



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:19 AM UTC

PDB ID : 7JMI / pdb_00007jmi
EMDB ID : EMD-22395
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
- Frame 29 - State 3 (S3)
Authors : Dashti, A.; des Georges, A.; Frank, J.; Ourmazd, A.
Deposited on : 2020-07-31
Resolution : 4.50 Å(reported)
Based on initial model : 5TB4

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

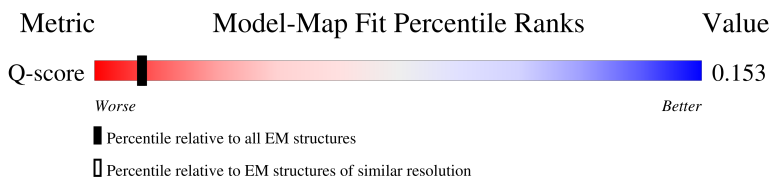
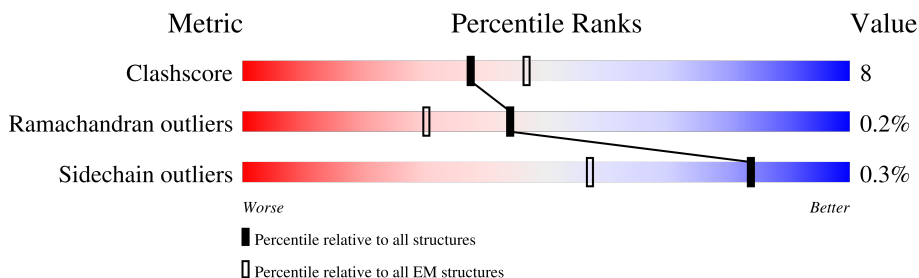
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

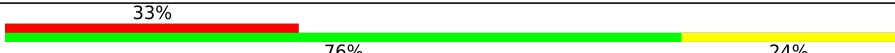
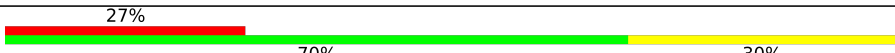
The reported resolution of this entry is 4.50 Å.

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.



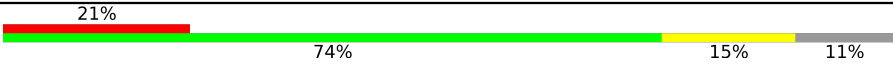
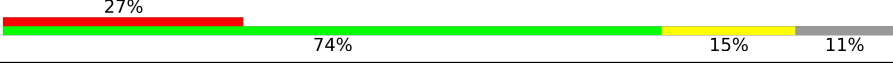
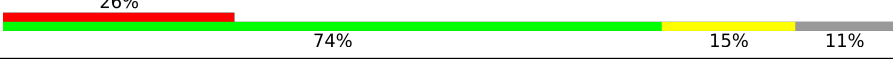
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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 ≥ 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	107	
1	F	107	
1	H	107	
1	J	107	

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Mol	Chain	Length	Quality of chain
2	B	4687	
2	E	4687	
2	G	4687	
2	I	4687	

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	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	F	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 type 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	G	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		

- 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	G	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	

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

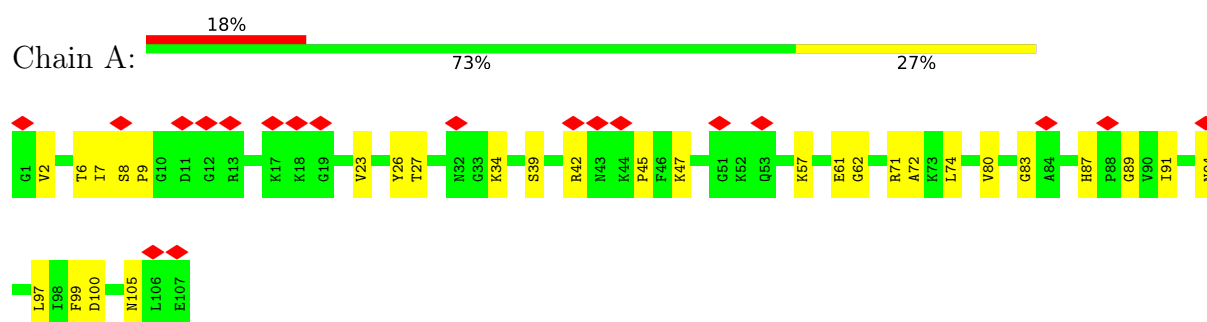
by depositor).

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

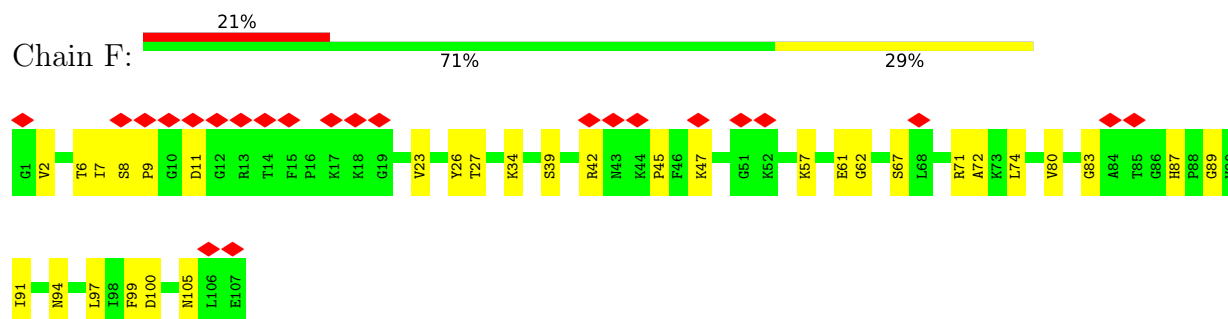
3 Residue-property plots [i](#)

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.

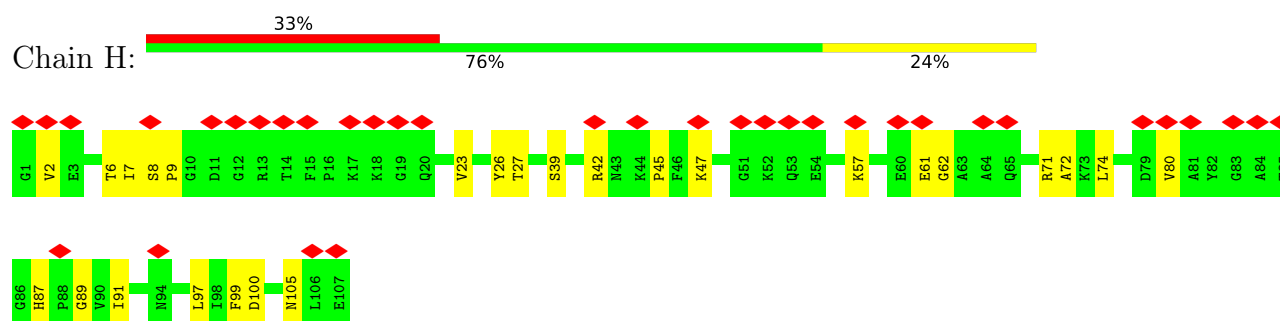
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



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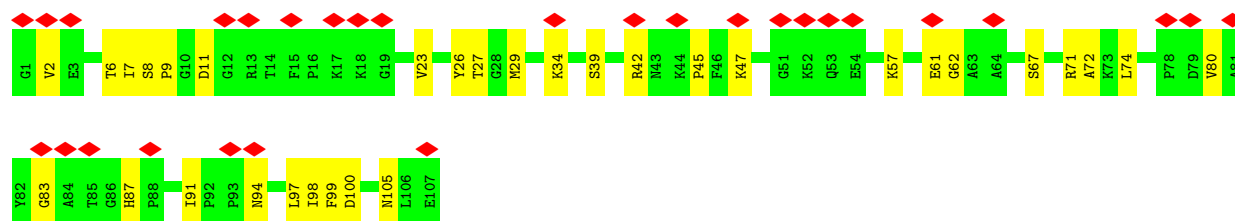


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

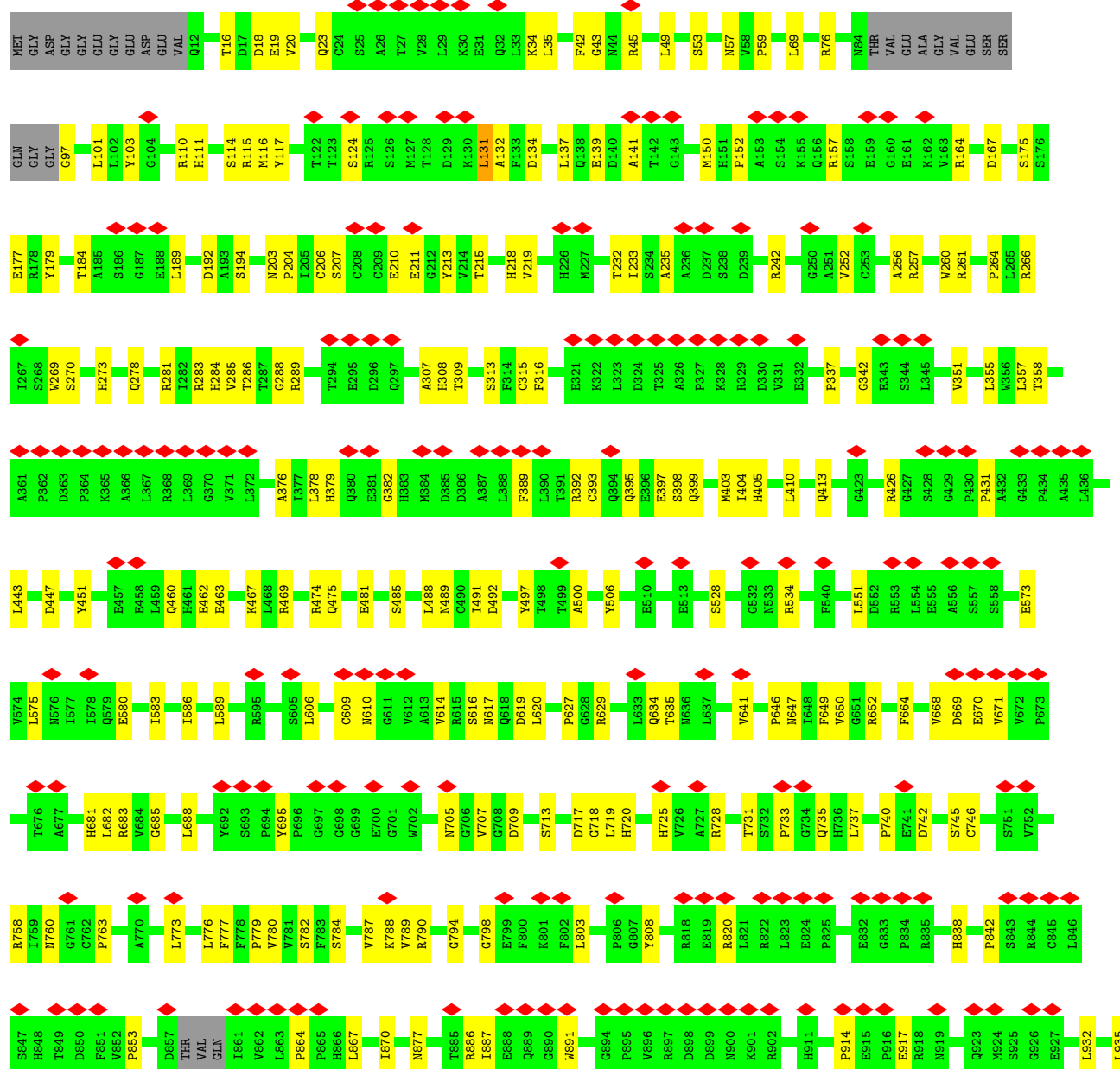
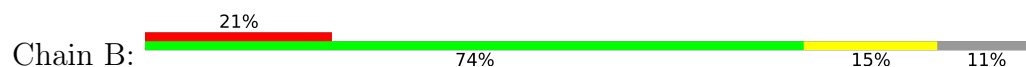


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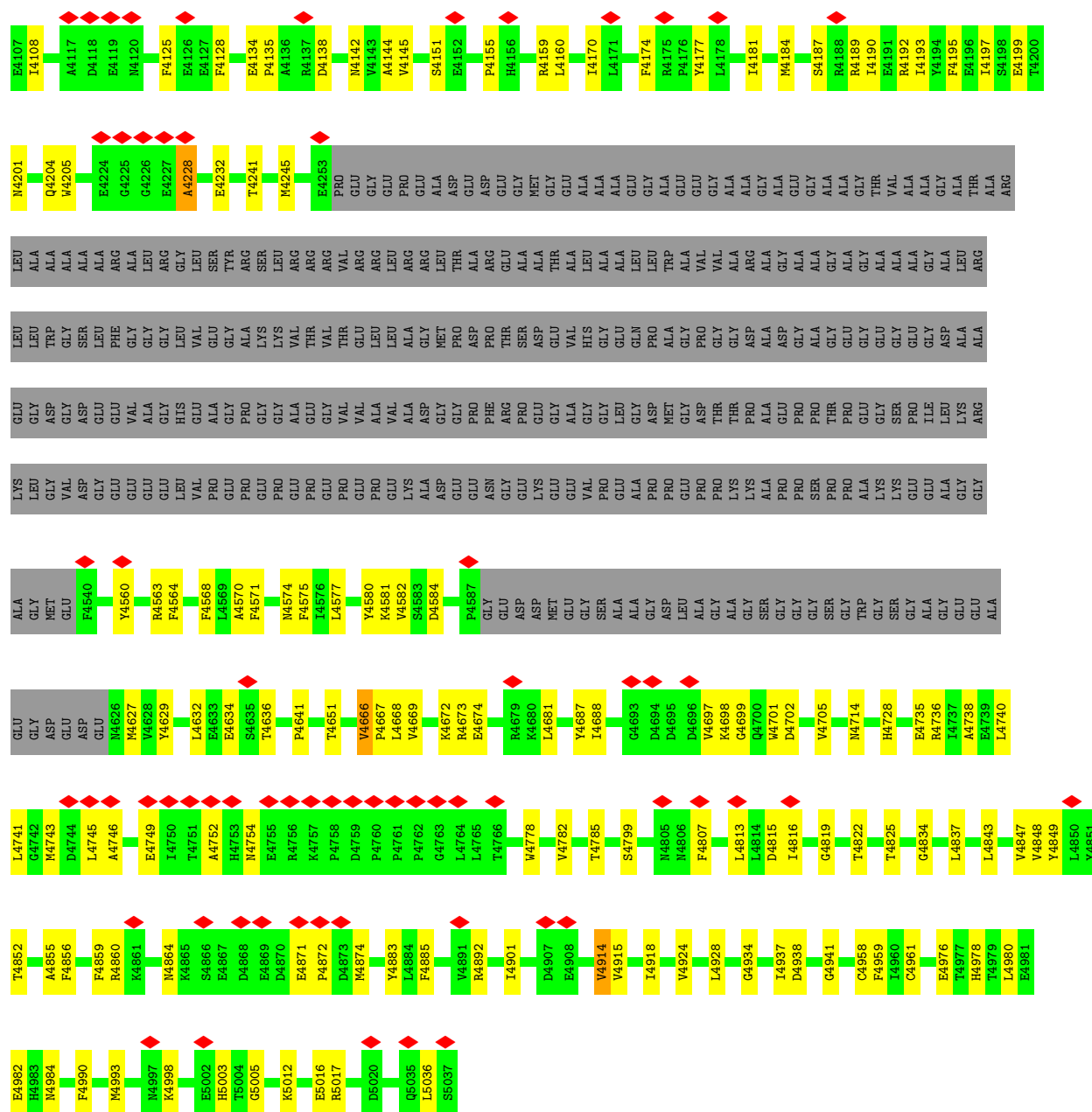




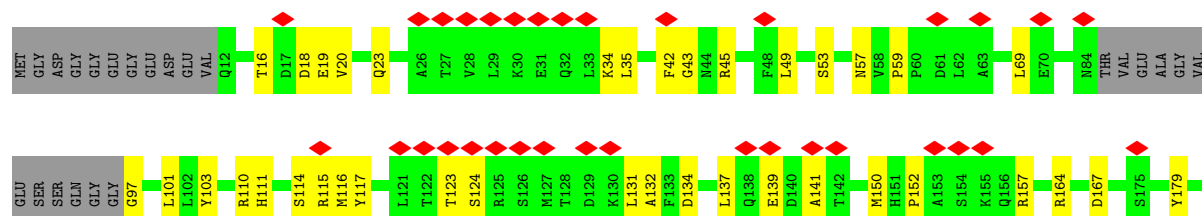
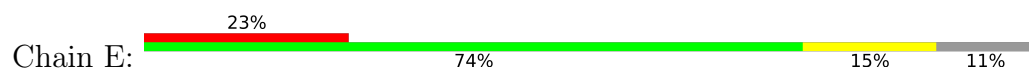
• Molecule 2: ryanodine receptor type 1

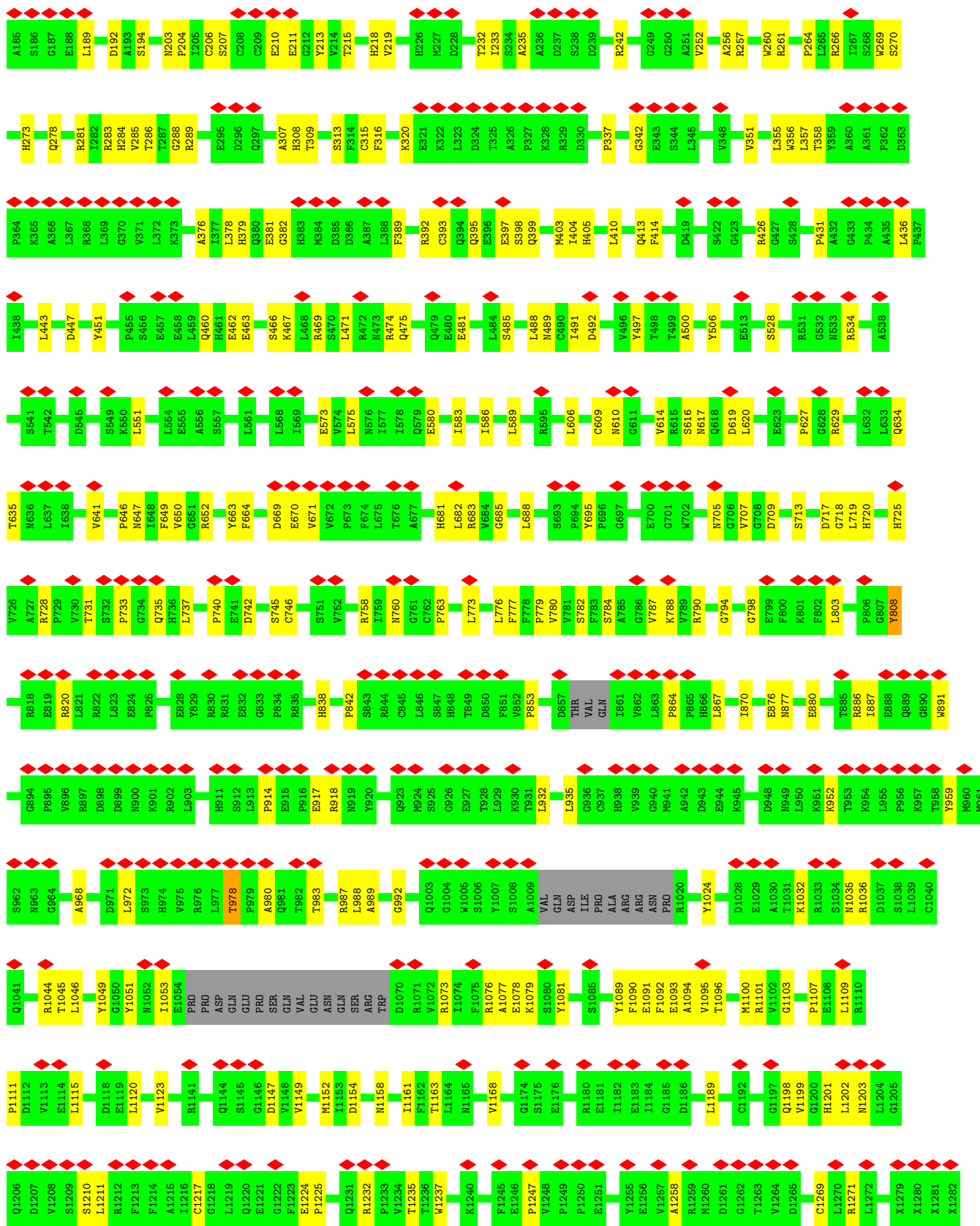


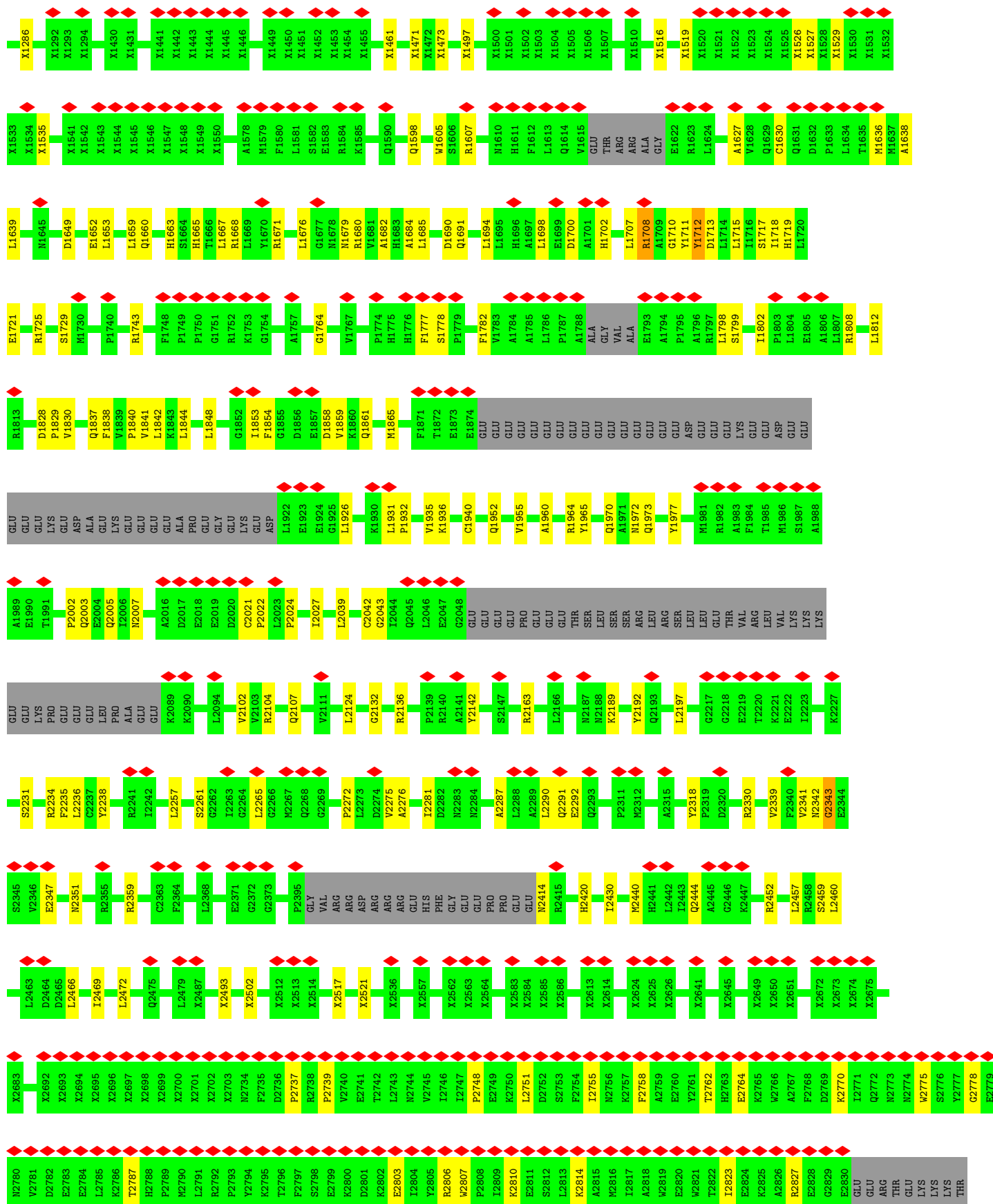




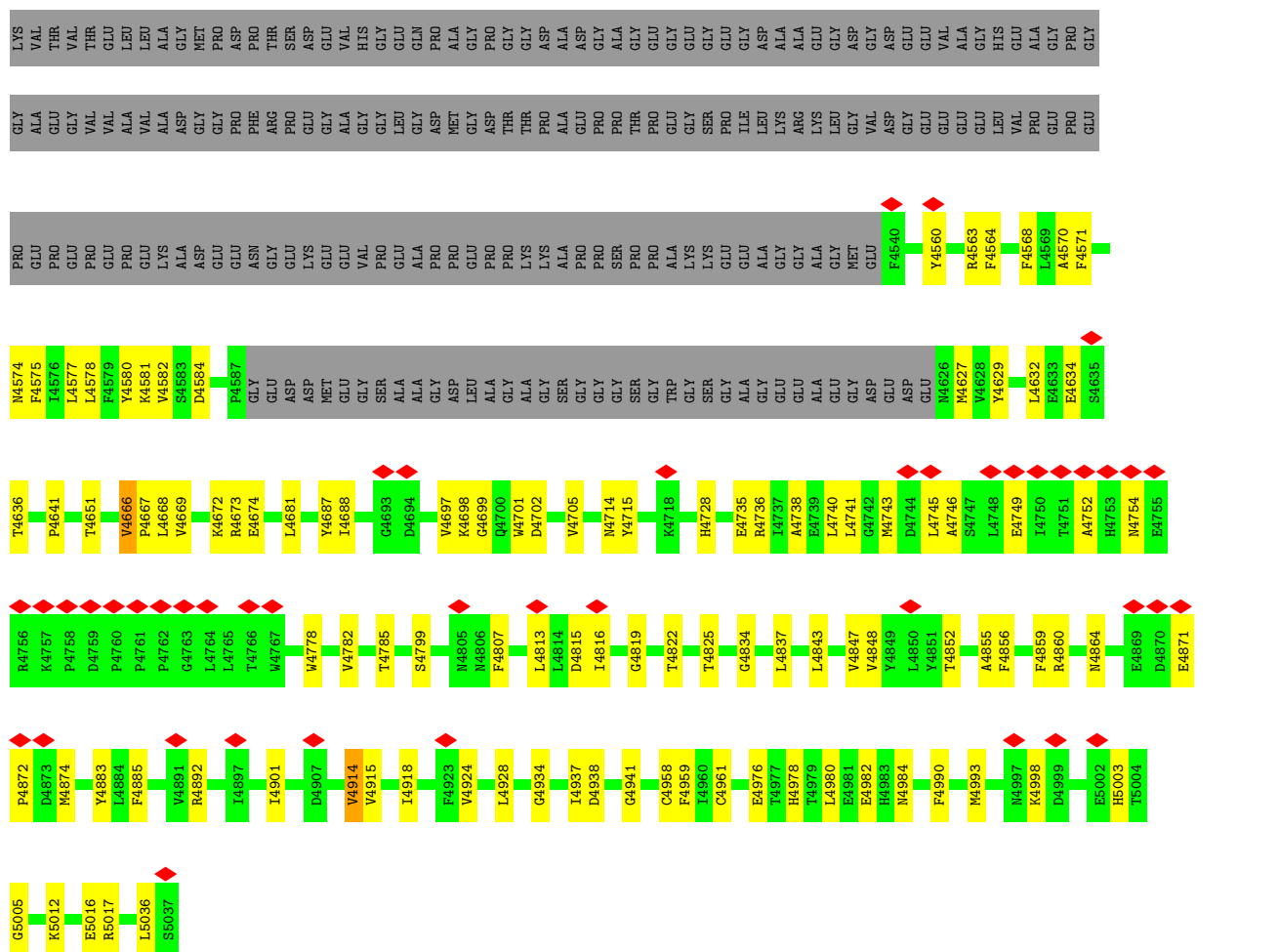
• Molecule 2: ryanodine receptor type 1



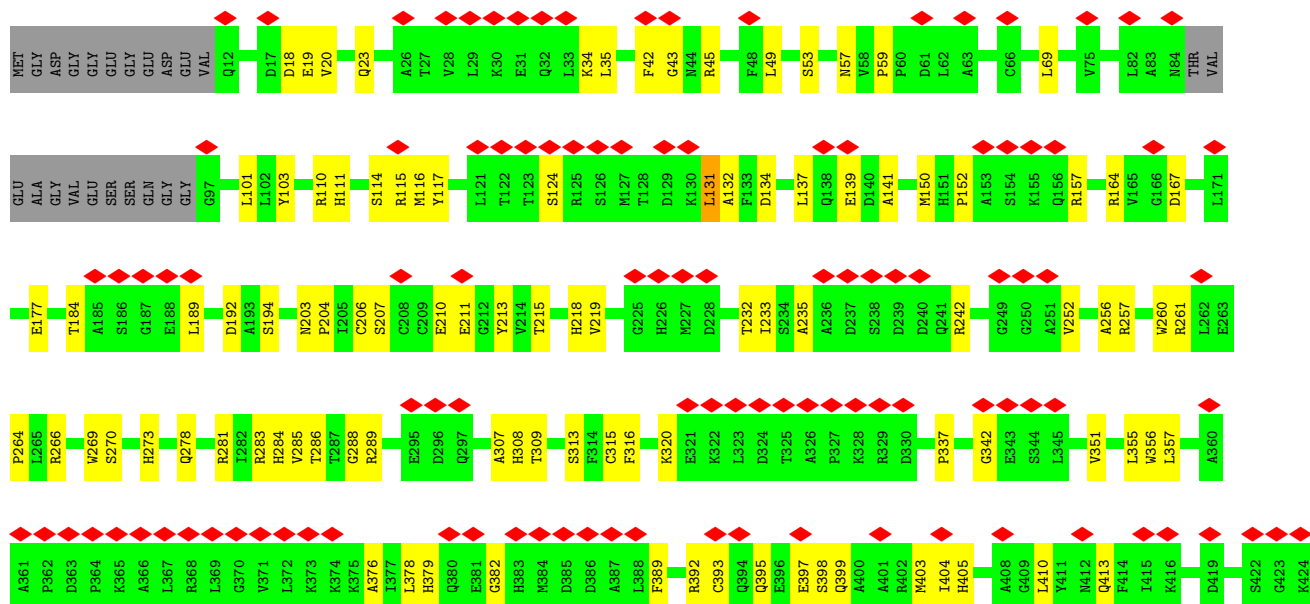
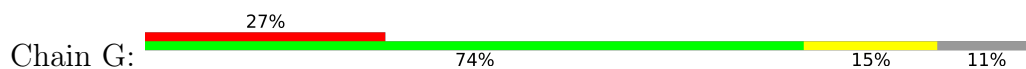


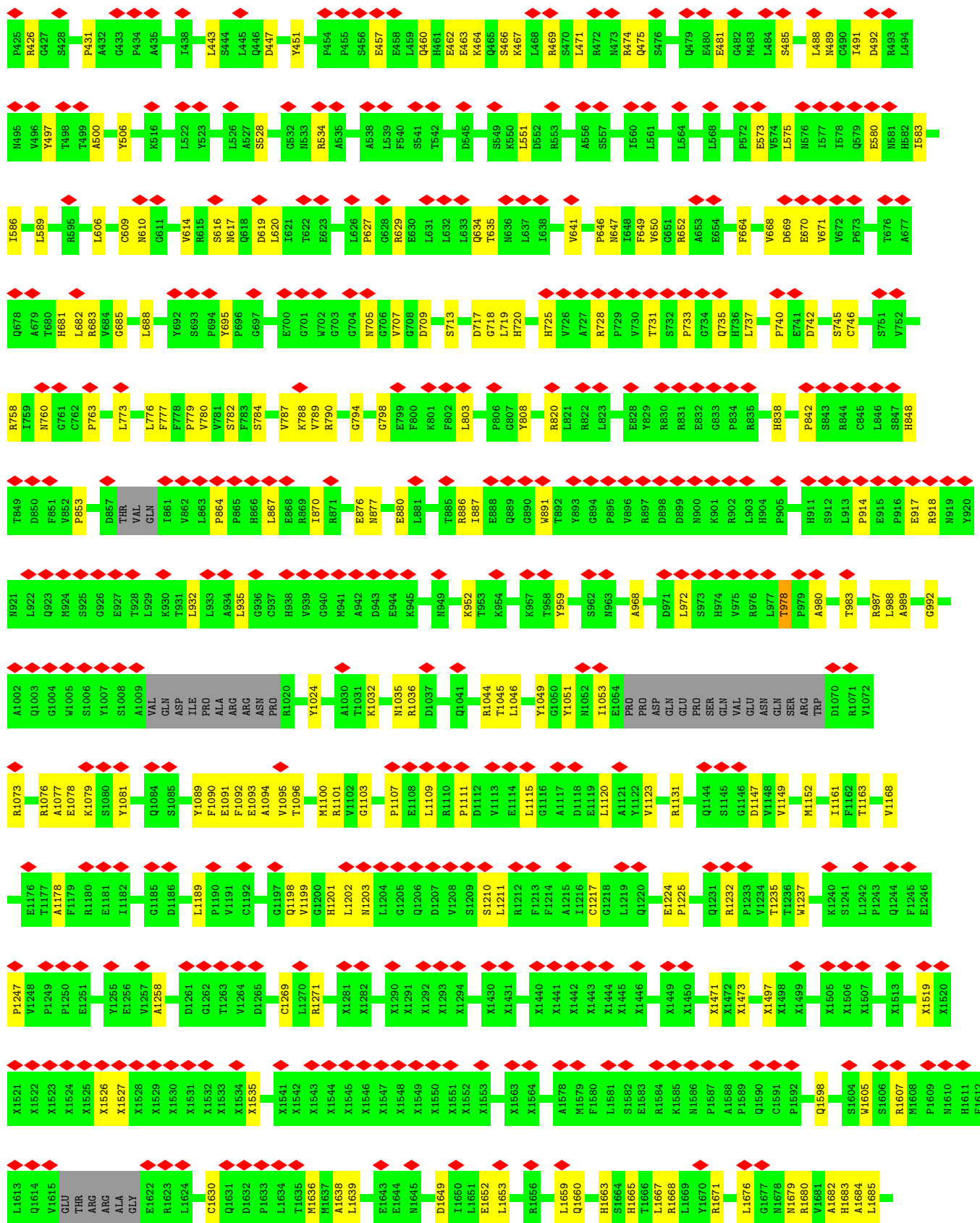






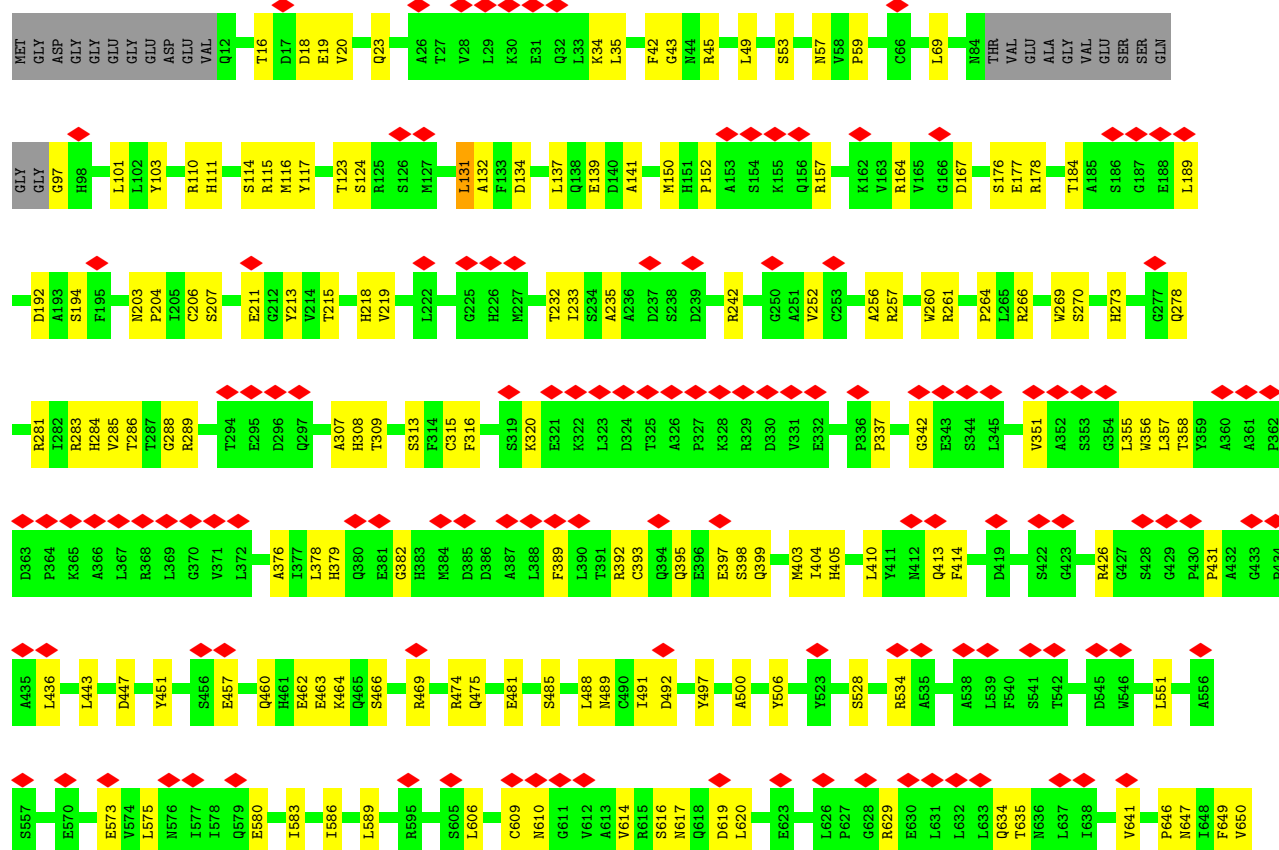
• Molecule 2: ryanodine receptor type 1







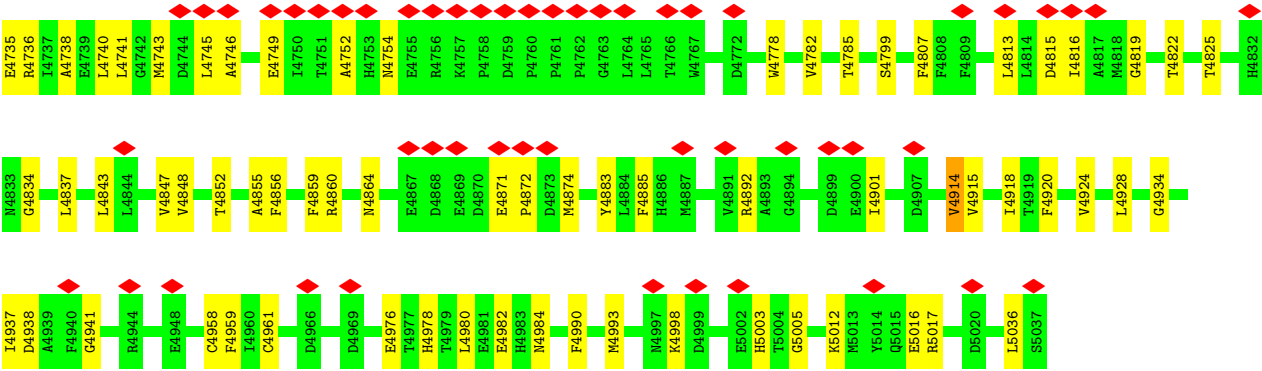






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X3196	X3197	X3221	X3235				X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3273				X3274	X3275	X3276	X3279				X3280	X3283	X3284	X3285	X3286	X3311				X3312	X3313	X3314	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357
K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	X2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2995		X3013	X3014	X3015	X3016	X3017	X3020		X3021	X3022	X3023	X3045	X3046	X3047	X3050		X3060	X3134	X3135	X3136	X3137	X3138	X3139	X3142	X3143	X3189		X3190	X3191	X3192	X3193	X3194	X3195										
S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	M2881	Y2882	H2883	T2884	N2885	W2886	G2887	R2888	K2889	K2890	E2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	T2900	H2902	L2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927						
P2748	E2749	K2750	L2751	D2752	S2753	F2754	I2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	H2787	E2788	P2789	M2790	L2791	R2792	P2793	T2794	K2795	T2796	F2797	S2798	E2799	K2800	L2801	K2802	E2803	L2804	Y2805	R2806	W2807					
X2562	X2563	X2564	X2565	X2566	X2586		X2598		X2604		X2610	X2611	X2614		X2618		X2645	X2646	X2649		X2650	X2651	X2652	X2653	X2654	X2655	X2673		X2674	X2691		X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	D2736	Y2737	R2738	Y2739	V2740	E2741	T2742	L2743	N2744	I2745	L2746	I2747							
A2455	I2456	L2457	R2458	S2459	L2460	V2461	L2463	D2464	D2465	L2466	V2467	G2468	L2469	T2470	S2471	L2472	F2473	L2474	Q2475	I2476	T2477	T2478	L2479	X2487	X2488	X2502		X2510	X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2526		X2529	X2530	X2531	X2532	X2533	X2536		X2537	X2554		X2561										
P2361	F2364		E2371	G2372	G2373	S2374	L2377	A2378	E2381	E2382	R2385		E2388		A2391	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	ARG	GLY	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	I2430	G2436	A2437	P2438	E2439	M2440	H2441	Q2444	A2445	G2446	K2447	G2448	L2451	R2452															
S2261	G2262	I2263	G2264	L2265	G2266	M2267	Q2268	G2269	D2274	V2275	A2276	L2281	D2282	N2283	N2284	A2287		L2288	A2289	Y2292	Q2291	E2292	L2295	E2296	A2303	L2307	L2314	A2315	Y2318	P2319	D2320	L2321	R2330	L2335	V2339	F2340	V2341	N2342	G2343	V2346	E2347	N2351	V2354	S2256	L2257	L2258	R2355	L2358																
L2138	P2139	R2140	A2141	Y2142	S2147	E2150	L2159	I2162	R2163	S2164	L2165	L2166	M2170	K2189	Y2192	Q2193	L2197	M2208	L2215	G2216	G2217	E2218	E2219	T2220	K2221	E2222	I2223	S2231	R2234	F2235	L2236	Y2238	R2241	H2125	G2132	F2251	L2254	S2255	L2257	L2258	E2259	M2260																						
PR0	GLU	GLU	THR	SER	LEU	SER	LEU	GLU	THR	VAL	ARG	LEU	VAL	LYS	LYS	LYS	GLU	LYS	GLU	PR0	GLU	GLU	GLU	PR0	ALA	GLU	GLU	K2099	K2090	L2094	V2102	V2103	R2104	W2105	A2106	Q2107	E2115	R2118	L2124	H2125	G2132	L2135	R2136	A2137	GLU	GLU	GLU																	
E1944	Q1952	V1955	L1958	A1959	A1960	R1964	Q1970	A1971	N1972	Q1973	Y1977	M1981	R1982	A1983	F1984	T1985	M1986	S1987	A1988	A1989	E1990	T1991	A1992	P2002	Q2003	E2005	Q2006	L2007	E2018	E2019	D2020	C2021	P2022	L2023	P2024	L2039	C2042	G2043	I2044	Q2045	L2046	E2047	G2048																					





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	791956	Depositor
Resolution determination method	OTHER	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	0.549	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.16	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	0.21	0/834	0.55	1/1123 (0.1%)
1	F	0.21	0/834	0.55	1/1123 (0.1%)
1	H	0.21	0/834	0.57	1/1123 (0.1%)
1	J	0.21	0/834	0.55	1/1123 (0.1%)
2	B	0.23	0/25428	0.58	4/34534 (0.0%)
2	E	0.23	0/25428	0.58	4/34534 (0.0%)
2	G	0.23	0/25428	0.58	4/34534 (0.0%)
2	I	0.23	0/25428	0.58	4/34534 (0.0%)
All	All	0.23	0/105048	0.58	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
2	B	0	16
2	E	0	16
2	G	0	16
2	I	0	16
All	All	0	64

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	G	4872	PRO	N-CA-C	-7.10	103.66	113.53
2	I	4872	PRO	N-CA-C	-7.10	103.66	113.53
2	E	4872	PRO	N-CA-C	-7.05	103.73	113.53
2	B	4872	PRO	N-CA-C	-7.04	103.75	113.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	8	SER	N-CA-C	5.75	120.73	113.25

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	LEU	Peptide
2	B	1676	LEU	Peptide
2	B	1690	ASP	Peptide
2	B	1712	TYR	Peptide
2	B	808	TYR	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	18	0
1	F	818	0	824	18	0
1	H	818	0	824	17	0
1	J	818	0	824	19	0
2	B	29369	0	24711	409	0
2	E	29369	0	24713	415	0
2	G	29369	0	24713	407	0
2	I	29369	0	24712	410	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	102145	1679	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1679 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:G:2318:TYR:HH	2:G:2414:ASN:N	1.88	0.72
2:I:2318:TYR:HH	2:I:2414:ASN:N	1.88	0.72
2:E:853:PRO:HB3	2:E:1024:TYR:H	1.56	0.71
2:I:853:PRO:HB3	2:I:1024:TYR:H	1.56	0.70
2:G:853:PRO:HB3	2:G:1024:TYR:H	1.56	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	105/107 (98%)	92 (88%)	13 (12%)	0	100	100
1	F	105/107 (98%)	92 (88%)	13 (12%)	0	100	100
1	H	105/107 (98%)	92 (88%)	13 (12%)	0	100	100
1	J	105/107 (98%)	92 (88%)	13 (12%)	0	100	100
2	B	3235/4687 (69%)	2890 (89%)	339 (10%)	6 (0%)	43	77
2	E	3235/4687 (69%)	2887 (89%)	342 (11%)	6 (0%)	43	77
2	G	3235/4687 (69%)	2892 (89%)	337 (10%)	6 (0%)	43	77
2	I	3235/4687 (69%)	2889 (89%)	340 (10%)	6 (0%)	43	77
All	All	13360/19176 (70%)	11926 (89%)	1410 (11%)	24 (0%)	44	77

5 of 24 Ramachandran outliers are listed below:

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

Continued on next page...

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Mol	Chain	Res	Type
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	88/88 (100%)	88 (100%)	0	100	100
1	F	88/88 (100%)	88 (100%)	0	100	100
1	H	88/88 (100%)	88 (100%)	0	100	100
1	J	88/88 (100%)	88 (100%)	0	100	100
2	B	2493/3209 (78%)	2485 (100%)	8 (0%)	86	84
2	E	2493/3209 (78%)	2485 (100%)	8 (0%)	86	84
2	G	2493/3209 (78%)	2485 (100%)	8 (0%)	86	84
2	I	2493/3209 (78%)	2485 (100%)	8 (0%)	86	84
All	All	10324/13188 (78%)	10292 (100%)	32 (0%)	84	84

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	3663	LEU
2	I	3805	LEU
2	E	3663	LEU
2	E	2339	VAL
2	I	4871	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 207 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	379	HIS
2	G	3960	GLN
2	I	4142	ASN
2	G	412	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	1775	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	G	12
2	B	12

Continued on next page...

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Mol	Chain	Number of breaks
2	I	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	G	3613:UNK	C	3639:THR	N	44.80
1	B	3613:UNK	C	3639:THR	N	44.74
1	I	3613:UNK	C	3639:THR	N	44.65
1	E	3613:UNK	C	3639:THR	N	44.57
1	B	3163:UNK	C	3170:UNK	N	16.54

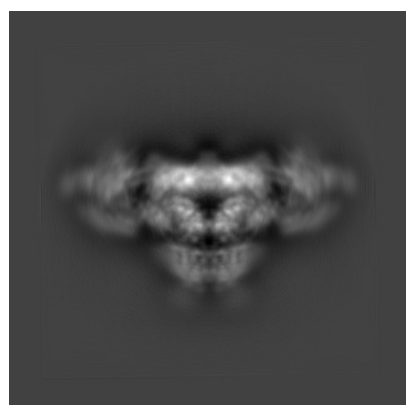
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22395. These allow visual inspection of the internal detail of the map and identification of artifacts.

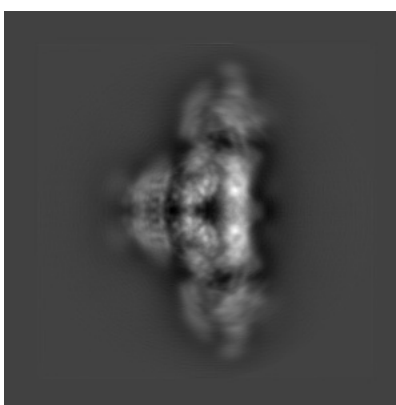
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

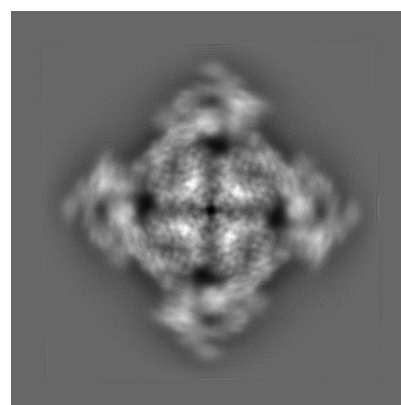
6.1.1 Primary map



X



Y

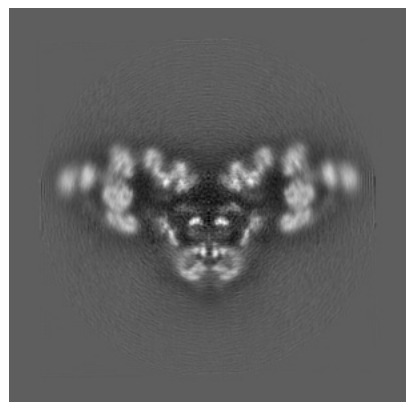


Z

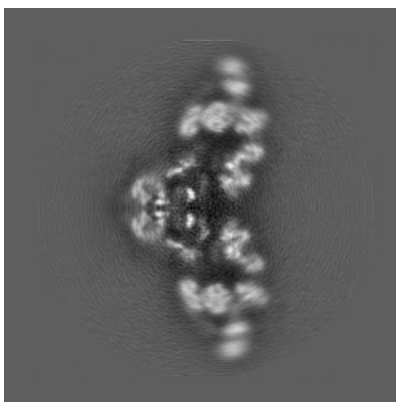
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

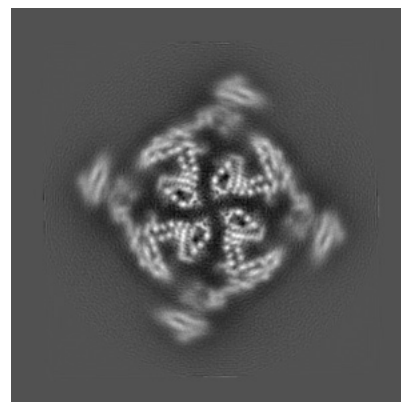
6.2.1 Primary map



X Index: 200



Y Index: 200

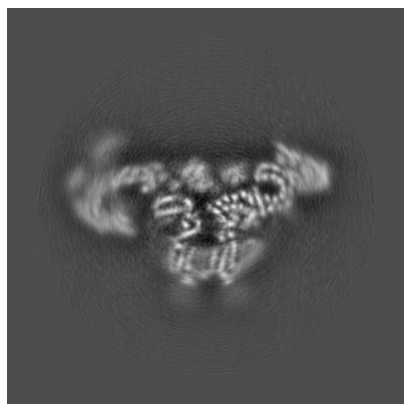


Z Index: 200

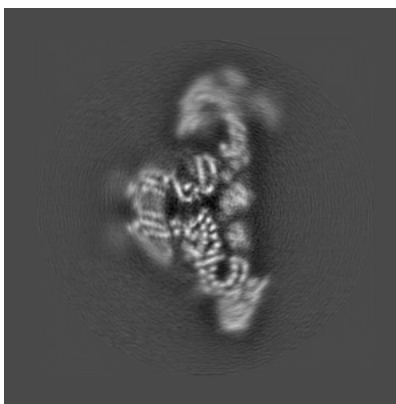
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

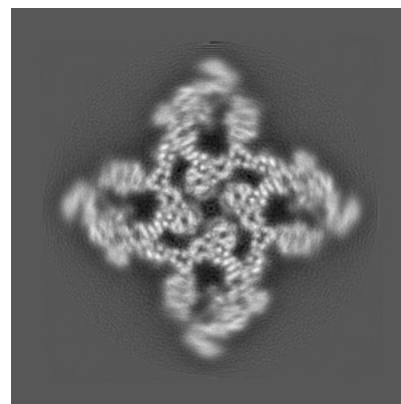
6.3.1 Primary map



X Index: 177



Y Index: 177



Z Index: 230

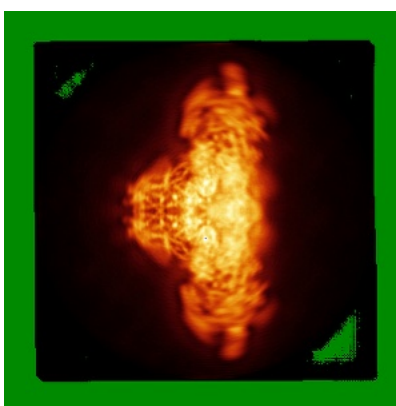
The images above show the largest variance slices of the map in three orthogonal directions.

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

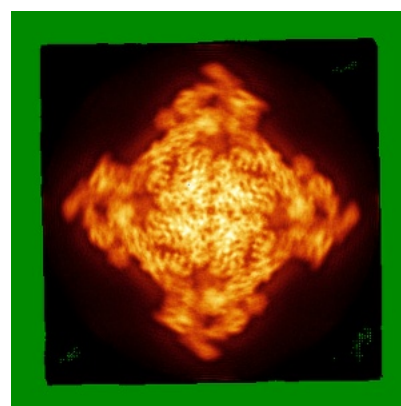
6.4.1 Primary map



X



Y

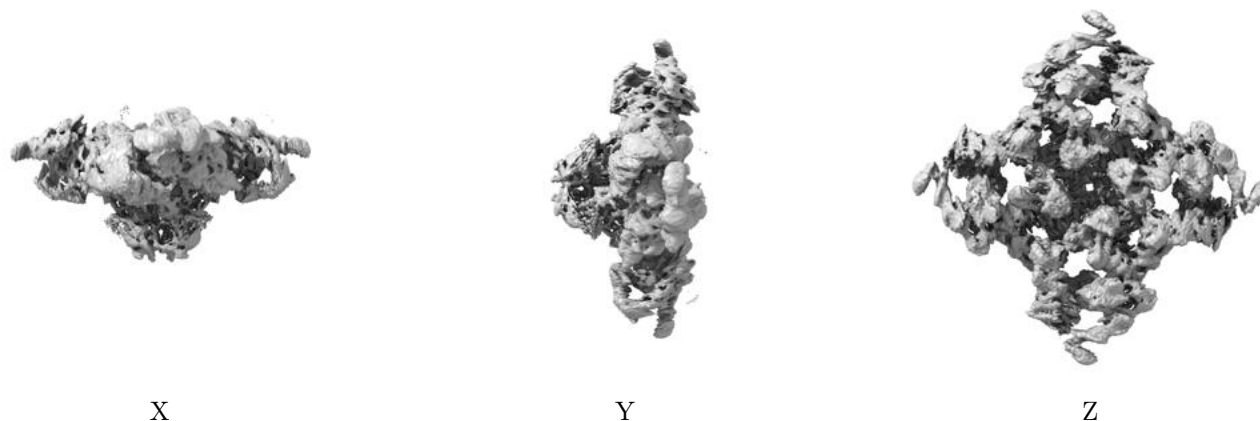


Z

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 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

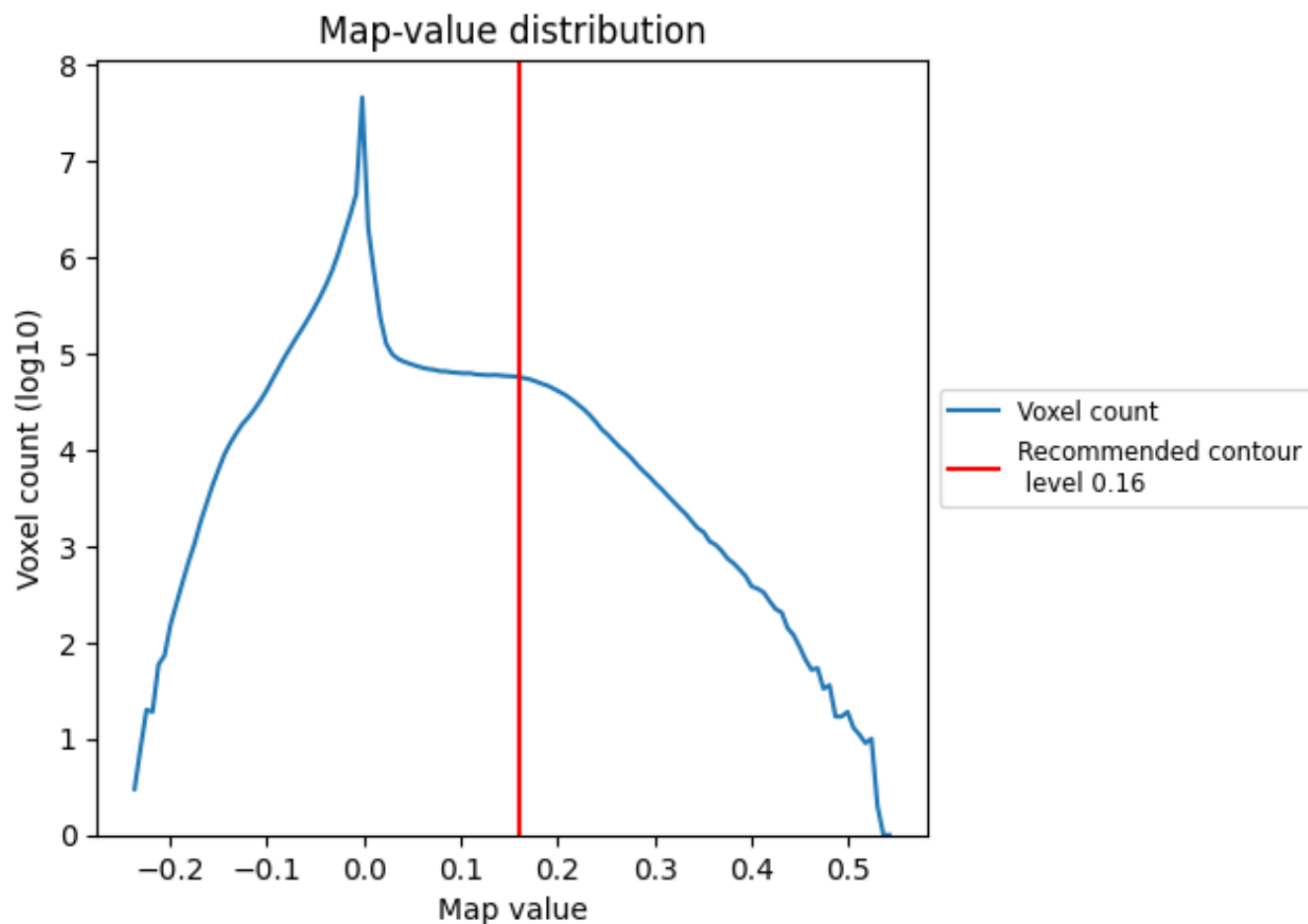
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

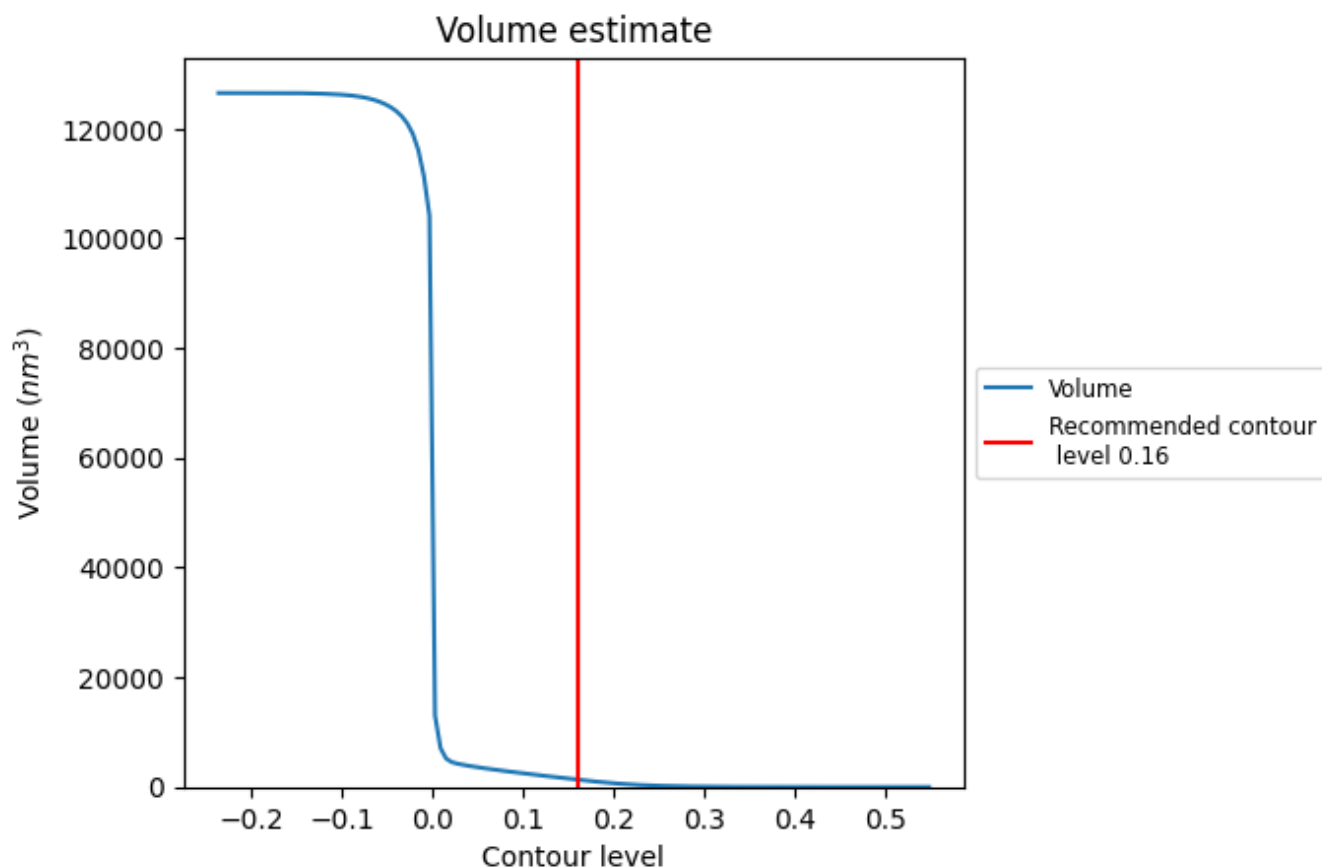
This section contains the results of statistical analysis of the map.

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.

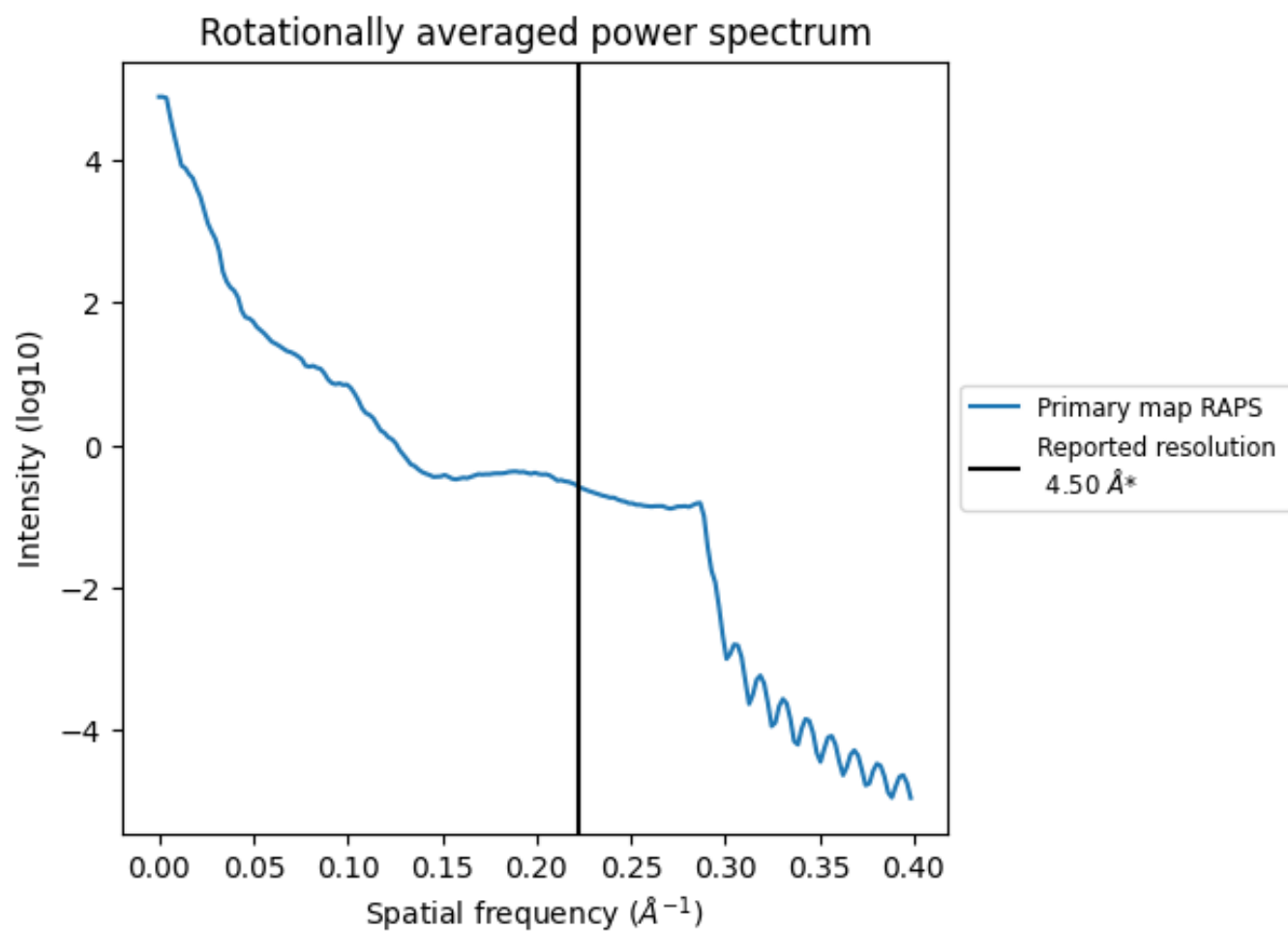
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1337 nm³; this corresponds to an approximate mass of 1208 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 0.222 Å⁻¹

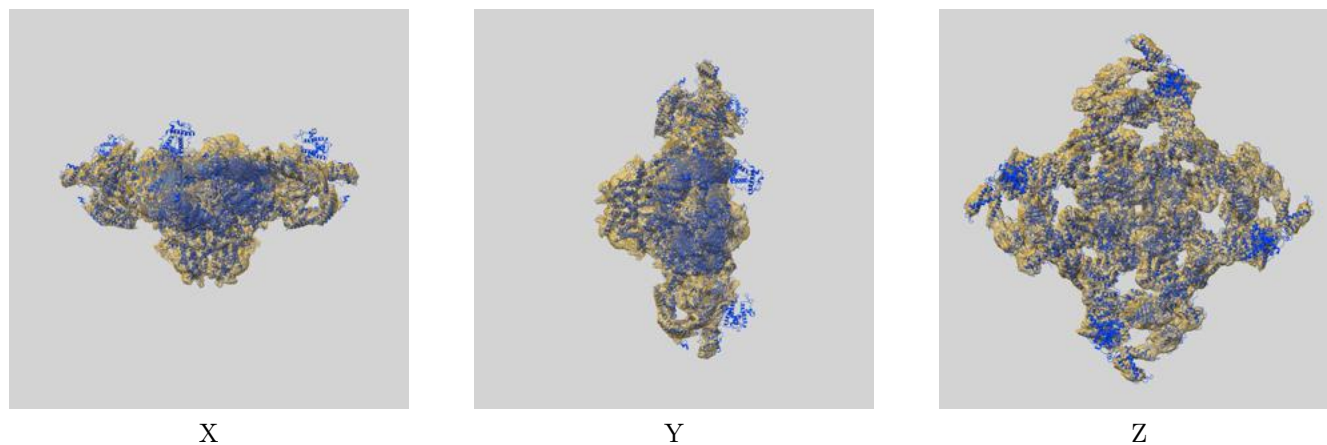
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

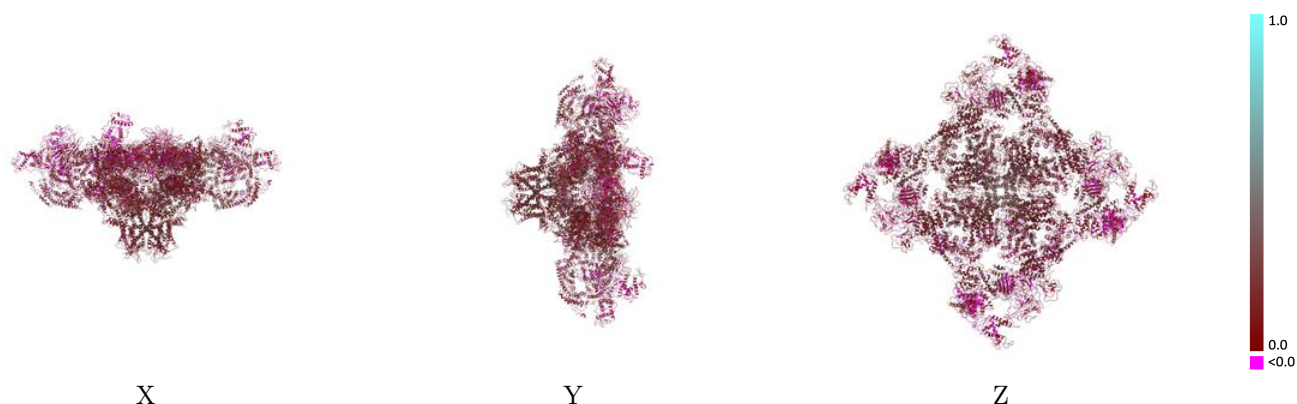
This section contains information regarding the fit between EMDB map EMD-22395 and PDB model 7JMI. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



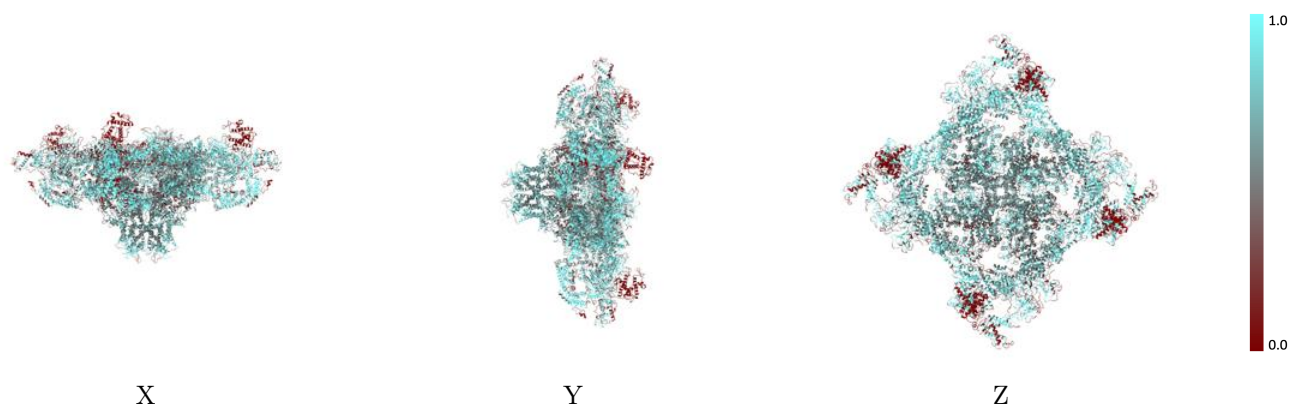
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



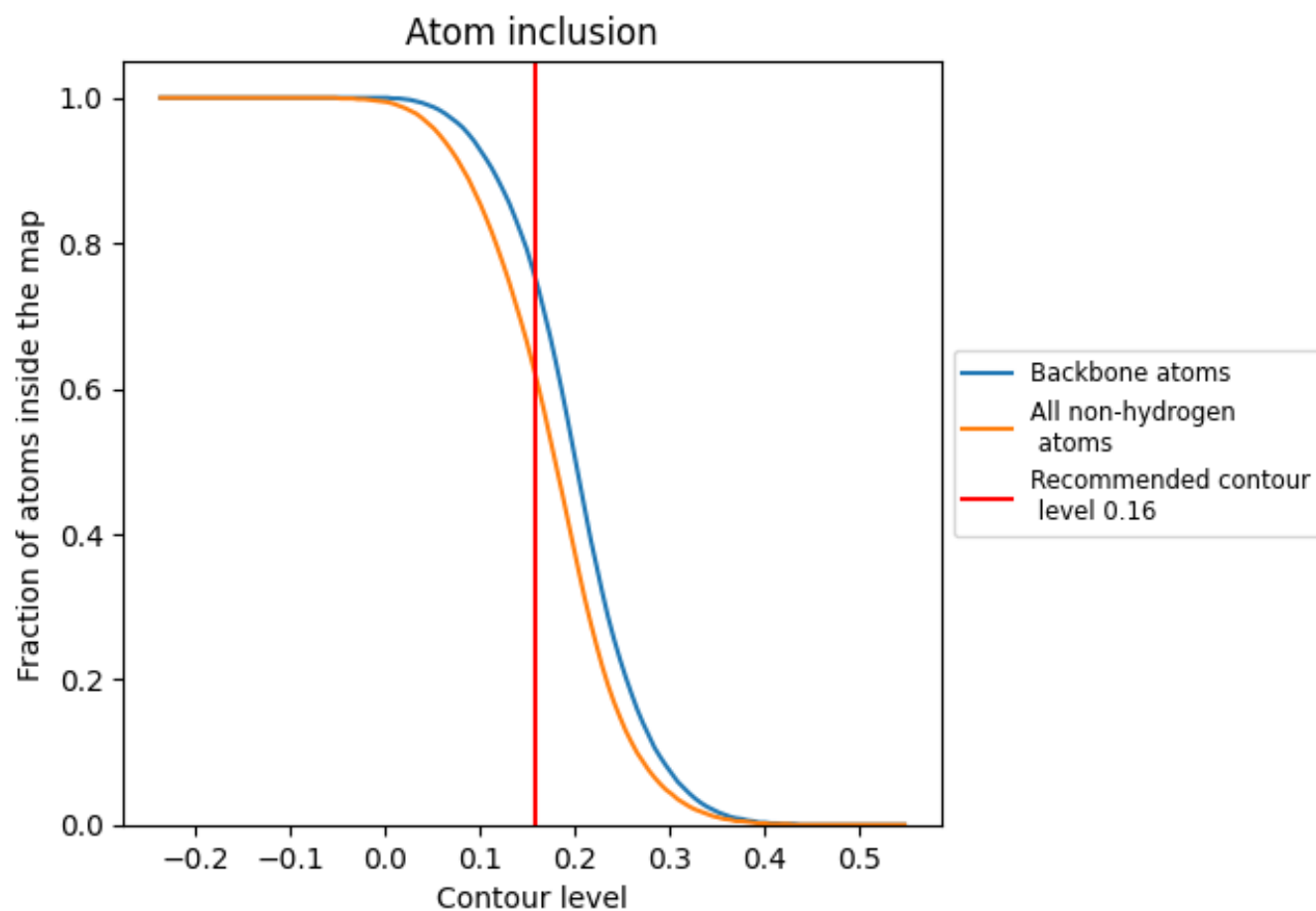
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6140	0.1530
A	0.7020	0.1430
B	0.6330	0.1730
E	0.6190	0.1580
F	0.6700	0.1150
G	0.5960	0.1340
H	0.6220	0.1130
I	0.6040	0.1490
J	0.6440	0.1220

1.0

0.0

<0.0