



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:19 PM UTC

PDB ID : 5J8V / pdb_00005j8v
EMDB ID : EMD-8073
Title : Structure of rabbit ryanodine receptor RyR1 open state activated by calcium ion
Authors : Wang, X.; Wei, R.; Yin, C.; Sun, F.
Deposited on : 2016-04-08
Resolution : 4.90 Å(reported)
Based on initial model : 3J8H

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:

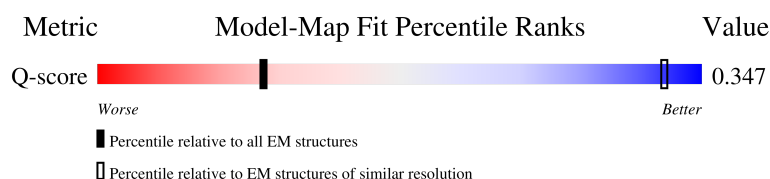
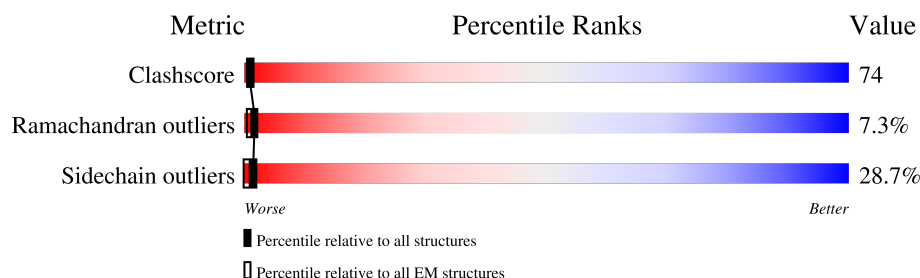
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.90 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	1274 (4.40 - 5.40)

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	5037	8% 37% 22% 7% 31%
1	B	5037	8% 37% 22% 7% 31%
1	C	5037	8% 37% 23% 7% 31%
1	D	5037	8% 37% 22% 7% 31%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 73616 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.

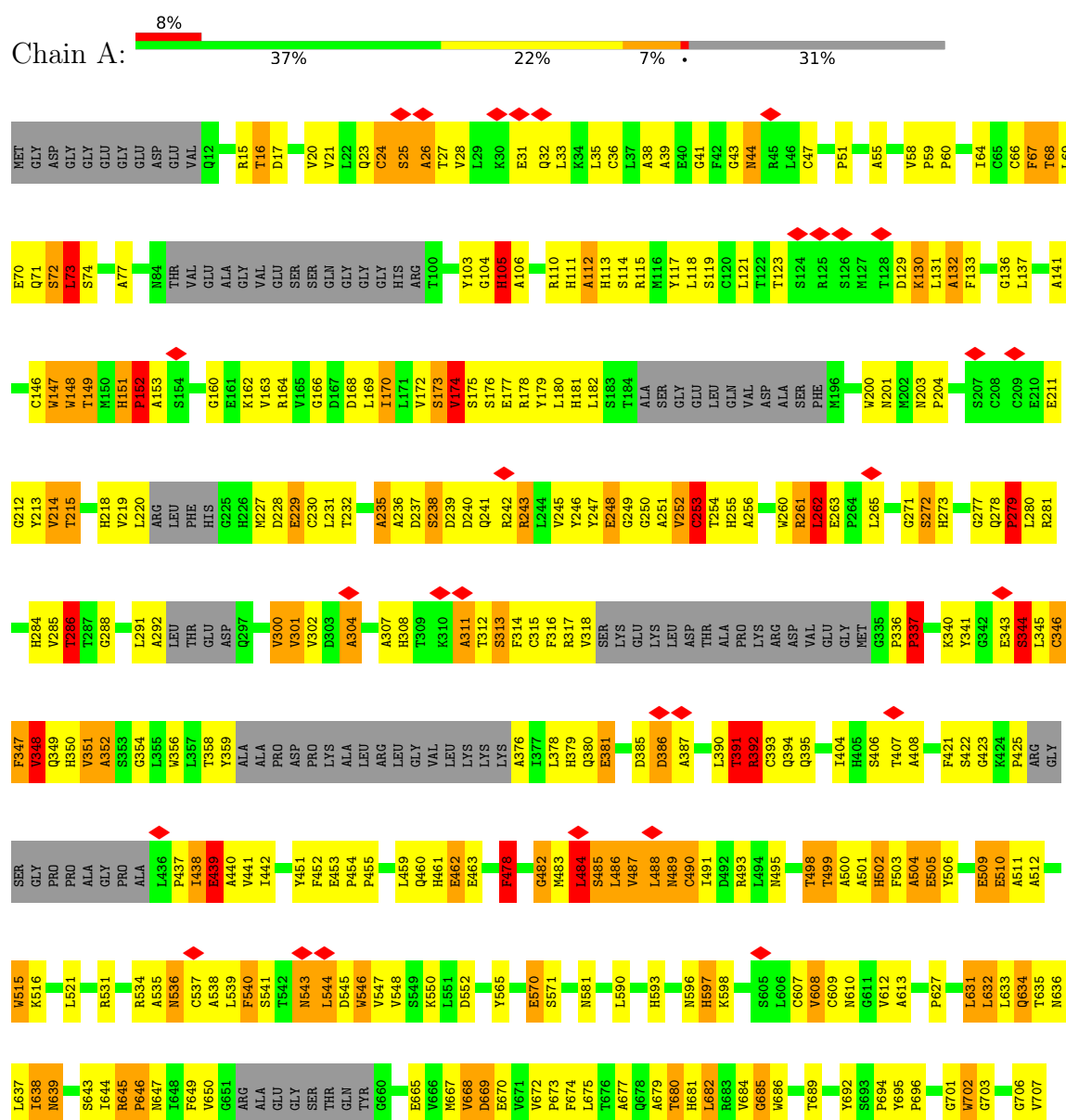
- Molecule 1 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	B	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	C	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	D	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0

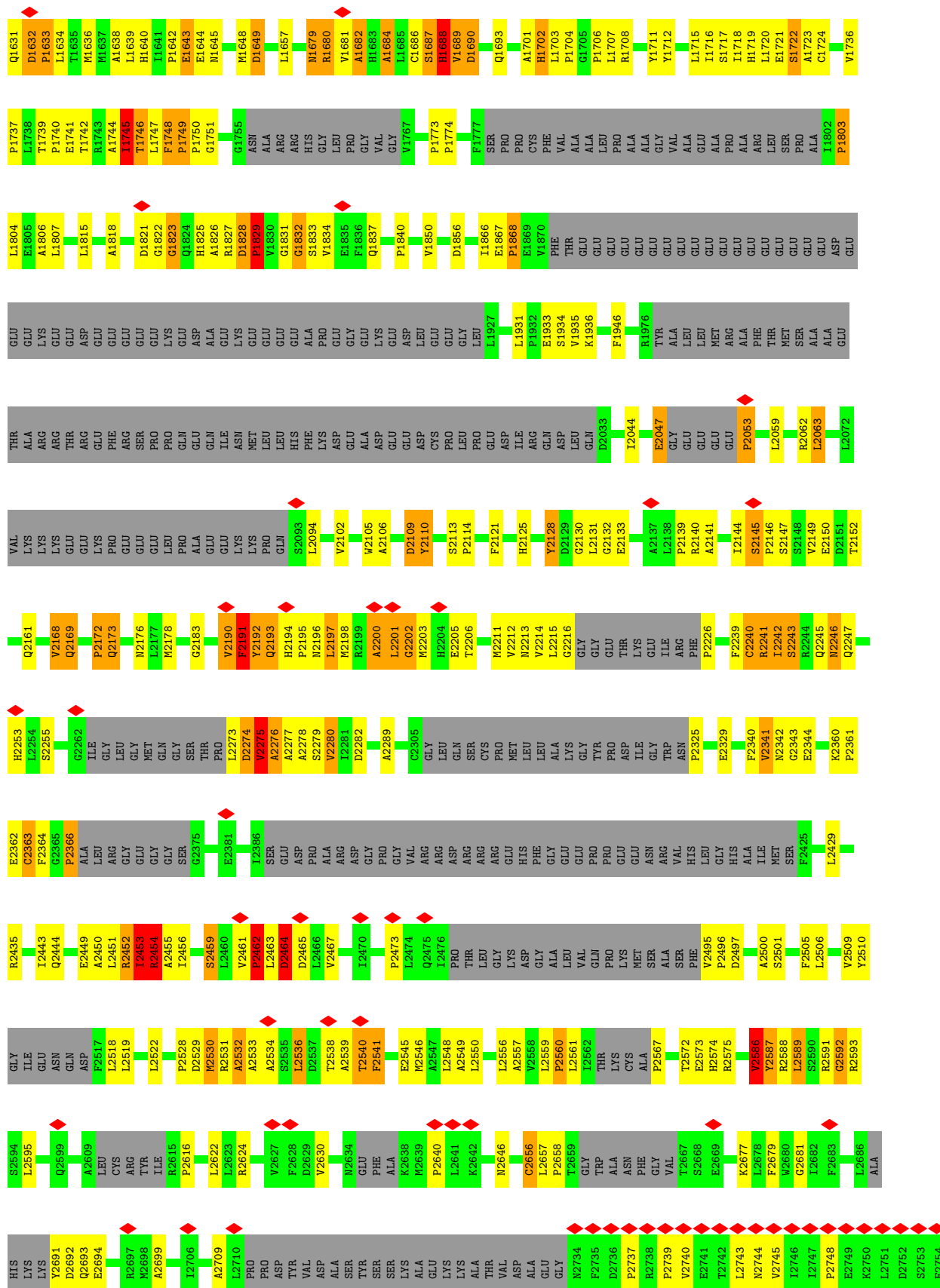
3 Residue-property plots

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 1

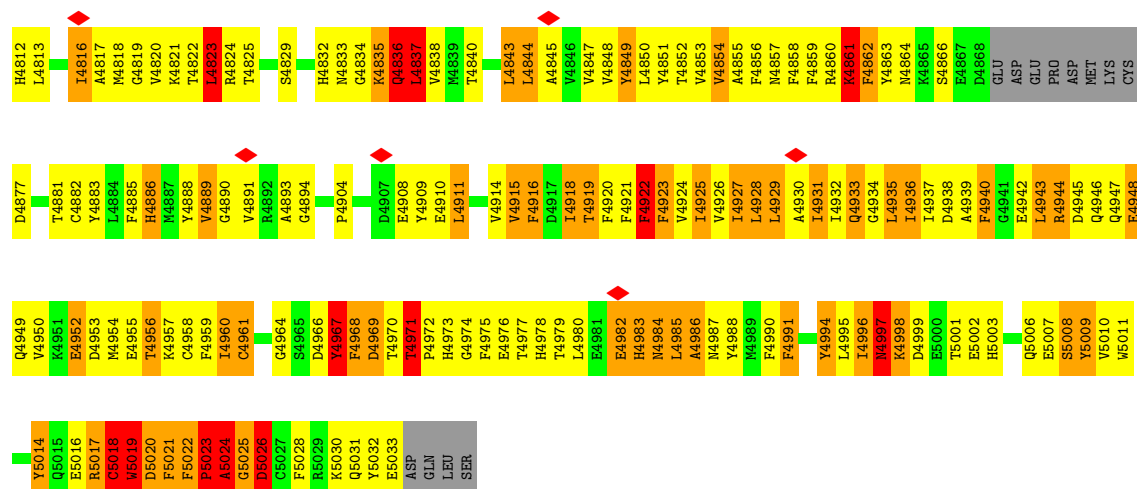




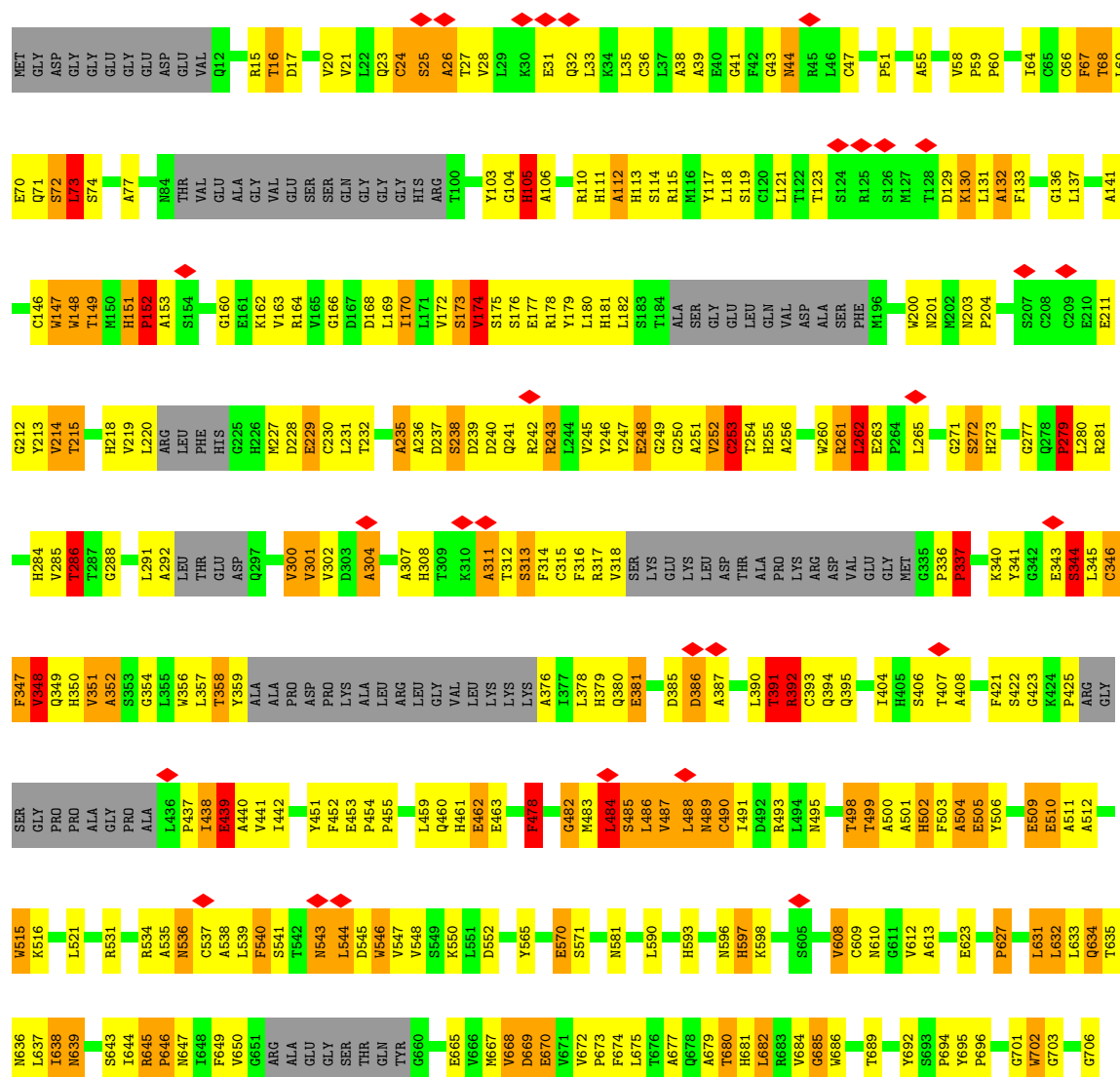




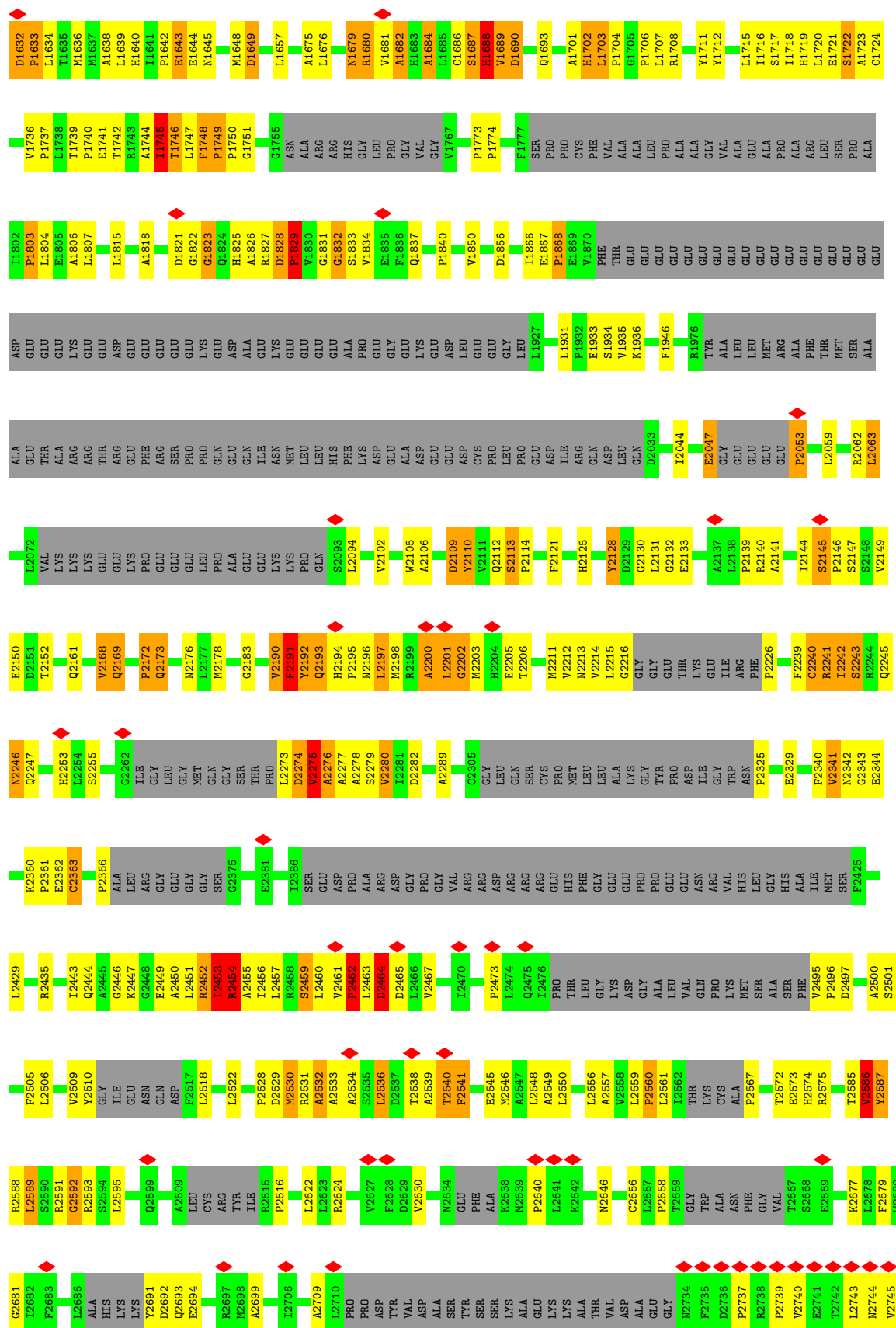




• Molecule 1: Ryanodine receptor 1

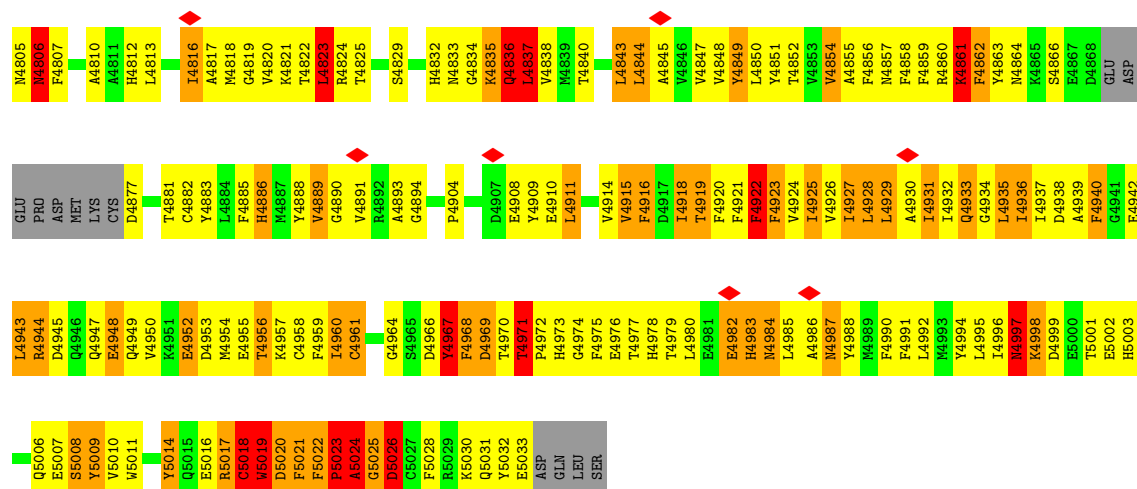




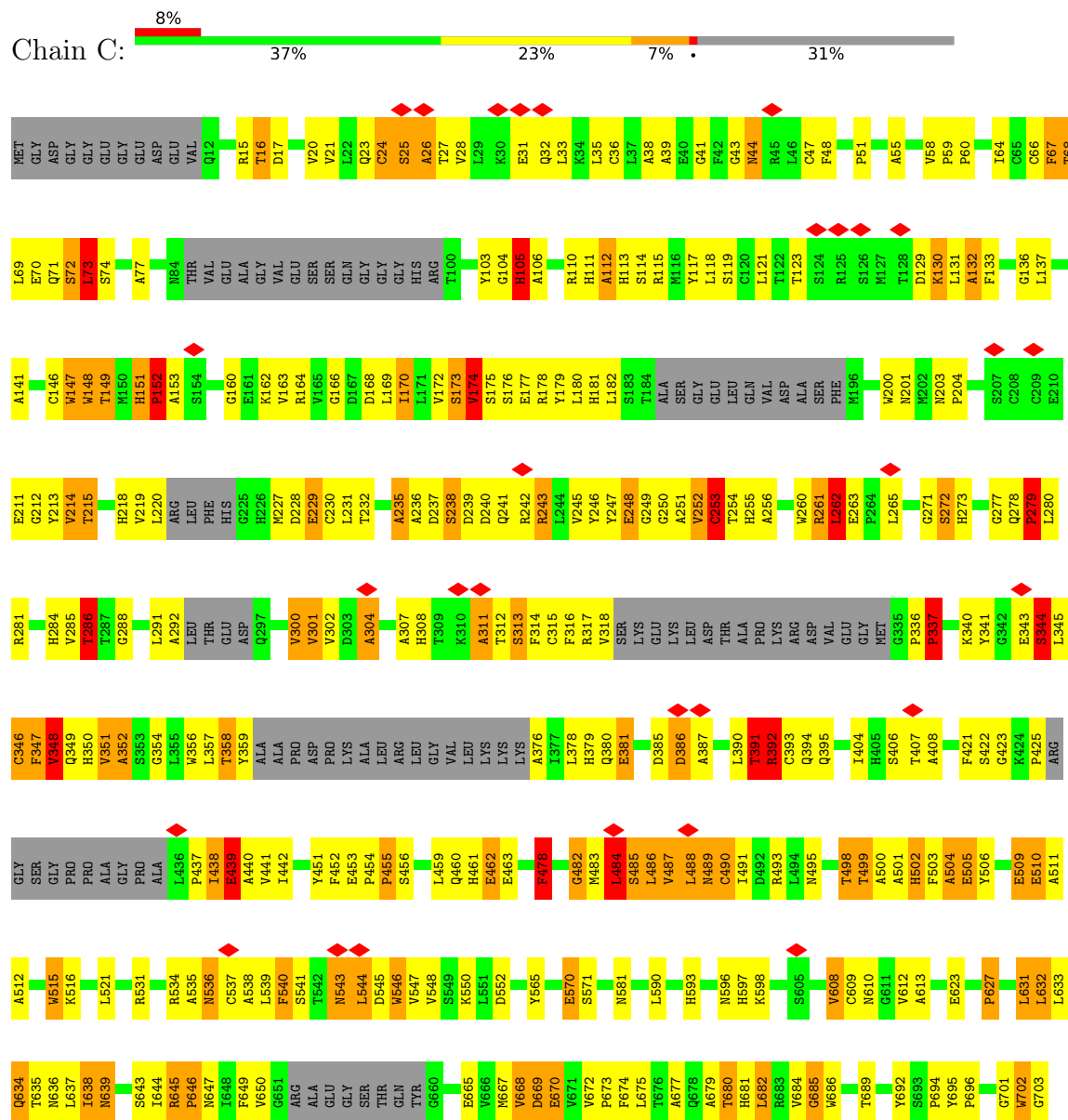








• Molecule 1: Ryanodine receptor 1



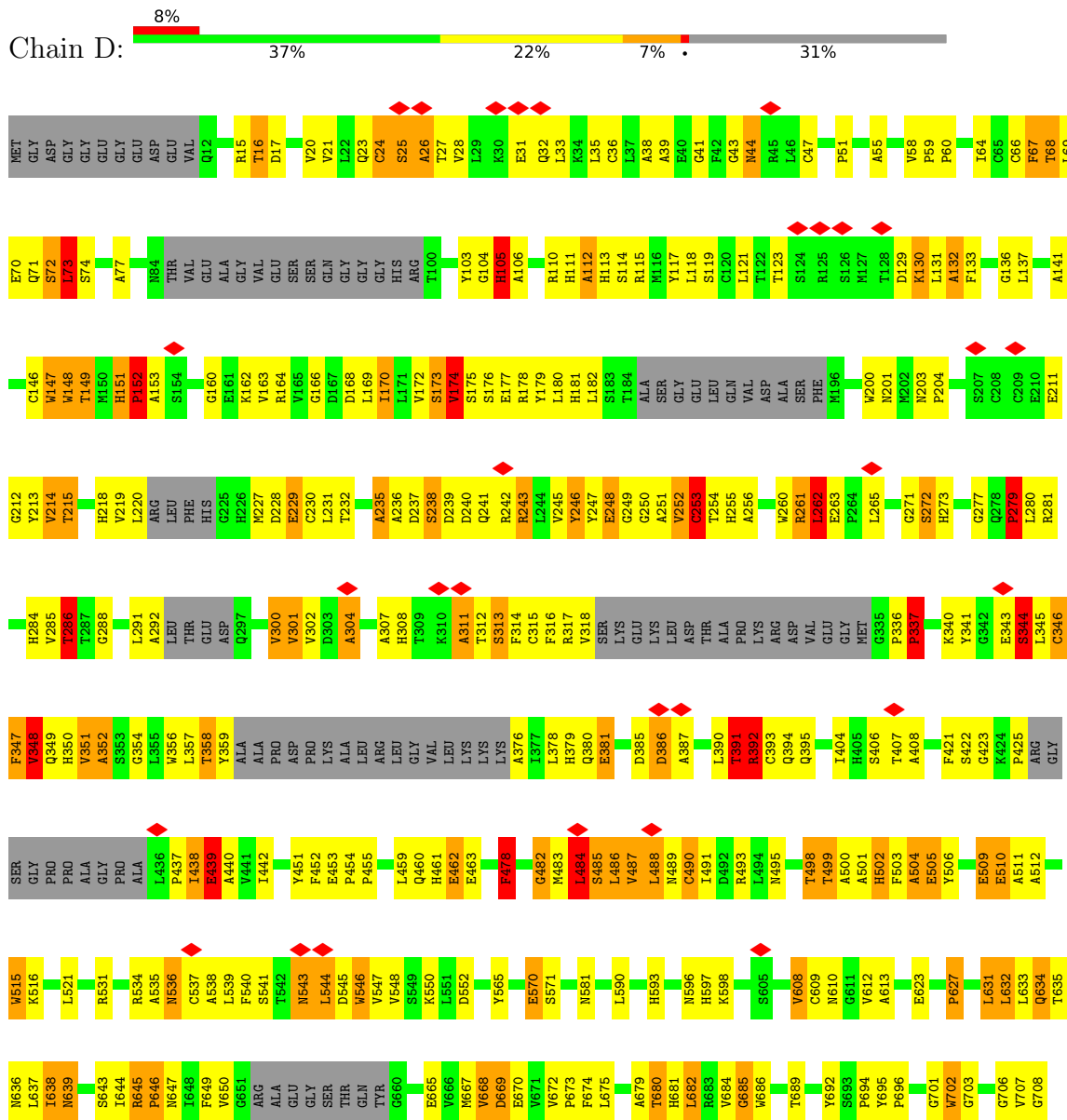




L2751	D2752	S2753	F2754	L2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	L2771	D2772	N2773	W2774	S2775	Y2776	Y2777	G2778	E2779	N2780	Y2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	F2789	M2790	L2791	R2792	N2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	D2806	W2807	P2808	L2809	K2810
E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	A2759	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLY	LYS	LYS	THR	ARG	LYS	ILE	GLN	THR	ALA	GLN	THR	Y2849	D2850	P2851	R2852	E2853	G2854	Y2855	N2856	P2857	Q2858	L2795	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	
L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	H2883	N2884	T2885	W2886	K2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	L2906	P2907	Y2908	D2909	T2910	L2911	T2912	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931		
M2932	N2933	G2934	Y2935	A2936	T2937	R2938	R2939	G2940	LEU	LYS	ASP	MET	GLU	LEU	THR	SER	ASN	THR	GLY	ARG	PHE	ALA	L2894	K2897	GLN	GLN	LEU	LEU	ARG	TRP	ASP	ILE	THR	GLN	THR	PHE	ILE	ALA	HIS	GLU	ALA	VAL	SER	GLY	ARG	VAL	GLU	LYS	PRO	HIS									
GLU	GLN	ILE	LYS	PHE	PHE	ALA	L2894	LEU	PRO	LEU	LEU	ASN	TYR	PHE	THR	ASN	HIS	CYS	LEU	Y3016	G3029	S3032	H3033	I3039	THR	SER	GLN	ALA	ARG	C3044	K3045	L3046	A3047	V3050	T3059	D3060	A3061	P3062	A3063	V3064	VAL	ASN	CYS	LEU	HIS	I3070	L3071	R3073	D3076										
K3082	P3085	F3086	L3087	V3088	C3089	A3090	GLY	LEU	ARG	SER	PHE	PHE	GLU	S3098	A3099	I3103	E3104	K3105	K3106	V3107	I3108	N3109	L3110	R3111	L3112	G3113	K3114	VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN	ASN	THR	TYR	T3132	T3133	P3138	F3152	GLY	ASP	ASP	VAL	ILE	L3158						
D3159	D3160	V3161	Q3162	V3163	S3164	C3165	Y3166	R3167	T3168	L3169	S3174	T3176	LYS	ASN	THR	THR	V3183	L3186	L3190	A3195	A3198	A3199	A3200	MET	PRO	VAL	A3204	F3205	L3206	E3207	P3208	Q3209	L3210	Y3213	S3217	VAL	TYR	THR	THR	LYS	SER	PRO	ARG	GLU	ARG	ALA	ILE	LEU	LEU	PRO									
ASN	SER	VAL	GLU	MET	CYS	PRO	ASP	PRO	VAL	LEU	ASP	ARG	MET	ALA	ASP	ILE	GLY	ALA	GLY	SER	GLY	ALA	ALA	ARG	TYR	THR	GLU	MET	PRO	HIS	ILE	ILE	T3273	L3274	P3275	M3276	L3277	C3278	S3279	Y3280	L3281	P3282	R3283	W3284	W3285	E3286	R3287	G3288	P3289	P3292	P3293	P3294							
A3295	L3296	P3297	P3301	P3302	P3303	C3304	T3305	A3306	N3313	SER	LEU	LEU	GLY	ASN	ILE	LEU	R3321	I3322	N3325	E3331	A3332	T3333	L3338	A3339	VAL	PHE	ALA	GLN	PRO	ILE	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	A3374								
E3377	Q3378	L3379	R3380	L3381	E3382	A3383	K3384	A3387	E3388	E3389	GLY	GLU	LEU	LEU	VAL	ASP	PHE	VAL	VAL	CYS	ASP	L3405	F3406	L3408	Y3409	P3410	L3411	Y3415	V3416	D3417	N3418	N3419	H3422	W3423	P3427	N3430	A3431	E3432	E3433	L3434	PHE	ARG	M3437	V3438	G3439	F3442	S3446												
K3452	E3453	E3454	E3455	Q3456	N3457	F3458	Q3461	L3470	THR	HIS	ASP	SER	K3475	S3476	K3477	G3482	S3486	G3487	G3488	SER	ASP	GLN	GLU	THR	LYS	LYS	LYS	ARG	GLY	ASP	ARG	T3451	V3416	D3417	N3418	N3419	H3422	W3423	P3427	N3430	A3431	E3432	E3433	L3434	PHE	ARG	M3437	V3438	G3439	F3442	S3446								
P3527	THR	ASP	GLN	ASP	LEU	ILE	MET	LEU	ALA	ALA	LYS	THR	ARG	THR	THR	THR	ASP	GLU	GLU	VAL	ARG	F3552	L3553	Q3554	Q3560	C3561	K3562	V3563	E3564	G3565	P3567	R3570	W3571	Q3572	ALA	LEU	THR	ARG	GLY	PRO	LEU	GLY	ASN	ARG	GLU	GLU	ASP	ALA	ASP	ASP	PRO	GLU							
LYS	ILE	VAL	ARG	ARG	VAL	GLN	VAL	SER	ALA	VAL	LEU	TYR	HIS	GLU	GLN	THR	GLU	PRO	TYR	LYS	SER	LYS	LYS	ALA	ALA	TRP	HIS	LYS	LEU	SER	LYS	GLN	ARG	GLY	ASP	ALA	VAL	VAL	CYS	PHE	THR	MET	PRO	LEU	TYR	ASN	LEU	P3645	T3646	H3647	R3648	K3658							



- Molecule 1: Ryanodine receptor 1

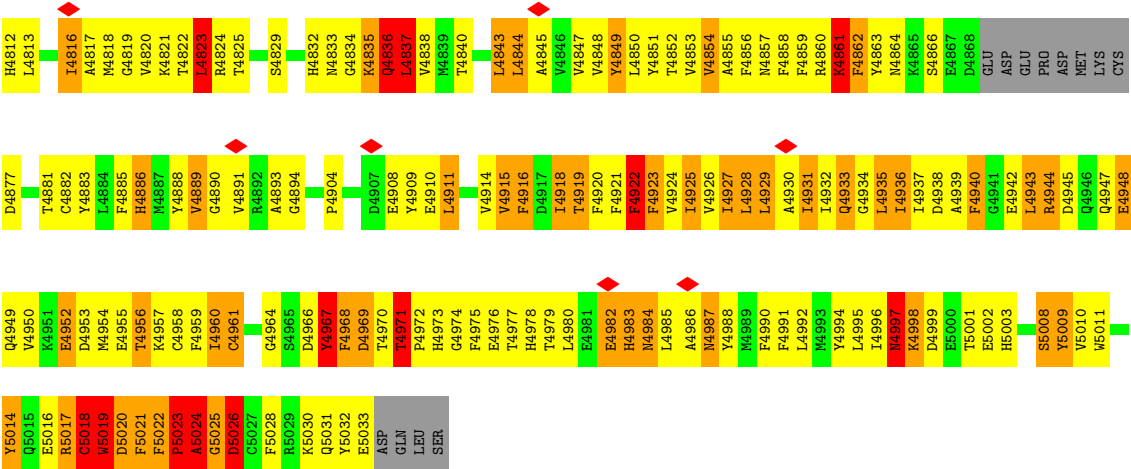


D709	D710	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L711	H838	L7
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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	41743	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	5400	Depositor
Magnification	100286	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.532	Depositor
Minimum map value	-0.339	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0967	Depositor
Map size ($\text{\AA}$)	547.232, 547.232, 547.232	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.396, 1.396, 1.396	Depositor

5 Model quality

5.1 Standard geometry

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	1.58	125/18508 (0.7%)	1.86	634/25601 (2.5%)
1	B	1.58	125/18508 (0.7%)	1.86	634/25601 (2.5%)
1	C	1.58	125/18508 (0.7%)	1.86	632/25601 (2.5%)
1	D	1.58	124/18508 (0.7%)	1.86	633/25601 (2.5%)
All	All	1.58	499/74032 (0.7%)	1.86	2533/102404 (2.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	3
1	B	1	3
1	C	1	3
1	D	1	3
All	All	4	12

The worst 5 of 499 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4859	PHE	CA-CB	-68.22	0.58	1.53
1	B	4859	PHE	CA-CB	-68.22	0.58	1.53
1	C	4859	PHE	CA-CB	-68.22	0.58	1.53
1	D	4859	PHE	CA-CB	-68.22	0.58	1.53
1	A	4691	GLN	CA-CB	-56.69	0.63	1.53

The worst 5 of 2533 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2047	GLU	N-CA-CB	-40.42	41.78	110.50
1	C	2047	GLU	N-CA-CB	-40.42	41.78	110.50
1	D	2047	GLU	N-CA-CB	-40.42	41.78	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2047	GLU	N-CA-CB	-40.41	41.80	110.50
1	B	1750	PRO	CA-C-N	-39.48	91.22	121.61

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	4691	GLN	CA
1	B	4691	GLN	CA
1	C	4691	GLN	CA
1	D	4691	GLN	CA

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2192	TYR	Mainchain
1	A	2586	VAL	Peptide
1	A	4091	LYS	Peptide
1	B	2192	TYR	Mainchain
1	B	2586	VAL	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	18404	0	9774	2137	0
1	B	18404	0	9774	2139	0
1	C	18404	0	9774	2141	0
1	D	18404	0	9774	2144	0
All	All	73616	0	39096	8320	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 74.

The worst 5 of 8320 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4978:HIS:HE2	1:D:4983:HIS:CD2	1.11	1.67
1:A:4235:VAL:HG21	1:A:5019:TRP:CZ3	1.15	1.67
1:C:4115:SER:HA	1:C:4128:PHE:CZ	1.23	1.66
1:A:4978:HIS:HE2	1:A:4983:HIS:CD2	1.11	1.66
1:B:4978:HIS:HE2	1:B:4983:HIS:CD2	1.11	1.65

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	3311/5037 (66%)	2865 (86%)	203 (6%)	243 (7%)	1	11
1	B	3311/5037 (66%)	2865 (86%)	204 (6%)	242 (7%)	1	11
1	C	3311/5037 (66%)	2865 (86%)	203 (6%)	243 (7%)	1	11
1	D	3311/5037 (66%)	2864 (86%)	205 (6%)	242 (7%)	1	11
All	All	13244/20148 (66%)	11459 (86%)	815 (6%)	970 (7%)	1	11

5 of 970 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	25	SER
1	A	26	ALA
1	A	44	ASN
1	A	67	PHE

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	317/4276 (7%)	225 (71%)	92 (29%)	0	3
1	B	317/4276 (7%)	227 (72%)	90 (28%)	0	3
1	C	317/4276 (7%)	226 (71%)	91 (29%)	0	3
1	D	317/4276 (7%)	226 (71%)	91 (29%)	0	3
All	All	1268/17104 (7%)	904 (71%)	364 (29%)	1	3

5 of 364 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4799	SER
1	D	3935	TRP
1	C	4844	LEU
1	C	4952	GLU
1	D	4241	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4776	GLN
1	D	2161	GLN
1	C	4803	HIS
1	C	4983	HIS
1	D	4553	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

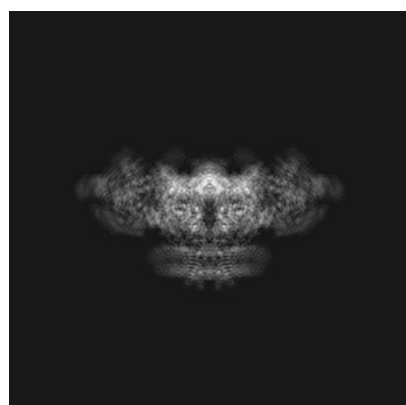
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8073. These allow visual inspection of the internal detail of the map and identification of artifacts.

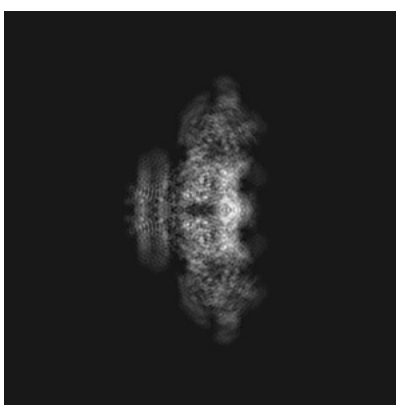
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

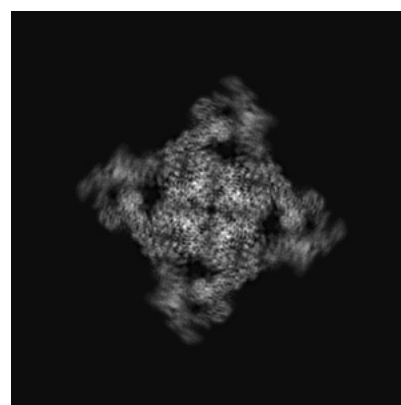
6.1.1 Primary map



X



Y



Z

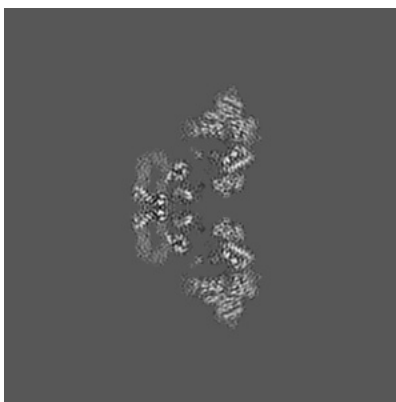
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

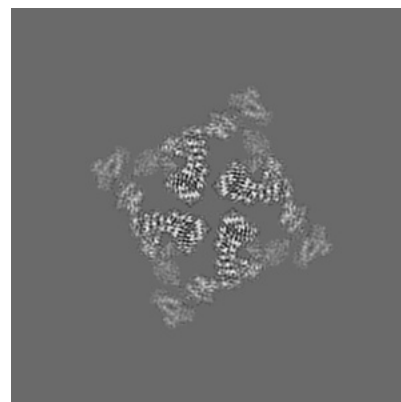
6.2.1 Primary map



X Index: 196



Y Index: 196



Z Index: 196

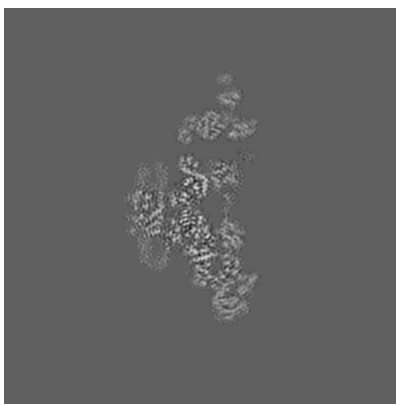
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

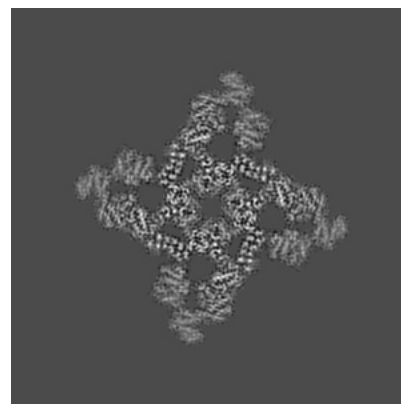
6.3.1 Primary map



X Index: 208



Y Index: 184

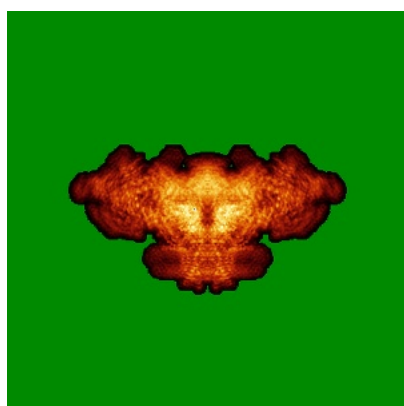


Z Index: 215

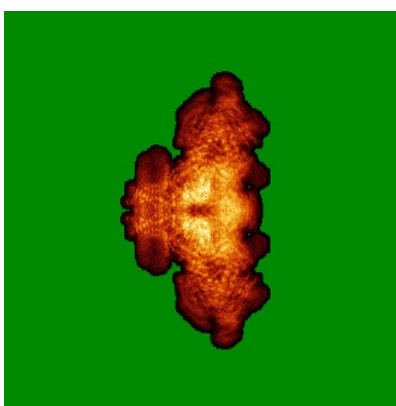
The images above show the largest variance slices of the map in three orthogonal directions.

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

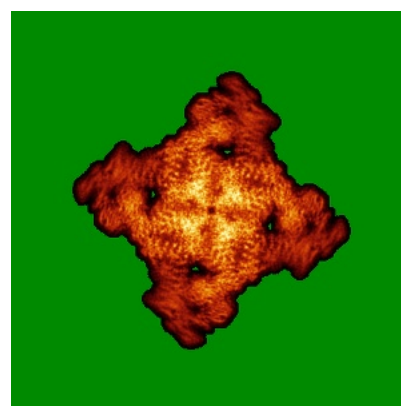
6.4.1 Primary map



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 0.0967. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

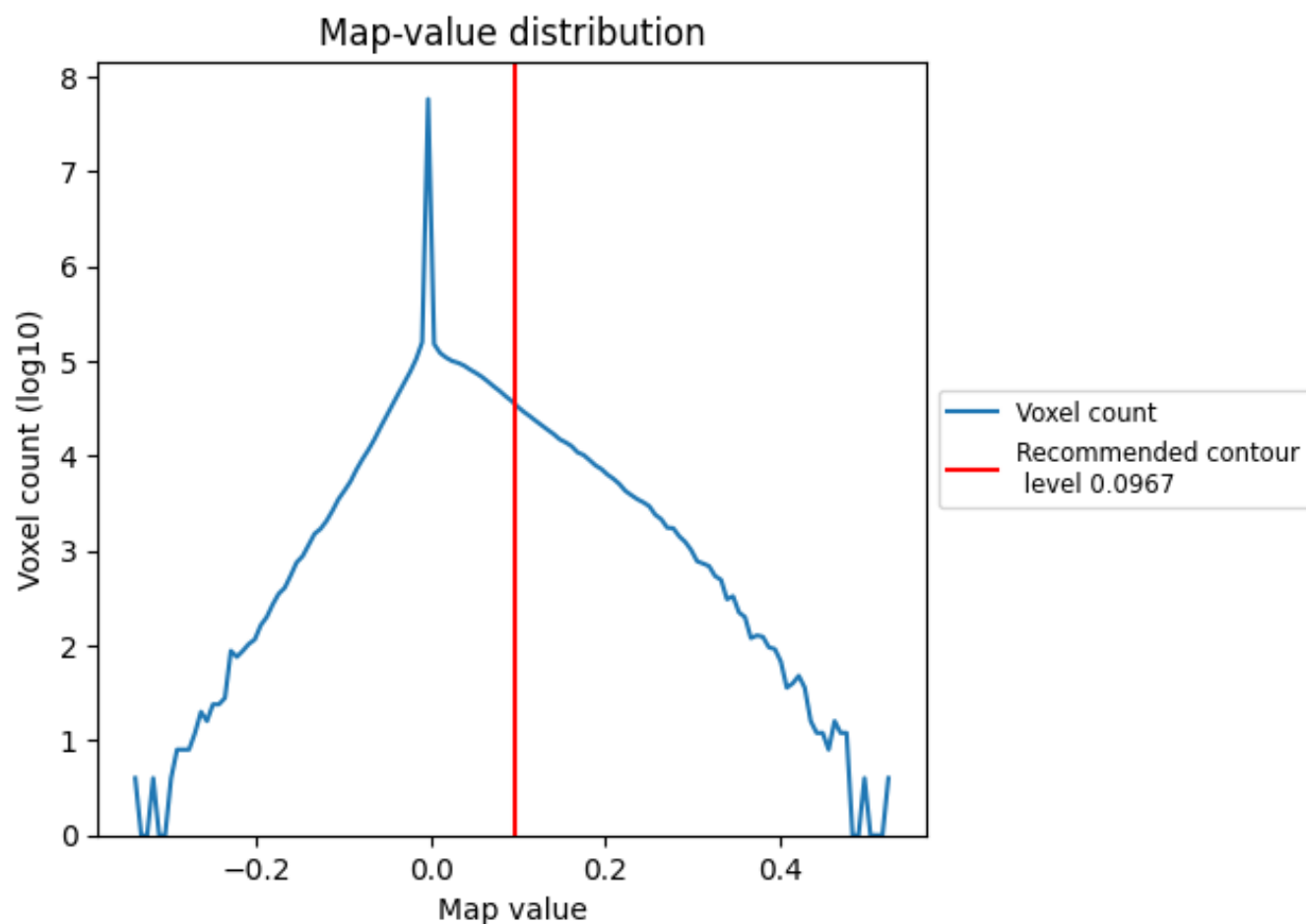
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

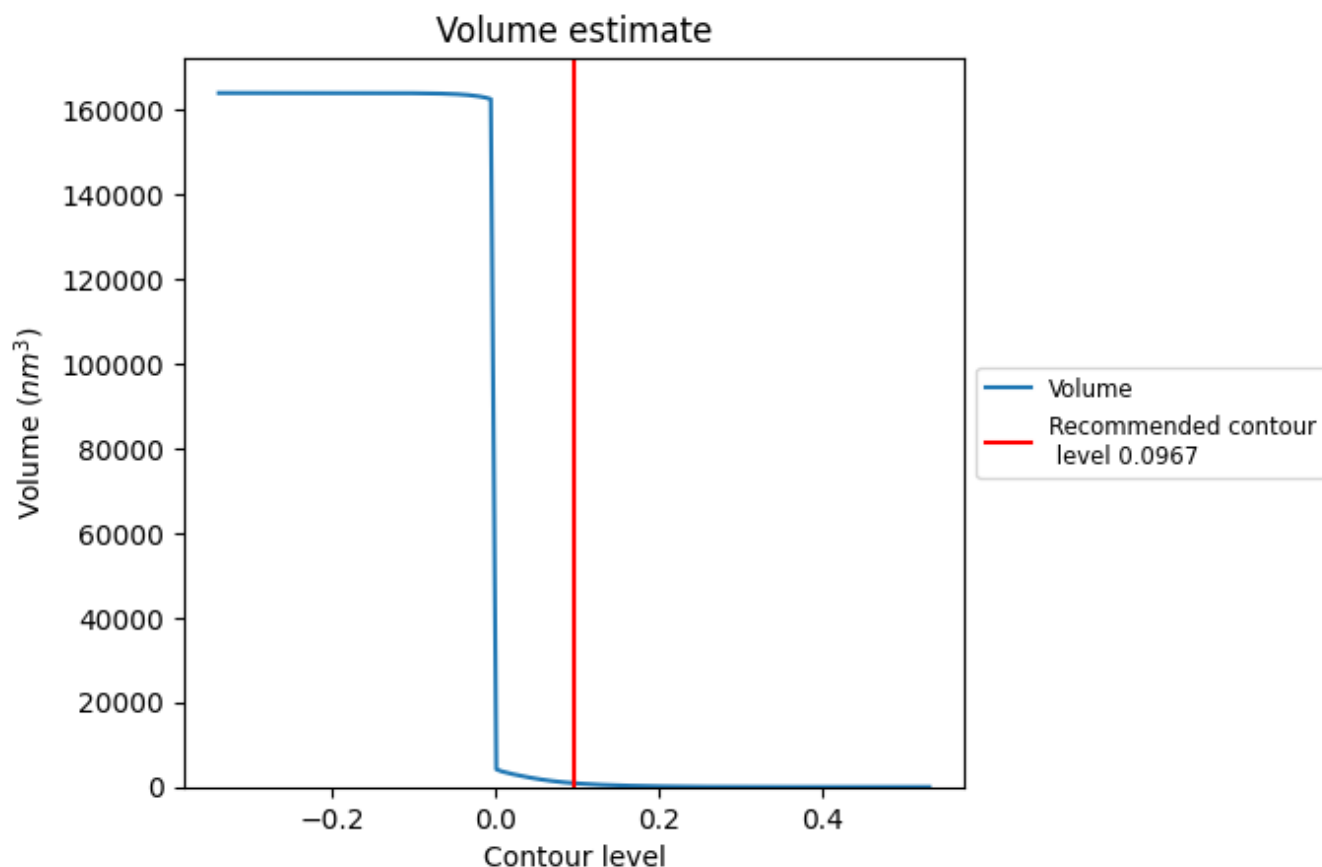
This section contains the results of statistical analysis of the map.

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.

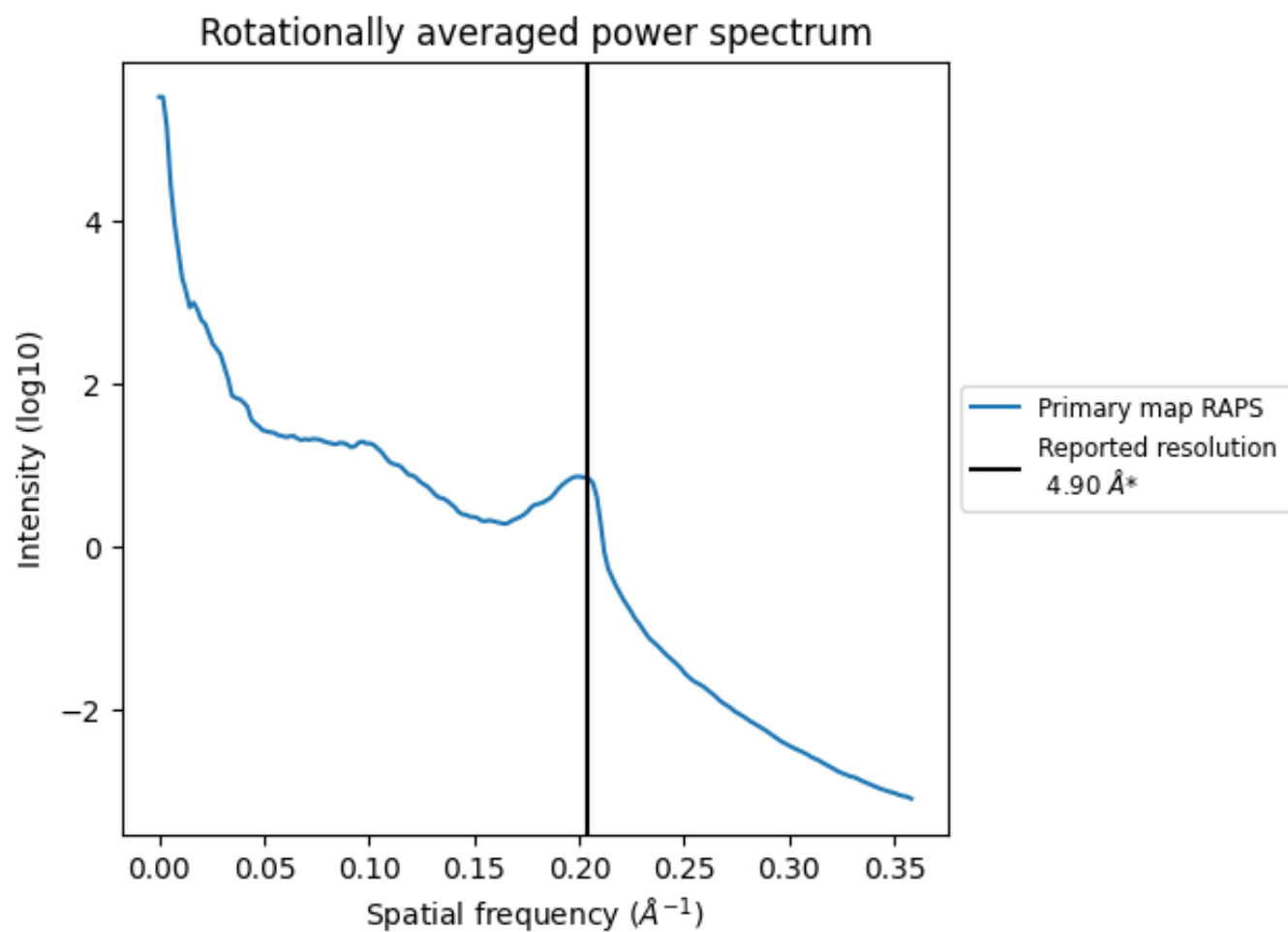
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 885 nm³; this corresponds to an approximate mass of 799 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 0.204 $\text{\AA}^{-1}$

8 Fourier-Shell correlation

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

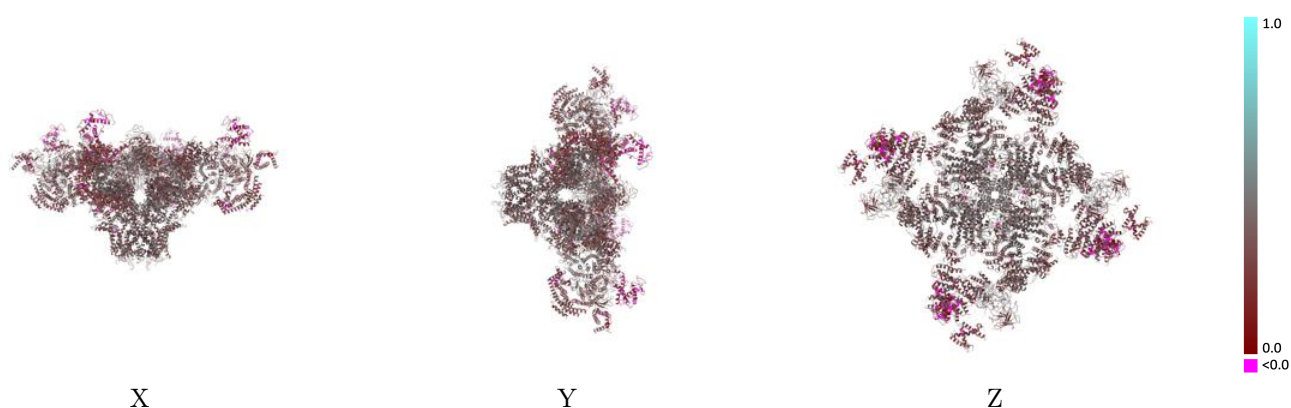
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8073 and PDB model 5J8V. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

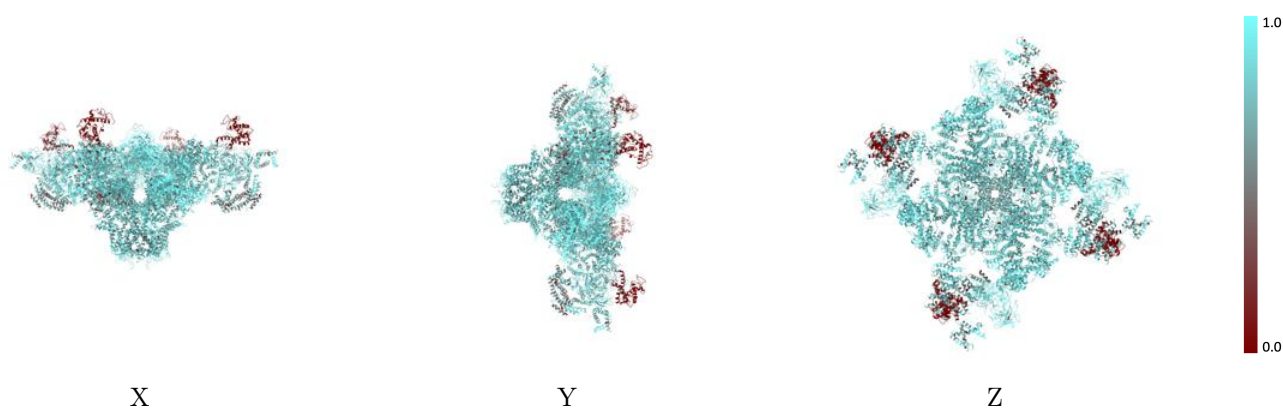
This section was not generated.

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



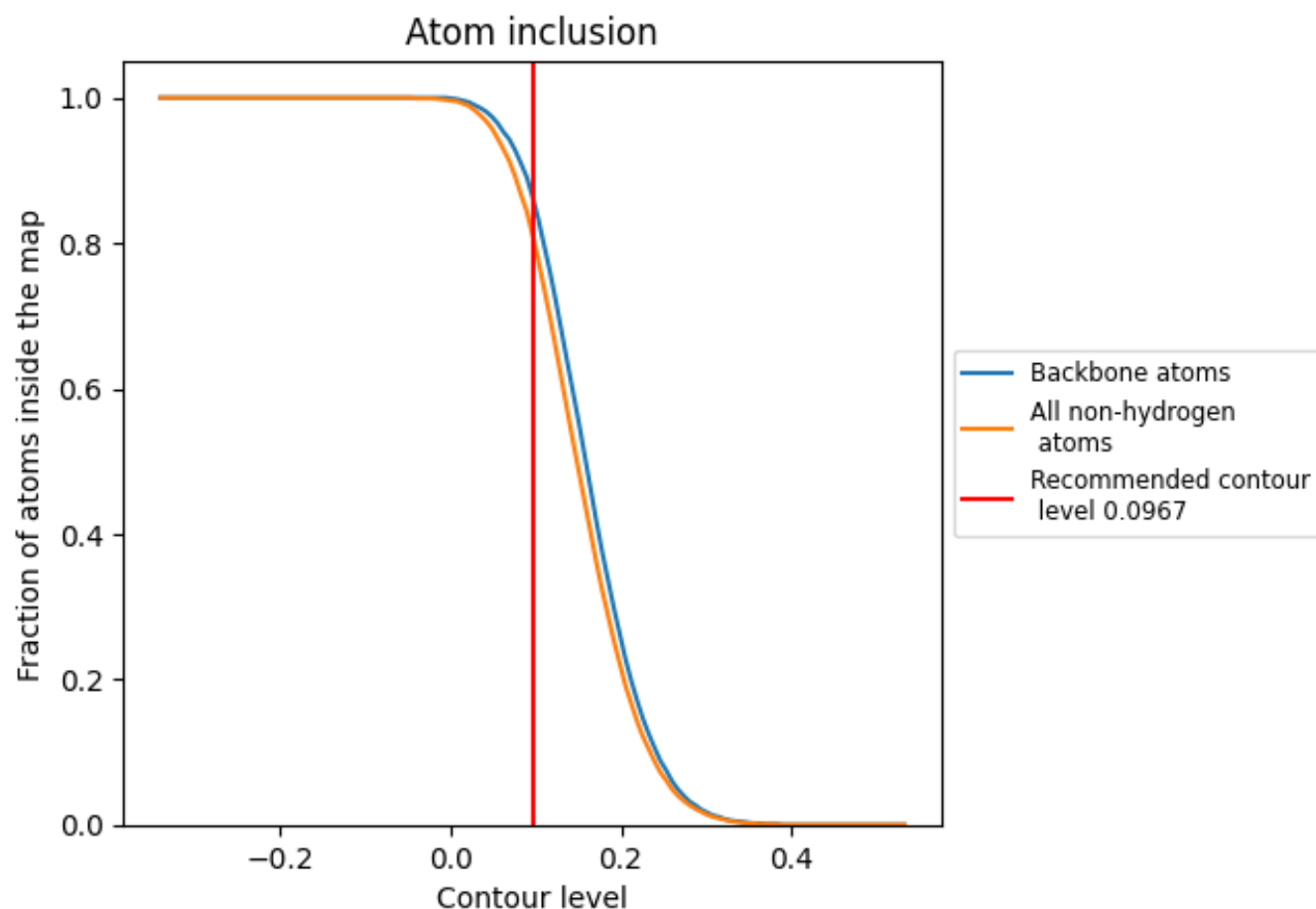
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0967).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.0967) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8100	0.3470
A	0.8090	0.3470
B	0.8100	0.3470
C	0.8100	0.3470
D	0.8090	0.3470

