



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 10:49 PM UTC

PDB ID : 6KPG / pdb_00006kpg
EMDB ID : EMD-0745
Title : Cryo-EM structure of CB1-G protein complex
Authors : Hua, T.; Li, X.T.; Wu, L.J.; Makriyannis, A.; Wang, Y.X.; Shen, L.; Liu, Z.J.
Deposited on : 2019-08-15
Resolution : 3.00 Å(reported)
Based on initial model : 6N4B

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

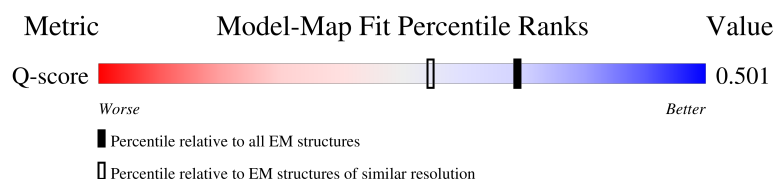
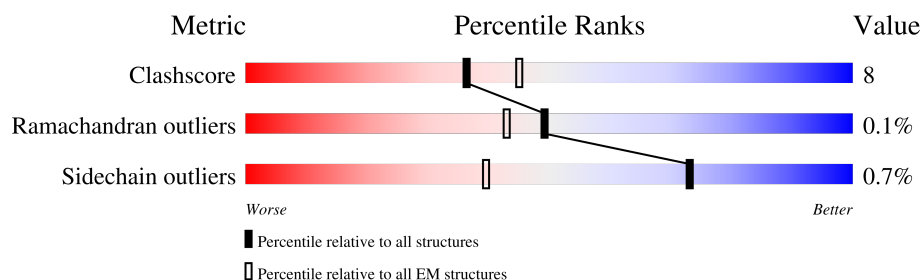
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	353	 6% 52% 12% 36%
2	B	346	 5% 76% 21% .
3	C	71	 20% 76% . 21%
4	R	469	 25% 48% 13% 39%

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Mol	Chain	Length	Quality of chain
5	S	259	7% 71% 18% 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8805 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 Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	225	Total	C	N	O	S	0	0
			1771	1131	295	332	13		

- 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	338	Total	C	N	O	S	0	0
			2592	1601	466	504	21		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	ILE	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873
B	-3	ARG	-	expression tag	UNP P62873
B	-2	ALA	-	expression tag	UNP P62873
B	-1	ARG	-	expression tag	UNP P62873
B	0	GLY	-	expression tag	UNP P62873
B	1	PHE	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	56	Total	C	N	O	S	0	0
			433	271	76	83	3		

- Molecule 4 is a protein called Cannabinoid receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	285	Total	C	N	O	S	0	0
			2223	1477	368	359	19		

There are 117 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-43	ALA	-	expression tag	UNP P21554
R	-42	ASP	-	expression tag	UNP P21554
R	-41	LEU	-	expression tag	UNP P21554
R	-40	GLU	-	expression tag	UNP P21554
R	-39	ASP	-	expression tag	UNP P21554
R	-38	ASN	-	expression tag	UNP P21554
R	-37	TRP	-	expression tag	UNP P21554
R	-36	GLU	-	expression tag	UNP P21554
R	-35	THR	-	expression tag	UNP P21554
R	-34	LEU	-	expression tag	UNP P21554
R	-33	ASN	-	expression tag	UNP P21554
R	-32	ASP	-	expression tag	UNP P21554
R	-31	ASN	-	expression tag	UNP P21554
R	-30	LEU	-	expression tag	UNP P21554
R	-29	LYS	-	expression tag	UNP P21554
R	-28	VAL	-	expression tag	UNP P21554
R	-27	ILE	-	expression tag	UNP P21554
R	-26	GLU	-	expression tag	UNP P21554
R	-25	LYS	-	expression tag	UNP P21554
R	-24	ALA	-	expression tag	UNP P21554
R	-23	ASP	-	expression tag	UNP P21554
R	-22	ASN	-	expression tag	UNP P21554
R	-21	ALA	-	expression tag	UNP P21554
R	-20	ALA	-	expression tag	UNP P21554
R	-19	GLN	-	expression tag	UNP P21554
R	-18	VAL	-	expression tag	UNP P21554
R	-17	LYS	-	expression tag	UNP P21554
R	-16	ASP	-	expression tag	UNP P21554
R	-15	ALA	-	expression tag	UNP P21554
R	-14	LEU	-	expression tag	UNP P21554
R	-13	THR	-	expression tag	UNP P21554
R	-12	LYS	-	expression tag	UNP P21554
R	-11	MET	-	expression tag	UNP P21554
R	-10	ARG	-	expression tag	UNP P21554
R	-9	ALA	-	expression tag	UNP P21554
R	-8	ALA	-	expression tag	UNP P21554
R	-7	ALA	-	expression tag	UNP P21554
R	-6	LEU	-	expression tag	UNP P21554
R	-5	ASP	-	expression tag	UNP P21554
R	-4	ALA	-	expression tag	UNP P21554
R	-3	GLN	-	expression tag	UNP P21554
R	-2	LYS	-	expression tag	UNP P21554

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-1	ALA	-	expression tag	UNP P21554
R	0	THR	-	expression tag	UNP P21554
R	1	PRO	-	expression tag	UNP P21554
R	2	PRO	-	expression tag	UNP P21554
R	3	LYS	-	expression tag	UNP P21554
R	4	LEU	-	expression tag	UNP P21554
R	5	GLU	-	expression tag	UNP P21554
R	6	ASP	-	expression tag	UNP P21554
R	7	LYS	-	expression tag	UNP P21554
R	8	SER	-	expression tag	UNP P21554
R	9	PRO	-	expression tag	UNP P21554
R	10	ASP	-	expression tag	UNP P21554
R	11	SER	-	expression tag	UNP P21554
R	12	PRO	-	expression tag	UNP P21554
R	13	GLU	-	expression tag	UNP P21554
R	14	MET	-	expression tag	UNP P21554
R	15	LYS	-	expression tag	UNP P21554
R	16	ASP	-	expression tag	UNP P21554
R	17	PHE	-	expression tag	UNP P21554
R	18	ARG	-	expression tag	UNP P21554
R	19	HIS	-	expression tag	UNP P21554
R	20	GLY	-	expression tag	UNP P21554
R	21	PHE	-	expression tag	UNP P21554
R	22	ASP	-	expression tag	UNP P21554
R	23	ILE	-	expression tag	UNP P21554
R	24	LEU	-	expression tag	UNP P21554
R	25	VAL	-	expression tag	UNP P21554
R	26	GLY	-	expression tag	UNP P21554
R	27	GLN	-	expression tag	UNP P21554
R	28	ILE	-	expression tag	UNP P21554
R	29	ASP	-	expression tag	UNP P21554
R	30	ASP	-	expression tag	UNP P21554
R	31	ALA	-	expression tag	UNP P21554
R	32	LEU	-	expression tag	UNP P21554
R	33	LYS	-	expression tag	UNP P21554
R	34	LEU	-	expression tag	UNP P21554
R	35	ALA	-	expression tag	UNP P21554
R	36	ASN	-	expression tag	UNP P21554
R	37	GLU	-	expression tag	UNP P21554
R	38	GLY	-	expression tag	UNP P21554
R	39	LYS	-	expression tag	UNP P21554
R	40	VAL	-	expression tag	UNP P21554

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Chain	Residue	Modelled	Actual	Comment	Reference
R	41	LYS	-	expression tag	UNP P21554
R	42	GLU	-	expression tag	UNP P21554
R	43	ALA	-	expression tag	UNP P21554
R	44	GLN	-	expression tag	UNP P21554
R	45	ALA	-	expression tag	UNP P21554
R	46	ALA	-	expression tag	UNP P21554
R	47	ALA	-	expression tag	UNP P21554
R	48	GLU	-	expression tag	UNP P21554
R	49	GLN	-	expression tag	UNP P21554
R	50	LEU	-	expression tag	UNP P21554
R	51	LYS	-	expression tag	UNP P21554
R	52	THR	-	expression tag	UNP P21554
R	53	THR	-	expression tag	UNP P21554
R	54	ARG	-	expression tag	UNP P21554
R	55	ASN	-	expression tag	UNP P21554
R	56	ALA	-	expression tag	UNP P21554
R	57	TYR	-	expression tag	UNP P21554
R	58	ILE	-	expression tag	UNP P21554
R	59	GLN	-	expression tag	UNP P21554
R	60	LYS	-	expression tag	UNP P21554
R	61	TYR	-	expression tag	UNP P21554
R	62	LEU	-	expression tag	UNP P21554
R	63	LEU	-	expression tag	UNP P21554
R	64	GLU	-	expression tag	UNP P21554
R	65	VAL	-	expression tag	UNP P21554
R	66	LEU	-	expression tag	UNP P21554
R	67	PHE	-	expression tag	UNP P21554
R	68	GLN	-	expression tag	UNP P21554
R	69	GLY	-	expression tag	UNP P21554
R	70	PRO	-	expression tag	UNP P21554
R	273	LYS	GLU	engineered mutation	UNP P21554
R	283	VAL	THR	engineered mutation	UNP P21554
R	340	GLU	ARG	engineered mutation	UNP P21554

- Molecule 5 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	231	Total	C	N	O	S	0	0
			1755	1117	294	334	10		

- Molecule 6 is (6 {a} {R},9 {R},10 {a} {R})-9-(hydroxymethyl)-3-(8-isothiocyanato-2-methyl-octan-2-yl)-6,6-dimethyl-6 {a},7,8,9,10,10 {a}-hexahydrobenzo[c]chromen-1-ol (CCD ID: 8D0) (formula: C₂₆H₃₉NO₃S) (labeled as "Ligand of Interest" by depositor).

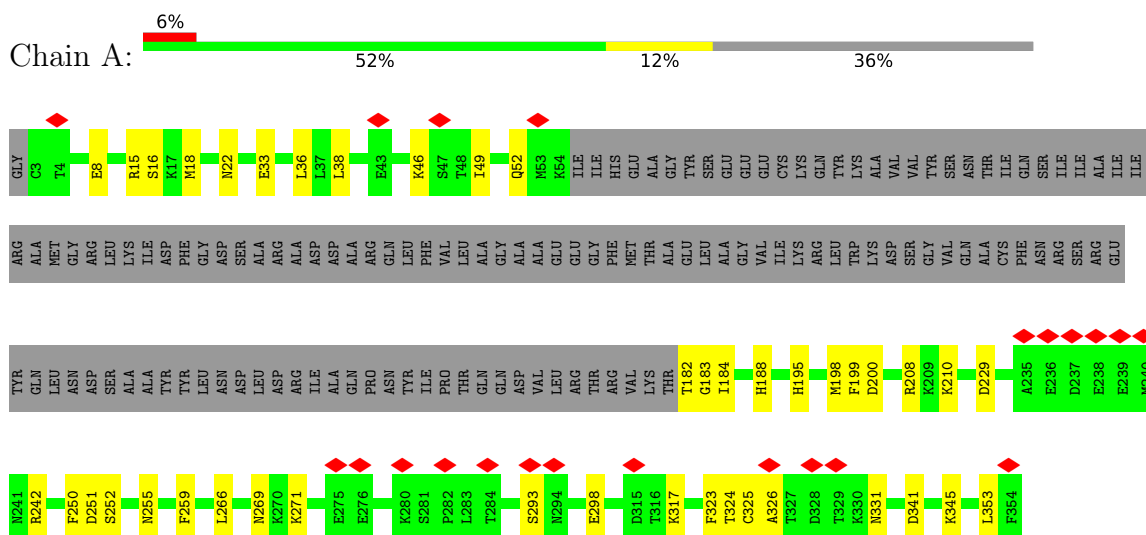


WORLDWIDE
PDB
PROTEIN DATA BANK

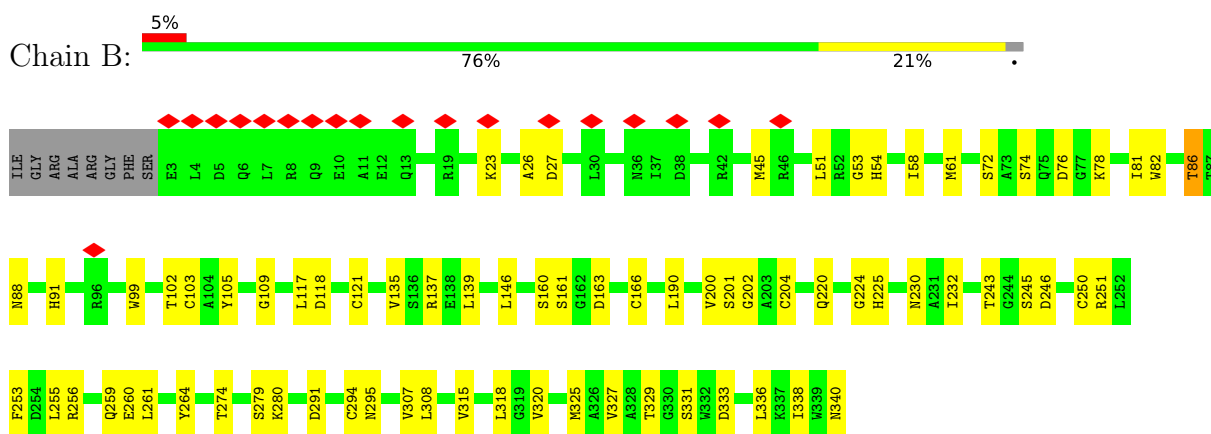
3 Residue-property plots

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.

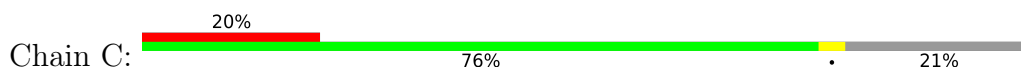
- Molecule 1: Guanine nucleotide-binding protein G(i) subunit alpha-1



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



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	505644	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 ($e^-/\text{\AA}^2$)	1.333	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.119	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	232.95999, 232.95999, 232.95999	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 8D0

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	0.49	0/1801	0.57	0/2421
2	B	0.67	0/2639	0.65	0/3577
3	C	0.32	0/439	0.49	0/592
4	R	0.30	0/2275	0.61	0/3092
5	S	0.50	0/1799	0.64	2/2441 (0.1%)
All	All	0.51	0/8953	0.61	2/12123 (0.0%)

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
2	B	0	1
5	S	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	223	TYR	N-CA-C	5.99	123.06	109.81
5	S	223	TYR	CA-CB-CG	-5.10	104.72	113.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	86	THR	Peptide

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Mol	Chain	Res	Type	Group
5	S	223	TYR	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	1771	0	1744	27	0
2	B	2592	0	2497	51	0
3	C	433	0	442	2	0
4	R	2223	0	2301	37	0
5	S	1755	0	1695	26	0
6	R	31	0	0	0	0
All	All	8805	0	8679	135	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 8.

All (135) 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:271:LYS:HG2	1:A:325:CYS:HB3	1.73	0.70
4:R:255:TRP:HE1	4:R:275:TYR:HB2	1.57	0.69
5:S:160:THR:HB	5:S:180:MET:HB2	1.78	0.66
2:B:160:SER:HB3	2:B:190:LEU:HD23	1.81	0.62
2:B:253:PHE:HA	2:B:260:GLU:HA	1.80	0.62
4:R:234:VAL:HA	4:R:237:PHE:HB3	1.80	0.61
5:S:91:THR:HB	5:S:119:VAL:HG22	1.82	0.61
2:B:51:LEU:HD12	2:B:336:LEU:HD22	1.81	0.60
5:S:176:LEU:HA	5:S:187:VAL:HG21	1.84	0.59
1:A:210:LYS:NZ	2:B:204:CYS:SG	2.72	0.59
1:A:251:ASP:OD1	1:A:255:ASN:ND2	2.35	0.59
1:A:33:GLU:HG2	1:A:195:HIS:HB3	1.84	0.58
1:A:208:ARG:NH2	1:A:252:SER:OG	2.37	0.58
5:S:109:ASP:N	5:S:109:ASP:OD1	2.36	0.58
2:B:74:SER:OG	2:B:76:ASP:OD1	2.22	0.57
2:B:325:MET:O	2:B:340:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:250:LEU:O	4:R:254:GLY:N	2.37	0.57
2:B:45:MET:HE3	2:B:308:LEU:HD21	1.87	0.57
4:R:389:ASN:OD1	4:R:393:ASN:ND2	2.36	0.57
5:S:9:GLY:O	5:S:18:ARG:NH1	2.37	0.57
2:B:320:VAL:HG22	2:B:327:VAL:HG22	1.86	0.56
1:A:341:ASP:OD1	1:A:345:LYS:NZ	2.39	0.56
4:R:247:ILE:O	4:R:275:TYR:OH	2.22	0.56
2:B:58:ILE:HD13	2:B:336:LEU:HD12	1.88	0.56
2:B:245:SER:OG	2:B:246:ASP:N	2.38	0.56
1:A:325:CYS:SG	1:A:326:ALA:N	2.79	0.56
5:S:180:MET:HE1	5:S:200:PHE:HB3	1.88	0.55
1:A:46:LYS:NZ	1:A:200:ASP:OD1	2.37	0.55
2:B:26:ALA:HB2	2:B:259:GLN:HE22	1.70	0.55
2:B:295:ASN:OD1	2:B:295:ASN:N	2.37	0.55
2:B:161:SER:OG	2:B:163:ASP:OD1	2.25	0.54
2:B:160:SER:HA	2:B:166:CYS:HA	1.90	0.53
4:R:153:TYR:OH	4:R:401:SER:OG	2.26	0.53
2:B:224:GLY:O	2:B:251:ARG:NH1	2.39	0.52
1:A:293:SER:N	1:A:298:GLU:OE1	2.41	0.52
4:R:229:THR:O	4:R:233:ALA:N	2.41	0.52
4:R:403:ASP:OD1	4:R:403:ASP:N	2.39	0.52
2:B:220:GLN:HA	3:C:22:GLU:HG3	1.90	0.52
2:B:220:GLN:NE2	2:B:255:LEU:O	2.43	0.52
5:S:39:GLN:HB2	5:S:45:LEU:HD23	1.91	0.52
1:A:229:ASP:HB2	1:A:242:ARG:HB2	1.92	0.52
1:A:49:ILE:HD11	1:A:269:ASN:HD21	1.74	0.52
2:B:318:LEU:HG	2:B:329:THR:HG22	1.92	0.51
5:S:190:ARG:NH2	5:S:211:ASP:OD2	2.43	0.51
4:R:198:ALA:HB1	4:R:245:ILE:HG12	1.93	0.51
2:B:72:SER:O	2:B:72:SER:OG	2.27	0.51
5:S:51:ILE:HG13	5:S:58:ILE:HG12	1.93	0.50
2:B:230:ASN:OD1	2:B:230:ASN:N	2.43	0.50
1:A:52:GLN:OE1	1:A:331:ASN:ND2	2.45	0.50
4:R:298:LEU:HD22	4:R:345:LEU:HD22	1.93	0.50
5:S:232:LYS:NZ	5:S:233:LEU:O	2.44	0.50
4:R:291:VAL:HA	4:R:349:LEU:HD11	1.93	0.50
2:B:295:ASN:HB3	2:B:307:VAL:HG22	1.94	0.49
4:R:236:ALA:HA	4:R:239:LEU:HG	1.94	0.49
2:B:261:LEU:HD22	3:C:30:VAL:HG13	1.94	0.49
4:R:150:ARG:NH1	4:R:403:ASP:OD2	2.46	0.49
4:R:401:SER:OG	4:R:403:ASP:OD1	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:72:ARG:HB3	5:S:79:LEU:HD12	1.96	0.48
4:R:126:LEU:HA	4:R:129:PHE:HB3	1.94	0.48
4:R:243:ILE:HA	4:R:246:VAL:HG22	1.94	0.48
2:B:76:ASP:OD1	2:B:76:ASP:N	2.36	0.48
2:B:250:CYS:HB2	2:B:264:TYR:HB2	1.95	0.48
2:B:201:SER:O	2:B:201:SER:OG	2.32	0.48
2:B:105:TYR:HE2	2:B:109:GLY:HA2	1.79	0.48
4:R:139:CYS:SG	4:R:140:VAL:N	2.86	0.47
5:S:175:LEU:HD21	5:S:178:TYR:HB3	1.95	0.47
1:A:353:LEU:HD22	4:R:214:ARG:HD3	1.97	0.47
2:B:53:GLY:H	2:B:82:TRP:HH2	1.62	0.47
4:R:287:LEU:HD11	4:R:352:LEU:HD12	1.97	0.47
5:S:166:LEU:HD13	5:S:215:TYR:CZ	2.50	0.47
1:A:188:HIS:HB3	1:A:195:HIS:HE1	1.80	0.47
4:R:395:ILE:HG23	4:R:399:LEU:HD23	1.97	0.47
4:R:109:MET:SD	4:R:109:MET:N	2.87	0.46
4:R:207:LEU:HD13	4:R:352:LEU:HD11	1.98	0.46
2:B:331:SER:OG	2:B:333:ASP:OD1	2.26	0.46
5:S:11:LEU:HD21	5:S:120:SER:HB3	1.97	0.46
1:A:184:ILE:HD11	1:A:199:PHE:HB3	1.97	0.46
1:A:15:ARG:HD3	5:S:102:TYR:HB3	1.98	0.46
2:B:102:THR:OG1	2:B:103:CYS:N	2.46	0.46
4:R:351:VAL:HA	4:R:354:ILE:HG22	1.97	0.46
2:B:294:CYS:HB2	2:B:308:LEU:HB2	1.97	0.45
4:R:154:HIS:O	4:R:158:SER:N	2.48	0.45
1:A:8:GLU:OE2	5:S:163:TYR:OH	2.25	0.45
1:A:259:PHE:O	1:A:317:LYS:NZ	2.46	0.45
4:R:143:HIS:NE2	4:R:411:MET:SD	2.89	0.45
4:R:197:THR:HG23	4:R:248:ALA:HB1	1.99	0.45
4:R:362:ILE:HG21	4:R:379:PHE:HB2	1.99	0.45
2:B:274:THR:OG1	2:B:315:VAL:O	2.25	0.45
5:S:4:LEU:HD12	5:S:110:PHE:HD2	1.82	0.45
4:R:234:VAL:HG13	4:R:237:PHE:HD2	1.82	0.44
5:S:47:TRP:HZ2	5:S:50:TYR:HB2	1.80	0.44
1:A:18:MET:O	1:A:22:ASN:ND2	2.50	0.44
5:S:218:MET:HE2	5:S:218:MET:HB3	1.87	0.44
2:B:54:HIS:NE2	2:B:72:SER:OG	2.45	0.44
2:B:202:GLY:H	2:B:232:ILE:HG13	1.82	0.44
5:S:99:SER:HB2	5:S:107:PRO:HB3	1.99	0.44
1:A:38:LEU:HD21	1:A:46:LYS:HB3	2.00	0.44
2:B:81:ILE:HD12	2:B:91:HIS:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:291:ASP:OD1	2:B:291:ASP:N	2.47	0.44
4:R:220:ARG:HD3	4:R:220:ARG:HA	1.75	0.44
2:B:86:THR:O	2:B:86:THR:OG1	2.33	0.44
5:S:83:MET:HE3	5:S:83:MET:HB2	1.76	0.44
2:B:86:THR:O	2:B:88:ASN:N	2.47	0.43
1:A:16:SER:HB2	2:B:88:ASN:HB3	2.00	0.43
2:B:23:LYS:HA	2:B:23:LYS:HD2	1.83	0.43
4:R:218:ILE:HG21	4:R:297:ILE:HA	2.01	0.43
5:S:18:ARG:HD3	5:S:18:ARG:HA	1.71	0.43
1:A:182:THR:HB	1:A:183:GLY:H	1.68	0.42
1:A:36:LEU:HB2	1:A:198:MET:HG2	2.00	0.42
2:B:279:SER:OG	2:B:280:LYS:N	2.52	0.42
2:B:137:ARG:HD3	2:B:137:ARG:HA	1.83	0.42
2:B:27:ASP:OD1	2:B:27:ASP:N	2.52	0.42
4:R:199:SER:O	4:R:203:SER:N	2.50	0.42
1:A:324:THR:OG1	1:A:331:ASN:OD1	2.31	0.42
1:A:271:LYS:HD3	1:A:323:PHE:HB3	2.01	0.42
2:B:61:MET:HE2	2:B:61:MET:HB2	1.89	0.42
2:B:51:LEU:HD11	2:B:338:ILE:HD11	2.01	0.42
2:B:121:CYS:HB3	2:B:139:LEU:HB2	2.02	0.41
4:R:125:THR:O	4:R:129:PHE:N	2.43	0.41
4:R:168:VAL:HA	4:R:171:VAL:HG22	2.01	0.41
2:B:118:ASP:OD1	2:B:118:ASP:N	2.52	0.41
2:B:256:ARG:HE	2:B:256:ARG:HB2	1.72	0.41
4:R:282:VAL:HA	4:R:285:VAL:HG22	2.02	0.41
1:A:250:PHE:HE2	1:A:266:LEU:HD13	1.85	0.41
4:R:287:LEU:HD12	4:R:287:LEU:HA	1.89	0.41
1:A:184:ILE:HD13	2:B:99:TRP:CD1	2.56	0.41
2:B:78:LYS:HD3	2:B:78:LYS:HA	1.90	0.41
4:R:158:SER:OG	4:R:241:TRP:NE1	2.48	0.41
4:R:298:LEU:HD12	4:R:298:LEU:HA	1.93	0.41
5:S:97:VAL:HG11	5:S:108:PHE:CD2	2.55	0.41
5:S:105:SER:O	5:S:179:ARG:NH2	2.53	0.40
5:S:167:GLN:NE2	5:S:171:GLN:O	2.53	0.40
2:B:99:TRP:HB3	2:B:117:LEU:HD12	2.02	0.40
2:B:225:HIS:NE2	2:B:243:THR:OG1	2.41	0.40
5:S:6:GLU:HG3	5:S:22:CYS:HB3	2.03	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	221/353 (63%)	206 (93%)	15 (7%)	0	100	100
2	B	336/346 (97%)	305 (91%)	31 (9%)	0	100	100
3	C	54/71 (76%)	49 (91%)	5 (9%)	0	100	100
4	R	281/469 (60%)	264 (94%)	17 (6%)	0	100	100
5	S	227/259 (88%)	211 (93%)	15 (7%)	1 (0%)	30	65
All	All	1119/1498 (75%)	1035 (92%)	83 (7%)	1 (0%)	49	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	S	223	TYR

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	189/304 (62%)	189 (100%)	0	100	100
2	B	278/286 (97%)	275 (99%)	3 (1%)	65	83
3	C	46/58 (79%)	46 (100%)	0	100	100
4	R	238/411 (58%)	236 (99%)	2 (1%)	73	86
5	S	191/209 (91%)	189 (99%)	2 (1%)	68	84
All	All	942/1268 (74%)	935 (99%)	7 (1%)	73	86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	135	VAL
2	B	146	LEU
2	B	200	VAL
4	R	222	LEU
4	R	309	ILE
5	S	86	LEU
5	S	183	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	195	HIS
1	A	269	ASN
1	A	322	HIS
2	B	16	ASN
2	B	44	GLN
2	B	91	HIS
2	B	119	ASN
2	B	175	GLN
2	B	237	ASN
2	B	340	ASN
3	C	18	GLN
3	C	24	ASN
4	R	261	GLN
4	R	302	HIS
4	R	310	GLN
5	S	82	GLN
5	S	113	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 [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	8D0	R	501	-	32,33,33	1.75	7 (21%)	47,48,48	1.62	10 (21%)

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	8D0	R	501	-	-	5/17/46/46	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	8D0	C10-C7	4.56	1.60	1.53
6	R	501	8D0	C13-C8	3.86	1.60	1.53
6	R	501	8D0	C4-C5	3.34	1.44	1.40
6	R	501	8D0	O1-C9	-2.97	1.41	1.47
6	R	501	8D0	C7-C8	-2.96	1.48	1.54
6	R	501	8D0	C5-C7	2.94	1.56	1.51
6	R	501	8D0	C6-C5	2.31	1.43	1.40

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	8D0	C25-N1-C26	-5.28	120.25	159.28
6	R	501	8D0	O3-C4-C5	3.17	127.13	118.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	8D0	C13-C8-C9	-3.06	109.61	114.89
6	R	501	8D0	C15-C9-C8	-2.63	108.37	112.81
6	R	501	8D0	C12-C13-C8	-2.51	107.98	111.89
6	R	501	8D0	C13-C12-C11	-2.48	107.67	112.36
6	R	501	8D0	C10-C7-C5	2.45	117.08	113.36
6	R	501	8D0	O1-C9-C16	2.43	112.10	105.92
6	R	501	8D0	O3-C4-C3	-2.27	113.34	119.45
6	R	501	8D0	C13-C8-C7	2.02	112.19	109.29

There are no chirality outliers.

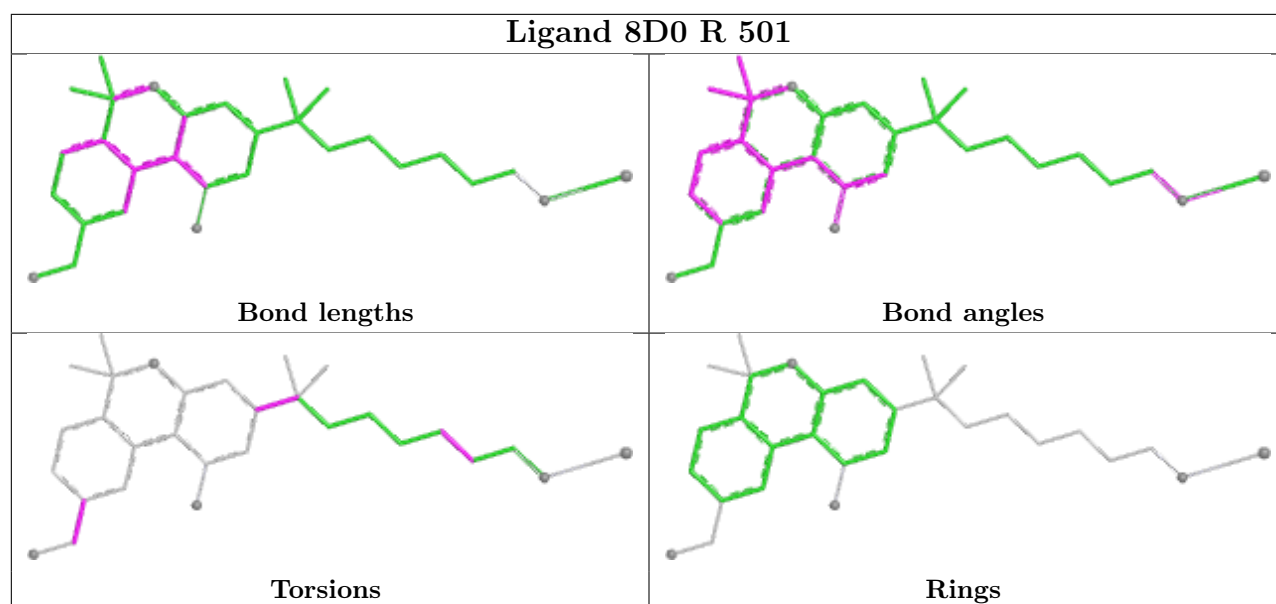
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	R	501	8D0	C10-C11-C14-O2
6	R	501	8D0	C12-C11-C14-O2
6	R	501	8D0	C22-C23-C24-C25
6	R	501	8D0	C20-C17-C2-C1
6	R	501	8D0	C20-C17-C2-C3

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.

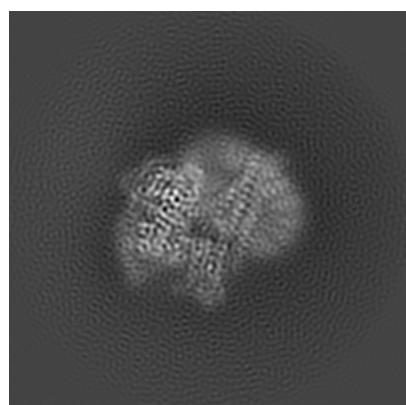
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0745. These allow visual inspection of the internal detail of the map and identification of artifacts.

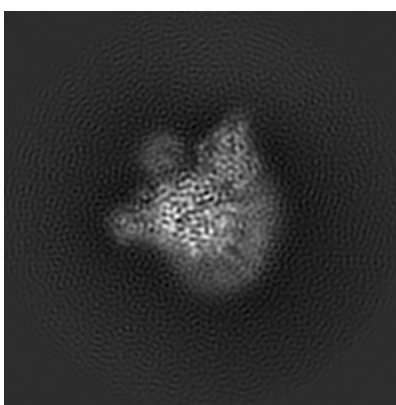
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

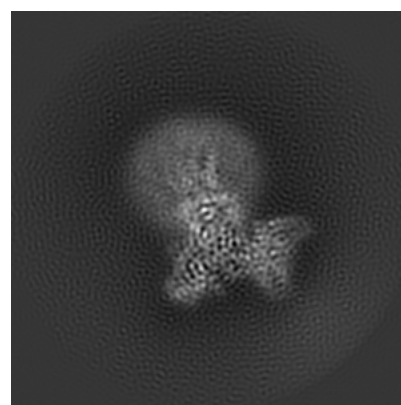
6.1.1 Primary map



X



Y

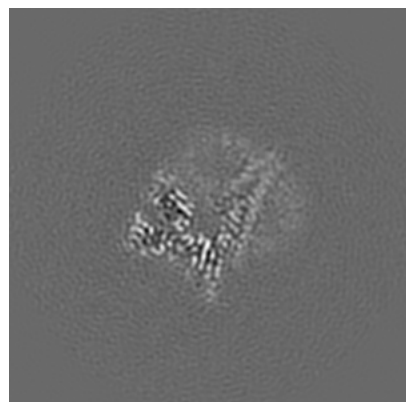


Z

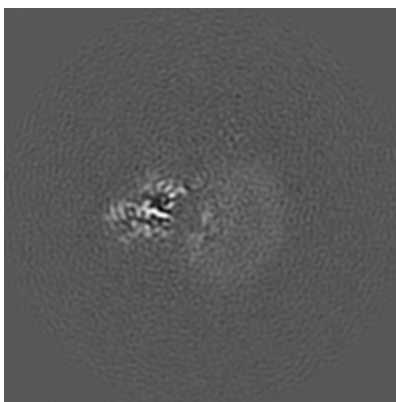
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

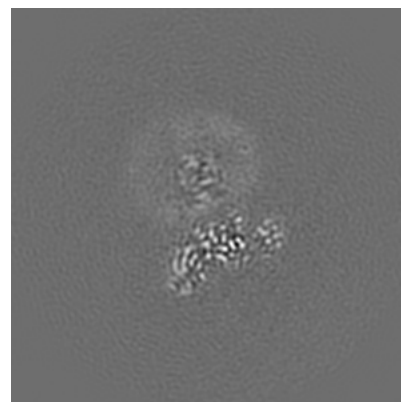
6.2.1 Primary map



X Index: 112



Y Index: 112

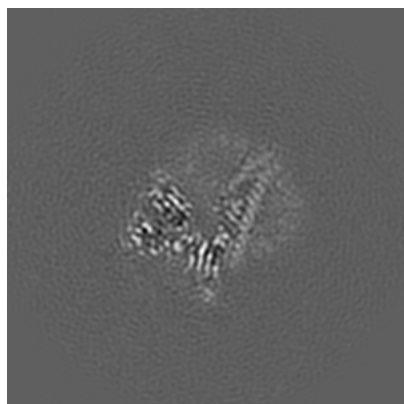


Z Index: 112

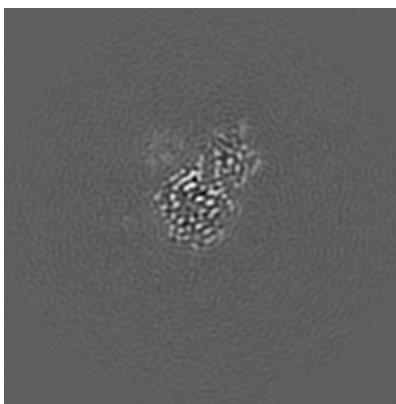
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

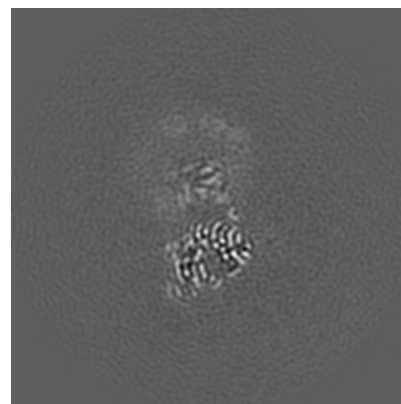
6.3.1 Primary map



X Index: 111



Y Index: 86

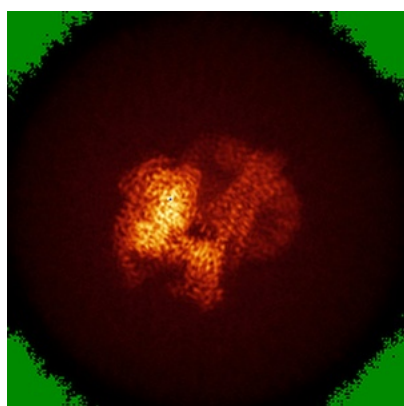


Z Index: 105

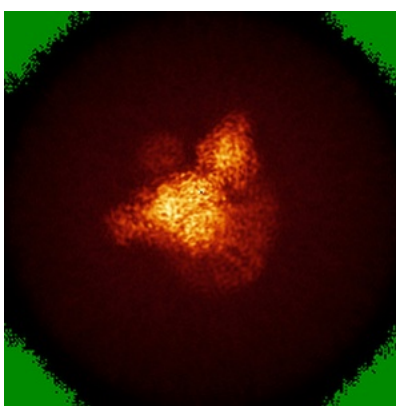
The images above show the largest variance slices of the map in three orthogonal directions.

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

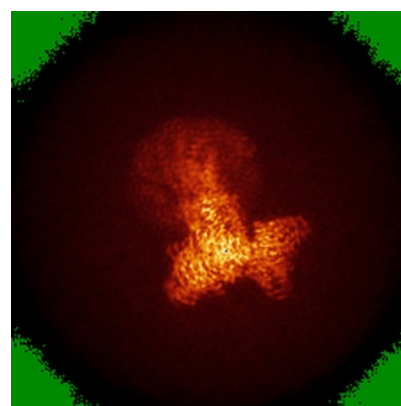
6.4.1 Primary map



X



Y

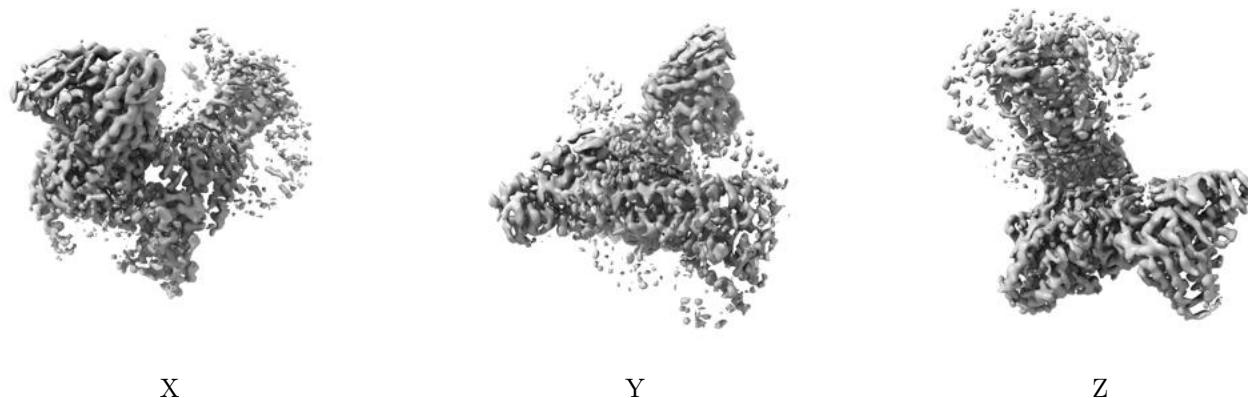


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

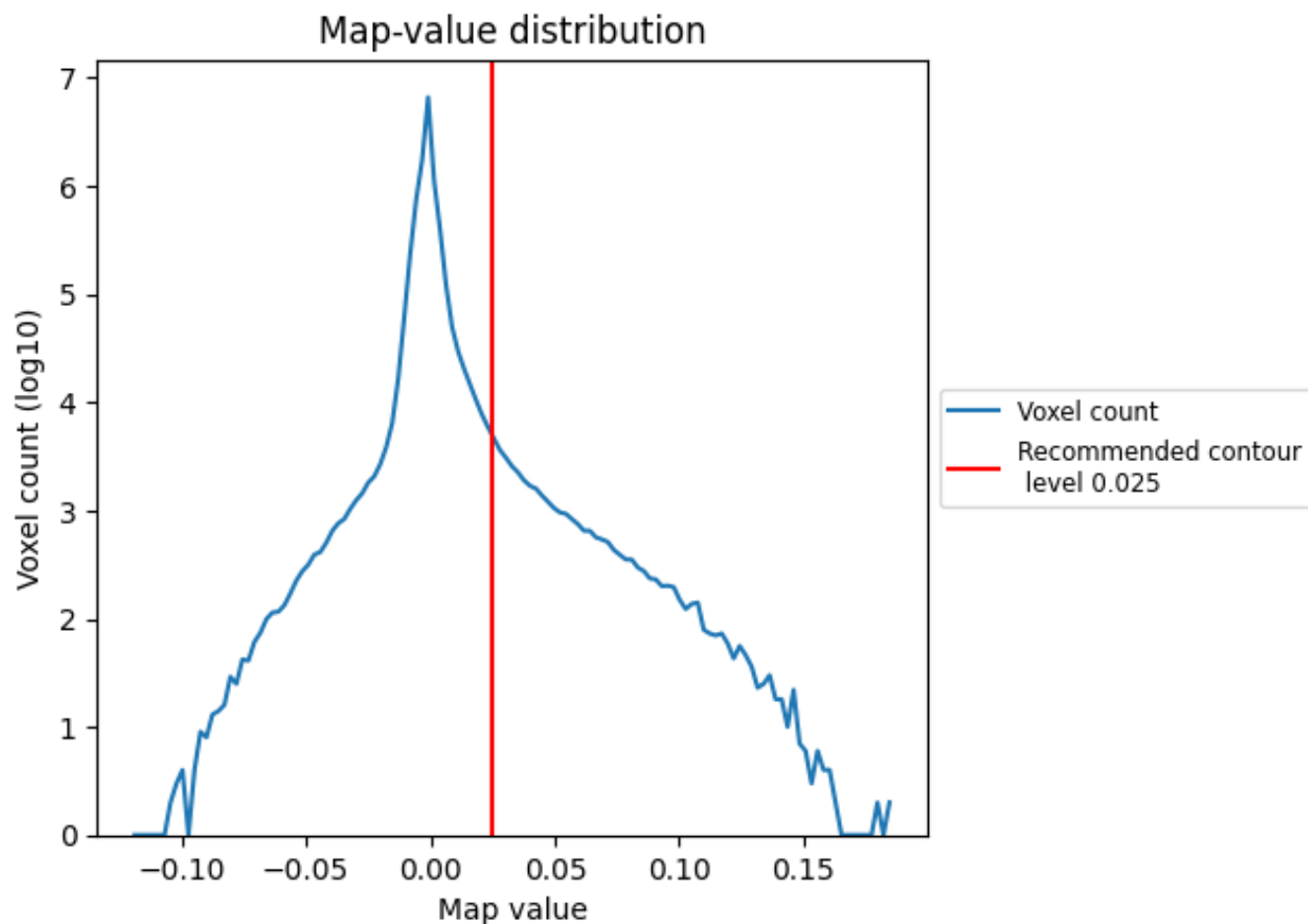
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

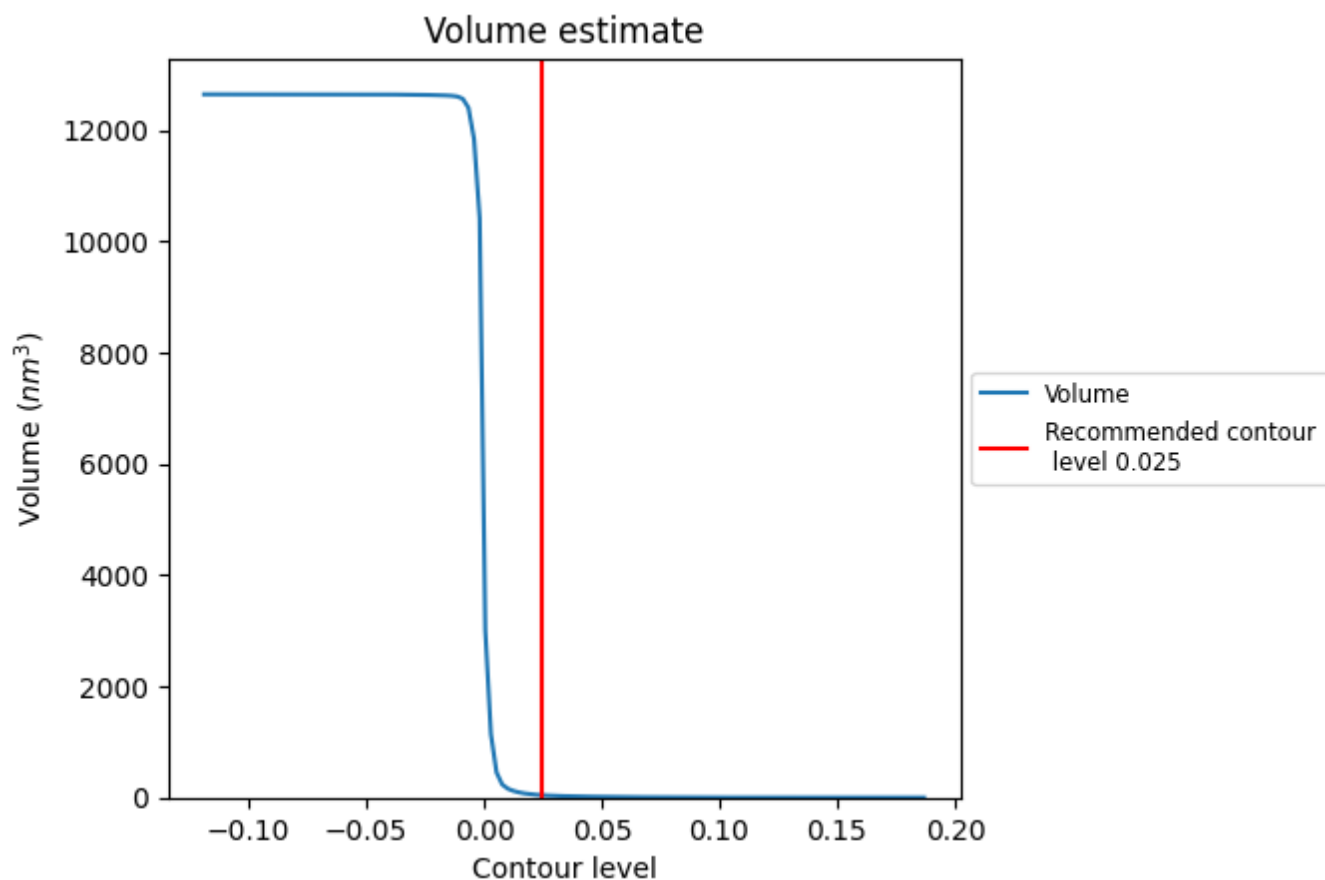
This section contains the results of statistical analysis of the map.

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.

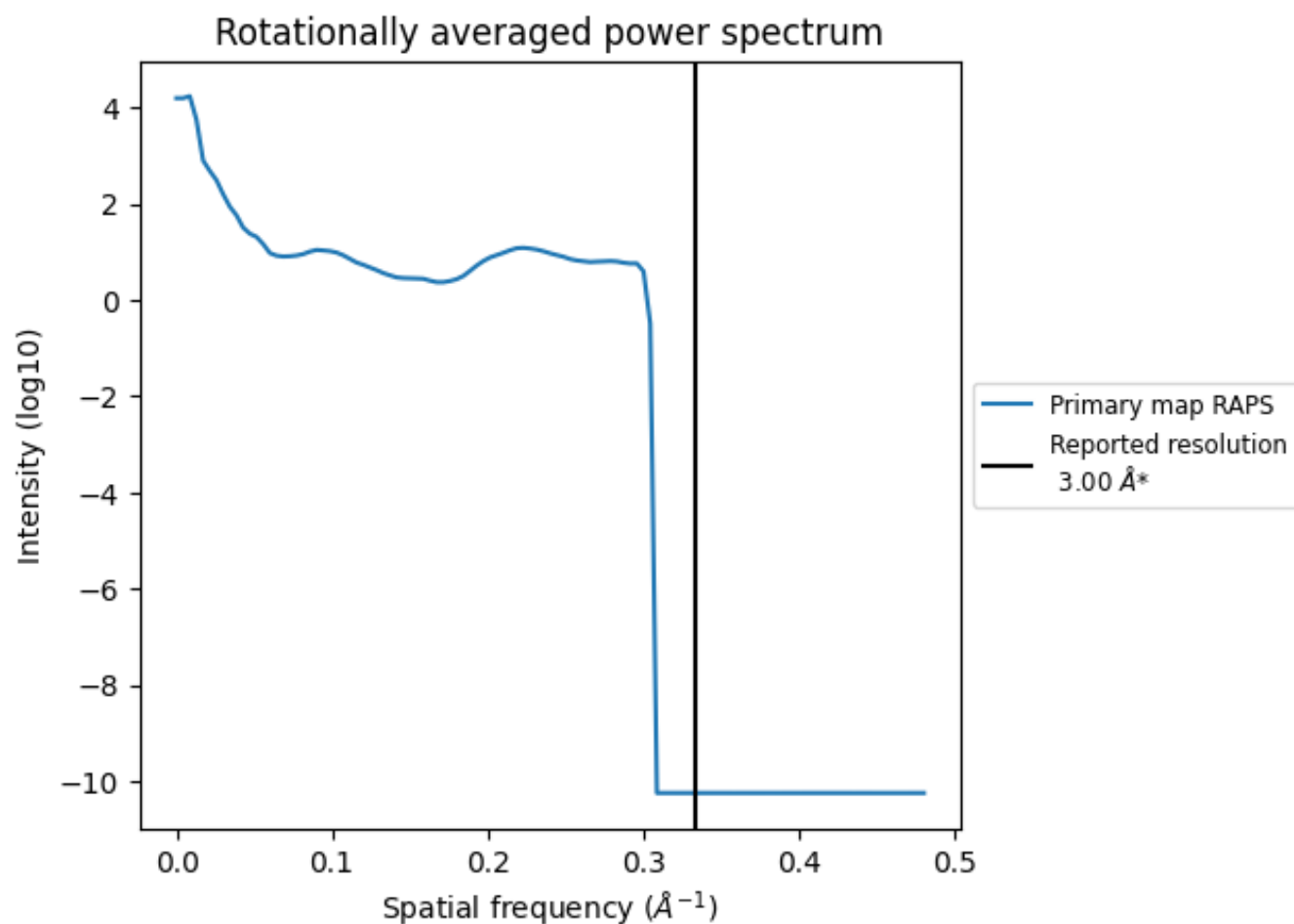
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 42 nm³; this corresponds to an approximate mass of 38 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 0.333 Å⁻¹

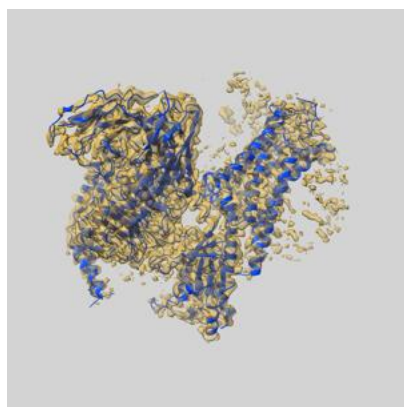
8 Fourier-Shell correlation

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

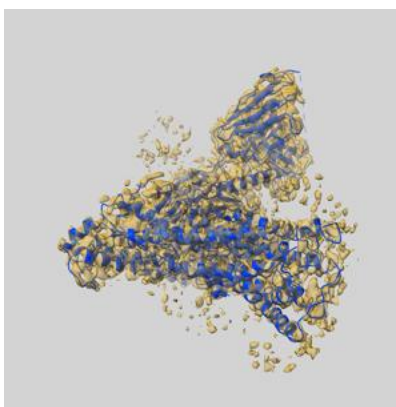
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0745 and PDB model 6KPG. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

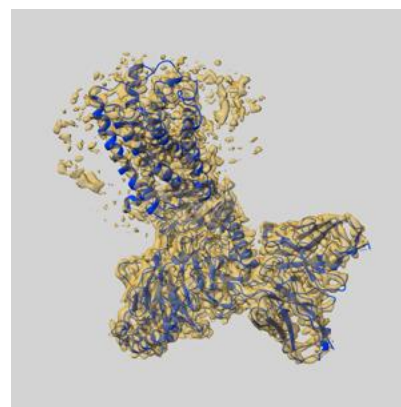
9.1 Map-model overlay [i](#)



X



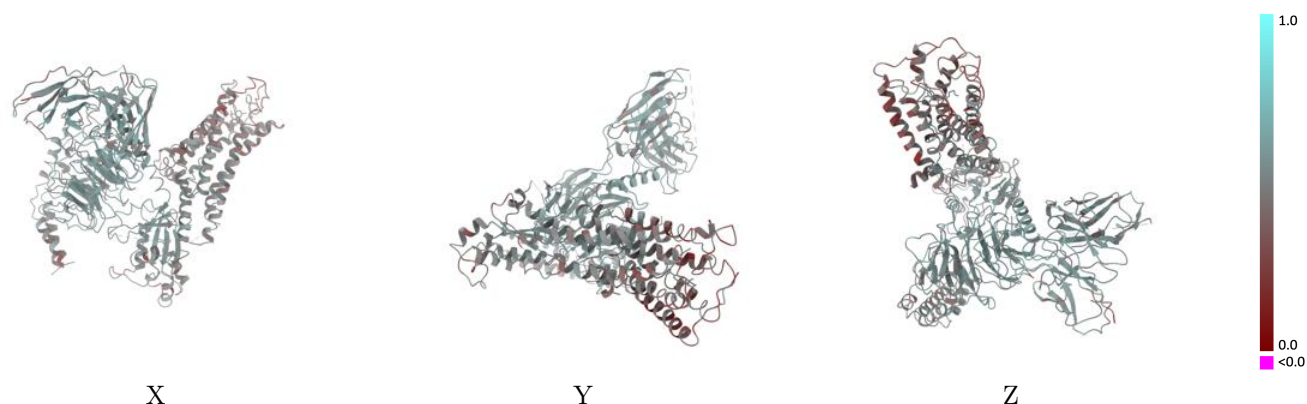
Y



Z

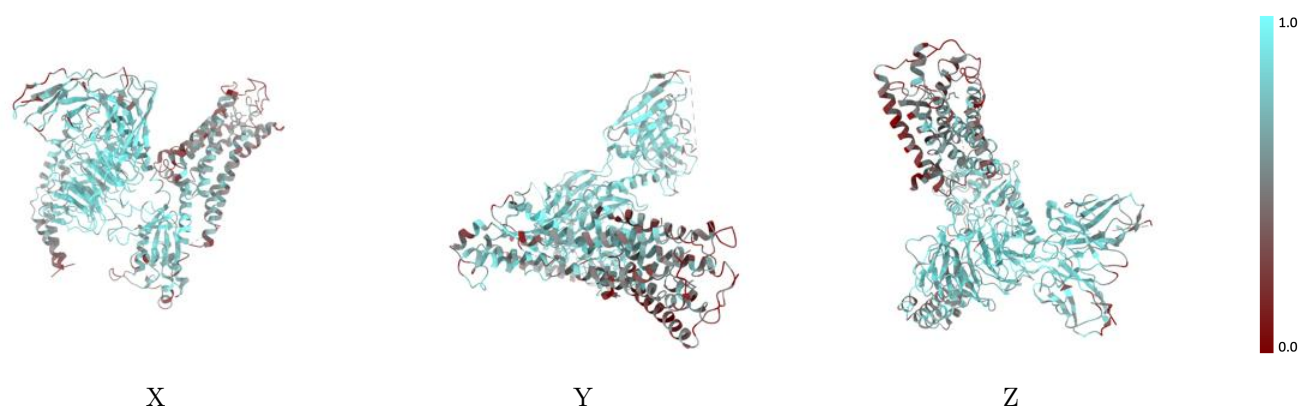
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



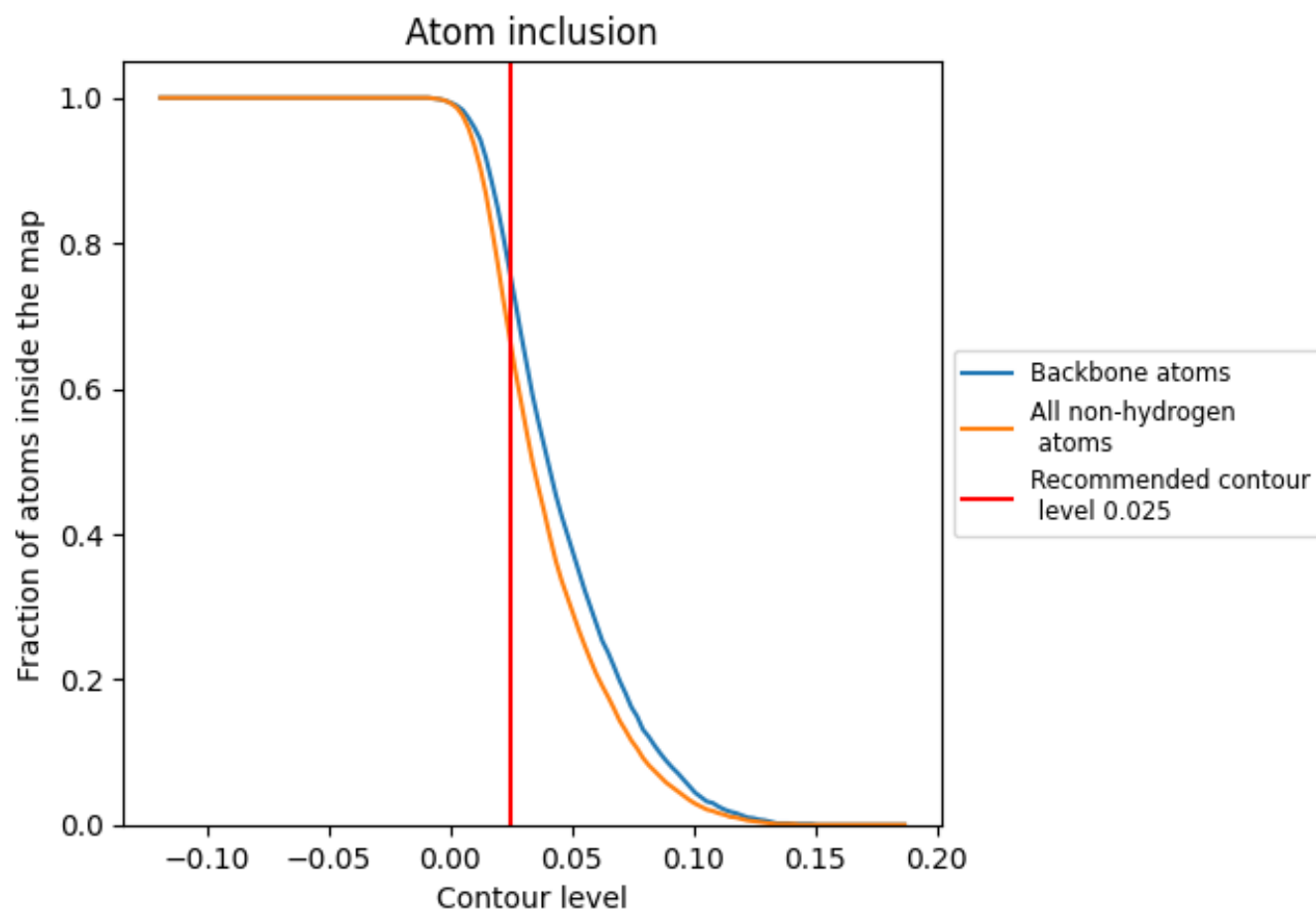
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 66% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6630	0.5010
A	0.7100	0.5160
B	0.7840	0.5410
C	0.5680	0.4970
R	0.4580	0.4200
S	0.7240	0.5320

