



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 07:13 PM EST

PDB ID : 7JMH
EMDB ID : EMD-22394
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
- Frame 35 - State 4 (S4)
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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

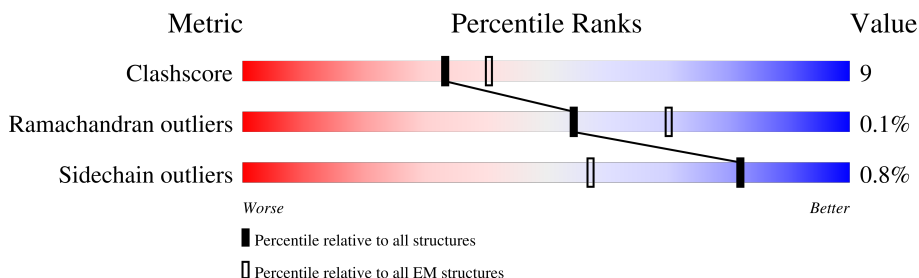
1 Overall quality at a glance

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	<div> <div>30%</div> <div>69%</div> <div>31%</div> </div>
1	F	107	<div> <div>44%</div> <div>68%</div> <div>32%</div> </div>
1	H	107	<div> <div>46%</div> <div>70%</div> <div>30%</div> </div>
1	J	107	<div> <div>43%</div> <div>67%</div> <div>33%</div> </div>
2	B	4687	<div> <div>34%</div> <div>71%</div> <div>18%</div> <div>11%</div> </div>
2	E	4687	<div> <div>38%</div> <div>71%</div> <div>18%</div> <div>11%</div> </div>
2	G	4687	<div> <div>44%</div> <div>70%</div> <div>18%</div> <div>11%</div> </div>
2	I	4687	<div> <div>43%</div> <div>71%</div> <div>18%</div> <div>11%</div> </div>

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 (three-letter code: 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 (three-letter code: CA) (formula: Ca) (labeled as "Ligand of

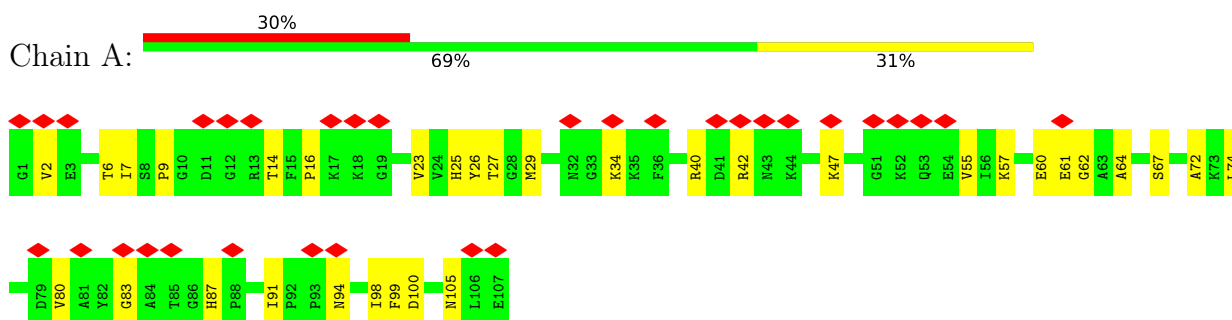
Interest" by depositor).

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

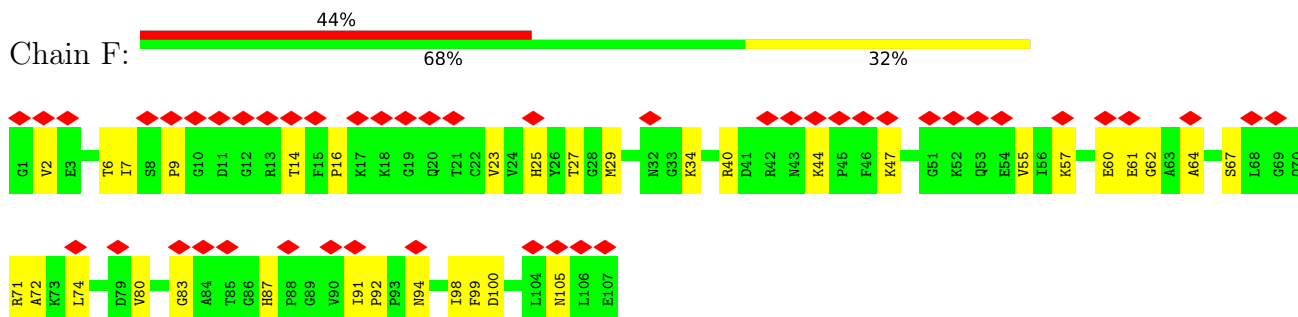
3 Residue-property plots [i](#)

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.

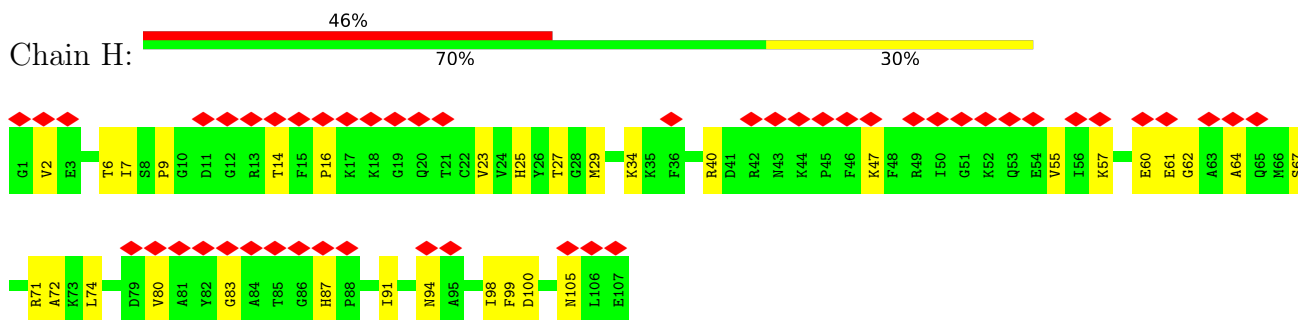
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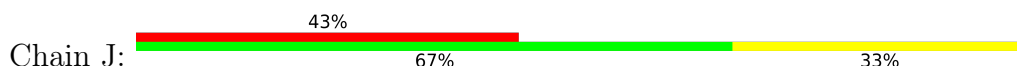
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

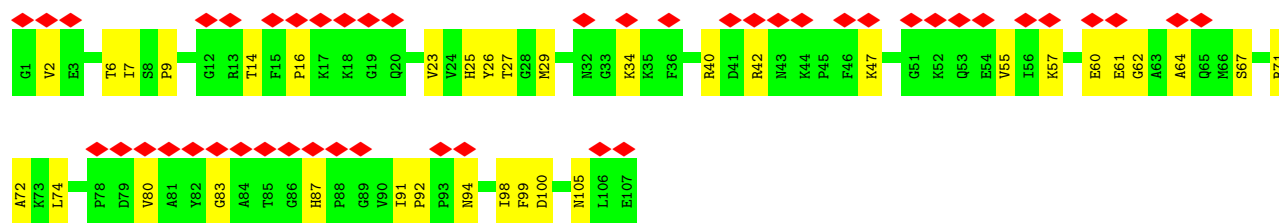


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

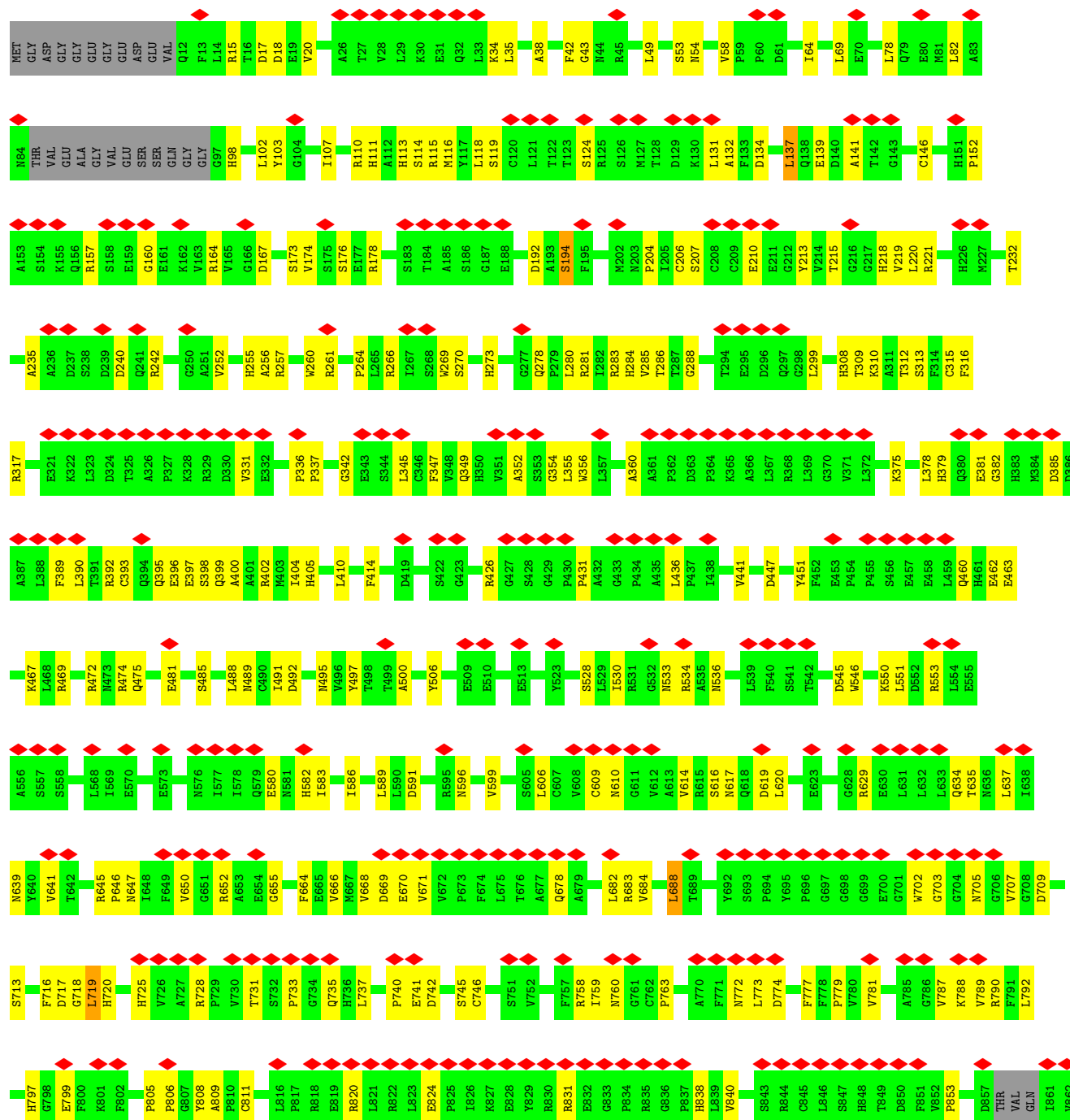


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





• Molecule 2: ryanodine receptor type 1



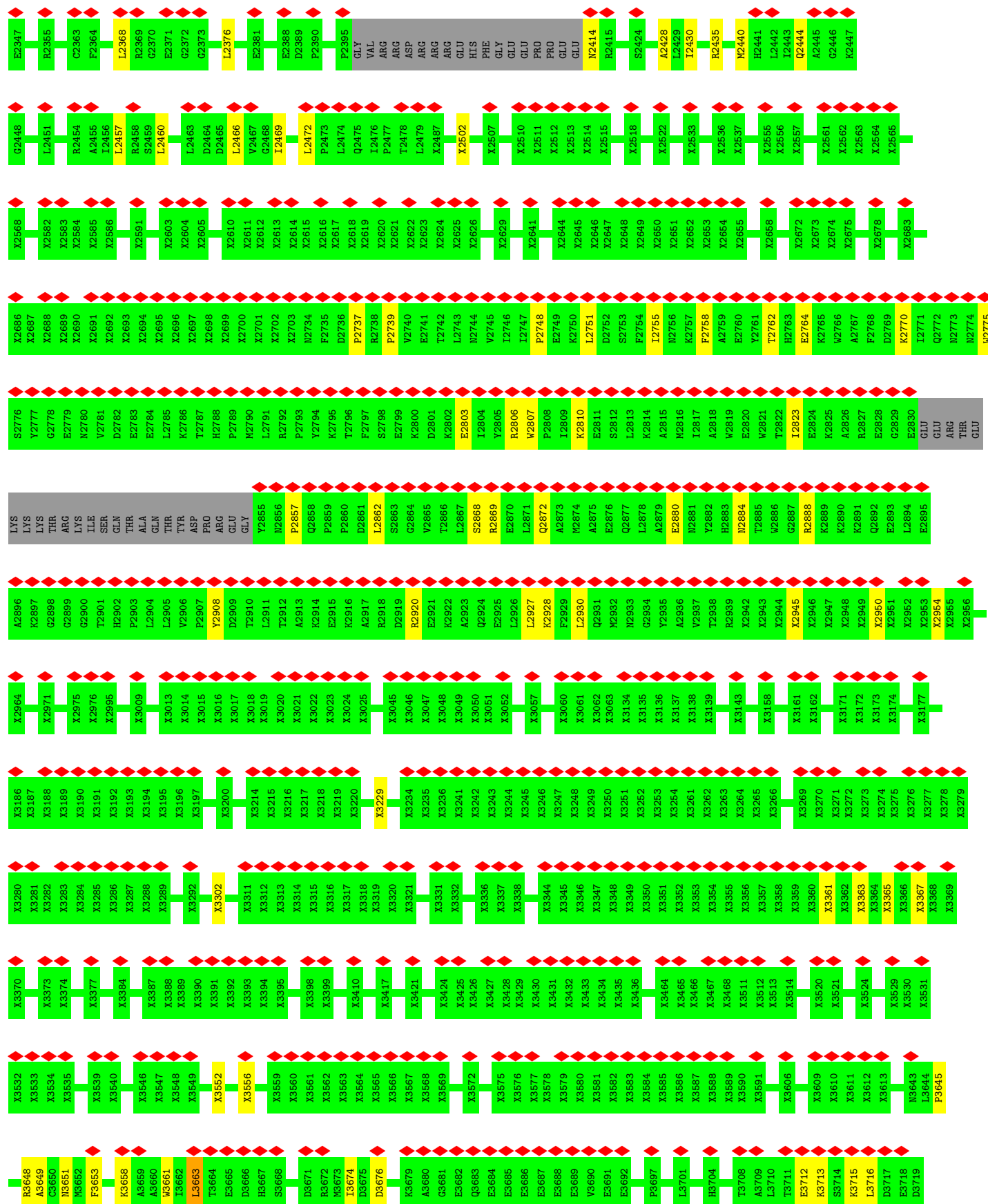


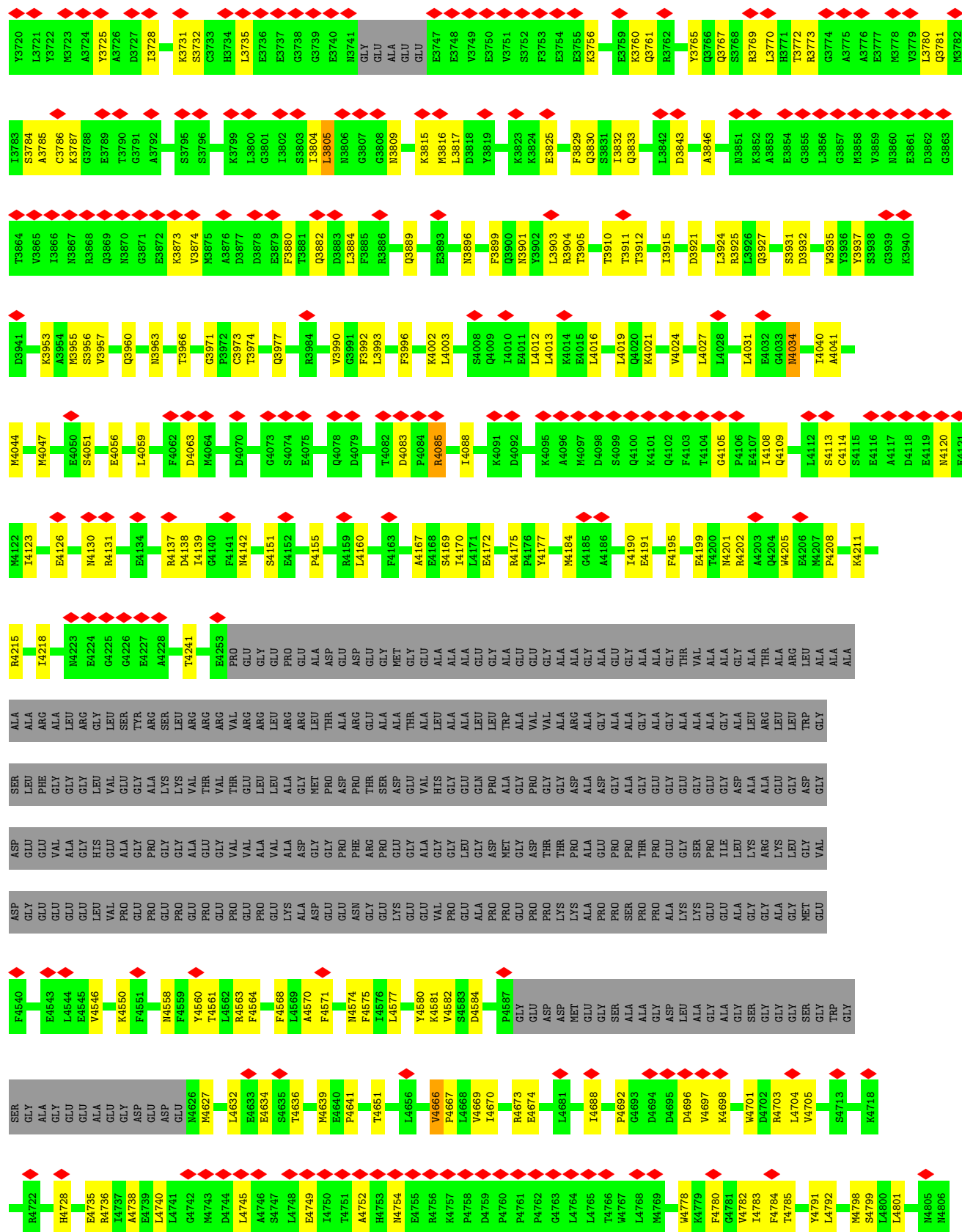


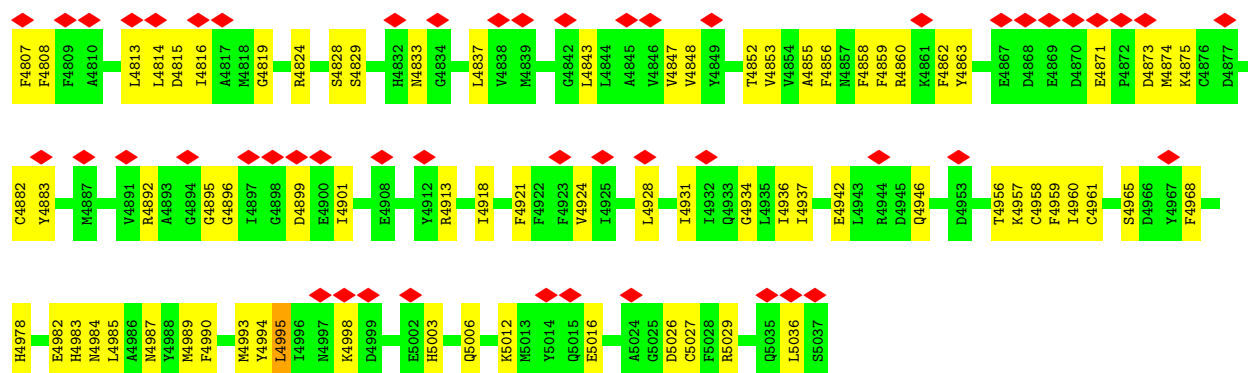


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SER	ARG	TRP	D1070	R1071	V1072	R1073	I1074	F1075	R1076	E1077	E1078	K1079	S1080	Y1081	T1082	V1083	Q1084	S1085	G1086	L1087	W1088	F1089	F1090	E1091	F1092	E1093	A1094	V1095	T1096	L1097	G1098	R1101	V1102	L1103	P1107	E1108	L1109	R1110	P1111	D1112	V1113	E1114	L1115	G1116	A1117	D1118	E1119	L1120	A1121	V1122	W1123	F1124	H1127	F1139	G1140		
Q1003	G1004	ARG	W1005	S1006	Y1007	S1008	A1009	VAL	GLN	ASP	ILE	PRO	ALA	ARG	ARG	ASN	PRO	R1020	Y1024	D1028	E1029	A1030	T1031	K1032	R1033	K1034	S1035	R1036	D1037	S1038	L1039	C1040	Q1041	M1042	V1043	R1044	T1045	L1046	L1047	G1048	Y1049	Y1051	N1052	I1053	E1054	PRO	PRO	ASP	GLN	GLU	PRO	SER	GLN	VAL	GLU	ASN	GLN
E927	T928	L929	K930	T931	L932	L935	H938	V939	G940	M941	A942	D943	E944	K945	A946	E947	N948	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	M960	M961	S962	N963	G964	A968	D971	L972	S973	H974	V975	R976	L977	T978	P979	Q980	A981	T982	T983	R987	L988	A989	G992	A1002						
D857	THR	VAL	GLN	T861	V862	L863	P864	P865	H866	L867	T870	K873	E876	H877	E880	L881	T885	R886	T887	E888	K889	G890	W891	T892	H893	G894	P895	V896	R897	D898	D899	H900	K901	R902	L903	H904	P905	H911	S912	L913	P914	E915	P916	E917	R918	N919	Y920	Q923	M924	S925	G926						
R790	F791	L792	G795	R796	H797	L798	E799	F800	K801	F802	L803	P806	G807	A809	P810	C811	H812	E813	L816	P817	R818	E819	R820	L821	R822	L823	E824	P825	T826	K827	E828	H829	R830	R831	E832	G833	P834	R835	C836	P837	H838	L839	W840	S843	R844	C845	R846	S847	T849	D850	F851	P852	R853				
V707	G708	D709	S713	D717	G718	L719	H720	H725	V726	A727	R728	F729	W730	T731	S732	P733	G734	Q735	H736	L737	L738	A739	P740	E741	D742	V743	V744	S745	C746	S751	V752	R758	L759	N760	G761	C762	P763	N772	L773	D774	G775	L776	F777	F778	P779	V780	V781	A785	V787	K788	V789						
L637	T638	N639	Y640	V641	L644	R645	P646	N647	T648	F649	V650	R651	R652	G655	Q658	W662	Y663	F664	E665	V666	V667	V668	D669	E670	V671	V672	P673	S674	L675	T676	A677	Q678	L682	R683	V684	G685	L688	Y692	S693	P694	Y695	P696	G697	G698	G699	E700	G701	W702	G703	G704	N705	G706					
I569	E570	S571	P572	E573	V574	L575	N576	I577	I578	Q579	R580	N581	H582	I583	I586	I587	S588	L589	L590	A591	G594	R595	N596	V599	L603	C504	S505	L506	C507	V508	C509	N610	G611	V614	R615	N617	D619	L620	L621	T622	E623	P627	G628	R629	E630	L631	L632	L633	T635	N636							
Y496	Y497	T498	A500	A501	H502	Y506	E513	A440	K516	V519	N520	Y523	E524	S528	L529	I530	R531	G532	N533	R534	A535	N536	C537	A538	L539	F540	S541	T542	N543	L544	D545	W546	V547	V548	S549	K550	L551	D552	R553	L554	E555	A556	S557	S558	G559	I560	L561	L564	Y565	L568							
P364	K365	A366	L367	R368	G370	V371	L372	K373	K374	K375	L378	H379	Q380	Y381	G382	H383	M384	D385	E453	A387	L388	F389	L390	T391	R392	C393	Q394	Q395	E396	E397	S398	Q399	A400	A401	R402	M403	I404	H405	S406	T407	A408	G409	L410	Y411	N412	K416	D419	S422	G423	K424	P425	G427	S428				
V285	T286	T287	G288	R289	E295	D296	Q297	A304	H308	T309	K310	A311	T312	S313	C315	F316	R317	V318	S319	K320	E321	K322	L323	D324	T325	A326	P327	K328	R329	D330	V331	P336	P337	Y341	G342	E343	S344	L345	C346	F347	V348	Q349	A352	S353	G354	L355	W356	A360	A361	P362	D363						

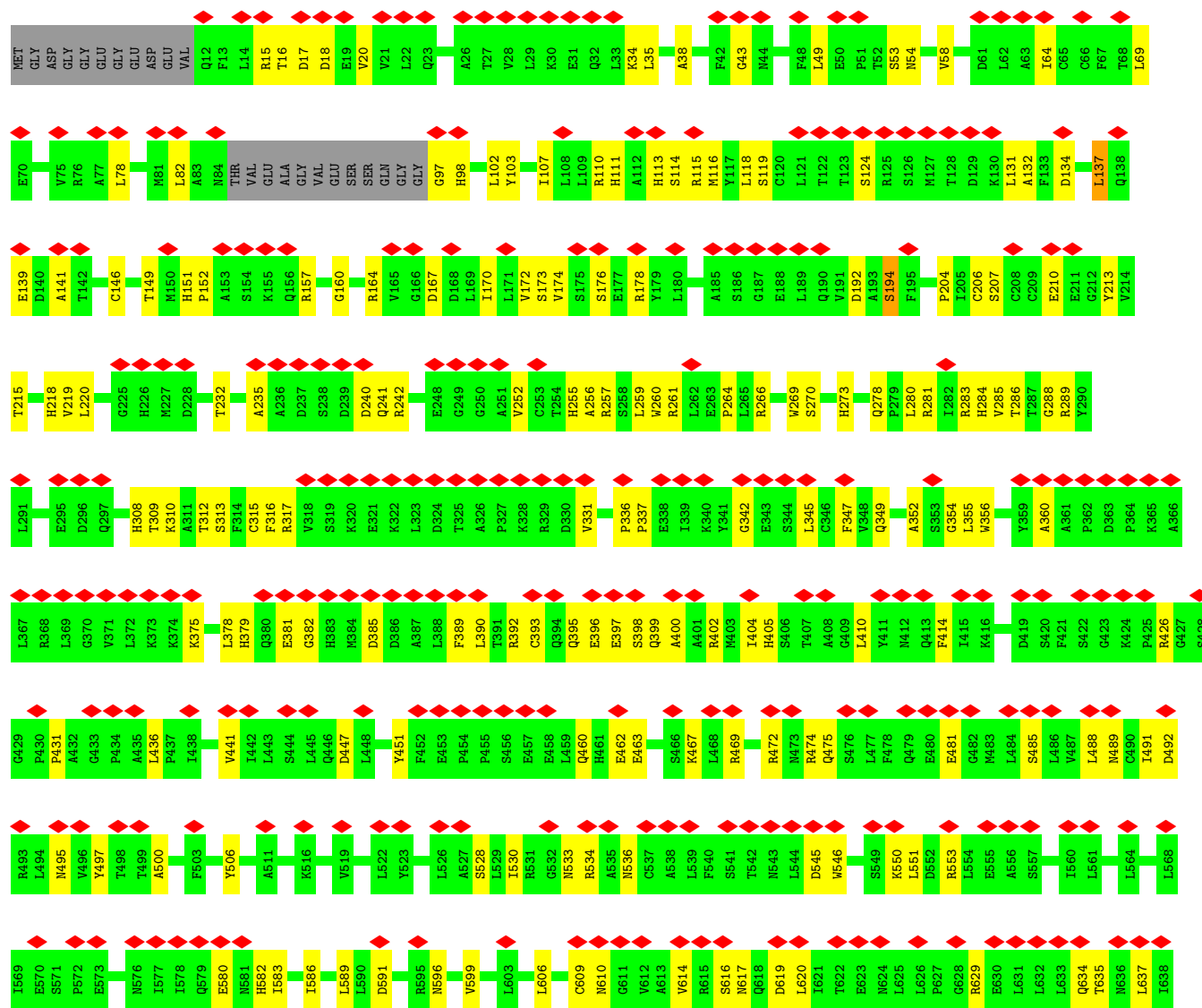
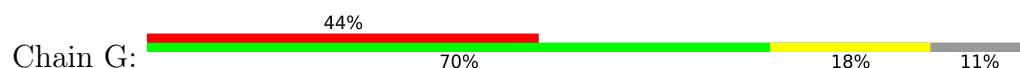


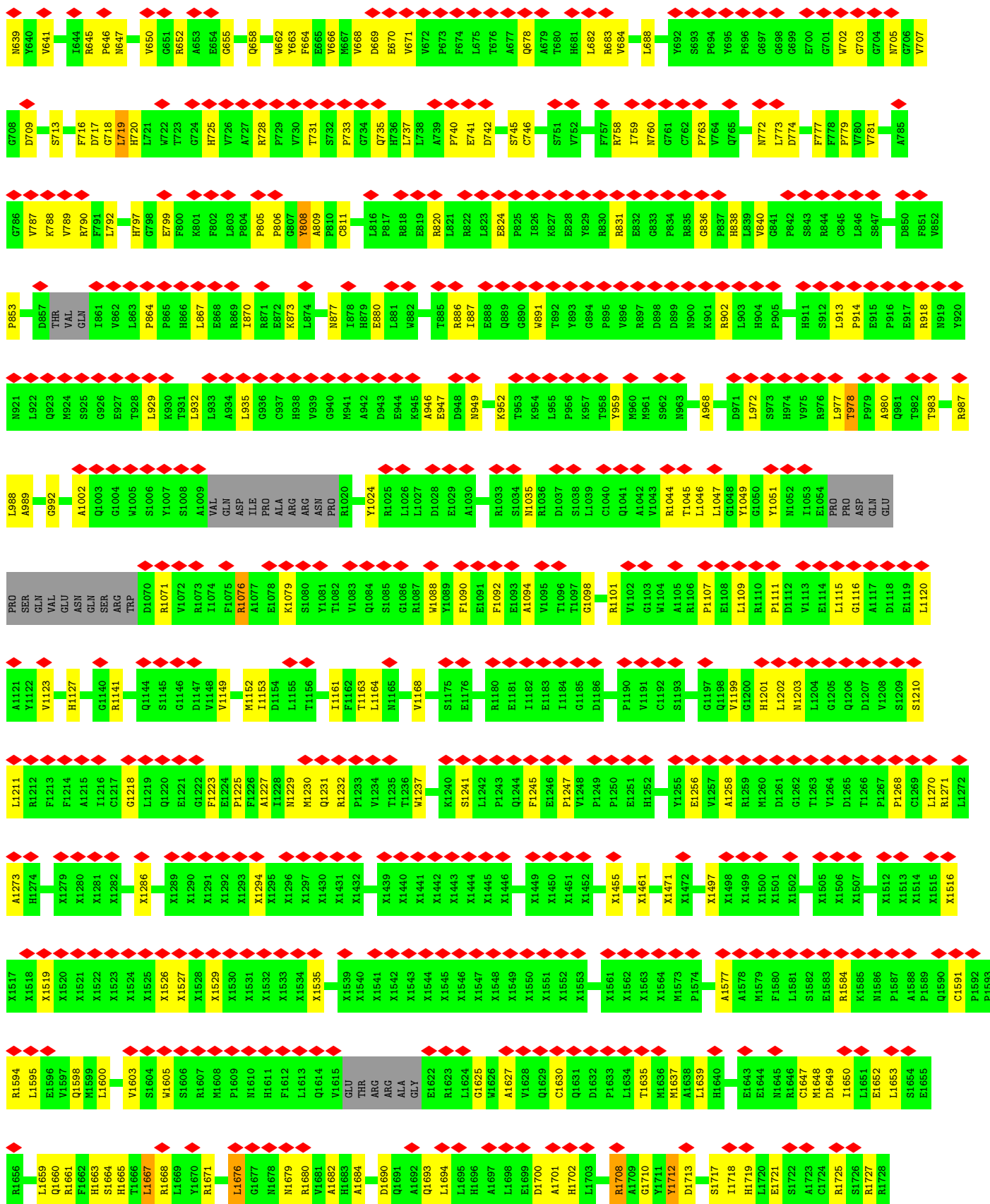






• Molecule 2: ryanodine receptor type 1

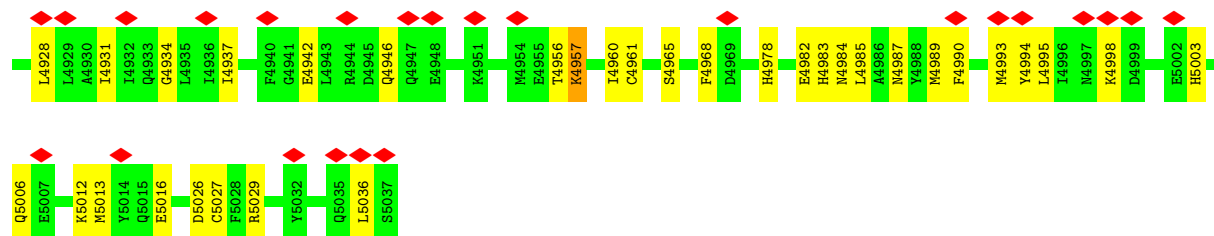




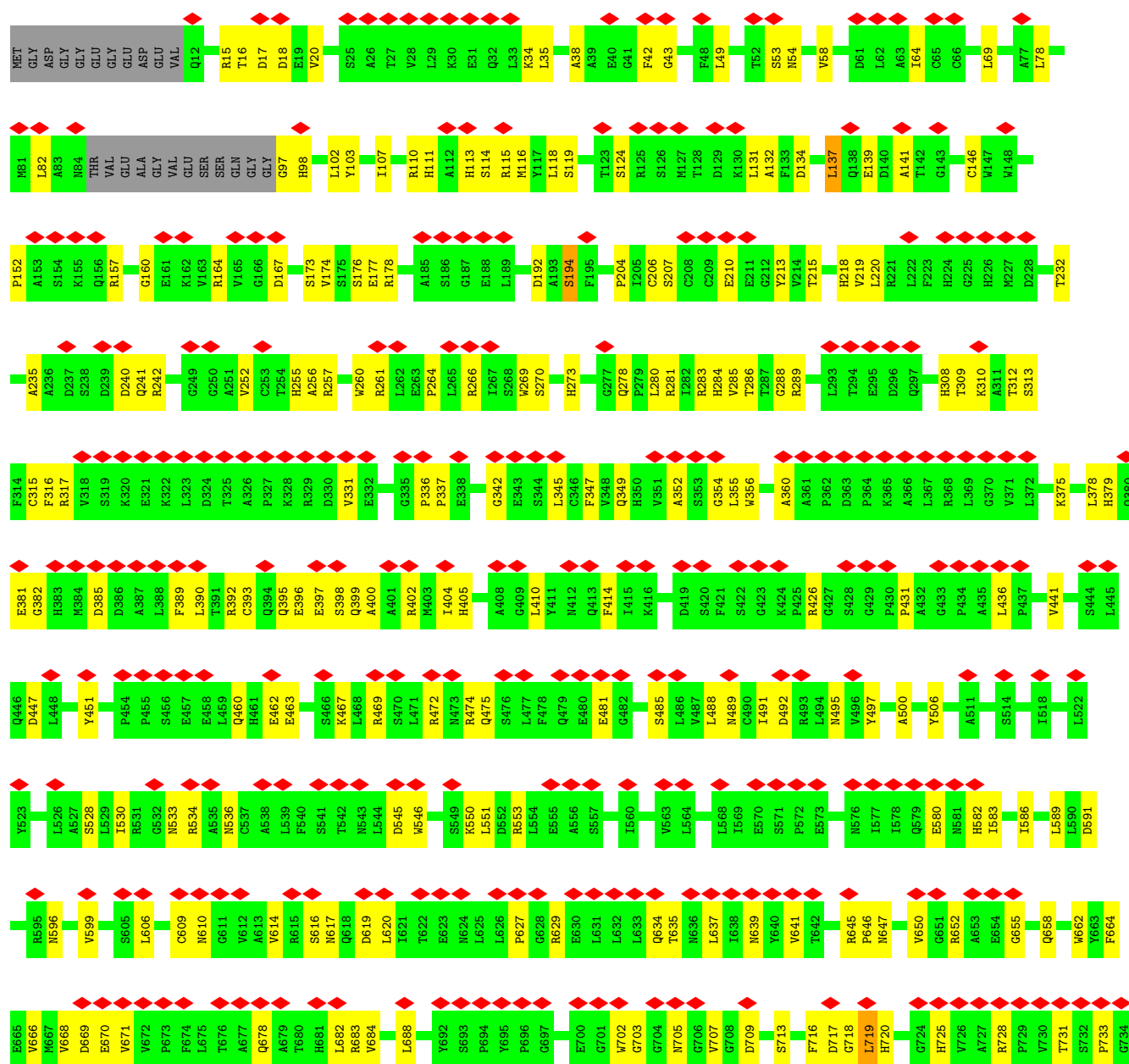
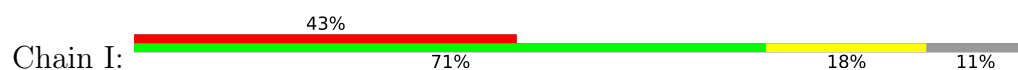


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X3377	X3380	X3381	X3384	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3398	X3399	X3409	X3410	X3413	X3414	X3415	X3416	X3417	X3418	X3419	X3420	X3421	X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437	X3438	X3439	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3514	X3515										
X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3324	X3325	X3328	X3332	X3333	X3337	X3338	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3373	X3374									
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X3045	X3046	X3047	X3048	X3049	X3053	X3056	X3057	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3158	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3177	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3198	X3199	X3200	X3214	X3215	X3216	X3217										
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F2754	I2755	H2756	K2757	F2758	A2759	E2760	V2761	T2762	H2763	E2764	K2765	A2766	A2767	F2768	D2769	K2770	I2771	Q2772	H2773	H2774	W2775	S2776	V2777	G2778	E2779	L2785	A2786	T2787	H2788	P2789	L2790	L2791	R2792	P2793	L2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	K2806	W2807	F2808	L2809	K2810	E2811	S2812	L2813						





• Molecule 2: ryanodine receptor type 1







LYS	LYS	THR	THR	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	ASP	PRO	ARG	GLU	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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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	0.486	Depositor
Minimum map value	-0.257	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.027	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	0.33	0/834	0.59	0/1123
1	F	0.33	0/834	0.59	0/1123
1	H	0.33	0/834	0.59	0/1123
1	J	0.33	0/834	0.59	0/1123
2	B	0.34	0/25428	0.58	6/34534 (0.0%)
2	E	0.34	0/25428	0.58	6/34534 (0.0%)
2	G	0.34	0/25428	0.58	6/34534 (0.0%)
2	I	0.34	0/25428	0.58	6/34534 (0.0%)
All	All	0.34	0/105048	0.58	24/142628 (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	23
2	E	0	23
2	G	0	23
2	I	0	23
All	All	0	92

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1667	LEU	CA-CB-CG	6.02	129.15	115.30
2	G	1667	LEU	CA-CB-CG	6.02	129.14	115.30
2	B	1667	LEU	CA-CB-CG	5.99	129.08	115.30
2	B	719	LEU	CA-CB-CG	5.98	129.06	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	719	LEU	CA-CB-CG	5.98	129.06	115.30

There are no chirality outliers.

5 of 92 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	LEU	Peptide
2	B	1676	LEU	Peptide
2	B	194	SER	Peptide
2	B	240	ASP	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	20	0
1	H	818	0	824	18	0
1	J	818	0	824	20	0
2	B	29369	0	24713	491	0
2	E	29369	0	24712	503	0
2	G	29369	0	24716	502	0
2	I	29369	0	24713	489	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	102150	2033	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 2033 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:4859:PHE:HA	2:G:4862:PHE:CD2	1.88	1.08
2:G:4859:PHE:HA	2:G:4862:PHE:HD2	1.28	0.97
2:E:4859:PHE:HA	2:E:4862:PHE:CD2	2.05	0.92
2:E:4859:PHE:HA	2:E:4862:PHE:HD2	1.43	0.83
2:G:4859:PHE:CA	2:G:4862:PHE:HD2	1.99	0.73

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%)	95 (90%)	10 (10%)	0	100	100
1	F	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	H	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	J	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
2	B	3235/4687 (69%)	2848 (88%)	382 (12%)	5 (0%)	47	81
2	E	3235/4687 (69%)	2849 (88%)	381 (12%)	5 (0%)	47	81
2	G	3235/4687 (69%)	2848 (88%)	382 (12%)	5 (0%)	47	81
2	I	3235/4687 (69%)	2850 (88%)	380 (12%)	5 (0%)	47	81
All	All	13360/19176 (70%)	11775 (88%)	1565 (12%)	20 (0%)	54	85

5 of 20 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

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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%)	2473 (99%)	20 (1%)	81	89
2	E	2493/3209 (78%)	2473 (99%)	20 (1%)	81	89
2	G	2493/3209 (78%)	2472 (99%)	21 (1%)	81	89
2	I	2493/3209 (78%)	2473 (99%)	20 (1%)	81	89
All	All	10324/13188 (78%)	10243 (99%)	81 (1%)	82	89

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	4913	ARG
2	I	4034	ASN
2	G	4984	ASN
2	I	1141	ARG
2	I	4798	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	4130	ASN
2	I	1719	HIS
2	G	4984	ASN
2	I	379	HIS

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Mol	Chain	Res	Type
2	I	3889	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	B	12
2	I	12

Continued on next page...

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Mol	Chain	Number of breaks
2	E	12
2	G	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	44.41
1	I	3613:UNK	C	3639:THR	N	44.36
1	E	3613:UNK	C	3639:THR	N	44.35
1	G	3613:UNK	C	3639:THR	N	44.35
1	B	3163:UNK	C	3170:UNK	N	16.42

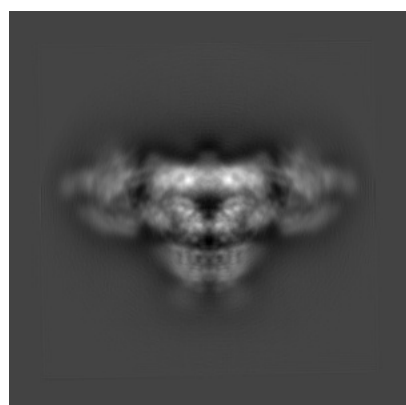
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22394. These allow visual inspection of the internal detail of the map and identification of artifacts.

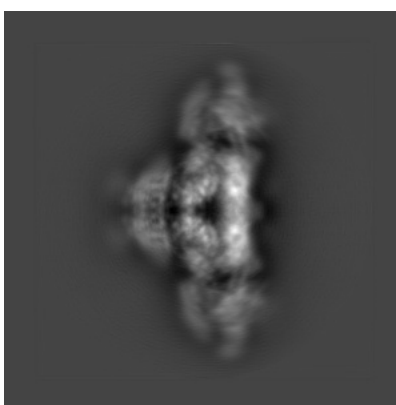
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

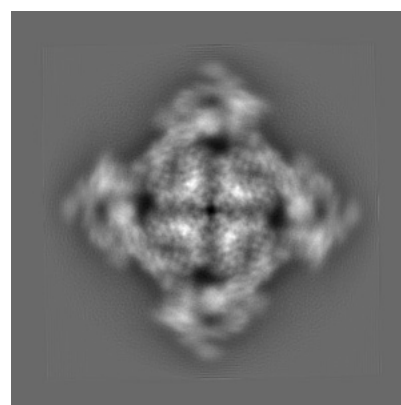
6.1.1 Primary map



X



Y

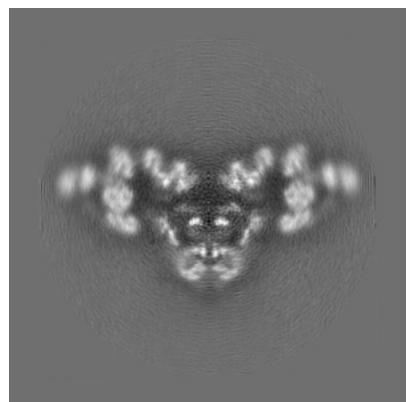


Z

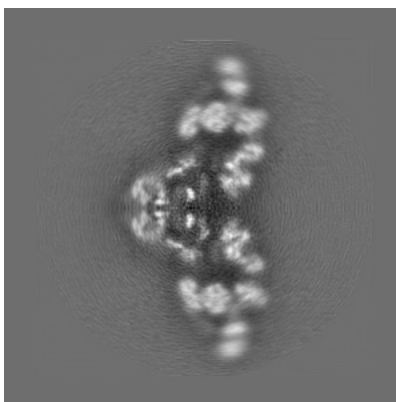
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

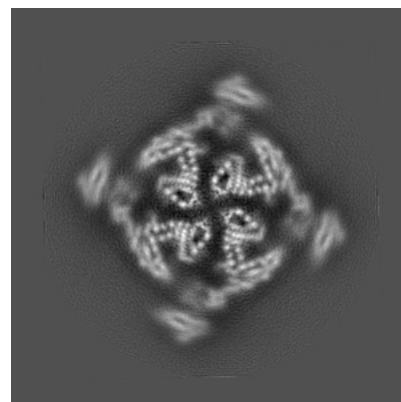
6.2.1 Primary map



X Index: 200



Y Index: 200

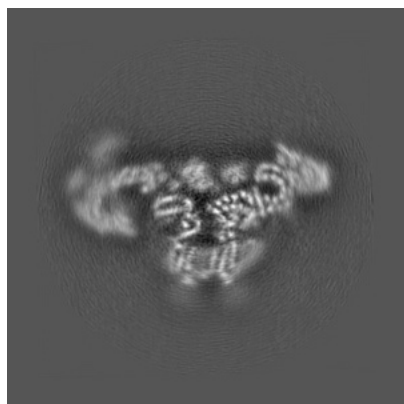


Z Index: 200

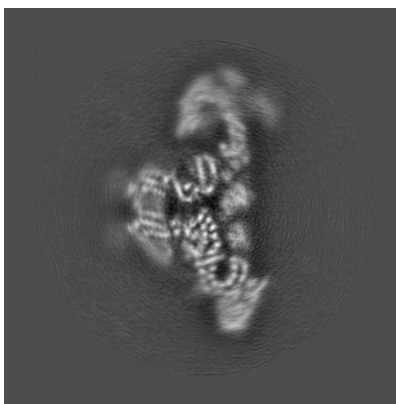
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

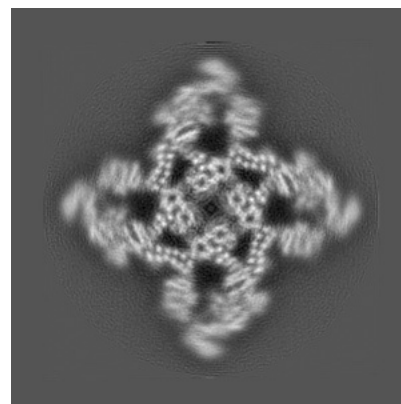
6.3.1 Primary map



X Index: 177



Y Index: 177



Z Index: 227

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

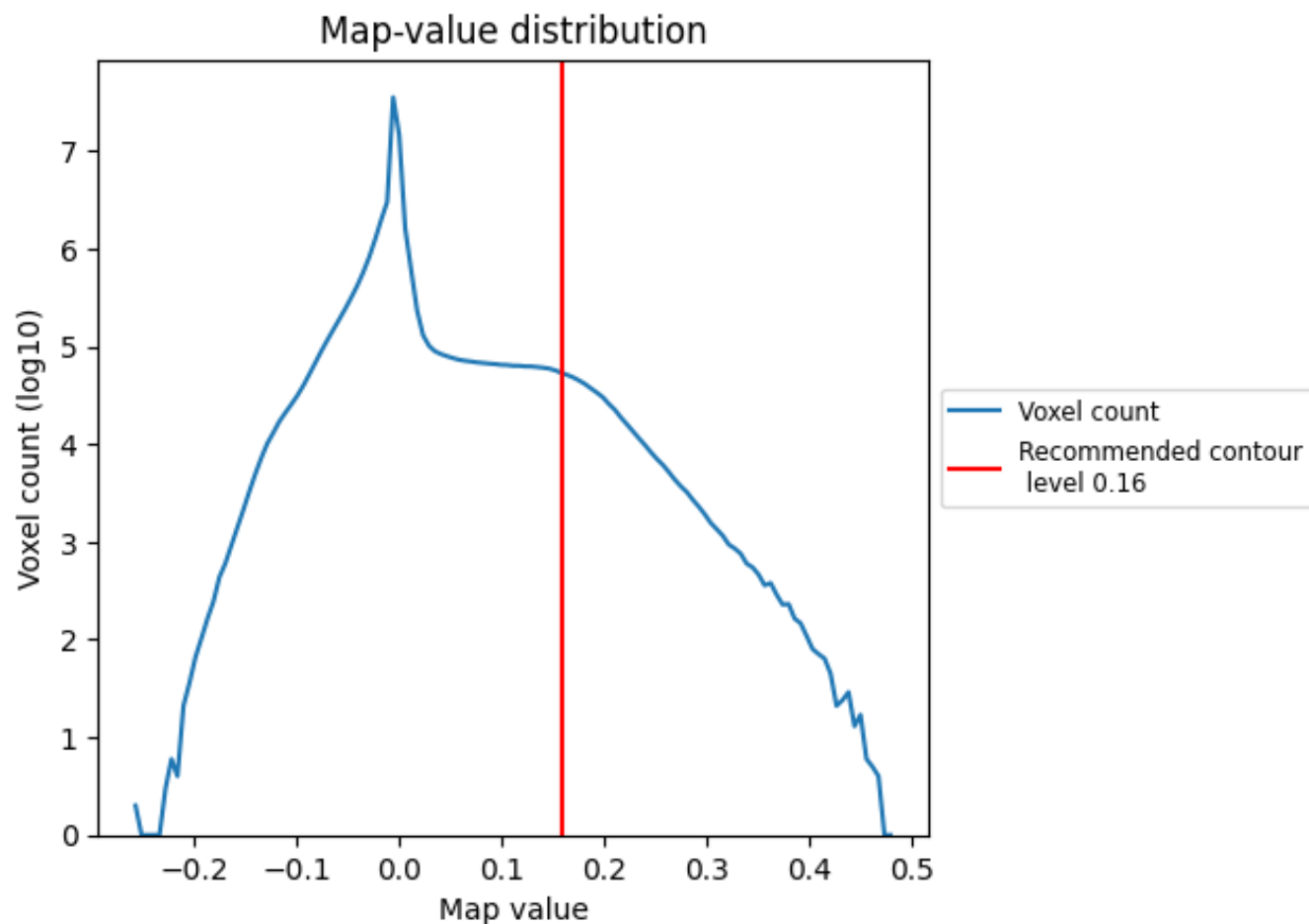
6.5 Mask visualisation

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

7 Map analysis [i](#)

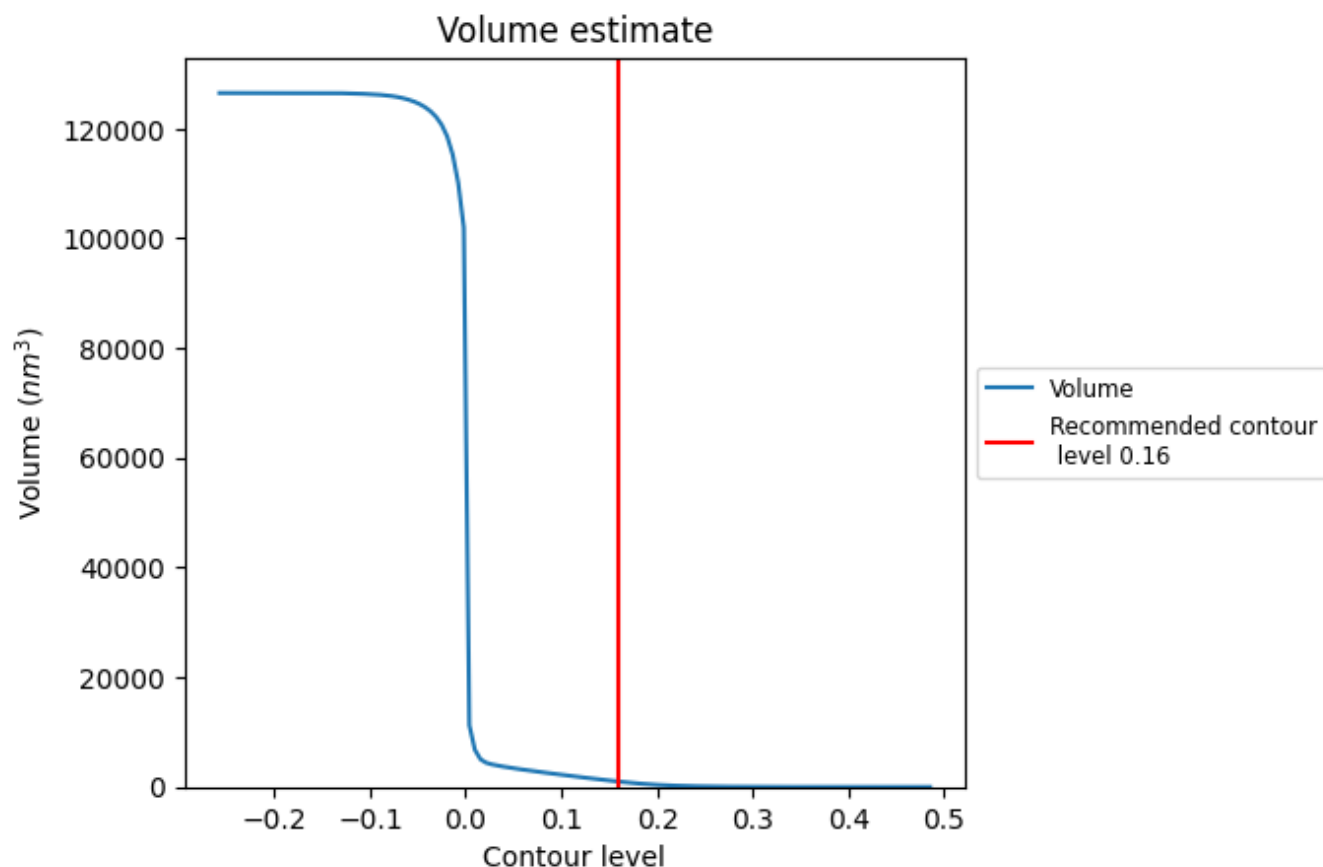
This section contains the results of statistical analysis of the map.

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.

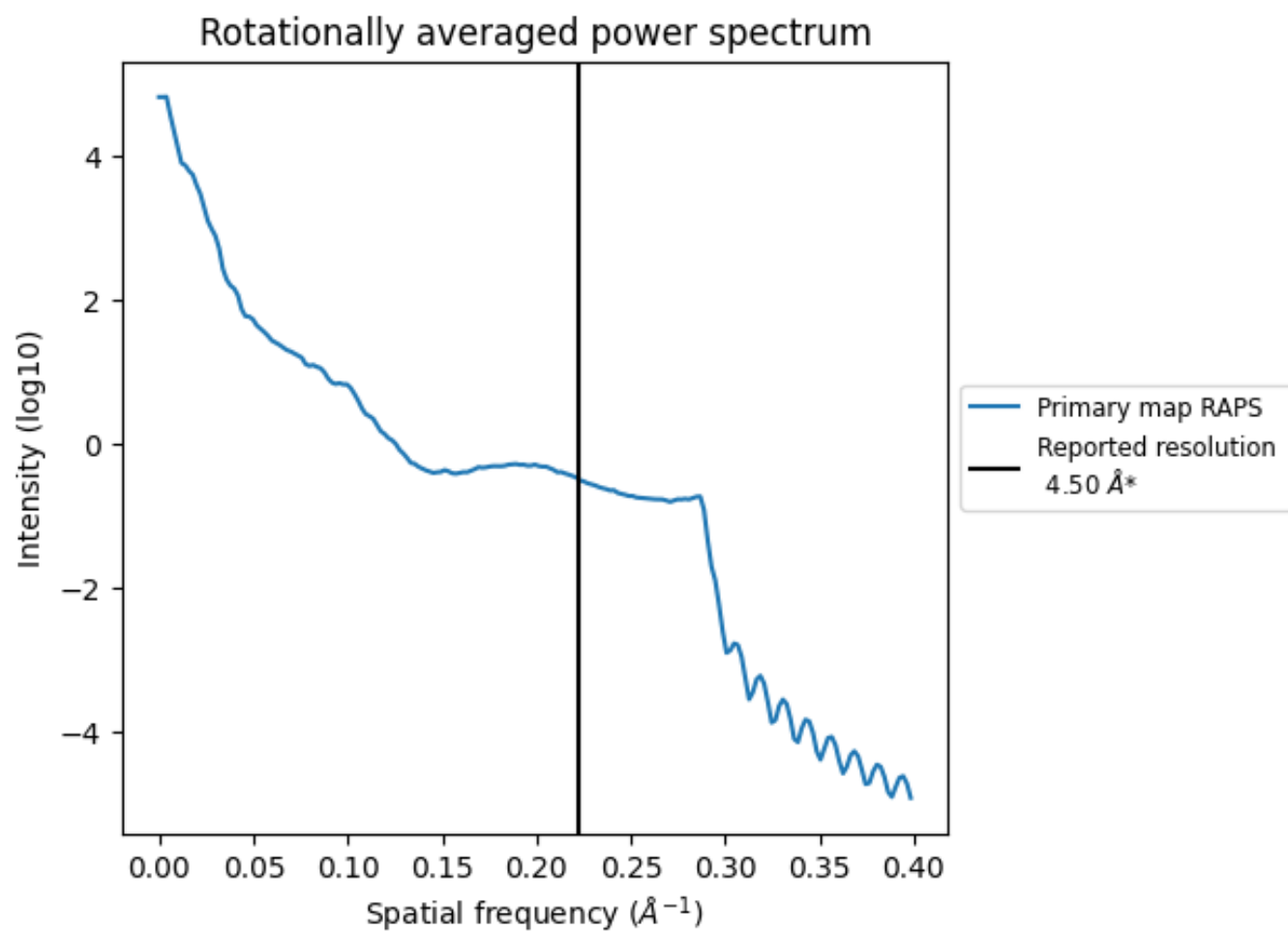
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 979 nm³; this corresponds to an approximate mass of 884 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

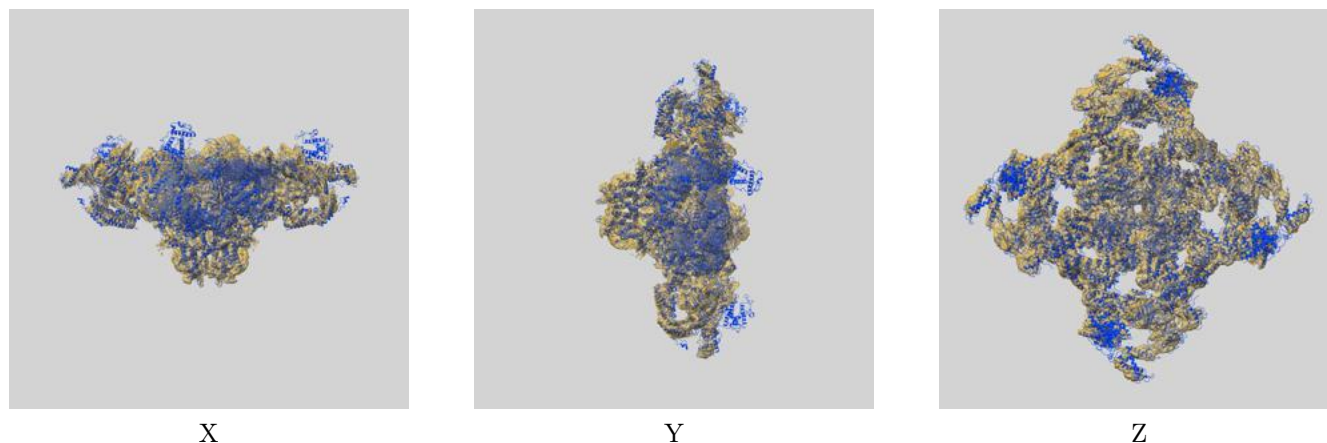
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

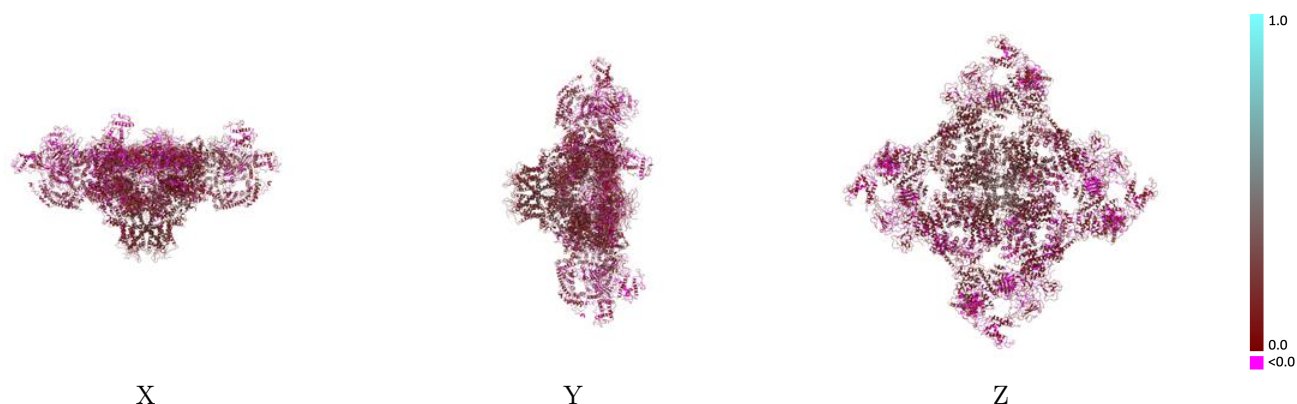
This section contains information regarding the fit between EMDB map EMD-22394 and PDB model 7JMH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



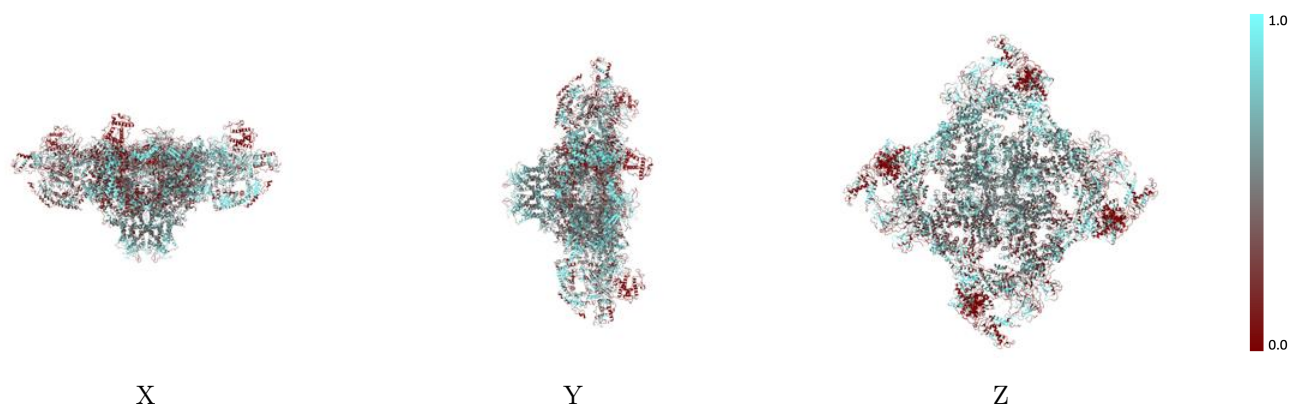
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



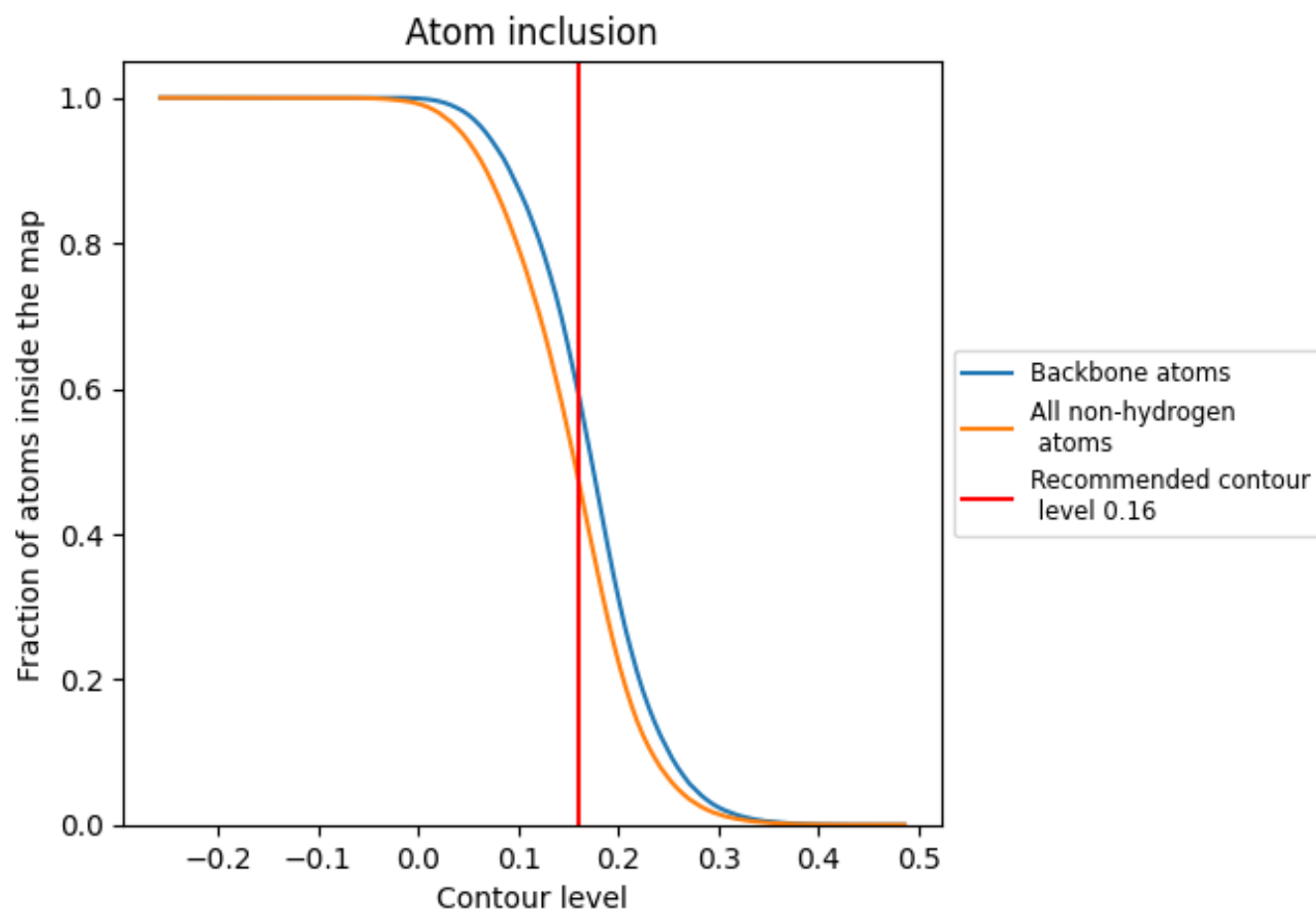
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 59% of all backbone atoms, 47% 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	<div></div> 0.4748	<div></div> 0.1320
A	<div></div> 0.5620	<div></div> 0.1390
B	<div></div> 0.5148	<div></div> 0.1680
E	<div></div> 0.4812	<div></div> 0.1330
F	<div></div> 0.4888	<div></div> 0.1070
G	<div></div> 0.4453	<div></div> 0.1070
H	<div></div> 0.4529	<div></div> 0.1190
I	<div></div> 0.4560	<div></div> 0.1230
J	<div></div> 0.4690	<div></div> 0.1180

