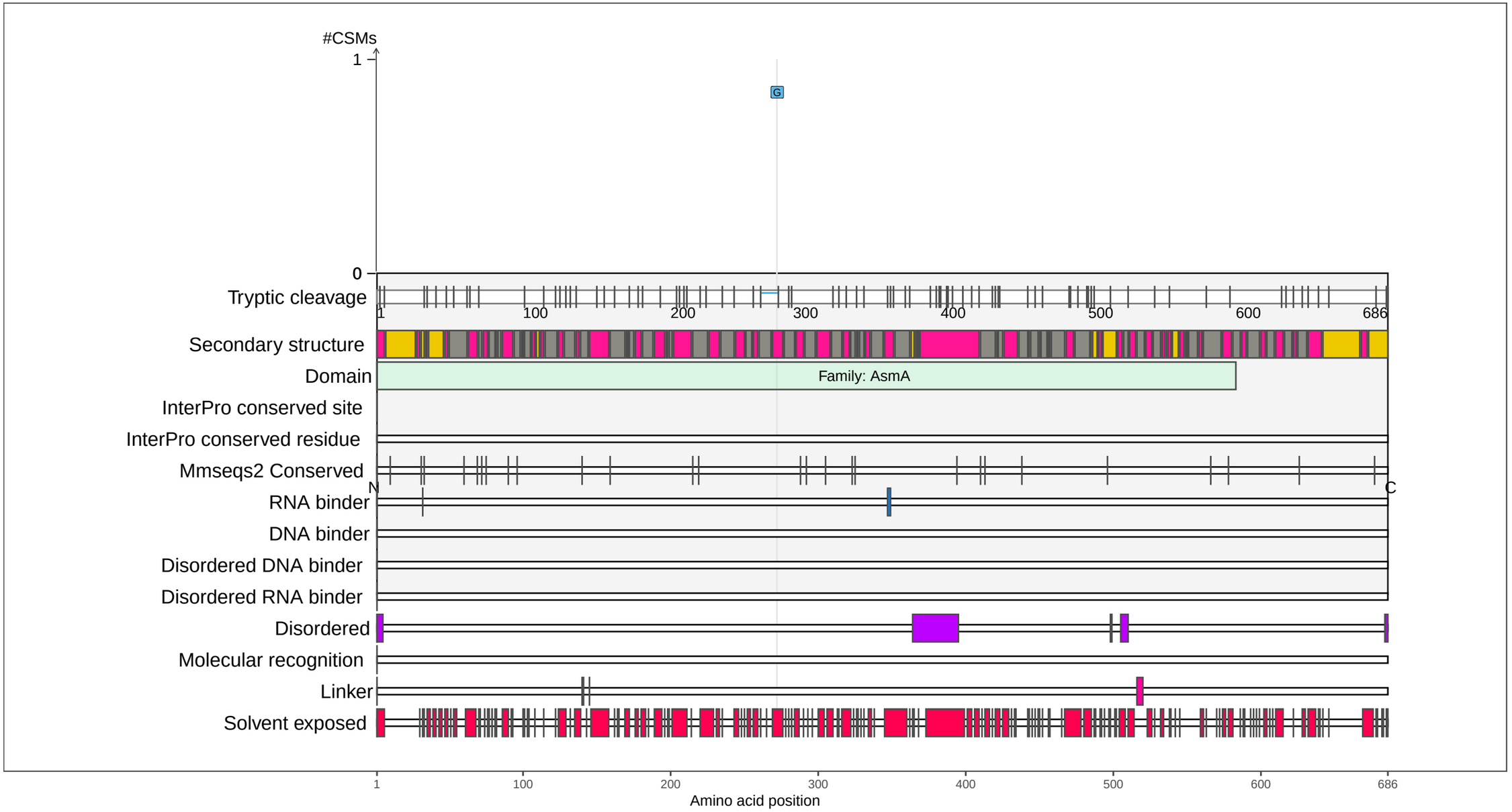
− RNA functions: not annotated



P37645
YHJG_ECOLI AsmA family protein YhjG

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.68 (Q 48)
PAXdb E.coli [ppm]: 1.34 (Q 55)

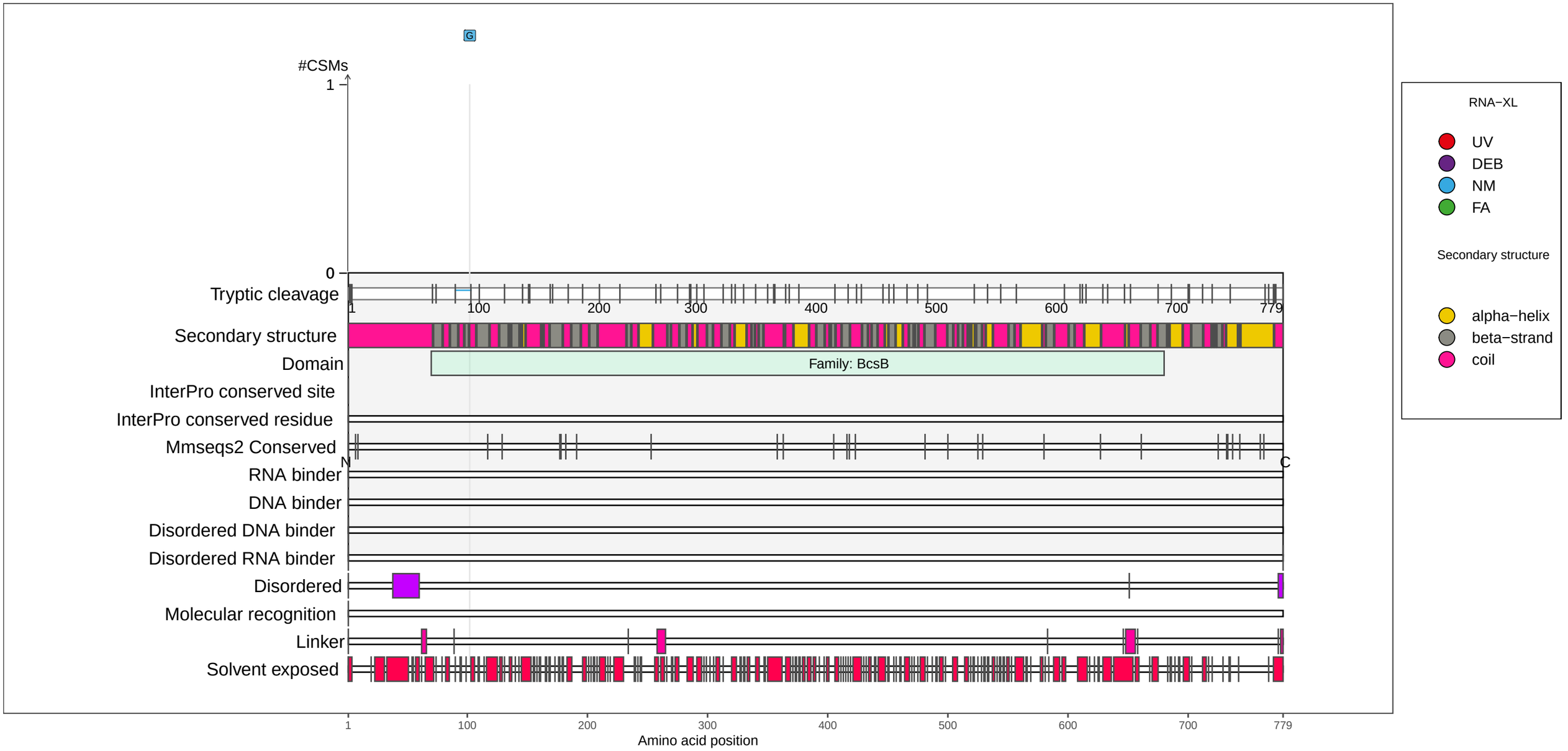
− RNA functions: not annotated



P37652
BCSB_ECOLI Cyclic di−GMP−binding protein

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.04 (Q 24)

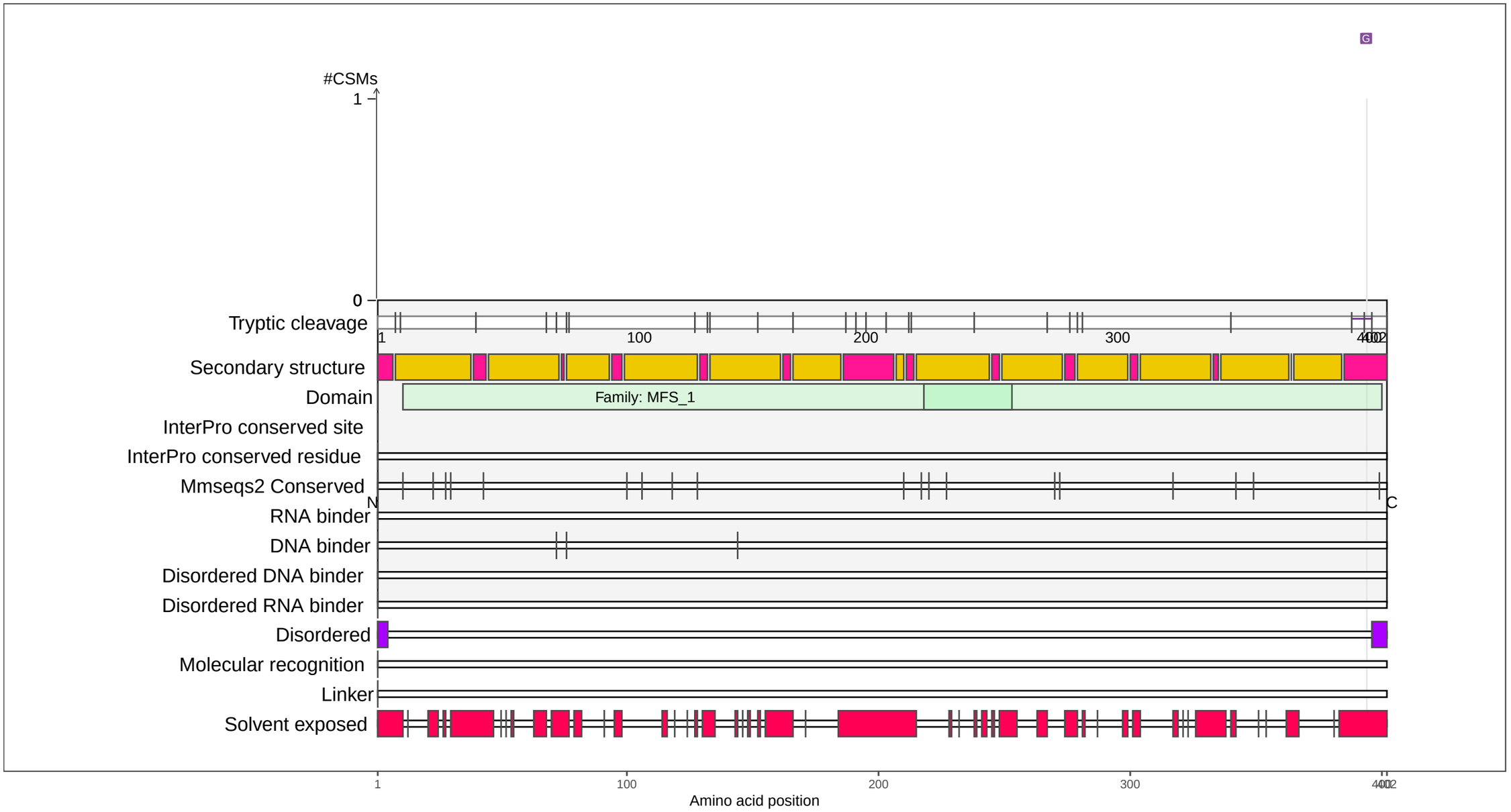
− RNA functions: not annotated



P37662
YHJX_ECOLI Uncharacterized MFS−type transporter YhjX

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.64 (Q 3)

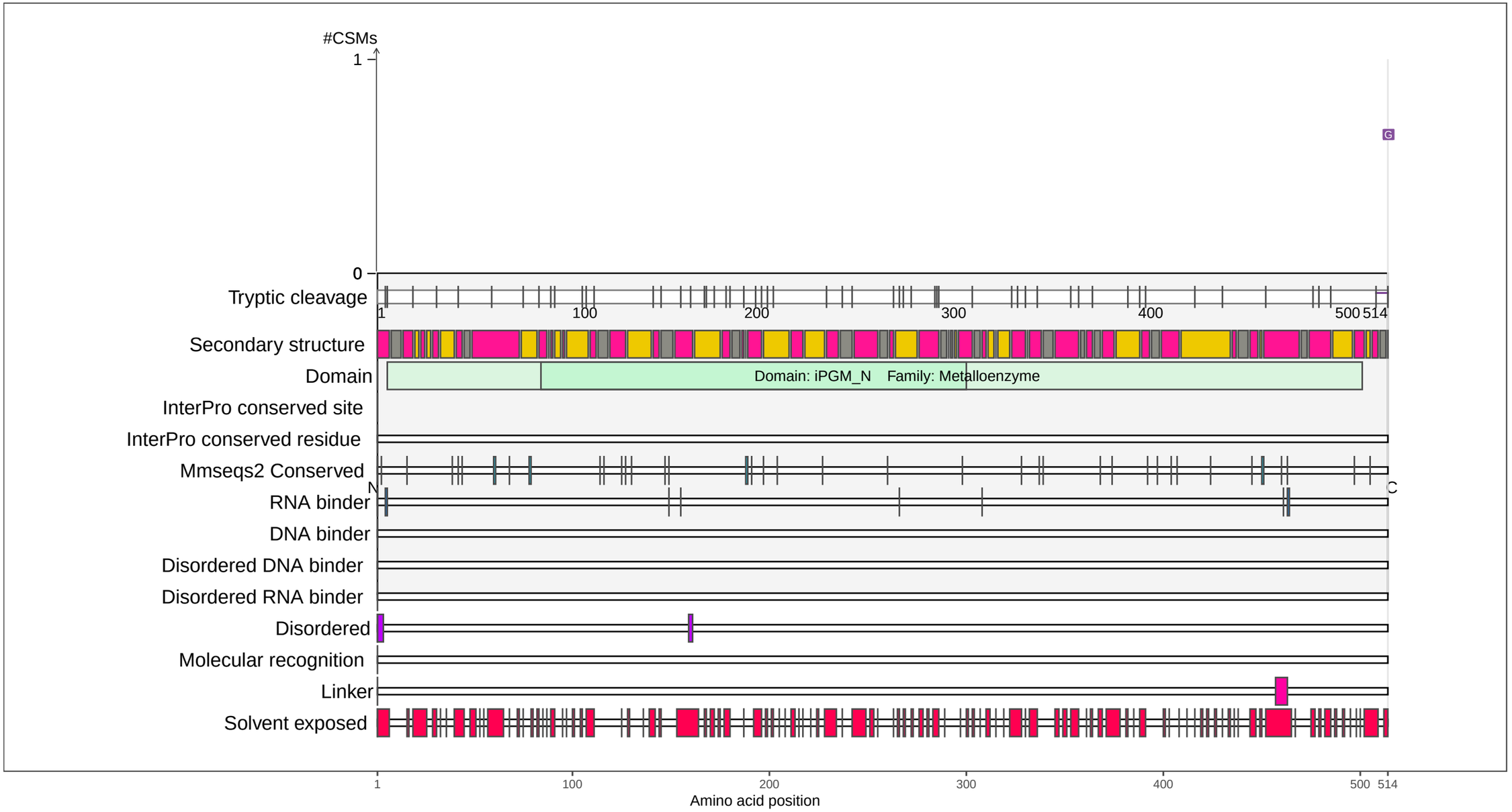
− RNA functions: not annotated



P37689
GPMI_ECOLI 2,3−bisphosphoglycerate−independent phosphoglycerate mutase

− Abundance:
tryptic [log10 Intensity]: 8.88 (Q 85)
PAXdb K12 strain [ppm]: 2.57 (Q 80)
PAXdb E.coli [ppm]: 2.67 (Q 89)

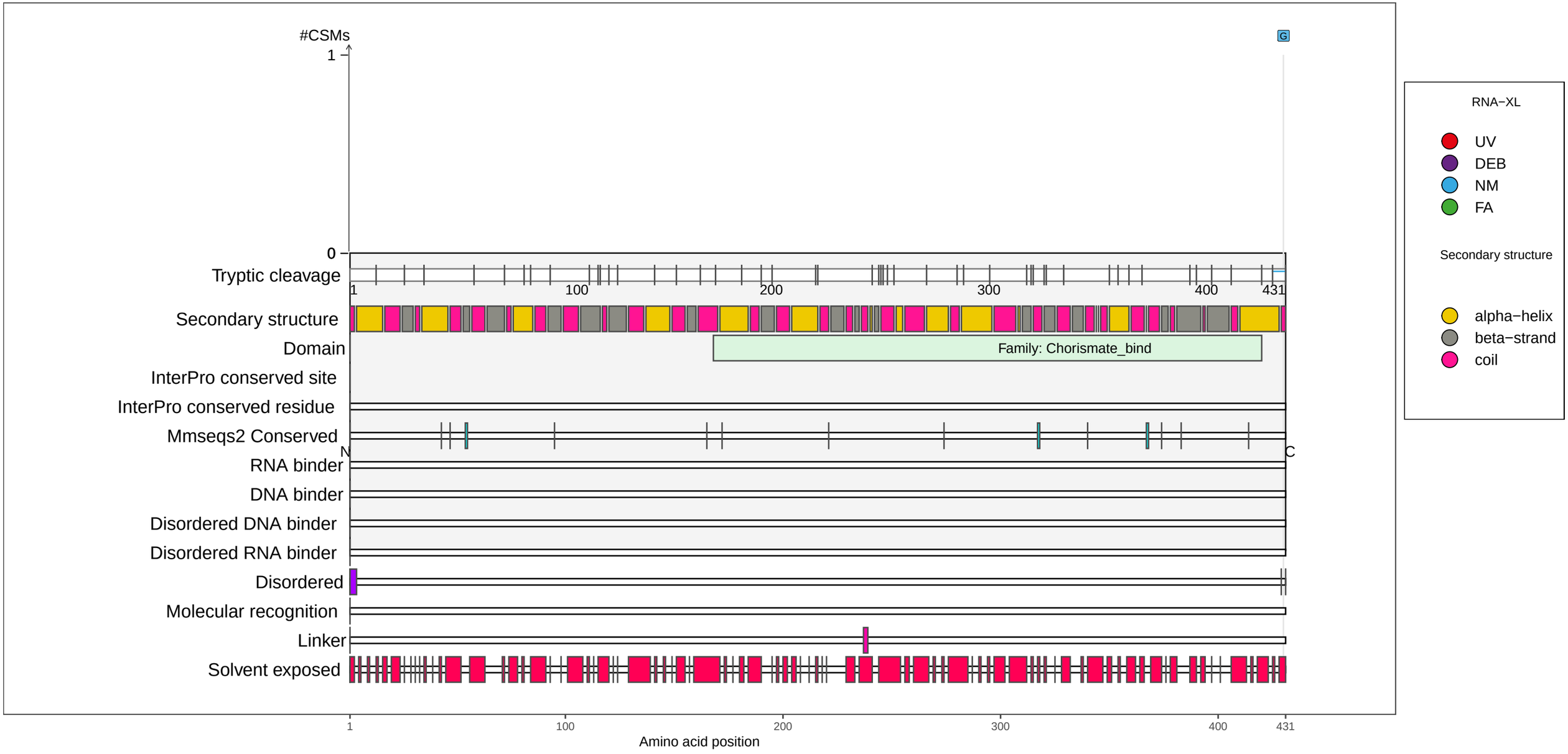
− RNA functions: not annotated



P38051
MENF_ECOLI Isochorismate synthase MenF

− Abundance:
tryptic [log10 Intensity]: 7.38 (Q 28)
PAXdb K12 strain [ppm]: 0.92 (Q 8)
PAXdb E.coli [ppm]: 0.12 (Q 27)

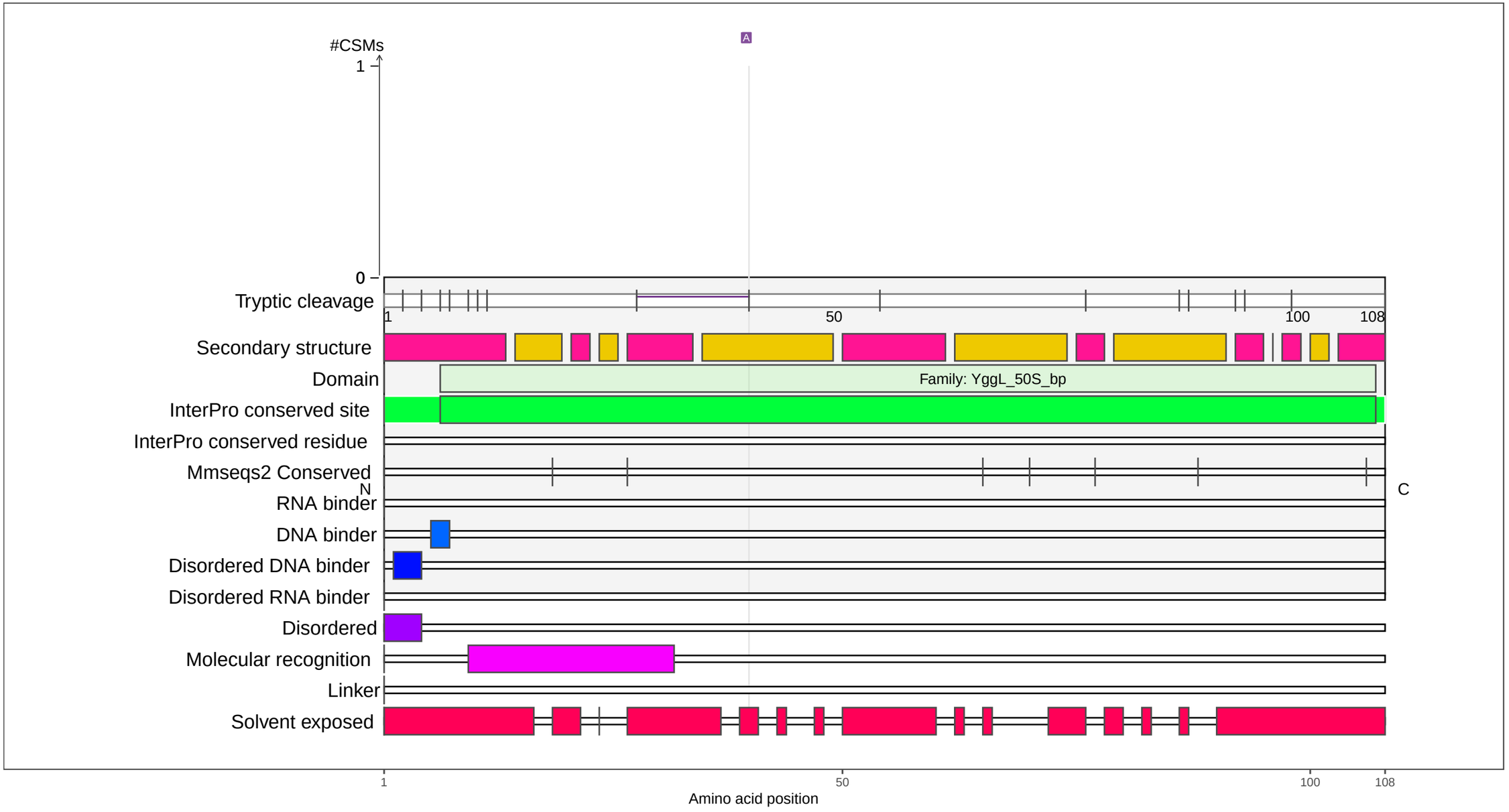
− RNA functions: not annotated

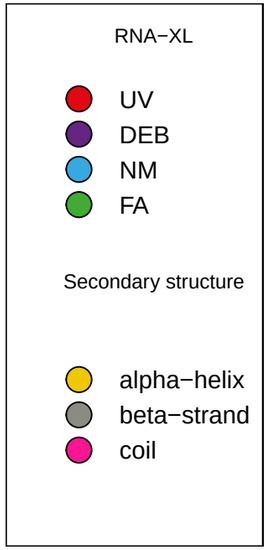


P38521
YGGL_ECOLI Uncharacterized protein YggL

− Abundance:
tryptic [log10 Intensity]: 7.95 (Q 56)
PAXdb K12 strain [ppm]: 2.32 (Q 71)
PAXdb E.coli [ppm]: 2.62 (Q 88)

− RNA functions: not annotated

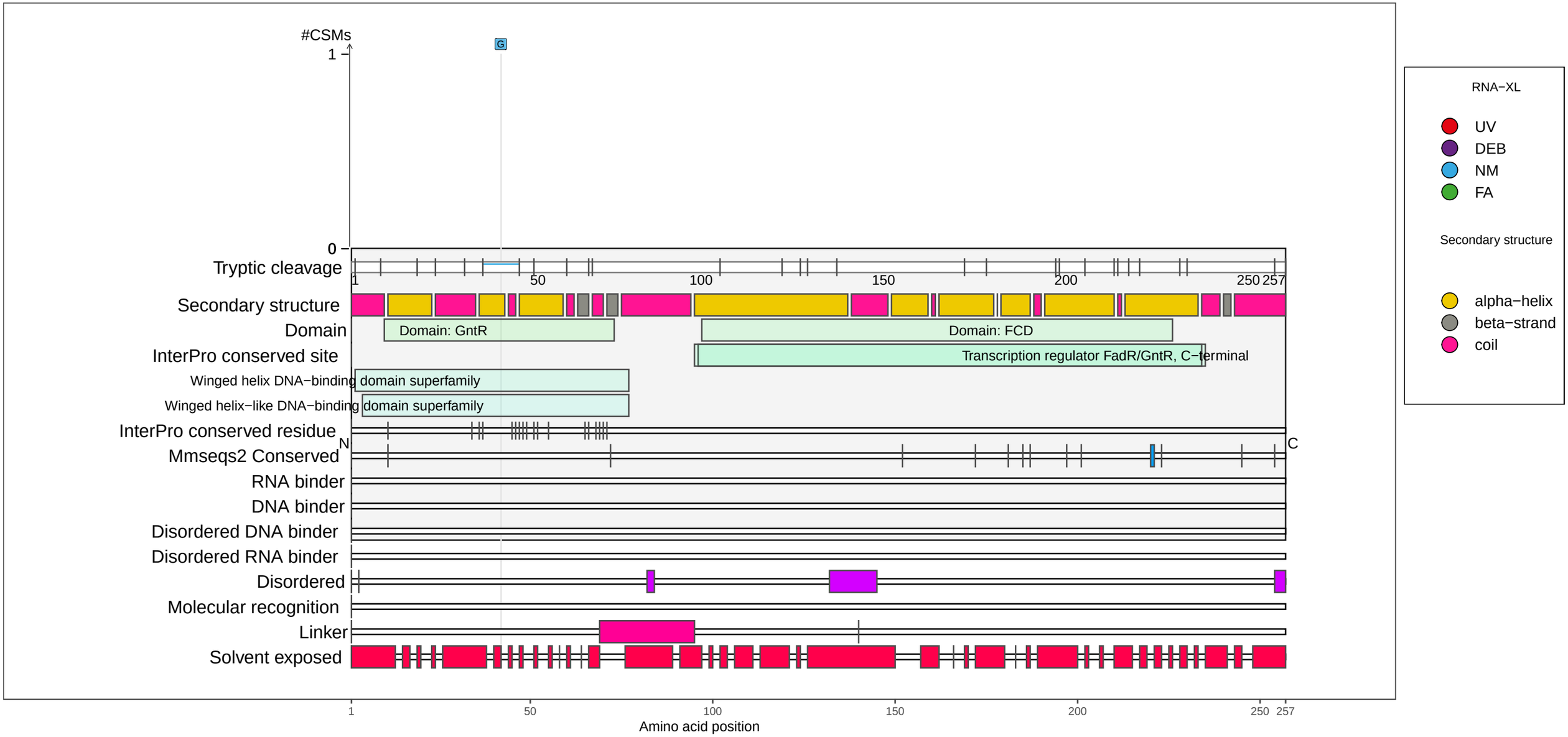




P39161
UXUR_ECOLI Uxu operon transcriptional regulator

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.41 (Q 34)

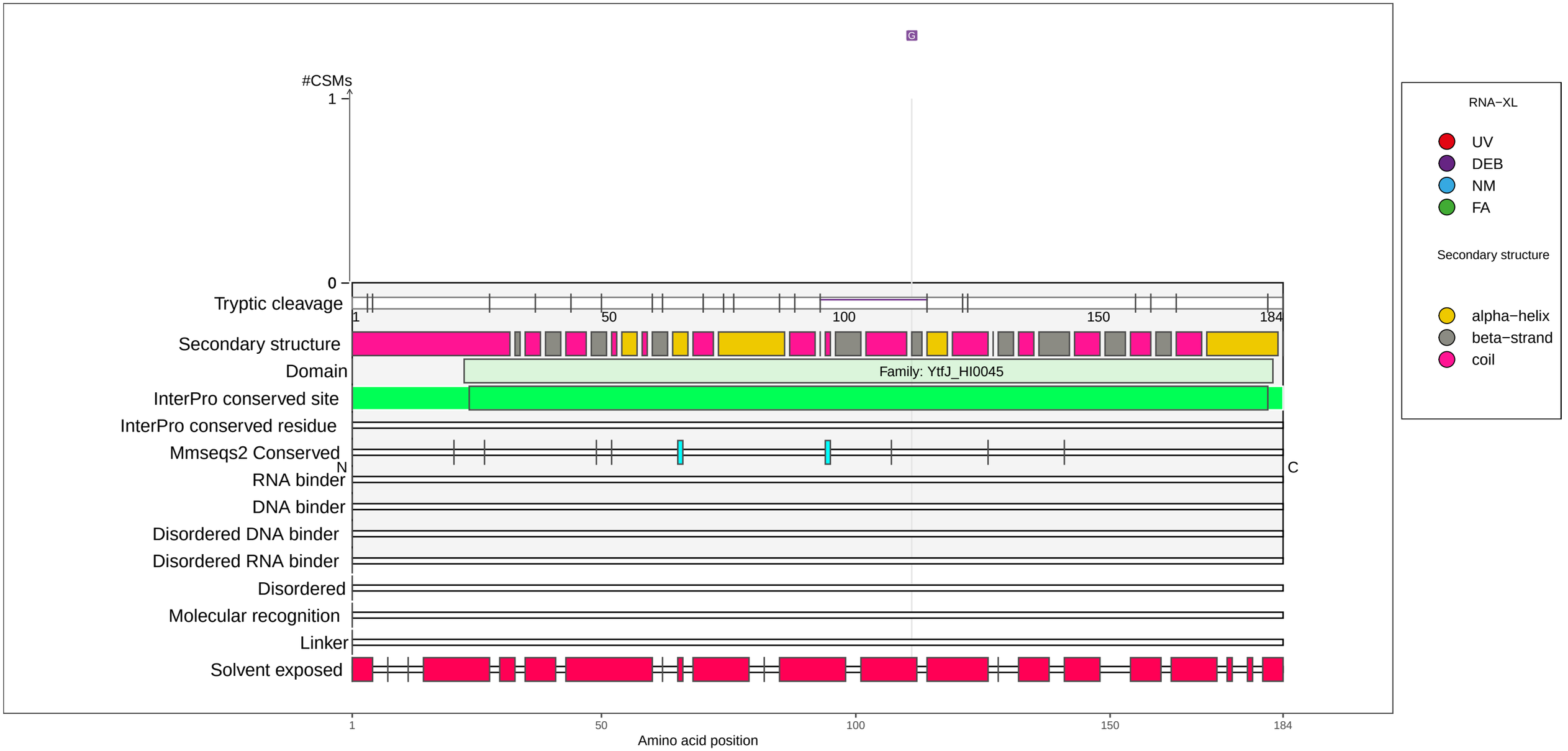
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P39187
YTFJ_ECOLI Uncharacterized protein YtfJ

− Abundance:
tryptic [log10 Intensity]: 7.04 (Q 15)
PAXdb K12 strain [ppm]: 2.06 (Q 62)
PAXdb E.coli [ppm]: 2.52 (Q 86)

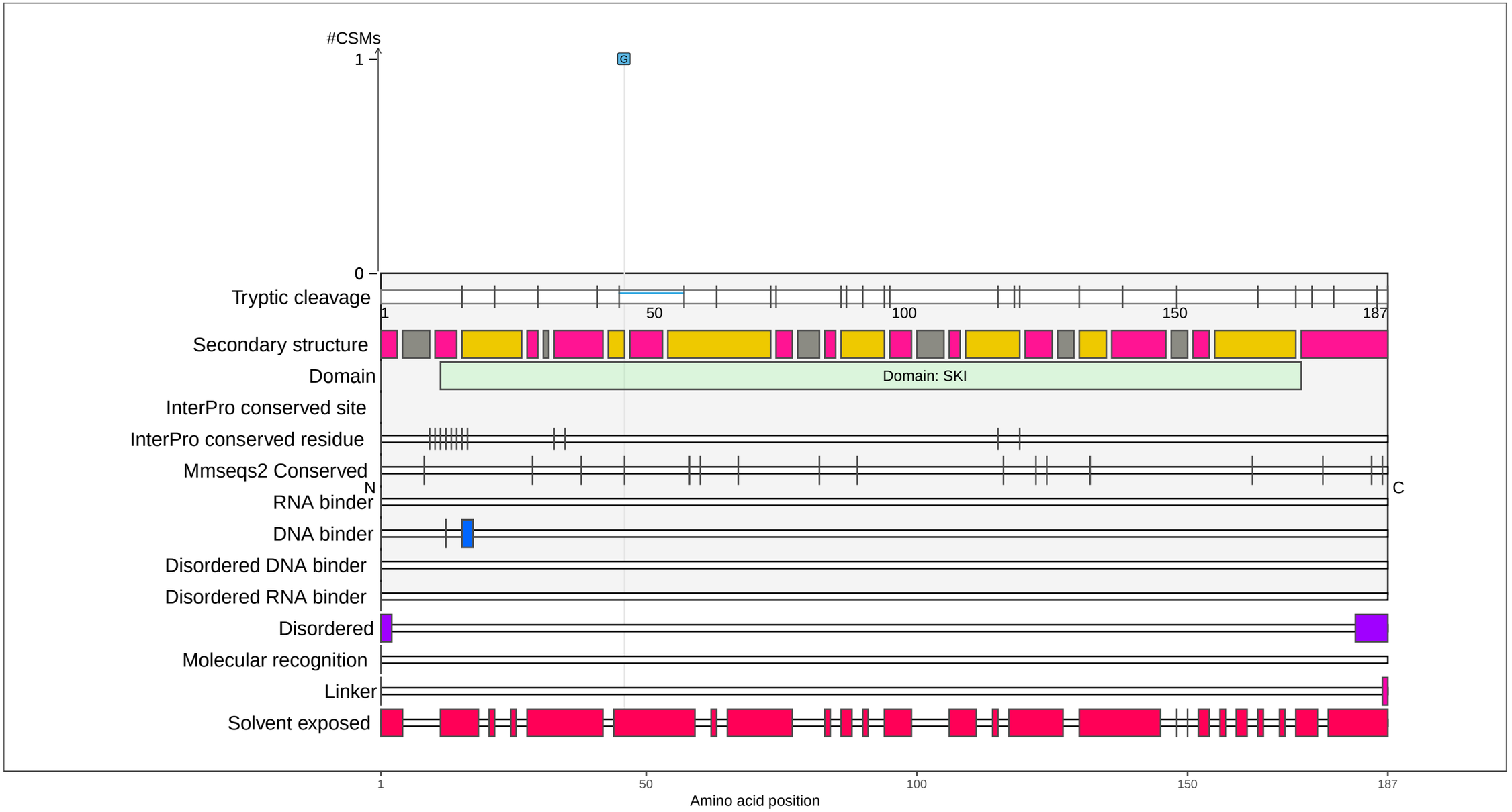
− RNA functions: not annotated



P39208
IDNK_ECOLI Thermosensitive gluconokinase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.61 (Q 14)

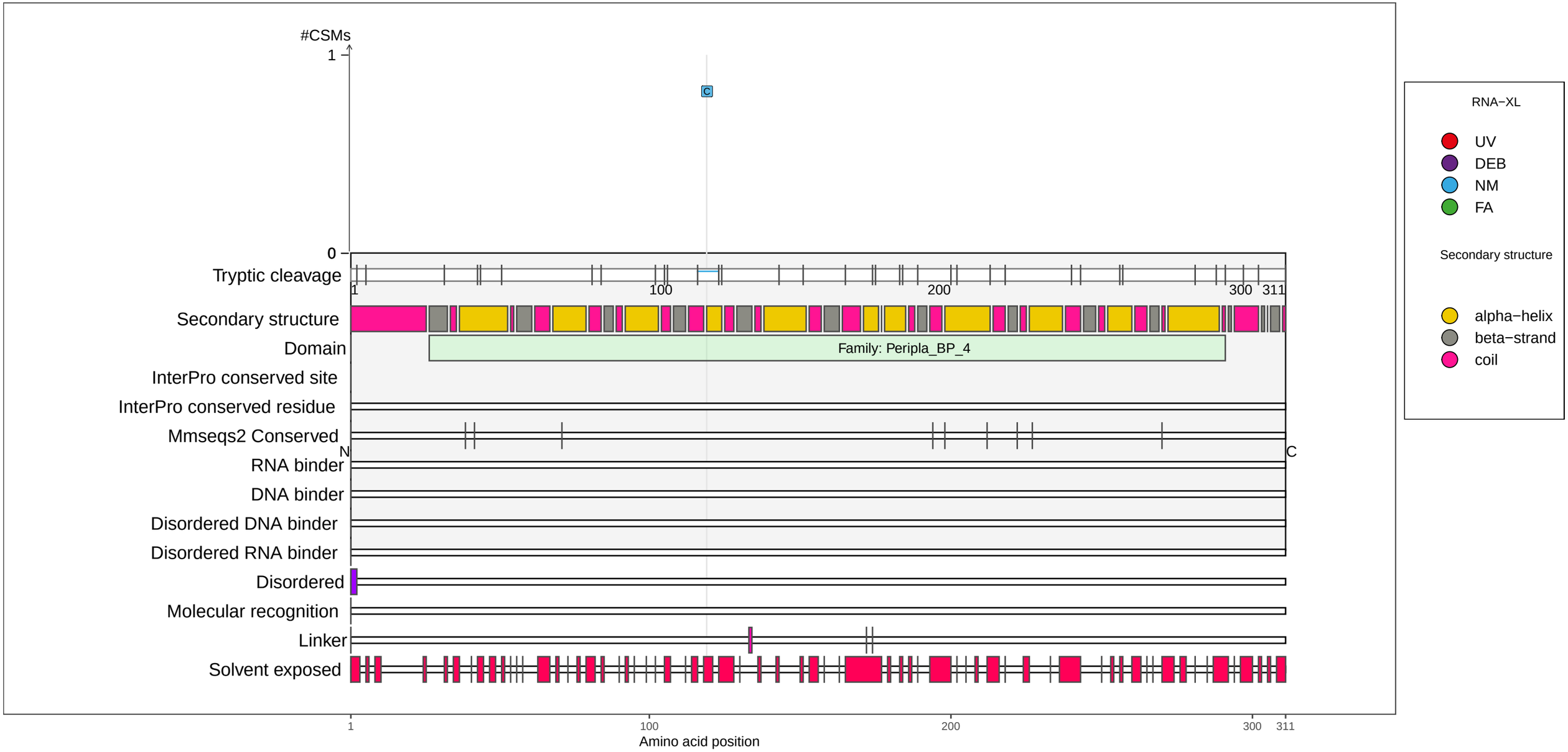
− RNA functions: not annotated



P39265
ALSB_ECOLI D−allose−binding periplasmic protein

− Abundance:
tryptic [log10 Intensity]: 7.41 (Q 30)
PAXdb K12 strain [ppm]: 2.43 (Q 75)
PAXdb E.coli [ppm]: 1.64 (Q 63)

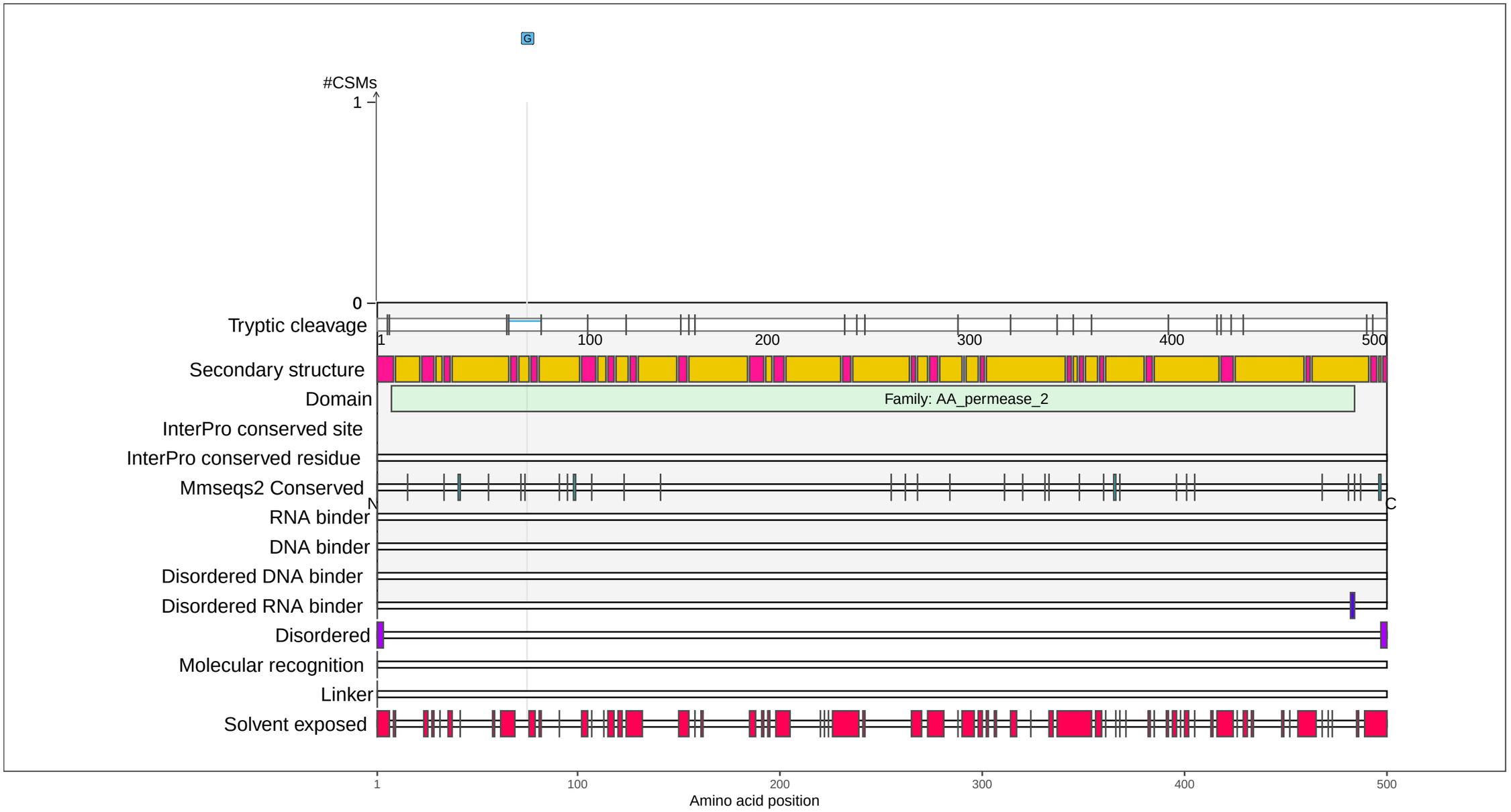
− RNA functions: not annotated

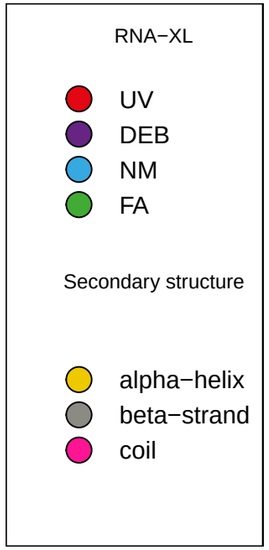


P39282
YJEM_ECOLI Inner membrane transporter YjeM

− Abundance:
tryptic [log10 Intensity]: 7.5 (Q 35)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

− RNA functions: not annotated

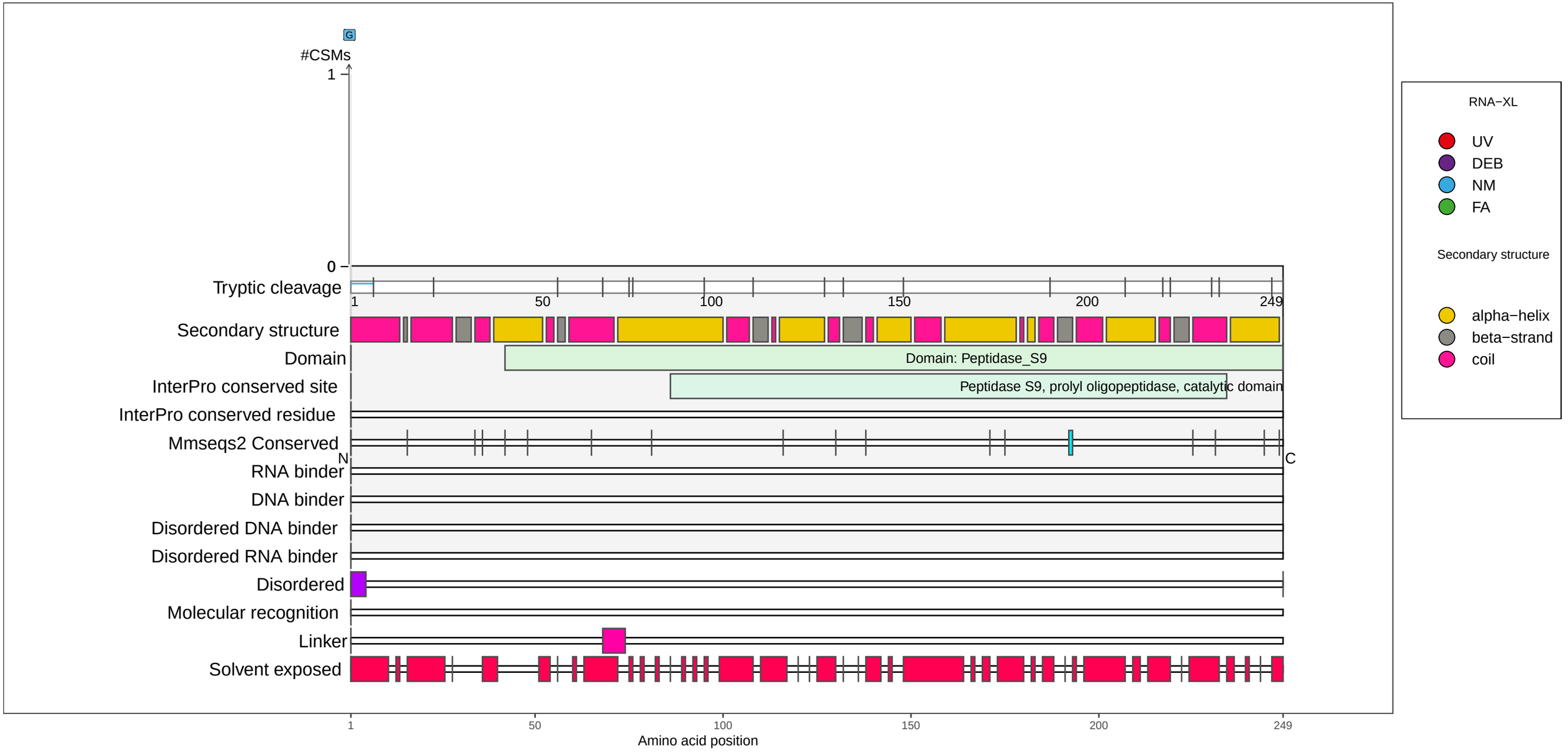




P39298
YJFP_ECOLI Esterase YjfP

− Abundance:
tryptic [log10 Intensity]: 7.54 (Q 37)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.15 (Q 51)

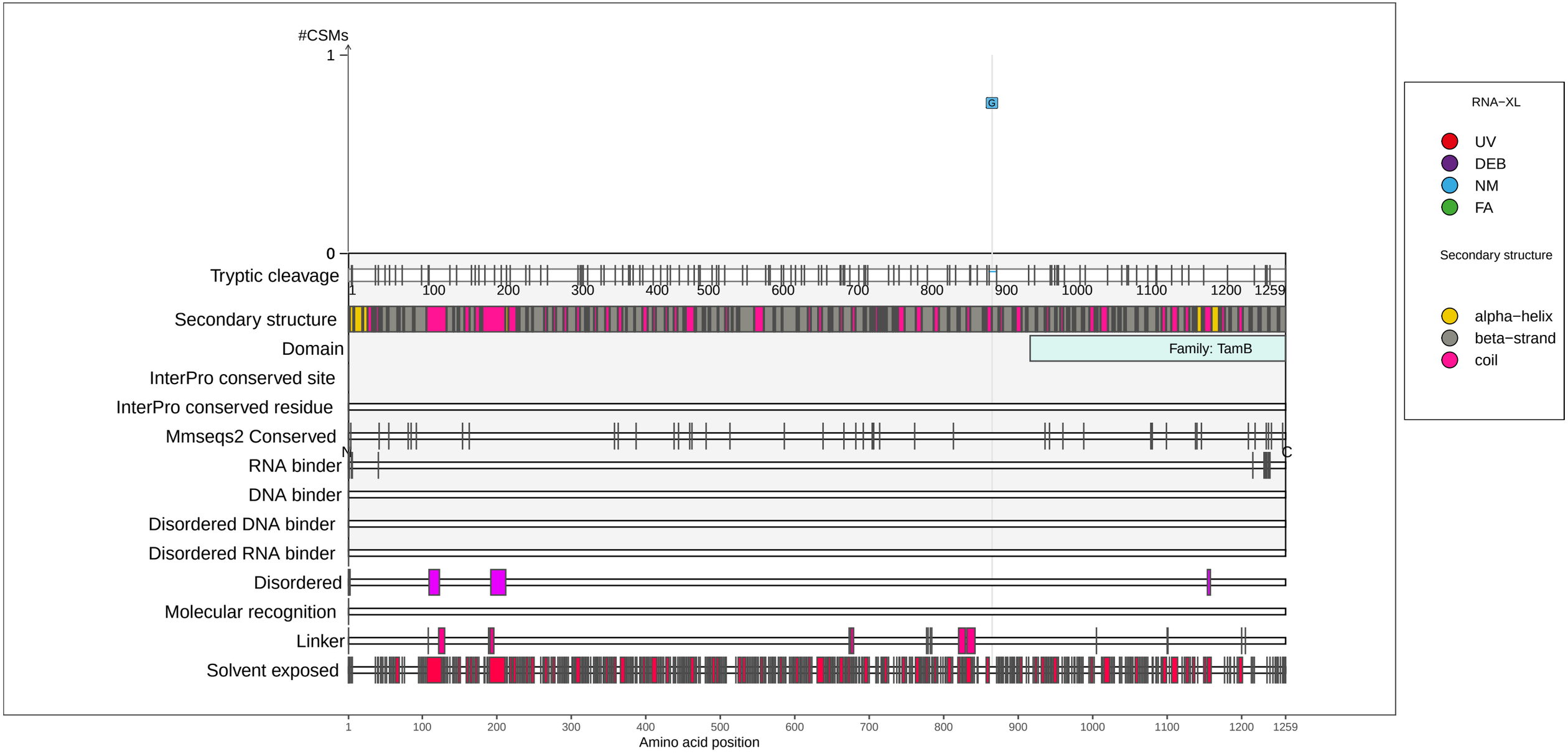
− RNA functions: not annotated



P39321
TAMB_ECOLI Translocation and assembly module subunit TamB

− Abundance:
tryptic [log10 Intensity]: 7.9 (Q 54)
PAXdb K12 strain [ppm]: 0.88 (Q 7)
PAXdb E.coli [ppm]: 0.53 (Q 37)

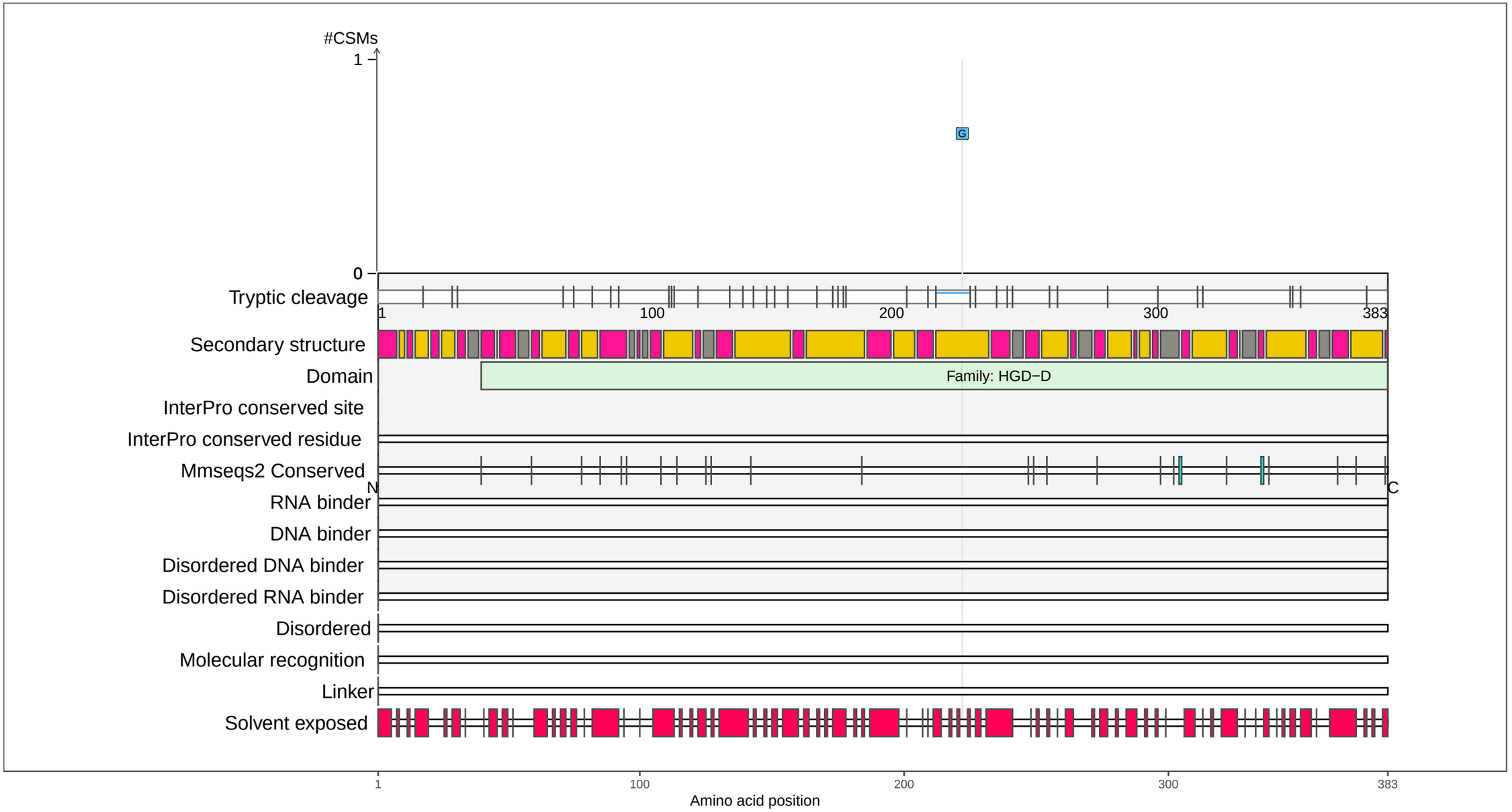
− RNA functions: not annotated



P39384
YJIM_ECOLI Putative dehydratase subunit YjiM

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.88 (Q 7)
PAXdb E.coli [ppm]: −0.76 (Q 12)

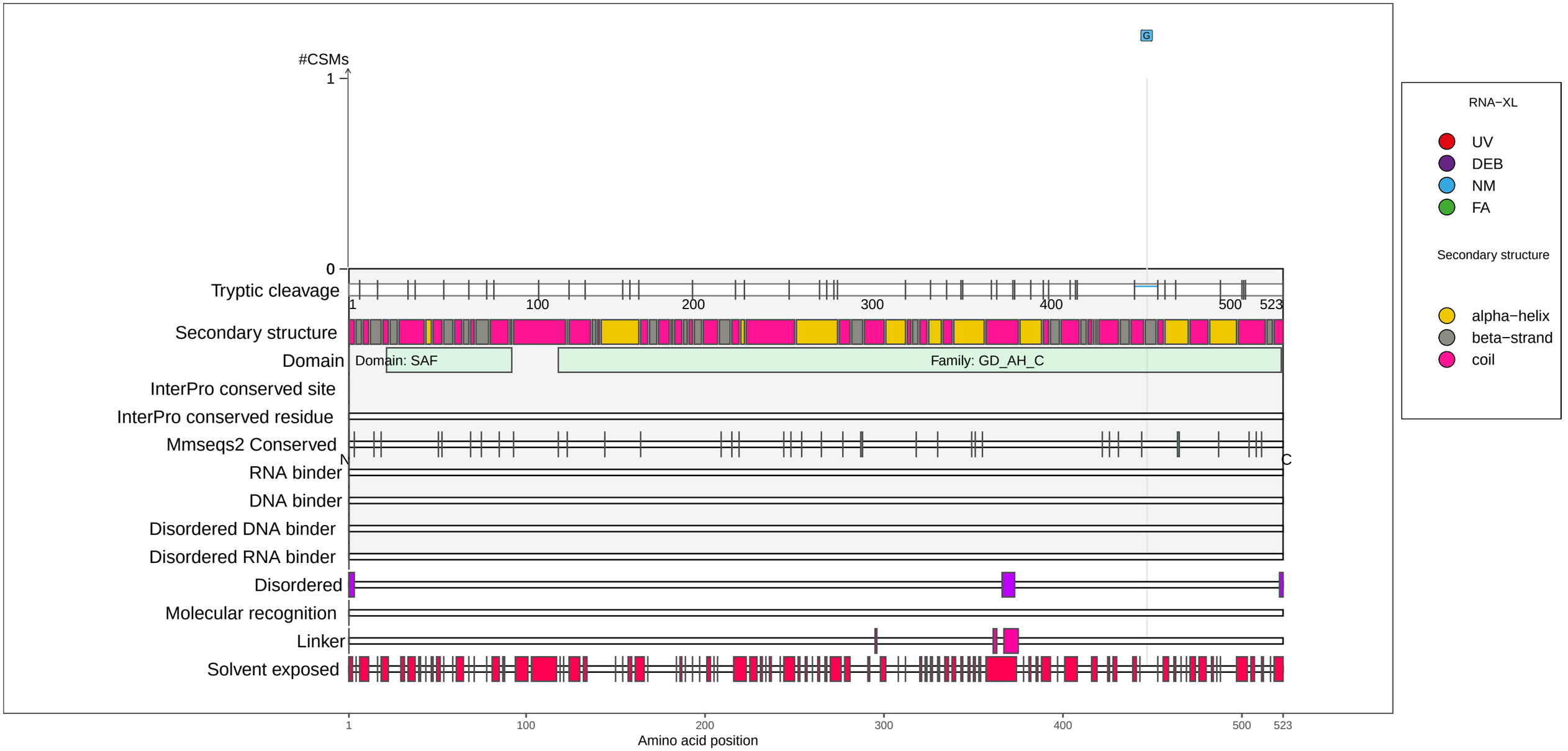
− RNA functions: not annotated



P39829
GARD_ECOLI Galactarate dehydratase (L−threo−forming)

− Abundance:
tryptic [log10 Intensity]: 7.64 (Q 42)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.43 (Q 34)

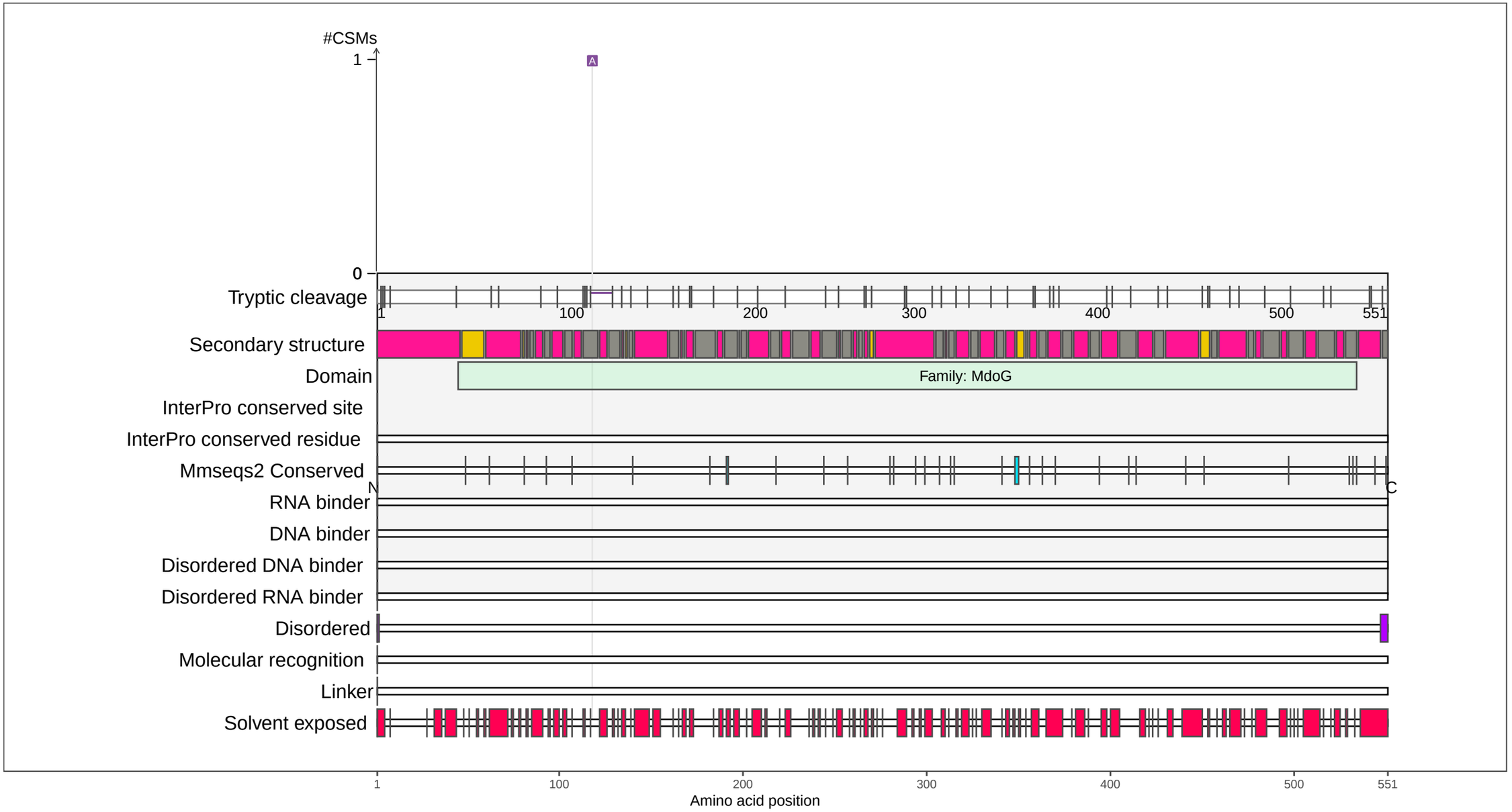
− RNA functions: not annotated



P40120
OPGD_ECOLI Glucans biosynthesis protein D

− Abundance:
tryptic [log10 Intensity]: 8.3 (Q 69)
PAXdb K12 strain [ppm]: 1.46 (Q 36)
PAXdb E.coli [ppm]: 1.37 (Q 56)

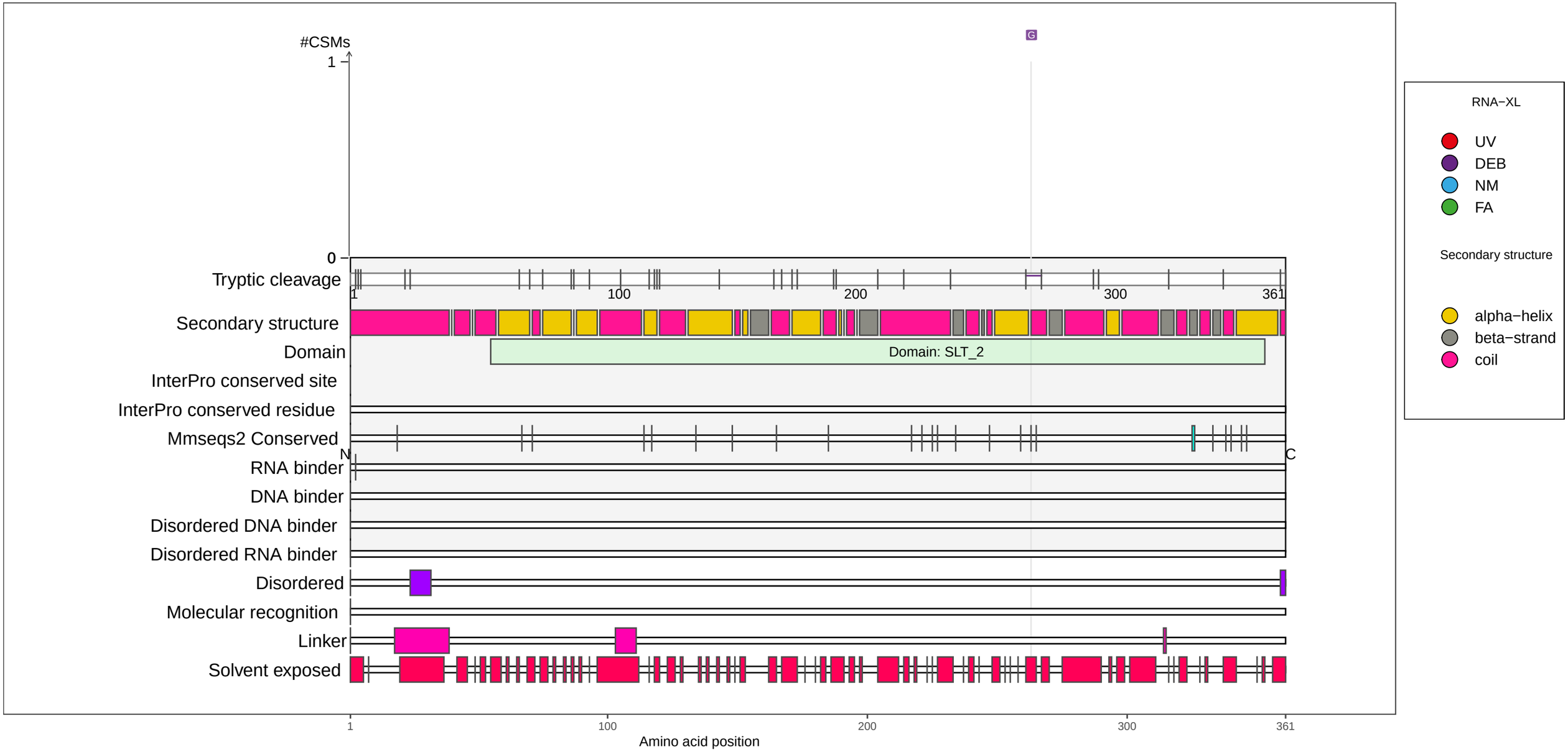
− RNA functions: not annotated



P41052
MLTB_ECOLI Membrane−bound lytic murein transglycosylase B

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 56)
PAXdb K12 strain [ppm]: 0.8 (Q 5)
PAXdb E.coli [ppm]: 0.98 (Q 47)

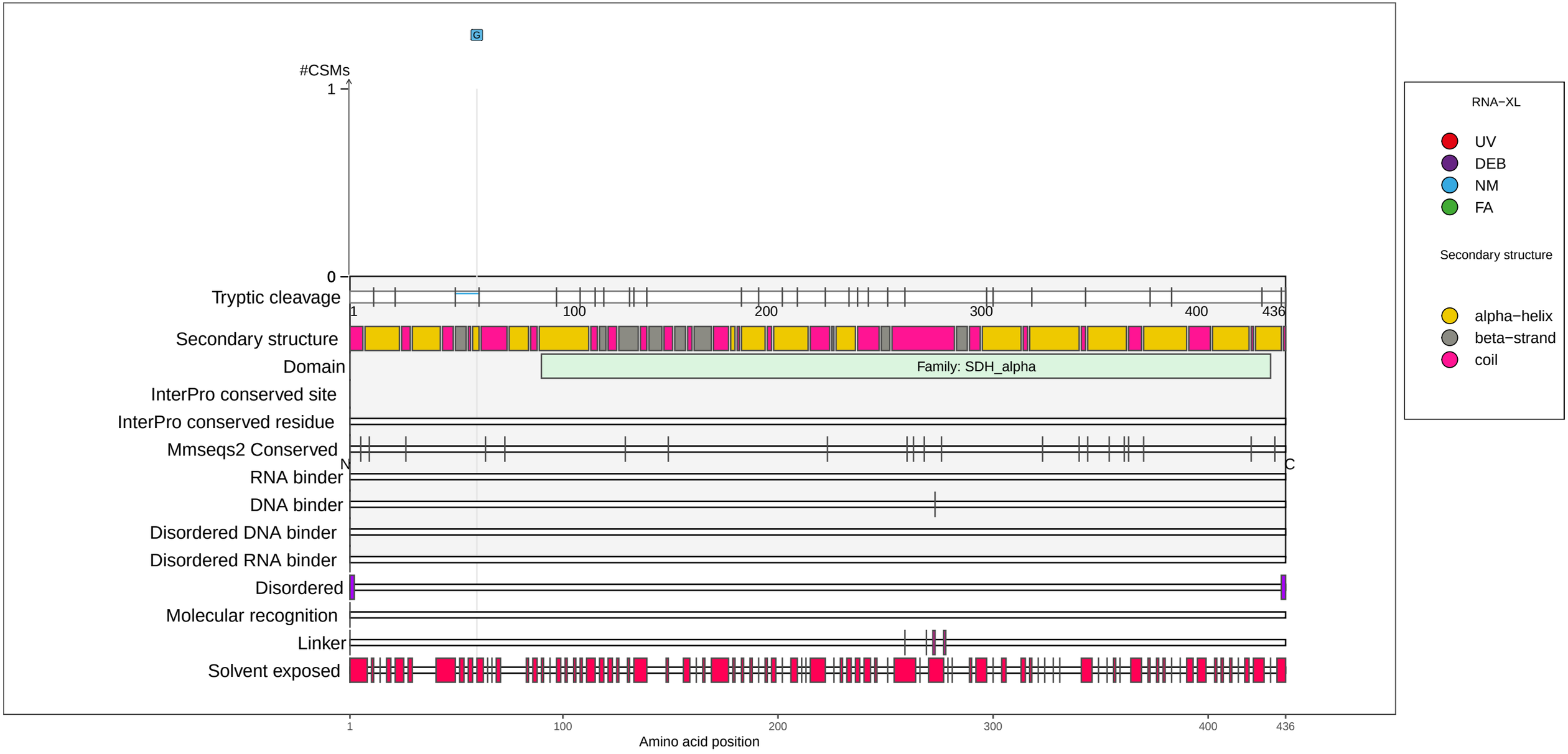
− RNA functions: not annotated



P42626
YHAM_ECOLI UPF0597 protein YhaM

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.94 (Q 10)

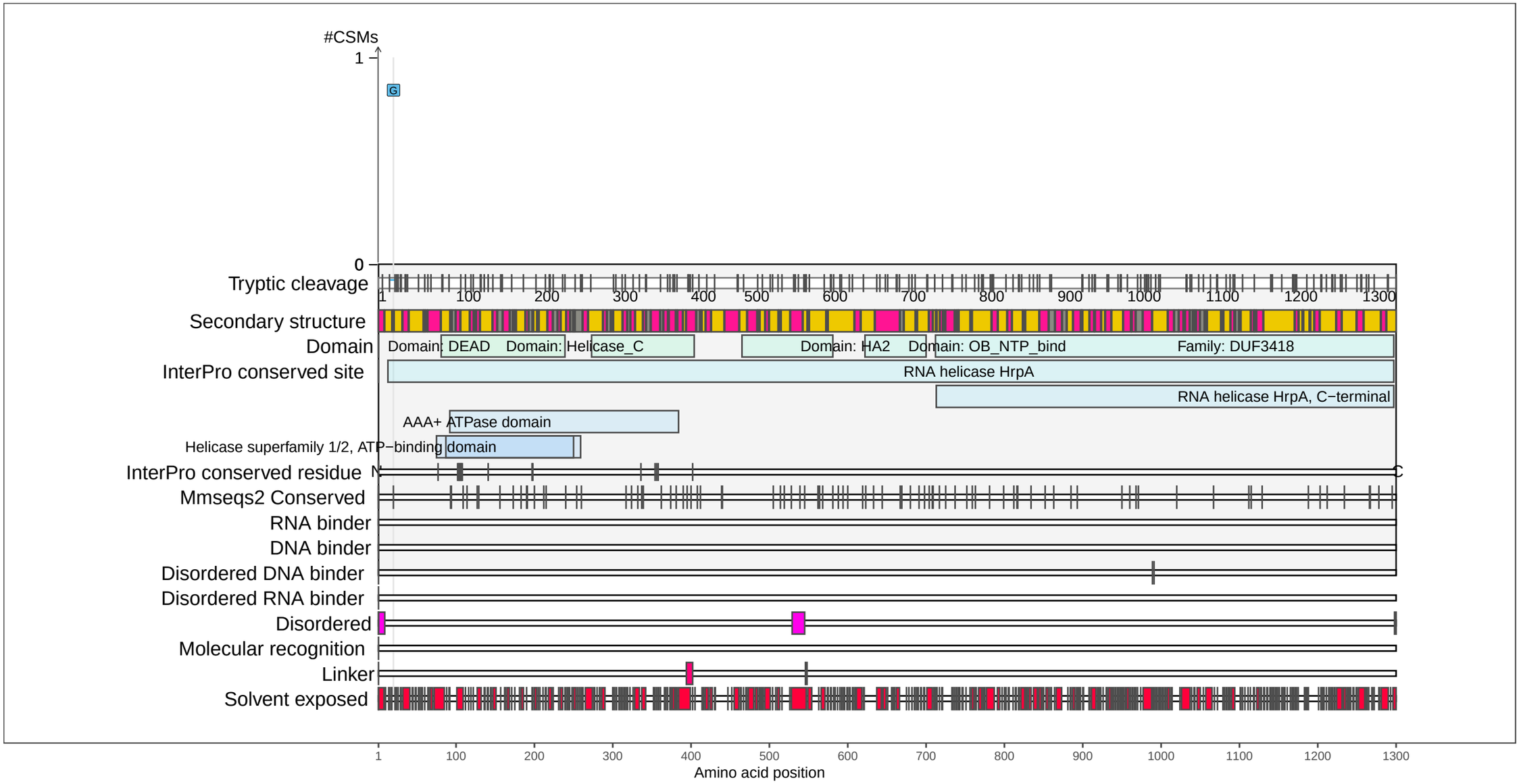
− RNA functions: not annotated

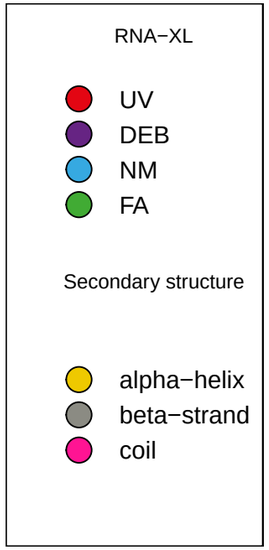


P43329
HRPA_ECOLI ATP−dependent RNA helicase HrpA

− Abundance:
tryptic [log10 Intensity]: 7.96 (Q 56)
PAXdb K12 strain [ppm]: 1.19 (Q 20)
PAXdb E.coli [ppm]: 1.43 (Q 58)

− RNA functions:
mRNA metabolic process; mRNA processing; RNA helicase activity; RNA metabolic process
RNA modification; RNA processing

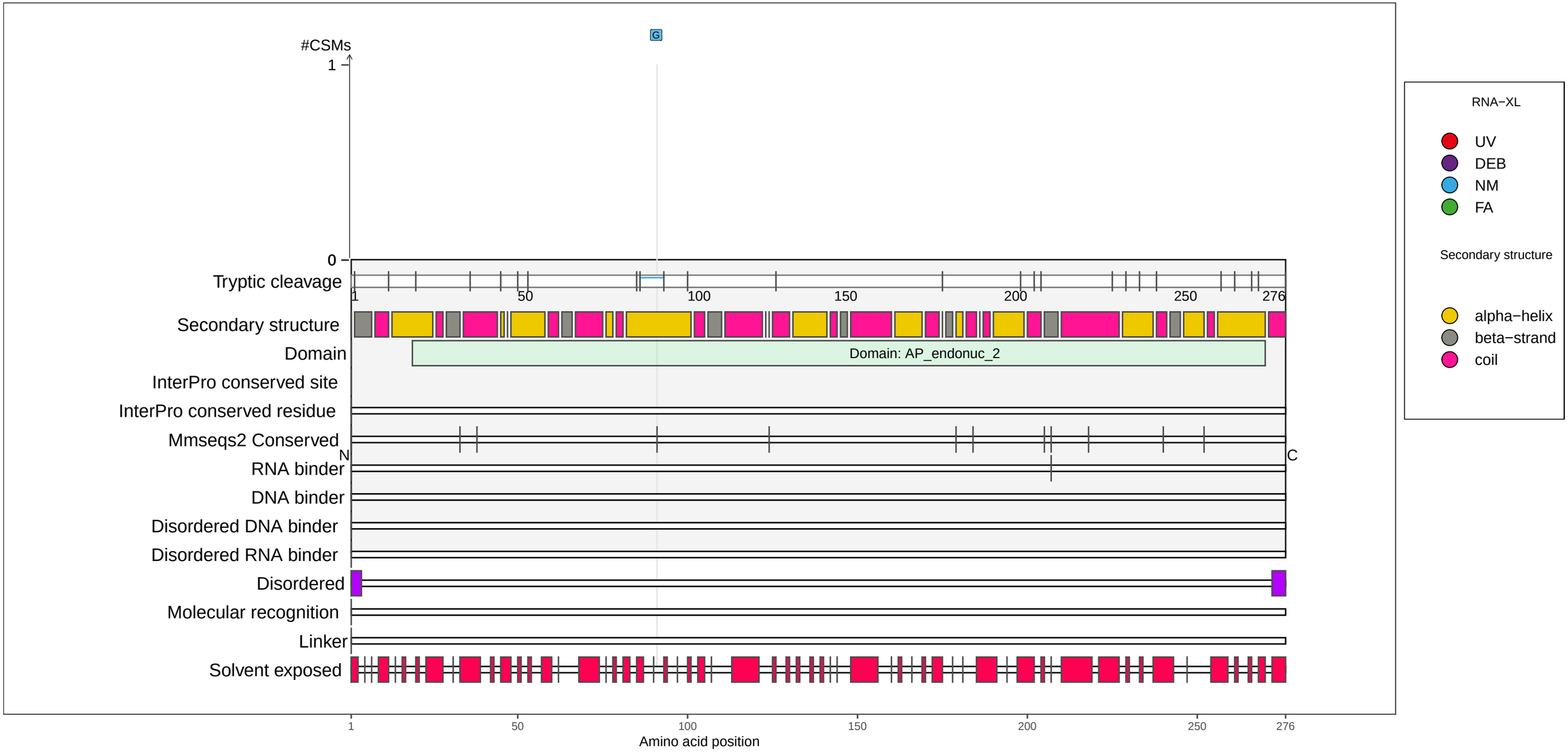




P45541
FRLC_ECOLI Fructoselysine 3−epimerase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.74 (Q 12)

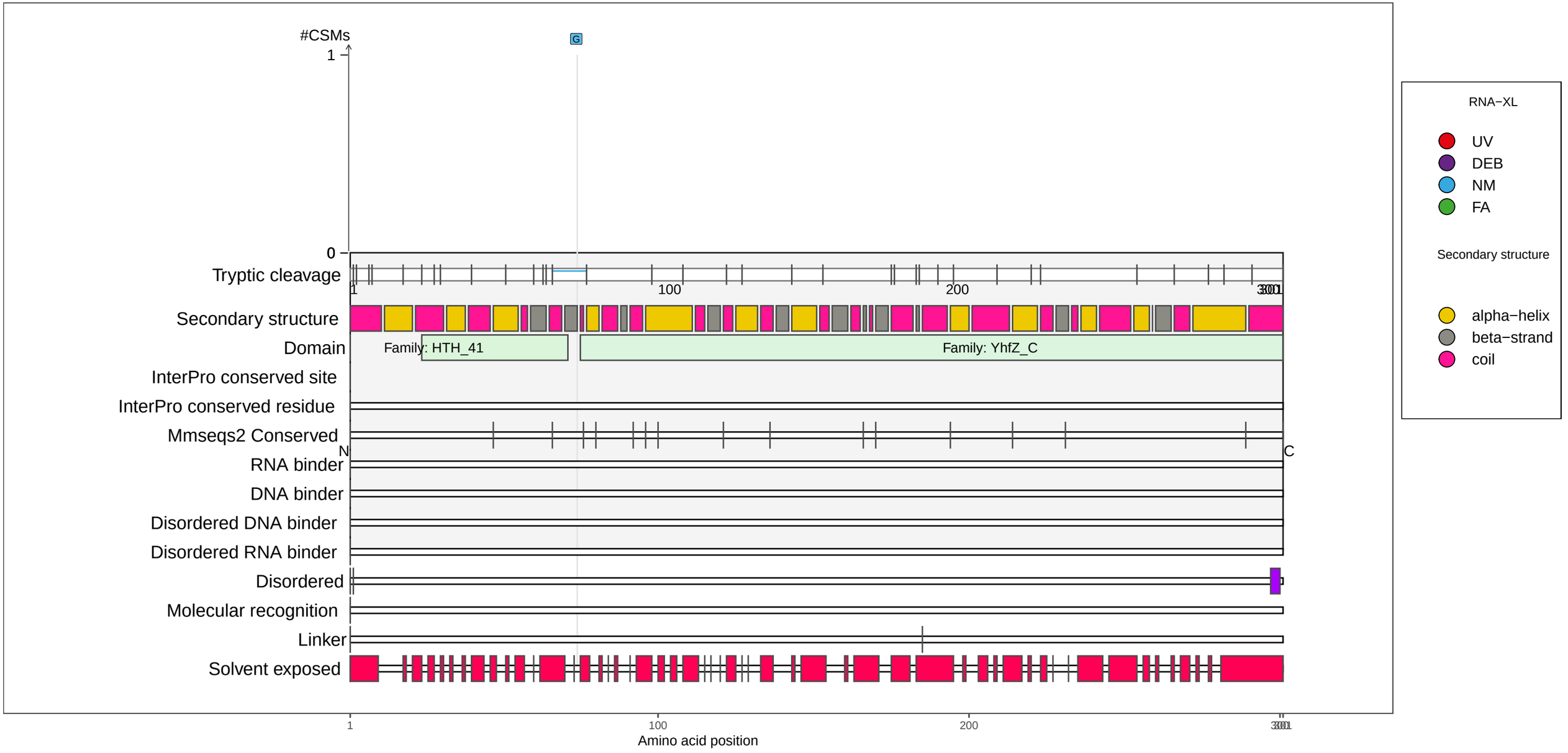
− RNA functions: not annotated



P45552
YHFZ_ECOLI Uncharacterized protein YhfZ

− Abundance:
tryptic [log10 Intensity]: 7.29 (Q 25)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.42 (Q 17)

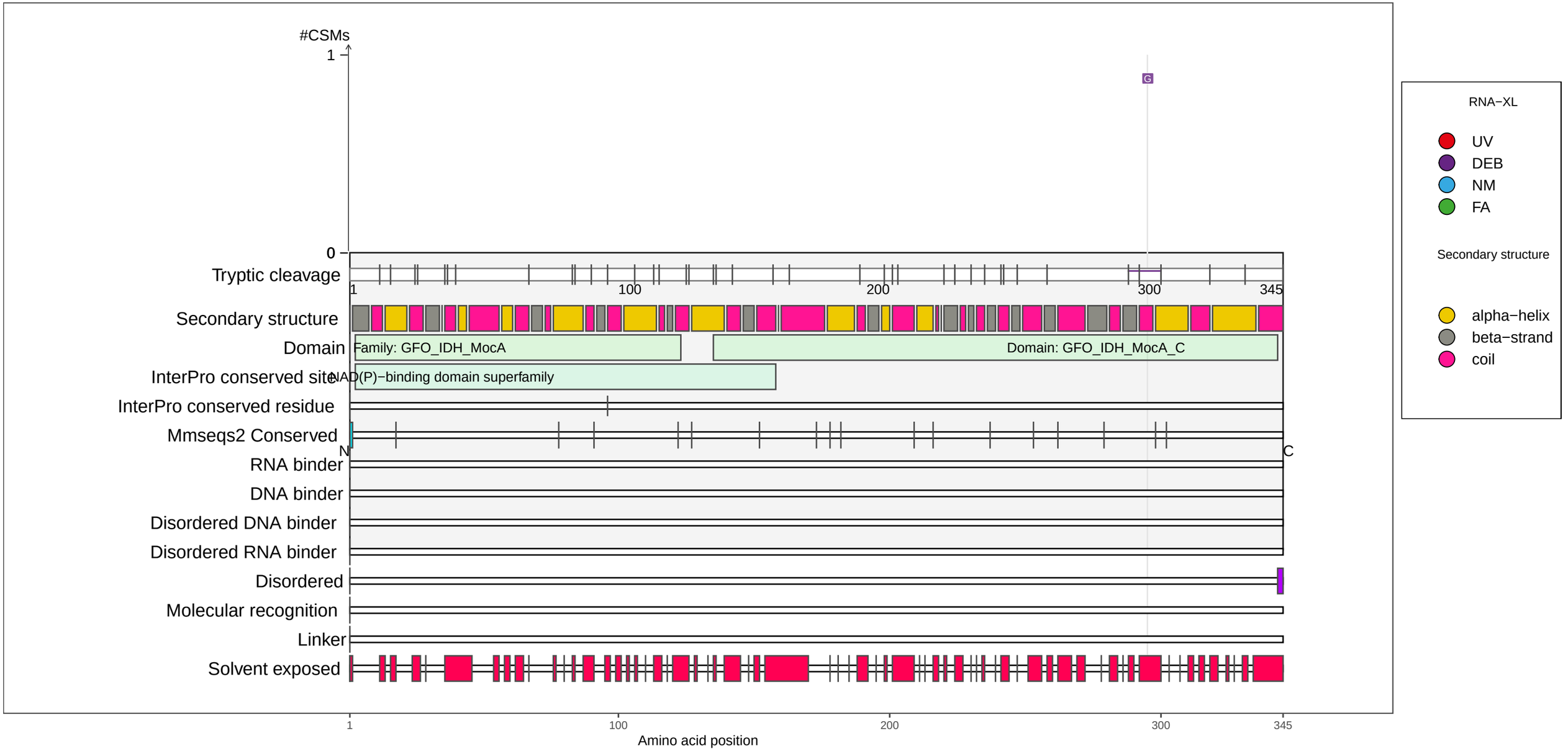
− RNA functions: not annotated



P46853
YHHX_ECOLI Uncharacterized oxidoreductase YhhX

− Abundance:
tryptic [log10 Intensity]: 8.92 (Q 86)
PAXdb K12 strain [ppm]: 1.56 (Q 42)
PAXdb E.coli [ppm]: 1.99 (Q 72)

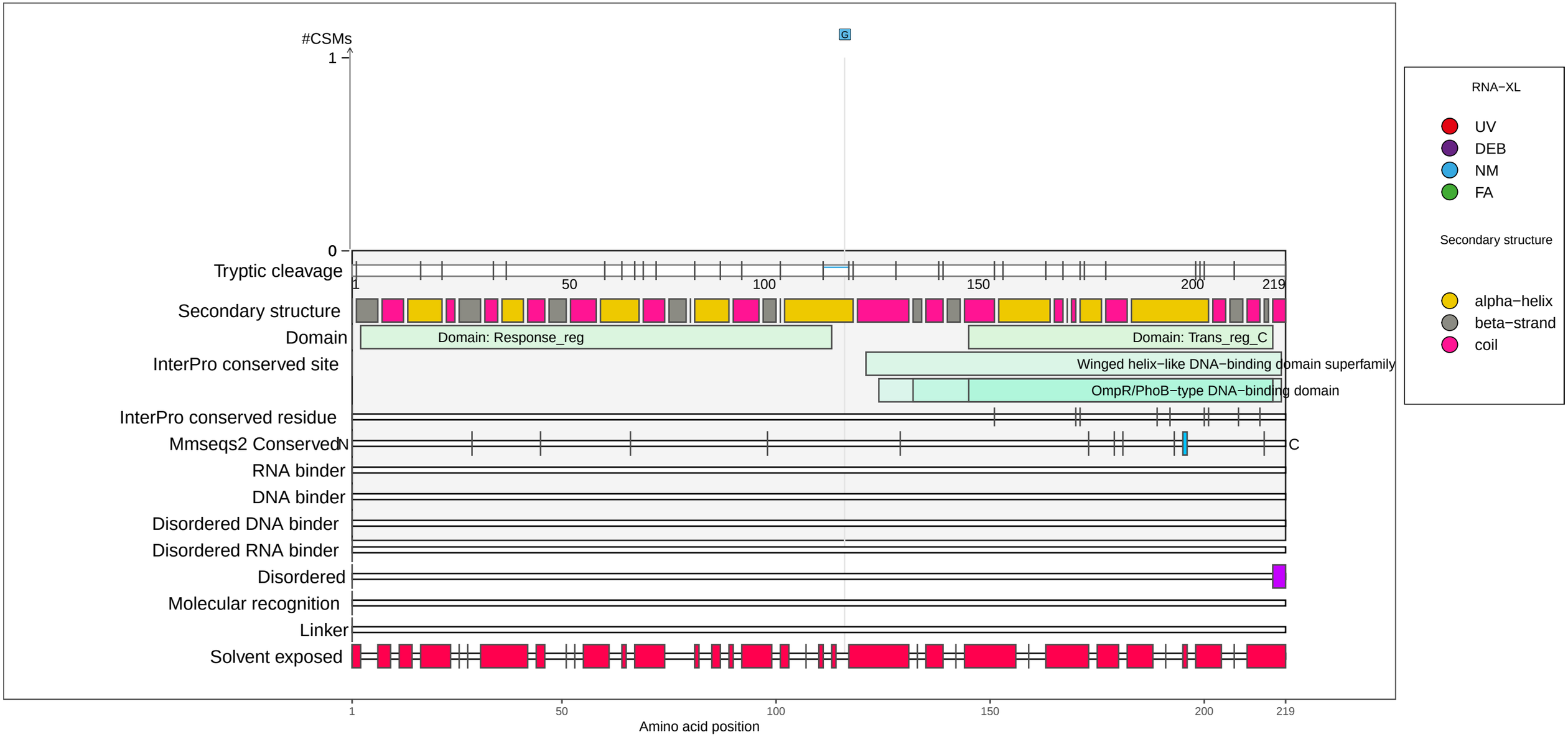
− RNA functions: not annotated



P52076
QSEB_ECOLI Transcriptional regulatory protein QseB

− Abundance:
tryptic [log10 Intensity]: 7.3 (Q 25)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.44 (Q 35)

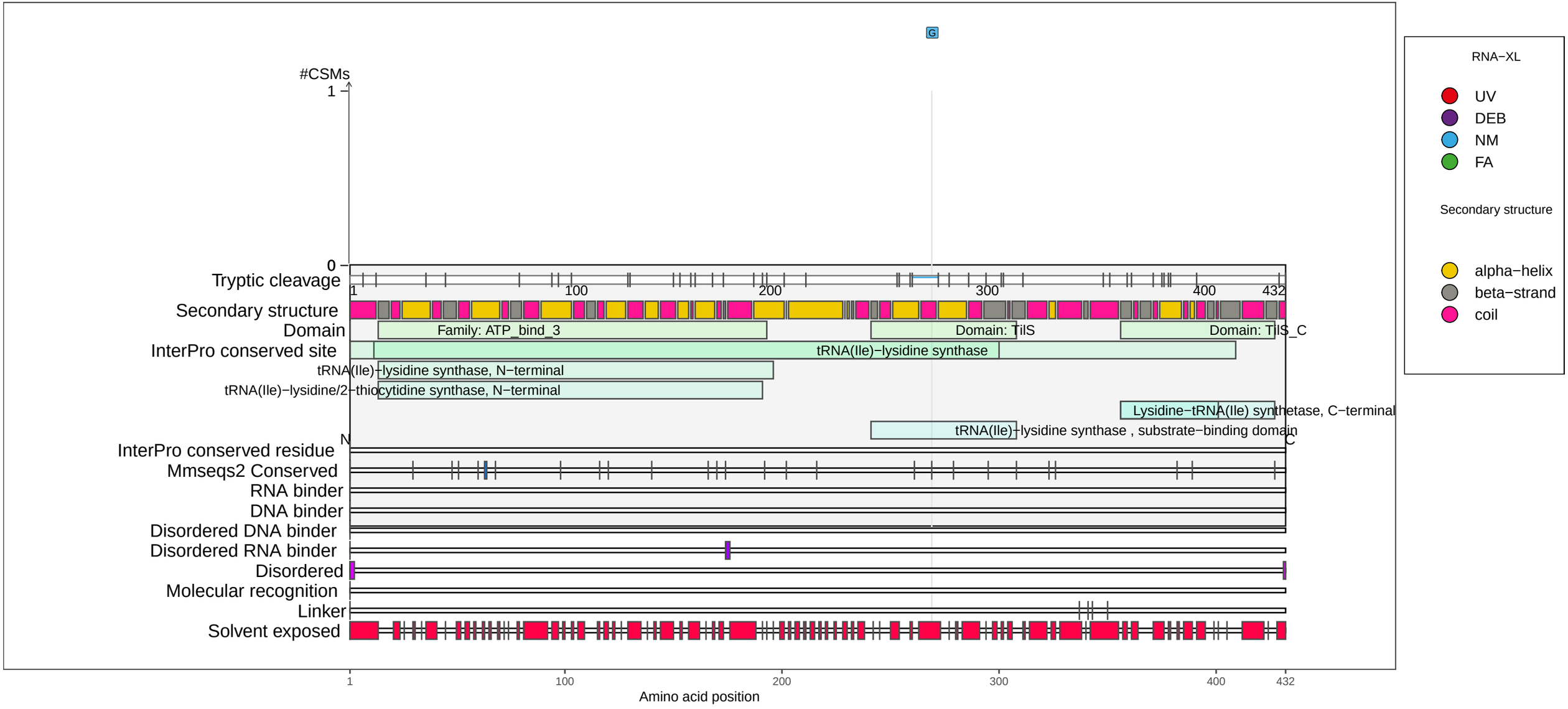
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P52097
TILS_ECOLI tRNA(Ile)−lysidine synthase

− Abundance:
tryptic [log10 Intensity]: 7.64 (Q 42)
PAXdb K12 strain [ppm]: 1.83 (Q 54)
PAXdb E.coli [ppm]: 1.1 (Q 50)

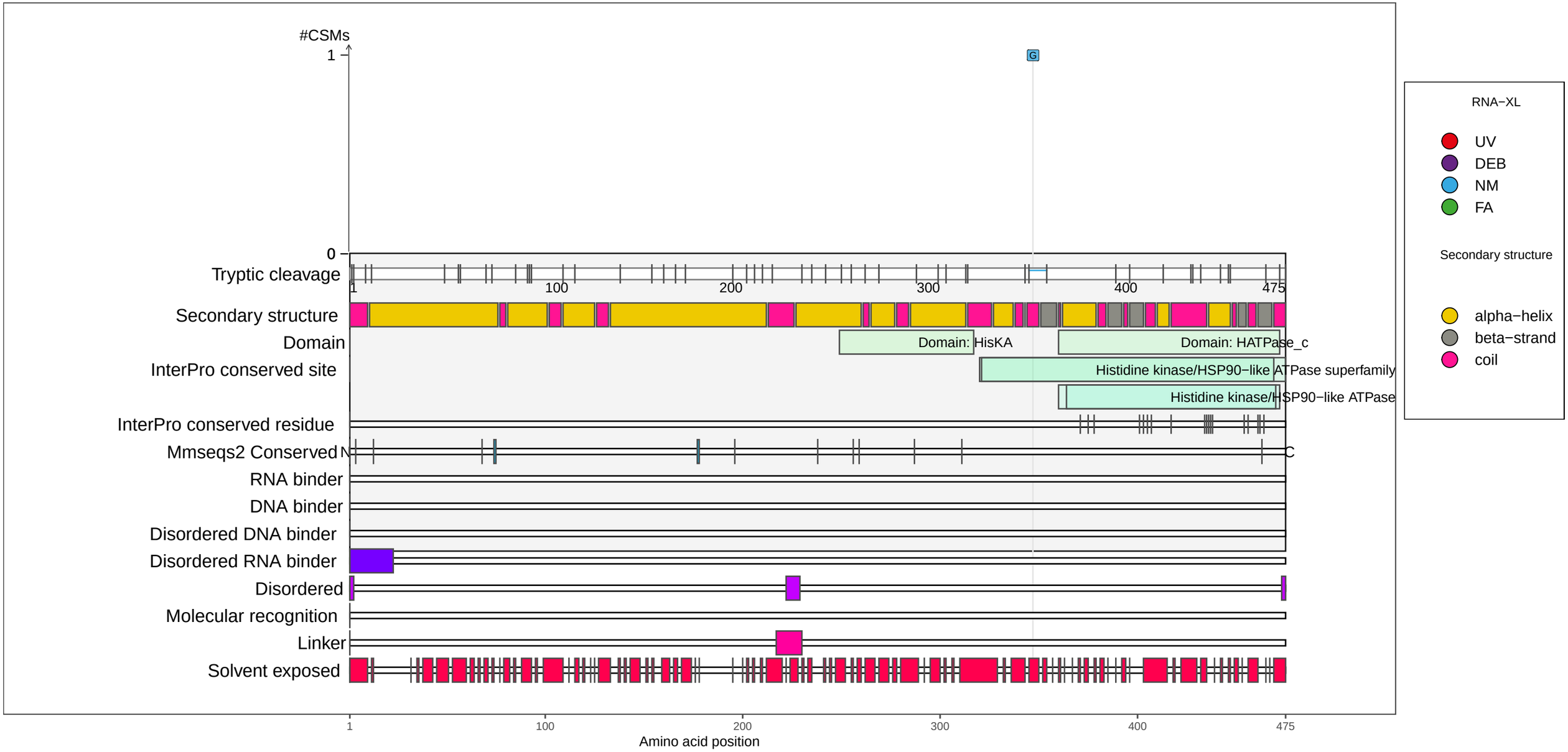
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA wobble base modification; tRNA wobble cytosine modification



P52101
GLRK_ECOLI Sensor histidine kinase GlrK

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.28 (Q 25)
PAXdb E.coli [ppm]: −0.63 (Q 14)

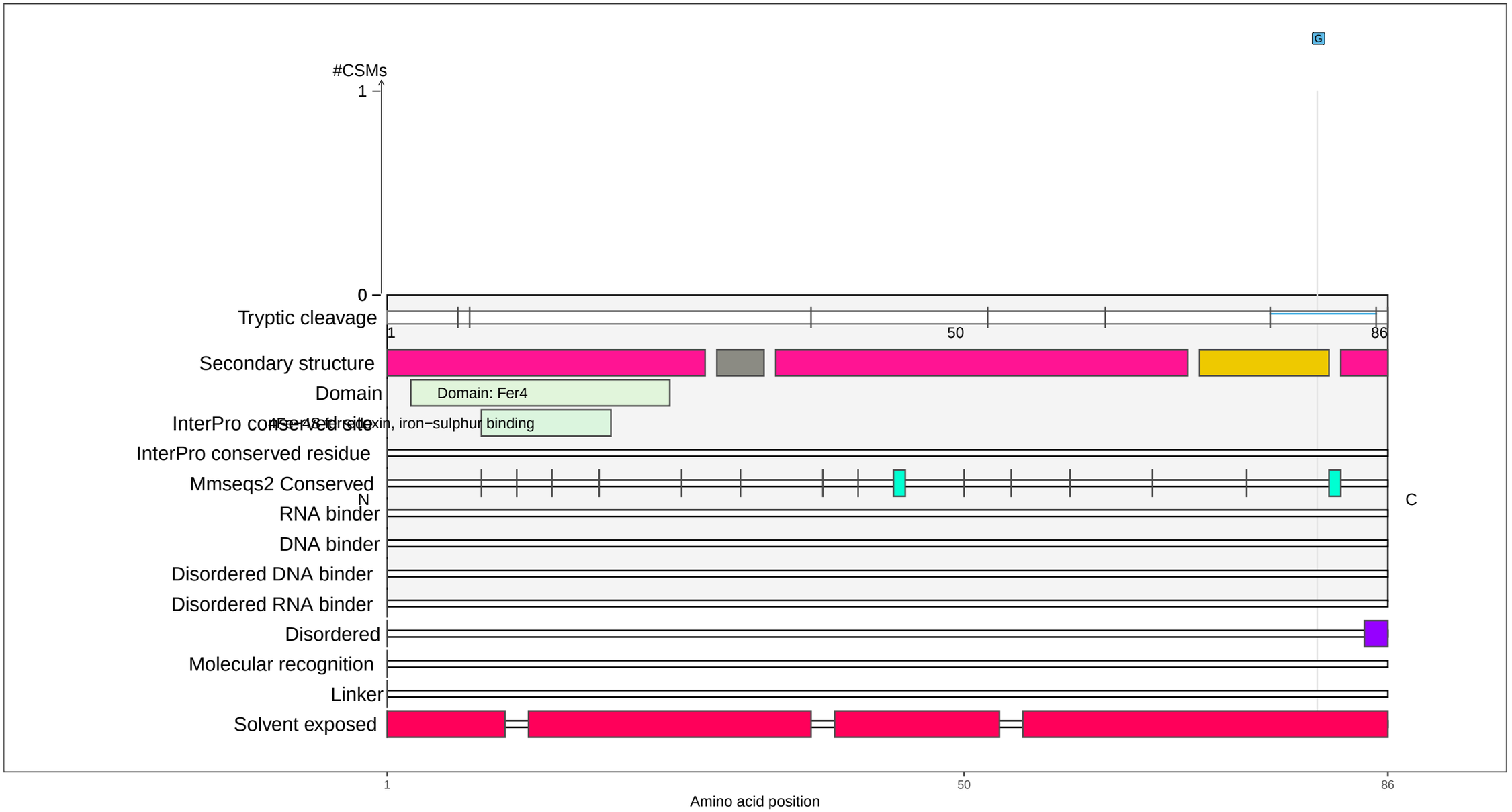
− RNA functions: not annotated



P52102
YFHL_ECOLI Ferredoxin YfhL

− Abundance:
tryptic [log10 Intensity]: 7.37 (Q 28)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.89 (Q 69)

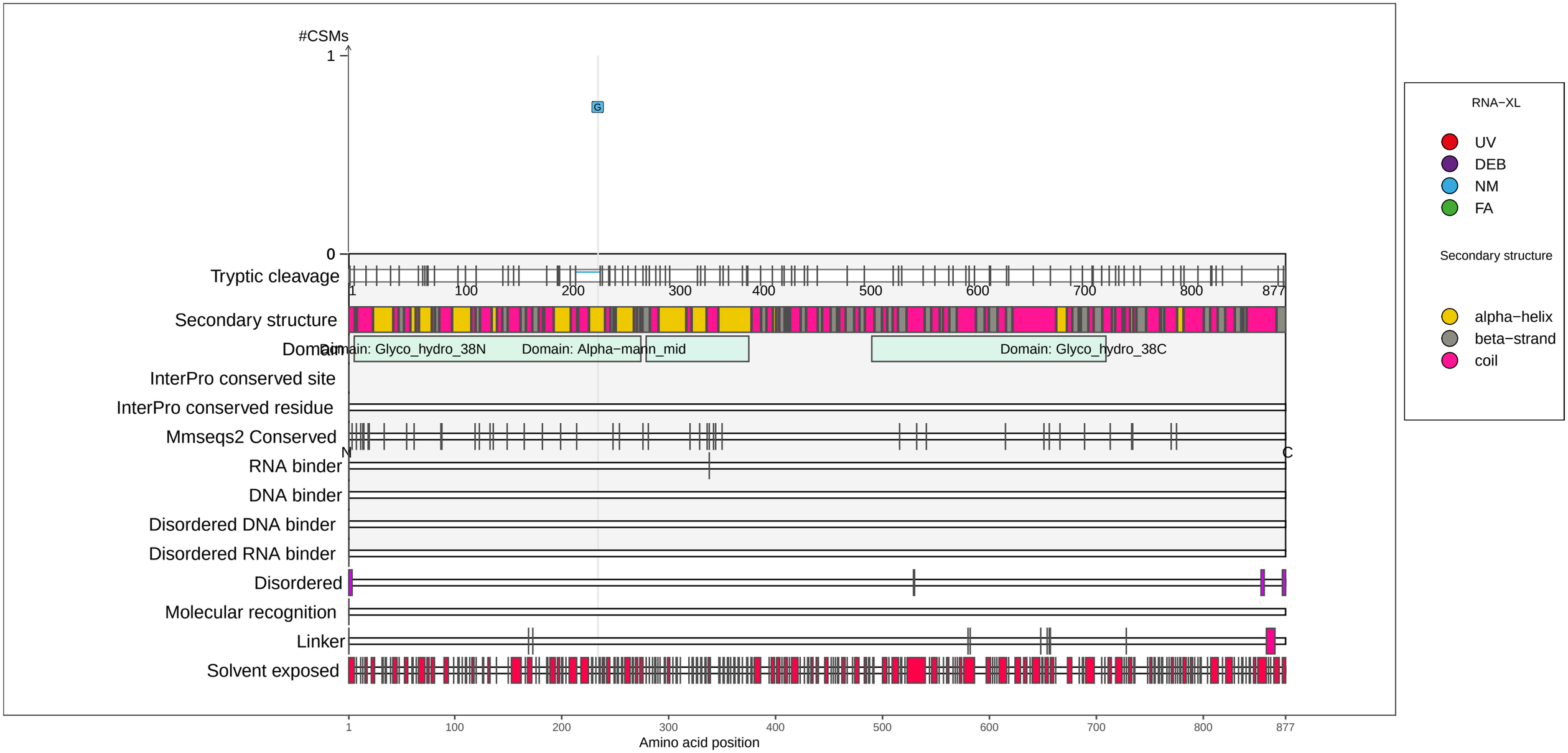
− RNA functions: not annotated



P54746
MNGB_ECOLI Mannosylglycerate hydrolase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.32 (Q 27)
PAXdb E.coli [ppm]: −0.22 (Q 20)

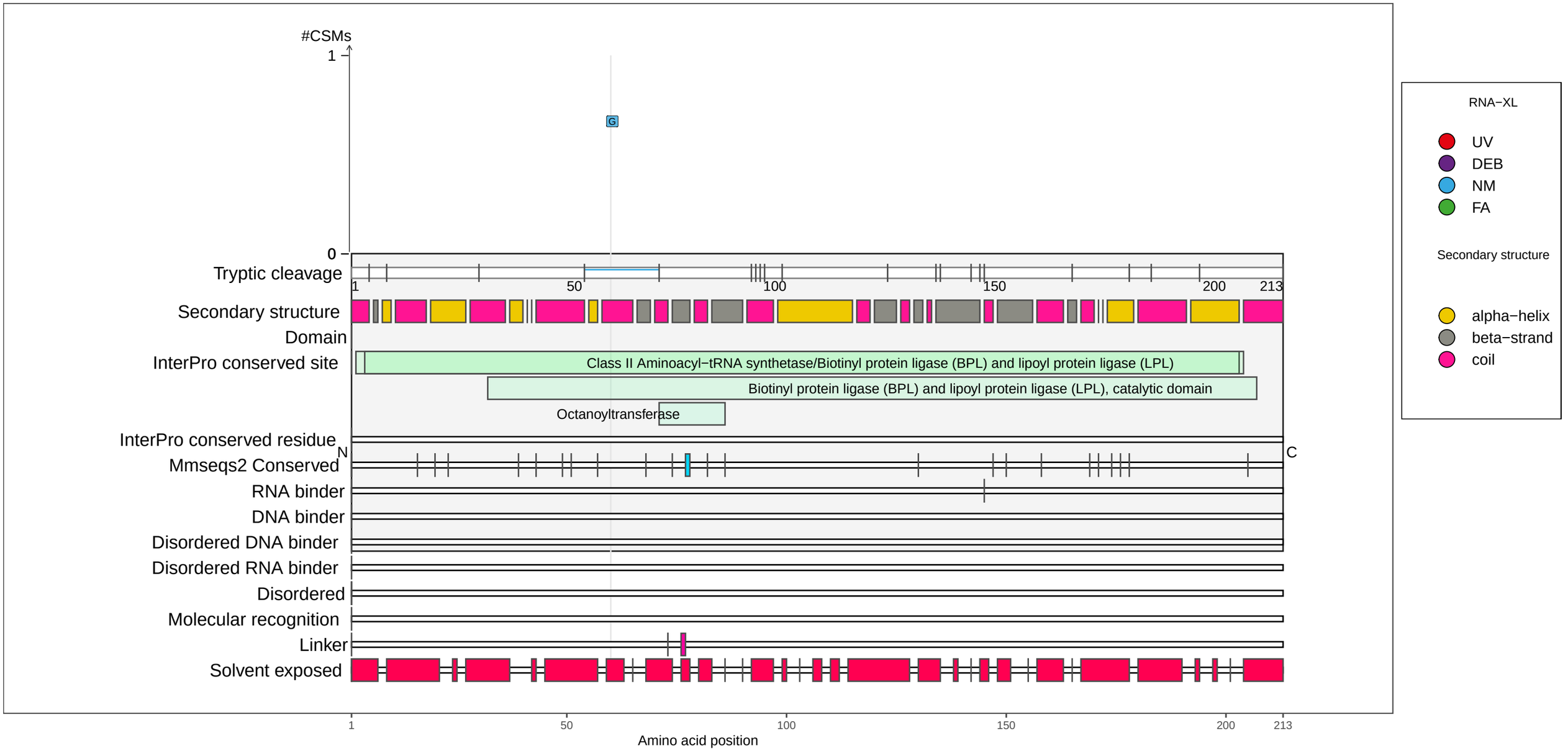
− RNA functions: not annotated



P60720
LIPB_ECOLI Octanoyltransferase

− Abundance:
tryptic [log10 Intensity]: 7.62 (Q 41)
PAXdb K12 strain [ppm]: 1.59 (Q 44)
PAXdb E.coli [ppm]: 1.19 (Q 52)

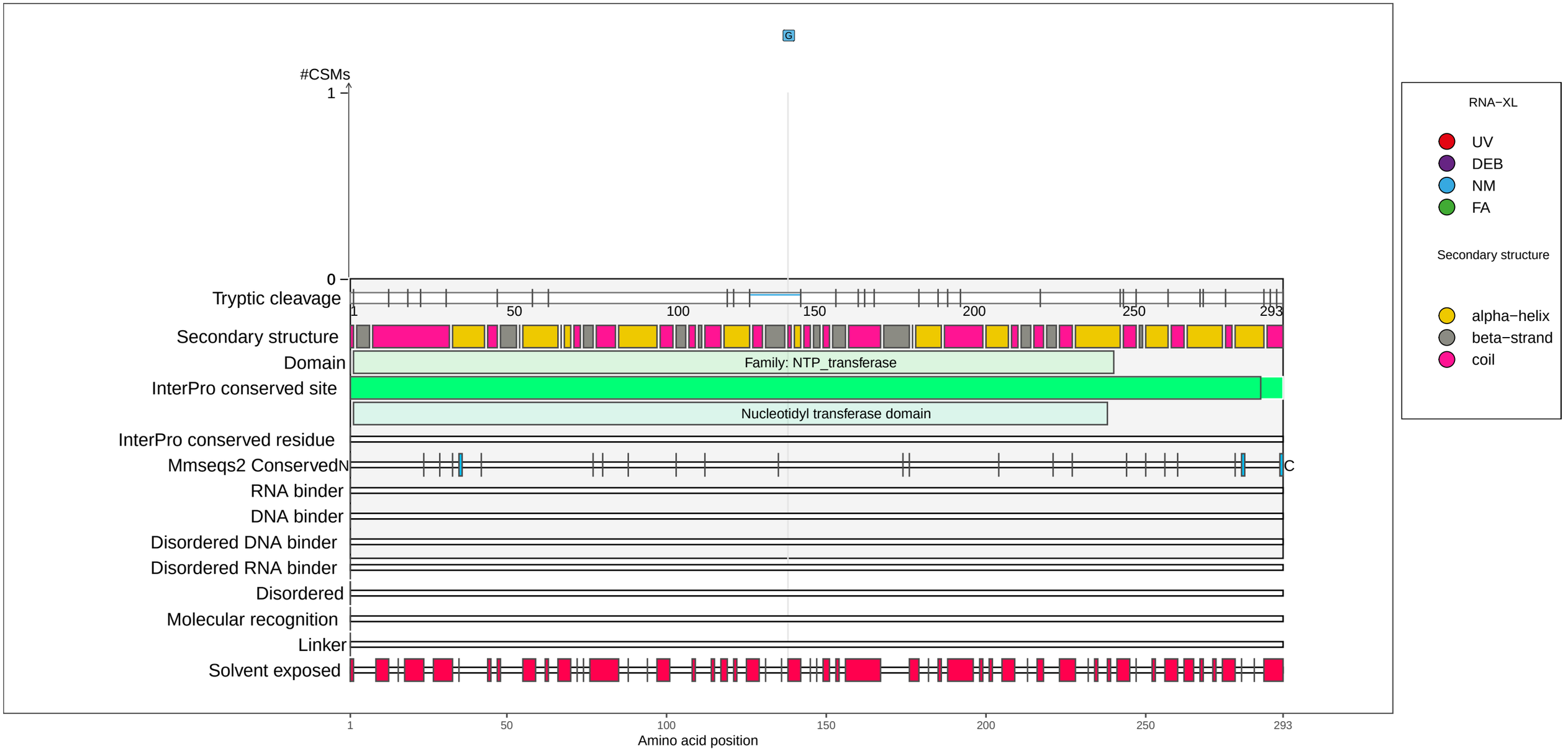
− RNA functions: not annotated



P61887
RMLA2_ECOLI Glucose−1−phosphate thymidylyltransferase 2

− Abundance:
tryptic [log10 Intensity]: 7.99 (Q 57)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.1 (Q 50)

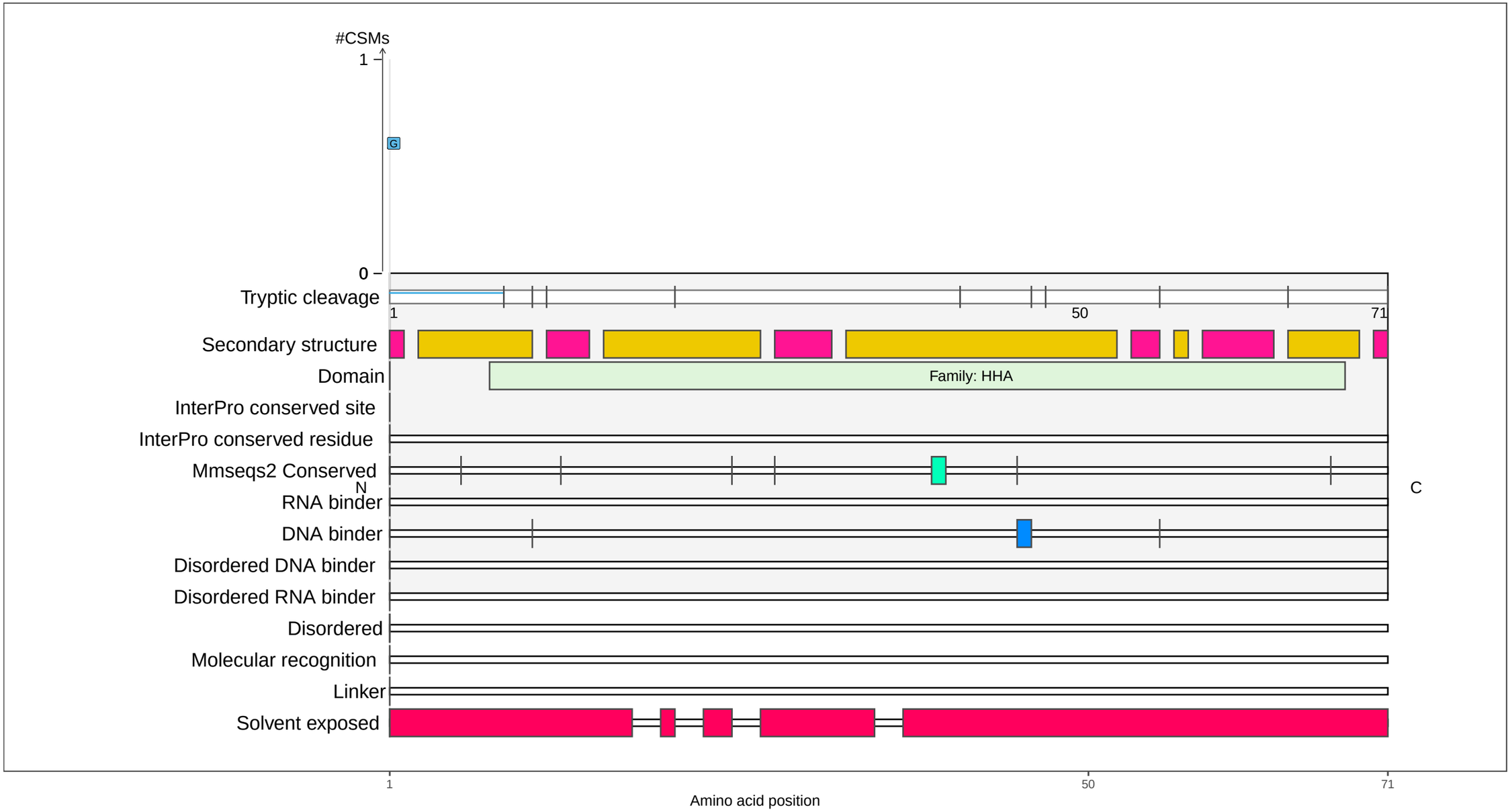
− RNA functions: not annotated



P64467
CNU_ECOLI OriC−binding nucleoid−associated protein

− Abundance:
tryptic [log10 Intensity]: 6.79 (Q 7)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.01 (Q 72)

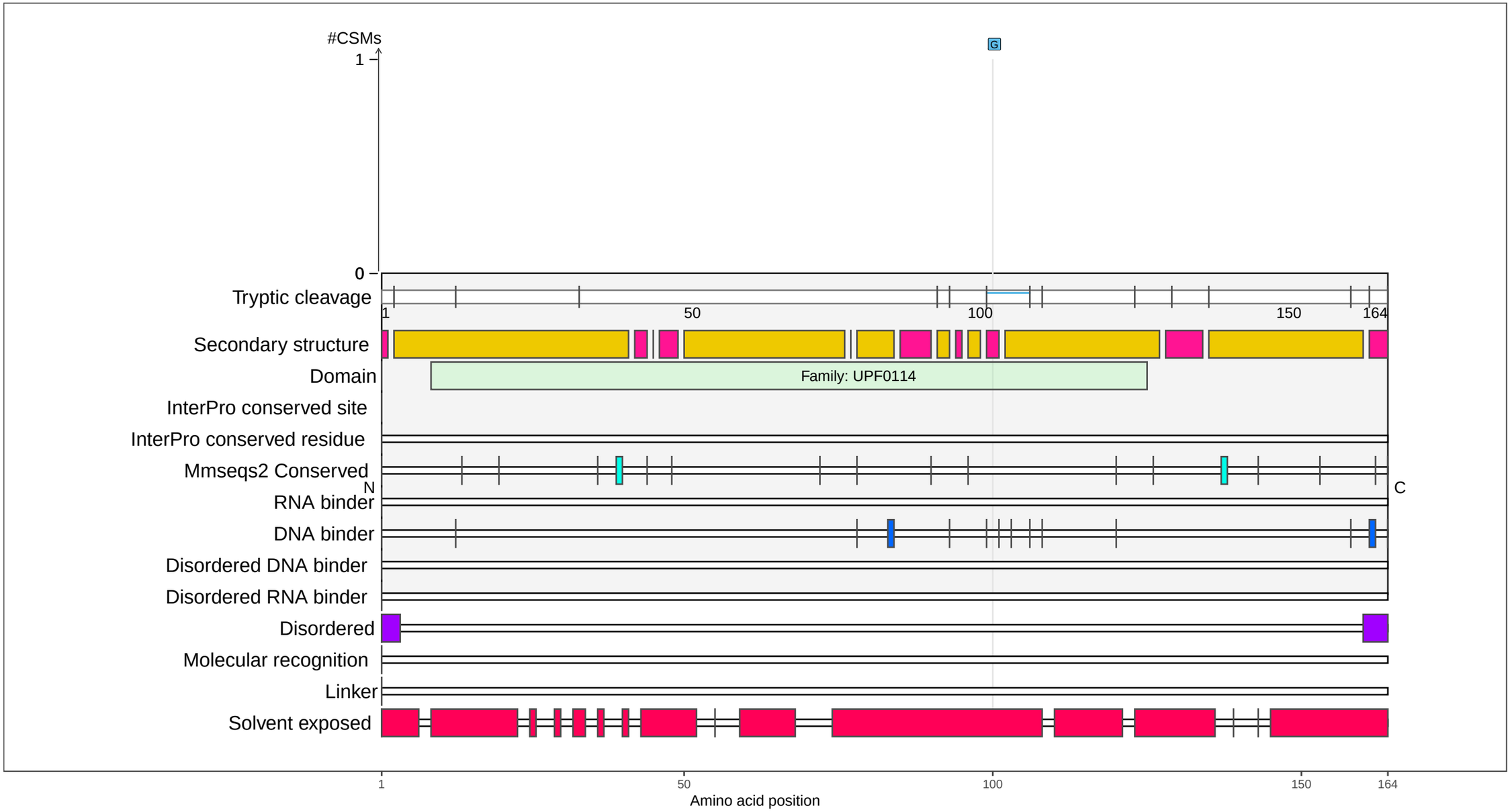
− RNA functions: not annotated

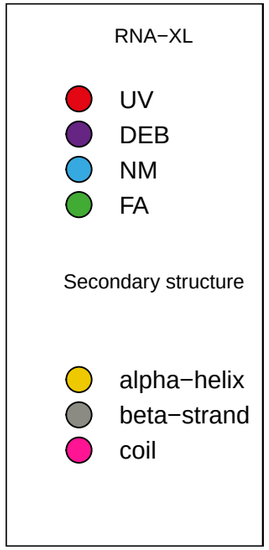


P67244
YQHA_ECOLI UPF0114 protein YqhA

− Abundance:
tryptic [log10 Intensity]: 8.07 (Q 60)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.26 (Q 54)

− RNA functions: not annotated

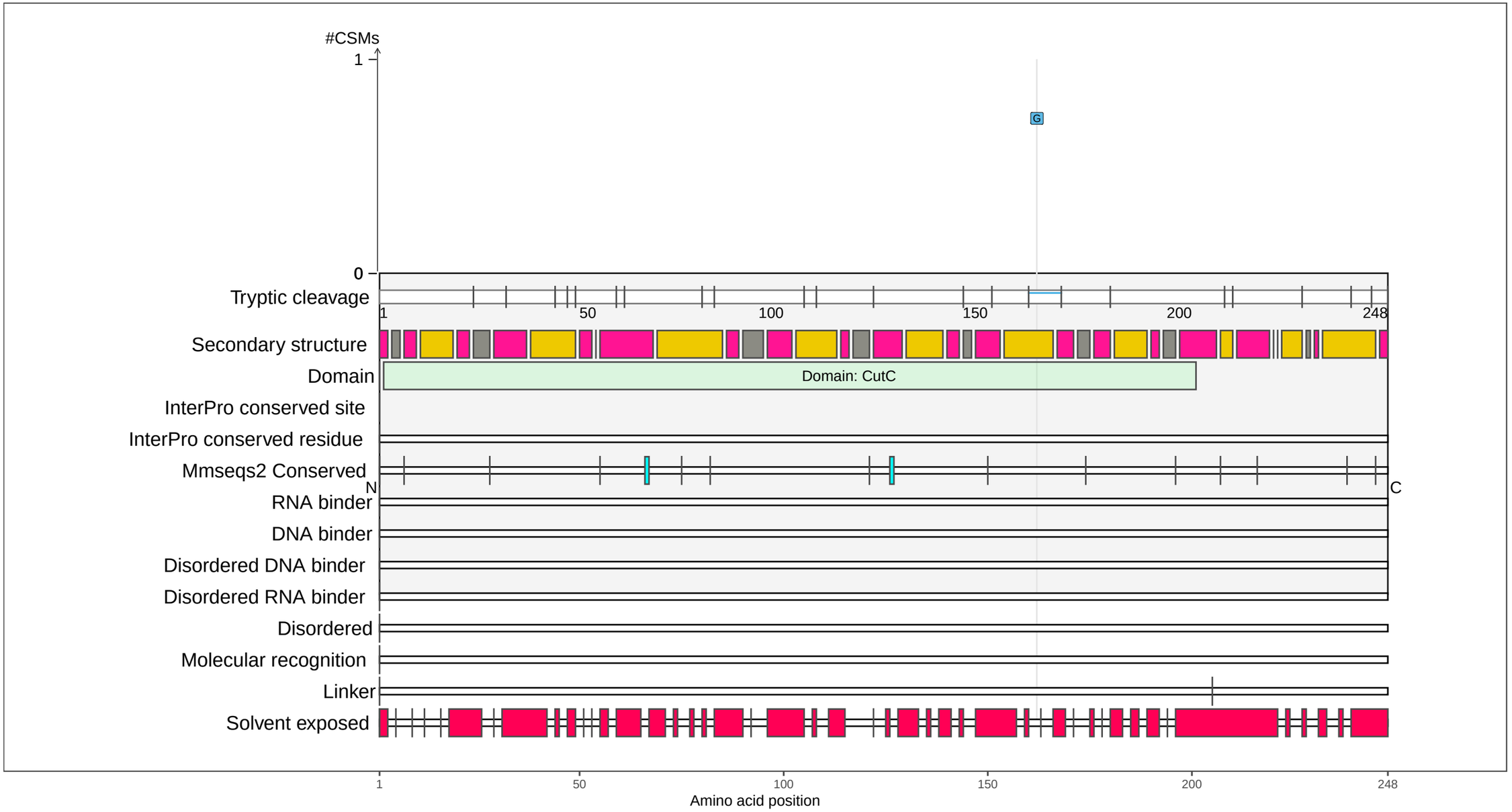


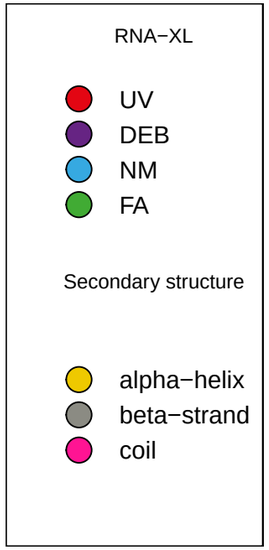


P67826
CUTC_ECOLI PF03932 family protein CutC

− Abundance:
tryptic [log10 Intensity]: 7.17 (Q 20)
PAXdb K12 strain [ppm]: 1.04 (Q 13)
PAXdb E.coli [ppm]: 1.68 (Q 64)

− RNA functions: not annotated

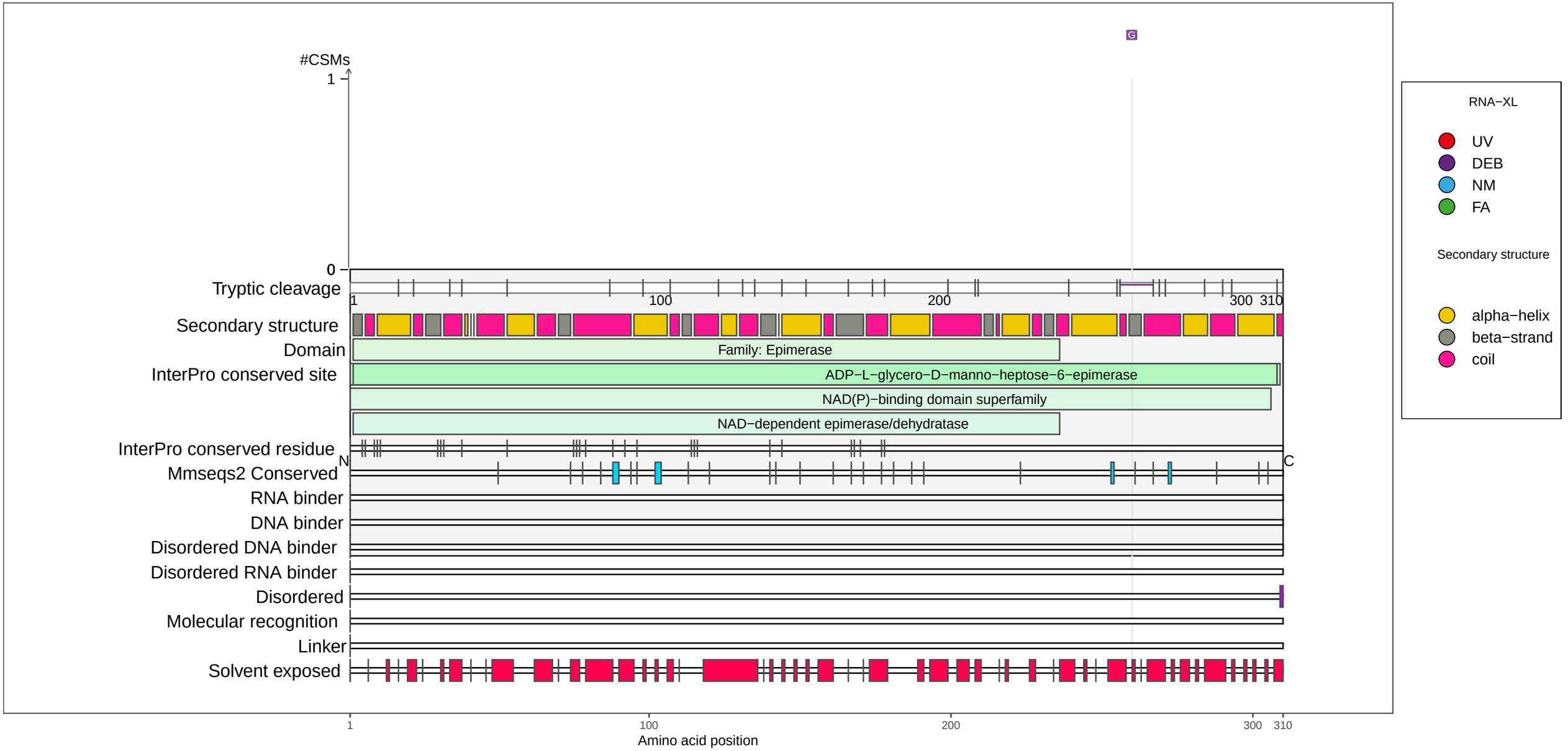




P67910
HLDD_ECOLI ADP−L−glycero−D−manno−heptose−6−epimerase

− Abundance:
tryptic [log10 Intensity]: 8.47 (Q 74)
PAXdb K12 strain [ppm]: 3.18 (Q 94)
PAXdb E.coli [ppm]: 2.98 (Q 94)

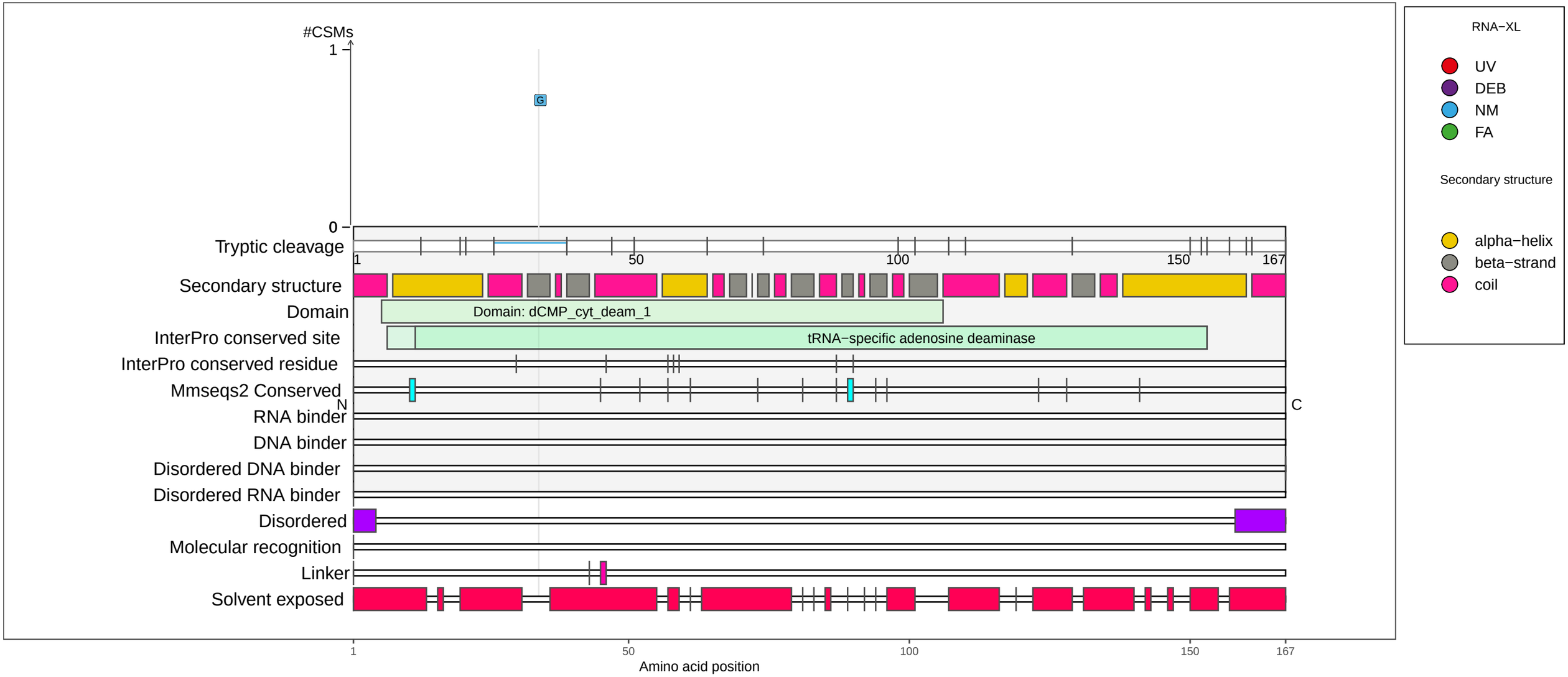
− RNA functions: not annotated



P68398
TADA_ECOLI tRNA−specific adenosine deaminase

− Abundance:
tryptic [log10 Intensity]: 7.38 (Q 29)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.33 (Q 55)

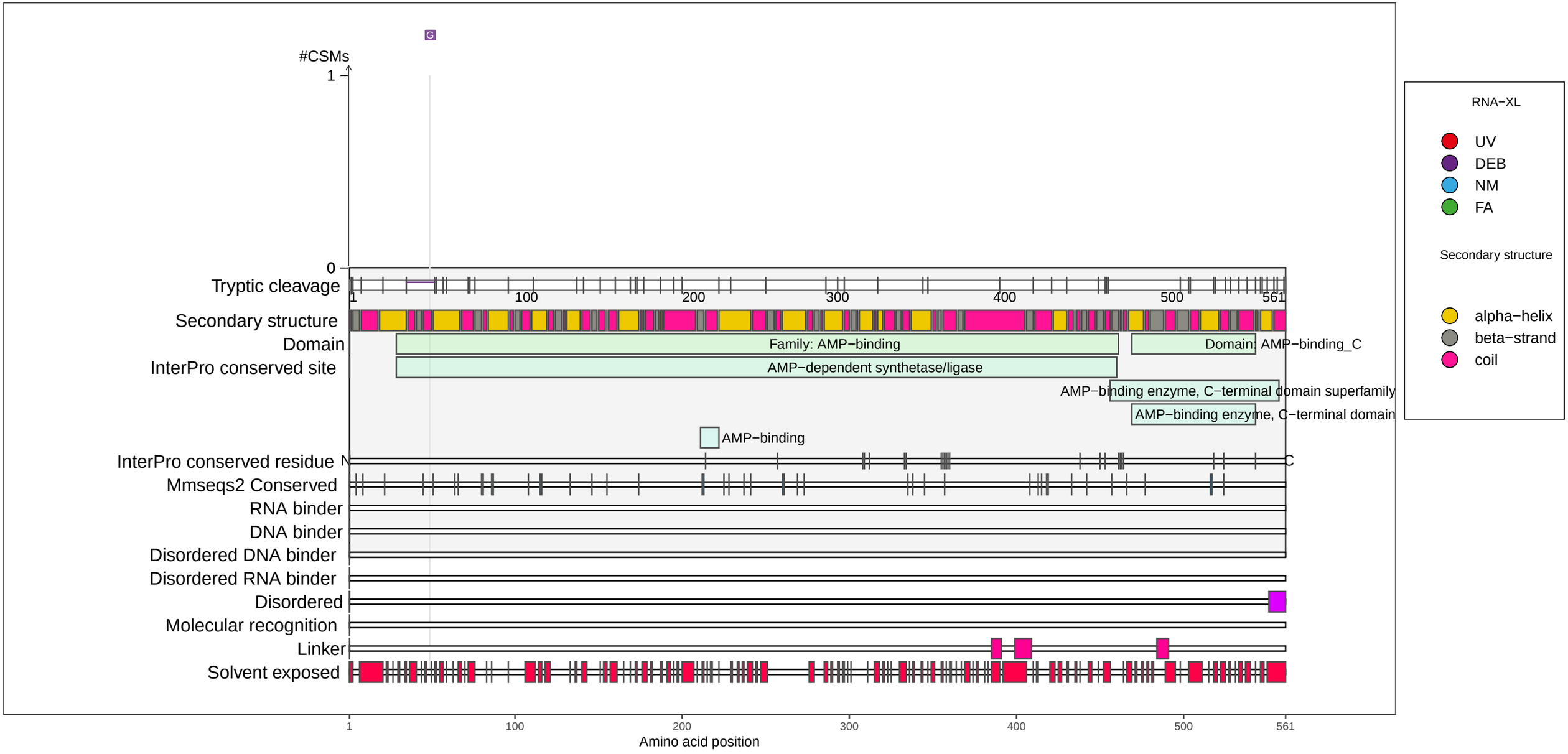
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA metabolic process; RNA modification
RNA processing; tRNA metabolic process; tRNA modification; tRNA processing
tRNA wobble adenosine to inosine editing; tRNA wobble base modification
tRNA−specific adenosine deaminase activity; tRNA−specific adenosine−34 deaminase activity
tRNA−specific adenosine−34 deaminase complex



P69451
LCFA_ECOLI Long−chain−fatty−acid−−CoA ligase

− Abundance:
tryptic [log10 Intensity]: 8 (Q 57)
PAXdb K12 strain [ppm]: 1.87 (Q 56)
PAXdb E.coli [ppm]: 1.59 (Q 62)

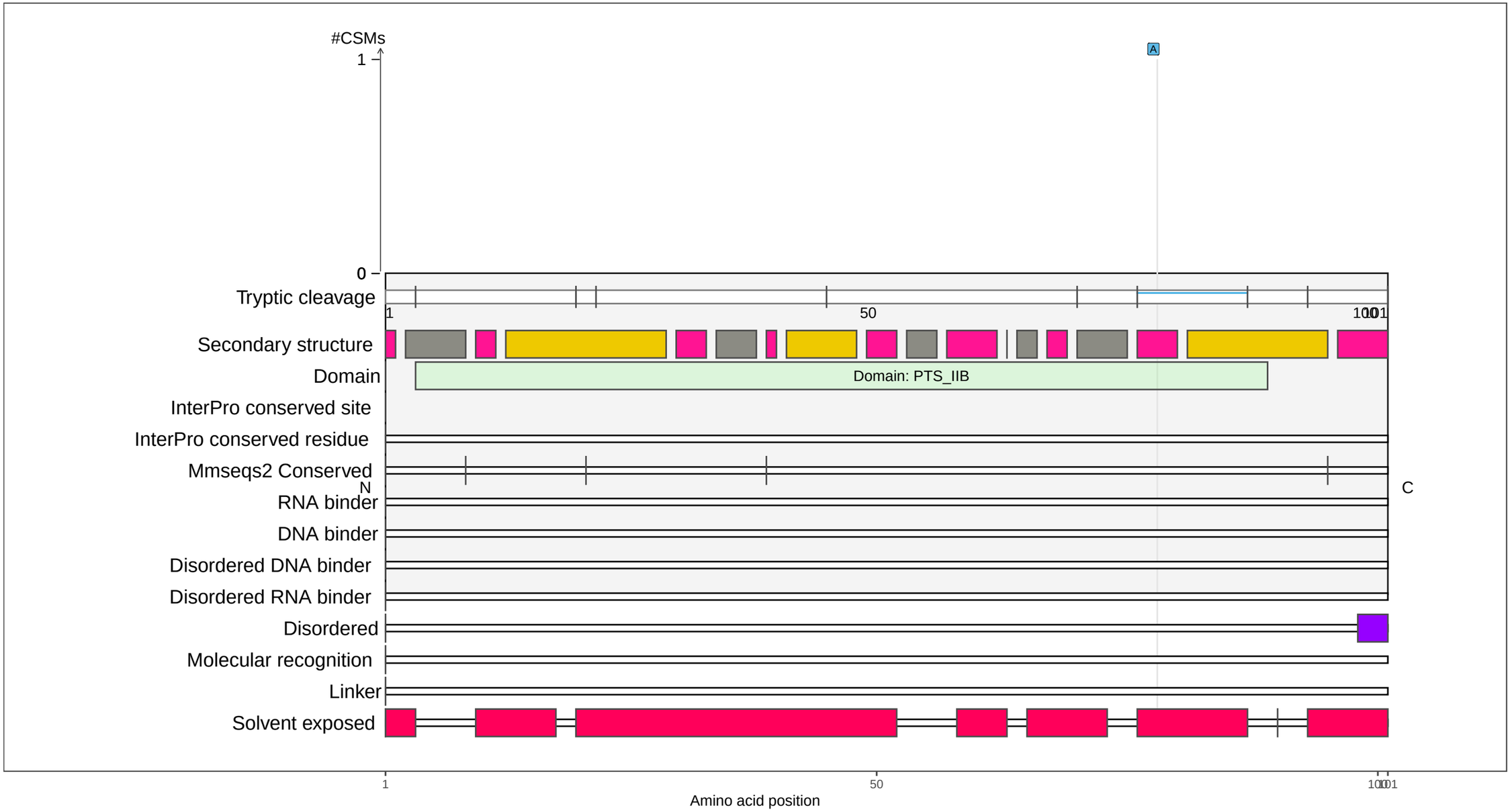
− RNA functions: not annotated



P69822
ULAB_ECOLI Ascorbate−specific PTS system EIIB component

− Abundance:
tryptic [log10 Intensity]: 7.92 (Q 54)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.43 (Q 58)

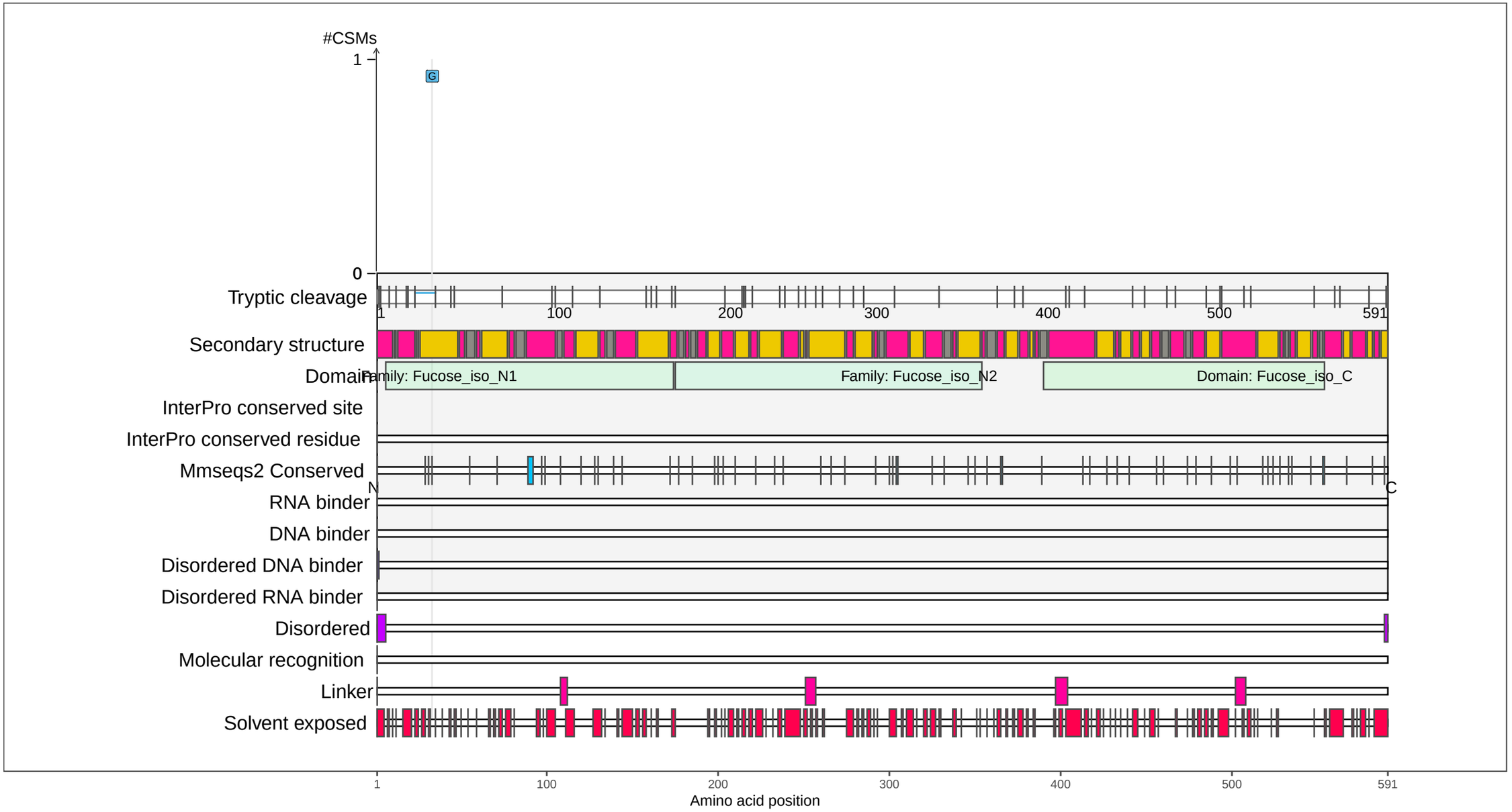
− RNA functions: not annotated



P69922
FUCI_ECOLI L−fucose isomerase

− Abundance:
tryptic [log10 Intensity]: 8.11 (Q 62)
PAXdb K12 strain [ppm]: 1.64 (Q 47)
PAXdb E.coli [ppm]: 0.49 (Q 36)

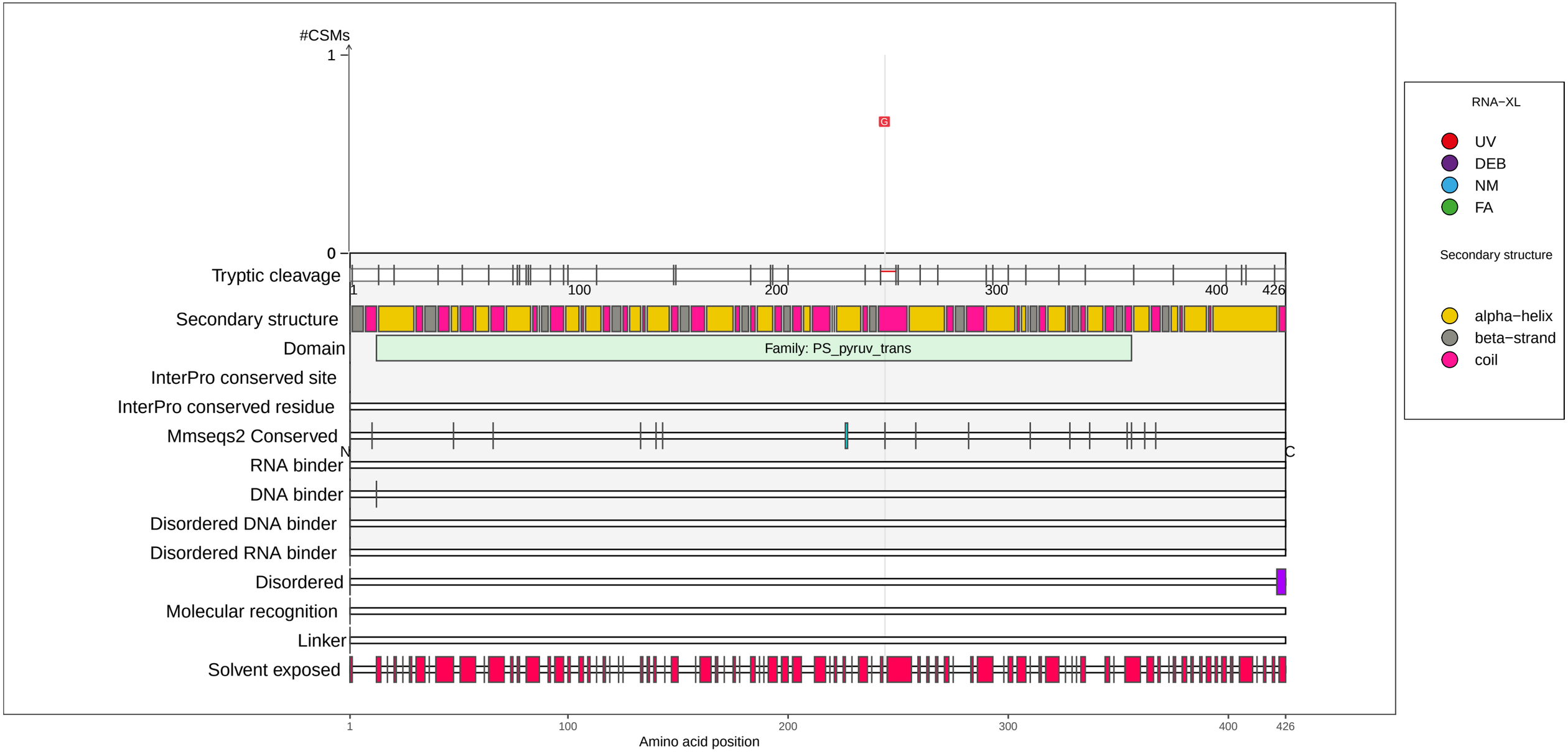
− RNA functions: not annotated



P71242
WCAK_ECOLI Colanic acid biosynthesis protein WcaK

− Abundance:
tryptic [log10 Intensity]: 7.33 (Q 26)
PAXdb K12 strain [ppm]: 0.93 (Q 9)
PAXdb E.coli [ppm]: −0.46 (Q 16)

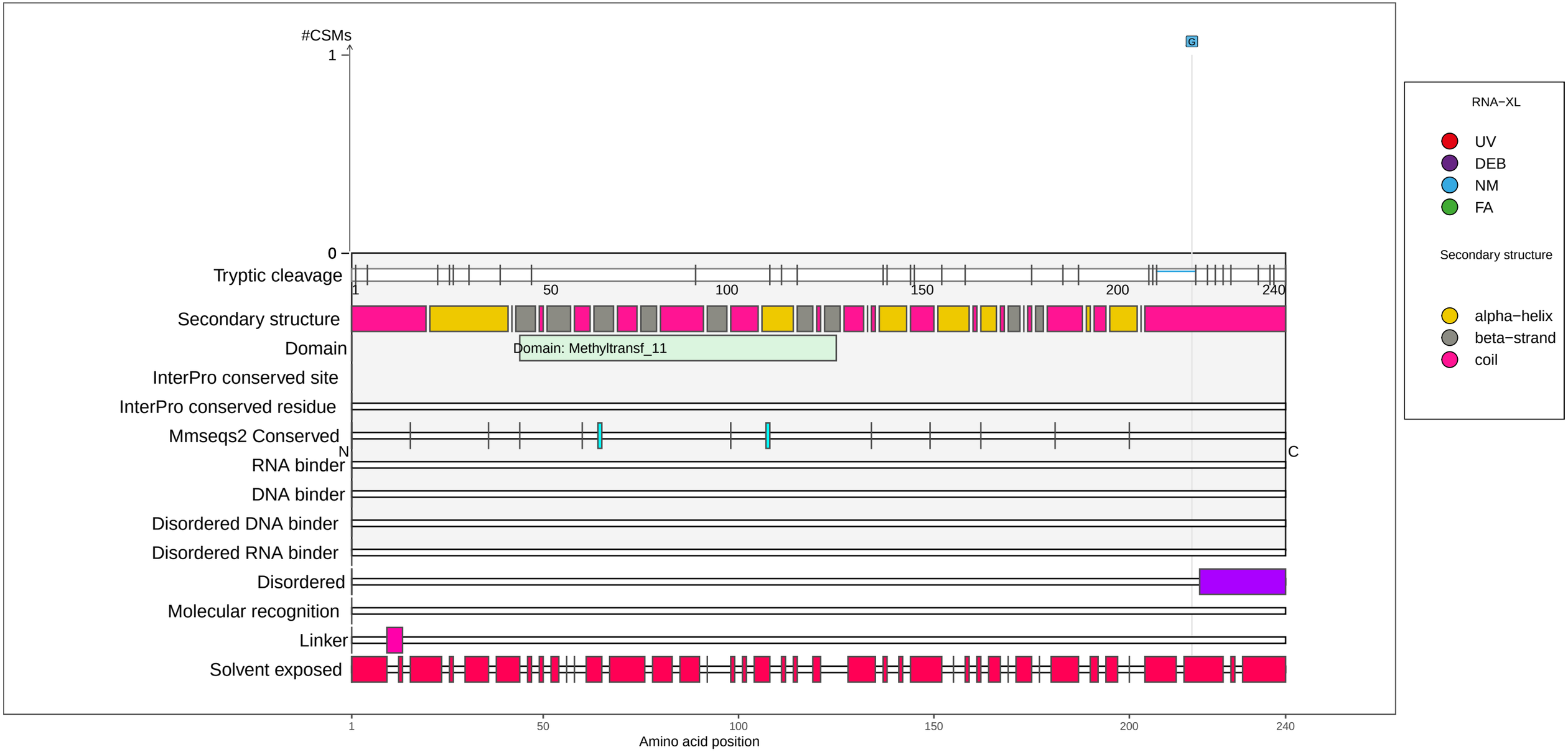
− RNA functions: not annotated



P75672
YAFS_ECOLI Uncharacterized protein YafS

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.95 (Q 9)

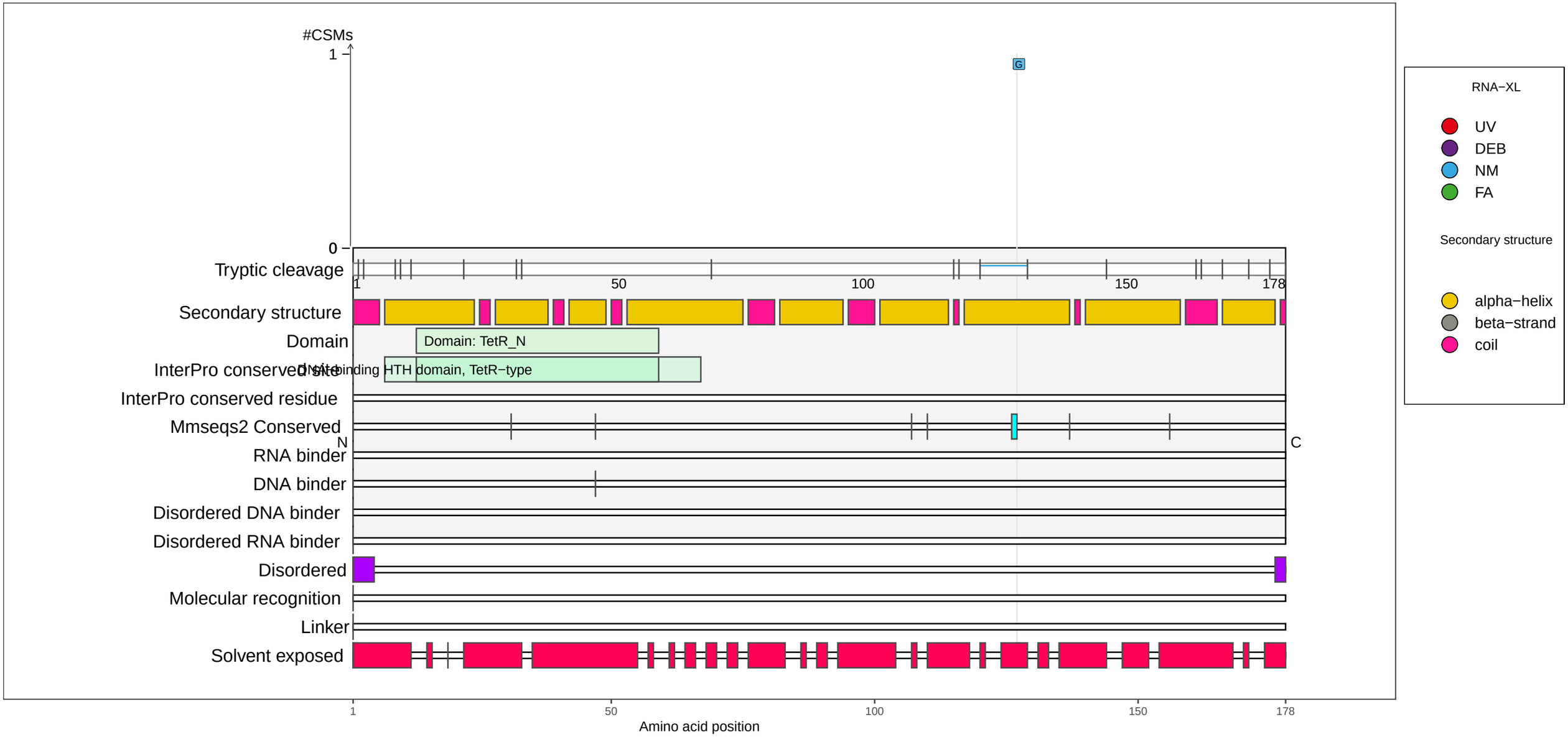
− RNA functions: not annotated



P75811
RCDA_ECOLI HTH−type transcriptional regulator RcdA

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 0.18 (Q 29)

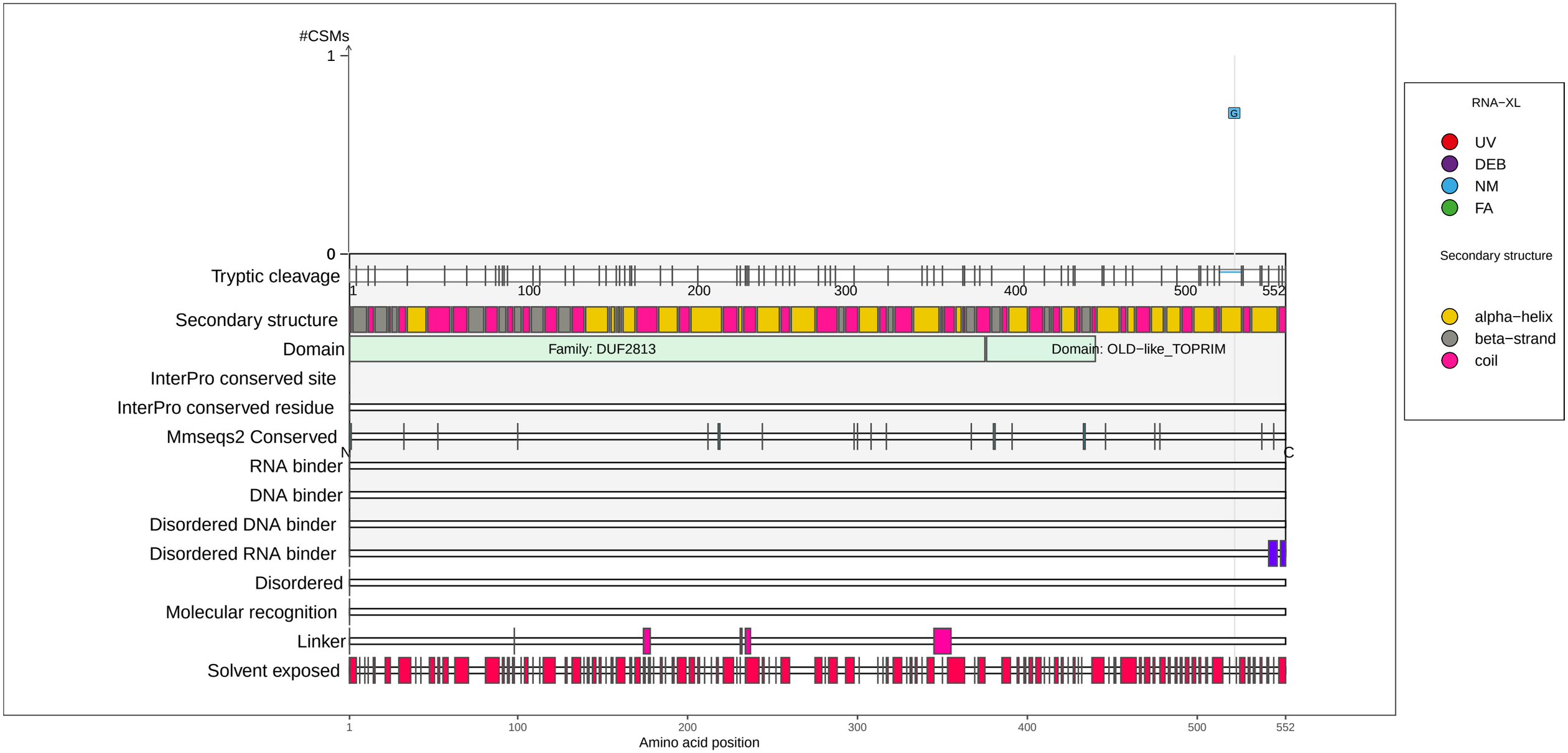
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P75828
YBJD_ECOLI Uncharacterized protein YbjD

− Abundance:
tryptic [log10 Intensity]: 6.64 (Q 4)
PAXdb K12 strain [ppm]: 0.98 (Q 10)
PAXdb E.coli [ppm]: 0.76 (Q 42)

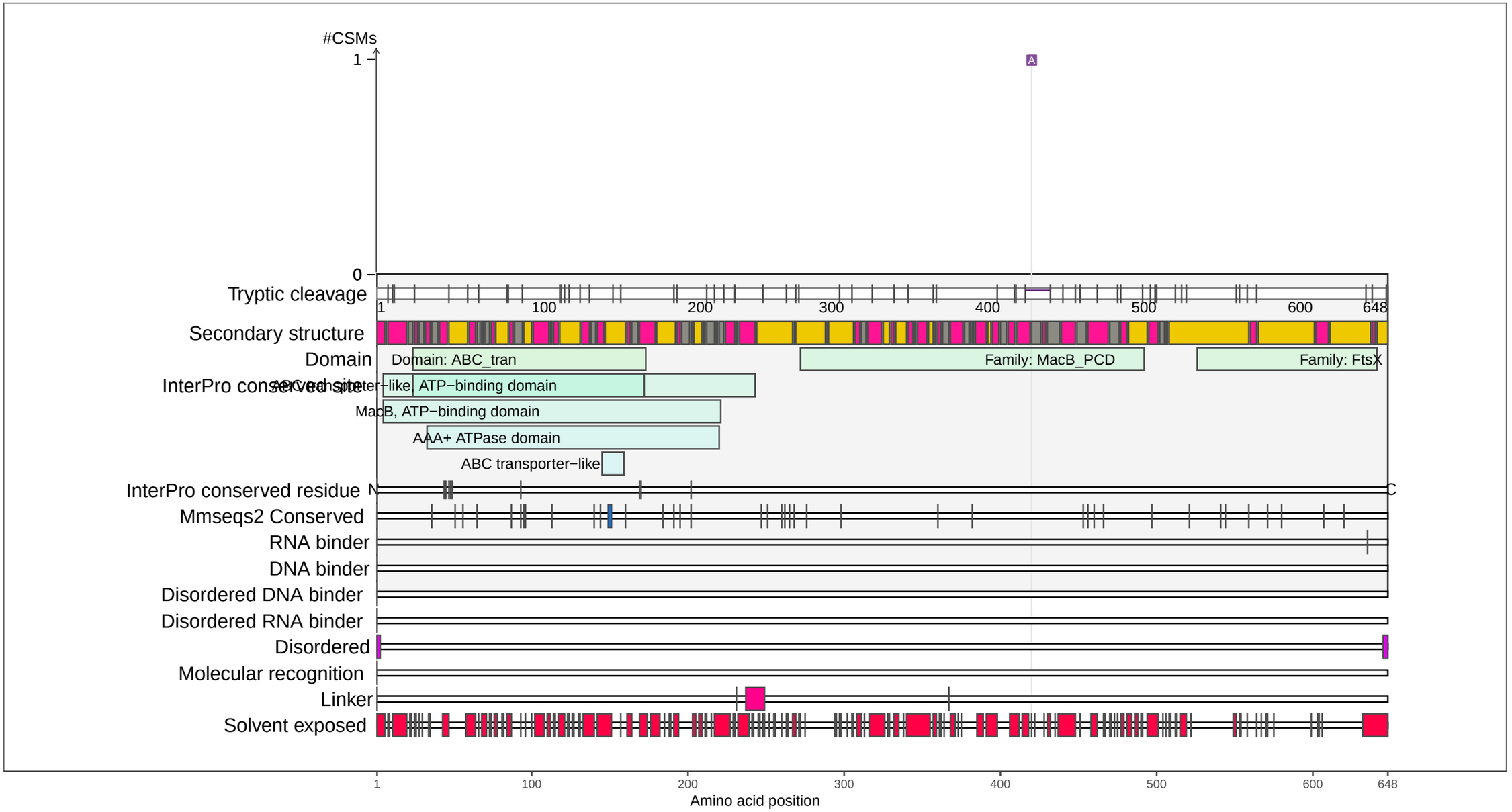
− RNA functions: not annotated



P75831
MACB_ECOLI Macrolide export ATP−binding/permease protein MacB

− Abundance:
tryptic [log10 Intensity]: 6.92 (Q 10)
PAXdb K12 strain [ppm]: 1.19 (Q 20)
PAXdb E.coli [ppm]: 0.35 (Q 32)

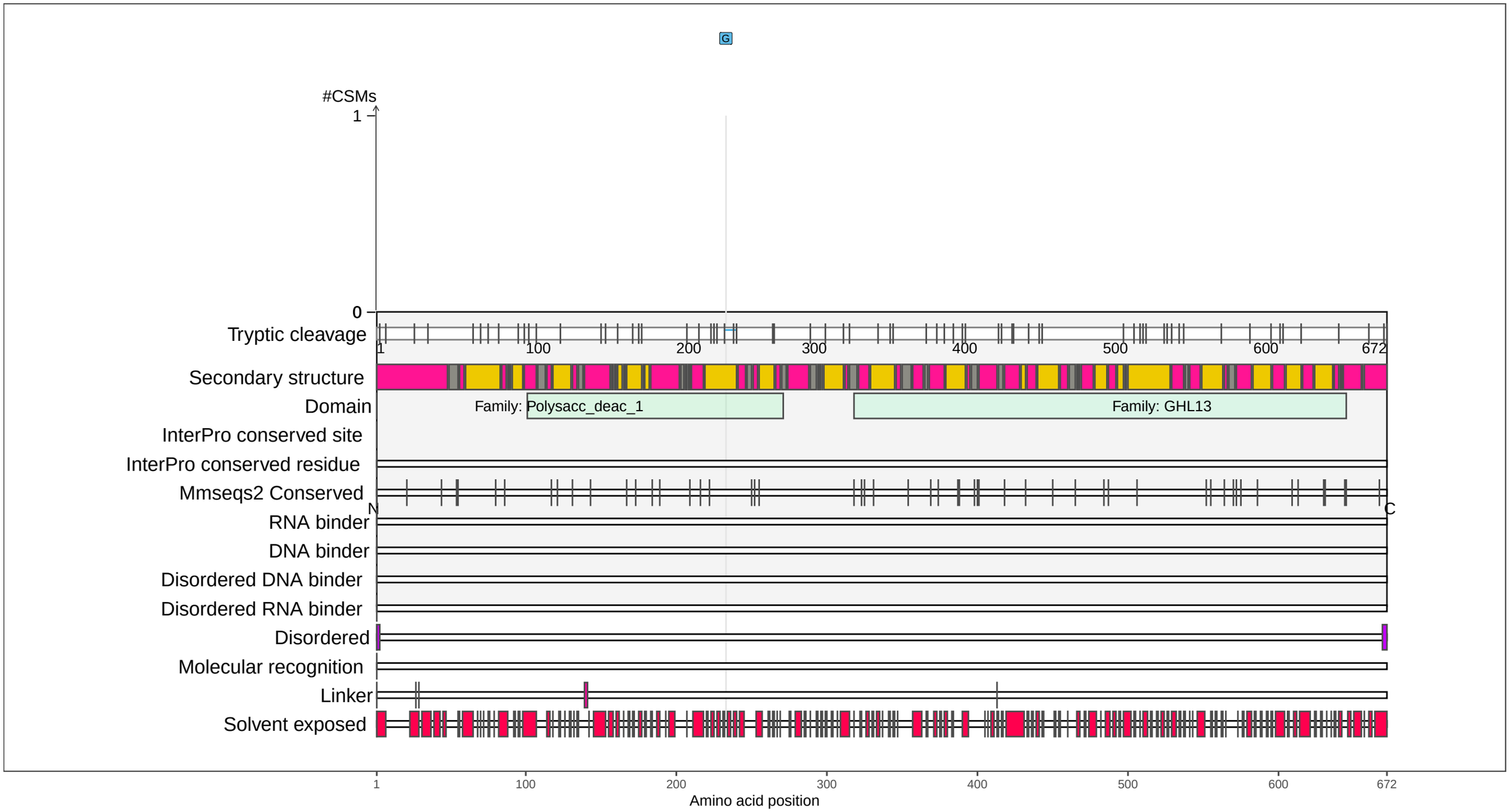
− RNA functions: not annotated



P75906
PGAB_ECOLI Poly−beta−1,6−N−acetyl−D−glucosamine N−deacetylase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −1.17 (Q 7)

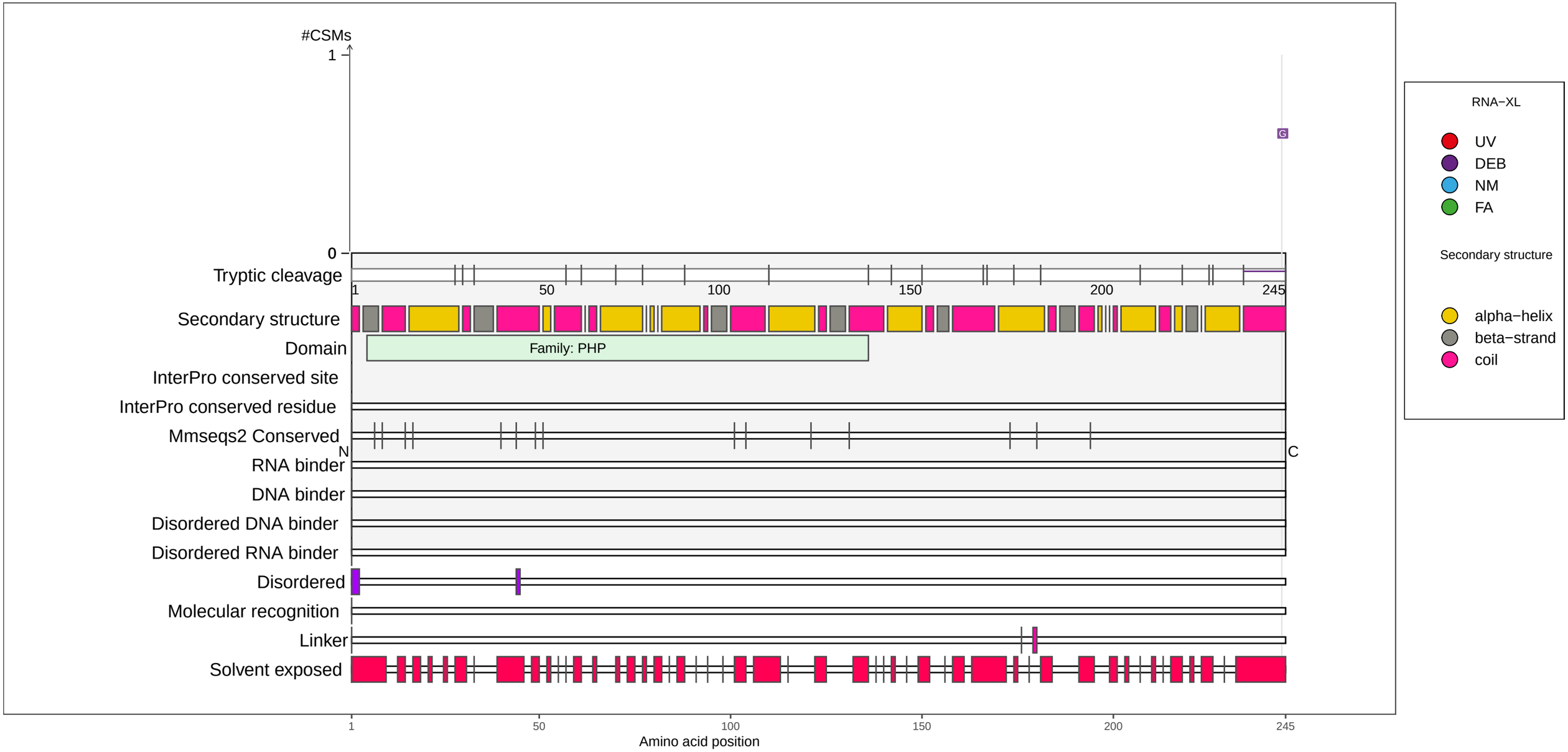
− RNA functions: not annotated



P75914
YCDX_ECOLI Probable phosphatase YcdX

− Abundance:
tryptic [log10 Intensity]: 8.26 (Q 68)
PAXdb K12 strain [ppm]: 2.14 (Q 65)
PAXdb E.coli [ppm]: 1.6 (Q 62)

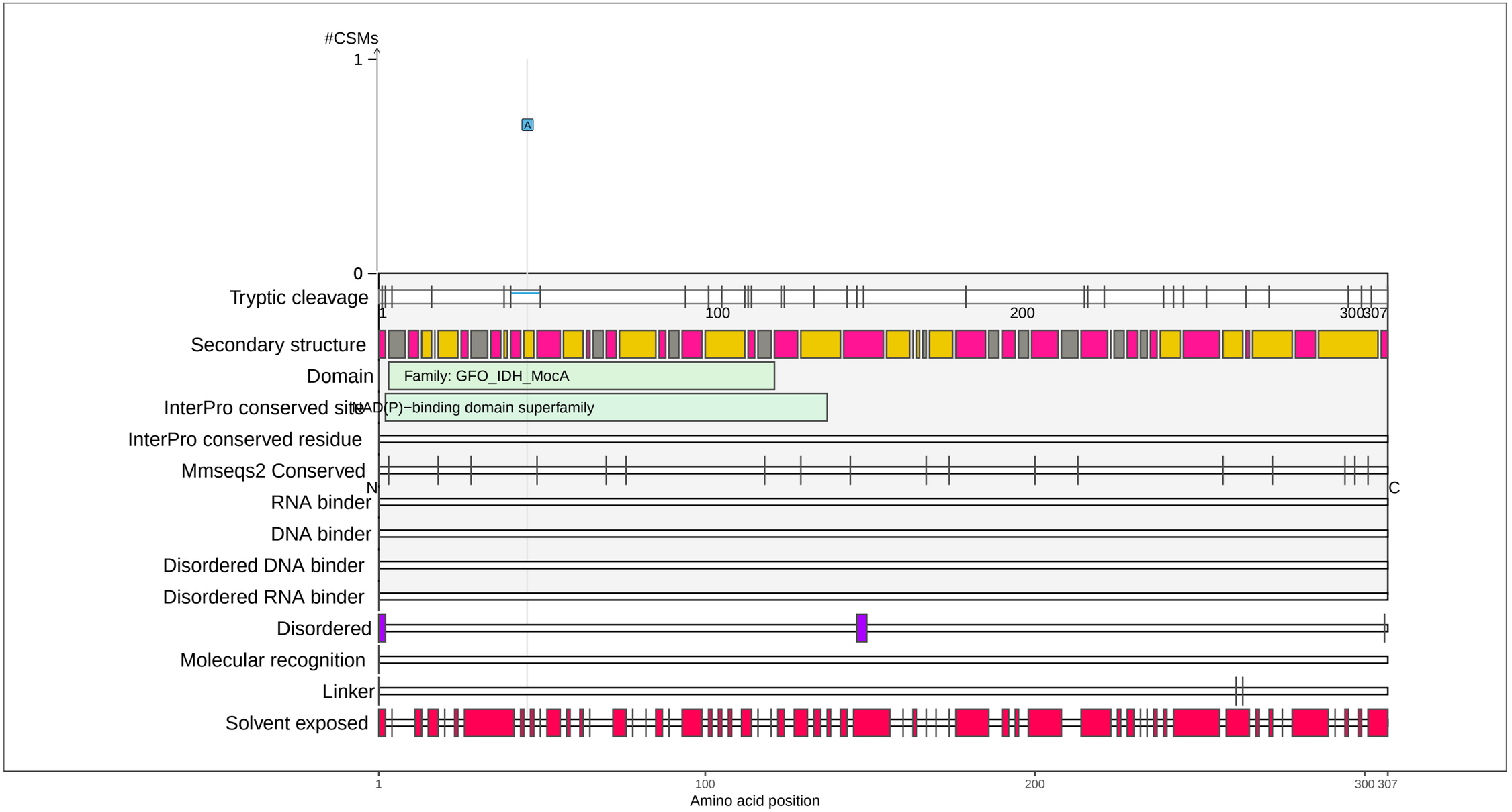
− RNA functions: not annotated

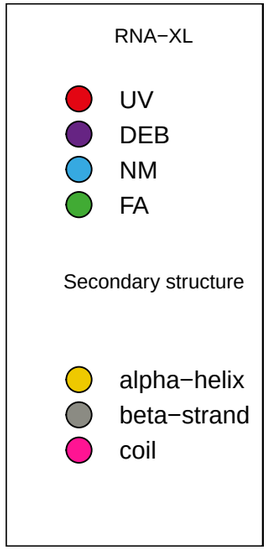


P75931
YCEM_ECOLI Putative oxidoreductase YceM

− Abundance:
tryptic [log10 Intensity]: 7.01 (Q 14)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.67 (Q 64)

− RNA functions: not annotated

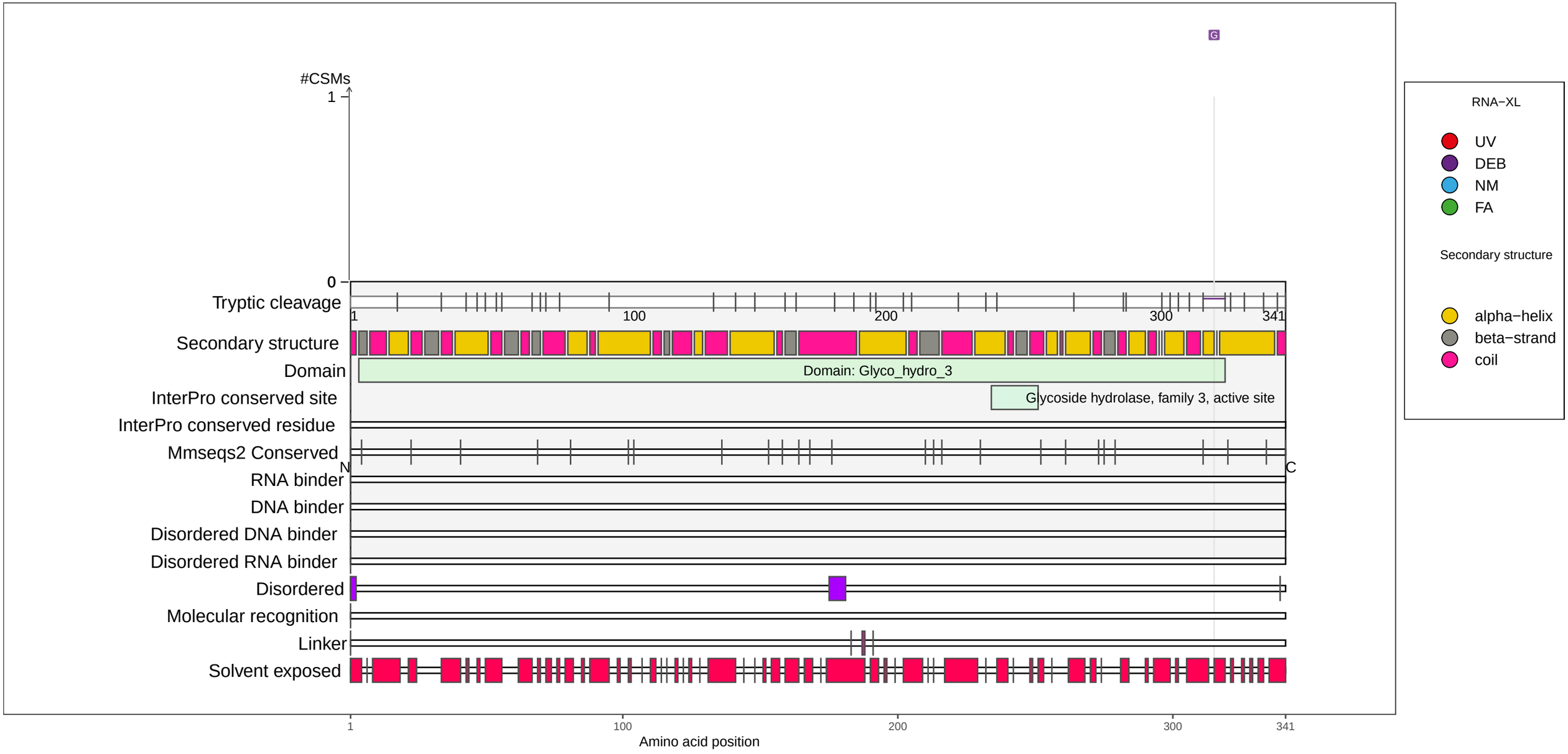




P75949
NAGZ_ECOLI Beta−hexosaminidase

− Abundance:
tryptic [log10 Intensity]: 7.59 (Q 39)
PAXdb K12 strain [ppm]: 2.49 (Q 77)
PAXdb E.coli [ppm]: 1.53 (Q 60)

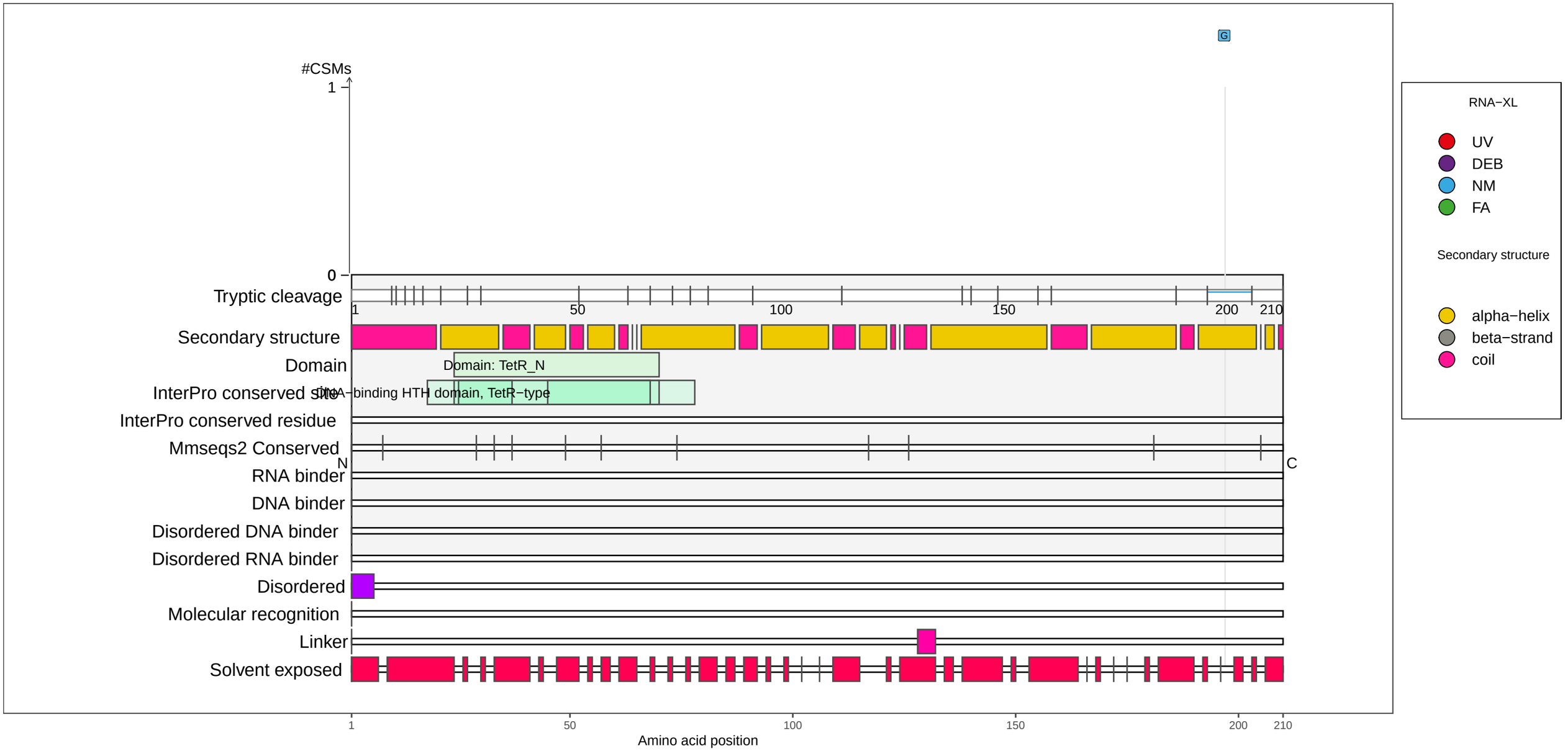
− RNA functions: not annotated



P75952
COMR_ECOLI HTH−type transcriptional repressor ComR

− Abundance:
tryptic [log10 Intensity]: 7.19 (Q 21)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.77 (Q 42)

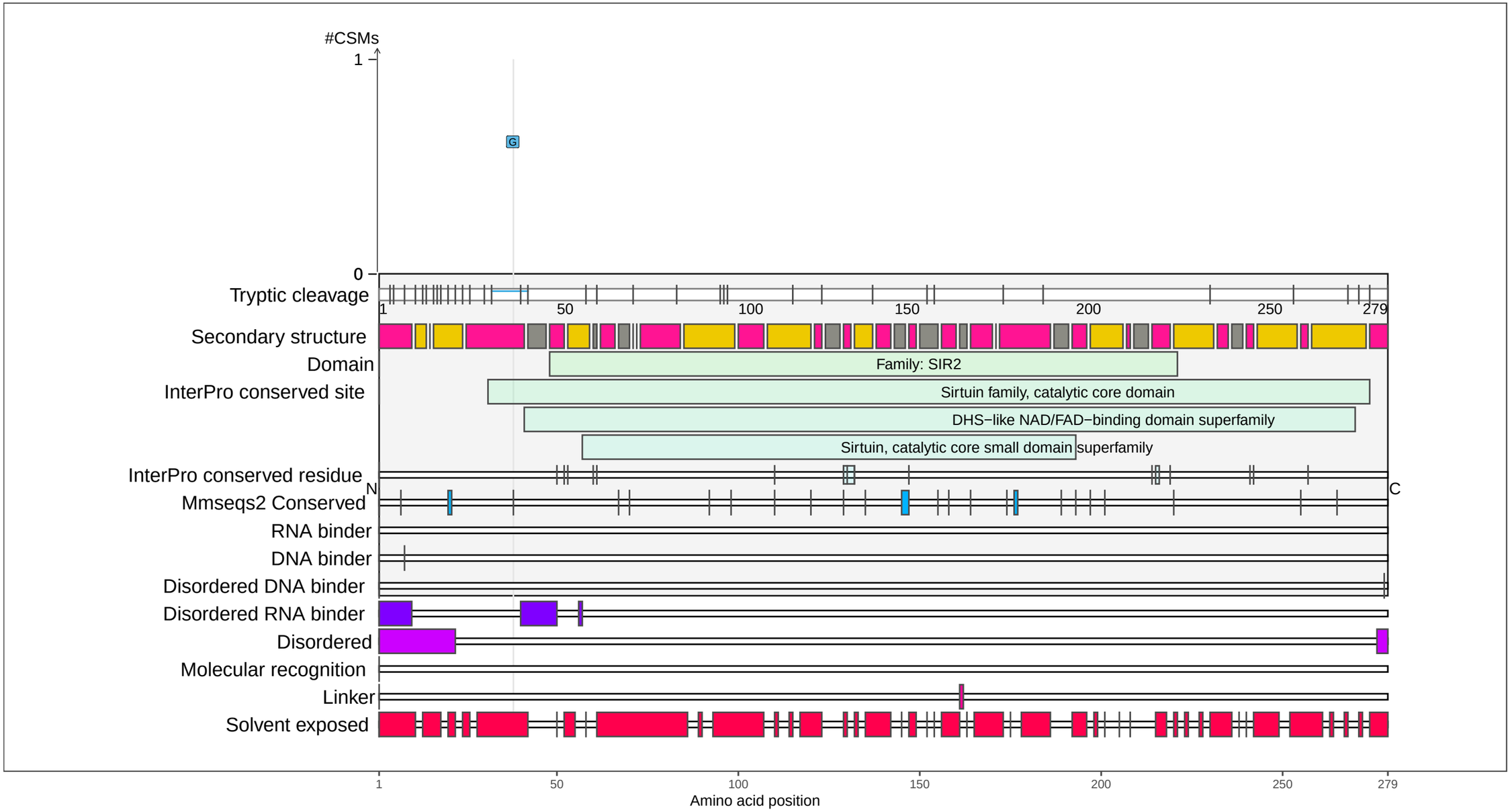
− RNA functions: not annotated



P75960
NPD_ECOLI NAD−dependent protein deacylase

− Abundance:
tryptic [log10 Intensity]: 7.44 (Q 32)
PAXdb K12 strain [ppm]: 1.06 (Q 13)
PAXdb E.coli [ppm]: 1.97 (Q 72)

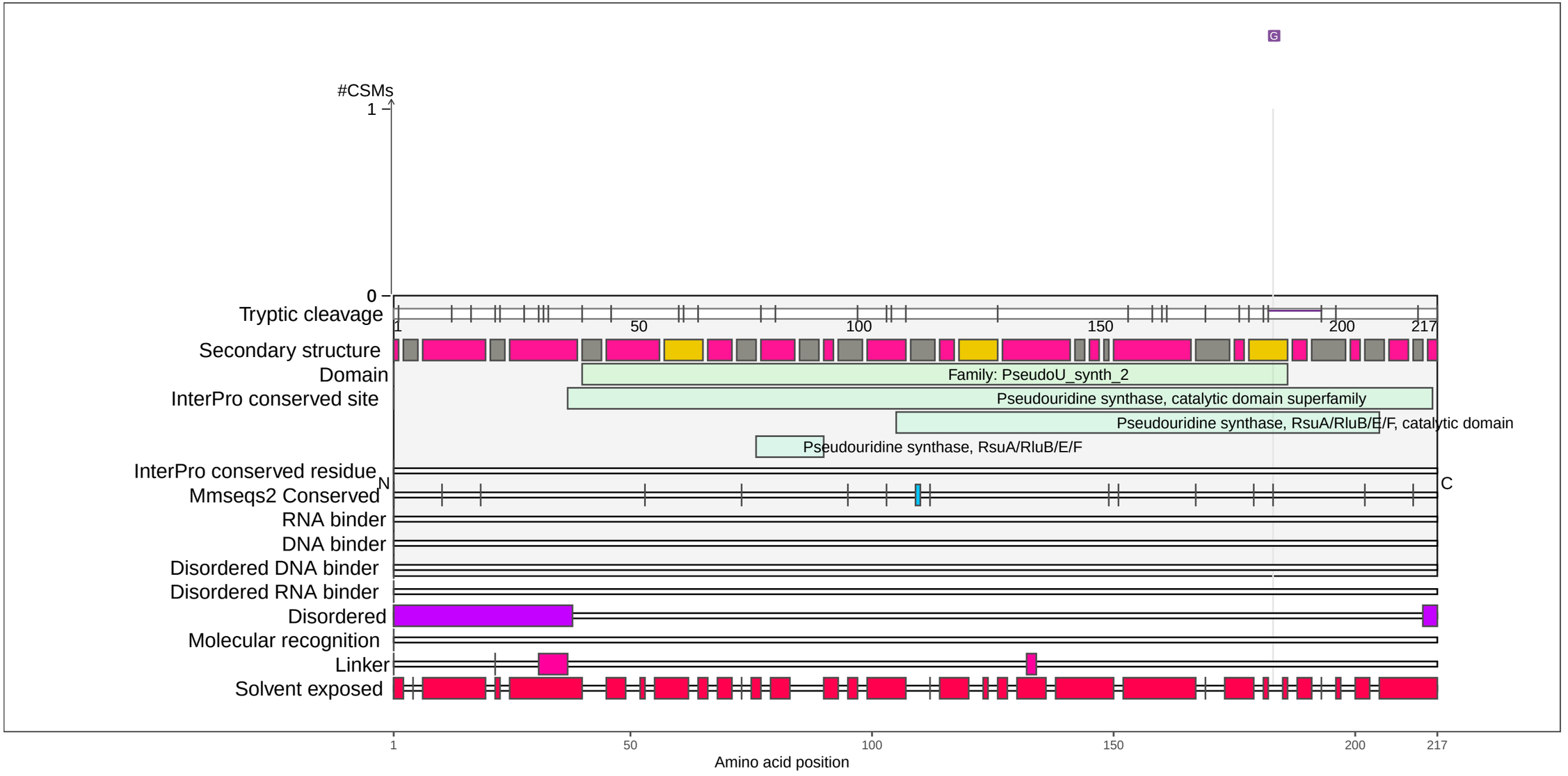
− RNA functions: not annotated



P75966
RLUE_ECOLI Ribosomal large subunit pseudouridine synthase E

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.01 (Q 11)
PAXdb E.coli [ppm]: 0.68 (Q 40)

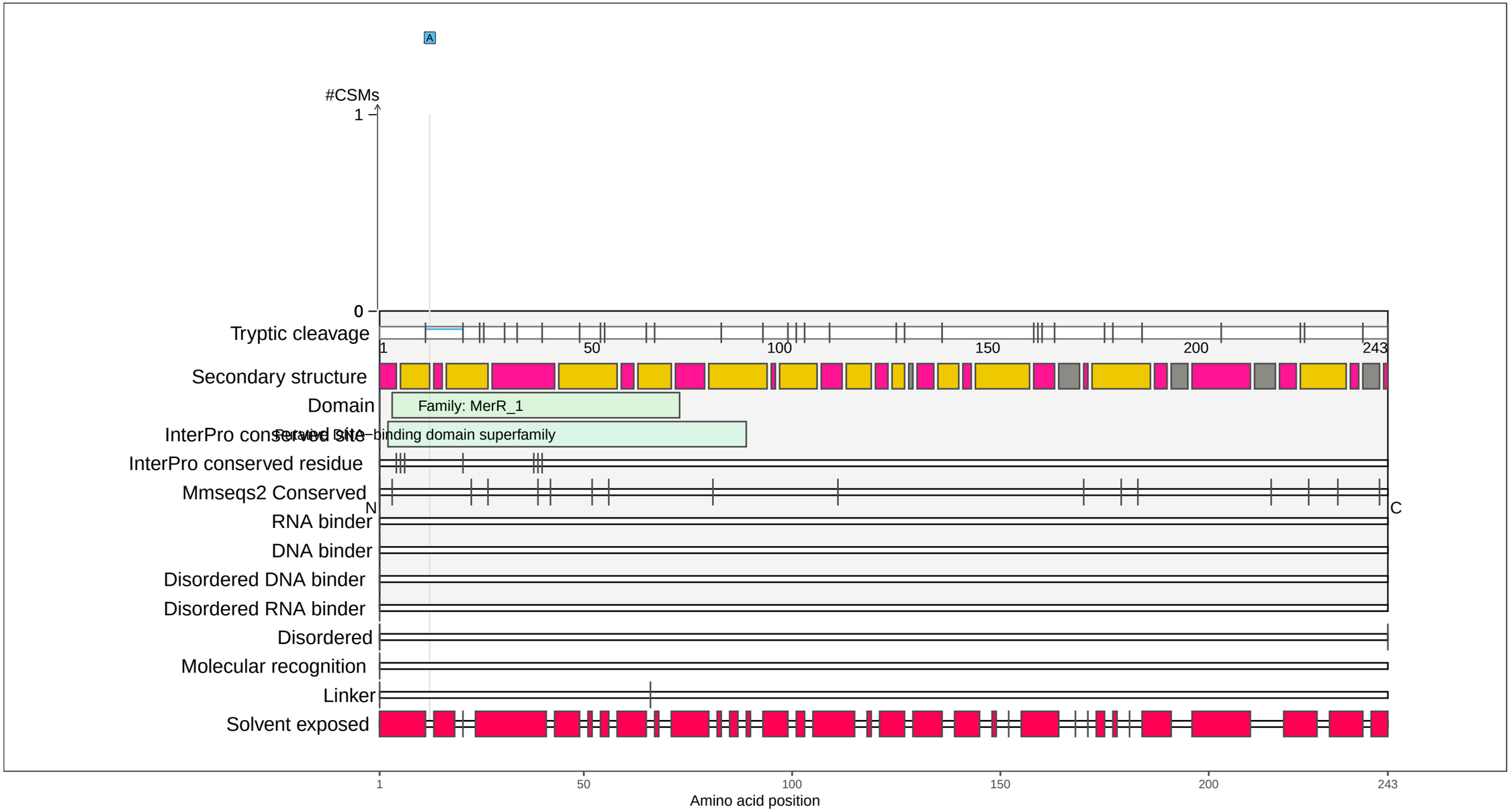
− RNA functions:
ncRNA metabolic process; ncRNA processing; RNA binding; RNA metabolic process
RNA modification; RNA processing; RNA pseudouridylate synthase; rRNA metabolic process
rRNA modification; rRNA processing; rRNA pseudouridine synthase activity
rRNA pseudouridine synthesis



P75989
BLUR_ECOLI HTH−type transcriptional repressor BluR

− Abundance:
tryptic [log10 Intensity]: 7.16 (Q 19)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.42 (Q 57)

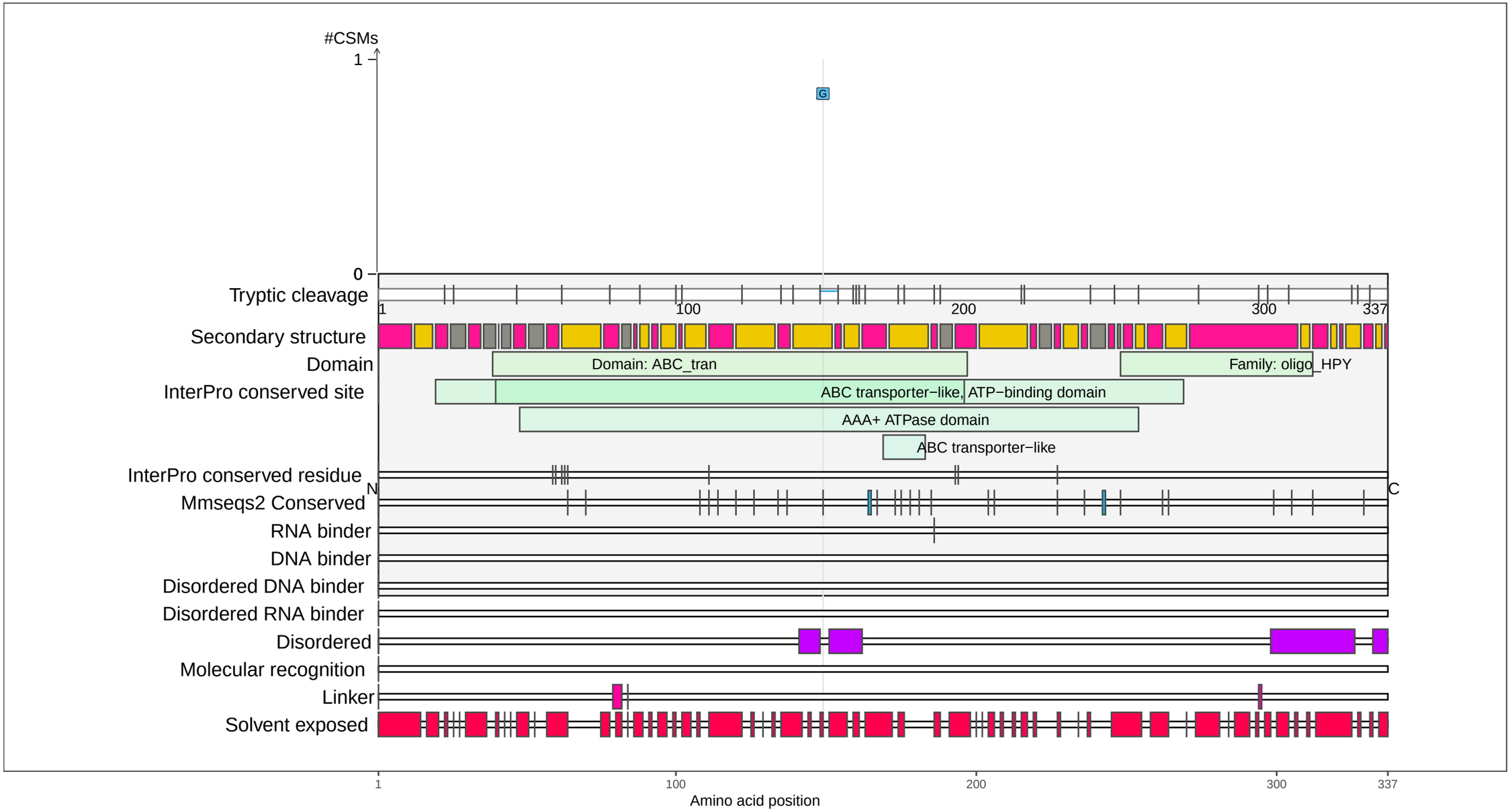
− RNA functions: not annotated

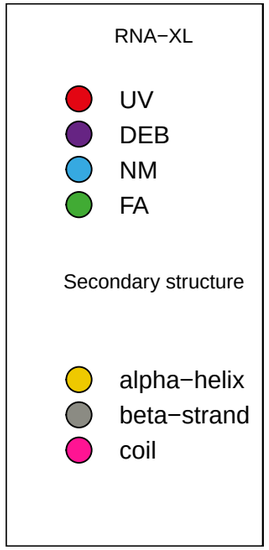


P76027
OPPD_ECOLI Oligopeptide transport ATP−binding protein OppD

− Abundance:
tryptic [log10 Intensity]: 6.25 (Q 1)
PAXdb K12 strain [ppm]: 1.31 (Q 27)
PAXdb E.coli [ppm]: 1.57 (Q 62)

− RNA functions: not annotated

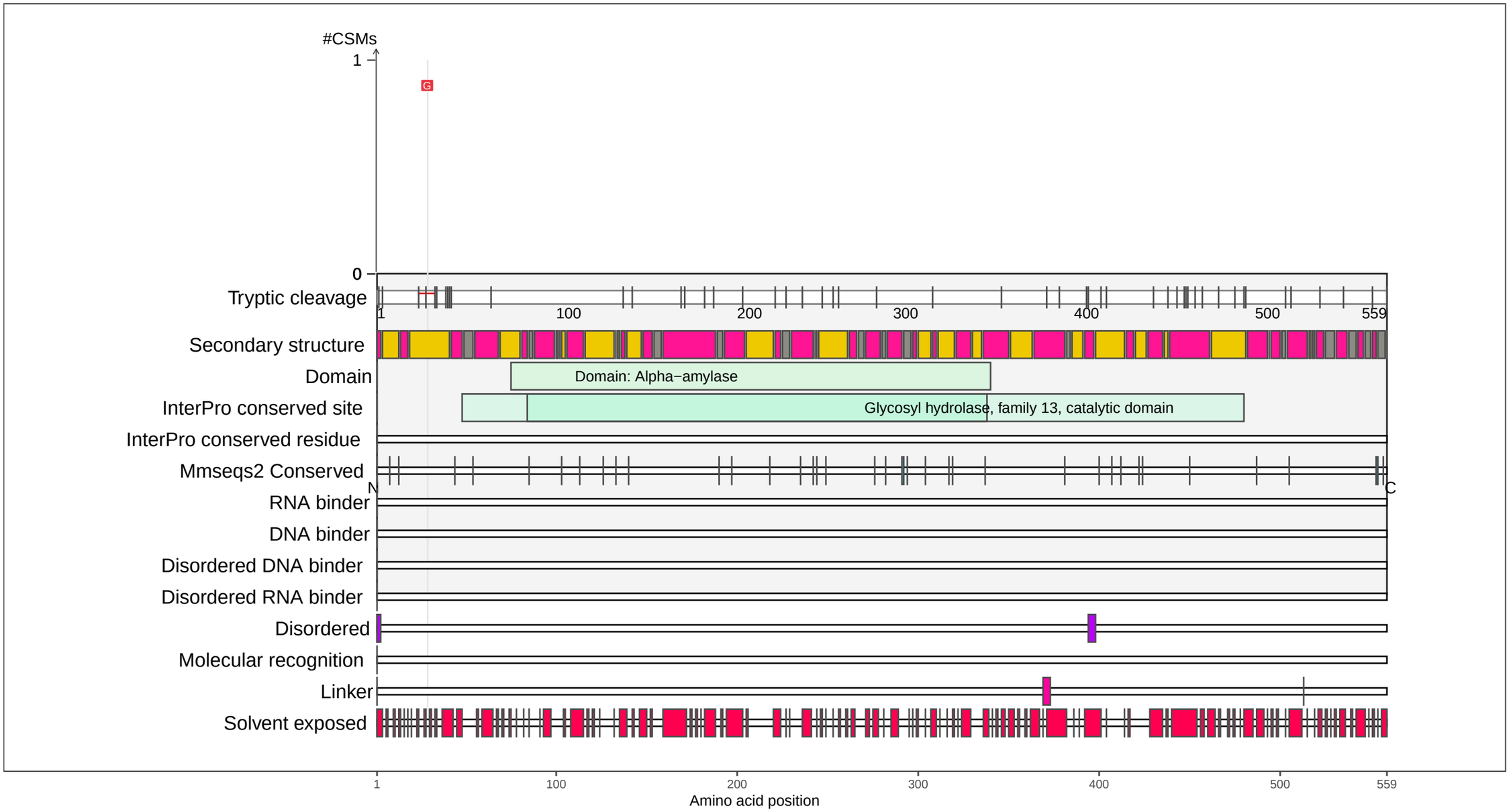


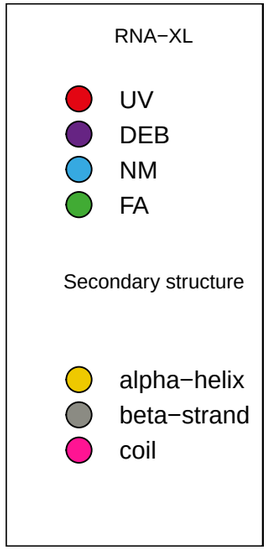


P76041
GGAP_ECOLI Glucosylglycerate phosphorylase

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.73 (Q 3)
PAXdb E.coli [ppm]: −0.69 (Q 13)

− RNA functions: not annotated

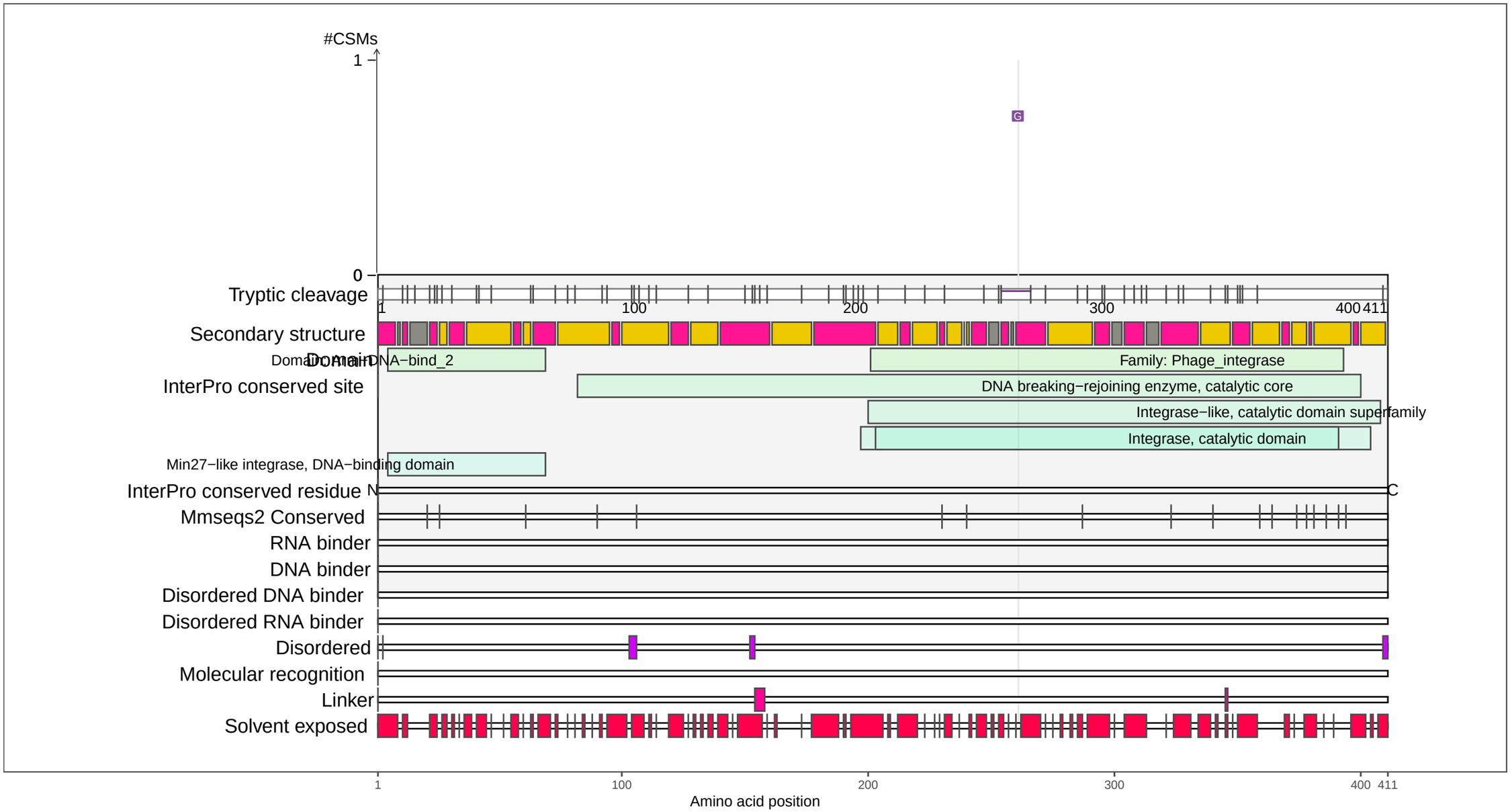




P76056
INTR_ECOLI Prophage integrase IntR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.77 (Q 4)
PAXdb E.coli [ppm]: −0.66 (Q 13)

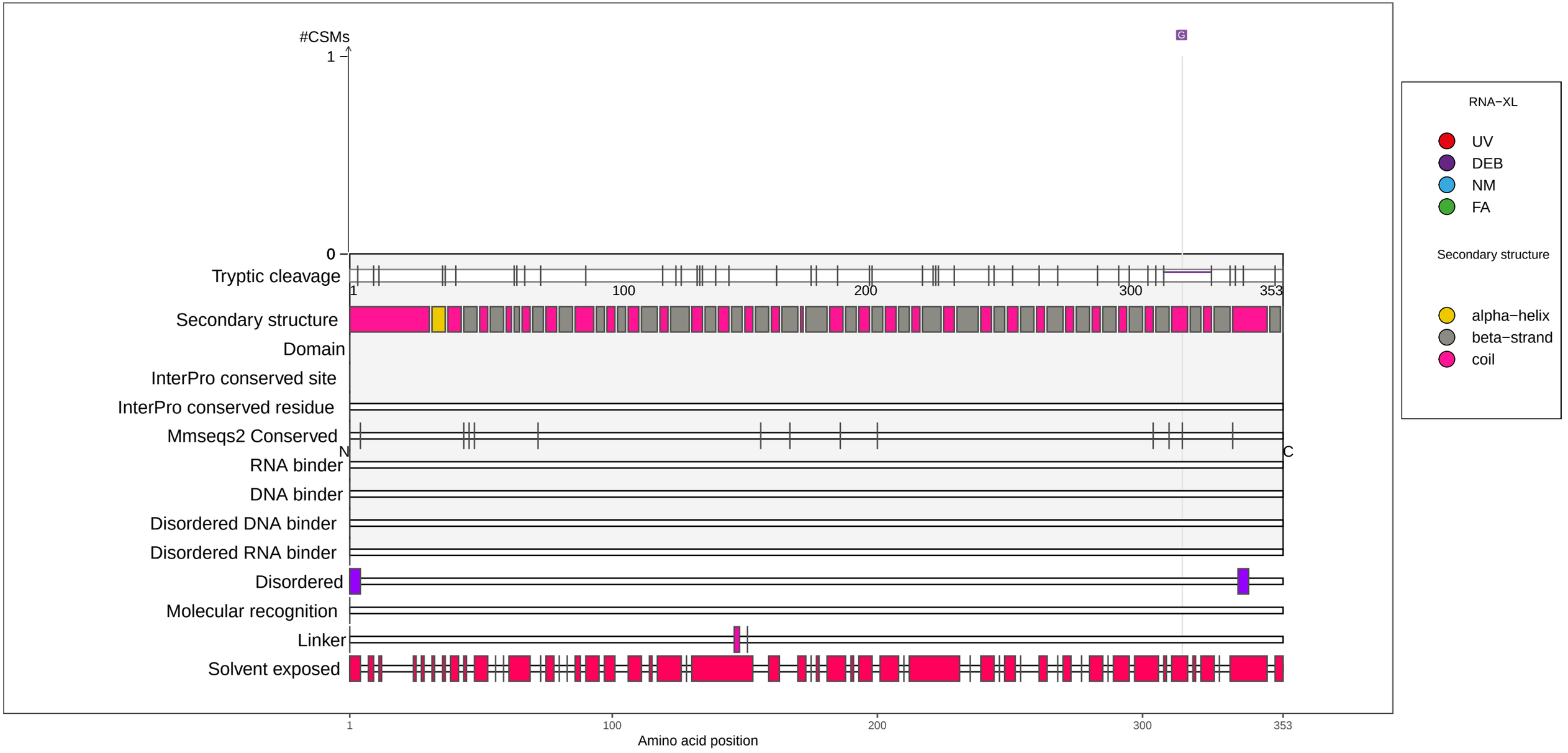
− RNA functions: not annotated



P76116
YNCE_ECOLI Uncharacterized protein YncE

− Abundance:
tryptic [log10 Intensity]: 8.85 (Q 85)
PAXdb K12 strain [ppm]: 1.46 (Q 36)
PAXdb E.coli [ppm]: 2.61 (Q 88)

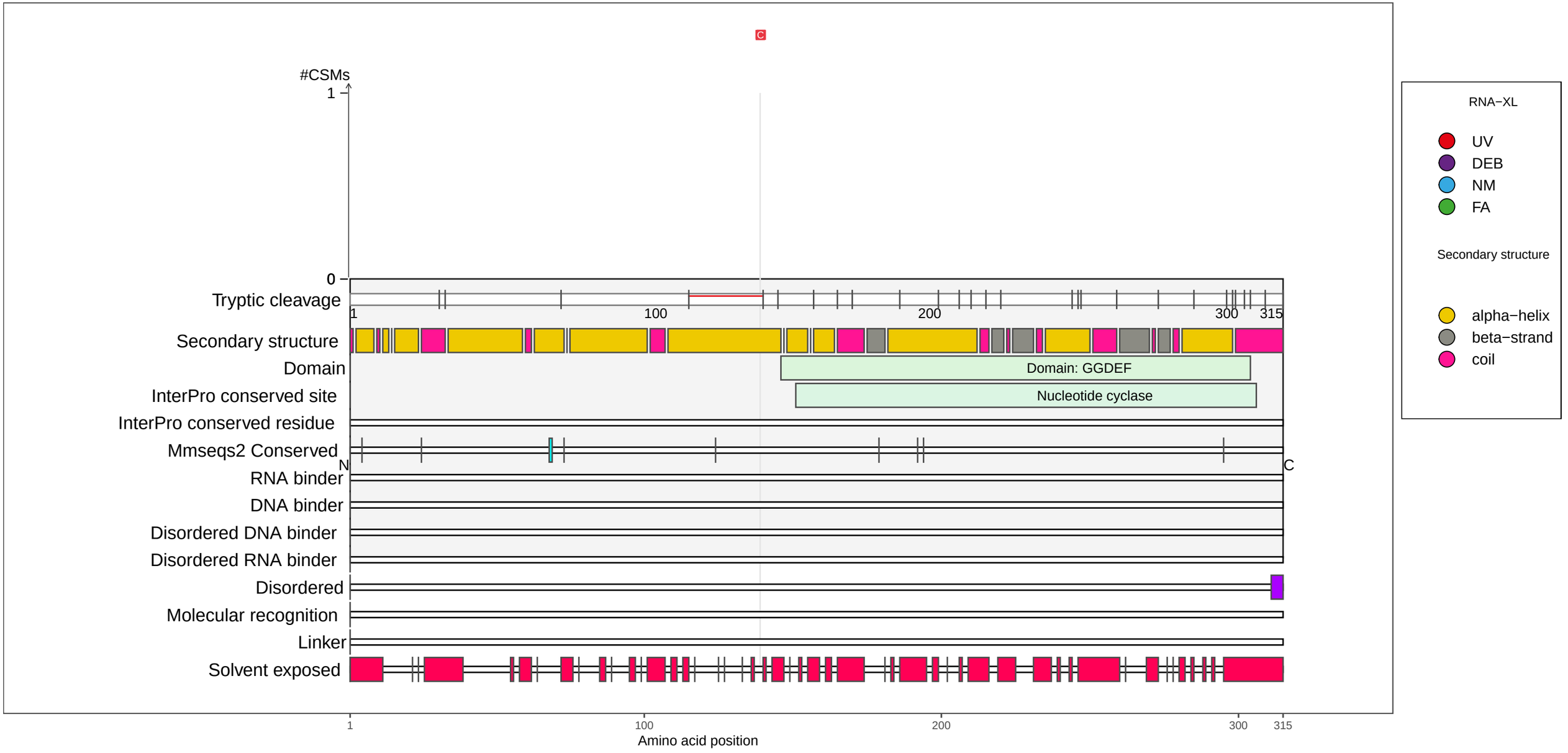
− RNA functions: not annotated



P76147
DGCF_ECOLI Probable diguanylate cyclase DgcF

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: −0.95 (Q 9)

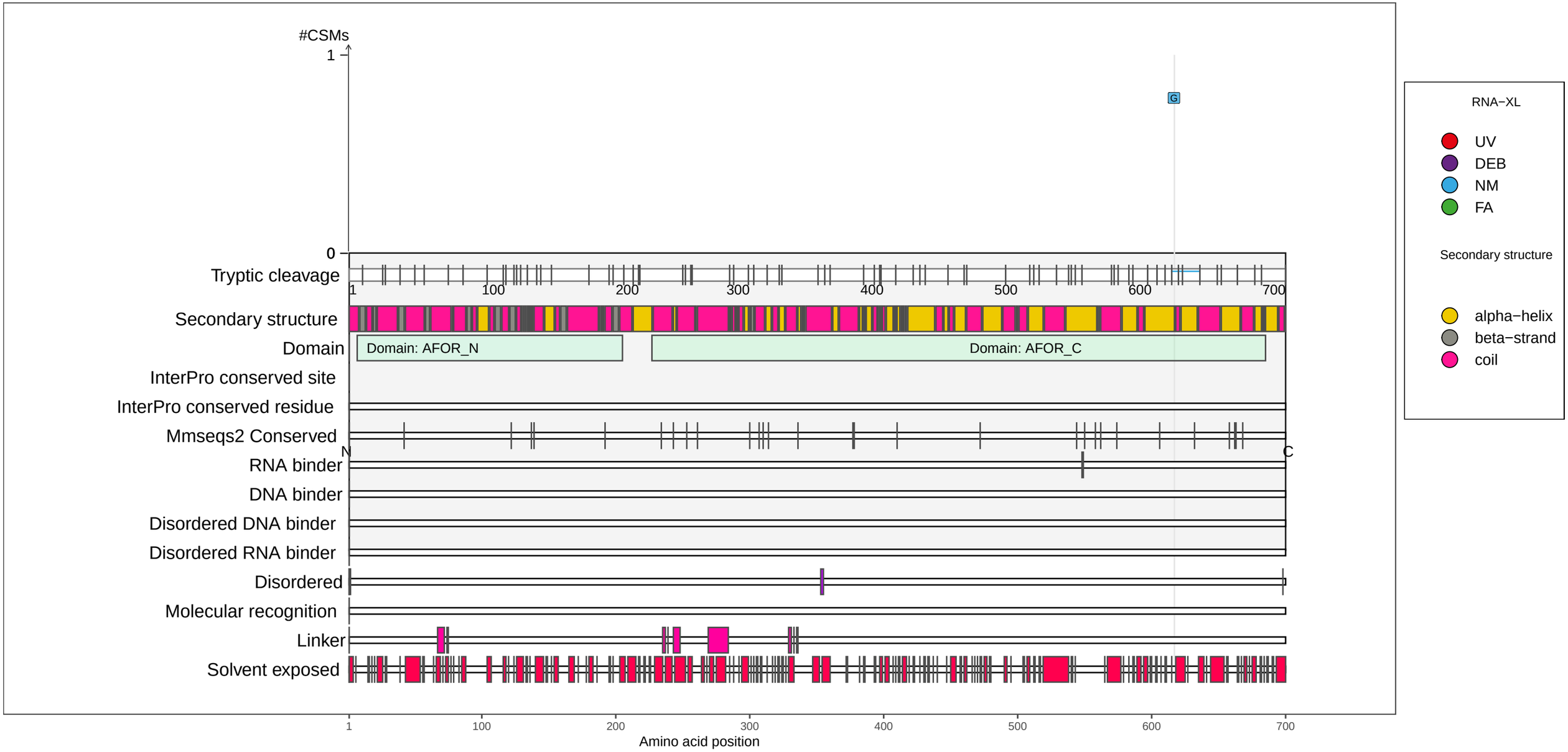
− RNA functions: not annotated



P76192
YDHV_ECOLI Uncharacterized oxidoreductase YdhV

− Abundance:
tryptic [log10 Intensity]: 8.97 (Q 88)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.46 (Q 35)

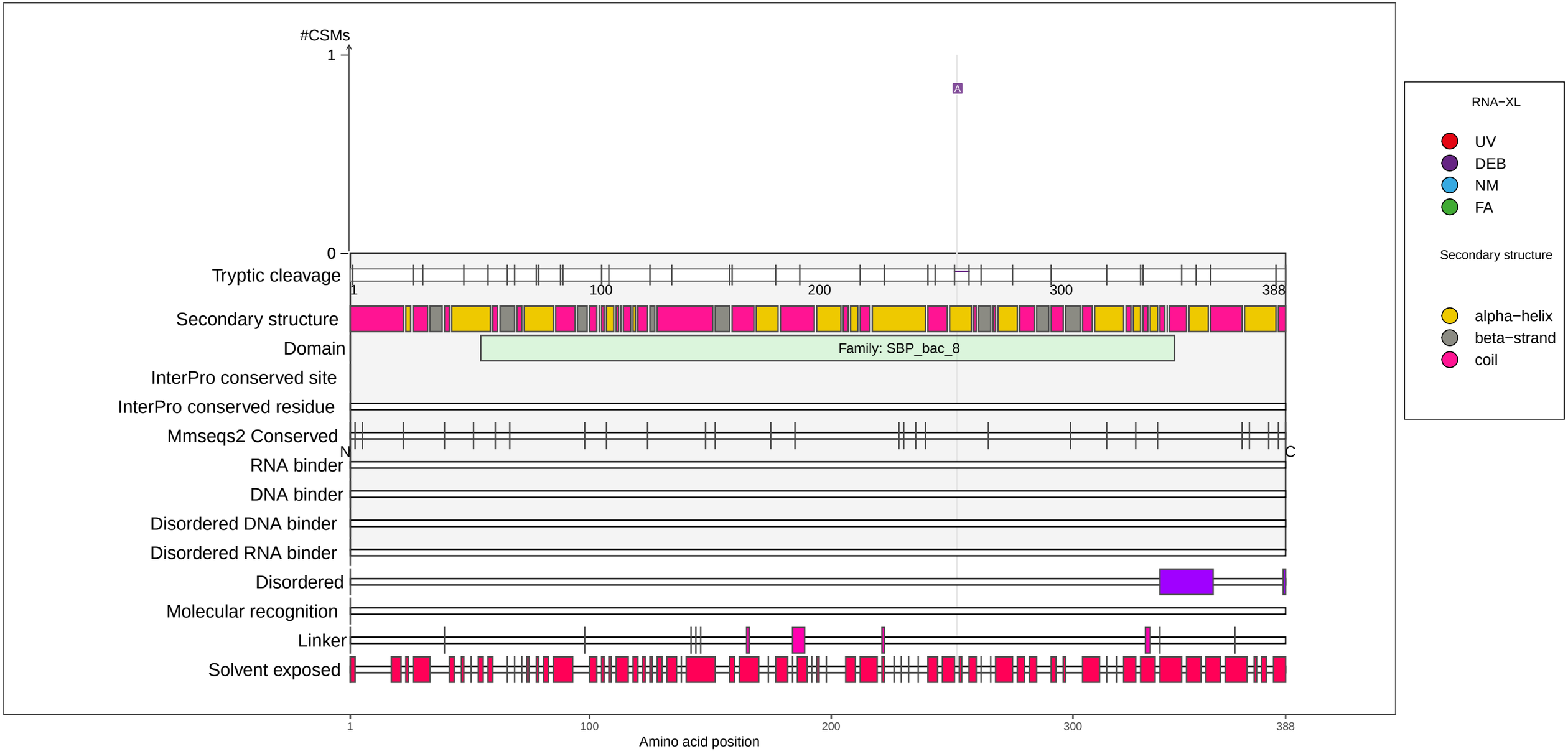
− RNA functions: not annotated



P76223
YNJB_ECOLI Protein YnjB

− Abundance:
tryptic [log10 Intensity]: 6.88 (Q 9)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.48 (Q 36)

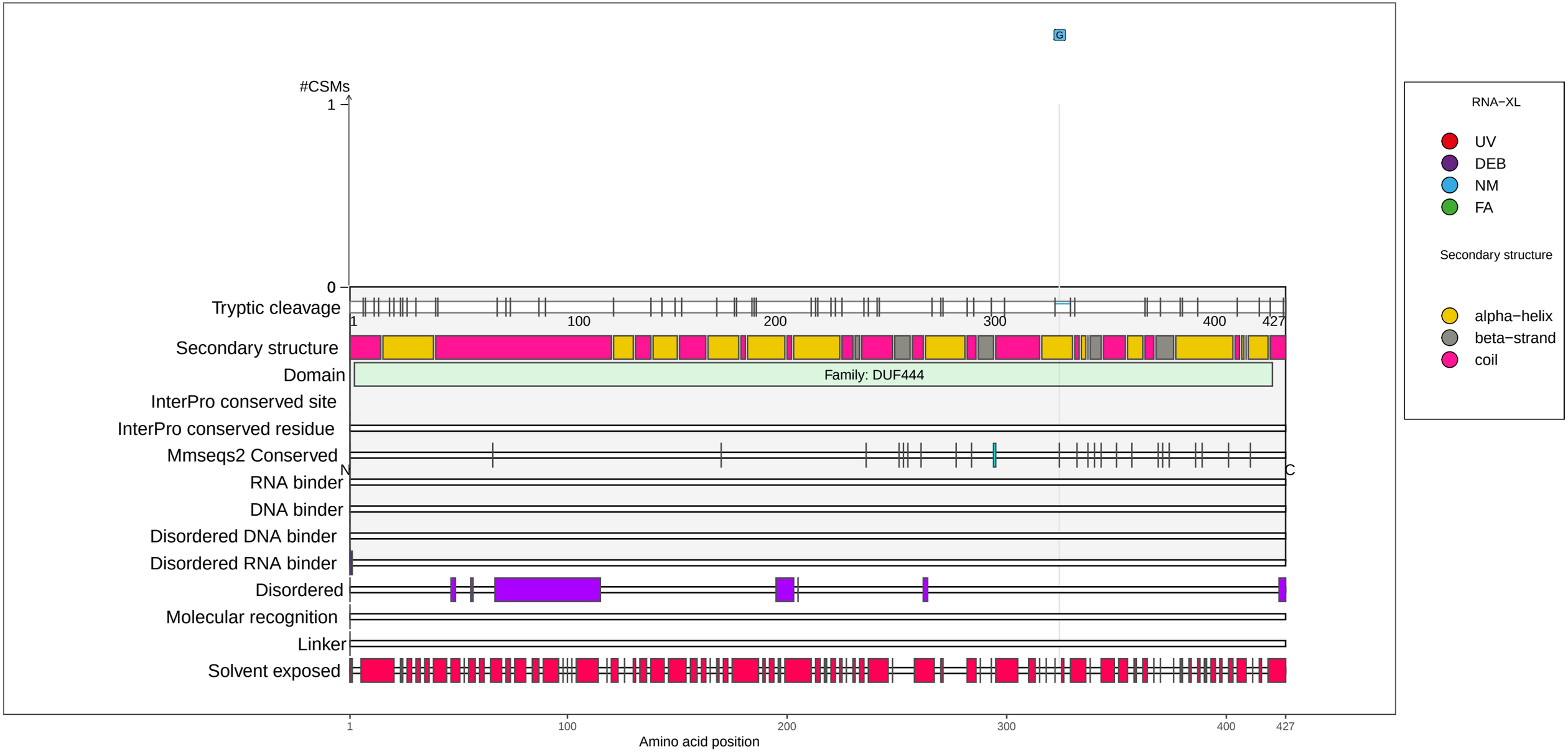
− RNA functions: not annotated



P76235
YEAH_ECOLI UPF0229 protein YeaH

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.8 (Q 43)

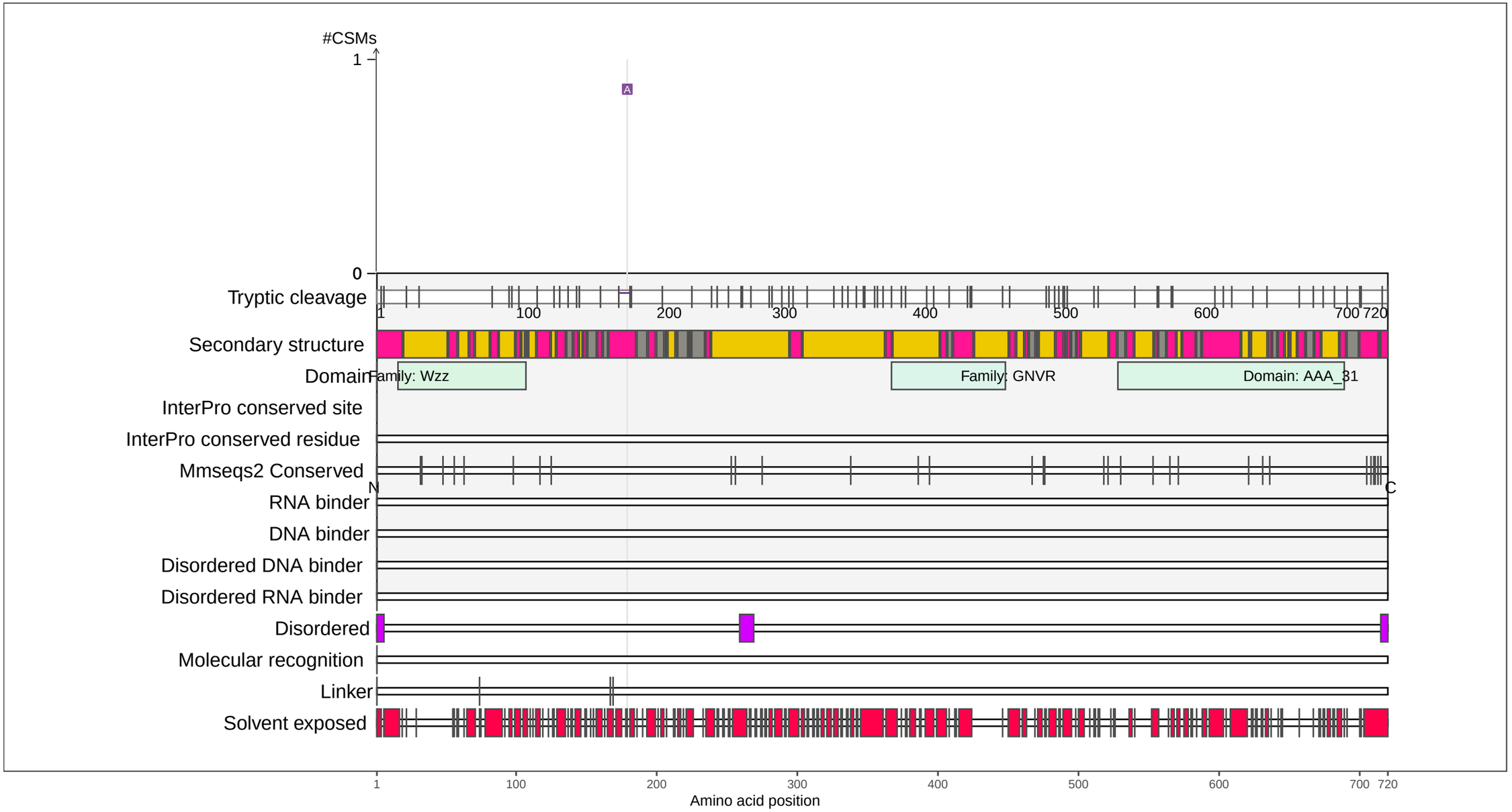
− RNA functions: not annotated

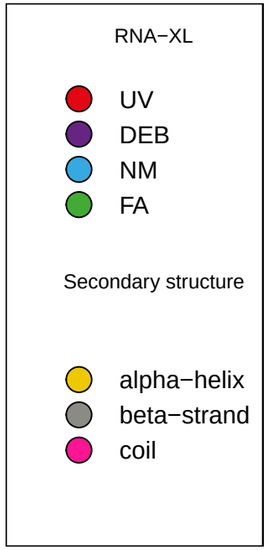


P76387
WZC_ECOLI Tyrosine−protein kinase wzc

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.66 (Q 2)
PAXdb E.coli [ppm]: −1.21 (Q 6)

− RNA functions: not annotated

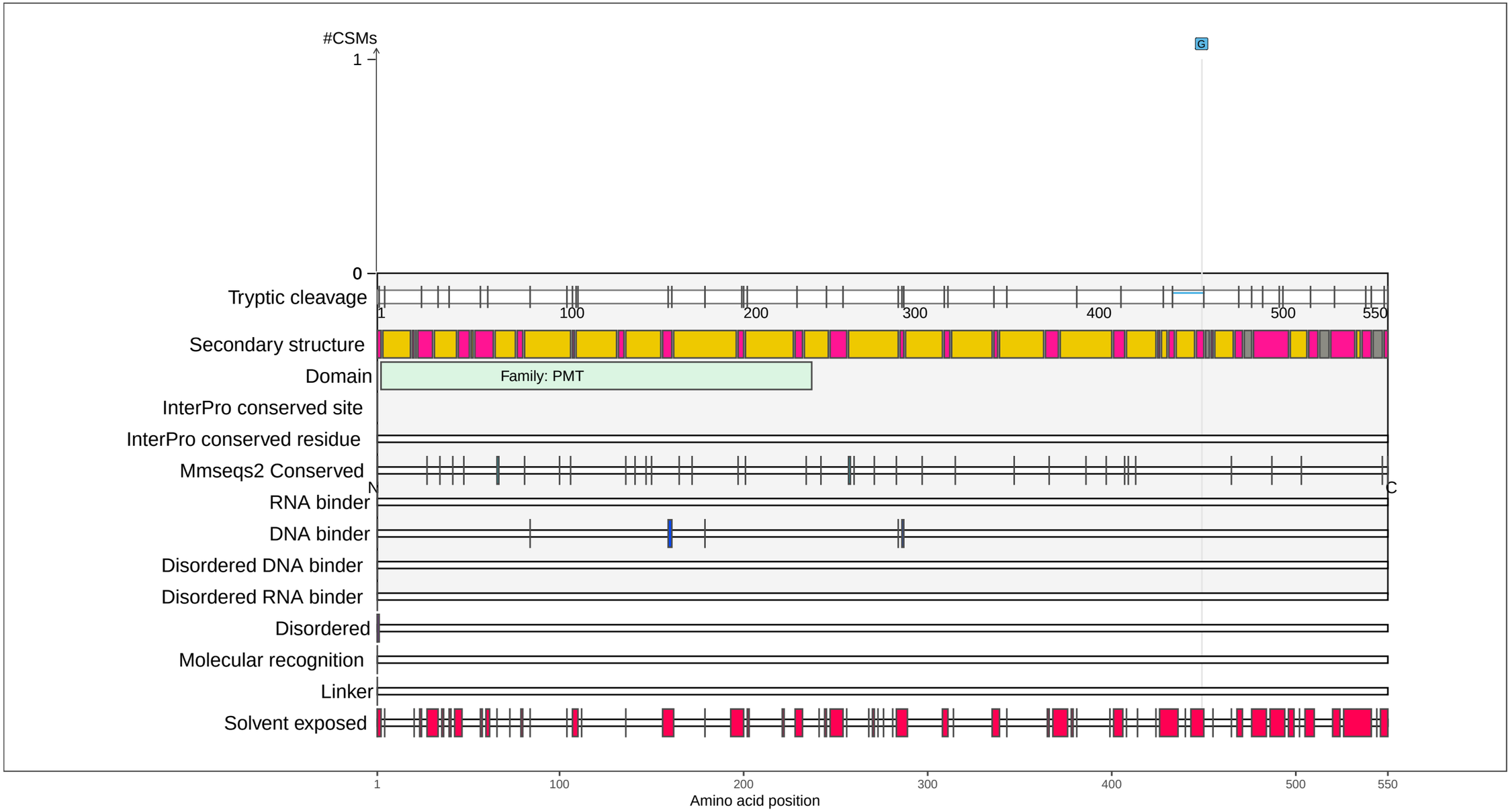




P76473
ARNT_ECOLI Undecaprenyl phosphate−alpha−4−amino−4−deoxy−L−arabinose arabinosyl transferase

− Abundance:
tryptic [log10 Intensity]: 8.1 (Q 61)
PAXdb K12 strain [ppm]: 1.09 (Q 15)
PAXdb E.coli [ppm]: −1.49 (Q 4)

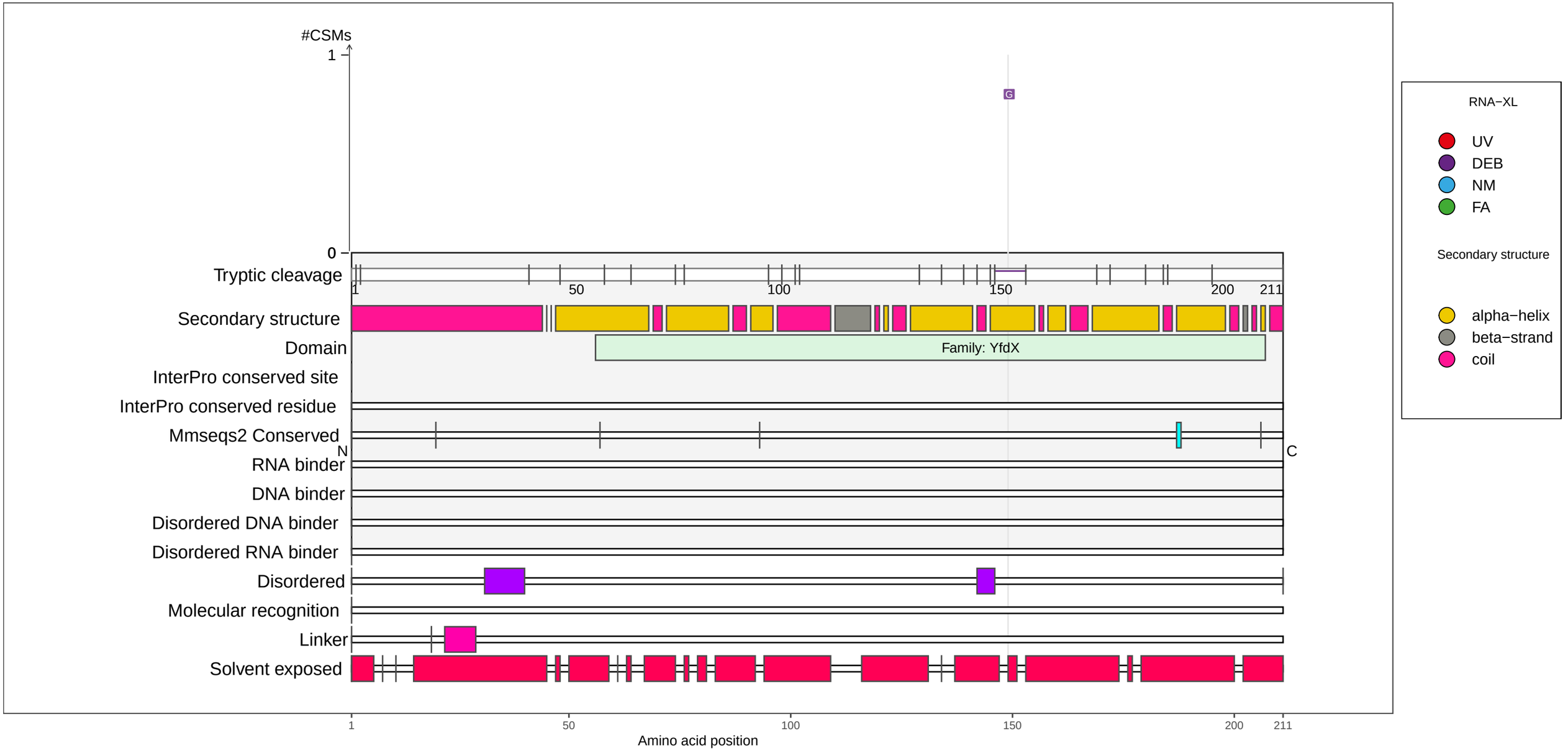
− RNA functions: not annotated



P76520
YFDX_ECOLI Protein YfdX

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.28 (Q 25)
PAXdb E.coli [ppm]: −0.6 (Q 14)

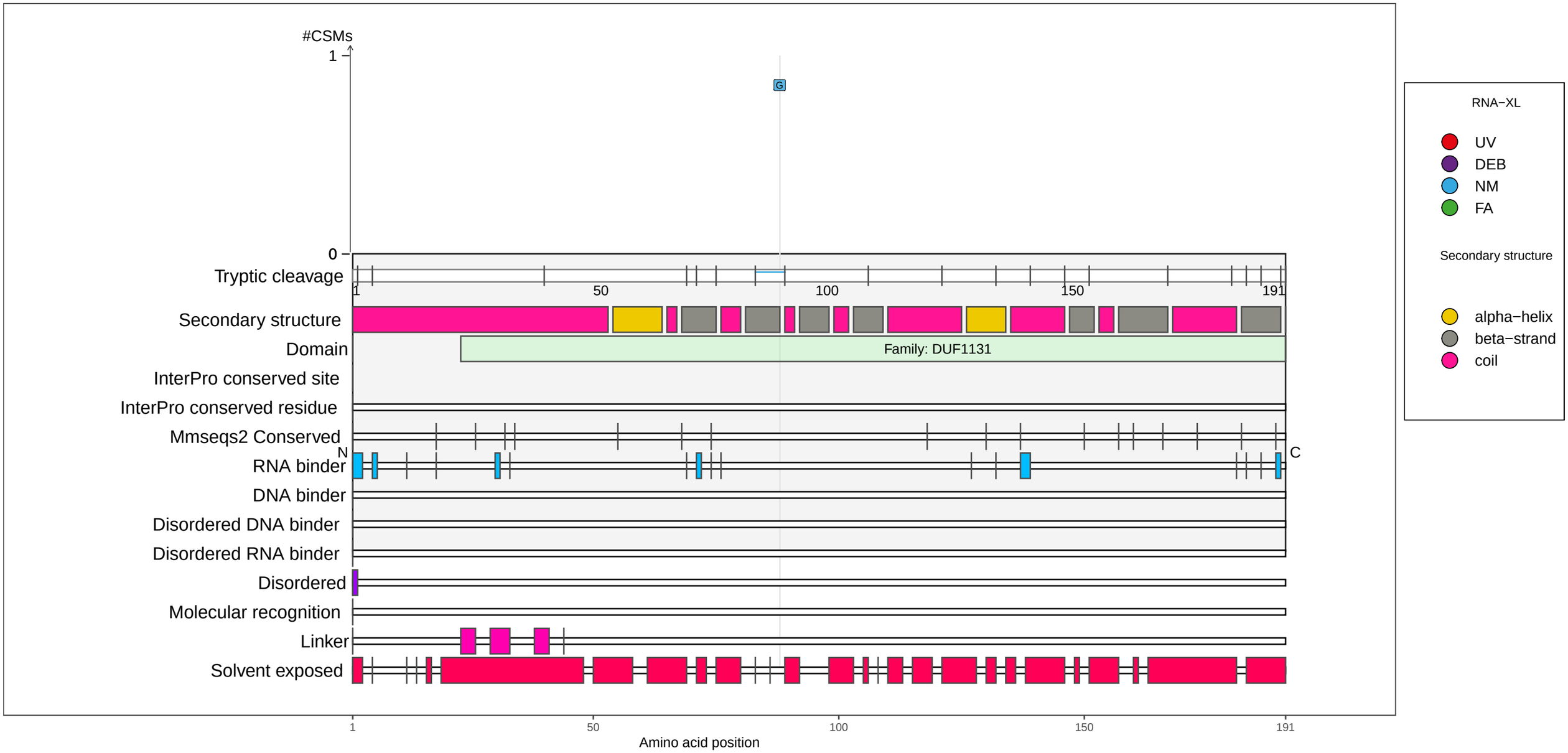
− RNA functions: not annotated



P76537
YFEY_ECOLI Uncharacterized protein YfeY

− Abundance:
tryptic [log10 Intensity]: 7.65 (Q 42)
PAXdb K12 strain [ppm]: 1.81 (Q 53)
PAXdb E.coli [ppm]: 1.22 (Q 53)

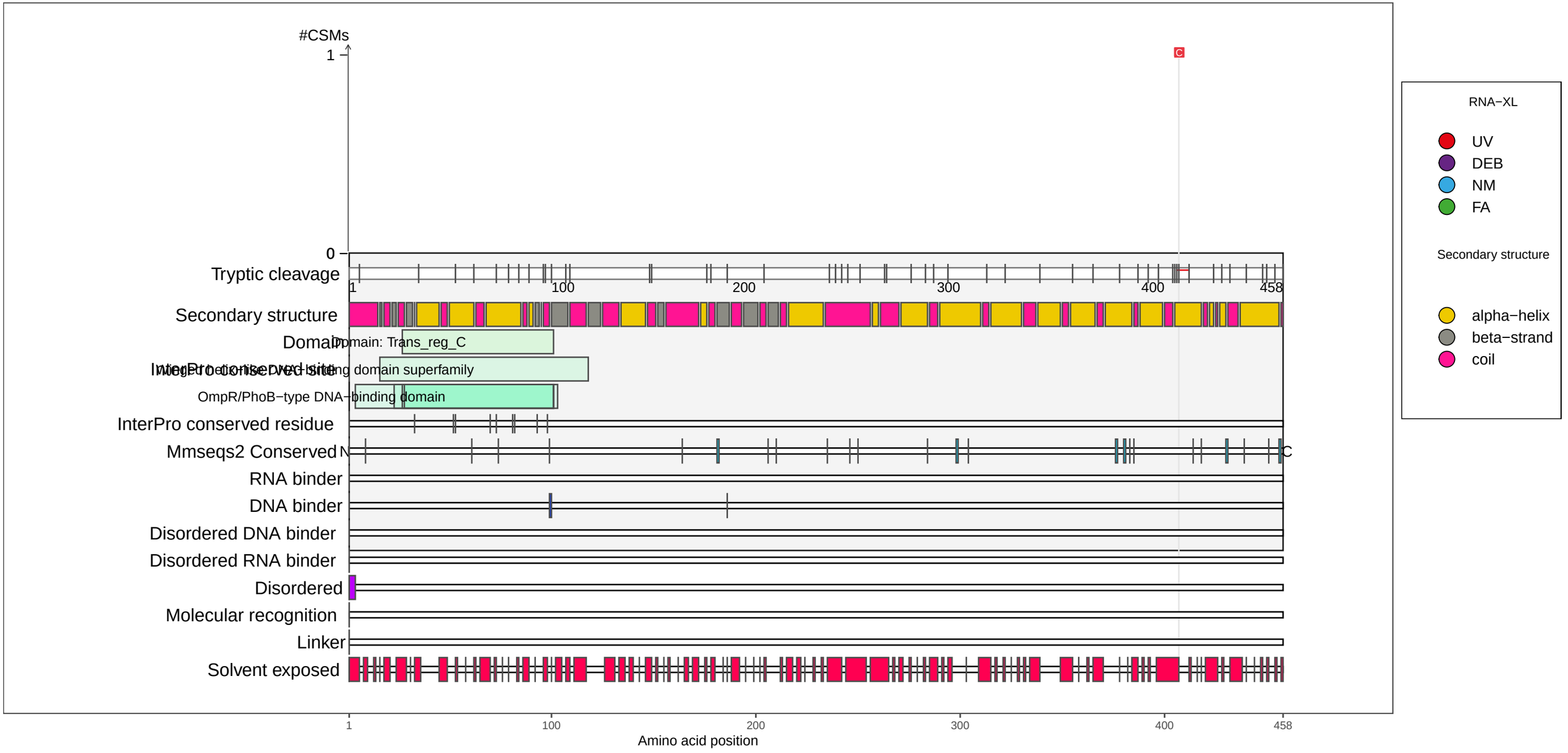
− RNA functions: not annotated



P76639
YGEH_ECOLI Uncharacterized protein YgeH

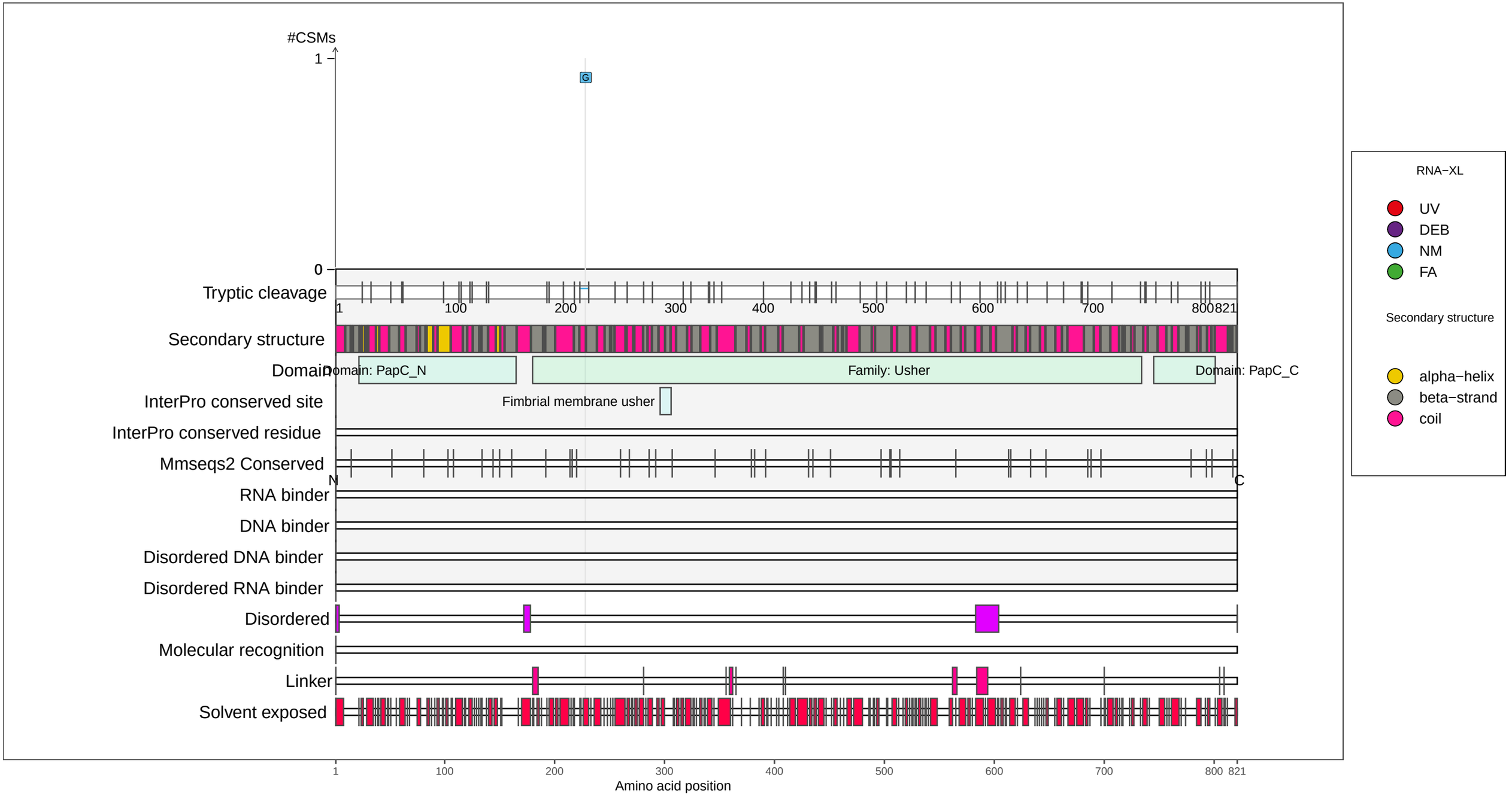
− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: NA (Q NA)

− RNA functions: not annotated



P76655
YQIG_ECOLI Putative outer membrane usher protein YqiG

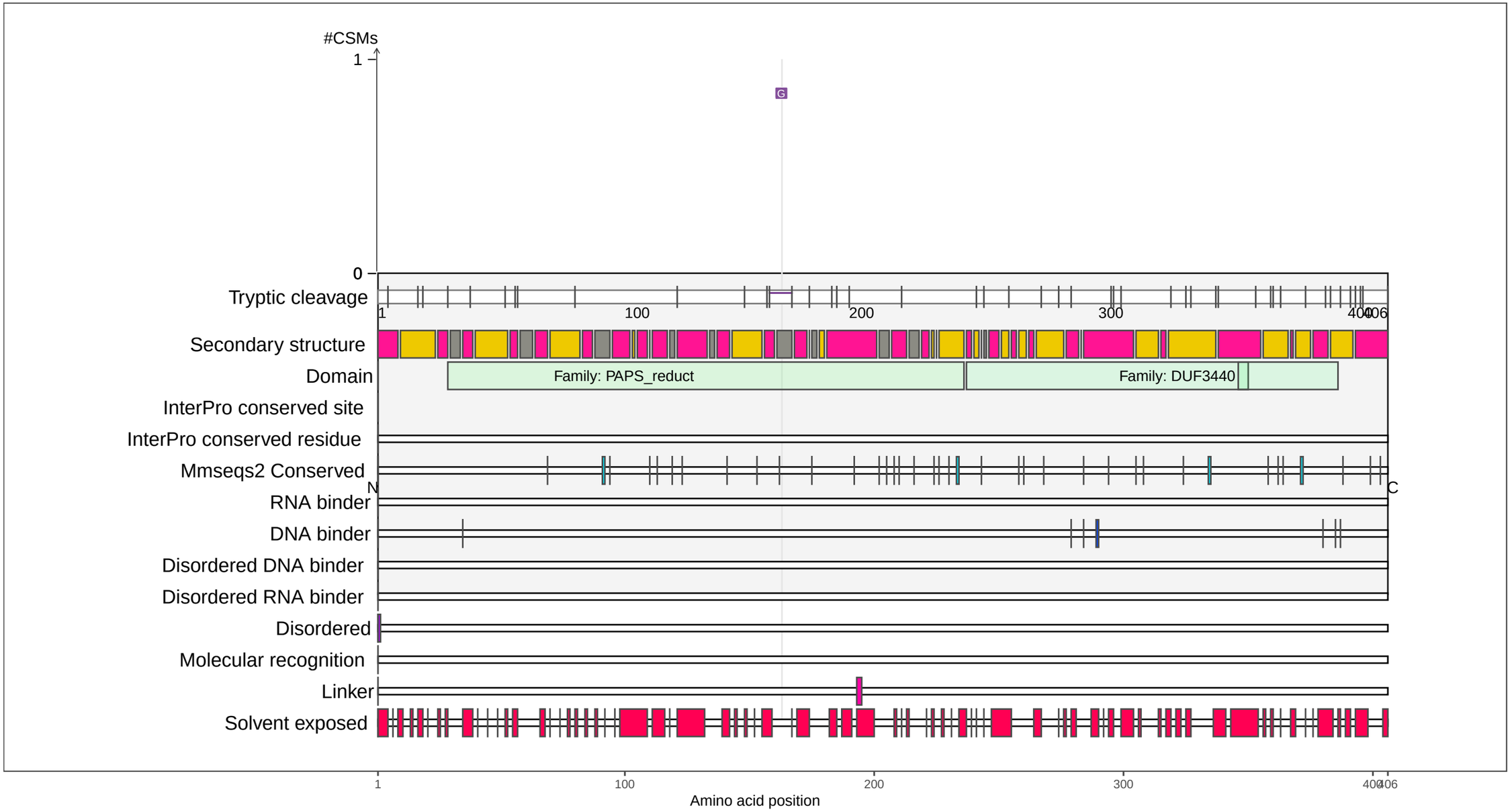
− RNA functions: not annotated

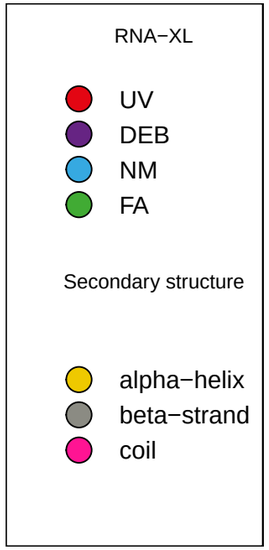


P77216
YBDN_ECOLI Uncharacterized protein YbdN

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.91 (Q 8)
PAXdb E.coli [ppm]: 0.64 (Q 39)

− RNA functions: not annotated

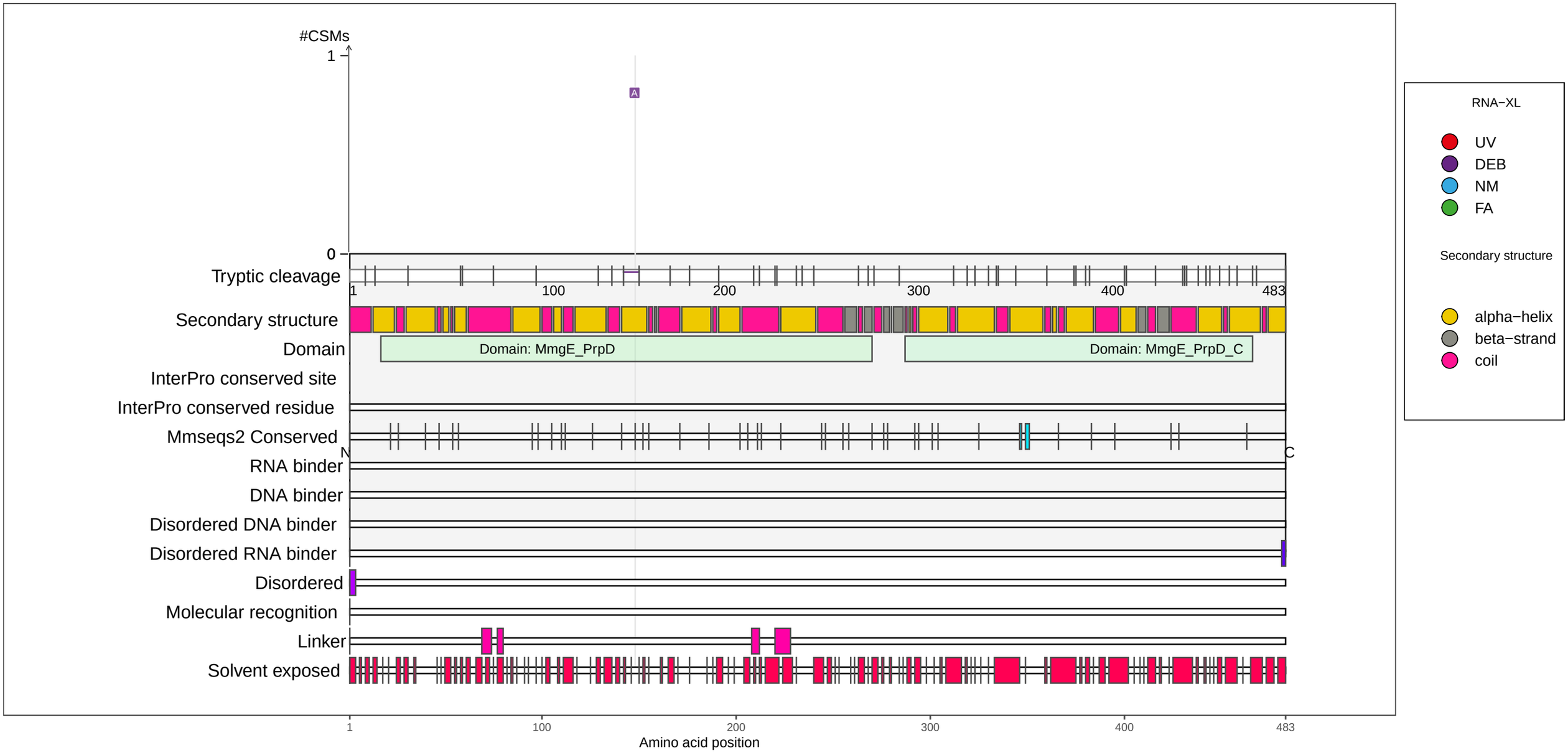




P77243
PRPD_ECOLI 2−methylcitrate dehydratase

− Abundance:
tryptic [log10 Intensity]: 8.87 (Q 85)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.19 (Q 77)

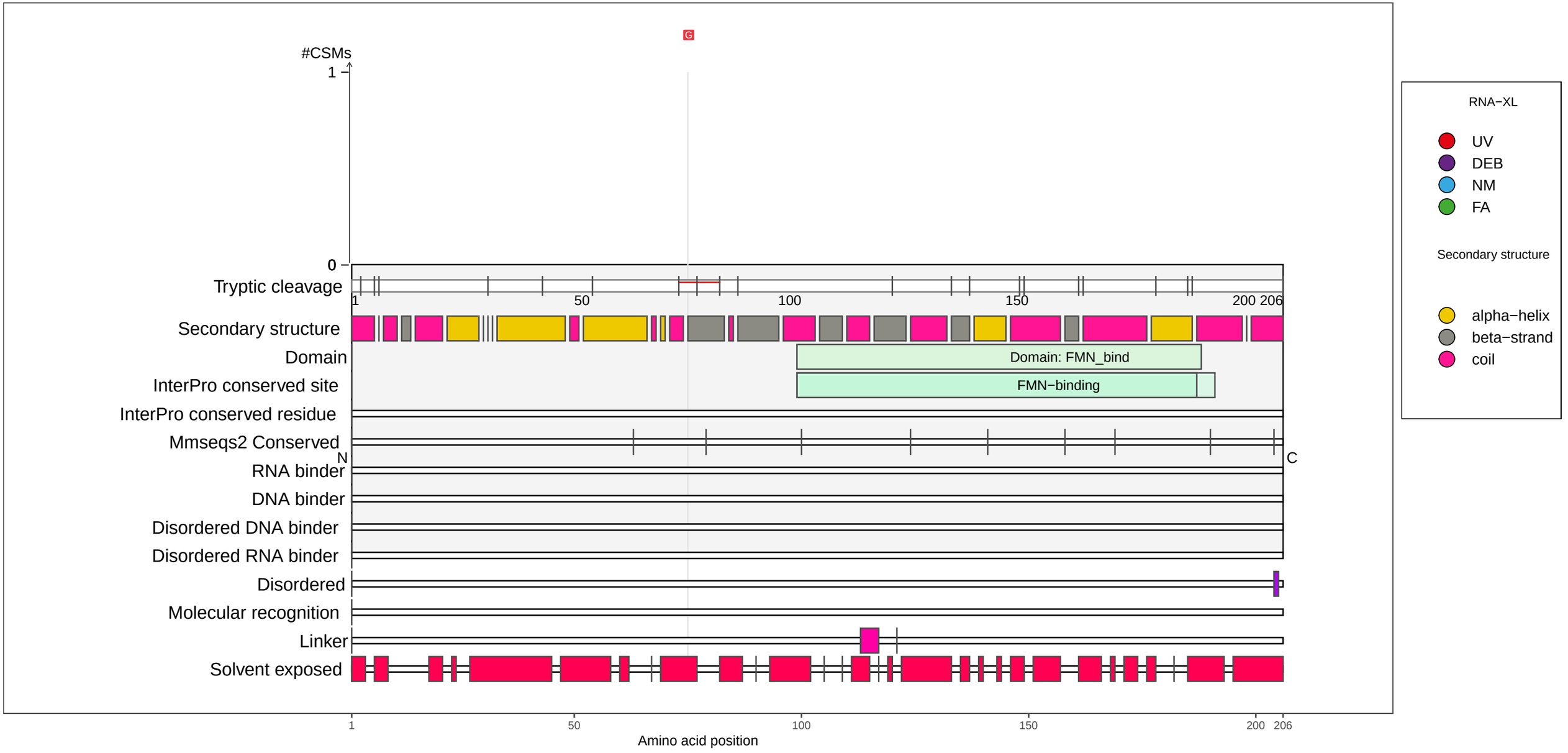
− RNA functions: not annotated



P77285
RSXG_ECOLI Ion−translocating oxidoreductase complex subunit G

− Abundance:
tryptic [log10 Intensity]: 7.05 (Q 15)
PAXdb K12 strain [ppm]: 1.95 (Q 59)
PAXdb E.coli [ppm]: 0.82 (Q 44)

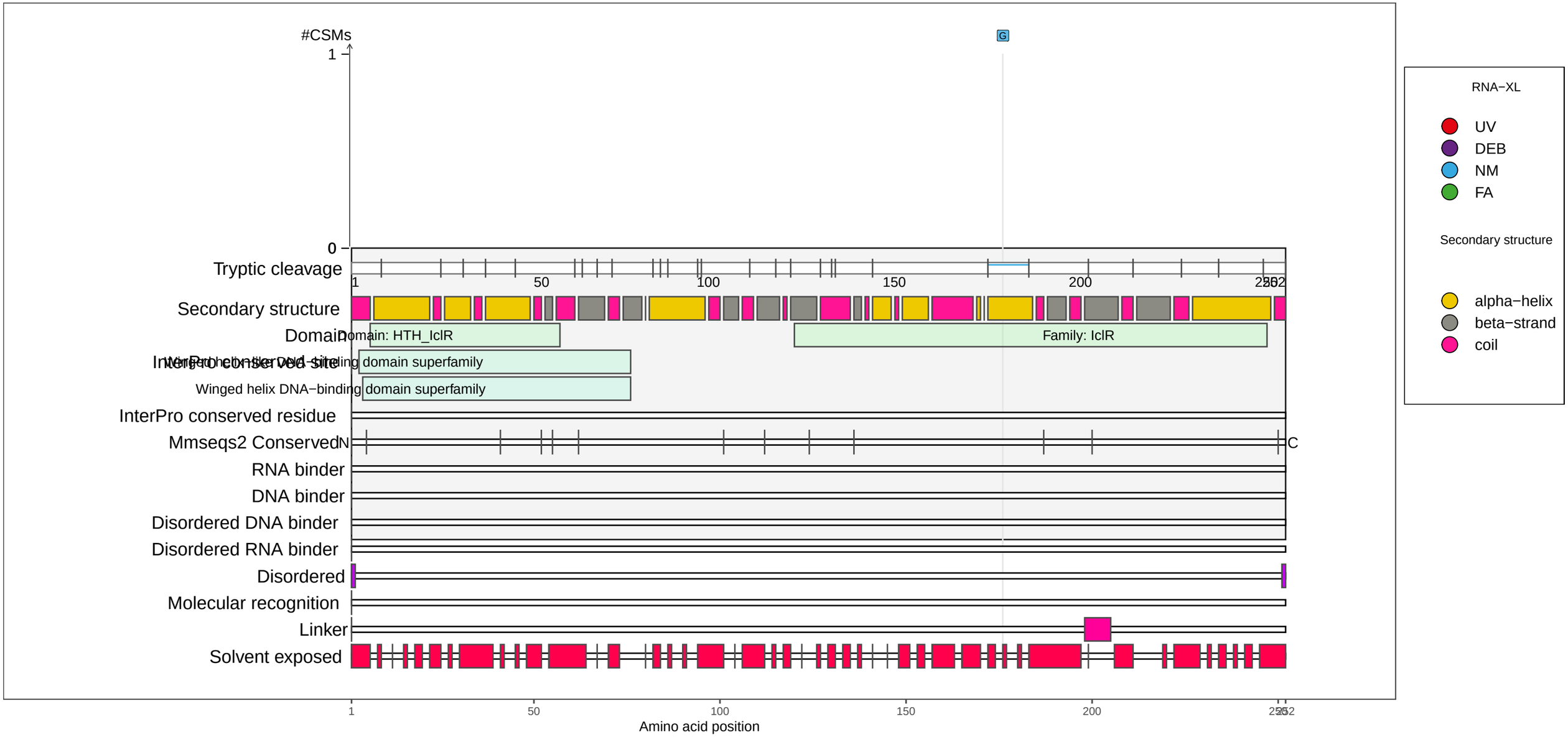
− RNA functions: not annotated



P77300
XYNR_ECOLI HTH−type transcriptional regulator XynR

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.83 (Q 44)

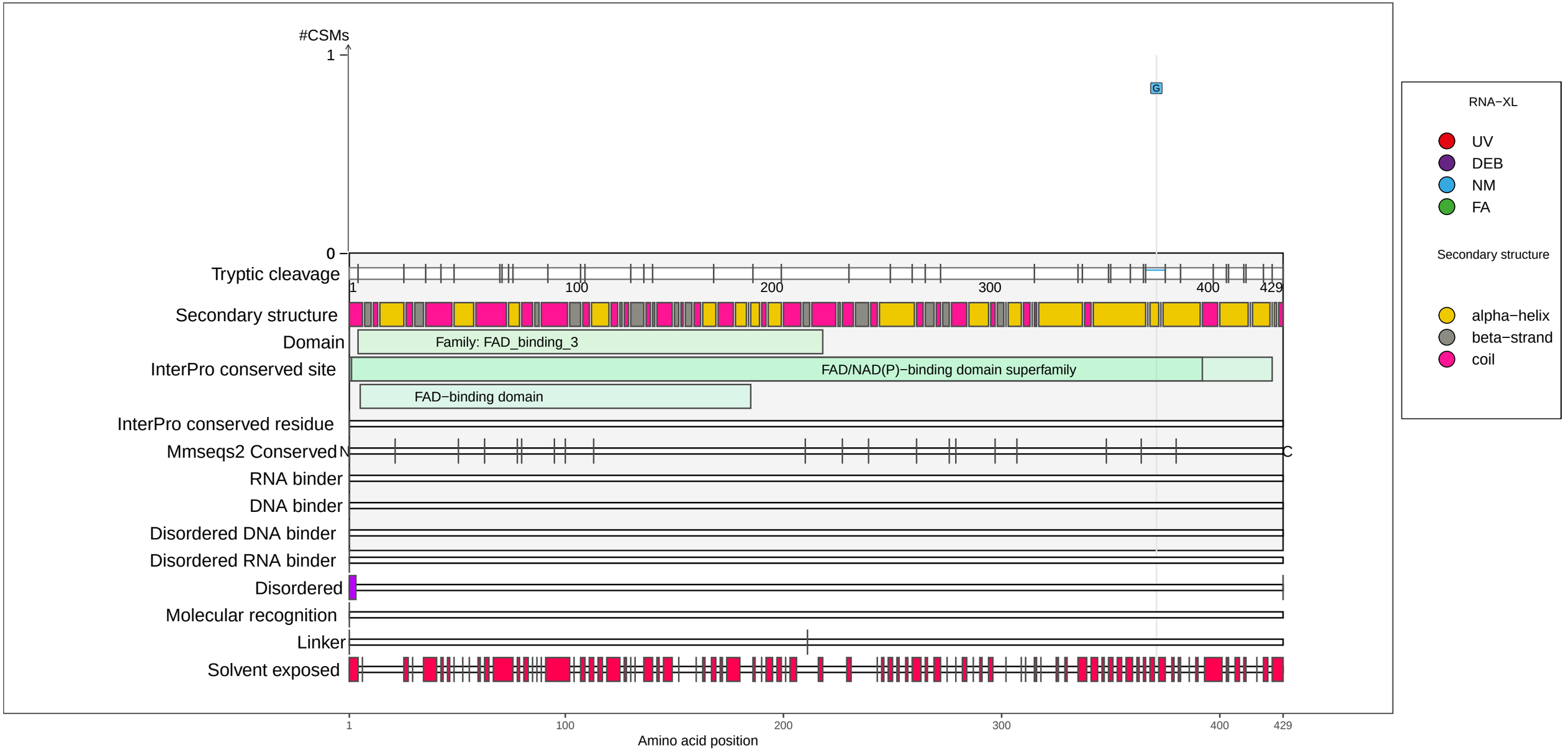
− RNA functions:
RNA biosynthetic process; RNA metabolic process



P77337
YDIS_ECOLI Probable electron transfer flavoprotein−quinone oxidoreductase YdiS

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.9 (Q 8)
PAXdb E.coli [ppm]: −1.85 (Q 2)

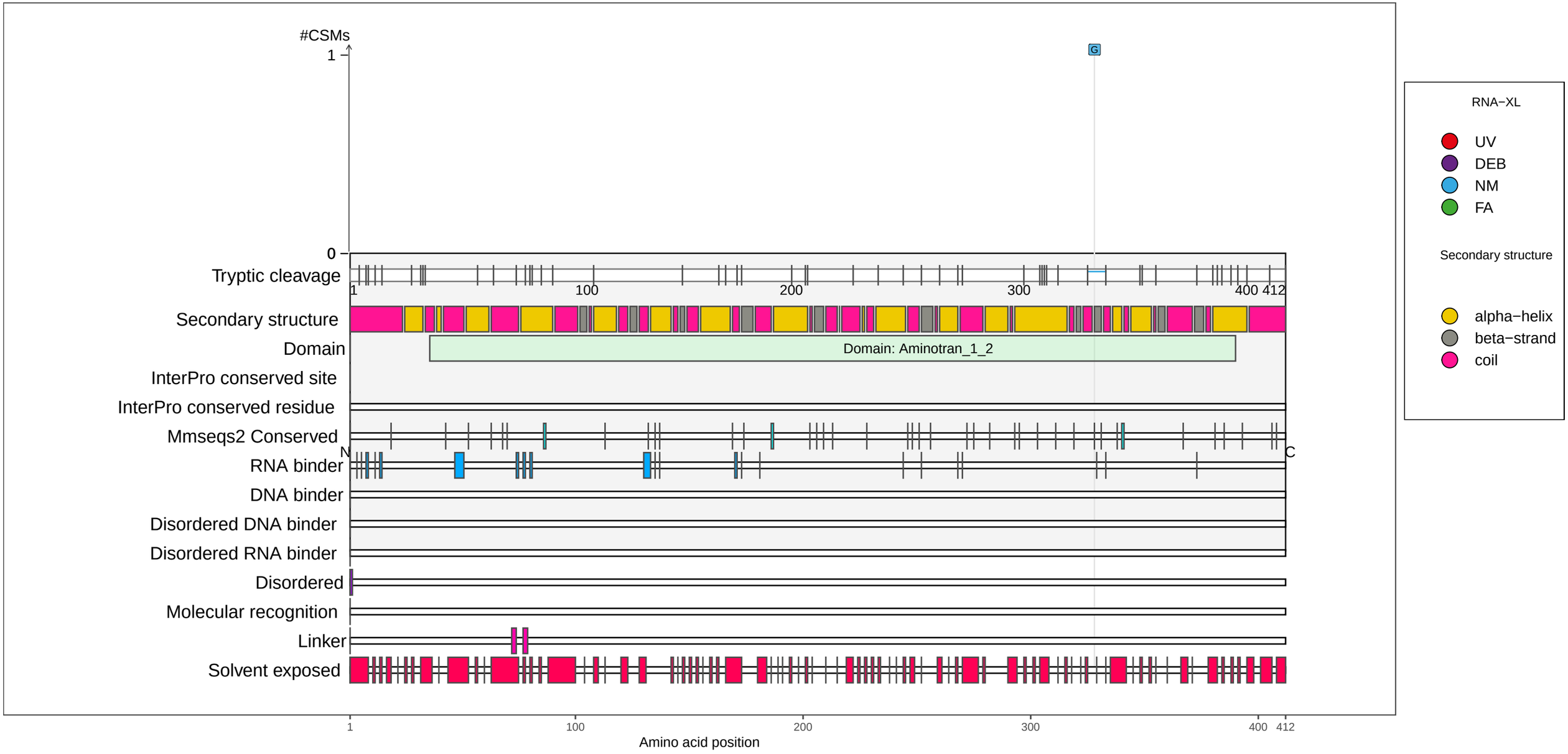
− RNA functions: not annotated



P77434
ALAC_ECOLI Glutamate−pyruvate aminotransferase AlaC

− Abundance:
tryptic [log10 Intensity]: 8.23 (Q 67)
PAXdb K12 strain [ppm]: 1.08 (Q 15)
PAXdb E.coli [ppm]: 1.55 (Q 61)

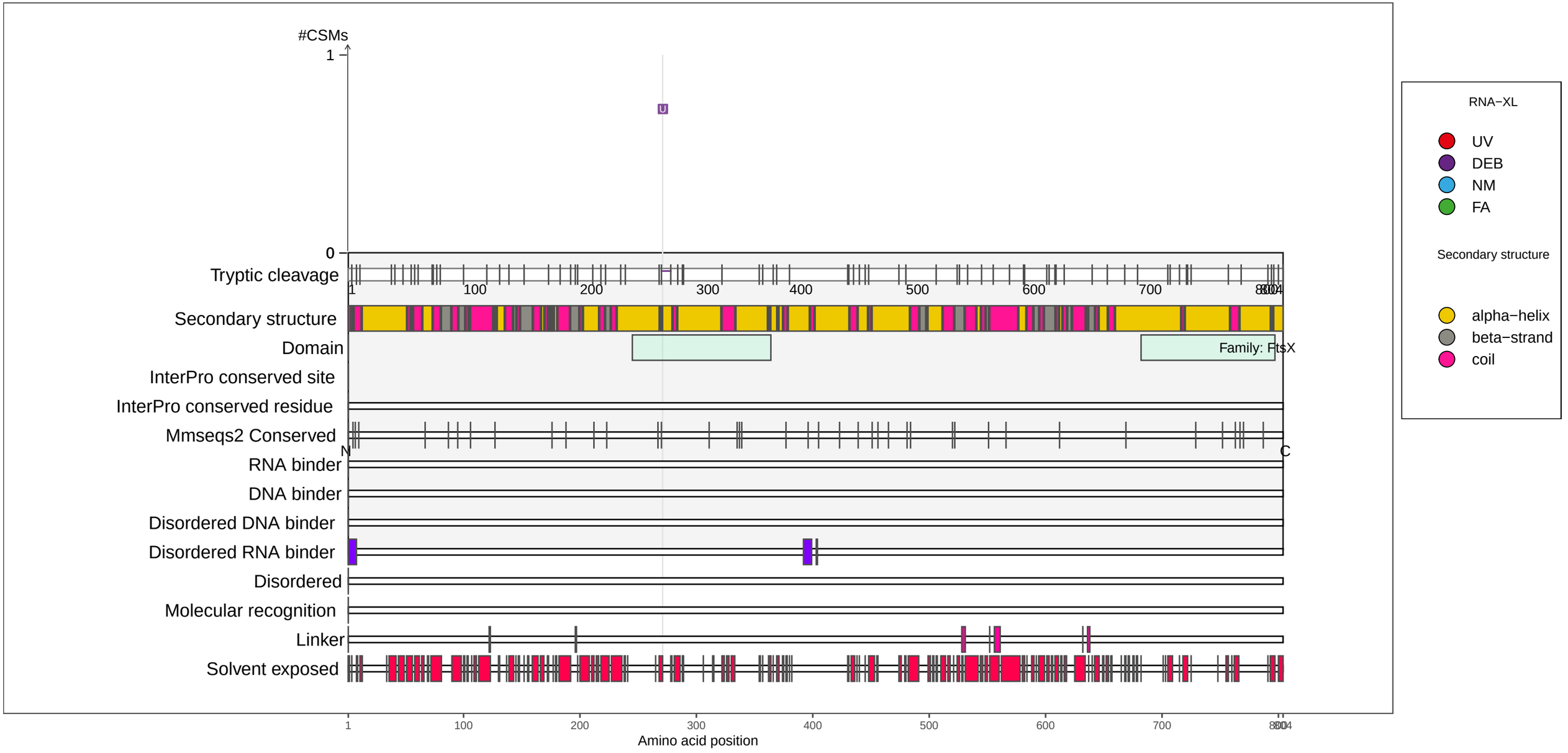
− RNA functions: not annotated



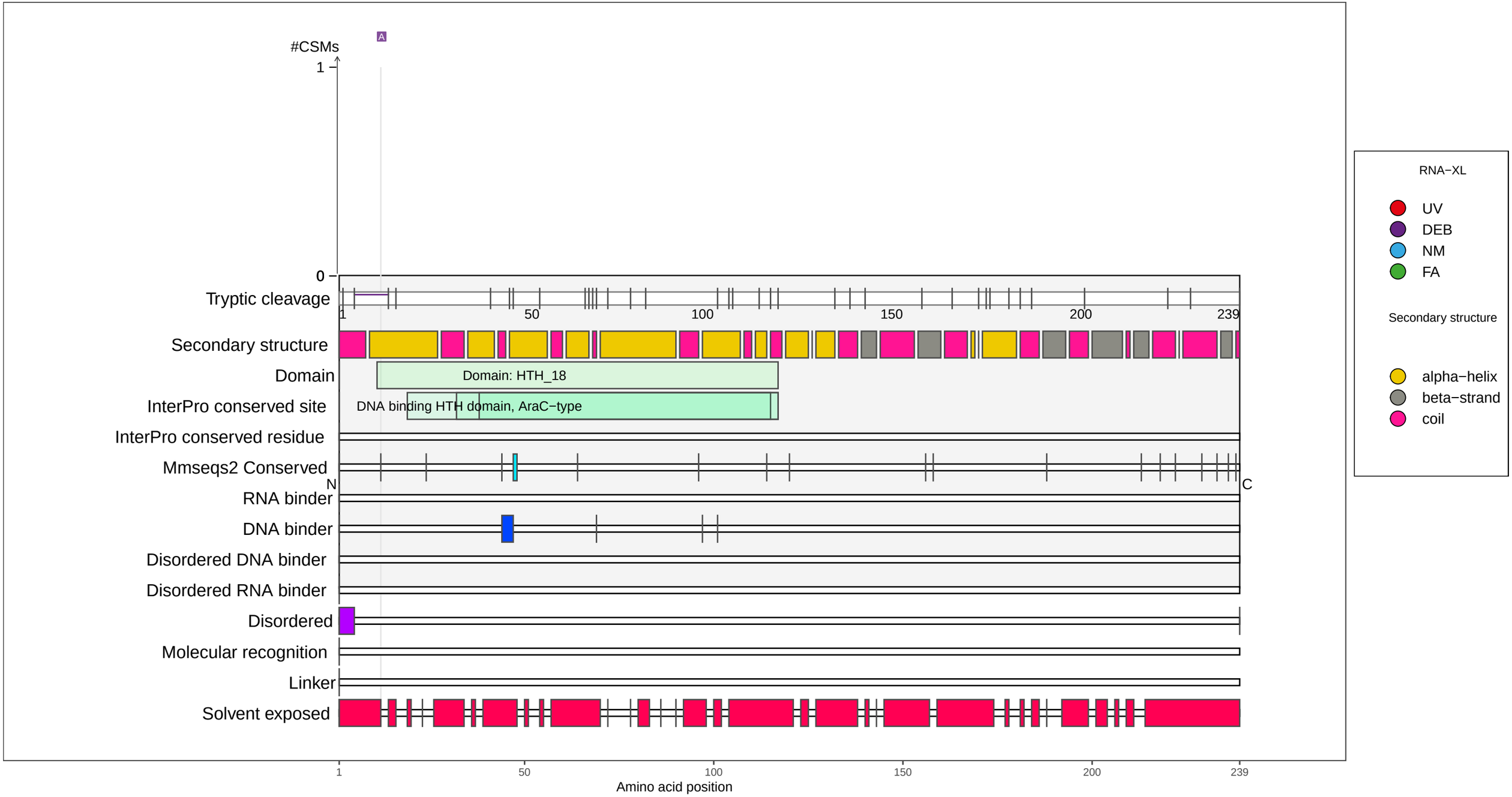
P77504
YBBP_ECOLI Uncharacterized ABC transporter permease YbbP

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 0.72 (Q 3)
PAXdb E.coli [ppm]: −0.04 (Q 24)

− RNA functions: not annotated



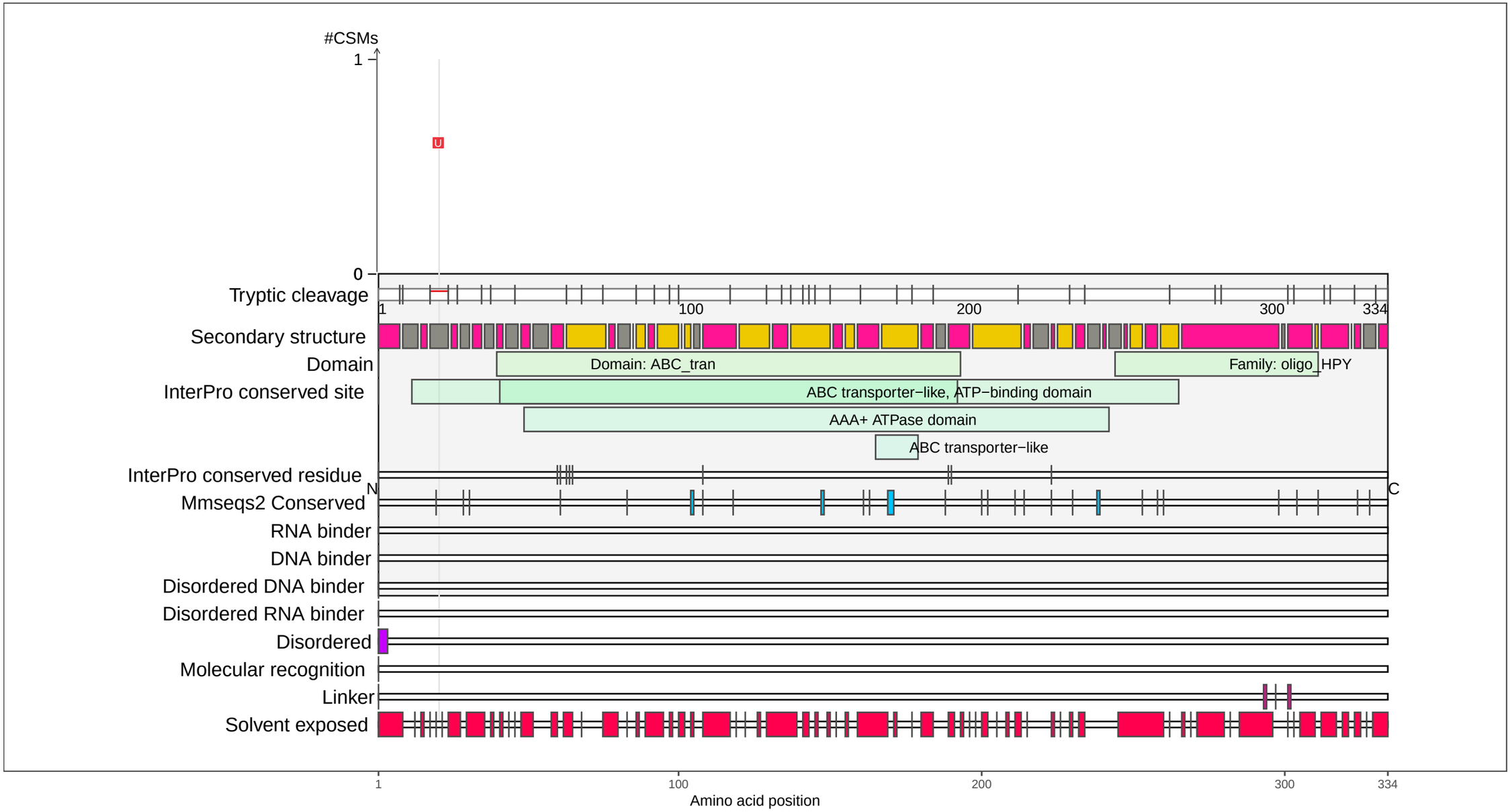
P77601
YKGA_ECOLI Putative HTH−type transcriptional regulator YkgA
− RNA functions: not annotated



P77737
OPPF_ECOLI Oligopeptide transport ATP−binding protein OppF

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: 1.39 (Q 32)
PAXdb E.coli [ppm]: 1.51 (Q 60)

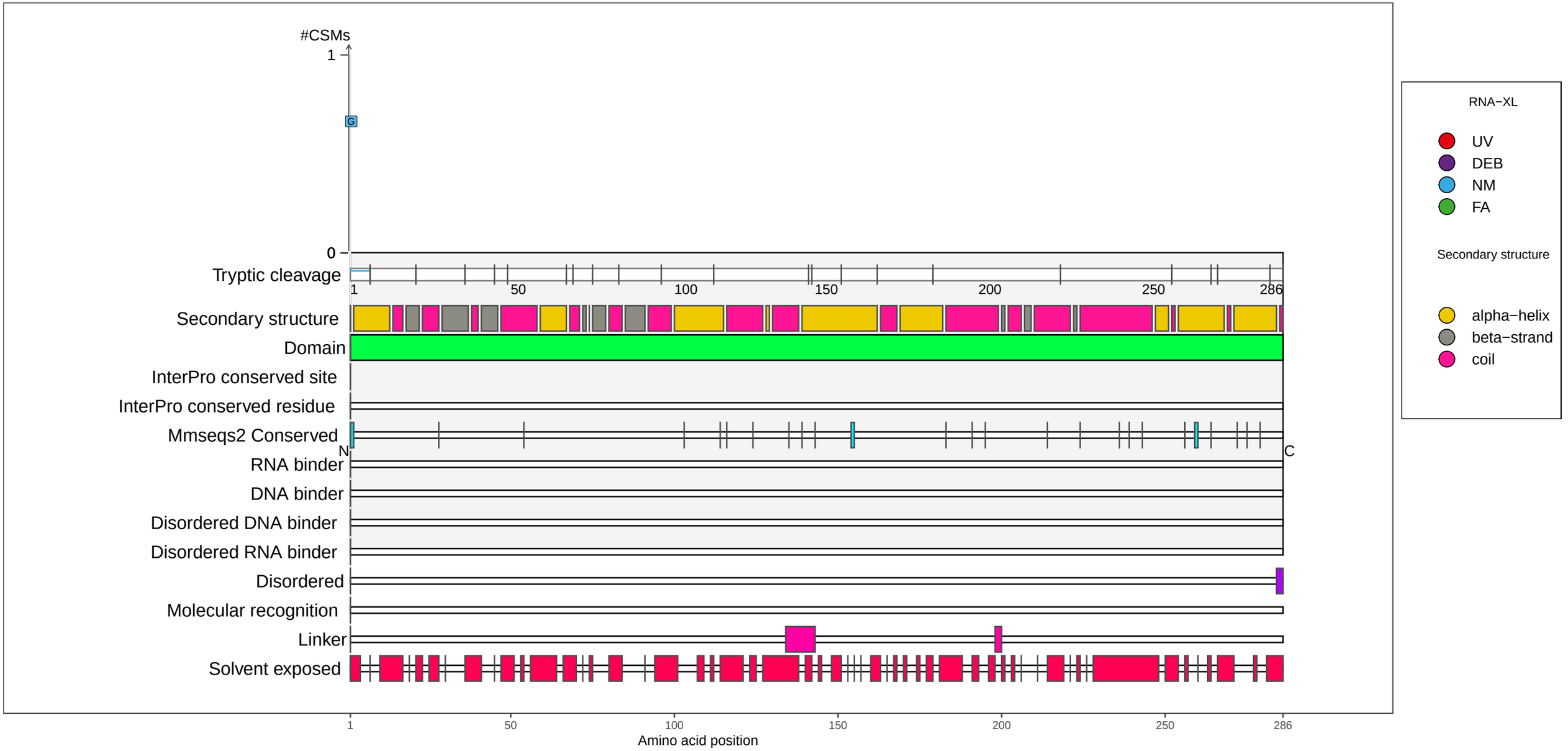
− RNA functions: not annotated



P77739
KT3K_ECOLI Probable ketoamine kinase YniA

− Abundance:
tryptic [log10 Intensity]: 8 (Q 58)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 2.26 (Q 79)

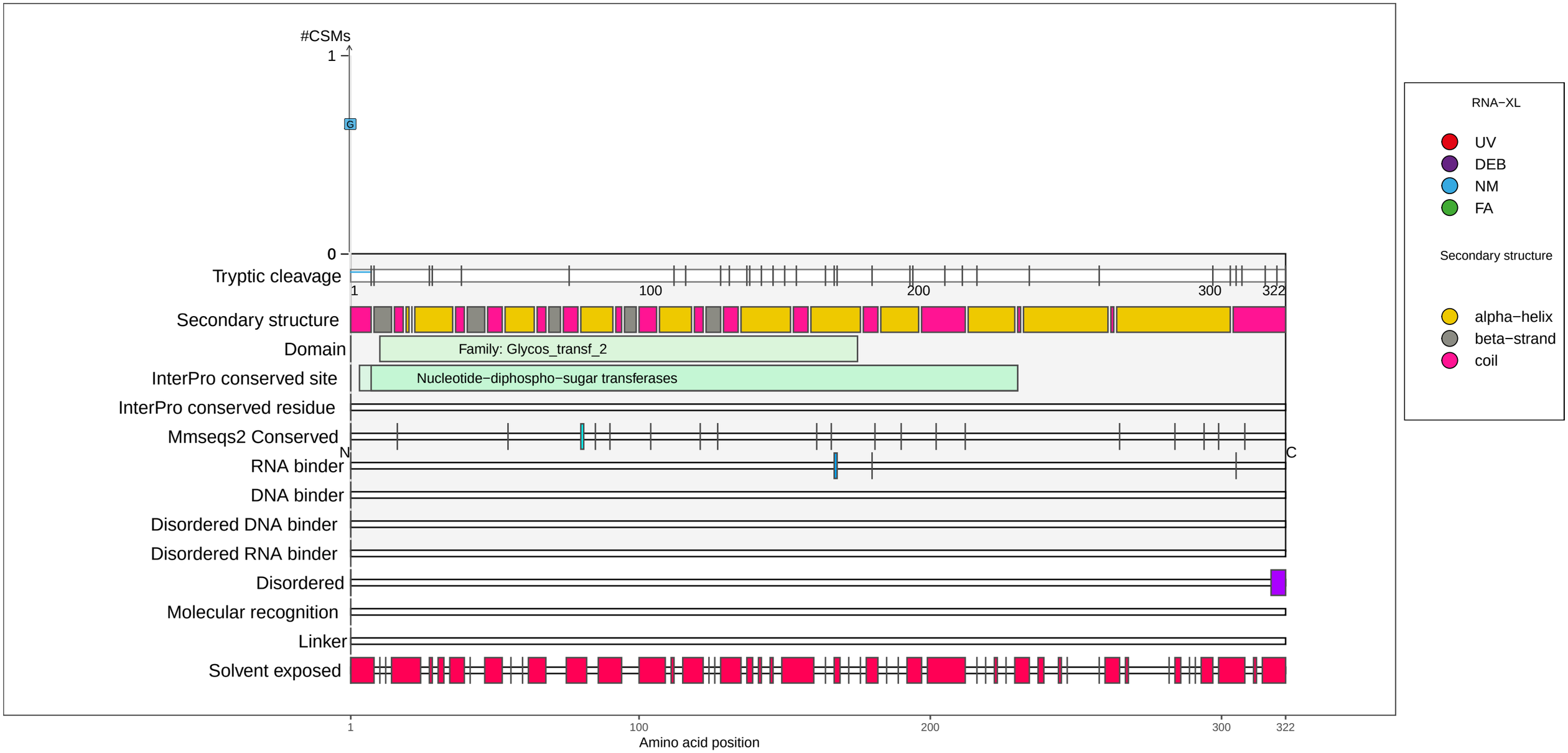
− RNA functions: not annotated



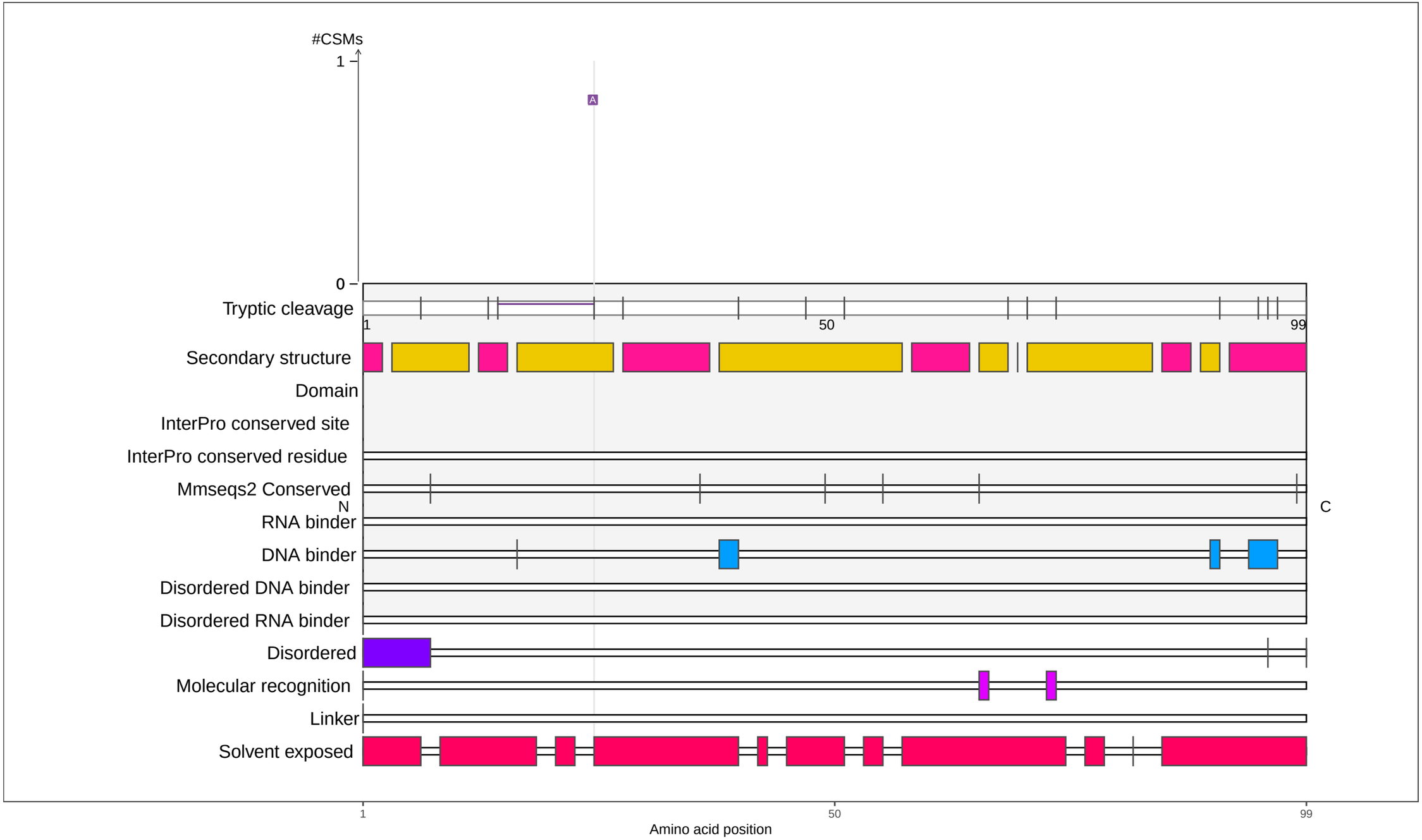
P77757
ARNC_ECOLI Undecaprenyl−phosphate 4−deoxy−4−formamido−L−arabinose transferase

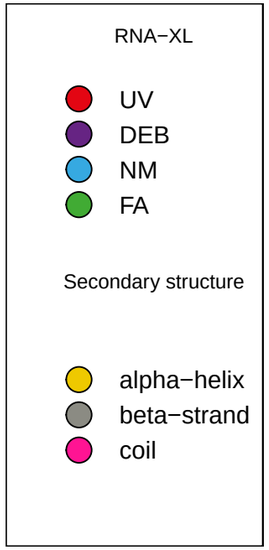
− Abundance:
tryptic [log10 Intensity]: 7.01 (Q 14)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.31 (Q 55)

− RNA functions: not annotated



Q46796
YGEP_ECOLI Putative protein YgeP
− RNA functions: not annotated

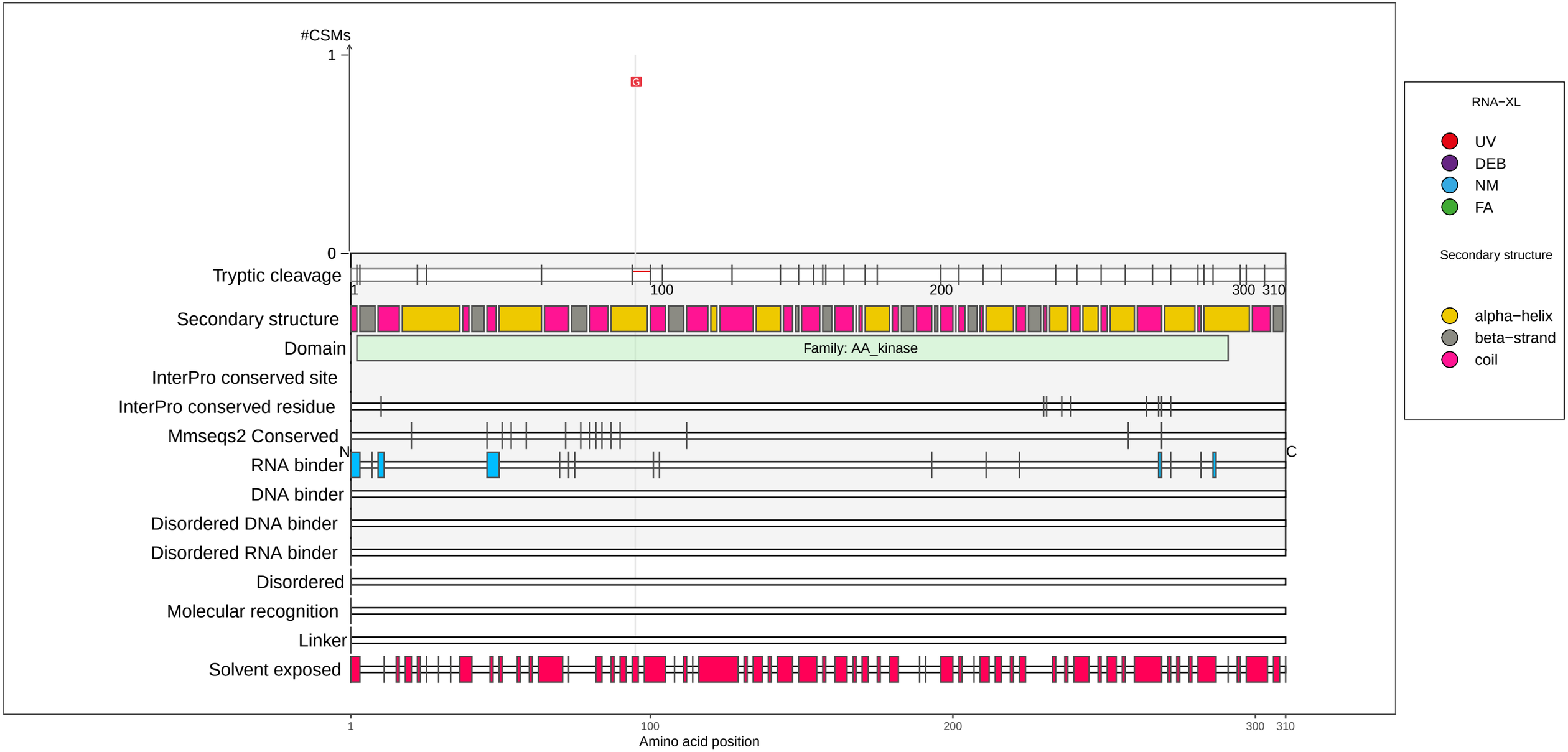




Q46807
ARCL_ECOLI Carbamate kinase−like protein YqeA

− Abundance:
tryptic [log10 Intensity]: NA (Q NA)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 1.16 (Q 51)

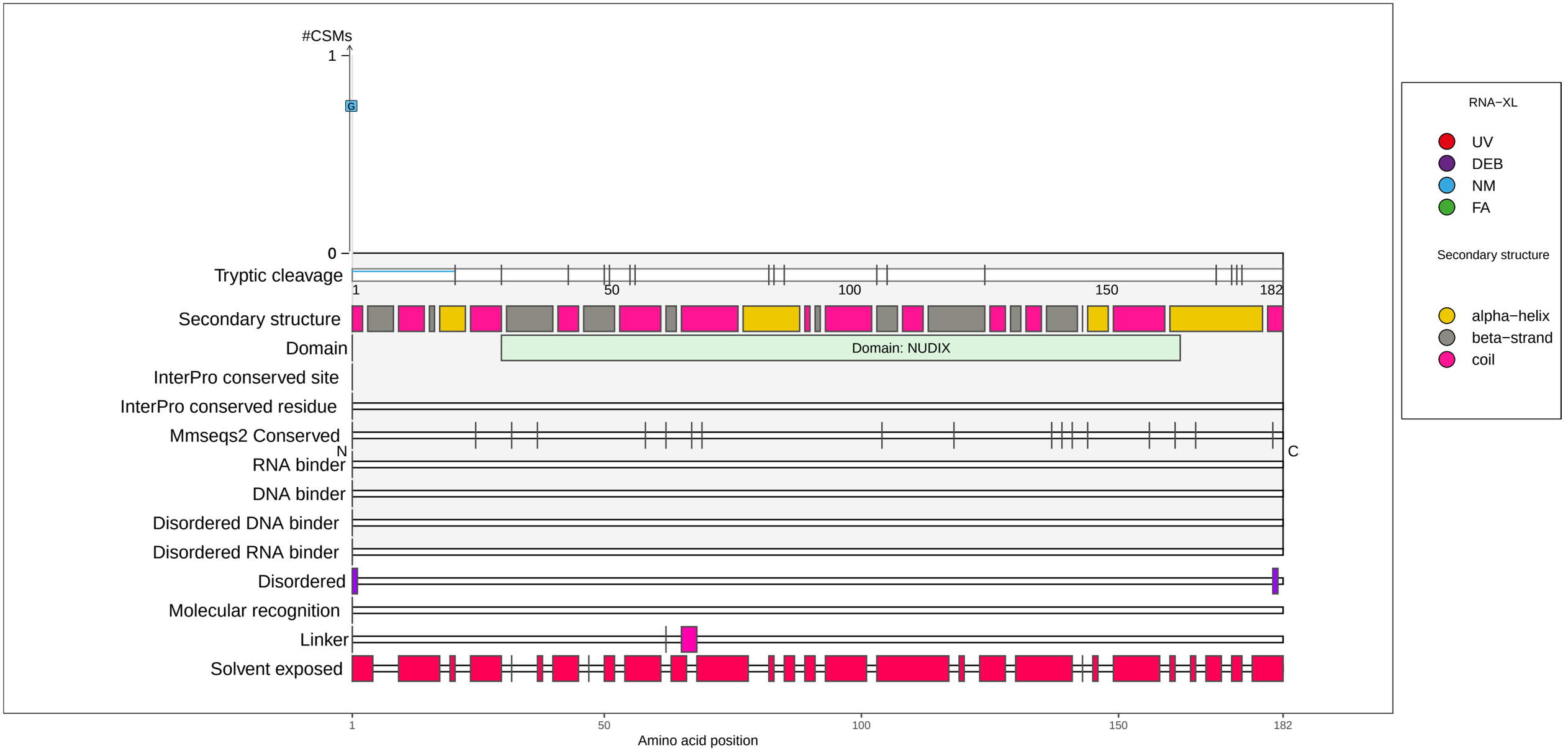
− RNA functions: not annotated



Q46822
IDI_ECOLI Isopentenyl−diphosphate Delta−isomerase

− Abundance:
tryptic [log10 Intensity]: 7.36 (Q 27)
PAXdb K12 strain [ppm]: NA (Q NA)
PAXdb E.coli [ppm]: 0.73 (Q 41)

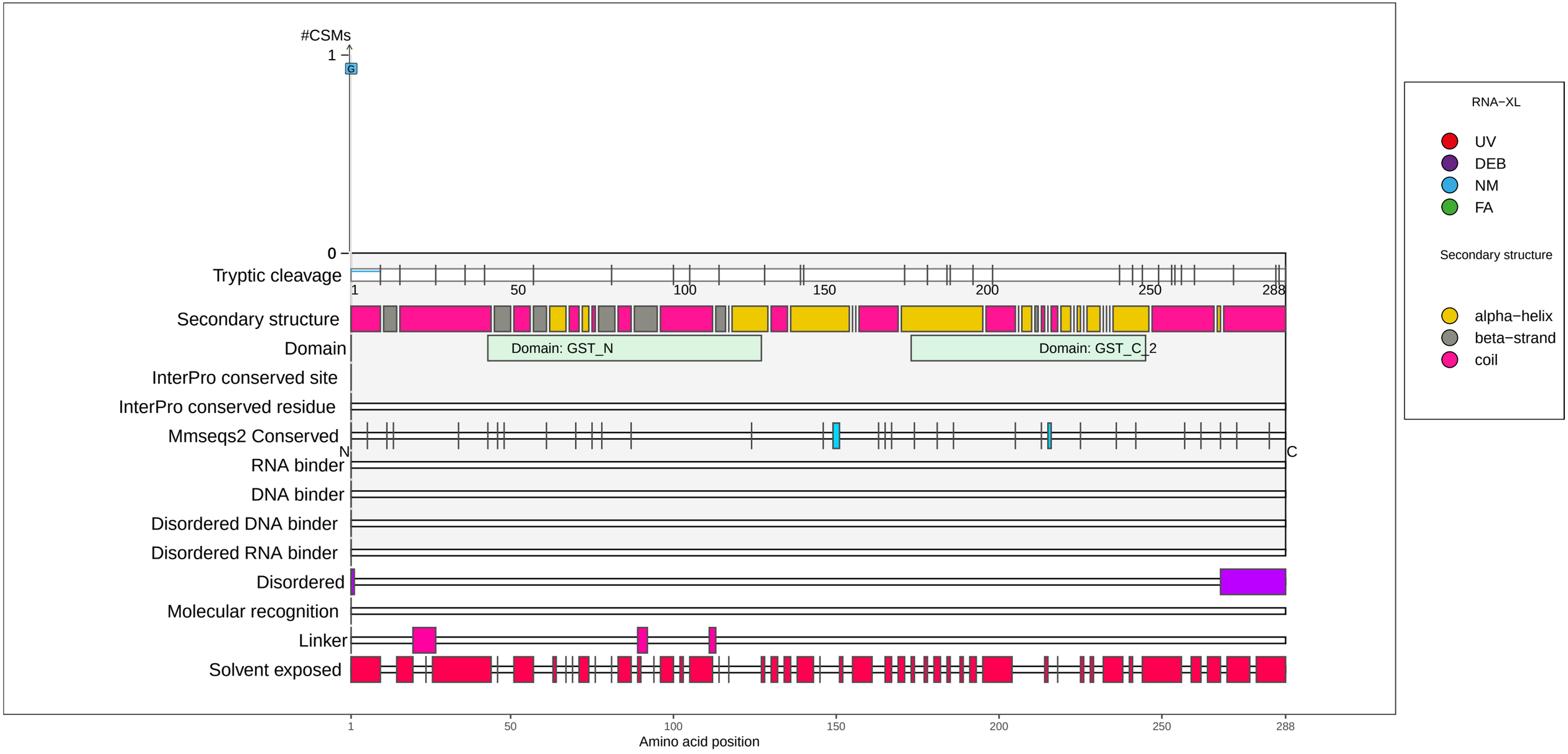
− RNA functions: not annotated



Q46845
YGHU_ECOLI Disulfide−bond oxidoreductase YghU

− Abundance:
tryptic [log10 Intensity]: 8.33 (Q 70)
PAXdb K12 strain [ppm]: 2.53 (Q 78)
PAXdb E.coli [ppm]: 2.57 (Q 87)

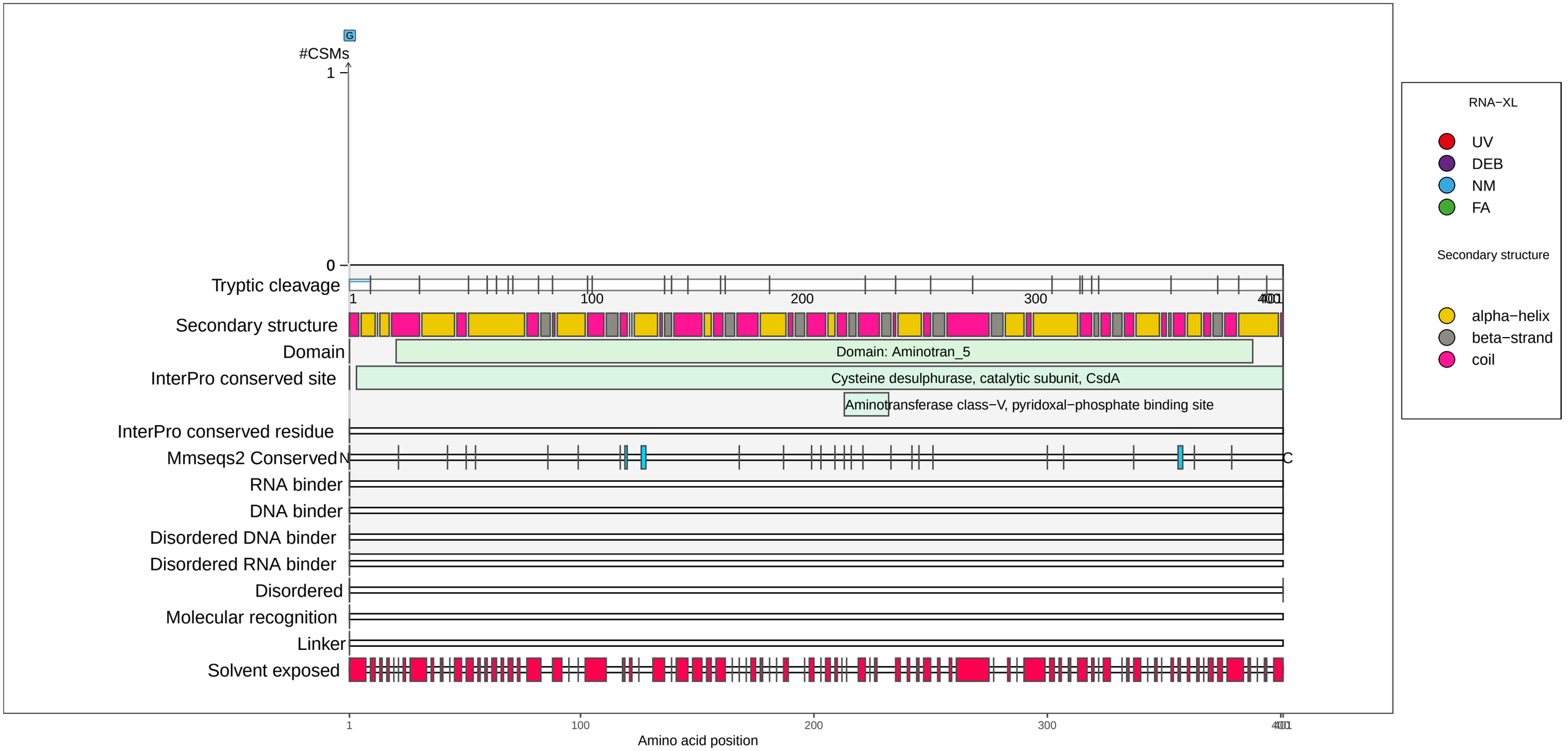
− RNA functions: not annotated



Q46925
CSDA_ECOLI Cysteine desulfurase CsdA

− Abundance:
tryptic [log10 Intensity]: 7.58 (Q 39)
PAXdb K12 strain [ppm]: 1.14 (Q 17)
PAXdb E.coli [ppm]: 1.43 (Q 58)

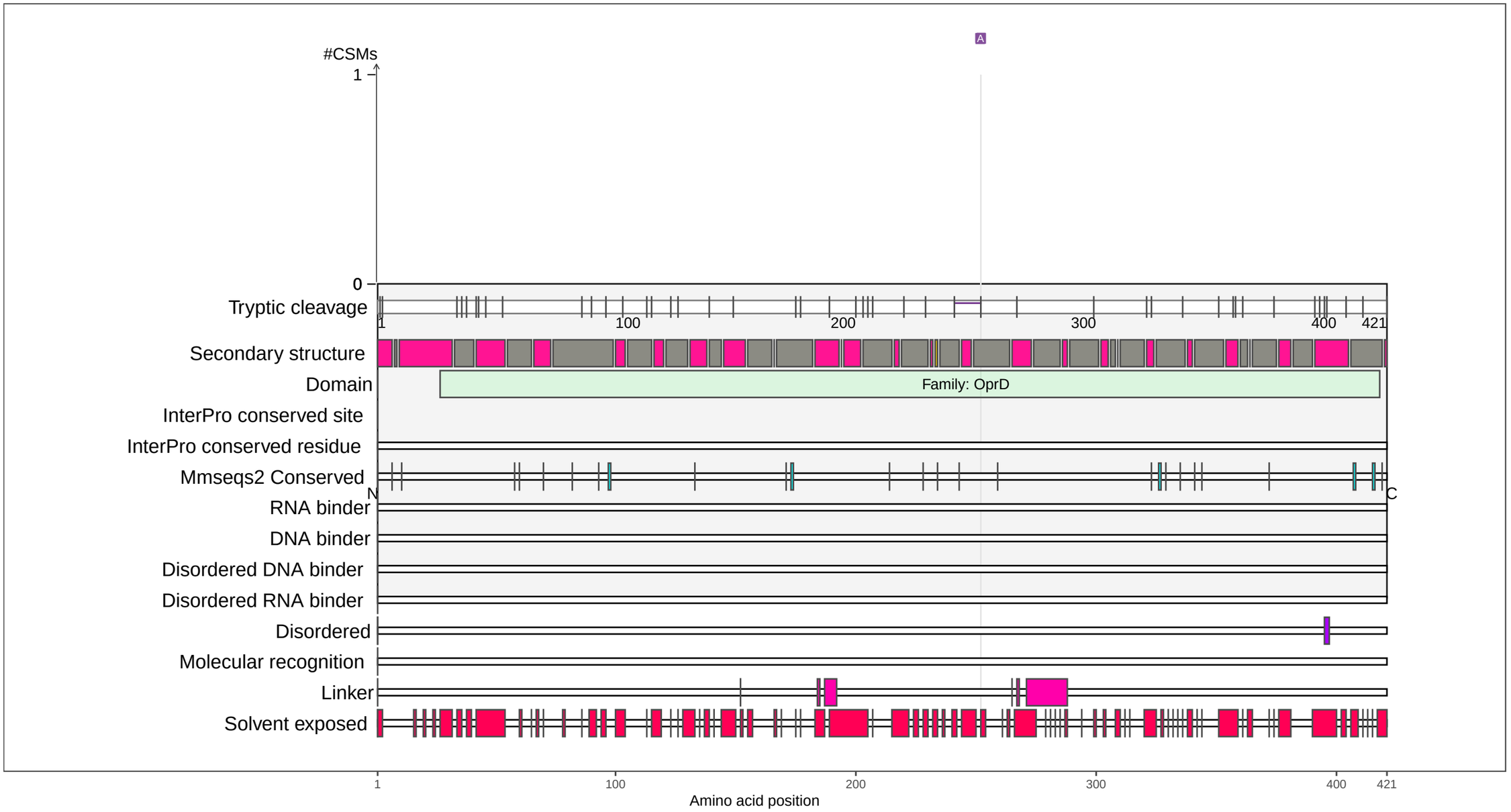
− RNA functions: not annotated



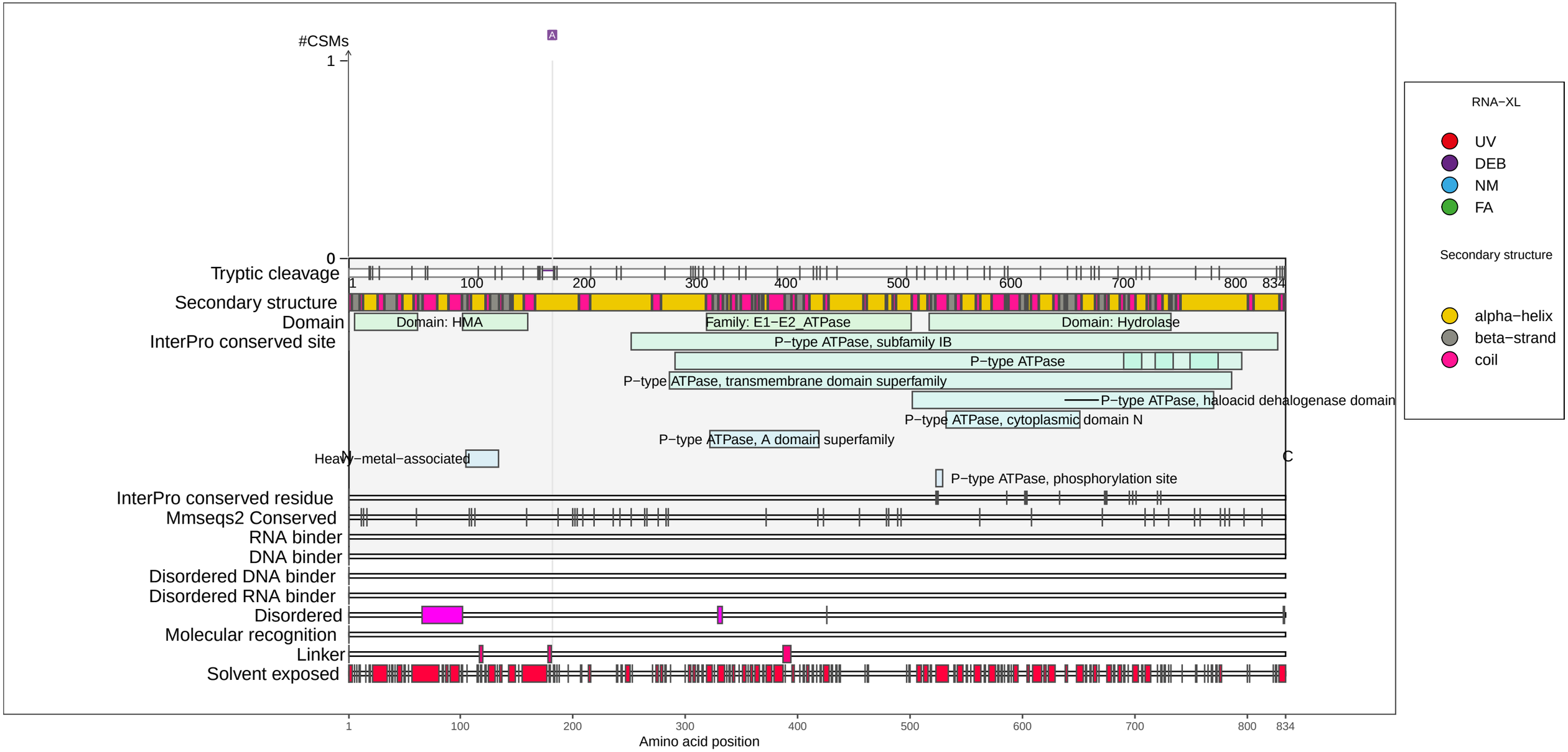
Q47706
UIDC_ECOLI Membrane−associated protein UidC

− Abundance:
tryptic [log10 Intensity]: 6.59 (Q 3)
PAXdb K12 strain [ppm]: 1.2 (Q 20)
PAXdb E.coli [ppm]: −0.99 (Q 9)

− RNA functions: not annotated



Q59385
COPA_ECOLI Copper−exporting P−type ATPase

− Abundance:
tryptic [log10 Intensity]: 7.45 (Q 33)
PAXdb K12 strain [ppm]: 2.17 (Q 66)
PAXdb E.coli [ppm]: 1.97 (Q 71)

− RNA functions: not annotated