



Full wwPDB EM Validation Report ⓘ

Feb 27, 2024 – 07:37 AM EST

PDB ID : 6V0J
EMDB ID : EMD-21000
Title : Lipophilic Envelope-spanning Tunnel B (LetB), Model 8
Authors : Isom, G.L.; Coudray, N.; MacRae, M.R.; McManus, C.T.; Ekiert, D.C.;
Bhabha, G.
Deposited on : 2019-11-18
Resolution : 3.78 Å (reported)
Based on initial model : 5UW2

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.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

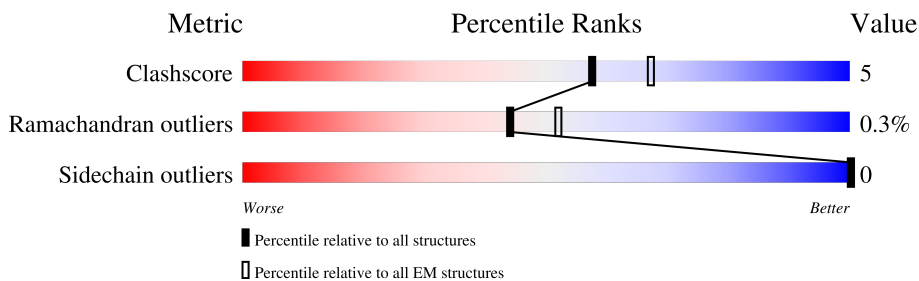
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.78 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	832	
1	B	832	
1	C	832	
1	D	832	
1	E	832	
1	F	832	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15252 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 Intermembrane transport protein YebT.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	335	Total 2542	C 1607	N 430	O 498	S 7	0	0
1	B	335	Total 2542	C 1607	N 430	O 498	S 7	0	0
1	C	335	Total 2542	C 1607	N 430	O 498	S 7	0	0
1	D	335	Total 2542	C 1607	N 430	O 498	S 7	0	0
1	E	335	Total 2542	C 1607	N 430	O 498	S 7	0	0
1	F	335	Total 2542	C 1607	N 430	O 498	S 7	0	0

PHE	ALA	ARG	GLY	GLY	THR	ARG	PHE	SER	VAL	VAL	THR	PRO	GLN	ILE	LEU	ALA	ALA	GLY	VAL	GLU
SER	ILE	ILE	VAL	GLY	ALA	PRO	GLU	ALA	PHE	GLY	LEU	LEU	GLY	ILE	GLY	THR	PRO	VAL	ALA	VAL
TRP	LEU	ALA	SER	GLY	THR	ALA	SER	LEU	GLY	GLY	THR	THR	GLY	VAL	ARG	THR	GLY	THR	PRO	THR
ARG	GLU	TRP	GLY	THR	ALA	LEU	PRO	LYS												

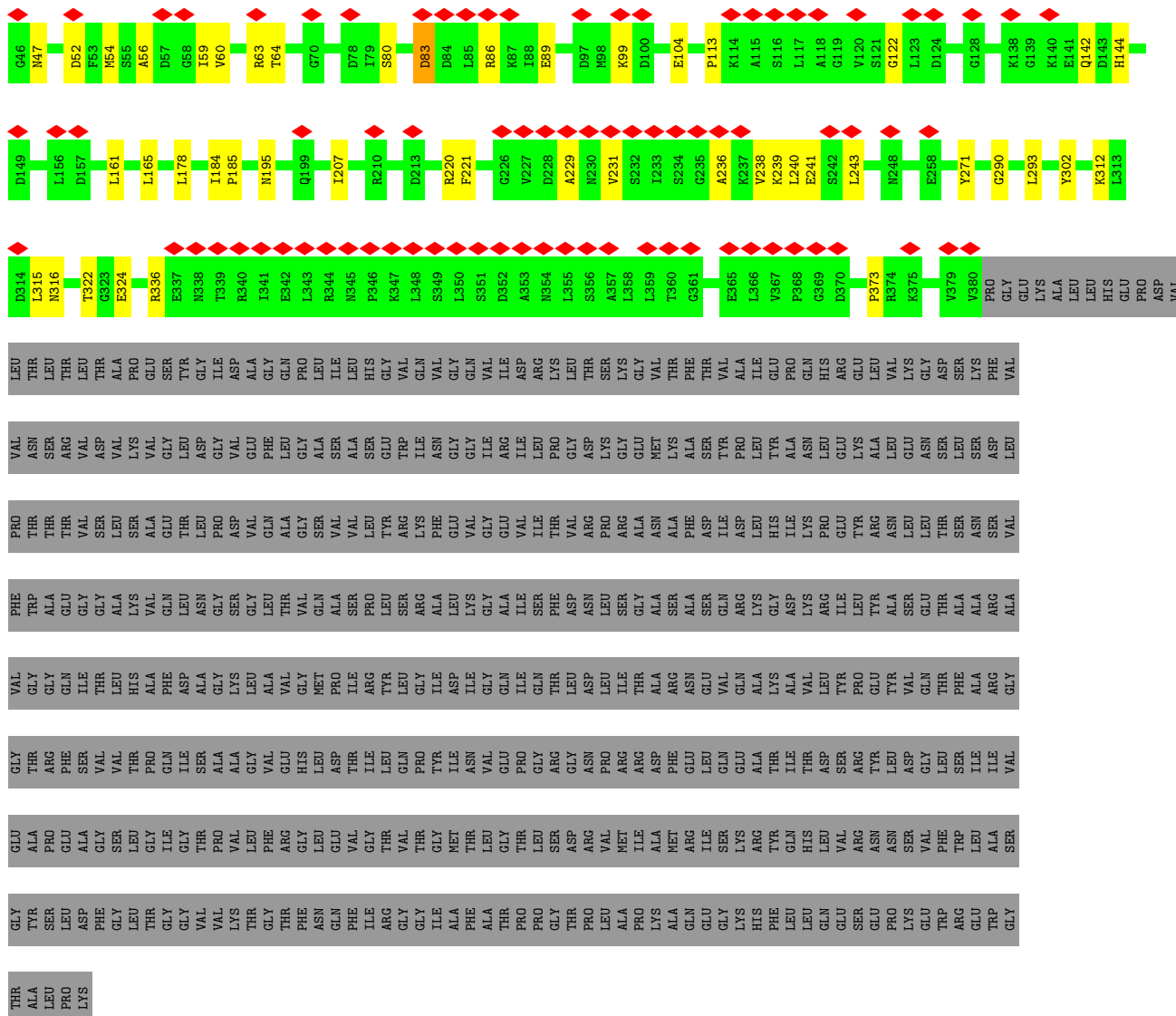
● Molecule 1: Intermembrane transport protein YebT



G46	M47	D52	F63	M54	A56	D67	G58	I59	V60	R63	T64	G70	D78	I79	S80	D83	D84	L85	R86	
D149	L156	D157	L161	M162	L165	L170	L178	I184	P185	N195	I207	I213	R220	F221	G226	V227	D228	A229	M230	
N316	T322	E324	R336	E337	N338	T339	R340	I341	E342	L343	R344	R345	P346	R347	L348	S349	S351	D352	A353	
THR	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ASN	SER	ARG	VAL	ASP	VAL	LYS	VAL	GLY	VAL	PHE	GLY	ALA	ALA	ALA	ALA	THR	TRP	VAL	ASN	GLY
THR	THR	THR	VAL	SER	ALA	ALA	THR	LEU	ASP	VAL	VAL	VAL	LEU	LEU	THR	ARG	LYS	PHE	GLY	VAL
TRP	ALA	GLU	GLY	ALA	VAL	GLN	VAL	THR	THR	VAL	ALA	ALA	PRO	THR	LEU	SER	ARG	ILE	ALA	LEU
GLY	GLY	ILE	THR	LEU	HIS	ALA	PHE	GLN	ASP	ALA	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR
THR	ARG	PHE	SER	VAL	THR	PRO	GLN	ILE	THR	ALA	ALA	THR	ILE	ILE	THR	ASN	ASP	ILE	ALA	VAL
ALA	PRO	GLU	ASP	ALA	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
TYR	SER	LEU	ASP	PHE	GLY	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
ALA	LEU	PRO	PRO	LYS																

● Molecule 1: Intermembrane transport protein YebT





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	21149	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.266	Depositor
Minimum map value	-0.132	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	366.8, 366.8, 366.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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	0.35	0/2583	0.57	1/3500 (0.0%)
1	B	0.35	0/2583	0.57	1/3500 (0.0%)
1	C	0.36	0/2583	0.61	1/3500 (0.0%)
1	D	0.35	0/2583	0.57	1/3500 (0.0%)
1	E	0.35	0/2583	0.57	1/3500 (0.0%)
1	F	0.35	0/2583	0.57	1/3500 (0.0%)
All	All	0.35	0/15498	0.58	6/21000 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	83	ASP	CB-CG-OD1	6.28	123.95	118.30
1	F	83	ASP	CB-CG-OD1	6.04	123.74	118.30
1	D	83	ASP	CB-CG-OD1	6.02	123.72	118.30
1	A	83	ASP	CB-CG-OD1	6.01	123.71	118.30
1	E	83	ASP	CB-CG-OD1	5.97	123.68	118.30
1	B	83	ASP	CB-CG-OD1	5.96	123.67	118.30

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	2542	0	2580	26	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2542	0	2580	30	0
1	C	2542	0	2580	29	0
1	D	2542	0	2580	30	0
1	E	2542	0	2580	30	0
1	F	2542	0	2580	28	0
All	All	15252	0	15480	152	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 5.

All (152) 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:231:VAL:HB	1:F:236:ALA:H	1.60	0.65
1:C:240:LEU:HG	1:C:241:GLU:HG3	1.83	0.61
1:B:231:VAL:HB	1:C:236:ALA:H	1.65	0.60
1:A:220:ARG:NH2	1:A:271:TYR:OH	2.37	0.57
1:B:220:ARG:NH2	1:B:271:TYR:OH	2.37	0.57
1:D:220:ARG:NH2	1:D:271:TYR:OH	2.37	0.57
1:C:231:VAL:HB	1:D:236:ALA:H	1.69	0.57
1:E:220:ARG:NH2	1:E:271:TYR:OH	2.37	0.57
1:E:56:ALA:HB1	1:E:59:ILE:HD12	1.87	0.57
1:F:220:ARG:NH2	1:F:271:TYR:OH	2.37	0.57
1:F:56:ALA:HB1	1:F:59:ILE:HD12	1.87	0.56
1:A:56:ALA:HB1	1:A:59:ILE:HD12	1.86	0.56
1:B:54:MET:HB3	1:B:86:ARG:HH22	1.71	0.56
1:B:56:ALA:HB1	1:B:59:ILE:HD12	1.87	0.56
1:E:240:LEU:HG	1:E:241:GLU:HG3	1.88	0.56
1:C:56:ALA:HB1	1:C:59:ILE:HD12	1.87	0.55
1:D:56:ALA:HB1	1:D:59:ILE:HD12	1.87	0.55
1:D:240:LEU:HG	1:D:241:GLU:HG3	1.88	0.55
1:A:54:MET:HB3	1:A:86:ARG:HH22	1.71	0.55
1:B:240:LEU:HG	1:B:241:GLU:HG3	1.88	0.54
1:F:240:LEU:HG	1:F:241:GLU:HG3	1.88	0.54
1:A:240:LEU:HG	1:A:241:GLU:HG3	1.88	0.54
1:E:54:MET:HB3	1:E:86:ARG:HH22	1.71	0.54
1:F:54:MET:HB3	1:F:86:ARG:HH22	1.71	0.54
1:D:54:MET:HB3	1:D:86:ARG:HH22	1.71	0.54
1:D:231:VAL:HB	1:E:236:ALA:H	1.72	0.54
1:D:336:ARG:HA	1:D:373:PRO:HA	1.90	0.54
1:A:236:ALA:H	1:F:231:VAL:HB	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:336:ARG:HA	1:E:373:PRO:HA	1.90	0.53
1:B:336:ARG:HA	1:B:373:PRO:HA	1.90	0.53
1:D:113:PRO:HA	1:D:122:GLY:HA3	1.91	0.53
1:A:113:PRO:HA	1:A:122:GLY:HA3	1.91	0.53
1:C:336:ARG:HA	1:C:373:PRO:HA	1.90	0.53
1:A:336:ARG:HA	1:A:373:PRO:HA	1.90	0.52
1:E:113:PRO:HA	1:E:122:GLY:HA3	1.91	0.52
1:F:336:ARG:HA	1:F:373:PRO:HA	1.90	0.52
1:B:113:PRO:HA	1:B:122:GLY:HA3	1.91	0.52
1:D:104:GLU:HG3	1:D:142:GLN:HB2	1.91	0.52
1:B:104:GLU:HG3	1:B:142:GLN:HB2	1.91	0.52
1:A:231:VAL:HB	1:B:236:ALA:H	1.73	0.52
1:A:104:GLU:HG3	1:A:142:GLN:HB2	1.91	0.51
1:B:247:VAL:HA	1:C:243:LEU:HD12	1.91	0.51
1:D:316:ASN:ND2	1:D:322:THR:OG1	2.44	0.51
1:F:113:PRO:HA	1:F:122:GLY:HA3	1.91	0.51
1:C:316:ASN:ND2	1:C:322:THR:OG1	2.43	0.51
1:B:316:ASN:ND2	1:B:322:THR:OG1	2.44	0.51
1:E:104:GLU:HG3	1:E:142:GLN:HB2	1.92	0.51
1:E:316:ASN:ND2	1:E:322:THR:OG1	2.44	0.51
1:F:104:GLU:HG3	1:F:142:GLN:HB2	1.91	0.51
1:C:220:ARG:NH2	1:C:271:TYR:OH	2.44	0.51
1:C:104:GLU:HG3	1:C:142:GLN:HB2	1.93	0.50
1:E:228:ASP:HB3	1:F:239:LYS:HG3	1.92	0.50
1:F:316:ASN:ND2	1:F:322:THR:OG1	2.44	0.50
1:A:316:ASN:ND2	1:A:322:THR:OG1	2.44	0.50
1:C:54:MET:HB3	1:C:86:ARG:HH22	1.77	0.50
1:C:247:VAL:HA	1:D:243:LEU:HD12	1.94	0.49
1:C:161:LEU:HB3	1:C:207:ILE:HB	1.96	0.48
1:C:228:ASP:HB3	1:D:239:LYS:HG3	1.95	0.48
1:C:113:PRO:HA	1:C:122:GLY:HA3	1.95	0.48
1:C:178:LEU:HD21	1:C:185:PRO:HB3	1.95	0.48
1:A:161:LEU:HB3	1:A:207:ILE:HB	1.97	0.47
1:B:161:LEU:HB3	1:B:207:ILE:HB	1.96	0.47
1:D:195:ASN:N	1:D:195:ASN:OD1	2.48	0.47
1:F:161:LEU:HB3	1:F:207:ILE:HB	1.97	0.47
1:C:60:VAL:HG13	1:C:63:ARG:H	1.81	0.46
1:C:312:LYS:HB3	1:C:324:GLU:HG2	1.97	0.46
1:D:161:LEU:HB3	1:D:207:ILE:HB	1.97	0.46
1:A:59:ILE:HG23	1:A:64:THR:HG21	1.98	0.46
1:E:195:ASN:OD1	1:E:195:ASN:N	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:312:LYS:HB3	1:B:324:GLU:HG2	1.98	0.46
1:D:59:ILE:HG23	1:D:64:THR:HG21	1.98	0.46
1:A:195:ASN:N	1:A:195:ASN:OD1	2.48	0.46
1:B:60:VAL:HG13	1:B:63:ARG:H	1.81	0.46
1:C:58:GLY:HA3	1:C:130:ASN:HD22	1.81	0.46
1:C:170:LEU:HD22	1:D:184:ILE:HG12	1.97	0.46
1:E:161:LEU:HB3	1:E:207:ILE:HB	1.96	0.46
1:A:312:LYS:HB3	1:A:324:GLU:HG2	1.97	0.46
1:B:59:ILE:HG23	1:B:64:THR:HG21	1.98	0.46
1:D:54:MET:SD	1:D:86:ARG:NH1	2.89	0.46
1:D:60:VAL:HG13	1:D:63:ARG:H	1.81	0.46
1:E:60:VAL:HG13	1:E:63:ARG:H	1.81	0.46
1:F:195:ASN:OD1	1:F:195:ASN:N	2.48	0.46
1:D:178:LEU:HD21	1:D:185:PRO:HB3	1.99	0.45
1:E:80:SER:O	1:E:89:GLU:N	2.50	0.45
1:F:54:MET:SD	1:F:86:ARG:NH1	2.89	0.45
1:A:60:VAL:HG13	1:A:63:ARG:H	1.81	0.45
1:B:290:GLY:HA2	1:B:293:LEU:HD12	1.99	0.45
1:E:170:LEU:HD22	1:F:184:ILE:HG12	1.98	0.45
1:F:312:LYS:HB3	1:F:324:GLU:HG2	1.97	0.45
1:E:59:ILE:HG23	1:E:64:THR:HG21	1.98	0.45
1:E:178:LEU:HD21	1:E:185:PRO:HB3	1.99	0.45
1:F:178:LEU:HD21	1:F:185:PRO:HB3	1.99	0.45
1:E:312:LYS:HB3	1:E:324:GLU:HG2	1.97	0.45
1:E:290:GLY:HA2	1:E:293:LEU:HD12	1.99	0.45
1:F:290:GLY:HA2	1:F:293:LEU:HD12	1.98	0.45
1:A:178:LEU:HD21	1:A:185:PRO:HB3	1.99	0.45
1:F:60:VAL:HG13	1:F:63:ARG:H	1.81	0.45
1:F:80:SER:O	1:F:89:GLU:N	2.49	0.45
1:A:80:SER:O	1:A:89:GLU:N	2.49	0.45
1:B:195:ASN:N	1:B:195:ASN:OD1	2.48	0.45
1:A:290:GLY:HA2	1:A:293:LEU:HD12	1.98	0.44
1:D:47:ASN:HB3	1:D:99:LYS:HZ2	1.83	0.44
1:F:59:ILE:HG23	1:F:64:THR:HG21	1.98	0.44
1:B:178:LEU:HD21	1:B:185:PRO:HB3	1.99	0.44
1:D:228:ASP:HB3	1:E:239:LYS:HE3	2.00	0.44
1:D:80:SER:O	1:D:89:GLU:N	2.49	0.44
1:D:229:ALA:HA	1:D:238:VAL:HG13	1.99	0.44
1:D:290:GLY:HA2	1:D:293:LEU:HD12	1.98	0.44
1:D:312:LYS:HB3	1:D:324:GLU:HG2	1.97	0.44
1:E:54:MET:SD	1:E:86:ARG:NH1	2.89	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:ASP:HB3	1:C:239:LYS:HG3	1.99	0.44
1:A:165:LEU:N	1:A:203:ILE:O	2.44	0.44
1:B:80:SER:O	1:B:89:GLU:N	2.49	0.44
1:F:229:ALA:HA	1:F:238:VAL:HG13	1.99	0.44
1:A:54:MET:SD	1:A:86:ARG:NH1	2.89	0.43
1:A:229:ALA:HA	1:A:238:VAL:HG13	1.99	0.43
1:B:229:ALA:HA	1:B:238:VAL:HG13	1.99	0.43
1:E:229:ALA:HA	1:E:238:VAL:HG13	1.99	0.43
1:A:52:ASP:OD2	1:A:144:HIS:NE2	2.52	0.43
1:B:52:ASP:OD2	1:B:144:HIS:NE2	2.52	0.43
1:B:54:MET:SD	1:B:86:ARG:NH1	2.89	0.43
1:C:59:ILE:HG23	1:C:64:THR:HG21	1.98	0.43
1:F:47:ASN:HB3	1:F:99:LYS:HZ2	1.83	0.43
1:F:52:ASP:OD2	1:F:144:HIS:NE2	2.52	0.43
1:E:47:ASN:HB3	1:E:99:LYS:HZ2	1.84	0.43
1:E:247:VAL:HA	1:F:243:LEU:HD12	2.01	0.43
1:B:47:ASN:HB3	1:B:99:LYS:HZ2	1.83	0.43
1:C:315:LEU:HD11	1:D:302:TYR:HD2	1.84	0.42
1:D:170:LEU:HD22	1:E:184:ILE:HG12	2.01	0.42
1:E:165:LEU:HD21	1:E:221:PHE:HD2	1.84	0.42
1:F:165:LEU:HD21	1:F:221:PHE:HD2	1.84	0.42
1:A:47:ASN:HB3	1:A:99:LYS:HZ2	1.84	0.42
1:B:315:LEU:HD11	1:C:302:TYR:HD2	1.84	0.42
1:E:52:ASP:OD2	1:E:144:HIS:NE2	2.52	0.42
1:E:315:LEU:HD11	1:F:302:TYR:HD2	1.83	0.42
1:B:165:LEU:HD21	1:B:221:PHE:HD2	1.84	0.42
1:A:302:TYR:HD2	1:F:315:LEU:HD11	1.85	0.42
1:D:52:ASP:OD2	1:D:144:HIS:NE2	2.52	0.42
1:B:170:LEU:HD22	1:C:184:ILE:HG12	2.02	0.41
1:C:80:SER:O	1:C:89:GLU:N	2.53	0.41
1:D:165:LEU:HD21	1:D:221:PHE:HD2	1.84	0.41
1:A:165:LEU:HD21	1:A:221:PHE:HD2	1.84	0.41
1:C:195:ASN:N	1:C:195:ASN:OD1	2.53	0.41
1:B:367:VAL:HA	1:B:368:PRO:HD3	1.92	0.41
1:C:215:VAL:HG12	1:C:262:ALA:HB3	2.03	0.41
1:B:204:ASP:OD1	1:B:204:ASP:N	2.54	0.41
1:A:204:ASP:OD1	1:A:204:ASP:N	2.54	0.40
1:E:367:VAL:HA	1:E:368:PRO:HD3	1.92	0.40
1:C:68:TYR:HB3	1:C:73:VAL:HG21	2.03	0.40
1:B:231:VAL:HG13	1:B:236:ALA:HB2	2.04	0.40
1:C:273:ASP:OD1	1:C:274:LEU:N	2.55	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:231:VAL:HG13	1:D:236:ALA:HB2	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	333/832 (40%)	313 (94%)	19 (6%)	1 (0%)	41	74
1	B	333/832 (40%)	313 (94%)	19 (6%)	1 (0%)	41	74
1	C	333/832 (40%)	313 (94%)	20 (6%)	0	100	100
1	D	333/832 (40%)	313 (94%)	19 (6%)	1 (0%)	41	74
1	E	333/832 (40%)	313 (94%)	19 (6%)	1 (0%)	41	74
1	F	333/832 (40%)	313 (94%)	19 (6%)	1 (0%)	41	74
All	All	1998/4992 (40%)	1878 (94%)	115 (6%)	5 (0%)	44	74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	ASP
1	B	83	ASP
1	D	83	ASP
1	E	83	ASP
1	F	83	ASP

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	281/683 (41%)	281 (100%)	0	100	100
1	B	281/683 (41%)	281 (100%)	0	100	100
1	C	281/683 (41%)	281 (100%)	0	100	100
1	D	281/683 (41%)	281 (100%)	0	100	100
1	E	281/683 (41%)	281 (100%)	0	100	100
1	F	281/683 (41%)	281 (100%)	0	100	100
All	All	1686/4098 (41%)	1686 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	164	HIS
1	A	316	ASN
1	B	47	ASN
1	B	164	HIS
1	B	316	ASN
1	C	47	ASN
1	C	164	HIS
1	C	316	ASN
1	D	47	ASN
1	D	164	HIS
1	D	316	ASN
1	E	47	ASN
1	E	164	HIS
1	E	316	ASN
1	F	47	ASN
1	F	164	HIS
1	F	316	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 monosaccharides 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.

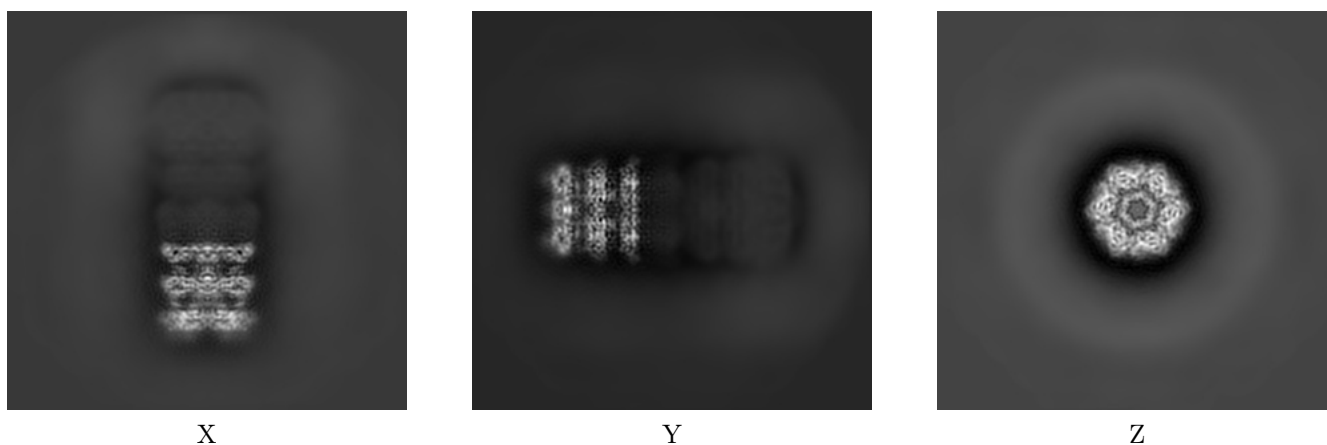
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21000. 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](#)

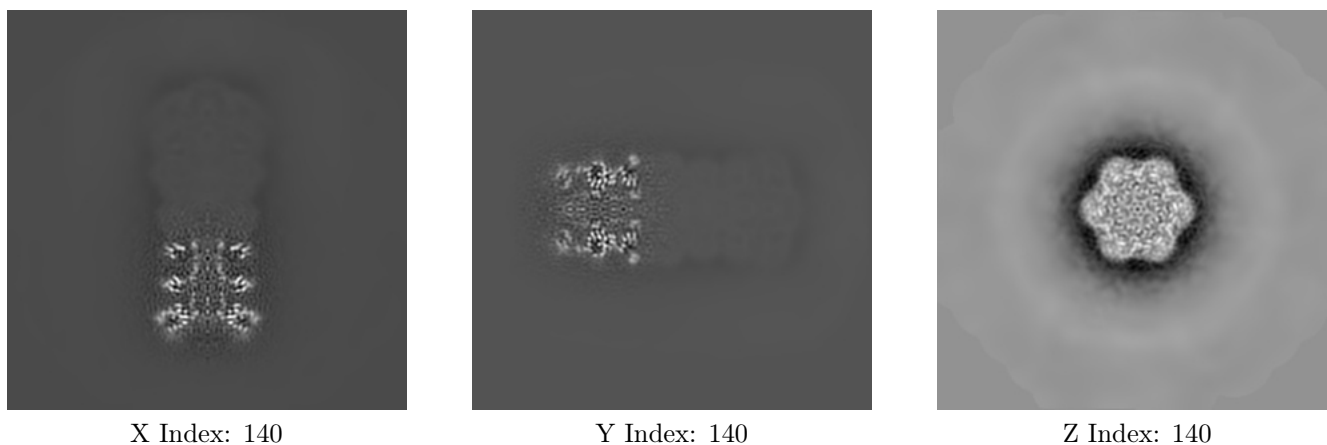
6.1.1 Primary map



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

6.2 Central slices [i](#)

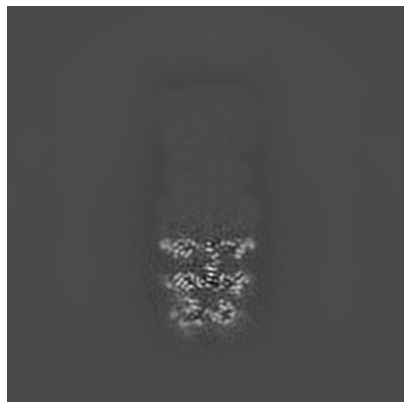
6.2.1 Primary map



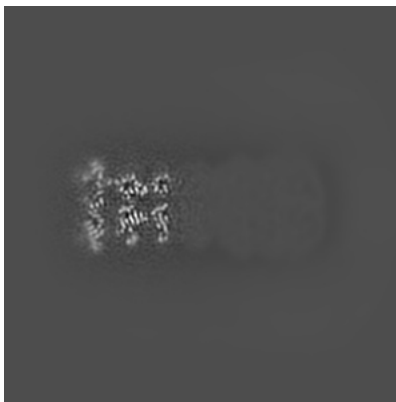
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

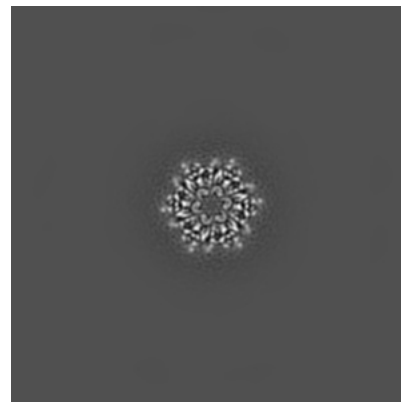
6.3.1 Primary map



X Index: 122



Y Index: 157



Z Index: 88

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

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

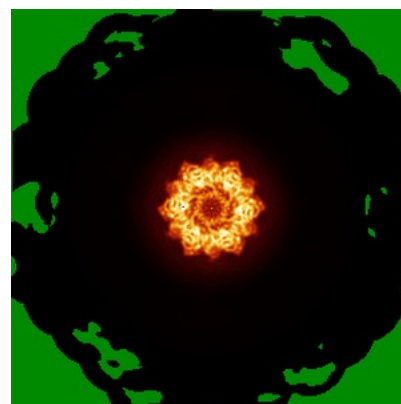
6.4.1 Primary map



X



Y

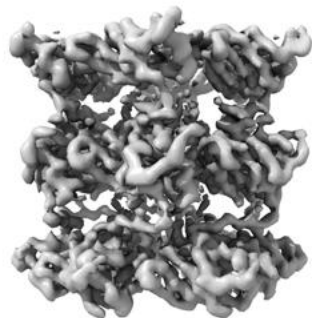


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

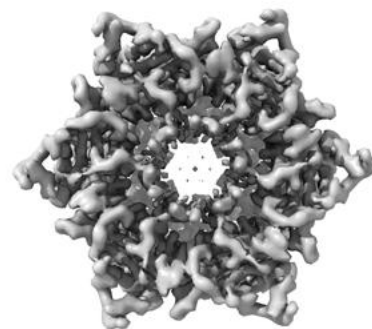
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

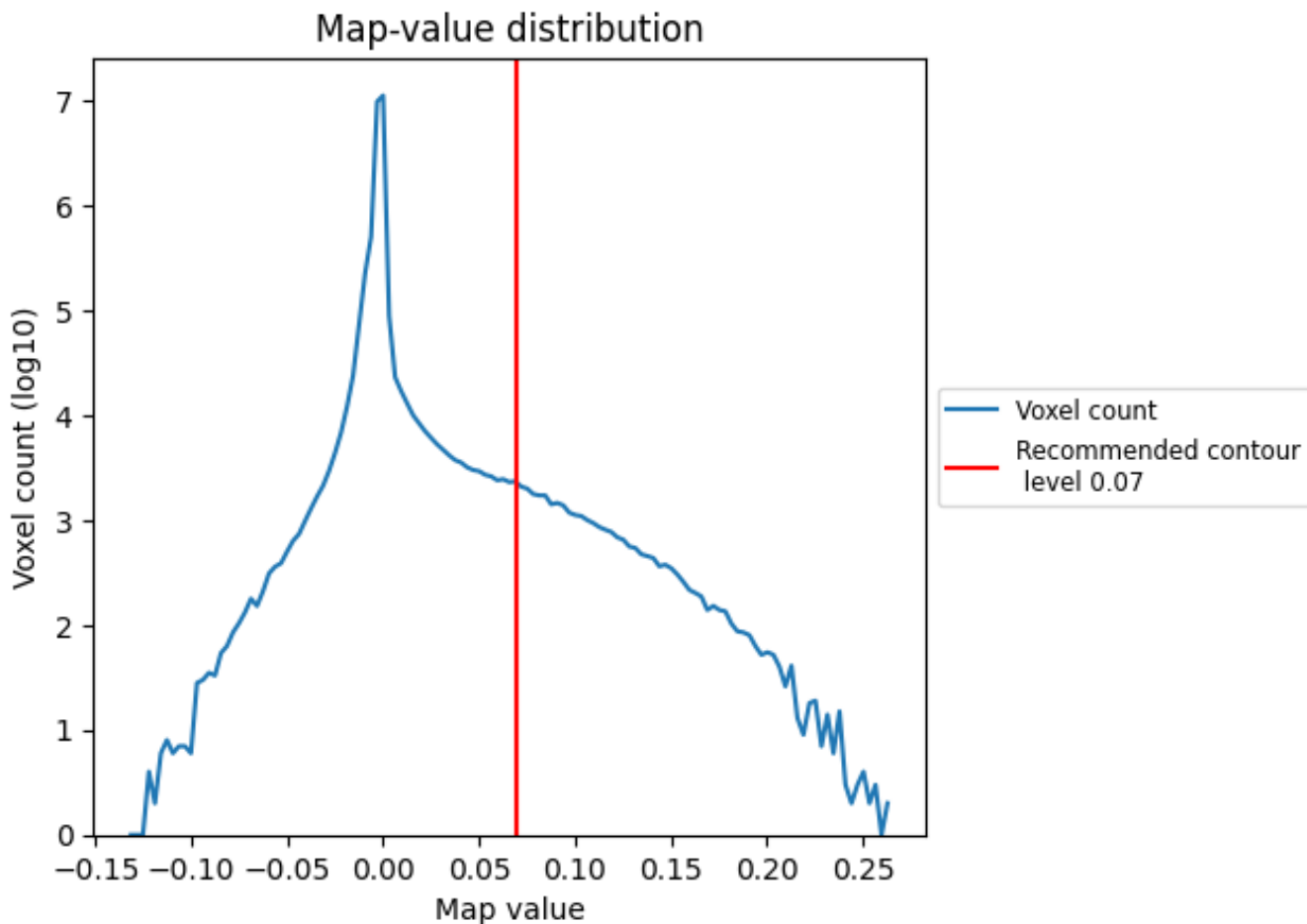
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

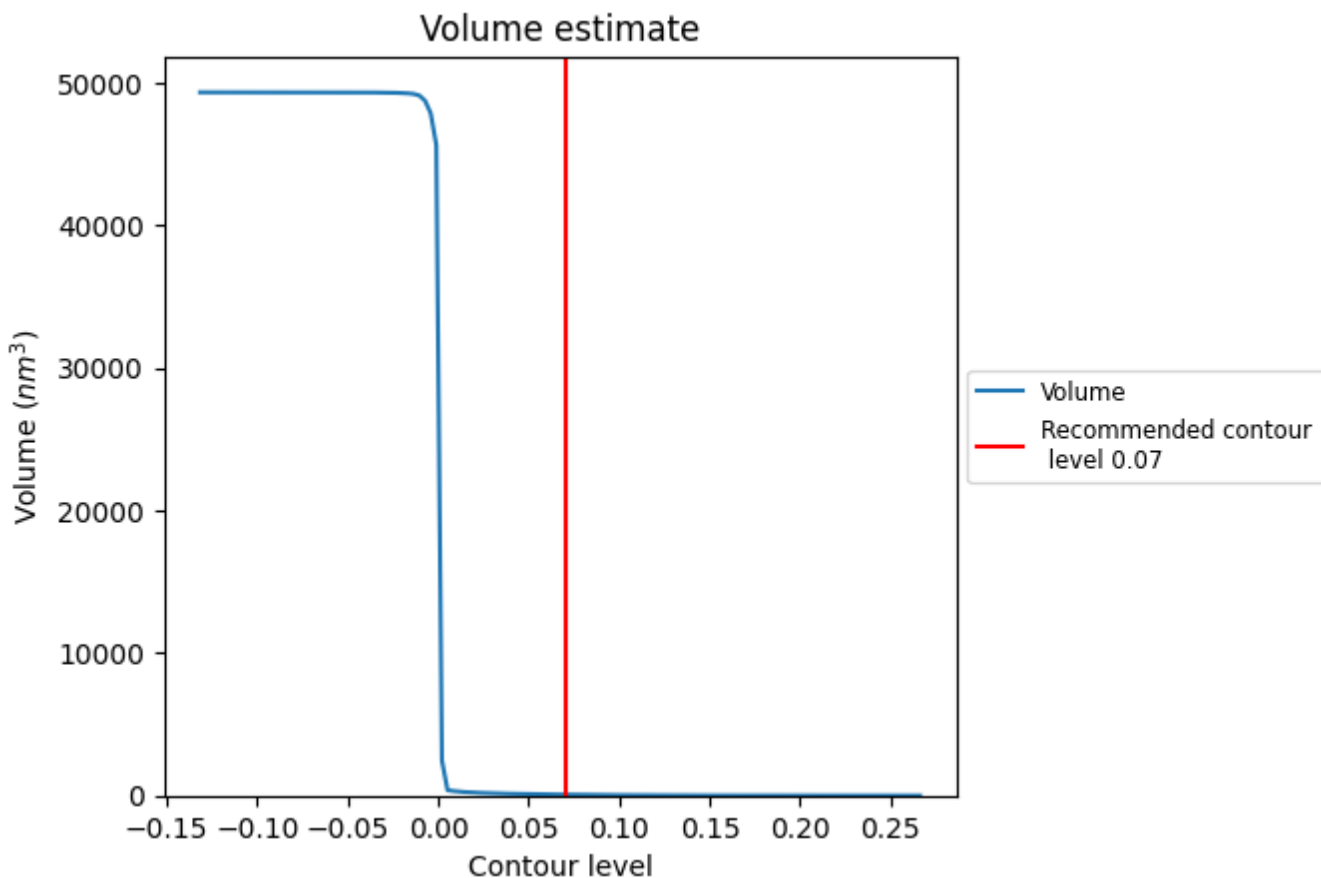
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

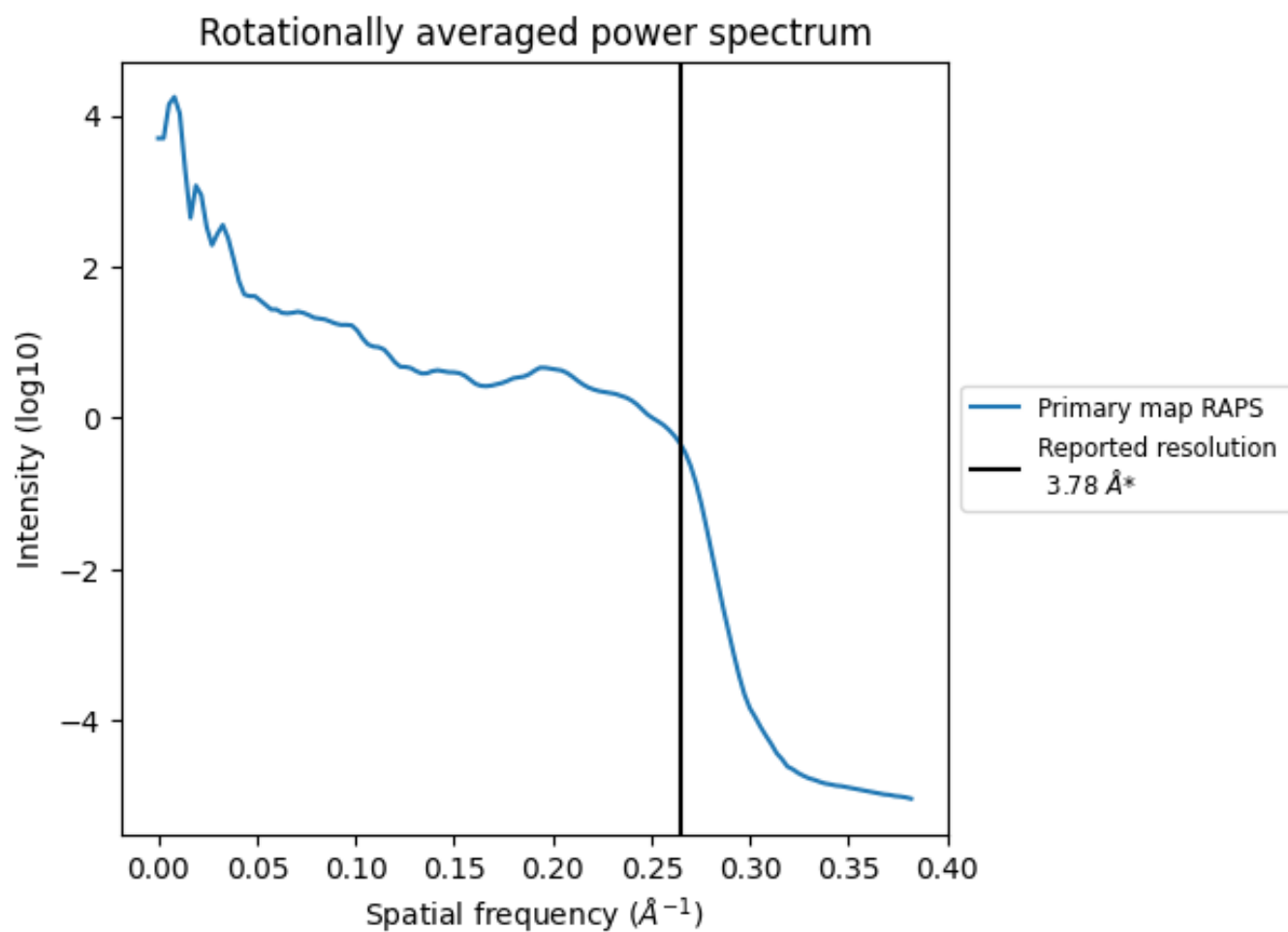
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 68 nm³; this corresponds to an approximate mass of 61 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 0.265\AA^{-1}

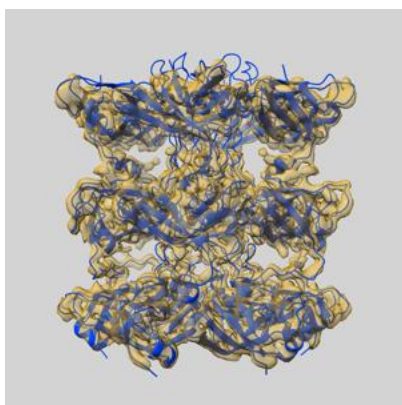
8 Fourier-Shell correlation

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

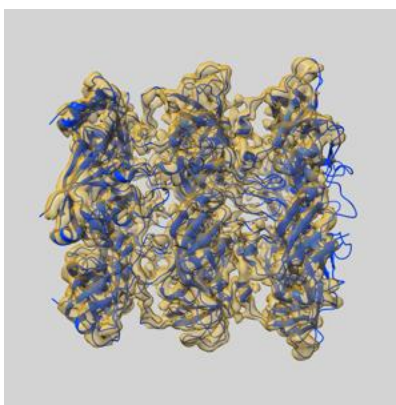
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21000 and PDB model 6V0J. Per-residue inclusion information can be found in section 3 on page 4.

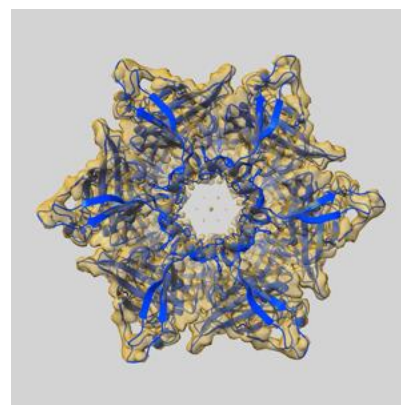
9.1 Map-model overlay [i](#)



X



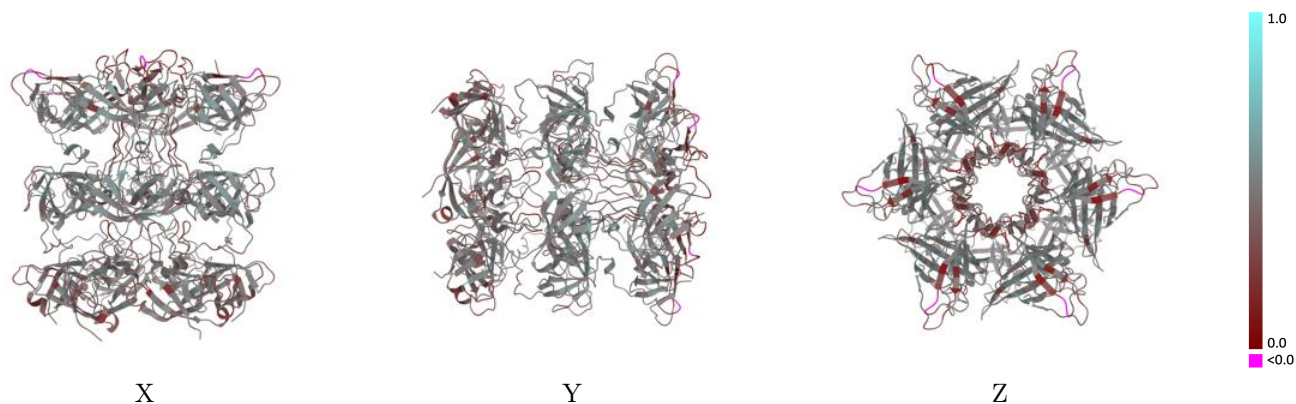
Y



Z

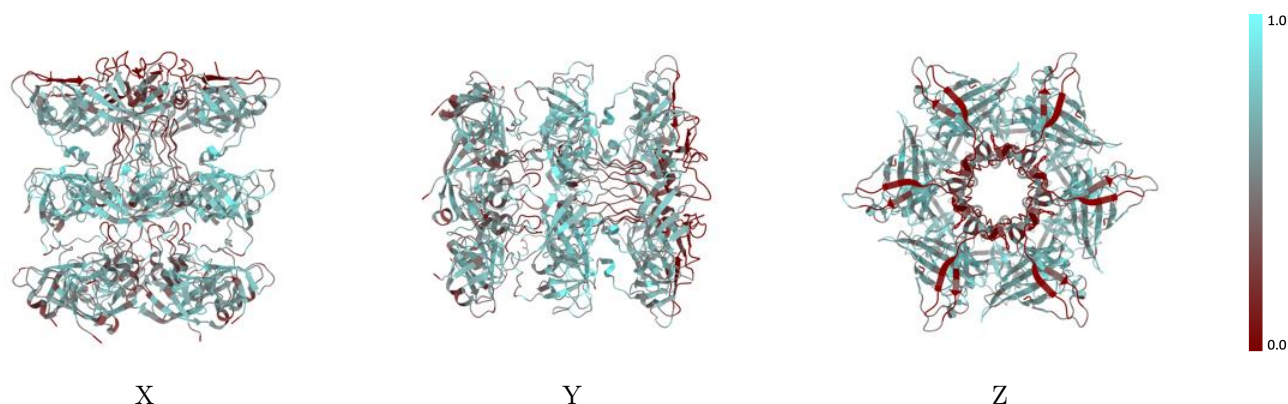
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



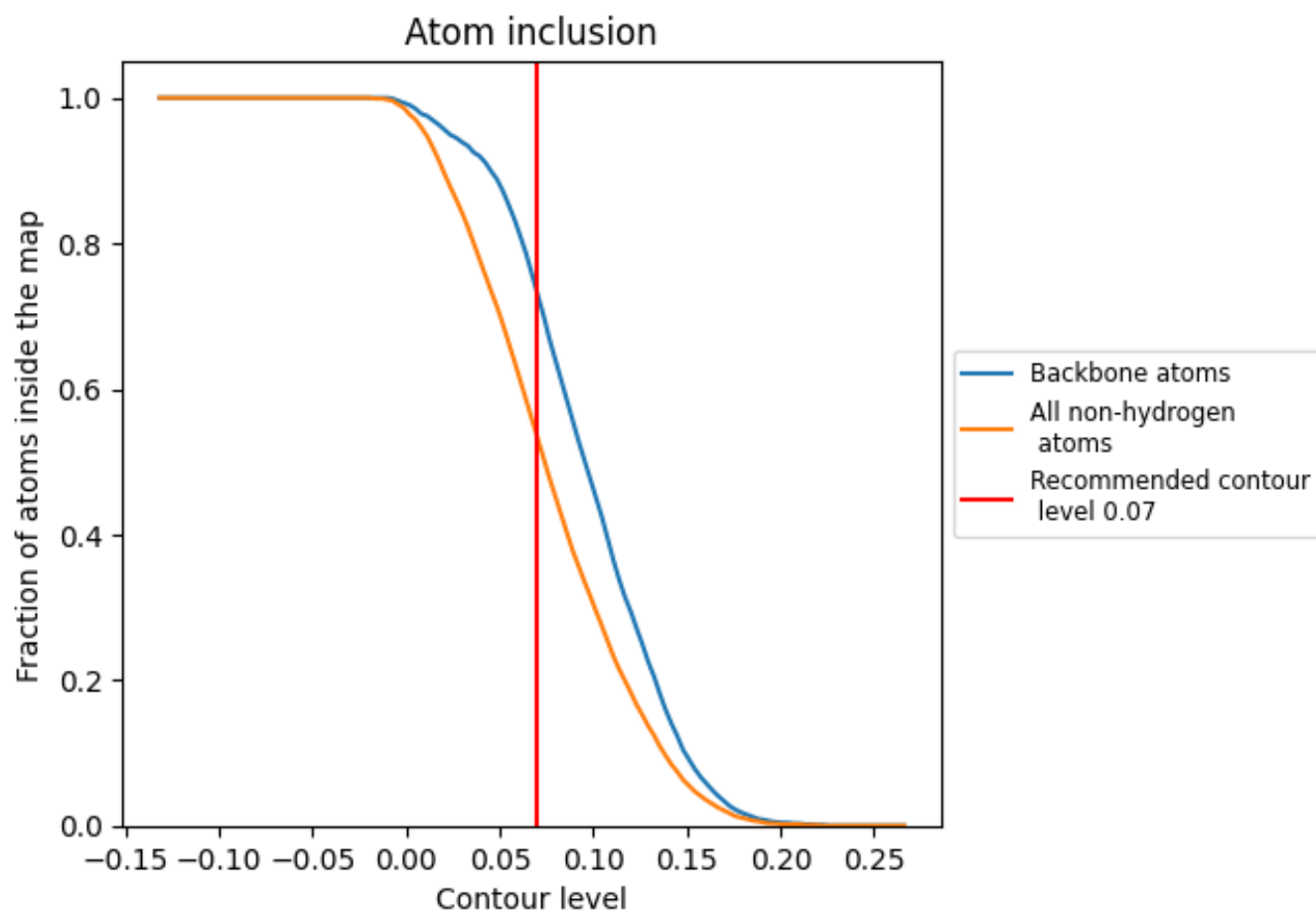
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 54% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5360	0.4190
A	0.5400	0.4210
B	0.5360	0.4190
C	0.5370	0.4180
D	0.5350	0.4170
E	0.5330	0.4180
F	0.5340	0.4200

