



## wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 05:45 AM UTC

PDB ID : 8DTY / pdb\_00008dtY  
EMDB ID : EMD-27711  
Title : Recombinant mouse RyR2 triple phosphomimetic mutant  
S2807D/S2813D/S2030D in complex with FKBP12.6 and nanodisc un-  
der closed-state conditions  
Authors : Iyer, K.A.; Hu, Y.; Murayama, T.; Samsó, M.  
Deposited on : 2022-07-26  
Resolution : 3.50 Å (reported)  
Based on initial model : 6WOU

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:

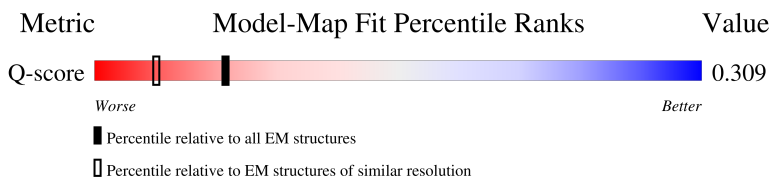
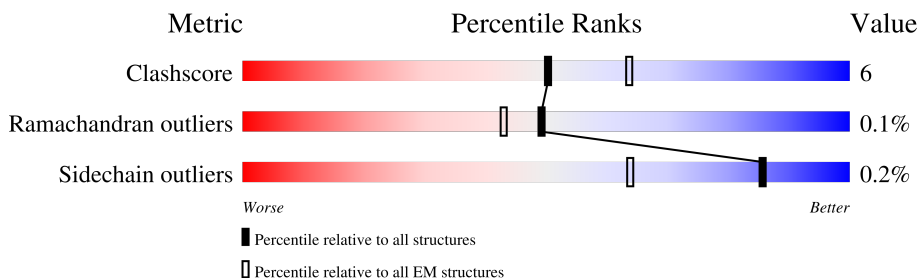
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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	13950 ( 3.00 - 4.00 )

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	E	107	 85% 15%
2	F	107	 85% 15%
2	G	107	 83% 17%
2	H	107	 85% 15%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 128772 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	4004	31374	19934	5355	5887	198	0	0
1	B	4004	31374	19934	5355	5887	198	0	0
1	C	4004	31374	19934	5355	5887	198	0	0
1	D	4004	31374	19934	5355	5887	198	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2030	ASP	SER	engineered mutation	UNP E9Q401
A	2807	ASP	SER	engineered mutation	UNP E9Q401
A	2813	ASP	SER	engineered mutation	UNP E9Q401
B	2030	ASP	SER	engineered mutation	UNP E9Q401
B	2807	ASP	SER	engineered mutation	UNP E9Q401
B	2813	ASP	SER	engineered mutation	UNP E9Q401
C	2030	ASP	SER	engineered mutation	UNP E9Q401
C	2807	ASP	SER	engineered mutation	UNP E9Q401
C	2813	ASP	SER	engineered mutation	UNP E9Q401
D	2030	ASP	SER	engineered mutation	UNP E9Q401
D	2807	ASP	SER	engineered mutation	UNP E9Q401
D	2813	ASP	SER	engineered mutation	UNP E9Q401

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	107	818	516	144	154	4	0	0
2	F	107	818	516	144	154	4	0	0
2	G	107	818	516	144	154	4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

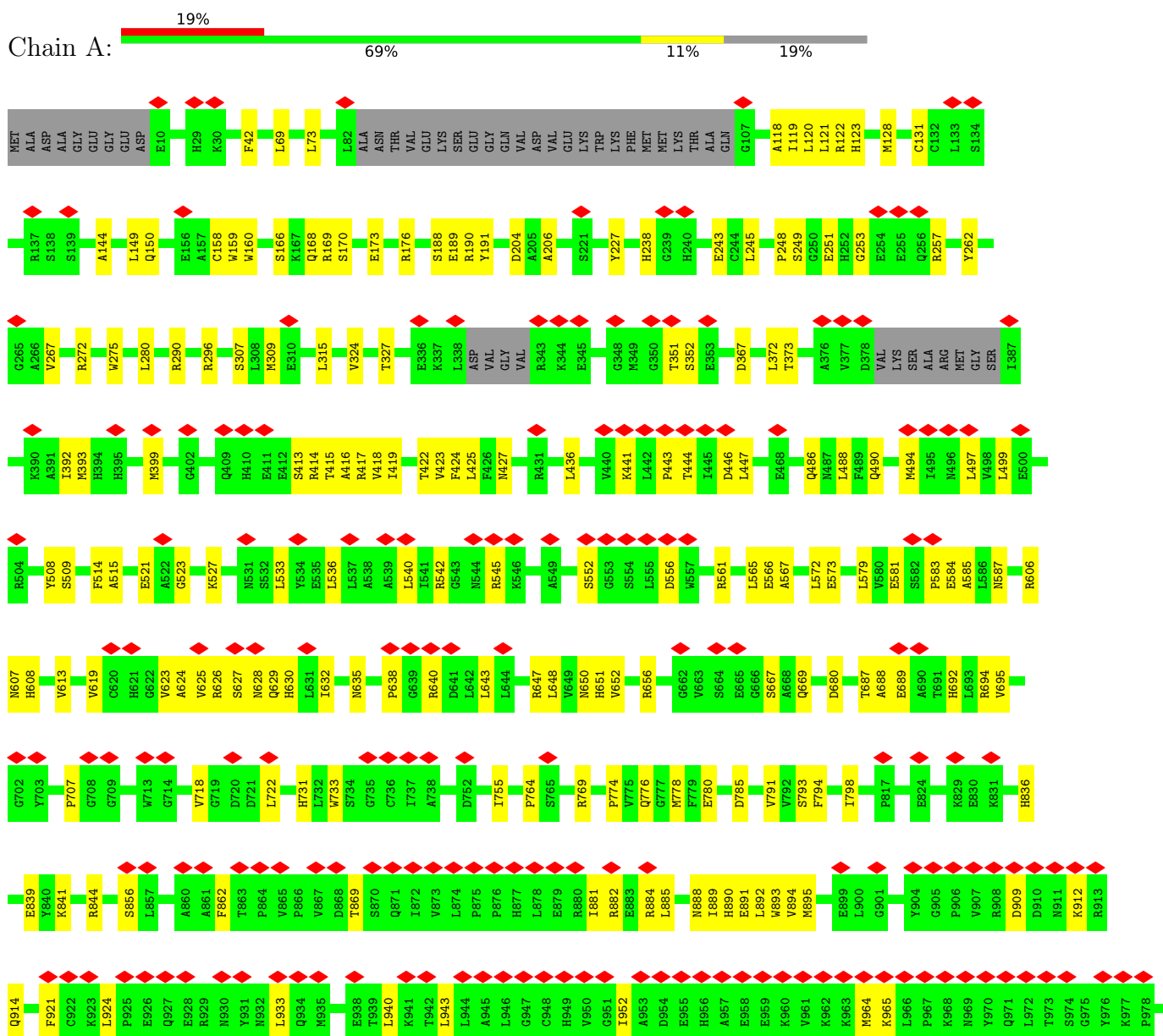
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

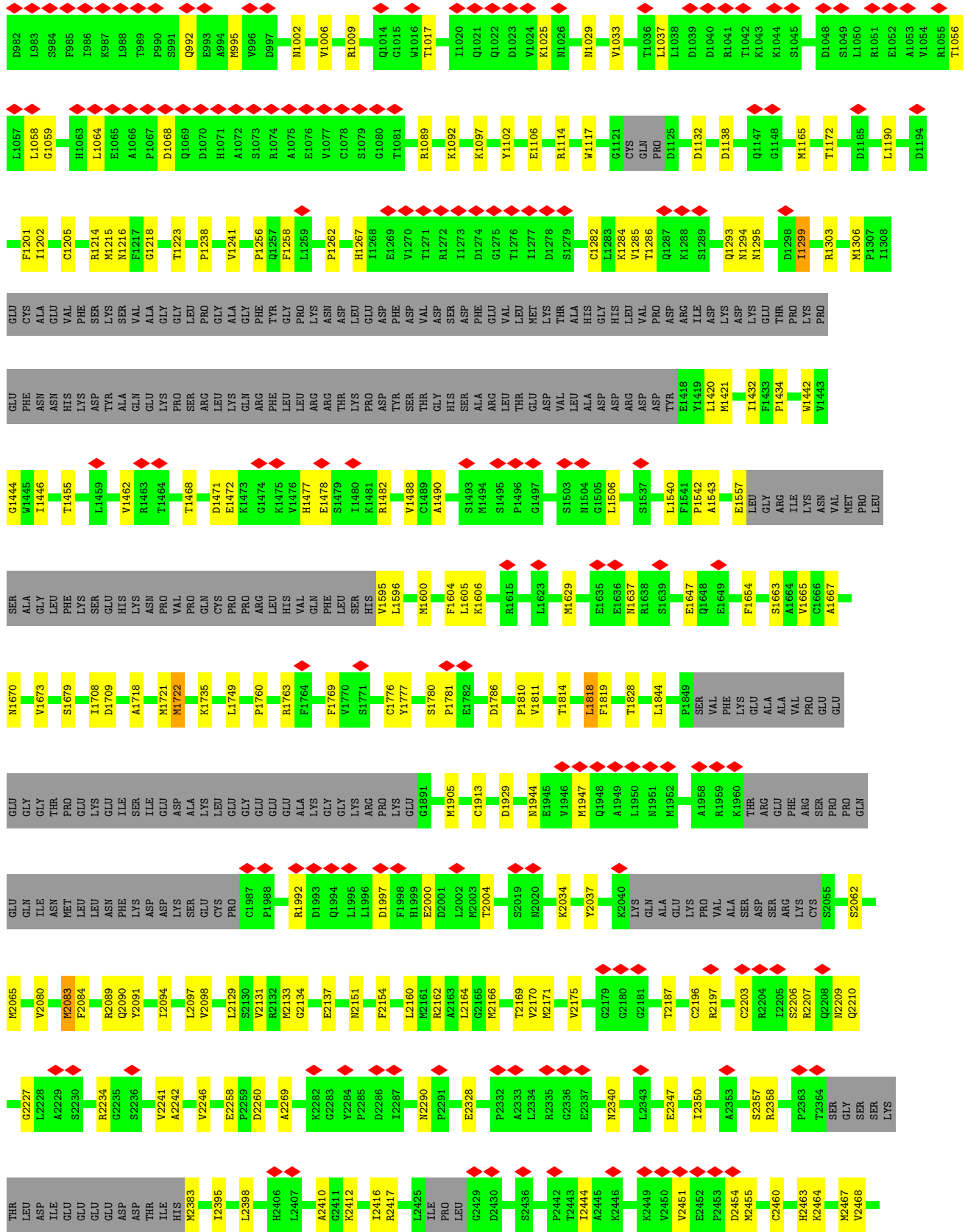
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	

### 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







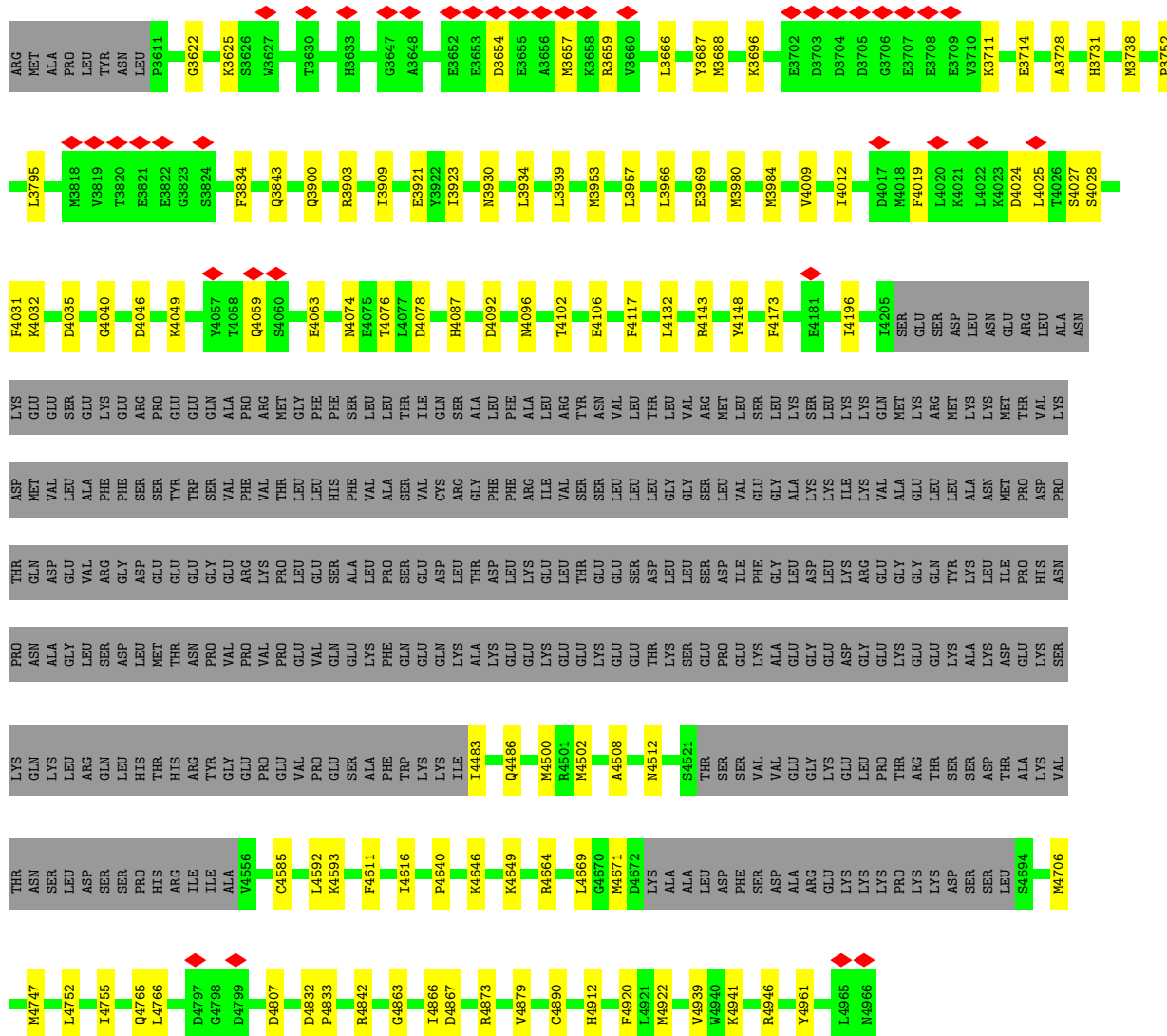




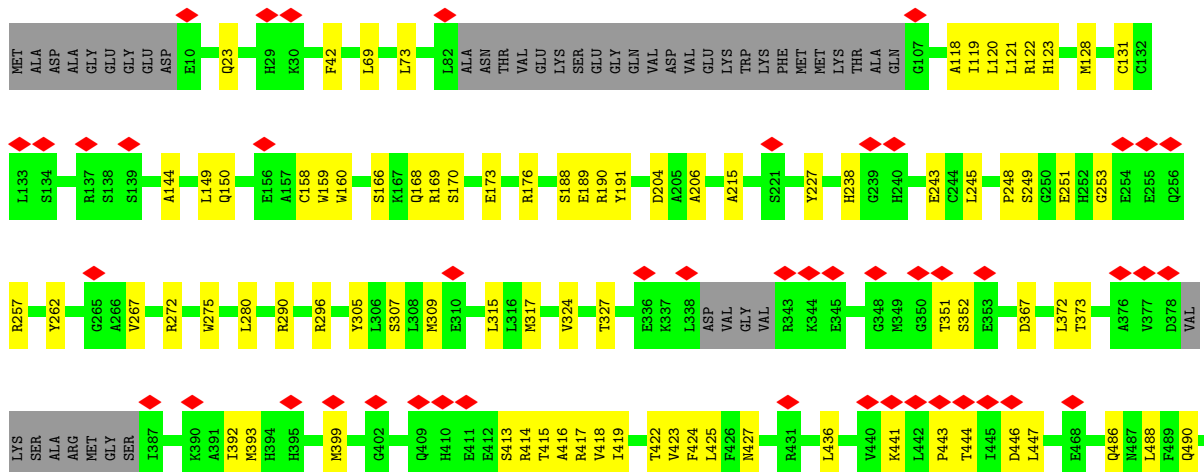
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L133	L134	R137	S138	S139	A144	L149	Q150	E156	A157	W158	W160	L69	S166	K167	Q168	R169	S170	E173	R176	S188	E189	R190	Y191	N198	S199	S200	D204	A205	A206	A215	S221	Y227	H238	G239	H240	E243	C244	L245	P248	G253	E254	E255																
Q256	R257	Y262	G265	A266	V267	R272	W275	L280	R280	R296	M309	E310	L315	V324	T327	E336	K337	F424	L338	ASP	VAL	GLY	VAL	R343	K344	E345	G348	M349	C350	T351	S352	E353	D367	L372	T373	A376	V377	D378	VAL	LYS	SER	ALA	ARG	MET														
GLY	SER	I387	K390	A391	T392	M393	H394	H395	M399	G402	Q409	H410	E411	S413	R414	T415	A416	R417	W418	I419	T422	V423	F424	L425	F426	M427	R431	L436	V440	K441	L442	P443	T444	I445	L446	L447	E468	Q486	N487	L488	F489	Q490	M494	I495	ALA	ALA	M496	L497	V498									
L499	E500	R504	S509	F514	A515	E521	A522	K527	N531	E532	L533	Y534	E535	L536	L537	D634	A538	A539	L540	I541	R542	G543	N544	R545	K546	A549	S552	G553	H551	S554	L555	D556	W557	R561	L565	E566	A567	L572	E573	L579	S582	P583	E584	A585	L586	N587	R606											
M607	H608	K609	V613	V619	C620	H621	G622	A624	V625	R626	N628	Q629	H630	L631	I632	G633	L634	A638	A639	L640	R640	D641	L642	L643	L644	R647	L648	M650	H651	V652	R656	G662	V663	S664	E665	G666	S667	Q669	D680	T687	A688	E689	A690	E691	H692	L693	R694											
V695	G702	Y703	P707	G709	W713	G714	V718	G719	D720	D721	L722	H731	L732	L733	S734	G735	C736	I737	A738	D752	I755	P764	S765	R769	P774	V775	G776	G777	M778	E780	D785	L791	V792	G793	F794	I798	P817	E824	K829	E830	K831																	
H836	E839	K841	R844	S856	L857	A860	A861	F862	T863	P864	V865	P866	V867	D868	T869	S870	Q871	I872	V873	L874	P875	H877	L878	E879	R880	I881	E882	G883	R884	L885	N888	I889	H890	E891	W892	V893	M895	E899	L900	G901	W902	Q903	Y904	G905	P906	V907	R908	D909	D910									
M911	K912	R913	Q914	F921	C922	K923	L924	P925	E926	Q927	E928	R929	M930	Y931	N932	L933	Q934	P935	D936	H937	S938	T939	L940	R941	T942	L943	A945	L946	G947	C948	H949	V950	R951	E952	A953	D954	E955	H956	A957	E958	E959	K960	V961	K962	L963	M964	K965	L966	P967	K968	N969	Y970	Q971	L972	S973	G974	G975	Y976
K977	P978	D982	L983	S984	F985	I986	K987	L988	T989	P990	S991	Q992	E993	A994	M995	V996	D997	N1002	V1006	R1009	Q1014	G1015	W1016	T1020	Q1021	D1022	V1024	K1025	N1026	M1029	V1033	T1036	L1037	D1039	D1040	R1041	T1042	K1043	K1044	S1045	D1048	S1049	L1050	R1051	E1052	A1053	V1054											
R1055	T1056	L1057	L1058	G1059	H1063	L1064	E1065	A1066	P1067	D1068	Q1069	D1070	H1071	A1072	S1073	R1074	A1075	E1076	V1077	C1078	S1079	G1080	T1081	R1089	K1092	K1097	Y1102	E1106	R1114	G1121	CYS	GLN	PRO	D1125	D1132	D1138	R1144	Q1147	M1165	T1172	D1185	L1190	A1191															
D1194	I1202	C1205	R1214	M1215	N1216	F1217	G1218	T1223	Q1233	P1238	V1241	P1256	Q1257	F1258	L1259	P1262	H1267	I1268	E1269	V1270	T1271	A1272	I1273	D1274	G1275	T1276	I1277	D1278	S1279	C1282	L1283	K1284	V1285	T1286	Q1287	K1288	S1289	Q1293	N1294	N1295	D1298	I1299	R1303															
M1306	F1307	I1308	GLU	ALA	GLU	VAL	PHE	M1215	SER	LYS	SER	VAL	ALA	GLY	LEU	PRO	GLY	ALA	PHE	TYR	GLY	PRO	LYS	ASN	ASP	LEU	LEU	ASP	PHE	VAL	LEU	VAL	LEU	MET	LYS	THR	ALA	HIS	GLY	HIS	LEU	VAL	ASP	ARG	ILE	LYS	ASP	GLY	THR									

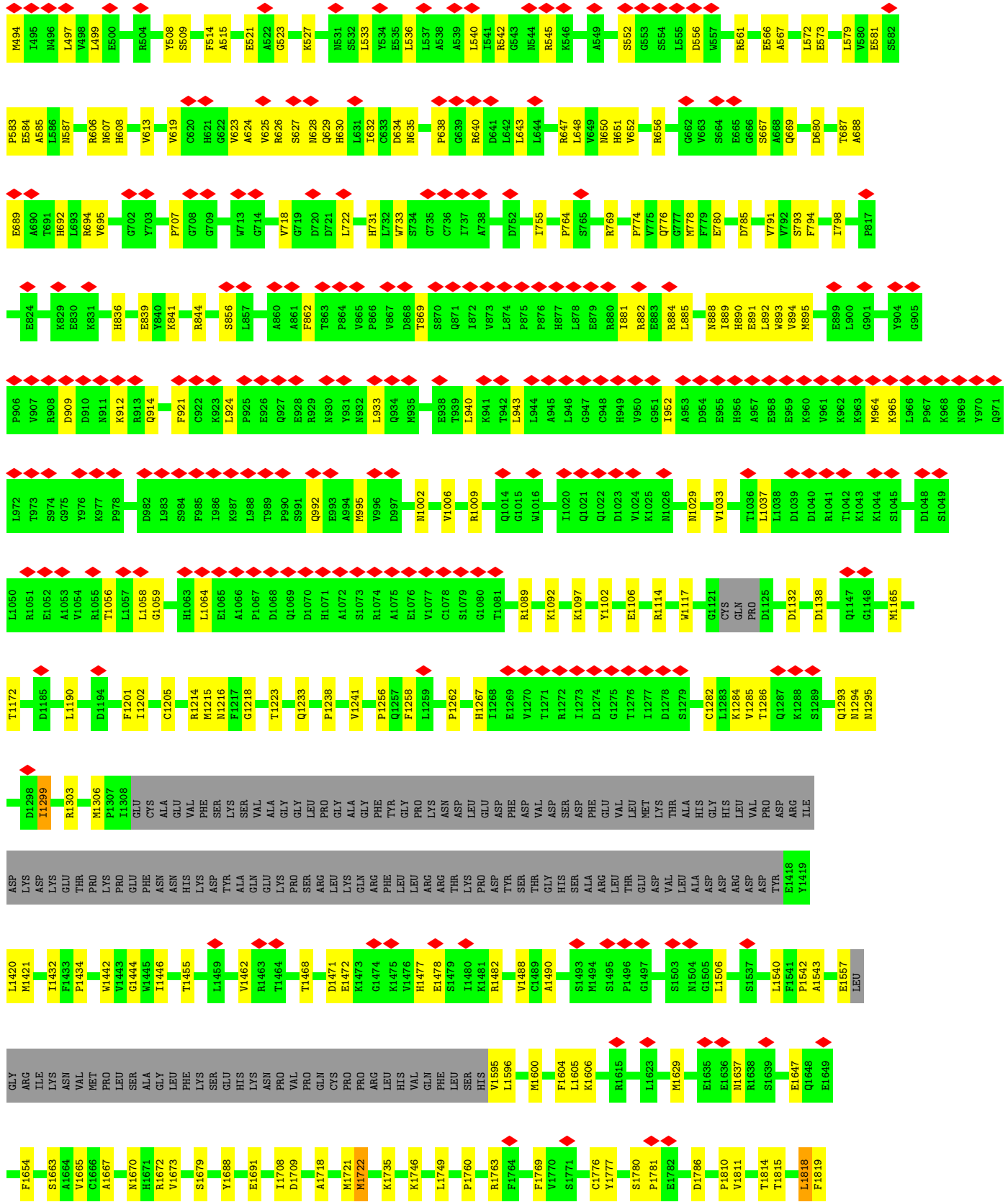




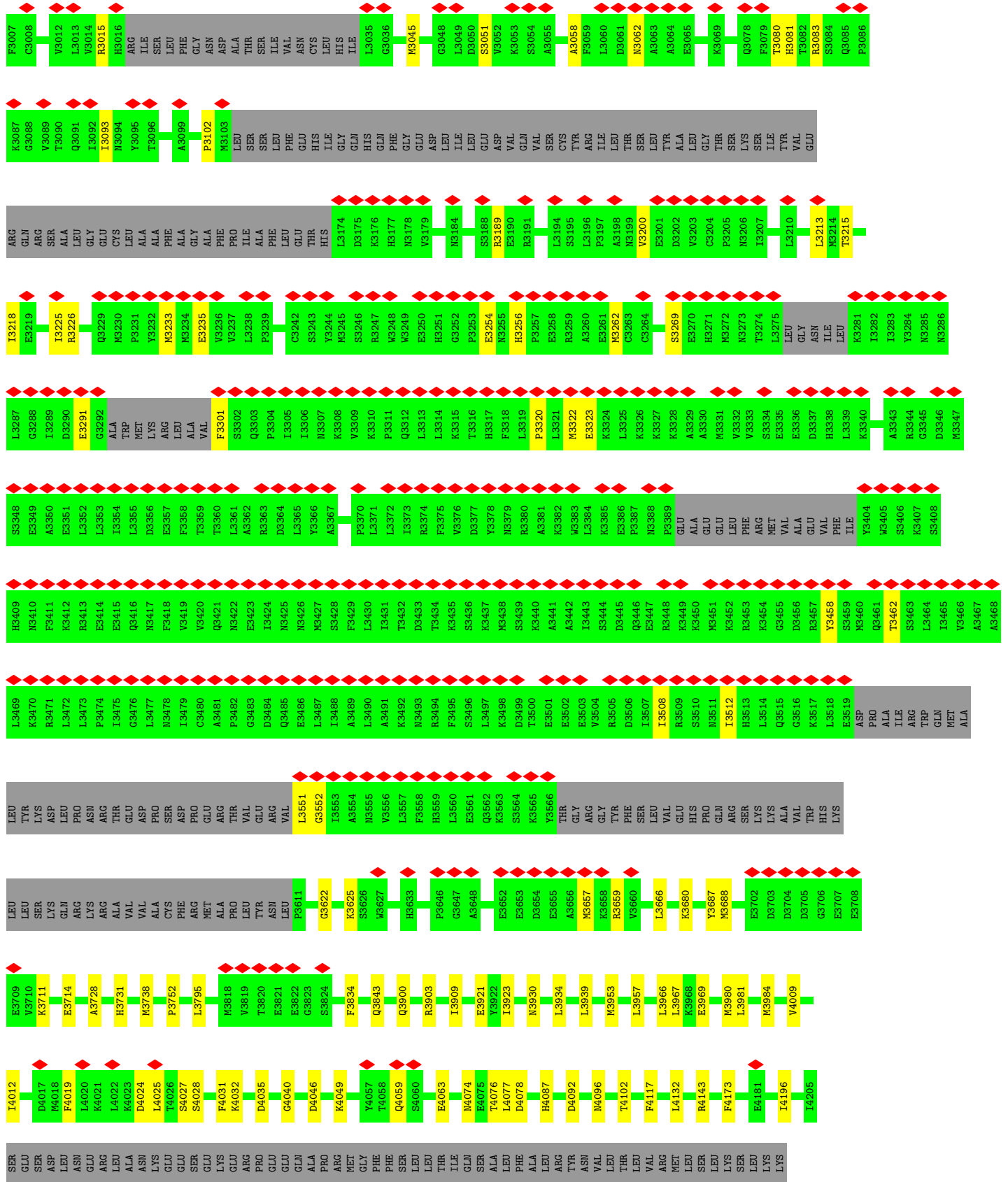


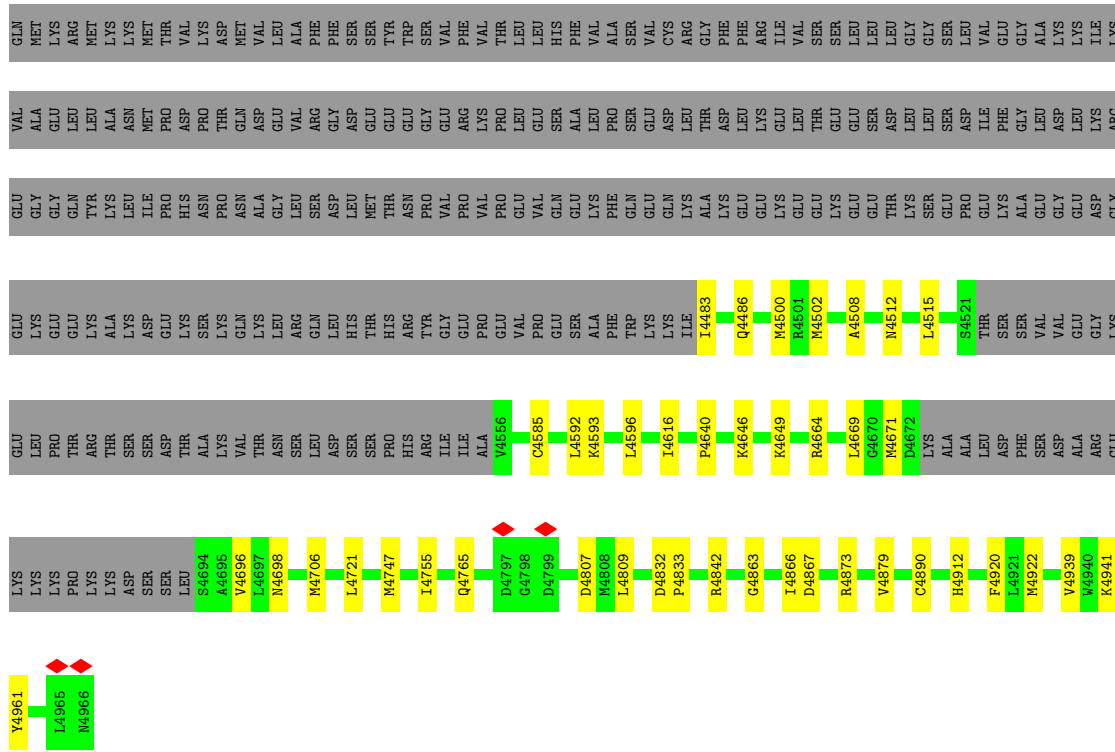
• Molecule 1: Ryanodine receptor 2



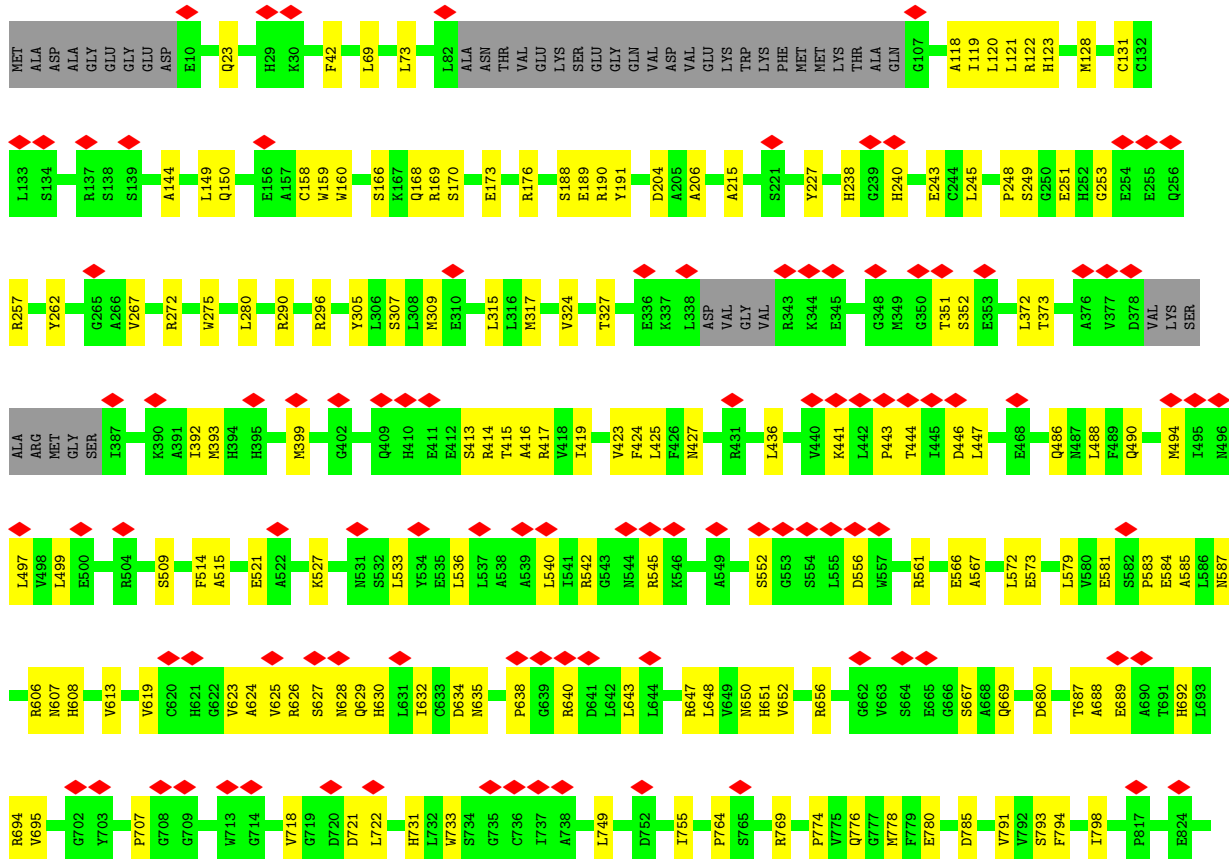




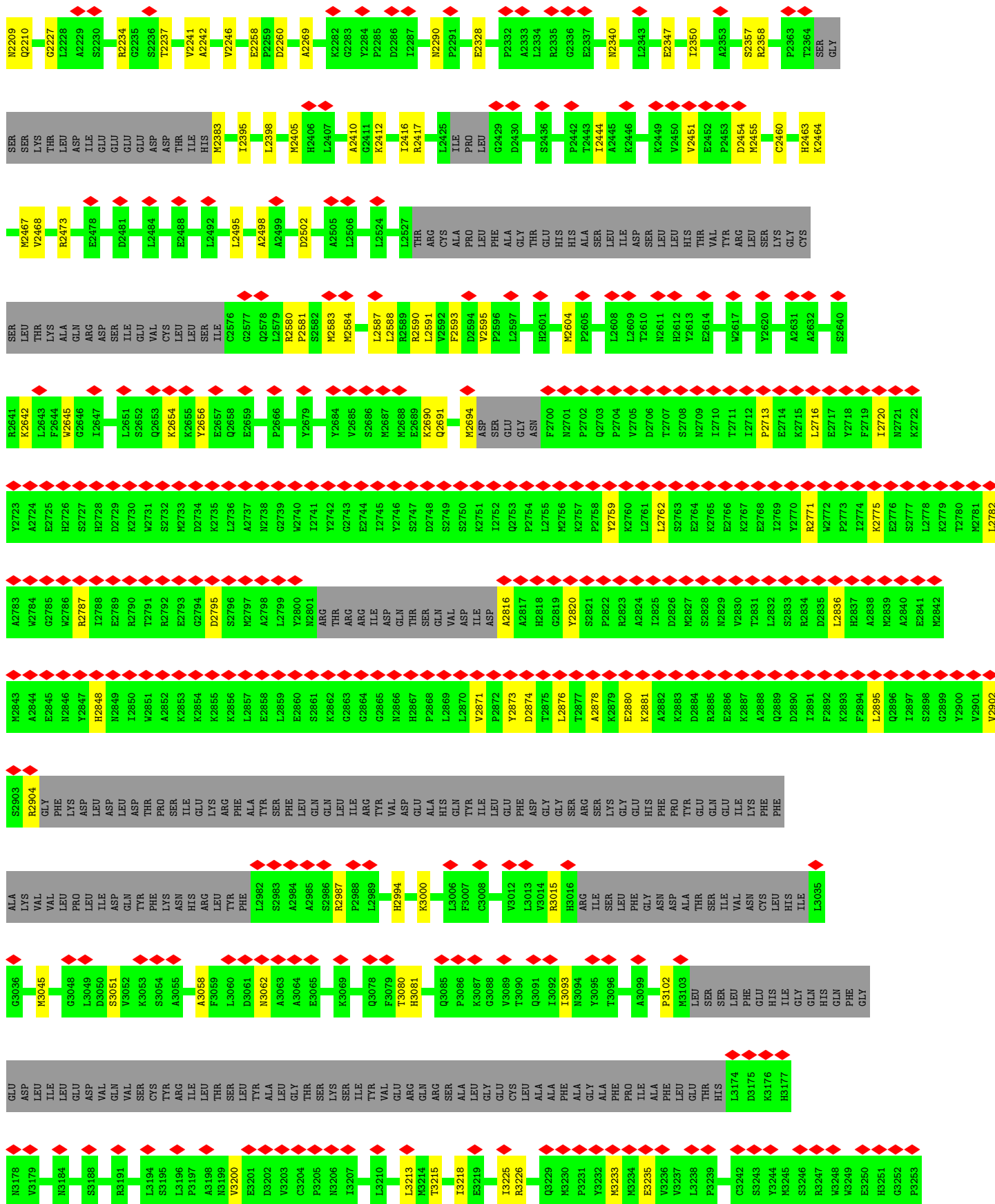




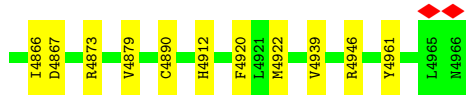
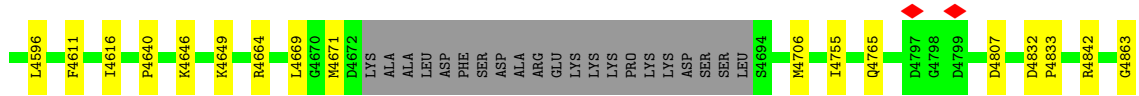
• Molecule 1: Ryanodine receptor 2



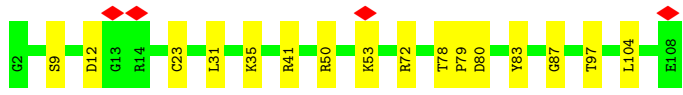
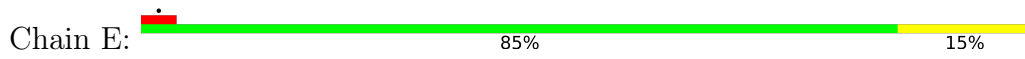




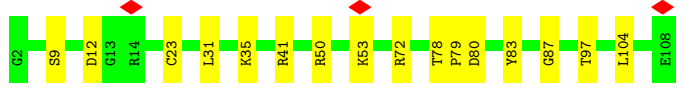
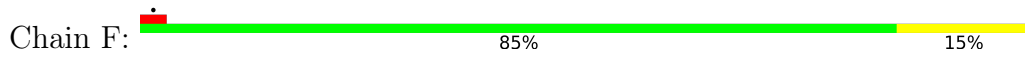




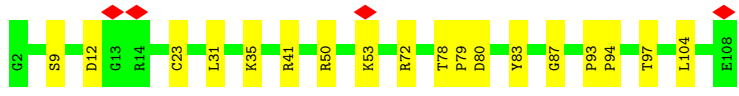
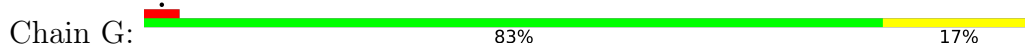
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



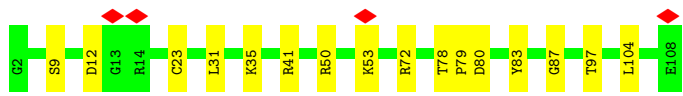
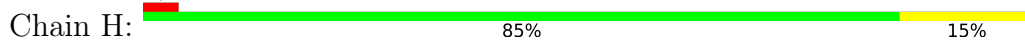
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



• 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, C4	Depositor
Number of particles used	406681	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	52.95	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.804	Depositor
Minimum map value	-1.458	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.24	Depositor
Map size ( $\text{\AA}$ )	496.80002, 496.80002, 496.80002	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.08, 1.08, 1.08	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	0.13	0/32026	0.32	0/43315
1	B	0.13	0/32026	0.32	0/43315
1	C	0.13	0/32026	0.32	0/43315
1	D	0.13	0/32026	0.32	0/43315
2	E	0.13	0/834	0.32	0/1123
2	F	0.13	0/834	0.32	0/1123
2	G	0.13	0/834	0.32	0/1123
2	H	0.13	0/834	0.32	0/1123
All	All	0.13	0/131440	0.32	0/177752

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	31374	0	30394	342	0
1	B	31374	0	30394	351	0
1	C	31374	0	30394	357	0
1	D	31374	0	30394	339	0
2	E	818	0	821	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	818	0	821	11	0
2	G	818	0	821	12	0
2	H	818	0	821	11	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	128772	0	124860	1409	0

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

The worst 5 of 1409 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:1629:MET:SD	1:A:1629:MET:N	2.61	0.73
1:D:1629:MET:SD	1:D:1629:MET:N	2.61	0.73
1:C:1629:MET:SD	1:C:1629:MET:N	2.61	0.72
1:D:1444:GLY:HA3	1:D:1488:VAL:HA	1.72	0.71
1:A:3843:GLN:HG3	1:A:3921:GLU:HG3	1.73	0.71

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	3952/4966 (80%)	3722 (94%)	224 (6%)	6 (0%)	43 74
1	B	3952/4966 (80%)	3724 (94%)	222 (6%)	6 (0%)	43 74
1	C	3952/4966 (80%)	3725 (94%)	221 (6%)	6 (0%)	43 74
1	D	3952/4966 (80%)	3722 (94%)	224 (6%)	6 (0%)	43 74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	F	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	G	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	H	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
All	All	16228/20292 (80%)	15285 (94%)	919 (6%)	24 (0%)	49	79

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1299	ILE
1	B	1299	ILE
1	C	1299	ILE
1	D	1299	ILE
1	A	1462	VAL

### 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	3331/4355 (76%)	3323 (100%)	8 (0%)	87	85
1	B	3331/4355 (76%)	3323 (100%)	8 (0%)	87	85
1	C	3331/4355 (76%)	3324 (100%)	7 (0%)	87	85
1	D	3331/4355 (76%)	3323 (100%)	8 (0%)	87	85
2	E	88/88 (100%)	88 (100%)	0	100	100
2	F	88/88 (100%)	88 (100%)	0	100	100
2	G	88/88 (100%)	88 (100%)	0	100	100
2	H	88/88 (100%)	88 (100%)	0	100	100
All	All	13676/17772 (77%)	13645 (100%)	31 (0%)	85	85

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4706	MET
1	D	2091	TYR
1	C	1818	LEU
1	D	2405	MET
1	D	1818	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 204 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1293	GLN
1	C	4637	GLN
2	F	44	ASN
1	C	1685	GLN
1	C	2801	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 [i](#)

There are no chain breaks in this entry.

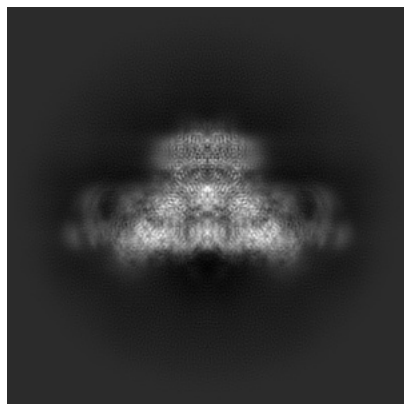
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27711. These allow visual inspection of the internal detail of the map and identification of artifacts.

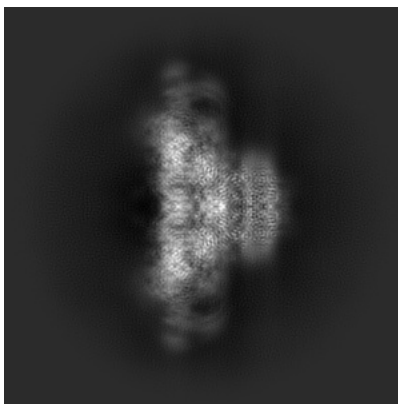
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

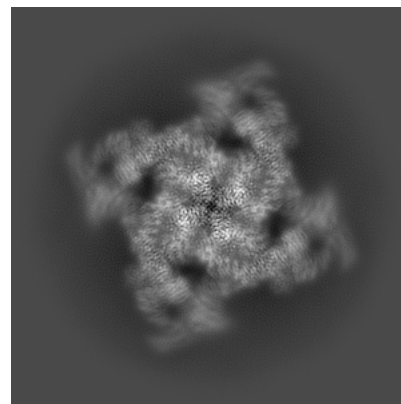
#### 6.1.1 Primary map



X

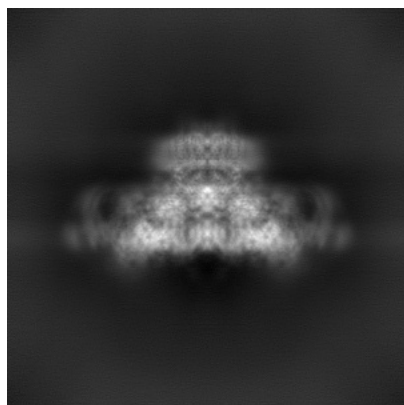


Y

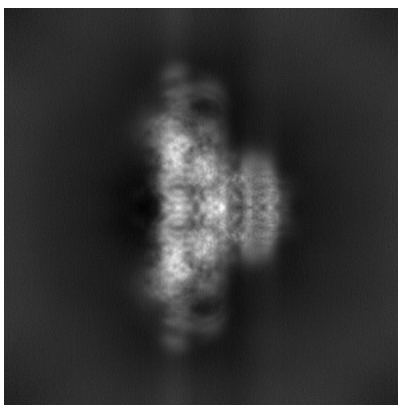


Z

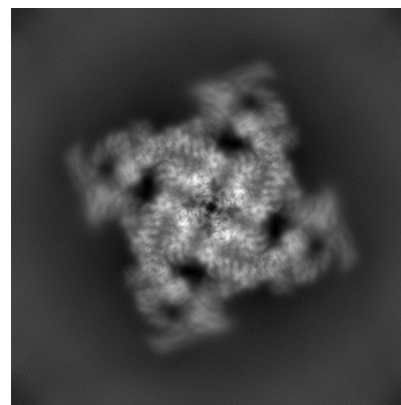
#### 6.1.2 Raw map



X



Y

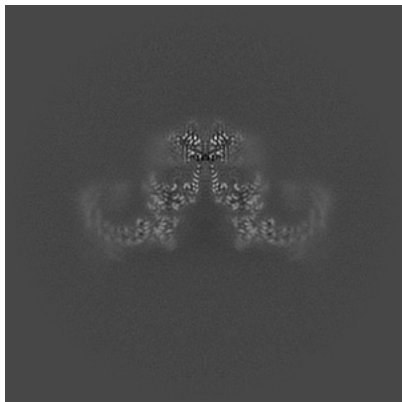


Z

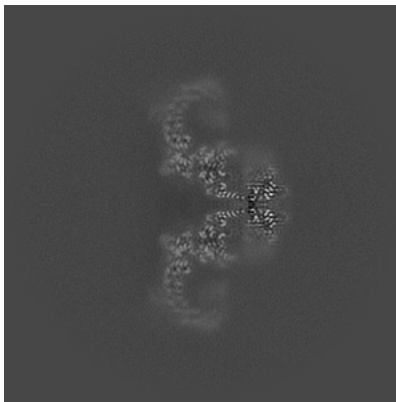
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

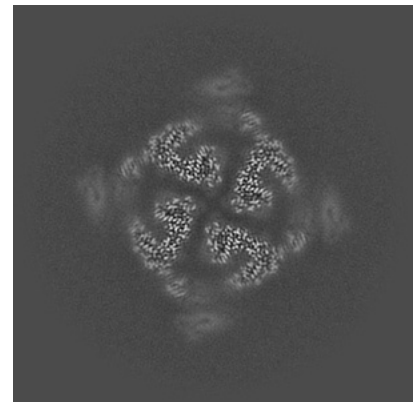
### 6.2.1 Primary map



X Index: 230

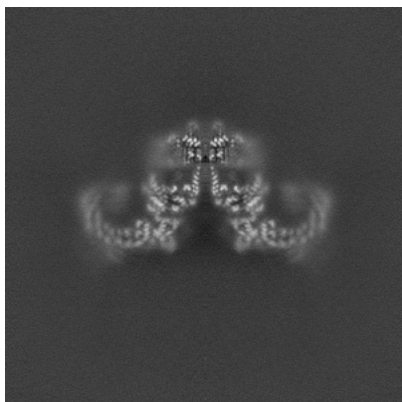


Y Index: 230

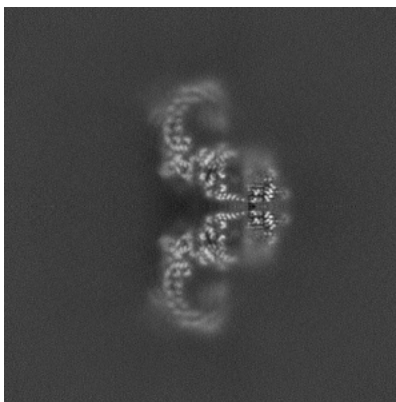


Z Index: 230

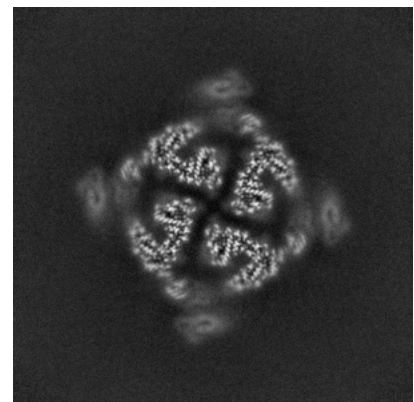
### 6.2.2 Raw map



X Index: 230



Y Index: 230

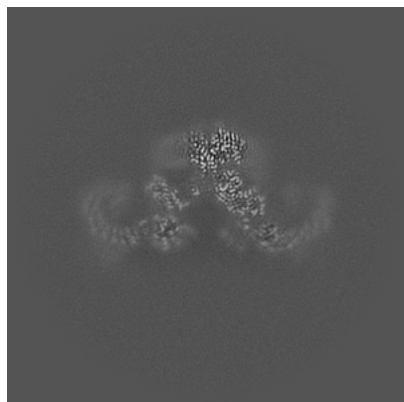


Z Index: 230

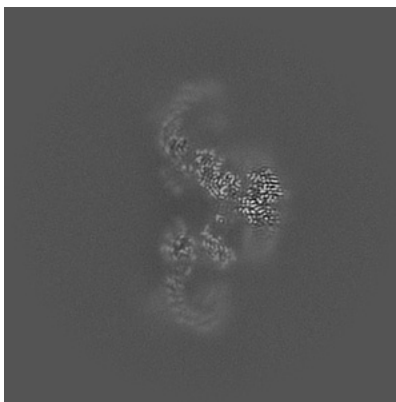
The images above show central slices of the map in three orthogonal directions.

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

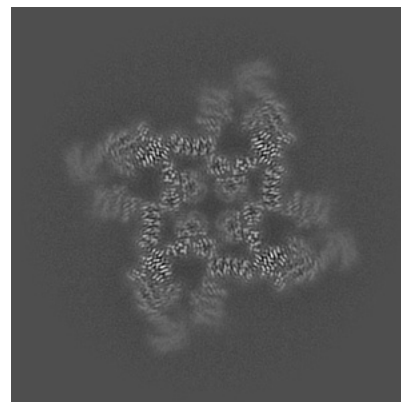
### 6.3.1 Primary map



X Index: 224

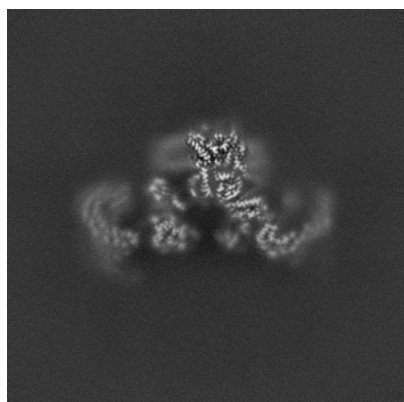


Y Index: 236

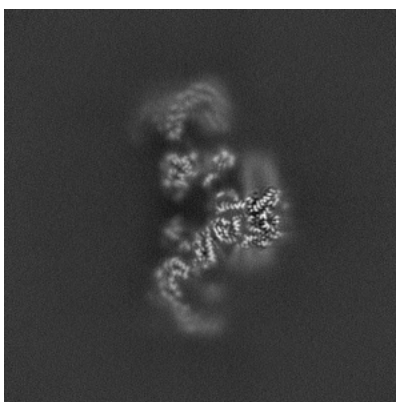


Z Index: 201

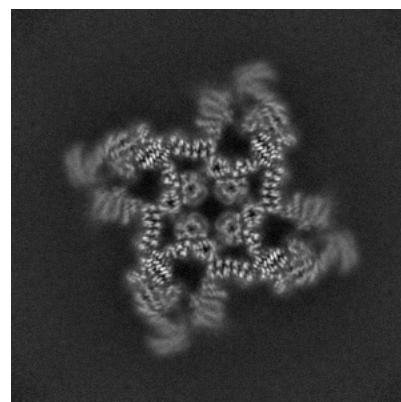
### 6.3.2 Raw map



X Index: 221



Y Index: 221

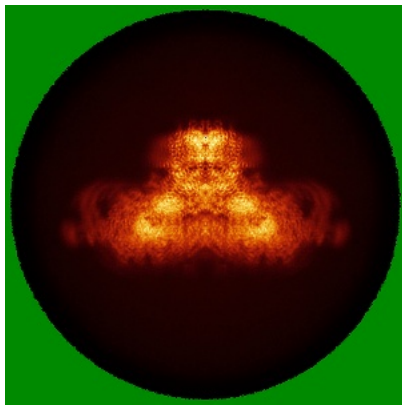


Z Index: 201

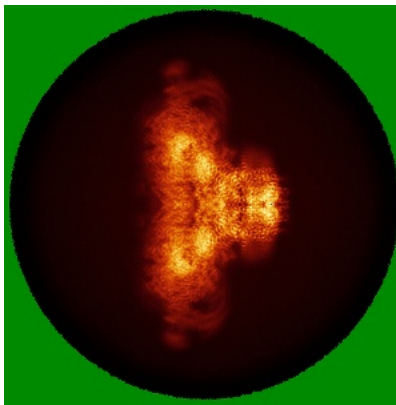
The images above show the largest variance slices of the map in three orthogonal directions.

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

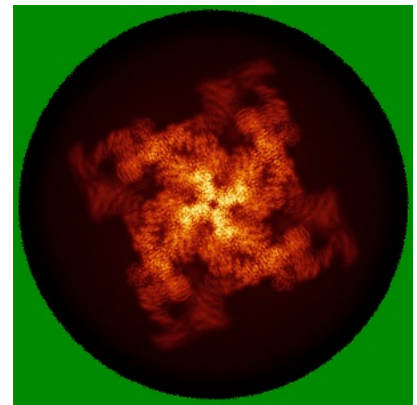
### 6.4.1 Primary map



X

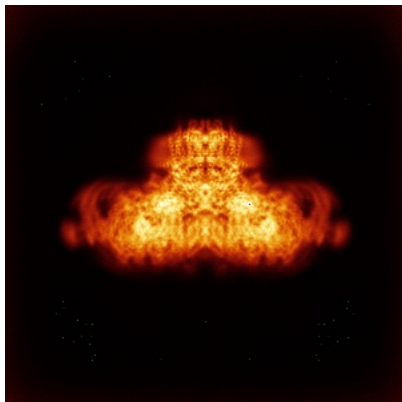


Y

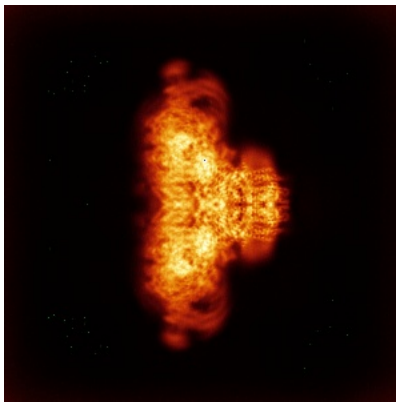


Z

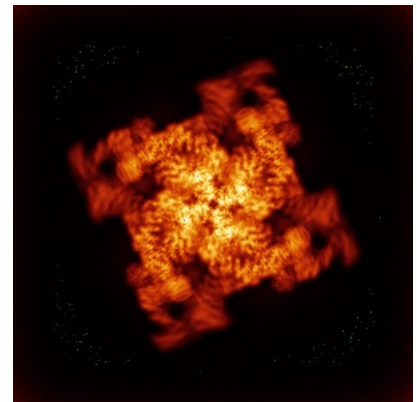
### 6.4.2 Raw map



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 0.24. 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.

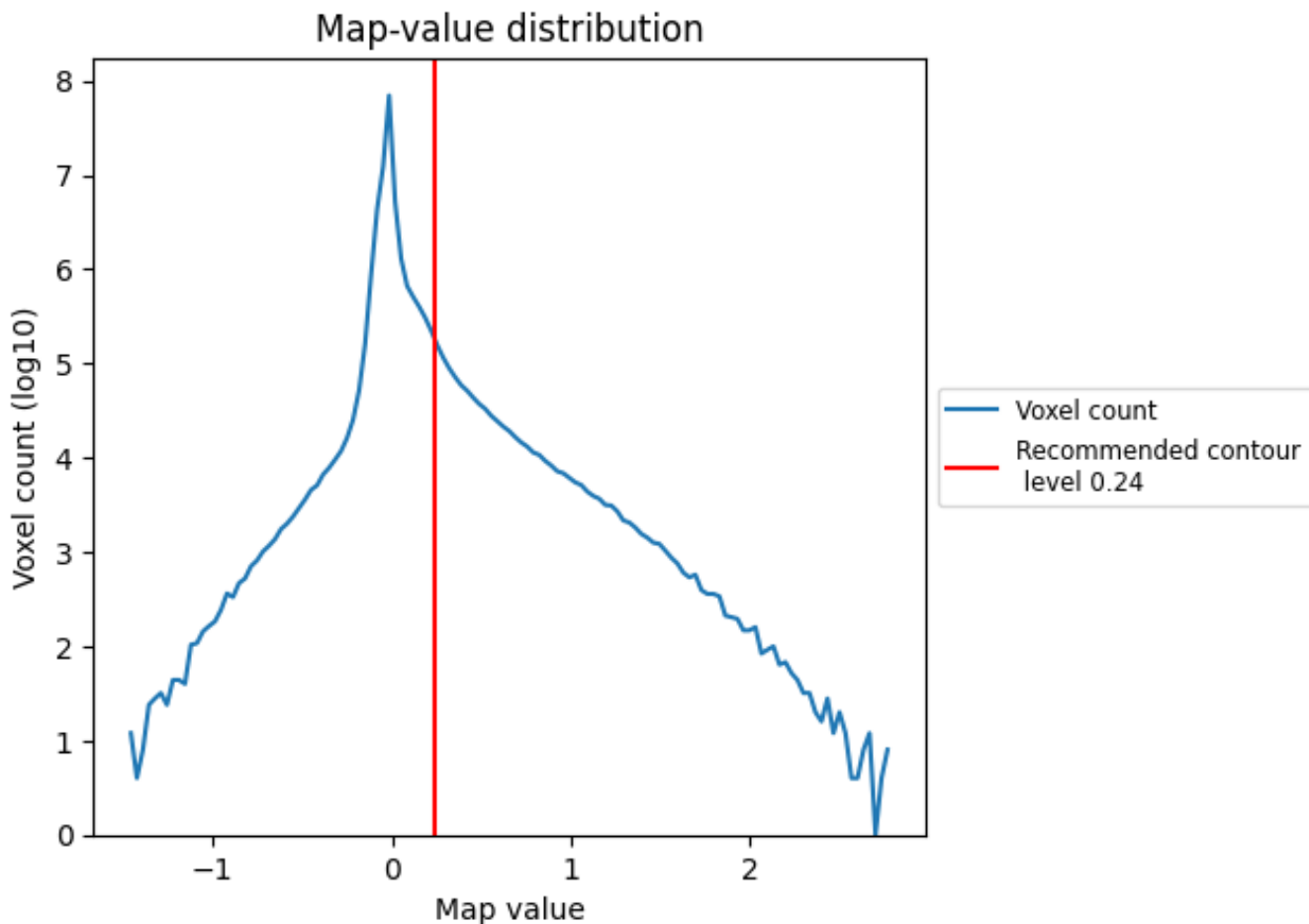
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

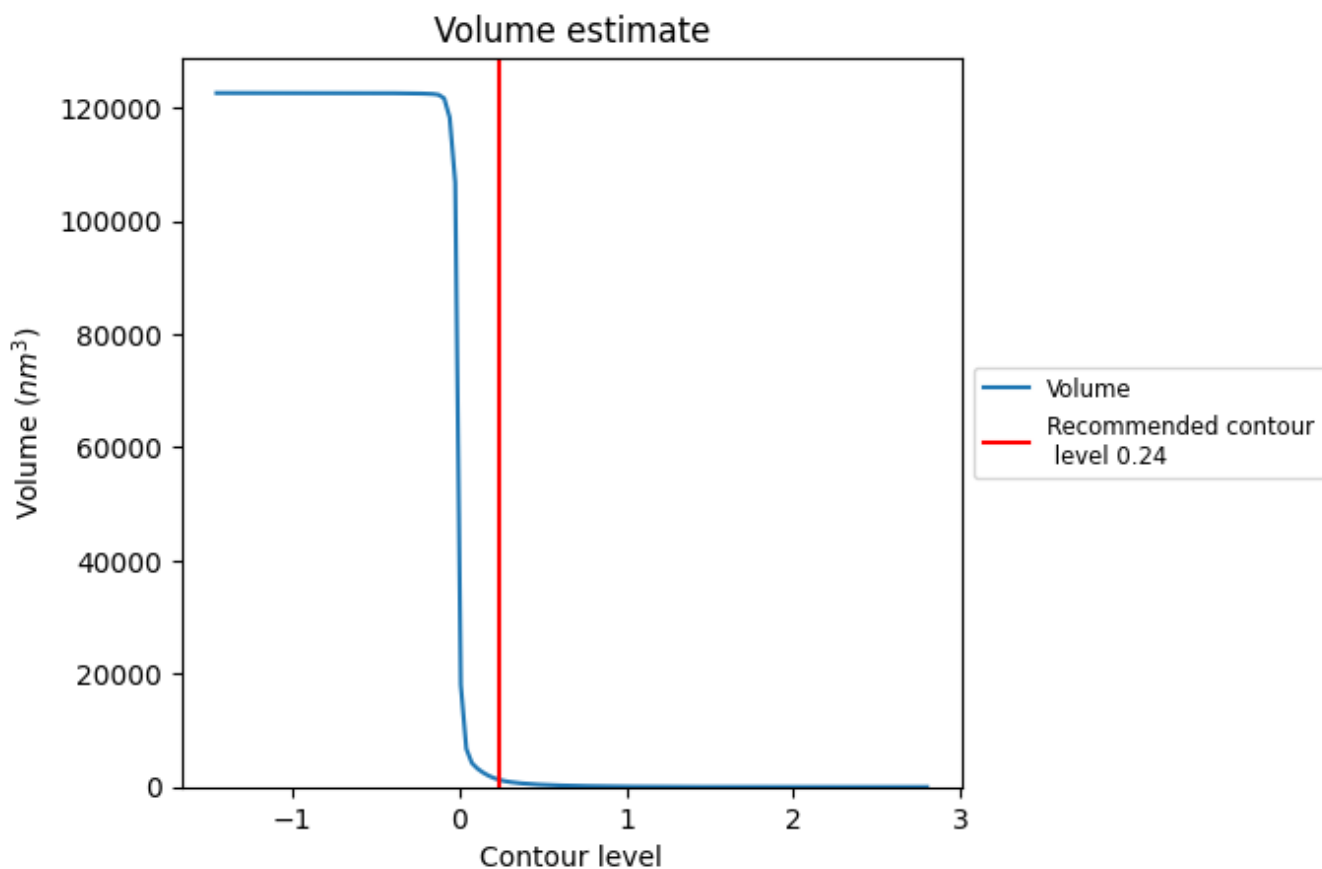
This section contains the results of statistical analysis of the map.

### 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.

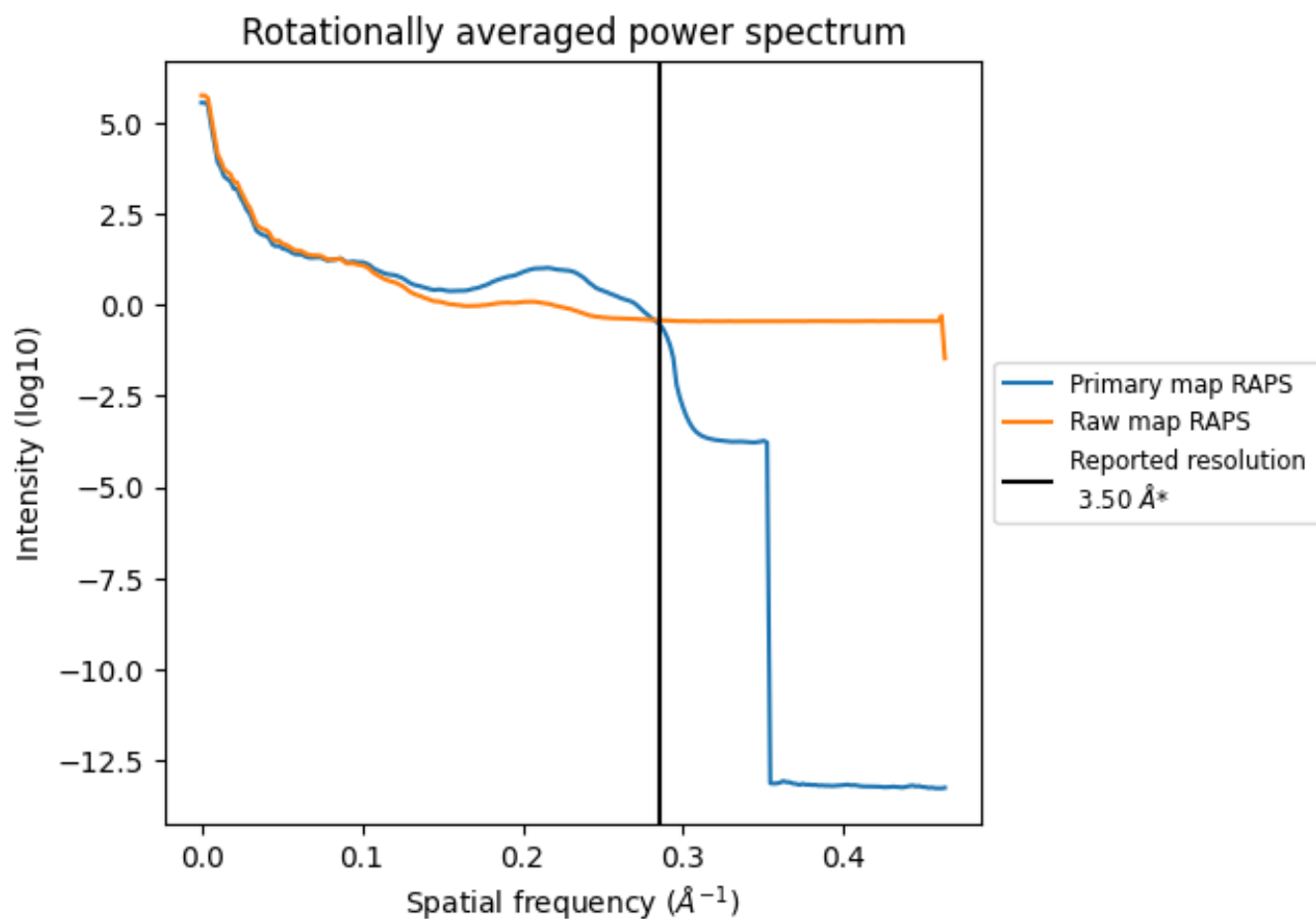
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1250  $\text{nm}^3$ ; this corresponds to an approximate mass of 1129 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](#)

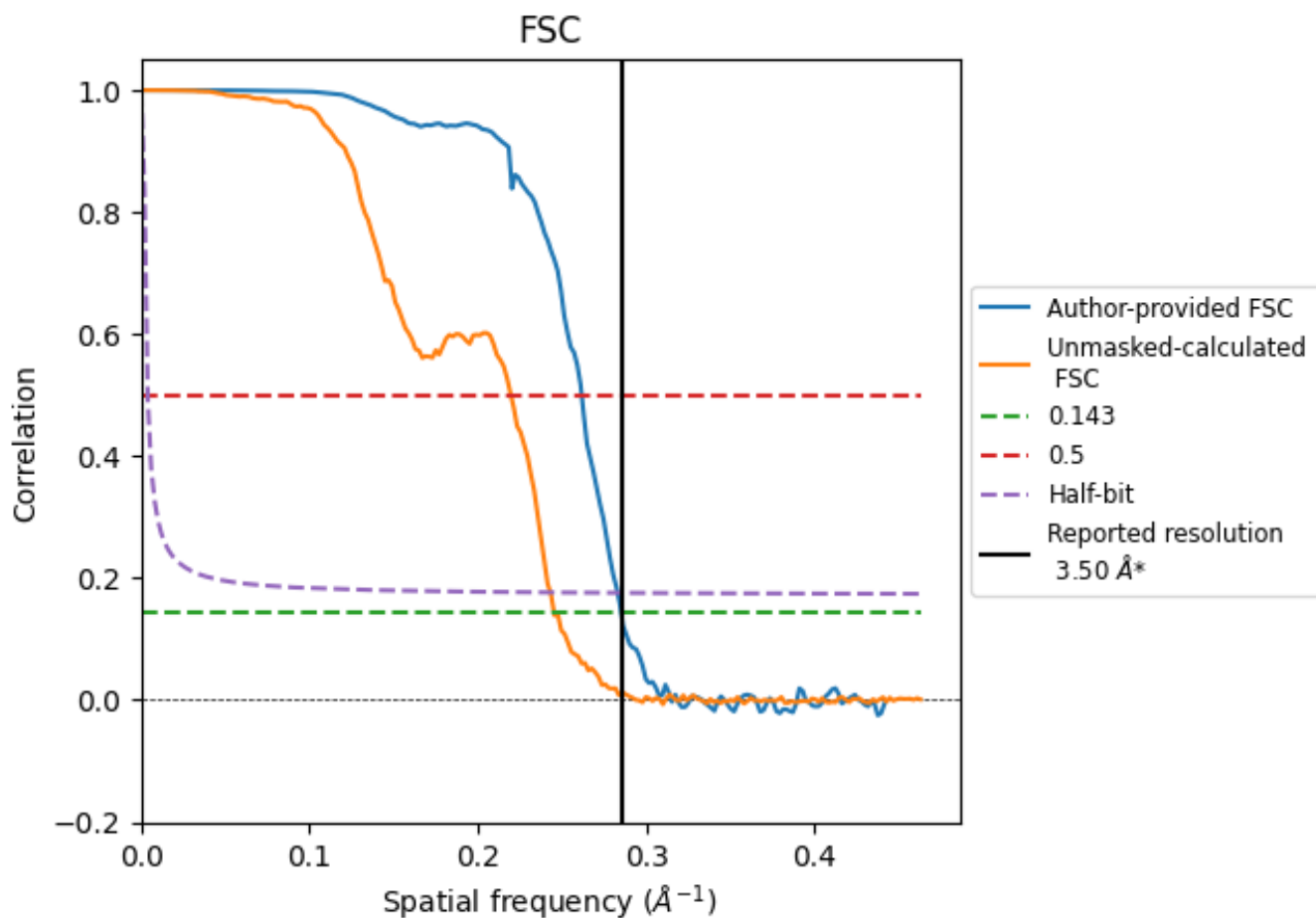


\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>

## 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](#)

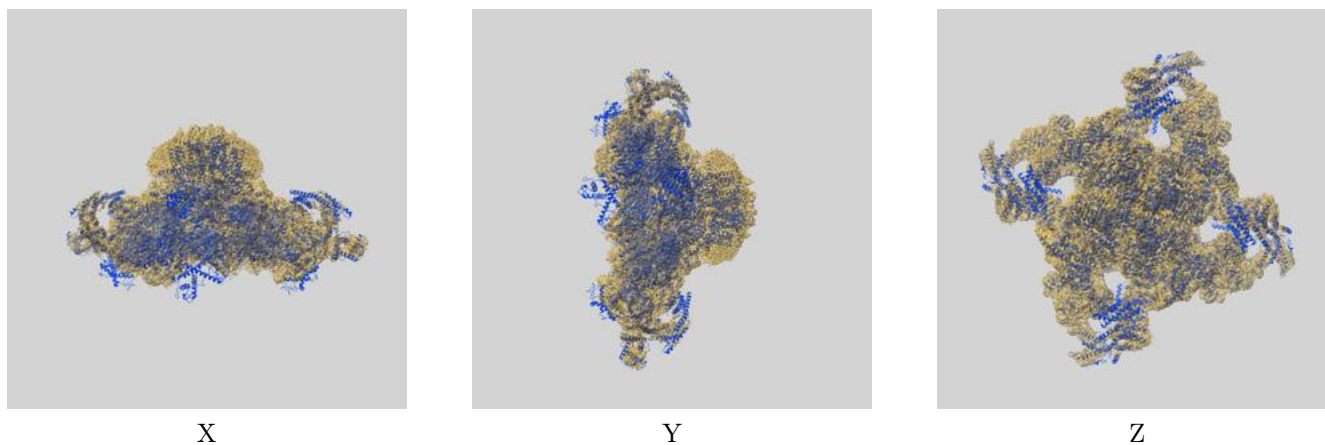
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.51	3.82	3.53
Unmasked-calculated*	4.08	4.55	4.11

\*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 4.08 differs from the reported value 3.5 by more than 10 %

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

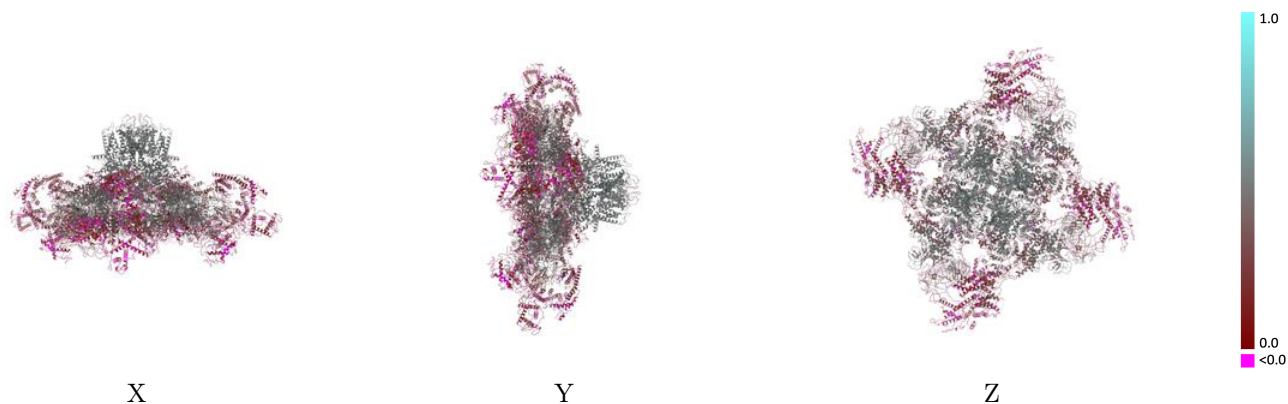
This section contains information regarding the fit between EMDB map EMD-27711 and PDB model 8DTY. Per-residue inclusion information can be found in section 3 on page 6.

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



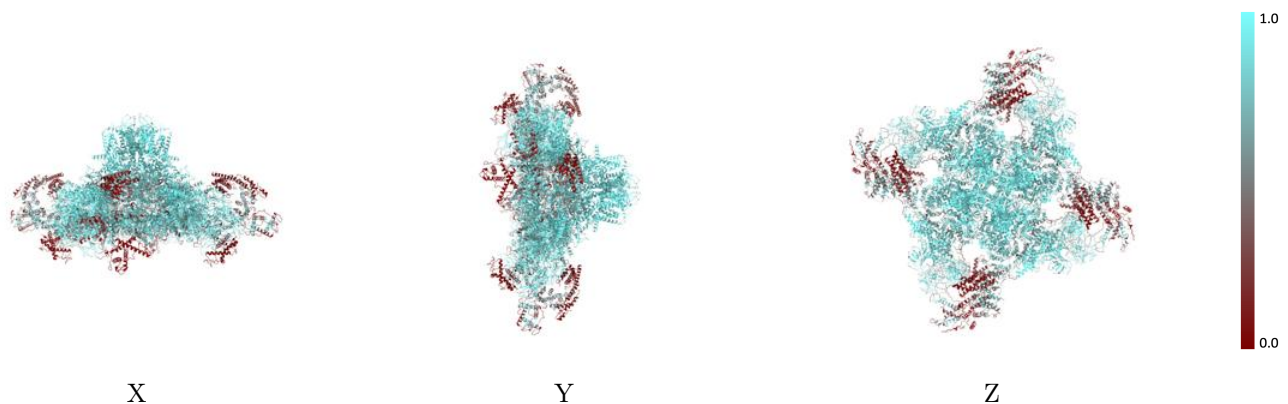
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



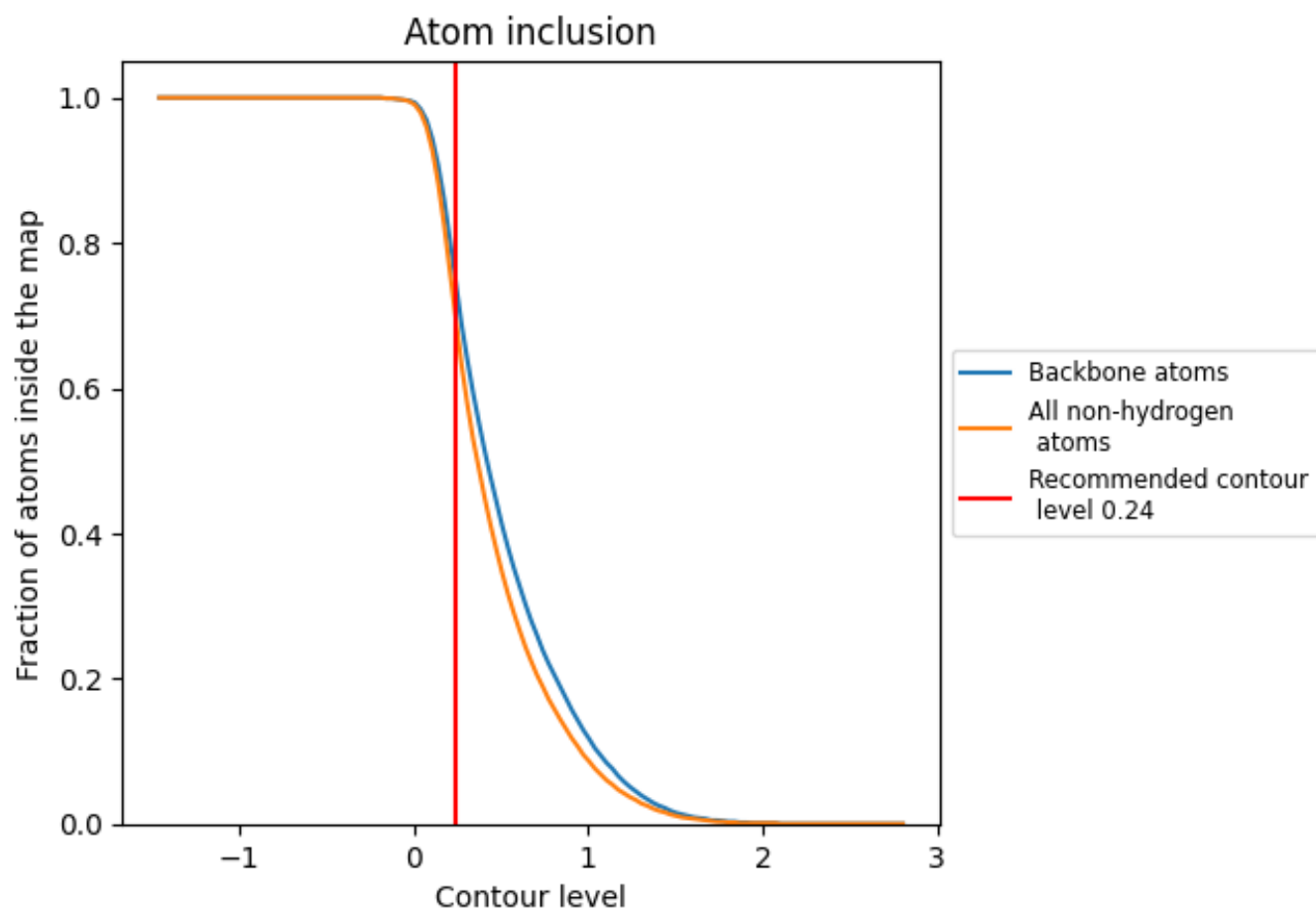
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.24).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 70% 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 (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6970	 0.3090
A	 0.6930	 0.3070
B	 0.6930	 0.3070
C	 0.6930	 0.3070
D	 0.6930	 0.3070
E	 0.8570	 0.3930
F	 0.8590	 0.3950
G	 0.8570	 0.3930
H	 0.8570	 0.3960

