



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:37 AM UTC

PDB ID : 7DGD / pdb_00007dgd
EMDB ID : EMD-30671
Title : apo state of class C GPCR
Authors : Zhang, J.Y.; Wu, L.J.; Luo, F.; Hua, T.; Liu, Z.J.
Deposited on : 2020-11-11
Resolution : 3.96 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:

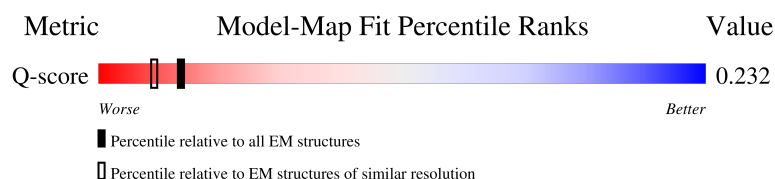
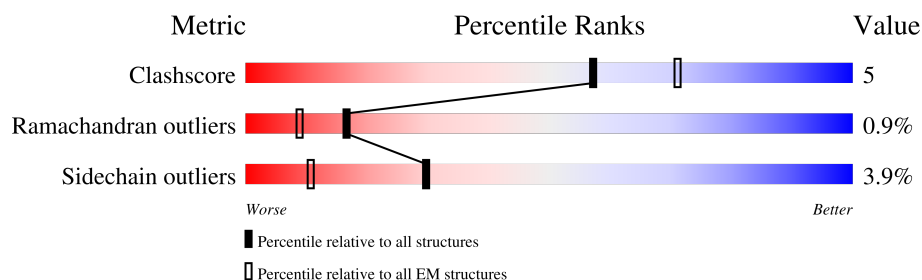
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.96 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	7646 (3.46 - 4.46)

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	833	 79% 14% • 6%
1	B	833	 79% 14% • 6%

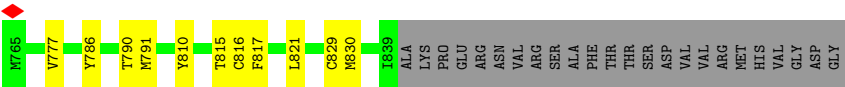
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12381 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 Metabotropic glutamate receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	786	Total	C	N	O	S	0	0
			6194	3982	1037	1126	49		
1	B	786	Total	C	N	O	S	0	0
			6187	3976	1037	1125	49		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	134512	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 ($e^-/\text{\AA}^2$)	1.78	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.925	Depositor
Minimum map value	-0.767	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	304.56, 304.56, 304.56	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.41, 1.41, 1.41	Depositor

5 Model quality

5.1 Standard geometry

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	0.89	0/6333	1.55	26/8591 (0.3%)
1	B	0.91	2/6325 (0.0%)	1.54	25/8580 (0.3%)
All	All	0.90	2/12658 (0.0%)	1.55	51/17171 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	2
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	80	GLU	CD-OE2	6.04	1.36	1.25
1	B	208	ASP	CG-OD2	5.91	1.36	1.25

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	309	VAL	N-CA-C	7.49	117.61	110.42
1	B	92	ASP	CA-CB-CG	7.09	119.69	112.60
1	A	308	VAL	CA-C-N	6.54	128.80	120.56
1	A	308	VAL	C-N-CA	6.54	128.80	120.56
1	B	318	ASP	CA-CB-CG	6.46	119.06	112.60
1	B	387	ASN	CA-CB-CG	6.31	118.91	112.60
1	A	512	ILE	N-CA-C	6.14	116.32	110.42
1	A	539	GLY	CA-C-N	5.96	128.59	120.54
1	A	539	GLY	C-N-CA	5.96	128.59	120.54
1	B	574	ASP	CA-CB-CG	5.94	118.54	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	317	SER	CA-C-N	5.92	129.01	120.38
1	A	317	SER	C-N-CA	5.92	129.01	120.38
1	B	107	ASP	CA-CB-CG	5.88	118.48	112.60
1	A	545	TRP	N-CA-C	5.84	117.31	111.07
1	A	780	ASN	CA-C-N	5.71	132.44	121.54
1	A	780	ASN	C-N-CA	5.71	132.44	121.54
1	B	810	TYR	CA-C-N	5.50	128.40	120.38
1	B	810	TYR	C-N-CA	5.50	128.40	120.38
1	B	572	ASN	CA-CB-CG	5.49	118.08	112.60
1	B	602	LEU	CA-C-N	5.49	126.07	119.98
1	B	602	LEU	C-N-CA	5.49	126.07	119.98
1	A	801	PHE	CA-C-N	5.45	125.66	120.43
1	A	801	PHE	C-N-CA	5.45	125.66	120.43
1	A	335	ASN	CA-CB-CG	5.44	118.04	112.60
1	B	483	ASN	CA-CB-CG	5.41	118.01	112.60
1	B	760	ASN	CA-C-N	5.38	125.95	119.98
1	B	760	ASN	C-N-CA	5.38	125.95	119.98
1	A	538	LYS	CA-C-N	5.33	131.87	121.41
1	A	538	LYS	C-N-CA	5.33	131.87	121.41
1	B	381	PRO	CA-C-N	5.32	125.88	119.98
1	B	381	PRO	C-N-CA	5.32	125.88	119.98
1	B	539	GLY	CA-C-N	5.30	127.92	120.28
1	B	539	GLY	C-N-CA	5.30	127.92	120.28
1	B	397	ASN	CA-CB-CG	5.26	117.86	112.60
1	A	583	VAL	CA-C-N	5.19	129.66	121.56
1	A	583	VAL	C-N-CA	5.19	129.66	121.56
1	A	255	ILE	CA-C-N	5.16	127.92	120.38
1	A	255	ILE	C-N-CA	5.16	127.92	120.38
1	B	259	ASP	CA-CB-CG	5.15	117.75	112.60
1	B	257	HIS	CE1-NE2-CD2	-5.15	103.85	109.00
1	A	231	HIS	CE1-NE2-CD2	-5.13	103.86	109.00
1	A	64	GLU	CA-C-N	5.13	129.69	122.46
1	A	64	GLU	C-N-CA	5.13	129.69	122.46
1	B	446	ASP	CA-CB-CG	5.07	117.67	112.60
1	A	55	HIS	CE1-NE2-CD2	-5.04	103.96	109.00
1	B	58	PRO	CA-C-N	5.03	128.37	120.82
1	B	58	PRO	C-N-CA	5.03	128.37	120.82
1	A	470	ASP	CA-CB-CG	5.02	117.62	112.60
1	A	442	MET	CA-C-N	5.01	126.35	120.09
1	A	442	MET	C-N-CA	5.01	126.35	120.09
1	B	365	ASN	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	353	TYR	Sidechain
1	A	499	THR	Peptide
1	A	589	SER	Peptide
1	A	672	TYR	Sidechain
1	B	161	GLY	Peptide
1	B	308	VAL	Peptide

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	6194	0	6226	56	0
1	B	6187	0	6221	65	0
All	All	12381	0	12447	119	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (119) 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:281:LEU:O	1:B:285:ARG:HG2	1.42	1.17
1:B:281:LEU:O	1:B:285:ARG:CG	1.93	1.16
1:B:281:LEU:O	1:B:285:ARG:CD	2.08	1.02
1:B:647:THR:HG23	1:B:663:LEU:HD11	1.52	0.91
1:B:281:LEU:O	1:B:285:ARG:HD3	1.69	0.91
1:A:648:LEU:HD11	1:A:812:ILE:HD11	1.64	0.80
1:B:634:ILE:HD11	1:B:678:LYS:HB2	1.67	0.76
1:A:507:ILE:HD11	1:A:512:ILE:HD13	1.68	0.74
1:B:285:ARG:NH2	1:B:520:VAL:HB	2.09	0.67
1:B:676:VAL:HG21	1:B:763:LEU:HD22	1.77	0.67
1:A:81:ALA:HB2	1:A:410:MET:HE3	1.79	0.64
1:A:81:ALA:HB1	1:A:414:ILE:HD11	1.79	0.64
1:B:720:LEU:HD22	1:B:759:TYR:CG	2.33	0.64
1:B:89:ILE:HD12	1:B:95:LEU:HD23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ILE:HG12	1:B:192:LEU:HD11	1.81	0.63
1:A:597:ILE:HD11	1:A:649:ILE:HG21	1.80	0.63
1:A:95:LEU:HD21	1:A:421:ALA:HB1	1.83	0.60
1:B:355:LEU:HD11	1:B:404:TYR:CD2	2.38	0.58
1:B:648:LEU:HD23	1:B:816:CYS:HB3	1.85	0.58
1:B:285:ARG:NH2	1:B:520:VAL:H	2.02	0.58
1:A:797:ILE:HG12	1:A:821:LEU:HD11	1.85	0.57
1:A:379:ARG:HH22	1:A:393:ILE:HD11	1.69	0.57
1:B:281:LEU:C	1:B:285:ARG:HG2	2.25	0.57
1:A:420:MET:HE1	1:A:450:LEU:HD21	1.88	0.56
1:B:359:LEU:HD21	1:B:383:HIS:NE2	2.22	0.54
1:B:764:ILE:HD11	1:B:791:MET:HB2	1.88	0.54
1:A:554:GLU:O	1:A:575:LEU:HD13	2.08	0.54
1:A:127:LEU:HD13	1:B:117:GLU:HG2	1.90	0.54
1:A:393:ILE:H	1:A:393:ILE:HD12	1.73	0.53
1:B:535:VAL:HG13	1:B:545:TRP:CD1	2.44	0.53
1:A:116:LEU:HD21	1:A:170:GLN:O	2.08	0.53
1:B:184:ALA:HB3	1:B:203:ARG:HB3	1.91	0.53
1:B:475:ALA:HB1	1:B:476:PRO:HD2	1.91	0.52
1:A:830:MET:HA	1:A:830:MET:HE2	1.90	0.52
1:A:648:LEU:HD23	1:A:816:CYS:HB3	1.92	0.52
1:A:673:SER:O	1:A:677:THR:HG23	2.09	0.52
1:B:357:LEU:HD21	1:B:362:ASN:HD22	1.75	0.51
1:A:338:ILE:HD11	1:A:512:ILE:HD11	1.92	0.51
1:A:661:ARG:HD3	1:A:725:ILE:HG12	1.93	0.51
1:A:227:VAL:HG12	1:A:286:VAL:HG23	1.92	0.51
1:A:676:VAL:HA	1:A:679:THR:HG22	1.92	0.50
1:B:790:THR:HG21	1:B:830:MET:HG2	1.93	0.50
1:A:400:LEU:H	1:A:400:LEU:HD12	1.77	0.50
1:A:693:ILE:HD12	1:B:693:ILE:HG13	1.92	0.50
1:B:680:ASN:HA	1:B:683:ALA:HB3	1.93	0.50
1:A:581:ILE:HD12	1:A:582:PRO:HD3	1.94	0.50
1:B:39:ALA:HB2	1:B:366:PRO:HD2	1.94	0.50
1:B:644:CYS:HA	1:B:663:LEU:HD22	1.94	0.49
1:B:445:ILE:H	1:B:445:ILE:HD12	1.77	0.49
1:B:189:SER:HB3	1:B:192:LEU:HD13	1.94	0.49
1:B:76:ILE:HD11	1:B:367:TRP:HB2	1.94	0.49
1:A:648:LEU:HD13	1:A:663:LEU:HD22	1.93	0.49
1:B:116:LEU:HD21	1:B:170:GLN:O	2.13	0.49
1:B:520:VAL:HG12	1:B:521:ARG:N	2.28	0.48
1:B:691:LYS:HD3	1:B:777:VAL:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ARG:HH11	1:B:203:ARG:HG2	1.77	0.48
1:B:285:ARG:HH22	1:B:520:VAL:H	1.60	0.48
1:B:634:ILE:HD11	1:B:678:LYS:CB	2.41	0.47
1:A:653:THR:H	1:A:656:SER:HB3	1.79	0.47
1:A:99:ILE:HD11	1:A:428:HIS:CE1	2.50	0.47
1:A:355:LEU:HD11	1:A:404:TYR:CD2	2.49	0.47
1:A:647:THR:HB	1:A:659:LEU:HD21	1.97	0.47
1:A:278:ARG:HD2	1:A:308:VAL:HG11	1.96	0.47
1:A:475:ALA:HB1	1:A:476:PRO:HD2	1.96	0.46
1:A:529:LEU:H	1:A:529:LEU:HD23	1.80	0.46
1:A:570:TRP:CD1	1:A:740:LYS:HZ1	2.33	0.46
1:B:284:ALA:HA	1:B:522:SER:HB3	1.97	0.46
1:A:570:TRP:HD1	1:A:581:ILE:HD13	1.80	0.46
1:B:285:ARG:HH22	1:B:520:VAL:HB	1.80	0.46
1:A:587:GLU:HG2	1:A:651:LYS:H	1.80	0.46
1:B:380:LEU:HD23	1:B:383:HIS:CD2	2.51	0.46
1:B:734:LEU:HD12	1:B:744:LEU:HD13	1.98	0.46
1:A:230:VAL:CG2	1:A:277:LEU:HD21	2.46	0.45
1:A:160:ILE:HD13	1:A:183:ILE:HD11	1.96	0.45
1:A:278:ARG:HA	1:A:281:LEU:HD21	1.98	0.45
1:A:380:LEU:HD21	1:A:394:CYS:SG	2.56	0.45
1:A:676:VAL:HG11	1:A:763:LEU:HD21	1.99	0.45
1:A:581:ILE:H	1:A:581:ILE:HG13	1.68	0.45
1:A:638:ILE:HG21	1:A:827:LEU:HD12	1.99	0.45
1:A:663:LEU:HD23	1:A:664:VAL:N	2.32	0.44
1:A:672:TYR:CE2	1:A:675:LEU:HD23	2.52	0.44
1:B:663:LEU:HA	1:B:667:SER:HB3	1.98	0.44
1:B:227:VAL:HG11	1:B:288:VAL:HG23	2.00	0.44
1:B:274:LEU:HD11	1:B:299:LEU:HD12	1.99	0.43
1:B:422:HIS:CD2	1:B:459:PHE:HB3	2.53	0.43
1:B:673:SER:O	1:B:677:THR:HG23	2.19	0.43
1:B:745:ILE:HG22	1:B:746:CYS:O	2.19	0.43
1:A:630:LEU:HD11	1:A:681:ARG:HD3	2.00	0.43
1:B:355:LEU:HD21	1:B:404:TYR:CG	2.54	0.43
1:B:535:VAL:HG22	1:B:545:TRP:NE1	2.33	0.43
1:A:497:VAL:O	1:A:507:ILE:HD12	2.19	0.43
1:B:535:VAL:HG13	1:B:545:TRP:CG	2.53	0.43
1:A:683:ALA:HB1	1:A:770:TYR:CD2	2.54	0.42
1:A:734:LEU:HD11	1:A:742:VAL:HG12	2.01	0.42
1:B:288:VAL:HG22	1:B:315:ILE:HD11	2.01	0.42
1:B:786:TYR:O	1:B:790:THR:HG23	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:817:PHE:CE2	1:B:821:LEU:HD11	2.54	0.42
1:A:225:THR:H	1:A:522:SER:CB	2.32	0.42
1:A:602:LEU:HD23	1:A:605:LEU:HD12	2.02	0.42
1:B:521:ARG:HD3	1:B:521:ARG:HA	1.43	0.42
1:A:662:LEU:HA	1:A:666:LEU:HD13	2.01	0.42
1:B:65:ARG:HH22	1:B:117:GLU:HB2	1.84	0.41
1:B:556:VAL:H	1:B:575:LEU:HB3	1.85	0.41
1:B:172:GLN:HE22	1:B:198:TYR:HA	1.84	0.41
1:B:192:LEU:HD23	1:B:201:PHE:CZ	2.55	0.41
1:B:790:THR:HG22	1:B:829:CYS:HB3	2.01	0.41
1:A:86:LEU:HD22	1:A:103:SER:HB3	2.01	0.41
1:A:350:PHE:CZ	1:A:354:PHE:HB2	2.56	0.41
1:A:774:THR:HB	1:A:784:ALA:HB1	2.03	0.41
1:A:127:LEU:HA	1:A:130:ILE:HG22	2.02	0.41
1:B:285:ARG:HB3	1:B:312:PHE:HB3	2.03	0.41
1:B:314:LEU:HD23	1:B:314:LEU:H	1.85	0.41
1:B:520:VAL:CG1	1:B:521:ARG:N	2.83	0.41
1:B:648:LEU:HD21	1:B:815:THR:OG1	2.20	0.41
1:B:105:ILE:N	1:B:105:ILE:HD12	2.36	0.41
1:B:634:ILE:HA	1:B:674:ALA:HB1	2.03	0.41
1:A:597:ILE:HD11	1:A:649:ILE:CG2	2.49	0.40
1:B:171:VAL:HG13	1:B:182:GLN:HE22	1.86	0.40
1:A:684:ARG:HE	1:A:699:ARG:HB3	1.87	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	782/833 (94%)	694 (89%)	78 (10%)	10 (1%)	9	41
1	B	782/833 (94%)	712 (91%)	66 (8%)	4 (0%)	24	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1564/1666 (94%)	1406 (90%)	144 (9%)	14 (1%)	16	48

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	SER
1	A	539	GLY
1	A	781	PHE
1	A	518	GLY
1	A	546	ILE
1	B	402	GLU
1	B	521	ARG
1	B	747	ASN
1	A	402	GLU
1	A	521	ARG
1	A	321	ALA
1	B	744	LEU
1	A	556	VAL
1	A	582	PRO

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	685/723 (95%)	663 (97%)	22 (3%)	34	56
1	B	684/723 (95%)	653 (96%)	31 (4%)	24	48
All	All	1369/1446 (95%)	1316 (96%)	53 (4%)	30	51

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	84	HIS
1	A	86	LEU
1	A	103	SER
1	A	111	HIS

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Mol	Chain	Res	Type
1	A	120	ILE
1	A	215	MET
1	A	217	ASP
1	A	274	LEU
1	A	335	ASN
1	A	377	GLN
1	A	398	GLU
1	A	445	ILE
1	A	484	LEU
1	A	535	VAL
1	A	544	CYS
1	A	553	ASN
1	A	557	GLN
1	A	581	ILE
1	A	676	VAL
1	A	679	THR
1	A	746	CYS
1	A	830	MET
1	B	82	MET
1	B	111	HIS
1	B	118	GLN
1	B	125	ASP
1	B	171	VAL
1	B	189	SER
1	B	205	VAL
1	B	220	LYS
1	B	227	VAL
1	B	268	LYS
1	B	276	LYS
1	B	281	LEU
1	B	359	LEU
1	B	371	PHE
1	B	387	ASN
1	B	429	HIS
1	B	440	ASP
1	B	446	ASP
1	B	483	ASN
1	B	521	ARG
1	B	524	CYS
1	B	541	VAL
1	B	547	CYS
1	B	572	ASN

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Mol	Chain	Res	Type
1	B	584	ARG
1	B	590	ASN
1	B	639	PHE
1	B	657	CYS
1	B	686	LEU
1	B	747	ASN
1	B	762	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	HIS
1	A	118	GLN
1	A	170	GLN
1	A	173	ASN
1	A	231	HIS
1	A	264	ASN
1	A	365	ASN
1	A	374	HIS
1	A	506	ASN
1	A	513	GLN
1	A	515	ASN
1	A	557	GLN
1	A	680	ASN
1	A	780	ASN
1	B	77	GLN
1	B	172	GLN
1	B	173	ASN
1	B	182	GLN
1	B	257	HIS
1	B	343	GLN
1	B	362	ASN
1	B	365	ASN
1	B	389	ASN
1	B	557	GLN
1	B	572	ASN
1	B	590	ASN
1	B	706	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

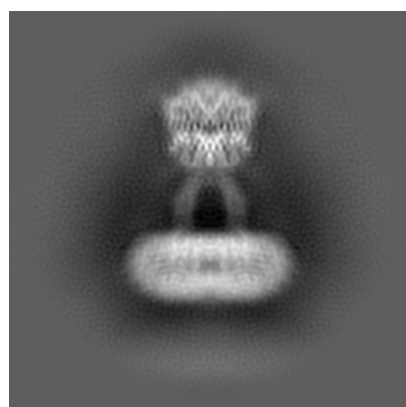
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30671. These allow visual inspection of the internal detail of the map and identification of artifacts.

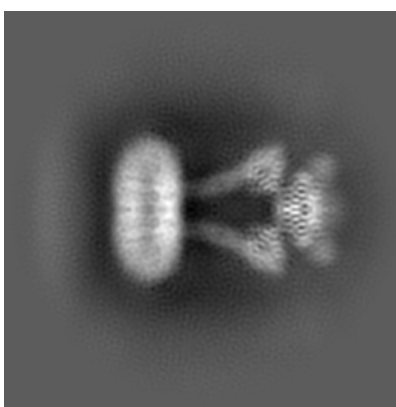
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

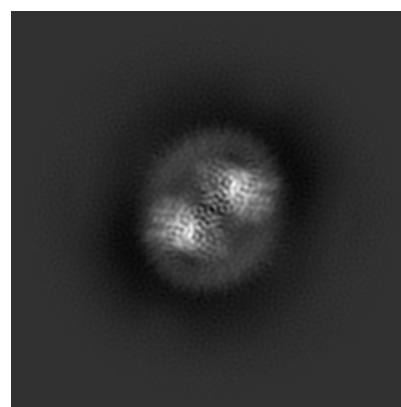
6.1.1 Primary map



X



Y

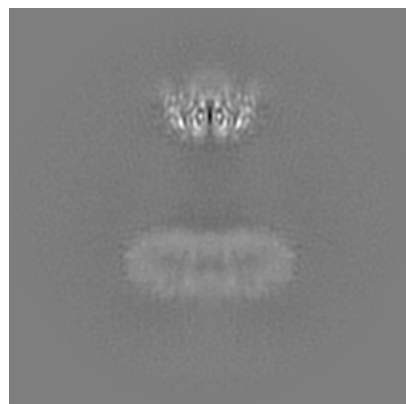


Z

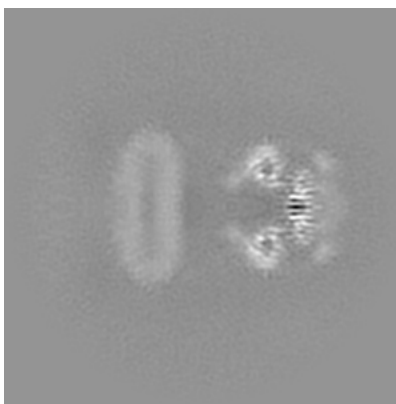
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

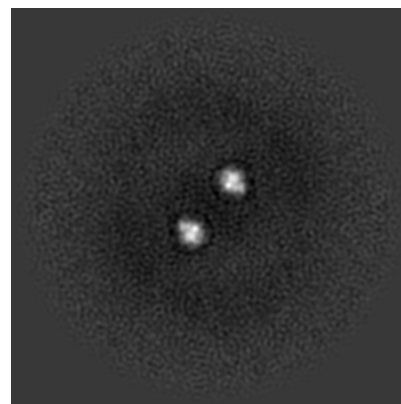
6.2.1 Primary map



X Index: 108



Y Index: 108

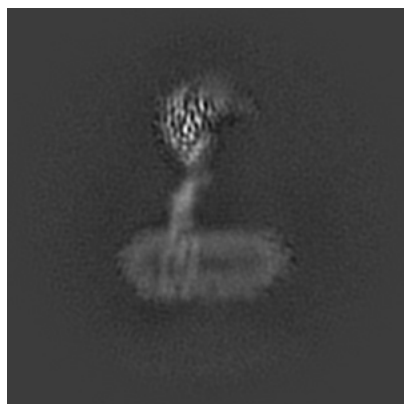


Z Index: 108

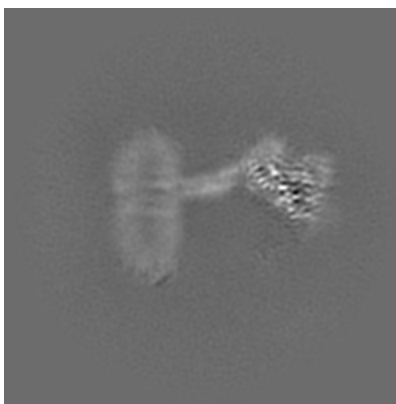
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

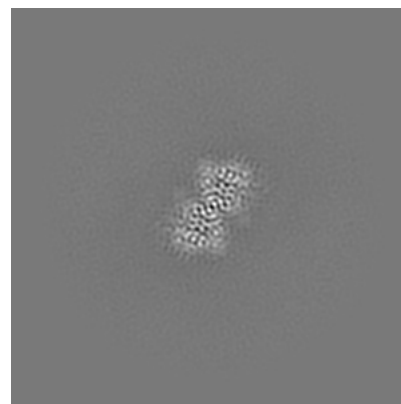
6.3.1 Primary map



X Index: 97



Y Index: 120

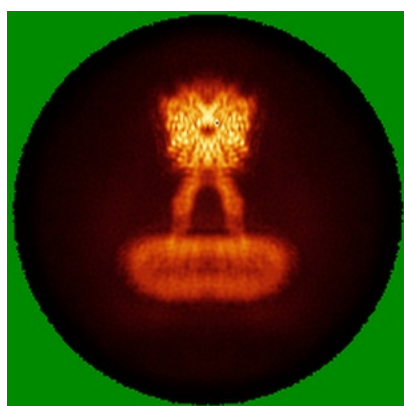


Z Index: 157

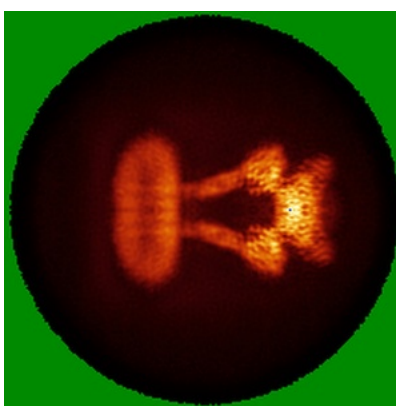
The images above show the largest variance slices of the map in three orthogonal directions.

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

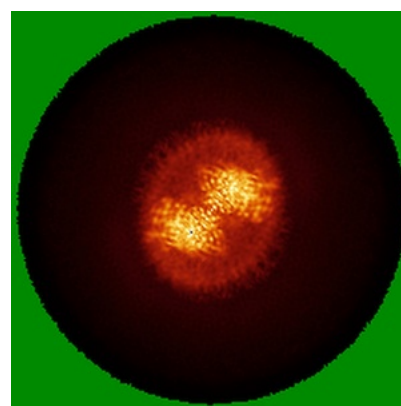
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

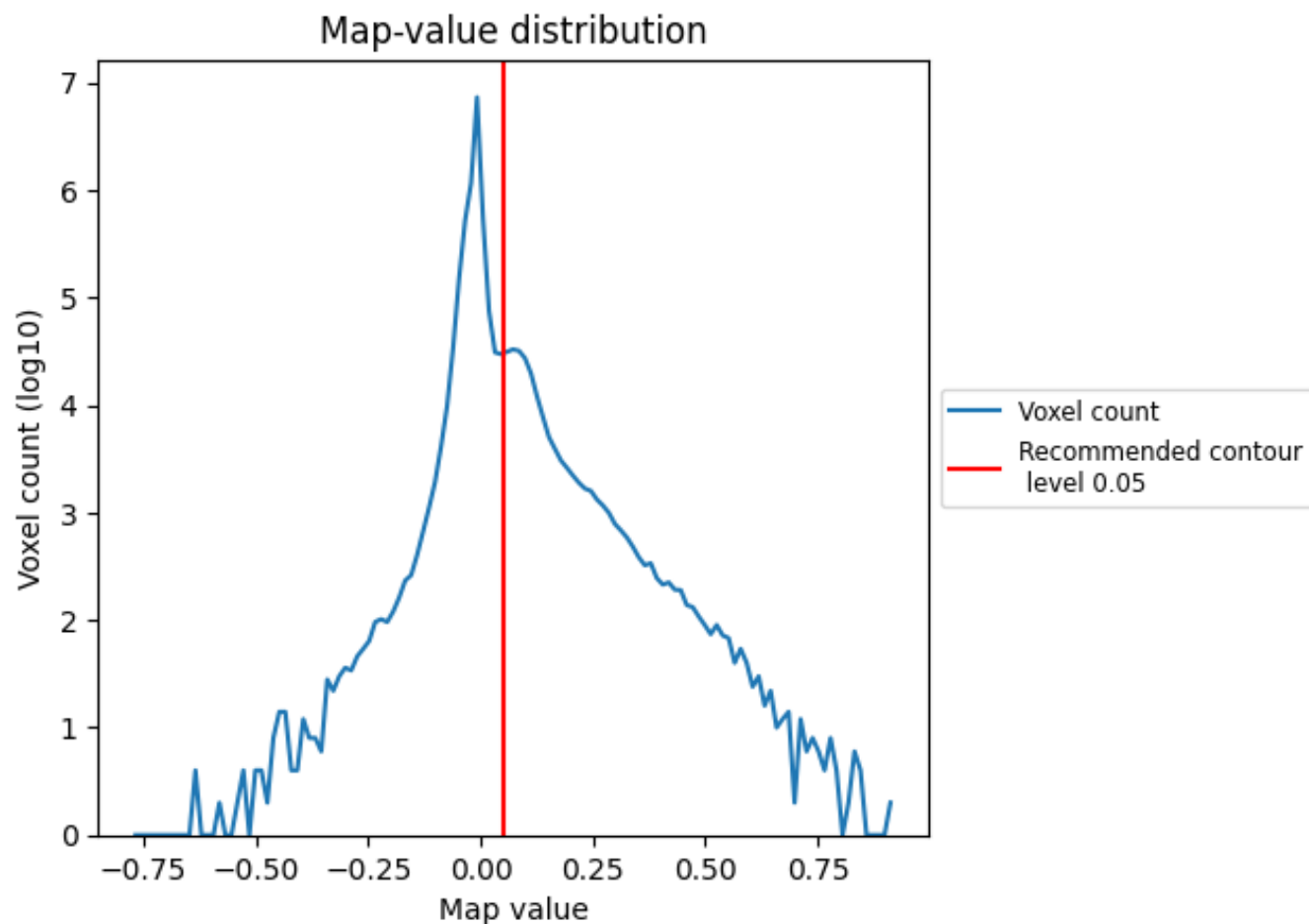
6.6 Mask visualisation

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

7 Map analysis [i](#)

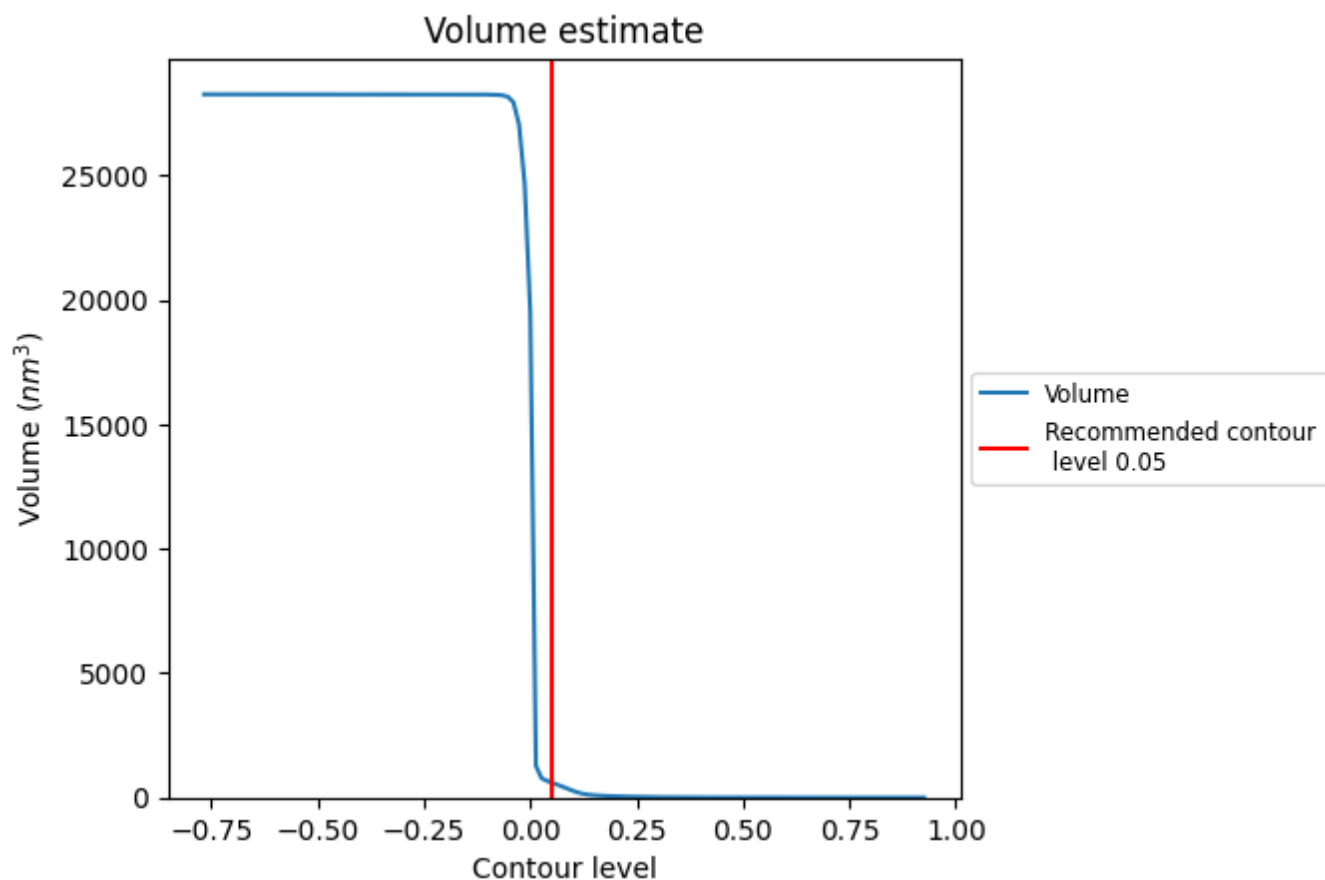
This section contains the results of statistical analysis of the map.

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.

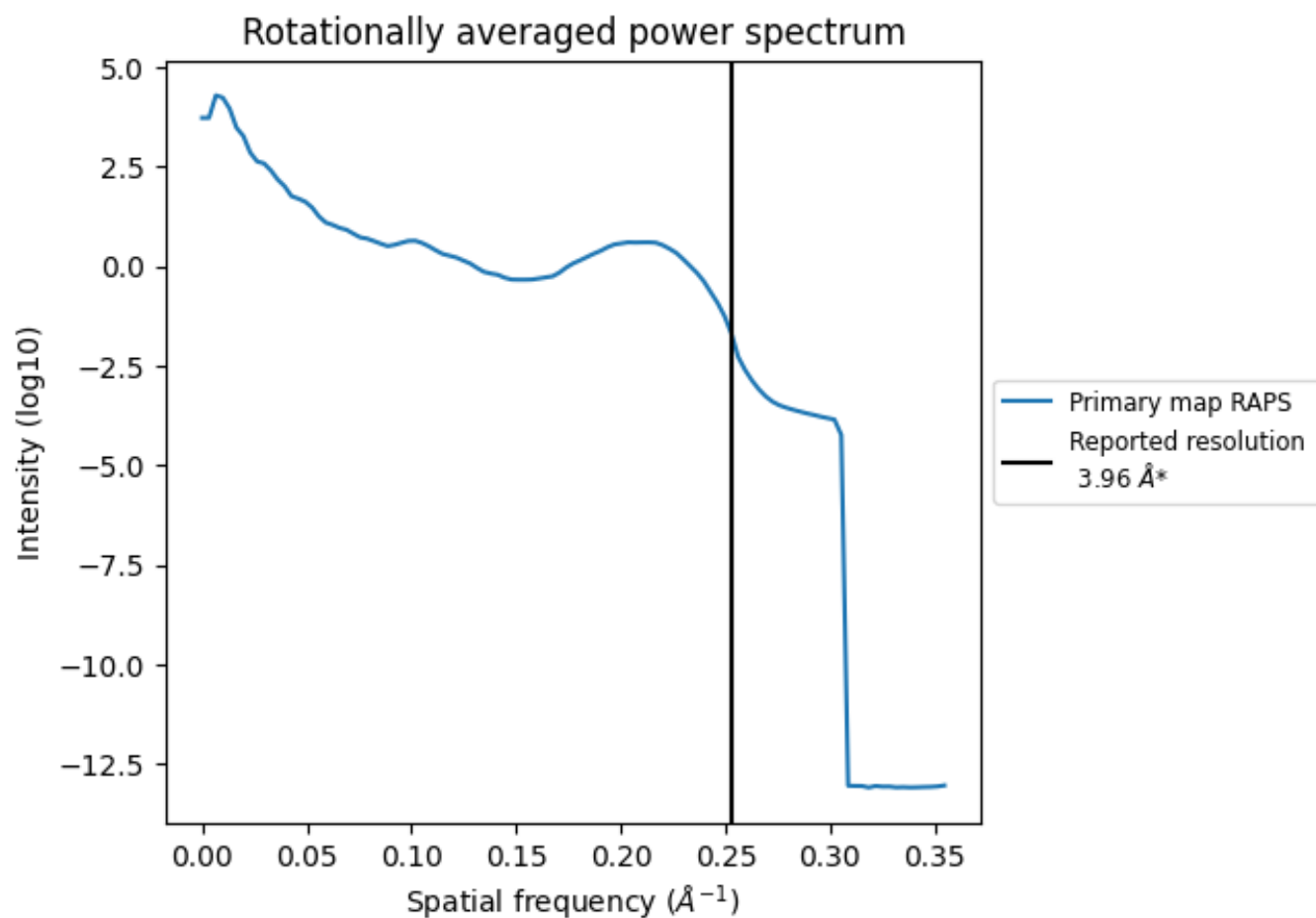
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 602 nm³; this corresponds to an approximate mass of 544 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 0.253 Å⁻¹

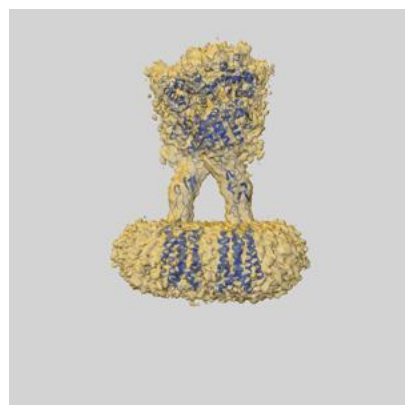
8 Fourier-Shell correlation

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

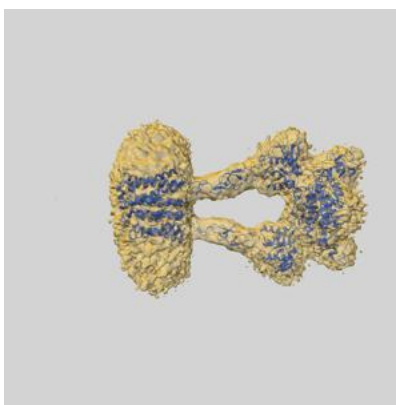
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30671 and PDB model 7DGD. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

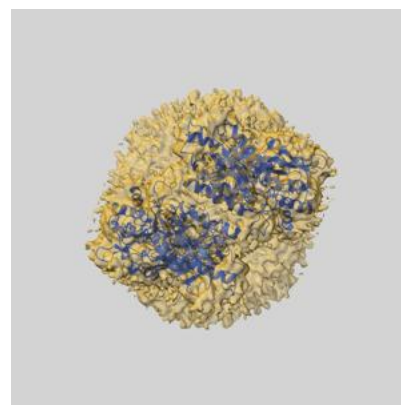
9.1 Map-model overlay [i](#)



X



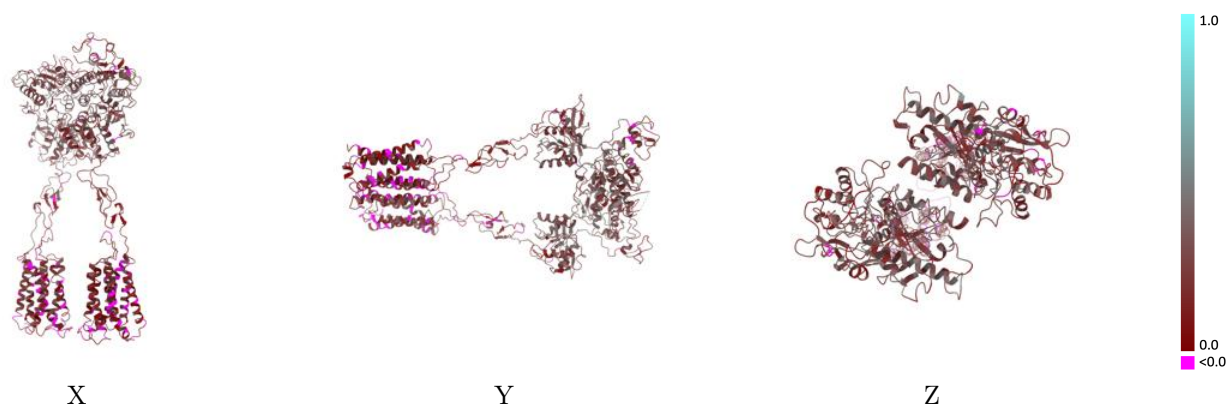
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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](#)

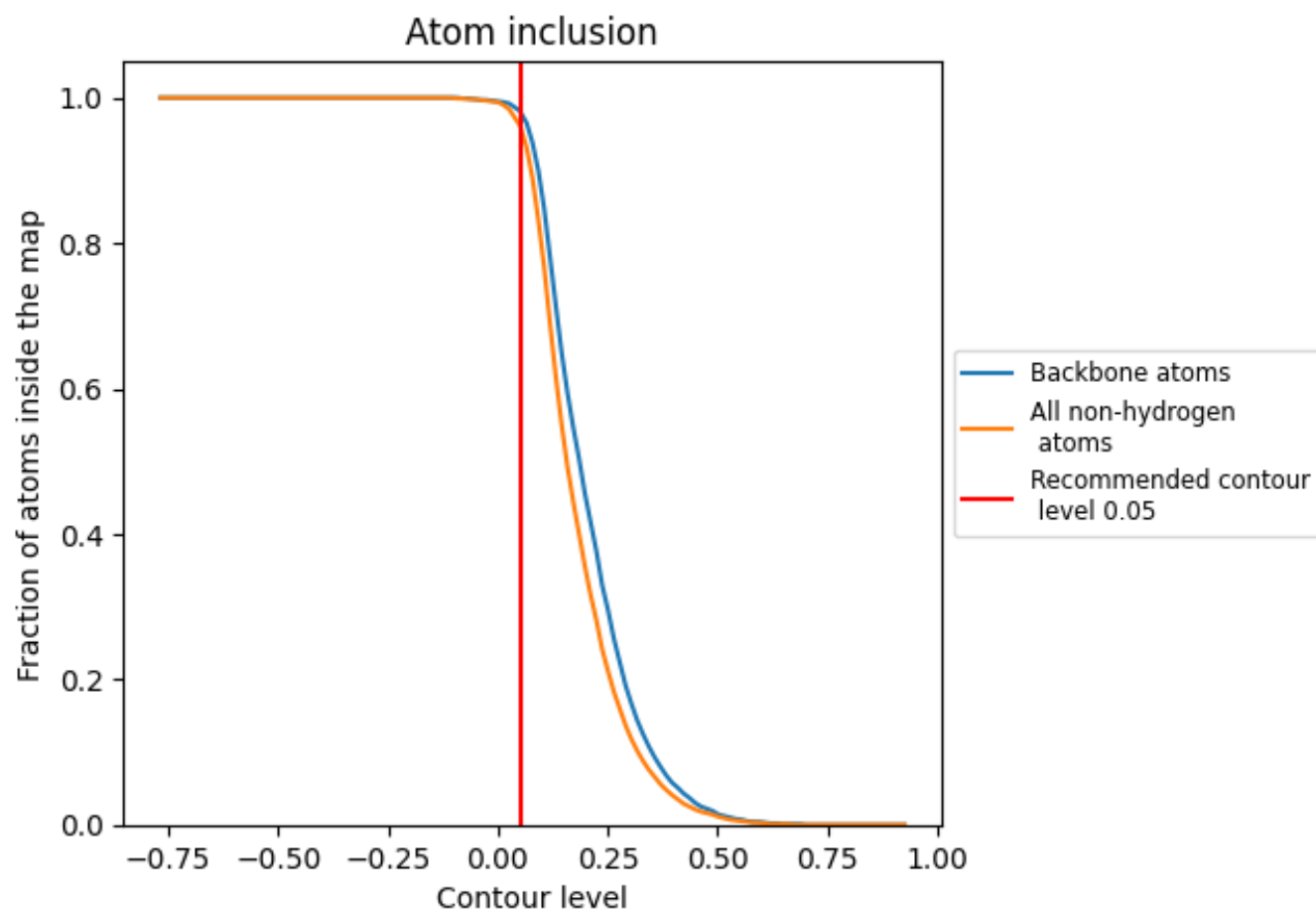


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9620	0.2320
A	0.9620	0.2300
B	0.9610	0.2350

