



wwPDB EM Validation Summary Report ⓘ

Oct 22, 2024 – 02:34 AM JST

PDB ID : 8GXQ
EMDB ID : EMD-34359
Title : PIC-Mediator in complex with +1 nucleosome (T40N) in MH-binding state
Authors : Chen, X.; Wang, X.; Liu, W.; Ren, Y.; Qu, X.; Li, J.; Yin, X.; Xu, Y.
Deposited on : 2022-09-21
Resolution : 5.04 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

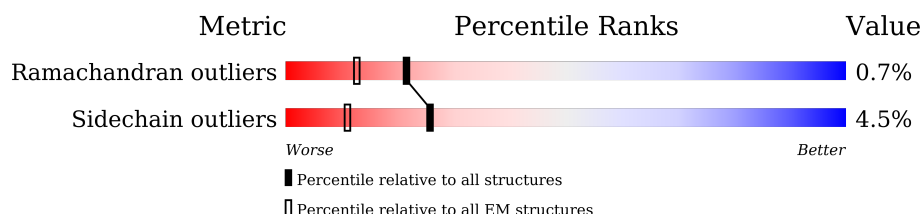
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.04 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.







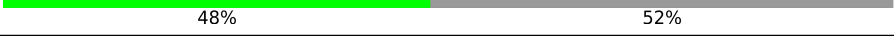


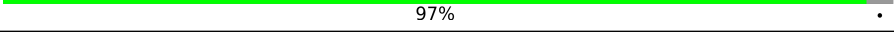
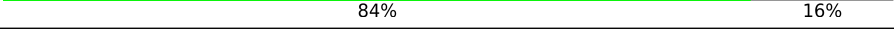
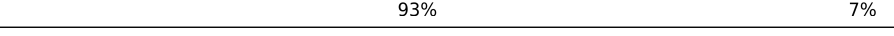
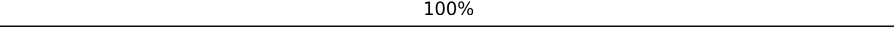
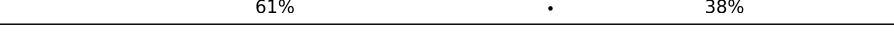
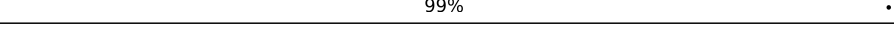
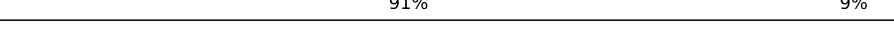
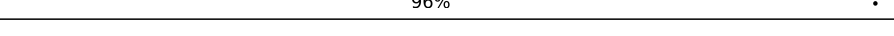
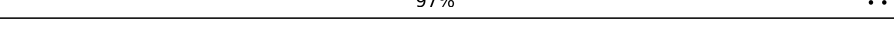
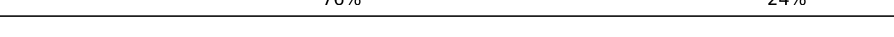

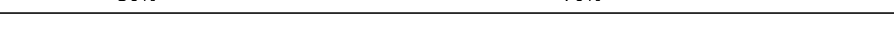






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	X	228	29% 71%
2	Y	228	29% 71%
3	BA	316	80% 20%
4	DA	1872	28% 70%
5	EA	439	42% 57%
6	FA	517	26% 73%
7	HA	760	94% 6%
8	NA	136	71% 26%
8	NE	136	74% 24%

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Mol	Chain	Length	Quality of chain
9	PA	1970	
10	DB	1199	
11	EB	291	
12	FB	249	
13	HB	548	
14	NB	103	
14	NF	103	
15	PB	1174	
16	HC	462	
17	PC	275	
18	PE	210	
19	PF	127	
20	PH	150	
21	PI	125	
22	PJ	67	
23	PK	117	
24	PL	58	
25	DP	339	
26	DQ	376	
27	DO	109	
28	Dc	929	
29	DD	1085	
29	Dd	1085	
30	DE	800	
30	De	800	



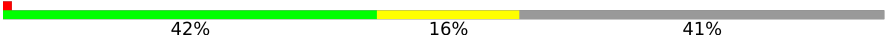







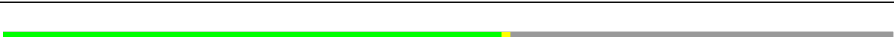


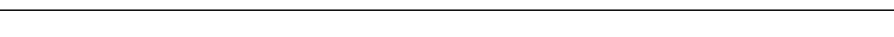
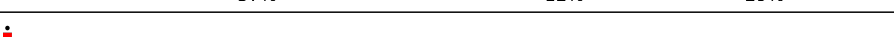
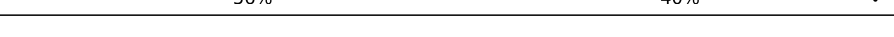



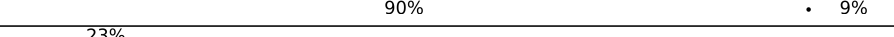
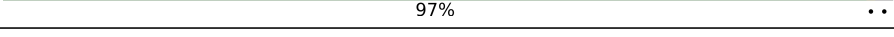




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Mol	Chain	Length	Quality of chain
31	DF	677	
31	Df	677	
32	DI	264	
32	Di	264	
33	DJ	218	
33	Dj	218	
34	Dk	211	
35	DL	161	
35	Dl	161	
36	Dm	124	
37	DG	349	
38	DH	310	
39	HD	309	
40	HE	308	
41	HG	395	
42	HH	782	
43	HF	71	
44	HI	346	
45	HJ	323	
46	PD	142	
47	PG	172	
48	g	233	
49	j	135	
50	n	1454	
51	s	244	

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Mol	Chain	Length	Quality of chain
52	u	144	
53	a	1581	
54	d	270	
55	f	246	
56	i	146	
57	m	131	
58	q	651	
59	z	600	
60	b	200	
61	c	311	
62	e	178	
63	l	178	
64	o	788	
65	h	268	
66	k	117	
67	r	208	
68	t	212	
69	v	200	
70	p	841	
71	w	1368	
72	x	989	
73	y	747	
74	NC	128	
74	NG	128	
75	ND	126	

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Mol	Chain	Length	Quality of chain
75	NH	126	<div><div></div><div>75%</div><div></div><div>25%</div></div>
76	NX	162	<div><div>8%</div><div></div><div>100%</div></div>
77	NY	162	<div><div></div><div>100%</div></div>

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 185972 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 DNA chain called DNA (228-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	67	Total	C	N	O	P	0	0
			1387	652	275	394	66		

- Molecule 2 is a DNA chain called DNA (228-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Y	67	Total	C	N	O	P	0	0
			1357	643	239	408	67		

- Molecule 3 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	252	Total	C	N	O	S	0	0
			1953	1224	346	366	17		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DA	558	Total	C	N	O	S	0	0
			4563	2913	791	832	27		

- Molecule 5 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EA	187	Total	C	N	O	S	0	0
			1535	964	275	285	11		

- Molecule 6 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FA	138	Total	C	N	O	S	0	0
			1138	719	208	208	3		

- Molecule 7 is a protein called General transcription and DNA repair factor IIIH helicase subunit XPD.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	HA	714	Total	C	N	O	S	0	0
			5751	3683	999	1040	29		

- Molecule 8 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	NA	100	Total	C	N	O		0	0
			498	298	100	100			
8	NE	103	Total	C	N	O		0	0
			511	305	103	103			

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	PA	1471	Total	C	N	O	S	0	0
			11628	7314	2064	2178	72		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 2.

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

- Molecule 11 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	EB	171	Total	C	N	O	S	0	0
			1403	895	243	261	4		

- Molecule 12 is a protein called General transcription factor IIF subunit 2.

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

- Molecule 13 is a protein called General transcription factor IIIH subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	HB	265	Total	C	N	O	S	0	0
			2167	1382	378	395	12		

- Molecule 14 is a protein called Histone H4.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	NB	80	Total	C	N	O	0	0
			391	231	80	80		
14	NF	86	Total	C	N	O	0	0
			421	249	86	86		

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	PB	1136	Total	C	N	O	S	0	0
			9076	5739	1597	1676	64		

- Molecule 16 is a protein called General transcription factor IIH subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	HC	390	Total	C	N	O	S	0	0
			3158	2050	545	551	12		

- Molecule 17 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 18 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	PE	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 19 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	PF	79	Total	C	N	O	S	0	0
			636	406	108	117	5		

- Molecule 20 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 21 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	PI	114	Total	C	N	O	S	0	0
			928	571	166	180	11		

- Molecule 22 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 23 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	PK	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 24 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	PL	44	Total	C	N	O	S	0	0
			373	231	72	64	6		

- Molecule 25 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	DP	179	Total	C	N	O	S	0	0
			1422	923	251	241	7		

- Molecule 26 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	DQ	113	Total	C	N	O	S	0	0
			930	585	152	189	4		

- Molecule 27 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	DO	99	Total	C	N	O	S	0	0
			806	510	142	151	3		

- Molecule 28 is a protein called Transcription initiation factor TFIID subunit 3.

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

- Molecule 29 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Dd	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		
29	DD	159	Total	C	N	O	S	0	0
			1330	830	248	249	3		

- Molecule 30 is a protein called Transcription initiation factor TFIID subunit 5.

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

- Molecule 31 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Df	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		
31	DF	408	Total	C	N	O	S	0	0
			3109	1970	542	579	18		

- Molecule 32 is a protein called Transcription initiation factor TFIID subunit 9.

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

- Molecule 33 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Dj	95	Total	C	N	O	S	0	0
			759	488	124	143	4		
33	DJ	90	Total	C	N	O	S	0	0
			720	466	115	135	4		

- Molecule 34 is a protein called Transcription initiation factor TFIID subunit 11.

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

- Molecule 35 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Dl	107	Total	C	N	O	S	0	0
			876	547	158	166	5		
35	DL	74	Total	C	N	O	S	0	0
			605	379	105	118	3		

- Molecule 36 is a protein called Transcription initiation factor TFIID subunit 13.

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

- Molecule 37 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DG	145	Total	C	N	O	S	0	0
			1180	748	217	211	4		

- Molecule 38 is a protein called Transcription initiation factor TFIID subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DH	209	Total	C	N	O	S	0	0
			1633	1034	283	311	5		

- Molecule 39 is a protein called CDK-activating kinase assembly factor MAT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	HD	306	Total	C	N	O	S	0	0
			2400	1498	424	465	13		

- Molecule 40 is a protein called General transcription factor IIH subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	HE	263	Total	C	N	O	S	0	0
			2066	1323	344	380	19		

- Molecule 41 is a protein called General transcription factor IIH subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	HG	347	Total	C	N	O	S	0	0
			2732	1726	471	508	27		

- Molecule 42 is a protein called General transcription and DNA repair factor IIH helicase subunit XPB.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	HH	605	Total	C	N	O	S	0	0
			4890	3127	848	885	30		

- Molecule 43 is a protein called General transcription factor IIH subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	HF	66	Total	C	N	O	S	0	0
			523	337	83	100	3		

- Molecule 44 is a protein called Cyclin-dependent kinase 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	HI	299	Total	C	N	O	S	0	0
			2374	1532	405	426	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
HI	41	ALA	LYS	engineered mutation	UNP P50613

- Molecule 45 is a protein called Cyclin-H.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	HJ	287	Total	C	N	O	S	0	0
			2307	1477	398	417	15		

- Molecule 46 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	PD	128	Total	C	N	O	S	0	0
			1050	656	178	212	4		

- Molecule 47 is a protein called DNA-directed RNA polymerase II subunit RPB7.

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

- Molecule 48 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	g	106	Total	C	N	O	S	0	0
			898	569	166	157	6		

- Molecule 49 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	j	122	Total	C	N	O	S	0	0
			840	527	151	159	3		

- Molecule 50 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	n	1015	Total	C	N	O	S	0	0
			7751	4941	1363	1405	42		

- Molecule 51 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	93	Total	C	N	O	S	0	0
			723	463	121	135	4		

- Molecule 52 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	117	Total	C	N	O	S	0	0
			886	552	146	184	4		

- Molecule 53 is a protein called Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	a	438	Total	C	N	O	S	0	0
			3430	2190	584	632	24		

- Molecule 54 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	d	158	Total	C	N	O	S	0	0
			1268	791	228	243	6		

- Molecule 55 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	f	167	Total	C	N	O	S	0	0
			1365	882	235	243	5		

- Molecule 56 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	i	73	Total	C	N	O	S	0	0
			605	382	107	110	6		

- Molecule 57 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	m	112	Total	C	N	O	S	0	0
			983	641	172	165	5		

- Molecule 58 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	q	555	Total	C	N	O	S	0	0
			4373	2765	783	805	20		

- Molecule 59 is a protein called Mediator of RNA polymerase II transcription subunit 26.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	97	Total	C	N	O	S	0	0
			765	472	136	154	3		

- Molecule 60 is a protein called Mediator of RNA polymerase II transcription subunit 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	b	115	Total	C	N	O	S	0	0
			899	563	155	172	9		

- Molecule 61 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c	263	Total	C	N	O	S	0	0
			2131	1356	379	385	11		

- Molecule 62 is a protein called Mediator of RNA polymerase II transcription subunit 28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	e	102	Total	C	N	O	S	0	0
			832	520	146	163	3		

- Molecule 63 is a protein called Mediator of RNA polymerase II transcription subunit 30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	l	126	Total	C	N	O	S	0	0
			1040	649	191	193	7		

- Molecule 64 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	o	156	Total	C	N	O	S	0	0
			1221	780	212	222	7		

- Molecule 65 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	h	190	Total	C	N	O	S	0	0
			1465	913	259	289	4		

- Molecule 66 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	k	112	Total	C	N	O	S	0	0
			879	537	163	175	4		

- Molecule 67 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	r	192	Total	C	N	O	S	0	0
			1535	973	271	276	15		

- Molecule 68 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	t	193	Total	C	N	O	S	0	0
			1499	955	247	280	17		

- Molecule 69 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	v	134	Total	C	N	O	S	0	0
			1083	668	185	226	4		

- Molecule 70 is a protein called Isoform 2 of Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	p	766	Total	C	N	O	S	0	0
			5983	3816	1026	1092	49		

- Molecule 71 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	w	1334	Total	C	N	O	S	0	0
			10774	6967	1827	1909	71		

- Molecule 72 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	x	897	Total	C	N	O	S	0	0
			7061	4524	1190	1293	54		

- Molecule 73 is a protein called Mediator of RNA polymerase II transcription subunit 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	y	210	Total	C	N	O	S	0	0
			1605	1030	264	302	9		

- Molecule 74 is a protein called HISTONE H2A.Z.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	NG	107	Total	C	N	O	0	0
			524	310	107	107		
74	NC	103	Total	C	N	O	0	0
			506	300	103	103		

- Molecule 75 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	ND	95	Total	C	N	O	0	0
			471	281	95	95		
75	NH	95	Total	C	N	O	0	0
			471	281	95	95		

- Molecule 76 is a DNA chain called DNA (162-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
76	NX	162	Total	C	N	O	P	0	0
			3078	1458	486	972	162		

- Molecule 77 is a DNA chain called DNA (162-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
77	NY	162	Total	C	N	O	P	0	0
			3561	1620	810	970	161		

- Molecule 78 is ZINC ION (three-letter code: ZN) (formula: Zn).

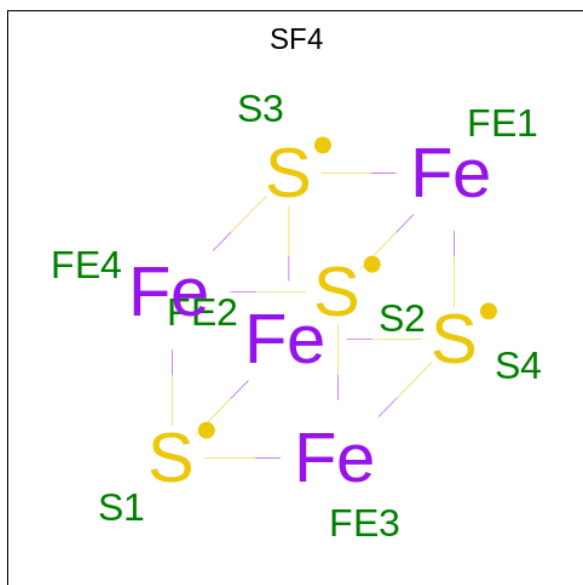
Mol	Chain	Residues	Atoms		AltConf
78	BA	1	Total	Zn	0
			1	1	
78	EA	1	Total	Zn	0
			1	1	
78	PA	2	Total	Zn	0
			2	2	
78	PB	1	Total	Zn	0
			1	1	
78	PC	1	Total	Zn	0
			1	1	
78	PI	2	Total	Zn	0
			2	2	
78	PJ	1	Total	Zn	0
			1	1	
78	PL	1	Total	Zn	0
			1	1	
78	HD	2	Total	Zn	0
			2	2	
78	HE	2	Total	Zn	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
78	HG	3	Total	Zn	0
			3	3	
78	c	1	Total	Zn	0
			1	1	
78	p	1	Total	Zn	0
			1	1	

- Molecule 79 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
79	HA	1	Total	Fe	S	0
			8	4	4	

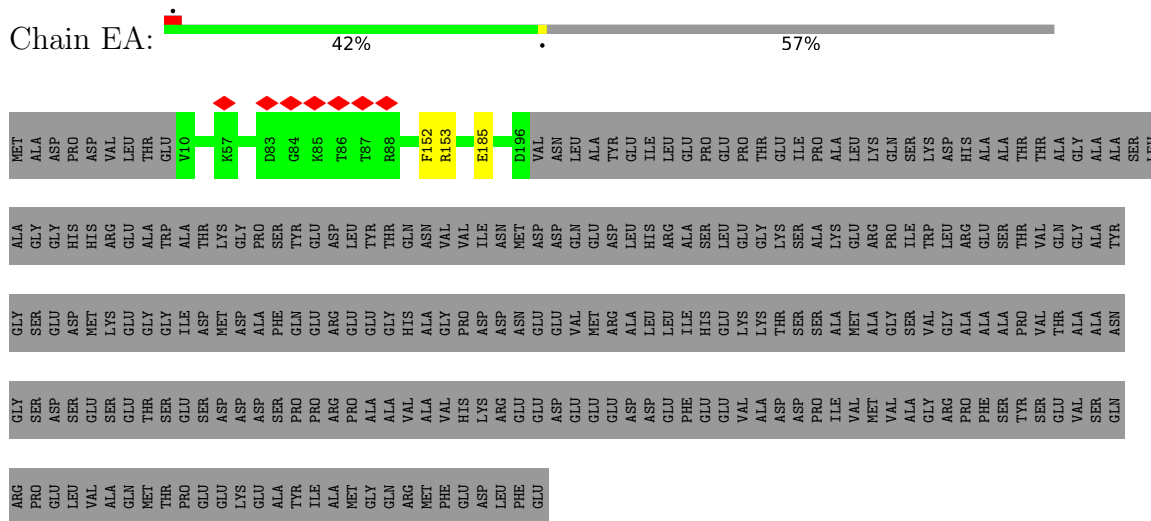
- Molecule 80 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	PA	1	Total	Mg	0
			1	1	

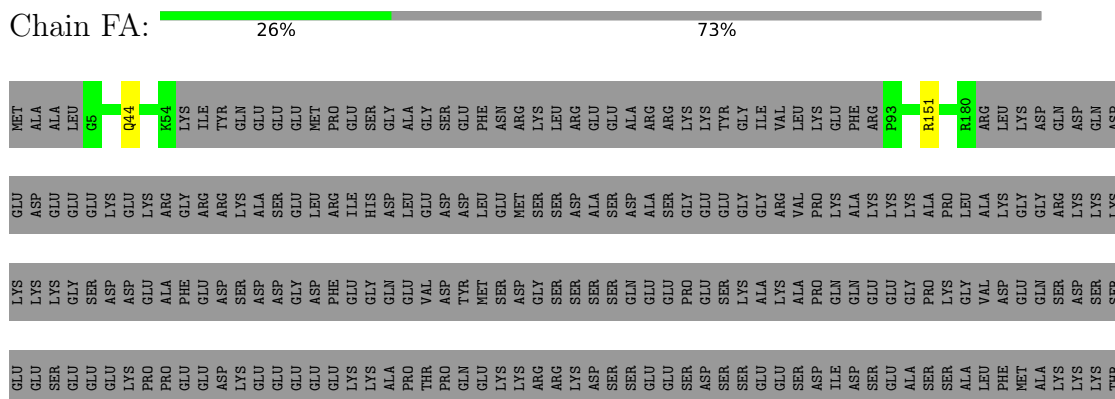


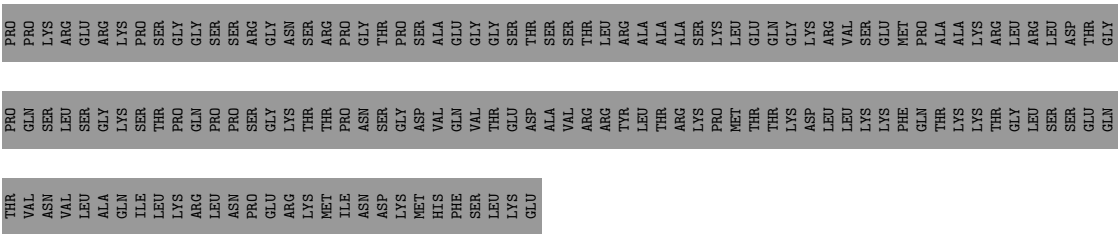
[illegible]

- Molecule 5: General transcription factor IIE subunit 1

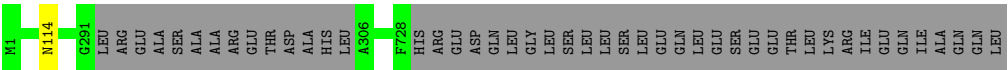


- Molecule 6: General transcription factor IIF subunit 1

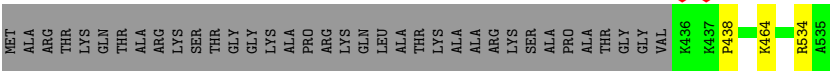




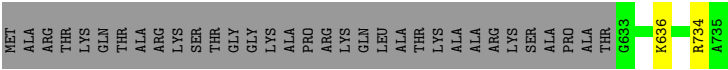
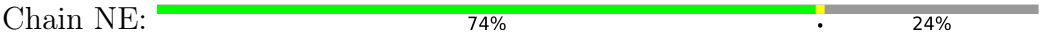
- Molecule 7: General transcription and DNA repair factor IIH helicase subunit XPD



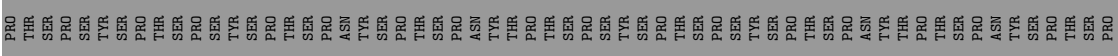
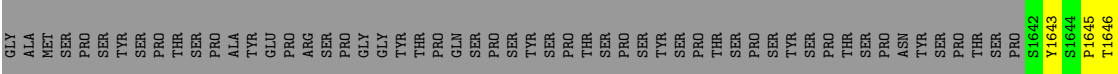
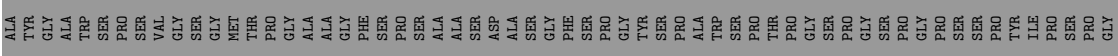
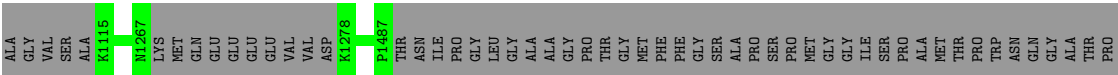
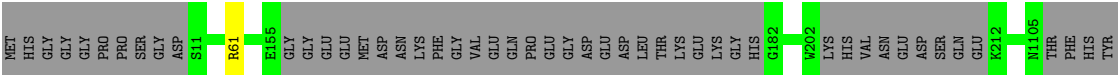
- Molecule 8: Histone H3

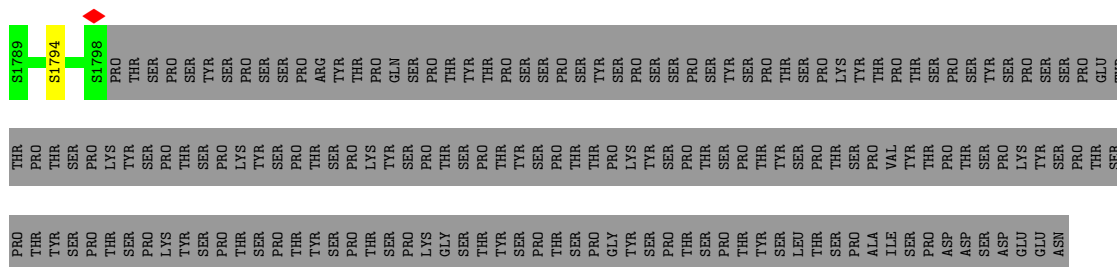


- Molecule 8: Histone H3

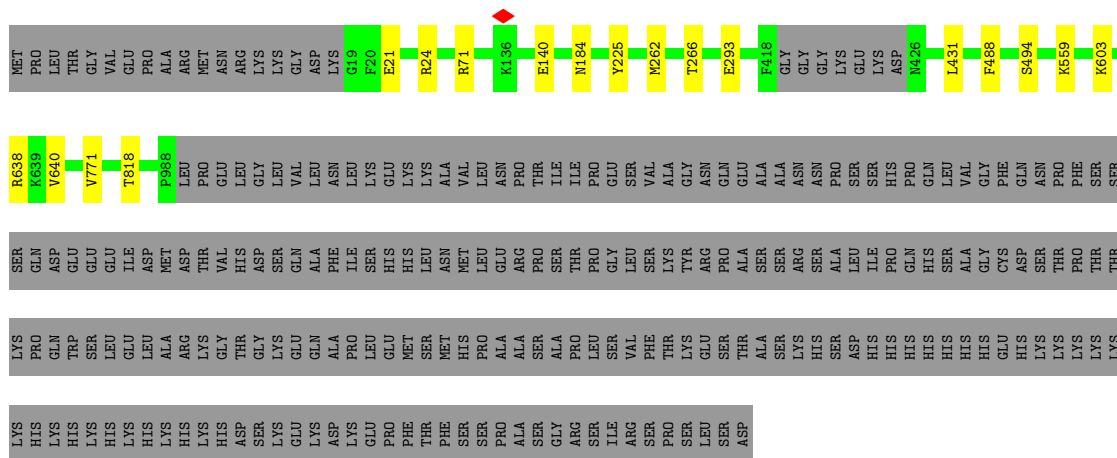


- Molecule 9: DNA-directed RNA polymerase subunit

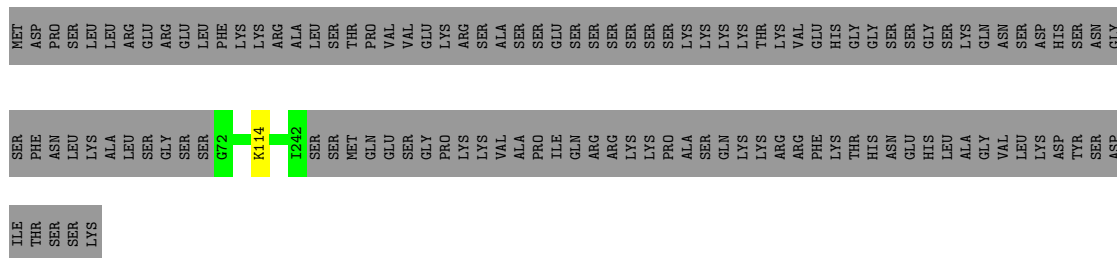




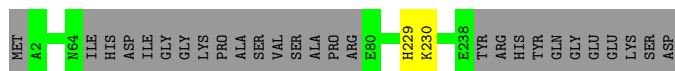
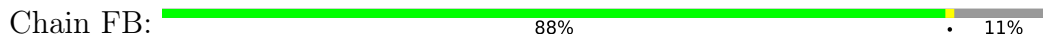
- Molecule 10: Transcription initiation factor TFIID subunit 2



- Molecule 11: Transcription initiation factor IIE subunit beta



- Molecule 12: General transcription factor IIF subunit 2

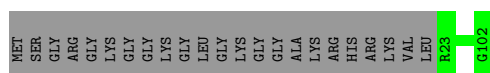
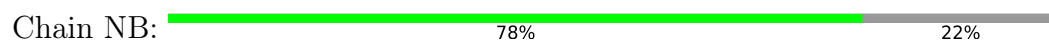


- Molecule 13: General transcription factor IIH subunit 1

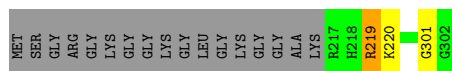
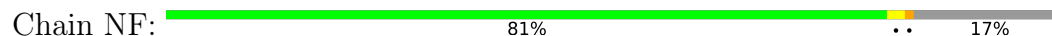




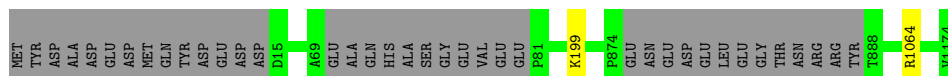
- Molecule 14: Histone H4



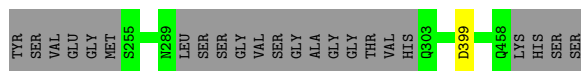
- Molecule 14: Histone H4



- Molecule 15: DNA-directed RNA polymerase subunit beta

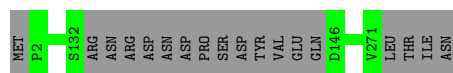


- Molecule 16: General transcription factor IIH subunit 4



- Molecule 17: DNA-directed RNA polymerase II subunit RPB3

Chain PC:  93% 7%



- Molecule 18: DNA-directed RNA polymerase II subunit E

Chain PE:  100%



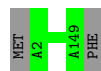
- Molecule 19: DNA-directed RNA polymerase II subunit F

Chain PF:  61% . 38%



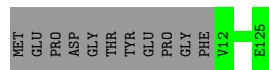
- Molecule 20: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain PH:  99% .



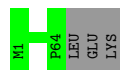
- Molecule 21: DNA-directed RNA polymerase II subunit RPB9

Chain PI:  91% 9%



- Molecule 22: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain PJ:  96% .



- Molecule 23: RNA_pol_L_2 domain-containing protein

Chain PK:  97% ..



- Molecule 24: RPB12

MET
ASP
THR
GLN
LYS
ASP
VAL
GLN
PRO
PRO
LYS
GLN
GLN
PRO
M15
R58

- Chain DP: 53% 47%

[illegible]

- Chain DQ:  30% 70%

[illegible]

SER
GLU
GLU
ASP
GLU
ASP
GLU
GLU
GLU
ASP
TYR
ASP
ASP
ASP
GLU
GLU
GLU
ASP
LYS
LYS
GLY
GLY
ALA
GLU
ASP
G307
Q308
V309
W376

- Chain DO: 89% . 9%

M1 R51 R82 D99 GLY LYS ASN THR GLY SER ASN THR THR GLU

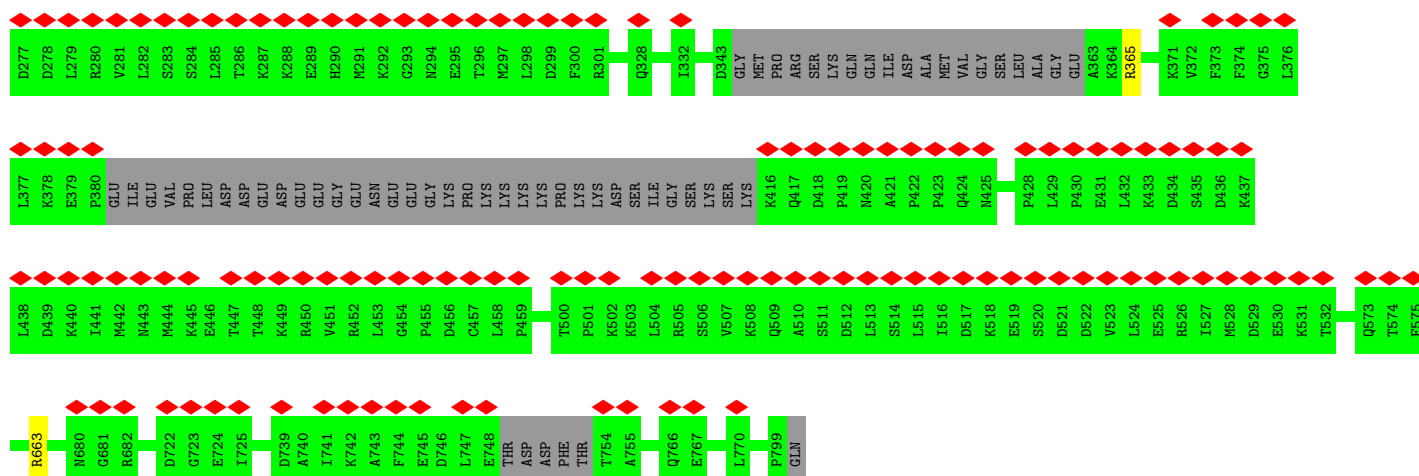
- Chain Dc:  5% 13% 86%

MI	R11	V12	S13	V14	A15	Q16	I17	C18	Q19	A20	L21	G22	W23	D24	S25	V26	Q27	L28	S29	A30	C31	H32	H85	N86	I87	E88	P89	F90	T91	F92	P93	H94	Q95	V106	P110	Q111	P112	G113	S114	K115	D116	A117	E118	E119	R120	K121	E122	P125	D126	Y127	LEU	PRO	PRO
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[illegible]

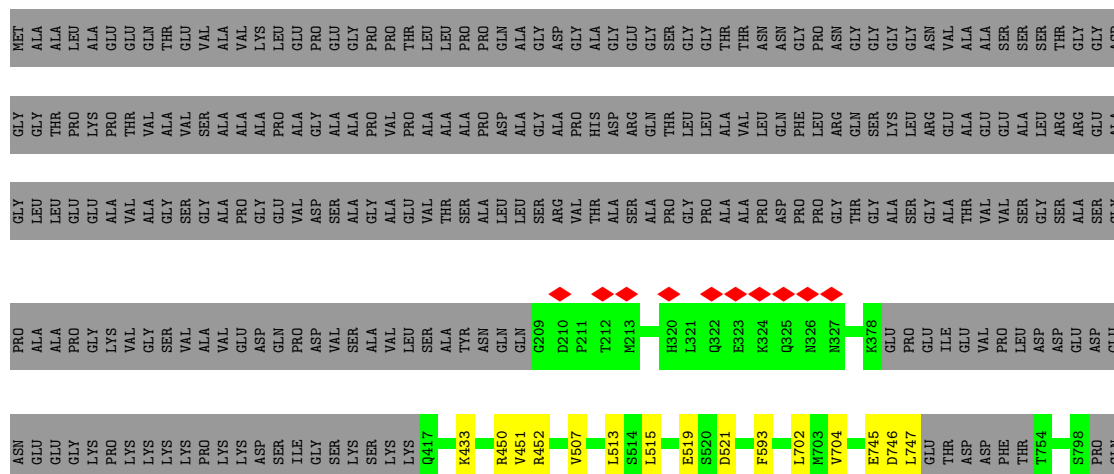
- Molecule 29: Transcription initiation factor TFIID subunit 4

[illegible]



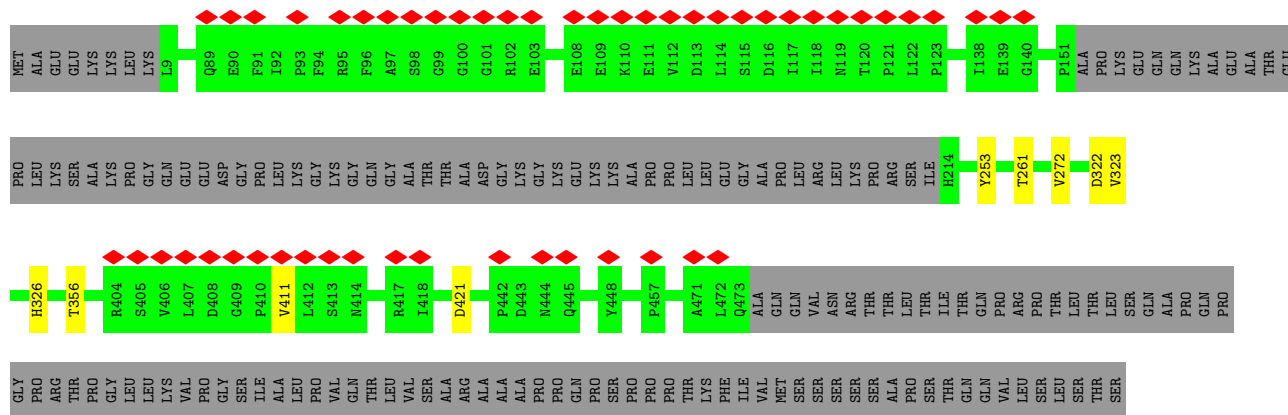
• Molecule 30: Transcription initiation factor TFIID subunit 5

Chain DE: 66% 32%

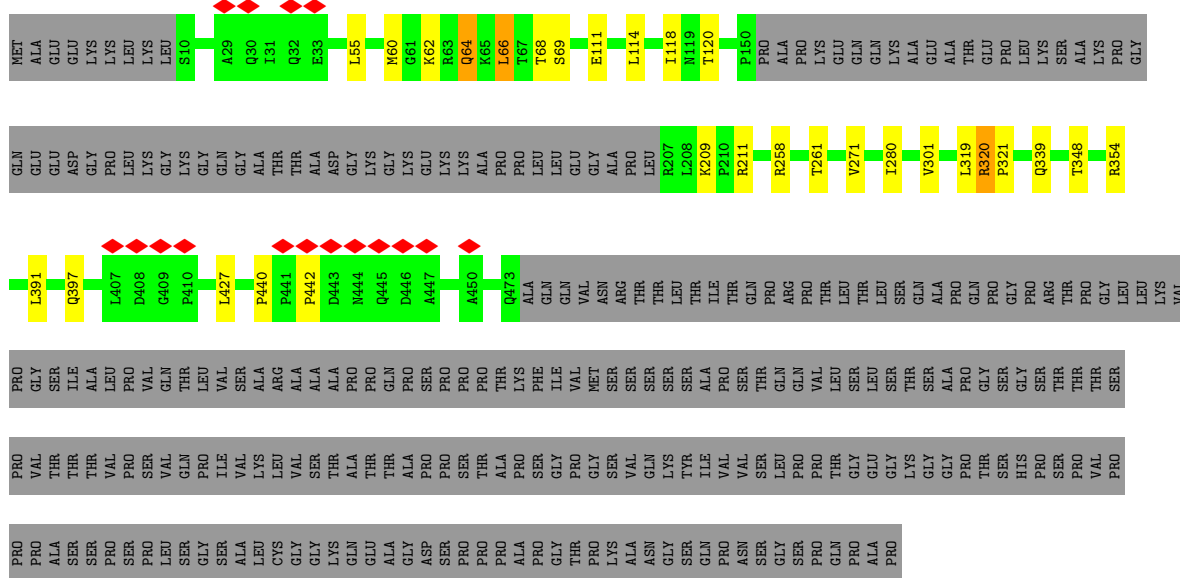


• Molecule 31: Transcription initiation factor TFIID subunit 6

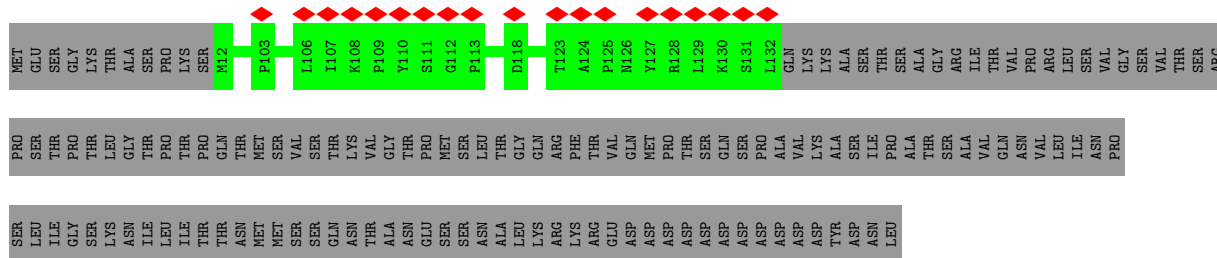
Chain Df: 8% 58% 40%



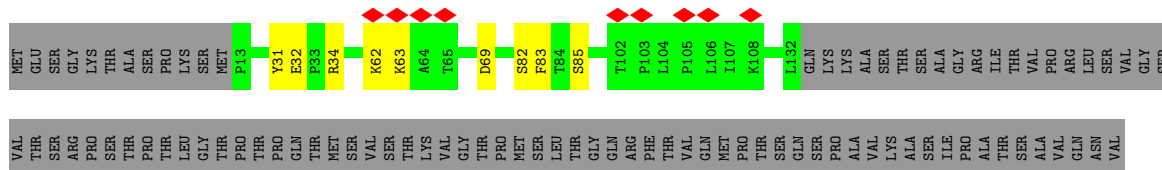
- Molecule 31: Transcription initiation factor TFIID subunit 6

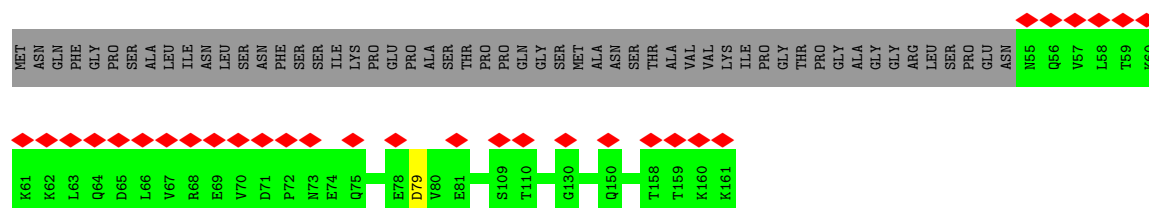


- Molecule 32: Transcription initiation factor TFIID subunit 9

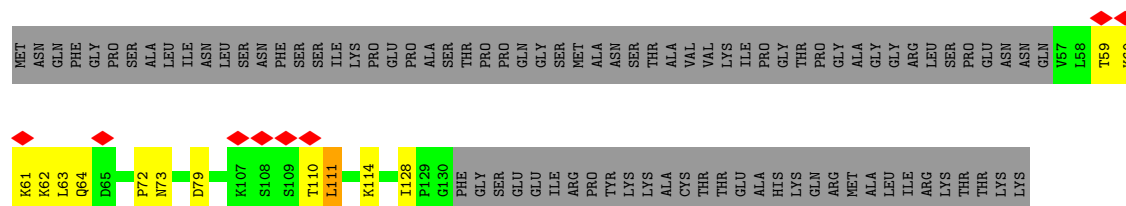
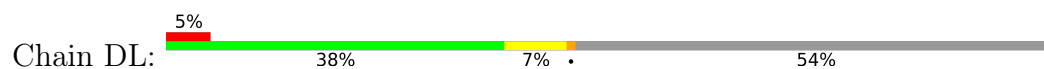


- Molecule 32: Transcription initiation factor TFIID subunit 9

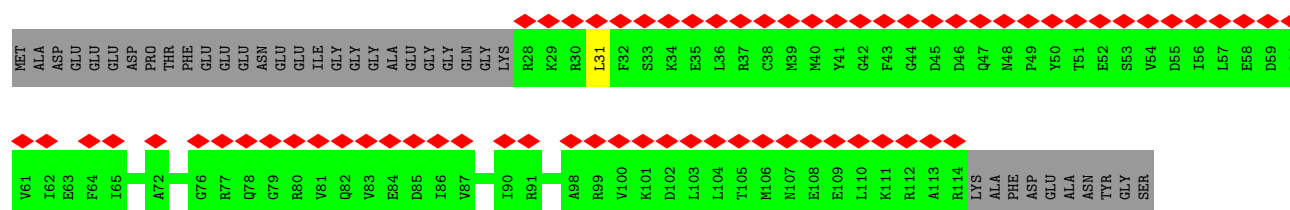
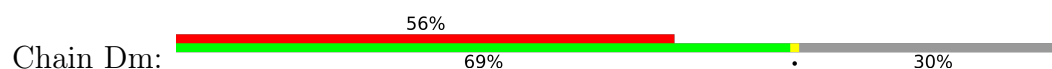




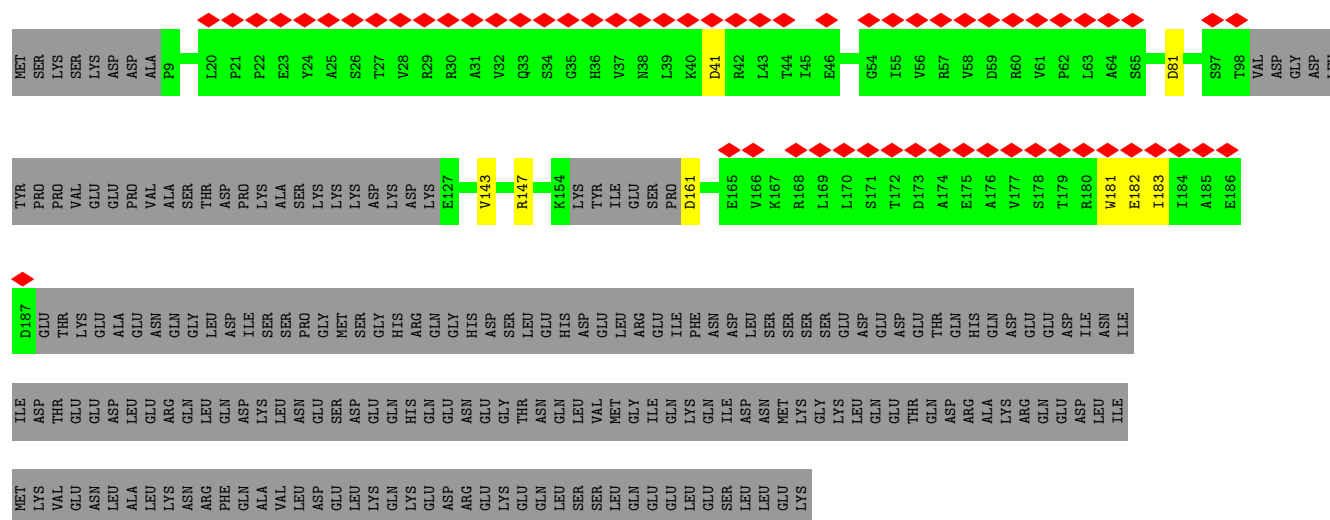
- Molecule 35: Transcription initiation factor TFIID subunit 12



- Molecule 36: Transcription initiation factor TFIID subunit 13



- Molecule 37: Transcription initiation factor TFIID subunit 7



- Molecule 38: Transcription initiation factor TFIID subunit 8

- Molecule 39: CDK-activating kinase assembly factor MAT1

M1	K10	T11	H28	R41	R54	K55	S56	Q126	K214	P217	P220	T225	L233	S234	P237	E242	L251	Q252	L253	E254	L263	E264	M265	R268	L272	V275	R276	Y287	T288	S289	C293	H294	R295	L304	F305	W306	GLN	PRO
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- Molecule 40: General transcription factor IIH subunit 3

NET	VAL	SER	ASP	GLU	GLU	L8	S62	H63	I64	F72	GLY	GLY	LYS	ASN	ARG	LEU	GLY	PHE	PHE	GLY	ASP	PRO	GLY	ASN	PRO	PRO	GLU	PHE	ASN	PRO	SER	G95	Z222	C257	H258	Z252	LEU	PRO	PRO	VAL	LEU	LYS	ALA	LYS	LYS	LYS	LYS	LEU	VAL	SER	ALA
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- Molecule 41: General transcription factor IIH subunit 2

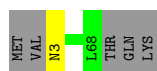
MET	ASP	GLU	GLU	GLU	PRO	GLY	R7	E24	ASP	GLU	GLY	SER	SER	LEU	LYS	ALA	THR	ILE	GLY	ASP	ILE	LEU	PHE	LYS	LYS	LYS	ARG	LYS	ARG	VAL	PHE	PHE	GLY	HIS	HIS	GLY	GLN	V63	A274	HIS	LEU	ASP	GLY	ASN	THR	E281	R343	H367	LYS	ILE	PRO	ALA	PRO	SER	GLY	VAL
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- Molecule 42: General transcription and DNA repair factor IIH helicase subunit XPB

[illegible]

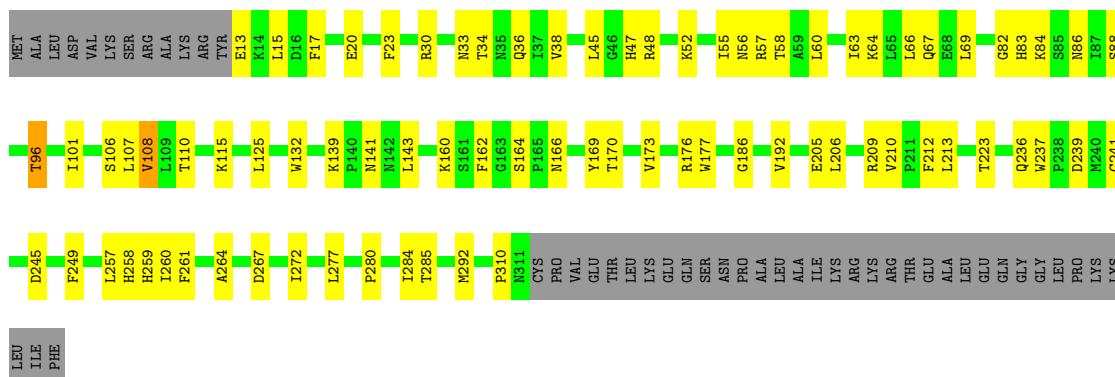
- Molecule 43: General transcription factor IIH subunit 5

Chain HF:  92% • 7%



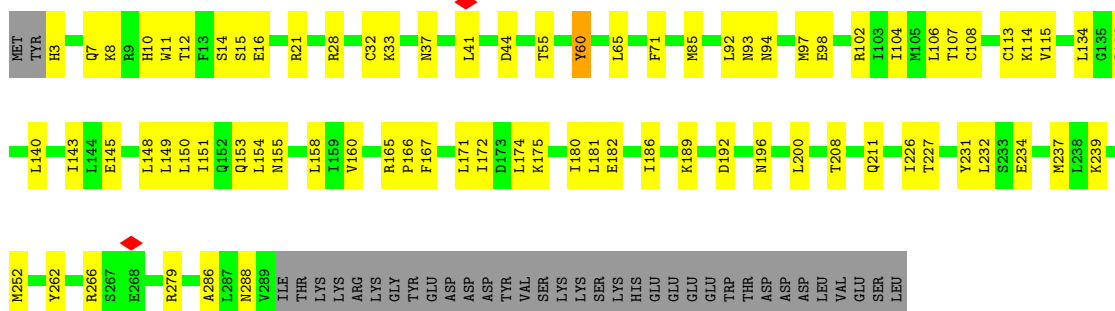
- Molecule 44: Cyclin-dependent kinase 7

Chain HI:  64% 22% • 14%



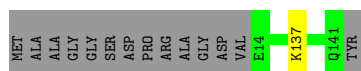
- Molecule 45: Cyclin-H

Chain HJ:  65% 24% 11%



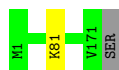
- Molecule 46: DNA-directed RNA polymerase II subunit RPB4

Chain PD:  89% • 10%



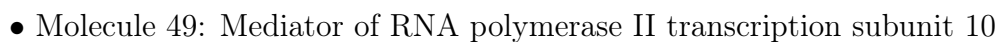
- Molecule 47: DNA-directed RNA polymerase II subunit RPB7

Chain PG:  99% ••



- Molecule 48: Mediator of RNA polymerase II transcription subunit 7

Response	Percentage
Yes	41%
No	1%
Don't know	55%



88% 10%

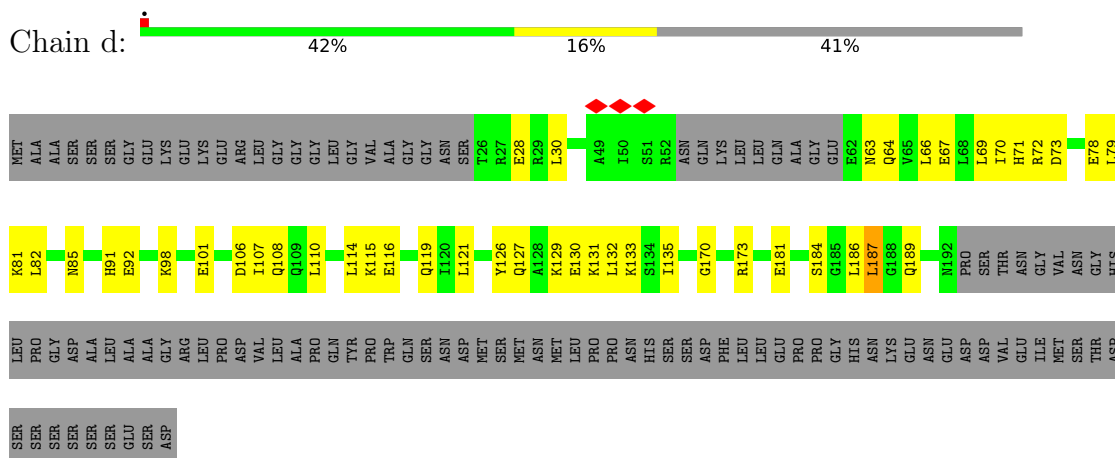


Response	Percentage
Yes	67%
No	2%
Don't know	30%

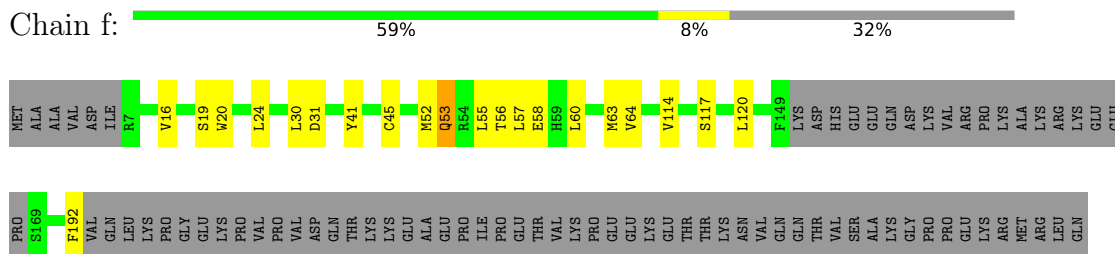


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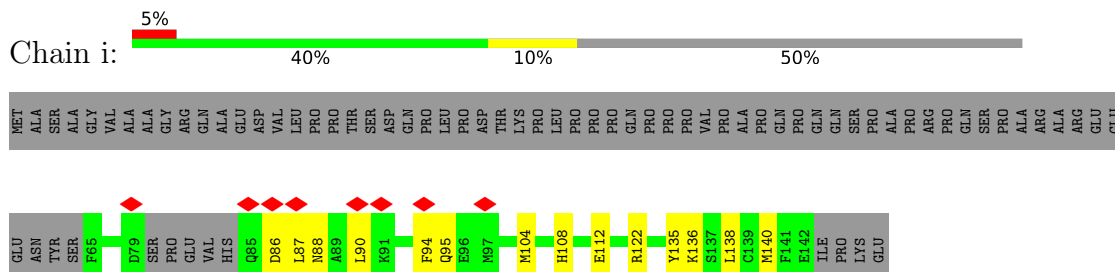
- Molecule 54: Mediator of RNA polymerase II transcription subunit 4



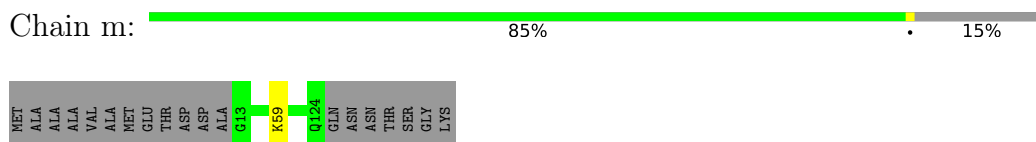
- Molecule 55: Mediator of RNA polymerase II transcription subunit 6



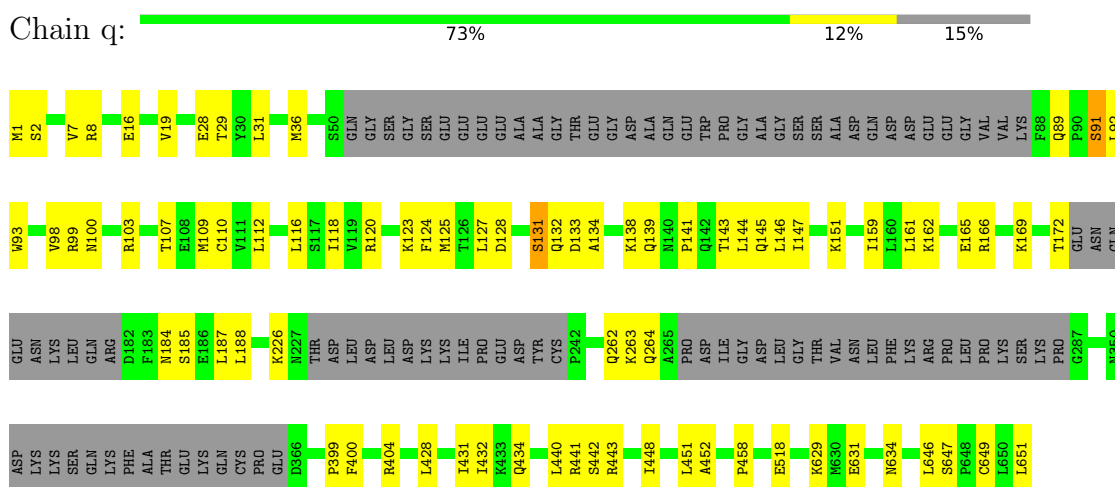
- Molecule 56: Mediator of RNA polymerase II transcription subunit 9



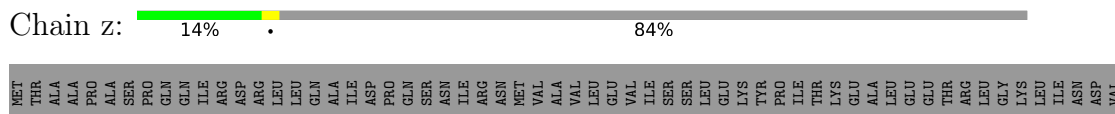
- Molecule 57: Mediator of RNA polymerase II transcription subunit 31

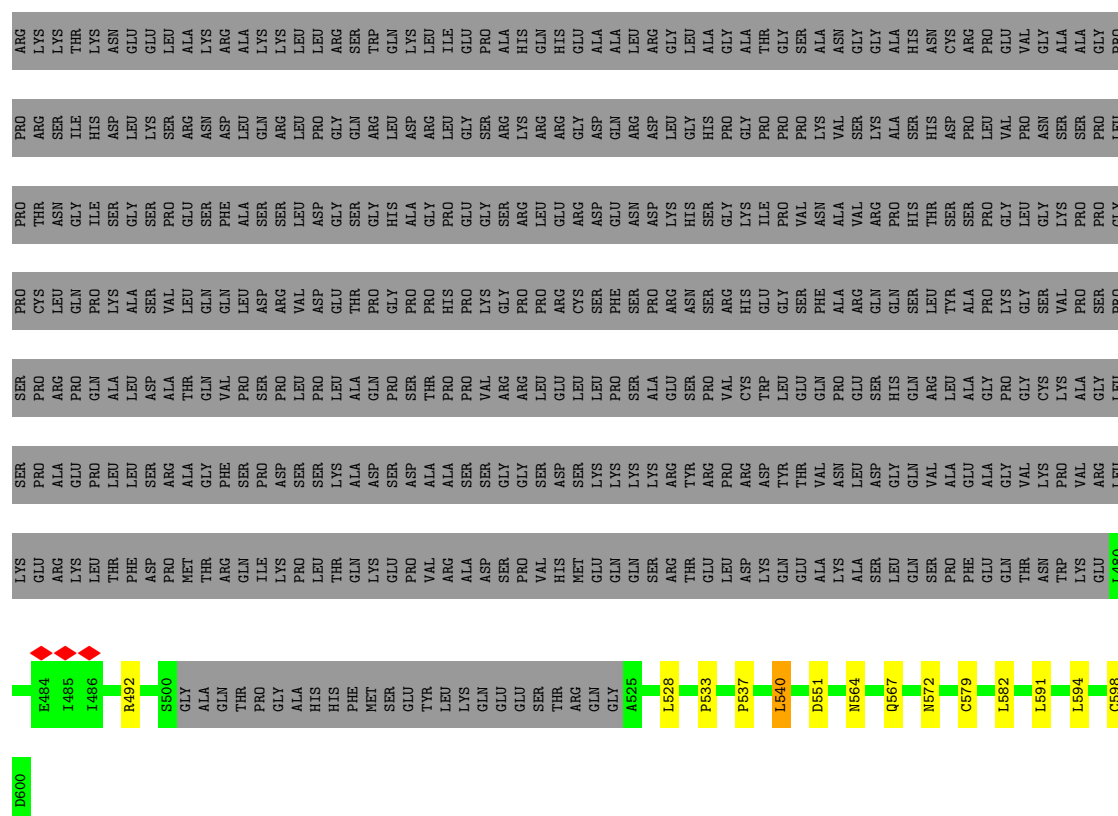


- Molecule 58: Mediator of RNA polymerase II transcription subunit 17



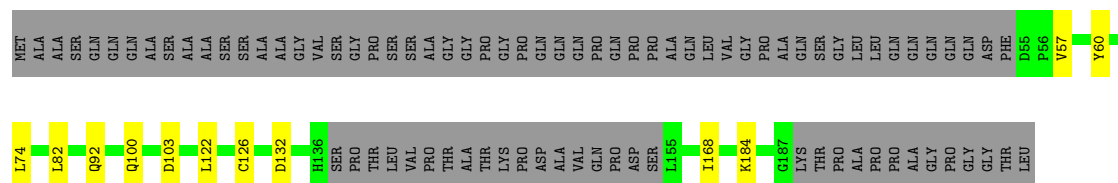
- Molecule 59: Mediator of RNA polymerase II transcription subunit 26





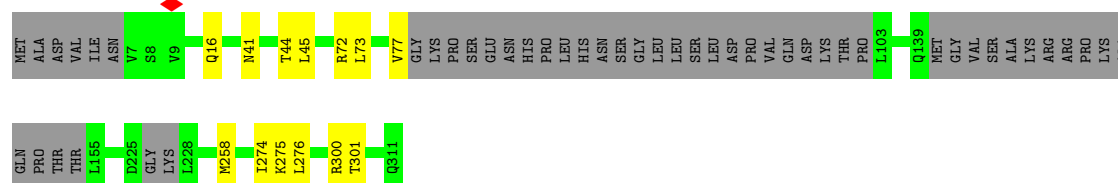
- Molecule 60: Mediator of RNA polymerase II transcription subunit 29

Chain b: 52% 6% 42%



- Molecule 61: Mediator of RNA polymerase II transcription subunit 27

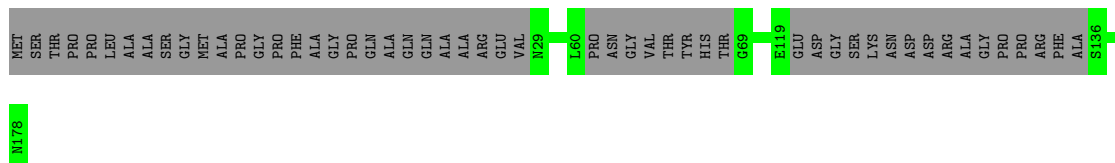
Chain c: 80% 15%



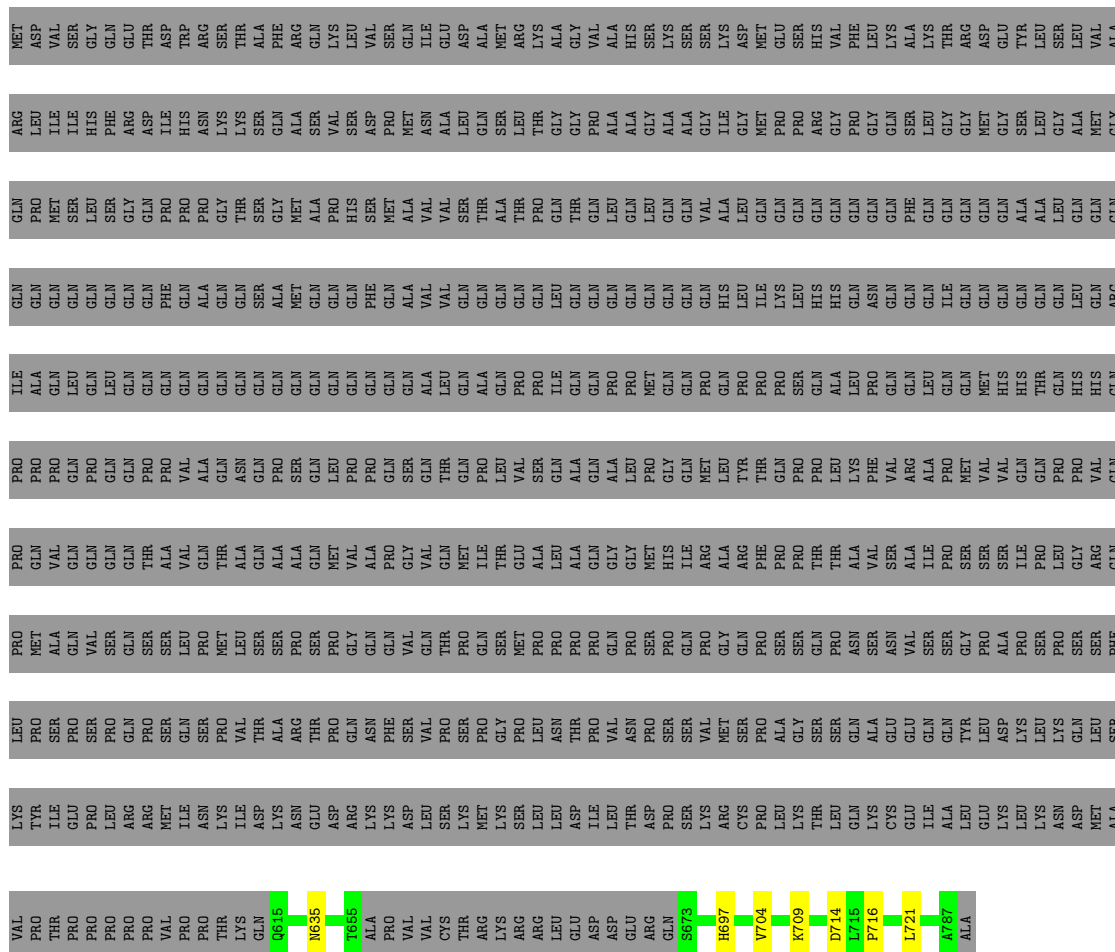
- Molecule 62: Mediator of RNA polymerase II transcription subunit 28

Chain e: 56% 43%

- Molecule 63: Mediator of RNA polymerase II transcription subunit 30

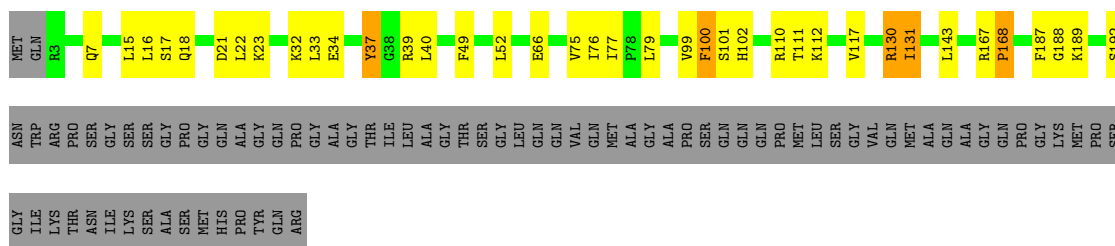


- Molecule 64: Mediator of RNA polymerase II transcription subunit 15

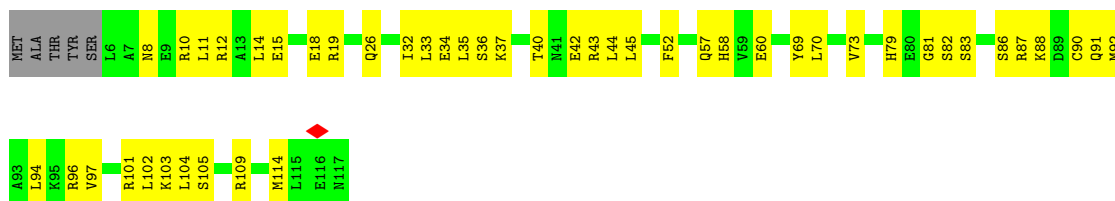


- Molecule 65: Isoform 2 of Mediator of RNA polymerase II transcription subunit 8

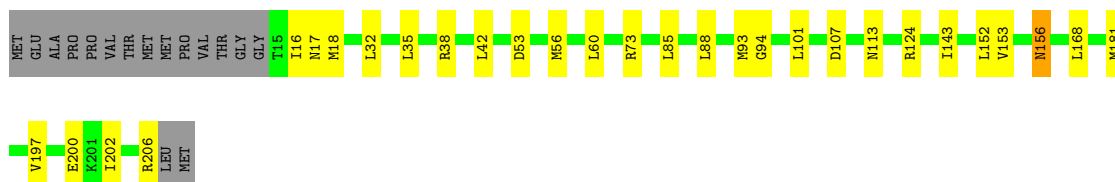
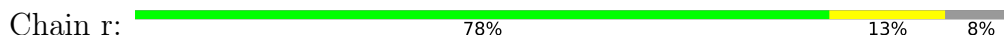




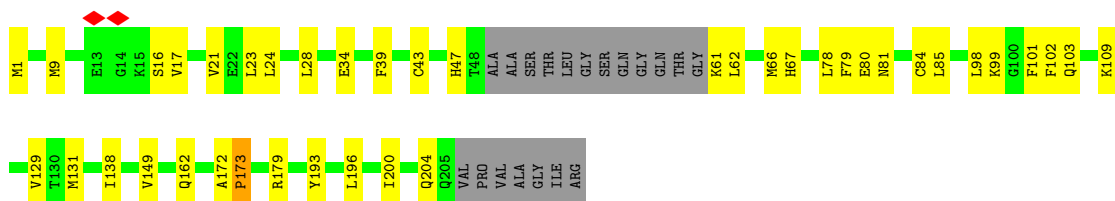
- Molecule 66: Mediator of RNA polymerase II transcription subunit 11



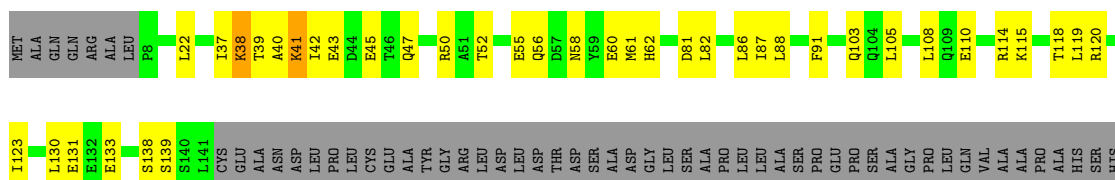
- Molecule 67: Mediator of RNA polymerase II transcription subunit 18



- Molecule 68: Mediator of RNA polymerase II transcription subunit 20




- Molecule 69: Mediator of RNA polymerase II transcription subunit 22



ALA
GLY
GLY
PRO
GLY
PRO
PRO
THR
GLU
HIS
ALA

- Molecule 70: Isoform 2 of Mediator of RNA polymerase II transcription subunit 16

Chain p:  90% 9%

MET CYS ASP LEU ARG ARG PRO PRO THR GLU HIS ALA
GLY GLY M12 M13 Y162 L170 D289 L295 E314
GLY LEU PRO VAL ASN ASN ILE PHE PHE GLN ILE ILE SER PRO VAL VAL GLY ASP LYS GLN PRO T335
T401 S408 ALA ALA PRO PRO ARG VAL ASP GLU PRO ALA MET LYS

ARG PRO ARG THR ALA GLY PRO ALA
V429 L443 L564 R634 GLN GLY SER LEU L639 C699 E703 G704 P705 D710 P727 P756
THR LEU PRO PRO SER ALA ALA THR LEU LEU ASP LEU LEU ARG
P841

- Molecule 71: Mediator of RNA polymerase II transcription subunit 23

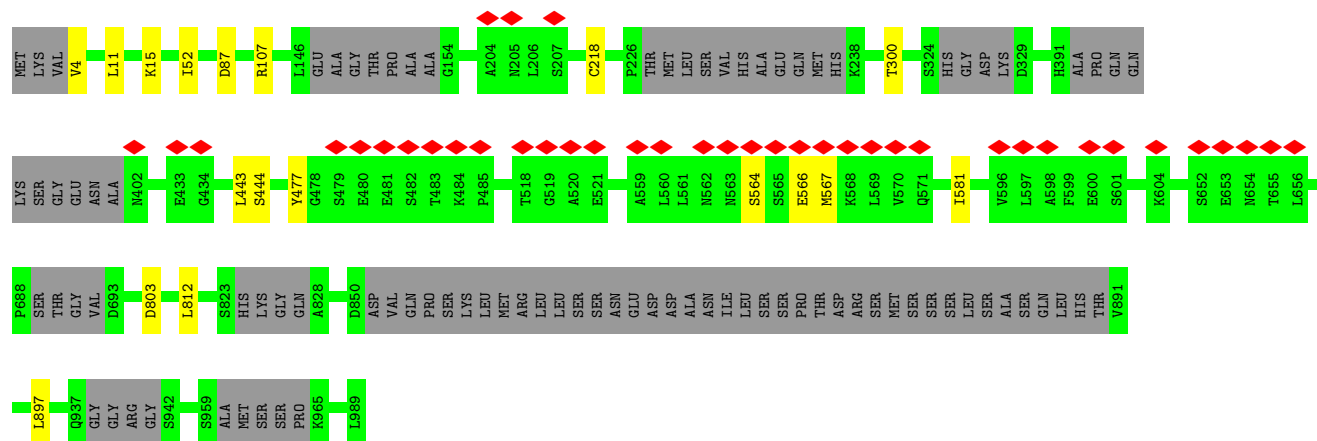
Chain w:  23% 97%

M1 E2 T3 Q4 S7 E11 F22 D32 T38 S39 G42 A43 F44 R45 Q46 G49 G50 L51 S52 Q53 E54 S55 H56 A84 M85 A86 V87 E88 T89 G90 L91 P94 R95 L96 V97 C98 E99 I102 N103 S104 D105 V122 R123 K124 I125 I126 G127 G128 V129
D130 Y131 K132 G133 V134 R135 D136 L137 L138 K139 V140 T141 L142 E143 K144 T145 L146 T147 A163 V166 I167 A168 Y169 I170 L171 E172 E173 N174 A175 C176 L177 L178 P179 A180 Y181 F182 A183 V184 T185 E186 I187 R188 K189 L190 Y191 P192 E193 G194 K195 L196 P197 V205 F208 V209 T211
F212 D244 P245 A246 T247 L255 Q292 H293 K294 Q295 R296 C297 P298 M425 Q460 R463 N464 R465 S466 G503 I504 M505 R506 T666 R667 F668 L669 S670 D671 P672 K673 D705 S706 I707 Q708 G709 T710 W711 C712 D713 W714 I715 L716 Q717 T718 T719 S720 S721 F722 T723 P724
H725 M726 W727 A728 S729 G737 P738 L739 Q740 A741 F742 F743 K744 W746 M747 V748 P749 Q750 E751 S752 R753 F754 M755 L756 K757 K758 M759 V760 E761 F762 E763 Y764 R765 K766 W767 K768 S769 S771 N772 N773 N774 D775 L776 T777 H779 W782 Q783 G784 S785 P786 L792 K795 M796
L797 L798 E799 T800 D801 H802 L803 H804 Q805 R809 S835 T836 S837 A838 G839 G840 Q841 Q842 L843 N844 K845 C846 T847 E848 I849 D852 K856 Y857 S873 H874 E875 G876 H877 E878 K892 P893 N894 D895 N898 S901 D902 F903 V904 K905 E906 H923 K926 K927
G936 L937 A938 E939 Q940 V941 D942 P943 P944 V945 Q946 I947 Q948 K1050 N1054 A1055 R1056 E1057 E1058 N1059 A1116 T1194 A1195 C1196 M1203 Q1261 T1264 R1265 L1279 N1280 V1281 D1282 Q1283 C1284 S1285 S1286 H1287 L1288 M1291 D1292 C1295 D1296 F1297 L1298 Y1299 K1302 Y1303 G1307
D1308 S1309 V1310 K1311 E1312 Q1313 V1314 E1315 I1316 I1317 I1318 C1319 M1320 L1321 L1322 K1323 A1324 L1325 K1326 L1327 L1328 L1329 A1330 F1331 I1332 T1333 H1334 ILE SER LYS MET GLU PRO PRO ALA ALA VAL PRO PRO GLN ALA MET ASN SER GLY SER PRO PRO PRO GLN SER VAL VAL VAL SER LEU VAL THR

GLN

- Molecule 72: Mediator of RNA polymerase II transcription subunit 24

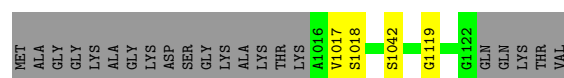
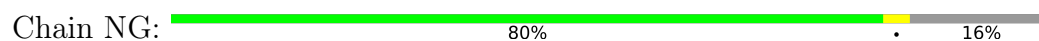
Chain x:  89% 9%




• Molecule 73: Mediator of RNA polymerase II transcription subunit 25

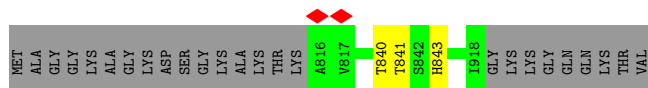


• Molecule 74: HISTONE H2A.Z




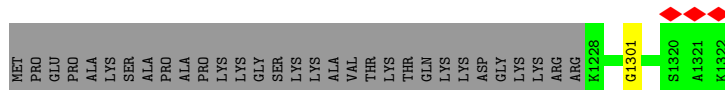
- Molecule 74: HISTONE H2A.Z

Chain NC:  78% 20%




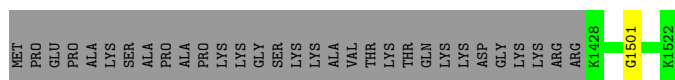
- Molecule 75: Histone H2B

Chain ND:  75% 25%



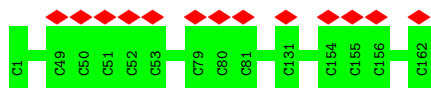
- Molecule 75: Histone H2B

Chain NH:  75% 25%



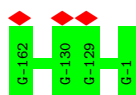
- Molecule 76: DNA (162-mer)

Chain NX:  8% 100%



- Molecule 77: DNA (162-mer)

Chain NY:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26458	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	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.678	Depositor
Minimum map value	-1.034	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.156	Depositor
Map size (\AA)	560.27997, 560.27997, 560.27997	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.3339999, 1.3339999, 1.3339999	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: SF4, 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	X	0.56	0/1561	0.82	1/2411 (0.0%)
2	Y	0.67	1/1516 (0.1%)	0.92	0/2334
3	BA	0.25	0/1983	0.40	0/2679
4	DA	0.51	0/4679	0.62	1/6320 (0.0%)
5	EA	0.33	0/1560	0.51	0/2097
6	FA	0.24	0/1167	0.41	0/1576
7	HA	0.25	0/5875	0.41	0/7955
8	NA	0.68	0/497	0.82	1/693 (0.1%)
8	NE	0.77	0/510	0.88	0/710
9	PA	0.27	0/11851	0.43	0/16014
10	DB	0.47	1/7993 (0.0%)	0.61	0/10836
11	EB	0.28	0/1427	0.46	0/1916
12	FB	0.26	0/1817	0.41	0/2445
13	HB	0.25	0/2210	0.40	0/2975
14	NB	0.76	0/390	0.84	0/539
14	NF	0.85	0/420	0.97	1/581 (0.2%)
15	PB	0.25	0/9257	0.42	0/12493
16	HC	0.28	0/3230	0.43	0/4376
17	PC	0.24	0/2102	0.42	0/2857
18	PE	0.24	0/1752	0.41	0/2366
19	PF	0.27	0/646	0.41	0/871
20	PH	0.24	0/1207	0.43	0/1628
21	PI	0.24	0/949	0.44	0/1284
22	PJ	0.26	0/516	0.41	0/696
23	PK	0.26	0/939	0.40	0/1271
24	PL	0.26	0/378	0.41	0/500
25	DP	0.25	0/1448	0.42	0/1948
26	DQ	0.25	0/945	0.42	0/1274
27	DO	0.25	0/816	0.43	0/1105
28	Dc	0.40	0/1035	0.54	0/1406
29	DD	0.42	0/1343	0.53	0/1795
29	Dd	0.29	0/1321	0.49	0/1772

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	DE	0.39	0/4469	0.56	0/6050
30	De	0.33	0/4433	0.55	0/6004
31	DF	0.50	0/3167	0.69	1/4303 (0.0%)
31	Df	0.42	0/3140	0.63	0/4268
32	DI	0.43	0/981	0.56	0/1332
32	Di	0.31	0/989	0.49	0/1343
33	DJ	0.30	0/736	0.49	1/998 (0.1%)
33	Dj	0.30	0/775	0.52	0/1049
34	Dk	0.31	0/799	0.48	0/1070
35	DL	0.44	0/613	0.65	1/829 (0.1%)
35	Dl	0.41	0/888	0.54	1/1194 (0.1%)
36	Dm	0.31	0/733	0.52	0/977
37	DG	0.52	0/1199	0.63	0/1612
38	DH	0.37	0/1673	0.58	1/2285 (0.0%)
39	HD	0.49	0/2436	0.68	3/3286 (0.1%)
40	HE	0.32	0/2103	0.47	0/2846
41	HG	0.25	0/2793	0.41	0/3780
42	HH	0.25	0/4994	0.40	0/6745
43	HF	0.27	0/529	0.49	1/714 (0.1%)
44	HI	0.67	0/2433	0.96	0/3302
45	HJ	0.73	0/2356	0.97	1/3185 (0.0%)
46	PD	0.30	0/1064	0.42	0/1428
47	PG	0.27	0/1382	0.45	0/1874
48	g	0.57	0/911	0.86	2/1219 (0.2%)
49	j	0.37	0/849	0.54	0/1150
50	n	0.36	0/7901	0.57	14/10731 (0.1%)
51	s	0.64	0/741	0.75	1/1002 (0.1%)
52	u	0.54	0/895	0.75	2/1215 (0.2%)
53	a	0.61	0/3507	0.78	1/4760 (0.0%)
54	d	0.62	0/1281	0.65	0/1718
55	f	0.55	0/1402	0.67	1/1905 (0.1%)
56	i	0.68	0/612	0.75	1/815 (0.1%)
57	m	0.27	0/1010	0.38	0/1359
58	q	0.49	1/4456 (0.0%)	0.56	0/6019
59	z	0.64	0/781	0.86	0/1067
60	b	0.51	0/911	0.63	0/1229
61	c	0.43	0/2172	0.56	0/2935
62	e	0.28	0/840	0.40	0/1128
63	l	0.26	0/1048	0.43	0/1405
64	o	0.41	0/1256	0.65	0/1724
65	h	0.63	0/1485	0.73	1/2008 (0.0%)
66	k	0.66	0/885	0.67	0/1190
67	r	0.59	0/1565	0.73	0/2106

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
68	t	0.70	0/1530	0.87	0/2066
69	v	0.66	0/1092	0.74	0/1468
70	p	0.65	0/6116	0.69	0/8311
71	w	0.56	0/11056	0.60	0/15023
72	x	0.58	0/7191	0.64	1/9728 (0.0%)
73	y	0.57	0/1645	0.64	0/2240
74	NC	0.80	0/505	0.86	0/700
74	NG	0.68	0/523	0.90	1/724 (0.1%)
75	ND	0.76	0/470	0.83	0/654
75	NH	0.66	0/470	0.85	0/654
76	NX	0.35	0/3401	0.84	0/5180
77	NY	0.40	0/4046	0.77	0/6310
All	All	0.45	3/190578 (0.0%)	0.60	39/259940 (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
39	HD	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	q	452	ALA	C-N	5.60	1.47	1.34
2	Y	36	DC	O3'-P	5.14	1.67	1.61
10	DB	494	SER	CA-CB	-5.06	1.45	1.52

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	g	128	PRO	N-CA-C	-7.74	91.97	112.10
50	n	1351	PRO	N-CA-CB	7.36	112.13	103.30
48	g	128	PRO	CA-N-CD	-7.30	101.28	111.50
50	n	1343	PRO	N-CA-CB	7.26	112.01	103.30
31	DF	320	ARG	CB-CG-CD	7.09	130.03	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	HD	126	GLN	Mainchain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BA	248/316 (78%)	246 (99%)	2 (1%)	0	100	100
4	DA	542/1872 (29%)	524 (97%)	15 (3%)	3 (1%)	22	60
5	EA	185/439 (42%)	183 (99%)	1 (0%)	1 (0%)	25	64
6	FA	134/517 (26%)	129 (96%)	5 (4%)	0	100	100
7	HA	710/760 (93%)	682 (96%)	28 (4%)	0	100	100
8	NA	98/136 (72%)	94 (96%)	2 (2%)	2 (2%)	6	31
8	NE	101/136 (74%)	96 (95%)	3 (3%)	2 (2%)	6	31
9	PA	1457/1970 (74%)	1406 (96%)	47 (3%)	4 (0%)	37	72
10	DB	959/1199 (80%)	910 (95%)	49 (5%)	0	100	100
11	EB	169/291 (58%)	164 (97%)	5 (3%)	0	100	100
12	FB	218/249 (88%)	213 (98%)	4 (2%)	1 (0%)	25	64
13	HB	253/548 (46%)	245 (97%)	8 (3%)	0	100	100
14	NB	78/103 (76%)	78 (100%)	0	0	100	100
14	NF	84/103 (82%)	77 (92%)	4 (5%)	3 (4%)	3	20
15	PB	1130/1174 (96%)	1093 (97%)	37 (3%)	0	100	100
16	HC	380/462 (82%)	363 (96%)	17 (4%)	0	100	100
17	PC	253/275 (92%)	241 (95%)	12 (5%)	0	100	100
18	PE	207/210 (99%)	203 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	PF	77/127 (61%)	76 (99%)	1 (1%)	0	100	100
20	PH	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
21	PI	112/125 (90%)	104 (93%)	8 (7%)	0	100	100
22	PJ	62/67 (92%)	61 (98%)	1 (2%)	0	100	100
23	PK	113/117 (97%)	112 (99%)	1 (1%)	0	100	100
24	PL	42/58 (72%)	40 (95%)	2 (5%)	0	100	100
25	DP	177/339 (52%)	175 (99%)	2 (1%)	0	100	100
26	DQ	109/376 (29%)	102 (94%)	7 (6%)	0	100	100
27	DO	97/109 (89%)	95 (98%)	2 (2%)	0	100	100
28	Dc	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
29	DD	153/1085 (14%)	146 (95%)	5 (3%)	2 (1%)	10	42
29	Dd	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
30	DE	540/800 (68%)	505 (94%)	33 (6%)	2 (0%)	30	68
30	De	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
31	DF	404/677 (60%)	376 (93%)	21 (5%)	7 (2%)	7	35
31	Df	399/677 (59%)	378 (95%)	20 (5%)	1 (0%)	37	72
32	DI	118/264 (45%)	113 (96%)	3 (2%)	2 (2%)	7	35
32	Di	119/264 (45%)	115 (97%)	4 (3%)	0	100	100
33	DJ	86/218 (39%)	82 (95%)	4 (5%)	0	100	100
33	Dj	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
34	Dk	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
35	DL	72/161 (45%)	62 (86%)	6 (8%)	4 (6%)	1	15
35	DI	105/161 (65%)	101 (96%)	4 (4%)	0	100	100
36	Dm	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
37	DG	139/349 (40%)	135 (97%)	4 (3%)	0	100	100
38	DH	207/310 (67%)	190 (92%)	13 (6%)	4 (2%)	6	32
39	HD	304/309 (98%)	267 (88%)	27 (9%)	10 (3%)	3	21
40	HE	259/308 (84%)	252 (97%)	7 (3%)	0	100	100
41	HG	341/395 (86%)	329 (96%)	12 (4%)	0	100	100
42	HH	601/782 (77%)	575 (96%)	26 (4%)	0	100	100
43	HF	64/71 (90%)	62 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	HI	297/346 (86%)	267 (90%)	18 (6%)	12 (4%)	2	18
45	HJ	285/323 (88%)	268 (94%)	14 (5%)	3 (1%)	12	46
46	PD	126/142 (89%)	122 (97%)	4 (3%)	0	100	100
47	PG	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
48	g	104/233 (45%)	99 (95%)	4 (4%)	1 (1%)	13	49
49	j	120/135 (89%)	117 (98%)	1 (1%)	2 (2%)	7	35
50	n	993/1454 (68%)	894 (90%)	80 (8%)	19 (2%)	6	32
51	s	91/244 (37%)	82 (90%)	7 (8%)	2 (2%)	5	29
52	u	113/144 (78%)	105 (93%)	5 (4%)	3 (3%)	4	25
53	a	430/1581 (27%)	386 (90%)	39 (9%)	5 (1%)	11	44
54	d	154/270 (57%)	143 (93%)	9 (6%)	2 (1%)	10	42
55	f	163/246 (66%)	149 (91%)	12 (7%)	2 (1%)	11	44
56	i	69/146 (47%)	65 (94%)	2 (3%)	2 (3%)	3	23
57	m	110/131 (84%)	106 (96%)	4 (4%)	0	100	100
58	q	543/651 (83%)	484 (89%)	52 (10%)	7 (1%)	10	42
59	z	93/600 (16%)	84 (90%)	6 (6%)	3 (3%)	3	21
60	b	111/200 (56%)	109 (98%)	1 (1%)	1 (1%)	14	50
61	c	255/311 (82%)	241 (94%)	14 (6%)	0	100	100
62	e	98/178 (55%)	92 (94%)	4 (4%)	2 (2%)	6	31
63	l	120/178 (67%)	115 (96%)	5 (4%)	0	100	100
64	o	152/788 (19%)	136 (90%)	12 (8%)	4 (3%)	4	25
65	h	188/268 (70%)	165 (88%)	15 (8%)	8 (4%)	2	17
66	k	110/117 (94%)	96 (87%)	12 (11%)	2 (2%)	7	34
67	r	190/208 (91%)	180 (95%)	6 (3%)	4 (2%)	5	30
68	t	189/212 (89%)	169 (89%)	16 (8%)	4 (2%)	5	30
69	v	132/200 (66%)	116 (88%)	10 (8%)	6 (4%)	2	17
70	p	756/841 (90%)	704 (93%)	50 (7%)	2 (0%)	37	72
71	w	1332/1368 (97%)	1262 (95%)	66 (5%)	4 (0%)	37	72
72	x	877/989 (89%)	828 (94%)	44 (5%)	5 (1%)	22	60
73	y	206/747 (28%)	196 (95%)	9 (4%)	1 (0%)	25	64
74	NC	101/128 (79%)	93 (92%)	5 (5%)	3 (3%)	3	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	NG	105/128 (82%)	94 (90%)	8 (8%)	3 (3%)	3	23
75	ND	93/126 (74%)	91 (98%)	1 (1%)	1 (1%)	12	46
75	NH	93/126 (74%)	89 (96%)	3 (3%)	1 (1%)	12	46
All	All	22102/36357 (61%)	20865 (94%)	1075 (5%)	162 (1%)	21	56

5 of 162 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	DA	498	PRO
4	DA	1158	SER
8	NA	534	ARG
9	PA	1666	PRO
12	FB	229	HIS

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	
3	BA	215/268 (80%)	215 (100%)	0	100	100
4	DA	495/1665 (30%)	460 (93%)	35 (7%)	12	32
5	EA	169/373 (45%)	167 (99%)	2 (1%)	67	79
6	FA	121/448 (27%)	119 (98%)	2 (2%)	56	72
7	HA	624/664 (94%)	623 (100%)	1 (0%)	92	94
9	PA	1302/1749 (74%)	1294 (99%)	8 (1%)	84	88
10	DB	876/1083 (81%)	859 (98%)	17 (2%)	52	70
11	EB	154/261 (59%)	153 (99%)	1 (1%)	84	88
12	FB	196/218 (90%)	195 (100%)	1 (0%)	86	89
13	HB	241/484 (50%)	241 (100%)	0	100	100
15	PB	994/1027 (97%)	992 (100%)	2 (0%)	92	94
16	HC	342/399 (86%)	340 (99%)	2 (1%)	84	88
17	PC	234/252 (93%)	234 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	PE	191/192 (100%)	191 (100%)	0	100	100
19	PF	69/111 (62%)	68 (99%)	1 (1%)	62	76
20	PH	129/131 (98%)	129 (100%)	0	100	100
21	PI	103/112 (92%)	103 (100%)	0	100	100
22	PJ	53/56 (95%)	53 (100%)	0	100	100
23	PK	104/106 (98%)	103 (99%)	1 (1%)	73	82
24	PL	41/55 (74%)	41 (100%)	0	100	100
25	DP	154/293 (53%)	154 (100%)	0	100	100
26	DQ	105/324 (32%)	105 (100%)	0	100	100
27	DO	90/98 (92%)	88 (98%)	2 (2%)	47	65
28	Dc	113/833 (14%)	111 (98%)	2 (2%)	54	71
29	DD	144/815 (18%)	136 (94%)	8 (6%)	17	39
29	Dd	146/815 (18%)	146 (100%)	0	100	100
30	DE	478/657 (73%)	465 (97%)	13 (3%)	40	59
30	De	475/657 (72%)	473 (100%)	2 (0%)	89	91
31	DF	324/574 (56%)	300 (93%)	24 (7%)	11	31
31	Df	322/574 (56%)	314 (98%)	8 (2%)	42	62
32	DI	106/235 (45%)	99 (93%)	7 (7%)	14	35
32	Di	107/235 (46%)	107 (100%)	0	100	100
33	DJ	79/154 (51%)	78 (99%)	1 (1%)	65	77
33	Dj	83/154 (54%)	83 (100%)	0	100	100
34	Dk	87/182 (48%)	87 (100%)	0	100	100
35	DL	69/141 (49%)	60 (87%)	9 (13%)	3	15
35	DI	98/141 (70%)	98 (100%)	0	100	100
36	Dm	80/106 (76%)	79 (99%)	1 (1%)	65	77
37	DG	133/322 (41%)	125 (94%)	8 (6%)	16	38
38	DH	181/270 (67%)	172 (95%)	9 (5%)	20	42
39	HD	251/283 (89%)	232 (92%)	19 (8%)	11	30
40	HE	234/272 (86%)	229 (98%)	5 (2%)	48	67
41	HG	311/352 (88%)	310 (100%)	1 (0%)	91	92
42	HH	536/688 (78%)	533 (99%)	3 (1%)	84	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	HF	59/64 (92%)	59 (100%)	0	100	100
44	HI	258/298 (87%)	189 (73%)	69 (27%)	0	3
45	HJ	252/296 (85%)	177 (70%)	75 (30%)	0	2
46	PD	118/126 (94%)	117 (99%)	1 (1%)	79	85
47	PG	152/153 (99%)	151 (99%)	1 (1%)	81	87
48	g	102/216 (47%)	94 (92%)	8 (8%)	10	29
49	j	66/124 (53%)	65 (98%)	1 (2%)	60	75
50	n	807/1271 (64%)	784 (97%)	23 (3%)	37	57
51	s	83/208 (40%)	73 (88%)	10 (12%)	4	16
52	u	95/119 (80%)	92 (97%)	3 (3%)	34	54
53	a	393/1391 (28%)	318 (81%)	75 (19%)	1	7
54	d	139/230 (60%)	95 (68%)	44 (32%)	0	2
55	f	149/223 (67%)	130 (87%)	19 (13%)	3	15
56	i	71/133 (53%)	60 (84%)	11 (16%)	2	11
57	m	102/115 (89%)	101 (99%)	1 (1%)	73	82
58	q	491/577 (85%)	416 (85%)	75 (15%)	2	11
59	z	89/512 (17%)	76 (85%)	13 (15%)	2	12
60	b	102/163 (63%)	91 (89%)	11 (11%)	5	19
61	c	238/280 (85%)	225 (94%)	13 (6%)	18	40
62	e	94/152 (62%)	94 (100%)	0	100	100
63	l	116/155 (75%)	116 (100%)	0	100	100
64	o	141/697 (20%)	138 (98%)	3 (2%)	48	67
65	h	161/225 (72%)	127 (79%)	34 (21%)	1	5
66	k	94/98 (96%)	49 (52%)	45 (48%)	0	0
67	r	169/183 (92%)	143 (85%)	26 (15%)	2	11
68	t	166/178 (93%)	128 (77%)	38 (23%)	0	4
69	v	122/173 (70%)	87 (71%)	35 (29%)	0	2
70	p	681/736 (92%)	671 (98%)	10 (2%)	60	75
71	w	1203/1232 (98%)	1200 (100%)	3 (0%)	92	94
72	x	789/864 (91%)	777 (98%)	12 (2%)	60	75
73	y	175/601 (29%)	172 (98%)	3 (2%)	56	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	19036/30622 (62%)	18179 (96%)	857 (4%)	26 45

5 of 857 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	d	63	ASN
58	q	146	LEU
69	v	43	GLU
54	d	82	LEU
54	d	30	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 257 such sidechains are listed below:

Mol	Chain	Res	Type
71	w	726	ASN
71	w	925	HIS
47	PG	124	ASN
46	PD	66	ASN
71	w	1320	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
79	SF4	HA	1000	7	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	SF4	HA	1000	7	-	-	0/6/5/5

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.

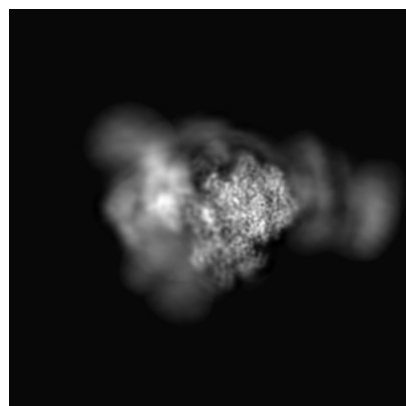
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34359. These allow visual inspection of the internal detail of the map and identification of artifacts.

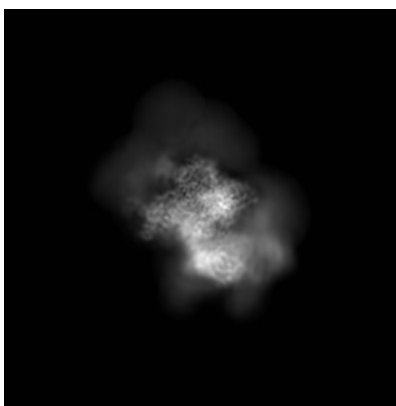
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

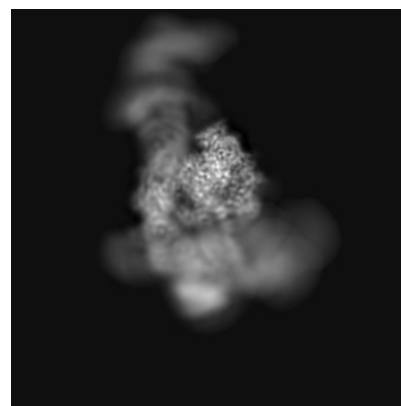
6.1.1 Primary map



X

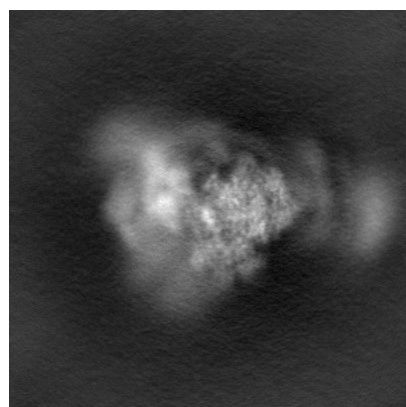


Y

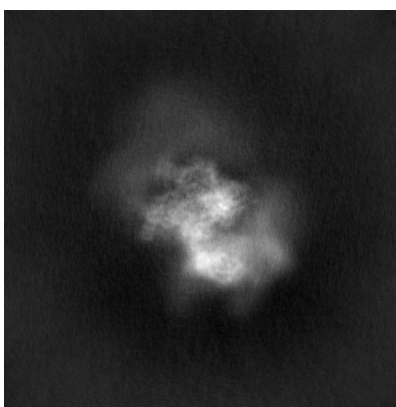


Z

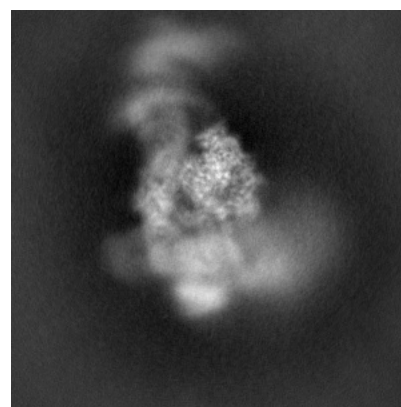
6.1.2 Raw map



X



Y

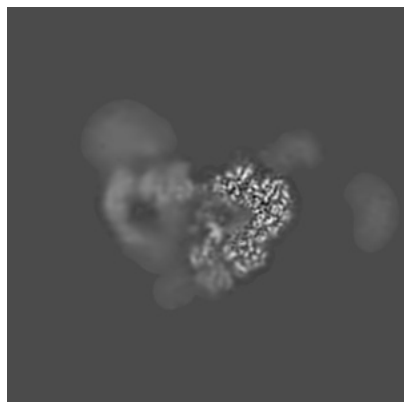


Z

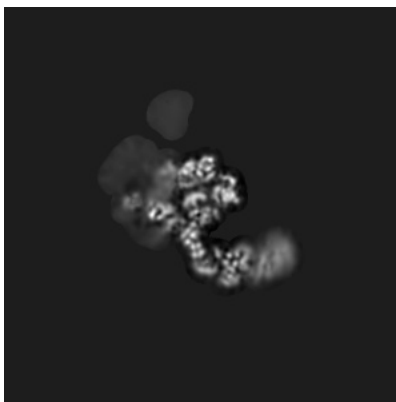
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

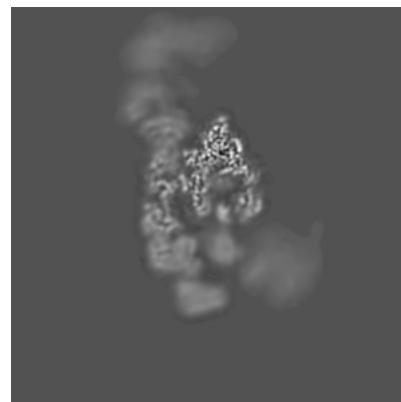
6.2.1 Primary map



X Index: 210

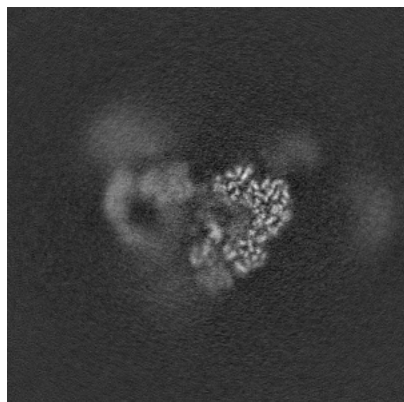


Y Index: 210

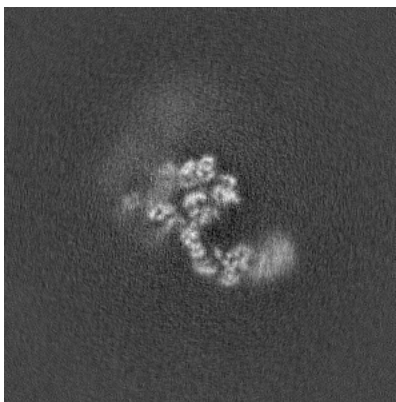


Z Index: 210

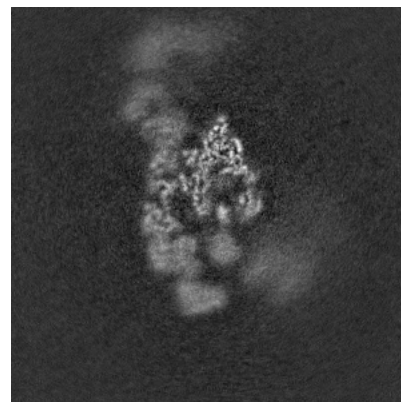
6.2.2 Raw map



X Index: 210



Y Index: 210

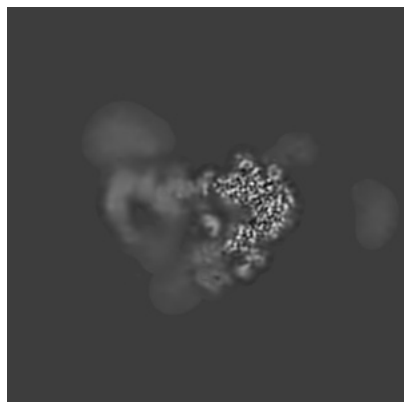


Z Index: 210

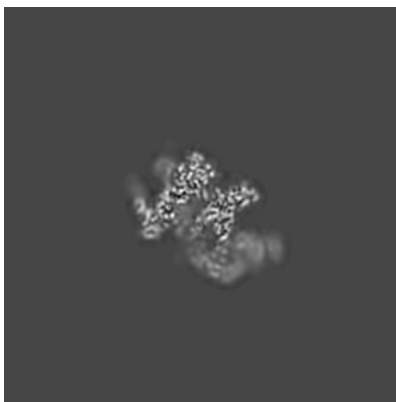
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

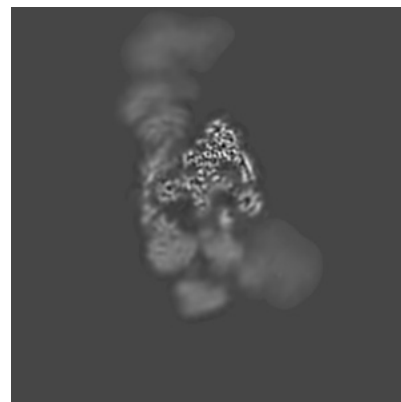
6.3.1 Primary map



X Index: 215

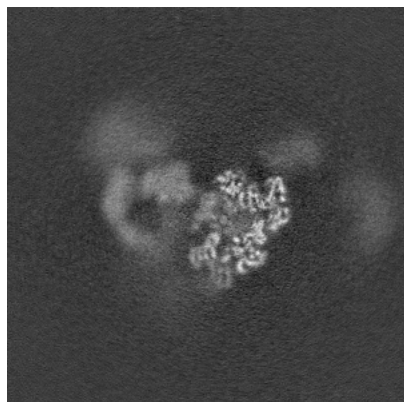


Y Index: 246

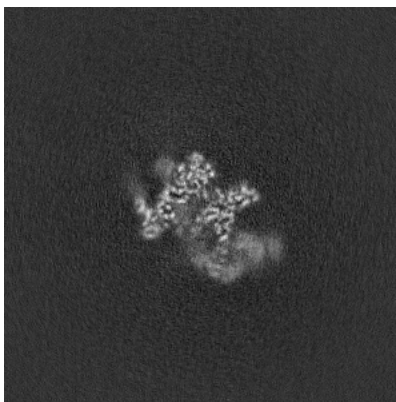


Z Index: 216

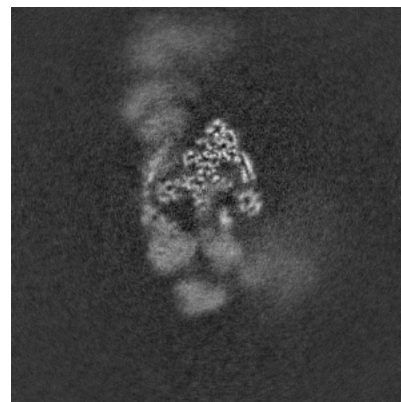
6.3.2 Raw map



X Index: 206



Y Index: 246

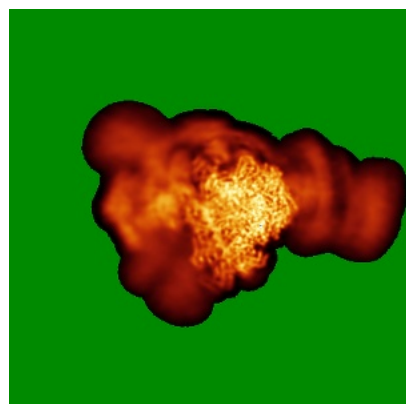


Z Index: 216

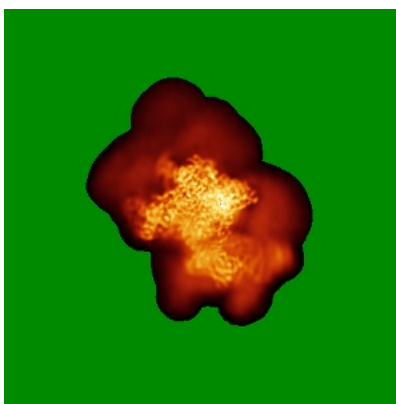
The images above show the largest variance slices of the map in three orthogonal directions.

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

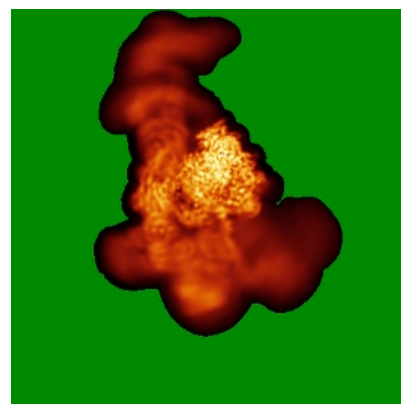
6.4.1 Primary map



X

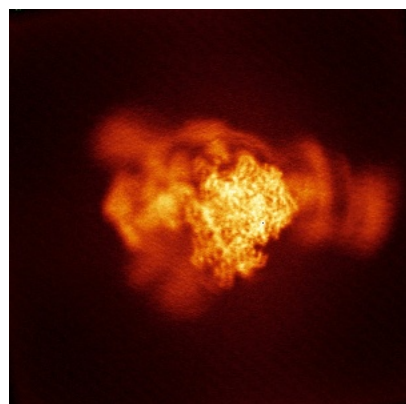


Y

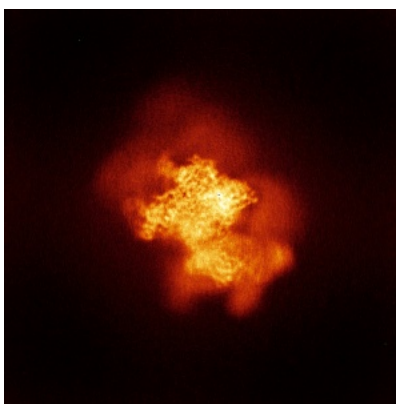


Z

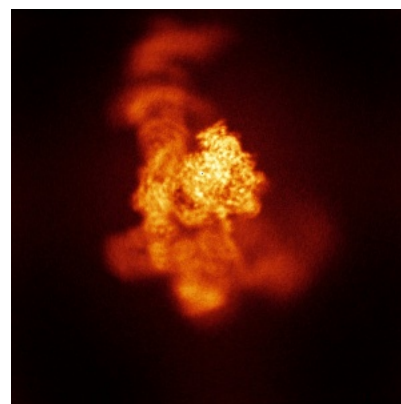
6.4.2 Raw map



X



Y

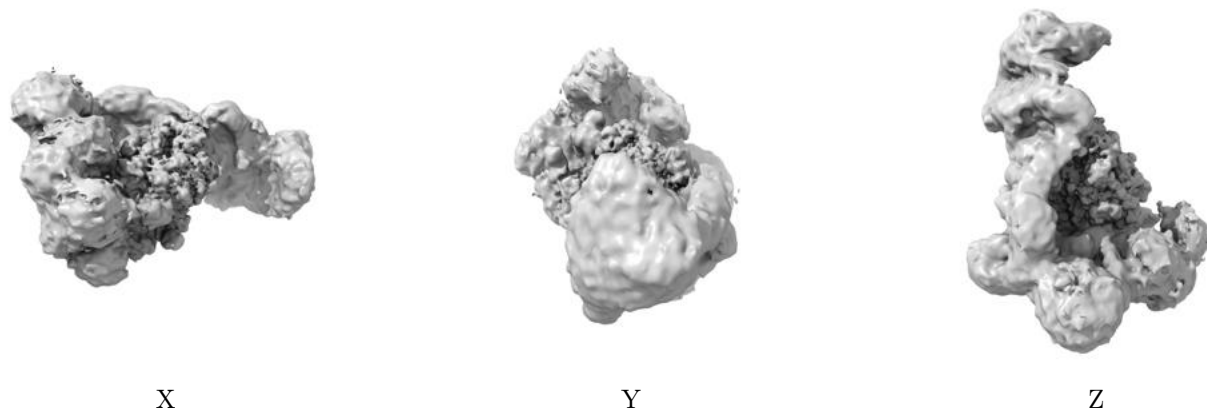


Z

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.

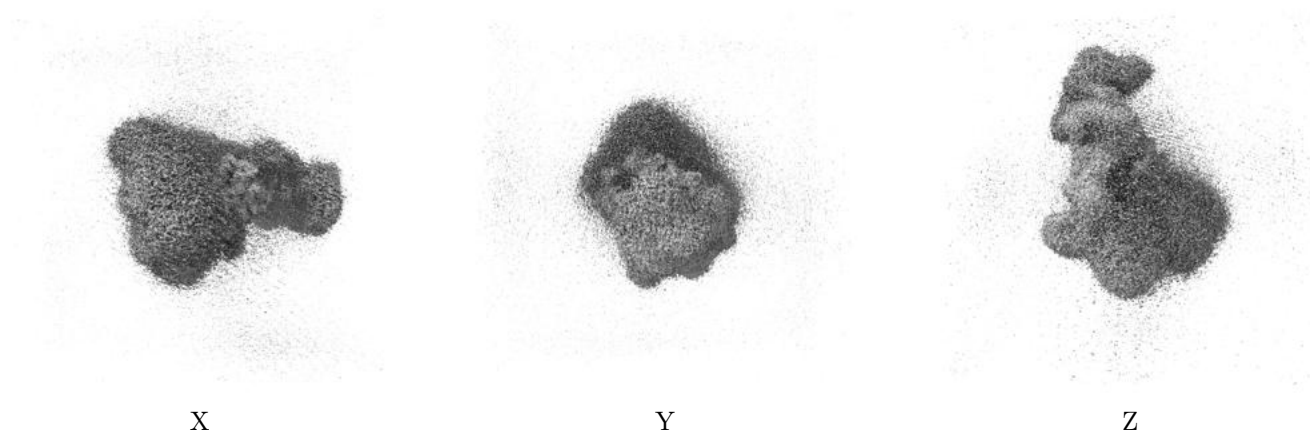
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.156. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

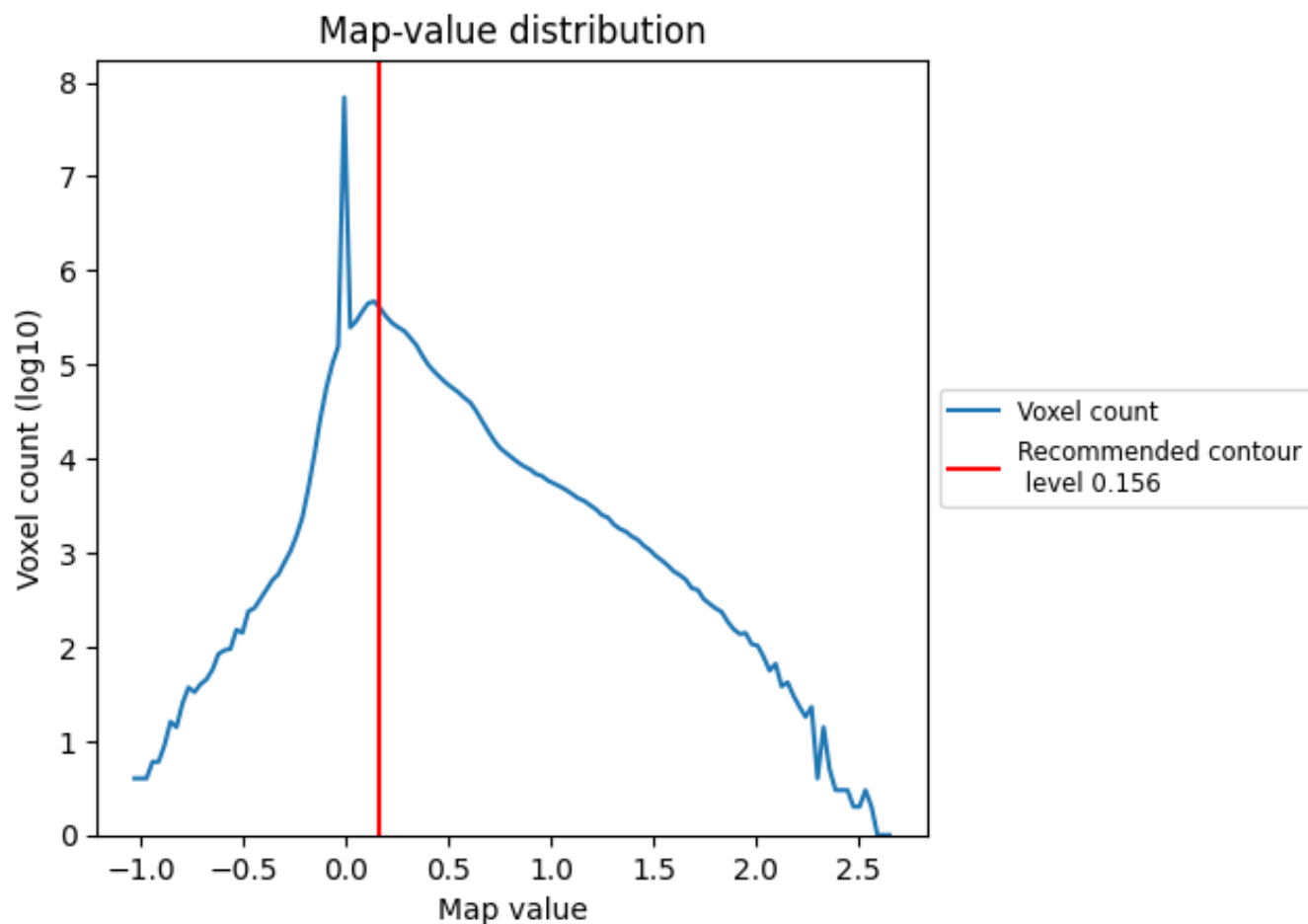
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

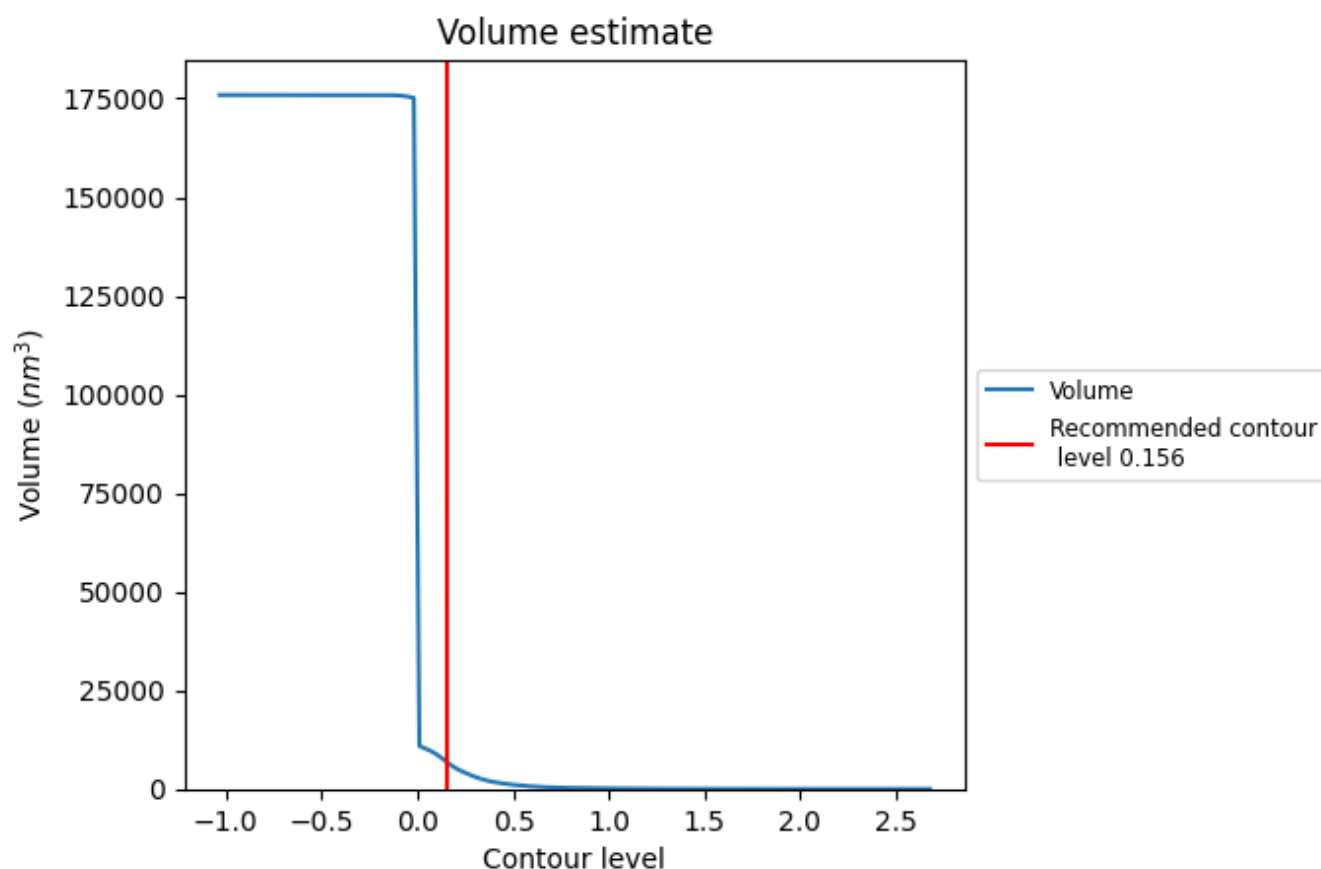
This section contains the results of statistical analysis of the map.

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.

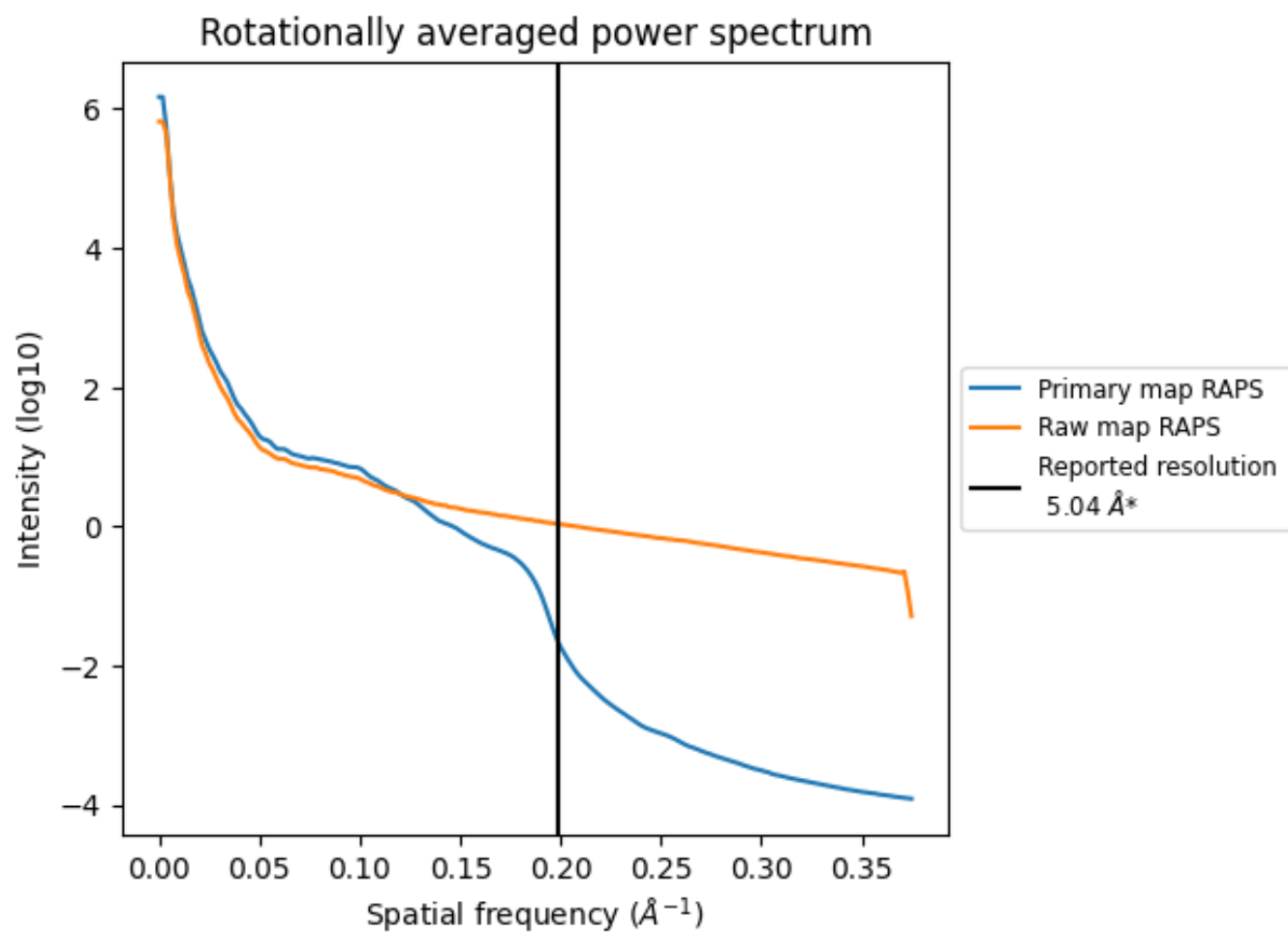
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6707 nm^3 ; this corresponds to an approximate mass of 6058 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 ⓘ

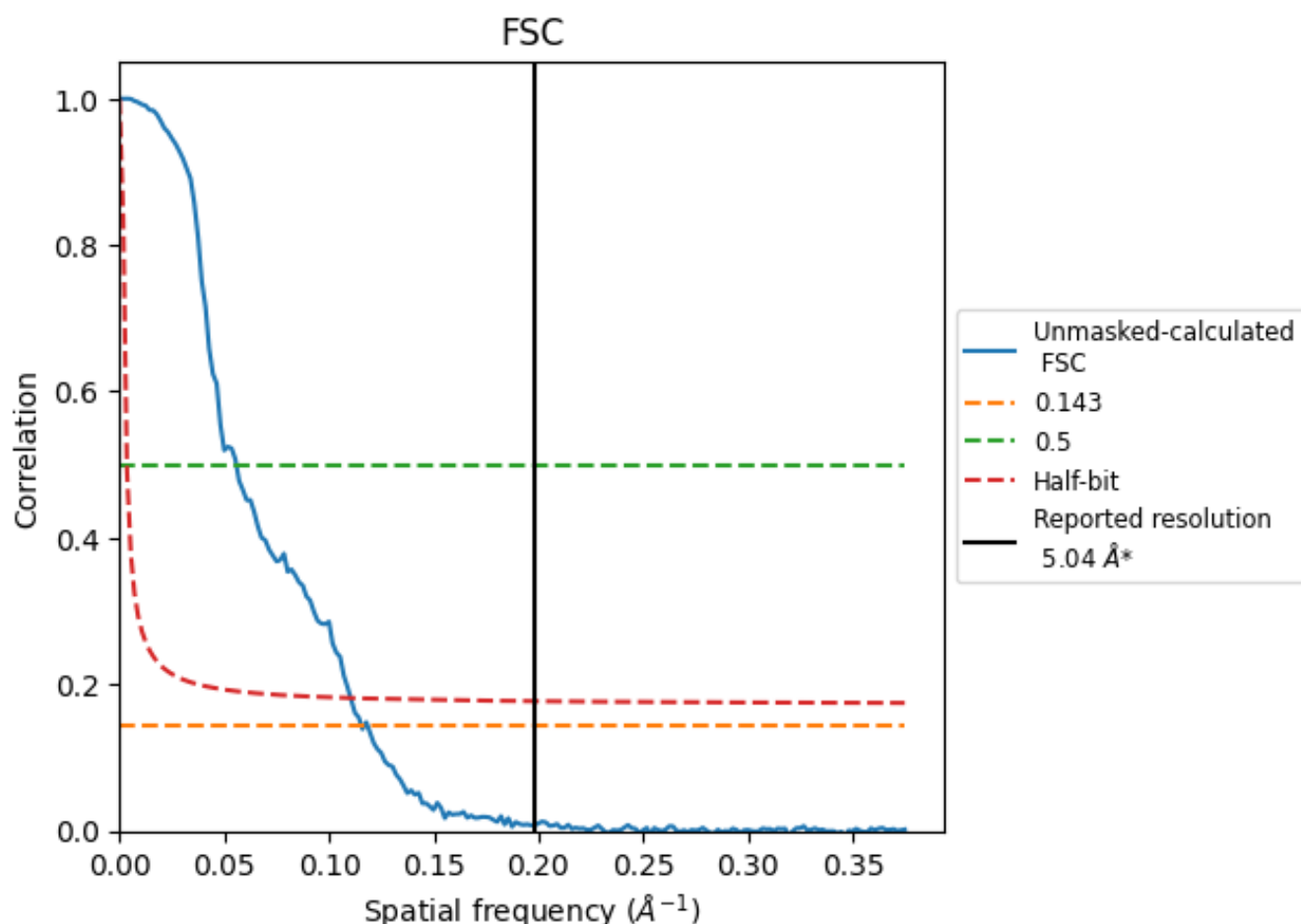


*Reported resolution corresponds to spatial frequency of 0.198 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.198 Å⁻¹

8.2 Resolution estimates [i](#)

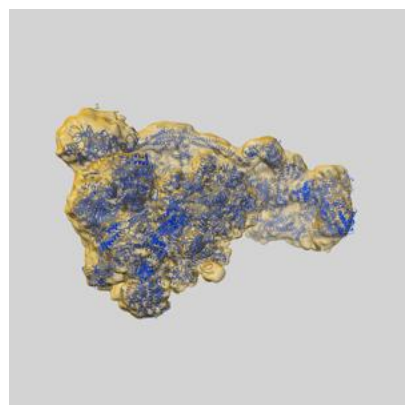
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.04	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.66	17.92	9.07

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.66 differs from the reported value 5.04 by more than 10 %

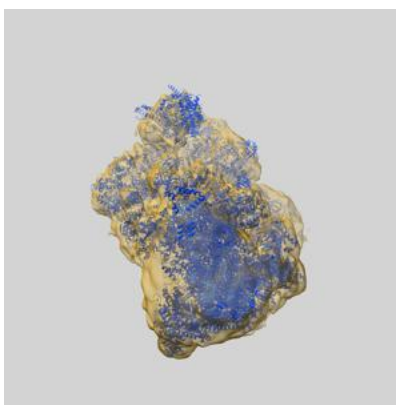
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34359 and PDB model 8GXQ. Per-residue inclusion information can be found in section [3](#) on page [20](#).

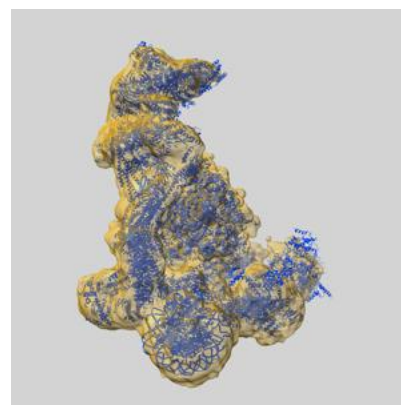
9.1 Map-model overlay [i](#)



X



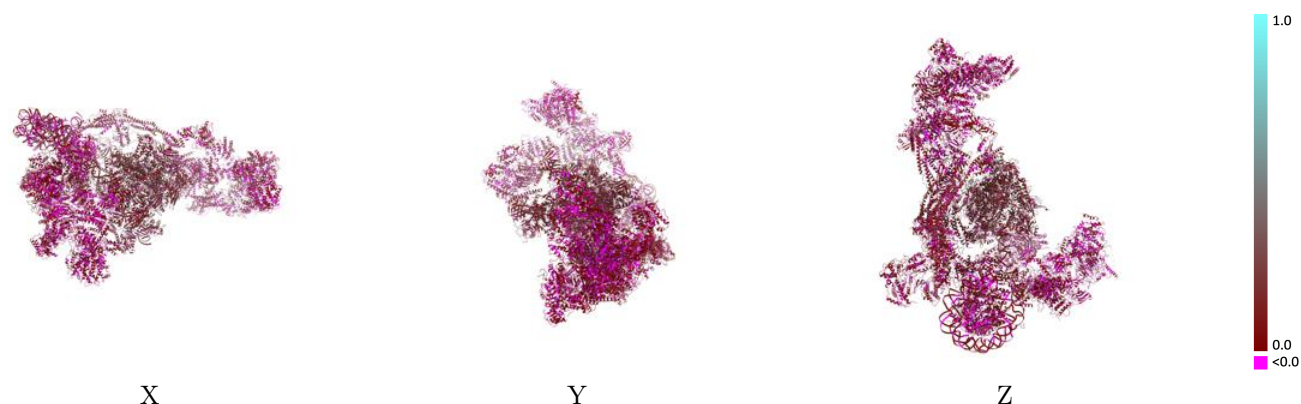
Y



Z

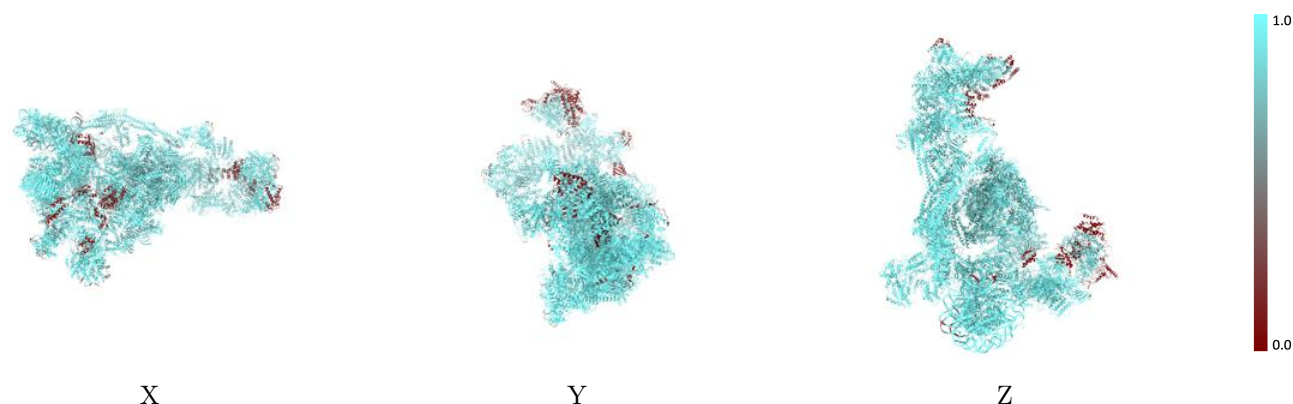
The images above show the 3D surface view of the map at the recommended contour level 0.156 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



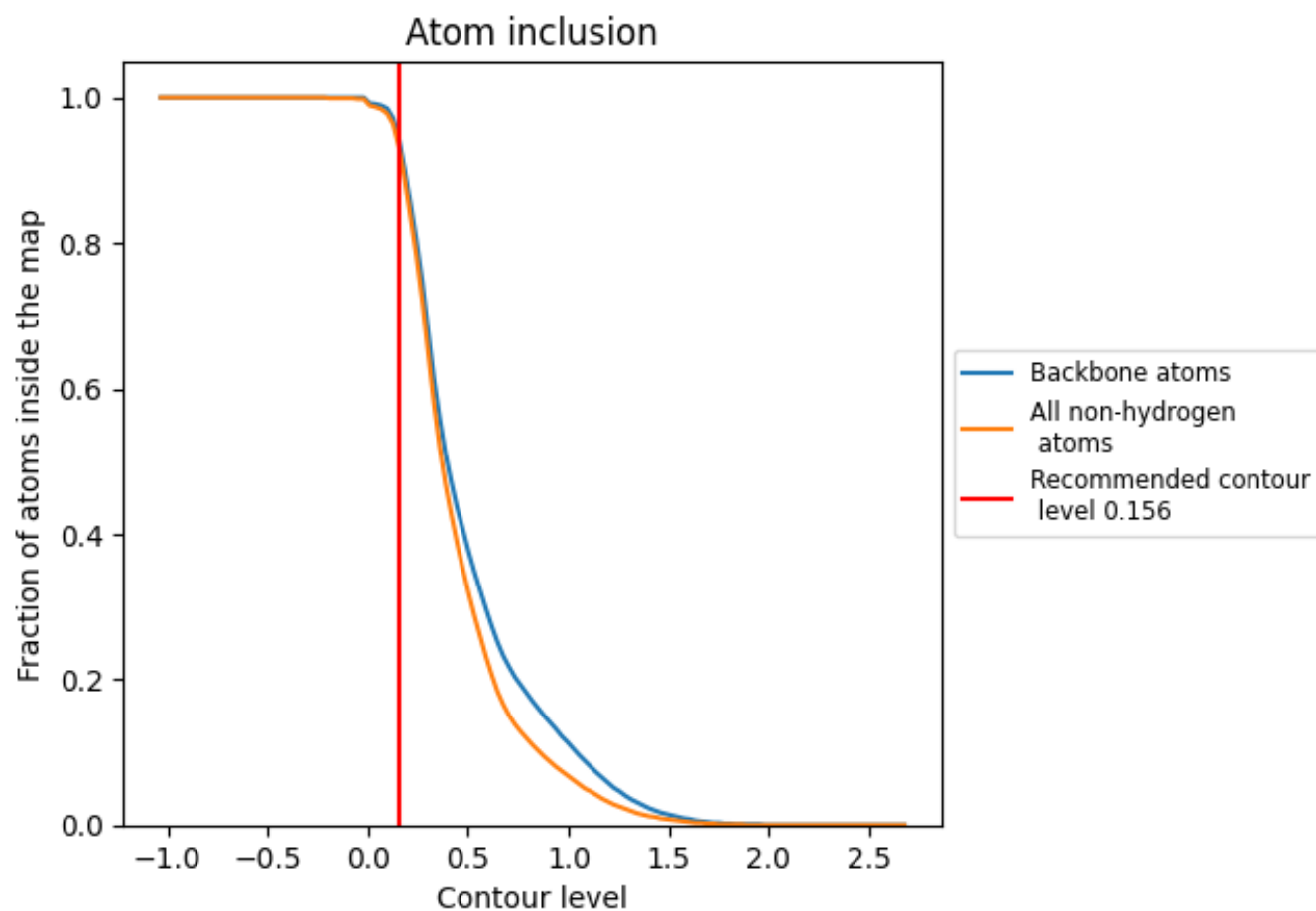
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.156).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.156) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.0840
BA	 0.9710	 0.1780
DA	 0.8720	 0.0300
DB	 0.9940	 0.0440
DD	 0.9020	 0.0440
DE	 0.9790	 0.0430
DF	 0.9610	 0.0410
DG	 0.5770	 0.0150
DH	 0.9980	 0.0490
DI	 0.9200	 0.0360
DJ	 0.9960	 0.0450
DL	 0.8450	 0.0330
DO	 0.9730	 0.1060
DP	 0.9830	 0.1390
DQ	 0.9680	 0.1190
Dc	 0.6200	 0.0290
Dd	 0.3480	 0.0030
De	 0.6780	 0.0240
Df	 0.8640	 0.0370
Di	 0.8370	 0.0200
Dj	 0.6600	 0.0400
Dk	 0.2270	 0.0000
DI	 0.6640	 0.0310
Dm	 0.2120	 0.0050
EA	 0.9500	 0.1120
EB	 0.9900	 0.1230
FA	 0.9870	 0.1360
FB	 0.9860	 0.1460
HA	 0.9980	 0.1150
HB	 0.9980	 0.0670
HC	 0.9970	 0.0860
HD	 0.9870	 0.1130
HE	 0.9980	 0.0490
HF	 1.0000	 0.0790
HG	 0.9990	 0.0690

























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Chain	Atom inclusion	Q-score
HH	 0.9940	 0.0730
HI	 0.9980	 0.0630
HJ	 0.9830	 0.0630
NA	 0.9800	 0.0770
NB	 1.0000	 0.0420
NC	 0.9840	 0.0110
ND	 0.9700	 0.0500
NE	 0.9940	 0.0710
NF	 1.0000	 0.0330
NG	 1.0000	 0.0430
NH	 1.0000	 0.0020
NX	 0.9070	 0.0340
NY	 0.9400	 0.0460
PA	 0.9560	 0.1830
PB	 0.9530	 0.2030
PC	 0.9630	 0.2080
PD	 0.9630	 0.1720
PE	 0.9790	 0.1790
PF	 0.9290	 0.2020
PG	 0.9720	 0.1580
PH	 0.9600	 0.1920
PI	 0.9780	 0.1840
PJ	 0.9540	 0.1870
PK	 0.9450	 0.2030
PL	 0.9800	 0.2110
X	 1.0000	 0.1830
Y	 0.9990	 0.1940
a	 0.9250	 0.0510
b	 0.9970	 0.0400
c	 0.9890	 0.0500
d	 0.9730	 0.0590
e	 0.9990	 0.0910
f	 0.9990	 0.1300
g	 1.0000	 0.1080
h	 0.9880	 0.1470
i	 0.8660	 0.0960
j	 1.0000	 0.0750
k	 0.9880	 0.1390
l	 1.0000	 0.0690
m	 1.0000	 0.0690
n	 0.9880	 0.0610
o	 0.9970	 0.0280

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Chain	Atom inclusion	Q-score
p	 0.9960	 0.0430
q	 0.9970	 0.0780
r	 0.9950	 0.1020
s	 1.0000	 0.0400
t	 0.9870	 0.0680
u	 1.0000	 0.0900
v	 0.9840	 0.1110
w	 0.7510	 0.0240
x	 0.9500	 0.0400
y	 0.9750	 0.0310
z	 0.9480	 0.0340