



Full wwPDB EM Validation Report ⓘ

Aug 18, 2025 – 06:19 PM JST

PDB ID : 9JBG / pdb_00009jbg
EMDB ID : EMD-61313
Title : Cryo-EM structure of the human LYCHOS in complex with lipids in the expanded state
Authors : Yu, S.; Liang, L.
Deposited on : 2024-08-27
Resolution : 3.76 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.dev126
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

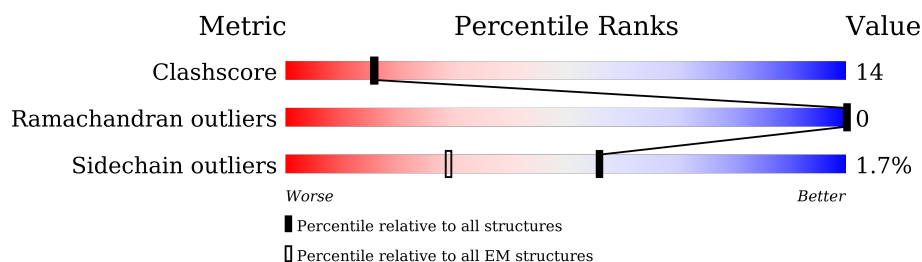
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.76 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	878	<div> <div>17%</div> <div>52%</div> <div>25%</div> <div>•</div> <div>21%</div> </div>
1	B	878	<div> <div>10%</div> <div>44%</div> <div>20%</div> <div>•</div> <div>35%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10187 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.

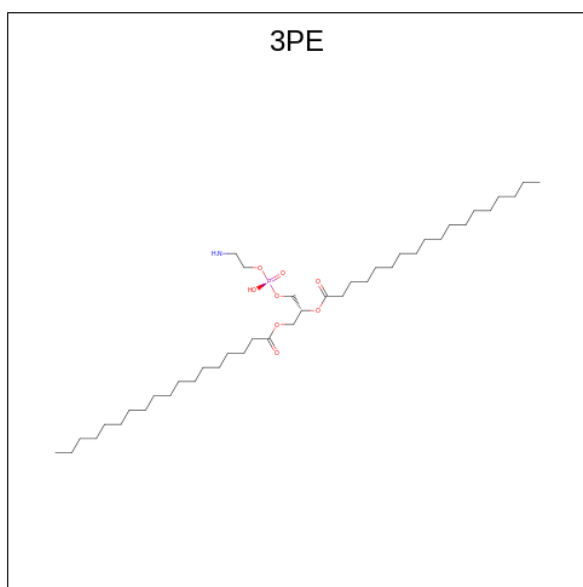
- Molecule 1 is a protein called Lysosomal cholesterol signaling protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	691	Total	C	N	O	S	0	0
			5452	3602	869	944	37		
1	B	568	Total	C	N	O	S	0	0
			4454	2983	690	753	28		

There are 16 discrepancies between the modelled and reference sequences:

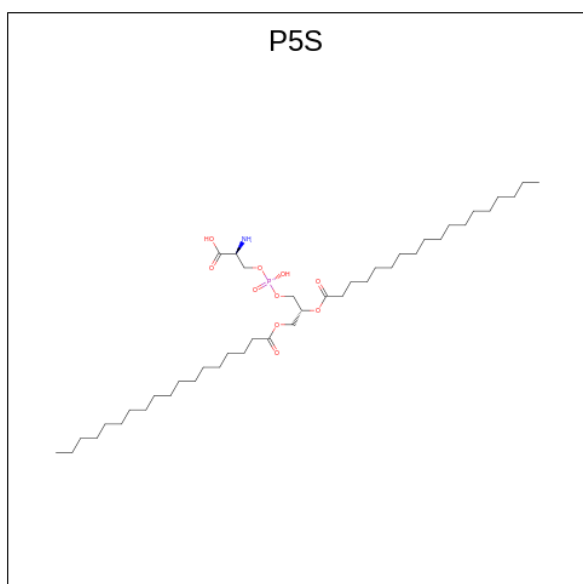
Chain	Residue	Modelled	Actual	Comment	Reference
A	871	SER	-	expression tag	UNP Q7Z3F1
A	872	ARG	-	expression tag	UNP Q7Z3F1
A	873	GLU	-	expression tag	UNP Q7Z3F1
A	874	ASN	-	expression tag	UNP Q7Z3F1
A	875	LEU	-	expression tag	UNP Q7Z3F1
A	876	TYR	-	expression tag	UNP Q7Z3F1
A	877	PHE	-	expression tag	UNP Q7Z3F1
A	878	GLN	-	expression tag	UNP Q7Z3F1
B	871	SER	-	expression tag	UNP Q7Z3F1
B	872	ARG	-	expression tag	UNP Q7Z3F1
B	873	GLU	-	expression tag	UNP Q7Z3F1
B	874	ASN	-	expression tag	UNP Q7Z3F1
B	875	LEU	-	expression tag	UNP Q7Z3F1
B	876	TYR	-	expression tag	UNP Q7Z3F1
B	877	PHE	-	expression tag	UNP Q7Z3F1
B	878	GLN	-	expression tag	UNP Q7Z3F1

- Molecule 2 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$) (labeled as "Ligand of Interest" by depositor).



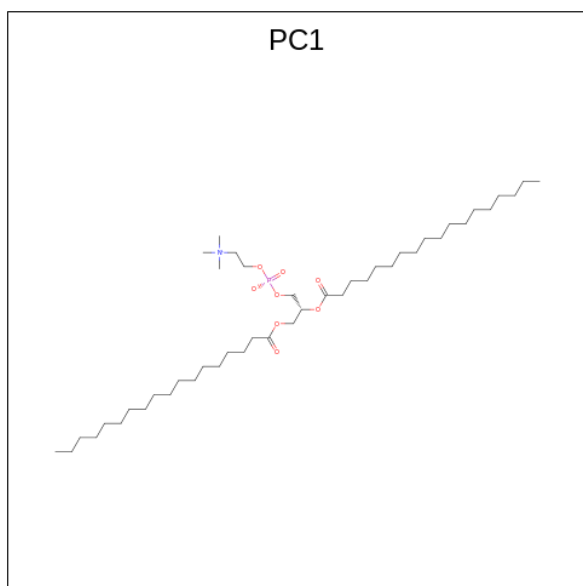
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			51	41	1	8	1	
2	A	1	Total	C	N	O	P	0
			51	41	1	8	1	
2	B	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 3 is O-[(R)-{[(2R)-2,3-bis(octadecanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (CCD ID: P5S) (formula: $C_{42}H_{82}NO_{10}P$) (labeled as "Ligand of Interest" by depositor).



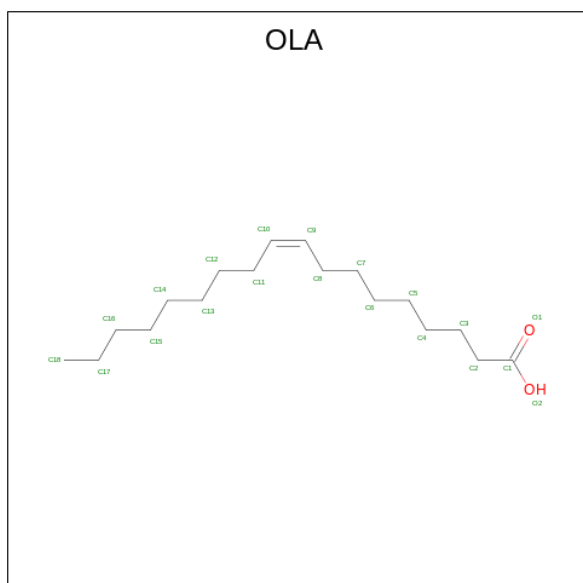
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			54	42	1	10	1	

- Molecule 4 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	N	O	P	0
			54	44	1	8	1	

- Molecule 5 is OLEIC ACID (CCD ID: OLA) (formula: $C_{18}H_{34}O_2$) (labeled as "Ligand of Interest" by depositor).

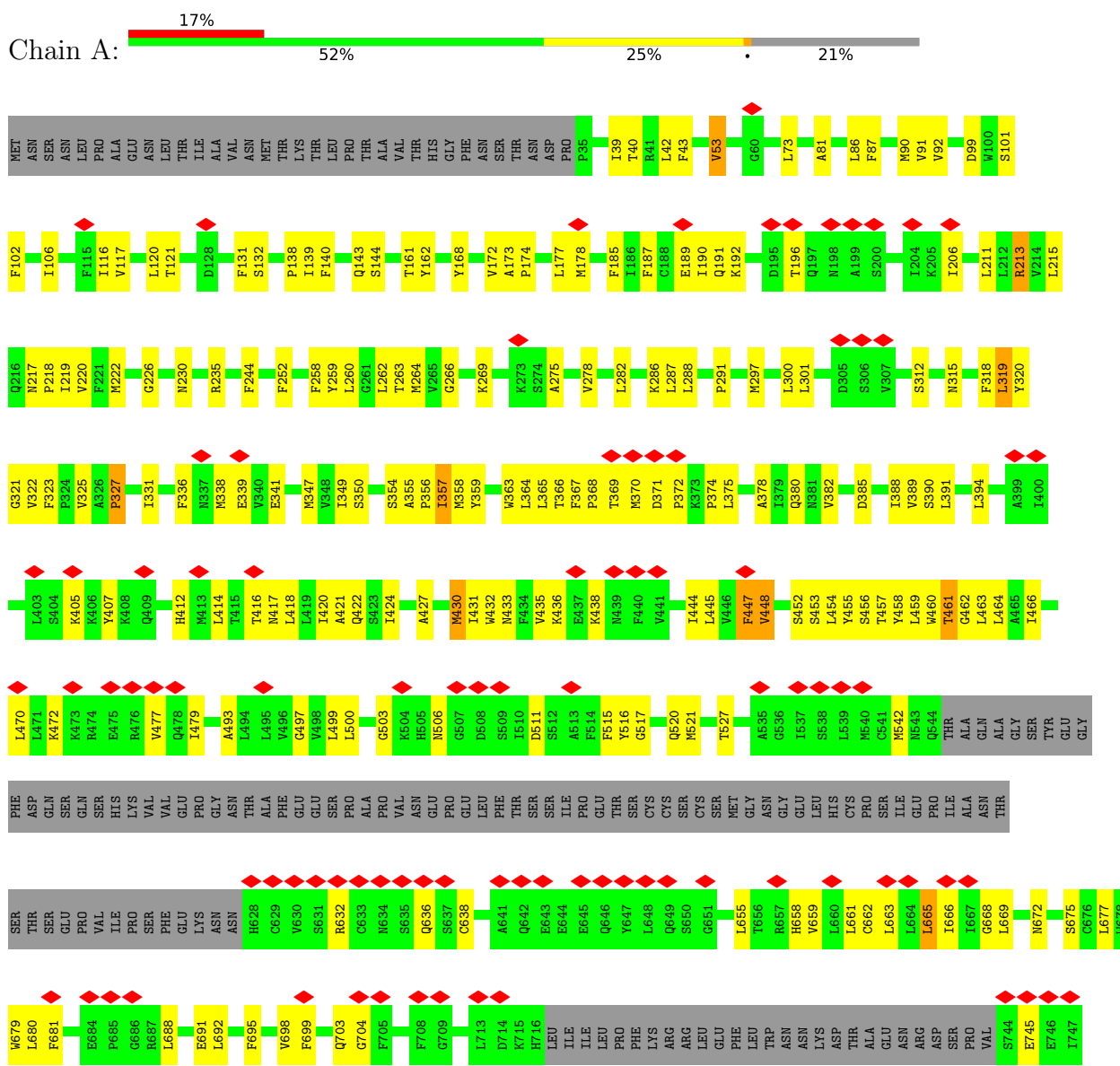


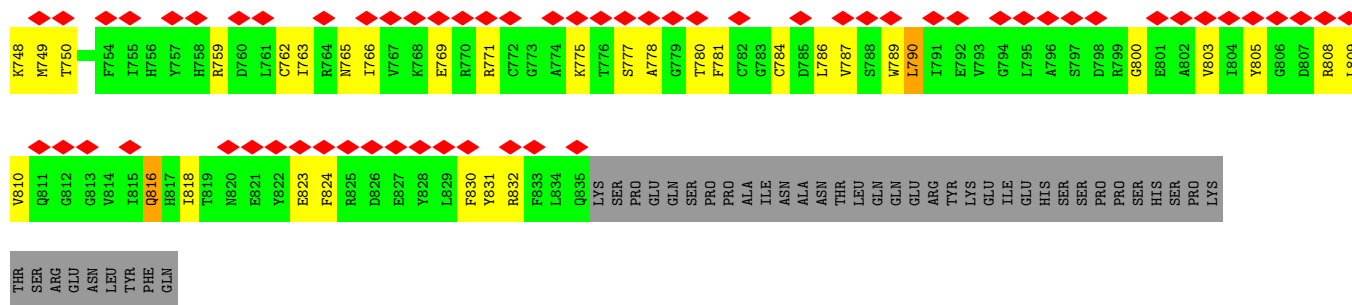
Mol	Chain	Residues	Atoms			AltConf
5	B	1	Total	C	O	0
			20	18	2	

3 Residue-property plots

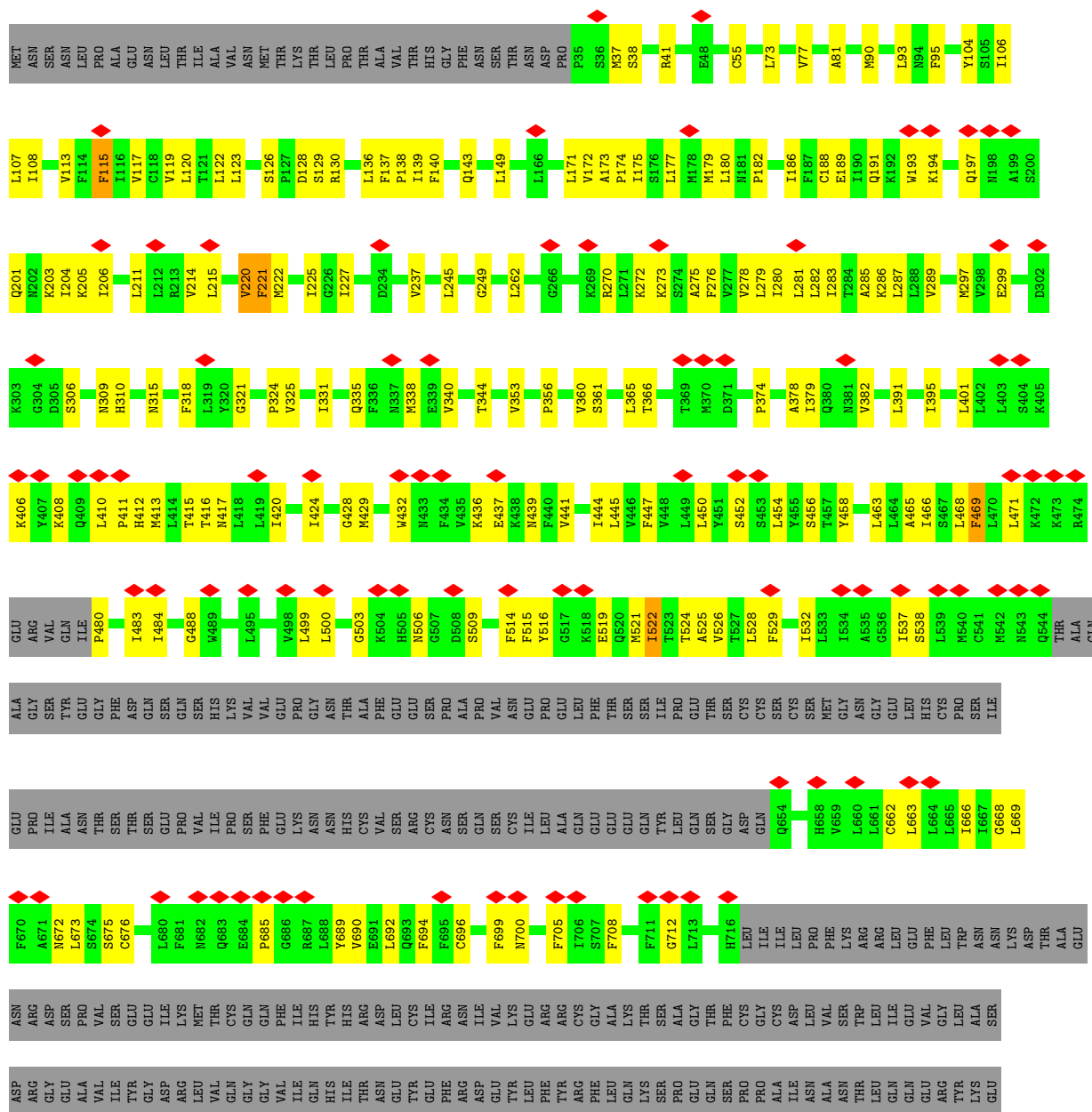
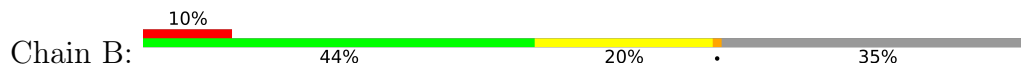
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Lysosomal cholesterol signaling protein





• Molecule 1: Lysosomal cholesterol signaling protein



ILE
GLU
HIS
SER
SER
PRO
PRO
SER
HIS
SER
PRO
LYS
THR
SER
ARG
GLU
ASN
LEU
TYR
PHE
GLN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20909	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 ($e^-/\text{\AA}^2$)	50.29	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.024	Depositor
Minimum map value	-0.686	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	323.2, 323.2, 323.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.808, 0.808, 0.808	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC1, OLA, 3PE, P5S

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	0.37	0/5577	0.68	3/7565 (0.0%)
1	B	0.36	0/4562	0.65	2/6198 (0.0%)
All	All	0.37	0/10139	0.67	5/13763 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	461	THR	N-CA-C	-5.91	104.92	111.36
1	B	522	ILE	N-CA-C	-5.43	105.42	110.53
1	A	327	PRO	CA-N-CD	-5.24	104.67	112.00
1	A	448	VAL	N-CA-C	-5.20	105.95	113.07
1	B	439	ASN	CB-CA-C	-5.16	110.21	117.23

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	5452	0	5615	174	0
1	B	4454	0	4658	124	0
2	A	102	0	164	4	0
2	B	51	0	82	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	54	0	80	4	0
4	B	54	0	88	0	0
5	B	20	0	33	0	0
All	All	10187	0	10720	299	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 14.

All (299) 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:428:GLY:HA3	1:B:450:LEU:HD22	1.62	0.82
1:A:102:PHE:CE1	1:A:106:ILE:HD11	2.24	0.72
1:A:444:ILE:O	1:A:448:VAL:HG23	1.91	0.71
1:A:258:PHE:CE2	1:A:262:LEU:HD11	2.25	0.71
1:A:258:PHE:CD2	1:A:262:LEU:HD11	2.30	0.67
1:A:102:PHE:CZ	1:A:106:ILE:HD11	2.30	0.67
1:A:258:PHE:O	1:A:262:LEU:HD12	1.95	0.66
1:B:685:PRO:HA	1:B:689:TYR:HB3	1.75	0.66
1:B:108:ILE:HG13	1:B:297:MET:SD	2.36	0.64
1:A:106:ILE:HG21	1:A:172:VAL:HG21	1.81	0.62
1:A:659:VAL:HA	1:A:662:CYS:SG	2.40	0.62
1:A:312:SER:HA	1:A:315:ASN:HD21	1.65	0.61
1:A:781:PHE:O	1:A:831:TYR:N	2.33	0.60
1:A:818:ILE:O	1:A:832:ARG:NH2	2.33	0.60
1:A:444:ILE:HA	1:A:447:PHE:CZ	2.37	0.59
1:A:499:LEU:O	1:A:503:GLY:N	2.34	0.59
1:B:115:PHE:C	1:B:115:PHE:CD2	2.83	0.57
1:A:448:VAL:HG21	1:A:515:PHE:CZ	2.40	0.57
1:A:323:PHE:HA	1:A:358:MET:HE2	1.87	0.56
1:A:339:GLU:O	1:A:341:GLU:N	2.36	0.56
1:A:39:ILE:HD13	1:A:363:TRP:CH2	2.40	0.56
1:B:465:ALA:HA	1:B:468:LEU:HG	1.87	0.56
1:A:173:ALA:O	1:A:177:LEU:HG	2.06	0.56
1:A:769:GLU:HB2	1:A:778:ALA:HA	1.87	0.56
1:A:388:ILE:HG13	1:A:430:MET:HE3	1.88	0.56
1:A:750:THR:HG21	1:A:808:ARG:CB	2.36	0.55
1:B:129:SER:HA	1:B:191:GLN:OE1	2.07	0.55
1:B:77:VAL:HA	1:B:81:ALA:HB3	1.87	0.55
1:B:382:VAL:HG21	1:B:694:PHE:CE2	2.42	0.55
1:A:786:LEU:O	1:A:790:LEU:HD22	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:VAL:HA	1:B:281:LEU:HD12	1.88	0.55
1:B:458:TYR:OH	1:B:672:ASN:ND2	2.39	0.55
1:B:463:LEU:HA	1:B:466:ILE:HG12	1.89	0.54
1:A:259:TYR:O	1:A:263:THR:HG23	2.08	0.54
1:A:244:PHE:CD2	3:A:903:P5S:H33A	2.42	0.54
1:B:285:ALA:HA	1:B:289:VAL:HB	1.89	0.54
1:B:286:LYS:NZ	1:B:321:GLY:O	2.31	0.54
1:B:672:ASN:O	1:B:676:CYS:N	2.41	0.54
1:A:457:THR:O	1:A:461:THR:HG23	2.07	0.54
1:A:632:ARG:O	1:A:636:GLN:NE2	2.40	0.54
1:A:675:SER:HB3	1:A:692:LEU:HD12	1.90	0.54
1:A:805:TYR:O	1:A:809:LEU:HG	2.07	0.54
1:B:119:VAL:HG23	1:B:120:LEU:HD23	1.90	0.54
1:B:526:VAL:HA	1:B:529:PHE:CE1	2.43	0.54
1:A:427:ALA:O	1:A:431:ILE:HG22	2.08	0.53
1:B:108:ILE:HD12	1:B:297:MET:HE2	1.90	0.53
1:B:108:ILE:HD12	1:B:297:MET:CE	2.39	0.53
1:A:73:LEU:HD13	1:B:73:LEU:HD13	1.89	0.53
1:A:315:ASN:HB2	1:A:365:LEU:HD23	1.89	0.53
1:A:818:ILE:HG23	1:A:830:PHE:O	2.08	0.53
1:B:465:ALA:HA	1:B:468:LEU:CG	2.39	0.53
1:A:679:TRP:HE3	1:A:680:LEU:HD13	1.74	0.52
1:A:454:LEU:O	1:A:457:THR:OG1	2.24	0.52
1:A:178:MET:HE2	1:A:220:VAL:HA	1.91	0.52
1:B:262:LEU:HD12	1:B:262:LEU:H	1.74	0.52
1:A:213:ARG:O	1:A:217:ASN:ND2	2.43	0.52
1:A:824:PHE:HA	1:A:831:TYR:CE1	2.45	0.52
1:A:91:VAL:O	1:A:230:ASN:ND2	2.43	0.52
1:A:116:ILE:O	1:A:120:LEU:HG	2.10	0.51
1:A:455:TYR:CD2	1:A:527:THR:HG21	2.45	0.51
1:A:762:CYS:HB3	1:A:765:ASN:HB3	1.92	0.51
1:B:340:VAL:O	1:B:344:THR:HG23	2.09	0.51
1:A:144:SER:HA	1:A:325:VAL:HA	1.93	0.51
1:A:92:VAL:O	1:A:235:ARG:NH1	2.43	0.51
1:A:99:ASP:OD1	1:A:101:SER:OG	2.22	0.51
1:A:472:LYS:HD3	1:A:542:MET:SD	2.51	0.51
1:A:816:GLN:HB3	1:A:832:ARG:HB3	1.92	0.51
1:B:275:ALA:O	1:B:278:VAL:HG12	2.11	0.51
1:B:412:HIS:O	1:B:415:THR:OG1	2.26	0.51
1:B:525:ALA:O	1:B:529:PHE:CD1	2.63	0.51
1:B:211:LEU:O	1:B:215:LEU:HD12	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:PRO:O	1:A:331:ILE:HG12	2.11	0.50
1:A:780:THR:HB	1:A:830:PHE:HB3	1.93	0.50
1:B:509:SER:HA	1:B:515:PHE:HA	1.92	0.50
1:B:411:PRO:HD3	1:B:471:LEU:HD11	1.93	0.50
1:B:391:LEU:HD23	1:B:395:ILE:HG12	1.92	0.50
1:B:668:GLY:O	1:B:672:ASN:N	2.36	0.50
1:A:800:GLY:O	1:A:803:VAL:HG12	2.11	0.50
1:A:370:MET:HE3	1:A:375:LEU:CD2	2.42	0.50
1:B:429:MET:HE3	1:B:429:MET:HA	1.94	0.50
1:A:781:PHE:CE2	1:A:786:LEU:HB2	2.47	0.49
1:B:179:MET:HB2	1:B:180:LEU:HD23	1.93	0.49
1:B:429:MET:O	1:B:432:TRP:HB2	2.12	0.49
1:A:312:SER:HA	1:A:315:ASN:ND2	2.28	0.49
1:A:830:PHE:C	1:A:831:TYR:HD2	2.20	0.49
1:A:372:PRO:HA	1:A:375:LEU:HG	1.95	0.49
1:A:745:GLU:C	1:A:749:MET:HE3	2.36	0.49
1:A:364:LEU:HA	1:A:367:PHE:HD2	1.77	0.49
1:A:460:TRP:CE3	1:A:463:LEU:HD22	2.48	0.49
1:A:39:ILE:HD12	1:A:40:THR:N	2.27	0.49
1:A:464:LEU:HD11	1:A:658:HIS:HB3	1.93	0.49
1:A:462:GLY:O	1:A:466:ILE:HG12	2.13	0.49
1:B:107:LEU:HD11	1:B:175:ILE:HG22	1.95	0.49
1:B:137:PHE:HB3	1:B:282:LEU:HD11	1.95	0.49
1:B:188:CYS:O	1:B:191:GLN:HB2	2.12	0.48
1:A:43:PHE:CD2	1:A:385:ASP:HB3	2.48	0.48
1:B:123:LEU:O	1:B:130:ARG:NH2	2.46	0.48
1:A:445:LEU:HA	1:A:448:VAL:HB	1.96	0.48
1:A:390:SER:HB2	1:A:704:GLY:HA3	1.96	0.48
1:A:355:ALA:HB3	1:A:356:PRO:HD3	1.95	0.48
1:A:244:PHE:CD2	3:A:903:P5S:C33	2.97	0.48
1:A:521:MET:HB3	1:A:680:LEU:HD21	1.95	0.48
1:A:455:TYR:HA	1:A:458:TYR:CD2	2.49	0.48
1:A:43:PHE:CZ	1:A:389:VAL:HG21	2.49	0.48
1:A:87:PHE:CE1	1:A:91:VAL:HG21	2.49	0.48
3:A:903:P5S:H54A	3:A:903:P5S:H39A	1.96	0.48
1:A:745:GLU:HA	1:A:748:LYS:HG2	1.95	0.48
1:B:222:MET:HE2	1:B:222:MET:HA	1.95	0.48
1:B:436:LYS:O	1:B:437:GLU:HB2	2.14	0.48
1:B:117:VAL:HG13	1:B:138:PRO:HB3	1.95	0.47
1:B:353:VAL:O	1:B:356:PRO:HD2	2.14	0.47
1:A:470:LEU:HB3	1:A:477:VAL:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:205:LYS:CG	1:B:206:ILE:HD12	2.44	0.47
1:A:448:VAL:HG11	1:A:515:PHE:CE2	2.50	0.47
1:B:136:LEU:HD12	1:B:338:MET:SD	2.55	0.47
1:A:391:LEU:HD13	1:A:430:MET:HE1	1.97	0.47
1:A:363:TRP:HA	1:A:366:THR:HG22	1.97	0.47
1:A:132:SER:HB2	1:A:191:GLN:HG2	1.97	0.47
1:B:173:ALA:O	1:B:177:LEU:HD22	2.15	0.47
1:B:201:GLN:HB3	1:B:204:ILE:HB	1.97	0.47
1:B:519:GLU:HA	1:B:522:ILE:HD12	1.96	0.47
1:B:318:PHE:CD2	1:B:365:LEU:HD11	2.50	0.47
1:A:81:ALA:HB1	1:A:252:PHE:HB2	1.96	0.47
1:B:685:PRO:HB3	1:B:690:VAL:HG23	1.97	0.47
1:A:771:ARG:HA	1:A:771:ARG:HD2	1.66	0.46
1:A:39:ILE:HG21	1:A:366:THR:HG21	1.97	0.46
1:A:327:PRO:HA	1:A:347:MET:HE1	1.97	0.46
1:A:370:MET:HE3	1:A:375:LEU:HD22	1.97	0.46
1:B:454:LEU:HD11	1:B:700:ASN:HD22	1.80	0.46
1:A:297:MET:N	1:A:297:MET:HE2	2.30	0.46
1:A:121:THR:HA	2:A:901:3PE:H281	1.97	0.46
1:A:414:LEU:HB2	1:A:460:TRP:HZ3	1.80	0.46
1:A:435:VAL:HA	1:A:438:LYS:HE3	1.97	0.46
1:A:456:SER:O	1:A:460:TRP:HB2	2.15	0.46
1:B:182:PRO:HG3	1:B:214:VAL:HG21	1.97	0.46
1:A:121:THR:HA	2:A:901:3PE:H251	1.97	0.46
1:A:421:ALA:HA	1:A:424:ILE:HD12	1.98	0.46
1:A:750:THR:HG21	1:A:808:ARG:HB3	1.98	0.46
1:B:360:VAL:HG23	1:B:361:SER:N	2.30	0.46
1:A:336:PHE:HB3	1:A:338:MET:SD	2.55	0.46
1:A:444:ILE:O	1:A:447:PHE:CD1	2.68	0.46
1:A:117:VAL:HG13	1:A:138:PRO:HG3	1.97	0.46
1:A:517:GLY:N	1:A:520:GLN:HE22	2.13	0.46
1:B:480:PRO:HD2	1:B:483:ILE:HD12	1.98	0.46
1:B:663:LEU:O	1:B:666:ILE:HG22	2.16	0.46
1:B:331:ILE:O	1:B:335:GLN:NE2	2.49	0.45
1:B:374:PRO:O	1:B:378:ALA:N	2.46	0.45
1:B:692:LEU:O	1:B:696:CYS:N	2.45	0.45
1:A:211:LEU:O	1:A:215:LEU:HD22	2.16	0.45
1:A:338:MET:SD	1:A:338:MET:N	2.89	0.45
1:B:119:VAL:O	1:B:123:LEU:HG	2.16	0.45
1:B:441:VAL:O	1:B:445:LEU:N	2.48	0.45
1:A:661:LEU:O	1:A:665:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:766:ILE:HG21	1:A:789:TRP:CE3	2.52	0.45
1:A:43:PHE:CE2	1:A:389:VAL:HG21	2.52	0.45
1:B:509:SER:HA	1:B:514:PHE:O	2.17	0.45
1:A:665:LEU:N	1:A:665:LEU:HD23	2.31	0.45
1:B:499:LEU:HD13	1:B:503:GLY:HA3	1.99	0.45
1:A:432:TRP:HH2	1:A:511:ASP:HA	1.82	0.45
1:B:139:ILE:HD12	1:B:139:ILE:HA	1.88	0.45
1:B:174:PRO:HA	1:B:177:LEU:HD23	1.98	0.45
1:B:193:TRP:CE2	1:B:197:GLN:O	2.70	0.45
1:A:414:LEU:HD22	1:A:463:LEU:HD21	1.99	0.45
1:A:422:GLN:NE2	1:A:703:GLN:HG3	2.32	0.44
1:A:679:TRP:CE3	1:A:680:LEU:HD13	2.51	0.44
1:A:745:GLU:O	1:A:748:LYS:N	2.50	0.44
1:A:90:MET:HE3	1:A:226:GLY:HA3	2.00	0.44
1:B:113:VAL:O	1:B:117:VAL:HG12	2.18	0.44
1:A:371:ASP:HB2	1:A:374:PRO:HD2	1.98	0.44
1:A:436:LYS:HD2	1:A:436:LYS:HA	1.74	0.44
1:A:638:CYS:SG	1:A:818:ILE:HB	2.57	0.44
1:A:516:TYR:CE1	1:A:520:GLN:HB3	2.53	0.44
1:A:824:PHE:HA	1:A:831:TYR:HE1	1.81	0.44
1:B:106:ILE:HD12	1:B:172:VAL:HG21	2.00	0.44
1:B:528:LEU:HB2	1:B:669:LEU:HD22	1.99	0.44
1:A:350:SER:O	1:A:354:SER:HB3	2.18	0.44
1:B:278:VAL:HG22	1:B:282:LEU:HD23	1.99	0.44
1:A:369:THR:O	1:A:370:MET:HG3	2.18	0.44
1:A:769:GLU:HG2	1:A:780:THR:C	2.43	0.44
1:B:122:LEU:O	1:B:130:ARG:NH1	2.51	0.44
1:B:140:PHE:O	1:B:325:VAL:HG11	2.17	0.44
1:B:276:PHE:O	1:B:280:ILE:HD12	2.18	0.44
1:A:300:LEU:HD12	1:A:301:LEU:HD23	1.99	0.44
1:A:318:PHE:HD2	1:A:365:LEU:HD21	1.83	0.44
1:A:695:PHE:HA	1:A:698:VAL:HG22	1.99	0.44
1:B:413:MET:O	1:B:417:ASN:ND2	2.50	0.44
1:A:168:TYR:O	1:A:172:VAL:HG12	2.17	0.44
2:A:901:3PE:H342	2:A:901:3PE:H272	2.00	0.44
1:B:93:LEU:HD23	1:B:95:PHE:CE1	2.53	0.44
1:A:775:LYS:HD3	1:A:775:LYS:HA	1.82	0.43
1:B:424:ILE:O	1:B:450:LEU:HD13	2.18	0.43
1:B:452:SER:O	1:B:456:SER:N	2.48	0.43
1:B:454:LEU:HD11	1:B:700:ASN:ND2	2.33	0.43
1:A:218:PRO:O	1:A:222:MET:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ALA:HA	1:A:278:VAL:HG22	2.01	0.43
1:A:688:LEU:O	1:A:691:GLU:HG2	2.19	0.43
1:A:784:CYS:O	1:A:787:VAL:HG12	2.18	0.43
1:B:189:GLU:O	1:B:193:TRP:N	2.51	0.43
1:B:526:VAL:HA	1:B:529:PHE:CZ	2.54	0.43
1:A:417:ASN:HA	1:A:420:ILE:HD12	2.01	0.43
1:B:484:ILE:O	1:B:488:GLY:N	2.52	0.43
1:A:172:VAL:HG11	1:A:320:TYR:CE1	2.53	0.43
1:B:128:ASP:HB3	1:B:194:LYS:NZ	2.34	0.43
1:B:245:LEU:O	1:B:249:GLY:N	2.40	0.43
1:A:677:LEU:O	1:A:681:PHE:CB	2.67	0.43
1:B:201:GLN:O	1:B:206:ILE:HD13	2.18	0.43
1:B:227:ILE:HD13	1:B:227:ILE:HA	1.90	0.43
1:B:469:PHE:CE2	1:B:538:SER:HB2	2.53	0.43
1:A:506:ASN:HA	1:A:516:TYR:HA	2.01	0.43
1:A:192:LYS:O	1:A:196:THR:N	2.51	0.43
1:A:259:TYR:CZ	1:A:263:THR:HG21	2.54	0.43
1:A:42:LEU:HD21	1:A:359:TYR:HA	2.01	0.42
1:B:173:ALA:HB3	1:B:174:PRO:HD3	2.00	0.42
1:B:306:SER:HB2	1:B:309:ASN:HB2	2.01	0.42
1:B:401:LEU:HB2	1:B:406:LYS:HB2	2.00	0.42
1:B:519:GLU:OE2	1:B:519:GLU:N	2.39	0.42
1:B:672:ASN:HA	1:B:675:SER:HB3	2.01	0.42
1:A:412:HIS:O	1:A:416:THR:HG22	2.19	0.42
1:A:139:ILE:O	1:A:143:GLN:HB2	2.19	0.42
1:A:173:ALA:HB3	1:A:174:PRO:HD3	2.02	0.42
1:B:506:ASN:HA	1:B:516:TYR:HB3	2.00	0.42
1:B:521:MET:HA	1:B:524:THR:HB	2.01	0.42
1:B:73:LEU:O	1:B:77:VAL:HG22	2.19	0.42
1:A:367:PHE:N	1:A:368:PRO:HD2	2.34	0.42
1:A:497:GLY:HA2	1:A:500:LEU:HG	2.01	0.42
1:B:416:THR:O	1:B:420:ILE:HG12	2.20	0.42
1:B:428:GLY:CA	1:B:450:LEU:HD22	2.41	0.42
1:A:266:GLY:O	1:A:269:LYS:NZ	2.38	0.42
1:B:299:GLU:HA	1:B:310:HIS:CE1	2.55	0.42
1:B:214:VAL:O	1:B:220:VAL:HG11	2.19	0.42
1:A:349:ILE:HD13	1:A:349:ILE:N	2.33	0.42
1:A:669:LEU:HA	1:A:672:ASN:OD1	2.20	0.42
1:A:217:ASN:HB3	1:A:219:ILE:HG12	2.02	0.41
1:A:459:LEU:HD21	1:A:527:THR:OG1	2.20	0.41
1:A:177:LEU:HD13	1:A:219:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:LYS:NZ	1:A:321:GLY:O	2.52	0.41
1:B:149:LEU:HD22	1:B:324:PRO:HG2	2.03	0.41
1:A:177:LEU:HD13	1:A:219:ILE:HD13	2.01	0.41
1:A:453:SER:O	1:A:456:SER:OG	2.29	0.41
3:A:903:P5S:H29	1:B:55:CYS:SG	2.60	0.41
1:B:38:SER:HB2	1:B:41:ARG:HE	1.84	0.41
1:B:379:ILE:HA	1:B:382:VAL:HG12	2.02	0.41
1:A:53:VAL:HG22	1:A:264:MET:HE2	2.02	0.41
1:A:405:LYS:HA	1:A:407:TYR:CE1	2.55	0.41
1:A:418:LEU:HD13	1:A:460:TRP:HB3	2.02	0.41
1:B:126:SER:O	1:B:130:ARG:HG3	2.20	0.41
1:B:522:ILE:O	1:B:526:VAL:HG23	2.20	0.41
1:A:185:PHE:O	1:A:189:GLU:HG2	2.20	0.41
1:B:237:VAL:HG21	1:B:245:LEU:HD12	2.03	0.41
1:A:287:LEU:HD23	1:A:357:ILE:HG21	2.01	0.41
1:A:371:ASP:O	1:A:375:LEU:HG	2.21	0.41
1:A:668:GLY:HA3	1:A:699:PHE:CE2	2.55	0.41
1:A:810:VAL:HG11	1:A:823:GLU:HG2	2.02	0.41
1:B:90:MET:O	1:B:93:LEU:HB3	2.20	0.41
1:B:117:VAL:HG23	2:B:903:3PE:H292	2.02	0.41
1:B:186:ILE:HA	1:B:189:GLU:HG2	2.02	0.41
1:B:221:PHE:CZ	1:B:225:ILE:HG13	2.56	0.41
1:A:187:PHE:HA	1:A:190:ILE:HD12	2.03	0.41
1:A:655:LEU:HD23	1:A:655:LEU:H	1.86	0.41
1:A:781:PHE:HE2	1:A:786:LEU:HB2	1.85	0.41
1:B:37:MET:SD	1:B:366:THR:CG2	3.09	0.41
1:B:283:ILE:HG23	1:B:287:LEU:HD23	2.02	0.41
1:B:529:PHE:HA	1:B:532:ILE:HD12	2.02	0.41
1:A:116:ILE:HG22	2:A:901:3PE:H2I1	2.02	0.41
1:A:140:PHE:CE1	1:A:282:LEU:HB3	2.56	0.41
1:A:378:ALA:O	1:A:382:VAL:HG12	2.21	0.41
1:A:448:VAL:O	1:A:448:VAL:HG12	2.21	0.41
1:A:677:LEU:O	1:A:681:PHE:HB3	2.21	0.41
1:A:745:GLU:O	1:A:749:MET:HE3	2.21	0.41
1:B:93:LEU:HD21	1:B:171:LEU:HD11	2.03	0.41
1:B:104:TYR:O	1:B:108:ILE:HG12	2.21	0.41
1:B:203:LYS:HB2	1:B:203:LYS:HE3	1.88	0.41
1:B:270:ARG:HD2	1:B:272:LYS:HD2	2.02	0.41
1:B:275:ALA:O	1:B:276:PHE:C	2.62	0.41
1:B:699:PHE:CD1	1:B:699:PHE:C	2.97	0.41
1:A:363:TRP:O	1:A:366:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:GLN:HE22	1:A:433:ASN:CG	2.29	0.41
1:A:394:LEU:HD23	1:A:394:LEU:HA	1.72	0.41
1:B:205:LYS:HG2	1:B:206:ILE:HD12	2.03	0.41
1:B:287:LEU:HD13	1:B:287:LEU:HA	1.95	0.41
1:B:408:LYS:HG2	1:B:410:LEU:HB2	2.02	0.41
1:A:288:LEU:C	1:A:291:PRO:HD2	2.46	0.40
1:B:143:GLN:O	1:B:286:LYS:HE3	2.21	0.40
1:A:86:LEU:HB3	1:A:90:MET:HE2	2.03	0.40
1:A:452:SER:HA	1:A:493:ALA:HB1	2.03	0.40
1:A:470:LEU:HD21	1:A:479:ILE:HD12	2.02	0.40
1:A:703:GLN:OE1	1:A:703:GLN:HA	2.21	0.40
1:B:444:ILE:O	1:B:447:PHE:HB3	2.21	0.40
1:B:669:LEU:O	1:B:673:LEU:N	2.52	0.40
1:B:708:PHE:O	1:B:712:GLY:N	2.54	0.40
1:A:161:THR:OG1	1:A:162:TYR:N	2.53	0.40
1:A:260:LEU:HA	1:A:263:THR:OG1	2.22	0.40
1:A:319:LEU:O	1:A:322:VAL:HG22	2.21	0.40
1:A:663:LEU:HA	1:A:666:ILE:HG12	2.04	0.40
1:A:759:ARG:O	1:A:763:ILE:HB	2.22	0.40
1:A:771:ARG:HA	1:A:777:SER:HA	2.04	0.40
1:B:275:ALA:O	1:B:279:LEU:HD13	2.21	0.40
1:A:131:PHE:CD1	1:A:190:ILE:HG21	2.57	0.40
1:B:273:LYS:H	1:B:273:LYS:HG2	1.63	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	685/878 (78%)	644 (94%)	41 (6%)	0	100	100
1	B	562/878 (64%)	535 (95%)	27 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1247/1756 (71%)	1179 (94%)	68 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	603/773 (78%)	593 (98%)	10 (2%)	56	73
1	B	494/773 (64%)	485 (98%)	9 (2%)	54	72
All	All	1097/1546 (71%)	1078 (98%)	19 (2%)	56	73

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	A	206	ILE
1	A	213	ARG
1	A	319	LEU
1	A	357	ILE
1	A	430	MET
1	A	447	PHE
1	A	665	LEU
1	A	790	LEU
1	A	816	GLN
1	B	115	PHE
1	B	220	VAL
1	B	221	PHE
1	B	315	ASN
1	B	469	PHE
1	B	500	LEU
1	B	537	ILE
1	B	662	CYS
1	B	705	PHE

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	69	GLN
1	A	89	ASN
1	A	217	ASN
1	A	315	ASN
1	A	337	ASN
1	A	381	ASN
1	A	658	HIS
1	A	682	ASN
1	A	693	GLN
1	A	700	ASN
1	B	63	ASN
1	B	380	GLN
1	B	412	HIS
1	B	417	ASN
1	B	439	ASN
1	B	672	ASN
1	B	700	ASN
1	B	716	HIS

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](#)

6 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
4	PC1	B	901	-	53,53,53	0.50	0	59,61,61	0.46	1 (1%)
5	OLA	B	902	-	19,19,19	0.78	1 (5%)	19,19,19	0.96	2 (10%)
2	3PE	A	901	-	50,50,50	0.28	0	53,55,55	0.29	0
3	P5S	A	903	-	52,53,53	0.39	0	56,60,60	0.40	0
2	3PE	A	902	-	50,50,50	0.51	0	53,55,55	0.68	3 (5%)
2	3PE	B	903	-	50,50,50	0.52	0	53,55,55	0.51	1 (1%)

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
4	PC1	B	901	-	-	14/57/57/57	-
5	OLA	B	902	-	-	9/17/17/17	-
2	3PE	A	901	-	-	23/54/54/54	-
3	P5S	A	903	-	-	21/59/59/59	-
2	3PE	A	902	-	-	20/54/54/54	-
2	3PE	B	903	-	-	18/54/54/54	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	902	OLA	C10-C9	2.69	1.47	1.31

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	902	3PE	C2-O21-C21	3.08	125.37	117.79
2	A	902	3PE	O12-P-O14	2.36	123.91	112.24
4	B	901	PC1	O12-P-O14	2.31	123.65	112.24
2	B	903	3PE	O12-P-O14	2.30	123.61	112.24
2	A	902	3PE	O21-C2-C1	2.03	115.76	108.40
5	B	902	OLA	C3-C2-C1	-2.01	109.41	114.47
5	B	902	OLA	O2-C1-C2	2.01	120.48	114.03

There are no chirality outliers.

All (105) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	3PE	C1-O11-P-O12
2	A	901	3PE	C22-C21-O21-C2
2	A	902	3PE	C1-O11-P-O12
2	A	902	3PE	C11-O13-P-O11
2	A	902	3PE	O13-C11-C12-N
2	A	902	3PE	C22-C21-O21-C2
2	B	903	3PE	C1-O11-P-O12
2	B	903	3PE	C1-O11-P-O13
2	B	903	3PE	O13-C11-C12-N
3	A	903	P5S	O-C-CA-N
3	A	903	P5S	N-CA-CB-OG
3	A	903	P5S	CB-OG-P12-O16
4	B	901	PC1	C11-O13-P-O12
4	B	901	PC1	C22-C21-O21-C2
2	A	901	3PE	O22-C21-O21-C2
2	A	902	3PE	O22-C21-O21-C2
4	B	901	PC1	O22-C21-O21-C2
2	B	903	3PE	C32-C31-O31-C3
2	B	903	3PE	O32-C31-O31-C3
3	A	903	P5S	C39-C38-O37-C2
3	A	903	P5S	OXT-C-CA-N
5	B	902	OLA	C1-C2-C3-C4
2	A	901	3PE	C2-C3-O31-C31
3	A	903	P5S	O47-C38-O37-C2
2	A	902	3PE	C1-O11-P-O13
2	B	903	3PE	C11-O13-P-O11
4	B	901	PC1	C11-O13-P-O11
2	A	902	3PE	C25-C26-C27-C28
4	B	901	PC1	C2A-C2B-C2C-C2D
3	A	903	P5S	C41-C42-C43-C44
2	A	901	3PE	C36-C37-C38-C39
2	A	902	3PE	C36-C37-C38-C39
5	B	902	OLA	C11-C12-C13-C14
2	A	902	3PE	C2D-C2E-C2F-C2G
2	A	901	3PE	C2D-C2E-C2F-C2G
2	A	902	3PE	C37-C38-C39-C3A
2	A	901	3PE	C2C-C2D-C2E-C2F
2	B	903	3PE	C37-C38-C39-C3A
2	B	903	3PE	C35-C36-C37-C38
4	B	901	PC1	C2D-C2E-C2F-C2G

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Mol	Chain	Res	Type	Atoms
2	A	902	3PE	C2E-C2F-C2G-C2H
4	B	901	PC1	C33-C34-C35-C36
3	A	903	P5S	C-CA-CB-OG
2	A	902	3PE	C1-C2-C3-O31
5	B	902	OLA	C3-C4-C5-C6
3	A	903	P5S	C21-C22-C23-C24
3	A	903	P5S	C20-C17-O19-C1
5	B	902	OLA	C11-C10-C9-C8
2	A	901	3PE	C2E-C2F-C2G-C2H
3	A	903	P5S	C1-C2-C3-O16
2	A	901	3PE	C3E-C3F-C3G-C3H
2	A	902	3PE	C2B-C2C-C2D-C2E
3	A	903	P5S	O37-C2-C3-O16
3	A	903	P5S	O18-C17-O19-C1
2	A	901	3PE	C3C-C3D-C3E-C3F
2	A	902	3PE	C26-C27-C28-C29
4	B	901	PC1	C37-C38-C39-C3A
2	A	901	3PE	C2B-C2C-C2D-C2E
2	A	901	3PE	C22-C23-C24-C25
3	A	903	P5S	C40-C41-C42-C43
2	A	901	3PE	C2F-C2G-C2H-C2I
2	A	901	3PE	C32-C31-O31-C3
2	A	901	3PE	O11-C1-C2-O21
2	A	901	3PE	O32-C31-O31-C3
2	A	902	3PE	C2-C1-O11-P
3	A	903	P5S	C2-C3-O16-P12
2	A	902	3PE	C11-O13-P-O12
2	B	903	3PE	C11-O13-P-O12
2	B	903	3PE	C11-O13-P-O14
3	A	903	P5S	CB-OG-P12-O15
4	B	901	PC1	C11-O13-P-O14
2	A	901	3PE	O11-C1-C2-C3
2	A	902	3PE	C12-C11-O13-P
4	B	901	PC1	O13-C11-C12-N
2	B	903	3PE	C2-C1-O11-P
5	B	902	OLA	C13-C14-C15-C16
3	A	903	P5S	C32-C33-C34-C35
3	A	903	P5S	C31-C32-C33-C34
4	B	901	PC1	C2E-C2F-C2G-C2H
3	A	903	P5S	C26-C27-C28-C29
2	A	902	3PE	O21-C2-C3-O31
2	B	903	3PE	C3C-C3D-C3E-C3F

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Mol	Chain	Res	Type	Atoms
5	B	902	OLA	C6-C7-C8-C9
5	B	902	OLA	C4-C5-C6-C7
4	B	901	PC1	C32-C33-C34-C35
2	A	901	3PE	C3-C2-O21-C21
2	A	902	3PE	C1-C2-O21-C21
3	A	903	P5S	C52-C53-C54-C55
2	A	901	3PE	C1-O11-P-O13
2	B	903	3PE	O11-C1-C2-C3
2	A	901	3PE	C34-C35-C36-C37
3	A	903	P5S	C29-C30-C31-C32
2	B	903	3PE	C31-C32-C33-C34
2	B	903	3PE	O31-C31-C32-C33
2	B	903	3PE	C3A-C3B-C3C-C3D
2	B	903	3PE	C34-C35-C36-C37
4	B	901	PC1	O31-C31-C32-C33
5	B	902	OLA	C5-C6-C7-C8
5	B	902	OLA	C9-C10-C11-C12
2	A	901	3PE	C37-C38-C39-C3A
2	B	903	3PE	O32-C31-C32-C33
2	A	902	3PE	C23-C24-C25-C26
4	B	901	PC1	O32-C31-C32-C33
2	A	901	3PE	C1-O11-P-O14
2	A	901	3PE	O21-C21-C22-C23

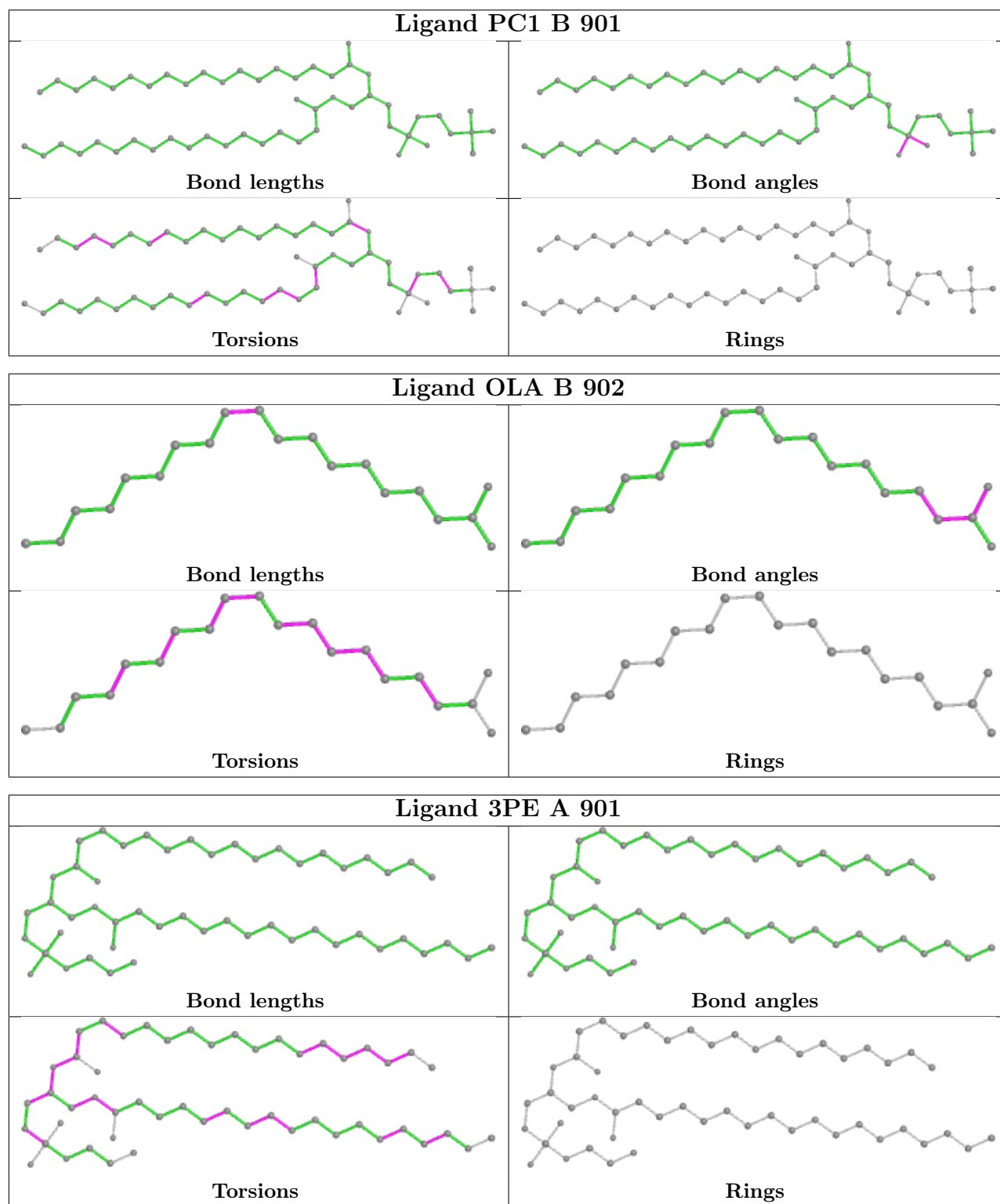
There are no ring outliers.

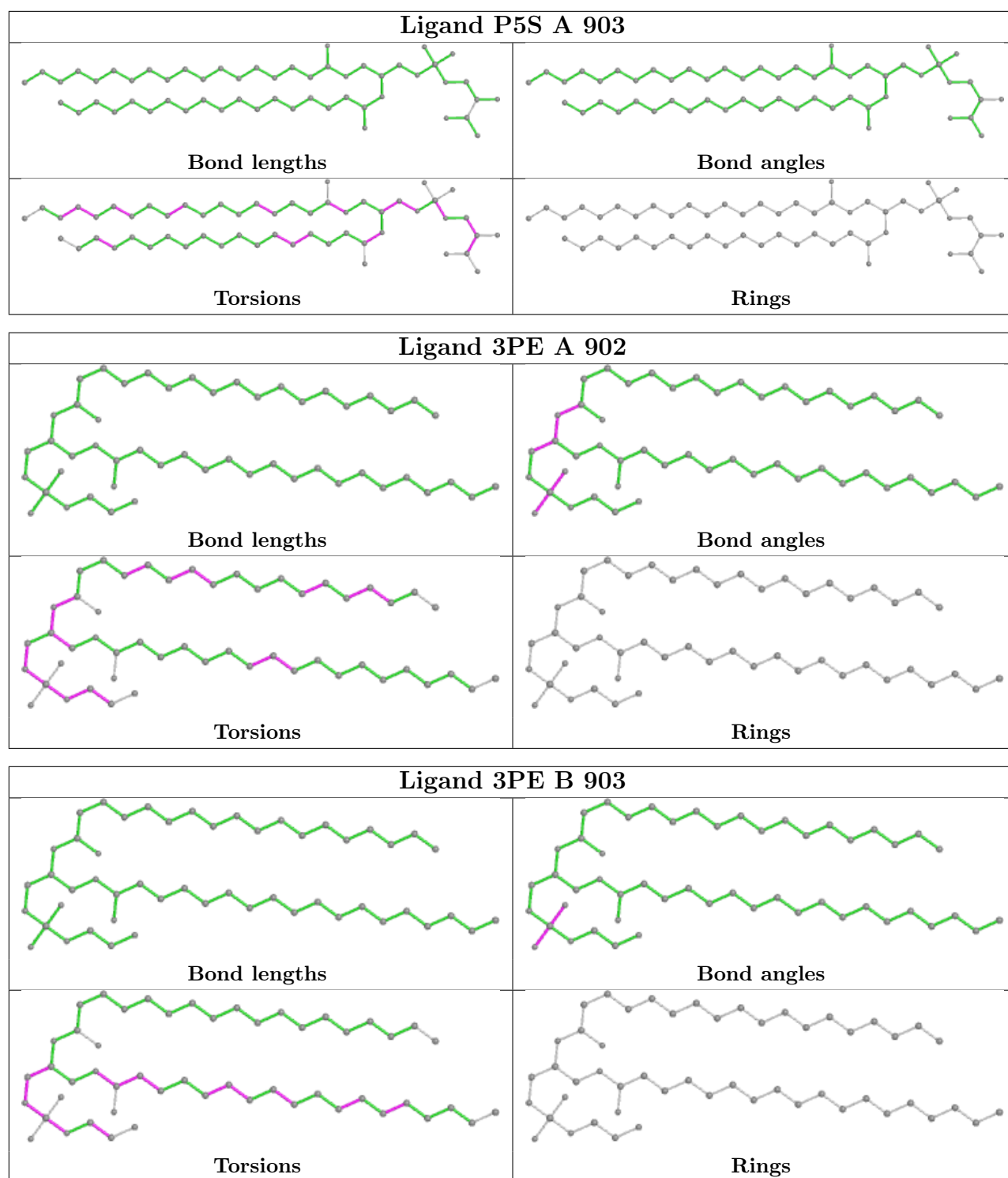
3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	3PE	4	0
3	A	903	P5S	4	0
2	B	903	3PE	1	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 ⓘ

There are no chain breaks in this entry.

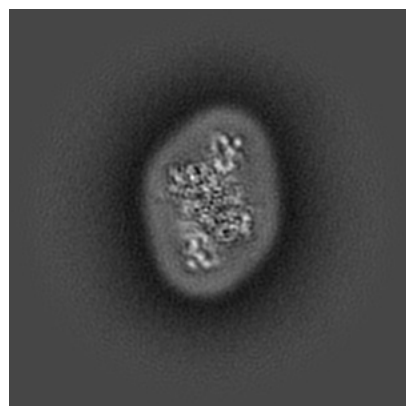
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61313. These allow visual inspection of the internal detail of the map and identification of artifacts.

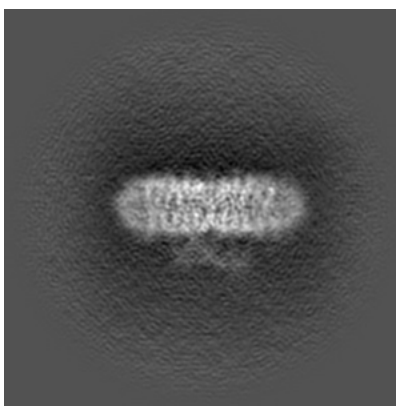
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

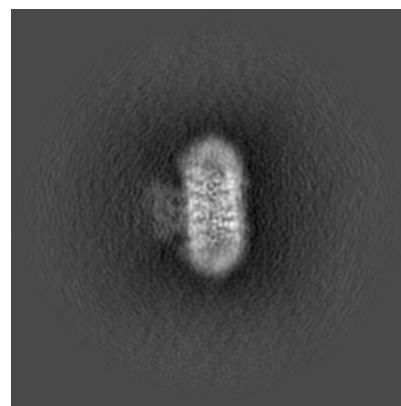
6.1.1 Primary map



X

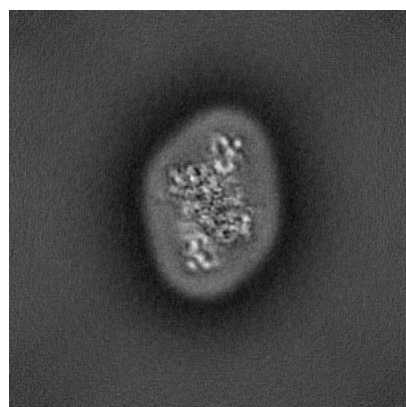


Y

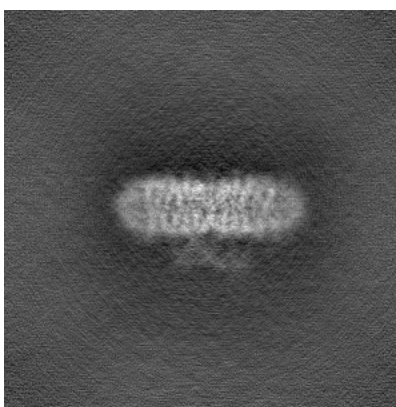


Z

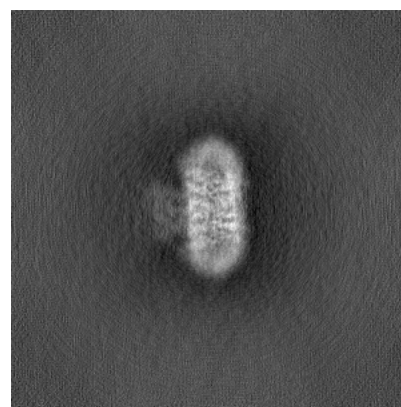
6.1.2 Raw map



X



Y

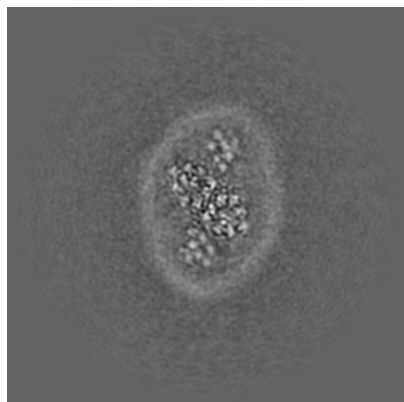


Z

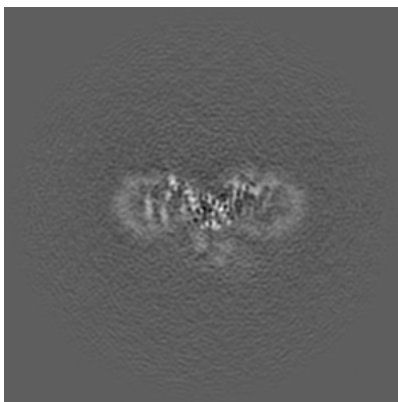
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

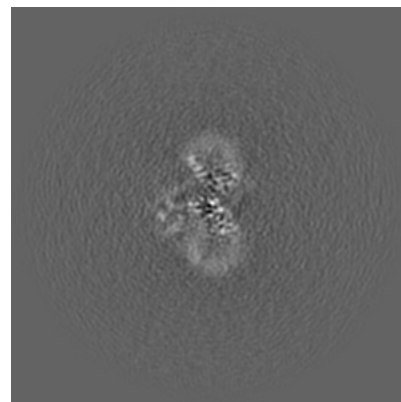
6.2.1 Primary map



X Index: 200

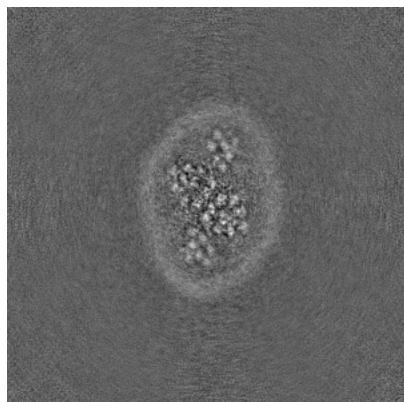


Y Index: 200

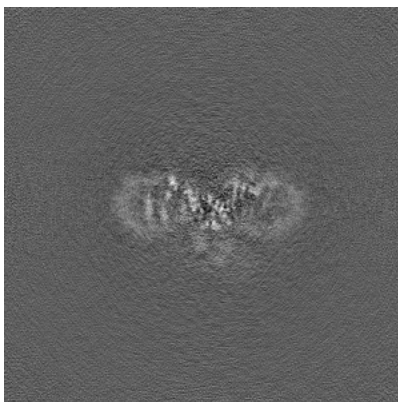


Z Index: 200

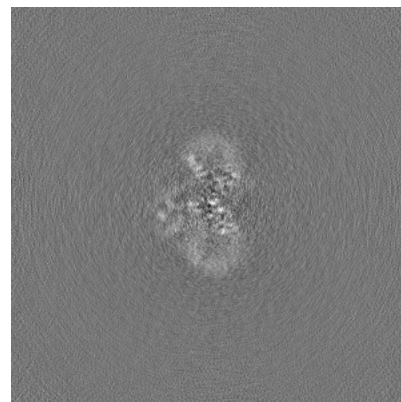
6.2.2 Raw map



X Index: 200



Y Index: 200

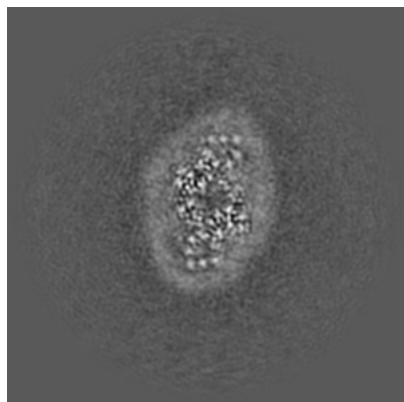


Z Index: 200

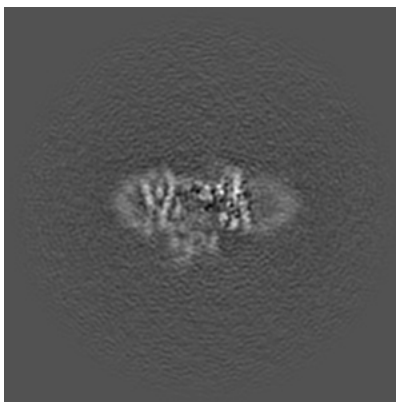
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

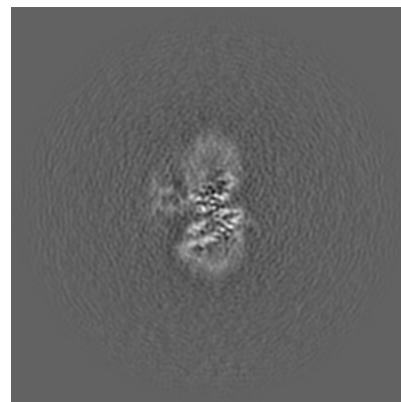
6.3.1 Primary map



X Index: 218

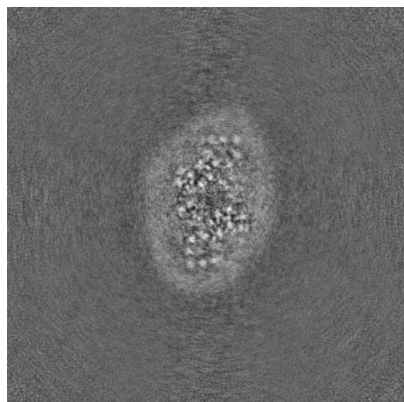


Y Index: 183

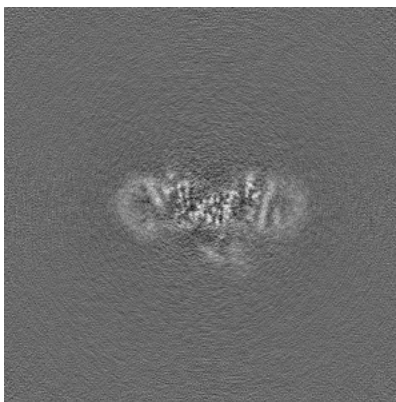


Z Index: 219

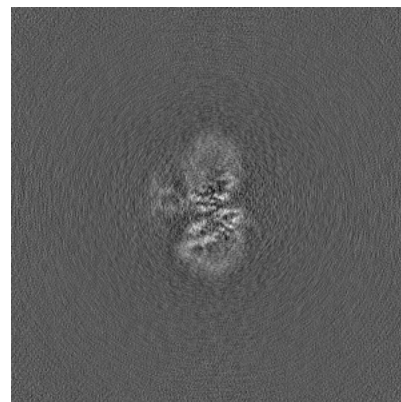
6.3.2 Raw map



X Index: 218



Y Index: 206

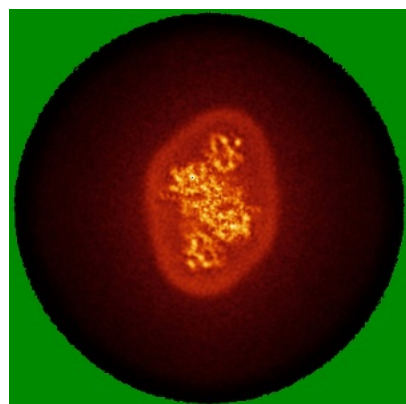


Z Index: 219

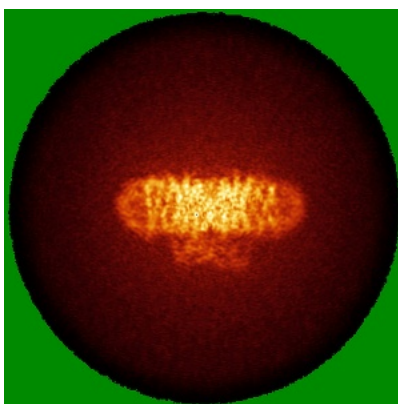
The images above show the largest variance slices of the map in three orthogonal directions.

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

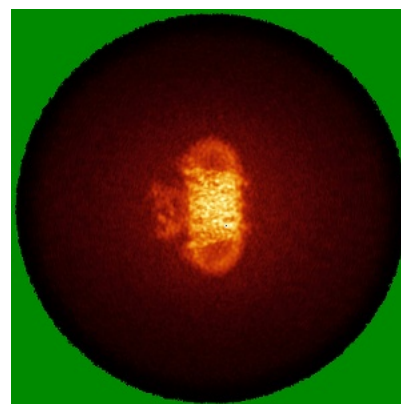
6.4.1 Primary map



X

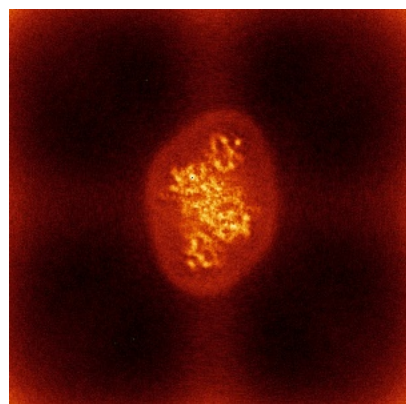


Y

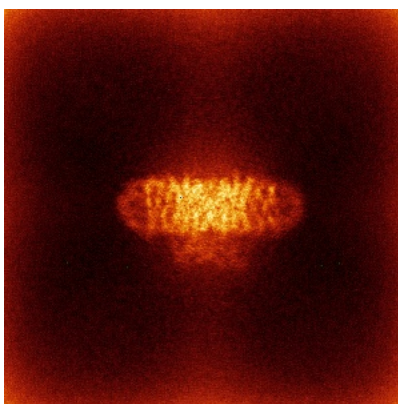


Z

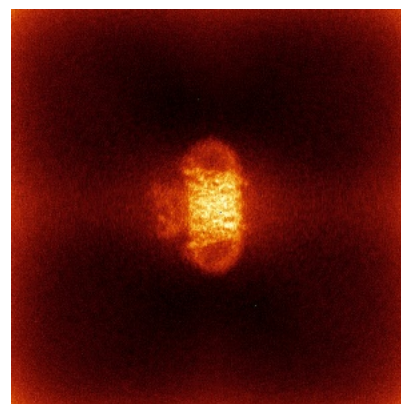
6.4.2 Raw map



X



Y

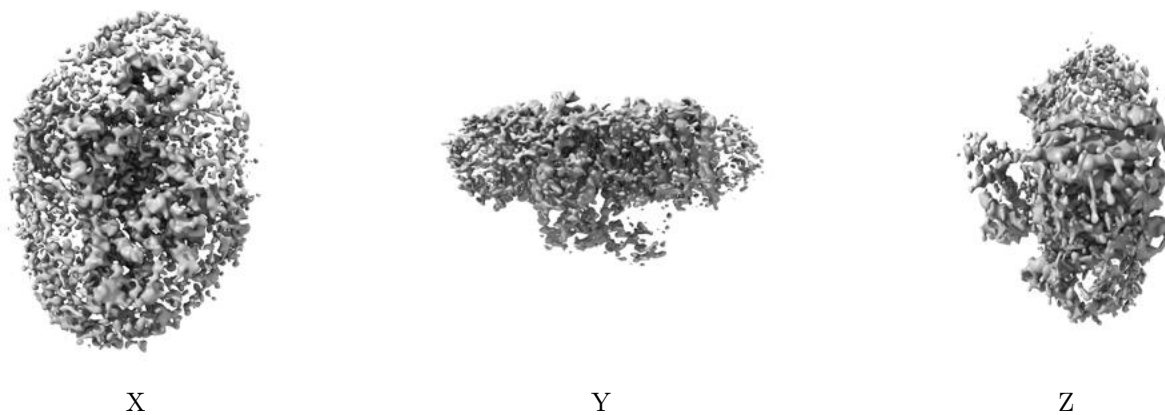


Z

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.

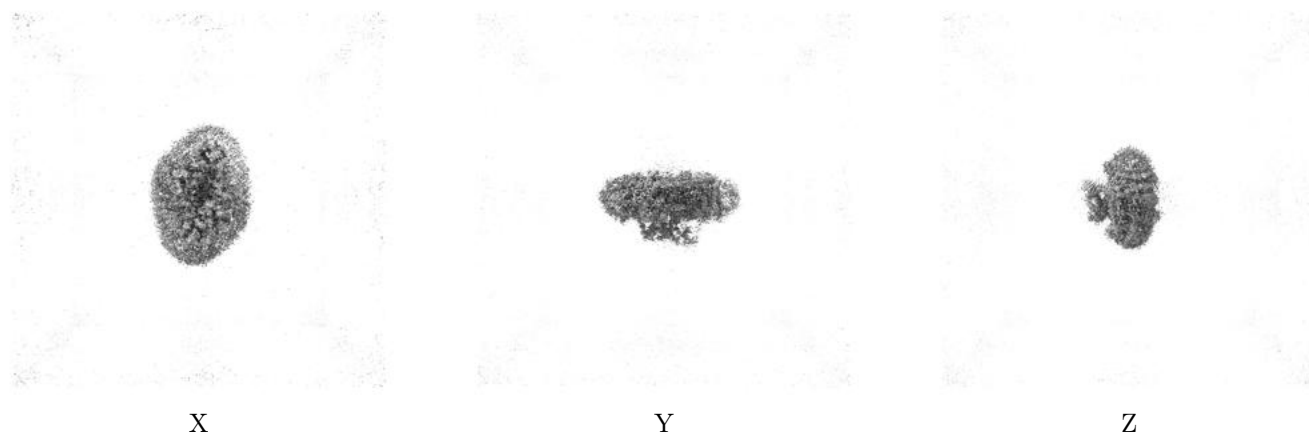
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

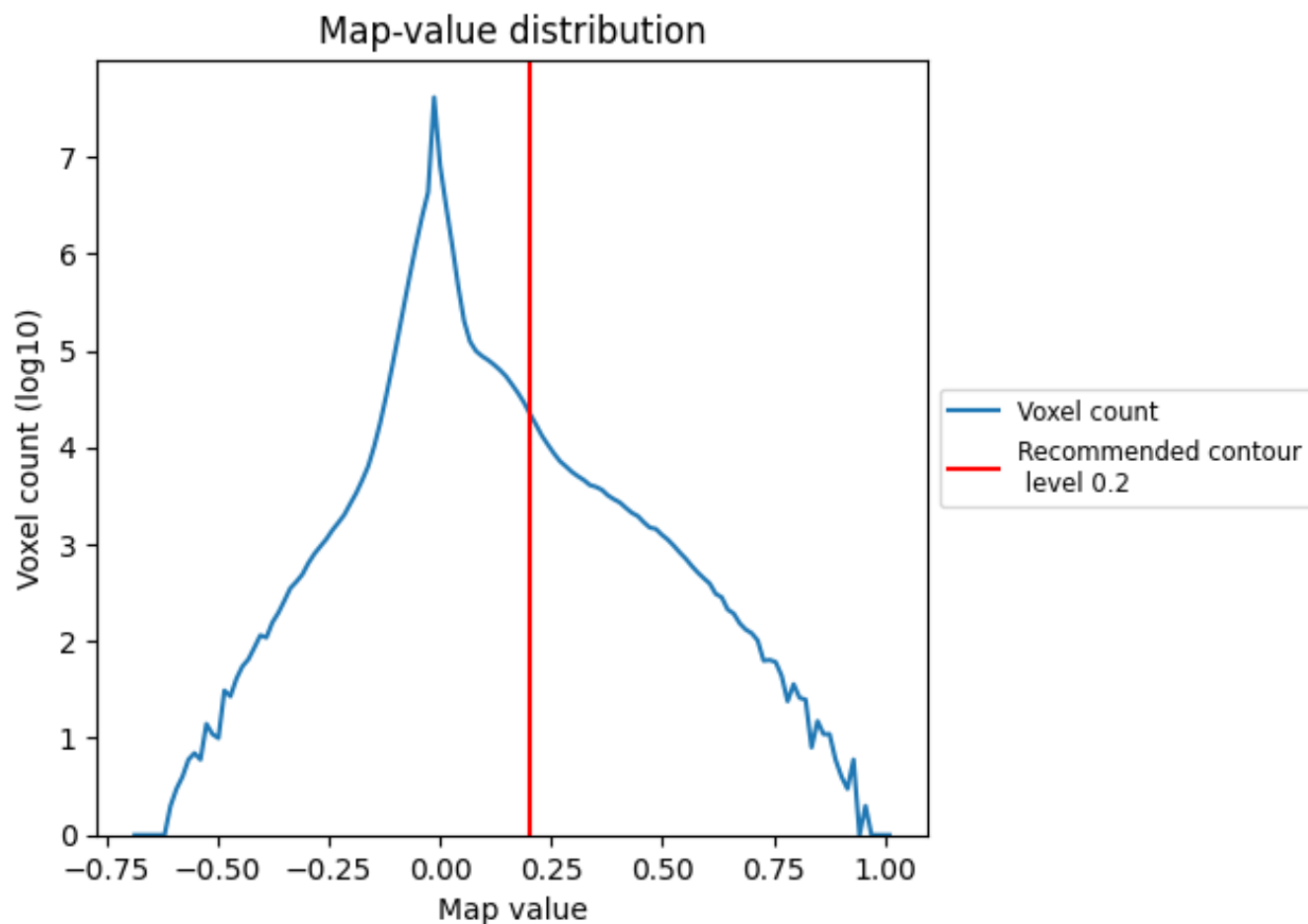
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

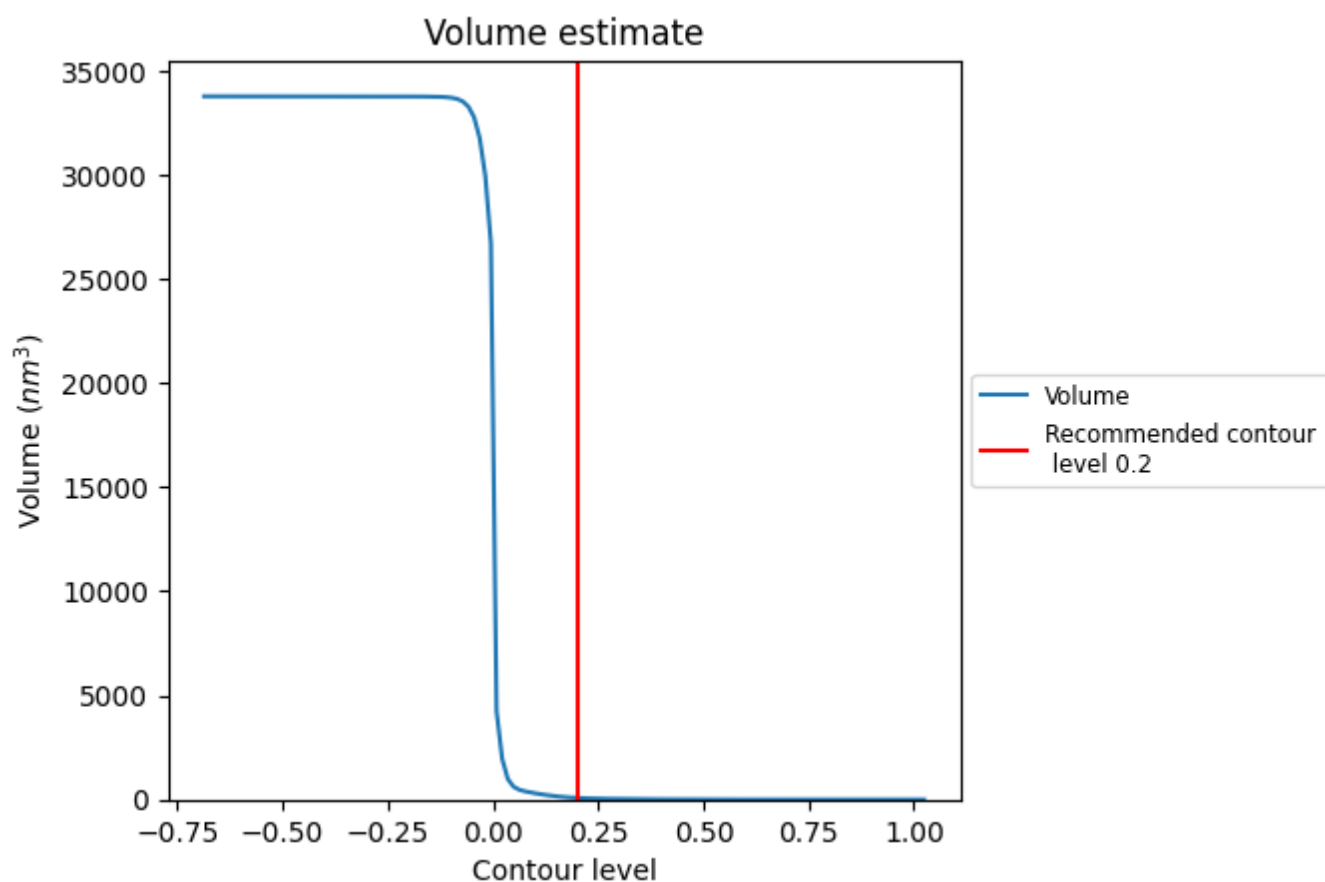
This section contains the results of statistical analysis of the map.

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.

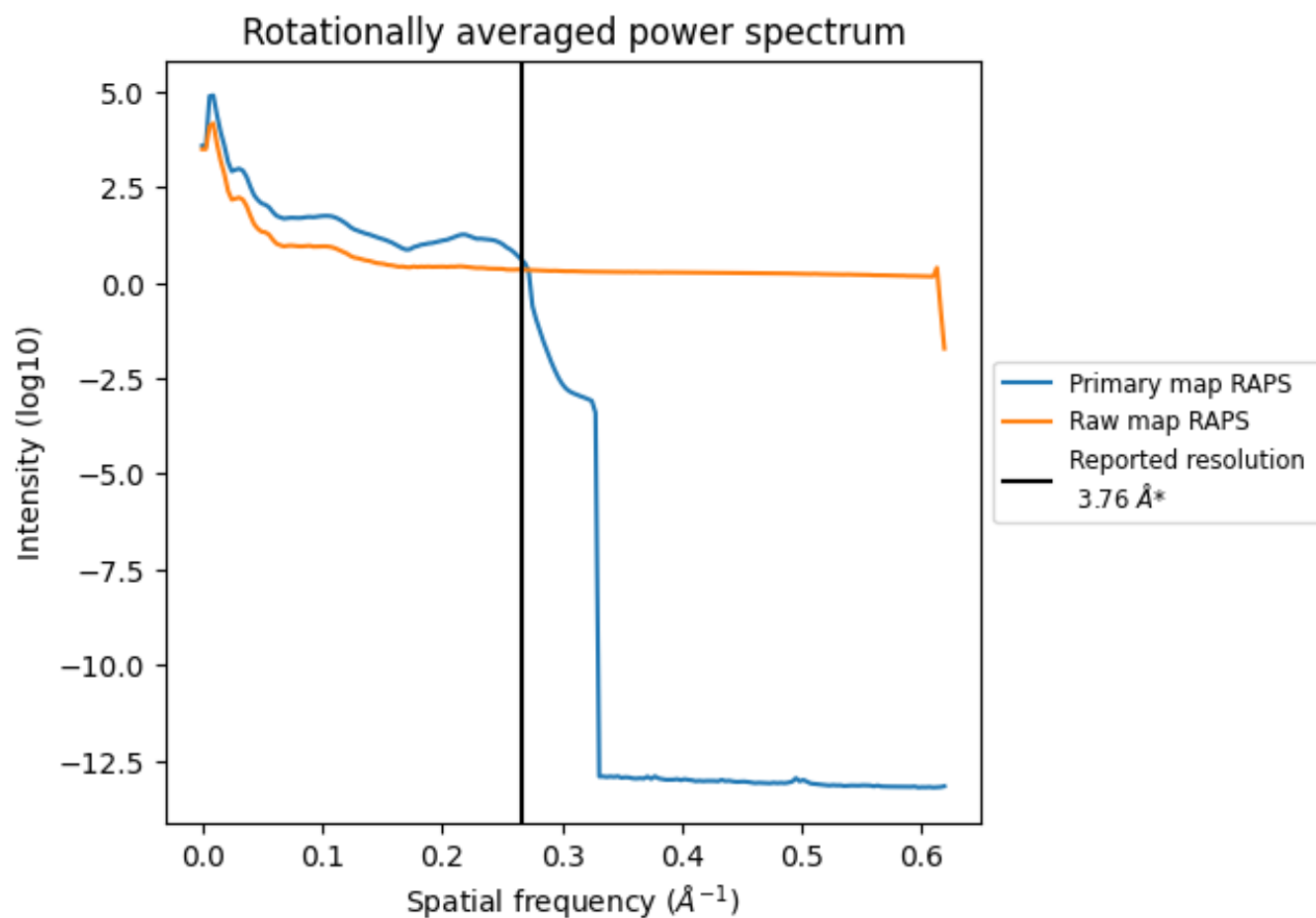
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 77 nm³; this corresponds to an approximate mass of 70 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 ⓘ

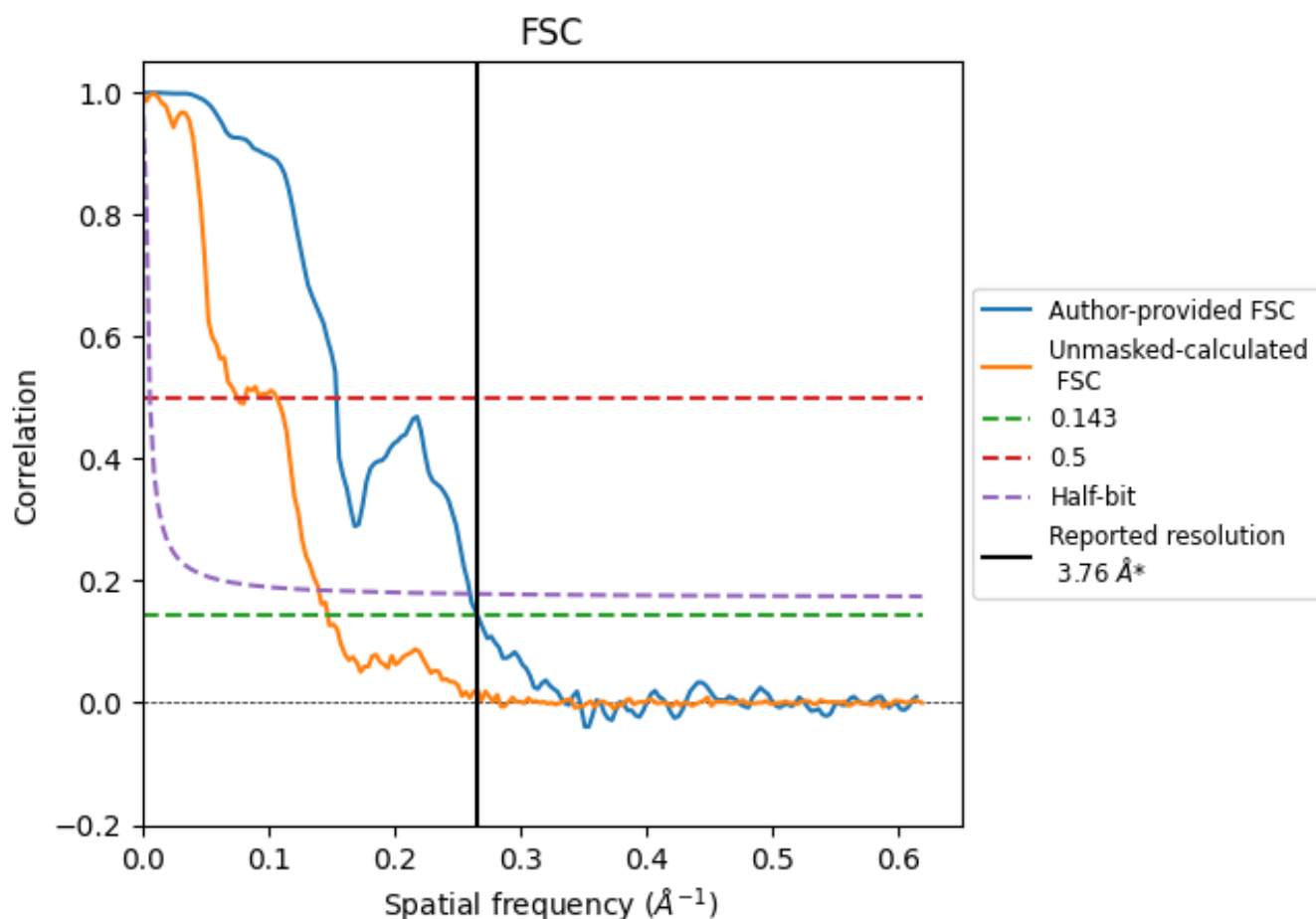


*Reported resolution corresponds to spatial frequency of 0.266 Å⁻¹

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 0.266 \AA^{-1}

8.2 Resolution estimates [i](#)

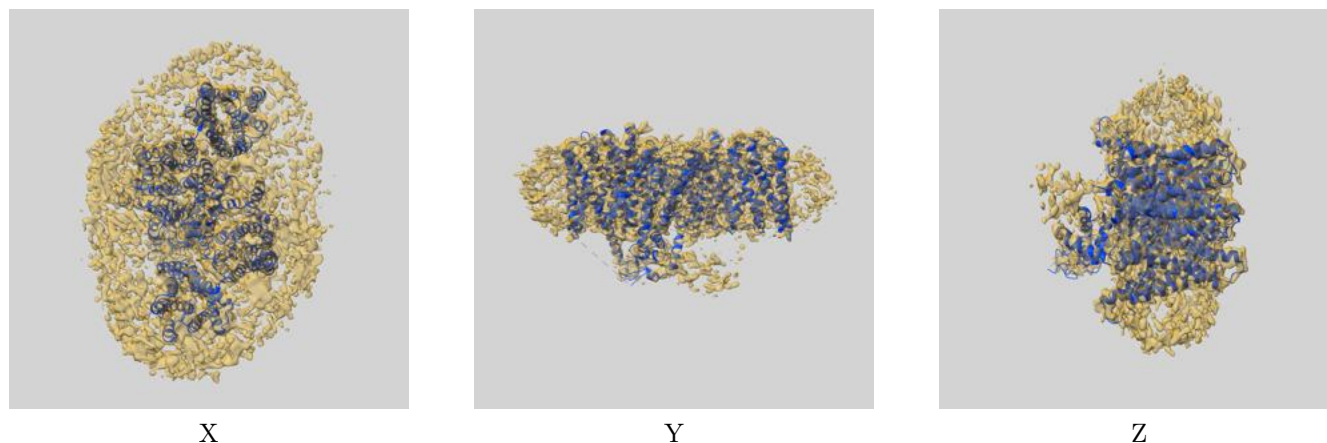
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.76	-	-
Author-provided FSC curve	3.76	6.49	3.84
Unmasked-calculated*	6.79	13.25	7.14

*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 6.79 differs from the reported value 3.76 by more than 10 %

9 Map-model fit [i](#)

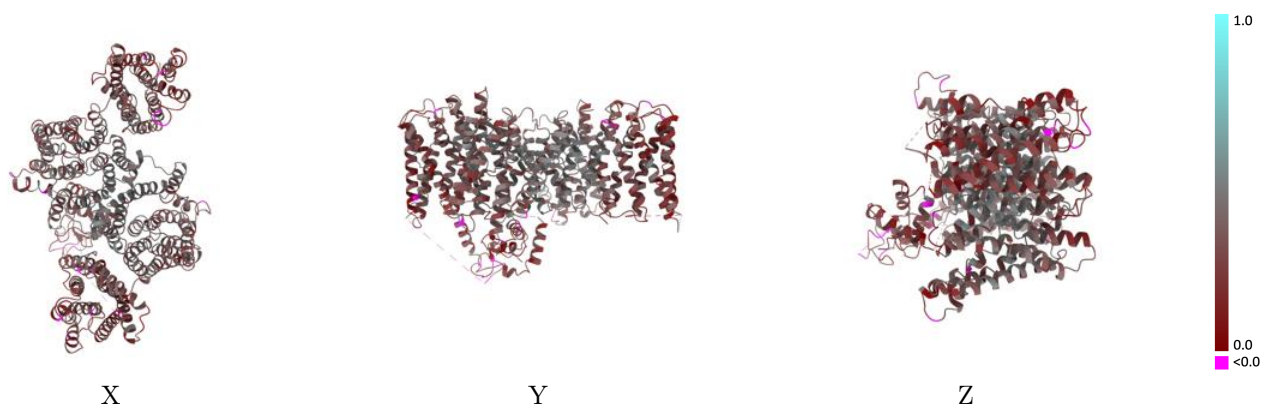
This section contains information regarding the fit between EMDB map EMD-61313 and PDB model 9JBG. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



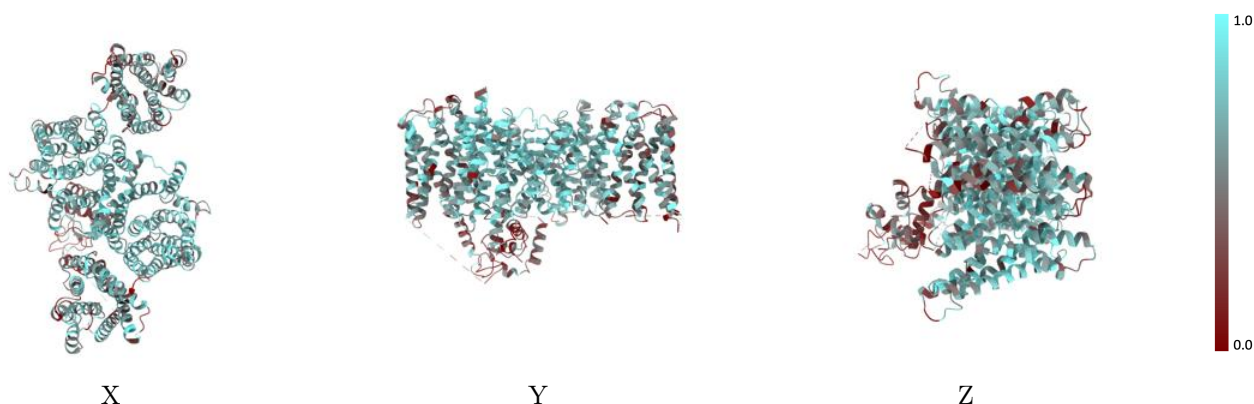
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



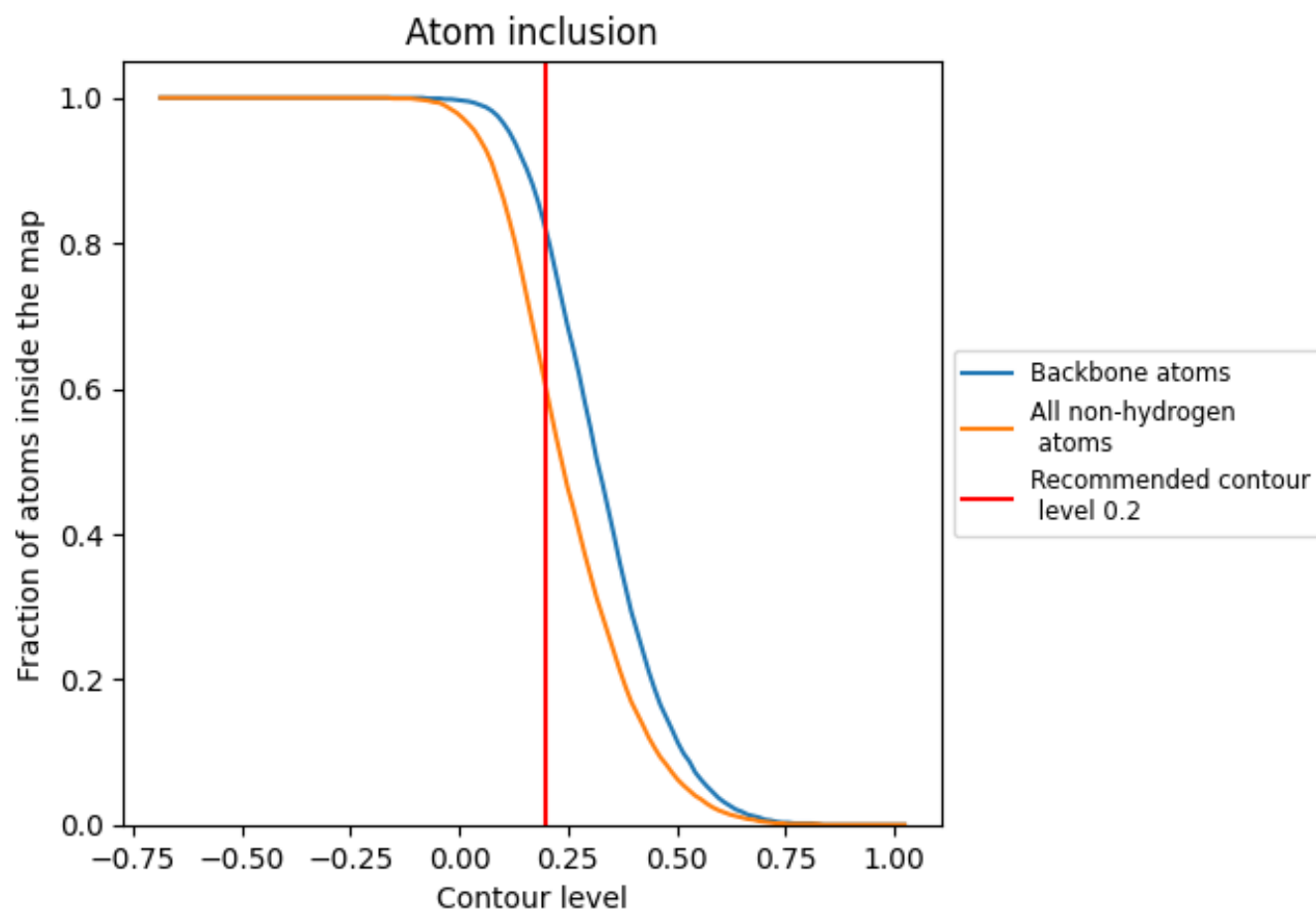
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 60% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6000	<div></div> 0.3240
A	<div></div> 0.5800	<div></div> 0.3130
B	<div></div> 0.6240	<div></div> 0.3380

