



## Full wwPDB EM Validation Report ⓘ

Nov 10, 2025 – 11:41 PM JST

PDB ID : 9WXM / pdb\_00009wxm  
EMDB ID : EMD-66350  
Title : Cryo-EM structure of the full-length GPR15L bound GPR15-Gi complex  
Authors : Han, S.; Wu, B.; Zhao, Q.  
Deposited on : 2025-09-25  
Resolution : 3.30 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev129  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.46

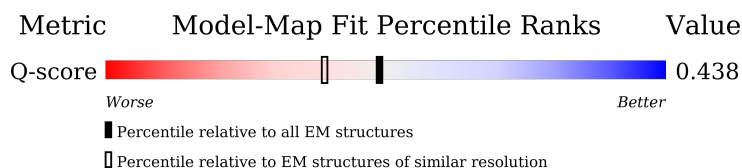
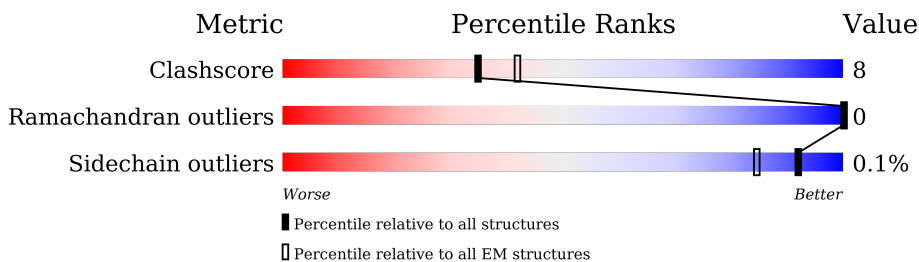
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	15087 ( 2.80 - 3.80 )

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  $\geq 3$ , 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	L	58	 10% 14% 76%
2	R	379	 59% 17% 24%
3	A	354	 58% 5% 38%
4	B	351	 11% 74% 22% .

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Mol	Chain	Length	Quality of chain
5	C	71	<div><div></div><div>38%</div><div>68%</div><div>8%</div><div>24%</div></div>
6	D	267	<div><div></div><div>67%</div><div>21%</div><div>12%</div></div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8643 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 Protein GPR15LG.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	L	14	Total	C	N	O	0	0
			105	71	16	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	0	GLY	-	expression tag	UNP Q6UWK7

- Molecule 2 is a protein called G-protein coupled receptor 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	287	Total	C	N	O	S	0	0
			2233	1485	366	363	19		

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-2	GLY	-	expression tag	UNP P49685
R	-1	ALA	-	expression tag	UNP P49685
R	0	PRO	-	expression tag	UNP P49685
R	331	GLU	-	expression tag	UNP P49685
R	332	PHE	-	expression tag	UNP P49685
R	333	LEU	-	expression tag	UNP P49685
R	334	GLU	-	expression tag	UNP P49685
R	335	VAL	-	expression tag	UNP P49685
R	336	LEU	-	expression tag	UNP P49685
R	337	PHE	-	expression tag	UNP P49685
R	338	GLN	-	expression tag	UNP P49685
R	339	GLY	-	expression tag	UNP P49685
R	340	PRO	-	expression tag	UNP P49685
R	341	TRP	-	expression tag	UNP P49685
R	342	SER	-	expression tag	UNP P49685
R	343	HIS	-	expression tag	UNP P49685

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Chain	Residue	Modelled	Actual	Comment	Reference
R	344	PRO	-	expression tag	UNP P49685
R	345	GLN	-	expression tag	UNP P49685
R	346	PHE	-	expression tag	UNP P49685
R	347	GLU	-	expression tag	UNP P49685
R	348	LYS	-	expression tag	UNP P49685
R	349	GLY	-	expression tag	UNP P49685
R	350	GLY	-	expression tag	UNP P49685
R	351	GLY	-	expression tag	UNP P49685
R	352	SER	-	expression tag	UNP P49685
R	353	GLY	-	expression tag	UNP P49685
R	354	GLY	-	expression tag	UNP P49685
R	355	GLY	-	expression tag	UNP P49685
R	356	SER	-	expression tag	UNP P49685
R	357	GLY	-	expression tag	UNP P49685
R	358	GLY	-	expression tag	UNP P49685
R	359	SER	-	expression tag	UNP P49685
R	360	ALA	-	expression tag	UNP P49685
R	361	TRP	-	expression tag	UNP P49685
R	362	SER	-	expression tag	UNP P49685
R	363	HIS	-	expression tag	UNP P49685
R	364	PRO	-	expression tag	UNP P49685
R	365	GLN	-	expression tag	UNP P49685
R	366	PHE	-	expression tag	UNP P49685
R	367	GLU	-	expression tag	UNP P49685
R	368	LYS	-	expression tag	UNP P49685
R	369	ASP	-	expression tag	UNP P49685
R	370	TYR	-	expression tag	UNP P49685
R	371	LYS	-	expression tag	UNP P49685
R	372	ASP	-	expression tag	UNP P49685
R	373	ASP	-	expression tag	UNP P49685
R	374	ASP	-	expression tag	UNP P49685
R	375	ASP	-	expression tag	UNP P49685
R	376	LYS	-	expression tag	UNP P49685

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	220	Total	C	N	O	S	0	0
			1699	1094	287	305	13		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	CYS	SER	conflict	UNP P08754
A	202	THR	GLY	conflict	UNP P08754
A	203	ALA	GLY	conflict	UNP P08754
A	245	ALA	GLU	conflict	UNP P08754
A	326	SER	ALA	conflict	UNP P08754

- 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
			2496	1546	445	485	20		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	initiating methionine	UNP P62873
B	-9	HIS	-	expression tag	UNP P62873
B	-8	HIS	-	expression tag	UNP P62873
B	-7	HIS	-	expression tag	UNP P62873
B	-6	HIS	-	expression tag	UNP P62873
B	-5	HIS	-	expression tag	UNP P62873
B	-4	HIS	-	expression tag	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873

- 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	C	54	Total	C	N	O	S	0	0
			357	226	61	69	1		

- Molecule 6 is a protein called scFv16.

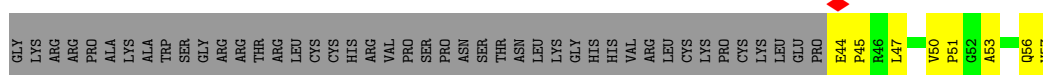
Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	234	Total	C	N	O	S	0	0
			1753	1115	293	335	10		

### 3 Residue-property plots [i](#)

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

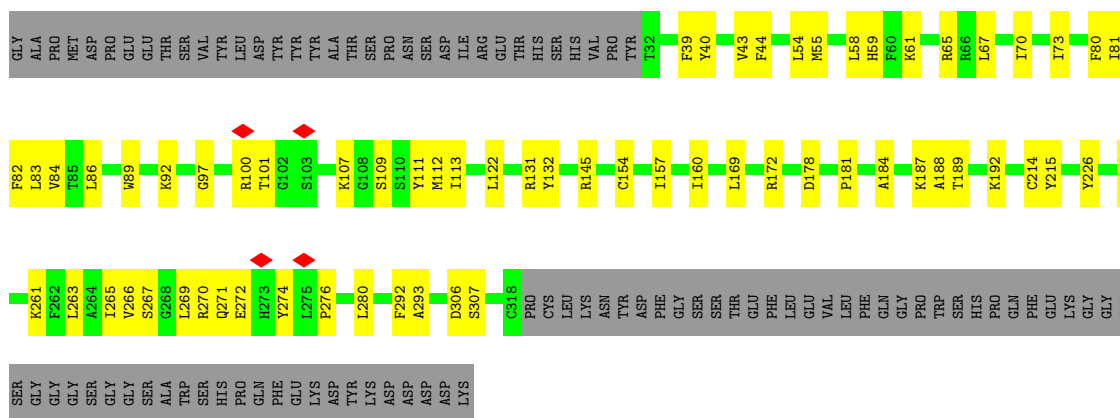
#### • Molecule 1: Protein GPR15LG

Chain L: 



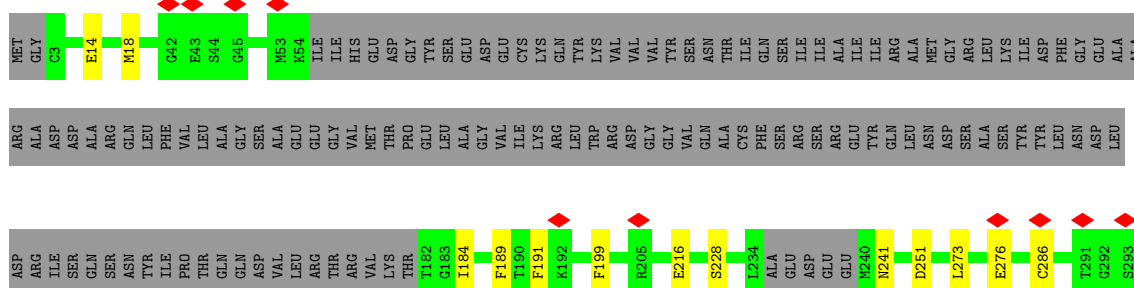
#### • Molecule 2: G-protein coupled receptor 15

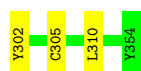
Chain R: 



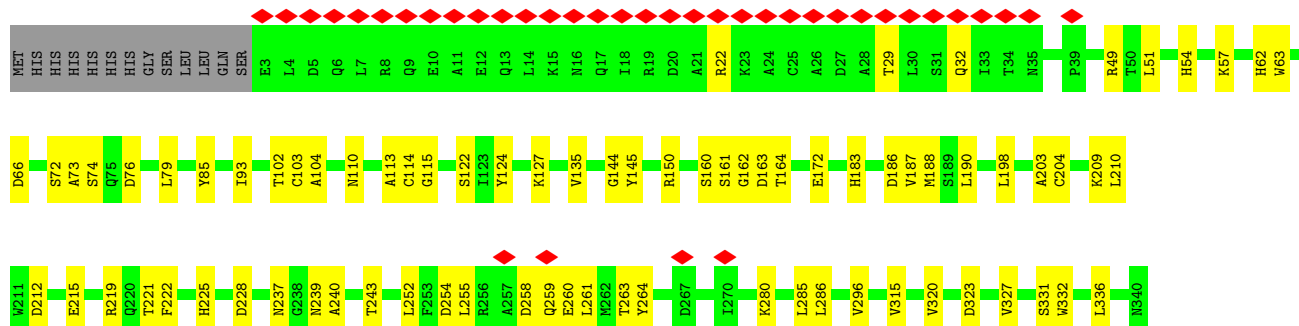
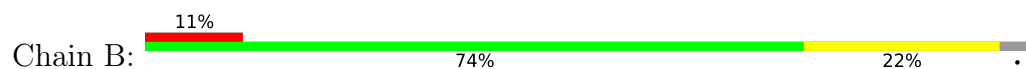
#### • Molecule 3: Guanine nucleotide-binding protein G(i) subunit alpha-3

Chain A: 

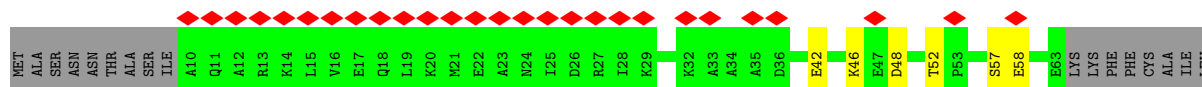
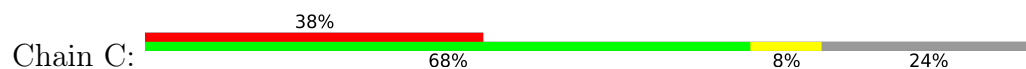




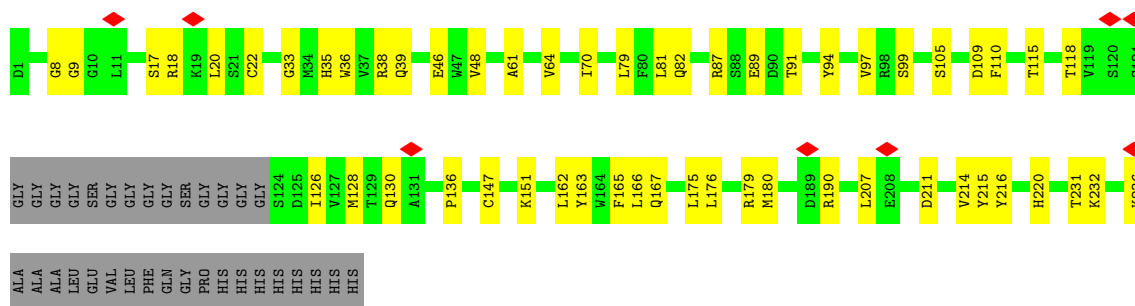
• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



• Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



• Molecule 6: scFv16





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	286873	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.246	Depositor
Minimum map value	-1.823	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.077	Depositor
Recommended contour level	0.5	Depositor
Map size ( $\text{\AA}$ )	274.176, 274.176, 274.176	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.071, 1.071, 1.071	Depositor

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	L	0.18	0/109	0.46	0/151
2	R	0.12	0/2291	0.33	0/3116
3	A	0.09	0/1728	0.25	0/2326
4	B	0.08	0/2543	0.24	0/3461
5	C	0.08	0/363	0.20	0/501
6	D	0.09	0/1796	0.26	0/2439
All	All	0.10	0/8830	0.28	0/11994

There are no bond length outliers.

There are no bond angle outliers.

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	L	105	0	103	6	0
2	R	2233	0	2309	38	0
3	A	1699	0	1643	9	0
4	B	2496	0	2326	48	0
5	C	357	0	309	3	0
6	D	1753	0	1678	32	0
All	All	8643	0	8368	133	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 (133) 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)
2:R:122:LEU:HB3	2:R:157:ILE:HD11	1.53	0.89
2:R:187:LYS:HG3	2:R:188:ALA:H	1.54	0.70
6:D:166:LEU:HB2	6:D:176:LEU:HD11	1.74	0.70
2:R:178:ASP:HB2	2:R:181:PRO:HG3	1.73	0.69
3:A:241:ASN:ND2	3:A:286:CYS:SG	2.65	0.69
6:D:215:TYR:HB2	6:D:231:THR:HB	1.76	0.67
4:B:22:ARG:O	4:B:259:GLN:NE2	2.28	0.67
3:A:216:GLU:OE1	4:B:57:LYS:NZ	2.29	0.65
4:B:225:HIS:HE2	4:B:243:THR:HG1	1.42	0.65
6:D:22:CYS:HB3	6:D:79:LEU:HB3	1.77	0.65
1:L:51:PRO:HB3	1:L:56:GLN:HB2	1.80	0.64
6:D:162:LEU:HB3	6:D:180:MET:HB2	1.79	0.64
2:R:55:MET:O	2:R:59:HIS:HB2	1.98	0.63
6:D:91:THR:HG23	6:D:118:THR:HA	1.79	0.63
2:R:276:PRO:HG2	2:R:280:LEU:HD23	1.82	0.62
4:B:51:LEU:HB2	4:B:336:LEU:HB2	1.80	0.62
6:D:214:VAL:HG22	6:D:232:LYS:HG2	1.80	0.62
4:B:110:ASN:HD22	4:B:127:LYS:HG3	1.64	0.61
2:R:226:TYR:HE1	2:R:234:LYS:HA	1.66	0.60
6:D:35:HIS:HB2	6:D:97:VAL:HB	1.83	0.59
4:B:198:LEU:HD23	4:B:210:LEU:HD21	1.84	0.59
2:R:261:LYS:O	2:R:265:ILE:HD12	2.02	0.59
2:R:107:LYS:NZ	2:R:172:ARG:O	2.35	0.58
6:D:33:GLY:N	6:D:99:SER:O	2.35	0.58
6:D:190:ARG:NH1	6:D:211:ASP:OD2	2.34	0.58
2:R:44:PHE:HA	2:R:83:LEU:HD13	1.86	0.57
6:D:17:SER:OG	6:D:82:GLN:OE1	2.24	0.56
2:R:100:ARG:NH1	2:R:101:THR:OG1	2.40	0.55
4:B:264:TYR:HE2	4:B:285:LEU:HD23	1.70	0.55
4:B:320:VAL:HG22	4:B:327:VAL:HG22	1.87	0.55
6:D:105:SER:O	6:D:179:ARG:NH2	2.39	0.55
6:D:207:LEU:HB2	6:D:211:ASP:HB2	1.88	0.55
2:R:187:LYS:HG3	2:R:188:ALA:N	2.22	0.55
4:B:210:LEU:HD22	4:B:255:LEU:HD22	1.89	0.54
5:C:48:ASP:O	5:C:52:THR:OG1	2.24	0.54
6:D:165:PHE:HB2	6:D:216:TYR:HB2	1.88	0.54
4:B:237:ASN:OD1	4:B:239:ASN:ND2	2.33	0.54
5:C:42:GLU:O	5:C:46:LYS:NZ	2.41	0.54
6:D:61:ALA:HB3	6:D:64:VAL:HG22	1.90	0.53
3:A:14:GLU:O	3:A:18:MET:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:74:SER:OG	4:B:76:ASP:OD1	2.25	0.53
4:B:280:LYS:HE3	4:B:323:ASP:HA	1.89	0.53
4:B:286:LEU:HD11	4:B:327:VAL:HG11	1.92	0.52
6:D:9:GLY:H	6:D:18:ARG:HH21	1.58	0.52
1:L:44:GLU:HA	1:L:47:LEU:HD23	1.92	0.52
4:B:172:GLU:OE1	4:B:172:GLU:N	2.26	0.52
6:D:36:TRP:CD2	6:D:81:LEU:HD22	2.45	0.52
2:R:58:LEU:HA	2:R:61:LYS:HD3	1.93	0.51
4:B:228:ASP:N	4:B:228:ASP:OD1	2.43	0.51
2:R:157:ILE:HA	2:R:160:ILE:HG22	1.93	0.51
4:B:252:LEU:HD22	4:B:261:LEU:HD12	1.92	0.51
6:D:130:GLN:HG2	6:D:147:CYS:HB3	1.91	0.51
4:B:186:ASP:N	4:B:204:CYS:SG	2.84	0.51
4:B:260:GLU:OE2	4:B:263:THR:OG1	2.28	0.51
2:R:70:ILE:HA	2:R:73:ILE:HG22	1.93	0.50
4:B:49:ARG:NH1	4:B:85:TYR:O	2.44	0.50
2:R:189:THR:HG23	2:R:192:LYS:H	1.77	0.50
6:D:39:GLN:NE2	6:D:167:GLN:OE1	2.38	0.50
2:R:40:TYR:HD1	2:R:86:LEU:HD21	1.77	0.49
6:D:136:PRO:HB2	6:D:236:LYS:HD2	1.95	0.49
4:B:73:ALA:HB2	4:B:103:CYS:HB3	1.94	0.49
4:B:144:GLY:HA3	4:B:163:ASP:N	2.27	0.49
6:D:36:TRP:CD1	6:D:81:LEU:HD13	2.47	0.49
4:B:212:ASP:OD2	4:B:219:ARG:NH2	2.41	0.49
2:R:43:VAL:HG11	2:R:292:PHE:HB3	1.95	0.49
4:B:209:LYS:HG2	4:B:221:THR:HG23	1.94	0.48
2:R:263:LEU:HA	2:R:266:VAL:HG12	1.94	0.48
2:R:270:ARG:HG3	2:R:272:GLU:HB2	1.96	0.48
4:B:212:ASP:HB3	4:B:215:GLU:HB3	1.94	0.48
4:B:240:ALA:HA	4:B:254:ASP:HA	1.96	0.48
4:B:104:ALA:HB3	4:B:113:ALA:HB3	1.95	0.48
4:B:222:PHE:HE1	4:B:258:ASP:HA	1.79	0.48
6:D:38:ARG:HD3	6:D:94:TYR:HE1	1.77	0.48
2:R:39:PHE:HZ	2:R:293:ALA:HB2	1.77	0.47
2:R:187:LYS:HZ3	2:R:188:ALA:HB3	1.79	0.47
4:B:188:MET:HE3	4:B:188:MET:HB3	1.79	0.47
3:A:228:SER:HB3	3:A:273:LEU:HD22	1.96	0.47
4:B:54:HIS:NE2	4:B:72:SER:OG	2.37	0.47
4:B:79:LEU:HB3	4:B:93:ILE:HB	1.95	0.47
6:D:180:MET:HG2	6:D:180:MET:O	2.13	0.47
4:B:187:VAL:HA	4:B:203:ALA:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:161:SER:OG	4:B:163:ASP:OD1	2.28	0.46
4:B:315:VAL:HA	4:B:331:SER:HA	1.98	0.46
4:B:114:CYS:HB3	4:B:122:SER:HB2	1.96	0.46
6:D:126:ILE:HG12	6:D:151:LYS:HD3	1.98	0.46
2:R:81:ILE:HA	2:R:84:VAL:HG22	1.98	0.45
2:R:92:LYS:HG3	2:R:97:GLY:HA2	1.98	0.45
6:D:20:LEU:HD12	6:D:81:LEU:HB3	1.98	0.45
2:R:54:LEU:O	2:R:58:LEU:HG	2.16	0.45
6:D:109:ASP:OD1	6:D:110:PHE:N	2.49	0.45
2:R:267:SER:OG	2:R:274:TYR:O	2.34	0.45
6:D:38:ARG:NE	6:D:46:GLU:OE2	2.50	0.45
1:L:53:ALA:H	2:R:89:TRP:HZ2	1.64	0.45
2:R:111:TYR:HB2	2:R:169:LEU:HD13	1.99	0.45
3:A:189:PHE:HE2	3:A:191:PHE:CE2	2.35	0.45
4:B:225:HIS:NE2	4:B:243:THR:OG1	2.34	0.45
2:R:82:PHE:CE1	2:R:113:ILE:HG23	2.52	0.44
3:A:184:ILE:HD11	3:A:199:PHE:HB3	1.99	0.44
4:B:264:TYR:CE2	4:B:285:LEU:HD23	2.52	0.44
6:D:48:VAL:HG13	6:D:64:VAL:HG21	2.00	0.44
2:R:131:ARG:NH1	2:R:215:TYR:OH	2.51	0.44
4:B:164:THR:OG1	4:B:183:HIS:O	2.34	0.44
4:B:286:LEU:HA	4:B:296:VAL:HA	1.99	0.44
1:L:56:GLN:HG2	1:L:57:VAL:H	1.84	0.43
4:B:145:TYR:O	4:B:162:GLY:N	2.51	0.43
4:B:102:THR:O	4:B:115:GLY:N	2.52	0.43
4:B:323:ASP:N	4:B:323:ASP:OD1	2.50	0.43
6:D:36:TRP:HD1	6:D:70:ILE:HD12	1.84	0.43
4:B:29:THR:OG1	4:B:32:GLN:OE1	2.31	0.43
6:D:128:MET:HE3	6:D:128:MET:HB3	1.84	0.43
2:R:80:PHE:O	2:R:84:VAL:HG13	2.19	0.43
2:R:306:ASP:OD1	2:R:307:SER:N	2.52	0.43
4:B:160:SER:HB2	4:B:190:LEU:HD23	2.01	0.43
3:A:251:ASP:HB3	3:A:310:LEU:HD13	2.01	0.42
1:L:44:GLU:N	1:L:45:PRO:HD2	2.34	0.42
2:R:65:ARG:HD3	2:R:65:ARG:HA	1.76	0.42
5:C:57:SER:OG	5:C:58:GLU:OE1	2.37	0.42
4:B:331:SER:OG	4:B:332:TRP:N	2.51	0.42
1:L:50:VAL:HG22	2:R:184:ALA:HB2	2.01	0.42
2:R:154:CYS:HA	2:R:157:ILE:HG22	2.02	0.42
6:D:87:ARG:HG2	6:D:89:GLU:H	1.85	0.42
4:B:62:HIS:CD2	4:B:63:TRP:H	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:163:TYR:HD2	6:D:175:LEU:HD11	1.83	0.41
2:R:109:SER:HA	2:R:112:MET:HG2	2.01	0.41
2:R:269:LEU:O	2:R:271:GLN:NE2	2.53	0.41
2:R:67:LEU:HD22	2:R:145:ARG:HH11	1.85	0.41
4:B:66:ASP:OD1	4:B:66:ASP:N	2.51	0.41
4:B:150:ARG:HA	4:B:150:ARG:HD3	1.88	0.41
6:D:8:GLY:O	6:D:115:THR:OG1	2.31	0.41
2:R:132:TYR:HB2	2:R:214:CYS:HB3	2.03	0.41
3:A:273:LEU:HA	3:A:276:GLU:HG3	2.03	0.41
3:A:302:TYR:HA	3:A:305:CYS:SG	2.61	0.41
4:B:124:TYR:CE2	4:B:135:VAL:HG22	2.56	0.41

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	L	12/58 (21%)	7 (58%)	5 (42%)	0	100	100
2	R	285/379 (75%)	268 (94%)	17 (6%)	0	100	100
3	A	214/354 (60%)	211 (99%)	3 (1%)	0	100	100
4	B	336/351 (96%)	323 (96%)	13 (4%)	0	100	100
5	C	52/71 (73%)	52 (100%)	0	0	100	100
6	D	230/267 (86%)	221 (96%)	9 (4%)	0	100	100
All	All	1129/1480 (76%)	1082 (96%)	47 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	L	11/51 (22%)	11 (100%)	0	100	100
2	R	243/333 (73%)	243 (100%)	0	100	100
3	A	170/311 (55%)	170 (100%)	0	100	100
4	B	254/293 (87%)	254 (100%)	0	100	100
5	C	28/58 (48%)	28 (100%)	0	100	100
6	D	188/216 (87%)	187 (100%)	1 (0%)	86	91
All	All	894/1262 (71%)	893 (100%)	1 (0%)	92	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	D	220	HIS

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

Mol	Chain	Res	Type
3	A	241	ASN
4	B	91	HIS
4	B	293	ASN
6	D	39	GLN
6	D	167	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](#)

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.



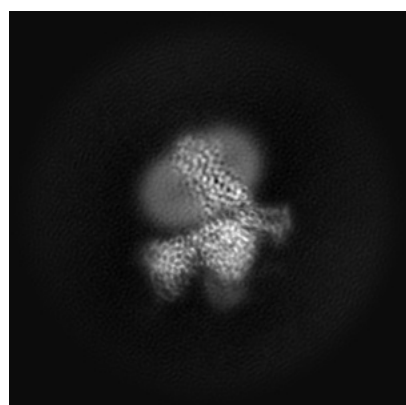
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66350. These allow visual inspection of the internal detail of the map and identification of artifacts.

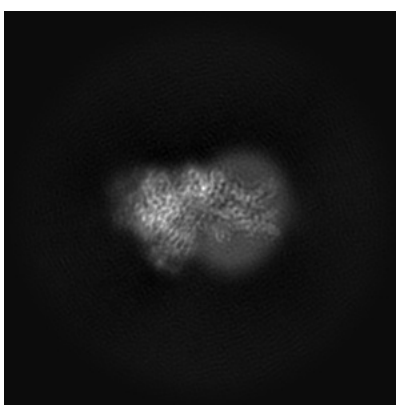
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

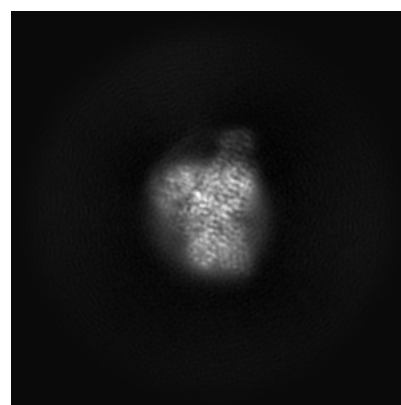
#### 6.1.1 Primary map



X



Y

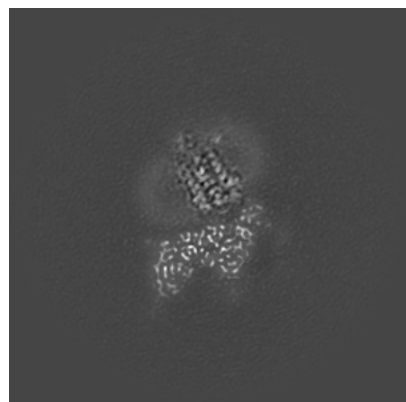


Z

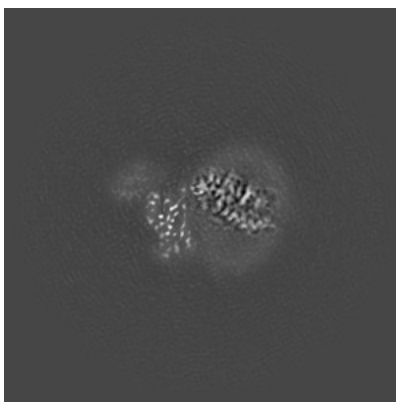
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

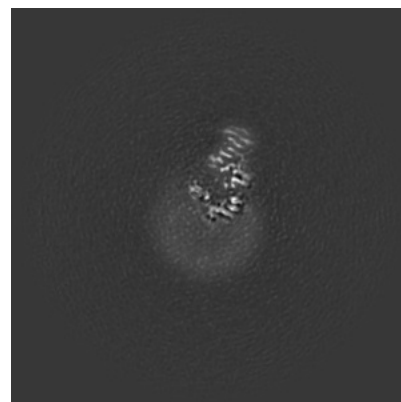
#### 6.2.1 Primary map



X Index: 128



Y Index: 128

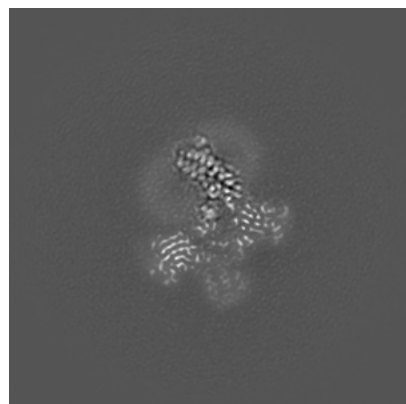


Z Index: 128

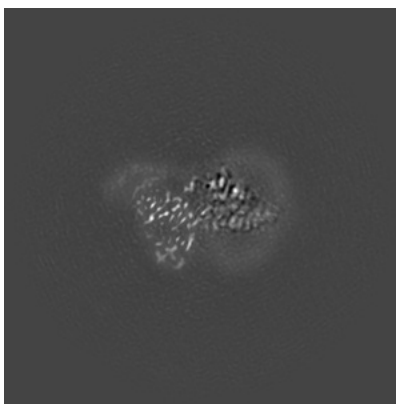
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

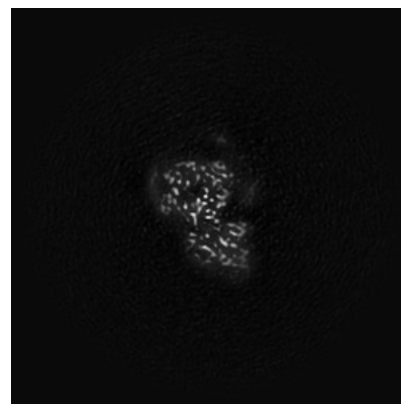
### 6.3.1 Primary map



X Index: 137



Y Index: 135

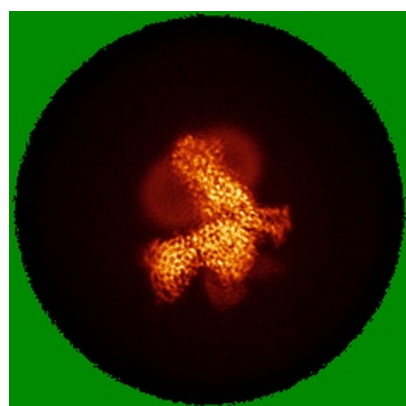


Z Index: 104

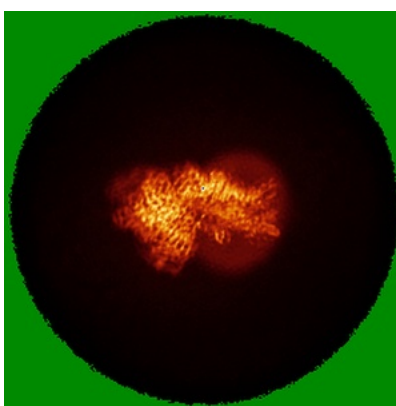
The images above show the largest variance slices of the map in three orthogonal directions.

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

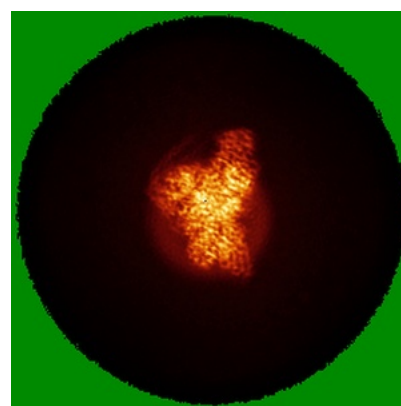
### 6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

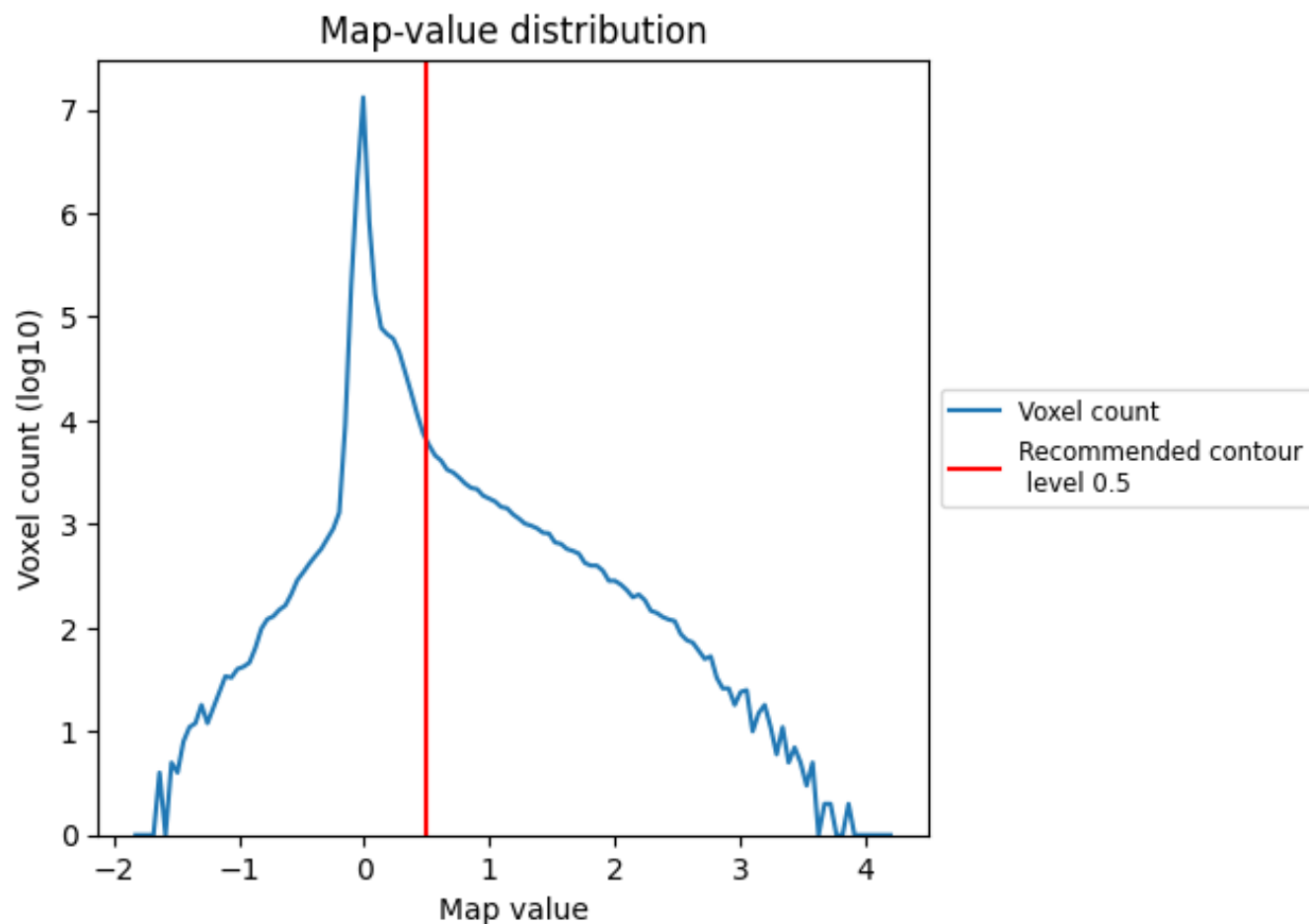
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

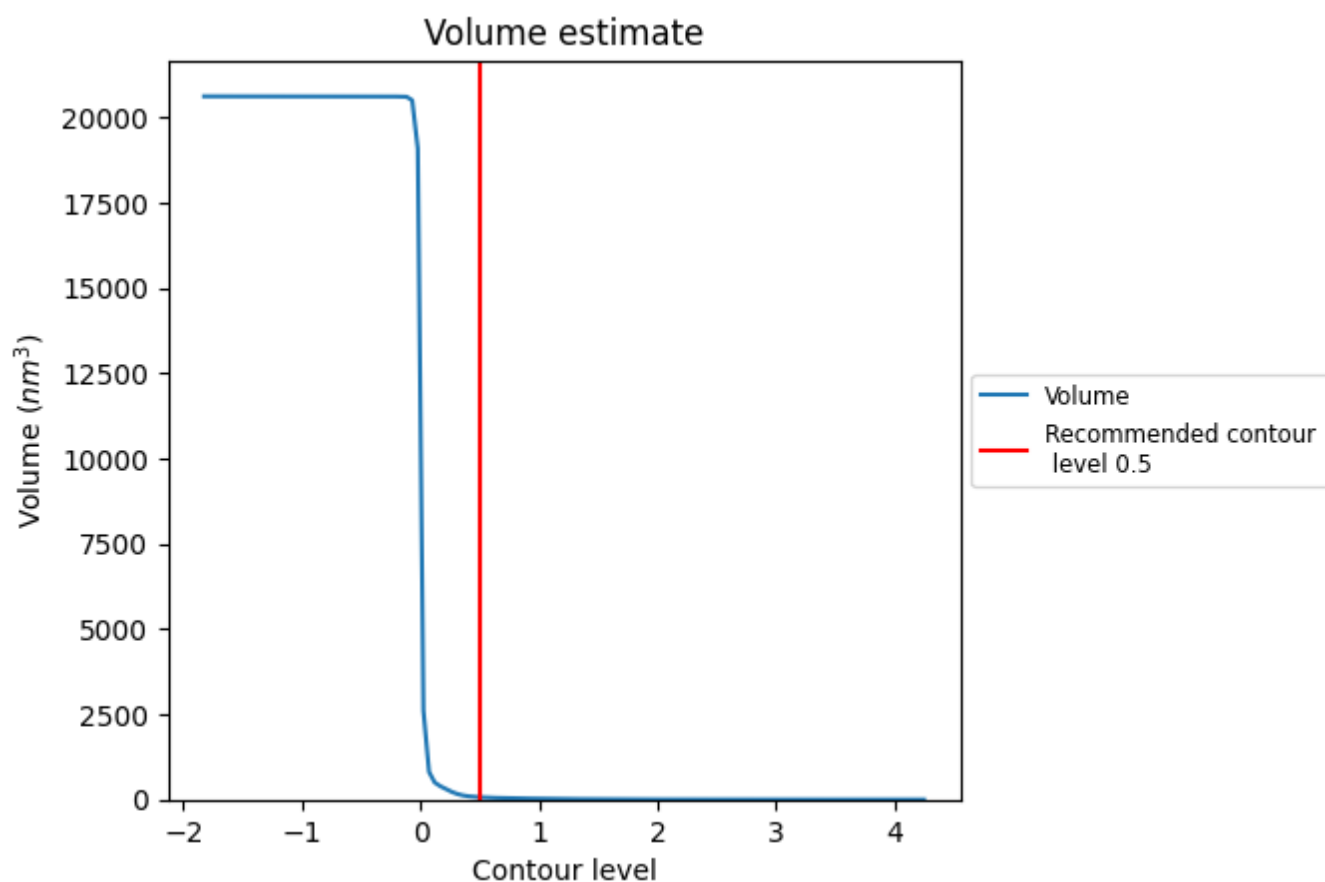
This section contains the results of statistical analysis of the map.

### 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.

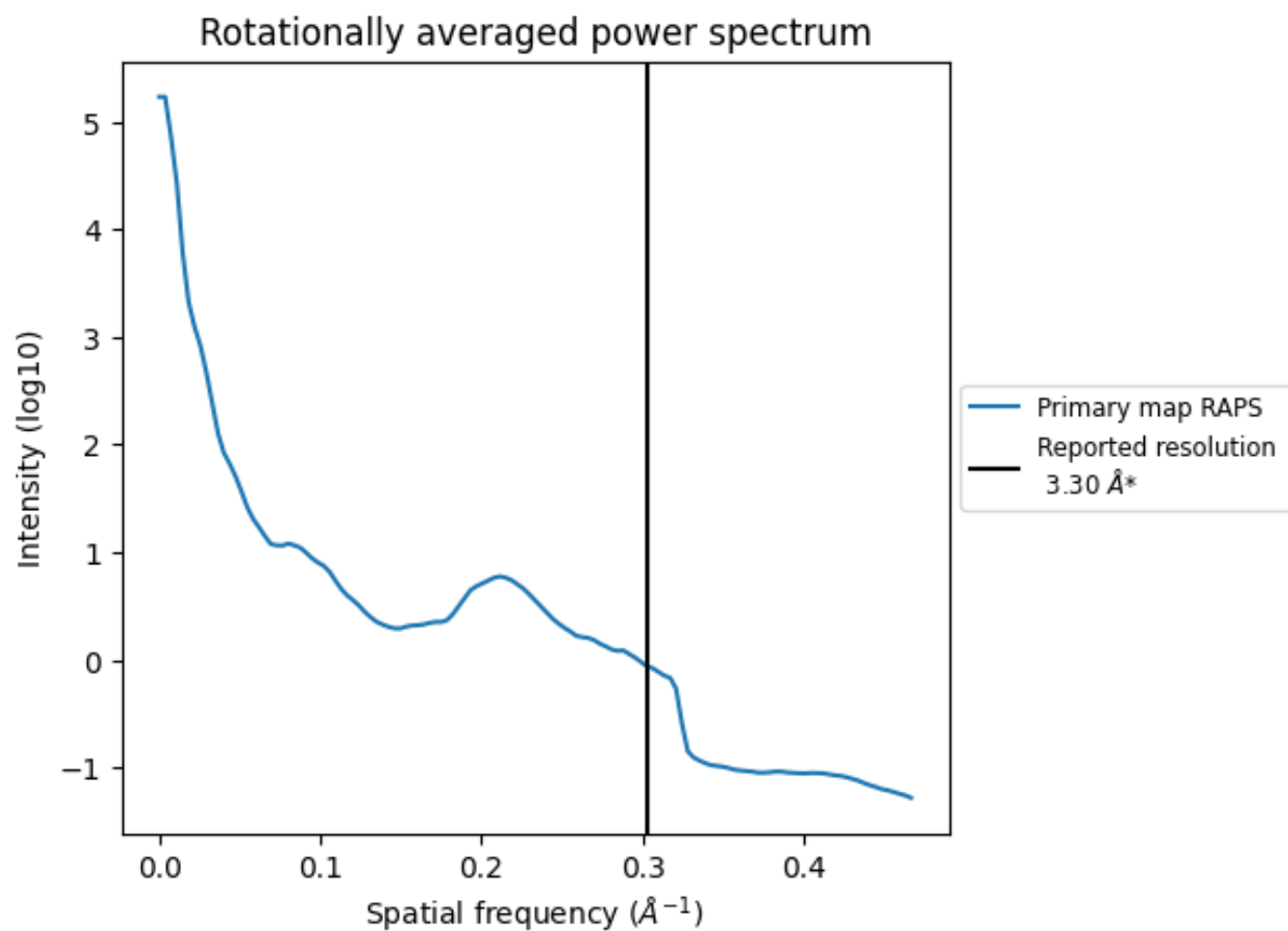
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 69  $\text{nm}^3$ ; this corresponds to an approximate mass of 62 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 0.303 Å<sup>-1</sup>

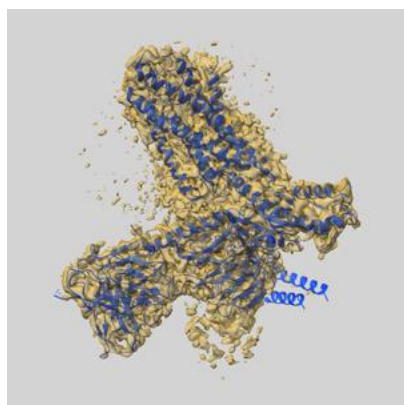
## 8 Fourier-Shell correlation

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

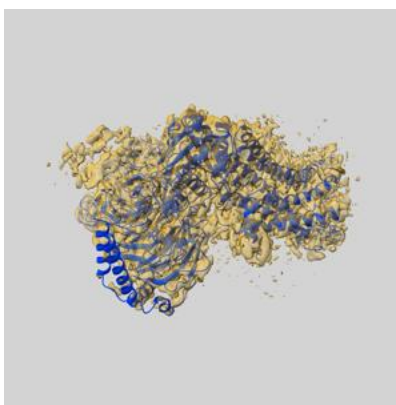
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66350 and PDB model 9WXM. Per-residue inclusion information can be found in section [3](#) on page [7](#).

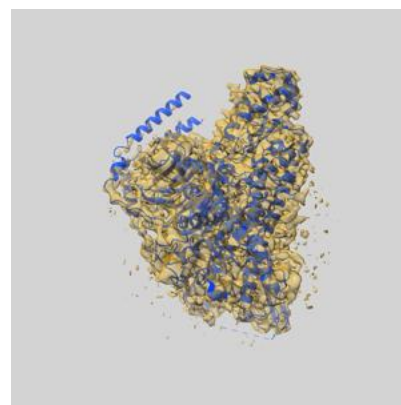
### 9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5 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.

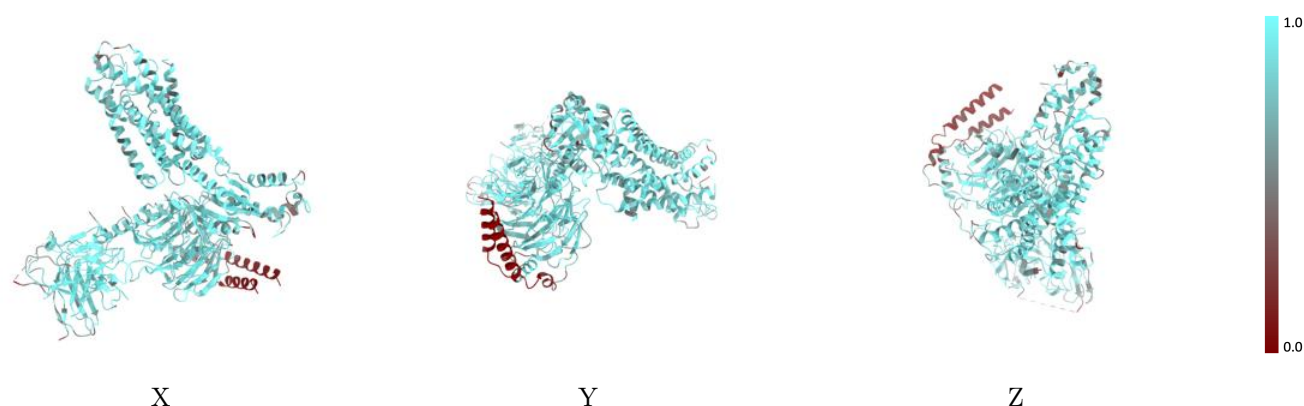


## 9.2 Q-score mapped to coordinate model [i](#)



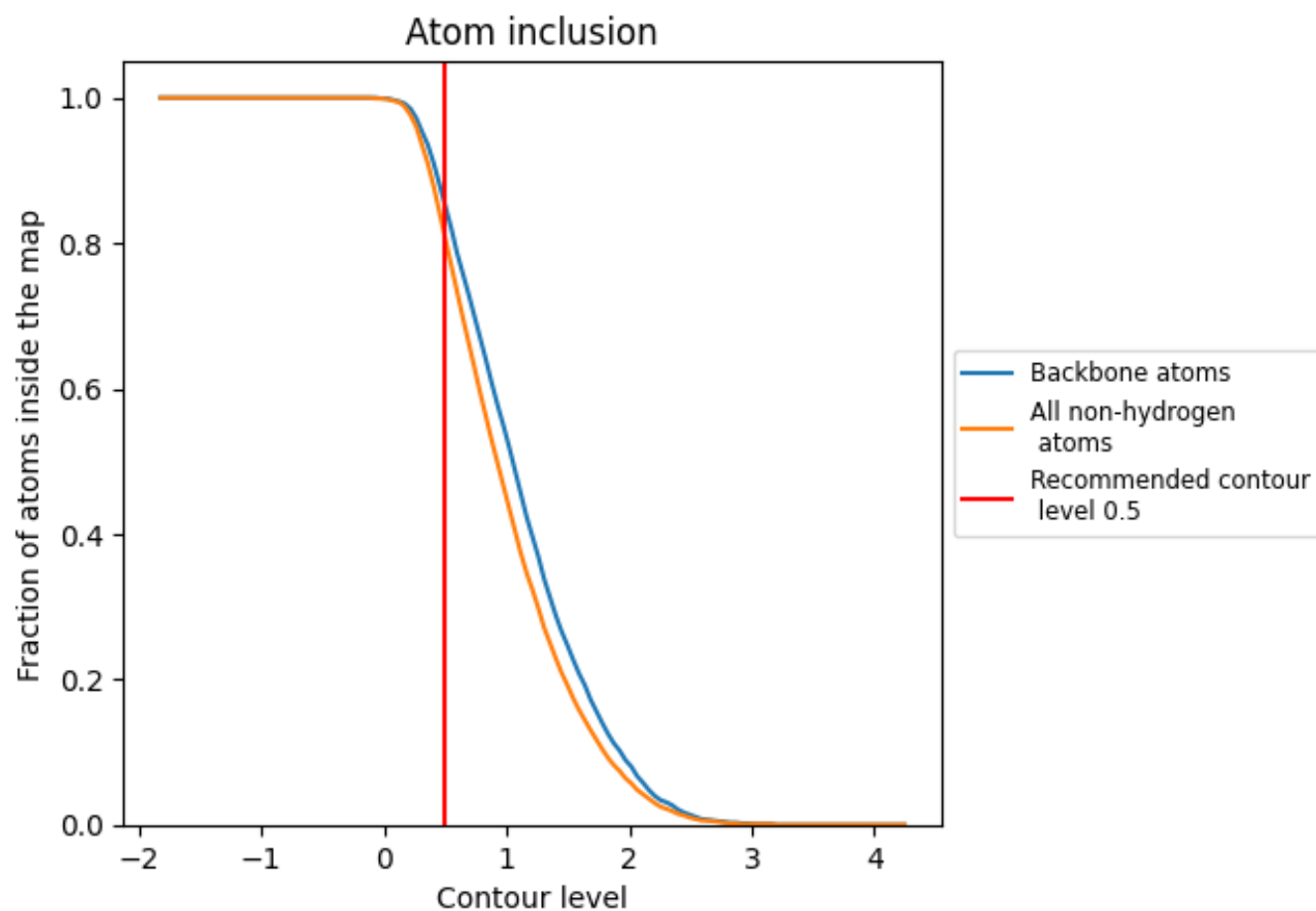
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8060</div>	<div><div></div>0.4380</div>
A	<div><div></div>0.8170</div>	<div><div></div>0.4610</div>
B	<div><div></div>0.7980</div>	<div><div></div>0.4490</div>
C	<div><div></div>0.4890</div>	<div><div></div>0.3310</div>
D	<div><div></div>0.8390</div>	<div><div></div>0.4780</div>
L	<div><div></div>0.6920</div>	<div><div></div>0.3680</div>
R	<div><div></div>0.8360</div>	<div><div></div>0.3980</div>

1.0

0.0

<0.0