



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 10:53 AM UTC

PDB ID : 8U8Z / pdb_00008u8z
EMDB ID : EMD-42030
Title : Cryo-EM structure of PsBphP in Pr state, extended DHp
Authors : Basore, K.; Burgie, E.S.; Vierstra, D.
Deposited on : 2023-09-18
Resolution : 3.25 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

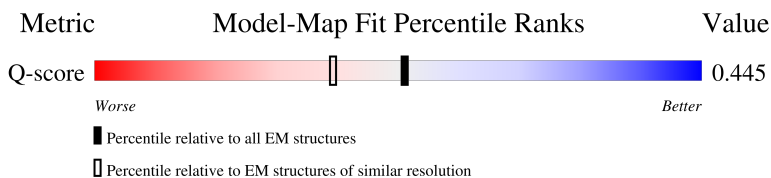
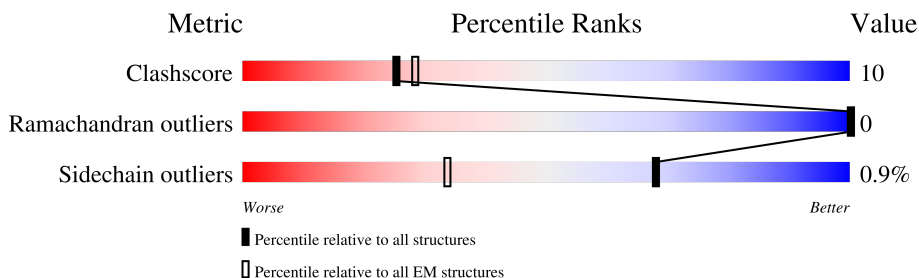
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14599 (2.75 - 3.75)

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	746	 52% 17% 31%
1	B	746	 51% 18% 31%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8147 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.

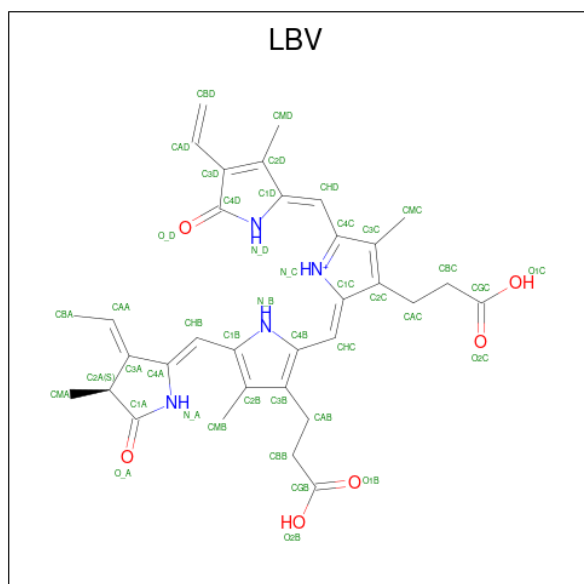
- Molecule 1 is a protein called histidine kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	517	Total	C	N	O	S	0	0
			4031	2531	712	765	23		
1	B	517	Total	C	N	O	S	0	0
			4030	2532	711	764	23		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q885D3
B	0	GLY	-	expression tag	UNP Q885D3

- Molecule 2 is 3-[2-[(Z)-[3-(2-carboxyethyl)-5-[(Z)-(4-ethenyl-3-methyl-5-oxidanylidene-pyrro- l-2-ylidene)methyl]-4-methyl-pyrrol-1-ium -2-ylidene]methyl]-5-[(Z)-[(3E)-3-ethylidene-4-methyl-5-oxidanylidene-pyrrolidin-2-ylidene]methyl]-4-methyl-1H-pyrrol-3-yl]propanoic acid (CCD ID: LBV) (formula: C₃₃H₃₇N₄O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			43	33	4	6	
2	B	1	Total	C	N	O	0
			43	33	4	6	

W216	Q351	L507	ASP	THR
L217	Q352	Q510	PRO	THR
R218	L355	V511	GLU	VAL
I219	L356	D522	ARG	GLY
L230	V360	E523	LEU	GLY
R235	V365	L524	PHE	ASN
P236	A366	V525	GLN	PRO
D237	I367	A526	VAL	THR
L249	R371	V527	LEU	GLY
R250	P382	V528	ILE	LEU
Y259	S383	S529	GLY	GLY
M260	D384	H530	ASN	LEU
S270	I385	D531	ALA	TYR
V271	R386	L532	ILE	ILE
S272	Y415	R533	THR	THR
C285	Q416	ASN	PRO	PRO
Y292	T417	PRO	GLN	ILE
R298	L418	MET	LYS	LYS
Q302	P428	THR	GLY	LEU
Q306	N433	VAL	ARG	GLY
I312	W437	ILE	VAL	ILE
M315	P452	SER	GLY	GLY
E316	R453	MET	ALA	SER
E319	K454	GLN	ALA	ASN
R322	P455	LYS	THR	GLN
Q323	L456	SER	LEU	GLY
R324	D459	PHE	ALA	THR
E325	ALA	SER	PRO	PHE
T326	SER	ASP	GLY	VAL
R327	THR	PRO	ALA	ARG
I328	LEU	HIS	MET	ARG
L334	R466	THR	LYS	THR
H335	L467	SER	SER	GLY
Q336	V478	ARG	ILE	GLY
R337	G490	ILE	ILE	ILE
H338	F493	THR	PRO	PRO
S341	L498	ALA	ASN	GLN
D342	L499	ASP	GLY	LEU
T343	R499	THR	PRO	PRO
F346	L503	MET	ASP	HIS
L349	N504	GLN	ILE	ILE
A350	D506	LYS	LYS	PHE
		VAL	ASN	GLU
		ALA	ARG	ARG
		SER	ALA	TYR
		MET	THR	
		ASN	ASN	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	119594	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 ($e^-/\text{\AA}^2$)	51.78	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.687	Depositor
Minimum map value	-0.270	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	262.8, 262.8, 262.8	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.65699995, 0.65699995, 0.65699995	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.14	0/4111	0.37	0/5586
1	B	0.13	0/4110	0.35	0/5585
All	All	0.13	0/8221	0.36	0/11171

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

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	4031	0	4000	92	0
1	B	4030	0	4003	84	0
2	A	43	0	33	2	0
2	B	43	0	33	1	0
All	All	8147	0	8069	169	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 10.

All (169) 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:B:135:ASN:OD1	1:B:138:ARG:NH1	2.08	0.86
1:A:139:MET:HE1	1:A:155:VAL:HG22	1.64	0.78
1:A:139:MET:HE3	1:A:159:GLU:HB2	1.65	0.78
1:A:235:ARG:HH11	1:A:240:GLN:HE22	1.31	0.76
1:A:428:PRO:HG3	1:A:499:ARG:HH22	1.50	0.75
1:B:334:LEU:O	1:B:338:MET:HG3	1.88	0.74
1:A:428:PRO:HG2	1:B:504:GLU:HG2	1.72	0.72
1:A:509:ARG:O	1:A:513:LYS:HG3	1.90	0.72
1:B:417:THR:HG23	1:B:418:LEU:HD12	1.73	0.71
1:A:78:ILE:HD11	1:A:95:MET:HE1	1.75	0.69
1:B:22:GLN:OE1	1:B:214:ARG:NH2	2.26	0.69
1:A:427:LEU:HD12	1:A:433:ASN:HD21	1.59	0.68
1:B:65:THR:HG23	1:B:67:ASP:H	1.59	0.68
1:A:159:GLU:HG3	1:A:163:MET:HE3	1.76	0.67
1:B:37:LYS:HG2	1:B:39:PRO:HD2	1.77	0.66
1:A:35:THR:CG2	1:A:45:GLN:HG2	2.27	0.65
1:B:127:ILE:HG23	1:B:132:ARG:HD2	1.79	0.64
1:B:146:ALA:O	1:B:315:MET:HE1	1.98	0.63
1:B:118:GLU:OE1	1:B:292:TYR:OH	2.16	0.63
1:A:176:GLU:H	1:A:176:GLU:CD	2.07	0.63
1:A:506:ASP:O	1:A:510:GLN:HG2	1.99	0.62
1:A:61:LEU:HD21	1:A:69:VAL:HG11	1.81	0.62
1:B:159:GLU:O	1:B:163:MET:HG2	2.00	0.62
1:B:78:ILE:HD11	1:B:95:MET:HE1	1.83	0.61
1:B:506:ASP:O	1:B:510:GLN:HG2	2.01	0.61
1:B:98:GLU:N	1:B:98:GLU:OE1	2.34	0.61
1:B:382:PRO:HA	1:B:385:ILE:HD12	1.81	0.61
1:B:146:ALA:HB1	1:B:151:THR:HG23	1.83	0.60
1:A:349:LEU:HD21	1:A:498:LEU:HD21	1.84	0.60
1:A:350:ALA:HB2	1:A:367:ILE:HD13	1.83	0.59
1:A:139:MET:HE3	1:A:159:GLU:CB	2.32	0.59
1:A:44:LEU:HD22	1:A:236:PRO:HD2	1.85	0.59
1:B:148:ASP:HB2	1:B:151:THR:HG22	1.85	0.59
1:B:350:ALA:HB2	1:B:367:ILE:HD13	1.85	0.58
1:B:97:VAL:HG12	1:B:98:GLU:OE1	2.05	0.57
1:B:218:ARG:NH2	1:B:272:SER:OG	2.38	0.57
1:B:31:GLY:HA2	1:B:119:ILE:HG13	1.86	0.57
1:A:19:GLU:HG2	1:A:207:GLN:HE22	1.70	0.56
1:A:146:ALA:O	1:A:315:MET:HE1	2.04	0.56
1:B:325:GLU:O	1:B:328:ILE:HG22	2.06	0.56
1:B:116:GLU:HB3	1:B:249:LEU:HD22	1.88	0.56
1:A:35:THR:HB	1:A:114:VAL:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD22	1:A:43:ILE:HA	1.87	0.55
1:A:324:ARG:HA	1:A:493:PHE:CE1	2.41	0.55
1:A:324:ARG:HG2	1:A:493:PHE:CD1	2.42	0.55
1:A:341:SER:OG	1:A:343:THR:OG1	2.22	0.54
1:A:151:THR:O	1:A:155:VAL:HG12	2.07	0.54
1:A:250:ARG:NH1	2:A:900:LBV:O2B	2.40	0.54
1:A:398:PRO:HB2	1:A:499:ARG:HE	1.72	0.54
1:A:389:HIS:NE2	1:A:432:ASP:OD1	2.41	0.53
1:A:506:ASP:OD1	1:A:510:GLN:NE2	2.35	0.53
1:A:306:GLN:OE1	1:B:144:HIS:ND1	2.42	0.53
1:A:153:TYR:O	1:A:157:VAL:HG13	2.09	0.52
1:B:41:LEU:HD13	1:B:66:LEU:HD12	1.90	0.52
1:B:34:PHE:HB3	1:B:36:LEU:HD21	1.90	0.52
1:A:74:TRP:HA	1:A:77:VAL:HG12	1.91	0.52
1:B:153:TYR:HB3	1:B:184:ALA:HB2	1.92	0.52
1:A:138:ARG:NH1	1:B:90:VAL:O	2.38	0.52
1:B:31:GLY:HA3	1:B:249:LEU:HD21	1.91	0.51
1:A:508:ALA:O	1:A:511:VAL:HG12	2.11	0.51
1:A:159:GLU:O	1:A:163:MET:HG2	2.11	0.51
1:A:31:GLY:HA3	1:A:249:LEU:HD21	1.93	0.51
1:B:194:PHE:HD1	1:B:197:LEU:HD12	1.75	0.51
1:B:525:VAL:HA	1:B:528:VAL:HG22	1.92	0.51
1:B:66:LEU:HD22	1:B:70:LEU:HB2	1.92	0.50
1:A:357:MET:HE1	1:A:377:GLY:HA3	1.92	0.50
1:A:194:PHE:HD1	1:A:197:LEU:HD12	1.76	0.50
1:A:507:LEU:HD22	1:B:503:LEU:HD23	1.93	0.50
1:B:19:GLU:HB3	1:B:207:GLN:HE22	1.77	0.50
1:B:105:LEU:HB2	1:B:116:GLU:OE1	2.12	0.50
1:B:349:LEU:HD21	1:B:498:LEU:HD21	1.93	0.50
1:B:452:PRO:HG3	1:B:478:VAL:HG21	1.94	0.50
1:A:17:ALA:HA	1:A:207:GLN:HE21	1.77	0.49
1:B:118:GLU:CD	1:B:298:ARG:HH22	2.21	0.49
1:A:294:SER:HB3	1:A:297:LEU:HD12	1.95	0.49
1:A:218:ARG:NH2	1:A:272:SER:OG	2.43	0.49
1:B:456:LEU:HD21	1:B:467:LEU:HD13	1.95	0.49
1:B:170:LEU:HD23	1:B:182:VAL:HG11	1.94	0.49
1:B:203:ASP:OD2	1:B:259:TYR:OH	2.20	0.49
1:A:144:HIS:ND1	1:B:306:GLN:OE1	2.45	0.48
1:A:153:TYR:HB3	1:A:184:ALA:HB2	1.95	0.48
1:A:35:THR:HG23	1:A:45:GLN:HG2	1.95	0.48
1:A:39:PRO:HG2	1:A:40:GLU:OE1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ARG:HD3	1:A:240:GLN:HE22	1.77	0.48
1:A:255:ILE:HD12	2:A:900:LBV:HAA1	1.96	0.48
1:B:153:TYR:O	1:B:157:VAL:HG13	2.13	0.48
1:A:170:LEU:HD23	1:A:182:VAL:HG11	1.96	0.47
1:A:398:PRO:HB3	1:A:499:ARG:HH21	1.78	0.47
1:A:428:PRO:CG	1:A:499:ARG:HH22	2.23	0.47
1:B:136:MET:O	1:B:139:MET:HE3	2.15	0.47
1:A:216:TRP:HA	1:A:272:SER:HB2	1.96	0.47
1:B:302:GLN:O	1:B:306:GLN:HG3	2.15	0.47
1:A:385:ILE:HG23	1:A:438:PHE:HZ	1.79	0.47
1:B:323:GLN:HB3	1:B:490:GLY:HA3	1.96	0.47
1:A:166:TYR:HD2	1:A:285:CYS:HB3	1.78	0.47
1:A:302:GLN:O	1:A:306:GLN:HG3	2.14	0.47
1:A:397:GLU:HG3	1:A:400:TYR:HD2	1.79	0.47
1:A:502:ALA:O	1:A:506:ASP:HB2	2.15	0.47
1:A:504:GLU:HG2	1:B:428:PRO:HG2	1.97	0.46
1:A:105:LEU:HB2	1:A:116:GLU:HG2	1.97	0.46
1:B:179:HIS:HB2	1:B:199:PHE:O	2.15	0.46
1:A:429:LYS:HE3	1:A:431:VAL:HB	1.97	0.46
1:B:102:PHE:HB3	1:B:117:LEU:HB3	1.98	0.46
1:B:129:TYR:CE1	1:B:133:THR:HG21	2.51	0.46
1:B:341:SER:OG	1:B:343:THR:OG1	2.27	0.46
1:B:360:VAL:HG21	1:B:437:TRP:CG	2.50	0.46
1:B:312:ILE:O	1:B:316:GLU:HG3	2.16	0.46
1:B:384:ASP:HB3	1:B:415:TYR:CE1	2.50	0.46
1:B:216:TRP:HA	1:B:272:SER:HB2	1.98	0.45
1:B:102:PHE:CE1	1:B:119:ILE:HG12	2.51	0.45
1:A:136:MET:HG2	1:B:136:MET:HG2	1.98	0.45
1:A:106:LEU:HD12	1:A:113:LEU:HD11	1.98	0.45
1:A:428:PRO:HG3	1:A:499:ARG:NH2	2.26	0.45
1:A:24:PRO:HG3	1:A:250:ARG:HG3	1.99	0.45
1:A:140:LEU:HD23	1:A:143:LEU:HD12	1.99	0.45
1:B:166:TYR:HD2	1:B:285:CYS:HB3	1.82	0.45
1:A:129:TYR:O	1:A:133:THR:OG1	2.29	0.44
1:A:37:LYS:HB2	1:A:42:THR:HG23	1.99	0.44
1:A:235:ARG:HD3	1:A:240:GLN:NE2	2.32	0.44
1:B:428:PRO:HG3	1:B:499:ARG:NH2	2.32	0.44
1:A:167:ASP:OD1	1:A:167:ASP:N	2.50	0.44
1:A:217:LEU:HD21	1:A:298:ARG:HB3	2.00	0.44
1:B:352:GLN:HG2	1:B:355:LEU:HB2	1.99	0.44
1:B:371:ARG:C	1:B:386:ARG:HH22	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:LEU:O	1:B:511:VAL:HG22	2.17	0.44
1:A:359:LEU:HD11	1:A:494:ALA:HB1	1.98	0.44
1:B:47:SER:HA	1:B:230:LEU:HD23	1.99	0.44
1:A:179:HIS:HB2	1:A:199:PHE:O	2.18	0.44
1:A:323:GLN:HB3	1:A:490:GLY:HA3	2.00	0.44
1:B:40:GLU:HB3	1:B:42:THR:HG23	2.00	0.43
1:A:127:ILE:HG23	1:A:132:ARG:HD2	1.99	0.43
1:A:338:MET:HG2	1:A:505:ASN:ND2	2.32	0.43
1:B:167:ASP:N	1:B:167:ASP:OD1	2.51	0.43
1:B:346:PHE:CE2	1:B:433:ASN:HB2	2.52	0.43
1:A:160:ILE:HD12	1:A:283:ILE:HG21	2.00	0.43
1:A:381:GLU:O	1:A:385:ILE:HG13	2.18	0.43
1:A:341:SER:HG	1:A:343:THR:HG1	1.56	0.43
1:A:441:GLU:OE2	1:A:482:GLY:N	2.41	0.43
1:A:457:ASN:OD1	1:A:457:ASN:N	2.45	0.43
1:B:219:ILE:HG21	1:B:298:ARG:NH1	2.32	0.43
1:B:527:VAL:O	1:B:531:ASP:N	2.42	0.43
1:B:218:ARG:HH11	1:B:270:SER:HB2	1.84	0.43
1:A:320:VAL:O	1:A:324:ARG:HG3	2.19	0.42
1:A:166:TYR:HE2	1:A:269:MET:HB2	1.84	0.42
1:B:35:THR:HG23	1:B:45:GLN:H	1.85	0.42
1:A:360:VAL:HG21	1:A:437:TRP:CG	2.54	0.42
1:B:217:LEU:HD21	1:B:298:ARG:HB3	2.02	0.42
1:B:454:LYS:HD2	1:B:454:LYS:HA	1.85	0.42
1:A:447:GLN:OE1	1:A:477:LYS:NZ	2.53	0.42
1:A:102:PHE:HB3	1:A:117:LEU:HB3	2.02	0.42
1:B:356:LEU:HD23	1:B:365:VAL:HG11	2.02	0.42
1:B:102:PHE:HE1	1:B:119:ILE:HG12	1.85	0.42
1:B:155:VAL:HG12	1:B:158:ARG:NH2	2.35	0.42
1:B:168:ARG:HH21	1:B:191:MET:HE3	1.84	0.42
1:B:154:GLU:OE2	1:B:154:GLU:HA	2.20	0.42
1:B:324:ARG:HG2	1:B:493:PHE:CD2	2.54	0.42
1:B:524:LEU:HD23	1:B:524:LEU:HA	1.91	0.42
1:B:250:ARG:NH1	2:B:900:LBV:O2B	2.43	0.41
1:B:323:GLN:HA	1:B:326:THR:HG22	2.03	0.41
1:A:323:GLN:HA	1:A:326:THR:HG22	2.01	0.41
1:A:70:LEU:HD23	1:A:70:LEU:HA	1.84	0.41
1:A:110:GLN:OE1	1:A:240:GLN:NE2	2.54	0.41
1:A:116:GLU:HB2	1:A:249:LEU:HD22	2.03	0.41
1:A:344:ASP:HA	1:A:509:ARG:CZ	2.51	0.41
1:A:385:ILE:HG13	1:A:385:ILE:H	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:HD23	1:B:152:LEU:HD23	2.03	0.41
1:B:319:GLU:OE2	1:B:322:ARG:NE	2.40	0.41
1:A:159:GLU:HA	1:A:159:GLU:OE1	2.20	0.40
1:B:235:ARG:NH2	1:B:237:ASP:OD1	2.54	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	513/746 (69%)	502 (98%)	11 (2%)	0	100	100
1	B	513/746 (69%)	501 (98%)	12 (2%)	0	100	100
All	All	1026/1492 (69%)	1003 (98%)	23 (2%)	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	441/633 (70%)	439 (100%)	2 (0%)	81	82
1	B	441/633 (70%)	435 (99%)	6 (1%)	59	72
All	All	882/1266 (70%)	874 (99%)	8 (1%)	68	76

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LEU
1	A	368	ILE
1	B	27	ILE
1	B	45	GLN
1	B	69	VAL
1	B	163	MET
1	B	260	MET
1	B	336	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	HIS
1	A	207	GLN
1	A	505	ASN
1	A	516	GLN
1	B	30	HIS
1	B	224	ASN
1	B	457	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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	LBV	B	900	1	46,46,46	1.08	2 (4%)	58,67,67	0.90	0
2	LBV	A	900	1	46,46,46	1.08	2 (4%)	58,67,67	0.93	2 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LBV	B	900	1	-	12/26/74/74	0/4/4/4
2	LBV	A	900	1	-	12/26/74/74	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	900	LBV	C1C-C2C	-3.42	1.40	1.45
2	A	900	LBV	C1C-C2C	-3.38	1.40	1.45
2	A	900	LBV	C4C-C3C	-2.51	1.40	1.45
2	B	900	LBV	C4C-C3C	-2.50	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	LBV	CMC-C3C-C4C	2.09	128.35	125.10
2	A	900	LBV	C4B-CHC-C1C	2.03	132.65	128.22

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	900	LBV	C2A-C3A-CAA-CBA
2	A	900	LBV	C4A-C3A-CAA-CBA
2	A	900	LBV	C3C-C4C-CHD-C1D
2	A	900	LBV	N_C-C4C-CHD-C1D
2	B	900	LBV	C2A-C3A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
2	B	900	LBV	C4A-C3A-CAA-CBA
2	B	900	LBV	C3C-C4C-CHD-C1D
2	B	900	LBV	N_C-C4C-CHD-C1D
2	B	900	LBV	N_D-C1D-CHD-C4C
2	A	900	LBV	N_B-C4B-CHC-C1C
2	A	900	LBV	N_D-C1D-CHD-C4C
2	B	900	LBV	N_C-C1C-CHC-C4B
2	B	900	LBV	N_B-C4B-CHC-C1C
2	A	900	LBV	N_C-C1C-CHC-C4B
2	B	900	LBV	C2C-C1C-CHC-C4B
2	A	900	LBV	C2D-C1D-CHD-C4C
2	B	900	LBV	C2D-C1D-CHD-C4C
2	A	900	LBV	C2C-C1C-CHC-C4B
2	A	900	LBV	C3B-C4B-CHC-C1C
2	B	900	LBV	C3B-C4B-CHC-C1C
2	A	900	LBV	CAC-CBC-CGC-O2C
2	A	900	LBV	CAC-CBC-CGC-O1C
2	B	900	LBV	CAC-CBC-CGC-O1C
2	B	900	LBV	CAC-CBC-CGC-O2C

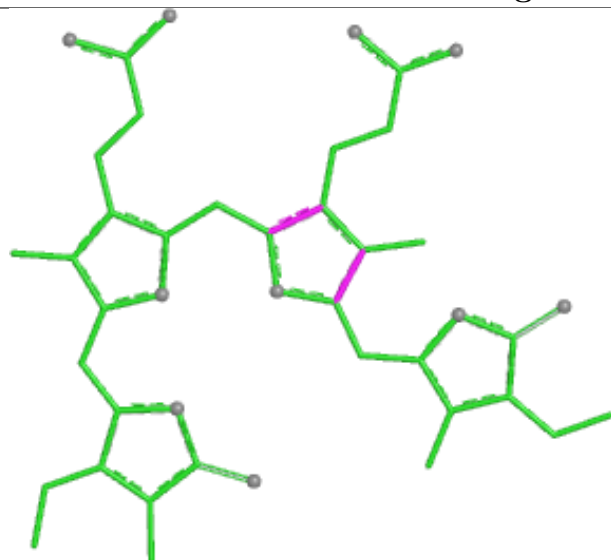
There are no ring outliers.

2 monomers are involved in 3 short contacts:

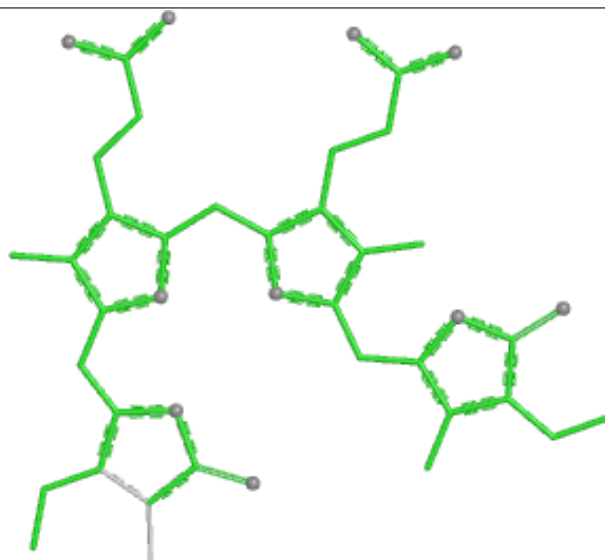
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	900	LBV	1	0
2	A	900	LBV	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

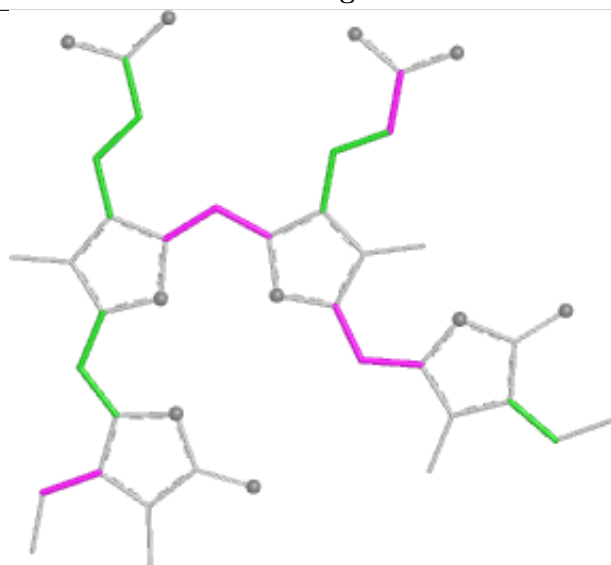
Ligand LBV B 900



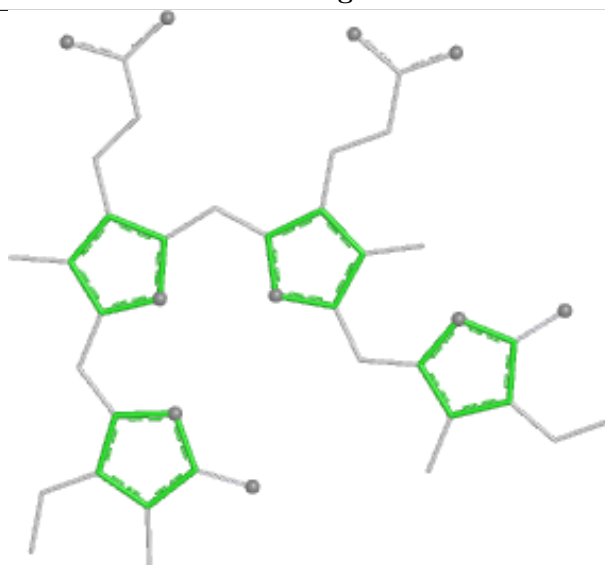
Bond lengths



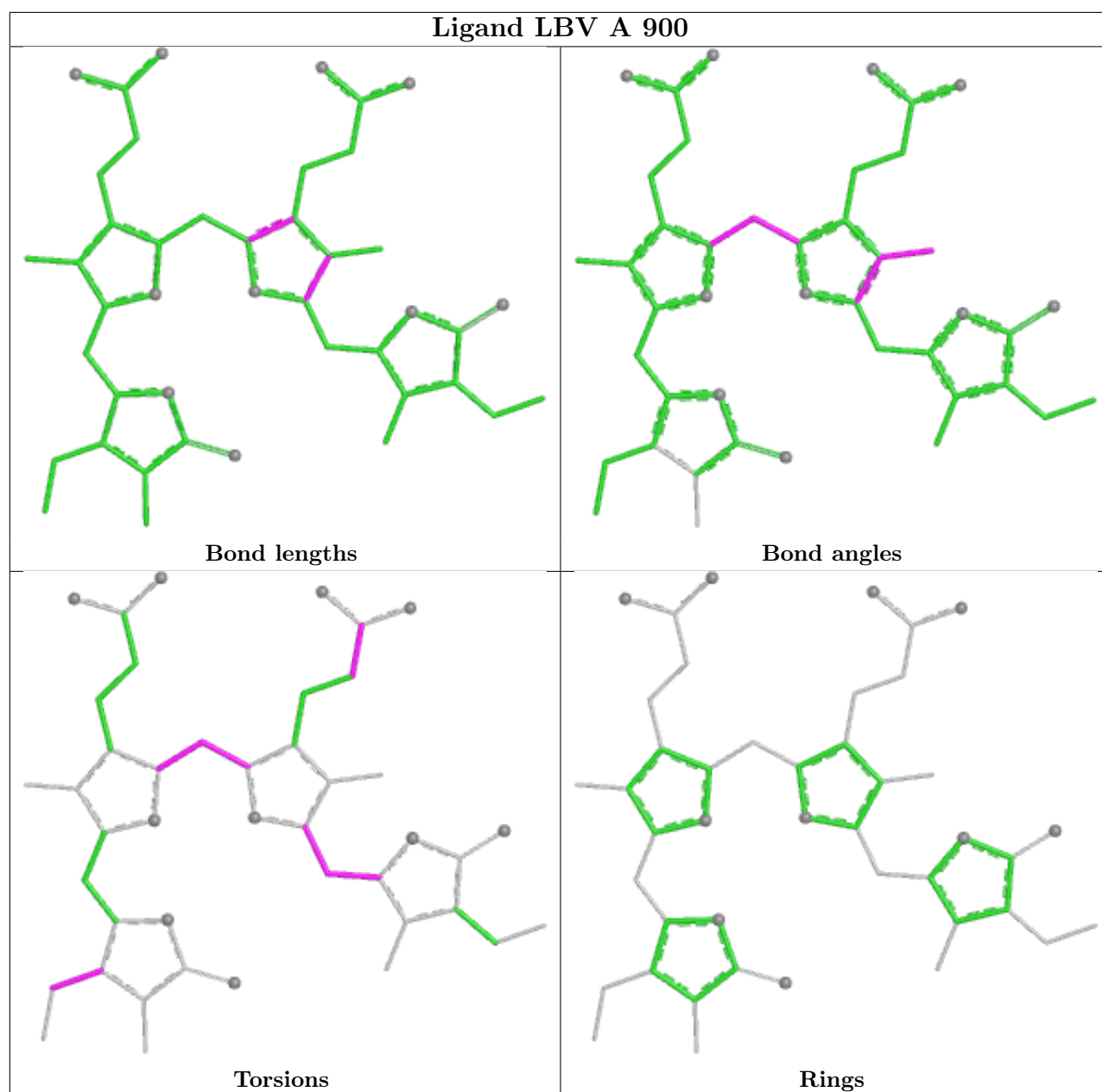
Bond angles



Torsions



Rings



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.

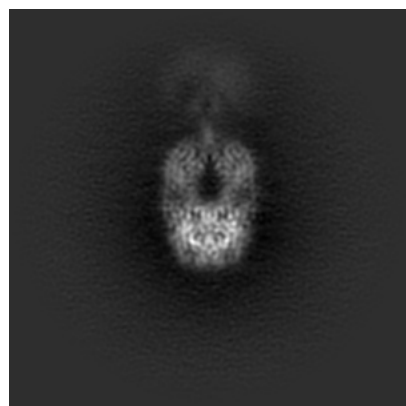
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42030. These allow visual inspection of the internal detail of the map and identification of artifacts.

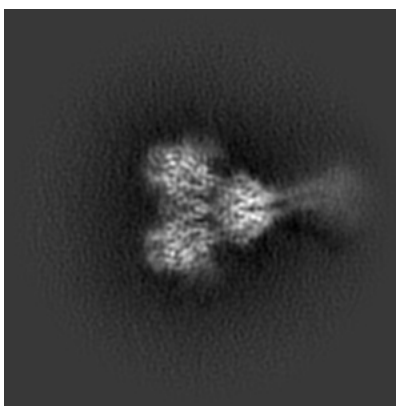
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

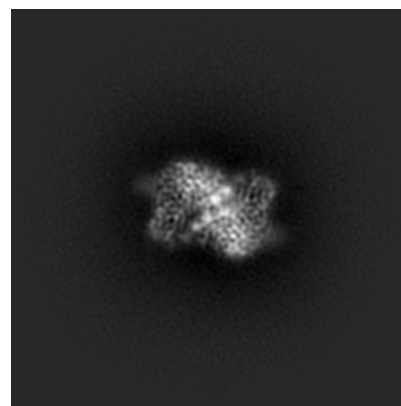
6.1.1 Primary map



X

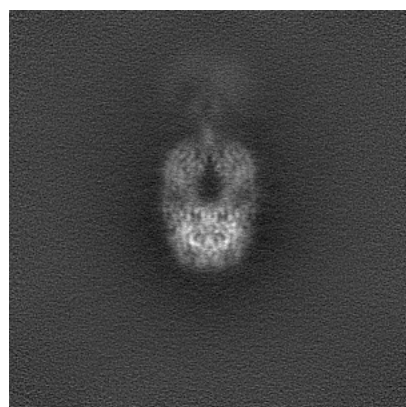


Y

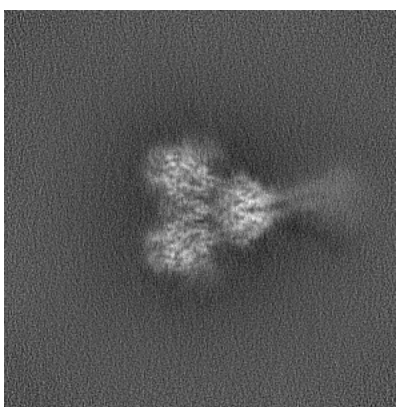


Z

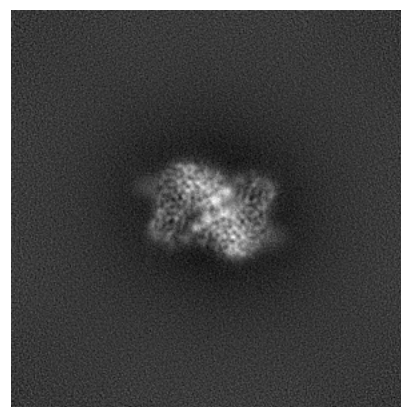
6.1.2 Raw map



X



Y

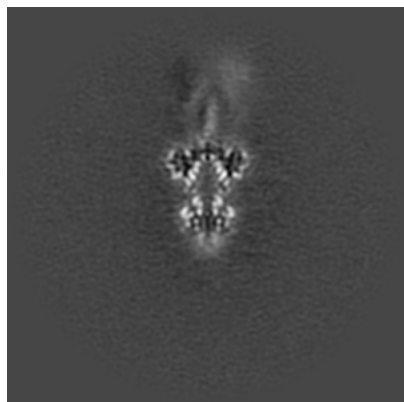


Z

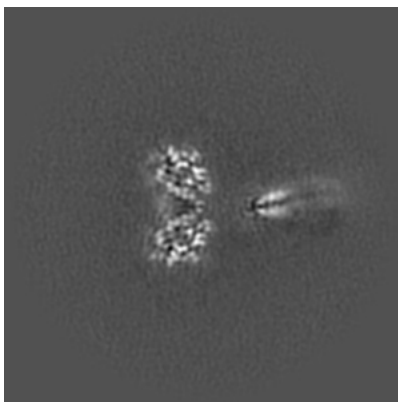
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

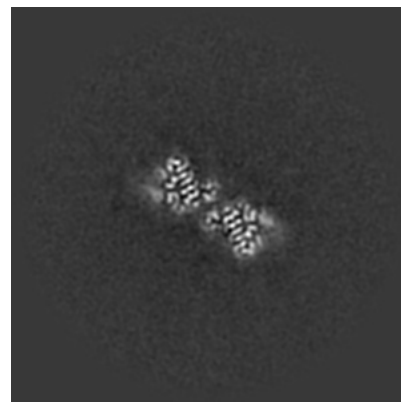
6.2.1 Primary map



X Index: 200

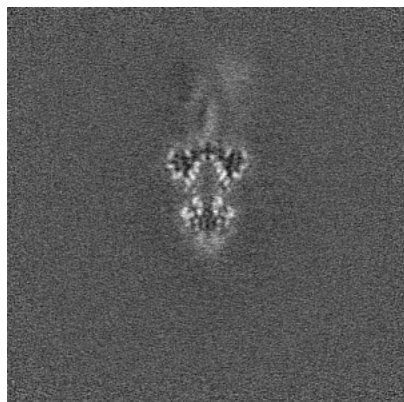


Y Index: 200

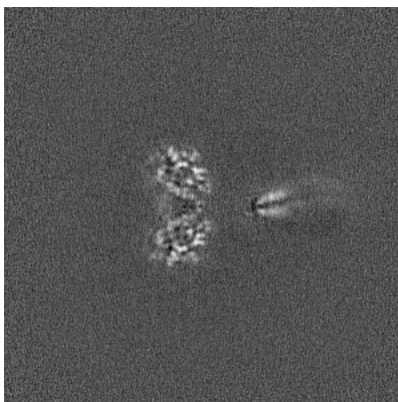


Z Index: 200

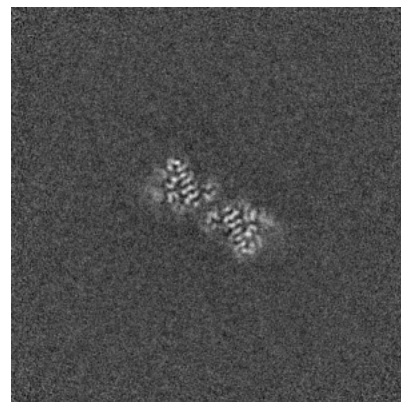
6.2.2 Raw map



X Index: 200



Y Index: 200

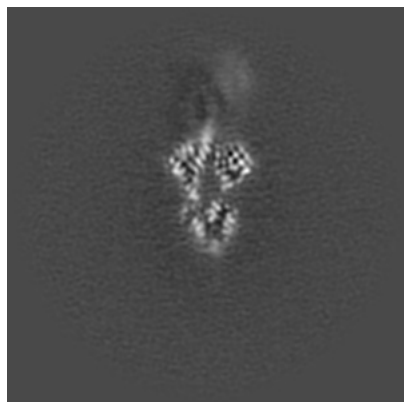


Z Index: 200

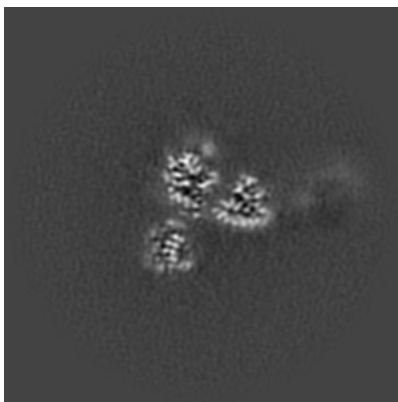
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

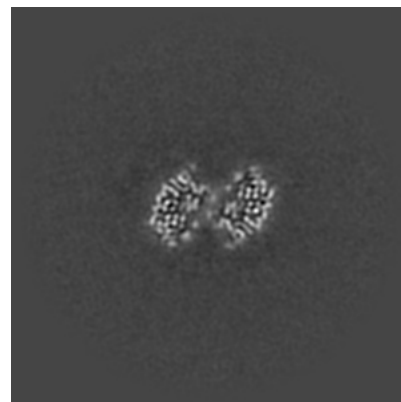
6.3.1 Primary map



X Index: 195

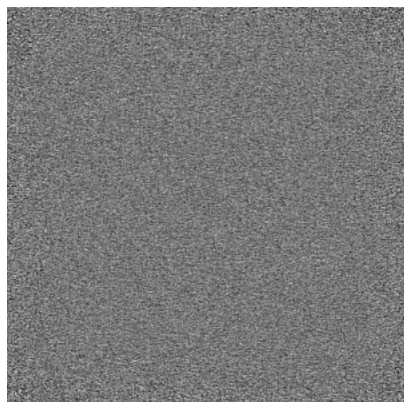


Y Index: 182

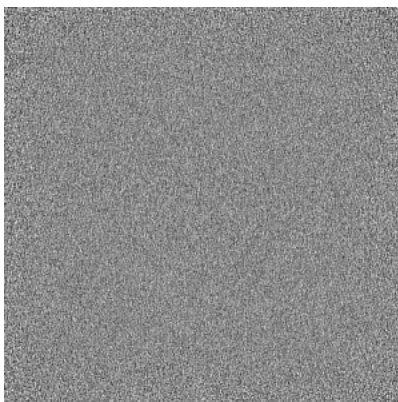


Z Index: 167

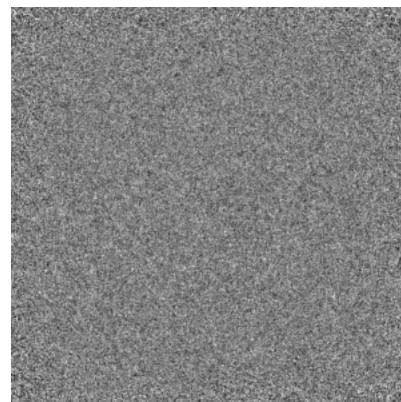
6.3.2 Raw map



X Index: 0



Y Index: 0

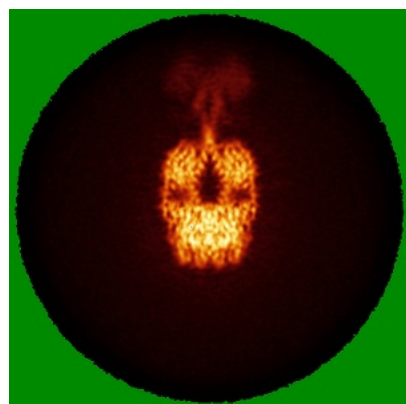


Z Index: 0

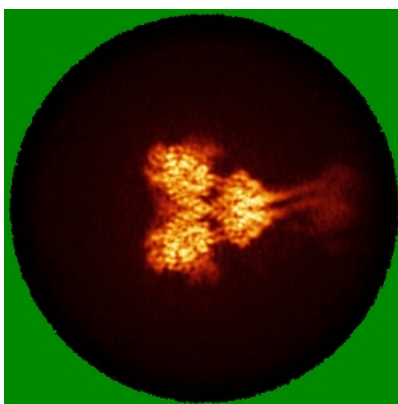
The images above show the largest variance slices of the map in three orthogonal directions.

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

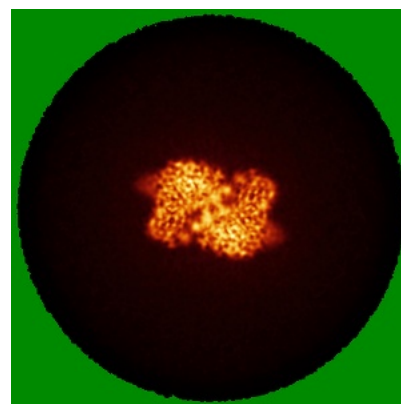
6.4.1 Primary map



X

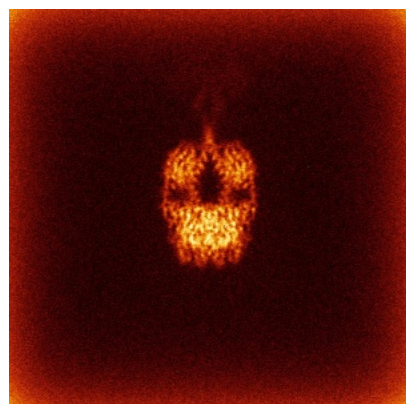


Y

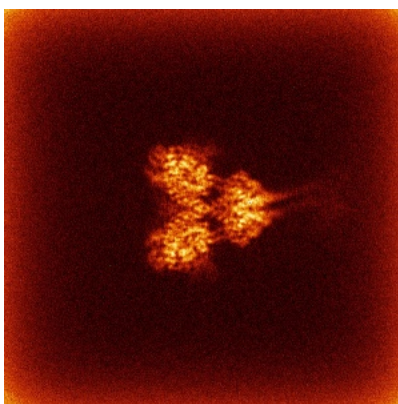


Z

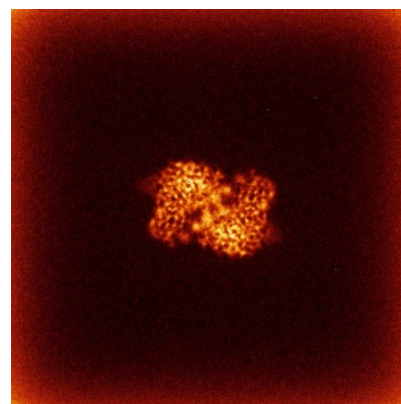
6.4.2 Raw map



X



Y

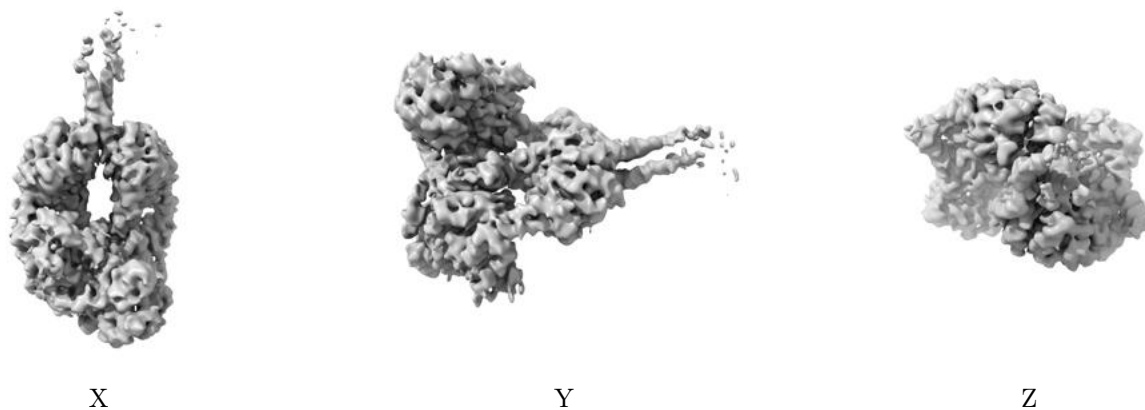


Z

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.

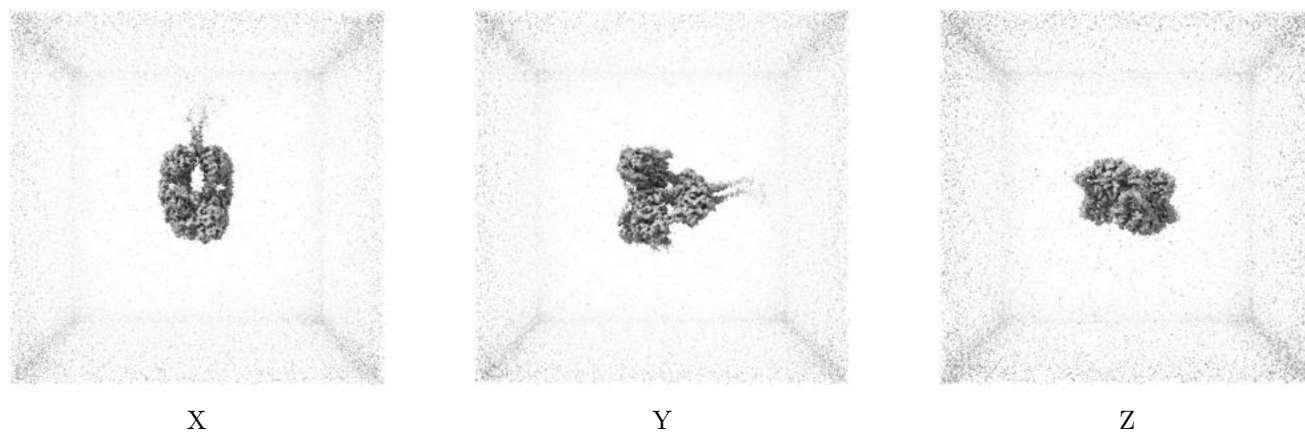
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

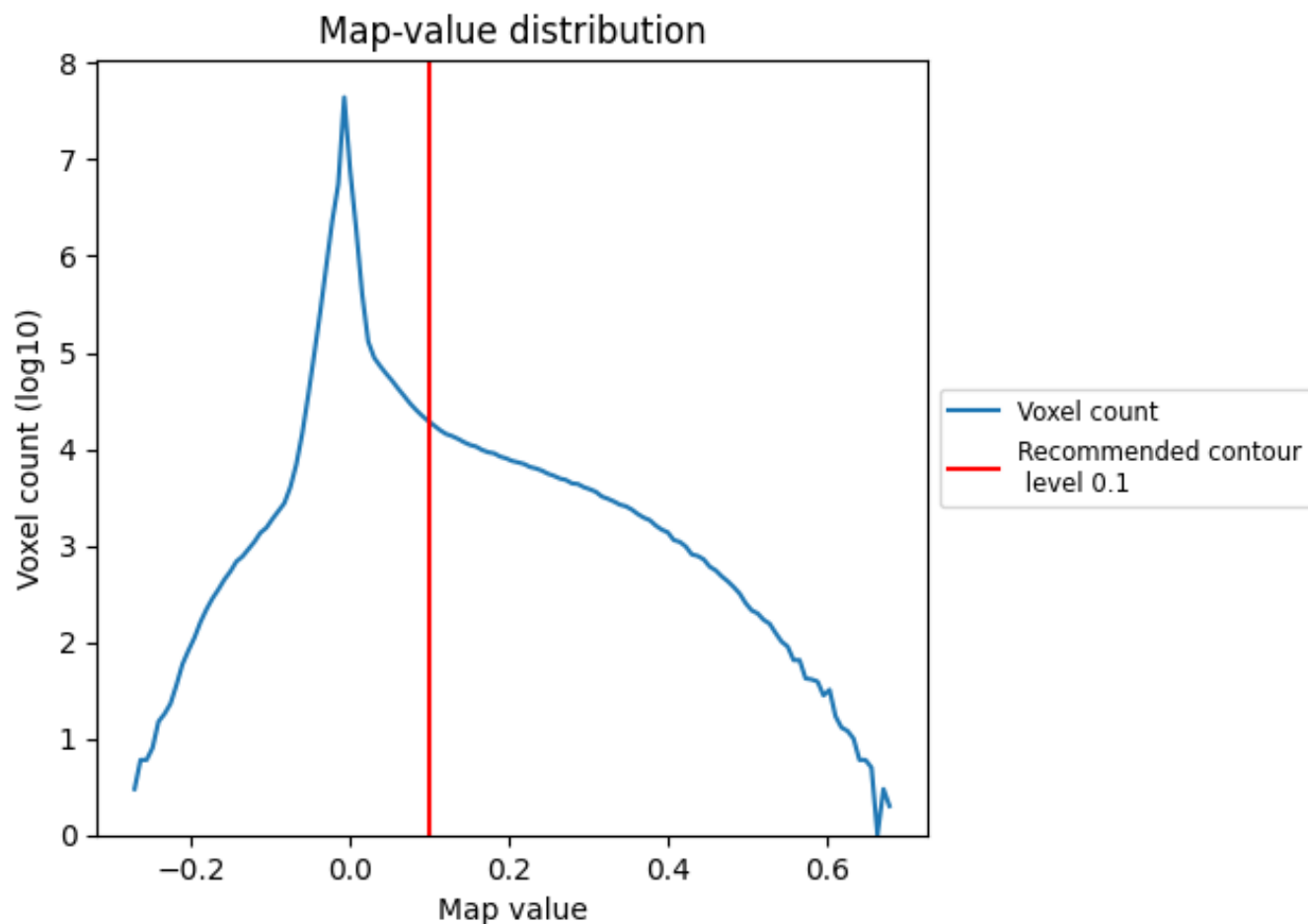
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

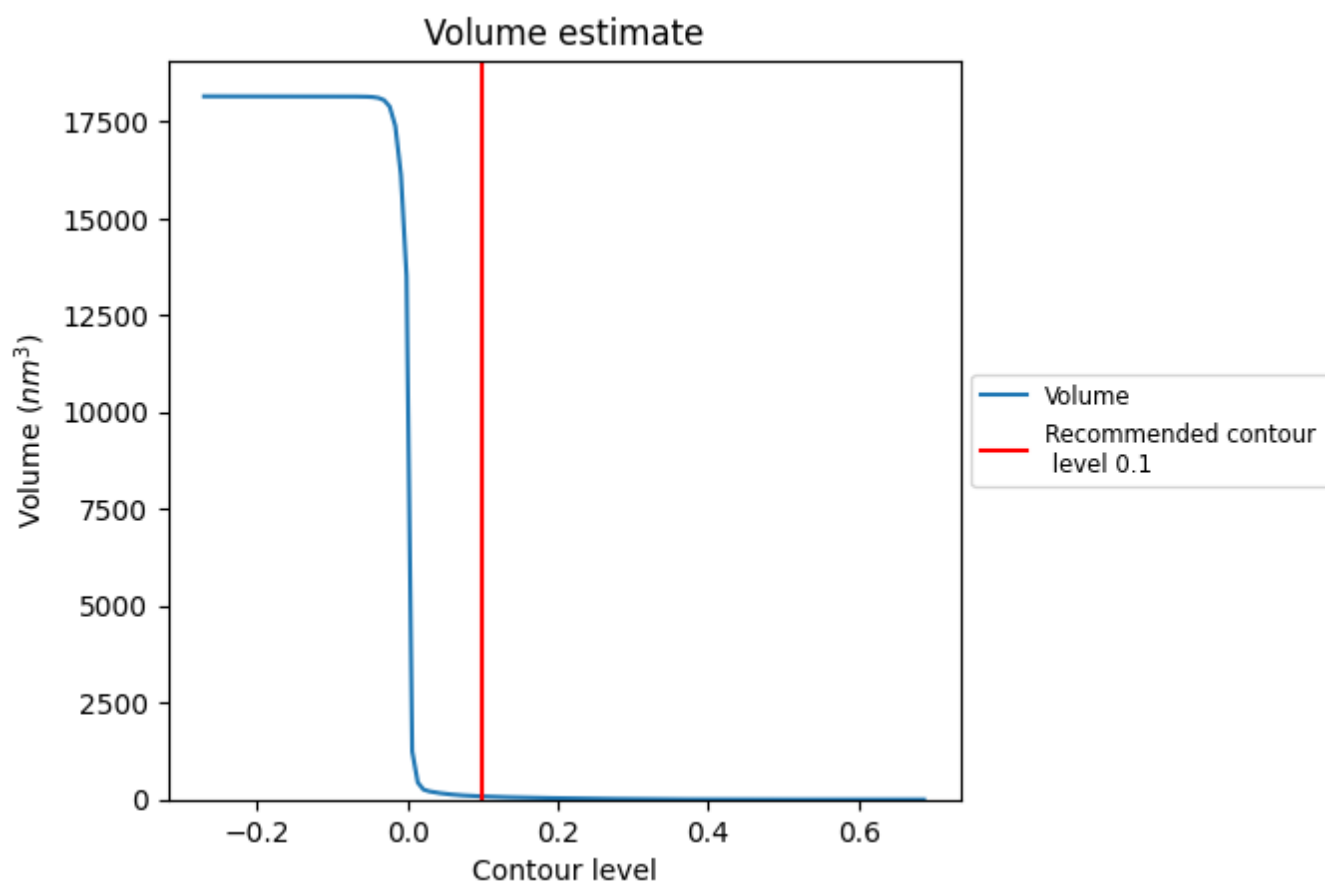
This section contains the results of statistical analysis of the map.

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.

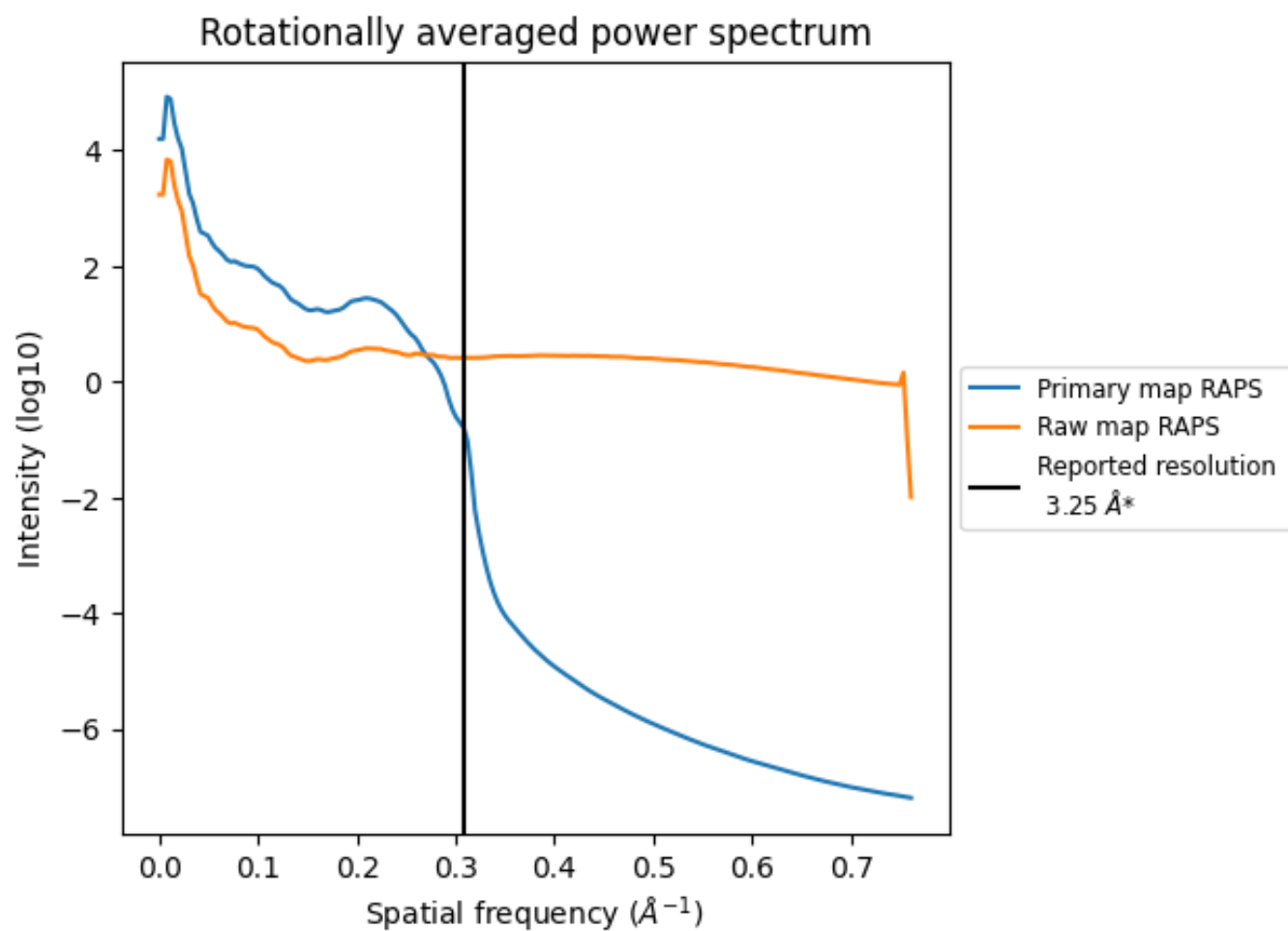
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 81 nm^3 ; this corresponds to an approximate mass of 74 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 ⓘ

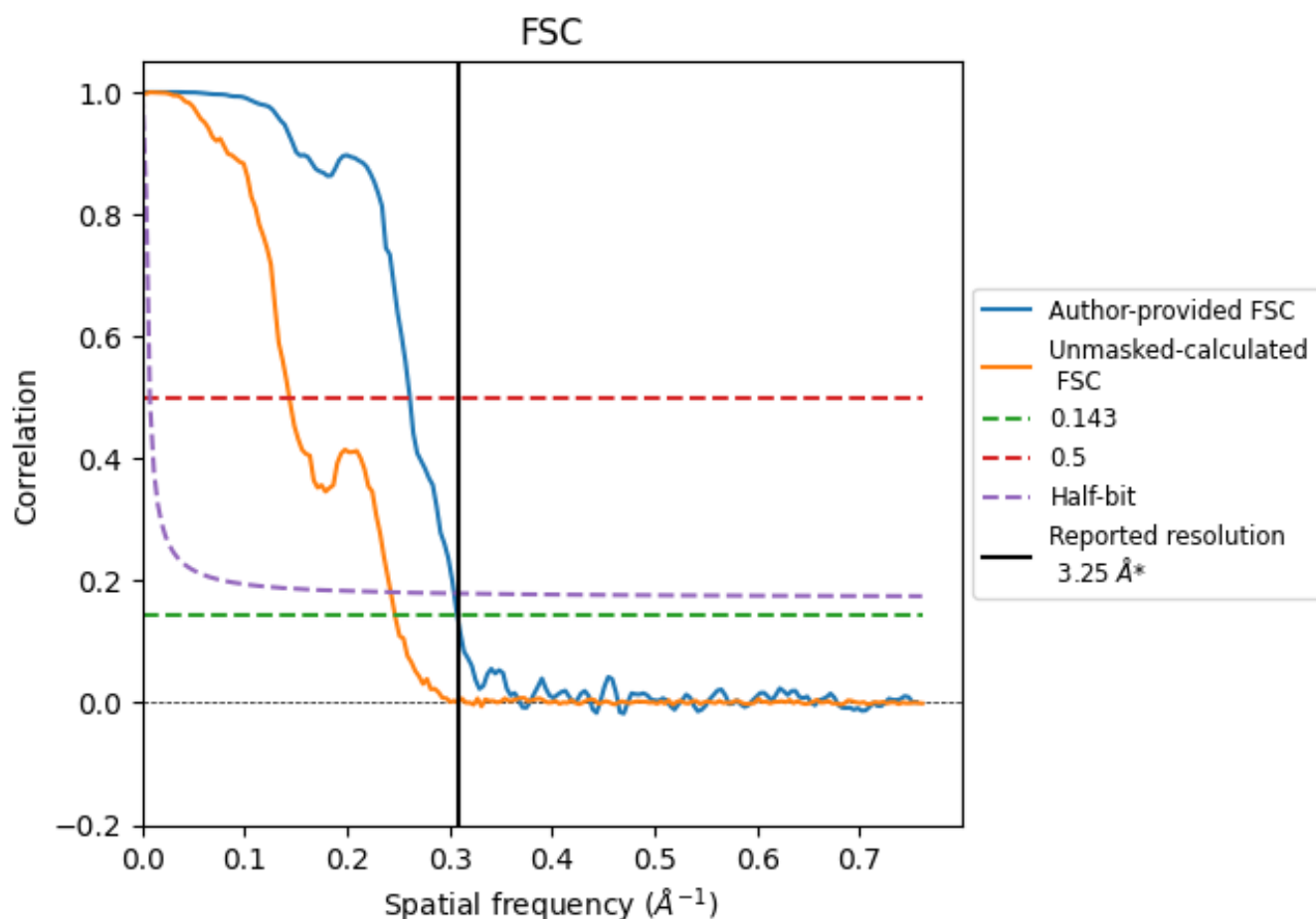


*Reported resolution corresponds to spatial frequency of $0.308 \text{ \AA}^{-1}$

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 0.308 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

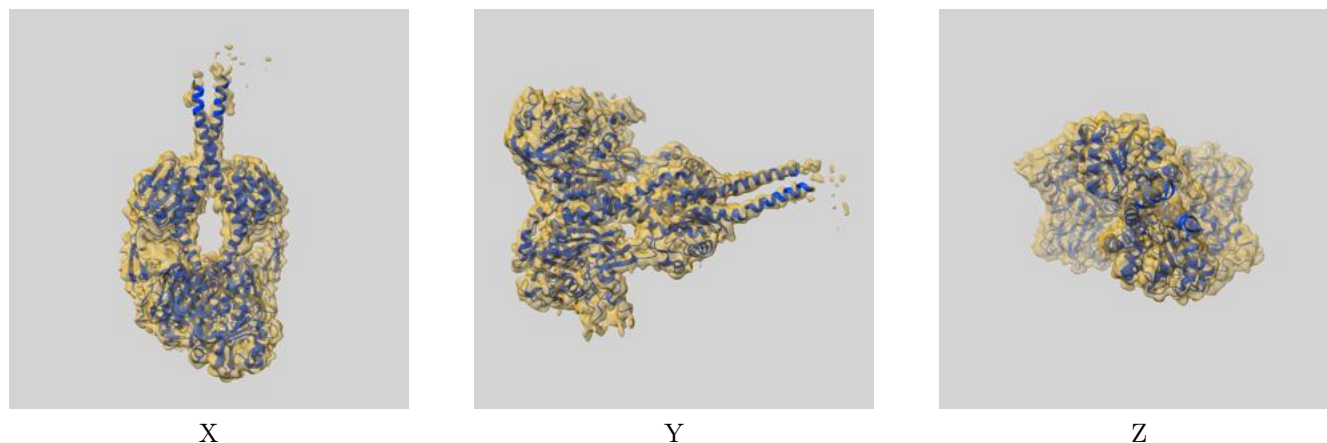
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	3.25	3.83	3.29
Unmasked-calculated*	4.05	6.97	4.12

*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 4.05 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

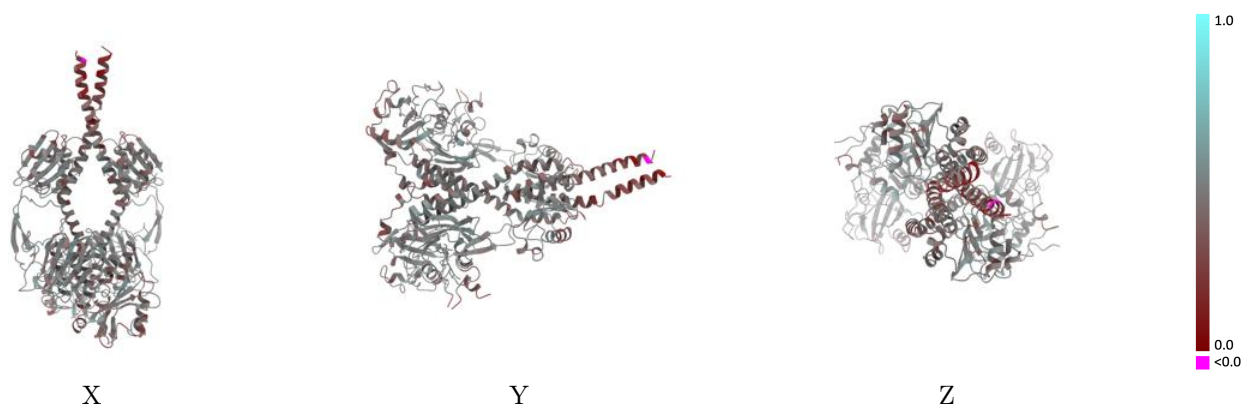
This section contains information regarding the fit between EMDB map EMD-42030 and PDB model 8U8Z. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



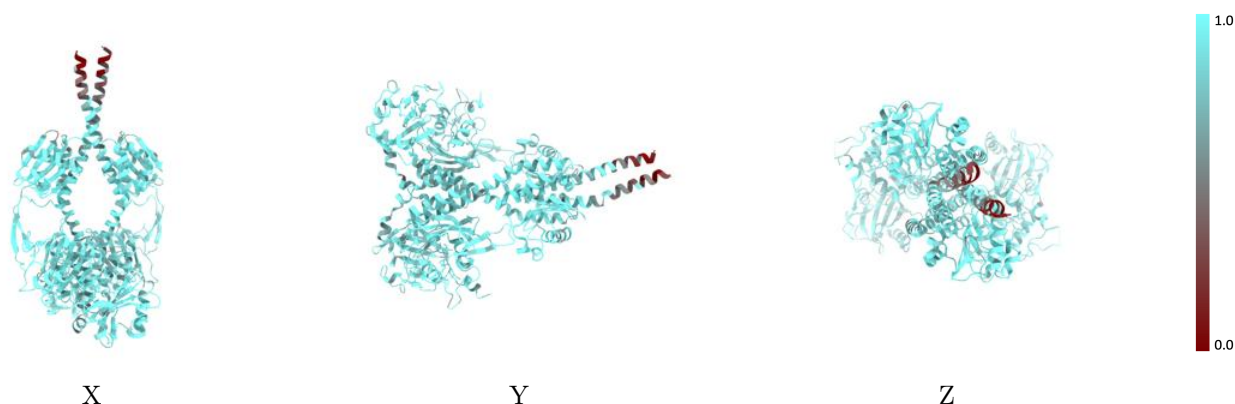
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



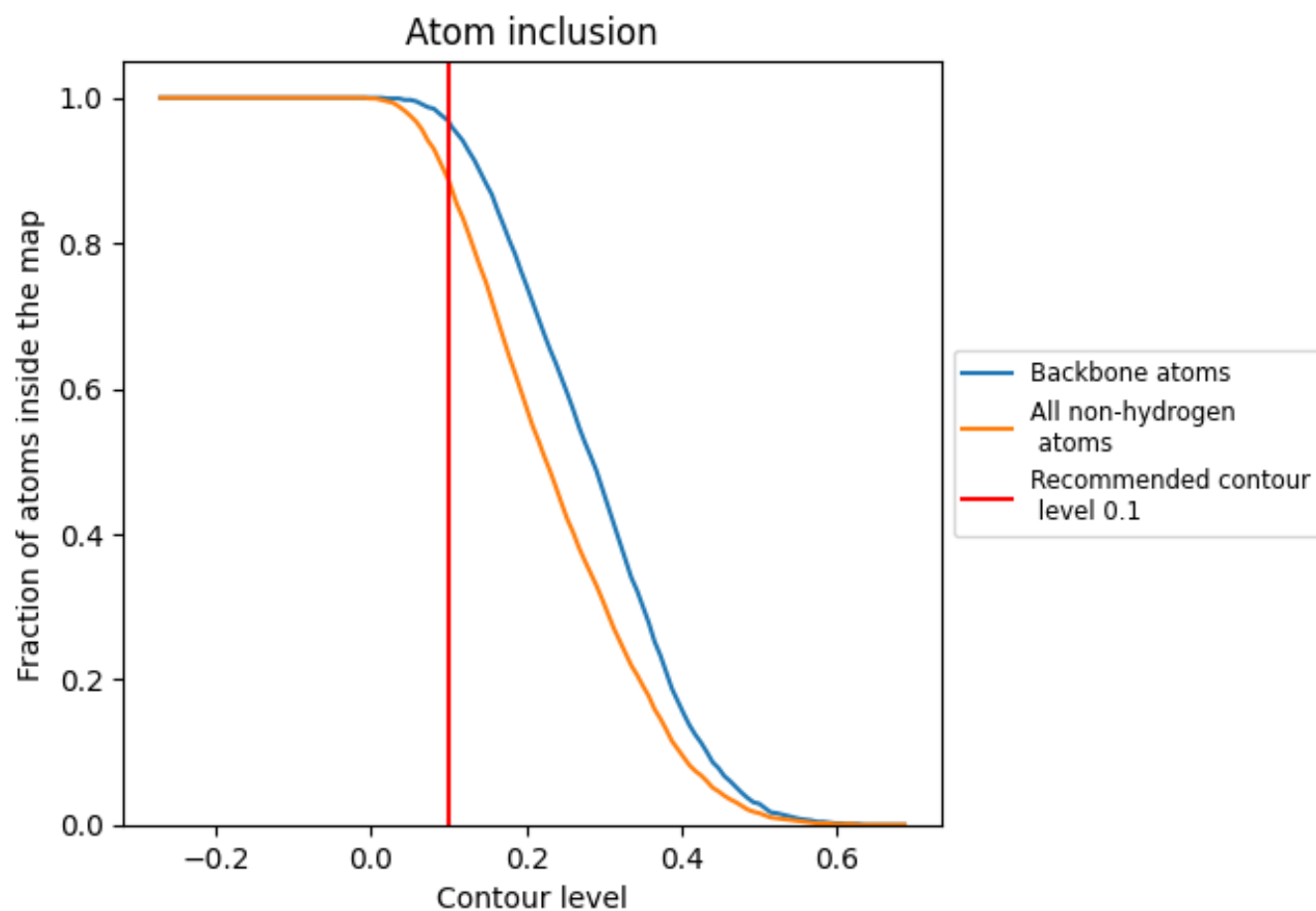
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 89% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8870	0.4450
A	0.8890	0.4430
B	0.8860	0.4470

