



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 03:48 AM UTC

PDB ID : 3JB9 / pdb_00003jb9
EMDB ID : EMD-6413
Title : Cryo-EM structure of the yeast spliceosome at 3.6 angstrom resolution
Authors : Yan, C.; Hang, J.; Wan, R.; Huang, M.; Wong, C.; Shi, Y.
Deposited on : 2015-08-09
Resolution : 3.60 Å(reported)
Based on initial models : 3J7P, 3U1L, 2XL2, 2YTC, 4YVD, 3LRV, 4I43, 4WZJ, 1GV2, 2BAY

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:

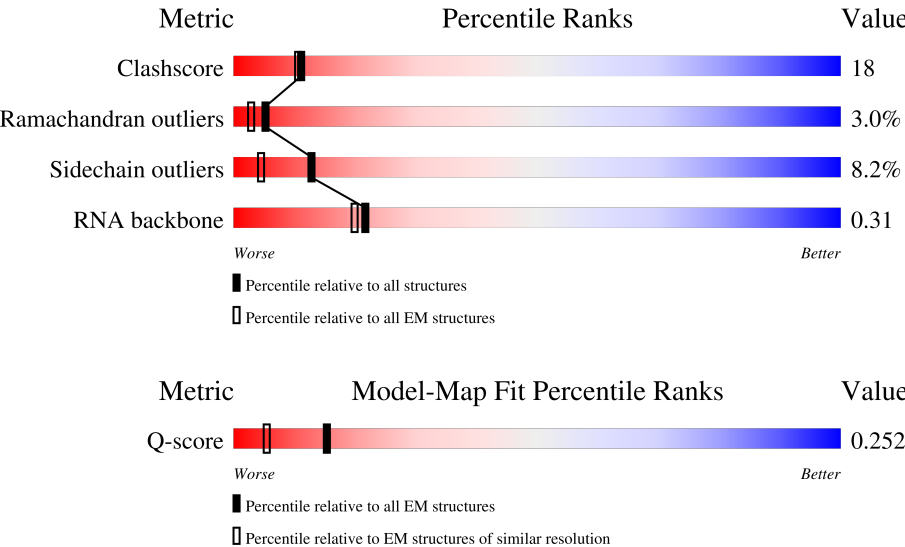
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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 i

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

The reported resolution of this entry is 3.60 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.



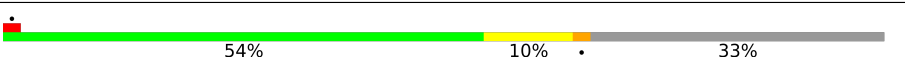
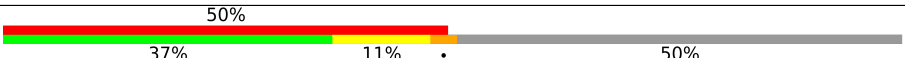
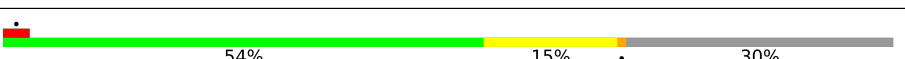
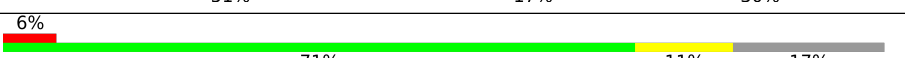
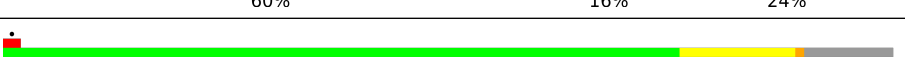
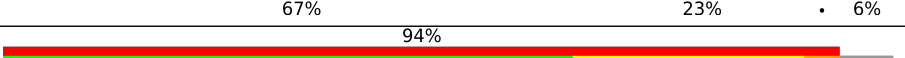
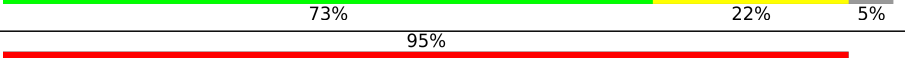
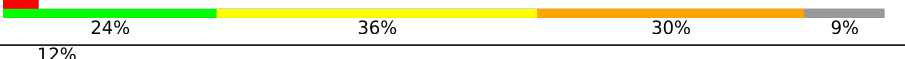
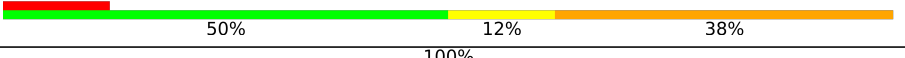
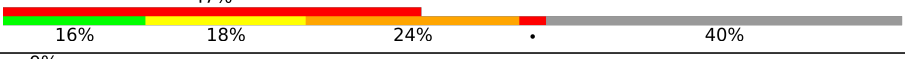
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	A	2363	7% 57% 21% 5% 17%
2	B	984	66% 23% 8%
3	C	120	35% 33% 18% 12%

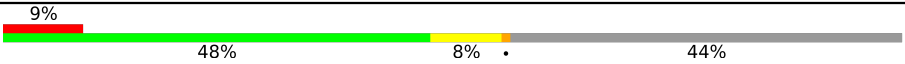
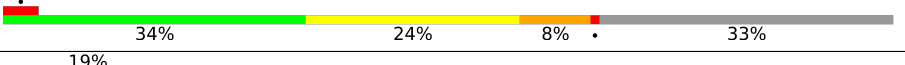
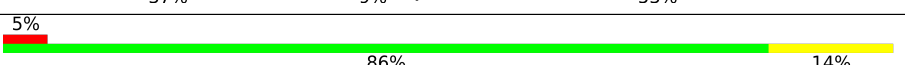
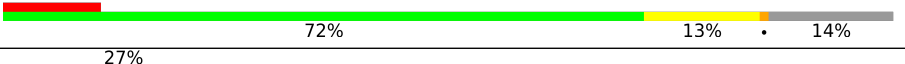
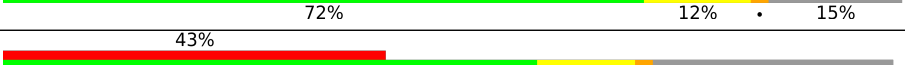
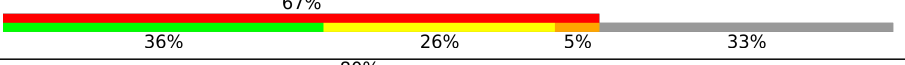
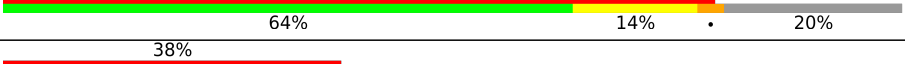
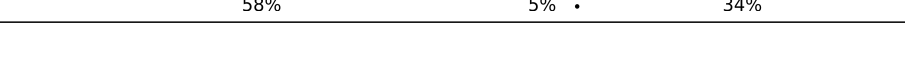
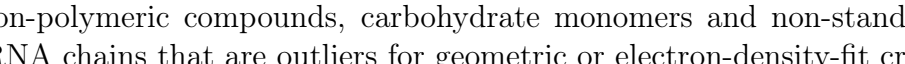
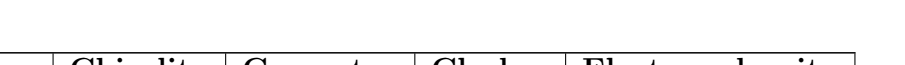
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	97	
4	Z	97	
5	E	147	
5	b	147	
6	F	117	
6	f	117	
7	G	115	
7	l	115	
8	H	84	
8	m	84	
9	I	78	
9	n	78	
10	J	77	
10	o	77	
11	K	473	
12	L	340	
13	M	557	
14	N	99	
15	O	8	
16	Q	13	
17	P	186	
18	S	488	
18	T	488	
18	U	488	
18	V	488	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
19	W	757	
20	Y	388	
21	a	354	
22	c	639	
23	d	155	
24	e	146	
25	g	558	
26	h	265	
27	i	187	
28	R	674	
29	r	790	
30	X	1284	
31	j	239	
32	k	111	
33	x	412	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	ZN	Y	501	-	-	X	-
36	ZN	a	402	-	-	X	-
36	ZN	e	201	-	-	X	-
36	ZN	e	202	-	-	X	-
36	ZN	e	203	-	-	X	-
37	ADP	X	1500	-	-	X	-

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 86551 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 Pre-mRNA-splicing factor spp42.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1964	Total	C	N	O	S	0	0
			16230	10413	2859	2893	65		

- Molecule 2 is a protein called Pre-mRNA-splicing factor cwf10.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	904	Total	C	N	O	S	0	0
			7196	4586	1235	1340	35		

- Molecule 3 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	105	Total	C	N	O	P	0	0
			2209	990	364	750	105		

- Molecule 4 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	96	Total	C	N	O	S	0	0
			760	470	147	136	7		
4	Z	80	Total	C	N	O	S	0	0
			639	396	118	118	7		

- Molecule 5 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	98	Total	C	N	O	S	0	0
			730	464	130	131	5		
5	b	74	Total	C	N	O	S	0	0
			576	365	99	107	5		

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			646	412	110	119	5		
6	f	82	Total	C	N	O	S	0	0
			646	412	110	119	5		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	95	Total	C	N	O	S	0	0
			751	472	141	134	4		
7	l	87	Total	C	N	O	S	0	0
			696	440	128	124	4		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	76	Total	C	N	O	S	0	0
			620	401	107	110	2		
8	m	76	Total	C	N	O	S	0	0
			620	401	107	110	2		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	73	Total	C	N	O	S	0	0
			570	369	95	104	2		
9	n	73	Total	C	N	O	S	0	0
			570	369	95	104	2		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	73	Total	C	N	O	S	0	0
			573	366	98	108	1		
10	o	73	Total	C	N	O	S	0	0
			573	366	98	108	1		

- Molecule 11 is a protein called Pre-mRNA-splicing factor prp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	373	Total	C	N	O	S	0	0
			2730	1720	492	505	13		

- Molecule 12 is a protein called Pre-mRNA-splicing factor cwf17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	293	Total	C	N	O	S	0	0
			2273	1425	407	430	11		

- Molecule 13 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	207	Total	C	N	O	S	0	0
			1661	1044	309	304	4		

- Molecule 14 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	90	Total	C	N	O	P	0	0
			1928	863	357	618	90		

- Molecule 15 is a RNA chain called RNA (5'-R(P*GP*UP*AP*UP*GP*UP*AP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	8	Total	C	N	O	P	0	0
			170	76	28	58	8		

- Molecule 16 is a RNA chain called RNA (5'-R(P*UP*UP*UP*AP*UP*AP*CP*UP*AP*A P*CP*AP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	13	Total	C	N	O	P	0	0
			270	122	44	91	13		

- Molecule 17 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	111	Total	C	N	O	P	0	0
			2323	1039	365	808	111		

- Molecule 18 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	132	Total	C	N	O	S	0	0
			1052	663	181	205	3		
18	T	134	Total	C	N	O	S	0	0
			1069	671	183	212	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	430	Total	C	N	O	S	0	0
			2864	1801	492	562	9		
18	V	131	Total	C	N	O	S	0	0
			1037	652	177	205	3		

- Molecule 19 is a protein called Pre-mRNA-splicing factor cdc5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	426	Total	C	N	O	S	0	0
			3024	1881	562	574	7		

- Molecule 20 is a protein called Pre-mRNA-splicing factor cwf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	261	Total	C	N	O	S	0	0
			2008	1252	365	381	10		

- Molecule 21 is a protein called Pre-mRNA-splicing factor cwf5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	255	Total	C	N	O	S	0	0
			1751	1088	324	325	14		

- Molecule 22 is a protein called Pre-mRNA-splicing factor cwf19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	300	Total	C	N	O	S	0	0
			2425	1541	422	447	15		

- Molecule 23 is a protein called Peptidyl-prolyl cis-trans isomerase ppi1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	155	Total	C	N	O	S	0	0
			1187	755	203	224	5		

- Molecule 24 is a protein called Pre-mRNA-splicing factor cwf14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	144	Total	C	N	O	S	0	0
			1176	733	216	214	13		

- Molecule 25 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	148	Total	C	N	O	S	0	0
			1013	631	181	200	1		

- Molecule 26 is a protein called Pre-mRNA-splicing factor cwf15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	90	Total	C	N	O	S	0	0
			752	467	146	138	1		

- Molecule 27 is a protein called Pre-mRNA-splicing factor cwf7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	161	Total	C	N	O	S	0	0
			1218	758	219	238	3		

- Molecule 28 is a protein called Pre-mRNA-splicing factor cwf4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	575	Total	C	N	O	S	0	0
			3800	2363	718	706	13		

- Molecule 29 is a protein called Pre-mRNA-splicing factor cwf3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	573	Total	C	N	O	S	0	0
			3299	2039	619	640	1		

- Molecule 30 is a protein called Pre-mRNA-splicing factor cwf11.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	1195	Total	C	N	O	S	0	0
			9764	6282	1619	1820	43		

- Molecule 31 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	160	Total	C	N	O	S	0	0
			1108	707	187	211	3		

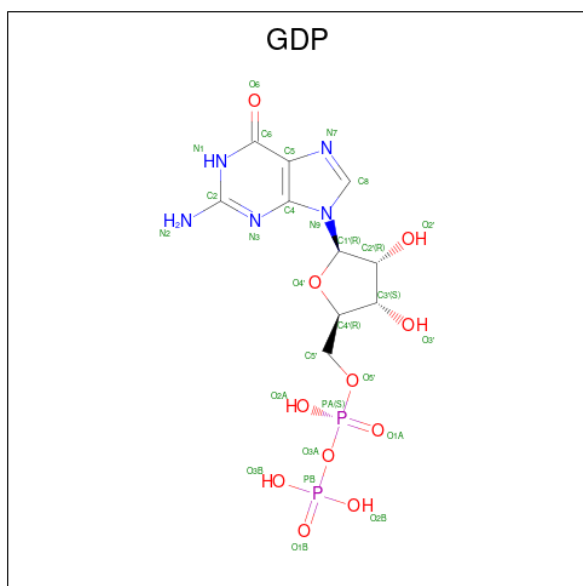
- Molecule 32 is a protein called Probable U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	89	Total	C	N	O	S	0	0
			618	405	102	109	2		

- Molecule 33 is a protein called unknown chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	x	272	Total	C	N	O	0	0
			1360	816	272	272		

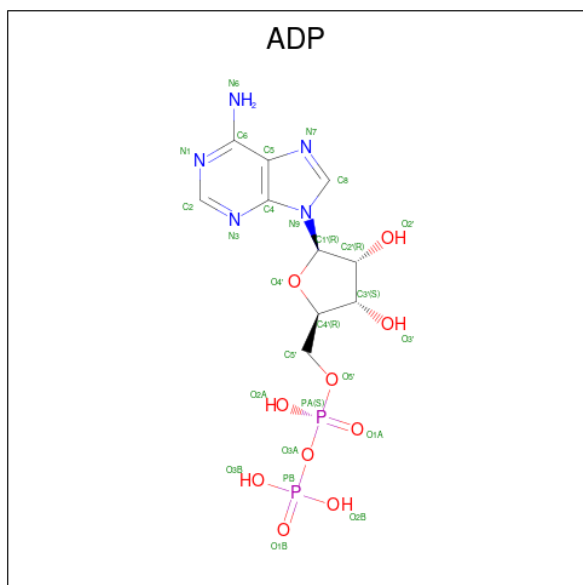
- Molecule 34 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
36	a	2	Total	Zn	0
			2	2	
36	c	1	Total	Zn	0
			1	1	
36	e	3	Total	Zn	0
			3	3	

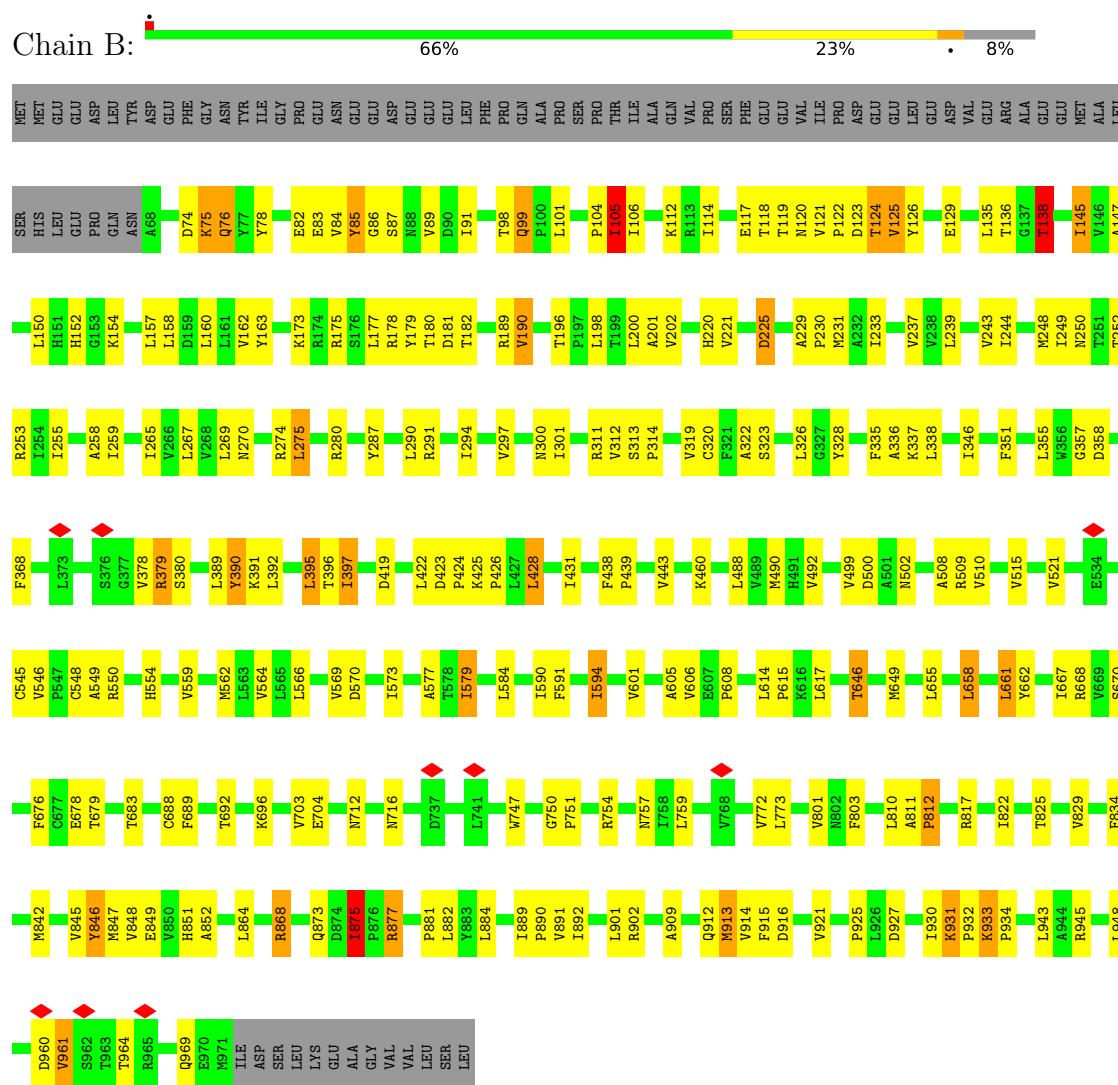
- Molecule 37 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



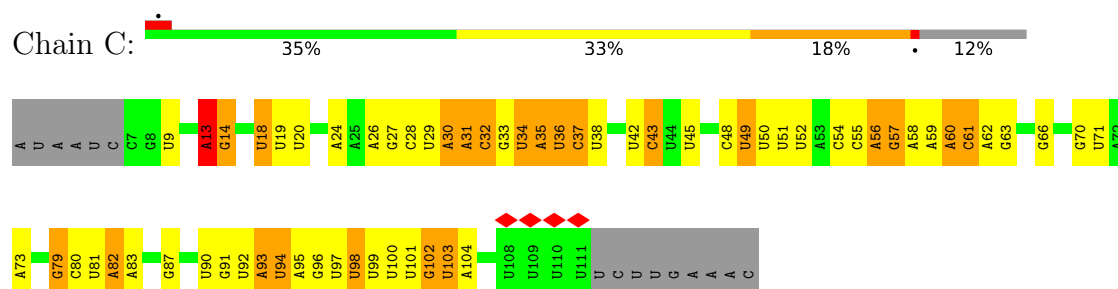
Mol	Chain	Residues	Atoms					AltConf
37	X	1	Total	C	N	O	P	0
			27	10	5	10	2	



- Molecule 2: Pre-mRNA-splicing factor cwf10

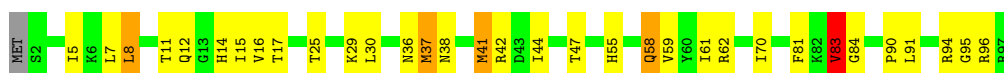


- Molecule 3: U5 snRNA



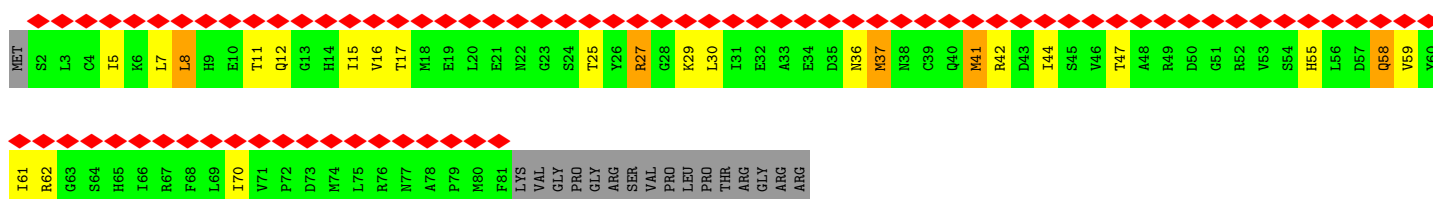
- Molecule 4: Small nuclear ribonucleoprotein Sm D3

Chain D: 



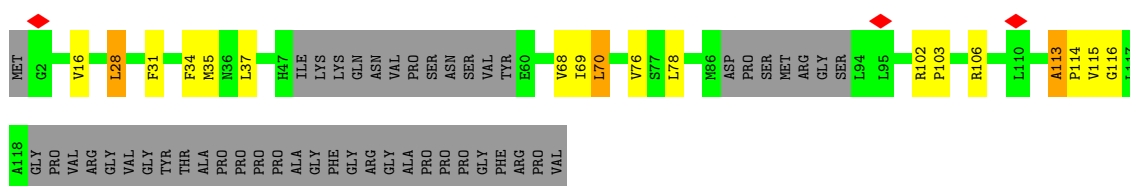
- Molecule 4: Small nuclear ribonucleoprotein Sm D3

Chain Z: 

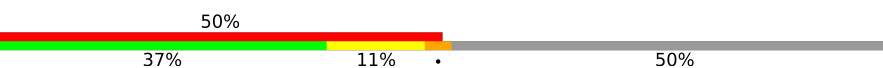


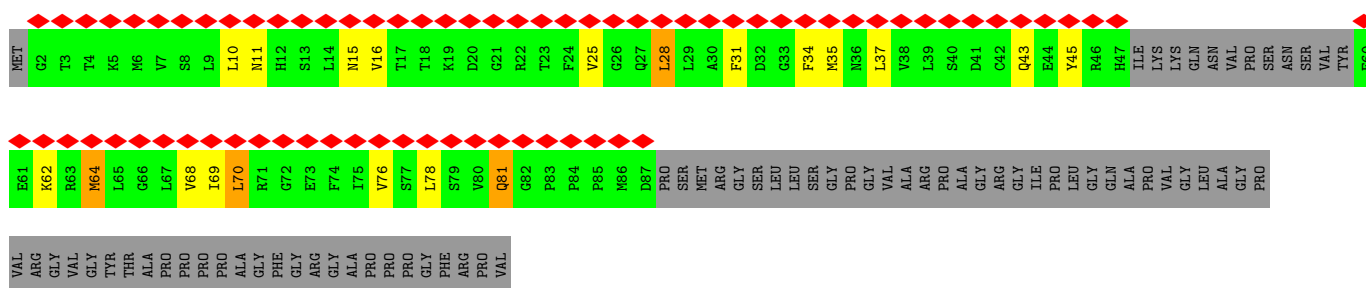
- Molecule 5: Small nuclear ribonucleoprotein-associated protein B

Chain E: 



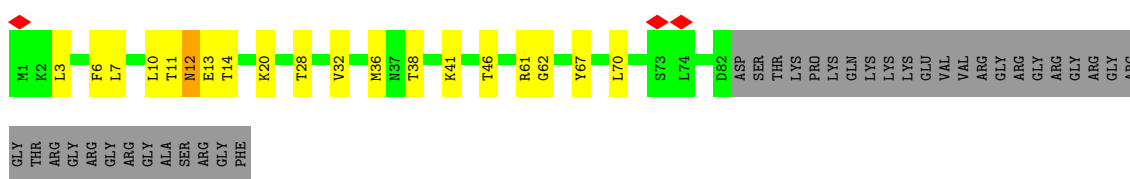
- Molecule 5: Small nuclear ribonucleoprotein-associated protein B

Chain b: 



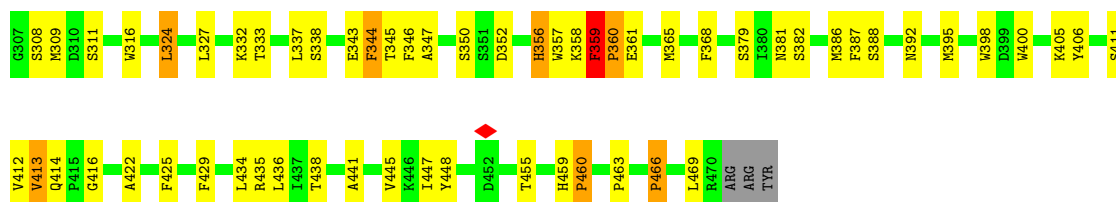
- Molecule 6: Small nuclear ribonucleoprotein Sm D1

Chain F: 

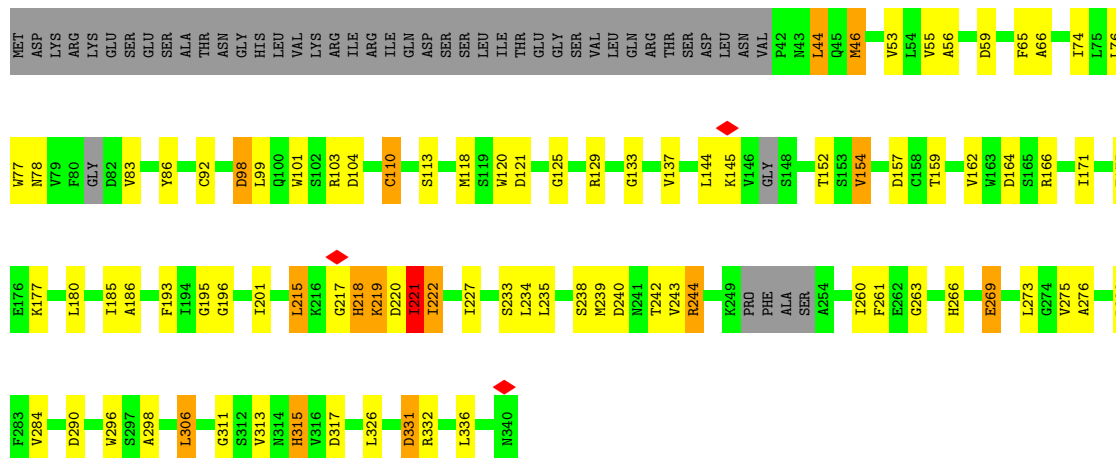


- Molecule 6: Small nuclear ribonucleoprotein Sm D1

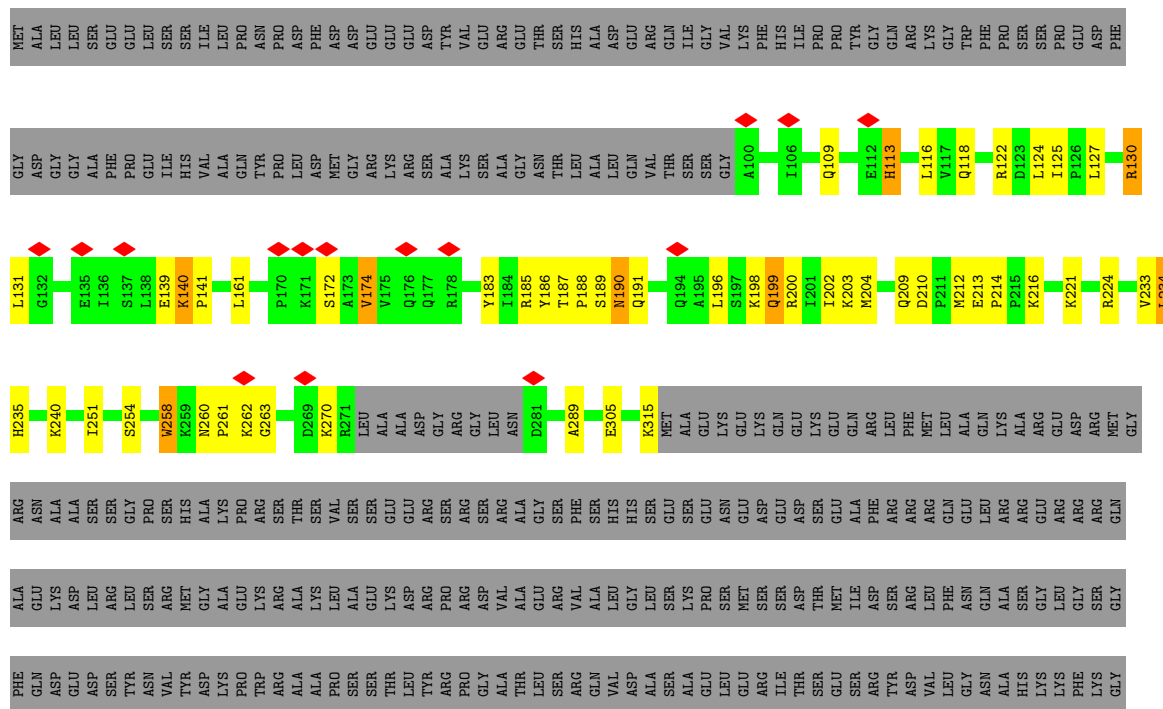




• Molecule 12: Pre-mRNA-splicing factor cwf17

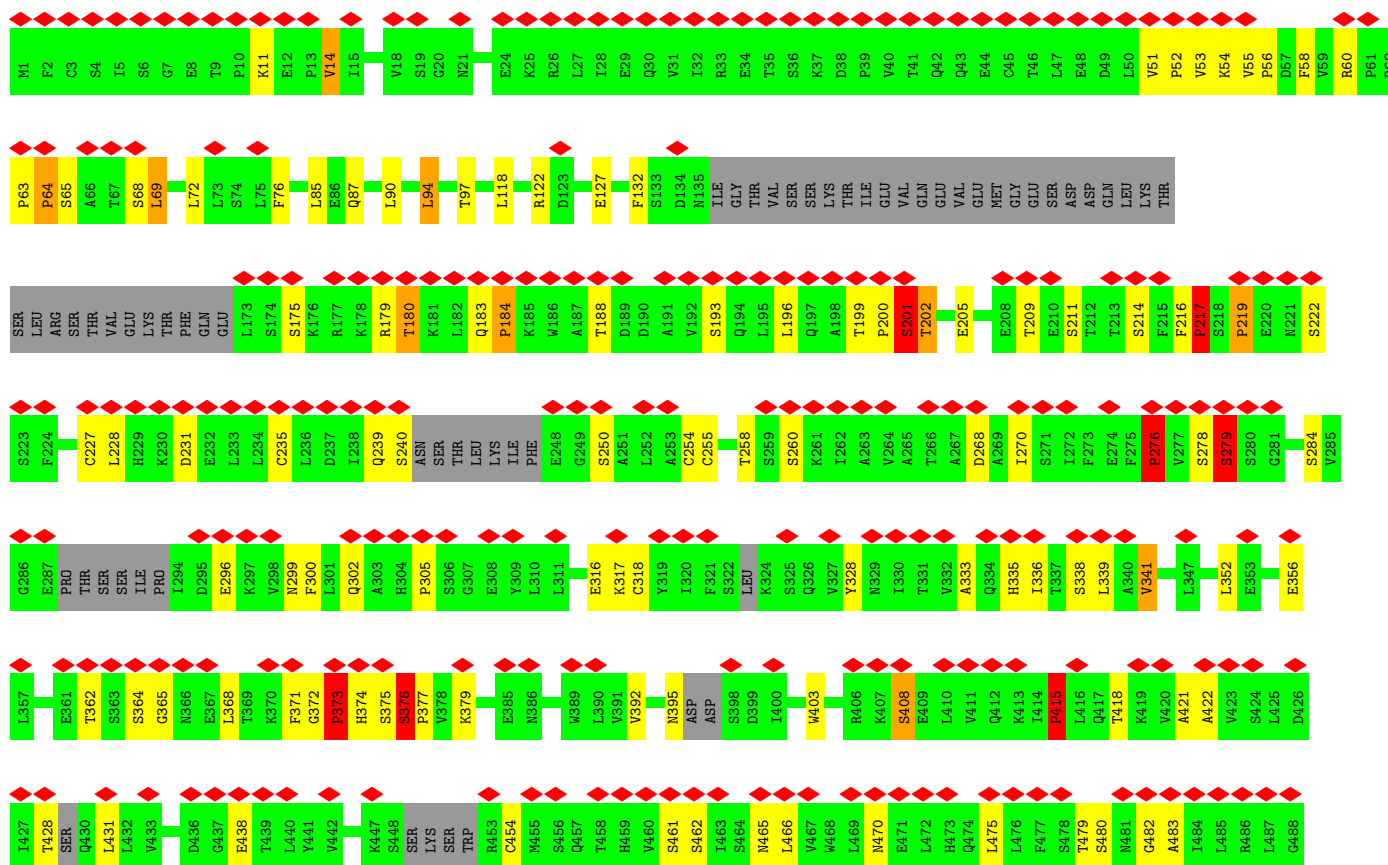


• Molecule 13: Pre-mRNA-processing protein 45



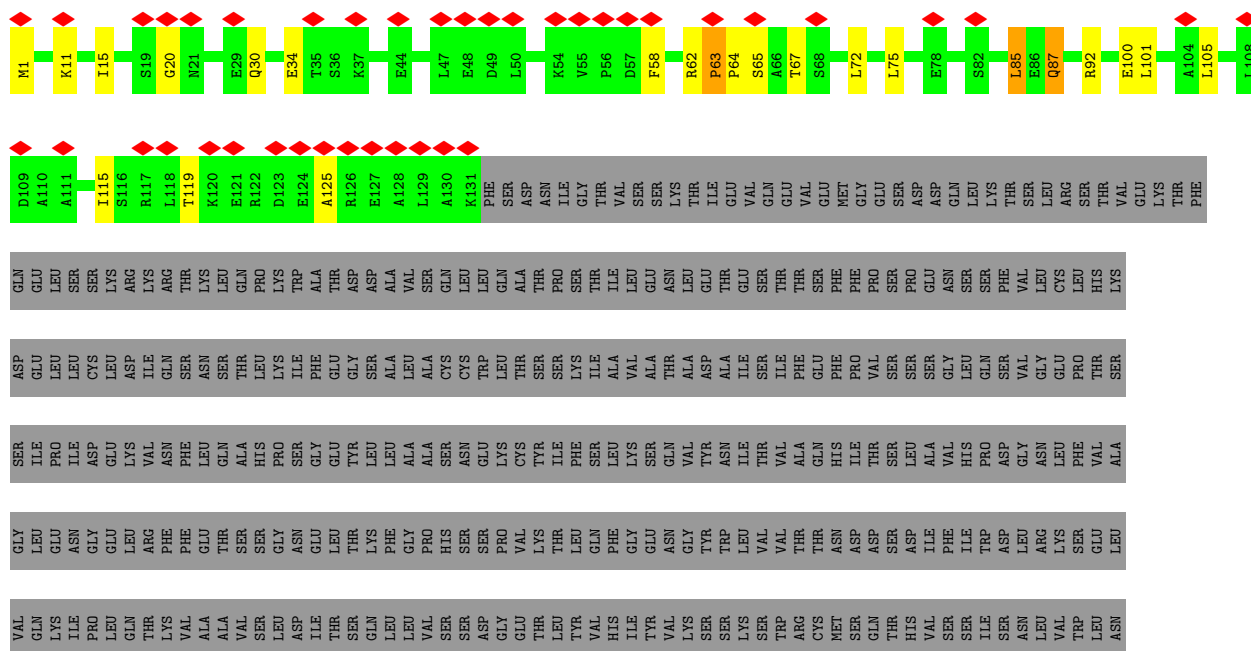


Chain U: 



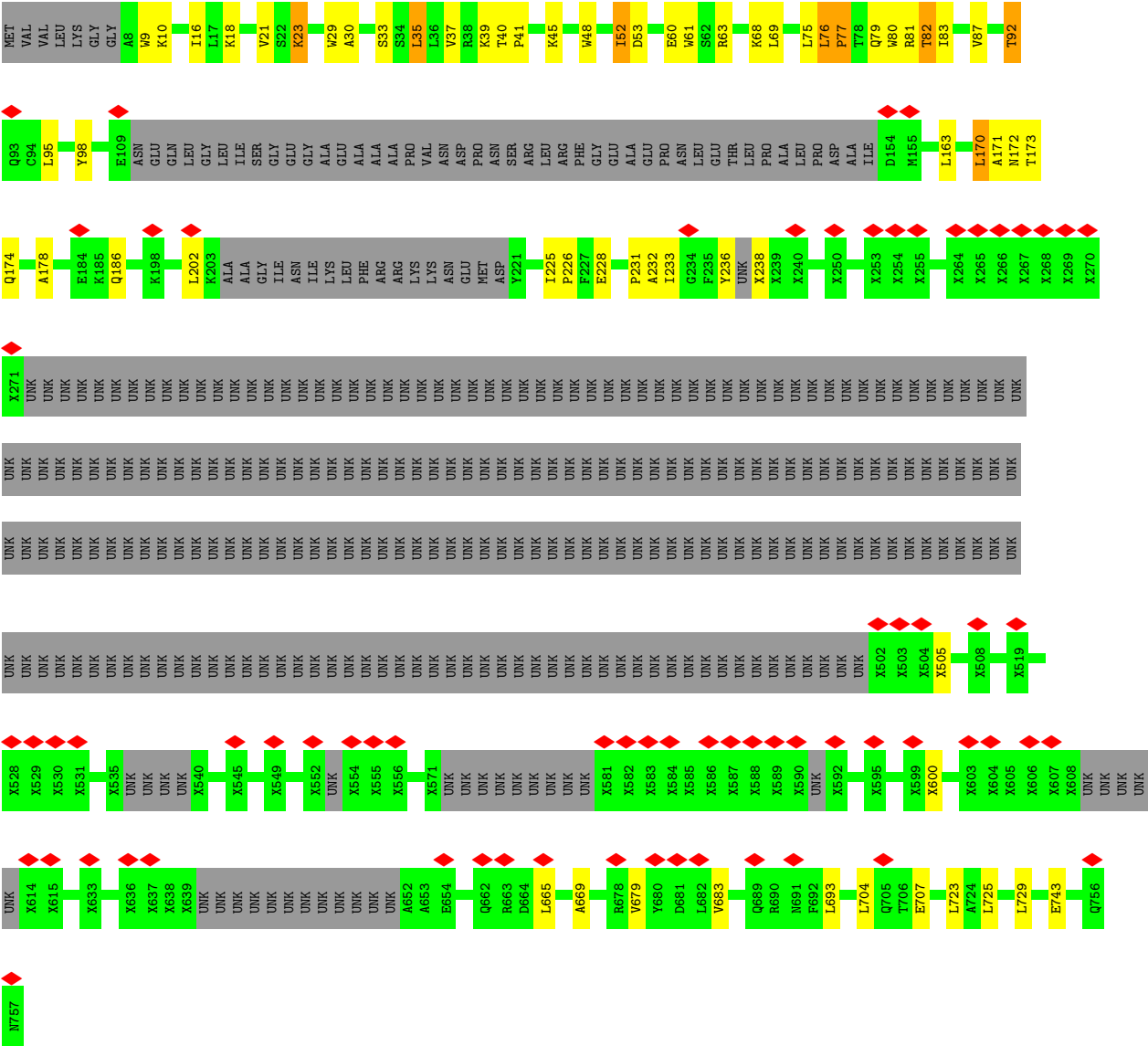
• Molecule 18: Pre-mRNA-processing factor 19

Chain V: 

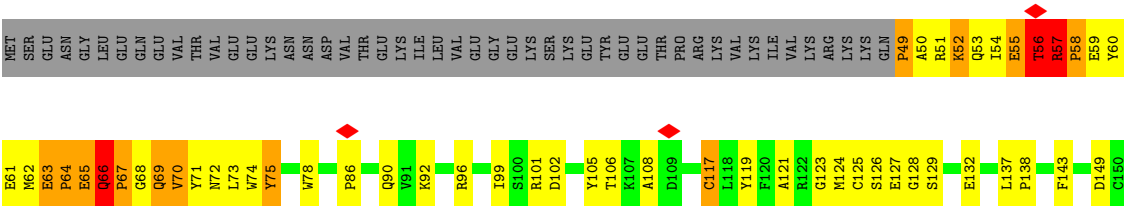
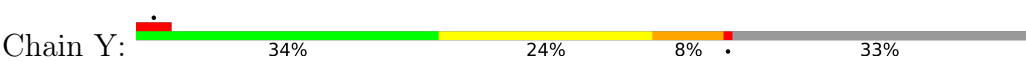


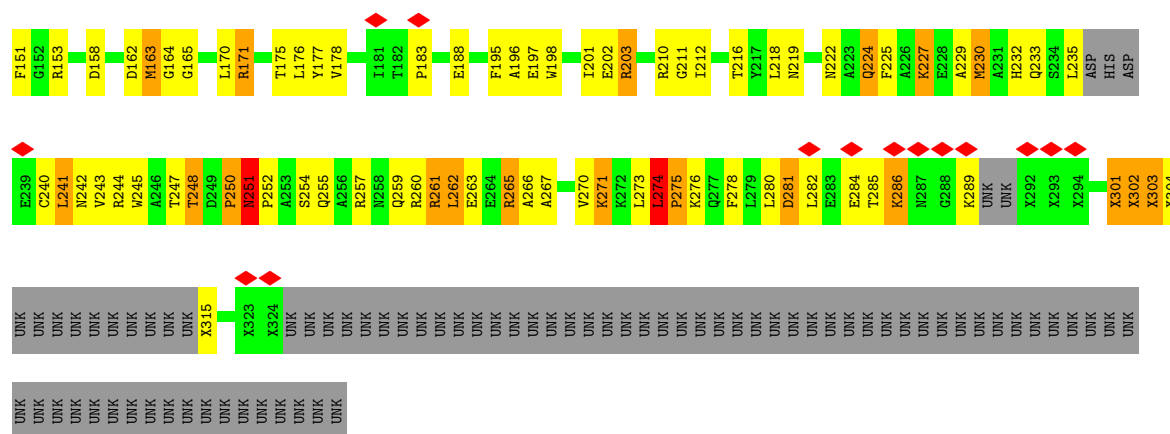
GLU
LEU
HIS
GLN
LEU
LEU
PHE
SER
THR
SER
ASN
GLY
ALA
ILE
LEU
ARG
LEU
GLY

• Molecule 19: Pre-mRNA-splicing factor cdc5

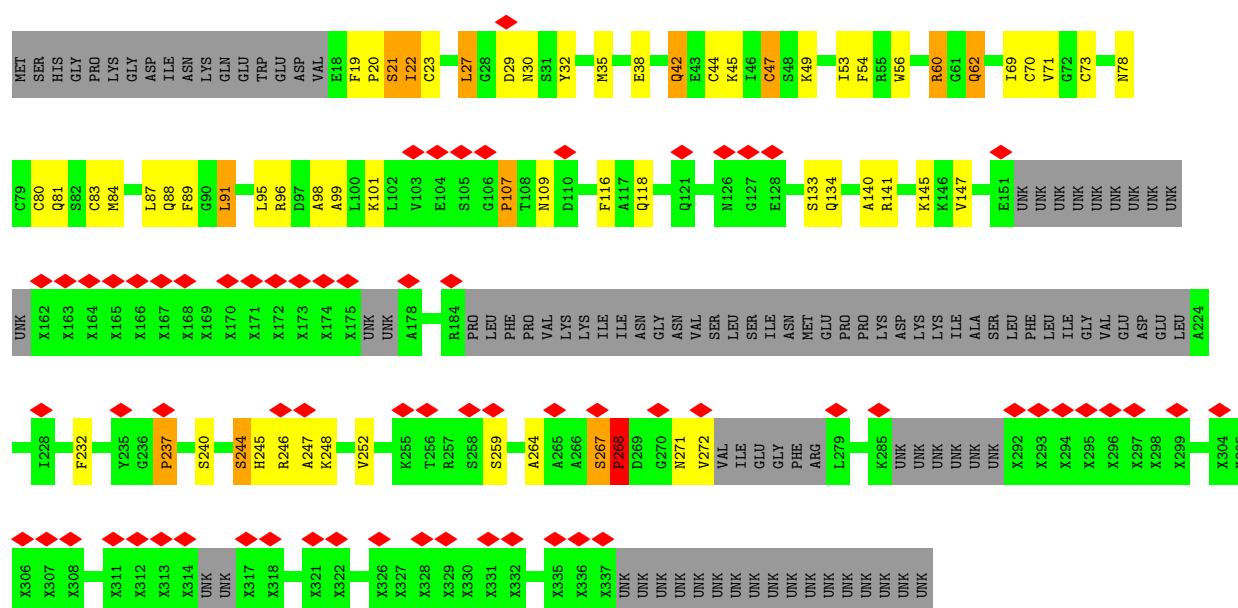


• Molecule 20: Pre-mRNA-splicing factor cwf2

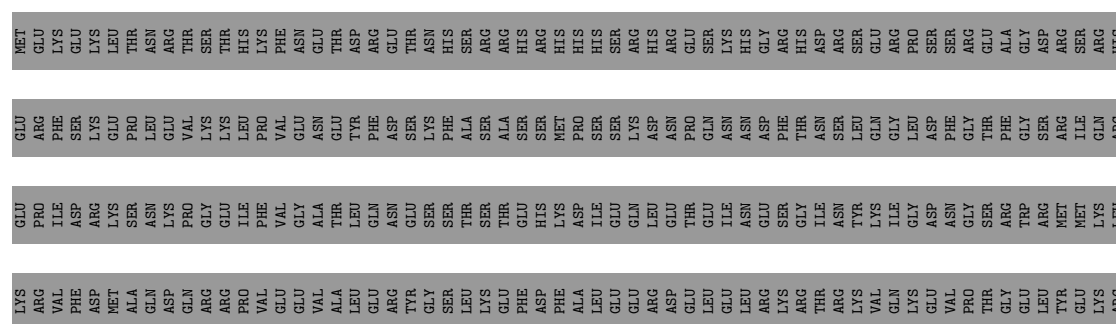
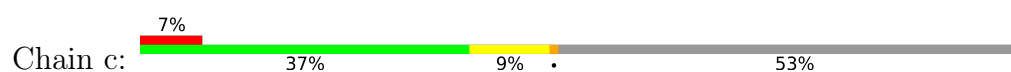


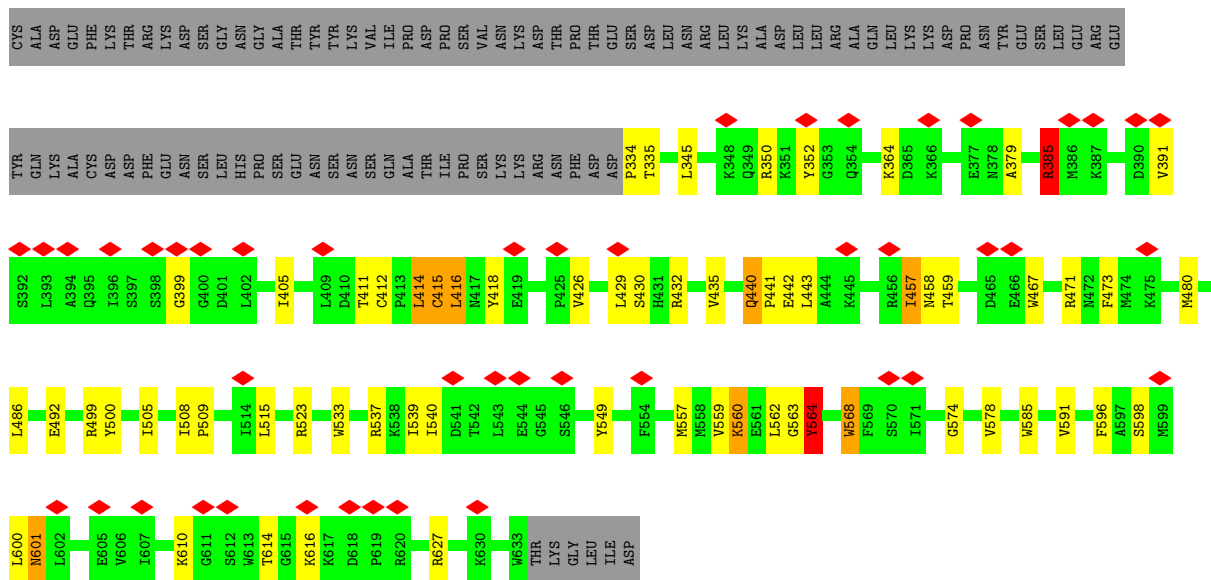


• Molecule 21: Pre-mRNA-splicing factor cwf5

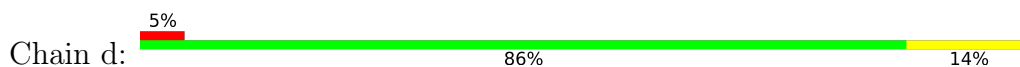


• Molecule 22: Pre-mRNA-splicing factor cwf19

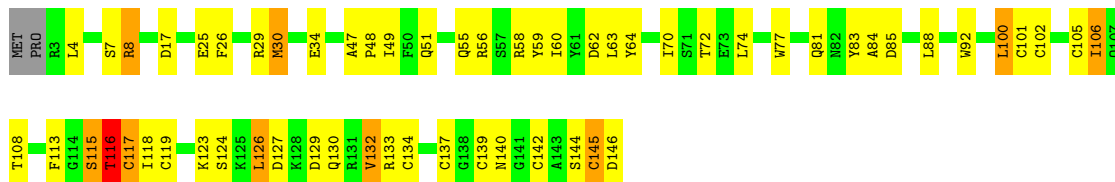




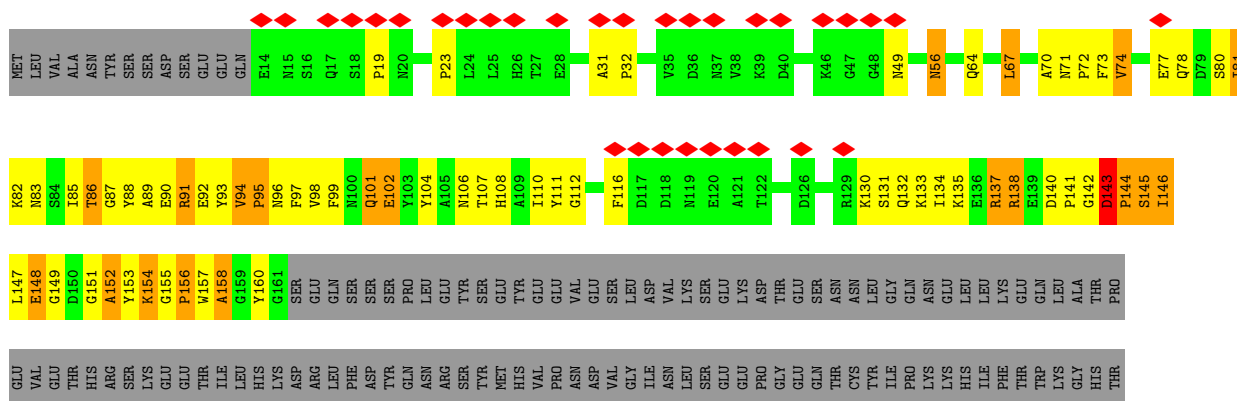
• Molecule 23: Peptidyl-prolyl cis-trans isomerase pp1l



• Molecule 24: Pre-mRNA-splicing factor cwf14

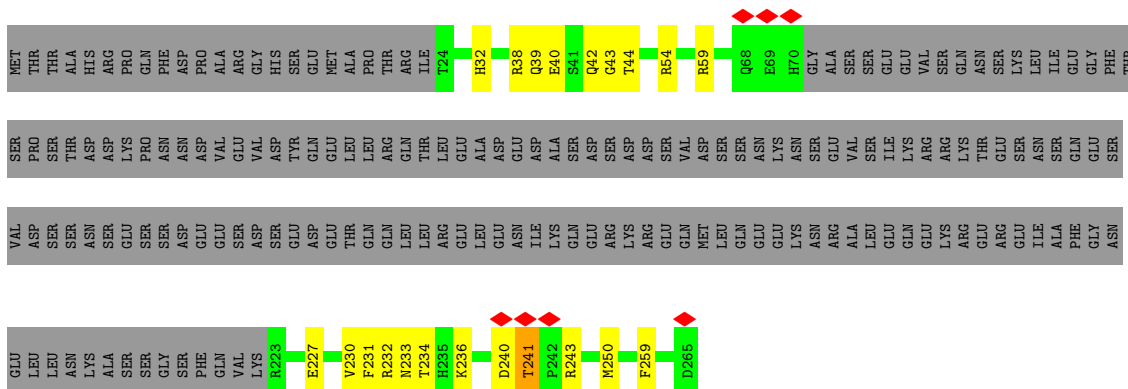


• Molecule 25: Pre-mRNA-processing factor 17

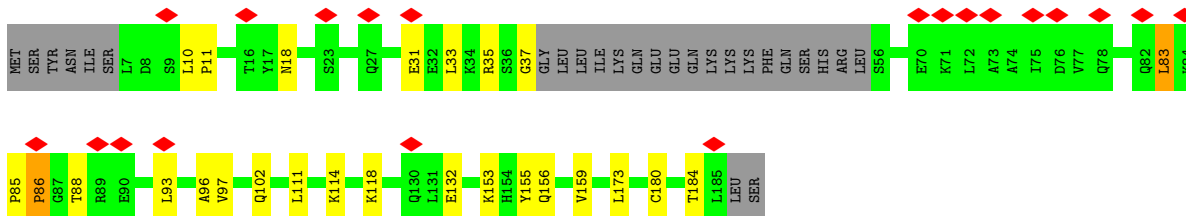




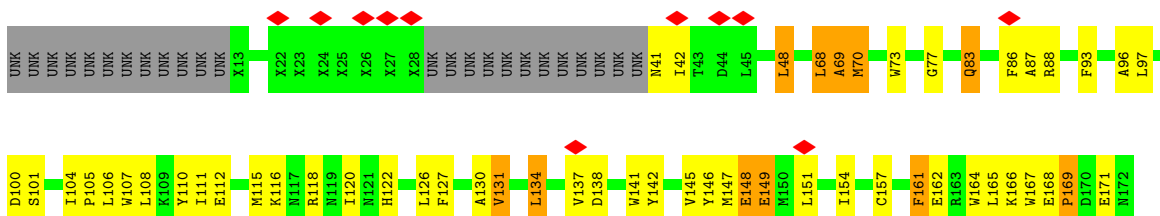
- Molecule 26: Pre-mRNA-splicing factor cwf15

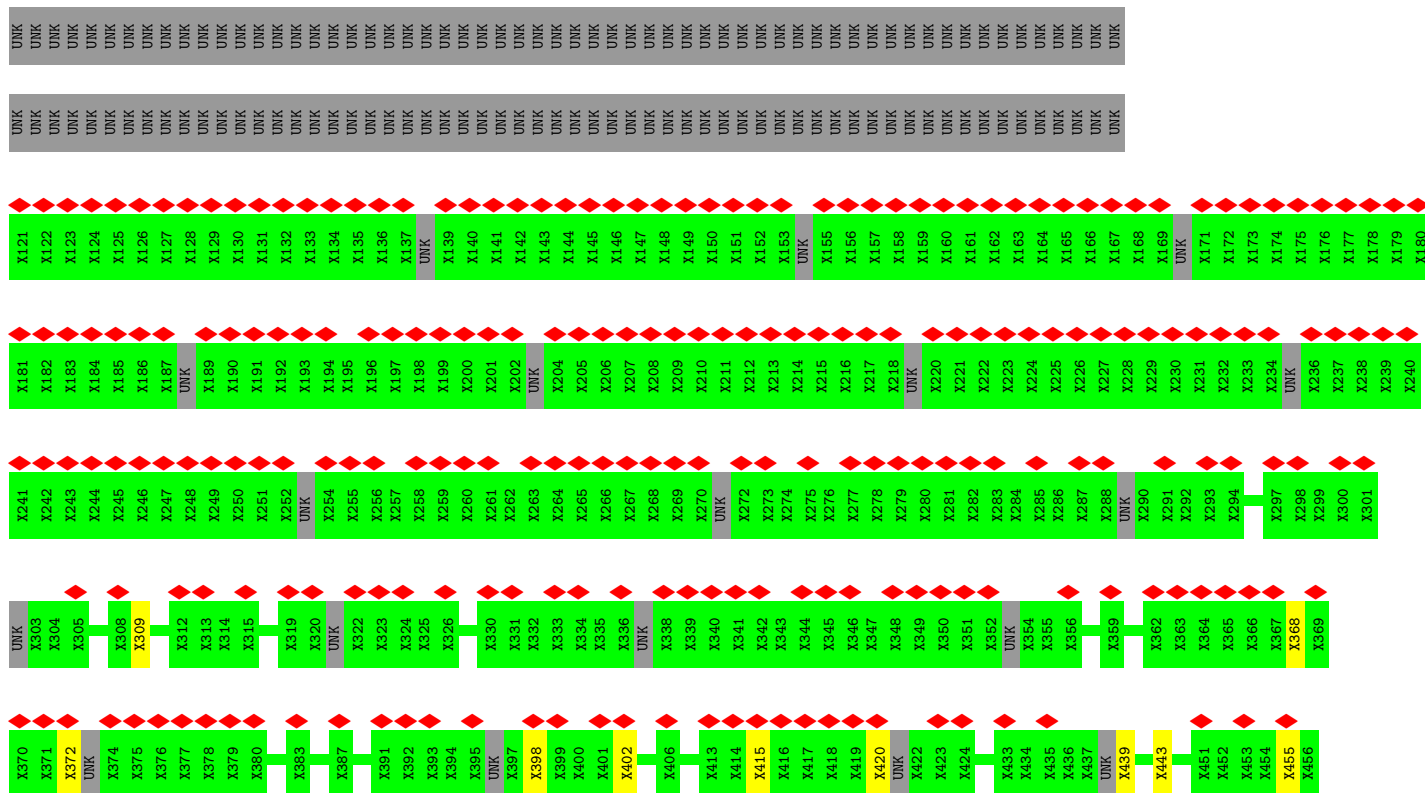


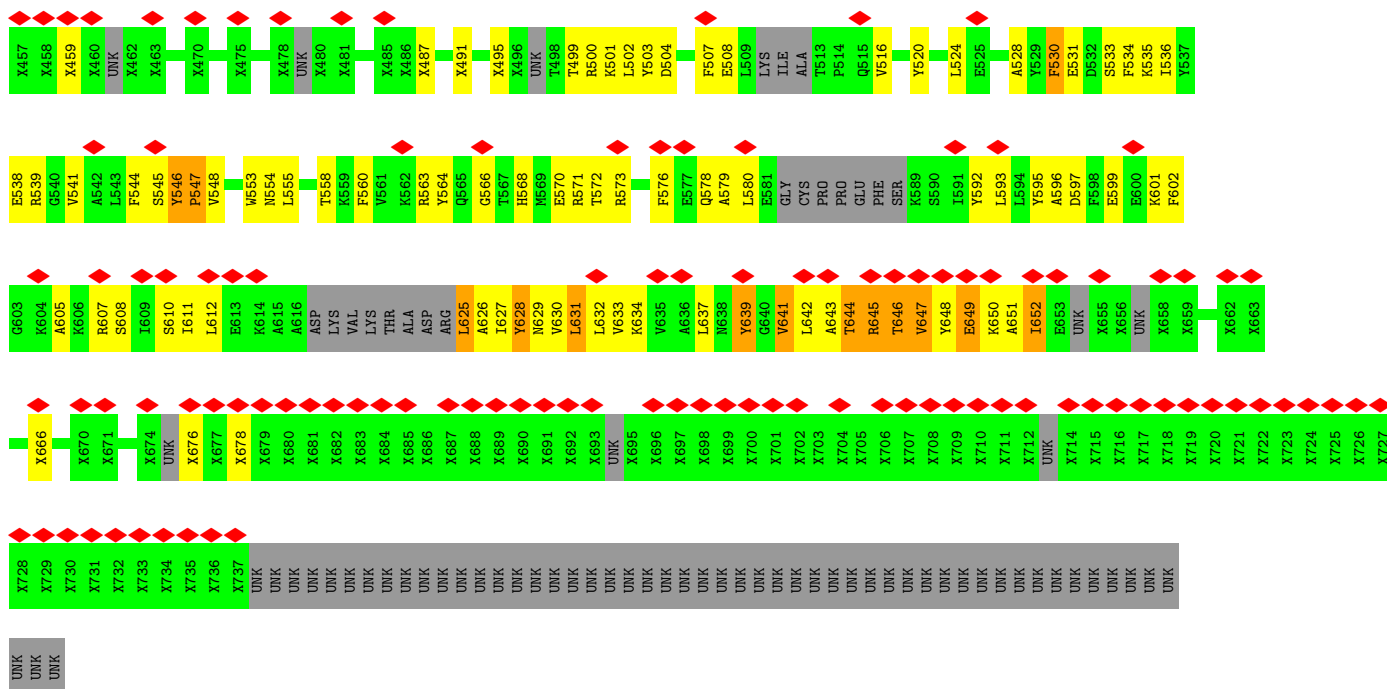
- Molecule 27: Pre-mRNA-splicing factor cwf7



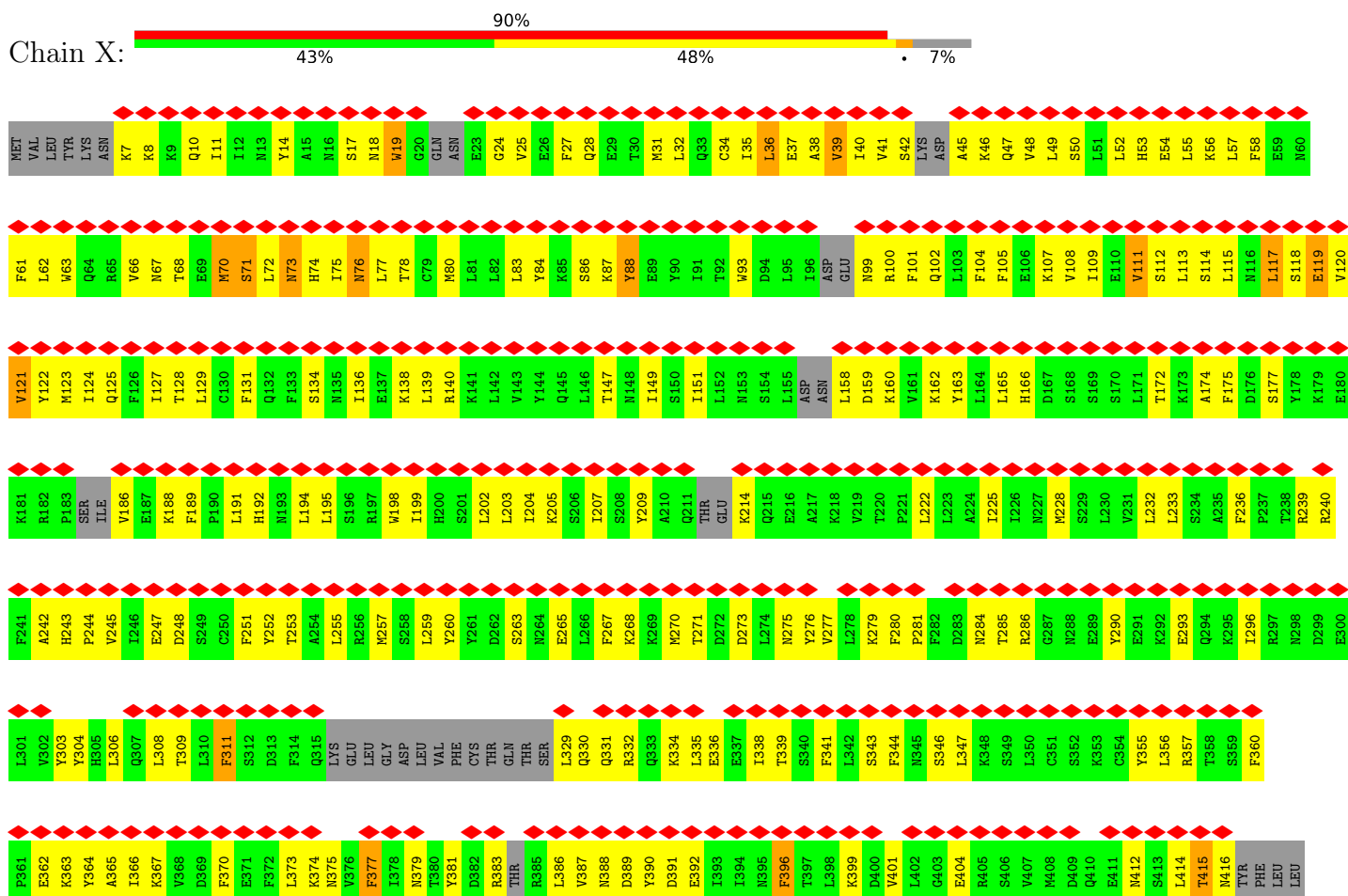
- Molecule 28: Pre-mRNA-splicing factor cwf4



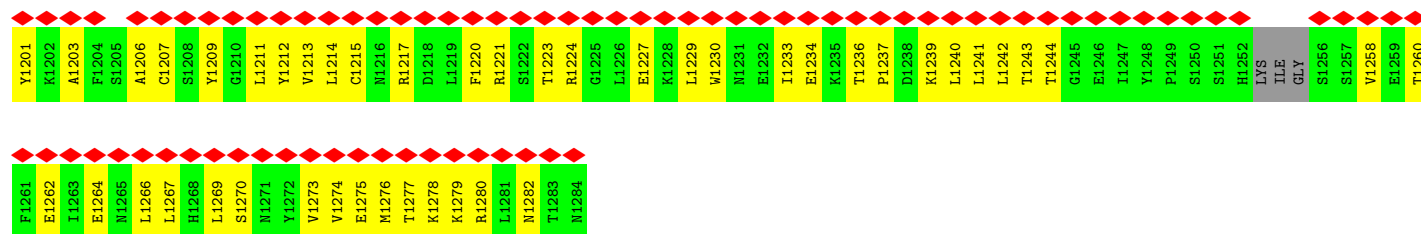




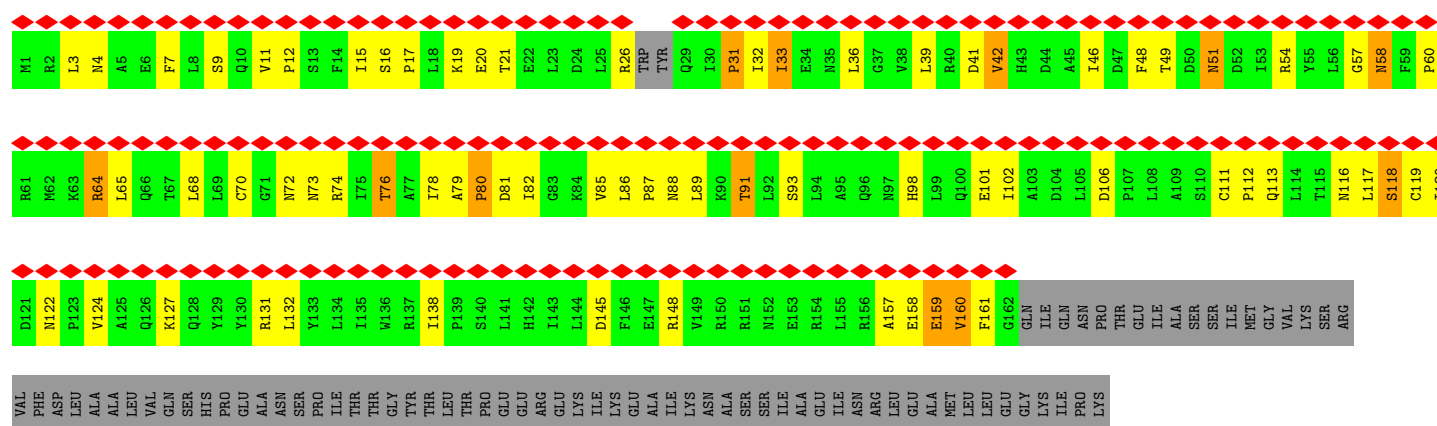
• Molecule 30: Pre-mRNA-splicing factor cwf11



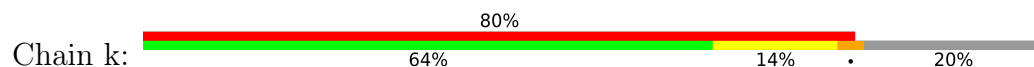
S1141	G1081	ASN	T961	T901	I641	W761	S721	Y601	K541	N481	GLN
Q1142	F1082	ASN	R962	Y902	Q642	F782	N722	R602	L542	N482	ASN
V1143	A1083	THR	L963	N903	A643	S783	R723	P603	L543	F483	
S1144	H1084		G964	K904	P644	M784	L724	K604	H544	K484	
L1145	E1085		T965	D905	G945	W785	Y725	Q605	G545	V485	
L1146	V1086		L966	N906	S946	W786	Y726	L606	N546	T486	
M1147	Q1087		K967	F907	H947	L787	Y727	K607	A547	S487	
E1148	F1088		E968	F908	D948	F788	N728	N608	L548	V488	
I1149	N1089		K969	D909	A949	W789	N729	F609	L549	S489	
I1150	V1090		G970	Y910	S950	L790	K730	F610	P550	P490	
S1151	F971		F971	A911	P951	L791	Q731	A611	L551	PRO	
V1152	C972		C972	T912	D952	W792	L732	L612	E552	GLN	
A1153	F973		F973	K913	T953	K793	E733	V613	GLY	ILE	
F1094	N974		N974	L914	A854	A794	S734	L614	V554	GLY	
K1095	N975		N975	Y915	L855	R795	I735	S615	T555	VAL	
G1096	L976		L976	G916	Y856	C796	L736	PRO	D556	L497	
S1097	I977		I977	E917	F957	F797	R737	GLU	F557	Q499	
Q1098	V978		V978	L918	R858	H798	G738	ALA	T558	F500	
E1099	N979		N979	E919	D859	W799	S739	GLN	I559	V501	
T1100	N980		N980	Y920	A860	GLY	Q740	N619	A560	K502	
E1101	S981		S981	N921	Y861	PRO	P741	K620	T561	C503	
P1102	Q982		Q982	F922	L862	L802	G742	W622	I562	Q504	
V1103	N983		N983	Q923	K963	L803	L743	L623	C563	M505	
S1104	I984		I984	Q924	R964	Y804	T744	D624	N564	L444	
G1105	Y1046		Y1046	L925	L865	L805	L745	L625	D565	G506	
V1106	E986		E986	E926	V866	S906	W746	N626	D566	L507	
K1107	S987		S987	E927	E967	D907	N747	I627	V567	R447	
Q1108	R988		R988	I928	K968	E908	G748	W629	S568	S508	
N1109	E1050		E1050	R929	Y869	GLY	P749	S630	P510	L449	
L1110	S1051		S1051	P930	L870	LYS	W750	GLY	PRO	Y450	
G1111	I1052		I1052	F931	N871	ASP	R751	GLN	PRO	A451	
E1112	S1053		S1053	G932	T872	THR	C752	THR	ASP	E452	
A1113	L993		L993	L933	W873	L814	G753	E693	S515	L453	
E1114	S1054		S1054	L934	D874	E915	K754	R634	A516	L454	
Y1115	C1056		C1056	R935	ASP	R816	H755	K636	L517	N455	
A1116	S1057		S1057	Y936	K876	V817	V756	E637	R518	F456	
V1117	S1058		S1058	Y937	D877	G818	L757	F638	D519	S457	
E1118	I1059		E1059	E938	S978	T819	W758	P639	L520	E458	
L1119	Y1060		Y1060	D939	V879	L820	C759	K640	K521	Q459	
F1180	P1061		P1061	Q940	D880	S821	L761	W641	N522	Y460	
V1181	L1062		L1062	E941	A881	S822	L762	F642	K581	R461	
I1182	Y1122		Y1122	L942	Y882	W823	L762	E643	S582	R462	
F1183	M1123		F1063	Y943	N883	T824	E763	D644	I583	L463	
R1184	R1124		R1004	A944	R884	S825	V764	L645	N584	S464	
M1125	L1125		L1005	L945	F885	W826	L765	F646	V585	I465	
L1126	V1066		V1006	C946	P886	L827	Q766	L647	Y586	K466	
G1127	D1068		D1007	Q947	F887	P828	D767	G648	F528	N467	
V1128	S1069		S1009	Q948	H888	G829	T768	P649	L529	A468	
K1189	G1009		K949	S949	S889	L830	W769	N651	C530	T469	
E1190	N1010		E950	R950	Y890	L831	S769	G650	L631	I470	
A1191	Q1011		Q951	F951	F891	R832	P770	T651	I532	N471	
S1192	Y1012		S952	I952	G892	E833	N771	P652	Y592	L472	
E1132	K1073		E953	G953	D893	T834	D772	D653	H593	THR	
V1134	SER		V954	C954	K894	G835	R773	I654	K536	LYS	
W1195	L1075		W955	T955	K894	R836	T774	C655	D637	ASP	
N1196	D1076		N956	Y956	S895	R837	W775	A656	M538	N476	
P1197	Y1077		P957	T957	K896	L837	V776	F657	E539	F478	
K1198	L1138		K958	S958	R897	A838	L777	P658	Y540	S479	
T1199	Y1139		T959	L959	P898	A839	S778	N659	G599	L480	
F1200	E1140		F960	S960	T899	S840	S780	A660	E600		



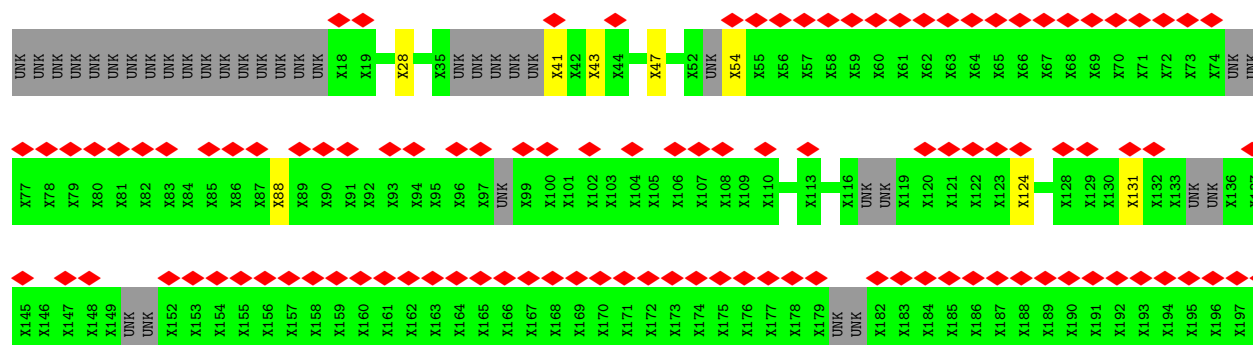
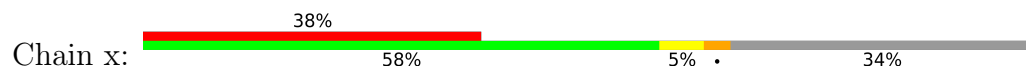
• Molecule 31: U2 small nuclear ribonucleoprotein A'

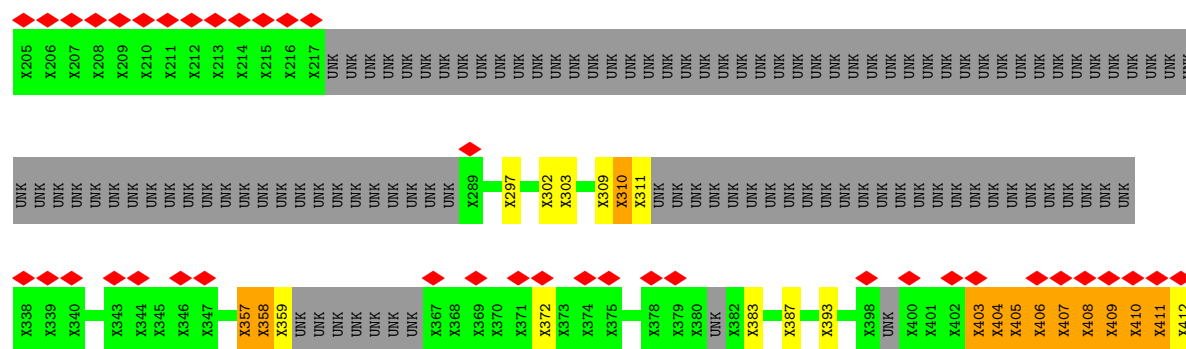


• Molecule 32: Probable U2 small nuclear ribonucleoprotein B'



• Molecule 33: unknown chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	112795	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	3.0	Depositor
Maximum defocus (nm)	1.5	Depositor
Magnification	Not provided	
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.189	Depositor
Minimum map value	-0.087	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0203	Depositor
Map size ($\text{\AA}$)	475.2, 475.2, 475.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/16654	0.79	13/22571 (0.1%)
2	B	0.46	0/7357	0.79	6/9980 (0.1%)
3	C	0.41	0/2463	0.79	2/3829 (0.1%)
4	D	0.39	0/772	0.71	0/1038
4	Z	0.37	0/648	0.69	0/871
5	E	0.42	0/741	0.75	1/998 (0.1%)
5	b	0.43	0/584	0.80	2/785 (0.3%)
6	F	0.40	0/654	0.67	0/885
6	f	0.40	0/654	0.67	0/885
7	G	0.39	0/760	0.71	2/1016 (0.2%)
7	l	0.39	0/705	0.71	2/945 (0.2%)
8	H	0.42	0/630	0.64	0/851
8	m	0.42	0/630	0.64	0/851
9	I	0.42	0/579	0.62	0/785
9	n	0.42	0/579	0.63	0/785
10	J	0.36	0/578	0.71	0/774
10	o	0.36	0/578	0.71	0/774
11	K	0.53	0/2539	0.93	10/3453 (0.3%)
12	L	0.40	0/2317	0.74	2/3130 (0.1%)
13	M	0.48	0/1698	0.79	2/2295 (0.1%)
14	N	0.39	0/2160	0.73	1/3365 (0.0%)
15	O	0.37	0/189	0.59	0/292
16	Q	0.36	0/300	0.63	0/463
17	P	0.85	23/2580 (0.9%)	1.25	34/4000 (0.8%)
18	S	0.45	0/1069	0.68	0/1449
18	T	0.44	0/1086	0.74	0/1472
18	U	1.24	32/2888 (1.1%)	1.01	10/3898 (0.3%)
18	V	0.45	0/1053	0.71	0/1429
19	W	0.42	0/2300	0.76	3/3087 (0.1%)
20	Y	0.55	7/1934 (0.4%)	0.91	8/2609 (0.3%)
21	a	0.57	3/1479 (0.2%)	0.89	2/1980 (0.1%)
22	c	0.44	0/2486	0.75	1/3360 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
23	d	0.46	0/1214	0.70	0/1646
24	e	0.47	0/1199	0.80	1/1609 (0.1%)
25	g	0.63	6/1033 (0.6%)	1.07	9/1412 (0.6%)
26	h	0.45	0/767	0.71	0/1028
27	i	0.44	0/1231	0.74	0/1657
28	R	0.41	0/2243	0.79	0/3016
29	r	0.50	0/1161	0.86	2/1565 (0.1%)
30	X	0.40	0/9957	0.83	10/13430 (0.1%)
31	j	1.49	14/1118 (1.3%)	2.25	61/1513 (4.0%)
32	k	0.98	3/624 (0.5%)	1.85	13/838 (1.6%)
All	All	0.55	88/82191 (0.1%)	0.86	197/112619 (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.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
11	K	0	2
20	Y	0	3
33	x	0	12
All	All	0	22

The worst 5 of 88 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	j	76	THR	CB-OG1	21.45	1.78	1.43
31	j	118	SER	CB-OG	20.24	1.82	1.42
31	j	58	ASN	CA-CB	-10.64	1.38	1.53
18	U	318	CYS	CB-SG	-9.93	1.48	1.81
18	U	227	CYS	CB-SG	-9.71	1.49	1.81

The worst 5 of 197 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	j	54	ARG	CD-NE-CZ	13.19	142.87	124.40
31	j	70	CYS	CA-C-N	12.14	131.63	120.10
31	j	70	CYS	C-N-CA	12.14	131.63	120.10
31	j	48	PHE	CA-CB-CG	11.44	125.23	113.80
21	a	237	PRO	N-CA-CB	11.26	110.77	103.23

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1191	THR	Peptide
1	A	1440	ILE	Peptide
1	A	187	PHE	Peptide
1	A	457	HIS	Peptide
1	A	964	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16230	0	16208	413	0
2	B	7196	0	7229	150	0
3	C	2209	0	1115	27	0
4	D	760	0	776	16	0
4	Z	639	0	640	19	0
5	E	730	0	753	16	0
5	b	576	0	584	33	0
6	F	646	0	694	7	0
6	f	646	0	694	27	0
7	G	751	0	772	9	0
7	l	696	0	710	56	0
8	H	620	0	641	8	0
8	m	620	0	641	8	0
9	I	570	0	590	16	0
9	n	570	0	590	25	0
10	J	573	0	602	7	0
10	o	573	0	602	7	0
11	K	2730	0	2435	87	0
12	L	2273	0	2226	117	0
13	M	1661	0	1689	63	0
14	N	1928	0	971	161	0
15	O	170	0	85	13	0
16	Q	270	0	138	23	0
17	P	2323	0	1178	219	0
18	S	1052	0	1073	19	0
18	T	1069	0	1084	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	U	2864	0	2384	56	0
18	V	1037	0	1052	15	0
19	W	3024	0	2433	48	0
20	Y	2008	0	1817	358	0
21	a	1751	0	1463	110	0
22	c	2425	0	2346	27	0
23	d	1187	0	1181	22	0
24	e	1176	0	1171	98	0
25	g	1013	0	826	194	0
26	h	752	0	729	8	0
27	i	1218	0	1163	22	0
28	R	3800	0	2469	128	0
29	r	3299	0	1614	154	0
30	X	9764	0	9707	608	0
31	j	1108	0	951	36	0
32	k	618	0	558	11	0
33	x	1360	0	300	59	0
34	B	28	0	12	0	0
35	N	4	0	0	0	0
36	Y	1	0	0	2	0
36	a	2	0	0	6	0
36	c	1	0	0	0	0
36	e	3	0	0	7	0
37	X	27	0	12	23	0
All	All	86551	0	76908	2967	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 18.

The worst 5 of 2967 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)
20:Y:278:PHE:CE2	21:a:141:ARG:HB2	1.24	1.60
14:N:26:U:H5	20:Y:244:ARG:CZ	1.03	1.57
12:L:195:GLY:CA	12:L:222:ILE:CD1	1.84	1.54
14:N:26:U:C5	20:Y:244:ARG:CZ	1.90	1.54
29:r:637:LEU:CD2	29:r:644:THR:HG21	1.15	1.54

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	A	1956/2363 (83%)	1657 (85%)	220 (11%)	79 (4%)	2	20
2	B	902/984 (92%)	783 (87%)	97 (11%)	22 (2%)	4	29
4	D	94/97 (97%)	80 (85%)	8 (8%)	6 (6%)	1	12
4	Z	78/97 (80%)	71 (91%)	6 (8%)	1 (1%)	9	39
5	E	92/147 (63%)	81 (88%)	9 (10%)	2 (2%)	5	30
5	b	70/147 (48%)	67 (96%)	3 (4%)	0	100	100
6	F	80/117 (68%)	72 (90%)	6 (8%)	2 (2%)	4	28
6	f	80/117 (68%)	72 (90%)	6 (8%)	2 (2%)	4	28
7	G	91/115 (79%)	88 (97%)	3 (3%)	0	100	100
7	l	83/115 (72%)	81 (98%)	2 (2%)	0	100	100
8	H	74/84 (88%)	69 (93%)	5 (7%)	0	100	100
8	m	74/84 (88%)	69 (93%)	5 (7%)	0	100	100
9	I	70/78 (90%)	64 (91%)	4 (6%)	2 (3%)	3	26
9	n	70/78 (90%)	65 (93%)	3 (4%)	2 (3%)	3	26
10	J	71/77 (92%)	66 (93%)	5 (7%)	0	100	100
10	o	71/77 (92%)	66 (93%)	5 (7%)	0	100	100
11	K	320/473 (68%)	246 (77%)	50 (16%)	24 (8%)	1	9
12	L	285/340 (84%)	239 (84%)	41 (14%)	5 (2%)	6	34
13	M	203/557 (36%)	172 (85%)	22 (11%)	9 (4%)	2	18
18	S	130/488 (27%)	122 (94%)	7 (5%)	1 (1%)	16	49
18	T	132/488 (27%)	123 (93%)	8 (6%)	1 (1%)	16	49
18	U	414/488 (85%)	383 (92%)	20 (5%)	11 (3%)	4	27
18	V	129/488 (26%)	121 (94%)	4 (3%)	4 (3%)	3	25
19	W	266/757 (35%)	244 (92%)	13 (5%)	9 (3%)	3	23
20	Y	234/388 (60%)	200 (86%)	24 (10%)	10 (4%)	2	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	a	189/354 (53%)	167 (88%)	18 (10%)	4 (2%)	5	31
22	c	298/639 (47%)	254 (85%)	31 (10%)	13 (4%)	2	18
23	d	153/155 (99%)	137 (90%)	13 (8%)	3 (2%)	6	32
24	e	142/146 (97%)	120 (84%)	17 (12%)	5 (4%)	3	23
25	g	146/558 (26%)	123 (84%)	15 (10%)	8 (6%)	1	14
26	h	86/265 (32%)	75 (87%)	7 (8%)	4 (5%)	2	17
27	i	157/187 (84%)	144 (92%)	10 (6%)	3 (2%)	6	33
28	R	248/674 (37%)	219 (88%)	20 (8%)	9 (4%)	2	22
29	r	130/790 (16%)	120 (92%)	6 (5%)	4 (3%)	3	25
30	X	1143/1284 (89%)	1032 (90%)	87 (8%)	24 (2%)	5	31
31	j	156/239 (65%)	140 (90%)	14 (9%)	2 (1%)	9	39
32	k	87/111 (78%)	85 (98%)	2 (2%)	0	100	100
All	All	9004/14646 (62%)	7917 (88%)	816 (9%)	271 (3%)	5	25

5 of 271 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	GLY
1	A	68	VAL
1	A	155	ARG
1	A	188	PRO
1	A	232	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1775/2138 (83%)	1557 (88%)	218 (12%)	4	23
2	B	809/881 (92%)	755 (93%)	54 (7%)	15	42
4	D	85/86 (99%)	75 (88%)	10 (12%)	5	24
4	Z	72/86 (84%)	63 (88%)	9 (12%)	4	22

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	80/118 (68%)	76 (95%)	4 (5%)	22	49
5	b	66/118 (56%)	61 (92%)	5 (8%)	12	39
6	F	77/102 (76%)	71 (92%)	6 (8%)	11	38
6	f	77/102 (76%)	71 (92%)	6 (8%)	11	38
7	G	81/101 (80%)	79 (98%)	2 (2%)	42	63
7	l	76/101 (75%)	75 (99%)	1 (1%)	61	72
8	H	69/76 (91%)	64 (93%)	5 (7%)	13	40
8	m	69/76 (91%)	64 (93%)	5 (7%)	13	40
9	I	64/69 (93%)	60 (94%)	4 (6%)	16	44
9	n	64/69 (93%)	60 (94%)	4 (6%)	16	44
10	J	63/67 (94%)	58 (92%)	5 (8%)	11	37
10	o	63/67 (94%)	58 (92%)	5 (8%)	11	37
11	K	261/278 (94%)	239 (92%)	22 (8%)	10	35
12	L	251/292 (86%)	235 (94%)	16 (6%)	16	43
13	M	182/477 (38%)	167 (92%)	15 (8%)	10	36
18	S	120/443 (27%)	112 (93%)	8 (7%)	15	42
18	T	123/443 (28%)	111 (90%)	12 (10%)	7	31
18	U	223/443 (50%)	205 (92%)	18 (8%)	11	36
18	V	118/443 (27%)	111 (94%)	7 (6%)	18	45
19	W	234/294 (80%)	216 (92%)	18 (8%)	12	38
20	Y	194/253 (77%)	165 (85%)	29 (15%)	3	17
21	a	142/222 (64%)	123 (87%)	19 (13%)	4	21
22	c	259/579 (45%)	234 (90%)	25 (10%)	8	31
23	d	129/129 (100%)	126 (98%)	3 (2%)	44	64
24	e	130/132 (98%)	120 (92%)	10 (8%)	12	38
25	g	78/496 (16%)	62 (80%)	16 (20%)	1	8
26	h	79/240 (33%)	69 (87%)	10 (13%)	4	22
27	i	118/163 (72%)	106 (90%)	12 (10%)	7	30
28	R	224/224 (100%)	196 (88%)	28 (12%)	4	22
29	r	117/136 (86%)	104 (89%)	13 (11%)	6	27
30	X	1106/1188 (93%)	1098 (99%)	8 (1%)	76	78

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	j	87/214 (41%)	83 (95%)	4 (5%)	24	51
32	k	49/96 (51%)	47 (96%)	2 (4%)	27	53
All	All	7814/11442 (68%)	7176 (92%)	638 (8%)	13	36

5 of 638 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	a	87	LEU
28	R	273	ARG
22	c	416	LEU
21	a	78	ASN
25	g	138	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 181 such sidechains are listed below:

Mol	Chain	Res	Type
21	a	118	GLN
29	r	629	ASN
22	c	349	GLN
27	i	130	GLN
30	X	416	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	N	89/99 (89%)	53 (59%)	12 (13%)
15	O	8/8 (100%)	3 (37%)	1 (12%)
16	Q	12/13 (92%)	4 (33%)	2 (16%)
17	P	106/186 (56%)	28 (26%)	8 (7%)
3	C	104/120 (86%)	54 (51%)	13 (12%)
All	All	319/426 (74%)	142 (44%)	36 (11%)

5 of 142 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	9	U
3	C	14	G
3	C	18	U
3	C	19	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	20	U

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	P	14	C
17	P	168	A
17	P	17	U
17	P	104	G
3	C	100	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 11 are monoatomic - leaving 2 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	$\# Z > 2$
37	ADP	X	1500	-	28,29,29	1.42	4 (14%)	43,45,45	1.85	9 (20%)
34	GDP	B	1000	-	29,30,30	1.44	4 (13%)	45,47,47	1.76	5 (11%)

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
37	ADP	X	1500	-	-	7/16/32/32	0/3/3/3
34	GDP	B	1000	-	-	5/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	X	1500	ADP	C5-C4	4.75	1.47	1.39
34	B	1000	GDP	PA-O3A	4.52	1.64	1.59
34	B	1000	GDP	C5-C4	3.03	1.47	1.38
37	X	1500	ADP	C5-C6	2.77	1.48	1.41
34	B	1000	GDP	C5-N7	-2.63	1.33	1.39

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B	1000	GDP	C5-C4-N3	-6.19	118.54	128.39
37	X	1500	ADP	C5-C4-N3	-5.84	118.68	126.72
34	B	1000	GDP	N9-C4-N3	5.22	136.40	125.95
37	X	1500	ADP	N3-C4-N9	4.63	135.04	127.17
34	B	1000	GDP	C2-N3-C4	4.60	120.23	112.30

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B	1000	GDP	C5'-O5'-PA-O3A
37	X	1500	ADP	C5'-O5'-PA-O3A
37	X	1500	ADP	C4'-C5'-O5'-PA
34	B	1000	GDP	C3'-C4'-C5'-O5'
37	X	1500	ADP	O4'-C1'-N9-C8

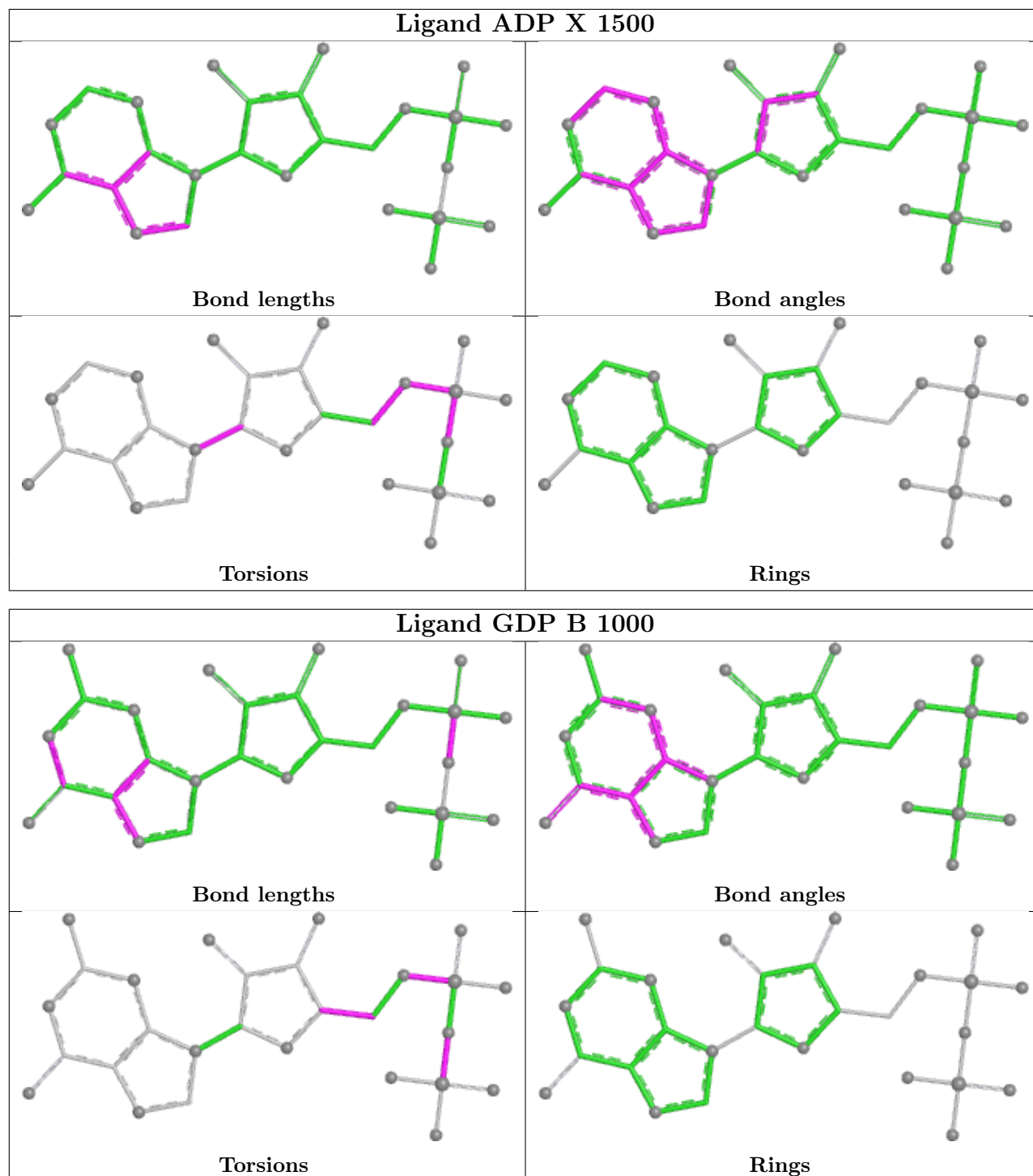
There are no ring outliers.

1 monomer is involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	X	1500	ADP	23	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

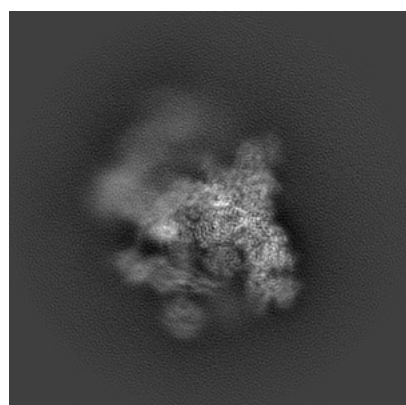
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6413. These allow visual inspection of the internal detail of the map and identification of artifacts.

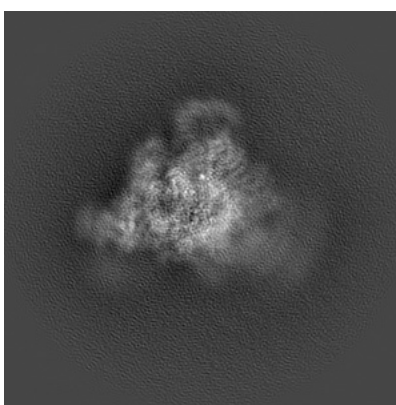
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

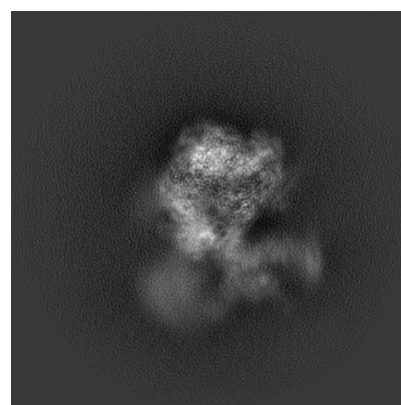
6.1.1 Primary map



X



Y

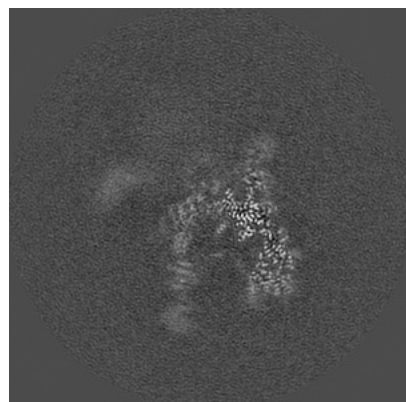


Z

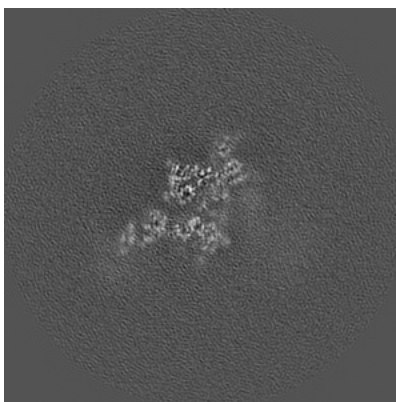
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

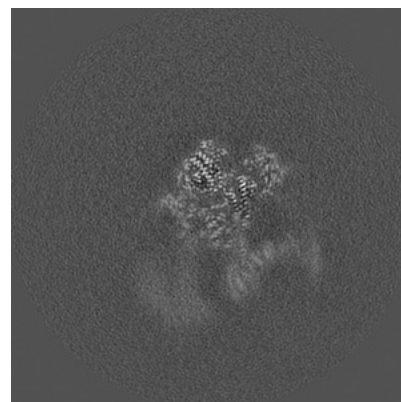
6.2.1 Primary map



X Index: 180



Y Index: 180

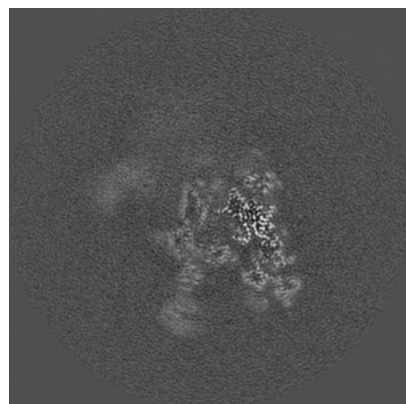


Z Index: 180

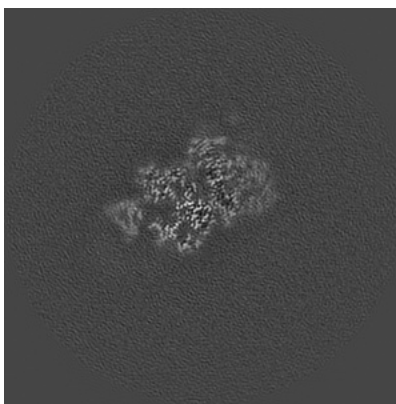
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

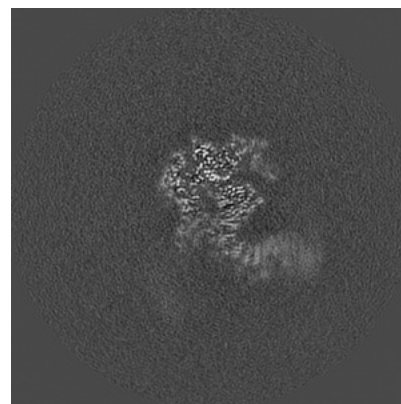
6.3.1 Primary map



X Index: 174



Y Index: 217

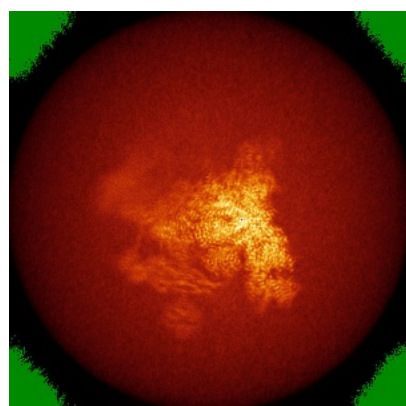


Z Index: 165

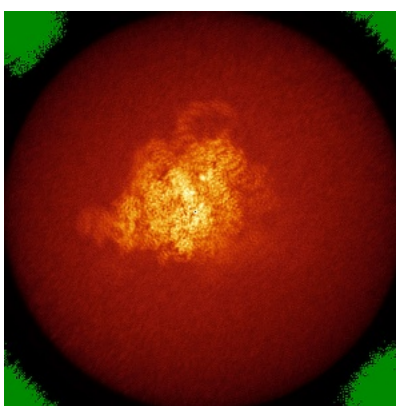
The images above show the largest variance slices of the map in three orthogonal directions.

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

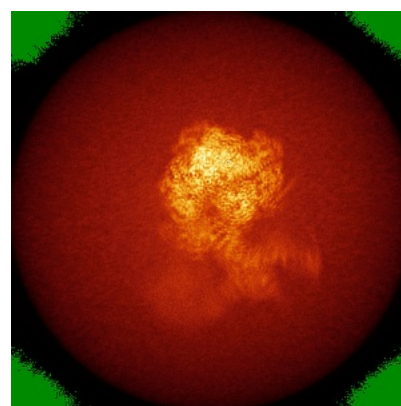
6.4.1 Primary map



X



Y

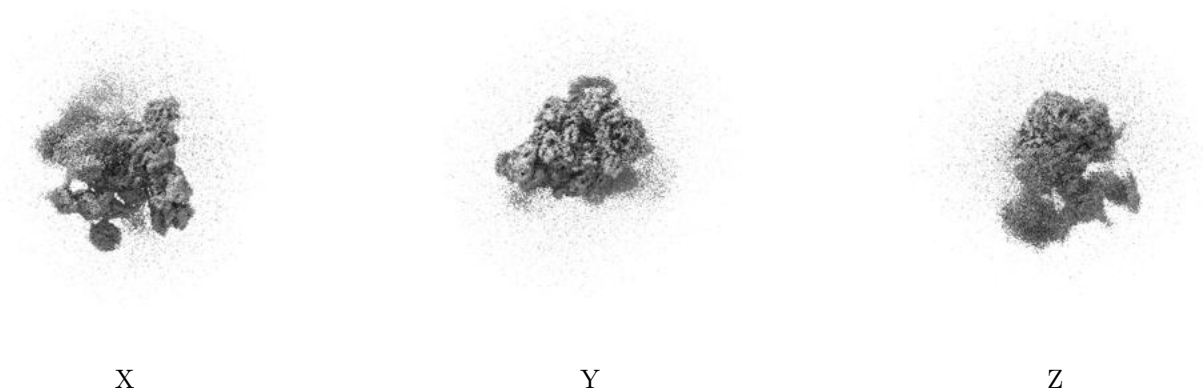


Z

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 0.0203. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

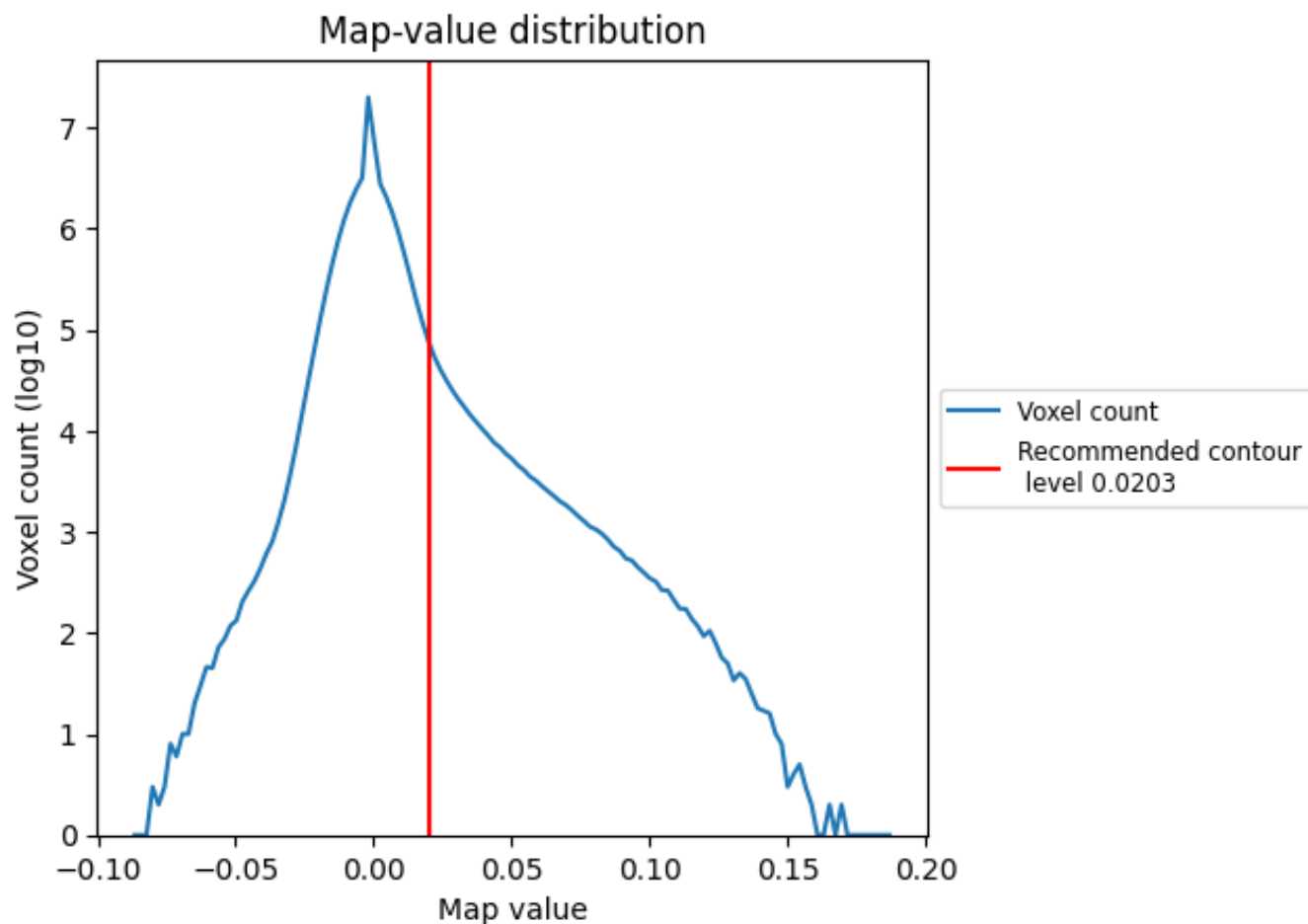
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

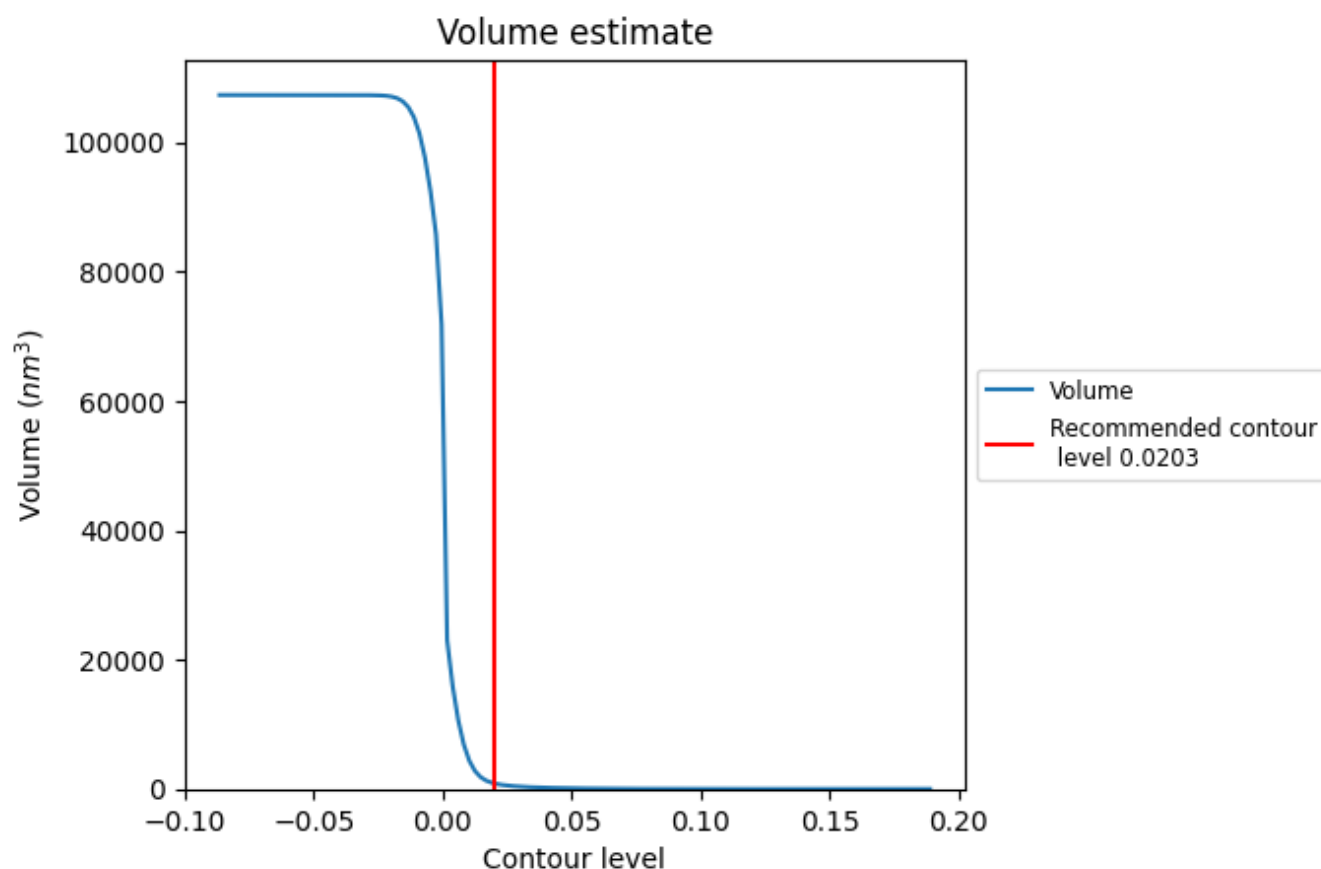
This section contains the results of statistical analysis of the map.

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.

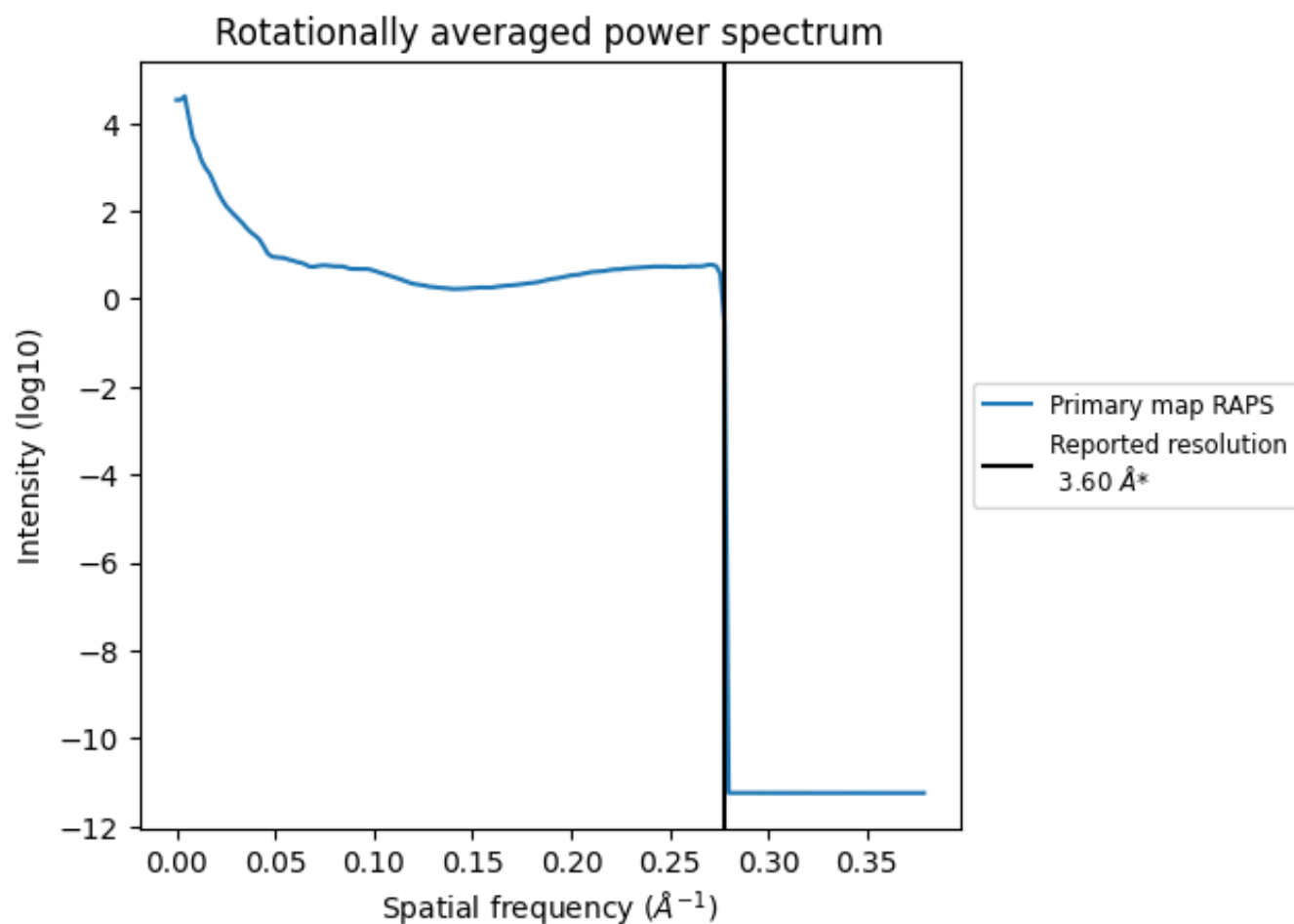
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 836 nm^3 ; this corresponds to an approximate mass of 755 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 0.278 Å⁻¹

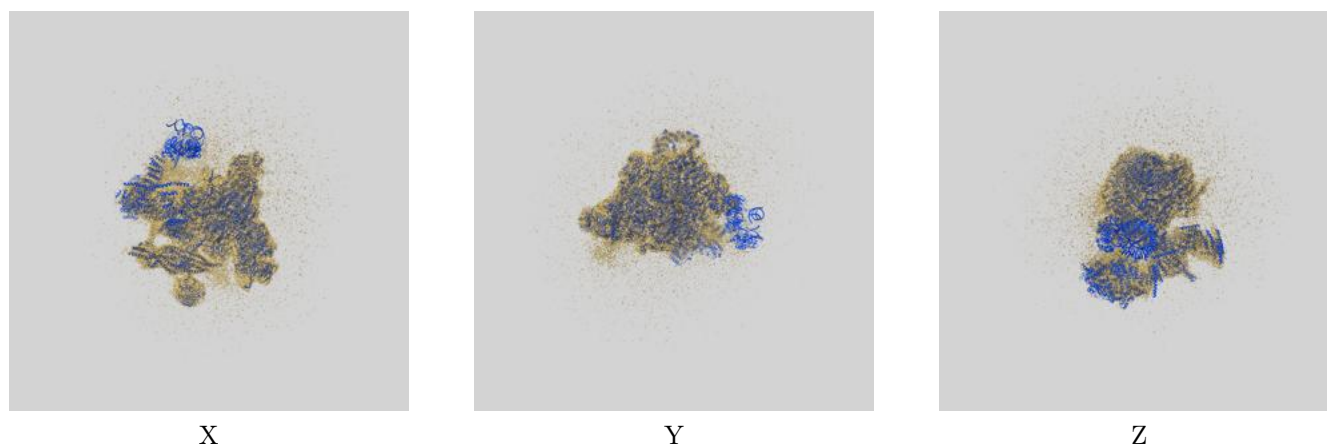
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

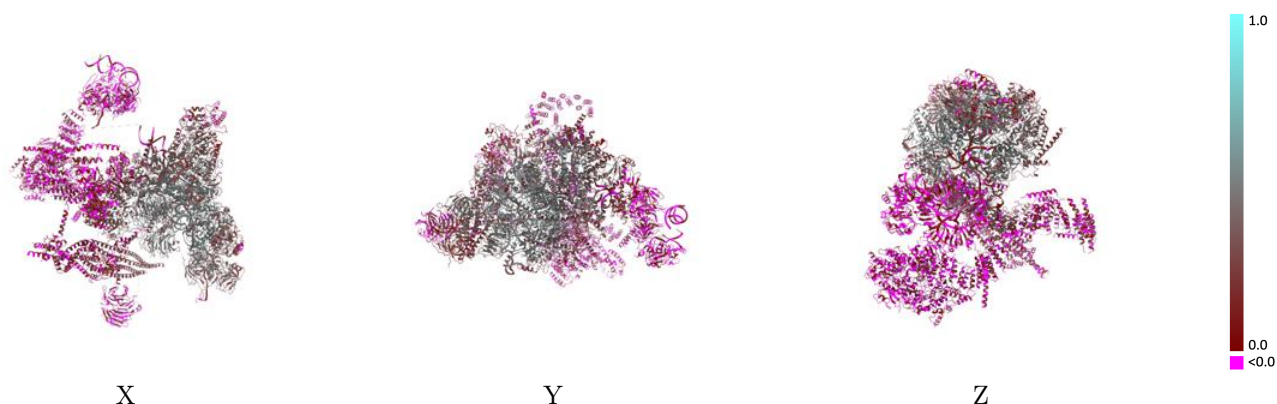
This section contains information regarding the fit between EMDB map EMD-6413 and PDB model 3JB9. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



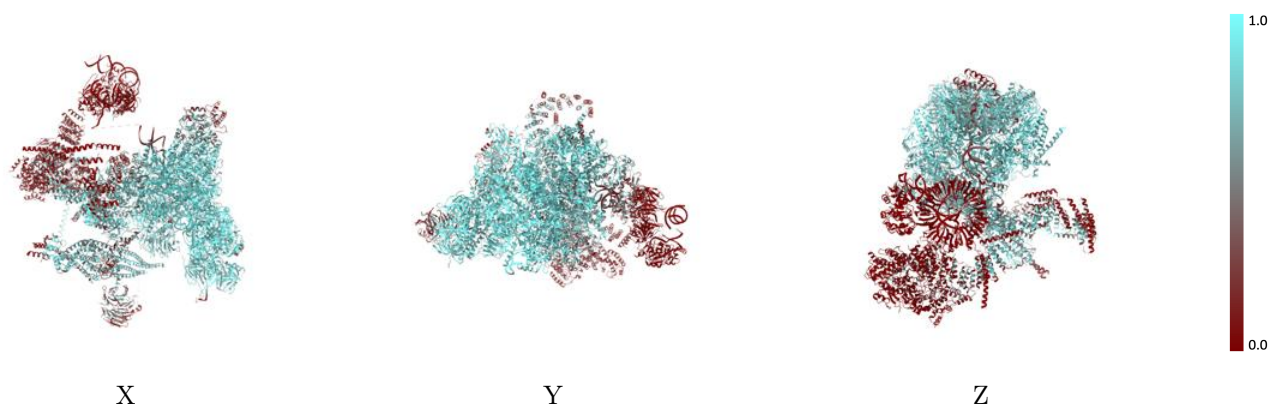
The images above show the 3D surface view of the map at the recommended contour level 0.0203 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



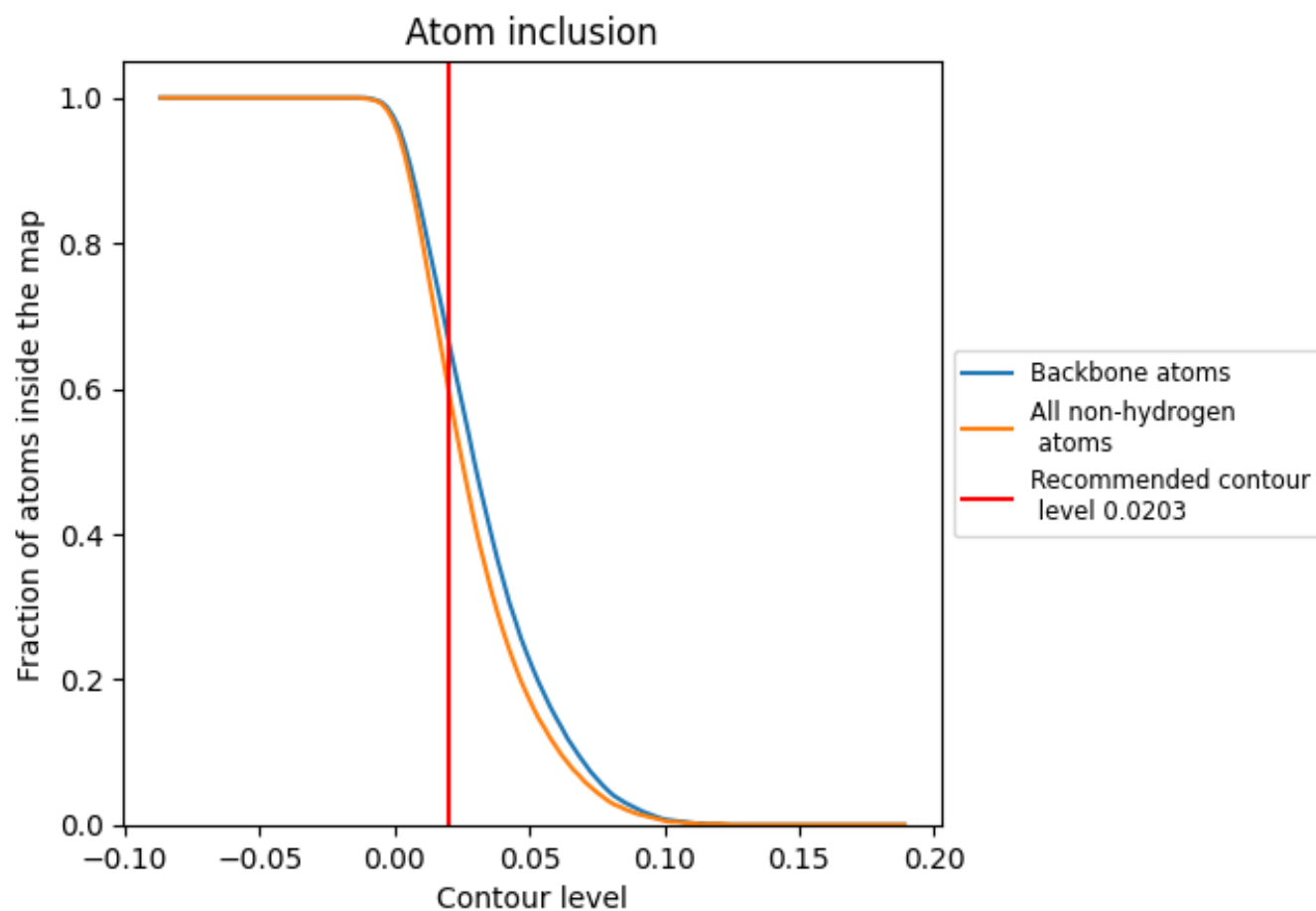
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0203).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 59% 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 (0.0203) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5930	 0.2520
A	 0.8040	 0.4010
B	 0.8680	 0.4180
C	 0.9290	 0.4420
D	 0.8890	 0.4500
E	 0.8480	 0.3960
F	 0.7740	 0.3100
G	 0.7330	 0.2220
H	 0.8070	 0.3130
I	 0.7740	 0.2540
J	 0.8220	 0.3800
K	 0.8760	 0.4390
L	 0.8580	 0.4210
M	 0.7380	 0.3490
N	 0.8110	 0.3390
O	 0.7120	 0.2310
P	 0.1830	 0.0590
Q	 0.2220	 0.0640
R	 0.6470	 0.2420
S	 0.5140	 0.1110
T	 0.6350	 0.1600
U	 0.3930	 0.0610
V	 0.5480	 0.1070
W	 0.6940	 0.2420
X	 0.0760	 0.0030
Y	 0.7700	 0.2860
Z	 0.0080	 0.0210
a	 0.6500	 0.2880
b	 0.0050	 0.0380
c	 0.6500	 0.3140
d	 0.7450	 0.3010
e	 0.8980	 0.4560
f	 0.0030	 0.0210
g	 0.7290	 0.3180
h	 0.7500	 0.4070



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.6580	 0.1600
j	 0.0040	 -0.0160
k	 0.0050	 0.0040
l	 0.0030	 -0.0040
m	 0.0000	 -0.0030
n	 0.0020	 -0.0110
o	 0.0040	 -0.0400
r	 0.4200	 0.0610
x	 0.4110	 0.0850