



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:20 AM UTC

PDB ID : 8PSF / pdb_00008psf
EMDB ID : EMD-17851
Title : Asymmetric unit of the yeast fatty acid synthase in non-rotated state with ACP at the acetyl transferase domain (FASx sample)
Authors : Singh, K.; Bunzel, G.; Graf, B.; Yip, K.M.; Stark, H.; Chari, A.
Deposited on : 2023-07-13
Resolution : 2.80 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:

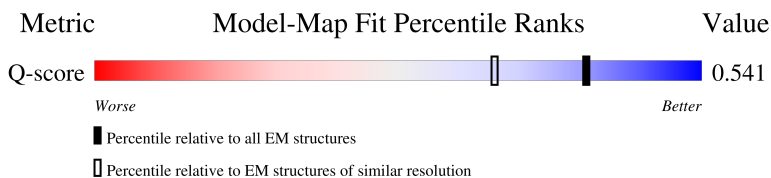
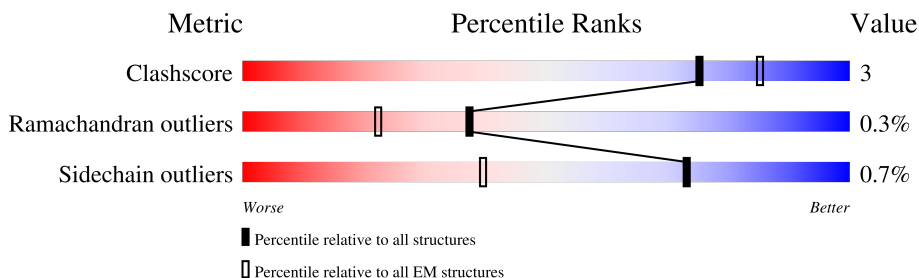
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	1887	
1	B	1887	
2	G	2051	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 29204 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.

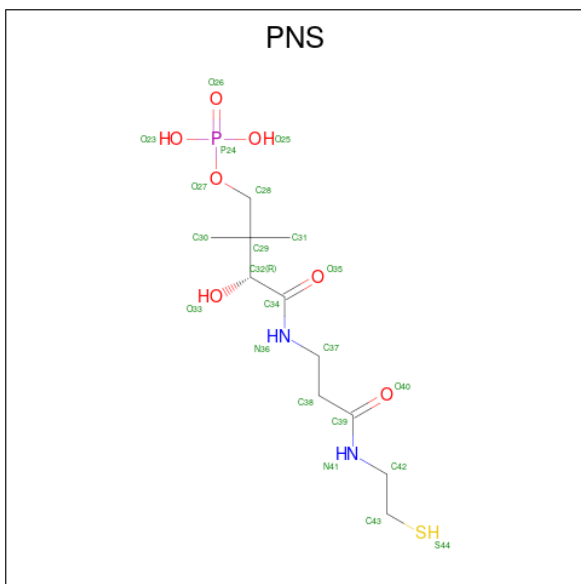
- Molecule 1 is a protein called Fatty acid synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1579	Total	C	N	O	S	0	0
			12346	7817	2084	2398	47		
1	B	163	Total	C	N	O		0	0
			802	475	163	164			

- Molecule 2 is a protein called Fatty acid synthase subunit beta.

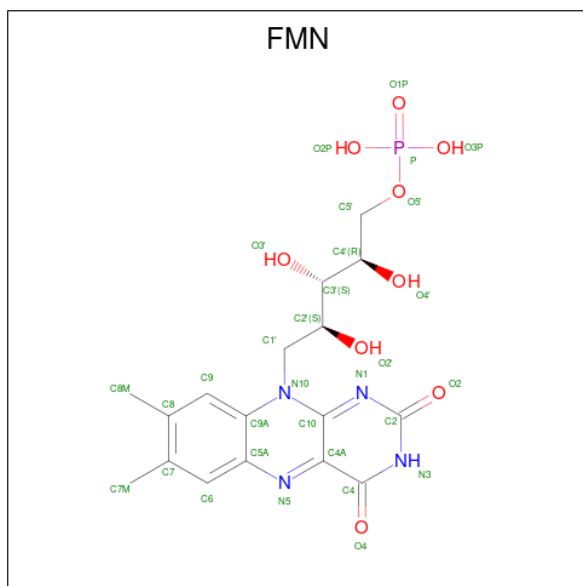
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	2034	Total	C	N	O	S	0	0
			16004	10258	2661	3029	56		

- Molecule 3 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
3	B	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).

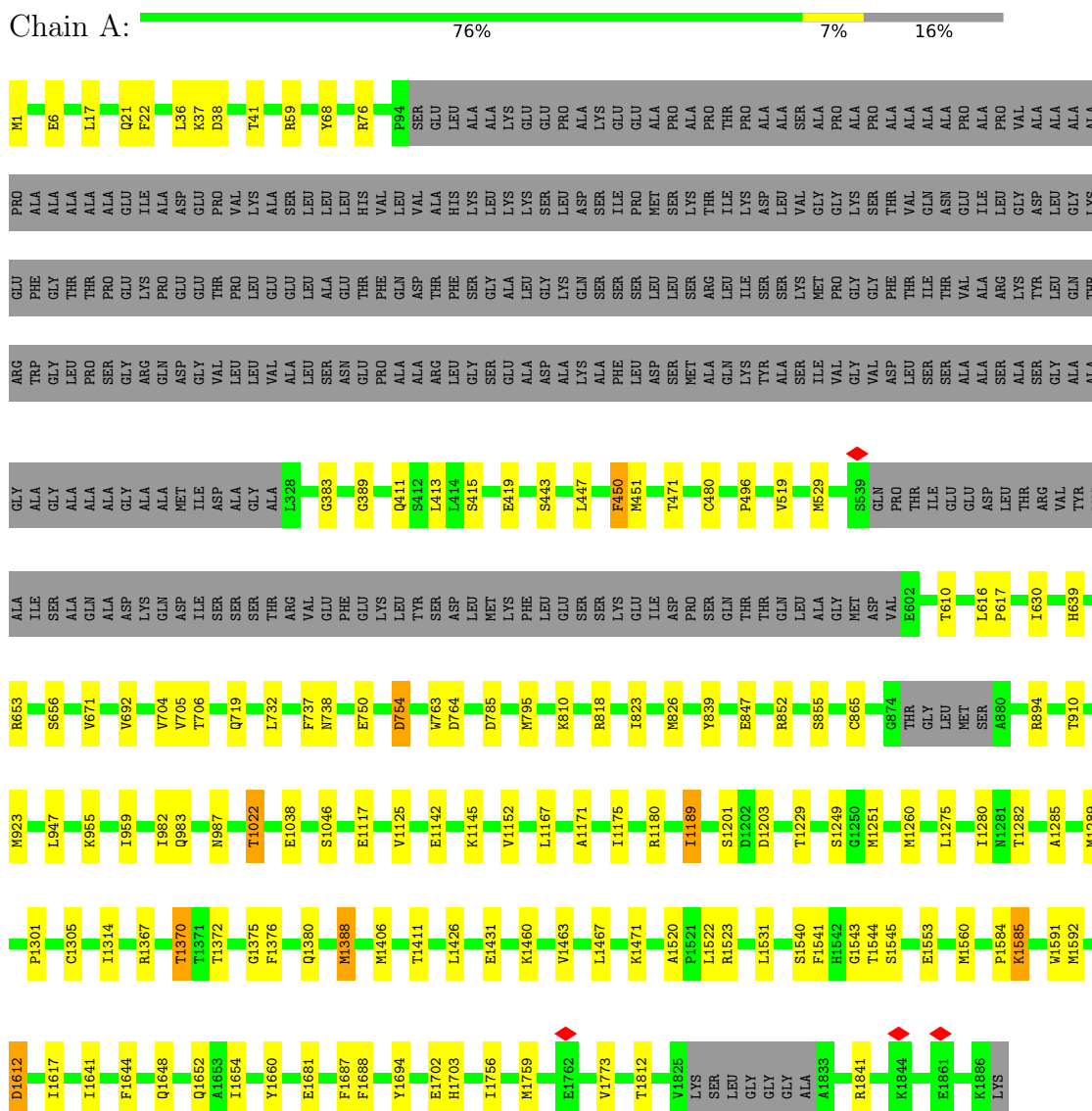


Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
4	G	1	31	17	4	9	1	0

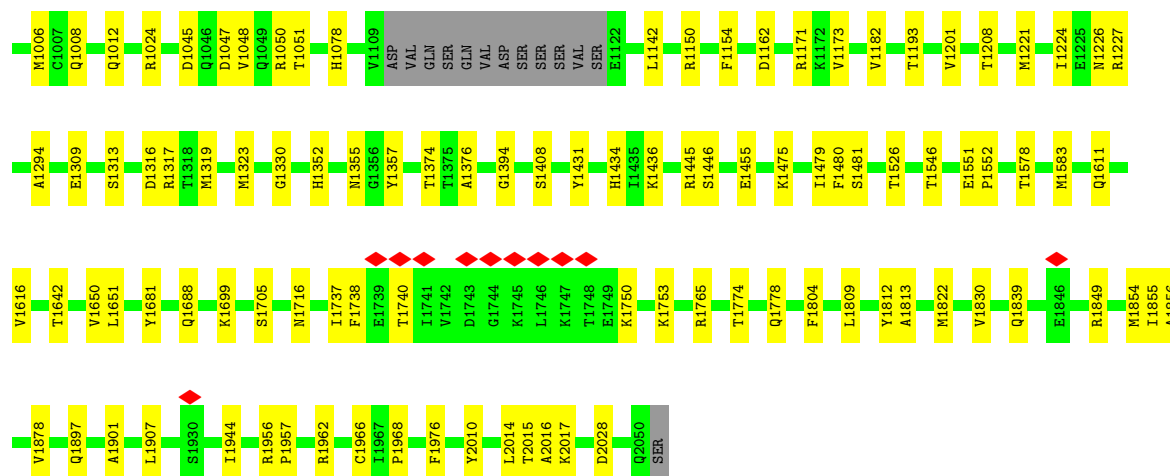
3 Residue-property plots [i](#)

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

- Molecule 1: Fatty acid synthase subunit alpha



- Molecule 1: Fatty acid synthase subunit alpha



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	149476	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	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.057	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0175	Depositor
Map size (Å)	253.19998, 253.19998, 253.19998	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	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: PNS, FMN

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	1.01	2/12579 (0.0%)	1.46	8/17001 (0.0%)
1	B	1.31	0/801	1.84	2/1111 (0.2%)
2	G	0.98	0/16369	1.45	4/22210 (0.0%)
All	All	1.00	2/29749 (0.0%)	1.47	14/40322 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1388	MET	C-O	-5.21	1.17	1.23
1	A	1688	PHE	C-O	-5.21	1.18	1.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	383	GLY	CA-C-O	-6.26	117.91	122.23
1	A	1282	THR	CA-CB-OG1	-6.03	100.56	109.60
2	G	1316	ASP	CA-CB-CG	5.72	118.32	112.60
2	G	599	PRO	N-CA-CB	-5.45	96.61	102.60
1	A	1375	GLY	CA-C-O	-5.43	118.69	122.22
2	G	65	LEU	CA-C-N	5.43	125.96	119.94
2	G	65	LEU	C-N-CA	5.43	125.96	119.94
1	A	450	PHE	CA-C-N	5.33	127.68	120.38
1	A	450	PHE	C-N-CA	5.33	127.68	120.38
1	A	1189	ILE	CB-CA-C	5.26	116.03	110.88
1	B	262	ASP	CA-C-N	5.16	125.71	119.98
1	B	262	ASP	C-N-CA	5.16	125.71	119.98
1	A	692	VAL	N-CA-C	-5.16	105.68	110.53
1	A	1376	PHE	CA-CB-CG	5.09	118.89	113.80

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	12346	0	12279	73	0
1	B	802	0	375	0	0
2	G	16004	0	15984	110	0
3	B	21	0	21	1	0
4	G	31	0	19	2	0
All	All	29204	0	28678	177	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 3.

All (177) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1560:MET:HE1	1:A:1652:GLN:HE22	1.52	0.73
2:G:1855:ILE:HG23	2:G:1907:LEU:HD23	1.74	0.69
1:A:1022:THR:HG21	1:A:1388:MET:HE3	1.76	0.67
2:G:894:ARG:NH1	2:G:898:ASP:OD2	2.29	0.66
1:A:826:MET:HE3	1:A:847:GLU:HG2	1.79	0.65
1:A:1471:LYS:HD3	1:A:1759:MET:SD	2.38	0.64
2:G:1142:LEU:HD22	2:G:1182:VAL:HG11	1.80	0.64
2:G:864:LEU:HD11	2:G:868:PHE:CZ	2.34	0.63
2:G:2015:THR:O	2:G:2017:LYS:N	2.33	0.62
1:A:1431:GLU:OE2	1:A:1523:ARG:NH1	2.34	0.60
2:G:1201:VAL:HG11	2:G:1226:ASN:HB2	1.83	0.60
1:A:529:MET:HE1	1:A:894:ARG:HG2	1.85	0.59
2:G:355:LYS:O	2:G:358:SER:OG	2.20	0.59
2:G:1323:MET:HE2	2:G:1357:TYR:HB2	1.85	0.58
2:G:526:ARG:NH2	2:G:546:GLU:OE2	2.36	0.58
2:G:1778:GLN:HG2	2:G:1809:LEU:HD12	1.86	0.58
1:A:1251:MET:HE1	1:A:1585:LYS:HD2	1.86	0.57
1:A:1285:ALA:O	1:A:1289:MET:HG3	2.05	0.57
1:A:17:LEU:HD23	2:G:2014:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:283:ILE:O	2:G:286:THR:HG22	2.06	0.56
1:A:987:ASN:HD21	2:G:993:GLN:HE22	1.53	0.56
1:A:1189:ILE:H	1:A:1380:GLN:HE21	1.55	0.55
2:G:1878:VAL:HG22	2:G:1944:ILE:HG12	1.88	0.55
1:A:704:VAL:HG23	1:A:763:TRP:CZ3	2.42	0.54
2:G:369:SER:HB2	2:G:428:HIS:HB2	1.90	0.54
1:A:706:THR:HB	1:A:737:PHE:HB3	1.90	0.54
1:A:795:MET:HE1	1:A:839:TYR:CD1	2.43	0.54
2:G:1750:LYS:O	2:G:1753:LYS:NZ	2.41	0.53
2:G:1856:ALA:O	2:G:1966:CYS:HA	2.08	0.53
1:A:1560:MET:HE1	1:A:1652:GLN:NE2	2.20	0.53
2:G:390:ASN:OD1	2:G:418:ASN:ND2	2.42	0.53
2:G:593:LEU:HB3	2:G:616:THR:HG23	1.91	0.53
2:G:1173:VAL:HG21	2:G:1221:MET:HE1	1.90	0.53
2:G:1445:ARG:NH1	2:G:1455:GLU:O	2.41	0.53
1:A:1426:LEU:HD12	1:A:1560:MET:HG3	1.91	0.53
2:G:1330:GLY:HA2	2:G:1374:THR:HG21	1.90	0.53
2:G:176:LEU:HD21	2:G:248:HIS:CE1	2.44	0.52
2:G:301:THR:HG21	2:G:448:VAL:HG21	1.91	0.52
2:G:600:CYS:SG	2:G:806:MET:HG2	2.49	0.52
2:G:597:MET:HA	4:G:2101:FMN:N5	2.24	0.52
2:G:1294:ALA:HB1	2:G:1319:MET:HE1	1.91	0.52
2:G:1002:HIS:CD2	2:G:1006:MET:HE2	2.45	0.52
2:G:234:ILE:N	2:G:235:PRO:CD	2.73	0.51
1:A:630:ILE:O	1:A:653:ARG:NH2	2.43	0.51
1:A:705:VAL:CG1	1:A:732:LEU:HD11	2.40	0.51
2:G:1738:PHE:HB3	2:G:1740:THR:HG23	1.92	0.51
2:G:898:ASP:O	2:G:1050:ARG:HA	2.10	0.51
1:A:443:SER:HA	1:A:447:LEU:HD23	1.92	0.51
1:A:415:SER:O	1:A:419:GLU:HG2	2.11	0.50
2:G:84:LEU:CD2	2:G:133:ALA:HB2	2.42	0.50
2:G:593:LEU:CB	2:G:616:THR:HG23	2.41	0.50
2:G:1854:MET:HG2	2:G:1901:ALA:HB2	1.93	0.50
1:A:41:THR:O	1:A:76:ARG:NH1	2.44	0.50
1:A:1431:GLU:OE1	1:A:1520:ALA:N	2.42	0.50
1:A:1411:THR:HA	1:A:1648:GLN:O	2.12	0.50
2:G:621:GLY:HA2	2:G:630:MET:CE	2.42	0.49
2:G:1778:GLN:HA	2:G:1809:LEU:HD11	1.94	0.49
2:G:50:ALA:HB3	2:G:53:GLU:OE1	2.11	0.49
2:G:159:ILE:HA	2:G:271:THR:O	2.12	0.49
1:A:1:MET:HE2	1:A:6:GLU:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:719:GLN:HG3	1:A:1612:ASP:HA	1.94	0.49
2:G:593:LEU:O	2:G:800:LEU:HA	2.12	0.49
2:G:372:ASN:HB3	2:G:515:LEU:HD11	1.94	0.49
1:A:764:ASP:OD1	1:A:810:LYS:NZ	2.42	0.49
1:A:705:VAL:HG12	1:A:732:LEU:HD11	1.95	0.49
2:G:338:MET:HE2	2:G:378:VAL:HG11	1.95	0.49
2:G:1854:MET:HE1	2:G:1976:PHE:HB2	1.94	0.48
1:A:1463:VAL:HB	1:A:1773:VAL:HG21	1.95	0.48
2:G:1809:LEU:C	2:G:1809:LEU:HD23	2.39	0.48
2:G:767:PHE:HD2	2:G:771:PHE:CE2	2.32	0.48
1:A:955:LYS:O	1:A:959:ILE:HG12	2.14	0.48
2:G:1956:ARG:N	2:G:1957:PRO:HD2	2.28	0.48
1:A:389:GLY:O	1:A:738:ASN:ND2	2.45	0.47
1:A:1117:GLU:O	1:A:1180:ARG:HD3	2.15	0.47
1:A:496:PRO:HG2	1:A:519:VAL:HG12	1.97	0.47
1:A:982:ILE:HD11	2:G:952:ARG:HD3	1.96	0.47
2:G:808:ALA:HB3	2:G:811:VAL:HG23	1.96	0.47
2:G:1355:ASN:ND2	2:G:1408:SER:OG	2.48	0.47
2:G:1804:PHE:CZ	2:G:2010:TYR:HB2	2.49	0.47
2:G:1045:ASP:HB2	2:G:1047:ASP:HB2	1.97	0.47
1:A:1531:LEU:HD21	1:A:1660:TYR:CZ	2.51	0.46
1:A:1260:MET:HE1	1:A:1275:LEU:HA	1.97	0.46
1:A:1406:MET:HE2	1:A:1654:ILE:HG12	1.97	0.46
2:G:109:LEU:HG	2:G:119:THR:HG21	1.98	0.46
2:G:598:THR:HA	2:G:599:PRO:HA	1.76	0.46
2:G:1313:SER:HB2	2:G:1319:MET:HE2	1.97	0.46
2:G:264:ARG:CZ	2:G:456:GLN:HG3	2.46	0.46
2:G:817:ALA:HA	2:G:1048:VAL:HG21	1.96	0.46
2:G:829:ASP:O	2:G:832:TRP:HD1	1.98	0.46
2:G:1352:HIS:CE1	2:G:1583:MET:HE3	2.51	0.46
1:A:983:GLN:HE22	2:G:962:LYS:HD2	1.80	0.46
1:A:1694:TYR:OH	2:G:1001:ASP:OD2	2.29	0.45
2:G:915:ALA:HA	2:G:1000:ILE:HD11	1.97	0.45
2:G:1154:PHE:O	2:G:1171:ARG:NH1	2.47	0.45
1:A:1584:PRO:HG3	1:A:1591:TRP:CE3	2.51	0.45
1:A:36:LEU:O	1:A:76:ARG:NH2	2.47	0.45
2:G:1048:VAL:O	2:G:1051:THR:OG1	2.29	0.45
1:A:1467:LEU:HD22	1:A:1756:ILE:HD11	1.97	0.45
2:G:142:ASN:O	2:G:147:ARG:NH2	2.49	0.45
2:G:168:ASP:OD1	2:G:171:GLU:HG2	2.16	0.45
2:G:33:LEU:HD21	2:G:80:PHE:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:767:PHE:O	2:G:799:PHE:HA	2.17	0.45
2:G:1434:HIS:HB3	2:G:1436:LYS:HE3	1.98	0.45
2:G:590:PRO:HG3	2:G:1078:HIS:CE1	2.51	0.45
1:A:1249:SER:HB3	1:A:1280:ILE:HG23	1.99	0.44
2:G:670:ARG:NH1	2:G:674:TYR:O	2.47	0.44
2:G:1309:GLU:O	2:G:1317:ARG:NH2	2.50	0.44
1:A:1541:PHE:CD2	1:A:1553:GLU:HG2	2.52	0.44
2:G:905:ALA:HA	2:G:917:MET:SD	2.57	0.44
2:G:1551:GLU:HB2	2:G:1552:PRO:HD3	1.99	0.44
1:A:1702:GLU:HG2	1:A:1703:HIS:CD2	2.52	0.44
2:G:750:MET:HE1	2:G:765:LEU:HD11	1.99	0.44
1:A:1167:LEU:HD12	1:A:1171:ALA:HB1	2.00	0.44
1:A:1229:THR:HB	1:A:1687:PHE:CD1	2.53	0.44
1:A:1201:SER:OG	1:A:1203:ASP:OD2	2.35	0.44
2:G:1716:ASN:OD1	2:G:1765:ARG:HA	2.18	0.44
1:A:37:LYS:HE2	1:A:68:TYR:CE1	2.53	0.44
1:A:451:MET:HE1	1:A:480:CYS:CB	2.48	0.44
1:A:1460:LYS:HG3	1:A:1773:VAL:O	2.17	0.44
1:A:1038:GLU:OE1	1:A:1046:SER:OG	2.30	0.44
2:G:1150:ARG:HD2	2:G:1193:THR:HG21	1.99	0.44
2:G:741:HIS:CD2	2:G:855:HIS:ND1	2.86	0.43
2:G:1008:GLN:OE1	2:G:1024:ARG:NH1	2.50	0.43
1:A:1553:GLU:HG3	1:A:1644:PHE:HE2	1.83	0.43
2:G:1962:ARG:HG2	2:G:1968:PRO:HD2	2.00	0.43
1:A:1592:MET:HE2	1:A:1641:ILE:HG23	2.00	0.43
2:G:1208:THR:O	2:G:1224:ILE:N	2.51	0.43
2:G:1611:GLN:O	2:G:1651:LEU:HD12	2.19	0.43
1:A:823:ILE:HD13	1:A:865:CYS:HB3	2.00	0.43
1:A:639:HIS:HB2	1:A:656:SER:OG	2.19	0.43
1:A:750:GLU:OE2	1:A:754:ASP:OD2	2.37	0.43
2:G:706:LYS:NZ	4:G:2101:FMN:O2'	2.52	0.42
2:G:1546:THR:HG21	2:G:1616:VAL:HG11	2.01	0.42
2:G:1699:LYS:HE3	2:G:1705:SER:HB2	2.01	0.42
2:G:1479:ILE:HG22	2:G:1480:PHE:O	2.19	0.42
2:G:273:HIS:CD2	2:G:488:VAL:HG11	2.54	0.42
2:G:1355:ASN:CB	2:G:1583:MET:HE1	2.49	0.42
1:A:471:THR:HG22	1:A:610:THR:HG21	2.01	0.42
1:A:1522:LEU:HD22	1:A:1560:MET:HE3	2.01	0.42
2:G:84:LEU:HD22	2:G:133:ALA:HB2	2.00	0.42
2:G:1355:ASN:HB3	2:G:1583:MET:HE1	2.02	0.42
1:A:616:LEU:N	1:A:617:PRO:CD	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:663:ILE:HB	2:G:664:PRO:HD3	2.02	0.42
2:G:1642:THR:HB	2:G:1651:LEU:HB3	2.02	0.42
2:G:1812:TYR:O	2:G:1813:ALA:C	2.63	0.42
2:G:1774:THR:HG22	2:G:1839:GLN:HE21	1.84	0.42
2:G:83:VAL:O	2:G:87:CYS:SG	2.63	0.42
2:G:1376:ALA:HA	2:G:1394:GLY:HA2	2.01	0.42
2:G:1431:TYR:CE1	2:G:1526:THR:HG22	2.55	0.42
1:A:1145:LYS:HA	1:A:1152:VAL:CG1	2.51	0.41
2:G:1822:MET:HE1	2:G:1830:VAL:HG21	2.02	0.41
1:A:1117:GLU:O	1:A:1180:ARG:HA	2.19	0.41
2:G:234:ILE:HA	2:G:237:SER:OG	2.20	0.41
1:A:1301:PRO:HB3	1:A:1314:ILE:HD12	2.02	0.41
1:A:1812:THR:OG1	1:A:1841:ARG:NH2	2.54	0.41
1:A:17:LEU:O	1:A:21:GLN:HB2	2.19	0.41
1:A:413:LEU:HD23	1:A:450:PHE:CE2	2.56	0.41
1:A:671:VAL:HG21	1:A:910:THR:HG22	2.02	0.41
1:A:1367:ARG:O	1:A:1370:THR:HB	2.21	0.41
1:A:1544:THR:O	1:A:1545:SER:HB3	2.20	0.41
3:B:1901:PNS:H421	2:G:370:LEU:HD11	2.03	0.41
2:G:1475:LYS:HB2	2:G:1481:SER:HB3	2.03	0.41
2:G:1854:MET:HG2	2:G:1901:ALA:CB	2.51	0.41
2:G:868:PHE:HB3	2:G:873:PHE:CE2	2.56	0.41
2:G:767:PHE:HD2	2:G:771:PHE:CZ	2.39	0.41
2:G:1849:ARG:HH12	2:G:1957:PRO:HB3	1.86	0.41
2:G:1854:MET:HE3	2:G:1976:PHE:H	1.86	0.41
2:G:942:THR:HB	2:G:1012:GLN:HB2	2.02	0.41
2:G:234:ILE:N	2:G:235:PRO:HD3	2.37	0.40
2:G:1854:MET:HE3	2:G:1976:PHE:N	2.36	0.40
1:A:852:ARG:HA	1:A:855:SER:OG	2.22	0.40
2:G:1227:ARG:NE	2:G:1551:GLU:OE2	2.53	0.40
1:A:764:ASP:OD2	1:A:818:ARG:HD3	2.22	0.40
1:A:1370:THR:HG22	1:A:1372:THR:H	1.85	0.40
1:A:59:ARG:HH22	2:G:1897:GLN:HE22	1.70	0.40
1:A:1125:VAL:HG11	1:A:1175:ILE:HD12	2.03	0.40
2:G:1681:TYR:O	2:G:1688:GLN:HG3	2.20	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	1569/1887 (83%)	1503 (96%)	62 (4%)	4 (0%)	36	66
1	B	161/1887 (8%)	152 (94%)	9 (6%)	0	100	100
2	G	2030/2051 (99%)	1918 (94%)	105 (5%)	7 (0%)	36	66
All	All	3760/5825 (64%)	3573 (95%)	176 (5%)	11 (0%)	37	66

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	2016	ALA
2	G	769	SER
1	A	22	PHE
1	A	1543	GLY
2	G	1578	THR
1	A	785	ASP
1	A	1585	LYS
2	G	97	GLU
2	G	1162	ASP
2	G	1737	ILE
2	G	839	PRO

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	1336/1566 (85%)	1323 (99%)	13 (1%)	68	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1/1566 (0%)	0	1 (100%)	0	0
2	G	1773/1789 (99%)	1766 (100%)	7 (0%)	84	94
All	All	3110/4921 (63%)	3089 (99%)	21 (1%)	73	91

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ASP
1	A	411	GLN
1	A	754	ASP
1	A	923	MET
1	A	947	LEU
1	A	1022	THR
1	A	1142	GLU
1	A	1305	CYS
1	A	1370	THR
1	A	1540	SER
1	A	1612	ASP
1	A	1617	ILE
1	A	1681	GLU
1	B	180	SER
2	G	35	GLU
2	G	86	LEU
2	G	425	SER
2	G	599	PRO
2	G	1446	SER
2	G	1650	VAL
2	G	2028	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	356	ASN
1	A	482	GLN
1	A	618	ASN
1	A	669	ASN
1	A	713	GLN
1	A	983	GLN
1	A	1000	GLN

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Mol	Chain	Res	Type
1	A	1380	GLN
1	A	1482	GLN
1	A	1542	HIS
1	A	1552	ASN
1	A	1601	ASN
1	A	1695	ASN
1	A	1703	HIS
1	A	1748	ASN
1	A	1843	ASN
2	G	85	ASN
2	G	155	GLN
2	G	165	ASN
2	G	245	GLN
2	G	330	ASN
2	G	440	ASN
2	G	566	HIS
2	G	640	GLN
2	G	718	ASN
2	G	723	HIS
2	G	725	ASN
2	G	747	HIS
2	G	760	HIS
2	G	896	ASN
2	G	993	GLN
2	G	1002	HIS
2	G	1078	HIS
2	G	1241	ASN
2	G	1306	ASN
2	G	1341	ASN
2	G	1352	HIS
2	G	1355	ASN
2	G	1432	GLN
2	G	1595	ASN
2	G	1611	GLN
2	G	1619	ASN
2	G	1839	GLN
2	G	1895	ASN
2	G	1897	GLN
2	G	1912	ASN
2	G	1939	HIS
2	G	1995	ASN
2	G	2013	ASN

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Mol	Chain	Res	Type
2	G	2020	GLN
2	G	2027	GLN
2	G	2044	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
4	FMN	G	2101	-	33,33,33	1.43	6 (18%)	48,50,50	1.35	7 (14%)
3	PNS	B	1901	1	15,20,21	0.57	0	18,26,29	1.42	4 (22%)

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	FMN	G	2101	-	-	1/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PNS	B	1901	1	-	6/24/26/27	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	2101	FMN	C9A-C5A	3.82	1.47	1.41
4	G	2101	FMN	C5A-N5	-2.66	1.34	1.39
4	G	2101	FMN	C8-C7	2.61	1.47	1.40
4	G	2101	FMN	C4-N3	-2.56	1.34	1.38
4	G	2101	FMN	C2-N3	-2.28	1.34	1.39
4	G	2101	FMN	C6-C5A	-2.15	1.36	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	2101	FMN	C4-C4A-N5	4.26	124.10	118.21
3	B	1901	PNS	C38-C39-N41	3.31	122.38	116.34
4	G	2101	FMN	C4A-C10-N10	3.21	121.07	116.48
3	B	1901	PNS	O40-C39-C38	-2.93	116.72	122.02
4	G	2101	FMN	O2P-P-O5'	2.77	113.88	106.67
4	G	2101	FMN	C10-N1-C2	2.66	122.62	116.85
4	G	2101	FMN	O3P-P-O5'	-2.59	99.92	106.67
4	G	2101	FMN	C10-C4A-N5	-2.15	120.41	124.81
3	B	1901	PNS	C31-C29-C28	2.13	111.74	108.22
4	G	2101	FMN	C4A-C10-N1	-2.12	119.40	124.59
3	B	1901	PNS	C42-N41-C39	2.02	126.59	122.82

There are no chirality outliers.

All (7) torsion outliers are listed below:

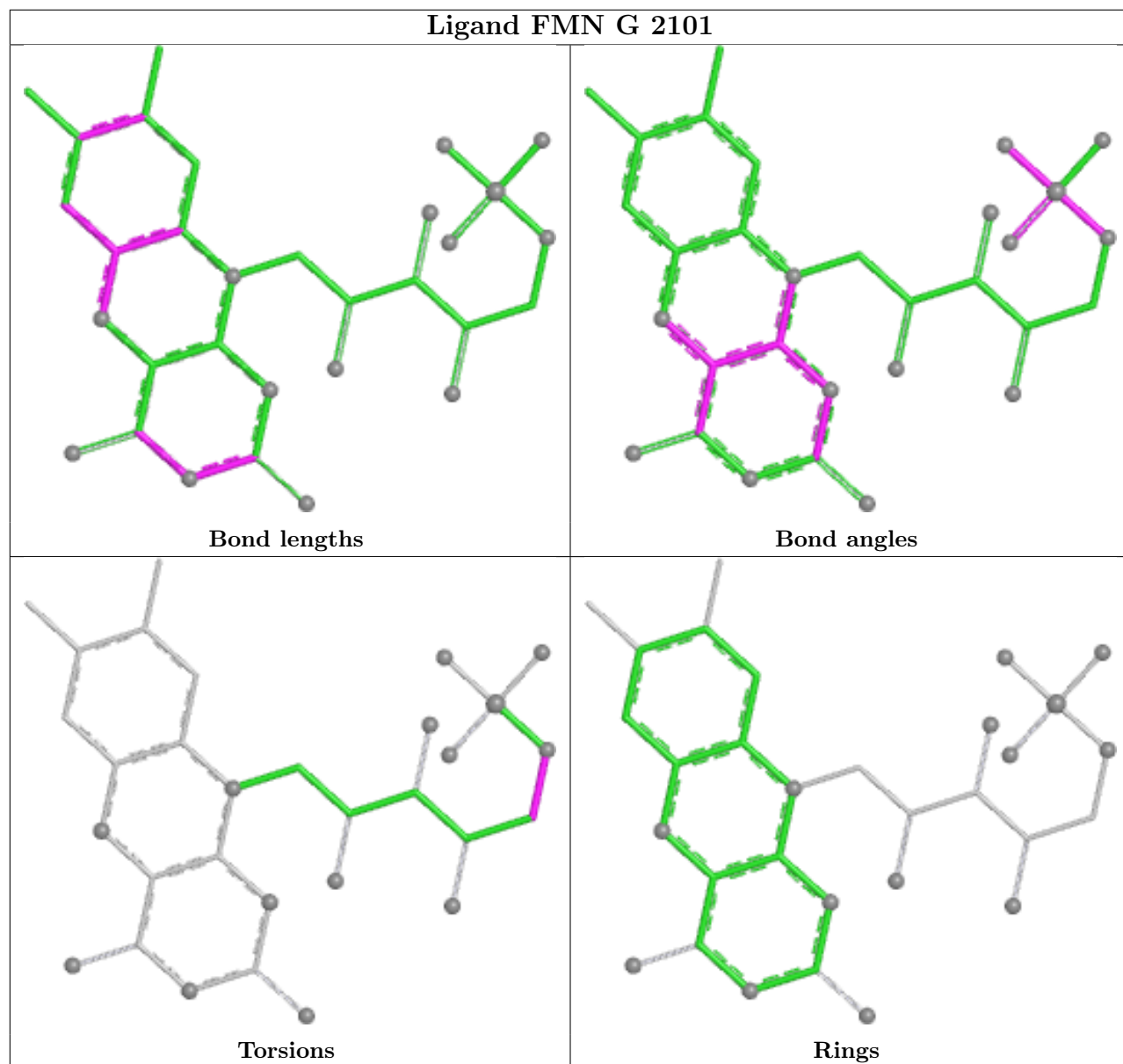
Mol	Chain	Res	Type	Atoms
3	B	1901	PNS	O27-C28-C29-C30
3	B	1901	PNS	O27-C28-C29-C31
3	B	1901	PNS	O27-C28-C29-C32
3	B	1901	PNS	N36-C37-C38-C39
3	B	1901	PNS	C38-C39-N41-C42
3	B	1901	PNS	O40-C39-N41-C42
4	G	2101	FMN	C4'-C5'-O5'-P

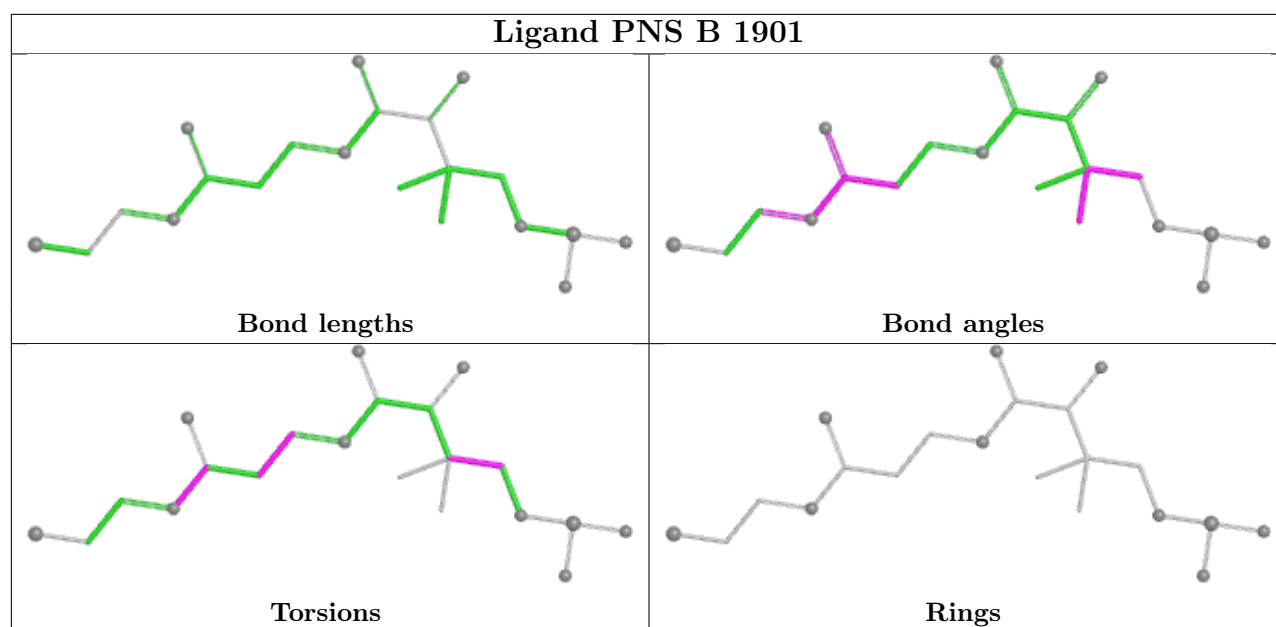
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	2101	FMN	2	0
3	B	1901	PNS	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 [i](#)

There are no chain breaks in this entry.

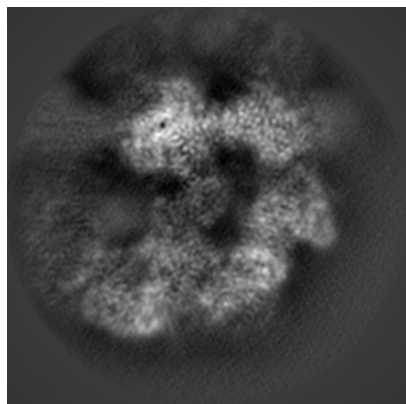
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17851. These allow visual inspection of the internal detail of the map and identification of artifacts.

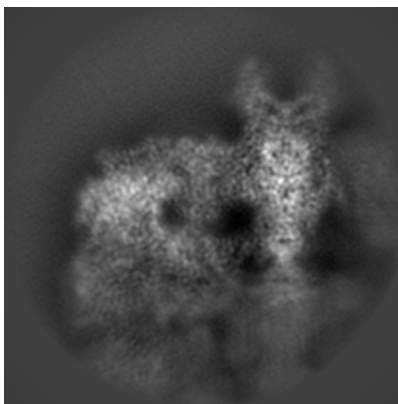
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

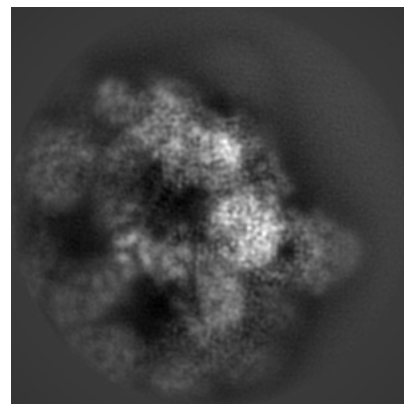
6.1.1 Primary map



X

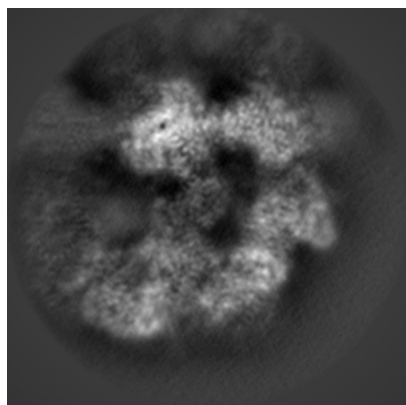


Y

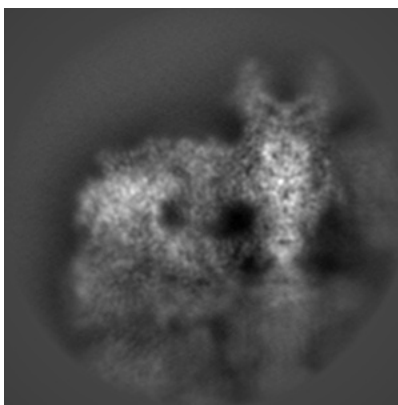


Z

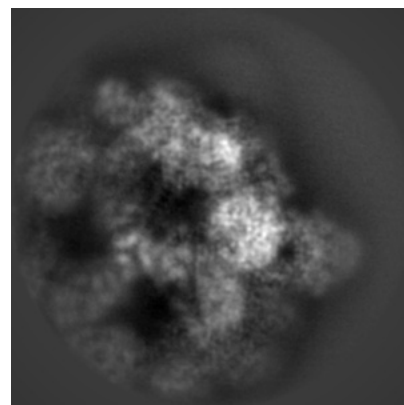
6.1.2 Raw map



X



Y

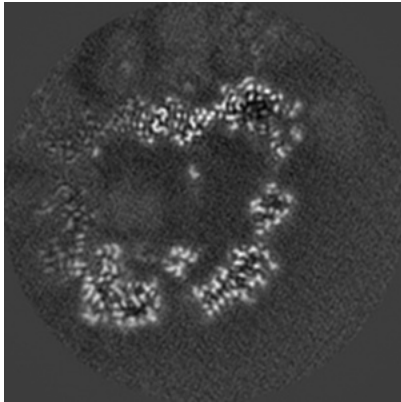


Z

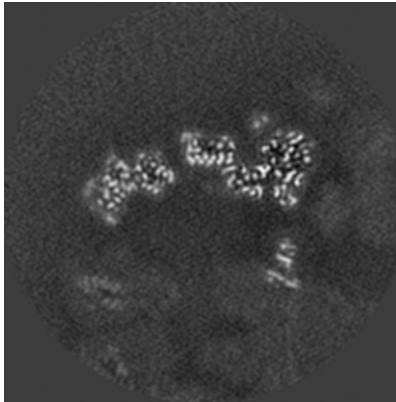
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

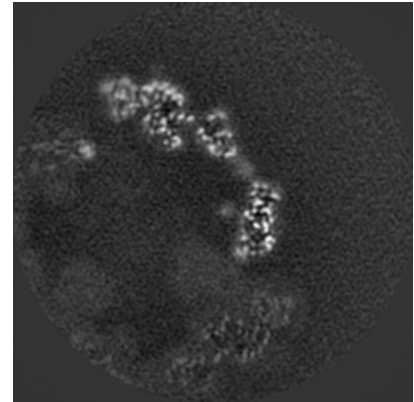
6.2.1 Primary map



X Index: 120

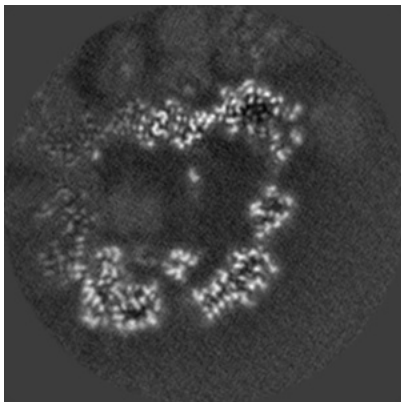


Y Index: 120

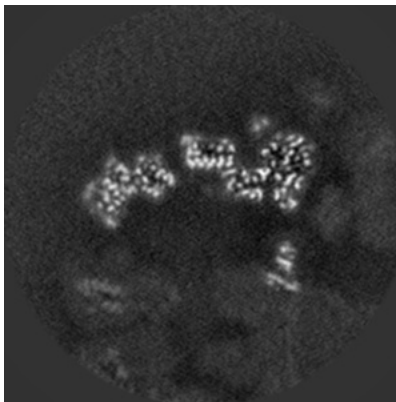


Z Index: 120

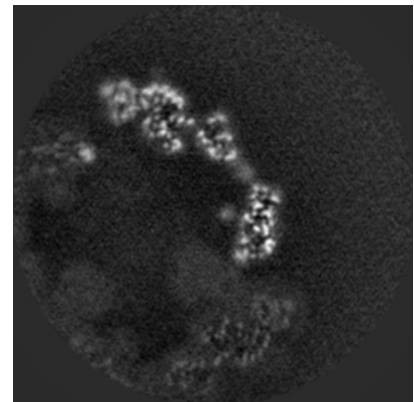
6.2.2 Raw map



X Index: 120



Y Index: 120

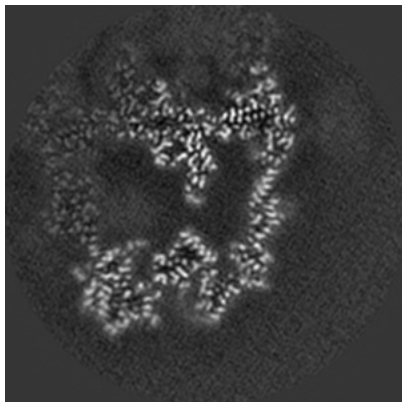


Z Index: 120

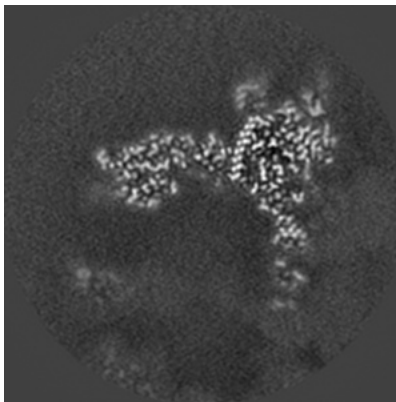
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

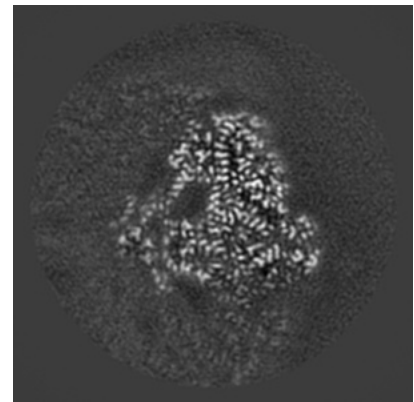
6.3.1 Primary map



X Index: 128

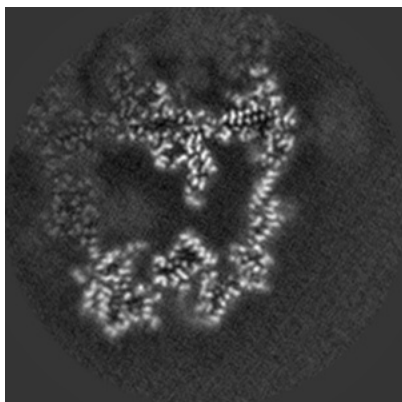


Y Index: 107

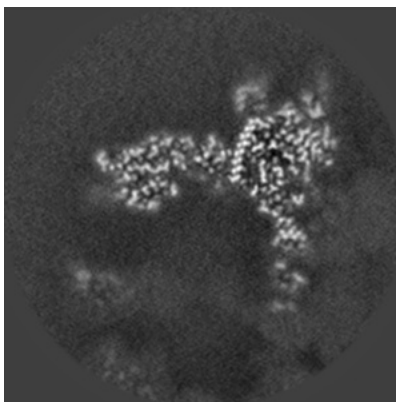


Z Index: 172

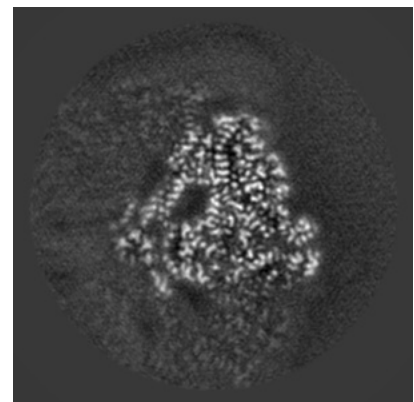
6.3.2 Raw map



X Index: 128



Y Index: 107

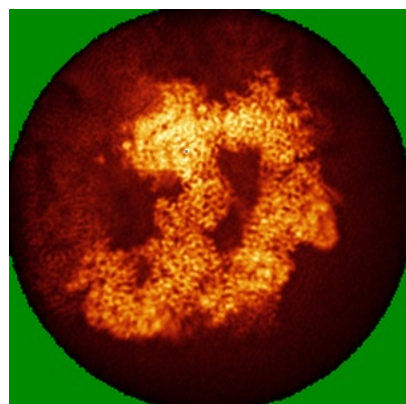


Z Index: 171

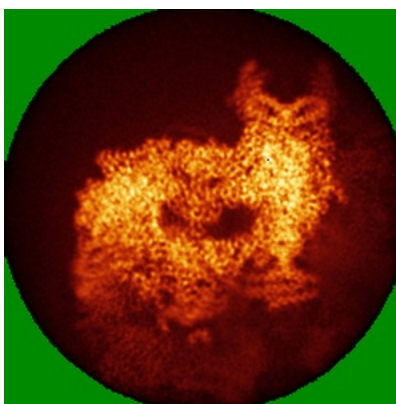
The images above show the largest variance slices of the map in three orthogonal directions.

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

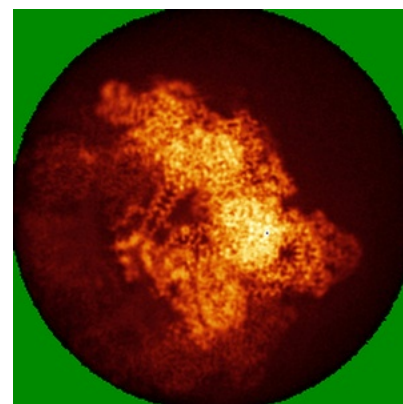
6.4.1 Primary map



X

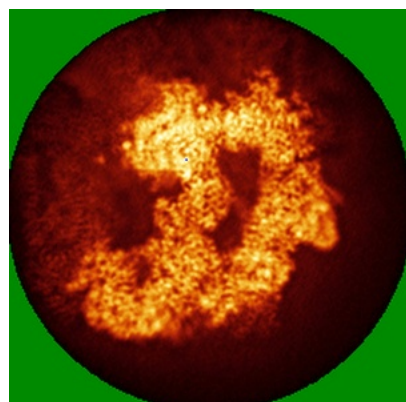


Y

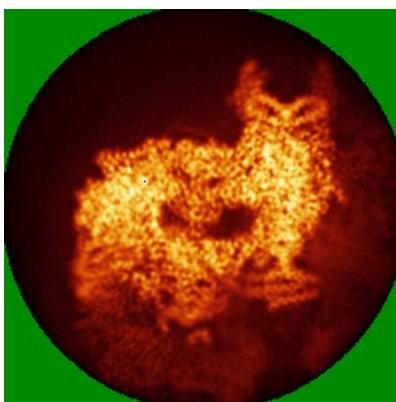


Z

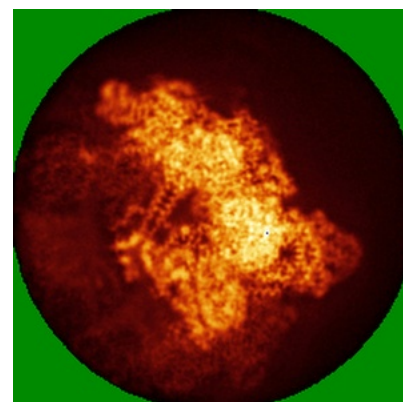
6.4.2 Raw map



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.

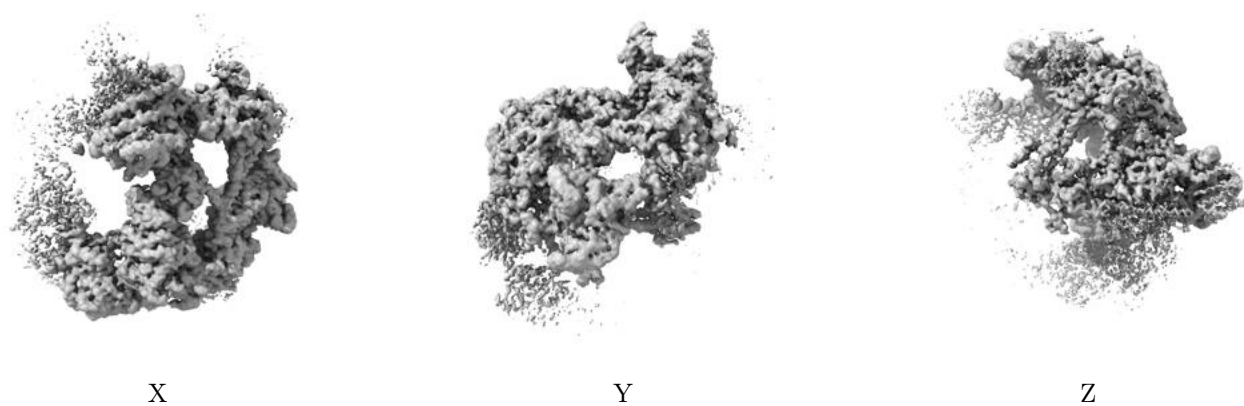
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

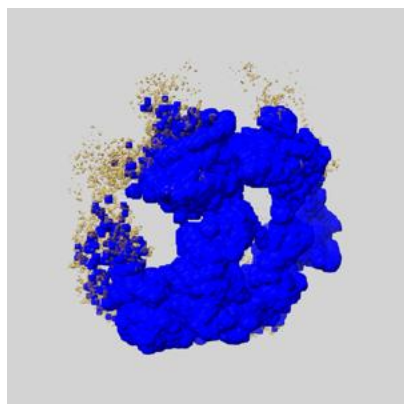
6.6 Mask visualisation [i](#)

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

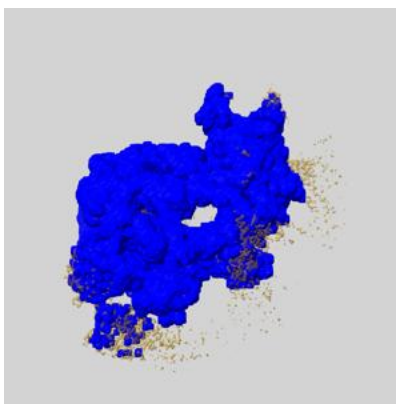
A mask typically either:

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

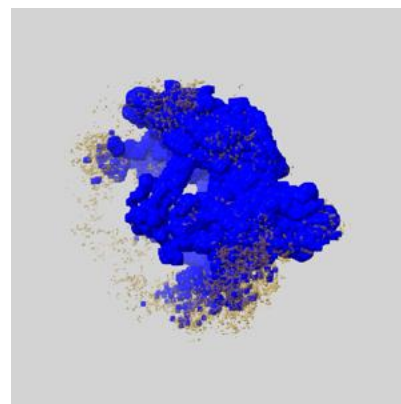
6.6.1 emd_17851_msk_1.map [i](#)



X



Y

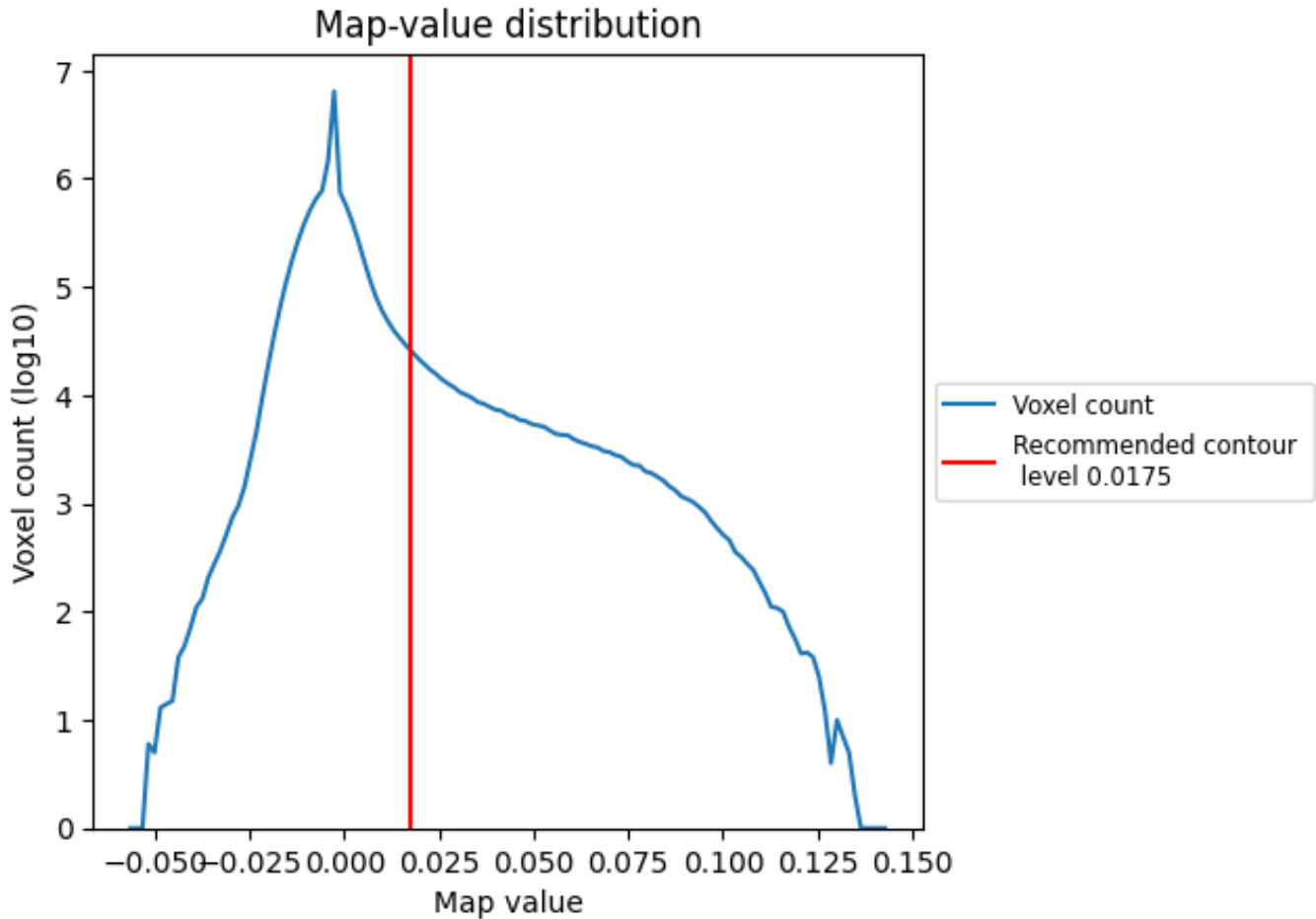


Z

7 Map analysis [i](#)

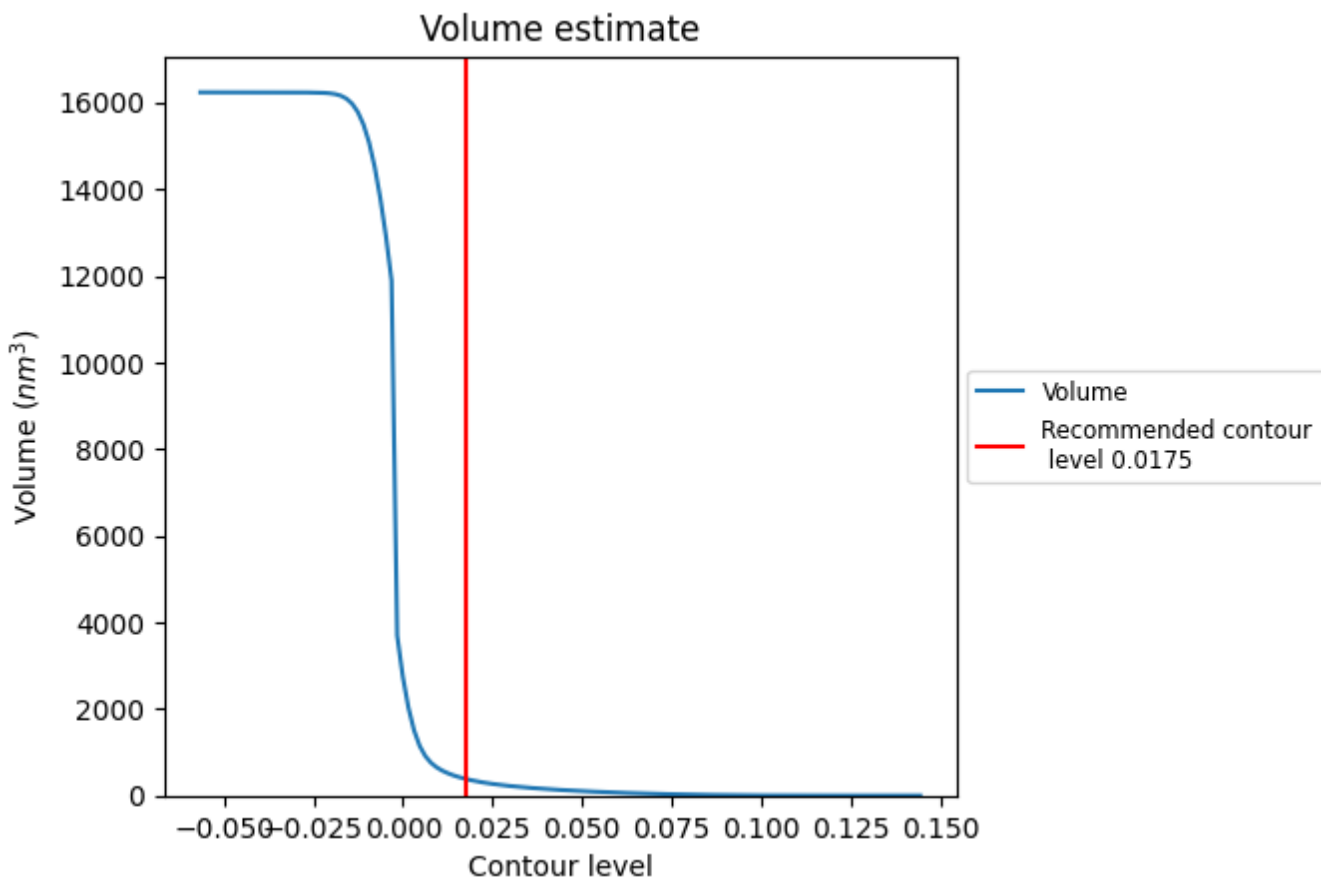
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

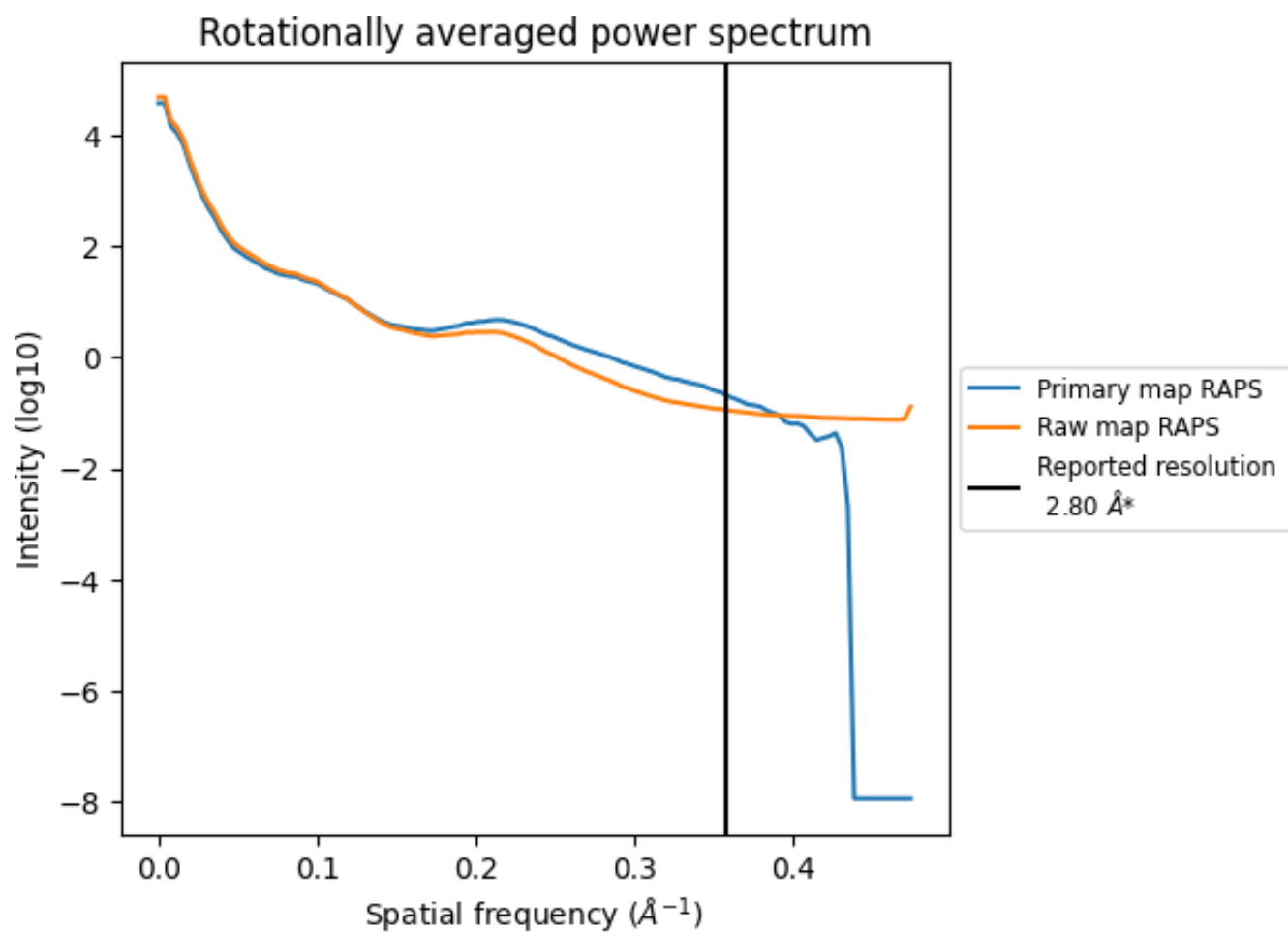
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 385 nm³; this corresponds to an approximate mass of 348 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](#)

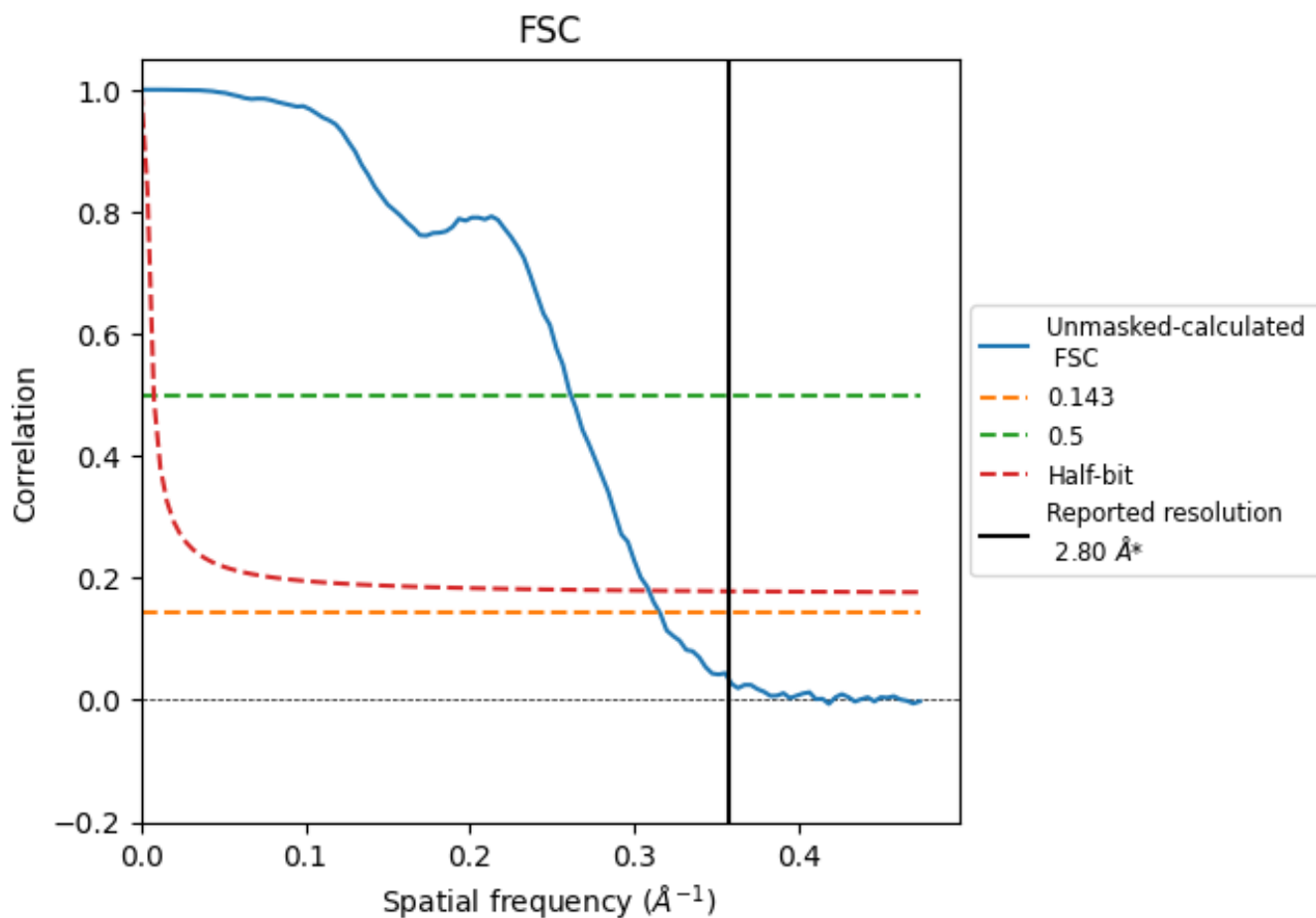


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

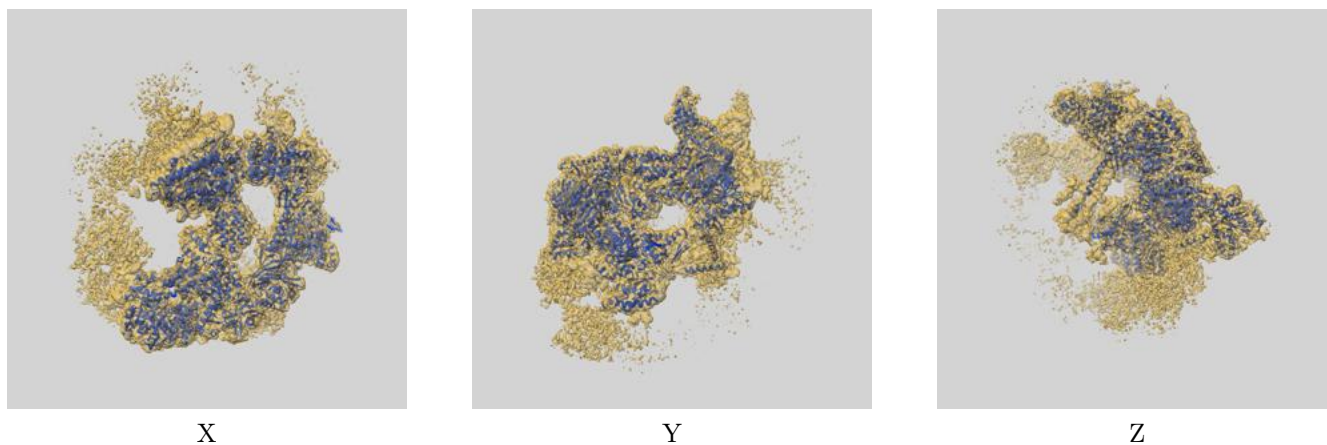
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.17	3.82	3.24

*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 3.17 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

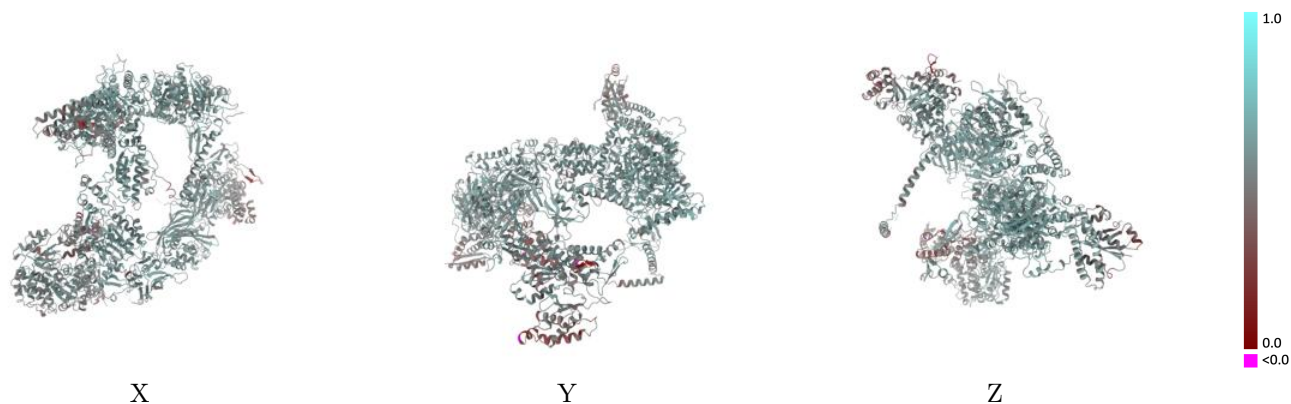
This section contains information regarding the fit between EMDB map EMD-17851 and PDB model 8PSF. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



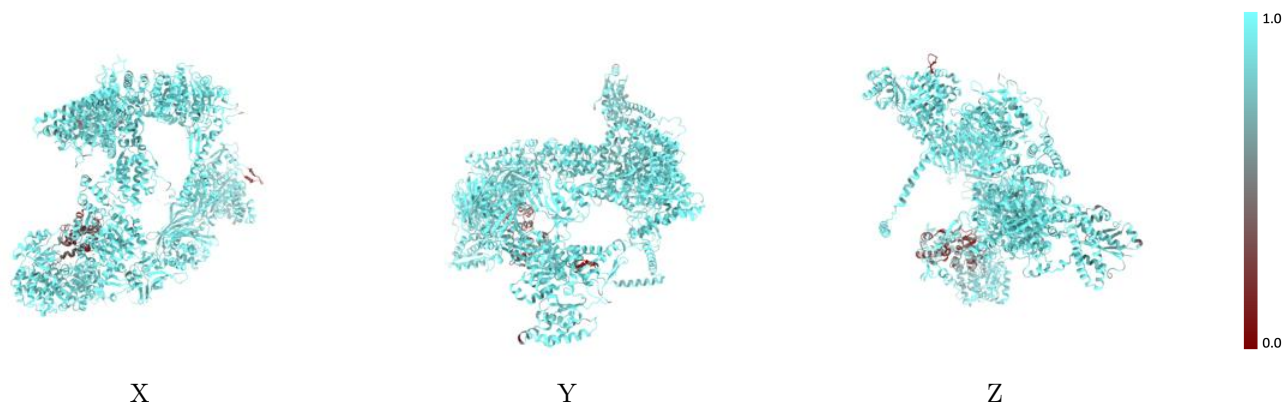
The images above show the 3D surface view of the map at the recommended contour level 0.0175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



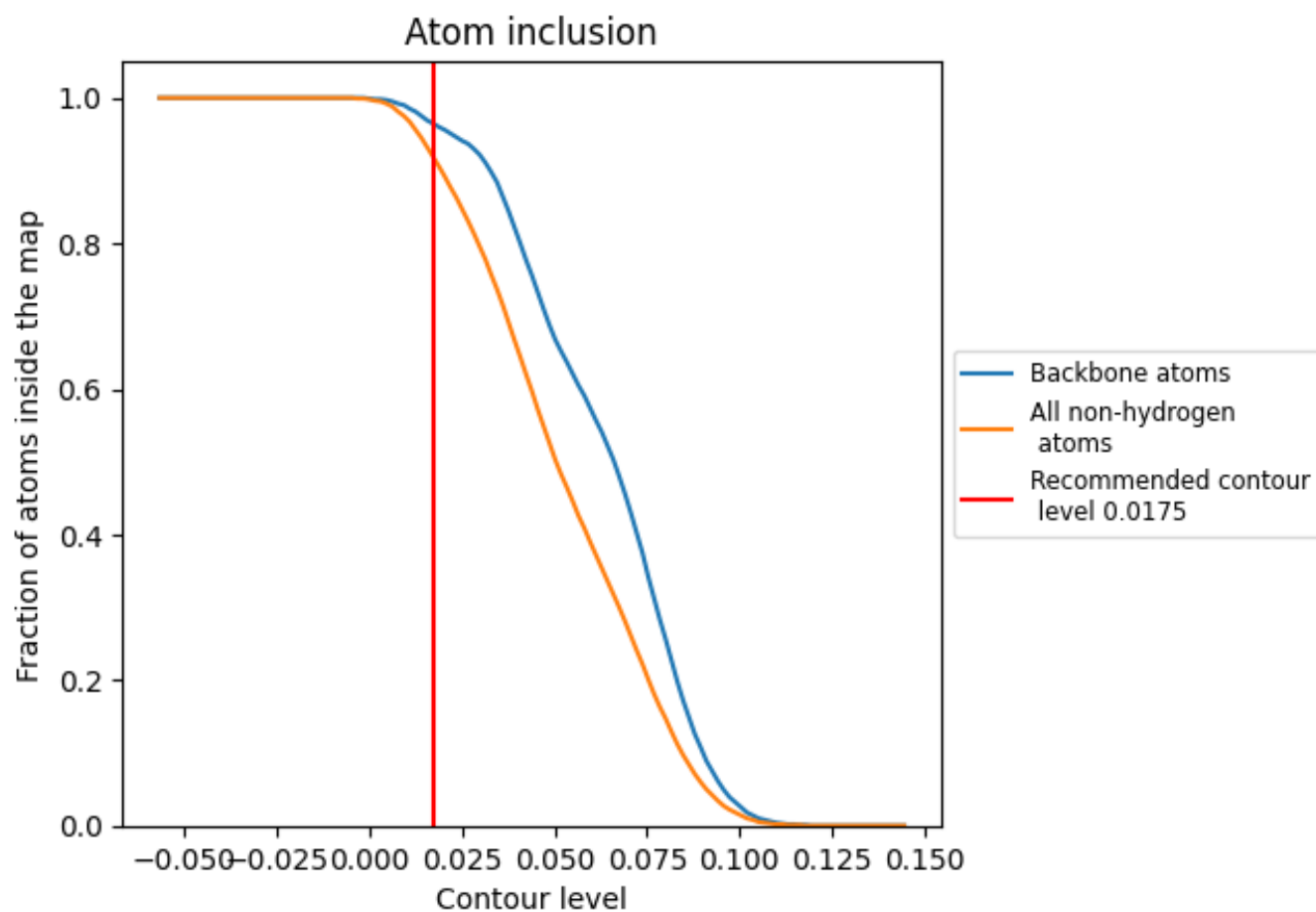
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0175).








9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.0175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9170	 0.5410
A	 0.9300	 0.5640
B	 0.2300	 0.3340
G	 0.9420	 0.5350

