



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 11:56 AM UTC

PDB ID : 7VMN / pdb\_00007vmn  
EMDB ID : EMD-33937  
Title : Structure of recombinant RyR2 (EGTA dataset, class 2, closed state)  
Authors : Kobayashi, T.; Tsutsumi, A.; Kurebayashi, N.; Kodama, M.; Kikkawa, M.;  
Murayama, T.; Ogawa, H.  
Deposited on : 2021-10-09  
Resolution : 3.50 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](mailto: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>.

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

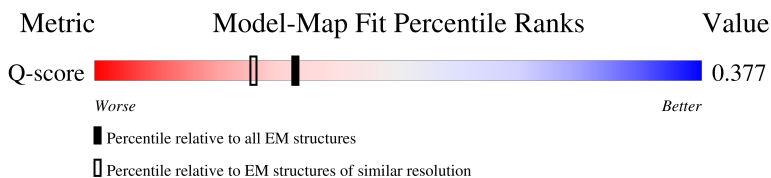
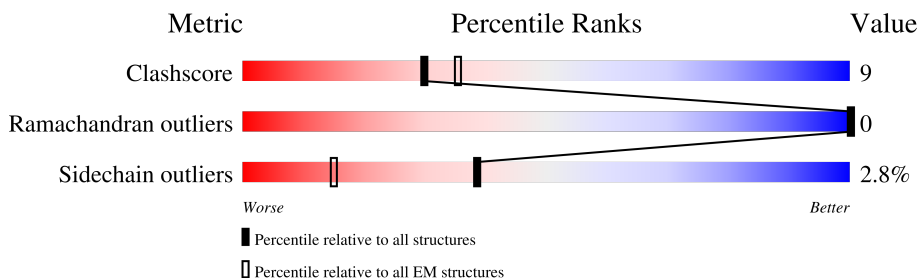
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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.



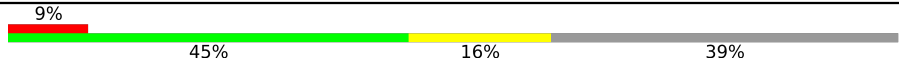
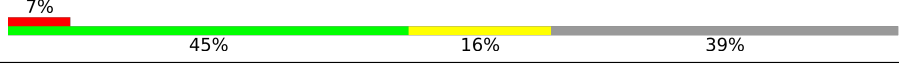
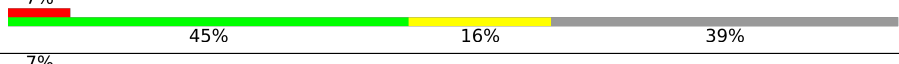
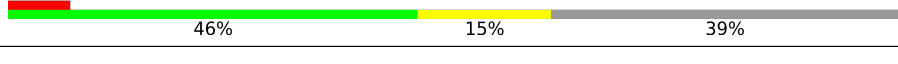
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13017 ( 3.02 - 4.02 )

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  $\geq 3$ , 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	
1	B	4966	
1	C	4966	
1	D	4966	

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Mol	Chain	Length	Quality of chain
2	G	176	 9% 45% 16% 39%
2	H	176	 7% 45% 16% 39%
2	I	176	 7% 45% 16% 39%
2	J	176	 7% 46% 15% 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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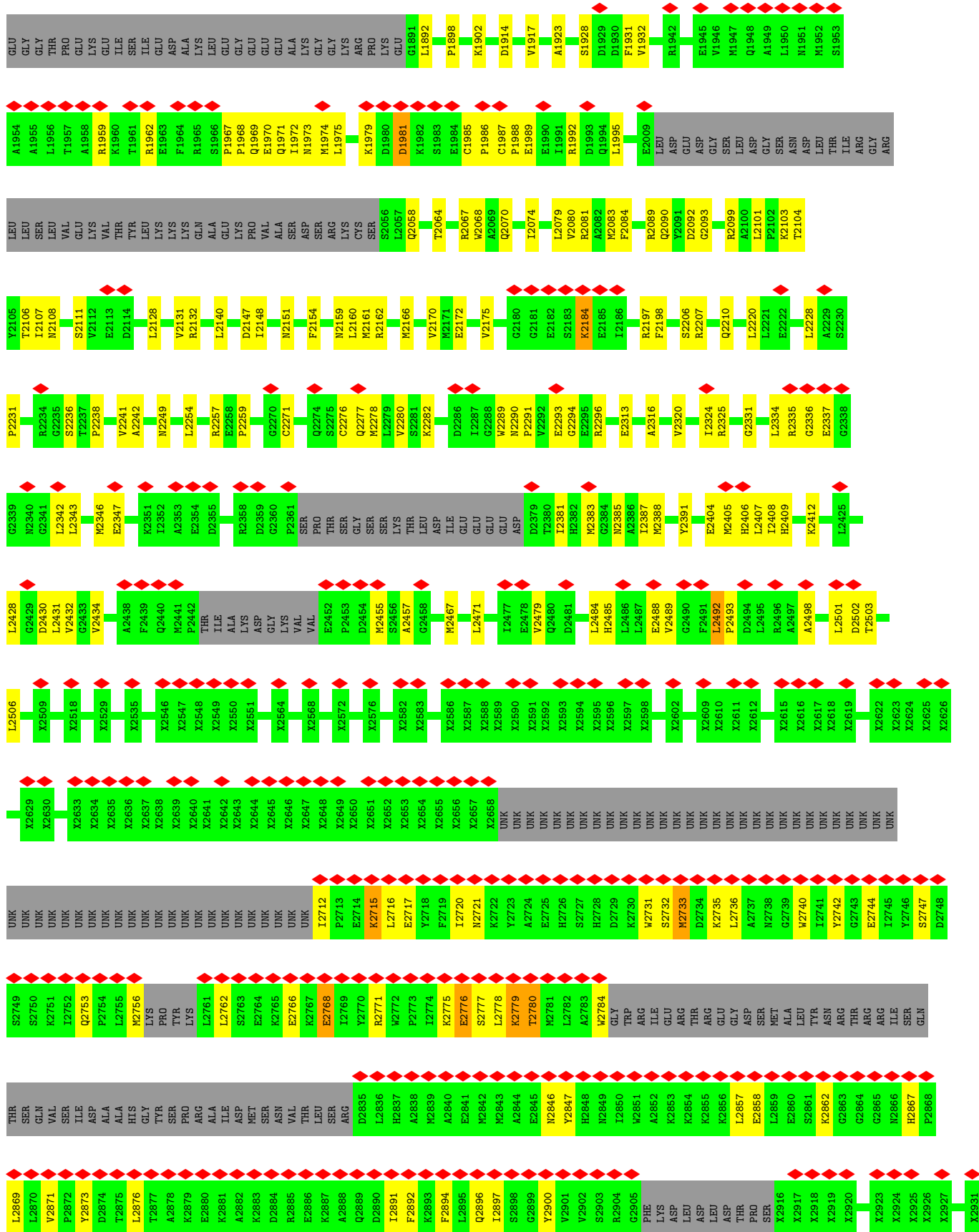
Chain	Residue	Modelled	Actual	Comment	Reference
J	-13	PRO	-	expression tag	UNP P68106
J	-12	GLN	-	expression tag	UNP P68106
J	-11	GLY	-	expression tag	UNP P68106
J	-10	GLN	-	expression tag	UNP P68106
J	-9	ARG	-	expression tag	UNP P68106
J	-8	GLU	-	expression tag	UNP P68106
J	-7	PRO	-	expression tag	UNP 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	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	



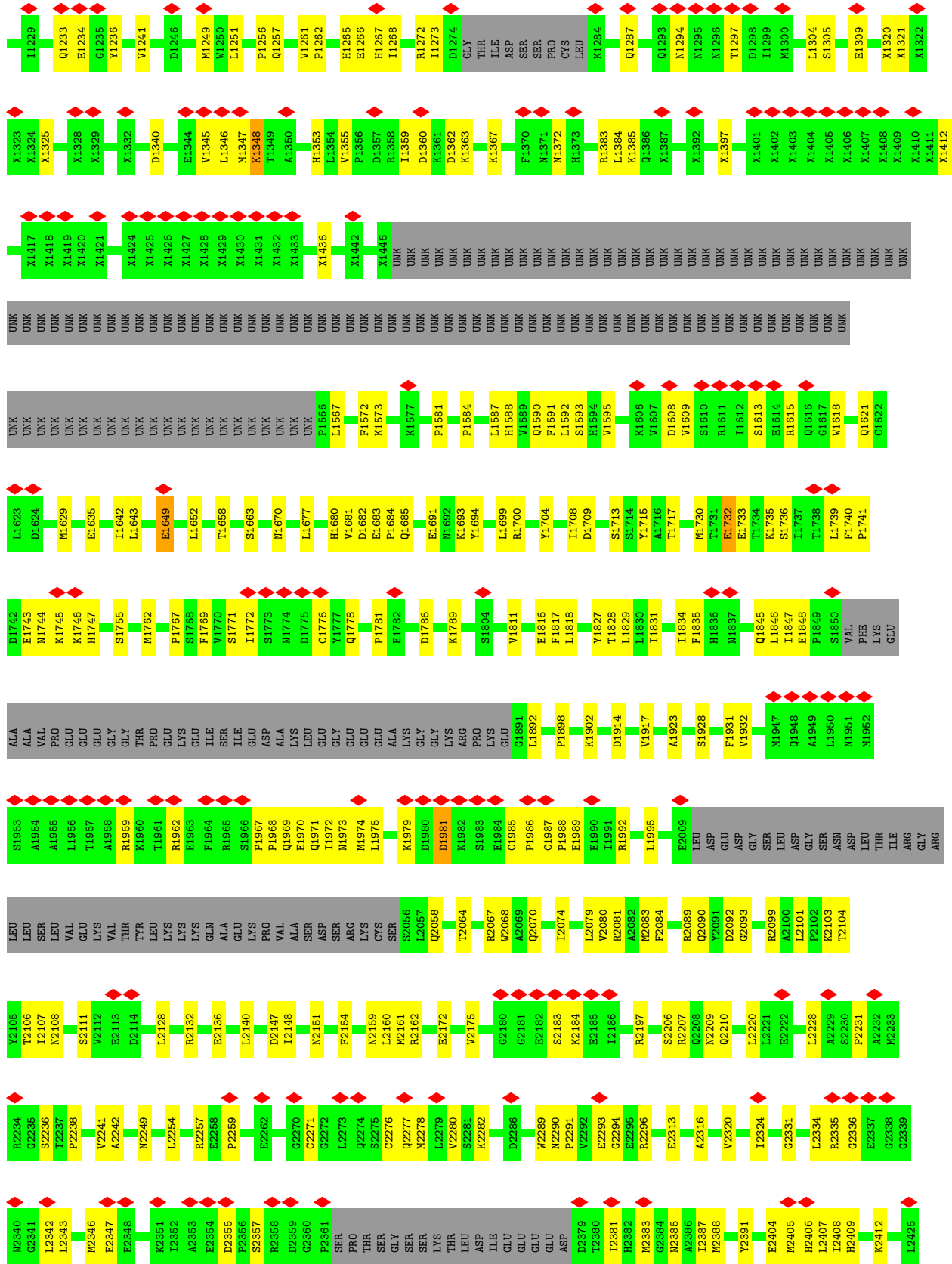




GLU	UNK	X2932	X3178	X3238	X3299	X3359	X3419	X3479	X3539	UNK	UNK	X2933	X3179	X3239	X3300	X3360	X3420	X3480	X3540	UNK	UNK	X2934	X3180	X3240	X3301	X3361	X3421	X3481	X3541	UNK	UNK	X2935	X3181	X3241	X3302	X3362	X3422	X3482	X3542	UNK	UNK	X2936	X3182	X3242	X3303	X3363	X3423	X3483	X3543	UNK	UNK	X2937	X3183	X3243	X3304	X3364	X3424	X3484	X3544	UNK	UNK	X2938	X3184	X3244	X3305	X3365	X3425	X3485	X3545	UNK	UNK	X2939	X3185	X3245	X3306	X3366	X3426	X3486	X3546	UNK	UNK	X2940	X3186	X3246	X3307	X3367	X3427	X3487	X3547	UNK	UNK	X2941	X3187	X3247	X3308	X3368	X3428	X3488	X3548	UNK	UNK	X2942	X3188	X3248	X3309	X3369	X3429	X3489	X3549	UNK	UNK	X2943	X3189	X3249	X3310	X3370	X3430	X3490	X3550	UNK	UNK	X2944	X3190	X3250	X3311	X3371	X3431	X3491	X3551	UNK	UNK	X2945	X3191	X3251	X3312	X3372	X3432	X3492	X3552	UNK	UNK	X2946	X3192	X3252	X3313	X3373	X3433	X3493	X3553	UNK	UNK	X2947	X3193	X3253	X3314	X3374	X3434	X3494	X3554	UNK	UNK	X2948	X3194	X3254	X3315	X3375	X3435	X3495	X3555	UNK	UNK	X2949	X3195	X3255	X3316	X3376	X3436	X3496	X3556	UNK	UNK	X2950	X3196	X3256	X3317	X3377	X3437	X3497	X3557	UNK	UNK	X2951	X3197	X3257	X3318	X3378	X3438	X3498	X3558	UNK	UNK	X2952	X3198	X3258	X3319	X3379	X3439	X3499	X3559	UNK	UNK	X2953	X3199	X3259	X3320	X3380	X3440	X3500	X3560	UNK	UNK	X2954	X3200	X3260	X3321	X3381	X3441	X3501	X3561	UNK	UNK	X2955	X3201	X3261	X3322	X3382	X3442	X3502	X3562	UNK	UNK	X2956	X3202	X3262	X3323	X3383	X3443	X3503	X3563	UNK	UNK	X2957	X3203	X3263	X3324	X3384	X3444	X3504	X3564	UNK	UNK	X2958	X3204	X3264	X3325	X3385	X3445	X3505	X3565	UNK	UNK	X2959	X3205	X3265	X3326	X3386	X3446	X3506	X3566	UNK	UNK	X2960	X3206	X3266	X3327	X3387	X3447	X3507	X3567	UNK	UNK	X2961	X3207	X3267	X3328	X3388	X3448	X3508	X3568	UNK	UNK	X2962	X3208	X3268	X3329	X3389	X3449	X3509	X3569	UNK	UNK	X2963	X3209	X3269	X3330	X3390	X3450	X3510	X3570	UNK	UNK	X2964	X3210	X3270	X3331	X3391	X3451	X3511	X3571	UNK	UNK	X2965	X3211	X3271	X3332	X3392	X3452	X3512	X3572	UNK	UNK	X2966	X3212	X3272	X3333	X3393	X3453	X3513	X3573	UNK	UNK	X2967	X3213	X3273	X3334	X3394	X3454	X3514	X3574	UNK	UNK	X2968	X3214	X3274	X3335	X3395	X3455	X3515	X3575	UNK	UNK	X2969	X3215	X3275	X3336	X3396	X3456	X3516	X3576	UNK	UNK	X2970	X3216	X3276	X3337	X3397	X3457	X3517	X3577	UNK	UNK	X2971	X3217	X3277	X3338	X3398	X3458	X3518	X3578	UNK	UNK	X2972	X3218	X3278	X3339	X3399	X3459	X3519	X3579	UNK	UNK	X2973	X3219	X3279	X3340	X3400	X3460	X3520	X3580	UNK	UNK	X2974	X3220	X3280	X3341	X3401	X3461	X3521	X3581	UNK	UNK	X2975	X3221	X3281	X3342	X3402	X3462	X3522	X3582	UNK	UNK	X2976	X3222	X3282	X3343	X3403	X3463	X3523	X3583	UNK	UNK	X2984	X3104	X3164	X3110	X3170	X3230	X3290	X3350	UNK	UNK	X2985	X3105	X3165	X3111	X3171	X3231	X3291	X3351	UNK	UNK	X2986	X3106	X3166	X3112	X3172	X3232	X3292	X3352	UNK	UNK	X2987	X3107	X3167	X3113	X3173	X3233	X3293	X3353	UNK	UNK	X2988	X3108	X3168	X3114	X3174	X3234	X3294	X3354	UNK	UNK	X2989	X3109	X3169	X3115	X3175	X3235	X3295	X3355	UNK	UNK	X2990	X3110	X3170	X3116	X3176	X3236	X3296	X3356	UNK	UNK	X2991	X3111	X3171	X3117	X3177	X3237	X3297	X3357	UNK	UNK	X2992	X3112	X3172	X3118	X3178	X3238	X3298	X3358	UNK	UNK	X2993	X3113	X3173	X3119	X3179	X3239	X3299	X3359	UNK	UNK	X2994	X3114	X3174	X3120	X3180	X3240	X3300	X3360	UNK	UNK	X2995	X3115	X3175	X3121	X3181	X3241	X3301	X3361	UNK	UNK	X2996	X3116	X3176	X3122	X3182	X3242	X3302	X3362	UNK	UNK	X2997	X3117	X3177	X3123	X3183	X3243	X3303	X3363	UNK	UNK	X2998	X3118	X3178	X3124	X3184	X3244	X3304	X3364	UNK	UNK	X2999	X3119	X3179	X3125	X3185	X3245	X3305	X3365	UNK	UNK	X3000	X3120	X3180	X3126	X3186	X3246	X3306	X3366	UNK	UNK	X3001	X3121	X3181	X3127	X3187	X3247	X3307	X3367	UNK	UNK	X3002	X3122	X3182	X3128	X3188	X3248	X3308	X3368	UNK	UNK	X3003	X3123	X3183	X3129	X3189	X3249	X3309	X3369	UNK	UNK	X3004	X3124	X3184	X3130	X3190	X3250	X3310	X3370	UNK	UNK	X3005	X3125	X3185	X3131	X3191	X3251	X3311	X3371	UNK	UNK	X3006	X3126	X3186	X3132	X3192	X3252	X3312	X3372	UNK	UNK	X3009	X3127	X3187	X3133	X3193	X3253	X3313	X3373	UNK	UNK	X3010	X3128	X3188	X3134	X3194	X3254	X3314	X3374	UNK	UNK	X3011	X3129	X3189	X3135	X3195	X3255	X3315	X3375	UNK	UNK	X3012	X3130	X3190	X3136	X3196	X3256	X3316	X3376	UNK	UNK	X3013	X3131	X3191	X3137	X3197	X3257	X3317	X3377	UNK	UNK	X3014	X3132	X3192	X3138	X3198	X3258	X3318	X3378	UNK	UNK	X3015	X3133	X3193	X3139	X3199	X3259	X3319	X3379	UNK	UNK	X3016	X3134	X3194	X3140	X3200	X3260	X3320	X3380	UNK	UNK	X3017	X3135	X3195	X3141	X3201	X3261	X3321	X3381	UNK	UNK	X3018	X3136	X3196	X3142	X3202	X3262	X3322	X3382	UNK	UNK	X3019	X3137	X3197	X3143	X3203	X3263	X3323	X3383	UNK	UNK	X3020	X3138	X3198	X3144	X3204	X3264	X3324	X3384	UNK	UNK	X3021	X3139	X3199	X3145	X3205	X3265	X3325	X3385	UNK	UNK	X3022	X3140	X3200	X3146	X3206	X3266	X3326	X3386	UNK	UNK	X3023	X3141	X3201	X3147	X3207	X3267	X3327	X3387	UNK	UNK	X3024	X3142	X3202	X3148	X3208	X3268	X3328	X3388	UNK	UNK	X3207	X3143	X3203	X3149	X3209	X3269	X3329	X3389	UNK	UNK	X3208	X3144	X3204	X3150	X3210	X3270	X3330	X3390	UNK	UNK	X3209	X3145	X3205	X3151	X3211	X3271	X3331	X3391	UNK	UNK	X3210	X3146	X3206	X3152	X3212	X3272	X3332	X3392	UNK	UNK	X3211	X3147	X3207	X3153	X3213	X3273	X3333	X3393	UNK	UNK	X3212	X3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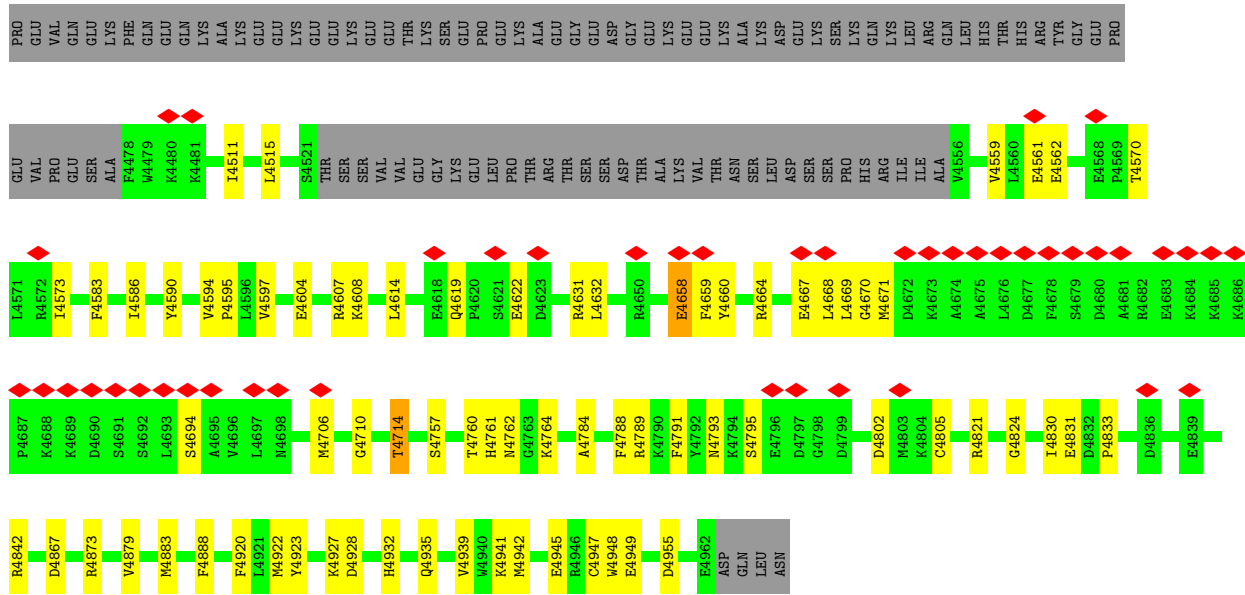




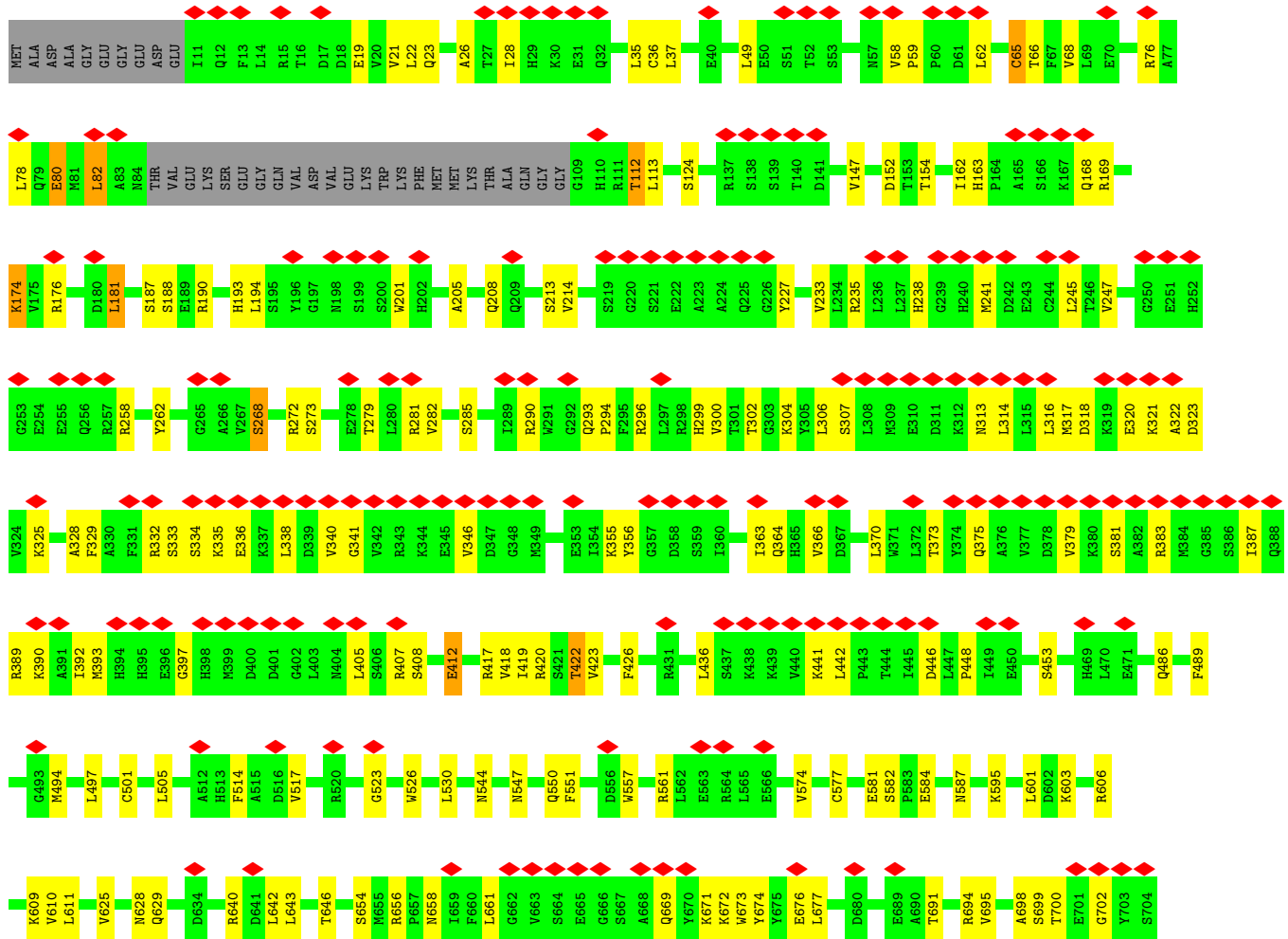








• Molecule 1: Ryanodine receptor 2























## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41197	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	0.120	Depositor
Minimum map value	-0.076	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.02	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	0.14	0/26895	0.36	0/36316
1	B	0.14	0/26895	0.36	0/36316
1	C	0.14	0/26895	0.36	0/36316
1	D	0.14	0/26895	0.36	0/36316
2	G	0.11	0/835	0.38	0/1123
2	H	0.11	0/835	0.38	0/1123
2	I	0.11	0/835	0.38	0/1123
2	J	0.11	0/835	0.38	0/1123
All	All	0.14	0/110920	0.36	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	26711	523	0
1	B	30071	0	26711	523	0
1	C	30071	0	26711	524	0
1	D	30071	0	26711	529	0
2	G	819	0	821	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	819	0	821	19	0
2	I	819	0	821	20	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	110128	2131	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 9.

The worst 5 of 2131 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:D:1772:ILE:HD11	2:J:57:ILE:HA	1.57	0.86
1:A:1233:GLN:HG3	1:B:3493:UNK:HA	1.56	0.86
1:A:4833:PRO:HB3	1:A:4842:ARG:HD3	1.61	0.82
1:C:4833:PRO:HB3	1:C:4842:ARG:HD3	1.61	0.81
1:D:76:ARG:O	1:D:80:GLU:HB2	1.81	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%)	3047 (94%)	208 (6%)	0	100	100
1	B	3255/4966 (66%)	3047 (94%)	208 (6%)	0	100	100
1	C	3255/4966 (66%)	3046 (94%)	209 (6%)	0	100	100
1	D	3255/4966 (66%)	3047 (94%)	208 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	105/176 (60%)	102 (97%)	3 (3%)	0	100	100
2	H	105/176 (60%)	102 (97%)	3 (3%)	0	100	100
2	I	105/176 (60%)	102 (97%)	3 (3%)	0	100	100
2	J	105/176 (60%)	102 (97%)	3 (3%)	0	100	100
All	All	13440/20568 (65%)	12595 (94%)	845 (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%)	2779 (97%)	83 (3%)	37	60
1	B	2862/3387 (84%)	2778 (97%)	84 (3%)	37	60
1	C	2862/3387 (84%)	2778 (97%)	84 (3%)	37	60
1	D	2862/3387 (84%)	2777 (97%)	85 (3%)	36	60
2	G	88/140 (63%)	88 (100%)	0	100	100
2	H	88/140 (63%)	88 (100%)	0	100	100
2	I	88/140 (63%)	88 (100%)	0	100	100
2	J	88/140 (63%)	88 (100%)	0	100	100
All	All	11800/14108 (84%)	11464 (97%)	336 (3%)	38	61

5 of 336 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3851	SER
1	D	1108	VAL
1	C	4076	THR
1	D	187	SER
1	D	2184	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 259 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	2150	ASN
1	D	3952	HIS
1	B	1944	ASN
1	B	1685	GLN
1	D	4200	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 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.

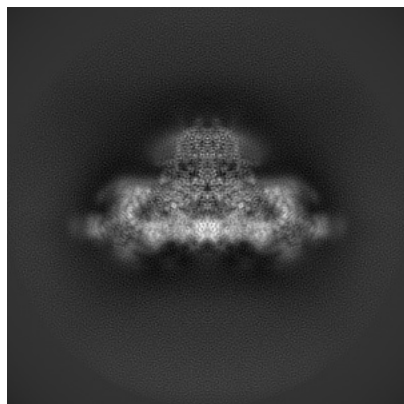
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33937. These allow visual inspection of the internal detail of the map and identification of artifacts.

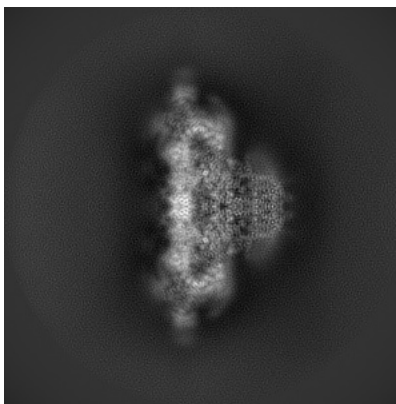
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

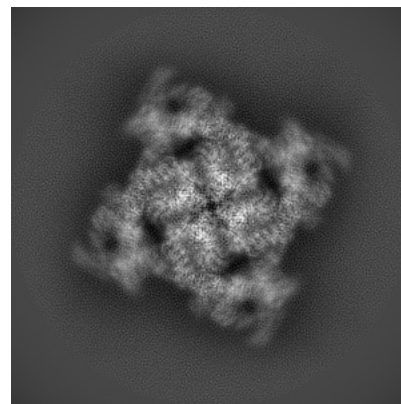
#### 6.1.1 Primary map



X

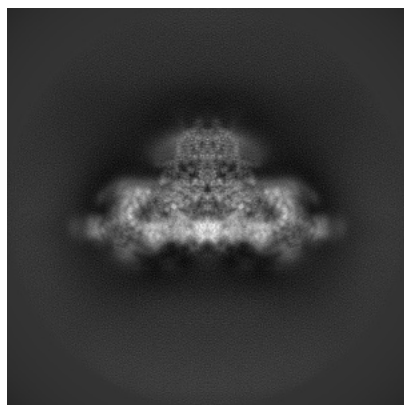


Y

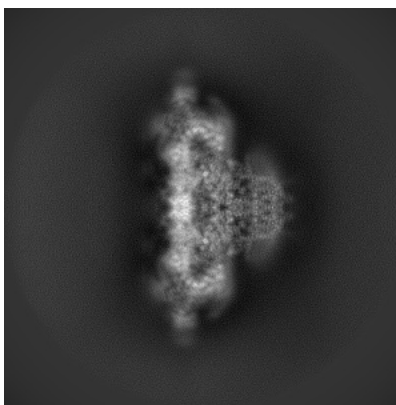


Z

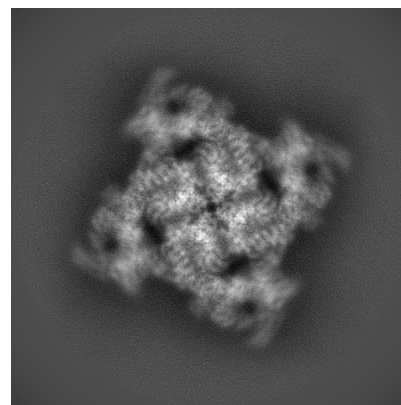
#### 6.1.2 Raw map



X



Y

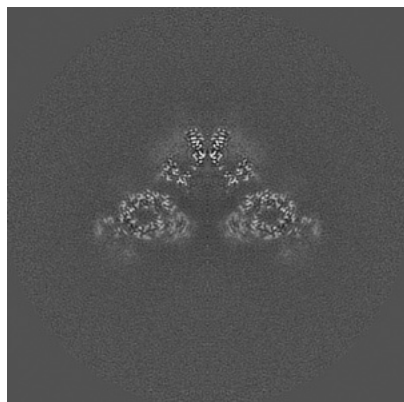


Z

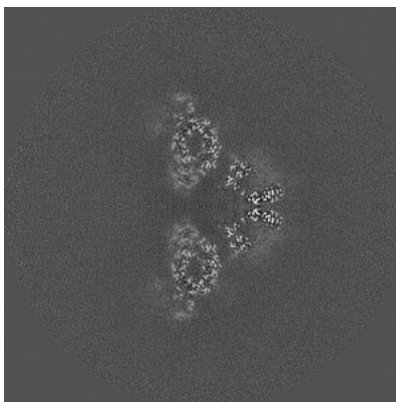
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

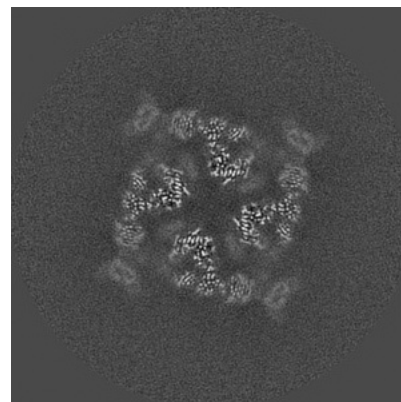
### 6.2.1 Primary map



X Index: 200

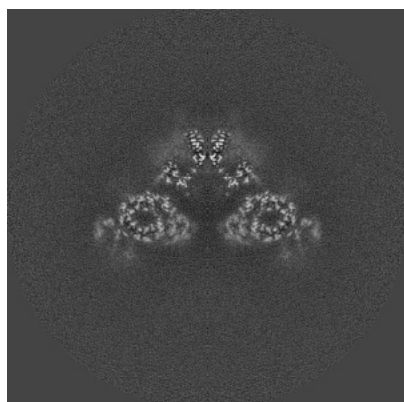


Y Index: 200

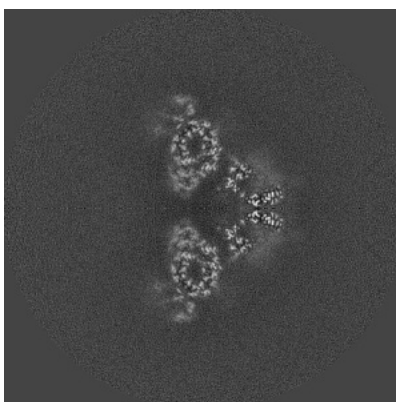


Z Index: 200

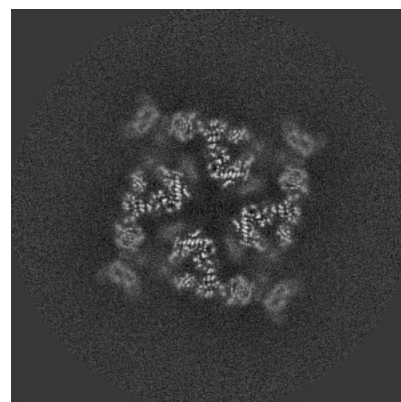
### 6.2.2 Raw map



X Index: 200



Y Index: 200

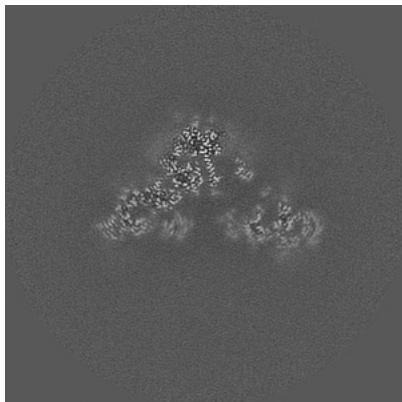


Z Index: 200

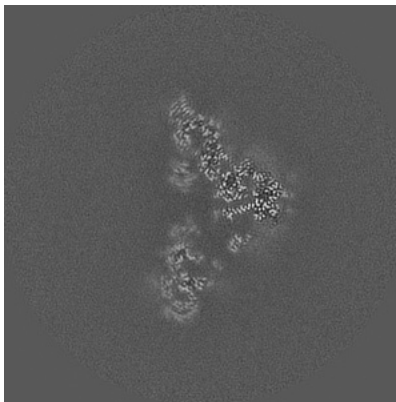
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

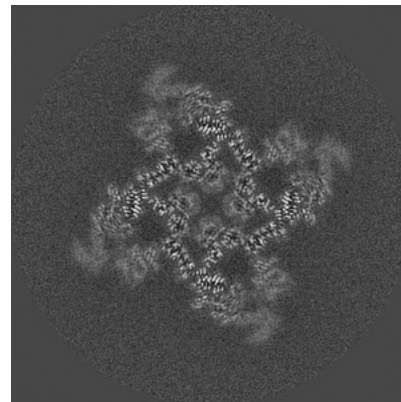
### 6.3.1 Primary map



X Index: 193

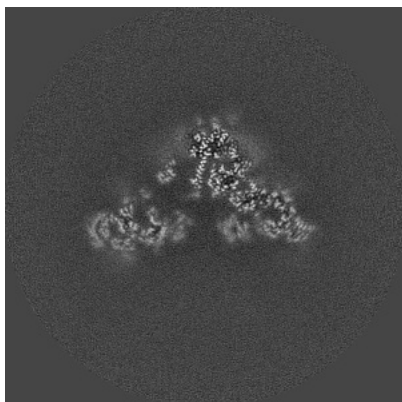


Y Index: 193

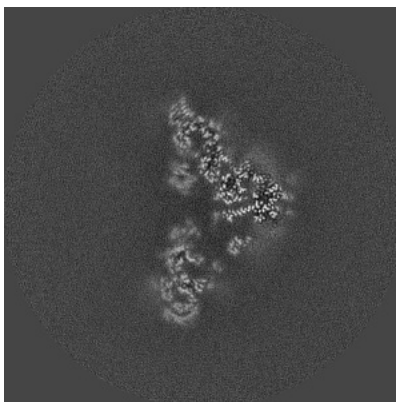


Z Index: 183

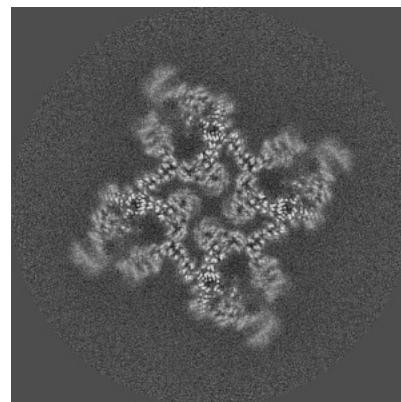
### 6.3.2 Raw map



X Index: 207



Y Index: 193

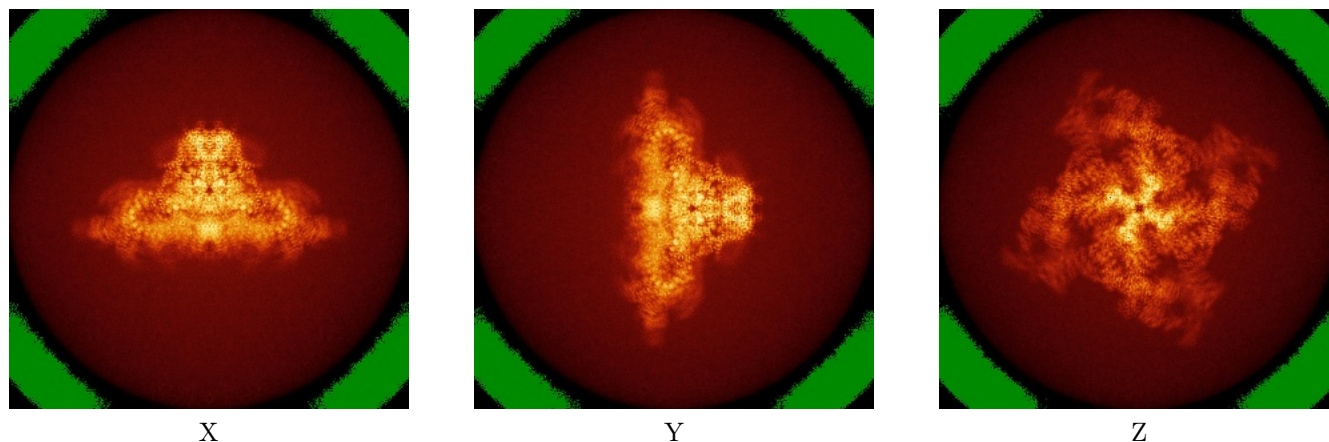


Z Index: 180

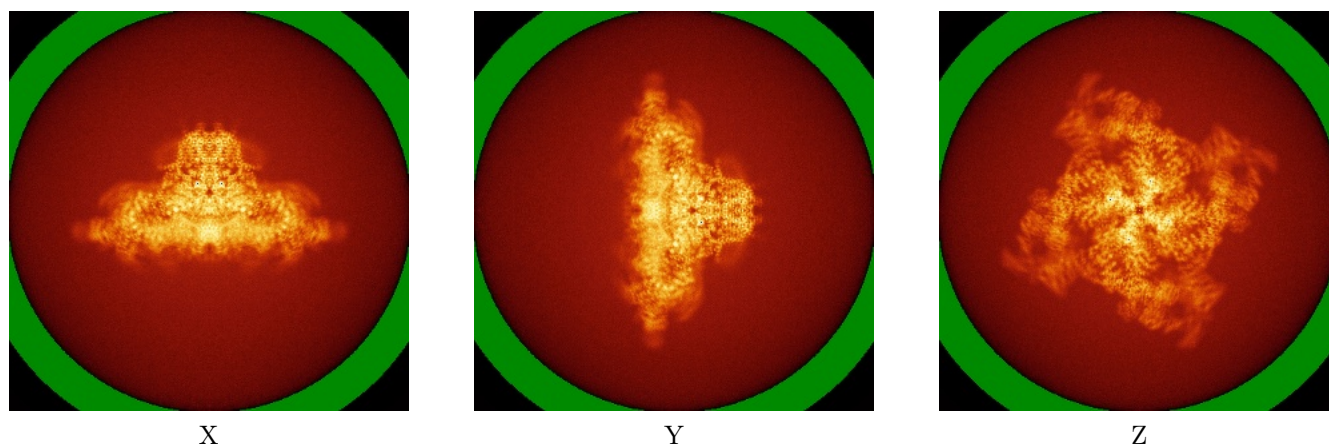
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



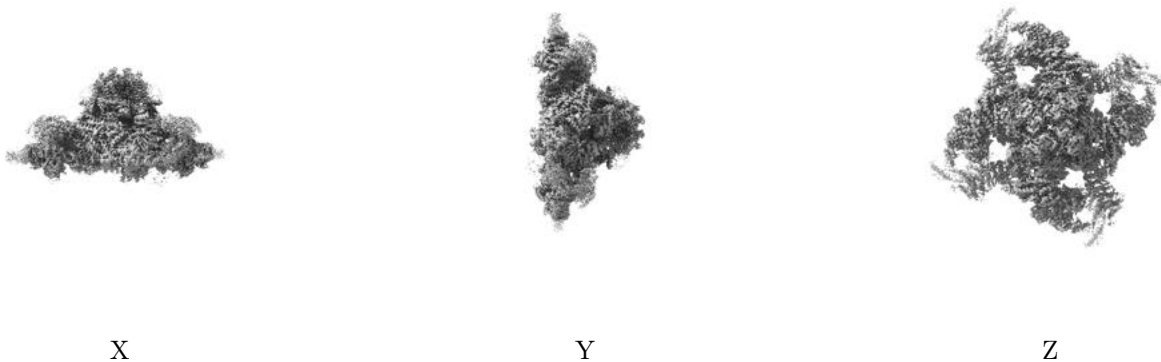
### 6.4.2 Raw map



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.

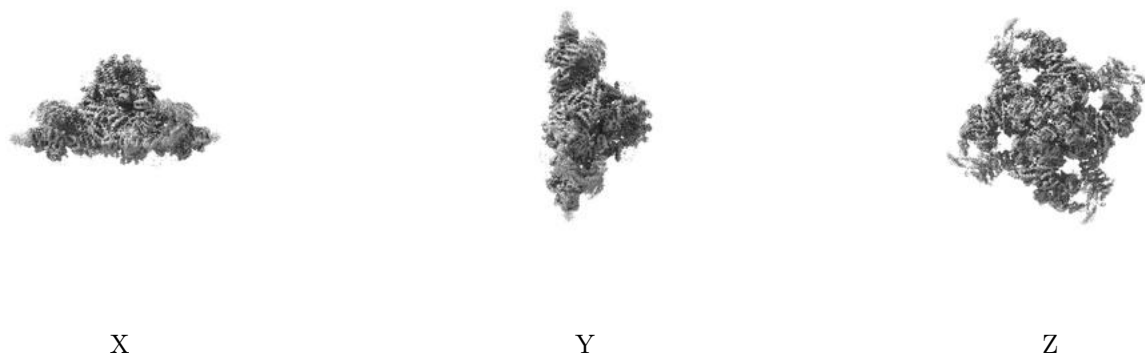
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

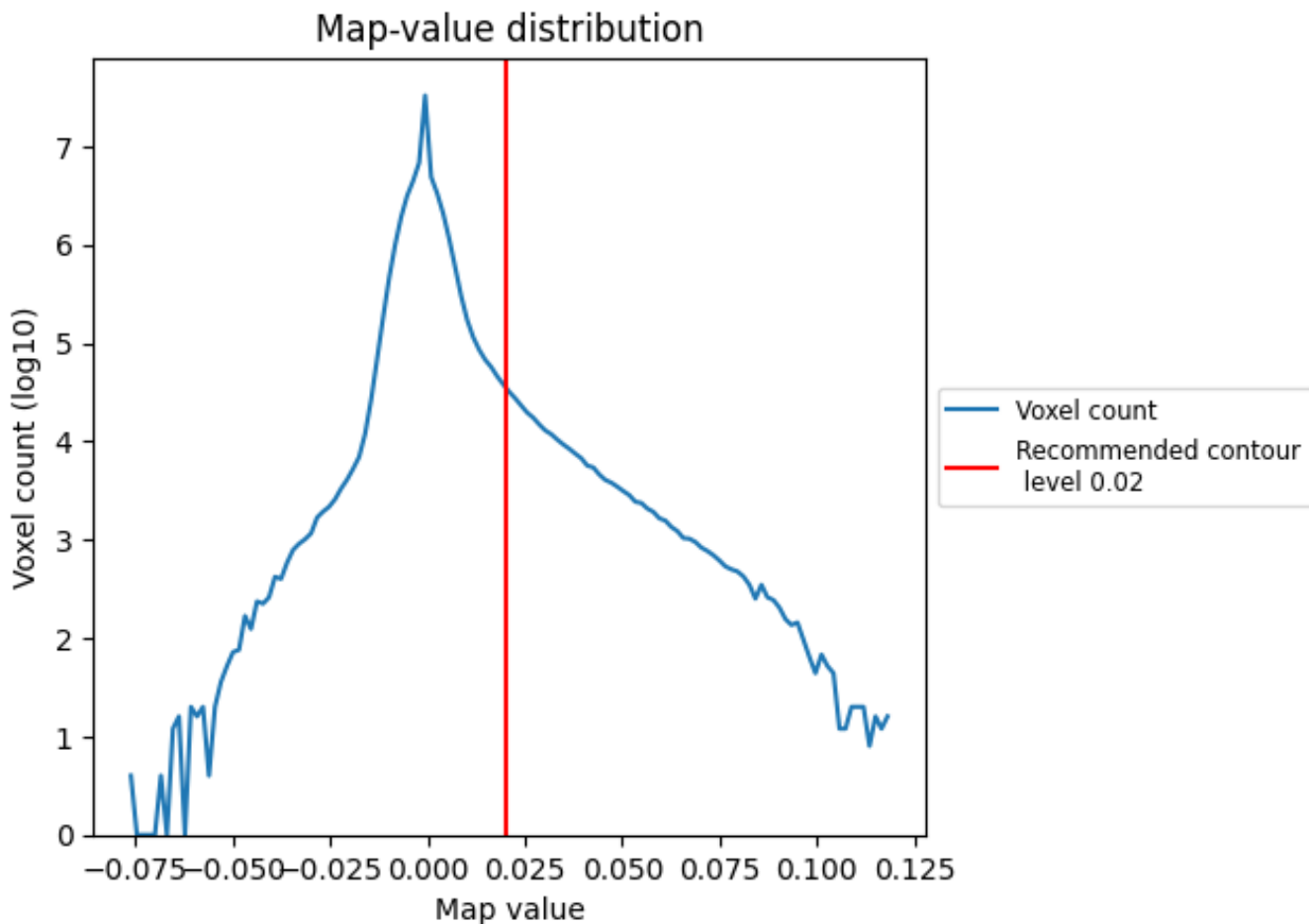
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

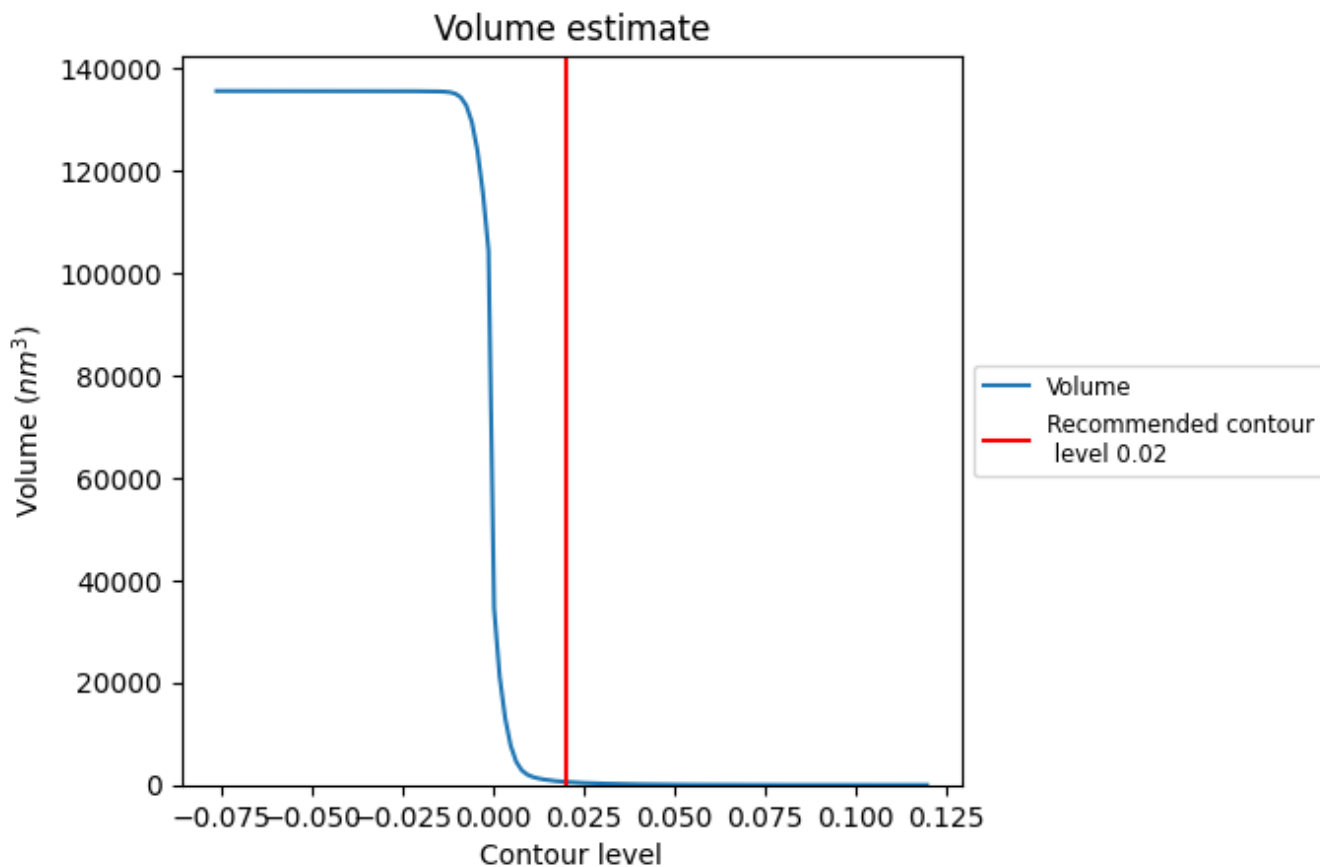
This section contains the results of statistical analysis of the map.

### 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.

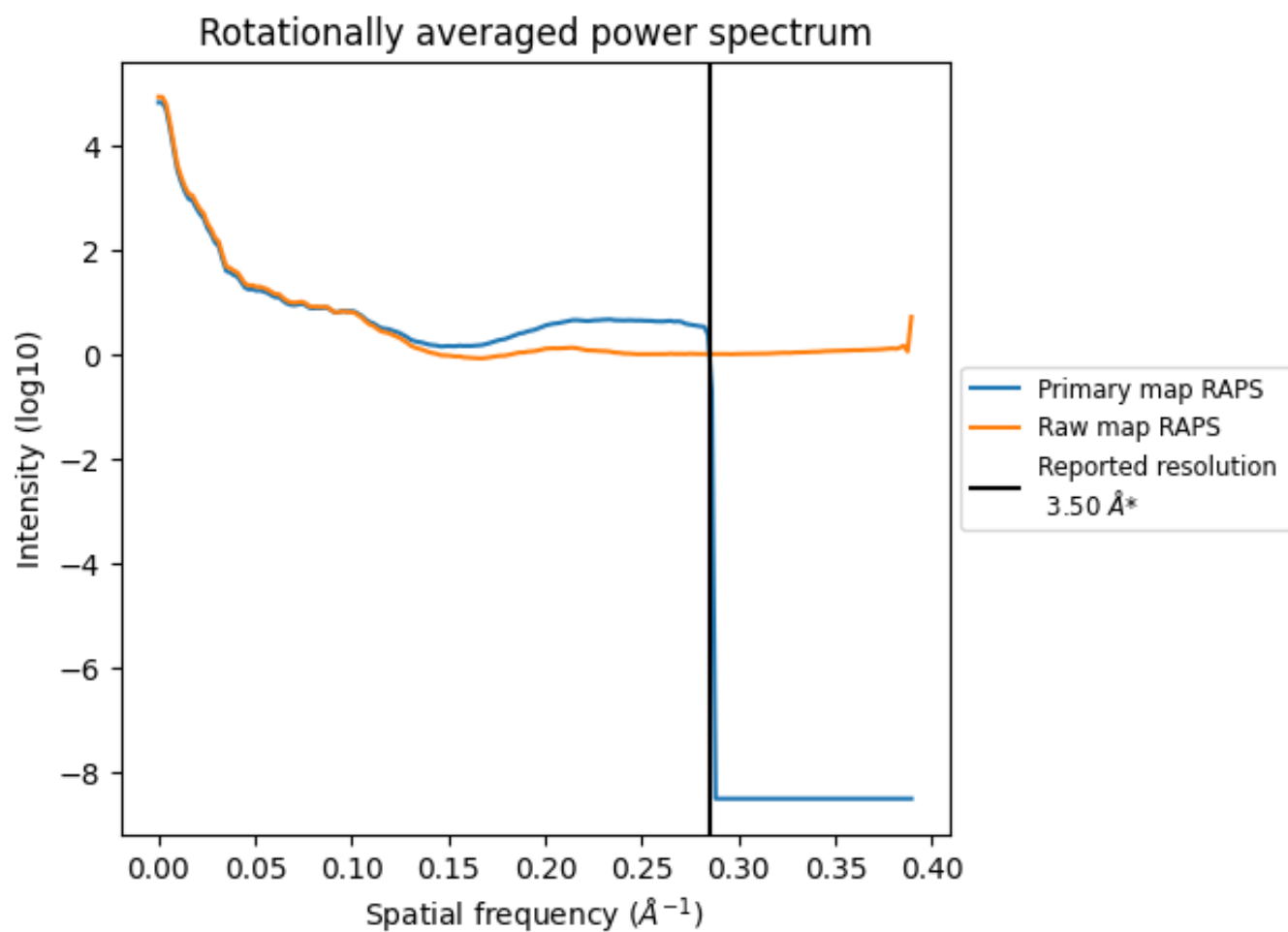
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 601 nm<sup>3</sup>; this corresponds to an approximate mass of 542 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

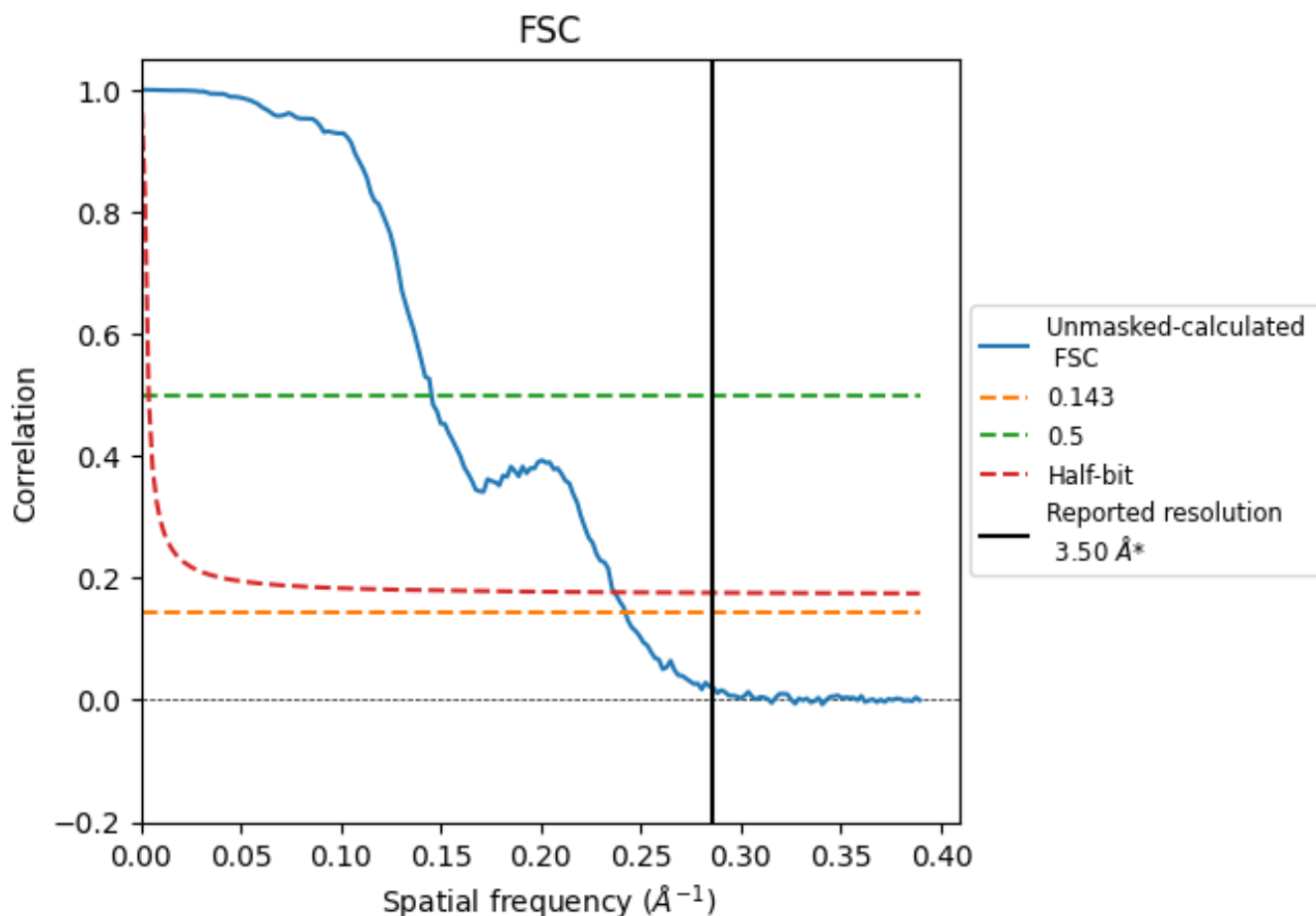


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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 0.286 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

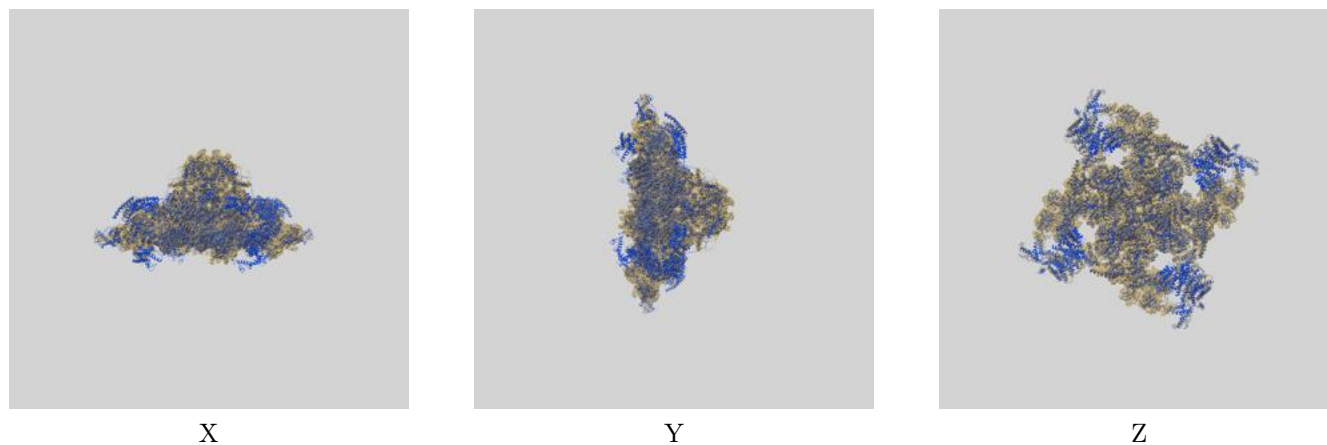
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.13	6.88	4.22

\*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 4.13 differs from the reported value 3.5 by more than 10 %

## 9 Map-model fit [i](#)

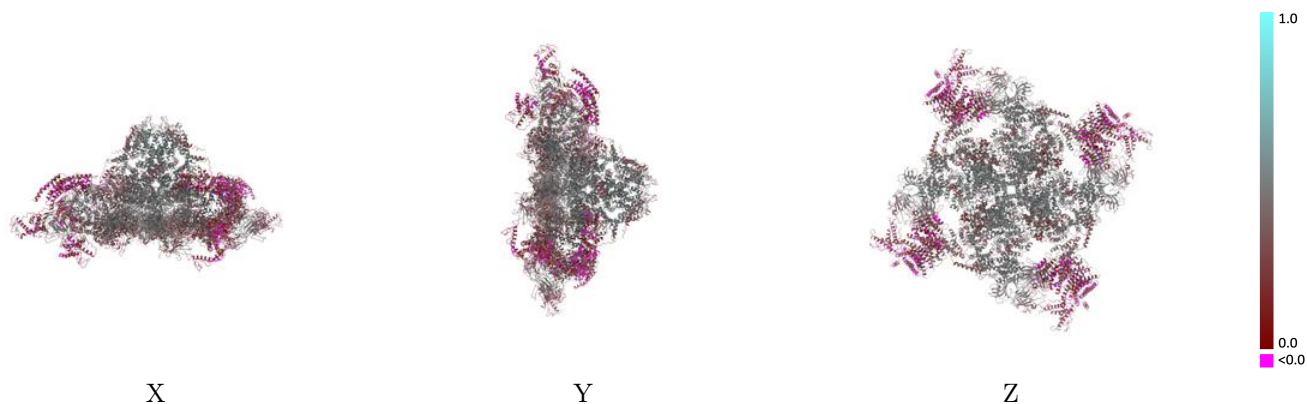
This section contains information regarding the fit between EMDB map EMD-33937 and PDB model 7VMN. Per-residue inclusion information can be found in section [3](#) on page [12](#).

### 9.1 Map-model overlay [i](#)



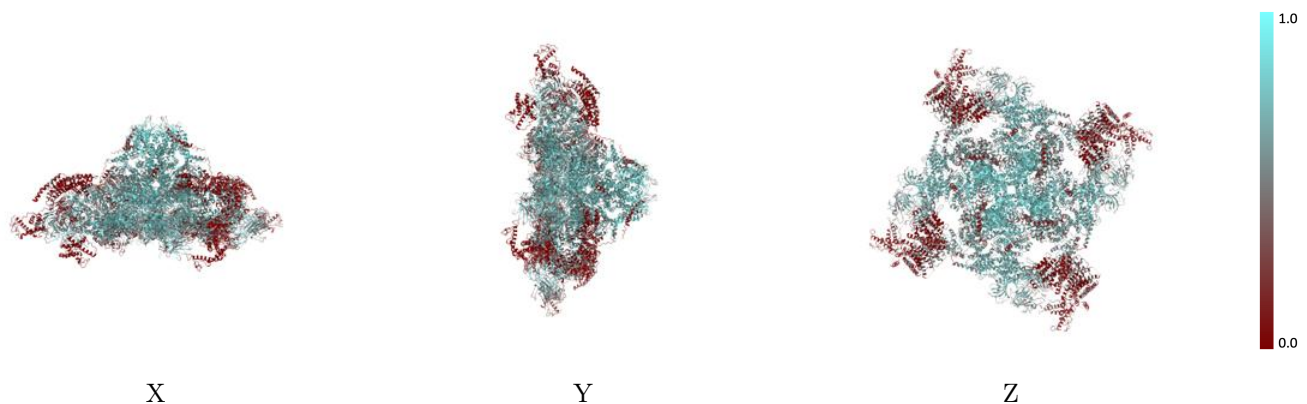
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



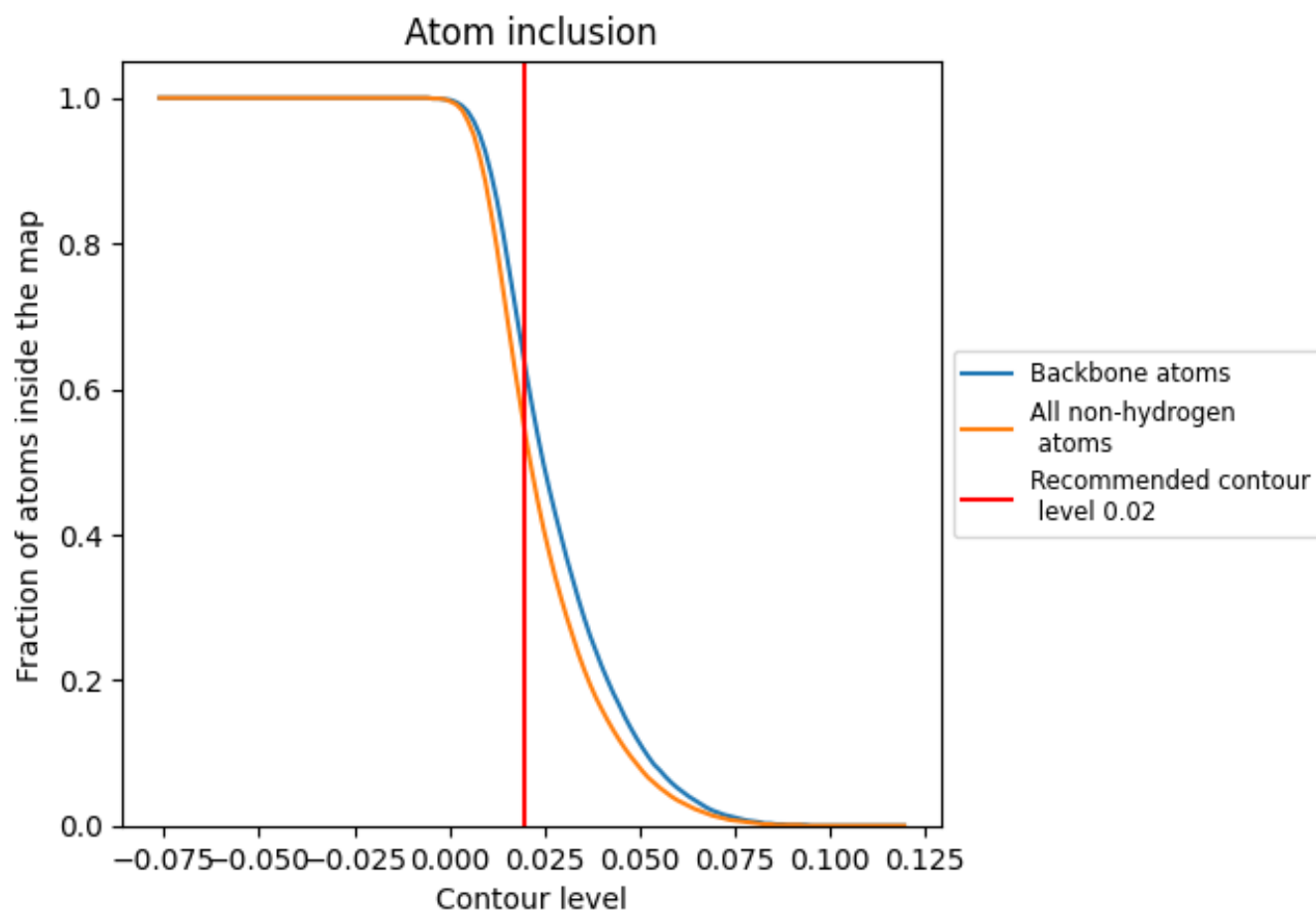
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 54% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5380	 0.3770
A	 0.5350	 0.3750
B	 0.5370	 0.3760
C	 0.5360	 0.3760
D	 0.5360	 0.3740
G	 0.6290	 0.4370
H	 0.6310	 0.4350
I	 0.6320	 0.4300
J	 0.6290	 0.4350

