



Full wwPDB EM Validation Report ⓘ

Mar 13, 2024 – 10:12 AM JST

PDB ID : 7YJM
EMDB ID : EMD-33874
Title : Cryo-EM structure of the monomeric atSPT-ORM1 complex
Authors : Xie, T.; Liu, P.; Gong, X.
Deposited on : 2022-07-20
Resolution : 3.20 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.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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

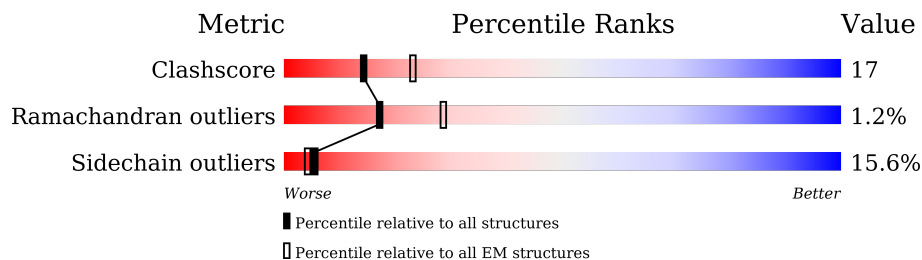
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	420	
2	B	489	
3	D	157	
4	E	62	
5	C	77	

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 8895 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 atLCB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	418	3230	2051	545	618	16	0	0

- Molecule 2 is a protein called Long chain base biosynthesis protein 2a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	471	3673	2347	638	667	21	0	0

- Molecule 3 is a protein called ORMDL family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	156	1277	847	210	210	10	0	0

- Molecule 4 is a protein called atLCB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	E	27	218	148	38	32	0	0

- Molecule 5 is a protein called Transmembrane protein, putative (DUF3317).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	48	436	299	67	67	3	0	0

There are 21 discrepancies between the modelled and reference sequences:

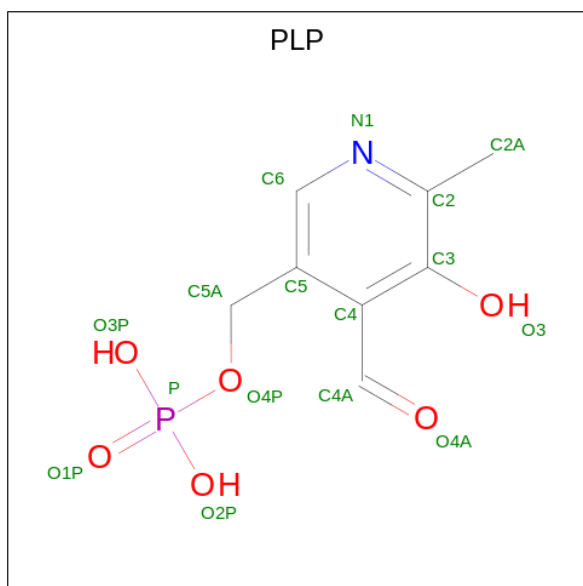
Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	initiating methionine	UNP A8MSB8
C	-19	ALA	-	expression tag	UNP A8MSB8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	ASP	-	expression tag	UNP A8MSB8
C	-17	TYR	-	expression tag	UNP A8MSB8
C	-16	LYS	-	expression tag	UNP A8MSB8
C	-15	ASP	-	expression tag	UNP A8MSB8
C	-14	ASP	-	expression tag	UNP A8MSB8
C	-13	ASP	-	expression tag	UNP A8MSB8
C	-12	ASP	-	expression tag	UNP A8MSB8
C	-11	LYS	-	expression tag	UNP A8MSB8
C	-10	SER	-	expression tag	UNP A8MSB8
C	-9	GLY	-	expression tag	UNP A8MSB8
C	-8	PRO	-	expression tag	UNP A8MSB8
C	-7	ASP	-	expression tag	UNP A8MSB8
C	-6	GLU	-	expression tag	UNP A8MSB8
C	-5	VAL	-	expression tag	UNP A8MSB8
C	-4	ASP	-	expression tag	UNP A8MSB8
C	-3	ALA	-	expression tag	UNP A8MSB8
C	-2	SER	-	expression tag	UNP A8MSB8
C	-1	GLY	-	expression tag	UNP A8MSB8
C	0	ARG	-	expression tag	UNP A8MSB8

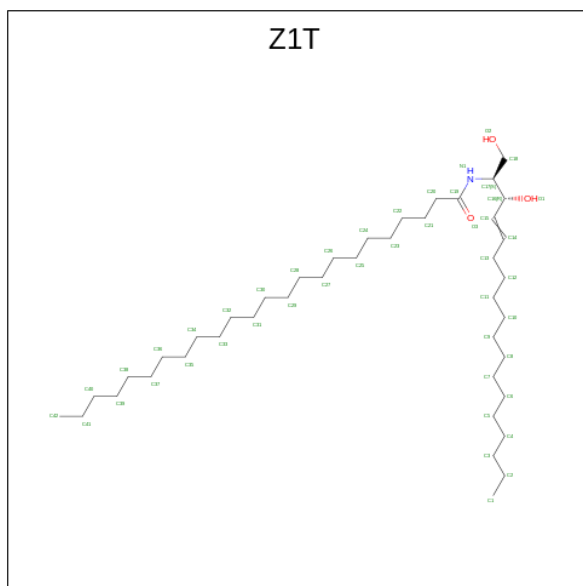
- Molecule 6 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
6	B	1	15	8	1	5	1	0

- Molecule 7 is N-[(2S,3R,4E)-1,3-dihydroxyoctadec-4-en-2-yl]tetracosanamide (three-letter

code: Z1T) (formula: $C_{42}H_{83}NO_3$) (labeled as "Ligand of Interest" by depositor).

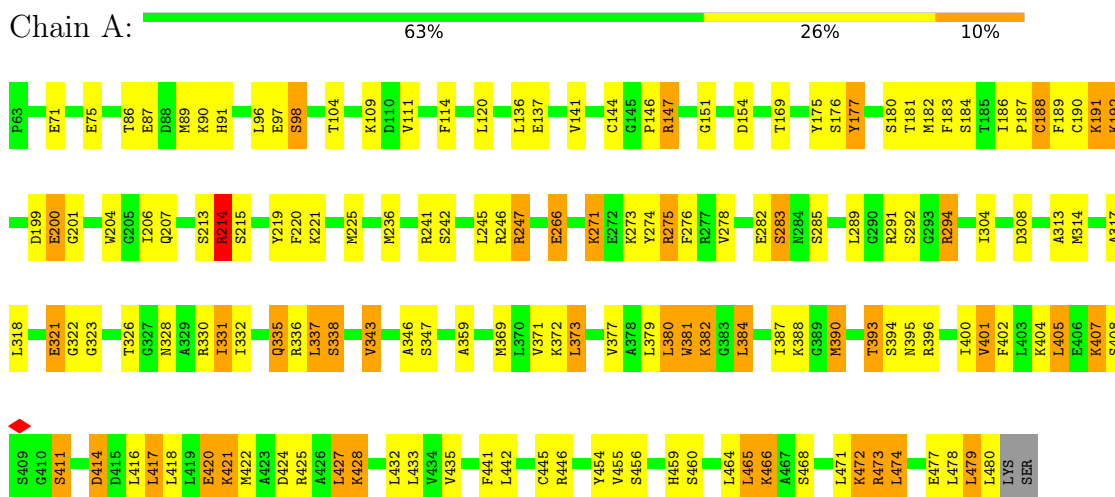


Mol	Chain	Residues	Atoms			AltConf	
			Total	C	N		O
7	D	1	46	42	1	3	0

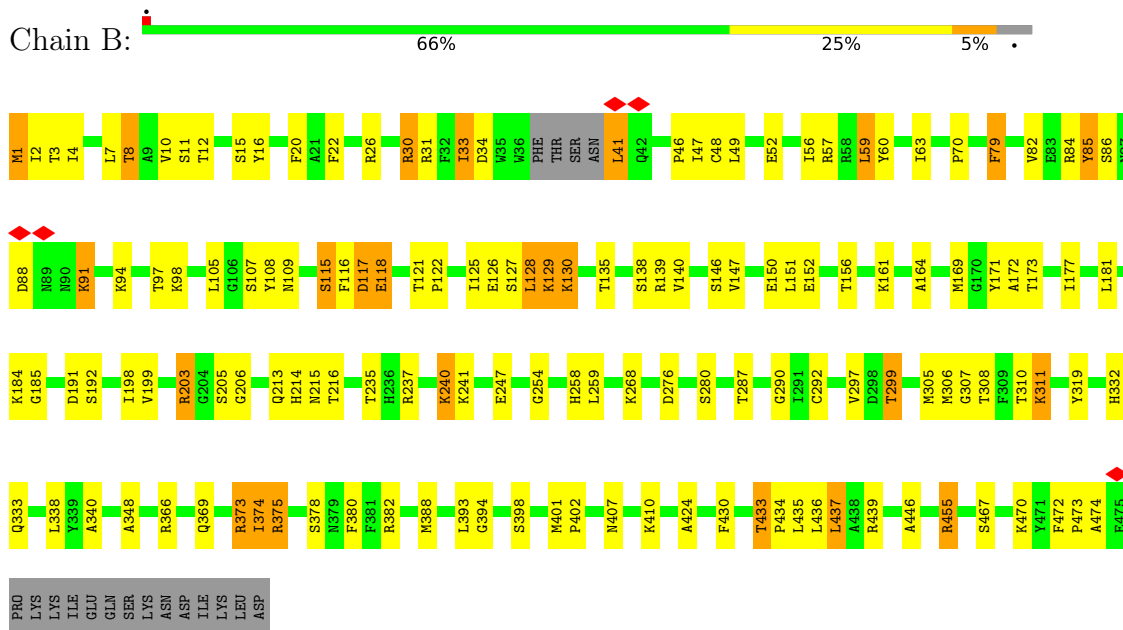
3 Residue-property plots

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

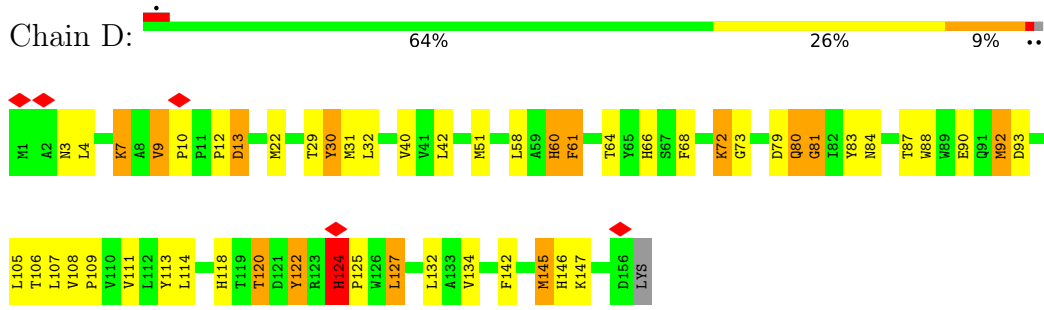
- Molecule 1: atLCB1



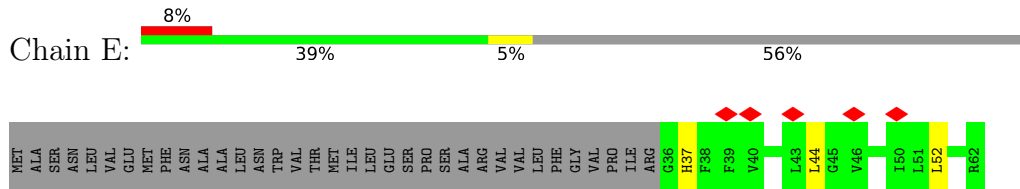
- Molecule 2: Long chain base biosynthesis protein 2a



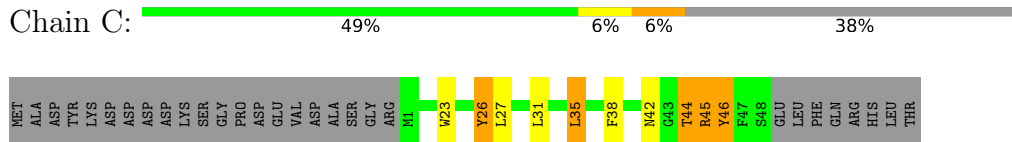
• Molecule 3: ORMDL family protein



• Molecule 4: atLCB1



• Molecule 5: Transmembrane protein, putative (DUF3317)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	115440	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.195	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.027	Depositor
Map size (\AA)	276.48, 276.48, 276.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PLP, Z1T

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	0.30	0/3289	0.45	0/4445
2	B	0.31	0/3755	0.45	0/5079
3	D	0.27	0/1324	0.43	0/1813
4	E	0.27	0/223	0.45	0/299
5	C	0.29	0/453	0.38	0/617
All	All	0.30	0/9044	0.45	0/12253

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	3230	0	3284	119	0
2	B	3673	0	3695	131	0
3	D	1277	0	1256	52	0
4	E	218	0	243	9	0
5	C	436	0	425	17	0
6	B	15	0	6	4	0
7	D	46	0	0	0	0
All	All	8895	0	8909	308	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 17.

All (308) 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)
2:B:311:LYS:NZ	6:B:501:PLP:C4A	1.86	1.39
2:B:433:THR:HG22	2:B:434:PRO:CD	1.67	1.23
2:B:311:LYS:HZ1	6:B:501:PLP:C4A	1.47	1.22
2:B:433:THR:HG21	2:B:439:ARG:HH21	0.98	1.15
2:B:433:THR:HG22	2:B:434:PRO:HD2	1.25	1.12
2:B:85:TYR:CE2	2:B:94:LYS:HB2	1.87	1.10
2:B:472:PHE:HB3	2:B:473:PRO:HD2	1.34	1.06
1:A:321:GLU:OE1	1:A:322:GLY:N	1.95	0.99
2:B:199:VAL:O	2:B:203:ARG:HG3	1.63	0.98
3:D:124:HIS:H	3:D:125:PRO:CD	1.77	0.97
2:B:433:THR:HG22	2:B:434:PRO:HD3	1.47	0.96
2:B:311:LYS:HZ3	6:B:501:PLP:C4A	1.70	0.95
2:B:433:THR:HG21	2:B:439:ARG:NH2	1.80	0.95
3:D:114:LEU:HD21	4:E:44:LEU:HD12	1.47	0.95
1:A:377:VAL:HG22	1:A:455:VAL:HG21	1.50	0.93
2:B:472:PHE:HB3	2:B:473:PRO:CD	1.97	0.93
2:B:88:ASP:O	2:B:91:LYS:HG3	1.70	0.91
1:A:241:ARG:HG3	1:A:241:ARG:HH11	1.34	0.90
3:D:124:HIS:H	3:D:125:PRO:HD2	1.36	0.90
2:B:85:TYR:HE2	2:B:94:LYS:HB2	1.34	0.90
2:B:455:ARG:HH21	2:B:455:ARG:HG2	1.37	0.89
2:B:433:THR:CG2	2:B:439:ARG:HH21	1.86	0.87
1:A:183:PHE:O	1:A:187:PRO:HG2	1.75	0.86
2:B:433:THR:CG2	2:B:434:PRO:CD	2.53	0.85
2:B:433:THR:CG2	2:B:434:PRO:HD2	2.07	0.83
1:A:441:PHE:HD2	2:B:333:GLN:OE1	1.61	0.83
1:A:192:LYS:HA	1:A:214:ARG:O	1.84	0.77
2:B:41:LEU:O	2:B:41:LEU:HD22	1.85	0.77
1:A:241:ARG:HG3	1:A:241:ARG:NH1	2.01	0.74
1:A:420:GLU:O	1:A:420:GLU:HG3	1.88	0.71
1:A:191:LYS:HG3	3:D:80:GLN:O	1.90	0.71
1:A:225:MET:HG3	1:A:266:GLU:HG3	1.72	0.70
2:B:375:ARG:HG2	2:B:375:ARG:NH2	2.05	0.70
3:D:108:VAL:N	3:D:109:PRO:HD2	2.06	0.70
1:A:407:LYS:O	1:A:407:LYS:HG3	1.92	0.70
2:B:198:ILE:HD11	2:B:276:ASP:OD1	1.92	0.69
2:B:375:ARG:HG2	2:B:375:ARG:HH21	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:PHE:O	1:A:187:PRO:CG	2.41	0.69
3:D:124:HIS:N	3:D:125:PRO:CD	2.52	0.69
1:A:465:LEU:HD12	1:A:465:LEU:O	1.94	0.68
2:B:30:ARG:HE	2:B:33:ILE:HG21	1.58	0.68
3:D:104:PHE:O	3:D:108:VAL:HG23	1.93	0.68
5:C:31:LEU:HG	5:C:31:LEU:O	1.93	0.67
3:D:108:VAL:N	3:D:109:PRO:CD	2.57	0.67
1:A:456:SER:H	1:A:459:HIS:HD2	1.41	0.66
1:A:411:SER:H	1:A:414:ASP:HB2	1.60	0.66
2:B:26:ARG:HH11	5:C:23:TRP:HZ2	1.42	0.66
1:A:187:PRO:HA	1:A:213:SER:HB3	1.77	0.66
3:D:9:VAL:HG22	3:D:10:PRO:HD2	1.77	0.66
1:A:273:LYS:HE3	1:A:274:TYR:CZ	2.31	0.65
1:A:418:LEU:HD12	1:A:418:LEU:O	1.97	0.65
2:B:117:ASP:OD2	2:B:366:ARG:NH1	2.29	0.64
2:B:215:ASN:OD1	2:B:258:HIS:ND1	2.29	0.64
1:A:136:LEU:HD11	1:A:141:VAL:HG22	1.80	0.64
1:A:120:LEU:HD23	1:A:317:ALA:HB1	1.79	0.64
2:B:433:THR:CG2	2:B:434:PRO:HD3	2.26	0.64
3:D:30:TYR:HD2	3:D:30:TYR:O	1.81	0.64
1:A:428:LYS:O	1:A:428:LYS:HG2	1.97	0.64
1:A:380:LEU:HG	1:A:380:LEU:O	1.97	0.63
2:B:52:GLU:OE2	2:B:52:GLU:HA	1.98	0.63
1:A:177:TYR:HB2	2:B:169:MET:SD	2.39	0.63
1:A:271:LYS:O	1:A:271:LYS:HG2	1.99	0.63
1:A:282:GLU:HB2	1:A:285:SER:OG	1.99	0.63
2:B:33:ILE:HD12	2:B:33:ILE:O	1.98	0.63
1:A:175:TYR:HB2	1:A:181:THR:HG22	1.80	0.62
1:A:181:THR:HG21	1:A:323:GLY:HA3	1.80	0.62
2:B:97:THR:HG22	2:B:98:LYS:H	1.63	0.62
1:A:183:PHE:O	1:A:187:PRO:CD	2.47	0.62
2:B:91:LYS:HB2	2:B:91:LYS:NZ	2.15	0.62
1:A:89:MET:O	1:A:89:MET:HG2	2.00	0.61
2:B:455:ARG:HG2	2:B:455:ARG:NH2	2.13	0.61
1:A:90:LYS:O	1:A:90:LYS:HG3	2.00	0.61
1:A:282:GLU:O	1:A:282:GLU:HG3	2.00	0.61
1:A:283:SER:HB3	1:A:313:ALA:H	1.65	0.61
1:A:175:TYR:OH	1:A:335:GLN:NE2	2.33	0.61
2:B:12:THR:HG21	2:B:436:LEU:HD12	1.82	0.61
2:B:308:THR:HG22	2:B:310:THR:H	1.65	0.61
2:B:33:ILE:O	2:B:33:ILE:HG23	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:150:GLU:O	2:B:150:GLU:HG2	2.00	0.61
1:A:393:THR:HG23	1:A:393:THR:O	2.00	0.60
3:D:120:THR:HG23	3:D:120:THR:O	2.00	0.60
1:A:304:ILE:O	1:A:304:ILE:HG12	2.01	0.60
1:A:381:TRP:CZ2	1:A:395:ASN:O	2.55	0.60
2:B:1:MET:CE	2:B:214:HIS:CD2	2.85	0.60
1:A:422:MET:HE1	1:A:479:LEU:HD21	1.82	0.60
3:D:118:HIS:HD1	4:E:37:HIS:CE1	2.18	0.60
3:D:108:VAL:H	3:D:109:PRO:HD2	1.67	0.60
1:A:120:LEU:HD12	1:A:369:MET:HG3	1.83	0.59
1:A:441:PHE:CD2	2:B:333:GLN:OE1	2.50	0.59
2:B:434:PRO:HG2	2:B:437:LEU:HD12	1.84	0.59
5:C:44:THR:HG23	5:C:44:THR:O	2.00	0.59
2:B:63:ILE:HG13	2:B:63:ILE:O	2.02	0.59
1:A:274:TYR:C	1:A:275:ARG:HG2	2.23	0.59
1:A:343:VAL:HG23	1:A:343:VAL:O	2.02	0.59
2:B:375:ARG:HH21	2:B:375:ARG:CG	2.15	0.59
2:B:98:LYS:HG2	2:B:98:LYS:O	2.02	0.58
2:B:393:LEU:HB2	2:B:402:PRO:HG2	1.85	0.58
1:A:98:SER:O	1:A:98:SER:OG	2.21	0.58
3:D:114:LEU:HD21	4:E:44:LEU:CD1	2.30	0.58
3:D:107:LEU:HD23	3:D:107:LEU:O	2.03	0.58
1:A:147:ARG:HG2	1:A:347:SER:HB3	1.86	0.58
1:A:400:ILE:HG22	1:A:400:ILE:O	2.04	0.58
2:B:97:THR:O	2:B:98:LYS:HB3	2.04	0.57
3:D:108:VAL:H	3:D:109:PRO:CD	2.17	0.57
1:A:169:THR:HG21	1:A:326:THR:HG22	1.86	0.57
2:B:247:GLU:HG3	2:B:276:ASP:HB3	1.86	0.57
1:A:104:THR:HG23	1:A:111:VAL:HG22	1.85	0.57
2:B:151:LEU:HD12	2:B:151:LEU:O	2.05	0.57
1:A:191:LYS:O	1:A:215:SER:HB3	2.04	0.57
5:C:35:LEU:O	5:C:35:LEU:HD12	2.05	0.57
2:B:130:LYS:HG3	2:B:130:LYS:O	2.04	0.57
2:B:151:LEU:HD22	2:B:348:ALA:HB1	1.85	0.56
3:D:122:TYR:CE2	4:E:37:HIS:ND1	2.73	0.56
1:A:466:LYS:O	1:A:466:LYS:HG2	2.05	0.56
1:A:418:LEU:HD21	1:A:479:LEU:CD1	2.35	0.56
2:B:382:ARG:O	2:B:382:ARG:HG3	2.05	0.56
2:B:147:VAL:HG12	2:B:147:VAL:O	2.06	0.56
2:B:382:ARG:NH1	2:B:398:SER:O	2.38	0.56
2:B:185:GLY:O	2:B:240:LYS:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:GLU:HB2	1:A:219:TYR:HB3	1.88	0.55
3:D:124:HIS:N	3:D:125:PRO:HD2	2.12	0.55
3:D:127:LEU:O	3:D:127:LEU:HD22	2.07	0.55
1:A:114:PHE:HB2	1:A:433:LEU:O	2.06	0.55
1:A:191:LYS:CG	3:D:80:GLN:O	2.55	0.55
1:A:377:VAL:HG22	1:A:455:VAL:CG2	2.31	0.55
1:A:384:LEU:HD13	1:A:468:SER:HB2	1.89	0.55
2:B:129:LYS:O	2:B:129:LYS:HG3	2.05	0.55
2:B:191:ASP:OD1	2:B:192:SER:N	2.40	0.55
2:B:472:PHE:CB	2:B:473:PRO:CD	2.74	0.54
1:A:477:GLU:O	1:A:477:GLU:HG3	2.06	0.54
2:B:1:MET:CE	2:B:214:HIS:HD2	2.19	0.54
3:D:113:TYR:CG	3:D:134:VAL:HG21	2.43	0.54
2:B:407:ASN:HB2	2:B:410:LYS:HG3	1.90	0.54
2:B:156:THR:HG23	2:B:161:LYS:O	2.08	0.53
1:A:111:VAL:HG21	1:A:433:LEU:HD23	1.90	0.53
2:B:254:GLY:O	2:B:394:GLY:HA2	2.09	0.53
2:B:299:THR:HG23	2:B:299:THR:O	2.08	0.53
1:A:427:LEU:HA	1:A:432:LEU:H	1.72	0.53
1:A:435:VAL:HG11	1:A:454:TYR:HE1	1.74	0.52
3:D:118:HIS:ND1	4:E:37:HIS:NE2	2.57	0.52
3:D:79:ASP:O	3:D:81:GLY:N	2.42	0.52
1:A:380:LEU:CD2	1:A:401:VAL:HG21	2.39	0.52
2:B:292:CYS:HA	2:B:297:VAL:HG12	1.91	0.52
2:B:56:ILE:HG22	2:B:56:ILE:O	2.09	0.52
5:C:45:ARG:HG2	5:C:45:ARG:NH2	2.25	0.52
2:B:91:LYS:NZ	2:B:91:LYS:CB	2.73	0.52
1:A:422:MET:HG3	1:A:474:LEU:HD23	1.91	0.52
1:A:380:LEU:HD23	1:A:401:VAL:HG21	1.92	0.51
3:D:73:GLY:HA2	3:D:83:TYR:O	2.10	0.51
2:B:116:PHE:CE1	2:B:121:THR:HG21	2.46	0.51
2:B:85:TYR:C	2:B:85:TYR:HD2	2.14	0.51
2:B:181:LEU:O	2:B:241:LYS:NZ	2.40	0.51
1:A:373:LEU:HD22	1:A:373:LEU:O	2.11	0.51
2:B:2:ILE:O	2:B:2:ILE:HG22	2.10	0.51
1:A:456:SER:H	1:A:459:HIS:CD2	2.27	0.51
2:B:169:MET:HG2	2:B:172:ALA:H	1.75	0.50
2:B:430:PHE:O	2:B:433:THR:O	2.29	0.50
1:A:247:ARG:HB3	1:A:276:PHE:CE1	2.47	0.50
2:B:128:LEU:HG	2:B:128:LEU:O	2.09	0.50
1:A:460:SER:O	1:A:464:LEU:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:MET:HE2	1:A:236:MET:HA	1.93	0.50
1:A:328:ASN:HD21	1:A:331:ILE:HB	1.77	0.50
1:A:318:LEU:HD22	1:A:359:ALA:HB3	1.93	0.50
1:A:418:LEU:HD21	1:A:479:LEU:HD11	1.93	0.50
2:B:433:THR:CB	2:B:434:PRO:CD	2.90	0.50
2:B:85:TYR:C	2:B:85:TYR:CD2	2.85	0.49
2:B:380:PHE:CD2	2:B:380:PHE:C	2.86	0.49
5:C:26:TYR:C	5:C:26:TYR:CD2	2.85	0.49
1:A:473:ARG:HD2	1:A:473:ARG:C	2.33	0.49
2:B:116:PHE:C	2:B:116:PHE:CD2	2.85	0.49
2:B:433:THR:CG2	2:B:439:ARG:NH2	2.59	0.49
1:A:175:TYR:CB	1:A:181:THR:HG22	2.41	0.49
5:C:46:TYR:CD1	5:C:46:TYR:C	2.85	0.49
1:A:91:HIS:ND1	1:A:91:HIS:N	2.60	0.49
1:A:241:ARG:NH1	1:A:241:ARG:CG	2.73	0.49
2:B:70:PRO:HG2	2:B:82:VAL:HB	1.94	0.49
1:A:71:GLU:O	1:A:75:GLU:HG3	2.12	0.48
1:A:336:ARG:HG2	1:A:336:ARG:HH21	1.78	0.48
1:A:380:LEU:CD2	1:A:455:VAL:HG11	2.43	0.48
2:B:139:ARG:HG3	2:B:139:ARG:NH1	2.28	0.48
1:A:372:LYS:O	1:A:372:LYS:HG2	2.12	0.48
2:B:382:ARG:NH2	2:B:394:GLY:HA3	2.29	0.48
1:A:346:ALA:HB2	2:B:310:THR:HG21	1.95	0.48
2:B:116:PHE:HD2	2:B:116:PHE:O	1.97	0.48
2:B:455:ARG:NH2	2:B:455:ARG:CG	2.73	0.48
2:B:139:ARG:HG3	2:B:139:ARG:HH11	1.78	0.48
3:D:92:MET:CE	3:D:105:LEU:HD12	2.43	0.48
3:D:87:THR:O	3:D:90:GLU:N	2.47	0.47
3:D:51:MET:HG3	3:D:51:MET:O	2.13	0.47
1:A:328:ASN:ND2	1:A:331:ILE:HB	2.30	0.47
1:A:186:ILE:N	1:A:187:PRO:CD	2.78	0.47
2:B:382:ARG:NH2	2:B:393:LEU:O	2.47	0.47
1:A:137:GLU:HG2	2:B:125:ILE:HD11	1.96	0.47
1:A:204:TRP:HA	1:A:207:GLN:HG2	1.97	0.47
3:D:64:THR:HG23	3:D:68:PHE:CD2	2.50	0.47
1:A:154:ASP:OD1	1:A:154:ASP:N	2.48	0.47
3:D:61:PHE:C	3:D:61:PHE:CD2	2.87	0.46
1:A:177:TYR:OH	2:B:340:ALA:HB1	2.16	0.46
1:A:182:MET:HG2	1:A:206:ILE:HG12	1.97	0.46
2:B:121:THR:HB	2:B:122:PRO:HD3	1.97	0.46
1:A:96:LEU:HD12	1:A:104:THR:OG1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:45:ARG:HG2	5:C:45:ARG:HH21	1.80	0.46
2:B:128:LEU:C	2:B:128:LEU:HD23	2.35	0.46
2:B:276:ASP:OD2	6:B:501:PLP:H2A2	2.16	0.46
3:D:106:THR:O	3:D:106:THR:HG22	2.13	0.46
1:A:271:LYS:HE2	1:A:278:VAL:HG23	1.97	0.46
3:D:72:LYS:HB3	3:D:72:LYS:HE2	1.61	0.46
2:B:374:ILE:HB	2:B:446:ALA:HB2	1.98	0.46
3:D:122:TYR:HE2	4:E:37:HIS:ND1	2.13	0.46
2:B:2:ILE:O	2:B:4:ILE:HG13	2.16	0.45
2:B:173:THR:O	2:B:177:ILE:HD13	2.17	0.45
3:D:60:HIS:O	3:D:60:HIS:ND1	2.50	0.45
3:D:68:PHE:N	3:D:68:PHE:CD1	2.84	0.45
3:D:118:HIS:ND1	4:E:37:HIS:CE1	2.84	0.45
1:A:421:LYS:O	1:A:421:LYS:HG3	2.16	0.45
1:A:213:SER:O	1:A:215:SER:N	2.49	0.45
1:A:405:LEU:HD23	1:A:405:LEU:O	2.16	0.45
2:B:369:GLN:O	2:B:373:ARG:HB2	2.16	0.45
2:B:118:GLU:H	2:B:118:GLU:HG3	1.57	0.45
2:B:30:ARG:O	2:B:33:ILE:HG22	2.17	0.45
3:D:60:HIS:O	3:D:60:HIS:CG	2.70	0.45
3:D:124:HIS:H	3:D:125:PRO:HD3	1.75	0.45
2:B:410:LYS:HE2	2:B:467:SER:O	2.17	0.45
1:A:388:LYS:CB	1:A:480:LEU:HD11	2.47	0.44
2:B:7:LEU:HD23	2:B:7:LEU:HA	1.75	0.44
1:A:294:ARG:HA	1:A:294:ARG:HD3	1.69	0.44
1:A:183:PHE:CD1	1:A:183:PHE:N	2.84	0.44
2:B:8:THR:O	2:B:8:THR:HG23	2.17	0.44
5:C:38:PHE:CD1	5:C:38:PHE:C	2.90	0.44
1:A:146:PRO:O	1:A:151:GLY:HA3	2.18	0.44
2:B:20:PHE:CD1	2:B:20:PHE:C	2.91	0.44
2:B:60:TYR:O	2:B:60:TYR:CD2	2.70	0.44
3:D:145:MET:HE3	3:D:145:MET:HB3	1.80	0.44
1:A:471:LEU:HD12	1:A:471:LEU:HA	1.85	0.44
2:B:213:GLN:HB3	2:B:216:THR:HG22	2.00	0.44
3:D:7:LYS:HE3	3:D:7:LYS:HB3	1.35	0.44
5:C:45:ARG:HH22	5:C:46:TYR:HB2	1.83	0.44
1:A:188:CYS:SG	1:A:335:GLN:HG3	2.58	0.44
3:D:111:VAL:HG12	3:D:111:VAL:O	2.16	0.44
5:C:38:PHE:CD1	5:C:38:PHE:O	2.70	0.44
5:C:38:PHE:O	5:C:38:PHE:CG	2.70	0.44
2:B:306:MET:HG2	2:B:307:GLY:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:116:PHE:CD2	2:B:116:PHE:O	2.70	0.43
1:A:96:LEU:H	1:A:96:LEU:HD23	1.84	0.43
1:A:472:LYS:HB2	1:A:472:LYS:HE2	1.76	0.43
2:B:1:MET:O	2:B:1:MET:HG3	2.18	0.43
3:D:66:HIS:O	3:D:66:HIS:CG	2.70	0.43
3:D:118:HIS:O	3:D:118:HIS:CD2	2.70	0.43
5:C:26:TYR:CD2	5:C:26:TYR:O	2.71	0.43
2:B:235:THR:O	2:B:237:ARG:N	2.46	0.43
5:C:46:TYR:O	5:C:46:TYR:CG	2.70	0.43
1:A:147:ARG:HE	1:A:147:ARG:HB3	1.62	0.43
1:A:388:LYS:HB2	1:A:480:LEU:HD11	2.00	0.43
1:A:435:VAL:HG11	1:A:454:TYR:CE1	2.54	0.43
2:B:16:TYR:OH	2:B:430:PHE:HB2	2.19	0.43
1:A:473:ARG:C	1:A:473:ARG:CD	2.87	0.43
2:B:85:TYR:HD2	2:B:85:TYR:O	2.02	0.43
5:C:46:TYR:CD1	5:C:46:TYR:O	2.72	0.43
1:A:136:LEU:HD23	2:B:125:ILE:HG12	1.99	0.43
1:A:394:SER:HB3	1:A:402:PHE:H	1.84	0.43
2:B:307:GLY:HA3	2:B:319:TYR:CE2	2.54	0.43
3:D:40:VAL:HG13	5:C:31:LEU:HD11	2.00	0.43
3:D:87:THR:O	3:D:88:TRP:C	2.57	0.43
1:A:332:ILE:HD13	1:A:332:ILE:HA	1.81	0.43
2:B:1:MET:HE1	2:B:214:HIS:CD2	2.53	0.43
3:D:118:HIS:CE1	4:E:37:HIS:NE2	2.86	0.43
2:B:213:GLN:HB3	2:B:216:THR:CG2	2.49	0.42
2:B:268:LYS:O	2:B:268:LYS:HG3	2.19	0.42
3:D:146:HIS:CE1	3:D:147:LYS:HG3	2.54	0.42
1:A:186:ILE:HB	1:A:187:PRO:HD3	2.01	0.42
1:A:479:LEU:HD13	1:A:479:LEU:HA	1.80	0.42
2:B:105:LEU:HB2	2:B:424:ALA:O	2.19	0.42
2:B:46:PRO:C	2:B:48:CYS:H	2.23	0.42
2:B:129:LYS:HB3	2:B:129:LYS:HE3	1.71	0.42
2:B:169:MET:CE	2:B:171:TYR:HB3	2.50	0.42
3:D:42:LEU:HD23	3:D:42:LEU:HA	1.91	0.42
2:B:94:LYS:HB3	2:B:94:LYS:HE3	1.79	0.42
1:A:382:LYS:HB3	1:A:382:LYS:HE3	1.62	0.42
2:B:59:LEU:O	2:B:59:LEU:HD23	2.19	0.42
3:D:127:LEU:HD23	3:D:127:LEU:HA	1.74	0.42
5:C:45:ARG:HH21	5:C:45:ARG:CG	2.33	0.42
1:A:380:LEU:HD22	1:A:455:VAL:HG11	2.01	0.42
1:A:411:SER:H	1:A:414:ASP:CB	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:LEU:HD23	1:A:416:LEU:HA	1.78	0.41
1:A:422:MET:CG	1:A:474:LEU:HD23	2.51	0.41
2:B:434:PRO:CG	2:B:437:LEU:HD12	2.50	0.41
3:D:60:HIS:ND1	3:D:60:HIS:C	2.73	0.41
1:A:337:LEU:H	1:A:337:LEU:HG	1.73	0.41
2:B:152:GLU:HG2	2:B:164:ALA:O	2.21	0.41
2:B:388:MET:O	2:B:470:LYS:HD3	2.20	0.41
2:B:79:PHE:C	2:B:79:PHE:CD2	2.93	0.41
2:B:140:VAL:HG11	2:B:338:LEU:HD23	2.03	0.41
1:A:199:ASP:OD1	1:A:220:PHE:CZ	2.73	0.41
2:B:332:HIS:CE1	2:B:333:GLN:HE21	2.38	0.41
2:B:79:PHE:HD2	2:B:79:PHE:O	2.03	0.41
1:A:189:PHE:CE1	1:A:331:ILE:HG12	2.56	0.41
1:A:188:CYS:SG	1:A:188:CYS:O	2.79	0.41
1:A:338:SER:O	1:A:338:SER:OG	2.34	0.41
1:A:387:ILE:CD1	1:A:390:MET:HG3	2.51	0.41
2:B:105:LEU:HD23	2:B:105:LEU:HA	1.94	0.41
2:B:259:LEU:HD23	2:B:297:VAL:HG11	2.01	0.40
3:D:107:LEU:HD13	4:E:52:LEU:HD21	2.03	0.40
3:D:118:HIS:O	3:D:118:HIS:CG	2.75	0.40
1:A:417:LEU:HD13	1:A:417:LEU:HA	1.90	0.40
2:B:184:LYS:HA	2:B:206:GLY:O	2.22	0.40
2:B:280:SER:O	2:B:290:GLY:HA2	2.22	0.40
2:B:287:THR:HG22	2:B:287:THR:O	2.22	0.40
3:D:132:LEU:HD12	3:D:132:LEU:HA	1.82	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	416/420 (99%)	365 (88%)	47 (11%)	4 (1%)	15 54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	467/489 (96%)	424 (91%)	40 (9%)	3 (1%)	25	64
3	D	154/157 (98%)	136 (88%)	12 (8%)	6 (4%)	3	22
4	E	25/62 (40%)	25 (100%)	0	0	100	100
5	C	46/77 (60%)	41 (89%)	5 (11%)	0	100	100
All	All	1108/1205 (92%)	991 (89%)	104 (9%)	13 (1%)	17	49

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	12	PRO
3	D	124	HIS
1	A	214	ARG
2	B	109	ASN
3	D	80	GLN
1	A	144	CYS
1	A	201	GLY
2	B	115	SER
2	B	474	ALA
3	D	13	ASP
1	A	401	VAL
3	D	81	GLY
3	D	122	TYR

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	361/363 (99%)	290 (80%)	71 (20%)	1	7
2	B	396/414 (96%)	347 (88%)	49 (12%)	4	21
3	D	138/139 (99%)	114 (83%)	24 (17%)	2	10
4	E	24/54 (44%)	24 (100%)	0	100	100
5	C	46/71 (65%)	39 (85%)	7 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	965/1041 (93%)	814 (84%)	151 (16%)	5 12

All (151) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	THR
1	A	87	GLU
1	A	97	GLU
1	A	98	SER
1	A	109	LYS
1	A	147	ARG
1	A	176	SER
1	A	177	TYR
1	A	180	SER
1	A	184	SER
1	A	188	CYS
1	A	190	CYS
1	A	191	LYS
1	A	192	LYS
1	A	200	GLU
1	A	214	ARG
1	A	221	LYS
1	A	242	SER
1	A	245	LEU
1	A	246	ARG
1	A	247	ARG
1	A	266	GLU
1	A	271	LYS
1	A	275	ARG
1	A	283	SER
1	A	289	LEU
1	A	291	ARG
1	A	292	SER
1	A	294	ARG
1	A	308	ASP
1	A	314	MET
1	A	321	GLU
1	A	330	ARG
1	A	331	ILE
1	A	335	GLN
1	A	337	LEU
1	A	338	SER

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Mol	Chain	Res	Type
1	A	343	VAL
1	A	371	VAL
1	A	373	LEU
1	A	379	LEU
1	A	380	LEU
1	A	381	TRP
1	A	382	LYS
1	A	384	LEU
1	A	390	MET
1	A	393	THR
1	A	396	ARG
1	A	404	LYS
1	A	405	LEU
1	A	407	LYS
1	A	408	SER
1	A	411	SER
1	A	414	ASP
1	A	417	LEU
1	A	420	GLU
1	A	421	LYS
1	A	424	ASP
1	A	425	ARG
1	A	427	LEU
1	A	428	LYS
1	A	442	LEU
1	A	445	CYS
1	A	446	ARG
1	A	465	LEU
1	A	466	LYS
1	A	472	LYS
1	A	473	ARG
1	A	474	LEU
1	A	478	LEU
1	A	479	LEU
2	B	1	MET
2	B	3	THR
2	B	8	THR
2	B	10	VAL
2	B	11	SER
2	B	15	SER
2	B	22	PHE
2	B	30	ARG

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Mol	Chain	Res	Type
2	B	31	ARG
2	B	33	ILE
2	B	34	ASP
2	B	41	LEU
2	B	47	ILE
2	B	49	LEU
2	B	57	ARG
2	B	59	LEU
2	B	79	PHE
2	B	84	ARG
2	B	85	TYR
2	B	86	SER
2	B	91	LYS
2	B	107	SER
2	B	108	TYR
2	B	115	SER
2	B	117	ASP
2	B	118	GLU
2	B	126	GLU
2	B	127	SER
2	B	128	LEU
2	B	129	LYS
2	B	130	LYS
2	B	135	THR
2	B	138	SER
2	B	146	SER
2	B	203	ARG
2	B	205	SER
2	B	240	LYS
2	B	299	THR
2	B	305	MET
2	B	311	LYS
2	B	373	ARG
2	B	374	ILE
2	B	375	ARG
2	B	378	SER
2	B	401	MET
2	B	433	THR
2	B	435	LEU
2	B	437	LEU
2	B	455	ARG
3	D	3	ASN

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Mol	Chain	Res	Type
3	D	4	LEU
3	D	7	LYS
3	D	9	VAL
3	D	13	ASP
3	D	22	MET
3	D	29	THR
3	D	30	TYR
3	D	31	MET
3	D	32	LEU
3	D	58	LEU
3	D	60	HIS
3	D	61	PHE
3	D	72	LYS
3	D	84	ASN
3	D	92	MET
3	D	93	ASP
3	D	96	GLN
3	D	99	THR
3	D	120	THR
3	D	124	HIS
3	D	127	LEU
3	D	142	PHE
3	D	145	MET
5	C	26	TYR
5	C	27	LEU
5	C	35	LEU
5	C	42	ASN
5	C	44	THR
5	C	45	ARG
5	C	46	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	335	GLN
1	A	459	HIS
2	B	214	HIS
2	B	333	GLN
3	D	3	ASN
3	D	96	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
7	Z1T	D	201	-	44,45,45	0.82	1 (2%)	45,47,47	1.20	2 (4%)
6	PLP	B	501	-	15,15,16	3.08	3 (20%)	20,22,23	1.19	1 (5%)

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
7	Z1T	D	201	-	-	26/48/48/48	-
6	PLP	B	501	-	-	3/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	501	PLP	C3-C2	7.94	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	501	PLP	C5-C4	7.51	1.48	1.40
7	D	201	Z1T	C15-C14	4.90	1.52	1.31
6	B	501	PLP	C3-C4	4.00	1.48	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	201	Z1T	C16-C15-C14	-4.48	114.79	124.79
7	D	201	Z1T	C13-C14-C15	-2.41	114.61	125.39
6	B	501	PLP	C6-N1-C2	2.20	123.23	119.17

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	501	PLP	C5A-O4P-P-O1P
6	B	501	PLP	C5A-O4P-P-O2P
6	B	501	PLP	C5A-O4P-P-O3P
7	D	201	Z1T	C16-C17-C18-O2
7	D	201	Z1T	C28-C29-C30-C31
7	D	201	Z1T	C32-C33-C34-C35
7	D	201	Z1T	C3-C4-C5-C6
7	D	201	Z1T	C26-C27-C28-C29
7	D	201	Z1T	C30-C31-C32-C33
7	D	201	Z1T	C23-C24-C25-C26
7	D	201	Z1T	C24-C25-C26-C27
7	D	201	Z1T	C37-C38-C39-C40
7	D	201	Z1T	C5-C6-C7-C8
7	D	201	Z1T	C1-C2-C3-C4
7	D	201	Z1T	C20-C21-C22-C23
7	D	201	Z1T	C6-C7-C8-C9
7	D	201	Z1T	C4-C5-C6-C7
7	D	201	Z1T	C39-C40-C41-C42
7	D	201	Z1T	C36-C37-C38-C39
7	D	201	Z1T	C25-C26-C27-C28
7	D	201	Z1T	O1-C16-C17-N1
7	D	201	Z1T	N1-C17-C18-O2
7	D	201	Z1T	C19-C20-C21-C22
7	D	201	Z1T	O1-C16-C17-C18
7	D	201	Z1T	C34-C35-C36-C37
7	D	201	Z1T	C9-C10-C11-C12
7	D	201	Z1T	C29-C30-C31-C32

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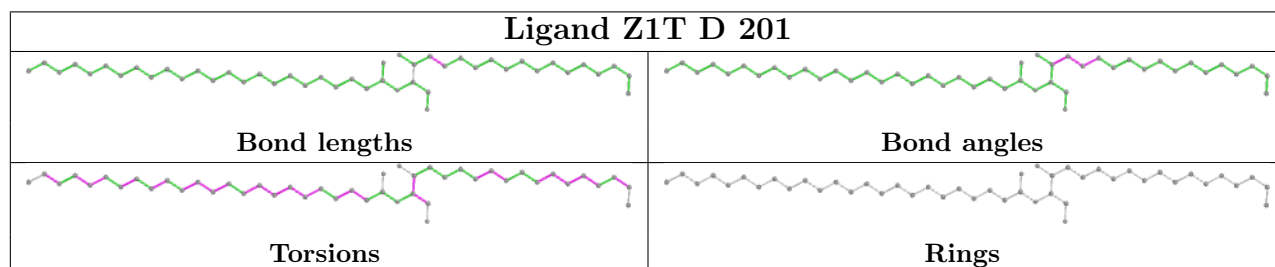
Mol	Chain	Res	Type	Atoms
7	D	201	Z1T	C10-C11-C12-C13
7	D	201	Z1T	C22-C23-C24-C25

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	501	PLP	4	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.



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.

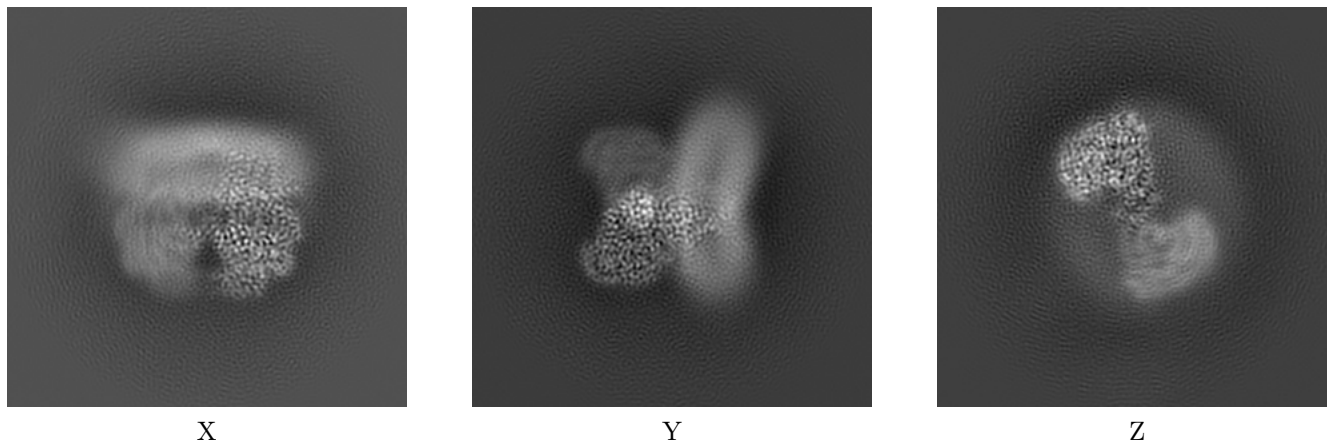
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33874. These allow visual inspection of the internal detail of the map and identification of artifacts.

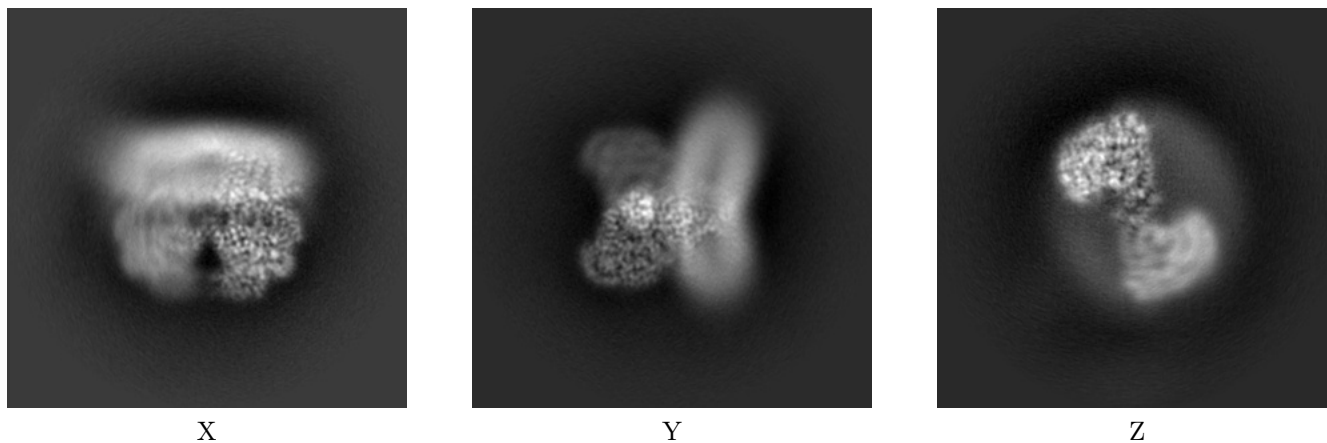
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



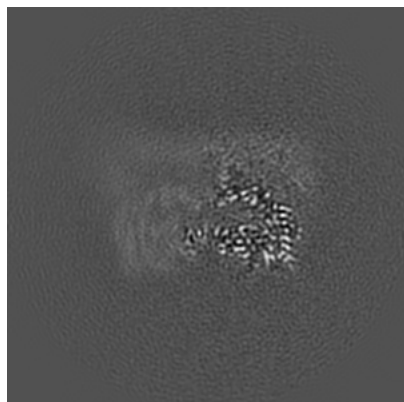
6.1.2 Raw map



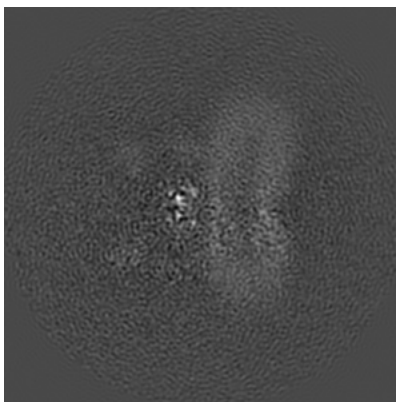
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

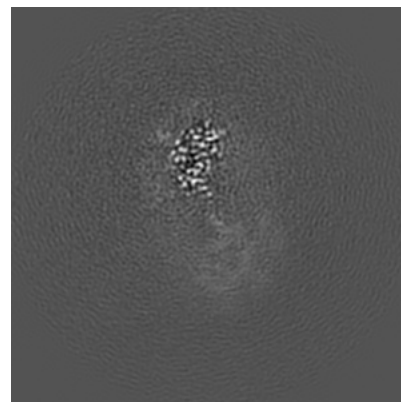
6.2.1 Primary map



X Index: 128

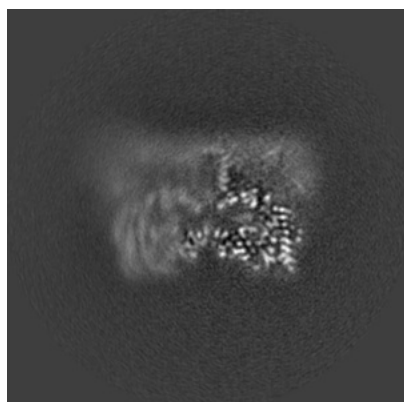


Y Index: 128

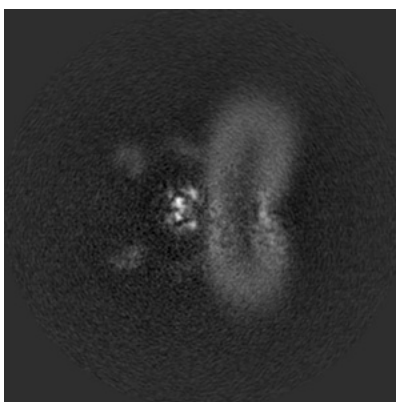


Z Index: 128

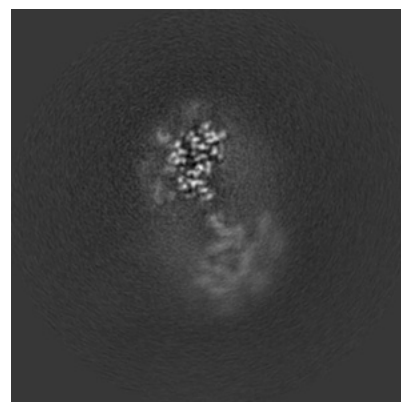
6.2.2 Raw map



X Index: 128



Y Index: 128

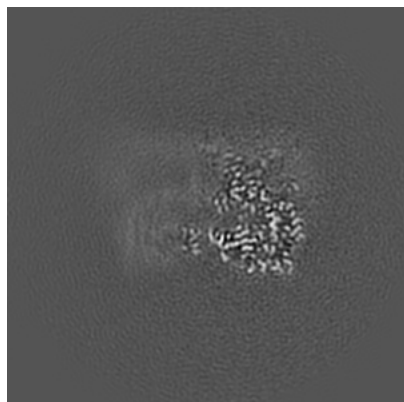


Z Index: 128

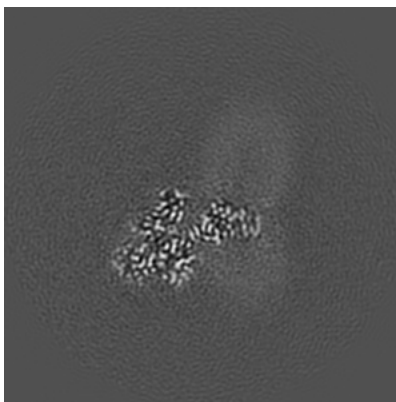
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

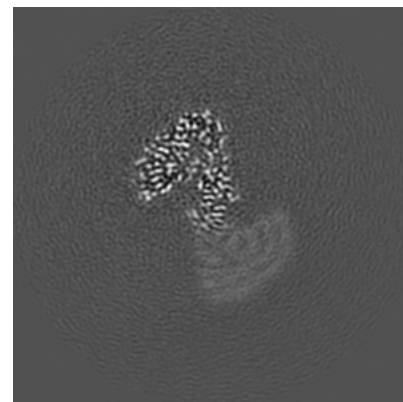
6.3.1 Primary map



X Index: 125

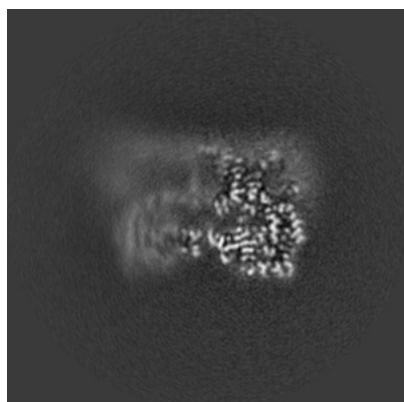


Y Index: 145

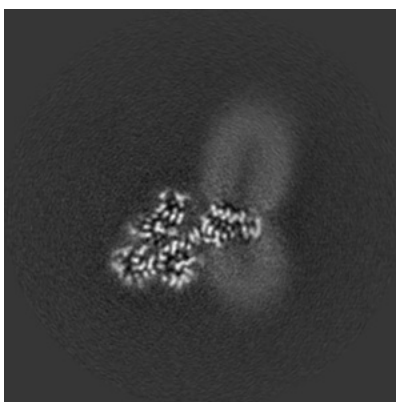


Z Index: 110

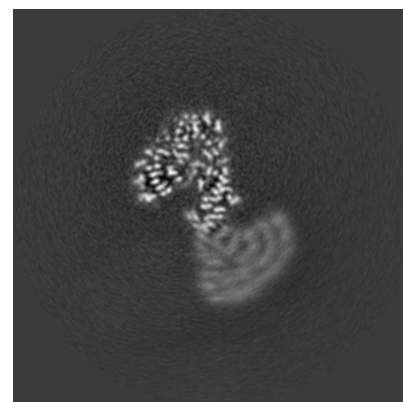
6.3.2 Raw map



X Index: 125



Y Index: 145

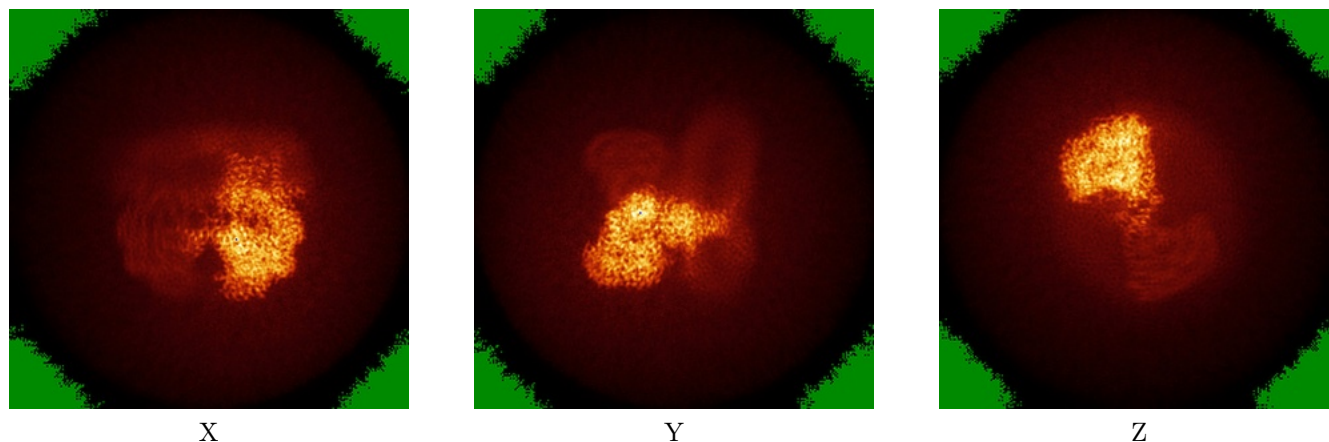


Z Index: 111

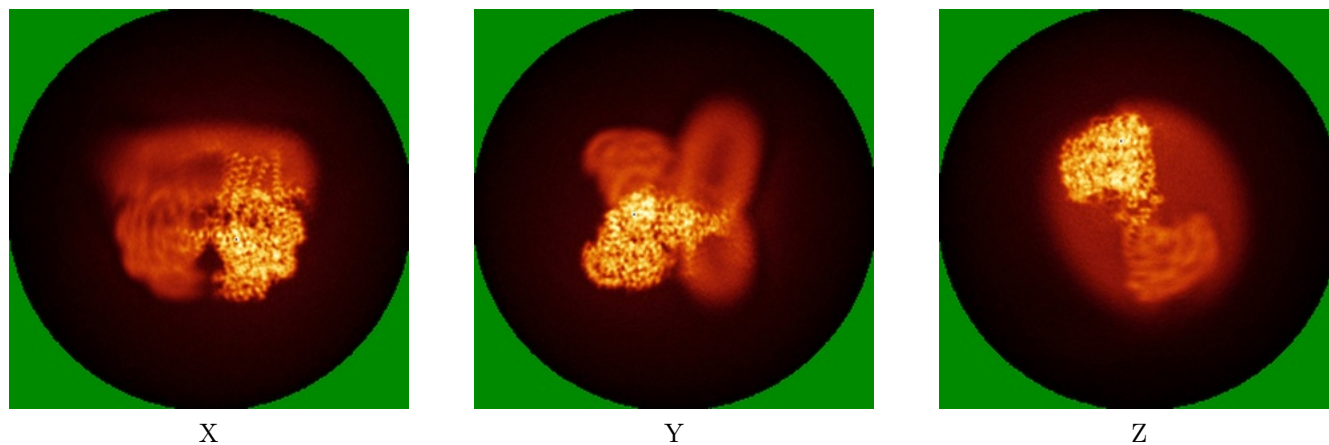
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



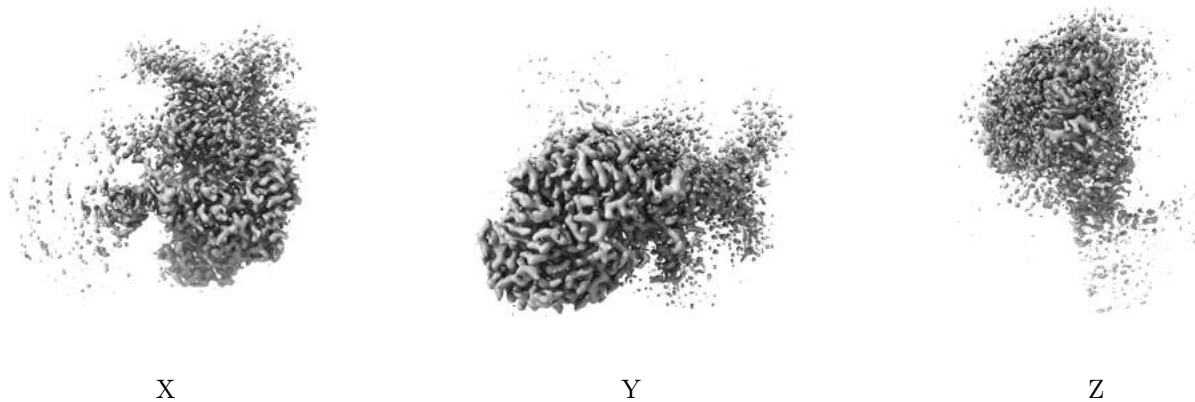
6.4.2 Raw map



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.

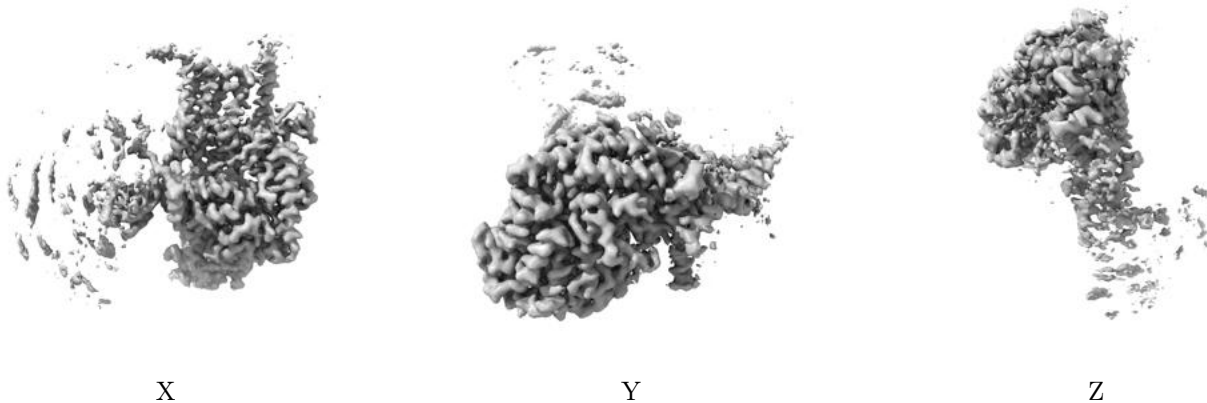
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. 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.

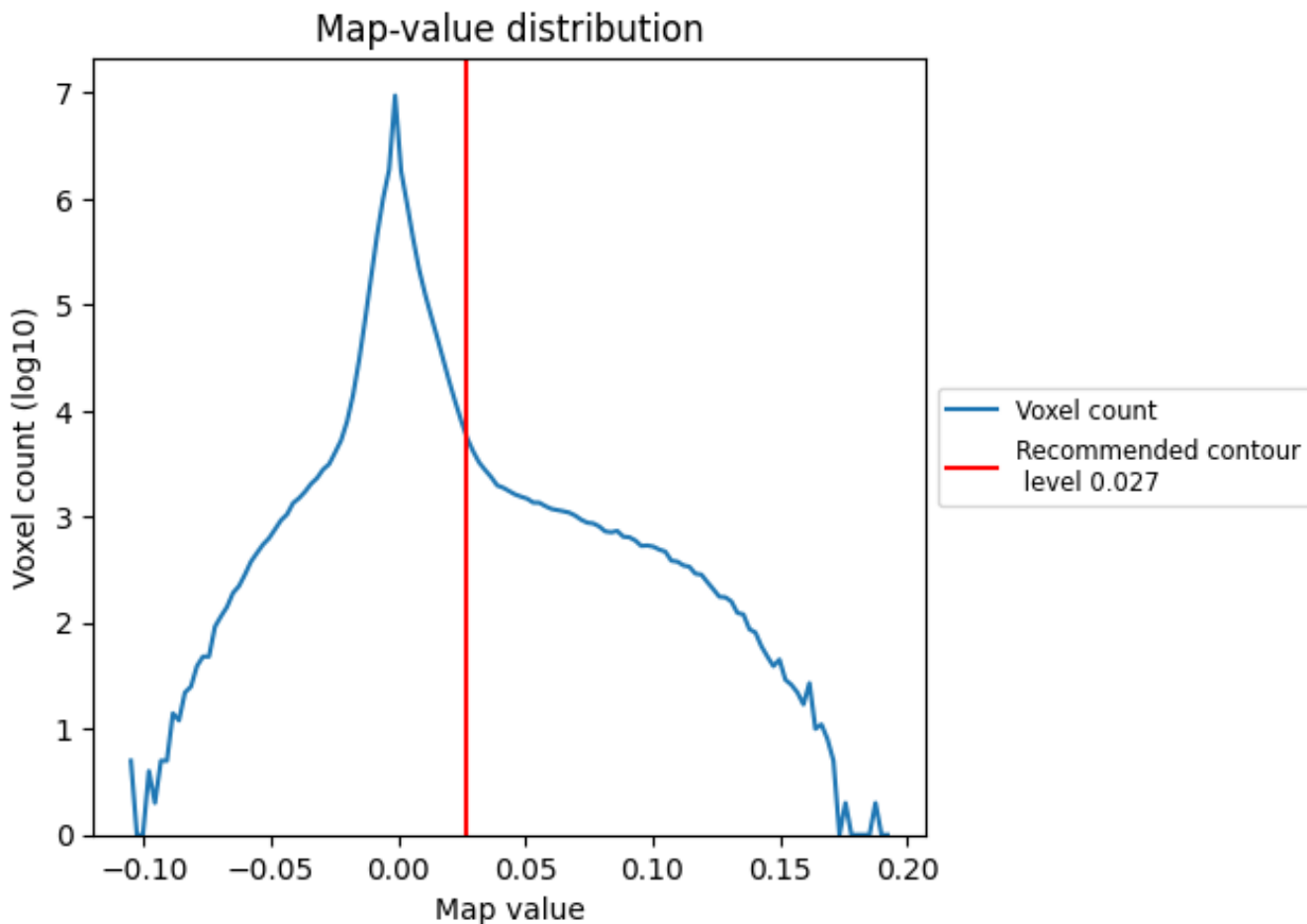
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

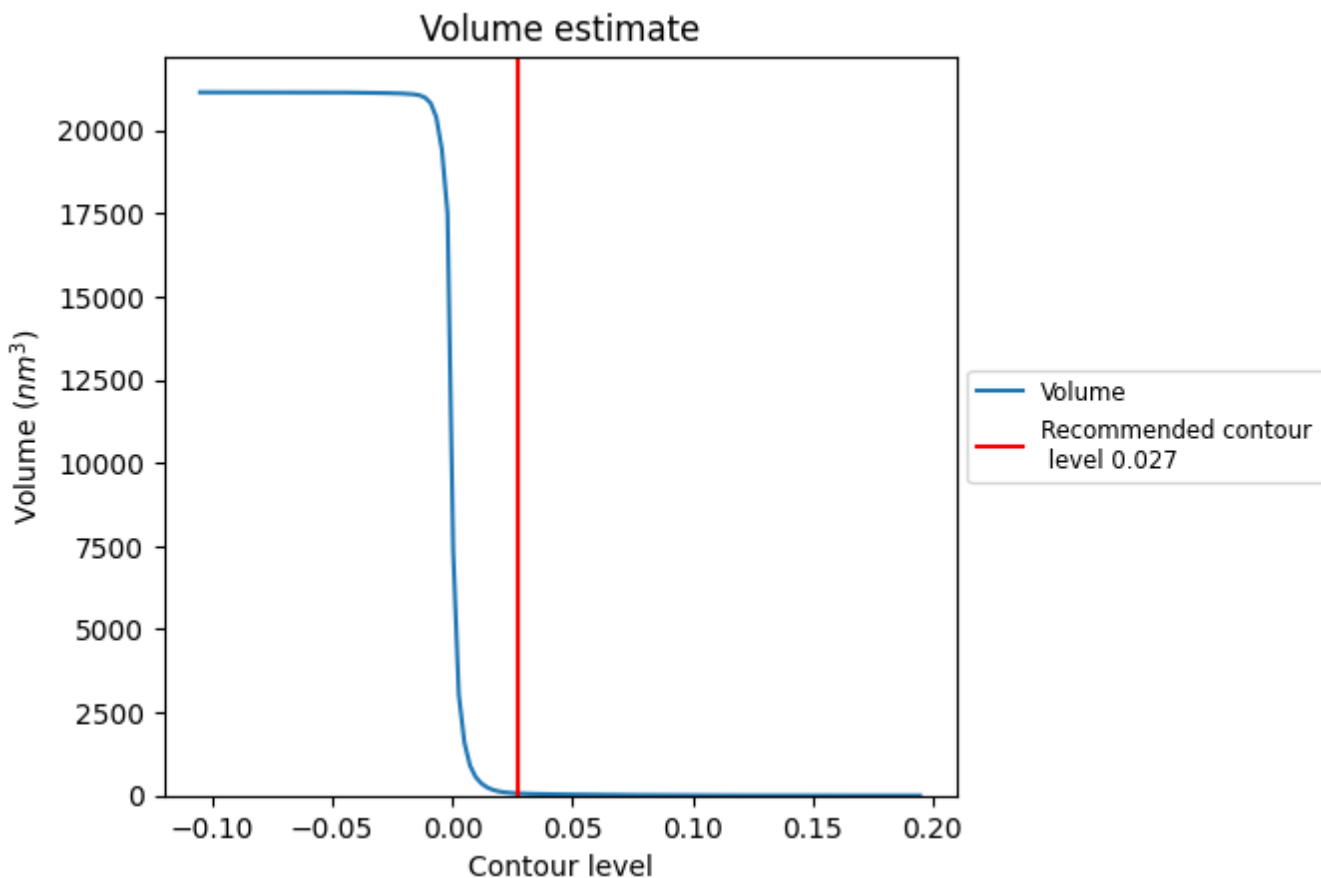
This section contains the results of statistical analysis of the map.

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.

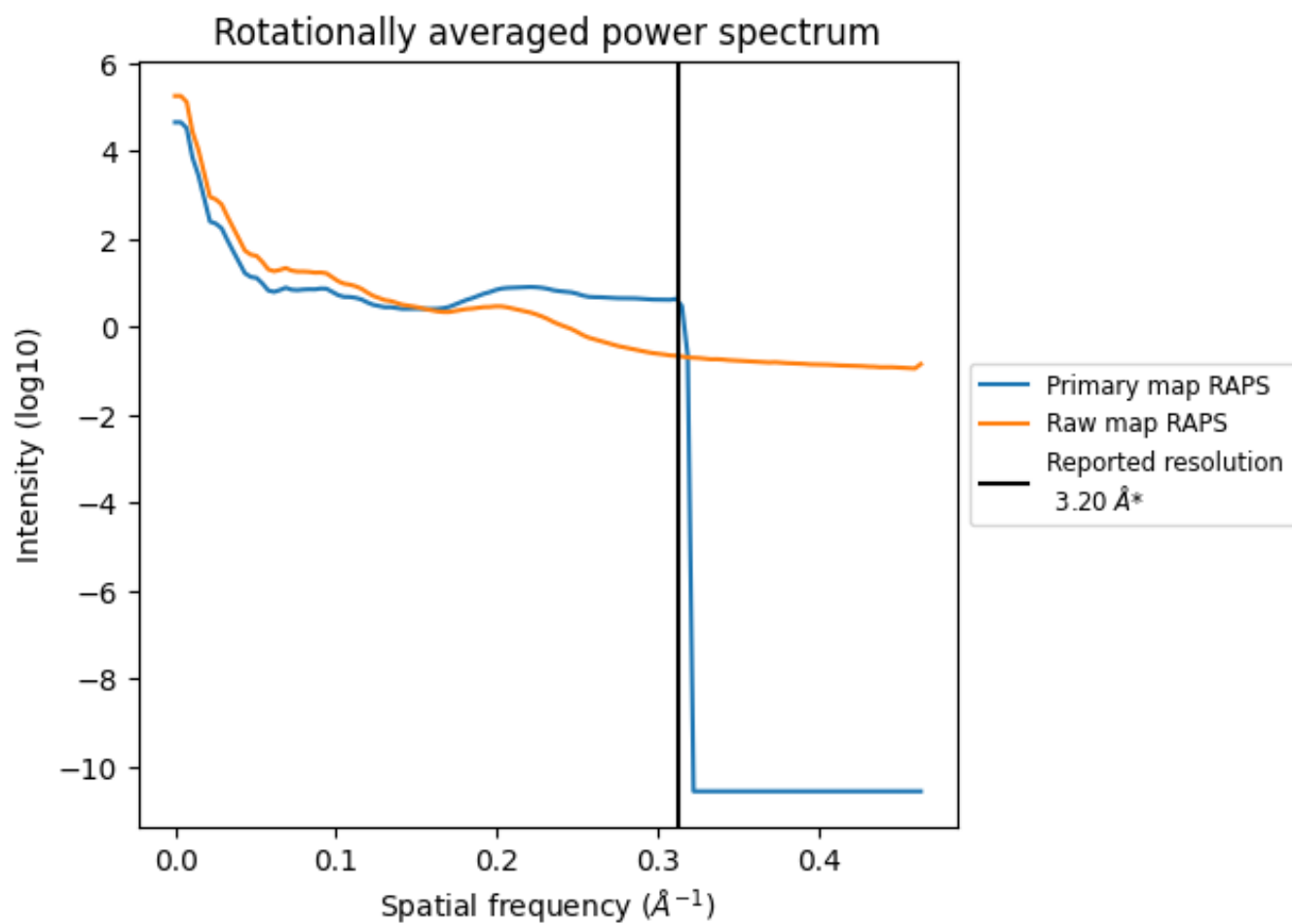
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 66 nm³; this corresponds to an approximate mass of 59 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](#)

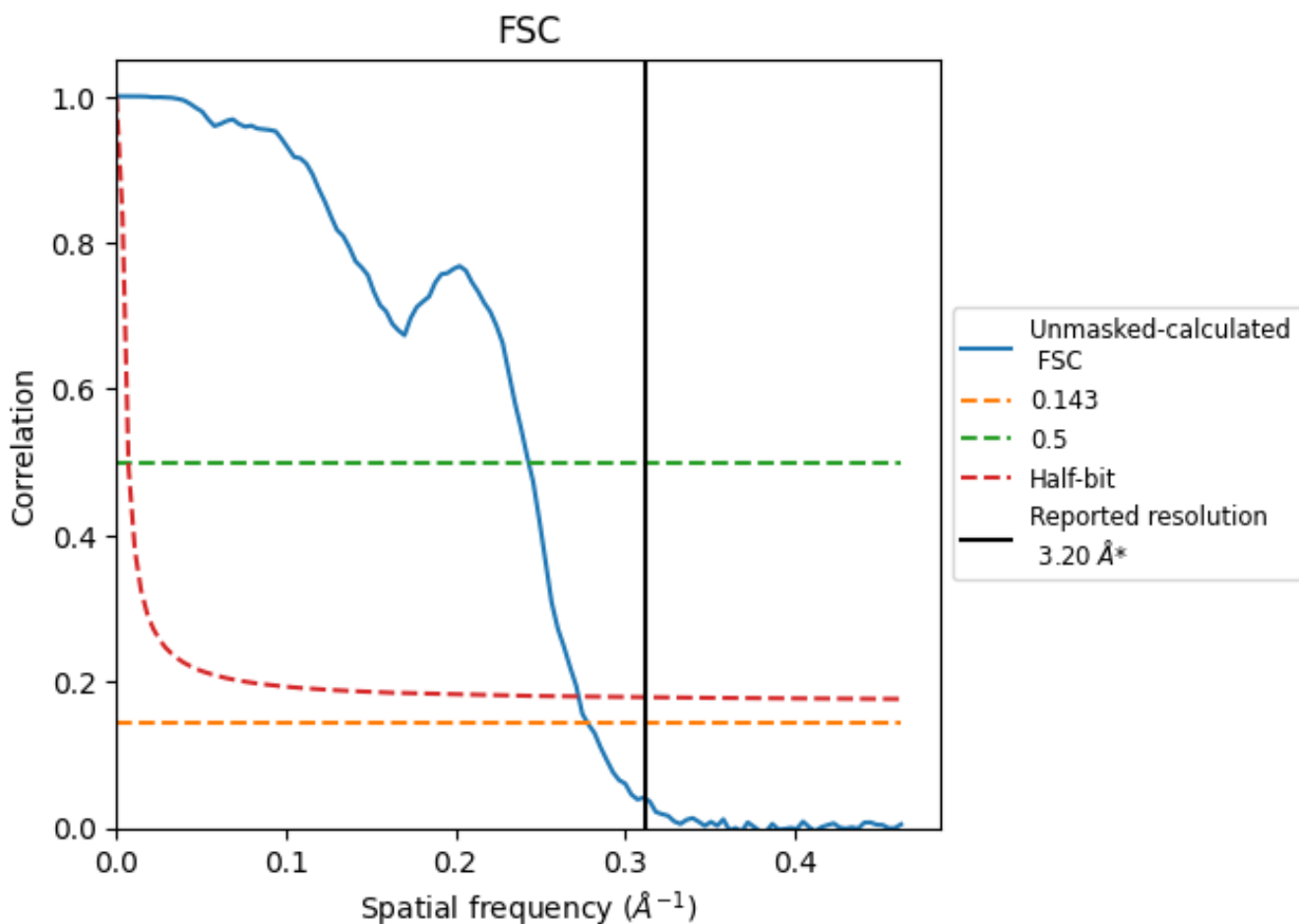


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

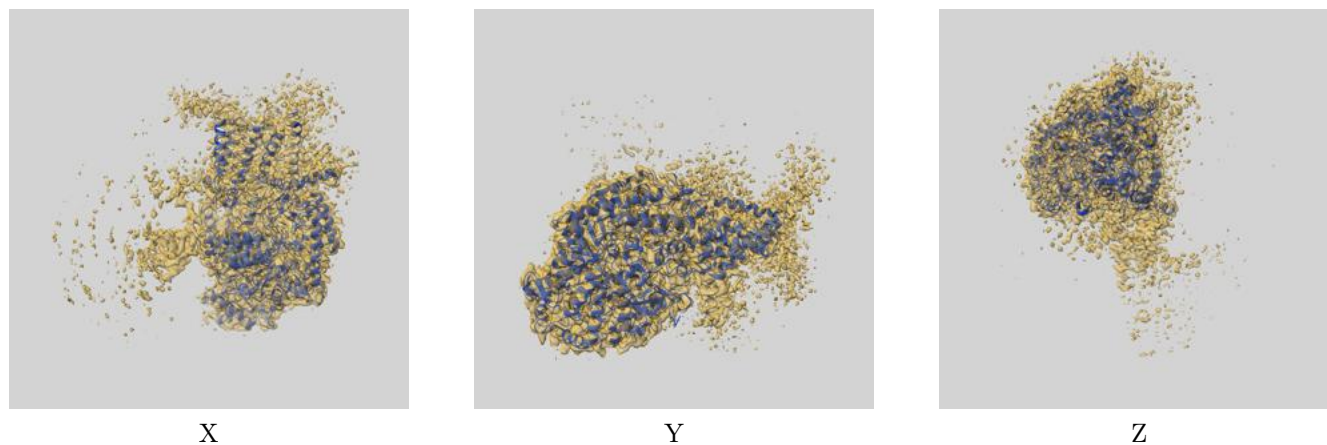
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	4.11	3.67

*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 3.60 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

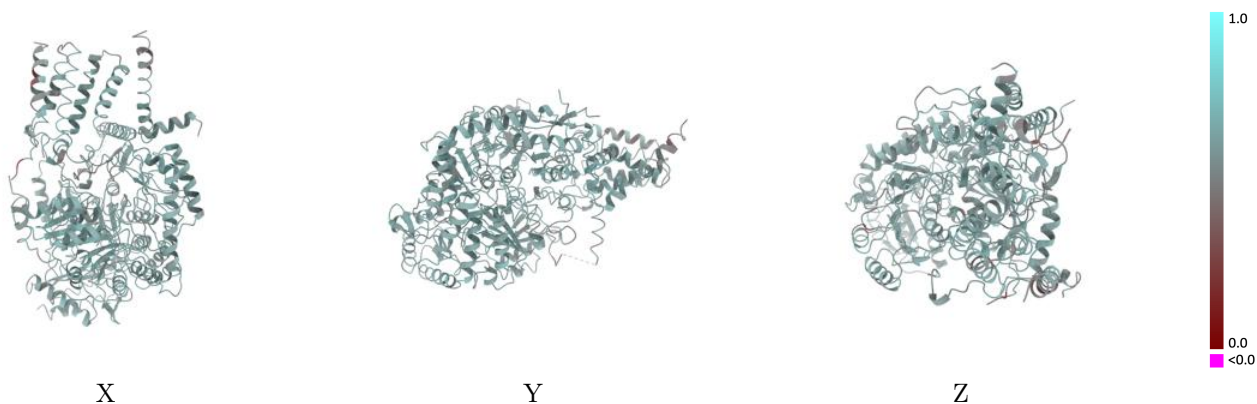
This section contains information regarding the fit between EMDB map EMD-33874 and PDB model 7YJM. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



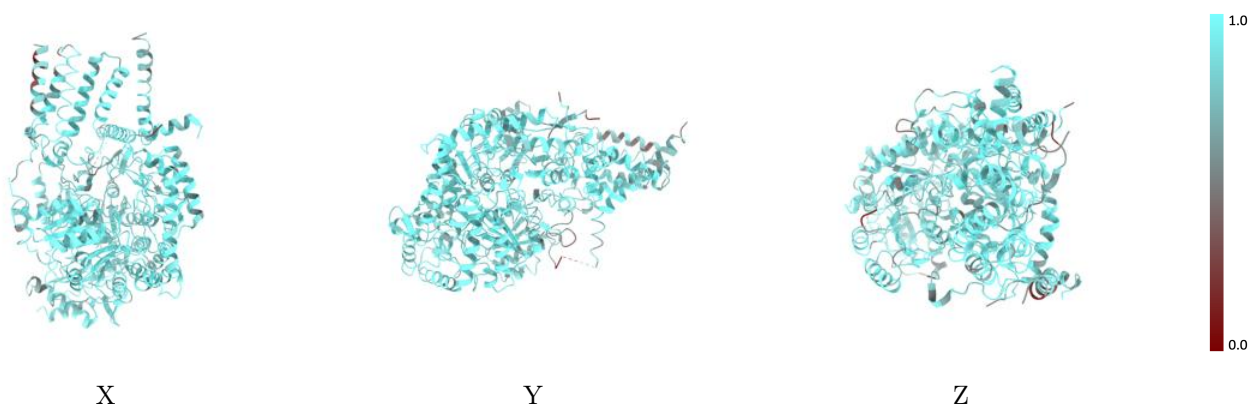
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



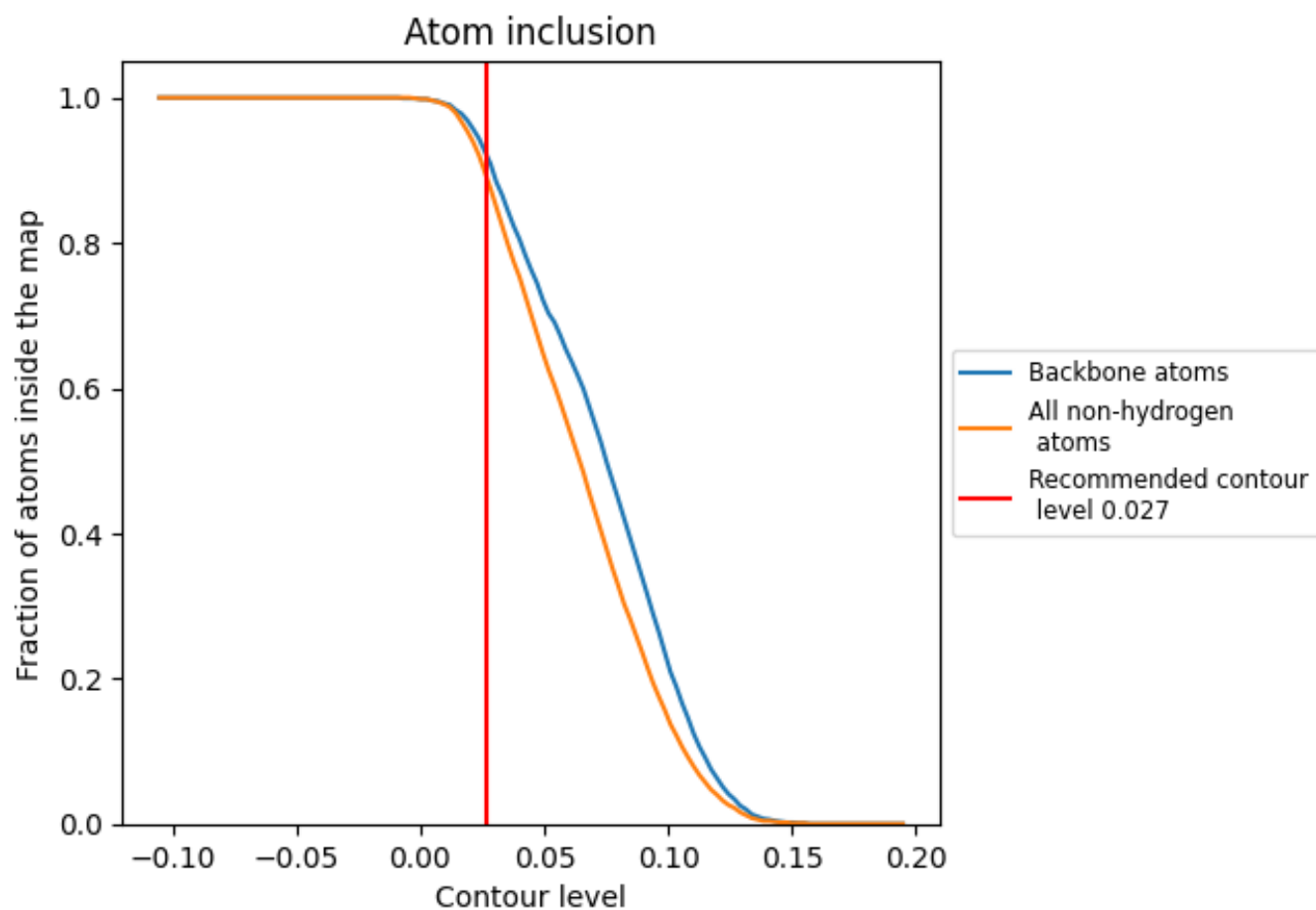
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).













9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.5850
A	 0.9060	 0.5910
B	 0.8990	 0.5900
C	 0.8450	 0.5570
D	 0.8740	 0.5800
E	 0.6380	 0.4920

