



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:24 PM UTC

PDB ID : 5T9M / pdb_00005t9m
EMDB ID : EMD-8372
Title : Structure of rabbit RyR1 (Ca²⁺-only dataset, class 1)
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;
Frank, J.
Deposited on : 2016-09-09
Resolution : 4.00 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:

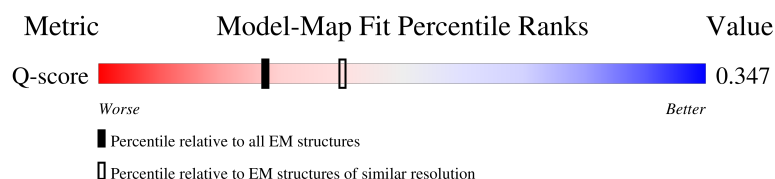
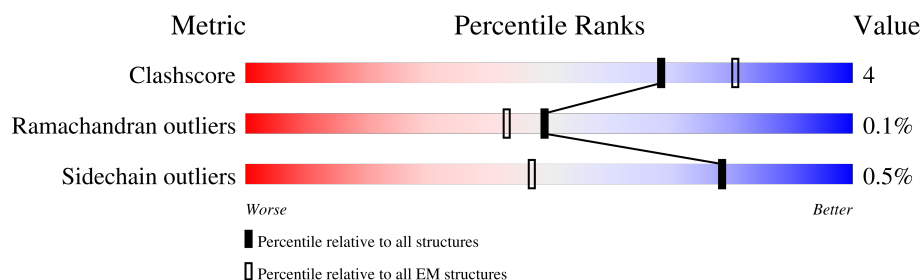
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.00 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.



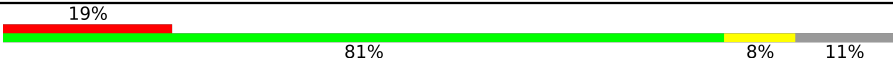
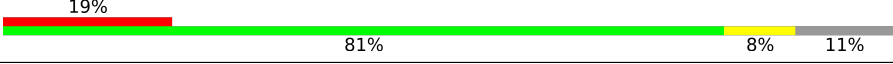
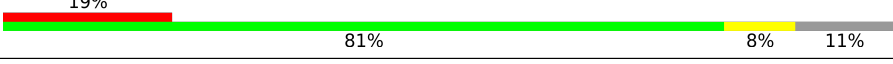
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	108	13% 88% 11%
1	F	108	14% 87% 12%
1	H	108	14% 87% 12%
1	J	108	13% 87% 12%

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Mol	Chain	Length	Quality of chain
2	B	4676	
2	E	4676	
2	G	4676	
2	I	4676	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 120756 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	J	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	E	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	I	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	G	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	

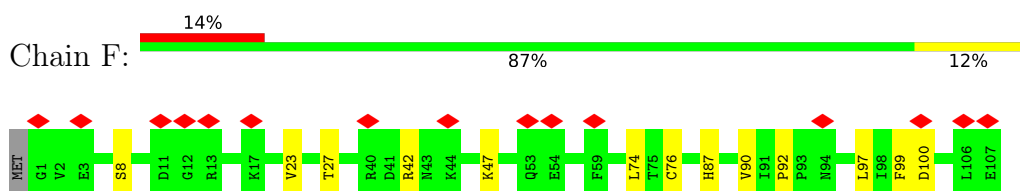
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Ca 1	0
4	E	1	Total 1	Ca 1	0
4	I	1	Total 1	Ca 1	0
4	G	1	Total 1	Ca 1	0

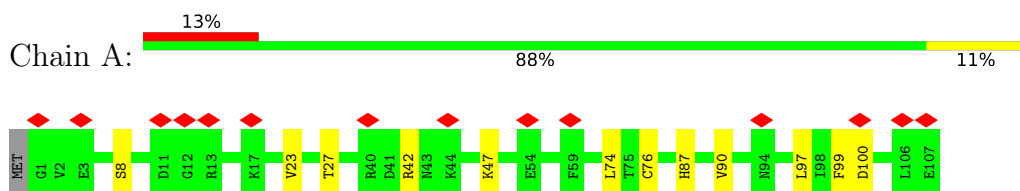
3 Residue-property plots [i](#)

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.

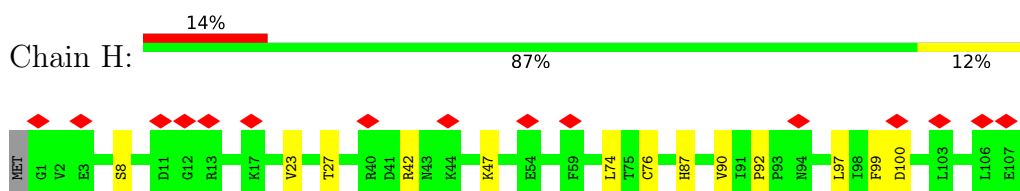
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



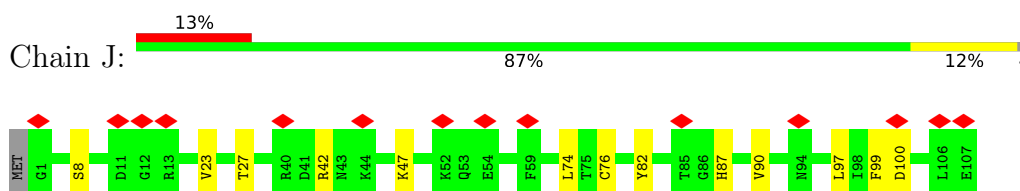
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



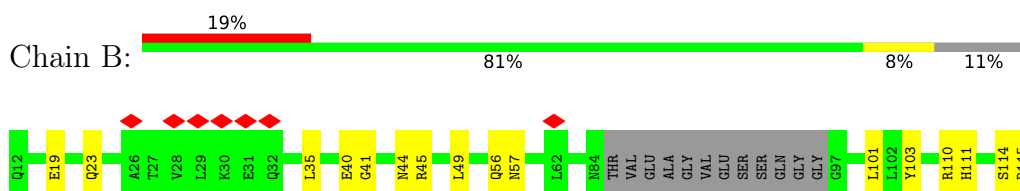
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

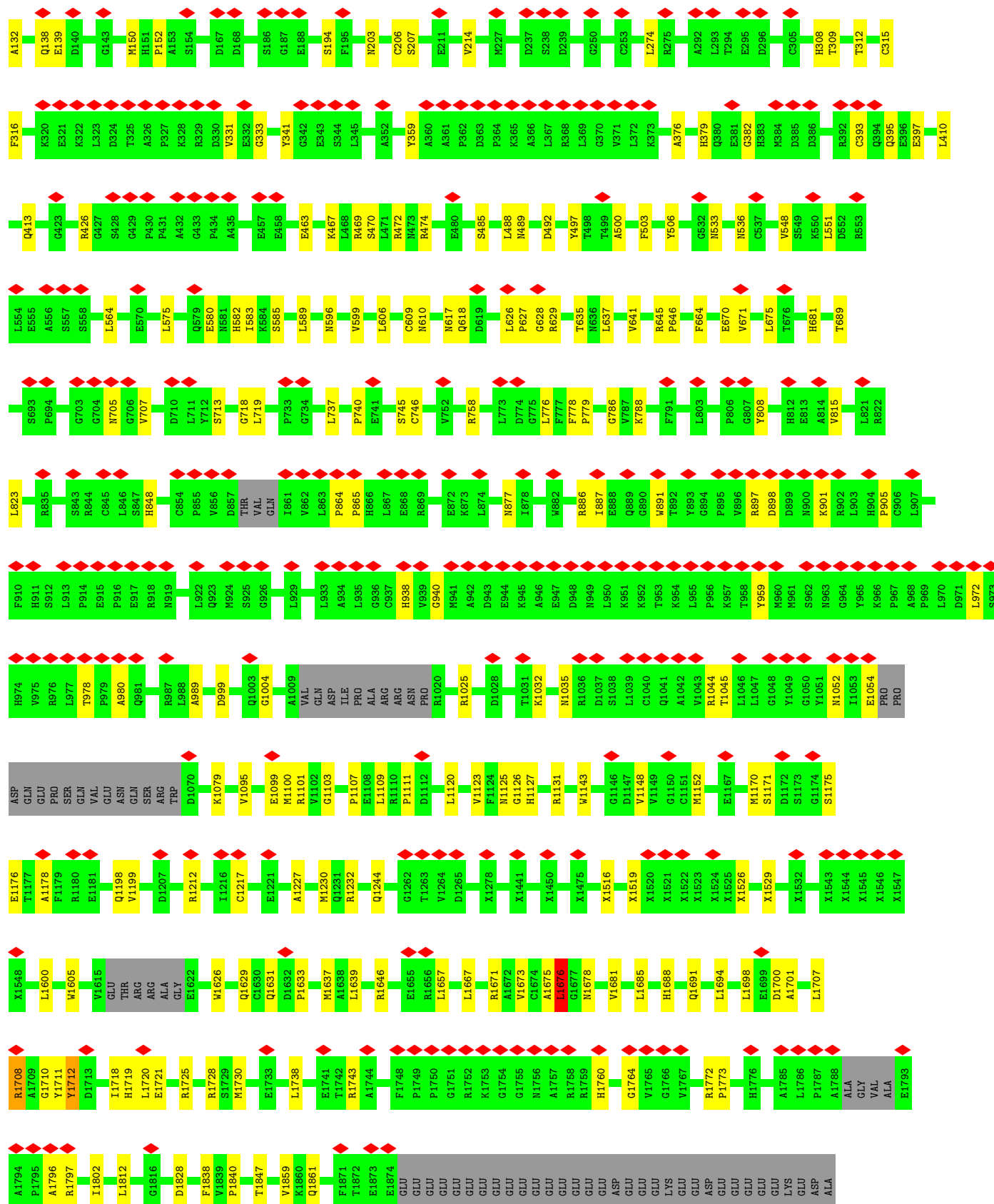


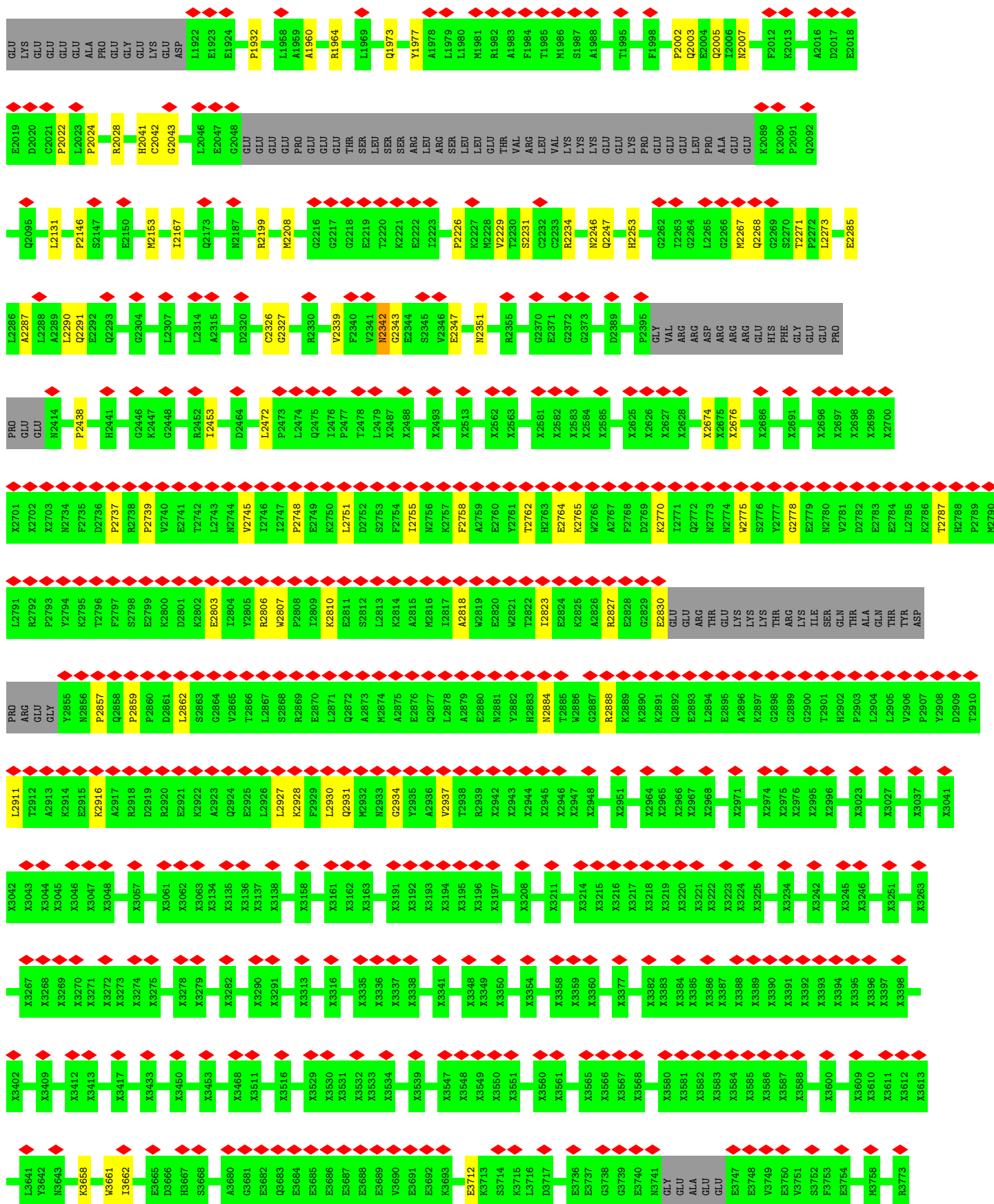
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

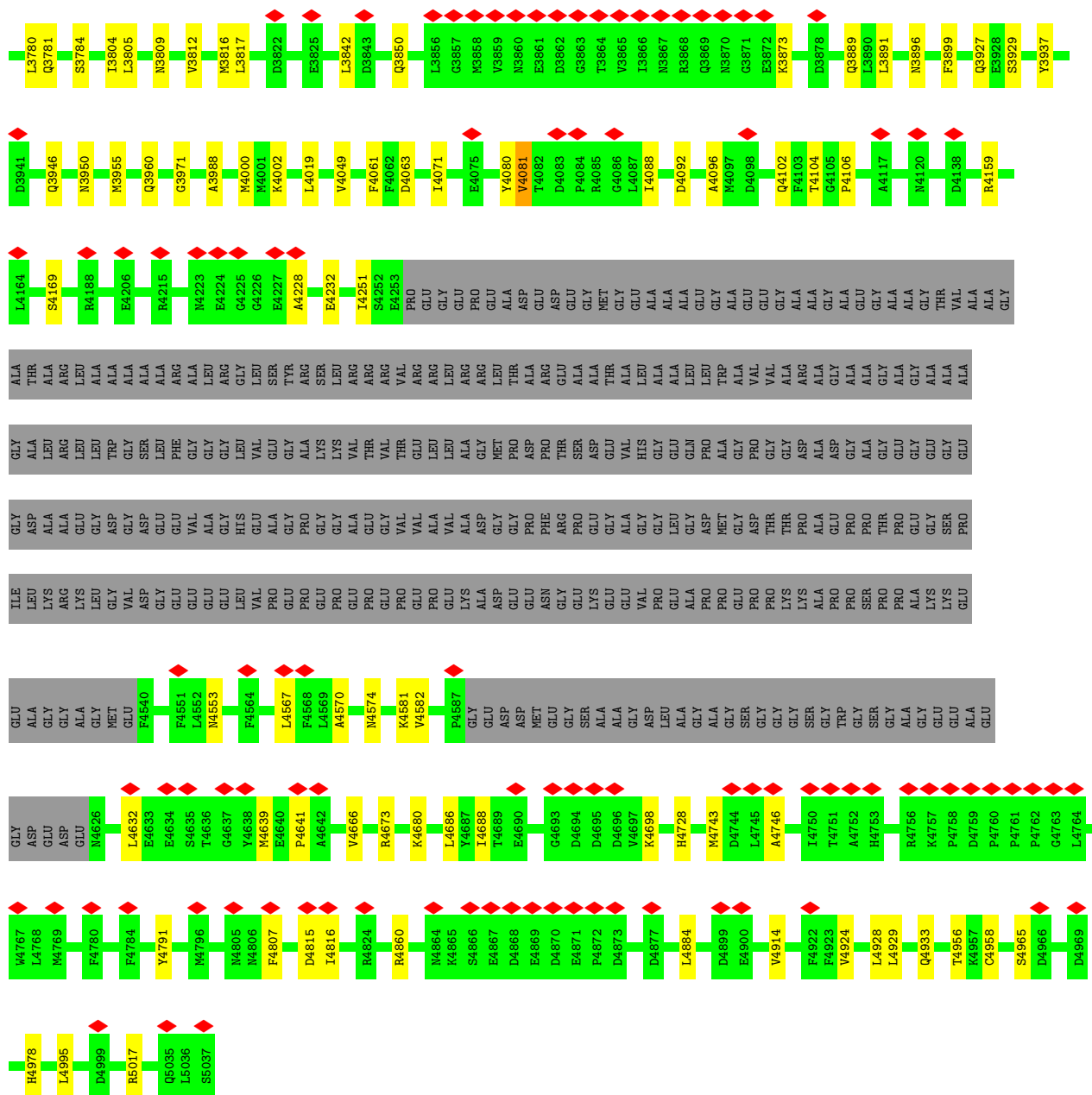


- Molecule 2: Ryanodine receptor 1



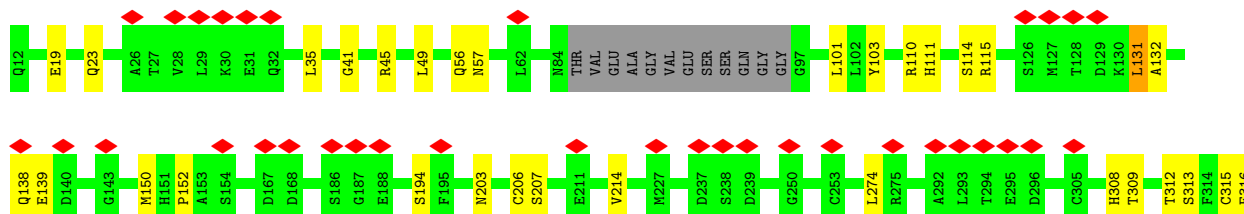


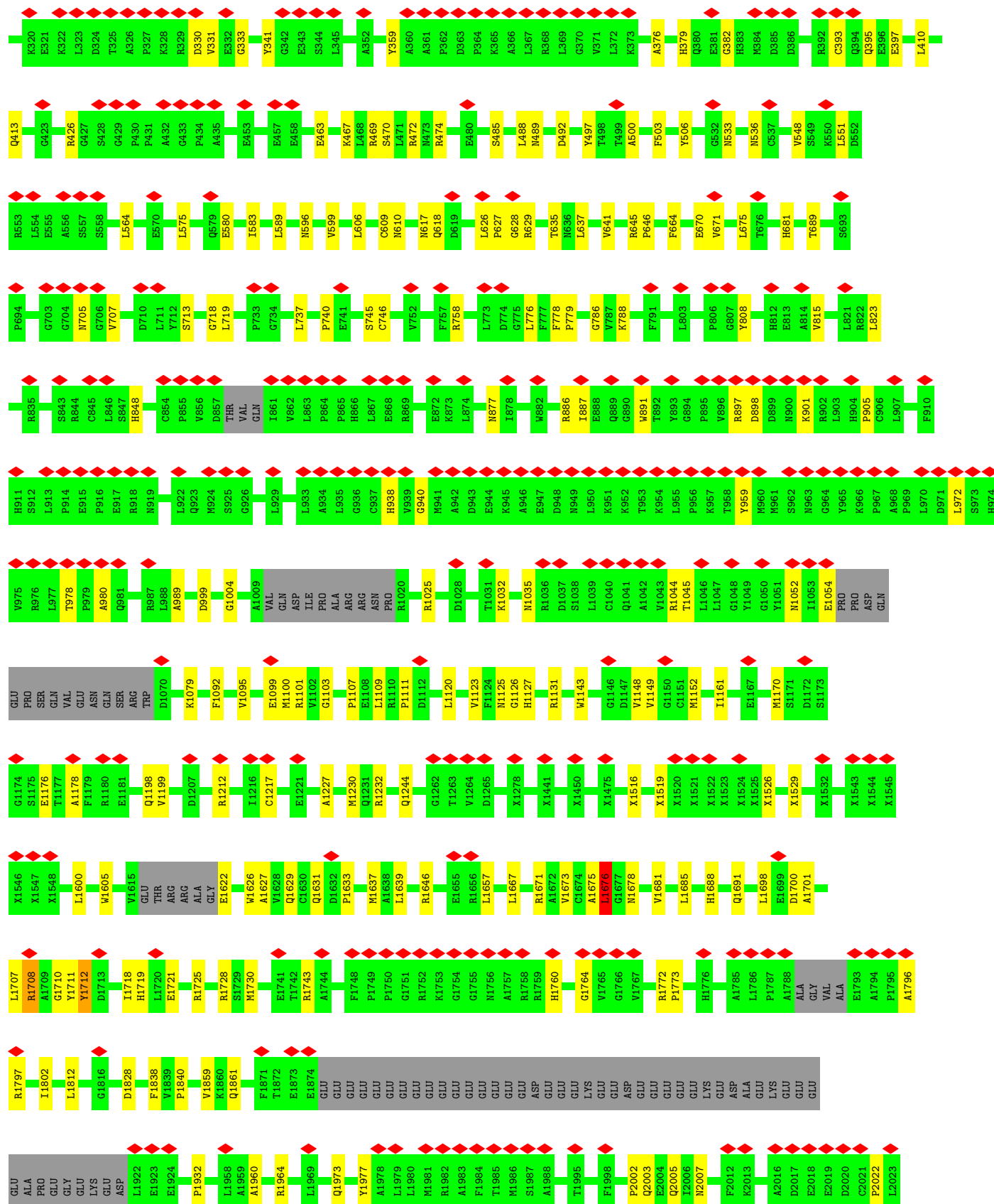




• Molecule 2: Ryanodine receptor 1

Chain E: 19% 81% 8% 11%

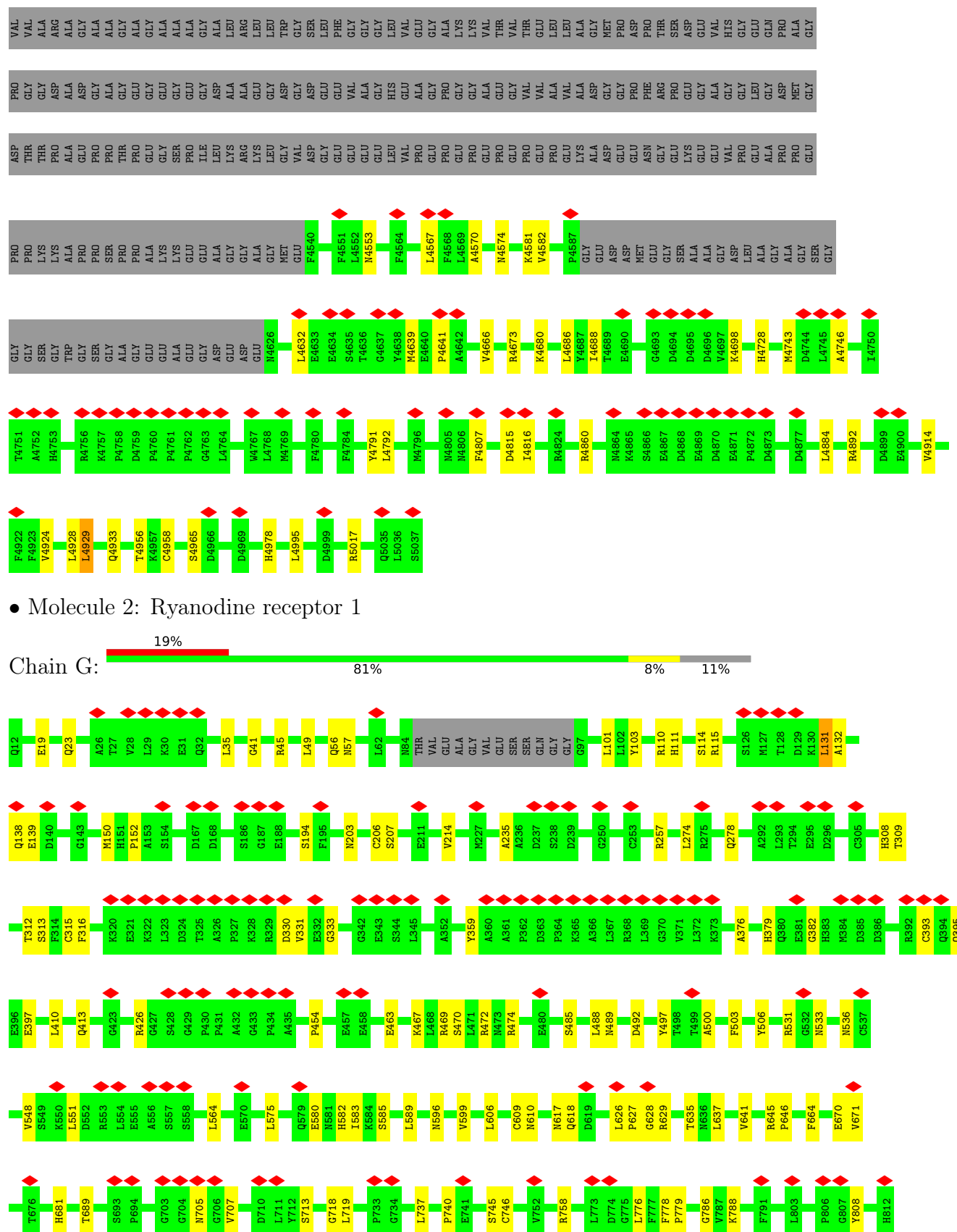






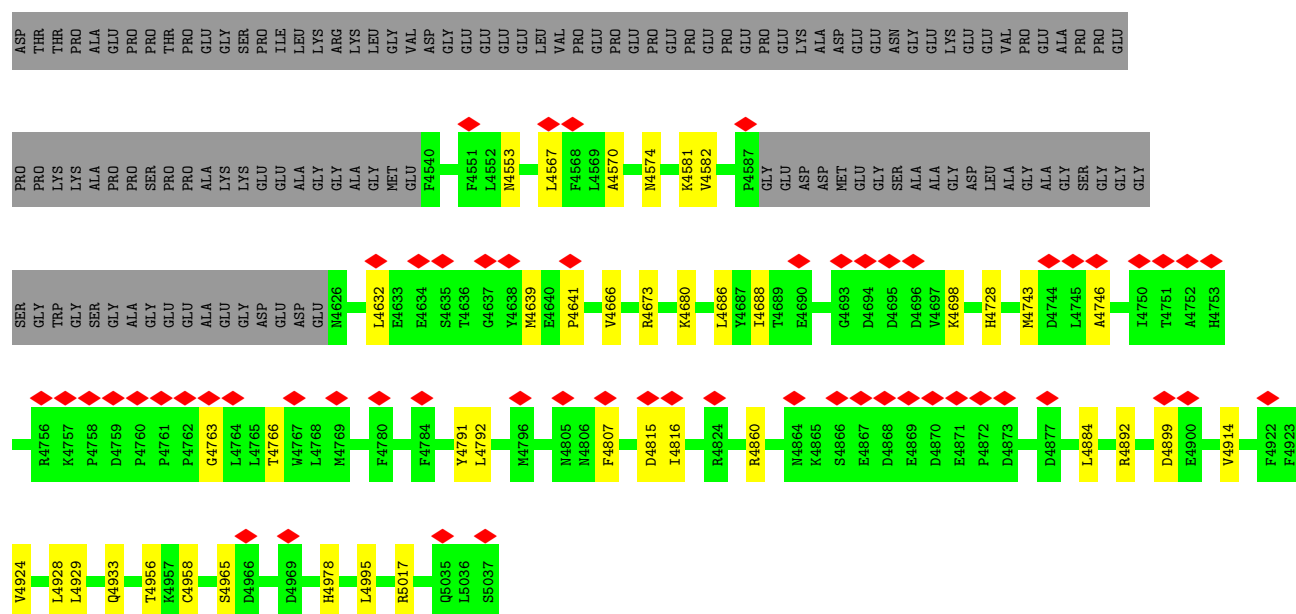


ALA	ALA	S9929	M3758	X3612	X3395	X3246	X3027	V2906	ALA	K2786	X2696	PHE
GLY	GLY	Y3937	R3773	X3613	X3396	X3251	X3037	P2907	GLN	T2787	X2697	GLY
ALA	ALA	D3941	L3780	L3641	X3397	X3254	X3037	Y2908	THR	H2788	X2698	GLU
GLY	GLY	Q3946	Q3781	N3643	X3398	X3263	X3041	D2909	TVR	P2789	X2699	GLU
ALA	ALA	Q3950	S3784	N3643	X3409	X3267	X3042	T2910	ASP	M2790	X2700	PRO
THR	THR	N3955	L3804	H3647	X3412	X3268	X3043	L2911	PRO	L2791	X2701	GLU
ALA	ALA	Q3960	L3805	K3658	X3413	X3269	X3044	T2912	ARG	L2792	X2702	GLU
GLY	GLY	Q3971	L3805	V3661	X3433	X3270	X3045	A2913	GLY	P2793	X2703	
ALA	ALA	Q3971	L3805	I3662	X3450	X3271	X3046	E2914		Y2794	N2734	
THR	THR	A3988	N3909	I3662	X3453	X3272	X3047	E2915		K2795	F2735	
ARG	ARG	M4000	V3812	D3665	X3467	X3273	X3048	K2916		T2796	D2736	
ALA	ALA	M4001	M3816	D3666	X3468	X3274	X3057	A2917		P2797	P2737	
ALA	ALA	M4002	L3817	H3667	X3468	X3275	X3061	D2918		S2798	R2738	
ALA	ALA	L4017	D3822	S3668	X3467	X3276	X3062	D2919		E2799	P2739	
ALA	ALA	L4018	E3825	A3680	X3467	X3278	X3063	R2920		K2800	V2740	
ALA	ALA	L4019	L3842	Q3683	X3468	X3279	X3063	E2921		D2801	E2741	
ALA	ALA	V4049	D3843	Q3683	X3511	X3282	X3134	A2922		T2742	T2742	
LEU	LEU	F4061	Q3850	E3684	X3516	X3290	X3135	Q2924		E2803	L2743	
GLY	GLY	F4062	L3856	E3684	X3529	X3291	X3136	E2925		I2804	N2744	
LEU	LEU	F4063	G3857	E3685	X3530	X3291	X3137	E2926		R2806	V2745	
SER	SER	I4071	G3857	E3686	X3531	X3313	X3161	L2927		R2807	I2746	
ARG	ARG	E4075	M3858	E3688	X3532	X3316	X3162	Q2928		P2808	P2748	
ARG	ARG	E4075	M3859	E3689	X3533	X3316	X3163	F2929		L2809	E2749	
ARG	ARG	E4075	N3860	V3690	X3534	X3335	X3191	L2930		K2810	K2750	
ARG	ARG	E4075	E3861	E3691	X3535	X3336	X3192	Q2931		E2811	L2751	
VAL	VAL	E4081	D3862	E3692	X3536	X3337	X3193	M2932		S2812	D2752	
ARG	ARG	T4082	G3863	K3693	X3537	X3338	X3194	N2933		L2813	S2753	
ARG	ARG	D4083	G3864	X3538	X3538	X3341	X3195	Q2935		K2814	F2754	
LEU	LEU	P4084	T3864	X3539	X3539	X3341	X3196	A2936		A2815	I2755	
ARG	ARG	R4085	V3865	X3540	X3540	X3341	X3197	T2937		M2816	N2756	
LEU	LEU	G4086	I3866	X3551	X3551	X3341	X3198	Q2938		L2817	K2757	
LEU	LEU	L4087	N3867	X3560	X3560	X3341	X3199	R2939		A2818	F2758	
ALA	ALA	L4088	N3867	X3561	X3561	X3354	X3208	X2942		N2881	A2759	
ALA	ALA	D4092	R3868	X3561	X3561	X3354	X3211	X2943		E2820	E2760	
GLU	GLU	A4092	Q3869	X3565	X3565	X3354	X3211	X2944		W2821	Y2761	
GLU	GLU	A4096	N3870	X3566	X3566	X3358	X3211	X2945		T2822	T2762	
GLY	GLY	M4097	G3871	X3567	X3567	X3358	X3211	X2946		E2824	H2763	
ALA	ALA	D4098	E3872	X3568	X3568	X3359	X3214	X2947		K2825	E2764	
ALA	ALA	Q4102	K3873	X3568	X3568	X3360	X3215	X2948		R2888	K2765	
ALA	ALA	F4103	D3878	X3580	X3580	X3377	X3216	X2951		K2889	W2766	
ALA	ALA	T4104	D3878	X3581	X3581	X3377	X3217	X2951		K2890	A2767	
LEU	LEU	G4106	Q3889	X3582	X3582	X3382	X3218	X2964		K2891	F2768	
LEU	LEU	G4106	L3890	X3583	X3583	X3383	X3219	X2965		K2892	D2769	
TRP	TRP	P4106	L3891	X3584	X3584	X3384	X3220	X2966		E2893	K2770	
ALA	ALA	A4117	N3896	X3585	X3585	X3385	X3221	X2967		L2894	I2771	
GLU	GLU			X3586	X3586	X3386	X3222	X2968		E2895	Q2772	
GLY	GLY			X3587	X3587	X3387	X3223	X2969		K2897	N2773	
GLY	GLY			X3588	X3588	X3388	X3224	X2971		L2896	N2774	
				X3600	X3600	X3390	X3225	X2974		L2897	W2775	
				X3609	X3609	X3391	X3234	X2975		G2899	S2776	
				X3610	X3610	X3392	X3242	X2976		K2900	Y2777	
				X3611	X3611	X3393	X3242	X2995		L2901	G2778	
						X3394	X3245	X2996		H2902	E2779	
								X3023		L2904	N2780	
										P2903	V2781	
										L2905	D2782	
										E2783	E2784	
										L2785		









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	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 K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.175	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.20	0/834	0.48	0/1123
1	F	0.20	0/834	0.48	0/1123
1	H	0.19	0/834	0.48	0/1123
1	J	0.20	0/834	0.48	0/1123
2	B	0.23	0/25428	0.52	5/34534 (0.0%)
2	E	0.23	0/25428	0.52	5/34534 (0.0%)
2	G	0.23	0/25428	0.52	5/34534 (0.0%)
2	I	0.23	0/25428	0.52	5/34534 (0.0%)
All	All	0.22	0/105048	0.52	20/142628 (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	F	0	1
1	H	0	1
1	J	0	1
2	B	0	14
2	E	0	14
2	G	0	14
2	I	0	14
All	All	0	60

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4639	MET	CA-C-N	5.37	134.91	121.80
2	B	4639	MET	C-N-CA	5.37	134.91	121.80
2	I	4639	MET	CA-C-N	5.37	134.89	121.80
2	I	4639	MET	C-N-CA	5.37	134.89	121.80
2	E	4639	MET	CA-C-N	5.35	134.87	121.80

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	SER	Peptide
2	B	139	GLU	Peptide
1	F	8	SER	Peptide
1	H	8	SER	Peptide
1	J	8	SER	Peptide

5.2 Too-close contacts

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	818	0	824	6	0
1	F	818	0	824	7	0
1	H	818	0	824	7	0
1	J	818	0	824	7	0
2	B	29369	0	24721	202	0
2	E	29369	0	24721	202	0
2	G	29369	0	24721	207	0
2	I	29369	0	24721	204	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	120756	0	102180	821	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 4.

The worst 5 of 821 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)
2:E:4958:CYS:SG	2:E:4978:HIS:CD2	2.72	0.83
2:G:4958:CYS:SG	2:G:4978:HIS:CD2	2.72	0.83
2:I:4958:CYS:SG	2:I:4978:HIS:CD2	2.72	0.82
2:B:4958:CYS:SG	2:B:4978:HIS:CD2	2.72	0.82
1:J:42:ARG:HG2	2:I:1691:GLN:HG2	1.72	0.70

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	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
1	F	105/108 (97%)	98 (93%)	7 (7%)	0	100	100
1	H	105/108 (97%)	98 (93%)	7 (7%)	0	100	100
1	J	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
2	B	3235/4676 (69%)	2881 (89%)	349 (11%)	5 (0%)	43	75
2	E	3235/4676 (69%)	2883 (89%)	347 (11%)	5 (0%)	43	75
2	G	3235/4676 (69%)	2879 (89%)	351 (11%)	5 (0%)	43	75
2	I	3235/4676 (69%)	2880 (89%)	350 (11%)	5 (0%)	43	75
All	All	13360/19136 (70%)	11913 (89%)	1427 (11%)	20 (0%)	49	81

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG

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Mol	Chain	Res	Type
2	E	1708	ARG
2	I	1708	ARG
2	G	1708	ARG
2	B	1932	PRO

5.3.2 Protein sidechains ⓘ

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	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3202 (78%)	2481 (100%)	12 (0%)	81	82
2	E	2493/3202 (78%)	2480 (100%)	13 (0%)	81	82
2	G	2493/3202 (78%)	2480 (100%)	13 (0%)	81	82
2	I	2493/3202 (78%)	2480 (100%)	13 (0%)	81	82
All	All	10324/13164 (78%)	10273 (100%)	51 (0%)	78	82

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	1600	LEU
2	I	4792	LEU
2	G	4929	LEU
2	I	1657	LEU
2	I	3805	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 221 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	105	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	I	2931	GLN
2	G	4984	ASN
2	G	3761	GLN
2	I	379	HIS

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 8 ligands modelled in this entry, 8 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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	I	12
2	B	12
2	G	12
2	E	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	3613:UNK	C	3639:THR	N	42.97
1	B	3613:UNK	C	3639:THR	N	42.95
1	G	3613:UNK	C	3639:THR	N	42.95
1	E	3613:UNK	C	3639:THR	N	42.94
1	B	3163:UNK	C	3170:UNK	N	16.52

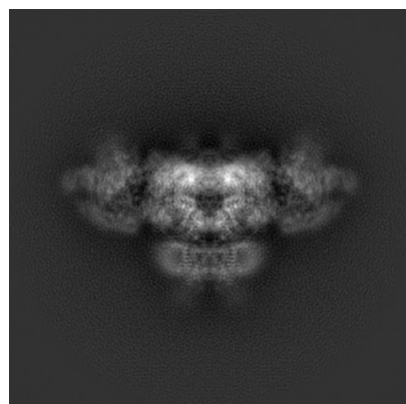
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8372. These allow visual inspection of the internal detail of the map and identification of artifacts.

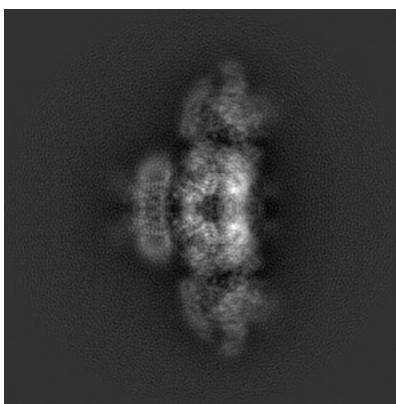
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

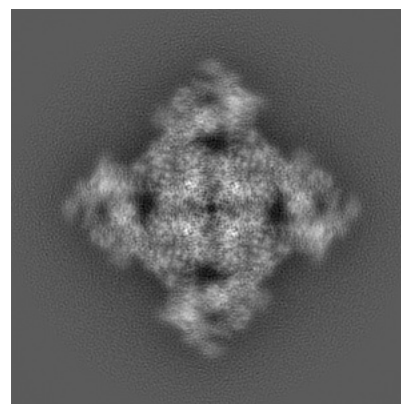
6.1.1 Primary map



X

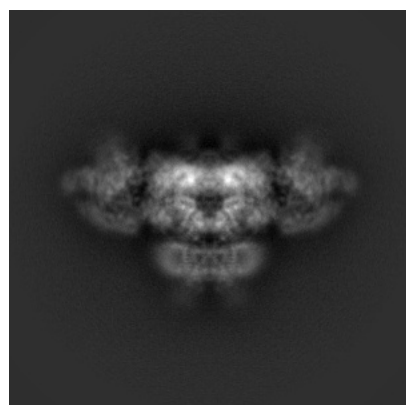


Y

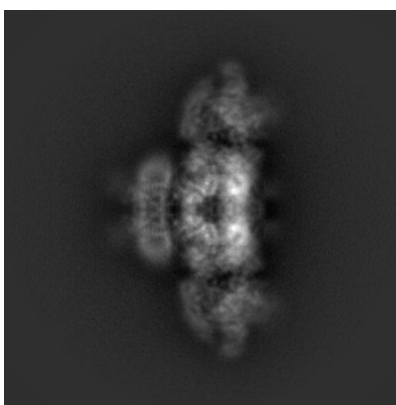


Z

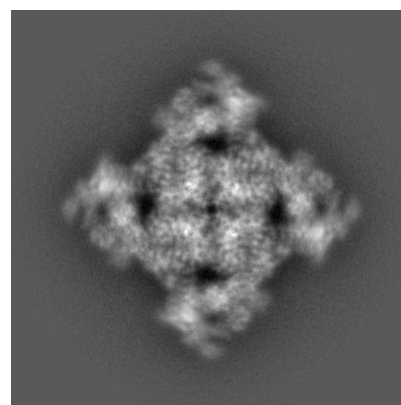
6.1.2 Raw map



X



Y

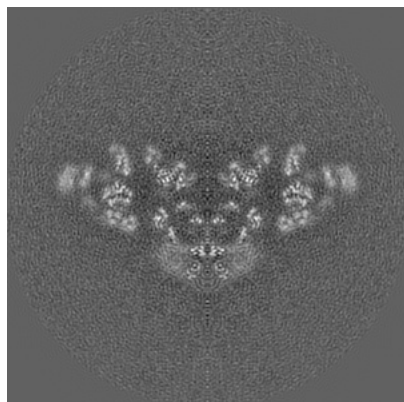


Z

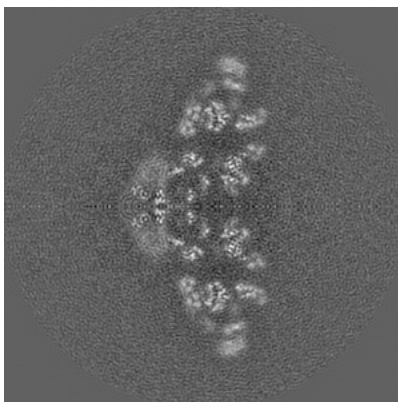
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

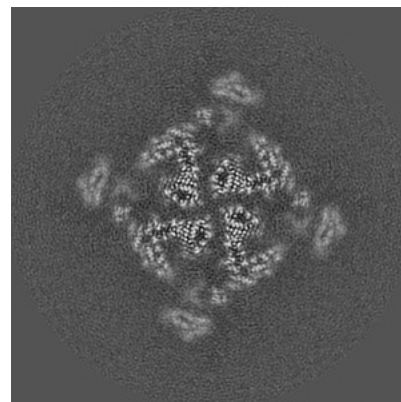
6.2.1 Primary map



X Index: 200

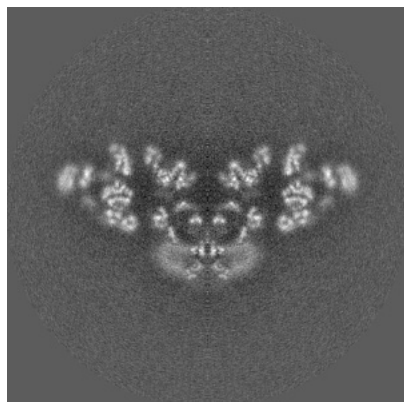


Y Index: 200

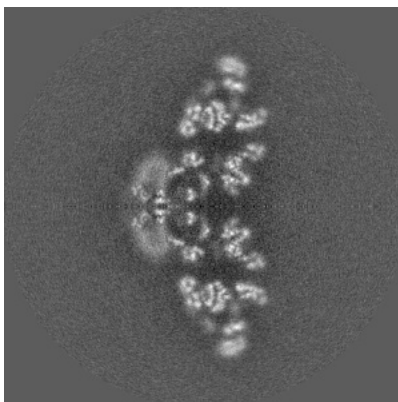


Z Index: 200

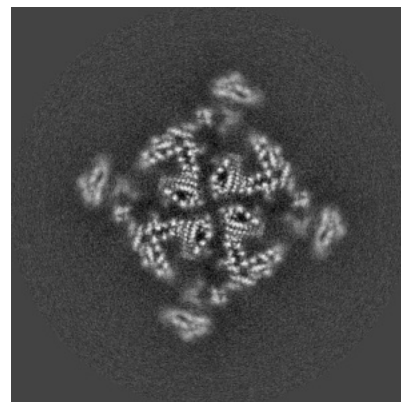
6.2.2 Raw map



X Index: 200



Y Index: 200

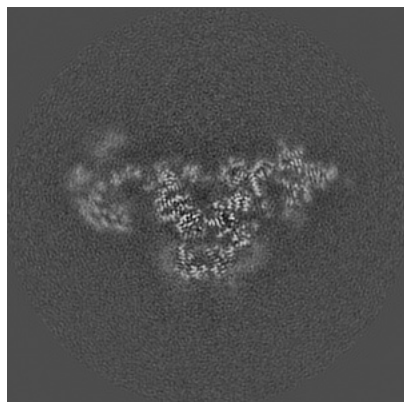


Z Index: 200

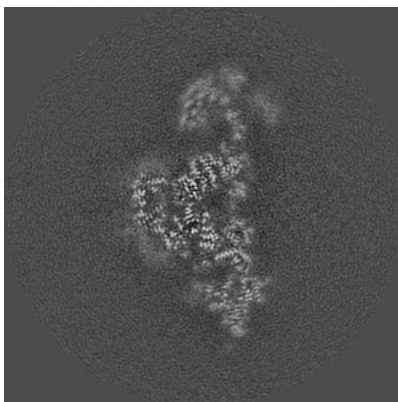
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

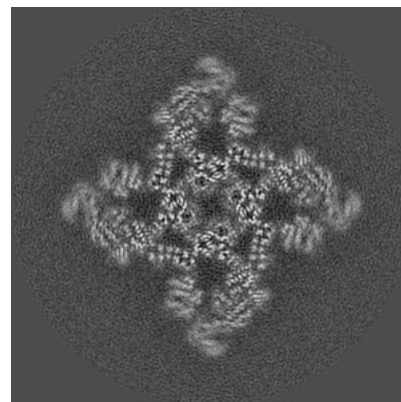
6.3.1 Primary map



X Index: 184

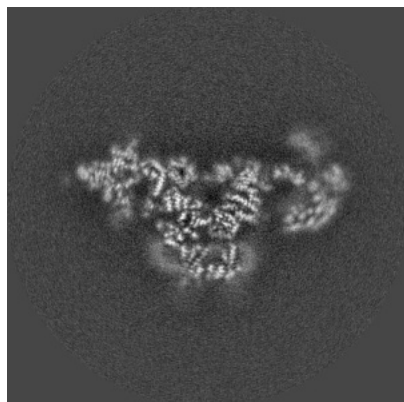


Y Index: 184

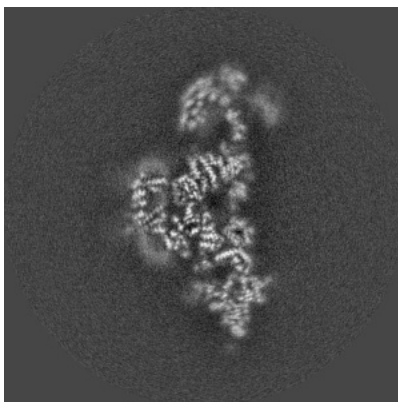


Z Index: 227

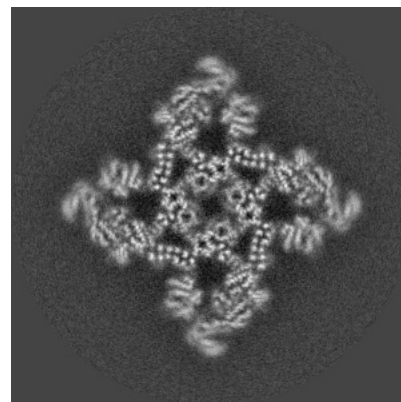
6.3.2 Raw map



X Index: 216



Y Index: 184

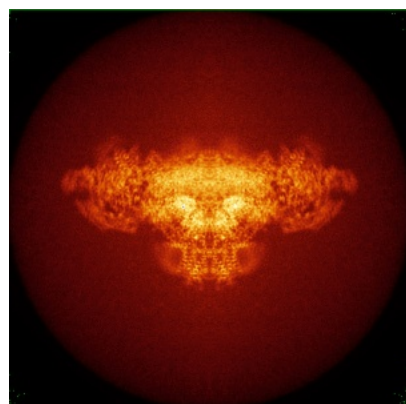


Z Index: 227

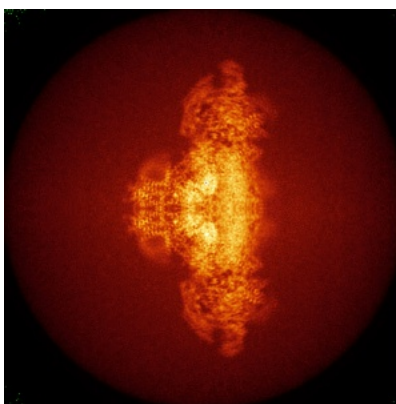
The images above show the largest variance slices of the map in three orthogonal directions.

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

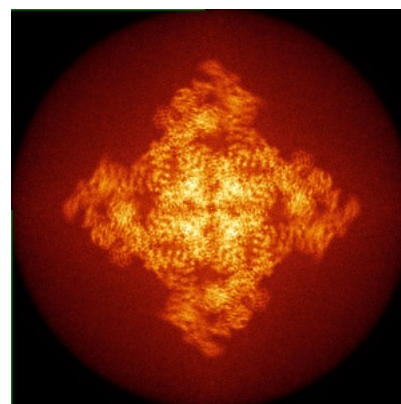
6.4.1 Primary map



X

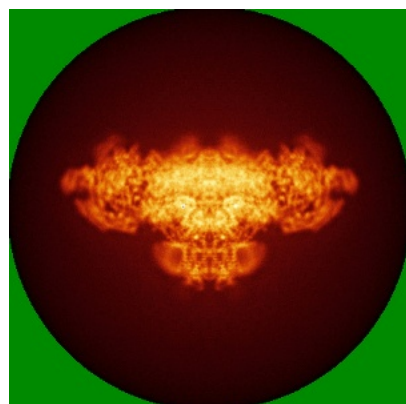


Y

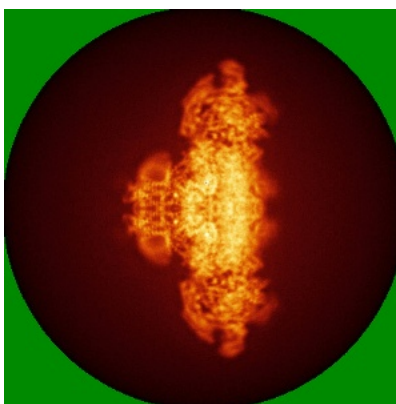


Z

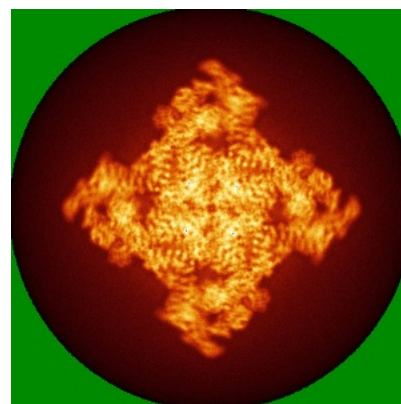
6.4.2 Raw map



X



Y

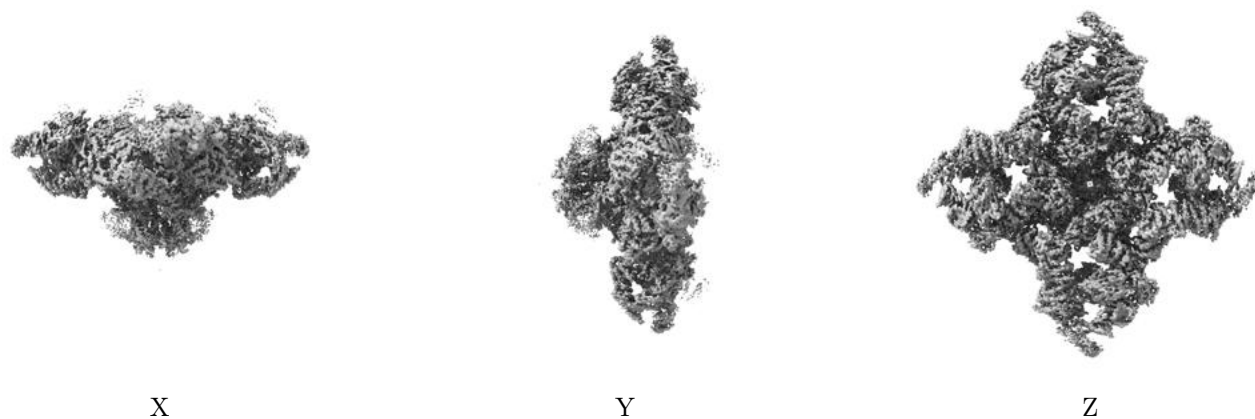


Z

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 0.04. 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



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.

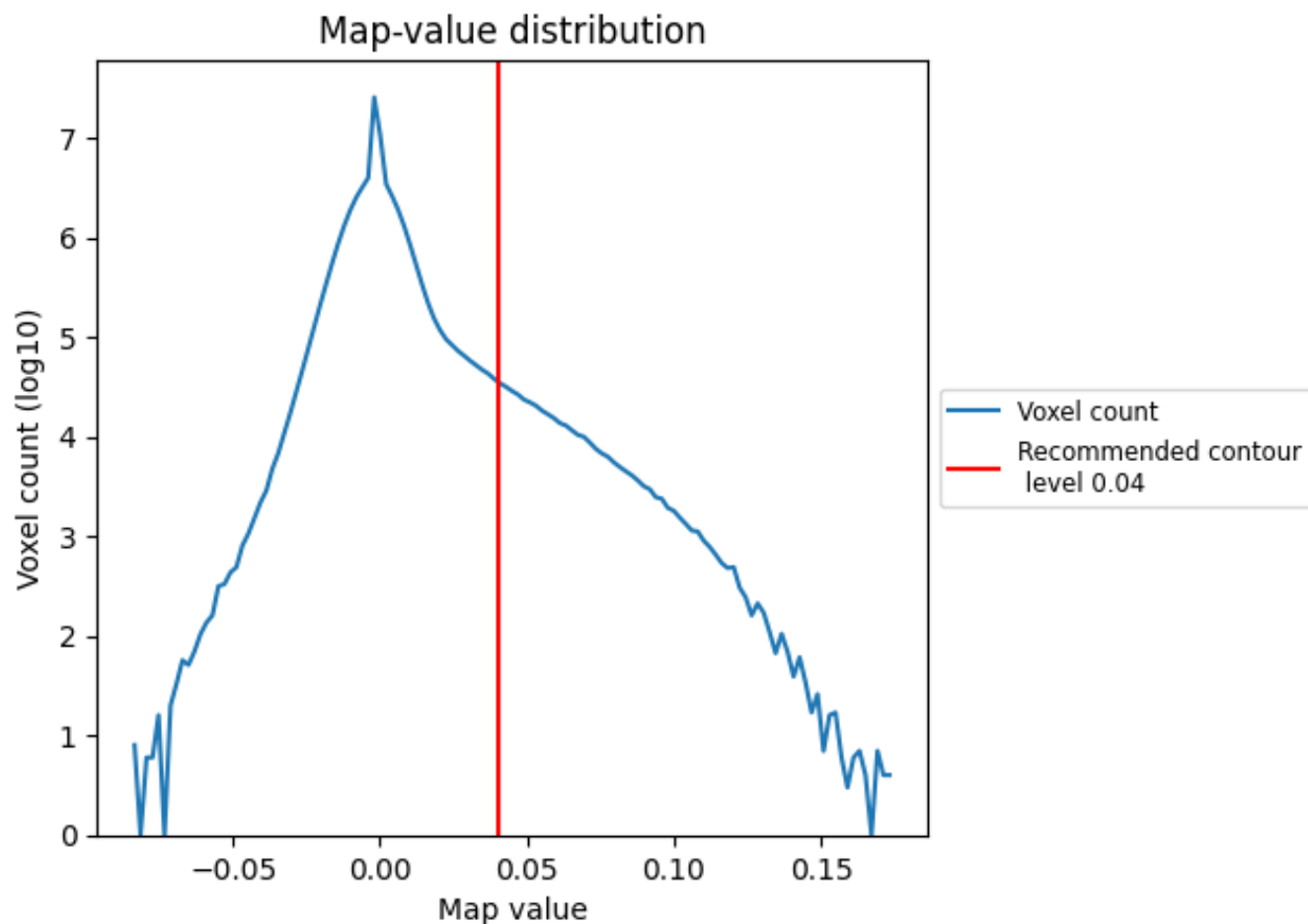
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

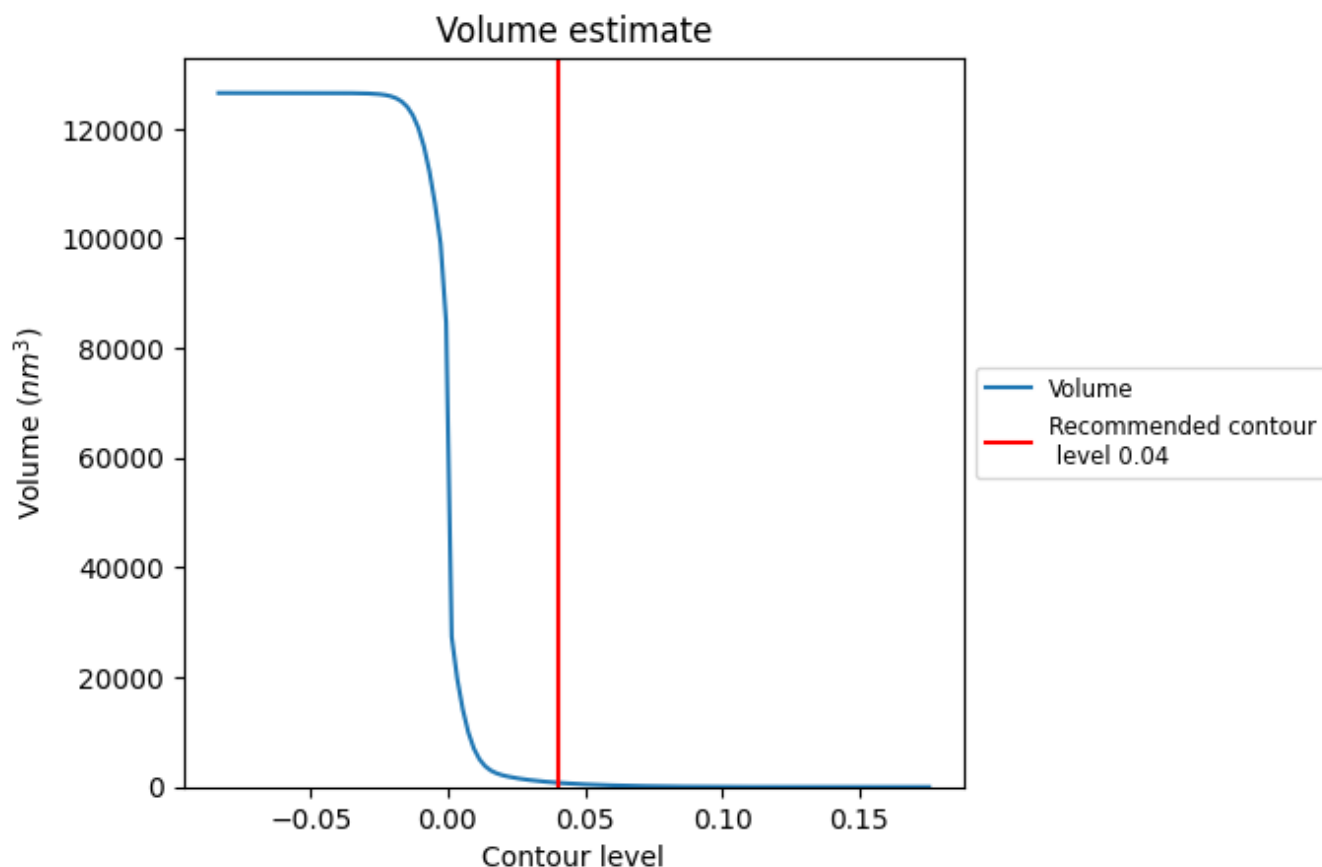
This section contains the results of statistical analysis of the map.

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.

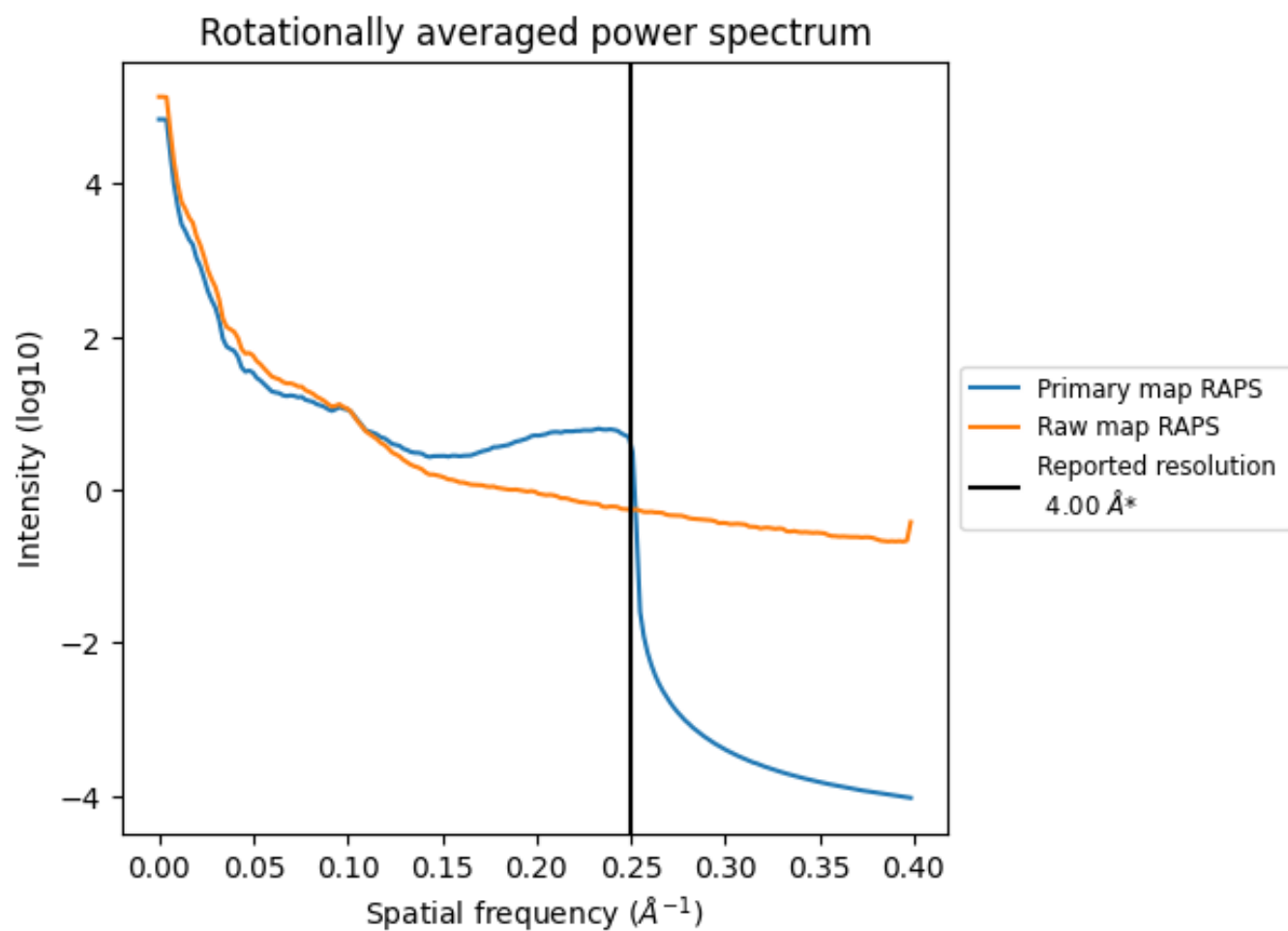
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 771 nm³; this corresponds to an approximate mass of 696 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 ⓘ

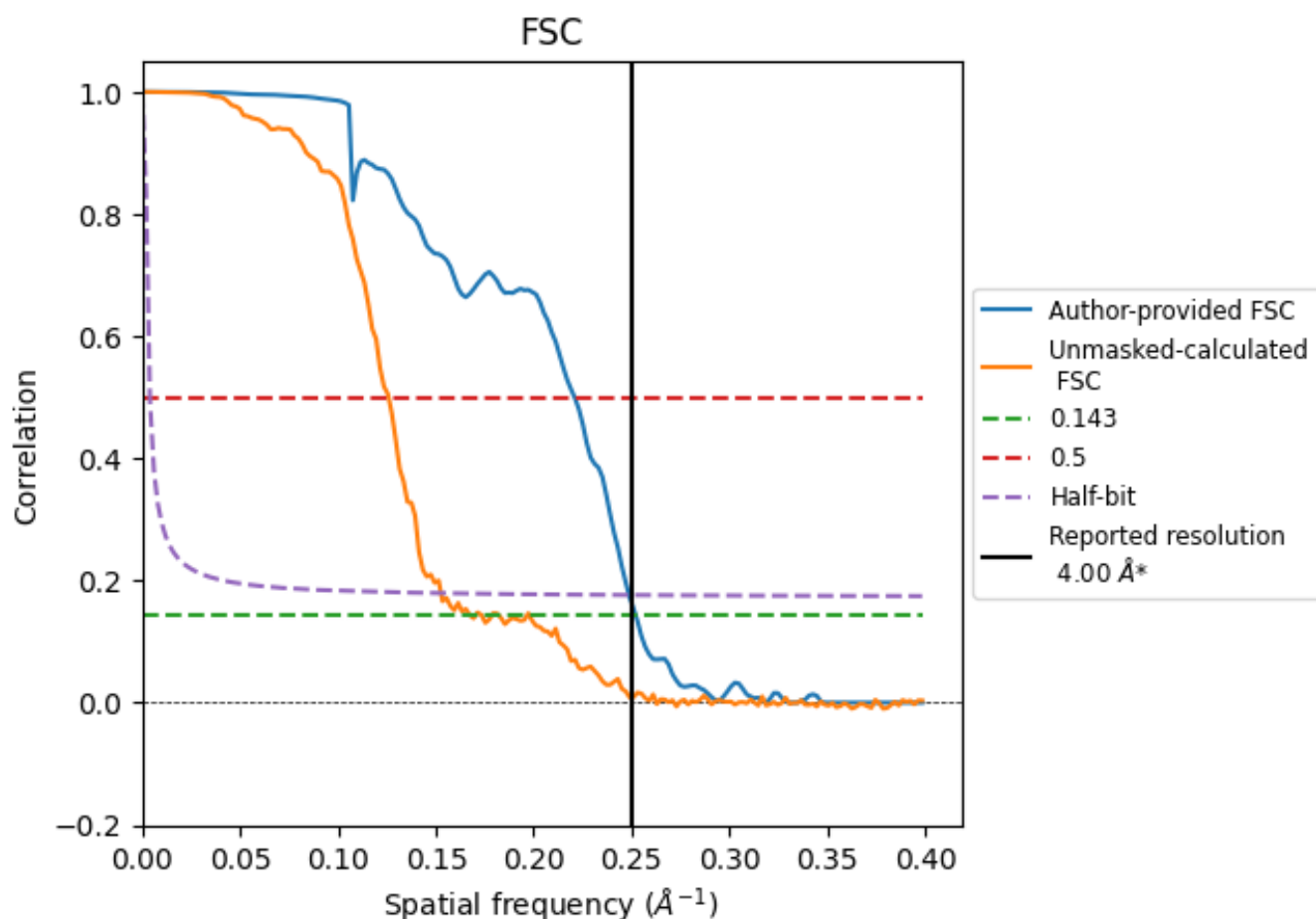


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

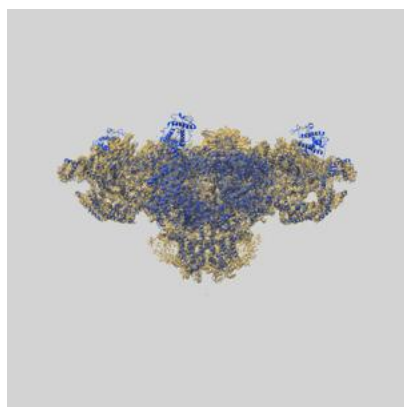
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.97	4.53	4.02
Unmasked-calculated*	5.97	7.95	6.55

*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 5.97 differs from the reported value 4.0 by more than 10 %

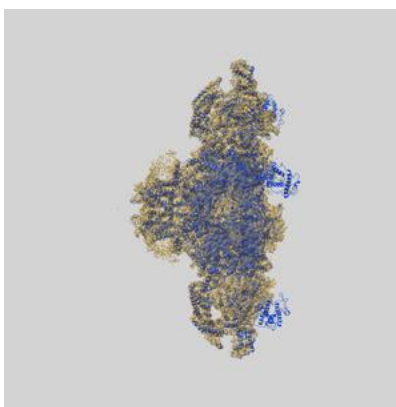
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8372 and PDB model 5T9M. Per-residue inclusion information can be found in section [3](#) on page [6](#).

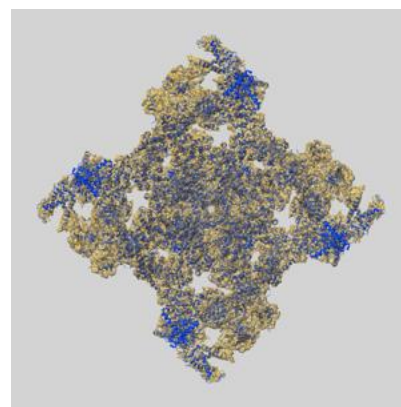
9.1 Map-model overlay [i](#)



X



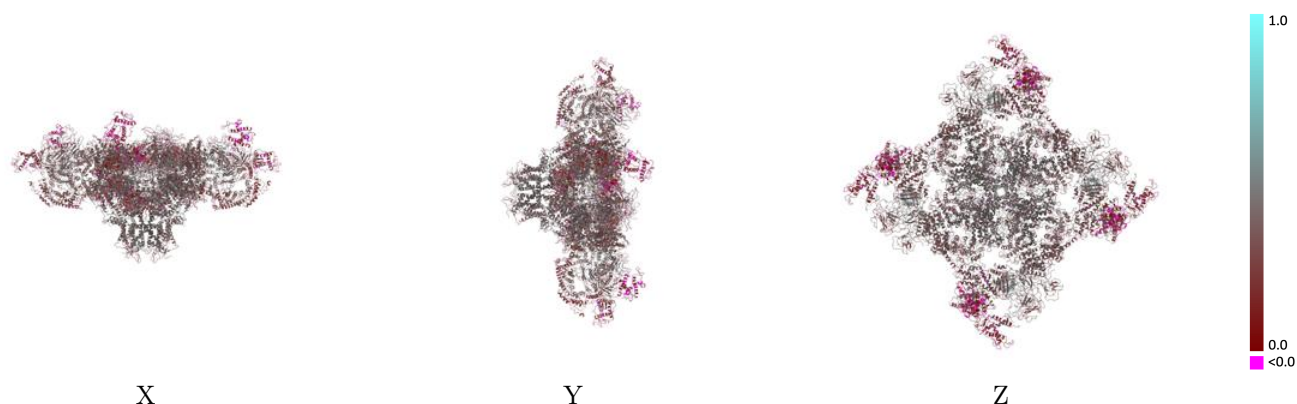
Y



Z

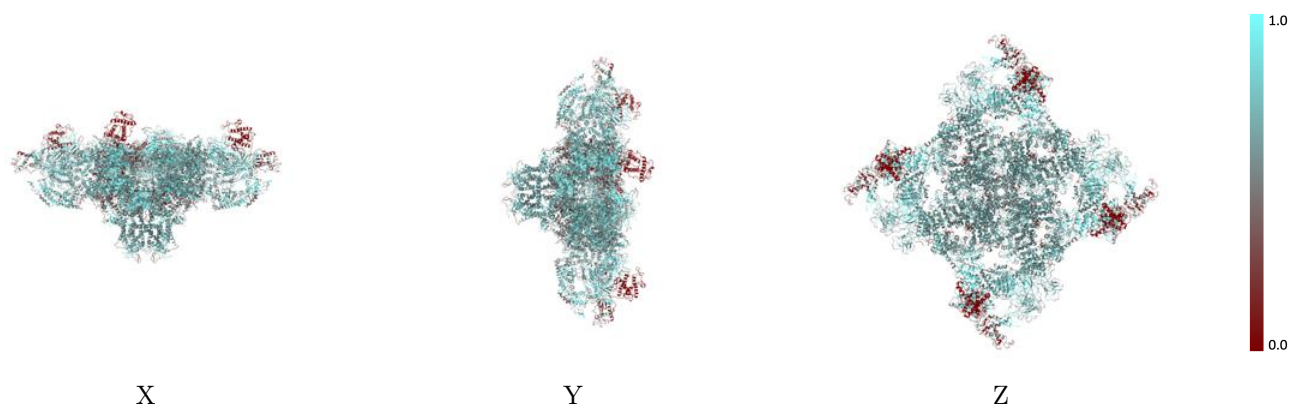
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



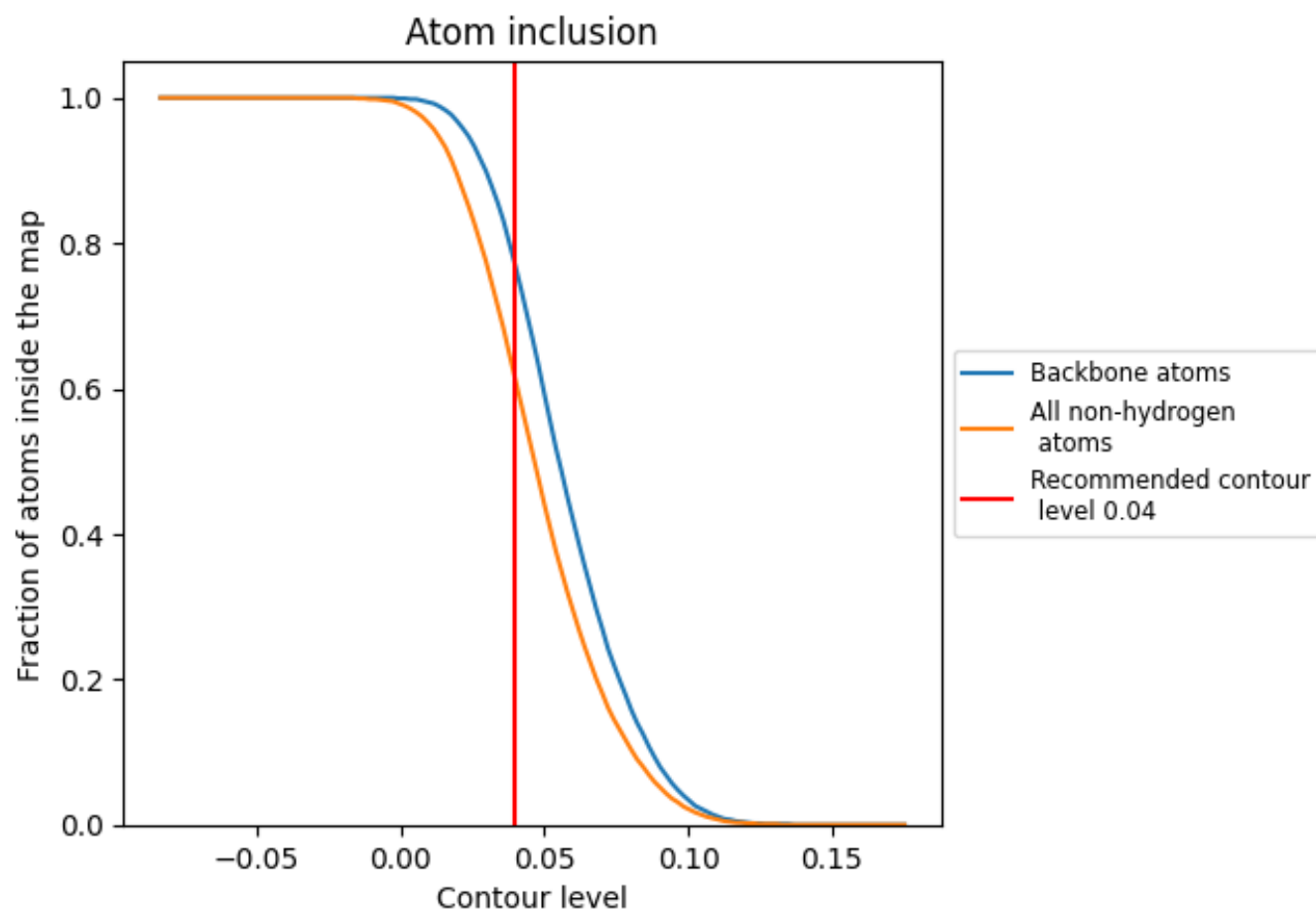
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 61% 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	0.6120	0.3470
A	0.6190	0.3590
B	0.6120	0.3470
E	0.6120	0.3470
F	0.6120	0.3630
G	0.6120	0.3470
H	0.6100	0.3650
I	0.6120	0.3470
J	0.6130	0.3660

1.0

0.0

<0.0