



## wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 07:15 PM EDT

PDB ID : 6MZD  
EMDB ID : EMD-9302  
Title : Human TFIID Lobe A canonical  
Authors : Patel, A.B.; Louder, R.K.; Greber, B.J.; Grunberg, S.; Luo, J.; Fang, J.; Liu, Y.; Ranish, J.; Hahn, S.; Nogales, E.  
Deposited on : 2018-11-05  
Resolution : 9.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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

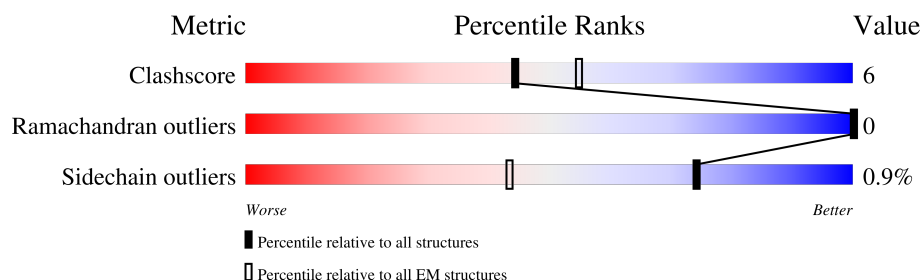
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 9.80 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.





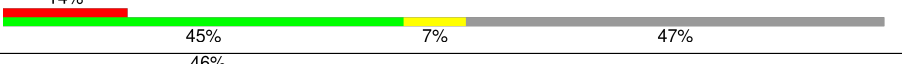
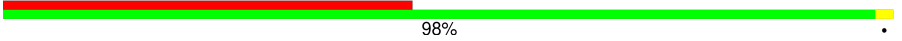
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1873	96%
2	C	929	9% 90%
3	D	1085	9% 91%
4	F	800	18% 48% 10% 41%
5	H	677	10% 89%
6	L	264	6% 36% 61%
7	N	218	11% 32% 6% 62%
8	P	211	14% 32% 9% 58%

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Mol	Chain	Length	Quality of chain
9	Q	161	
10	S	124	
11	T	339	
12	Y	96	

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 11120 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 Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	71	Total	C	N	O	S	1	0
			526	326	84	115	1		

- Molecule 2 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	93	Total	C	N	O	S	0	0
			742	467	128	141	6		

- Molecule 3 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	102	Total	C	N	O	0	0
			686	423	130	133		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	473	Total	C	N	O	S	0	0
			3646	2314	638	679	15		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	72	Total	C	N	O	S	0	0
			551	345	92	109	5		

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	104	Total	C	N	O	S	0	0
			732	456	129	142	5		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	82	Total	C	N	O	S	0	0
			645	413	102	126	4		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	89	Total	C	N	O	S	0	0
			707	447	127	128	5		

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	74	Total	C	N	O	S	0	0
			611	381	107	120	3		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	S	45	Total	C	N	O	S	0	0
			365	233	54	73	5		

- Molecule 11 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	T	180	Total	C	N	O	S	0	0
			1429	927	252	243	7		

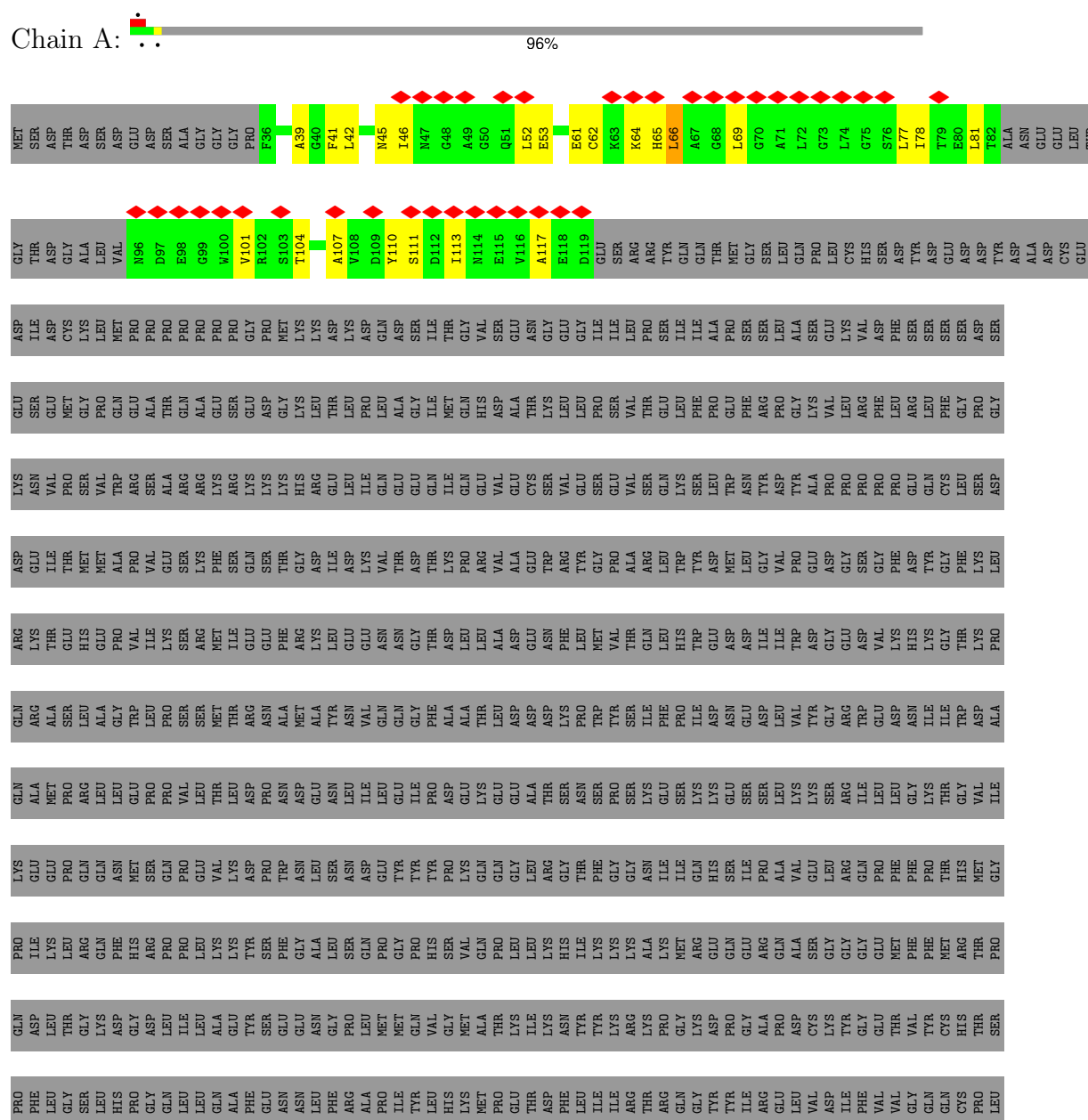
- Molecule 12 is a protein called poly(UNK).

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Y	96	Total	C	N	O	0	0
			480	288	96	96		

### 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: Transcription initiation factor TFIID subunit 1



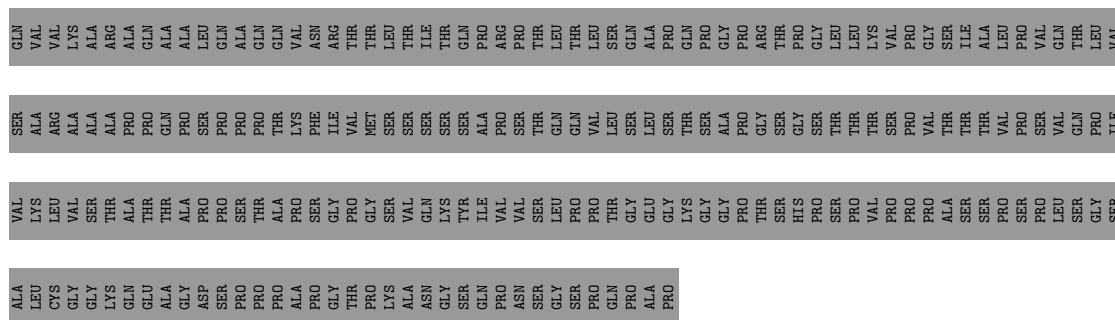




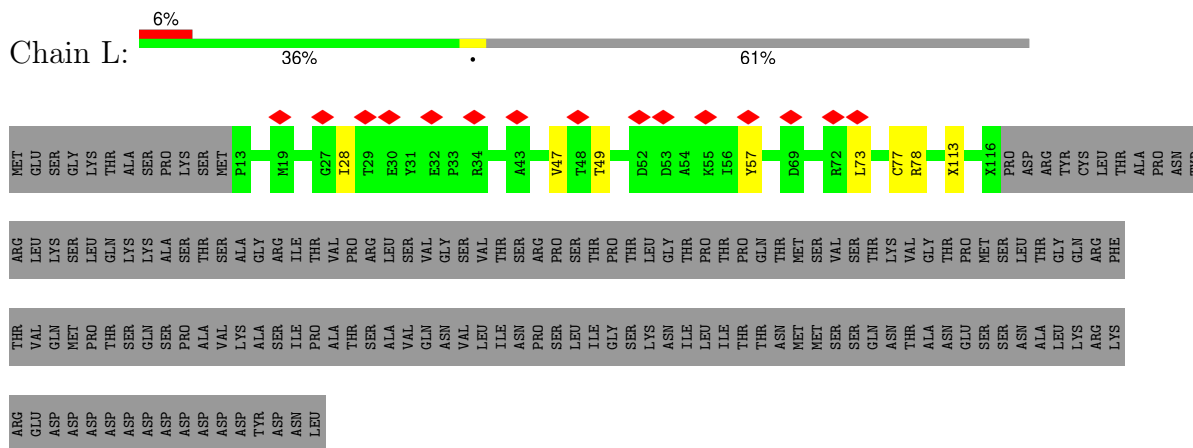




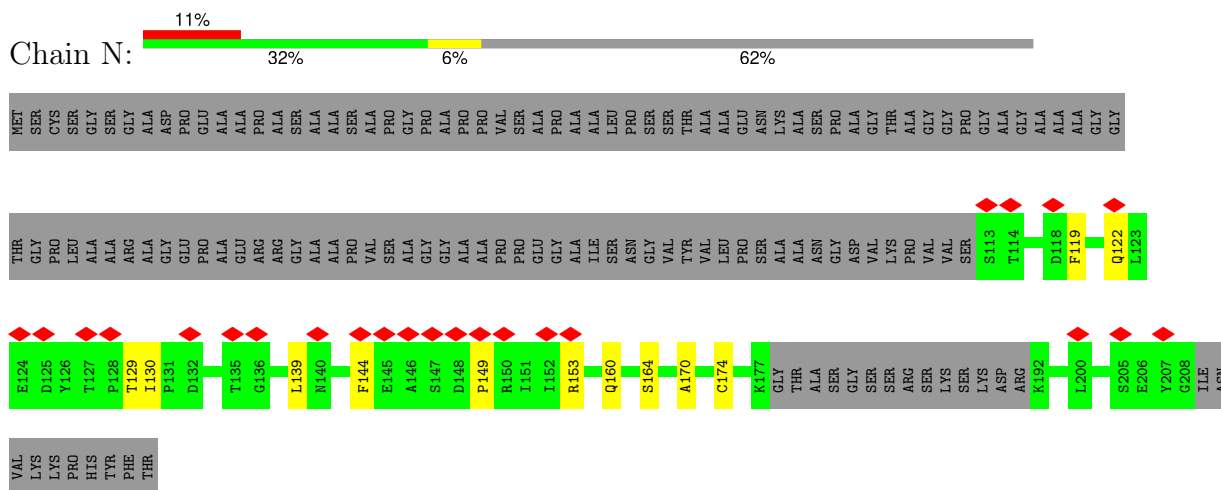




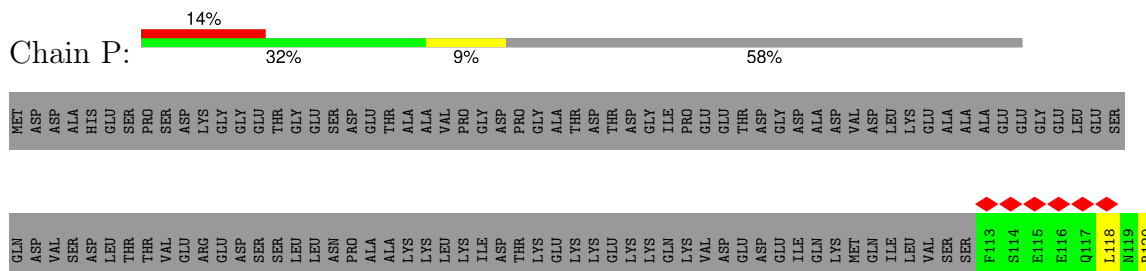
- Molecule 6: Transcription initiation factor TFIID subunit 9



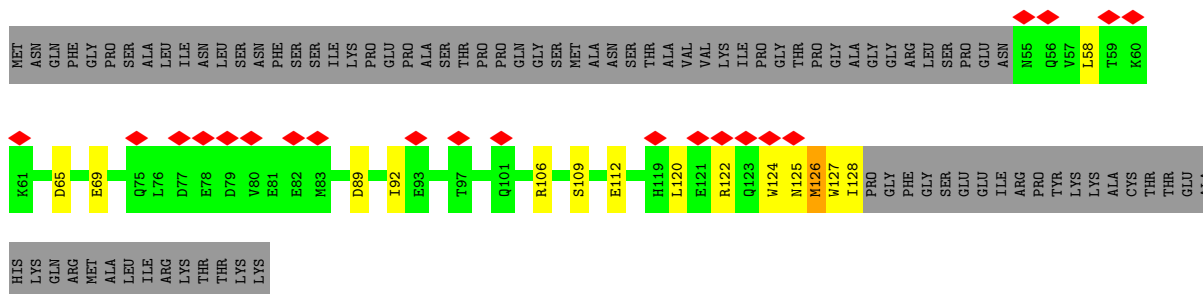
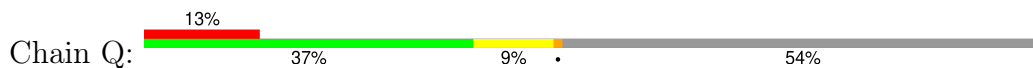
- Molecule 7: Transcription initiation factor TFIID subunit 10



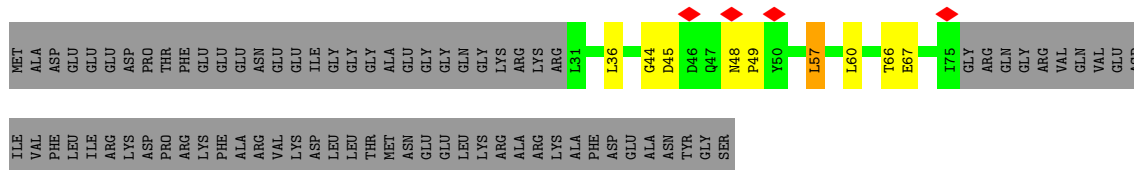
- Molecule 8: Transcription initiation factor TFIID subunit 11



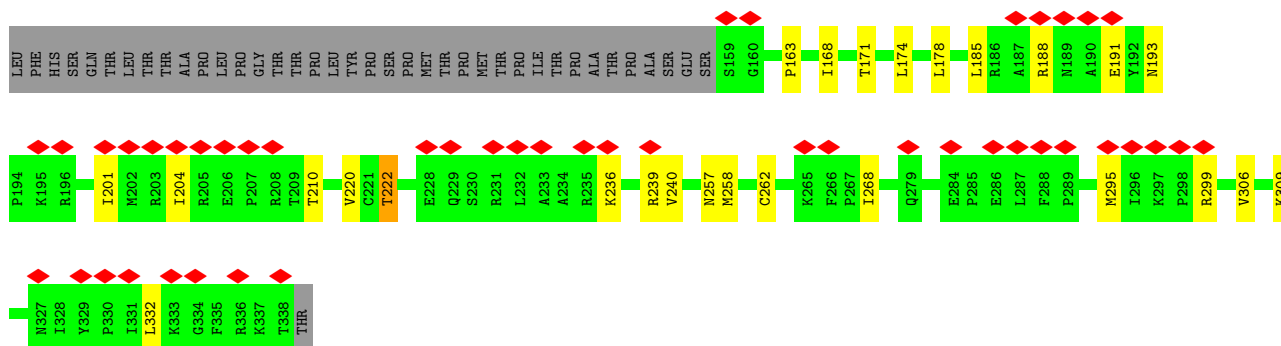
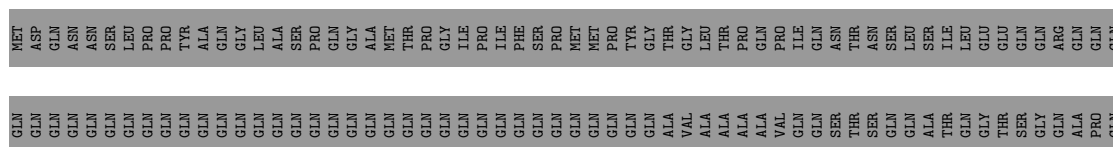
- Molecule 9: Transcription initiation factor TFIID subunit 12



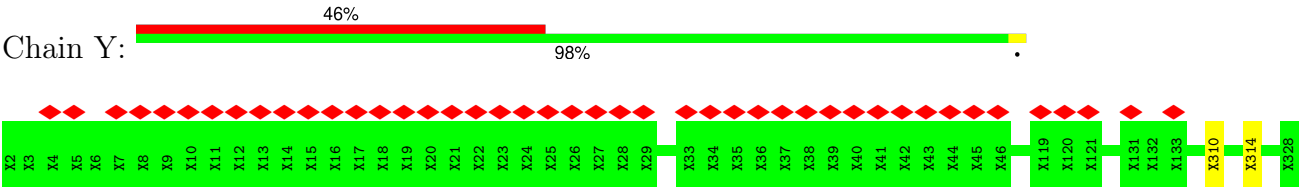
- Molecule 10: Transcription initiation factor TFIID subunit 13



- Molecule 11: TATA-box-binding protein



- Molecule 12: poly(UNK)



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	107900	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.352	Depositor
Minimum map value	-0.126	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	380.16, 380.16, 380.16	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0/531	0.71	2/716 (0.3%)
2	C	0.28	0/757	0.52	0/1027
3	D	0.34	0/692	0.61	1/945 (0.1%)
4	F	0.27	0/3537	0.58	0/4802
5	H	0.25	0/555	0.46	0/746
6	L	0.25	0/705	0.48	0/955
7	N	0.27	0/657	0.47	0/891
8	P	0.37	0/719	0.72	4/965 (0.4%)
9	Q	0.31	0/618	0.62	1/835 (0.1%)
10	S	0.28	0/371	0.52	0/498
11	T	0.31	0/1455	0.55	0/1958
All	All	0.29	0/10597	0.58	8/14338 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	F	0	3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	192	ARG	CG-CD-NE	6.62	125.71	111.80
1	A	69	LEU	CA-CB-CG	6.27	129.72	115.30
8	P	192	ARG	CB-CG-CD	-5.65	96.92	111.60
8	P	192	ARG	CA-CB-CG	5.64	125.81	113.40
3	D	908	GLN	CB-CG-CD	5.42	125.69	111.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	F	668	HIS	Peptide
4	F	721	ARG	Peptide
4	F	783	LEU	Peptide

## 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	526	0	483	16	0
2	C	742	0	719	8	0
3	D	686	0	572	8	0
4	F	3646	0	3312	48	0
5	H	551	0	552	5	0
6	L	732	0	624	6	0
7	N	645	0	640	7	0
8	P	707	0	730	24	0
9	Q	611	0	610	16	0
10	S	365	0	351	10	0
11	T	1429	0	1521	18	0
12	Y	480	0	112	1	0
All	All	11120	0	10226	132	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 6.

The worst 5 of 132 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:D:908:GLN:HG2	8:P:192:ARG:HD3	1.61	0.83
8:P:195:LYS:HE2	9:Q:127:TRP:H	1.45	0.80
3:D:904:HIS:HA	8:P:192:ARG:HH21	1.50	0.76
1:A:62:CYS:O	1:A:66:LEU:HB2	1.84	0.76
2:C:34:ARG:HG2	2:C:66:GLN:HE22	1.53	0.73

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	67/1873 (4%)	62 (92%)	5 (8%)	0	100	100
2	C	91/929 (10%)	89 (98%)	2 (2%)	0	100	100
3	D	100/1085 (9%)	93 (93%)	7 (7%)	0	100	100
4	F	429/800 (54%)	382 (89%)	47 (11%)	0	100	100
5	H	70/677 (10%)	65 (93%)	5 (7%)	0	100	100
6	L	96/264 (36%)	93 (97%)	3 (3%)	0	100	100
7	N	78/218 (36%)	75 (96%)	3 (4%)	0	100	100
8	P	87/211 (41%)	86 (99%)	1 (1%)	0	100	100
9	Q	72/161 (45%)	71 (99%)	1 (1%)	0	100	100
10	S	43/124 (35%)	43 (100%)	0	0	100	100
11	T	178/339 (52%)	177 (99%)	1 (1%)	0	100	100
All	All	1311/6681 (20%)	1236 (94%)	75 (6%)	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	55/1669 (3%)	54 (98%)	1 (2%)	54	71
2	C	83/833 (10%)	83 (100%)	0	100	100
3	D	52/815 (6%)	51 (98%)	1 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	F	367/619 (59%)	365 (100%)	2 (0%)	86	89
5	H	60/574 (10%)	60 (100%)	0	100	100
6	L	61/229 (27%)	60 (98%)	1 (2%)	58	73
7	N	71/154 (46%)	71 (100%)	0	100	100
8	P	78/182 (43%)	78 (100%)	0	100	100
9	Q	70/141 (50%)	69 (99%)	1 (1%)	62	75
10	S	42/106 (40%)	40 (95%)	2 (5%)	21	43
11	T	155/293 (53%)	153 (99%)	2 (1%)	65	77
All	All	1094/5615 (20%)	1084 (99%)	10 (1%)	74	83

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	S	57	LEU
11	T	193	ASN
11	T	222	THR
4	F	607	ARG
6	L	73	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
10	S	48	ASN
11	T	327	ASN
4	F	336	HIS
4	F	626	HIS
4	F	710	HIS

### 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	Y	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	143:UNK	C	309:UNK	N	54.12
1	Y	52:UNK	C	119:UNK	N	47.22

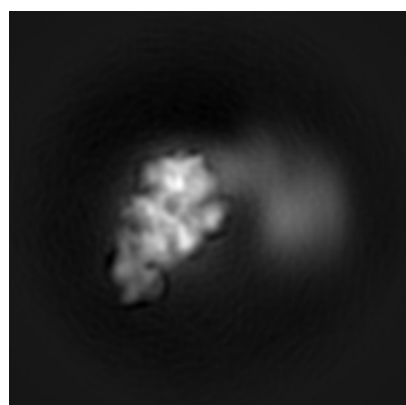
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9302. These allow visual inspection of the internal detail of the map and identification of artifacts.

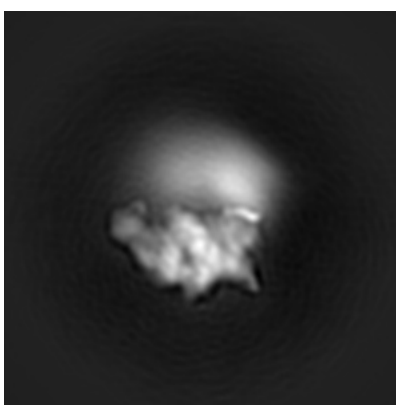
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

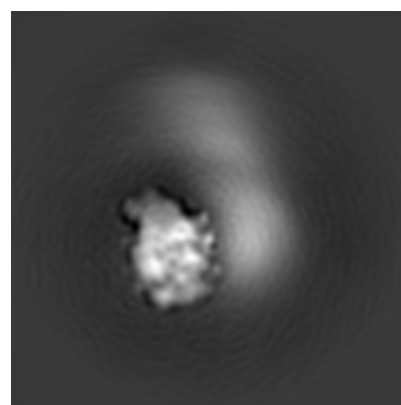
#### 6.1.1 Primary map



X



Y

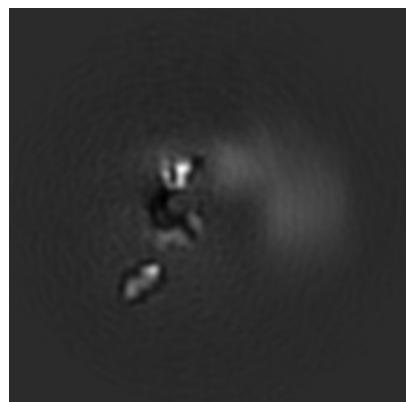


Z

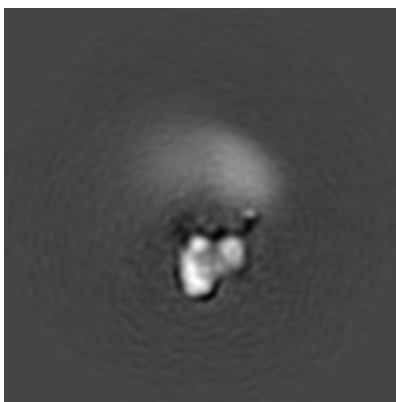
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

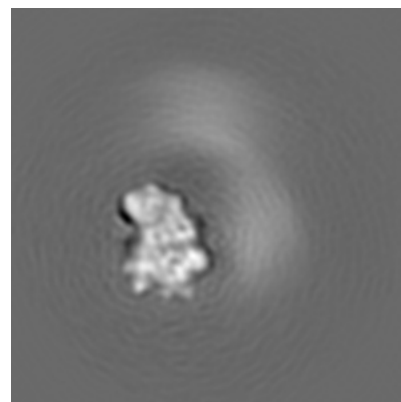
#### 6.2.1 Primary map



X Index: 144



Y Index: 144

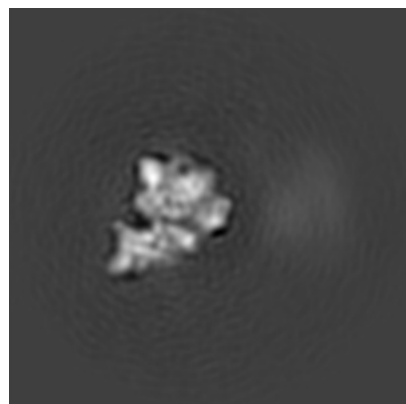


Z Index: 144

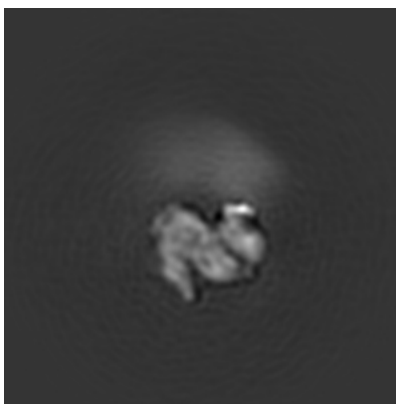
The images above show central slices of the map in three orthogonal directions.

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

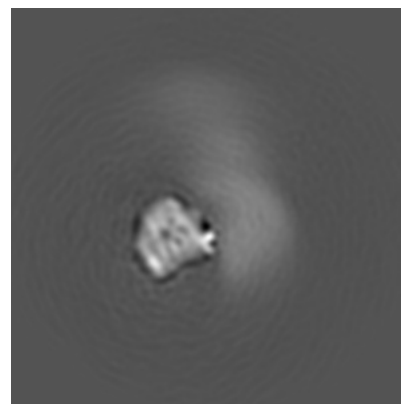
### 6.3.1 Primary map



X Index: 104



Y Index: 124

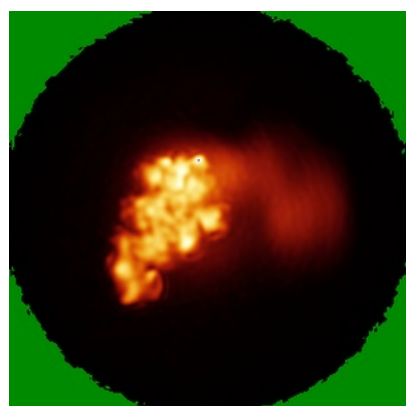


Z Index: 164

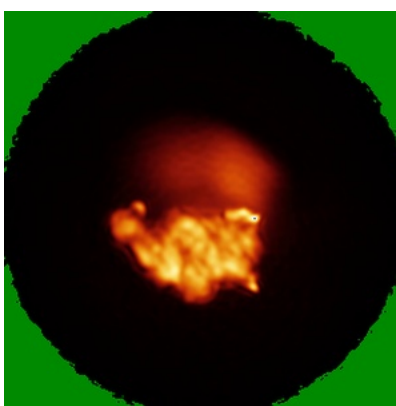
The images above show the largest variance slices of the map in three orthogonal directions.

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

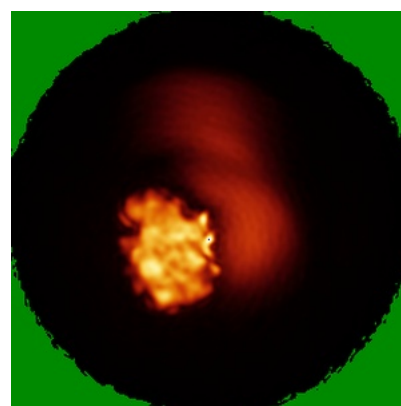
### 6.4.1 Primary map



X



Y

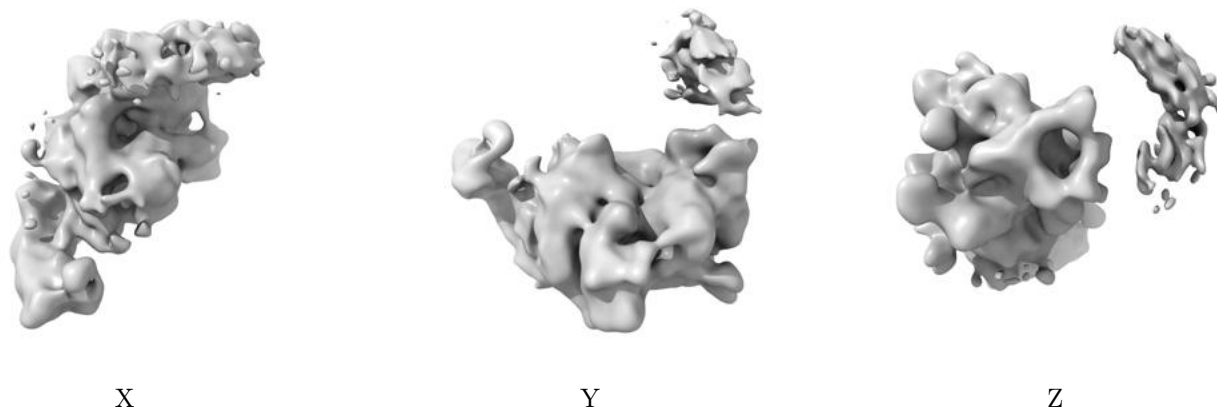


Z

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 [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

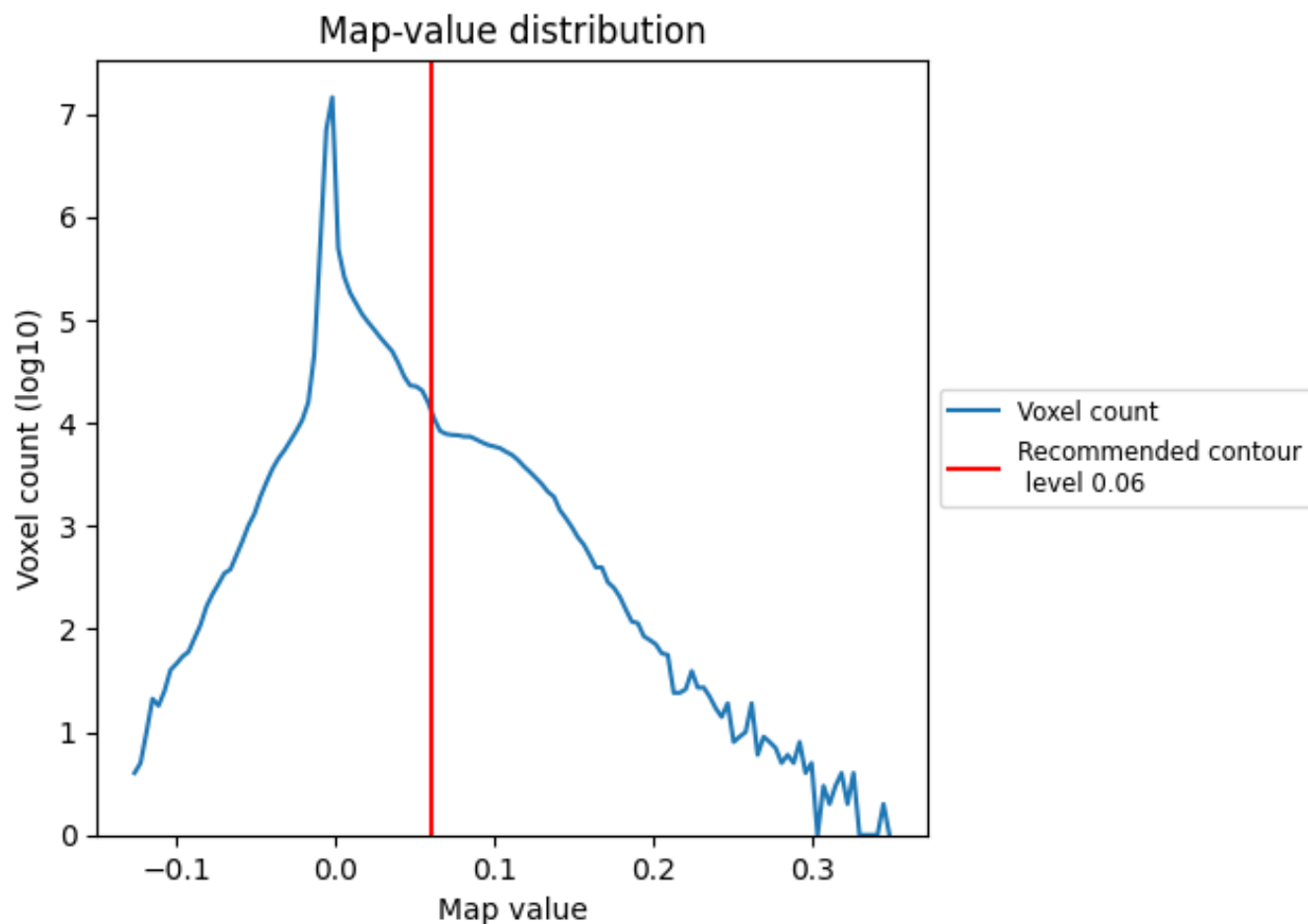
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

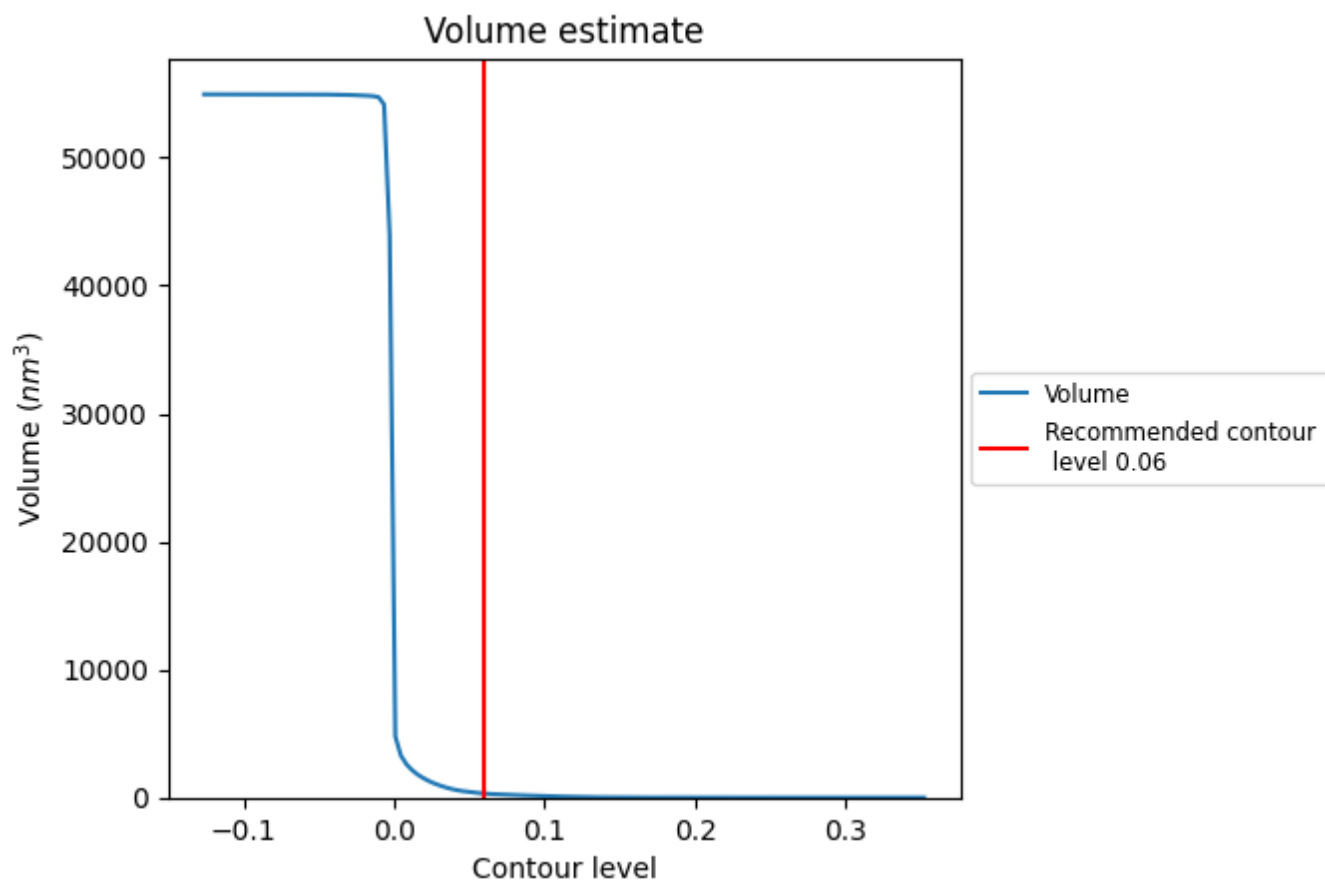
This section contains the results of statistical analysis of the map.

### 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](#)

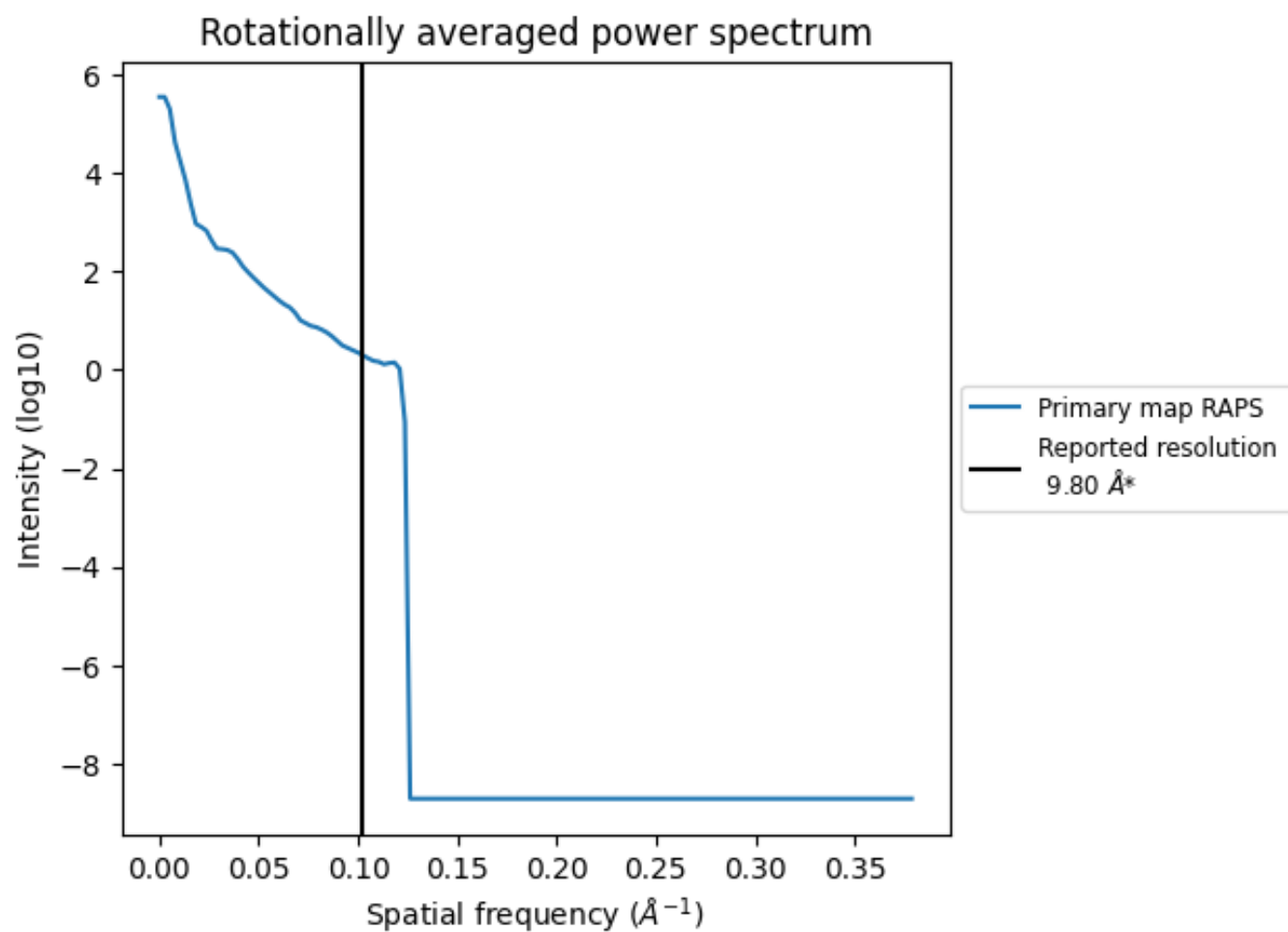


The volume at the recommended contour level is 312  $\text{nm}^3$ ; this corresponds to an approximate mass of 282 kDa.

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 0.102 Å<sup>-1</sup>

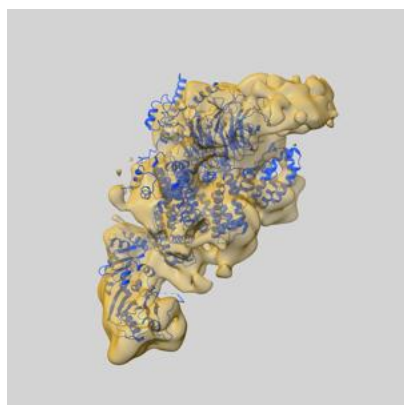
## 8 Fourier-Shell correlation ⓘ

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

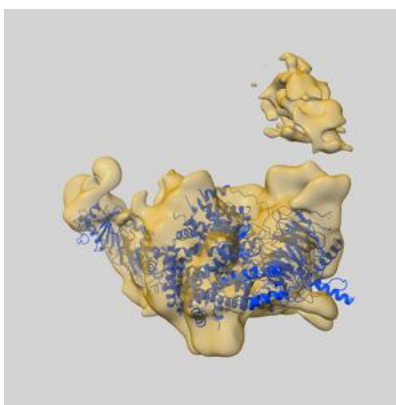
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9302 and PDB model 6MZD. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

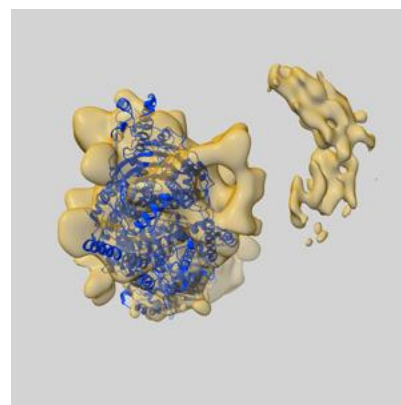
### 9.1 Map-model overlay [i](#)



X



Y



Z

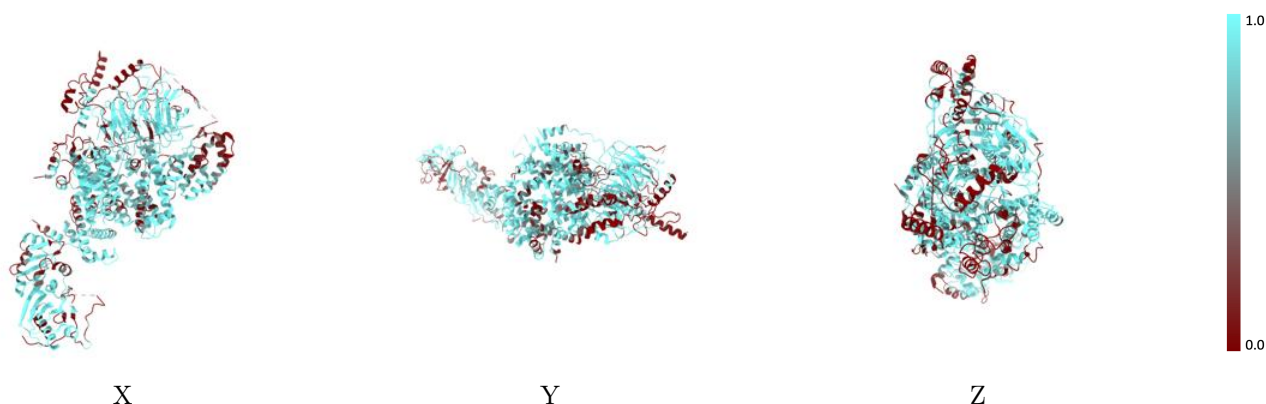
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



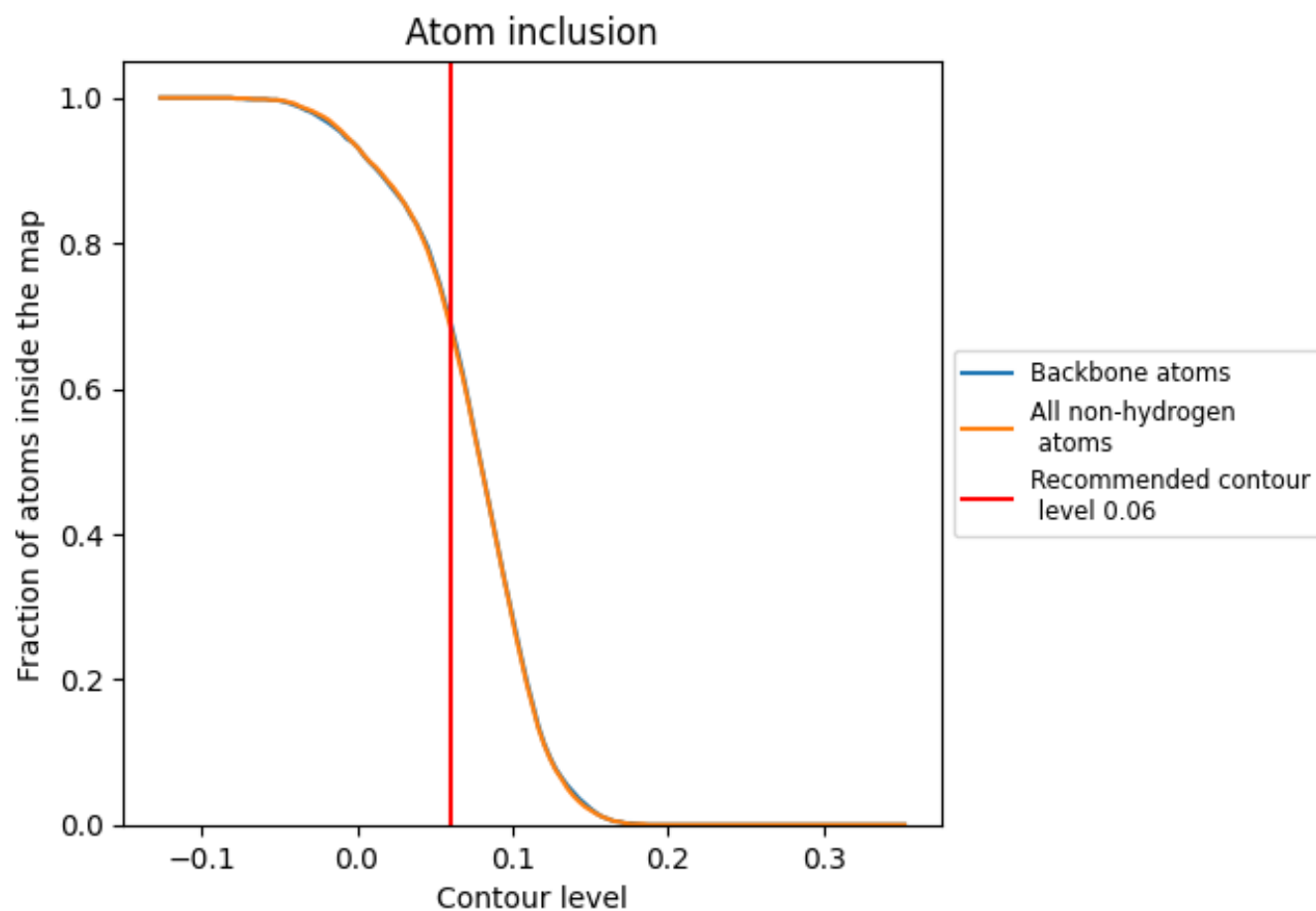
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).



























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 69% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6860	 0.0180
A	 0.4330	 -0.0090
C	 0.8270	 0.0490
D	 0.6610	 0.0290
F	 0.6800	 0.0030
H	 0.7870	 -0.0170
L	 0.7610	 0.0290
N	 0.6770	 0.0230
P	 0.6100	 0.0090
Q	 0.6640	 0.0400
S	 0.8530	 0.0330
T	 0.7130	 0.0430
Y	 0.5420	 0.0190

