



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:46 AM UTC

PDB ID : 9GD0 / pdb_00009gd0
EMDB ID : EMD-51238
Title : Structure of a hexasome-nucleosome complex with a dyad-to-dyad distance of 103 bp.
Authors : Engholm, M.; Roske, J.J.; Oberbeckmann, E.; Dienemann, C.; Lidschreiber, M.; Cramer, P.; Farnung, L.
Deposited on : 2024-08-04
Resolution : 2.80 Å(reported)

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.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

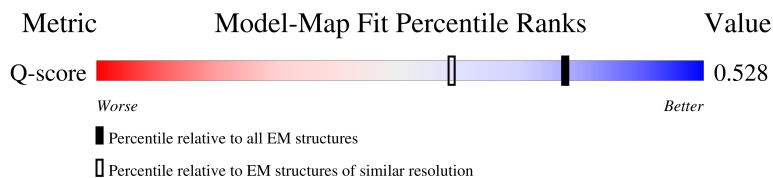
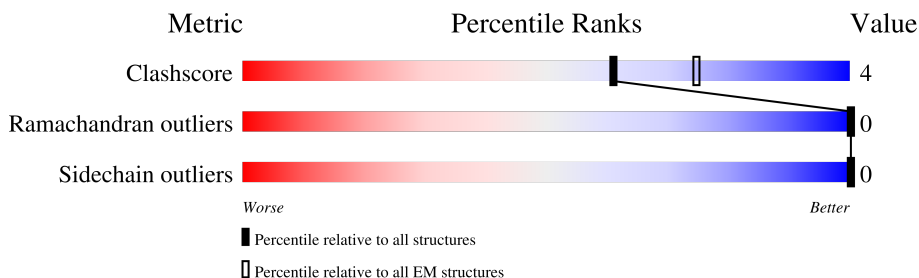
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	136	 68% 30%
1	E	136	 68% 30%
1	K	136	 51% 46%
1	O	136	 65% 5% 29%

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Mol	Chain	Length	Quality of chain
2	B	103	 69%7%24%
2	F	103	 72%•25%
2	L	103	 •68%•28%
2	P	103	 6%67%11%22%
3	C	130	 5%82%•16%
3	G	130	 •76%•21%
3	M	130	 •78%•21%
4	D	123	 •71%•28%
4	H	123	 •72%•26%
4	N	123	 •72%•27%
5	I	250	 8%65%35%
6	J	250	 10%60%40%•

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 20207 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
1	A	95	Total	C	N	O	S	0	0
			784	495	150	136	3		
1	E	95	Total	C	N	O	S	0	0
			784	495	150	136	3		
1	K	73	Total	C	N	O	S	0	0
			592	376	109	104	3		
1	O	96	Total	C	N	O	S	0	0
			795	501	154	137	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	GLY	conflict	UNP P84233
E	102	ALA	GLY	conflict	UNP P84233
K	102	ALA	GLY	conflict	UNP P84233
O	102	ALA	GLY	conflict	UNP P84233

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	78	Total	C	N	O	S	0	0
			622	393	120	108	1		
2	F	77	Total	C	N	O	S	0	0
			614	389	119	105	1		
2	L	74	Total	C	N	O	S	0	0
			591	371	116	103	1		
2	P	80	Total	C	N	O	S	0	0
			644	408	125	110	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	109	Total	C	N	O	0	0
			840	528	163	149		
3	G	103	Total	C	N	O	0	0
			795	501	155	139		
3	M	103	Total	C	N	O	0	0
			795	501	155	139		

There are 6 discrepancies between the modelled and reference sequences:

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

- Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	89	Total	C	N	O	S	0	0
			694	438	122	132	2		
4	H	91	Total	C	N	O	S	0	0
			708	447	125	134	2		
4	N	90	Total	C	N	O	S	0	0
			699	441	123	133	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	initiating methionine	UNP P02281
D	29	THR	SER	conflict	UNP P02281
H	0	MET	-	initiating methionine	UNP P02281
H	29	THR	SER	conflict	UNP P02281
N	0	MET	-	initiating methionine	UNP P02281
N	29	THR	SER	conflict	UNP P02281

- Molecule 5 is a DNA chain called DNA (250-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	250	Total	C	N	O	P	0	0
			5090	2419	917	1504	250		

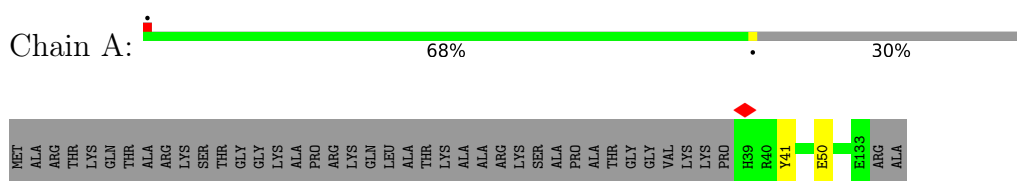
- Molecule 6 is a DNA chain called DNA (250-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	J	250	5160	2441	973	1496	250	0	0

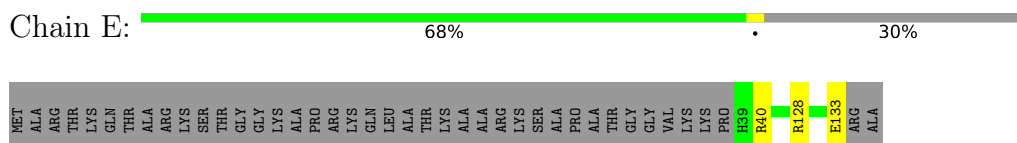
3 Residue-property plots [i](#)

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.

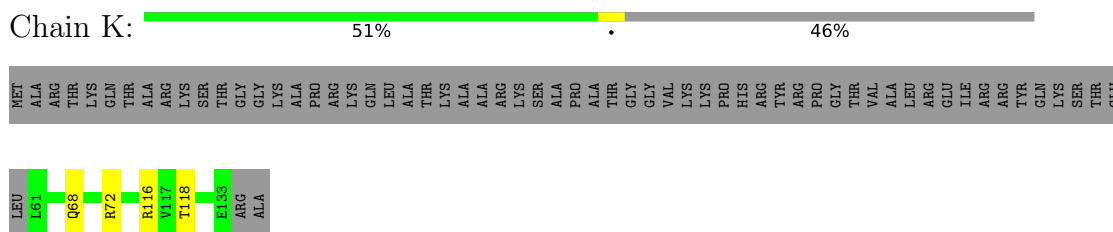
- Molecule 1: Histone H3.2



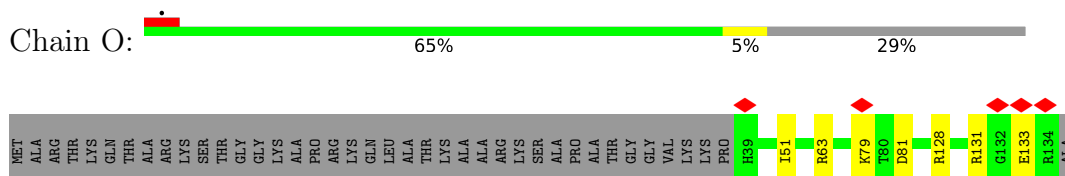
- Molecule 1: Histone H3.2



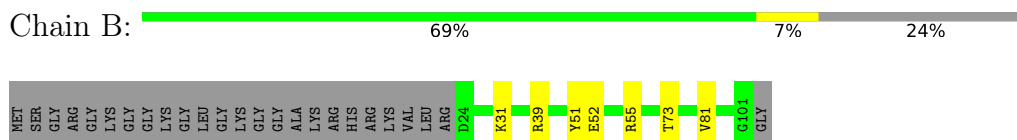
- Molecule 1: Histone H3.2



- Molecule 1: Histone H3.2

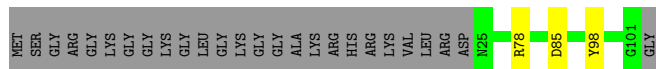


- Molecule 2: Histone H4



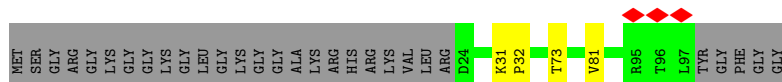
- Molecule 2: Histone H4

Chain F:  72% 25%



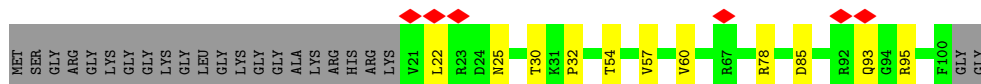
- Molecule 2: Histone H4

Chain L:  68% 28%



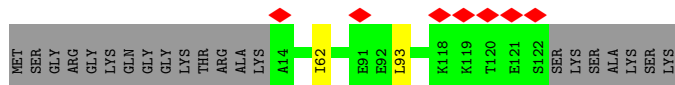
- Molecule 2: Histone H4

Chain P:  67% 11% 22% 6%



- Molecule 3: Histone H2A type 1

Chain C:  82% 16% 5%



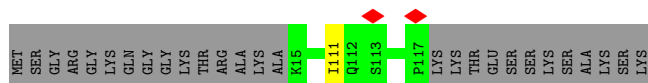
- Molecule 3: Histone H2A type 1

Chain G:  76% 21%



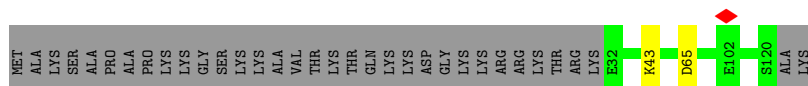
- Molecule 3: Histone H2A type 1

Chain M:  78% 21%

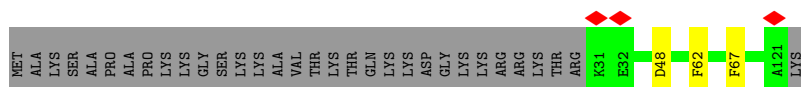


- Molecule 4: Histone H2B 1.1

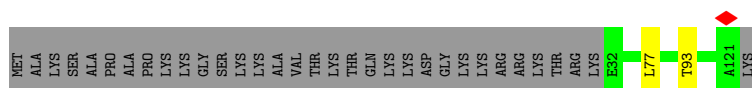
Chain D:  71% 28%



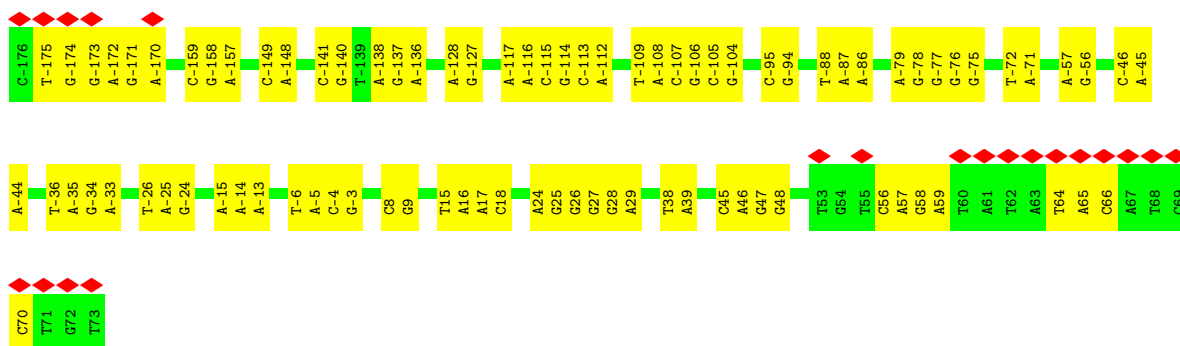
• Molecule 4: Histone H2B 1.1



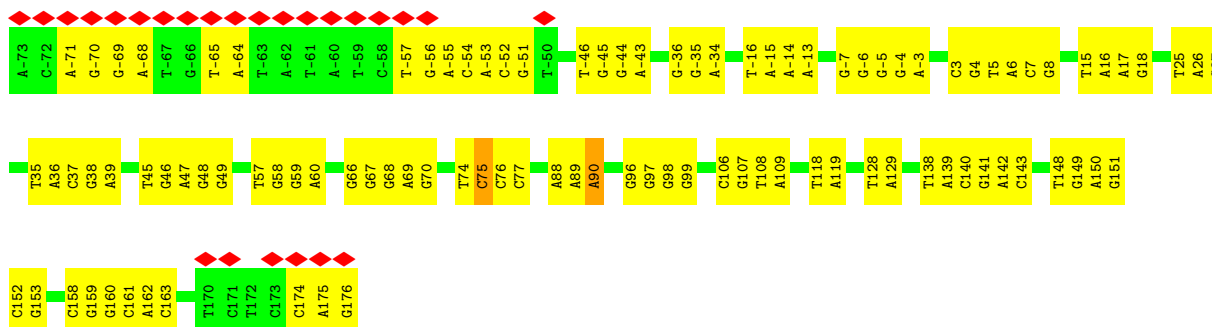
• Molecule 4: Histone H2B 1.1



• Molecule 5: DNA (250-MER)



• Molecule 6: DNA (250-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	143477	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 ($e^-/\text{\AA}^2$)	41.1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	64.582	Depositor
Minimum map value	-20.900	Depositor
Average map value	-0.005	Depositor
Map value standard deviation	1.153	Depositor
Recommended contour level	8	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	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	0.19	0/795	0.39	0/1067
1	E	0.19	0/795	0.40	0/1067
1	K	0.22	0/599	0.40	0/804
1	O	0.20	0/806	0.38	0/1081
2	B	0.22	0/629	0.41	0/843
2	F	0.22	0/621	0.41	0/832
2	L	0.23	0/596	0.41	0/799
2	P	0.19	0/651	0.39	0/873
3	C	0.17	0/850	0.36	0/1147
3	G	0.17	0/805	0.36	0/1088
3	M	0.19	0/805	0.39	0/1088
4	D	0.18	0/705	0.43	0/951
4	H	0.20	0/719	0.41	0/969
4	N	0.22	0/710	0.42	0/958
5	I	0.31	0/5701	0.63	2/8788 (0.0%)
6	J	0.30	0/5797	0.65	4/8954 (0.0%)
All	All	0.26	0/21584	0.55	6/31309 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	90	DA	C2'-C3'-O3'	-7.29	100.57	111.50
6	J	76	DC	C2'-C3'-O3'	-5.93	102.60	111.50
5	I	-57	DA	C2'-C3'-O3'	-5.89	102.66	111.50
5	I	-56	DG	C2'-C3'-O3'	-5.87	102.69	111.50
6	J	75	DC	C2'-C3'-O3'	-5.80	102.81	111.50

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	784	0	820	2	0
1	E	784	0	820	2	0
1	K	592	0	621	2	0
1	O	795	0	833	5	0
2	B	622	0	660	4	0
2	F	614	0	656	2	0
2	L	591	0	636	2	0
2	P	644	0	690	6	0
3	C	840	0	895	1	0
3	G	795	0	846	3	0
3	M	795	0	846	1	0
4	D	694	0	709	2	0
4	H	708	0	727	3	0
4	N	699	0	714	1	0
5	I	5090	0	2808	60	0
6	J	5160	0	2804	71	0
All	All	20207	0	16085	160	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.

The worst 5 of 160 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)
4:N:77:LEU:HD13	4:N:93:THR:HG23	1.76	0.68
1:A:50:GLU:OE2	2:B:39:ARG:NH1	2.27	0.67
6:J:150:DA:H2''	6:J:151:DG:C8	2.37	0.60
5:I:-86:DA:H4'	1:O:63:ARG:HD3	1.84	0.59
6:J:140:DC:H2''	6:J:141:DG:C8	2.39	0.58

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	93/136 (68%)	93 (100%)	0	0	100	100
1	E	93/136 (68%)	93 (100%)	0	0	100	100
1	K	71/136 (52%)	71 (100%)	0	0	100	100
1	O	94/136 (69%)	93 (99%)	1 (1%)	0	100	100
2	B	76/103 (74%)	76 (100%)	0	0	100	100
2	F	75/103 (73%)	74 (99%)	1 (1%)	0	100	100
2	L	72/103 (70%)	72 (100%)	0	0	100	100
2	P	78/103 (76%)	78 (100%)	0	0	100	100
3	C	107/130 (82%)	105 (98%)	2 (2%)	0	100	100
3	G	101/130 (78%)	100 (99%)	1 (1%)	0	100	100
3	M	101/130 (78%)	100 (99%)	1 (1%)	0	100	100
4	D	87/123 (71%)	87 (100%)	0	0	100	100
4	H	89/123 (72%)	89 (100%)	0	0	100	100
4	N	88/123 (72%)	88 (100%)	0	0	100	100
All	All	1225/1715 (71%)	1219 (100%)	6 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	83/111 (75%)	83 (100%)	0	100	100
1	E	83/111 (75%)	83 (100%)	0	100	100
1	K	63/111 (57%)	63 (100%)	0	100	100
1	O	84/111 (76%)	84 (100%)	0	100	100
2	B	64/79 (81%)	64 (100%)	0	100	100
2	F	63/79 (80%)	63 (100%)	0	100	100
2	L	62/79 (78%)	62 (100%)	0	100	100
2	P	67/79 (85%)	67 (100%)	0	100	100
3	C	87/102 (85%)	87 (100%)	0	100	100
3	G	82/102 (80%)	82 (100%)	0	100	100
3	M	82/102 (80%)	82 (100%)	0	100	100
4	D	76/103 (74%)	76 (100%)	0	100	100
4	H	77/103 (75%)	77 (100%)	0	100	100
4	N	76/103 (74%)	76 (100%)	0	100	100
All	All	1049/1375 (76%)	1049 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
4	N	81	ASN
3	M	24	GLN
2	F	27	GLN
1	E	93	GLN
2	L	25	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

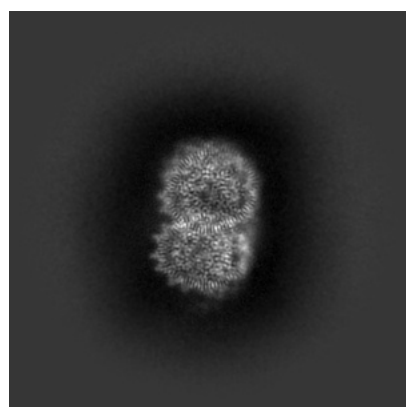
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51238. These allow visual inspection of the internal detail of the map and identification of artifacts.

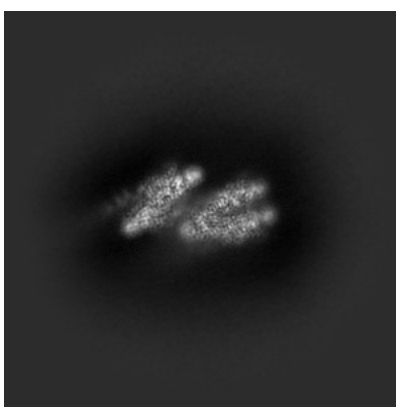
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

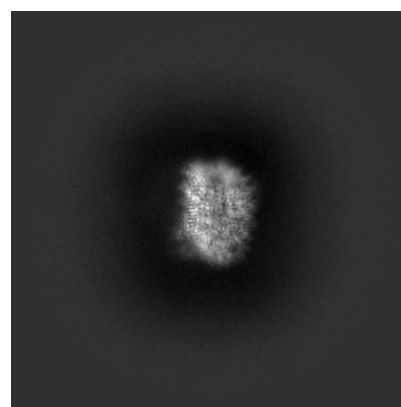
6.1.1 Primary map



X



Y

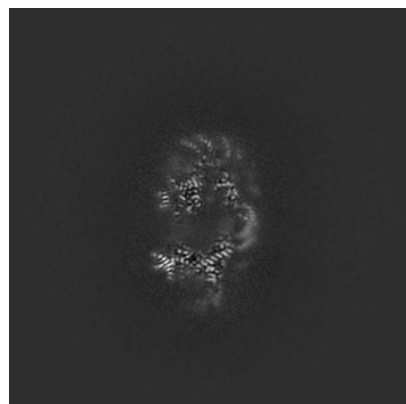


Z

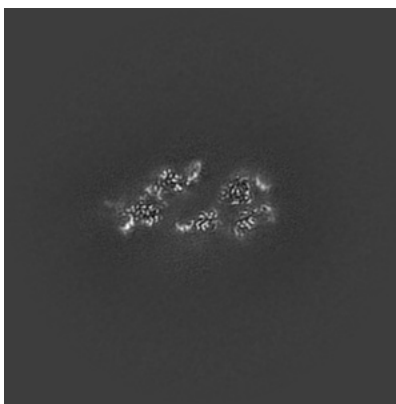
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

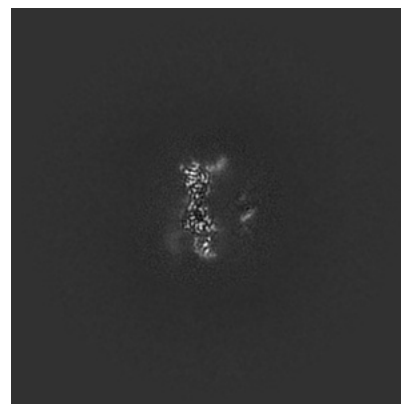
6.2.1 Primary map



X Index: 160



Y Index: 160

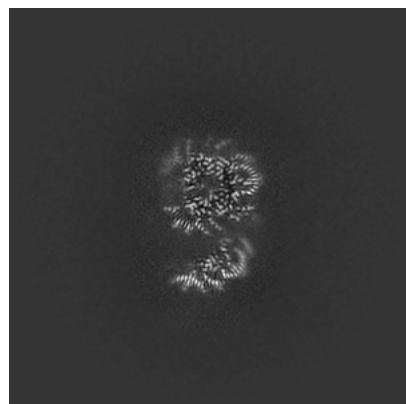


Z Index: 160

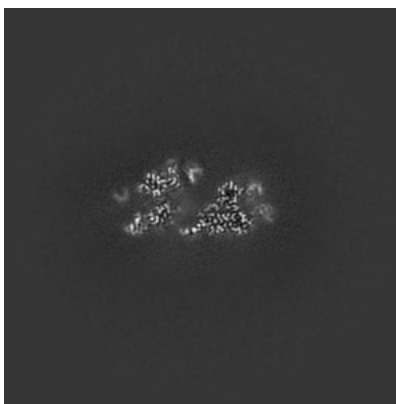
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

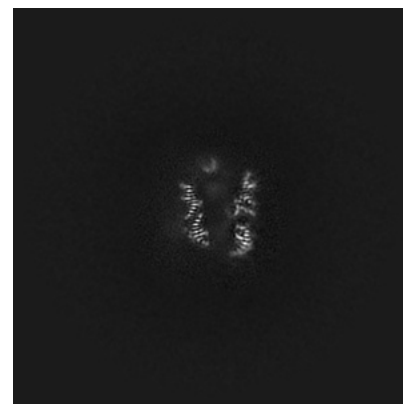
6.3.1 Primary map



X Index: 148



Y Index: 174

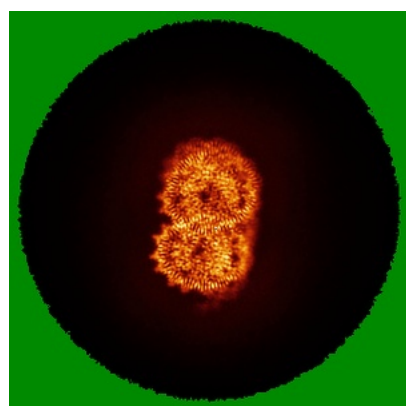


Z Index: 147

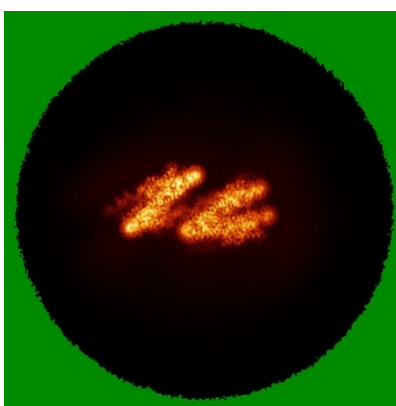
The images above show the largest variance slices of the map in three orthogonal directions.

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

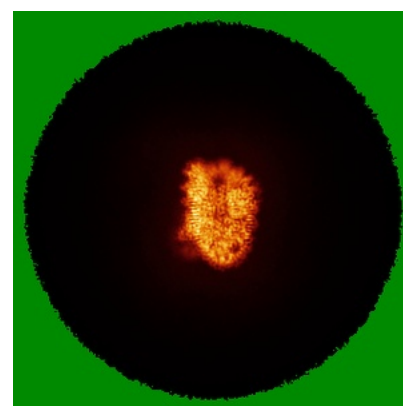
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

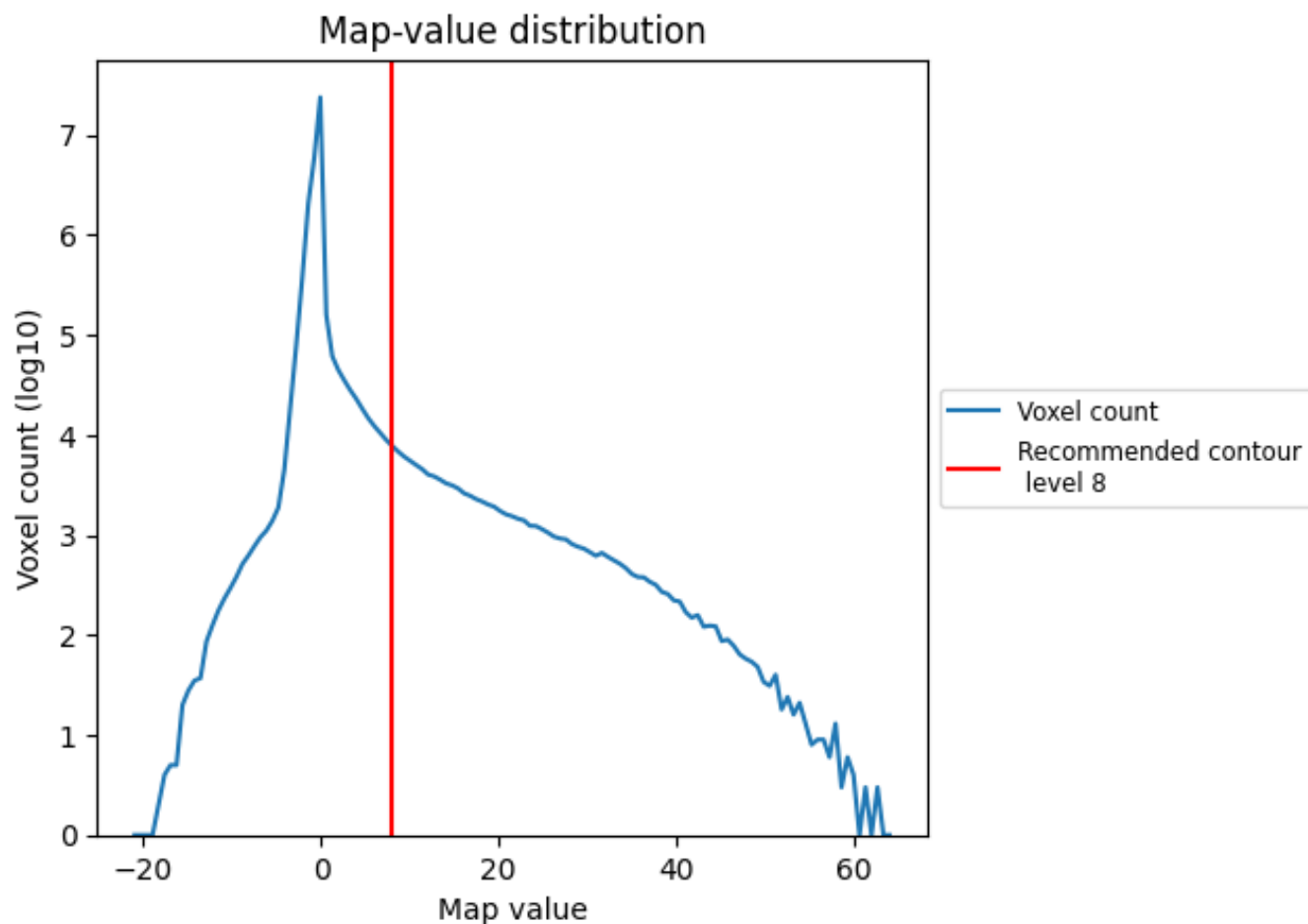
6.6 Mask visualisation

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

7 Map analysis [i](#)

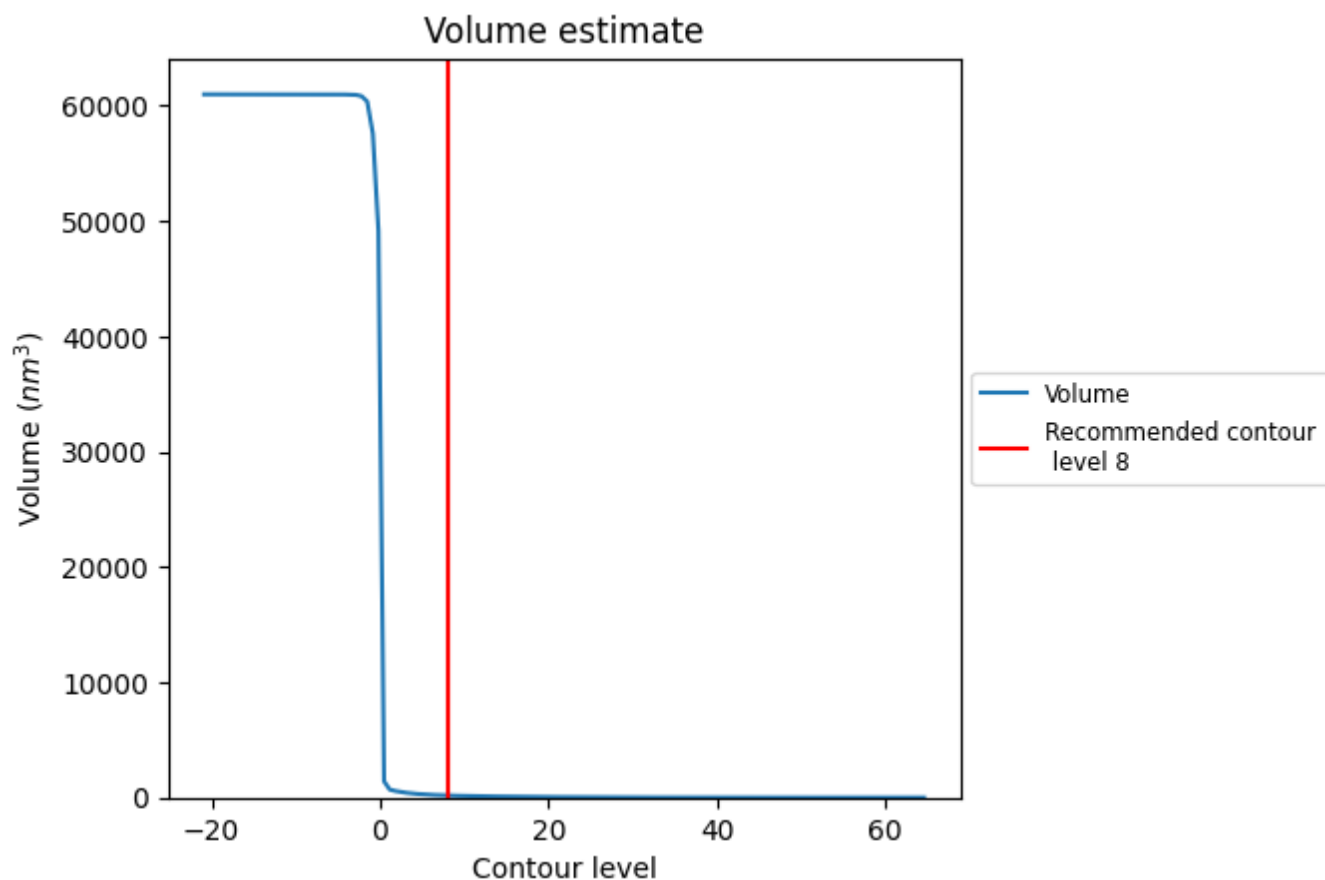
This section contains the results of statistical analysis of the map.

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.

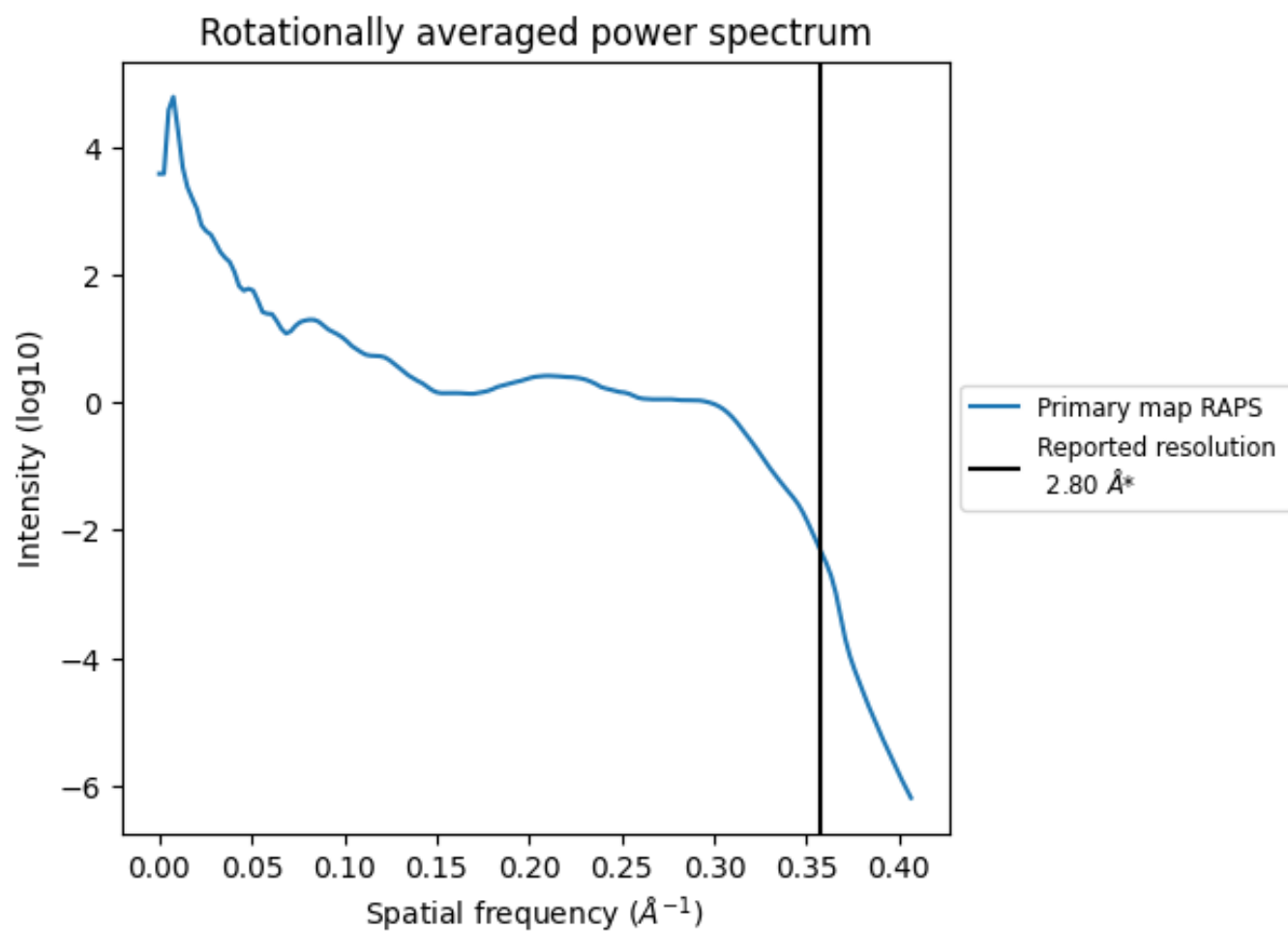
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm^3 ; this corresponds to an approximate mass of 162 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

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

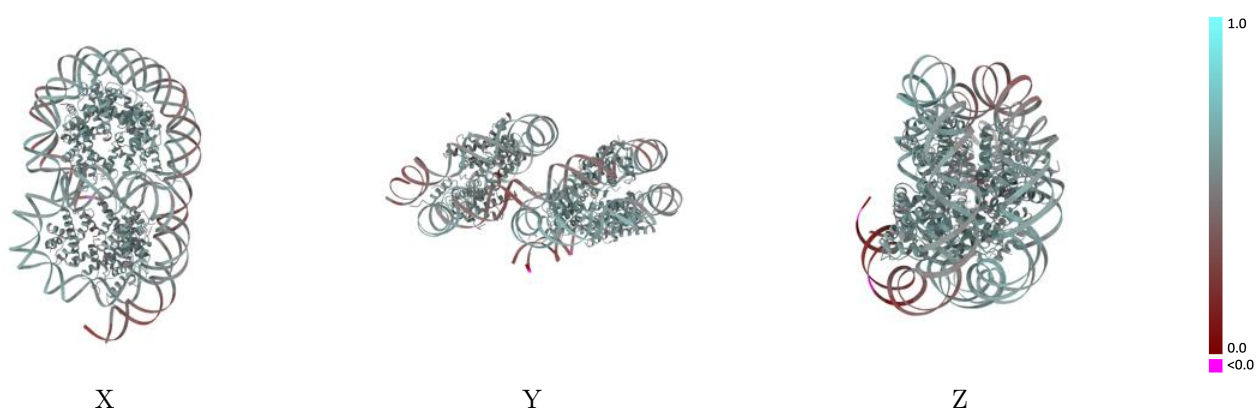
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-51238 and PDB model 9GD0. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

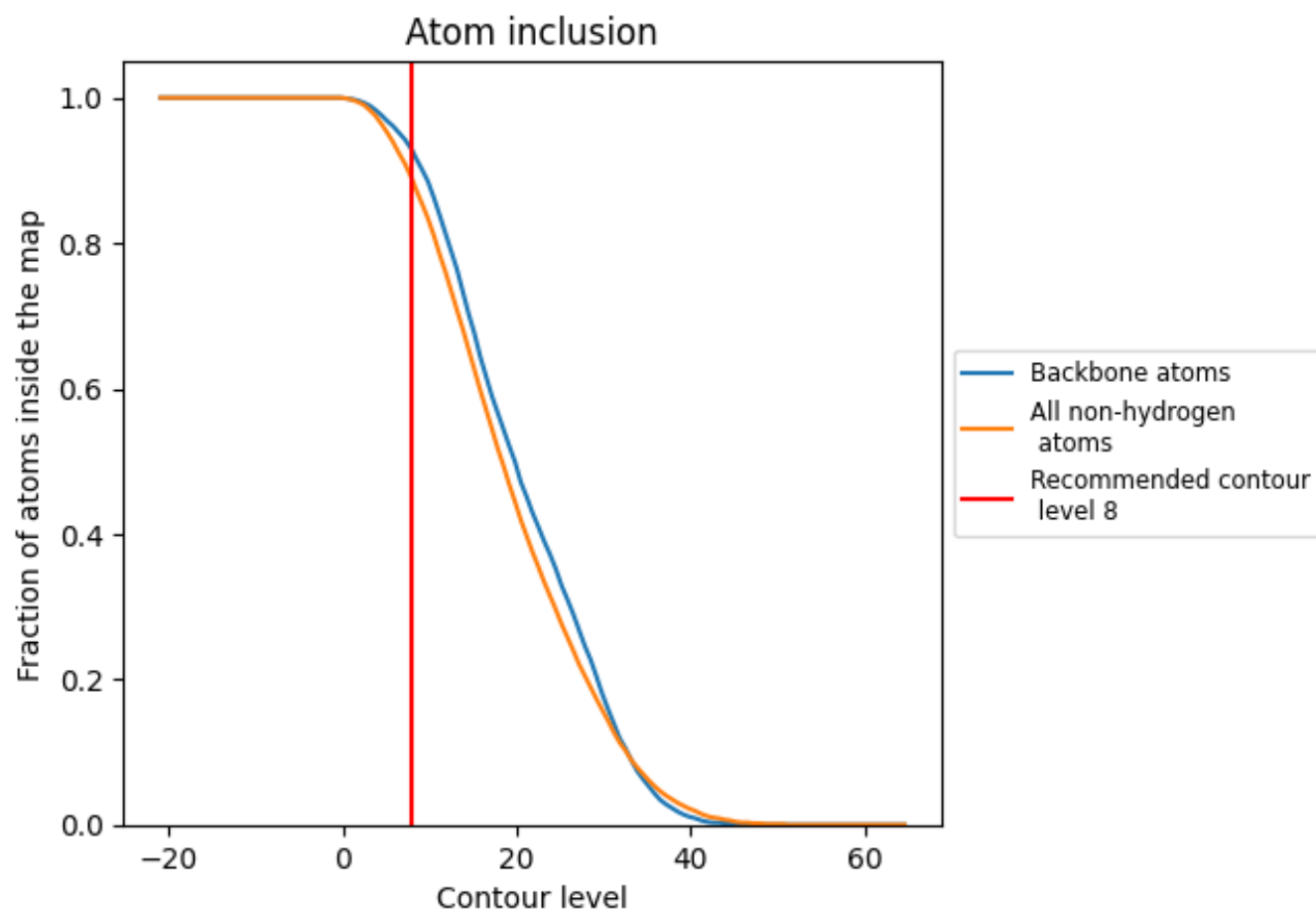


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 89% 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 (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8880	 0.5280
A	 0.9180	 0.5780
B	 0.9500	 0.5940
C	 0.8650	 0.5570
D	 0.9310	 0.5730
E	 0.9520	 0.5860
F	 0.9680	 0.5970
G	 0.8930	 0.5670
H	 0.9290	 0.5540
I	 0.8630	 0.4980
J	 0.8650	 0.5000
K	 0.9550	 0.5570
L	 0.8980	 0.5220
M	 0.9160	 0.5350
N	 0.9500	 0.5350
O	 0.8650	 0.5270
P	 0.8300	 0.5210

