



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 06:39 AM UTC

PDB ID : 8XZH / pdb_00008xzh
EMDB ID : EMD-38796
Title : Cryo-EM structure of the MM07-bound human APLNR-Gi complex
Authors : Wang, W.; Ji, S.; Zhang, Y.
Deposited on : 2024-01-21
Resolution : 2.60 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

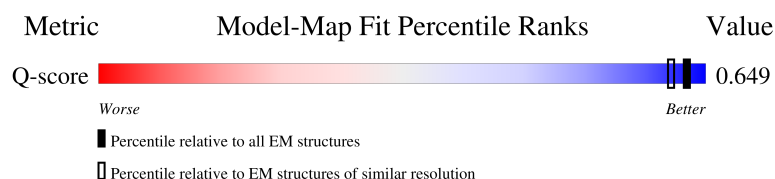
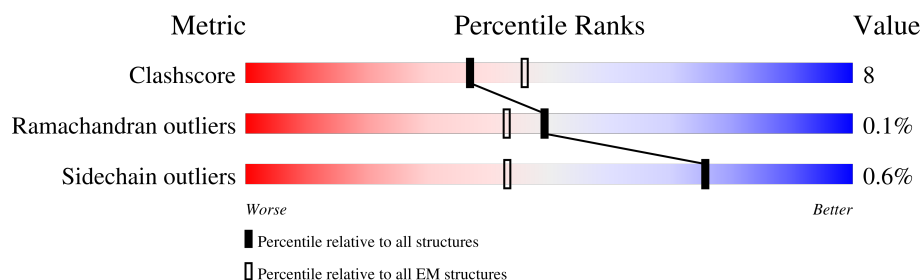
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.60 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	8728 (2.10 - 3.10)

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	380	
2	A	354	
3	B	339	
4	G	71	

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Mol	Chain	Length	Quality of chain
5	S	256	23% 77% 10%
6	L	13	38% 23% 62%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9048 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 Apelin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	303	Total	C	N	O	S	0	0
			2419	1604	385	408	22		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	218	Total	C	N	O	S	0	0
			1743	1110	293	327	13		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ASN	SER	conflict	UNP P63096
A	203	ALA	GLY	conflict	UNP P63096
A	245	ALA	GLU	conflict	UNP P63096
A	326	SER	ALA	conflict	UNP P63096

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	339	Total	C	N	O	S	0	0
			2592	1599	464	508	21		

- 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	55	Total	C	N	O	S	0	0
			416	261	74	78	3		

- Molecule 5 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	231	Total	C	N	O	S	0	0
			1773	1126	294	343	10		

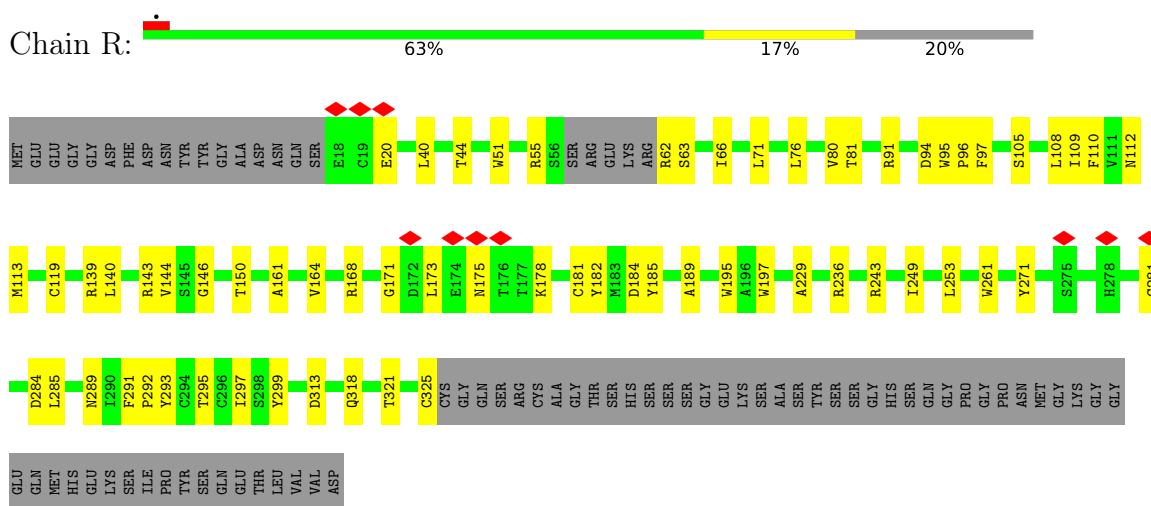
- Molecule 6 is a protein called MM07.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	13	Total	C	N	O	S	0	0
			105	67	22	13	3		

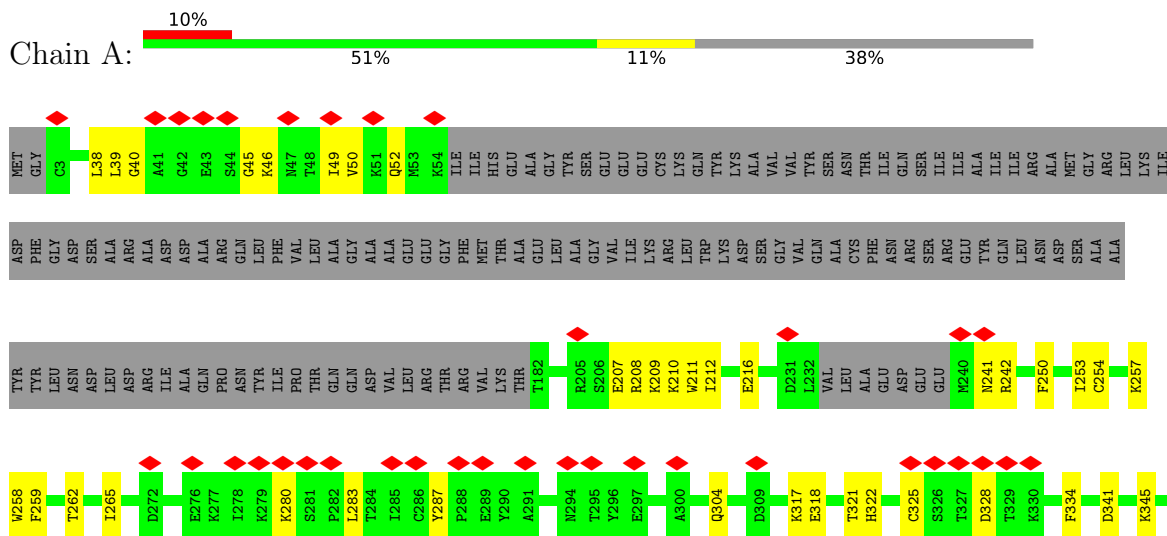
3 Residue-property plots

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.

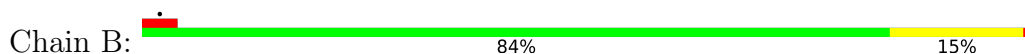
• Molecule 1: Apelin receptor

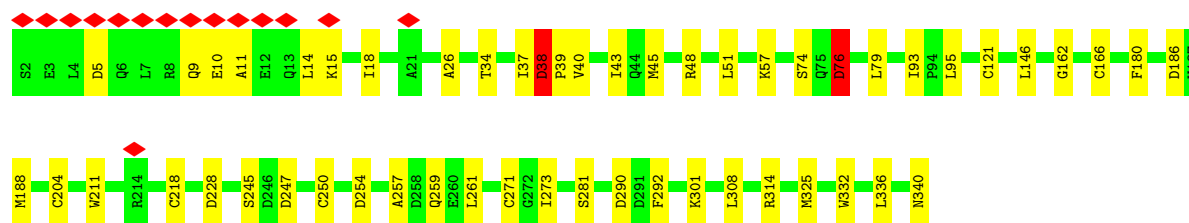


• Molecule 2: Guanine nucleotide-binding protein G(i) subunit alpha-1

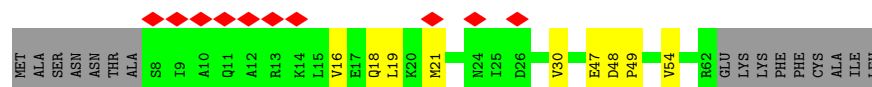


• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

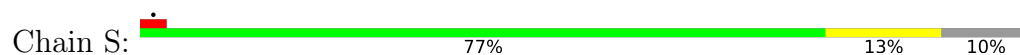




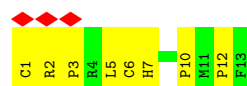
- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 5: scFv16



- Molecule 6: MM07



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92120	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.288	Depositor
Minimum map value	-0.065	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0285	Depositor
Map size (Å)	184.576, 184.576, 184.576	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.824, 0.824, 0.824	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.68	0/2488	0.61	0/3396
2	A	0.47	0/1772	0.58	0/2378
3	B	0.55	0/2639	0.70	3/3578 (0.1%)
4	G	0.39	0/422	0.57	0/571
5	S	0.46	0/1817	0.54	0/2464
6	L	0.51	0/109	0.64	0/145
All	All	0.55	0/9247	0.62	3/12532 (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
5	S	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	76	ASP	N-CA-C	-7.96	103.47	113.02
3	B	38	ASP	CA-C-N	7.53	127.69	120.31
3	B	38	ASP	C-N-CA	7.53	127.69	120.31

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	S	179	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	R	2419	0	2433	48	0
2	A	1743	0	1729	26	0
3	B	2592	0	2484	42	0
4	G	416	0	421	8	0
5	S	1773	0	1708	20	0
6	L	105	0	109	12	0
All	All	9048	0	8884	136	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 (136) 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:B:37:ILE:O	3:B:38:ASP:HB2	1.57	1.02
1:R:281:CYS:HA	1:R:284:ASP:HB2	1.68	0.76
3:B:10:GLU:O	3:B:14:LEU:HG	1.86	0.75
5:S:67:ARG:NH2	5:S:90:ASP:OD2	2.20	0.74
1:R:108:LEU:O	1:R:112:ASN:ND2	2.22	0.72
2:A:207:GLU:HG3	2:A:209:LYS:HG2	1.71	0.72
2:A:259:PHE:O	2:A:317:LYS:NZ	2.24	0.68
3:B:51:LEU:HB2	3:B:336:LEU:HB2	1.77	0.66
2:A:254:CYS:O	2:A:317:LYS:NZ	2.27	0.66
1:R:249:ILE:O	1:R:253:LEU:HG	1.97	0.65
1:R:229:ALA:O	1:R:243:ARG:NH1	2.31	0.63
1:R:91:ARG:NH2	1:R:94:ASP:OD2	2.32	0.62
3:B:14:LEU:HD11	4:G:16:VAL:HG13	1.80	0.62
3:B:261:LEU:HD22	4:G:30:VAL:HG13	1.80	0.61
1:R:271:TYR:HD2	6:L:5:LEU:HD11	1.65	0.61
1:R:81:THR:HG21	1:R:105:SER:OG	2.01	0.61
2:A:322:HIS:HB2	2:A:334:PHE:CE1	2.35	0.61
2:A:304:GLN:HG3	2:A:321:THR:HG21	1.82	0.60
5:S:137:VAL:HB	5:S:207:LEU:HD13	1.82	0.60
1:R:109:ILE:HD12	6:L:10:PRO:HB3	1.82	0.60
1:R:171:GLY:HA3	1:R:182:TYR:HE2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:81:THR:O	1:R:81:THR:HG22	2.02	0.60
1:R:109:ILE:HD12	6:L:10:PRO:CB	2.32	0.60
1:R:168:ARG:NH1	6:L:6:CYS:O	2.29	0.60
2:A:262:THR:O	2:A:317:LYS:HE3	2.03	0.59
5:S:190:ARG:NH2	5:S:211:ASP:OD2	2.36	0.58
3:B:57:LYS:HD3	3:B:332:TRP:CG	2.38	0.58
1:R:62:ARG:NH1	1:R:313:ASP:OD2	2.37	0.58
3:B:281:SER:OG	4:G:48:ASP:OD2	2.17	0.57
5:S:155:HIS:HD2	5:S:157:ASN:H	1.51	0.56
3:B:14:LEU:CD1	4:G:16:VAL:HG13	2.35	0.56
3:B:40:VAL:HG12	3:B:40:VAL:O	2.06	0.56
3:B:57:LYS:HD3	3:B:332:TRP:CD2	2.41	0.56
4:G:47:GLU:O	4:G:49:PRO:HD3	2.05	0.56
3:B:211:TRP:CZ3	3:B:218:CYS:HB2	2.41	0.56
2:A:210:LYS:HD2	3:B:188:MET:HE2	1.88	0.55
3:B:14:LEU:HD13	4:G:19:LEU:HB2	1.87	0.55
2:A:325:CYS:N	2:A:328:ASP:OD2	2.40	0.55
1:R:95:TRP:CE2	1:R:97:PHE:HB2	2.42	0.55
3:B:79:LEU:HG	3:B:95:LEU:HD21	1.89	0.54
1:R:76:LEU:O	1:R:80:VAL:HB	2.08	0.53
1:R:271:TYR:CD2	6:L:5:LEU:HD11	2.44	0.53
5:S:52:SER:HB2	5:S:57:THR:HB	1.89	0.53
2:A:208:ARG:HG2	2:A:211:TRP:CZ2	2.44	0.53
6:L:2:ARG:HB3	6:L:3:PRO:HD3	1.91	0.53
1:R:51:TRP:O	1:R:55:ARG:HB2	2.08	0.52
2:A:341:ASP:OD1	2:A:345:LYS:HE3	2.09	0.52
1:R:321:THR:O	1:R:325:CYS:N	2.41	0.52
3:B:325:MET:HE1	4:G:54:VAL:HG21	1.92	0.52
1:R:295:THR:HG22	1:R:299:TYR:CE1	2.44	0.52
5:S:40:ALA:HB3	5:S:43:LYS:HB2	1.92	0.52
3:B:14:LEU:O	3:B:18:ILE:HG13	2.10	0.52
5:S:162:LEU:HD13	5:S:200:PHE:CD1	2.44	0.52
2:A:209:LYS:NZ	3:B:228:ASP:OD2	2.37	0.51
5:S:34:MET:HG2	5:S:72:ARG:NH2	2.25	0.51
1:R:94:ASP:O	1:R:96:PRO:HD3	2.11	0.51
1:R:195:TRP:HB3	6:L:2:ARG:HE	1.76	0.51
1:R:285:LEU:O	1:R:289:ASN:ND2	2.44	0.51
3:B:26:ALA:HB2	3:B:259:GLN:HE22	1.75	0.51
5:S:155:HIS:CD2	5:S:157:ASN:H	2.28	0.50
3:B:37:ILE:O	3:B:38:ASP:CB	2.42	0.50
2:A:265:ILE:HG23	2:A:334:PHE:HE2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:140:LEU:O	1:R:144:VAL:HG22	2.12	0.49
2:A:46:LYS:O	2:A:50:VAL:HG23	2.12	0.49
5:S:212:VAL:HG11	5:S:235:LEU:HD23	1.95	0.49
2:A:241:ASN:OD1	2:A:242:ARG:N	2.45	0.49
2:A:322:HIS:HB2	2:A:334:PHE:CZ	2.47	0.49
3:B:250:CYS:SG	3:B:273:ILE:HD13	2.52	0.49
1:R:161:ALA:O	1:R:164:VAL:HG22	2.12	0.49
3:B:76:ASP:OD1	3:B:76:ASP:N	2.40	0.48
1:R:110:PHE:CE1	6:L:12:PRO:HD2	2.48	0.48
3:B:166:CYS:HB2	3:B:180:PHE:HB2	1.95	0.48
3:B:254:ASP:CB	3:B:261:LEU:HD11	2.43	0.47
1:R:109:ILE:HG21	6:L:10:PRO:HB2	1.97	0.47
3:B:121:CYS:HB2	3:B:146:LEU:HD21	1.96	0.47
3:B:34:THR:HA	3:B:37:ILE:HG23	1.95	0.47
2:A:38:LEU:HG	2:A:46:LYS:HE3	1.97	0.47
1:R:181:CYS:O	6:L:7:HIS:HB3	2.15	0.47
1:R:289:ASN:O	1:R:292:PRO:HD2	2.15	0.47
1:R:139:ARG:O	1:R:143:ARG:HG3	2.15	0.47
1:R:291:PHE:CD2	6:L:5:LEU:HD13	2.50	0.46
1:R:40:LEU:O	1:R:44:THR:HG23	2.15	0.46
5:S:4:LEU:HD22	5:S:22:CYS:SG	2.56	0.46
5:S:69:THR:HG23	5:S:82:GLN:HB3	1.96	0.46
1:R:62:ARG:HG3	1:R:63:SER:O	2.16	0.46
1:R:71:LEU:HD13	1:R:119:CYS:HB2	1.98	0.46
1:R:81:THR:CG2	1:R:105:SER:OG	2.64	0.46
3:B:48:ARG:HE	3:B:340:ASN:HB3	1.81	0.46
5:S:149:SER:OG	5:S:151:LYS:O	2.31	0.46
1:R:184:ASP:OD1	1:R:184:ASP:N	2.46	0.46
3:B:5:ASP:O	3:B:9:GLN:HG2	2.15	0.46
2:A:210:LYS:HE3	3:B:204:CYS:SG	2.55	0.45
1:R:91:ARG:NH1	1:R:96:PRO:HG3	2.31	0.45
3:B:301:LYS:HB3	3:B:301:LYS:NZ	2.31	0.45
5:S:22:CYS:HB3	5:S:79:LEU:HB3	1.97	0.45
1:R:113:MET:HG3	1:R:261:TRP:CH2	2.51	0.45
5:S:168:ARG:NH1	5:S:174:GLN:OE1	2.46	0.44
2:A:40:GLY:HA3	2:A:46:LYS:HD2	1.98	0.44
5:S:137:VAL:HG12	5:S:143:VAL:HG11	1.99	0.44
6:L:1:CYS:SG	6:L:3:PRO:HD2	2.58	0.44
1:R:146:GLY:O	1:R:150:THR:HG23	2.18	0.44
3:B:162:GLY:HA2	3:B:186:ASP:HB3	2.00	0.44
5:S:137:VAL:HB	5:S:207:LEU:CD1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:173:LEU:HG	1:R:175:ASN:HB2	2.00	0.43
2:A:250:PHE:O	2:A:253:ILE:HG22	2.18	0.43
5:S:32:PHE:O	5:S:72:ARG:NH2	2.50	0.43
2:A:39:LEU:CD1	2:A:253:ILE:HG12	2.49	0.43
3:B:290:ASP:HA	3:B:314:ARG:HG3	2.00	0.43
1:R:293:TYR:O	1:R:297:ILE:HG13	2.19	0.42
3:B:79:LEU:HB2	3:B:93:ILE:HB	2.02	0.42
1:R:95:TRP:NE1	1:R:97:PHE:HB2	2.34	0.42
3:B:45:MET:HB2	3:B:308:LEU:HD22	2.01	0.42
3:B:292:PHE:N	3:B:292:PHE:CD1	2.87	0.42
1:R:236:ARG:NH1	2:A:318:GLU:HG3	2.35	0.42
4:G:18:GLN:O	4:G:21:MET:HG3	2.19	0.42
3:B:74:SER:CB	3:B:76:ASP:OD1	2.67	0.42
3:B:74:SER:HB3	3:B:76:ASP:OD1	2.20	0.42
3:B:257:ALA:O	3:B:259:GLN:HG3	2.19	0.42
1:R:20:GLU:O	1:R:285:LEU:HD11	2.19	0.41
3:B:11:ALA:O	3:B:15:LYS:HG3	2.20	0.41
1:R:185:TYR:O	1:R:189:ALA:N	2.53	0.41
2:A:250:PHE:HA	2:A:253:ILE:HG22	2.02	0.41
5:S:65:LYS:HE3	5:S:65:LYS:HB2	1.93	0.41
1:R:189:ALA:HB2	1:R:197:TRP:CD1	2.55	0.41
2:A:45:GLY:O	2:A:49:ILE:HG12	2.20	0.41
3:B:271:CYS:HB2	3:B:290:ASP:HB2	2.02	0.41
1:R:105:SER:O	1:R:109:ILE:HG13	2.20	0.41
3:B:38:ASP:HA	3:B:39:PRO:HD3	1.83	0.41
1:R:66:ILE:HG12	1:R:150:THR:HG21	2.03	0.41
2:A:257:LYS:HE3	2:A:258:TRP:CE2	2.56	0.41
1:R:94:ASP:HB2	1:R:178:LYS:HD2	2.03	0.41
2:A:212:ILE:HD12	2:A:212:ILE:HA	1.93	0.41
2:A:283:LEU:HD11	2:A:287:TYR:CD1	2.56	0.41
3:B:40:VAL:CG1	3:B:43:ILE:HD11	2.51	0.40
3:B:245:SER:HB3	3:B:247:ASP:OD1	2.21	0.40
5:S:83:MET:HE1	5:S:117:LEU:HD22	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	R	299/380 (79%)	281 (94%)	18 (6%)	0	100	100
2	A	212/354 (60%)	208 (98%)	4 (2%)	0	100	100
3	B	337/339 (99%)	319 (95%)	17 (5%)	1 (0%)	36	58
4	G	53/71 (75%)	51 (96%)	2 (4%)	0	100	100
5	S	227/256 (89%)	222 (98%)	5 (2%)	0	100	100
6	L	11/13 (85%)	8 (73%)	3 (27%)	0	100	100
All	All	1139/1413 (81%)	1089 (96%)	49 (4%)	1 (0%)	49	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	38	ASP

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	263/327 (80%)	262 (100%)	1 (0%)	84	93
2	A	190/305 (62%)	187 (98%)	3 (2%)	55	79
3	B	278/282 (99%)	276 (99%)	2 (1%)	76	89
4	G	43/58 (74%)	43 (100%)	0	100	100
5	S	195/208 (94%)	195 (100%)	0	100	100
6	L	12/12 (100%)	12 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	981/1192 (82%)	975 (99%)	6 (1%)	76	91

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	318	GLN
2	A	52	GLN
2	A	216	GLU
2	A	280	LYS
3	B	38	ASP
3	B	76	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	46	ASN
2	A	52	GLN
2	A	213	HIS
2	A	322	HIS
3	B	6	GLN
3	B	32	GLN
3	B	91	HIS
3	B	110	ASN
3	B	259	GLN
4	G	11	GLN
4	G	24	ASN
5	S	82	GLN
5	S	155	HIS

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

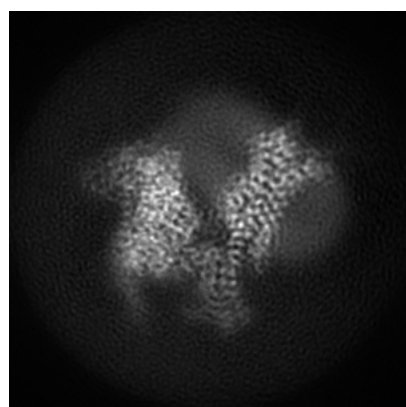
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38796. These allow visual inspection of the internal detail of the map and identification of artifacts.

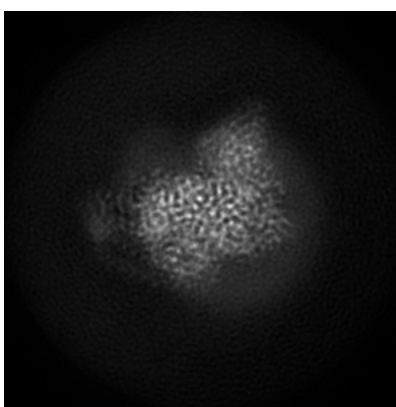
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

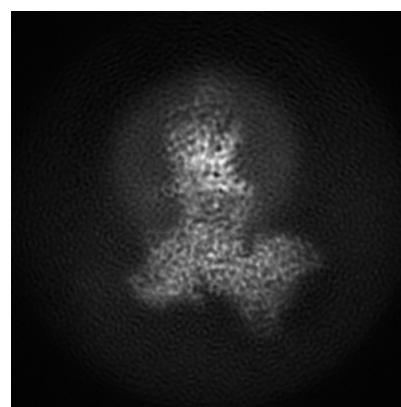
6.1.1 Primary map



X



Y

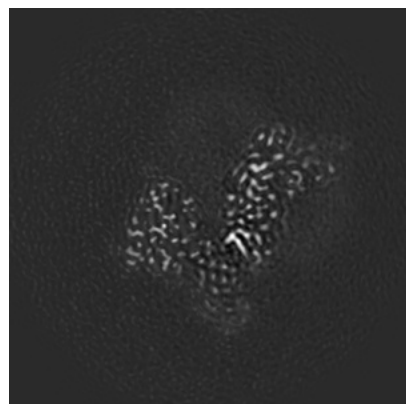


Z

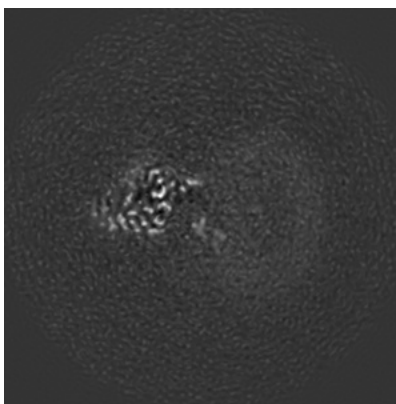
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

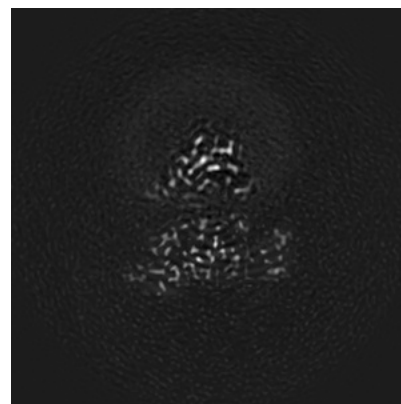
6.2.1 Primary map



X Index: 112



Y Index: 112

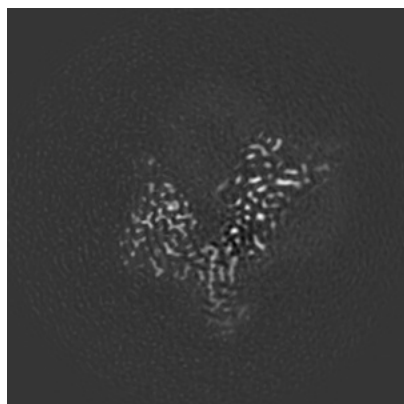


Z Index: 112

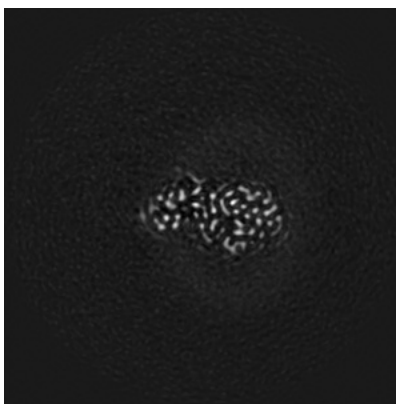
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

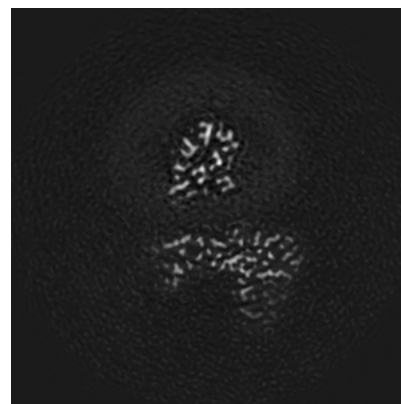
6.3.1 Primary map



X Index: 114



Y Index: 140



Z Index: 121

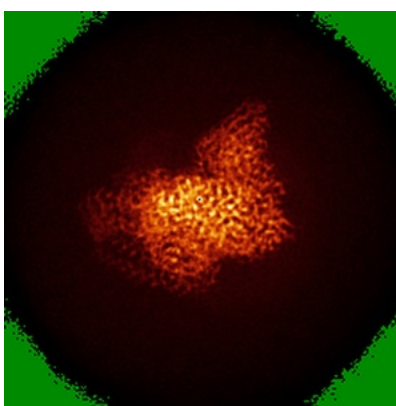
The images above show the largest variance slices of the map in three orthogonal directions.

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

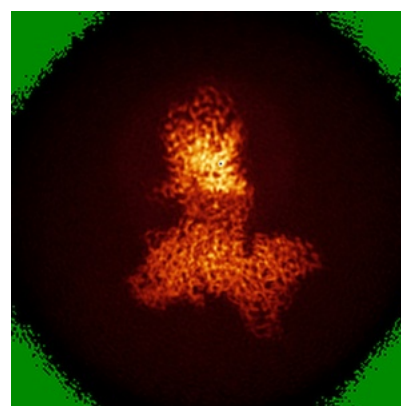
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

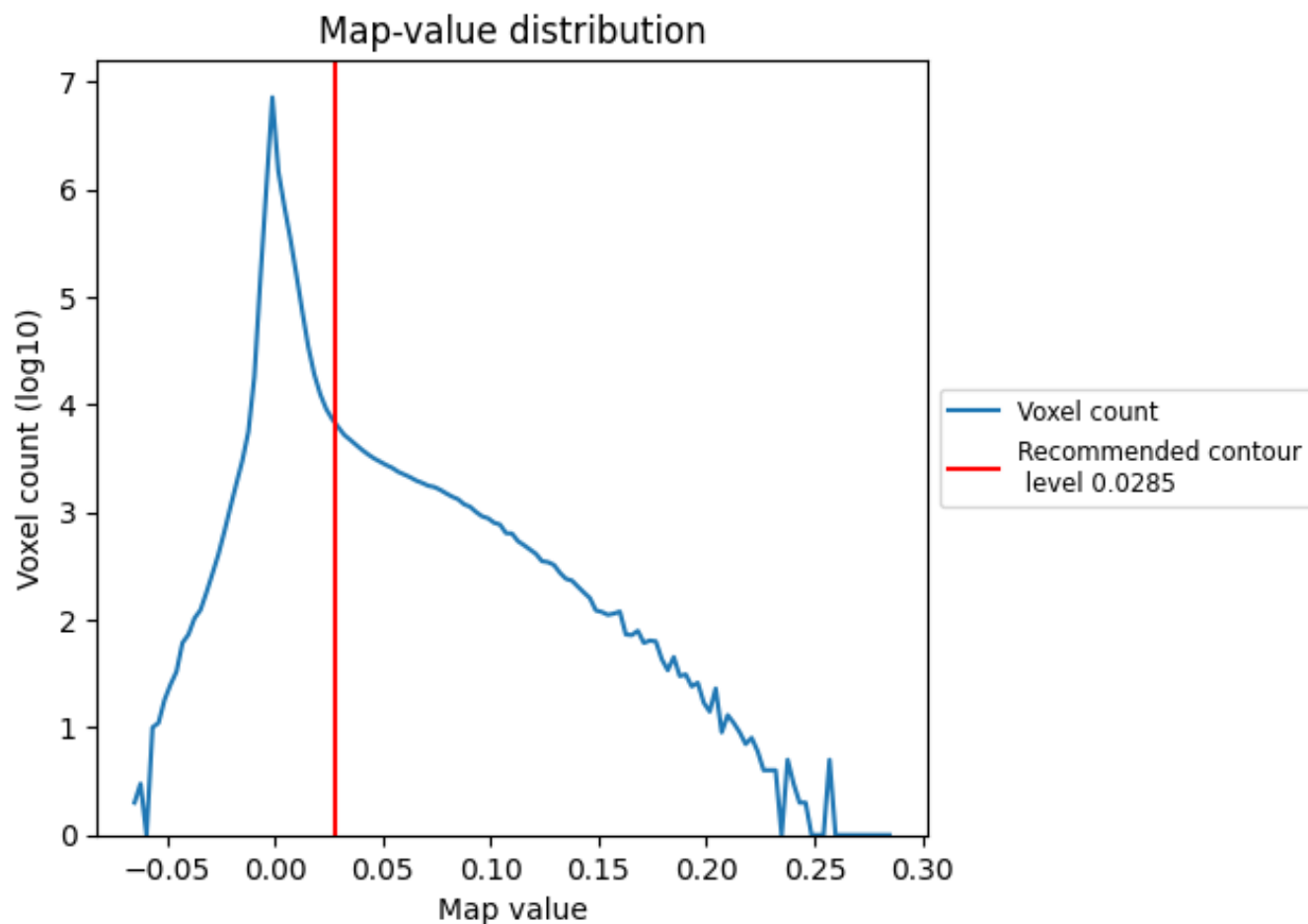
6.6 Mask visualisation

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

7 Map analysis [i](#)

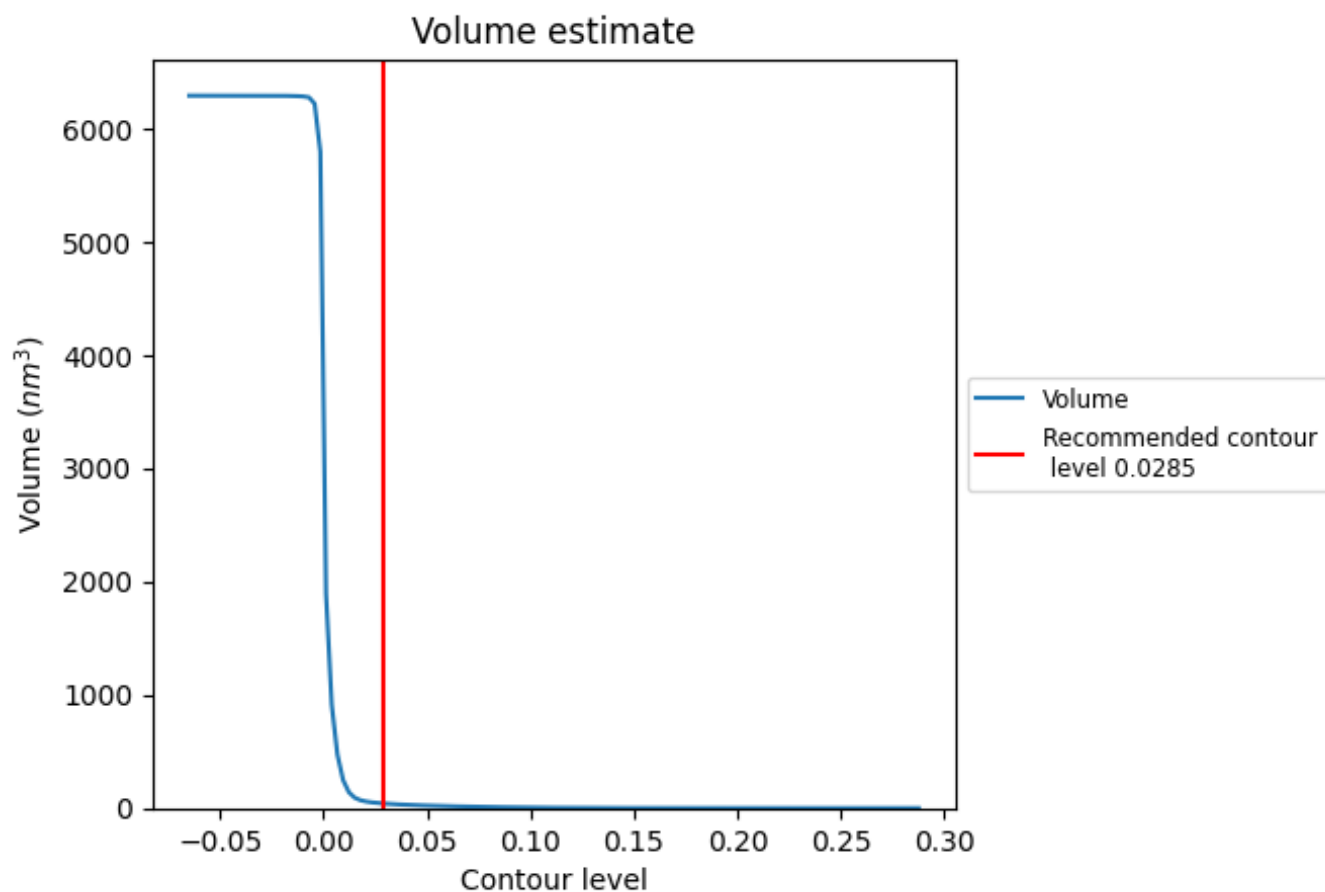
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

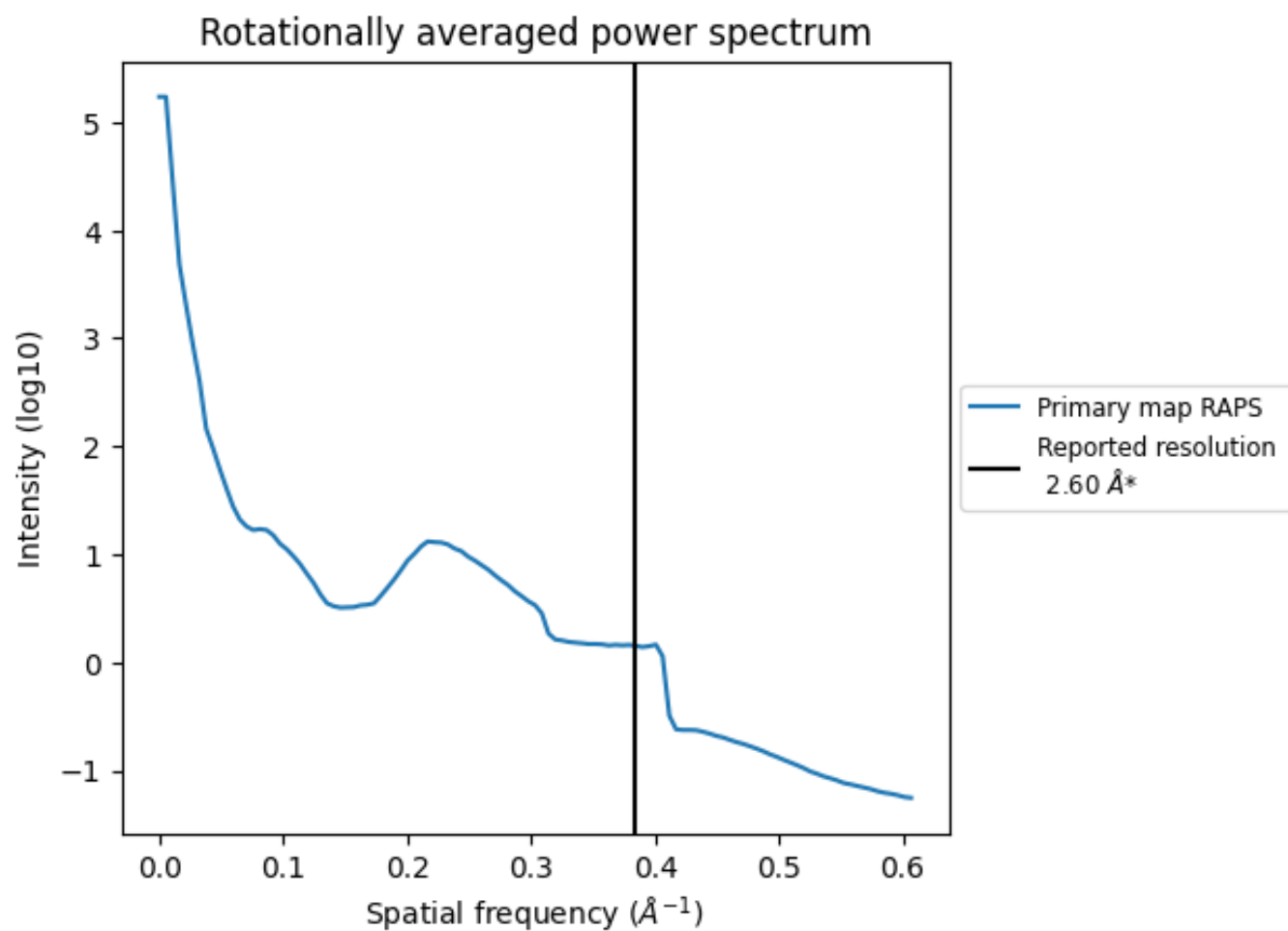
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 42 nm^3 ; 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 0.385 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 EMD map EMD-38796 and PDB model 8XZH. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

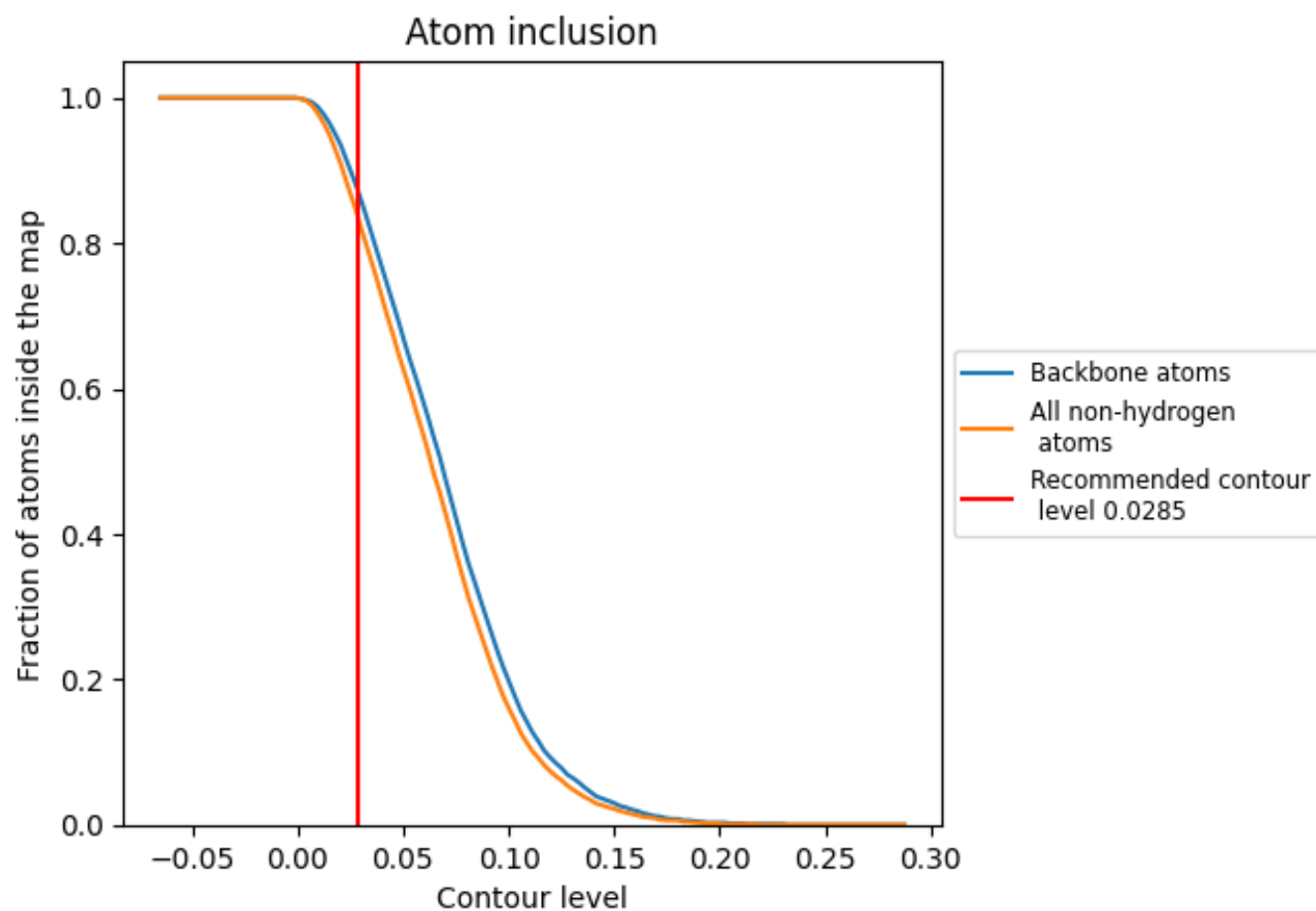


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.0285) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8380	0.6490
A	0.7380	0.6250
B	0.8990	0.7020
G	0.6820	0.6090
L	0.7230	0.5340
R	0.8450	0.5850
S	0.8820	0.7000

1.0

0.0

<0.0