



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:30 PM UTC

PDB ID : 3J8H / pdb_00003j8h
EMDB ID : EMD-2807
Title : Structure of the rabbit ryanodine receptor RyR1 in complex with FKBP12 at 3.8 Angstrom resolution
Authors : Yan, Z.; Bai, X.; Yan, C.; Wu, J.; Scheres, S.H.W.; Shi, Y.; Yan, N.
Deposited on : 2014-10-26
Resolution : 3.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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

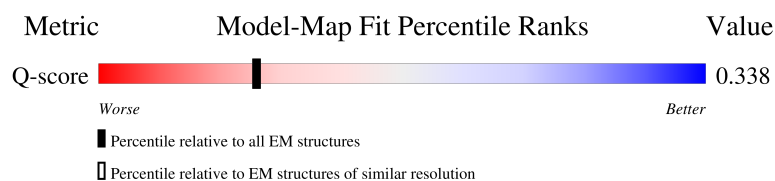
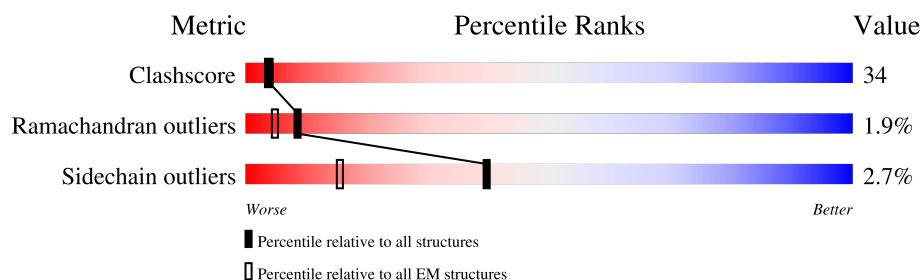
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	4599	
1	C	4599	
1	E	4599	
1	G	4599	

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Mol	Chain	Length	Quality of chain
2	B	107	 59% 40% .
2	D	107	 61% 38% .
2	F	107	 59% 40% .
2	H	107	 59% 40% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ZN	A	6000	-	-	X	-
3	ZN	C	6000	-	-	X	-
3	ZN	E	6000	-	-	X	-
3	ZN	G	6000	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 111160 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	3660	Total	C	N	O	S	1	0
			26957	17143	4683	4974	157		
1	C	3660	Total	C	N	O	S	1	0
			26957	17143	4683	4974	157		
1	E	3660	Total	C	N	O	S	1	0
			26957	17143	4683	4974	157		
1	G	3660	Total	C	N	O	S	1	0
			26957	17143	4683	4974	157		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

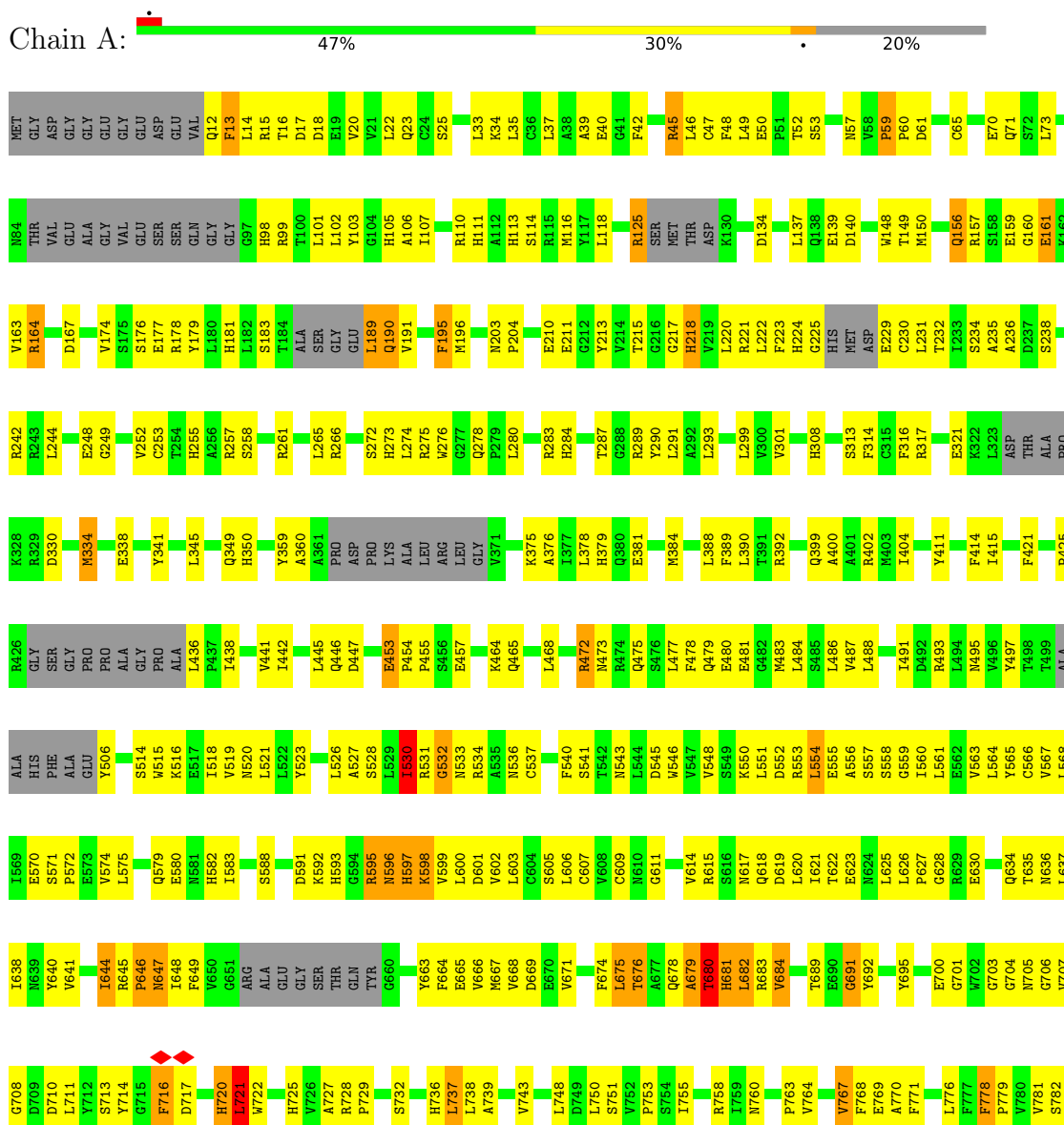
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	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 1





L3805	Y3722	V2937	L2867	R2806	L2743	V2503	ARG	F2337	H2253	L2185	R2104	V1955	GLU
M3806	M3723	T2938	S2868	R2806	M2744	L2804	ARG	A2338	Y2256	M2186	E2108	E1956	GLU
Y3725	A3724	R2939	R2869	I2809	V2745	F2505	ARG	L2339	L2257	N2188	L2257	S1957	GLU
N3809	A3726	H3647	E2870	K2810	L2746	Y2510	PHE	F2340	L2258	K2189	S2113	F1961	ASP
Q3813	B3727	R3648	L2871	E2811	L2747	GLY	HIS	V2341	E2259	N2190	Q2116	A1962	GLU
L3817	L3728	A3649	Q2872	L2812	L2748	I2511	GLY	N2342	N2260	F2191	L2116	E1963	GLU
A3730	M3729	C3650	A2873	K2814	P2749	GLU	GLU	Q2343	L2283	Y2192	L2116	R1964	GLU
K3731	K3731	N3657	A2875	M2816	E2750	N2514	PRO	V2346	GLY	P2195	L2123	R1965	LYS
L3820	S3732	Y3657	A2876	L2817	F2751	F2517	PRO	N2349	LEU	N2196	L2124	V1966	LYS
V3826	C3733	I3662	Q2877	A2818	D2752	V2521	GLU	A2350	GLY	L2197	H2125	V1966	LYS
G3827	F3828	H3667	E2880	W2819	S2753	L2522	GLU	N2351	GLN	R2198	R2126	L1969	ASP
F3829	S3668	S3668	L2754	A2820	F2754	ASP	ASN	V2354	GLY	R2199	Q2127	L1972	GLU
Q3830	F3669	F3670	N2755	H2821	N2756	V2525	ARG	R2355	SER	A2200	D2128	S1975	GLU
S3831	E3670	E3671	N2756	T2822	K2757	P2529	HIS	L2357	T2271	L2201	Y2129	S1975	GLU
L3835	GLU	D3672	F2758	L2823	P2759	P2529	LEU	R2358	P2272	M2203	E2133	S2058	LYS
M3836	ASN	R3672	A2759	L2823	A2759	A2533	GLU	I2358	V2275	H2204	L2134	S2058	LYS
R3837	GLY	M3673	E2760	K2825	E2760	L2537	GLU	R2359	A2276	T2206	L2136	S2061	ASP
T3838	GLU	L3674	Y2761	A2826	Y2761	THR	GLU	K2360	A2277	R2207	A2137	R2062	ALA
C3839	ALA	D3675	T2762	E2827	T2762	THR	GLU	P2361	A2278	M2208	L2138	L2063	GLU
S3840	GLU	D3676	H2763	R2828	H2763	ALA	GLU	E2362	S2279	E2209	P2139	L2066	LYS
V3841	GLU	L3677	E2764	G2829	E2764	THR	GLU	CYS	V2280	V2210	V2280	L2066	GLU
L3842	GLU	S3678	K2765	G2830	K2765	THR	GLU	PHE	T2281	M2211	A2141	L2066	GLU
D3843	VAL	K3679	F2768	GLU	F2768	THR	GLU	ARG	D2282	V2212	Y2142	T2069	GLU
L3844	VAL	GLY	D2769	GLU	D2769	THR	GLU	GLY	A2437	M2213	T2143	R2071	GLU
R3849	GLN	GLN	K2770	THR	K2770	THR	GLU	SER	L2286	V2214	T2144	R2072	ALA
Q3766	GLU	GLU	T2771	THR	T2771	THR	GLU	GLY	V2289	G2216	P2146	VAL	GLU
Q3767	GLU	GLU	Q2772	THR	Q2772	THR	GLU	GLY	V2299	GLY	V2149	LYS	GLY
S3768	GLU	GLU	N2773	LYS	N2773	LYS	GLU	GLY	S2300	GLU	E2150	LYS	LYS
R3769	GLU	GLU	N2774	LYS	N2774	LYS	GLU	GLY	Y2301	THR	D2151	GLU	GLU
L2904	GLU	GLU	W2775	THR	W2775	THR	GLU	SER	L2307	LYS	T2152	ASP	ASP
L2905	VAL	VAL	S2776	ARG	S2776	ARG	GLY	GLY	L2307	ILE	L2155	PRO	LYS
V2906	GLU	GLU	Y2777	ILE	Y2777	ILE	LYS	G2375	GLN	ARG	L2156	GLU	GLU
P2907	GLU	GLU	G2778	SER	G2778	SER	GLY	L2376	CYS	PHE	L2156	GLU	GLU
Y2908	LYS	LYS	E2779	GLN	E2779	GLN	GLY	I2380	PRO	ARG	L2159	GLU	GLU
D2909	GLN	GLN	N2780	THR	N2780	THR	GLU	A2383	PRO	P2226	L2159	GLU	GLU
T2910	ALA	ALA	Y2781	ALA	Y2781	ALA	GLU	I2384	LEU	K2227	G2160	LEU	LEU
L2911	GLN	GLN	D2782	THR	D2782	THR	GLU	R2385	ALA	T2230	Q2161	PRO	ALA
T2912	THR	THR	E2783	THR	E2783	THR	GLU	I2386	LYS	R2234	T2162	ALA	L1931
A2913	THR	THR	E2784	THR	E2784	THR	GLU	SER	GLY	R2234	R2163	P1932	P1932
K2914	GLN	GLN	L2785	THR	L2785	THR	GLU	ASP	TVR	C2237	S2164	GLU	L1937
E2915	THR	THR	K2786	THR	K2786	THR	GLU	PRO	ASP	Y2238	L2166	LYS	LYS
R2918	THR	THR	T2787	THR	T2787	THR	GLU	PRO	ASP	F2239	V2168	PRO	PRO
D2919	THR	THR	H2788	THR	H2788	THR	GLU	ALA	ILE	G2240	GLN	S2093	GLN
R2920	THR	THR	P2789	THR	P2789	THR	GLU	ALA	ILE	R2241	MET	L2094	L1943
E2921	THR	THR	W2790	THR	W2790	THR	GLU	ASP	TRP	I2242	GLY	E2095	E1944
Q2924	THR	THR	L2791	THR	L2791	THR	GLU	GLY	ASN	Q2245	Q2173	L2097	Y1945
L2927	THR	THR	R2792	THR	R2792	THR	GLU	PRO	C2326	Q2247	N2246	C1947	F1946
K2928	THR	THR	P2793	THR	P2793	THR	GLU	VAL	E2329	Q2247	M2178	V2098	C1947
F2929	THR	THR	Y2794	THR	Y2794	THR	GLU	ARG	E2330	S2249	M2100	S2099	D1948
Q2931	THR	THR	K2795	THR	K2795	THR	GLU	ARG	Y2331		L2182	H2101	Q1952
W2932	THR	THR	L2796	THR	L2796	THR	GLU	ASP					
N2933	THR	THR	S2797	THR	S2797	THR	GLU	ASP					
G2934	THR	THR	E2798	THR	E2798	THR	GLU	ASP					
Y2935	THR	THR	K2800	THR	K2800	THR	GLU	ASP					
A2936	THR	THR	D2801	THR	D2801	THR	GLU	ASP					
			E2803	THR	E2803	THR	GLU	ASP					



Chain C:



WORLDWIDE
PDB
PROTEIN DATA BANK







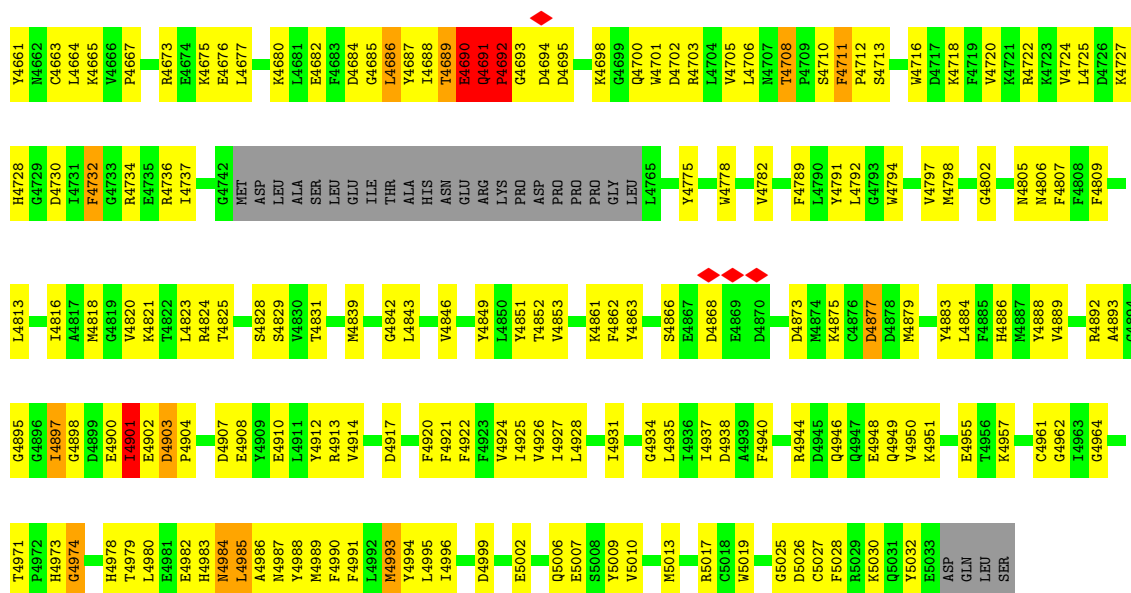






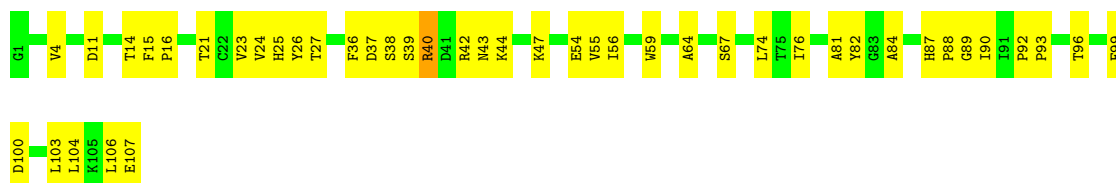






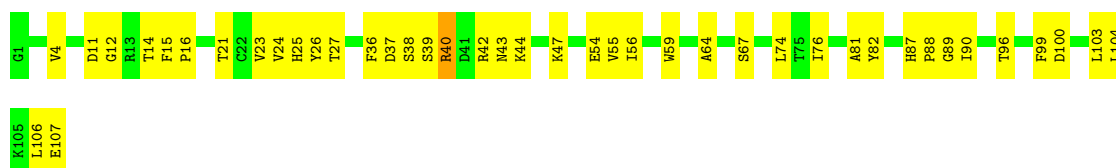
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain B: 59% 40%



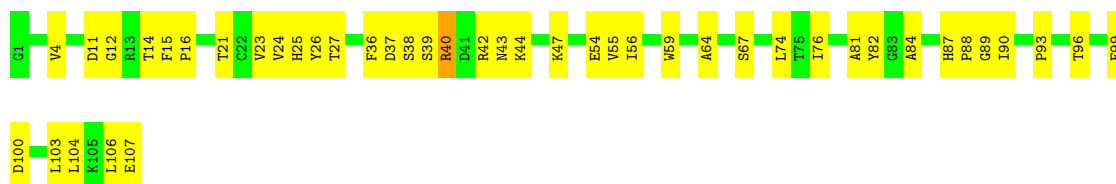
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain D: 61% 38%

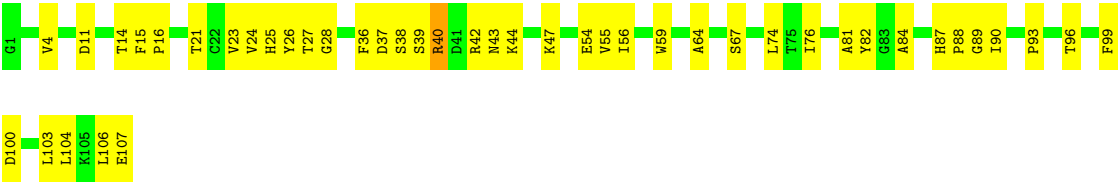


• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain F: 59% 40%



• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	65872	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Contrast transfer function parameters were estimated using CTFFIND3	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	5600	Depositor
Magnification	104748	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.336	Depositor
Minimum map value	-0.183	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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

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	0.44	6/24616 (0.0%)	0.92	89/33295 (0.3%)
1	C	0.44	6/24616 (0.0%)	0.92	89/33295 (0.3%)
1	E	0.44	6/24616 (0.0%)	0.92	89/33295 (0.3%)
1	G	0.44	6/24616 (0.0%)	0.92	89/33295 (0.3%)
2	B	0.33	0/851	0.81	0/1146
2	D	0.33	0/851	0.81	0/1146
2	F	0.33	0/851	0.81	0/1146
2	H	0.33	0/851	0.81	0/1146
All	All	0.43	24/101868 (0.0%)	0.92	356/137764 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	C	0	3
1	E	0	3
1	G	0	3
All	All	0	12

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	679	ALA	C-O	6.54	1.31	1.23
1	C	679	ALA	C-O	6.54	1.31	1.23
1	E	679	ALA	C-O	6.54	1.31	1.23
1	G	679	ALA	C-O	6.54	1.31	1.23
1	A	4903	ASP	C-N	6.10	1.40	1.33

The worst 5 of 356 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	THR	N-CA-C	-15.19	89.69	110.35
1	C	680	THR	N-CA-C	-15.19	89.69	110.35
1	E	680	THR	N-CA-C	-15.19	89.69	110.35
1	G	680	THR	N-CA-C	-15.19	89.69	110.35
1	A	1764	GLY	N-CA-C	15.13	149.05	113.18

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1253	PRO	Peptide
1	A	1867	GLU	Peptide
1	A	646	PRO	Peptide
1	C	1253	PRO	Peptide
1	C	646	PRO	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	26957	0	23849	1758	0
1	C	26957	0	23849	1763	0
1	E	26957	0	23849	1749	0
1	G	26957	0	23849	1758	0
2	B	832	0	831	44	0
2	D	832	0	831	44	0
2	F	832	0	831	43	0
2	H	832	0	831	43	0
3	A	1	0	0	2	0
3	C	1	0	0	2	0
3	E	1	0	0	2	0
3	G	1	0	0	2	0
All	All	111160	0	98720	7047	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 34.

The worst 5 of 7047 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:2198:MET:HE3	1:A:2203:MET:SD	1.19	1.70
1:C:2198:MET:HE3	1:C:2203:MET:SD	1.19	1.68
1:E:2198:MET:HE3	1:E:2203:MET:SD	1.19	1.66
1:G:2198:MET:HE3	1:G:2203:MET:SD	1.19	1.65
1:E:554:LEU:HD11	1:E:593:HIS:CE1	1.12	1.64

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	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	6	32
1	C	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	6	32
1	E	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	6	32
1	G	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	6	32
2	B	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
2	D	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
2	F	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
2	H	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
All	All	12384/18824 (66%)	11492 (93%)	652 (5%)	240 (2%)	8	32

5 of 240 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	737	LEU
1	A	807	GLY
1	A	827	LYS

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Continued from previous page...

Mol	Chain	Res	Type
1	A	852	VAL
1	A	1254	HIS

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	2507/3406 (74%)	2438 (97%)	69 (3%)	38	58
1	C	2507/3406 (74%)	2438 (97%)	69 (3%)	38	58
1	E	2507/3406 (74%)	2438 (97%)	69 (3%)	38	58
1	G	2507/3406 (74%)	2438 (97%)	69 (3%)	38	58
2	B	89/89 (100%)	88 (99%)	1 (1%)	65	73
2	D	89/89 (100%)	88 (99%)	1 (1%)	65	73
2	F	89/89 (100%)	88 (99%)	1 (1%)	65	73
2	H	89/89 (100%)	88 (99%)	1 (1%)	65	73
All	All	10384/13980 (74%)	10104 (97%)	280 (3%)	40	59

5 of 280 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	806	PRO
1	G	982	THR
1	G	3708	THR
1	C	979	PRO
1	C	865	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 247 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4947	GLN
1	G	2773	ASN
1	E	1558	HIS

Continued on next page...

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Mol	Chain	Res	Type
1	G	2253	HIS
1	G	3994	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	36

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Mol	Chain	Number of breaks
1	C	36
1	E	36
1	G	36

The worst 5 of 144 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	3572:UNK	C	3645:PRO	N	56.50
1	C	3572:UNK	C	3645:PRO	N	56.50
1	E	3572:UNK	C	3645:PRO	N	56.50
1	G	3572:UNK	C	3645:PRO	N	56.50
1	A	2712:UNK	C	2734:ASN	N	35.36

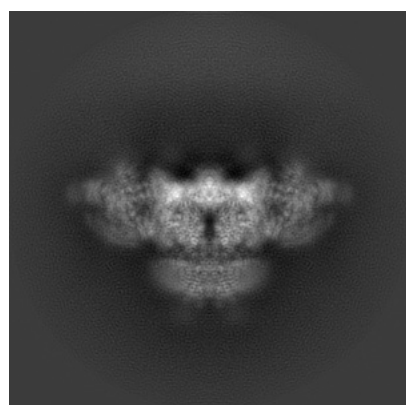
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2807. These allow visual inspection of the internal detail of the map and identification of artifacts.

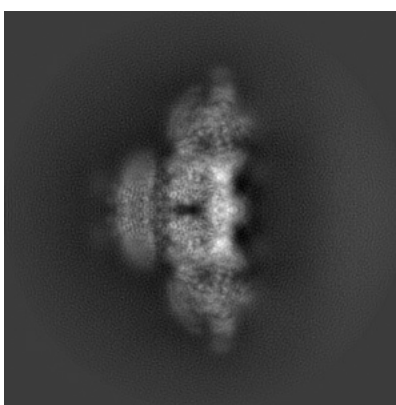
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

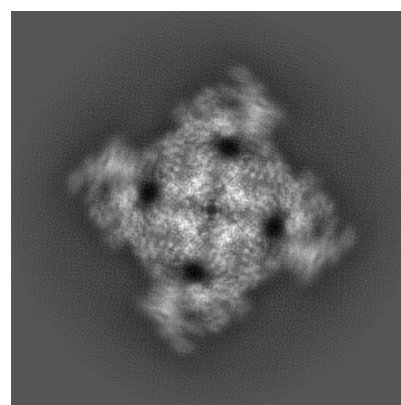
6.1.1 Primary map



X



Y

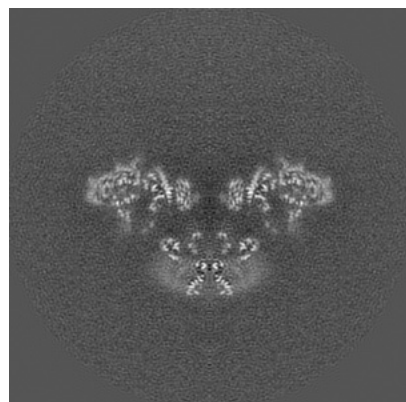


Z

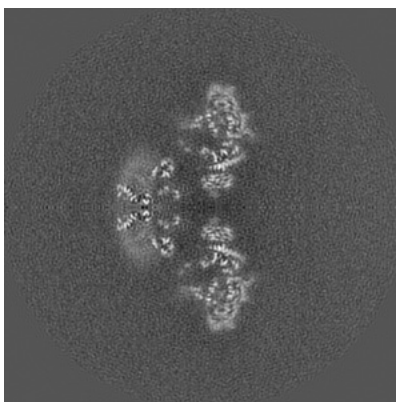
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

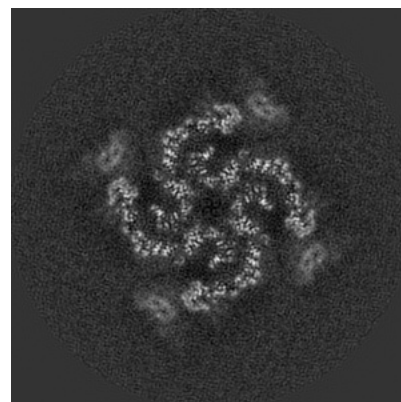
6.2.1 Primary map



X Index: 180



Y Index: 180

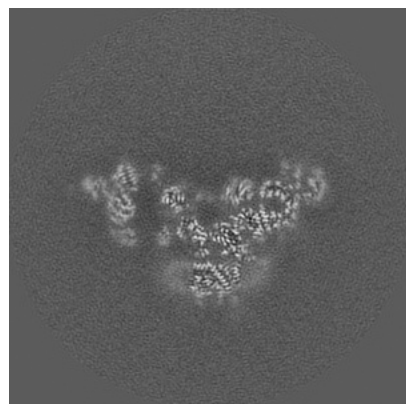


Z Index: 180

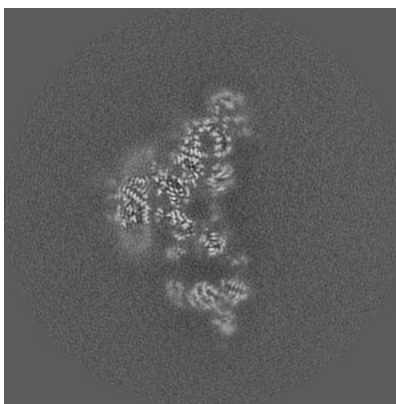
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

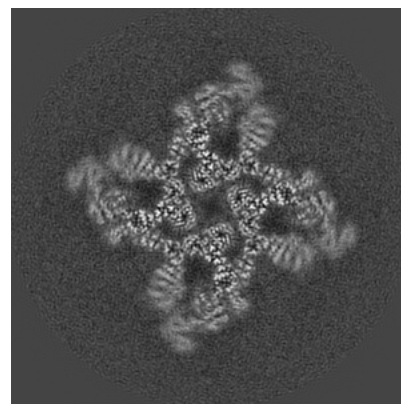
6.3.1 Primary map



X Index: 169



Y Index: 191

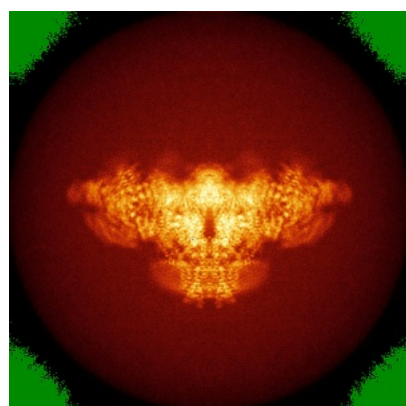


Z Index: 193

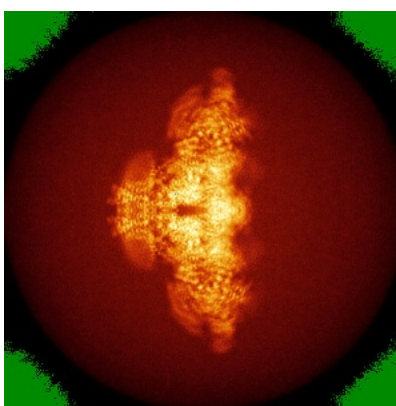
The images above show the largest variance slices of the map in three orthogonal directions.

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

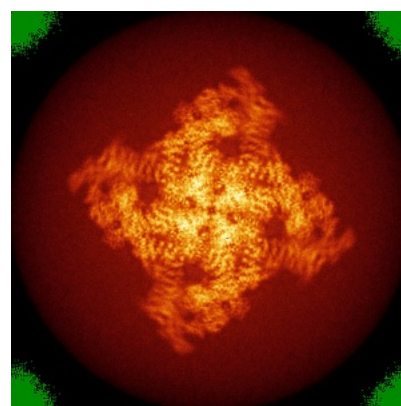
6.4.1 Primary map



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

This section was not generated.

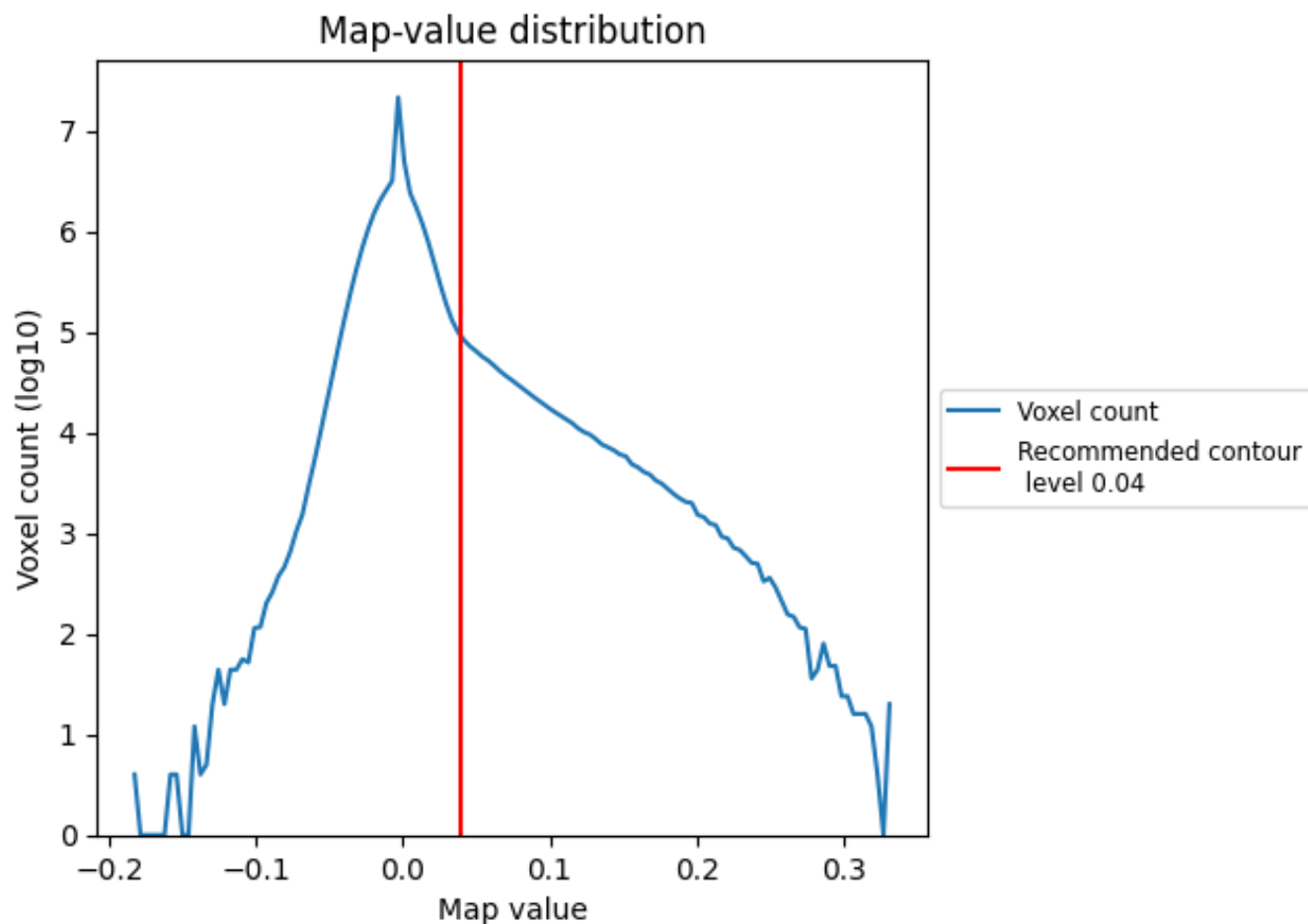
6.6 Mask visualisation

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

7 Map analysis [i](#)

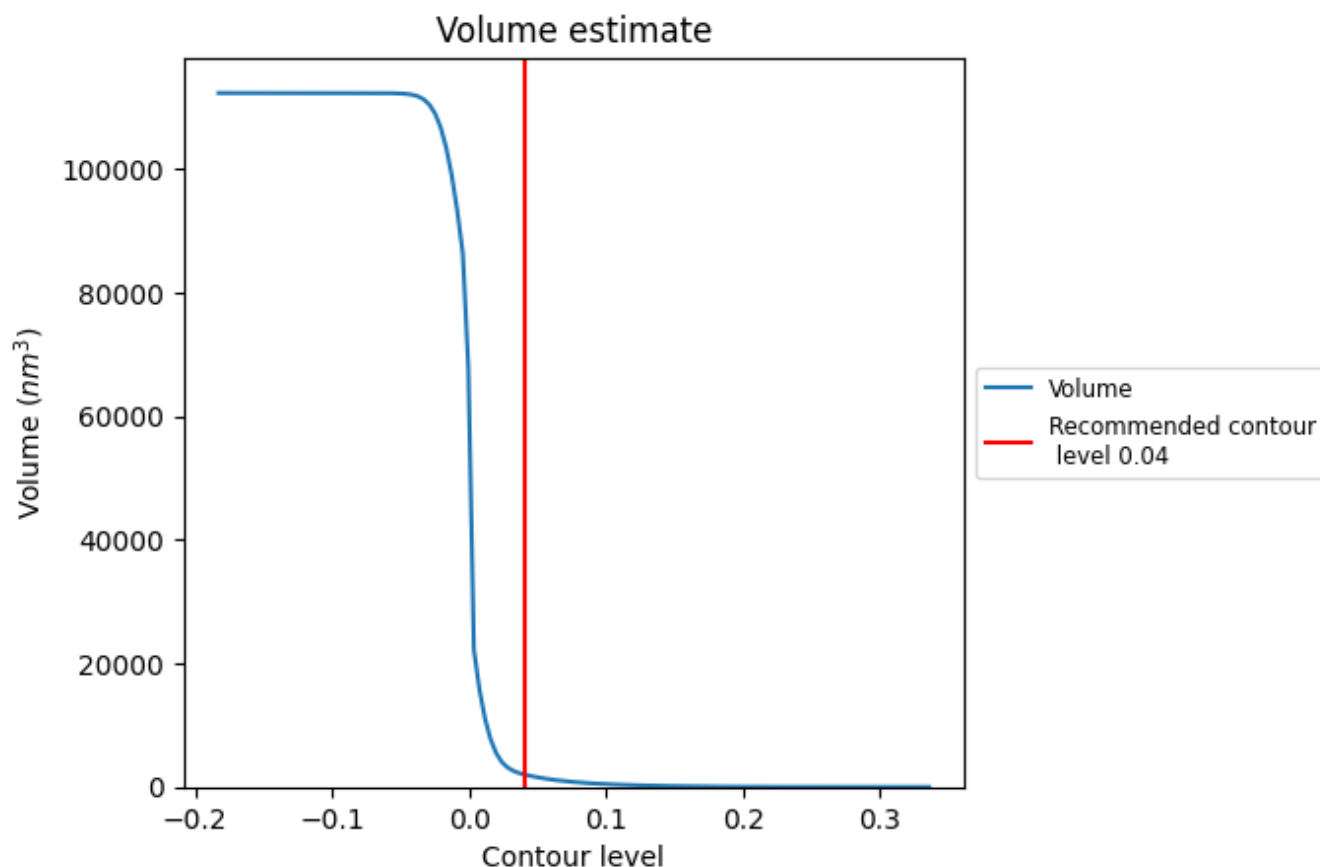
This section contains the results of statistical analysis of the map.

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.

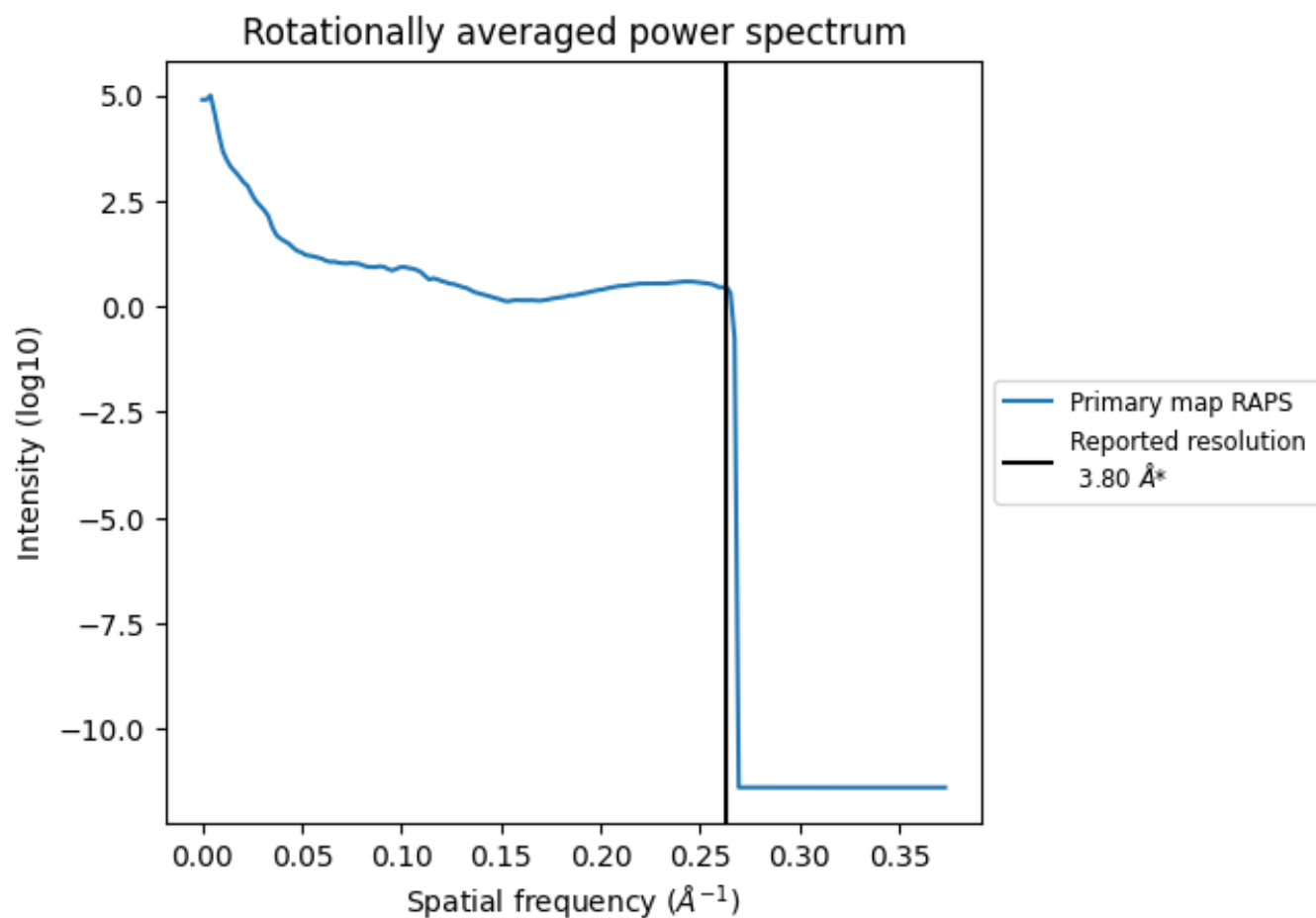
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2026 nm³; this corresponds to an approximate mass of 1830 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 0.263 Å⁻¹

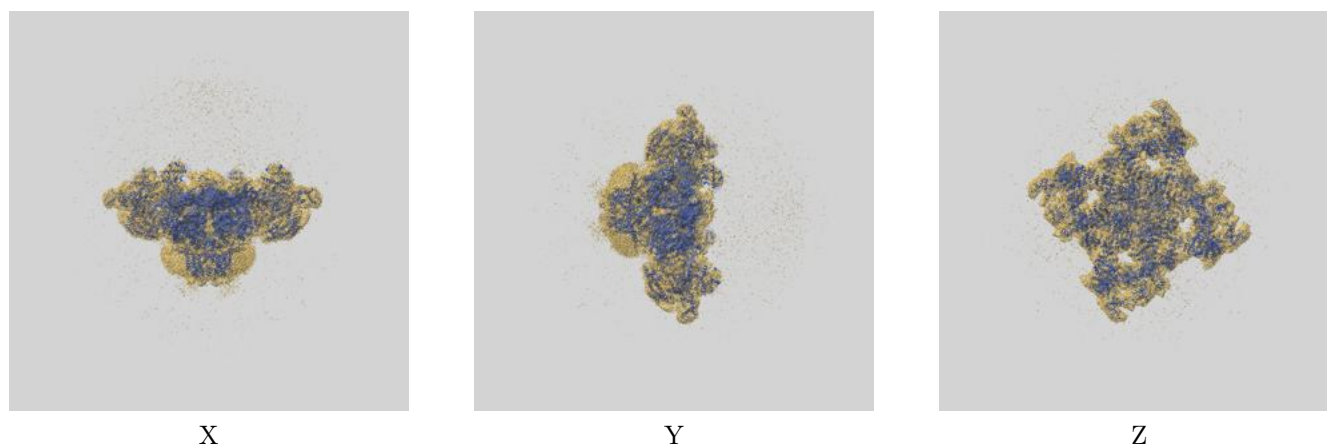
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

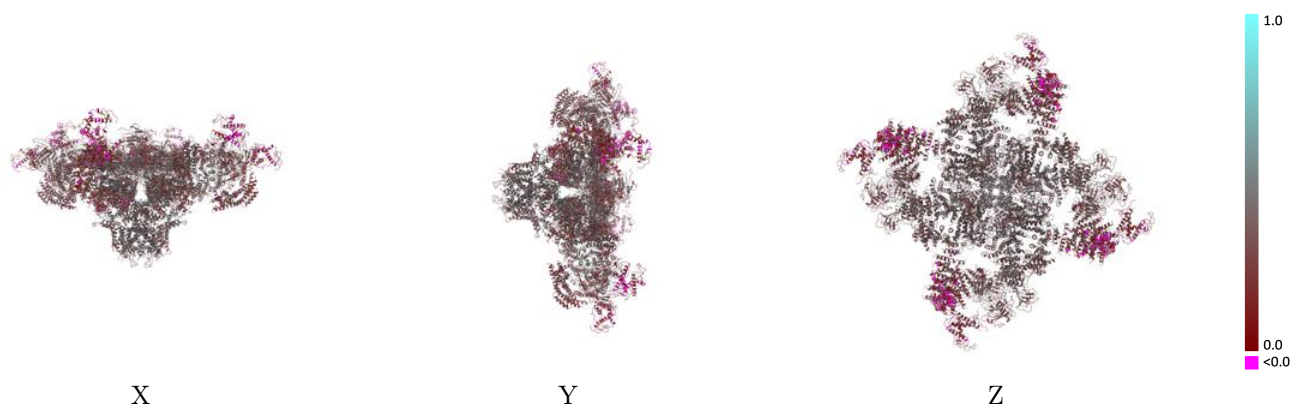
This section contains information regarding the fit between EMDB map EMD-2807 and PDB model 3J8H. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



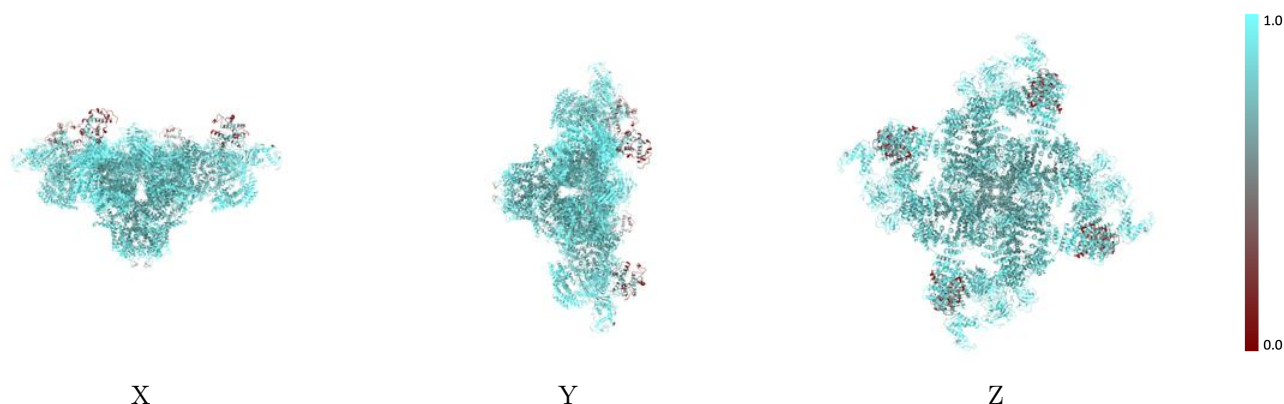
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



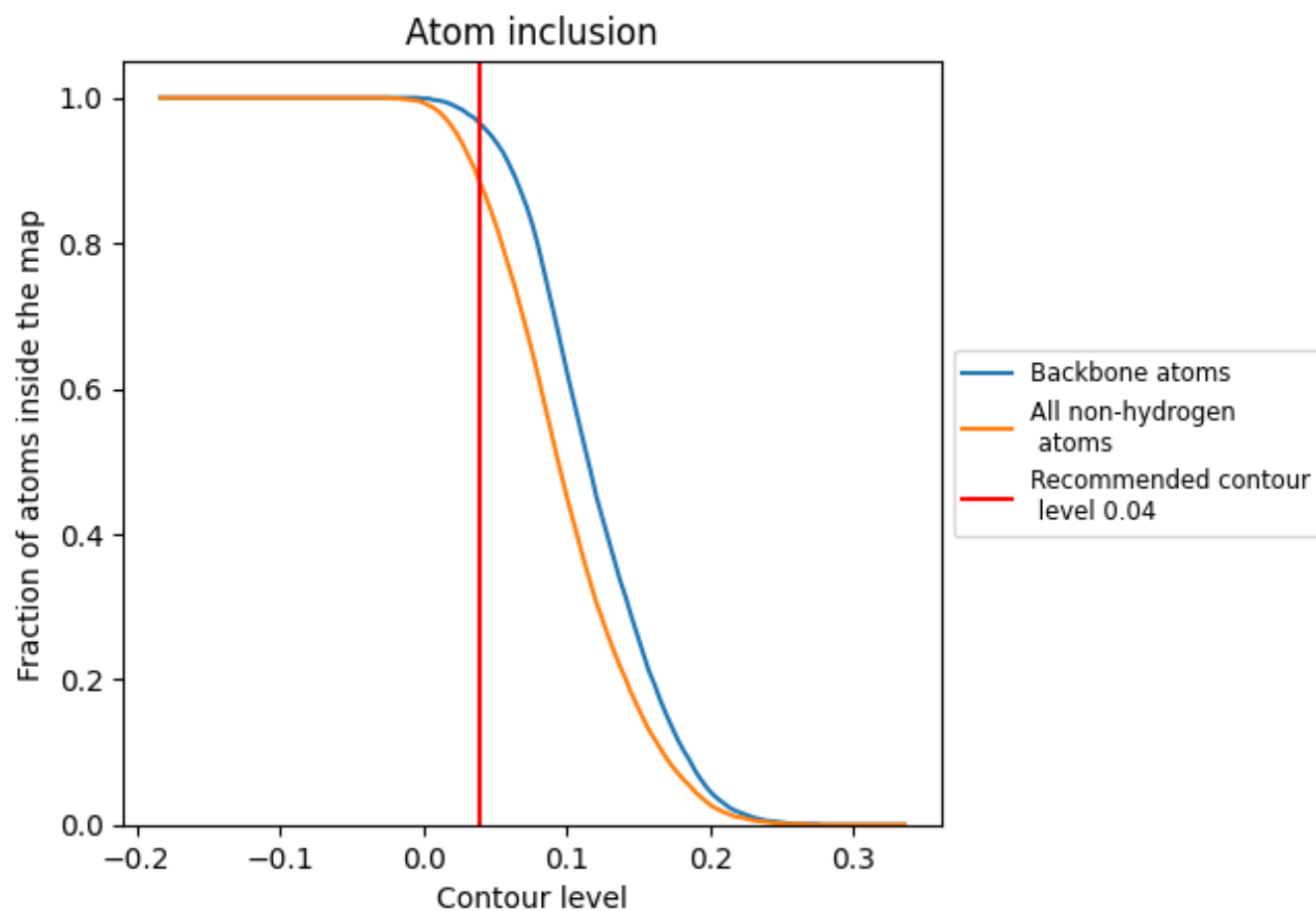
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8820	0.3380
A	0.8810	0.3380
B	0.9190	0.3580
C	0.8810	0.3380
D	0.9190	0.3570
E	0.8810	0.3380
F	0.9190	0.3540
G	0.8810	0.3380
H	0.9190	0.3590

1.0

0.0

<0.0