



Full wwPDB EM Validation Report ⓘ

Dec 2, 2024 – 02:11 PM JST

PDB ID : 8JQG
EMDB ID : EMD-36571
Title : Cryo EM map of full length PLC gamma 2
Authors : Shin, Y.-C.; Liao, M.
Deposited on : 2023-06-14
Resolution : 3.72 Å (reported)

This is a Full wwPDB EM Validation 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

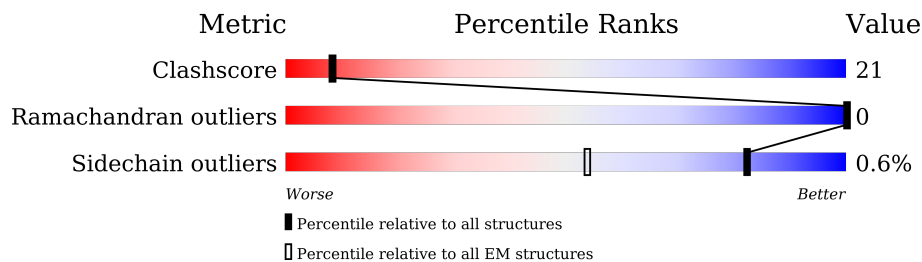
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.72 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1265	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8708 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.

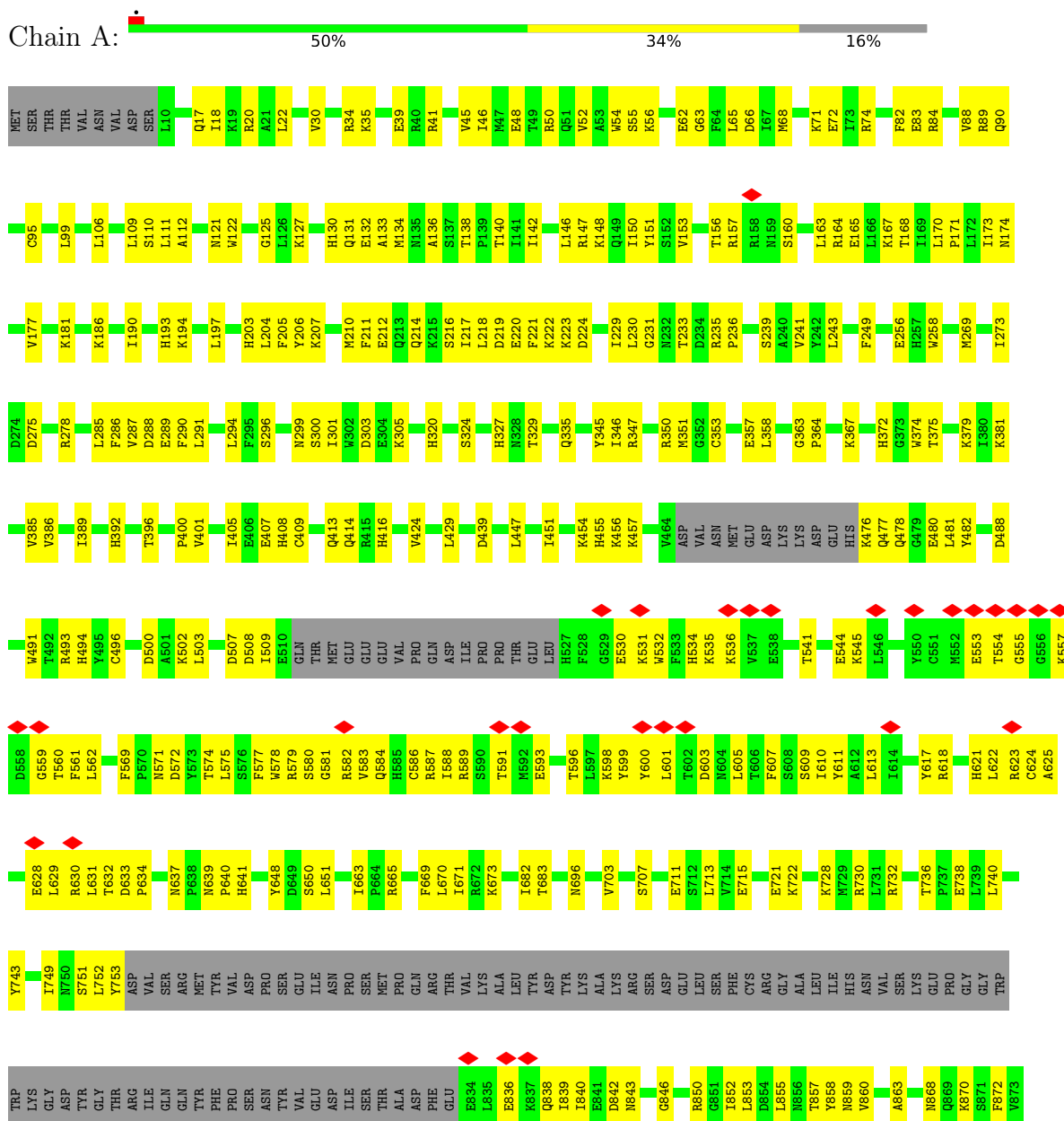
- Molecule 1 is a protein called 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1061	8708	5548	1494	1622	44	0	0

3 Residue-property plots i

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2



F874	F875	L876	E877	K878	K879	Q880	D883	E887	F888	A889	T890	D891	R892	V893	E894	E895	L896	F897	E898	W899	F900	Q901	S902	I903	R904	F905	I906	T907	W908	LYS	ILE	ASP	THR	LYS	GLU	ASN	ASN	ASN	MET	LYS	TYR	TRP	GLU	K922	I926	A927	I928	L933	K938	P939	T940	S941	K942	T943	K944
D945	N946	L947	P950	D951	F952	R953	F954	I955	R956	S957	F958	D964	R967	R968	L975	K976	Y977	K980	Y985	F986	F987	D993	N996	F999	F1000	R1001	L1002	F1014	A1017	D1018	K1019	Y1020	M1021	Q1022	M1023	L1027	Q1039	P1040	M1043	R1044	D1049	P1050	M1051												
I1069	L1069	M1061	T1062	L1063	T1064	V1065	K1066	V1067	L1068	I969	A1070	R1071	L1076	I1080	A1081	C1082	P1083	F1084	V1085	E1086	V1087	E1088	L1088	C1090	G1091	D1106	N1107	G1108	P1111	I1112	Q1117	F1122	E1123	I1124	Y1125	D1126	P1127	M1128	F1131	L1132	R1133	F1134	V1136	Y1137	E1138	N1146	F1147	L1148	A1149	H1150					
A1151	T1152	I1155	F1162	R1163	S1164	L1167	Y1171	A1178	S1179	L1180	L1181	V1182	E1185	M1186	R1187	P1188	V1189	L1190	GLU	SER	GLU	GLU	GLU	GLU	GLU	LEU	TYR	SER	SER	CYS	ARG	GLN	LEU	ARG	ARG	ARG	GLN	GLN	GLN	LEU	PHE	LEU	TYR	ASP	THR	HIS	GLN	ASN	ASN	LEU	ARG	ARG	ASN		
ALA	ASN	ARG	ASP	ALA	LEU	VAL	LYS	GLU	PHE	SER	VAL	ASN	GLU	ASN	GLN	LEU	LEU	LEU	TYR	GLN	GLU	LYS	ASN	LYS	ARG	LEU	GLU	GLU	ARG	VAL	SER	SER	ASN	SER	LYS	PHE	TYR	SER	ALA	LEU	LEU	LEU	ASP	THR	HIS	GLN	ASN	ASN	LEU	ARG	ARG	ASN			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	189652	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53.0932	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.982	Depositor
Minimum map value	-1.785	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.075	Depositor
Recommended contour level	0.3	Depositor
Map size (\AA)	237.6, 237.6, 237.6	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/8910	0.55	0/12025

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	8708	0	8605	368	0
All	All	8708	0	8605	368	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 21.

All (368) 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:578:TRP:HE1	1:A:581:GLY:H	1.13	0.92
1:A:491:TRP:HZ2	1:A:868:ASN:HB2	1.40	0.85
1:A:491:TRP:CZ2	1:A:868:ASN:HB2	2.10	0.85
1:A:623:ARG:HG2	1:A:628:GLU:HG2	1.62	0.81
1:A:939:PRO:HA	1:A:955:ILE:HG22	1.63	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:PHE:HE1	1:A:249:PHE:CE1	1.97	0.81
1:A:106:LEU:HD11	1:A:347:ARG:HE	1.46	0.81
1:A:22:LEU:HD21	1:A:122:TRP:HA	1.64	0.79
1:A:530:GLU:HG2	1:A:532:TRP:CE2	2.17	0.79
1:A:153:VAL:HG21	1:A:165:GLU:HB3	1.63	0.78
1:A:621:HIS:NE2	1:A:630:ARG:HG2	2.01	0.76
1:A:216:SER:HB3	1:A:1112:ILE:HD11	1.68	0.76
1:A:587:ARG:HE	1:A:589:ARG:HD3	1.52	0.74
1:A:621:HIS:HD2	1:A:630:ARG:N	1.86	0.74
1:A:482:TYR:HB2	1:A:889:ALA:HB3	1.70	0.73
1:A:899:TRP:O	1:A:903:ILE:HD12	1.90	0.72
1:A:996:ASN:HD22	1:A:1021:MET:HB2	1.55	0.72
1:A:74:ARG:NH1	1:A:346:ILE:HD13	2.04	0.72
1:A:838:GLN:NE2	1:A:842:ASP:OD2	2.24	0.71
1:A:72:GLU:HG2	1:A:350:ARG:HD3	1.71	0.70
1:A:457:LYS:HD2	1:A:938:LYS:HB2	1.73	0.70
1:A:534:HIS:CE1	1:A:562:LEU:HG	2.26	0.70
1:A:574:THR:HA	1:A:588:ILE:H	1.56	0.70
1:A:219:ASP:O	1:A:222:LYS:HB3	1.92	0.69
1:A:233:THR:HA	1:A:235:ARG:HH12	1.56	0.69
1:A:481:LEU:HD22	1:A:890:THR:HG22	1.75	0.69
1:A:599:TYR:HE1	1:A:613:LEU:HB2	1.57	0.69
1:A:599:TYR:CE1	1:A:613:LEU:HB2	2.29	0.68
1:A:530:GLU:HB2	1:A:611:TYR:OH	1.92	0.68
1:A:22:LEU:HD11	1:A:125:GLY:HA3	1.75	0.68
1:A:600:TYR:CD2	1:A:603:ASP:HA	2.29	0.68
1:A:593:GLU:HB3	1:A:598:LYS:HG3	1.76	0.68
1:A:409:CYS:O	1:A:414:GLN:NE2	2.28	0.67
1:A:858:TYR:HA	1:A:878:PRO:HA	1.77	0.67
1:A:68:MET:HG2	1:A:133:ALA:HB1	1.75	0.66
1:A:578:TRP:CE3	1:A:583:VAL:HG22	2.30	0.66
1:A:903:ILE:HA	1:A:906:ILE:HD12	1.76	0.66
1:A:99:LEU:HB3	1:A:106:LEU:HD23	1.77	0.66
1:A:218:LEU:HD12	1:A:230:LEU:HD11	1.78	0.65
1:A:637:ASN:O	1:A:640:PRO:HD3	1.96	0.65
1:A:39:GLU:HG3	1:A:41:ARG:HH11	1.62	0.65
1:A:1027:LEU:HB2	1:A:1131:PHE:HZ	1.60	0.64
1:A:621:HIS:CD2	1:A:630:ARG:HB3	2.32	0.64
1:A:579:ARG:N	1:A:582:ARG:O	2.25	0.64
1:A:74:ARG:HH12	1:A:346:ILE:CD1	2.11	0.64
1:A:901:GLN:HA	1:A:904:ARG:HD3	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ARG:NH1	1:A:346:ILE:CD1	2.60	0.63
1:A:243:LEU:HA	1:A:269:MET:HE1	1.81	0.63
1:A:407:GLU:O	1:A:408:HIS:ND1	2.32	0.63
1:A:1167:LEU:HD21	1:A:1180:LEU:HD13	1.81	0.63
1:A:1040:PRO:HG2	1:A:1128:ASN:HB2	1.81	0.63
1:A:223:LYS:HG2	1:A:224:ASP:H	1.64	0.63
1:A:221:PHE:CE1	1:A:249:PHE:CE1	2.84	0.62
1:A:999:PRO:HD3	1:A:1020:TYR:HB3	1.82	0.62
1:A:1027:LEU:HB2	1:A:1131:PHE:CZ	2.35	0.62
1:A:68:MET:CG	1:A:133:ALA:HB1	2.30	0.62
1:A:170:LEU:HD23	1:A:177:VAL:HG22	1.81	0.62
1:A:599:TYR:CZ	1:A:607:PHE:HB2	2.33	0.62
1:A:45:VAL:HG22	1:A:52:VAL:HG22	1.81	0.62
1:A:82:PHE:HE1	1:A:110:SER:HB3	1.65	0.61
1:A:588:ILE:HA	1:A:601:LEU:HD21	1.83	0.61
1:A:130:HIS:O	1:A:134:MET:HG2	2.00	0.61
1:A:221:PHE:CE1	1:A:249:PHE:CD1	2.89	0.61
1:A:493:ARG:HD2	1:A:509:ILE:HG21	1.82	0.61
1:A:596:THR:OG1	1:A:598:LYS:NZ	2.34	0.61
1:A:190:ILE:HG23	1:A:204:LEU:HD22	1.84	0.60
1:A:857:THR:HA	1:A:879:LYS:HD2	1.83	0.60
1:A:150:ILE:O	1:A:153:VAL:HG12	2.01	0.60
1:A:621:HIS:CD2	1:A:630:ARG:HG2	2.36	0.60
1:A:303:ASP:OD2	1:A:305:LYS:NZ	2.35	0.60
1:A:1089:ILE:HG21	1:A:1124:ILE:HD11	1.83	0.60
1:A:859:ASN:OD1	1:A:879:LYS:NZ	2.35	0.60
1:A:1023:MET:HE3	1:A:1131:PHE:HE2	1.66	0.59
1:A:1022:GLN:OE1	1:A:1133:ARG:NH1	2.31	0.59
1:A:1090:CYS:HB2	1:A:1131:PHE:HB2	1.84	0.59
1:A:286:PHE:O	1:A:290:PHE:N	2.34	0.59
1:A:621:HIS:CD2	1:A:630:ARG:N	2.70	0.59
1:A:707:SER:HB2	1:A:1080:ILE:HB	1.84	0.59
1:A:18:ILE:HD12	1:A:121:ASN:CG	2.23	0.59
1:A:385:VAL:O	1:A:389:ILE:HG13	2.03	0.59
1:A:329:THR:HB	1:A:345:TYR:CE1	2.37	0.59
1:A:329:THR:HB	1:A:345:TYR:HE1	1.68	0.59
1:A:578:TRP:HA	1:A:583:VAL:HA	1.85	0.58
1:A:71:LYS:HB3	1:A:72:GLU:OE1	2.03	0.58
1:A:72:GLU:HG2	1:A:350:ARG:CD	2.33	0.58
1:A:221:PHE:HE1	1:A:249:PHE:CD1	2.21	0.58
1:A:530:GLU:HG3	1:A:531:LYS:N	2.19	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:641:HIS:CD2	1:A:713:LEU:HD12	2.38	0.58
1:A:211:PHE:HE2	1:A:236:PRO:HA	1.68	0.58
1:A:589:ARG:HB2	1:A:600:TYR:CE2	2.39	0.58
1:A:648:TYR:HE2	1:A:670:LEU:HD22	1.67	0.58
1:A:876:LEU:HD23	1:A:887:GLU:H	1.68	0.57
1:A:975:LEU:HD12	1:A:1050:PRO:HG3	1.86	0.57
1:A:363:GLY:H	1:A:413:GLN:HE22	1.52	0.57
1:A:170:LEU:HD12	1:A:173:ILE:HD11	1.86	0.57
1:A:186:LYS:O	1:A:190:ILE:HG12	2.03	0.57
1:A:872:PHE:HB3	1:A:896:LEU:HD22	1.87	0.57
1:A:206:TYR:HE1	1:A:210:MET:HE2	1.69	0.57
1:A:456:LYS:HA	1:A:939:PRO:HG2	1.86	0.57
1:A:477:GLN:NE2	1:A:898:GLU:OE2	2.35	0.57
1:A:480:GLU:HB2	1:A:493:ARG:HH11	1.70	0.56
1:A:222:LYS:HE2	1:A:231:GLY:O	2.04	0.56
1:A:350:ARG:HA	1:A:396:THR:HG21	1.87	0.56
1:A:351:MET:SD	1:A:1014:PHE:CD2	2.99	0.56
1:A:496:CYS:HB3	1:A:503:LEU:HD21	1.87	0.56
1:A:530:GLU:HG2	1:A:532:TRP:NE1	2.20	0.56
1:A:749:ILE:O	1:A:753:TYR:OH	2.24	0.56
1:A:488:ASP:OD2	1:A:665:ARG:NH2	2.39	0.56
1:A:1066:LYS:NZ	1:A:1117:GLN:O	2.34	0.56
1:A:1067:VAL:HA	1:A:1182:VAL:HG12	1.87	0.56
1:A:1150:HIS:HD1	1:A:1152:THR:HG23	1.71	0.56
1:A:648:TYR:HB3	1:A:651:LEU:HG	1.88	0.56
1:A:671:ILE:HD12	1:A:682:ILE:HB	1.87	0.56
1:A:1112:ILE:HG23	1:A:1112:ILE:O	2.06	0.55
1:A:530:GLU:CG	1:A:531:LYS:N	2.70	0.55
1:A:50:ARG:HH22	1:A:140:THR:HG22	1.71	0.55
1:A:580:SER:O	1:A:580:SER:OG	2.23	0.55
1:A:591:THR:HG23	1:A:600:TYR:OH	2.07	0.55
1:A:55:SER:HB2	1:A:62:GLU:H	1.71	0.55
1:A:71:LYS:CB	1:A:72:GLU:OE1	2.55	0.55
1:A:401:VAL:HG12	1:A:451:ILE:HG12	1.88	0.55
1:A:561:PHE:HB3	1:A:631:LEU:HD22	1.89	0.55
1:A:575:LEU:HD13	1:A:601:LEU:HD11	1.89	0.55
1:A:579:ARG:HD2	1:A:584:GLN:HB2	1.89	0.55
1:A:1063:LEU:HD22	1:A:1065:VAL:HG23	1.89	0.55
1:A:221:PHE:CE2	1:A:290:PHE:HE2	2.25	0.55
1:A:429:LEU:HD21	1:A:933:LEU:HD11	1.87	0.55
1:A:621:HIS:CD2	1:A:630:ARG:CB	2.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:GLU:CG	1:A:531:LYS:H	2.20	0.54
1:A:1001:ARG:NH2	1:A:1051:MET:SD	2.81	0.54
1:A:296:SER:O	1:A:1164:SER:OG	2.24	0.54
1:A:648:TYR:CE2	1:A:670:LEU:HD22	2.42	0.54
1:A:858:TYR:HD2	1:A:876:LEU:HB3	1.72	0.54
1:A:951:ASP:OD2	1:A:953:ARG:NH1	2.41	0.54
1:A:233:THR:HA	1:A:235:ARG:NH1	2.22	0.54
1:A:347:ARG:O	1:A:351:MET:HB2	2.08	0.54
1:A:940:THR:O	1:A:956:ARG:NH1	2.40	0.54
1:A:90:GLN:HG2	1:A:112:ALA:HB1	1.90	0.54
1:A:839:ILE:O	1:A:843:ASN:ND2	2.41	0.54
1:A:30:VAL:HG22	1:A:111:LEU:HD22	1.90	0.54
1:A:34:ARG:HG2	1:A:35:LYS:HG2	1.90	0.54
1:A:374:TRP:O	1:A:478:GLN:NE2	2.36	0.54
1:A:993:ASP:OD1	1:A:993:ASP:N	2.39	0.53
1:A:632:THR:OG1	1:A:633:ASP:OD2	2.22	0.53
1:A:299:ASN:ND2	1:A:1162:PHE:O	2.38	0.53
1:A:571:ASN:O	1:A:571:ASN:ND2	2.41	0.53
1:A:572:ASP:OD2	1:A:587:ARG:NH1	2.42	0.53
1:A:82:PHE:CE1	1:A:110:SER:HB3	2.42	0.53
1:A:216:SER:HB3	1:A:1112:ILE:CD1	2.37	0.53
1:A:74:ARG:HD3	1:A:392:HIS:NE2	2.24	0.53
1:A:291:LEU:HD23	1:A:1071:ARG:HH21	1.75	0.53
1:A:863:ALA:H	1:A:874:PHE:HA	1.74	0.53
1:A:502:LYS:HE2	1:A:852:ILE:HD11	1.90	0.52
1:A:534:HIS:HE1	1:A:562:LEU:HG	1.72	0.52
1:A:1167:LEU:HB2	1:A:1178:ALA:HB1	1.92	0.52
1:A:214:GLN:HB2	1:A:217:ILE:HD11	1.92	0.52
1:A:938:LYS:O	1:A:955:ILE:N	2.41	0.52
1:A:1023:MET:HE3	1:A:1131:PHE:CE2	2.43	0.52
1:A:146:LEU:HD11	1:A:206:TYR:HD2	1.73	0.52
1:A:605:LEU:HB2	1:A:617:TYR:OH	2.10	0.52
1:A:738:GLU:OE1	1:A:738:GLU:N	2.30	0.52
1:A:532:TRP:HB3	1:A:634:PRO:HB3	1.92	0.52
1:A:273:ILE:HG21	1:A:278:ARG:HD2	1.92	0.51
1:A:164:ARG:HD2	1:A:554:THR:OG1	2.10	0.51
1:A:892:ARG:HH12	1:A:893:VAL:HG12	1.76	0.51
1:A:863:ALA:HB2	1:A:875:ILE:HG13	1.92	0.51
1:A:351:MET:SD	1:A:1014:PHE:HD2	2.34	0.51
1:A:500:ASP:O	1:A:502:LYS:HG3	2.11	0.51
1:A:860:VAL:HG11	1:A:903:ILE:HB	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ILE:HG13	1:A:205:PHE:HB2	1.93	0.51
1:A:221:PHE:CE2	1:A:290:PHE:CE2	2.99	0.51
1:A:18:ILE:HD12	1:A:121:ASN:OD1	2.12	0.50
1:A:218:LEU:HD23	1:A:291:LEU:HD12	1.93	0.50
1:A:381:LYS:O	1:A:385:VAL:HG23	2.12	0.50
1:A:400:PRO:HG3	1:A:447:LEU:HB3	1.93	0.50
1:A:534:HIS:HB3	1:A:637:ASN:HD21	1.76	0.50
1:A:218:LEU:CD2	1:A:291:LEU:HD12	2.42	0.50
1:A:624:CYS:SG	1:A:625:ALA:N	2.83	0.50
1:A:530:GLU:CD	1:A:531:LYS:H	2.15	0.50
1:A:350:ARG:HE	1:A:392:HIS:HD2	1.60	0.50
1:A:22:LEU:CD1	1:A:125:GLY:HA3	2.42	0.49
1:A:985:VAL:HG11	1:A:1002:LEU:HD21	1.94	0.49
1:A:943:THR:HG22	1:A:946:ASN:HB3	1.94	0.49
1:A:872:PHE:CE1	1:A:893:VAL:HB	2.47	0.49
1:A:880:GLN:OE1	1:A:883:ASP:N	2.45	0.49
1:A:151:TYR:CZ	1:A:157:ARG:HB2	2.48	0.49
1:A:221:PHE:CZ	1:A:229:ILE:HG21	2.48	0.49
1:A:711:GLU:N	1:A:715:GLU:OE1	2.45	0.49
1:A:210:MET:O	1:A:214:GLN:HG2	2.13	0.49
1:A:751:SER:OG	1:A:752:LEU:N	2.42	0.48
1:A:214:GLN:HB2	1:A:217:ILE:CD1	2.43	0.48
1:A:621:HIS:NE2	1:A:630:ARG:CG	2.75	0.48
1:A:65:LEU:HD13	1:A:109:LEU:HD23	1.96	0.48
1:A:372:HIS:O	1:A:375:THR:OG1	2.31	0.48
1:A:947:LEU:HD12	1:A:977:TYR:CG	2.48	0.48
1:A:1050:PRO:HB2	1:A:1051:MET:HE2	1.94	0.48
1:A:1084:PHE:CE1	1:A:1137:TYR:HB2	2.48	0.48
1:A:617:TYR:CD2	1:A:622:LEU:HB3	2.49	0.48
1:A:203:HIS:ND1	1:A:207:LYS:HE3	2.28	0.48
1:A:613:LEU:HG	1:A:617:TYR:CE1	2.48	0.48
1:A:876:LEU:HD21	1:A:888:PHE:CE2	2.49	0.48
1:A:300:SER:HA	1:A:1164:SER:O	2.14	0.48
1:A:142:ILE:HG23	1:A:206:TYR:HE2	1.79	0.48
1:A:363:GLY:H	1:A:413:GLN:NE2	2.11	0.48
1:A:71:LYS:O	1:A:72:GLU:CG	2.62	0.47
1:A:507:ASP:OD1	1:A:508:ASP:N	2.38	0.47
1:A:577:PHE:HE1	1:A:586:CYS:HB2	1.79	0.47
1:A:855:LEU:HD23	1:A:906:ILE:HD13	1.96	0.47
1:A:892:ARG:HB2	1:A:895:GLU:HB2	1.96	0.47
1:A:1061:MET:HE2	1:A:1127:PRO:HB3	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:GLN:HG3	1:A:291:LEU:HD11	1.97	0.47
1:A:324:SER:OG	1:A:353:CYS:HA	2.15	0.47
1:A:164:ARG:O	1:A:168:THR:HG23	2.14	0.47
1:A:544:GLU:OE2	1:A:545:LYS:NZ	2.47	0.47
1:A:1063:LEU:HD12	1:A:1155:ILE:HD11	1.95	0.47
1:A:66:ASP:OD1	1:A:148:LYS:NZ	2.41	0.47
1:A:358:LEU:HB2	1:A:405:ILE:HD13	1.95	0.47
1:A:663:ILE:HG22	1:A:743:TYR:CG	2.50	0.47
1:A:39:GLU:HB2	1:A:41:ARG:HD3	1.97	0.47
1:A:541:THR:HA	1:A:544:GLU:HG2	1.97	0.47
1:A:876:LEU:HD11	1:A:888:PHE:HE2	1.80	0.46
1:A:127:LYS:O	1:A:131:GLN:HG2	2.15	0.46
1:A:553:GLU:OE2	1:A:554:THR:HG22	2.16	0.46
1:A:559:GLY:HA2	1:A:578:TRP:O	2.15	0.46
1:A:46:ILE:O	1:A:50:ARG:N	2.48	0.46
1:A:1039:GLN:NE2	1:A:1043:MET:SD	2.86	0.46
1:A:17:GLN:HG3	1:A:20:ARG:HH12	1.81	0.46
1:A:351:MET:SD	1:A:1014:PHE:CE2	3.08	0.46
1:A:588:ILE:HA	1:A:601:LEU:CD2	2.44	0.46
1:A:836:GLU:HA	1:A:839:ILE:HD12	1.98	0.46
1:A:1085:VAL:HG22	1:A:1136:VAL:HG12	1.97	0.46
1:A:18:ILE:CD1	1:A:121:ASN:OD1	2.64	0.46
1:A:530:GLU:CG	1:A:532:TRP:CE2	2.96	0.46
1:A:1019:LYS:HG3	1:A:1133:ARG:CZ	2.46	0.46
1:A:1014:PHE:HA	1:A:1021:MET:CE	2.45	0.46
1:A:164:ARG:NH2	1:A:165:GLU:OE2	2.48	0.46
1:A:958:PHE:HB2	1:A:985:VAL:HG22	1.97	0.46
1:A:728:LYS:HB2	1:A:728:LYS:HE2	1.66	0.46
1:A:18:ILE:CD1	1:A:121:ASN:CG	2.85	0.45
1:A:71:LYS:O	1:A:72:GLU:HG3	2.16	0.45
1:A:74:ARG:HH12	1:A:346:ILE:HD12	1.81	0.45
1:A:1059:ILE:HG22	1:A:1125:TYR:HE1	1.82	0.45
1:A:1076:LEU:HD21	1:A:1148:LEU:HD23	1.97	0.45
1:A:364:PRO:HG3	1:A:379:LYS:NZ	2.32	0.45
1:A:1070:ALA:HB3	1:A:1111:PRO:HG2	1.98	0.45
1:A:146:LEU:HD11	1:A:206:TYR:CD2	2.51	0.45
1:A:903:ILE:O	1:A:907:THR:HG23	2.17	0.45
1:A:1082:CYS:SG	1:A:1106:ASP:N	2.84	0.45
1:A:560:THR:O	1:A:578:TRP:N	2.50	0.45
1:A:456:LYS:HD2	1:A:926:ILE:HD11	1.98	0.45
1:A:840:ILE:HG23	1:A:846:GLY:C	2.37	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1000:PHE:CE2	1:A:1091:GLY:HA2	2.51	0.45
1:A:71:LYS:O	1:A:72:GLU:CD	2.54	0.45
1:A:561:PHE:CD1	1:A:631:LEU:HB3	2.51	0.45
1:A:621:HIS:CD2	1:A:630:ARG:CG	3.00	0.45
1:A:569:PHE:CD1	1:A:587:ARG:NH1	2.85	0.45
1:A:855:LEU:HD12	1:A:855:LEU:HA	1.83	0.45
1:A:1107:ASN:O	1:A:1111:PRO:HB3	2.17	0.45
1:A:599:TYR:OH	1:A:607:PHE:HB2	2.17	0.44
1:A:622:LEU:O	1:A:628:GLU:HA	2.16	0.44
1:A:301:ILE:HA	1:A:1163:ARG:HD2	1.99	0.44
1:A:589:ARG:HB2	1:A:600:TYR:CD2	2.51	0.44
1:A:1068:LEU:HD23	1:A:1068:LEU:HA	1.82	0.44
1:A:52:VAL:HB	1:A:65:LEU:HD22	1.98	0.44
1:A:630:ARG:NH1	1:A:631:LEU:O	2.51	0.44
1:A:367:LYS:HG3	1:A:416:HIS:NE2	2.32	0.44
1:A:941:SER:H	1:A:942:LYS:NZ	2.14	0.44
1:A:241:VAL:N	1:A:285:LEU:O	2.44	0.44
1:A:88:VAL:HG13	1:A:89:ARG:HD2	2.00	0.44
1:A:132:GLU:O	1:A:136:ALA:N	2.50	0.44
1:A:219:ASP:O	1:A:222:LYS:N	2.45	0.44
1:A:544:GLU:HB2	1:A:583:VAL:HG11	1.99	0.44
1:A:83:GLU:HB2	1:A:84:ARG:HH12	1.83	0.44
1:A:1162:PHE:HB3	1:A:1181:LEU:HD11	2.00	0.44
1:A:530:GLU:HG3	1:A:531:LYS:H	1.80	0.44
1:A:1022:GLN:HG2	1:A:1150:HIS:CE1	2.52	0.44
1:A:174:ASN:OD1	1:A:1108:GLY:HA3	2.18	0.44
1:A:320:HIS:HB3	1:A:1044:ARG:HD3	1.99	0.43
1:A:345:TYR:OH	1:A:357:GLU:O	2.25	0.43
1:A:1136:VAL:O	1:A:1148:LEU:HB2	2.18	0.43
1:A:386:VAL:HG13	1:A:424:VAL:HG21	2.00	0.43
1:A:454:LYS:HE2	1:A:955:ILE:HG21	2.01	0.43
1:A:532:TRP:HZ2	1:A:611:TYR:CE2	2.36	0.43
1:A:1059:ILE:HG13	1:A:1189:VAL:HG21	1.98	0.43
1:A:721:GLU:OE1	1:A:722:LYS:HG2	2.18	0.43
1:A:1018:ASP:OD1	1:A:1019:LYS:N	2.46	0.43
1:A:1138:GLU:HB3	1:A:1148:LEU:HD11	2.00	0.43
1:A:181:LYS:HE3	1:A:181:LYS:HB2	1.74	0.43
1:A:532:TRP:CH2	1:A:610:ILE:HB	2.53	0.43
1:A:71:LYS:C	1:A:72:GLU:OE1	2.55	0.43
1:A:455:HIS:HE1	1:A:926:ILE:HG23	1.83	0.43
1:A:447:LEU:HA	1:A:447:LEU:HD23	1.81	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:ARG:NE	1:A:589:ARG:HD3	2.27	0.43
1:A:599:TYR:OH	1:A:609:SER:O	2.31	0.43
1:A:163:LEU:HD11	1:A:167:LYS:HE3	2.00	0.43
1:A:545:LYS:HA	1:A:545:LYS:HD3	1.90	0.43
1:A:1023:MET:SD	1:A:1090:CYS:HB3	2.59	0.43
1:A:153:VAL:CG2	1:A:165:GLU:HB3	2.40	0.43
1:A:156:THR:O	1:A:157:ARG:HG2	2.19	0.43
1:A:221:PHE:CZ	1:A:249:PHE:CD1	3.07	0.43
1:A:941:SER:O	1:A:941:SER:OG	2.36	0.43
1:A:507:ASP:HB2	1:A:850:ARG:HG3	2.01	0.43
1:A:673:LYS:C	1:A:673:LYS:HD3	2.39	0.43
1:A:476:LYS:HE2	1:A:476:LYS:HB2	1.86	0.43
1:A:530:GLU:HG2	1:A:532:TRP:CZ2	2.54	0.43
1:A:532:TRP:HZ2	1:A:611:TYR:CE1	2.36	0.43
1:A:639:ASN:HB3	1:A:641:HIS:CE1	2.54	0.43
1:A:736:THR:O	1:A:740:LEU:N	2.47	0.43
1:A:220:GLU:C	1:A:222:LYS:N	2.72	0.42
1:A:275:ASP:HB3	1:A:278:ARG:HG3	2.01	0.42
1:A:696:ASN:HB2	1:A:703:VAL:HG12	1.99	0.42
1:A:669:PHE:HA	1:A:683:THR:O	2.19	0.42
1:A:707:SER:OG	1:A:1080:ILE:N	2.50	0.42
1:A:928:ILE:HD12	1:A:928:ILE:H	1.84	0.42
1:A:481:LEU:HD11	1:A:899:TRP:CH2	2.54	0.42
1:A:968:ARG:HA	1:A:968:ARG:HD3	1.82	0.42
1:A:1049:ASP:OD1	1:A:1049:ASP:N	2.53	0.42
1:A:621:HIS:HD2	1:A:629:LEU:C	2.23	0.42
1:A:980:LYS:HA	1:A:980:LYS:HD3	1.82	0.42
1:A:239:SER:O	1:A:287:VAL:N	2.50	0.42
1:A:618:ARG:HG2	1:A:631:LEU:O	2.18	0.42
1:A:1019:LYS:HG3	1:A:1133:ARG:NE	2.34	0.42
1:A:218:LEU:HD12	1:A:230:LEU:CD1	2.47	0.42
1:A:286:PHE:HB2	1:A:289:GLU:CD	2.40	0.42
1:A:650:SER:O	1:A:651:LEU:HD23	2.19	0.42
1:A:1064:THR:OG1	1:A:1185:GLU:HB3	2.19	0.42
1:A:48:GLU:HB3	1:A:147:ARG:HG2	2.02	0.42
1:A:950:PRO:HB3	1:A:977:TYR:CD1	2.55	0.42
1:A:193:HIS:ND1	1:A:194:LYS:N	2.68	0.41
1:A:964:ASP:O	1:A:967:ILE:HG22	2.20	0.41
1:A:138:THR:OG1	1:A:296:SER:HB2	2.21	0.41
1:A:229:ILE:HG21	1:A:249:PHE:HB2	2.01	0.41
1:A:1062:THR:HG23	1:A:1187:ARG:HB2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:PHE:CZ	1:A:290:PHE:HZ	2.38	0.41
1:A:327:HIS:CG	1:A:987:PRO:HD2	2.54	0.41
1:A:898:GLU:HA	1:A:901:GLN:OE1	2.20	0.41
1:A:1083:PRO:HA	1:A:1137:TYR:O	2.20	0.41
1:A:1089:ILE:HD11	1:A:1122:PHE:CD2	2.55	0.41
1:A:212:GLU:OE2	1:A:236:PRO:HB3	2.20	0.41
1:A:217:ILE:C	1:A:219:ASP:N	2.72	0.41
1:A:1017:ALA:HB2	1:A:1171:TYR:CD1	2.55	0.41
1:A:456:LYS:O	1:A:926:ILE:HD13	2.20	0.41
1:A:730:ARG:HD2	1:A:732:ARG:NH2	2.35	0.41
1:A:1087:VAL:HG22	1:A:1134:PHE:HD1	1.86	0.41
1:A:1138:GLU:OE1	1:A:1146:ASN:HB3	2.21	0.41
1:A:54:TRP:CE2	1:A:63:GLY:HA3	2.56	0.41
1:A:193:HIS:ND1	1:A:194:LYS:HG3	2.36	0.41
1:A:218:LEU:HD21	1:A:291:LEU:HB2	2.02	0.41
1:A:477:GLN:OE1	1:A:478:GLN:N	2.54	0.41
1:A:870:LYS:HD3	1:A:870:LYS:HA	1.86	0.41
1:A:256:GLU:OE1	1:A:258:TRP:NE1	2.51	0.41
1:A:335:GLN:HB3	1:A:372:HIS:CE1	2.56	0.41
1:A:535:LYS:HB3	1:A:536:LYS:H	1.65	0.41
1:A:610:ILE:H	1:A:610:ILE:HG12	1.72	0.41
1:A:876:LEU:HD13	1:A:876:LEU:HA	1.91	0.41
1:A:82:PHE:CZ	1:A:95:CYS:HB3	2.56	0.40
1:A:294:LEU:O	1:A:1164:SER:HB3	2.20	0.40
1:A:555:GLY:O	1:A:557:LYS:HG2	2.22	0.40
1:A:569:PHE:CG	1:A:587:ARG:HD3	2.56	0.40
1:A:160:SER:HA	1:A:197:LEU:O	2.21	0.40
1:A:1124:ILE:HD13	1:A:1124:ILE:HA	1.93	0.40
1:A:1137:TYR:HD1	1:A:1146:ASN:O	2.04	0.40
1:A:1137:TYR:CD1	1:A:1147:PHE:HA	2.55	0.40
1:A:171:PRO:HB3	1:A:1080:ILE:HD11	2.04	0.40
1:A:574:THR:HA	1:A:587:ARG:HA	2.03	0.40
1:A:663:ILE:HG22	1:A:743:TYR:CD1	2.57	0.40
1:A:212:GLU:HA	1:A:212:GLU:OE1	2.21	0.40
1:A:56:LYS:HA	1:A:56:LYS:HE2	2.04	0.40

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	1051/1265 (83%)	997 (95%)	54 (5%)	0	100 100

There are no Ramachandran outliers to report.

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	965/1158 (83%)	959 (99%)	6 (1%)	84 90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	ASP
1	A	439	ASP
1	A	494	HIS
1	A	853	LEU
1	A	945	ASP
1	A	1138	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	621	HIS
1	A	637	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1025	HIS
1	A	1031	ASN

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](#)

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.

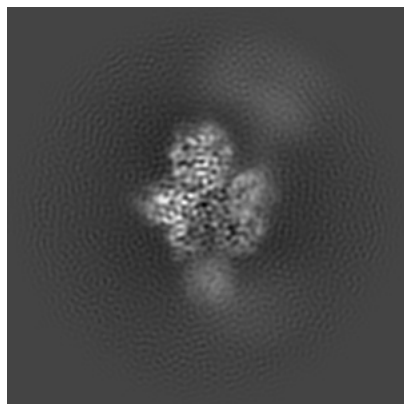
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36571. These allow visual inspection of the internal detail of the map and identification of artifacts.

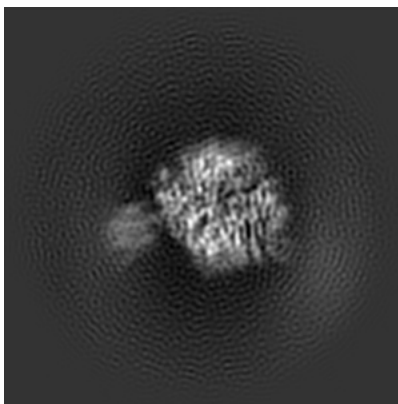
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

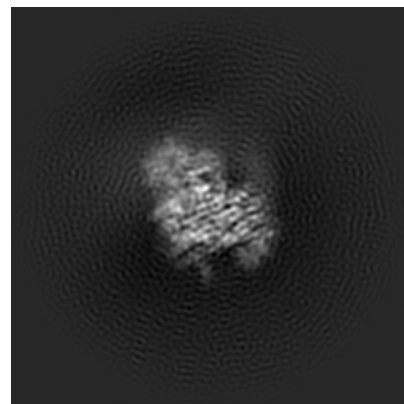
6.1.1 Primary map



X

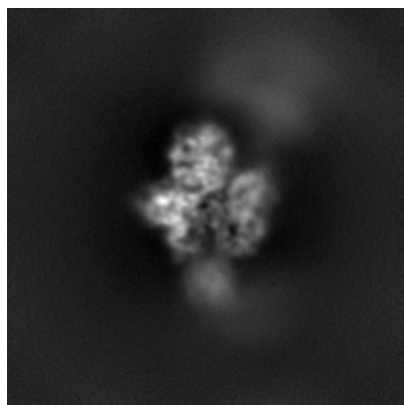


Y

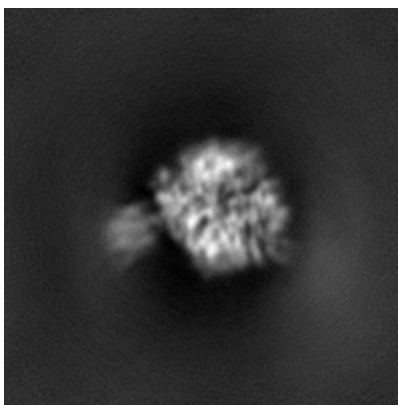


Z

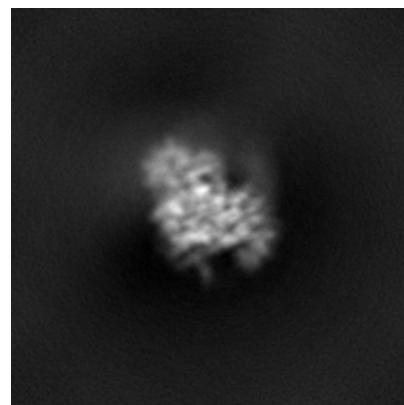
6.1.2 Raw map



X



Y

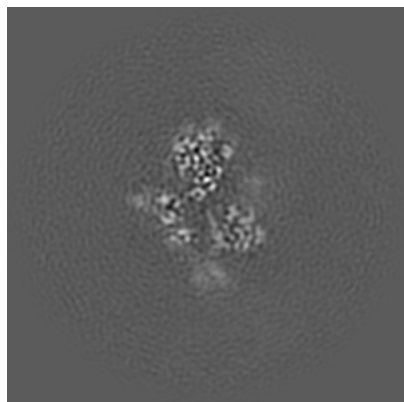


Z

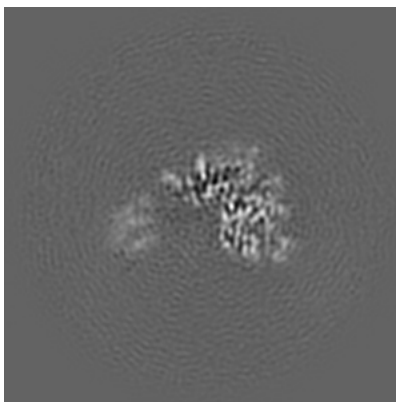
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

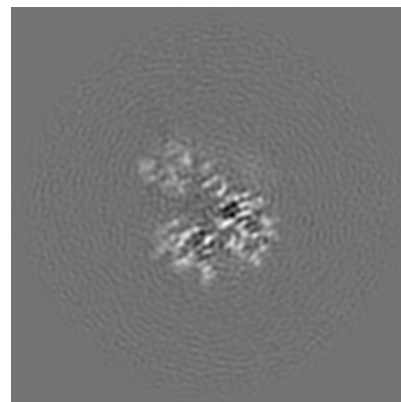
6.2.1 Primary map



X Index: 108

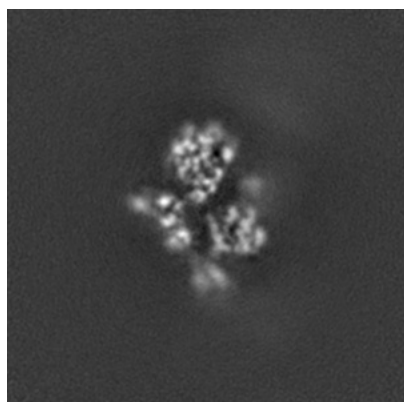


Y Index: 108

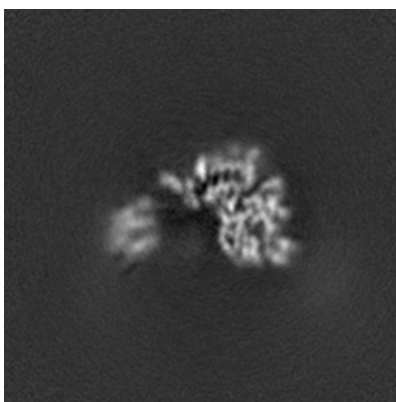


Z Index: 108

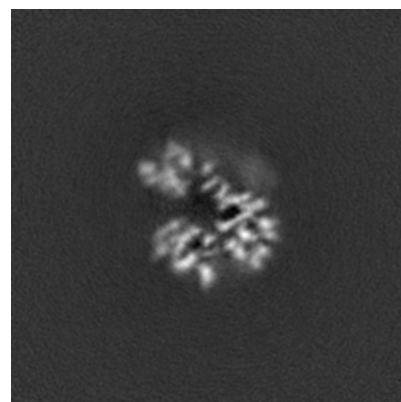
6.2.2 Raw map



X Index: 108



Y Index: 108

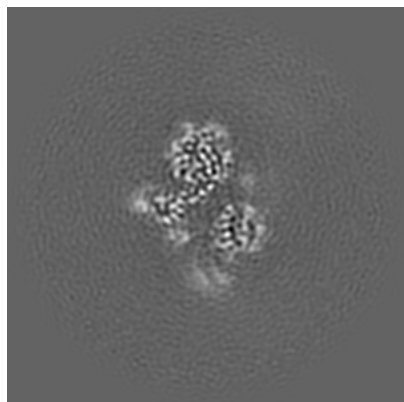


Z Index: 108

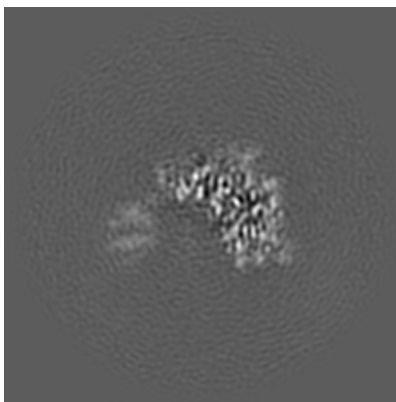
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

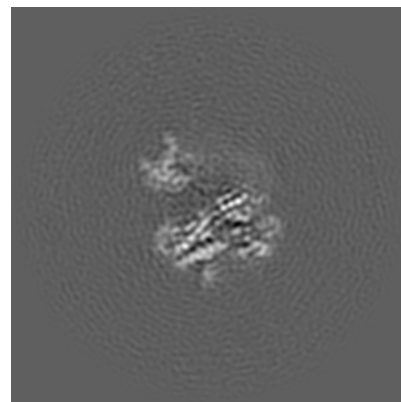
6.3.1 Primary map



X Index: 105

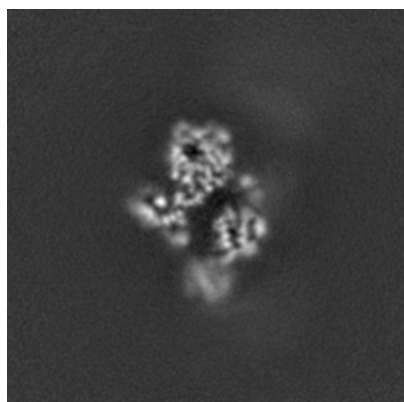


Y Index: 105

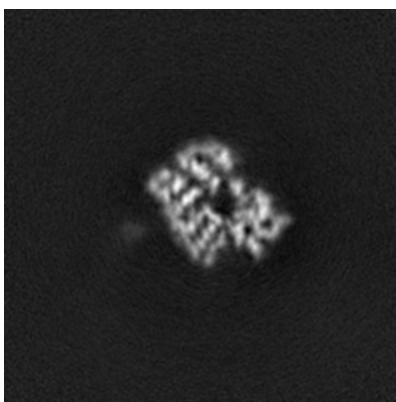


Z Index: 111

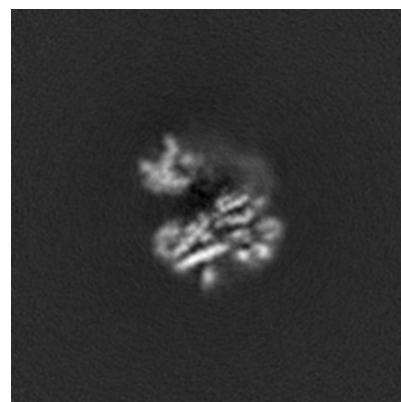
6.3.2 Raw map



X Index: 103



Y Index: 92

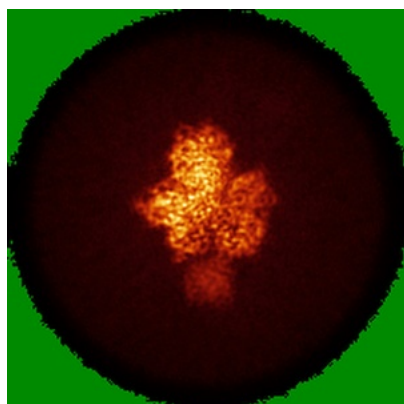


Z Index: 111

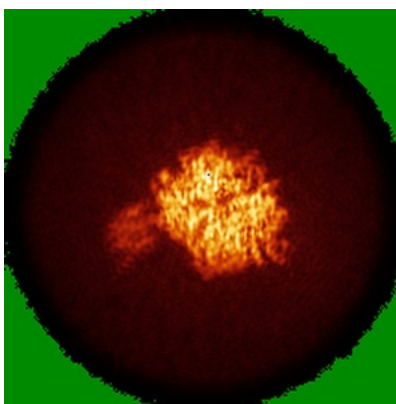
The images above show the largest variance slices of the map in three orthogonal directions.

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

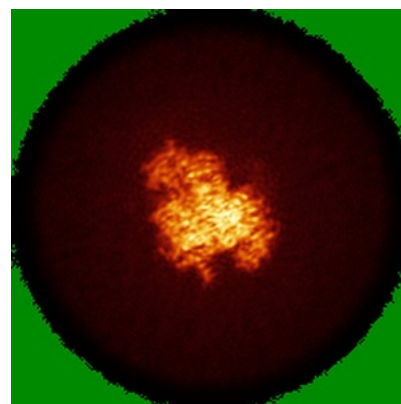
6.4.1 Primary map



X

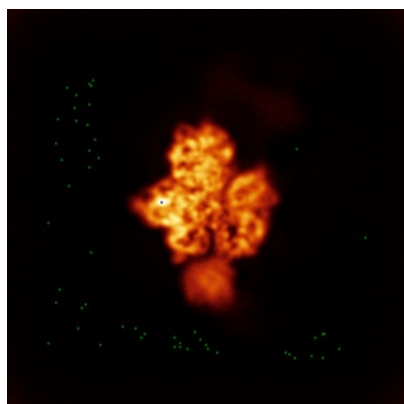


Y

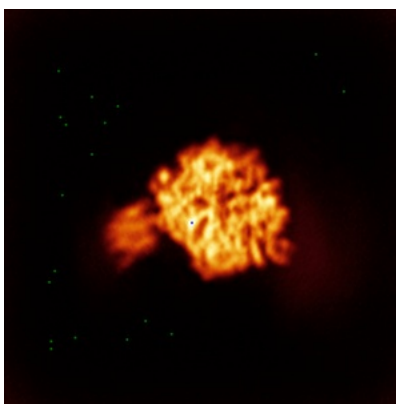


Z

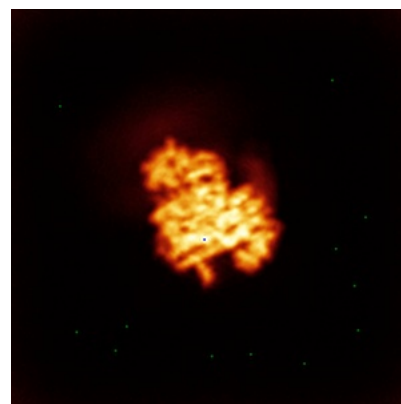
6.4.2 Raw map



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.

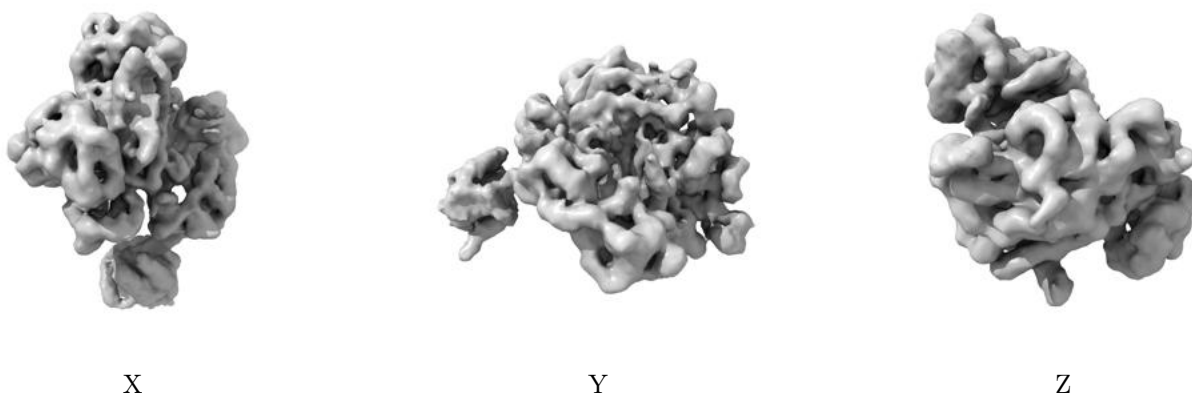
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

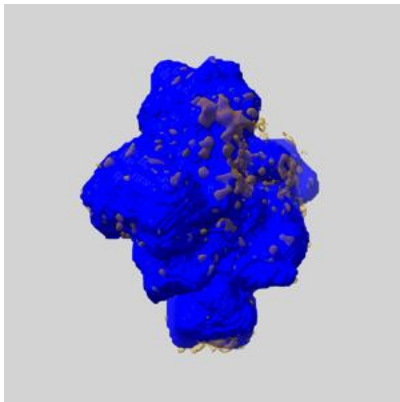
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

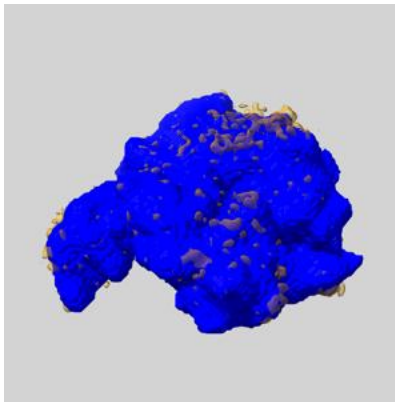
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

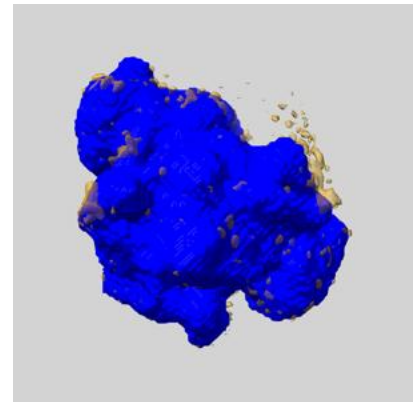
6.6.1 emd_36571_msk_1.map [i](#)



X



Y

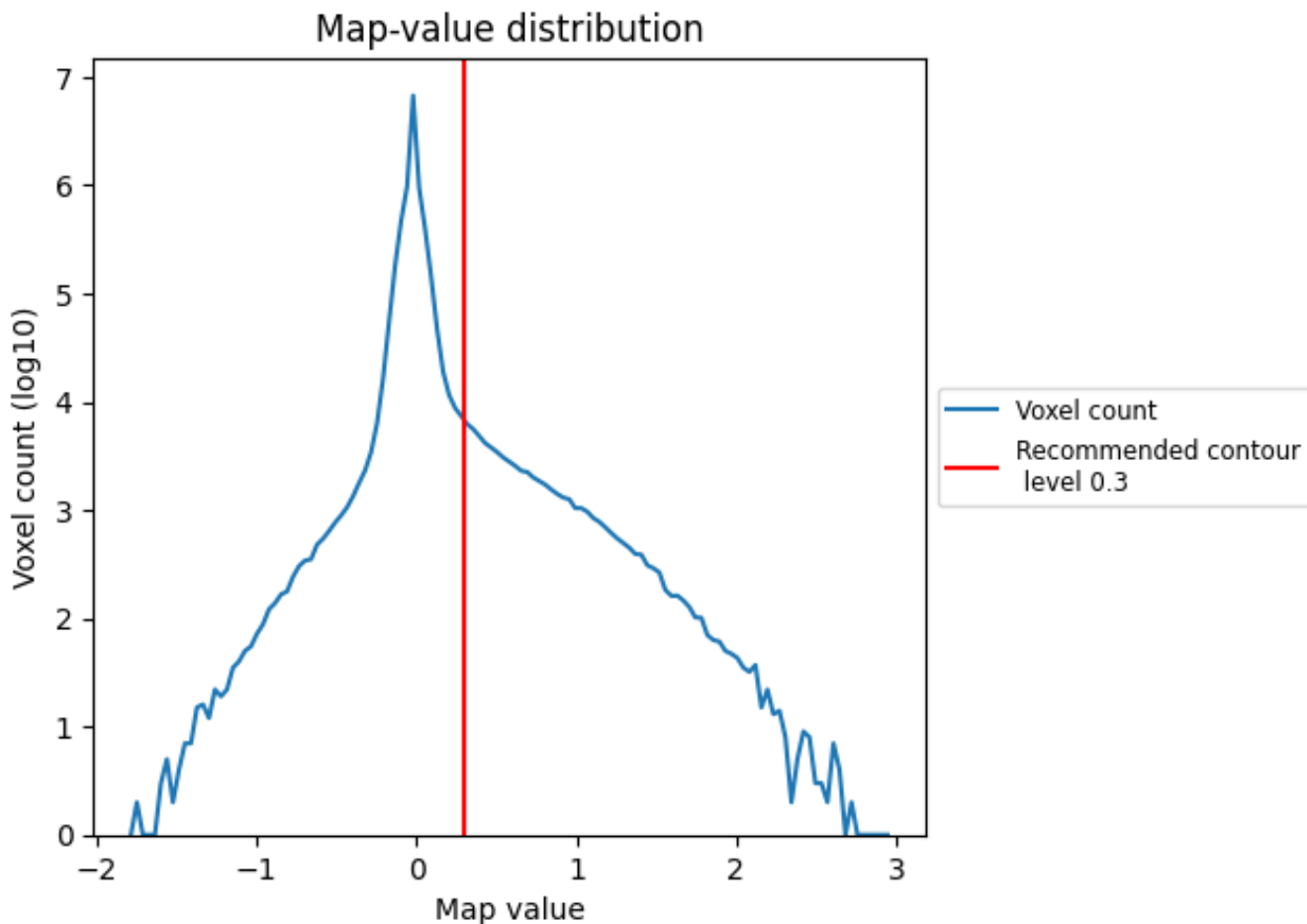


Z

7 Map analysis [i](#)

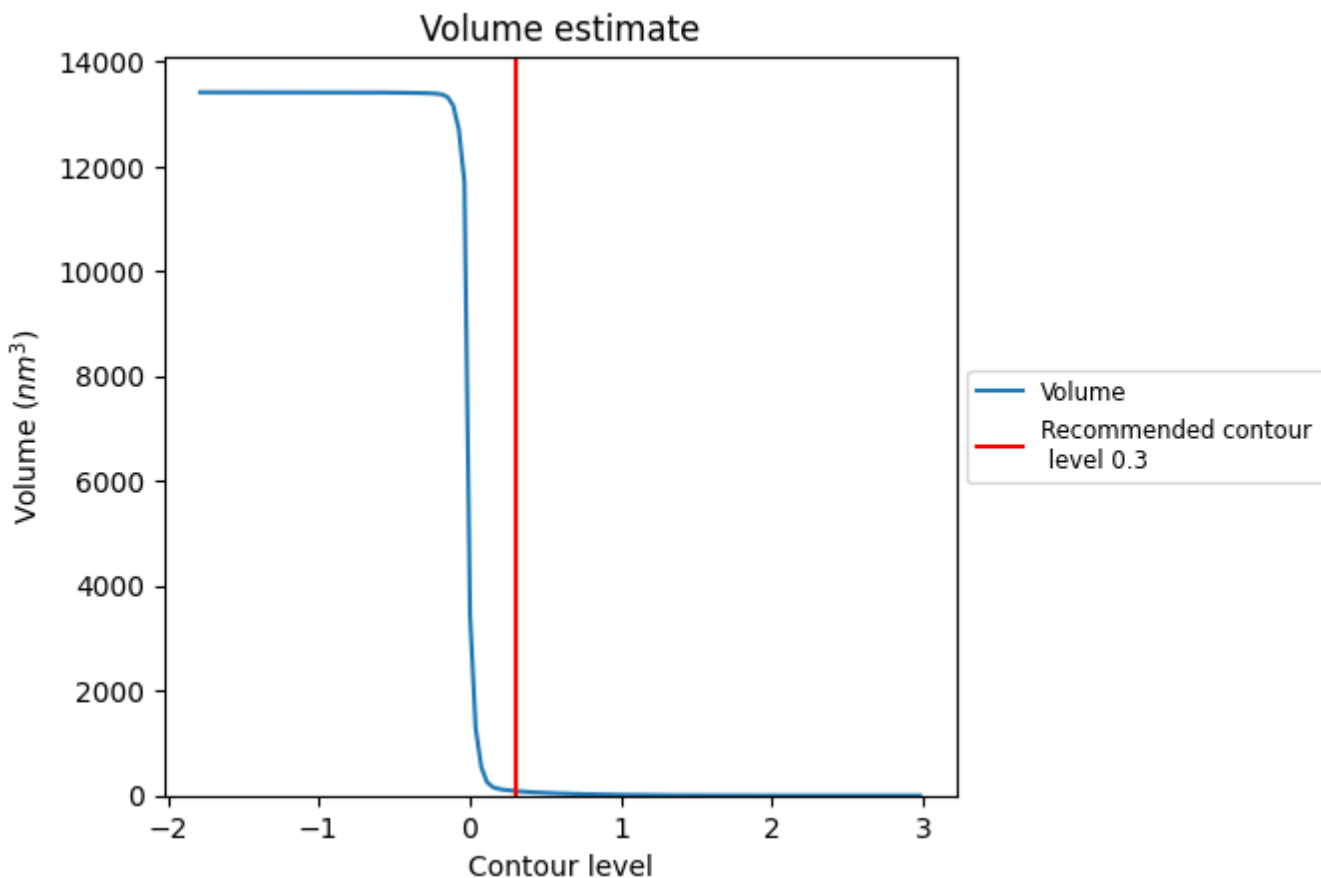
This section contains the results of statistical analysis of the map.

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.

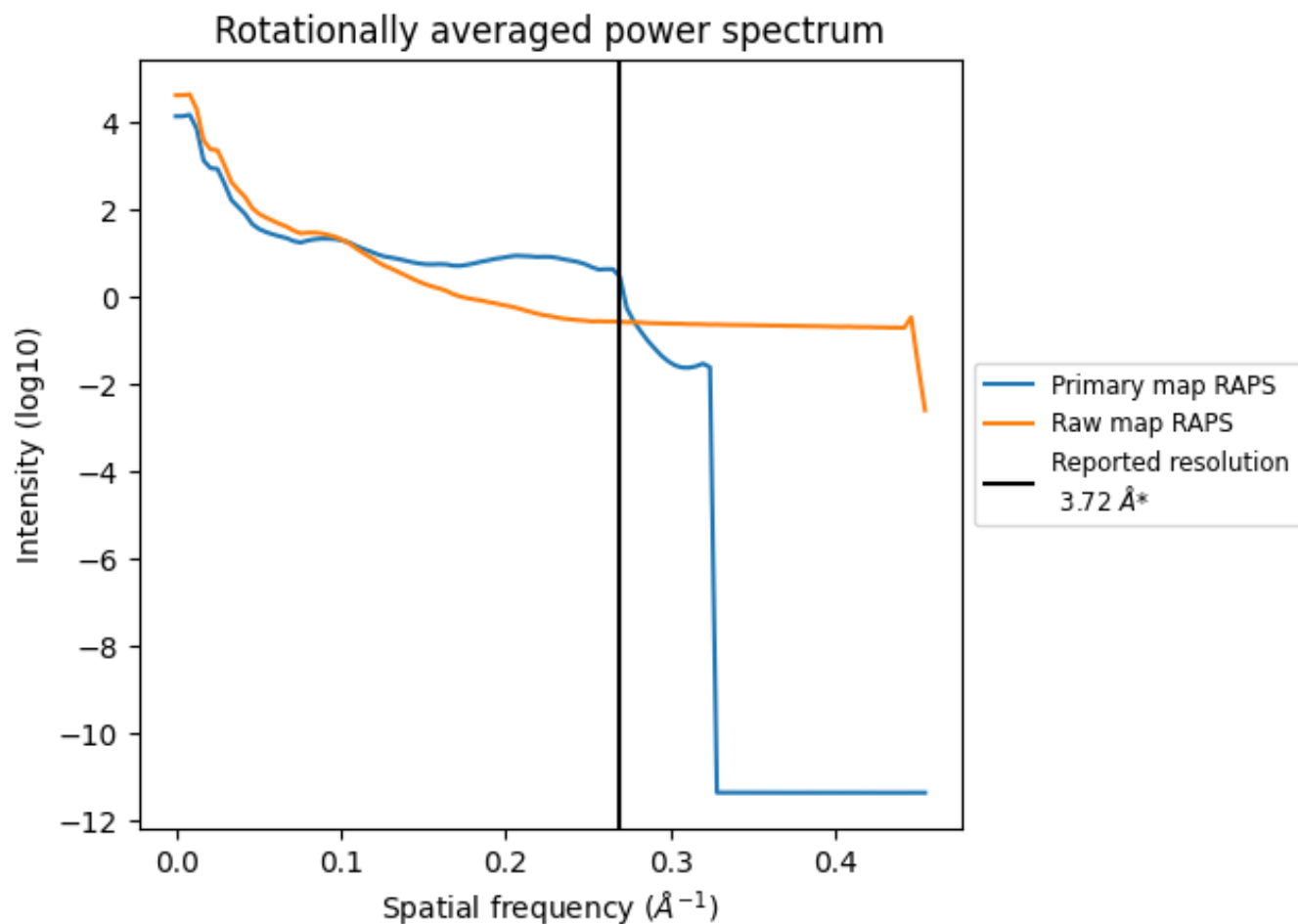
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 88 nm³; this corresponds to an approximate mass of 79 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 i

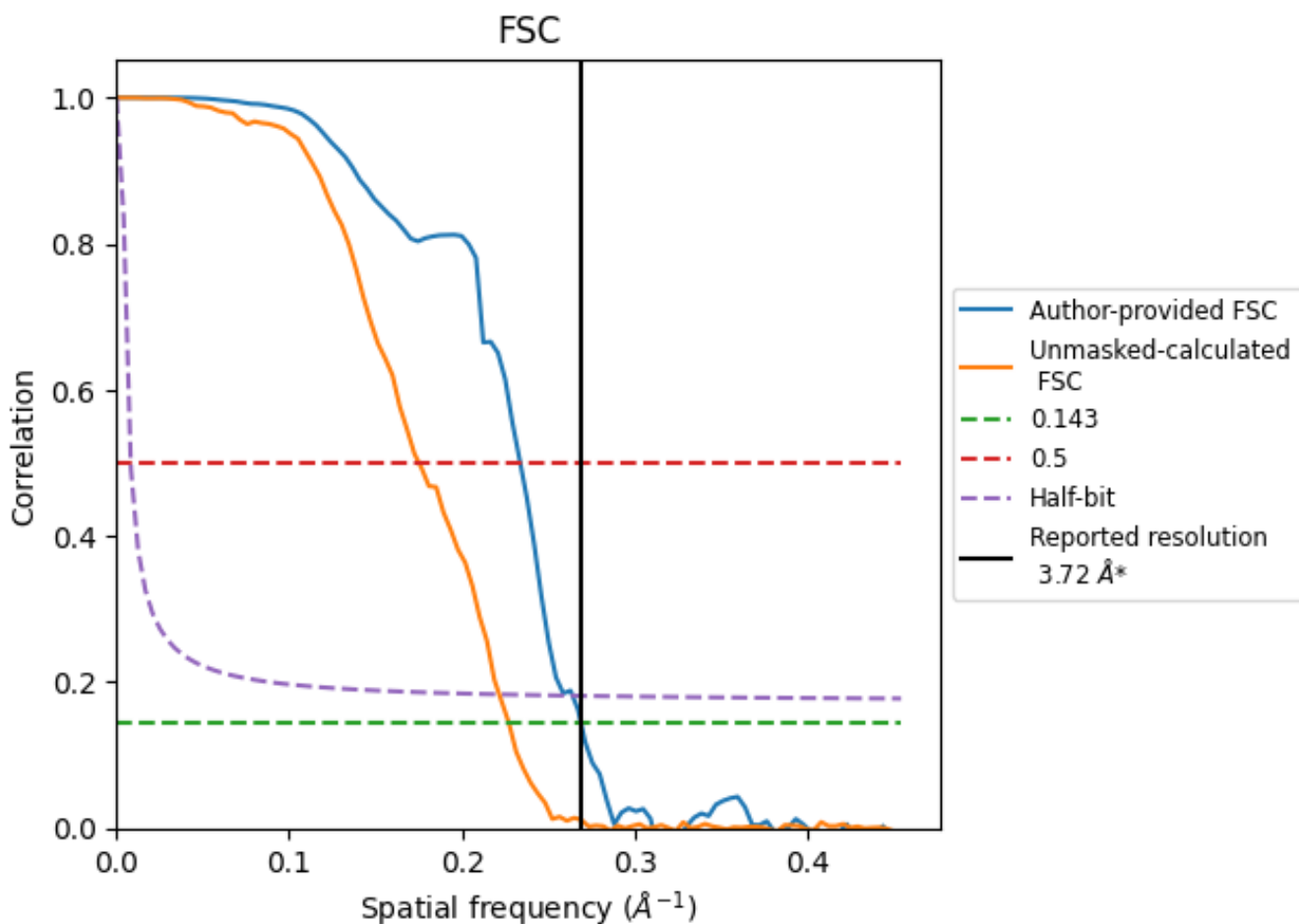


*Reported resolution corresponds to spatial frequency of 0.269 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.269 Å⁻¹

8.2 Resolution estimates [i](#)

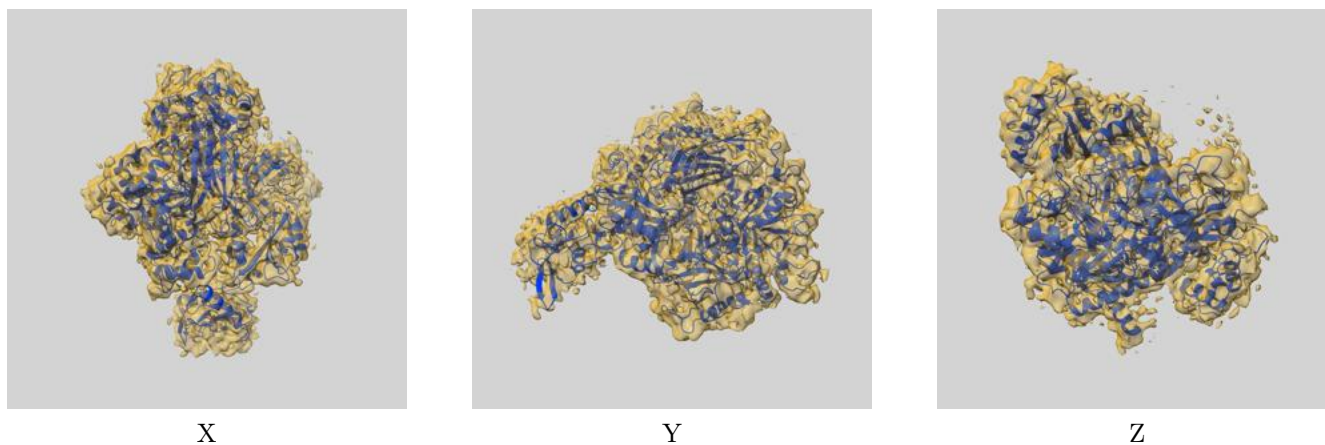
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.72	-	-
Author-provided FSC curve	3.72	4.28	3.79
Unmasked-calculated*	4.40	5.71	4.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.40 differs from the reported value 3.72 by more than 10 %

9 Map-model fit [i](#)

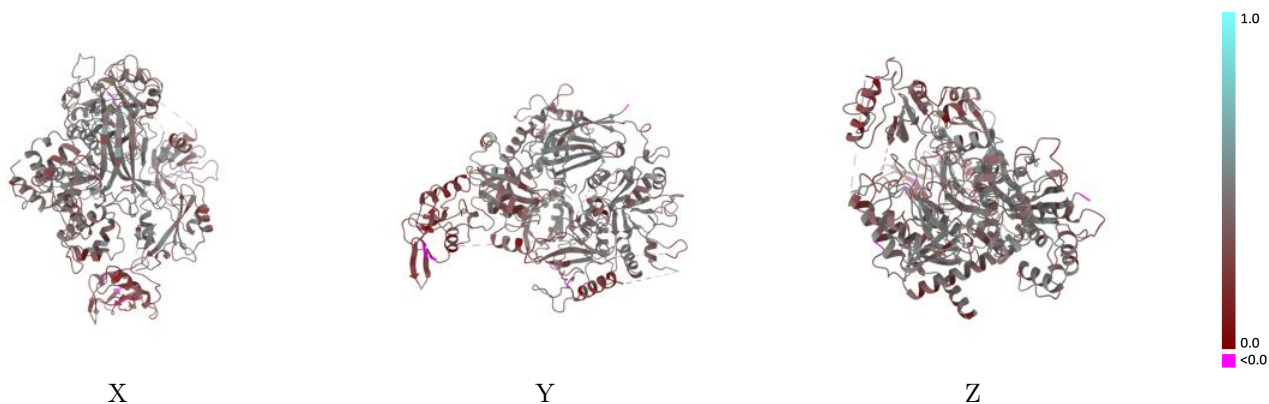
This section contains information regarding the fit between EMDB map EMD-36571 and PDB model 8JQG. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)



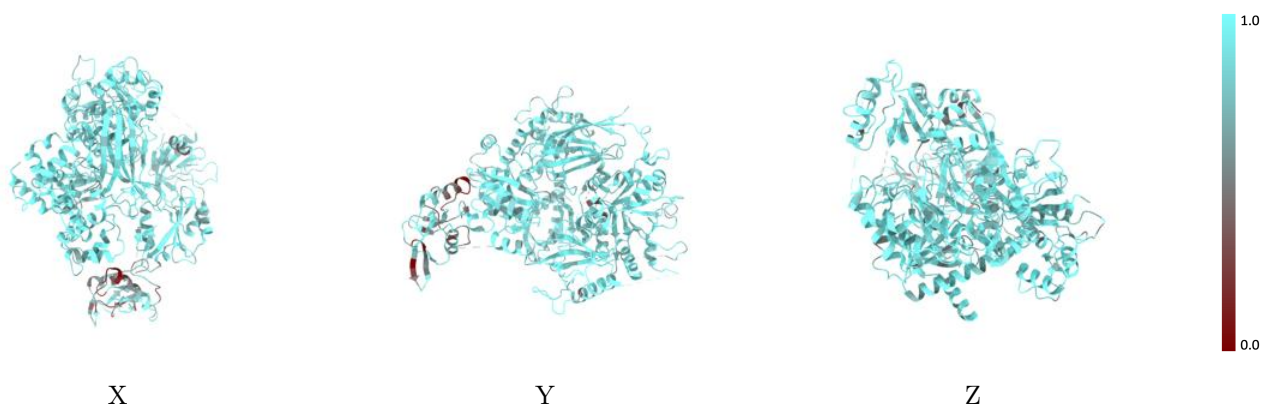
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



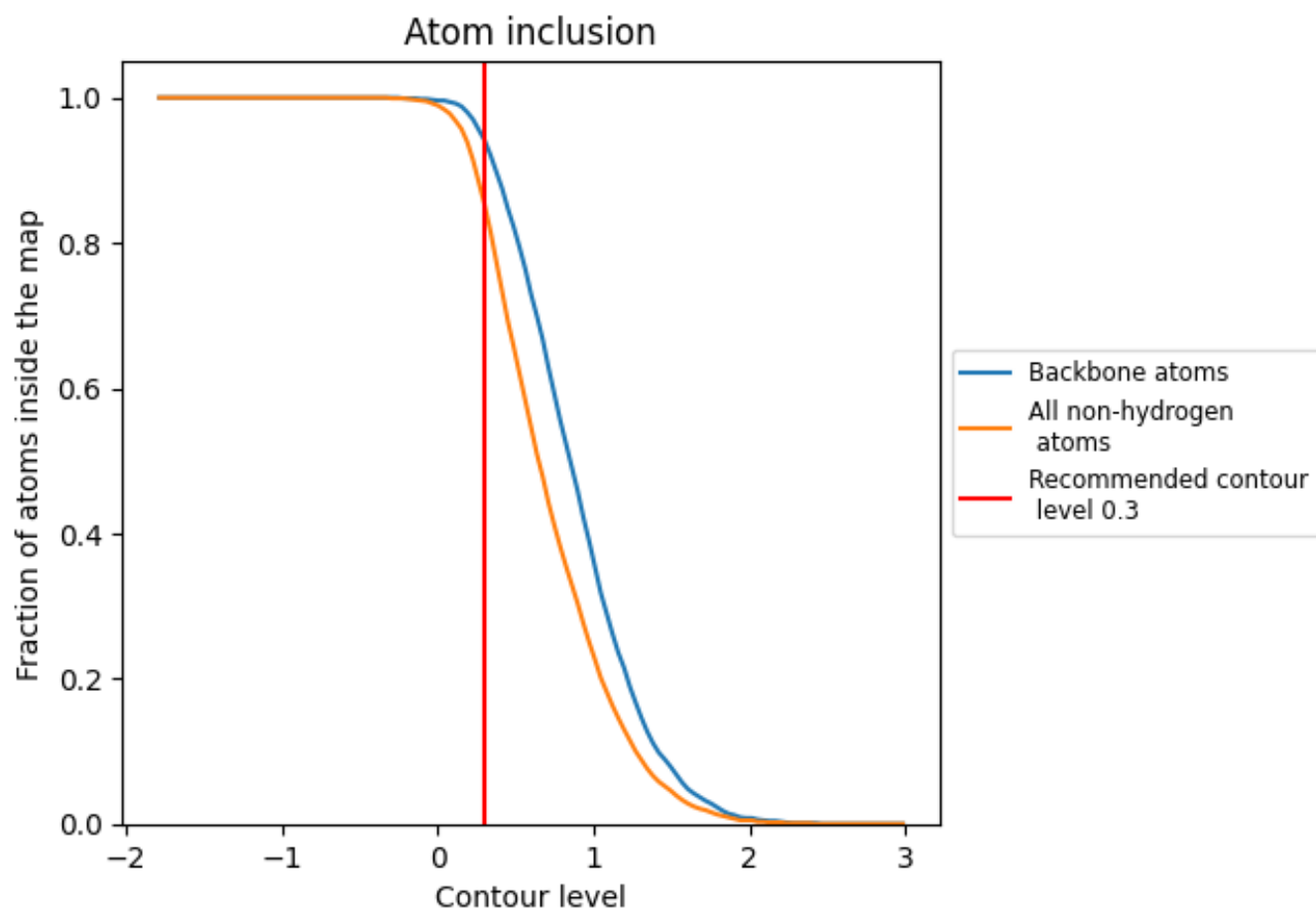
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).





9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8520	 0.3840
A	 0.8520	 0.3840

