



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 05:51 AM UTC

PDB ID : 8JIP / pdb_00008jip
EMDB ID : EMD-36323
Title : Cryo-EM structure of the GLP-1R/GCGR dual agonist MEDI0382-bound human GLP-1R-Gs complex
Authors : Yang, L.; Zhou, Q.T.; Dai, A.T.; Zhao, F.H.; Chang, R.L.; Ying, T.L.; Wu, B.L.; Yang, D.H.; Wang, M.W.; Cong, Z.T.
Deposited on : 2023-05-27
Resolution : 2.85 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:

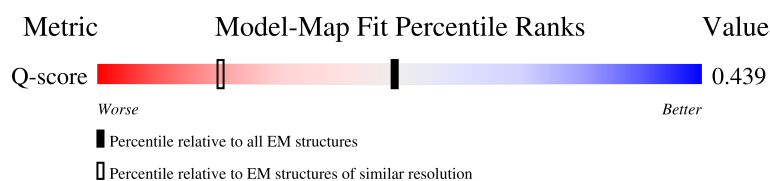
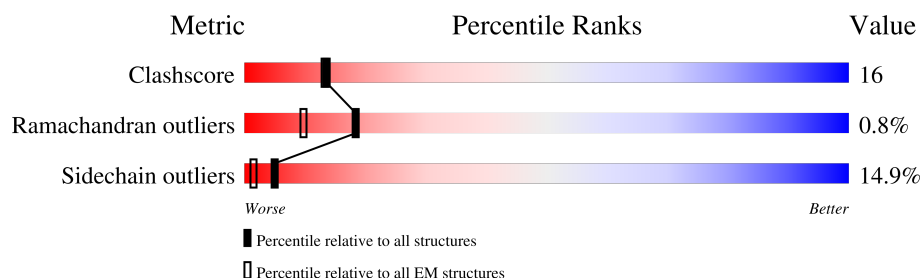
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.85 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	11965 (2.35 - 3.35)

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	R	440	18% 49% 28% 10% 12%
2	A	361	48% 15% 5% 32%
3	P	29	59% 31% 10%
4	B	345	8% 76% 20%

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Mol	Chain	Length	Quality of chain
5	G	70	 39% 66% 10% 20%
6	N	140	 9% 71% 19% 10%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9399 atoms, of which 37 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 Glucagon-like peptide 1 receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	386	Total	C	N	O	S	0	0
			3109	2057	501	532	19		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	245	Total	C	N	O	S	0	0
			2016	1273	361	374	8		

- Molecule 3 is a protein called MEDI0382.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	P	29	Total	C	N	O	0	0
			231	143	38	50		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	338	Total	C	N	O	S	0	0
			2590	1599	464	506	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P54311
B	-3	GLY	-	expression tag	UNP P54311
B	-2	SER	-	expression tag	UNP P54311
B	-1	LEU	-	expression tag	UNP P54311
B	0	LEU	-	expression tag	UNP P54311
B	1	GLN	-	expression tag	UNP P54311

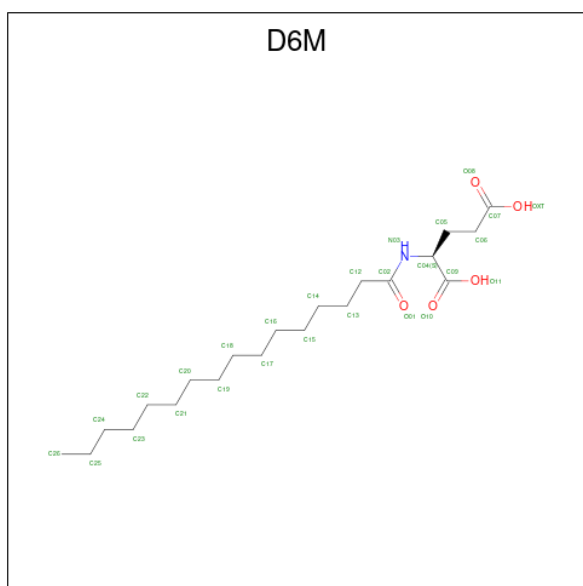
- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	56	Total	C	N	O	S	0	0
			429	269	76	81	3		

- Molecule 6 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	126	Total	C	N	O	S	0	0
			961	599	168	188	6		

- Molecule 7 is N-hexadecanoyl-L-glutamic acid (CCD ID: D6M) (formula: $C_{21}H_{39}NO_5$) (labeled as "Ligand of Interest" by depositor).

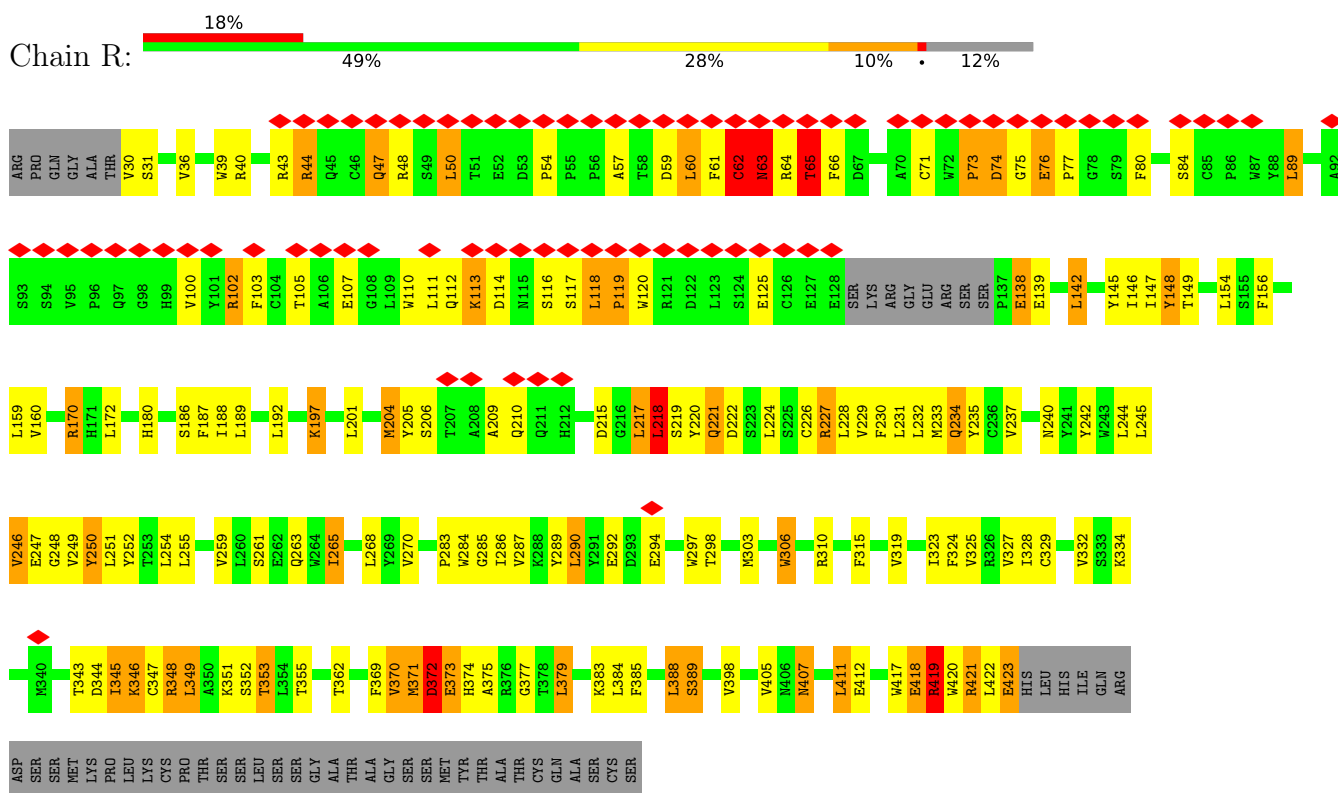


Mol	Chain	Residues	Atoms					AltConf
7	P	1	Total	C	H	N	O	0
			63	21	37	1	4	

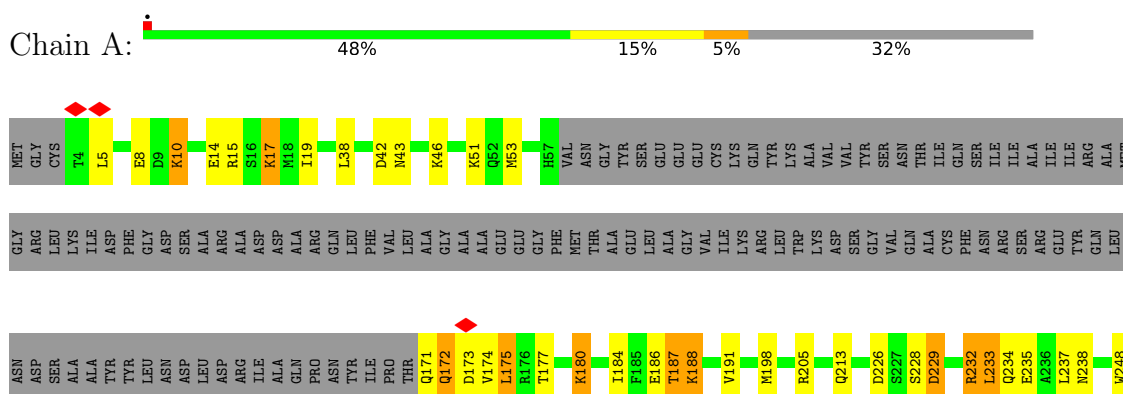
3 Residue-property plots

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

• Molecule 1: Glucagon-like peptide 1 receptor



• Molecule 2: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	796065	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 ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.496	Depositor
Minimum map value	-0.261	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.059	Depositor
Map size ($\text{\AA}$)	247.68001, 247.68001, 247.68001	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	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: D6M

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	R	0.58	1/3203 (0.0%)	0.96	22/4373 (0.5%)
2	A	0.45	0/2055	0.72	11/2772 (0.4%)
3	P	0.80	0/236	0.97	1/318 (0.3%)
4	B	0.24	0/2637	0.41	0/3577
5	G	0.20	0/435	0.44	0/587
6	N	0.17	0/981	0.39	0/1329
All	All	0.44	1/9547 (0.0%)	0.72	34/12956 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	218	LEU	C-O	-5.55	1.17	1.24

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	64	ARG	N-CA-C	-9.29	102.32	114.31
2	A	292	THR	CA-C-N	-8.04	111.89	120.66
2	A	292	THR	C-N-CA	-8.04	111.89	120.66
1	R	353	THR	N-CA-C	-7.99	104.13	114.04
1	R	379	LEU	N-CA-C	-7.95	102.56	111.07
1	R	73	PRO	N-CA-C	7.39	121.96	110.80
1	R	40	ARG	N-CA-C	-7.25	103.10	112.23
1	R	250	TYR	N-CA-C	-7.04	103.22	111.03
2	A	281	GLU	N-CA-C	-6.96	104.30	114.39
1	R	329	CYS	N-CA-C	-6.89	103.70	111.14
1	R	407	ASN	N-CA-C	6.81	119.57	111.33
1	R	149	THR	N-CA-C	-6.47	105.36	113.20
1	R	84	SER	N-CA-C	6.43	118.63	110.33
2	A	228	SER	N-CA-C	-6.35	107.38	114.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	119	PRO	N-CA-C	6.17	120.33	110.40
1	R	210	GLN	N-CA-C	-6.09	104.76	111.82
1	R	229	VAL	N-CA-C	5.83	117.26	110.62
2	A	53	MET	N-CA-C	-5.81	106.23	113.38
2	A	287	THR	CA-C-N	-5.80	113.80	119.78
2	A	287	THR	C-N-CA	-5.80	113.80	119.78
1	R	89	LEU	CA-C-N	-5.70	112.64	118.85
1	R	89	LEU	C-N-CA	-5.70	112.64	118.85
1	R	244	LEU	N-CA-C	-5.63	105.29	111.82
1	R	62	CYS	N-CA-C	-5.62	98.84	110.80
2	A	311	GLU	N-CA-C	-5.51	105.19	111.14
3	P	25	TRP	N-CA-C	-5.51	106.40	113.23
1	R	39	TRP	N-CA-C	-5.46	106.46	113.23
1	R	419	ARG	N-CA-C	-5.36	105.34	111.07
2	A	279	PHE	CA-C-N	-5.34	113.43	120.96
2	A	279	PHE	C-N-CA	-5.34	113.43	120.96
1	R	344	ASP	N-CA-C	-5.19	104.94	113.50
2	A	340	ARG	N-CA-C	-5.15	105.11	111.40
1	R	218	LEU	CA-C-N	5.02	126.97	120.44
1	R	218	LEU	C-N-CA	5.02	126.97	120.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	3109	0	3019	155	0
2	A	2016	0	1975	50	0
3	P	231	0	203	14	0
4	B	2590	0	2490	61	0
5	G	429	0	441	13	0
6	N	961	0	928	15	0
7	P	26	37	37	4	0
All	All	9362	37	9093	296	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 16.

All (296) 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)
3:P:10:LYS:NZ	7:P:101:D6M:C07	1.71	1.53
4:B:39:PRO:HA	4:B:301:LYS:CE	1.47	1.43
4:B:39:PRO:CA	4:B:301:LYS:HE2	1.49	1.42
1:R:237:VAL:HG11	3:P:1:HIS:HD2	1.07	1.17
4:B:262:MET:HB3	4:B:264:TYR:CE1	1.78	1.17
1:R:289:TYR:HB2	1:R:297:TRP:HZ2	1.12	1.13
4:B:262:MET:HB3	4:B:264:TYR:HE1	1.04	1.12
1:R:227:ARG:HH11	1:R:227:ARG:HB2	1.11	1.12
4:B:300:LEU:HD23	5:G:38:MET:HE1	1.32	1.06
1:R:289:TYR:HB2	1:R:297:TRP:CZ2	1.92	1.05
1:R:237:VAL:HG11	3:P:1:HIS:CD2	1.92	1.03
2:A:356:ARG:HH11	2:A:356:ARG:HB2	1.19	1.02
4:B:39:PRO:CB	4:B:301:LYS:HE2	1.93	0.98
1:R:217:LEU:O	1:R:221:GLN:HB2	1.62	0.98
2:A:232:ARG:HG2	2:A:232:ARG:HH11	1.30	0.96
4:B:39:PRO:CA	4:B:301:LYS:CE	2.26	0.92
3:P:10:LYS:HZ2	7:P:101:D6M:C07	1.73	0.92
4:B:39:PRO:HA	4:B:301:LYS:NZ	1.85	0.91
4:B:262:MET:CB	4:B:264:TYR:HE1	1.85	0.90
4:B:262:MET:CB	4:B:264:TYR:CE1	2.56	0.88
4:B:39:PRO:HA	4:B:301:LYS:HE2	0.88	0.87
2:A:356:ARG:HH11	2:A:356:ARG:CB	1.88	0.87
1:R:142:LEU:HD12	1:R:142:LEU:O	1.76	0.86
5:G:21:MET:HE2	5:G:21:MET:O	1.74	0.85
2:A:233:LEU:O	2:A:233:LEU:HD12	1.76	0.85
1:R:206:SER:HA	1:R:209:ALA:HB3	1.58	0.84
4:B:300:LEU:CD2	5:G:38:MET:HE1	2.08	0.84
1:R:48:ARG:HG3	1:R:48:ARG:HH11	1.43	0.83
1:R:227:ARG:HH11	1:R:227:ARG:CB	1.90	0.82
1:R:421:ARG:HH11	1:R:421:ARG:HG3	1.41	0.81
1:R:48:ARG:HD2	1:R:48:ARG:O	1.84	0.78
2:A:276:GLU:OE1	2:A:276:GLU:N	2.16	0.78
1:R:50:LEU:HD12	1:R:50:LEU:O	1.83	0.78
1:R:170:ARG:HG3	1:R:170:ARG:HH11	1.50	0.77
3:P:10:LYS:CE	7:P:101:D6M:C07	2.63	0.77
1:R:421:ARG:HG3	1:R:421:ARG:NH1	1.98	0.74
2:A:268:VAL:HG11	2:A:301:VAL:HG12	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:39:ALA:O	5:G:43:ALA:HB2	1.89	0.73
4:B:39:PRO:HB3	4:B:301:LYS:HE2	1.69	0.73
1:R:234:GLN:HG3	1:R:284:TRP:CZ3	2.24	0.72
1:R:227:ARG:HB2	1:R:227:ARG:NH1	1.96	0.72
4:B:296:VAL:HG23	4:B:296:VAL:O	1.90	0.70
2:A:233:LEU:HD12	2:A:233:LEU:C	2.15	0.70
3:P:2:SER:HA	3:P:5:THR:HG22	1.72	0.70
1:R:423:GLU:HA	1:R:423:GLU:OE1	1.93	0.69
6:N:65:LYS:O	6:N:67:ARG:NH1	2.25	0.69
1:R:348:ARG:NE	1:R:348:ARG:O	2.26	0.69
1:R:47:GLN:HA	1:R:47:GLN:OE1	1.93	0.68
1:R:118:LEU:O	1:R:118:LEU:HG	1.94	0.68
1:R:419:ARG:NH1	1:R:419:ARG:HG3	2.08	0.68
6:N:3:GLN:HE22	6:N:5:GLN:HB2	1.58	0.68
1:R:349:LEU:C	1:R:349:LEU:HD23	2.18	0.68
1:R:419:ARG:HG3	1:R:419:ARG:HH11	1.58	0.68
4:B:296:VAL:HG22	4:B:306:GLY:CA	2.24	0.67
1:R:138:GLU:HA	1:R:138:GLU:OE2	1.94	0.67
2:A:232:ARG:HG2	2:A:232:ARG:NH1	2.02	0.67
4:B:233:CYS:SG	4:B:234:PHE:N	2.65	0.66
4:B:296:VAL:CG2	4:B:306:GLY:HA3	2.24	0.66
2:A:38:LEU:HD21	2:A:46:LYS:HG3	1.78	0.66
1:R:186:SER:OG	1:R:240:ASN:HA	1.96	0.66
1:R:44:ARG:HG3	1:R:44:ARG:HH11	1.61	0.65
1:R:142:LEU:HD12	1:R:142:LEU:C	2.20	0.65
6:N:71:SER:HB2	6:N:80:TYR:HB2	1.78	0.65
2:A:276:GLU:H	2:A:276:GLU:CD	2.05	0.65
4:B:296:VAL:HG22	4:B:306:GLY:HA3	1.80	0.64
1:R:306:TRP:HH2	3:P:1:HIS:ND1	1.95	0.64
2:A:356:ARG:HB2	2:A:356:ARG:NH1	2.04	0.64
2:A:359:GLU:N	2:A:359:GLU:OE1	2.31	0.63
4:B:300:LEU:HD12	4:B:300:LEU:H	1.62	0.63
1:R:219:SER:HA	1:R:222:ASP:OD1	1.99	0.63
5:G:21:MET:HE2	5:G:21:MET:C	2.23	0.63
1:R:160:VAL:HG12	1:R:188:ILE:CD1	2.29	0.62
1:R:170:ARG:HH11	1:R:170:ARG:CG	2.12	0.62
1:R:250:TYR:O	1:R:251:LEU:C	2.42	0.62
1:R:421:ARG:HD3	1:R:421:ARG:O	1.99	0.62
1:R:48:ARG:HH11	1:R:48:ARG:CG	2.13	0.62
1:R:306:TRP:HH2	3:P:1:HIS:CE1	2.17	0.61
1:R:310:ARG:NH1	1:R:372:ASP:HB2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:186:GLU:HG2	2:A:198:MET:HB3	1.83	0.61
1:R:54:PRO:HD2	1:R:73:PRO:HD2	1.80	0.61
1:R:217:LEU:HD13	1:R:217:LEU:N	2.16	0.61
6:N:83:MET:HE1	6:N:86:LEU:HG	1.83	0.61
6:N:22:CYS:HB2	6:N:79:LEU:HD13	1.81	0.61
2:A:356:ARG:HH11	2:A:356:ARG:CG	2.15	0.60
1:R:30:VAL:HG12	1:R:30:VAL:O	2.01	0.60
1:R:44:ARG:HE	1:R:47:GLN:HB2	1.66	0.60
1:R:419:ARG:HH11	1:R:419:ARG:CG	2.14	0.60
4:B:234:PHE:HE1	4:B:238:GLY:HA2	1.66	0.59
4:B:300:LEU:HD23	5:G:38:MET:CE	2.21	0.59
1:R:44:ARG:HH11	1:R:44:ARG:CG	2.17	0.58
1:R:230:PHE:CD2	1:R:298:THR:HG22	2.38	0.58
4:B:320:VAL:HG23	4:B:327:VAL:HG22	1.86	0.58
1:R:48:ARG:HD2	1:R:48:ARG:C	2.28	0.58
1:R:224:LEU:HD23	1:R:224:LEU:O	2.02	0.58
1:R:251:LEU:HD13	2:A:358:TYR:CZ	2.39	0.58
1:R:234:GLN:HG3	1:R:284:TRP:CH2	2.38	0.57
1:R:306:TRP:CH2	3:P:1:HIS:ND1	2.73	0.57
2:A:278:TYR:CD1	2:A:278:TYR:N	2.72	0.57
2:A:172:GLN:H	2:A:172:GLN:NE2	2.01	0.57
4:B:295:ASN:HB3	4:B:304:ARG:HG3	1.87	0.57
1:R:230:PHE:CE2	1:R:298:THR:HG22	2.40	0.56
1:R:231:LEU:HD23	1:R:231:LEU:O	2.04	0.56
6:N:39:GLN:HB2	6:N:45:LEU:HD13	1.86	0.56
4:B:331:SER:OG	4:B:333:ASP:OD1	2.22	0.56
4:B:264:TYR:CD1	4:B:264:TYR:N	2.72	0.56
4:B:270:ILE:HG13	4:B:270:ILE:O	2.06	0.56
2:A:275:ILE:O	2:A:275:ILE:HD12	2.06	0.55
3:P:2:SER:HA	3:P:5:THR:CG2	2.36	0.55
1:R:113:LYS:H	1:R:113:LYS:HD2	1.70	0.55
1:R:242:TYR:O	1:R:246:VAL:HG13	2.05	0.55
5:G:48:ASP:HB3	5:G:51:LEU:HD23	1.88	0.55
1:R:248:GLY:O	1:R:323:ILE:HG21	2.07	0.55
1:R:232:LEU:HD12	1:R:232:LEU:O	2.07	0.55
6:N:100:PRO:HD2	6:N:107:CYS:SG	2.47	0.55
2:A:234:GLN:O	2:A:234:GLN:NE2	2.41	0.54
1:R:246:VAL:O	1:R:246:VAL:HG23	2.07	0.54
1:R:421:ARG:HH11	1:R:421:ARG:CG	2.14	0.54
1:R:145:TYR:CD1	1:R:145:TYR:C	2.85	0.54
2:A:42:ASP:OD1	2:A:43:ASN:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:160:VAL:HG12	1:R:188:ILE:HD13	1.89	0.54
4:B:290:ASP:OD1	4:B:314:ARG:NE	2.38	0.54
1:R:148:TYR:CD1	1:R:148:TYR:C	2.86	0.54
4:B:33:ILE:HG23	4:B:34:THR:HG23	1.90	0.54
1:R:180:HIS:CE1	1:R:247:GLU:OE2	2.61	0.54
1:R:245:LEU:HD12	1:R:245:LEU:O	2.08	0.53
1:R:372:ASP:HA	1:R:383:LYS:NZ	2.23	0.53
4:B:298:ASP:HB2	4:B:301:LYS:HB2	1.90	0.53
2:A:226:ASP:OD2	2:A:229:ASP:HB3	2.10	0.52
1:R:48:ARG:HG3	1:R:48:ARG:NH1	2.19	0.52
1:R:324:PHE:CD1	1:R:324:PHE:C	2.87	0.52
1:R:44:ARG:NE	1:R:44:ARG:HA	2.25	0.52
1:R:44:ARG:NH1	1:R:44:ARG:HB3	2.25	0.51
1:R:348:ARG:NH2	1:R:352:SER:OG	2.43	0.51
4:B:58:ILE:O	4:B:316:SER:OG	2.23	0.51
2:A:356:ARG:NH1	2:A:356:ARG:CG	2.73	0.51
1:R:156:PHE:HE1	1:R:188:ILE:HG23	1.75	0.51
1:R:44:ARG:NE	1:R:44:ARG:CA	2.73	0.51
1:R:160:VAL:HG12	1:R:188:ILE:HD11	1.91	0.51
1:R:385:PHE:O	1:R:389:SER:OG	2.25	0.50
1:R:420:TRP:CE3	1:R:420:TRP:C	2.89	0.50
4:B:139:LEU:HD12	4:B:169:TRP:CE3	2.47	0.50
1:R:388:LEU:N	1:R:388:LEU:HD23	2.26	0.50
1:R:226:CYS:SG	1:R:227:ARG:N	2.84	0.50
2:A:229:ASP:OD2	2:A:232:ARG:HD3	2.11	0.50
1:R:57:ALA:CB	1:R:75:GLY:O	2.60	0.50
1:R:349:LEU:HG	1:R:349:LEU:O	2.10	0.50
4:B:39:PRO:HB3	4:B:301:LYS:CE	2.40	0.50
4:B:296:VAL:CG2	4:B:306:GLY:CA	2.88	0.50
2:A:339:ILE:HD12	2:A:339:ILE:C	2.36	0.50
4:B:323:ASP:OD1	4:B:323:ASP:N	2.41	0.50
4:B:210:LEU:HD23	4:B:219:ARG:HB2	1.94	0.50
1:R:44:ARG:CG	1:R:44:ARG:NH1	2.75	0.49
2:A:172:GLN:H	2:A:172:GLN:CD	2.21	0.49
2:A:232:ARG:NH1	2:A:232:ARG:CG	2.73	0.49
1:R:57:ALA:HB2	1:R:76:GLU:HA	1.94	0.49
1:R:170:ARG:CG	1:R:170:ARG:NH1	2.73	0.49
1:R:385:PHE:CD1	1:R:385:PHE:C	2.91	0.49
4:B:294:CYS:HB2	4:B:308:LEU:HB2	1.93	0.49
1:R:204:MET:HG3	1:R:221:GLN:HE21	1.77	0.49
1:R:345:ILE:H	1:R:345:ILE:HG12	1.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:283:PRO:O	1:R:287:VAL:HG23	2.13	0.48
3:P:1:HIS:ND1	3:P:1:HIS:N	2.60	0.48
1:R:44:ARG:NH2	1:R:44:ARG:O	2.46	0.48
4:B:160:SER:HB2	4:B:190:LEU:HD23	1.94	0.48
5:G:19:LEU:HD22	5:G:19:LEU:O	2.13	0.48
1:R:370:VAL:HG13	1:R:371:MET:SD	2.54	0.48
4:B:296:VAL:HG22	4:B:306:GLY:C	2.38	0.48
1:R:66:PHE:HD1	1:R:71:CYS:HB3	1.79	0.48
1:R:255:LEU:N	1:R:255:LEU:HD23	2.28	0.48
2:A:205:ARG:NH2	4:B:186:ASP:OD1	2.47	0.48
1:R:306:TRP:HZ2	3:P:1:HIS:N	2.12	0.48
1:R:116:SER:O	1:R:116:SER:OG	2.31	0.47
1:R:50:LEU:HD12	1:R:50:LEU:C	2.38	0.47
1:R:103:PHE:H	1:R:120:TRP:HD1	1.62	0.47
2:A:314:ARG:O	2:A:317:THR:OG1	2.29	0.47
1:R:159:LEU:HD13	1:R:187:PHE:HB3	1.97	0.47
1:R:233:MET:C	1:R:235:TYR:H	2.23	0.47
4:B:296:VAL:O	4:B:296:VAL:CG2	2.60	0.47
1:R:327:VAL:O	1:R:327:VAL:HG12	2.15	0.47
1:R:315:PHE:O	1:R:319:VAL:HG23	2.14	0.47
1:R:114:ASP:HB2	1:R:117:SER:HB2	1.97	0.46
1:R:44:ARG:HB3	1:R:44:ARG:CZ	2.46	0.46
1:R:156:PHE:CE1	1:R:188:ILE:HG23	2.50	0.46
1:R:231:LEU:HB2	1:R:297:TRP:CZ3	2.50	0.46
1:R:377:GLY:C	1:R:379:LEU:N	2.72	0.46
2:A:10:LYS:HA	2:A:10:LYS:HD3	1.40	0.46
1:R:57:ALA:HB2	1:R:75:GLY:O	2.15	0.46
1:R:217:LEU:N	1:R:217:LEU:CD1	2.77	0.46
2:A:265:ALA:O	2:A:266:GLU:C	2.58	0.46
1:R:102:ARG:HA	1:R:120:TRP:CD1	2.51	0.46
2:A:17:LYS:HA	2:A:17:LYS:HD3	1.66	0.46
1:R:65:THR:HB	1:R:66:PHE:H	1.49	0.46
1:R:286:ILE:O	1:R:290:LEU:HB2	2.15	0.46
4:B:278:PHE:CE1	4:B:285:LEU:HD13	2.51	0.46
2:A:180:LYS:HB2	2:A:180:LYS:HE2	1.58	0.46
2:A:278:TYR:H	2:A:278:TYR:HD1	1.63	0.46
4:B:127:LYS:HD3	4:B:127:LYS:HA	1.77	0.46
4:B:266:HIS:HB3	4:B:269:ILE:HG12	1.98	0.46
1:R:227:ARG:HH11	1:R:227:ARG:CG	2.29	0.45
5:G:25:ILE:HD12	5:G:26:ASP:H	1.81	0.45
1:R:230:PHE:CE2	1:R:298:THR:CG2	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:213:GLN:HG2	2:A:248:TRP:CD1	2.50	0.45
2:A:298:ASP:O	2:A:301:VAL:HG22	2.16	0.45
1:R:180:HIS:ND1	1:R:247:GLU:OE2	2.48	0.45
2:A:234:GLN:HE21	2:A:238:ASN:HD21	1.62	0.45
1:R:48:ARG:CG	1:R:48:ARG:NH1	2.73	0.45
1:R:420:TRP:O	1:R:420:TRP:CD2	2.70	0.45
4:B:303:ASP:O	4:B:304:ARG:C	2.59	0.45
1:R:374:HIS:O	1:R:375:ALA:C	2.60	0.45
1:R:417:TRP:CH2	1:R:421:ARG:NH1	2.85	0.45
2:A:307:PHE:O	2:A:307:PHE:CG	2.69	0.45
1:R:248:GLY:C	1:R:323:ILE:HD13	2.42	0.45
6:N:112:SER:O	6:N:118:ARG:NH2	2.39	0.45
1:R:324:PHE:O	1:R:324:PHE:CG	2.70	0.45
1:R:371:MET:HE2	1:R:371:MET:HB2	1.70	0.45
1:R:154:LEU:HD13	7:P:101:D6M:H262	1.99	0.45
4:B:161:SER:OG	4:B:163:ASP:OD1	2.32	0.44
1:R:44:ARG:CZ	1:R:44:ARG:CB	2.94	0.44
1:R:110:TRP:HD1	1:R:119:PRO:HB3	1.82	0.44
1:R:48:ARG:C	1:R:48:ARG:CD	2.89	0.44
1:R:377:GLY:C	1:R:379:LEU:H	2.26	0.44
6:N:37:VAL:HG13	6:N:95:TYR:HB2	1.99	0.44
1:R:231:LEU:CD1	1:R:285:GLY:HA3	2.47	0.44
2:A:175:LEU:HD13	2:A:175:LEU:HA	1.79	0.44
4:B:159:THR:OG1	4:B:169:TRP:NE1	2.41	0.44
1:R:204:MET:HE3	1:R:221:GLN:CG	2.47	0.44
1:R:420:TRP:CE3	1:R:420:TRP:O	2.70	0.44
5:G:39:ALA:O	5:G:43:ALA:CB	2.63	0.44
1:R:220:TYR:CD1	1:R:220:TYR:O	2.70	0.44
6:N:51:ILE:HG12	6:N:55:GLY:HA2	1.99	0.44
1:R:205:TYR:HB3	1:R:206:SER:H	1.56	0.44
1:R:218:LEU:O	1:R:222:ASP:N	2.51	0.44
1:R:252:TYR:O	1:R:252:TYR:CG	2.70	0.44
1:R:289:TYR:O	1:R:289:TYR:CG	2.70	0.44
4:B:39:PRO:CB	4:B:301:LYS:CE	2.79	0.44
4:B:298:ASP:CB	4:B:301:LYS:HB2	2.47	0.44
1:R:324:PHE:CD1	1:R:324:PHE:O	2.70	0.43
1:R:306:TRP:CZ2	3:P:1:HIS:N	2.87	0.43
1:R:411:LEU:N	1:R:411:LEU:HD23	2.32	0.43
1:R:418:GLU:CD	1:R:418:GLU:C	2.85	0.43
2:A:310:ASP:HA	2:A:313:LEU:HB2	2.00	0.43
1:R:346:LYS:HD2	1:R:346:LYS:HA	1.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:303:MET:HE2	1:R:373:GLU:HB3	1.99	0.43
1:R:328:ILE:O	1:R:328:ILE:HG22	2.18	0.43
4:B:325:MET:O	4:B:340:ASN:ND2	2.51	0.43
1:R:254:LEU:C	1:R:255:LEU:HD23	2.43	0.43
2:A:191:VAL:HG21	2:A:339:ILE:HD13	1.99	0.43
4:B:286:LEU:HB3	4:B:318:LEU:HD21	2.01	0.43
3:P:18:ARG:HA	3:P:18:ARG:HD3	1.49	0.43
1:R:306:TRP:HA	1:R:306:TRP:CE3	2.54	0.43
6:N:20:LEU:HB2	6:N:81:LEU:HB2	2.01	0.42
6:N:51:ILE:HB	6:N:70:ILE:HD12	2.02	0.42
2:A:356:ARG:O	2:A:356:ARG:HG2	2.19	0.42
4:B:235:PHE:CG	4:B:236:PRO:HD2	2.55	0.42
2:A:276:GLU:N	2:A:276:GLU:CD	2.73	0.42
1:R:102:ARG:HE	1:R:102:ARG:HB3	1.66	0.42
2:A:249:LEU:HA	2:A:252:ILE:HD13	2.01	0.42
2:A:268:VAL:CG1	2:A:301:VAL:HG12	2.43	0.42
4:B:296:VAL:HG22	4:B:306:GLY:O	2.19	0.42
1:R:417:TRP:HH2	1:R:421:ARG:HH12	1.66	0.42
4:B:165:THR:HG22	4:B:181:THR:HG22	2.02	0.42
1:R:306:TRP:HA	1:R:306:TRP:HE3	1.85	0.42
2:A:46:LYS:HB3	2:A:46:LYS:HE3	1.75	0.42
1:R:63:ASN:HD22	1:R:63:ASN:HA	1.56	0.41
1:R:422:LEU:HA	1:R:422:LEU:HD23	1.77	0.41
1:R:204:MET:HE3	1:R:221:GLN:HG2	2.02	0.41
4:B:51:LEU:HB3	4:B:82:TRP:CZ3	2.54	0.41
1:R:186:SER:OG	1:R:240:ASN:CA	2.66	0.41
1:R:197:LYS:HE3	1:R:197:LYS:HB3	1.66	0.41
1:R:347:CYS:O	1:R:347:CYS:SG	2.79	0.41
2:A:186:GLU:H	2:A:186:GLU:HG3	1.68	0.41
4:B:274:THR:HG21	4:B:316:SER:HA	2.02	0.41
1:R:289:TYR:O	1:R:289:TYR:CD2	2.74	0.41
5:G:19:LEU:HD22	5:G:19:LEU:C	2.46	0.41
1:R:231:LEU:HD13	1:R:297:TRP:HZ3	1.86	0.41
4:B:245:SER:HB2	4:B:247:ASP:OD1	2.20	0.41
4:B:297:TRP:CE2	4:B:304:ARG:HB2	2.56	0.41
5:G:19:LEU:C	5:G:19:LEU:CD2	2.93	0.41
6:N:6:GLU:OE2	6:N:6:GLU:N	2.53	0.41
1:R:102:ARG:HB2	1:R:110:TRP:CE3	2.55	0.41
2:A:340:ARG:HA	2:A:340:ARG:HD3	1.67	0.41
4:B:244:GLY:HA3	4:B:273:ILE:HG21	2.02	0.41
1:R:160:VAL:CG1	1:R:188:ILE:HD11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:298:ASP:HA	2:A:299:PRO:HD3	1.97	0.41
4:B:276:VAL:HG13	4:B:285:LEU:HD11	2.02	0.41
6:N:64:VAL:O	6:N:64:VAL:HG13	2.21	0.41
1:R:110:TRP:HB2	1:R:111:LEU:H	1.69	0.40
1:R:59:ASP:HB3	1:R:60:LEU:H	1.66	0.40
1:R:233:MET:C	1:R:235:TYR:N	2.79	0.40
2:A:187:THR:O	2:A:188:LYS:C	2.65	0.40
4:B:219:ARG:H	4:B:219:ARG:HG2	1.61	0.40
6:N:104:THR:HG22	6:N:106:ASP:H	1.86	0.40
2:A:229:ASP:OD2	2:A:232:ARG:HB2	2.22	0.40
4:B:12:GLU:O	4:B:16:ASN:ND2	2.54	0.40
1:R:265:ILE:HD13	1:R:265:ILE:HA	1.94	0.40
5:G:34:ALA:O	5:G:38:MET:HG2	2.22	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	R	382/440 (87%)	337 (88%)	38 (10%)	7 (2%)	6	15
2	A	241/361 (67%)	221 (92%)	19 (8%)	1 (0%)	30	48
3	P	27/29 (93%)	25 (93%)	1 (4%)	1 (4%)	2	5
4	B	336/345 (97%)	321 (96%)	15 (4%)	0	100	100
5	G	54/70 (77%)	53 (98%)	1 (2%)	0	100	100
6	N	124/140 (89%)	121 (98%)	3 (2%)	0	100	100
All	All	1164/1385 (84%)	1078 (93%)	77 (7%)	9 (1%)	18	31

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	62	CYS
1	R	63	ASN
1	R	65	THR
2	A	272	LYS
3	P	3	GLN
1	R	74	ASP
1	R	234	GLN
1	R	372	ASP
1	R	77	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	R	327/392 (83%)	244 (75%)	83 (25%)	0	0
2	A	218/316 (69%)	184 (84%)	34 (16%)	2	4
3	P	24/24 (100%)	16 (67%)	8 (33%)	0	0
4	B	279/287 (97%)	258 (92%)	21 (8%)	12	26
5	G	45/57 (79%)	42 (93%)	3 (7%)	15	31
6	N	104/116 (90%)	104 (100%)	0	100	100
All	All	997/1192 (84%)	848 (85%)	149 (15%)	5	5

All (149) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	31	SER
1	R	36	VAL
1	R	43	ARG
1	R	44	ARG
1	R	47	GLN
1	R	50	LEU
1	R	60	LEU
1	R	61	PHE
1	R	62	CYS
1	R	63	ASN

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Mol	Chain	Res	Type
1	R	65	THR
1	R	74	ASP
1	R	76	GLU
1	R	80	PHE
1	R	89	LEU
1	R	100	VAL
1	R	102	ARG
1	R	105	THR
1	R	107	GLU
1	R	112	GLN
1	R	113	LYS
1	R	118	LEU
1	R	125	GLU
1	R	138	GLU
1	R	139	GLU
1	R	142	LEU
1	R	146	ILE
1	R	147	ILE
1	R	148	TYR
1	R	170	ARG
1	R	172	LEU
1	R	189	LEU
1	R	192	LEU
1	R	197	LYS
1	R	201	LEU
1	R	204	MET
1	R	215	ASP
1	R	217	LEU
1	R	218	LEU
1	R	221	GLN
1	R	227	ARG
1	R	228	LEU
1	R	246	VAL
1	R	249	VAL
1	R	259	VAL
1	R	261	SER
1	R	263	GLN
1	R	265	ILE
1	R	268	LEU
1	R	270	VAL
1	R	290	LEU
1	R	292	GLU

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Mol	Chain	Res	Type
1	R	294	GLU
1	R	306	TRP
1	R	325	VAL
1	R	332	VAL
1	R	334	LYS
1	R	343	THR
1	R	345	ILE
1	R	346	LYS
1	R	348	ARG
1	R	349	LEU
1	R	351	LYS
1	R	353	THR
1	R	355	THR
1	R	362	THR
1	R	369	PHE
1	R	370	VAL
1	R	371	MET
1	R	372	ASP
1	R	373	GLU
1	R	384	LEU
1	R	388	LEU
1	R	389	SER
1	R	398	VAL
1	R	405	VAL
1	R	407	ASN
1	R	411	LEU
1	R	412	GLU
1	R	418	GLU
1	R	419	ARG
1	R	421	ARG
1	R	423	GLU
2	A	5	LEU
2	A	8	GLU
2	A	10	LYS
2	A	14	GLU
2	A	15	ARG
2	A	17	LYS
2	A	19	ILE
2	A	51	LYS
2	A	171	GLN
2	A	172	GLN
2	A	173	ASP

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Mol	Chain	Res	Type
2	A	174	VAL
2	A	175	LEU
2	A	177	THR
2	A	180	LYS
2	A	184	ILE
2	A	187	THR
2	A	188	LYS
2	A	229	ASP
2	A	232	ARG
2	A	233	LEU
2	A	235	GLU
2	A	237	LEU
2	A	267	LYS
2	A	268	VAL
2	A	275	ILE
2	A	278	TYR
2	A	284	ARG
2	A	286	THR
2	A	289	GLU
2	A	292	THR
2	A	308	ILE
2	A	356	ARG
2	A	359	GLU
3	P	1	HIS
3	P	2	SER
3	P	11	SER
3	P	15	ASP
3	P	18	ARG
3	P	20	GLN
3	P	26	LEU
3	P	27	GLU
4	B	4	LEU
4	B	123	ILE
4	B	127	LYS
4	B	133	VAL
4	B	134	ARG
4	B	135	VAL
4	B	136	SER
4	B	178	THR
4	B	213	VAL
4	B	214	ARG
4	B	215	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	B	217	MET
4	B	220	GLN
4	B	221	THR
4	B	264	TYR
4	B	298	ASP
4	B	300	LEU
4	B	301	LYS
4	B	303	ASP
4	B	304	ARG
4	B	307	VAL
5	G	19	LEU
5	G	21	MET
5	G	25	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	63	ASN
1	R	82	ASN
1	R	99	HIS
1	R	221	GLN
1	R	234	GLN
1	R	240	ASN
1	R	363	HIS
1	R	394	GLN
2	A	24	GLN
2	A	172	GLN
2	A	195	ASN
2	A	238	ASN
2	A	338	ASN
3	P	20	GLN
4	B	44	GLN
4	B	125	ASN
4	B	183	HIS
5	G	24	ASN
6	N	3	GLN
6	N	5	GLN
6	N	123	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
7	D6M	P	101	-	24,25,26	0.62	0	27,27,29	0.90	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	D6M	P	101	-	-	4/27/27/28	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

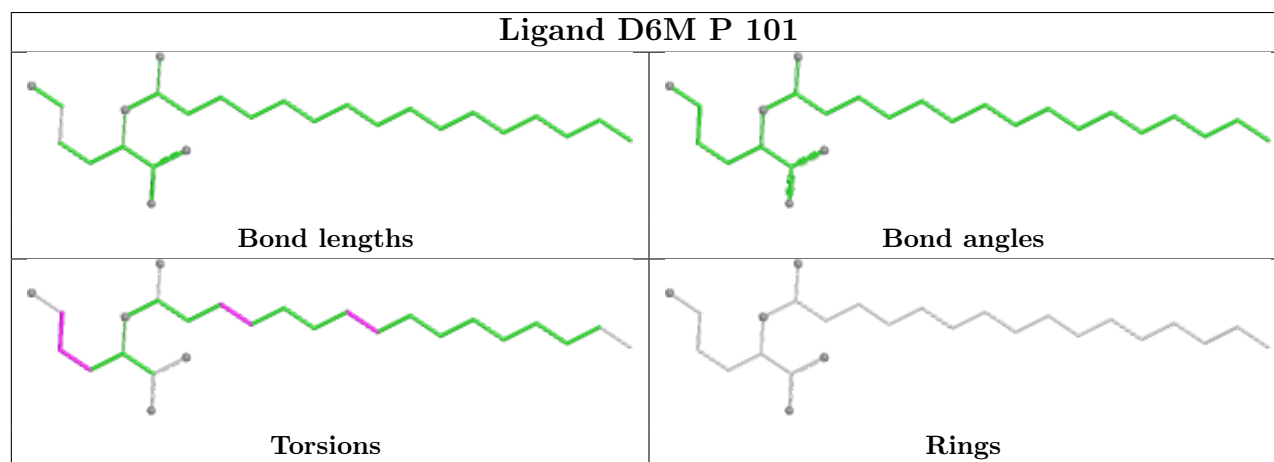
Mol	Chain	Res	Type	Atoms
7	P	101	D6M	C05-C06-C07-O08
7	P	101	D6M	C16-C17-C18-C19
7	P	101	D6M	C04-C05-C06-C07
7	P	101	D6M	C12-C13-C14-C15

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	P	101	D6M	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

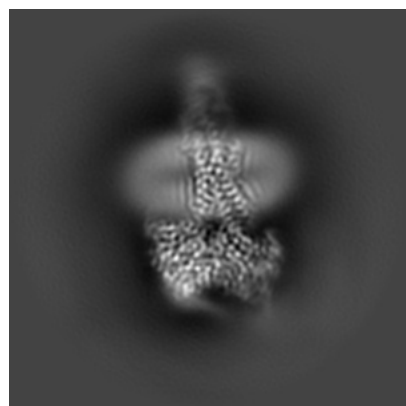
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36323. These allow visual inspection of the internal detail of the map and identification of artifacts.

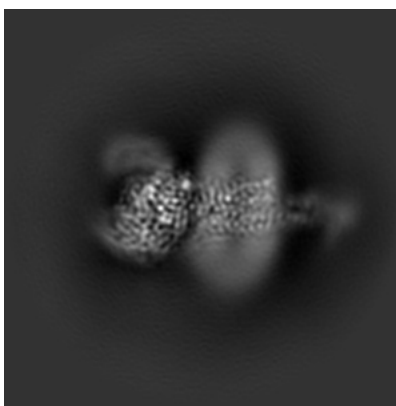
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

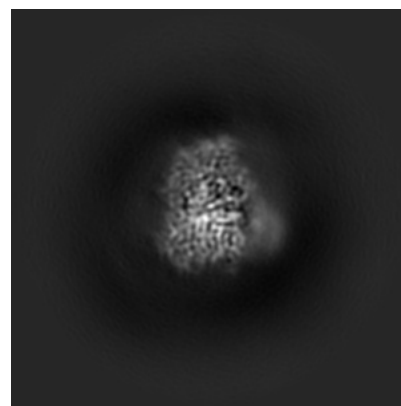
6.1.1 Primary map



X

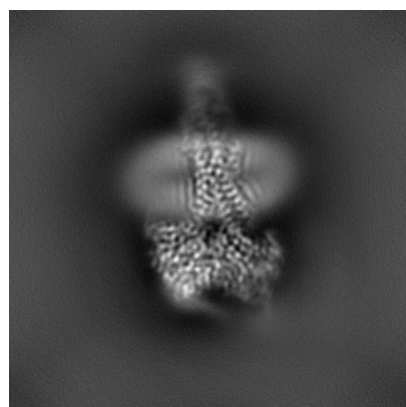


Y

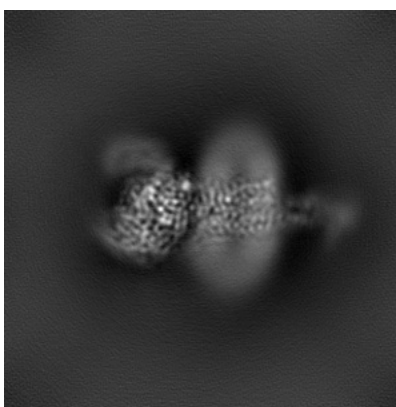


Z

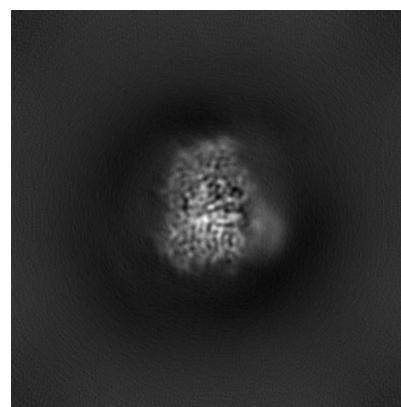
6.1.2 Raw map



X



Y

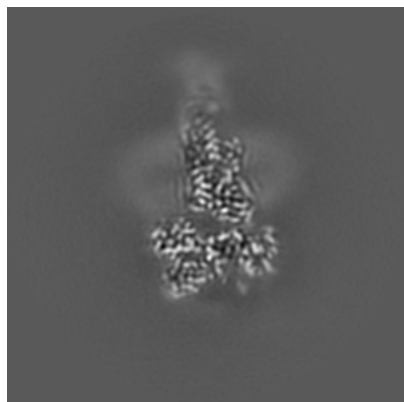


Z

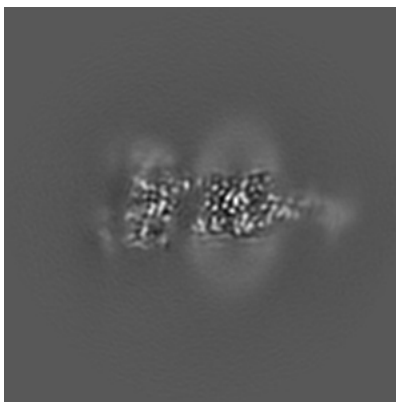
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

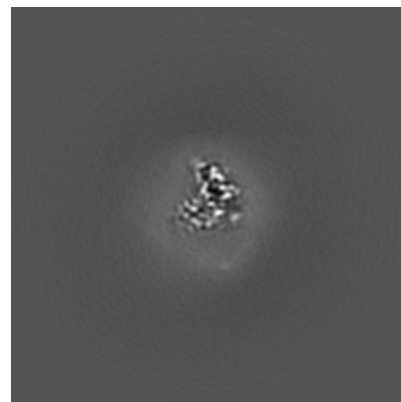
6.2.1 Primary map



X Index: 144

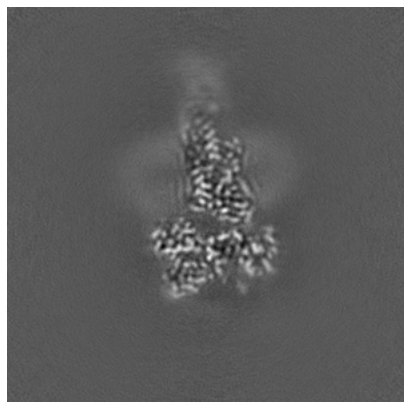


Y Index: 144

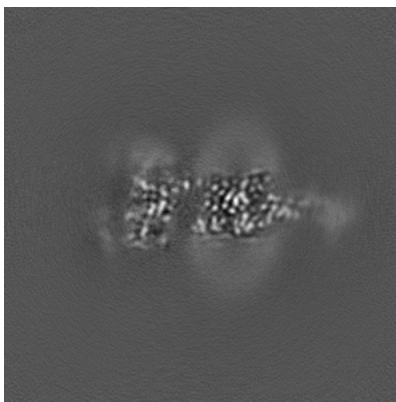


Z Index: 144

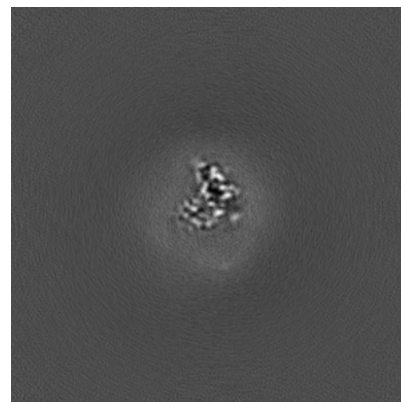
6.2.2 Raw map



X Index: 144



Y Index: 144

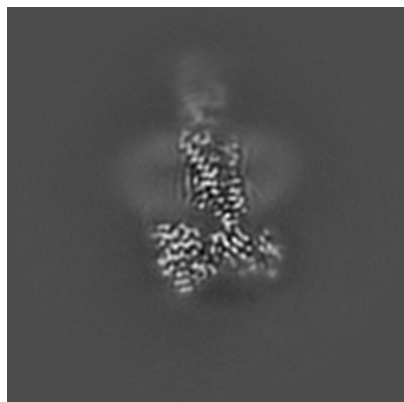


Z Index: 144

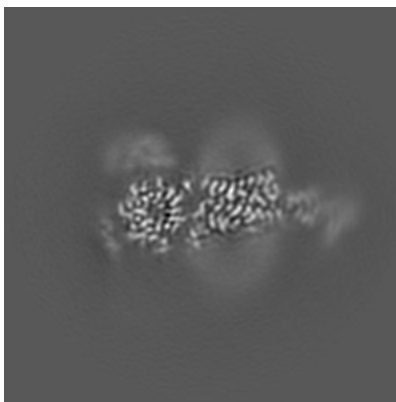
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

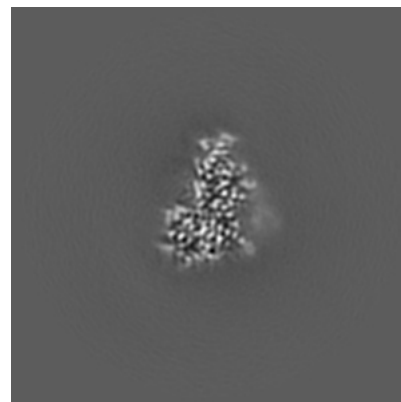
6.3.1 Primary map



X Index: 150

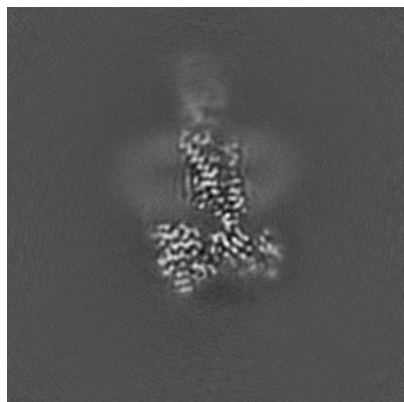


Y Index: 136

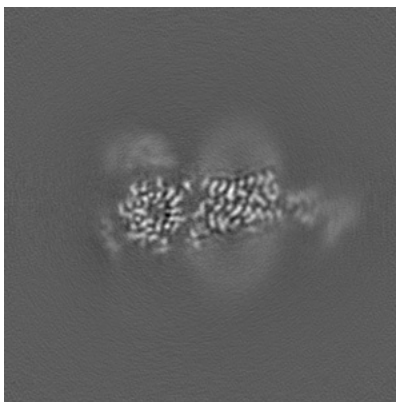


Z Index: 115

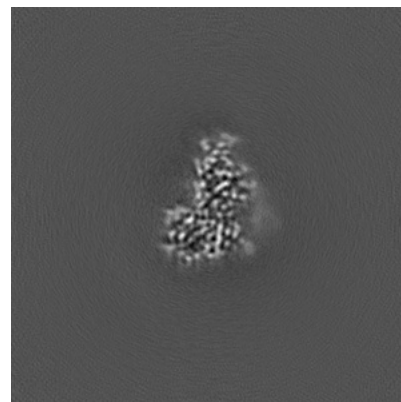
6.3.2 Raw map



X Index: 150



Y Index: 136

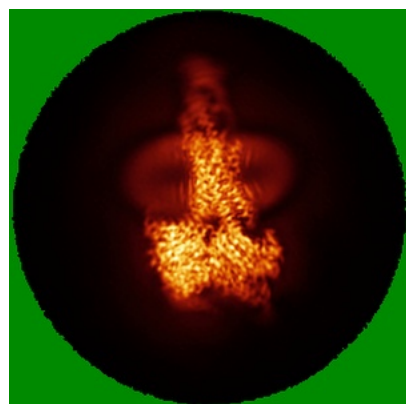


Z Index: 116

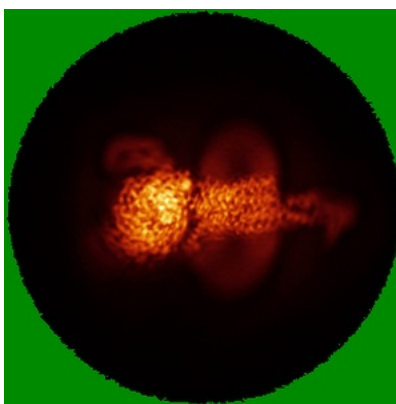
The images above show the largest variance slices of the map in three orthogonal directions.

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

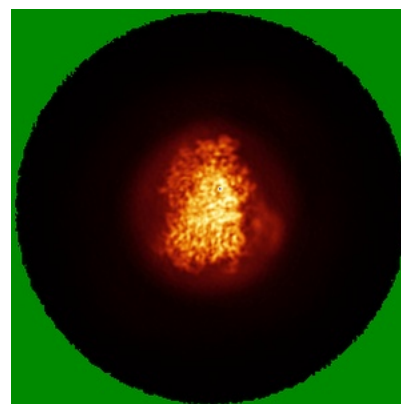
6.4.1 Primary map



X

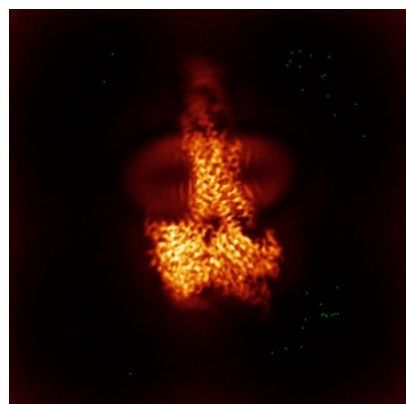


Y

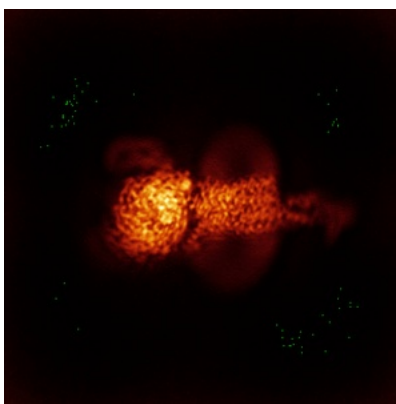


Z

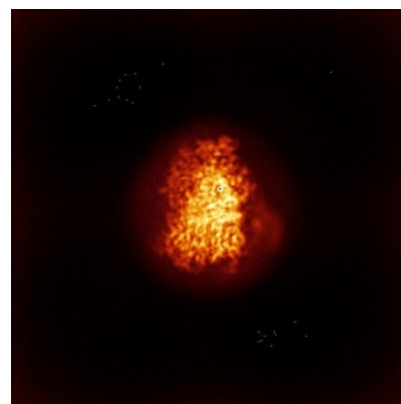
6.4.2 Raw map



X



Y

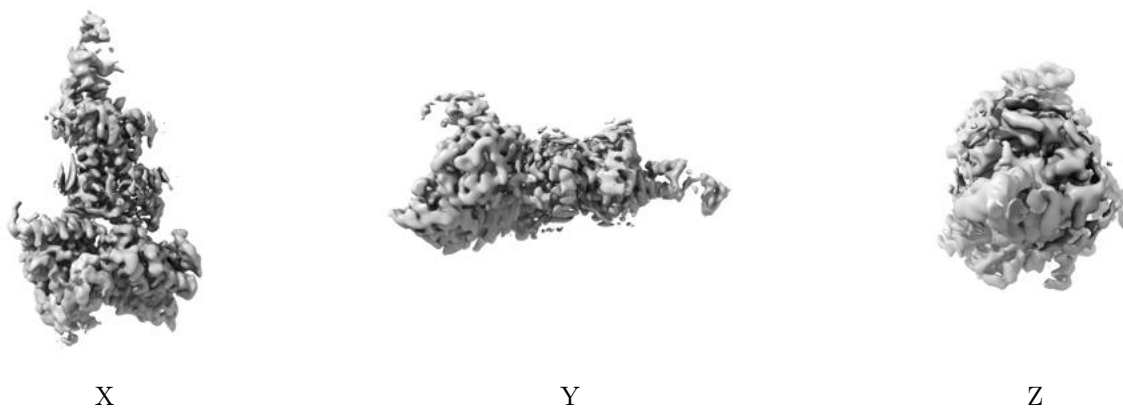


Z

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.

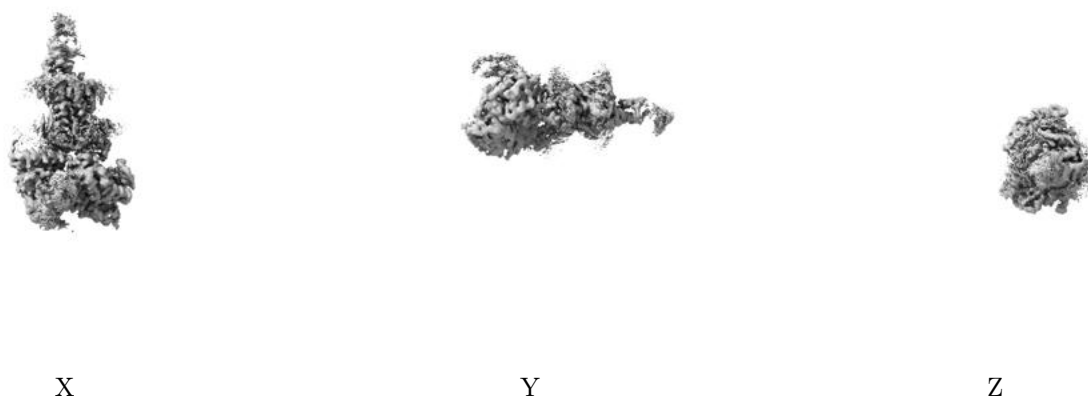
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.059. 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.

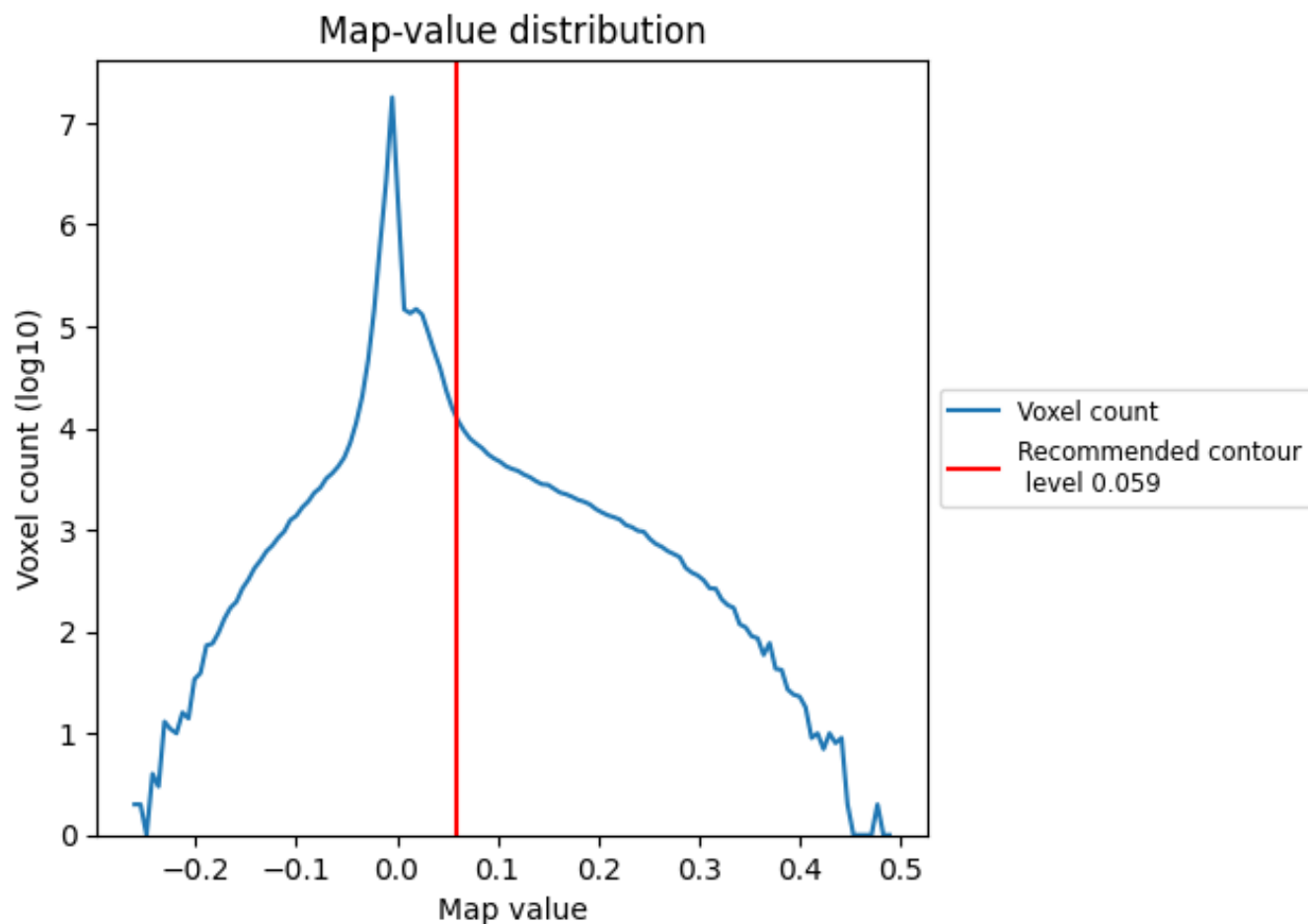
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

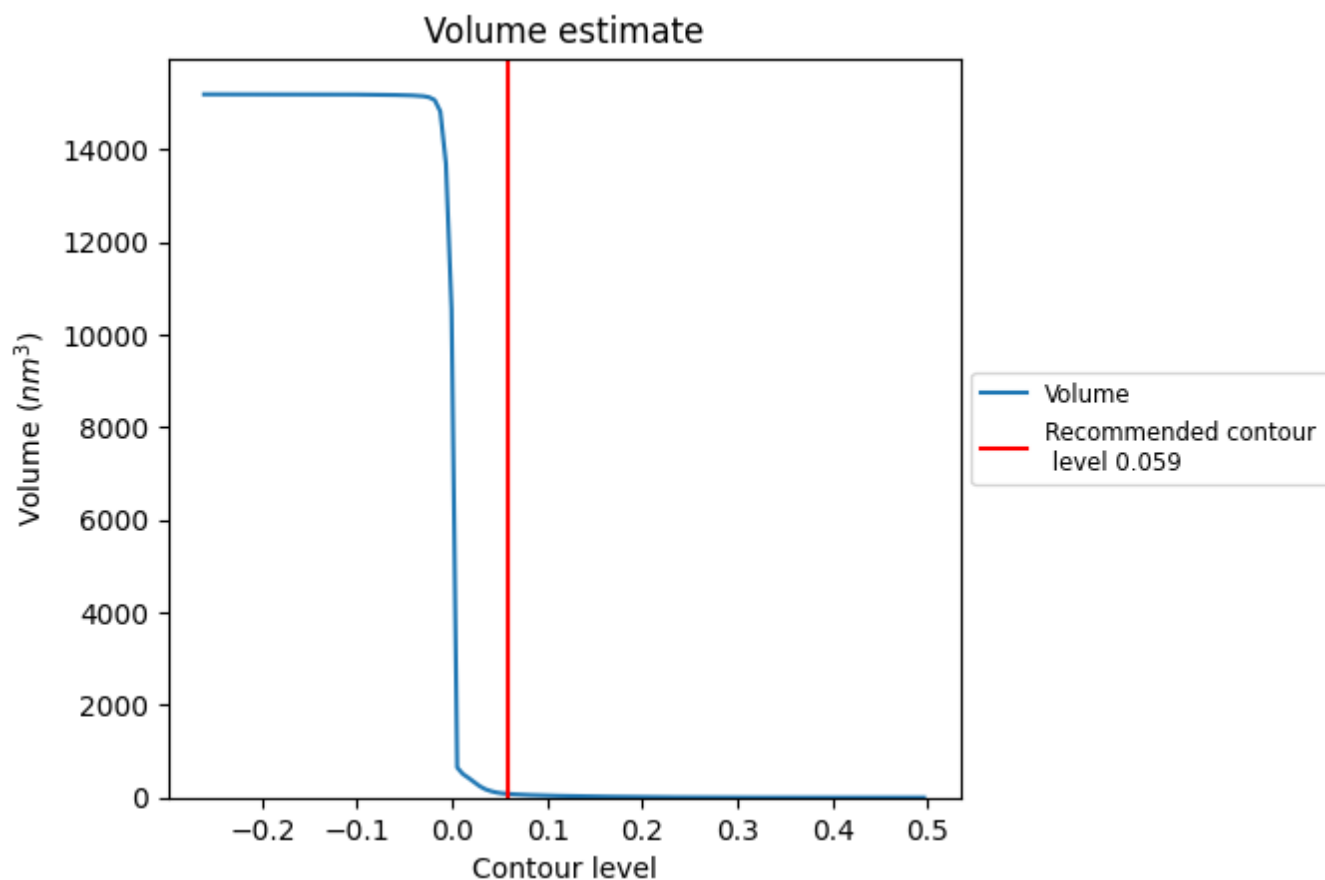
This section contains the results of statistical analysis of the map.

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.

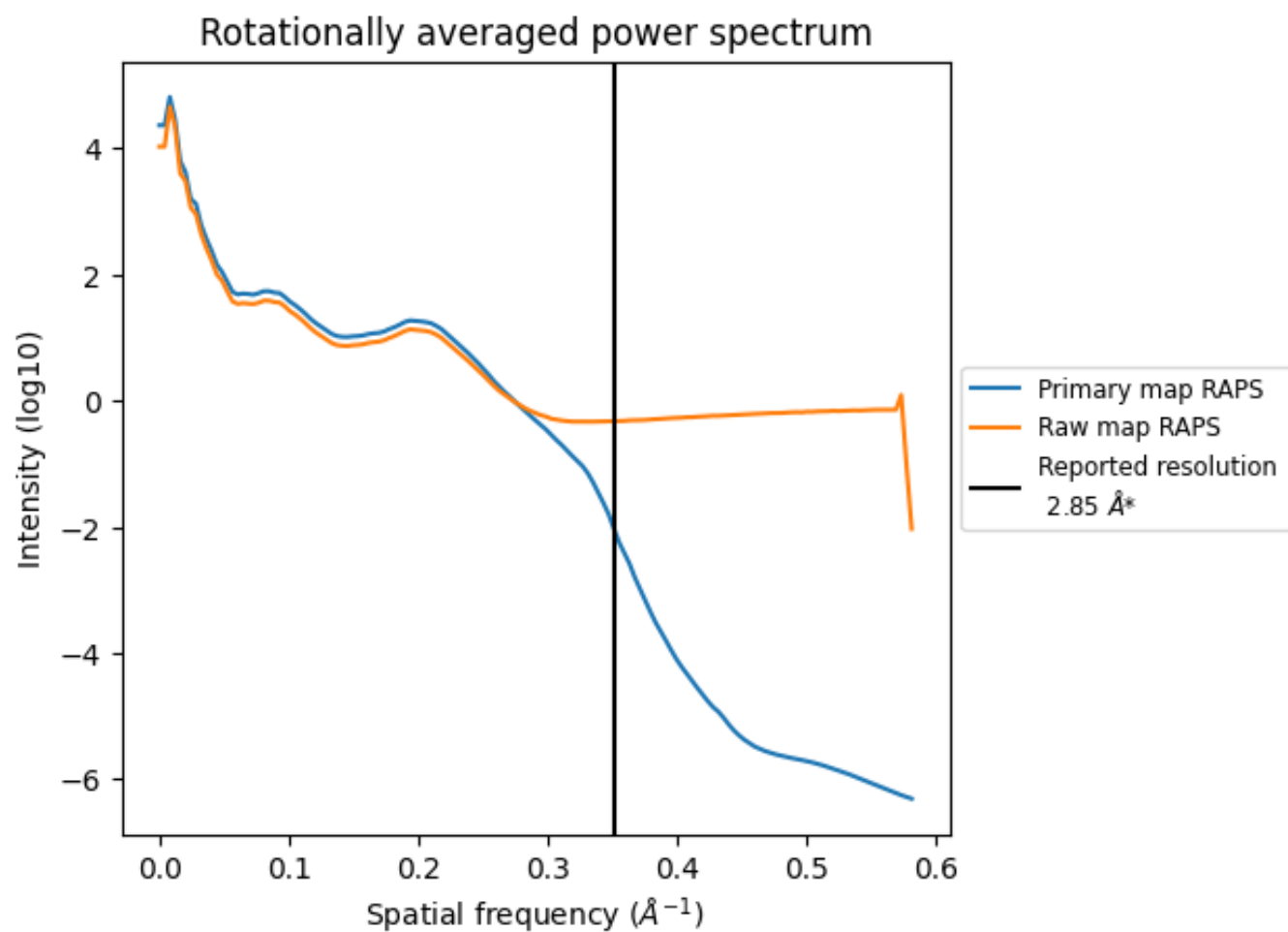
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 78 nm^3 ; this corresponds to an approximate mass of 71 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 ⓘ

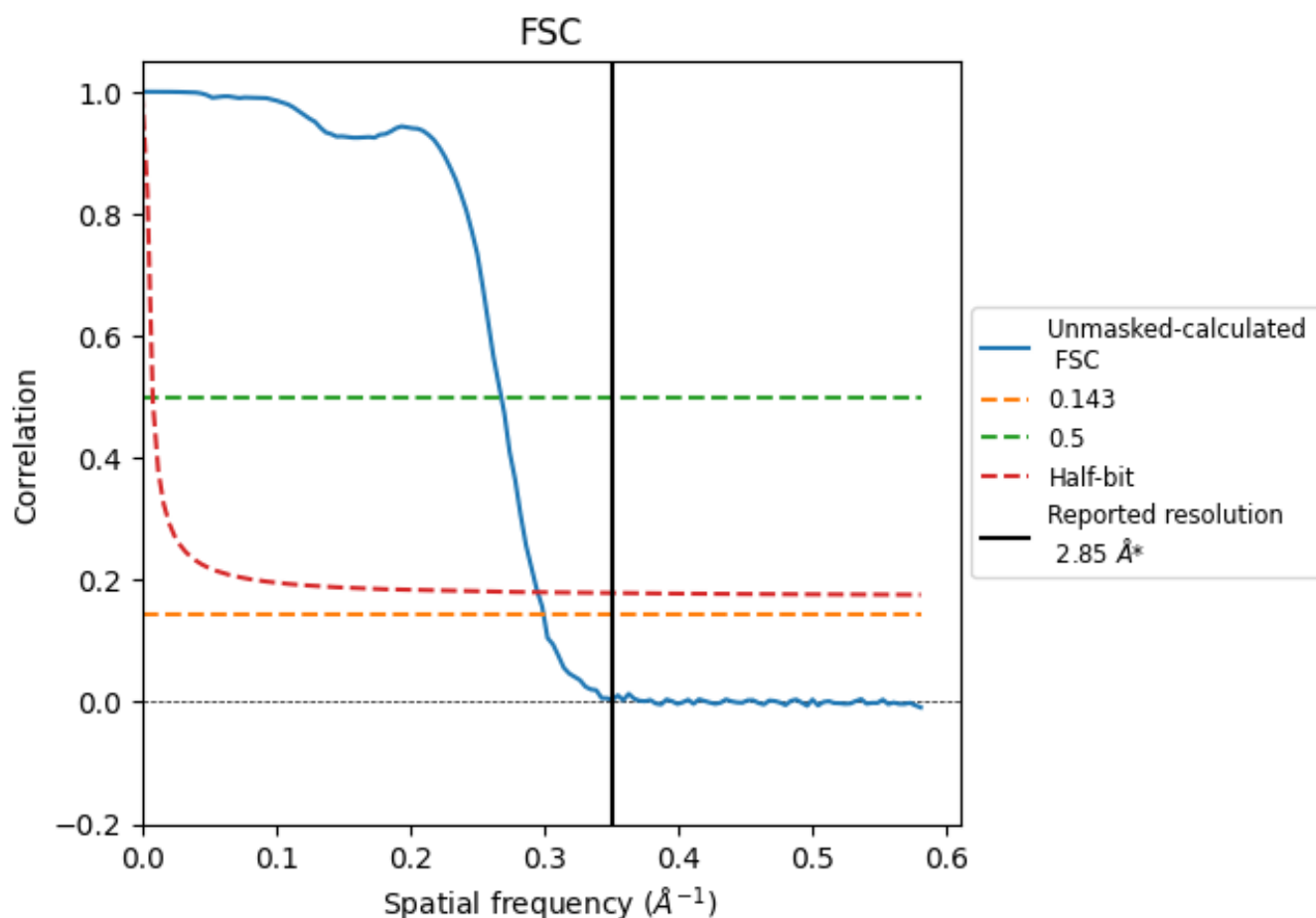


*Reported resolution corresponds to spatial frequency of $0.351 \text{ \AA}^{-1}$

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 0.351 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

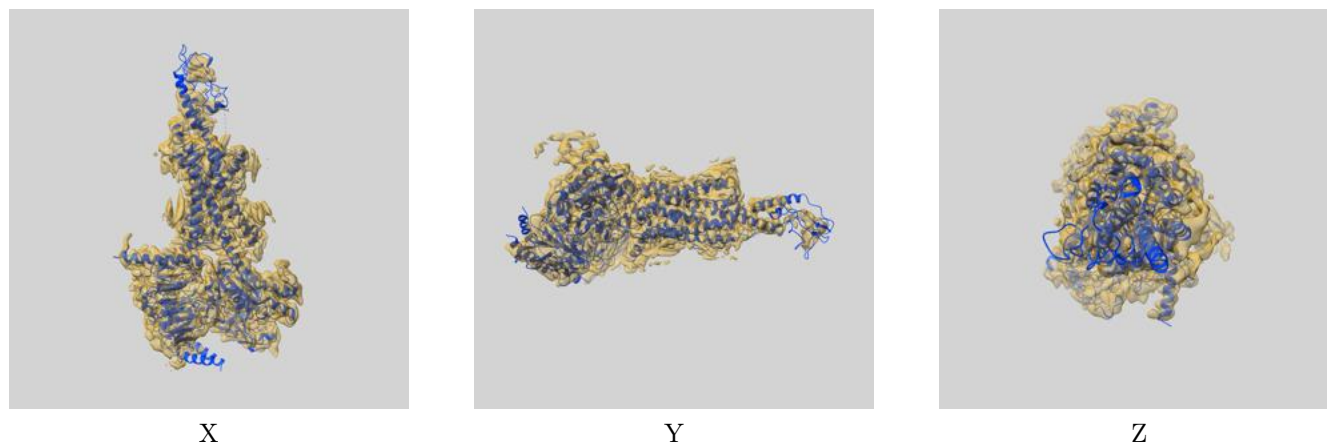
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.34	3.73	3.39

*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 3.34 differs from the reported value 2.85 by more than 10 %

9 Map-model fit [i](#)

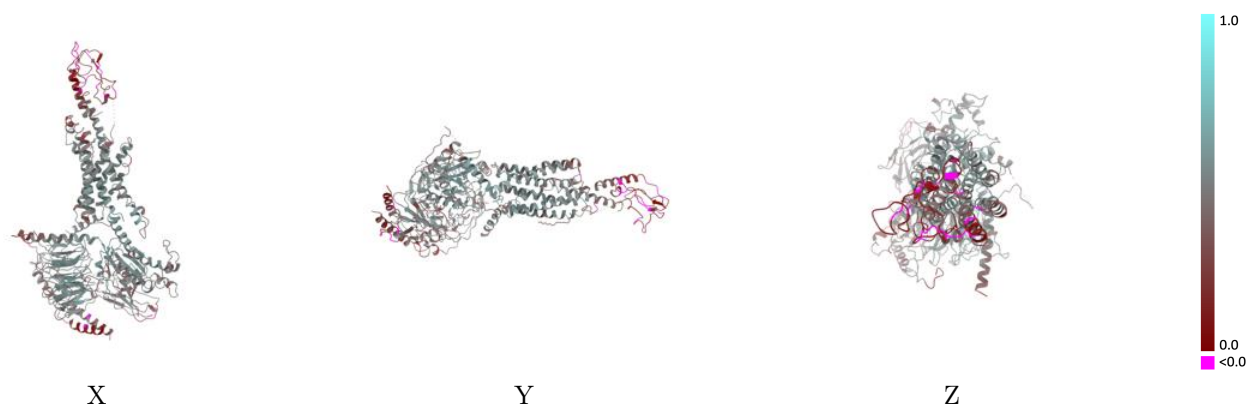
This section contains information regarding the fit between EMDB map EMD-36323 and PDB model 8JIP. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



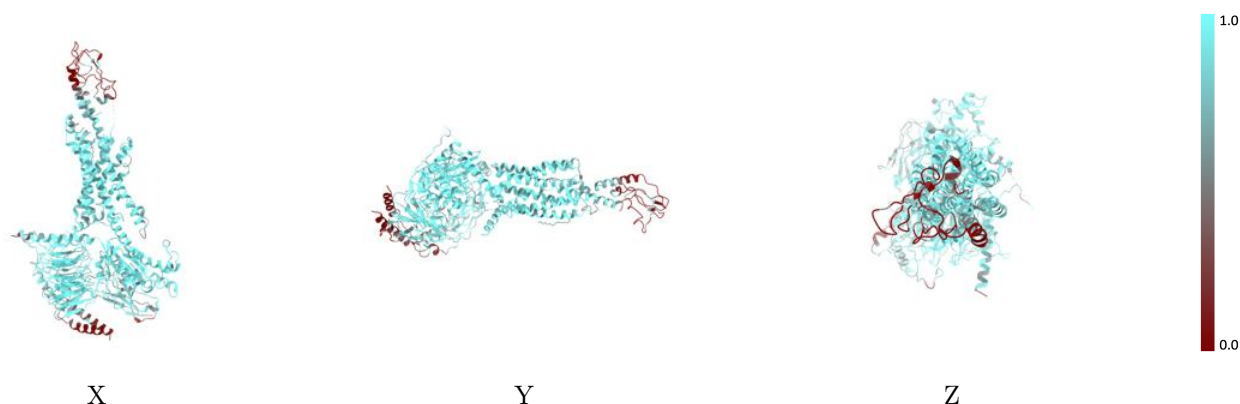
The images above show the 3D surface view of the map at the recommended contour level 0.059 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



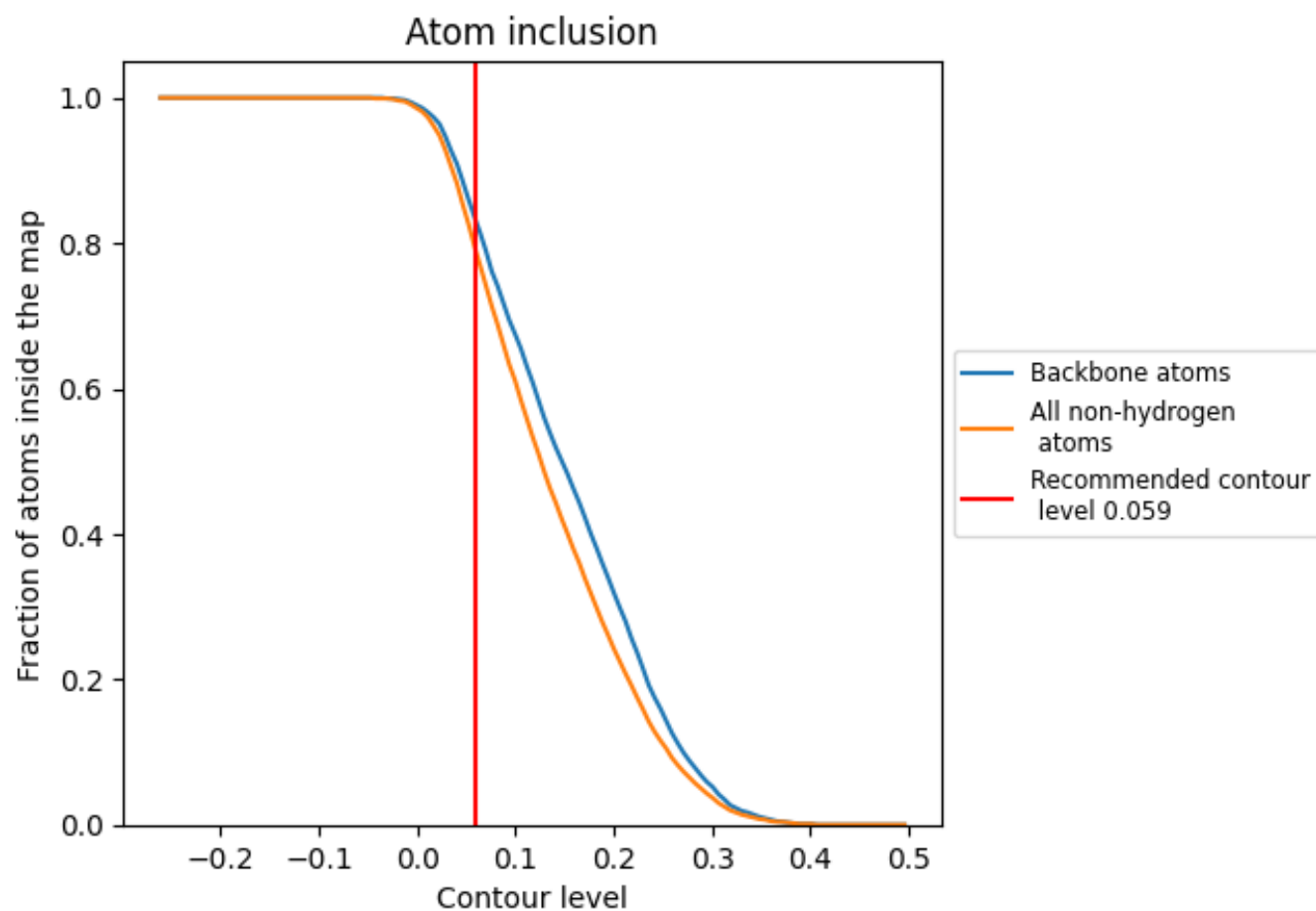
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.059).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 79% 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 (0.059) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7930	0.4390
A	0.8930	0.4890
B	0.8560	0.4800
G	0.4690	0.2890
N	0.7880	0.4090
P	0.7980	0.4390
R	0.7230	0.4030

1.0

0.0

<0.0