



Full wwPDB EM Validation Report ⓘ

Nov 22, 2022 – 12:14 PM JST

PDB ID : 7EG8
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 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:

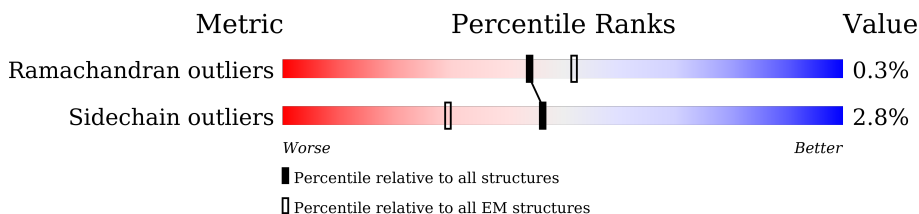
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1872	
2	B	1199	
3	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	51% 63% 33%
8	I	264	31% 45% 55%
8	i	264	46% 46% 54%
9	J	218	22% 41% 59%
9	j	218	44% 44% 56%
10	L	161	47% 45% 53%
10	l	161	66% 65% 34%
11	O	109	17% 82% 7% 11%
12	P	339	47% 6% 48%
13	Q	376	8% 31% 68%
14	R	316	9% 75% 21%
15	S	517	21% 79%
16	T	249	22% 80% 9% 11%
17	X	85	75% 98%
18	Y	85	69% 99%
19	c	929	14% 13% 86%
20	k	211	46% 46% 54%
21	m	124	70% 69% 30%
22	o	1970	5% 72% 28%
23	p	1174	96%
24	q	275	93% 7%
25	r	142	25% 89% 10%
26	s	210	99%
27	t	127	62% 38%
28	u	172	15% 99%

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Mol	Chain	Length	Quality of chain
29	v	150	 99%
30	w	125	 91% 9%
31	x	67	 96%
32	y	117	 100%
33	z	58	 76% 24%

2 Entry composition [i](#)

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
			Total	C	N	O	S		
1	A	602	4927	3142	858	899	28	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	164	1366	851	256	255	4	0	0
3	d	158	1307	814	238	252	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	546	4364	2766	757	820	21	0	0
4	e	539	4327	2746	748	814	19	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	404	3081	1954	537	572	18	0	0
5	f	403	3081	1954	533	576	18	0	0

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

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

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

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

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

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

- Molecule 22 is a protein called RPB1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 31 is a protein called RPB10.

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

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

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

- Molecule 33 is a protein called RPB12.

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

- Molecule 34 is ZINC ION (three-letter code: 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	

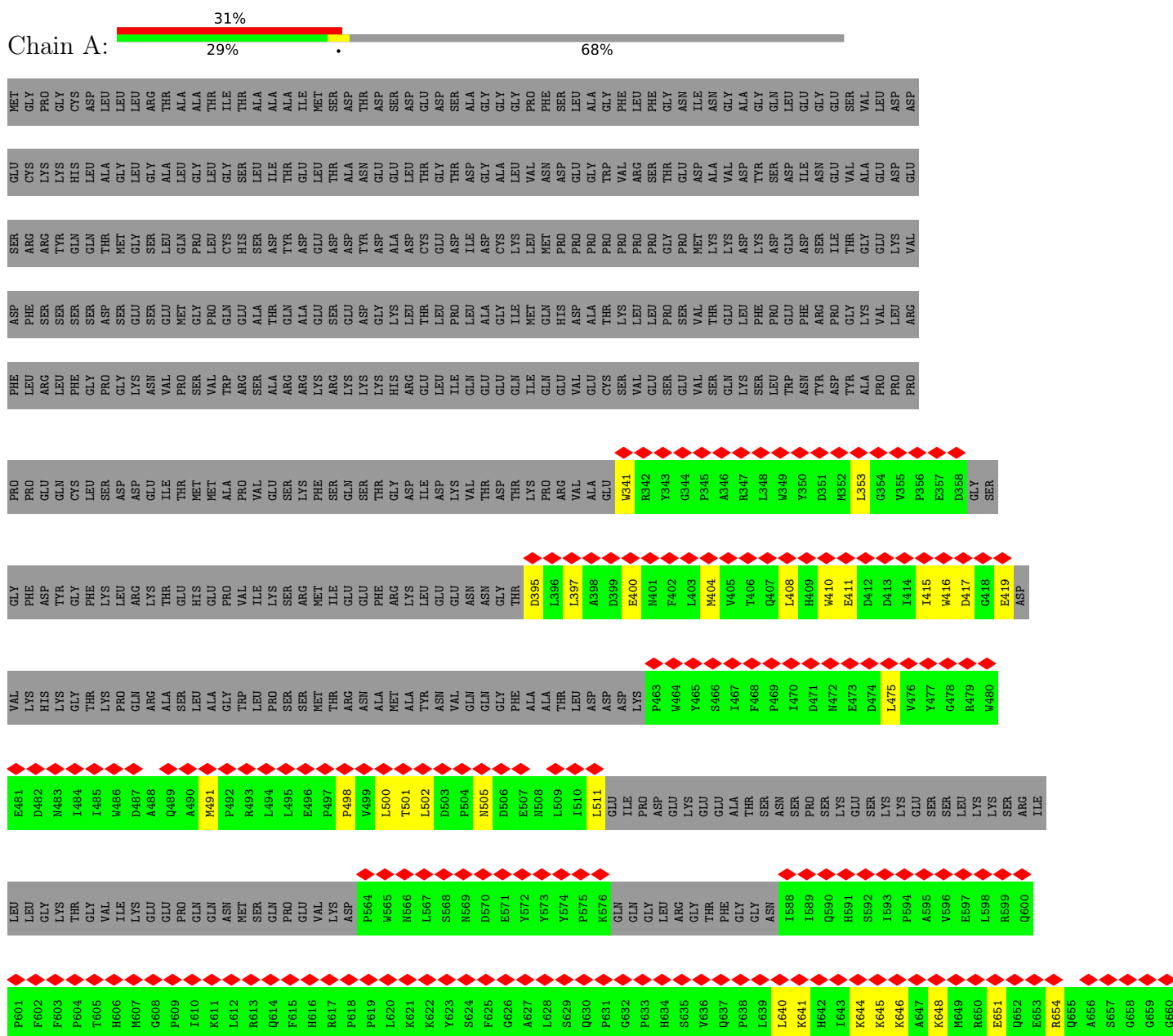
- Molecule 35 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

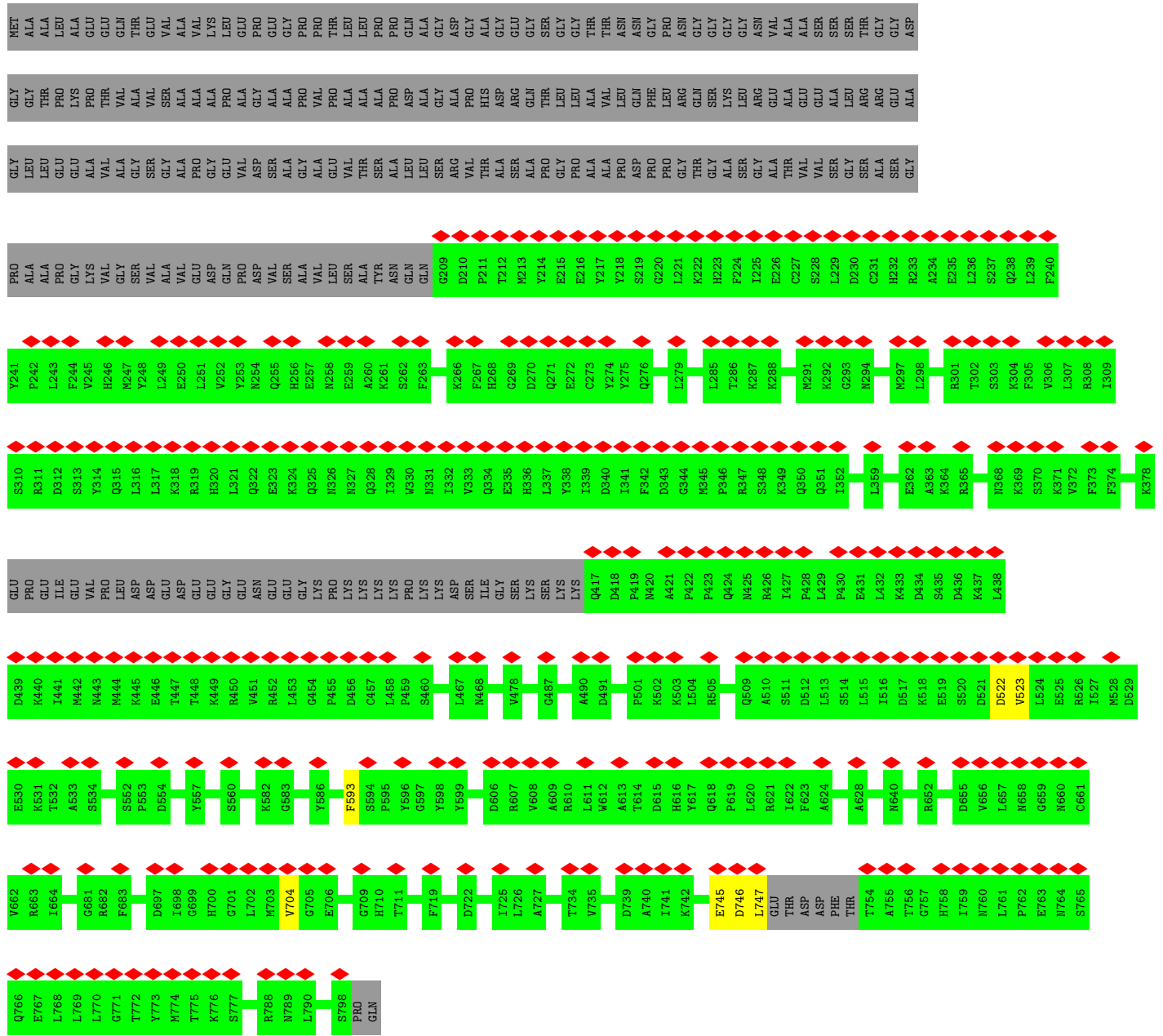
3 Residue-property plots

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.

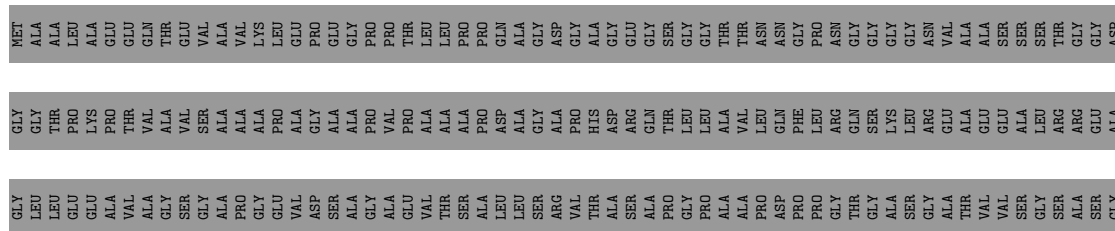
- Molecule 1: Transcription initiation factor TFIID subunit 1



E661	M662	F663	F664	M665	R666	T667	P668	Q669	D670	L671	T672	G673	K674	D675	G676	D677	L678	I679	L680	A681	E682	Y683	S684	E685	E686	M687	G688	P689	L690	M691	Q692	V694	G695	T698	K699	I700	K701	K702	Y703	Y704	K705	R706	K707	P708	G709	K710	D711	P712	G713	A714	P715	D716	C717	K718	Y719	G720	E721														
T722	Y724	C725	H726	T727	S728	P729	F730	L731	G732	S733	L734	H735	P736	Q737	Q738	L739	L740	Q741	A742	F743	E744	N745	N746	L747	F748	R749	A750	P751	I752	Y753	L754	H755	K756	F757	P758	E759	T760	D761	F762	L763	I764	I765	R766	M767	R768	Q769	G770	Y771	Y772	I773	R774	E775	L776	V777	D778	I779	F780	E781													
V782	G783	Q784	Q785	C786	P787	L788	F789	E790	V791	P792	G793	P794	N795	S796	K797	R798	A799	N800	T801	H802	I803	R804	D805	F806	L807	Q808	V809	F810	I811	Y812	R813	L814	F815	W816	K817	S818	K819	D820	R821	P822	R823	R824	I825	R826	M827	E828	D829	I830	K831	K832	A833	F834	P835	S836	H837	S838	E839	S840	S841												
I842	R843	K844	R845	L846	K847	L848	C849	A850	A851	F852	K853	R854	T855	G856	M857	D858	S859	N860	W861	W862	I863	R864	K865	S866	D867	F868	R869	L870	P871	T872	R873	L874	E875	I876	R877	A878	M879	V880	S881	P882	E883	Q884	A887	Y888	Y889	S890	A893	A894	E895	Q896	R897	L898	K899	D900	A901	G902	T903														
G903	L904	P905	R906	H907	L908	I909	S910	R911	E912	H913	V914	M915	L916	G917	F918	D919	R920	E921	H922	R923	T924	A925	L926	K927	F928	G929	H930	R931	L932	R933	H934	T935	R936	A937	F938	I939	A940	A941	M942	K943	G944	K945	C946	L947	L948	E949	V950	T951	G952	V953	A954	D955	P956	T957	G958	C959	G960	E961	G962	F963											
S964	Y965	V966	K967	V968	P969	N970	K971	PRO	THR	GLN	ASN	GLU	ASP	ASP	GLN	MET	LYS	PRO	GLN	PRO	VAL	LYS	THR	THR	D992	A993	D994	L995	Y996	R997	L998	S999	L1000	K1001	M1002	A1003	K1004	K1005	L1006	L1007	R1008	K1009	F1010	G1011	V1012	P1013	E1014	E1015	E1016	I1017	K1018	K1019	L1020	S1021	R1022	H1023															
E1024	V1025	I1026	D1027	V1028	V1029	R1030	T1031	M1032	S1033	T1034	E1035	GLN	ALA	ARG	LYS	ASN	GLY	GLY	PRO	PRO	MET	SER	LYS	VAL	PHE	ALA	ARG	GLY	SER	R1052	F1053	S1054	V1055	A1056	E1057	H1058	Q1059	E1060	L1061	Y1062	K1063	E1064	E1065	C1066	Q1067	R1068	I1069	F1070	D1071	L1072	Q1073	M1074	K1075	V1076	L1077	S1078	S1079	T1080	V1081	L1082	L1083										
S1084	T1085	ASP	THR	ASP	SER	SER	ALA	GLU	ASP	SER	PHE	GLY	MET	GLY	LYS	ASN	ILE	GLU	ASN	ASN	LEU	LEU	GLM	ASN	LYS	ALA	ARG	THR	SER	R1052	F1053	S1054	V1055	A1056	E1057	H1058	Q1059	E1060	L1061	Y1062	K1063	E1064	E1065	C1066	Q1067	R1068	I1069	F1070	D1071	L1072	Q1073	M1074	K1075	V1076	L1077	S1078	S1079	T1080	V1081	L1082	L1083										
ASN	HIS	ARG	ASP	ASP	T1150	A1151	S1152	V1153	T1154	S1155	L1156	H1157	S1158	S1159	A1160	T1161	G1162	R1163	C1164	L1165	K1166	T1167	V1168	R1169	T1170	F1171	R1172	D1173	E1174	E1175	G1176	K1177	E1178	Y1179	V1180	R1181	C1182	E1183	T1184	V1185	R1186	K1187	F1188	A1189	V1190	I1191	D1192	A1193	Y1194	V1195	R1196	I1197	R1198	T1199	T1200	D1202	E1203														
E1204	F1205	ILE	ARG	LYS	PHE	ALA	LEU	LEU	PHE	HIS	ASP	GLU	ARG	LYS	PRO	TYR	GLN	ARG	ARG	ILE	GLN	PRO	SER	LEU	LEU	LYS	ARG	ARG	ASN	ARG	GLN	GLY	THR	VAL	HIS	ASN	ASP	ASN	GLY	LEU	MET	GLY	LEU	LEU	ASP	ALA	ILE	ASN	ASP	ASP	LEU	ASP	LEU	ASP	THR	ASP	ASP	LEU	ASP	ASP	ASP	GLN									
CYS	GLY	ALA	CYS	GLY	ILE	ILE	GLY	HIS	ASP	ARG	THR	ASN	ARG	LYS	PHE	PRO	ASN	GLY	LEU	TYR	GLN	ARG	LEU	LEU	LYS	ARG	ARG	ASN	ARG	GLN	GLY	THR	VAL	HIS	ASN	ASP	ASN	GLY	LEU	MET	GLY	LEU	LEU	ASP	ALA	ILE	ASN	ASP	ASP	LEU	ASP	THR	ASP	ASP	LEU	ASP	ASP	ASP	GLN												
VAL	LEU	GLY	GLN	LEU	ILE	GLY	SER	ILE	ILE	VAL	ASN	ASP	GLU	ARG	ARG	VAL	VAL	ASN	ASN	VAL	VAL	VAL	VAL	LYS	ARG	ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL										
THR	LEU	SER	ILE	LEU	GLU	SER	ILE	ILE	ILE	VAL	ASN	ASP	GLU	ARG	ARG	VAL	VAL	ASN	ASN	VAL	VAL	VAL	LYS	ASP	LEU	CYS	TYR	VAL	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR							
GLU	PHE	ARG	GLU	HIS	LEU	GLU	LEU	LEU	VAL	ASN	ASP	GLU	ARG	TYR	GLY	PRO	LYS	HIS	SER	THR	TRP	PRO	PHE	HIS	LYS	ASP	LEU	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL



● Molecule 4: Transcription initiation factor TFIID subunit 5

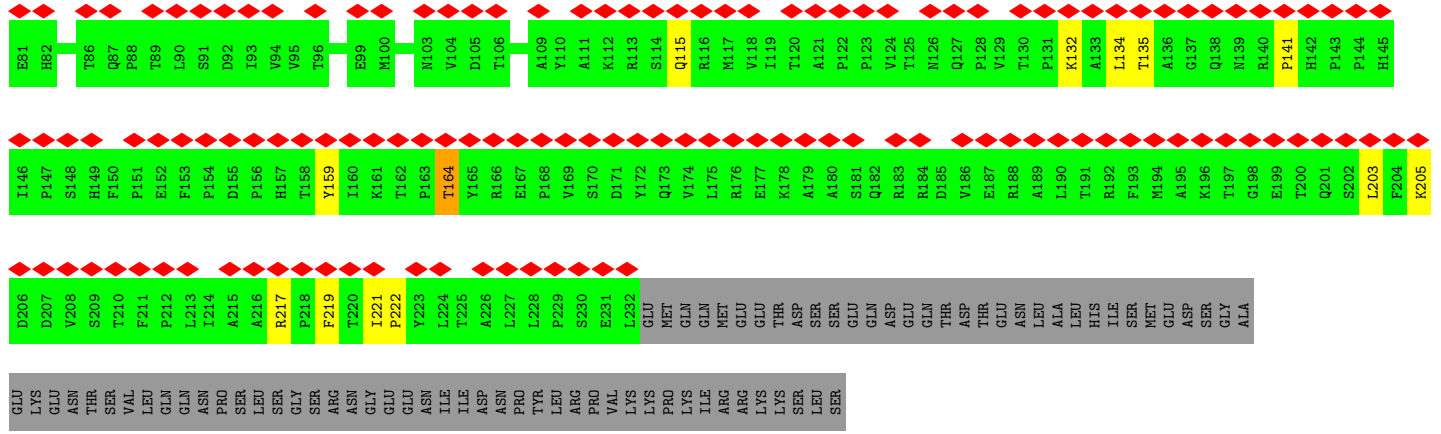


PRO	ALA	ALA	PRO	GLY	LYS	VAL	GLY	SER	VAL	ALA	VAL	GLU	ASP	PRO	PRO	ASP	VAL	SER	ALA	VAL	L202	S203	A204	Y205	N206	Q207	Q208	G209	D210	P211	T212	M213	Y214	E215	E216	Y217	Y218	S219	G220	L221	K222	H223	F224	I225	E226	C227	S228	L229	D230	C231	H232	R233	A234	E235	L236	S237	Q238	L239	F240	
Y241	P242	L243	F244	V245	H246	M247	Y248	L249	E250	L251	V252	Y253	N254	Q255	H256	E257	N258	E259	A260	K261	S262	F263	F264	E265	K266	F267	H268	G269	D270	Q271	E272	C273	Y274	Y275	Q276	D277	L278	L279	R280	V281	L282	S283	S284	L285	T286	K287	K288	E289	H290	M291	K292	G293	N294	E295	T296	N297	D298	F300		
R301	T302	S303	K304	F305	V306	L307	R308	I309	S310	R311	D312	S313	Y314	Q315	L316	L317	K318	R319	H320	L321	Q322	E323	K324	Q325	N326	N327	Q328	I329	W330	N331	I332	V333	Q334	L335	E336	H336	L337	L338	I339	D340	I341	F342	D343	GLY	MET	PRO	LYS	ARG	SER	LYS	GLN	E289	I218	ALA	ALA	VAL	GLY	SER	LEU	ALA
GLY	GLU	A363	K364	R365	E366	A367	N368	K369	S370	K371	V372	F373	F374	G375	L376	L377	K378	E379	F380	GLU	I381	GLU	VAL	PRO	LEU	ASP	GLU	GLU	GLU	GLU	ASN	GLU	GLY	LYS	PRO	LYS	LYS	LYS	ASP	SER	I381	GLY	GLY	SER	SER	LYS	K416	Q417	D418	P419	M420									
A421	P422	P423	Q424	M425	R426	I427	P428	L429	P430	E431	L432	K433	D434	S435	D436	K437	L438	D439	K440	I441	M442	M443	M444	K445	E446	T447	T448	K449	R450	V451	R452	L453	G454	P455	D456	C457	L458	P459	S460	I461	C462	F463	Y464	T465	F466	L467	M468	A469	Y470	Q471	G472	L473	T474	A475	V476	D477	T478	D480		
D481	S482	S483	L484	I485	A486	G487	G488	F489	A490	D491	S492	T493	D494	R495	V496	W497	S498	V499	T500	I501	K502	K503	L504	R505	S506	V507	K508	Q509	A510	S511	D512	L513	S514	L515	I516	D517	K518	E519	S520	D521	V522	V523	L524	E525	R526	I527	N528	D529	E530	K531	A533	S534	A535	E536	L536	K537	I538	L539	Y540	
H541	S542	S543	L544	I545	V546	G547	G548	A549	S550	D551	S552	P553	D554	R555	N556	W557	L558	L559	S560	S561	K562	E563	D564	G565	T566	V567	R568	L569	W570	S571	L572	Q573	L574	F575	T576	C577	L578	V579	G580	Y581	D582	G583	H584	N585	V586	P587	V588	W589	D590	T591	Q592	F593	S594	P595	Y596	G597	I598	Y599	F600	
V601	S602	G603	G604	H605	D606	R607	V608	A609	R610	L611	S612	T613	G614	D615	H616	Q618	P619	L620	R621	I622	F623	A624	G625	H626	L627	A628	D629	V630	N631	C632	T633	R634	F635	H636	P637	N638	S639	N640	Y641	A643	T644	G645	S646	A647	D648	R649	T650	V651	R652	L653	W654	D655	V656	L657	N658	G659	N660			
C661	V662	R663	L664	F665	T666	H667	H668	K669	G670	P671	L672	H673	L674	L675	T676	F677	S678	N680	G681	R682	F683	L684	A685	T686	G687	A688	T689	D690	G691	R692	V693	L694	L695	W696	D697	L698	G699	H700	G701	L702	M703	V704	G705	E706	L707	K708	G709	H710	T711	D712	T713	V714	C715	S716	L717	R718	F719	S720		
R721	D722	G723	E724	L725	L726	A727	S728	G729	S730	M731	D732	M733	T734	W735	R736	L737	W738	D739	I740	K741	A742	A743	F744	E745	D746	L747	E748	THR	ASP	ASP	PHE	THR	T754	A755	T756	G757	H758	L759	N760	L761	P762	E763	N764	S765	Q766	E767	L768	L769	L770	G771	T772	M773	T774	T775	K776	S777	T778	P779	W780	
V781	H782	L783	H784	F785	T786	R787	R788	M789	L790	V791	L792	A793	A794	G795	A796	Y797	S798	F799	GLN	L14	P15	S16	E17	S18	M19	K20	V21	V22	A23	E24	S25	M26	G27	I28	A29	Q30	I31	L136	S137	I138	E139	G140	C141	Q142	P143	D41	A51	Q52	D53	R63	Q64	T67	A74	M79	P82	L83	A88	Q89		
I92	P93	A97	F106	Y107	E108	E109	K110	E111	V112	D113	L114	S115	I118	M119	T120	P121	P122	P123	R124	L127	K132	W135	L136	S137	I138	E139	G140	C141	Q142	P143	A144	I145	P146	E147	M148	P149	P150	PRO	ALA	PRO	LYS	GLU	GLN	GLN	LYS	ALA	ALA	GLU	THR	PRO	PRO	LEU	LYS							

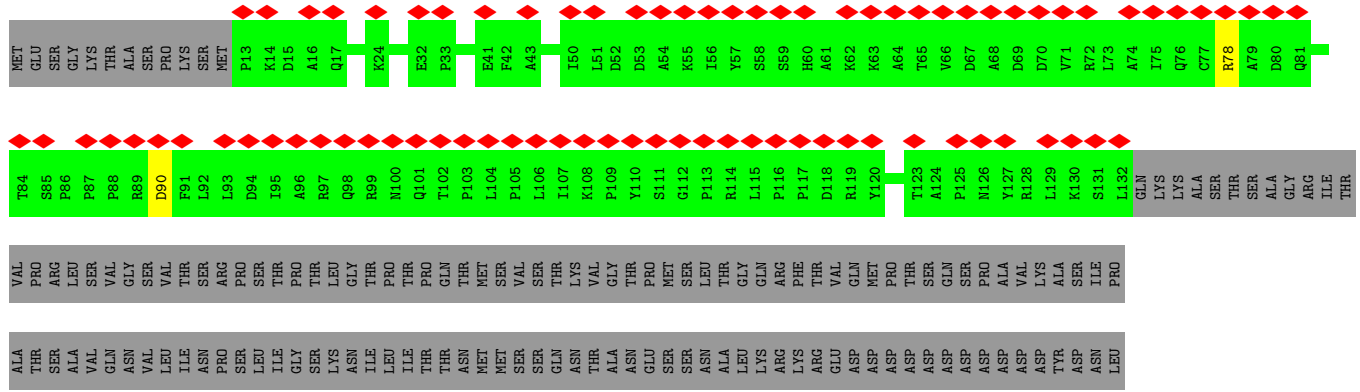
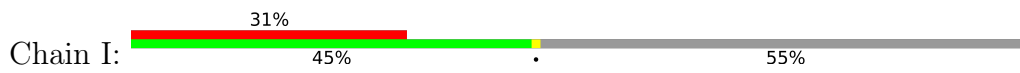
• Molecule 5: Transcription initiation factor TFIID subunit 6



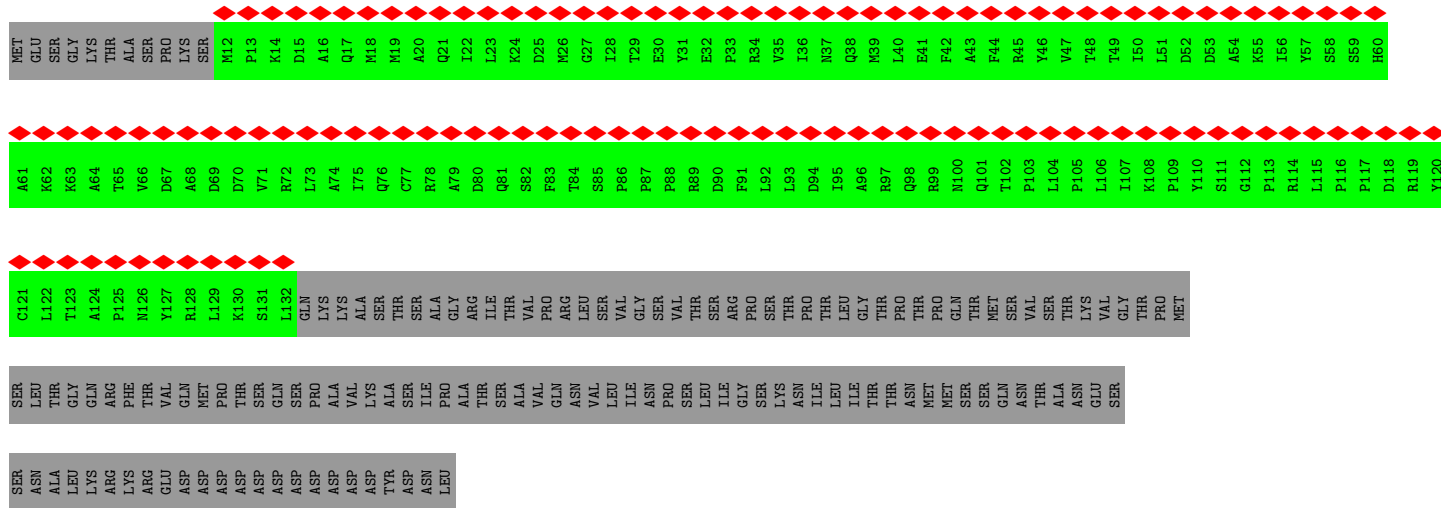
MET	ALA	GLU	GLY	LYS	LEU	LYS	SER	ASN	THR	VAL	L14	P15	S16	E17	S18	M19	K20	V21	V22	A23	E24	S25	M26	G27	I28	A29	Q30	I31	L136	S137	I138	E139	G140	C141	Q142	P143	D41	A51	Q52	D53	R63	Q64	T67	A74	M79	P82	L83	A88	Q89				
I92	P93	A97	F106	Y107	E108	E109	K110	E111	V112	D113	L114	S115	I118	M119	T120	P121	P122	P123	R124	L127	K132	W135	L136	S137	I138	E139	G140	C141	Q142	P143	A144	I145	P146	E147	M148	P149	P150	PRO	ALA	PRO	LYS	GLU	GLN	GLN	LYS	ALA	ALA	GLU	THR	PRO	PRO	LEU	LYS



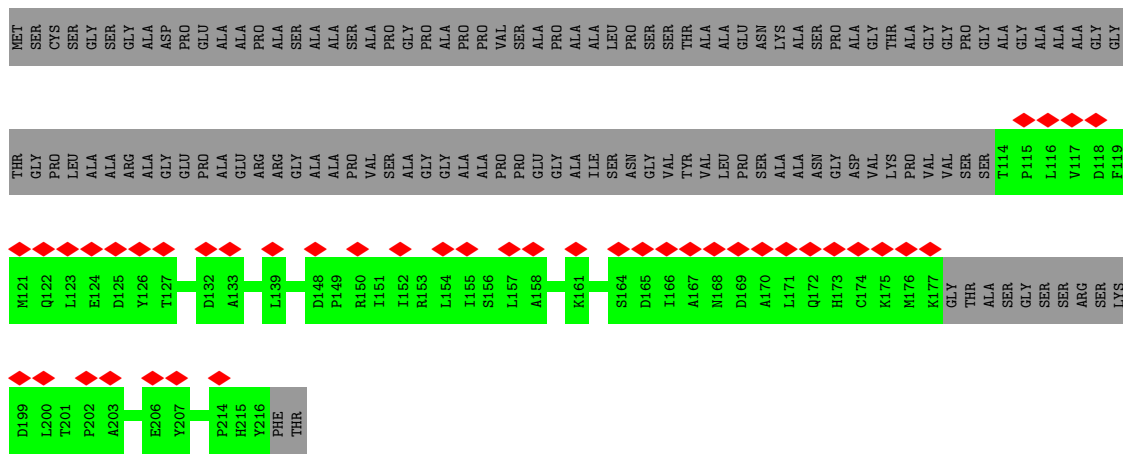
• Molecule 8: Transcription initiation factor TFIID subunit 9



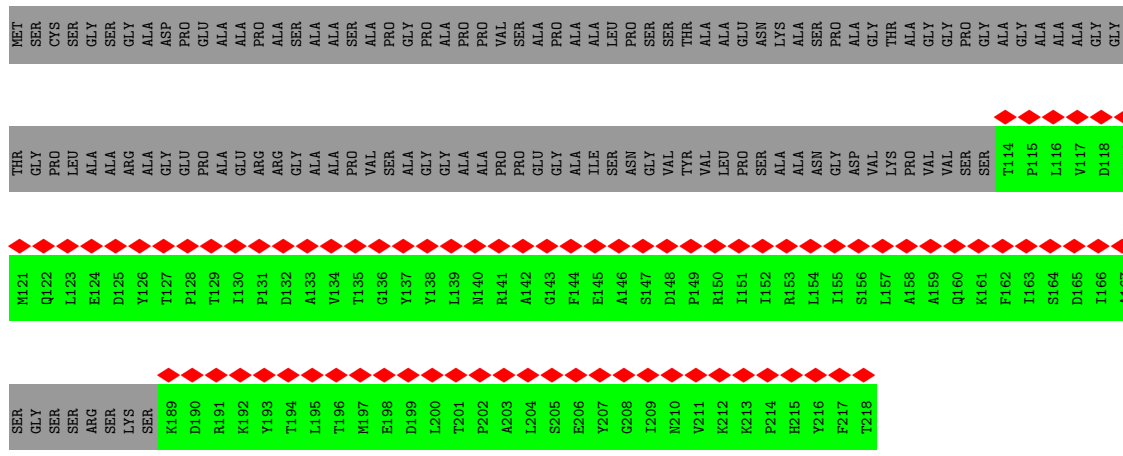
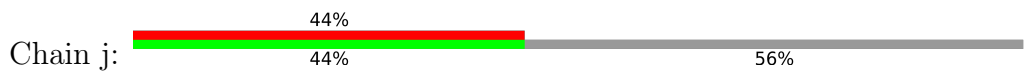
• Molecule 8: Transcription initiation factor TFIID subunit 9



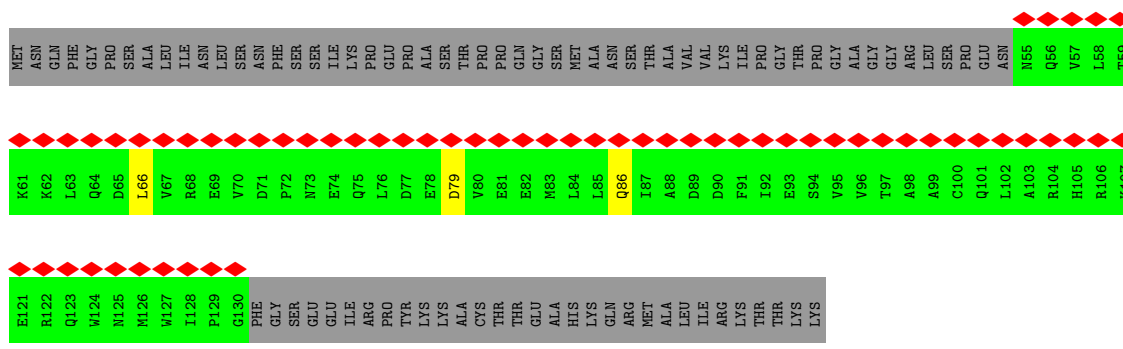
• Molecule 9: Transcription initiation factor TFIID subunit 10



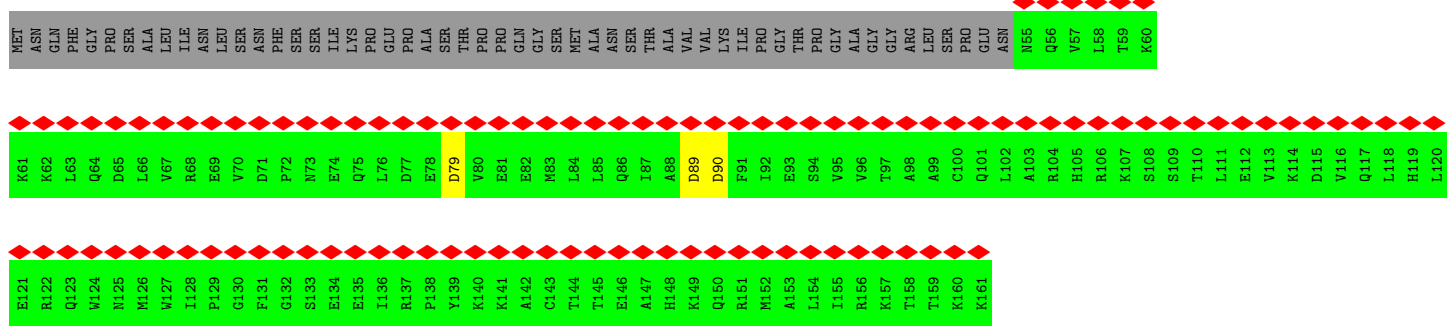
• Molecule 9: Transcription initiation factor TFIID subunit 10



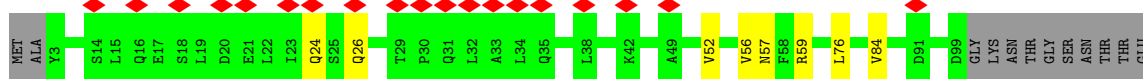
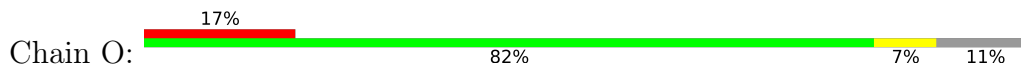
• Molecule 10: Transcription initiation factor TFIID subunit 12



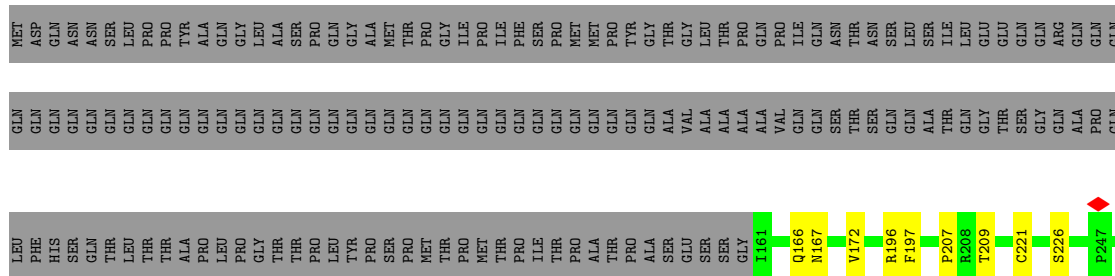
• Molecule 10: Transcription initiation factor TFIID subunit 12



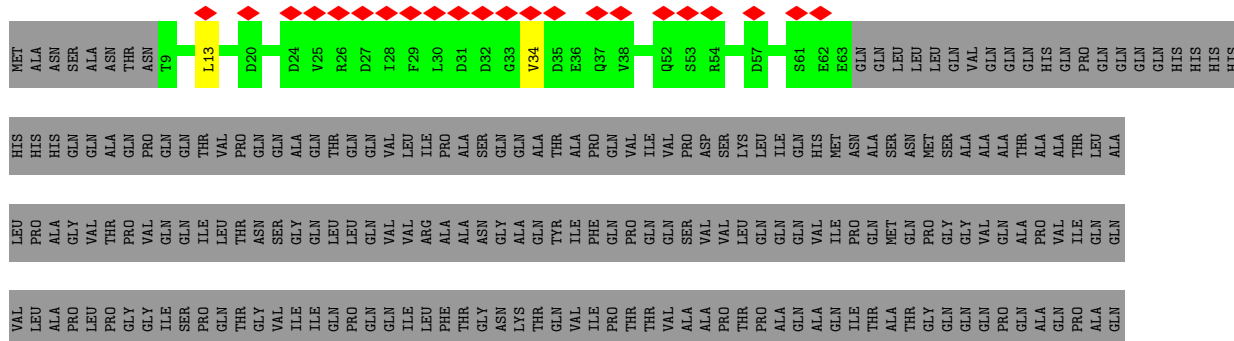
• Molecule 11: Transcription initiation factor IIA subunit 2

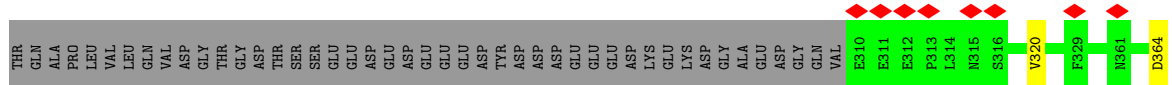


• Molecule 12: TATA-box-binding protein



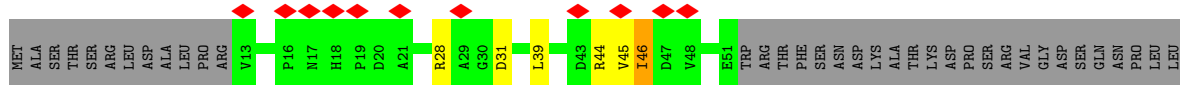
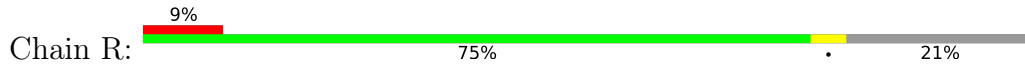
• Molecule 13: Transcription initiation factor IIA subunit 1





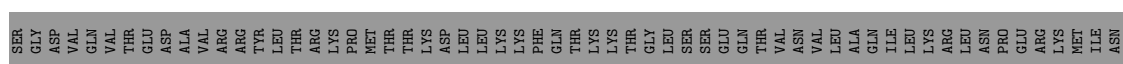
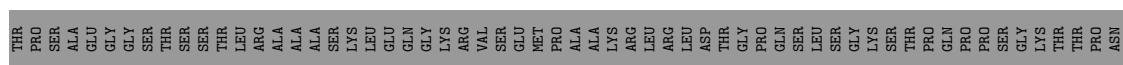
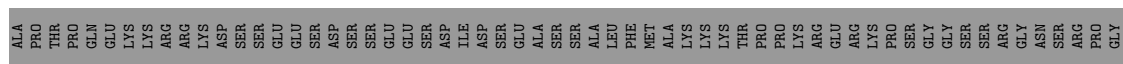
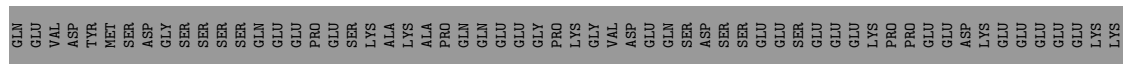
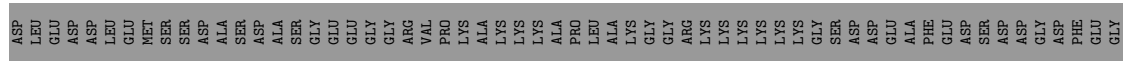
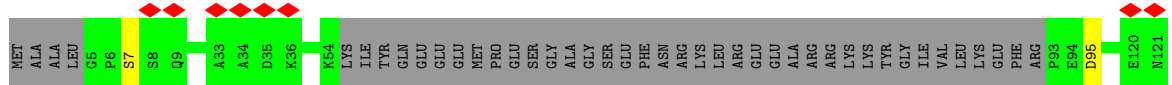
#376

• Molecule 14: Transcription initiation factor IIB



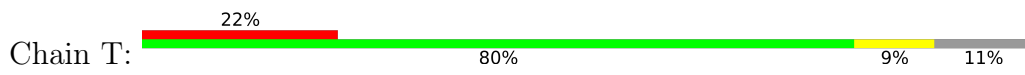
D288
F306
D307
T308
V310
D311
K312
L313
Q314
L316

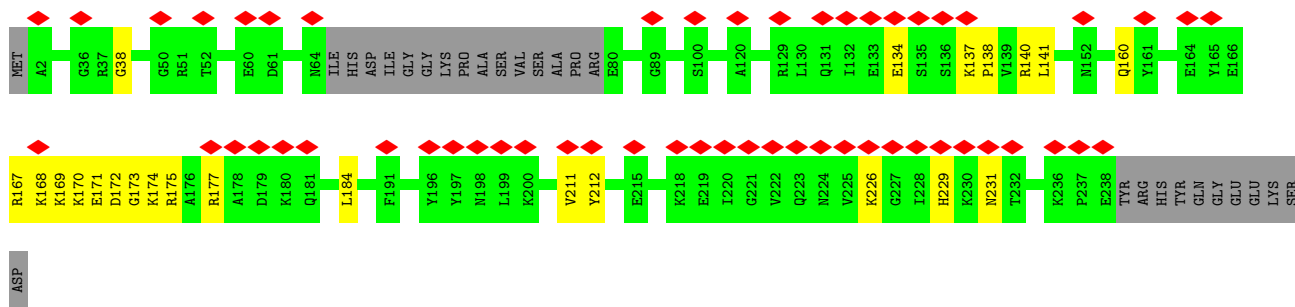
• Molecule 15: General transcription factor IIF subunit 1



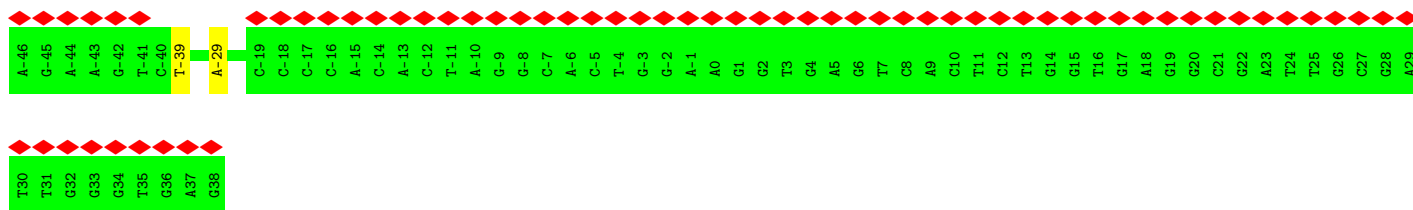
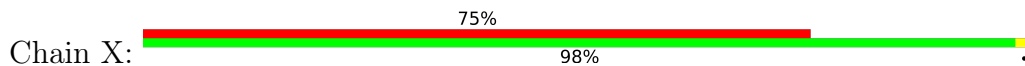
ASP
LYS
HIS
PHE
SER
LEU
GLU

• Molecule 16: General transcription factor IIF subunit 2





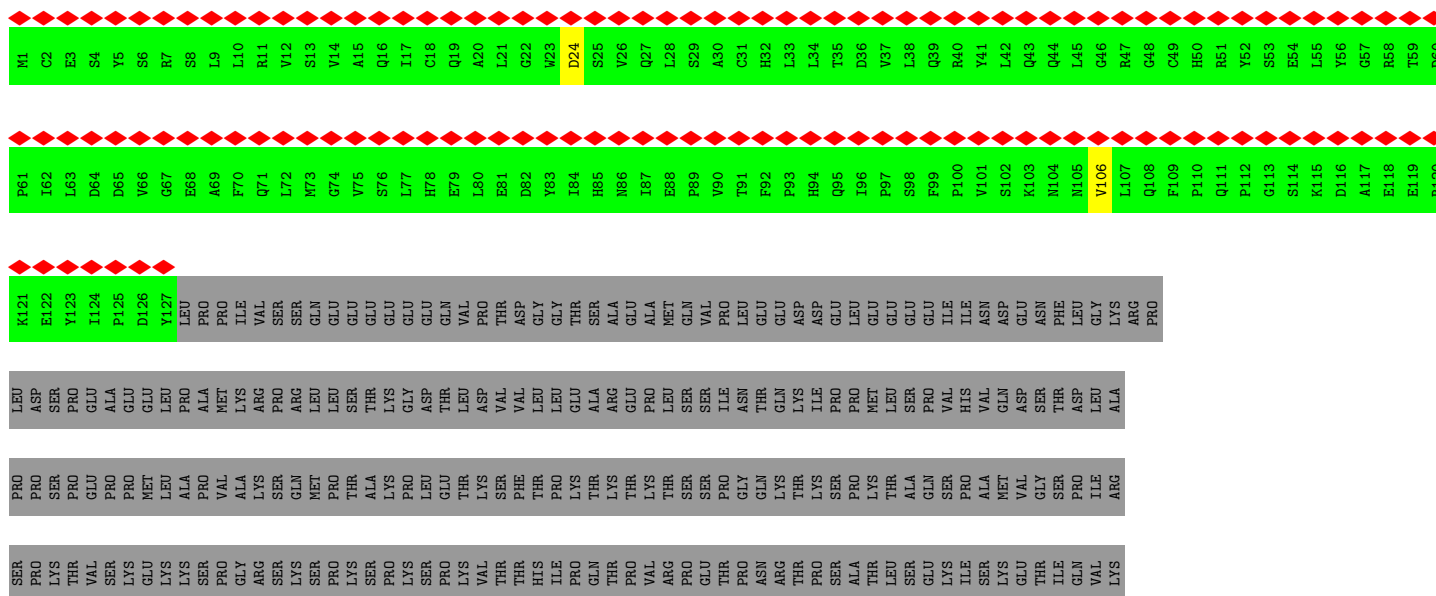
• Molecule 17: DNA (85-MER)

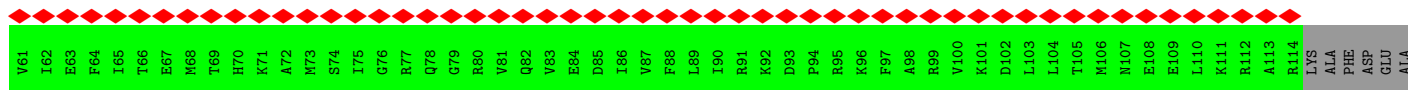


• Molecule 18: DNA (85-MER)



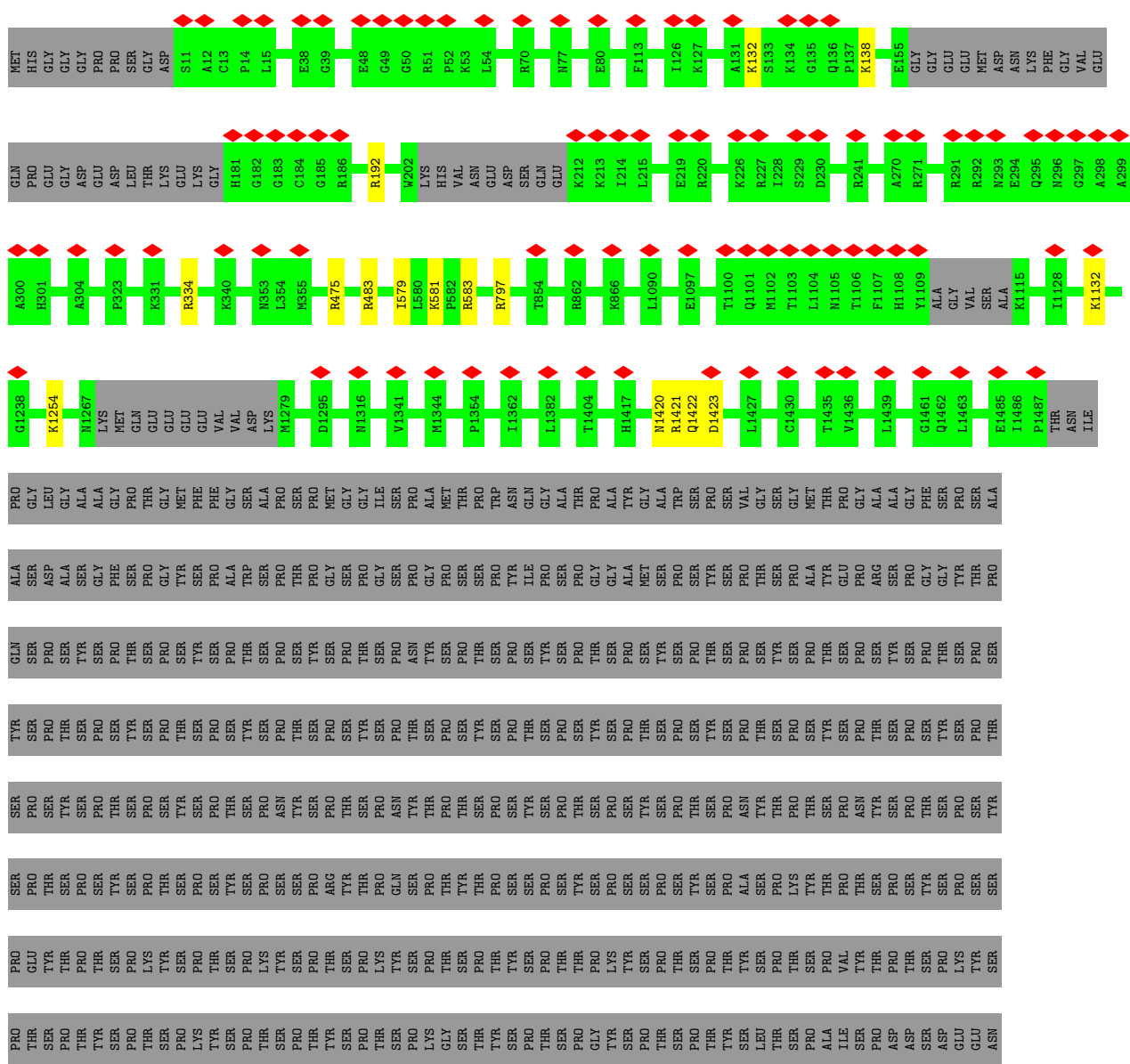
• Molecule 19: Transcription initiation factor TFIID subunit 3





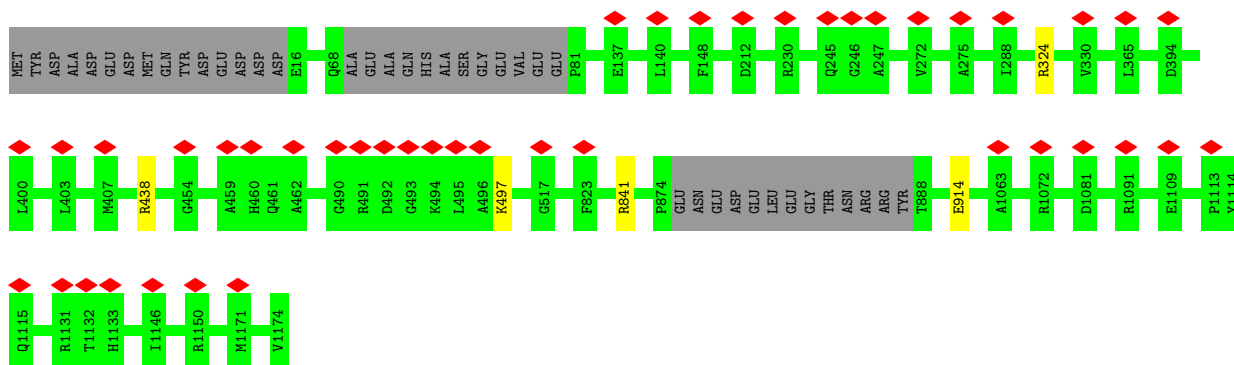
ASN
TYR
GLY
SER

• Molecule 22: RPB1

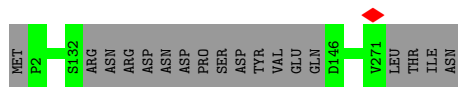


• Molecule 23: DNA-directed RNA polymerase subunit beta

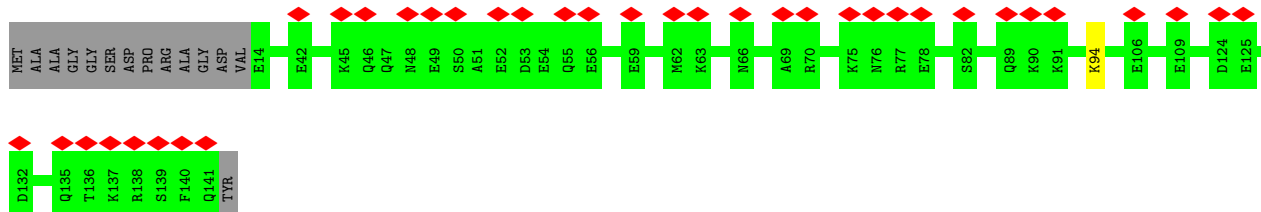
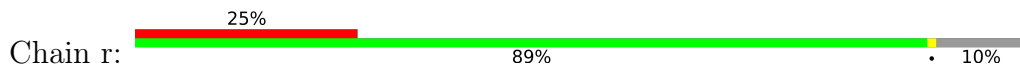




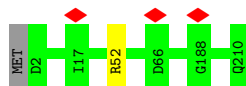
• Molecule 24: DNA-directed RNA polymerase II subunit RPB3



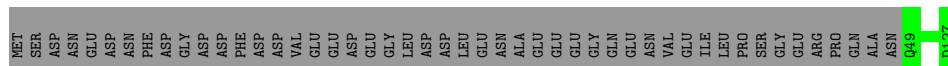
• Molecule 25: DNA-directed RNA polymerase II subunit RPB4



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

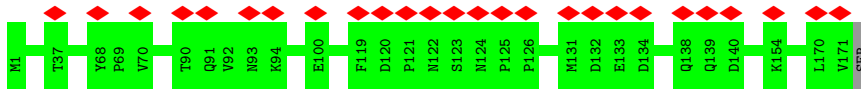


• Molecule 27: DNA-directed RNA polymerase II subunit F



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





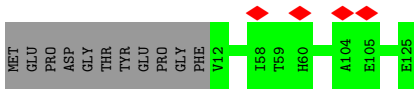
- Molecule 29: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain v: 99%



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

Chain w: 91% 9%



- Molecule 31: RPB10

Chain x: 96%



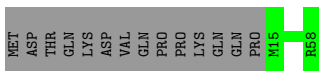
- Molecule 32: RNA_pol_L_2 domain-containing protein

Chain y: 100%



- Molecule 33: RPB12

Chain z: 76% 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 (\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 (\AA)	1.38, 1.38, 1.38	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.65	0/6810
2	B	0.47	0/7993	0.60	0/10836
3	D	0.45	0/1379	0.58	0/1843
3	d	0.29	0/1321	0.49	0/1772
4	E	0.35	0/4469	0.55	0/6050
4	e	0.33	0/4433	0.55	0/6004
5	F	0.50	0/3139	0.67	0/4264
5	f	0.40	0/3140	0.63	0/4268
6	G	0.51	0/1199	0.63	0/1612
7	H	0.41	0/1673	0.60	0/2285
8	I	0.32	0/981	0.50	0/1332
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	0.36	0/630	0.57	0/852
10	l	0.29	0/888	0.55	3/1194 (0.3%)
11	O	0.50	0/781	0.74	0/1061
12	P	0.61	0/1438	0.75	1/1935 (0.1%)
13	Q	0.44	0/1013	0.60	0/1366
14	R	0.33	0/1966	0.56	0/2655
15	S	0.32	0/896	0.49	0/1213
16	T	0.49	0/1817	0.67	0/2445
17	X	0.77	1/1966 (0.1%)	1.00	1/3034 (0.0%)
18	Y	0.67	1/1942 (0.1%)	0.90	0/2993
19	c	0.39	0/1035	0.54	0/1406
20	k	0.30	0/799	0.47	0/1070
21	m	0.31	0/733	0.51	0/977
22	o	0.34	0/11516	0.50	0/15548
23	p	0.37	0/9243	0.47	0/12475
24	q	0.39	0/2102	0.46	0/2857
25	r	0.26	0/1019	0.47	0/1374
26	s	0.30	0/1751	0.46	0/2366

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	t	0.37	0/645	0.47	0/871
28	u	0.29	0/1365	0.47	0/1853
29	v	0.37	0/1207	0.49	0/1628
30	w	0.30	0/948	0.46	0/1284
31	x	0.43	0/516	0.45	0/696
32	y	0.35	0/956	0.44	0/1294
33	z	0.38	0/377	0.44	0/500
All	All	0.42	2/84810 (0.0%)	0.58	5/115397 (0.0%)

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

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	X	-39	DT	C1'-N1	5.03	1.55	1.49
18	Y	10	DT	C1'-N1	5.02	1.55	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	P	167	ASN	CB-CA-C	-6.91	96.59	110.40
17	X	-29	DA	C1'-O4'-C4'	-6.06	104.04	110.10
10	1	79	ASP	CB-CG-OD2	5.21	122.98	118.30
10	1	89	ASP	CB-CG-OD2	5.18	122.96	118.30
10	1	90	ASP	CB-CG-OD2	5.16	122.95	118.30

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 [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%)	544 (93%)	35 (6%)	5 (1%)	17	57
2	B	959/1199 (80%)	913 (95%)	46 (5%)	0	100	100
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%)	25	66
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	373 (93%)	23 (6%)	4 (1%)	15	54
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%)	8	38
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%)	4	26
12	P	175/339 (52%)	162 (93%)	11 (6%)	2 (1%)	14	52
13	Q	118/376 (31%)	110 (93%)	7 (6%)	1 (1%)	19	60
14	R	247/316 (78%)	235 (95%)	10 (4%)	2 (1%)	19	60
15	S	104/517 (20%)	102 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	T	218/249 (88%)	198 (91%)	15 (7%)	5 (2%)	6	34
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%)	51	86
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
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%)	44	77

All (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
11	O	52	VAL
13	Q	320	VAL
1	A	661	GLU
4	E	522	ASP
4	E	704	VAL
11	O	26	GLN
14	R	46	ILE
5	F	413	SER
12	P	207	PRO
16	T	173	GLY

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Mol	Chain	Res	Type
16	T	231	ASN
5	F	64	GLN
5	F	439	ARG
11	O	84	VAL
16	T	226	LYS
22	o	583	ARG
1	A	640	LEU
7	H	134	LEU
7	H	164	THR
12	P	298	PRO
14	R	247	GLY
16	T	38	GLY
16	T	138	PRO
1	A	498	PRO
4	E	523	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	536/1665 (32%)	484 (90%)	52 (10%)	8 27
2	B	876/1083 (81%)	851 (97%)	25 (3%)	42 64
3	D	147/815 (18%)	117 (80%)	30 (20%)	1 7
3	d	146/815 (18%)	145 (99%)	1 (1%)	84 90
4	E	478/657 (73%)	474 (99%)	4 (1%)	81 89
4	e	475/657 (72%)	473 (100%)	2 (0%)	91 94
5	F	320/574 (56%)	304 (95%)	16 (5%)	24 49
5	f	322/574 (56%)	312 (97%)	10 (3%)	40 62
6	G	133/322 (41%)	126 (95%)	7 (5%)	22 47
7	H	181/270 (67%)	171 (94%)	10 (6%)	21 47
8	I	106/235 (45%)	104 (98%)	2 (2%)	57 75
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%)	68 (96%)	3 (4%)	30	54
10	l	98/141 (70%)	98 (100%)	0	100	100
11	O	84/98 (86%)	79 (94%)	5 (6%)	19	44
12	P	153/293 (52%)	137 (90%)	16 (10%)	7	24
13	Q	111/324 (34%)	108 (97%)	3 (3%)	44	65
14	R	213/268 (80%)	201 (94%)	12 (6%)	21	46
15	S	93/448 (21%)	91 (98%)	2 (2%)	52	71
16	T	196/218 (90%)	178 (91%)	18 (9%)	9	29
19	c	113/833 (14%)	111 (98%)	2 (2%)	59	77
20	k	87/182 (48%)	87 (100%)	0	100	100
21	m	80/106 (76%)	79 (99%)	1 (1%)	69	81
22	o	1257/1748 (72%)	1242 (99%)	15 (1%)	71	83
23	p	993/1027 (97%)	988 (100%)	5 (0%)	88	93
24	q	234/252 (93%)	234 (100%)	0	100	100
25	r	106/126 (84%)	105 (99%)	1 (1%)	78	87
26	s	191/192 (100%)	190 (100%)	1 (0%)	88	93
27	t	69/111 (62%)	69 (100%)	0	100	100
28	u	147/153 (96%)	147 (100%)	0	100	100
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%)	8473 (97%)	243 (3%)	46	65

All (243) 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

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Mol	Chain	Res	Type
1	A	397	LEU
1	A	400	GLU
1	A	404	MET
1	A	408	LEU
1	A	410	TRP
1	A	411	GLU
1	A	415	ILE
1	A	416	TRP
1	A	417	ASP
1	A	419	GLU
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	641	LYS
1	A	644	LYS
1	A	645	LYS
1	A	646	LYS
1	A	648	LYS
1	A	651	GLU
1	A	654	ARG
1	A	667	THR
1	A	685	GLU
1	A	711	ASP
1	A	727	THR
1	A	730	PHE
1	A	797	LYS
1	A	798	ARG
1	A	828	GLU
1	A	943	LYS
1	A	970	ASN
1	A	971	LYS
1	A	992	ASP
1	A	994	ASP
1	A	995	LEU
1	A	996	ARG
1	A	1020	LEU
1	A	1022	ARG
1	A	1029	VAL

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Mol	Chain	Res	Type
1	A	1052	ARG
1	A	1054	SER
1	A	1062	TYR
1	A	1064	GLU
1	A	1069	ILE
1	A	1165	LEU
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	488	PHE
2	B	559	LYS
2	B	603	LYS
2	B	638	ARG
2	B	640	VAL
2	B	771	VAL
2	B	816	VAL
2	B	817	ARG
2	B	818	THR
2	B	819	LEU
2	B	820	ASP
2	B	944	LEU
2	B	945	CYS
2	B	983	ARG
2	B	987	LEU
3	D	893	GLU
3	D	929	LYS
3	D	932	ASP
3	D	933	ARG
3	D	936	GLN
3	D	938	SER
3	D	939	ASP
3	D	941	ARG
3	D	944	LEU
3	D	945	LYS

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Mol	Chain	Res	Type
3	D	946	PHE
3	D	947	PHE
3	D	948	GLU
3	D	949	GLN
3	D	950	LEU
3	D	951	ASP
3	D	952	GLN
3	D	953	ILE
3	D	955	LYS
3	D	957	ARG
3	D	958	LYS
3	D	959	ASP
3	D	962	GLU
3	D	965	ILE
3	D	967	MET
3	D	968	ARG
3	D	1002	ARG
3	D	1003	ASP
3	D	1054	ARG
3	D	1056	THR
4	E	593	PHE
4	E	745	GLU
4	E	746	ASP
4	E	747	LEU
5	F	63	ARG
5	F	92	ILE
5	F	136	LEU
5	F	258	ARG
5	F	261	THR
5	F	271	VAL
5	F	280	ILE
5	F	301	VAL
5	F	317	LEU
5	F	326	HIS
5	F	348	THR
5	F	354	ARG
5	F	397	GLN
5	F	408	ASP
5	F	411	VAL
5	F	427	LEU
6	G	41	ASP
6	G	81	ASP

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Mol	Chain	Res	Type
6	G	143	VAL
6	G	147	ARG
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	205	LYS
7	H	217	ARG
7	H	219	PHE
7	H	221	ILE
8	I	78	ARG
8	I	90	ASP
10	L	66	LEU
10	L	79	ASP
10	L	86	GLN
11	O	24	GLN
11	O	56	VAL
11	O	57	ASN
11	O	59	ARG
11	O	76	LEU
12	P	166	GLN
12	P	172	VAL
12	P	196	ARG
12	P	197	PHE
12	P	209	THR
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	309	LYS
12	P	312	LEU
12	P	313	THR
12	P	317	VAL
13	Q	13	LEU

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Mol	Chain	Res	Type
13	Q	34	VAL
13	Q	364	ASP
14	R	28	ARG
14	R	31	ASP
14	R	39	LEU
14	R	44	ARG
14	R	45	VAL
14	R	46	ILE
14	R	114	MET
14	R	120	GLU
14	R	137	ARG
14	R	139	ASN
14	R	142	PHE
14	R	189	LYS
15	S	7	SER
15	S	95	ASP
16	T	134	GLU
16	T	137	LYS
16	T	140	ARG
16	T	141	LEU
16	T	160	GLN
16	T	167	ARG
16	T	168	LYS
16	T	169	LYS
16	T	170	LYS
16	T	171	GLU
16	T	172	ASP
16	T	174	LYS
16	T	175	ARG
16	T	177	ARG
16	T	184	LEU
16	T	211	VAL
16	T	212	TYR
16	T	229	HIS
19	c	24	ASP
19	c	106	VAL
3	d	888	LYS
4	e	365	ARG
4	e	663	ARG
5	f	253	TYR
5	f	261	THR
5	f	272	VAL

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Mol	Chain	Res	Type
5	f	322	ASP
5	f	323	VAL
5	f	326	HIS
5	f	356	THR
5	f	408	ASP
5	f	412	LEU
5	f	421	ASP
21	m	31	LEU
22	o	132	LYS
22	o	138	LYS
22	o	192	ARG
22	o	334	ARG
22	o	475	ARG
22	o	483	ARG
22	o	579	ILE
22	o	581	LYS
22	o	797	ARG
22	o	1132	LYS
22	o	1254	LYS
22	o	1420	ASN
22	o	1421	ARG
22	o	1422	GLN
22	o	1423	ASP
23	p	324	ARG
23	p	438	ARG
23	p	497	LYS
23	p	841	ARG
23	p	914	GLU
25	r	94	LYS
26	s	52	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) 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	590	GLN
1	A	637	GLN
1	A	860	ASN
1	A	896	GLN

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Mol	Chain	Res	Type
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	765	ASN
2	B	813	ASN
2	B	908	GLN
2	B	916	ASN
3	D	936	GLN
3	D	943	GLN
3	D	981	GLN
3	D	998	GLN
4	E	254	ASN
4	E	268	HIS
4	E	327	ASN
4	E	351	GLN
4	E	616	HIS
4	E	640	ASN
5	F	52	GLN
5	F	119	ASN
5	F	221	GLN
5	F	270	ASN
5	F	273	GLN
5	F	274	ASN
5	F	275	ASN
5	F	316	GLN
6	G	48	HIS
7	H	145	HIS
7	H	201	GLN
8	I	21	GLN

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Mol	Chain	Res	Type
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	8	ASN
11	O	13	ASN
11	O	27	GLN
11	O	31	GLN
11	O	57	ASN
12	P	167	ASN
13	Q	60	HIS
13	Q	352	HIS
13	Q	361	ASN
14	R	139	ASN
16	T	158	ASN
16	T	181	GLN
16	T	182	HIS
16	T	208	GLN
19	c	104	ASN
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	60	HIS
8	i	81	GLN
10	l	73	ASN
10	l	105	HIS
21	m	107	ASN
22	o	123	ASN
22	o	278	HIS
22	o	289	GLN
22	o	296	ASN
22	o	311	GLN
22	o	372	ASN
22	o	507	GLN

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Mol	Chain	Res	Type
22	o	620	HIS
22	o	721	HIS
22	o	731	ASN
22	o	739	ASN
22	o	809	HIS
22	o	913	ASN
22	o	950	ASN
22	o	1005	HIS
22	o	1230	GLN
22	o	1248	ASN
22	o	1332	GLN
22	o	1397	HIS
22	o	1445	HIS
22	o	1462	GLN
23	p	111	ASN
23	p	139	GLN
23	p	287	HIS
23	p	525	ASN
23	p	570	ASN
23	p	749	HIS
23	p	842	HIS
23	p	1021	HIS
23	p	1094	GLN
23	p	1117	HIS
23	p	1120	ASN
25	r	19	GLN
26	s	133	GLN
28	u	60	GLN
29	v	131	ASN
32	y	2	ASN
32	y	29	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

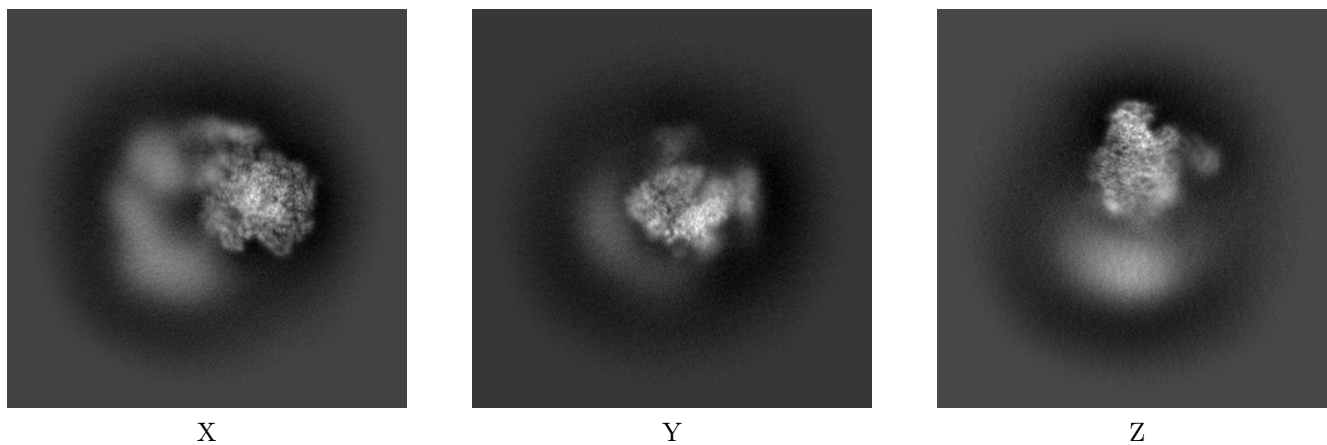
6 Map visualisation [i](#)

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](#)

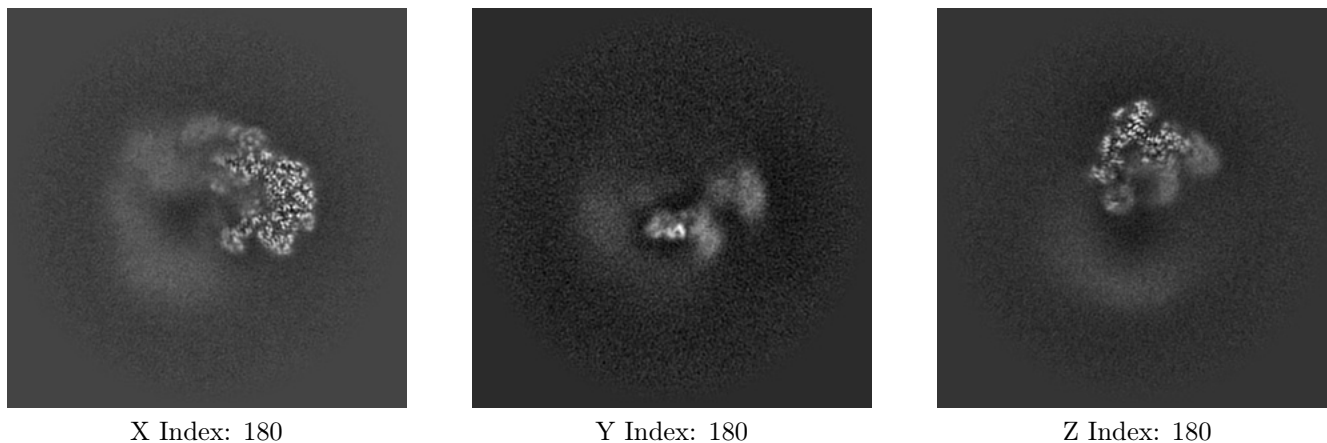
6.1.1 Primary map



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

6.2 Central slices [i](#)

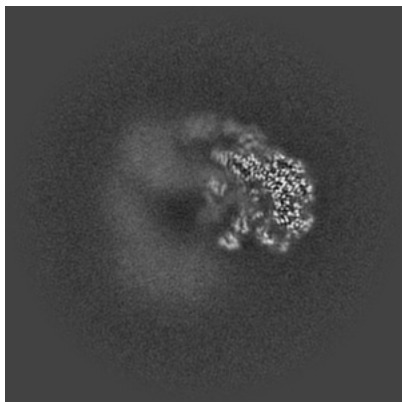
6.2.1 Primary map



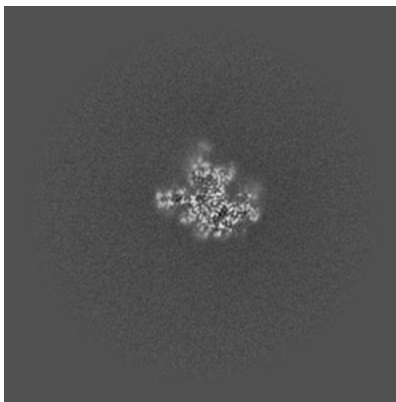
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

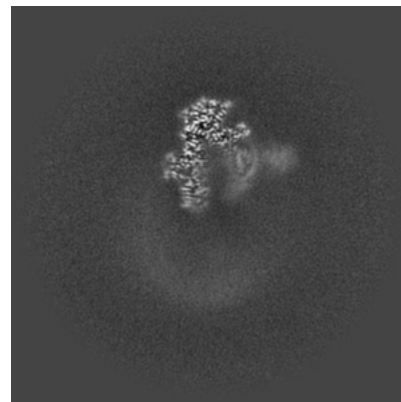
6.3.1 Primary map



X Index: 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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.19. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

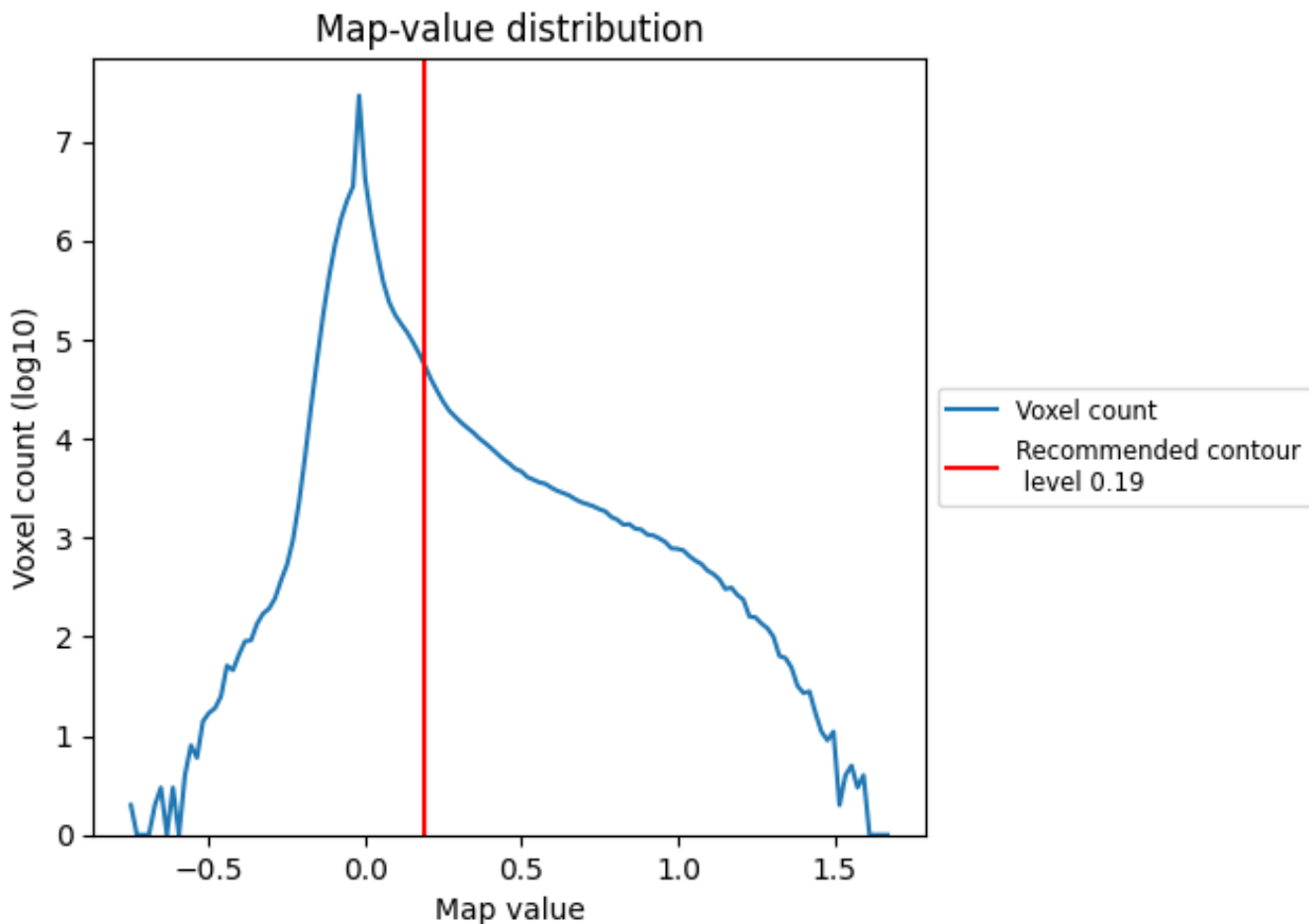
6.5 Mask visualisation

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

7 Map analysis [i](#)

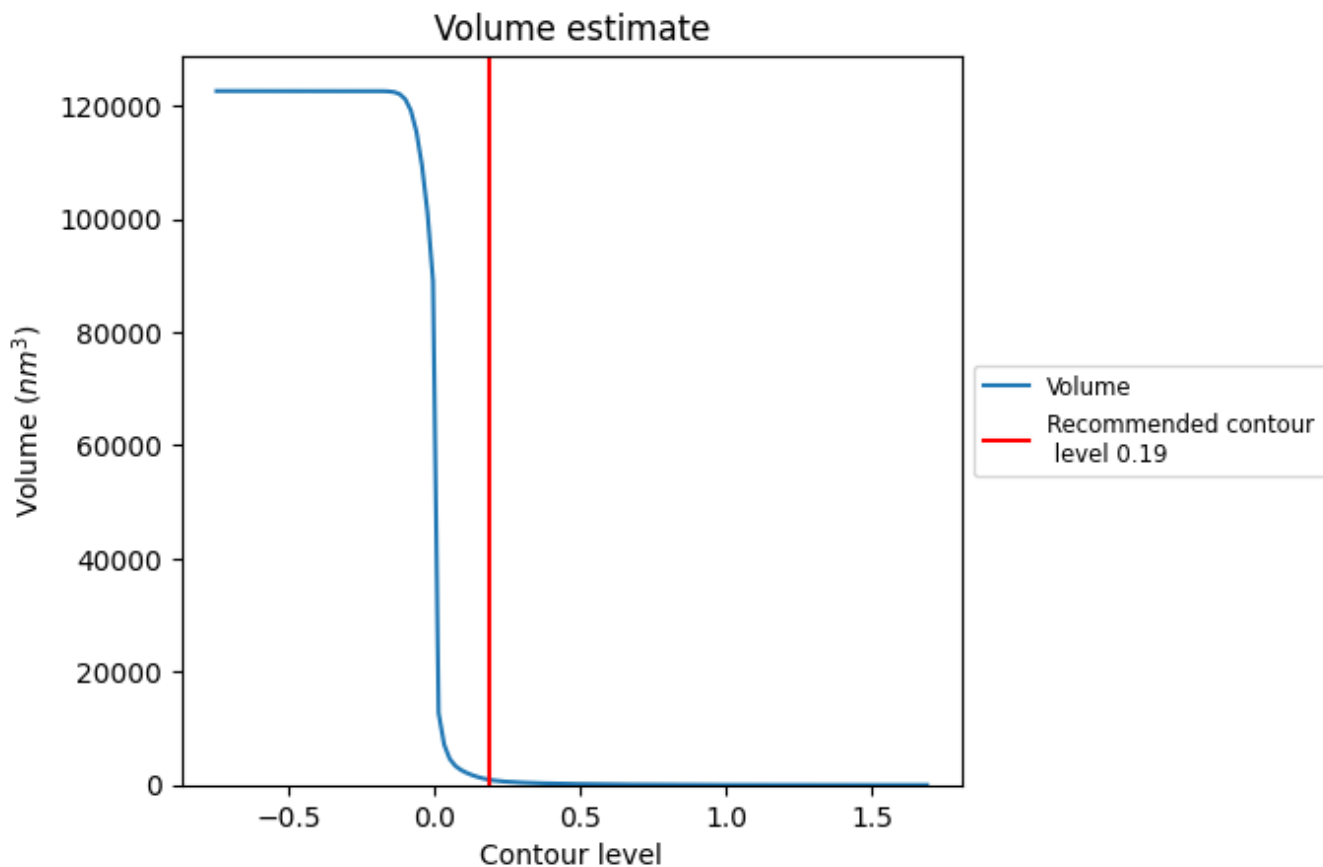
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

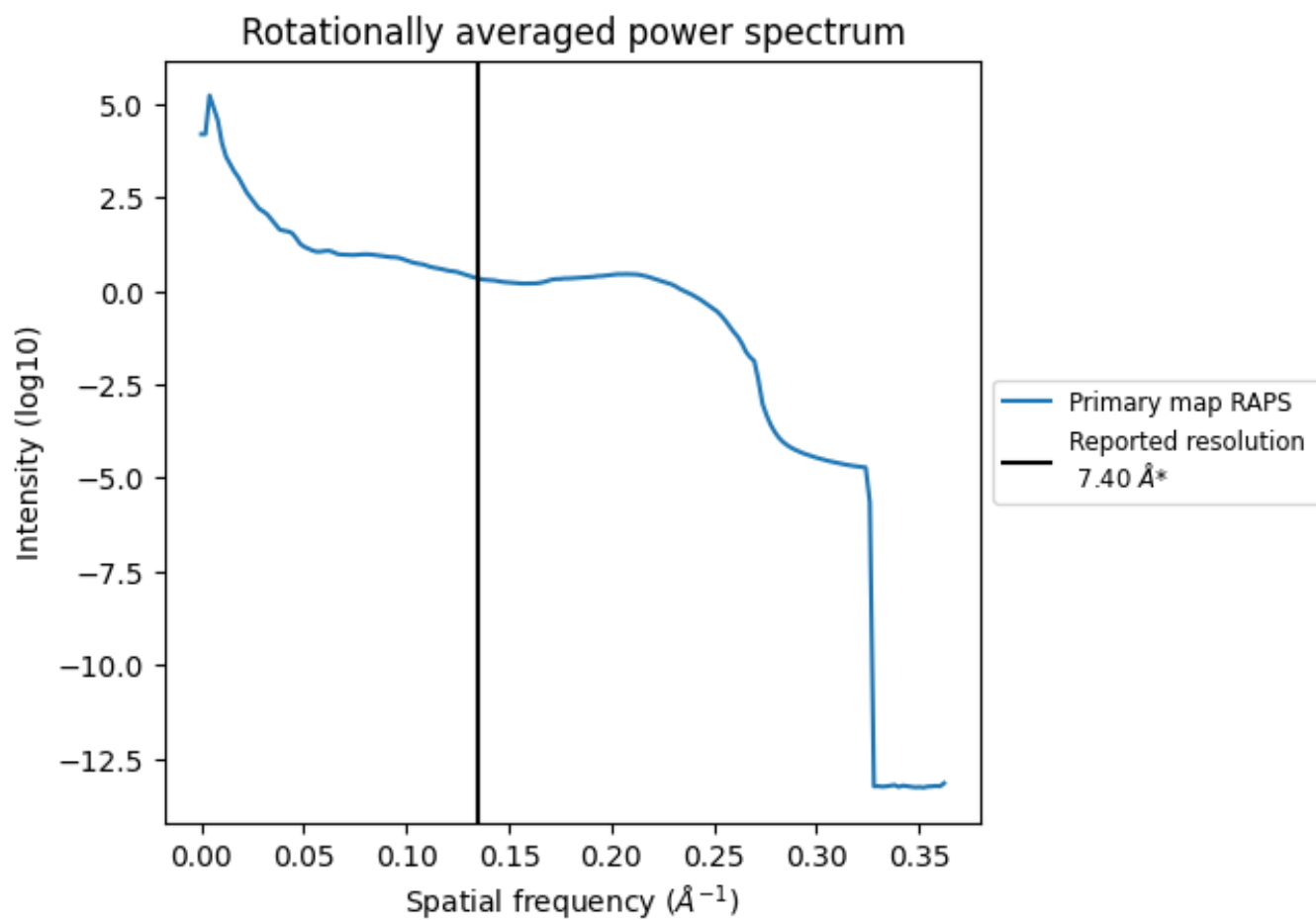
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 917 nm^3 ; 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 i



*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

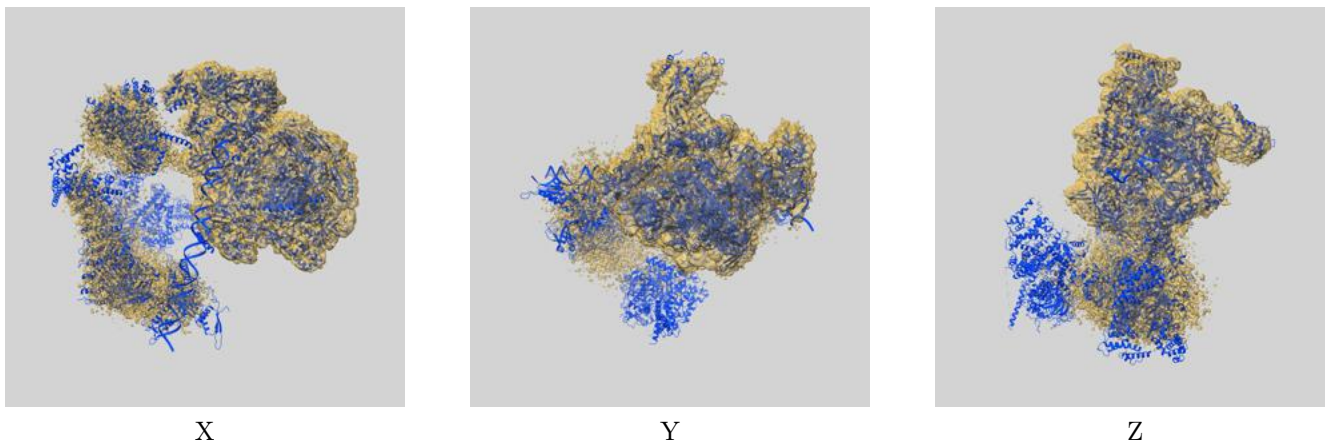
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

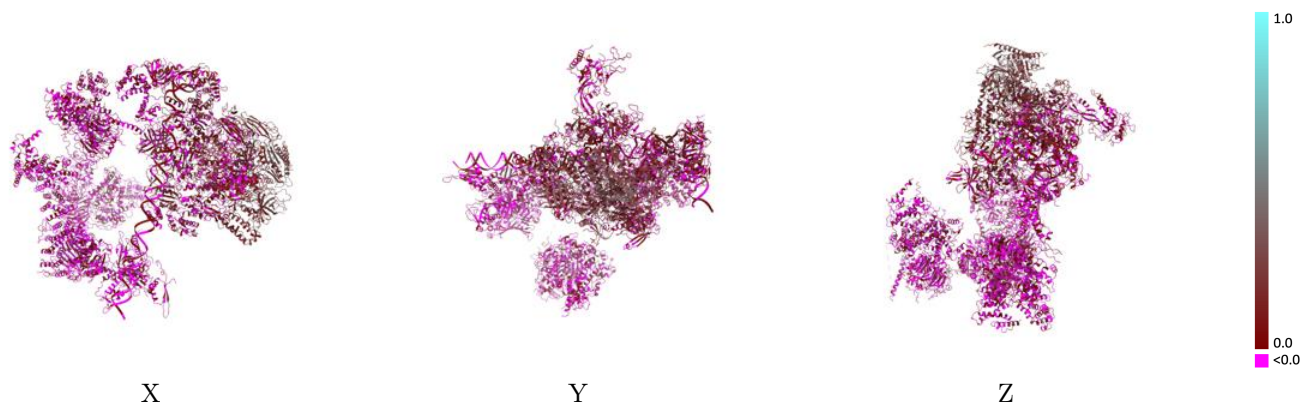
This section contains information regarding the fit between EMDB map EMD-31108 and PDB model 7EG8. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



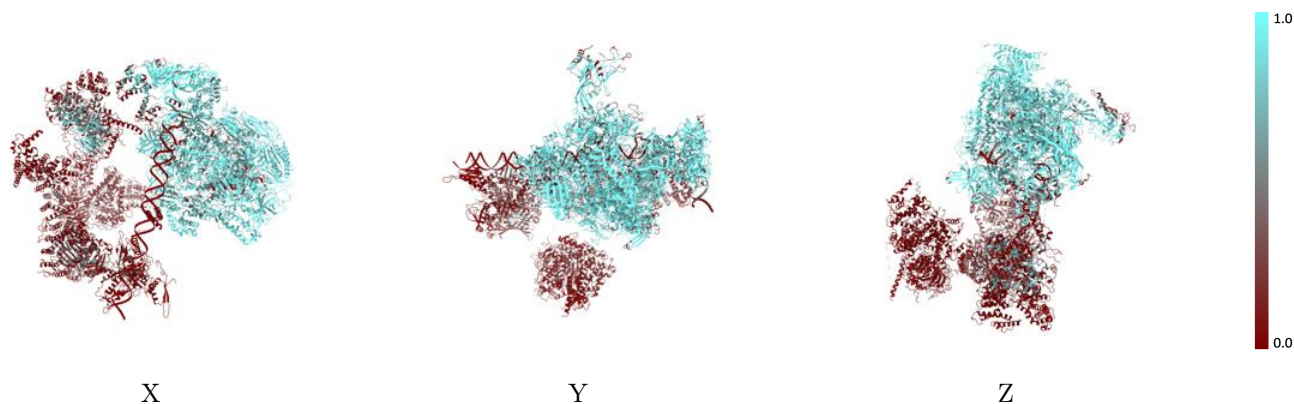
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



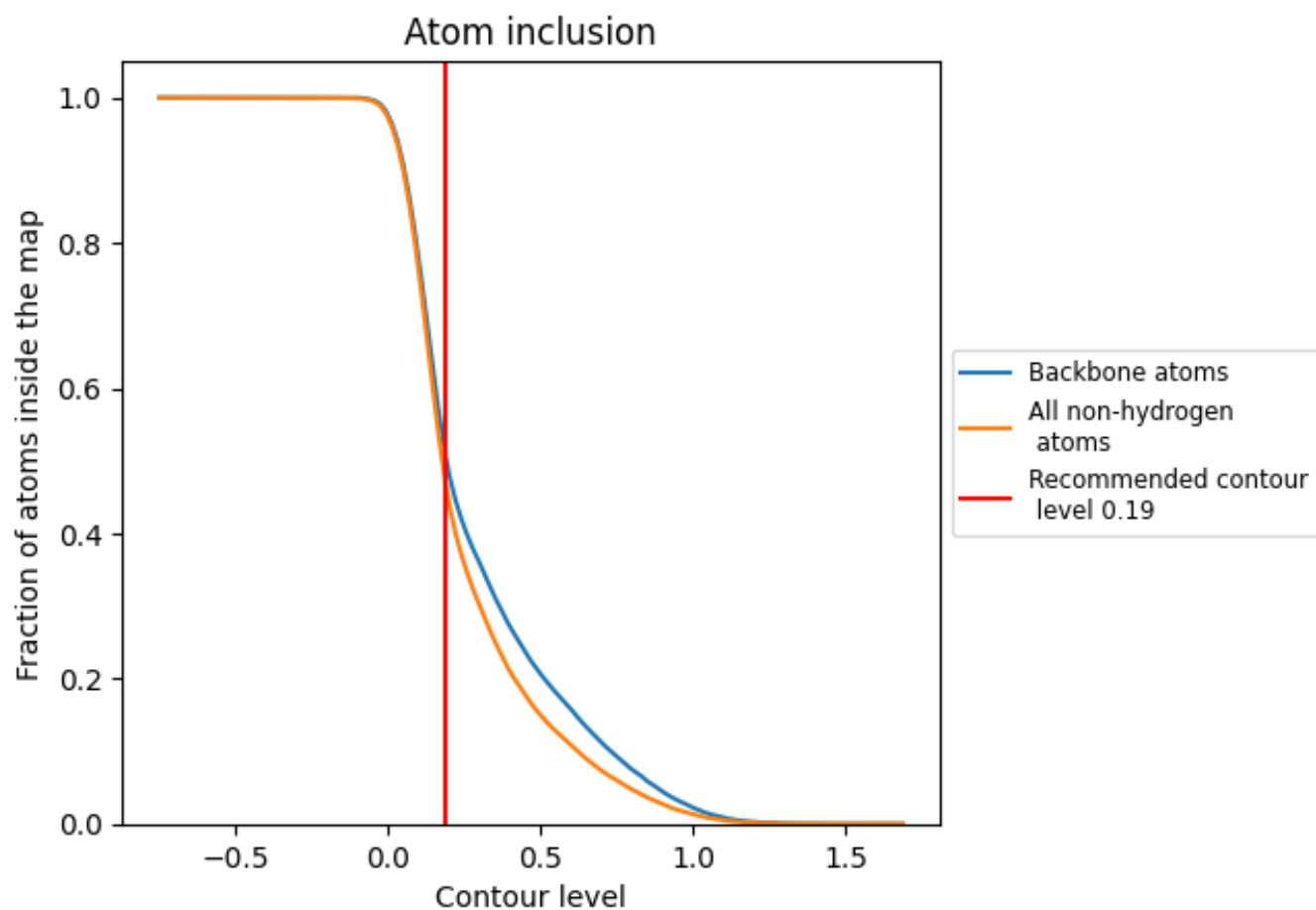
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.19).







































































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	 0.4701	 0.0740
A	 0.0573	 -0.0030
B	 0.1576	 -0.0020
D	 0.1772	 0.0200
E	 0.4078	 0.0150
F	 0.1705	 0.0150
G	 0.0383	 0.0120
H	 0.2116	 0.0060
I	 0.3091	 0.0320
J	 0.3759	 0.0070
L	 0.0408	 0.0510
O	 0.7371	 0.0280
P	 0.9274	 0.0760
Q	 0.7067	 0.0260
R	 0.7953	 0.0950
S	 0.9087	 0.0710
T	 0.6794	 0.0610
X	 0.2467	 0.0420
Y	 0.2987	 0.0290
c	 0.0030	 -0.0170
d	 0.0000	 0.0130
e	 0.0068	 -0.0070
f	 0.0555	 0.0020
i	 0.0032	 0.0160
j	 0.0000	 0.0210
k	 0.0000	 -0.0100
l	 0.0012	 -0.0020
m	 0.0000	 -0.0130
o	 0.8424	 0.1510
p	 0.8459	 0.1660
q	 0.9574	 0.3080
r	 0.6828	 0.0570
s	 0.8600	 0.1060
t	 0.9286	 0.1960
u	 0.7779	 0.0630



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Chain	Atom inclusion	Q-score
v	 0.9500	 0.2600
w	 0.8877	 0.1830
x	 0.9313	 0.2950
y	 0.9290	 0.2800
z	 0.9579	 0.2160