



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 01:56 PM UTC

PDB ID : 5U0S / pdb_00005u0s
EMDB ID : EMD-8480
Title : Cryo-EM structure of the Mediator-RNAPII complex
Authors : Tsai, K.-L.; Yu, X.; Gopalan, S.; Chao, T.-C.; Zhang, Y.; Florens, L.; Washburn, M.P.; Murakami, K.; Conaway, R.C.; Conaway, J.W.; Asturias, F.
Deposited on : 2016-11-26
Resolution : 7.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

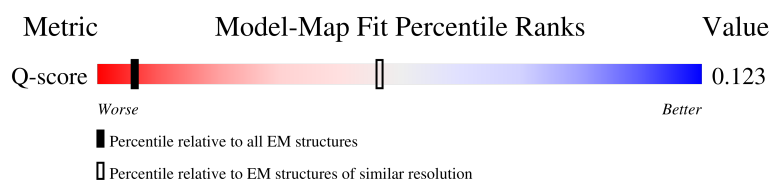
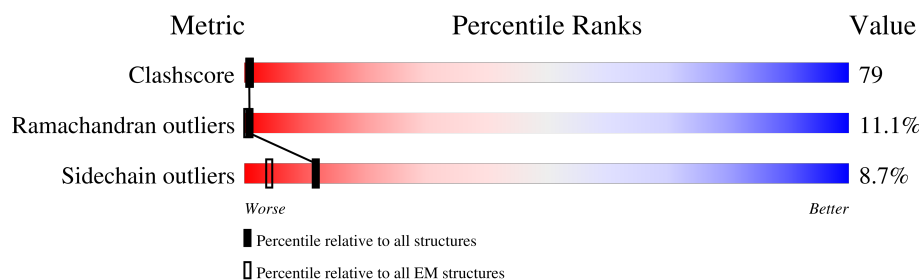
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	370 (7.30 - 8.30)

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	F	216	
2	H	200	
3	Q	545	
4	R	207	

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Mol	Chain	Length	Quality of chain
5	T	193	
6	K	116	
7	V	136	
8	N	931	
9	D	239	
10	G	376	
11	U	138	
12	3	139	
13	2	273	
14	I	121	
15	S	139	
16	J	132	
17	a	1752	
18	b	1210	
19	c	297	
20	d	135	
21	e	210	
22	f	142	
23	g	172	
24	h	125	
25	i	113	
26	j	71	
27	k	123	
28	l	63	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 51548 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 Mediator complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	188	Total	C	N	O	S	0	0
			1534	979	258	288	9		

- Molecule 2 is a protein called Mediator complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	182	Total	C	N	O	S	0	0
			1493	941	257	292	3		

- Molecule 3 is a protein called Mediator complex subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	500	Total	C	N	O	S	0	0
			3787	2393	651	725	18		

- Molecule 4 is a protein called Mediator complex subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	207	Total	C	N	O	S	0	0
			1694	1082	288	316	8		

- Molecule 5 is a protein called Mediator complex subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	T	176	Total	C	N	O	S	0	0
			1435	938	234	258	5		

- Molecule 6 is a protein called Mediator complex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	98	Total	C	N	O	S	0	0
			769	486	128	154	1		

- Molecule 7 is a protein called Mediator complex subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V	118	Total	C	N	O	S	0	0
			949	599	161	187	2		

- Molecule 8 is a protein called Mediator complex subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	520	Total	C	N	O	S	0	0
			3887	2498	683	698	8		

- Molecule 9 is a protein called Mediator complex subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	D	96	Total	C	N	O	0	0
			480	288	96	96		

- Molecule 10 is a protein called Mediator complex subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	G	194	Total	C	N	O	0	0
			965	577	194	194		

- Molecule 11 is a protein called Mediator complex subunit 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	U	122	Total	C	N	O	0	0
			608	364	122	122		

- Molecule 12 is a protein called Mediator complex subunit 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	3	103	Total	C	N	O	0	0
			515	309	103	103		

- Molecule 13 is a protein called Mediator complex subunit 27.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	2	78	Total	C	N	O	0	0
			388	232	78	78		

- Molecule 14 is a protein called Mediator complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	75	Total	C	N	O	0	0
			374	224	75	75		

- Molecule 15 is a protein called Mediator complex subunit 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	S	122	Total	C	N	O	0	0
			610	366	122	122		

- Molecule 16 is a protein called Mediator complex subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	J	131	Total	C	N	O	0	0
			655	393	131	131		

- Molecule 17 is a protein called RNA polymerase II subunit Rpb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	1490	Total	C	N	O	S	0	0
			11761	7388	2065	2238	70		

- Molecule 18 is a protein called RNA polymerase II subunit Rpb2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	1150	Total	C	N	O	S	0	0
			9180	5772	1630	1716	62		

- Molecule 19 is a protein called RNA polymerase II subunit Rpb3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c	263	Total	C	N	O	S	0	0
			2088	1315	355	406	12		

- Molecule 20 is a protein called RNA polymerase II subunit Rpb4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	d	125	Total	C	N	O	S	0	0
			988	619	166	197	6		

- Molecule 21 is a protein called RNA polymerase II subunit Rpb5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	e	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		

- Molecule 22 is a protein called RNA polymerase II subunit Rpb6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	f	83	Total	C	N	O	S	0	0
			656	416	112	125	3		

- Molecule 23 is a protein called RNA polymerase II subunit Rpb7.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	g	170	Total	C	N	O	S	0	0
			1330	860	217	247	6		

- Molecule 24 is a protein called RNA polymerase II subunit Rpb8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	h	124	Total	C	N	O	S	0	0
			996	631	167	195	3		

- Molecule 25 is a protein called RNA polymerase II subunit Rpb9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	i	111	Total	C	N	O	S	0	0
			902	551	164	176	11		

- Molecule 26 is a protein called RNA polymerase II subunit Rpb10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	64	Total	C	N	O	S	0	0
			518	330	87	94	7		

- Molecule 27 is a protein called RNA polymerase II subunit Rpb11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	119	Total	C	N	O	S	0	0
			955	608	159	182	6		

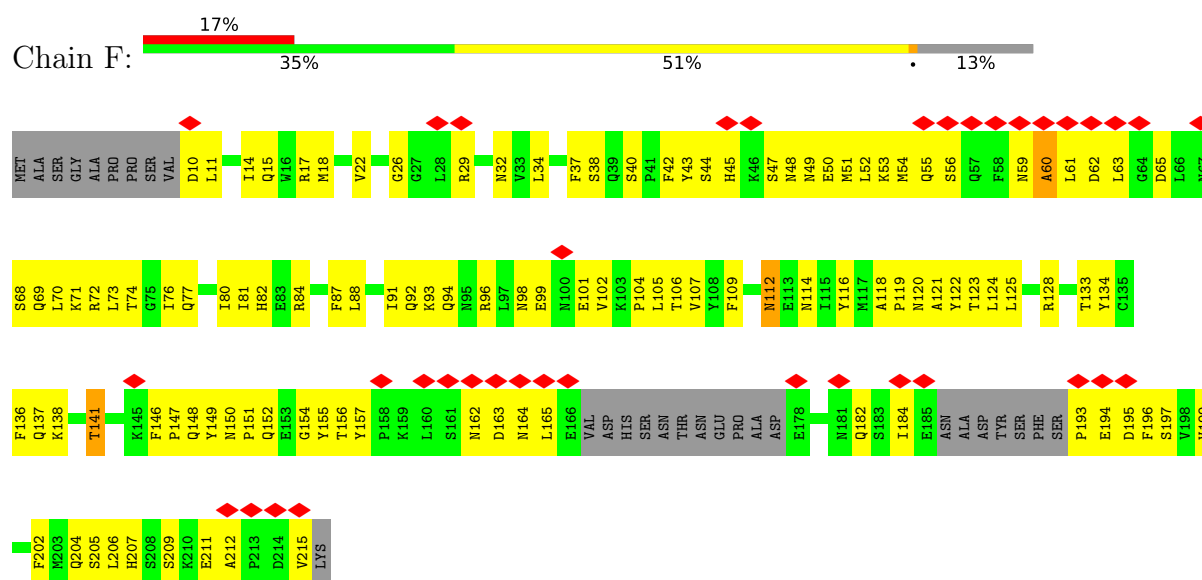
- Molecule 28 is a protein called RNA polymerase II subunit Rpb12.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	45	Total	C	N	O	S	0	0
			368	225	74	61	8		

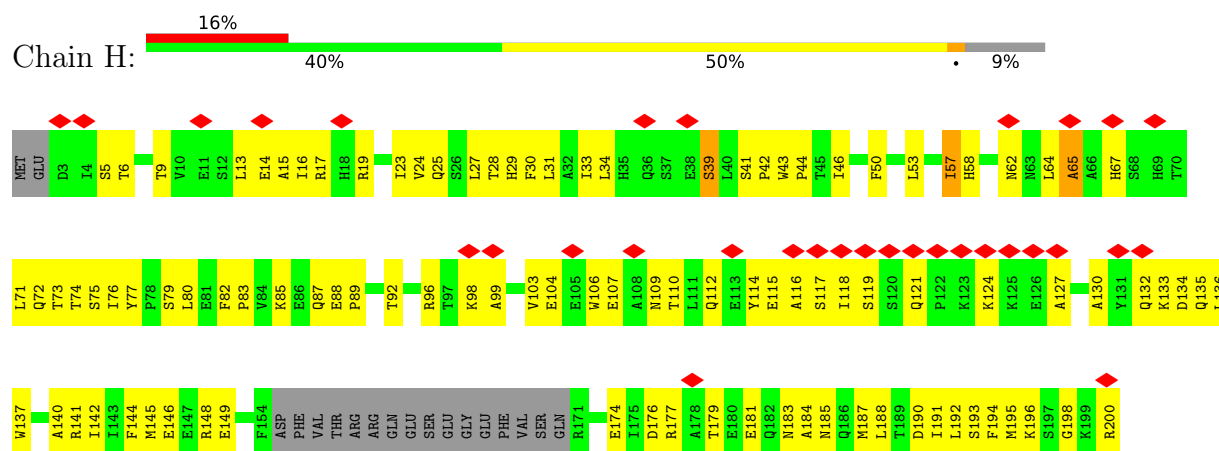
3 Residue-property plots

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.

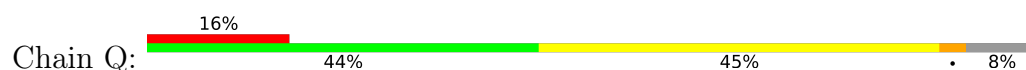
• Molecule 1: Mediator complex subunit 6

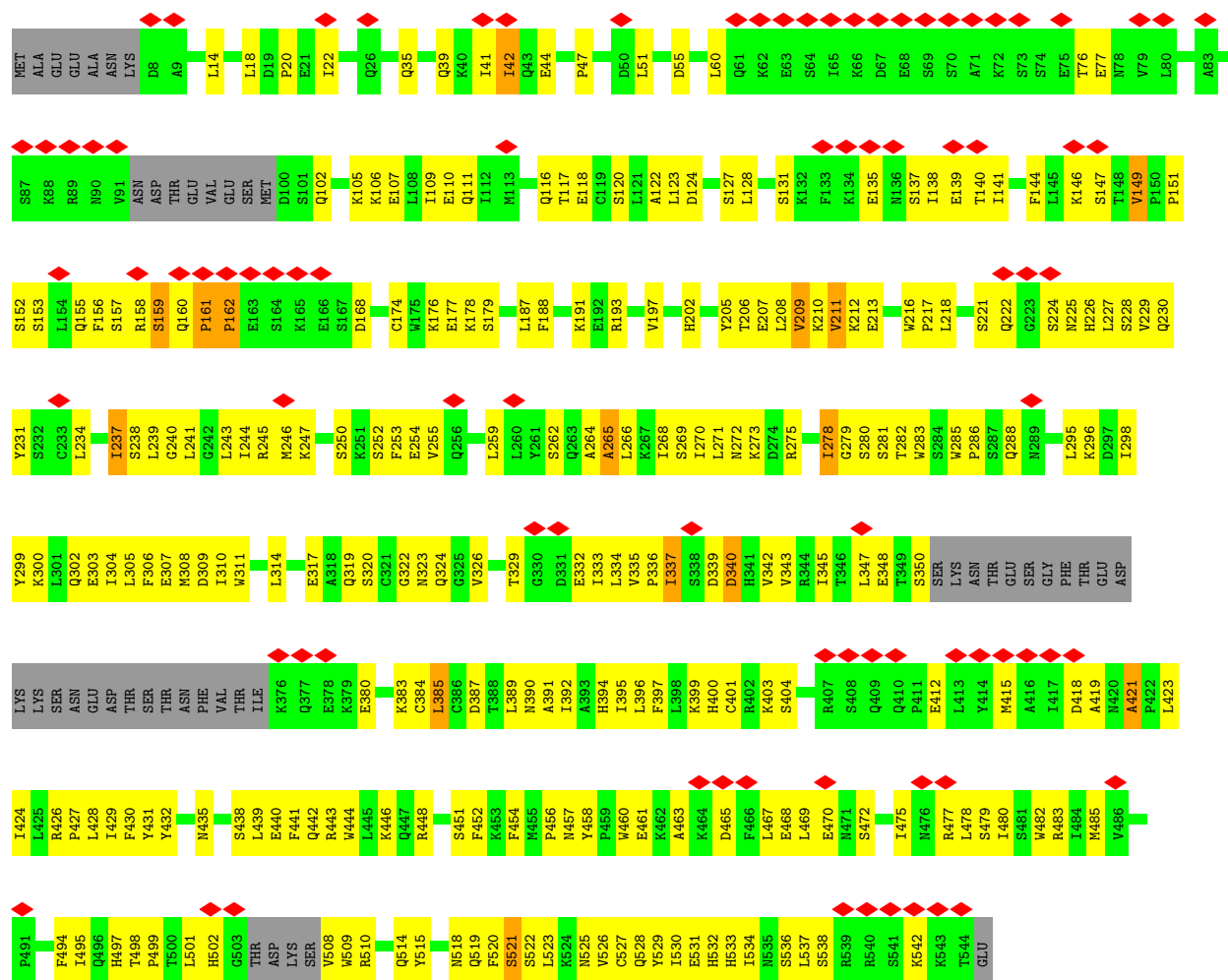


• Molecule 2: Mediator complex subunit 8

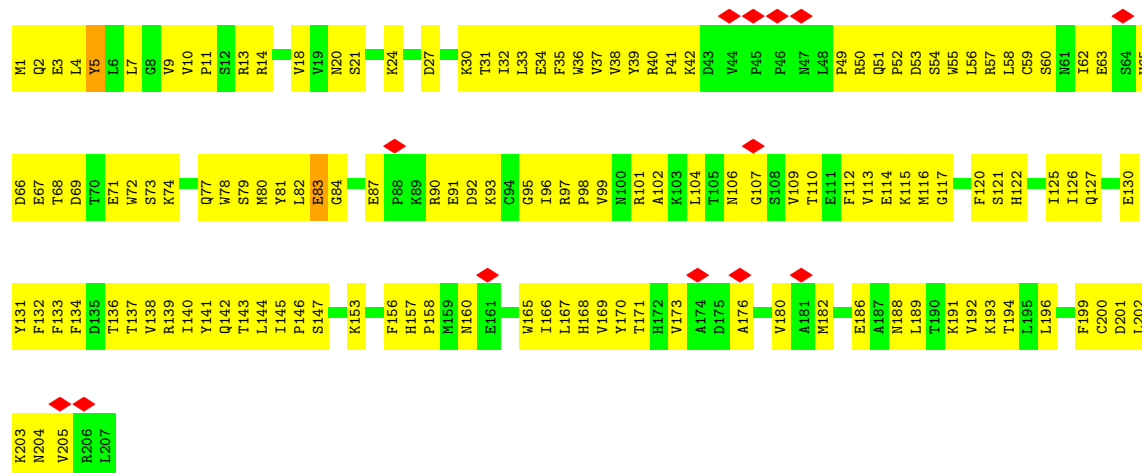


• Molecule 3: Mediator complex subunit 17

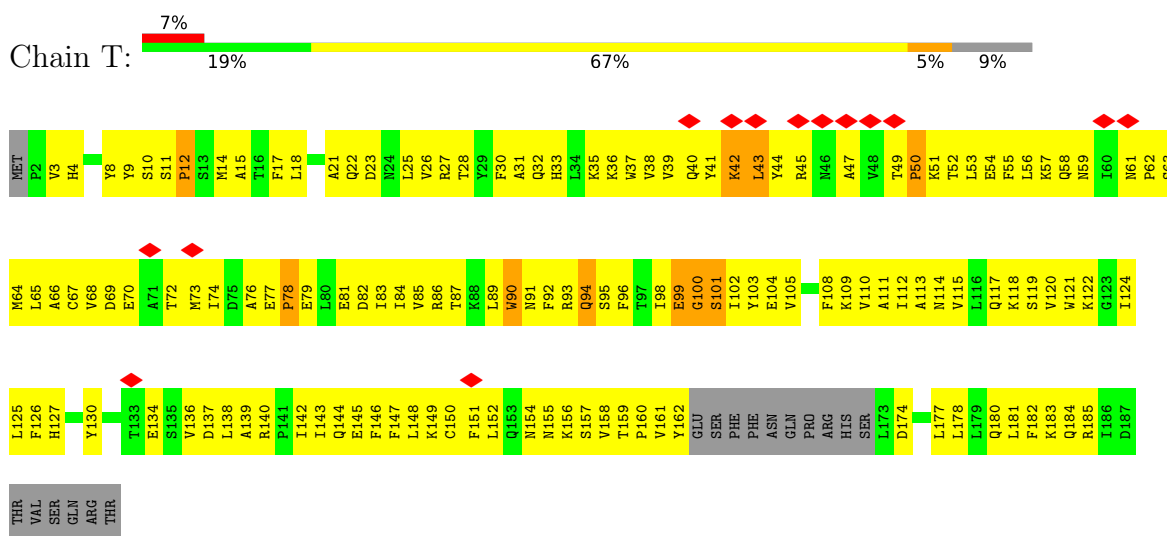




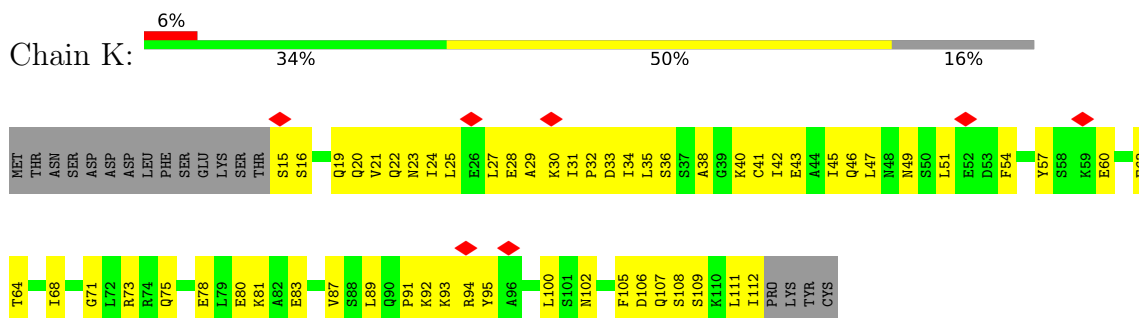
• Molecule 4: Mediator complex subunit 18



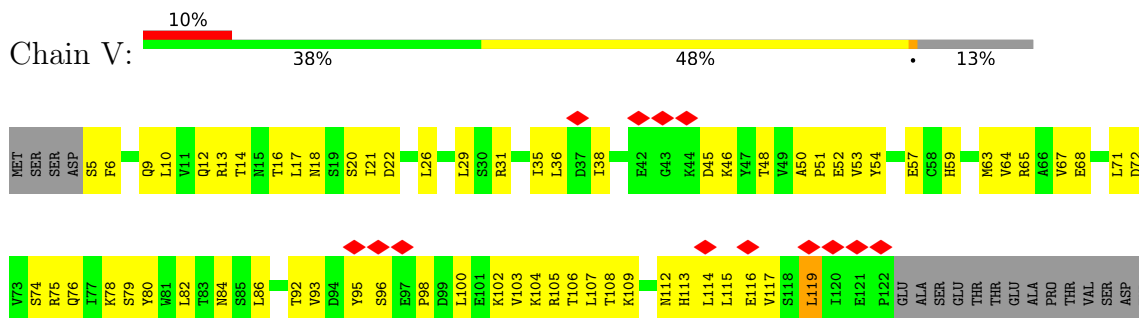
• Molecule 5: Mediator complex subunit 20



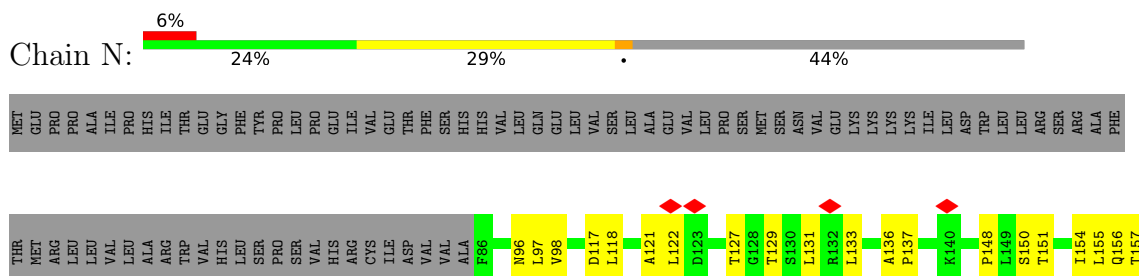
- Molecule 6: Mediator complex subunit 11

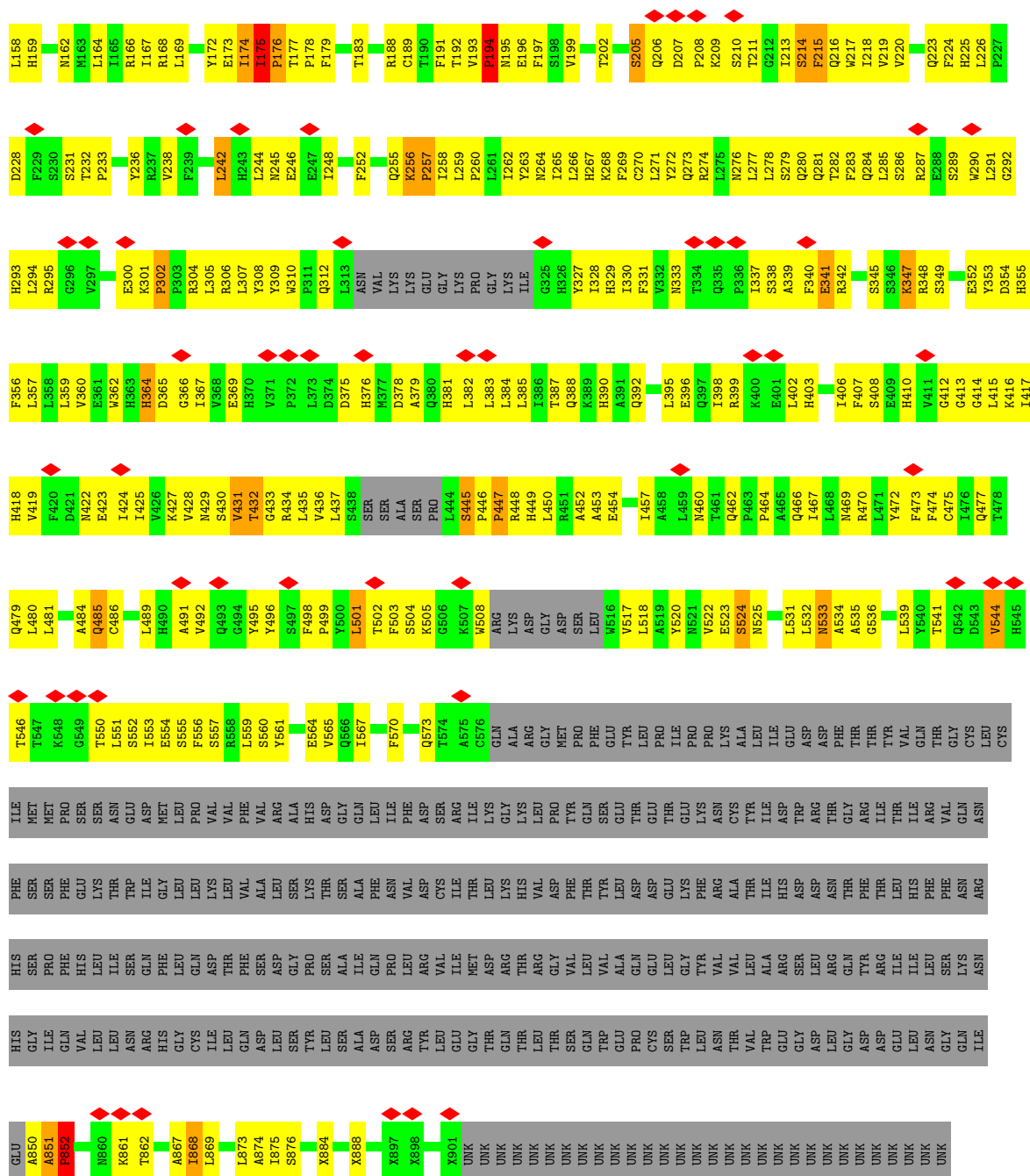


● Molecule 7: Mediator complex subunit 22



- Molecule 8: Mediator complex subunit 14

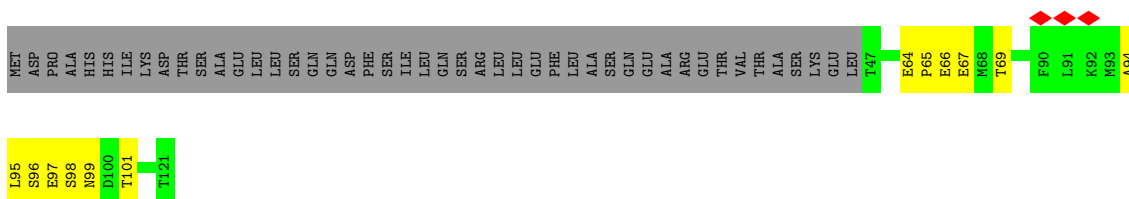




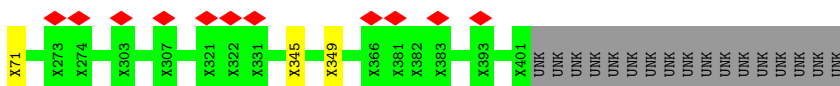
• Molecule 9: Mediator complex subunit 4

Chain D: 38% 60%

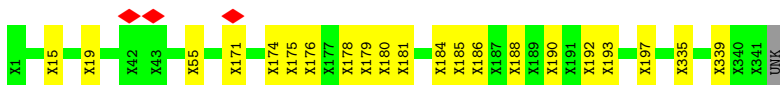




Chain S: 8% 86% 12%



Chain J: 83% 16%

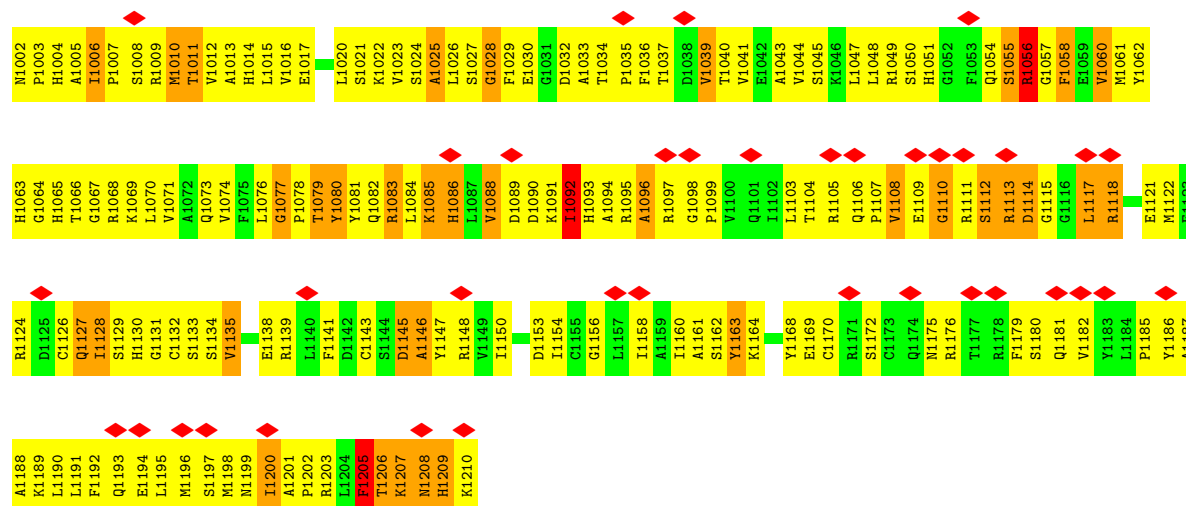


Chain a:

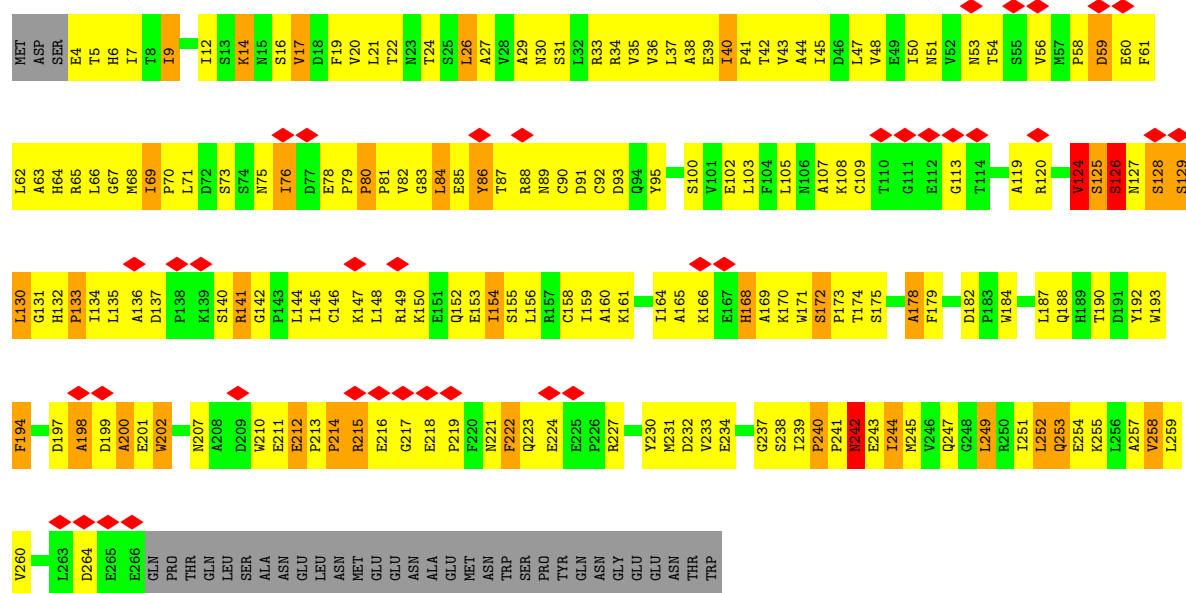


D1007	R1008	T1009	T1010	R1011	D1012	V1013	N1016	A1017	T1018	L1019	L1020	F1021	L1022	I1023	L1024	L1025	R1026	S1027	K1028	F1029	A1030	V1031	K1032	Y1038	R1039	L1040	K1041	K1042	V1043	A1044	F1045	E1046	I1047	M1048	M1049	E1050	E1051	V1052	E1053	V1061	S1062	P1063	G1064	E1065	M1066	V1067	G1068	L1070	A1071	A1072	Q1073	S1074	I1075	G1076	E1077				
L945	C946	R947	F948	I949	F950	P951	K952	G953	D954	A955	R956	W957	P958	L959	P960	V961	N962	S963	Q964	R965	I966	I967	Q968	N969	A970	L971	Q972	I973	F974	R975	L976	E977	A978	K979	K980	P981	T982	D983	L984	L985	P986	S987	D988	I989	I990	L993	L996	I997	K998	A999	L1000	A1071	A1072	Q1073	S1074	I1075	G1076	E1077	
B876	D877	L878	D880	A881	T882	L883	V884	E885	Y886	Q887	V888	F889	D890	S891	L892	R893	L894	S895	Q896	K900	Y903	R904	I905	D906	L907	M908	E909	D910	R911	Y916	M917	E918	N919	S920	I921	E922	N923	D924	S925	S926	V927	Q928	D929	E933	E934	Q937	L938	V939	A940	R941	E942	E943	L944						
T815	F816	Q817	E818	F819	F820	F821	L822	A823	N824	A825	C826	R827	E828	G829	L830	T833	A834	V835	K836	T837	A838	E839	T840	G841	T842	T843	Q844	R845	R846	L847	V848	K849	A850	R851	E852	D853	V854	M855	V856	R857	V858	D859	G860	T861	R863	N864	A865	M866	C867	D868	T869	R870	N808	S809	Y810	L811	R812	G813	C875
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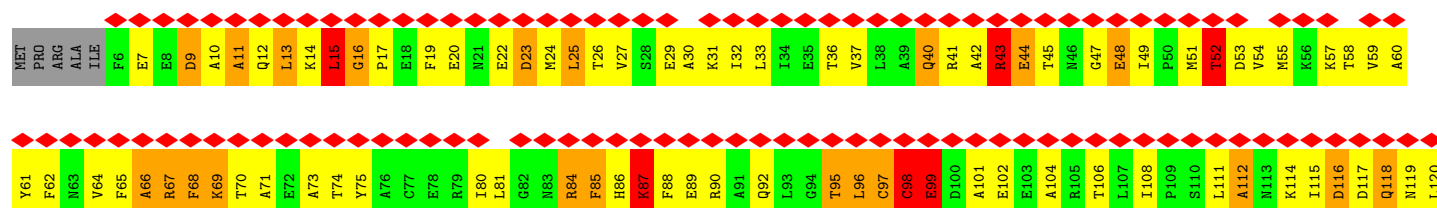
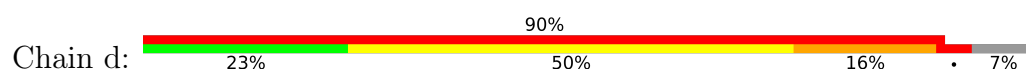
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T945	D880	C818	S753	N629	N563	L500	I439	A316	F189	I189	ALA
N946	K881	Y819	P754	P630	T564	H501	T440	L317	E249	I190	ALA
Q947	S820	S820	R755	N631	K565	N502	N441	D318	N250	N191	ASP
E948	G821	E695	N756	S632	K566	T503	G442	Y319	G580	G192	SER
D949	Y822	A696	T757	E633	V566	H504	L443	D320	S251	S193	ASN
L950	D885	N823	Y758	E634	F567	H505	L444	G321	G252	E194	VAL
K951	G886	Q824	Q759	R635	V568	H506	L445	K322	Q253	K196	PRO
K952	E826	E826	S760	R636	N569	G506	S446	R323	T254	E194	ILE
G953	S827	W700	A761	R637	N570	H507	S447	G324	I255	V196	GLY
V954	I828	A702	H762	E637	V508	C509	A448	G325	L259	I197	GLU
K955	I829	G703	G763	L638	L573	P510	T449	S325	P260	I198	GLU
K956	M830	Y704	K764	C639	G574	C509	G450	T326	Y261	Q200	TRP
K957	N831	E705	M767	L640	V575	A511	M451	T327	G262	E201	VAL
K958	Q832	V706	L771	E643	H576	E512	M452	G328	R263	R202	GLU
S959	Q833	W707	L772	E644	R577	T513	G454	V329	S264	S203	GLU
G960	I835	E708	T773	H644	P579	E515	Q455	T330	P267	A204	GLU
G961	S834	W708	T774	L645	A580	Q517	R457	R331	I268	A205	GLU
G962	I835	E709	Y774	L646	H581	A518	S458	E332	V269	I207	GLU
G963	Q838	L710	Q775	Q646	T583	C519	M459	K333	V208	V208	GLU
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G965	F840	A713	R777	L648	T585	L521	M461	R335	V210	V210	GLU
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G967	F842	R715	T780	K652	L587	K523	V463	Y337	K212	K212	GLU
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G969	H846	K717	A782	D654	L589	L525	V465	R339	I283	I283	GLU
G970	T847	Q718	L783	R655	R590	S526	Q467	K344	L284	L284	GLU
G971	Y848	P718	L784	D656	R591	L527	V468	D341	D280	D280	GLU
G972	T849	A719	L785	K657	H592	N528	M469	I342	I342	I342	GLU
G973	D850	Q720	Y786	L657	L593	S529	N470	Q343	S217	S217	GLU
G974	Q851	P721	L787	D658	I601	Y530	R471	K344	P218	P218	GLU
G975	E852	W722	K793	P659	V602	V531	T472	E345	I219	I219	GLU
G976	K853	V724	H794	E660	R603	S532	T473	E346	A220	A220	GLU
G977	K854	H725	A795	D661	P604	V533	F474	I347	Y221	Y221	GLU
G978	I855	Q726	L796	R662	L605	G534	A475	Y289	V222	V222	GLU
G979	G856	W727	T797	K663	R606	S535	S476	D290	C164	C164	GLU
G980	M857	T728	R798	G664	E607	P536	T477	I350	I165	I165	GLU
G981	T858	H729	Y799	T666	K608	S537	L478	T351	L166	L166	GLU
G982	E861	Q730	S797	A667	E609	A538	S479	T352	R226	R226	GLU
G983	B862	E731	N798	L668	L610	P539	L481	M353	G168	G168	GLU
G984	B863	W732	Y799	V669	R611	I540	R482	E294	V169	V169	GLU
G985	E864	H733	Q800	L669	L612	I541	R483	Q295	A228	A228	GLU
G986	B865	P734	L801	S670	F613	E542	T484	G355	S170	S170	GLU
G987	B866	W735	K802	S671	T614	F543	M485	F356	D171	D171	GLU
G988	E867	A736	F803	G672	D615	E544	T486	R359	L174	L174	GLU
G989	B868	Q736	R804	L673	A616	E545	P487	M300	Y175	Y175	GLU
G990	B869	T737	E805	L674	G617	E546	I488	K301	D176	D176	GLU
G991	B870	W738	L806	E675	L616	E547	G489	P302	L177	L177	GLU
G992	B871	Q739	R807	E676	R619	E548	R490	C303	N178	N178	GLU
G993	B872	I740	A808	L677	C620	E549	R491	G365	E179	E179	GLU
G994	B873	W741	L809	D678	R621	E550	D491	E306	C180	C180	GLU
G995	B874	L742	K811	E679	R622	E551	G492	A307	P181	P181	GLU
G996	B875	I743	L812	E680	P622	E552	K493	E308	I182	I182	GLU
G997	B876	Q744	L813	E681	L624	E553	L494	R370	Q240	Q240	GLU
G998	B877	W745	L814	E682	F624	E554	L495	M371	I241	I241	GLU
G999	B878	P746	W814	E683	L625	E555	A495	I310	K242	K242	GLU
G1000	B879	F747	Y814	E684	T684	E556	K496	Q311	M244	M244	GLU
G1001	B880	D749	W815	E685	M686	P557		D312	A245	A245	GLU



• Molecule 19: RNA polymerase II subunit Rpb3

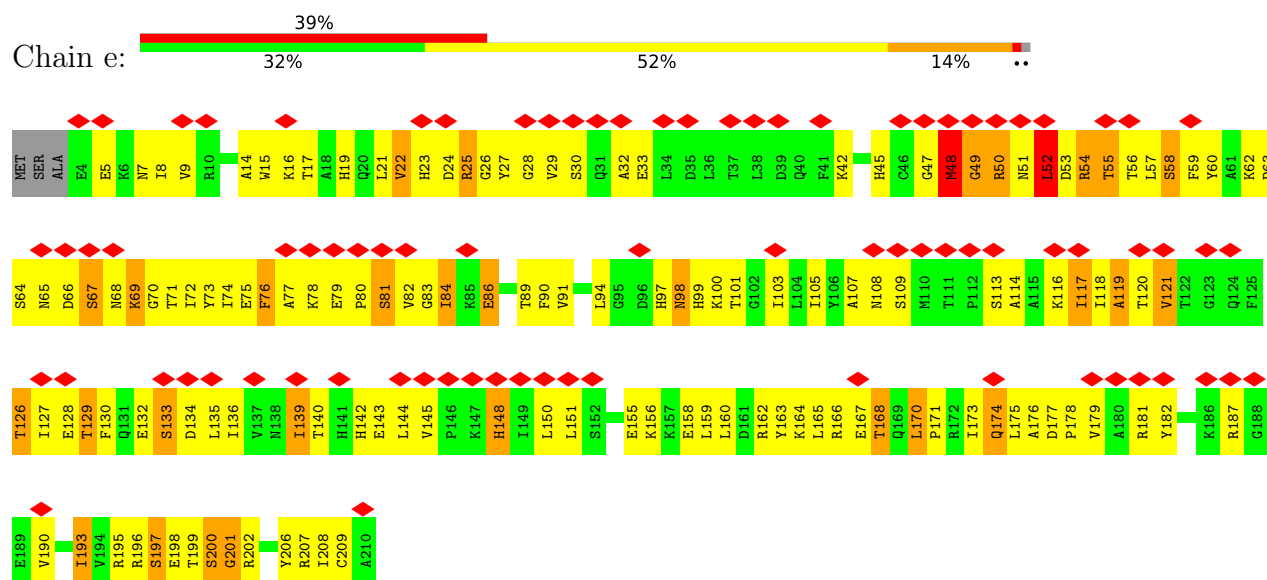


• Molecule 20: RNA polymerase II subunit Rpb4

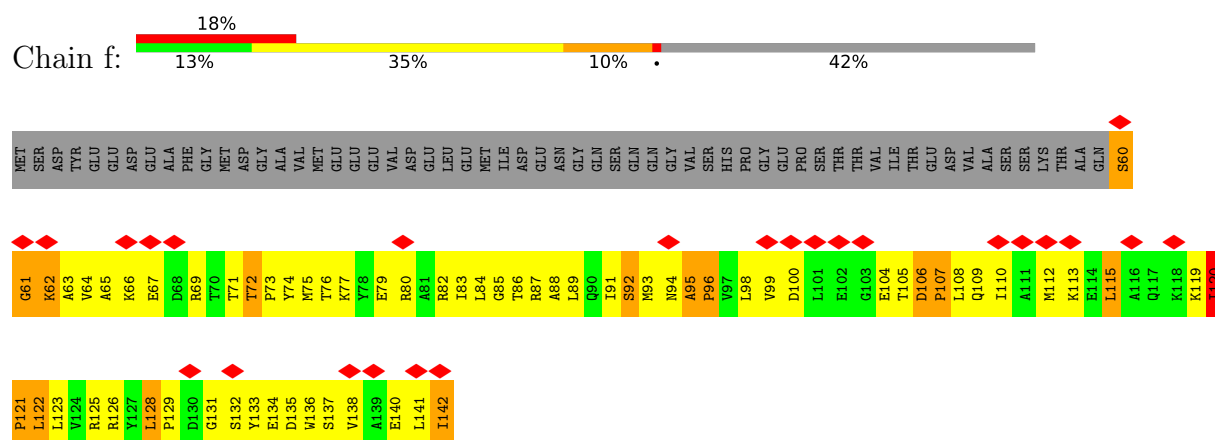




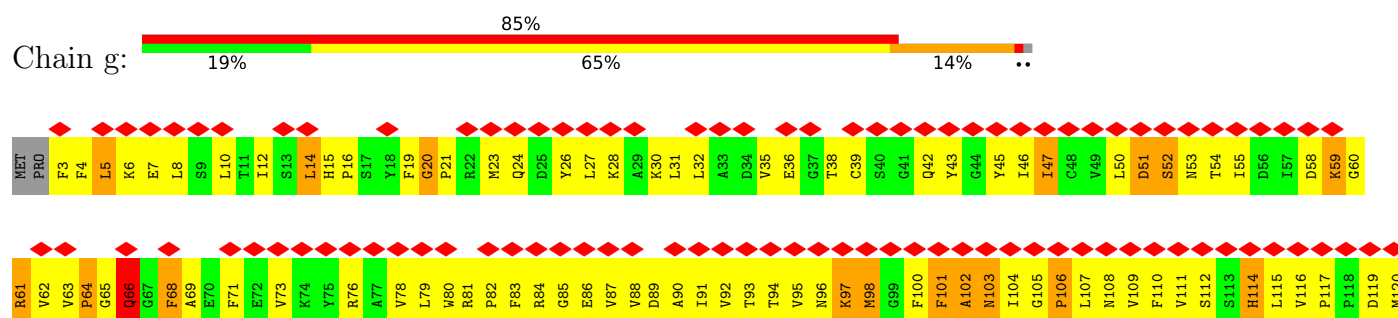
• Molecule 21: RNA polymerase II subunit Rpb5



• Molecule 22: RNA polymerase II subunit Rpb6

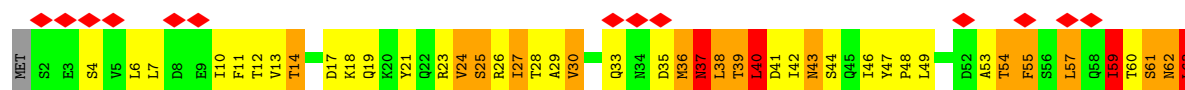


• Molecule 23: RNA polymerase II subunit Rpb7

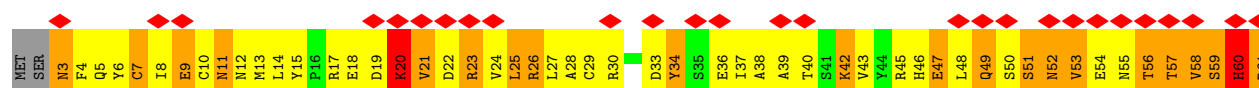




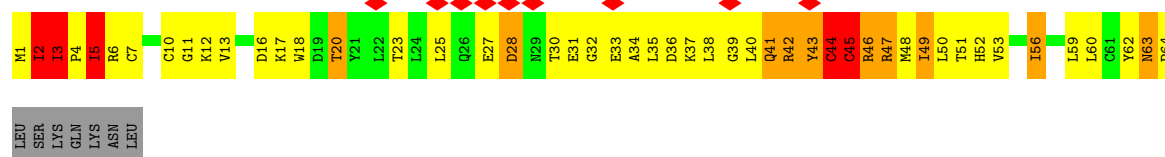
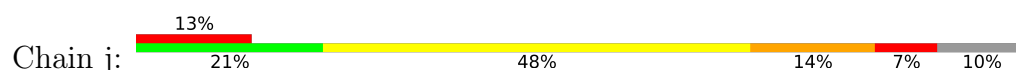
• Molecule 24: RNA polymerase II subunit Rpb8



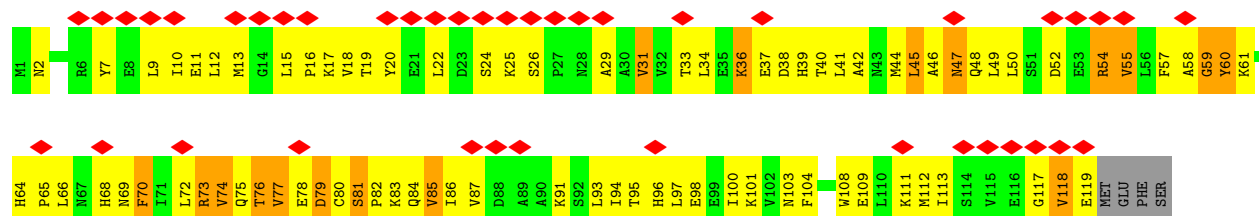
• Molecule 25: RNA polymerase II subunit Rpb9



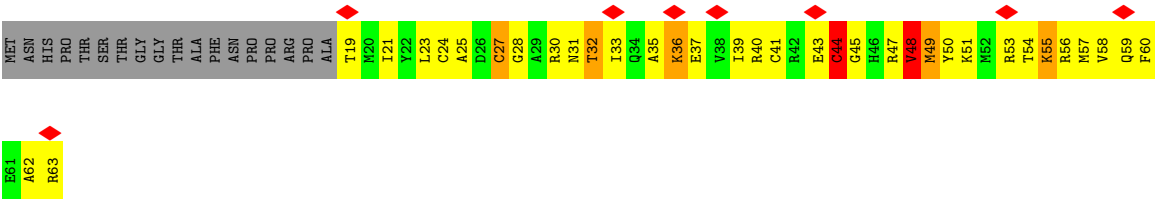
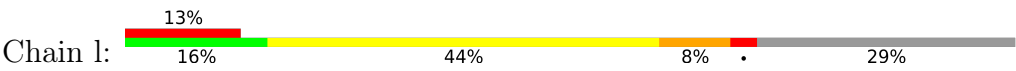
• Molecule 26: RNA polymerase II subunit Rpb10



• Molecule 27: RNA polymerase II subunit Rpb11



• Molecule 28: RNA polymerase II subunit Rpb12



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	3862	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	9.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.229	Depositor
Minimum map value	-0.114	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	461.12, 461.12, 461.12	wwPDB
Map dimensions	176, 176, 176	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.62, 2.62, 2.62	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	F	0.36	0/1570	0.82	2/2126 (0.1%)
2	H	0.38	0/1523	0.82	0/2063
3	Q	0.39	0/3856	0.87	11/5223 (0.2%)
4	R	0.36	0/1739	0.86	4/2362 (0.2%)
5	T	0.46	2/1469 (0.1%)	1.17	12/1992 (0.6%)
6	K	0.41	0/778	0.83	0/1049
7	V	0.37	0/963	0.76	1/1309 (0.1%)
8	N	0.40	0/3865	0.97	15/5275 (0.3%)
10	G	0.50	0/961	1.07	5/1336 (0.4%)
11	U	0.44	0/606	0.95	1/844 (0.1%)
12	3	0.42	0/514	1.05	4/718 (0.6%)
13	2	0.37	0/382	0.91	0/524
14	I	0.42	0/373	0.90	0/520
17	a	0.54	3/11983 (0.0%)	0.87	37/16197 (0.2%)
18	b	0.58	3/9360 (0.0%)	0.91	36/12643 (0.3%)
19	c	0.59	0/2135	0.95	10/2904 (0.3%)
20	d	0.30	0/1000	0.65	1/1348 (0.1%)
21	e	0.50	0/1695	0.90	7/2287 (0.3%)
22	f	0.68	0/666	1.12	10/901 (1.1%)
23	g	0.33	0/1361	0.78	2/1847 (0.1%)
24	h	0.53	0/1010	0.88	2/1363 (0.1%)
25	i	0.26	0/921	0.53	0/1246
26	j	0.78	0/526	1.13	4/709 (0.6%)
27	k	0.59	0/972	0.90	0/1317
28	l	0.46	0/371	0.84	0/491
All	All	0.50	8/50599 (0.0%)	0.90	164/68594 (0.2%)

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.

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Mol	Chain	#Chirality outliers	#Planarity outliers
-----	-------	---------------------	---------------------

Mol	Chain	#Chirality outliers	#Planarity outliers
8	N	0	2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	a	346	LEU	C-N	-7.42	1.23	1.33
18	b	1150	ILE	C-N	6.76	1.43	1.33
18	b	480	HIS	C-N	6.41	1.42	1.33
5	T	101	SER	C-N	6.28	1.41	1.33
18	b	1011	THR	CA-CB	-5.72	1.48	1.53

The worst 5 of 164 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	T	100	GLY	CA-C-N	17.75	153.64	121.70
5	T	100	GLY	C-N-CA	17.75	153.64	121.70
5	T	100	GLY	CA-C-O	-10.46	110.37	121.35
17	a	997	ILE	N-CA-C	-10.32	102.64	112.96
8	N	445	SER	CA-C-N	10.19	127.00	119.66

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	N	256	LYS	Peptide
8	N	302	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1534	0	1484	114	0
2	H	1493	0	1467	107	0
3	Q	3787	0	3544	283	0
4	R	1694	0	1670	148	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	T	1435	0	1448	198	0
6	K	769	0	783	69	0
7	V	949	0	961	69	0
8	N	3887	0	3543	322	0
9	D	480	0	101	11	0
10	G	965	0	402	6	0
11	U	608	0	265	4	0
12	3	515	0	209	17	0
13	2	388	0	155	14	0
14	I	374	0	163	6	0
15	S	610	0	138	2	0
16	J	655	0	144	12	0
17	a	11761	0	11738	3370	0
18	b	9180	0	9164	1711	0
19	c	2088	0	2044	333	0
20	d	988	0	977	375	0
21	e	1663	0	1684	213	0
22	f	656	0	679	78	0
23	g	1330	0	1329	424	0
24	h	996	0	1006	169	0
25	i	902	0	843	280	0
26	j	518	0	532	101	0
27	k	955	0	968	126	0
28	l	368	0	381	39	0
All	All	51548	0	47822	7818	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 79.

The worst 5 of 7818 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:a:1161:PRO:HG2	17:a:1190:LYS:CG	1.29	1.60
8:N:192:THR:C	8:N:194:PRO:HD3	1.19	1.59
23:g:100:PHE:HB2	23:g:111:VAL:CG1	1.34	1.58
3:Q:135:GLU:HB3	20:d:128:SER:CB	1.29	1.57
17:a:267:ASP:CB	17:a:268:LEU:HB2	1.35	1.56

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	F	182/216 (84%)	154 (85%)	24 (13%)	4 (2%)	5	29
2	H	178/200 (89%)	161 (90%)	15 (8%)	2 (1%)	11	46
3	Q	492/545 (90%)	424 (86%)	55 (11%)	13 (3%)	4	25
4	R	205/207 (99%)	177 (86%)	23 (11%)	5 (2%)	4	27
5	T	172/193 (89%)	141 (82%)	21 (12%)	10 (6%)	1	14
6	K	96/116 (83%)	88 (92%)	7 (7%)	1 (1%)	12	49
7	V	116/136 (85%)	107 (92%)	8 (7%)	1 (1%)	14	51
8	N	489/931 (52%)	382 (78%)	72 (15%)	35 (7%)	1	11
10	G	186/376 (50%)	166 (89%)	18 (10%)	2 (1%)	11	46
11	U	118/138 (86%)	110 (93%)	5 (4%)	3 (2%)	4	26
12	3	101/139 (73%)	76 (75%)	9 (9%)	16 (16%)	0	2
13	2	66/273 (24%)	62 (94%)	3 (4%)	1 (2%)	8	40
14	I	73/121 (60%)	67 (92%)	3 (4%)	3 (4%)	2	18
17	a	1486/1752 (85%)	937 (63%)	276 (19%)	273 (18%)	0	2
18	b	1142/1210 (94%)	735 (64%)	244 (21%)	163 (14%)	0	3
19	c	261/297 (88%)	178 (68%)	56 (22%)	27 (10%)	0	6
20	d	123/135 (91%)	85 (69%)	20 (16%)	18 (15%)	0	3
21	e	205/210 (98%)	137 (67%)	43 (21%)	25 (12%)	0	4
22	f	81/142 (57%)	57 (70%)	16 (20%)	8 (10%)	0	7
23	g	168/172 (98%)	128 (76%)	24 (14%)	16 (10%)	0	8
24	h	122/125 (98%)	73 (60%)	27 (22%)	22 (18%)	0	2
25	i	109/113 (96%)	46 (42%)	27 (25%)	36 (33%)	0	0
26	j	62/71 (87%)	41 (66%)	15 (24%)	6 (10%)	0	7
27	k	117/123 (95%)	80 (68%)	24 (20%)	13 (11%)	0	5
28	l	43/63 (68%)	23 (54%)	12 (28%)	8 (19%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6393/8004 (80%)	4635 (72%)	1047 (16%)	711 (11%)	1 5

5 of 711 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	Q	319	GLN
4	R	50	ARG
5	T	101	SER
8	N	175	ILE
8	N	194	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	F	171/198 (86%)	171 (100%)	0	100 100
2	H	168/185 (91%)	167 (99%)	1 (1%)	78 83
3	Q	389/509 (76%)	389 (100%)	0	100 100
4	R	191/191 (100%)	191 (100%)	0	100 100
5	T	161/178 (90%)	161 (100%)	0	100 100
6	K	88/108 (82%)	88 (100%)	0	100 100
7	V	112/129 (87%)	112 (100%)	0	100 100
8	N	369/799 (46%)	369 (100%)	0	100 100
17	a	1296/1536 (84%)	1089 (84%)	207 (16%)	2 11
18	b	1012/1064 (95%)	900 (89%)	112 (11%)	6 20
19	c	236/267 (88%)	217 (92%)	19 (8%)	11 31
20	d	106/115 (92%)	89 (84%)	17 (16%)	2 11
21	e	182/184 (99%)	170 (93%)	12 (7%)	15 37
22	f	71/121 (59%)	65 (92%)	6 (8%)	10 29
23	g	146/148 (99%)	136 (93%)	10 (7%)	14 36
24	h	113/114 (99%)	99 (88%)	14 (12%)	4 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	i	103/105 (98%)	80 (78%)	23 (22%)	1	6
26	j	59/66 (89%)	46 (78%)	13 (22%)	1	6
27	k	109/113 (96%)	100 (92%)	9 (8%)	10	30
28	l	39/53 (74%)	34 (87%)	5 (13%)	4	15
All	All	5121/6183 (83%)	4673 (91%)	448 (9%)	12	29

5 of 448 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	b	352	THR
28	l	27	CYS
18	b	870	THR
27	k	72	LEU
25	i	17	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 158 such sidechains are listed below:

Mol	Chain	Res	Type
18	b	985	HIS
23	g	53	ASN
18	b	1086	HIS
19	c	247	GLN
25	i	79	HIS

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	S	6
16	J	3
9	D	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	56:UNK	C	160:UNK	N	39.54
1	J	204:UNK	C	310:UNK	N	28.97
1	S	265:UNK	C	271:UNK	N	28.24
1	S	366:UNK	C	381:UNK	N	25.63
1	S	287:UNK	C	301:UNK	N	18.84

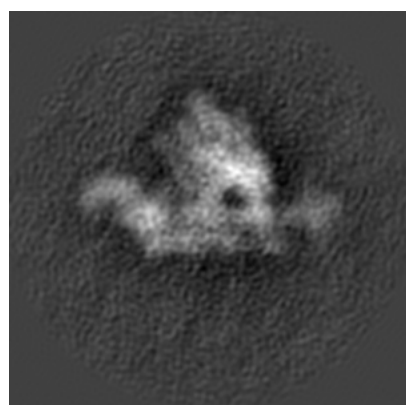
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8480. These allow visual inspection of the internal detail of the map and identification of artifacts.

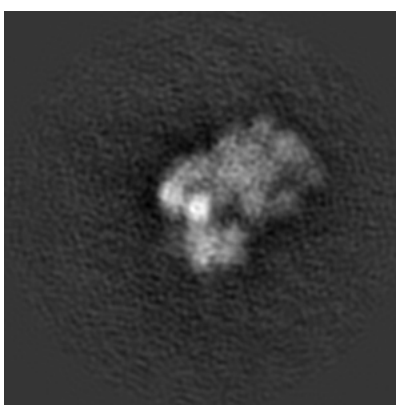
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

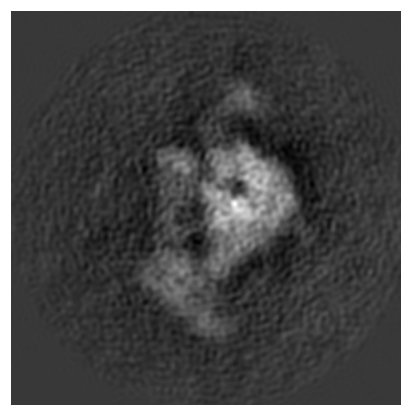
6.1.1 Primary map



X



Y

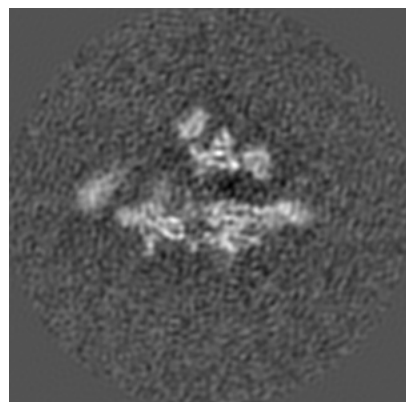


Z

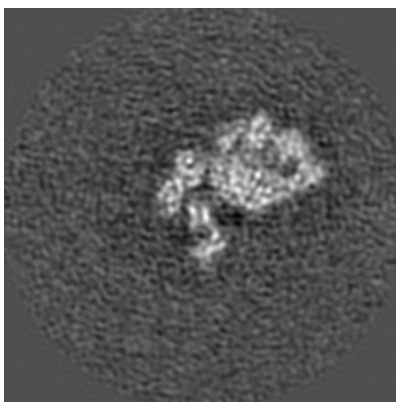
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

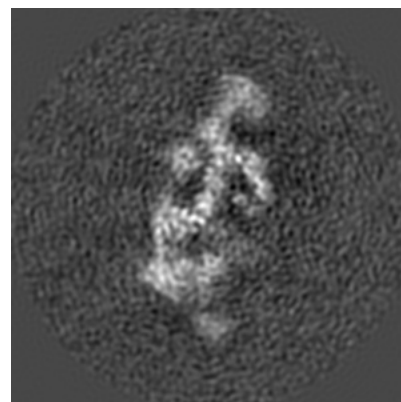
6.2.1 Primary map



X Index: 88



Y Index: 88

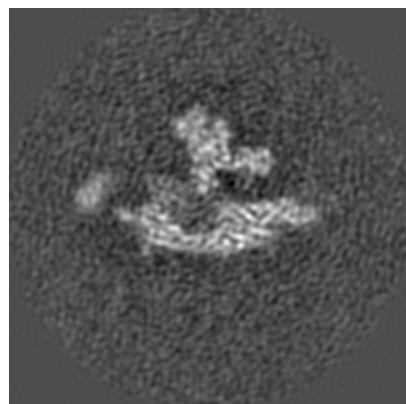


Z Index: 88

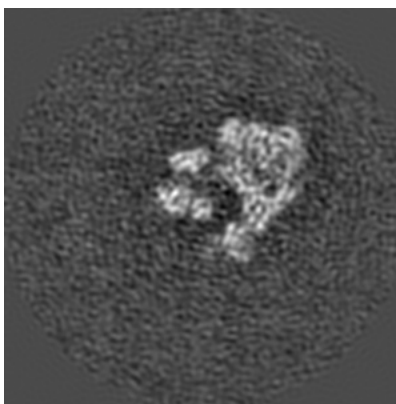
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

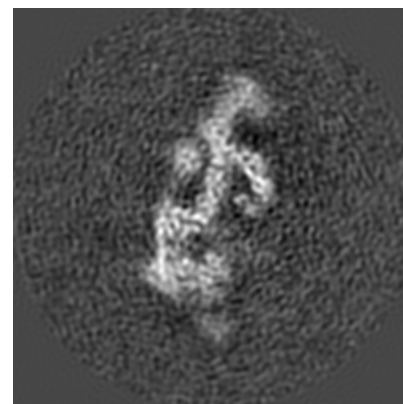
6.3.1 Primary map



X Index: 91



Y Index: 94

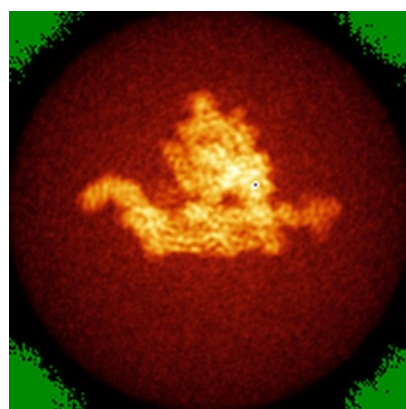


Z Index: 87

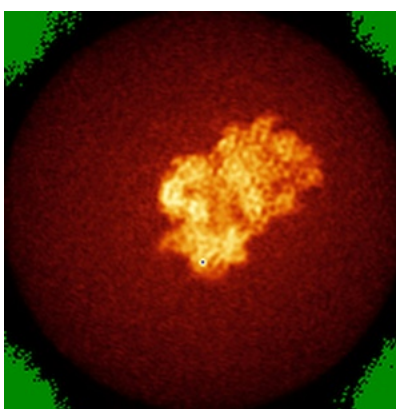
The images above show the largest variance slices of the map in three orthogonal directions.

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

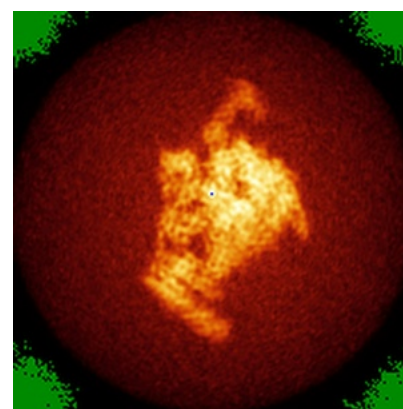
6.4.1 Primary map



X



Y

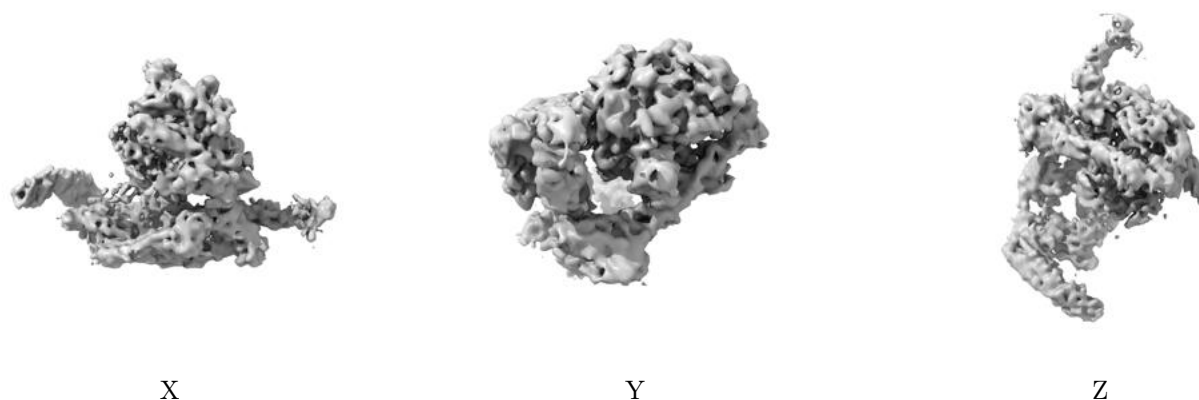


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

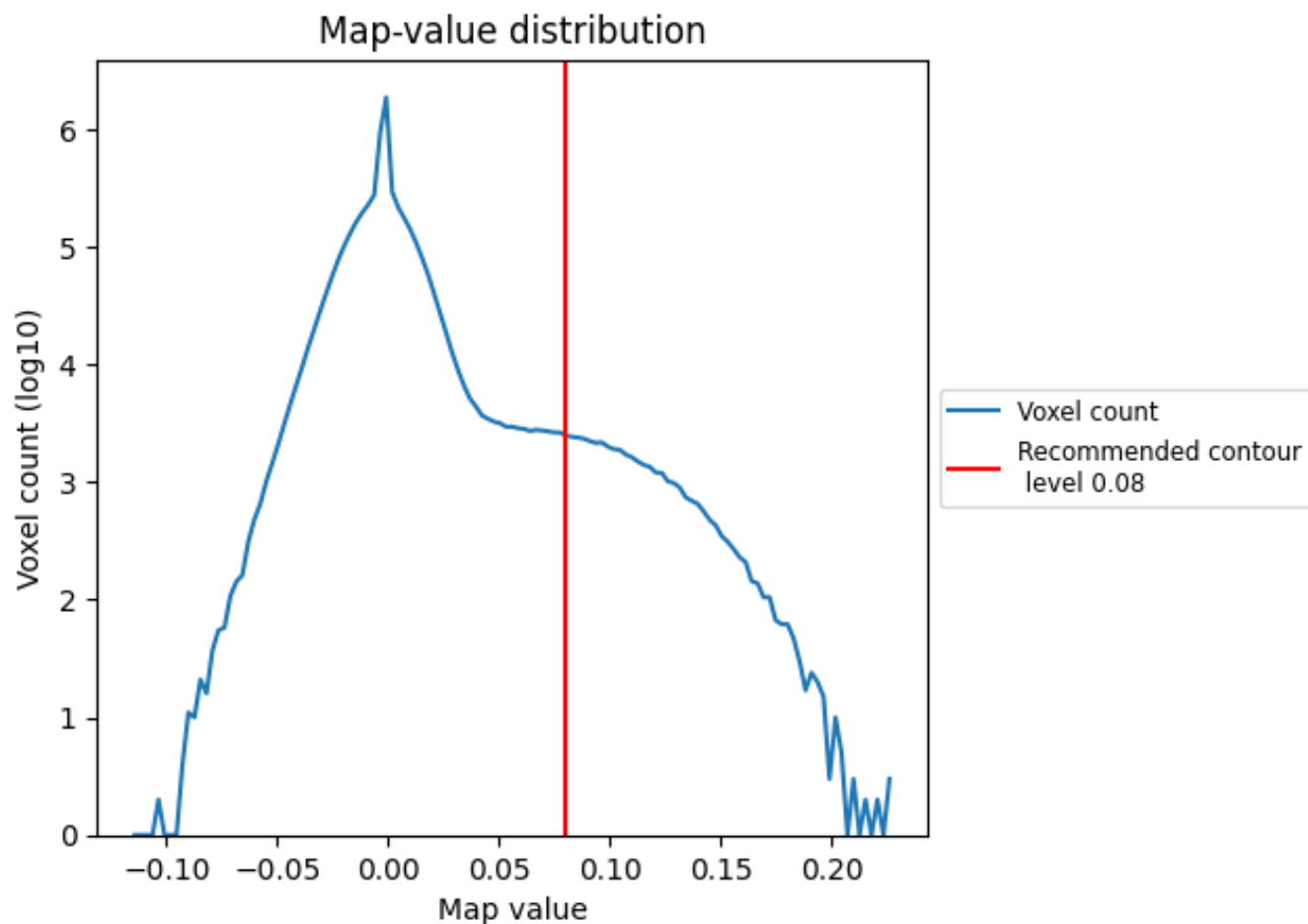
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

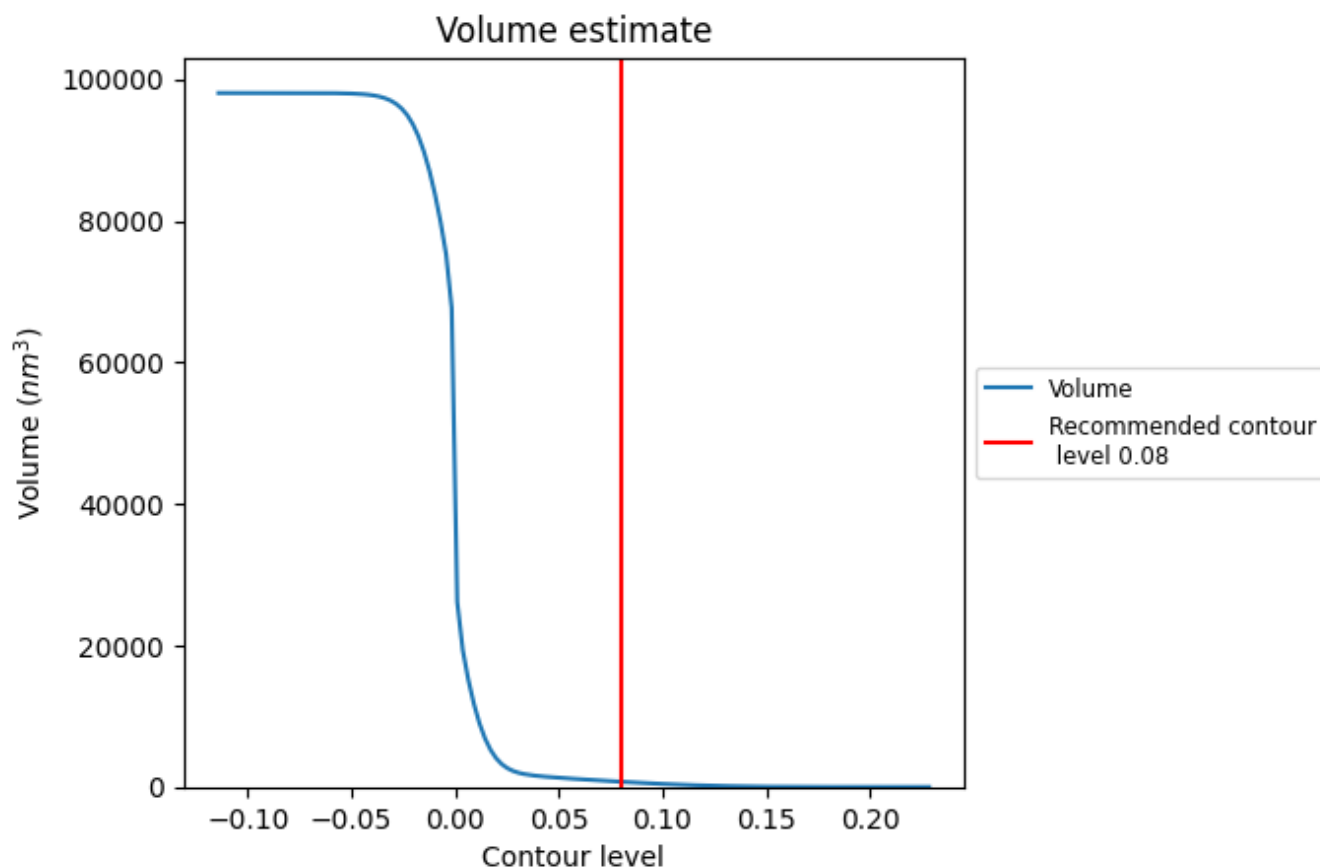
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

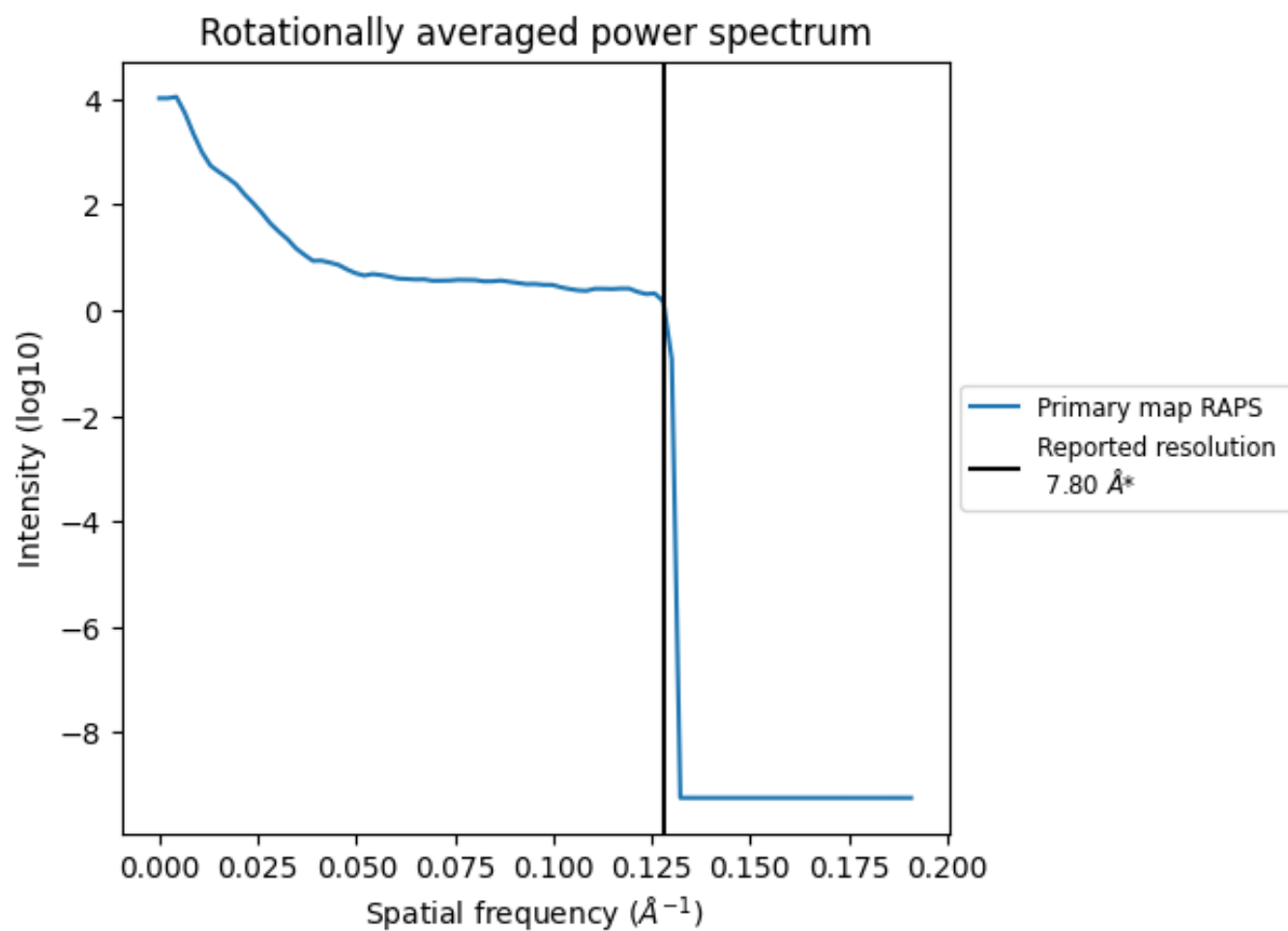
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 735 nm^3 ; this corresponds to an approximate mass of 664 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 0.128 Å⁻¹

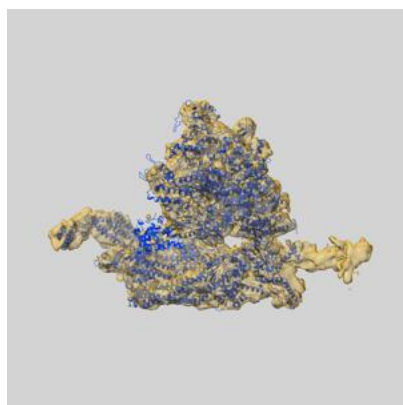
8 Fourier-Shell correlation

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

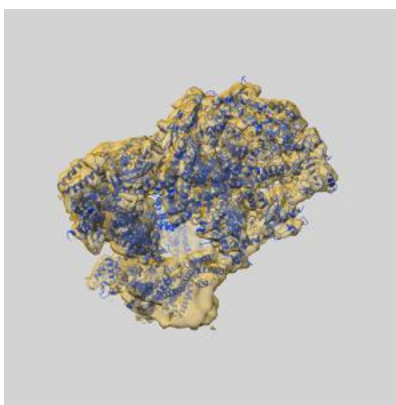
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8480 and PDB model 5U0S. Per-residue inclusion information can be found in section [3](#) on page [9](#).

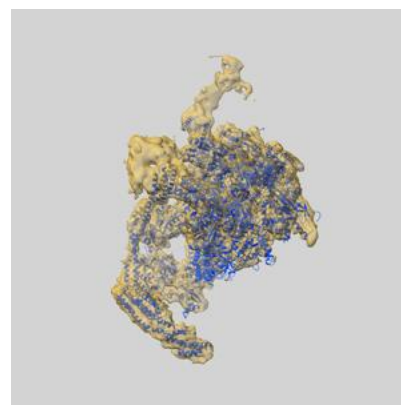
9.1 Map-model overlay [i](#)



X



Y



Z

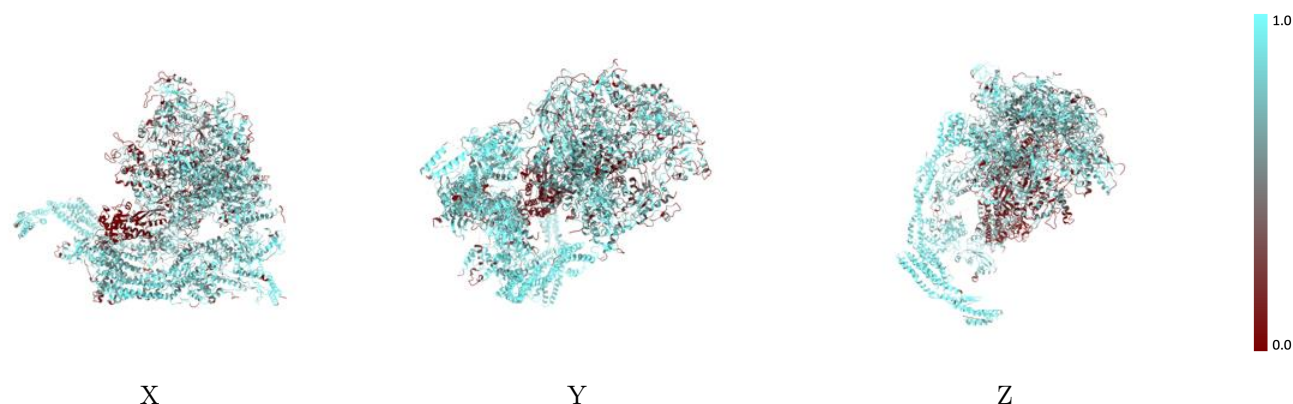
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



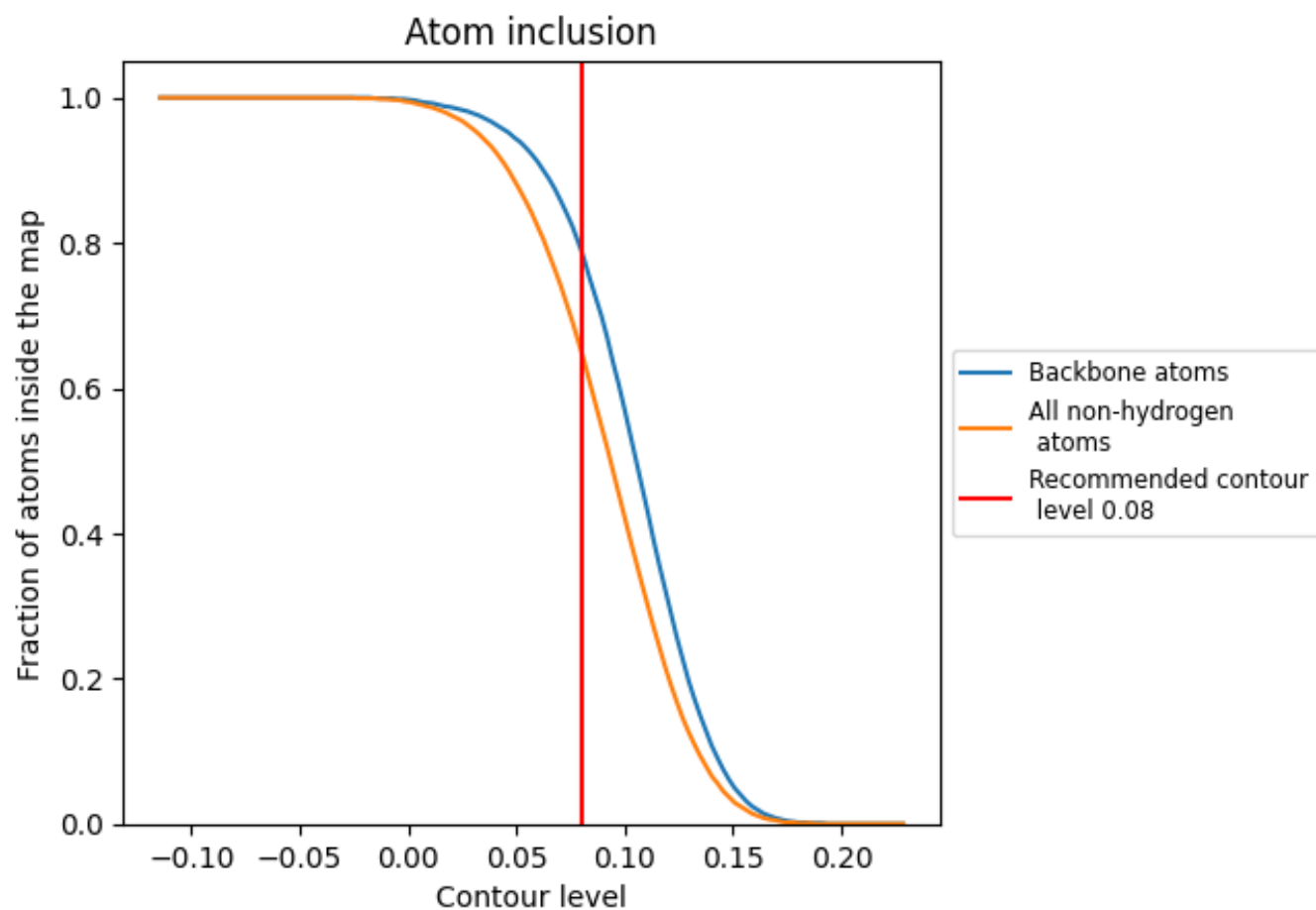
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 65% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6510	 0.1230
2	 0.9430	 0.2260
3	 0.9440	 0.2070
D	 0.9040	 0.2350
F	 0.7220	 0.1270
G	 0.9510	 0.2160
H	 0.6980	 0.1620
I	 0.9470	 0.2090
J	 0.9650	 0.1540
K	 0.8310	 0.1410
N	 0.7830	 0.1550
Q	 0.7090	 0.1510
R	 0.7780	 0.1390
S	 0.8950	 0.1070
T	 0.8170	 0.1470
U	 0.9290	 0.1950
V	 0.7990	 0.1510
a	 0.5630	 0.1050
b	 0.6170	 0.1000
c	 0.7060	 0.1160
d	 0.0250	 0.0450
e	 0.5410	 0.1010
f	 0.5840	 0.1210
g	 0.1180	 0.0370
h	 0.6740	 0.1180
i	 0.4990	 0.0900
j	 0.7100	 0.0990
k	 0.5410	 0.1320
l	 0.6190	 0.0870

