



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:22 AM UTC

PDB ID : 7EGE / pdb_00007ege
EMDB ID : EMD-31114
Title : TFIID in canonical conformation
Authors : Chen, X.; Wu, Z.; Li, J.; Zhao, D.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 9.00 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.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

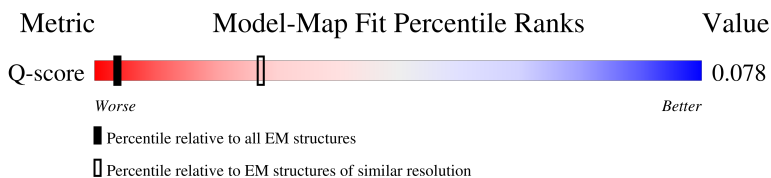
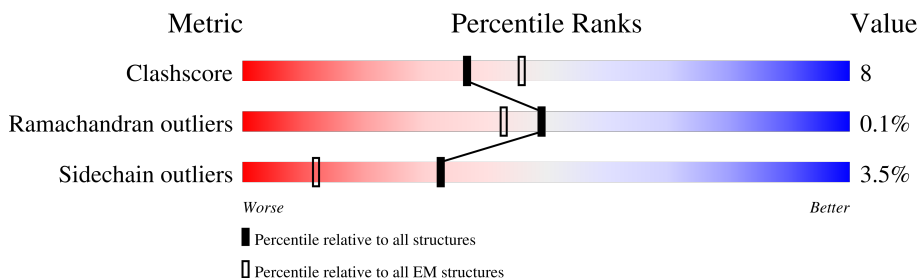
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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.



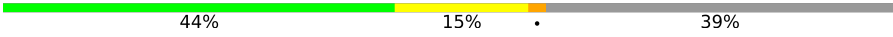
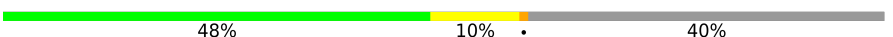
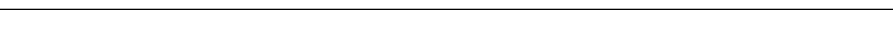
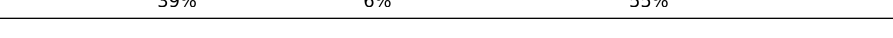
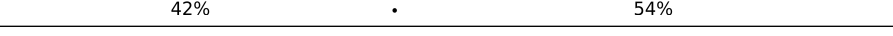
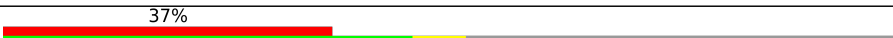
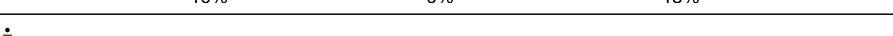
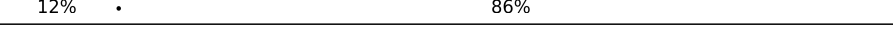
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	257 (8.50 - 9.50)

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	D	1085	
3	d	1085	

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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	P	339	
12	c	929	
13	k	211	
14	m	124	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 41435 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	154	Total	C	N	O	S	0	0
			1266	789	231	243	3		
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	547	Total	C	N	O	S	0	0
			4376	2774	759	822	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
			3149	1997	551	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 TATA-box-binding protein.

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

- Molecule 12 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 13 is a protein called Transcription initiation factor TFIID subunit 11.

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

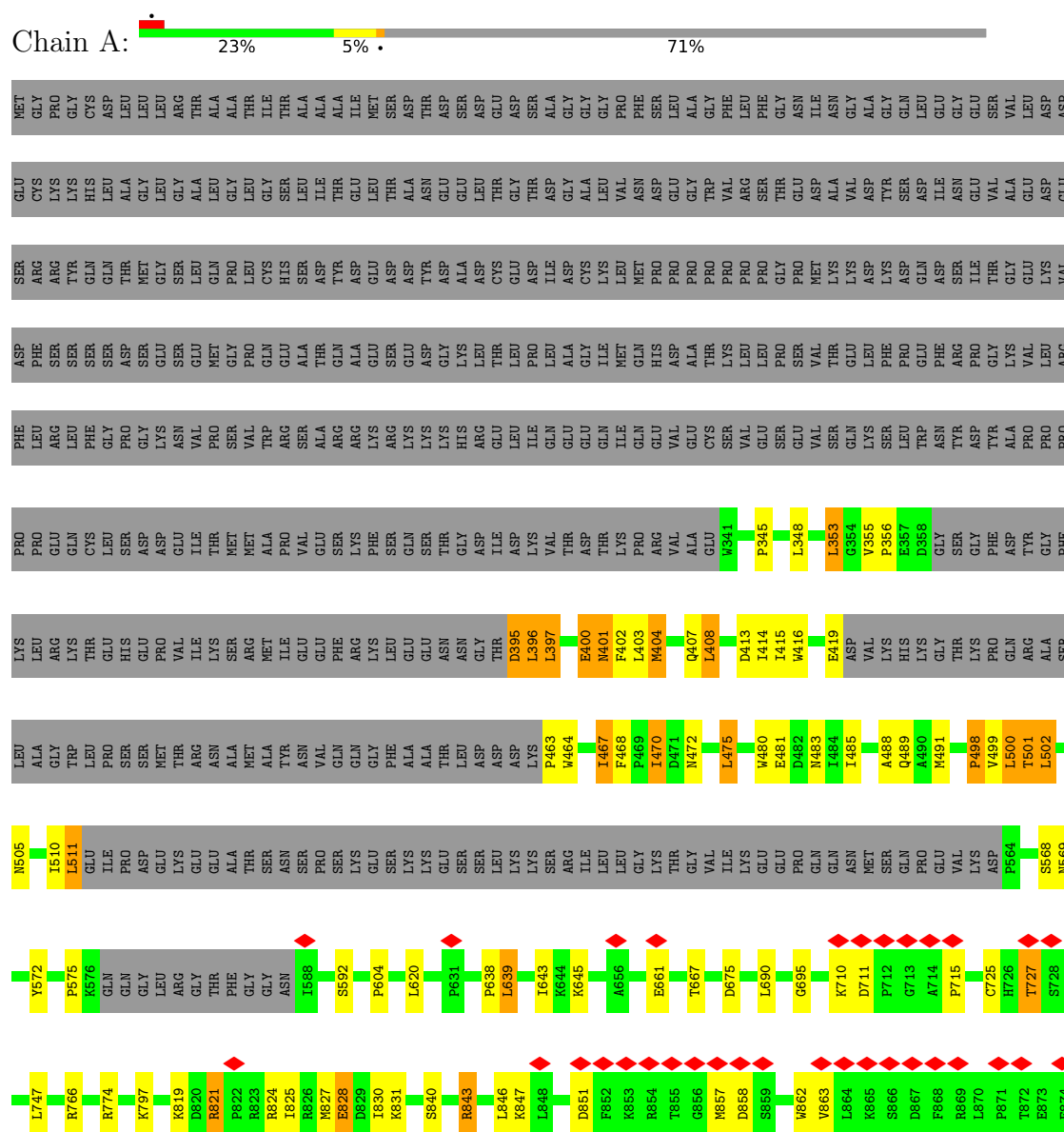
- Molecule 14 is a protein called Transcription initiation factor TFIID subunit 13.

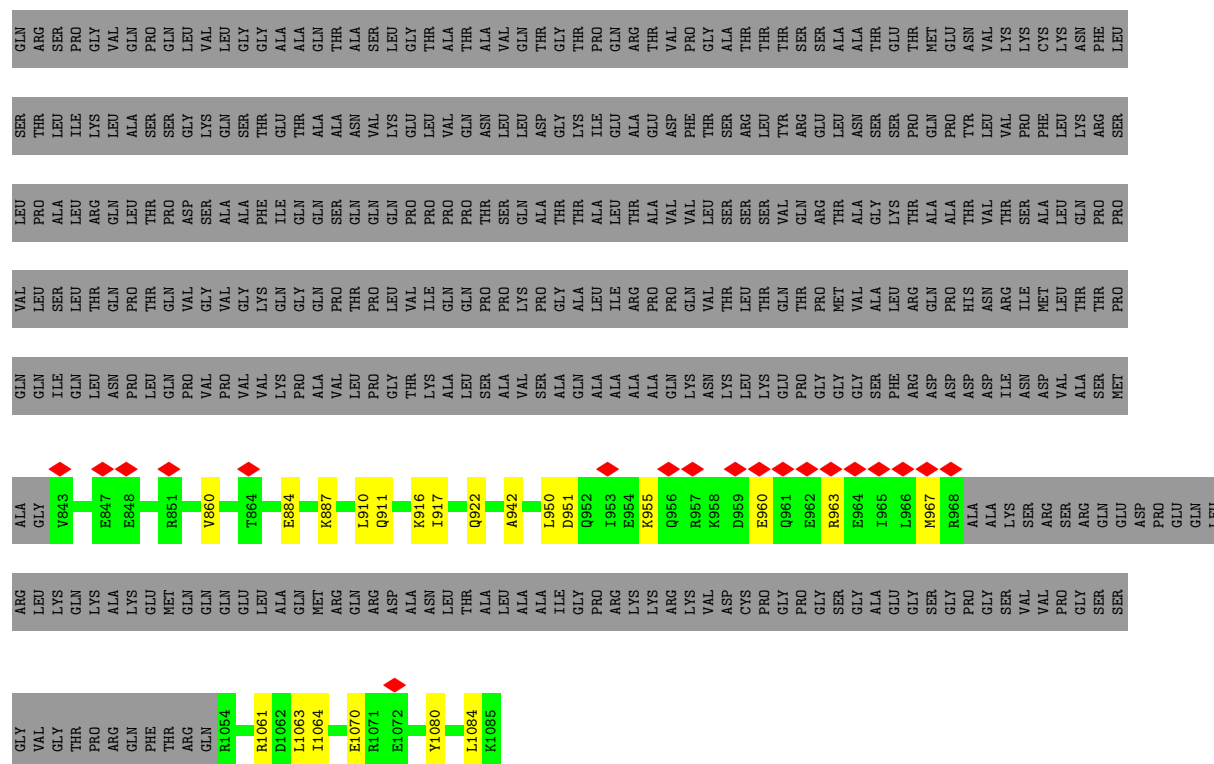
Mol	Chain	Residues	Atoms					AltConf	Trace
14	m	87	Total	C	N	O	S	0	0
			724	456	131	131	6		

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.

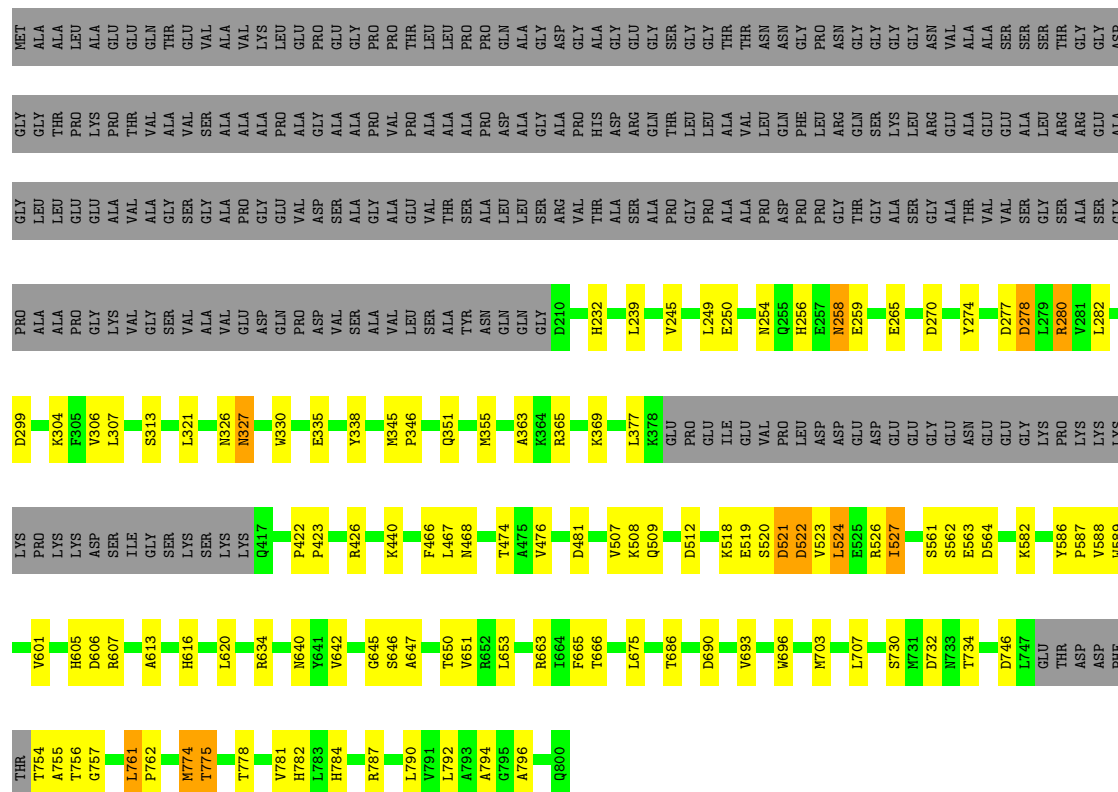
- Molecule 1: Transcription initiation factor TFIID subunit 1



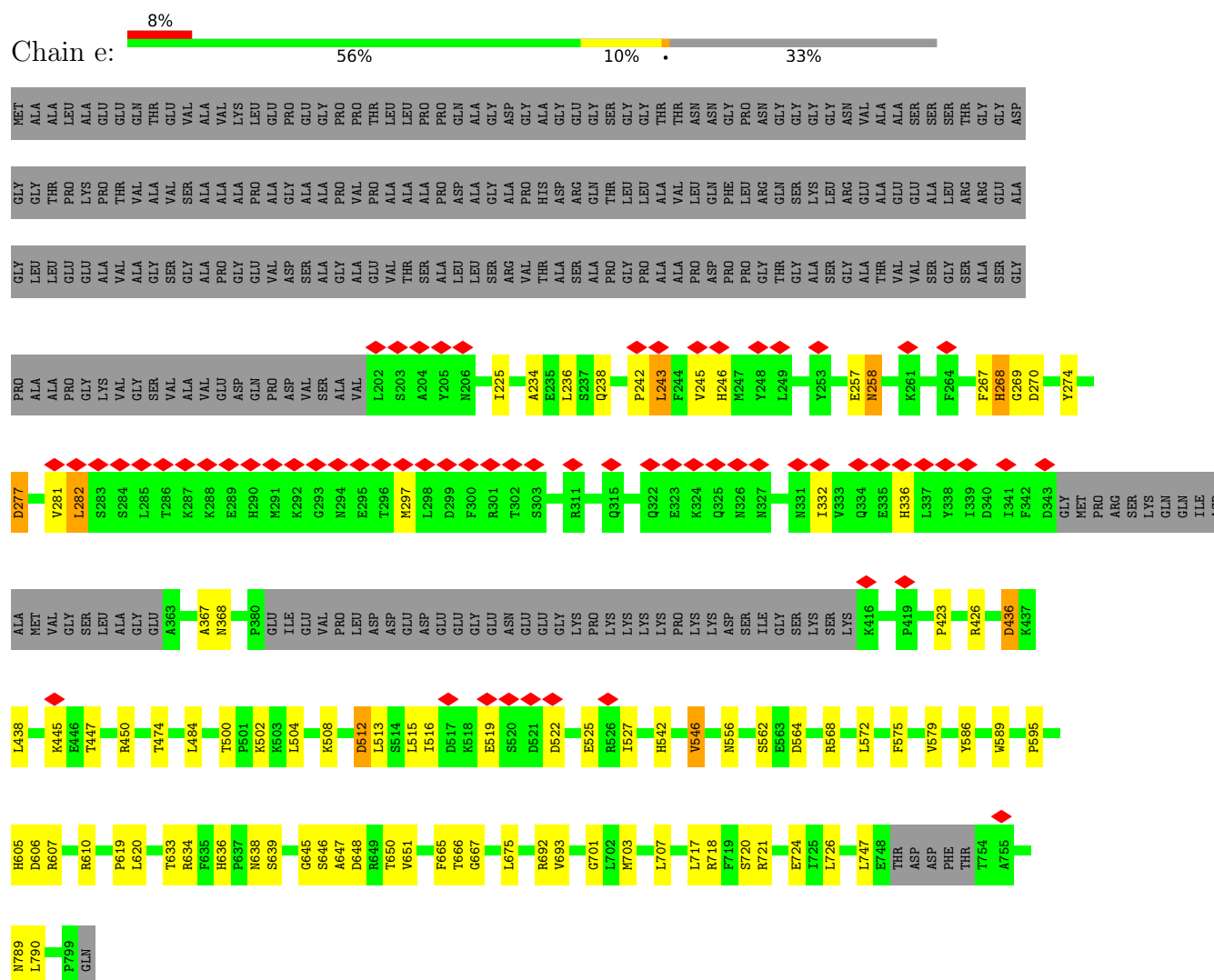


• Molecule 4: Transcription initiation factor TFIID subunit 5

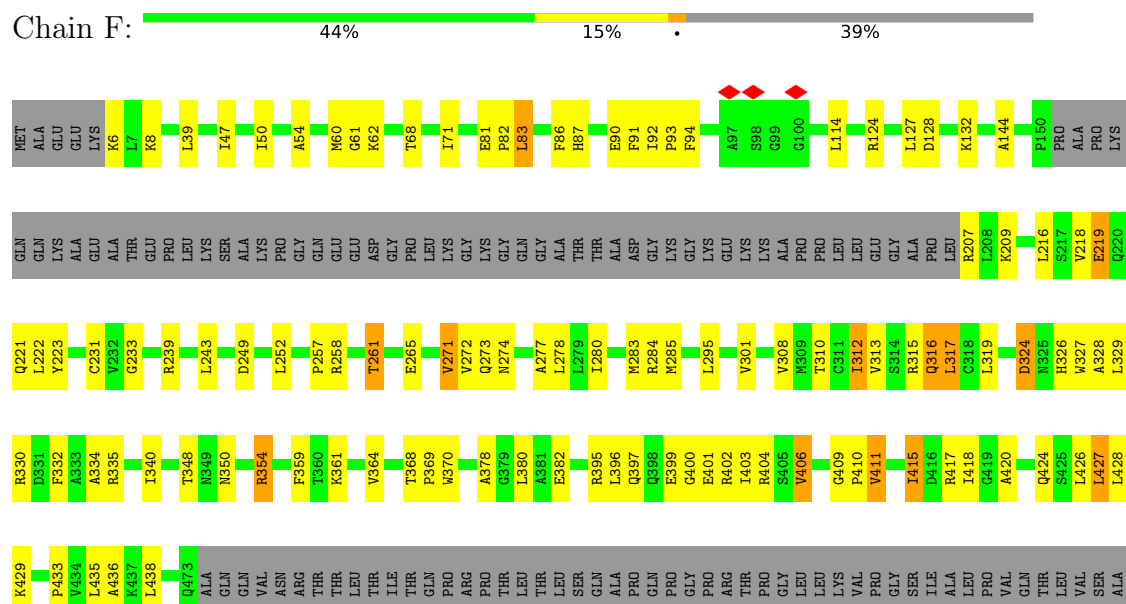
Chain E: 54% 13% 32%



• Molecule 4: Transcription initiation factor TFIID subunit 5



- Molecule 5: Transcription initiation factor TFIID subunit 6



Chain H:

Sequence logo for Chain H. The y-axis represents information content in bits. The x-axis shows positions 1 to 100. A bar chart at the top indicates the percentage of conserved positions: 52% (green), 15% (yellow), and 33% (grey).

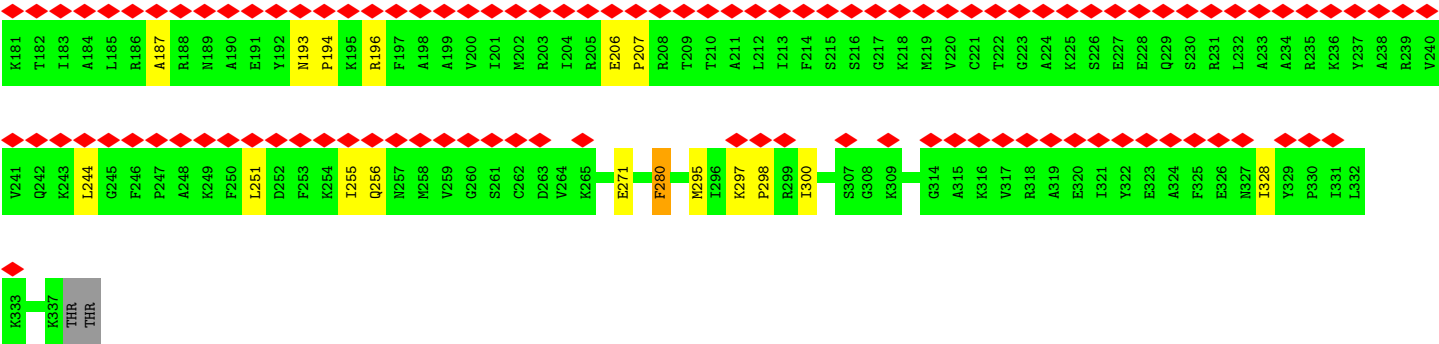
Position	Amino Acid	Information Content (bits)
1	GLU	0.15
2	GLU	0.15
3	THR	0.15
4	LYS	0.15
5	ASP	0.15
6	PRO	0.15
7	LYS	0.15
8	ILE	0.15
9	ARG	0.15
10	ARG	0.15
11	LYS	0.15
12	LYS	0.15
13	SER	0.15
14	LEU	0.15
15	SER	0.15
16	THR	0.15
17	ASP	0.15
18	THR	0.15
19	ASN	0.15
20	LEU	0.15
21	ALA	0.15
22	ALA	0.15
23	HIS	0.15
24	ILE	0.15
25	SER	0.15
26	MET	0.15
27	LYS	0.15
28	GLU	0.15
29	ASP	0.15
30	SER	0.15
31	GLY	0.15
32	ALA	0.15
33	GLU	0.15
34	LYS	0.15
35	GLU	0.15
36	ASN	0.15
37	THR	0.15
38	VAL	0.15
39	LEU	0.15
40	GLN	0.15
41	GLN	0.15
42	ASN	0.15
43	PRO	0.15
44	SER	0.15
45	LEU	0.15
46	SER	0.15
47	GLY	0.15
48	SER	0.15
49	ASN	0.15
50	GLY	0.15
51	GLU	0.15
52	GLU	0.15
53	ASN	0.15
54	ILE	0.15
55	ASP	0.15
56	ASN	0.15
57	PRO	0.15
58	TYR	0.15
59	LEU	0.15
60	ARG	0.15
61	PRO	0.15
62	GLN	0.15
63	GLU	0.15
64	GLU	0.15
65	ASP	0.15
66	GLU	0.15
67	ASN	0.15
68	ILE	0.15
69	ASP	0.15
70	ASN	0.15
71	L227	0.15
72	L224	0.15
73	GLU	0.15
74	GLU	0.15
75	P218	0.15
76	A216	0.15
77	ASN	0.15
78	ARG	0.15
79	L213	0.15
80	S209	0.15
81	LEU	0.15
82	TYR	0.15
83	M194	0.15
84	F193	0.15
85	R192	0.15
86	Y186	0.15
87	R183	0.15
88	R176	0.15
89	L175	0.15
90	V174	0.15
91	D171	0.15
92	T162	0.15
93	K161	0.15
94	I160	0.15
95	Y159	0.15
96	T158	0.15
97	H157	0.15
98	F153	0.15
99	ALA	0.15
100	LEU	0.15

[illegible][illegible]

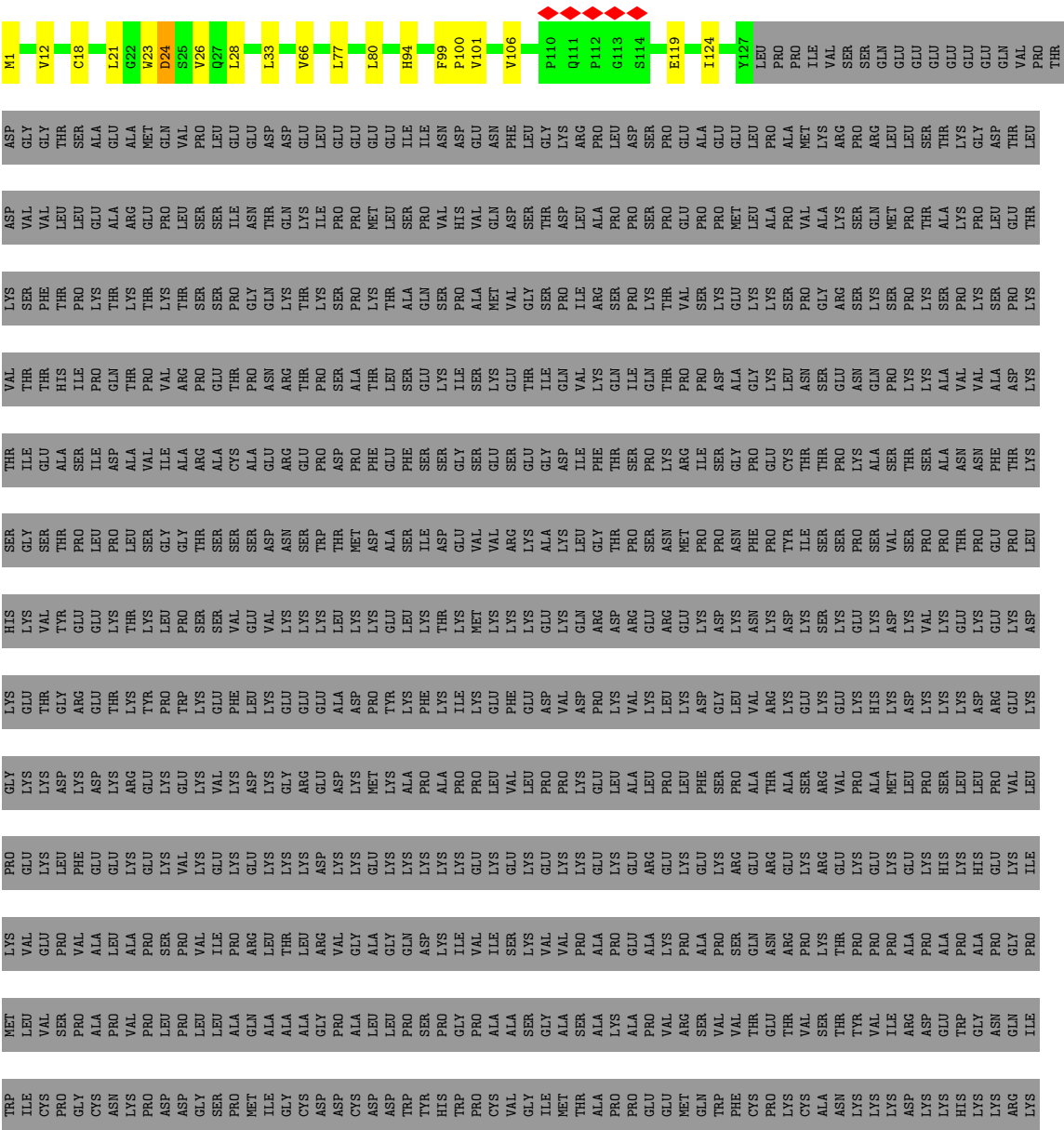
Chain J: 32%

Chain I: 9%

Chain K: 59%



• Molecule 12: Transcription initiation factor TFIID subunit 3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66920	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	0.043	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0062	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	0.63	0/4621	0.95	7/6240 (0.1%)
2	B	0.46	2/7993 (0.0%)	0.68	7/10836 (0.1%)
3	D	0.46	0/1279	0.74	0/1714
3	d	0.47	0/1321	0.71	2/1772 (0.1%)
4	E	0.45	1/4482 (0.0%)	0.72	3/6069 (0.0%)
4	e	0.54	1/4433 (0.0%)	0.76	0/6004
5	F	0.63	1/3207 (0.0%)	1.01	8/4354 (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	0.69	3/1662 (0.2%)	0.92	6/2272 (0.3%)
8	I	0.22	0/981	0.43	0/1332
8	i	0.20	0/989	0.40	0/1343
9	J	0.83	0/736	1.15	2/998 (0.2%)
9	j	0.73	0/775	0.96	0/1049
10	L	0.69	0/630	1.14	1/852 (0.1%)
10	l	0.58	0/888	0.87	0/1194
11	P	0.55	0/1438	0.78	1/1935 (0.1%)
12	c	0.47	0/1035	0.67	0/1406
13	k	0.28	0/799	0.53	1/1070 (0.1%)
14	m	0.84	0/733	1.18	1/977 (0.1%)
All	All	0.54	8/42332 (0.0%)	0.81	46/57286 (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	-7.52	1.15	1.24
7	H	27	ASP	C-O	-7.23	1.15	1.24
7	H	31	LEU	C-O	-6.39	1.16	1.24
2	B	61	ASN	C-O	-6.14	1.18	1.24
4	E	524	LEU	C-O	5.83	1.30	1.24

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	491	HIS	N-CA-C	-9.45	100.98	111.28
5	f	149	PRO	O-C-N	8.87	125.39	121.31
4	E	756	THR	N-CA-C	-8.32	103.27	113.50
7	H	32	ALA	N-CA-C	-8.26	102.23	111.07
1	A	356	PRO	N-CA-C	7.90	124.80	114.68

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	4505	0	4424	96	0
2	B	7796	0	7751	88	0
3	D	1266	0	1272	28	0
3	d	1307	0	1318	14	0
4	E	4376	0	4256	81	0
4	e	4327	0	4197	59	0
5	F	3149	0	3104	103	0
5	f	3081	0	3012	69	0
6	G	1171	0	1222	16	0
7	H	1622	0	1595	40	0
8	I	959	0	969	13	0
8	i	967	0	977	10	0
9	J	720	0	719	14	0
9	j	759	0	759	13	0
10	L	622	0	620	20	0
10	l	876	0	893	10	0
11	P	1412	0	1506	14	0
12	c	1011	0	975	18	0
13	k	785	0	818	9	0
14	m	724	0	744	23	0
All	All	41435	0	41131	625	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 625 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:1200:THR:O	1:A:1204:GLU:HG2	1.52	1.08
9:J:192:LYS:HE3	9:J:192:LYS:N	1.78	0.98
1:A:725:CYS:O	1:A:725:CYS:SG	2.22	0.98
11:P:271:GLU:CD	13:k:122:GLU:HG2	1.91	0.95
1:A:467:ILE:H	5:F:221:GLN:NE2	1.65	0.94

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%)	513 (96%)	19 (4%)	1 (0%)	43	78
2	B	959/1199 (80%)	911 (95%)	48 (5%)	0	100	100
3	D	148/1085 (14%)	143 (97%)	5 (3%)	0	100	100
3	d	154/1085 (14%)	149 (97%)	5 (3%)	0	100	100
4	E	541/800 (68%)	516 (95%)	24 (4%)	1 (0%)	43	78
4	e	531/800 (66%)	482 (91%)	48 (9%)	1 (0%)	43	78
5	F	408/677 (60%)	391 (96%)	16 (4%)	1 (0%)	43	78
5	f	399/677 (59%)	380 (95%)	19 (5%)	0	100	100
6	G	138/349 (40%)	135 (98%)	3 (2%)	0	100	100
7	H	207/310 (67%)	194 (94%)	13 (6%)	0	100	100
8	I	118/264 (45%)	115 (98%)	3 (2%)	0	100	100
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	l	105/161 (65%)	100 (95%)	5 (5%)	0	100	100
11	P	175/339 (52%)	165 (94%)	9 (5%)	1 (1%)	21	59
12	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
13	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
14	m	85/124 (68%)	82 (96%)	3 (4%)	0	100	100
All	All	5092/11743 (43%)	4837 (95%)	248 (5%)	7 (0%)	49	83

5 of 7 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%)	445 (91%)	42 (9%)	10	29
2	B	876/1083 (81%)	863 (98%)	13 (2%)	57	72
3	D	139/815 (17%)	136 (98%)	3 (2%)	45	64
3	d	146/815 (18%)	144 (99%)	2 (1%)	59	72
4	E	480/657 (73%)	467 (97%)	13 (3%)	39	61
4	e	475/657 (72%)	462 (97%)	13 (3%)	39	61
5	F	329/574 (57%)	309 (94%)	20 (6%)	17	38
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%)	173 (97%)	5 (3%)	38	60
8	I	106/235 (45%)	106 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	P	153/293 (52%)	150 (98%)	3 (2%)	48	66
12	c	113/833 (14%)	111 (98%)	2 (2%)	51	68
13	k	87/182 (48%)	87 (100%)	0	100	100
14	m	80/106 (76%)	71 (89%)	9 (11%)	5	19
All	All	4541/9906 (46%)	4384 (96%)	157 (4%)	32	53

5 of 157 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	L	114	LYS
5	f	356	THR
12	c	24	ASP
4	e	438	LEU
14	m	58	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	273	GLN
10	L	117	GLN
10	l	105	HIS
5	F	326	HIS
7	H	126	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.

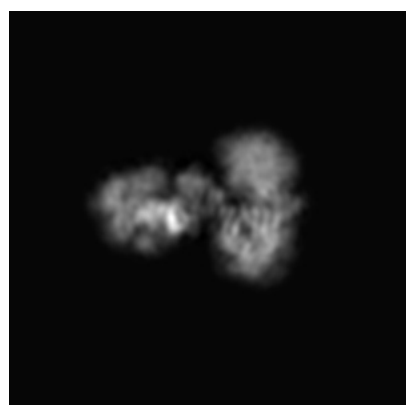
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31114. These allow visual inspection of the internal detail of the map and identification of artifacts.

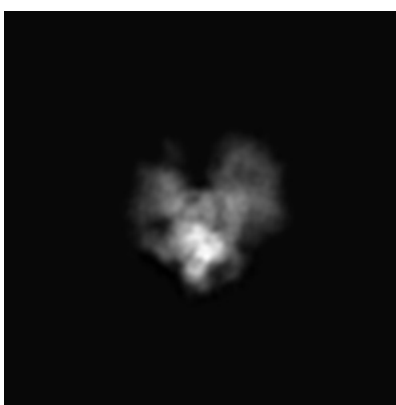
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

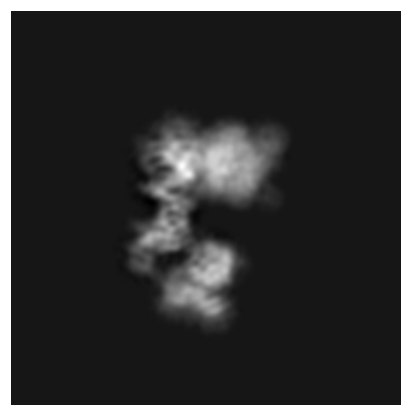
6.1.1 Primary map



X



Y

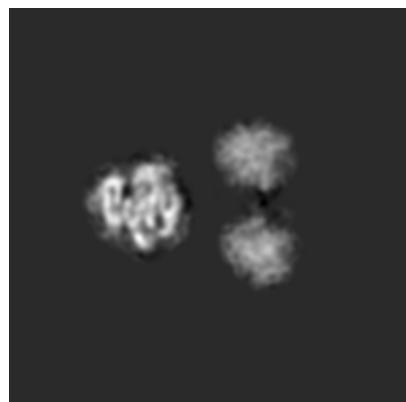


Z

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

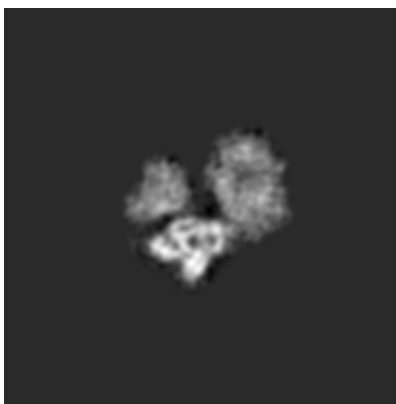
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 131



Y Index: 205

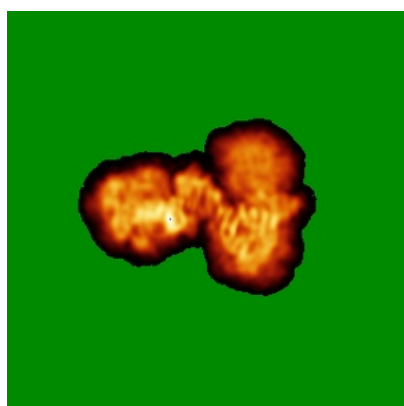


Z Index: 155

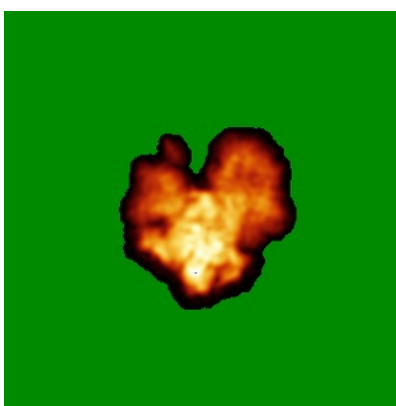
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

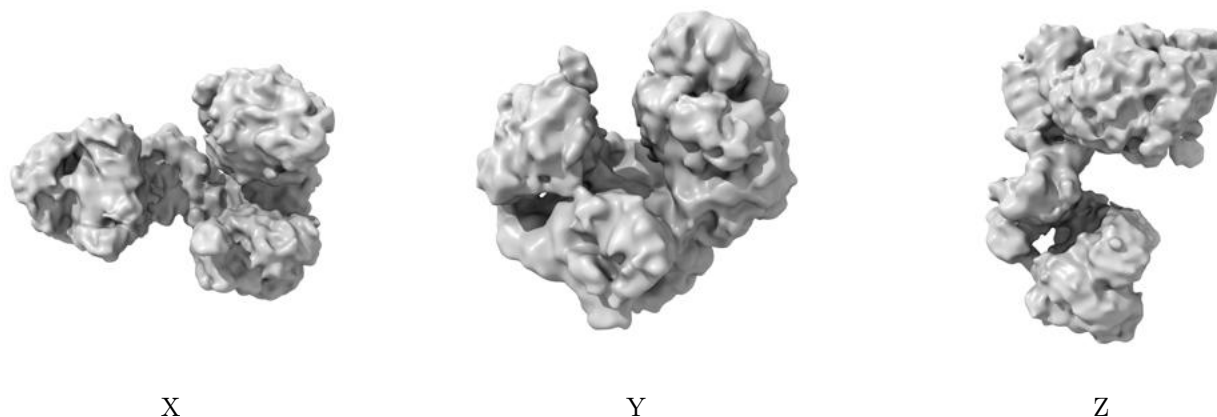


Z

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 0.0062. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

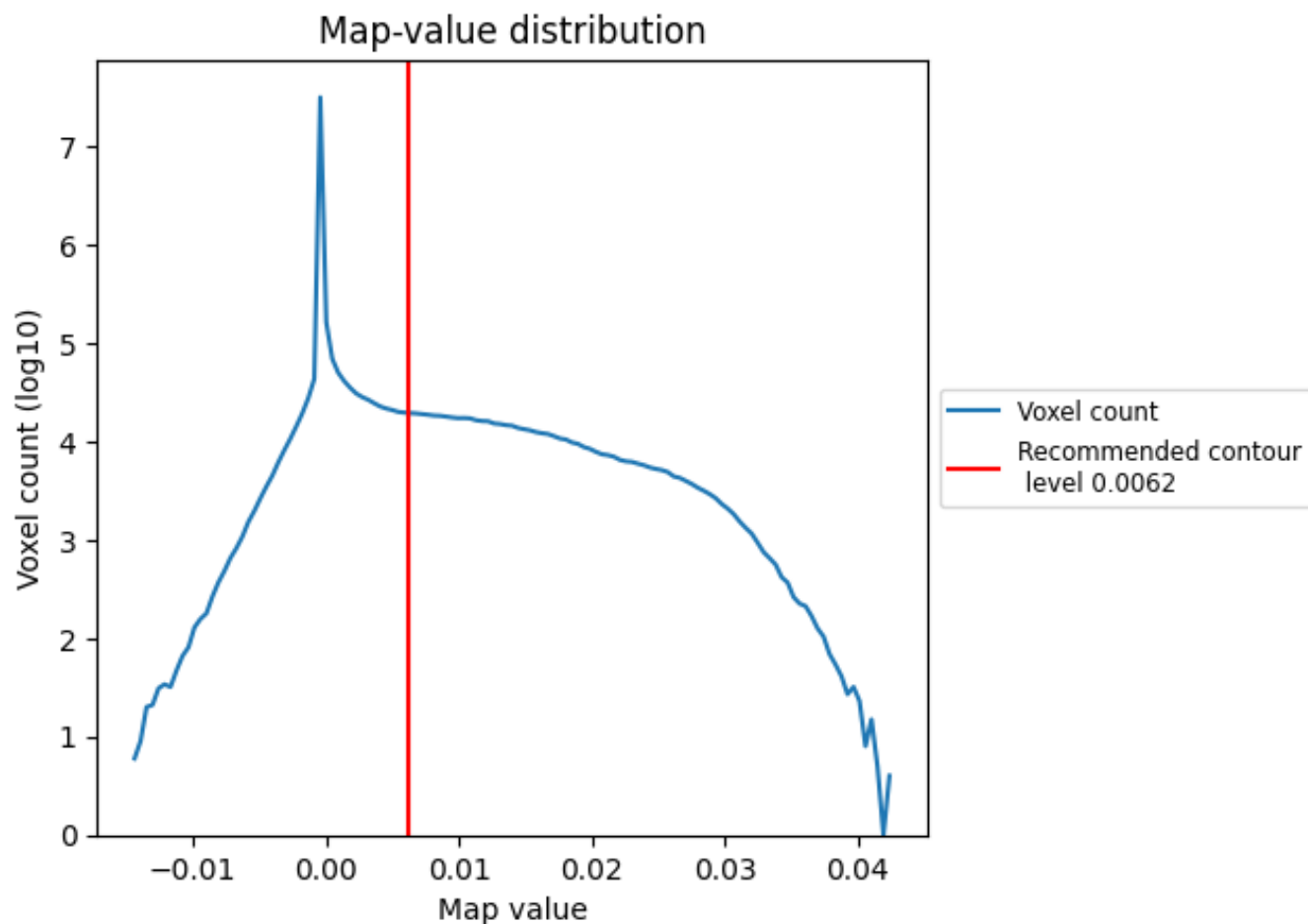
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

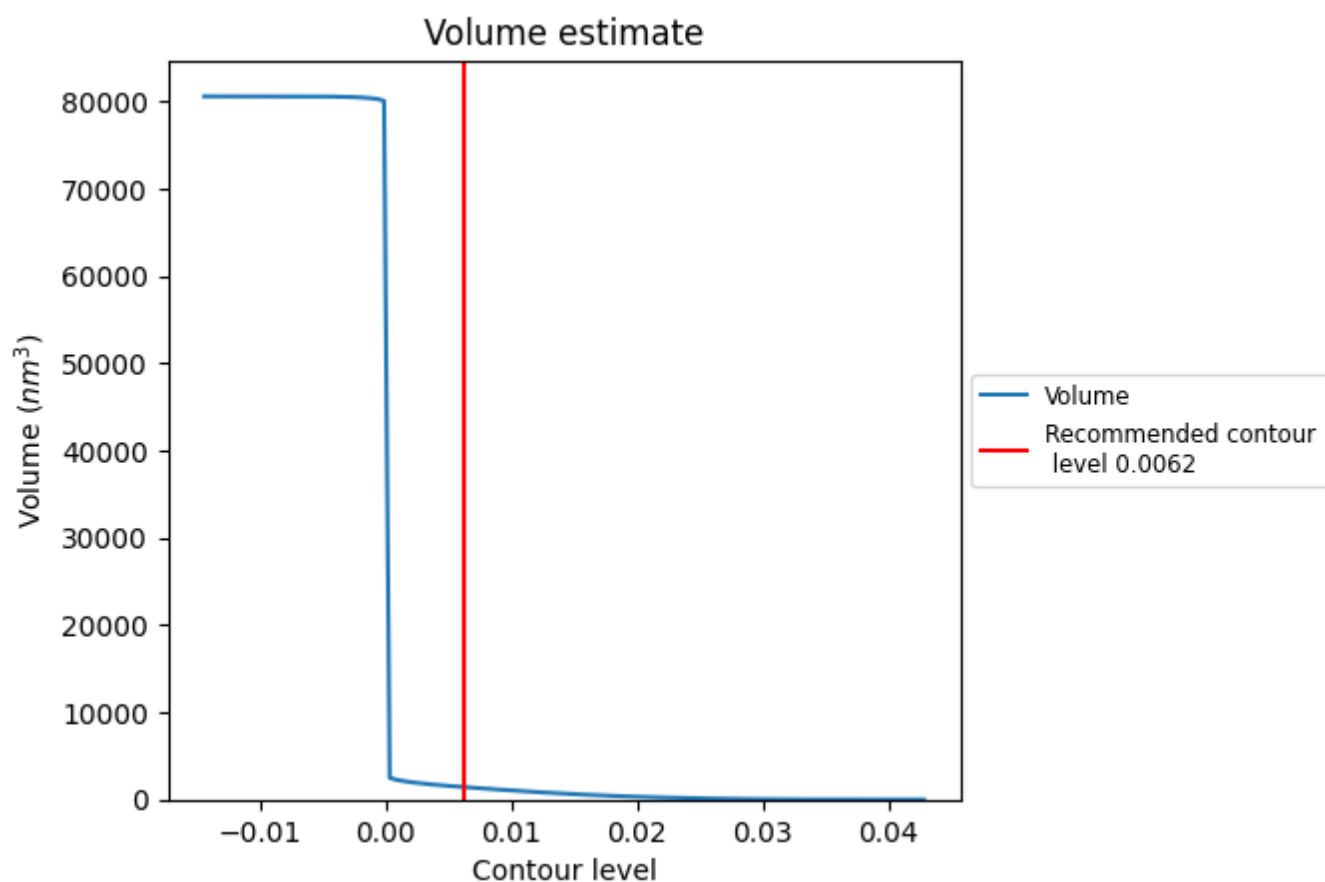
This section contains the results of statistical analysis of the map.

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.

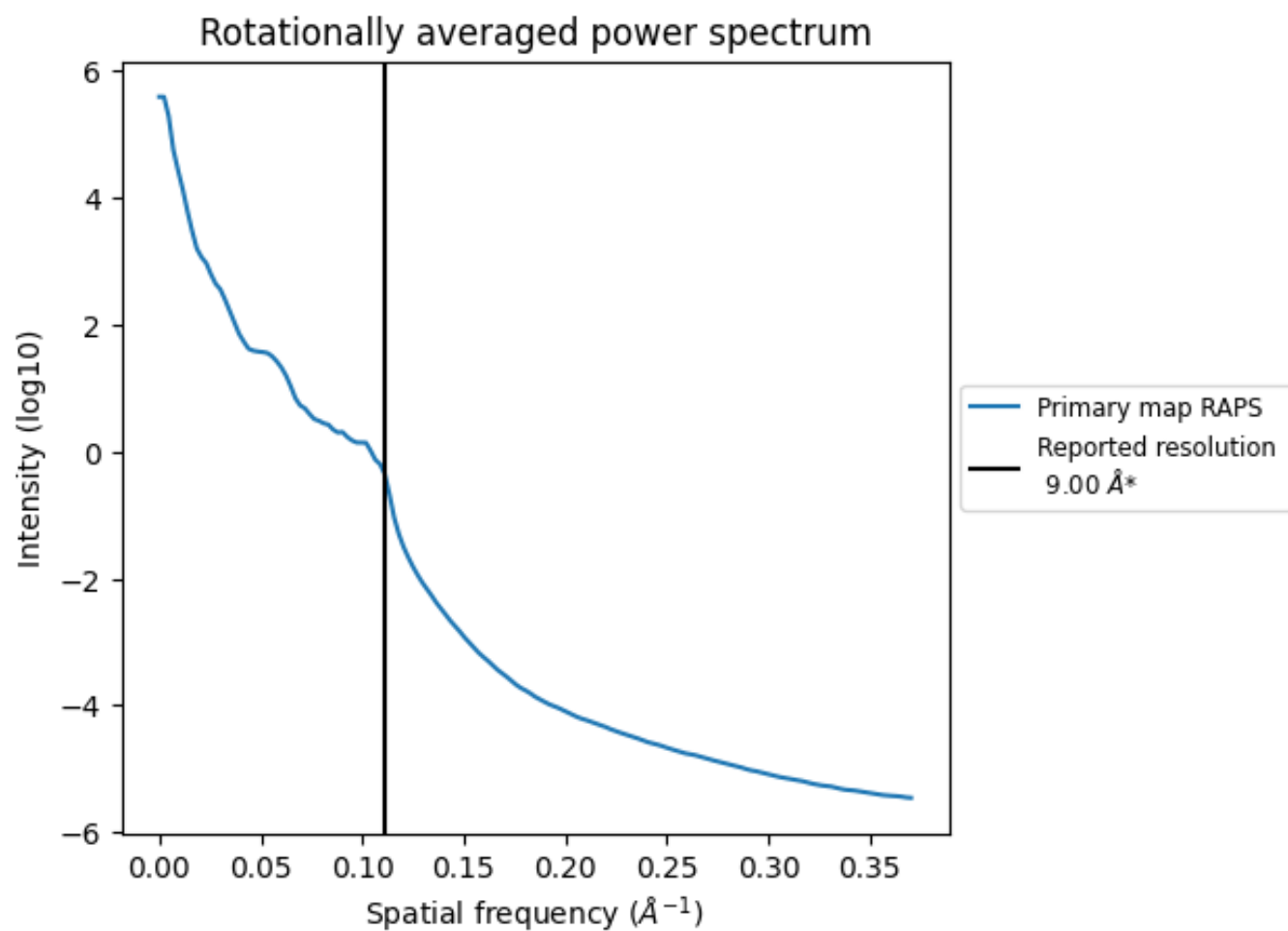
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1436 nm³; this corresponds to an approximate mass of 1297 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 0.111 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-31114 and PDB model 7EGE. 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](#)

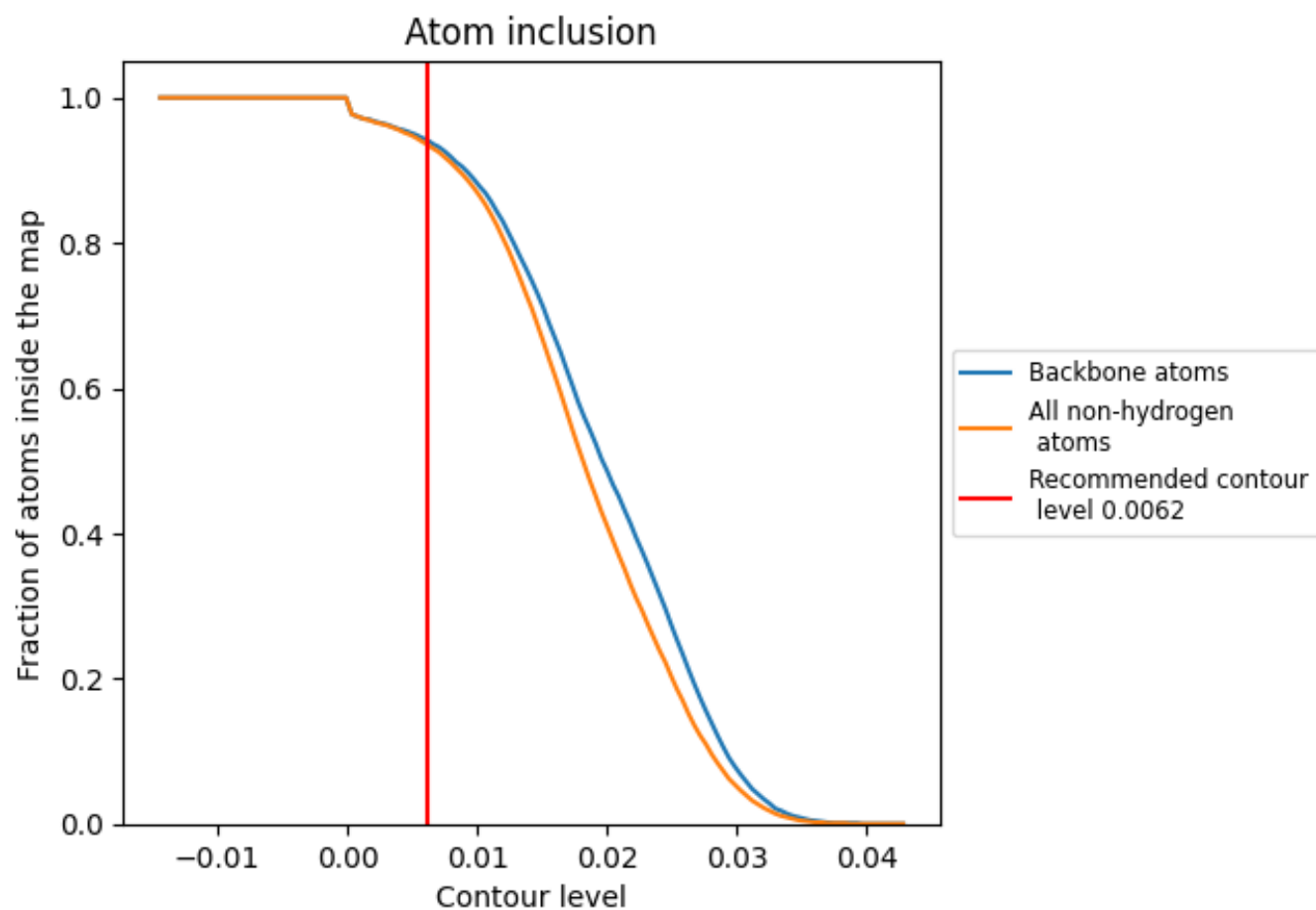


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.0062) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9350	 0.0780
A	 0.8710	 0.0530
B	 0.9940	 0.1120
D	 0.9880	 0.1000
E	 0.9970	 0.0960
F	 0.9910	 0.1180
G	 0.9310	 0.0470
H	 0.9890	 0.1270
I	 1.0000	 0.1280
J	 1.0000	 0.0770
L	 1.0000	 0.1190
P	 0.2660	 -0.0100
c	 0.9630	 0.0470
d	 0.8670	 0.0310
e	 0.8610	 0.0280
f	 0.9880	 0.1120
i	 0.9990	 0.0490
j	 1.0000	 0.0410
k	 0.9790	 0.0440
l	 0.9880	 0.0310
m	 0.9960	 0.0160

