



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:31 AM UTC

PDB ID : 7EGI / pdb_00007egi
EMDB ID : EMD-31118
Title : TFIID in rearranged conformation
Authors : Chen, X.; Wu, Z.; Li, J.; Zhao, D.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 9.82 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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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:

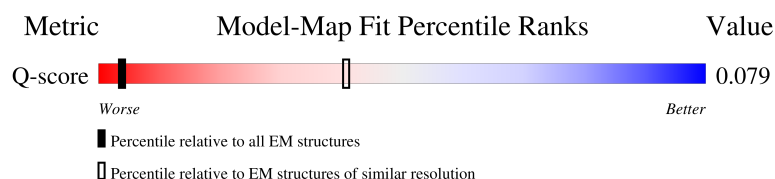
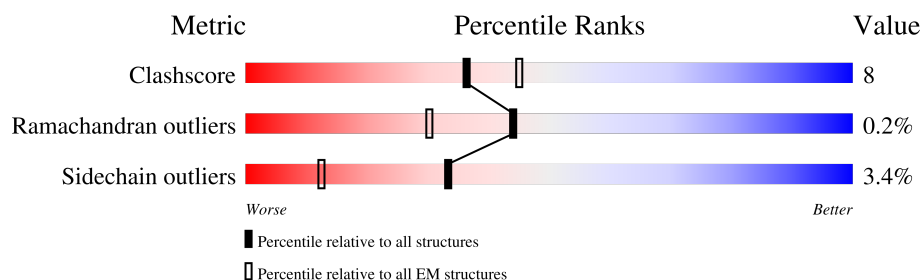
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.82 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.



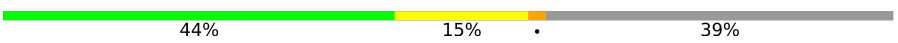
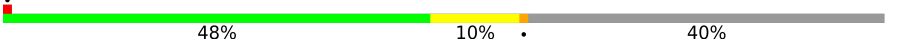
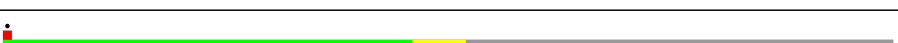
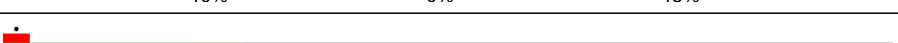
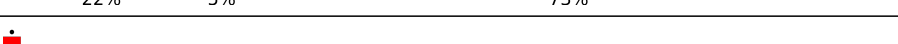
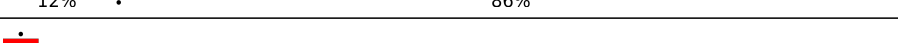
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	143 (9.40 - 10.31)

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	 23% 5% 71%
2	B	1199	 69% 11% 20%
3	D	1085	 14% 82%
3	d	1085	 12% 85%

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Mol	Chain	Length	Quality of chain
4	E	800	
4	e	800	
5	F	677	
5	f	677	
6	G	349	
7	H	310	
8	I	264	
8	i	264	
9	J	218	
9	j	218	
10	L	161	
10	l	161	
11	O	109	
12	P	339	
13	Q	376	
14	c	929	
15	k	211	
16	m	124	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 43358 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	549	Total	C	N	O	S	0	0
			4505	2879	781	818	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	963	Total	C	N	O	S	0	0
			7796	5011	1315	1412	58		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	197	Total	C	N	O	S	0	0
			1614	997	302	310	5		
3	d	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	545	Total	C	N	O	S	0	0
			4359	2765	756	817	21		
4	e	539	Total	C	N	O	S	0	0
			4327	2746	748	814	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	412	Total	C	N	O	S	0	0
			3143	1994	548	583	18		
5	f	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	144	Total	C	N	O	S	0	0
			1171	742	215	210	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	209	Total	C	N	O	S	0	0
			1622	1026	281	310	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	120	Total	C	N	O	S	0	0
			959	610	166	177	6		
8	i	121	Total	C	N	O	S	0	0
			967	615	167	178	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	90	Total	C	N	O	S	0	0
			720	466	115	135	4		
9	j	95	Total	C	N	O	S	0	0
			759	488	124	143	4		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	76	Total	C	N	O	S	0	0
			622	388	109	122	3		
10	l	107	Total	C	N	O	S	0	0
			876	547	158	166	5		

- Molecule 11 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	97	Total	C	N	O	S	0	0
			771	491	133	145	2		

- Molecule 12 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	177	Total	C	N	O	S	0	0
			1412	918	249	238	7		

- Molecule 13 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	101	Total	C	N	O	S	0	0
			827	524	139	160	4		

- Molecule 14 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	c	127	Total	C	N	O	S	0	0
			1011	638	174	193	6		

- Molecule 15 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	k	98	Total	C	N	O	S	0	0
			785	499	142	139	5		

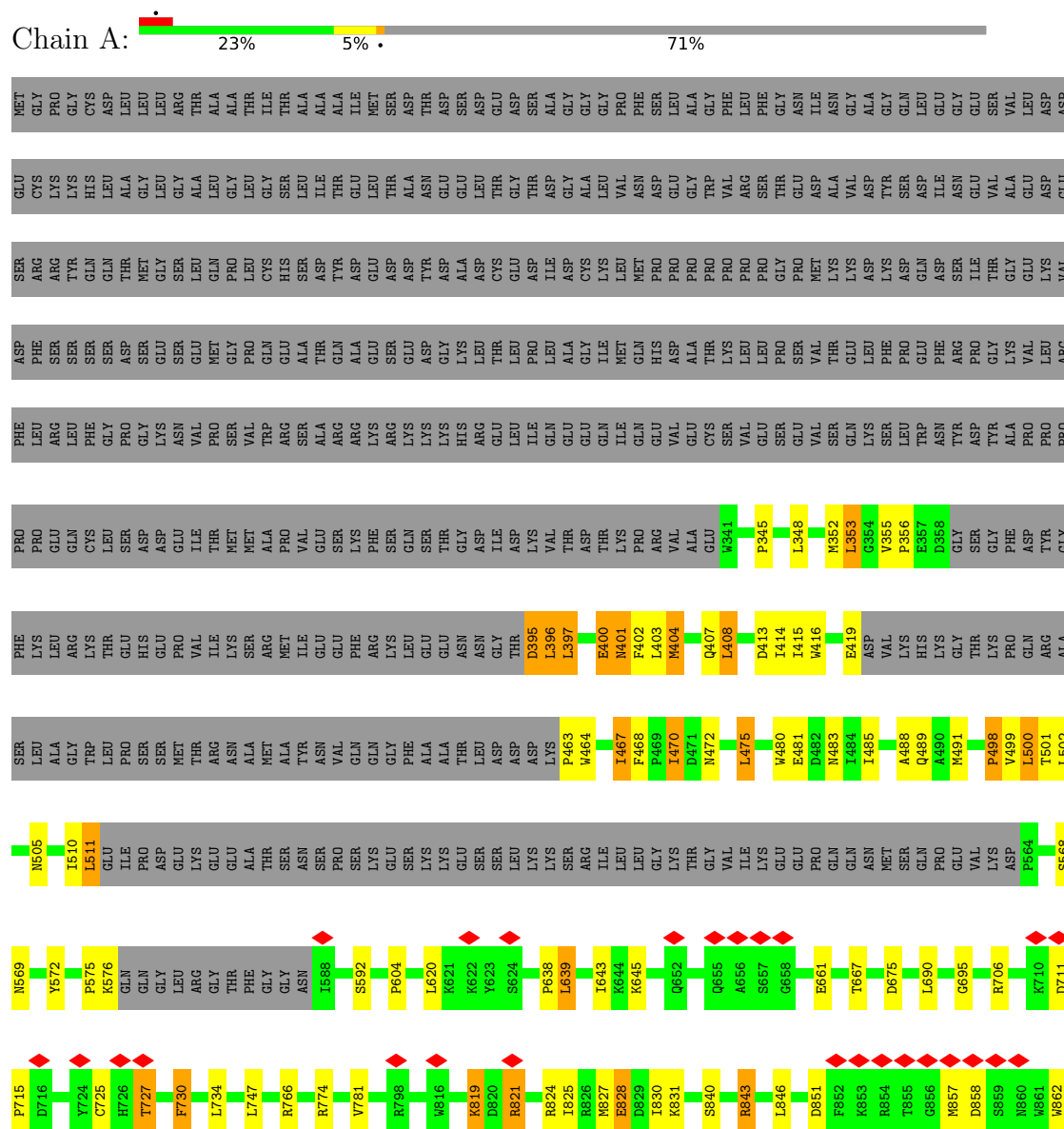
- Molecule 16 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m	87	Total	C	N	O	S	0	0
			724	456	131	131	6		

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 2: Transcription initiation factor TFIID subunit 2

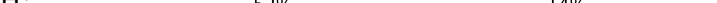
Chain B:  69% 11% • 20%





[illegible]

- Molecule 7: Transcription initiation factor TFIID subunit 8

Chain H:  52% 14% 33%

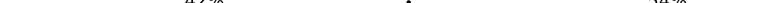
[illegible]

- Molecule 8: Transcription initiation factor TFIID subunit 9

Chain I: 38% 7% 55%

THR	ASP	ALA	GLY	MET
	ASN	SER	ARG	GLU
LEU		PRO	THR	SER
		ALA	VAL	LYS
		THR	PRO	THR
		SER	ARG	ALA
		ALA	LEU	SER
		VAL	SER	PRO
		GLN	VAL	LYS
		ASN	GLY	SER
		VAL	SER	MET
		LEU	VAL	P13
		ILE	THR	
		ASN	SER	M19
		PRO	ARG	A20
		SER	PRO	Q21
		LEU	SER	I22
		ILE	THR	L23
		GLY	PRO	K24
		LYS	THR	
		ASN	LEU	I28
		ILE	GLY	
		LEU	THR	E32
		ILE	PRO	
		THR	THR	V35
		THR	PRO	
		THR	GLN	Q38
		ASN	THR	
		MET	MET	E41
		MET	SER	F42
		SER	VAL	A43
		GLY	SER	F44
		GLN	THR	R45
		ASN	LYS	
		THR	VAL	L51
		ALA	GLY	
		ASN	THR	K63
		GLU	PRO	A64
		SER	MET	
		SER	SER	
		ASN	LEU	D69
		ALA	THR	
		LEU	GLY	S82
		LYS	GLN	
		ARG	ARG	R119
		LYS	PHE	Y120
		ARG	THR	
		GLU	VAL	T123
		ASP	GLN	
		ASP	MET	L129
		ASP	PRO	
		ASP	THR	L132
		ASP	SER	GLN
		ASP	GLN	LYS
		ASP	SER	LYS
		ASP	PRO	ALA
		ASP	ALA	SER
		ASP	VAL	THR
		ASP	LYS	SER

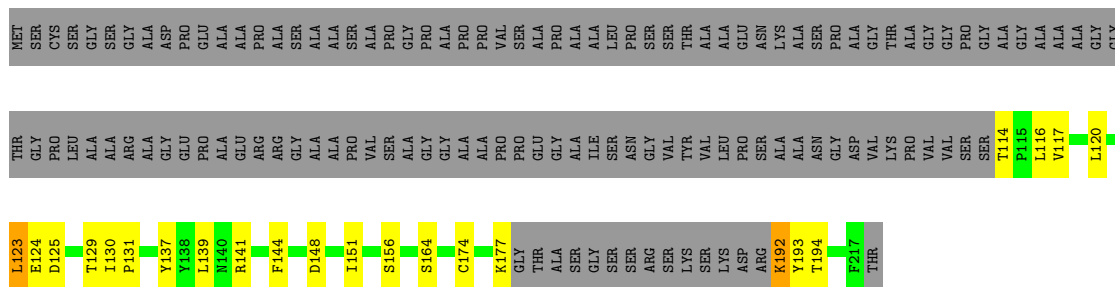
- Molecule 8: Transcription initiation factor TFIID subunit 9

Chain i:  42% . 54%

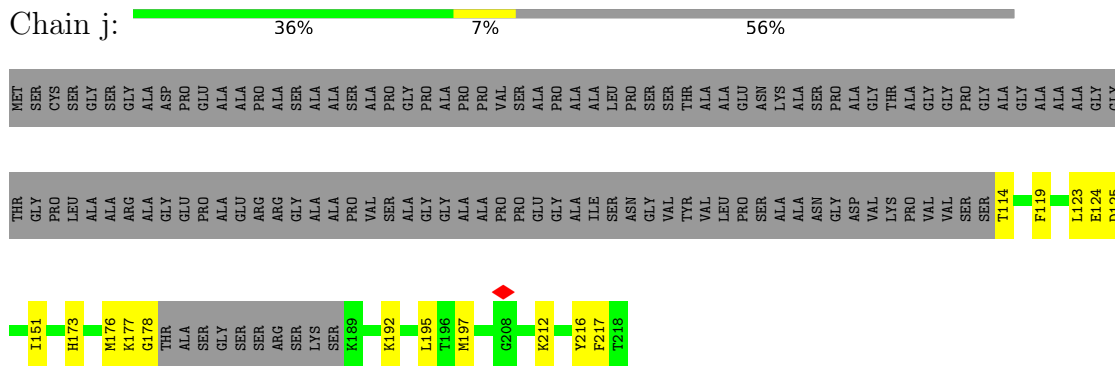
[illegible]

- Molecule 9: Transcription initiation factor TFIID subunit 10

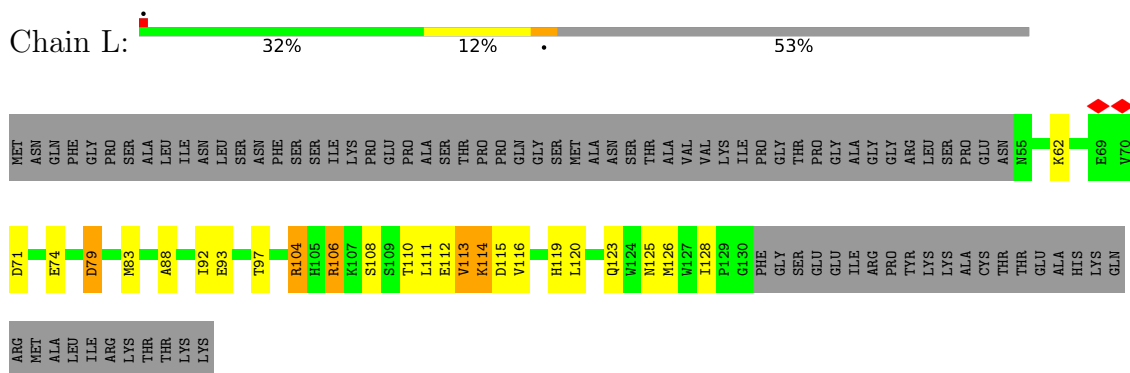
Chain J:  31% 10% 59%



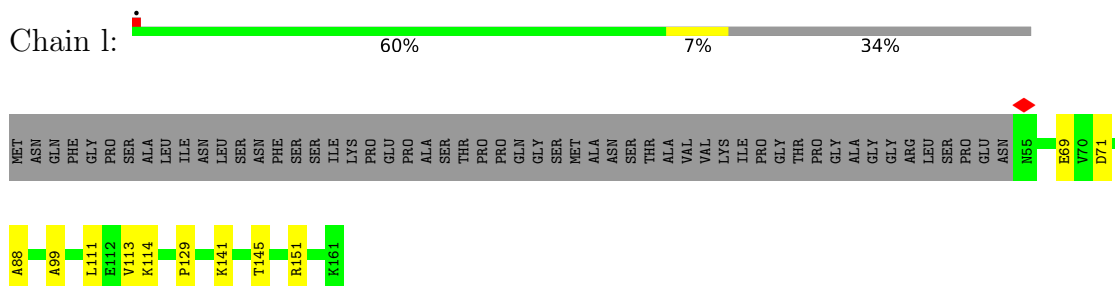
- Molecule 9: Transcription initiation factor TFIID subunit 10



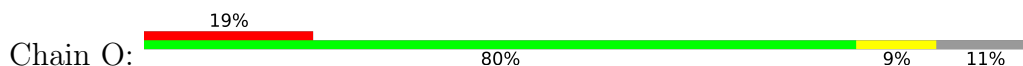
- Molecule 10: Transcription initiation factor TFIID subunit 12

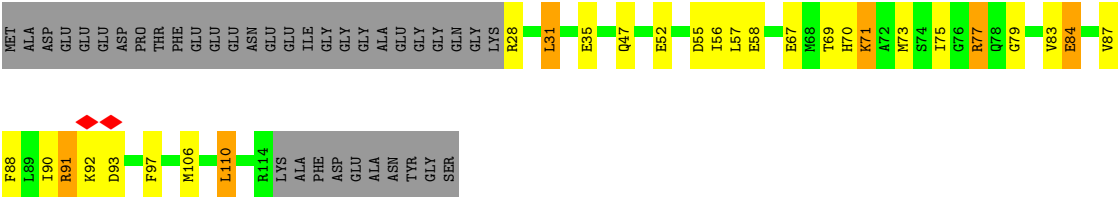


- Molecule 10: Transcription initiation factor TFIID subunit 12



- Molecule 11: Transcription initiation factor IIA subunit 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64496	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.040	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	432.0, 432.0, 432.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	0.62	0/4621	0.95	7/6240 (0.1%)
2	B	0.46	2/7993 (0.0%)	0.68	7/10836 (0.1%)
3	D	0.58	0/1628	0.83	0/2178
3	d	0.47	0/1321	0.71	2/1772 (0.1%)
4	E	0.45	1/4465 (0.0%)	0.72	3/6045 (0.0%)
4	e	0.54	1/4433 (0.0%)	0.77	0/6004
5	F	0.63	1/3201 (0.0%)	1.00	7/4347 (0.2%)
5	f	0.46	0/3140	0.80	6/4268 (0.1%)
6	G	0.68	0/1190	0.94	1/1601 (0.1%)
7	H	0.70	3/1662 (0.2%)	0.93	8/2272 (0.4%)
8	I	0.20	0/981	0.41	0/1332
8	i	0.20	0/989	0.40	0/1343
9	J	0.83	0/736	1.15	4/998 (0.4%)
9	j	0.73	0/775	0.97	0/1049
10	L	0.68	0/630	1.13	1/852 (0.1%)
10	l	0.58	0/888	0.88	0/1194
11	O	0.30	0/781	0.73	0/1061
12	P	0.55	0/1438	0.78	1/1935 (0.1%)
13	Q	0.34	0/842	0.69	0/1134
14	c	0.48	0/1035	0.67	0/1406
15	k	0.28	0/799	0.53	1/1070 (0.1%)
16	m	0.84	0/733	1.18	1/977 (0.1%)
All	All	0.54	8/44281 (0.0%)	0.81	49/59914 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	28	ASN	C-O	-7.56	1.15	1.24
7	H	27	ASP	C-O	-7.14	1.15	1.24
7	H	31	LEU	C-O	-6.34	1.16	1.24
2	B	61	ASN	C-O	-6.02	1.18	1.24
4	e	445	LYS	C-O	5.71	1.30	1.24

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	491	HIS	N-CA-C	-9.51	100.91	111.28
5	f	149	PRO	O-C-N	9.18	125.53	121.31
4	E	756	THR	N-CA-C	-8.38	103.19	113.50
7	H	32	ALA	N-CA-C	-8.20	102.29	111.07
1	A	356	PRO	N-CA-C	7.90	124.79	114.68

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4505	0	4424	109	0
2	B	7796	0	7751	84	0
3	D	1614	0	1634	42	0
3	d	1307	0	1318	15	0
4	E	4359	0	4245	76	0
4	e	4327	0	4197	59	0
5	F	3143	0	3093	101	0
5	f	3081	0	3012	64	0
6	G	1171	0	1222	17	0
7	H	1622	0	1595	37	0
8	I	959	0	969	15	0
8	i	967	0	977	9	0
9	J	720	0	719	14	0
9	j	759	0	759	14	0
10	L	622	0	620	22	0
10	l	876	0	893	9	0
11	O	771	0	764	11	0
12	P	1412	0	1506	18	0
13	Q	827	0	794	12	0
14	c	1011	0	975	17	0
15	k	785	0	818	9	0
16	m	724	0	744	25	0
All	All	43358	0	43029	667	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 8.

The worst 5 of 667 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:576:LYS:HG2	1:A:943:LYS:CD	1.33	1.53
1:A:576:LYS:CG	1:A:943:LYS:HD3	1.38	1.51
1:A:1200:THR:O	1:A:1204:GLU:HG2	1.52	1.08
9:J:192:LYS:HE3	9:J:192:LYS:N	1.78	0.99
1:A:725:CYS:O	1:A:725:CYS:SG	2.22	0.97

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	533/1872 (28%)	514 (96%)	18 (3%)	1 (0%)	43	78
2	B	959/1199 (80%)	912 (95%)	47 (5%)	0	100	100
3	D	191/1085 (18%)	182 (95%)	9 (5%)	0	100	100
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	539/800 (67%)	515 (96%)	23 (4%)	1 (0%)	43	78
4	e	531/800 (66%)	482 (91%)	48 (9%)	1 (0%)	43	78
5	F	408/677 (60%)	390 (96%)	17 (4%)	1 (0%)	43	78
5	f	399/677 (59%)	383 (96%)	16 (4%)	0	100	100
6	G	138/349 (40%)	135 (98%)	3 (2%)	0	100	100
7	H	207/310 (67%)	193 (93%)	13 (6%)	1 (0%)	24	63
8	I	118/264 (45%)	115 (98%)	3 (2%)	0	100	100
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	J	86/218 (39%)	82 (95%)	4 (5%)	0	100	100
9	j	91/218 (42%)	85 (93%)	4 (4%)	2 (2%)	5	29
10	L	74/161 (46%)	72 (97%)	2 (3%)	0	100	100
10	l	105/161 (65%)	100 (95%)	5 (5%)	0	100	100
11	O	95/109 (87%)	86 (90%)	9 (10%)	0	100	100
12	P	175/339 (52%)	165 (94%)	9 (5%)	1 (1%)	21	59
13	Q	97/376 (26%)	89 (92%)	8 (8%)	0	100	100
14	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
15	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
16	m	85/124 (68%)	82 (96%)	3 (4%)	0	100	100
All	All	5325/12228 (44%)	5054 (95%)	263 (5%)	8 (0%)	44	78

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	523	VAL
4	e	522	ASP
9	j	124	GLU
5	F	411	VAL
9	j	177	LYS

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	487/1665 (29%)	444 (91%)	43 (9%)	9	28
2	B	876/1083 (81%)	863 (98%)	13 (2%)	57	72
3	D	175/815 (22%)	167 (95%)	8 (5%)	24	45
3	d	146/815 (18%)	144 (99%)	2 (1%)	59	72
4	E	478/657 (73%)	465 (97%)	13 (3%)	39	61
4	e	475/657 (72%)	462 (97%)	13 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	328/574 (57%)	309 (94%)	19 (6%)	18	40
5	f	322/574 (56%)	312 (97%)	10 (3%)	35	56
6	G	132/322 (41%)	124 (94%)	8 (6%)	17	38
7	H	178/270 (66%)	174 (98%)	4 (2%)	45	64
8	I	106/235 (45%)	106 (100%)	0	100	100
8	i	107/235 (46%)	107 (100%)	0	100	100
9	J	79/154 (51%)	72 (91%)	7 (9%)	9	28
9	j	83/154 (54%)	82 (99%)	1 (1%)	63	75
10	L	71/141 (50%)	66 (93%)	5 (7%)	14	35
10	l	98/141 (70%)	97 (99%)	1 (1%)	68	78
11	O	84/98 (86%)	84 (100%)	0	100	100
12	P	153/293 (52%)	150 (98%)	3 (2%)	48	66
13	Q	91/324 (28%)	89 (98%)	2 (2%)	45	64
14	c	113/833 (14%)	111 (98%)	2 (2%)	51	68
15	k	87/182 (48%)	87 (100%)	0	100	100
16	m	80/106 (76%)	71 (89%)	9 (11%)	5	19
All	All	4749/10328 (46%)	4586 (97%)	163 (3%)	33	54

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	L	79	ASP
5	f	253	TYR
10	L	114	LYS
4	e	258	ASN
5	f	366	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	79	ASN
15	k	205	HIS
7	H	145	HIS
15	k	202	ASN
5	f	30	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

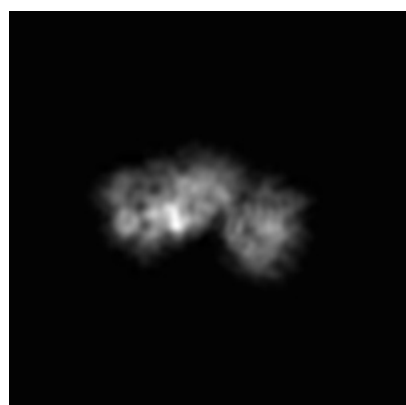
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31118. These allow visual inspection of the internal detail of the map and identification of artifacts.

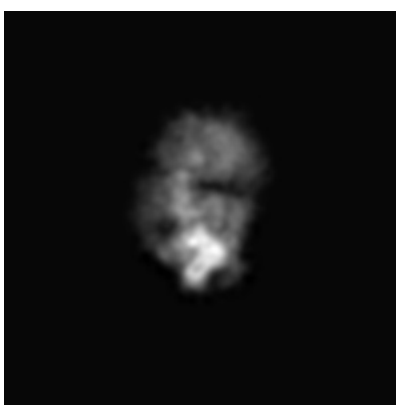
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

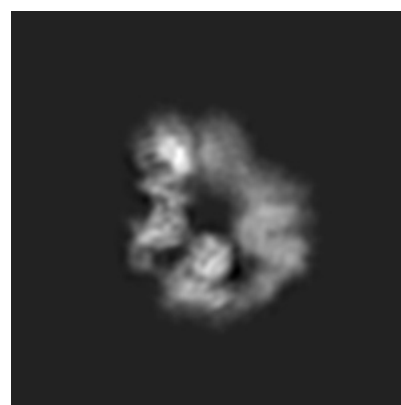
6.1.1 Primary map



X



Y

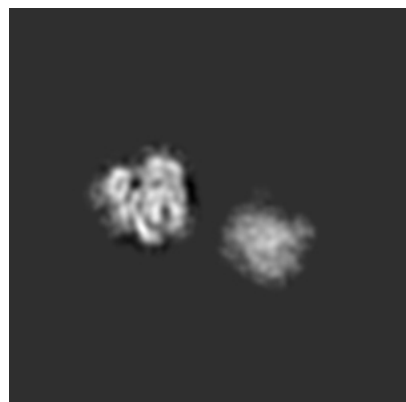


Z

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

6.2 Central slices [i](#)

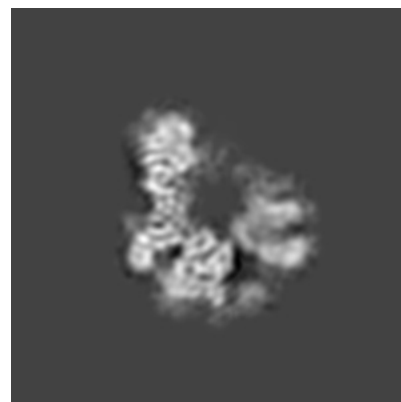
6.2.1 Primary map



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: 132



Y Index: 133

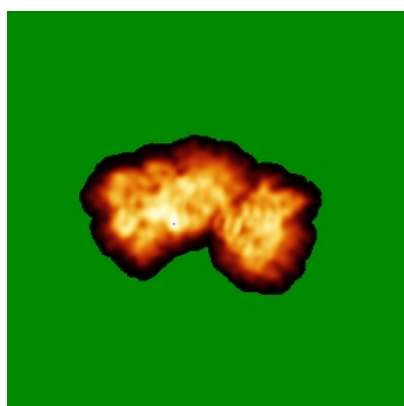


Z Index: 155

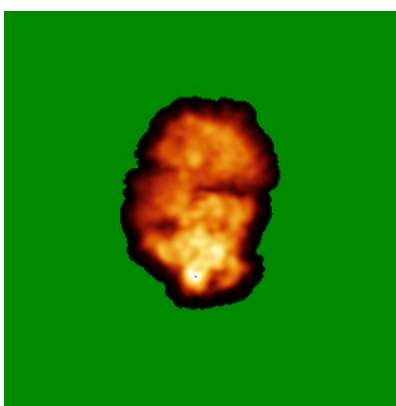
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

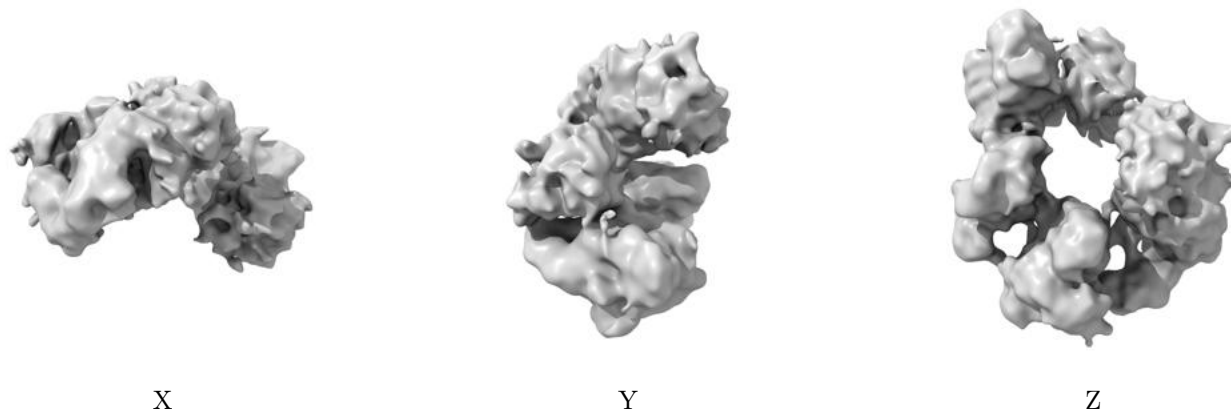


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

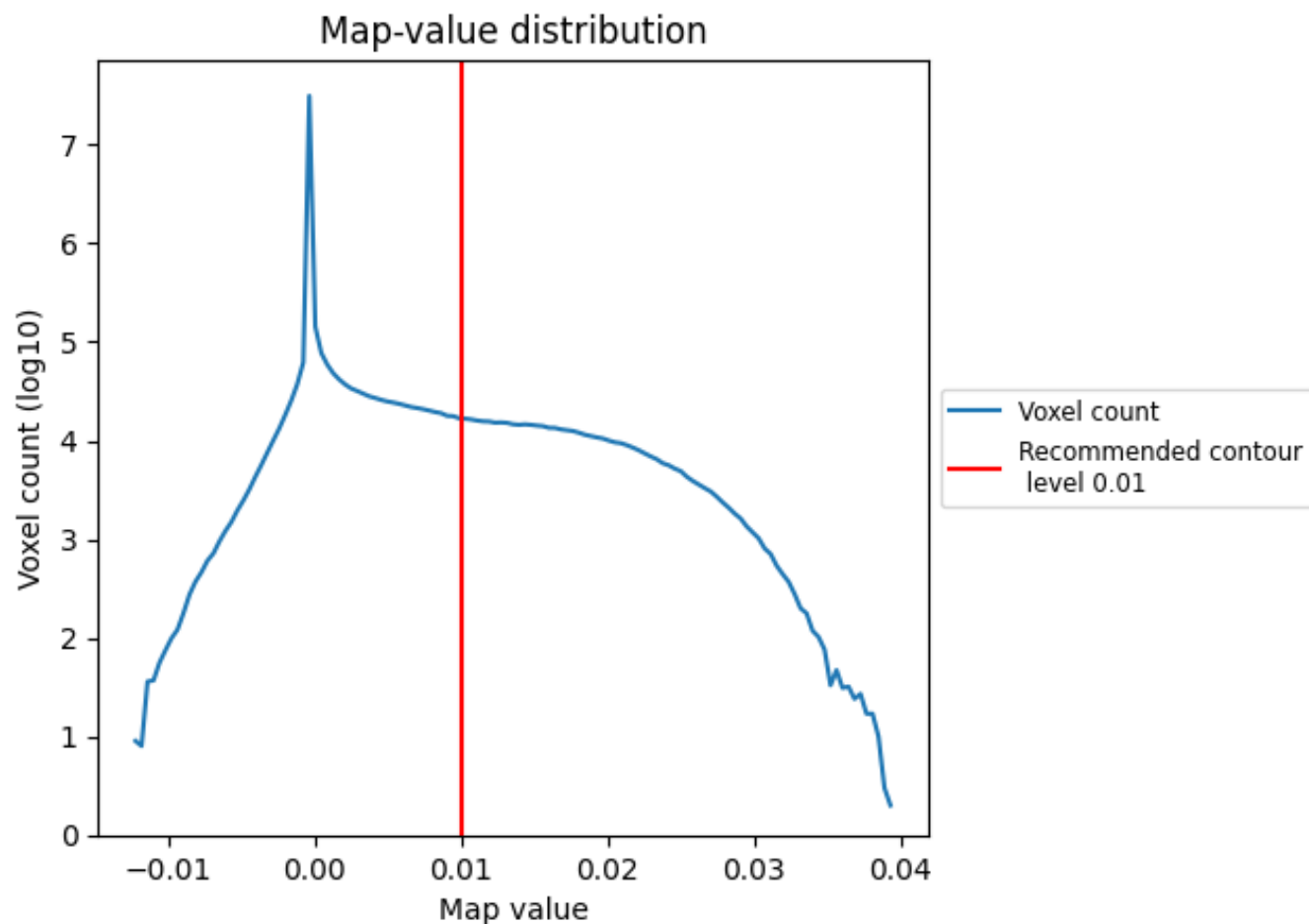
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

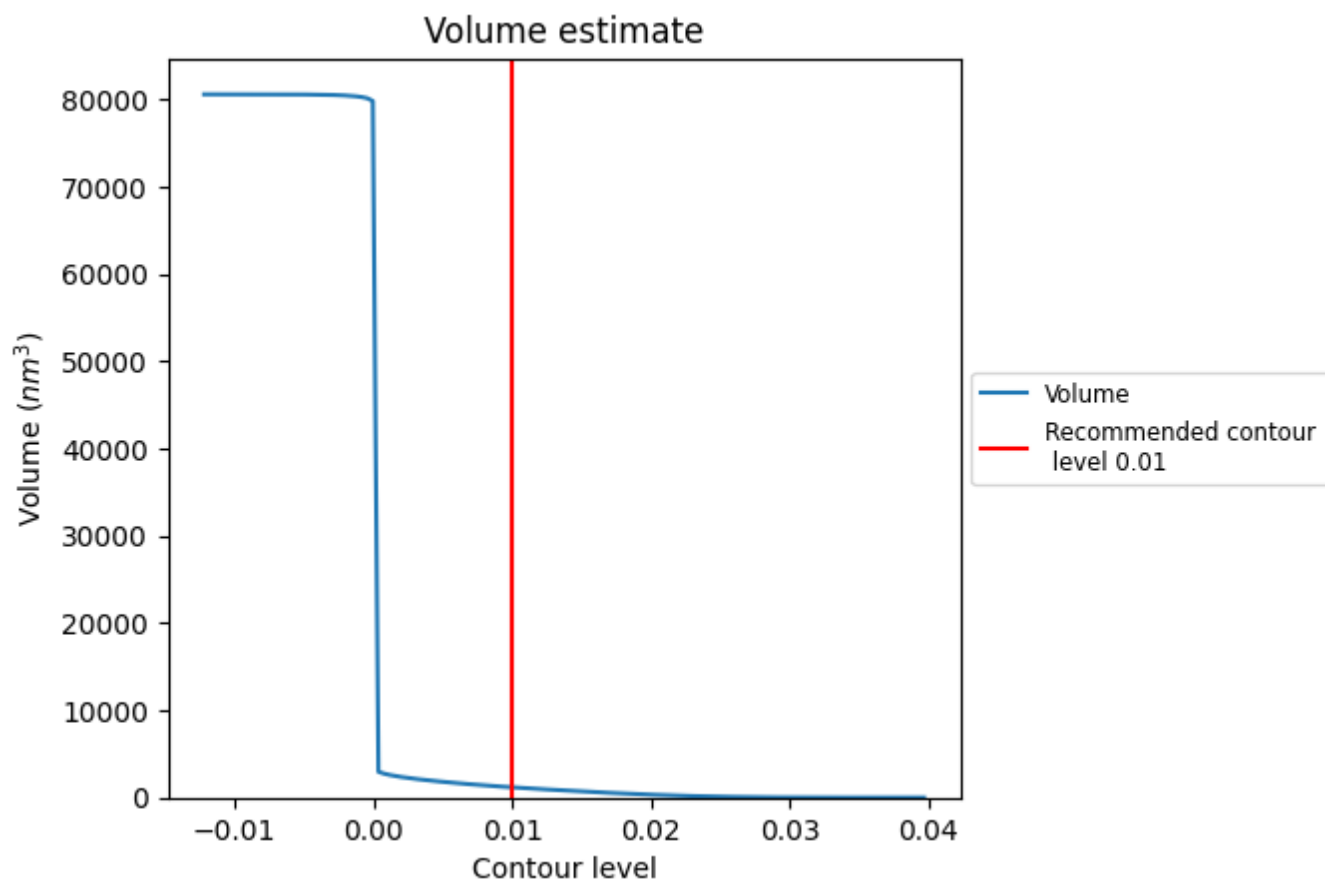
This section contains the results of statistical analysis of the map.

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.

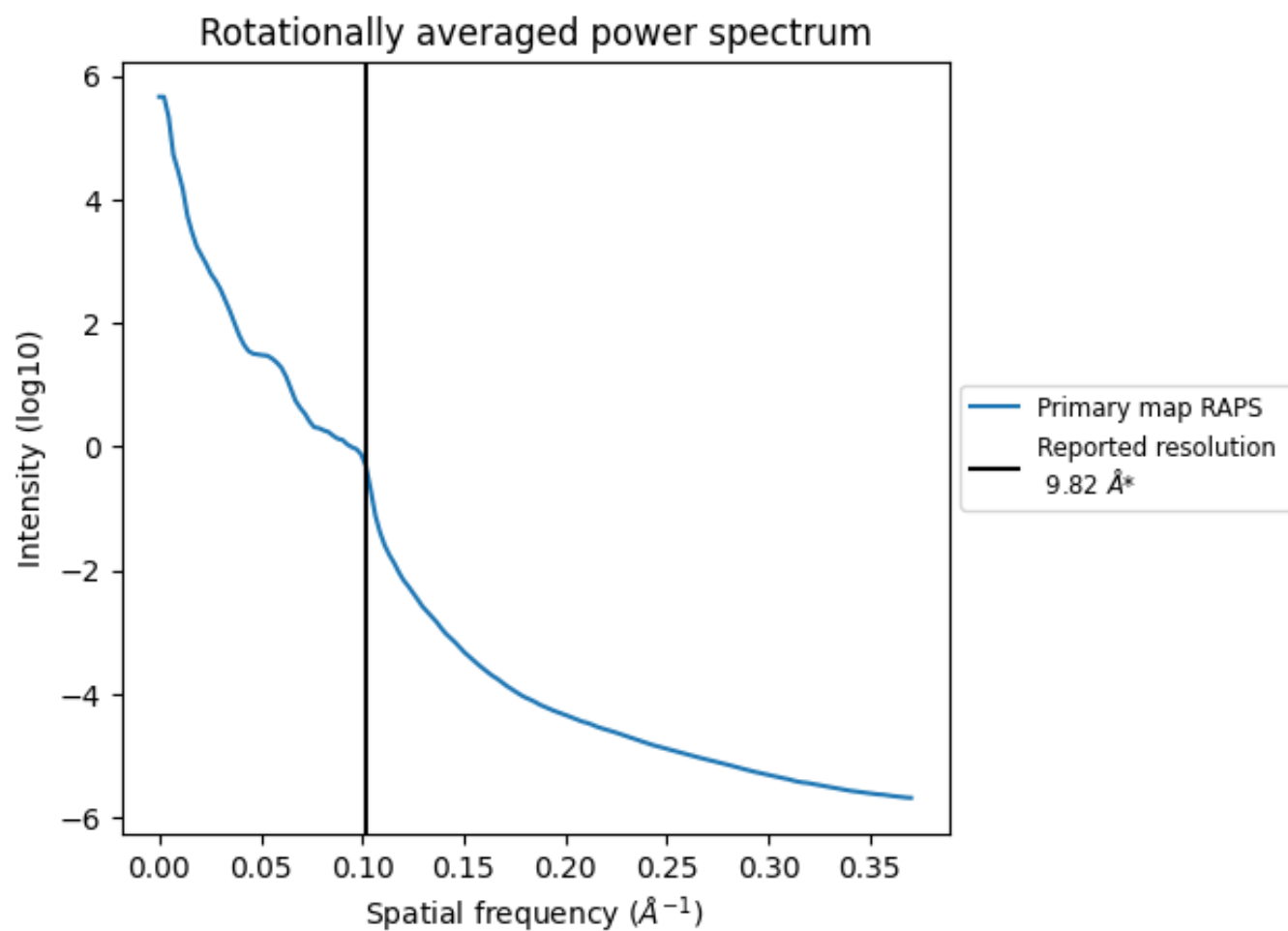
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1175 nm³; this corresponds to an approximate mass of 1062 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⁻¹

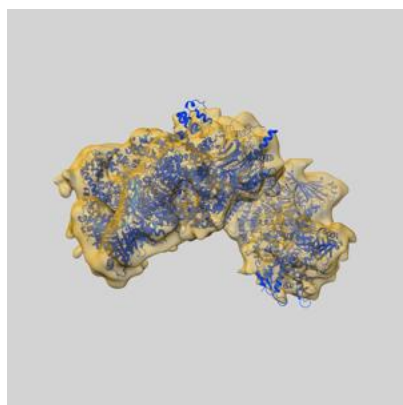
8 Fourier-Shell correlation

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

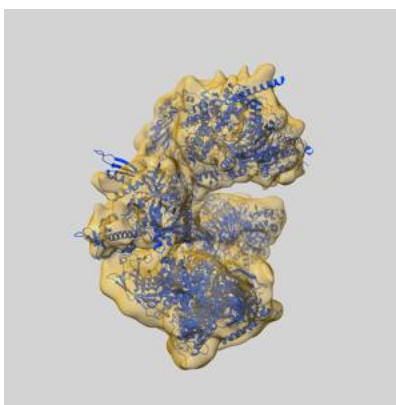
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31118 and PDB model 7EGI. Per-residue inclusion information can be found in section [3](#) on page [7](#).

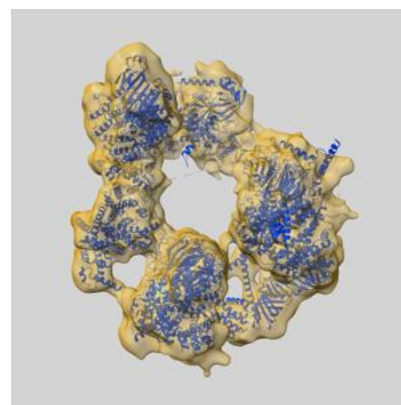
9.1 Map-model overlay [i](#)



X



Y



Z

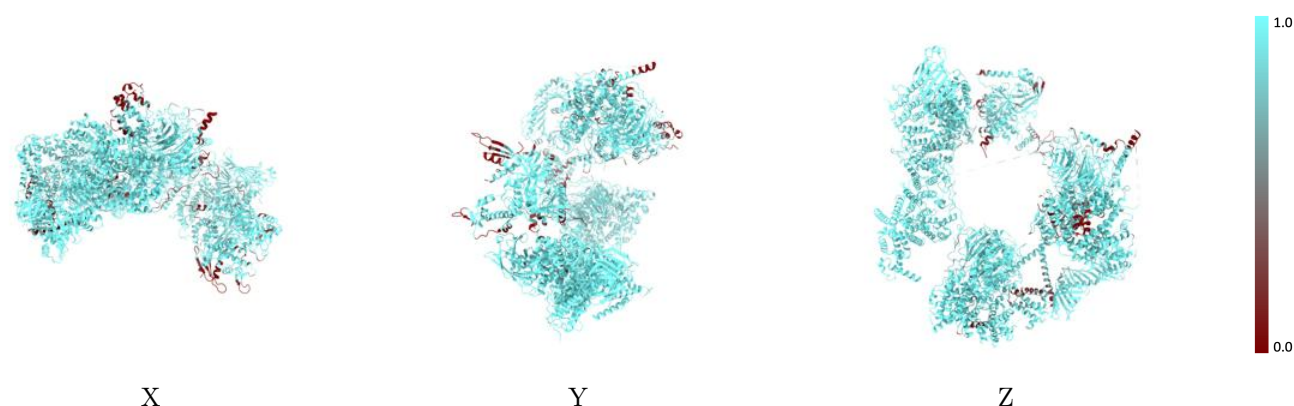
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



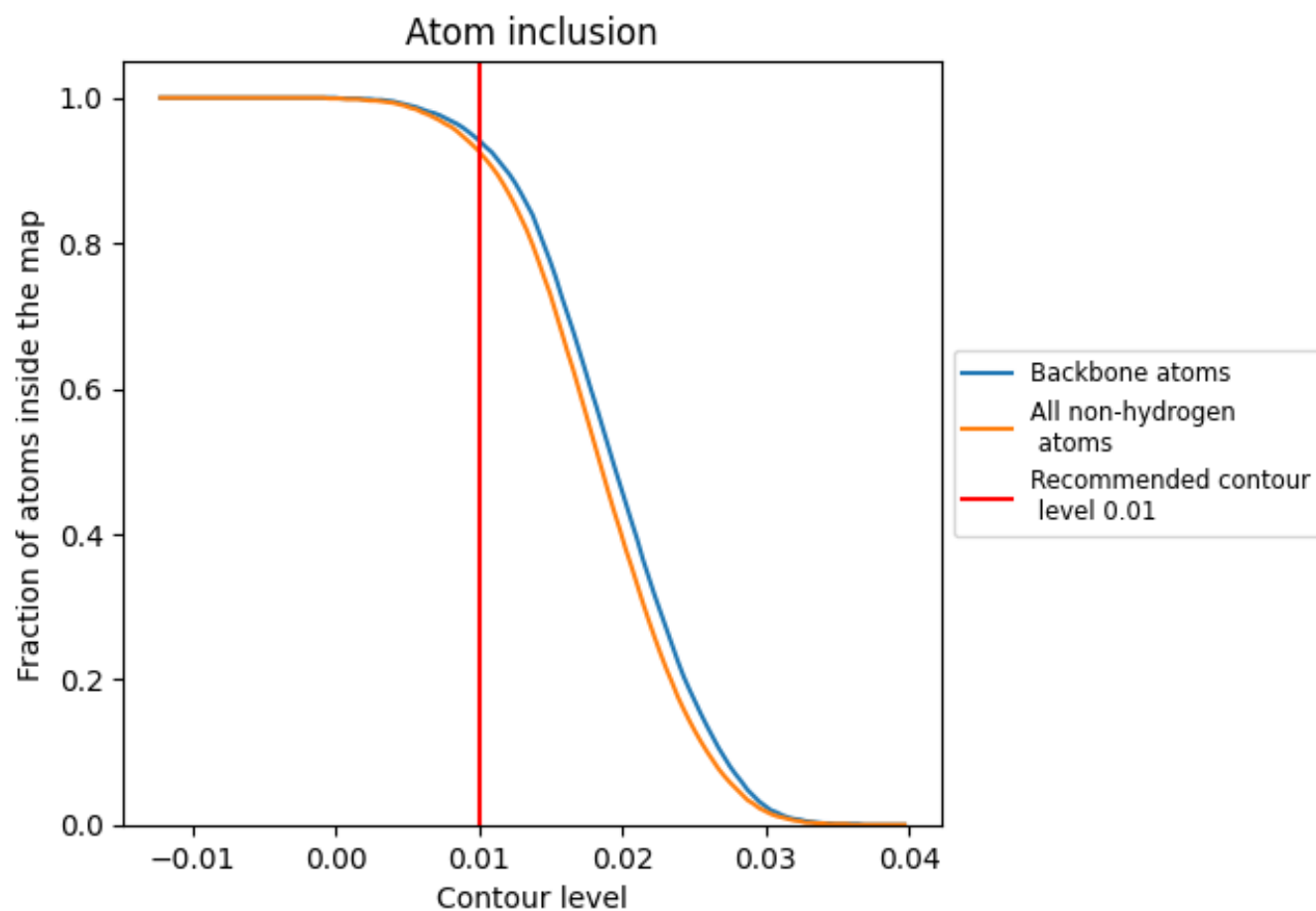
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.0790
A	 0.8380	 0.0620
B	 0.9800	 0.0950
D	 0.8530	 0.0940
E	 0.9730	 0.0850
F	 0.9700	 0.1150
G	 0.8270	 0.0320
H	 0.9720	 0.1260
I	 0.9710	 0.1130
J	 0.9960	 0.1020
L	 0.9760	 0.1130
O	 0.7740	 0.0740
P	 0.9650	 0.0700
Q	 0.8870	 0.0520
c	 0.8690	 0.0420
d	 0.9030	 0.0490
e	 0.8480	 0.0310
f	 0.9590	 0.0980
i	 0.9780	 0.0700
j	 0.9660	 0.0590
k	 0.8960	 0.0510
l	 0.9700	 0.0740
m	 0.9500	 0.0700

