



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 09:10 AM EST

PDB ID : 3J8H
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.

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) : 2.31.3

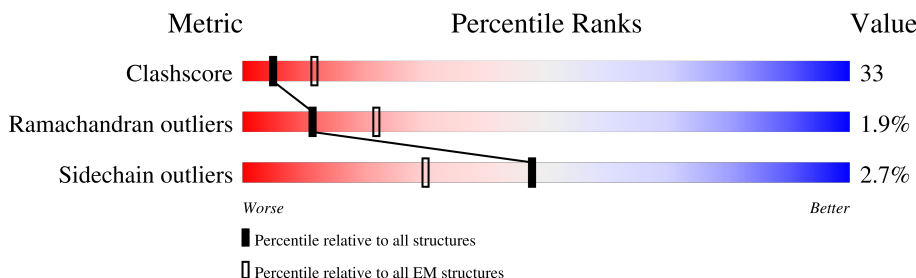
1 Overall quality at a glance

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)
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	4599	
1	C	4599	
1	E	4599	
1	G	4599	
2	B	107	
2	D	107	
2	F	107	
2	H	107	

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		

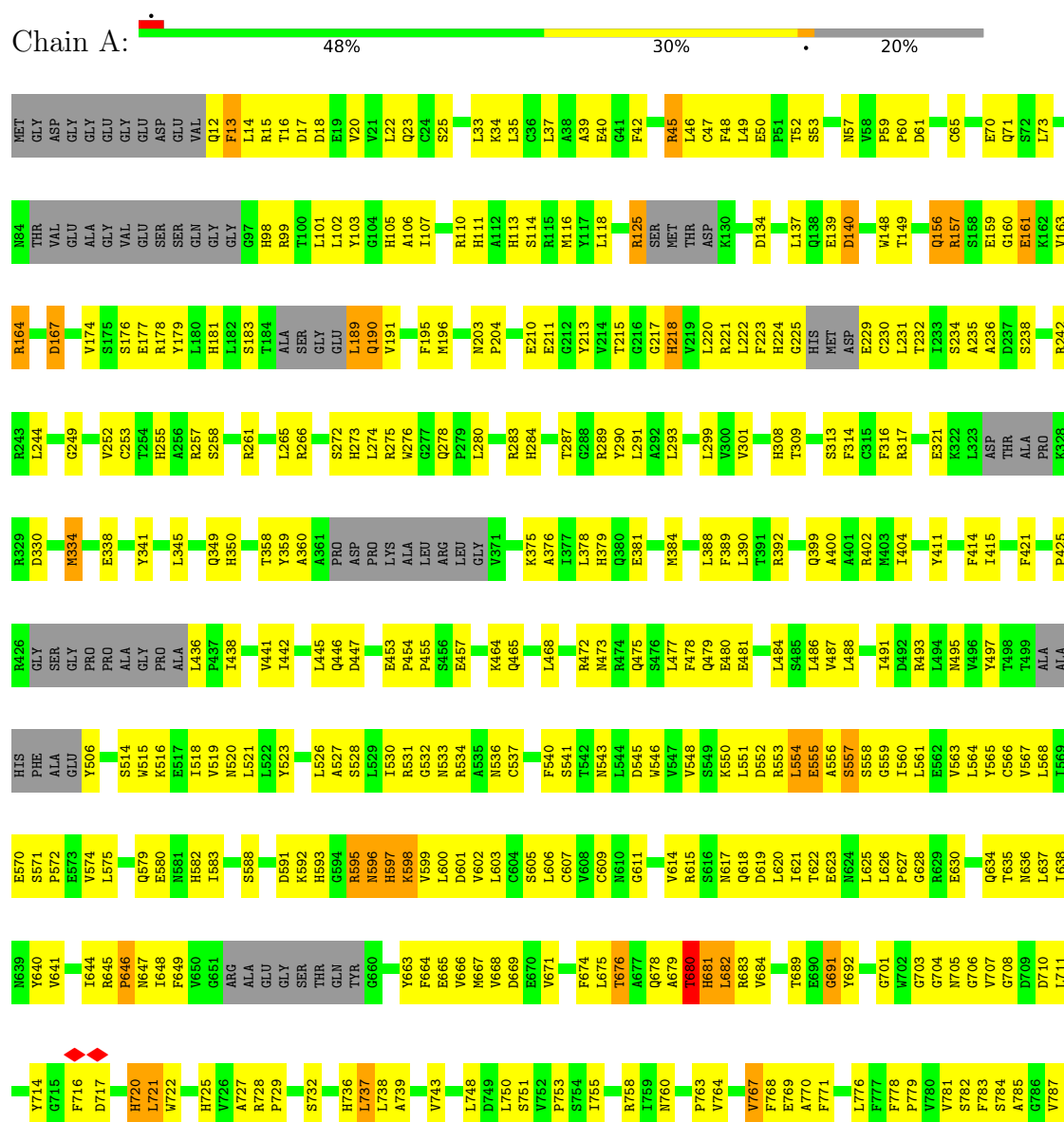
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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









Chain C:









Frequency	Percentage
Often	48%
Sometimes	29%
Rarely	20%



L283	L284	E1285	M1286	F1287	F1288	L289	S1292	L1293	L1294	V1295	F1296	F1297	HIS	HIS	HIS	PHE	ARG	CYS	THR	THR	GLY	GLN	F1139	G1140	W1143	D1147	V1148	C1151	G1152	H1153	L1154	L1155	T1156	E1157	N1158	I1161	V1168	MET	SER	GLY	SER	GLY	SER	GLU	F1178	L1189	P1190	C1192	S1193	L1194	G1195	P1196	Q1197	V1199	G1200	H1201	G1205	Q1206	D1207	V1208	S1209	S1210	L1211	R1212	L1283	L1284	G1249	V1252	C1253	T1254	A1256	R1257	S1258	R1261	L1265	R1266	L1280	R1283	H1284	T1287	C1288	R1289	Y1290	L1291	A1292	M1293	L1298	L1299	V1300	V1301	R1308	S1313	F1314	C1315	F1316	R1317	E1321	K1322	L1323	ASP	THR	ALA	ALA	PRO	K1328	R1330	D1339																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
GLU	ALA	GLU	GLY	GLY	LYS	GLU	THR	ALA	LYS	GLY	GLY	THR	PRO	GLY	GLY	THR	GLN	GLN	GLN	PRO	GLN	F1139	G1140	W1143	D1147	V1148	C1151	G1152	H1153	L1154	L1155	T1156	E1157	N1158	I1161	V1168	MET	SER	GLY	SER	GLU	F1178	L1189	P1190	C1192	S1193	L1194	G1195	P1196	Q1197	V1199	G1200	H1201	G1205	Q1206	D1207	V1208	S1209	S1210	L1211	R1212	GLU	ALA	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY



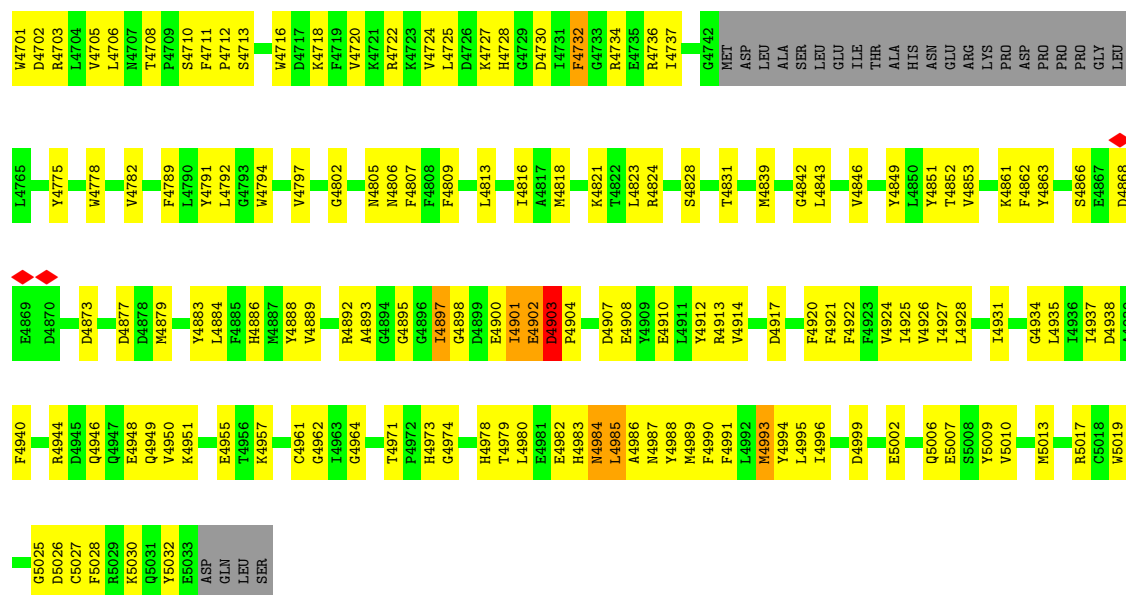






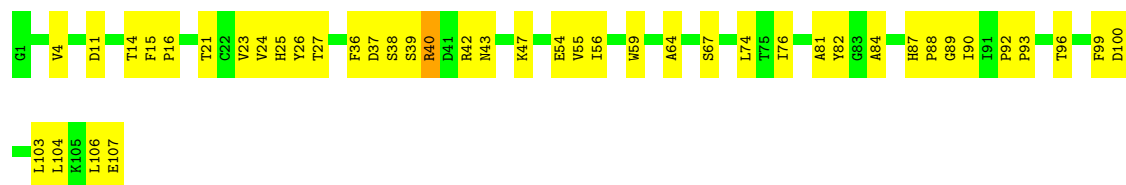
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LYS	Q2772	THR	T2544	GLU	LEU	E2285	V2212	R2140	L2066	GLU	V1845	P1773	D1700	A1627
LYS	N2773	THR	A2547	MET	ARG	L2286	N2213	A2141	L2066	ASP	S1846	P1774	H1701	V1628
THR	N2774	THR	A2547	LEU	GLU	L2286	V2214	T2142	L2066	ALA	T1847	H1775	H1702	L1628
LYS	N2775	THR	L2550	ILE	GLY	S2300	L2215	T2143	T2069	LYS	L1848	H1776	L1703	L1634
LYS	S2776	THR	N2551	GLN	GLY	Y2301	G2216	T2144	T2070	GLU	V1850	F1777	P1704	T1636
ILE	V2777	THR	R2552	ALA	SER	L2307	GLY	P2146	R2071	GLU	G1851	P1780	G1705	M1637
GLN	Q2778	THR	Y2553	GLY	G2237	L2307	GLU	P2146	L2072	GLU	G1852	C1781	L1707	A1637
LYS	Q2779	THR	L2554	LYS	THR	SER	THR	V2149	VAL	GLU	I1853	F1782	R1708	A1638
LYS	C2555	THR	C2555	GLY	LYS	GLN	LYS	D2151	L2070	ALA	F1854	V1783	Y1712	L1639
LYS	L2556	THR	L2556	PRO	ILE	GLY	LYS	T2152	T2070	PRO	D1855	A1784	L1713	H1640
LYS	A2557	THR	A2557	MET	ARG	TYR	ARG	L2152	T2070	GLY	E1857	ALA	L1714	I1641
LYS	E2449	THR	E2449	GLY	PHE	ASP	PHE	T2152	T2070	GLY	D1858	LEU	L1715	P1642
LYS	R2452	THR	R2452	LEU	GLY	LEU	P2226	L2156	T2070	GLY	D1859	PRO	L1716	E1643
LYS	I2453	THR	I2453	LEU	GLY	LEU	K2227	L2159	T2070	GLY	K1860	ALA	L1720	R1646
LYS	R2454	THR	R2454	LEU	GLY	LEU	K2227	L2159	T2070	GLY	I1862	VAL	E1721	C1647
LYS	A2455	THR	A2455	LEU	GLY	LEU	K2227	L2159	T2070	GLY	I1863	ALA	E1721	M1648
LYS	L2456	THR	L2456	LEU	GLY	LEU	K2227	L2159	T2070	GLY	R1864	ALA	E1721	D1649
LYS	L2457	THR	L2457	LEU	GLY	LEU	K2227	L2159	T2070	GLY	M1865	ALA	E1721	I1650
LYS	R2458	THR	R2458	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1867	ALA	E1721	L1652
LYS	X2465	THR	X2465	LEU	GLY	LEU	K2227	L2159	T2070	GLY	P1868	ARG	E1721	S1654
LYS	X2466	THR	X2466	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	E1655
LYS	X2467	THR	X2467	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1656
LYS	P2496	THR	P2496	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	D2497	THR	D2497	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	H2498	THR	H2498	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	K2499	THR	K2499	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	A2500	THR	A2500	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	S2501	THR	S2501	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	N2502	THR	N2502	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	V2503	THR	V2503	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	L2504	THR	L2504	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	F2505	THR	F2505	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	Y2510	THR	Y2510	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	GLY	THR	GLY	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	ILE	THR	ILE	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	GLU	THR	GLU	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	N2514	THR	N2514	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	F2517	THR	F2517	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	V2521	THR	V2521	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	L2522	THR	L2522	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	V2525	THR	V2525	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	P2529	THR	P2529	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	A2533	THR	A2533	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	L2537	THR	L2537	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	ASP	THR	ASP	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	E2760	THR	E2760	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	Y2761	THR	Y2761	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	T2762	THR	T2762	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	L2823	THR	L2823	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	E2824	THR	E2824	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	K2825	THR	K2825	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	A2826	THR	A2826	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	R2827	THR	R2827	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	D2828	THR	D2828	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	G2829	THR	G2829	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	G2900	THR	G2900	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	H2901	THR	H2901	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657
LYS	P2903	THR	P2903	LEU	GLY	LEU	K2227	L2159	T2070	GLY	E1869	ARG	E1721	L1657

L2904	L2905	V2906	F2907	V2908	D2909	T2910	L2911	T2912	A2913	K3694	K3695	D2914	D2915	D2918	D2919	R2920	E2921	D2924	L2927	K2928	F2929	L2930	Q2931	D2932	N2933	Q2934	D2935	D2936	V2937	T2938	R2939	H3647	R3648	A3649	C3650	N3651	Y3657	T3662	H3667	S3668	F3669	E3670	D3671	R3672	K3673	I3674	D3675	D3676	L3677	S3678	K3679	A3680	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
GLN	GLU	GLU	GLU	GLU	GLU	VAL	GLU	GLY	LYS	K3694	P3695	D3696	H3699	GLY	GLY	Q3700	L3701	V3702	F3705	T3708	A3709	E3712	S3795	S3796	K3713	S3714	T3797	L3798	K3799	Y3722	M3723	A3724	Y3725	A3726	D3727	I3728	Q3813	L3817	L3820	V3826	G3827	F3828	F3829	K3830	S3831	L3835	M3836	Q3837	T3838	C3839	S3840	V3841	L3842	E3750	V3751																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
Q3766	Q3767	S3768	R3769	K3852	ALA	GLU	GLY	GLY	GLY	M3778	V3779	L3780	K3781	M3782	A3785	C3786	K3787	K3788	E3789	T3790	M3793	V3794	S3795	S3796	K3713	S3714	T3797	L3798	K3799	I3802	L3805	A3806	N3809	Q3813	L3817	L3820	V3826	G3827	F3828	F3829	K3830	S3831	L3835	M3836	Q3837	T3838	C3839	S3840	V3841	L3842	D3843																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
L3844	R3849	K3852	ALA	GLU	GLU	GLY	LEU	GLY	MET	M4001	S3929	L3930	F3933	Q4005	Q4006	D4007	Y3934	Y3935	Y3936	Y3937	S3938	K3940	D3941	V3942	L3943	F3951	A3954	M3955	S3956	V3957	A3958	V3961	F3962	I3963	T3966	E3967	Y3968	Q3970	G3971	C3972	C3973	T3974	G3975	N3976	Q3977	L3980	S3983	R3984	E4050	S4051	S4052	N4054																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
V3990	G3991	F3992	L3993	H3994	V3995	F3996	A3997	H3998	M3999	M4000	M4001	K4002	L4003	Q4004	Q4005	D4006	Y3934	Y3935	Y3936	Y3937	S3938	K3940	D3941	V3942	L3943	F3951	A3954	M3955	S3956	V3957	A3958	V3961	F3962	I3963	T3966	E3967	Y3968	Q3970	G3971	C3972	C3973	T3974	G3975	N3976	Q3977	L3980	S3983	R3984	E4050	S4051	S4052	N4054																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
V4055	E4056	M4057	L4058	L4059	K4060	F4061	F4062	D4063	M4064	PHE	LEU	LYS	LEU	LYS	ASP	L4071	V4072	G4073	S4074	F4077	D4083	P4084	L4087	L4088	L4089	L4090	L4091	L4092	L4093	Q4100	Q4101	Q4102	P4106	E4107	L4108	L4109	F4110	L4111	L4112	S4113	N4120	L4123	L4124	L4125	L4126	L4127	L4128	L4129	L4130	L4131	L4132	L4133	L4134	L4135	L4136	L4137	L4138	L4139	L4140	L4141	L4142	L4143	L4144	L4145	L4146	L4147	L4148	L4149	L4150																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
L4146	L4147	T4148	M4149	L4150	V4154	F4155	H4156	D4157	F4158	R4159	L4160	R4161	L4164	F4165	H4166	E4167	E4168	A4172	R4175	L4178	G4179	R4180	E4181	E4182	S4187	R4188	R4189	L4190	E4191	L4192	L4193	Y4194	F4195	E4196	L4197	L4198	L4199	L4200	L4201	L4202	L4203	L4204	L4205	L4206	L4207	L4208	L4209	L4210	L4211	L4212	L4213	L4214	L4215	L4216	L4217	L4218	F4219	D4220	V4221	V4222	M4223	E4224	G4225	G4226	E4227	A4228	F4234																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
V4235	C4238	E4239	L4242	F4243	T4247	Y4251	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	



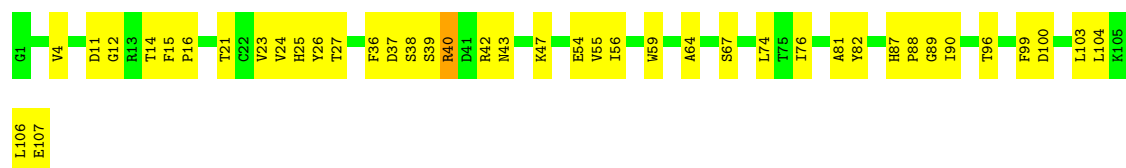
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain B: 60% 39%



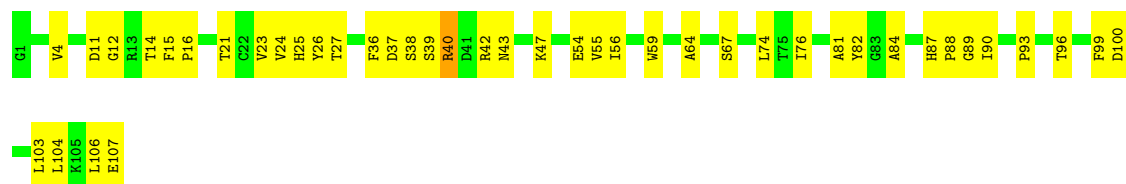
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain D: 62% 37%



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

Chain F: 60% 39%



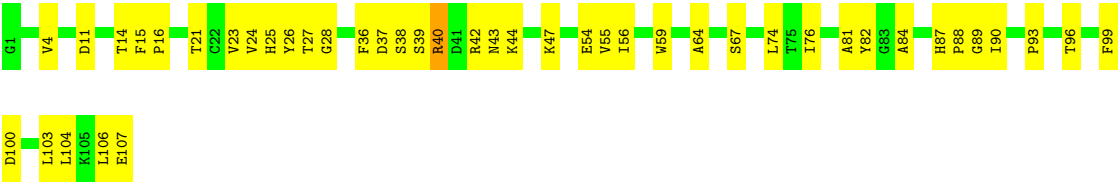
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H:

59%

40%

.



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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	2/24616 (0.0%)	0.59	19/33295 (0.1%)
1	C	0.33	2/24616 (0.0%)	0.59	19/33295 (0.1%)
1	E	0.33	2/24616 (0.0%)	0.59	19/33295 (0.1%)
1	G	0.33	2/24616 (0.0%)	0.59	19/33295 (0.1%)
2	B	0.26	0/851	0.45	0/1146
2	D	0.26	0/851	0.45	0/1146
2	F	0.26	0/851	0.45	0/1146
2	H	0.26	0/851	0.45	0/1146
All	All	0.33	8/101868 (0.0%)	0.59	76/137764 (0.1%)

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 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1544	PRO	N-CD	5.20	1.55	1.47
1	C	1544	PRO	N-CD	5.20	1.55	1.47
1	E	1544	PRO	N-CD	5.20	1.55	1.47
1	G	1544	PRO	N-CD	5.20	1.55	1.47
1	A	1763	PRO	N-CD	5.05	1.54	1.47

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1764	GLY	N-CA-C	14.38	149.05	113.10
1	C	1764	GLY	N-CA-C	14.38	149.05	113.10
1	E	1764	GLY	N-CA-C	14.38	149.05	113.10
1	G	1764	GLY	N-CA-C	14.38	149.05	113.10
1	A	1765	VAL	N-CA-CB	-9.67	90.23	111.50

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	1705	0
1	C	26957	0	23849	1709	0
1	E	26957	0	23849	1698	0
1	G	26957	0	23849	1714	0
2	B	832	0	831	41	0
2	D	832	0	831	42	0
2	F	832	0	831	42	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	6845	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 33.

The worst 5 of 6845 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:E:554:LEU:HD11	1:E:593:HIS:CE1	1.12	1.64
1:G:554:LEU:HD11	1:G:593:HIS:CE1	1.12	1.63
1:A:554:LEU:HD11	1:A:593:HIS:CE1	1.12	1.62
1:C:554:LEU:HD11	1:C:593:HIS:CE1	1.12	1.61
1:G:1961:PHE:CZ	1:G:2063:LEU:HD23	1.36	1.60

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%)	7	41
1	C	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	7	41
1	E	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	7	41
1	G	2991/4599 (65%)	2776 (93%)	155 (5%)	60 (2%)	7	41
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%)	11	42

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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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%)	2439 (97%)	68 (3%)	44	69
1	C	2507/3406 (74%)	2439 (97%)	68 (3%)	44	69
1	E	2507/3406 (74%)	2439 (97%)	68 (3%)	44	69
1	G	2507/3406 (74%)	2439 (97%)	68 (3%)	44	69
2	B	89/89 (100%)	88 (99%)	1 (1%)	73	85
2	D	89/89 (100%)	88 (99%)	1 (1%)	73	85
2	F	89/89 (100%)	88 (99%)	1 (1%)	73	85
2	H	89/89 (100%)	88 (99%)	1 (1%)	73	85
All	All	10384/13980 (74%)	10108 (97%)	276 (3%)	48	69

5 of 276 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	851	PHE
1	G	1055	PRO
1	G	4006	ASP
1	C	979	PRO
1	C	865	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 221 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	156	GLN
1	E	2100	HIS
2	H	25	HIS

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Mol	Chain	Res	Type
1	G	2196	ASN
1	E	278	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 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

Continued on next page...

Continued from previous page...

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

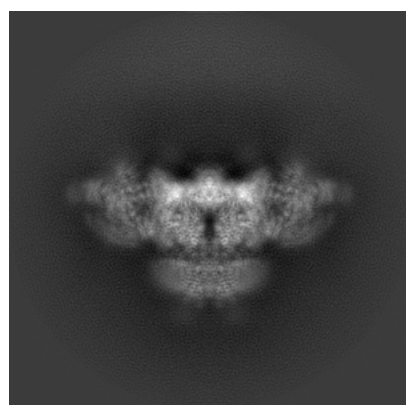
6 Map visualisation [i](#)

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.

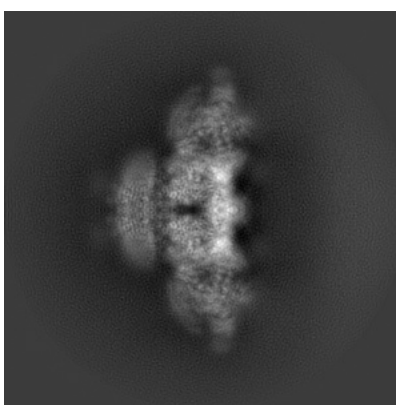
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

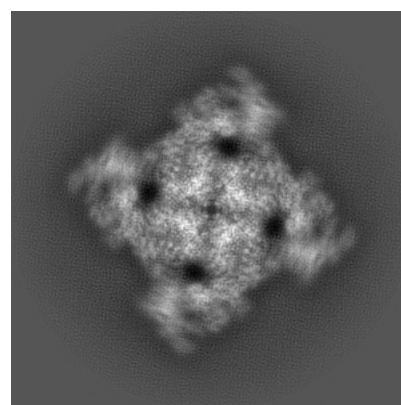
6.1.1 Primary map



X



Y

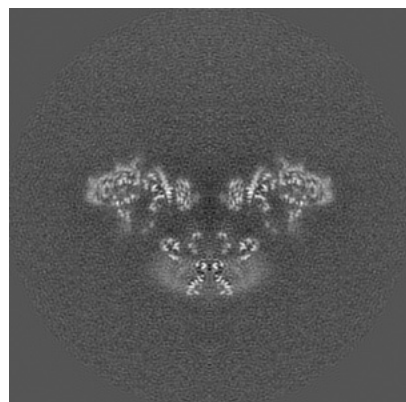


Z

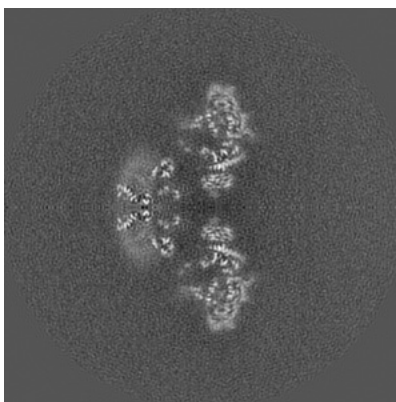
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

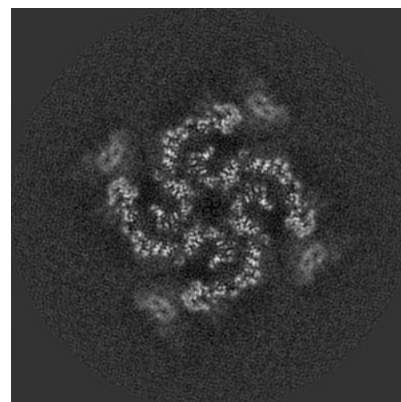
6.2.1 Primary map



X Index: 180



Y Index: 180

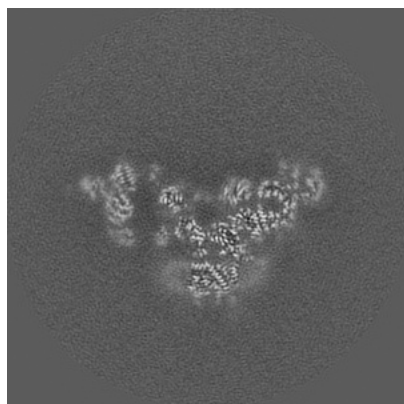


Z Index: 180

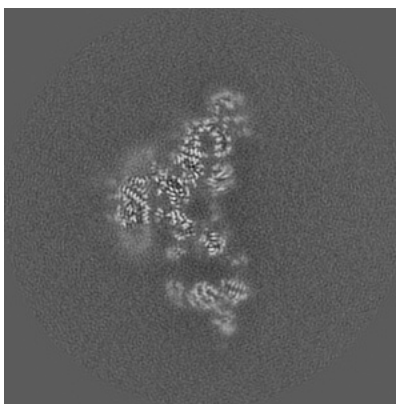
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

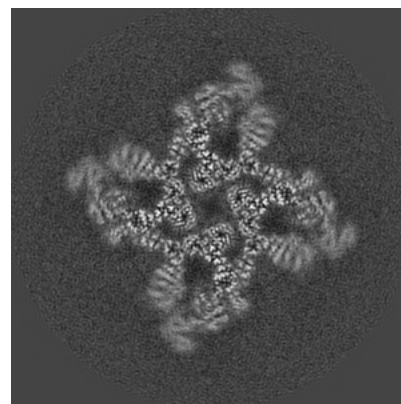
6.3.1 Primary map



X Index: 169



Y Index: 191

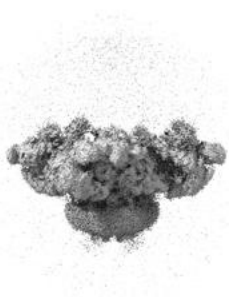


Z Index: 193

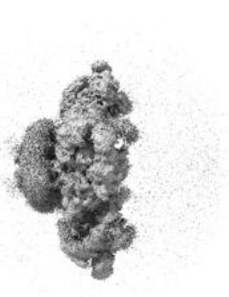
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

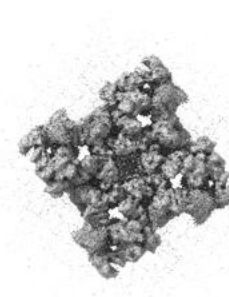
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

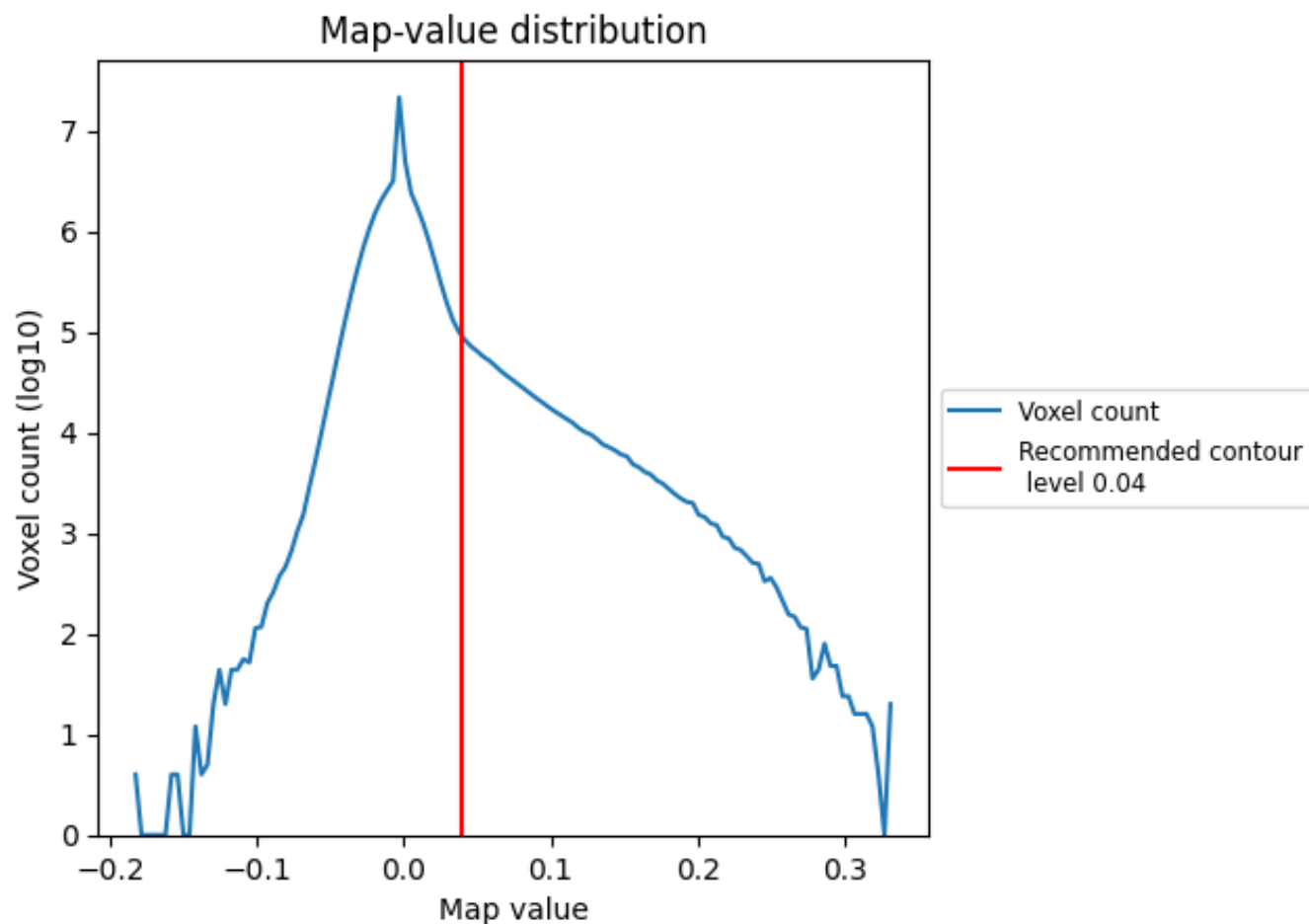
6.5 Mask visualisation

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

7 Map analysis [i](#)

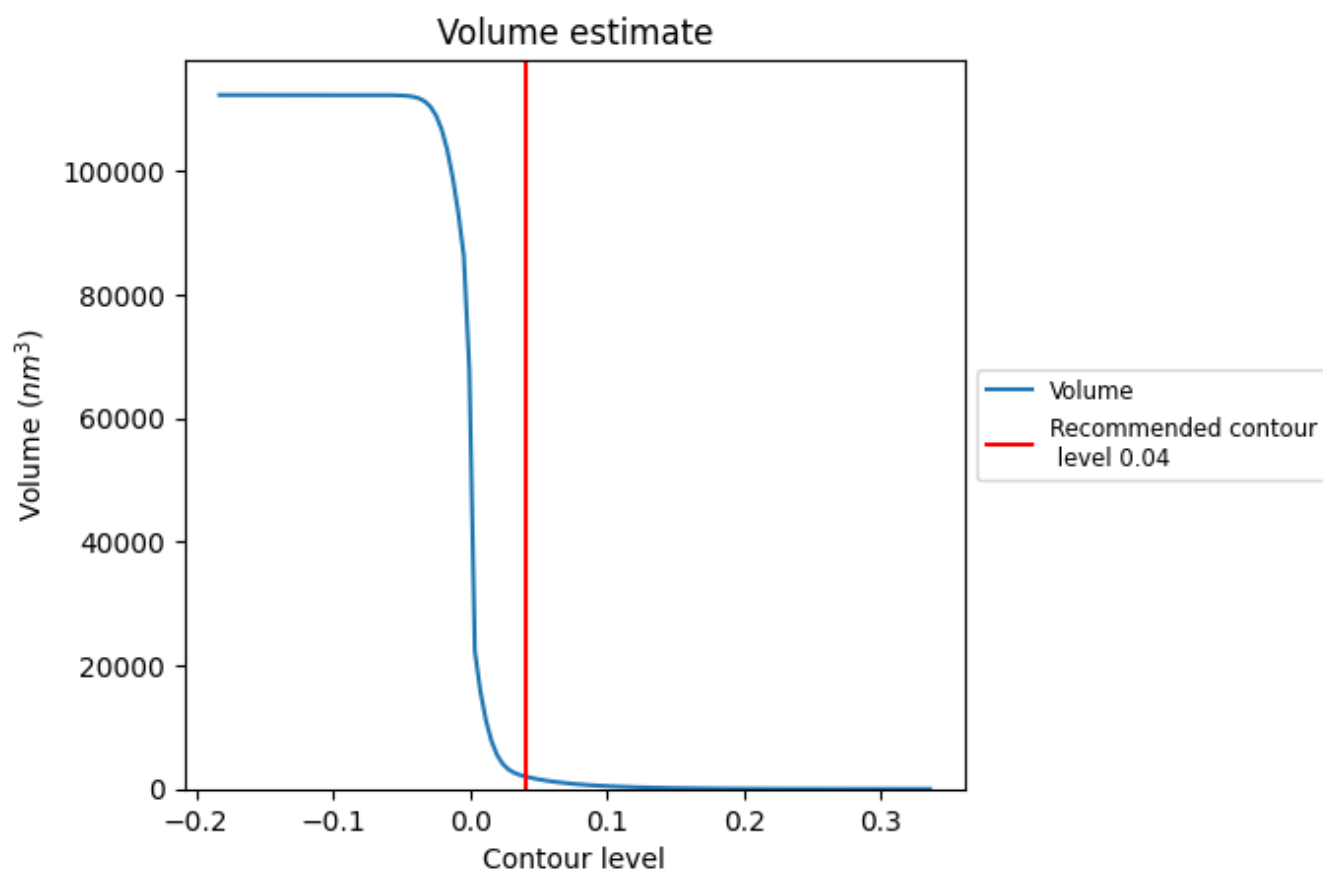
This section contains the results of statistical analysis of the map.

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.

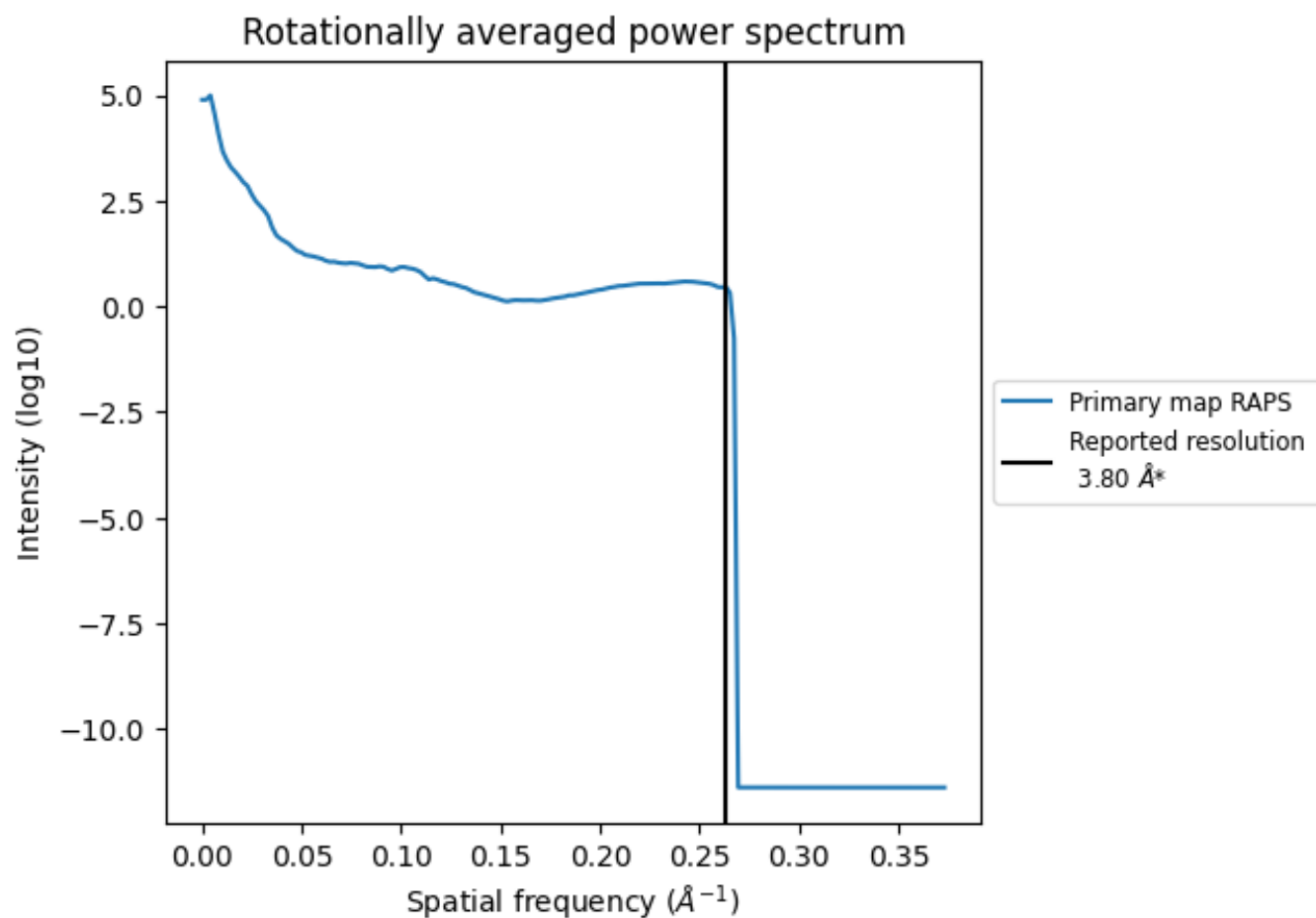
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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

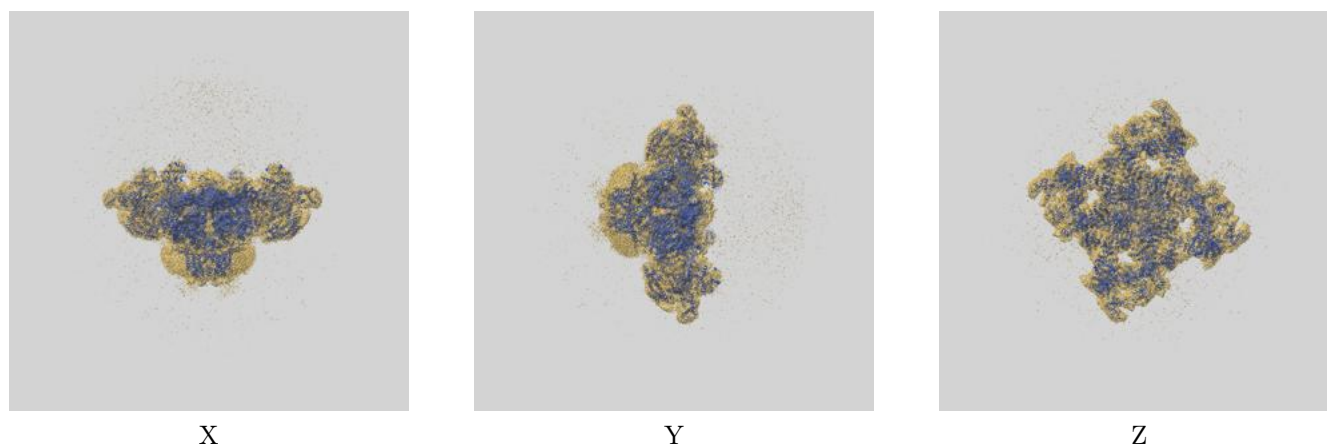
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

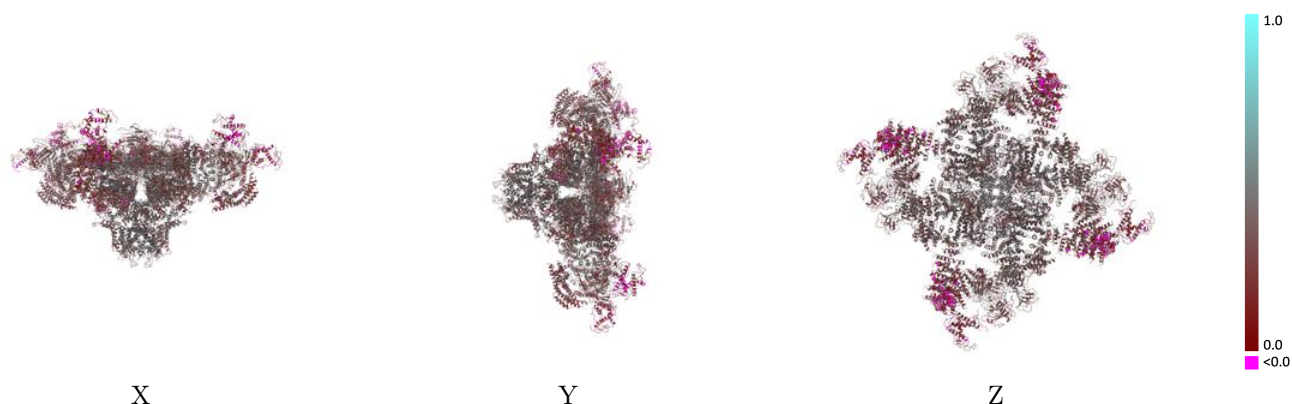
This section contains information regarding the fit between EMDB map EMD-2807 and PDB model 3J8H. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



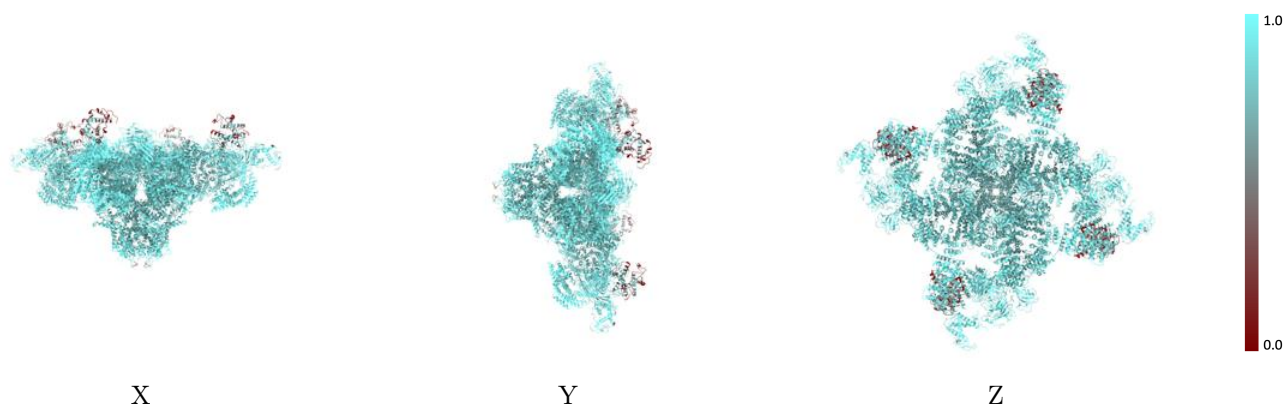
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



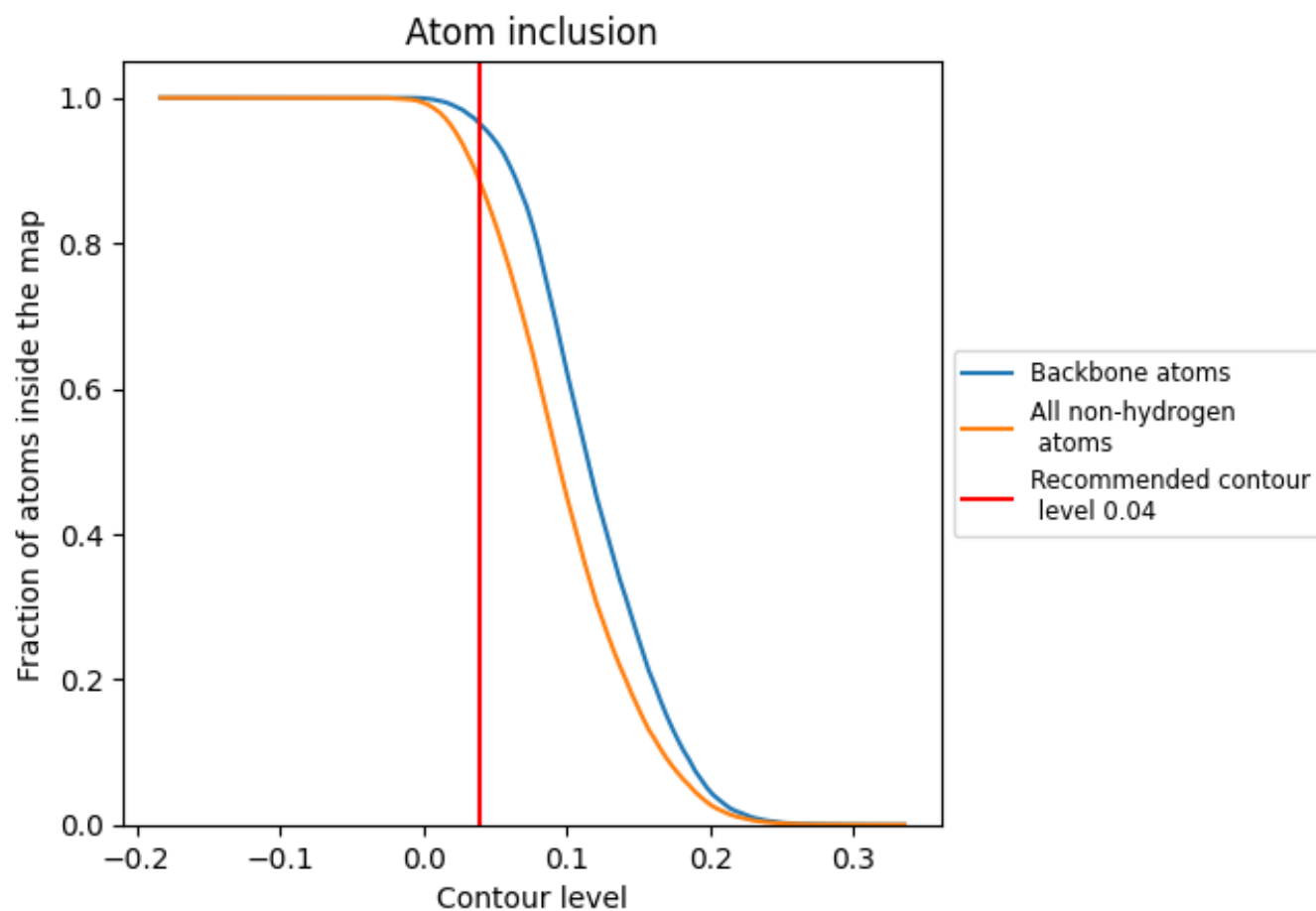
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	<div><div></div></div> 0.8824	<div><div></div></div> 0.3380
A	<div><div></div></div> 0.8813	<div><div></div></div> 0.3380
B	<div><div></div></div> 0.9191	<div><div></div></div> 0.3580
C	<div><div></div></div> 0.8813	<div><div></div></div> 0.3380
D	<div><div></div></div> 0.9191	<div><div></div></div> 0.3570
E	<div><div></div></div> 0.8813	<div><div></div></div> 0.3380
F	<div><div></div></div> 0.9191	<div><div></div></div> 0.3540
G	<div><div></div></div> 0.8813	<div><div></div></div> 0.3380
H	<div><div></div></div> 0.9191	<div><div></div></div> 0.3590

1.0

0.0

<0.0