



Full wwPDB EM Validation Report ⓘ

Oct 1, 2024 – 04:47 PM JST

PDB ID : 8IJB
EMDB ID : EMD-35484
Title : Cryo-EM structure of human HCAR2-Gi complex with acipimox
Authors : Pan, X.; Fang, Y.
Deposited on : 2023-02-27
Resolution : 3.23 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
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) : 2.39

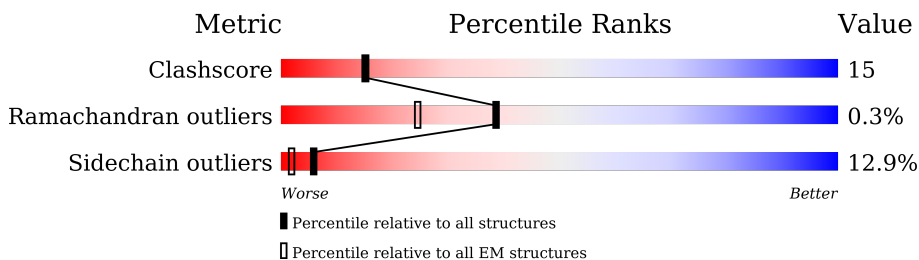
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 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	294	 46% 40% 12% •
2	B	337	 71% 26% •
3	C	351	 47% 12% • 38%
4	G	56	 23% 75% 20% 5%
5	S	248	 66% 25% • 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8842 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 Hydroxycarboxylic acid receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	294	Total	C	N	O	S	0	0
			2301	1532	381	368	20		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	337	Total	C	N	O	S	0	0
			2592	1599	466	506	21		

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	216	Total	C	N	O	S	0	0
			1712	1089	285	326	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	203	ALA	GLY	engineered mutation	UNP P63096
C	326	SER	ALA	engineered mutation	UNP P63096

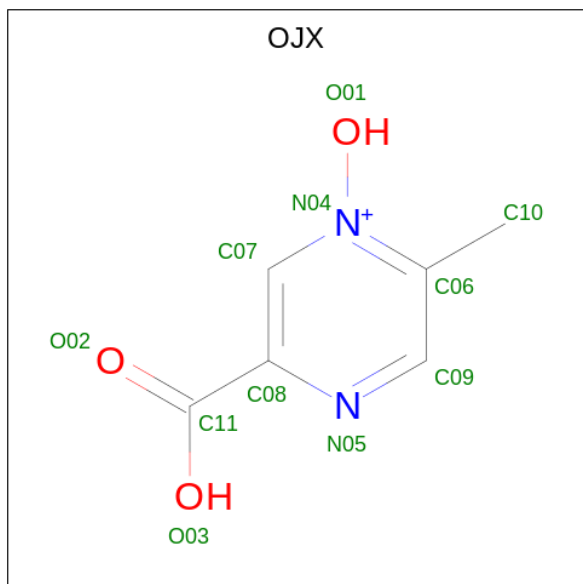
- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	56	Total	C	N	O	S	0	0
			434	271	76	84	3		

- Molecule 5 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	233	Total	C	N	O	S	0	0
			1792	1135	296	351	10		

- Molecule 6 is 5-methyl-4-oxidanyl-pyrazin-4-ium-2-carboxylic acid (three-letter code: OJX) (formula: $C_6H_7N_2O_3$) (labeled as "Ligand of Interest" by depositor).

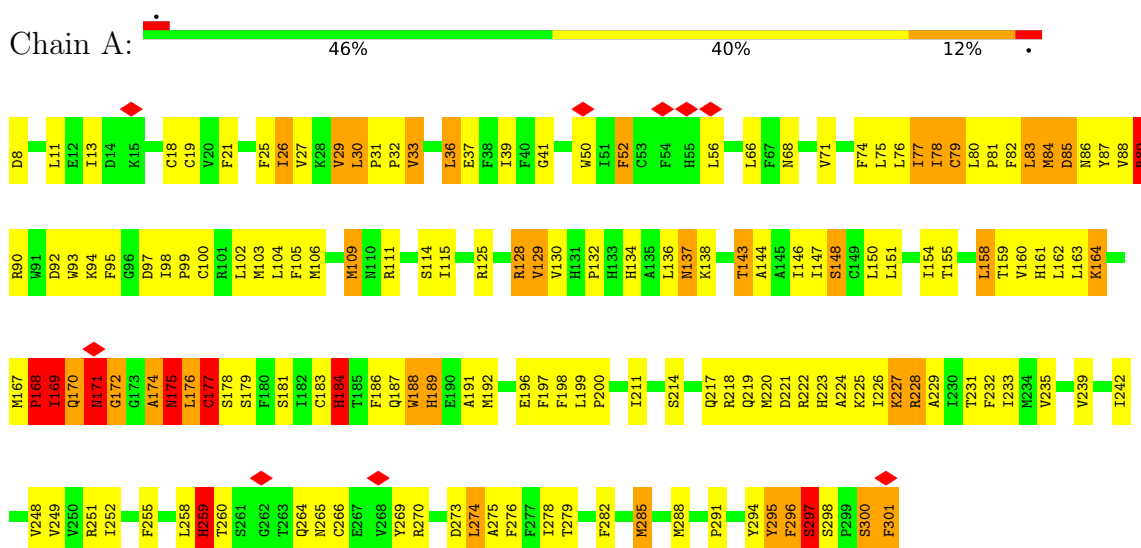


Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			11	6	2	3	

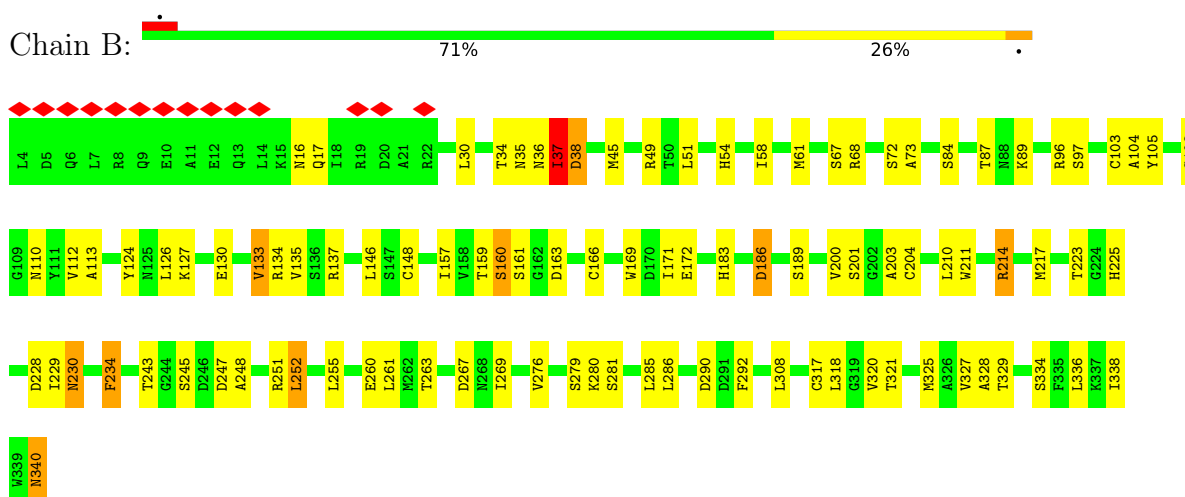
3 Residue-property plots [i](#)

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: Hydroxycarboxylic acid receptor 2



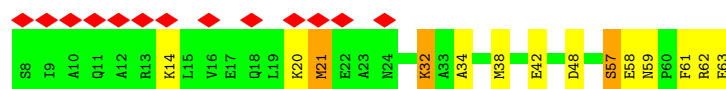
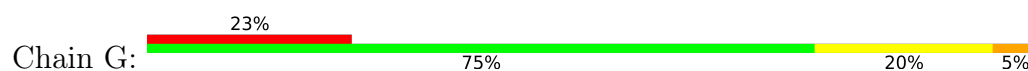
• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



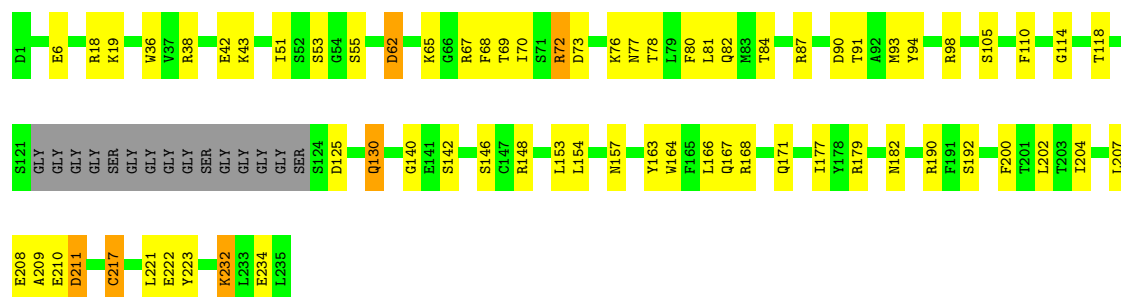
• Molecule 3: Guanine nucleotide-binding protein G(i) subunit alpha-1



- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 5: scFv16



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	221940	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 ($e^-/\text{\AA}^2$)	56	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.682	Depositor
Minimum map value	-0.395	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.1	Depositor
Map size (\AA)	272.0, 272.0, 272.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.52	1/2366 (0.0%)	1.16	30/3222 (0.9%)
2	B	0.26	0/2639	0.63	5/3577 (0.1%)
3	C	0.29	0/1741	0.75	8/2339 (0.3%)
4	G	0.30	0/440	0.62	1/592 (0.2%)
5	S	0.29	0/1836	0.57	0/2488
All	All	0.36	1/9022 (0.0%)	0.81	44/12218 (0.4%)

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
5	S	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	168	PRO	N-CD	6.16	1.56	1.47

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	SER	N-CA-CB	19.02	139.03	110.50
1	A	171	ASN	CB-CA-C	18.98	148.37	110.40
1	A	294	TYR	N-CA-C	12.77	145.47	111.00
2	B	35	ASN	N-CA-CB	-12.54	88.02	110.60
1	A	259	HIS	CB-CA-C	-12.54	85.32	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	323	PHE	N-CA-C	-12.50	77.24	111.00
1	A	295	TYR	N-CA-CB	-12.41	88.26	110.60
1	A	300	SER	CB-CA-C	-11.71	87.84	110.10
3	C	324	THR	N-CA-CB	-11.28	88.87	110.30
1	A	168	PRO	CB-CA-C	10.95	139.39	112.00
1	A	175	ASN	N-CA-CB	-10.26	92.13	110.60
1	A	169	ILE	N-CA-CB	9.71	133.13	110.80
3	C	327	THR	N-CA-C	-9.50	85.34	111.00
1	A	296	PHE	N-CA-C	-9.47	85.44	111.00
1	A	184	HIS	CB-CA-C	-9.20	92.00	110.40
1	A	177	CYS	N-CA-C	8.86	134.91	111.00
2	B	37	ILE	N-CA-C	-8.72	87.47	111.00
1	A	260	THR	N-CA-C	-8.57	87.87	111.00
1	A	174	ALA	CB-CA-C	-8.46	97.40	110.10
1	A	301	PHE	N-CA-C	-8.34	88.50	111.00
1	A	171	ASN	N-CA-C	-7.71	90.19	111.00
1	A	300	SER	N-CA-C	7.62	131.57	111.00
1	A	89	ARG	N-CA-C	-7.25	91.42	111.00
3	C	327	THR	CB-CA-C	7.24	131.16	111.60
1	A	172	GLY	N-CA-C	-7.21	95.06	113.10
2	B	36	ASN	N-CA-C	-7.20	91.56	111.00
1	A	174	ALA	N-CA-CB	-7.01	100.28	110.10
3	C	328	ASP	N-CA-CB	-6.89	98.20	110.60
1	A	184	HIS	N-CA-C	6.65	128.96	111.00
1	A	260	THR	N-CA-CB	6.63	122.89	110.30
1	A	175	ASN	CB-CA-C	6.45	123.31	110.40
2	B	37	ILE	N-CA-CB	6.42	125.56	110.80
1	A	168	PRO	N-CA-CB	6.38	110.95	103.30
3	C	328	ASP	N-CA-C	6.37	128.20	111.00
1	A	294	TYR	CB-CA-C	-6.25	97.91	110.40
1	A	298	SER	N-CA-C	-6.18	94.32	111.00
1	A	168	PRO	N-CA-C	-6.14	96.14	112.10
1	A	301	PHE	N-CA-CB	6.10	121.58	110.60
1	A	297	SER	CB-CA-C	-5.94	98.81	110.10
2	B	38	ASP	CB-CG-OD1	5.91	123.62	118.30
3	C	328	ASP	CB-CA-C	-5.64	99.11	110.40
1	A	176	LEU	N-CA-C	5.37	125.50	111.00
4	G	21	MET	CA-CB-CG	5.08	121.94	113.30
3	C	323	PHE	CB-CA-C	5.00	120.40	110.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111	ARG	Sidechain
1	A	128	ARG	Sidechain
1	A	228	ARG	Sidechain
1	A	89	ARG	Sidechain
5	S	223	TYR	Peptide

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	2301	0	2279	124	0
2	B	2592	0	2499	51	0
3	C	1712	0	1672	39	0
4	G	434	0	442	12	0
5	S	1792	0	1724	37	0
6	A	11	0	0	0	0
All	All	8842	0	8616	256	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 15.

All (256) 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:259:HIS:CG	1:A:259:HIS:O	1.92	1.14
1:A:176:LEU:HD12	1:A:176:LEU:O	1.54	1.04
1:A:259:HIS:O	1:A:259:HIS:CD2	2.09	1.04
1:A:31:PRO:HB2	1:A:32:PRO:HD3	1.58	0.86
5:S:94:TYR:O	5:S:114:GLY:HA2	1.75	0.86
1:A:291:PRO:HA	1:A:295:TYR:HD2	1.39	0.85
1:A:86:ASN:O	1:A:89:ARG:O	1.94	0.83
1:A:151:LEU:HA	1:A:154:ILE:HD12	1.59	0.83
2:B:159:THR:HG1	2:B:169:TRP:HE1	1.22	0.82
1:A:187:GLN:HG3	1:A:189:HIS:H	1.43	0.82
1:A:143:THR:HA	1:A:146:ILE:HD12	1.65	0.79
1:A:297:SER:OG	1:A:297:SER:O	1.97	0.77
4:G:58:GLU:N	4:G:58:GLU:OE2	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD12	1:A:39:ILE:HD11	1.67	0.76
1:A:291:PRO:HA	1:A:295:TYR:CD2	2.20	0.75
2:B:54:HIS:HE2	2:B:72:SER:HG	1.32	0.75
1:A:36:LEU:HA	1:A:39:ILE:HG12	1.69	0.72
3:C:290:TYR:CD1	3:C:302:TYR:CE2	2.78	0.71
1:A:115:ILE:HD12	1:A:196:GLU:HG3	1.73	0.70
1:A:160:VAL:HG23	1:A:163:LEU:HD12	1.74	0.69
3:C:290:TYR:CD1	3:C:291:ALA:N	2.62	0.68
3:C:290:TYR:CD1	3:C:302:TYR:HE2	2.11	0.68
3:C:322:HIS:CE1	3:C:323:PHE:O	2.47	0.68
3:C:44:SER:OG	3:C:46:LYS:NZ	2.27	0.67
1:A:300:SER:O	1:A:300:SER:OG	2.13	0.67
1:A:36:LEU:HA	1:A:39:ILE:CG1	2.25	0.65
2:B:276:VAL:HG13	2:B:285:LEU:HD11	1.78	0.65
5:S:91:THR:HG23	5:S:118:THR:HA	1.78	0.65
1:A:168:PRO:HB2	1:A:170:GLN:OE1	1.97	0.65
5:S:190:ARG:NH2	5:S:211:ASP:OD2	2.29	0.65
1:A:144:ALA:O	1:A:148:SER:OG	2.15	0.65
2:B:110:ASN:HD22	2:B:127:LYS:HD2	1.61	0.64
3:C:348:LEU:HB3	3:C:354:PHE:HB2	1.80	0.64
2:B:286:LEU:HD22	2:B:327:VAL:HG11	1.80	0.64
2:B:34:THR:HG22	4:G:38:MET:HE2	1.78	0.63
2:B:34:THR:HG22	4:G:38:MET:CE	2.30	0.62
1:A:176:LEU:HD12	1:A:176:LEU:C	2.13	0.61
1:A:154:ILE:O	1:A:158:LEU:HG	2.00	0.61
3:C:322:HIS:ND1	3:C:323:PHE:O	2.34	0.61
1:A:170:GLN:C	1:A:174:ALA:O	2.39	0.60
1:A:187:GLN:HG3	1:A:189:HIS:HB2	1.83	0.60
3:C:208:ARG:O	3:C:212:ILE:HB	2.00	0.60
5:S:43:LYS:HE2	5:S:43:LYS:N	2.16	0.60
1:A:169:ILE:HB	1:A:176:LEU:HB3	1.83	0.59
5:S:130:GLN:NE2	5:S:217:CYS:SG	2.64	0.59
2:B:325:MET:O	2:B:340:ASN:ND2	2.36	0.59
1:A:223:HIS:CD2	1:A:225:LYS:HG2	2.37	0.59
2:B:320:VAL:HG22	2:B:327:VAL:HG22	1.84	0.59
2:B:45:MET:HG3	2:B:308:LEU:HD11	1.85	0.59
2:B:67:SER:HB2	2:B:321:THR:HB	1.83	0.59
5:S:153:LEU:HD23	5:S:221:LEU:HD12	1.84	0.58
1:A:74:PHE:O	1:A:78:ILE:HG23	2.03	0.58
1:A:26:ILE:HD11	1:A:90:ARG:HG3	1.86	0.58
1:A:74:PHE:O	1:A:77:ILE:HG13	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:201:SER:HG	2:B:211:TRP:HE1	1.50	0.58
4:G:57:SER:O	4:G:62:ARG:NH2	2.38	0.57
5:S:36:TRP:HD1	5:S:70:ILE:HD11	1.69	0.57
1:A:92:ASP:OD1	1:A:174:ALA:HB1	2.03	0.56
5:S:73:ASP:HB3	5:S:78:THR:HG22	1.84	0.56
1:A:170:GLN:O	1:A:171:ASN:C	2.44	0.56
1:A:129:VAL:HG11	1:A:211:ILE:HG23	1.88	0.56
4:G:59:ASN:ND2	4:G:61:PHE:O	2.35	0.56
3:C:243:MET:O	3:C:247:MET:HG3	2.06	0.55
2:B:108:SER:OG	2:B:110:ASN:OD1	2.17	0.54
2:B:318:LEU:HD12	2:B:329:THR:HG22	1.89	0.54
5:S:98:ARG:HD3	5:S:110:PHE:HB3	1.90	0.54
4:G:14:LYS:O	4:G:14:LYS:NZ	2.40	0.54
1:A:148:SER:HA	1:A:151:LEU:HD12	1.90	0.54
4:G:48:ASP:OD1	4:G:48:ASP:N	2.40	0.54
5:S:168:ARG:NH1	5:S:210:GLU:O	2.41	0.54
1:A:37:GLU:HA	1:A:288:MET:CE	2.38	0.54
1:A:295:TYR:C	1:A:296:PHE:O	2.33	0.53
2:B:16:ASN:OD1	2:B:17:GLN:N	2.41	0.53
2:B:279:SER:OG	2:B:280:LYS:N	2.41	0.53
2:B:126:LEU:HA	2:B:133:VAL:HG12	1.90	0.53
2:B:248:ALA:HB1	2:B:269:ILE:HG22	1.91	0.53
5:S:62:ASP:HA	5:S:65:LYS:HZ2	1.74	0.53
2:B:229:ILE:HA	2:B:245:SER:HA	1.89	0.53
4:G:32:LYS:NZ	4:G:32:LYS:HB3	2.24	0.53
5:S:62:ASP:HA	5:S:65:LYS:NZ	2.24	0.53
2:B:161:SER:OG	2:B:163:ASP:OD1	2.27	0.52
3:C:8:GLU:OE2	5:S:163:TYR:OH	2.27	0.52
3:C:349:LYS:HG3	3:C:354:PHE:HD2	1.74	0.52
2:B:130:GLU:N	2:B:130:GLU:OE2	2.42	0.52
5:S:6:GLU:OE1	5:S:114:GLY:N	2.42	0.51
1:A:167:MET:N	1:A:168:PRO:HD3	2.25	0.51
1:A:169:ILE:HG13	1:A:177:CYS:H	1.75	0.51
1:A:199:LEU:HB3	1:A:200:PRO:HD3	1.93	0.51
1:A:31:PRO:O	1:A:84:MET:SD	2.68	0.50
1:A:137:ASN:OD1	1:A:137:ASN:N	2.44	0.50
1:A:32:PRO:O	1:A:36:LEU:HD22	2.11	0.50
1:A:275:ALA:O	1:A:279:THR:HG23	2.12	0.50
1:A:171:ASN:ND2	1:A:176:LEU:HD22	2.27	0.50
1:A:218:ARG:HB2	1:A:220:MET:HG2	1.93	0.50
3:C:322:HIS:CG	3:C:323:PHE:H	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:89:LYS:NZ	3:C:20:ASP:OD2	2.39	0.50
3:C:290:TYR:HD1	3:C:302:TYR:HE2	1.57	0.50
1:A:219:GLN:O	1:A:222:ARG:NH1	2.44	0.49
2:B:157:ILE:HG22	2:B:169:TRP:HB2	1.94	0.49
2:B:186:ASP:OD1	2:B:186:ASP:N	2.45	0.49
3:C:353:LEU:HD23	3:C:353:LEU:H	1.77	0.49
1:A:161:HIS:O	1:A:164:LYS:NZ	2.35	0.49
1:A:186:PHE:HZ	1:A:191:ALA:HB2	1.78	0.49
1:A:279:THR:O	1:A:282:PHE:HB2	2.13	0.49
2:B:281:SER:OG	4:G:48:ASP:OD2	2.21	0.48
5:S:232:LYS:HD2	5:S:234:GLU:HB3	1.94	0.48
1:A:29:VAL:O	1:A:33:VAL:HG12	2.13	0.48
1:A:159:THR:HA	1:A:161:HIS:CE1	2.47	0.48
1:A:104:LEU:HD13	1:A:179:SER:HB3	1.94	0.48
1:A:170:GLN:O	1:A:174:ALA:O	2.31	0.48
3:C:290:TYR:CD1	3:C:302:TYR:CD2	3.01	0.48
5:S:51:ILE:HD11	5:S:55:SER:HA	1.95	0.48
3:C:206:SER:OG	3:C:211:TRP:NE1	2.45	0.48
1:A:66:LEU:HB3	1:A:295:TYR:HE1	1.78	0.48
1:A:144:ALA:HA	1:A:147:ILE:HD12	1.95	0.48
1:A:26:ILE:HG22	1:A:30:LEU:HD23	1.96	0.48
3:C:9:ASP:OD2	5:S:157:ASN:ND2	2.47	0.48
5:S:18:ARG:HG3	5:S:19:LYS:N	2.28	0.48
1:A:249:VAL:O	1:A:252:ILE:HG13	2.14	0.48
2:B:30:LEU:HD13	4:G:34:ALA:HB1	1.96	0.48
1:A:30:LEU:O	1:A:33:VAL:HG13	2.14	0.48
1:A:37:GLU:HA	1:A:288:MET:HE3	1.95	0.48
2:B:137:ARG:NH1	2:B:172:GLU:O	2.46	0.48
1:A:214:SER:O	1:A:218:ARG:HG3	2.14	0.47
2:B:225:HIS:NE2	2:B:243:THR:OG1	2.38	0.47
1:A:26:ILE:H	1:A:26:ILE:HG13	1.52	0.47
1:A:97:ASP:HB2	1:A:168:PRO:HG3	1.96	0.47
1:A:229:ALA:O	1:A:233:ILE:HG12	2.14	0.47
5:S:171:GLN:N	5:S:171:GLN:OE1	2.47	0.47
1:A:89:ARG:HB2	1:A:92:ASP:HB2	1.96	0.47
2:B:73:ALA:HB2	2:B:103:CYS:SG	2.55	0.47
2:B:112:VAL:HG22	2:B:124:TYR:HB2	1.97	0.47
3:C:304:GLN:HG3	3:C:321:THR:HG21	1.95	0.47
2:B:61:MET:HG3	2:B:317:CYS:HB2	1.96	0.47
1:A:89:ARG:H	1:A:89:ARG:HG2	1.48	0.46
5:S:166:LEU:HD12	5:S:167:GLN:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ARG:HG3	1:A:92:ASP:O	2.16	0.46
1:A:248:VAL:O	1:A:252:ILE:HG23	2.15	0.46
2:B:228:ASP:OD1	2:B:228:ASP:N	2.48	0.46
5:S:105:SER:O	5:S:179:ARG:NH2	2.49	0.46
2:B:225:HIS:CE1	2:B:251:ARG:HD2	2.51	0.46
1:A:11:LEU:HD11	1:A:13:ILE:HG23	1.98	0.46
3:C:251:ASP:OD1	3:C:255:ASN:ND2	2.49	0.46
1:A:78:ILE:HG13	1:A:79:CYS:N	2.30	0.46
1:A:89:ARG:NH1	1:A:94:LYS:HG2	2.31	0.46
5:S:208:GLU:N	5:S:208:GLU:OE2	2.49	0.46
1:A:31:PRO:HB2	1:A:32:PRO:CD	2.38	0.46
5:S:140:GLY:N	5:S:207:LEU:O	2.37	0.46
1:A:95:PHE:O	1:A:99:PRO:HD2	2.16	0.45
2:B:328:ALA:HB2	2:B:338:ILE:HD13	1.97	0.45
3:C:272:ASP:N	3:C:272:ASP:OD1	2.49	0.45
1:A:221:ASP:HA	1:A:226:ILE:HG21	1.99	0.45
5:S:42:GLU:OE2	5:S:42:GLU:HA	2.16	0.45
5:S:67:ARG:NH2	5:S:90:ASP:OD2	2.50	0.45
1:A:184:HIS:CG	1:A:258:LEU:HD11	2.51	0.45
2:B:160:SER:OG	2:B:166:CYS:SG	2.64	0.45
1:A:68:ASN:O	1:A:71:VAL:HG12	2.17	0.45
1:A:218:ARG:HH11	1:A:218:ARG:HB3	1.81	0.45
2:B:58:ILE:HG13	2:B:334:SER:HA	1.97	0.45
3:C:254:CYS:O	3:C:317:LYS:NZ	2.50	0.45
3:C:53:MET:HG2	3:C:332:VAL:HG22	1.98	0.45
1:A:82:PHE:HA	1:A:85:ASP:OD2	2.17	0.44
1:A:167:MET:N	1:A:168:PRO:CD	2.81	0.44
2:B:214:ARG:HB3	2:B:214:ARG:NH1	2.32	0.44
5:S:209:ALA:O	5:S:210:GLU:HB3	2.17	0.44
1:A:170:GLN:HA	1:A:175:ASN:HA	1.99	0.44
1:A:273:ASP:O	1:A:276:PHE:HB3	2.17	0.44
2:B:200:VAL:HG22	2:B:234:PHE:HE1	1.82	0.44
1:A:85:ASP:O	1:A:89:ARG:HG2	2.17	0.44
1:A:105:PHE:HA	1:A:162:LEU:HD13	1.98	0.44
2:B:252:LEU:HD23	2:B:261:LEU:HB2	1.99	0.44
3:C:322:HIS:CG	3:C:323:PHE:O	2.71	0.44
1:A:197:PHE:CD2	1:A:248:VAL:HG21	2.52	0.44
1:A:227:LYS:O	1:A:231:THR:HG23	2.16	0.44
4:G:21:MET:HE2	4:G:21:MET:N	2.33	0.44
1:A:95:PHE:CD1	1:A:95:PHE:N	2.85	0.44
5:S:69:THR:HG23	5:S:82:GLN:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:68:PHE:HB3	5:S:81:LEU:HD11	1.99	0.44
1:A:161:HIS:O	1:A:164:LYS:HG3	2.17	0.44
1:A:282:PHE:HA	1:A:285:MET:CE	2.48	0.44
2:B:157:ILE:HB	2:B:171:ILE:HD11	2.00	0.43
1:A:168:PRO:C	1:A:170:GLN:N	2.72	0.43
1:A:187:GLN:HG3	1:A:189:HIS:N	2.22	0.43
1:A:188:TRP:CZ2	1:A:192:MET:HG3	2.52	0.43
5:S:87:ARG:HE	5:S:87:ARG:HB3	1.67	0.43
1:A:134:HIS:CE1	1:A:136:LEU:H	2.37	0.43
5:S:42:GLU:C	5:S:43:LYS:HE2	2.37	0.43
1:A:223:HIS:HD2	1:A:224:ALA:N	2.16	0.43
5:S:53:SER:HA	5:S:72:ARG:NH1	2.33	0.43
1:A:36:LEU:N	1:A:36:LEU:HD13	2.33	0.43
1:A:85:ASP:O	1:A:86:ASN:C	2.56	0.43
1:A:223:HIS:CD2	1:A:224:ALA:N	2.87	0.43
3:C:283:LEU:HB2	3:C:290:TYR:HD2	1.83	0.43
4:G:20:LYS:HG3	4:G:21:MET:CE	2.48	0.43
3:C:277:LYS:HB2	3:C:277:LYS:HE2	1.78	0.43
1:A:97:ASP:O	1:A:98:ILE:C	2.56	0.43
1:A:147:ILE:O	1:A:151:LEU:HG	2.18	0.43
2:B:245:SER:OG	2:B:247:ASP:OD1	2.37	0.43
3:C:306:GLN:HE21	3:C:306:GLN:HB3	1.61	0.43
5:S:6:GLU:CD	5:S:114:GLY:H	2.22	0.43
3:C:313:ARG:H	3:C:313:ARG:HG2	1.70	0.43
2:B:251:ARG:NH1	2:B:260:GLU:OE1	2.51	0.42
5:S:76:LYS:NZ	5:S:76:LYS:HB2	2.34	0.42
1:A:171:ASN:HB2	1:A:175:ASN:C	2.39	0.42
1:A:265:ASN:OD1	1:A:265:ASN:N	2.51	0.42
1:A:26:ILE:HD12	1:A:27:VAL:H	1.84	0.42
1:A:56:LEU:HD12	1:A:301:PHE:CE1	2.55	0.42
1:A:85:ASP:O	1:A:88:VAL:HG22	2.19	0.42
5:S:153:LEU:HD12	5:S:200:PHE:CZ	2.54	0.42
1:A:84:MET:O	1:A:88:VAL:HG13	2.19	0.42
1:A:170:GLN:C	1:A:171:ASN:O	2.54	0.42
2:B:37:ILE:HD13	2:B:37:ILE:HA	1.68	0.42
3:C:271:LYS:HD2	3:C:323:PHE:HB3	2.01	0.42
5:S:164:TRP:HB2	5:S:177:ILE:HB	2.01	0.42
1:A:21:PHE:CE2	1:A:270:ARG:HA	2.54	0.42
2:B:124:TYR:CE2	2:B:135:VAL:HG22	2.55	0.42
3:C:268:LEU:HD12	3:C:323:PHE:CZ	2.55	0.42
5:S:211:ASP:OD1	5:S:211:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:PHE:CE1	1:A:56:LEU:HD22	2.55	0.42
3:C:302:TYR:HE1	3:C:306:GLN:OE1	2.02	0.42
1:A:184:HIS:CD2	1:A:258:LEU:HD11	2.54	0.41
1:A:187:GLN:O	1:A:188:TRP:C	2.59	0.41
2:B:210:LEU:HD13	2:B:255:LEU:HD11	2.01	0.41
3:C:212:ILE:HD12	3:C:212:ILE:HA	1.84	0.41
1:A:83:LEU:HG	1:A:87:TYR:CZ	2.55	0.41
3:C:210:LYS:HA	3:C:210:LYS:HD2	1.67	0.41
3:C:290:TYR:CD1	3:C:290:TYR:C	2.91	0.41
3:C:322:HIS:CG	3:C:323:PHE:N	2.88	0.41
1:A:251:ARG:HG3	1:A:255:PHE:CE2	2.55	0.41
1:A:258:LEU:HG	1:A:259:HIS:N	2.35	0.41
2:B:230:ASN:OD1	2:B:230:ASN:N	2.53	0.41
1:A:109:MET:HE3	1:A:109:MET:HB3	1.82	0.41
1:A:282:PHE:HA	1:A:285:MET:HE1	2.02	0.41
1:A:37:GLU:HA	1:A:288:MET:HE1	2.02	0.41
1:A:56:LEU:HD12	1:A:301:PHE:CZ	2.55	0.41
1:A:93:TRP:NE1	1:A:100:CYS:HB2	2.36	0.41
2:B:104:ALA:HB3	2:B:113:ALA:HB3	2.03	0.41
2:B:183:HIS:CE1	2:B:203:ALA:HB2	2.56	0.41
3:C:24:ARG:HG2	3:C:24:ARG:HH11	1.85	0.41
3:C:227:LEU:HD21	3:C:268:LEU:HB3	2.03	0.41
3:C:283:LEU:HB2	3:C:290:TYR:CD2	2.56	0.41
1:A:41:GLY:HA3	1:A:77:ILE:HG21	2.03	0.41
1:A:130:VAL:C	1:A:132:PRO:HD3	2.42	0.41
1:A:171:ASN:N	1:A:174:ALA:O	2.54	0.41
1:A:232:PHE:O	1:A:235:VAL:HG12	2.21	0.41
1:A:296:PHE:N	1:A:296:PHE:CD1	2.87	0.41
3:C:230:TYR:O	3:C:230:TYR:CG	2.74	0.41
5:S:142:SER:HA	5:S:204:ILE:O	2.20	0.41
1:A:239:VAL:HA	1:A:242:ILE:HG22	2.03	0.40
2:B:51:LEU:HD23	2:B:87:THR:HG22	2.03	0.40
2:B:186:ASP:O	2:B:204:CYS:N	2.54	0.40
2:B:68:ARG:O	2:B:84:SER:OG	2.34	0.40
1:A:186:PHE:CZ	1:A:191:ALA:HB2	2.55	0.40
1:A:232:PHE:CE2	1:A:297:SER:O	2.74	0.40
1:A:274:LEU:HG	1:A:275:ALA:N	2.37	0.40
1:A:278:ILE:HD13	1:A:278:ILE:HA	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	292/294 (99%)	249 (85%)	40 (14%)	3 (1%)	13	44
2	B	335/337 (99%)	314 (94%)	21 (6%)	0	100	100
3	C	210/351 (60%)	197 (94%)	13 (6%)	0	100	100
4	G	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
5	S	229/248 (92%)	214 (93%)	15 (7%)	0	100	100
All	All	1120/1286 (87%)	1024 (91%)	93 (8%)	3 (0%)	38	67

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	PRO
1	A	259	HIS
1	A	172	GLY

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	242/267 (91%)	183 (76%)	59 (24%)	0	2
2	B	280/280 (100%)	255 (91%)	25 (9%)	8	29
3	C	185/304 (61%)	169 (91%)	16 (9%)	8	31
4	G	46/46 (100%)	42 (91%)	4 (9%)	8	30
5	S	198/201 (98%)	179 (90%)	19 (10%)	7	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	951/1098 (87%)	828 (87%)	123 (13%)	6 15

All (123) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASP
1	A	18	CYS
1	A	19	CYS
1	A	25	PHE
1	A	26	ILE
1	A	29	VAL
1	A	30	LEU
1	A	33	VAL
1	A	36	LEU
1	A	50	TRP
1	A	52	PHE
1	A	75	LEU
1	A	76	LEU
1	A	77	ILE
1	A	78	ILE
1	A	79	CYS
1	A	80	LEU
1	A	81	PRO
1	A	83	LEU
1	A	84	MET
1	A	85	ASP
1	A	89	ARG
1	A	102	LEU
1	A	103	MET
1	A	106	MET
1	A	109	MET
1	A	114	SER
1	A	125	ARG
1	A	128	ARG
1	A	129	VAL
1	A	137	ASN
1	A	138	LYS
1	A	143	THR
1	A	148	SER
1	A	150	LEU
1	A	155	THR
1	A	158	LEU

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Mol	Chain	Res	Type
1	A	164	LYS
1	A	169	ILE
1	A	170	GLN
1	A	171	ASN
1	A	175	ASN
1	A	177	CYS
1	A	178	SER
1	A	181	SER
1	A	183	CYS
1	A	184	HIS
1	A	188	TRP
1	A	189	HIS
1	A	198	PHE
1	A	217	GLN
1	A	227	LYS
1	A	228	ARG
1	A	264	GLN
1	A	266	CYS
1	A	269	TYR
1	A	274	LEU
1	A	285	MET
1	A	297	SER
2	B	37	ILE
2	B	38	ASP
2	B	49	ARG
2	B	96	ARG
2	B	97	SER
2	B	105	TYR
2	B	133	VAL
2	B	134	ARG
2	B	146	LEU
2	B	148	CYS
2	B	160	SER
2	B	186	ASP
2	B	189	SER
2	B	214	ARG
2	B	217	MET
2	B	223	THR
2	B	230	ASN
2	B	234	PHE
2	B	252	LEU
2	B	263	THR

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Mol	Chain	Res	Type
2	B	267	ASP
2	B	290	ASP
2	B	292	PHE
2	B	336	LEU
2	B	340	ASN
3	C	6	SER
3	C	20	ASP
3	C	28	GLU
3	C	38	LEU
3	C	53	MET
3	C	188	HIS
3	C	207	GLU
3	C	230	TYR
3	C	272	ASP
3	C	286	CYS
3	C	293	SER
3	C	296	TYR
3	C	302	TYR
3	C	325	CYS
3	C	328	ASP
3	C	353	LEU
4	G	32	LYS
4	G	42	GLU
4	G	57	SER
4	G	63	GLU
5	S	38	ARG
5	S	62	ASP
5	S	72	ARG
5	S	77	ASN
5	S	80	PHE
5	S	84	THR
5	S	93	MET
5	S	125	ASP
5	S	130	GLN
5	S	146	SER
5	S	148	ARG
5	S	154	LEU
5	S	182	ASN
5	S	192	SER
5	S	202	LEU
5	S	211	ASP
5	S	217	CYS

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Mol	Chain	Res	Type
5	S	222	GLU
5	S	232	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	ASN
1	A	171	ASN
1	A	223	HIS
1	A	259	HIS
3	C	306	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](#)

1 ligand is 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	$\# Z > 2$
6	OJX	A	401	-	10,11,11	0.97	0	8,15,15	1.62	2 (25%)

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
6	OJX	A	401	-	-	0/4/4/4	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	401	OJX	C11-C08-N05	2.99	122.90	117.54
6	A	401	OJX	C07-C08-N05	-2.04	119.29	121.99

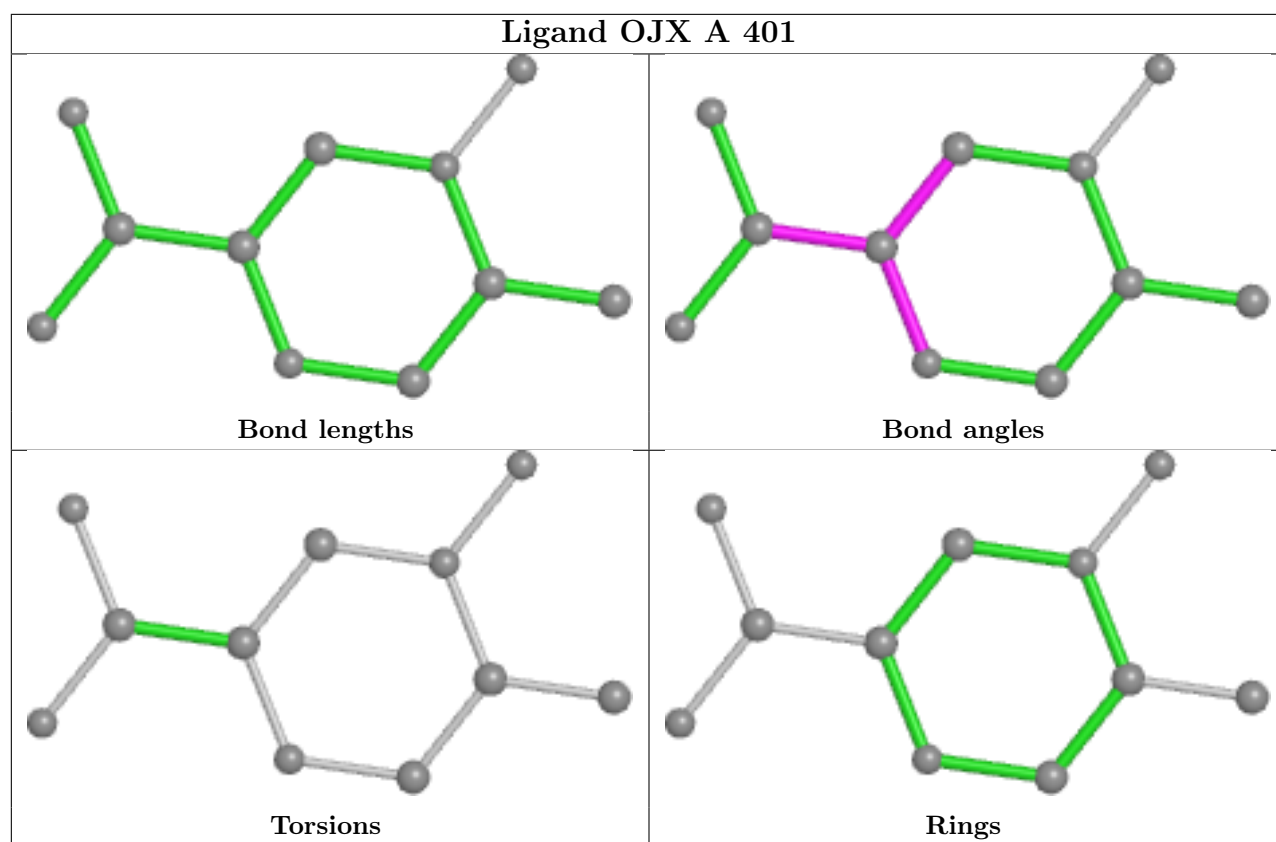
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

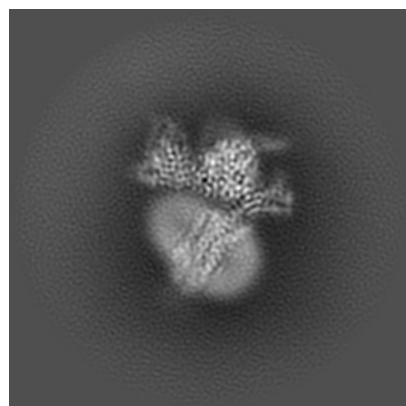
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35484. These allow visual inspection of the internal detail of the map and identification of artifacts.

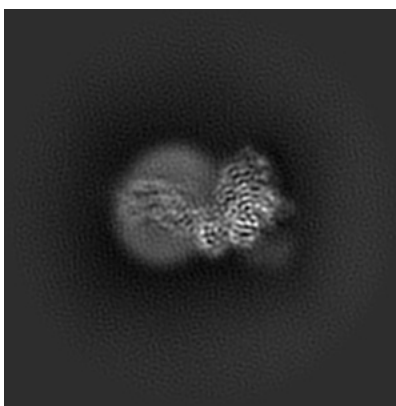
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

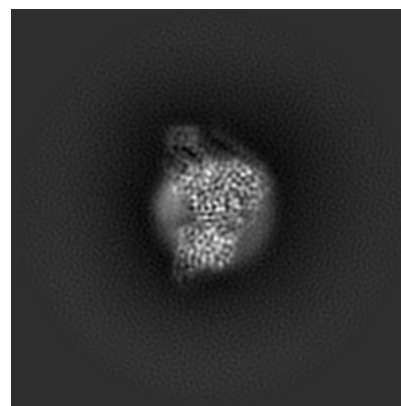
6.1.1 Primary map



X

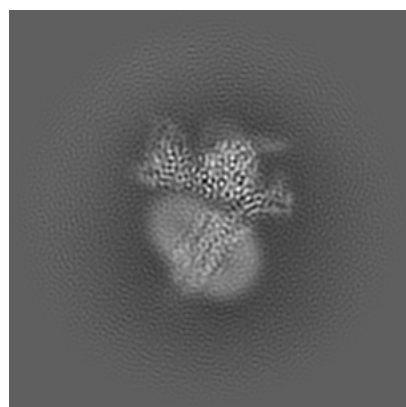


Y

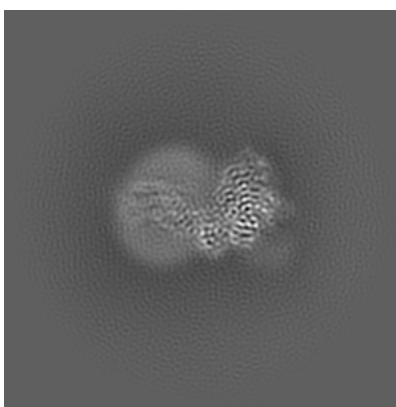


Z

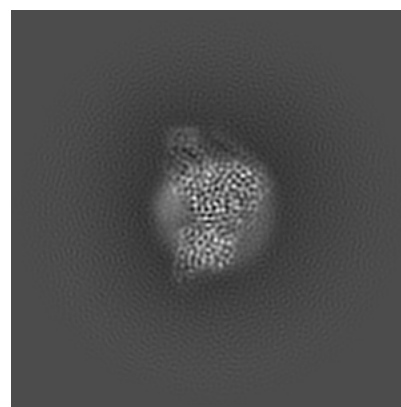
6.1.2 Raw map



X



Y

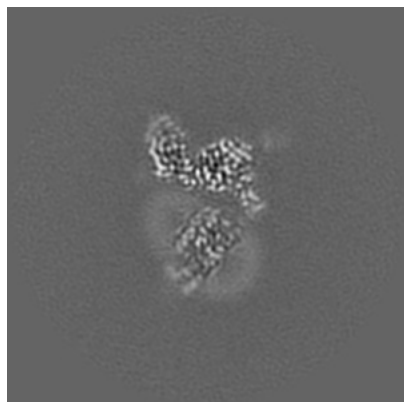


Z

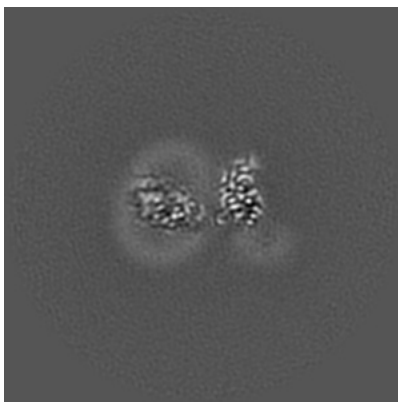
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

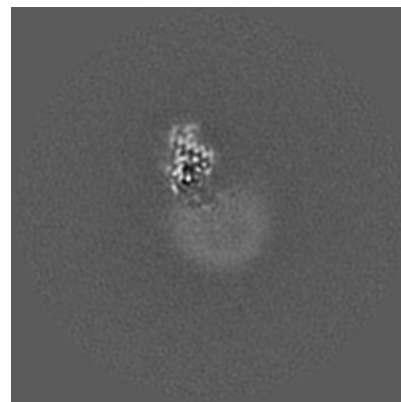
6.2.1 Primary map



X Index: 160

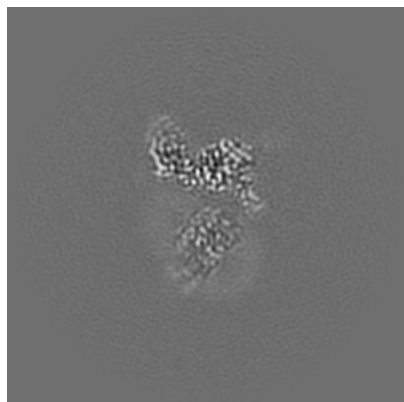


Y Index: 160

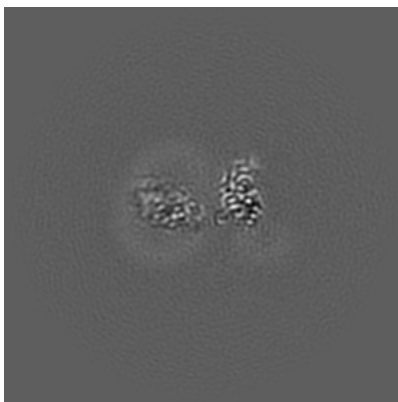


Z Index: 160

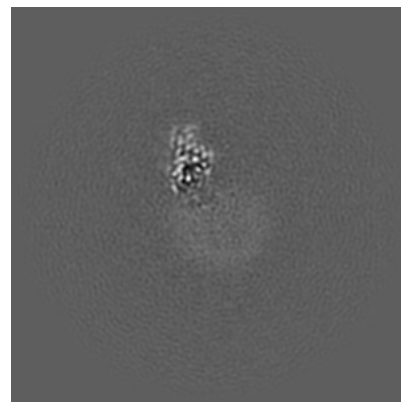
6.2.2 Raw map



X Index: 160



Y Index: 160

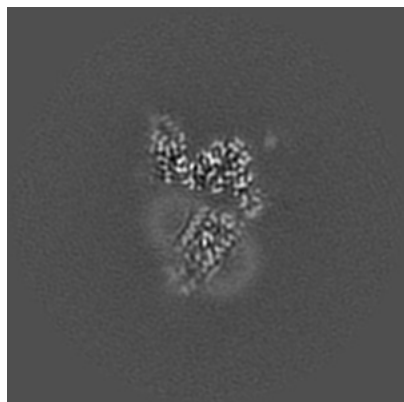


Z Index: 160

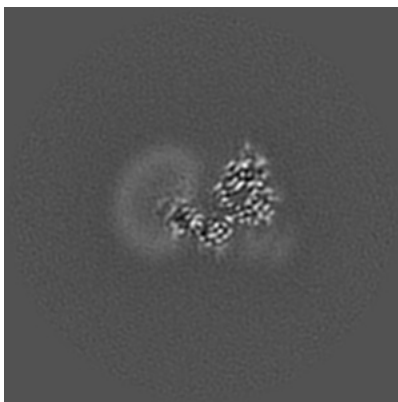
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

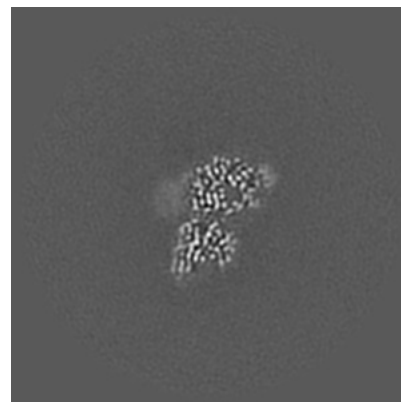
6.3.1 Primary map



X Index: 158

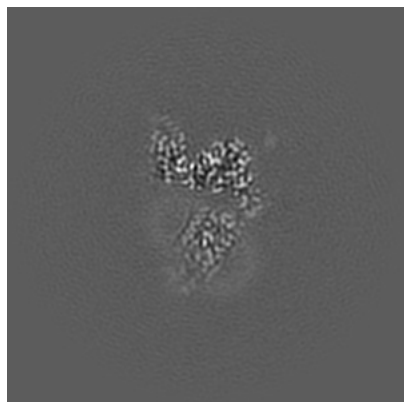


Y Index: 179

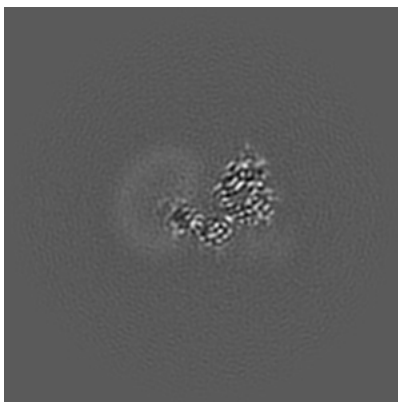


Z Index: 196

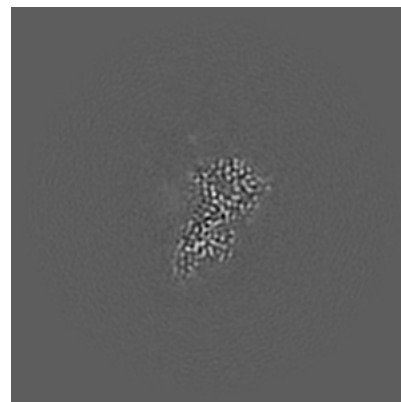
6.3.2 Raw map



X Index: 158



Y Index: 179

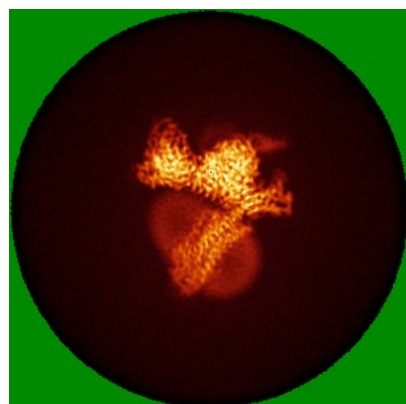


Z Index: 191

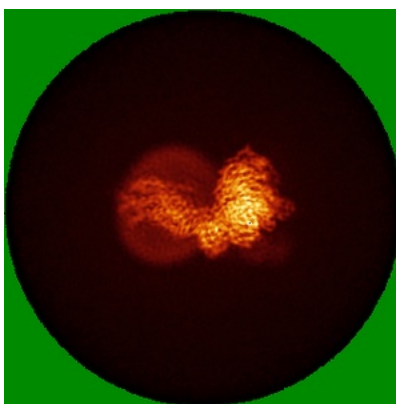
The images above show the largest variance slices of the map in three orthogonal directions.

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

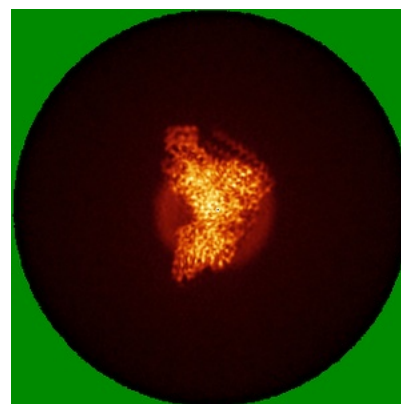
6.4.1 Primary map



X

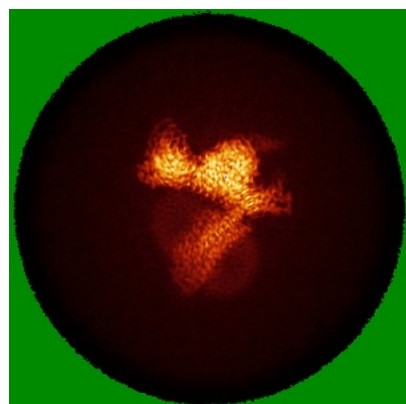


Y

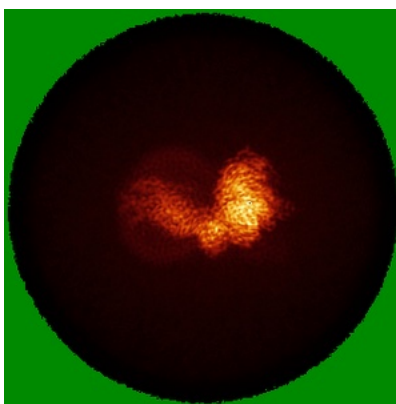


Z

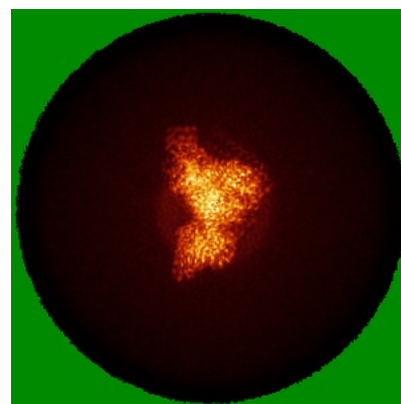
6.4.2 Raw map



X



Y

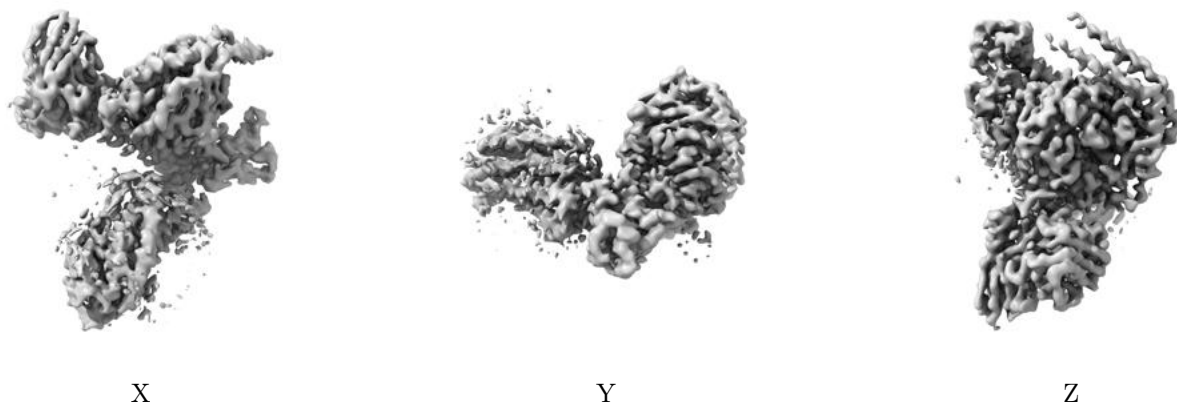


Z

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

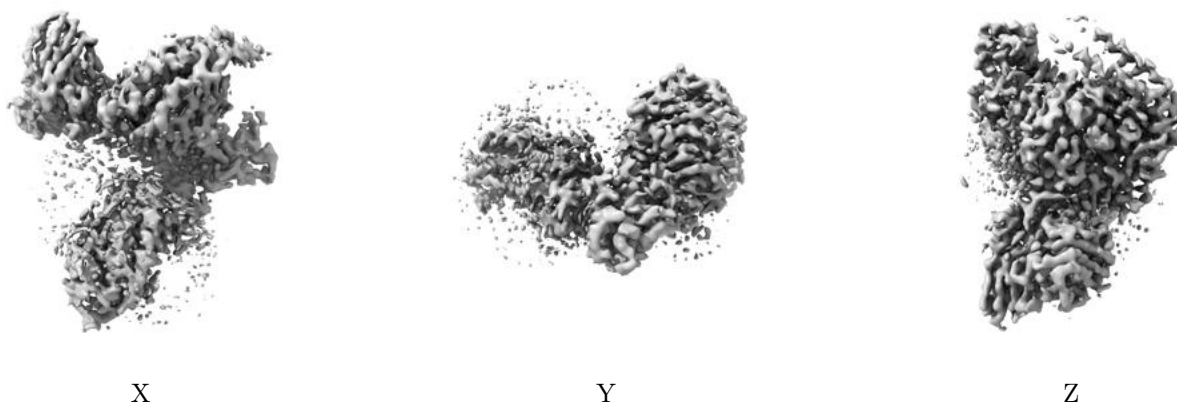
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

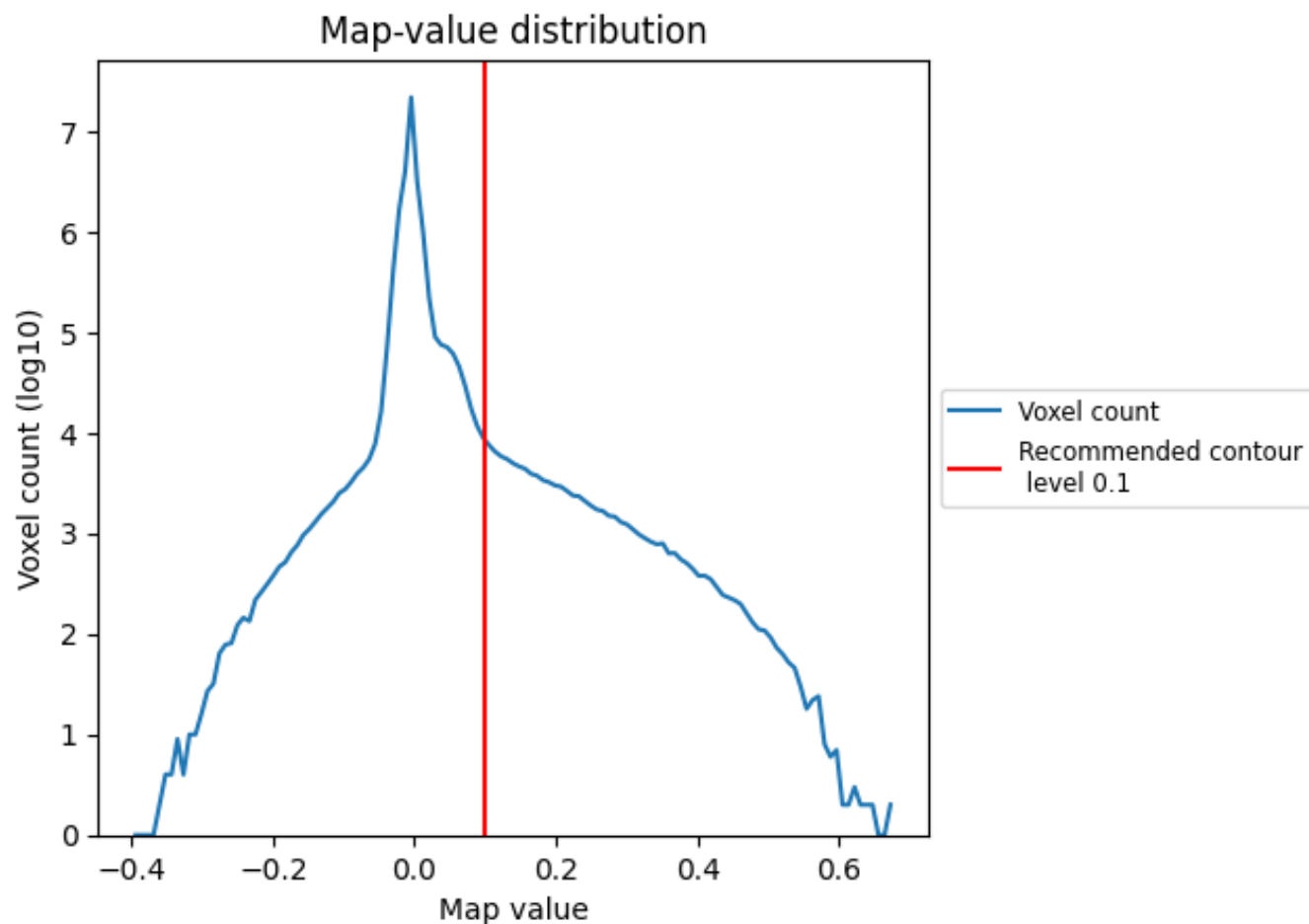
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

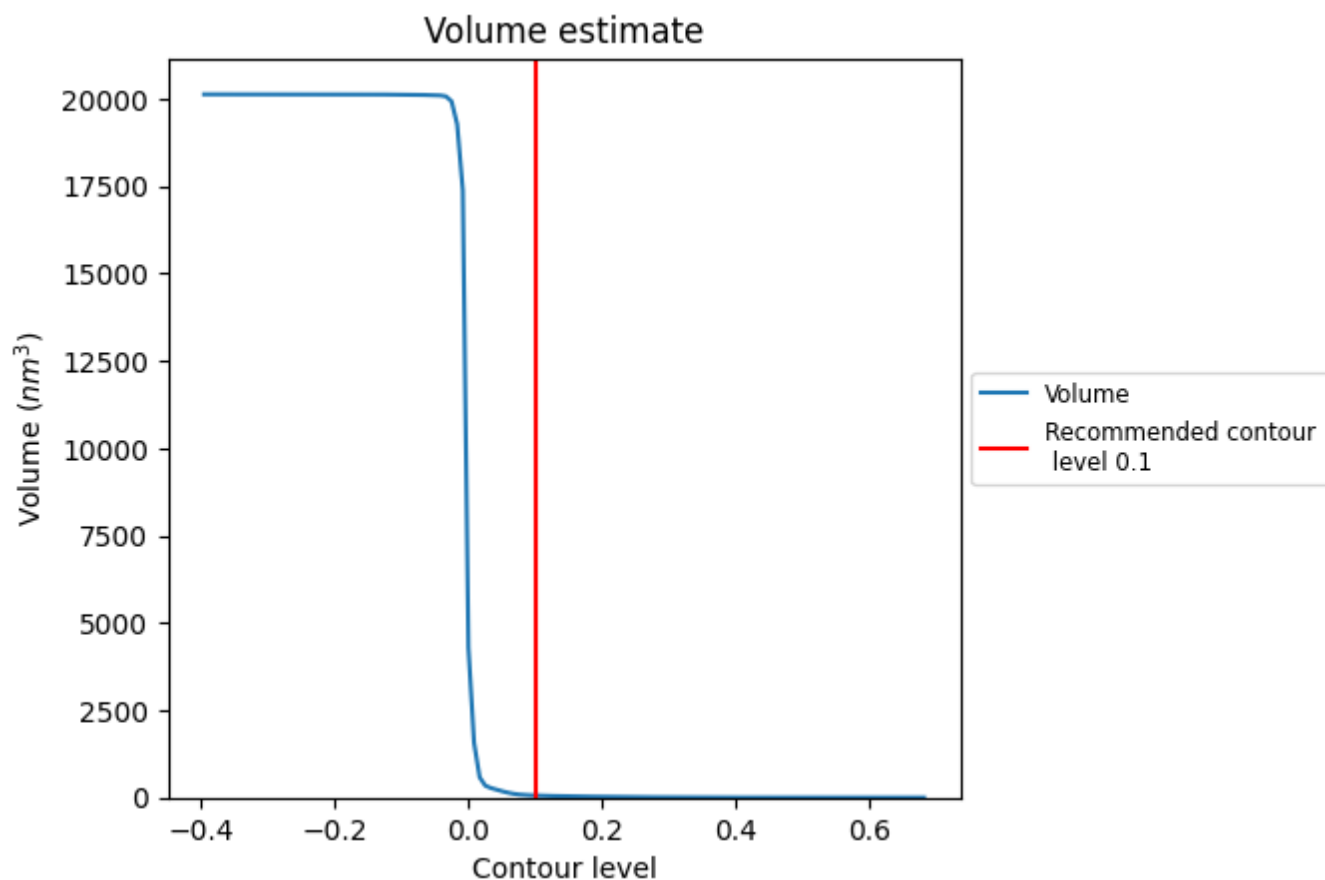
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

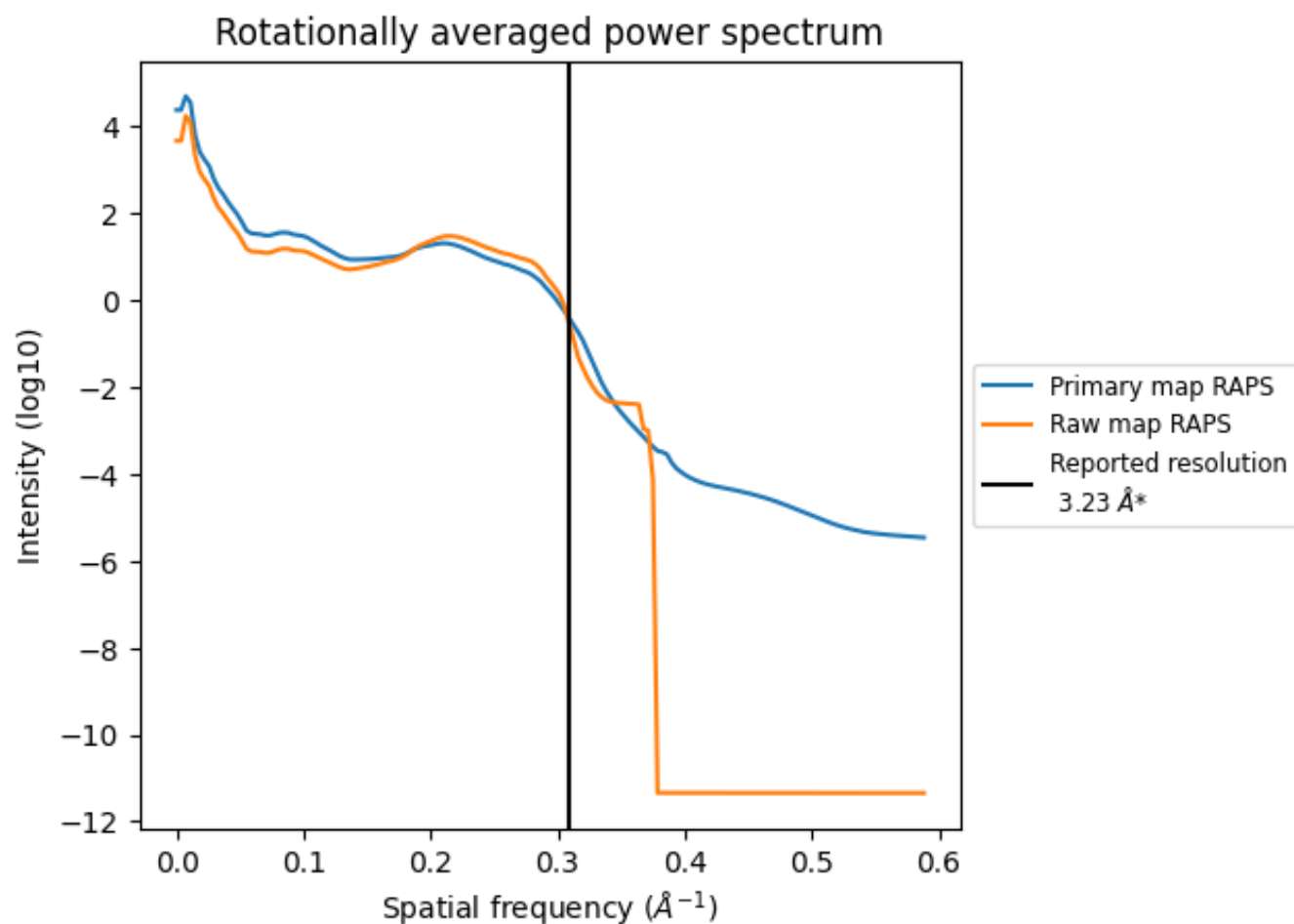
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 59 nm³; this corresponds to an approximate mass of 54 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 ⓘ

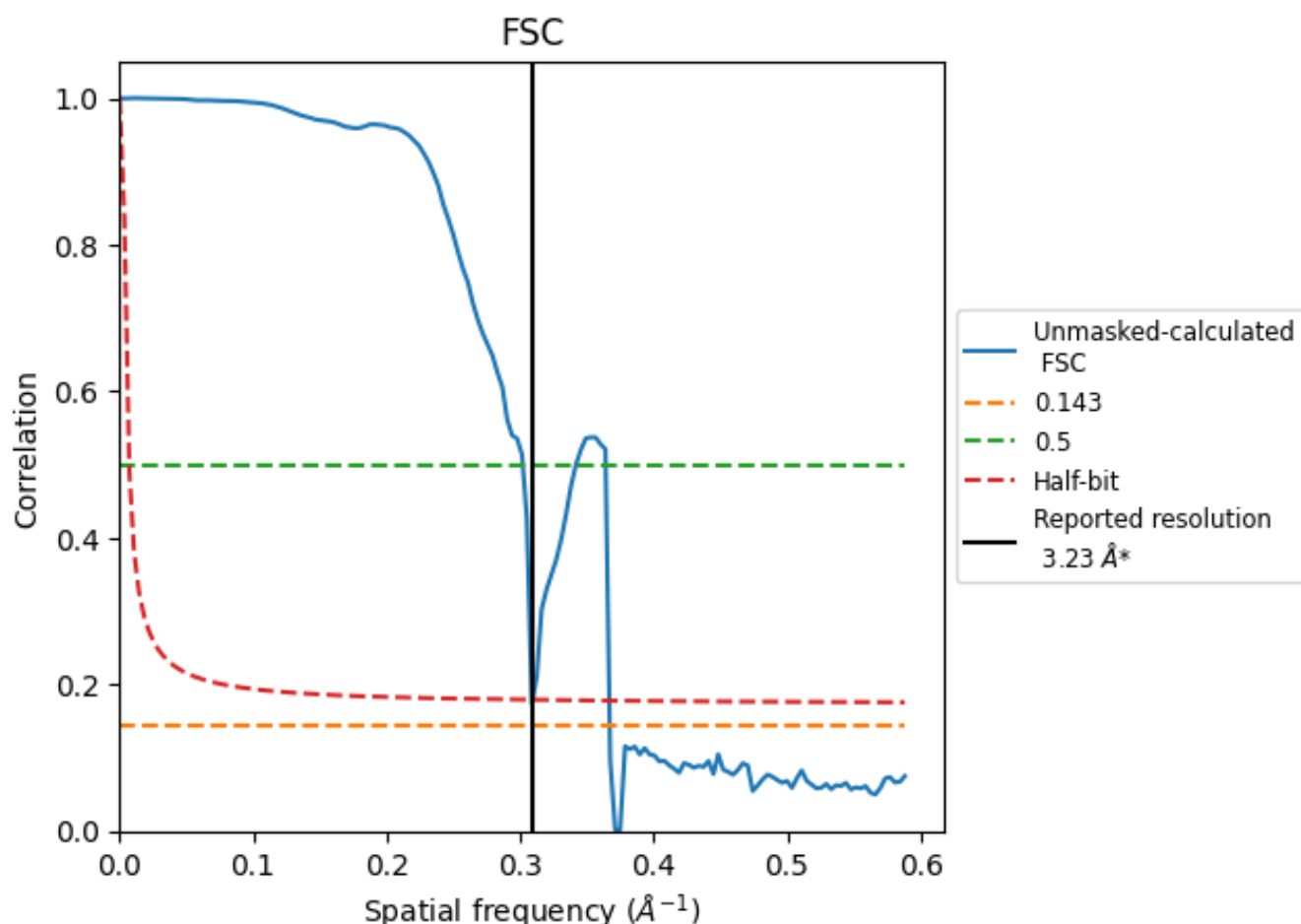


*Reported resolution corresponds to spatial frequency of 0.310 Å⁻¹

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 0.310 \AA^{-1}

8.2 Resolution estimates [i](#)

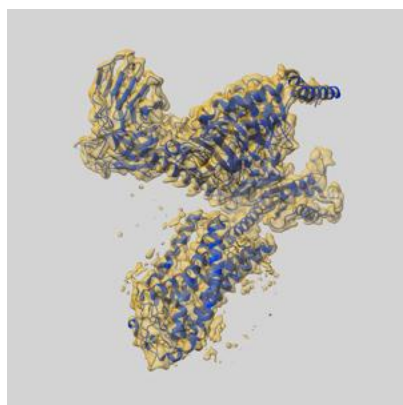
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.72	3.31	3.24

*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 2.72 differs from the reported value 3.23 by more than 10 %

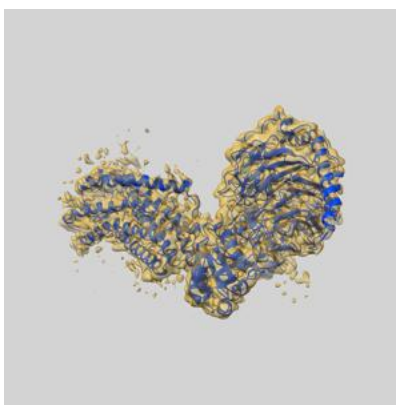
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35484 and PDB model 8IJB. Per-residue inclusion information can be found in section 3 on page 5.

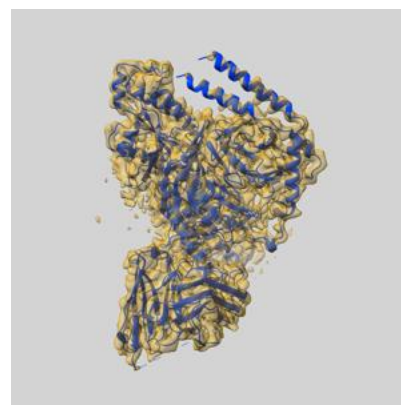
9.1 Map-model overlay [i](#)



X



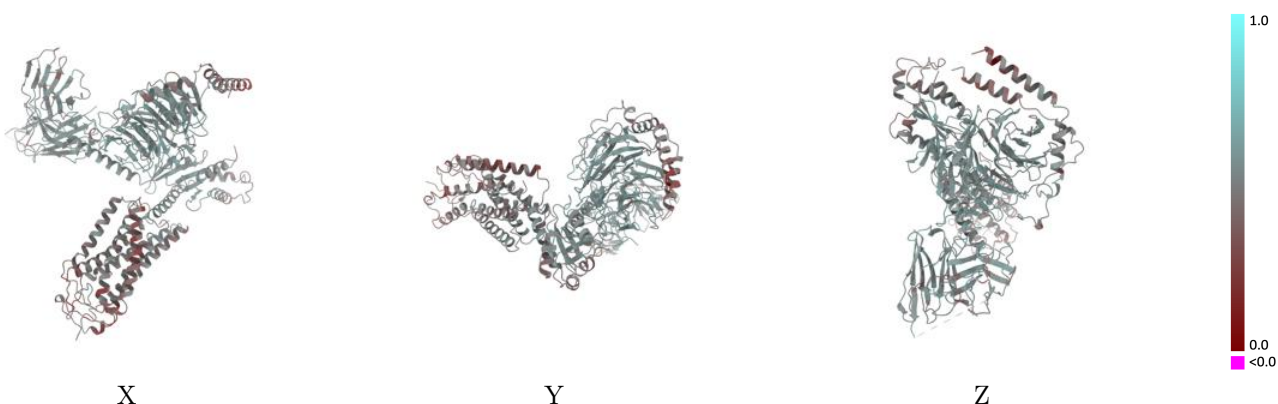
Y



Z

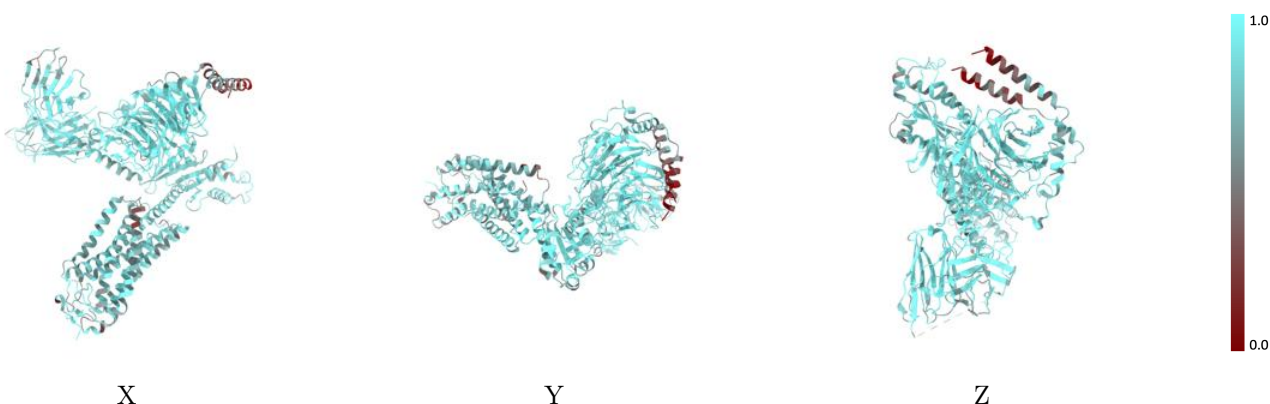
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



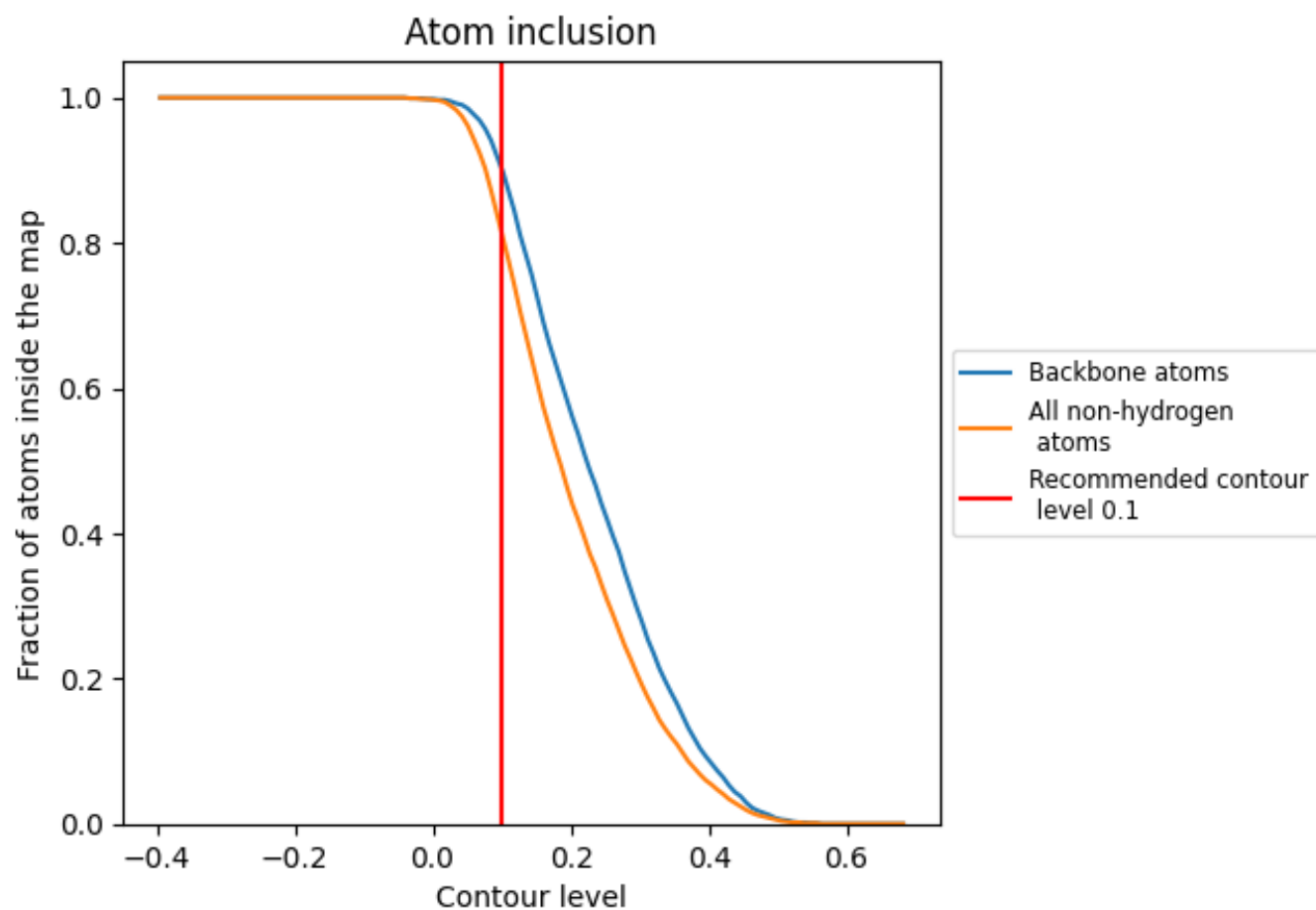
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8140	<div></div> 0.4970
A	<div></div> 0.7560	<div></div> 0.4350
B	<div></div> 0.8580	<div></div> 0.5330
C	<div></div> 0.8330	<div></div> 0.5090
G	<div></div> 0.6370	<div></div> 0.4620
S	<div></div> 0.8520	<div></div> 0.5230

