



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 11:01 AM UTC

PDB ID : 8KGK / pdb_00008kgk
EMDB ID : EMD-37224
Title : Cryo-EM structure of the GPR61-Gs complex
Authors : Nie, Y.; Qiu, Z.; Zheng, S.
Deposited on : 2023-08-19
Resolution : 3.16 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

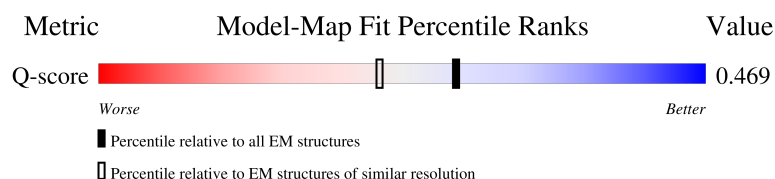
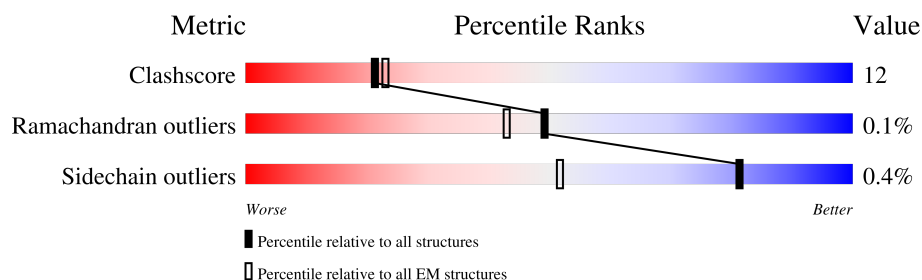
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.16 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	14474 (2.66 - 3.66)

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	390	
2	B	249	
3	C	357	
4	D	71	

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Mol	Chain	Length	Quality of chain
5	E	160	 A horizontal bar chart showing the quality of chain E. The bar is divided into three segments: a green segment representing 64%, a yellow segment representing 15%, and a grey segment representing 21%. A small red dot is visible at the beginning of the green segment.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7476 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 G-protein coupled receptor 61.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	256	Total	C	N	O	S	0	0
			1888	1248	307	317	16		

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP Q9BZJ8
A	-7	TYR	-	expression tag	UNP Q9BZJ8
A	-6	LYS	-	expression tag	UNP Q9BZJ8
A	-5	ASP	-	expression tag	UNP Q9BZJ8
A	-4	ASP	-	expression tag	UNP Q9BZJ8
A	-3	ASP	-	expression tag	UNP Q9BZJ8
A	-2	ASP	-	expression tag	UNP Q9BZJ8
A	-1	LYS	-	expression tag	UNP Q9BZJ8
A	0	ALA	-	expression tag	UNP Q9BZJ8
A	366	LEU	-	expression tag	UNP Q9BZJ8
A	367	GLU	-	expression tag	UNP Q9BZJ8
A	368	VAL	-	expression tag	UNP Q9BZJ8
A	369	LEU	-	expression tag	UNP Q9BZJ8
A	370	PHE	-	expression tag	UNP Q9BZJ8
A	371	GLN	-	expression tag	UNP Q9BZJ8
A	372	GLY	-	expression tag	UNP Q9BZJ8
A	373	PRO	-	expression tag	UNP Q9BZJ8
A	374	LEU	-	expression tag	UNP Q9BZJ8
A	375	GLU	-	expression tag	UNP Q9BZJ8
A	376	VAL	-	expression tag	UNP Q9BZJ8
A	377	LEU	-	expression tag	UNP Q9BZJ8
A	378	PHE	-	expression tag	UNP Q9BZJ8
A	379	GLN	-	expression tag	UNP Q9BZJ8
A	380	GLY	-	expression tag	UNP Q9BZJ8
A	381	PRO	-	expression tag	UNP Q9BZJ8

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	229	Total	C	N	O	S	0	0
			1804	1144	325	328	7		

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	13	ARG	GLY	engineered mutation	UNP P38405
B	14	ASN	VAL	engineered mutation	UNP P38405
B	15	GLU	ASP	engineered mutation	UNP P38405
B	18	ALA	GLU	engineered mutation	UNP P38405
B	19	GLN	ARG	engineered mutation	UNP P38405
B	33	ASP	GLU	engineered mutation	UNP P38405
B	34	LYS	ARG	engineered mutation	UNP P38405
B	35	GLN	LEU	engineered mutation	UNP P38405
B	36	VAL	ALA	engineered mutation	UNP P38405
B	38	ARG	LYS	engineered mutation	UNP P38405
B	49	ASP	GLY	engineered mutation	UNP P38405
B	50	ASN	GLU	engineered mutation	UNP P38405
B	196	GLY	-	linker	UNP P38405
B	197	GLY	-	linker	UNP P38405
B	198	SER	-	linker	UNP P38405
B	199	GLY	-	linker	UNP P38405
B	200	GLY	-	linker	UNP P38405
B	201	SER	-	linker	UNP P38405
B	202	GLY	-	linker	UNP P38405
B	203	GLY	-	linker	UNP P38405
B	249	ASP	ALA	engineered mutation	UNP P63092
B	252	ASP	SER	engineered mutation	UNP P63092
B	?	-	ASN	deletion	UNP P63092
B	?	-	MET	deletion	UNP P63092
B	?	-	VAL	deletion	UNP P63092
B	?	-	ILE	deletion	UNP P63092
B	?	-	ARG	deletion	UNP P63092
B	?	-	GLU	deletion	UNP P63092
B	?	-	ASP	deletion	UNP P63092
B	?	-	ASN	deletion	UNP P63092
B	?	-	GLN	deletion	UNP P63092
B	?	-	THR	deletion	UNP P63092
B	362	ALA	ILE	engineered mutation	UNP P63092
B	365	ILE	VAL	engineered mutation	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	C	339	Total	C	N	O	S	1	0
			2503	1549	441	491	22		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	HIS	-	expression tag	UNP P62873
C	-15	HIS	-	expression tag	UNP P62873
C	-14	HIS	-	expression tag	UNP P62873
C	-13	HIS	-	expression tag	UNP P62873
C	-12	HIS	-	expression tag	UNP P62873
C	-11	HIS	-	expression tag	UNP P62873
C	-10	LEU	-	expression tag	UNP P62873
C	-9	GLU	-	expression tag	UNP P62873
C	-8	VAL	-	expression tag	UNP P62873
C	-7	LEU	-	expression tag	UNP P62873
C	-6	PHE	-	expression tag	UNP P62873
C	-5	GLN	-	expression tag	UNP P62873
C	-4	GLY	-	expression tag	UNP P62873
C	-3	PRO	-	expression tag	UNP P62873
C	-2	GLY	-	expression tag	UNP P62873
C	-1	SER	-	expression tag	UNP P62873
C	0	SER	-	expression tag	UNP P62873
C	1	GLY	-	expression tag	UNP P62873

- 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	D	56	Total	C	N	O	S	0	0
			353	220	62	69	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	68	SER	CYS	engineered mutation	UNP P59768

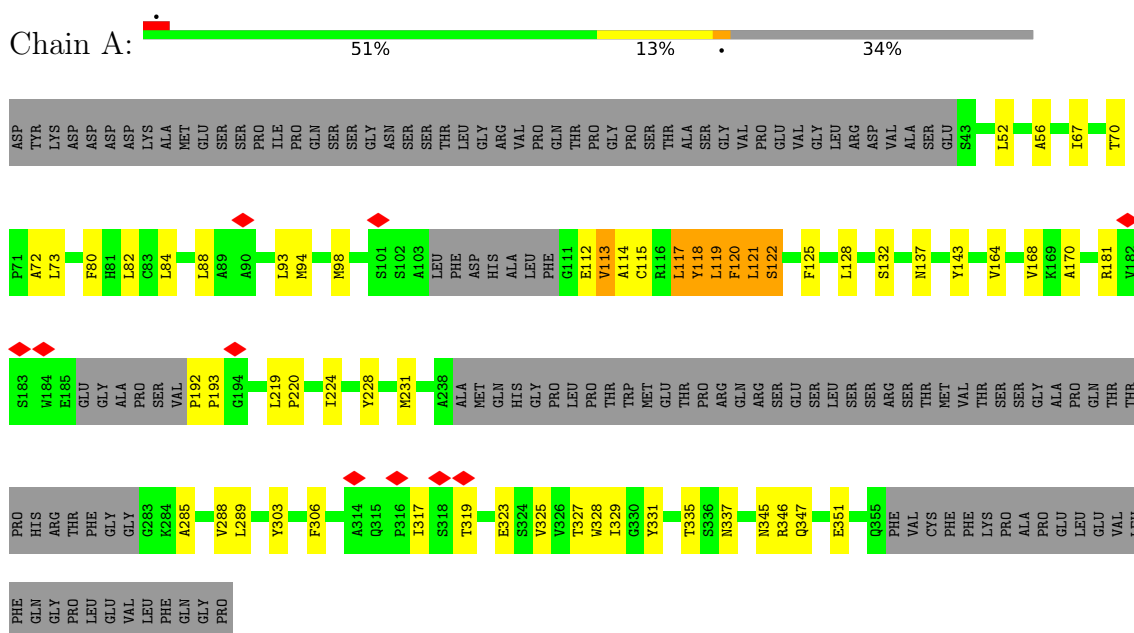
- Molecule 5 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	126	Total	C	N	O	S	0	0
			928	577	163	182	6		

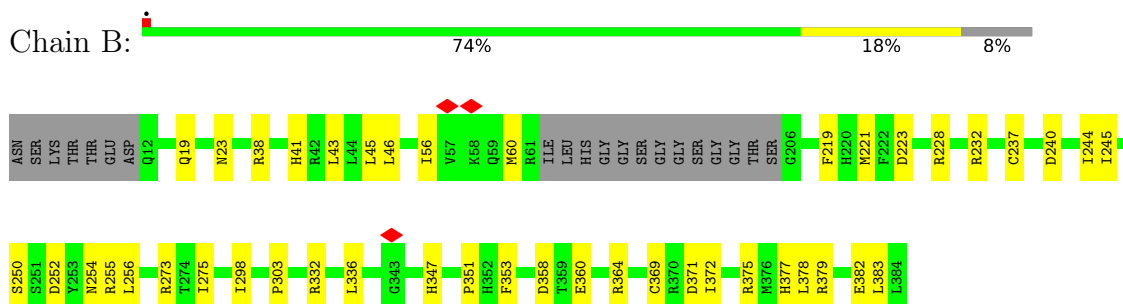
3 Residue-property plots

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: G-protein coupled receptor 61

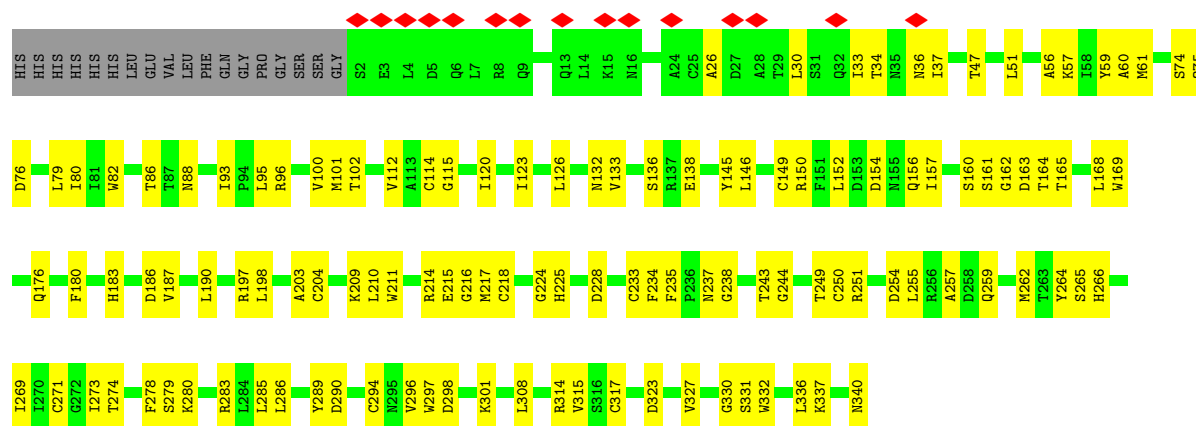


• Molecule 2: Guanine nucleotide-binding protein G(olf) subunit alpha, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

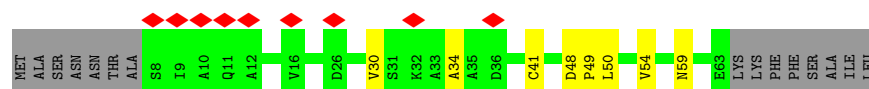


• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1

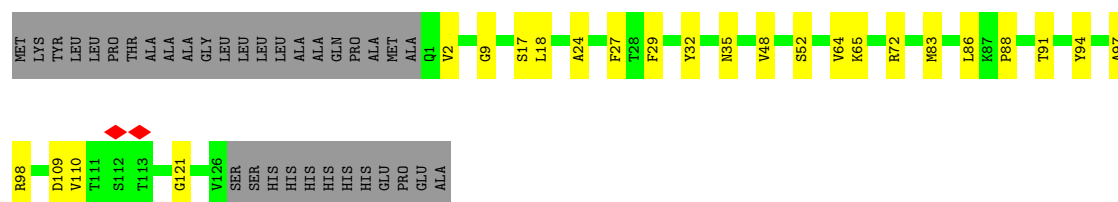




- Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 5: Nanobody 35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	192672	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)	870	Depositor
Maximum defocus (nm)	2480	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.134	Depositor
Minimum map value	-2.097	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	194.40001, 194.40001, 194.40001	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	A	0.76	10/1932 (0.5%)	0.66	9/2641 (0.3%)
2	B	0.11	0/1841	0.27	0/2492
3	C	0.13	0/2550	0.33	0/3472
4	D	0.09	0/359	0.26	0/497
5	E	0.12	0/947	0.36	0/1287
All	All	0.40	10/7629 (0.1%)	0.43	9/10389 (0.1%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	115	CYS	N-CA	-11.67	1.32	1.46
1	A	117	LEU	C-O	-9.59	1.12	1.24
1	A	114	ALA	C-O	-9.06	1.13	1.24
1	A	112	GLU	C-O	-8.73	1.14	1.24
1	A	113	VAL	C-O	-6.39	1.16	1.24
1	A	118	TYR	C-O	-5.94	1.17	1.24
1	A	115	CYS	CA-CB	-5.21	1.45	1.53
1	A	120	PHE	C-O	-5.17	1.18	1.24
1	A	122	SER	CA-C	-5.13	1.46	1.52
1	A	112	GLU	CA-C	-5.02	1.46	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	115	CYS	O-C-N	-7.53	114.14	122.12
1	A	112	GLU	N-CA-C	-7.37	103.25	111.28
1	A	115	CYS	N-CA-CB	6.98	120.38	110.12
1	A	192	PRO	CA-C-N	-6.42	111.81	119.84
1	A	192	PRO	C-N-CA	-6.42	111.81	119.84
1	A	121	LEU	N-CA-C	-6.15	104.69	111.82
1	A	114	ALA	CA-C-N	6.04	128.37	120.28
1	A	114	ALA	C-N-CA	6.04	128.37	120.28
1	A	115	CYS	N-CA-C	-5.96	104.79	111.28

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	A	1888	0	1860	35	0
2	B	1804	0	1691	38	0
3	C	2503	0	2315	95	0
4	D	353	0	278	8	0
5	E	928	0	871	18	0
All	All	7476	0	7015	171	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 12.

All (171) 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:C:283:ARG:NH1	3:C:298:ASP:OD1	2.15	0.80
3:C:271:CYS:HB3	3:C:290:ASP:HB2	1.68	0.76
2:B:250:SER:HA	2:B:256:LEU:HD21	1.68	0.75
1:A:117:LEU:HG	1:A:121:LEU:HD23	1.69	0.75
3:C:79:LEU:HG	3:C:95:LEU:HD11	1.68	0.74
2:B:43:LEU:HB2	2:B:221:MET:HB3	1.70	0.73
5:E:29:PHE:O	5:E:72:ARG:NH2	2.24	0.70
3:C:160:SER:HB2	3:C:190:LEU:HD23	1.72	0.70
3:C:51:LEU:HB2	3:C:336:LEU:HB2	1.74	0.70
3:C:79:LEU:HD11	3:C:114:CYS:HB3	1.76	0.68
3:C:30:LEU:HD13	4:D:34:ALA:HB1	1.75	0.67
5:E:52:SER:O	5:E:72:ARG:NH1	2.28	0.67
3:C:56:ALA:HB1	3:C:75:GLN:HE21	1.59	0.67
2:B:228:ARG:NH1	3:C:186:ASP:OD1	2.28	0.66
1:A:52:LEU:HD11	1:A:328:TRP:HZ3	1.59	0.66
3:C:26:ALA:HB2	3:C:259:GLN:HE22	1.61	0.65
3:C:59:TYR:HE2	3:C:75:GLN:HB3	1.62	0.65
3:C:234:PHE:HE1	3:C:238:GLY:HA2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:57:LYS:NZ	3:C:75:GLN:OE1	2.31	0.64
3:C:112:VAL:HG13	3:C:126:LEU:HD11	1.78	0.64
3:C:198:LEU:HB3	3:C:210:LEU:HD11	1.79	0.63
2:B:336:LEU:HD11	2:B:351:PRO:HG3	1.80	0.63
3:C:264:TYR:HE2	3:C:285:LEU:HD13	1.62	0.63
5:E:94:TYR:O	5:E:121:GLY:HA2	2.00	0.62
3:C:210:LEU:HD22	3:C:255:LEU:HD12	1.83	0.61
3:C:198:LEU:HD13	3:C:210:LEU:HD21	1.83	0.60
3:C:152:LEU:HD12	3:C:156:GLN:HG2	1.84	0.60
3:C:115:GLY:HA3	3:C:146:LEU:HD22	1.83	0.59
1:A:231:MET:SD	2:B:383:LEU:HD22	2.42	0.59
3:C:86:THR:OG1	3:C:88:ASN:OD1	2.12	0.59
3:C:74:SER:OG	3:C:76:ASP:OD1	2.20	0.59
3:C:274:THR:HG22	3:C:314:ARG:HH21	1.66	0.58
3:C:30:LEU:HD12	3:C:33:ILE:HB	1.84	0.58
3:C:279:SER:OG	4:D:48:ASP:OD1	2.20	0.58
1:A:325:VAL:O	1:A:329:ILE:HD12	2.04	0.57
3:C:225:HIS:HE2	3:C:243:THR:HG1	1.52	0.57
2:B:369:CYS:HA	2:B:372:ILE:HD12	1.85	0.57
5:E:9:GLY:HA2	5:E:18:LEU:HD23	1.87	0.57
1:A:164:VAL:O	1:A:168:VAL:HG23	2.04	0.57
1:A:82:LEU:HD21	1:A:337:ASN:HB3	1.86	0.57
3:C:257:ALA:HB1	4:D:30:VAL:HG12	1.86	0.57
5:E:2:VAL:HG21	5:E:98:ARG:HH21	1.70	0.56
5:E:29:PHE:HE2	5:E:72:ARG:HG3	1.71	0.56
1:A:70:THR:HG22	1:A:72:ALA:H	1.69	0.56
1:A:303:TYR:HE2	1:A:327:THR:HG23	1.69	0.56
3:C:266:HIS:HB3	3:C:269:ILE:HG12	1.88	0.56
3:C:57:LYS:HB2	3:C:332:TRP:HA	1.88	0.56
3:C:283:ARG:HD3	4:D:41:CYS:SG	2.46	0.56
5:E:17:SER:HA	5:E:83:MET:O	2.06	0.56
1:A:317:ILE:HG22	1:A:319:THR:HG23	1.87	0.55
1:A:120:PHE:HD2	1:A:121:LEU:HD22	1.71	0.55
2:B:303:PRO:HG2	5:E:65:LYS:HD2	1.89	0.55
3:C:80:ILE:HG22	3:C:82:TRP:CD1	2.41	0.55
3:C:274:THR:HG21	3:C:314:ARG:HE	1.72	0.55
1:A:346:ARG:NH2	2:B:382:GLU:OE2	2.41	0.54
5:E:94:TYR:O	5:E:121:GLY:CA	2.56	0.54
1:A:93:LEU:HD11	1:A:122:SER:HA	1.89	0.54
3:C:233[A]:CYS:SG	3:C:234:PHE:N	2.79	0.54
3:C:259:GLN:HE21	4:D:30:VAL:HG11	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:HD11	1:A:328:TRP:CZ3	2.43	0.53
2:B:244:ILE:HG13	2:B:275:ILE:HG21	1.90	0.53
1:A:67:ILE:HG21	1:A:80:PHE:HB2	1.90	0.52
3:C:168:LEU:HB2	3:C:180:PHE:HE1	1.75	0.52
3:C:225:HIS:HE2	3:C:251:ARG:HB2	1.74	0.52
3:C:34:THR:O	3:C:301:LYS:NZ	2.43	0.52
5:E:48:VAL:HG13	5:E:64:VAL:HG21	1.92	0.52
3:C:100:VAL:HG21	3:C:114:CYS:HB2	1.91	0.52
2:B:240:ASP:OD2	3:C:75:GLN:NE2	2.42	0.51
3:C:273:ILE:HG12	3:C:289:TYR:CE1	2.45	0.51
3:C:157:ILE:HG22	3:C:169:TRP:HB2	1.92	0.51
3:C:96:ARG:NH1	3:C:138:GLU:OE2	2.44	0.51
2:B:240:ASP:CG	3:C:75:GLN:HE22	2.18	0.51
3:C:249:THR:HG22	3:C:265:SER:HB3	1.93	0.51
1:A:143:TYR:O	2:B:377:HIS:ND1	2.43	0.50
3:C:30:LEU:HD23	3:C:262:MET:HE1	1.92	0.50
3:C:132:ASN:OD1	3:C:133:VAL:N	2.44	0.50
3:C:183:HIS:CE1	3:C:209:LYS:HG3	2.47	0.50
3:C:161:SER:OG	3:C:163:ASP:OD1	2.25	0.50
3:C:286:LEU:HG	3:C:296:VAL:HG22	1.94	0.50
3:C:36:ASN:OD1	3:C:37:ILE:N	2.45	0.49
3:C:145:TYR:O	3:C:162:GLY:N	2.44	0.49
2:B:232:ARG:HH21	3:C:204:CYS:HB3	1.76	0.49
3:C:279:SER:HB2	4:D:50:LEU:HD22	1.95	0.49
2:B:43:LEU:HD13	2:B:245:ILE:HD11	1.95	0.49
2:B:252:ASP:O	2:B:256:LEU:HG	2.13	0.49
2:B:19:GLN:NE2	3:C:86:THR:OG1	2.46	0.48
2:B:232:ARG:NE	3:C:228:ASP:OD2	2.45	0.48
3:C:47:THR:HG21	3:C:337:LYS:HE2	1.94	0.48
3:C:197:ARG:HD3	3:C:214:ARG:HE	1.79	0.48
3:C:93:ILE:HG12	3:C:133:VAL:HG21	1.95	0.47
2:B:19:GLN:NE2	3:C:88:ASN:OD1	2.44	0.47
5:E:24:ALA:HB1	5:E:27:PHE:CZ	2.48	0.47
1:A:84:LEU:O	1:A:88:LEU:HD13	2.15	0.47
1:A:327:THR:HG22	1:A:331:TYR:CE2	2.50	0.47
2:B:23:ASN:HD22	3:C:88:ASN:HD22	1.63	0.47
3:C:180:PHE:CE2	3:C:216:GLY:HA2	2.50	0.47
1:A:94:MET:O	1:A:98:MET:HG2	2.14	0.47
3:C:235:PHE:HD1	3:C:237:ASN:H	1.62	0.47
3:C:61:MET:HG3	3:C:317:CYS:HB3	1.98	0.46
3:C:280:LYS:HD2	3:C:323:ASP:C	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:ARG:O	2:B:347:HIS:ND1	2.49	0.46
2:B:41:HIS:HB2	2:B:219:PHE:CD1	2.51	0.45
3:C:149:CYS:O	3:C:150:ARG:NH1	2.46	0.45
3:C:211:TRP:HD1	3:C:218:CYS:HA	1.81	0.45
3:C:161:SER:OG	3:C:165:THR:O	2.33	0.45
1:A:346:ARG:NE	2:B:379:ARG:O	2.36	0.45
3:C:314:ARG:O	3:C:332:TRP:N	2.46	0.45
2:B:237:CYS:SG	3:C:101:MET:HE2	2.57	0.45
5:E:83:MET:HB3	5:E:86:LEU:HD11	1.99	0.45
3:C:224:GLY:O	3:C:251:ARG:NH1	2.47	0.45
5:E:88:PRO:O	5:E:91:THR:HG22	2.17	0.45
3:C:60:ALA:HB3	3:C:102:THR:HA	1.99	0.44
1:A:288:VAL:HG11	2:B:383:LEU:HD11	1.98	0.44
3:C:51:LEU:HB3	3:C:82:TRP:CZ3	2.51	0.44
1:A:345:ASN:C	1:A:347:GLN:H	2.26	0.44
2:B:252:ASP:OD1	2:B:255:ARG:HB2	2.18	0.44
5:E:110:VAL:HG12	5:E:110:VAL:O	2.18	0.44
1:A:73:LEU:HD11	1:A:351:GLU:HG3	1.99	0.44
3:C:274:THR:OG1	3:C:315:VAL:O	2.32	0.44
2:B:254:ASN:OD1	2:B:255:ARG:N	2.50	0.44
2:B:332:ARG:HD3	2:B:353:PHE:HZ	1.82	0.44
3:C:120:ILE:HG21	3:C:138:GLU:HB3	1.99	0.44
2:B:56:ILE:HG22	2:B:60:MET:SD	2.58	0.44
1:A:219:LEU:HB3	1:A:220:PRO:HD3	2.00	0.43
1:A:303:TYR:HD2	1:A:327:THR:HA	1.83	0.43
4:D:54:VAL:HG11	4:D:59:ASN:HB3	2.00	0.43
1:A:306:PHE:HE2	1:A:323:GLU:HB3	1.83	0.43
2:B:45:LEU:HD23	2:B:223:ASP:HB2	2.01	0.43
3:C:123:ILE:O	3:C:136:SER:N	2.49	0.43
1:A:82:LEU:HD13	1:A:132:SER:HB2	2.00	0.43
1:A:117:LEU:HG	1:A:121:LEU:CD2	2.42	0.43
2:B:38:ARG:HH11	2:B:38:ARG:HG2	1.83	0.42
2:B:23:ASN:ND2	3:C:88:ASN:HD22	2.16	0.42
3:C:163:ASP:O	3:C:164:THR:OG1	2.32	0.42
3:C:234:PHE:CE1	3:C:238:GLY:HA2	2.48	0.42
1:A:119:LEU:HD12	1:A:119:LEU:HA	1.65	0.42
3:C:187:VAL:HA	3:C:203:ALA:HA	2.01	0.42
3:C:254:ASP:HB3	3:C:257:ALA:HB3	2.02	0.42
3:C:286:LEU:HD22	3:C:327:VAL:HG11	2.02	0.42
1:A:285:ALA:HB1	2:B:383:LEU:HD23	2.02	0.42
3:C:250:CYS:HB2	3:C:264:TYR:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:59:TYR:CE2	3:C:75:GLN:HB3	2.49	0.42
1:A:93:LEU:HD12	1:A:125:PHE:HD2	1.85	0.41
1:A:228:TYR:HB3	1:A:289:LEU:HD12	2.02	0.41
3:C:211:TRP:CD1	3:C:218:CYS:HA	2.55	0.41
2:B:298:ILE:H	2:B:298:ILE:HD12	1.85	0.41
3:C:244:GLY:HA3	3:C:273:ILE:HG21	2.02	0.41
3:C:154:ASP:OD1	3:C:154:ASP:N	2.53	0.41
3:C:289:TYR:HH	3:C:297:TRP:HZ2	1.62	0.41
2:B:378:LEU:HD23	2:B:378:LEU:HA	1.83	0.41
1:A:128:LEU:HD22	1:A:170:ALA:CB	2.50	0.41
3:C:215:GLU:OE1	3:C:217:MET:N	2.53	0.41
3:C:294:CYS:HB2	3:C:308:LEU:HB2	2.03	0.41
5:E:32:TYR:O	5:E:72:ARG:NH2	2.54	0.41
5:E:35:ASN:OD1	5:E:97:ALA:HB3	2.21	0.41
2:B:46:LEU:HA	2:B:46:LEU:HD23	1.80	0.41
1:A:137:ASN:ND2	1:A:224:ILE:HD13	2.36	0.41
3:C:176:GLN:HA	3:C:176:GLN:OE1	2.21	0.41
3:C:278:PHE:CZ	3:C:285:LEU:HD12	2.56	0.41
3:C:315:VAL:HA	3:C:331:SER:HA	2.02	0.41
2:B:371:ASP:HB3	2:B:375:ARG:NH1	2.36	0.41
1:A:118:TYR:HD2	1:A:119:LEU:HD13	1.85	0.40
2:B:353:PHE:O	2:B:364:ARG:NH1	2.49	0.40
2:B:358:ASP:OD1	2:B:360:GLU:HG2	2.21	0.40
3:C:317:CYS:HB2	3:C:330:GLY:H	1.86	0.40
4:D:49:PRO:HB3	4:D:54:VAL:HG22	2.04	0.40
5:E:109:ASP:O	5:E:109:ASP:OD1	2.39	0.40
1:A:56:ALA:HB2	1:A:335:THR:OG1	2.21	0.40
3:C:61:MET:HE2	3:C:61:MET:HB2	1.96	0.40
3:C:340:ASN:C	3:C:340:ASN:HD22	2.29	0.40
5:E:17:SER:C	5:E:18:LEU:HD12	2.47	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	A	248/390 (64%)	240 (97%)	7 (3%)	1 (0%)	30	59
2	B	225/249 (90%)	220 (98%)	5 (2%)	0	100	100
3	C	338/357 (95%)	328 (97%)	10 (3%)	0	100	100
4	D	54/71 (76%)	54 (100%)	0	0	100	100
5	E	124/160 (78%)	120 (97%)	4 (3%)	0	100	100
All	All	989/1227 (81%)	962 (97%)	26 (3%)	1 (0%)	49	76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/329 (57%)	186 (98%)	3 (2%)	55	71
2	B	178/220 (81%)	178 (100%)	0	100	100
3	C	255/297 (86%)	255 (100%)	0	100	100
4	D	24/58 (41%)	24 (100%)	0	100	100
5	E	96/129 (74%)	96 (100%)	0	100	100
All	All	742/1033 (72%)	739 (100%)	3 (0%)	81	84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	VAL
1	A	119	LEU
1	A	181	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	19	GLN
2	B	23	ASN
2	B	218	ASN
2	B	257	GLN
3	C	183	HIS
3	C	259	GLN
3	C	293	ASN
5	E	3	GLN

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.

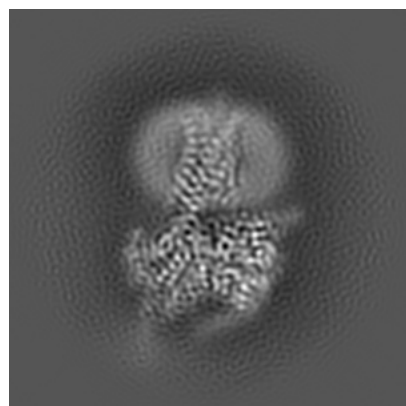
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37224. These allow visual inspection of the internal detail of the map and identification of artifacts.

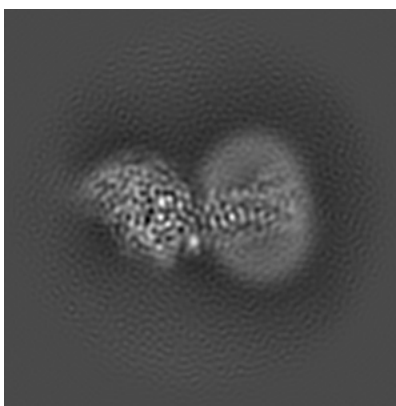
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

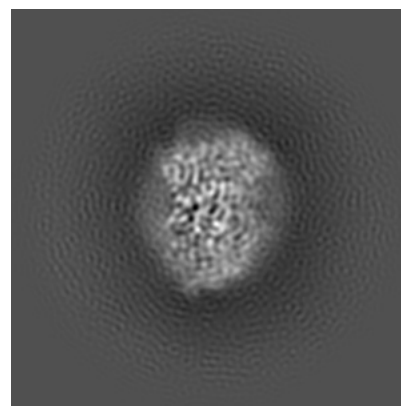
6.1.1 Primary map



X

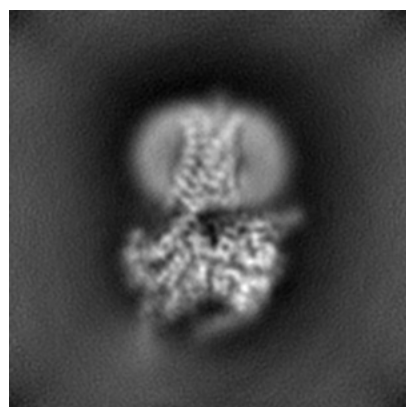


Y

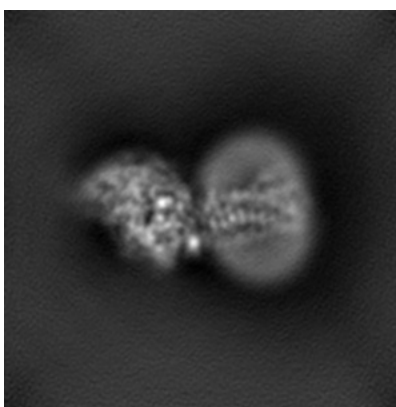


Z

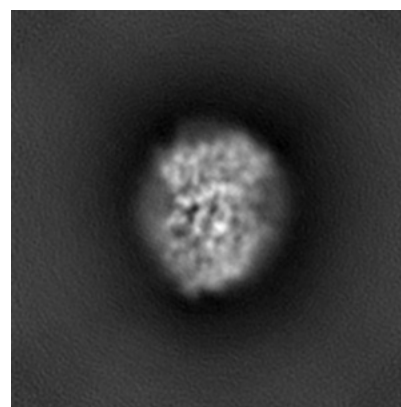
6.1.2 Raw map



X



Y

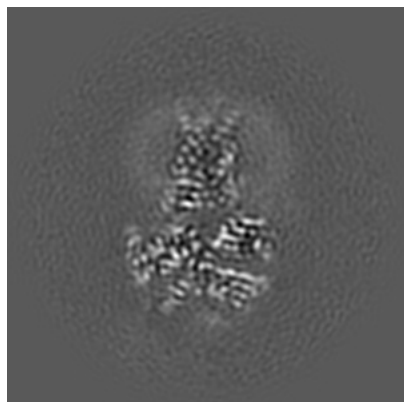


Z

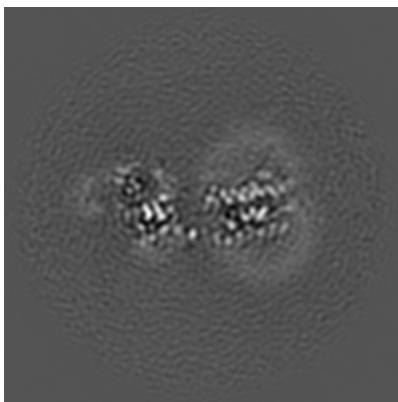
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

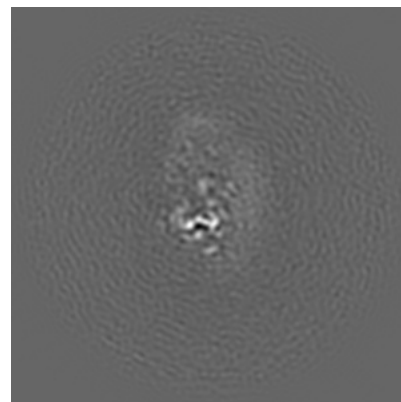
6.2.1 Primary map



X Index: 90

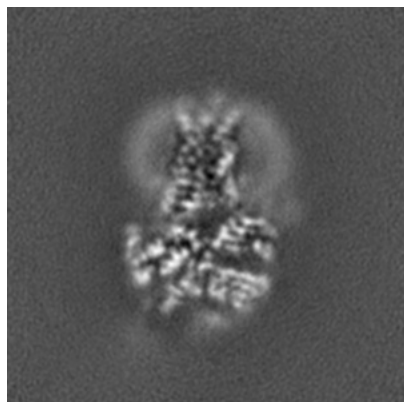


Y Index: 90

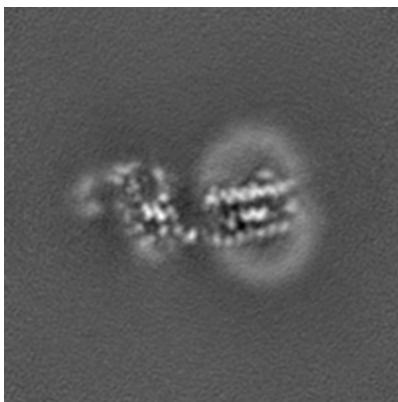


Z Index: 90

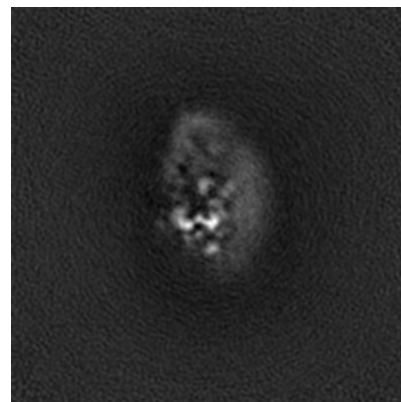
6.2.2 Raw map



X Index: 90



Y Index: 90

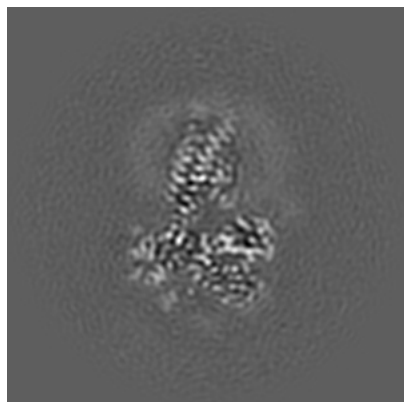


Z Index: 90

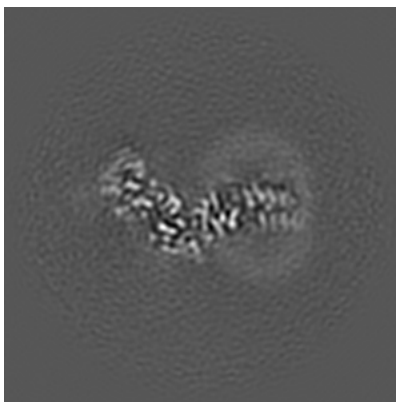
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

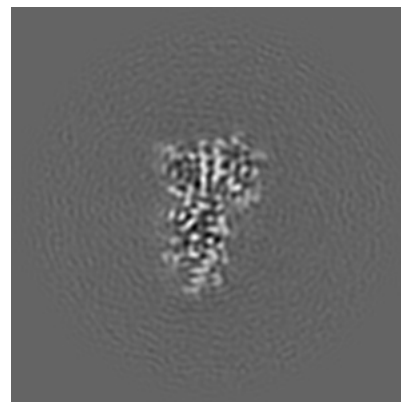
6.3.1 Primary map



X Index: 86

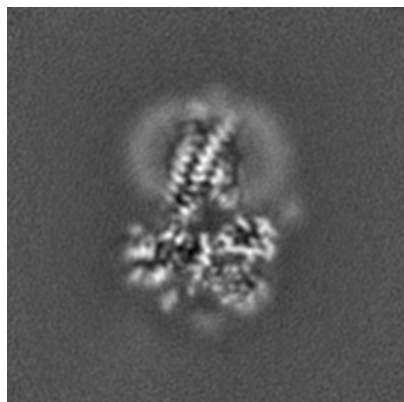


Y Index: 83

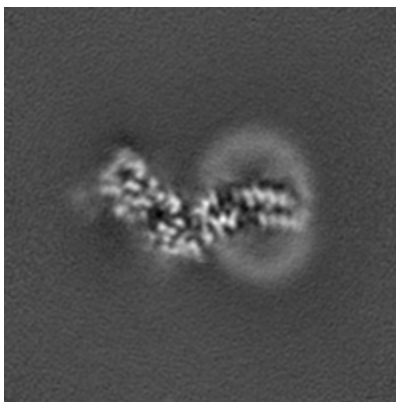


Z Index: 70

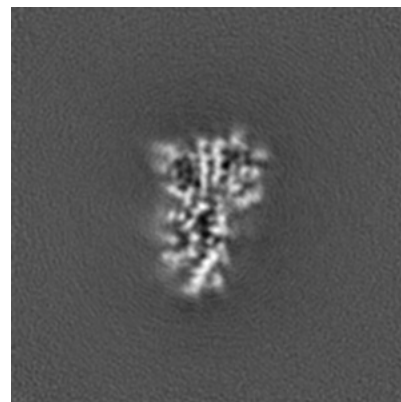
6.3.2 Raw map



X Index: 86



Y Index: 83

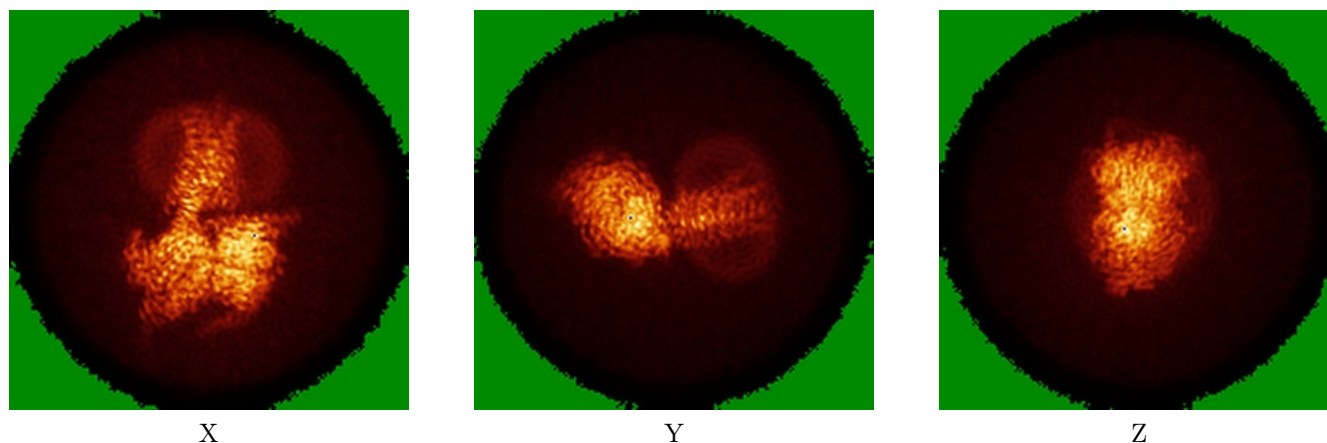


Z Index: 70

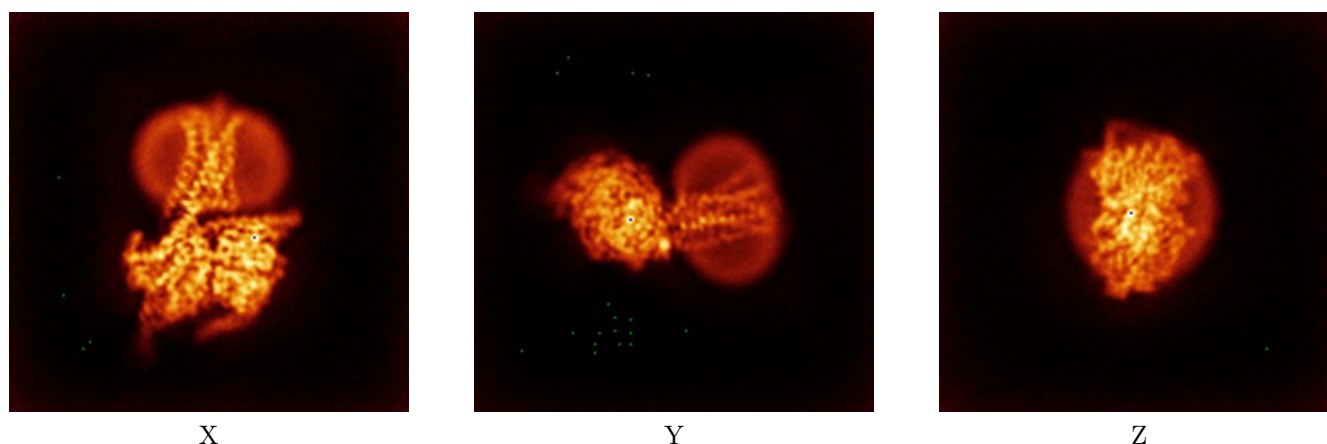
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

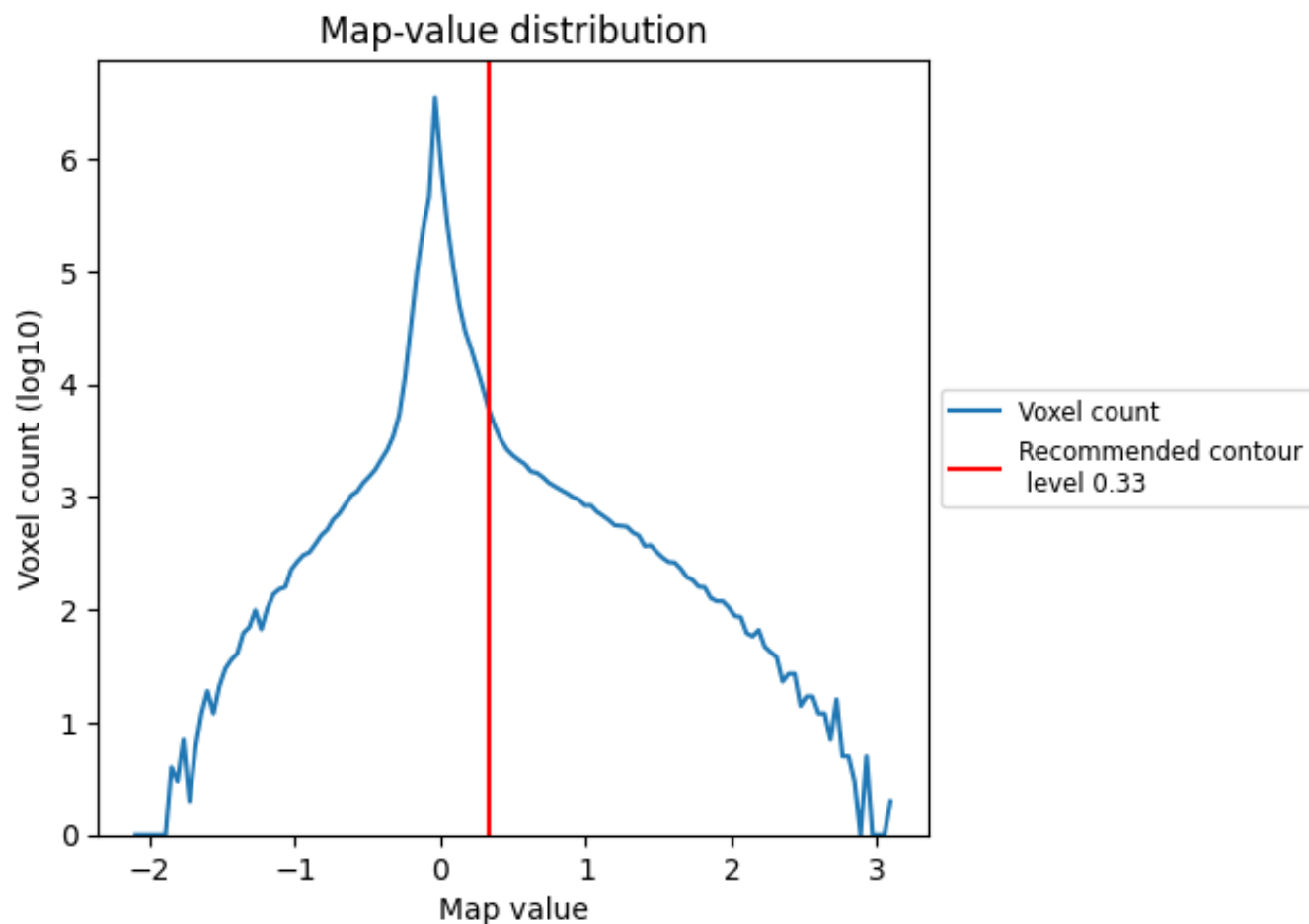
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

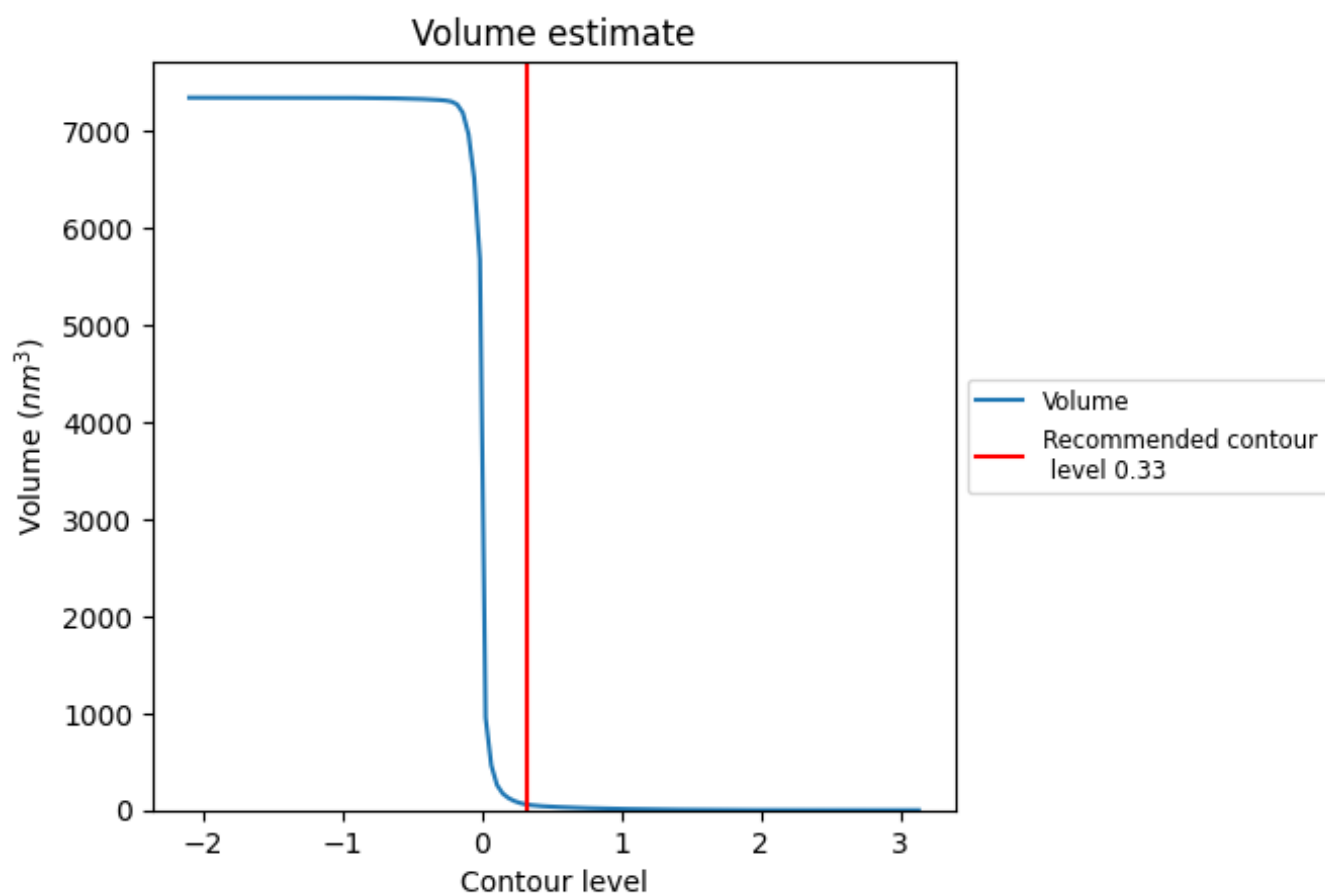
This section contains the results of statistical analysis of the map.

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.

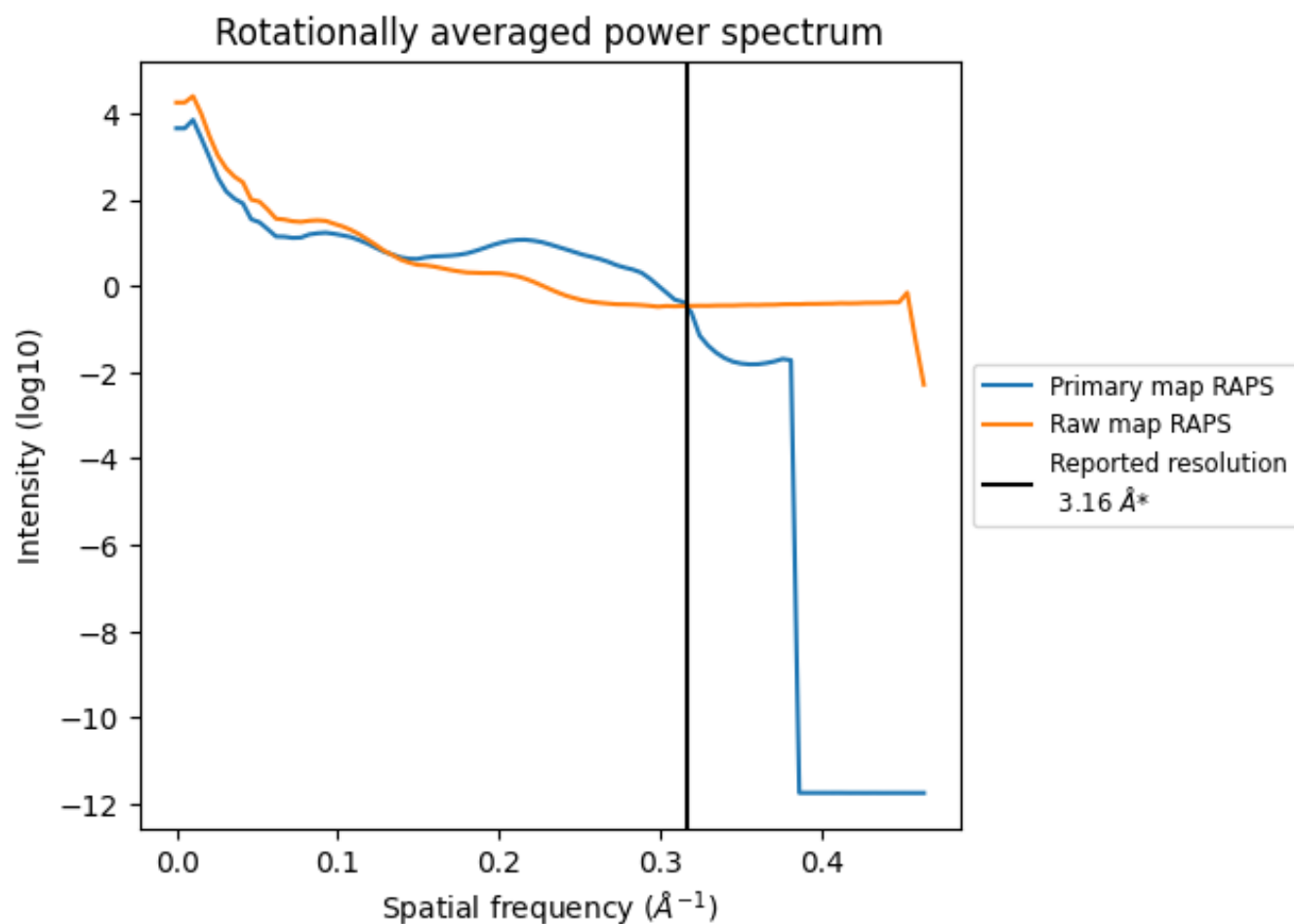
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 57 nm^3 ; this corresponds to an approximate mass of 51 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 ⓘ

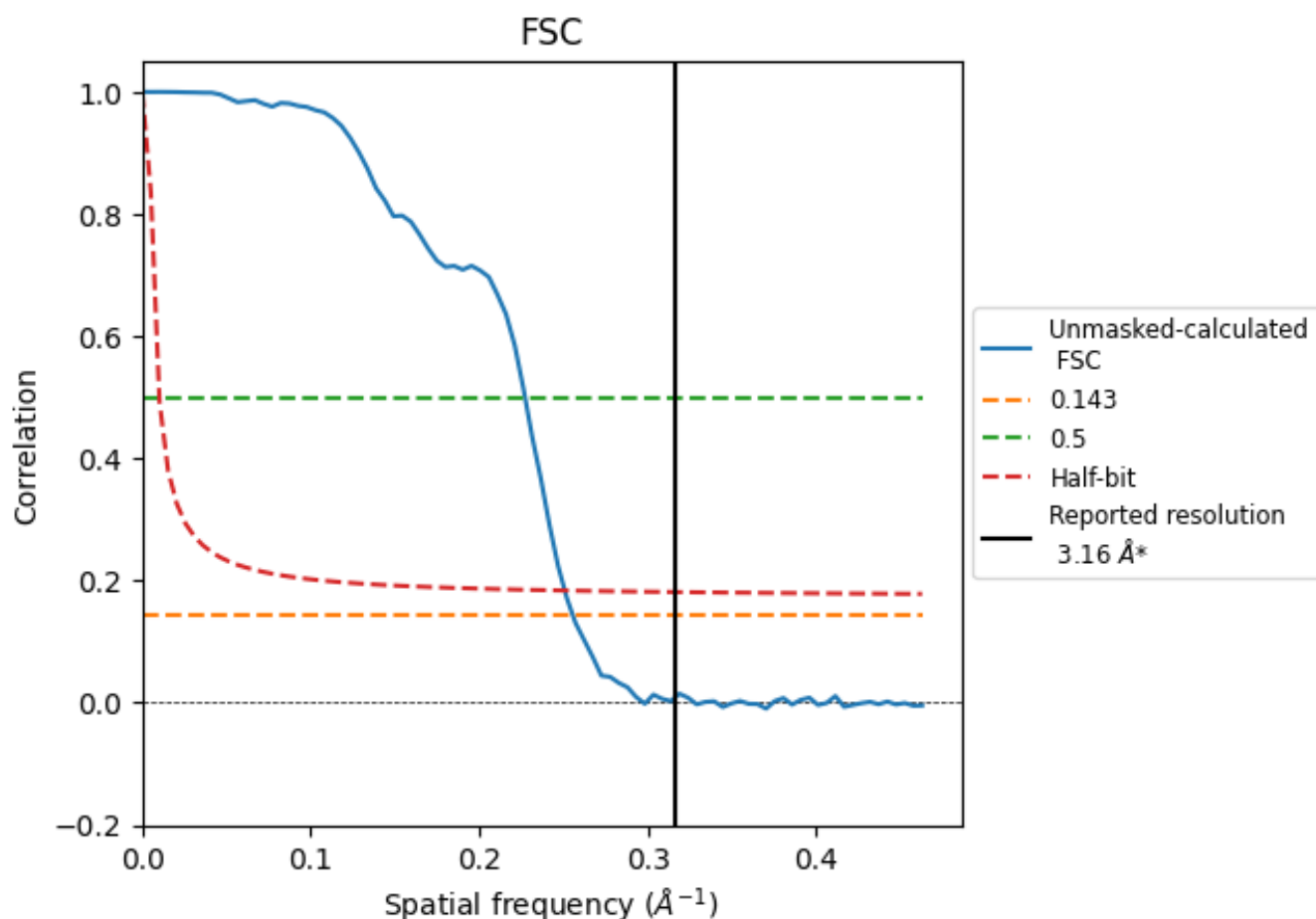


*Reported resolution corresponds to spatial frequency of $0.316 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.316 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

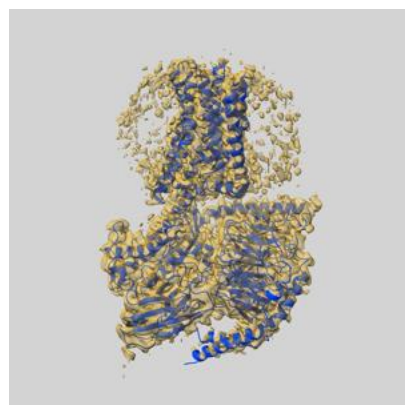
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.91	4.40	3.99

*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 3.91 differs from the reported value 3.16 by more than 10 %

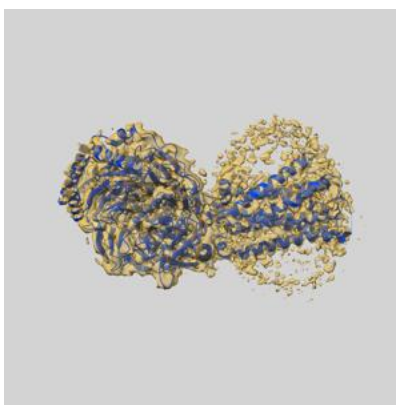
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37224 and PDB model 8KGK. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

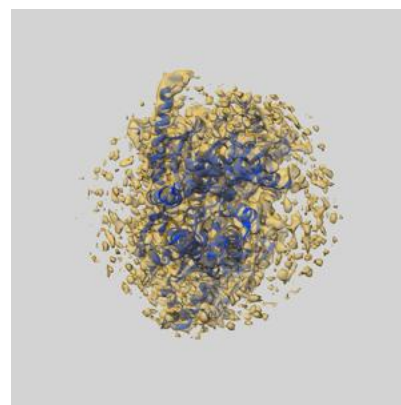
9.1 Map-model overlay [i](#)



X



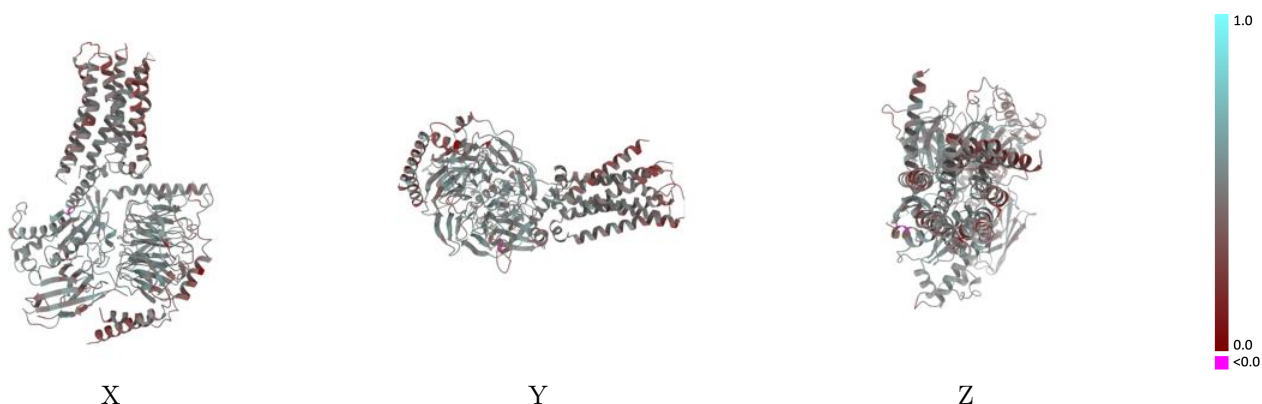
Y



Z

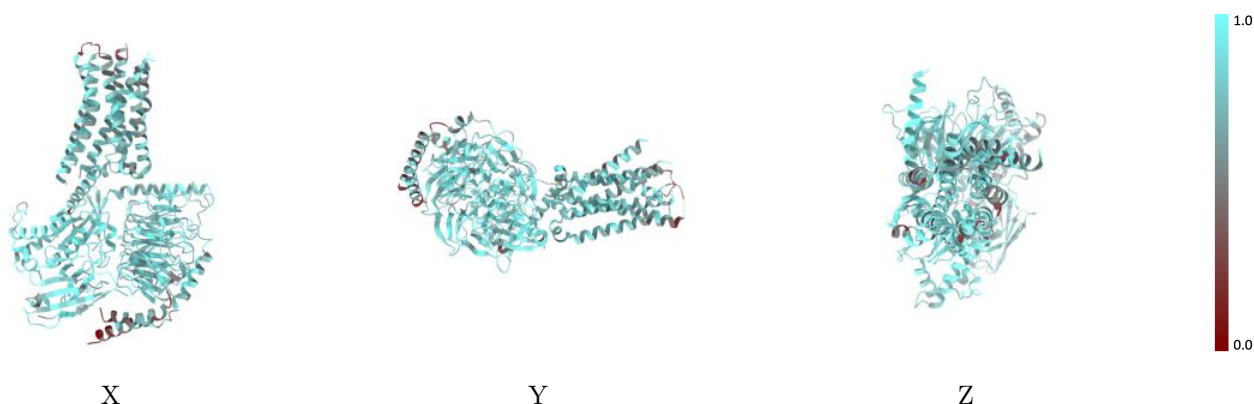
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



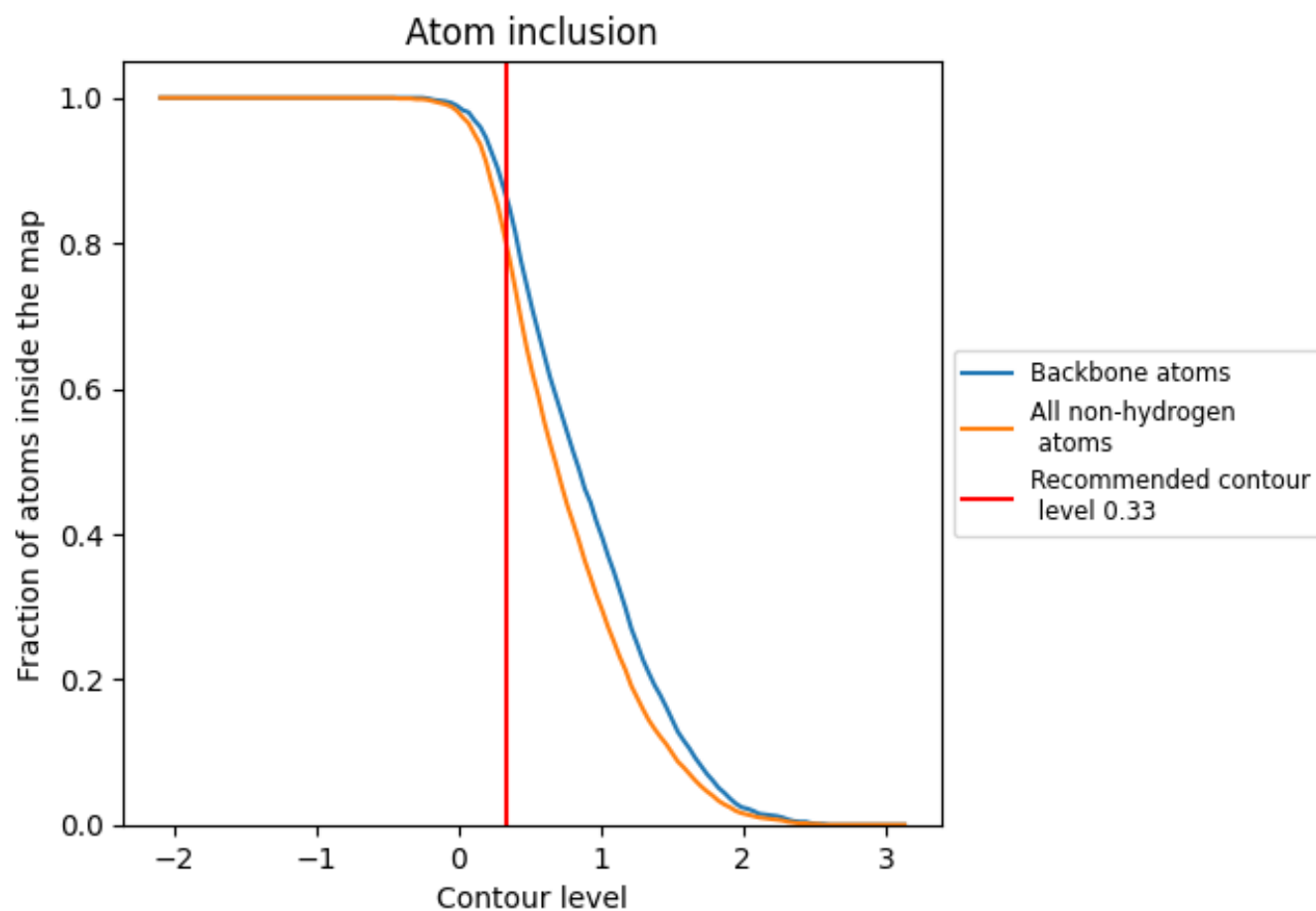
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 80% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.4690
A	0.7470	0.4290
B	0.8590	0.4920
C	0.8070	0.4870
D	0.6540	0.3980
E	0.8370	0.4840

