



Full wwPDB EM Validation Report ⓘ

Oct 14, 2024 – 07:34 PM JST

PDB ID : 7EG9
EMDB ID : EMD-31109
Title : TFIID-based intermediate PIC on SCP promoter
Authors : Chen, X.; Qi, Y.; Wang, X.; Wu, Z.; Li, J.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 3.70 Å(reported)

This is a Full wwPDB EM Validation 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:

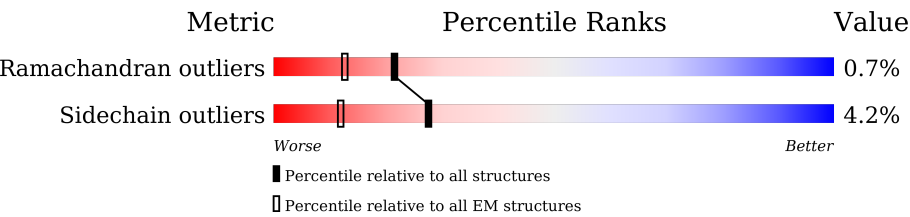
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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)
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 ≥ 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	
4	E	800	
4	e	800	
5	F	677	
5	f	677	
6	G	349	

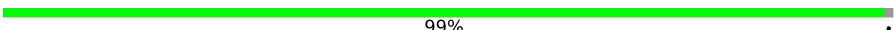


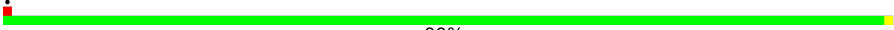

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Mol	Chain	Length	Quality of chain
7	H	310	
8	I	264	
8	i	264	
9	J	218	
9	j	218	
10	L	161	
10	l	161	
11	O	109	
12	P	339	
13	Q	376	
14	R	316	
15	S	517	
16	T	249	
17	U	439	
18	V	291	
19	X	79	
20	Y	79	
21	c	929	
22	k	211	
23	m	124	
24	o	1970	
25	p	1174	
26	q	275	
27	r	142	
28	s	210	

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Mol	Chain	Length	Quality of chain
29	t	127	 62%38%
30	v	150	 99%.
31	w	125	 91%9%
32	x	67	 87%9%.
33	y	117	 99%.
34	z	58	 76%24%
35	u	172	 98%..

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 84318 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	602	Total	C	N	O	S	0	0
			4927	3142	858	899	28		

- 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	163	Total	C	N	O	S	0	0
			1361	848	255	254	4		
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	546	Total	C	N	O	S	0	0
			4364	2766	757	820	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	404	Total	C	N	O	S	0	0
			3081	1954	537	572	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	145	Total	C	N	O	S	0	0
			1180	748	217	211	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
			1633	1034	283	311	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	89	Total	C	N	O	S	0	0
			709	457	114	134	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	122	Total	C	N	O	S	0	0
			996	623	162	207	4		

- Molecule 14 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	248	Total	C	N	O	S	0	0
			1913	1200	338	358	17		

- Molecule 15 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	134	Total	C	N	O	S	0	0
			1101	698	199	202	2		

- Molecule 16 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	103	Total	C	N	O	S	0	0
			789	492	142	154	1		

- Molecule 17 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	179	Total	C	N	O	S	0	0
			1476	932	261	272	11		

- Molecule 18 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	172	Total	C	N	O	S	0	0
			1400	890	242	264	4		

- Molecule 19 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	71	Total	C	N	O	P	0	0
			1470	691	287	421	71		

- Molecule 20 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	71	Total	C	N	O	P	0	0
			1441	683	256	431	71		

- Molecule 21 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 22 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 23 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 24 is a protein called RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	o	1427	Total	C	N	O	S	0	0
			11308	7114	2023	2099	72		

- Molecule 25 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	1134	Total	C	N	O	S	0	0
			9062	5732	1595	1671	64		

- Molecule 26 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

- Molecule 27 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	r	128	Total	C	N	O	S	0	0
			1005	632	172	197	4		

- Molecule 28 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 29 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	t	79	Total	C	N	O	S	0	0
			635	406	108	116	5		

- Molecule 30 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 31 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	w	114	Total	C	N	O	S	0	0
			927	571	166	179	11		

- Molecule 32 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	x	64	Total	C	N	O	S	0	0
			507	328	86	87	6		

- Molecule 33 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 34 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	z	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

- Molecule 35 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	u	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 36 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	R	1	Total	Zn	0
			1	1	
36	U	1	Total	Zn	0
			1	1	
36	o	2	Total	Zn	0
			2	2	
36	p	1	Total	Zn	0
			1	1	
36	q	1	Total	Zn	0
			1	1	
36	w	2	Total	Zn	0
			2	2	
36	x	1	Total	Zn	0
			1	1	
36	z	1	Total	Zn	0
			1	1	

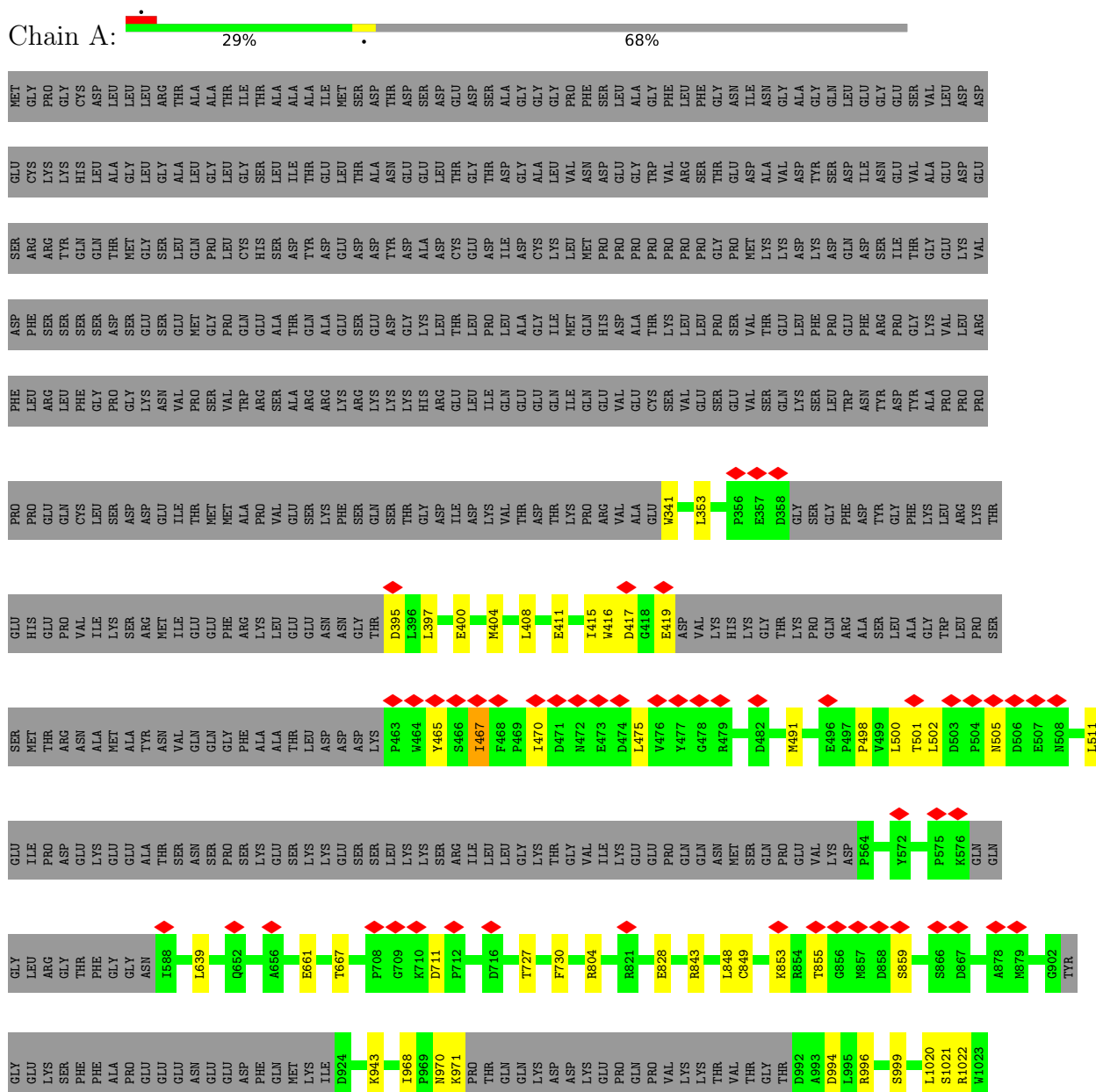
- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

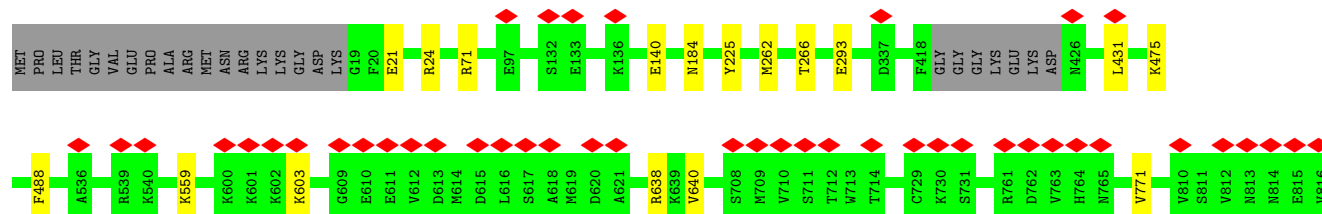
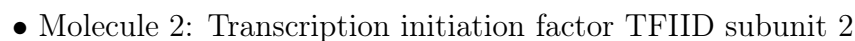
Mol	Chain	Residues	Atoms		AltConf
37	o	1	Total	Mg	0
			1	1	

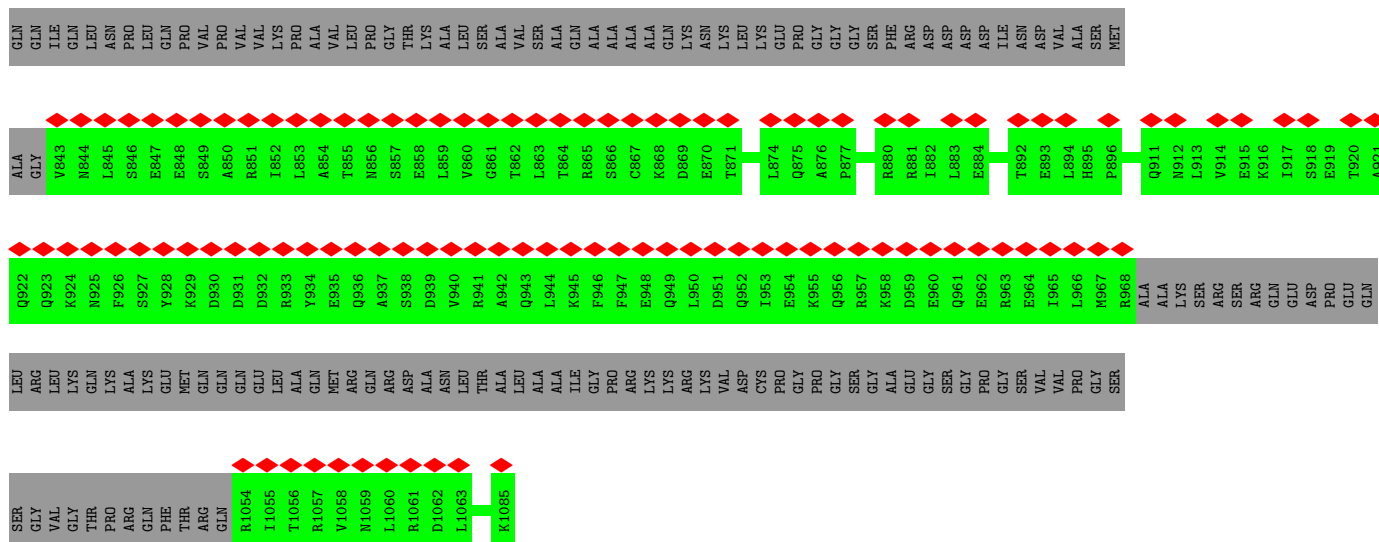
3 Residue-property plots

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.

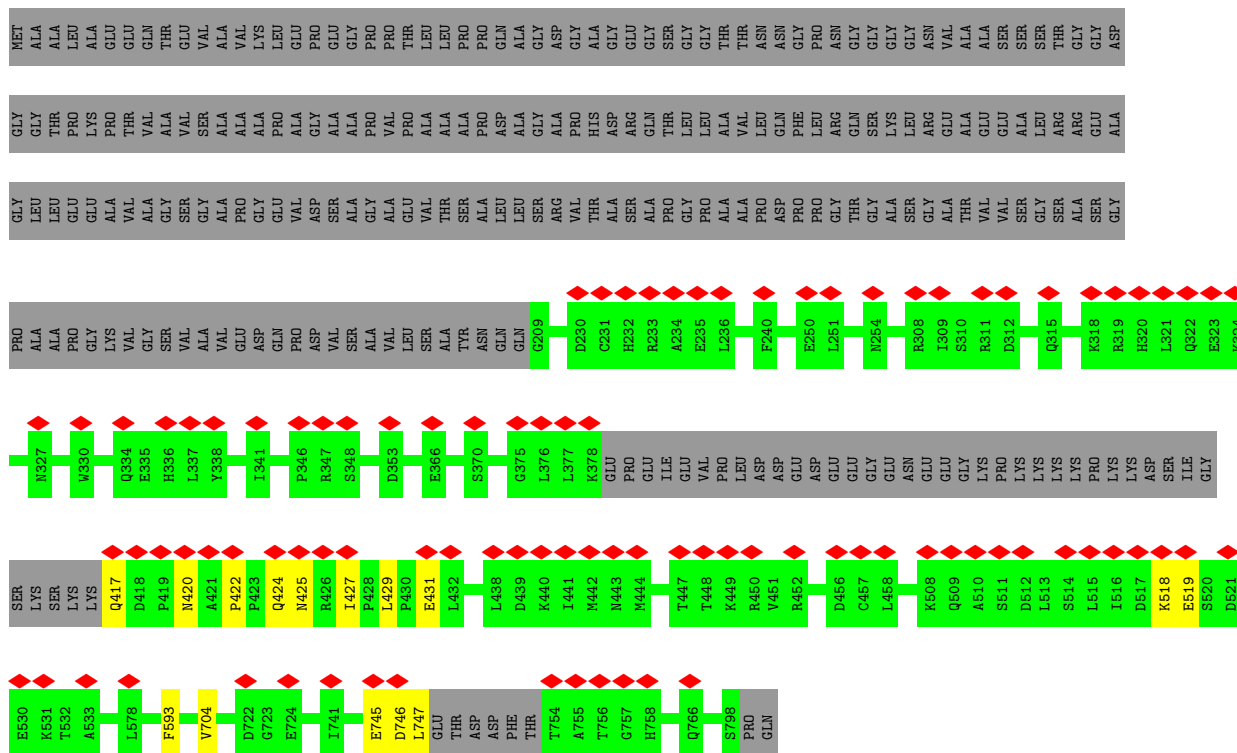
- Molecule 1: Transcription initiation factor TFIID subunit 1



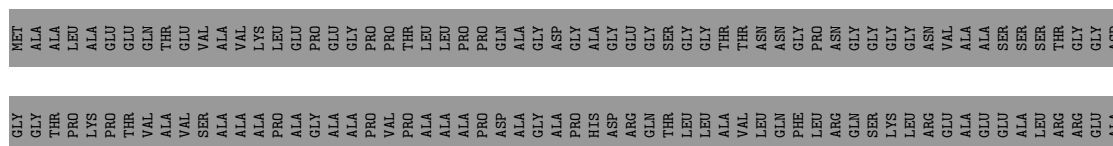




- Molecule 4: Transcription initiation factor TFIID subunit 5

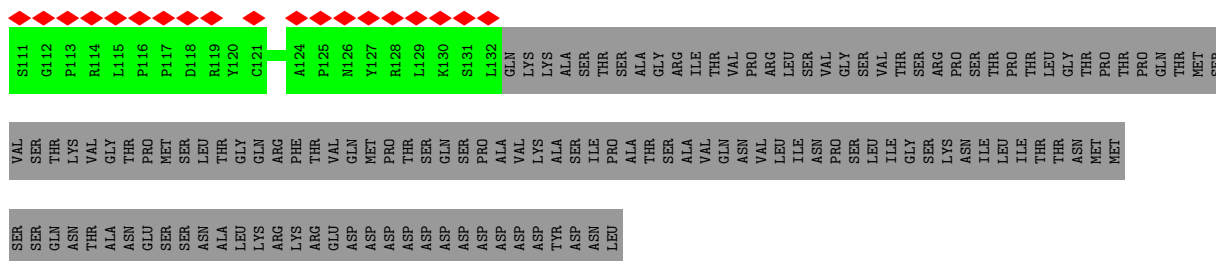


- Molecule 4: Transcription initiation factor TFIID subunit 5

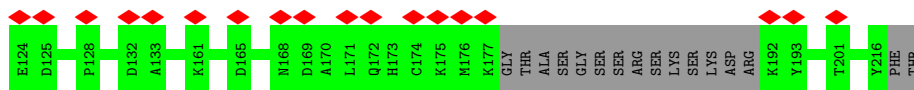
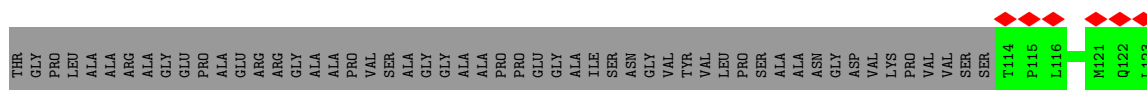
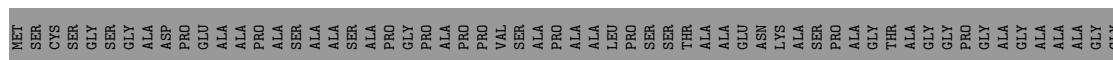




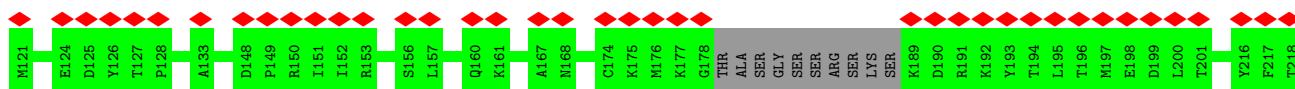
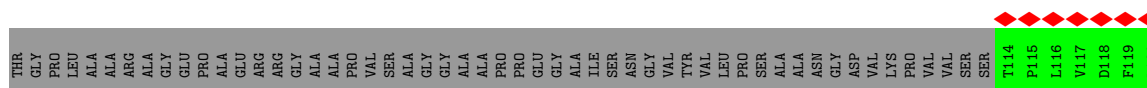
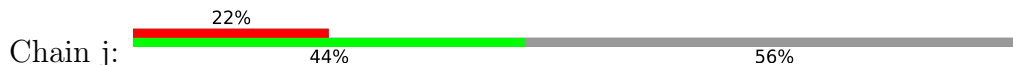




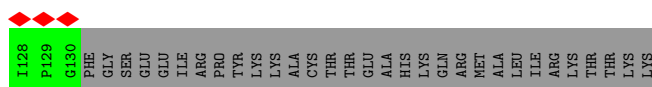
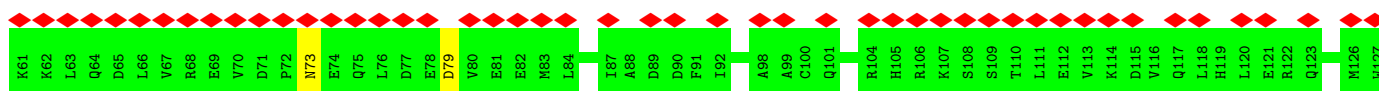
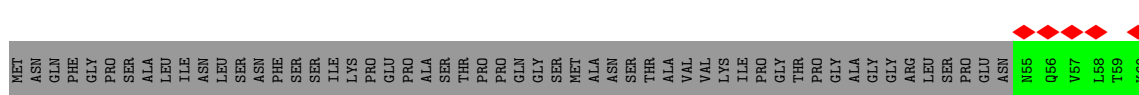
- Molecule 9: Transcription initiation factor TFIID subunit 10



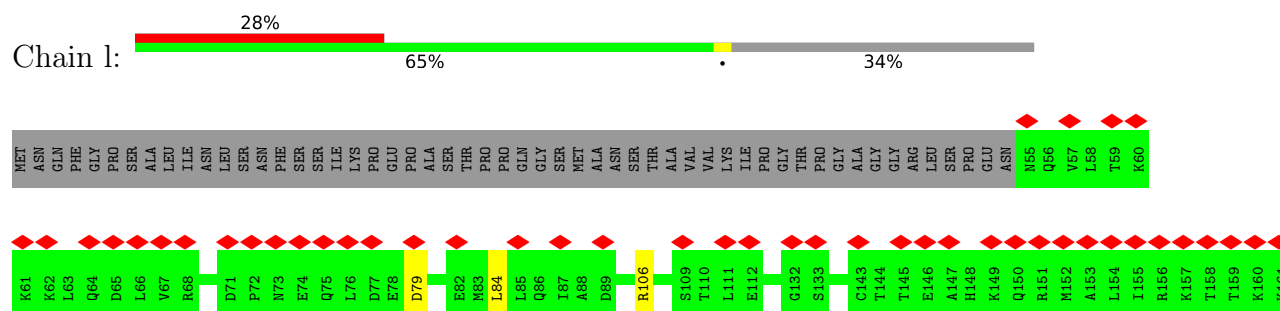
- Molecule 9: Transcription initiation factor TFIID subunit 10



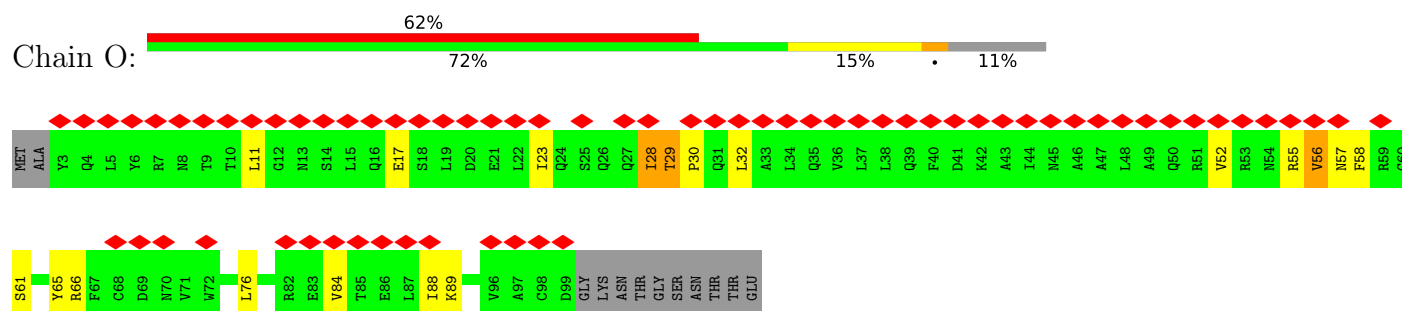
- Molecule 10: Transcription initiation factor TFIID subunit 12



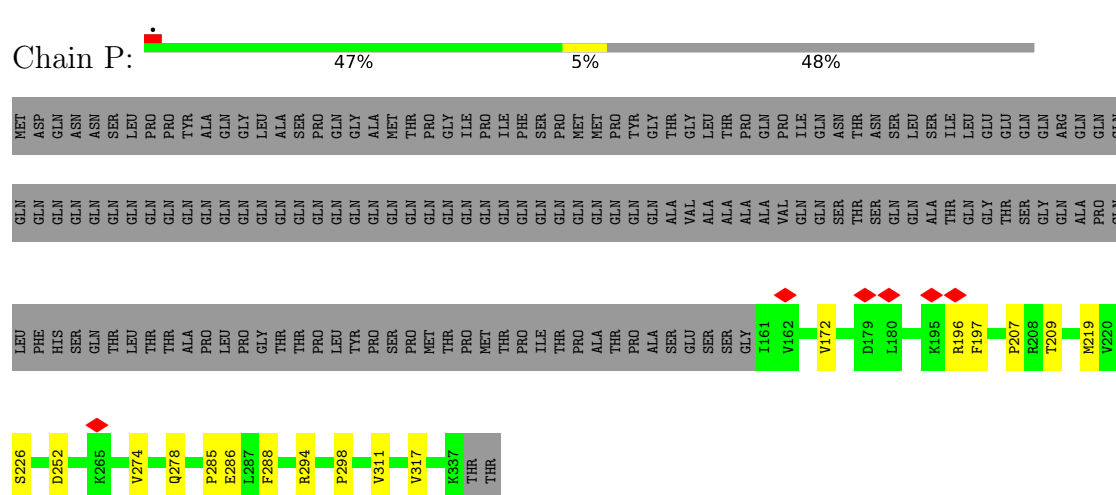
- Molecule 10: Transcription initiation factor TFIID subunit 12



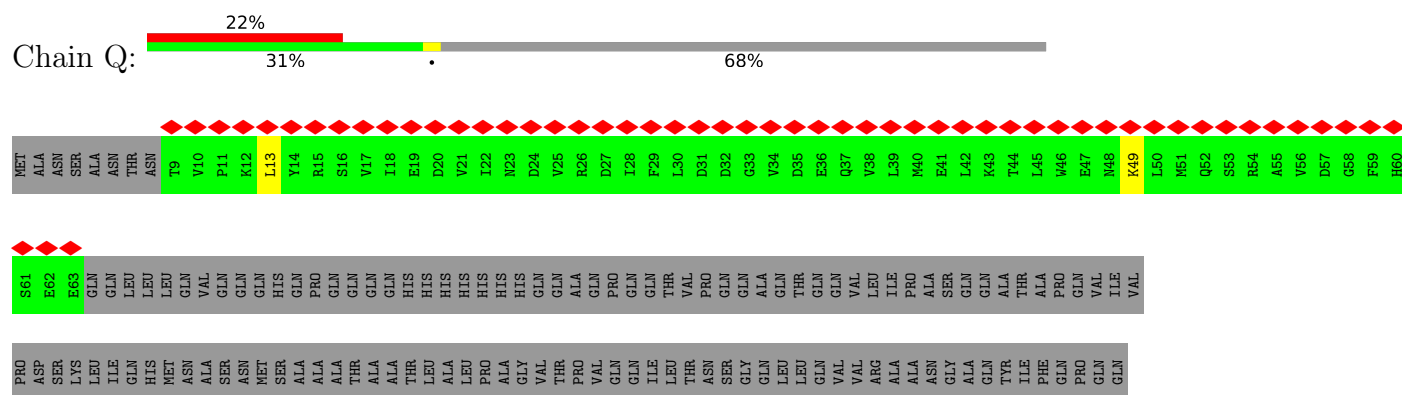
- Molecule 11: Transcription initiation factor IIA subunit 2

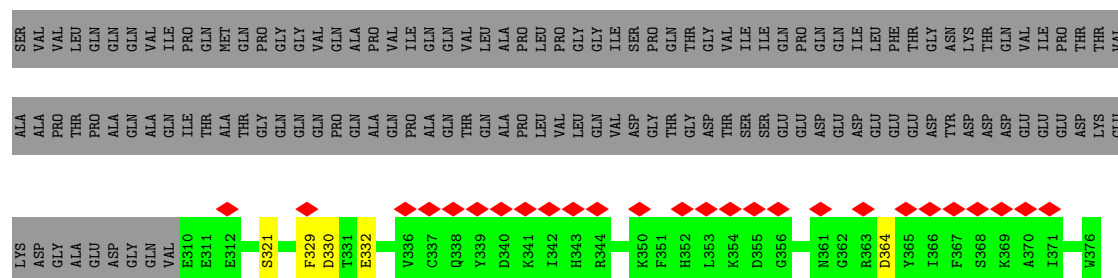


- Molecule 12: TATA-box-binding protein

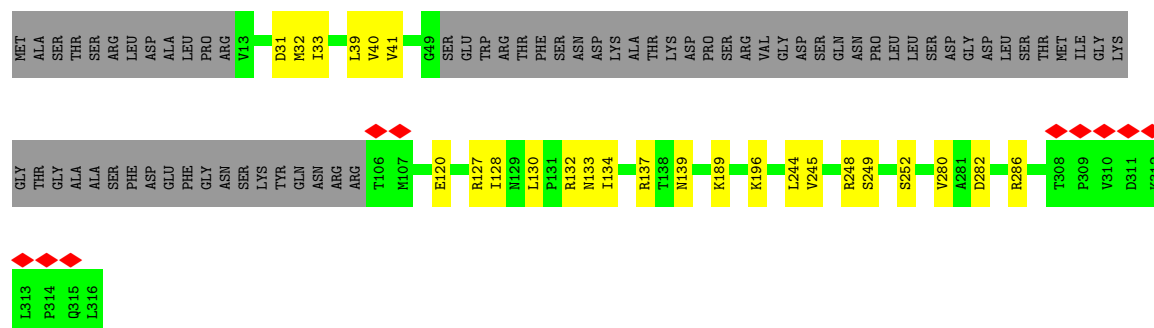


- Molecule 13: Transcription initiation factor IIA subunit 1

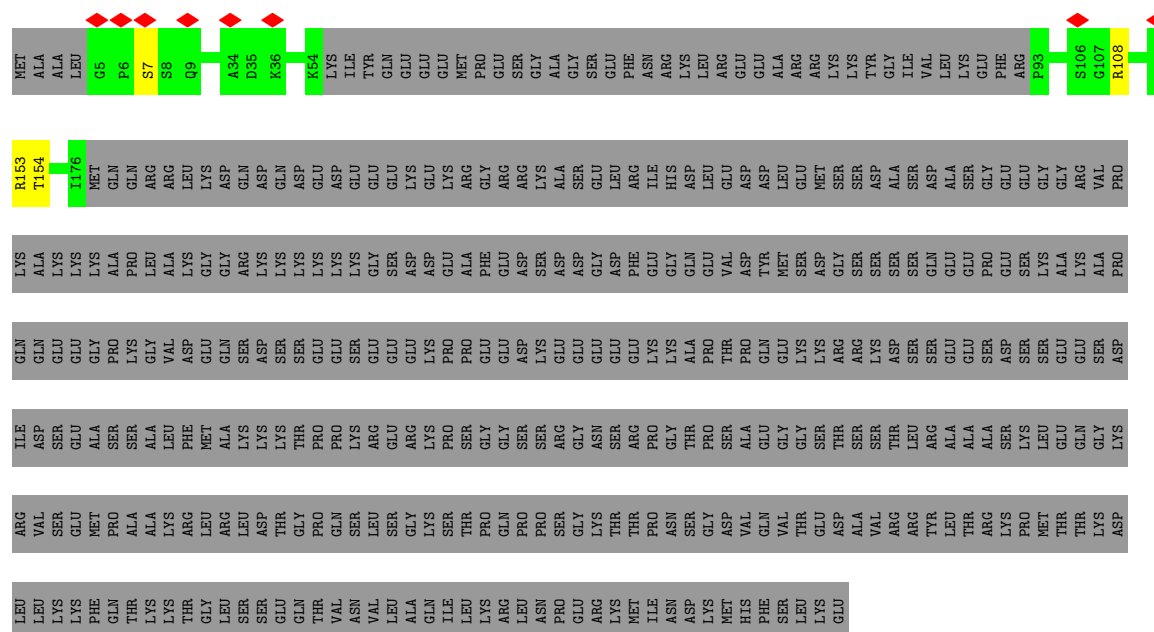




• Molecule 14: Transcription initiation factor IIB



• Molecule 15: General transcription factor IIF subunit 1



• Molecule 16: General transcription factor IIF subunit 2





[illegible]

- Molecule 22: Transcription initiation factor TFIID subunit 11



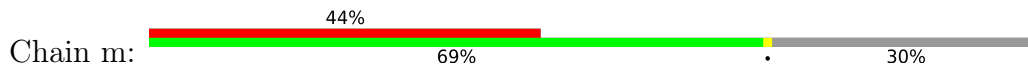
NET	ASP	ASP	ASP	HIS	GLU	SER	PRO	SER	ASP	LYS	GLY	GLY	GLU	THR	ALA	ALA	VAL	PRO	PRO	ASP	ASP	PRO	GLY	ALA	THR	THR	THR	ILE	PRO	GLU	GLU	GLU	THR	THR	ASP	GLY	ASP	ALA	ALA	ASP	VAL	ASP	LEU	LYS	GLU	ALA	ALA	ALA	GLU	GLU	GLY	GLY	LEU	GLU	GLF
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[illegible]

Y121	E122	M123	Y124	R125	R126	S127	A128	I129	P130	K131	A132	A133	I134	I138	Q139	S140	I141	T142	G143	T144	S145	V146	S147	Q148	M149	I152	A153	M154	S155	G156	I157	S158	K159	V162	G163	E164	V165	V166	E167	E168	A169	L170	D171	V172	C173	E174	K175	V176	G177	E178	M179	P180	P181	L182	Q183	A184
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Diagram illustrating a sequence of nodes (K185, H186, M187, R188, E189, A190, V191, R192, R193, F211) connected by arrows. The nodes are arranged in a horizontal sequence. The first nine nodes (K185 to R193) are grouped together in a blue box, and the final node (F211) is in a red box. Red diamonds are positioned above each node. A red arrow points from R193 to F211.

- Molecule 23: Transcription initiation factor TFIID subunit 13



MET	ALA	ASP	GLU	GLU	GLU	ASP	PRO	THR	PHE	GLU	GLU	GLU	ASN	GLU	GLU	ILE	GLY	GLY	GLY	ALA	GLU	GLY	GLY	GLN	GLY	LYS	R28	R29	R30	L31	F32	S33	R34	R35	R36	L36	R37	R38	M39	M40	Y41	G42	F43	G44	D45	D46	Q47	M48	P49	Y50	T51	E52	S53	V54	D55	I56	L65	S66
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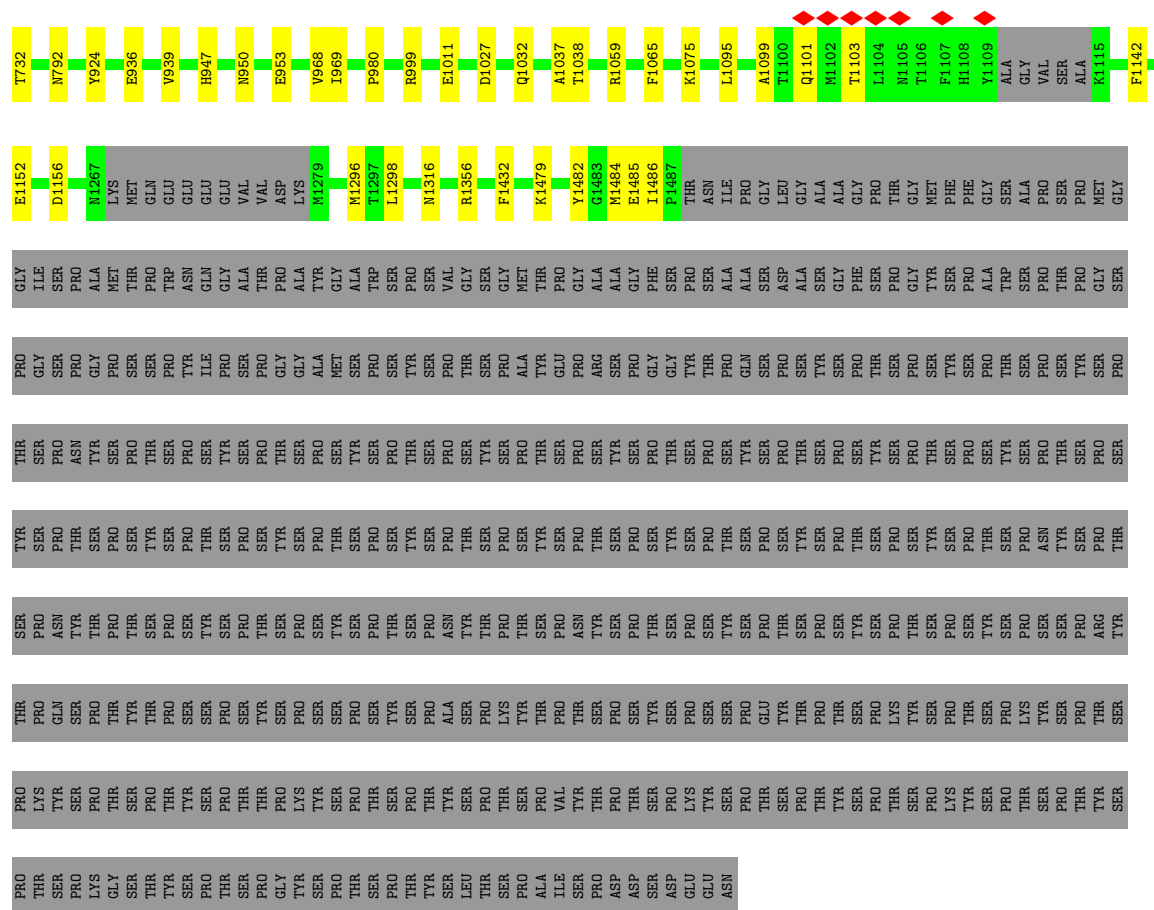
G76	R77	Q78	G79	Q82	D85	R86	V87	F88	L89	D93	P94	R95	K96	F97	A98	K101	D102	L103	L104	T105	M106	N107	E108	E109	L110	K111	R112	A113	L114	LYS	ALA	PHE	ASP	GLU	ALA	ASN	TYR	GLY
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- Molecule 24: RPB1



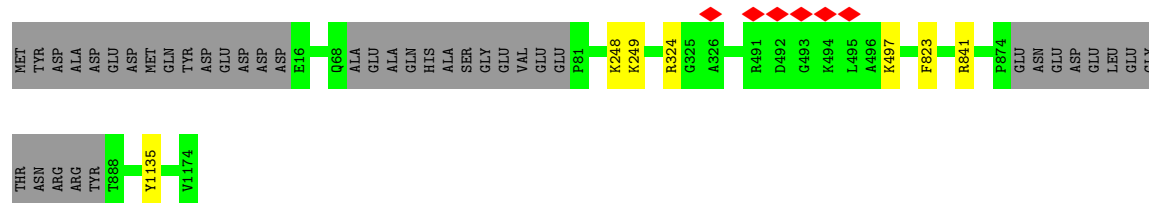
MET
 HIS
 GLY
 GLY
 GLY
 PRO
 PRO
 SER
 GLY
 ASP
 S11
 A12
 C13
 P14
 L15
 R16
 T17
 C114
 R134
 G135
 E155
 GLY
 GLY
 GLY
 GLU
 MET
 ASP
 ASN
 LYS
 PHE
 GLY
 VAL
 GLU
 GLN
 PRO
 GLU
 GLY
 ASP
 ASP
 GLU
 LEU
 THR
 LYS
 LYS
 LYS
 GLY
 H181
 R193
 W202
 LYS
 HIS
 VAL
 ASN
 GLU
 CTD

SER		GLN
GLU		
K212		L215
R292		
N296		D297
D297		
A299		A300
A300		
H301		V302
V302		
I303		A304
A304		
E305		L322
L322		
R327		S332
S332		
R364		K417
K417		
I420		A421
A421		
I427		D428
D428		
L429		D437
D437		
F458		M459
M459		
R460		Q461
Q461		
L486		L503
L503		
Q539		K581
K581		
P582		R583
R583		
Q703		N723
N723		
T728		



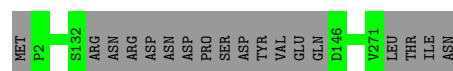
• Molecule 25: DNA-directed RNA polymerase subunit beta

Chain p: 96%



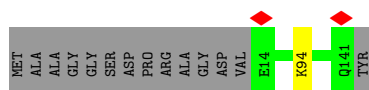
• Molecule 26: DNA-directed RNA polymerase II subunit RPB3

Chain q: 93% 7%



• Molecule 27: DNA-directed RNA polymerase II subunit RPB4

Chain r: 89% 10%



- Molecule 28: DNA-directed RNA polymerase II subunit E

Chain s: 99%



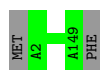
- Molecule 29: DNA-directed RNA polymerase II subunit F

Chain t: 62% 38%



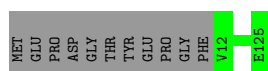
- Molecule 30: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain v: 99%



- Molecule 31: DNA-directed RNA polymerase II subunit RPB9

Chain w: 91% 9%



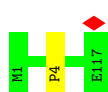
- Molecule 32: RPB10

Chain x: 87% 9%



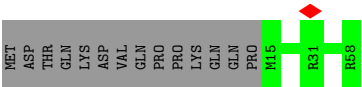
- Molecule 33: RNA_pol_L_2 domain-containing protein

Chain y: 99%



- Molecule 34: RPB12

Chain z: 76% 24%



- Molecule 35: DNA-directed RNA polymerase II subunit RPB7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57889	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	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	1.158	Depositor
Minimum map value	-0.399	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.13	Depositor
Map size (\AA)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.52	0/5046	0.67	1/6810 (0.0%)
2	B	0.47	0/7993	0.62	1/10836 (0.0%)
3	D	0.44	0/1374	0.56	0/1836
3	d	0.28	0/1321	0.49	0/1772
4	E	0.36	0/4469	0.56	0/6050
4	e	0.32	0/4433	0.55	0/6004
5	F	0.51	0/3139	0.72	0/4264
5	f	0.41	0/3140	0.63	0/4268
6	G	0.51	0/1199	0.65	0/1612
7	H	0.42	0/1673	0.59	0/2285
8	I	0.34	0/981	0.57	1/1332 (0.1%)
8	i	0.30	0/989	0.46	0/1343
9	J	0.31	0/724	0.50	0/982
9	j	0.30	0/775	0.52	0/1049
10	L	0.32	0/630	0.59	1/852 (0.1%)
10	l	0.34	0/888	0.57	1/1194 (0.1%)
11	O	0.57	0/781	0.78	0/1061
12	P	0.62	0/1438	0.75	0/1935
13	Q	0.44	0/1013	0.69	1/1366 (0.1%)
14	R	0.37	0/1941	0.59	0/2622
15	S	0.34	0/1130	0.53	0/1528
16	T	0.26	0/799	0.53	0/1077
17	U	0.51	0/1499	0.75	3/2012 (0.1%)
18	V	0.48	0/1424	0.72	2/1913 (0.1%)
19	X	0.88	0/1653	1.11	0/2552
20	Y	0.79	0/1611	0.98	0/2481
21	c	0.39	0/1035	0.54	0/1406
22	k	0.30	0/799	0.47	0/1070
23	m	0.31	0/733	0.51	0/977
24	o	0.49	0/11516	0.68	1/15548 (0.0%)
25	p	0.37	0/9243	0.47	1/12475 (0.0%)
26	q	0.38	0/2102	0.46	0/2857

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	r	0.27	0/1019	0.47	0/1374
28	s	0.30	0/1751	0.45	0/2366
29	t	0.37	0/645	0.46	0/871
30	v	0.37	0/1207	0.49	0/1628
31	w	0.30	0/948	0.45	0/1284
32	x	0.49	0/516	0.65	0/696
33	y	0.36	0/956	0.46	0/1294
34	z	0.38	0/377	0.45	0/500
35	u	0.33	0/1382	0.53	0/1874
All	All	0.45	0/86292	0.62	13/117256 (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
11	O	0	1
17	U	0	1
All	All	0	2

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	883	PHE	C-N-CA	-7.06	104.04	121.70
17	U	94	ILE	O-C-N	6.62	133.29	122.70
18	V	139	PHE	CB-CA-C	-6.26	97.88	110.40
13	Q	330	ASP	CB-CA-C	6.21	122.82	110.40
18	V	234	GLU	CB-CA-C	-5.73	98.94	110.40
1	A	843	ARG	CG-CD-NE	5.71	123.79	111.80
25	p	1135	TYR	CB-CA-C	5.41	121.23	110.40
17	U	140	GLU	CB-CA-C	-5.38	99.63	110.40
10	L	79	ASP	CB-CG-OD2	5.19	122.97	118.30
10	l	79	ASP	CB-CG-OD2	5.15	122.93	118.30
8	I	114	ARG	CB-CA-C	5.09	120.58	110.40
24	o	950	ASN	CB-CA-C	-5.05	100.31	110.40
17	U	128	LYS	N-CA-CB	5.01	119.62	110.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	O	17	GLU	Mainchain
17	U	161	VAL	Mainchain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	584/1872 (31%)	553 (95%)	27 (5%)	4 (1%)	19	51
2	B	959/1199 (80%)	908 (95%)	50 (5%)	1 (0%)	48	78
3	D	157/1085 (14%)	150 (96%)	7 (4%)	0	100	100
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	540/800 (68%)	497 (92%)	40 (7%)	3 (1%)	22	54
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	367 (92%)	24 (6%)	9 (2%)	5	31
5	f	399/677 (59%)	377 (94%)	22 (6%)	0	100	100
6	G	139/349 (40%)	134 (96%)	5 (4%)	0	100	100
7	H	207/310 (67%)	188 (91%)	15 (7%)	4 (2%)	6	35
8	I	118/264 (45%)	109 (92%)	5 (4%)	4 (3%)	3	26
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
9	J	85/218 (39%)	82 (96%)	3 (4%)	0	100	100
9	j	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
10	L	74/161 (46%)	69 (93%)	5 (7%)	0	100	100
10	l	105/161 (65%)	100 (95%)	5 (5%)	0	100	100
11	O	95/109 (87%)	76 (80%)	13 (14%)	6 (6%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	P	175/339 (52%)	164 (94%)	8 (5%)	3 (2%)	7	36
13	Q	118/376 (31%)	108 (92%)	9 (8%)	1 (1%)	16	49
14	R	244/316 (77%)	228 (93%)	15 (6%)	1 (0%)	30	62
15	S	130/517 (25%)	127 (98%)	2 (2%)	1 (1%)	16	49
16	T	99/249 (40%)	95 (96%)	3 (3%)	1 (1%)	13	44
17	U	175/439 (40%)	155 (89%)	16 (9%)	4 (2%)	5	31
18	V	170/291 (58%)	133 (78%)	25 (15%)	12 (7%)	1	13
21	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
22	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
23	m	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
24	o	1417/1970 (72%)	1280 (90%)	124 (9%)	13 (1%)	14	47
25	p	1128/1174 (96%)	1052 (93%)	76 (7%)	0	100	100
26	q	253/275 (92%)	226 (89%)	27 (11%)	0	100	100
27	r	126/142 (89%)	119 (94%)	7 (6%)	0	100	100
28	s	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
29	t	77/127 (61%)	74 (96%)	3 (4%)	0	100	100
30	v	146/150 (97%)	132 (90%)	14 (10%)	0	100	100
31	w	112/125 (90%)	103 (92%)	9 (8%)	0	100	100
32	x	62/67 (92%)	60 (97%)	2 (3%)	0	100	100
33	y	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	14	47
34	z	42/58 (72%)	38 (90%)	4 (10%)	0	100	100
35	u	169/172 (98%)	156 (92%)	12 (7%)	1 (1%)	22	54
All	All	10028/18627 (54%)	9288 (93%)	671 (7%)	69 (1%)	21	51

All (69) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1158	SER
5	F	323	VAL
5	F	345	SER
5	F	415	ILE
7	H	141	PRO
8	I	105	PRO
8	I	109	PRO

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Mol	Chain	Res	Type
11	O	28	ILE
11	O	29	THR
11	O	30	PRO
11	O	52	VAL
13	Q	321	SER
17	U	71	PHE
17	U	119	ARG
18	V	171	ILE
18	V	205	ASP
24	o	461	GLN
24	o	1059	ARG
35	u	154	LYS
1	A	849	CYS
7	H	226	ALA
12	P	285	PRO
18	V	79	ALA
18	V	173	GLU
24	o	114	CYS
24	o	723	ASN
24	o	969	ILE
24	o	1038	THR
24	o	1103	THR
4	E	422	PRO
5	F	64	GLN
12	P	207	PRO
18	V	134	ASP
24	o	17	THR
24	o	1037	ALA
4	E	429	LEU
5	F	439	ARG
11	O	56	VAL
11	O	84	VAL
16	T	38	GLY
17	U	145	PHE
18	V	139	PHE
18	V	172	GLU
18	V	206	LYS
18	V	208	CYS
18	V	225	VAL
24	o	581	LYS
24	o	1099	ALA
2	B	880	TYR

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Mol	Chain	Res	Type
7	H	134	LEU
7	H	164	THR
8	I	107	ILE
15	S	153	ARG
17	U	74	CYS
18	V	212	VAL
5	F	314	SER
5	F	432	ALA
12	P	298	PRO
18	V	177	ASN
24	o	968	VAL
33	y	4	PRO
8	I	113	PRO
5	F	433	PRO
1	A	467	ILE
1	A	498	PRO
4	E	704	VAL
5	F	364	VAL
14	R	280	VAL
24	o	980	PRO

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	536/1665 (32%)	484 (90%)	52 (10%)	6	28
2	B	876/1083 (81%)	856 (98%)	20 (2%)	45	64
3	D	147/815 (18%)	130 (88%)	17 (12%)	4	22
3	d	146/815 (18%)	146 (100%)	0	100	100
4	E	478/657 (73%)	464 (97%)	14 (3%)	37	59
4	e	475/657 (72%)	473 (100%)	2 (0%)	89	93
5	F	320/574 (56%)	298 (93%)	22 (7%)	13	39
5	f	322/574 (56%)	313 (97%)	9 (3%)	38	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	G	133/322 (41%)	121 (91%)	12 (9%)	8	31
7	H	181/270 (67%)	169 (93%)	12 (7%)	14	41
8	I	106/235 (45%)	97 (92%)	9 (8%)	8	33
8	i	107/235 (46%)	107 (100%)	0	100	100
9	J	78/154 (51%)	78 (100%)	0	100	100
9	j	83/154 (54%)	83 (100%)	0	100	100
10	L	71/141 (50%)	70 (99%)	1 (1%)	62	76
10	l	98/141 (70%)	96 (98%)	2 (2%)	50	68
11	O	84/98 (86%)	69 (82%)	15 (18%)	1	9
12	P	153/293 (52%)	138 (90%)	15 (10%)	6	27
13	Q	111/324 (34%)	106 (96%)	5 (4%)	23	50
14	R	211/268 (79%)	187 (89%)	24 (11%)	4	23
15	S	117/448 (26%)	114 (97%)	3 (3%)	41	61
16	T	85/218 (39%)	85 (100%)	0	100	100
17	U	163/373 (44%)	130 (80%)	33 (20%)	1	7
18	V	154/261 (59%)	116 (75%)	38 (25%)	0	4
21	c	113/833 (14%)	111 (98%)	2 (2%)	54	71
22	k	87/182 (48%)	87 (100%)	0	100	100
23	m	80/106 (76%)	79 (99%)	1 (1%)	65	77
24	o	1257/1748 (72%)	1207 (96%)	50 (4%)	27	52
25	p	993/1027 (97%)	987 (99%)	6 (1%)	84	90
26	q	234/252 (93%)	234 (100%)	0	100	100
27	r	106/126 (84%)	105 (99%)	1 (1%)	75	84
28	s	191/192 (100%)	190 (100%)	1 (0%)	86	92
29	t	69/111 (62%)	69 (100%)	0	100	100
30	v	129/131 (98%)	129 (100%)	0	100	100
31	w	103/112 (92%)	103 (100%)	0	100	100
32	x	53/56 (95%)	47 (89%)	6 (11%)	4	23
33	y	106/106 (100%)	106 (100%)	0	100	100
34	z	41/55 (74%)	41 (100%)	0	100	100
35	u	152/153 (99%)	150 (99%)	2 (1%)	65	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	8949/15965 (56%)	8575 (96%)	374 (4%)	27	51

All (374) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	341	TRP
1	A	353	LEU
1	A	395	ASP
1	A	397	LEU
1	A	400	GLU
1	A	404	MET
1	A	408	LEU
1	A	411	GLU
1	A	415	ILE
1	A	416	TRP
1	A	417	ASP
1	A	419	GLU
1	A	465	TYR
1	A	467	ILE
1	A	470	ILE
1	A	475	LEU
1	A	491	MET
1	A	500	LEU
1	A	501	THR
1	A	502	LEU
1	A	505	ASN
1	A	511	LEU
1	A	639	LEU
1	A	661	GLU
1	A	667	THR
1	A	711	ASP
1	A	727	THR
1	A	730	PHE
1	A	804	ARG
1	A	828	GLU
1	A	848	LEU
1	A	853	LYS
1	A	855	THR
1	A	859	SER
1	A	943	LYS
1	A	968	ILE
1	A	970	ASN

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Mol	Chain	Res	Type
1	A	971	LYS
1	A	994	ASP
1	A	996	ARG
1	A	999	SER
1	A	1020	LEU
1	A	1021	SER
1	A	1022	ARG
1	A	1024	GLU
1	A	1026	ILE
1	A	1029	VAL
1	A	1052	ARG
1	A	1055	VAL
1	A	1165	LEU
1	A	1181	ARG
1	A	1203	GLU
2	B	21	GLU
2	B	24	ARG
2	B	71	ARG
2	B	140	GLU
2	B	184	ASN
2	B	225	TYR
2	B	262	MET
2	B	266	THR
2	B	293	GLU
2	B	431	LEU
2	B	475	LYS
2	B	488	PHE
2	B	559	LYS
2	B	603	LYS
2	B	638	ARG
2	B	640	VAL
2	B	771	VAL
2	B	817	ARG
2	B	819	LEU
2	B	820	ASP
3	D	941	ARG
3	D	947	PHE
3	D	949	GLN
3	D	963	ARG
3	D	964	GLU
3	D	966	LEU
3	D	968	ARG

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Mol	Chain	Res	Type
3	D	986	GLN
3	D	990	GLU
3	D	991	MET
3	D	992	GLN
3	D	993	GLN
3	D	1000	ARG
3	D	1002	ARG
3	D	1006	LEU
3	D	1054	ARG
3	D	1055	ILE
4	E	417	GLN
4	E	420	ASN
4	E	424	GLN
4	E	425	ASN
4	E	427	ILE
4	E	431	GLU
4	E	518	LYS
4	E	519	GLU
4	E	522	ASP
4	E	526	ARG
4	E	593	PHE
4	E	745	GLU
4	E	746	ASP
4	E	747	LEU
5	F	221	GLN
5	F	222	LEU
5	F	258	ARG
5	F	261	THR
5	F	271	VAL
5	F	276	LEU
5	F	280	ILE
5	F	301	VAL
5	F	312	ILE
5	F	315	ARG
5	F	317	LEU
5	F	339	GLN
5	F	343	HIS
5	F	348	THR
5	F	354	ARG
5	F	358	THR
5	F	367	LYS
5	F	391	LEU

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Mol	Chain	Res	Type
5	F	397	GLN
5	F	408	ASP
5	F	427	LEU
5	F	433	PRO
6	G	41	ASP
6	G	42	ARG
6	G	44	THR
6	G	46	GLU
6	G	81	ASP
6	G	143	VAL
6	G	147	ARG
6	G	154	LYS
6	G	161	ASP
6	G	181	TRP
6	G	182	GLU
6	G	183	ILE
7	H	115	GLN
7	H	132	LYS
7	H	135	THR
7	H	159	TYR
7	H	164	THR
7	H	203	LEU
7	H	206	ASP
7	H	217	ARG
7	H	220	THR
7	H	221	ILE
7	H	225	THR
7	H	227	LEU
8	I	101	GLN
8	I	102	THR
8	I	104	LEU
8	I	105	PRO
8	I	106	LEU
8	I	107	ILE
8	I	108	LYS
8	I	110	TYR
8	I	111	SER
10	L	73	ASN
11	O	11	LEU
11	O	23	ILE
11	O	28	ILE
11	O	29	THR

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Mol	Chain	Res	Type
11	O	32	LEU
11	O	55	ARG
11	O	56	VAL
11	O	57	ASN
11	O	58	PHE
11	O	61	SER
11	O	65	TYR
11	O	66	ARG
11	O	76	LEU
11	O	88	ILE
11	O	89	LYS
12	P	172	VAL
12	P	196	ARG
12	P	197	PHE
12	P	209	THR
12	P	219	MET
12	P	221	CYS
12	P	226	SER
12	P	252	ASP
12	P	274	VAL
12	P	278	GLN
12	P	286	GLU
12	P	288	PHE
12	P	294	ARG
12	P	311	VAL
12	P	317	VAL
13	Q	13	LEU
13	Q	49	LYS
13	Q	329	PHE
13	Q	332	GLU
13	Q	364	ASP
14	R	31	ASP
14	R	32	MET
14	R	33	ILE
14	R	39	LEU
14	R	40	VAL
14	R	41	VAL
14	R	120	GLU
14	R	127	ARG
14	R	128	ILE
14	R	130	LEU
14	R	132	ARG

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Mol	Chain	Res	Type
14	R	133	ASN
14	R	134	ILE
14	R	137	ARG
14	R	139	ASN
14	R	189	LYS
14	R	196	LYS
14	R	244	LEU
14	R	245	VAL
14	R	248	ARG
14	R	249	SER
14	R	252	SER
14	R	282	ASP
14	R	286	ARG
15	S	7	SER
15	S	108	ARG
15	S	154	THR
17	U	15	LYS
17	U	16	ARG
17	U	17	LEU
17	U	28	ILE
17	U	39	ARG
17	U	45	GLU
17	U	72	ILE
17	U	73	LYS
17	U	75	ARG
17	U	76	MET
17	U	77	ARG
17	U	95	ASN
17	U	99	LEU
17	U	105	TYR
17	U	111	ARG
17	U	112	ARG
17	U	113	ARG
17	U	126	SER
17	U	139	LEU
17	U	145	PHE
17	U	168	MET
17	U	171	LYS
17	U	174	ARG
17	U	175	THR
17	U	176	LEU
17	U	179	ARG

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Mol	Chain	Res	Type
17	U	184	ILE
17	U	185	GLU
17	U	190	LEU
17	U	191	LEU
17	U	193	GLU
17	U	194	THR
17	U	199	LEU
18	V	88	ARG
18	V	99	LEU
18	V	100	ASP
18	V	107	GLN
18	V	132	VAL
18	V	142	LYS
18	V	144	ASN
18	V	146	ARG
18	V	147	ASP
18	V	149	LYS
18	V	151	LEU
18	V	153	ARG
18	V	154	LEU
18	V	155	LEU
18	V	157	GLN
18	V	159	ASP
18	V	160	GLN
18	V	161	ARG
18	V	163	LEU
18	V	167	LEU
18	V	168	LEU
18	V	169	GLU
18	V	171	ILE
18	V	175	LEU
18	V	188	GLN
18	V	193	ASN
18	V	204	ASN
18	V	206	LYS
18	V	207	SER
18	V	208	CYS
18	V	210	PHE
18	V	211	SER
18	V	213	ASP
18	V	215	GLU
18	V	221	ARG

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Mol	Chain	Res	Type
18	V	229	ASP
18	V	230	GLU
18	V	235	GLU
21	c	24	ASP
21	c	106	VAL
4	e	365	ARG
4	e	663	ARG
5	f	214	HIS
5	f	253	TYR
5	f	261	THR
5	f	272	VAL
5	f	322	ASP
5	f	323	VAL
5	f	326	HIS
5	f	356	THR
5	f	421	ASP
10	l	84	LEU
10	l	106	ARG
23	m	31	LEU
24	o	13	CYS
24	o	15	LEU
24	o	16	ARG
24	o	114	CYS
24	o	364	ARG
24	o	417	LYS
24	o	420	ILE
24	o	421	ARG
24	o	427	ILE
24	o	428	ASP
24	o	429	LEU
24	o	437	ASP
24	o	458	PHE
24	o	460	ARG
24	o	461	GLN
24	o	486	LEU
24	o	503	LEU
24	o	539	GLN
24	o	581	LYS
24	o	583	ARG
24	o	703	GLN
24	o	728	THR
24	o	732	THR

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Mol	Chain	Res	Type
24	o	792	ASN
24	o	924	TYR
24	o	936	GLU
24	o	939	VAL
24	o	947	HIS
24	o	953	GLU
24	o	999	ARG
24	o	1011	GLU
24	o	1027	ASP
24	o	1032	GLN
24	o	1065	PHE
24	o	1075	LYS
24	o	1095	LEU
24	o	1101	GLN
24	o	1142	PHE
24	o	1152	GLU
24	o	1156	ASP
24	o	1296	MET
24	o	1298	LEU
24	o	1316	ASN
24	o	1356	ARG
24	o	1432	PHE
24	o	1479	LYS
24	o	1482	TYR
24	o	1484	MET
24	o	1485	GLU
24	o	1486	ILE
25	p	248	LYS
25	p	249	LYS
25	p	324	ARG
25	p	497	LYS
25	p	823	PHE
25	p	841	ARG
27	r	94	LYS
28	s	52	ARG
32	x	14	VAL
32	x	19	GLU
32	x	26	GLN
32	x	28	GLU
32	x	30	THR
32	x	31	GLU
35	u	144	ARG

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Mol	Chain	Res	Type
35	u	163	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (113) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	401	ASN
1	A	472	ASN
1	A	489	GLN
1	A	569	ASN
1	A	634	HIS
1	A	896	GLN
1	A	1058	HIS
1	A	1073	GLN
2	B	30	HIS
2	B	137	HIS
2	B	176	HIS
2	B	183	GLN
2	B	184	ASN
2	B	235	HIS
2	B	348	GLN
2	B	432	HIS
2	B	439	HIS
2	B	450	GLN
2	B	509	ASN
2	B	644	GLN
2	B	652	GLN
2	B	745	GLN
2	B	750	GLN
2	B	813	ASN
2	B	908	GLN
2	B	916	ASN
3	D	875	GLN
3	D	936	GLN
3	D	949	GLN
3	D	992	GLN
4	E	254	ASN
4	E	268	HIS
4	E	327	ASN
4	E	351	GLN
4	E	616	HIS
5	F	52	GLN
5	F	119	ASN

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Mol	Chain	Res	Type
5	F	221	GLN
5	F	270	ASN
5	F	273	GLN
5	F	274	ASN
5	F	275	ASN
5	F	302	HIS
5	F	316	GLN
6	G	10	HIS
6	G	15	GLN
6	G	48	HIS
7	H	145	HIS
7	H	201	GLN
8	I	21	GLN
8	I	38	GLN
8	I	60	HIS
8	I	98	GLN
9	J	160	GLN
9	J	173	HIS
9	J	210	ASN
10	L	105	HIS
10	L	117	GLN
11	O	57	ASN
13	Q	37	GLN
13	Q	60	HIS
13	Q	343	HIS
13	Q	352	HIS
13	Q	361	ASN
14	R	139	ASN
15	S	44	GLN
17	U	123	ASN
18	V	117	GLN
18	V	177	ASN
18	V	193	ASN
18	V	209	GLN
3	d	912	ASN
3	d	1069	ASN
4	e	294	ASN
4	e	320	HIS
4	e	336	HIS
4	e	616	HIS
5	f	325	ASN
8	i	81	GLN

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Mol	Chain	Res	Type
10	l	105	HIS
23	m	107	ASN
24	o	267	GLN
24	o	353	ASN
24	o	465	HIS
24	o	539	GLN
24	o	673	GLN
24	o	721	HIS
24	o	739	ASN
24	o	740	GLN
24	o	792	ASN
24	o	861	GLN
24	o	1032	GLN
24	o	1036	ASN
24	o	1101	GLN
24	o	1230	GLN
24	o	1420	ASN
24	o	1462	GLN
25	p	111	ASN
25	p	139	GLN
25	p	287	HIS
25	p	370	HIS
25	p	525	ASN
25	p	570	ASN
25	p	749	HIS
25	p	1021	HIS
25	p	1073	GLN
25	p	1120	ASN
27	r	19	GLN
30	v	131	ASN
31	w	22	ASN
33	y	2	ASN
33	y	29	ASN
35	u	60	GLN

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](#)

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

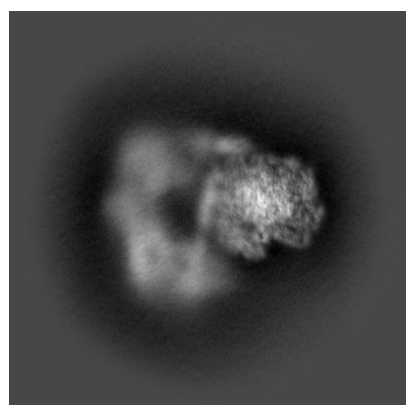
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31109. These allow visual inspection of the internal detail of the map and identification of artifacts.

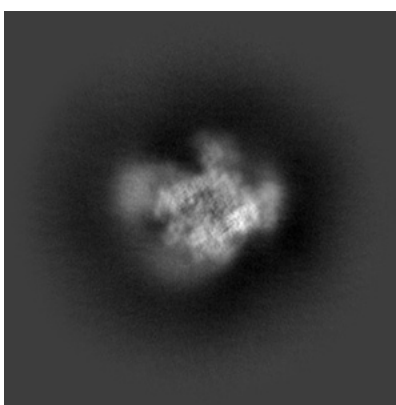
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

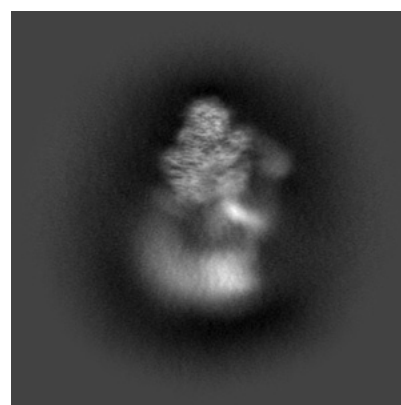
6.1.1 Primary map



X



Y

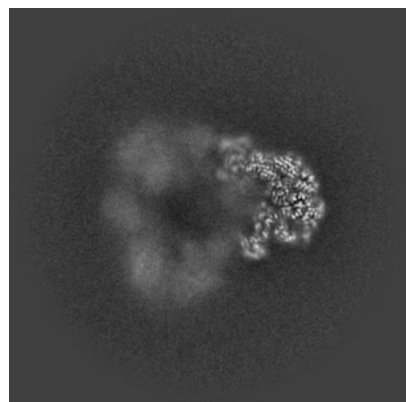


Z

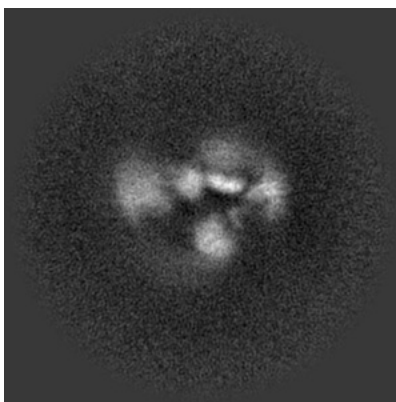
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

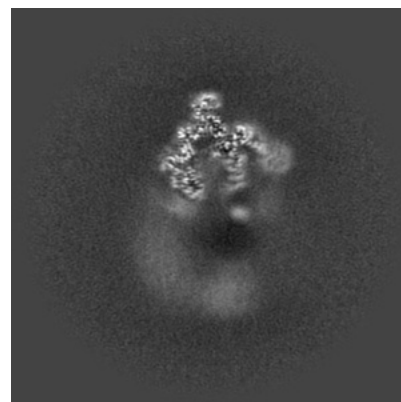
6.2.1 Primary map



X Index: 240



Y Index: 240

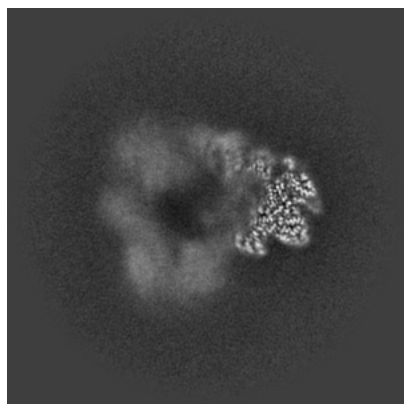


Z Index: 240

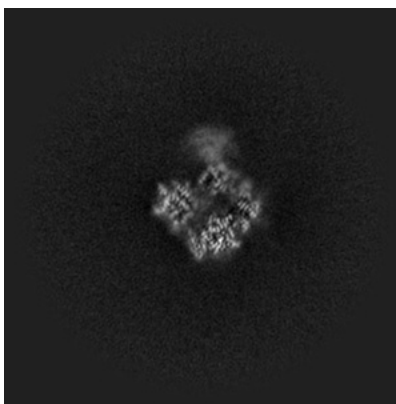
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

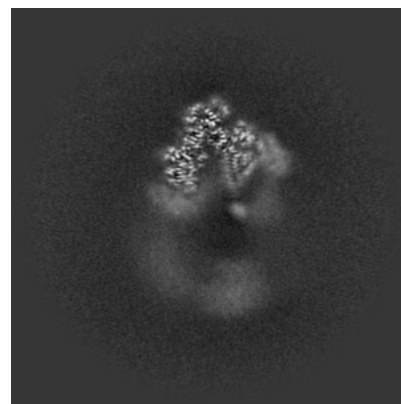
6.3.1 Primary map



X Index: 250



Y Index: 299

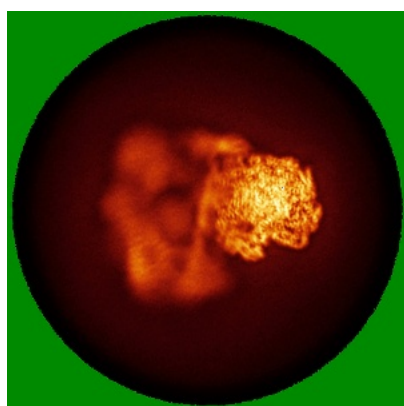


Z Index: 252

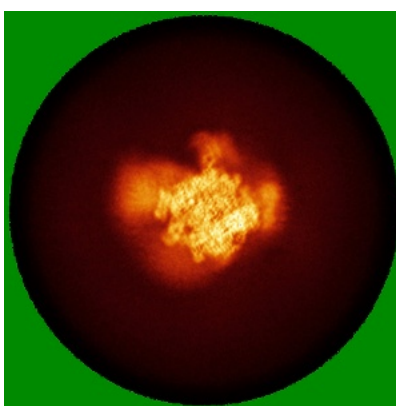
The images above show the largest variance slices of the map in three orthogonal directions.

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

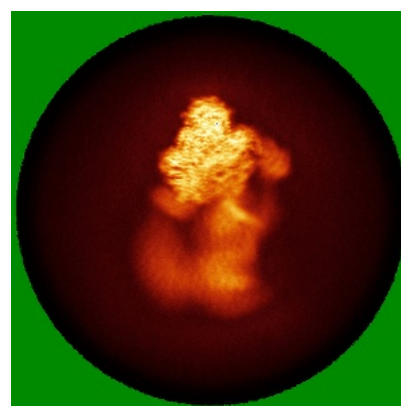
6.4.1 Primary map



X



Y

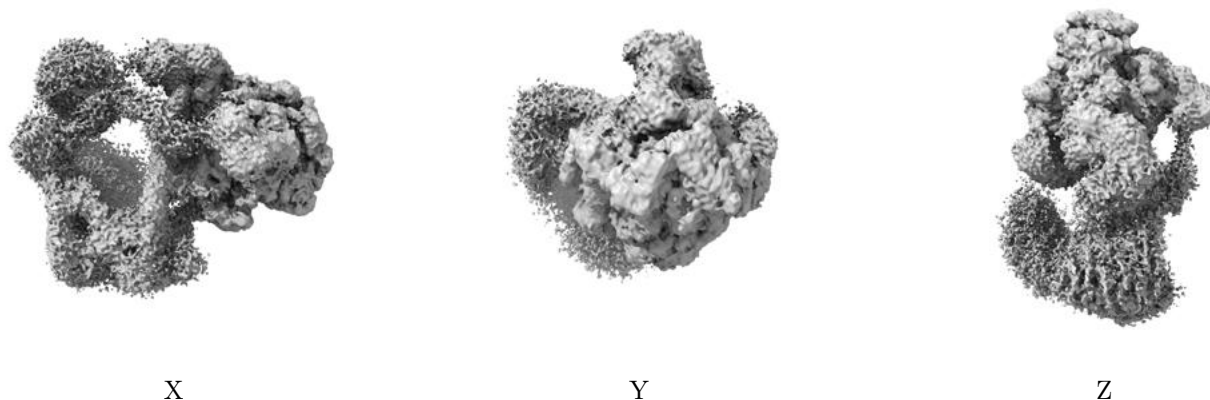


Z

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

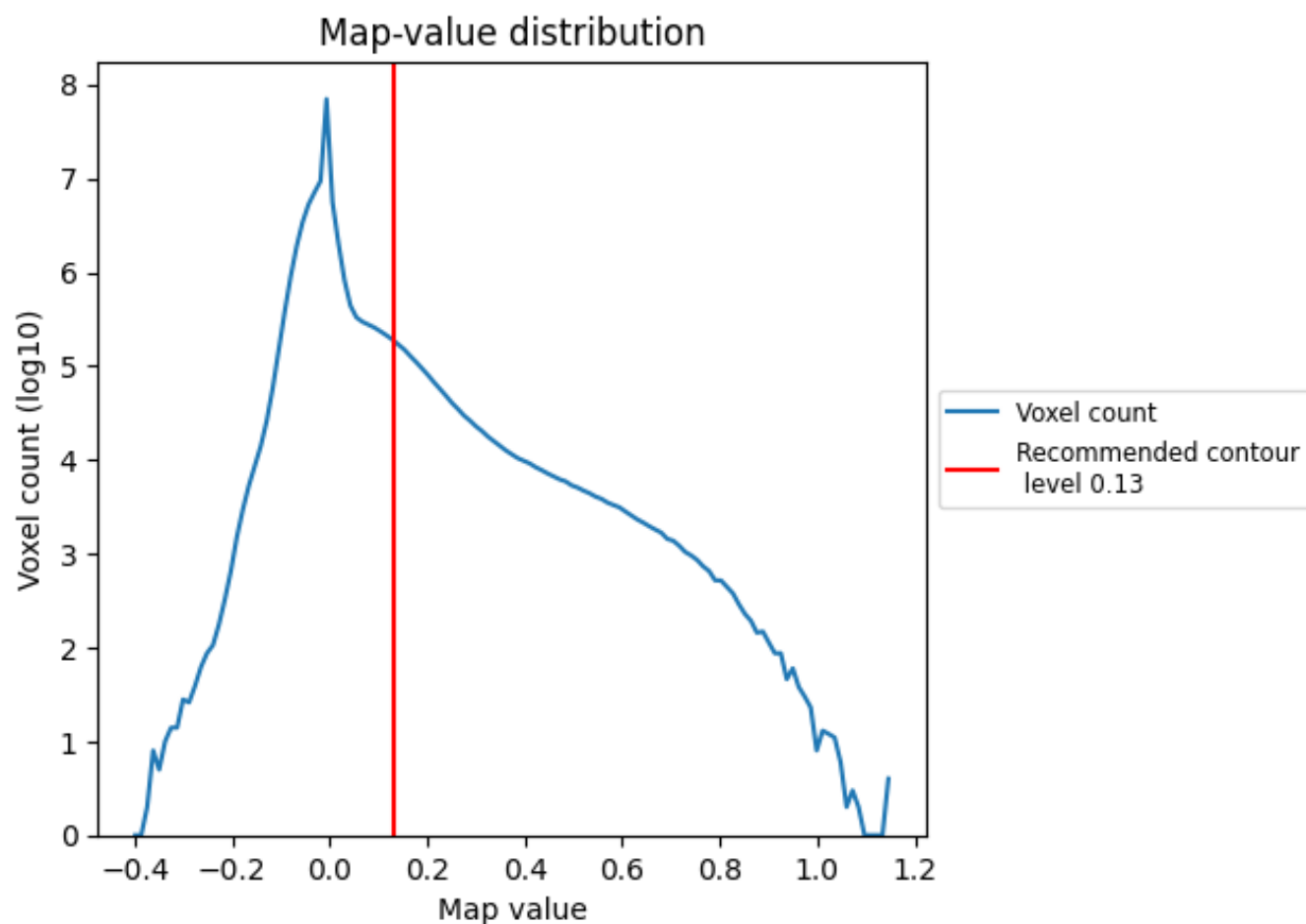
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

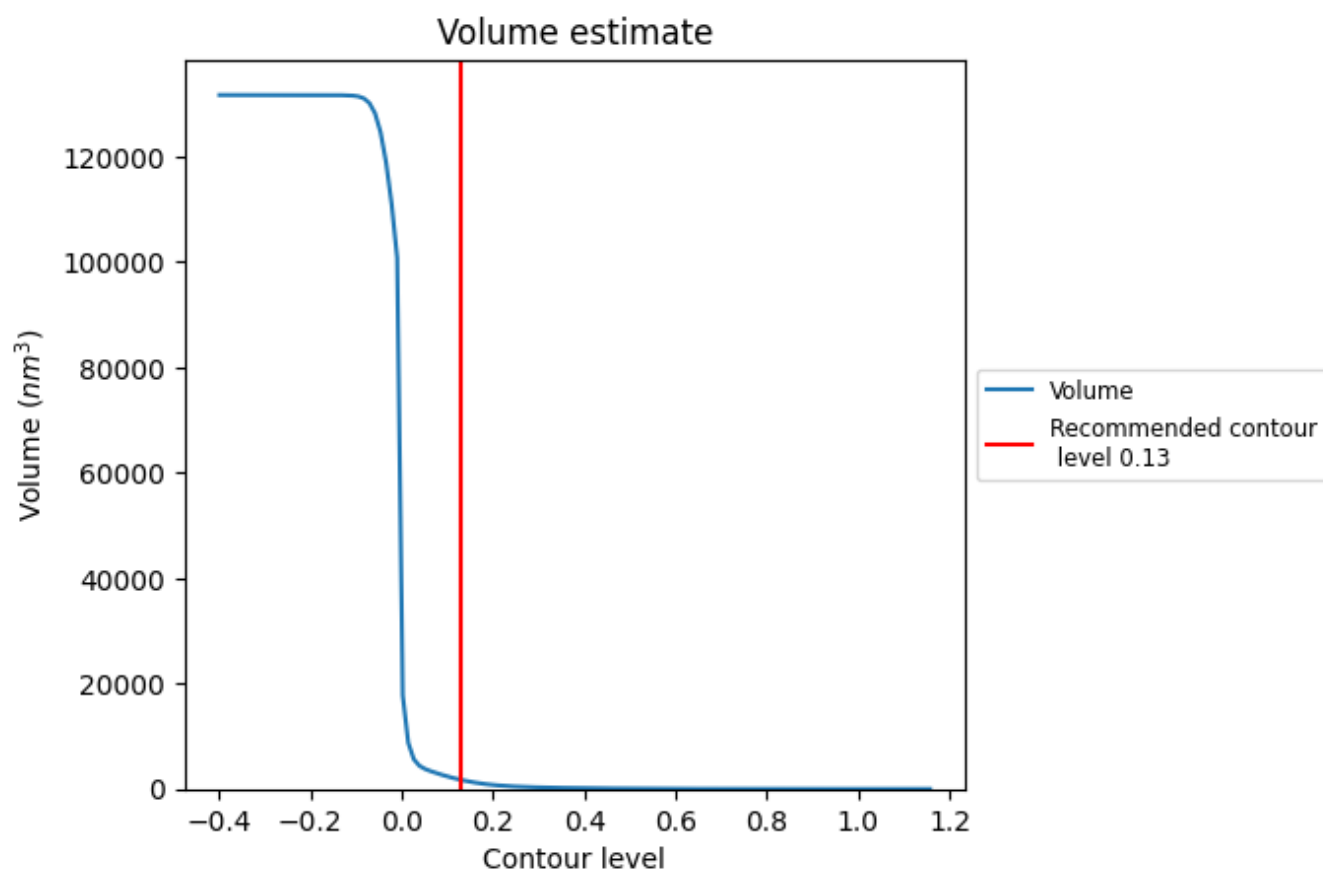
This section contains the results of statistical analysis of the map.

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.

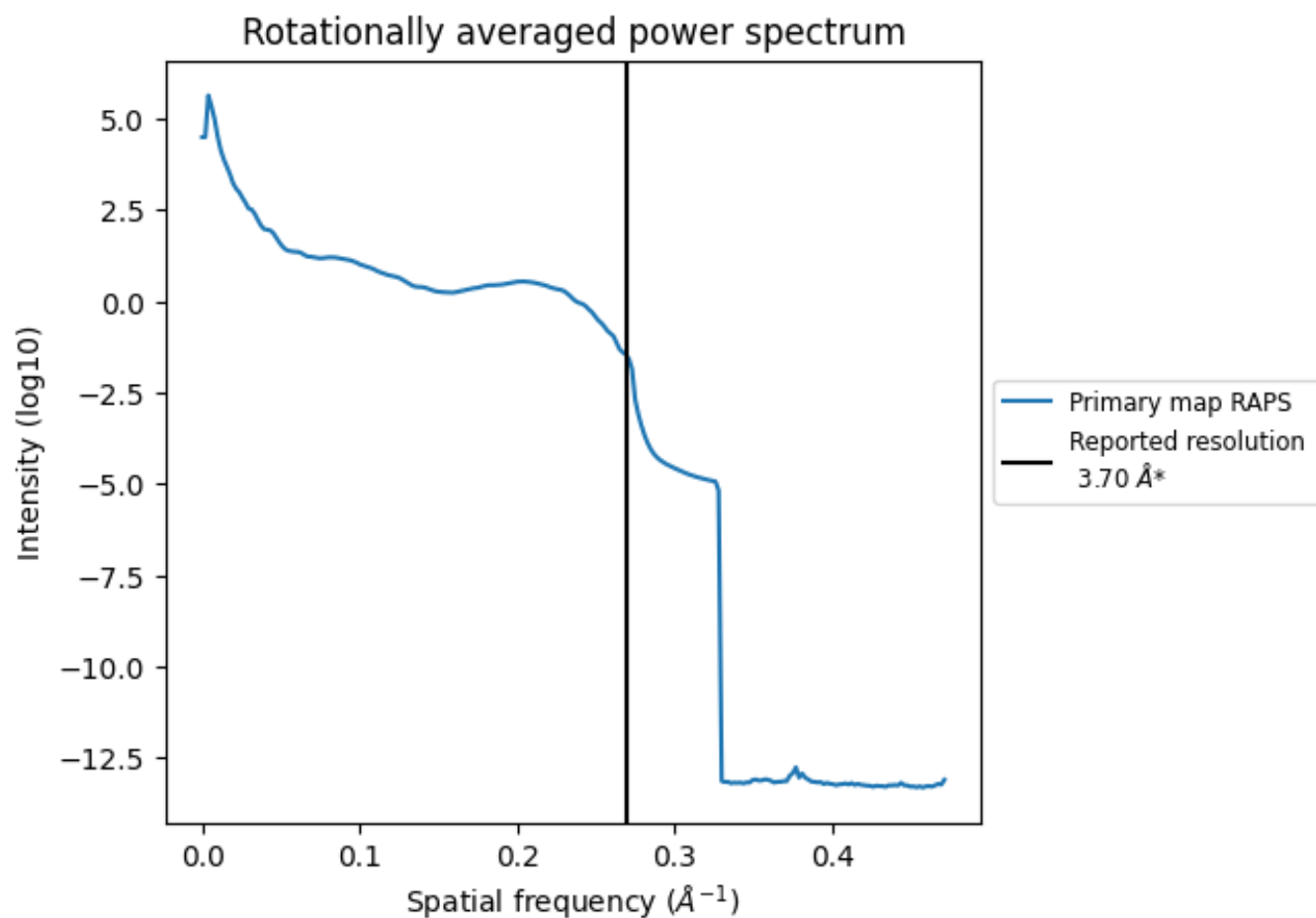
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1729 nm^3 ; this corresponds to an approximate mass of 1562 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 0.270 \AA^{-1}

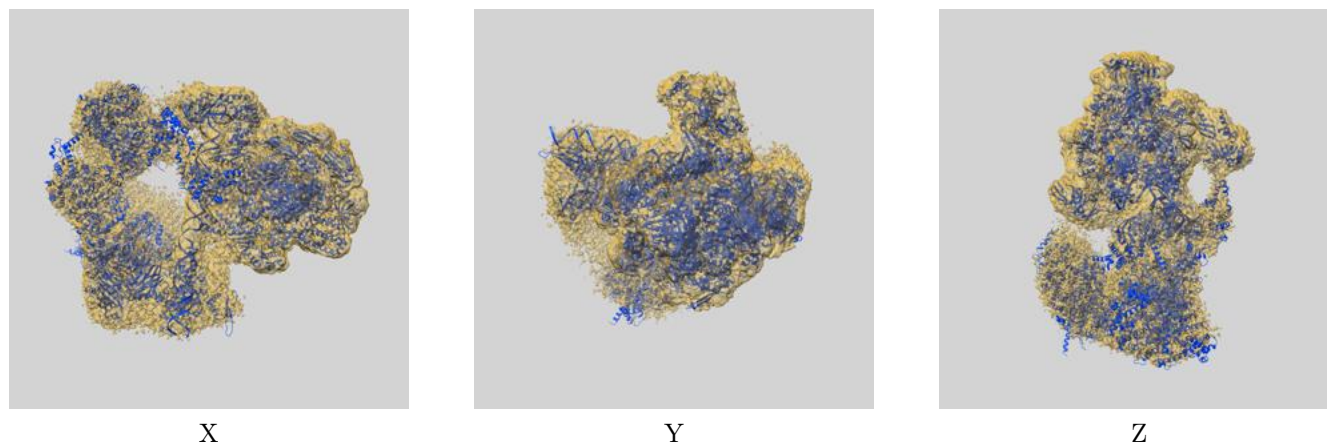
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

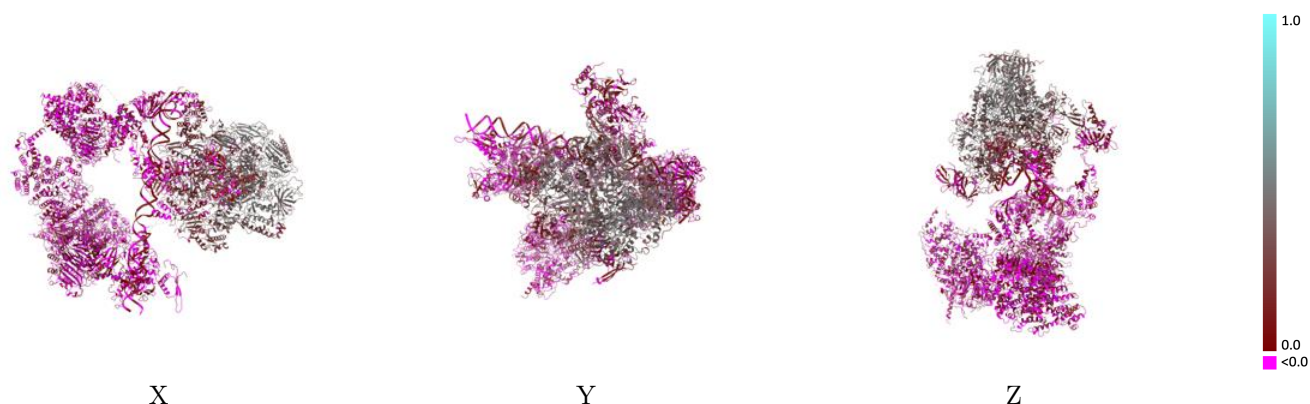
This section contains information regarding the fit between EMDB map EMD-31109 and PDB model 7EG9. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



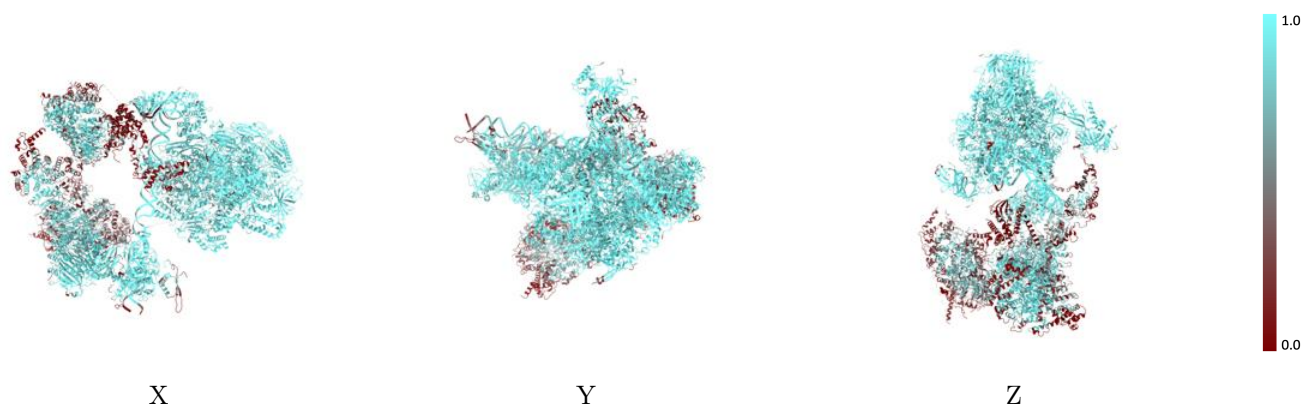
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



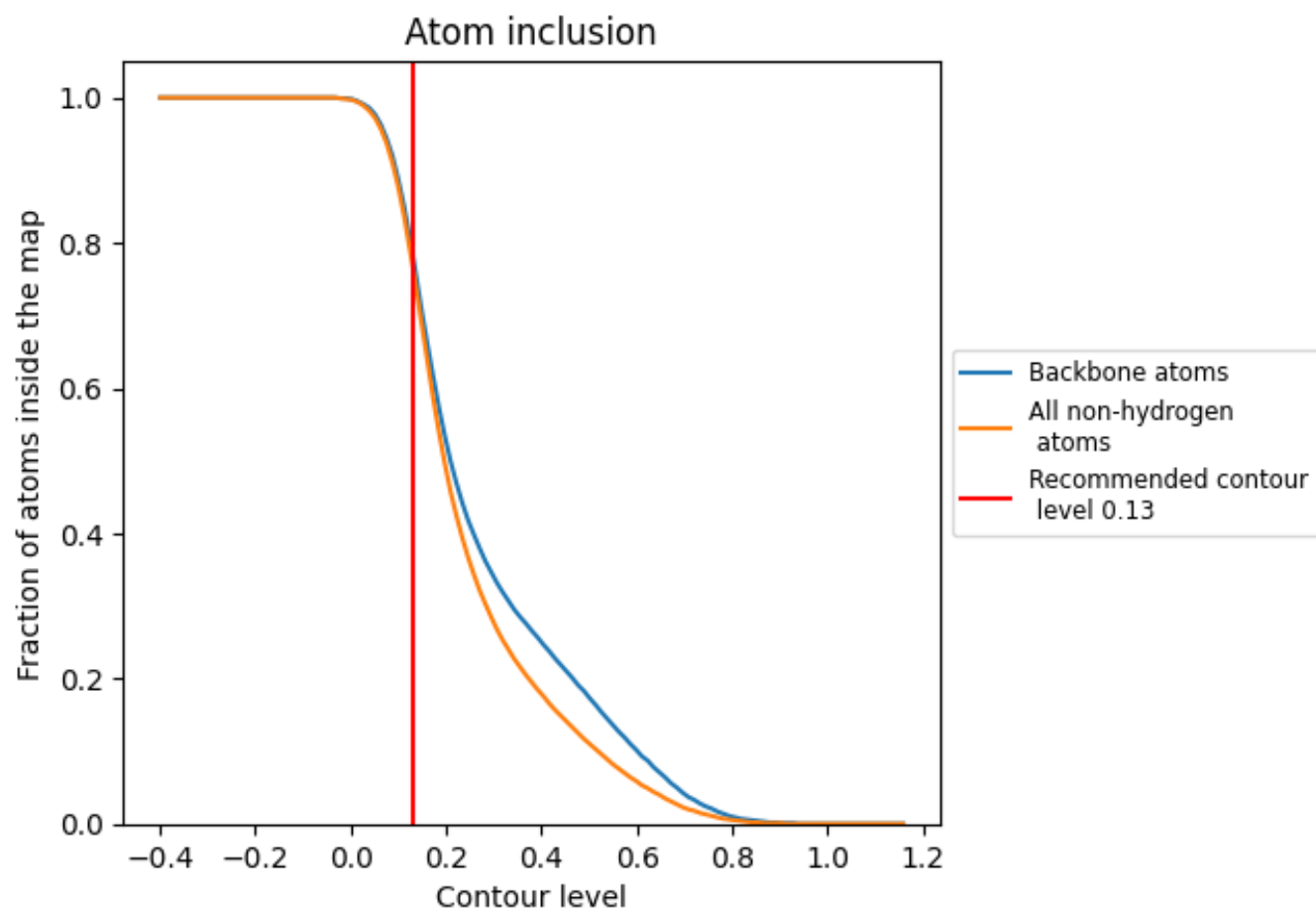
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).





































































9.4 Atom inclusion ⓘ



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.1370
A	 0.8320	 0.0160
B	 0.9040	 0.0370
D	 0.2970	 0.0010
E	 0.7600	 0.0140
F	 0.5210	 0.0090
G	 0.8760	 -0.0040
H	 0.6060	 -0.0030
I	 0.7100	 0.0160
J	 0.6810	 -0.0010
L	 0.2210	 -0.0060
O	 0.3060	 -0.0150
P	 0.9460	 0.0130
Q	 0.3010	 0.0030
R	 0.9090	 0.1460
S	 0.8920	 0.0820
T	 0.8840	 0.0670
U	 0.4200	 -0.0010
V	 0.2480	 0.0100
X	 0.8830	 0.0620
Y	 0.8220	 0.0720
c	 0.4010	 -0.0170
d	 0.3100	 0.0110
e	 0.4380	 -0.0020
f	 0.6670	 0.0200
i	 0.4870	 -0.0100
j	 0.4170	 -0.0160
k	 0.3100	 -0.0000
l	 0.5020	 0.0270
m	 0.2930	 -0.0060
o	 0.9340	 0.3050
p	 0.9620	 0.3760
q	 0.9920	 0.4220
r	 0.9510	 0.1150
s	 0.9820	 0.3140



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Chain	Atom inclusion	Q-score
t	 0.9970	 0.4100
u	 0.9720	 0.1760
v	 0.9920	 0.3870
w	 0.9880	 0.3280
x	 0.9880	 0.4410
y	 0.9680	 0.3950
z	 0.9780	 0.3530