



## Full wwPDB EM Validation Report ⓘ

Jul 9, 2025 – 08:12 PM JST

PDB ID : 9LWP / pdb\_00009lwp  
EMDB ID : EMD-63455  
Title : Cryo-EM structure of the unliganded human BRS3-Gq complex  
Authors : Li, J.; Li, C.; Zhou, Q.; Han, W.; Fang, M.; Xu, Y.; Mai, Y.; Cui, J.; Xu, H.;  
Zhang, Y.; Wang, M.  
Deposited on : 2025-02-16  
Resolution : 2.93 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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.44

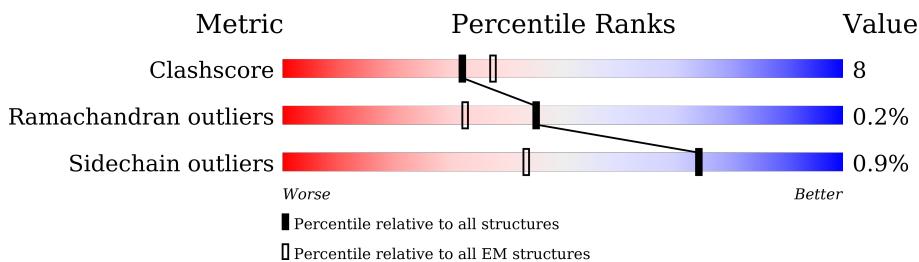
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.93 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	R	612	
2	A	246	
3	B	345	
4	G	70	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6844 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 Bombesin receptor subtype-3, Oplophorus-luciferin 2-monooxygenase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	271	Total	C	N	O	S	0	0
			2165	1448	349	357	11		

There are 85 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-15	MET	-	initiating methionine	UNP P32247
R	-14	LYS	-	expression tag	UNP P32247
R	-13	THR	-	expression tag	UNP P32247
R	-12	ILE	-	expression tag	UNP P32247
R	-11	ILE	-	expression tag	UNP P32247
R	-10	ALA	-	expression tag	UNP P32247
R	-9	LEU	-	expression tag	UNP P32247
R	-8	SER	-	expression tag	UNP P32247
R	-7	TYR	-	expression tag	UNP P32247
R	-6	ILE	-	expression tag	UNP P32247
R	-5	PHE	-	expression tag	UNP P32247
R	-4	CYS	-	expression tag	UNP P32247
R	-3	LEU	-	expression tag	UNP P32247
R	-2	VAL	-	expression tag	UNP P32247
R	-1	PHE	-	expression tag	UNP P32247
R	0	ALA	-	expression tag	UNP P32247
R	400	GLY	-	linker	UNP P32247
R	401	SER	-	linker	UNP P32247
R	402	SER	-	linker	UNP P32247
R	403	GLY	-	linker	UNP P32247
R	404	GLY	-	linker	UNP P32247
R	405	GLY	-	linker	UNP P32247
R	406	GLY	-	linker	UNP P32247
R	407	SER	-	linker	UNP P32247
R	408	GLY	-	linker	UNP P32247
R	409	GLY	-	linker	UNP P32247
R	410	GLY	-	linker	UNP P32247

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Chain	Residue	Modelled	Actual	Comment	Reference
R	411	GLY	-	linker	UNP P32247
R	412	SER	-	linker	UNP P32247
R	413	SER	-	linker	UNP P32247
R	414	GLY	-	linker	UNP P32247
R	415	VAL	-	linker	UNP P32247
R	419	GLU	ALA	conflict	UNP Q9GV45
R	426	GLU	GLN	conflict	UNP Q9GV45
R	430	ALA	GLY	conflict	UNP Q9GV45
R	433	LEU	GLN	conflict	UNP Q9GV45
R	442	VAL	LEU	conflict	UNP Q9GV45
R	446	LEU	PHE	conflict	UNP Q9GV45
R	448	ASN	ALA	conflict	UNP Q9GV45
R	450	ALA	GLY	conflict	UNP Q9GV45
R	458	ARG	LYS	conflict	UNP Q9GV45
R	459	ILE	VAL	conflict	UNP Q9GV45
R	461	ARG	LEU	conflict	UNP Q9GV45
R	466	ALA	GLY	conflict	UNP Q9GV45
R	469	ILE	ALA	conflict	UNP Q9GV45
R	482	ALA	GLY	conflict	UNP Q9GV45
R	483	ASP	PHE	conflict	UNP Q9GV45
R	486	ALA	GLY	conflict	UNP Q9GV45
R	487	GLN	LEU	conflict	UNP Q9GV45
R	490	GLU	MET	conflict	UNP Q9GV45
R	491	VAL	ILE	conflict	UNP Q9GV45
R	505	VAL	ILE	conflict	UNP Q9GV45
R	508	PRO	HIS	conflict	UNP Q9GV45
R	522	LEU	ILE	conflict	UNP Q9GV45
R	523	ASN	ASP	conflict	UNP Q9GV45
R	530	GLU	PRO	conflict	UNP Q9GV45
R	539	LYS	GLN	conflict	UNP Q9GV45
R	553	ILE	TYR	conflict	UNP Q9GV45
R	559	THR	ASN	conflict	UNP Q9GV45
R	564	MET	LEU	conflict	UNP Q9GV45
R	572	SER	-	expression tag	UNP Q9GV45
R	573	GLY	-	expression tag	UNP Q9GV45
R	574	GLY	-	expression tag	UNP Q9GV45
R	575	SER	-	expression tag	UNP Q9GV45
R	576	GLU	-	expression tag	UNP Q9GV45
R	577	ASN	-	expression tag	UNP Q9GV45
R	578	LEU	-	expression tag	UNP Q9GV45
R	579	TYR	-	expression tag	UNP Q9GV45
R	580	PHE	-	expression tag	UNP Q9GV45

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Chain	Residue	Modelled	Actual	Comment	Reference
R	581	GLN	-	expression tag	UNP Q9GV45
R	582	GLY	-	expression tag	UNP Q9GV45
R	583	GLY	-	expression tag	UNP Q9GV45
R	584	SER	-	expression tag	UNP Q9GV45
R	585	ALA	-	expression tag	UNP Q9GV45
R	586	GLY	-	expression tag	UNP Q9GV45
R	587	SER	-	expression tag	UNP Q9GV45
R	588	ALA	-	expression tag	UNP Q9GV45
R	589	HIS	-	expression tag	UNP Q9GV45
R	590	HIS	-	expression tag	UNP Q9GV45
R	591	HIS	-	expression tag	UNP Q9GV45
R	592	HIS	-	expression tag	UNP Q9GV45
R	593	HIS	-	expression tag	UNP Q9GV45
R	594	HIS	-	expression tag	UNP Q9GV45
R	595	HIS	-	expression tag	UNP Q9GV45
R	596	HIS	-	expression tag	UNP Q9GV45

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	211	Total	C	N	O	S	0	0
			1650	1050	291	302	7		

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	CYS	conflict	UNP P04899
A	31	ARG	ALA	conflict	UNP P04899
A	33	THR	GLU	conflict	UNP P04899
A	34	LEU	VAL	conflict	UNP P04899
A	35	ARG	LYS	conflict	UNP P04899
A	42	ASP	GLY	conflict	UNP P63092
A	43	ASN	GLU	conflict	UNP P63092
A	58	GLY	-	linker	UNP P63092
A	59	GLY	-	linker	UNP P63092
A	60	SER	-	linker	UNP P63092
A	61	GLY	-	linker	UNP P63092
A	62	GLY	-	linker	UNP P63092
A	63	SER	-	linker	UNP P63092
A	64	GLY	-	linker	UNP P63092
A	65	GLY	-	linker	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	111	ASP	ALA	conflict	UNP P63092
A	114	ASP	SER	conflict	UNP P63092
A	124	ASP	LEU	conflict	UNP P63092
A	195	LYS	ASP	conflict	UNP P63092
A	198	VAL	LEU	conflict	UNP P63092
A	199	ASP	ARG	conflict	UNP P63092
A	210	ILE	TYR	conflict	UNP P63092
A	224	ALA	ILE	conflict	UNP P63092
A	227	ILE	VAL	conflict	UNP P63092
A	232	LYS	ARG	conflict	UNP P63092
A	236	LEU	GLN	conflict	UNP P63092
A	237	GLN	ARG	conflict	UNP P63092
A	239	ASN	HIS	conflict	UNP P63092
A	242	GLU	GLN	conflict	UNP P63092
A	244	ASN	GLU	conflict	UNP P63092
A	246	VAL	LEU	conflict	UNP P63092

- 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	338	Total	C	N	O	S	0	0
			2600	1604	467	508	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

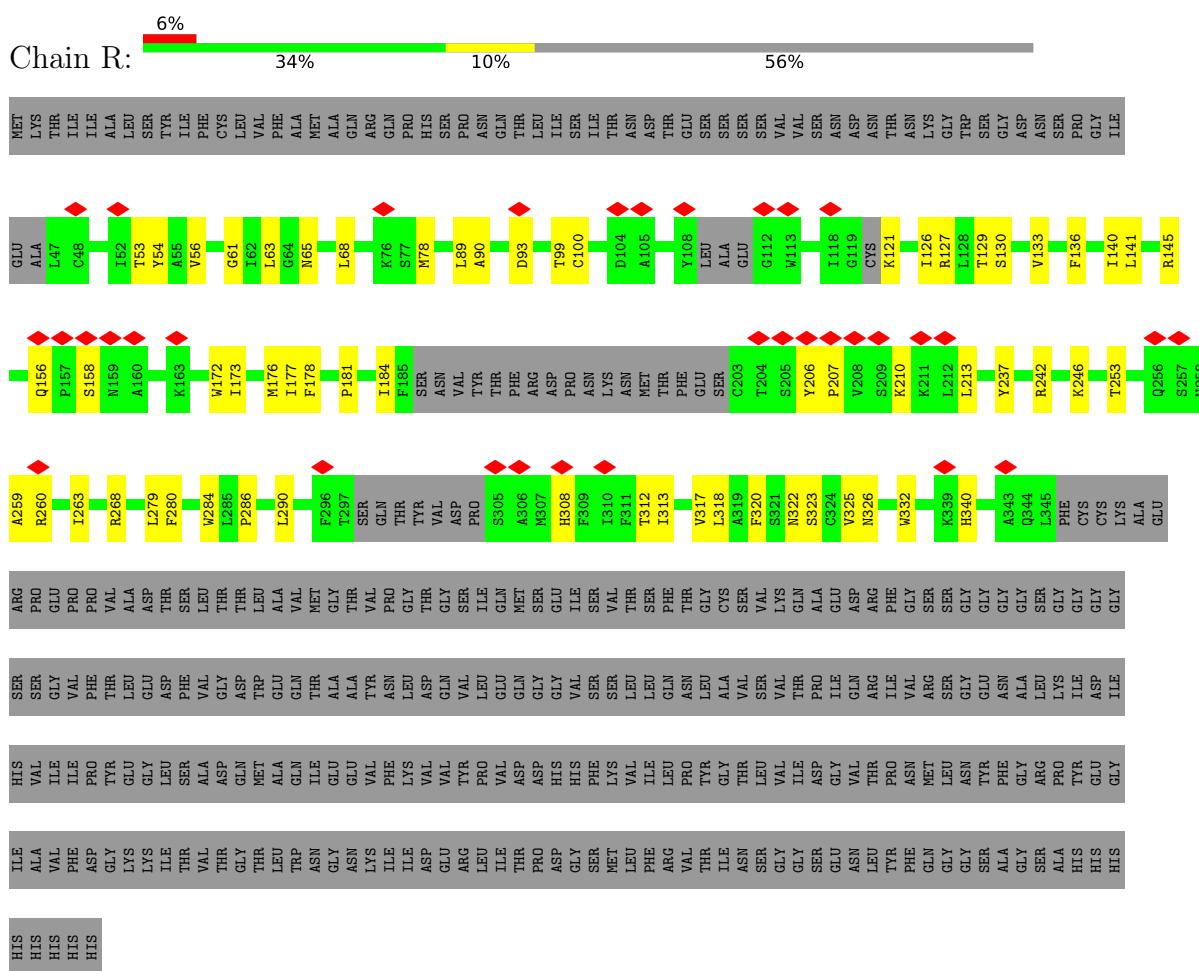
- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

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

### 3 Residue-property plots

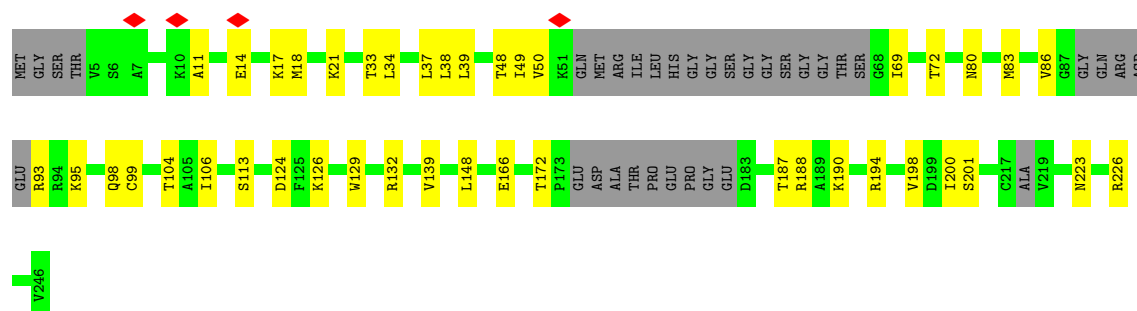
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Bombesin receptor subtype-3,Oplophorus-luciferin 2-monooxygenase catalytic subunit

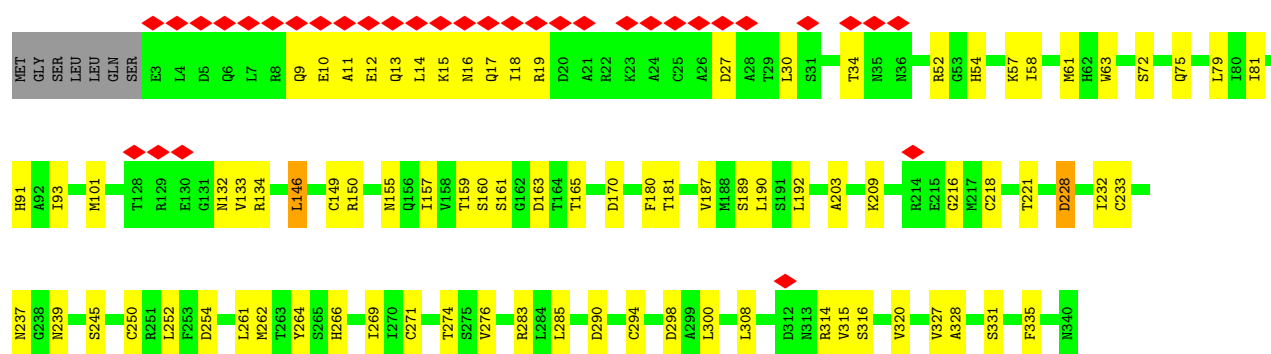
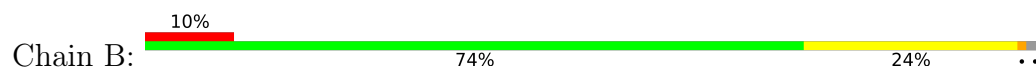


- Molecule 2: Guanine nucleotide-binding protein G(i) subunit alpha-2,Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

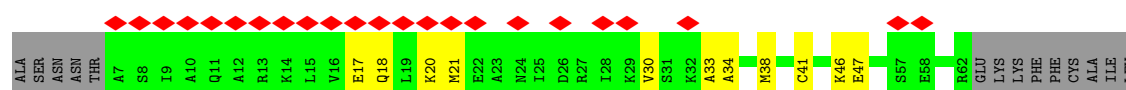




- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



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



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	693649	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	80	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	4.560	Depositor
Minimum map value	-3.020	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.265	Depositor
Map size (Å)	274.176, 274.176, 274.176	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.071, 1.071, 1.071	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	0.14	0/2217	0.30	0/3009
2	A	0.10	0/1677	0.26	0/2264
3	B	0.11	0/2647	0.30	0/3589
4	G	0.12	0/435	0.32	0/587
All	All	0.12	0/6976	0.29	0/9449

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 [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	R	2165	0	2283	33	0
2	A	1650	0	1585	24	0
3	B	2600	0	2505	52	0
4	G	429	0	441	10	0
All	All	6844	0	6814	114	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 (114) 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:271:CYS:HB2	3:B:290:ASP:HB2	1.67	0.77
3:B:218:CYS:O	4:G:18:GLN:NE2	2.20	0.73
1:R:268:ARG:NH2	1:R:332:TRP:O	2.24	0.71
1:R:290:LEU:HD11	1:R:312:THR:HG22	1.75	0.69
3:B:34:THR:HG21	3:B:300:LEU:HD22	1.75	0.68
3:B:58:ILE:O	3:B:316:SER:OG	2.10	0.68
1:R:65:ASN:ND2	1:R:93:ASP:OD2	2.26	0.68
3:B:132:ASN:HD21	3:B:134:ARG:HH21	1.41	0.68
3:B:250:CYS:HB2	3:B:264:TYR:HB2	1.76	0.67
3:B:160:SER:HB3	3:B:190:LEU:HD23	1.77	0.67
4:G:47:GLU:N	4:G:47:GLU:OE1	2.28	0.66
1:R:61:GLY:O	1:R:65:ASN:ND2	2.27	0.65
3:B:294:CYS:HB3	3:B:308:LEU:HB2	1.78	0.64
3:B:237:ASN:HD21	3:B:239:ASN:HB2	1.62	0.64
1:R:89:LEU:HD12	1:R:141:LEU:HD12	1.78	0.64
3:B:320:VAL:HG22	3:B:327:VAL:HG22	1.78	0.64
2:A:49:ILE:HG23	2:A:50:VAL:HG23	1.80	0.64
3:B:54:HIS:HE2	3:B:72:SER:HG	1.45	0.63
2:A:34:LEU:HD23	2:A:104:THR:HG21	1.81	0.63
3:B:30:LEU:HD23	3:B:262:MET:HB2	1.80	0.62
1:R:145:ARG:NH1	1:R:237:TYR:OH	2.32	0.62
2:A:132:ARG:NH1	2:A:132:ARG:HB2	2.15	0.61
2:A:172:THR:HB	2:A:188:ARG:HG2	1.82	0.61
1:R:313:ILE:O	1:R:317:VAL:HG23	2.01	0.60
3:B:27:ASP:H	4:G:30:VAL:HG12	1.65	0.60
3:B:16:ASN:OD1	3:B:19:ARG:NH2	2.35	0.59
3:B:155:ASN:ND2	3:B:170:ASP:OD1	2.35	0.58
1:R:279:LEU:HD23	1:R:325:VAL:HG11	1.86	0.58
3:B:93:ILE:HG12	3:B:133:VAL:HG21	1.87	0.57
3:B:209:LYS:HG2	3:B:221:THR:HG23	1.88	0.56
3:B:79:LEU:HD23	3:B:93:ILE:HD12	1.89	0.55
2:A:126:LYS:HG3	2:A:200:ILE:HG23	1.88	0.55
4:G:34:ALA:O	4:G:38:MET:HG3	2.07	0.55
2:A:113:SER:HB2	2:A:148:LEU:HB2	1.89	0.54
3:B:252:LEU:HD23	3:B:261:LEU:HD23	1.90	0.54
3:B:266:HIS:HB3	3:B:269:ILE:HG12	1.89	0.54
3:B:276:VAL:HG13	3:B:285:LEU:HD11	1.90	0.54
3:B:161:SER:OG	3:B:163:ASP:OD1	2.22	0.53
1:R:54:TYR:OH	1:R:100:CYS:SG	2.60	0.53
1:R:286:PRO:HG3	1:R:318:LEU:HD23	1.91	0.53
2:A:93:ARG:NH2	2:A:124:ASP:OD2	2.34	0.53
2:A:33:THR:HG22	2:A:80:ASN:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:189:SER:HB3	3:B:232:ILE:HG22	1.90	0.52
3:B:57:LYS:HE2	3:B:75:GLN:HG3	1.92	0.52
4:G:17:GLU:O	4:G:21:MET:HG3	2.09	0.52
1:R:317:VAL:HA	1:R:320:PHE:CE2	2.44	0.52
3:B:290:ASP:OD1	3:B:314:ARG:HD2	2.09	0.51
2:A:14:GLU:O	2:A:18:MET:HG2	2.11	0.51
2:A:129:TRP:HZ3	2:A:139:VAL:HB	1.74	0.51
2:A:11:ALA:O	2:A:14:GLU:HG3	2.11	0.50
2:A:106:ILE:HB	2:A:139:VAL:HG22	1.92	0.50
1:R:284:TRP:CD1	1:R:322:ASN:HD22	2.29	0.50
3:B:254:ASP:HB2	3:B:261:LEU:HD22	1.94	0.50
1:R:126:ILE:HA	1:R:129:THR:HG22	1.93	0.50
3:B:9:GLN:O	3:B:12:GLU:HG3	2.12	0.50
2:A:132:ARG:HB2	2:A:132:ARG:HH11	1.76	0.49
2:A:38:LEU:HD22	2:A:83:MET:HE3	1.95	0.49
3:B:10:GLU:O	3:B:13:GLN:HG3	2.12	0.49
3:B:146:LEU:HD11	3:B:159:THR:HB	1.95	0.48
3:B:14:LEU:O	3:B:17:GLN:HG3	2.13	0.48
3:B:149:CYS:HB2	3:B:157:ILE:HD11	1.95	0.48
2:A:194:ARG:O	2:A:198:VAL:HG23	2.14	0.48
3:B:150:ARG:HB2	3:B:192:LEU:HD23	1.95	0.48
1:R:308:HIS:O	1:R:312:THR:HG23	2.14	0.47
1:R:136:PHE:O	1:R:140:ILE:HG12	2.14	0.47
2:A:69:ILE:HD12	2:A:86:VAL:HG22	1.97	0.47
3:B:228:ASP:C	3:B:245:SER:HG	2.21	0.46
2:A:129:TRP:NE1	2:A:201:SER:O	2.49	0.46
1:R:253:THR:O	1:R:260:ARG:NH1	2.49	0.46
3:B:14:LEU:HD22	4:G:20:LYS:HD3	1.99	0.45
2:A:37:LEU:HD21	2:A:39:LEU:HD22	1.99	0.45
3:B:61:MET:HE1	3:B:63:TRP:CD1	2.50	0.45
4:G:20:LYS:HA	4:G:20:LYS:HD2	1.75	0.45
1:R:93:ASP:CG	1:R:323:SER:HB2	2.41	0.45
4:G:46:LYS:HG3	4:G:47:GLU:OE1	2.17	0.45
1:R:184:ILE:HD12	1:R:206:TYR:HE1	1.81	0.45
2:A:95:LYS:O	2:A:98:GLN:HG3	2.17	0.44
1:R:133:VAL:HG12	1:R:172:TRP:HA	1.98	0.44
2:A:14:GLU:HA	2:A:17:LYS:HG2	1.98	0.44
1:R:210:LYS:HB3	1:R:213:LEU:HB2	1.99	0.44
3:B:274:THR:OG1	3:B:315:VAL:O	2.24	0.44
3:B:15:LYS:O	3:B:18:ILE:HG22	2.17	0.44
3:B:283:ARG:NE	3:B:298:ASP:OD1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:165:THR:HG22	3:B:181:THR:HG22	2.00	0.44
3:B:290:ASP:HA	3:B:314:ARG:HG3	2.00	0.43
3:B:254:ASP:OD2	4:G:33:ALA:HB1	2.18	0.43
1:R:68:LEU:HD22	1:R:90:ALA:HB2	2.01	0.43
3:B:81:ILE:HB	3:B:91:HIS:HB2	2.00	0.43
4:G:38:MET:HA	4:G:41:CYS:SG	2.59	0.43
1:R:99:THR:HG21	1:R:127:ARG:HB2	2.00	0.43
1:R:280:PHE:HA	1:R:322:ASN:ND2	2.35	0.42
1:R:130:SER:HA	1:R:133:VAL:HG22	2.02	0.42
3:B:187:VAL:HA	3:B:203:ALA:HA	2.00	0.42
1:R:53:THR:HA	1:R:56:VAL:HG22	2.02	0.41
1:R:121:LYS:HB3	1:R:121:LYS:HE3	1.80	0.41
2:A:223:ASN:OD1	2:A:226:ARG:NH1	2.53	0.41
1:R:78:MET:SD	1:R:340:HIS:ND1	2.93	0.41
1:R:323:SER:HA	1:R:326:ASN:HD22	1.85	0.41
2:A:18:MET:HA	2:A:21:LYS:HG2	2.02	0.41
2:A:187:THR:HA	2:A:190:LYS:HG2	2.03	0.41
1:R:242:ARG:HH11	1:R:246:LYS:HD3	1.85	0.41
2:A:99:CYS:SG	3:B:101:MET:HE3	2.60	0.41
1:R:207:PRO:HG2	1:R:210:LYS:HG2	2.01	0.41
3:B:11:ALA:O	3:B:14:LEU:HG	2.20	0.41
3:B:233:CYS:SG	3:B:276:VAL:HG12	2.61	0.41
3:B:314:ARG:C	3:B:331:SER:HG	2.27	0.41
1:R:259:ALA:O	1:R:263:ILE:HG12	2.20	0.41
3:B:61:MET:HE3	3:B:328:ALA:HB3	2.03	0.41
3:B:283:ARG:HA	3:B:283:ARG:HD2	1.91	0.41
3:B:52:ARG:HG2	3:B:335:PHE:CE1	2.57	0.40
1:R:173:ILE:O	1:R:177:ILE:HG12	2.22	0.40
3:B:261:LEU:HD12	3:B:261:LEU:HA	1.80	0.40
1:R:178:PHE:O	1:R:181:PRO:HD2	2.22	0.40
3:B:180:PHE:CE1	3:B:216:GLY:HA2	2.56	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	261/612 (43%)	247 (95%)	12 (5%)	2 (1%)	16	38
2	A	201/246 (82%)	200 (100%)	1 (0%)	0	100	100
3	B	336/345 (97%)	323 (96%)	13 (4%)	0	100	100
4	G	54/70 (77%)	53 (98%)	1 (2%)	0	100	100
All	All	852/1273 (67%)	823 (97%)	27 (3%)	2 (0%)	45	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	156	GLN
1	R	158	SER

### 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	243/531 (46%)	241 (99%)	2 (1%)	79	87
2	A	169/213 (79%)	166 (98%)	3 (2%)	54	75
3	B	281/287 (98%)	279 (99%)	2 (1%)	81	89
4	G	45/57 (79%)	45 (100%)	0	100	100
All	All	738/1088 (68%)	731 (99%)	7 (1%)	74	85

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

Mol	Chain	Res	Type
1	R	63	LEU
1	R	176	MET
2	A	48	THR
2	A	72	THR
2	A	166	GLU
3	B	146	LEU

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Mol	Chain	Res	Type
3	B	228	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	258	HIS
1	R	322	ASN
2	A	119	GLN
3	B	156	GLN
3	B	220	GLN
3	B	237	ASN
3	B	239	ASN
3	B	293	ASN
3	B	340	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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.

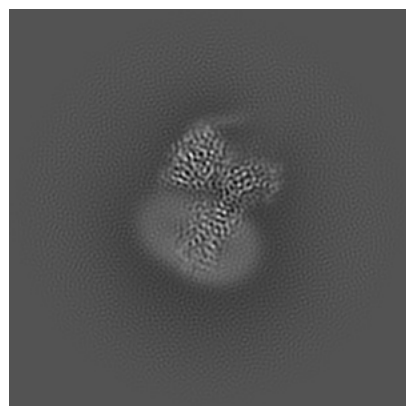
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63455. These allow visual inspection of the internal detail of the map and identification of artifacts.

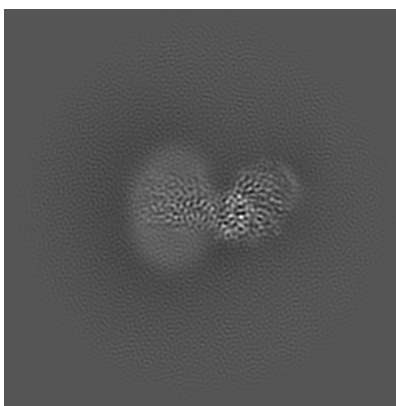
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

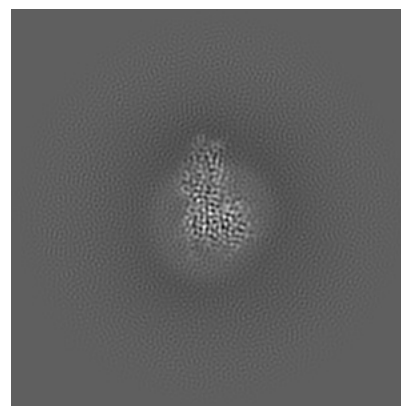
#### 6.1.1 Primary map



X

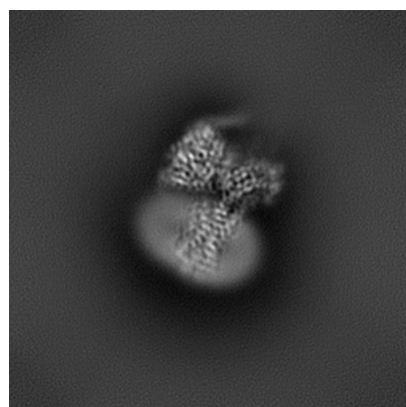


Y

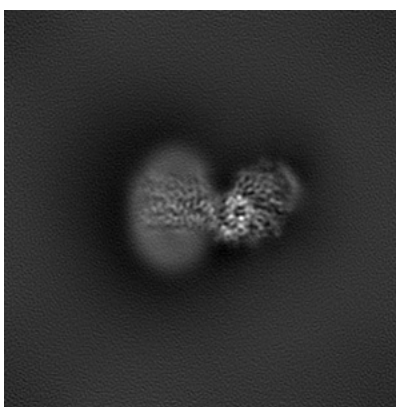


Z

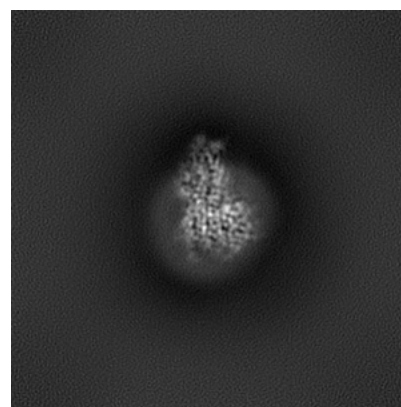
#### 6.1.2 Raw map



X



Y

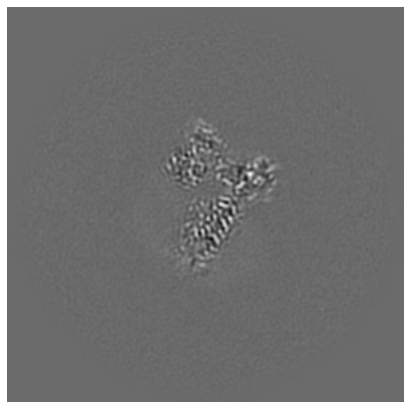


Z

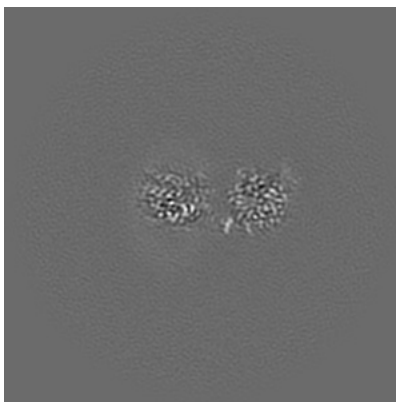
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

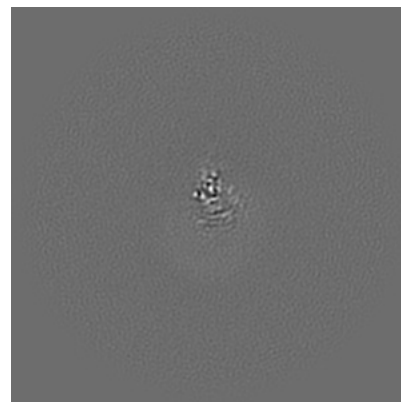
### 6.2.1 Primary map



X Index: 128

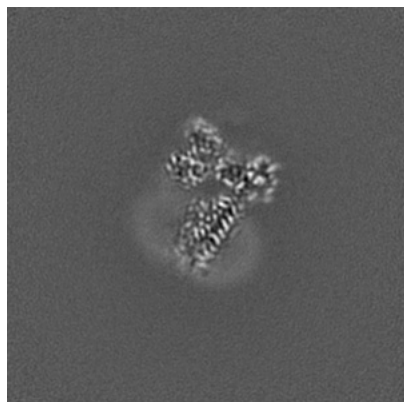


Y Index: 128

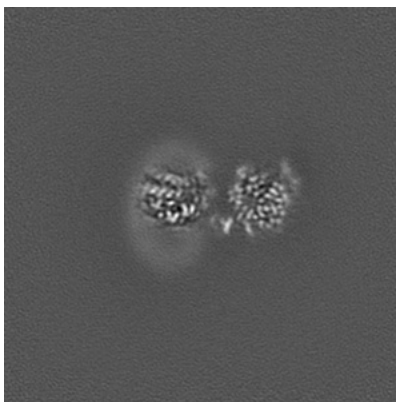


Z Index: 128

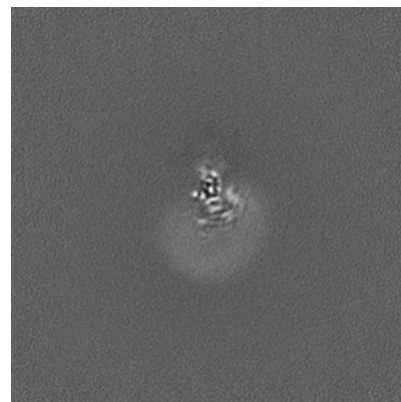
### 6.2.2 Raw map



X Index: 128



Y Index: 128

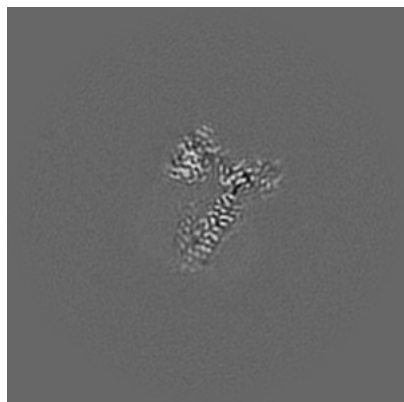


Z Index: 128

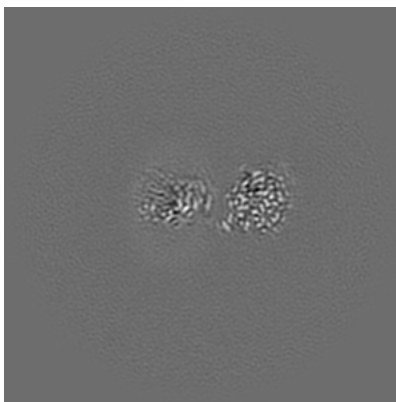
The images above show central slices of the map in three orthogonal directions.

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

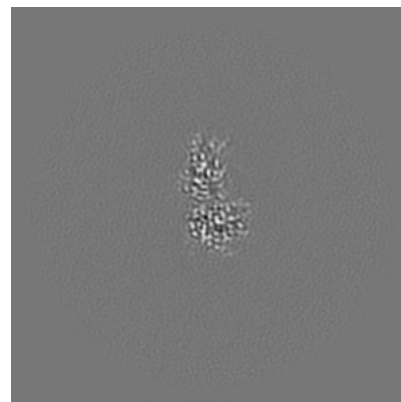
### 6.3.1 Primary map



X Index: 123

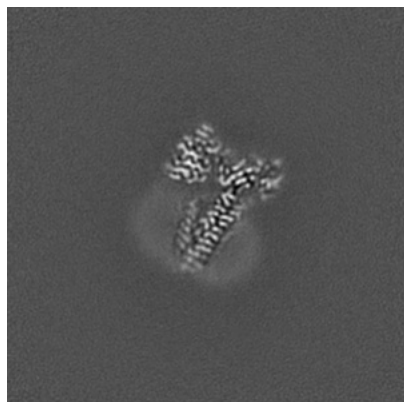


Y Index: 124

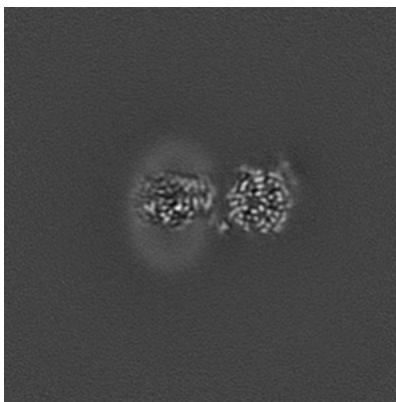


Z Index: 151

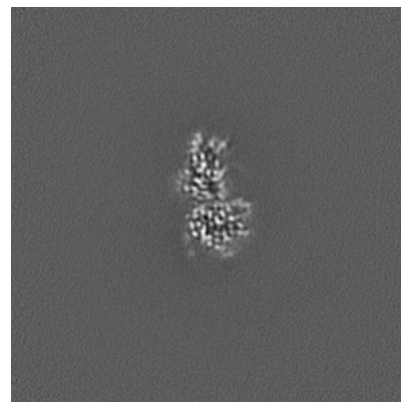
### 6.3.2 Raw map



X Index: 123



Y Index: 125

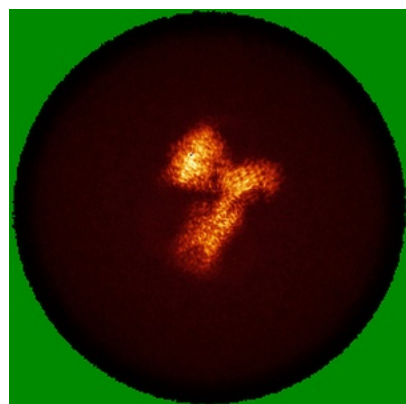


Z Index: 151

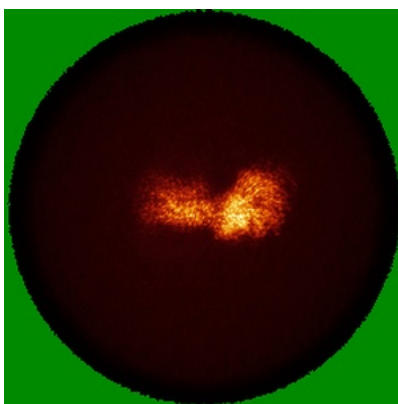
The images above show the largest variance slices of the map in three orthogonal directions.

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

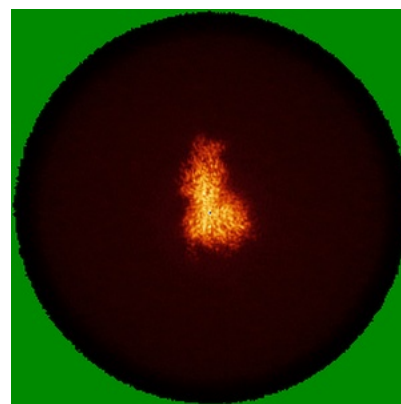
### 6.4.1 Primary map



X

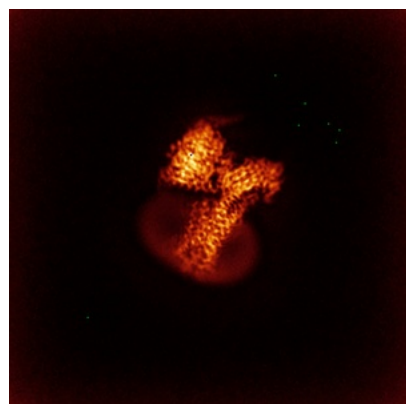


Y

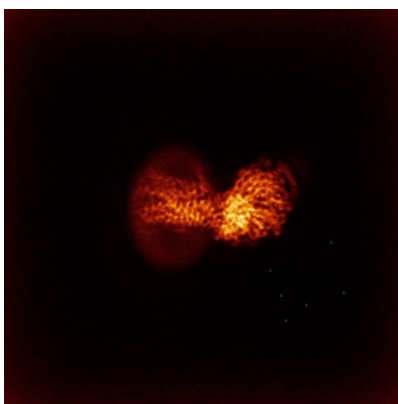


Z

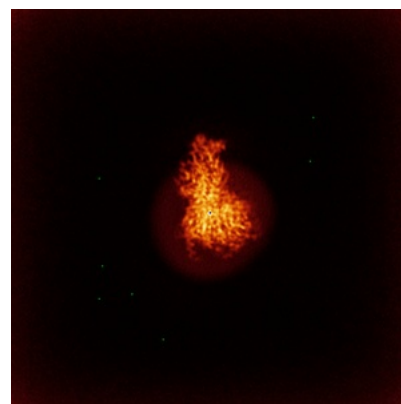
### 6.4.2 Raw map



X



Y

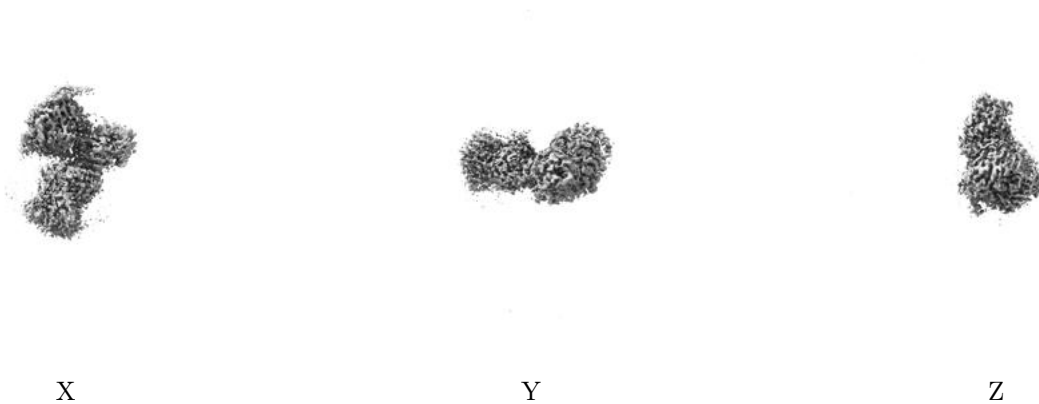


Z

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.

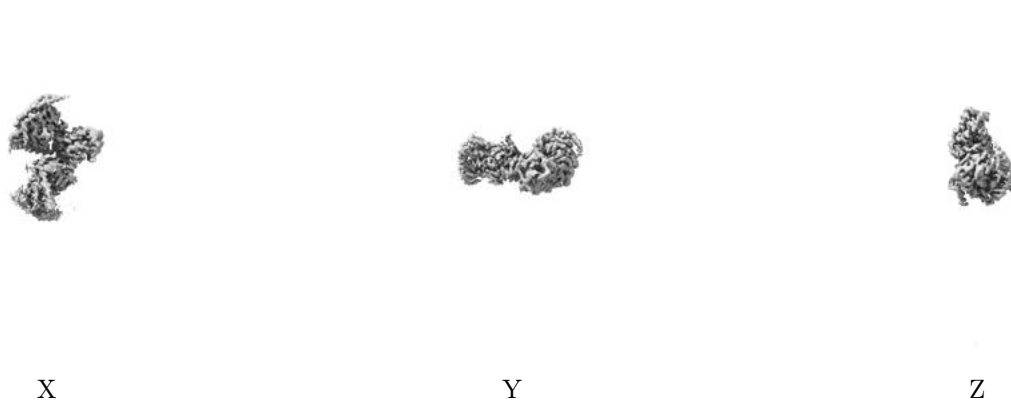
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.265. 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.

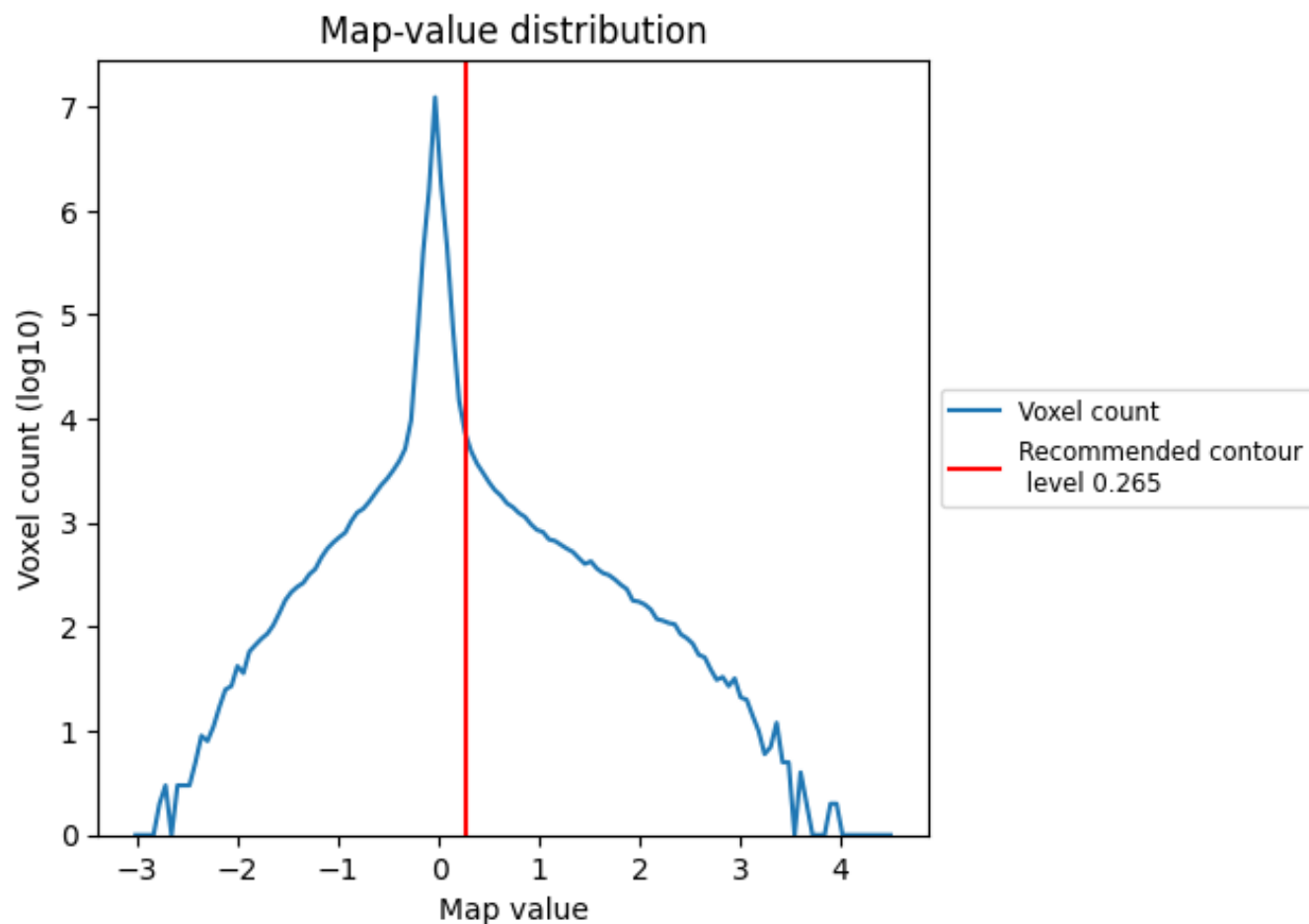
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

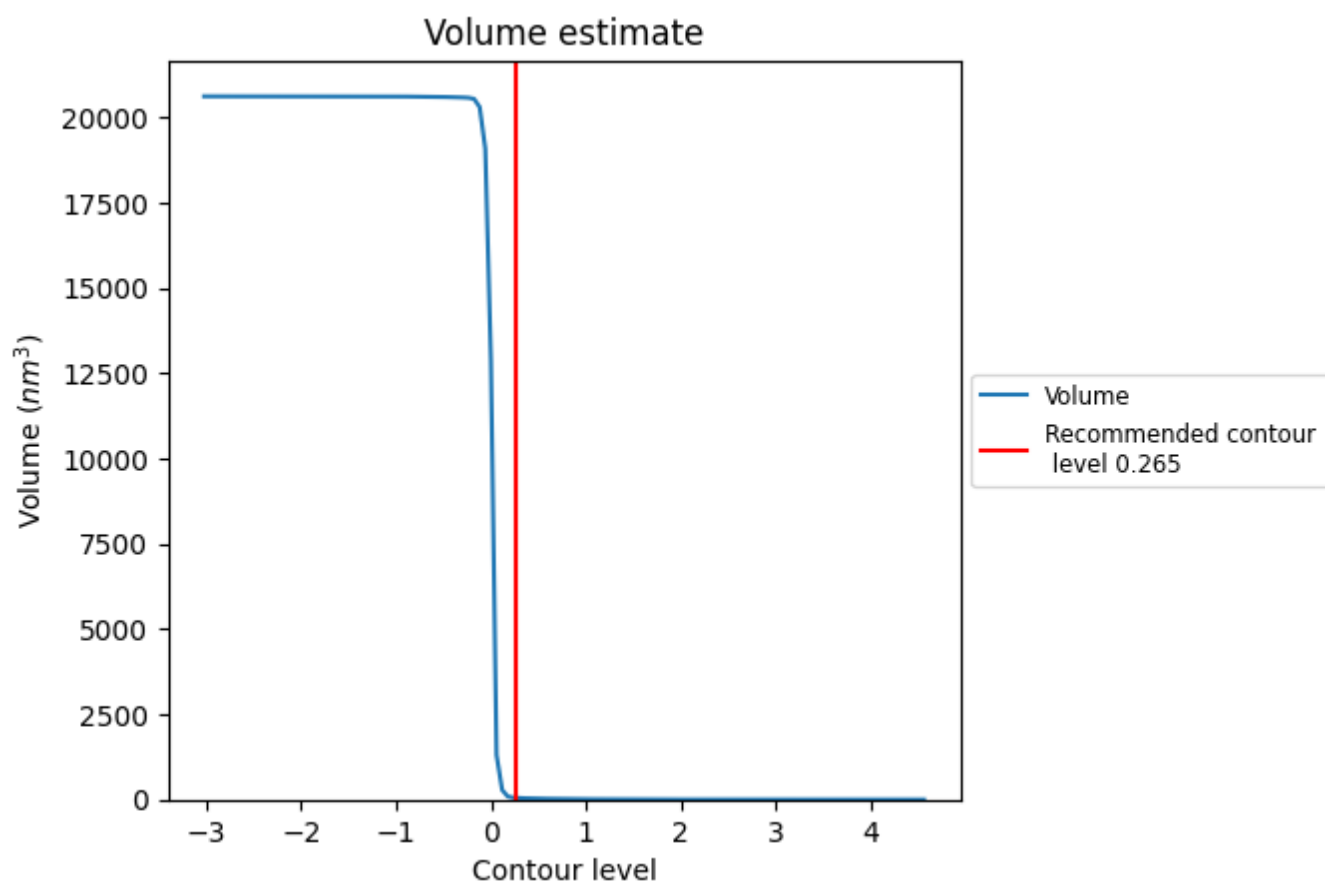
This section contains the results of statistical analysis of the map.

### 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.

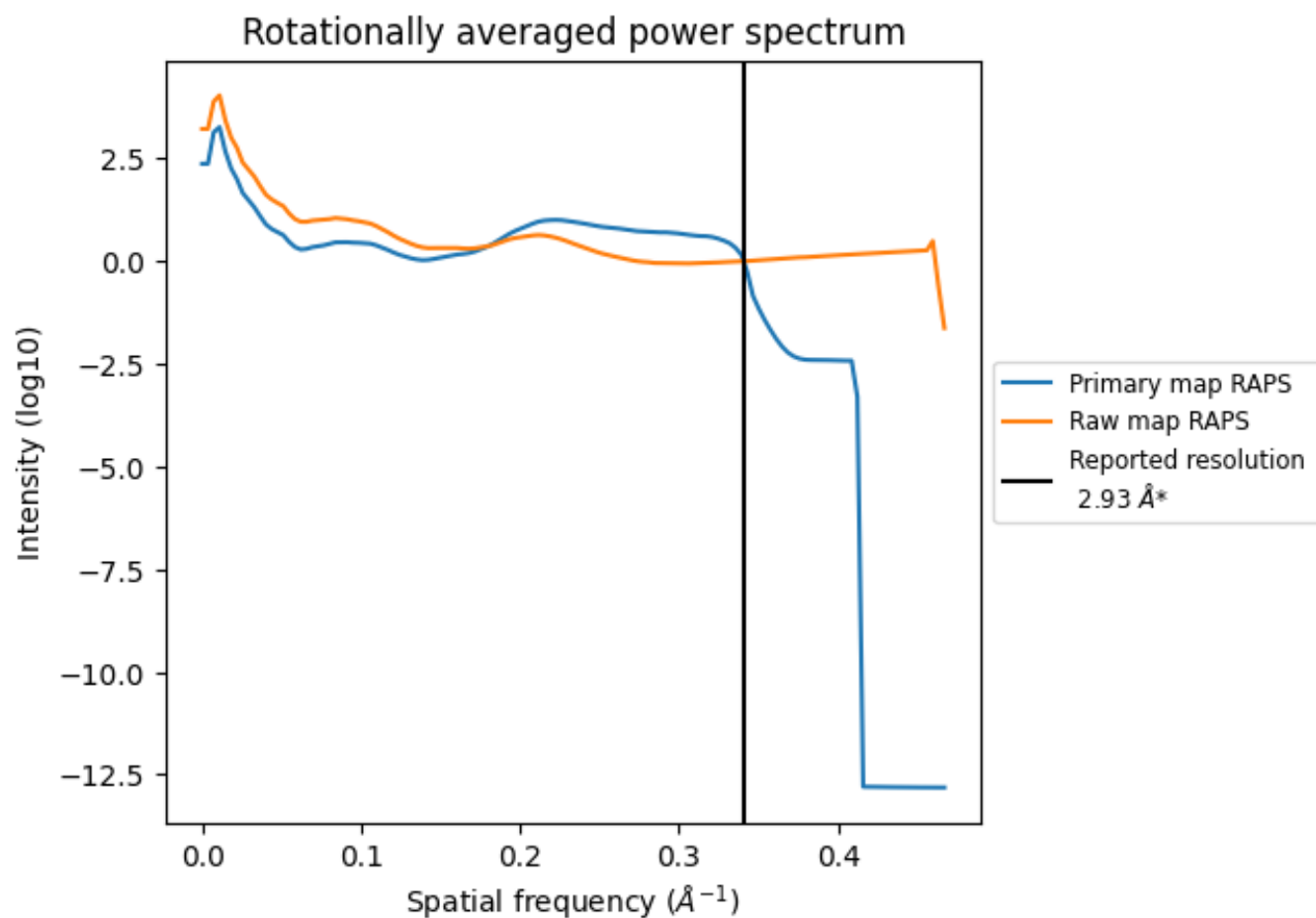
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 51 nm<sup>3</sup>; this corresponds to an approximate mass of 46 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 ⓘ

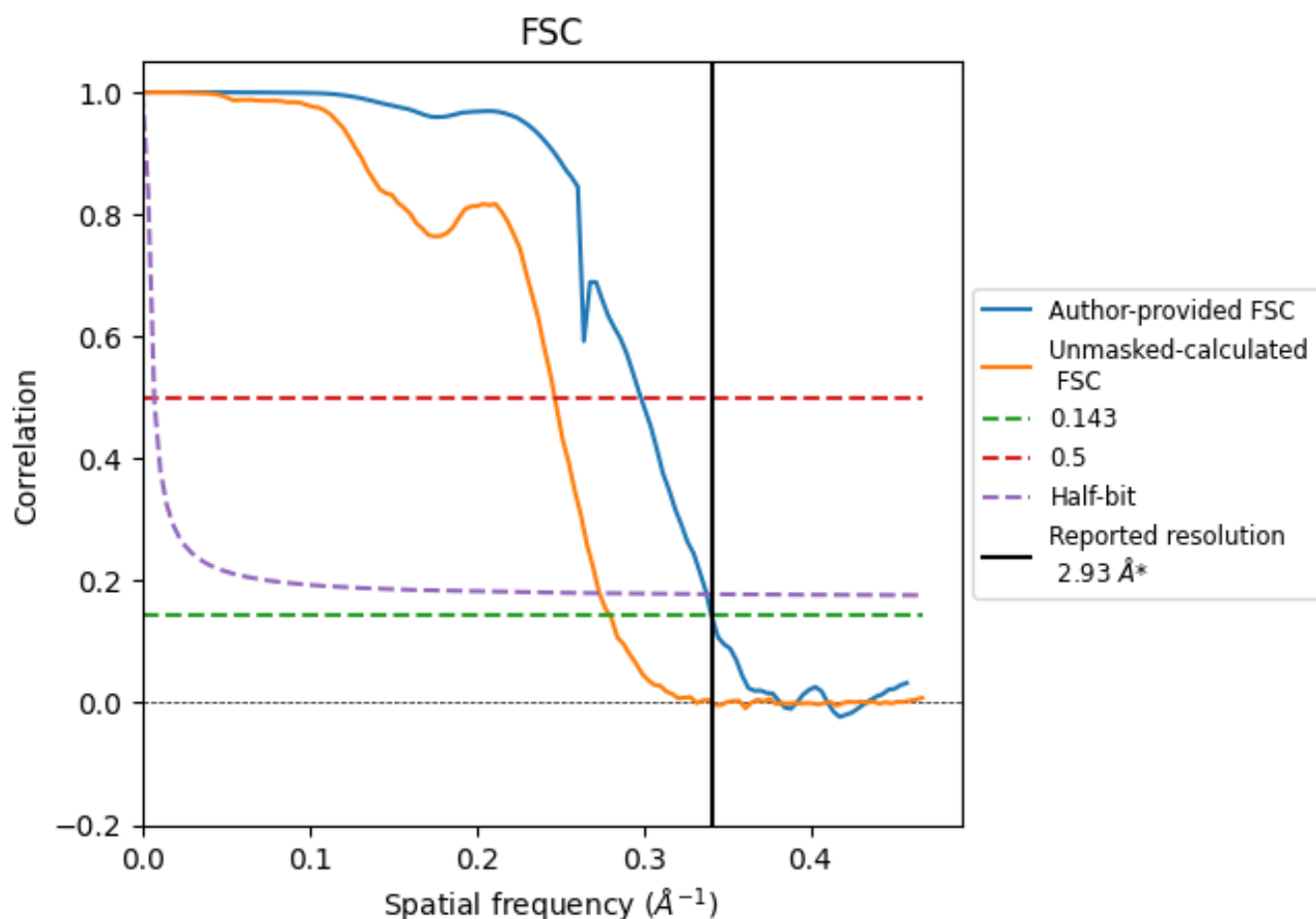


\*Reported resolution corresponds to spatial frequency of 0.341 Å<sup>-1</sup>

## 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 0.341  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

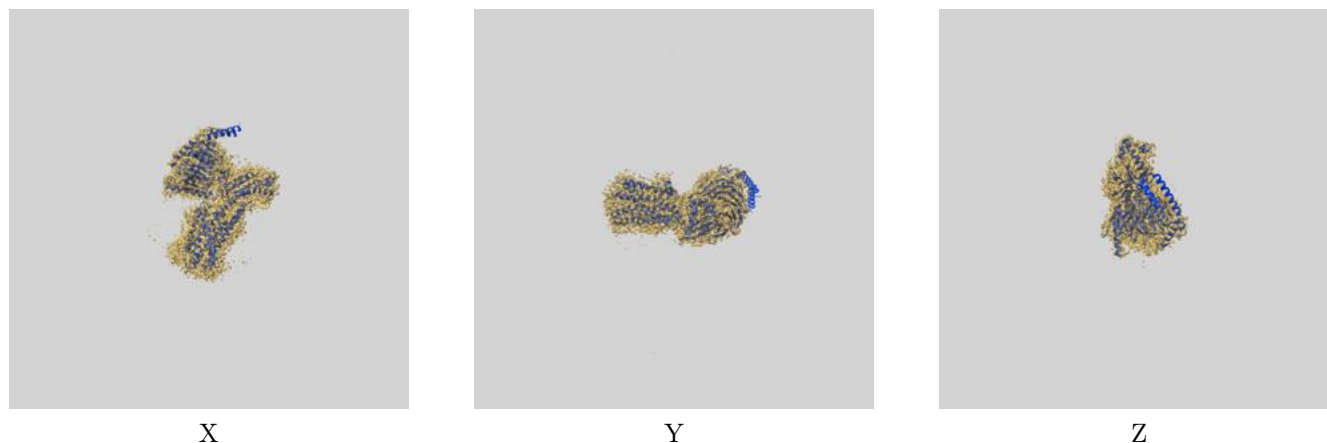
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	2.93	3.35	2.96
Unmasked-calculated*	3.57	4.05	3.65

\*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 3.57 differs from the reported value 2.93 by more than 10 %

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

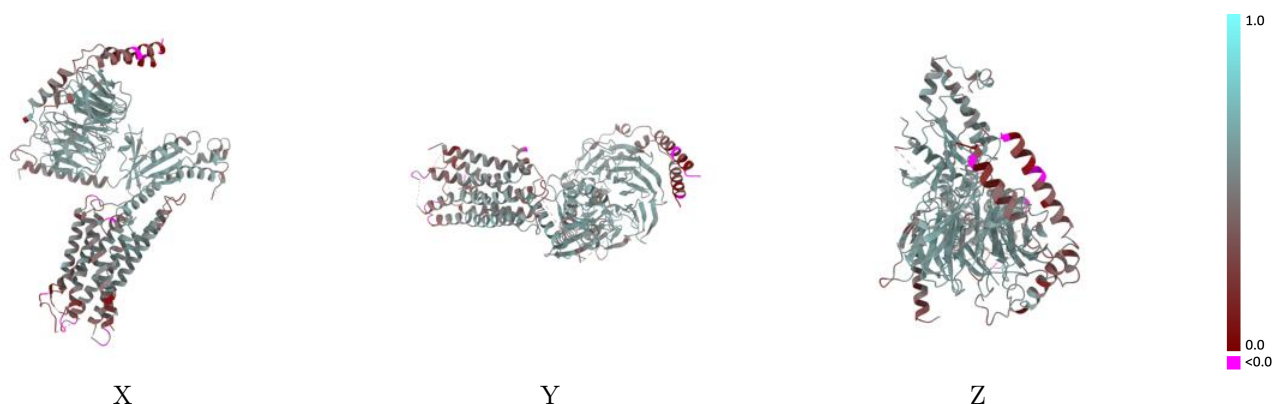
This section contains information regarding the fit between EMDB map EMD-63455 and PDB model 9LWP. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

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



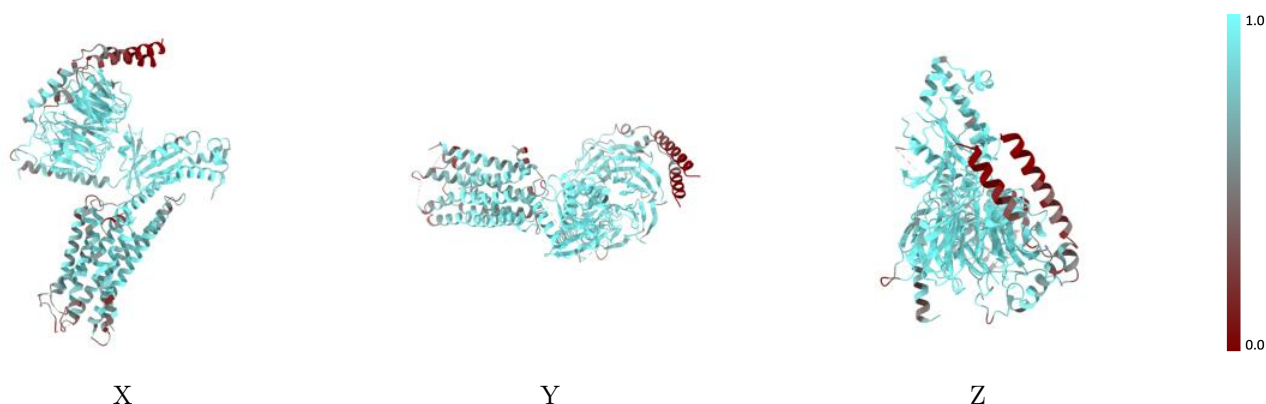
The images above show the 3D surface view of the map at the recommended contour level 0.265 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



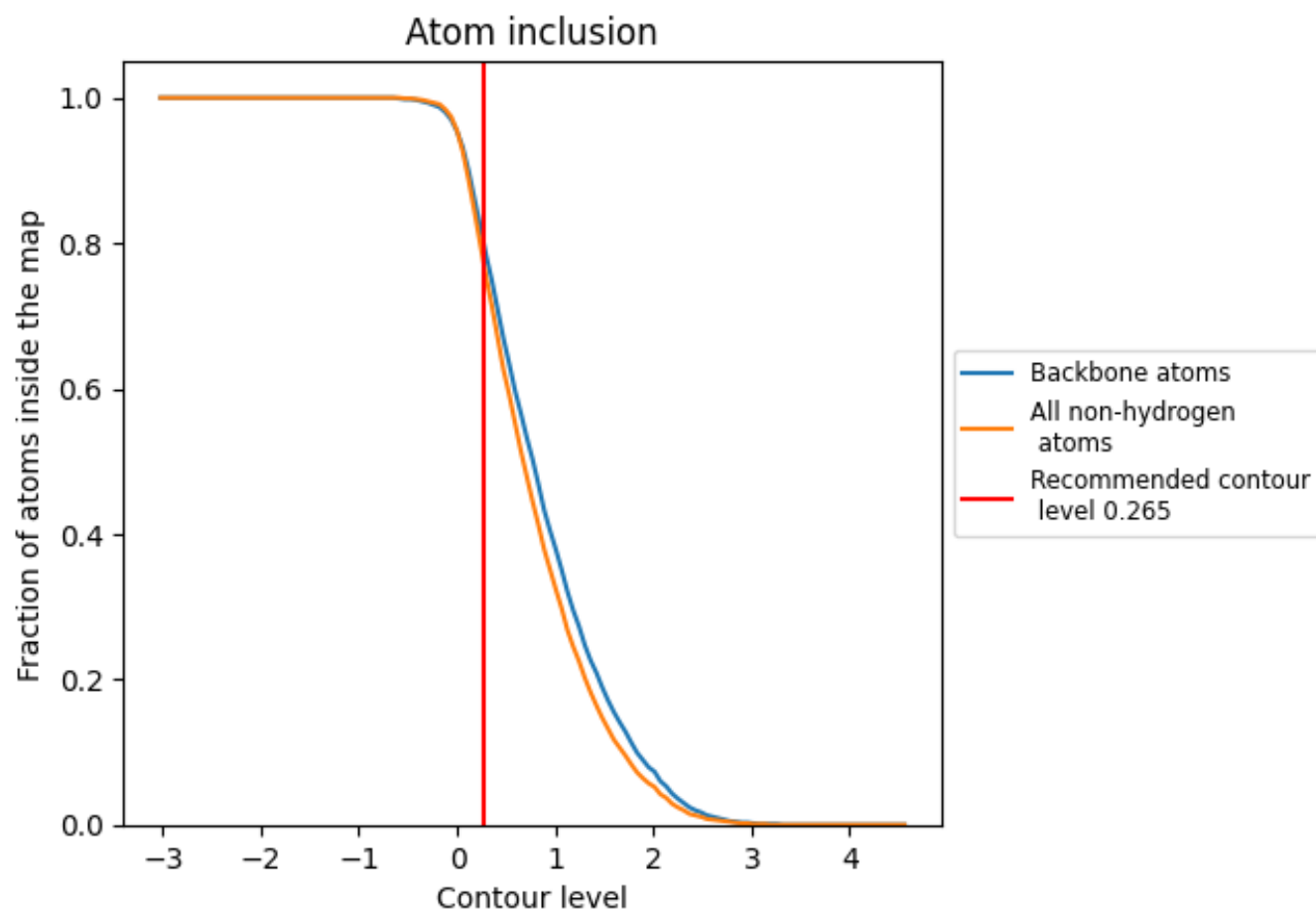
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.265).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 78% 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 (0.265) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7780	<div></div> 0.4850
A	<div></div> 0.8820	<div></div> 0.5380
B	<div></div> 0.8180	<div></div> 0.5290
G	<div></div> 0.4830	<div></div> 0.3520
R	<div></div> 0.7100	<div></div> 0.4190

