wwPDB EM Validation Summary Report (i)

Oct 26, 2026 – 04:57 PM JST

PDB ID	:	26IQ / pdb_000026iq
EMDB ID	:	EMD-80685
Title	:	Structure of recombinant RyR2 in complex with Ryanozole in the open conformation (Ca2+ dataset)
Authors	:	Otori, Y.; Takeuchi, S.; Ogawa, H.
Deposited on	:	2026-05-01
Resolution	:	2.89 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

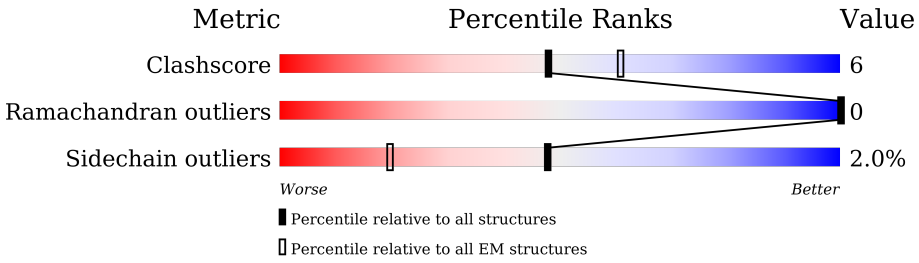
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

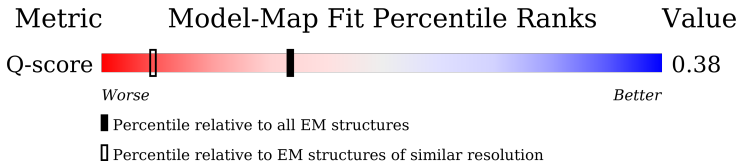
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12148 (2.39 - 3.39)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	4966	21% 59% 11% 30%
1	B	4966	21% 59% 11% 30%
1	C	4966	21% 59% 11% 30%
1	D	4966	21% 59% 11% 30%

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Mol	Chain	Length	Quality of chain
2	G	176	
2	H	176	
2	I	176	
2	J	176	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 228412 atoms, of which 113440 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ryanodine receptor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	3493	Total	C	H	N	O	S	0	0
			55424	17764	27527	4746	5197	190		
1	B	3493	Total	C	H	N	O	S	0	0
			55424	17764	27527	4746	5197	190		
1	C	3493	Total	C	H	N	O	S	0	0
			55424	17764	27527	4746	5197	190		
1	D	3493	Total	C	H	N	O	S	0	0
			55424	17764	27527	4746	5197	190		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	G	107	Total	C	H	N	O	S	0	0
			1640	516	821	144	155	4		
2	H	107	Total	C	H	N	O	S	0	0
			1640	516	821	144	155	4		
2	I	107	Total	C	H	N	O	S	0	0
			1640	516	821	144	155	4		
2	J	107	Total	C	H	N	O	S	0	0
			1640	516	821	144	155	4		

There are 276 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-67	MET	-	initiating methionine	UNP P68106
G	-66	GLY	-	expression tag	UNP P68106
G	-65	SER	-	expression tag	UNP P68106
G	-64	SER	-	expression tag	UNP P68106
G	-63	HIS	-	expression tag	UNP P68106
G	-62	HIS	-	expression tag	UNP P68106
G	-61	HIS	-	expression tag	UNP P68106
G	-60	HIS	-	expression tag	UNP P68106
G	-59	HIS	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-58	HIS	-	expression tag	UNP P68106
G	-57	SER	-	expression tag	UNP P68106
G	-56	SER	-	expression tag	UNP P68106
G	-55	GLY	-	expression tag	UNP P68106
G	-54	LEU	-	expression tag	UNP P68106
G	-53	VAL	-	expression tag	UNP P68106
G	-52	PRO	-	expression tag	UNP P68106
G	-51	ARG	-	expression tag	UNP P68106
G	-50	GLY	-	expression tag	UNP P68106
G	-49	SER	-	expression tag	UNP P68106
G	-48	HIS	-	expression tag	UNP P68106
G	-47	MET	-	expression tag	UNP P68106
G	-46	ALA	-	expression tag	UNP P68106
G	-45	SER	-	expression tag	UNP P68106
G	-44	MET	-	expression tag	UNP P68106
G	-43	ASP	-	expression tag	UNP P68106
G	-42	GLU	-	expression tag	UNP P68106
G	-41	LYS	-	expression tag	UNP P68106
G	-40	THR	-	expression tag	UNP P68106
G	-39	THR	-	expression tag	UNP P68106
G	-38	GLY	-	expression tag	UNP P68106
G	-37	TRP	-	expression tag	UNP P68106
G	-36	ARG	-	expression tag	UNP P68106
G	-35	GLY	-	expression tag	UNP P68106
G	-34	GLY	-	expression tag	UNP P68106
G	-33	HIS	-	expression tag	UNP P68106
G	-32	VAL	-	expression tag	UNP P68106
G	-31	VAL	-	expression tag	UNP P68106
G	-30	GLU	-	expression tag	UNP P68106
G	-29	GLY	-	expression tag	UNP P68106
G	-28	LEU	-	expression tag	UNP P68106
G	-27	ALA	-	expression tag	UNP P68106
G	-26	GLY	-	expression tag	UNP P68106
G	-25	GLU	-	expression tag	UNP P68106
G	-24	LEU	-	expression tag	UNP P68106
G	-23	GLU	-	expression tag	UNP P68106
G	-22	GLN	-	expression tag	UNP P68106
G	-21	LEU	-	expression tag	UNP P68106
G	-20	ARG	-	expression tag	UNP P68106
G	-19	ALA	-	expression tag	UNP P68106
G	-18	ARG	-	expression tag	UNP P68106
G	-17	LEU	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-16	GLU	-	expression tag	UNP P68106
G	-15	HIS	-	expression tag	UNP P68106
G	-14	HIS	-	expression tag	UNP P68106
G	-13	PRO	-	expression tag	UNP P68106
G	-12	GLN	-	expression tag	UNP P68106
G	-11	GLY	-	expression tag	UNP P68106
G	-10	GLN	-	expression tag	UNP P68106
G	-9	ARG	-	expression tag	UNP P68106
G	-8	GLU	-	expression tag	UNP P68106
G	-7	PRO	-	expression tag	UNP P68106
G	-6	GLY	-	expression tag	UNP P68106
G	-5	SER	-	expression tag	UNP P68106
G	-4	GLY	-	expression tag	UNP P68106
G	-3	GLY	-	expression tag	UNP P68106
G	-2	SER	-	expression tag	UNP P68106
G	-1	GLY	-	expression tag	UNP P68106
G	0	GLY	-	expression tag	UNP P68106
G	1	THR	-	expression tag	UNP P68106
H	-67	MET	-	initiating methionine	UNP P68106
H	-66	GLY	-	expression tag	UNP P68106
H	-65	SER	-	expression tag	UNP P68106
H	-64	SER	-	expression tag	UNP P68106
H	-63	HIS	-	expression tag	UNP P68106
H	-62	HIS	-	expression tag	UNP P68106
H	-61	HIS	-	expression tag	UNP P68106
H	-60	HIS	-	expression tag	UNP P68106
H	-59	HIS	-	expression tag	UNP P68106
H	-58	HIS	-	expression tag	UNP P68106
H	-57	SER	-	expression tag	UNP P68106
H	-56	SER	-	expression tag	UNP P68106
H	-55	GLY	-	expression tag	UNP P68106
H	-54	LEU	-	expression tag	UNP P68106
H	-53	VAL	-	expression tag	UNP P68106
H	-52	PRO	-	expression tag	UNP P68106
H	-51	ARG	-	expression tag	UNP P68106
H	-50	GLY	-	expression tag	UNP P68106
H	-49	SER	-	expression tag	UNP P68106
H	-48	HIS	-	expression tag	UNP P68106
H	-47	MET	-	expression tag	UNP P68106
H	-46	ALA	-	expression tag	UNP P68106
H	-45	SER	-	expression tag	UNP P68106
H	-44	MET	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-43	ASP	-	expression tag	UNP P68106
H	-42	GLU	-	expression tag	UNP P68106
H	-41	LYS	-	expression tag	UNP P68106
H	-40	THR	-	expression tag	UNP P68106
H	-39	THR	-	expression tag	UNP P68106
H	-38	GLY	-	expression tag	UNP P68106
H	-37	TRP	-	expression tag	UNP P68106
H	-36	ARG	-	expression tag	UNP P68106
H	-35	GLY	-	expression tag	UNP P68106
H	-34	GLY	-	expression tag	UNP P68106
H	-33	HIS	-	expression tag	UNP P68106
H	-32	VAL	-	expression tag	UNP P68106
H	-31	VAL	-	expression tag	UNP P68106
H	-30	GLU	-	expression tag	UNP P68106
H	-29	GLY	-	expression tag	UNP P68106
H	-28	LEU	-	expression tag	UNP P68106
H	-27	ALA	-	expression tag	UNP P68106
H	-26	GLY	-	expression tag	UNP P68106
H	-25	GLU	-	expression tag	UNP P68106
H	-24	LEU	-	expression tag	UNP P68106
H	-23	GLU	-	expression tag	UNP P68106
H	-22	GLN	-	expression tag	UNP P68106
H	-21	LEU	-	expression tag	UNP P68106
H	-20	ARG	-	expression tag	UNP P68106
H	-19	ALA	-	expression tag	UNP P68106
H	-18	ARG	-	expression tag	UNP P68106
H	-17	LEU	-	expression tag	UNP P68106
H	-16	GLU	-	expression tag	UNP P68106
H	-15	HIS	-	expression tag	UNP P68106
H	-14	HIS	-	expression tag	UNP P68106
H	-13	PRO	-	expression tag	UNP P68106
H	-12	GLN	-	expression tag	UNP P68106
H	-11	GLY	-	expression tag	UNP P68106
H	-10	GLN	-	expression tag	UNP P68106
H	-9	ARG	-	expression tag	UNP P68106
H	-8	GLU	-	expression tag	UNP P68106
H	-7	PRO	-	expression tag	UNP P68106
H	-6	GLY	-	expression tag	UNP P68106
H	-5	SER	-	expression tag	UNP P68106
H	-4	GLY	-	expression tag	UNP P68106
H	-3	GLY	-	expression tag	UNP P68106
H	-2	SER	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	GLY	-	expression tag	UNP P68106
H	0	GLY	-	expression tag	UNP P68106
H	1	THR	-	expression tag	UNP P68106
I	-67	MET	-	initiating methionine	UNP P68106
I	-66	GLY	-	expression tag	UNP P68106
I	-65	SER	-	expression tag	UNP P68106
I	-64	SER	-	expression tag	UNP P68106
I	-63	HIS	-	expression tag	UNP P68106
I	-62	HIS	-	expression tag	UNP P68106
I	-61	HIS	-	expression tag	UNP P68106
I	-60	HIS	-	expression tag	UNP P68106
I	-59	HIS	-	expression tag	UNP P68106
I	-58	HIS	-	expression tag	UNP P68106
I	-57	SER	-	expression tag	UNP P68106
I	-56	SER	-	expression tag	UNP P68106
I	-55	GLY	-	expression tag	UNP P68106
I	-54	LEU	-	expression tag	UNP P68106
I	-53	VAL	-	expression tag	UNP P68106
I	-52	PRO	-	expression tag	UNP P68106
I	-51	ARG	-	expression tag	UNP P68106
I	-50	GLY	-	expression tag	UNP P68106
I	-49	SER	-	expression tag	UNP P68106
I	-48	HIS	-	expression tag	UNP P68106
I	-47	MET	-	expression tag	UNP P68106
I	-46	ALA	-	expression tag	UNP P68106
I	-45	SER	-	expression tag	UNP P68106
I	-44	MET	-	expression tag	UNP P68106
I	-43	ASP	-	expression tag	UNP P68106
I	-42	GLU	-	expression tag	UNP P68106
I	-41	LYS	-	expression tag	UNP P68106
I	-40	THR	-	expression tag	UNP P68106
I	-39	THR	-	expression tag	UNP P68106
I	-38	GLY	-	expression tag	UNP P68106
I	-37	TRP	-	expression tag	UNP P68106
I	-36	ARG	-	expression tag	UNP P68106
I	-35	GLY	-	expression tag	UNP P68106
I	-34	GLY	-	expression tag	UNP P68106
I	-33	HIS	-	expression tag	UNP P68106
I	-32	VAL	-	expression tag	UNP P68106
I	-31	VAL	-	expression tag	UNP P68106
I	-30	GLU	-	expression tag	UNP P68106
I	-29	GLY	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-28	LEU	-	expression tag	UNP P68106
I	-27	ALA	-	expression tag	UNP P68106
I	-26	GLY	-	expression tag	UNP P68106
I	-25	GLU	-	expression tag	UNP P68106
I	-24	LEU	-	expression tag	UNP P68106
I	-23	GLU	-	expression tag	UNP P68106
I	-22	GLN	-	expression tag	UNP P68106
I	-21	LEU	-	expression tag	UNP P68106
I	-20	ARG	-	expression tag	UNP P68106
I	-19	ALA	-	expression tag	UNP P68106
I	-18	ARG	-	expression tag	UNP P68106
I	-17	LEU	-	expression tag	UNP P68106
I	-16	GLU	-	expression tag	UNP P68106
I	-15	HIS	-	expression tag	UNP P68106
I	-14	HIS	-	expression tag	UNP P68106
I	-13	PRO	-	expression tag	UNP P68106
I	-12	GLN	-	expression tag	UNP P68106
I	-11	GLY	-	expression tag	UNP P68106
I	-10	GLN	-	expression tag	UNP P68106
I	-9	ARG	-	expression tag	UNP P68106
I	-8	GLU	-	expression tag	UNP P68106
I	-7	PRO	-	expression tag	UNP P68106
I	-6	GLY	-	expression tag	UNP P68106
I	-5	SER	-	expression tag	UNP P68106
I	-4	GLY	-	expression tag	UNP P68106
I	-3	GLY	-	expression tag	UNP P68106
I	-2	SER	-	expression tag	UNP P68106
I	-1	GLY	-	expression tag	UNP P68106
I	0	GLY	-	expression tag	UNP P68106
I	1	THR	-	expression tag	UNP P68106
J	-67	MET	-	initiating methionine	UNP P68106
J	-66	GLY	-	expression tag	UNP P68106
J	-65	SER	-	expression tag	UNP P68106
J	-64	SER	-	expression tag	UNP P68106
J	-63	HIS	-	expression tag	UNP P68106
J	-62	HIS	-	expression tag	UNP P68106
J	-61	HIS	-	expression tag	UNP P68106
J	-60	HIS	-	expression tag	UNP P68106
J	-59	HIS	-	expression tag	UNP P68106
J	-58	HIS	-	expression tag	UNP P68106
J	-57	SER	-	expression tag	UNP P68106
J	-56	SER	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-55	GLY	-	expression tag	UNP P68106
J	-54	LEU	-	expression tag	UNP P68106
J	-53	VAL	-	expression tag	UNP P68106
J	-52	PRO	-	expression tag	UNP P68106
J	-51	ARG	-	expression tag	UNP P68106
J	-50	GLY	-	expression tag	UNP P68106
J	-49	SER	-	expression tag	UNP P68106
J	-48	HIS	-	expression tag	UNP P68106
J	-47	MET	-	expression tag	UNP P68106
J	-46	ALA	-	expression tag	UNP P68106
J	-45	SER	-	expression tag	UNP P68106
J	-44	MET	-	expression tag	UNP P68106
J	-43	ASP	-	expression tag	UNP P68106
J	-42	GLU	-	expression tag	UNP P68106
J	-41	LYS	-	expression tag	UNP P68106
J	-40	THR	-	expression tag	UNP P68106
J	-39	THR	-	expression tag	UNP P68106
J	-38	GLY	-	expression tag	UNP P68106
J	-37	TRP	-	expression tag	UNP P68106
J	-36	ARG	-	expression tag	UNP P68106
J	-35	GLY	-	expression tag	UNP P68106
J	-34	GLY	-	expression tag	UNP P68106
J	-33	HIS	-	expression tag	UNP P68106
J	-32	VAL	-	expression tag	UNP P68106
J	-31	VAL	-	expression tag	UNP P68106
J	-30	GLU	-	expression tag	UNP P68106
J	-29	GLY	-	expression tag	UNP P68106
J	-28	LEU	-	expression tag	UNP P68106
J	-27	ALA	-	expression tag	UNP P68106
J	-26	GLY	-	expression tag	UNP P68106
J	-25	GLU	-	expression tag	UNP P68106
J	-24	LEU	-	expression tag	UNP P68106
J	-23	GLU	-	expression tag	UNP P68106
J	-22	GLN	-	expression tag	UNP P68106
J	-21	LEU	-	expression tag	UNP P68106
J	-20	ARG	-	expression tag	UNP P68106
J	-19	ALA	-	expression tag	UNP P68106
J	-18	ARG	-	expression tag	UNP P68106
J	-17	LEU	-	expression tag	UNP P68106
J	-16	GLU	-	expression tag	UNP P68106
J	-15	HIS	-	expression tag	UNP P68106
J	-14	HIS	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-13	PRO	-	expression tag	UNP P68106
J	-12	GLN	-	expression tag	UNP P68106
J	-11	GLY	-	expression tag	UNP P68106
J	-10	GLN	-	expression tag	UNP P68106
J	-9	ARG	-	expression tag	UNP P68106
J	-8	GLU	-	expression tag	UNP P68106
J	-7	PRO	-	expression tag	UNP P68106
J	-6	GLY	-	expression tag	UNP P68106
J	-5	SER	-	expression tag	UNP P68106
J	-4	GLY	-	expression tag	UNP P68106
J	-3	GLY	-	expression tag	UNP P68106
J	-2	SER	-	expression tag	UNP P68106
J	-1	GLY	-	expression tag	UNP P68106
J	0	GLY	-	expression tag	UNP P68106
J	1	THR	-	expression tag	UNP P68106

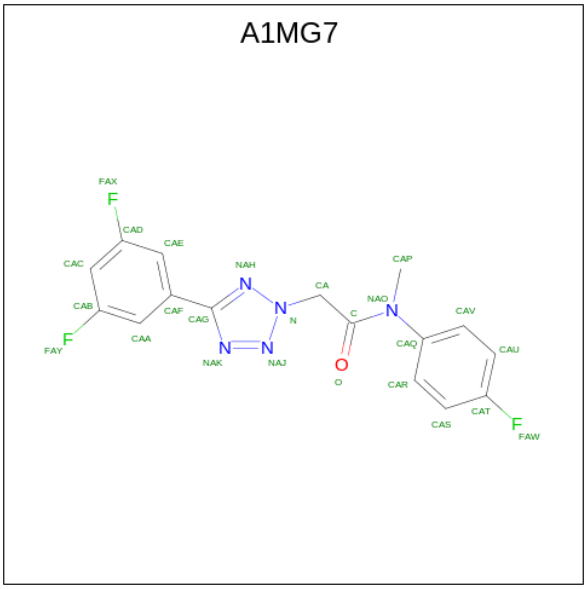
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total Zn 1 1	0
3	B	1	Total Zn 1 1	0
3	C	1	Total Zn 1 1	0
3	D	1	Total Zn 1 1	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
4	A	1	Total Ca 1 1	0
4	B	1	Total Ca 1 1	0
4	C	1	Total Ca 1 1	0
4	D	1	Total Ca 1 1	0

- Molecule 5 is Ryanozole (CCD ID: A1MG7) (formula: $C_{16}H_{12}F_3N_5O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total	C	F	H	N	O	0
			37	16	3	12	5	1	
5	B	1	Total	C	F	H	N	O	0
			37	16	3	12	5	1	
5	C	1	Total	C	F	H	N	O	0
			37	16	3	12	5	1	
5	D	1	Total	C	F	H	N	O	0
			37	16	3	12	5	1	

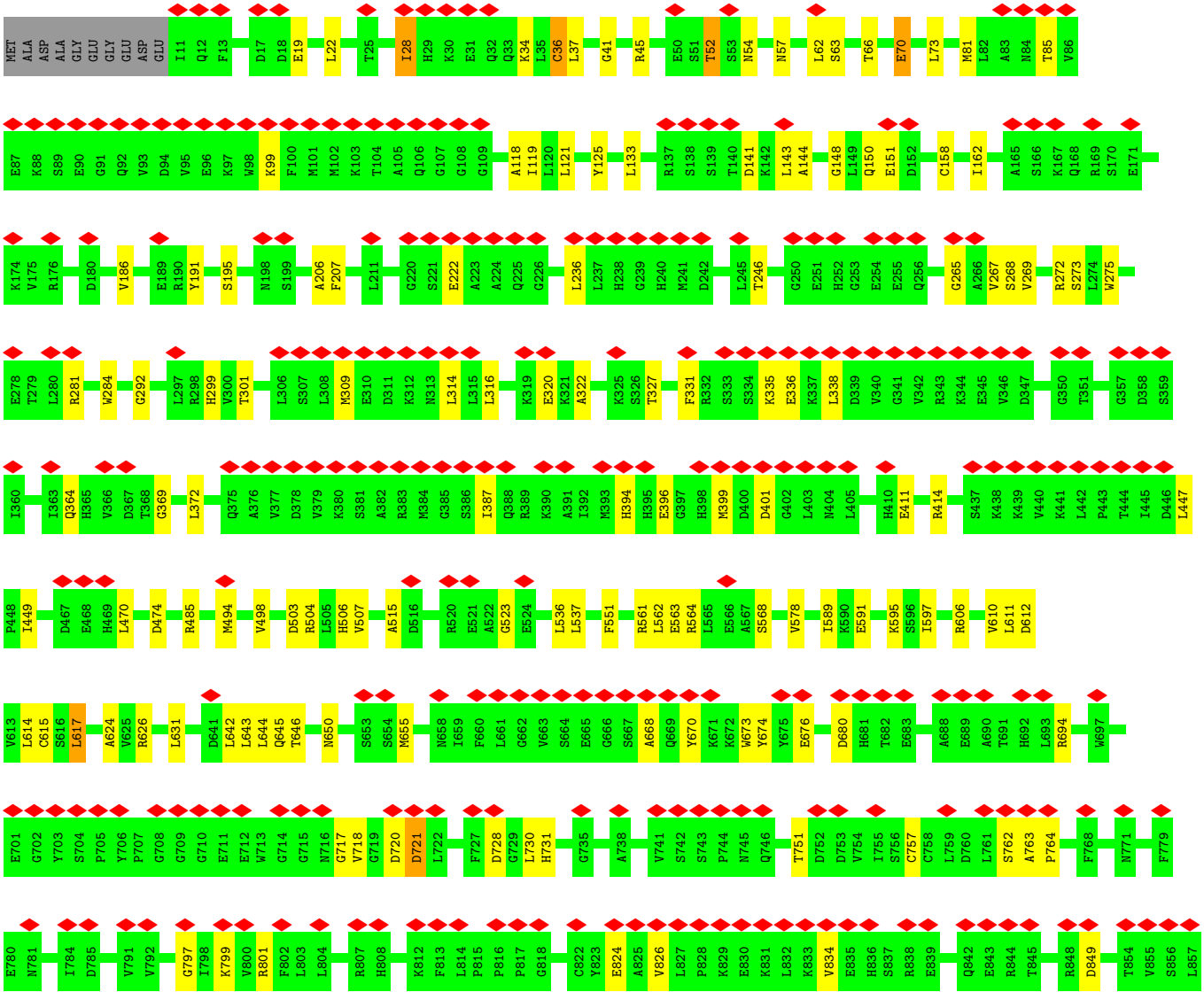
3 Residue-property plots (i)

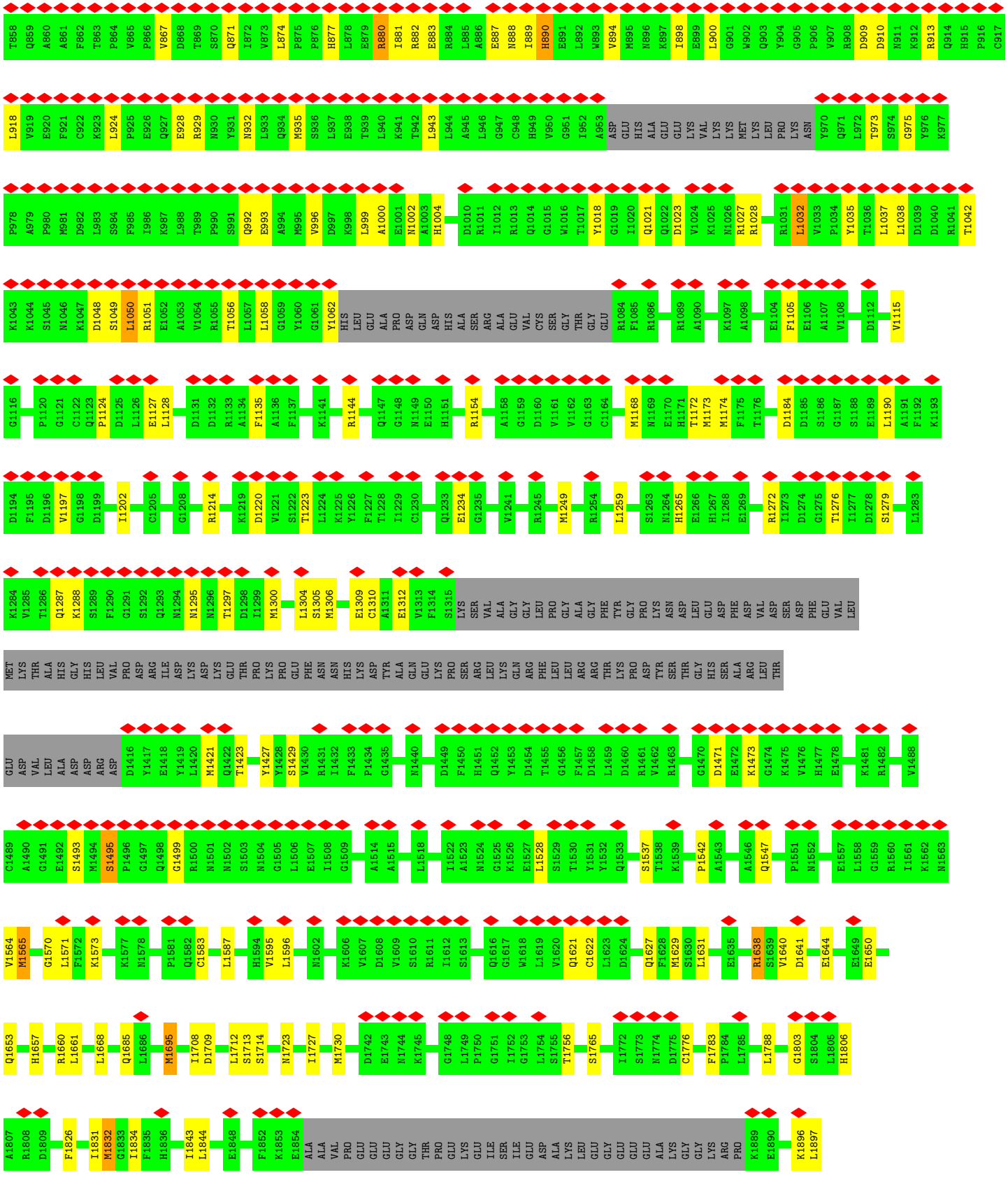
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

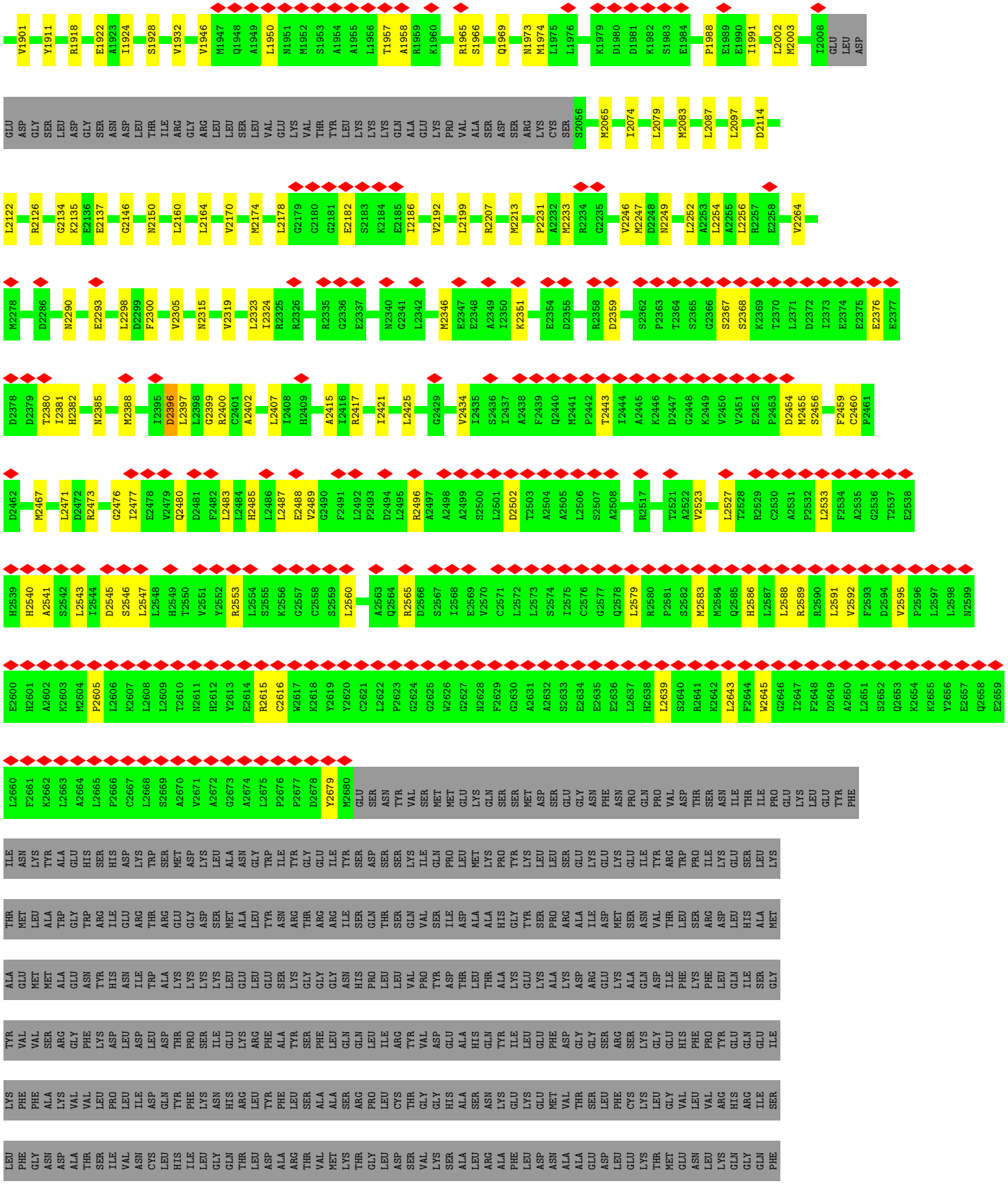
- Molecule 1: Ryanodine receptor 2

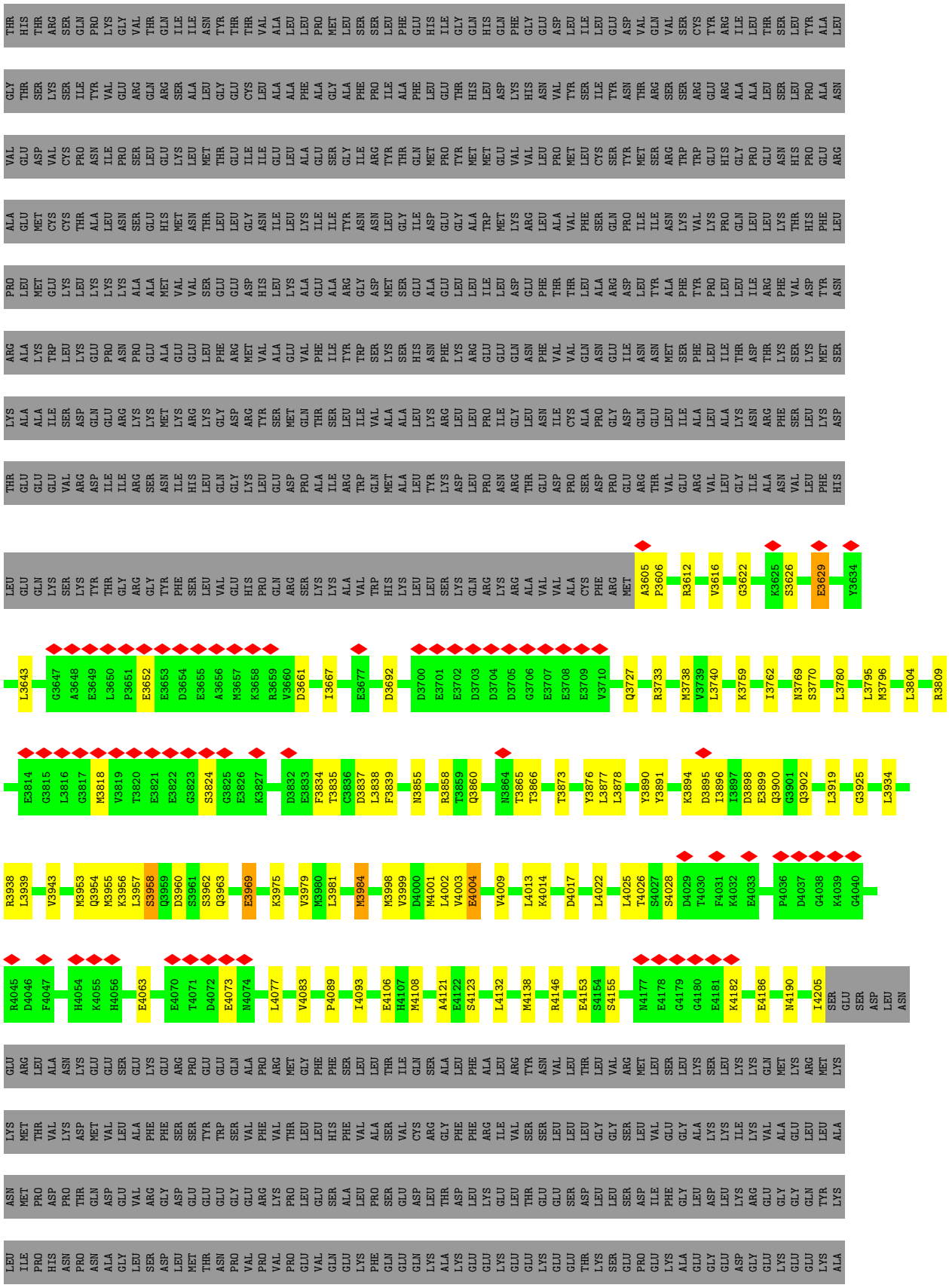
Chain A:

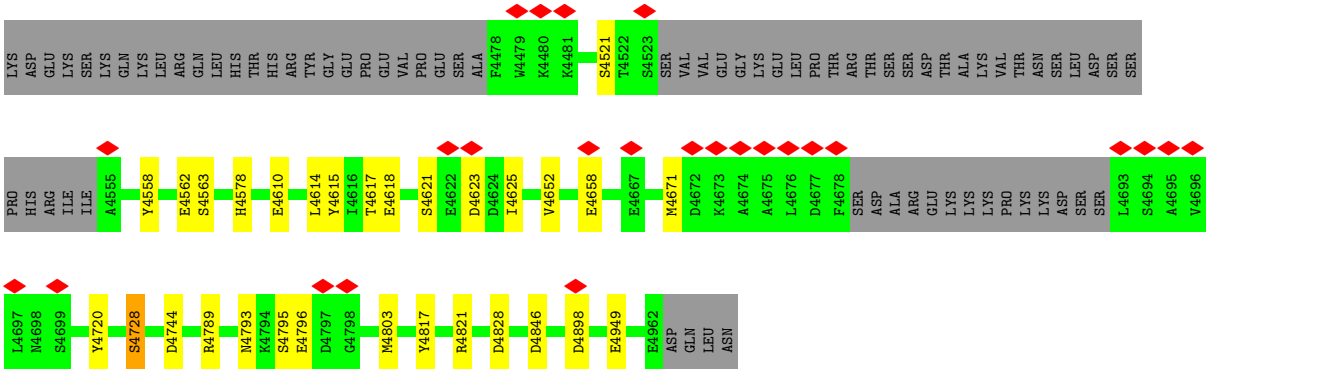





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L918 V919 E920 F921 C922 K923 L924 P925 E926 Q927 E928 R929 N930 Y931 N932 L933 Q934 M935 S936 L937 E938 T939 L940 K941 T942 L943 L944 A945 L946 G947 C948 H949 V950 G951 I952 A953 ASP GLU HIS ALA GLU GLU LYS VAL LYS LYS MET LYS LEU PRO LYS ASN Y970 Q971 L972 T973 S974 G975 Y976 K977
P978 A979 P980 M981 D982 L983 S984 F985 I986 K987 L988 T989 P990 S991 Q992 E993 A994 M995 V996 D997 K998 L999 A1000 E1001 N1002 A1003 H1004 D1010 R1011 I1012 R1013 Q1014 G1015 W1016 T1017 Y1018 G1019 I1020 Q1021 Q1022 D1023 V1024 K1025 N1026 R1027 R1028 R1031 L1032 V1033 P1034 Y1035 T1036 L1037 L1038 D1039 D1040 R1041 T1042
K1043 K1044 S1045 N1046 K1047 D1048 S1049 L1050 R1051 E1052 A1053 V1054 R1055 T1056 L1057 L1058 G1059 Y1060 G1061 Y1062 HIS LEU GLU ALA PRO ASP GLN ASP HIS ALA SER ARG ALA GLU VAL CYS SER GLY THR GLY GLU R1084 F1085 R1086 R1089 A1090 K1097 A1098 E1104 F1105 E1106 A1107 V1108 D1112 V1115
G1116 P1120 G1121 C1122 Q1123 P1124 D1125 L1126 E1127 L1128 D1131 D1132 R1133 A1134 F1135 A1136 F1137 K1141 R1144 Q1147 G1148 N1149 E1150 H1151 R1154 A1158 G1159 D1160 V1161 V1162 G1163 C1164 M1168 N1169 E1170 H1171 T1172 M1173 M1174 F1175 T1176 D1184 D1185 S1186 G1187 S1188 E1189 L1190 A1191 F1192 K1193
D1194 F1195 D1196 V1197 G1198 D1199 I1202 C1205 G1208 R1214 K1219 D1220 V1221 S1222 T1223 L1224 K1225 Y1226 F1227 T1228 I1229 C1230 Q1233 E1234 G1235 V1241 R1245 M1249 R1254 L1259 S1263 N1264 H1265 E1266 H1267 I1268 E1269 R1272 I1273 D1274 G1275 T1276 I1277 D1278 S1279 L1283
K1284 V1285 T1286 Q1287 K1288 S1289 F1290 G1291 S1292 Q1293 N1294 N1295 N1296 T1297 D1298 I1299 M1300 L1304 S1305 M1306 E1309 C1310 A1311 E1312 V1313 F1314 S1315 LYS SER VAL ALA GLY GLY LEU PRO GLY ALA GLY PHE TYR GLY PRO LYS ASN ASP LEU GLU ASP PHE ASP VAL ASP SER ASP PHE GLU VAL LEU
MET LYS THR ALA HIS GLY HIS LEU VAL PRO ASP ARG ILE ASP LYS ASP LYS GLU THR PRO LYS PRO GLU PHE ASN ASN HIS LYS ASP TYR ALA GLN GLU LYS PRO SER ARG LEU LYS GLN ARG PHE LEU LEU ARG ARG THR LYS PRO ASP TYR SER THR GLY HIS SER ALA ARG LEU THR
GLU ASP VAL LEU ALA ASP ASP ARG ASP D1416 Y1417 E1418 Y1419 L1420 M1421 Q1422 T1423 Y1427 Y1428 S1429 V1430 R1431 I1432 F1433 P1434 G1435 N1440 D1449 F1450 H1451 Q1452 Y1453 D1454 T1455 G1456 F1457 D1458 L1459 D1460 R1461 V1462 R1463 G1470 D1471 E1472 K1473 G1474 K1475 V1476 H1477 E1478 K1481 R1482 V1488
C1489 A1490 G1491 E1492 S1493 M1494 S1495 P1496 G1497 Q1498 G1499 R1500 N1501 N1502 S1503 N1504 G1505 L1506 E1507 I1508 G1509 A1514 A1515 L1518 I1522 A1523 N1524 G1525 K1526 E1527 L1528 S1529 T1530 Y1531 Y1532 Q1533 S1537 T1538 K1539 P1542 A1543 A1546 Q1547 P1551 N1552 E1557 L1558 G1559 R1560 I1561 K1562 N1563
V1564 M1565 G1570 L1571 F1572 K1573 K1577 N1578 P1581 Q1582 C1583 L1587 H1594 V1595 L1596 N1602 K1606 V1607 D1608 V1609 S1610 R1611 I1612 S1613 Q1616 G1617 W1618 L1619 V1620 Q1621 C1622 L1623 D1624 Q1627 F1628 M1629 S1630 L1631 E1635 R1638 S1639 V1640 D1641 E1644 E1649 E1650
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A1807 R1808 D1809 F1826 I1831 M1832 G1833 I1834 F1835 H1836 I1843 L1844 E1848 F1852 K1853 E1854 ALA ALA VAL PRO GLU GLU GLU GLU GLY GLY THR PRO GLU LYS GLU ILE SER ILE GLU ASP ALA LYS LEU GLU GLY GLY GLU GLU GLU ALA LYS GLY GLY LYS ARG PRO K1889 E1890 K1896 L1897


V1901 Y1911 R1918 E1922 A1923 I1924 S1928 V1932 V1946 M1947 Q1948 A1949 L1950 N1951 M1952 S1963 A1954 A1955 L1956 T1957 A1958 R1959 K1960 R1965 S1966 Q1969 N1973 M1974 L1975 L1976 K1979 D1980 D1981 K1982 S1983 E1984 P1988 E1989 E1990 I1991 L2002 M2003 I2008 GLU LEU ASP
GLU ASP GLY SER LEU ASP GLY SER ASN ASP LEU THR ILE ARG GLY ARG LEU LEU SER LEU VAL GLU LYS VAL THR TYR LEU LYS LYS LYS GLN ALA GLU LYS PRO VAL ALA SER ASP SER ARG LYS CYS SER S2056 M2065 I2074 L2079 M2083 L2087 L2097 D2114
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L2660 F2661 K2662 L2663 A2664 L2665 P2666 C2667 L2668 S2669 A2670 V2671 A2672 G2673 A2674 L2675 P2676 P2677 D2678 Y2679 M2680 GLU SER ASN TYR VAL SER MET MET GLU LYS GLN SER SER MET ASP SER GLU GLY ASN PHE ASN PRO GLN PRO VAL ASP THR SER ASN ILE THR ILE PRO GLU LYS LEU GLU TYR PHE
ILE ASN LYS TYR ALA GLU HIS SER HIS ASP LYS TRP SER MET ASP LYS LEU ALA ASN GLY TRP ILE TYR SER ASP SER SER LYS LEU LEU SER GLU GLU LYS ASP GLU LYS GLU ILE TYR ARG TRP PRO ILE LYS GLU SER LEU LYS
THR MET LEU ALA TRP GLY TRP ARG ILE GLU ARG THR ARG GLU GLY ASP SER MET ALA LEU TYR ASN ARG THR ARG ARG ILE SER GLN THR SER GLN VAL SER ILE ASP ALA ALA HIS GLY TYR SER PRO ARG ALA ILE ASP MET SER ASN VAL THR LEU SER ARG ASP LEU HIS ALA MET
ALA GLU MET MET ALA GLU ASN TYR HIS ASN ILE TRP ALA LYS LYS LYS LEU GLU LEU GLU SER LYS GLY GLY GLY ASN HIS PRO LEU LEU VAL PRO TYR ASP THR LEU THR ALA LYS GLU LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU GLU GLY SER
TYR VAL VAL SER ARG GLY PHE LYS ASP LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN TYR ILE LEU GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR GLU GLN GLU ILE
LYS PHE PHE ALA LYS VAL VAL LEU PRO LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY HIS ALA SER ASN LYS GLU LYS GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU VAL ARG HIS ARG ILE SER
LEU PHE GLY ASN ASP ALA THR SER ILE VAL ASN CYS LEU HIS ILE LEU GLY GLN THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS SER ALA LEU ARG ALA PHE LEU ASP ASN ALA ALA GLU ASP LEU GLU LYS LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE

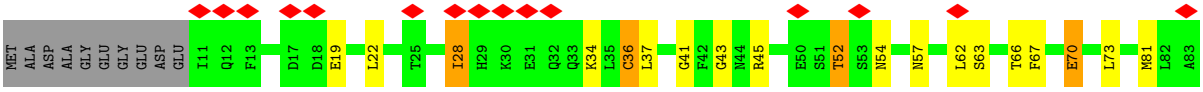


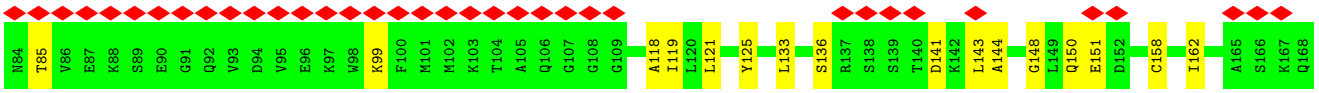


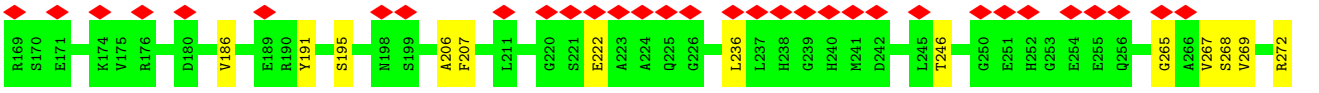
• Molecule 1: Ryanodine receptor 2

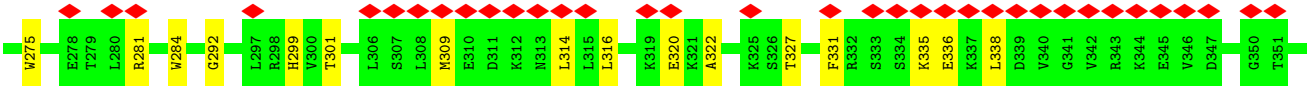
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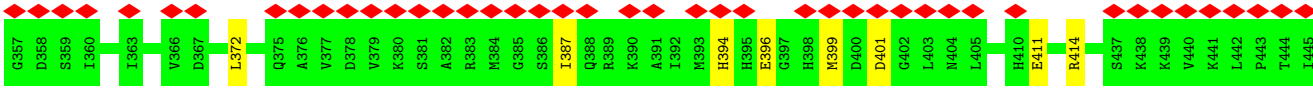


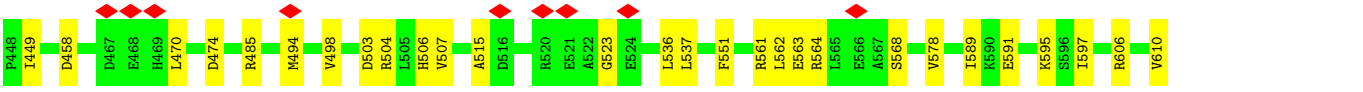


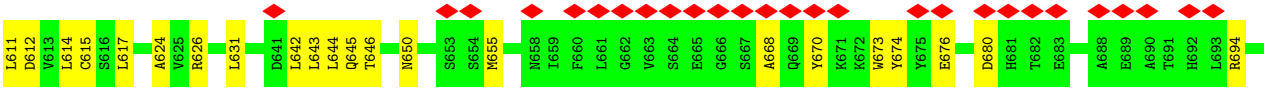


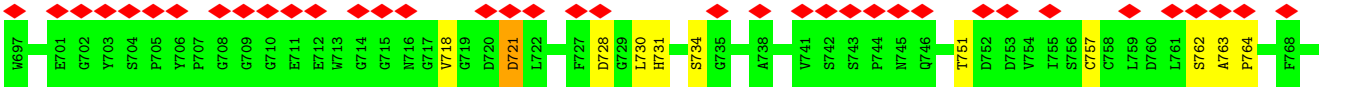


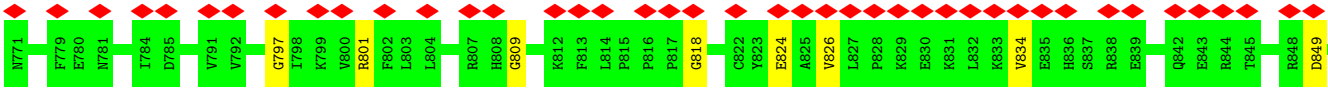


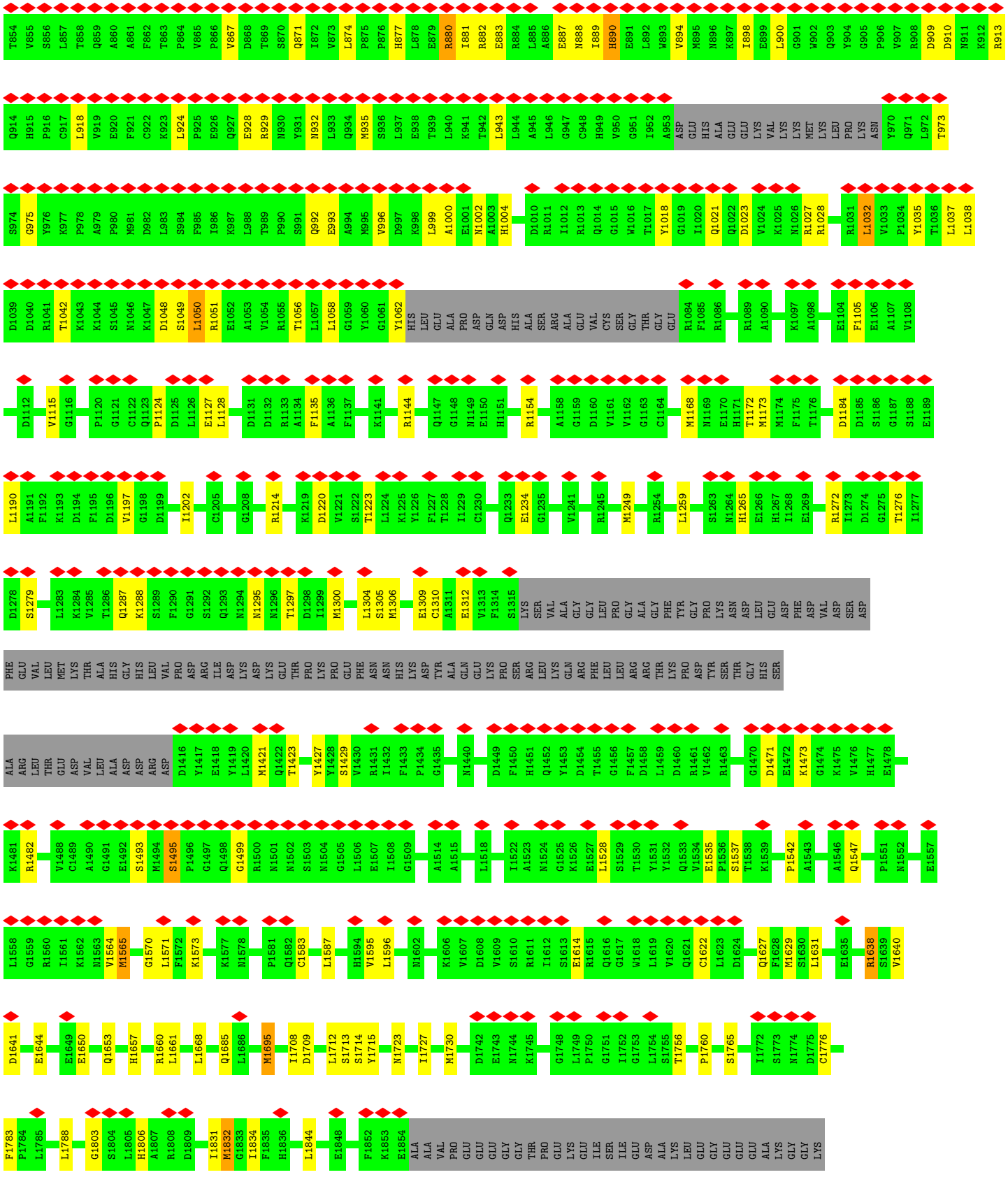


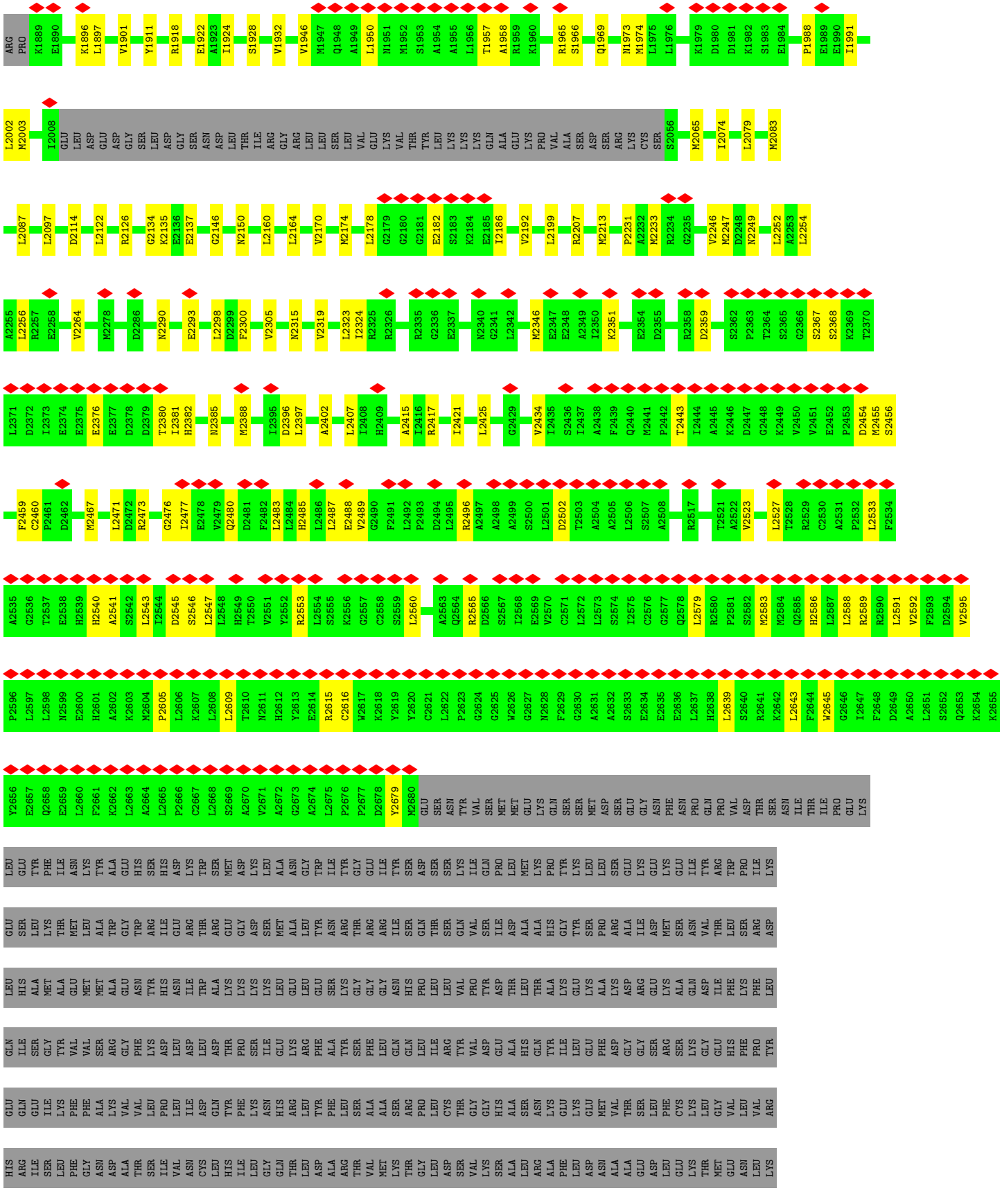


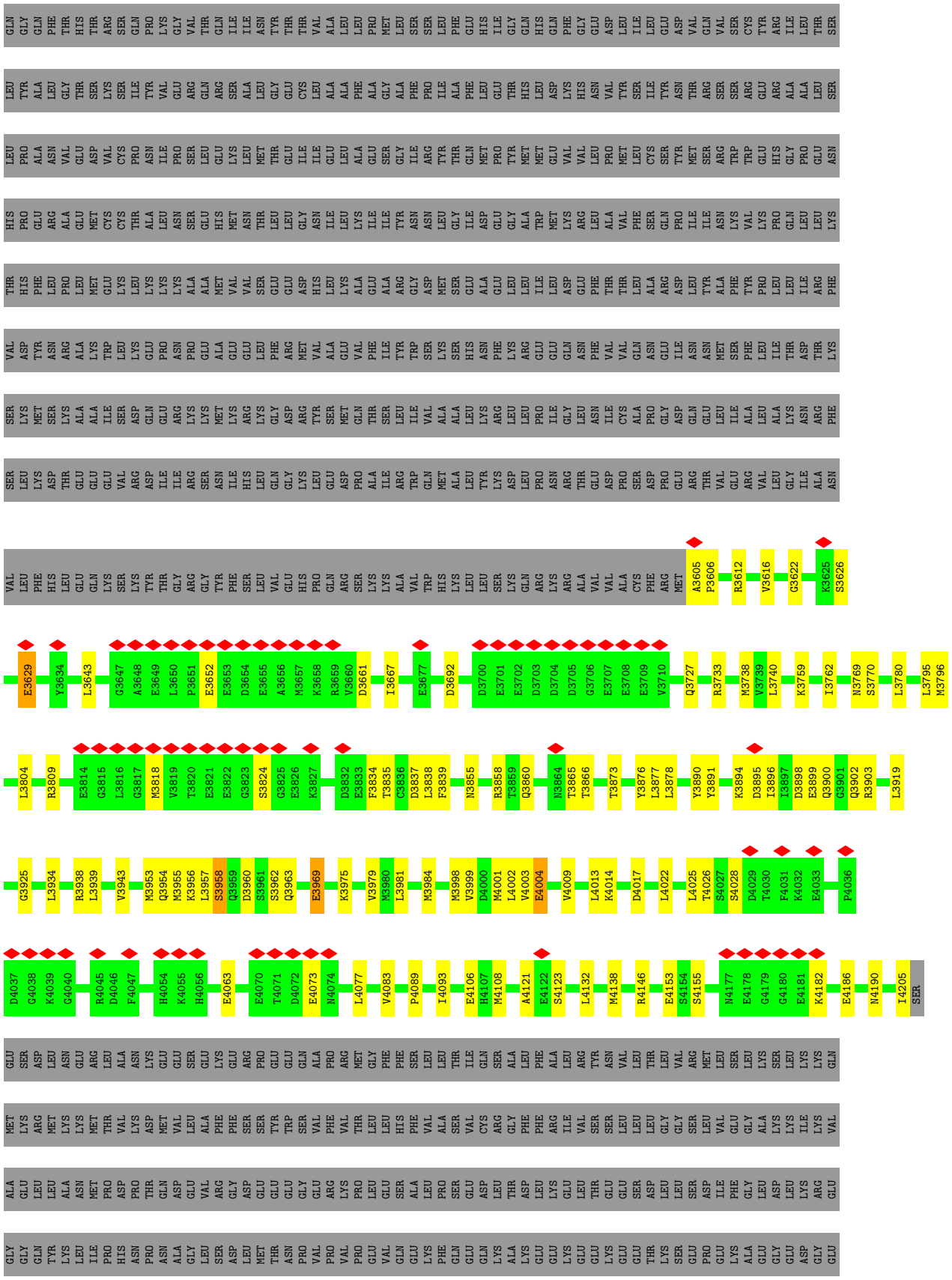


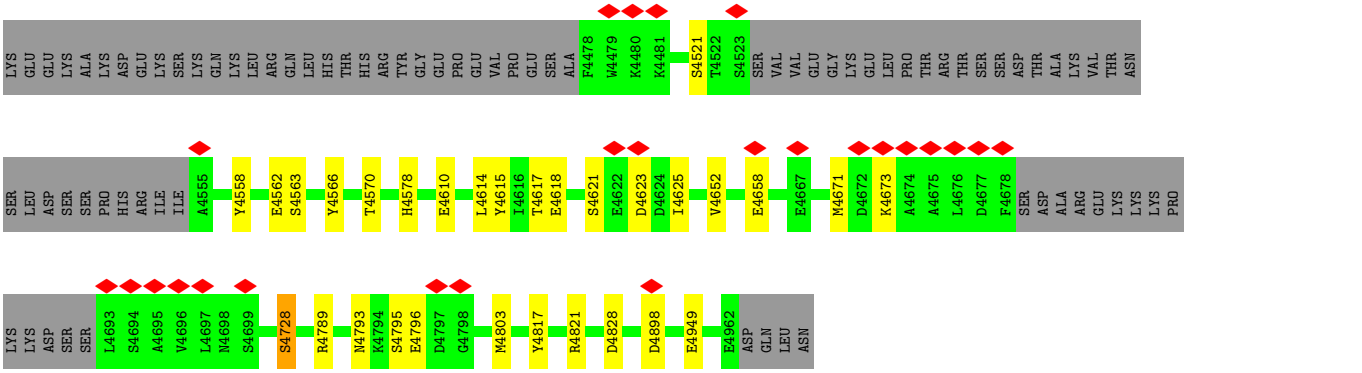





T854 V855 S856 L857 T858 Q859 A860 A861 F862 T863 P864 V865 P866 V867 D868 T869 S870 Q871 I872 V873 L874 P875 P876 H877 L878 E879 R880 I881 R882 E883 R884 L885 A886 E887 N888 I889 H890 E891 L892 W893 V894 M895 N896 K897 I898 E899 L900 G901 W902 Q903 Y904 G905 P906 V907 R908 D909 D910 N911 K912 R913
Q914 H915 P916 C917 L918 V919 E920 F921 C922 K923 L924 P925 E926 Q927 E928 R929 N930 Y931 N932 L933 Q934 M935 S936 L937 E938 T939 L940 K941 T942 L943 L944 A945 L946 G947 C948 H949 V950 G951 I952 A953 ASP GLU HIS ALA GLU GLU LYS VAL LYS LYS MET LYS LEU PRO LYS ASN Y970 Q971 L972 T973
S974 G975 Y976 K977 P978 A979 P980 M981 D982 L983 S984 F985 I986 K987 L988 T989 P990 S991 Q992 E993 A994 M995 V996 D997 K998 L999 A1000 E1001 N1002 A1003 H1004 D1010 R1011 I1012 R1013 Q1014 G1015 W1016 T1017 Y1018 G1019 I1020 Q1021 Q1022 D1023 V1024 K1025 N1026 R1027 R1028 R1031 L1032 V1033 P1034 Y1035 T1036 L1037 L1038
D1039 D1040 R1041 T1042 K1043 K1044 S1045 N1046 K1047 D1048 S1049 L1050 R1051 E1052 A1053 V1054 R1055 T1056 L1057 L1058 G1059 Y1060 G1061 Y1062 HIS LEU GLU ALA PRO ASP GLN ASP HIS ALA SER ARG ALA GLU VAL CYS SER GLY THR GLY GLU R1084 F1085 R1086 R1089 A1090 K1097 A1098 E1104 F1105 E1106 A1107 V1108
D1112 V1115 G1116 P1120 G1121 C1122 Q1123 P1124 D1125 L1126 E1127 L1128 D1131 D1132 R1133 A1134 F1135 A1136 F1137 K1141 R1144 Q1147 G1148 N1149 E1150 H1151 R1154 A1158 G1159 D1160 V1161 V1162 G1163 C1164 M1168 N1169 E1170 H1171 T1172 M1173 M1174 F1175 T1176 D1184 D1185 S1186 G1187 S1188 E1189
L1190 A1191 F1192 K1193 D1194 F1195 D1196 V1197 G1198 D1199 I1202 C1205 G1208 R1214 K1219 D1220 V1221 S1222 T1223 L1224 K1225 Y1226 F1227 T1228 I1229 C1230 Q1233 E1234 G1235 V1241 R1245 M1249 R1254 L1259 S1263 N1264 H1265 E1266 H1267 I1268 E1269 R1272 I1273 D1274 G1275 T1276 I1277
D1278 S1279 L1283 K1284 V1285 T1286 Q1287 K1288 S1289 F1290 G1291 S1292 Q1293 N1294 N1295 N1296 T1297 D1298 I1299 M1300 L1304 S1305 M1306 E1309 C1310 A1311 E1312 V1313 F1314 S1315 LYS SER VAL ALA GLY GLY LEU PRO GLY GLY ALA GLY PHE TYR GLY PRO LYS ASN ASP LEU GLU ASP PHE ASP VAL ASP SER ASP
PHE GLU VAL LEU MET LYS THR ALA HIS GLY HIS LEU VAL PRO ASP ARG ILE ASP LYS ASP LYS GLU THR PRO LYS PRO GLU PHE ASN ASN HIS LYS ASP TYR ALA GLN GLU LYS PRO SER ARG LEU LYS GLN ARG PHE LEU LEU ARG ARG THR LYS PRO ASP TYR SER THR GLY HIS SER
ALA ARG LEU THR GLU ASP VAL LEU ALA ASP ASP ARG ASP D1416 Y1417 E1418 Y1419 L1420 M1421 Q1422 T1423 Y1427 Y1428 S1429 V1430 R1431 I1432 F1433 P1434 G1435 N1440 D1449 F1450 H1451 Q1452 Y1453 D1454 T1455 G1456 F1457 D1458 L1459 D1460 R1461 V1462 R1463 G1470 D1471 E1472 K1473 G1474 K1475 V1476 H1477 E1478
K1481 R1482 V1488 C1489 A1490 G1491 E1492 S1493 M1494 S1495 P1496 G1497 Q1498 G1499 R1500 N1501 N1502 S1503 N1504 G1505 L1506 E1507 I1508 G1509 A1514 A1515 L1518 I1522 A1523 N1524 G1525 K1526 E1527 L1528 S1529 T1530 Y1531 Y1532 Q1533 V1534 E1535 P1536 S1537 T1538 K1539 P1542 A1543 A1546 Q1547 P1551 N1552 E1557
L1558 G1559 R1560 I1561 K1562 N1563 V1564 M1565 G1570 L1571 F1572 K1573 K1577 N1578 P1581 Q1582 C1583 L1587 H1594 V1595 L1596 N1602 K1606 V1607 D1608 V1609 S1610 R1611 I1612 S1613 E1614 R1615 Q1616 G1617 W1618 L1619 V1620 Q1621 C1622 L1623 D1624 Q1627 F1628 M1629 S1630 L1631 E1635 R1638 S1639 V1640
D1641 E1644 E1649 E1650 Q1653 H1657 R1660 L1661 L1668 Q1685 L1686 M1695 I1708 D1709 L1712 S1713 S1714 Y1715 N1723 I1727 M1730 D1742 E1743 N1744 K1745 G1748 L1749 P1750 G1751 I1752 G1753 L1754 S1755 T1756 P1760 S1765 I1772 S1773 N1774 D1775 C1776
F1783 P1784 L1785 L1788 G1803 S1804 L1805 H1806 A1807 R1808 D1809 I1831 M1832 G1833 I1834 F1835 H1836 L1844 E1848 F1852 K1853 E1854 ALA ALA VAL PRO GLU GLU GLU GLY GLY THR PRO GLU LYS GLU ILE SER ILE GLU ASP ALA LYS LEU GLU GLY GLU GLU GLU GLU ALA LYS GLY GLY LYS


ARG PRO K1889 E1890 K1896 L1897 V1901 Y1911 R1918 E1922 A1923 I1924 S1928 V1932 V1946 M1947 Q1948 A1949 L1950 N1951 M1952 S1953 A1964 A1955 L1956 T1957 A1958 R1959 K1960 R1965 S1966 Q1969 N1973 M1974 L1975 L1976 K1979 D1980 D1981 K1982 S1983 E1984 P1988 E1989 E1990 I1991
L2002 M2003 I2008 GLU LEU ASP GLU ASP GLY SER LEU ASP GLY SER ASN ASP LEU THR ILE ARG GLY ARG LEU LEU SER LEU VAL GLU LYS VAL THR TYR LEU LYS LYS LYS GLN ALA GLU LYS PRO VAL ALA SER ASP SER ARG LYS CYS SER S2056 M2065 I2074 L2079 M2083
L2087 L2097 D2114 L2122 R2126 G2134 K2135 E2136 E2137 G2146 N2150 L2160 L2164 V2170 M2174 L2178 G2179 G2180 G2181 E2182 S2183 K2184 E2185 I2186 V2192 L2199 R2207 M2213 P2231 A2232 M2233 R2234 G2235 V2246 M2247 D2248 N2249 L2252 A2253 L2254
A2255 L2256 R2257 E2258 V2264 M2278 D2286 N2290 E2293 L2298 D2299 F2300 V2305 N2315 V2319 L2323 I2324 R2325 R2326 R2335 G2336 E2337 N2340 G2341 L2342 M2346 E2347 E2348 A2349 I2350 K2351 E2354 D2355 R2358 D2359 S2362 P2363 T2364 S2365 G2366 S2367 S2368 K2369 T2370
L2371 D2372 I2373 E2374 E2375 E2376 E2377 D2378 D2379 T2380 I2381 H2382 N2385 M2388 I2395 D2396 L2397 A2402 L2407 I2408 H2409 A2415 I2416 R2417 I2421 L2425 G2429 V2434 I2435 S2436 I2437 A2438 F2439 Q2440 M2441 P2442 T2443 I2444 A2445 K2446 D2447 G2448 K2449 V2450 V2451 E2452 P2453 D2454 M2455 S2456
F2459 C2460 P2461 D2462 M2467 L2471 D2472 R2473 G2476 I2477 E2478 V2479 Q2480 D2481 P2482 L2483 L2484 H2485 L2486 L2487 E2488 V2489 G2490 P2491 L2492 P2493 D2494 L2495 R2496 A2497 A2498 A2499 S2500 L2501 D2502 T2503 A2504 A2505 L2506 S2507 A2508 R2517 T2521 A2522 V2523 L2527 T2528 R2529 C2530 A2531 P2532 L2533 F2534
A2535 G2536 T2537 E2538 H2539 H2540 A2541 S2542 L2543 I2544 D2545 S2546 L2547 L2548 H2549 T2550 V2551 Y2552 R2553 L2554 S2555 K2556 G2557 C2558 S2559 L2560 A2563 Q2564 R2565 D2566 S2567 I2568 E2569 V2570 C2571 L2572 L2573 S2574 I2575 C2576 G2577 Q2578 L2579 R2580 P2581 S2582 M2583 M2584 Q2585 H2586 L2587 L2588 R2589 R2590 L2591 V2592 F2593 D2594 V2595
P2596 L2597 L2598 N2599 E2600 H2601 A2602 K2603 M2604 P2605 L2606 K2607 L2608 L2609 T2610 N2611 H2612 Y2613 E2614 R2615 C2616 W2617 K2618 Y2619 Y2620 C2621 L2622 P2623 G2624 G2625 W2626 G2627 N2628 F2629 G2630 A2631 A2632 S2633 E2634 E2635 E2636 L2637 H2638 L2639 S2640 R2641 K2642 L2643 F2644 W2645 G2646 I2647 F2648 D2649 A2650 L2651 S2652 Q2653 K2654 K2655
Y2656 E2657 Q2658 E2659 L2660 F2661 K2662 L2663 A2664 L2665 P2666 C2667 L2668 S2669 A2670 V2671 A2672 G2673 A2674 L2675 P2676 P2677 D2678 Y2679 M2680 GLU SER ASN TYR VAL SER MET MET GLU LYS GLN SER SER MET ASP SER GLU GLY ASN PHE ASN PRO GLN PRO VAL ASP THR SER ASN ILE THR ILE PRO GLU LYS
LEU GLU TYR PHE ILE ASN LYS TYR ALA GLU HIS SER HIS ASP LYS TRP SER MET ASP LYS LEU ALA ASN GLY TRP ILE TYR SER ASP SER SER LYS ILE GLN PRO LEU MET LYS PRO TYR LYS LEU GLU SER GLU LYS GLU ILE TYR ARG PRO PRO ILE LYS
GLU SER LEU LYS THR MET LEU ALA TRP GLY TRP ARG ILE GLU ARG THR ARG GLU GLY ASP SER MET ALA LEU TYR ASN ARG THR ARG ARG ILE SER GLN THR SER GLN VAL SER ILE ASP ALA ALA HIS GLY TYR SER PRO ARG ALA ILE ASP MET SER ASN VAL THR LEU SER ARG ASP
LEU HIS ALA MET ALA GLU MET MET ALA GLU ASN TYR HIS ASN ILE TRP ALA LYS LYS LYS LYS LEU GLU GLU GLU SER LYS GLY GLY ASN HIS PRO LEU LEU LEU VAL PRO TYR ASP THR LEU THR ALA LYS GLU LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU
GLN ILE SER GLY TYR VAL VAL SER ARG GLY PHE LYS ASP LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN TYR ILE LEU LEU GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR
GLU GLN GLU ILE LYS PHE PHE ALA LYS VAL VAL LEU PRO LEU LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY HIS ALA SER ASN LYS GLU LYS GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU VAL ARG
HIS ARG ILE SER LEU PHE GLY ASN ASP ALA THR SER THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS SER ALA LEU ARG ALA PHE LEU ASP ASN ALA ALA GLU ASP GLU LYS THR MET GLU ASN LEU LYS

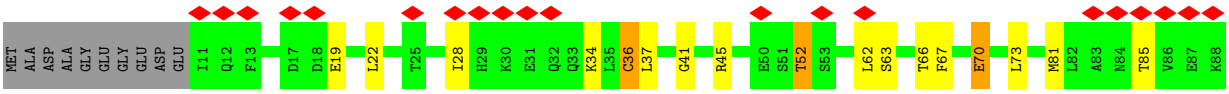


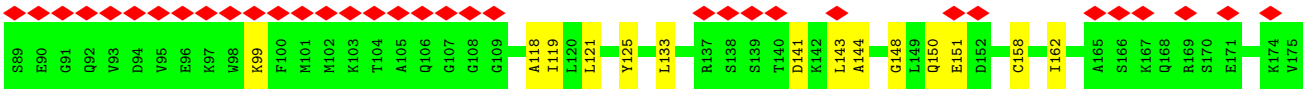


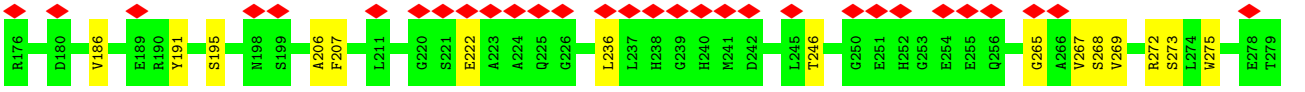
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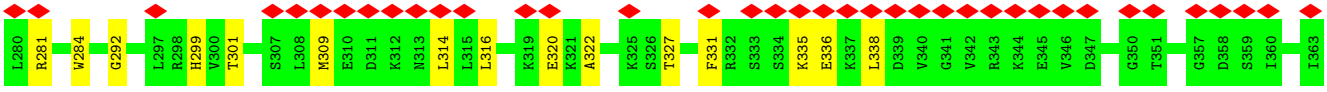
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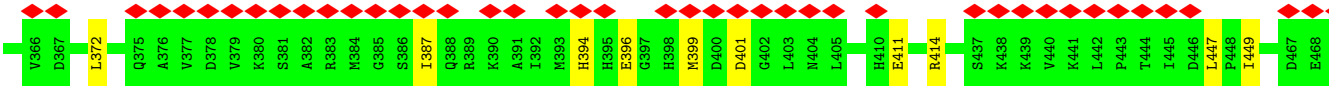




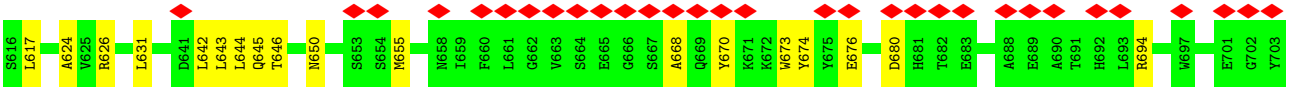


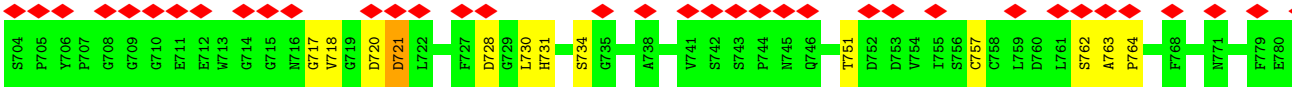


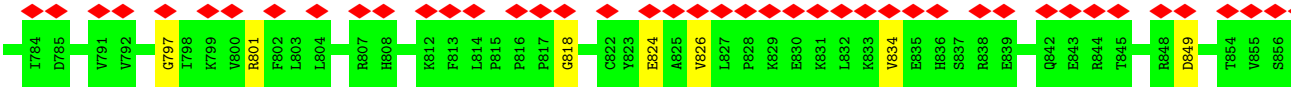




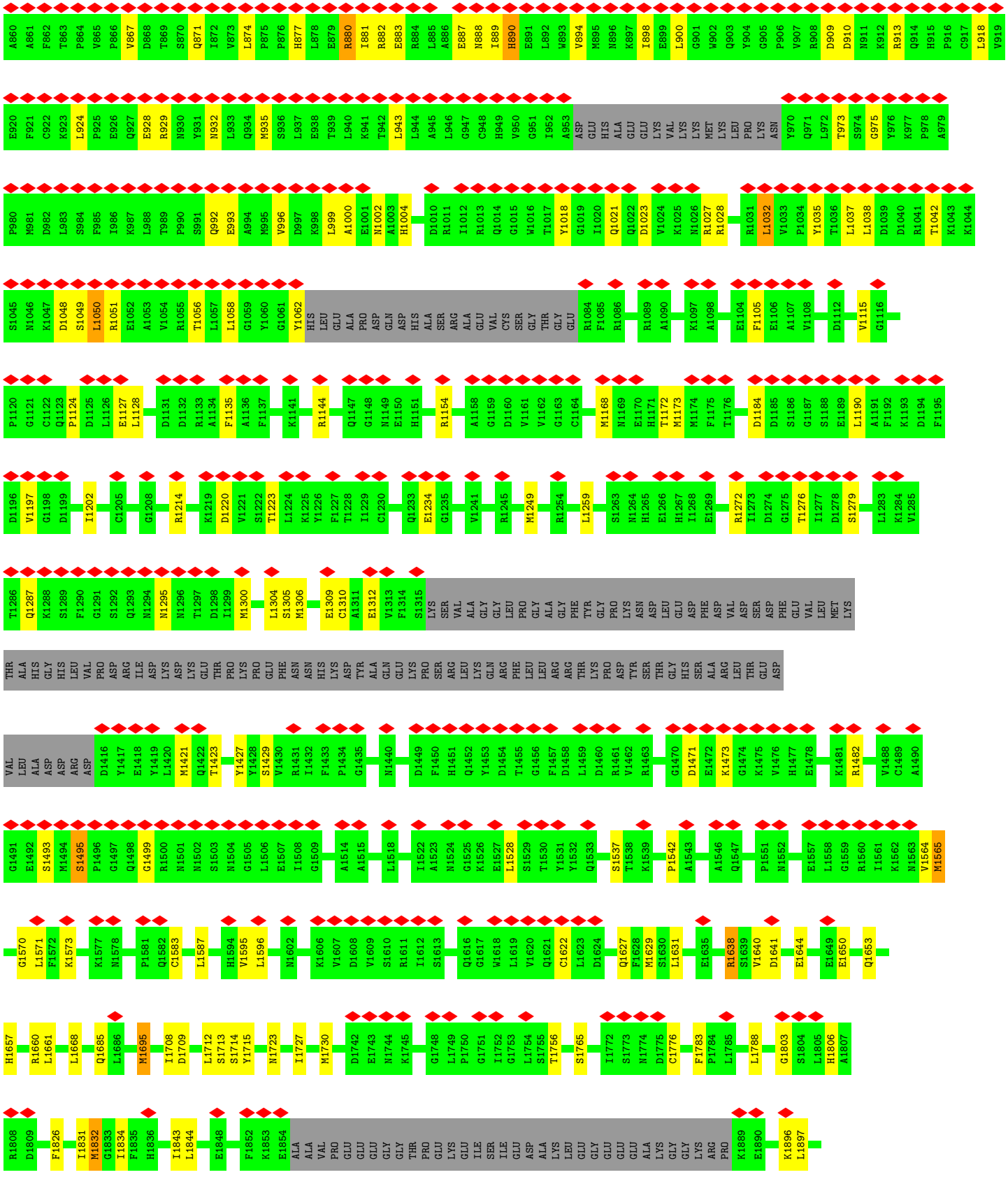


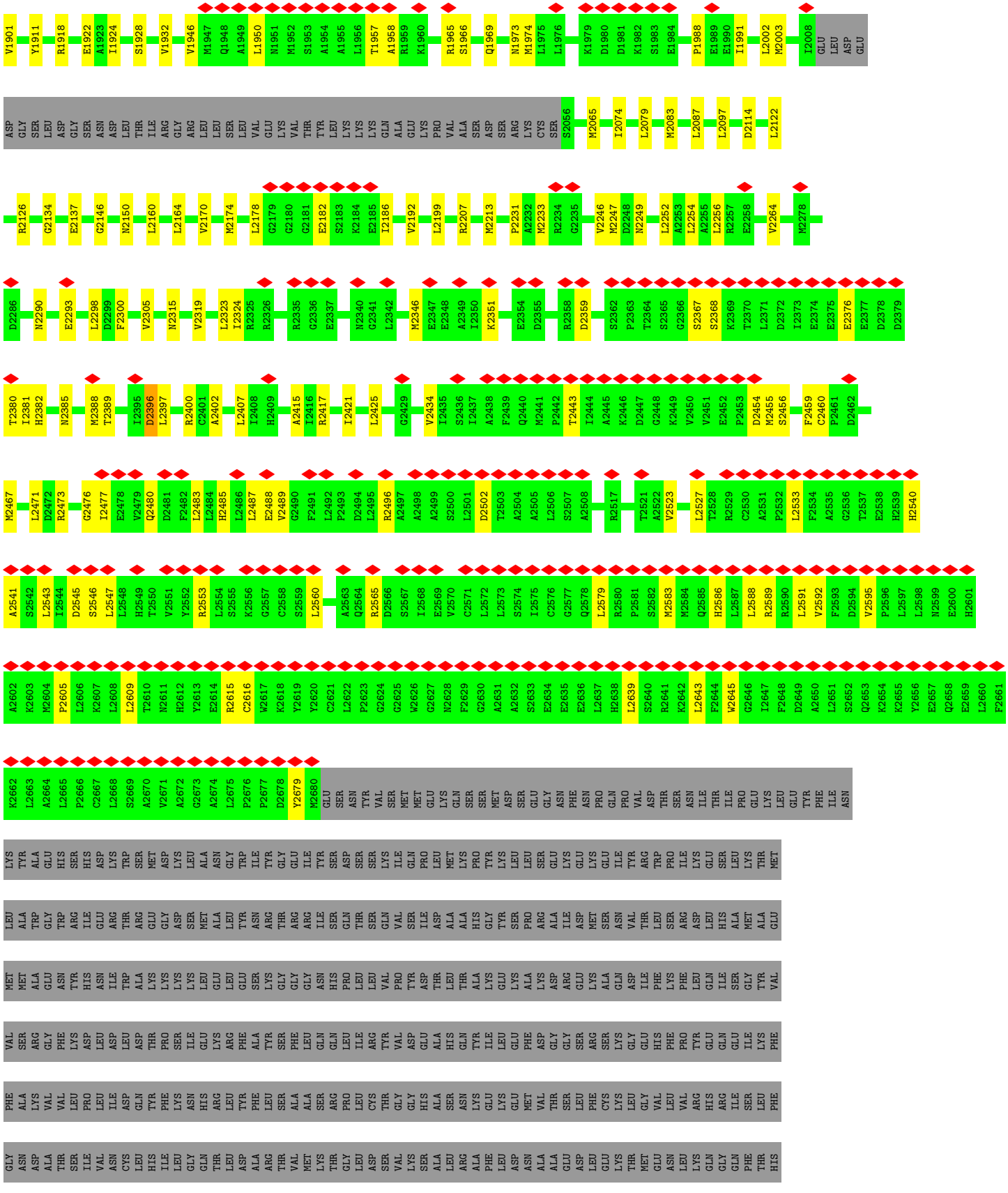


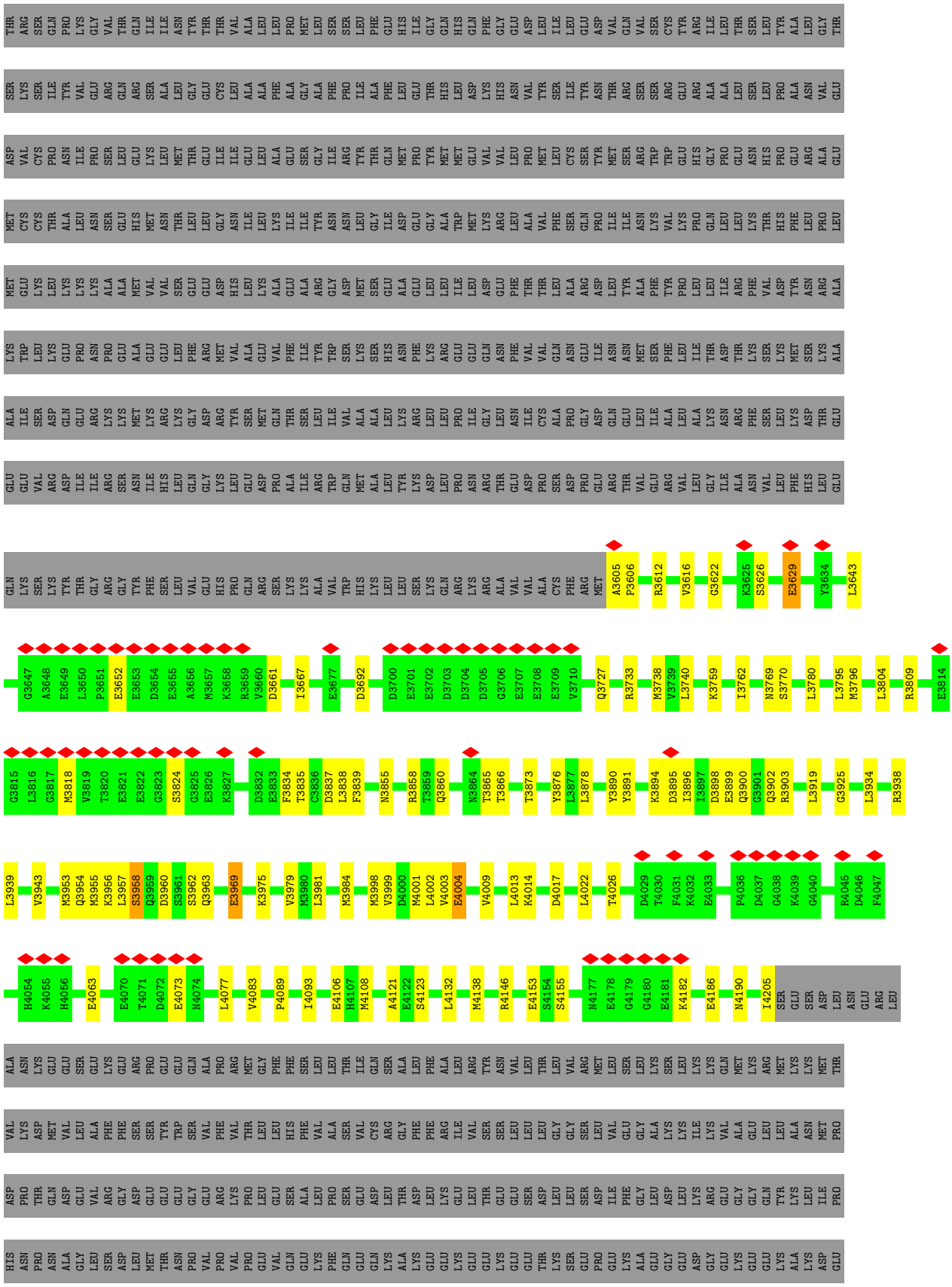


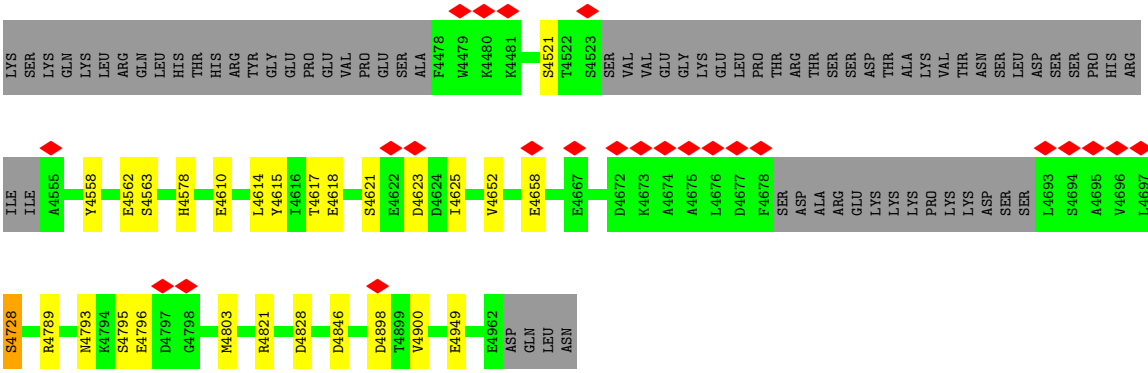





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E920 F921 C922 K923 L924 P925 E926 Q927 E928 R929 N930 Y931 N932 L933 Q934 M935 S936 L937 E938 T939 L940 K941 T942 L943 L944 A945 L946 G947 C948 H949 V950 G951 I952 A953 ASP GLU HIS ALA GLU GLU LYS VAL LYS LYS MET LYS LEU PRO LYS ASN Y970 Q971 L972 T973 S974 G975 Y976 K977 P978 A979
P980 M981 D982 L983 S984 F985 I986 K987 L988 T989 P990 S991 Q992 E993 A994 M995 V996 D997 K998 L999 A1000 E1001 N1002 A1003 H1004 D1010 R1011 I1012 R1013 Q1014 G1015 W1016 T1017 Y1018 G1019 I1020 Q1021 Q1022 D1023 V1024 K1025 N1026 R1027 R1028 R1031 L1032 V1033 P1034 Y1035 T1036 L1037 L1038 D1039 D1040 R1041 T1042 K1043 K1044
S1045 N1046 K1047 D1048 S1049 L1050 R1051 E1052 A1053 V1054 R1055 T1056 L1057 L1058 G1059 Y1060 G1061 Y1062 HIS LEU GLU ALA PRO ASP GLN ASP HIS ALA SER ARG ALA GLU VAL CYS SER GLY THR GLY GLU R1084 F1085 R1086 R1089 A1090 K1097 A1098 E1104 F1105 E1106 A1107 V1108 D1112 V1115 G1116
P1120 G1121 C1122 Q1123 P1124 D1125 L1126 E1127 L1128 D1131 D1132 R1133 A1134 F1135 A1136 F1137 K1141 R1144 Q1147 G1148 N1149 E1150 H1151 R1154 A1158 G1159 D1160 V1161 V1162 G1163 C1164 M1168 N1169 E1170 H1171 T1172 M1173 M1174 F1175 T1176 D1184 D1185 S1186 G1187 S1188 E1189 L1190 A1191 F1192 K1193 D1194 F1195
D1196 V1197 G1198 D1199 I1202 C1205 G1208 R1214 K1219 D1220 V1221 S1222 T1223 L1224 K1225 Y1226 F1227 T1228 I1229 C1230 Q1233 E1234 G1235 V1241 R1245 M1249 R1254 L1259 S1263 N1264 H1265 E1266 H1267 I1268 E1269 R1272 I1273 D1274 G1275 T1276 I1277 D1278 S1279 L1283 K1284 V1285
T1286 Q1287 K1288 S1289 F1290 G1291 S1292 Q1293 N1294 N1295 N1296 T1297 D1298 I1299 M1300 L1304 S1305 M1306 E1309 C1310 A1311 E1312 V1313 F1314 S1315 LYS SER VAL ALA GLY GLY LEU PRO GLY ALA GLY PHE TYR GLY PRO LYS ASN ASP LEU GLU ASP PHE ASP VAL ASP SER ASP PHE GLU VAL LEU MET LYS
THR ALA HIS GLY HIS LEU VAL PRO ASP ARG ILE ASP LYS ASP LYS GLU THR PRO LYS PRO GLU PHE ASN ASN HIS LYS ASP TYR ALA GLN GLU LYS PRO SER ARG LEU LYS GLN ARG PHE LEU LEU ARG ARG THR LYS PRO ASP TYR SER THR GLY HIS SER ALA ARG LEU THR GLU ASP
VAL LEU ALA ASP ASP ARG ASP D1416 Y1417 E1418 Y1419 L1420 M1421 Q1422 T1423 Y1427 Y1428 S1429 V1430 R1431 I1432 F1433 P1434 G1435 N1440 D1449 F1450 H1451 Q1452 Y1453 D1454 T1455 G1456 F1457 D1458 L1459 D1460 R1461 V1462 R1463 G1470 D1471 E1472 K1473 G1474 K1475 V1476 H1477 E1478 K1481 R1482 V1488 C1489 A1490
G1491 E1492 S1493 M1494 S1495 P1496 G1497 Q1498 G1499 R1500 N1501 N1502 S1503 N1504 G1505 L1506 E1507 I1508 G1509 A1514 A1515 L1518 I1522 A1523 N1524 G1525 K1526 E1527 L1528 S1529 T1530 Y1531 Y1532 Q1533 S1537 T1538 K1539 P1542 A1543 A1546 Q1547 P1551 N1552 E1557 L1558 G1559 R1560 I1561 K1562 N1563 V1564 M1565
G1570 L1571 F1572 K1573 K1577 N1578 P1581 Q1582 C1583 L1587 H1594 V1595 L1596 N1602 K1606 V1607 D1608 V1609 S1610 R1611 I1612 S1613 Q1616 G1617 W1618 L1619 V1620 Q1621 C1622 L1623 D1624 Q1627 F1628 M1629 S1630 L1631 E1635 R1638 S1639 V1640 D1641 E1644 E1649 E1650 Q1653
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R1808 D1809 F1826 I1831 M1832 G1833 I1834 F1835 H1836 I1843 L1844 E1848 F1852 K1853 E1854 ALA ALA VAL PRO GLU GLU GLU GLY GLY THR PRO GLU LYS GLU ILE SER ILE GLU ASP ALA LYS LEU GLU GLY GLU GLU GLU ALA LYS GLY GLY LYS ARG PRO K1889 E1890 K1896 L1897


V1901 Y1911 R1918 E1922 A1923 I1924 S1928 V1932 V1946 M1947 Q1948 A1949 L1950 N1951 M1952 S1953 A1954 A1955 L1956 T1957 A1958 R1959 K1960 R1965 S1966 Q1969 N1973 M1974 L1975 L1976 K1979 D1980 D1981 K1982 S1983 E1984 P1988 E1989 E1990 I1991 L2002 M2003 I2008 GLU LEU ASP GLU
ASP GLY SER LEU ASP GLY SER ASN ASP LEU THR ILE ARG GLY ARG LEU LEU SER LEU VAL GLU LYS VAL THR TYR LEU LYS LYS GLN ALA GLU LYS PRO VAL ALA SER ASP SER ARG LYS CYS SER S2056 M2065 I2074 L2079 M2083 L2087 L2097 D2114 L2122
R2126 G2134 E2137 G2146 N2150 L2160 L2164 V2170 M2174 L2178 G2179 G2180 G2181 E2182 S2183 K2184 E2185 I2186 V2192 L2199 R2207 M2213 P2231 A2232 M2233 R2234 G2235 V2246 M2247 D2248 N2249 L2252 A2253 L2254 A2255 L2256 R2257 E2258 V2264 M2278
D2286 N2290 E2293 L2298 D2299 F2300 V2305 N2315 V2319 L2323 I2324 R2325 R2326 R2335 G2336 E2337 N2340 G2341 L2342 M2346 E2347 E2348 A2349 I2350 K2351 E2354 D2355 R2358 D2359 S2362 P2363 T2364 S2365 G2366 S2367 S2368 K2369 T2370 L2371 D2372 I2373 E2374 E2375 E2376 E2377 D2378 D2379
T2380 I2381 H2382 N2385 M2388 T2389 I2395 D2396 L2397 R2400 C2401 A2402 L2407 I2408 H2409 A2415 I2416 R2417 I2421 L2425 G2429 V2434 I2435 S2436 I2437 A2438 F2439 Q2440 M2441 P2442 T2443 I2444 A2445 K2446 D2447 G2448 K2449 V2450 V2451 E2452 P2453 D2454 M2455 S2456 F2459 C2460 P2461 D2462
M2467 L2471 D2472 R2473 G2476 I2477 E2478 V2479 Q2480 D2481 F2482 L2483 L2484 H2485 L2486 L2487 E2488 V2489 G2490 F2491 L2492 P2493 D2494 L2495 R2496 A2497 A2498 A2499 S2500 L2501 D2502 T2503 A2504 A2505 L2506 S2507 A2508 R2517 T2521 A2522 V2523 L2527 T2528 R2529 C2530 A2531 P2532 L2533 F2534 A2535 G2536 T2537 E2538 H2539 H2540
A2541 S2542 L2543 T2544 D2545 L2546 S2547 L2548 H2549 T2550 V2551 Y2552 R2553 L2554 S2555 K2556 G2557 C2558 S2559 L2560 A2563 Q2564 R2565 D2566 S2567 I2568 E2569 V2570 C2571 L2572 L2573 S2574 I2575 C2576 G2577 Q2578 L2579 R2580 P2581 S2582 M2583 M2584 Q2585 H2586 L2587 L2588 R2589 R2590 L2591 V2592 F2593 D2594 V2595 P2596 L2597 L2598 N2599 E2600 H2601
A2602 K2603 M2604 P2605 L2606 K2607 L2608 L2609 T2610 N2611 H2612 Y2613 E2614 R2615 C2616 W2617 K2618 Y2619 Y2620 C2621 L2622 P2623 G2624 G2625 W2626 G2627 N2628 F2629 G2630 A2631 A2632 S2633 E2634 E2635 E2636 L2637 H2638 L2639 S2640 R2641 K2642 L2643 F2644 W2645 G2646 I2647 F2648 D2649 A2650 L2651 S2652 Q2653 K2654 K2655 Y2656 E2657 Q2658 E2659 L2660 F2661
K2662 L2663 A2664 L2665 P2666 C2667 L2668 S2669 A2670 V2671 A2672 G2673 A2674 L2675 P2676 P2677 D2678 Y2679 M2680 GLU SER ASN TYR VAL SER MET MET GLU LYS GLN SER SER MET ASP SER GLU GLY ASN PHE ASN PRO GLN PRO VAL ASP THR SER ASN ILE THR ILE PRO GLU LYS LEU GLU TYR PHE ILE ASN
LYS TYR ALA GLU HIS SER HIS ASP LYS TRP SER MET ASP LYS LEU ALA ASN GLY TRP ILE TYR GLY GLU ILE TYR SER ASP SER SER LYS ILE GLN PRO LEU MET MET LYS PRO TYR LYS LEU SER GLU LYS GLU LYS SER GLU LEU LYS THR MET
LEU ALA TRP GLY TRP ARG THR ARG ILE GLU ARG GLU GLY ASP SER MET ALA LEU TYR ASN ARG THR ARG ARG ILE SER GLN THR SER GLN VAL SER ILE ASP ALA ALA HIS GLY TYR SER PRO ARG ALA ILE ASP MET SER ASN VAL THR LEU SER ARG ASP LEU HIS ALA MET ALA GLU
MET MET ALA GLU ASN TYR HIS ASN ILE TRP ALA LYS LYS LYS LEU GLU LEU GLU SER LYS GLY GLY GLY ASN HIS PRO LEU LEU VAL PRO TYR ASP THR LEU THR ALA LYS GLU LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU GLN ILE SER GLY TYR VAL
VAL SER ARG GLY PHE LYS ASP LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN TYR ILE LEU GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR GLU GLN GLU ILE LYS PHE
PHE ALA LYS VAL VAL LEU PRO LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY HIS ALA SER ASN LYS GLU LYS GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU VAL ARG HIS ARG ILE SER LEU PHE
GLY ASN ASP ALA THR SER ILE VAL ASN CYS LEU HIS ILE LEU GLY GLN THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS SER ALA LEU ARG ALA PHE LEU ASP ASN ALA ALA GLU ASP LEU GLU LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE THR HIS

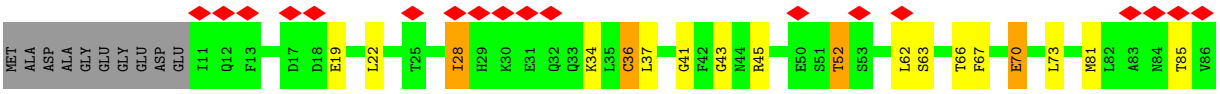

THR ARG SER GLN PRO LYS GLY VAL THR GLN ILE ILE ASN TYR THR THR VAL ALA LEU LEU PRO MET LEU SER SER LEU PHE GLU HIS ILE GLY GLN HIS GLN PHE GLY GLU ASP LEU ILE LEU GLU ASP SER CYS TYR ARG ILE LEU THR SER LEU TYR ALA LEU GLY VAL THR
SER LYS SER ILE TYR VAL GLU ARG GLN ARG SER ALA LEU GLY GLU CYS LEU ALA ALA PHE PRO ILE ALA PHE LEU GLU THR HIS LEU ASP LYS HIS ASN VAL TYR SER ILE TYR ASN THR ARG SER SER ARG GLU ARG ALA ALA LEU SER LEU PRO ALA ASN VAL GLU
ASP VAL CYS PRO ASN ILE PRO SER LEU GLU LYS LEU MET THR GLU ILE ILE GLU LEU ALA GLU SER GLY ILE ARG TYR THR GLN MET PRO TYR MET MET GLU VAL VAL LEU PRO MET LEU CYS SER TYR MET SER ARG TRP TRP GLU HIS GLY PRO GLU LEU ASN HIS PRO GLU PRO ARG ALA GLU
MET CYS CYS THR ALA LEU ASN SER GLU HIS MET ASN THR LEU LEU GLY ASN ILE LEU LYS ILE ILE TYR ASN ASN LEU GLY ILE ASP GLU GLY ALA TRP MET LYS ARG LEU ALA VAL PHE SER GLN PRO ILE ILE ASN LYS VAL LYS PRO GLN LEU LEU LEU LYS THR HIS PHE LEU PRO LEU
MET GLU LYS LEU LYS LYS LYS ALA ALA MET VAL VAL SER GLU GLU GLU ASP HIS LEU LYS ALA GLU VAL PHE ILE ALA ARG GLY ASP MET SER GLU ALA ALA LEU ALA ARG ASP LEU TYR ALA PHE TYR PRO LEU LEU LEU ILE ARG PHE VAL ASP TYR ASN ARG ALA
LYS TRP LEU LYS GLU PRO ASN PRO GLU GLU ALA ALA MET VAL GLU VAL ALA GLU LEU PHE ILE TYR TRP SER LYS SER HIS ASN PHE LYS ARG GLU GLU GLN ASN PHE VAL VAL VAL GLN ASN GLU ILE ASN ASN MET SER PHE LEU ILE THR ASP THR LYS SER LYS MET SER LYS LYS
ALA ILE SER ASP GLN GLU ARG LYS LYS MET LYS ARG LYS GLY ASP ARG TYR SER MET GLN THR SER LEU ILE VAL ALA ALA LEU LYS ARG LEU LEU PRO ILE GLY LEU ASN ILE CYS ALA PRO GLY ASP GLN GLU LEU ILE ALA LEU LEU ILE ALA LYS ASN ARG PHE SER LEU LYS ASP THR GLU
GLU GLU VAL ARG ASP ILE ILE ARG SER ASN ILE HIS LEU GLN GLY LYS LEU GLU ASP PRO ALA ILE ARG TRP GLN MET ALA LEU TYR LYS ASP LEU PRO LEU GLU VAL ASP PRO GLN GLU ARG THR VAL GLU ARG VAL LEU LEU ASP PRO ASN ARG THR GLU ASP PRO SER ASP PRO GLU ARG THR VAL GLU ARG VAL LEU GLY ILE ALA ASN ARG PHE VAL LEU LEU PHE HIS LEU GLU
GLN LYS SER LYS TYR THR GLY ARG GLY TYR PHE SER LEU VAL GLU HIS PRO GLN ARG SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG LYS ARG ALA VAL VAL ALA CYS PHE ARG MET A3605 P3606 R3612 V3616 G3622 K3625 S3626 E3629 Y3634 L3643
G3647 A3648 E3649 L3650 P3651 E3652 E3653 D3654 E3655 A3656 M3657 K3658 R3659 V3660 D3661 I3667 E3677 D3692 D3700 E3701 E3702 D3703 D3704 D3705 G3706 E3707 E3708 E3709 V3710 Q3727 R3733 M3738 V3739 L3740 K3759 I3762 N3769 S3770 L3780 L3795 M3796 L3804 R3809 E3814
G3815 L3816 G3817 M3818 V3819 T3820 E3821 E3822 G3823 S3824 G3825 E3826 K3827 D3832 E3833 F3834 T3835 C3836 D3837 L3838 F3839 N3855 R3858 T3859 Q3860 N3864 T3865 T3866 T3873 Y3876 L3877 L3878 Y3890 Y3891 K3894 D3895 I3896 I3897 D3898 E3899 Q3900 G3901 Q3902 R3903 L3919 G3925 L3934 R3938
L3939 V3943 M3953 Q3954 M3955 K3956 L3957 S3958 Q3959 D3960 S3961 S3962 Q3963 E3969 K3975 V3979 M3980 L3981 M3984 M3998 V3999 D4000 M4001 L4002 V4003 E4004 V4009 L4013 K4014 D4017 L4022 T4026 D4029 T4030 F4031 K4032 E4033 P4036 D4037 G4038 K4039 G4040 R4045 D4046 F4047
H4054 K4055 H4056 E4063 E4070 T4071 D4072 E4073 N4074 L4077 V4083 P4089 I4093 E4106 H4107 M4108 A4121 E4122 S4123 L4132 M4138 R4146 E4153 S4154 S4155 N4177 E4178 G4179 G4180 E4181 K4182 E4186 N4190 I4205 SER GLU SER ASP LEU ASN GLU ARG LEU
ALA ASN LYS GLU GLU SER GLU LYS GLU ARG PRO GLU GLU GLN ALA PRO ARG MET GLY PHE PHE SER LEU LEU THR ILE GLN SER ALA LEU PHE ALA LEU ARG TYR ASN VAL LEU THR LEU VAL ARG MET LEU SER LEU LYS LYS GLN MET LYS ARG MET LYS LYS MET THR
VAL LYS ASP MET VAL LEU ALA PHE PHE SER SER TYR TRP SER VAL PHE VAL THR LEU LEU HIS PHE VAL ALA SER VAL CYS ARG GLY PHE PHE ARG ILE VAL SER SER LEU LEU LEU GLY GLY SER LEU VAL GLU GLY ALA LYS LYS ILE LYS VAL ALA GLU LEU LEU GLU ALA ASN MET PRO
ASP PRO THR GLN ASP GLU VAL ARG GLY ASP GLU GLU GLY GLU ARG LYS PRO LEU GLU SER ALA LEU PRO SER GLU ASP LEU ASP THR GLU LEU ASP LEU GLU GLU SER ASP LEU SER ASP ILE PHE GLY LEU ASP LEU LYS ARG GLU GLY GLY GLN TYR LYS LEU ILE PRO
HIS ASN PRO ASN ALA GLY LEU SER ASP LEU MET THR ASN PRO VAL PRO VAL PRO GLU VAL GLN GLU LYS PHE GLN GLU GLU GLN LYS GLU LYS GLU GLU LYS LYS GLU GLU GLU THR LYS SER GLU PRO GLU LYS ALA GLY GLU GLY GLU ASP GLY GLU LYS GLU GLU LYS ALA LYS ASP GLU



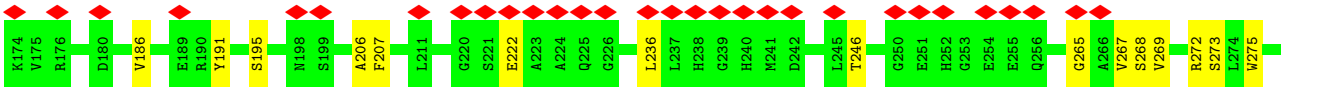
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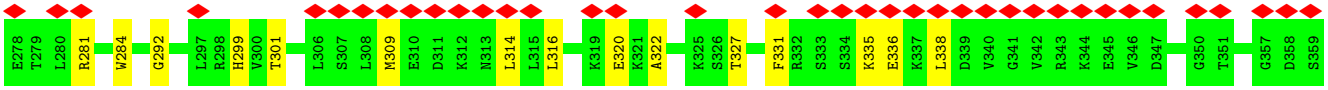
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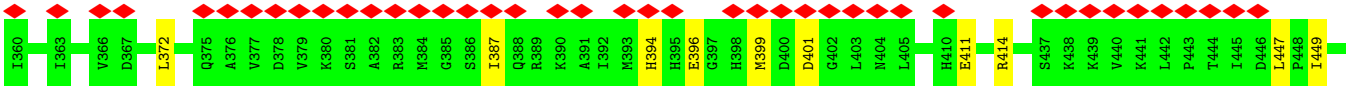


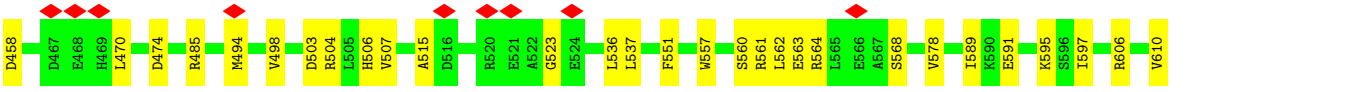


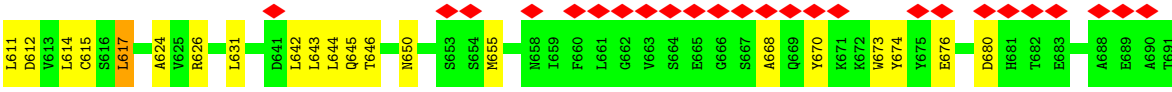


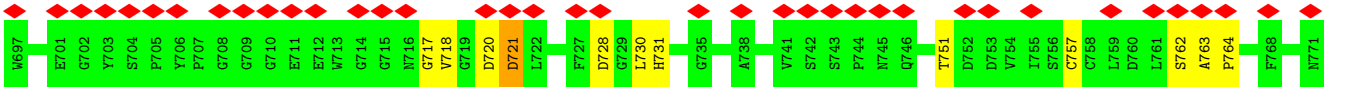


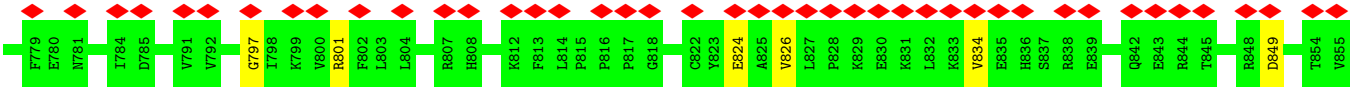


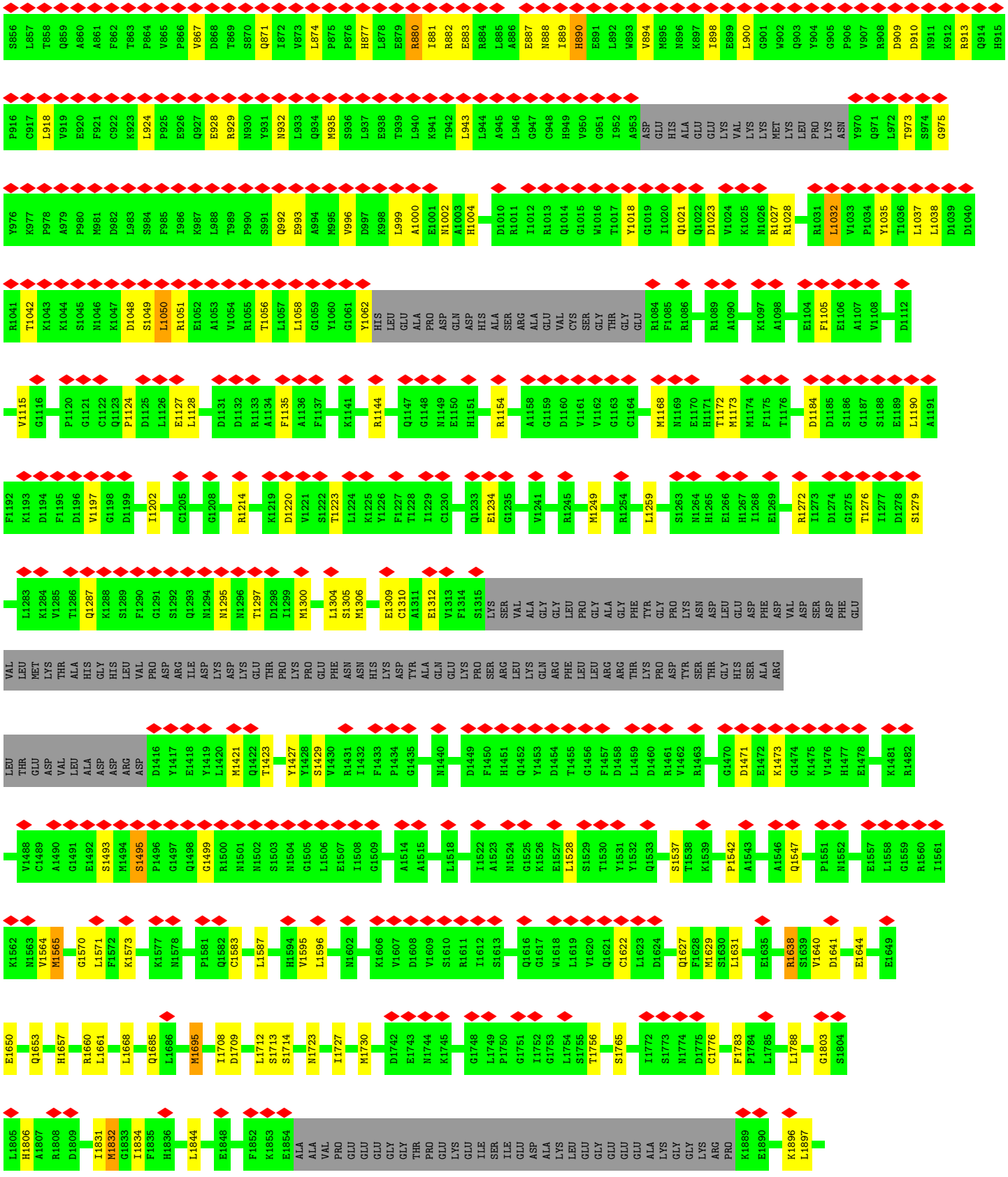


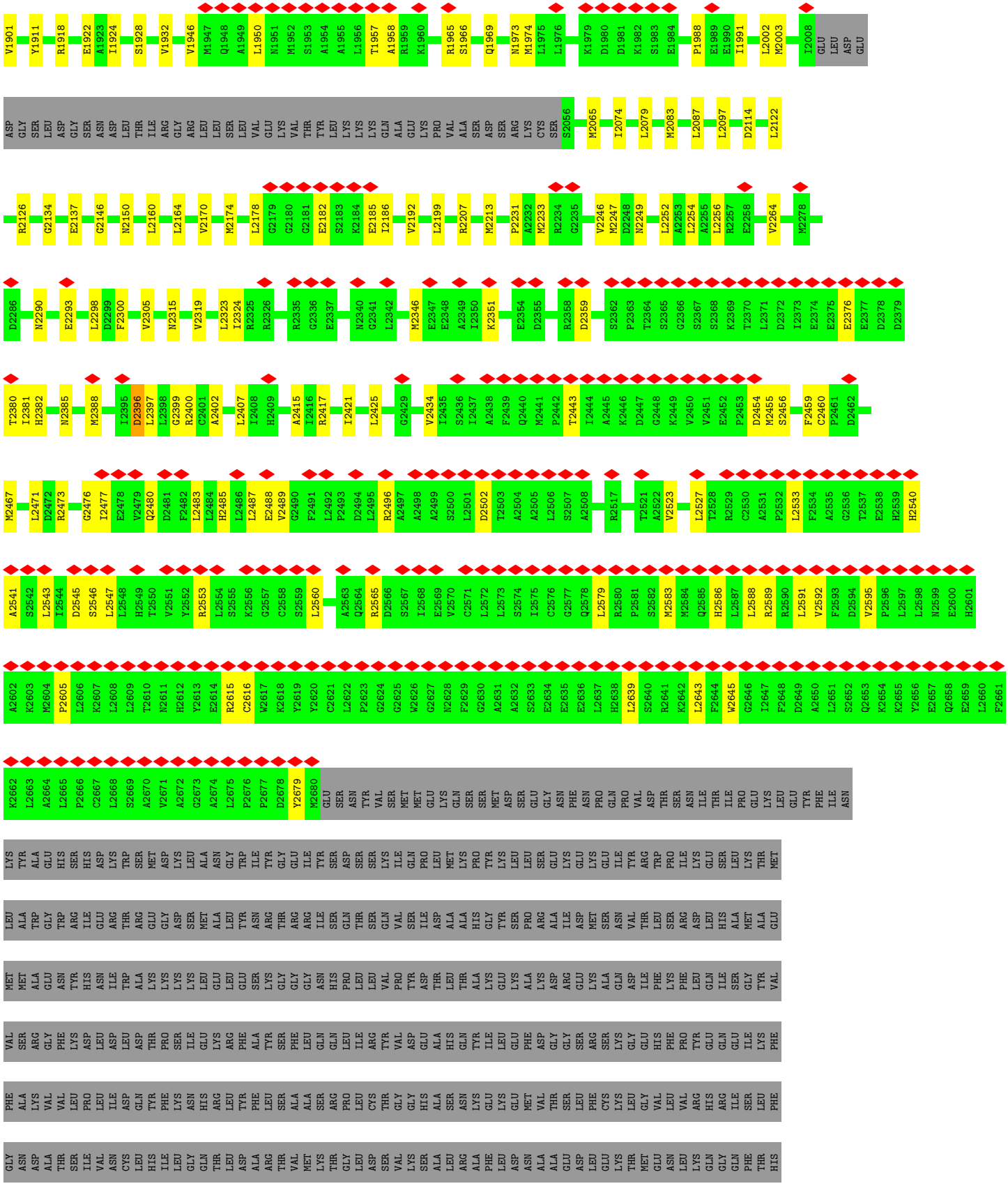


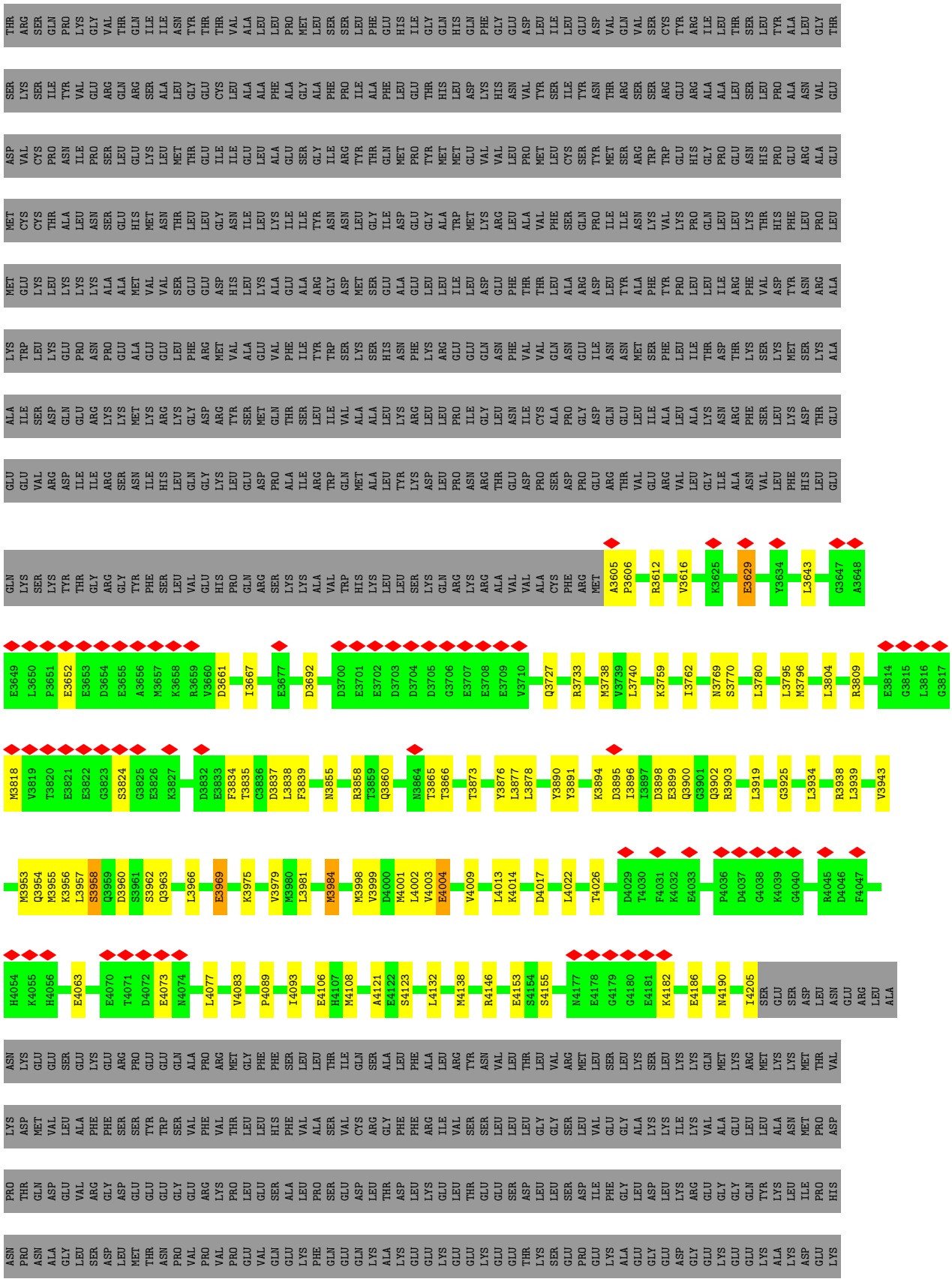


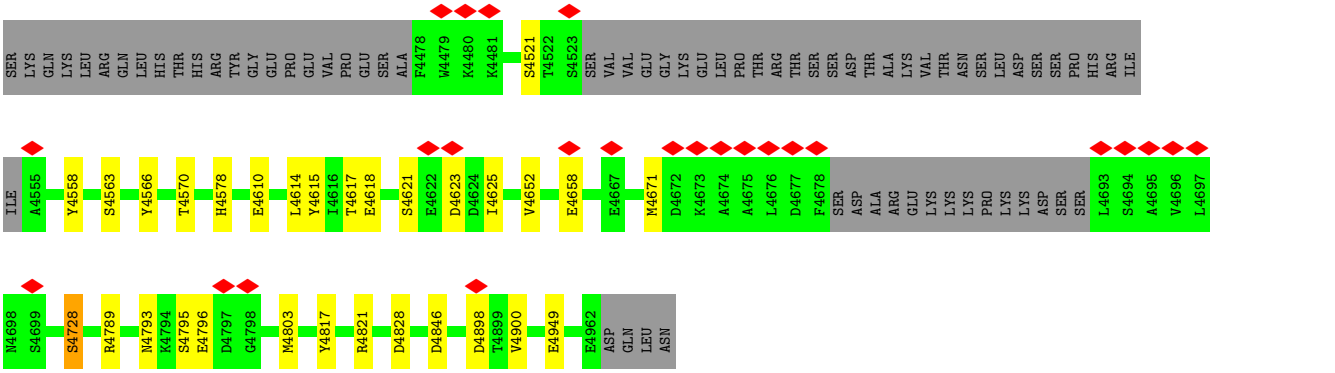





S856 L857 T858 Q859 A860 A861 F862 T863 P864 V865 P866 V867 D868 T869 S870 Q871 I872 V873 L874 P875 P876 H877 L878 E879 R880 I881 R882 E883 R884 L885 A886 E887 N888 I889 H890 E891 L892 W893 V894 M895 N896 K897 I898 E899 L900 G901 W902 Q903 Y904 G905 P906 V907 R908 D909 D910 N911 K912 R913 Q914 H915
P916 C917 L918 V919 E920 F921 C922 K923 L924 P925 E926 Q927 E928 R929 N930 Y931 N932 L933 Q934 M935 S936 L937 E938 T939 L940 K941 T942 L943 L944 A945 L946 G947 C948 H949 V950 G951 I952 A953 ASP GLU HIS ALA GLU GLU LYS VAL LYS LYS MET LYS LEU PRO LYS ASN Y970 Q971 L972 T973 S974 G975
Y976 K977 P978 A979 P980 M981 D982 L983 S984 F985 I986 K987 L988 T989 P990 S991 Q992 E993 A994 M995 V996 D997 K998 L999 A1000 E1001 N1002 A1003 H1004 D1010 R1011 I1012 R1013 Q1014 G1015 W1016 T1017 Y1018 G1019 I1020 Q1021 Q1022 D1023 V1024 K1025 N1026 R1027 R1028 R1031 L1032 V1033 P1034 Y1035 T1036 L1037 L1038 D1039 D1040
R1041 T1042 K1043 K1044 S1045 N1046 K1047 D1048 S1049 L1050 R1051 E1052 A1053 V1054 R1055 T1056 L1057 L1058 G1059 Y1060 G1061 Y1062 HIS LEU GLU ALA PRO ASP GLN ASP HIS ALA SER ARG ALA GLU VAL CYS SER GLY THR GLY GLU R1084 F1085 R1086 R1089 A1090 K1097 A1098 E1104 F1105 E1106 A1107 V1108 D1112
V1115 G1116 P1120 G1121 C1122 Q1123 P1124 D1125 L1126 E1127 L1128 D1131 D1132 R1133 A1134 F1135 A1136 F1137 K1141 R1144 Q1147 G1148 N1149 E1150 H1151 R1154 A1158 G1159 D1160 V1161 V1162 G1163 C1164 M1168 N1169 E1170 H1171 T1172 M1173 M1174 F1175 T1176 D1184 D1185 S1186 G1187 S1188 E1189 L1190 A1191
F1192 K1193 D1194 F1195 D1196 V1197 G1198 D1199 I1202 C1205 G1208 R1214 K1219 D1220 V1221 S1222 T1223 L1224 K1225 Y1226 F1227 T1228 I1229 C1230 Q1233 E1234 G1235 V1241 R1245 M1249 R1254 L1259 S1263 N1264 H1265 E1266 H1267 I1268 E1269 R1272 T1273 D1274 G1275 T1276 I1277 D1278 S1279
L1283 K1284 V1285 T1286 Q1287 K1288 S1289 F1290 G1291 S1292 Q1293 N1294 N1295 N1296 T1297 D1298 I1299 M1300 L1304 S1305 M1306 E1309 C1310 A1311 E1312 V1313 F1314 S1315 LYS SER VAL ALA GLY GLY LEU PRO GLY ALA GLY PHE TYR GLY PRO LYS ASN ASP LEU GLU ASP PHE ASP VAL ASP SER ASP PHE GLU
VAL LEU MET LYS THR ALA HIS GLY HIS LEU VAL PRO ASP ARG ILE ASP LYS ASP LYS GLU THR PRO LYS PRO GLU PHE ASN ASN HIS LYS ASP TYR ALA GLN GLU LYS PRO SER ARG LEU LYS GLN ARG PHE LEU LEU ARG ARG THR LYS PRO ASP TYR SER THR GLY HIS SER ALA ARG
LEU THR GLU ASP VAL LEU ALA ASP ASP ARG ASP D1416 Y1417 E1418 Y1419 L1420 M1421 Q1422 T1423 Y1427 Y1428 S1429 V1430 R1431 I1432 F1433 P1434 G1435 N1440 D1449 F1450 H1451 Q1452 Y1453 D1454 T1455 G1456 F1457 D1458 L1459 D1460 R1461 V1462 R1463 G1470 D1471 E1472 K1473 G1474 K1475 V1476 H1477 E1478 K1481 R1482
V1488 C1489 A1490 G1491 E1492 S1493 M1494 S1495 P1496 G1497 Q1498 G1499 R1500 N1501 N1502 S1503 N1504 G1505 L1506 E1507 I1508 G1509 A1514 A1515 L1518 I1522 A1523 N1524 G1525 K1526 E1527 L1528 S1529 T1530 Y1531 Y1532 Q1533 S1537 T1538 K1539 P1542 A1543 A1546 Q1547 P1551 N1552 E1557 L1558 G1559 R1560 I1561
K1562 N1563 V1564 M1565 G1570 L1571 F1572 K1573 K1577 N1578 P1581 Q1582 C1583 L1587 H1594 V1595 L1596 N1602 K1606 V1607 D1608 V1609 S1610 R1611 I1612 S1613 Q1616 G1617 W1618 L1619 V1620 Q1621 C1622 L1623 D1624 Q1627 F1628 M1629 S1630 L1631 E1635 R1638 S1639 V1640 D1641 E1644 E1649
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L1805 H1806 A1807 R1808 D1809 I1831 M1832 G1833 I1834 F1835 H1836 L1844 E1848 F1852 K1853 E1854 ALA ALA VAL PRO GLU GLU GLY GLY GLY THR PRO GLU LYS GLU ILE SER ILE GLU ASP ALA LYS LEU GLU GLY GLY GLU GLU GLU ALA LYS GLY GLY LYS ARG PRO K1889 E1890 K1896 L1897

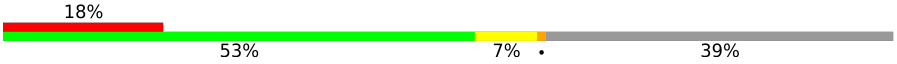

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ASP GLY SER LEU ASP GLY SER ASN ASP LEU THR ILE ARG GLY ARG LEU LEU SER LEU VAL GLU LYS VAL THR TYR LEU LYS LYS GLN ALA GLU LYS PRO VAL ALA SER ASP SER ARG LYS CYS SER S2056 M2065 I2074 L2079 M2083 L2087 L2097 D2114 L2122
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D2286 N2290 E2293 L2298 D2299 F2300 V2305 N2315 V2319 L2323 I2324 R2325 R2326 R2335 G2336 E2337 N2340 G2341 L2342 M2346 E2347 E2348 A2349 I2350 K2351 E2354 D2355 R2358 D2359 S2362 P2363 T2364 S2365 G2366 S2367 S2368 K2369 T2370 L2371 D2372 I2373 E2374 E2375 E2376 E2377 D2378 D2379
T2380 I2381 H2382 N2385 M2388 I2395 D2396 L2397 L2398 G2399 R2400 C2401 A2402 L2407 I2408 H2409 A2415 I2416 R2417 I2421 L2425 G2429 V2434 I2435 S2436 I2437 A2438 F2439 Q2440 M2441 P2442 T2443 I2444 A2445 K2446 D2447 G2448 K2449 V2450 V2451 E2452 P2453 D2454 M2455 S2456 F2459 C2460 P2461 D2462
M2467 L2471 D2472 R2473 G2476 I2477 E2478 V2479 Q2480 D2481 F2482 L2483 L2484 H2485 L2486 L2487 E2488 V2489 G2490 F2491 L2492 P2493 D2494 L2495 R2496 A2497 A2498 A2499 S2500 L2501 D2502 T2503 A2504 A2505 L2506 S2507 A2508 R2517 T2521 A2522 V2523 L2527 T2528 R2529 C2530 A2531 P2532 L2533 F2534 A2535 G2536 T2537 E2538 H2539 H2540
A2541 S2542 L2543 T2544 D2545 L2606 S2546 K2607 L2547 L2608 L2548 L2609 H2549 T2610 T2550 N2611 V2551 H2612 Y2552 Y2613 R2553 E2614 L2554 R2615 S2555 C2616 K2556 W2617 G2557 K2618 C2558 Y2619 S2559 Y2620 L2560 C2621 A2563 L2622 Q2564 P2623 R2565 G2624 D2566 G2625 S2567 W2626 I2568 G2627 E2569 N2628 V2570 F2629 C2571 G2630 L2572 A2631 L2573 A2632 S2574 S2633 I2575 E2634 C2576 E2635 G2577 E2636 Q2578 L2637 L2579 H2638 R2580 L2639 P2581 S2640 S2582 R2641 M2583 K2642 M2584 L2643 Q2585 F2644 H2586 W2645 L2587 G2646 L2588 I2647 R2589 F2648 R2590 D2649 L2591 A2650 V2592 L2651 F2593 S2652 D2594 Q2653 V2595 K2654 P2596 K2655 L2597 Y2656 L2598 E2657 N2599 Q2658 E2600 E2659 H2601 L2660 F2661
K2662 L2663 A2664 L2665 P2666 C2667 L2668 S2669 A2670 V2671 A2672 G2673 A2674 L2675 P2676 P2677 D2678 Y2679 M2680 GLU SER ASN TYR VAL SER MET MET GLU LYS GLN SER SER MET ASP SER GLU GLY ASN PHE ASN PRO GLN PRO VAL ASP THR SER ASN ILE THR ILE PRO GLU LYS LEU GLU TYR PHE ILE ASN
LYS TYR ALA GLU HIS SER HIS ASP LYS TRP SER MET ASP LYS LEU ALA ASN GLY TRP ILE TYR GLY GLU ILE TYR SER ASP SER SER LYS ILE GLN PRO LEU MET MET LYS PRO TYR LYS LEU SER GLU LYS LYS GLU ILE TYR ARG TRP PRO ILE LYS GLU SER LEU LYS THR MET
LEU ALA TRP GLY TRP ARG ILE GLU ARG THR ARG GLU GLY ASP SER MET ALA LEU TYR ASN ARG THR ARG ARG ILE SER GLN THR SER GLN VAL SER ILE ASP ALA ALA HIS GLY TYR SER PRO ARG ALA ILE ASP MET SER ASN VAL THR LEU SER ARG ASP LEU HIS ALA MET ALA GLU
MET MET ALA GLU ASN TYR HIS ASN ILE TRP ALA LYS LYS LYS LEU GLU LEU GLU SER LYS GLY GLY GLY ASN HIS PRO LEU LEU VAL PRO TYR ASP THR LEU THR ALA LYS GLU LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU GLN ILE ILE SER GLY TYR VAL
VAL SER ARG GLY PHE LYS ASP LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN TYR ILE LEU GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR GLU GLN ILE GLU LYS PHE
PHE ALA LYS VAL VAL LEU PRO LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY HIS ALA SER ASN LYS GLU LYS GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU VAL ARG HIS ARG ILE SER LEU PHE
GLY ASN ASP ALA THR SER ILE VAL ASN CYS LEU HIS ILE LEU GLY GLN THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS SER ALA LEU ARG ALA PHE LEU ASP ASN ALA ALA GLU ASP LEU GLU LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE THR HIS

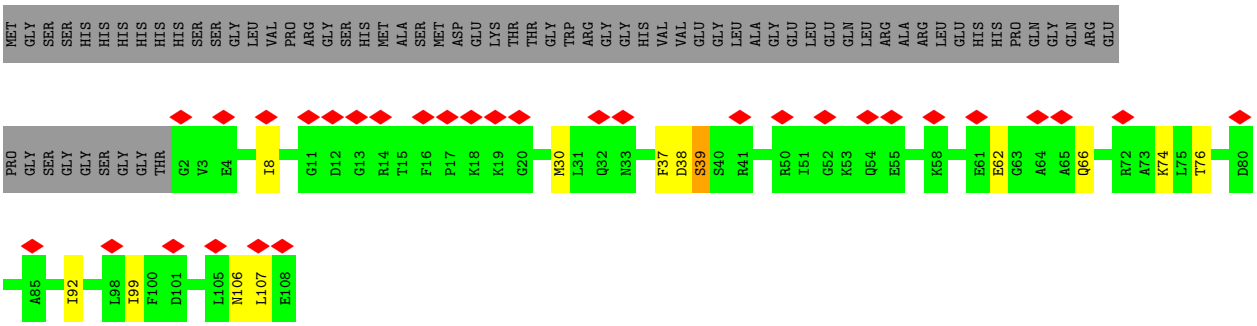




• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain G:

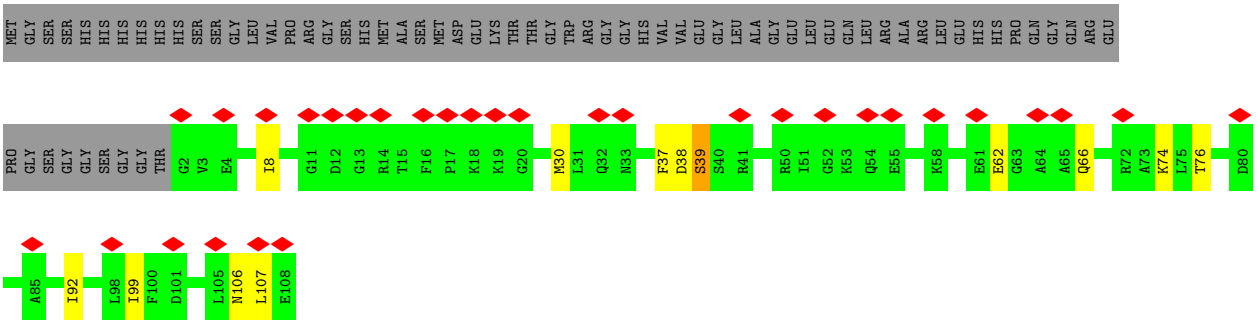




• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain H:

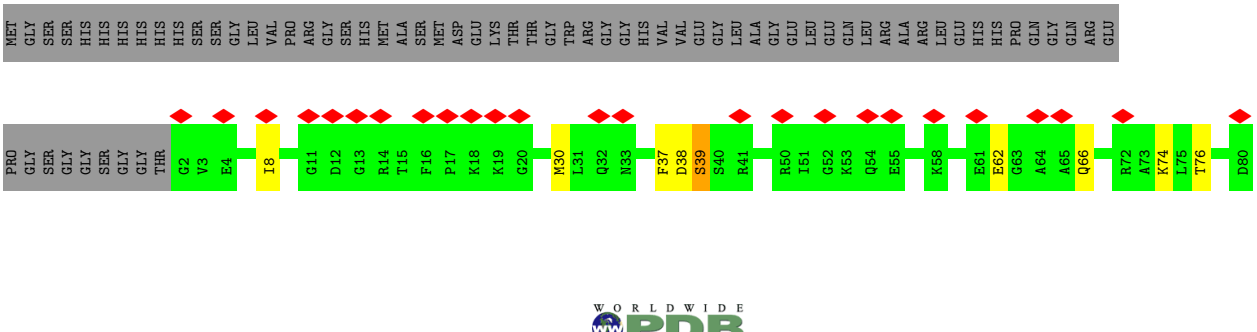


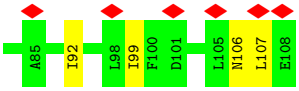


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain I:





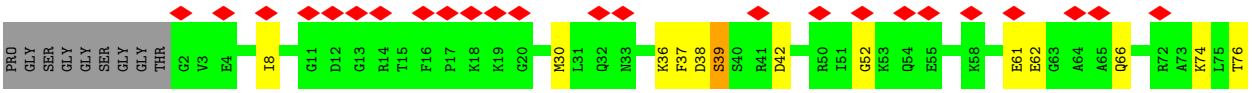


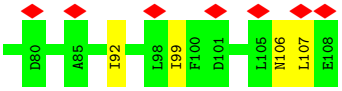
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain J:









4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	366532	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.185	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	471.04, 471.04, 471.04	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.92, 0.92, 0.92	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, ZN, A1MG7

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.19	0/28507	0.41	1/38529 (0.0%)
1	B	0.19	0/28507	0.41	1/38529 (0.0%)
1	C	0.19	0/28507	0.41	1/38529 (0.0%)
1	D	0.19	0/28507	0.41	1/38529 (0.0%)
2	G	0.16	0/835	0.40	0/1123
2	H	0.16	0/835	0.40	0/1123
2	I	0.16	0/835	0.40	0/1123
2	J	0.16	0/835	0.39	0/1123
All	All	0.19	0/117368	0.41	4/158608 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1832	MET	CB-CG-SD	5.17	128.23	112.70
1	C	1832	MET	CB-CG-SD	5.17	128.22	112.70
1	A	1832	MET	CB-CG-SD	5.16	128.19	112.70
1	D	1832	MET	CB-CG-SD	5.16	128.18	112.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3925	GLY	Peptide
1	B	3925	GLY	Peptide
1	C	3925	GLY	Peptide
1	D	3925	GLY	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	27897	27527	27526	342	0
1	B	27897	27527	27526	342	0
1	C	27897	27527	27526	337	0
1	D	27897	27527	27526	336	0
2	G	819	821	821	7	0
2	H	819	821	821	7	0
2	I	819	821	821	7	0
2	J	819	821	821	10	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	25	12	0	0	0
5	B	25	12	0	0	0
5	C	25	12	0	0	0
5	D	25	12	0	0	0
All	All	114972	113440	113388	1351	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1351 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3934:LEU:HD12	1:C:3939:LEU:HD22	1.47	0.97
1:D:3934:LEU:HD12	1:D:3939:LEU:HD22	1.47	0.97
1:B:3934:LEU:HD12	1:B:3939:LEU:HD22	1.47	0.96
1:A:3934:LEU:HD12	1:A:3939:LEU:HD22	1.47	0.95
1:A:889:ILE:HG21	1:A:935:MET:HE1	1.66	0.78

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3473/4966 (70%)	3381 (97%)	92 (3%)	0	100	100
1	B	3473/4966 (70%)	3381 (97%)	92 (3%)	0	100	100
1	C	3473/4966 (70%)	3381 (97%)	92 (3%)	0	100	100
1	D	3473/4966 (70%)	3381 (97%)	92 (3%)	0	100	100
2	G	105/176 (60%)	94 (90%)	11 (10%)	0	100	100
2	H	105/176 (60%)	94 (90%)	11 (10%)	0	100	100
2	I	105/176 (60%)	94 (90%)	11 (10%)	0	100	100
2	J	105/176 (60%)	94 (90%)	11 (10%)	0	100	100
All	All	14312/20568 (70%)	13900 (97%)	412 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	3056/4355 (70%)	2994 (98%)	62 (2%)	48 78
1	B	3056/4355 (70%)	2995 (98%)	61 (2%)	48 78
1	C	3056/4355 (70%)	2996 (98%)	60 (2%)	48 78
1	D	3056/4355 (70%)	2994 (98%)	62 (2%)	48 78
2	G	88/140 (63%)	87 (99%)	1 (1%)	65 88
2	H	88/140 (63%)	87 (99%)	1 (1%)	65 88
2	I	88/140 (63%)	87 (99%)	1 (1%)	65 88
2	J	88/140 (63%)	87 (99%)	1 (1%)	65 88
All	All	12576/17980 (70%)	12327 (98%)	249 (2%)	48 78

5 of 249 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4155	SER
1	D	2443	THR
1	C	1050	LEU
1	D	2396	ASP
1	D	4132	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4926	ASN
1	D	3766	ASN
1	C	4935	GLN
1	D	1648	GLN
1	D	4487	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	A1MG7	B	5003	-	27,27,27	1.62	6 (22%)	36,38,38	2.50	10 (27%)
5	A1MG7	A	5003	-	27,27,27	1.62	5 (18%)	36,38,38	2.50	10 (27%)
5	A1MG7	D	5003	-	27,27,27	1.62	5 (18%)	36,38,38	2.50	10 (27%)
5	A1MG7	C	5003	-	27,27,27	1.61	5 (18%)	36,38,38	2.51	10 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	A1MG7	B	5003	-	-	0/16/16/16	0/3/3/3
5	A1MG7	A	5003	-	-	0/16/16/16	0/3/3/3
5	A1MG7	D	5003	-	-	0/16/16/16	0/3/3/3
5	A1MG7	C	5003	-	-	0/16/16/16	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	5003	A1MG7	C-NAO	4.78	1.45	1.35
5	D	5003	A1MG7	C-NAO	4.78	1.45	1.35
5	A	5003	A1MG7	C-NAO	4.76	1.45	1.35
5	C	5003	A1MG7	C-NAO	4.76	1.45	1.35
5	A	5003	A1MG7	N-NAH	3.35	1.37	1.33

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	5003	A1MG7	CAG-NAH-N	7.98	108.02	101.70
5	B	5003	A1MG7	CAG-NAH-N	7.95	107.99	101.70
5	A	5003	A1MG7	CAG-NAH-N	7.94	107.99	101.70
5	D	5003	A1MG7	CAG-NAH-N	7.89	107.94	101.70
5	C	5003	A1MG7	NAH-N-NAJ	-7.38	107.77	114.03

There are no chirality outliers.

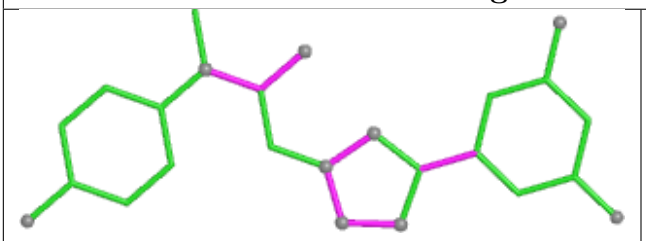
There are no torsion outliers.

There are no ring outliers.

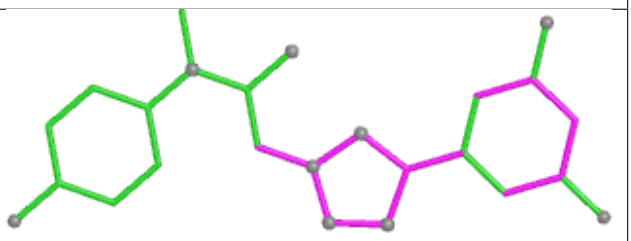
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

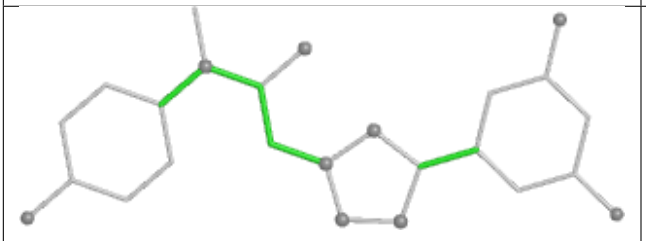
Ligand A1MG7 B 5003



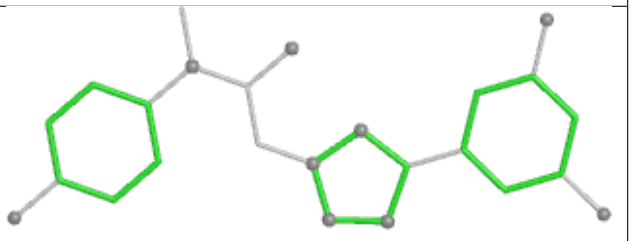
Bond lengths



Bond angles

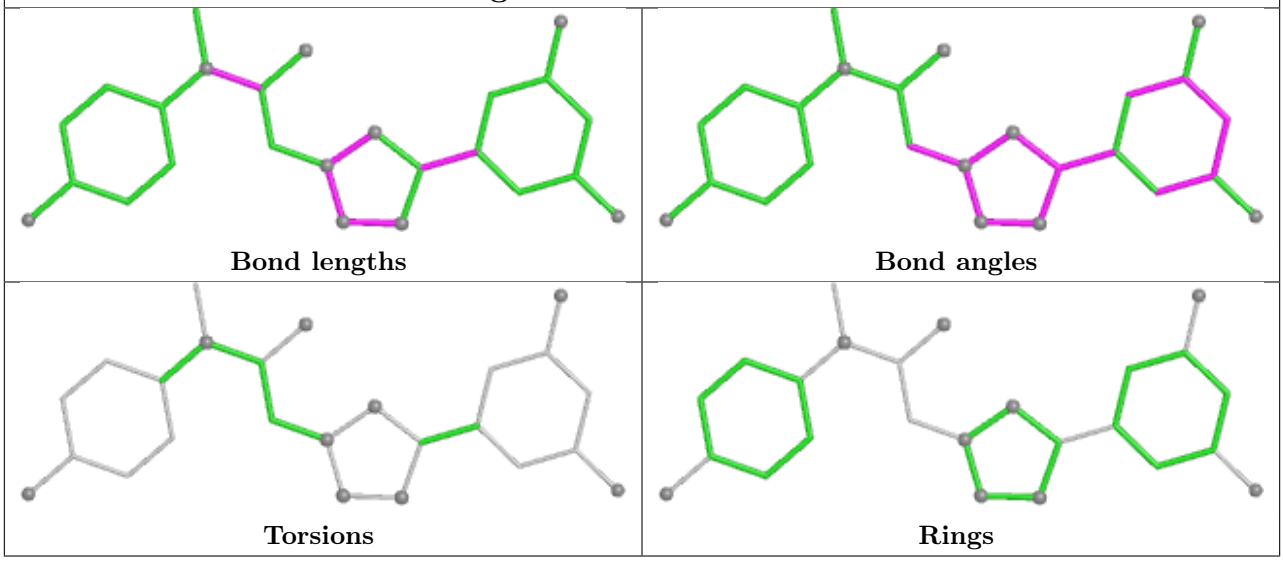


Torsions

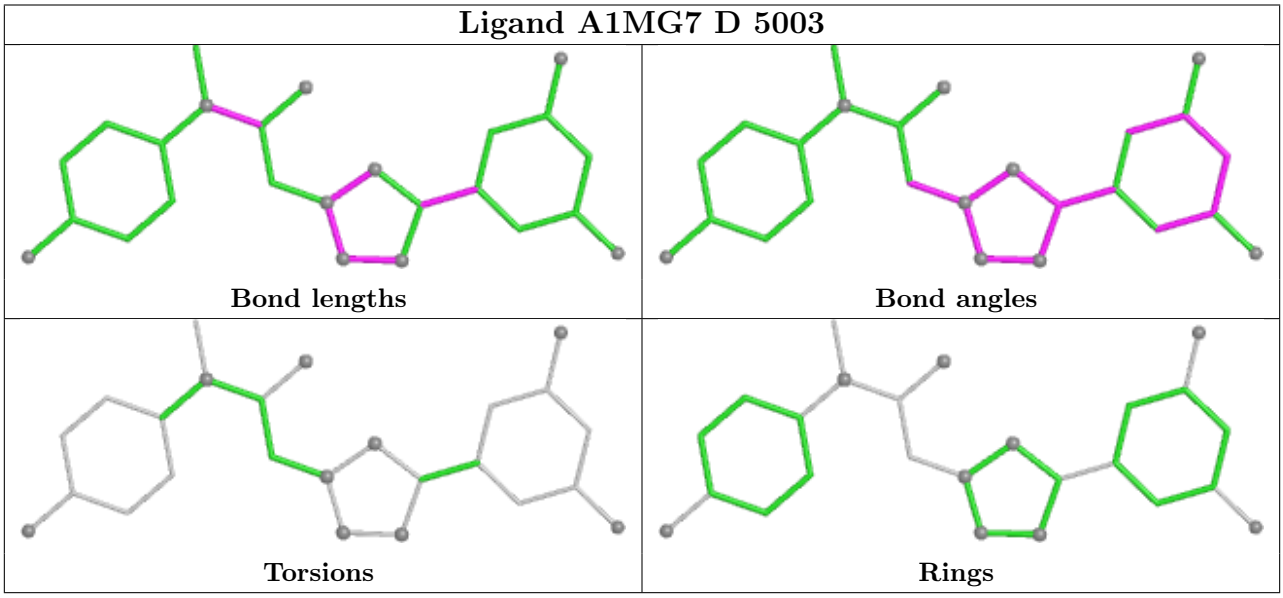


Rings

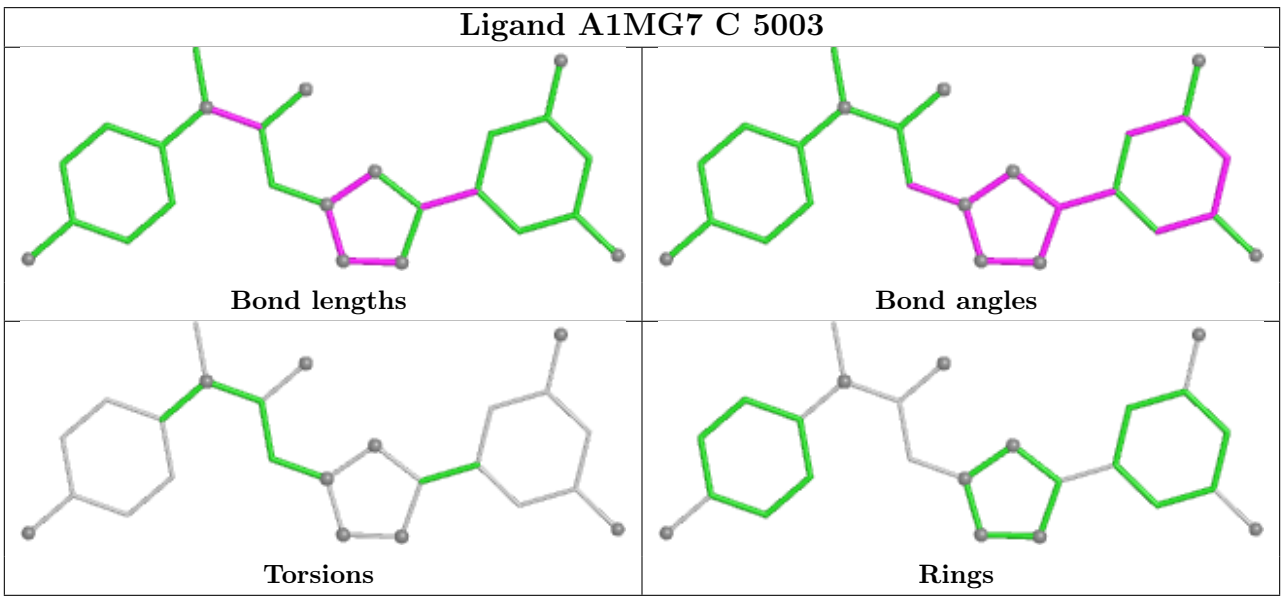
Ligand A1MG7 A 5003



Ligand A1MG7 D 5003



Ligand A1MG7 C 5003



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

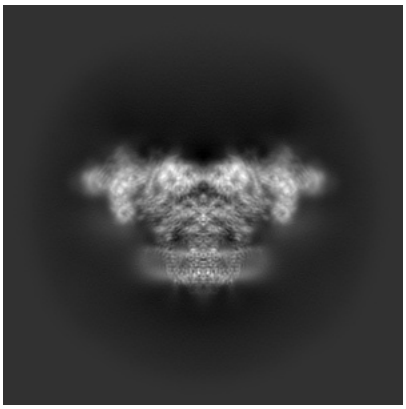
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-80685. These allow visual inspection of the internal detail of the map and identification of artifacts.

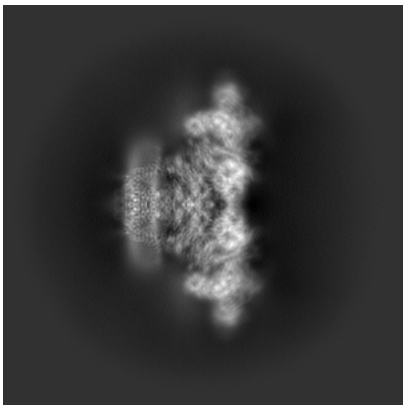
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

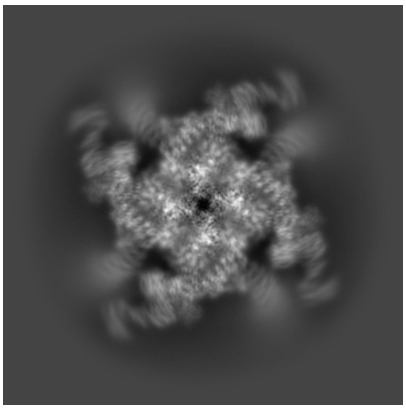
6.1.1 Primary map



X

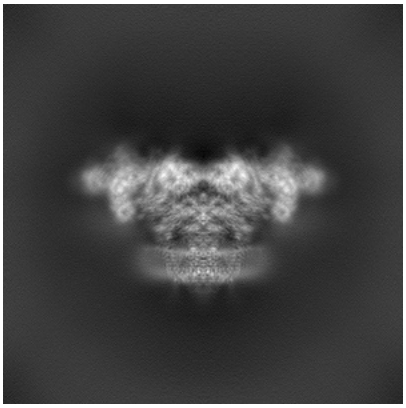


Y

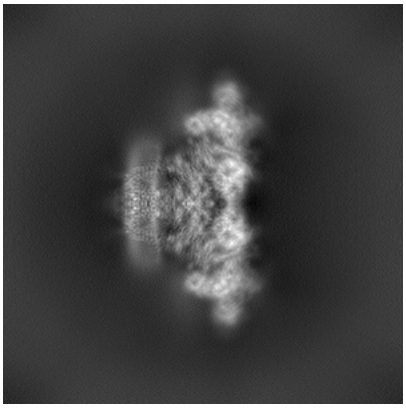


Z

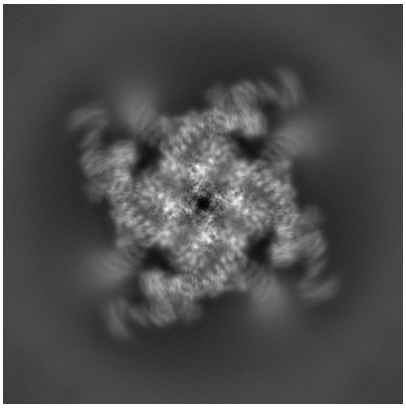
6.1.2 Raw map



X



Y

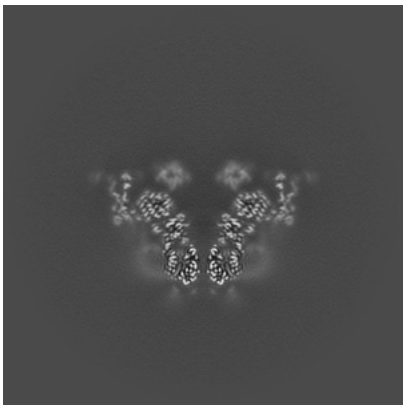


Z

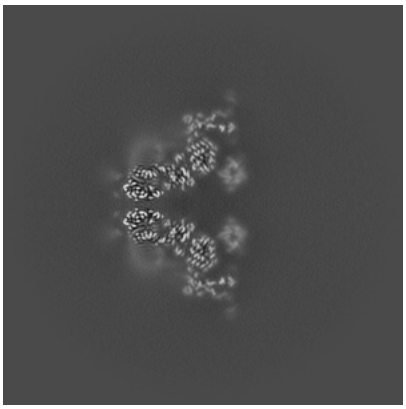
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

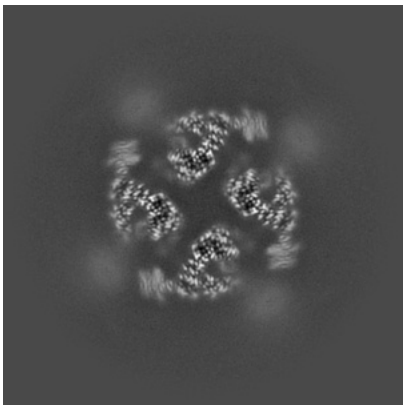
6.2.1 Primary map



X Index: 256

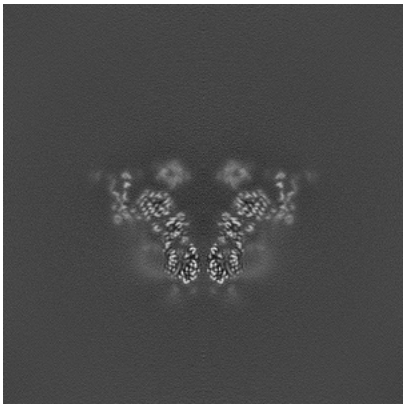


Y Index: 256

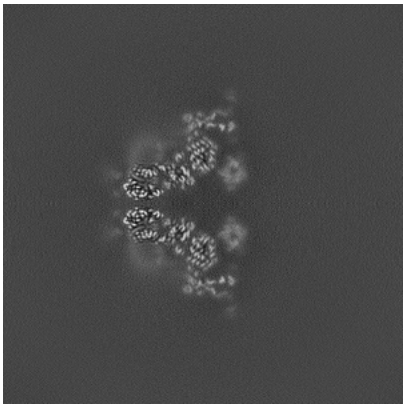


Z Index: 256

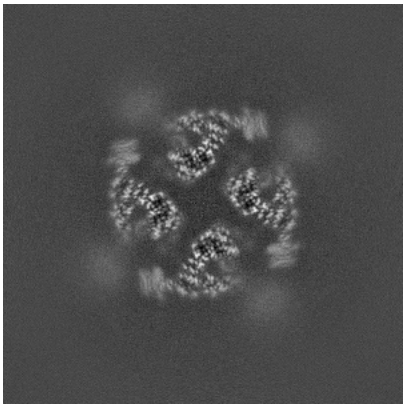
6.2.2 Raw map



X Index: 256



Y Index: 256

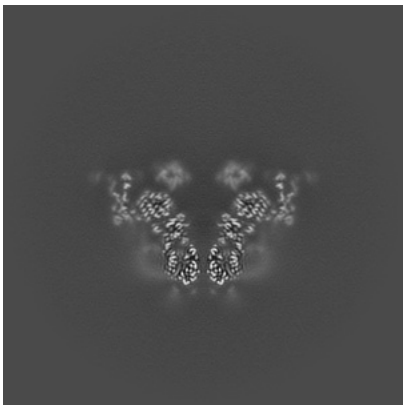


Z Index: 256

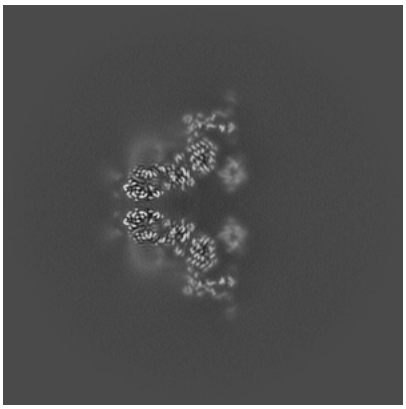
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

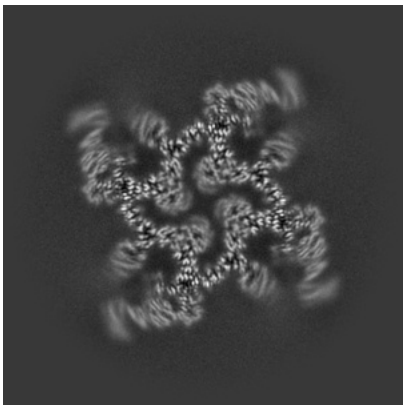
6.3.1 Primary map



X Index: 256

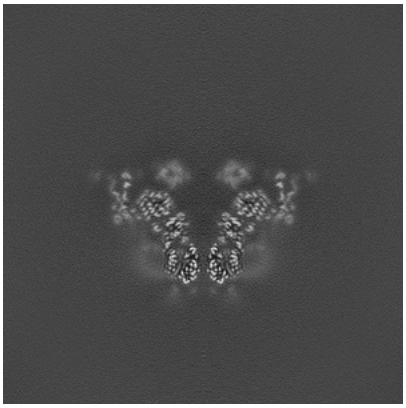


Y Index: 256

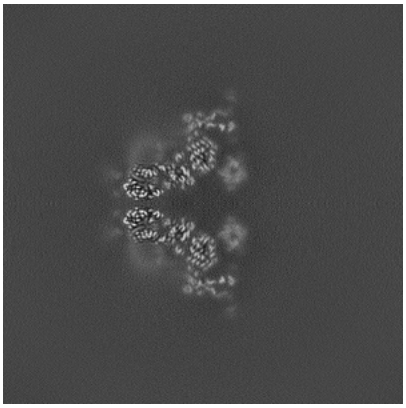


Z Index: 290

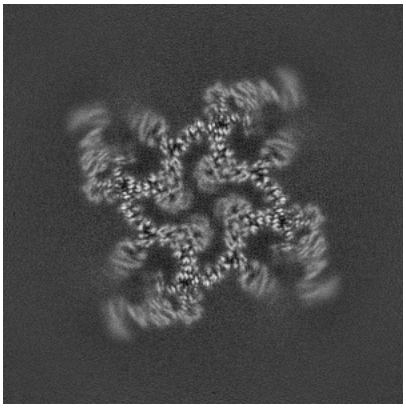
6.3.2 Raw map



X Index: 256



Y Index: 256

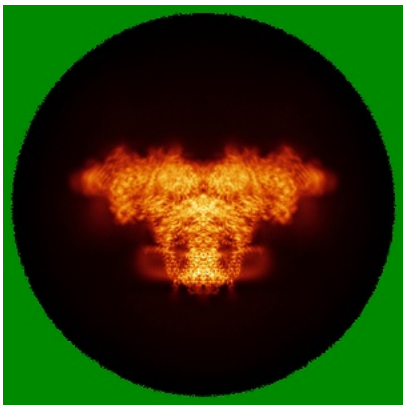


Z Index: 290

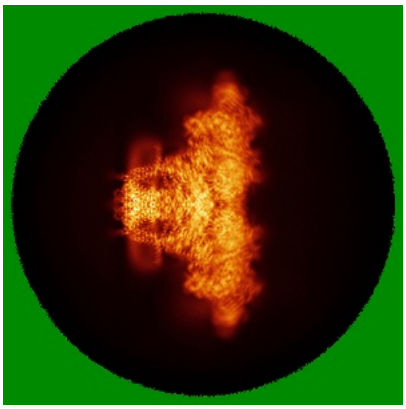
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

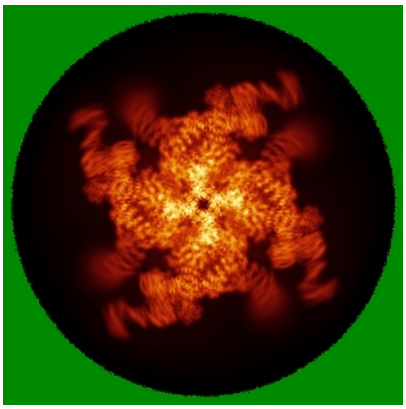
6.4.1 Primary map



X

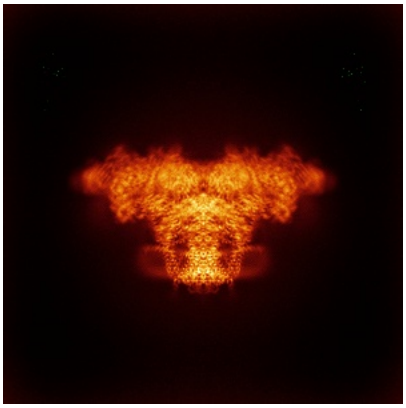


Y

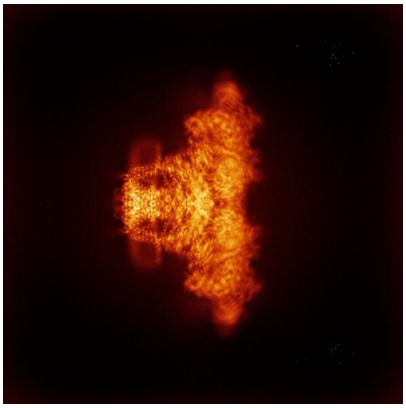


Z

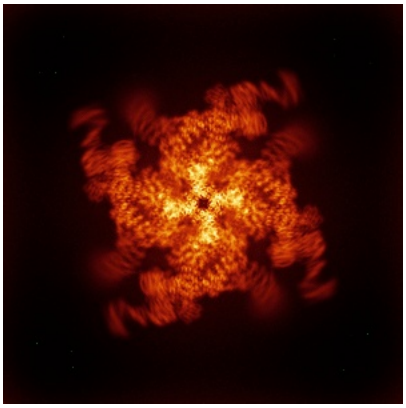
6.4.2 Raw map



X



Y

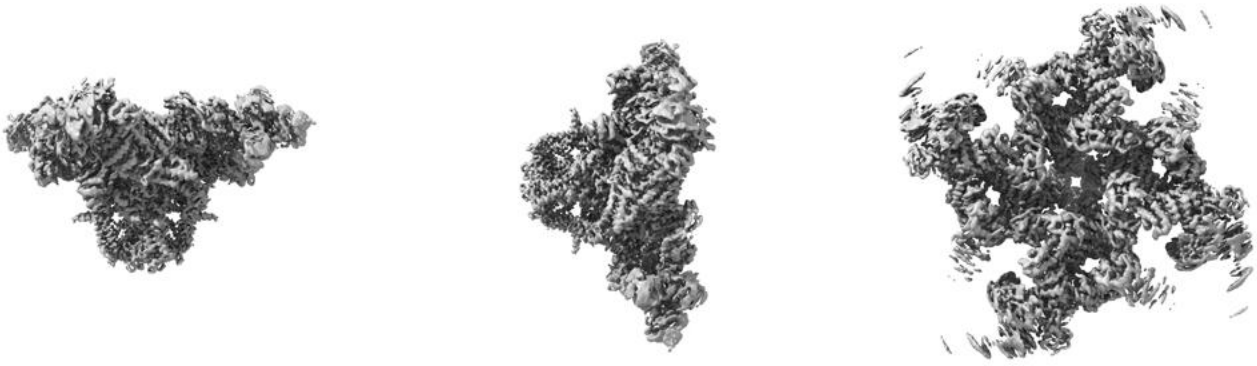


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

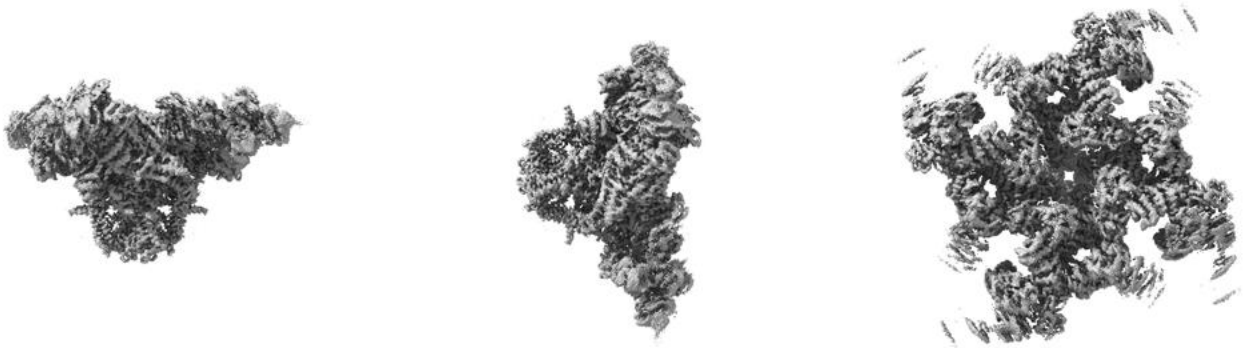
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

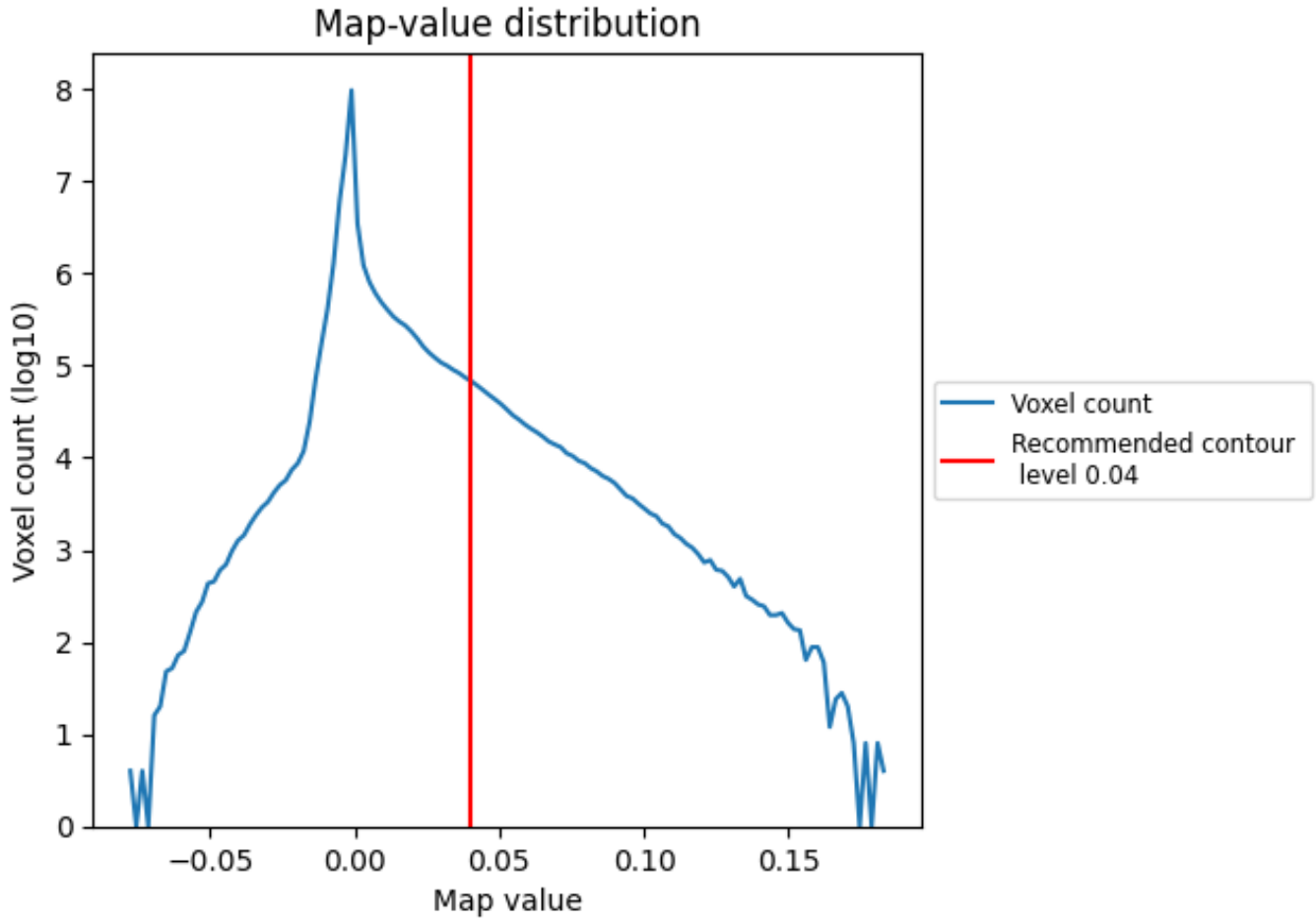
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

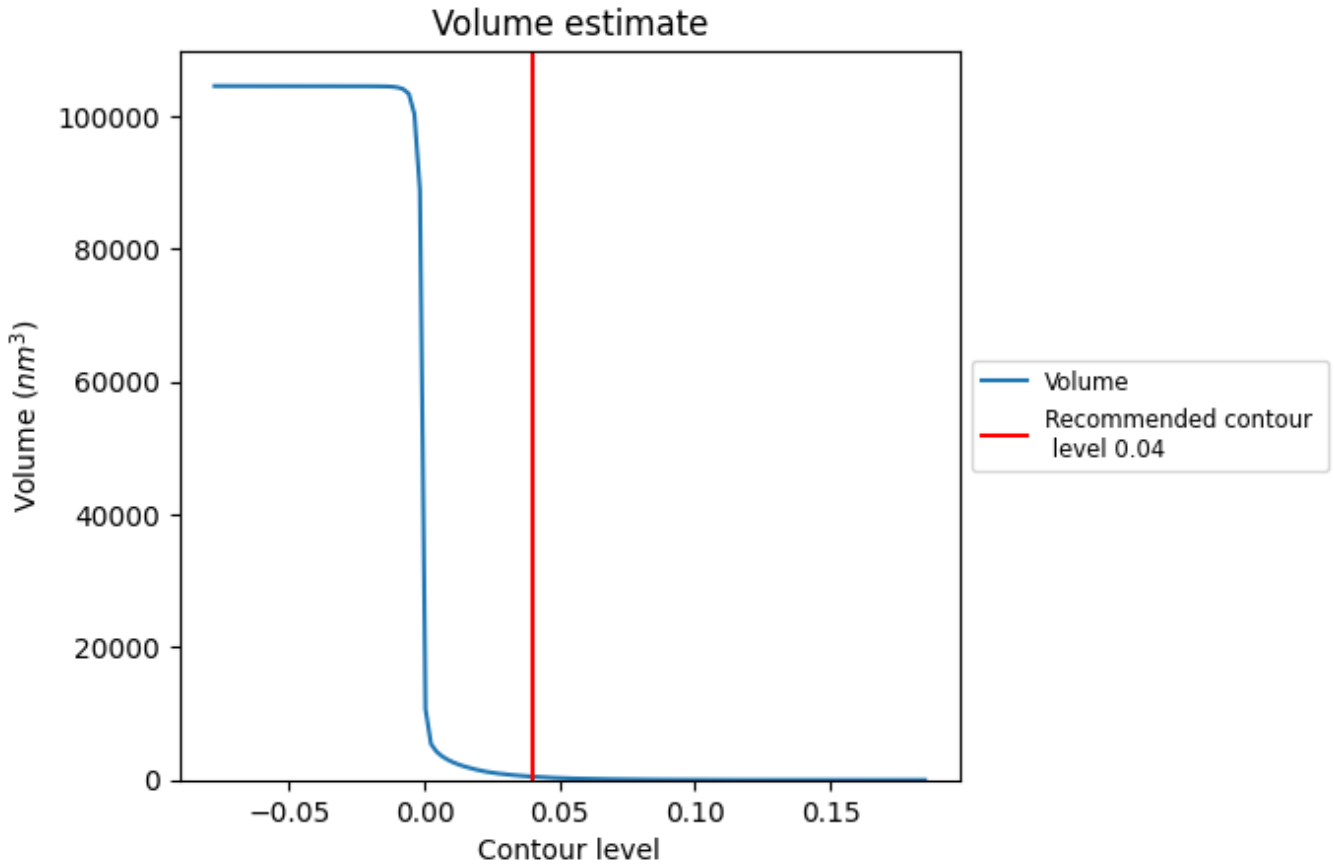
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

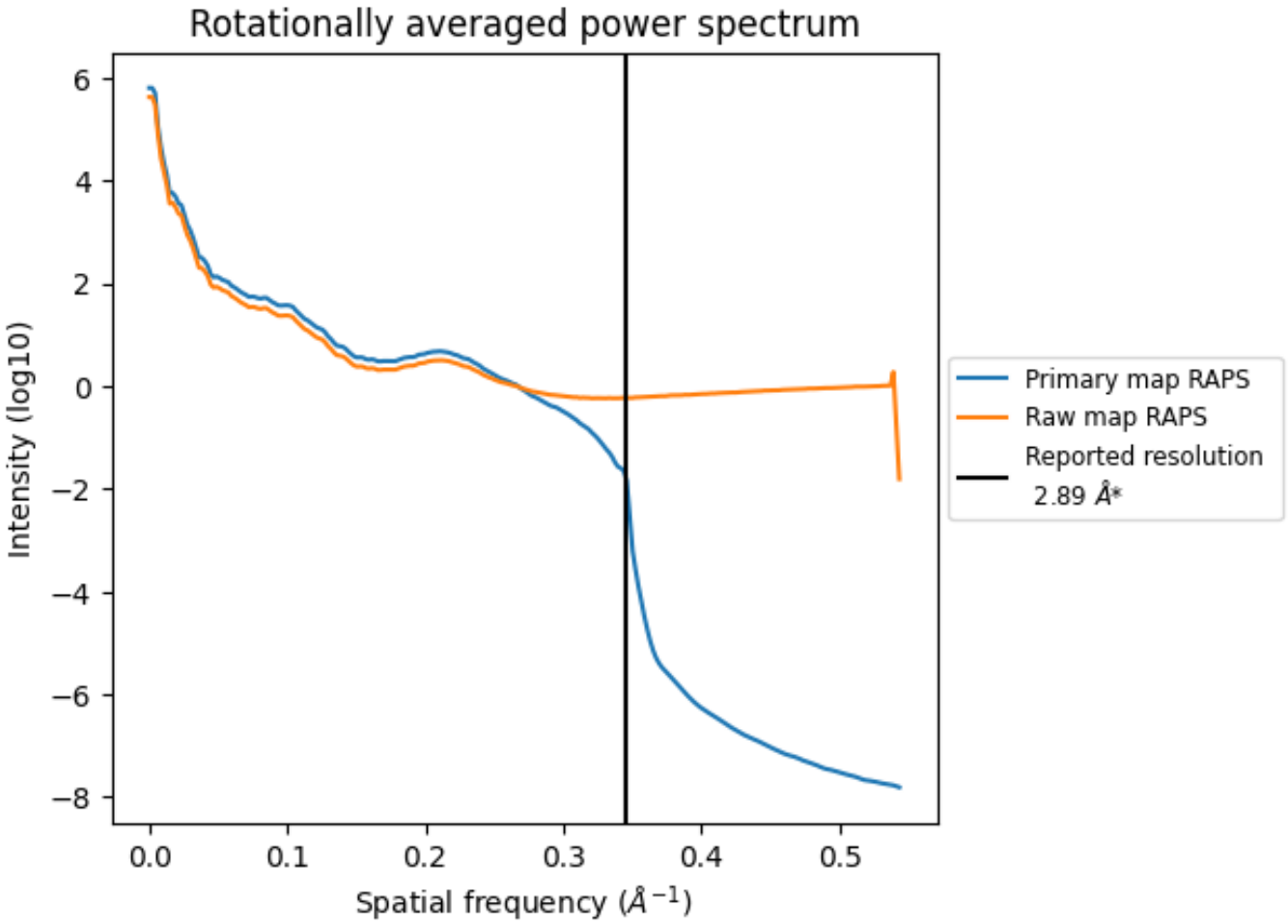
7.2 Volume estimate (i)



The volume at the recommended contour level is 500 nm^3; this corresponds to an approximate mass of 452 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

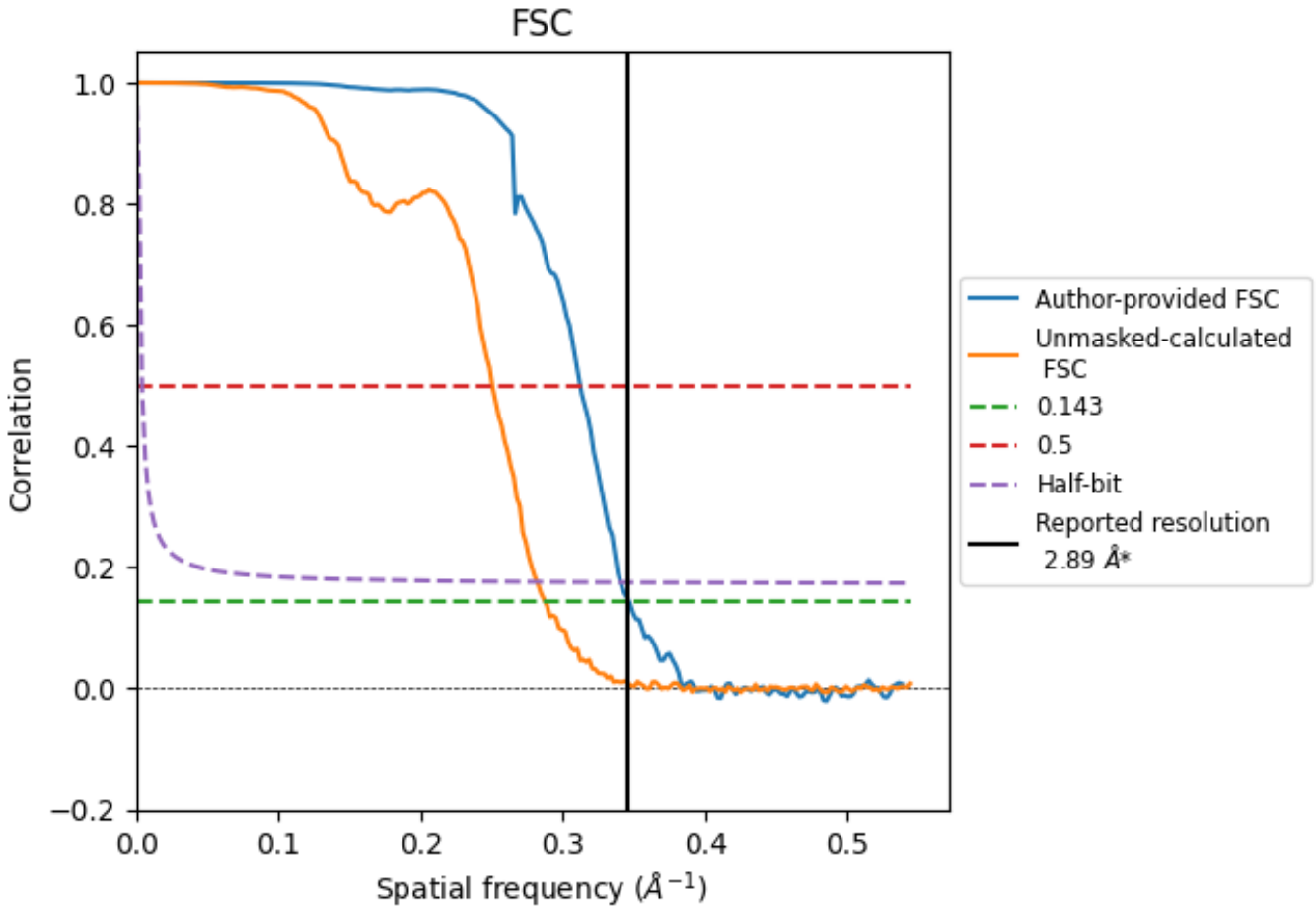


*Reported resolution corresponds to spatial frequency of 0.346 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.346 Å^{-1}

8.2 Resolution estimates (i)

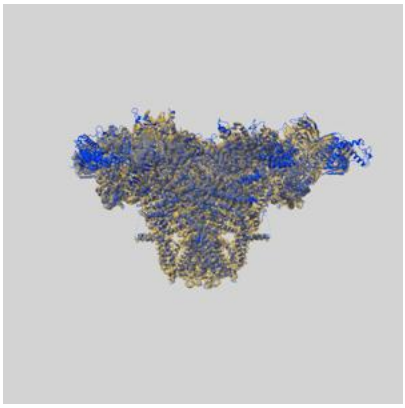
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.89	3.20	2.94
Unmasked-calculated*	3.48	4.00	3.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.48 differs from the reported value 2.89 by more than 10 %

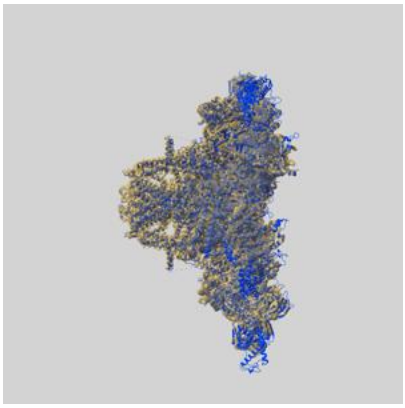
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-80685 and PDB model 26IQ. Per-residue inclusion information can be found in section 3 on page 13.

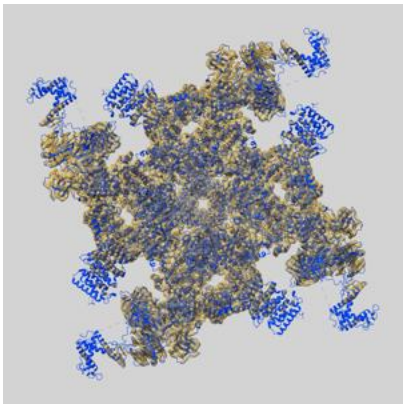
9.1 Map-model overlay



X



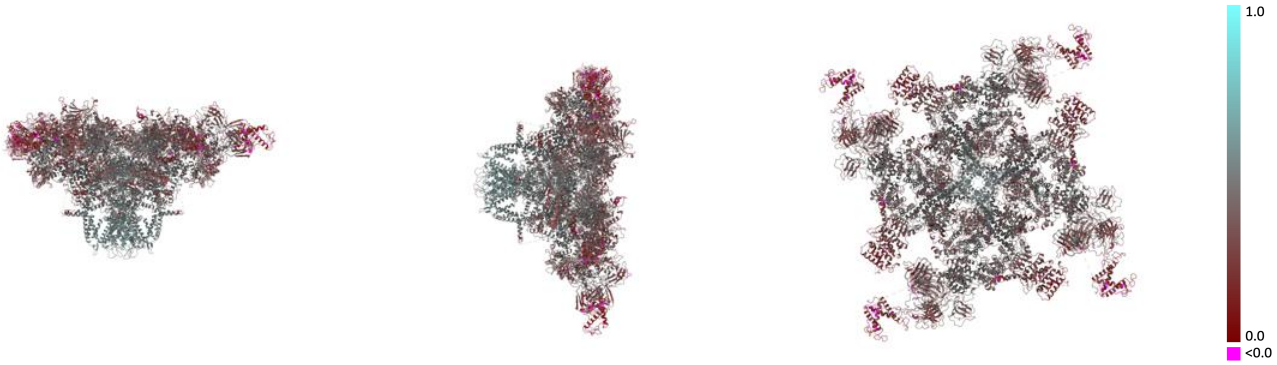
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

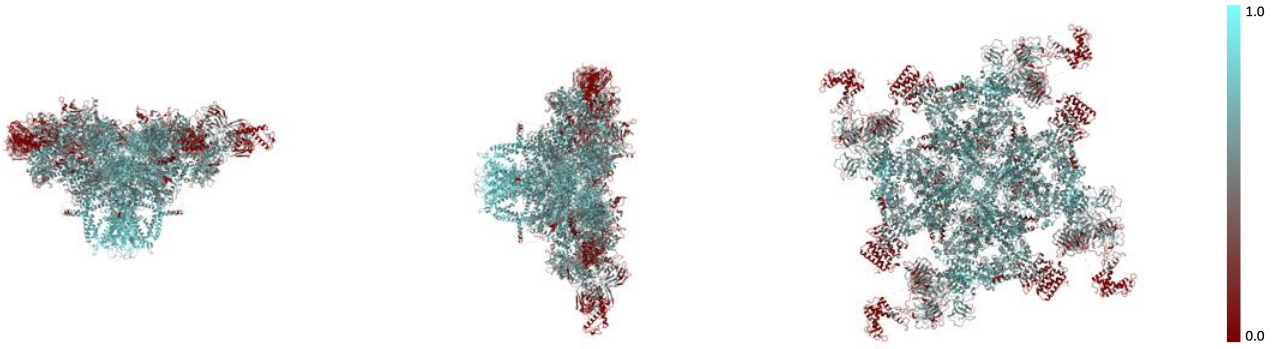
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

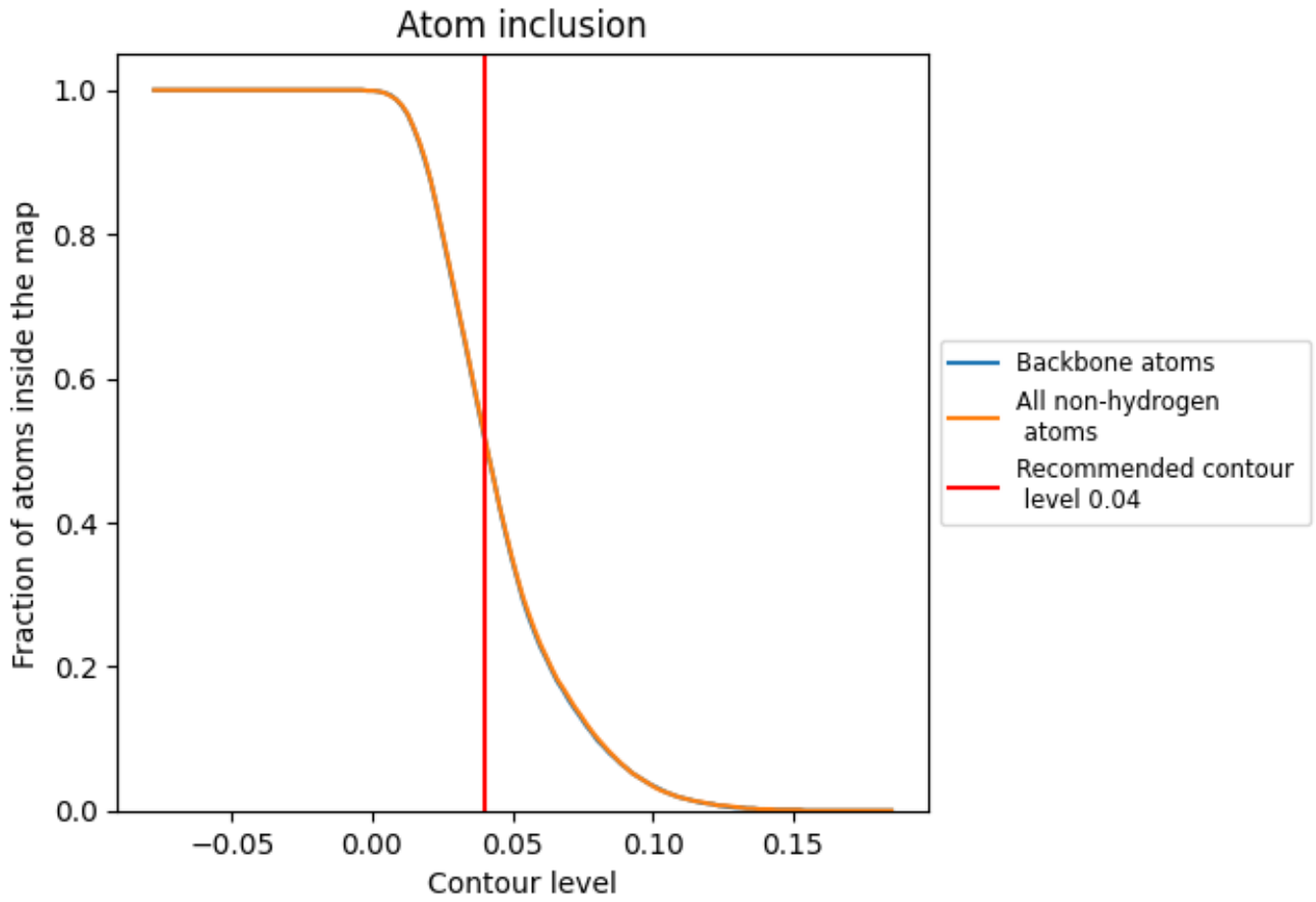
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion (i)



At the recommended contour level, 52% of all backbone atoms, 52% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5200	0.3800
A	0.5290	0.3810
B	0.5290	0.3800
C	0.5290	0.3800
D	0.5290	0.3800
G	0.5120	0.3910
H	0.5120	0.3900
I	0.5120	0.3880
J	0.5100	0.3920

