



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 01:51 PM EST

PDB ID : 6MZL
EMDB ID : EMD-9305
Title : Human TFIID canonical state
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 : 23.00 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.dev43
MolProbity : 4.02b-467
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

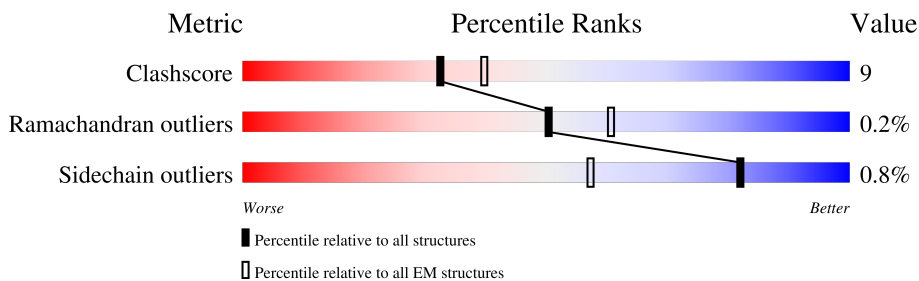
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 23.00 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	1872	
2	B	1199	
3	C	929	
4	D	1085	
4	E	1085	
5	F	800	
5	G	800	
6	H	677	

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Mol	Chain	Length	Quality of chain
7	I	677	
8	J	349	
9	K	310	
10	L	264	
10	M	264	
11	N	218	
11	O	218	
12	P	211	
13	Q	161	
13	R	161	
14	S	124	
15	T	339	
16	Y	96	
17	Z	238	

2 Entry composition i

There are 17 unique types of molecules in this entry. The entry contains 36618 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
			Total	C	N	O	S		
1	A	472	3772	2397	659	693	23	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	968	7832	5031	1322	1421	58	0	0

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

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

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

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

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 5, TAF5.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	329	2494	1575	439	464	16	0	0

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	339	2520	1585	445	474	16	0	0

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	J	123	998	638	184	172	4	0	0

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 8, TAF8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	K	202	1449	906	260	278	5	0	0

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 9, TAF9.

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

- Molecule 11 is a protein called Transcription initiation factor TFIID subunit 10.

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

- Molecule 12 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 13 is a protein called Transcription initiation factor TFIID subunit 12.

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

- Molecule 14 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 15 is a protein called TATA-box-binding protein.

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

- Molecule 16 is a protein called poly(UNK).

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

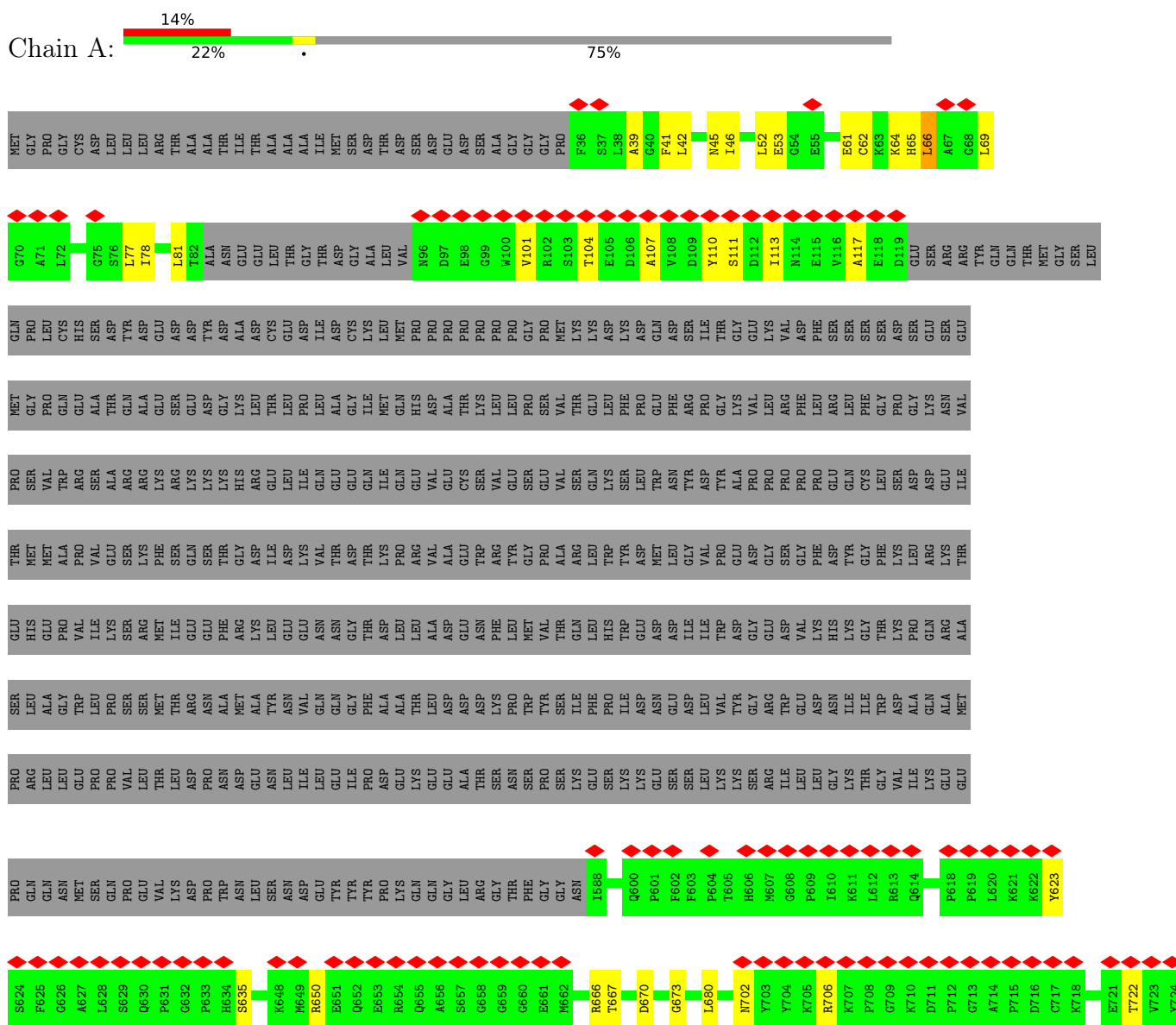
- Molecule 17 is a protein called poly(UNK).

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Z	238	Total	C	N	O	0	0
			1190	714	238	238		

3 Residue-property plots

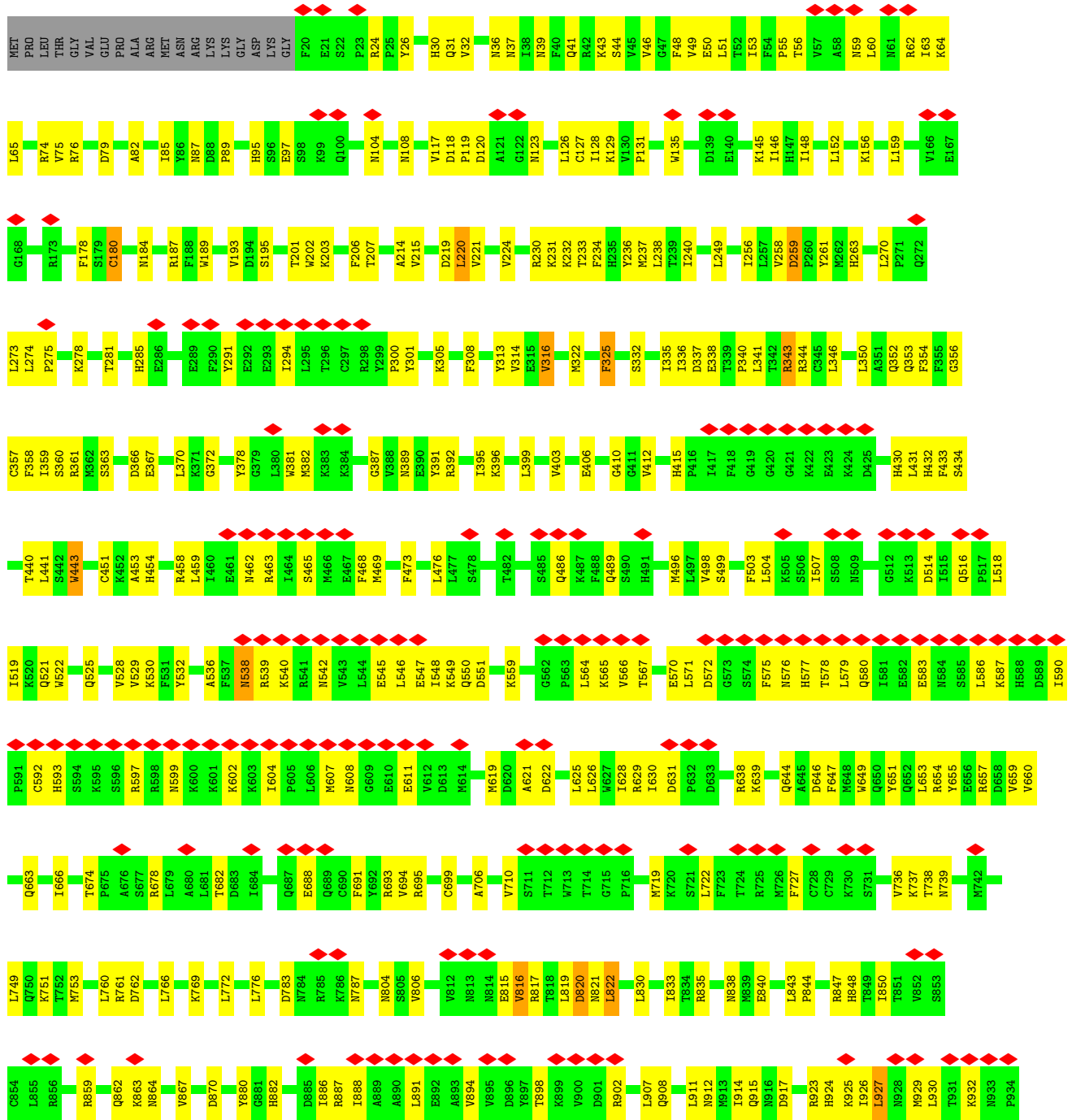
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

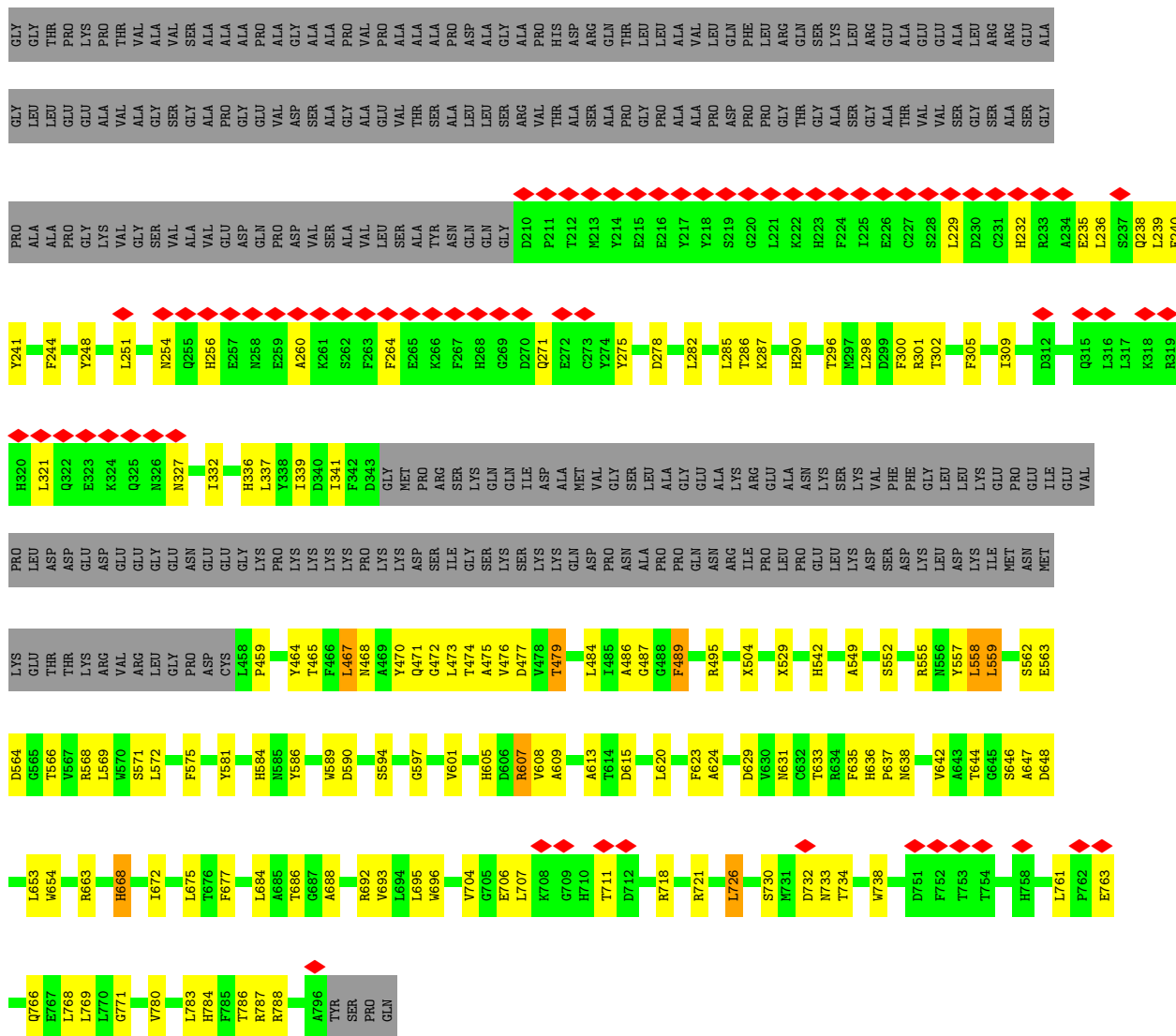
- Molecule 1: Transcription initiation factor TFIID subunit 1



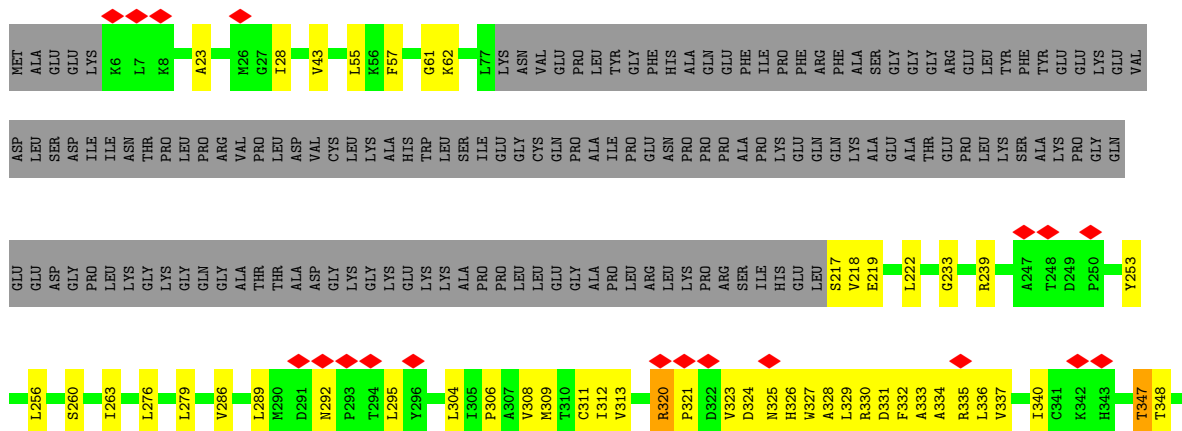
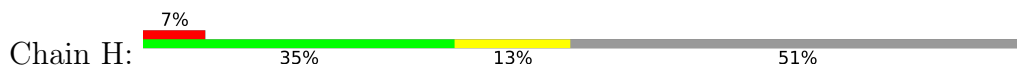
TYR	GLY	SER	LEU	THR	GLY	GLU	PRO	ASP	PRO	ASP	LYS	ASN	THR	GLN	THR	THR	ASP	PHE	SER	SER	ILE	GLY	GLY	TYR	VAL	VAL	SER	GLU	GLU	GLY	GLU	GLU	GLN	GLU	GLY	GLY	GLY	GLY	VAL	VAL	LEU	SER	GLN	VAL	VAL	HIS	LEU	SER	ASP	GLU	GLU	ASP	ASP	GLY	ASP	PHE
HIS	SER	ILE	ALA	GLY	ASP	SER	ASP	LEU	ASP	SER	ASP	ASN	THR	GLN	THR	THR	ASP	PHE	SER	SER	ILE	GLY	GLY	TYR	VAL	VAL	SER	GLU	GLU	GLY	GLU	GLU	GLN	GLU	GLY	GLY	GLY	VAL	VAL	LEU	SER	GLN	VAL	VAL	HIS	LEU	SER	ASP	GLU	GLU	ASP	ASP	GLY	ASP	PHE	

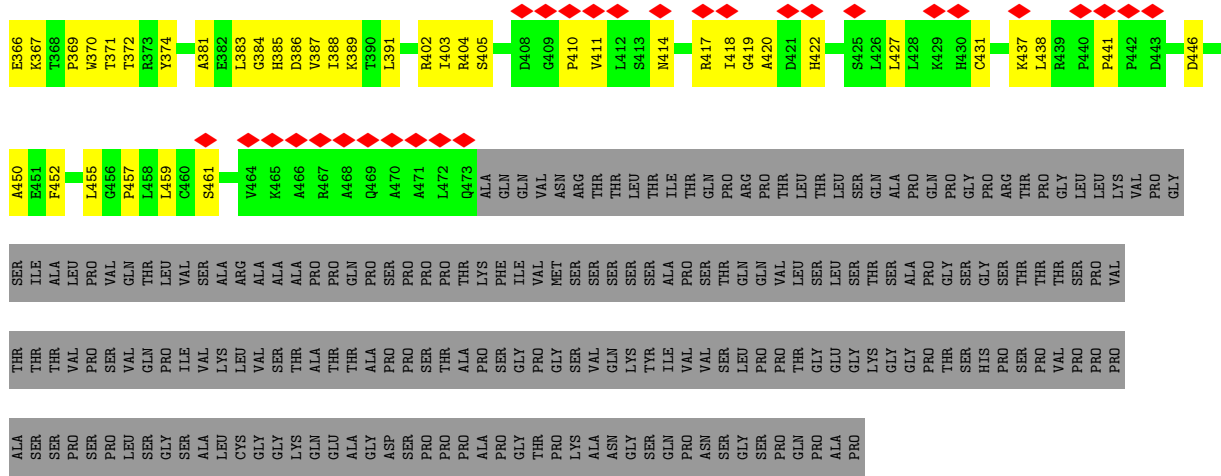
● Molecule 2: Transcription initiation factor TFIID subunit 2



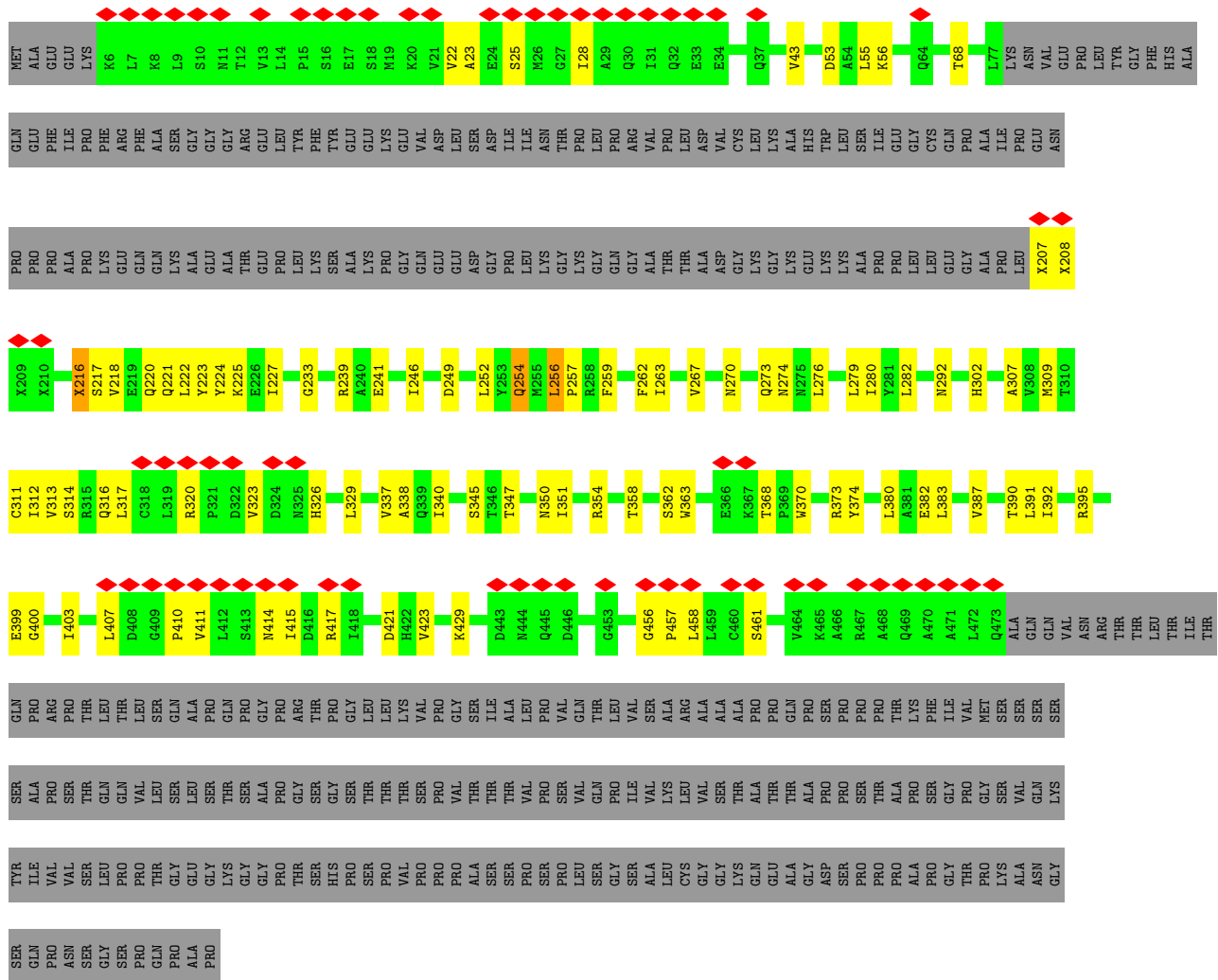
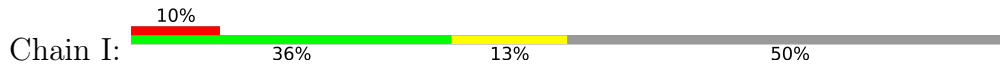


- Molecule 6: Transcription initiation factor TFIID subunit 6

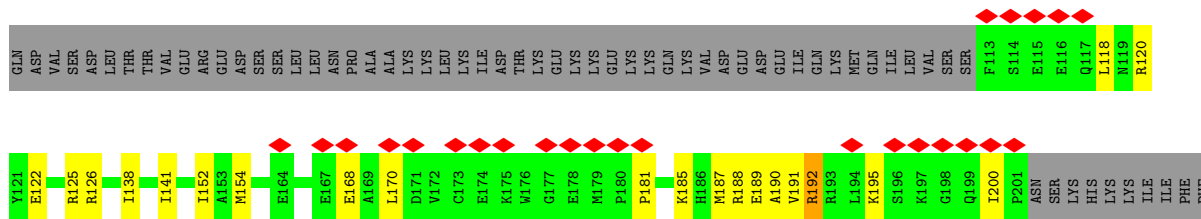




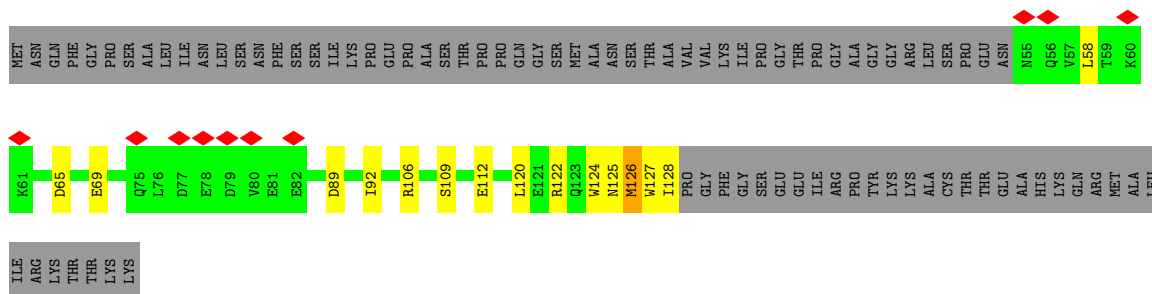
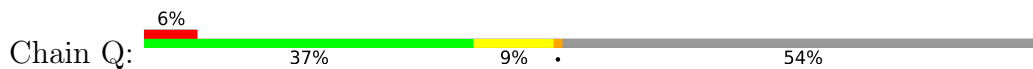
• Molecule 7: Transcription initiation factor TFIID subunit 6



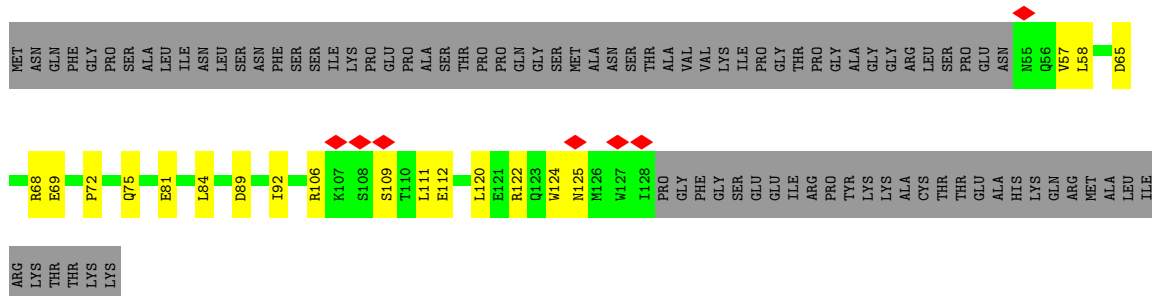
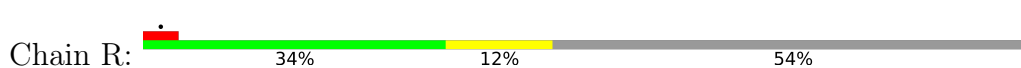
• Molecule 8: Transcription initiation factor TFIID subunit 7



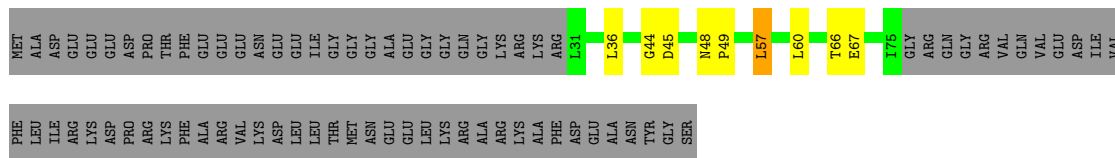
• Molecule 13: Transcription initiation factor TFIID subunit 12



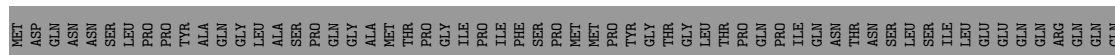
• Molecule 13: Transcription initiation factor TFIID subunit 12

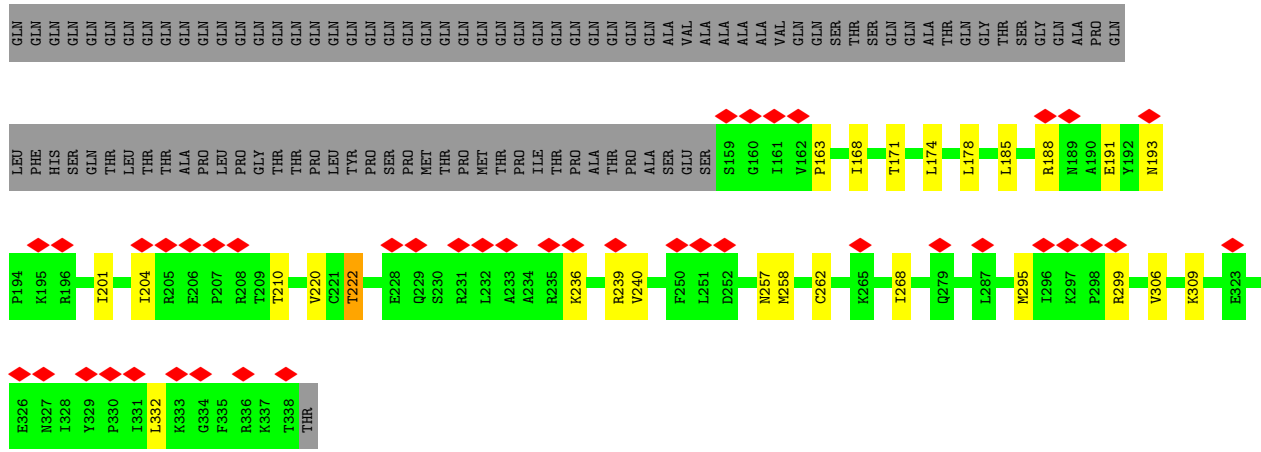


• Molecule 14: Transcription initiation factor TFIID subunit 13

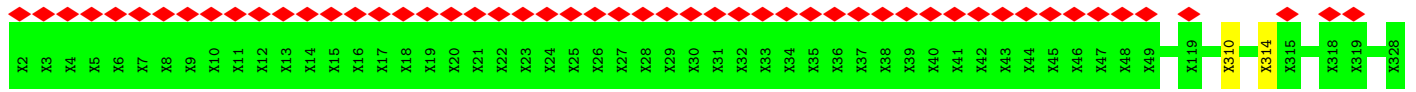


• Molecule 15: TATA-box-binding protein

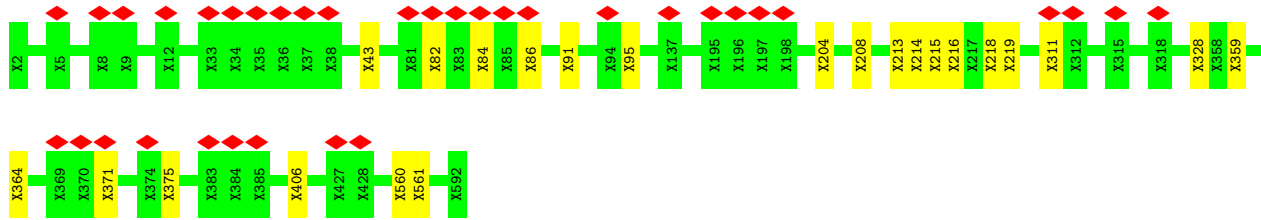
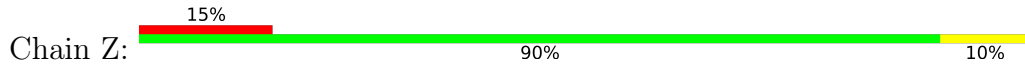




• Molecule 16: poly(UNK)



• Molecule 17: poly(UNK)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
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	0.065	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	380.16, 380.16, 380.16	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	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	0.27	0/3858	0.53	2/5193 (0.0%)
2	B	0.57	2/8029 (0.0%)	0.74	3/10882 (0.0%)
3	C	0.28	0/757	0.52	0/1027
4	D	0.34	0/692	0.61	1/945 (0.1%)
4	E	0.31	0/692	0.50	0/945
5	F	0.27	0/3537	0.58	0/4802
5	G	0.52	0/3537	0.72	2/4802 (0.0%)
6	H	0.46	0/2533	0.66	0/3439
7	I	0.44	0/2506	0.64	0/3402
8	J	0.26	0/1017	0.53	0/1370
9	K	0.43	0/1212	0.59	0/1640
10	L	0.25	0/705	0.48	0/955
10	M	0.37	0/705	0.59	0/955
11	N	0.27	0/657	0.47	0/891
11	O	0.38	0/657	0.51	0/891
12	P	0.37	0/719	0.72	4/965 (0.4%)
13	Q	0.31	0/618	0.62	1/835 (0.1%)
13	R	0.33	0/618	0.55	0/835
14	S	0.28	0/371	0.52	0/498
15	T	0.31	0/1455	0.55	0/1958
All	All	0.42	2/34875 (0.0%)	0.64	13/47230 (0.0%)

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
1	A	0	1
2	B	0	17
5	F	0	3
5	G	0	8
6	H	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	I	0	4
9	K	0	2
10	M	0	1
17	Z	0	1
All	All	0	43

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	443	TRP	CB-CG	-7.44	1.36	1.50
2	B	381	TRP	CB-CG	-5.07	1.41	1.50

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	220	LEU	CA-CB-CG	7.67	132.93	115.30
12	P	192	ARG	CG-CD-NE	6.62	125.71	111.80
2	B	927	LEU	CA-CB-CG	-6.32	100.76	115.30
1	A	69	LEU	CA-CB-CG	6.27	129.72	115.30
5	G	726	LEU	CB-CG-CD2	-6.05	100.72	111.00

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	949	GLU	Peptide
2	B	193	VAL	Peptide
2	B	259	ASP	Peptide
2	B	316	VAL	Peptide
2	B	325	PHE	Peptide

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	3772	0	3742	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	7832	0	7789	217	0
3	C	742	0	719	8	0
4	D	686	0	572	8	0
4	E	686	0	572	13	0
5	F	3646	0	3312	48	0
5	G	3646	0	3312	95	0
6	H	2494	0	2474	58	0
7	I	2520	0	2422	61	0
8	J	998	0	1055	12	0
9	K	1449	0	1281	33	0
10	L	732	0	624	6	0
10	M	732	0	623	13	0
11	N	645	0	640	7	0
11	O	645	0	640	15	0
12	P	707	0	730	24	0
13	Q	611	0	610	16	0
13	R	611	0	610	16	0
14	S	365	0	351	10	0
15	T	1429	0	1521	18	0
16	Y	480	0	112	1	0
17	Z	1190	0	280	16	0
All	All	36618	0	33991	655	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 9.

The worst 5 of 655 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)
1:A:874:GLU:HG2	2:B:468:PHE:HZ	1.27	0.99
2:B:566:VAL:O	2:B:577:HIS:HA	1.64	0.97
2:B:532:TYR:O	2:B:551:ASP:HB2	1.67	0.94
2:B:50:GLU:HA	2:B:146:ILE:O	1.70	0.92
1:A:874:GLU:HG2	2:B:468:PHE:CZ	2.04	0.91

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	462/1872 (25%)	454 (98%)	7 (2%)	1 (0%)	47	81
2	B	966/1199 (81%)	781 (81%)	183 (19%)	2 (0%)	47	81
3	C	91/929 (10%)	89 (98%)	2 (2%)	0	100	100
4	D	100/1085 (9%)	93 (93%)	7 (7%)	0	100	100
4	E	100/1085 (9%)	94 (94%)	6 (6%)	0	100	100
5	F	429/800 (54%)	382 (89%)	47 (11%)	0	100	100
5	G	429/800 (54%)	352 (82%)	77 (18%)	0	100	100
6	H	325/677 (48%)	293 (90%)	31 (10%)	1 (0%)	41	77
7	I	326/677 (48%)	292 (90%)	32 (10%)	2 (1%)	25	66
8	J	119/349 (34%)	117 (98%)	2 (2%)	0	100	100
9	K	149/310 (48%)	133 (89%)	15 (10%)	1 (1%)	22	63
10	L	96/264 (36%)	93 (97%)	3 (3%)	0	100	100
10	M	96/264 (36%)	89 (93%)	7 (7%)	0	100	100
11	N	78/218 (36%)	75 (96%)	3 (4%)	0	100	100
11	O	78/218 (36%)	74 (95%)	4 (5%)	0	100	100
12	P	87/211 (41%)	86 (99%)	1 (1%)	0	100	100
13	Q	72/161 (45%)	71 (99%)	1 (1%)	0	100	100
13	R	72/161 (45%)	68 (94%)	4 (6%)	0	100	100
14	S	43/124 (35%)	43 (100%)	0	0	100	100
15	T	178/339 (52%)	177 (99%)	1 (1%)	0	100	100
All	All	4296/11743 (37%)	3856 (90%)	433 (10%)	7 (0%)	50	81

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	950	VAL

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Mol	Chain	Res	Type
7	I	256	LEU
6	H	321	PRO
7	I	257	PRO
9	K	218	PRO

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	407/1665 (24%)	403 (99%)	4 (1%)	76	86
2	B	879/1083 (81%)	872 (99%)	7 (1%)	81	89
3	C	83/833 (10%)	83 (100%)	0	100	100
4	D	52/815 (6%)	51 (98%)	1 (2%)	57	75
4	E	52/815 (6%)	52 (100%)	0	100	100
5	F	367/619 (59%)	365 (100%)	2 (0%)	88	93
5	G	367/619 (59%)	362 (99%)	5 (1%)	67	80
6	H	260/574 (45%)	259 (100%)	1 (0%)	91	94
7	I	252/564 (45%)	251 (100%)	1 (0%)	91	94
8	J	113/322 (35%)	113 (100%)	0	100	100
9	K	132/223 (59%)	132 (100%)	0	100	100
10	L	61/229 (27%)	60 (98%)	1 (2%)	62	79
10	M	61/229 (27%)	60 (98%)	1 (2%)	62	79
11	N	71/154 (46%)	71 (100%)	0	100	100
11	O	71/154 (46%)	71 (100%)	0	100	100
12	P	78/182 (43%)	78 (100%)	0	100	100
13	Q	70/141 (50%)	69 (99%)	1 (1%)	67	80
13	R	70/141 (50%)	69 (99%)	1 (1%)	67	80
14	S	42/106 (40%)	40 (95%)	2 (5%)	25	51
15	T	155/293 (53%)	153 (99%)	2 (1%)	69	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3643/9761 (37%)	3614 (99%)	29 (1%)	82 89

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	G	558	LEU
15	T	193	ASN
5	G	607	ARG
13	R	125	ASN
5	G	589	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
11	N	122	GLN
11	O	122	GLN
15	T	193	ASN
2	B	924	HIS
2	B	912	ASN

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 monosaccharides 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
17	Z	8
16	Y	2

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Z	95:UNK	C	119:UNK	N	129.81
1	Z	52:UNK	C	81:UNK	N	116.40
1	Z	143:UNK	C	195:UNK	N	95.92
1	Z	223:UNK	C	309:UNK	N	54.56
1	Y	143:UNK	C	309:UNK	N	54.12

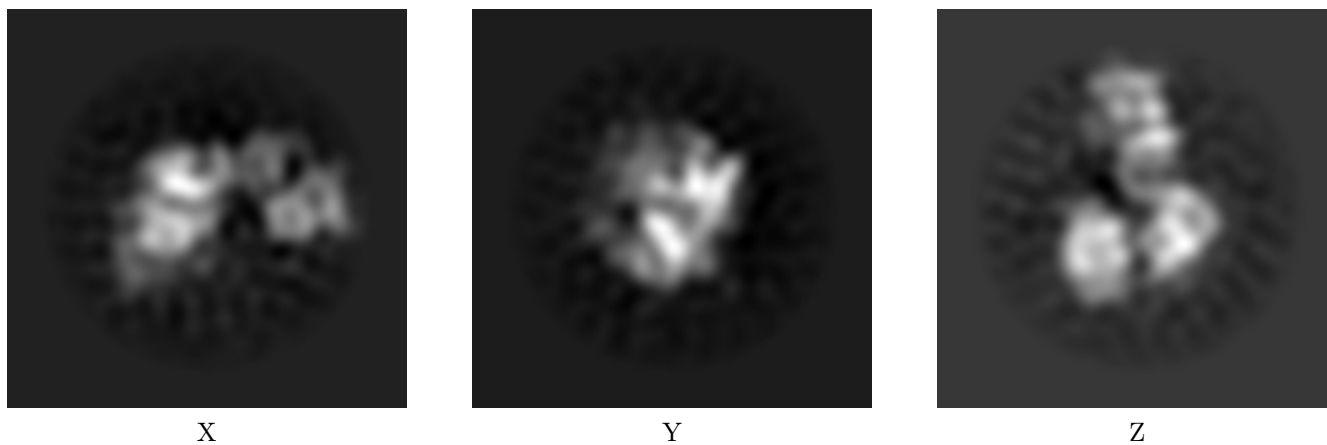
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9305. 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](#)

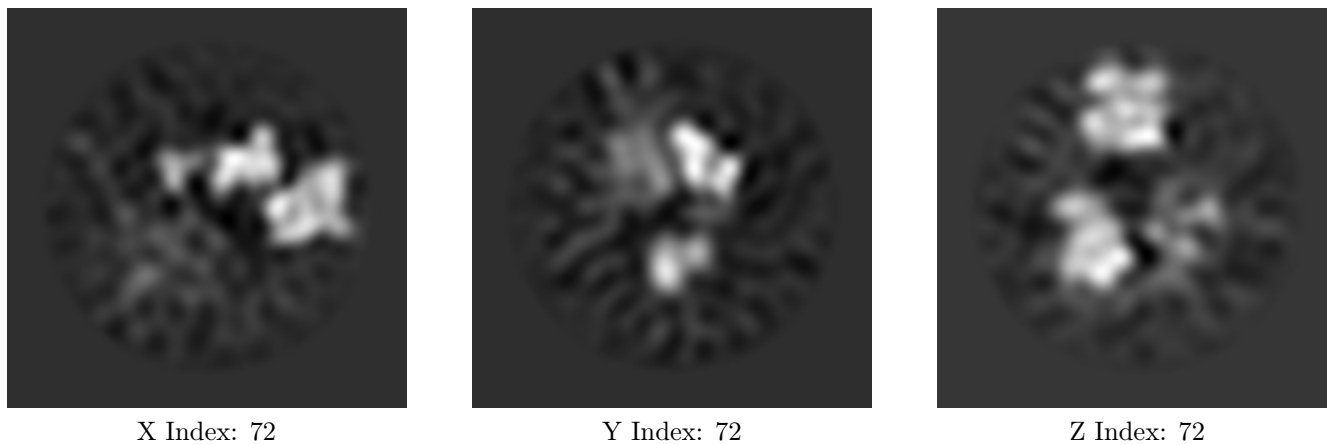
6.1.1 Primary map



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

6.2 Central slices [i](#)

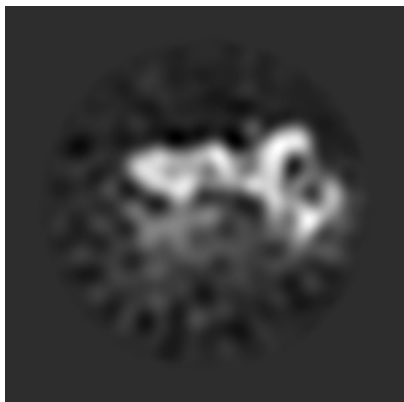
6.2.1 Primary map



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: 79



Y Index: 62

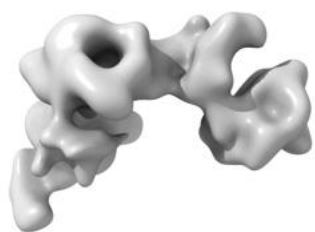


Z Index: 80

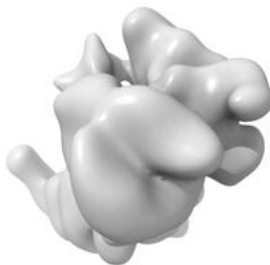
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

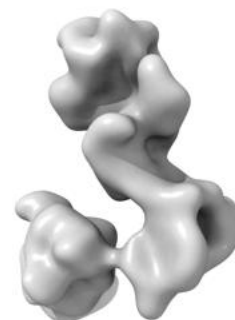
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

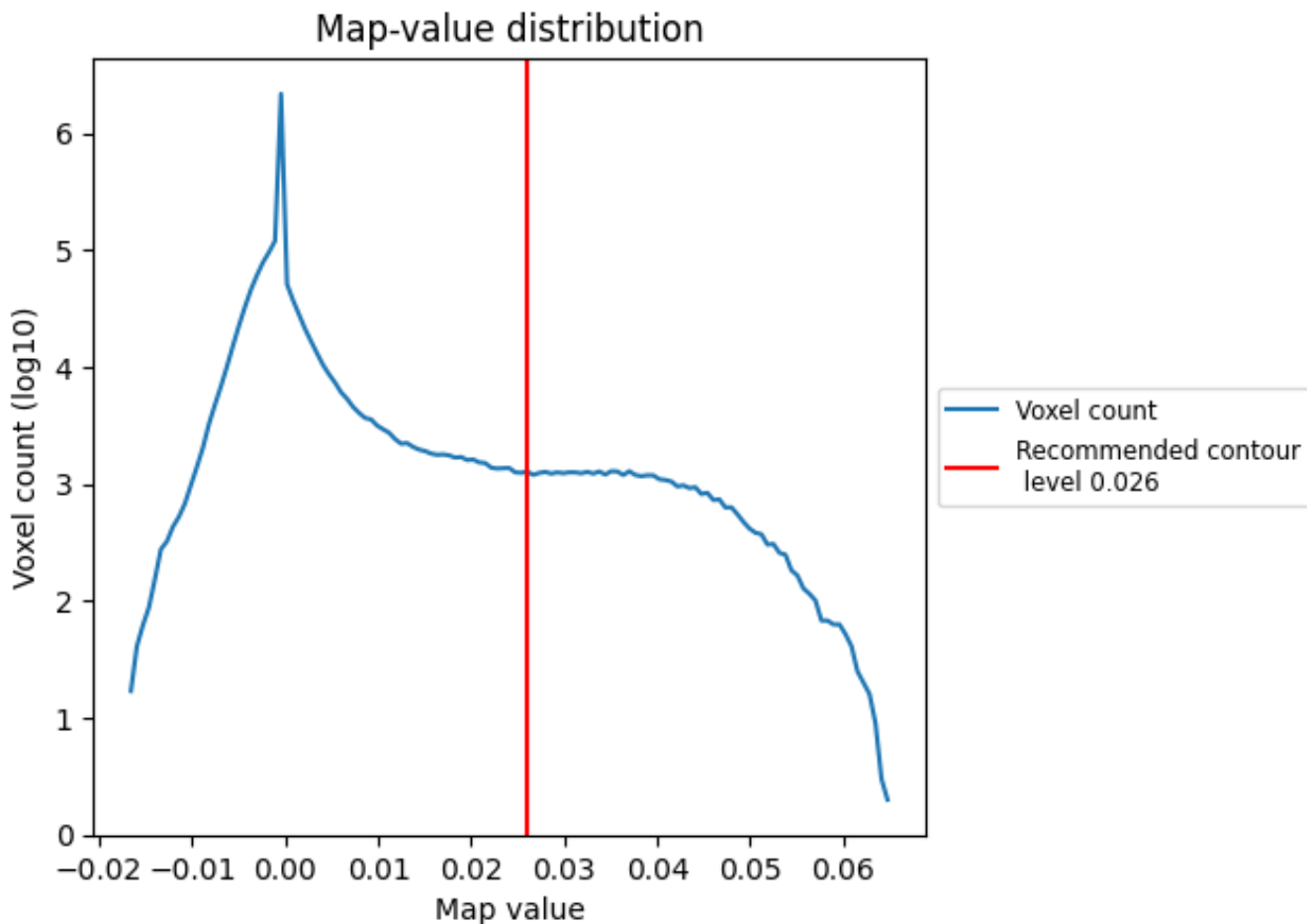
6.5 Mask visualisation

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

7 Map analysis [i](#)

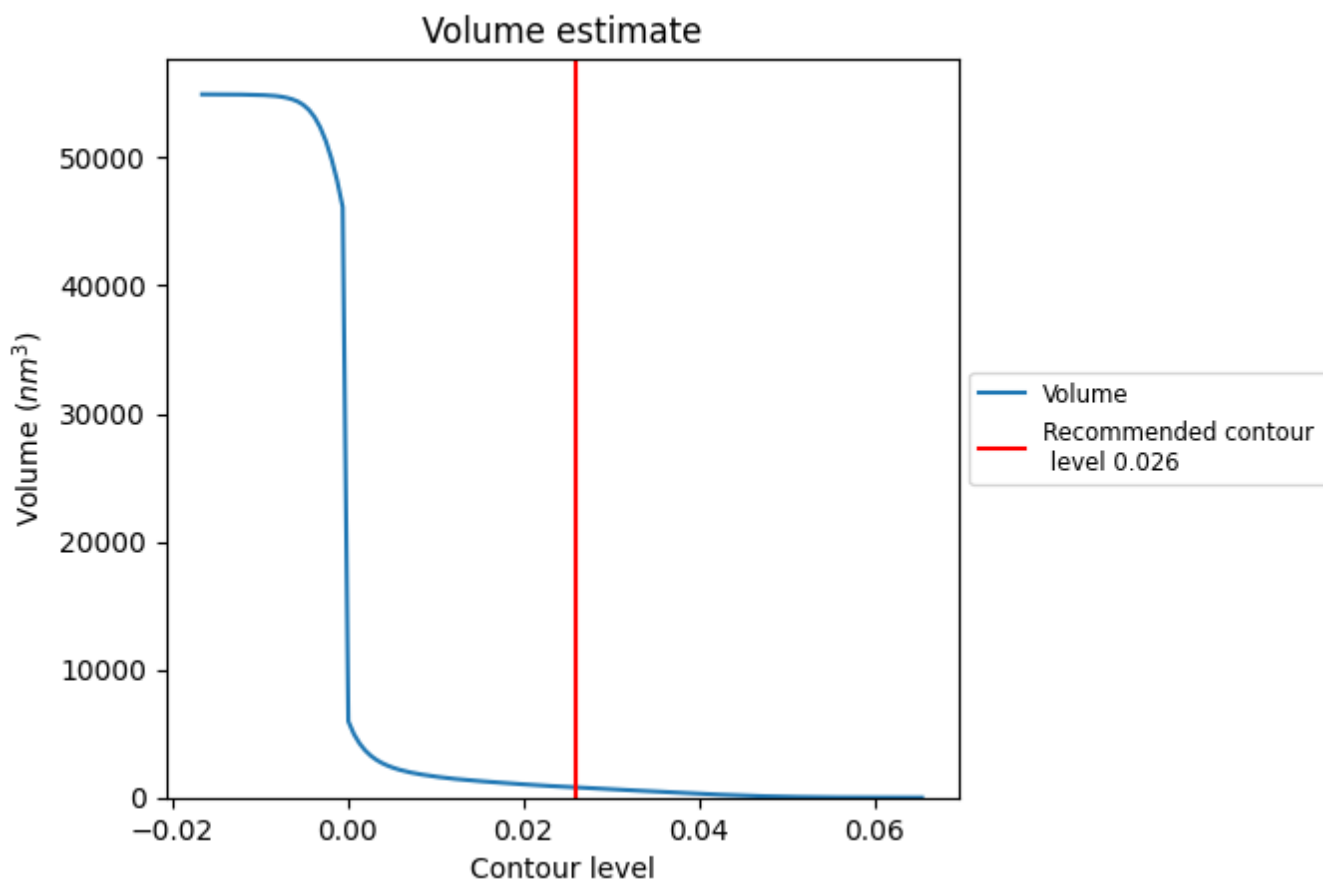
This section contains the results of statistical analysis of the map.

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.

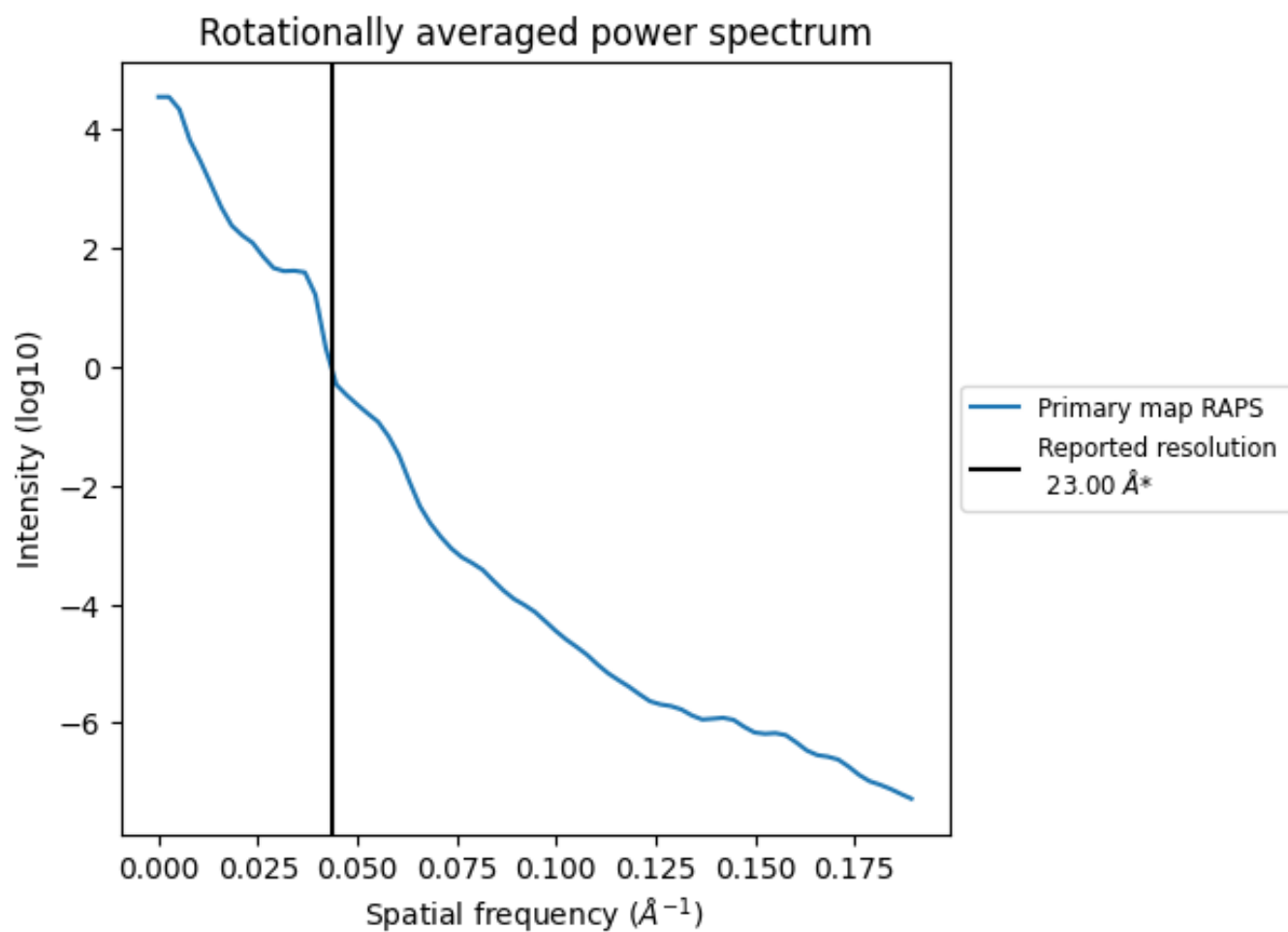
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 794 nm³; this corresponds to an approximate mass of 717 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 0.043 Å⁻¹

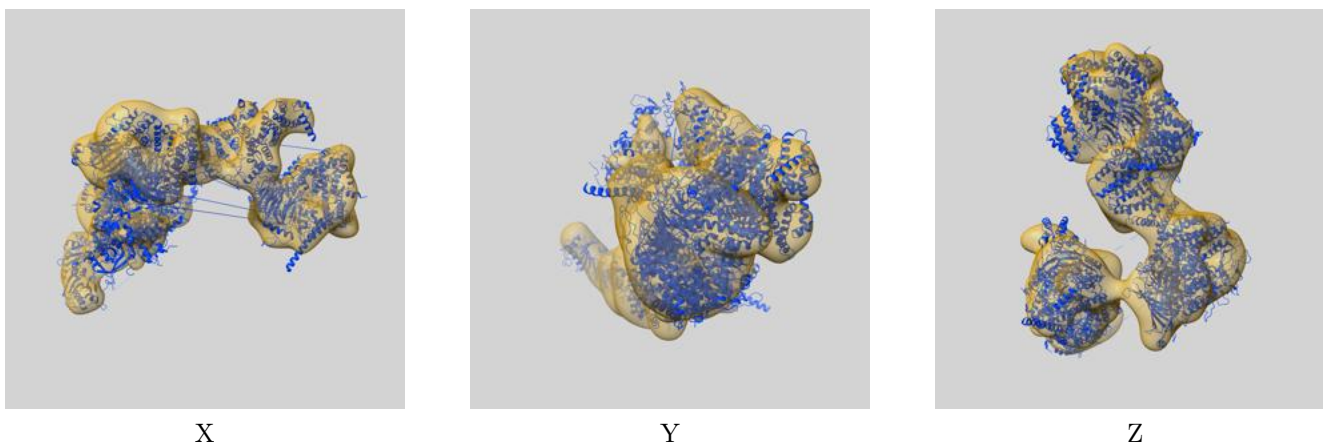
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

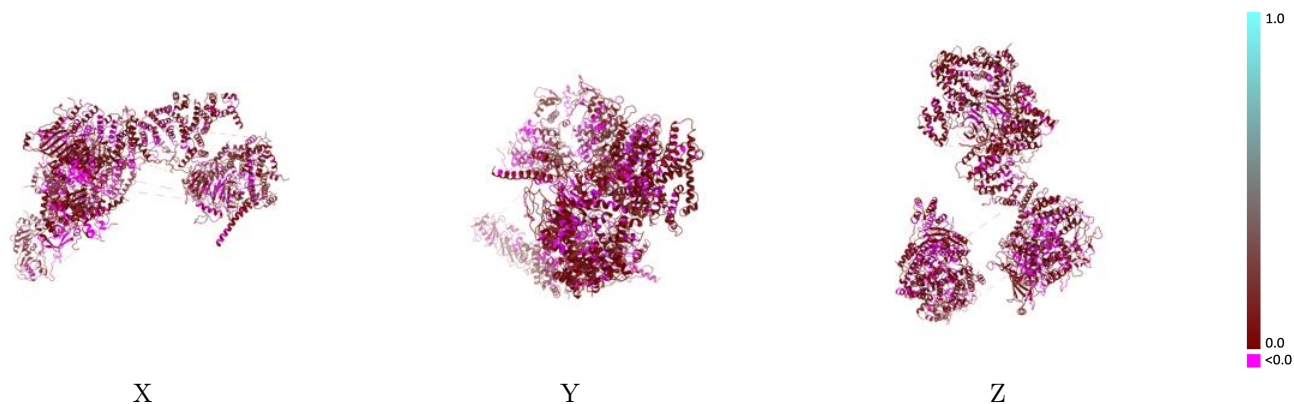
This section contains information regarding the fit between EMDB map EMD-9305 and PDB model 6MZL. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



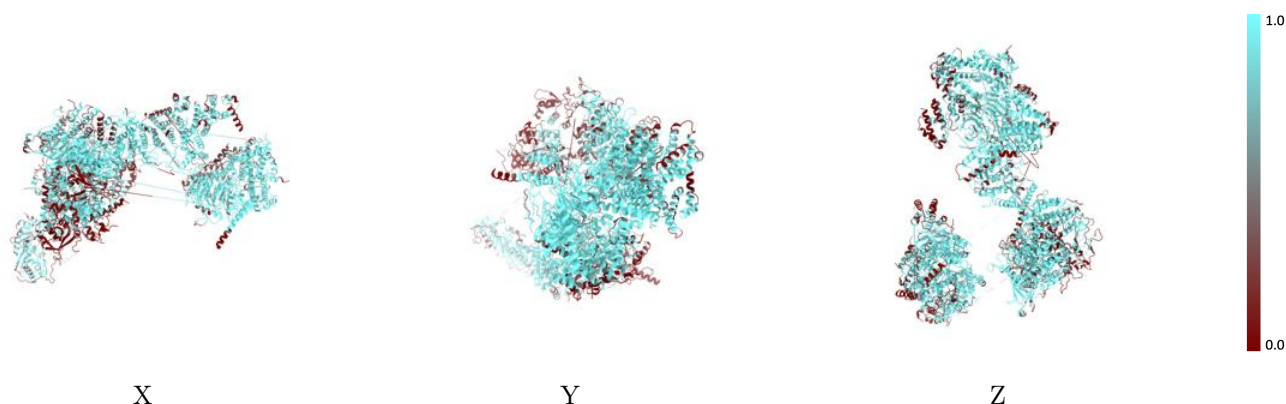
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



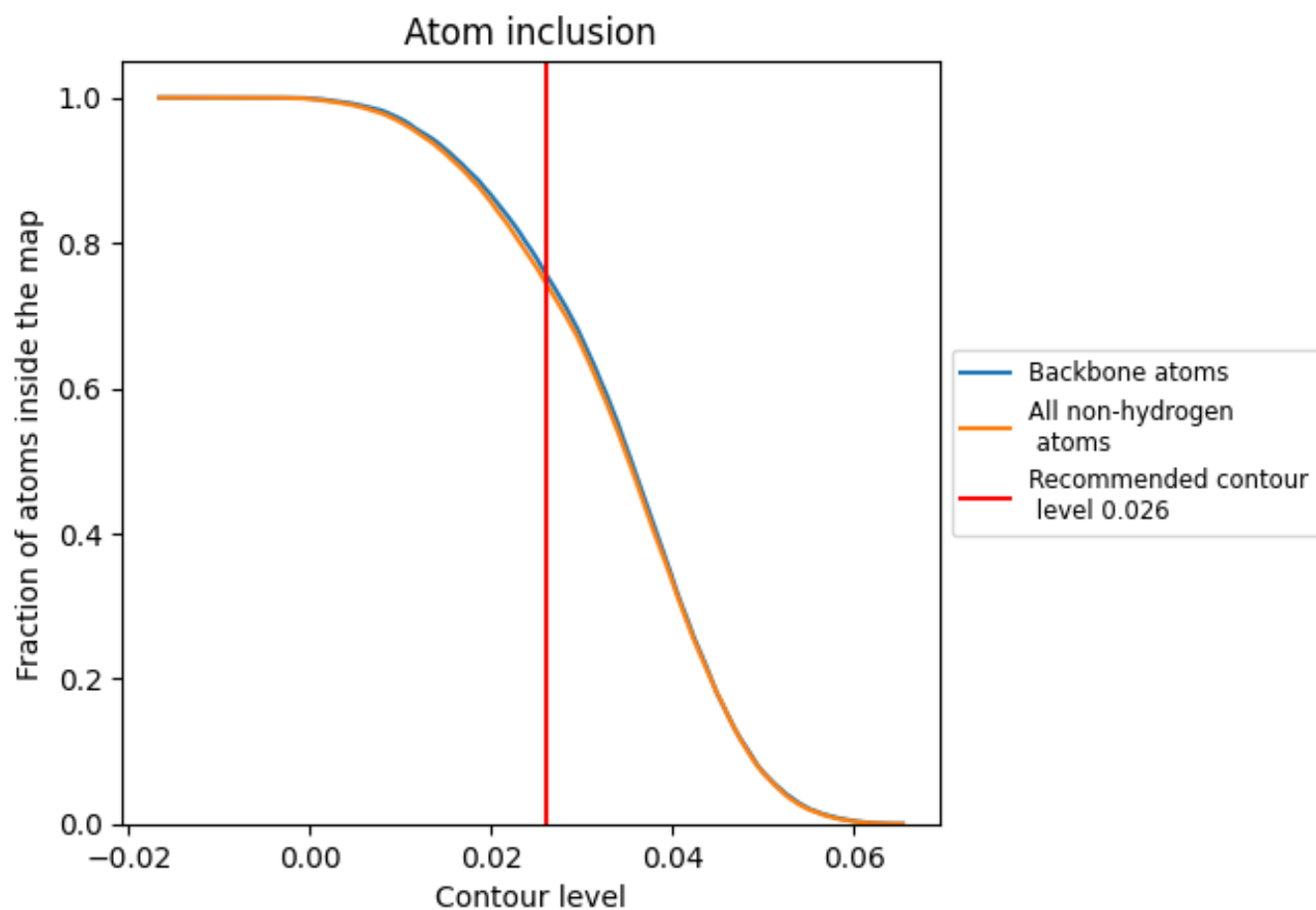
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 75% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7460	 0.0510
A	 0.4127	 0.0390
B	 0.7835	 0.0480
C	 0.9420	 0.0820
D	 0.6922	 0.0730
E	 0.7923	 0.0700
F	 0.7465	 0.0340
G	 0.8162	 0.0530
H	 0.8452	 0.0500
I	 0.8021	 0.0650
J	 0.2058	 0.0100
K	 0.9386	 0.0760
L	 0.9362	 0.0420
M	 0.7171	 0.0580
N	 0.8628	 0.0590
O	 0.9432	 0.0750
P	 0.6942	 0.0320
Q	 0.8170	 0.0450
R	 0.8403	 0.0710
S	 0.9668	 0.0990
T	 0.7176	 0.0690
Y	 0.4792	 0.0320
Z	 0.8571	 0.0550

