



Full wwPDB EM Validation Report ⓘ

Oct 1, 2024 – 11:33 AM JST

PDB ID : 7VVL
EMDB ID : EMD-32143
Title : PTH-bound human PTH1R in complex with Gs (class2)
Authors : Kobayashi, K.; Kusakizako, T.; Miyauchi, H.; Tomita, A.; Kobayashi, K.;
Shihoya, W.; Yamashita, K.; Nishizawa, T.; Kato, H.E.; Nureki, O.
Deposited on : 2021-11-06
Resolution : 2.80 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.dev113
MolProbity : 4.02b-467
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) : 2.39

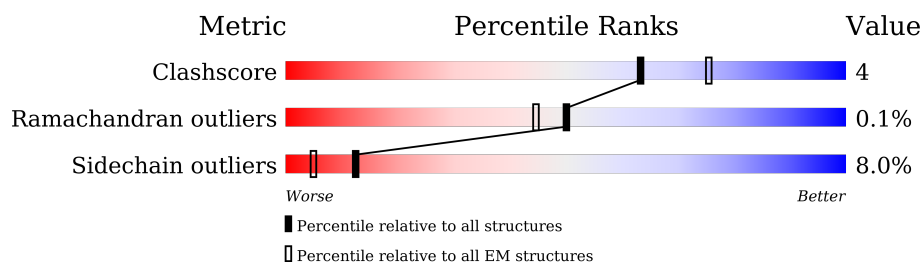
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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 ≥ 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	380	
2	B	351	
3	G	68	
4	N	137	
5	P	34	
6	R	473	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8725 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	230	Total	C	N	O	S	0	0
			1901	1200	343	351	7		

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	ASP	GLY	engineered mutation	UNP P63092
A	50	ASN	GLU	engineered mutation	UNP P63092
A	63	TYR	LEU	engineered mutation	UNP P63092
A	249	ASP	ALA	engineered mutation	UNP P63092
A	252	ASP	SER	engineered mutation	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	MET	deletion	UNP P63092
A	?	-	VAL	deletion	UNP P63092
A	?	-	ILE	deletion	UNP P63092
A	?	-	ARG	deletion	UNP P63092
A	?	-	GLU	deletion	UNP P63092
A	?	-	ASP	deletion	UNP P63092
A	?	-	ASN	deletion	UNP P63092
A	?	-	GLN	deletion	UNP P63092
A	?	-	THR	deletion	UNP P63092
A	362	ALA	ILE	engineered mutation	UNP P63092
A	365	ILE	VAL	engineered mutation	UNP P63092

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	335	Total	C	N	O	S	0	0
			2519	1559	447	492	21		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	expression tag	UNP P54311
B	-9	HIS	-	expression tag	UNP P54311
B	-8	HIS	-	expression tag	UNP P54311
B	-7	HIS	-	expression tag	UNP P54311
B	-6	HIS	-	expression tag	UNP P54311
B	-5	HIS	-	expression tag	UNP P54311
B	-4	HIS	-	expression tag	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 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	53	Total	C	N	O	S	0	0
			392	246	68	75	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	68	SER	-	expression tag	UNP P63212

- Molecule 4 is a protein called nanobody Nb35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			968	603	170	189	6		

- Molecule 5 is a protein called Parathyroid hormone.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	P	34	Total	C	N	O	S	0	0
			280	174	55	49	2		

- Molecule 6 is a protein called Parathyroid hormone/parathyroid hormone-related peptide receptor.

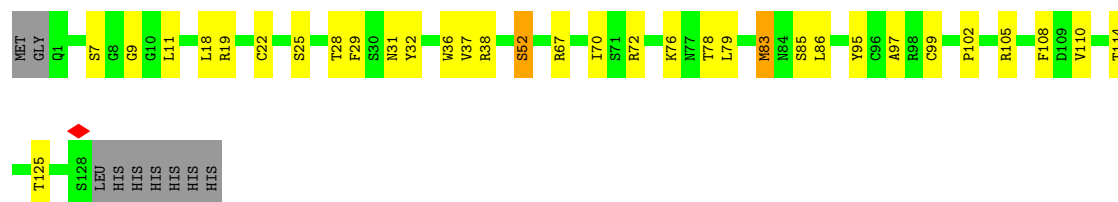
Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	346	Total	C	N	O	S	0	0
			2664	1764	440	446	14		

There are 8 discrepancies between the modelled and reference sequences:

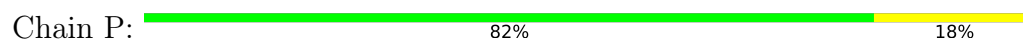
Chain	Residue	Modelled	Actual	Comment	Reference
R	19	ASP	-	expression tag	UNP Q03431
R	20	TYR	-	expression tag	UNP Q03431
R	21	LYS	-	expression tag	UNP Q03431
R	22	ASP	-	expression tag	UNP Q03431
R	23	ASP	-	expression tag	UNP Q03431
R	24	ASP	-	expression tag	UNP Q03431
R	25	ASP	-	expression tag	UNP Q03431
R	26	LYS	-	expression tag	UNP Q03431

- Molecule 7 is water.

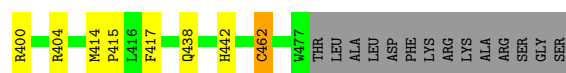
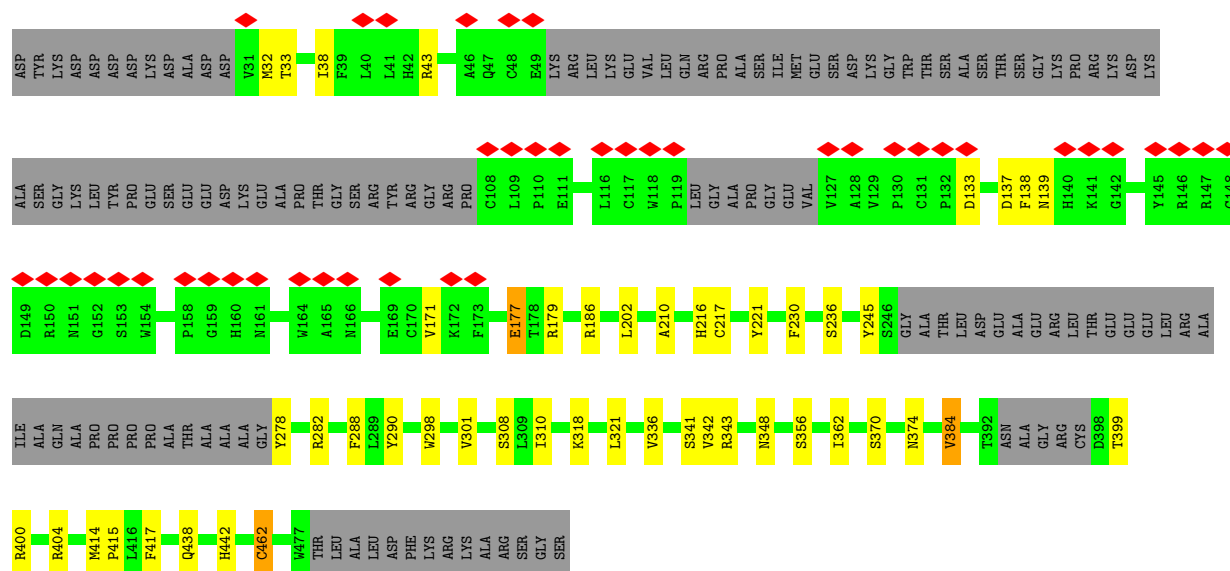
Mol	Chain	Residues	Atoms		AltConf
7	R	1	Total	O	0
			1	1	



• Molecule 5: Parathyroid hormone



• Molecule 6: Parathyroid hormone/parathyroid hormone-related peptide receptor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	490054	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64.319	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.233	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.019	Depositor
Map size (\AA)	152.72046, 152.72046, 152.72046	wwPDB
Map dimensions	138, 138, 138	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.10667, 1.10667, 1.10667	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	0.68	0/1938	0.89	3/2609 (0.1%)
2	B	0.73	0/2566	0.91	2/3486 (0.1%)
3	G	0.68	0/398	0.85	0/541
4	N	0.69	0/988	0.88	0/1339
5	P	0.72	0/284	0.82	0/378
6	R	0.70	0/2736	0.85	0/3731
All	All	0.70	0/8910	0.88	5/12084 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	A	346	ARG	NE-CZ-NH1	5.39	122.99	120.30
2	B	49	ARG	NE-CZ-NH1	5.11	122.86	120.30
2	B	197	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	A	379	ARG	NE-CZ-NH2	-5.01	117.80	120.30

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	A	1901	0	1861	12	0
2	B	2519	0	2388	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	392	0	383	3	0
4	N	968	0	931	14	0
5	P	280	0	283	5	0
6	R	2664	0	2520	24	0
7	R	1	0	0	0	0
All	All	8725	0	8366	68	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 4.

All (68) 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:B:49:ARG:NH1	2:B:85:TYR:O	2.31	0.64
6:R:282:ARG:NH1	6:R:348:ASN:OD1	2.30	0.64
6:R:177:GLU:CB	6:R:179:ARG:HE	2.10	0.64
4:N:28:THR:OG1	4:N:31:ASN:ND2	2.29	0.63
1:A:234:TRP:HB2	2:B:117:LEU:HD21	1.82	0.62
6:R:310:ILE:HG21	6:R:384:VAL:HG11	1.83	0.59
4:N:37:VAL:HG23	4:N:95:TYR:HB2	1.84	0.59
2:B:54:HIS:NE2	2:B:72:SER:OG	2.27	0.59
2:B:22:ARG:O	2:B:259:GLN:NE2	2.36	0.57
6:R:438:GLN:O	6:R:442:HIS:ND1	2.26	0.57
1:A:332:ARG:NH2	1:A:333:ASP:OD1	2.39	0.56
2:B:57:LYS:HB2	2:B:332:TRP:HA	1.88	0.55
6:R:342:VAL:HG11	6:R:362:ILE:HD13	1.90	0.54
6:R:221:TYR:CE1	6:R:321:LEU:HD11	2.43	0.54
2:B:237:ASN:HD21	2:B:239:ASN:HB2	1.74	0.53
2:B:247:ASP:HA	4:N:102:PRO:HG3	1.92	0.52
5:P:17:SER:HA	5:P:20:ARG:NH1	2.25	0.51
2:B:166:CYS:HB2	2:B:180:PHE:HB2	1.92	0.51
1:A:228:ARG:NH1	2:B:186:ASP:OD1	2.45	0.50
1:A:378:LEU:HD21	6:R:310:ILE:HD11	1.94	0.49
4:N:36:TRP:HD1	4:N:70:ILE:HD12	1.76	0.49
4:N:67:ARG:NH1	4:N:85:SER:O	2.44	0.49
1:A:230:GLU:OE1	1:A:232:ARG:NH1	2.31	0.49
1:A:270:ARG:O	1:A:270:ARG:NH1	2.43	0.49
2:B:250:CYS:HB2	2:B:264:TYR:HB2	1.95	0.48
4:N:83:MET:HG2	4:N:86:LEU:HD21	1.95	0.48
6:R:462:CYS:SG	6:R:462:CYS:O	2.72	0.48
2:B:146:LEU:HD21	2:B:159:THR:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:P:11:LEU:HD23	6:R:245:TYR:CE2	2.48	0.48
6:R:290:TYR:HA	6:R:336:VAL:HG21	1.96	0.47
6:R:298:TRP:CZ3	6:R:301:VAL:HG11	2.49	0.47
1:A:332:ARG:HD2	1:A:336:LEU:HD12	1.96	0.47
4:N:29:PHE:O	4:N:72:ARG:NH2	2.48	0.47
2:B:43:ILE:HG12	2:B:305:ALA:HB1	1.97	0.46
6:R:399:THR:OG1	6:R:400:ARG:N	2.47	0.46
2:B:245:SER:OG	2:B:247:ASP:OD1	2.34	0.46
4:N:9:GLY:HA2	4:N:18:LEU:HD21	1.98	0.46
6:R:356:SER:O	6:R:356:SER:OG	2.20	0.45
2:B:99:TRP:HB3	2:B:117:LEU:HD12	1.99	0.45
4:N:32:TYR:CZ	4:N:102:PRO:HB3	2.52	0.44
5:P:16:ASN:OD1	6:R:33:THR:HA	2.17	0.44
1:A:213:GLN:NE2	1:A:216:LYS:HA	2.32	0.44
5:P:20:ARG:NE	6:R:137:ASP:OD1	2.47	0.43
4:N:52:SER:O	4:N:72:ARG:NH1	2.47	0.43
2:B:236:PRO:HB2	3:G:40:TYR:CE2	2.54	0.43
6:R:210:ALA:O	6:R:216:HIS:NE2	2.40	0.43
1:A:284:GLN:HG3	1:A:353:PHE:HB3	2.01	0.43
6:R:414:MET:HB2	6:R:415:PRO:HD3	2.00	0.43
1:A:209:GLU:HG3	1:A:222:PHE:CE1	2.54	0.43
6:R:177:GLU:CB	6:R:179:ARG:HH21	2.30	0.43
6:R:202:LEU:HD13	6:R:230:PHE:HB3	2.01	0.43
2:B:248:ALA:HB1	2:B:269:ILE:HG22	2.01	0.43
5:P:23:TRP:NE1	6:R:38:ILE:HG12	2.34	0.42
4:N:11:LEU:HD23	4:N:11:LEU:HA	1.85	0.42
2:B:30:LEU:HB3	2:B:262:MET:HG3	2.02	0.42
1:A:374:GLN:NE2	6:R:310:ILE:O	2.53	0.42
2:B:49:ARG:HH21	3:G:61:PHE:C	2.23	0.42
2:B:51:LEU:HD12	2:B:336:LEU:HD22	2.02	0.42
6:R:343:ARG:HA	6:R:343:ARG:HD2	1.82	0.42
4:N:28:THR:OG1	4:N:28:THR:O	2.38	0.41
2:B:262:MET:HE3	2:B:302:ALA:HB2	2.02	0.41
1:A:313:ASP:OD1	1:A:313:ASP:N	2.50	0.41
4:N:22:CYS:HB3	4:N:79:LEU:HB3	2.03	0.41
6:R:374:ASN:ND2	6:R:417:PHE:O	2.51	0.41
2:B:84:SER:HB2	3:G:61:PHE:HE1	1.86	0.41
6:R:138:PHE:CE1	6:R:171:VAL:HG12	2.55	0.41
2:B:196:THR:OG1	2:B:197:ARG:NH2	2.55	0.40
4:N:97:ALA:CB	4:N:110:VAL:HG13	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	226/380 (60%)	221 (98%)	5 (2%)	0	100	100
2	B	333/351 (95%)	314 (94%)	19 (6%)	0	100	100
3	G	51/68 (75%)	49 (96%)	2 (4%)	0	100	100
4	N	126/137 (92%)	122 (97%)	4 (3%)	0	100	100
5	P	32/34 (94%)	29 (91%)	3 (9%)	0	100	100
6	R	336/473 (71%)	321 (96%)	14 (4%)	1 (0%)	37	67
All	All	1104/1443 (76%)	1056 (96%)	47 (4%)	1 (0%)	50	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	R	177	GLU

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	203/338 (60%)	184 (91%)	19 (9%)	7	23
2	B	265/293 (90%)	245 (92%)	20 (8%)	11	33
3	G	39/56 (70%)	36 (92%)	3 (8%)	10	31
4	N	104/114 (91%)	91 (88%)	13 (12%)	3	12
5	P	31/33 (94%)	30 (97%)	1 (3%)	34	68
6	R	256/405 (63%)	240 (94%)	16 (6%)	15	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	898/1239 (72%)	826 (92%)	72 (8%)	12	30

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLU
1	A	28	LYS
1	A	38	ARG
1	A	61	ARG
1	A	209	GLU
1	A	224	VAL
1	A	251	SER
1	A	256	LEU
1	A	270	ARG
1	A	289	GLU
1	A	304	GLU
1	A	307	ARG
1	A	313	ASP
1	A	332	ARG
1	A	339	SER
1	A	347	HIS
1	A	355	CYS
1	A	360	GLU
1	A	363	ARG
2	B	27	ASP
2	B	38	ASP
2	B	59	TYR
2	B	61	MET
2	B	67	SER
2	B	70	LEU
2	B	78	LYS
2	B	79	LEU
2	B	86	THR
2	B	105	TYR
2	B	122	SER
2	B	146	LEU
2	B	173	THR
2	B	189	SER
2	B	197	ARG
2	B	201	SER
2	B	249	THR
2	B	277	SER

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Mol	Chain	Res	Type
2	B	336	LEU
2	B	340	ASN
3	G	29	LYS
3	G	36	ASP
3	G	62	ARG
4	N	7	SER
4	N	19	ARG
4	N	25	SER
4	N	38	ARG
4	N	52	SER
4	N	76	LYS
4	N	78	THR
4	N	83	MET
4	N	99	CYS
4	N	105	ARG
4	N	108	PHE
4	N	114	THR
4	N	125	THR
5	P	19	GLU
6	R	32	MET
6	R	43	ARG
6	R	133	ASP
6	R	139	ASN
6	R	186	ARG
6	R	217	CYS
6	R	236	SER
6	R	278	TYR
6	R	288	PHE
6	R	308	SER
6	R	318	LYS
6	R	341	SER
6	R	370	SER
6	R	384	VAL
6	R	404	ARG
6	R	462	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	32	GLN
2	B	237	ASN
3	G	59	ASN

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Mol	Chain	Res	Type
4	N	31	ASN
6	R	223	HIS
6	R	402	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.

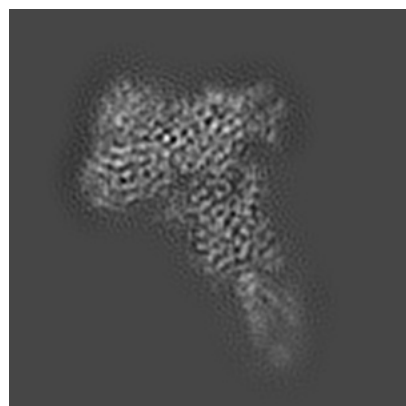
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32143. These allow visual inspection of the internal detail of the map and identification of artifacts.

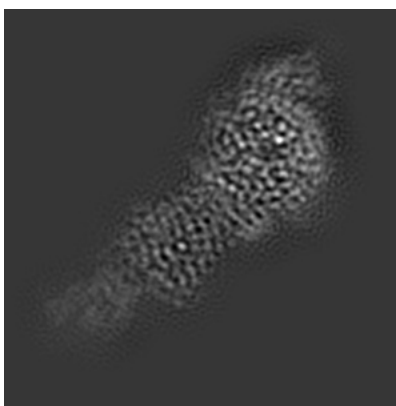
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

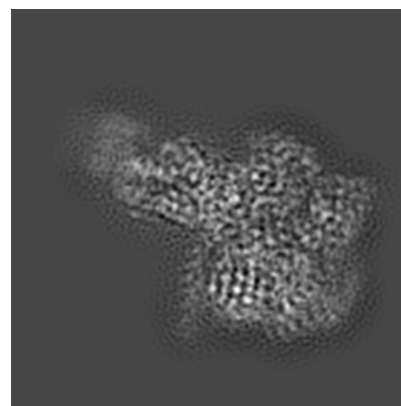
6.1.1 Primary map



X

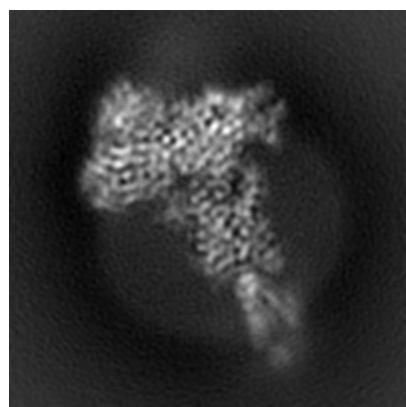


Y

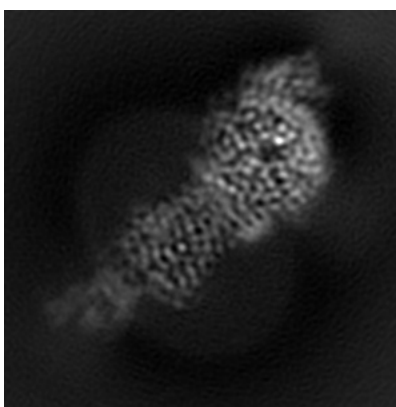


Z

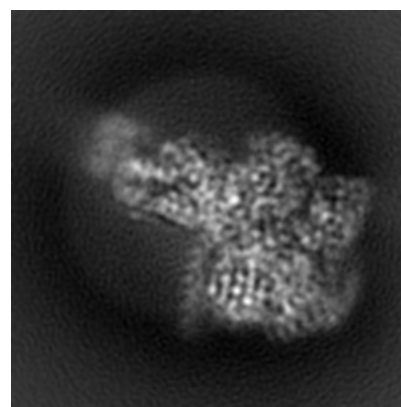
6.1.2 Raw map



X



Y

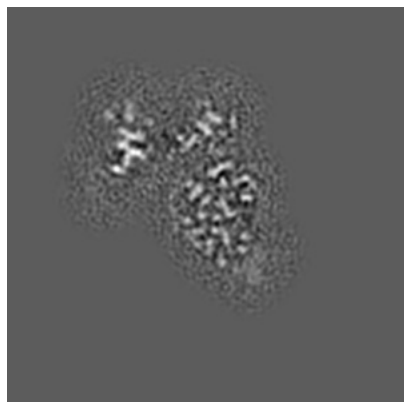


Z

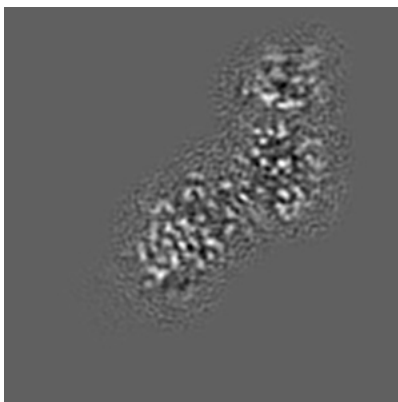
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

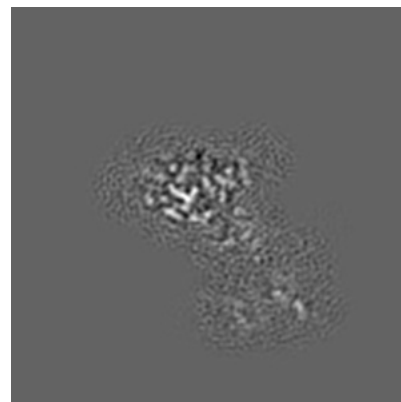
6.2.1 Primary map



X Index: 69

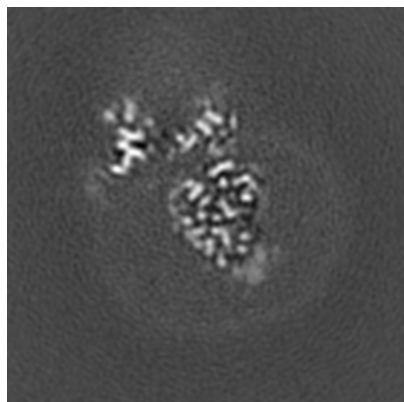


Y Index: 69

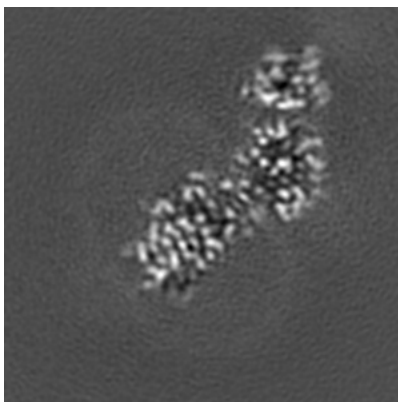


Z Index: 69

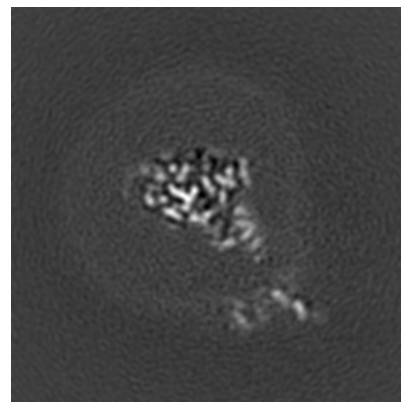
6.2.2 Raw map



X Index: 69



Y Index: 69

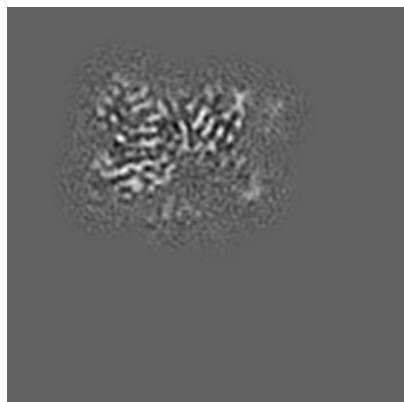


Z Index: 69

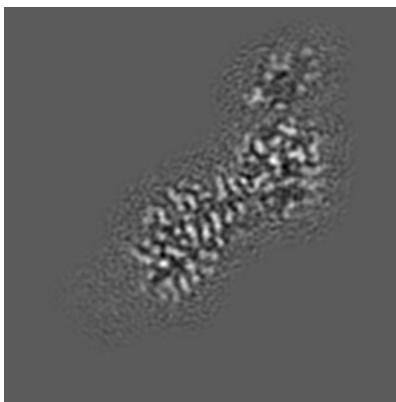
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 83

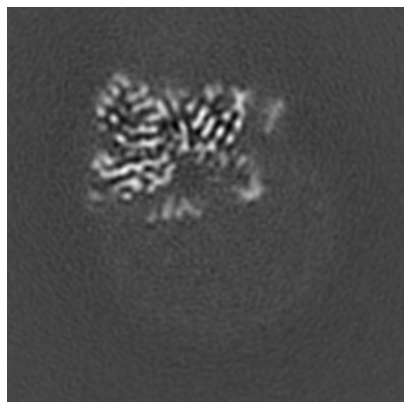


Y Index: 72

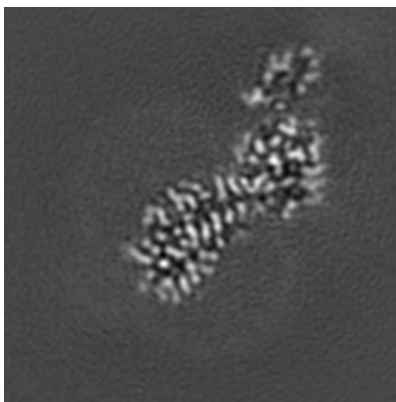


Z Index: 95

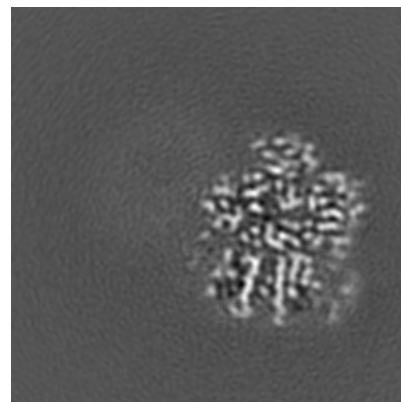
6.3.2 Raw map



X Index: 83



Y Index: 72

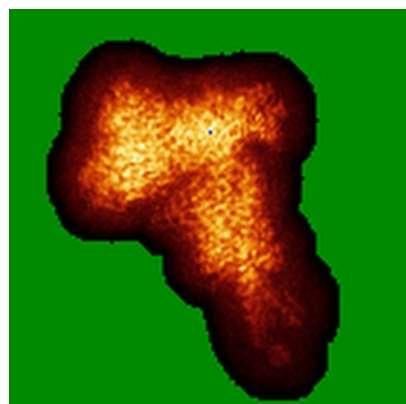


Z Index: 95

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

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

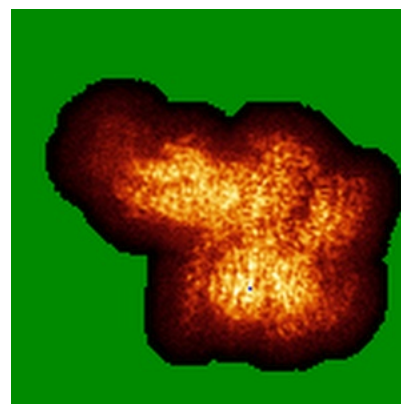
6.4.1 Primary map



X

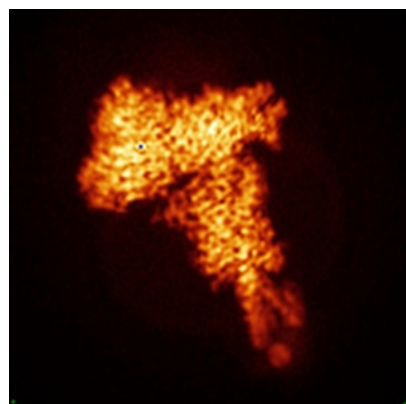


Y

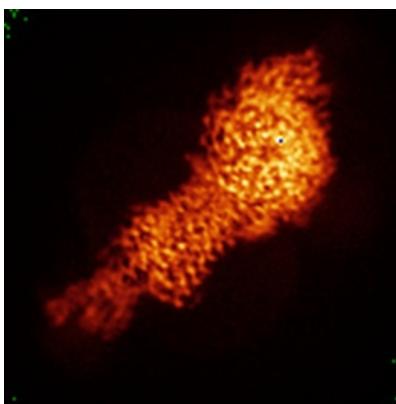


Z

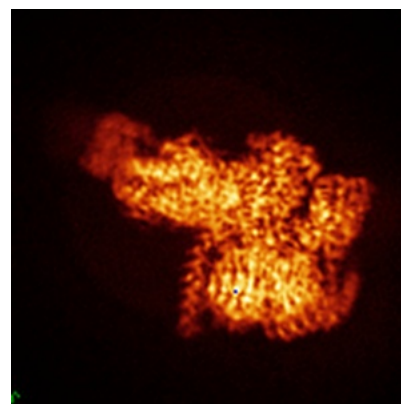
6.4.2 Raw map



X



Y

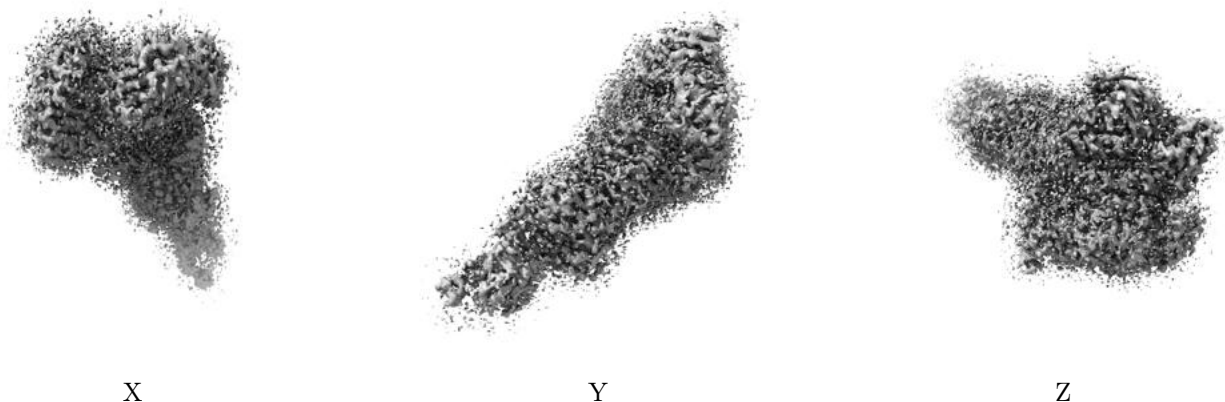


Z

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.

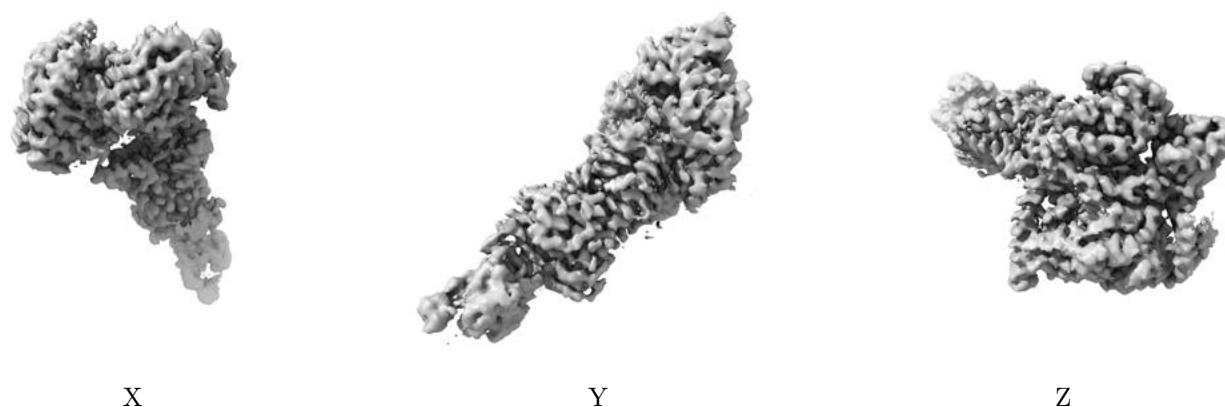
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.019. 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.

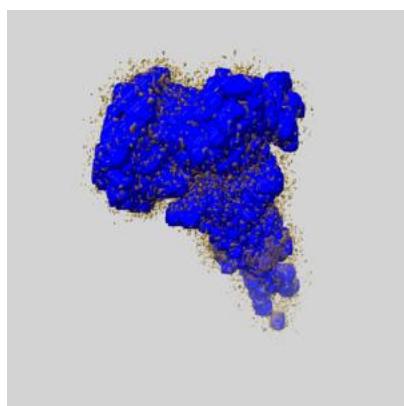
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

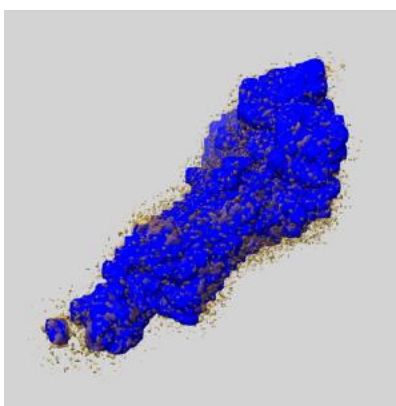
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

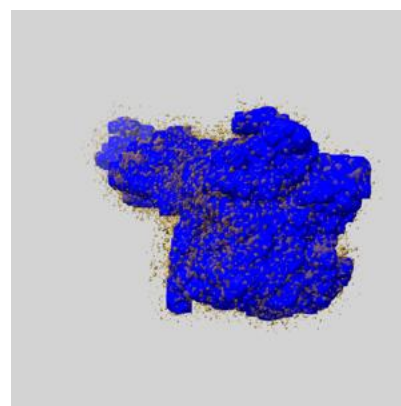
6.6.1 emd_32143_msk_1.map [i](#)



X



Y

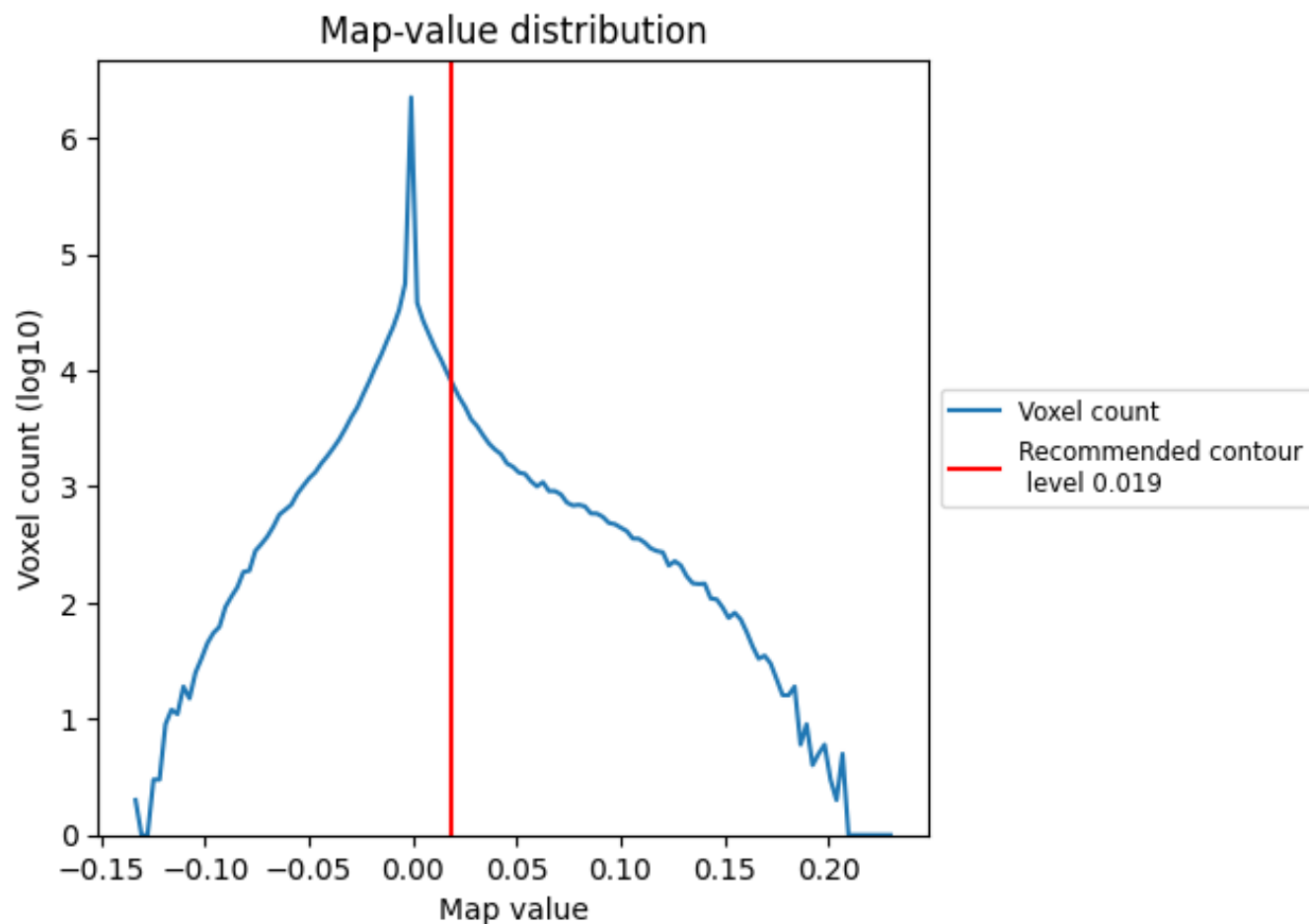


Z

7 Map analysis [i](#)

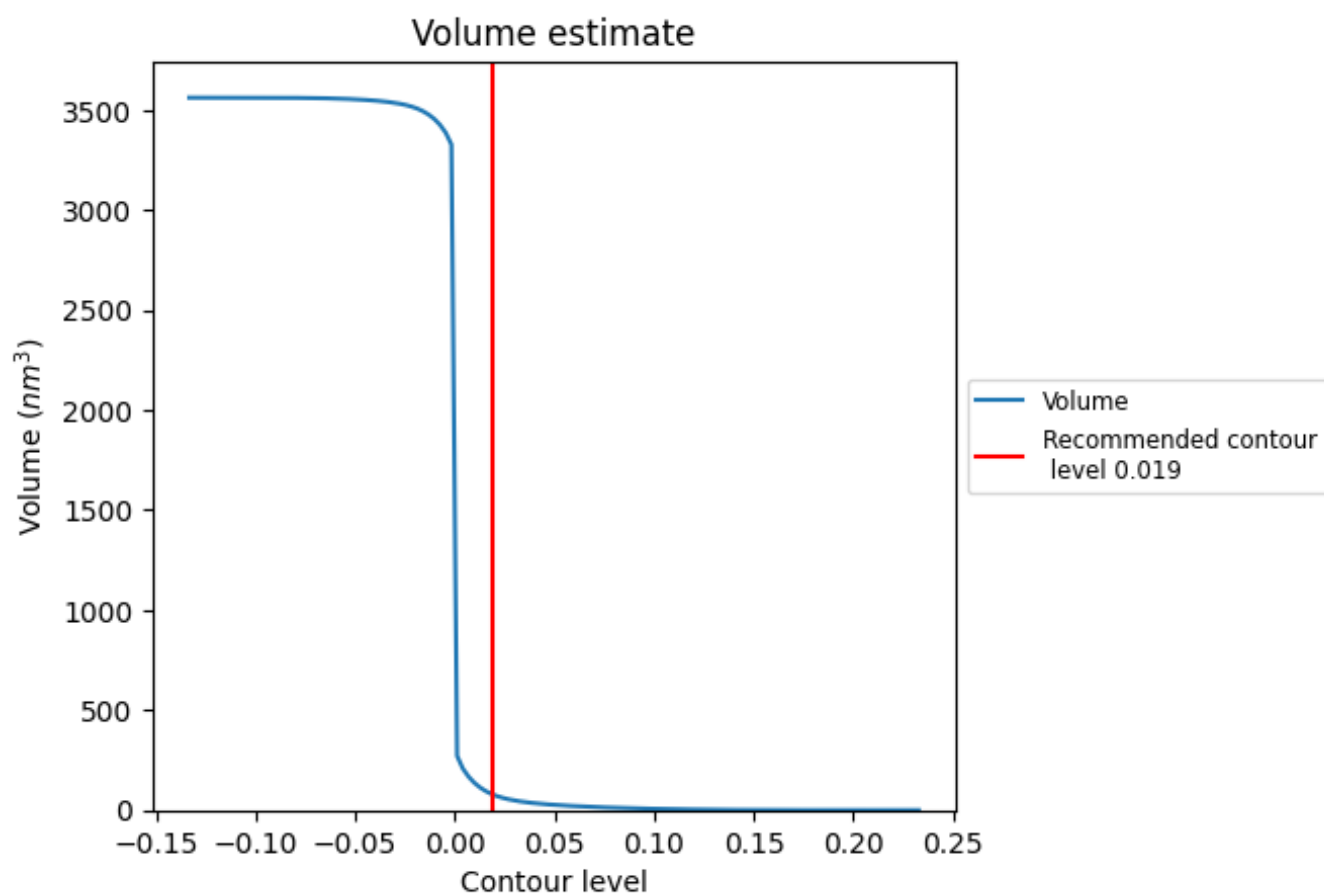
This section contains the results of statistical analysis of the map.

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.

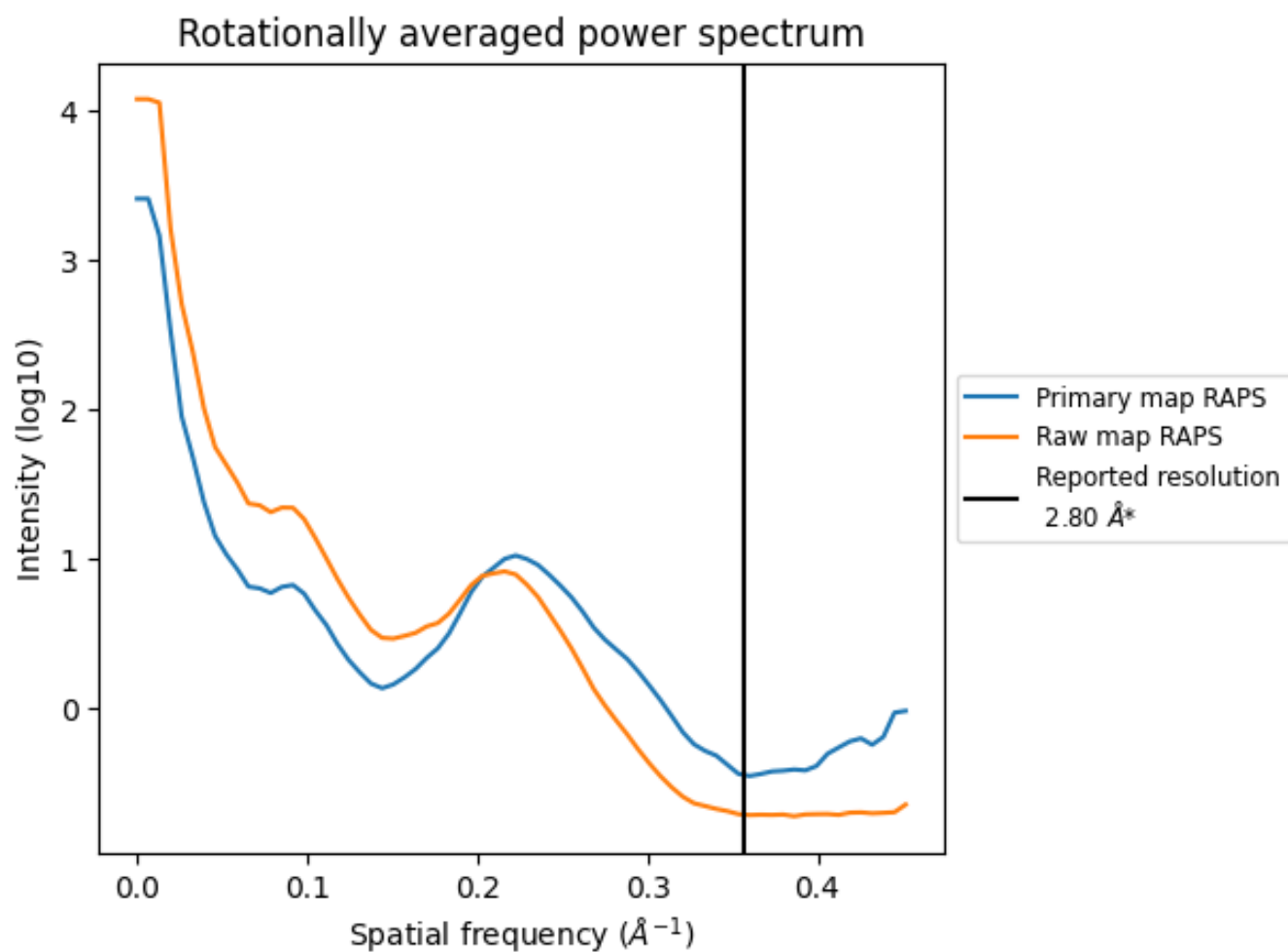
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79 nm^3 ; this corresponds to an approximate mass of 71 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 ⓘ

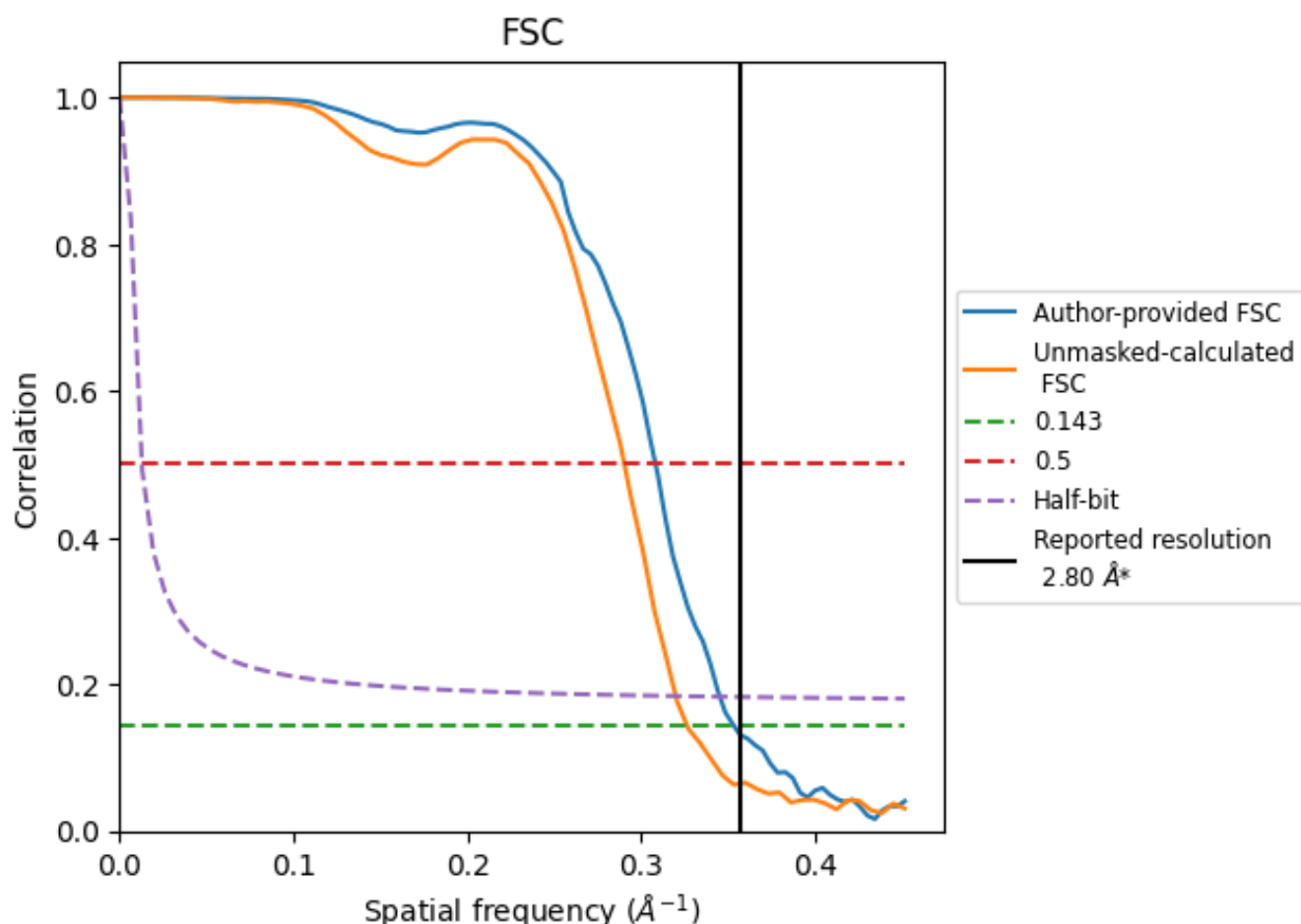


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 \AA^{-1}

8.2 Resolution estimates [i](#)

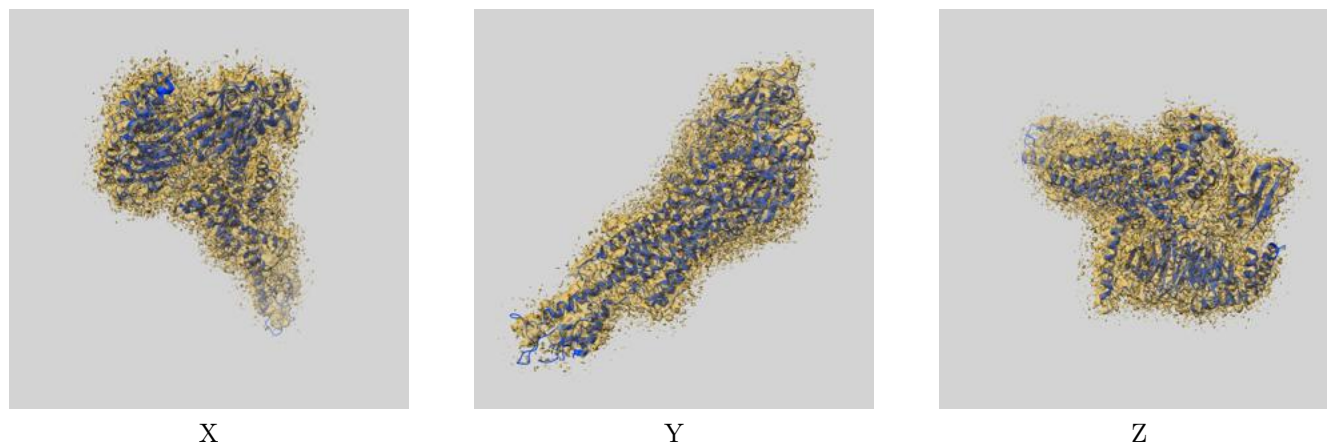
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.83	3.24	2.89
Unmasked-calculated*	3.06	3.44	3.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

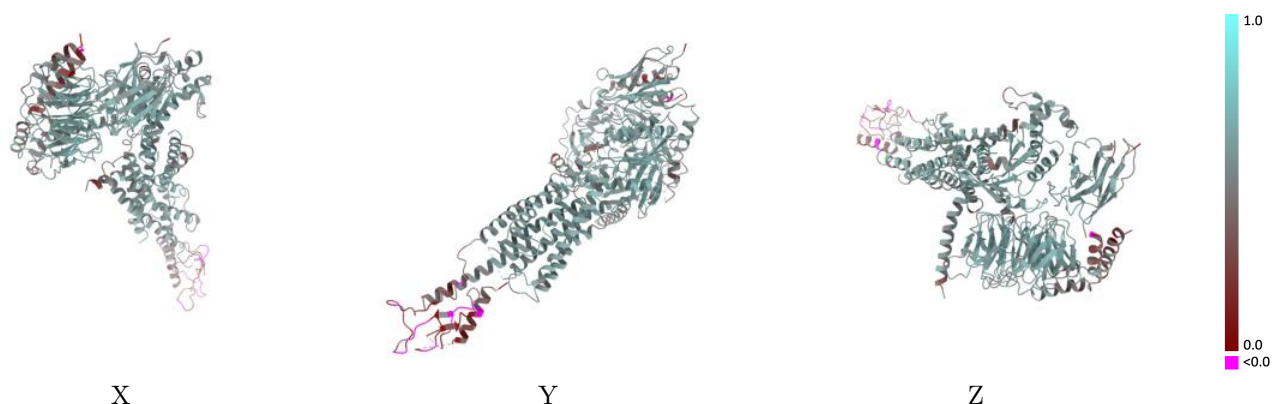
This section contains information regarding the fit between EMDB map EMD-32143 and PDB model 7VVL. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



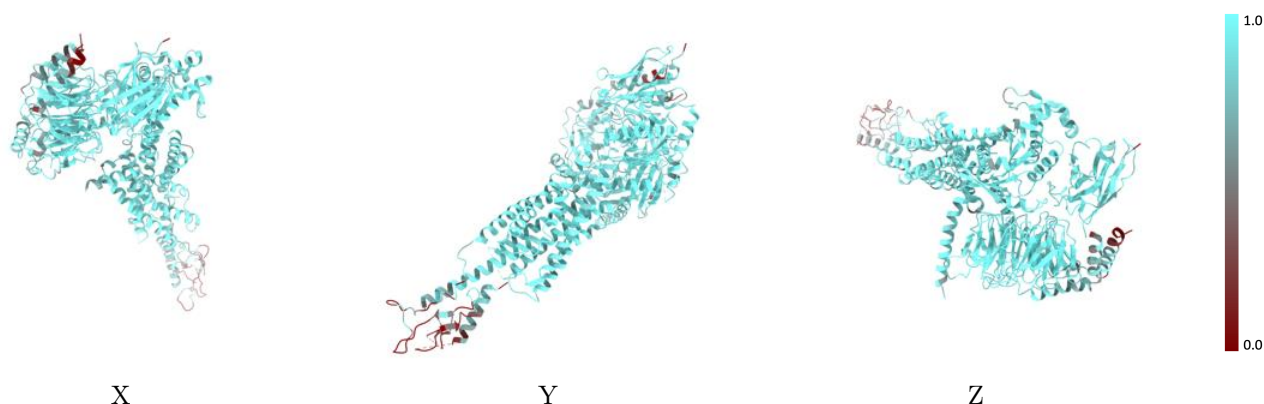
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



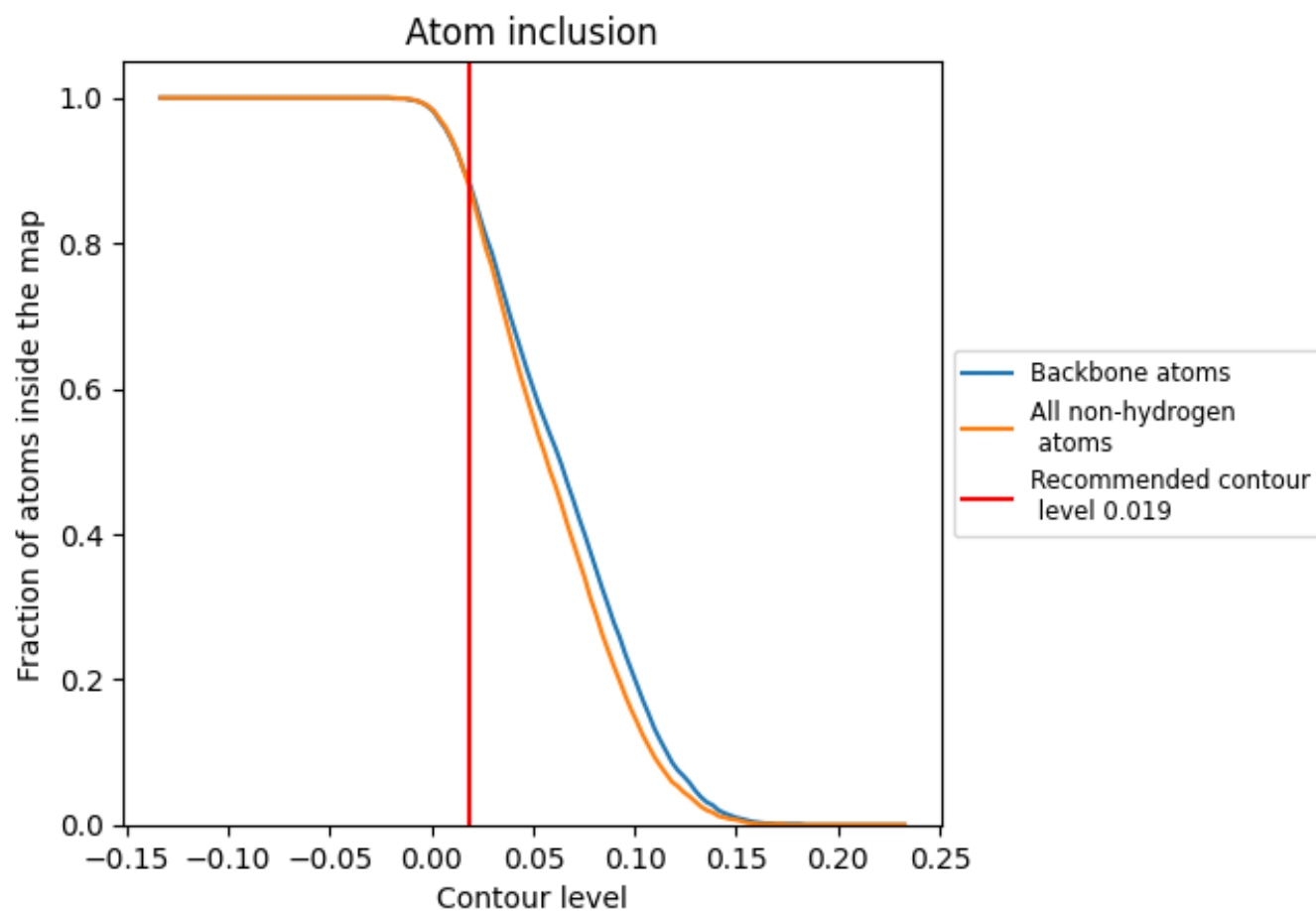
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8750	<div><div></div></div> 0.5400
A	<div><div></div></div> 0.9190	<div><div></div></div> 0.5730
B	<div><div></div></div> 0.9190	<div><div></div></div> 0.5800
G	<div><div></div></div> 0.7700	<div><div></div></div> 0.4710
N	<div><div></div></div> 0.9120	<div><div></div></div> 0.5680
P	<div><div></div></div> 0.8330	<div><div></div></div> 0.4880
R	<div><div></div></div> 0.8080	<div><div></div></div> 0.4860

1.0

0.0

<0.0