



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 02:17 AM EST

PDB ID : 6VEN
EMDB ID : EMD-21157
Title : Yeast COMPASS in complex with a ubiquitinated nucleosome
Authors : Worden, E.J.; Wolberger, C.
Deposited on : 2020-01-02
Resolution : 3.37 Å(reported)
Based on initial models : 6BX3, 6NJ9, 6CHG

This is a wwPDB EM Validation Summary 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:

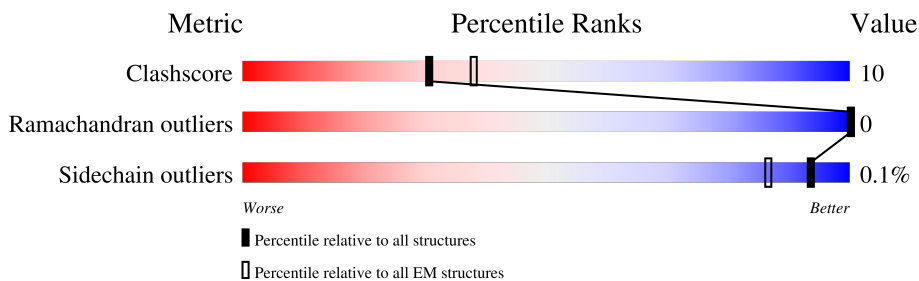
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.37 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	135	
1	E	135	
2	B	102	
2	F	102	
3	C	129	
3	G	129	
4	D	122	
4	H	122	

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Mol	Chain	Length	Quality of chain
5	I	146	52% 48%
6	J	146	47% 53%
7	K	80	18% 64% 30% 6%
8	L	315	68% 30%
9	M	426	65% 28% 7%
10	N	358	8% 49% 12% 39%
11	O	505	15% 44% 18% 38%
12	P	175	17% 21% 76%
12	Q	175	10% 10% 7% 83%
13	R	391	13% 25% 8% 67%

2 Entry composition i

There are 15 unique types of molecules in this entry. The entry contains 24028 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 Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	106	Total 871	C 548	N 171	O 151	S 1	0	0
1	E	97	Total 802	C 508	N 155	O 138	S 1	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	NLE	LYS	engineered mutation	UNP P84233
A	90	NLE	MET	engineered mutation	UNP P84233
A	102	ALA	GLY	engineered mutation	UNP P84233
A	120	NLE	MET	engineered mutation	UNP P84233
E	4	NLE	LYS	engineered mutation	UNP P84233
E	90	NLE	MET	engineered mutation	UNP P84233
E	102	ALA	GLY	engineered mutation	UNP P84233
E	120	NLE	MET	engineered mutation	UNP P84233

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	81	Total 646	C 407	N 126	O 112	S 1	0	0
2	F	80	Total 644	C 408	N 125	O 110	S 1	0	0

- Molecule 3 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	103	Total 795	C 501	N 155	O 139	0	0
3	G	106	Total 818	C 516	N 160	O 142	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	99	ARG	GLY	engineered mutation	UNP P06897
C	123	SER	ALA	engineered mutation	UNP P06897
G	99	ARG	GLY	engineered mutation	UNP P06897
G	123	SER	ALA	engineered mutation	UNP P06897

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	93	Total	C	N	O	S	0	0
			727	457	130	137	3		
4	H	94	Total	C	N	O	S	0	0
			732	460	131	138	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	32	THR	SER	engineered mutation	UNP P02281
D	120	CYS	LYS	engineered mutation	UNP P02281
H	32	THR	SER	engineered mutation	UNP P02281
H	120	CYS	LYS	engineered mutation	UNP P02281

- Molecule 5 is a DNA chain called 601 DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		

- Molecule 6 is a DNA chain called 601 DNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		

- Molecule 7 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	75	Total	C	N	O	S	0	0
			597	376	104	116	1		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	GLY	-	expression tag	UNP P0CG48
K	-2	SER	-	expression tag	UNP P0CG48
K	-1	HIS	-	expression tag	UNP P0CG48
K	0	MET	-	expression tag	UNP P0CG48
K	76	CYS	GLY	engineered mutation	UNP P0CG48

- Molecule 8 is a protein called COMPASS component SWD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L	308	2367	1500	394	454	19	0	0

- Molecule 9 is a protein called COMPASS component SWD1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	M	395	3183	2032	523	614	14	0	0

- Molecule 10 is a protein called Histone-lysine N-methyltransferase, H3 lysine-4 specific.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	N	218	1710	1072	315	314	9	0	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	723	MET	-	expression tag	UNP P38827
N	724	HIS	-	expression tag	UNP P38827
N	725	HIS	-	expression tag	UNP P38827
N	726	HIS	-	expression tag	UNP P38827
N	727	HIS	-	expression tag	UNP P38827
N	728	HIS	-	expression tag	UNP P38827
N	729	HIS	-	expression tag	UNP P38827
N	730	GLY	-	expression tag	UNP P38827
N	731	SER	-	expression tag	UNP P38827
N	732	SER	-	expression tag	UNP P38827
N	733	ASP	-	expression tag	UNP P38827
N	734	TYR	-	expression tag	UNP P38827
N	735	LYS	-	expression tag	UNP P38827
N	736	ASP	-	expression tag	UNP P38827
N	737	HIS	-	expression tag	UNP P38827
N	738	ASP	-	expression tag	UNP P38827

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Chain	Residue	Modelled	Actual	Comment	Reference
N	739	GLY	-	expression tag	UNP P38827
N	740	ASP	-	expression tag	UNP P38827
N	741	TYR	-	expression tag	UNP P38827
N	742	LYS	-	expression tag	UNP P38827
N	743	ASP	-	expression tag	UNP P38827
N	744	HIS	-	expression tag	UNP P38827
N	745	ASP	-	expression tag	UNP P38827
N	746	ILE	-	expression tag	UNP P38827
N	747	ASP	-	expression tag	UNP P38827
N	748	TYR	-	expression tag	UNP P38827
N	749	LYS	-	expression tag	UNP P38827
N	750	ASP	-	expression tag	UNP P38827
N	751	ASP	-	expression tag	UNP P38827
N	752	ASP	-	expression tag	UNP P38827
N	753	ASP	-	expression tag	UNP P38827
N	754	LYS	-	expression tag	UNP P38827
N	755	GLU	-	expression tag	UNP P38827
N	756	ASN	-	expression tag	UNP P38827
N	757	LEU	-	expression tag	UNP P38827
N	758	TYR	-	expression tag	UNP P38827
N	759	PHE	-	expression tag	UNP P38827
N	760	GLN	-	expression tag	UNP P38827
N	761	GLY	-	expression tag	UNP P38827

- Molecule 11 is a protein called COMPASS component BRE2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	O	315	2595	1667	428	491	9	0	0

- Molecule 12 is a protein called COMPASS component SDC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	P	42	336	212	60	63	1	0	0
12	Q	29	225	142	40	42	1	0	0

- Molecule 13 is a protein called COMPASS component SPP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	R	129	966	605	164	189	8	0	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-37	MET	-	expression tag	UNP Q03012
R	-36	TRP	-	expression tag	UNP Q03012
R	-35	SER	-	expression tag	UNP Q03012
R	-34	HIS	-	expression tag	UNP Q03012
R	-33	PRO	-	expression tag	UNP Q03012
R	-32	GLN	-	expression tag	UNP Q03012
R	-31	PHE	-	expression tag	UNP Q03012
R	-30	GLU	-	expression tag	UNP Q03012
R	-29	LYS	-	expression tag	UNP Q03012
R	-28	GLY	-	expression tag	UNP Q03012
R	-27	GLY	-	expression tag	UNP Q03012
R	-26	GLY	-	expression tag	UNP Q03012
R	-25	SER	-	expression tag	UNP Q03012
R	-24	GLY	-	expression tag	UNP Q03012
R	-23	GLY	-	expression tag	UNP Q03012
R	-22	GLY	-	expression tag	UNP Q03012
R	-21	SER	-	expression tag	UNP Q03012
R	-20	GLY	-	expression tag	UNP Q03012
R	-19	GLY	-	expression tag	UNP Q03012
R	-18	SER	-	expression tag	UNP Q03012
R	-17	SER	-	expression tag	UNP Q03012
R	-16	ALA	-	expression tag	UNP Q03012
R	-15	TRP	-	expression tag	UNP Q03012
R	-14	SER	-	expression tag	UNP Q03012
R	-13	HIS	-	expression tag	UNP Q03012
R	-12	PRO	-	expression tag	UNP Q03012
R	-11	GLN	-	expression tag	UNP Q03012
R	-10	PHE	-	expression tag	UNP Q03012
R	-9	GLU	-	expression tag	UNP Q03012
R	-8	LYS	-	expression tag	UNP Q03012
R	-7	GLY	-	expression tag	UNP Q03012
R	-6	SER	-	expression tag	UNP Q03012
R	-5	GLU	-	expression tag	UNP Q03012
R	-4	ASN	-	expression tag	UNP Q03012
R	-3	LEU	-	expression tag	UNP Q03012
R	-2	TYR	-	expression tag	UNP Q03012
R	-1	PHE	-	expression tag	UNP Q03012

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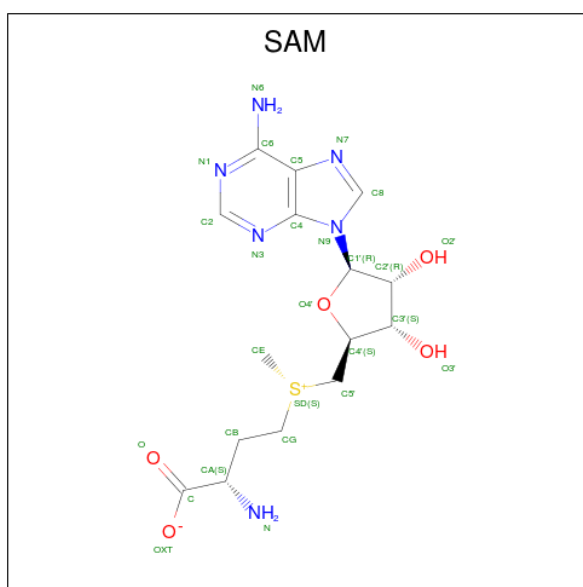
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Chain	Residue	Modelled	Actual	Comment	Reference
R	0	GLN	-	expression tag	UNP Q03012
R	1	GLY	-	expression tag	UNP Q03012

- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
14	N	1	Total Zn 1 1	0

- Molecule 15 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: C₁₅H₂₂N₆O₅S).



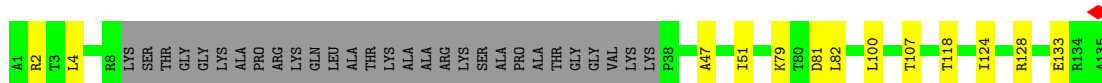
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
15	N	1	27	15	6	5	1	0

3 Residue-property plots [i](#)

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

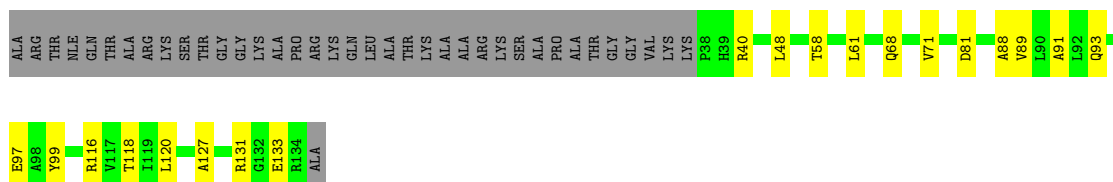
- Molecule 1: Histone H3.2

Chain A: 



- Molecule 1: Histone H3.2

Chain E: 



- Molecule 2: Histone H4

Chain B: 



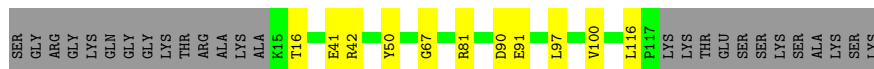
- Molecule 2: Histone H4

Chain F: 



- Molecule 3: Histone H2A type 1

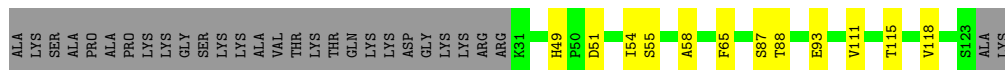
Chain C: 



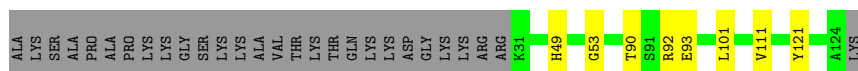
• Molecule 3: Histone H2A type 1



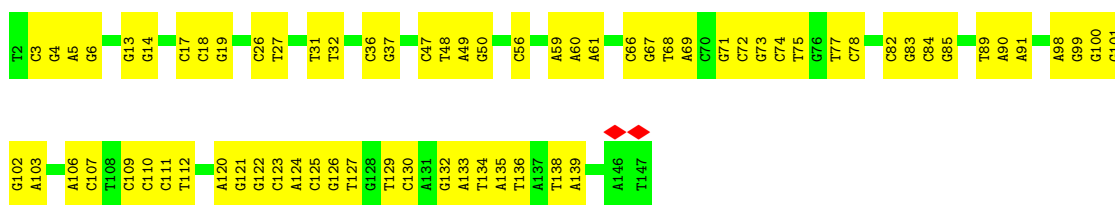
• Molecule 4: Histone H2B 1.1



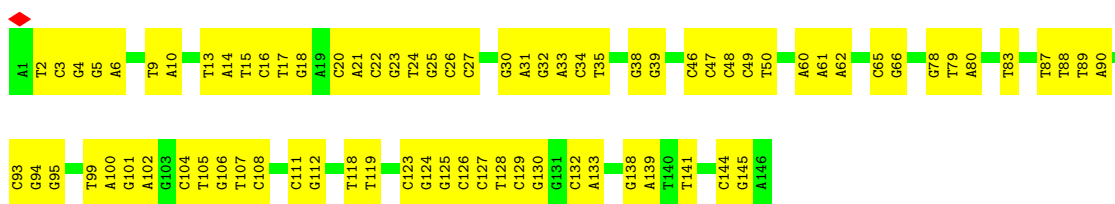
• Molecule 4: Histone H2B 1.1



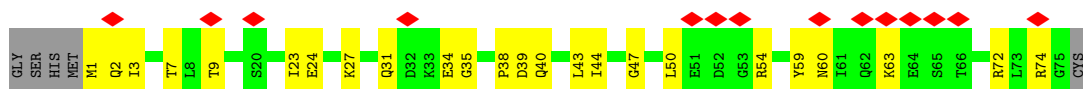
• Molecule 5: 601 DNA (146-MER)



• Molecule 6: 601 DNA (146-MER)



• Molecule 7: Ubiquitin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	650847	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)	-1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.104	Depositor
Minimum map value	-0.055	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0128	Depositor
Map size (Å)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NLE, SAM, ZN

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	0.30	0/855	0.43	0/1140
1	E	0.31	0/796	0.43	0/1065
2	B	0.33	0/653	0.46	0/873
2	F	0.32	0/651	0.45	0/873
3	C	0.31	0/805	0.43	0/1088
3	G	0.30	0/828	0.44	0/1117
4	D	0.30	0/738	0.44	0/994
4	H	0.30	0/743	0.44	0/1001
5	I	0.57	0/3333	0.95	0/5137
6	J	0.56	0/3381	0.92	0/5221
7	K	0.25	0/603	0.50	0/811
8	L	0.26	0/2417	0.51	0/3281
9	M	0.28	0/3259	0.48	0/4438
10	N	0.26	0/1732	0.44	0/2317
11	O	0.27	0/2651	0.52	0/3575
12	P	0.25	0/341	0.51	0/463
12	Q	0.32	0/227	0.62	0/307
13	R	0.29	0/983	0.56	0/1335
All	All	0.38	0/24996	0.65	0/35036

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	871	0	918	9	0
1	E	802	0	843	14	0
2	B	646	0	687	8	0
2	F	644	0	690	12	0
3	C	795	0	846	10	0
3	G	818	0	877	10	0
4	D	727	0	747	10	0
4	H	732	0	752	9	0
5	I	2975	0	1639	47	0
6	J	3011	0	1639	55	0
7	K	597	0	626	17	0
8	L	2367	0	2330	63	0
9	M	3183	0	3085	87	0
10	N	1710	0	1723	32	0
11	O	2595	0	2506	68	0
12	P	336	0	345	6	0
12	Q	225	0	226	9	0
13	R	966	0	827	28	0
14	N	1	0	0	0	0
15	N	27	0	22	2	0
All	All	24028	0	21328	445	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 10.

The worst 5 of 445 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)
11:O:130:GLU:HA	11:O:241:LEU:HB2	1.67	0.76
8:L:9:GLY:HA3	8:L:309:CYS:HB3	1.72	0.71
11:O:66:TYR:HA	11:O:323:PHE:O	1.91	0.70
8:L:97:ALA:HB1	8:L:116:MET:HB2	1.73	0.69
8:L:290:VAL:HA	8:L:304:ALA:HA	1.73	0.69

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	99/135 (73%)	92 (93%)	7 (7%)	0	100	100
1	E	93/135 (69%)	86 (92%)	7 (8%)	0	100	100
2	B	79/102 (78%)	77 (98%)	2 (2%)	0	100	100
2	F	78/102 (76%)	76 (97%)	2 (3%)	0	100	100
3	C	101/129 (78%)	99 (98%)	2 (2%)	0	100	100
3	G	104/129 (81%)	104 (100%)	0	0	100	100
4	D	91/122 (75%)	87 (96%)	4 (4%)	0	100	100
4	H	92/122 (75%)	89 (97%)	3 (3%)	0	100	100
7	K	73/80 (91%)	71 (97%)	2 (3%)	0	100	100
8	L	302/315 (96%)	283 (94%)	19 (6%)	0	100	100
9	M	387/426 (91%)	356 (92%)	31 (8%)	0	100	100
10	N	210/358 (59%)	190 (90%)	20 (10%)	0	100	100
11	O	297/505 (59%)	281 (95%)	16 (5%)	0	100	100
12	P	40/175 (23%)	36 (90%)	4 (10%)	0	100	100
12	Q	25/175 (14%)	24 (96%)	1 (4%)	0	100	100
13	R	125/391 (32%)	111 (89%)	14 (11%)	0	100	100
All	All	2196/3401 (65%)	2062 (94%)	134 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	88/107 (82%)	88 (100%)	0	100	100
1	E	83/107 (78%)	83 (100%)	0	100	100
2	B	66/78 (85%)	66 (100%)	0	100	100
2	F	67/78 (86%)	67 (100%)	0	100	100
3	C	82/101 (81%)	82 (100%)	0	100	100
3	G	84/101 (83%)	84 (100%)	0	100	100
4	D	80/102 (78%)	80 (100%)	0	100	100
4	H	80/102 (78%)	80 (100%)	0	100	100
7	K	68/72 (94%)	68 (100%)	0	100	100
8	L	272/279 (98%)	271 (100%)	1 (0%)	91	95
9	M	359/388 (92%)	358 (100%)	1 (0%)	92	96
10	N	179/318 (56%)	179 (100%)	0	100	100
11	O	282/449 (63%)	282 (100%)	0	100	100
12	P	38/162 (24%)	38 (100%)	0	100	100
12	Q	25/162 (15%)	25 (100%)	0	100	100
13	R	91/355 (26%)	91 (100%)	0	100	100
All	All	1944/2961 (66%)	1942 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	L	104	PHE
9	M	236	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
9	M	361	ASN
10	N	931	ASN
10	N	903	ASN
11	O	116	GLN
8	L	239	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

5 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	NLE	A	120	1	6,7,8	0.46	0	2,7,9	0.43	0
1	NLE	E	90	1	6,7,8	0.54	0	2,7,9	0.47	0
1	NLE	A	90	1	6,7,8	0.55	0	2,7,9	0.46	0
1	NLE	E	120	1	6,7,8	0.44	0	2,7,9	0.40	0
1	NLE	A	4	1	6,7,8	0.49	0	2,7,9	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	NLE	A	120	1	-	0/5/6/8	-
1	NLE	E	90	1	-	0/5/6/8	-
1	NLE	A	90	1	-	3/5/6/8	-
1	NLE	E	120	1	-	0/5/6/8	-
1	NLE	A	4	1	-	0/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	90	NLE	CA-CB-CG-CD
1	A	90	NLE	C-CA-CB-CG
1	A	90	NLE	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	120	NLE	1	0
1	A	4	NLE	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	SAM	N	1102	-	24,29,29	0.66	0	23,42,42	0.85	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	SAM	N	1102	-	-	5/12/33/33	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
15	N	1102	SAM	C5-C6-N6	2.26	123.79	120.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

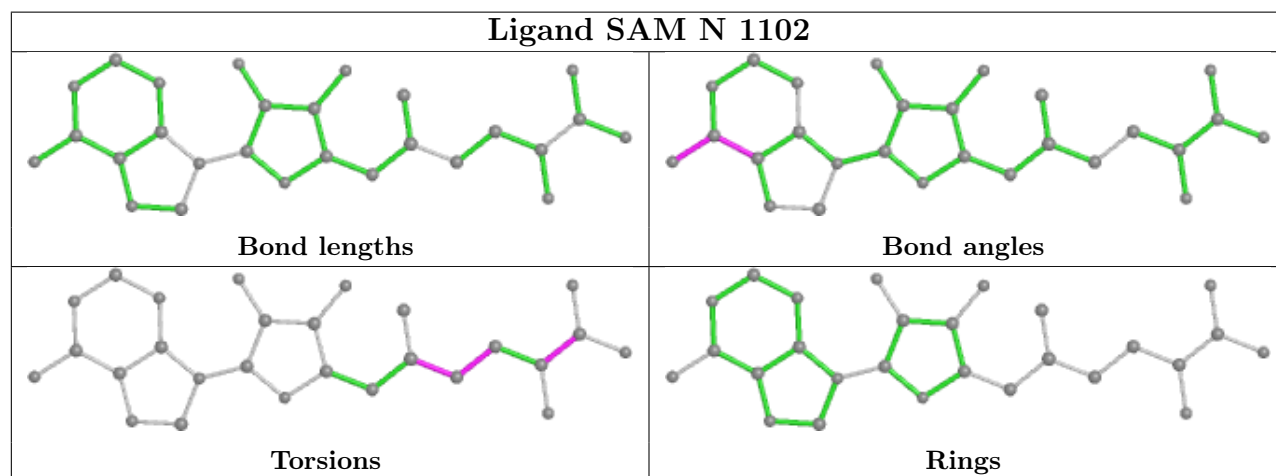
Mol	Chain	Res	Type	Atoms
15	N	1102	SAM	CA-CB-CG-SD
15	N	1102	SAM	CB-CG-SD-CE
15	N	1102	SAM	O-C-CA-CB
15	N	1102	SAM	OXT-C-CA-CB
15	N	1102	SAM	CB-CG-SD-C5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	N	1102	SAM	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

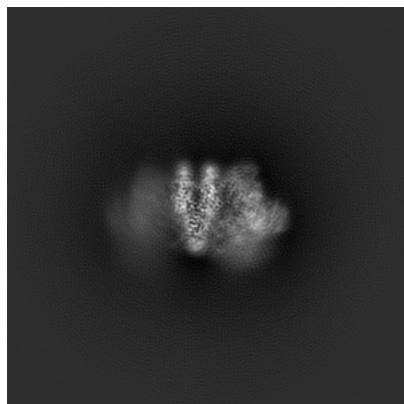
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21157. These allow visual inspection of the internal detail of the map and identification of artifacts.

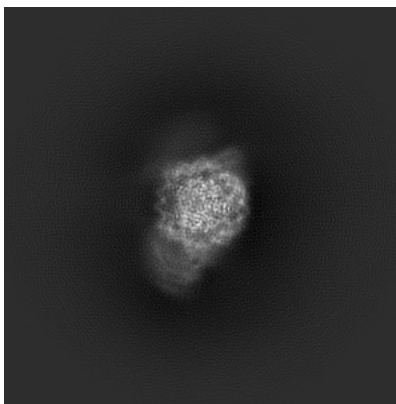
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

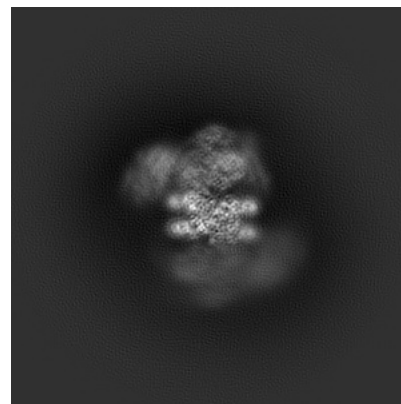
6.1.1 Primary map



X

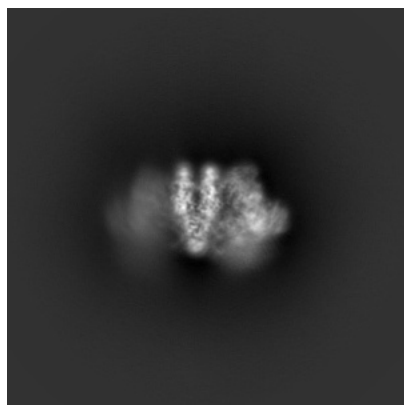


Y

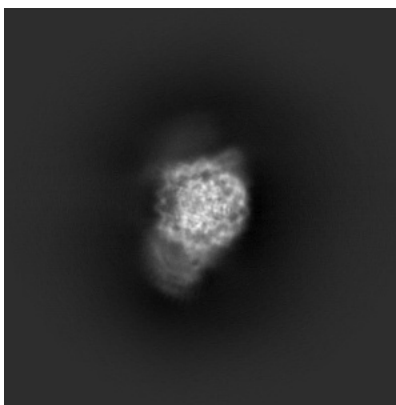


Z

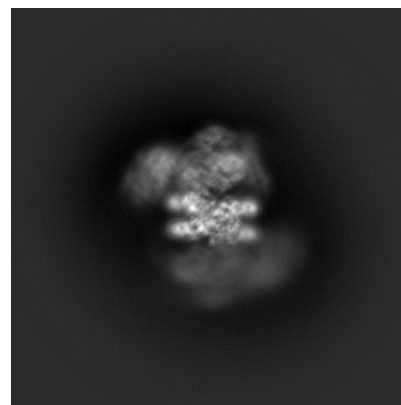
6.1.2 Raw map



X



Y

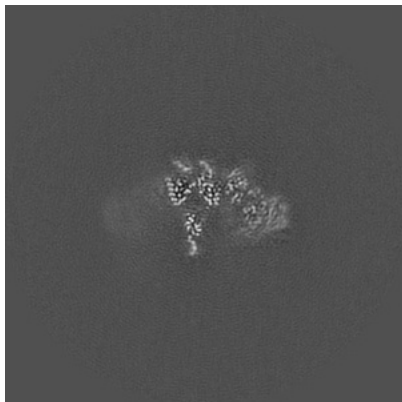


Z

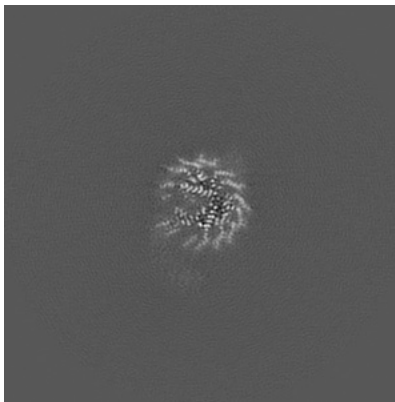
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

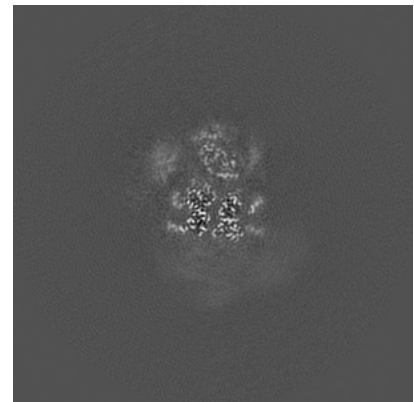
6.2.1 Primary map



X Index: 200

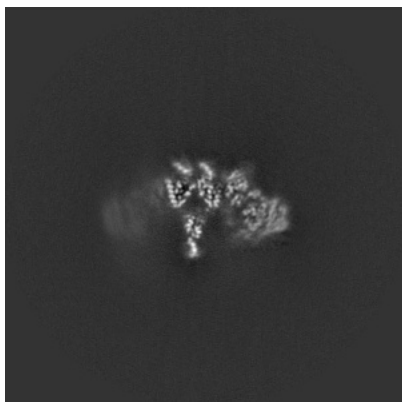


Y Index: 200

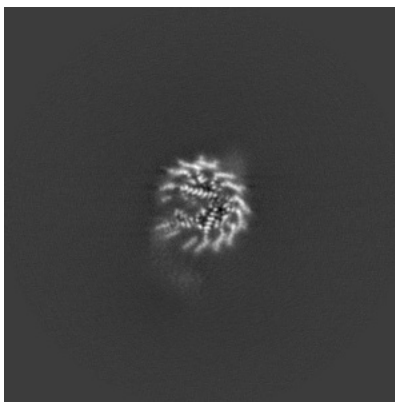


Z Index: 200

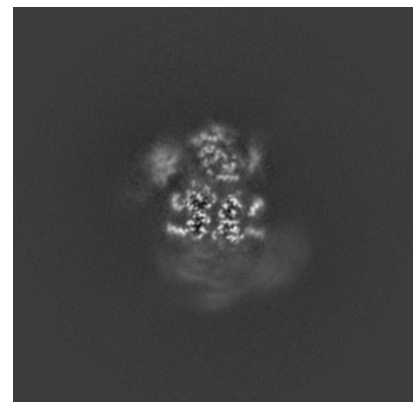
6.2.2 Raw map



X Index: 200



Y Index: 200

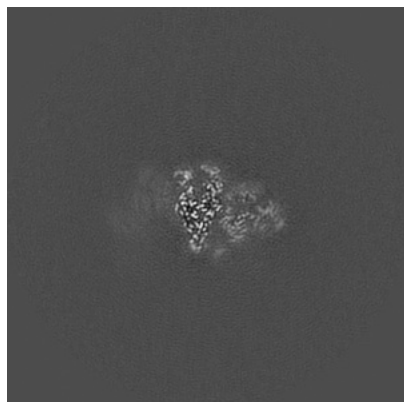


Z Index: 200

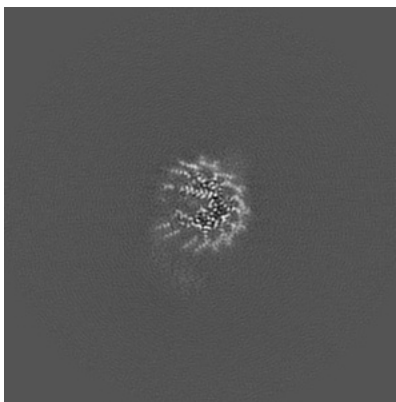
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

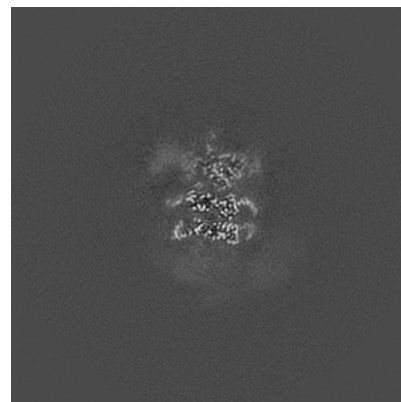
6.3.1 Primary map



X Index: 186

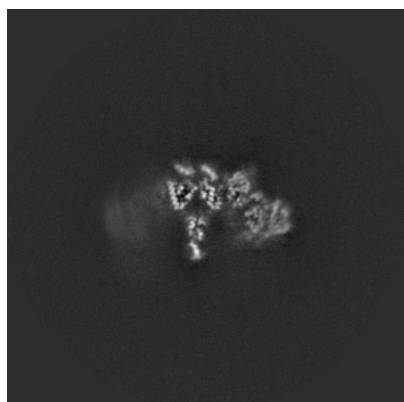


Y Index: 201

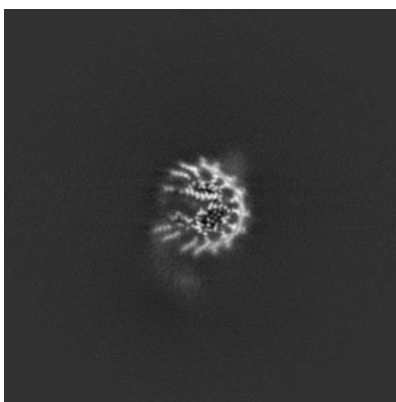


Z Index: 208

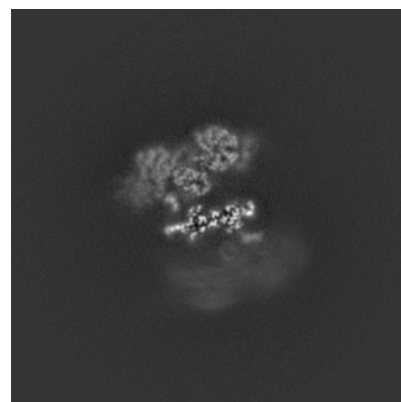
6.3.2 Raw map



X Index: 201



Y Index: 202



Z Index: 186

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

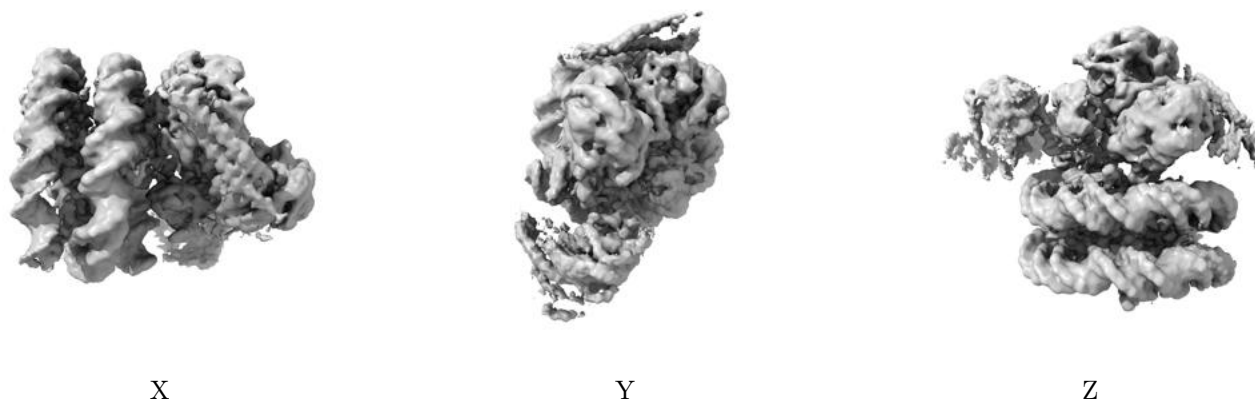
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0128. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

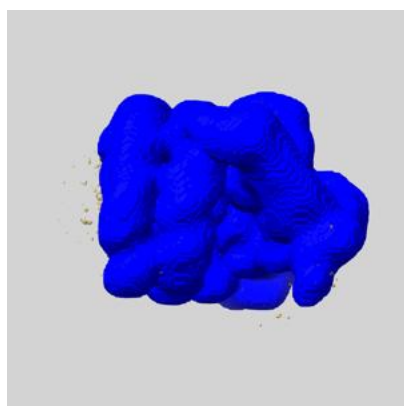
6.5 Mask visualisation [i](#)

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

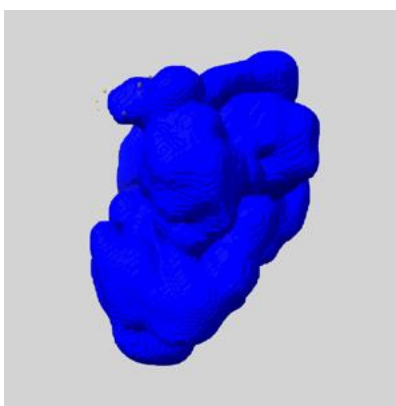
A mask typically either:

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

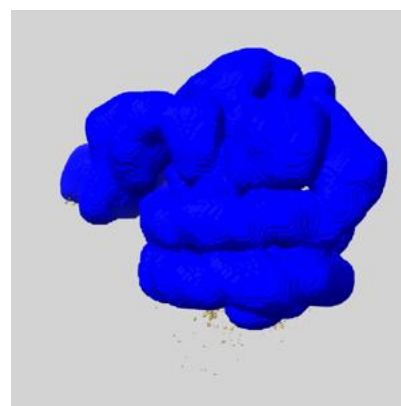
6.5.1 emd_21157_msk_1.map [i](#)



X



Y

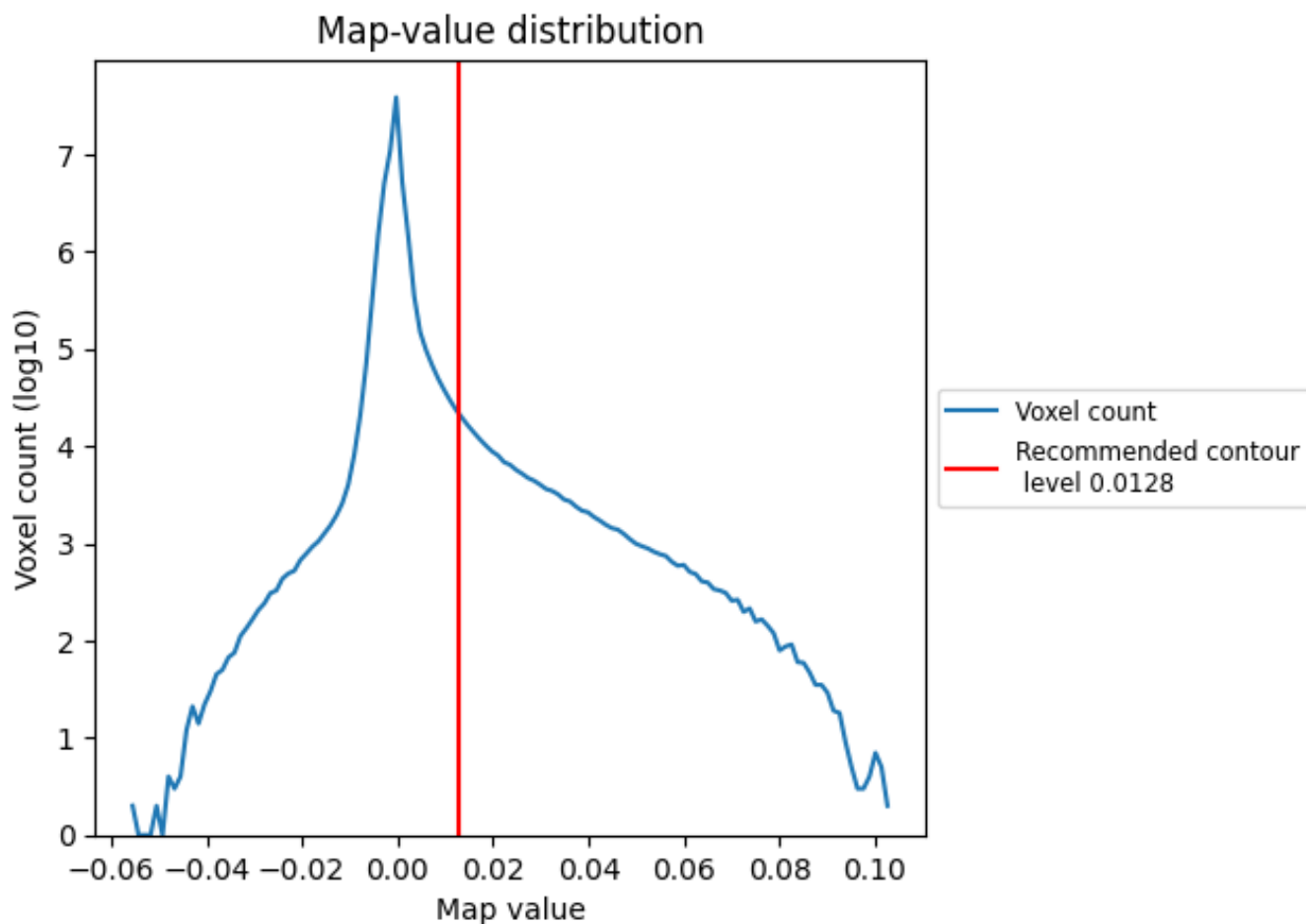


Z

7 Map analysis [i](#)

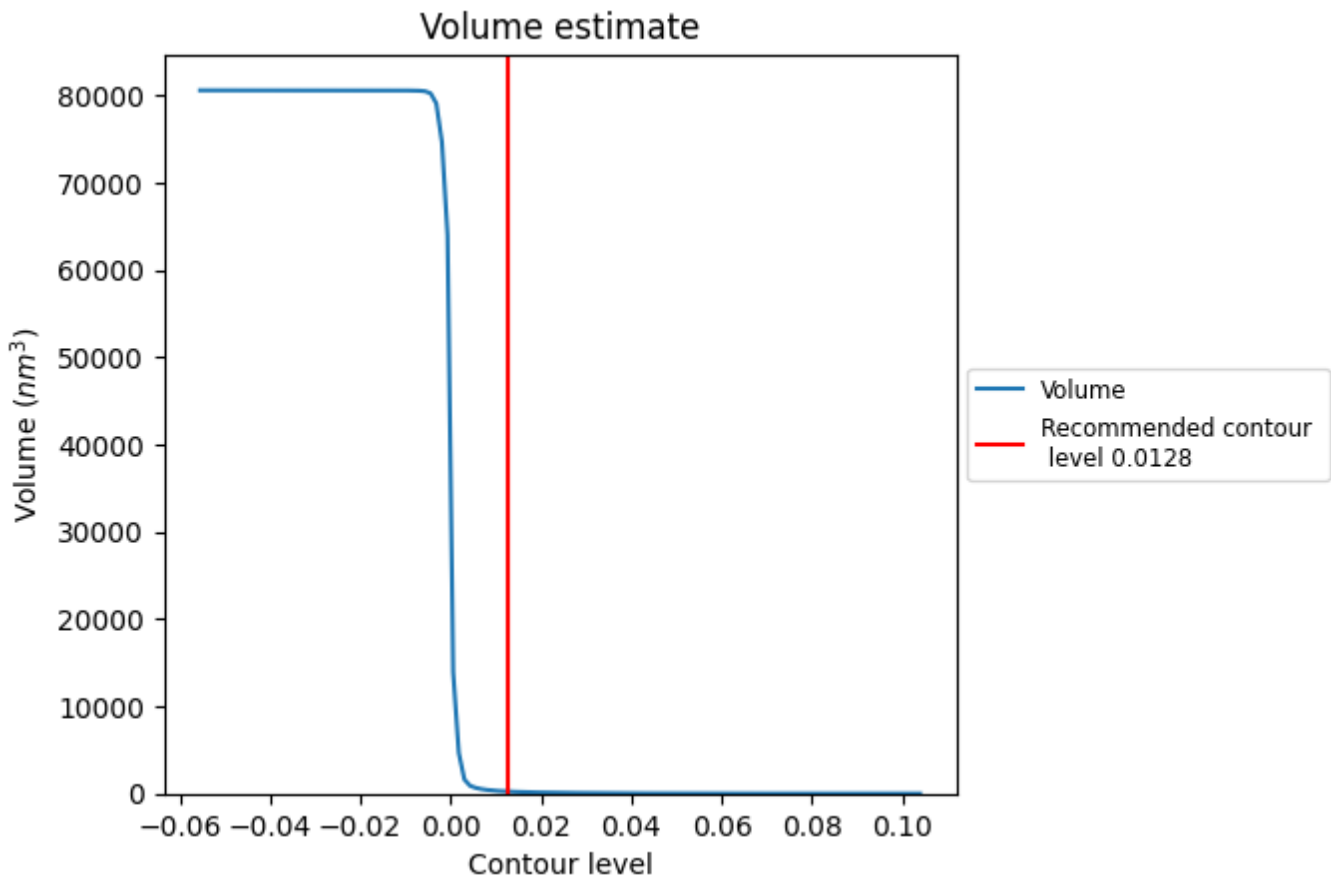
This section contains the results of statistical analysis of the map.

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.

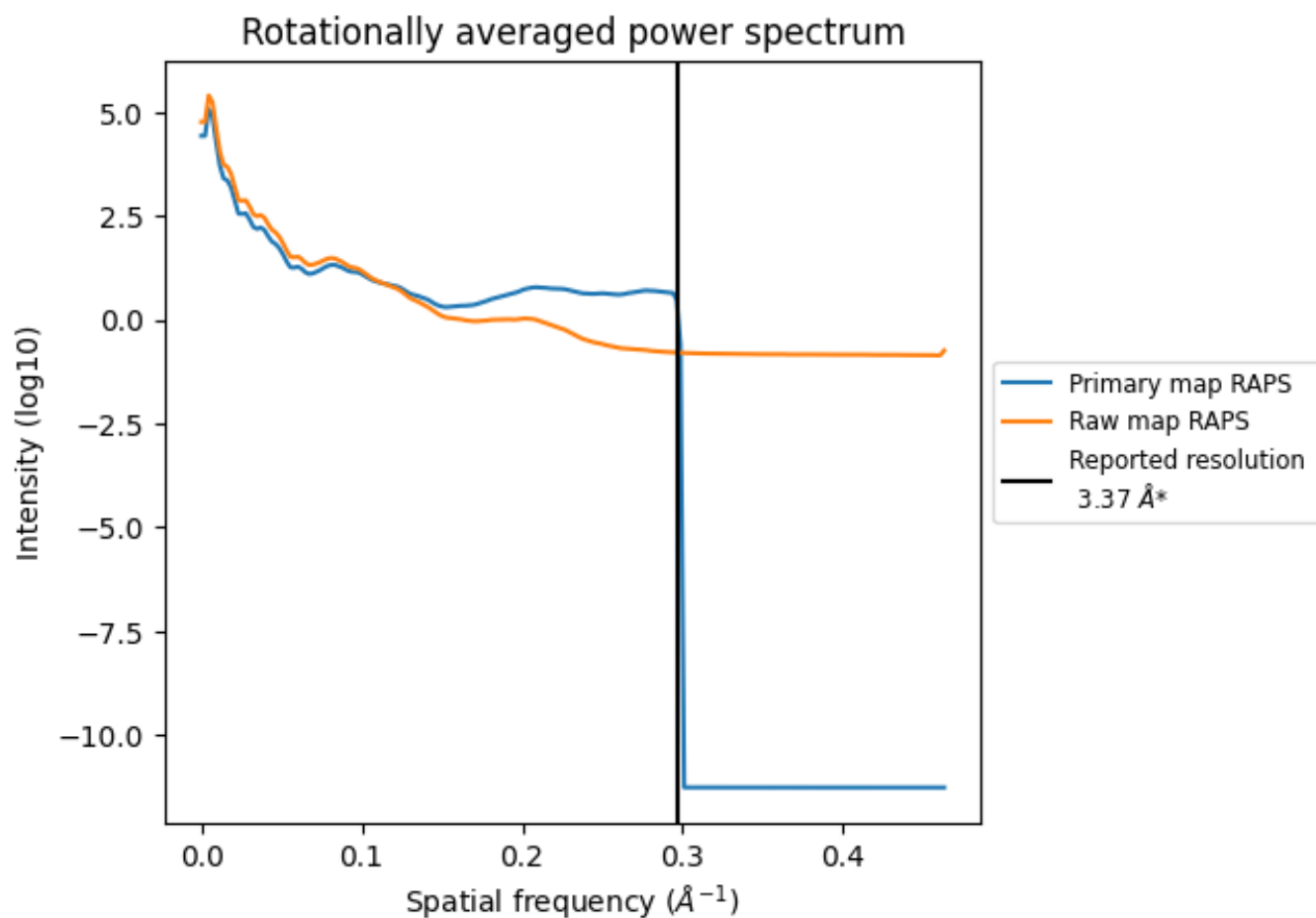
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 231 nm³; this corresponds to an approximate mass of 209 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 [i](#)

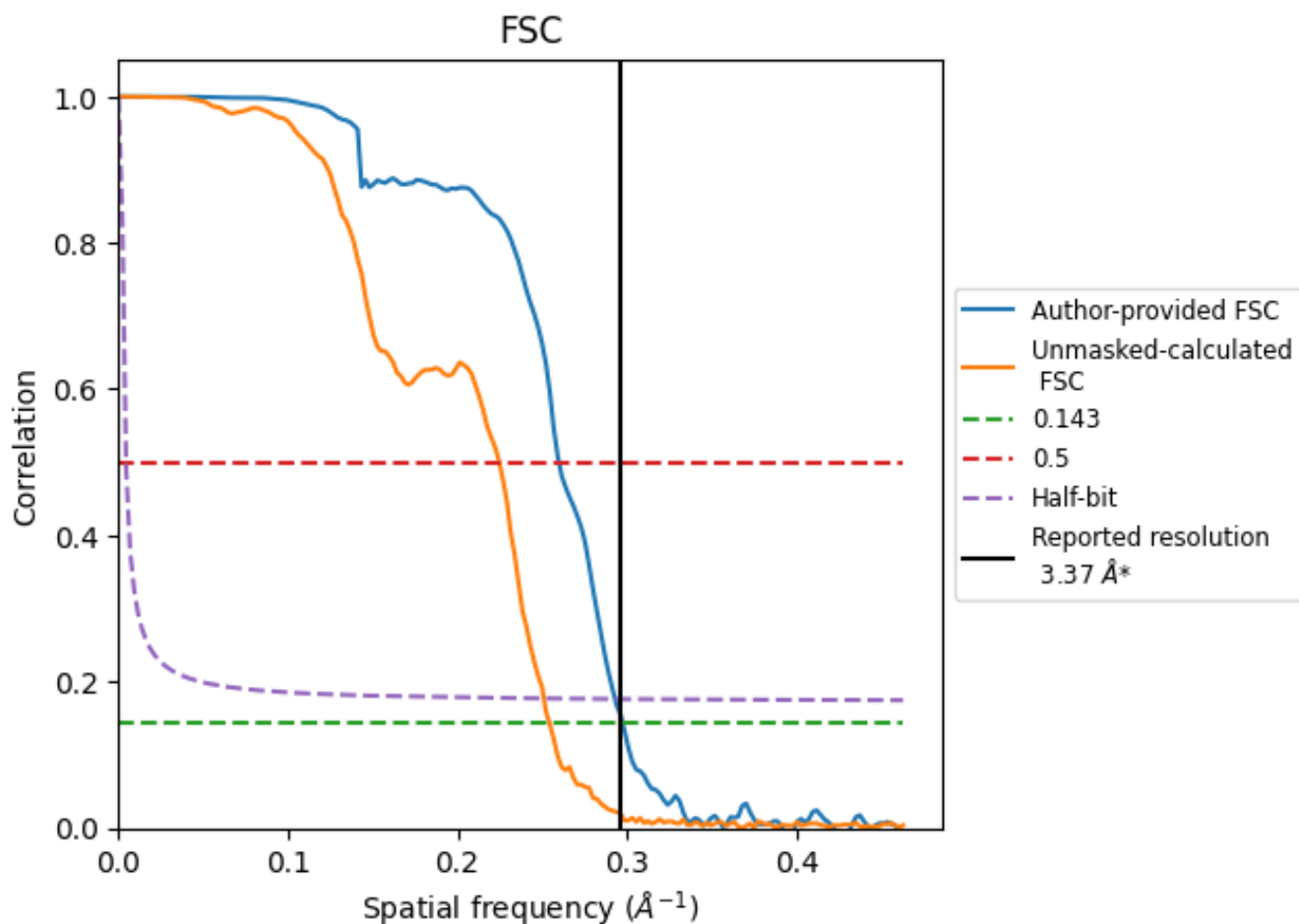


*Reported resolution corresponds to spatial frequency of 0.297 \AA^{-1}

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 0.297 Å⁻¹

8.2 Resolution estimates [i](#)

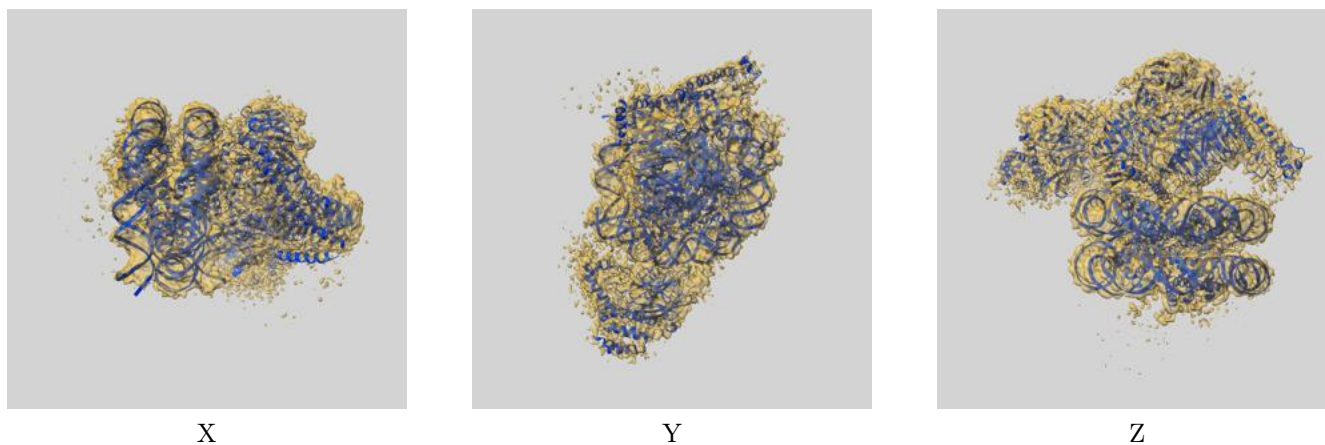
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.37	-	-
Author-provided FSC curve	3.36	3.85	3.41
Unmasked-calculated*	3.93	4.45	3.98

*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 3.93 differs from the reported value 3.37 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21157 and PDB model 6VEN. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



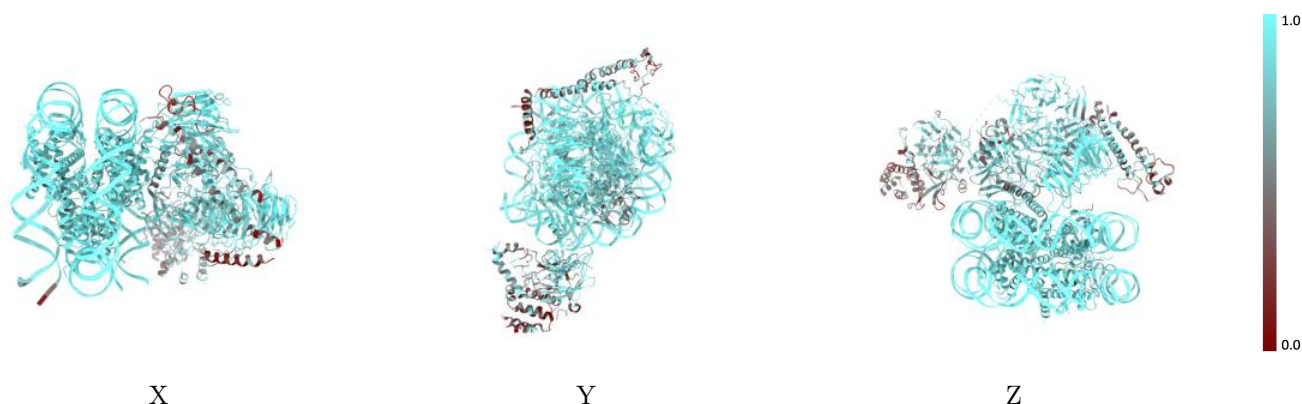
The images above show the 3D surface view of the map at the recommended contour level 0.0128 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



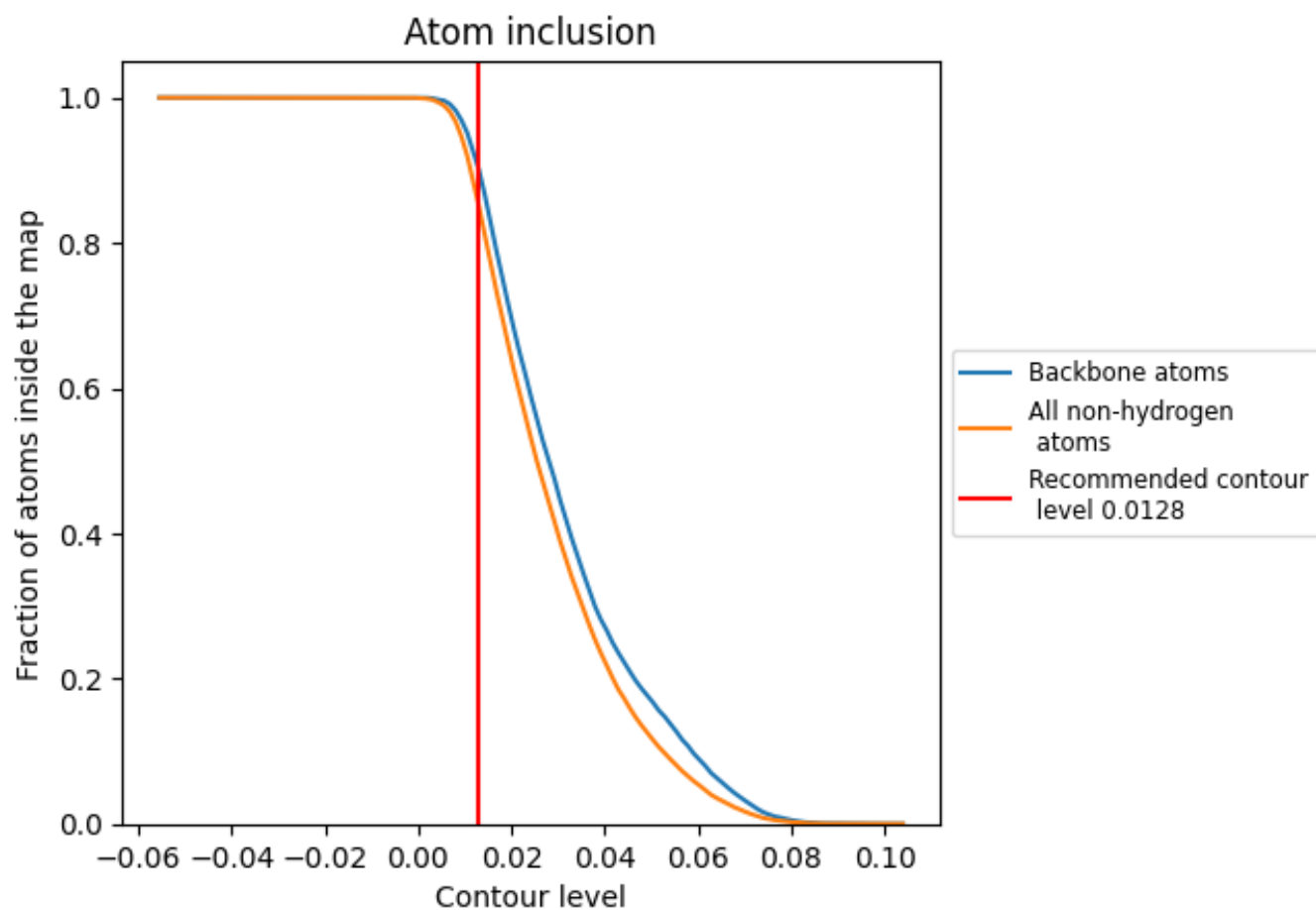
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0128).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.0128) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8566	 0.4490
A	 0.9581	 0.5560
B	 0.9629	 0.5530
C	 0.9558	 0.5530
D	 0.9535	 0.5430
E	 0.9559	 0.5500
F	 0.9579	 0.5540
G	 0.9470	 0.5550
H	 0.9497	 0.5490
I	 0.9667	 0.4590
J	 0.9734	 0.4620
K	 0.6071	 0.3220
L	 0.9046	 0.4550
M	 0.9139	 0.4920
N	 0.7645	 0.4600
O	 0.6048	 0.2620
P	 0.3354	 0.2150
Q	 0.3864	 0.2430
R	 0.5110	 0.2680

