



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 02:14 PM UTC

PDB ID : 7EG8 / pdb_00007eg8
EMDB ID : EMD-31108
Title : TFIID-based core PIC on PUMA promoter
Authors : Chen, X.; Qi, Y.; Hou, H.; Wang, X.; Wu, Z.; Li, J.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 7.40 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:

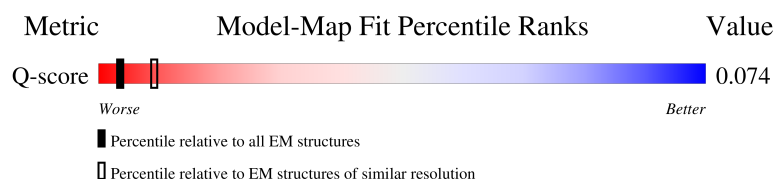
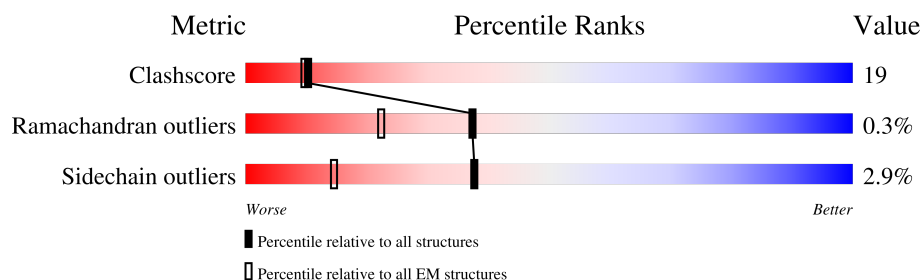
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.40 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	412 (6.90 - 7.90)

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	31% 22% 9% . 68%
2	B	1199	70% 65% 14% . 20%
3	D	1085	13% 9% . . 85%
3	d	1085	15% 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	R	316	
15	S	517	
16	T	249	
17	X	85	
18	Y	85	
19	c	929	
20	k	211	
21	m	124	
22	o	1970	
23	p	1174	

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Mol	Chain	Length	Quality of chain
24	q	275	
25	r	142	
26	s	210	
27	t	127	
28	u	172	
29	v	150	
30	w	125	
31	x	67	
32	y	117	
33	z	58	

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 82798 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	164	Total	C	N	O	S	0	0
			1366	851	256	255	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	251	Total	C	N	O	S	0	0
			1938	1214	344	363	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	108	Total	C	N	O	S	0	0
			872	558	153	159	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	222	Total	C	N	O	S	0	0
			1788	1127	320	338	3		

- Molecule 17 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	85	Total	C	N	O	P	0	0
			1751	829	329	508	85		

- Molecule 18 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	85	Total	C	N	O	P	0	0
			1734	824	313	512	85		

- Molecule 19 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 20 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 21 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 22 is a protein called RPB1.

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

- Molecule 23 is a protein called DNA-directed RNA polymerase subunit beta.

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

- Molecule 24 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 25 is a protein called DNA-directed RNA polymerase II subunit RPB4.

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

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

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

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

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

- Molecule 28 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	u	171	Total	C	N	O	S	0	0
			1334	867	216	243	8		

- Molecule 29 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 30 is a protein called DNA-directed RNA polymerase II subunit RPB9.

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

- Molecule 31 is a protein called RPB10.

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

- Molecule 32 is a protein called RNA_pol_L_2 domain-containing protein.

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

- Molecule 33 is a protein called RPB12.

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

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

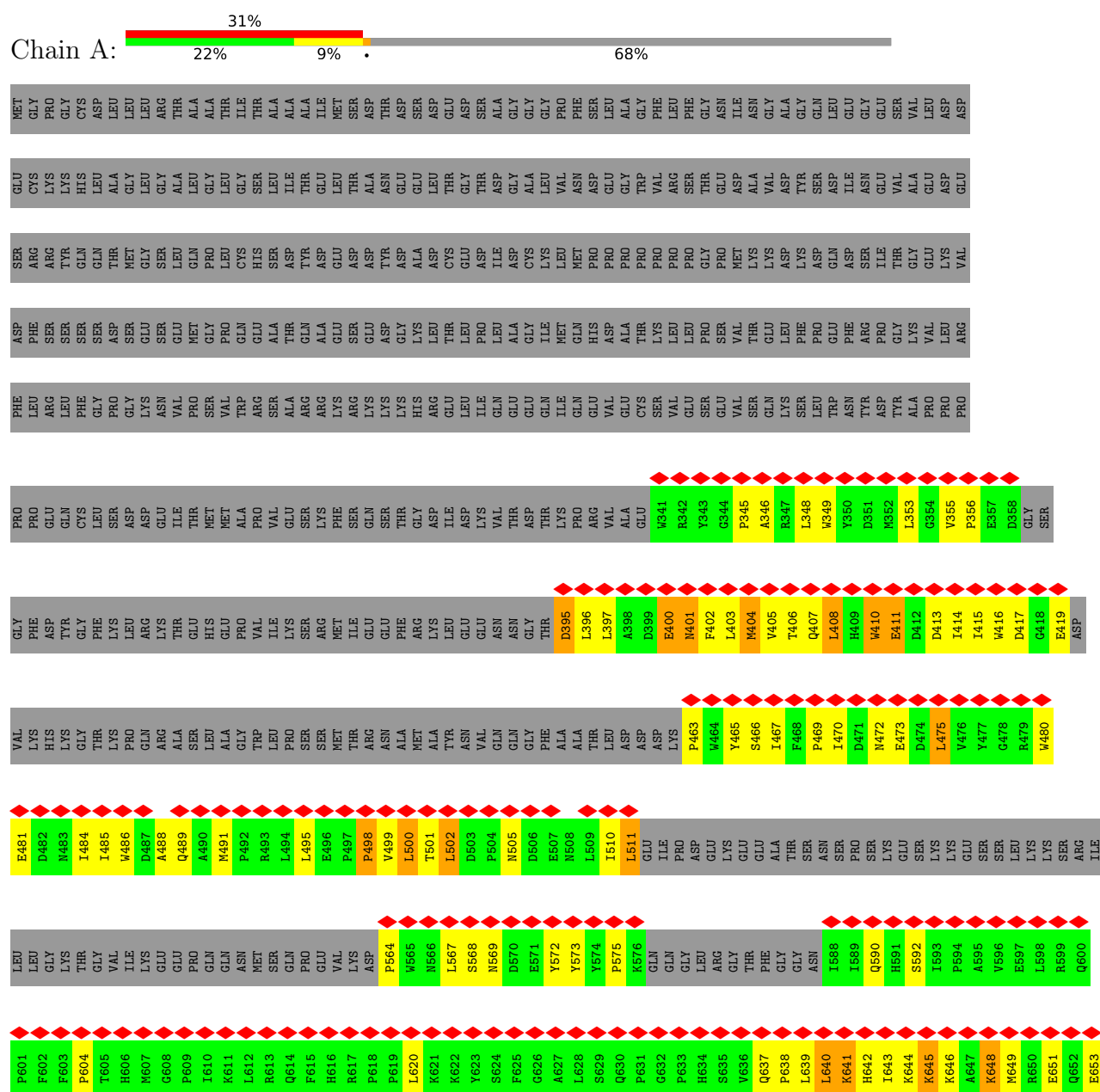
- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

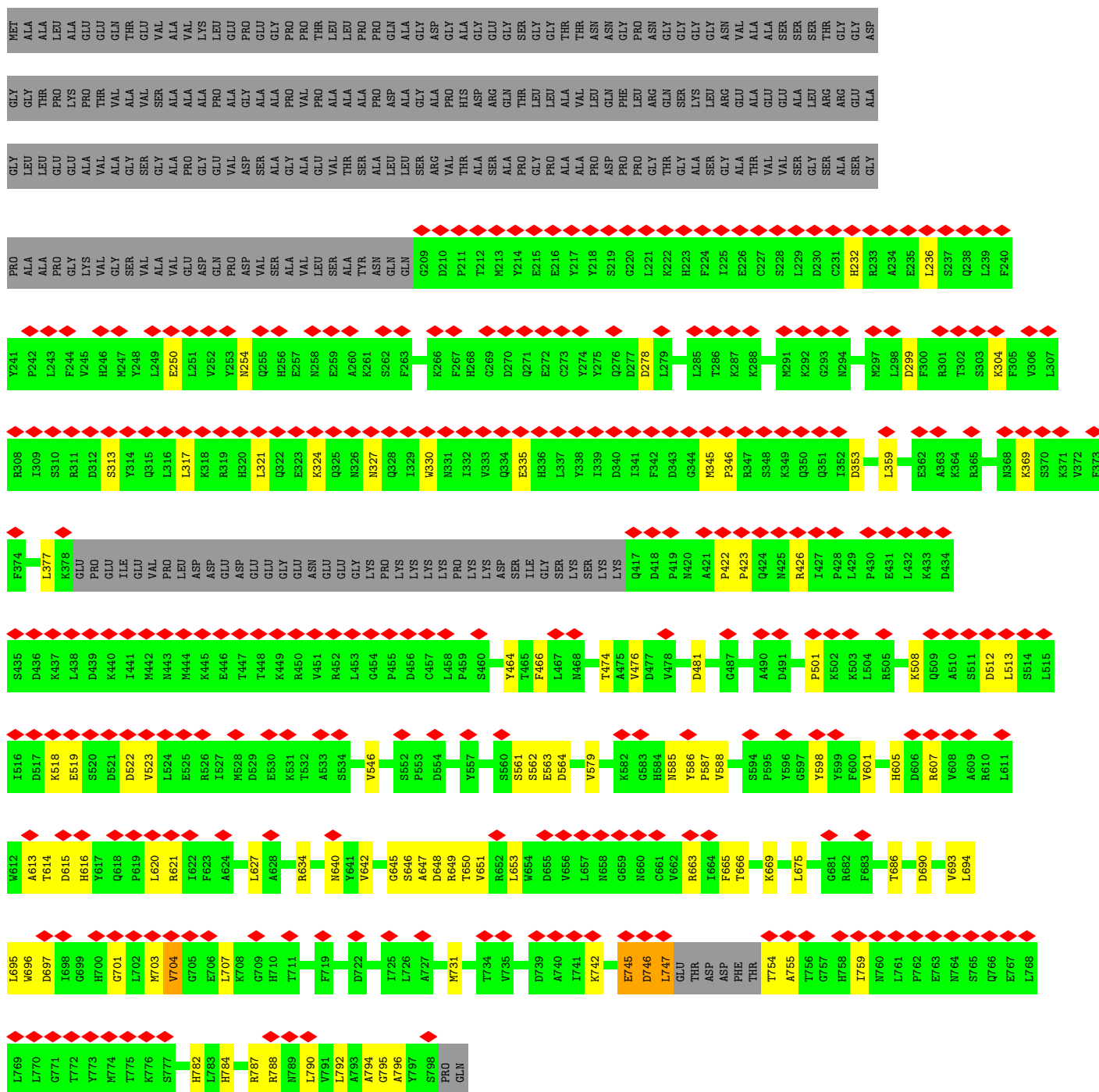
3 Residue-property plots

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.

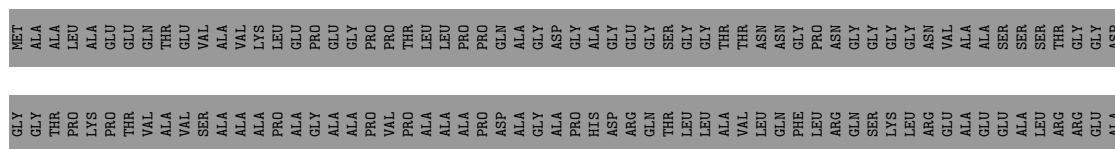
- Molecule 1: Transcription initiation factor TFIID subunit 1

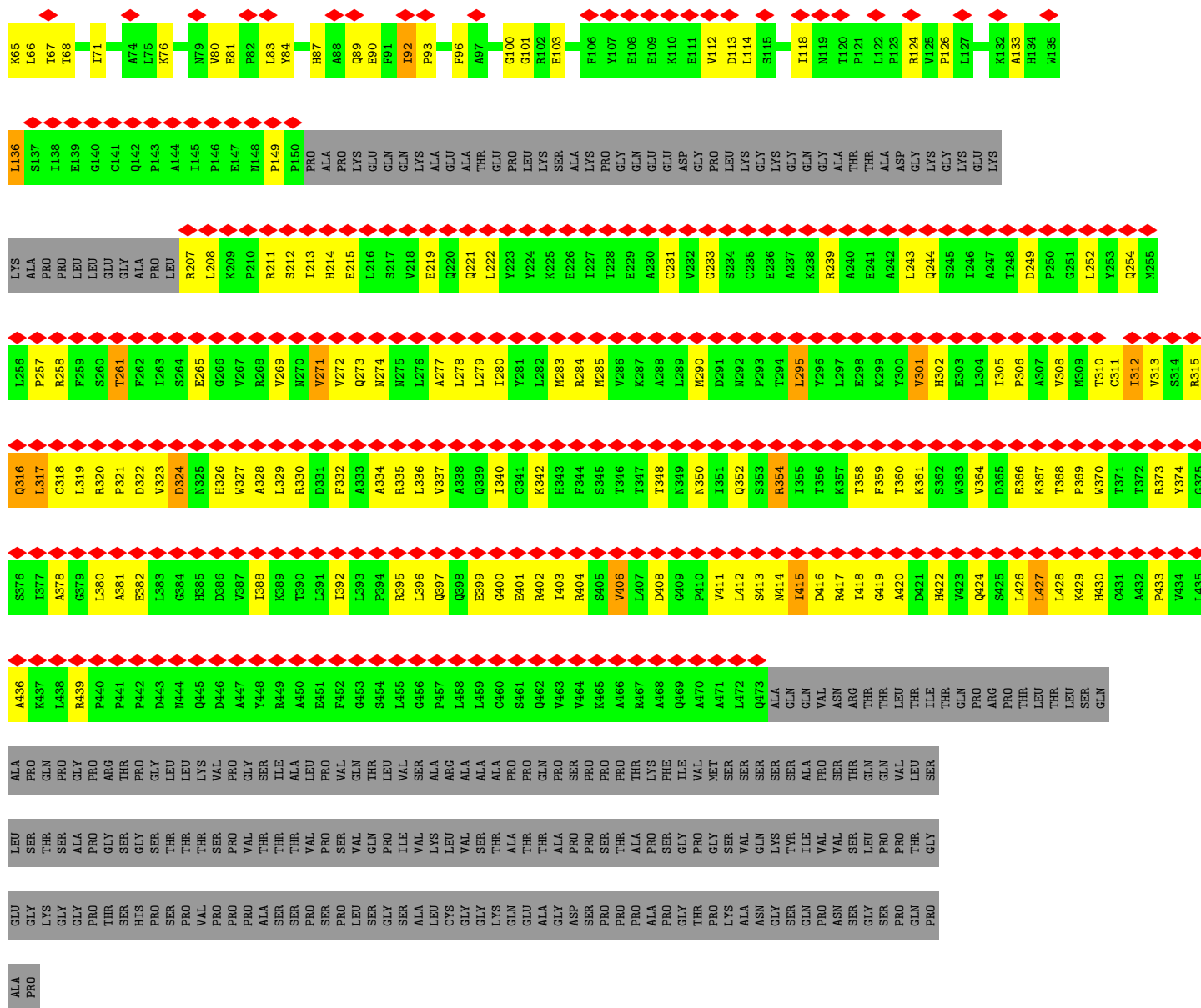


GLN	VAL	PHE	GLU	THR	VAL	CYS	E1204	ASN	S1084	E1024	S964	GLY	I843	V782	T722	E861
ALA	ARG	GLU	F1205	HIS	ASP	GLY	V1205	HIS	T1085	V1025	Y965	GLU	R843	G783	V723	M662
PHE	ASP	GLY	ILE	ASP	THR	ALA	I1026	ASP	ASP	I1026	V966	LYS	X844	Q784	Y724	F663
PHE	ASP	GLY	LYS	ASP	THR	GLN	D1027	THR	ASP	D1027	K967	PHE	R845	Q785	C725	F664
ILE	ASP	ALA	PHE	ASP	SER	SER	V1028	SER	SER	V1028	P968	ALA	R846	C786	T727	M665
LEU	ASP	LEU	ALA	ASP	SER	SER	R1029	SER	SER	R1029	N970	PRO	K947	L788	S729	T667
LEU	ASP	LEU	ALA	ASP	ALA	ALA	T1031	ASP	ALA	T1031	K971	GLU	C949	F789	P729	P668
ASP	ASP	ASP	ASP	ASP	GLU	GLU	S1032	ASP	GLU	S1032	PRO	ASN	D851	V791	F730	Q669
GLN	GLN	GLN	GLN	ASP	ASP	ASP	M1033	ASP	GLN	M1033	THR	GLU	F852	G792	L731	D670
ASP	ASP	ASP	ASP	ASP	ASP	ASP	T1034	ASP	GLN	T1034	GLN	GLU	K853	G793	G732	L671
ASP	ASP	ASP	ASP	ASP	ASP	ASP	E1035	ASP	GLU	E1035	GLN	GLU	R854	G794	L734	T672
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLN	ASP	GLU	GLN	PRO	LYS	T855	N795	H735	G673
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ALA	ASP	GLY	ALA	ASP	GLY	R854	G796	P736	K674
ASP	ASP	ASP	ASP	ASP	ASP	ASP	ARG	ASP	GLY	ARG	GLY	LYS	G856	S797	G737	D675
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L739	L678
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L740	I679
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L741	L680
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L742	A681
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L743	E682
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L747	E686
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L748	M687
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L749	G688
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L750	P689
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L751	L690
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L754	Q693
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L755	V694
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L756	G695
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L758	K699
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L761	T702
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L764	K705
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L765	T706
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L766	K707
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L767	P708
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L768	G709
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L771	P712
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L772	G713
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L773	A714
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L774	P715
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L775	D716
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L776	C717
ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L777	K718
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ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLY	ASP	GLY	GLY	PRO	GLN	S859	N800	L781	

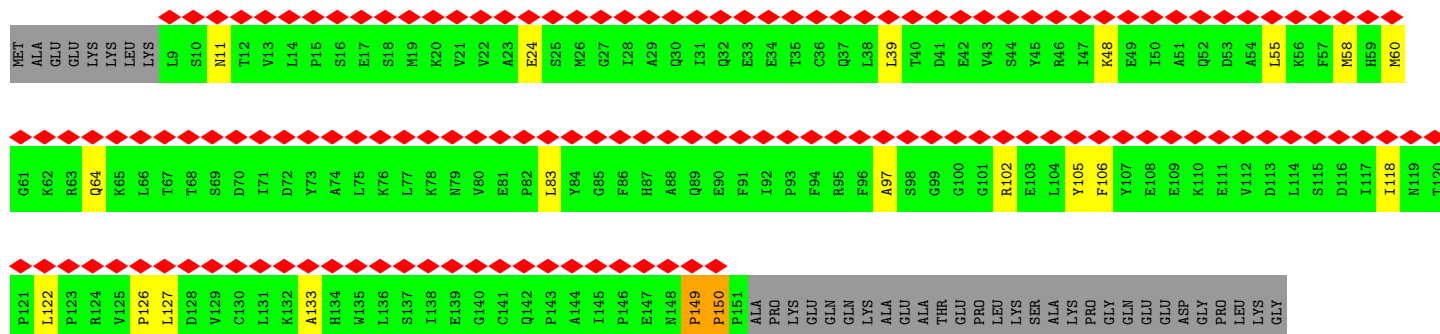


• Molecule 4: Transcription initiation factor TFIID subunit 5



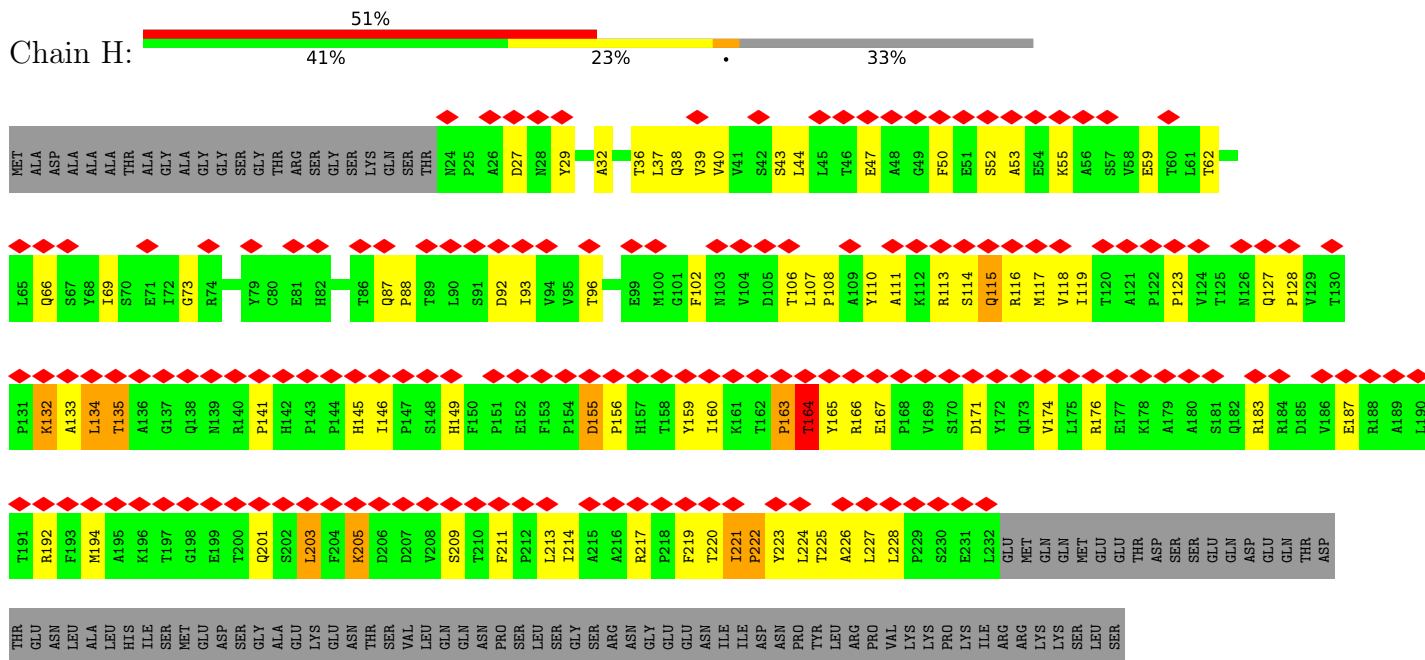


• Molecule 5: Transcription initiation factor TFIID subunit 6

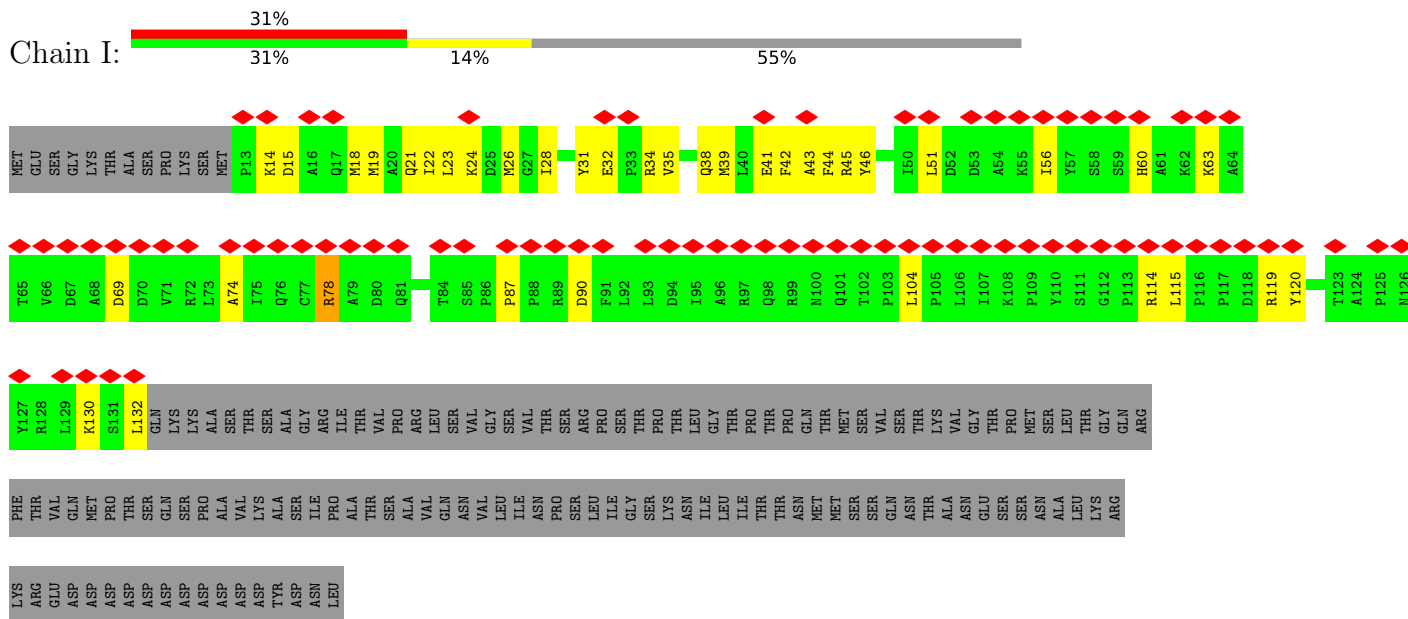




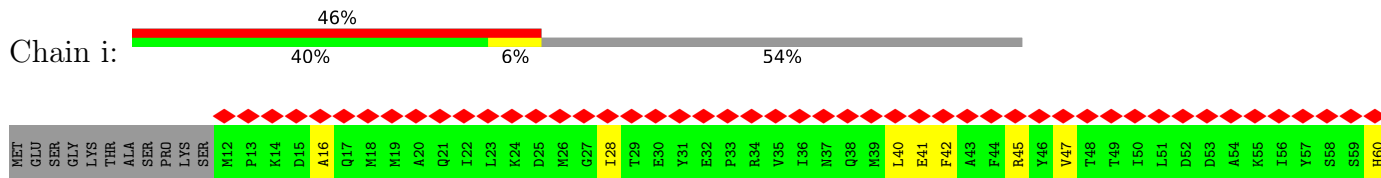
- Molecule 7: Transcription initiation factor TFIID subunit 8

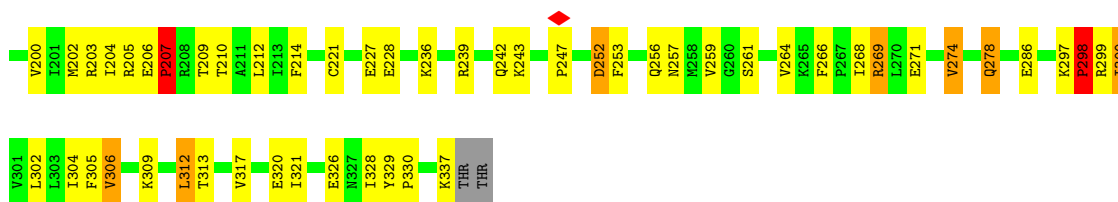


- Molecule 8: Transcription initiation factor TFIID subunit 9

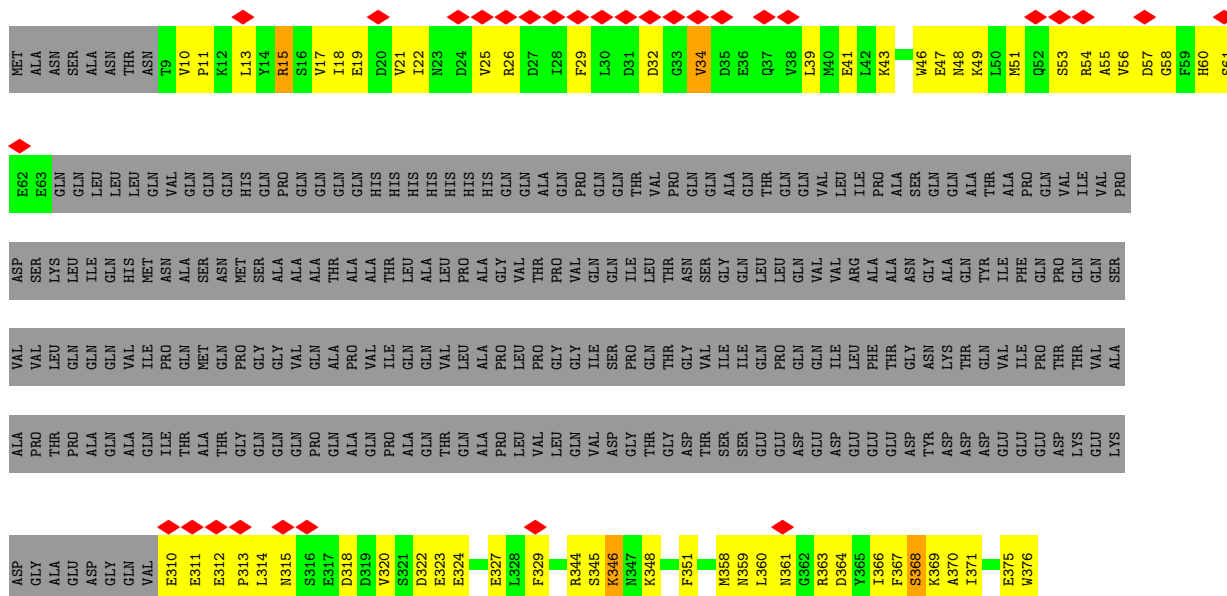


- Molecule 8: Transcription initiation factor TFIID subunit 9

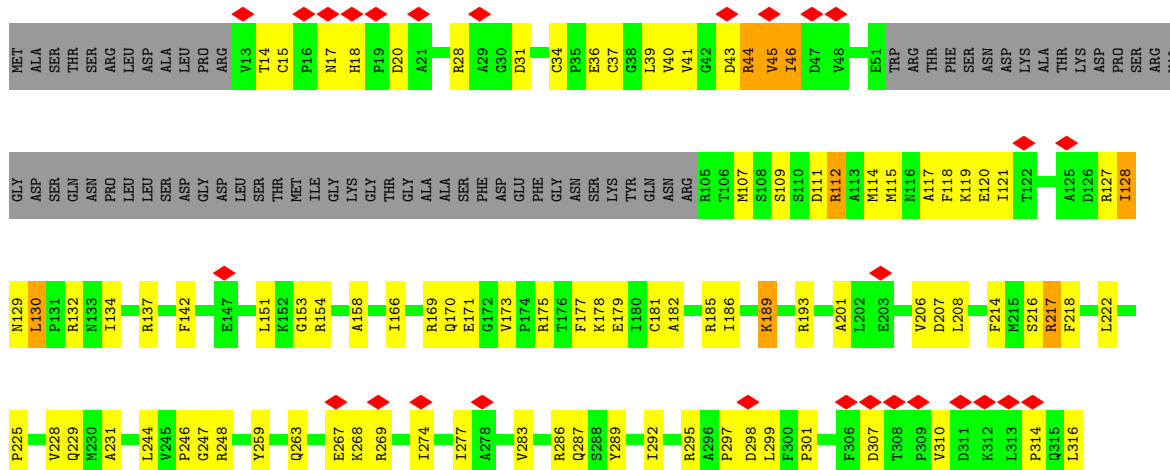




• Molecule 13: Transcription initiation factor IIA subunit 1

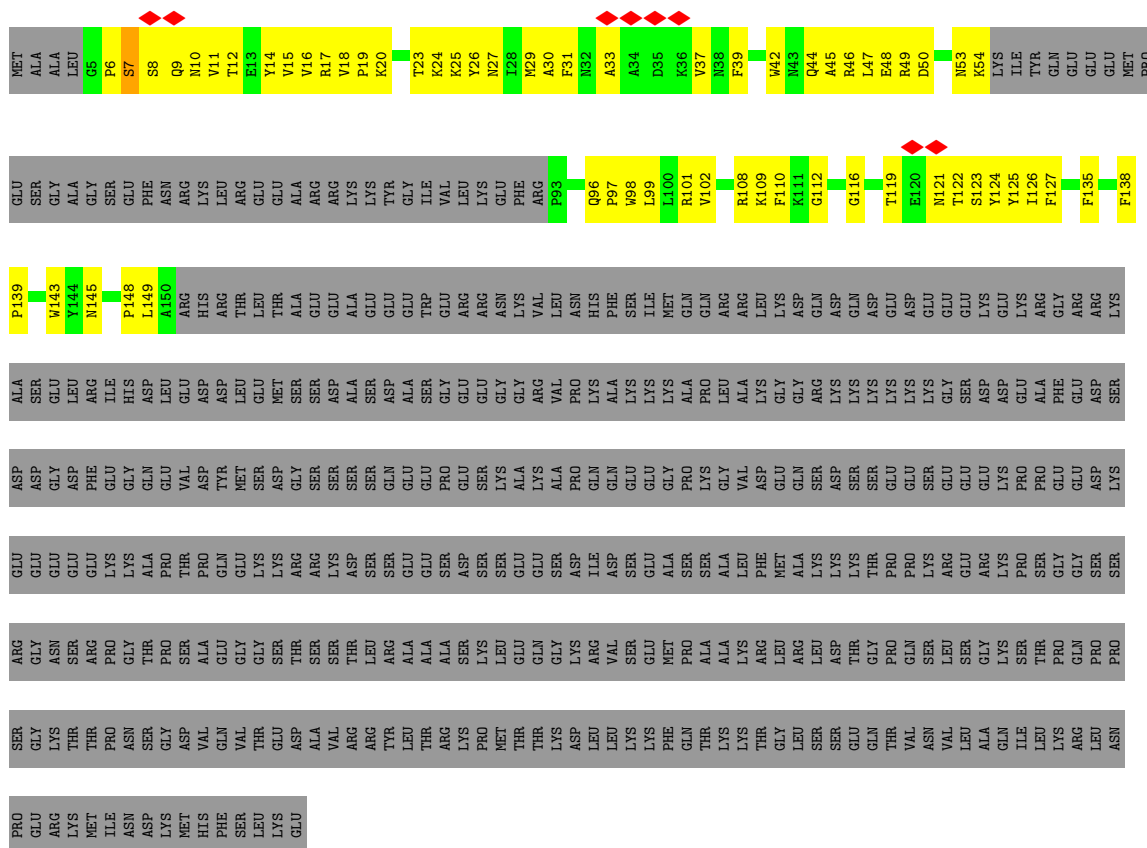


• Molecule 14: Transcription initiation factor IIB

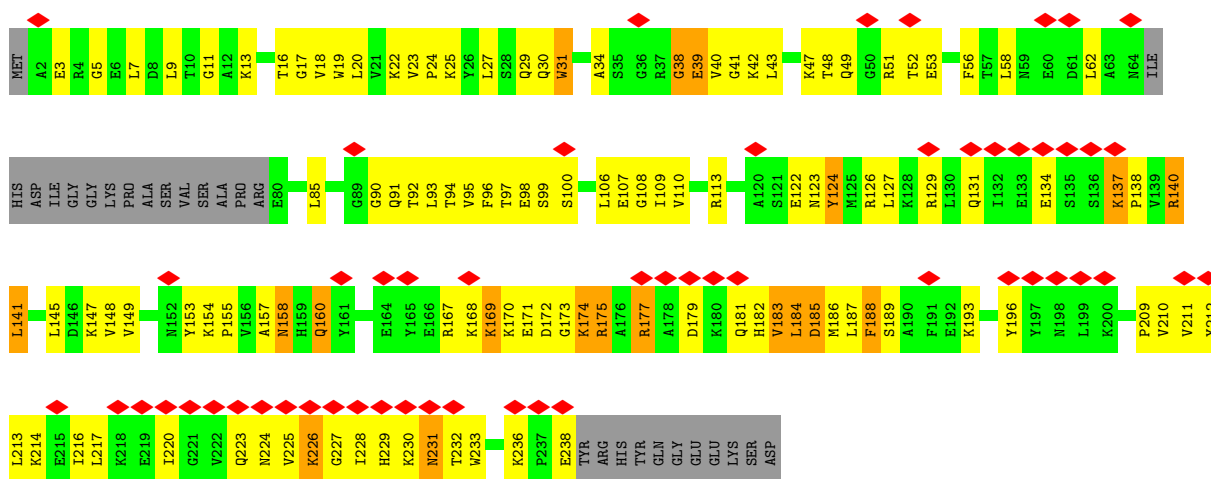


• Molecule 15: General transcription factor IIF subunit 1

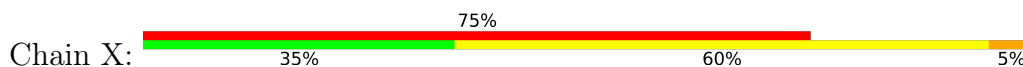


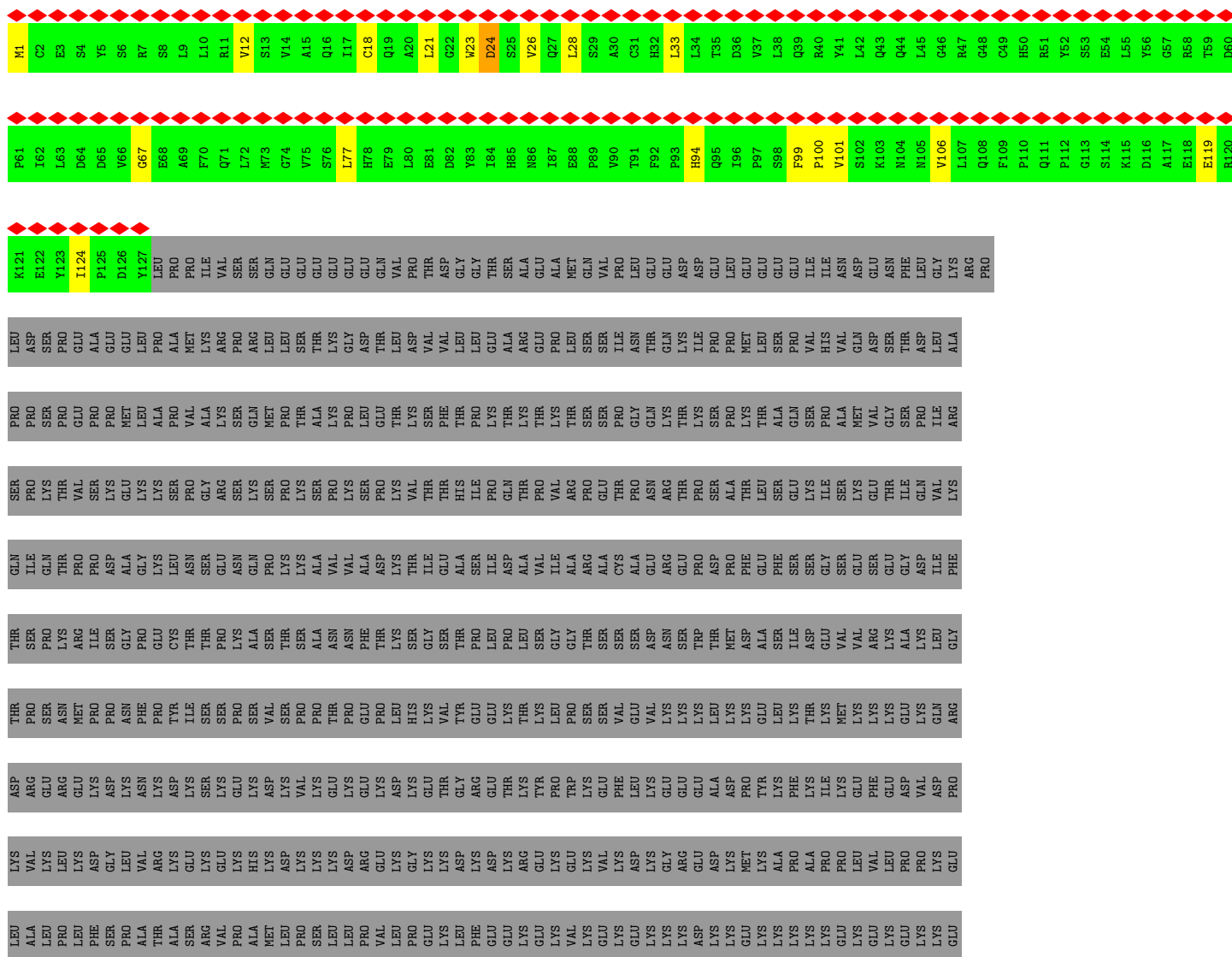


- Molecule 16: General transcription factor IIF subunit 2



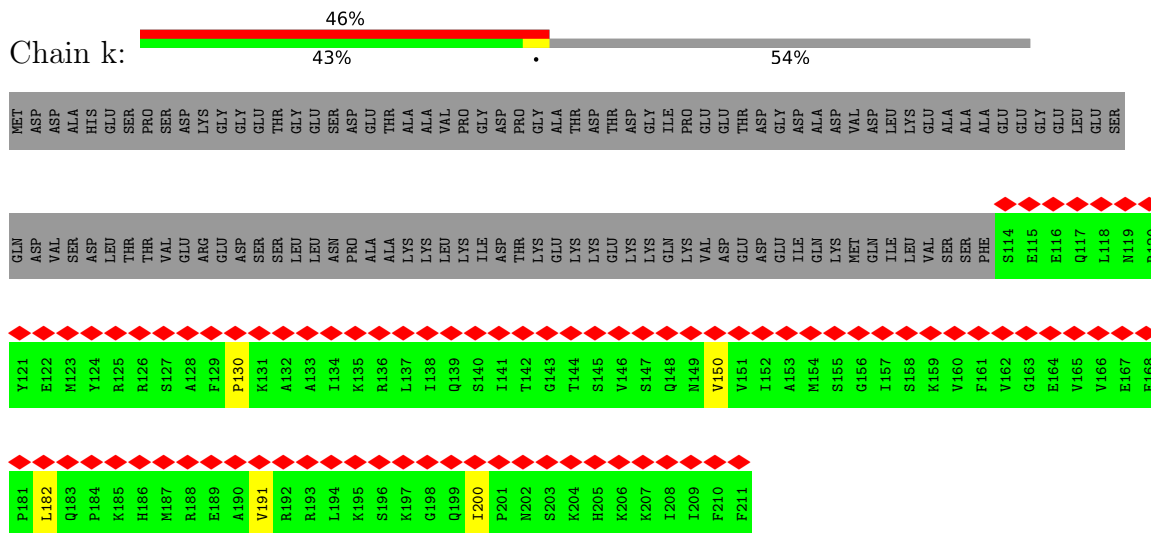
- Molecule 17: DNA (85-MER)



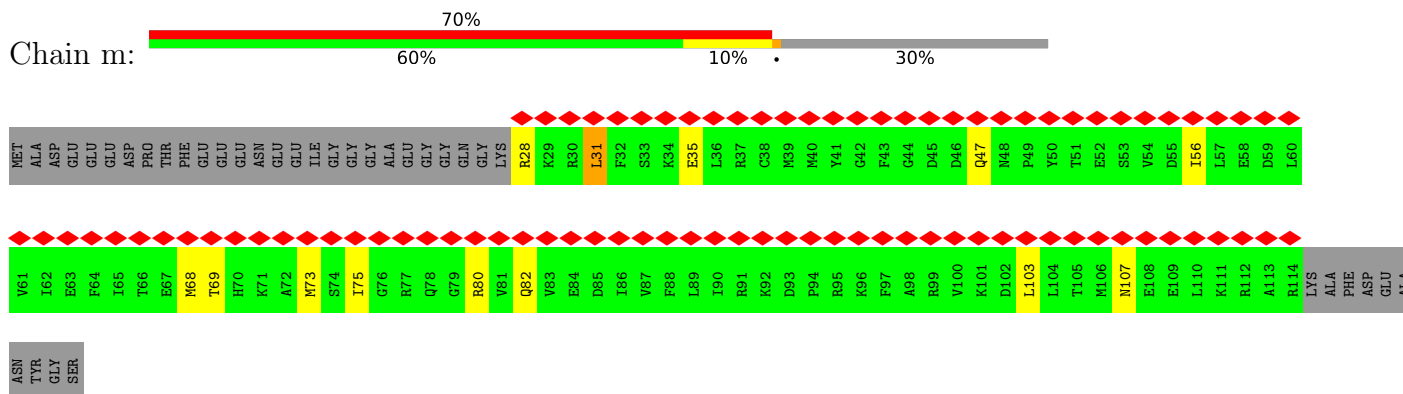


[illegible]

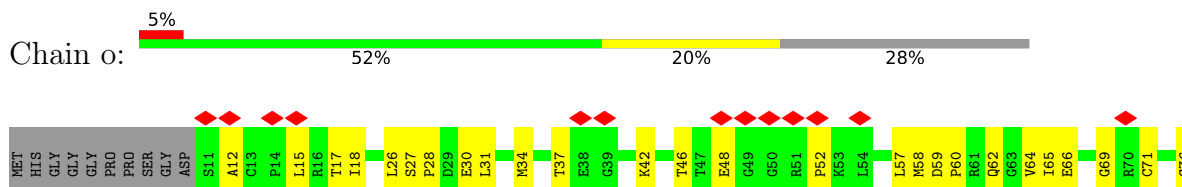
- Molecule 20: Transcription initiation factor TFIID subunit 11



- Molecule 21: Transcription initiation factor TFIID subunit 13

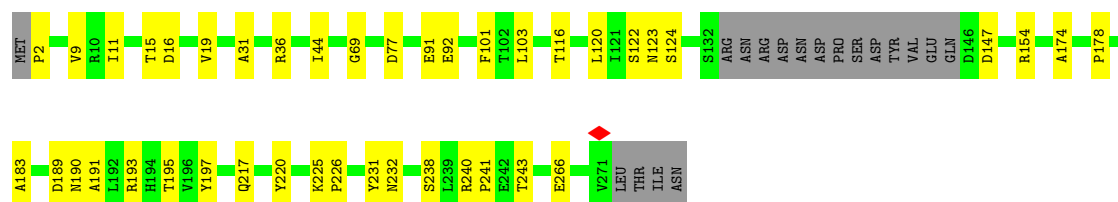


- Molecule 22: RPB1

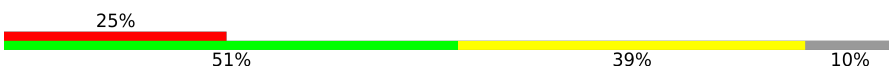


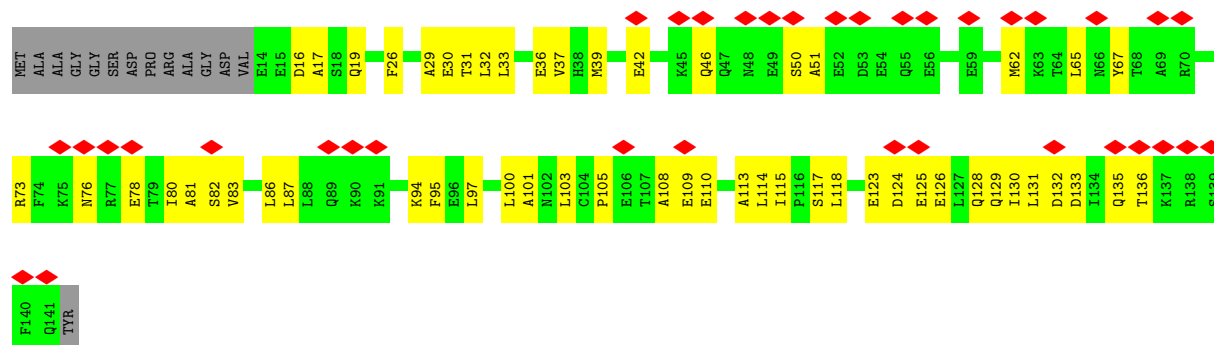


Chain q: 



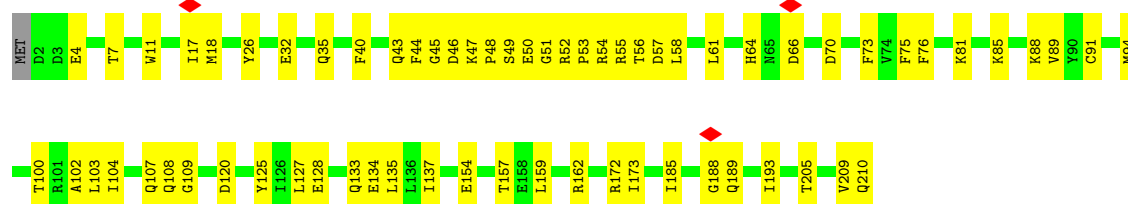
- Molecule 25: DNA-directed RNA polymerase II subunit RPB4

Chain r: 



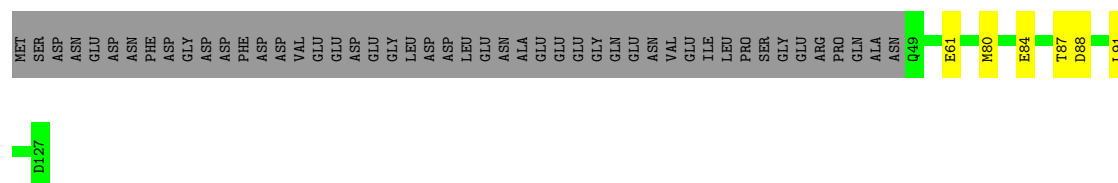
- Molecule 26: DNA-directed RNA polymerase II subunit E

Chain s: 



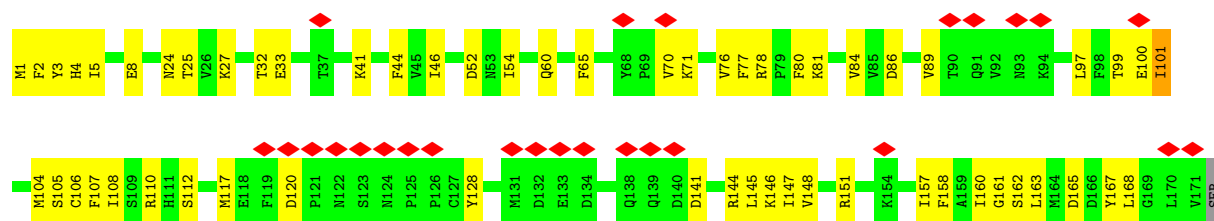
- Molecule 27: DNA-directed RNA polymerase II subunit F

Chain t: 



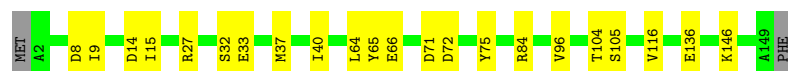
- Molecule 28: DNA-directed RNA polymerase II subunit RPB7

Chain u: 



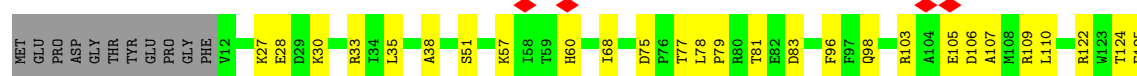
- Molecule 29: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain v: 84% 15% .



- Molecule 30: DNA-directed RNA polymerase II subunit RPB9

Chain w: 70% 22% 9% .



- Molecule 31: RPB10

Chain x: 82% 13% .



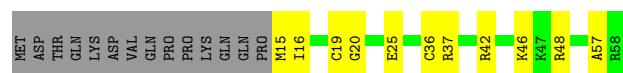
- Molecule 32: RNA_pol_L_2 domain-containing protein

Chain y: 85% 15% .



- Molecule 33: RPB12

Chain z: 57% 19% 24% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7186	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	1.689	Depositor
Minimum map value	-0.746	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.19	Depositor
Map size ($\text{\AA}$)	496.8, 496.8, 496.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.38, 1.38, 1.38	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.70	0/5046	0.96	7/6810 (0.1%)
2	B	0.48	1/7993 (0.0%)	0.70	7/10836 (0.1%)
3	D	0.61	0/1379	0.92	5/1843 (0.3%)
3	d	0.25	0/1321	0.47	0/1772
4	E	0.34	0/4469	0.58	1/6050 (0.0%)
4	e	0.29	0/4433	0.53	0/6004
5	F	0.68	1/3139 (0.0%)	1.02	5/4264 (0.1%)
5	f	0.47	0/3140	0.80	6/4268 (0.1%)
6	G	0.68	0/1199	0.95	1/1612 (0.1%)
7	H	0.55	0/1673	0.80	3/2285 (0.1%)
8	I	0.33	0/981	0.54	1/1332 (0.1%)
8	i	0.21	0/989	0.40	0/1343
9	J	0.28	0/724	0.50	0/982
9	j	0.22	0/775	0.44	0/1049
10	L	0.49	0/630	0.86	1/852 (0.1%)
10	l	0.32	0/888	0.61	0/1194
11	O	0.73	0/781	1.19	8/1061 (0.8%)
12	P	0.93	0/1438	1.25	4/1935 (0.2%)
13	Q	0.58	0/1013	1.02	3/1366 (0.2%)
14	R	0.48	0/1966	1.04	9/2655 (0.3%)
15	S	0.35	0/896	0.79	0/1213
16	T	0.74	0/1817	1.15	9/2445 (0.4%)
17	X	0.39	0/1966	0.72	4/3034 (0.1%)
18	Y	0.37	0/1942	0.68	2/2993 (0.1%)
19	c	0.48	0/1035	0.67	0/1406
20	k	0.29	0/799	0.53	1/1070 (0.1%)
21	m	0.31	0/733	0.55	0/977
22	o	0.31	0/11516	0.53	2/15548 (0.0%)
23	p	0.31	0/9243	0.47	1/12475 (0.0%)
24	q	0.32	0/2102	0.44	0/2857
25	r	0.17	0/1019	0.45	0/1374
26	s	0.22	0/1751	0.47	0/2366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	t	0.29	0/645	0.48	0/871
28	u	0.20	0/1365	0.45	0/1853
29	v	0.29	0/1207	0.47	0/1628
30	w	0.23	0/948	0.45	0/1284
31	x	0.36	0/516	0.44	0/696
32	y	0.31	0/956	0.47	0/1294
33	z	0.28	0/377	0.43	0/500
All	All	0.44	2/84810 (0.0%)	0.70	80/115397 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	61	ASN	C-O	-6.04	1.18	1.24
5	F	395	ARG	C-O	5.72	1.32	1.24

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	491	HIS	N-CA-C	-9.45	100.97	111.28
14	R	112	ARG	N-CA-C	-9.32	101.12	111.28
14	R	130	LEU	CA-C-N	9.13	129.21	119.90
14	R	130	LEU	C-N-CA	9.13	129.21	119.90
11	O	58	PHE	N-CA-C	9.11	120.26	108.24

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	821	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4927	0	4869	327	0
2	B	7796	0	7751	216	0
3	D	1366	0	1390	154	0
3	d	1307	0	1318	28	0
4	E	4364	0	4244	103	0
4	e	4327	0	4197	47	0
5	F	3081	0	3014	429	0
5	f	3081	0	3012	89	0
6	G	1180	0	1235	59	0
7	H	1633	0	1621	236	0
8	I	959	0	968	206	0
8	i	967	0	977	46	0
9	J	709	0	710	101	0
9	j	759	0	759	17	0
10	L	622	0	620	117	0
10	l	876	0	891	81	0
11	O	771	0	763	185	0
12	P	1412	0	1506	105	0
13	Q	996	0	926	176	0
14	R	1938	0	1977	109	0
15	S	872	0	848	233	0
16	T	1788	0	1819	359	0
17	X	1751	0	954	96	0
18	Y	1734	0	956	99	0
19	c	1011	0	975	26	0
20	k	785	0	818	8	0
21	m	724	0	744	13	0
22	o	11308	0	11428	290	0
23	p	9062	0	9107	223	0
24	q	2059	0	2008	32	0
25	r	1005	0	964	65	0
26	s	1720	0	1737	50	0
27	t	635	0	665	5	0
28	u	1334	0	1333	70	0
29	v	1186	0	1147	14	0
30	w	927	0	859	19	0
31	x	507	0	523	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	y	937	0	959	13	0
33	z	372	0	379	10	0
34	R	1	0	0	0	0
34	o	2	0	0	0	0
34	p	1	0	0	0	0
34	q	1	0	0	0	0
34	w	2	0	0	0	0
34	x	1	0	0	0	0
34	z	1	0	0	0	0
35	o	1	0	0	0	0
All	All	82798	0	80971	3113	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 19.

The worst 5 of 3113 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)
16:T:124:TYR:CE1	23:p:596:ILE:HD13	1.22	1.67
5:F:47:ILE:HG21	8:I:19:MET:SD	1.09	1.65
16:T:124:TYR:CG	23:p:596:ILE:HD11	1.20	1.62
5:F:48:LYS:CG	8:I:22:ILE:HG23	1.17	1.60
8:I:60:HIS:CE1	10:L:118:LEU:CD2	1.84	1.59

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	584/1872 (31%)	544 (93%)	35 (6%)	5 (1%)	14	51
2	B	959/1199 (80%)	913 (95%)	46 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	158/1085 (15%)	141 (89%)	17 (11%)	0	100	100
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	540/800 (68%)	503 (93%)	34 (6%)	3 (1%)	21	59
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	373 (93%)	23 (6%)	4 (1%)	12	48
5	f	399/677 (59%)	377 (94%)	22 (6%)	0	100	100
6	G	139/349 (40%)	135 (97%)	4 (3%)	0	100	100
7	H	207/310 (67%)	184 (89%)	19 (9%)	4 (2%)	6	32
8	I	118/264 (45%)	114 (97%)	4 (3%)	0	100	100
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%)	67 (90%)	7 (10%)	0	100	100
10	l	105/161 (65%)	101 (96%)	4 (4%)	0	100	100
11	O	95/109 (87%)	85 (90%)	7 (7%)	3 (3%)	3	21
12	P	175/339 (52%)	162 (93%)	11 (6%)	2 (1%)	11	46
13	Q	118/376 (31%)	110 (93%)	7 (6%)	1 (1%)	16	54
14	R	247/316 (78%)	235 (95%)	10 (4%)	2 (1%)	16	54
15	S	104/517 (20%)	102 (98%)	2 (2%)	0	100	100
16	T	218/249 (88%)	198 (91%)	15 (7%)	5 (2%)	5	28
19	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
20	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
21	m	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
22	o	1417/1970 (72%)	1306 (92%)	110 (8%)	1 (0%)	48	83
23	p	1128/1174 (96%)	1054 (93%)	74 (7%)	0	100	100
24	q	253/275 (92%)	226 (89%)	27 (11%)	0	100	100
25	r	126/142 (89%)	119 (94%)	7 (6%)	0	100	100
26	s	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
27	t	77/127 (61%)	73 (95%)	4 (5%)	0	100	100
28	u	169/172 (98%)	156 (92%)	13 (8%)	0	100	100
29	v	146/150 (97%)	133 (91%)	13 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	w	112/125 (90%)	103 (92%)	9 (8%)	0	100	100
31	x	62/67 (92%)	59 (95%)	3 (5%)	0	100	100
32	y	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
33	z	42/58 (72%)	38 (90%)	4 (10%)	0	100	100
All	All	9780/17897 (55%)	9122 (93%)	628 (6%)	30 (0%)	37	72

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1000	LEU
1	A	1158	SER
5	F	323	VAL
7	H	141	PRO
7	H	222	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%)	477 (89%)	59 (11%)	6	20
2	B	876/1083 (81%)	855 (98%)	21 (2%)	43	64
3	D	147/815 (18%)	113 (77%)	34 (23%)	1	5
3	d	146/815 (18%)	145 (99%)	1 (1%)	76	81
4	E	478/657 (73%)	475 (99%)	3 (1%)	78	83
4	e	475/657 (72%)	473 (100%)	2 (0%)	84	84
5	F	320/574 (56%)	300 (94%)	20 (6%)	16	37
5	f	322/574 (56%)	310 (96%)	12 (4%)	30	51
6	G	133/322 (41%)	126 (95%)	7 (5%)	20	41
7	H	181/270 (67%)	170 (94%)	11 (6%)	17	38
8	I	106/235 (45%)	104 (98%)	2 (2%)	50	67
8	i	107/235 (46%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	67 (94%)	4 (6%)	19	40
10	l	98/141 (70%)	98 (100%)	0	100	100
11	O	84/98 (86%)	77 (92%)	7 (8%)	10	30
12	P	153/293 (52%)	134 (88%)	19 (12%)	4	16
13	Q	111/324 (34%)	108 (97%)	3 (3%)	39	61
14	R	213/268 (80%)	201 (94%)	12 (6%)	19	40
15	S	93/448 (21%)	92 (99%)	1 (1%)	65	76
16	T	196/218 (90%)	177 (90%)	19 (10%)	8	24
19	c	113/833 (14%)	111 (98%)	2 (2%)	51	68
20	k	87/182 (48%)	87 (100%)	0	100	100
21	m	80/106 (76%)	79 (99%)	1 (1%)	61	74
22	o	1257/1748 (72%)	1248 (99%)	9 (1%)	76	81
23	p	993/1027 (97%)	990 (100%)	3 (0%)	86	86
24	q	234/252 (93%)	234 (100%)	0	100	100
25	r	106/126 (84%)	106 (100%)	0	100	100
26	s	191/192 (100%)	191 (100%)	0	100	100
27	t	69/111 (62%)	69 (100%)	0	100	100
28	u	147/153 (96%)	146 (99%)	1 (1%)	76	81
29	v	129/131 (98%)	129 (100%)	0	100	100
30	w	103/112 (92%)	103 (100%)	0	100	100
31	x	53/56 (95%)	53 (100%)	0	100	100
32	y	106/106 (100%)	106 (100%)	0	100	100
33	z	41/55 (74%)	41 (100%)	0	100	100
All	All	8716/15331 (57%)	8463 (97%)	253 (3%)	38	58

5 of 253 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	E	746	ASP
16	T	211	VAL
6	G	183	ILE

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Mol	Chain	Res	Type
16	T	184	LEU
5	f	411	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 172 such sidechains are listed below:

Mol	Chain	Res	Type
20	k	186	HIS
23	p	56	GLN
21	m	107	ASN
22	o	620	HIS
23	p	537	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](#)

Of 10 ligands modelled in this entry, 10 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.

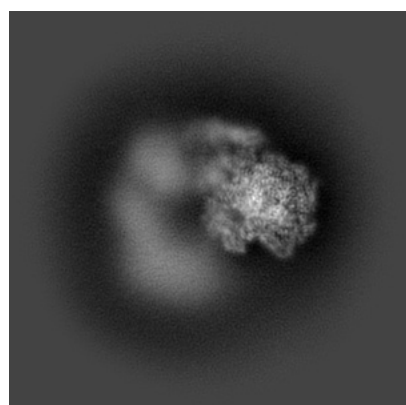
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31108. These allow visual inspection of the internal detail of the map and identification of artifacts.

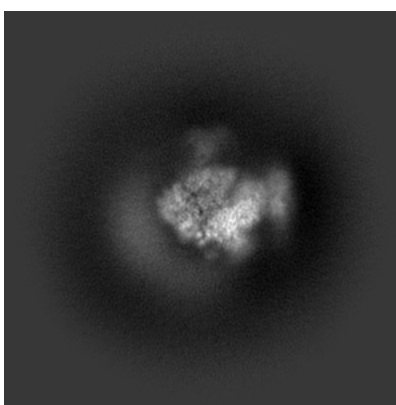
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

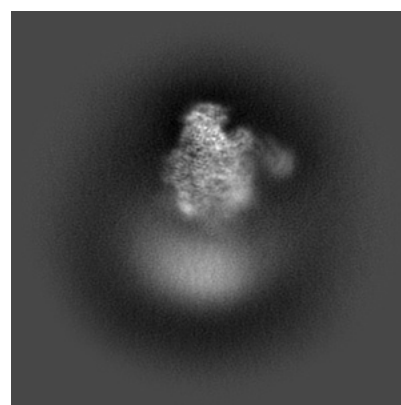
6.1.1 Primary map



X



Y

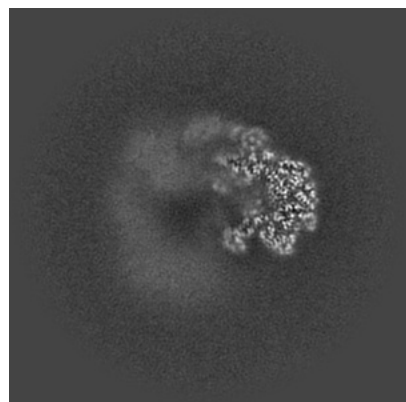


Z

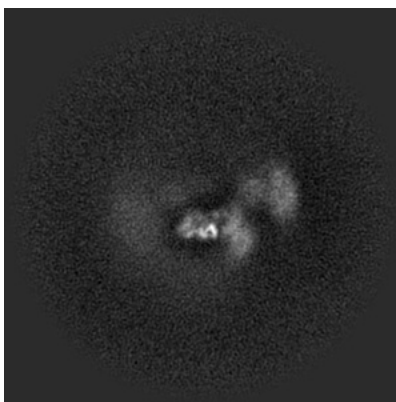
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

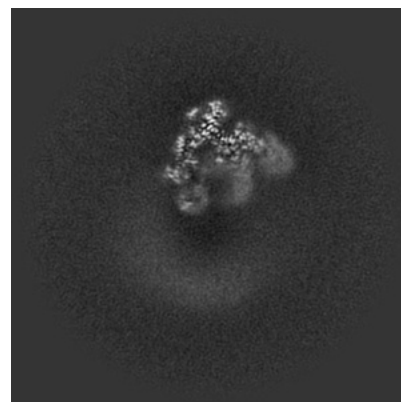
6.2.1 Primary map



X Index: 180



Y Index: 180

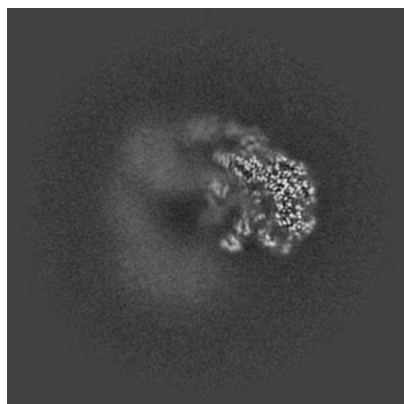


Z Index: 180

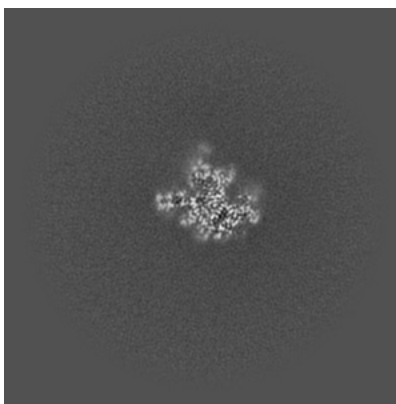
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

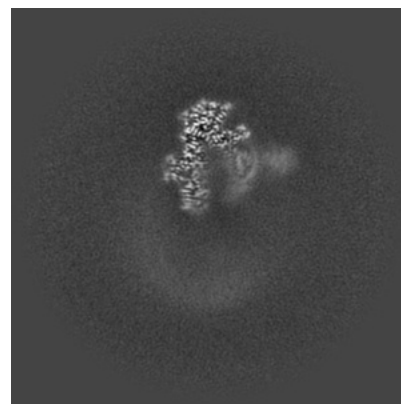
6.3.1 Primary map



X Index: 176



Y Index: 244

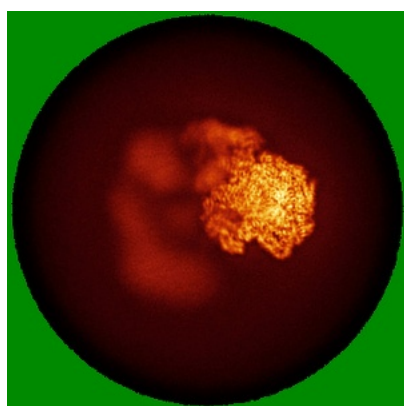


Z Index: 190

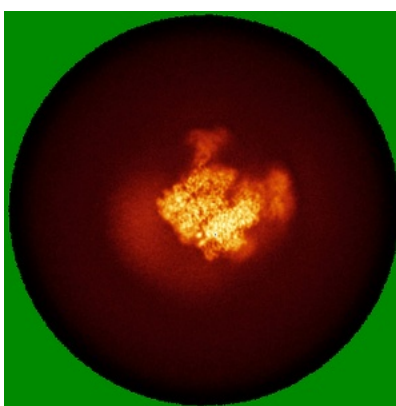
The images above show the largest variance slices of the map in three orthogonal directions.

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

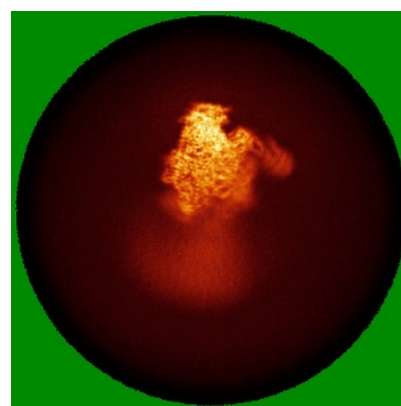
6.4.1 Primary map



X



Y

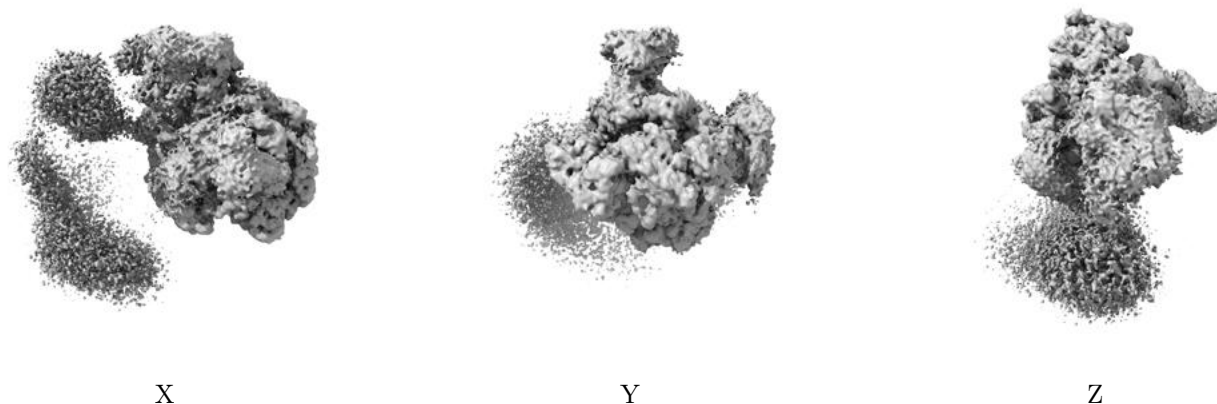


Z

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

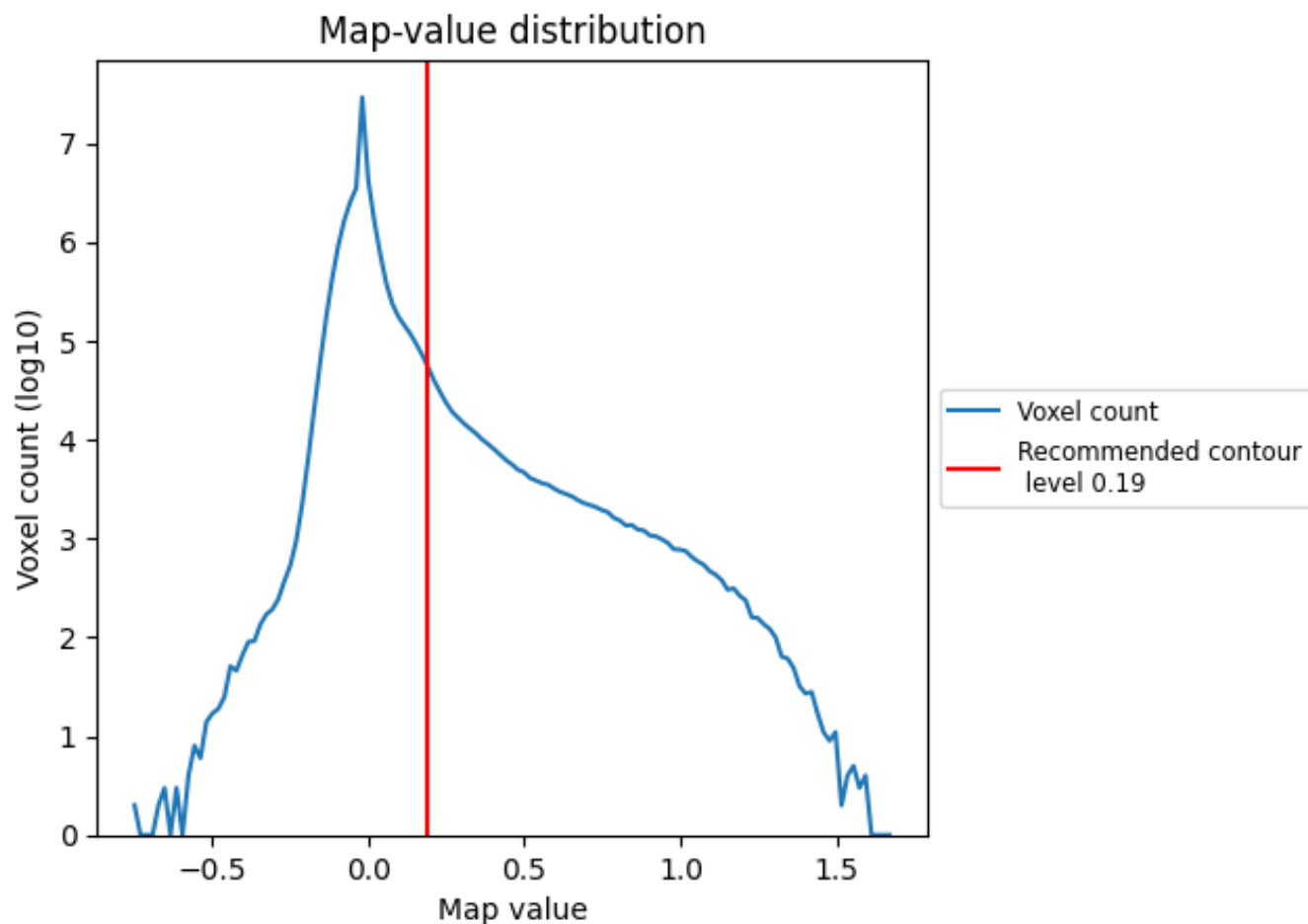
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

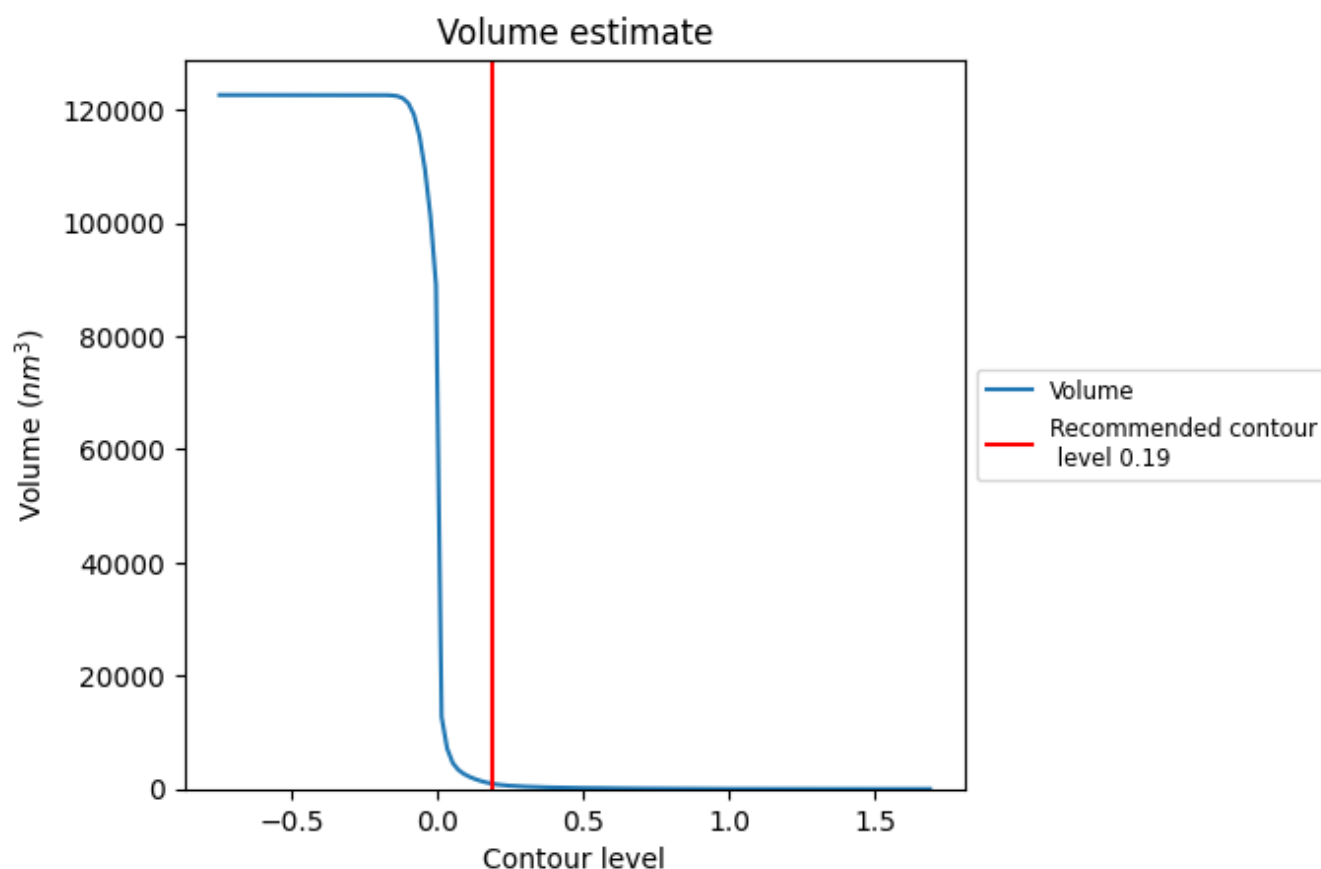
This section contains the results of statistical analysis of the map.

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.

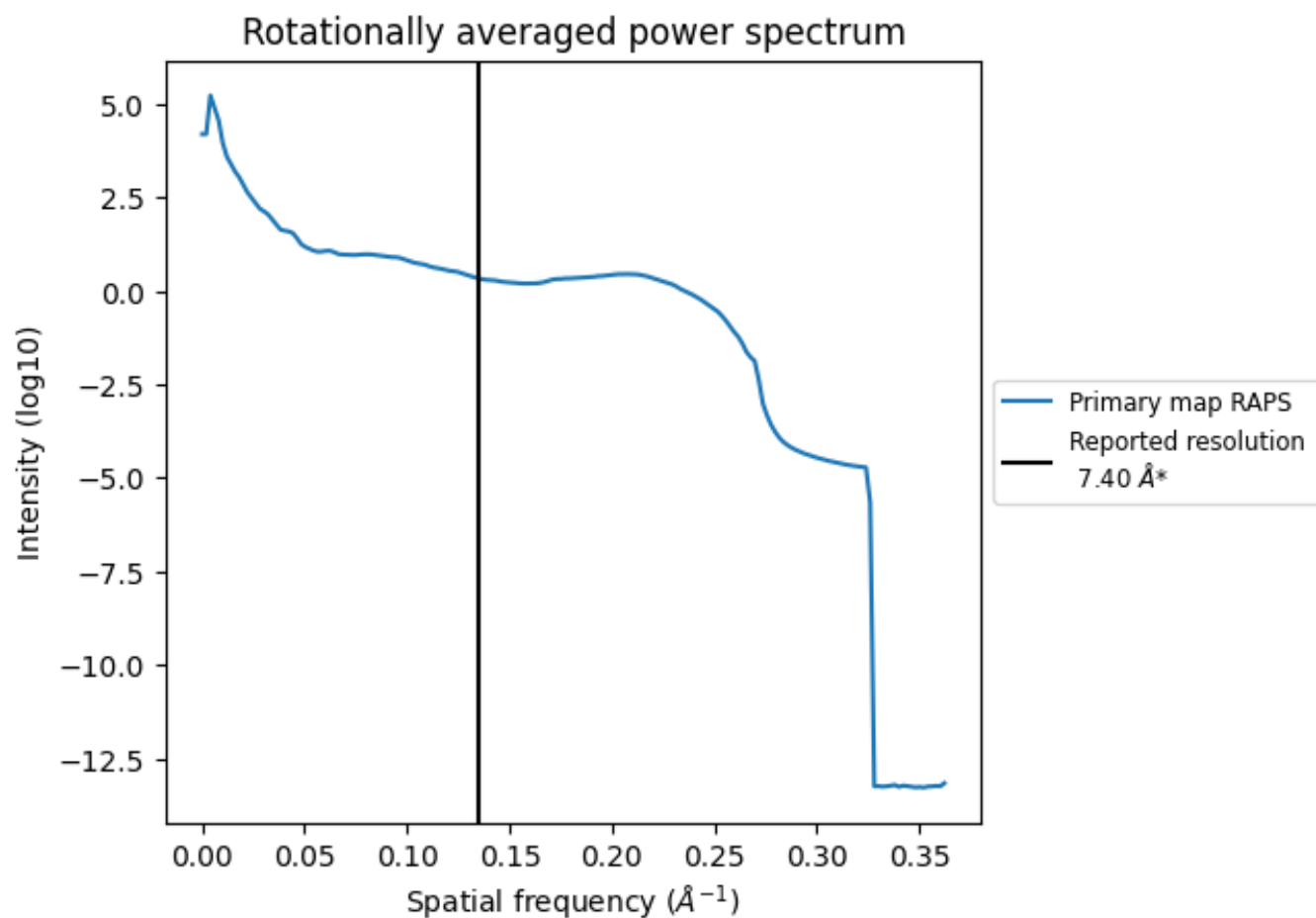
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 917 nm³; this corresponds to an approximate mass of 828 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 0.135 Å⁻¹

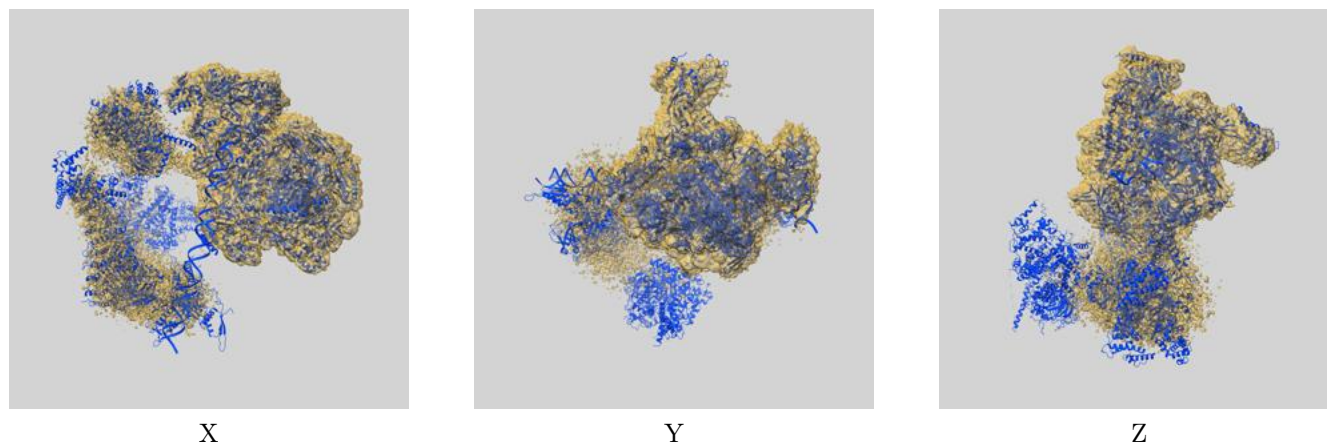
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

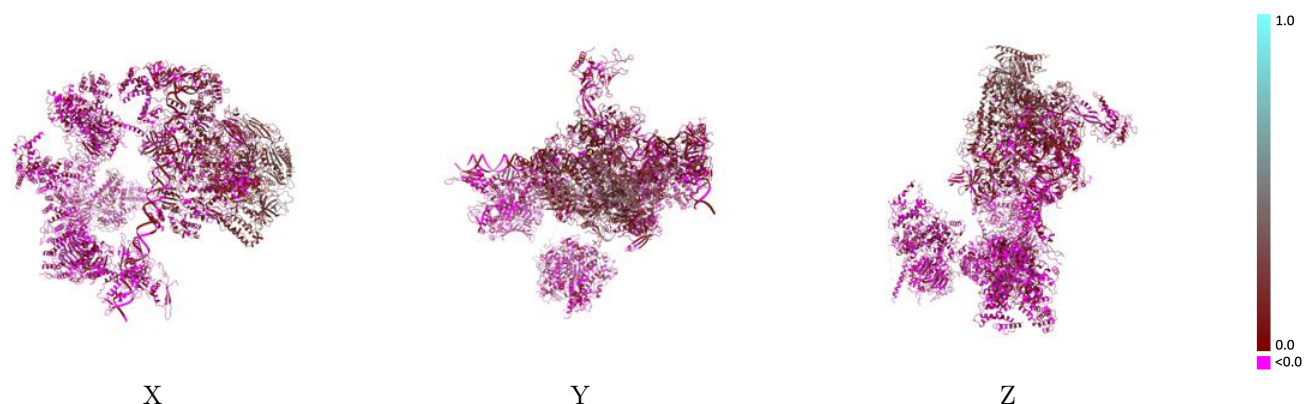
This section contains information regarding the fit between EMDB map EMD-31108 and PDB model 7EG8. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



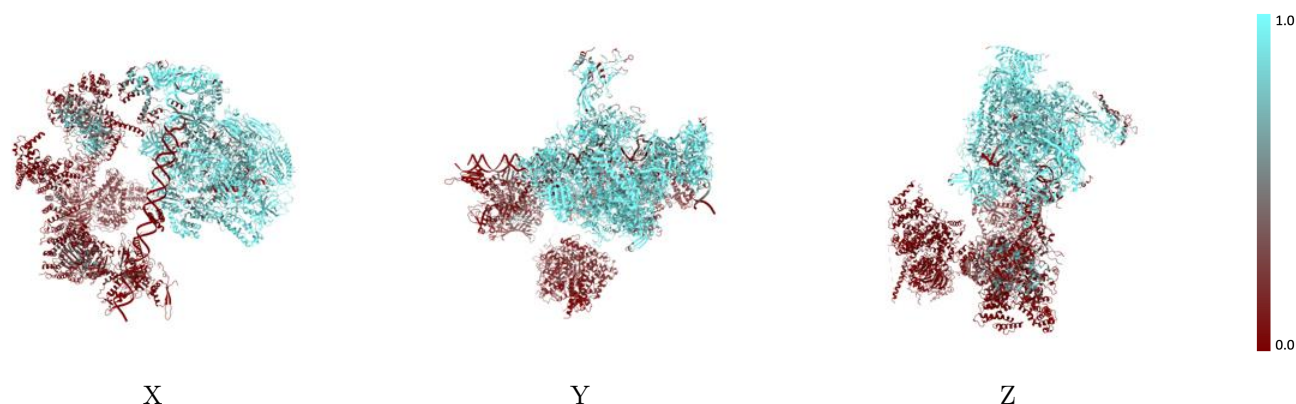
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



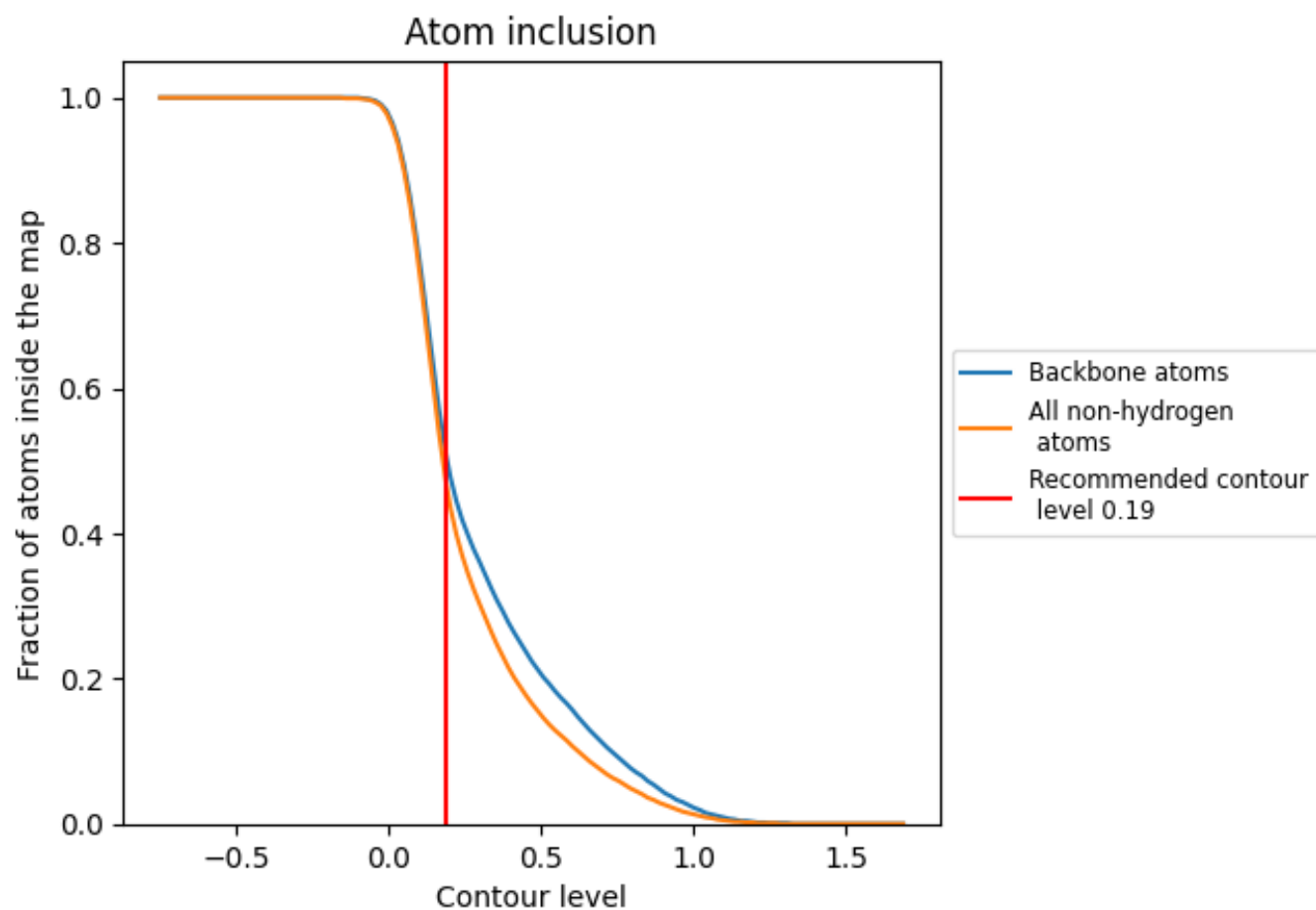
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.19).

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 47% 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 (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4700	 0.0740
A	 0.0570	 -0.0030
B	 0.1580	 -0.0020
D	 0.1770	 0.0200
E	 0.4080	 0.0150
F	 0.1710	 0.0150
G	 0.0380	 0.0120
H	 0.2120	 0.0060
I	 0.3090	 0.0320
J	 0.3760	 0.0080
L	 0.0410	 0.0510
O	 0.7370	 0.0280
P	 0.9270	 0.0760
Q	 0.7070	 0.0260
R	 0.7950	 0.0950
S	 0.9090	 0.0710
T	 0.6790	 0.0610
X	 0.2470	 0.0420
Y	 0.2990	 0.0290
c	 0.0030	 -0.0170
d	 0.0000	 0.0130
e	 0.0070	 -0.0070
f	 0.0560	 0.0020
i	 0.0030	 0.0160
j	 0.0000	 0.0210
k	 0.0000	 -0.0100
l	 0.0010	 -0.0020
m	 0.0000	 -0.0130
o	 0.8420	 0.1510
p	 0.8460	 0.1660
q	 0.9570	 0.3080
r	 0.6830	 0.0570
s	 0.8600	 0.1060
t	 0.9290	 0.1960
u	 0.7780	 0.0630



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Chain	Atom inclusion	Q-score
v	 0.9500	 0.2600
w	 0.8880	 0.1830
x	 0.9310	 0.2950
y	 0.9290	 0.2800
z	 0.9580	 0.2160