



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:35 AM UTC

PDB ID : 5YZG / pdb_00005yzg
EMDB ID : EMD-6864
Title : The Cryo-EM Structure of Human Catalytic Step I Spliceosome (C complex)
at 4.1 angstrom resolution
Authors : Zhan, X.; Yan, C.; Zhang, X.; Lei, J.; Shi, Y.
Deposited on : 2017-12-14
Resolution : 4.10 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:

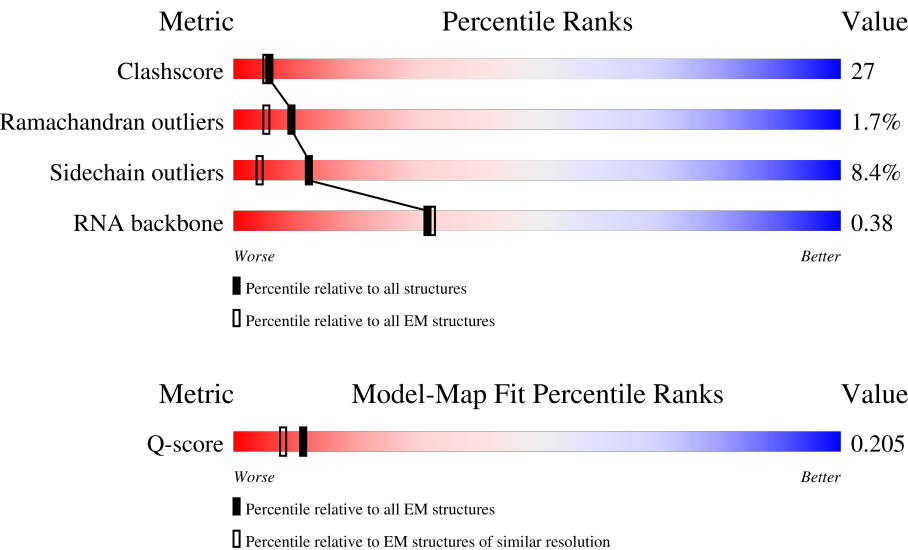
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	2335	6% 62% 26% 8%
2	B	117	8% 32% 26% 13% 28%
3	C	972	49% 31% 8% 11%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	2136	
5	E	357	
6	F	107	
7	G	275	
8	H	188	
9	I	855	
10	J	848	
11	K	225	
12	L	802	
13	y	307	
14	M	243	
15	N	144	
16	O	420	
17	P	229	
18	R	536	
19	S	166	
20	T	514	
21	Q	1485	
22	U	2752	
23	V	908	
24	W	579	
25	X	425	
26	Y	323	
27	Z	1227	
28	q	504	

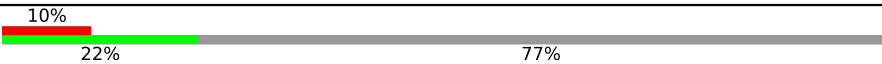
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	r	504	
28	s	504	
28	t	504	
29	u	411	
30	v	148	
31	w	174	
32	x	703	
33	a	126	
33	h	126	
34	b	229	
34	i	229	
35	c	119	
35	j	119	
36	d	118	
36	k	118	
37	f	86	
37	m	86	
38	e	92	
38	l	92	
39	g	76	
39	n	76	
40	o	255	
41	p	225	
42	1	301	
43	2	646	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
44	3	754	
45	4	37	

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
46	IHP	A	3000	-	-	X	-
50	ZN	N	202	-	-	X	-
50	ZN	Y	400	-	-	X	-

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 103906 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-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2253	Total	C	N	O	S	0	0
			17519	11136	3147	3166	70		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	P	0	0
			1768	792	295	597	84		

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	862	Total	C	N	O	S	0	0
			6795	4344	1138	1281	32		

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	1908	Total	C	N	O	0	0
			7632	3816	1908	1908		

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	299	Total	C	N	O	S	0	0
			2338	1470	410	445	13		

- Molecule 6 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 7 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	88	Total	C	N	O	P	0	0
			1641	727	238	589	87		

- Molecule 8 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	139	Total	C	N	O	P	0	0
			2946	1317	507	983	139		

- Molecule 9 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	559	Total	C	N	O	0	0
			2757	1639	559	559		

- Molecule 10 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	571	Total	C	N	O	S	0	0
			3829	2385	720	718	6		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	152	Total	C	N	O	S	0	0
			979	611	177	189	2		

- Molecule 12 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	419	Total	C	N	O	S	0	0
			2885	1809	534	537	5		

- Molecule 13 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	y	112	Total	C	N	O	S	0	0
			704	440	130	133	1		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	91	Total	C	N	O	S	0	0
			775	482	146	145	2		

- Molecule 15 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	143	Total	C	N	O	S	0	0
			1184	746	217	209	12		

- Molecule 16 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	283	Total	C	N	O	S	0	0
			2277	1430	403	424	20		

- Molecule 17 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	96	Total	C	N	O	S	0	0
			829	508	162	157	2		

- Molecule 18 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	245	Total	C	N	O	P	S	0	0
			1962	1231	353	364	2	12		

- Molecule 19 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1236	787	215	227	7		

- Molecule 20 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	313	Total	C	N	O	S	0	0
			2461	1554	447	452	8		

- Molecule 21 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Q	1322	Total	C	N	O	0	0
			5288	2644	1322	1322		

- Molecule 22 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	26	Total	C	N	O	S	0	0
			193	120	36	36	1		

- Molecule 23 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	452	Total	C	N	O	S	0	0
			3410	2194	590	611	15		

- Molecule 24 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	440	Total	C	N	O	S	0	0
			2310	1296	487	523	4		

- Molecule 25 is a protein called Pre-mRNA-splicing factor CWC25 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	71	Total	C	N	O	0	0
			480	297	95	88		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	145	GLN	LYS	conflict	UNP Q9NXXE8
X	149	PRO	LYS	conflict	UNP Q9NXXE8

- Molecule 26 is a protein called Coiled-coil domain-containing protein 94.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	204	Total	C	N	O	S	0	0
			1426	898	259	261	8		

- Molecule 27 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Z	635	Total	C	N	O	0	0
			2540	1270	635	635		

- Molecule 28 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	q	132	Total	C	N	O	S	0	0
			918	581	156	178	3		
28	r	131	Total	C	N	O	S	0	0
			901	572	149	177	3		
28	s	374	Total	C	N	O		1	0
			1497	749	374	374			
28	t	67	Total	C	N	O	S	0	0
			476	300	83	92	1		

- Molecule 29 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	u	390	Total	C	N	O	S	0	0
			3126	1974	545	588	19		

- Molecule 30 is a protein called Protein mago nashi homolog 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	144	Total	C	N	O	S	0	0
			1196	772	200	221	3		

- Molecule 31 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	w	91	Total	C	N	O	S	0	0
			730	463	122	142	3		

- Molecule 32 is a protein called Protein CASC3.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	x	25	Total	C	N	O	0	0
			216	136	39	41		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	80	Total	C	N	O	S	0	0
			621	388	110	117	6		
33	a	77	Total	C	N	O	S	0	0
			609	381	108	115	5		

- Molecule 34 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	86	Total	C	N	O	S	0	0
			690	434	126	123	7		
34	b	83	Total	C	N	O	S	0	0
			675	426	123	119	7		

- Molecule 35 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	82	Total	C	N	O	S	0	0
			649	413	113	119	4		
35	c	81	Total	C	N	O	S	0	0
			641	409	112	116	4		

- Molecule 36 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	85	Total	C	N	O	S	0	0
			688	432	125	126	5		
36	d	97	Total	C	N	O	S	0	0
			768	482	141	140	5		

- Molecule 37 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	74	Total	C	N	O	S	0	0
			576	373	95	103	5		
37	f	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 38 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	79	Total	C	N	O	S	0	0
			652	412	116	119	5		

- Molecule 39 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	68	Total	C	N	O	S	0	0
			533	339	95	93	6		
39	g	74	Total	C	N	O	S	0	0
			569	358	102	103	6		

- Molecule 40 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	162	Total	C	N	O	S	0	0
			1277	817	219	238	3		

- Molecule 41 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	94	Total	C	N	O	S	0	0
			760	488	135	132	5		

- Molecule 42 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	1	243	Total	C	N	O	0	0
			972	486	243	243		

- Molecule 43 is a protein called Peptidylprolyl isomerase domain and WD repeat-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	2	416	Total	C	N	O	0	0
			1664	832	416	416		

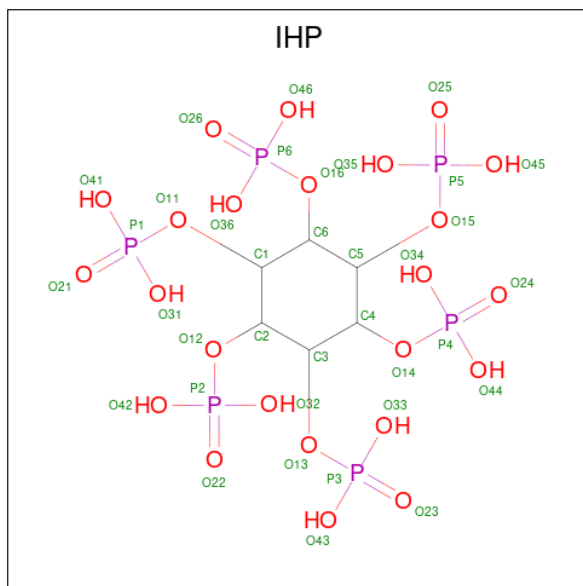
- Molecule 44 is a protein called Peptidyl-prolyl cis-trans isomerase G.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	3	171	Total	C	N	O	0	0
			684	342	171	171		

- Molecule 45 is a protein called UNKNOWN.

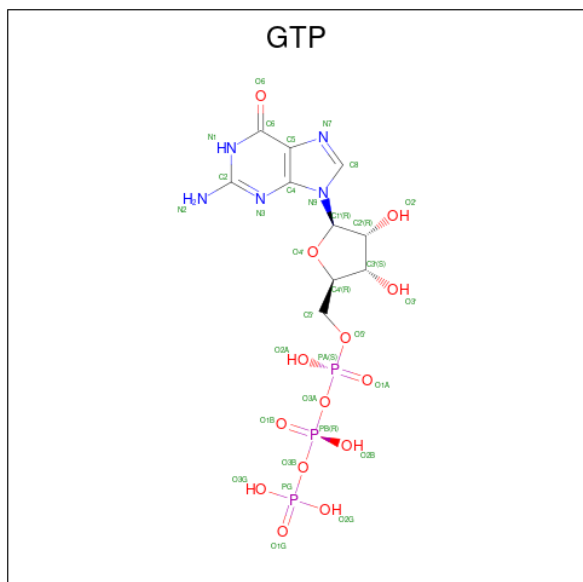
Mol	Chain	Residues	Atoms				AltConf	Trace
45	4	37	Total	C	N	O	0	0
			184	110	37	37		

- Molecule 46 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
46	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 47 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

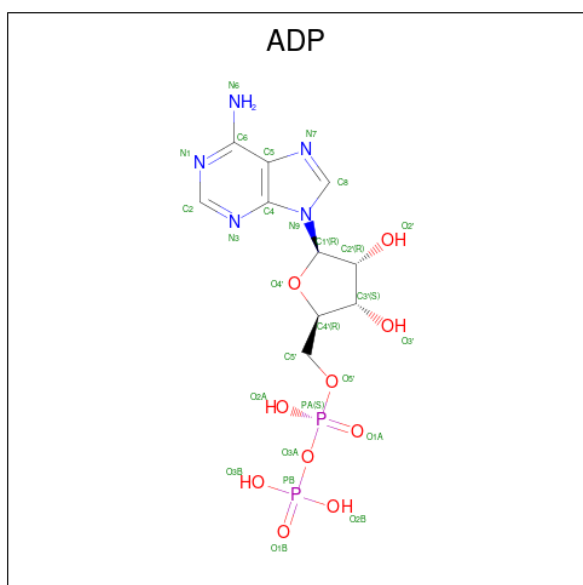


Mol	Chain	Residues	Atoms					AltConf
47	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	C	1	Total	Mg	0
			1	1	
48	F	5	Total	Mg	0
			5	5	
48	u	1	Total	Mg	0
			1	1	

- Molecule 49 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

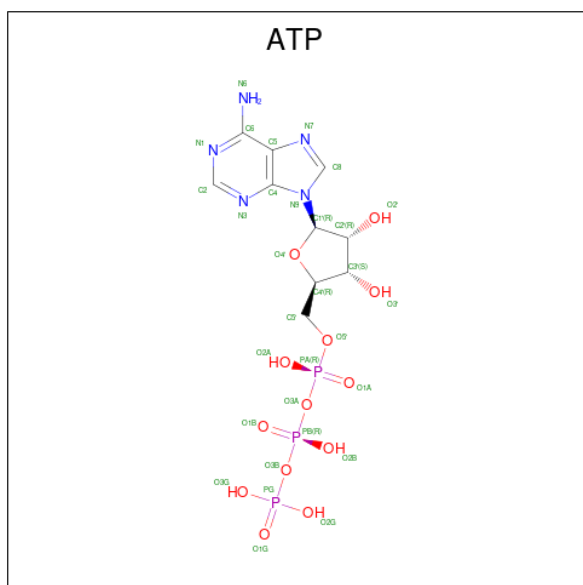
Mol	Chain	Residues	Atoms		AltConf
50	N	3	Total	Zn	0
			3	3	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
50	O	3	Total 3	Zn 3	0
50	Y	1	Total 1	Zn 1	0

- Molecule 51 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

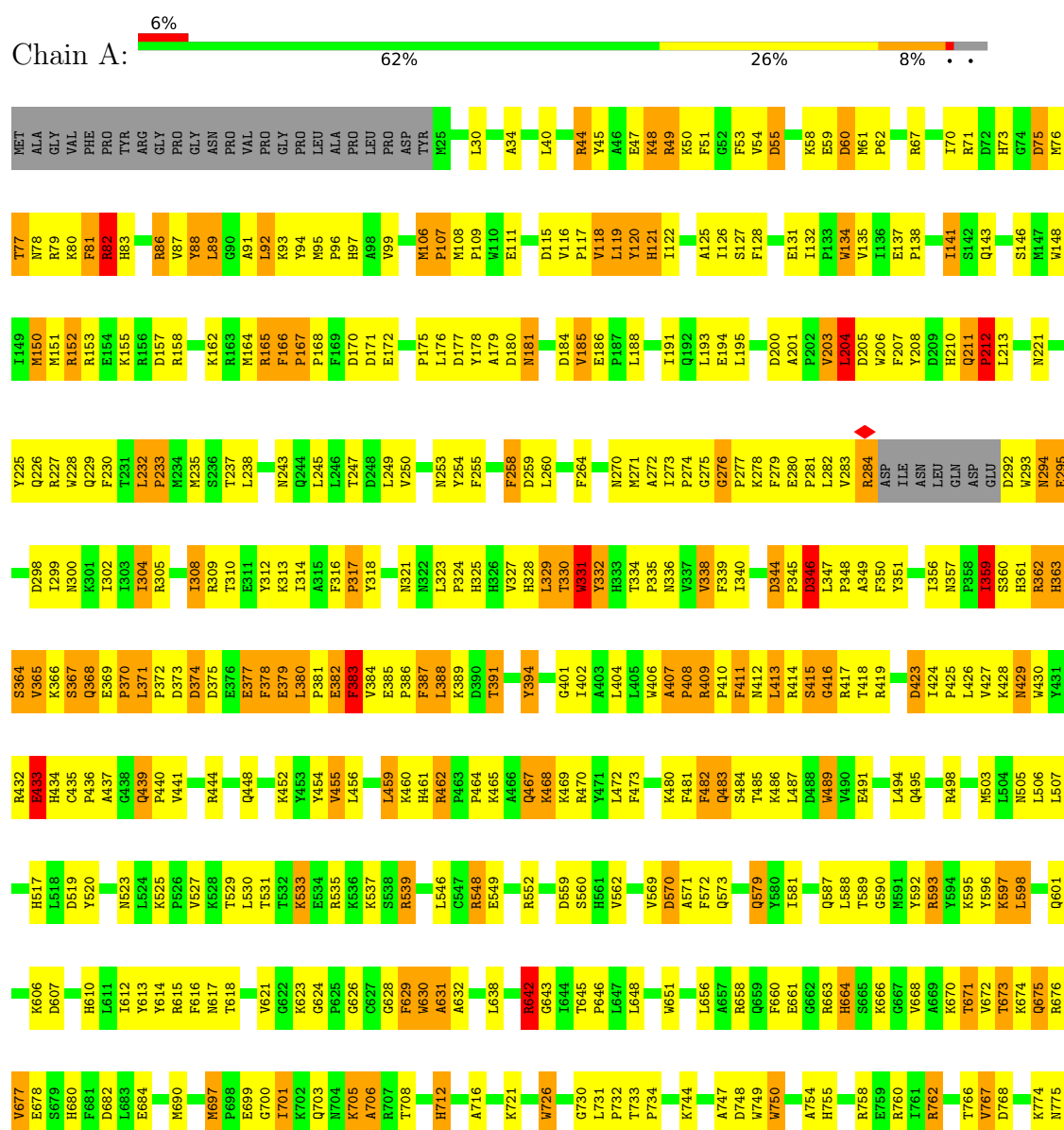


Mol	Chain	Residues	Atoms					AltConf
51	u	1	Total 31	C 10	N 5	O 13	P 3	0

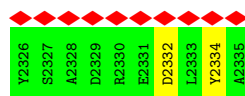
3 Residue-property plots

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.

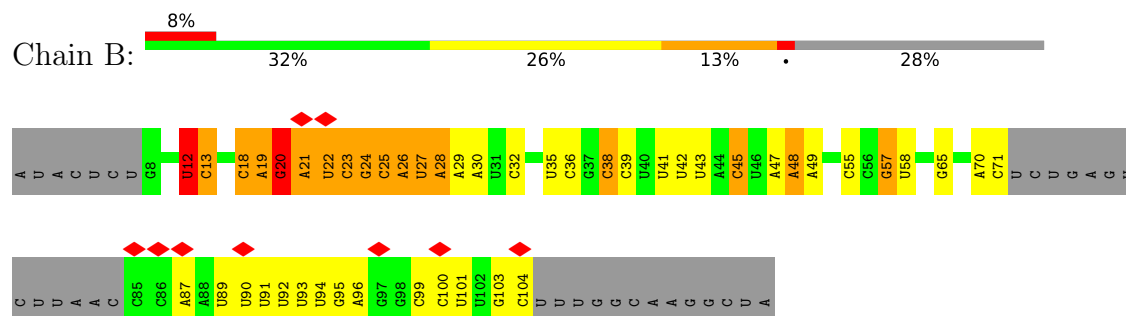
• Molecule 1: Pre-mRNA-processing-splicing factor 8



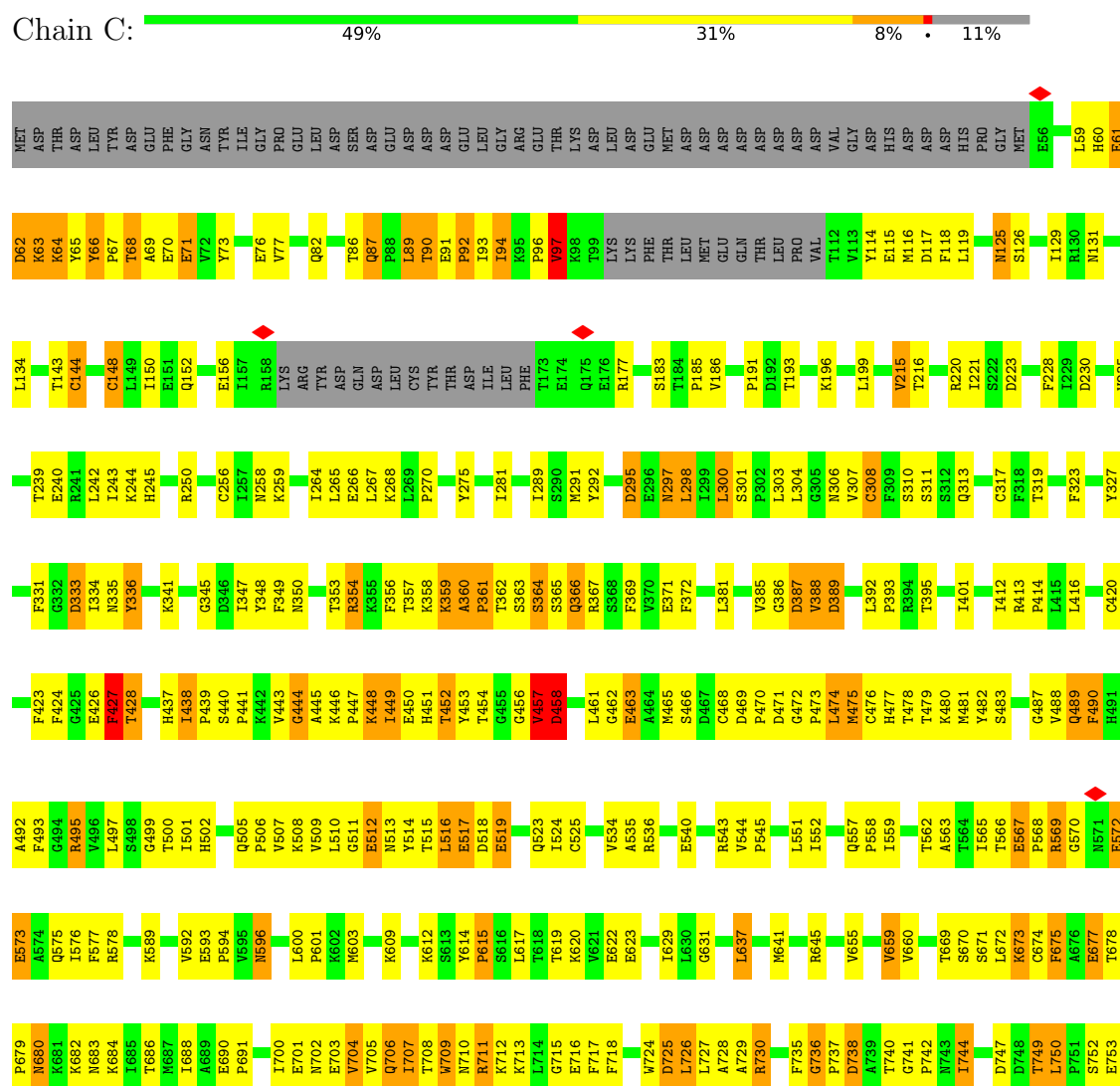




• Molecule 2: U5 snRNA

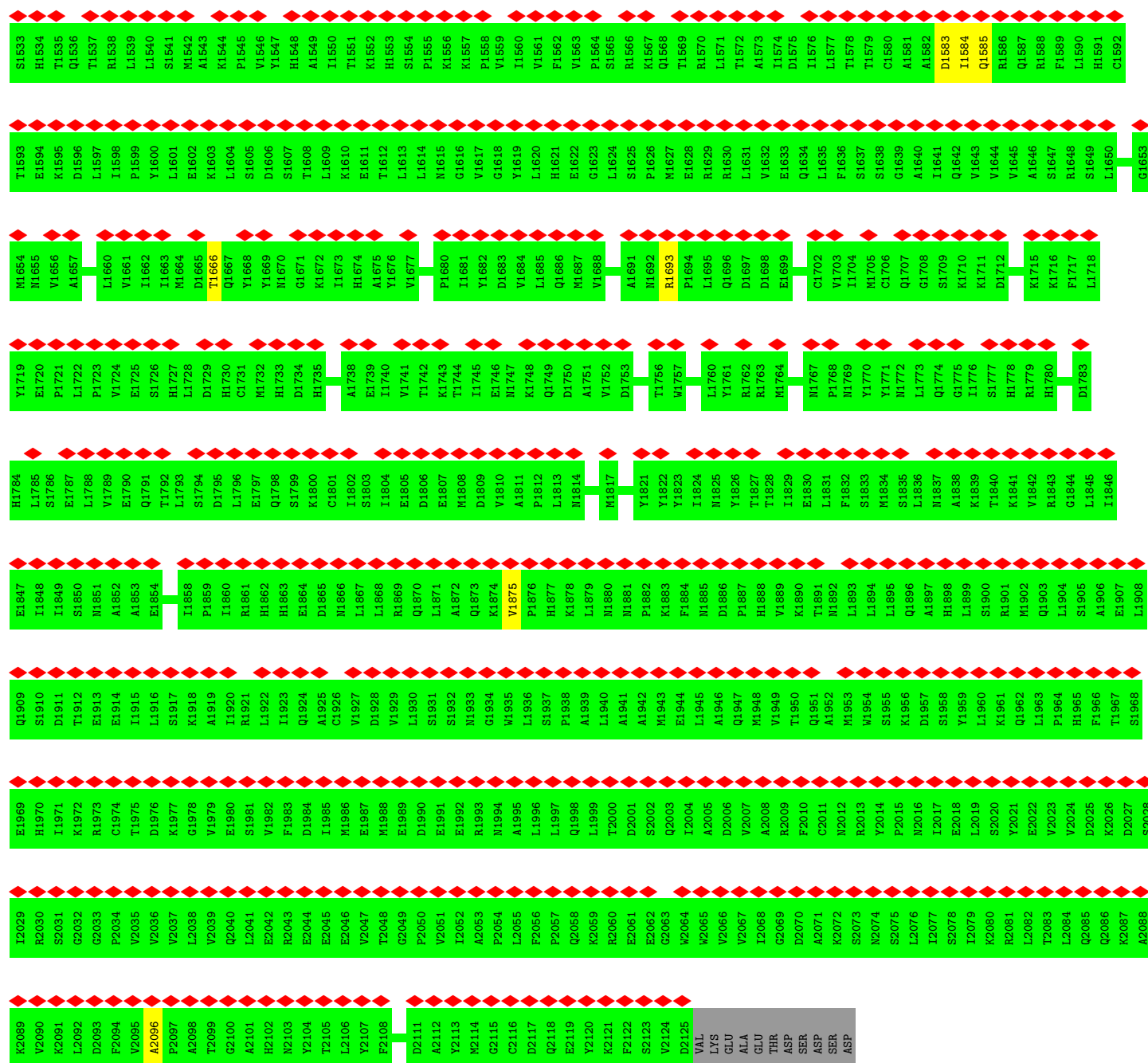


• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



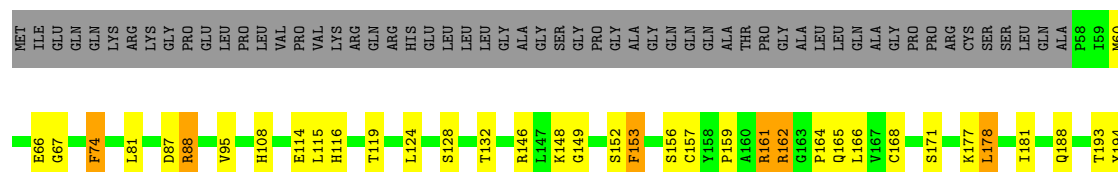




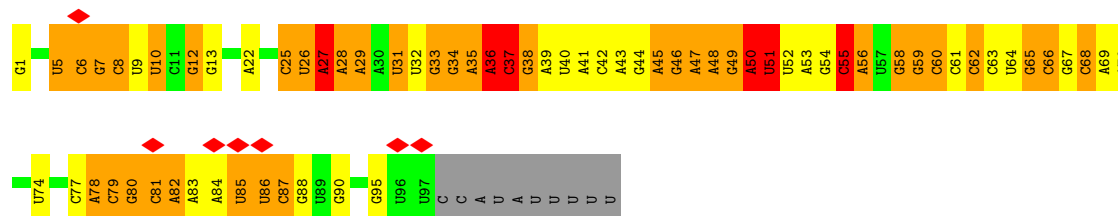
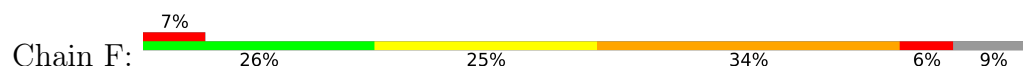


- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

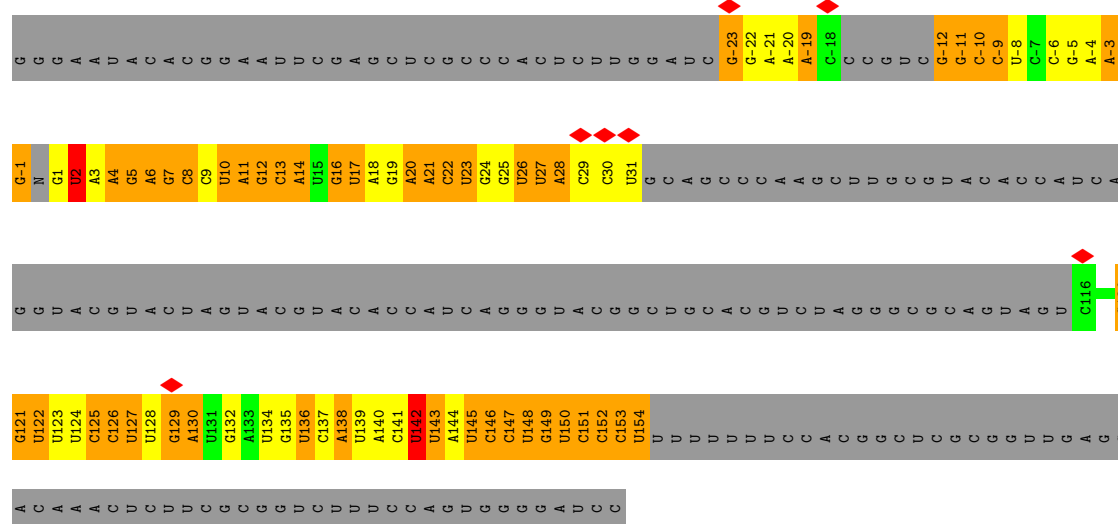
Chain E: 57% 22% 16%



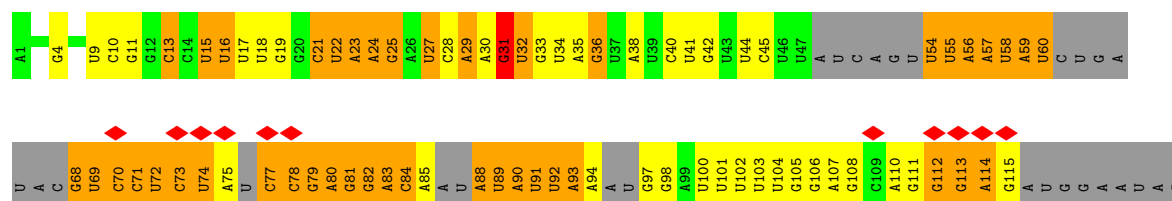
- Molecule 6: U6 snRNA

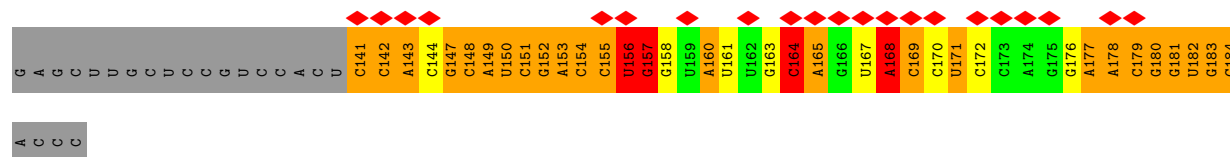


- Molecule 7: Pre-mRNA

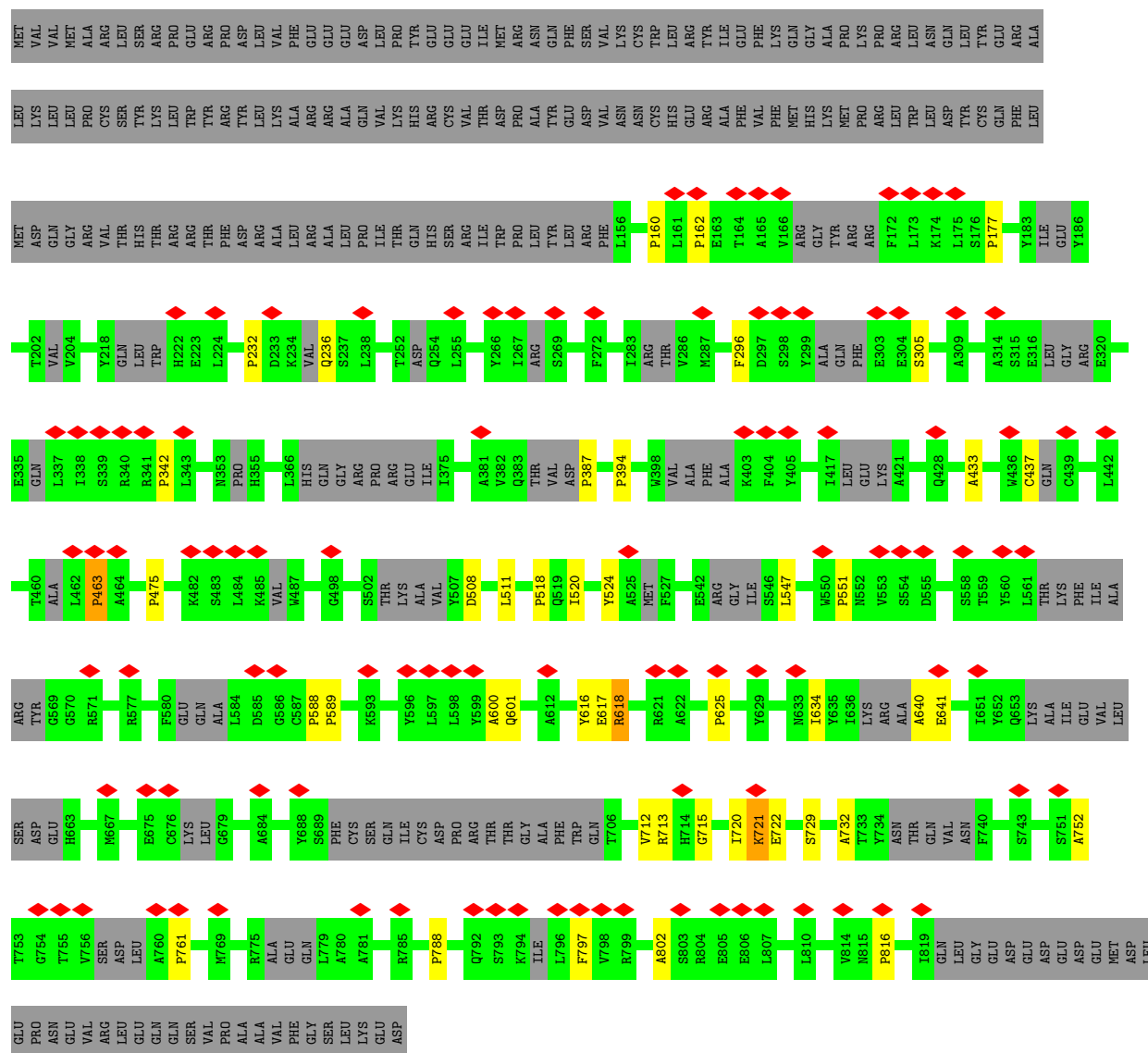


- Molecule 8: U2 snRNA

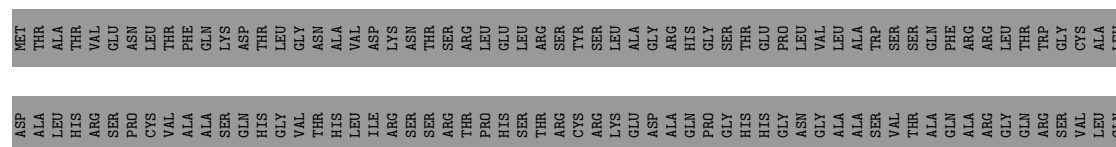


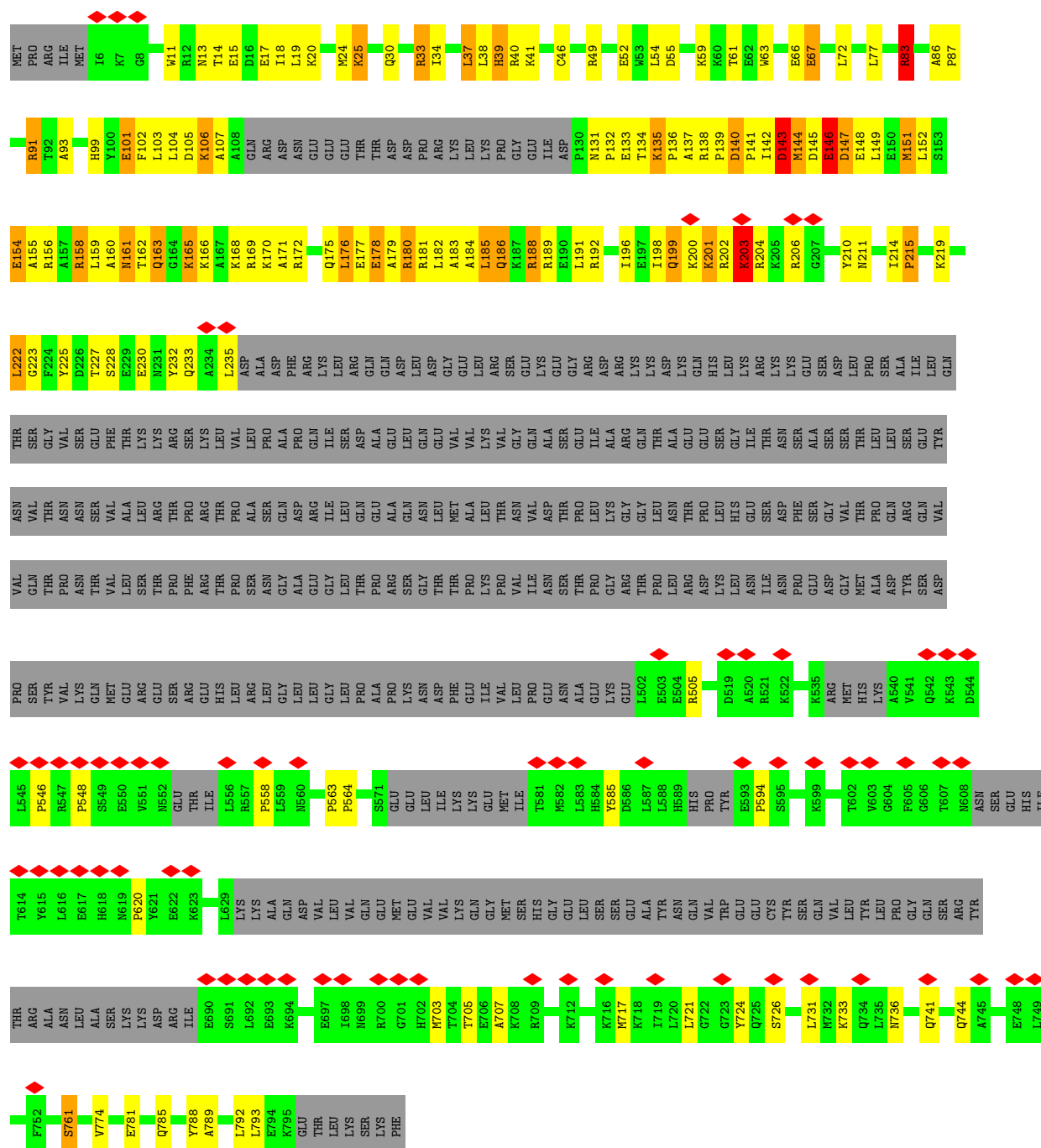


• Molecule 9: Pre-mRNA-splicing factor SYF1

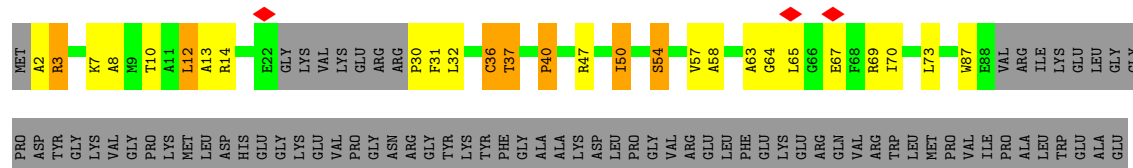


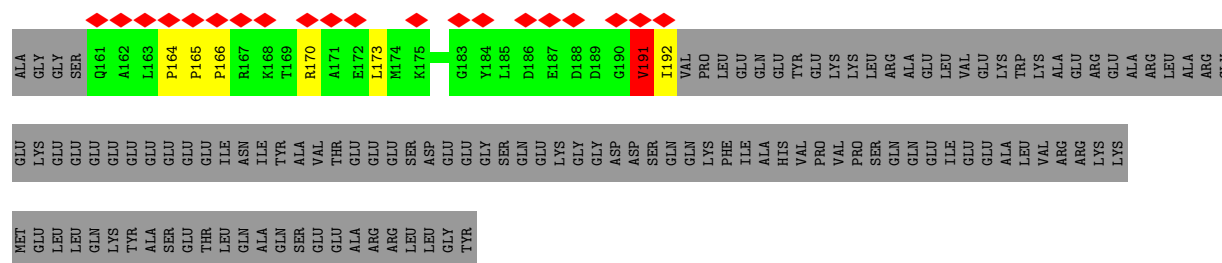
• Molecule 10: Crooked neck-like protein 1



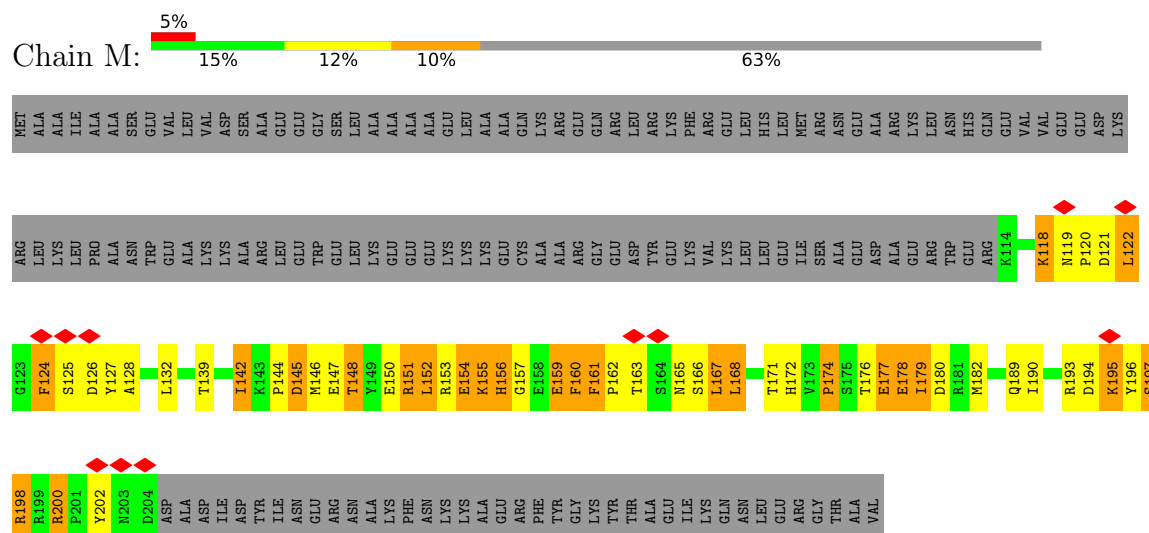


• Molecule 13: Pre-mRNA-splicing factor ISY1 homolog

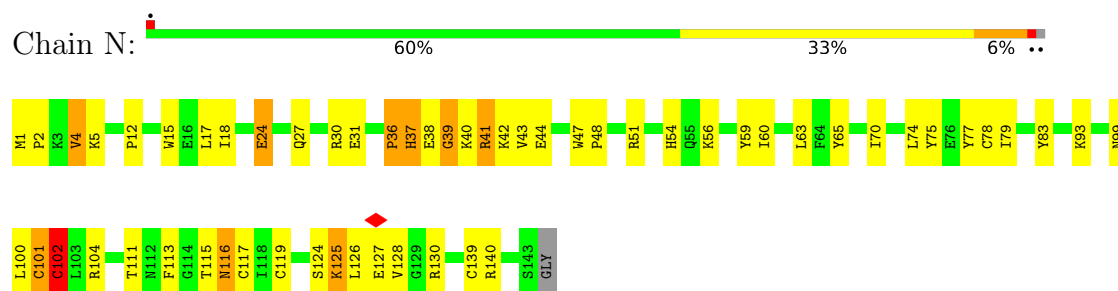




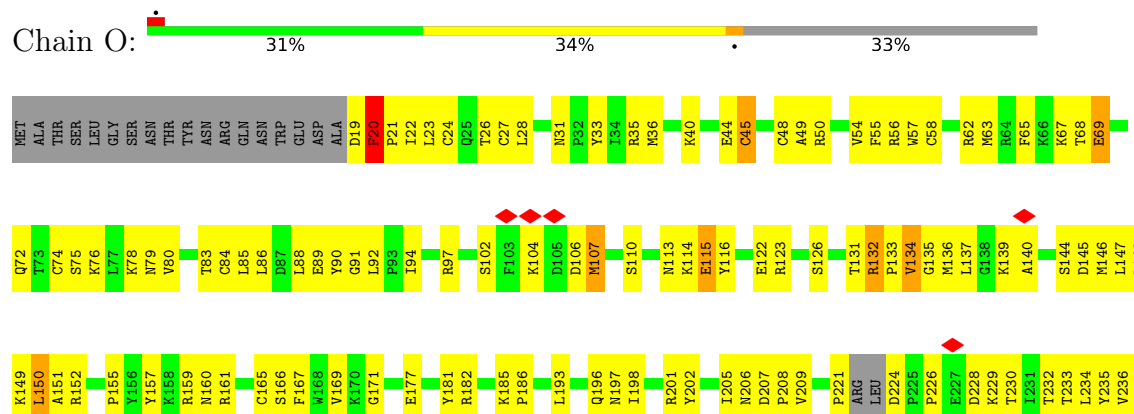
• Molecule 14: Pre-mRNA-splicing factor SYF2



• Molecule 15: Protein BUD31 homolog

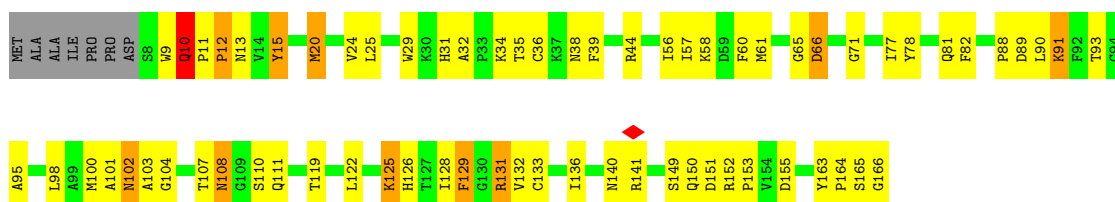


• Molecule 16: Pre-mRNA-splicing factor RBM22

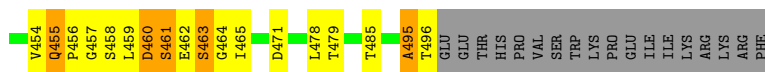
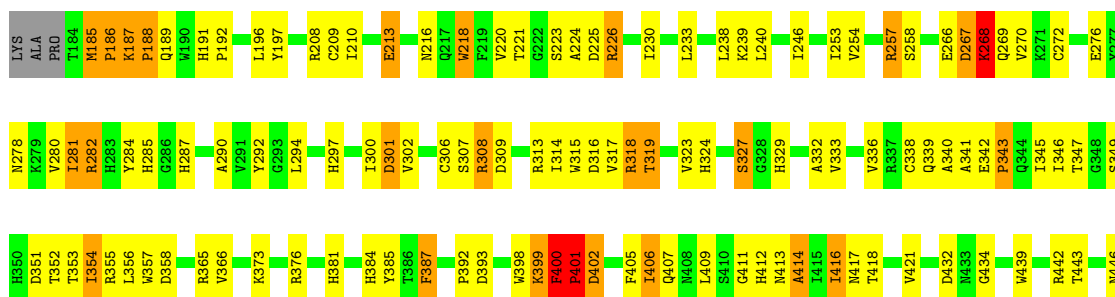
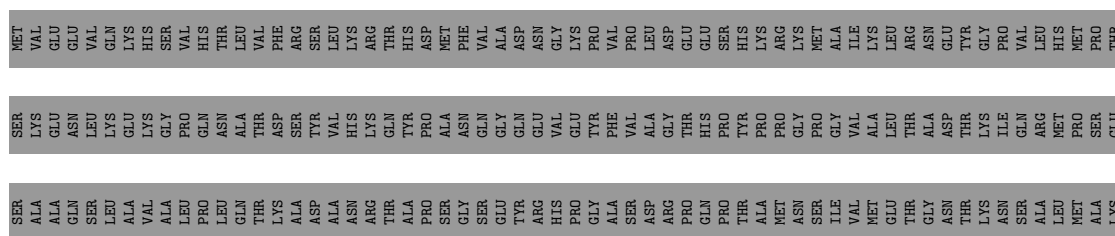
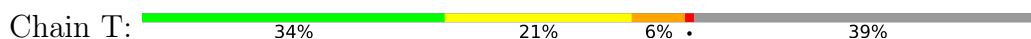




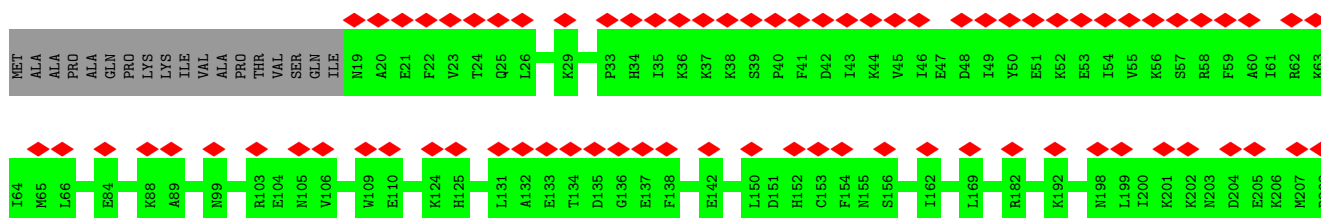
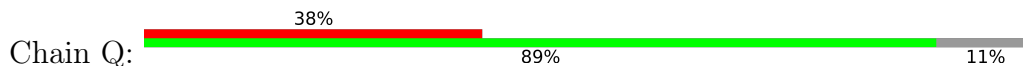
- Molecule 19: Peptidyl-prolyl cis-trans isomerase-like 1



- Molecule 20: Pleiotropic regulator 1



- Molecule 21: Intron-binding protein aquarius



GLU	P1334	M1255	D1176	L1088	F892	V783	T717	P614	S445	Q316	P209
VAL	T1335	T1259	F1177	H1097	G896	I784		R615	C446	T317	E210
THR	E1336	V1260						P616	E447		A211
GLN	PRO	D1261	N1181			Y790	I721	N617		L321	R212
GLU	PHE	V1182	V1182	I1104	L902	P791	E722	L618	A451	T322	E213
THR	PRO	E1183	E1183	K1105	A903	S986	H723	R619	L452	T323	Q214
VAL	T1340	F1263	D1184	M1106	I906	Q794	L724		L455	N324	
ALA	T1341	Q1264	F1185			P795		N632	T461	E325	L222
LEU	T1342	G1265	Q1186	F1109	V912	K796	S727				
VAL	R1342	G1266		Q1110		R797	F728	Q636		T328	I230
SER	K1343	Q1267	E1190	K1111	K917			T639	T461		
ALA	N1344	Q1267	S1191	Y1112		I800	N732	N640	L467	D332	P237
PRO	G1345	M1268	E1192	M1113	G920	Q801	V733	N640	L467		L238
GLU	E1192	D1269	E1192	S1113	V921	F802	K734	T641	L472	P346	S239
ALA	D1346	I1270	G995	M1114	P922	T803	V735	I642			E240
ASN	R1347	Y1198	E995	M1115	G923	Q815	V736	Q643	S497	E363	P241
THR	P1348	Q1199	C997	E1116	G923	Q815	T737	N644	GLU		
PRO	L1272	N1200	F998	Q1117		P816	V737	G645	TVR	K367	V242
GLN				S1118	S926		E738	G645			T243
ALA	L1275	V1207	I1001			M820	D739	A646	G501	P371	M244
ALA	E1351	V1208	K1002	G1127	M941	V821	F740	E647	G500	L372	D245
THR	V1352	A1209	K1003	V1128	S942	B822	A741	D648		L377	K246
SER	Q1353	L1210			R943		L742				V247
PRO	I1354	F1211	T1006	Q1136	W944	P825	Q743	K662	I514		
GLU	T1211	M1212	Q1007	G1137	E945		ILE		V519	L390	F253
GLU	F1211	M1212	L1008	E1138	E946	G828	PRO	L676	V520	L390	
THR	I1355	M1212	L1008	A1139	Y947	N839	F747		E521	P391	D259
ASP	K1356	M1212	L1008	R1140	I948			T679	V522	K392	L260
THR	R1285	Y1213	L1016	E1141	S949	H842	T750	C681	I527	N393	E261
SER	D1286	G1214	L1016	S1142	K950	N843	F751	V682	E527	D396	A262
CYS	M1358	M1214	L1017	L1143	V951	F844	P752		E529	T396	
ARG	P1359	C1215	R1018	C1144	K952	P845	V753	D685	N530	T397	D275
GLN	Q1360		C1039	M1145	N953	E846	ARG	W686	K550		
GLU		L1216	G1039	L1146	LYS	Q847	GLY	H688	K550	K400	C283
THR	F1364	L1217	A1042	Y1147	GLY	Q847	LYS	E401		E401	Y284
PRO	V1365	G1218	L1017	E1147	SER		LYS	F402		F402	L285
ALA	V1365	Y1219	L1018	M1148	THR	L859	GLY	L403		L403	S286
PHE	Y1366	P1220	R1018	W1149	LEU		LYS	L404		L404	N287
GLN	Y1366	A1221	M1145			E864	LYS	L407			L288
THR	N1298	L1221	L1146		P959		LYS				R290
ASP	L1299	D1222	L1146		D960	M867	ARG	L407			V289
THR	G1300	K1223	Y1147		V961		LYS				R291
THR	L1301	L1224	M1148		T962	I871	ASP	L407			E292
PRO	Y1302	S1225			E963	D872	VAL	R414			R293
SER					V964	E873	GLU	R414			E293
GLU					S965	R874	ASP	R415			D294
ALA					T966	H875	GLU	I418			G295
ALA	Y1379				F967	L876	THR	Q419			H296
ALA					P968	L877	GLU				
PRO	H1380				P969	R878	THR	L589			L297
PRO	Q1381				F970	L879	GLU	V590			F298
LEU					H971	G880	THR				S299
LEU					E972	H881	GLU				Q300
GLN					Y973	GLY	THR	I432			I433
PRO					F974	GLU	GLU	I433			S299
PRO					A975	E884	THR	W434			Q300
ALA					N976		THR	D435			D303
ALA					N976		THR	E436			M304
MET					A977		THR	M437			
VAL					PRO		THR	P440			F307
GLU					GLN		THR	T441			E311
GLY					PRO		THR	E442			
GLU					GLN		THR	Y443			N314
					PRO		THR	D713			D315

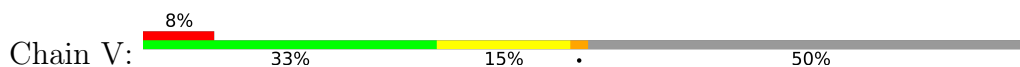
Chain U: 99%





PRO	GLN	PRO	SER	THR	ALA	THR	ALA	ILE	ASP	SER
PRO	SER	SER	SER	ALA	GLN	PRO	ALA	ALA	ARG	HIS
SER	SER	SER	SER	PRO	ALA	LYS	GLU	THR	SER	ALA
ARG	SER	GLU	ALA	GLU	GLY	VAL	PRO	ARG	THR	ALA
ASP	PRO	ALA	VAL	ARG	GLY	ALA	PRO	VAL	THR	PRO
GLN	SER	SER	GLY	GLY	SER	SER	ALA	ALA	PRO	ASN
GLN	PRO	GLU	ALA	GLU	GLY	GLN	GLN	SER	ILE	PRO
SER	SER	PRO	PRO	ARG	SER	SER	PRO	GLY	ALA	GLY
SER	SER	GLY	GLY	PRO	SER	LEU	SER	SER	SER	SER
GLU	ARG	PRO	PRO	GLU	SER	ALA	THR	GLN	ARG	ARG
ARG	GLY	ALA	GLN	GLU	SER	VAL	ALA	SER	ALA	ALA
GLY	SER	PRO	ALA	THR	SER	ALA	MET	ARG	ALA	ALA
ARG	ARG	PRO	LYS	ALA	SER	SER	THR	ALA	THR	LEU
GLY	GLN	PHO	PHO	LYS	SER	SER	THR	GLU	SER	ALA
ARG	ALA	SER	ALA	ARG	SER	SER	THR	ARG	PRO	PRO
GLY	ARG	ALA	ALA	LYS	SER	SER	THR	ALA	ALA	ALA
GLY	PRO	ARG	PRO	ARG	SER	SER	SER	PRO	PRO	SER
ASP	LYS	ARG	LYS	ARG	SER	SER	SER	SER	LEU	LEU
SER	SER	SER	LYS	SER	SER	SER	ALA	PRO	THR	THR
ARG	ARG	PHO	PHO	SER	SER	SER	GLY	SER	SER	ALA
PRO	PRO	PRO	PRO	SER	SER	SER	ASP	SER	ALA	ARG
SER	SER	GLY	GLY	SER	SER	SER	HIS	ARG	ARG	ARG
HIS	SER	GLU	GLU	SER	SER	SER	GLY	MET	MET	WET
LYS	ARG	ARG	ARG	SER	SER	SER	GLY	GLY	GLY	ALA
ARG	ARG	ANG	ANG	SER	SER	SER	MET	GLN	GLN	PRO
ARG	ARG	ANG	ANG	SER	SER	SER	LEU	ALA	ALA	ALA
GLU	ARG	ARG	ARG	SER	SER	SER	VAL	SER	PRO	LEU
THR	PRO	PRO	PRO	SER	SER	GLY	PRO	GLN	SER	GLY
PRO	SER	LYS	LYS	SER	SER	SER	PRO	ASN	LEU	ASN
PRO	PRO	PRO	PRO	SER	SER	SER	VAL	LEU	PRO	PRO
ARG	ARG	ILE	ILE	SER	SER	ASP	PRO	PRO	PRO	THR
PRO	PRO	ASP	ASP	SER	SER	SER	HIS	ALA	PRO	PRO
MET	ARG	SER	SER	SER	SER	GLU	SER	GLN	ARG	ARG
ARG	HIS	ANG	ANG	SER	SER	GLY	VAL	ASP	VAL	PRO
ARG	ARG	ASP	ASP	SER	SER	SER	GLY	PRO	GLN	PRO
SER	SER	ARG	ARG	SER	SER	PRO	PRO	SER	SER	ALA
SER	SER	LEU	LEU	SER	SER	VAL	PRO	PRO	TYR	TYR
PRO	PRO	TYR	TYR	SER	SER	GLU	PRO	VAL	GLU	VAL
				SER	SER	VAL	GLY	SER	PRO	ARG
				SER	SER	ALA	ALA	PHE	ALA	GLY
				SER	SER	LEU	GLN	SER	ARG	ARG
				SER	SER	LYS	GLN	GLN	THR	THR
				SER	SER	ARG	PRO	ASP	GLN	ASP
				SER	SER	VAL	SER	SER	ARG	PRO
				SER	SER	PRO	ALA	ARG	PRO	PRO
				SER	SER	PRO	LEU	CYS	LEU	LEU
				SER	SER	PRO	ALA	ALA	ALA	ALA

- Molecule 23: Pre-mRNA-splicing factor CWC22 homolog



F612	Q532	A462	A400	R192	K298	GLU	SER
E613	Y533		I401	G193	G311	LEU	TYR
GLY	D534	S465	K402	R194		ASP	ASP
LEU	T535	S466	K403	G195		PRO	SER
LEU	I536	L467	E404	L196	F316	LEU	SER
PRO	H537	D468	E405	L197		LEU	MET
ARG		F469	I405	S198	R320	THR	GLU
D619	E540	E470	L406			ARG	SER
M620	T541	C471	ASP	L202	E325	THR	LYS
P621	C472	A473	GLU			GLY	PRO
R622	N546	H474	GLY	L207	D329	ARG	SER
M623	V547	A475	ASP	A207	K330	ALA	ASP
T624	A548	K475	THR		R331	TYR	GLY
R625	K549	L476	ASP	V214	G332	ILE	HIS
	M550	L477	SER	Y215	Q333	PRO	LYS
N629	F551	K478	ASN	A216	G334	PRO	ARG
F630	A552		THR	A217	M335	ALA	ARG
P631	H553	E483	ASP	L218	F340	LYS	GLU
		S484	GLN	L219		LEU	ASN
T634	Y556	Q485	GLN	A220		ARG	GLU
G637	T557	T486	ASP	K225	R343	GLU	LEU
G638	D558	K487	ALA	E231	K344	ILE	ASN
L639	S559	E488	GLY	L232		THR	TVR
	LEU	L489	SER	I233	I352	GLN	ASP
T640	PRO	C490	GLU	G235	I353	GLN	ARG
D641	W562	M491	GLU		I354	ILE	ASN
E642		M492	GLU	L234	E355	THR	SER
	L565	I493	GLU	K235	G356	ASP	SER
L643			GLU		L357	GLU	PRO
R644	S571	C496	GLU	R247	D358	TYR	TYR
E645	E572	C497	GLU	K250		PRO	GLU
L647	T574	R501	GLU	R156	Q155	GLY	GLN
G648	T575	T502	GLY	M157		ARG	GLU
ASN	T576	Y503	GLY	L252	R158	ASN	ARG
THR	T577	E504	GLU		S158	PRO	SER
PRO	S578	K505	GLU	V260	K164	GLU	PRO
LYS	S579	F506	ASP	A261	S165	THR	ARG
ILE	R580	F507	GLU	L263	I166	SER	ASP
VAL			GLU	L264		VAL	ASP
ALA	K584	L510	GLY		I170	GLN	TYR
GLN	I585	A511	GLN	A269		SER	PHE
ALA	F586	G512	LYS	C274		SER	ASP
PRO	F587	R513	VAL		V173	THR	TYR
ASP	Q588	F514	THR	M277	I175	ALA	SER
VAL	E589	G515	ILE	L278	S176	GLN	ARG
GLU			HIS	T279	M177	GLU	ASP
GLN	L596	E520	LYS	E283	I178	PRO	TYR
ASN	P597	Y521	ASP	R284	S179	ALA	GLU
LYS		E523	LYS		I180	THR	GLU
SER	N600	E524	T448	M287	I181	LYS	HIS
SER	A601	S523	E449	L277		LYS	SER
PRO	R602	S524		T279		ARG	ARG
SER	L603	F525	L462	E283		GLU	ASP
SER		E526			M387	ALA	GLU
SER	E606	G527	F455	R284		THR	GLU
SER	T607	I528	R456	D388		LYS	SER
SER	L608	F529	R457	D287		ARG	ARG
ALA	Q609	K530	L458	D288		LYS	GLY
		E531			E393	ASP	ASP

[illegible]

- Molecule 24: Pre-mRNA-processing factor 17



MET	SER	ALA	ALA	ILE	ALA	ALA	LEU	ALA	ALA	SER	TYR	GLY	GLY	GLY	GLY	GLU	SER	SER	ASP	ASP	ASP	CYS	PRO	LEU	PRO	ALA	ALA	ALA	ASP	SER	SER	LEU	MET	HIS	THR	LEU	LYS	SER	PRO	SER	SER	SER	LYS	PRO	SER	LEU	VAL	VAL	VAL	ASP	SER	ALA	ALA	PRO	GLU	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ALA	VAL	LYS	GLU	ASP	LEU	GLU	THR	GLY	VAL	HIS	LEU	ASP	PRO	ALA	VAL	LYS	GLU	VAL	GLN	TYR	ASN	P93	P84	M88	F99	E92	F93	G94	P95	E96	N97	P98	F99	R100	T101	Q102	Q103	A104	A105	A106	P107	R108	M109	M110	L111	S112	G113	A114	A115	E116	P117	A118	H119	I120	N121	D122
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

M124	F125	E126	Q127	Q128	R129	U130	T131	F132	A133	T134	Y135	G136	Y137	A138	L139	D140	D144	H145	H146	Q147	V148	S149	K150	K151	I152	I153	G154	S155	V156	E157	E158	A159	E160	K161	Q163	L164	L165	T166	V167	F168	E169	T170	G171	Q172	K173	E176	K177	R178	K179	K180	F181	K182	D185	A186	S187
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

[illegible]

GLN
 GLY
 ARG
 ARG
 SER
 TYR
 LEU
 HIS
 ILE
 PRO
 PRO
 GLN
 ASP
 VAL
 GLY
 VAL
 ASN
 LEU
 ARG
 SER
 THR
 MET
 PRO
 PRO
 PRO
 GLU
 LYS
 C274
 Y275
 K278
 K279
 Q280
 I281
 G286
 H287
 T288
 K289
 G290
 Y291
 S292
 F297
 P298
 L299
 S300
 G301
 H302
 M309
 V318
 Y319
 G320
 E321
 R322
 L325
 I329
 G330
 H334

S332	F340	G344	Y352	D353	R354	T361	T371	N372	R373	P376	F381	N382	E385	D386	K387	V392	K399	S407	G408	E409	D415	R416	H417	L418	G419	A420	D438	A457	E458	P459	S460	M461	H462	S463	M464	T468	L469	S470	Q479	S480	M481	D482	M483
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Molecule 25: Pre-mRNA-splicing factor CWC25 homolog



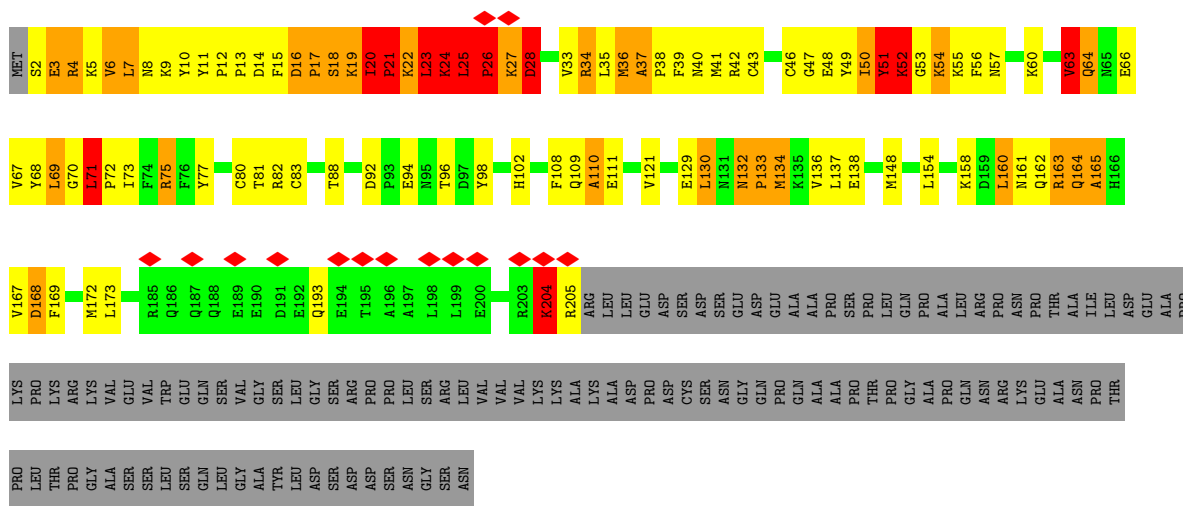
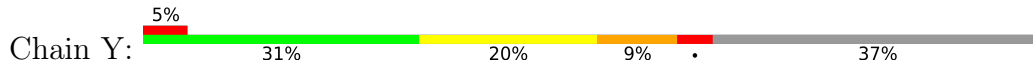
MET
G2
D6
L6
N7
L8
K9
S10
S11
W12
H13
P14
Q15
T16
L17
E21
W24
K25
Q28
X29
H30
A31
A32
E33
R34
K35
K36
I37
E38
E39
L40
Q41
E46
E47
R48
A49
R50
E51
E52
M53
E58
D59
V60
G61
A62
V63
K64
D71
W72
MET
TVR
CLN

PRO	GLY	GLY	MET	VAL	ASN	ARG	ASP	GLU	TYR	LEU	LEU	GLY	ARG	PRO	ILE	LYS	ASP	TYR	VAL	PHE	GLU	GLY	LYS	MET	GLU	GLY	LYS	ALA	GLY	CYS	SER	GLU	THR	GLY	LEU	LEU	PRO	PRO	GLY	GLY	GLY	ASN	ALA	ALA	SER	SER	LYS	ILE	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

[illegible]

- Molecule 26: Coiled-coil domain-containing protein 94

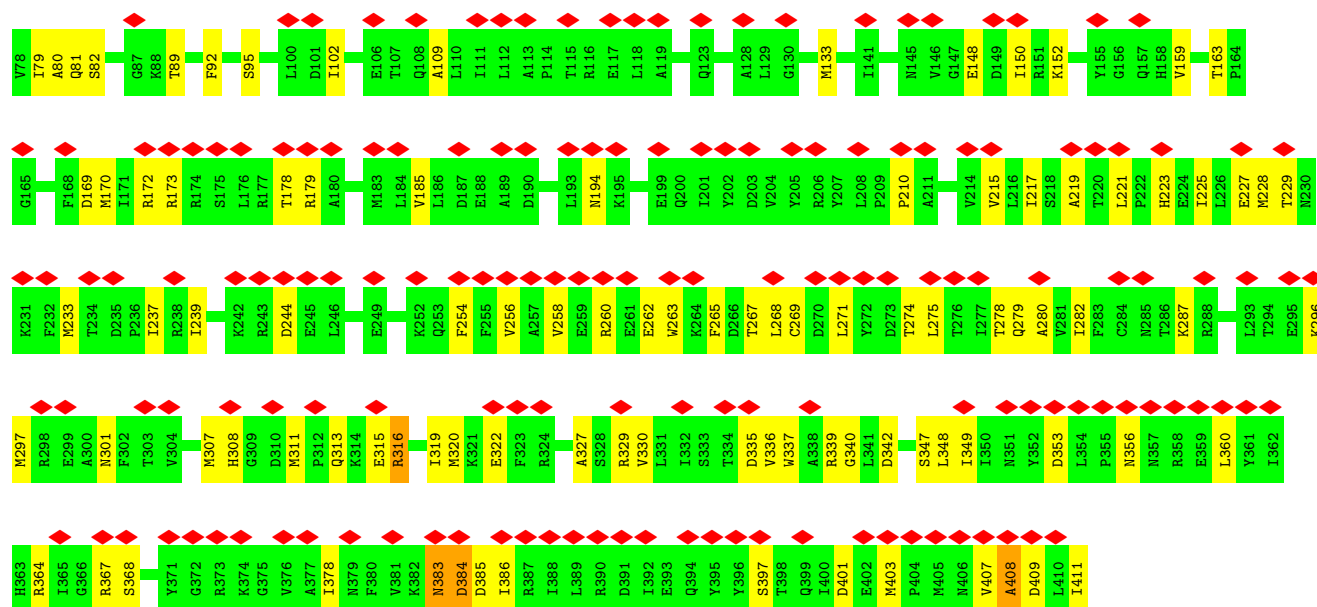


- Molecule 27: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16

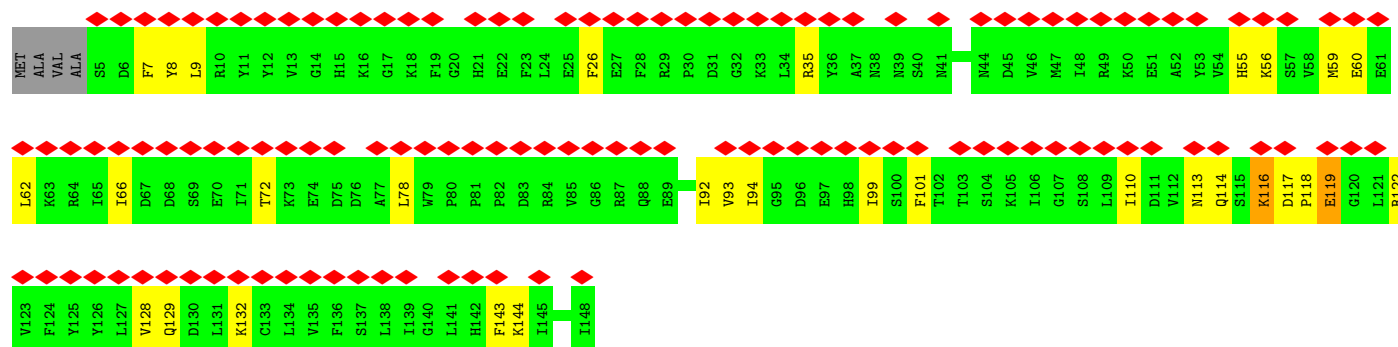
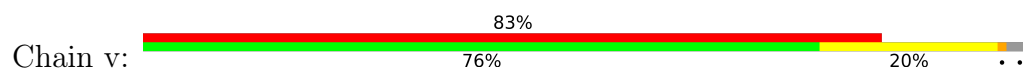


LYS	GLU	ASP	ARG	PRO	GLU	MET
LYS	GLU	ASP	ARG	PRO	GLU	MET
ILE	GLY	SER	GLU	GLY	ARG	GLY
SER	ILE	ARG	ARG	VAL	THR	GLU
ALA	SER	ASP	ASP	SER	LYS	SER
GLN	PHE	HIS	GLY	GLU	ASP	GLU
ARG	ASP	ARG	GLY	GLU	ASP	ASP
THR	THR	LEU	SER	PHE	GLY	ALA
GLN	GLU	SER	GLU	THR	GLU	SER
GLU	GLU	THR	ARG	GLU	ILE	ARG
ASN	GLU	ARG	SER	ARG	LYS	HIS
ASP	ARG	ASP	SER	SER	LYS	ARG
ASN	GLN	ARG	ARG	ARG	LYS	LEU
GLU	TRP	ASP	ASN	GLN	SER	GLU
GLU	GLU	SER	ASN	GLN	LYS	GLY
TRP	ASP	VAL	PRO	ARG	VAL	THR
GLU	ASP	ARG	GLU	GLU	SER	LEU
THR	GLN	GLY	SER	ARG	TYR	GLY
ASN	ARG	LYS	PRO	ARG	LYS	ILE
ASN	GLN	LYS	ARG	ARG	CYS	CYS
GLU	GLN	THR	ARG	GLU	ASP	LYS
MET	ALA	SER	HIS	HIS	TRP	VAL
LEU	ALA	ASP	GLY	GLY	GLU	GLY
THR	ARG	PRO	ARG	VAL	GLU	GLY
SER	ASP	THR	LYS	TYR	SER	LEU
GLY	TRP	PRO	ASP	ALA	LYS	ILE
VAL	VAL	LEU	ALA	SER	ASP	CYS
VAL	MET	PRO	ALA	SER	ASP	LYS
HIS	MET	THR	THR	LYS	GLN	SER
ARG	ASP	PRO	PRO	GLU	LYS	LYS
LEU	GLU	SER	SER	GLU	ASP	SER
GLU	GLY	TYR	ARG	LYS	ALA	ALA
VAL	ASP	LYS	ARG	THR	GLU	ALA
ASP	ASP	THR	THR	ASP	GLU	SER
ASP	GLU	ASN	TRP	LYS	GLU	GLU
PHE	PHE	GLY	GLU	LYS	GLY	GLN
GLU	ASN	TRP	GLU	GLU	ASP	HIS
GLU	GLU	ALA	GLU	LYS	VAL	VAL
ASP	LEU	ASP	SER	ARG	ALA	LYS
ASN	LEU	ARG	GLY	ASP	GLY	LYS
ALA	TYR	ARG	TYR	ARG	GLN	PRO
ALA	SER	HIS	GLY	ASP	ASN	ALA
LYS	LYS	LEU	SER	TYR	ILE	PRO
VAL	GLU	GLY	ARG	ASP	ARG	ARG
HIS	HIS	SER	SER	ARG	LYS	PRO
LEU	TYR	THR	ARG	LYS	ASP	SER
MET	VAL	PRO	SER	ARG	ARG	LEU
VAL	ARG	ARG	GLN	ARG	HIS	LEU
ASN	ARG	SER	TRP	ARG	TYR	GLY
LEU	ARG	SER	GLU	ASP	ARG	LEU
LEU	GLU	ARG	SER	GLU	SER	ASP
VAL	GLN	GLY	PRO	ARG	ALA	LEU
PRO	HIS	ARG	SER	ASP	ARG	LEU
PHE	LEU	GLY	PRO	ASP	VAL	ALA
ASP	HIS	ARG	THR	SER	GLU	SER
LEU	LYS	ARG	PRO	ARG	THR	LEU
ASP	GLN	GLU	SER	HIS	THR	LYS
GLY	LYS	GLU	TYR	SER	SER	ARG
ARG	GLN	GLY	ARG	SER	HIS	ARG

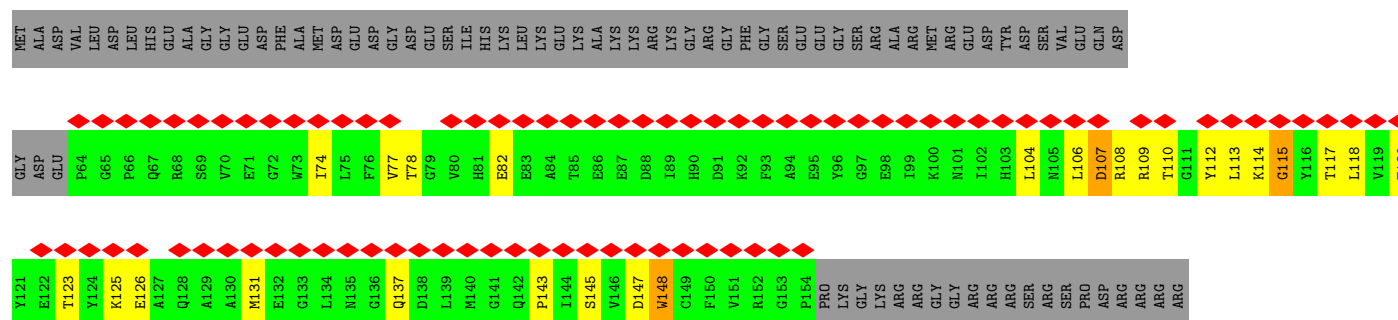
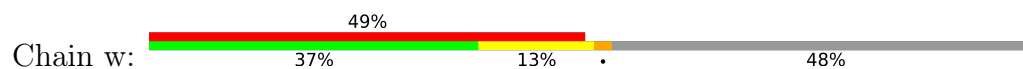




• Molecule 30: Protein mago nashi homolog 2

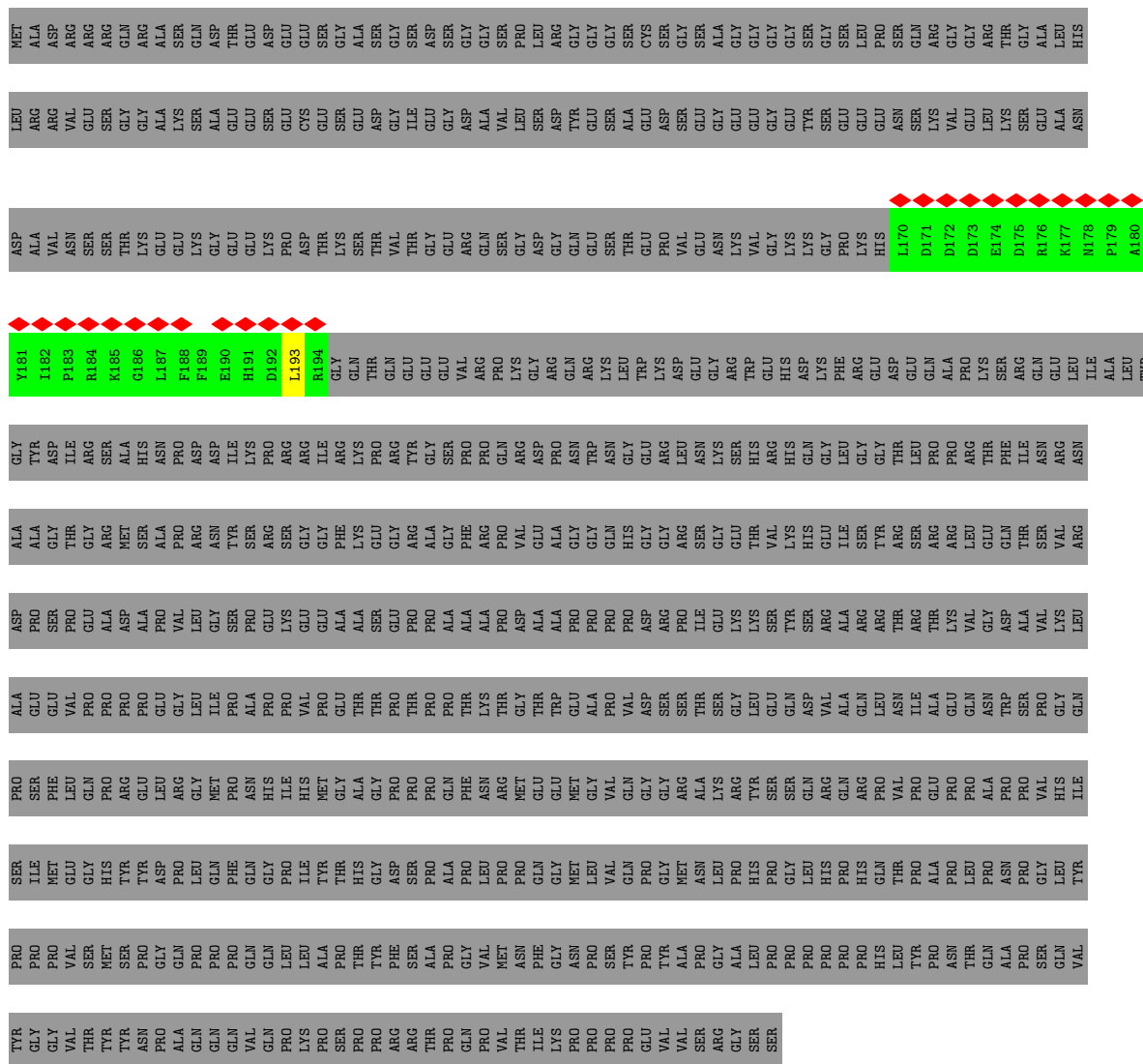


• Molecule 31: RNA-binding protein 8A

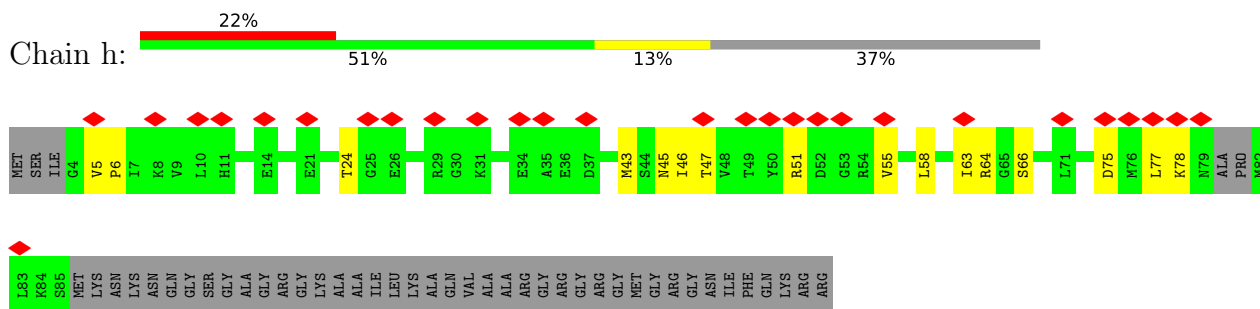


• Molecule 32: Protein CASC3

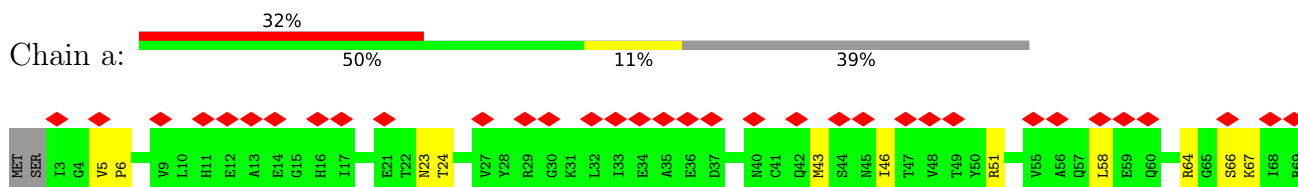


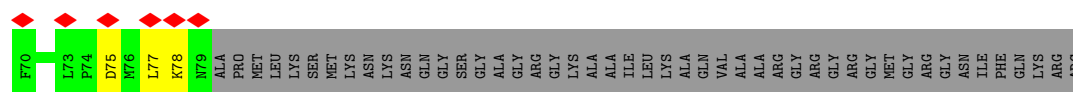


- Molecule 33: Small nuclear ribonucleoprotein Sm D3

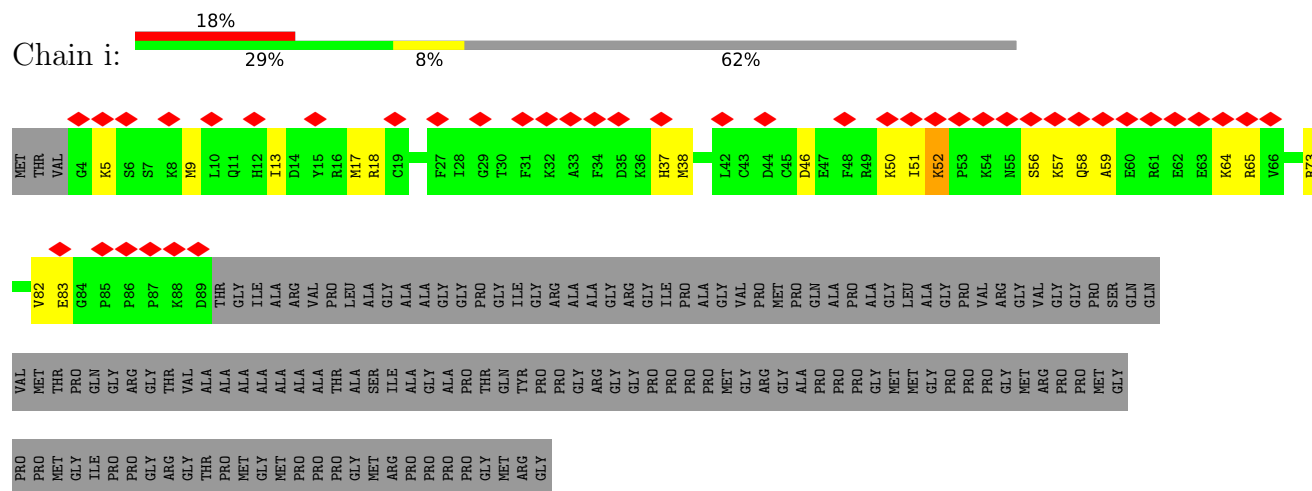


- Molecule 33: Small nuclear ribonucleoprotein Sm D3

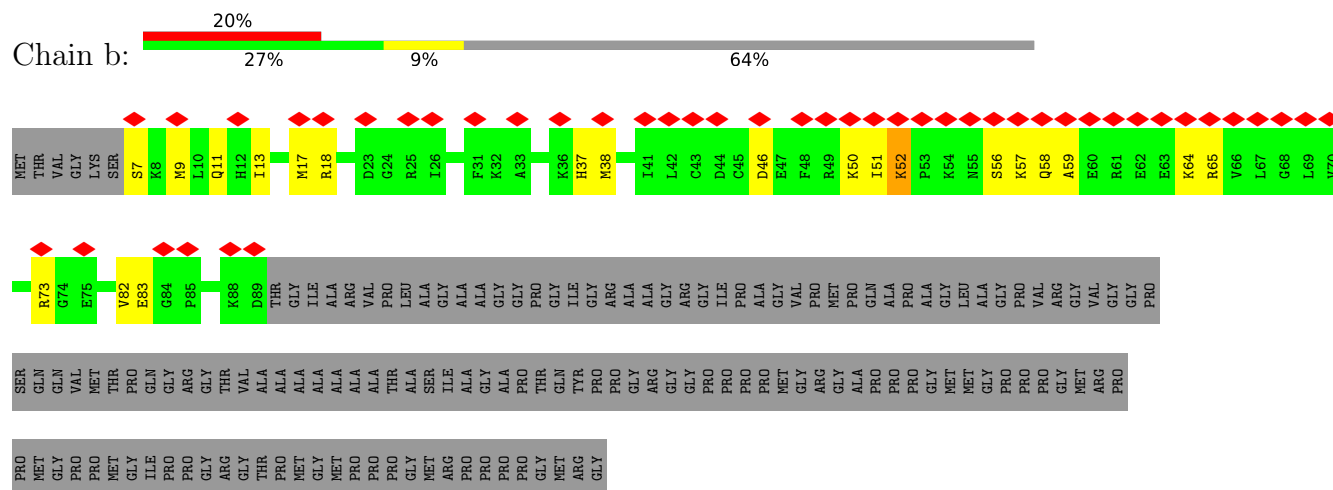




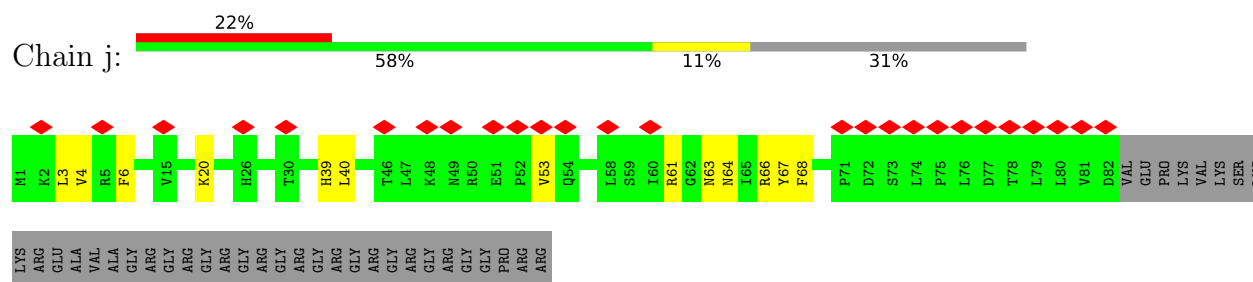
- Molecule 34: Small nuclear ribonucleoprotein-associated proteins B and B'



- Molecule 34: Small nuclear ribonucleoprotein-associated proteins B and B'

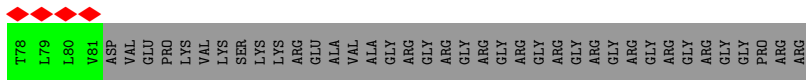


- Molecule 35: Small nuclear ribonucleoprotein Sm D1

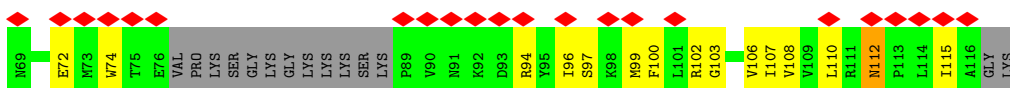
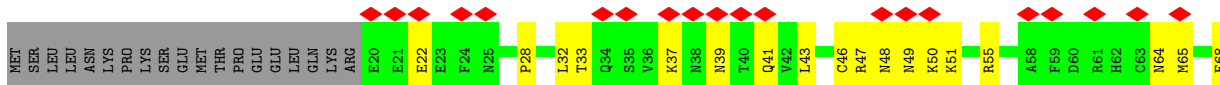


- Molecule 35: Small nuclear ribonucleoprotein Sm D1

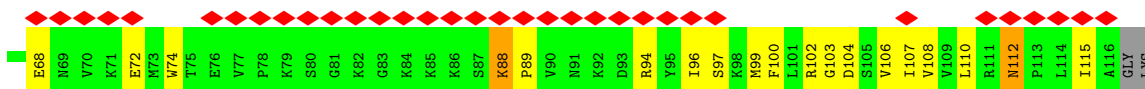
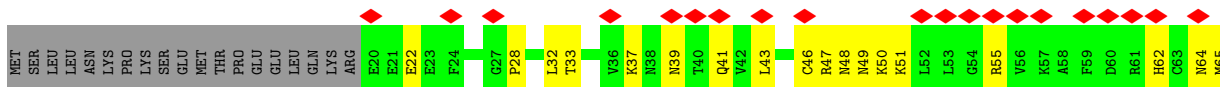




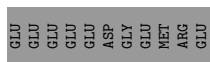
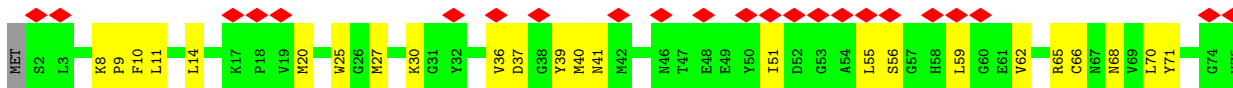
- Molecule 36: Small nuclear ribonucleoprotein Sm D2



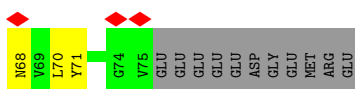
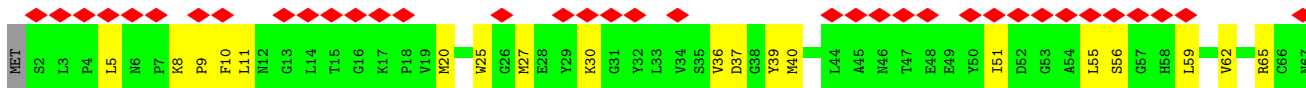
- Molecule 36: Small nuclear ribonucleoprotein Sm D2



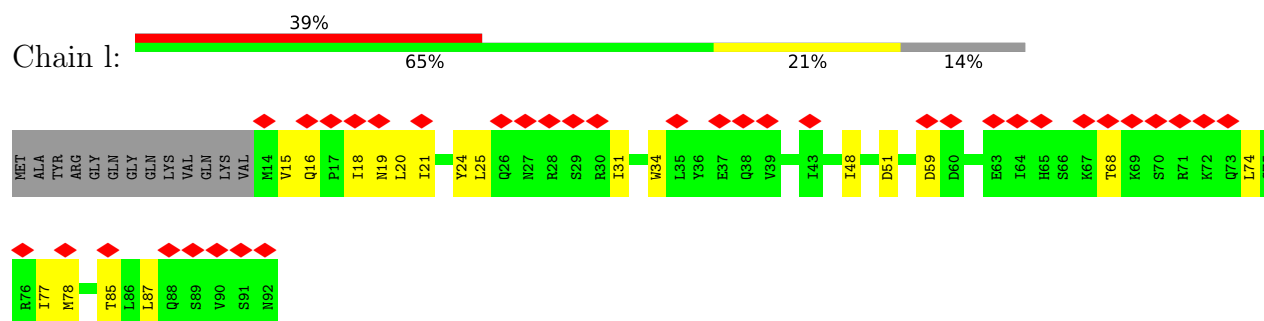
- Molecule 37: Small nuclear ribonucleoprotein F



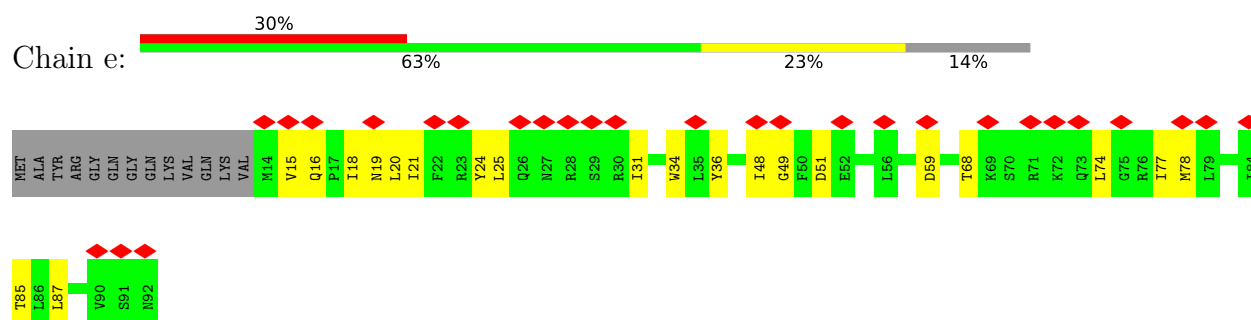
- Molecule 37: Small nuclear ribonucleoprotein F



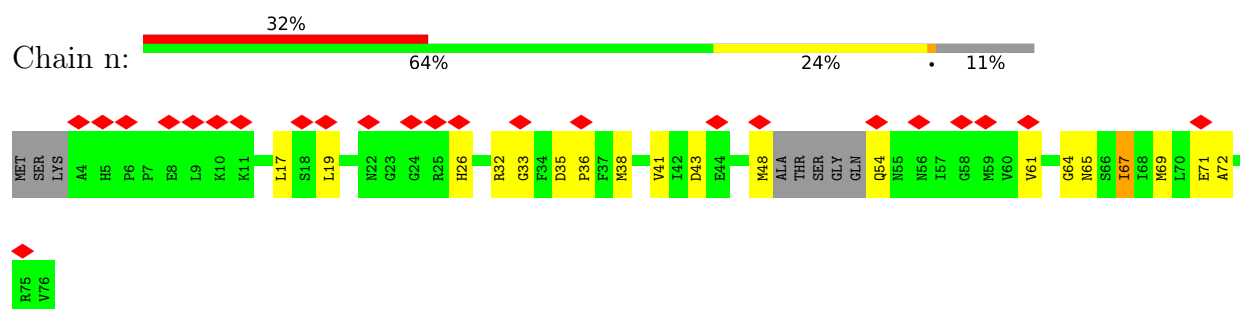
- Molecule 38: Small nuclear ribonucleoprotein E



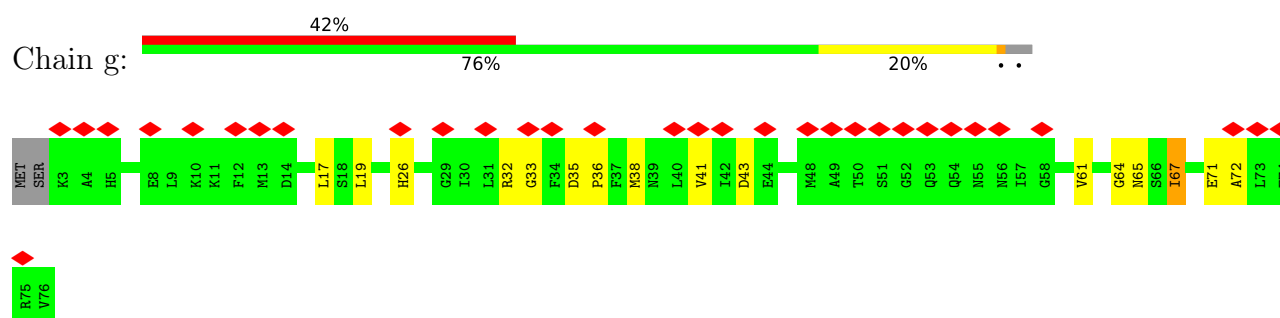
- Molecule 38: Small nuclear ribonucleoprotein E



- Molecule 39: Small nuclear ribonucleoprotein G



- Molecule 39: Small nuclear ribonucleoprotein G

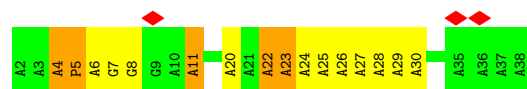


- Molecule 40: U2 small nuclear ribonucleoprotein A'



[illegible]

- Molecule 45: UNKNOWN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	53633	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.209	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.029	Depositor
Map size ($\text{\AA}$)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.338, 1.338, 1.338	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, ZN, ATP, GTP, MG, IHP, SEP

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	1.29	90/17966 (0.5%)	1.34	108/24251 (0.4%)
2	B	0.69	1/1970 (0.1%)	0.96	6/3060 (0.2%)
3	C	1.09	11/6946 (0.2%)	1.28	41/9436 (0.4%)
4	D	0.55	0/7628	1.17	29/9528 (0.3%)
5	E	0.87	0/2392	1.00	6/3242 (0.2%)
6	F	0.58	0/2323	0.99	12/3619 (0.3%)
7	G	0.70	7/1820 (0.4%)	0.93	5/2819 (0.2%)
8	H	0.86	25/3283 (0.8%)	1.43	64/5096 (1.3%)
9	I	0.53	0/2724	0.91	18/3738 (0.5%)
10	J	0.81	2/3870 (0.1%)	1.14	6/5252 (0.1%)
11	K	1.08	12/981 (1.2%)	1.02	6/1317 (0.5%)
12	L	0.86	5/2914 (0.2%)	1.18	17/3929 (0.4%)
13	y	0.76	4/707 (0.6%)	1.12	5/953 (0.5%)
14	M	0.71	0/791	1.10	1/1058 (0.1%)
15	N	1.15	1/1210 (0.1%)	1.16	4/1622 (0.2%)
16	O	1.04	3/2324 (0.1%)	1.05	3/3135 (0.1%)
17	P	1.01	1/841 (0.1%)	1.29	3/1117 (0.3%)
18	R	1.03	8/1976 (0.4%)	1.34	11/2651 (0.4%)
19	S	0.81	0/1268	1.13	8/1714 (0.5%)
20	T	1.44	13/2526 (0.5%)	1.42	26/3443 (0.8%)
21	Q	0.38	0/5279	0.92	1/6583 (0.0%)
22	U	1.44	3/196 (1.5%)	1.53	4/265 (1.5%)
23	V	0.76	1/3453 (0.0%)	1.03	3/4640 (0.1%)
24	W	0.85	3/2336 (0.1%)	1.24	19/3027 (0.6%)
25	X	0.63	0/486	1.02	3/658 (0.5%)
26	Y	0.74	7/1450 (0.5%)	1.39	26/1975 (1.3%)
27	Z	0.87	2/2528 (0.1%)	1.75	38/3139 (1.2%)
28	q	0.98	9/929 (1.0%)	1.00	6/1260 (0.5%)
28	r	0.97	9/912 (1.0%)	1.02	6/1239 (0.5%)
28	s	3.23	4/1497 (0.3%)	1.30	4/1866 (0.2%)
28	t	0.91	6/480 (1.2%)	0.85	0/650
29	u	0.45	0/3175	1.00	14/4286 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	v	0.40	0/1225	0.84	3/1648 (0.2%)
31	w	0.40	0/748	0.98	4/1012 (0.4%)
32	x	0.46	0/221	0.92	0/296
33	a	0.63	0/616	0.85	0/830
33	h	0.65	0/627	0.86	0/842
34	b	0.71	0/685	1.01	3/913 (0.3%)
34	i	0.73	0/700	1.03	4/933 (0.4%)
35	c	0.74	0/649	0.98	0/877
35	j	0.74	0/657	0.98	0/888
36	d	0.94	0/778	1.10	2/1045 (0.2%)
36	k	0.95	0/696	1.07	1/935 (0.1%)
37	f	1.03	0/588	1.08	0/795
37	m	1.04	1/588 (0.2%)	1.08	0/795
38	e	0.85	0/660	1.06	1/886 (0.1%)
38	l	0.85	0/660	1.06	1/886 (0.1%)
39	g	0.71	0/576	0.95	1/771 (0.1%)
39	n	0.70	0/539	0.95	1/718 (0.1%)
40	o	0.81	0/1294	2.06	56/1754 (3.2%)
41	p	0.77	0/774	1.71	13/1035 (1.3%)
42	1	0.55	0/970	0.96	0/1209
43	2	0.85	0/1649	0.99	0/2035
44	3	0.97	1/682 (0.1%)	1.08	3/849 (0.4%)
45	4	0.65	0/184	1.38	3/255 (1.2%)
All	All	0.99	229/105947 (0.2%)	1.20	599/142775 (0.4%)

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	6
3	C	0	3
4	D	0	1
10	J	0	1
12	L	0	1
13	y	0	1
14	M	0	1
15	N	0	1
18	R	0	1
20	T	0	2
26	Y	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
27	Z	0	29
28	s	0	4
36	d	0	1
36	k	0	1
All	All	0	56

The worst 5 of 229 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	s	481[A]	VAL	N-CA	82.34	2.43	1.46
28	s	481[B]	VAL	N-CA	82.34	2.43	1.46
1	A	642	ARG	CD-NE	14.92	1.67	1.46
28	q	47	LEU	CB-CG	14.02	1.81	1.53
28	r	47	LEU	CB-CG	13.93	1.81	1.53

The worst 5 of 599 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	s	481[A]	VAL	N-CA-C	-26.68	68.71	108.46
28	s	481[B]	VAL	N-CA-C	-26.68	68.71	108.46
40	o	55	ARG	CD-NE-CZ	13.22	142.90	124.40
20	T	187	LYS	CA-C-N	13.12	132.88	119.76
20	T	187	LYS	C-N-CA	13.12	132.88	119.76

There are no chirality outliers.

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	642	ARG	Sidechain

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	17519	0	16642	1178	0
2	B	1768	0	897	66	0
3	C	6795	0	6807	612	0
4	D	7632	0	1994	27	0
5	E	2338	0	2272	160	0
6	F	2075	0	1048	199	0
7	G	1641	0	835	255	0
8	H	2946	0	1494	261	0
9	I	2757	0	1234	24	0
10	J	3829	0	2907	133	0
11	K	979	0	741	23	0
12	L	2885	0	2427	278	0
13	y	704	0	525	46	0
14	M	775	0	767	102	0
15	N	1184	0	1190	72	0
16	O	2277	0	2260	176	0
17	P	829	0	814	74	0
18	R	1962	0	2011	286	0
19	S	1236	0	1210	183	0
20	T	2461	0	2420	156	0
21	Q	5288	0	1361	0	0
22	U	193	0	196	24	0
23	V	3410	0	3287	205	0
24	W	2310	0	1360	332	0
25	X	480	0	401	122	0
26	Y	1426	0	1210	274	0
27	Z	2540	0	677	12	0
28	q	918	0	801	16	0
28	r	901	0	777	14	0
28	s	1497	0	406	2	0
28	t	476	0	434	7	0
29	u	3126	0	3167	98	0
30	v	1196	0	1182	35	0
31	w	730	0	690	29	0
32	x	216	0	202	1	0
33	a	609	0	620	9	0
33	h	621	0	623	16	0
34	b	675	0	702	32	0
34	i	690	0	712	15	0
35	c	641	0	689	15	0
35	j	649	0	693	13	0
36	d	768	0	797	31	0
36	k	688	0	709	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	f	576	0	589	22	0
37	m	576	0	589	21	0
38	e	652	0	668	21	0
38	l	652	0	668	20	0
39	g	569	0	581	13	0
39	n	533	0	555	19	0
40	o	1277	0	1297	30	0
41	p	760	0	783	11	0
42	1	972	0	284	1	0
43	2	1664	0	449	11	0
44	3	684	0	198	0	0
45	4	184	0	180	34	0
46	A	36	0	6	10	0
47	C	32	0	12	7	0
48	C	1	0	0	0	0
48	F	5	0	0	0	0
48	u	1	0	0	0	0
49	D	54	0	24	1	0
50	N	3	0	0	2	0
50	O	3	0	0	0	0
50	Y	1	0	0	2	0
51	u	31	0	12	1	0
All	All	103906	0	79086	4873	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 27.

The worst 5 of 4873 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)
19:S:57:ILE:HD13	24:W:97:ASN:CB	1.21	1.66
12:L:191:LEU:HD21	13:y:57:VAL:CB	1.24	1.64
1:A:1772:PHE:CD2	1:A:1813:ARG:HG2	1.21	1.63
28:r:47:LEU:CB	28:r:47:LEU:CG	1.81	1.59
1:A:853:LYS:HE2	7:G:148:U:C5	1.36	1.57

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	2247/2335 (96%)	2100 (94%)	107 (5%)	40 (2%)	6	35
3	C	856/972 (88%)	779 (91%)	57 (7%)	20 (2%)	5	31
4	D	1900/2136 (89%)	1799 (95%)	96 (5%)	5 (0%)	36	70
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	25
9	I	493/855 (58%)	475 (96%)	10 (2%)	8 (2%)	7	37
10	J	530/848 (62%)	483 (91%)	30 (6%)	17 (3%)	3	24
11	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	4	27
12	L	401/802 (50%)	375 (94%)	19 (5%)	7 (2%)	7	36
13	y	106/307 (34%)	98 (92%)	8 (8%)	0	100	100
14	M	89/243 (37%)	80 (90%)	3 (3%)	6 (7%)	1	14
15	N	141/144 (98%)	126 (89%)	12 (8%)	3 (2%)	5	32
16	O	279/420 (66%)	247 (88%)	26 (9%)	6 (2%)	5	31
17	P	92/229 (40%)	82 (89%)	9 (10%)	1 (1%)	11	44
18	R	235/536 (44%)	207 (88%)	14 (6%)	14 (6%)	1	15
19	S	157/166 (95%)	144 (92%)	10 (6%)	3 (2%)	6	34
20	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	21
21	Q	1304/1485 (88%)	1279 (98%)	25 (2%)	0	100	100
22	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	2	20
23	V	444/908 (49%)	413 (93%)	26 (6%)	5 (1%)	11	44
24	W	436/579 (75%)	385 (88%)	32 (7%)	19 (4%)	2	20
25	X	69/425 (16%)	65 (94%)	2 (3%)	2 (3%)	3	26
26	Y	202/323 (62%)	182 (90%)	6 (3%)	14 (7%)	1	13
27	Z	611/1227 (50%)	517 (85%)	61 (10%)	33 (5%)	1	17
28	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	25
28	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	7	37

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	s	369/504 (73%)	352 (95%)	16 (4%)	1 (0%)	36	70
28	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	39
29	u	388/411 (94%)	376 (97%)	9 (2%)	3 (1%)	16	52
30	v	142/148 (96%)	138 (97%)	4 (3%)	0	100	100
31	w	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	11	44
32	x	23/703 (3%)	22 (96%)	1 (4%)	0	100	100
33	a	75/126 (60%)	74 (99%)	1 (1%)	0	100	100
33	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
34	b	81/229 (35%)	79 (98%)	2 (2%)	0	100	100
34	i	84/229 (37%)	82 (98%)	2 (2%)	0	100	100
35	c	79/119 (66%)	76 (96%)	3 (4%)	0	100	100
35	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
36	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
36	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
37	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
37	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
38	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
38	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
39	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
39	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
40	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	41
41	p	92/225 (41%)	90 (98%)	2 (2%)	0	100	100
42	1	239/301 (79%)	232 (97%)	7 (3%)	0	100	100
43	2	386/646 (60%)	358 (93%)	20 (5%)	8 (2%)	5	32
44	3	167/754 (22%)	165 (99%)	2 (1%)	0	100	100
45	4	35/37 (95%)	29 (83%)	2 (6%)	4 (11%)	0	5
All	All	14867/26150 (57%)	13893 (93%)	719 (5%)	255 (2%)	9	36

5 of 255 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP

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	1778/2108 (84%)	1628 (92%)	150 (8%)	10	32
3	C	760/866 (88%)	694 (91%)	66 (9%)	9	31
5	E	256/300 (85%)	243 (95%)	13 (5%)	21	45
10	J	241/751 (32%)	216 (90%)	25 (10%)	7	24
11	K	54/196 (28%)	46 (85%)	8 (15%)	3	15
12	L	193/709 (27%)	155 (80%)	38 (20%)	1	9
13	y	33/256 (13%)	30 (91%)	3 (9%)	9	29
14	M	85/209 (41%)	61 (72%)	24 (28%)	0	3
15	N	130/130 (100%)	124 (95%)	6 (5%)	24	47
16	O	253/361 (70%)	248 (98%)	5 (2%)	48	66
17	P	90/203 (44%)	80 (89%)	10 (11%)	6	22
18	R	210/457 (46%)	153 (73%)	57 (27%)	0	3
19	S	129/134 (96%)	120 (93%)	9 (7%)	14	38
20	T	269/441 (61%)	252 (94%)	17 (6%)	16	40
22	U	21/2432 (1%)	16 (76%)	5 (24%)	1	5
23	V	324/838 (39%)	305 (94%)	19 (6%)	18	42
24	W	115/502 (23%)	73 (64%)	42 (36%)	0	1
25	X	33/381 (9%)	20 (61%)	13 (39%)	0	1
26	Y	114/289 (39%)	85 (75%)	29 (25%)	0	4
28	q	78/435 (18%)	71 (91%)	7 (9%)	9	30
28	r	76/435 (18%)	65 (86%)	11 (14%)	3	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	t	40/435 (9%)	37 (92%)	3 (8%)	12	35
29	u	344/361 (95%)	337 (98%)	7 (2%)	48	66
30	v	132/134 (98%)	131 (99%)	1 (1%)	73	77
31	w	76/143 (53%)	75 (99%)	1 (1%)	61	72
32	x	23/581 (4%)	23 (100%)	0	100	100
33	a	68/101 (67%)	68 (100%)	0	100	100
33	h	68/101 (67%)	68 (100%)	0	100	100
34	b	76/167 (46%)	73 (96%)	3 (4%)	28	51
34	i	77/167 (46%)	74 (96%)	3 (4%)	28	51
35	c	76/101 (75%)	74 (97%)	2 (3%)	40	61
35	j	77/101 (76%)	75 (97%)	2 (3%)	40	61
36	d	88/110 (80%)	87 (99%)	1 (1%)	65	74
36	k	80/110 (73%)	79 (99%)	1 (1%)	61	72
37	f	63/74 (85%)	61 (97%)	2 (3%)	34	56
37	m	63/74 (85%)	61 (97%)	2 (3%)	34	56
38	e	74/84 (88%)	74 (100%)	0	100	100
38	l	74/84 (88%)	74 (100%)	0	100	100
39	g	62/66 (94%)	61 (98%)	1 (2%)	55	69
39	n	59/66 (89%)	58 (98%)	1 (2%)	53	68
40	o	138/218 (63%)	132 (96%)	6 (4%)	26	49
41	p	82/195 (42%)	79 (96%)	3 (4%)	30	52
45	4	1/1 (100%)	1 (100%)	0	100	100
All	All	7083/15907 (44%)	6487 (92%)	596 (8%)	12	32

5 of 596 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	W	126	GLU
35	j	40	LEU
24	W	160	GLU
24	W	108	ARG
26	Y	24	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
38	l	65	HIS
33	a	60	GLN
11	K	171	GLN
10	J	221	ASN
34	b	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	82/117 (70%)	17 (20%)	6 (7%)
6	F	96/107 (89%)	45 (46%)	17 (17%)
7	G	85/275 (30%)	50 (58%)	8 (9%)
8	H	132/188 (70%)	26 (19%)	4 (3%)
All	All	395/687 (57%)	138 (34%)	35 (8%)

5 of 138 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	G	23	U
7	G	146	C
8	H	156	U
6	F	35	A
6	F	34	G

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
18	SEP	R	224	18	8,9,10	0.84	0	7,12,14	1.19	0
18	SEP	R	232	18	8,9,10	0.75	0	7,12,14	1.46	1 (14%)

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
18	SEP	R	224	18	-	3/6/8/10	-
18	SEP	R	232	18	-	3/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	R	232	SEP	OG-CB-CA	-2.55	105.67	108.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	R	224	SEP	CB-OG-P-O1P
18	R	224	SEP	CB-OG-P-O2P
18	R	224	SEP	CB-OG-P-O3P
18	R	232	SEP	N-CA-CB-OG
18	R	232	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	R	232	SEP	3	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 19 ligands modelled in this entry, 14 are monoatomic - leaving 5 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
49	ADP	D	2202	-	28,29,29	1.36	4 (14%)	43,45,45	1.86	9 (20%)
51	ATP	u	702	48	32,33,33	1.22	3 (9%)	48,52,52	1.84	8 (16%)
46	IHP	A	3000	-	36,36,36	1.03	2 (5%)	60,60,60	1.74	15 (25%)
49	ADP	D	2201	-	28,29,29	1.44	5 (17%)	43,45,45	1.79	7 (16%)
47	GTP	C	1500	48	33,34,34	1.45	5 (15%)	50,54,54	2.05	10 (20%)

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
49	ADP	D	2202	-	-	2/16/32/32	0/3/3/3
51	ATP	u	702	48	-	0/22/38/38	0/3/3/3
46	IHP	A	3000	-	-	6/30/54/54	0/1/1/1
49	ADP	D	2201	-	-	8/16/32/32	0/3/3/3
47	GTP	C	1500	48	-	8/22/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	D	2201	ADP	C5-C4	4.77	1.47	1.39
49	D	2202	ADP	C5-C4	4.46	1.47	1.39
47	C	1500	GTP	C5-N7	-3.75	1.31	1.39
47	C	1500	GTP	C6-N1	-3.29	1.32	1.38
51	u	702	ATP	C4-N9	-3.19	1.31	1.37

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	C	1500	GTP	C5-C4-N3	-7.08	117.12	128.39
51	u	702	ATP	C5-C4-N3	-6.36	117.96	126.72
49	D	2202	ADP	C5-C4-N3	-6.35	117.97	126.72
47	C	1500	GTP	C2-N3-C4	5.99	122.62	112.30
49	D	2201	ADP	C5-C4-N3	-5.86	118.65	126.72

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

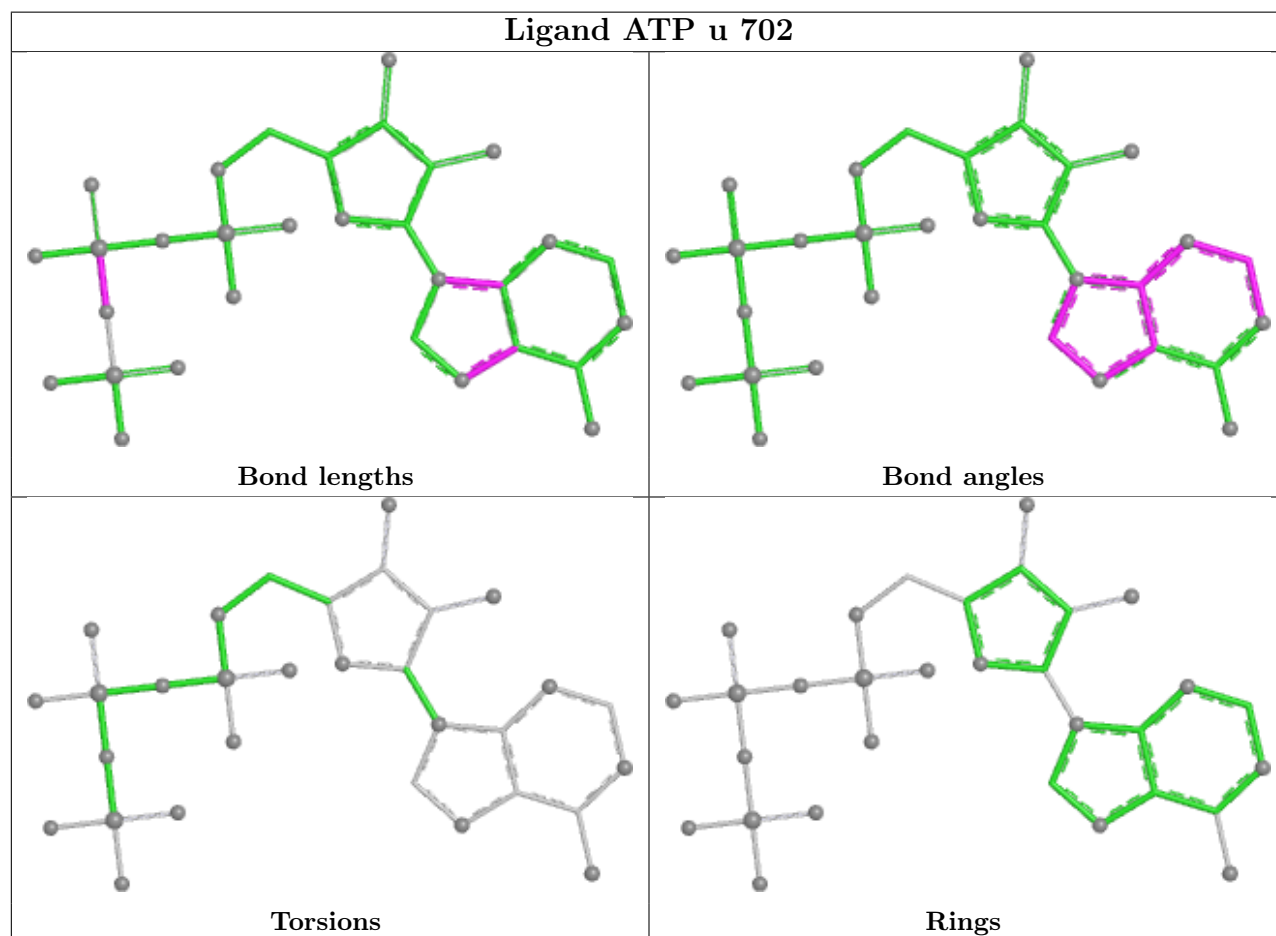
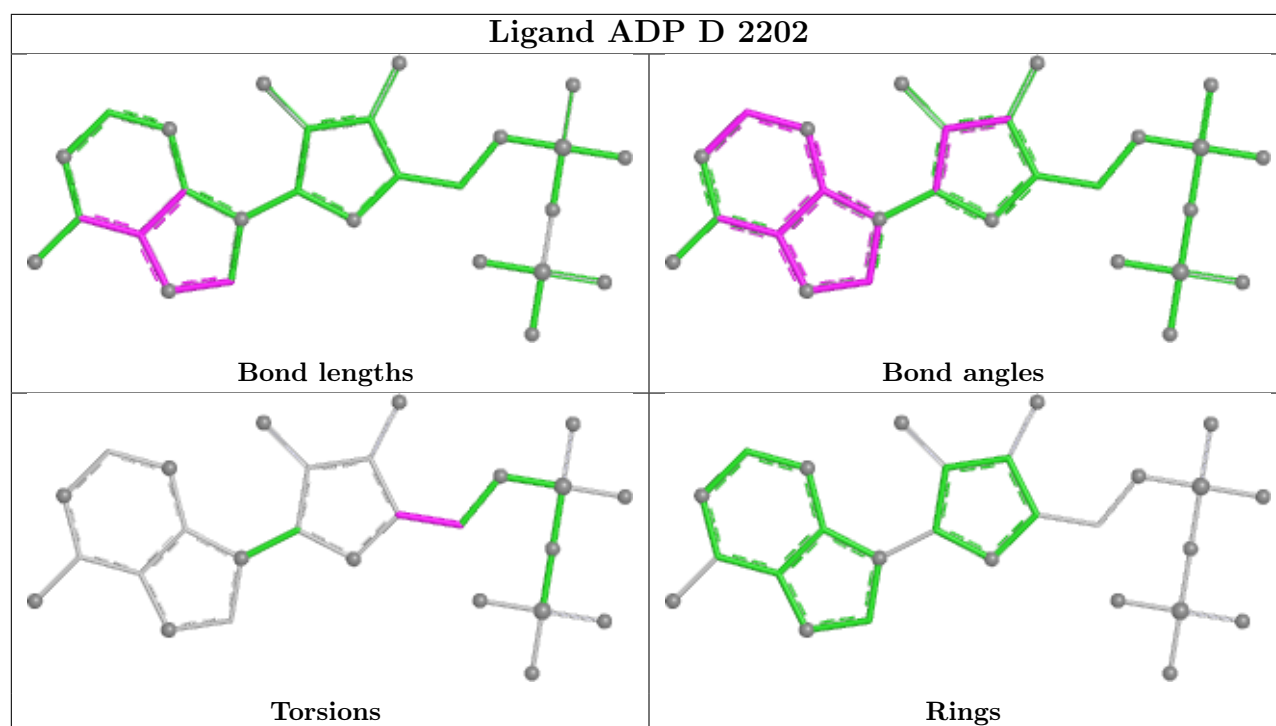
Mol	Chain	Res	Type	Atoms
46	A	3000	IHP	C4-C5-O15-P5
46	A	3000	IHP	C6-C5-O15-P5
47	C	1500	GTP	PB-O3B-PG-O3G
47	C	1500	GTP	C5'-O5'-PA-O1A
47	C	1500	GTP	C5'-O5'-PA-O2A

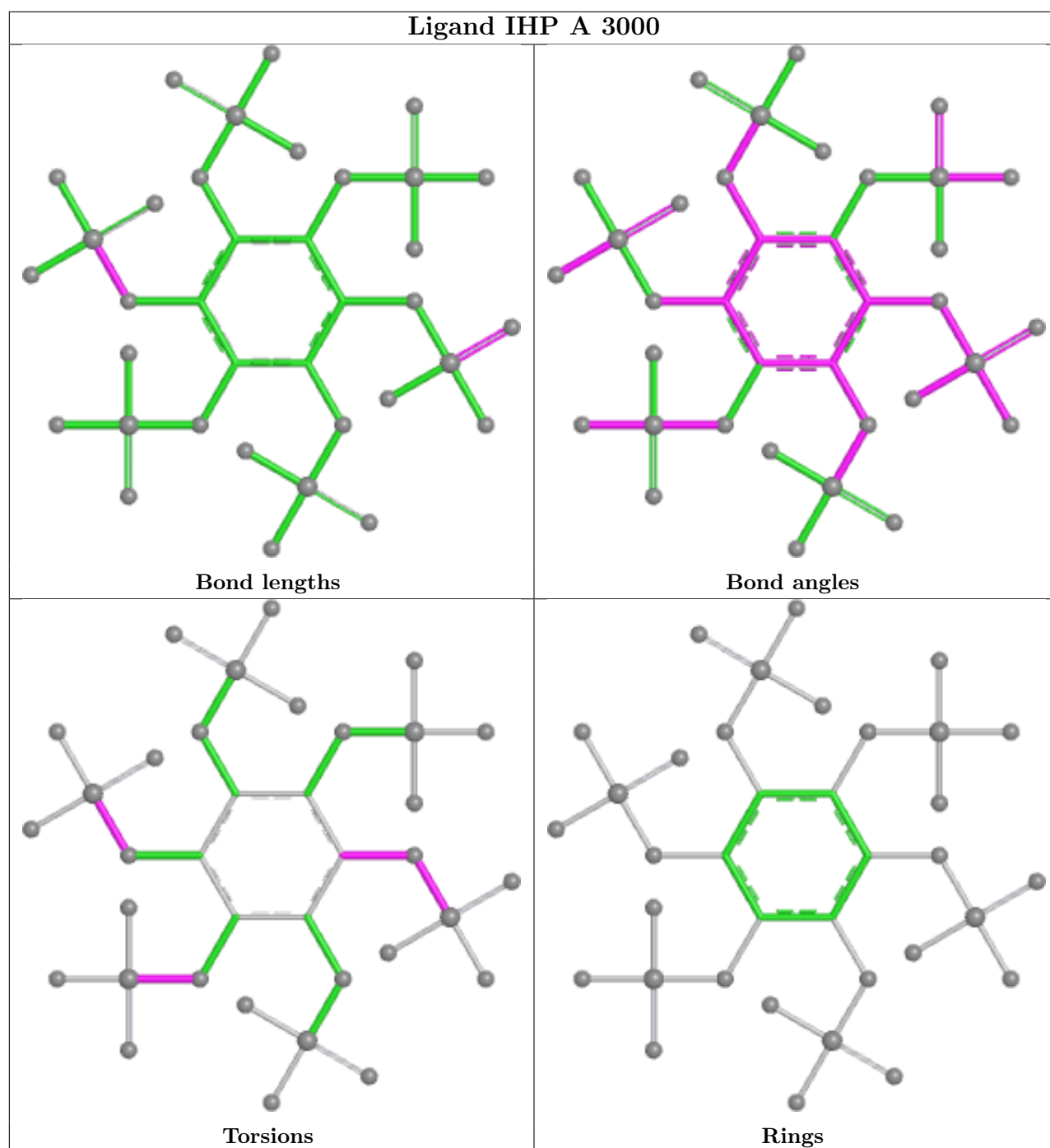
There are no ring outliers.

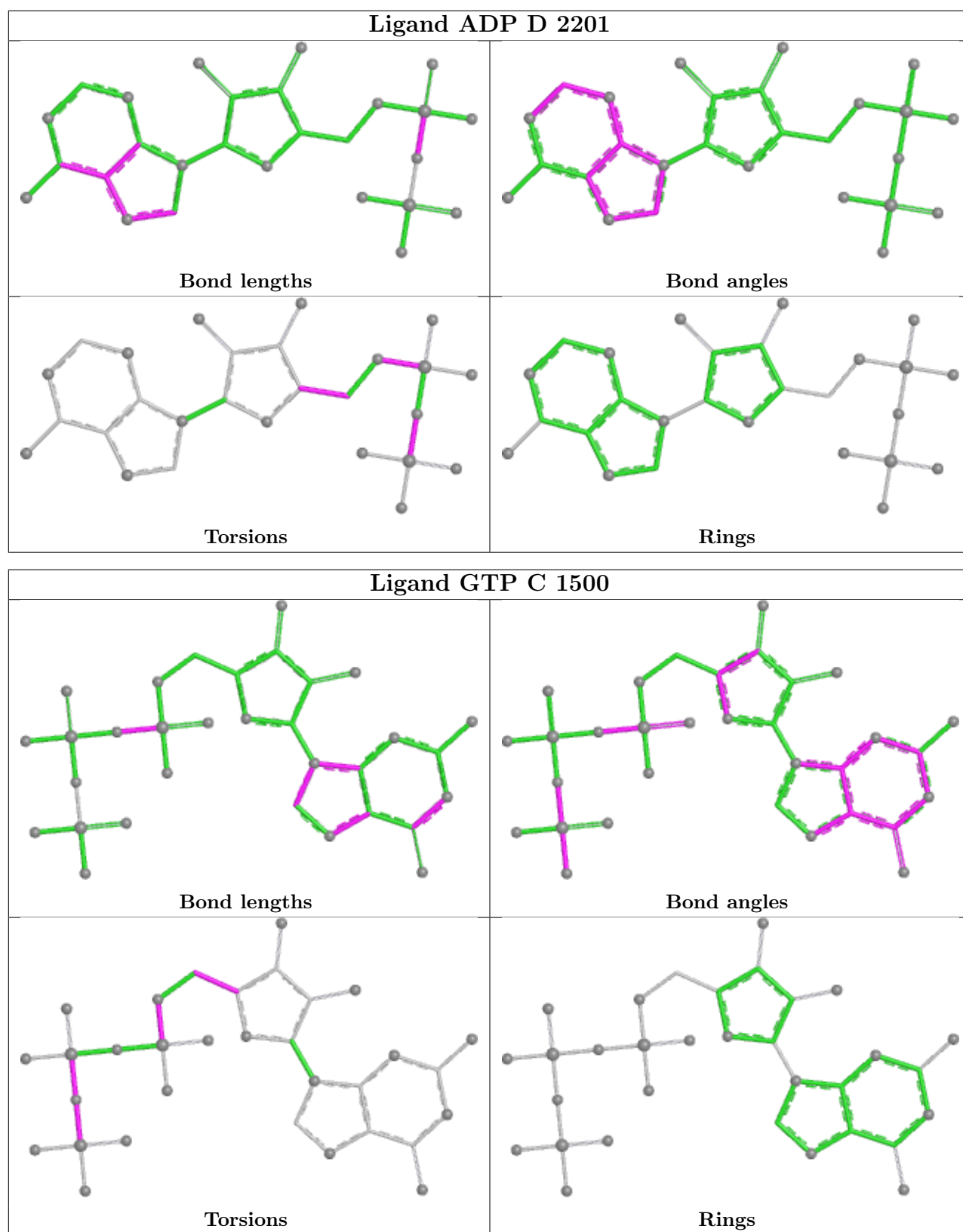
4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
51	u	702	ATP	1	0
46	A	3000	IHP	10	0
49	D	2201	ADP	1	0
47	C	1500	GTP	7	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

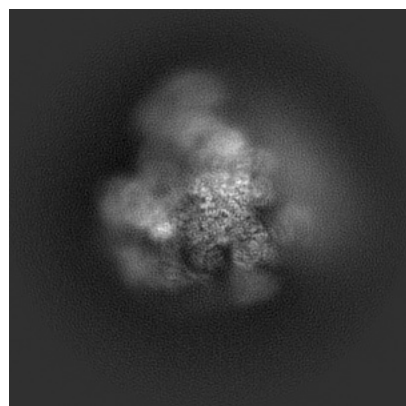
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6864. These allow visual inspection of the internal detail of the map and identification of artifacts.

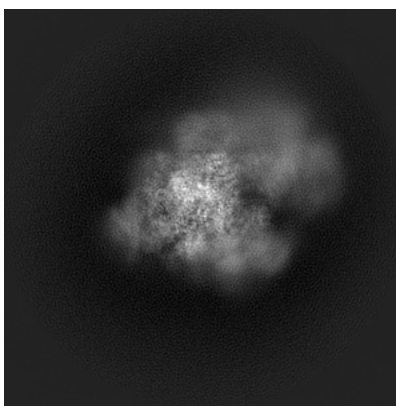
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

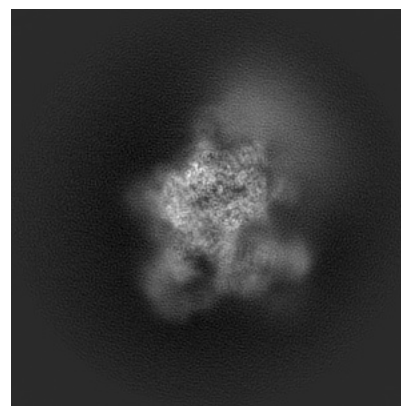
6.1.1 Primary map



X

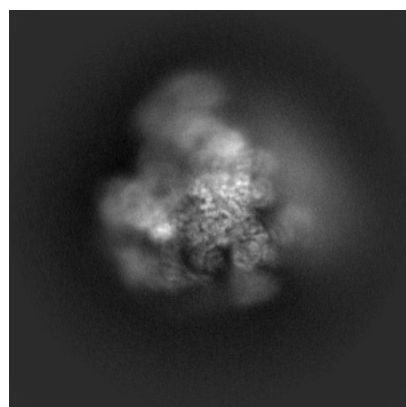


Y

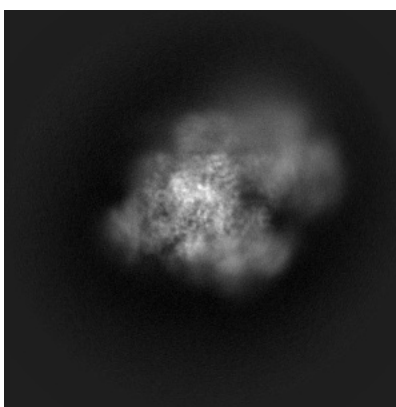


Z

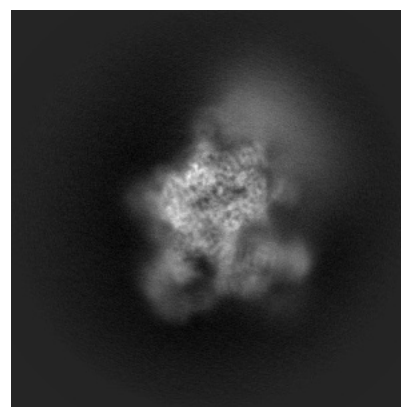
6.1.2 Raw map



X



Y

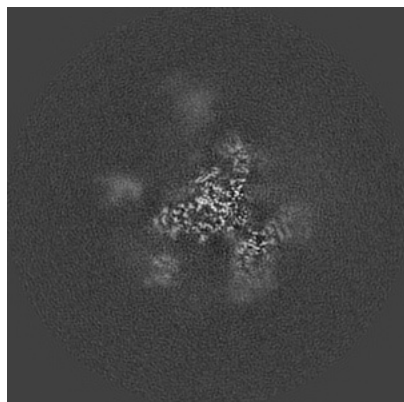


Z

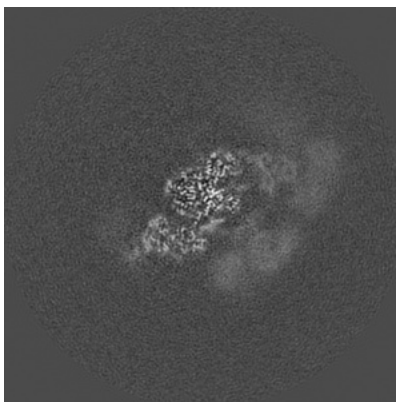
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

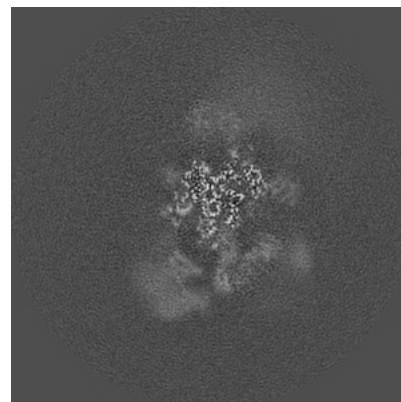
6.2.1 Primary map



X Index: 200

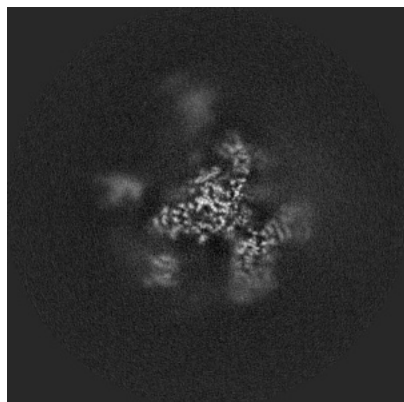


Y Index: 200

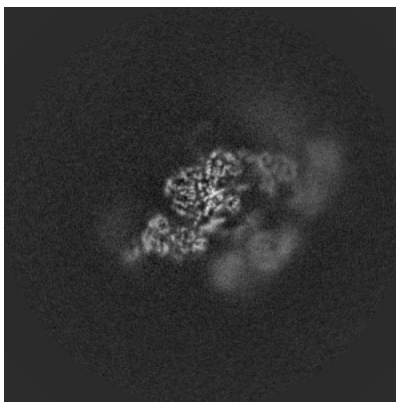


Z Index: 200

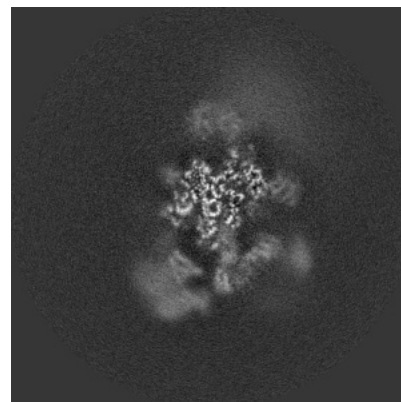
6.2.2 Raw map



X Index: 200



Y Index: 200

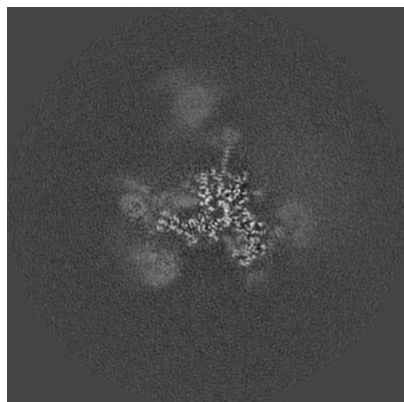


Z Index: 200

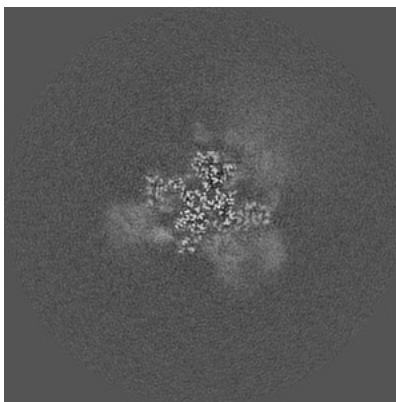
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

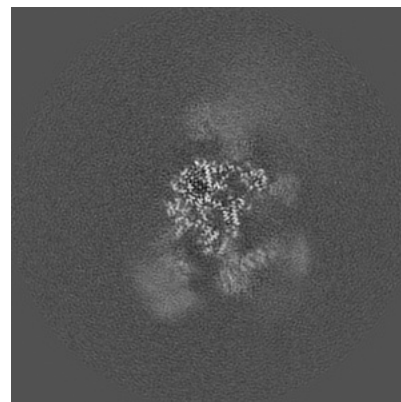
6.3.1 Primary map



X Index: 210

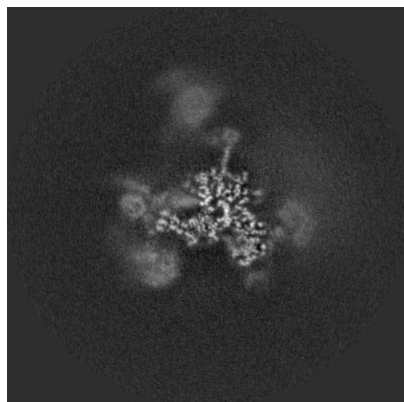


Y Index: 229

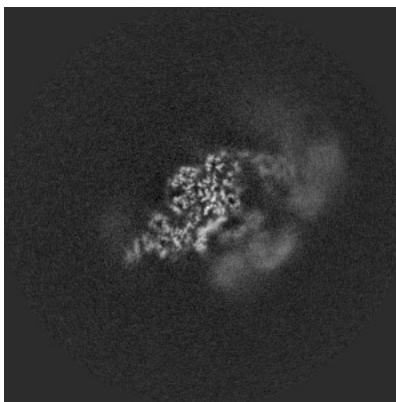


Z Index: 194

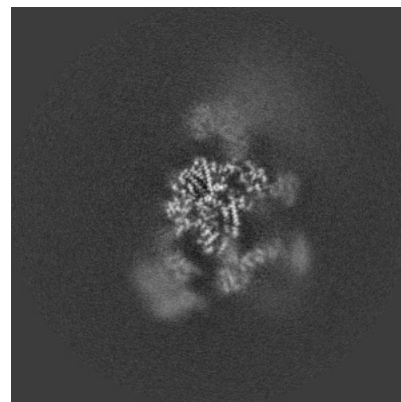
6.3.2 Raw map



X Index: 210



Y Index: 197

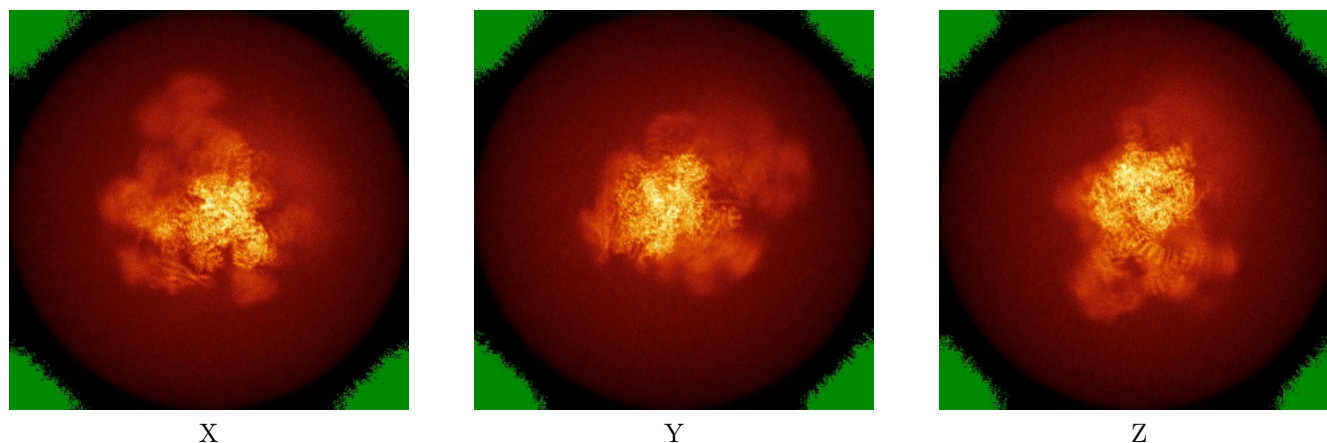


Z Index: 195

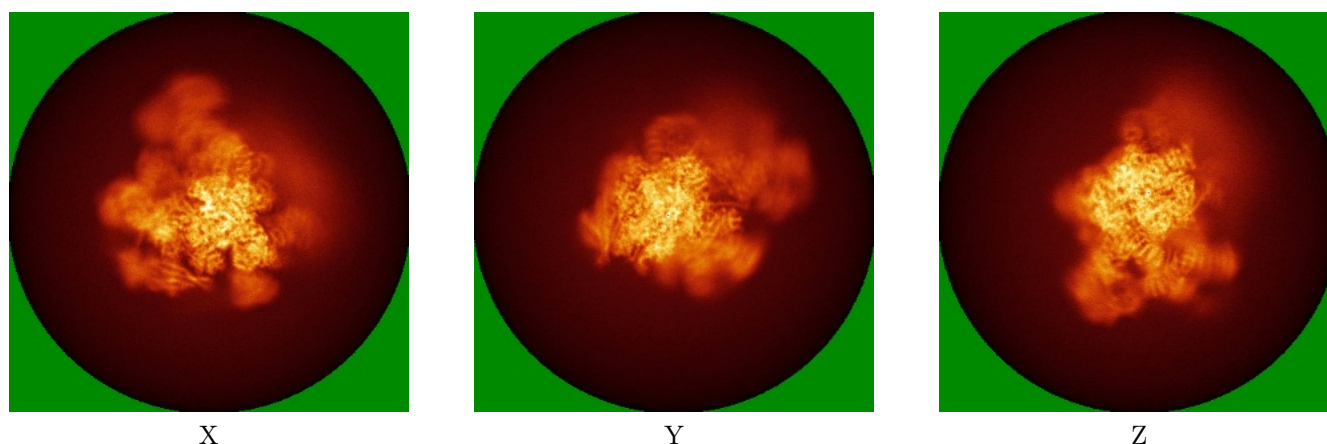
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

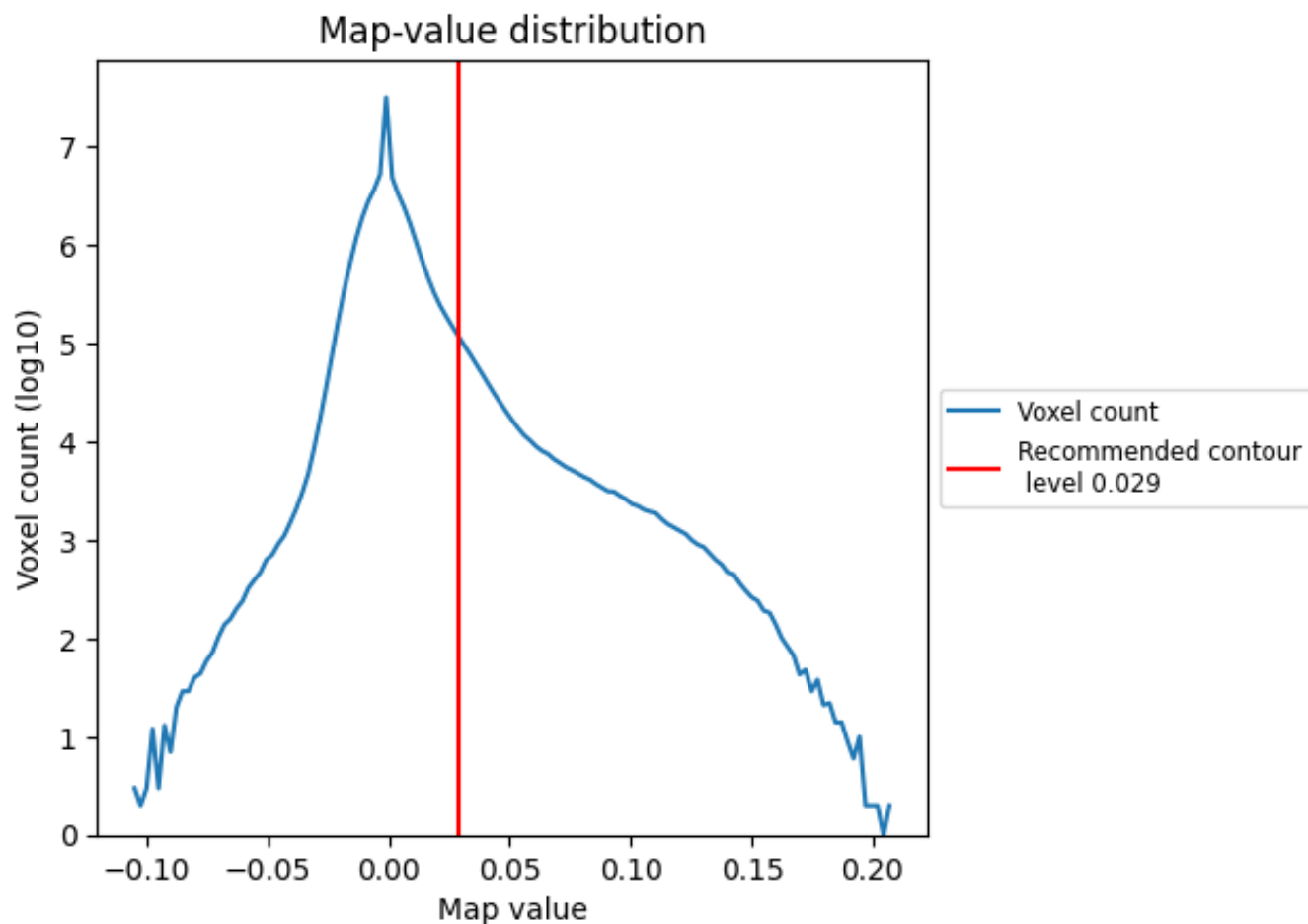
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

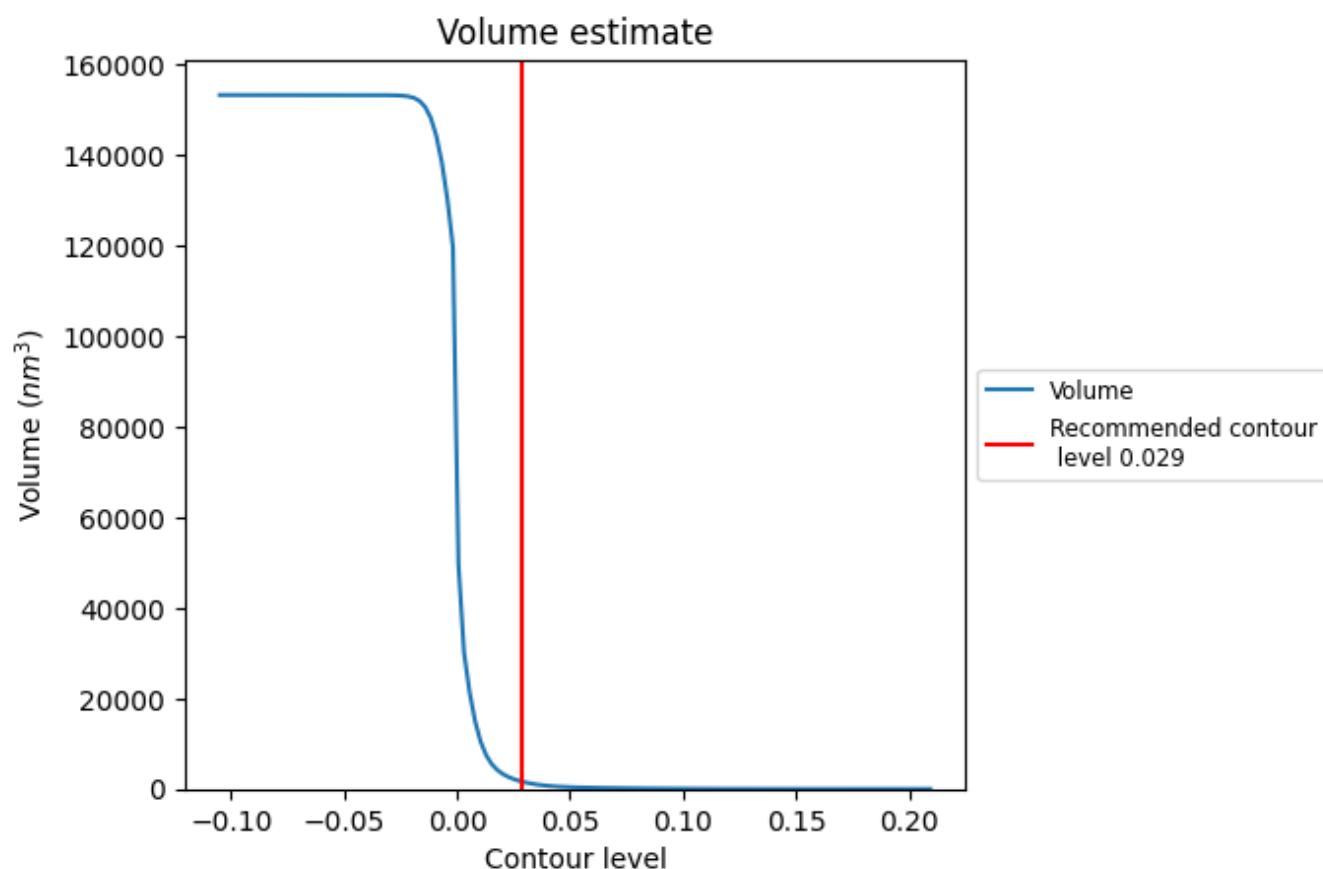
This section contains the results of statistical analysis of the map.

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.

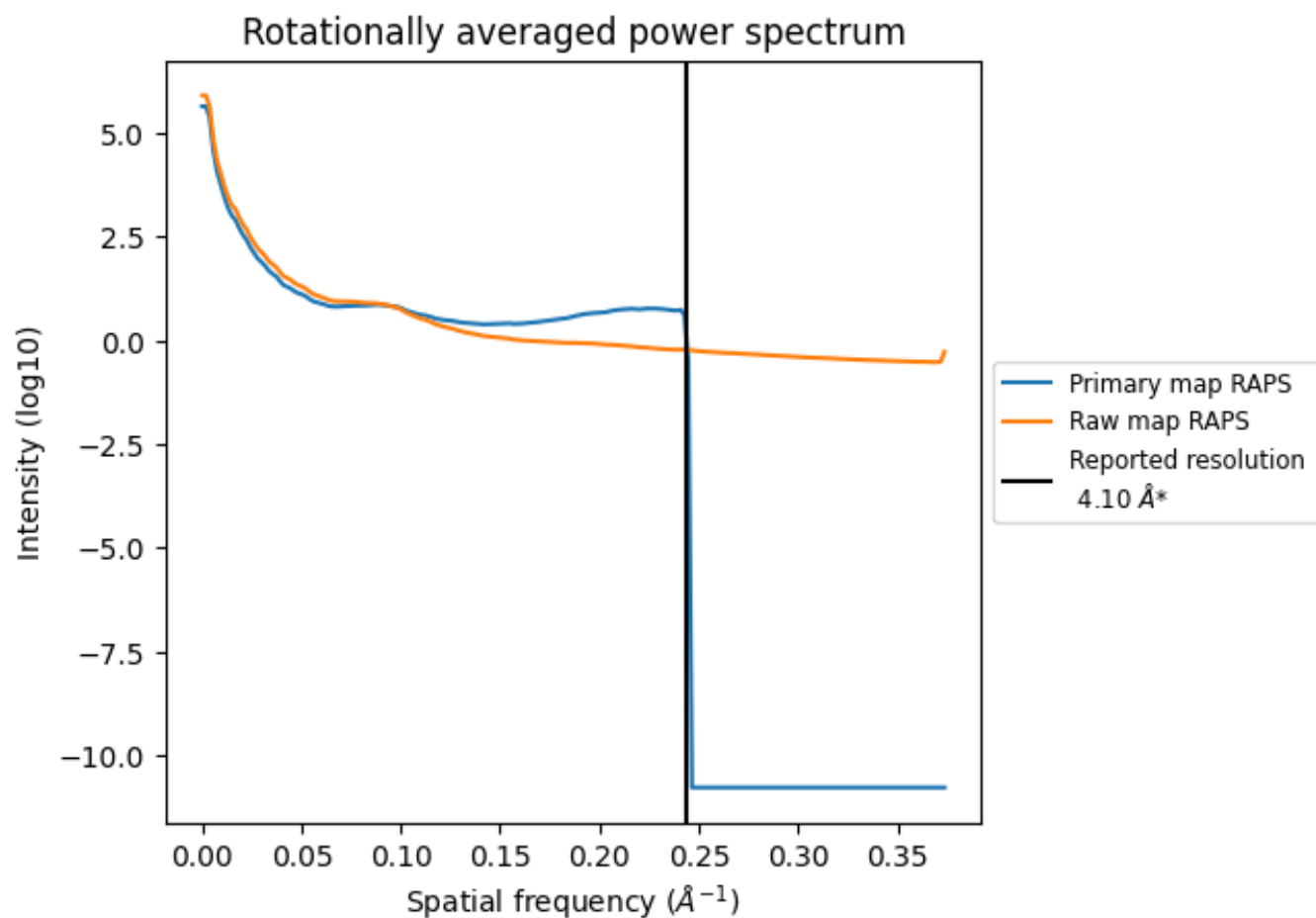
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1595 nm³; this corresponds to an approximate mass of 1441 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 ⓘ

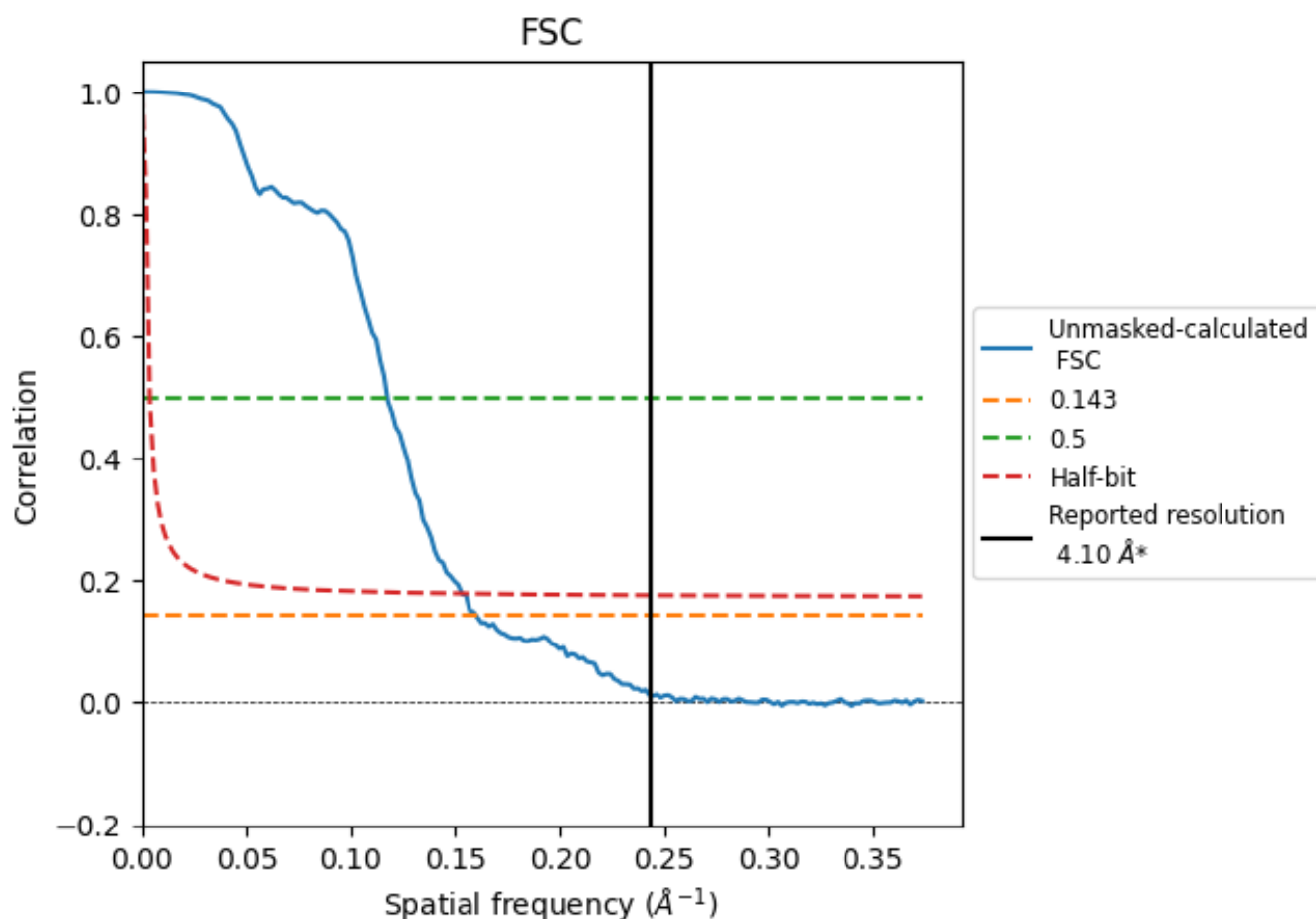


*Reported resolution corresponds to spatial frequency of 0.244 $\text{\AA}^{-1}$

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

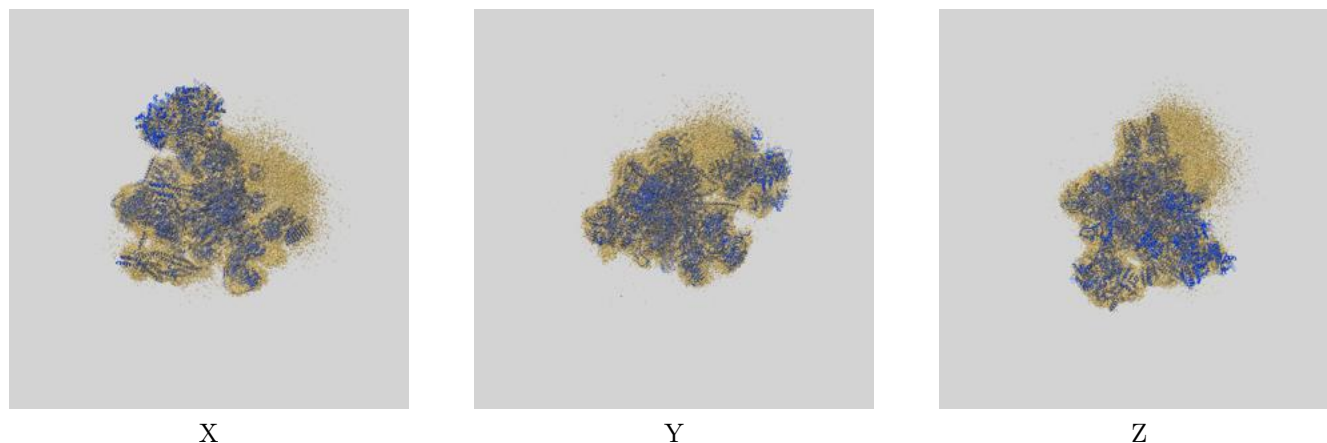
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.25	8.52	6.53

*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 6.25 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

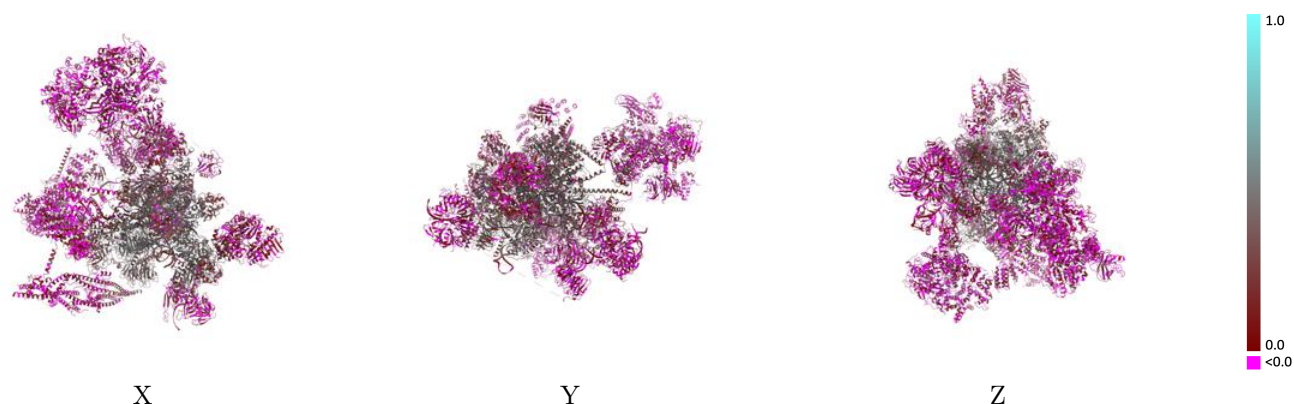
This section contains information regarding the fit between EMDB map EMD-6864 and PDB model 5YZG. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



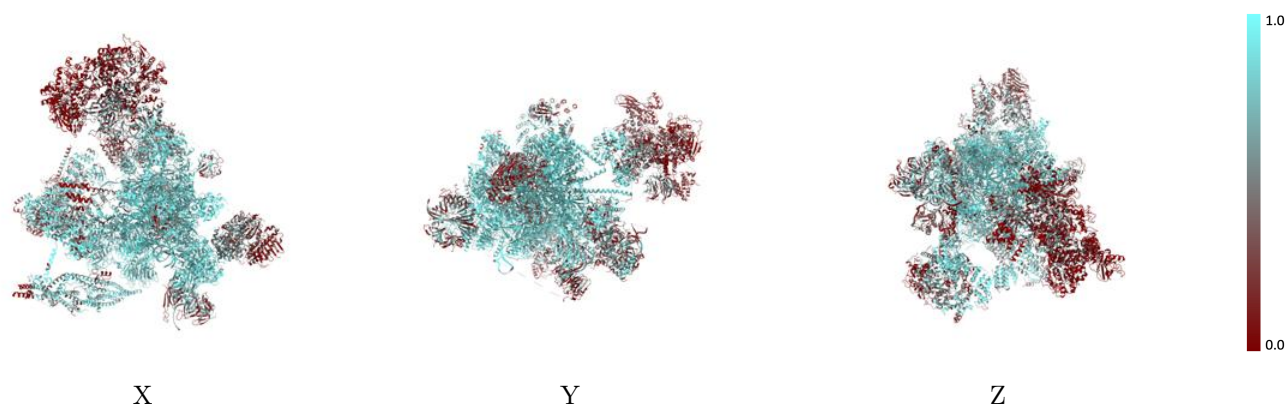
The images above show the 3D surface view of the map at the recommended contour level 0.029 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



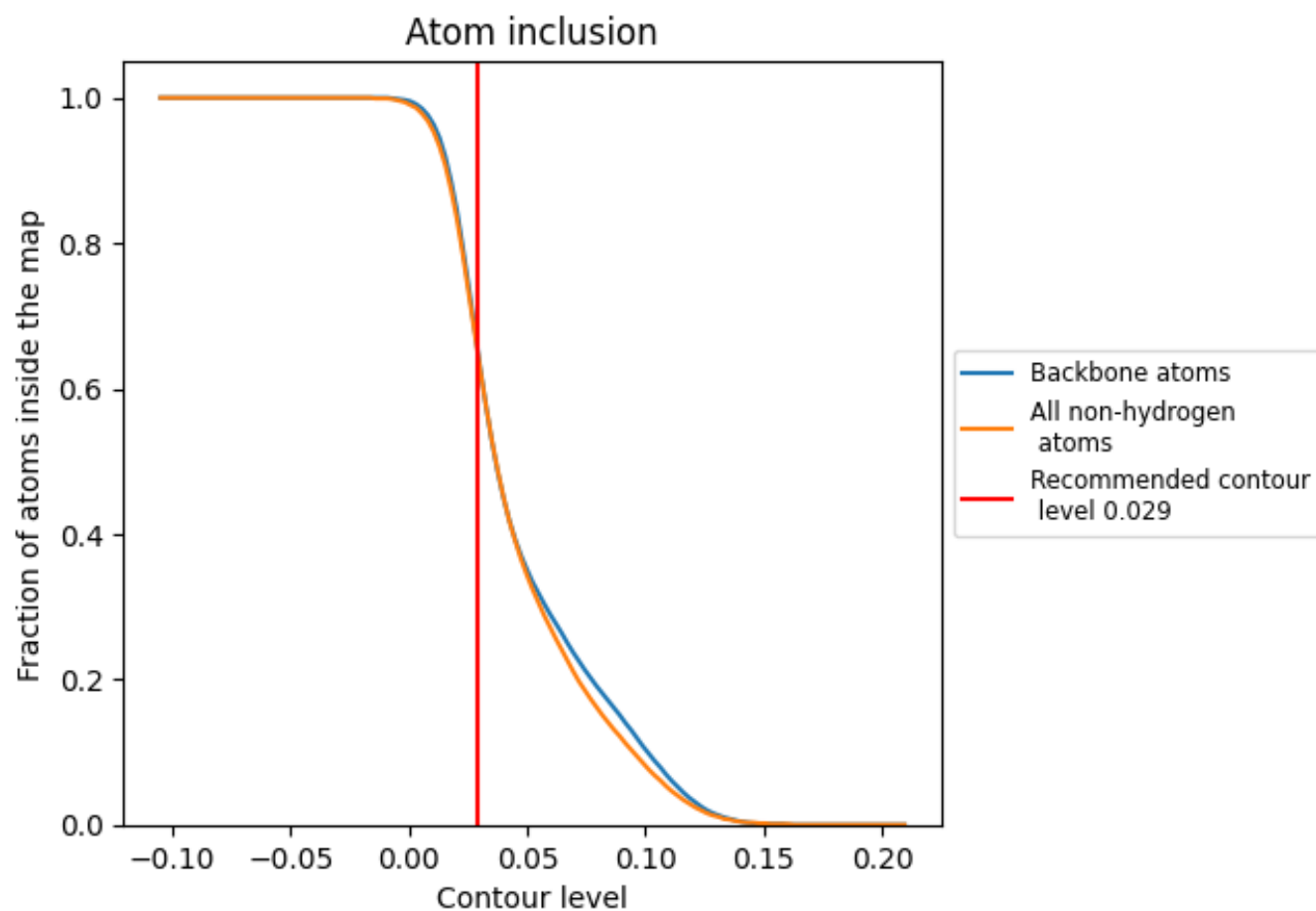
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.029).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% 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 (0.029) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6510	 0.2050
1	 0.7200	 0.1430
2	 0.4000	 0.0390
3	 0.4680	 0.1560
4	 0.8700	 0.3750
A	 0.8370	 0.3780
B	 0.8520	 0.2730
C	 0.8680	 0.3820
D	 0.1460	 0.0280
E	 0.8900	 0.3500
F	 0.8650	 0.2960
G	 0.8510	 0.2700
H	 0.6310	 0.0890
I	 0.7740	 0.0680
J	 0.7230	 0.2200
K	 0.7130	 0.0690
L	 0.7540	 0.2330
M	 0.6960	 0.2110
N	 0.8730	 0.4120
O	 0.8470	 0.3230
P	 0.8100	 0.3700
Q	 0.4890	 0.0330
R	 0.8270	 0.3610
S	 0.8430	 0.3040
T	 0.9240	 0.4440
U	 0.9360	 0.4430
V	 0.6770	 0.2120
W	 0.7040	 0.1780
X	 0.8270	 0.3130
Y	 0.8360	 0.3570
Z	 0.6210	 0.1250
a	 0.3930	 0.0090
b	 0.3740	 0.0240
c	 0.4240	 0.0370
d	 0.4010	 0.0410



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	 0.5360	 0.0140
f	 0.4080	 0.0310
g	 0.4810	 0.0080
h	 0.5260	 0.0240
i	 0.4030	 -0.0170
j	 0.4980	 0.0360
k	 0.4200	 0.0330
l	 0.4910	 -0.0020
m	 0.5670	 0.0230
n	 0.5660	 0.0530
o	 0.1710	 0.0460
p	 0.3100	 -0.0180
q	 0.4200	 0.0250
r	 0.6580	 0.0370
s	 0.4310	 0.0090
t	 0.5920	 0.0430
u	 0.4450	 0.0850
v	 0.1650	 0.0720
w	 0.1540	 0.0230
x	 0.0860	 0.0040
y	 0.7300	 0.1960