



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 11:22 AM UTC

PDB ID : 7VML / pdb_00007vml
EMDB ID : EMD-33935
Title : Structure of recombinant RyR2 (EGTA dataset, class 1&2, closed state)
Authors : Kobayashi, T.; Tsutsumi, A.; Kurebayashi, N.; Kodama, M.; Kikkawa, M.;
Murayama, T.; Ogawa, H.
Deposited on : 2021-10-09
Resolution : 3.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

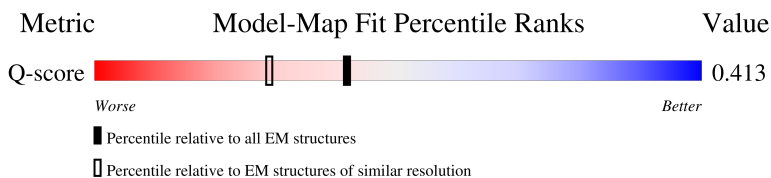
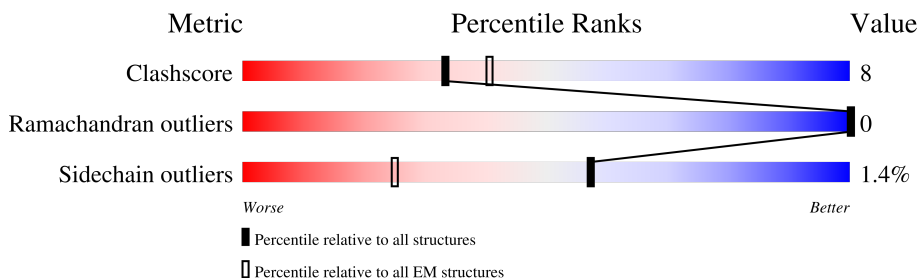
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.30 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.



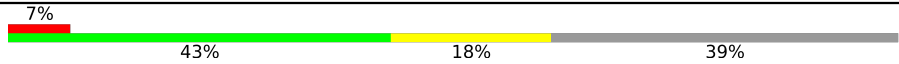
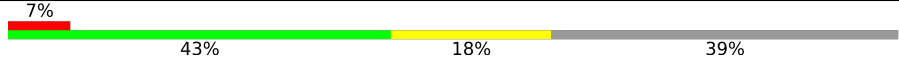
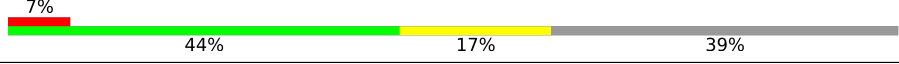
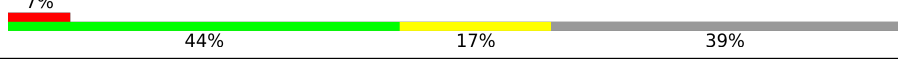
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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 $\leq 5\%$. 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	<p>29% (Poor fit), 66% (0 outliers), 15% (1 outlier), 19% (2+ outliers)</p>
1	B	4966	<p>29% (Poor fit), 66% (0 outliers), 15% (1 outlier), 19% (2+ outliers)</p>
1	C	4966	<p>29% (Poor fit), 66% (0 outliers), 15% (1 outlier), 19% (2+ outliers)</p>
1	D	4966	<p>29% (Poor fit), 66% (0 outliers), 15% (1 outlier), 19% (2+ outliers)</p>

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Mol	Chain	Length	Quality of chain
2	G	176	 7% 43% 18% 39%
2	H	176	 7% 43% 18% 39%
2	I	176	 7% 44% 17% 39%
2	J	176	 7% 44% 17% 39%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 123564 atoms, of which 0 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
			Total	C	N	O	S		
1	A	4044	30071	19035	5243	5617	176	0	0
1	B	4044	30071	19035	5243	5617	176	0	0
1	C	4044	30071	19035	5243	5617	176	0	0
1	D	4044	30071	19035	5243	5617	176	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	107	819	516	144	155	4	0	0
2	H	107	819	516	144	155	4	0	0
2	I	107	819	516	144	155	4	0	0
2	J	107	819	516	144	155	4	0	0

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

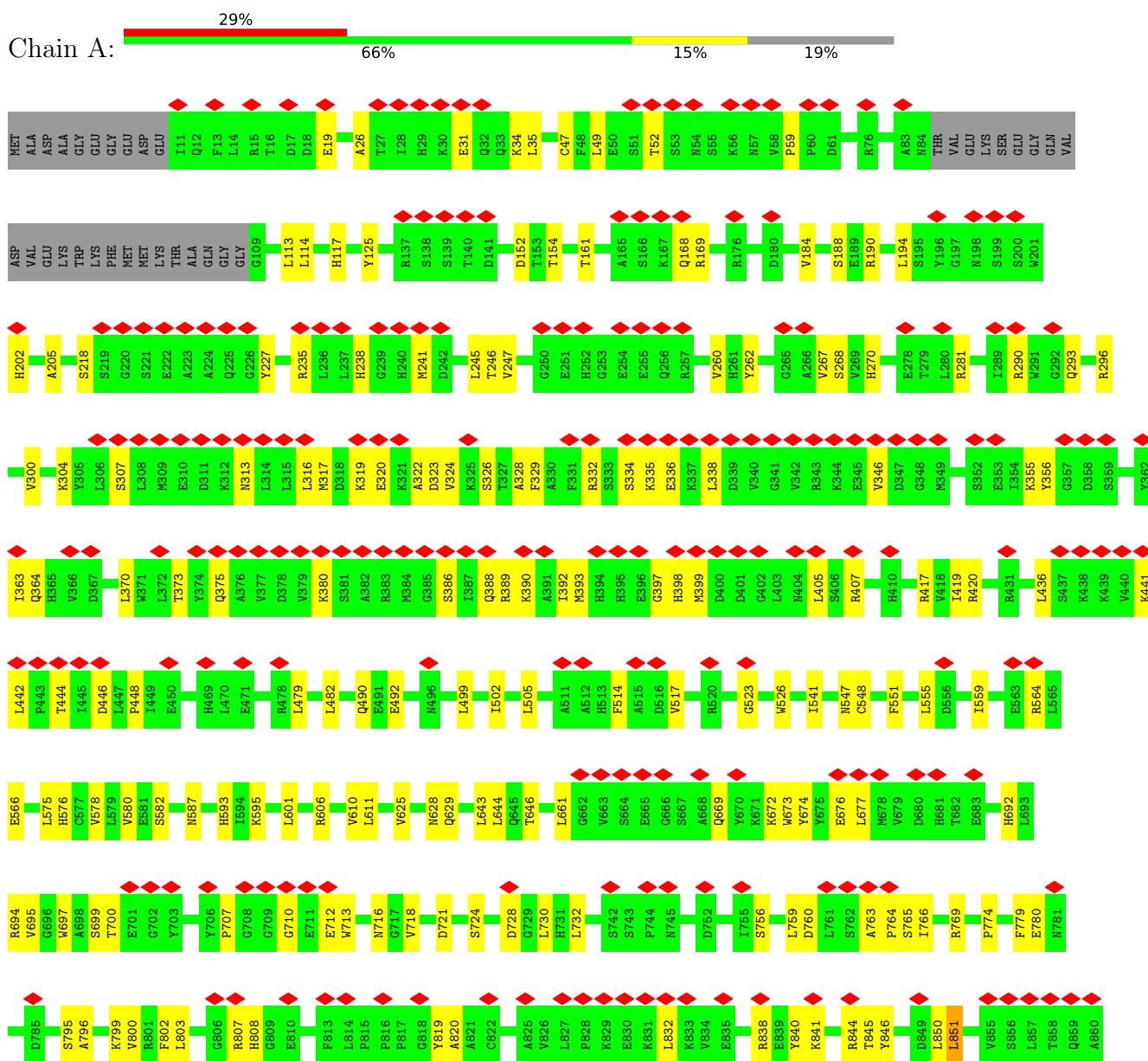
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

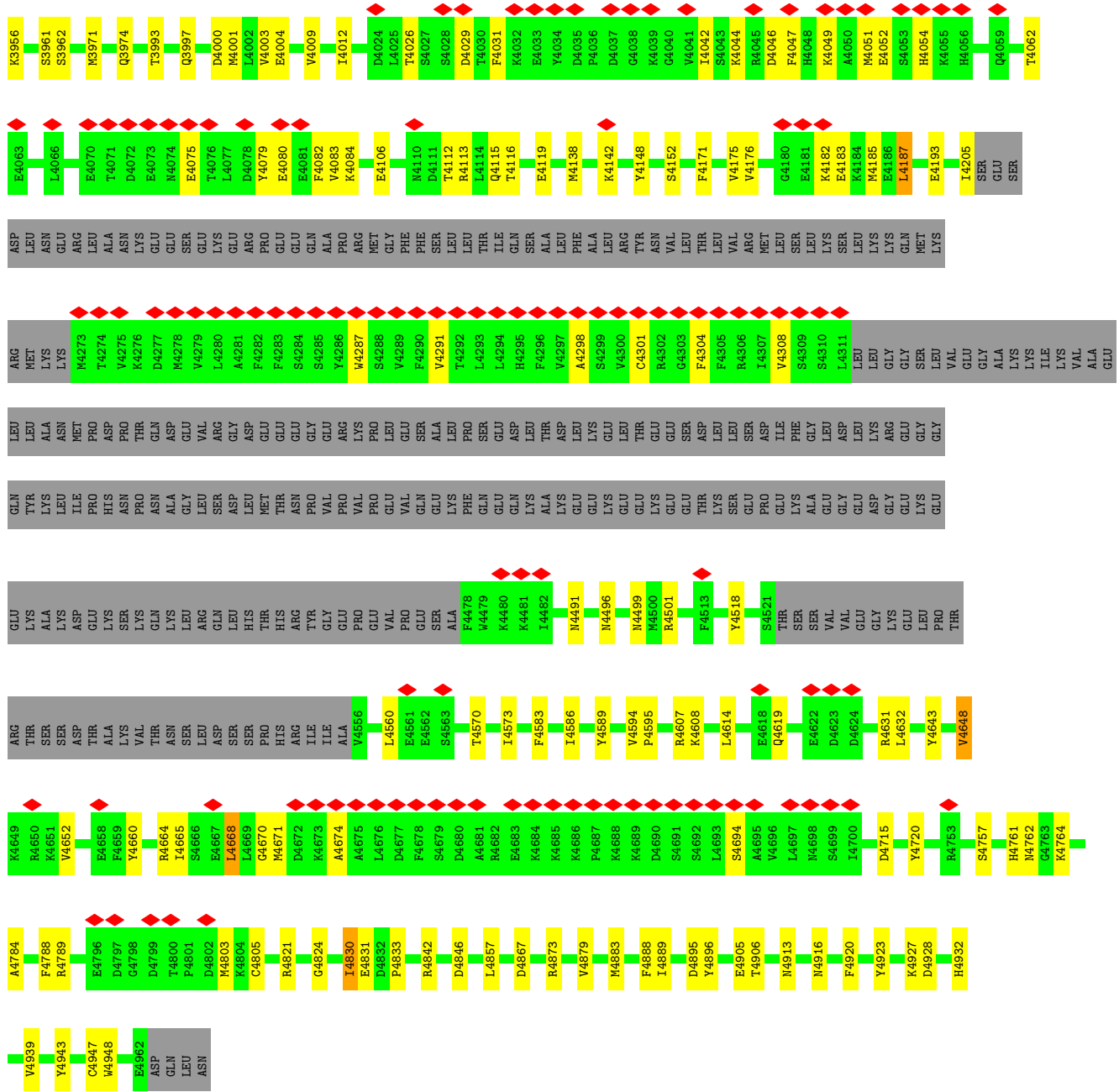
3 Residue-property plots

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.

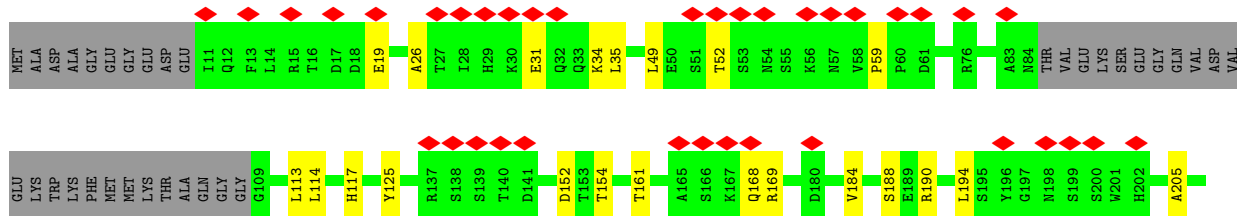
• Molecule 1: Ryanodine receptor 2

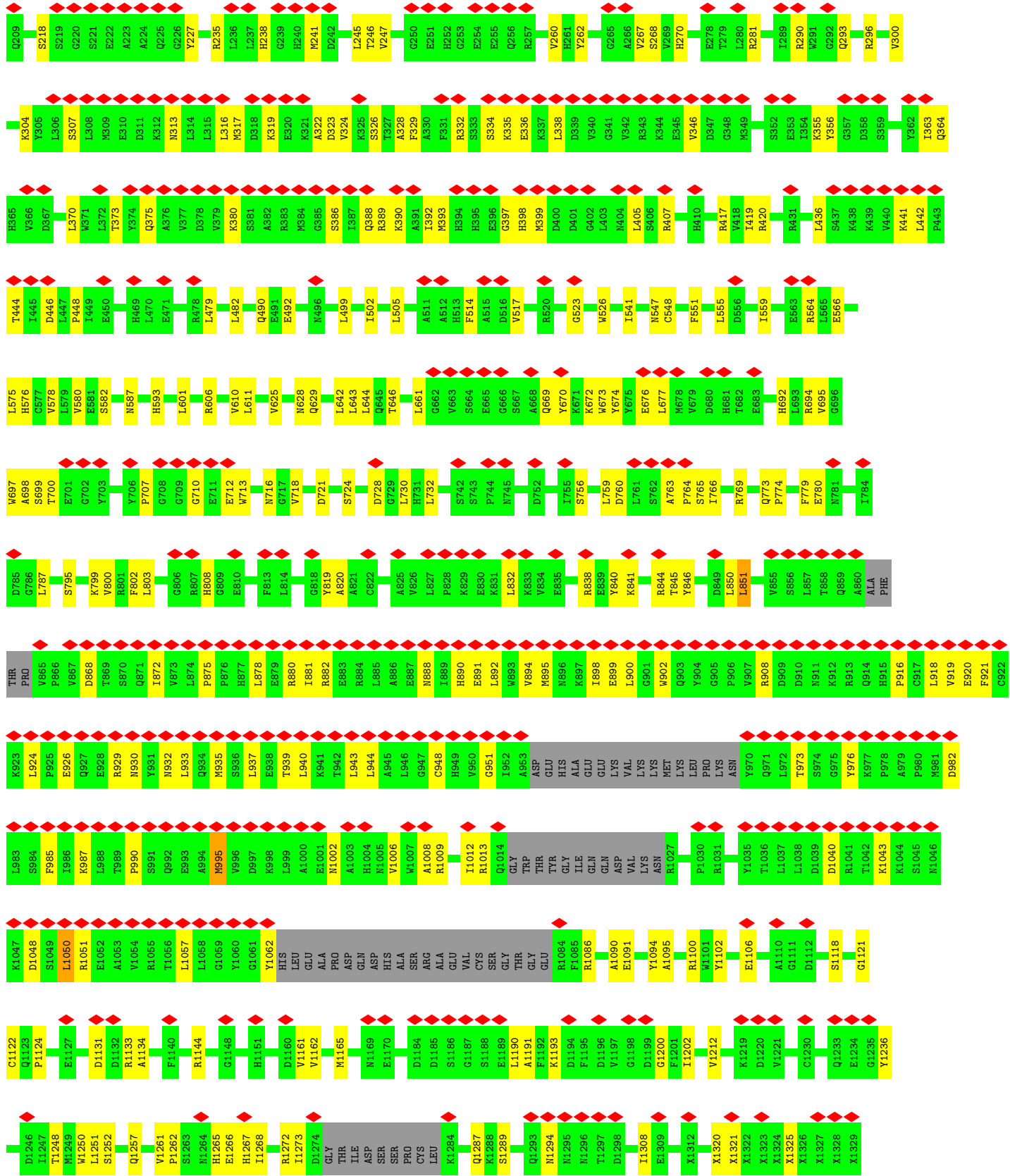


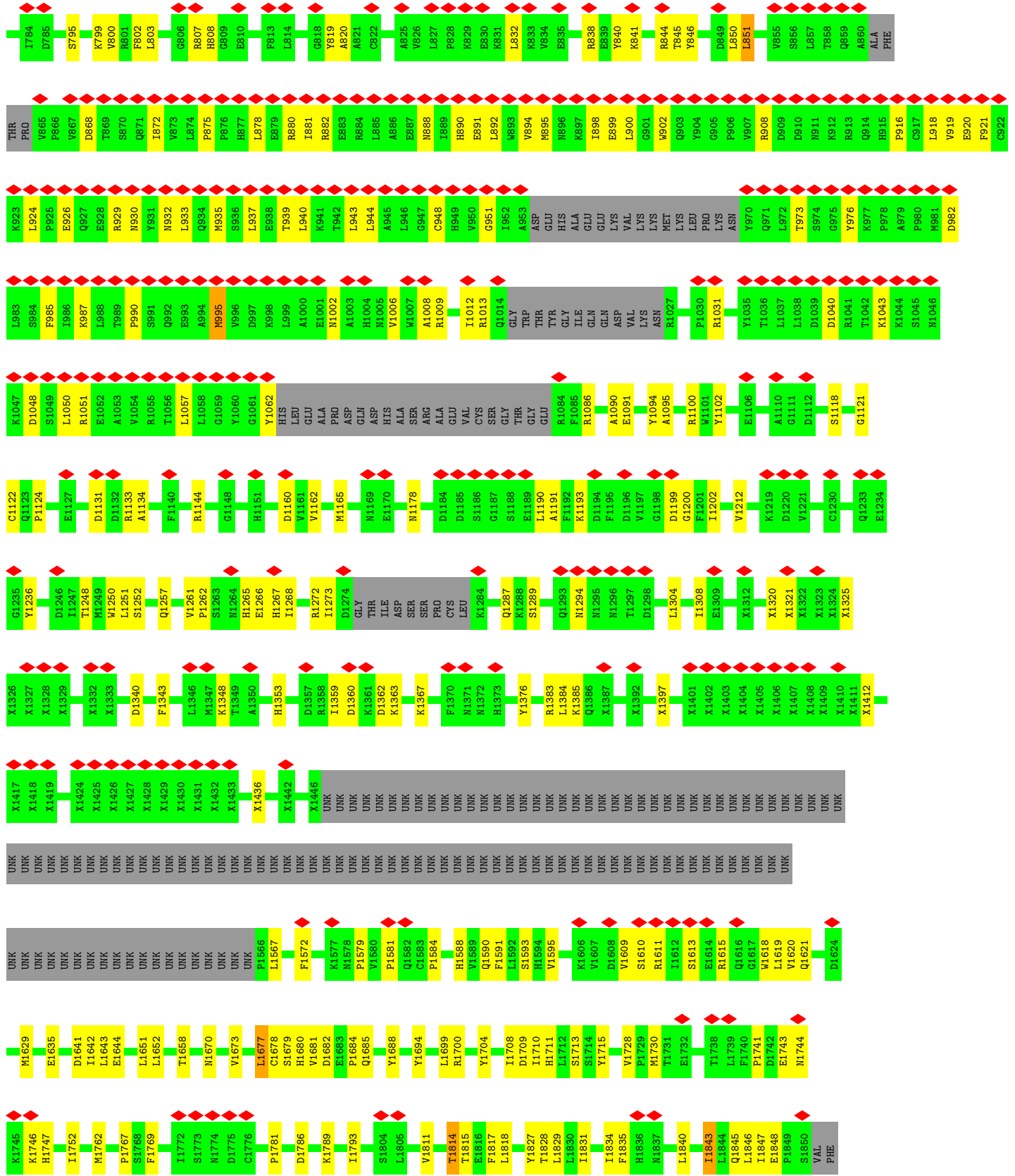
X2977	UNK	X3158	X3218	X3278	X3338	X3398	X3477	X3518	X3578	X3659	G3815	X2978	UNK	X3159	X3219	X3279	X3339	X3399	UNK	X3478	X3519	X3579	L3669	L3816	X2979	UNK	X3160	X3220	X3280	X3340	X3400	X3460	X3520	X3580	X3660	L3817	L3816	X2982	UNK	X3161	UNK	X3281	X3341	X3401	X3461	X3521	X3581	X3661	L3818	L3817	X2983	UNK	X3162	UNK	X3282	X3342	X3402	X3462	X3522	X3582	X3662	L3819	V3819	X2984	UNK	X3163	UNK	X3283	X3343	X3403	X3463	X3523	X3583	X3663	L3820	T3820	X2985	UNK	X3164	UNK	X3284	X3344	X3404	X3464	X3524	X3584	X3664	L3821	E3821	X2986	UNK	X3165	UNK	X3285	X3345	X3405	X3465	X3525	X3585	X3665	L3822	E3822	X2987	UNK	X3166	UNK	X3286	X3346	X3406	X3466	X3526	X3586	X3666	L3823	G3823	X2988	UNK	X3167	UNK	X3287	X3347	X3407	X3467	X3527	X3587	X3667	L3824	S3824	X2989	UNK	X3168	UNK	X3288	X3348	X3408	X3468	X3528	X3588	X3668	L3825	G3825	X2990	UNK	X3169	UNK	X3289	X3349	X3409	X3469	X3529	X3589	X3669	L3826	E3826	X2991	UNK	X3170	UNK	X3290	X3350	X3410	X3470	X3530	X3590	X3670	L3827	K3827	X2992	UNK	X3171	UNK	X3291	X3351	X3411	X3471	X3531	X3591	X3671	L3828	V3828	X2993	UNK	X3172	UNK	X3292	X3352	X3412	X3472	X3532	X3592	X3672	L3829	L3829	X2994	UNK	X3173	UNK	X3293	X3353	X3413	X3473	X3533	X3593	X3673	L3830	Q3830	X2995	UNK	X3174	UNK	X3294	X3354	X3414	X3474	X3534	X3594	X3674	L3831	D3831	X2996	UNK	X3175	UNK	X3295	X3355	X3415	X3475	X3535	X3595	X3675	L3832	D3832	X2997	UNK	X3176	UNK	X3296	X3356	X3416	X3476	X3536	X3596	X3676	L3833	G3833	X2998	UNK	X3177	UNK	X3297	X3357	X3417	X3477	X3537	X3597	X3677	L3834	F3834	X2999	UNK	X3178	UNK	X3298	X3358	X3418	X3478	X3538	X3598	X3678	L3835	R3835	X3000	UNK	X3179	UNK	X3299	X3359	X3419	X3479	X3539	X3599	X3679	L3836	F3836	X3001	UNK	X3180	UNK	X3300	X3360	X3420	X3480	X3540	X3600	X3680	L3837	L3837	X3002	UNK	X3181	UNK	X3301	X3361	X3421	X3481	X3541	X3601	X3681	L3838	R3838	X3003	UNK	X3182	UNK	X3302	X3362	X3422	X3482	X3542	X3602	X3682	L3839	L3839	X3004	UNK	X3183	UNK	X3303	X3363	X3423	X3483	X3543	X3603	X3683	L3840	F3840	X3005	UNK	X3184	UNK	X3304	X3364	X3424	X3484	X3544	X3604	X3684	L3841	R3841	X3006	UNK	X3185	UNK	X3305	X3365	X3425	X3485	X3545	X3605	X3685	L3842	L3842	X3007	UNK	X3186	UNK	X3306	X3366	X3426	X3486	X3546	X3606	X3686	L3843	Q3843	X3008	UNK	X3187	UNK	X3307	X3367	X3427	X3487	X3547	X3607	X3687	L3844	R3844	X3009	UNK	X3188	UNK	X3308	X3368	X3428	X3488	X3548	X3608	X3688	L3845	L3845	X3010	UNK	X3189	UNK	X3309	X3369	X3429	X3489	X3549	X3609	X3689	L3846	L3846	X3011	UNK	X3190	UNK	X3310	X3370	X3430	X3490	X3550	X3610	X3690	L3847	L3847	X3012	UNK	X3191	UNK	X3311	X3371	X3431	X3491	X3551	X3611	X3691	L3848	L3848	X3013	UNK	X3192	UNK	X3312	X3372	X3432	X3492	X3552	X3612	X3692	L3849	L3849	X3014	UNK	X3193	UNK	X3313	X3373	X3433	X3493	X3553	X3613	X3693	L3850	L3850	X3015	UNK	X3194	UNK	X3314	X3374	X3434	X3494	X3554	X3614	X3694	L3851	L3851	X3016	UNK	X3195	UNK	X3315	X3375	X3435	X3495	X3555	X3615	X3695	L3852	L3852	X3017	UNK	X3196	UNK	X3316	X3376	X3436	X3496	X3556	X3616	X3696	L3853	L3853	X3018	UNK	X3197	UNK	X3317	X3377	X3437	X3497	X3557	X3617	X3697	L3854	L3854	X3019	UNK	X3198	UNK	X3318	X3378	X3438	X3498	X3558	X3618	X3698	L3855	L3855	X3020	UNK	X3199	UNK	X3319	X3379	X3439	X3499	X3559	X3619	X3699	L3856	L3856	X3021	UNK	X3200	UNK	X3320	X3380	X3440	X3500	X3560	X3620	X3700	L3857	L3857	X3022	UNK	X3201	UNK	X3321	X3381	X3441	X3501	X3561	X3621	X3701	L3858	L3858	X3023	UNK	X3202	UNK	X3322	X3382	X3442	X3502	X3562	X3622	X3702	L3859	L3859	X3024	UNK	X3203	UNK	X3323	X3383	X3443	X3503	X3563	X3623	X3703	L3860	L3860	X3025	UNK	X3204	UNK	X3324	X3384	X3444	X3504	X3564	X3624	X3704	L3861	L3861	X3026	UNK	X3205	UNK	X3325	X3385	X3445	X3505	X3565	X3625	X3705	L3862	L3862	X3027	UNK	X3206	UNK	X3326	X3386	X3446	X3506	X3566	X3626	X3706	L3863	L3863	X3028	UNK	X3207	UNK	X3327	X3387	X3447	X3507	X3567	X3627	X3707	L3864	L3864	X3029	UNK	X3208	UNK	X3328	X3388	X3448	X3508	X3568	X3628	X3708	L3865	L3865	UNK	UNK	X3209	UNK	X3329	X3389	X3449	X3509	X3569	X3629	X3709	L3866	L3866	UNK	UNK	X3210	UNK	X3330	X3390	X3450	X3510	X3570	X3630	X3710	L3867	L3867	UNK	UNK	X3211	UNK	X3331	X3391	X3451	X3511	X3571	X3631	X3711	L3868	L3868	UNK	UNK	X3212	UNK	X3332	X3392	X3452	X3512	X3572	X3632	X3712	L3869	L3869	UNK	UNK	X3213	UNK	X3333	X3393	X3453	X3513	X3573	X3633	X3713	L3870	L3870	UNK	UNK	X3214	UNK	X3334	X3394	X3454	X3514	X3574	X3634	X3714	L3871	L3871	UNK	UNK	X3215	UNK	X3335	X3395	X3455	X3515	X3575	X3635	X3715	L3872	L3872	UNK	UNK	X3216	UNK	X3336	X3396	X3456	X3516	X3576	X3636	X3716	L3873	L3873	UNK	UNK	X3217	UNK	X3337	X3397	X3457	X3517	X3577	X3637	X3717	L3874	L3874	UNK	UNK	X3218	UNK	X3338	X3398	X3458	X3518	X3578	X3638	X3718	L3875	L3875	UNK	UNK	X3219	UNK	X3339	X3399	X3459	X3519	X3579	X3639	X3719	L3876	L3876	UNK	UNK	X3220	UNK	X3340	X3400	X3460	X3520	X3580	X3640	X3720	L3877	L3877	UNK	UNK	X3221	UNK	X3341	X3401	X3461	X3521	X3581	X3641	X3721	L3878	L3878	UNK	UNK	X3222	UNK	X3342	X3402	X3462	X3522	X3582	X3642	X3722	L3879	L3879	UNK	UNK	X3223	UNK	X3343	X3403	X3463	X3523	X3583	X3643	X3723	L3880	L3880	UNK	UNK	X3224	UNK	X3344	X3404	X3464	X3524	X3584	X3644	X3724	L3881	L3881	UNK	UNK	X3225	UNK	X3345	X3405	X3465	X3525	X3585	X3645	X3725	L3882	L3882	UNK	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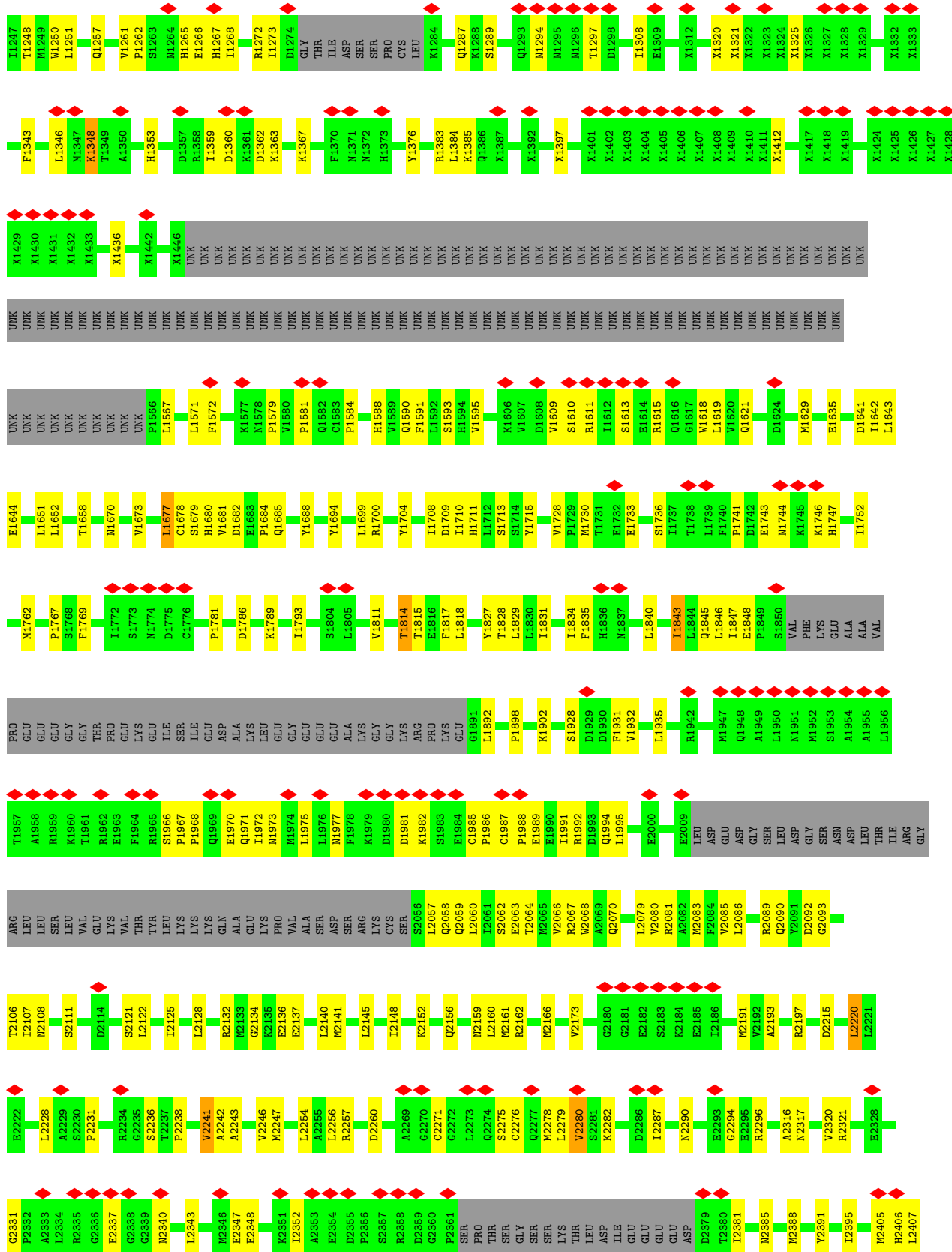


• Molecule 1: Ryanodine receptor 2

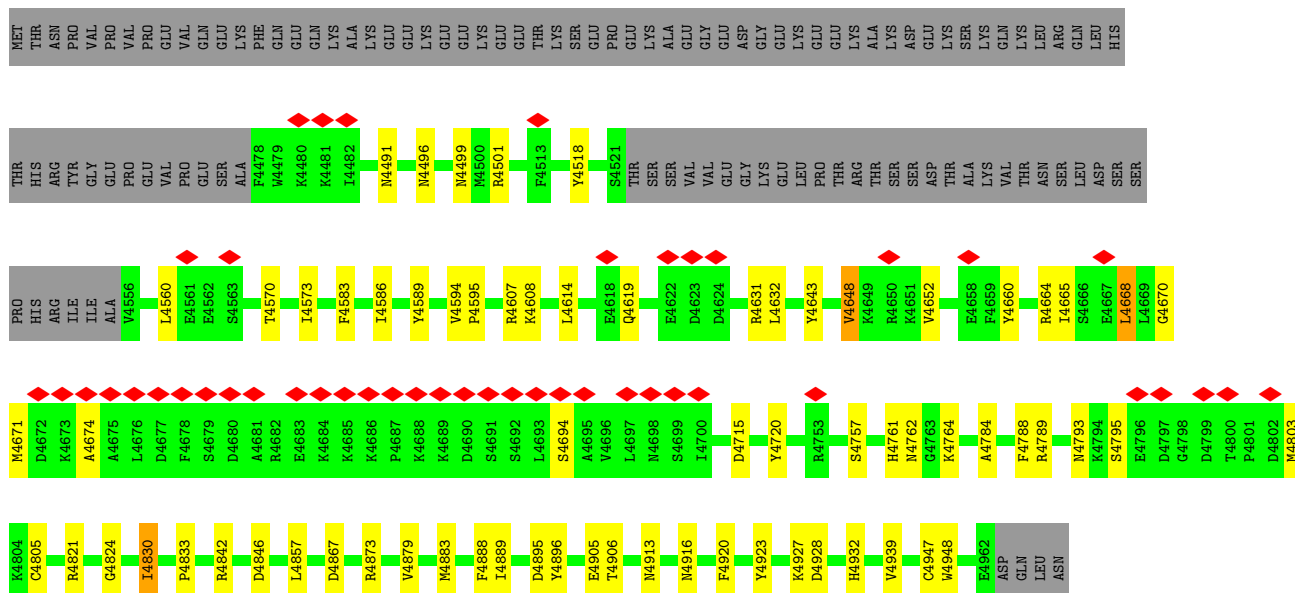




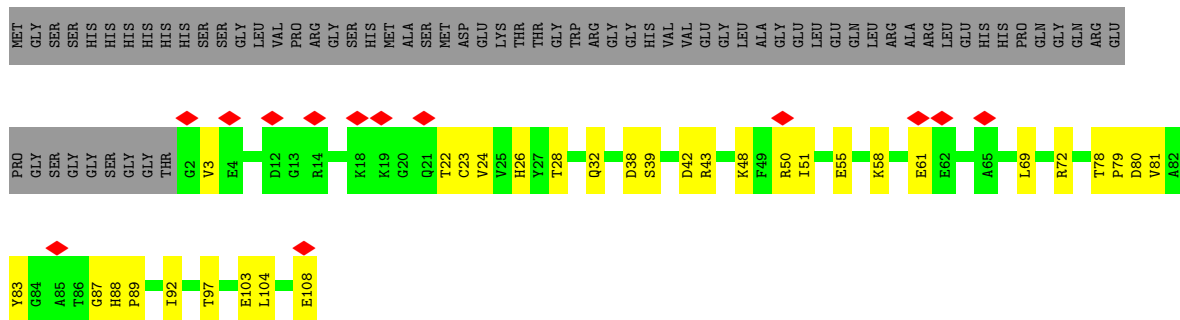




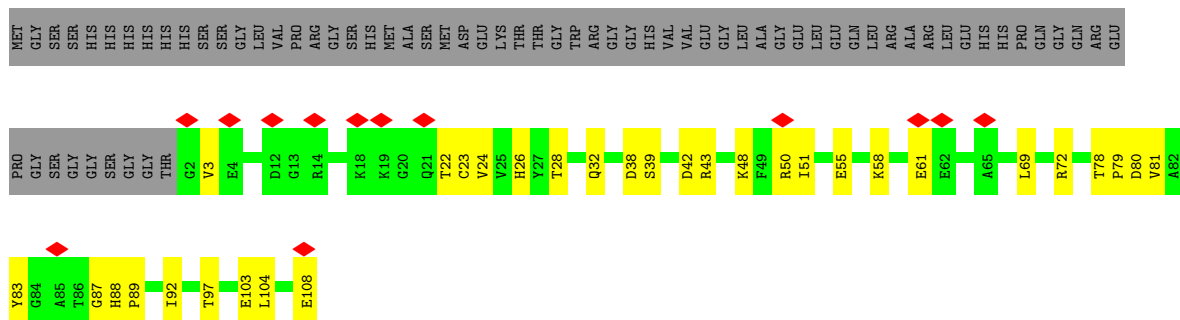
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GLU	Y4286	GLU	E4106	I4012	D3832	UNK	X3531	UNK	X3411	X3351	X3291
GLY	W4287	GLN	M4110	D4024	E3833	UNK	X3532	UNK	X3412	X3352	X3292
ARG	S4288	ALA	D4111	L4025	F3834	UNK	X3533	UNK	X3413	X3353	X3293
PRO	V4289	ARG	R4043	T4026	R3840	UNK	X3534	UNK	X3414	X3354	X3294
LYS	F4290	MET	Q3843	S4027	Q3843	UNK	X3535	UNK	X3415	X3355	X3295
LEU	V4291	GLY	N3864	S4028	T3865	UNK	X3536	UNK	X3416	X3356	X3296
GLU	T4292	PHE	Q4028	S4029	N3869	UNK	X3537	UNK	X3417	X3357	X3297
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LEU	H4295	LEU	T3865	F4031	T3865	UNK	X3540	UNK	X3420	X3360	X3300
PRO	H4296	LEU	T3865	F4031	T3865	UNK	X3541	UNK	X3421	X3361	X3301
SER	F4296	THR	Q3727	F4031	T3865	UNK	X3542	UNK	X3422	X3362	X3302
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GLU	F4305	VAL	I3762	F4031	T3865	UNK	X3552	UNK	X3432	X3372	X3312
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LEU	LEU	LEU	M4001	F4031	T3865	UNK	X3573	UNK	X3453	X3393	X3333
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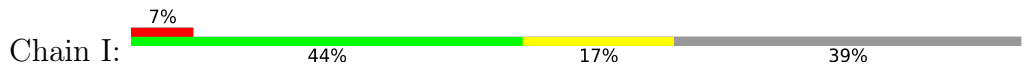
● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

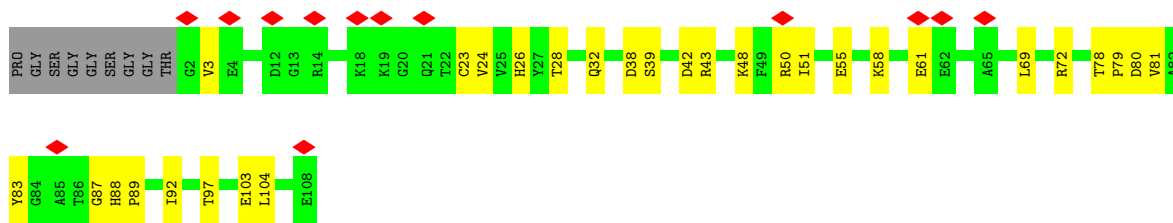


● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

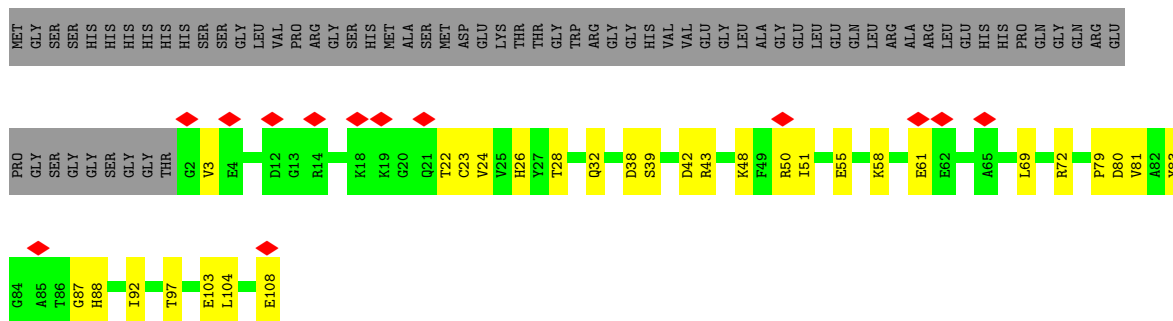
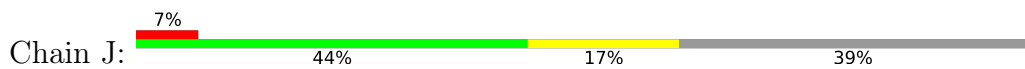


● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B





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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	264902	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.091	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	513.60004, 513.60004, 513.60004	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.284, 1.284, 1.284	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.12	0/26895	0.33	0/36316
1	B	0.12	0/26895	0.33	0/36316
1	C	0.12	0/26895	0.33	0/36316
1	D	0.12	0/26895	0.33	0/36316
2	G	0.10	0/835	0.34	0/1123
2	H	0.10	0/835	0.34	0/1123
2	I	0.10	0/835	0.34	0/1123
2	J	0.10	0/835	0.34	0/1123
All	All	0.12	0/110920	0.33	0/149756

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	30071	0	26715	470	0
1	B	30071	0	26715	471	0
1	C	30071	0	26714	475	0
1	D	30071	0	26715	461	0
2	G	819	0	821	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	819	0	821	19	0
2	I	819	0	821	18	0
2	J	819	0	821	17	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
All	All	123564	0	110143	1935	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 8.

The worst 5 of 1935 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:A:838:ARG:H	1:A:841:LYS:HZ1	1.23	0.87
1:C:838:ARG:H	1:C:841:LYS:HZ1	1.24	0.85
1:B:838:ARG:H	1:B:841:LYS:HZ1	1.24	0.84
1:D:2406:HIS:HA	1:D:2409:HIS:HB3	1.62	0.82
1:C:2406:HIS:HA	1:C:2409:HIS:HB3	1.62	0.81

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	3255/4966 (66%)	3049 (94%)	206 (6%)	0	100	100
1	B	3255/4966 (66%)	3053 (94%)	202 (6%)	0	100	100
1	C	3255/4966 (66%)	3051 (94%)	204 (6%)	0	100	100
1	D	3255/4966 (66%)	3050 (94%)	205 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	105/176 (60%)	103 (98%)	2 (2%)	0	100	100
2	H	105/176 (60%)	103 (98%)	2 (2%)	0	100	100
2	I	105/176 (60%)	103 (98%)	2 (2%)	0	100	100
2	J	105/176 (60%)	103 (98%)	2 (2%)	0	100	100
All	All	13440/20568 (65%)	12615 (94%)	825 (6%)	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	2862/3387 (84%)	2823 (99%)	39 (1%)	59	73
1	B	2862/3387 (84%)	2823 (99%)	39 (1%)	59	73
1	C	2862/3387 (84%)	2823 (99%)	39 (1%)	59	73
1	D	2862/3387 (84%)	2823 (99%)	39 (1%)	59	73
2	G	88/140 (63%)	86 (98%)	2 (2%)	44	66
2	H	88/140 (63%)	86 (98%)	2 (2%)	44	66
2	I	88/140 (63%)	86 (98%)	2 (2%)	44	66
2	J	88/140 (63%)	86 (98%)	2 (2%)	44	66
All	All	11800/14108 (84%)	11636 (99%)	164 (1%)	57	73

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4152	SER
1	D	2220	LEU
1	C	4803	MET
1	D	995	MET
1	D	2901	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 269 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1944	ASN
1	D	2157	HIS
1	D	4641	ASN
1	B	2088	HIS
1	B	1744	ASN

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

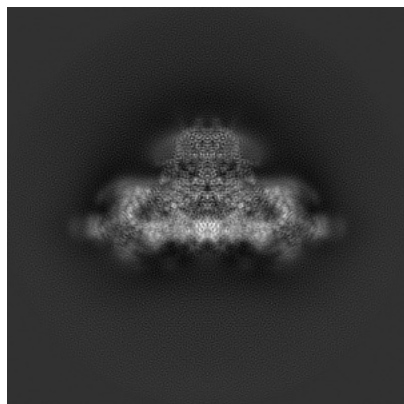
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33935. These allow visual inspection of the internal detail of the map and identification of artifacts.

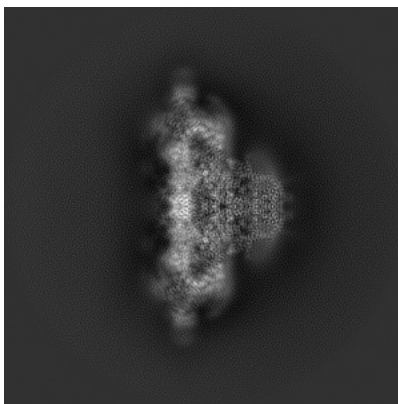
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

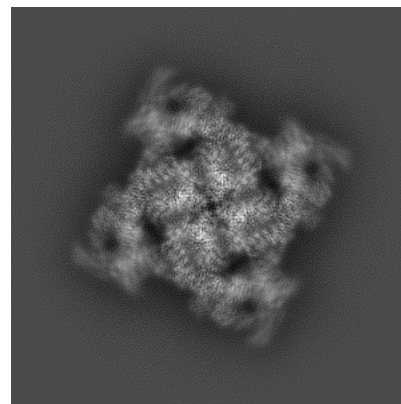
6.1.1 Primary map



X

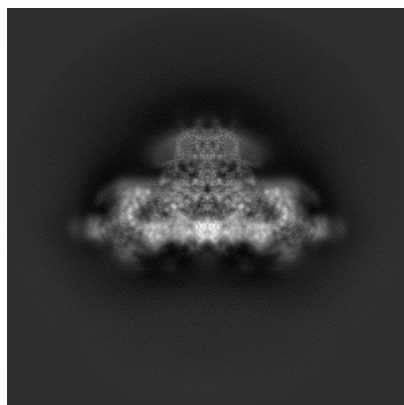


Y

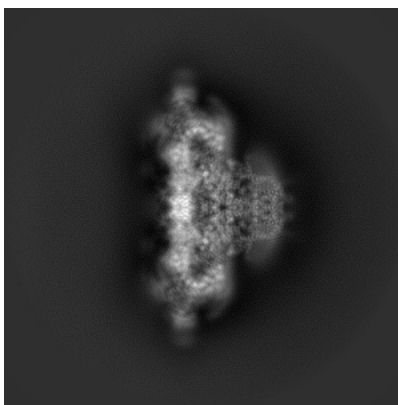


Z

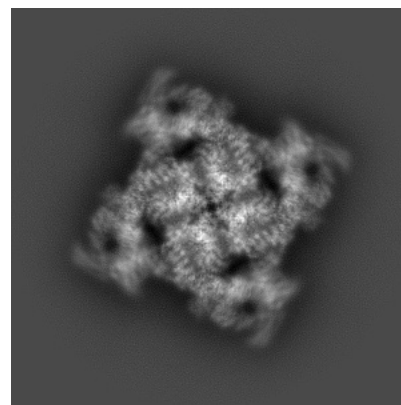
6.1.2 Raw map



X



Y

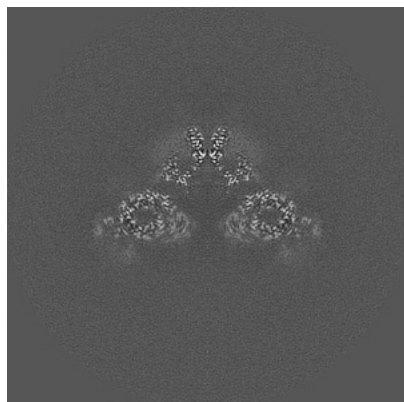


Z

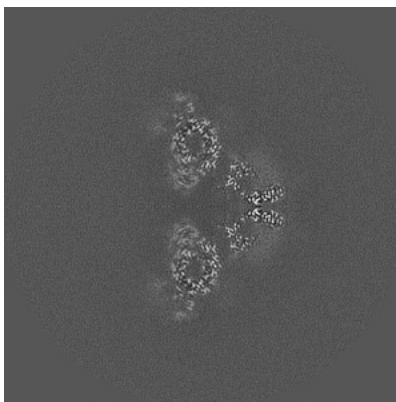
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

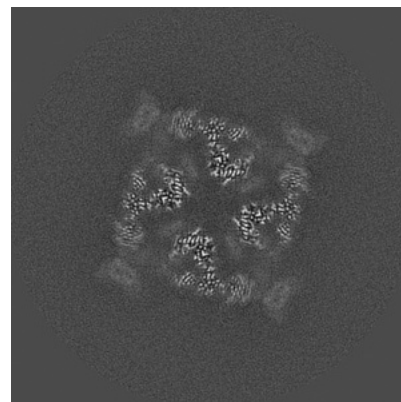
6.2.1 Primary map



X Index: 200

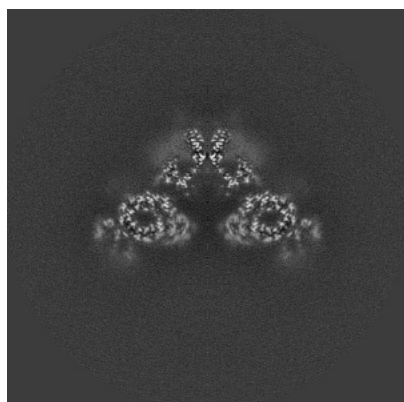


Y Index: 200

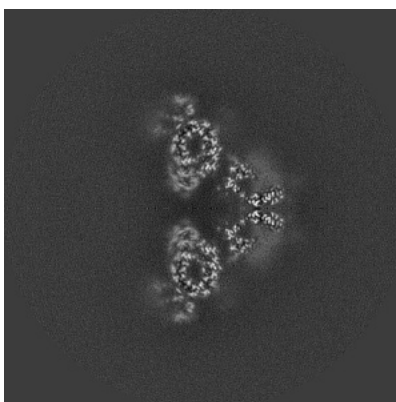


Z Index: 200

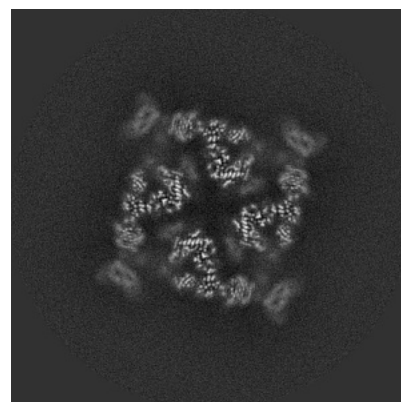
6.2.2 Raw map



X Index: 200



Y Index: 200

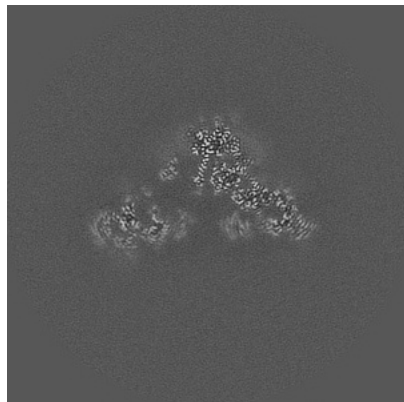


Z Index: 200

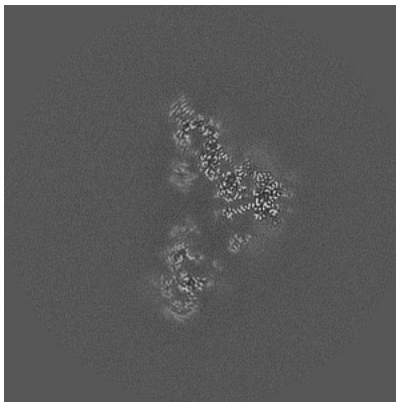
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

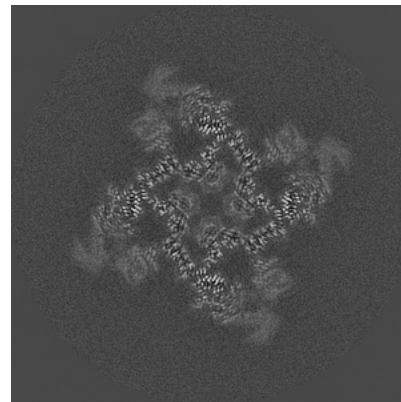
6.3.1 Primary map



X Index: 207

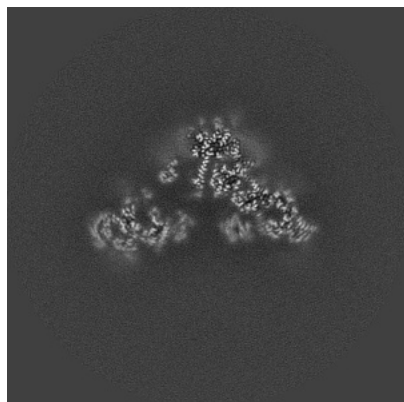


Y Index: 193

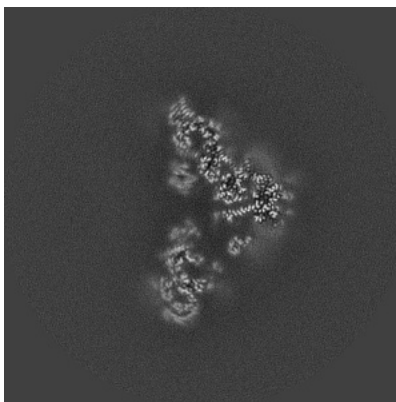


Z Index: 183

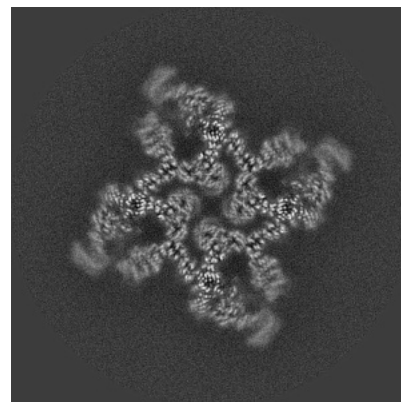
6.3.2 Raw map



X Index: 207



Y Index: 193

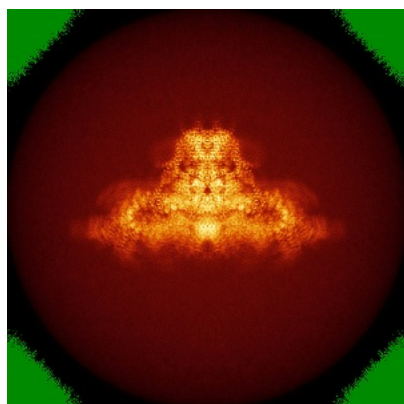


Z Index: 180

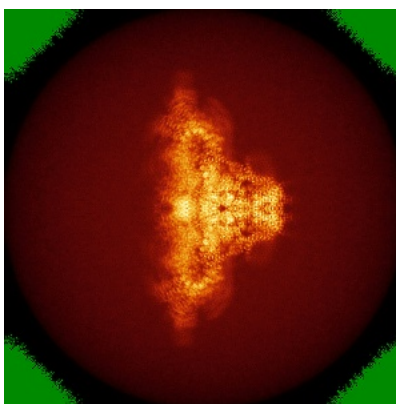
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

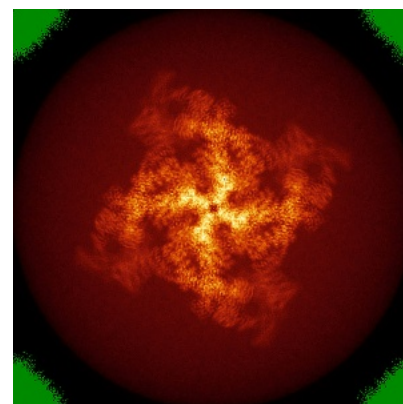
6.4.1 Primary map



X

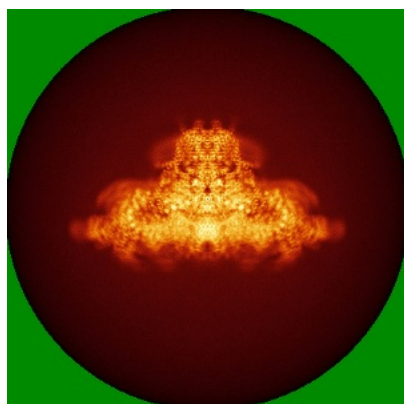


Y

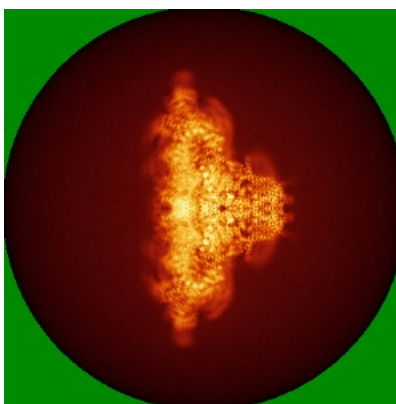


Z

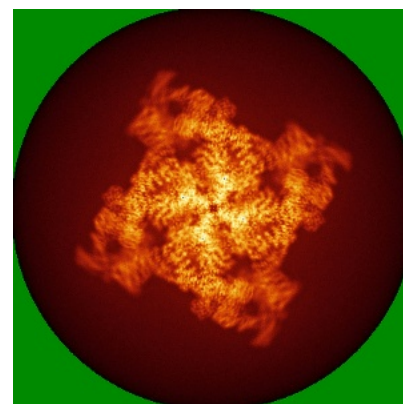
6.4.2 Raw map



X



Y

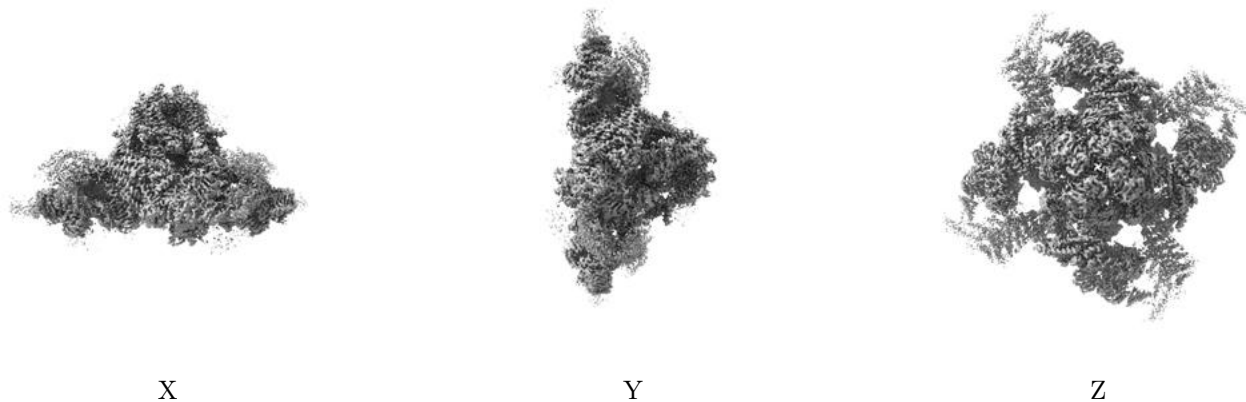


Z

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.

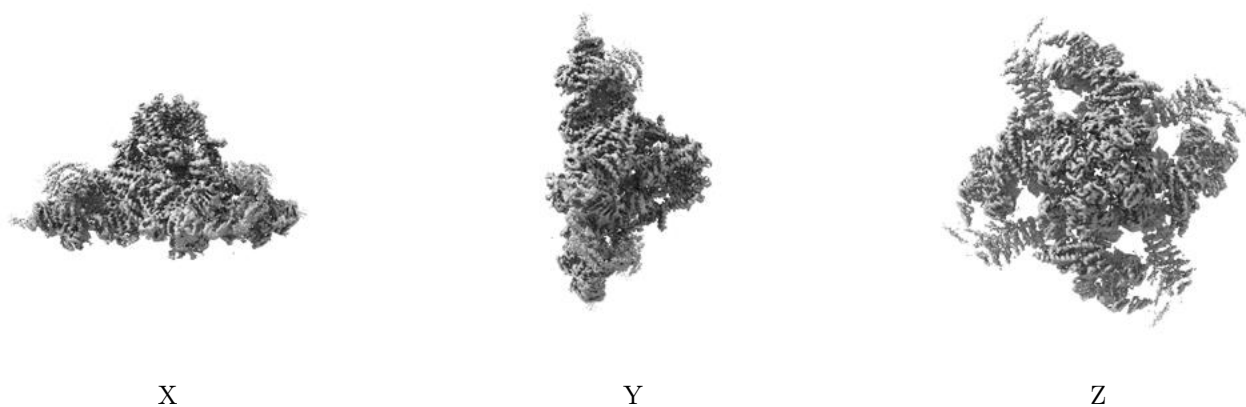
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.023. 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



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.

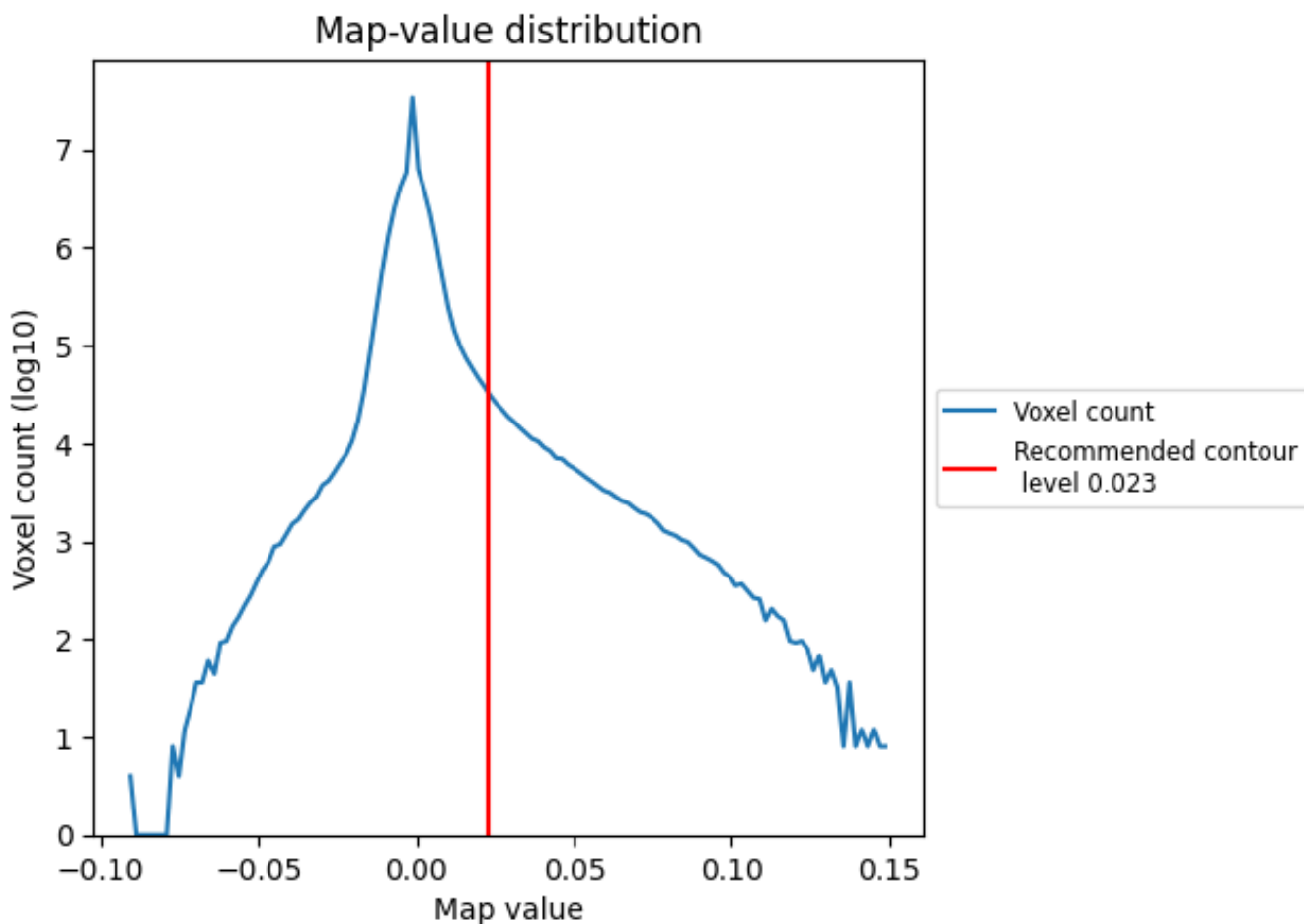
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

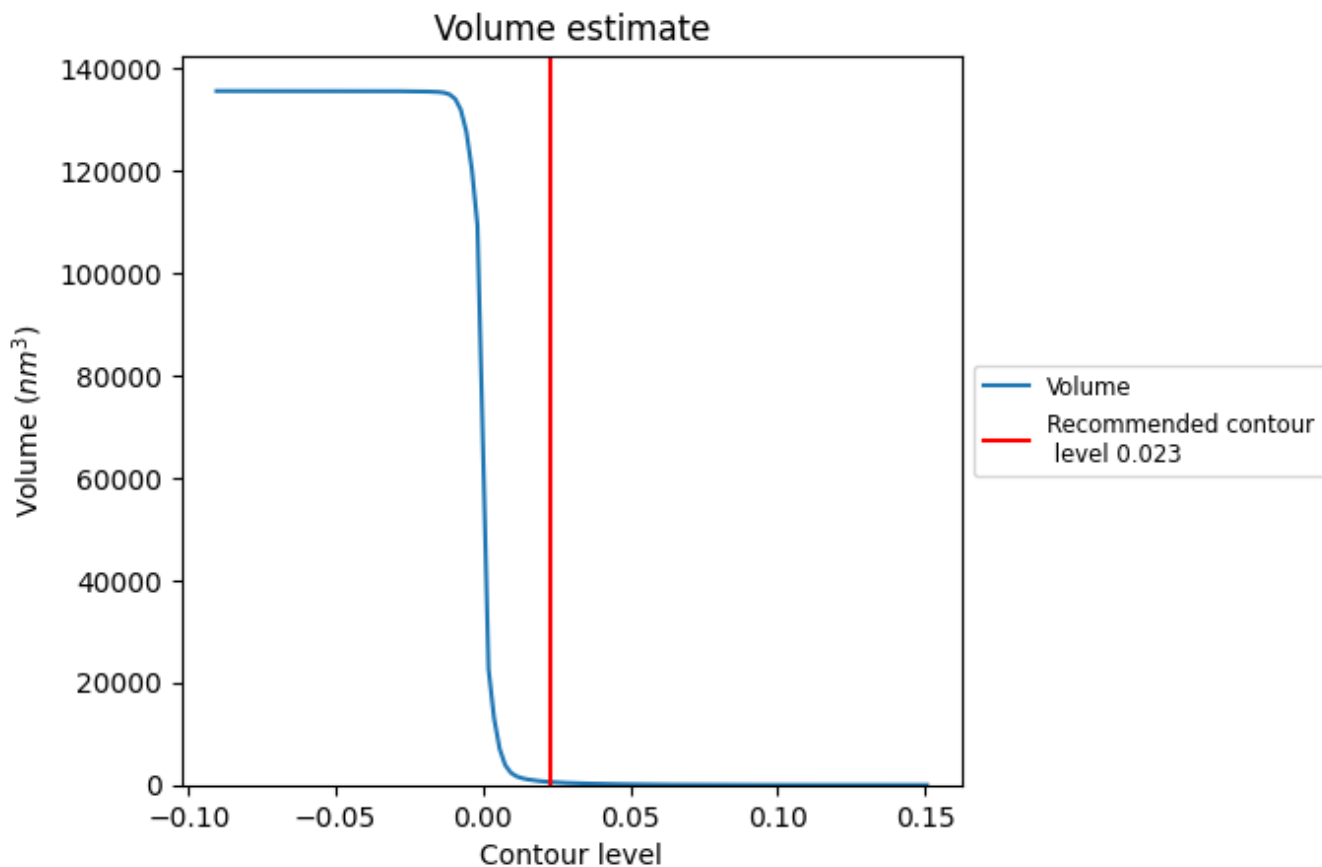
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

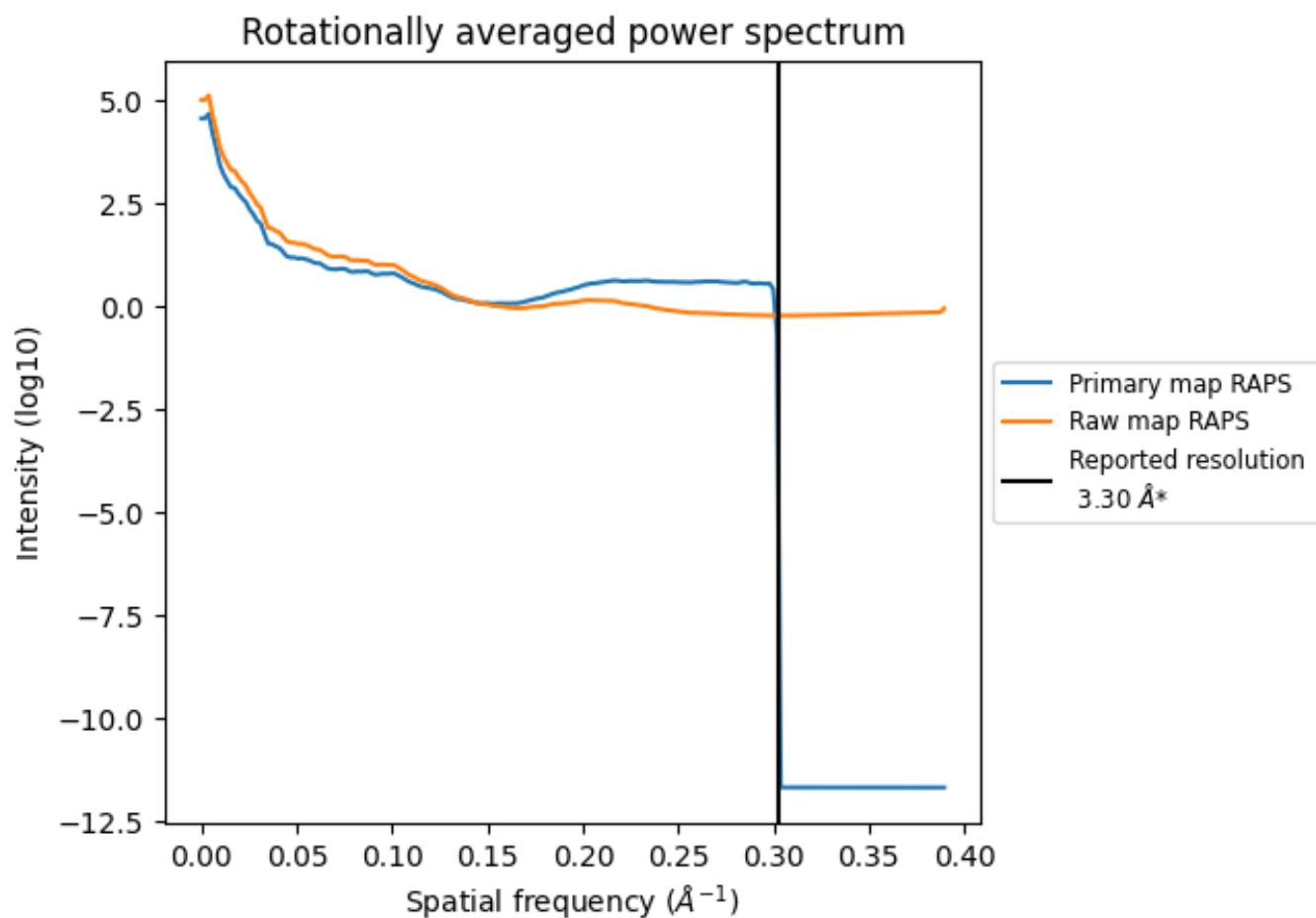
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm^3 ; this corresponds to an approximate mass of 513 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](#)

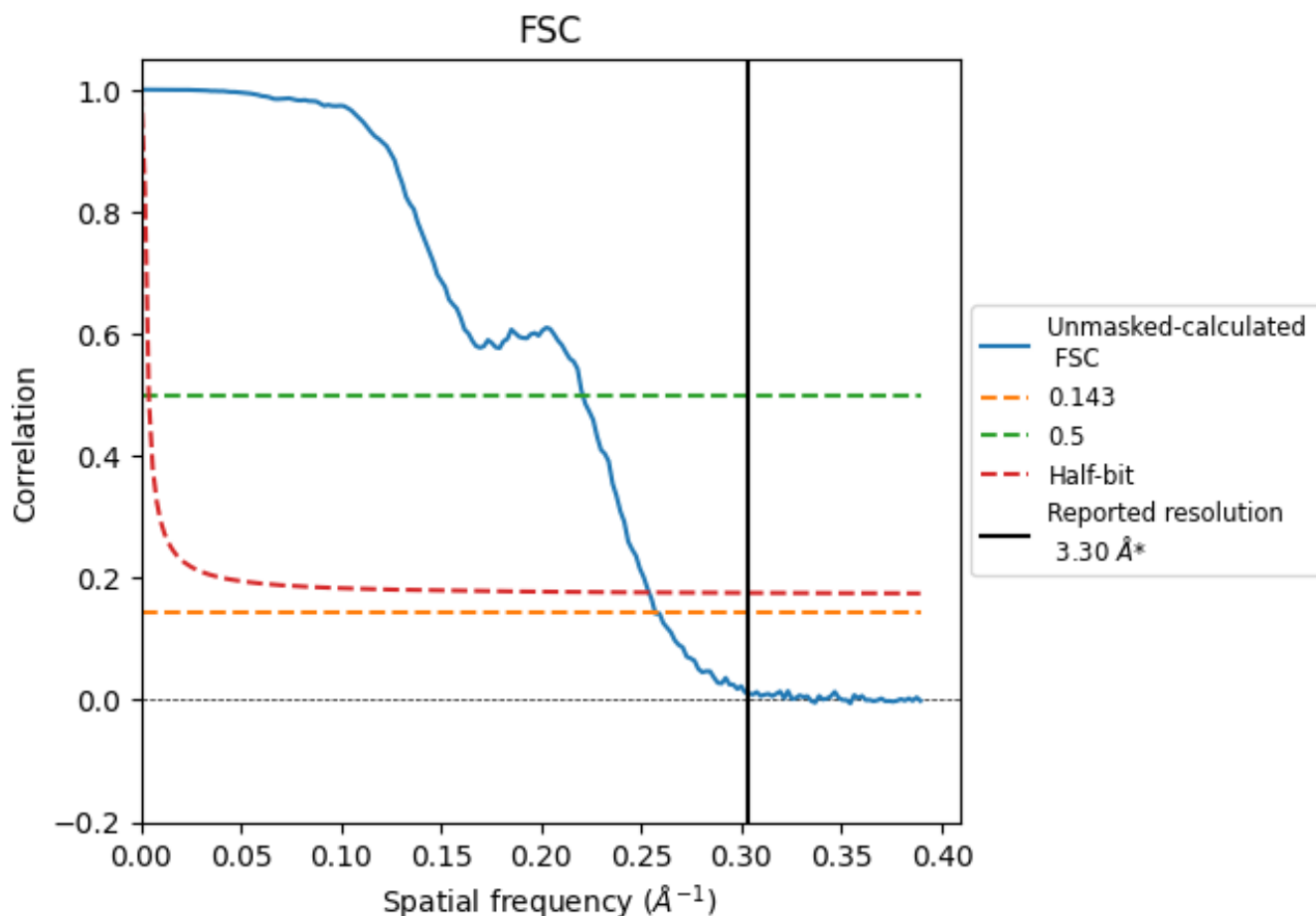


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

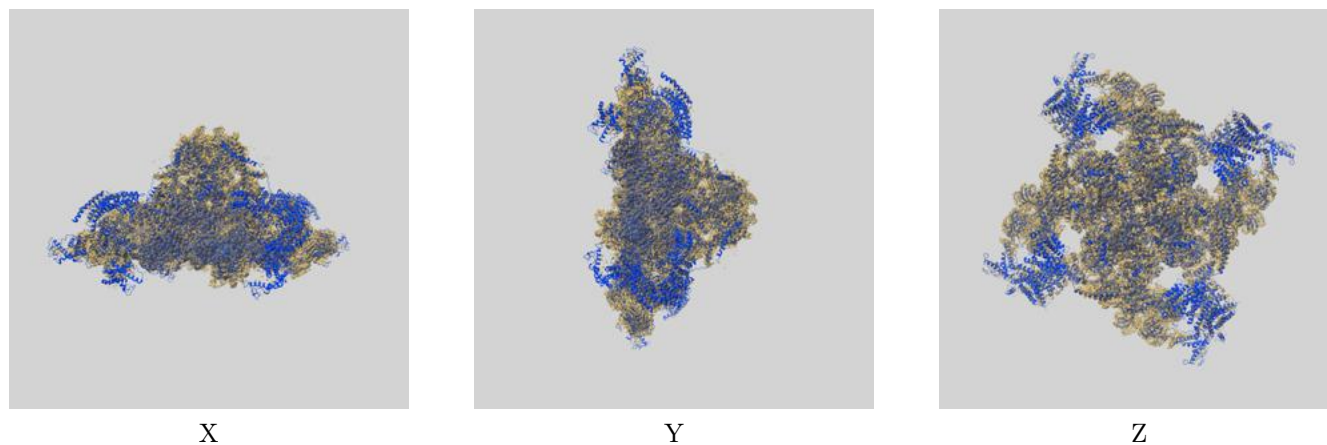
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.89	4.53	3.94

*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 3.89 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

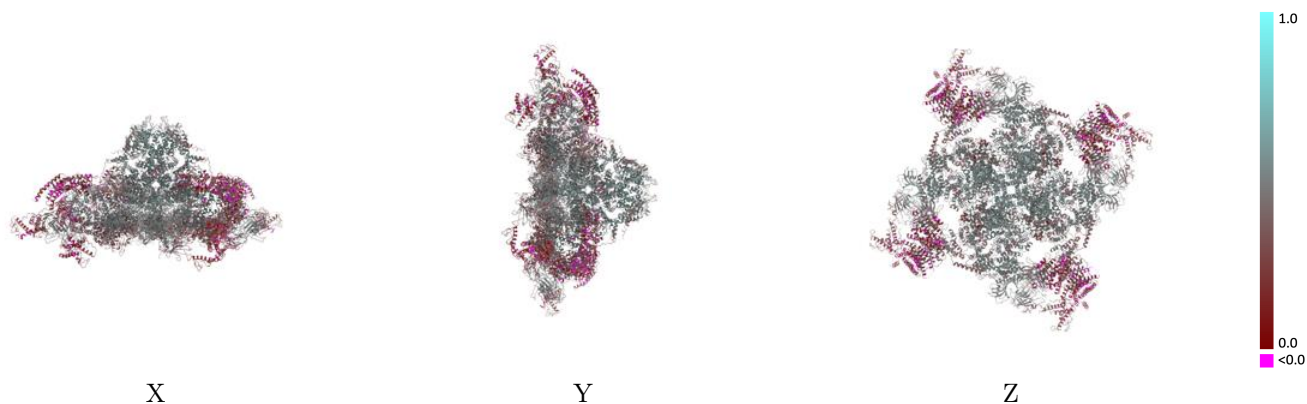
This section contains information regarding the fit between EMDB map EMD-33935 and PDB model 7VML. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



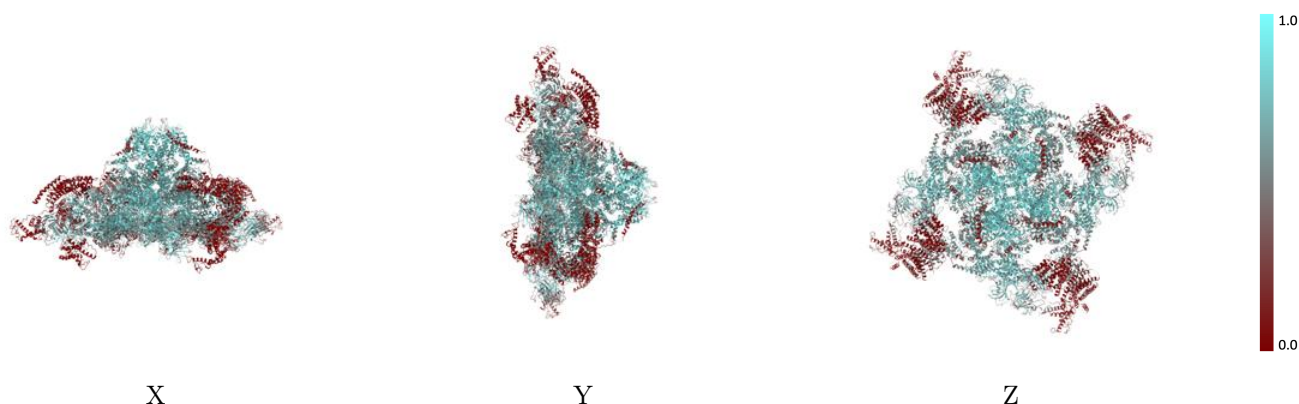
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [\(i\)](#)



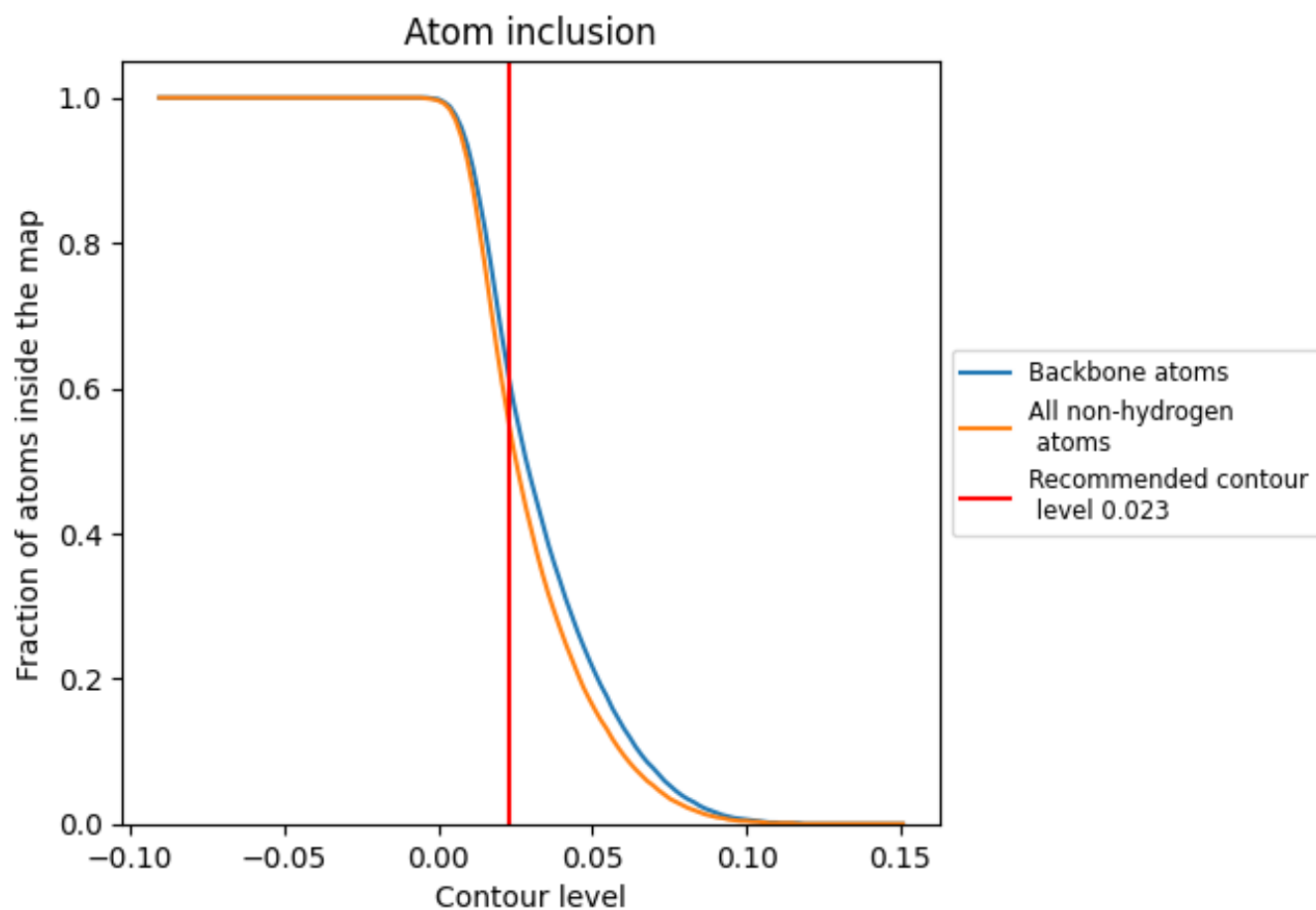
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [\(i\)](#)



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 (0.023).



















9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 55% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5490	 0.4130
A	 0.5470	 0.4110
B	 0.5460	 0.4120
C	 0.5460	 0.4110
D	 0.5460	 0.4110
G	 0.6550	 0.4790
H	 0.6490	 0.4800
I	 0.6480	 0.4770
J	 0.6520	 0.4770

