



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 10:29 AM UTC

PDB ID : 5Z58 / pdb_00005z58
EMDB ID : EMD-6891
Title : Cryo-EM structure of a human activated spliceosome (early Bact) at 4.9 angstrom.
Authors : Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on : 2018-01-17
Resolution : 4.90 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

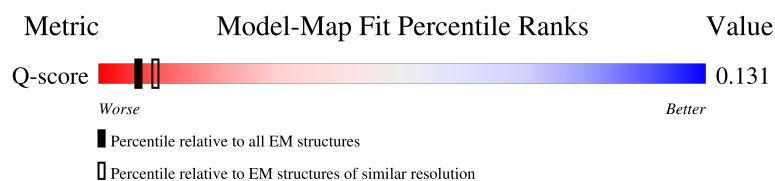
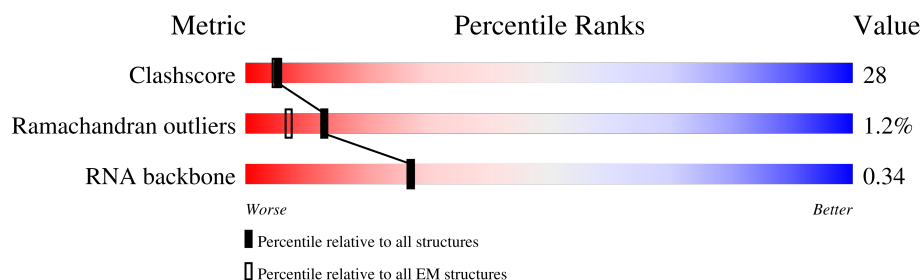
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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	
2	B	117	
3	C	972	
4	D	2136	

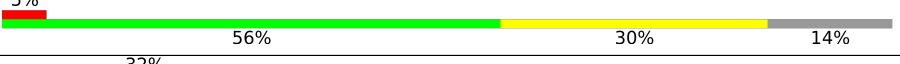
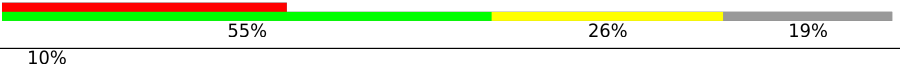
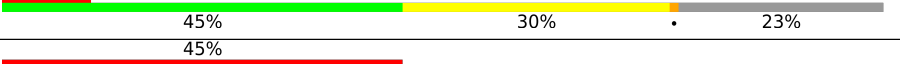
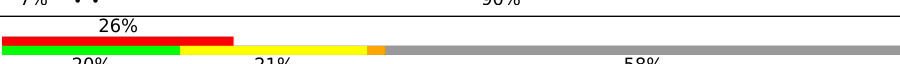
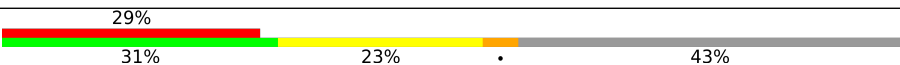
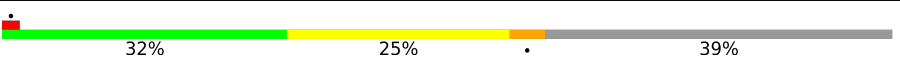
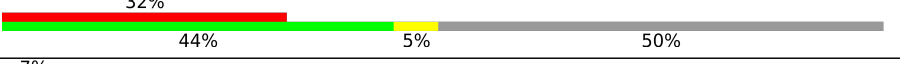
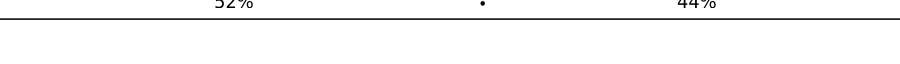
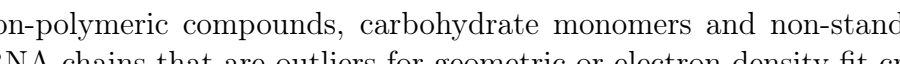
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Mol	Chain	Length	Quality of chain
5	E	357	
6	a	126	
6	h	126	
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	
22	2	895	

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Mol	Chain	Length	Quality of chain
23	3	1217	
24	4	424	
25	5	125	
26	6	110	
27	7	86	
28	J	848	
29	L	802	
30	M	343	
31	P	229	
32	R	540	
33	T	514	
34	V	908	
35	X	396	
36	Y	322	
37	Z	619	
38	z	472	
39	x	1041	

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
41	GTP	C	1500	-	-	X	-

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 94673 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	2211	Total	C	N	O	S	0	0
			18165	11706	3163	3220	76		

- 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	860	Total	C	N	O	S	0	0
			6716	4294	1120	1270	32		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	1722	Total	C	N	O		0	0
			8528	5084	1722	1722			

- 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 protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	81	Total	C	N	O		0	0
			399	237	81	81			

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Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total	C	N	O	0	0
			393	233	80	80		

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total	C	N	O	0	0
			405	241	82	82		
7	i	86	Total	C	N	O	0	0
			422	250	86	86		

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total	C	N	O	0	0
			406	242	82	82		
8	j	82	Total	C	N	O	0	0
			406	242	82	82		

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total	C	N	O	0	0
			480	286	97	97		
9	k	85	Total	C	N	O	0	0
			422	252	85	85		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total	C	N	O	0	0
			361	213	74	74		
10	m	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total	C	N	O	0	0
			391	233	79	79		
11	l	79	Total	C	N	O	0	0
			391	233	79	79		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total	C	N	O	0	0
			363	215	74	74		
12	n	68	Total	C	N	O	0	0
			334	198	68	68		

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total	C	N	O	P	0	0
			1988	889	363	643	93		

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total	C	N	O	P	0	0
			1545	689	240	539	77		

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total	C	N	O	P	0	0
			2886	1289	499	962	136		

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total	C	N	O	0	0
			804	480	162	162		

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total	C	N	O	0	0
			813	483	165	165		

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	437	Total	C	N	O	S	0	0
			2369	1448	460	458	3		

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	v	98	Total	C	N	O	0	0
			486	290	98	98		

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	1038	Total	C	N	O	S	0	0
			7702	4900	1347	1415	40		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	183	Total	C	N	O	S	0	0
			1252	809	213	226	4		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1177	Total	C	N	O	S	0	0
			9220	5854	1566	1755	45		

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4	78	Total	C	N	O	0	0
			527	345	83	99		

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	108	Total	C	N	O	S	0	0
			807	512	142	150	3		

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	89	Total	C	N	O	S	0	0
			670	410	119	128	13		

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	522	Total	C	N	O	S	0	0
			3463	2156	653	648	6		

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	132	Total	C	N	O	S	0	0
			1077	691	188	194	4		

- Molecule 30 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	36	Total	C	N	O	S	0	0
			267	167	45	52	3		

- Molecule 31 is a protein called Spliceosome-associated protein CWC15 homolog.

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

- Molecule 32 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	309	Total	C	N	O	S	0	0
			2314	1454	413	435	12		

- Molecule 33 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 34 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	V	451	Total	C	N	O		0	0
			2238	1336	451	451			

- Molecule 35 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 36 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	104	Total	C	N	O	S	0	0
			737	466	126	143	2		

- Molecule 37 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Z	113	Total	C	N	O		0	0
			755	474	147	134			

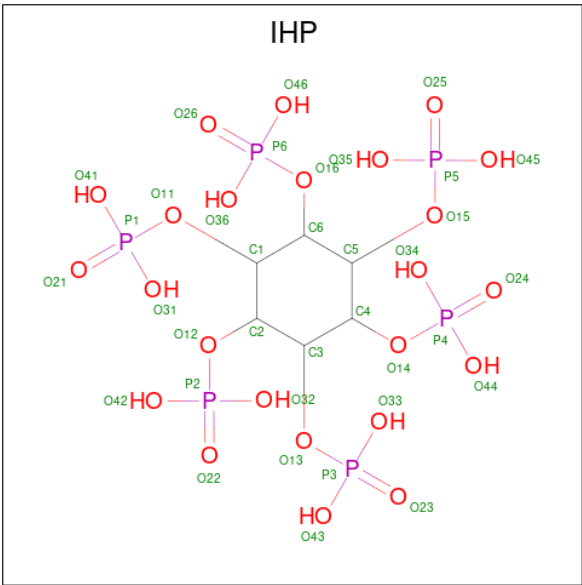
- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	z	177	Total	C	N	O	S	1	0
			1381	869	241	266	5		

- Molecule 39 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

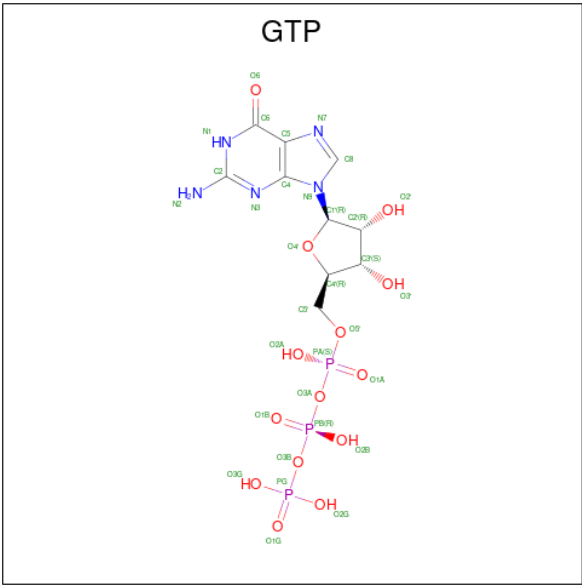
Mol	Chain	Residues	Atoms					AltConf	Trace
39	x	583	Total	C	N	O		0	0
			2882	1715	583	584			

- Molecule 40 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆).



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

- Molecule 41 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 42 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

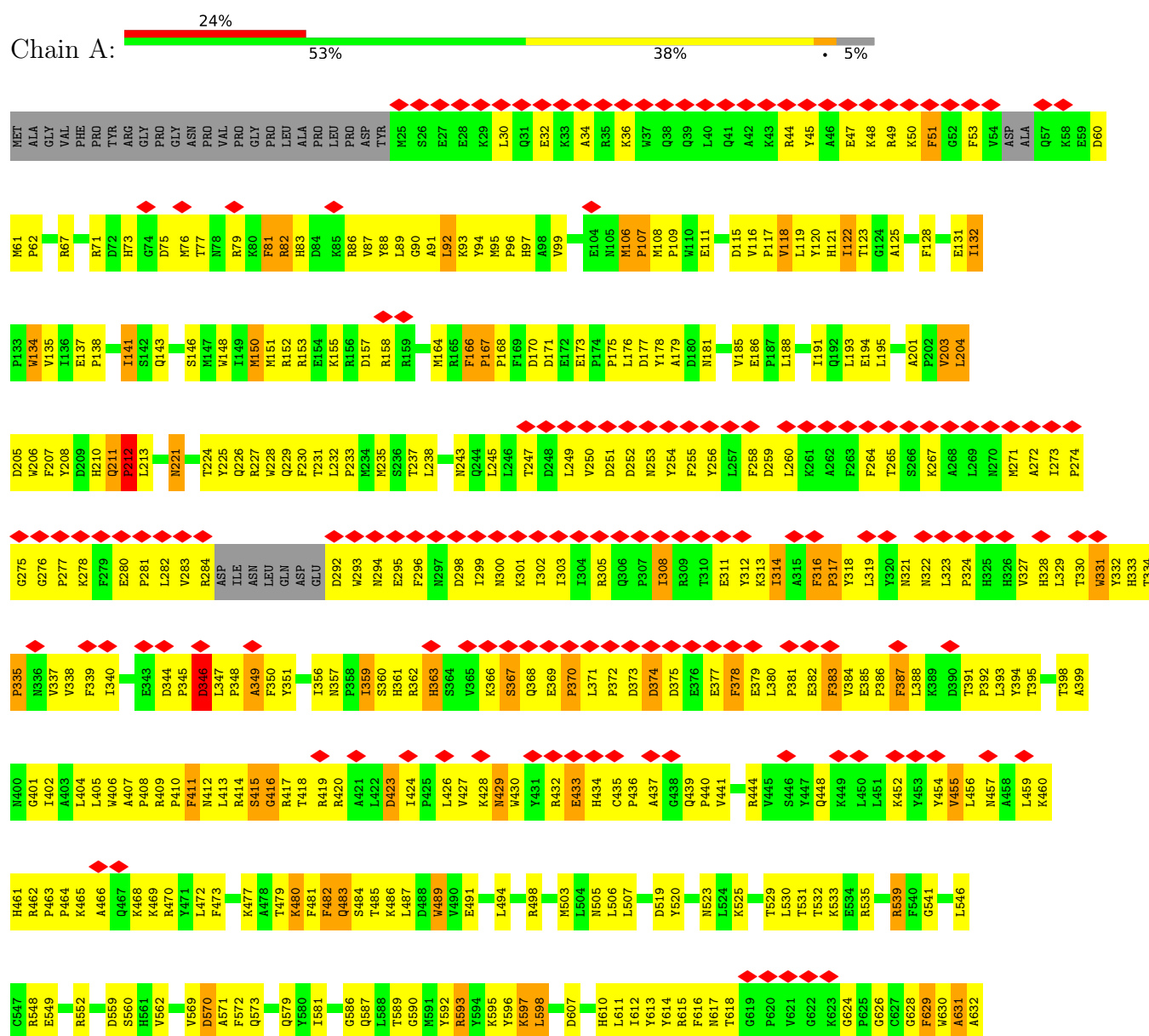
- Molecule 43 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
43	6	3	Total 3	Zn 3	0
43	M	1	Total 1	Zn 1	0

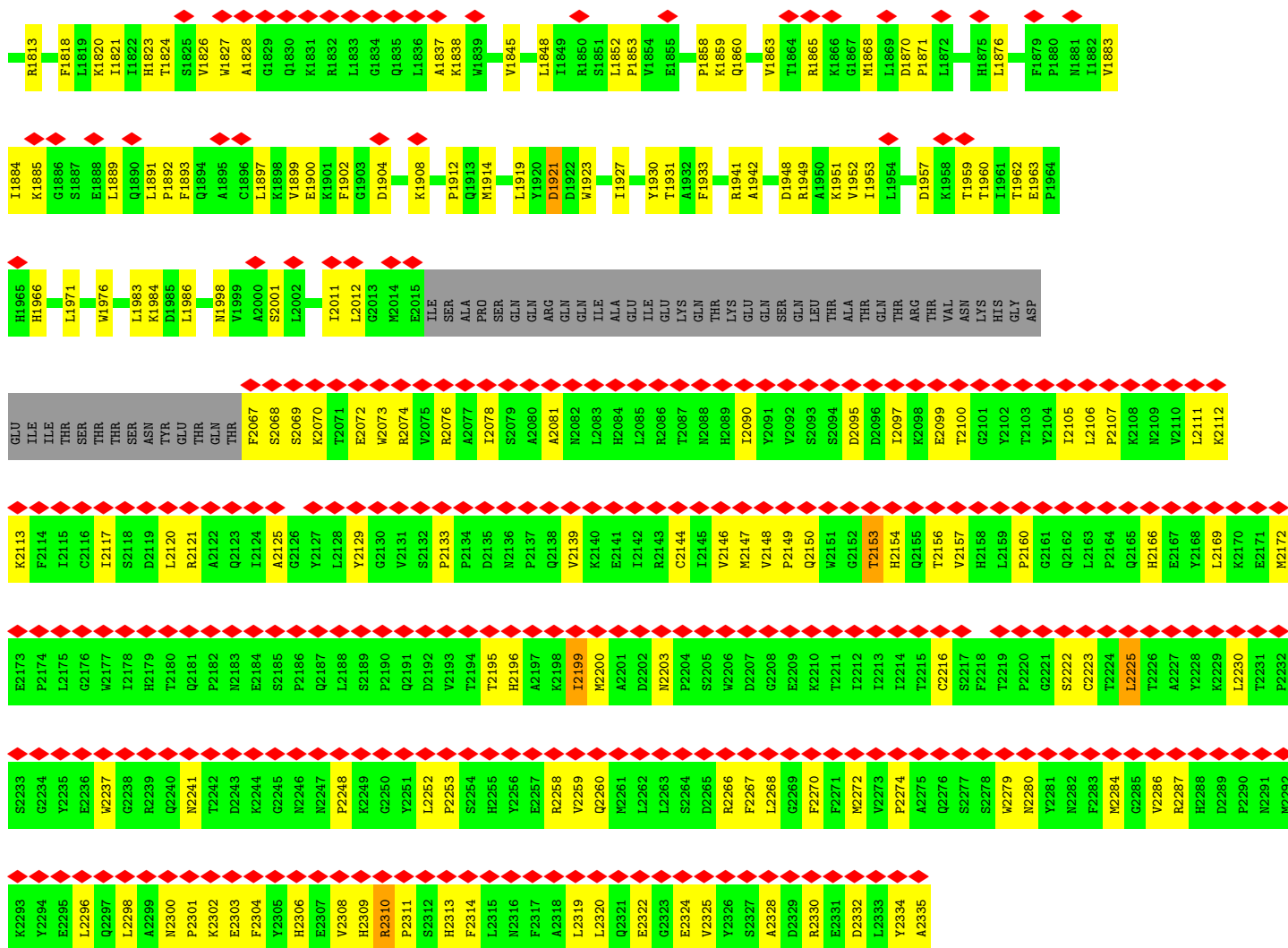
3 Residue-property plots

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.

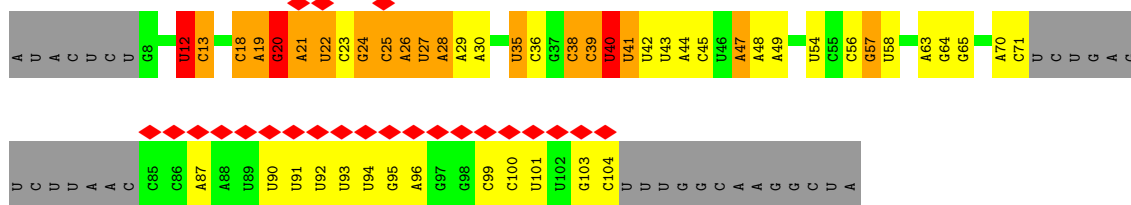
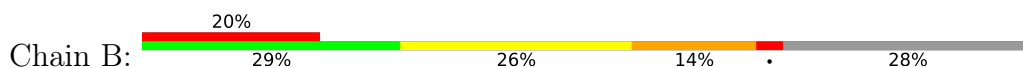
• Molecule 1: Pre-mRNA-processing-splicing factor 8



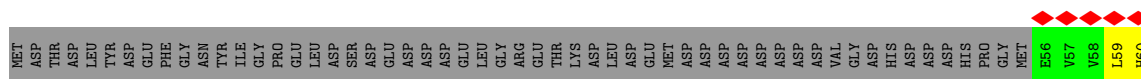
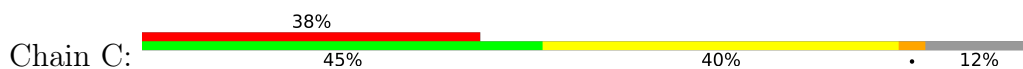




• Molecule 2: U5 snRNA

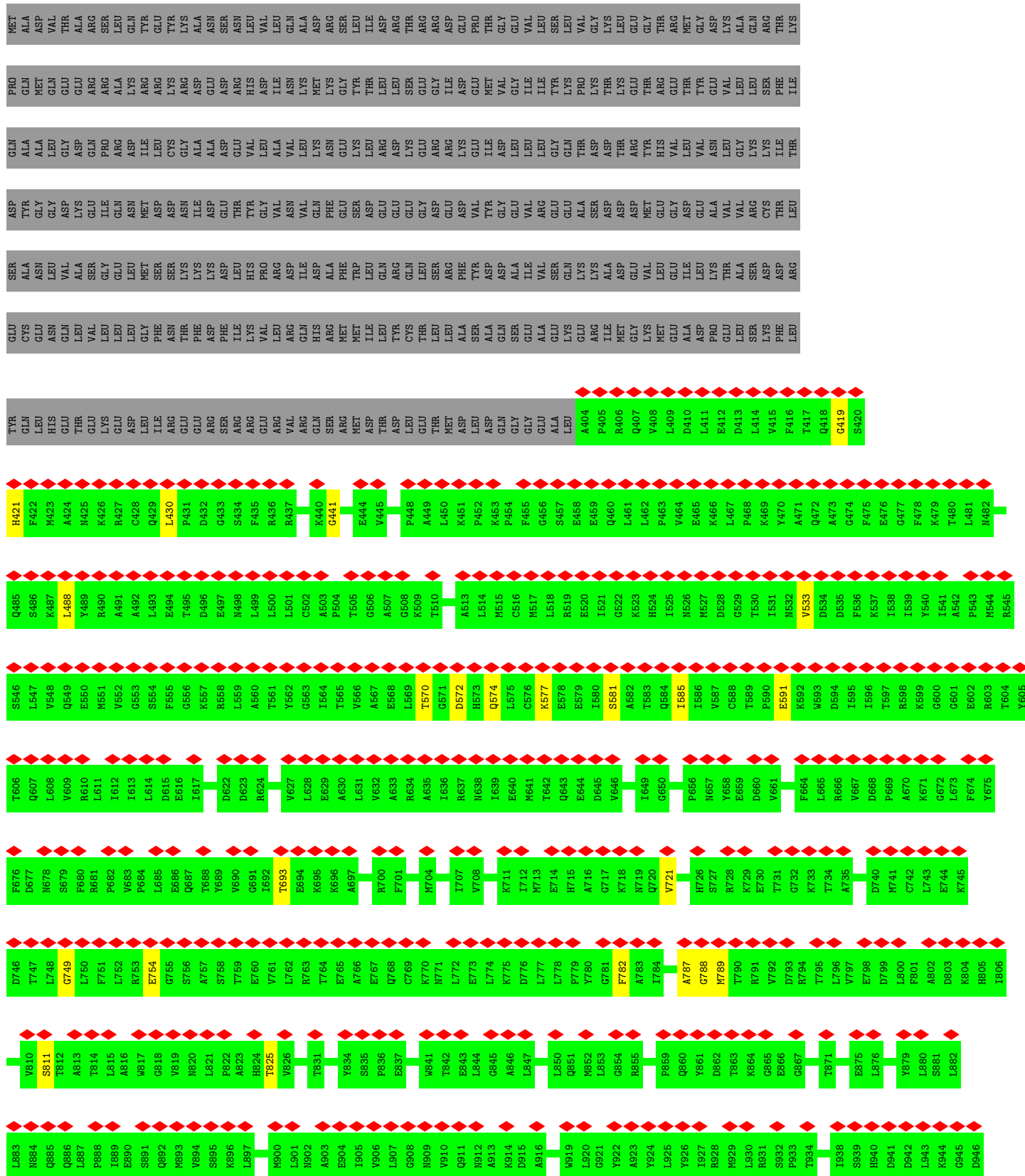


• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



SER	E61	M123	P185	N258	G332	I401	P473	S533	P594	E668	A729	K790	S880
ILE	D62	D124	V186	K289	D333	L401	L474	V534	V595	E669	R730	I791	F881
SER	K63	N125	T187	D261	I334	L408	L475	A535	N596	T669	S731	L792	G882
PHE	K64	N126	V188	R262	N335	K409	C476	R536	P597	S670	I732	D793	F883
ASP	Y65	E127	V189	L263	Y336	L410	H477	E537	S598	S671	W733	A794	E884
PRO	Y66	L128	L190	L264	F339	L411	T478	E540	E599	L672	A795	W795	T885
MET	P67	L129	L191	L265	G344	L412	K480	E541	L600	K673	F735	W796	L886
LEU	T68	R130	P191	E266	G345	P414	K481	Y541	P601	C674	G736	A797	R887
GLU	A69	N131	T193	P270	L343	L415	K482	Y542	K602	A676	D738	Q798	Q892
LEU	E70	G136	G195	P271	G444	L416	S483	R543	M603	E677	A739	E799	Q893
LEU	E71	G137	L199	Y275	Y348	L418	T484	V544	G606	T678	T740	F800	Q894
ALA	V72	G138	L200	R279	F349	V419	D485	P545	L607	P679	G741	L801	A895
ASP	V73	L139	F200	H280	N350	C420	D486	A546	R608	N680	P742	H802	F896
VAL	E76	H137	F201	I281	P351	F423	G487	G547	K609	K681	W743	I744	S897
LEU	E77	L138	F202	I282	K352	G425	V488	Y548	K612	N683	L745	L746	L898
ASN	E78	H140	I202	D283	T353	E426	Q489	V550	S613	N686	L747	W748	S899
TRP	E79	H141	M203	E284	R354	T427	F490	L551	Y614	T685	I749	Q807	H902
VAL	I80	G141	D204	G287	K355	T428	A492	L552	P615	T686	T749	I808	H903
LEU	V81	K142	H208	L288	F356	C434	F493	G554	S616	M687	W751	I809	V907
ASP	Q82	T143	G144	I289	K357	G437	G494	V555	L617	I688	L750	P810	Q908
PRO	E83	F145	T215	S290	K358	I438	R495	V556	T619	A689	S751	T811	Q909
MET	E84	G148	V216	M291	K359	I439	V496	P558	K620	E690	W752	V815	G909
	D85	L149	A217	Y292	P361	P439	L497	P568	V621	E753	E753	W816	D910
	Q87	L150	G218	I294	T362	S440	S486	V569	E622	L692	W754	Y817	P911
	P88	E151	L219	S293	S363	K442	S499	V560	E623	E693	D755	S818	L912
	L89	Q152	R220	T294	S364	V443	T500	K561	S624	K694	W756	M822	D913
	E91	P155	I221	D295	S365	G444	H502	A563	E626	G695	K757	A823	K914
	P92	E156	G223	E296	Q366	A445	A504	T562	H627	G696	A757	T824	S915
	I93	ILE	D224	L298	R367	K446	G505	V566	V628	E700	W758	R825	I916
	I94	ARG	G225	N297	S368	P447	P506	E567	L629	E701	L759	R826	V917
	K95	L299	V225	L299	S369	I449	V507	P568	L630	E703	W761	E829	R919
	P96	ASP	V226	L300	F369	E450	K508	R569	G631	E704	W762	P830	P920
	V97	LYS	L227	L301	V370	H451	V509	G570	T632	W705	Q763	V843	E922
	K98	THR	F228	L302	E371	T452	L510	N571	L635	Q706	W764	W846	P923
	T99	THR	I229	L303	F372	Y453	E512	E572	Y636	I707	W765	P852	Q924
	LYS	GLN	D230	G305	E375	G456	N513	E573	L637	T708	S765	R853	P925
	LYS	LEU	A231	G306	P376	V457	L514	A574	L638	W709	W766	R854	A926
	PHE	CYS	A232	N306	L377	D458	T515	Q575	M641	W710	I767	G855	P927
	THR	THR	E233	V307	Y378	S459	E516	F577	K646	R711	Q771	R856	Q928
	LEU	THR	G234	C308	K379	D460	D518	R578	E649	K712	W772	I863	A930
	MET	LEU	V235	F309	L380	L461	E519	P579	S649	K713	G773	L714	R931
	GLU	ASP	M236	S310	A382	G462	E520	L580	E650	G715	T774	E716	G932
	LEU	ILE		S311	Q383	E463	S522	K581	L651	F717	R775	F718	F933
	THR	PHE		S312	V384	D463	S523	F582	D652	F718	E776	F719	M934
	PRO	VAL	T239	G317	V385	M465	Q524	N583	D653	Q719	L779	Q799	R939
	VAL	E174	R241	F318	G386	S466	L524	T584	K654	T720	G780	C780	R940
	T112	Q175	E242	T319	D387	D467	E525	T585	V655	K721	D781	D781	K941
	V113	K244	L242	T319	A382	G467	C526	S586	A656	Y722	E782	E782	G942
	Y114	R177	H245	F323	D389	E464	C527	V587	D657	W723	L783	L783	L943
	E115	G178	A246	T326	T390	M466	T526	I588	P657	D724	W784	W784	I878
	M116	V179	R250	Y327	S391	S466	T527	V587	D658	W725	R785	R785	I879
	D117	G180	V253	T330	T392	S466	C528	V587	P659	L726	N786	N786	SER
	F118	I181	T254	F331	P393	D468	C529	I589	V660	L727	K788	K788	GLU
	L119	K182	V255	F331	L399	D469	C530	V591	T661	A728	F789	F789	ASP
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	T184					G472							

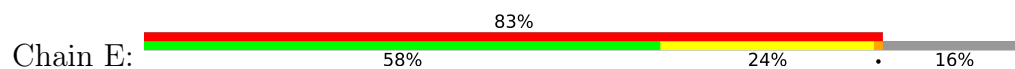
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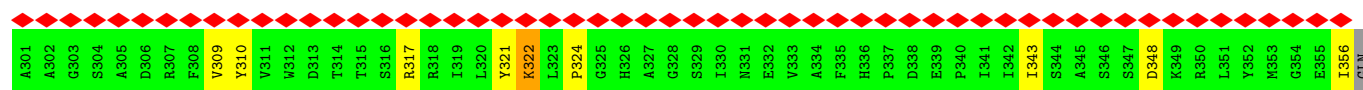
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P947	L948	L949	D950	Q951	R952	D955				L956	V957	H958	T959	A960	A961	L962	H963	L964	D965	K966	H967	V970				K971	Y972	D973	K974	K975	T976	G977	H978	F979	Q980	V981	T982	E983	L984	G985	R986	H990				Y991	Y992	E993	T994	D995	T997	V998	Q999	T1000	Y1001	N1002	Q1003	L1004	L1005	K1006	P1007	T1008	L1009	S1010

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Q1749	D1809	R1869	V1929	E1989	G2049	M2109
D1750	V1810	Q1870	L1930	D1990	P2050	S2110
A1751	A1811	L1871	S1931	E1991	V2051	D2111
V1752	P1812	A1872	S1932	E1992	T2052	A2112
D1753	L1813	Q1873	N1933	R1993	A2053	Y2113
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T1756	G1816	P1876	L1936	L1996	L2056	C2116
W1757	M1817	H1877	S1937	L1997	P2057	D2117
T1758	I1818	K1878	P1938	Q1998	Q2058	Q2118
F1759	A1819	L1879	A1939	L1999	R2059	Y2119
L1760	A1820	N1880	L1940	T2000	R2060	E2120
V1761	Y1821	M1881	A1941	D2001	E2061	K2121
R1762	Y1822	P1882	A1942	S2002	E2062	F2122
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Q1766	Y1826	D1886	A1946	D2006	V2066	VAL
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M1769	I1829	V1889	V1949	R2009	G2069	ALA
Y1770	E1830	K1890	T1950	F2010	D2070	GLY
Y1771	L1831	T1891	Q1951	C2011	A2071	THR
M1772	F1832	N1892	A1952	N2012	K2072	ASP
L1773	S1833	L1893	M1953	R2013	S2073	ALA
Q1774	M1834	L1894	W1954	T2014	N2074	GLY
G1775	S1835	L1895	S1955	P2015	S2075	GLN
T1776	L1836	Q1896	L1956	N2016	T2076	GLN
S1777	N1837	A1897	D1957	T2017	T2077	THR
H1778	A1838	H1898	S1958	E2018	S2078	PRO
R1779	K1839	L1899	Y1959	L2019	T2079	GLY
H1780	T1840	S1900	L1960	S2020	K2080	ALA
L1781	K1841	R1901	K1961	Y2021	R2081	LEU
S1782	V1842	M1902	Q1962	E2022	L2082	LEU
D1783	R1843	Q1903	L1963	V2023	T2083	GLN
H1784	G1844	L1904	P1964	V2024	L2084	GLY
L1785	L1845	S1905	H1965	D2025	Q2085	PRO
S1786	L1846	A1906	F1966	K2026	Q2086	ARG
E1787	E1847	L1907	T1967	D2027	K2087	CYS
L1788	I1848	L1908	S1968	S2028	A2088	SER
V1789	I1849	Q1909	E1969	L2029	K2089	LEU
E1790	S1850	S1910	H1970	R2030	V2090	GLN
Q1791	N1851	D1911	I1971	S2031	K2091	ALA
T1792	A1852	T1912	K1972	G2032	L2092	P58
L1793	A1853	E1913	R1973	G2033	D2093	I59
S1794	E1854	E1914	G1974	P2034	F2094	M60
D1795	Y1855	L1915	T1975	V2035	V2095	
L1796	E1856	L1916	T1976	V2036	A2096	
E1797	N1857	S1917	K1977	V2037	P2097	
Q1798	I1858	K1918	G1978	L2038	A2098	
S1799	P1859	A1919	V1979	V2039	T2099	
K1800	I1860	I1920	E1980	Q2040	G2100	
C1801	R1861	R1921	S1981	L2041	A2101	
T1802	H1862	L1922	V1982	E2042	H2102	
S1803	H1863	I1923	F1983	R2043	N2103	
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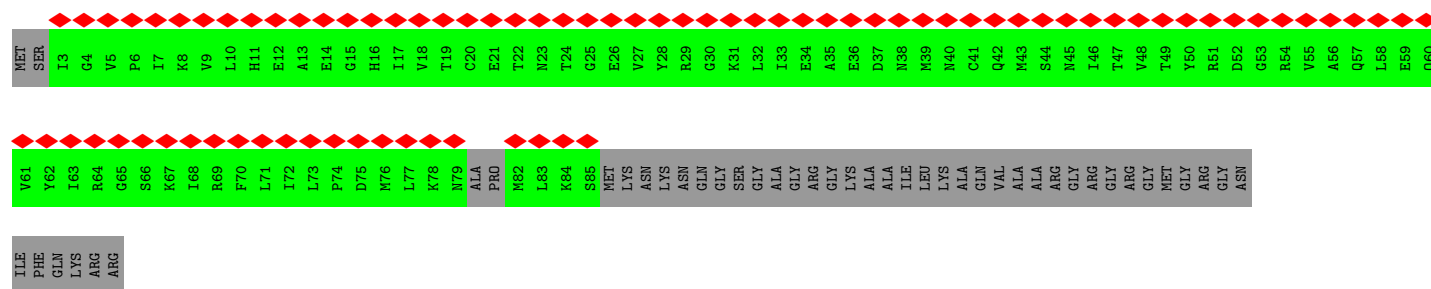
• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



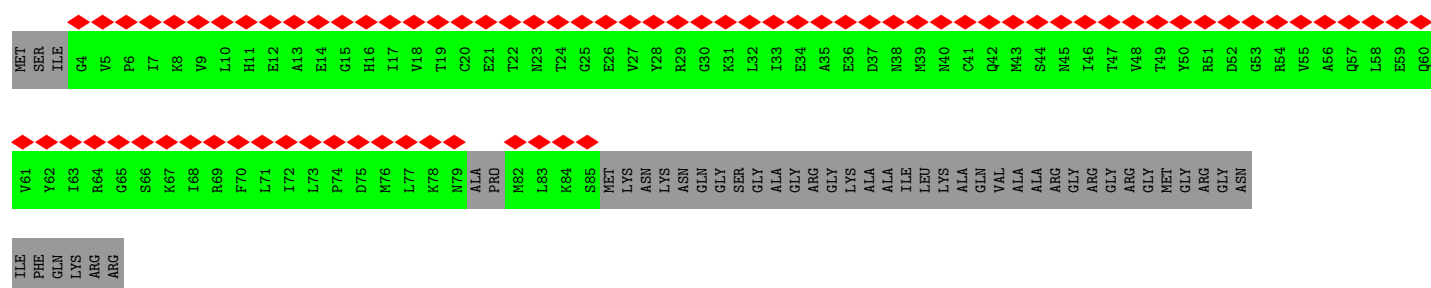
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ARG	E66	S126	A186	E246
GLY	G67	A127	L187	G247
PRO	E68	S128	Q188	S248
LEU	V69	T129	T189	Y249
LEU	Y70	D130	F190	L250
LEU	C71	K131	Q191	L251
VAL	C72	T132	N192	S252
PRO	K73	V133	L193	M253
VAL	F74	A134	Y194	A254
LYS	H75	V135	Q195	M255
ARG	P76	W136	V196	D256
GLN	N77	D137	L197	N257
ARG	G78	S138	A198	T258
HIS	S79	E139	V199	V259
GLU	T80	T140	T200	R260
LEU	L81	G141	F201	V261
LEU	Y82	E142	N202	W262
GLY	S83	R143	D203	D263
ALA	A84	V144	T204	V264
GLY	G85	K145	S205	R265
ASP	F86	R146	D206	P266
SER	D87	L147	Q207	F267
SER	B88	K148	T208	A268
ASP	L89	G149	T209	P269
GLY	I90	H150	S210	K270
GLN	L91	T151	G211	E271
THR	L92	S152	G212	R272
PRO	W93	F153	T213	C273
GLY	N94	V154	D214	V274
ALA	V95	N155	N215	K275
LEU	Y96	S156	D216	L276
LEU	G97	C157	T217	F277
LEU	D98	Y158	K218	Q278
LEU	C99	P159	V219	G279
LEU	D100	A160	W220	N280
GLN	N101	R161	D221	V281
GLN	Y102	R162	L222	H282
GLN	A103	G163	R223	M283
GLY	T104	P164	Q224	F284
GLY	L105	Q165	N225	E285
PRO	K106	L166	K226	K286
PRO	G107	V167	L227	N287
ARG	H108	C168	T228	L288
SER	S109	T169	Y229	L289
SER	G110	G170	T230	R290
LEU	A111	S171	N231	C291
LEU	V112	D172	R232	S292
GLN	M113	D173	G233	W293
ALA	E114	G174	H234	S294
P58	L115	T175	A235	P295
I59	H116	V176	D236	D296
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	N118	L178	V238	S298
	T119	W179	T239	K299
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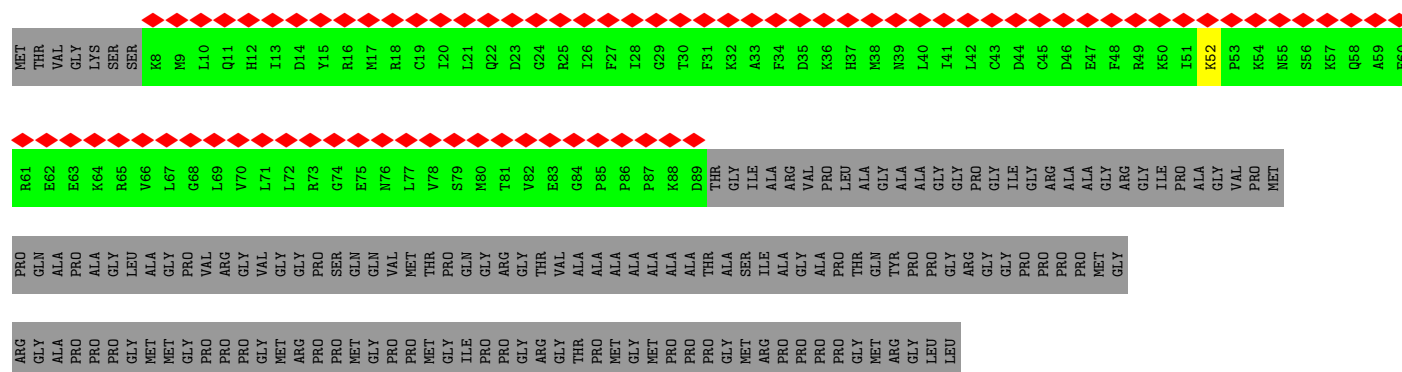
• Molecule 6: Small nuclear ribonucleoprotein Sm D3



• Molecule 6: Small nuclear ribonucleoprotein Sm D3

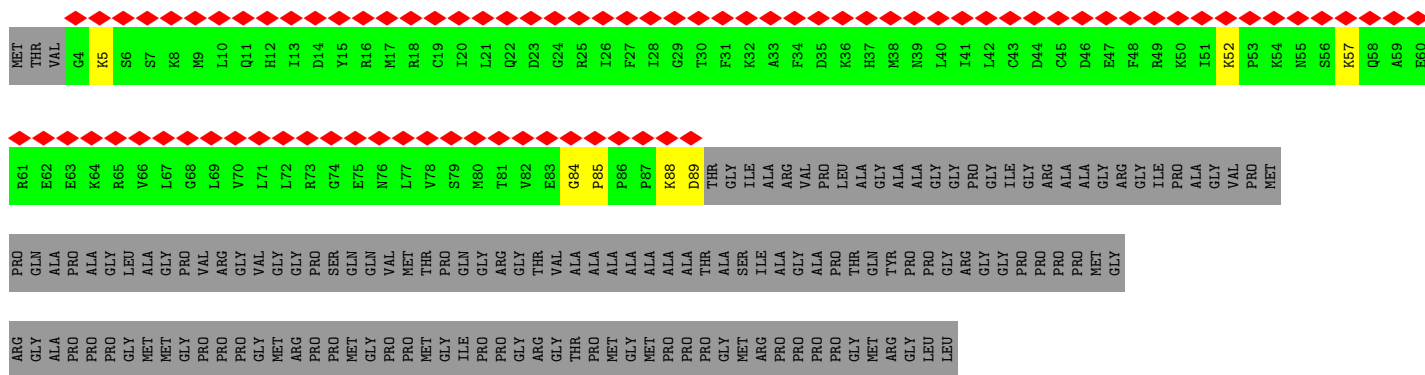


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

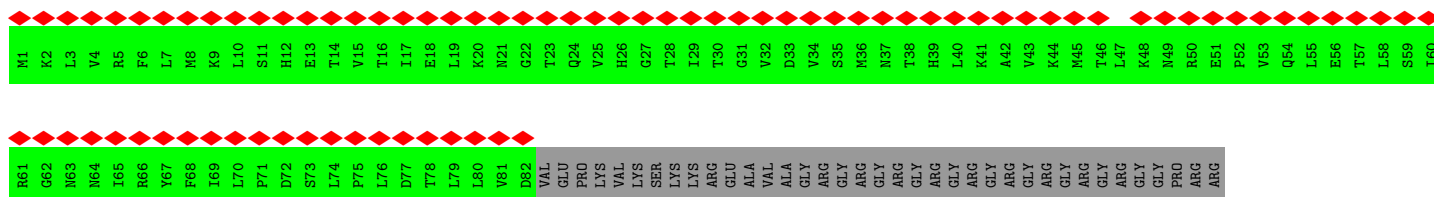


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'





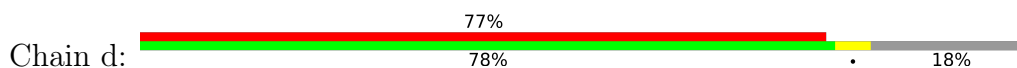
- Molecule 8: Small nuclear ribonucleoprotein Sm D1



- Molecule 8: Small nuclear ribonucleoprotein Sm D1



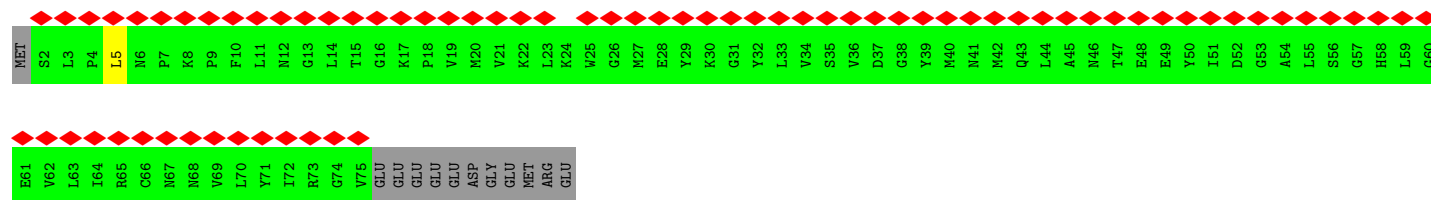
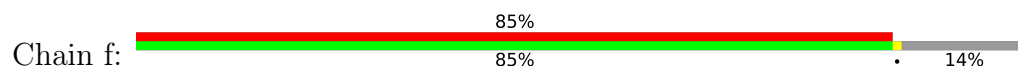
- Molecule 9: Small nuclear ribonucleoprotein Sm D2



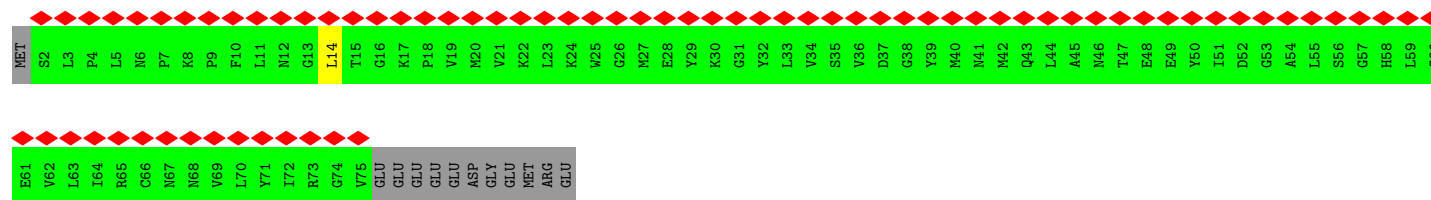
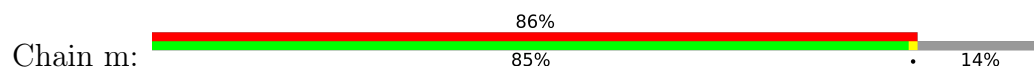
- Molecule 9: Small nuclear ribonucleoprotein Sm D2



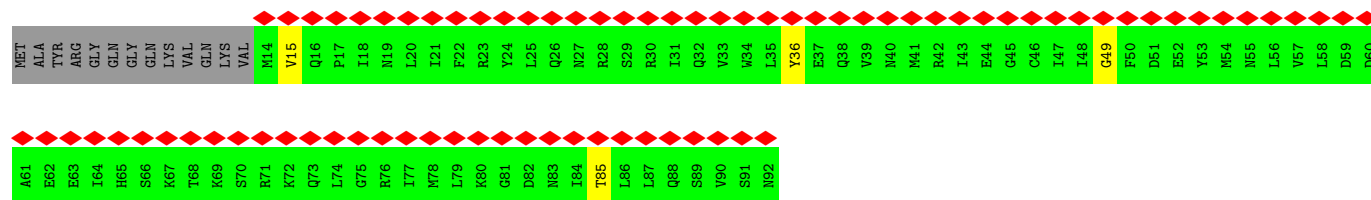
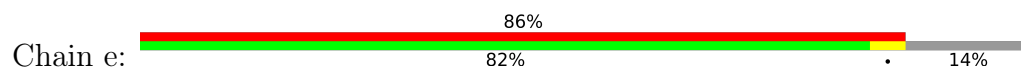
- Molecule 10: Small nuclear ribonucleoprotein F



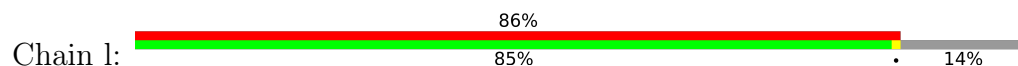
- Molecule 10: Small nuclear ribonucleoprotein F



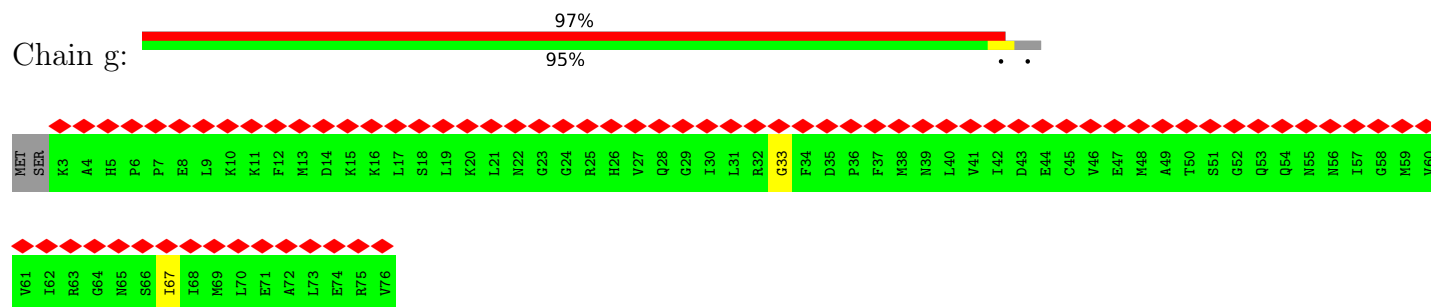
- Molecule 11: Small nuclear ribonucleoprotein E



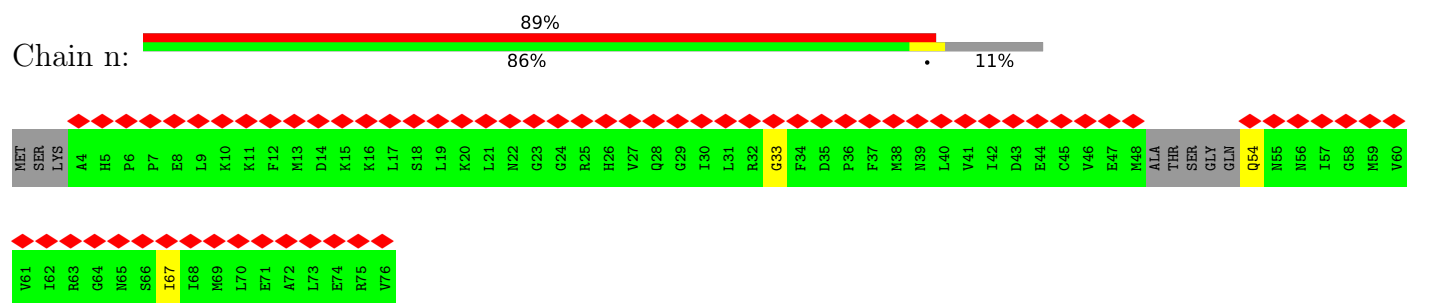
- Molecule 11: Small nuclear ribonucleoprotein E



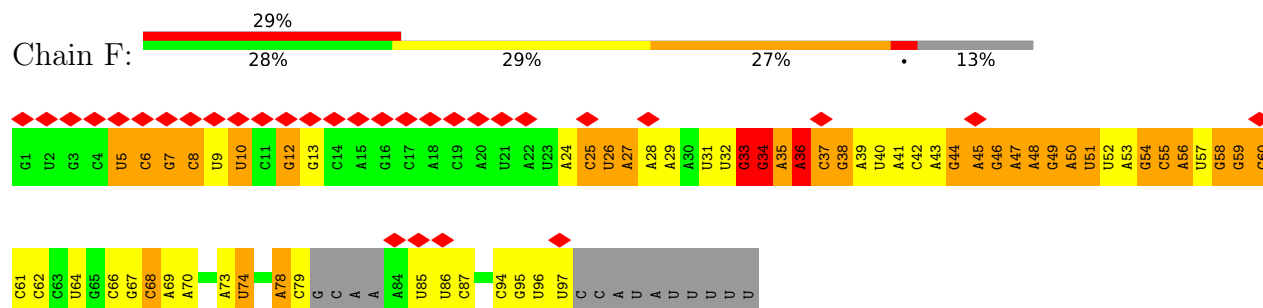
Chain g:



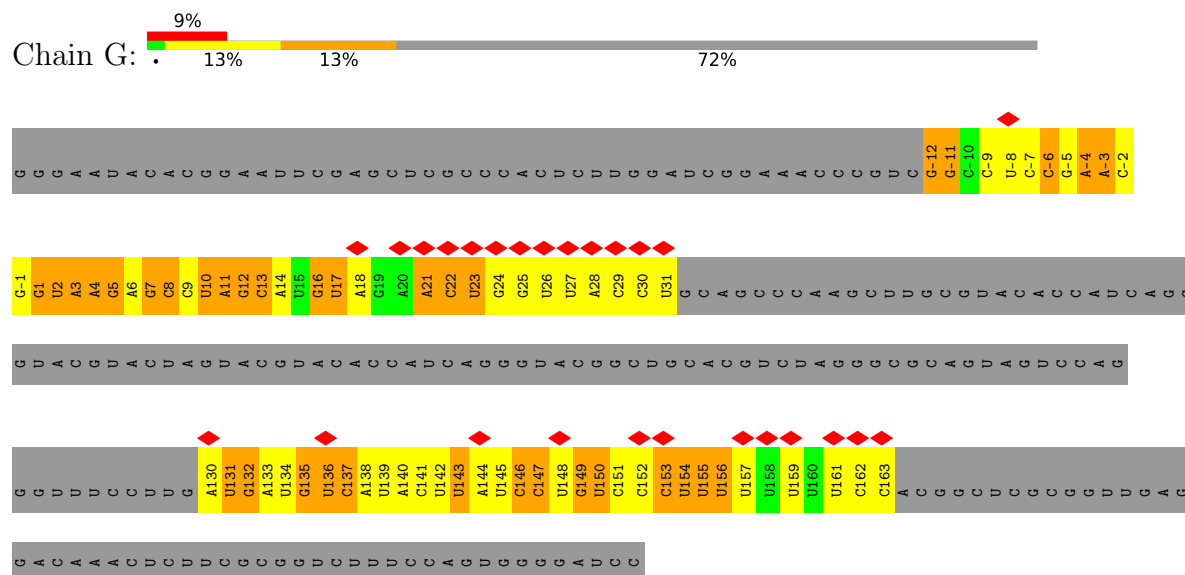
Chain n:

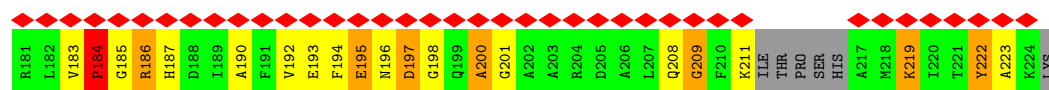


Chain F:

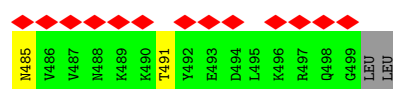
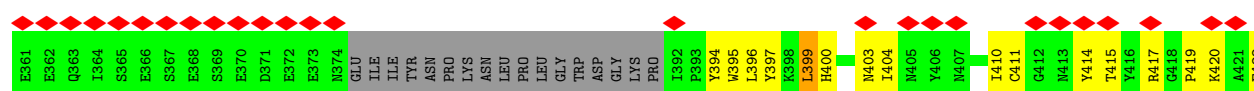
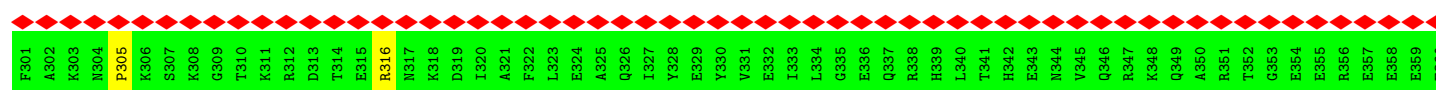
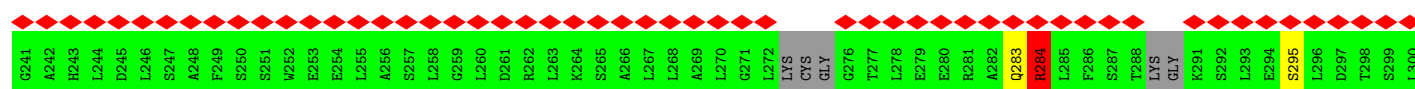
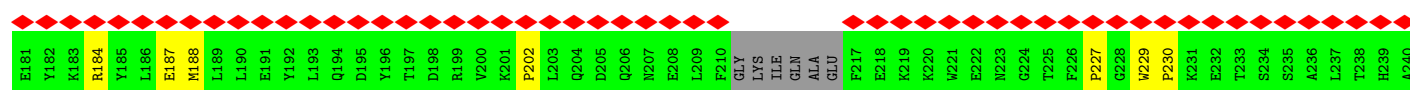
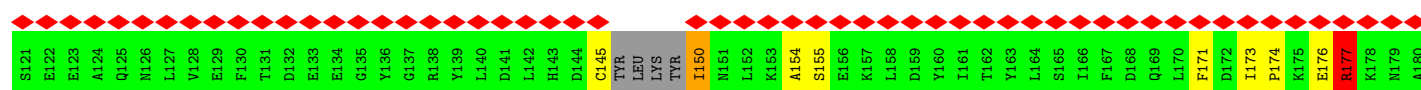
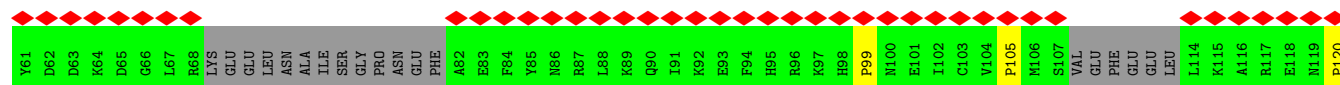
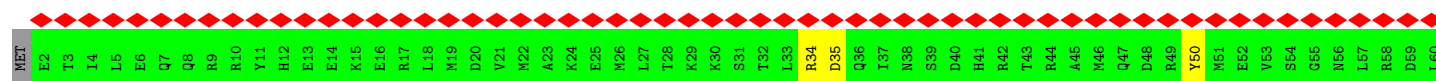
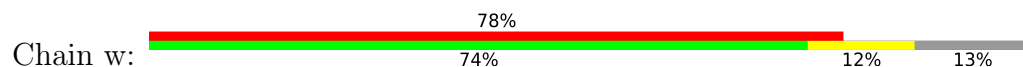


Chain G:

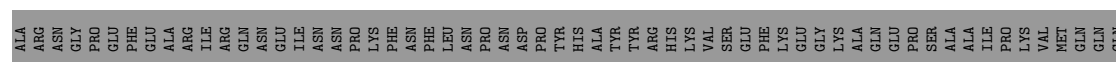
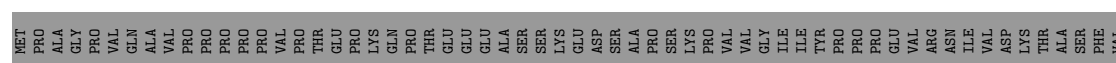




• Molecule 18: Splicing factor 3A subunit 3



• Molecule 19: Splicing factor 3A subunit 1



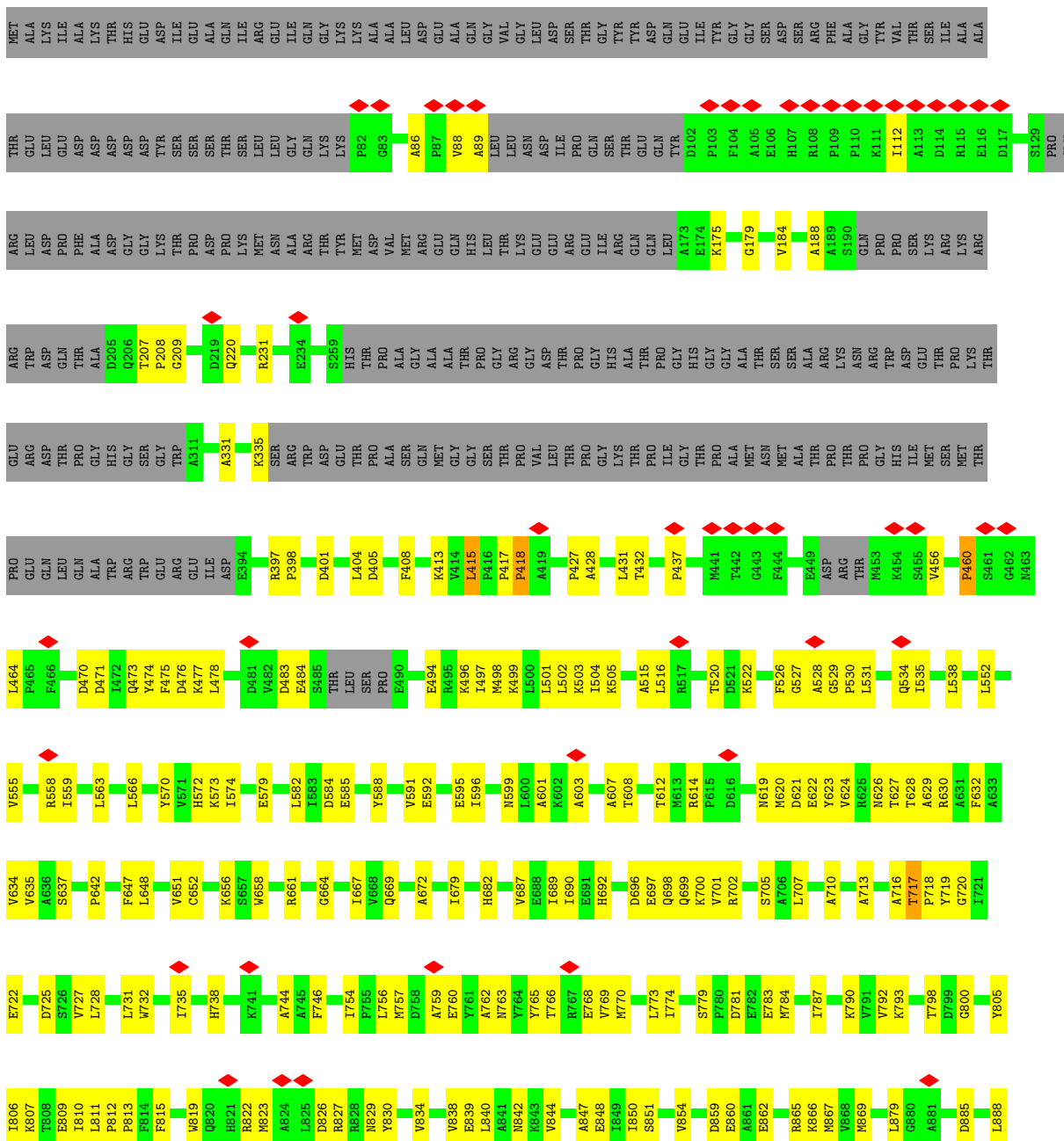
ILE	HIS	LEU	LEU	ALA	GLY	VAL	GLN	VAL	PHE	GLY	THR	GLN	HIS	VAL	PRO	MET	LYS	THR	GLU	THR	GLU	ALA	PRO	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU</
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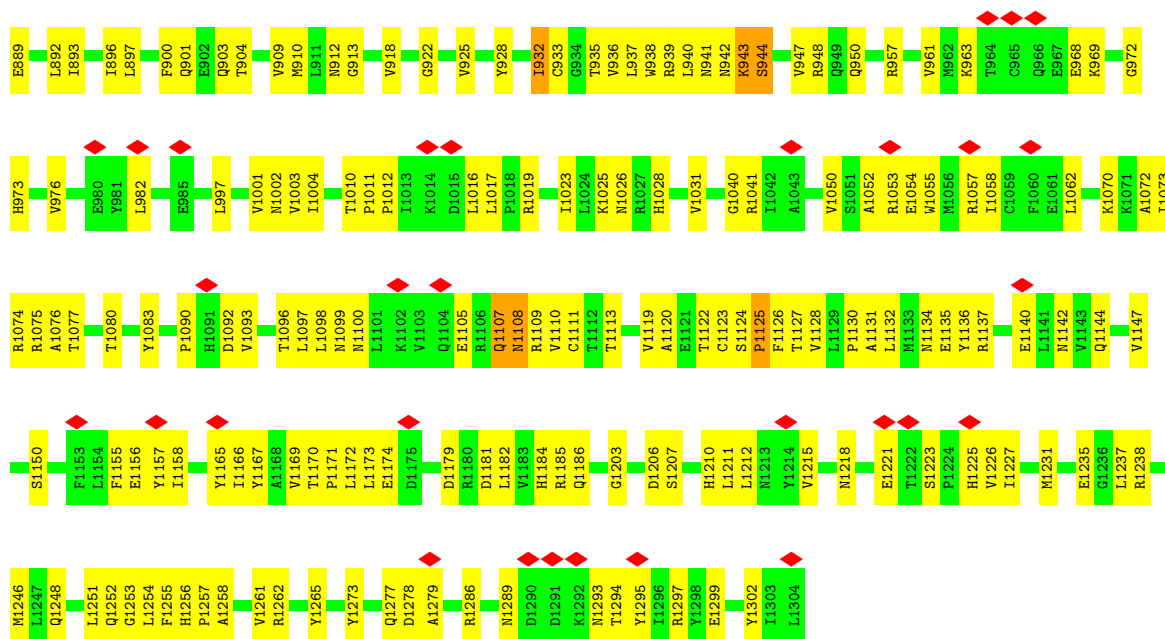
● Molecule 20: Splicing factor 3A subunit 2



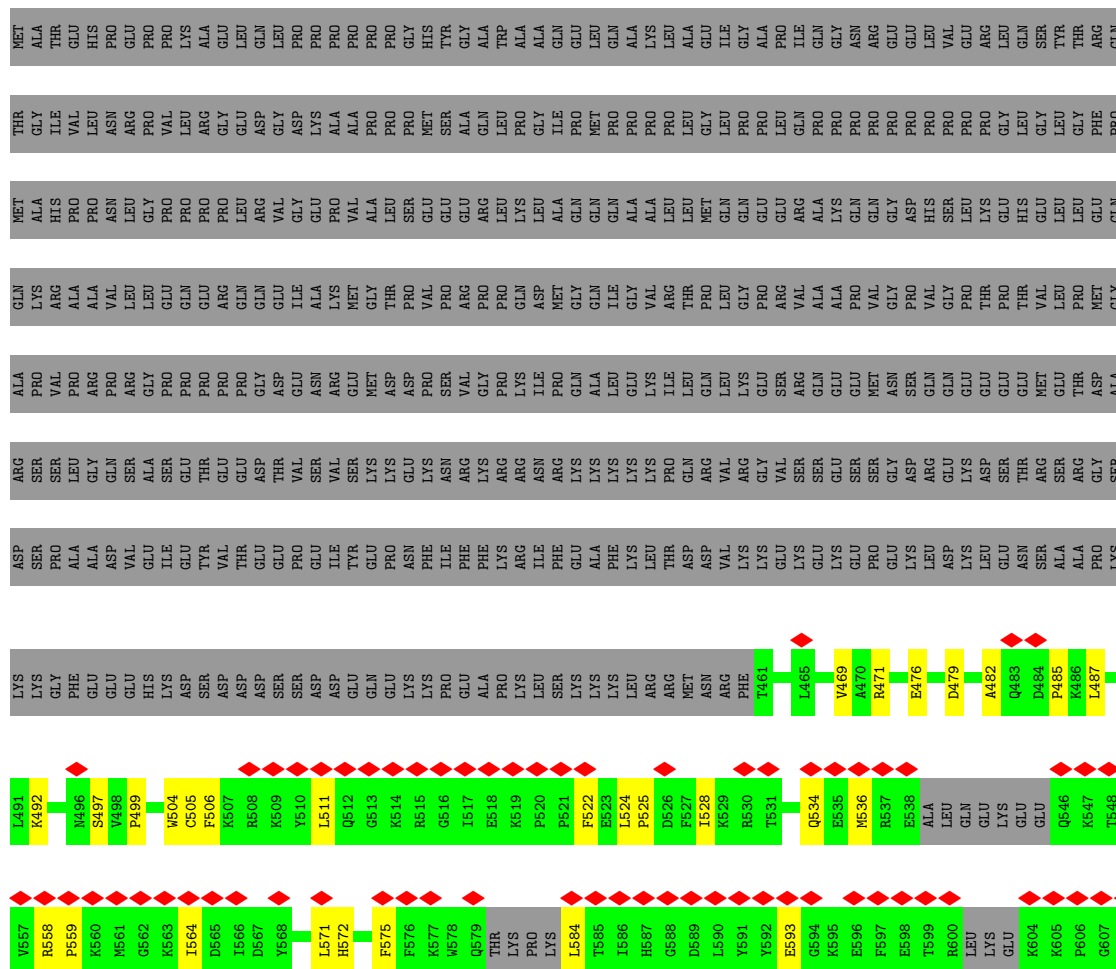
MET	ASP	PHE	GLN	HIS	ARG	PRO	GLY	LYS	THR	GLY	GLY	VAL	ALA	SER	SER	SER	GLU	ASN	ALA	ARG	ASP	ARG	GLU	ARG	LEU	ALA	LEU	THR	THR	ILE	ASP	ILE	ASN	LYS	ASP	PRO	PRO	TYR	PHE	MET	LYS	ASN	HIS	LEU	GLY	SER	TYR	GLU	LYS	CYS	LEU	CYS	LEU							
THR	LEU	HIS	ASN	ASN	GLU	GLY	SER	TYR	LEU	ALA	HIS	THR	GLN	GLY	GLY	LYS	LYS	ASN	LEU	ALA	ARG	ALA	LYS	GLU	LYS	ALA	GLU	GLN	PRO	PRO	ALA	ALA	LYS	VAL	VAL	VAL	VAL	VAL	LYS	LYS	PHE	VAL	LYS	ILE	GLY	SER	TYR	GLU	R114	P115	G116	Y117	K118	W119	T120					
	K121	Q122	R123	D124	S125	E126	M127	G128	Q129	Q130	S131	LEU	PHE	GLN	ILE	ASP	Y138	P139	E140	T141	A142	GLU	GLY	ILE	M146	P147	R148	H149	R150	F151	M152	S153	A154	Y155	E156	Q157	R158	ILE	GLU	PRO	D162	D163	R164	R165	W166	Q167	Y168	L169	Y170	M171	A172	A173	E174	P175	Y176	E177	T178	Y179	A180	
F181	K182	V183	P184	S185	R186	E187	I188	D189	K190	A191	E192	G193	K194	F195	W196	T197	H198	W199	N200	R201	E202	T203	K204	Q205	F206	F207	L208	Q209	F210	H211	F212	K213	M214	E215	K216	P217	P218	A219	P220	P221	S222	L223	PRO	ALA	GLY	PRO	PRO	PRO	GLY	VAL	LYS	ARG	PRO	PRO	PRO	PRO	LEU	MET	ASN	GLY

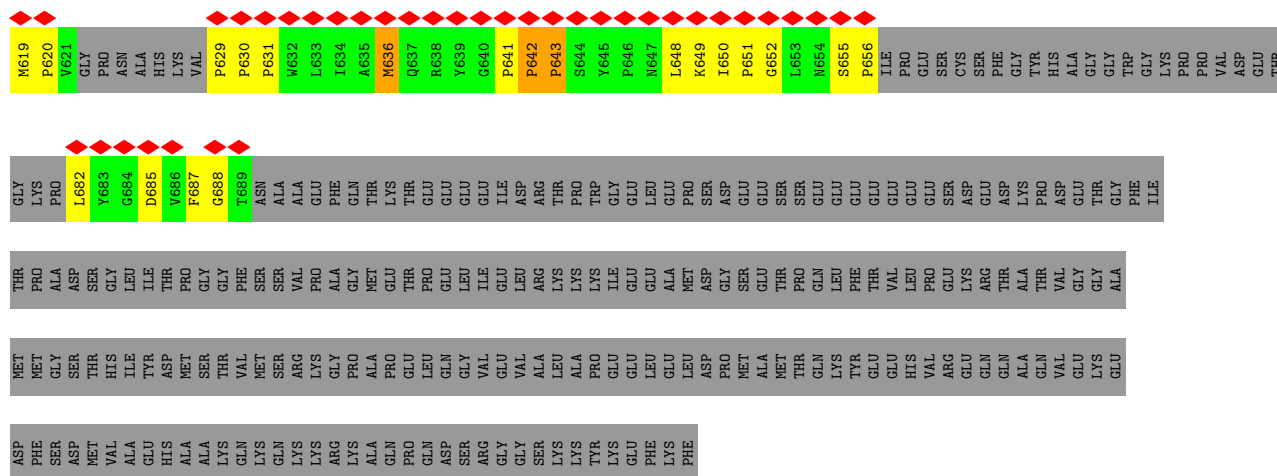
- Molecule 21: Splicing factor 3B subunit 1



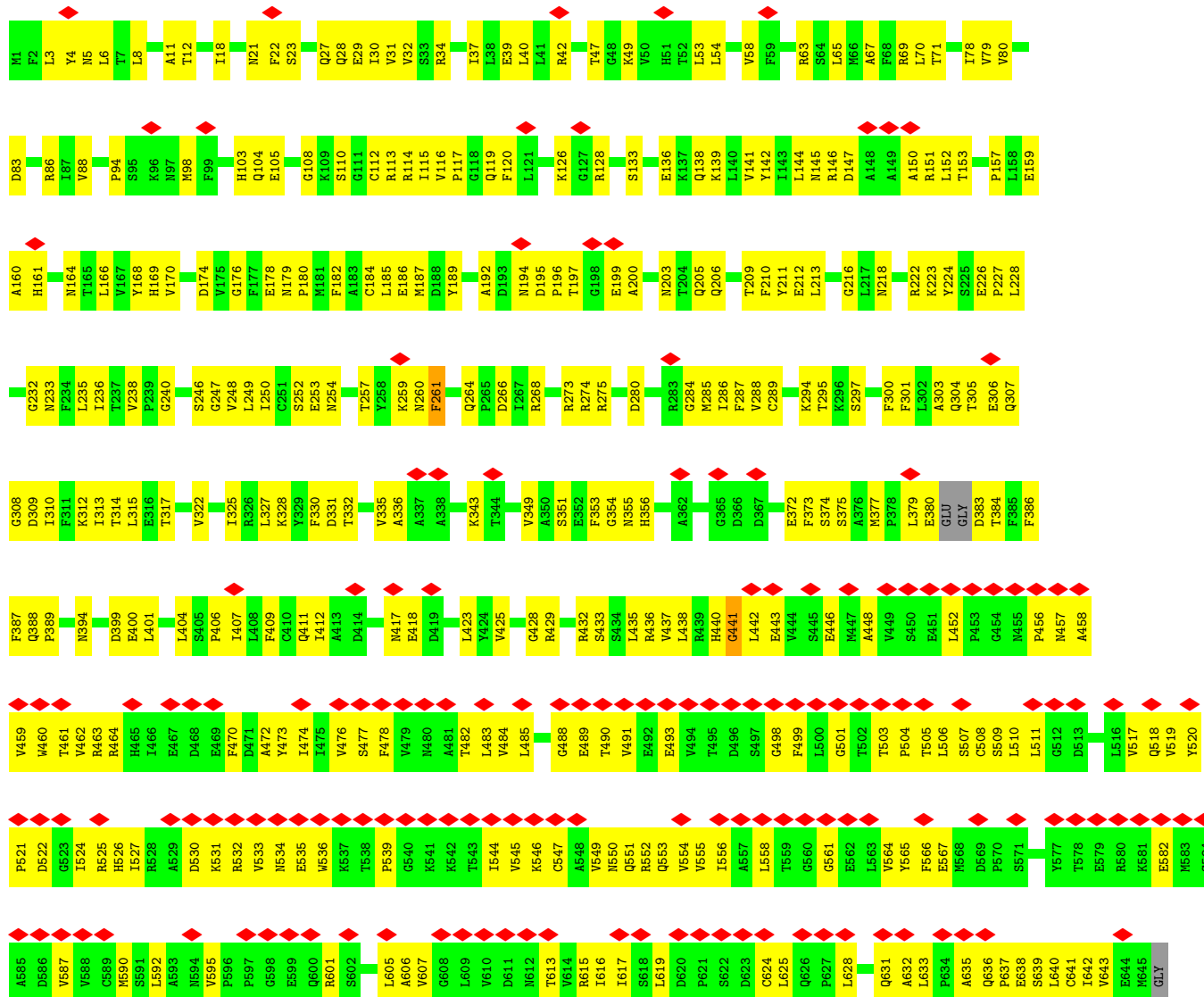


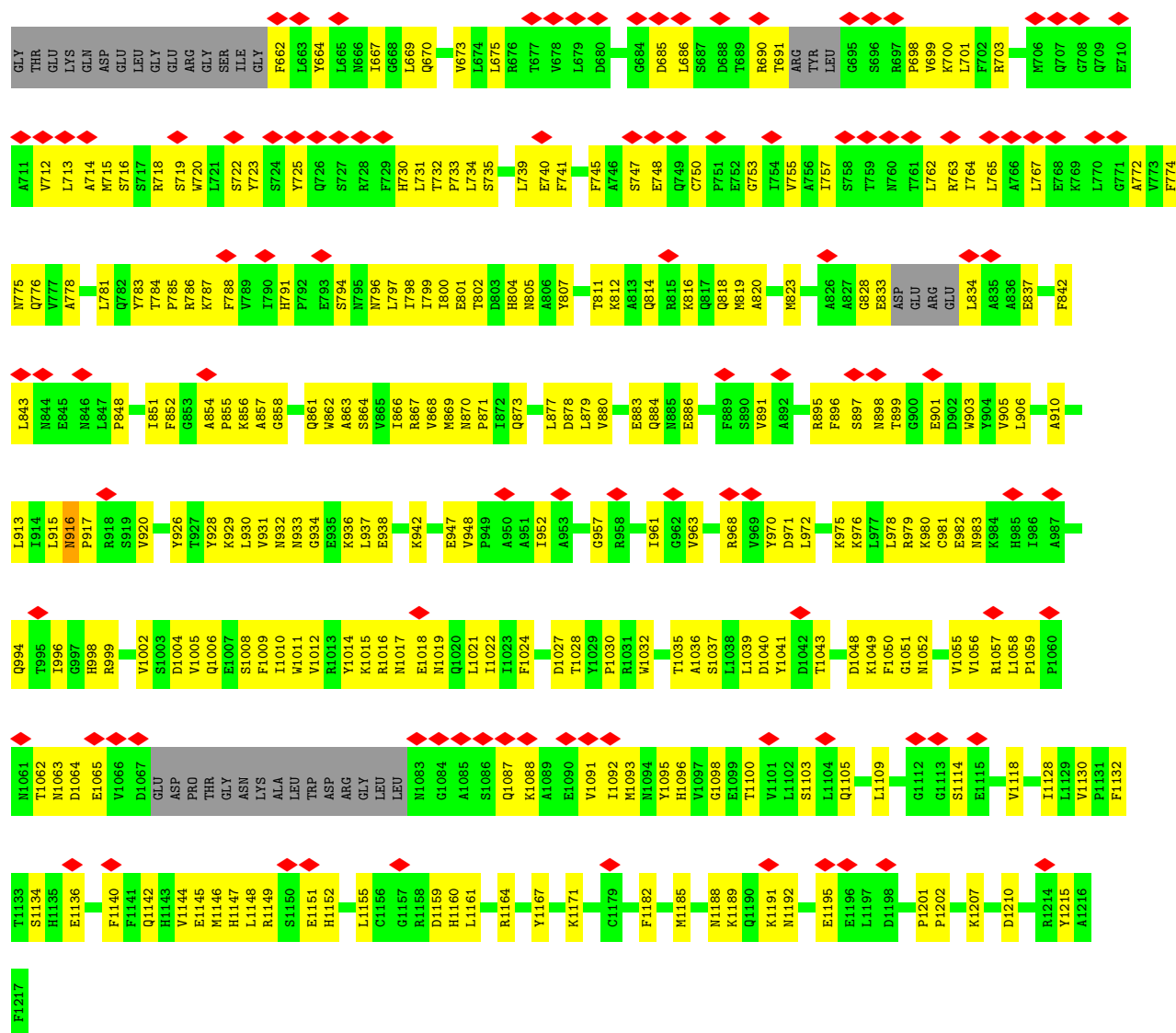
• Molecule 22: Splicing factor 3B subunit 2



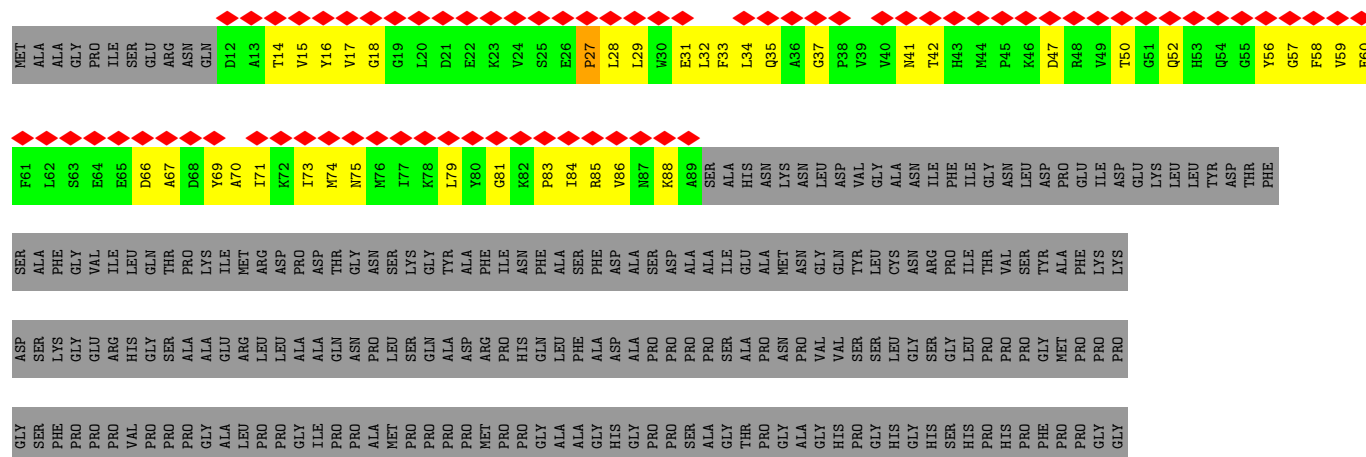


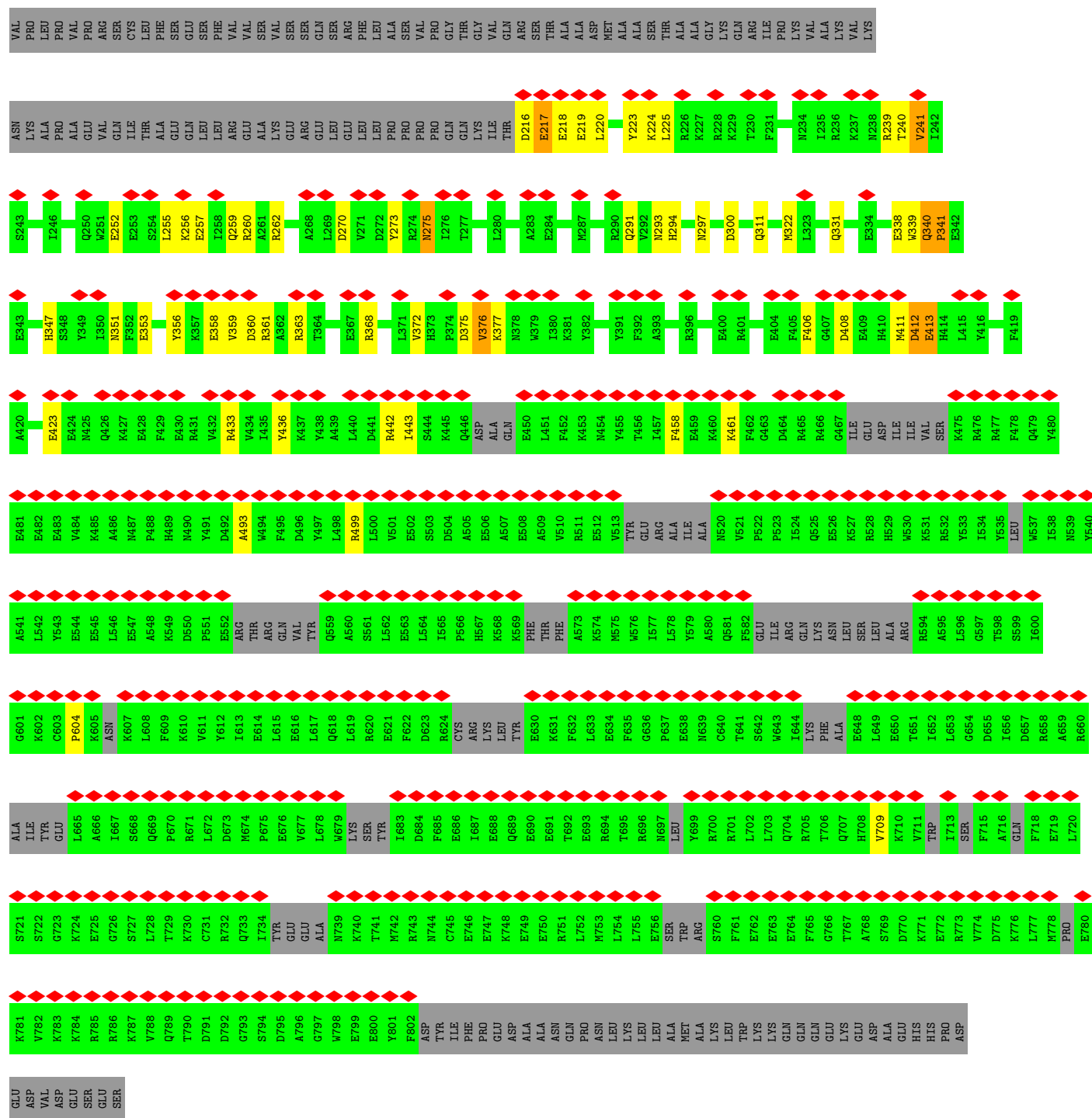
• Molecule 23: Splicing factor 3B subunit 3



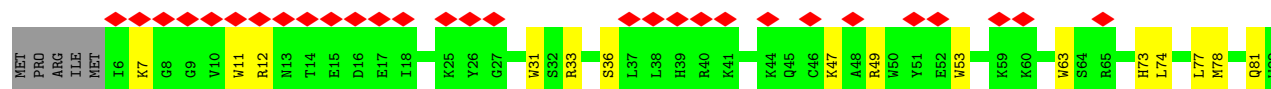


• Molecule 24: Splicing factor 3B subunit 4





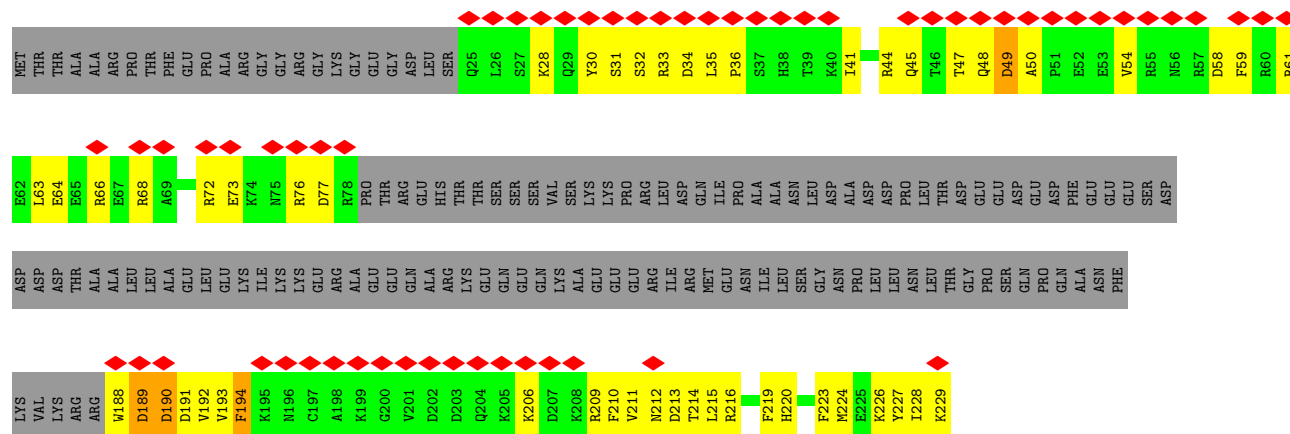
• Molecule 29: Cell division cycle 5-like protein



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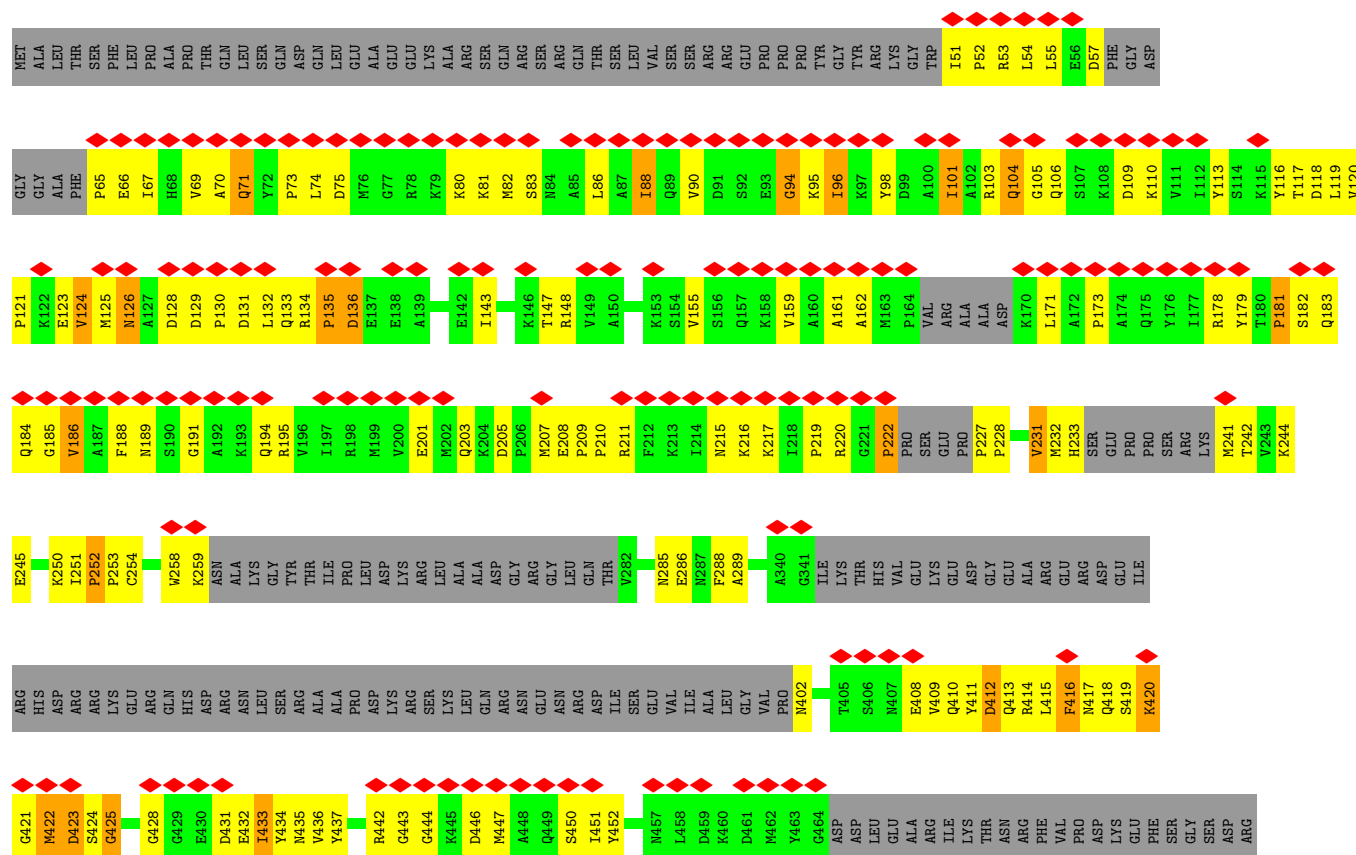
• Molecule 31: Spliceosome-associated protein CWC15 homolog

Chain P: 26% 20% 21% 58%

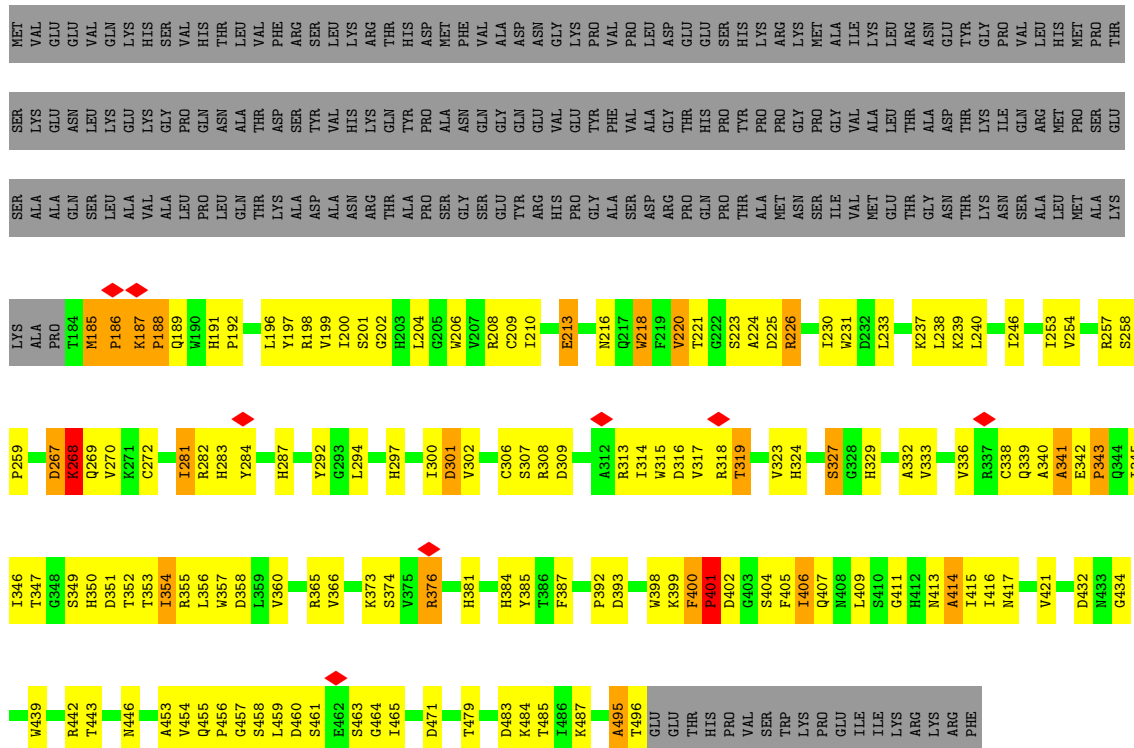
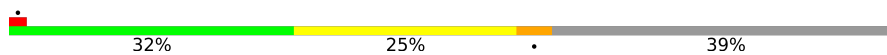


• Molecule 32: Skip

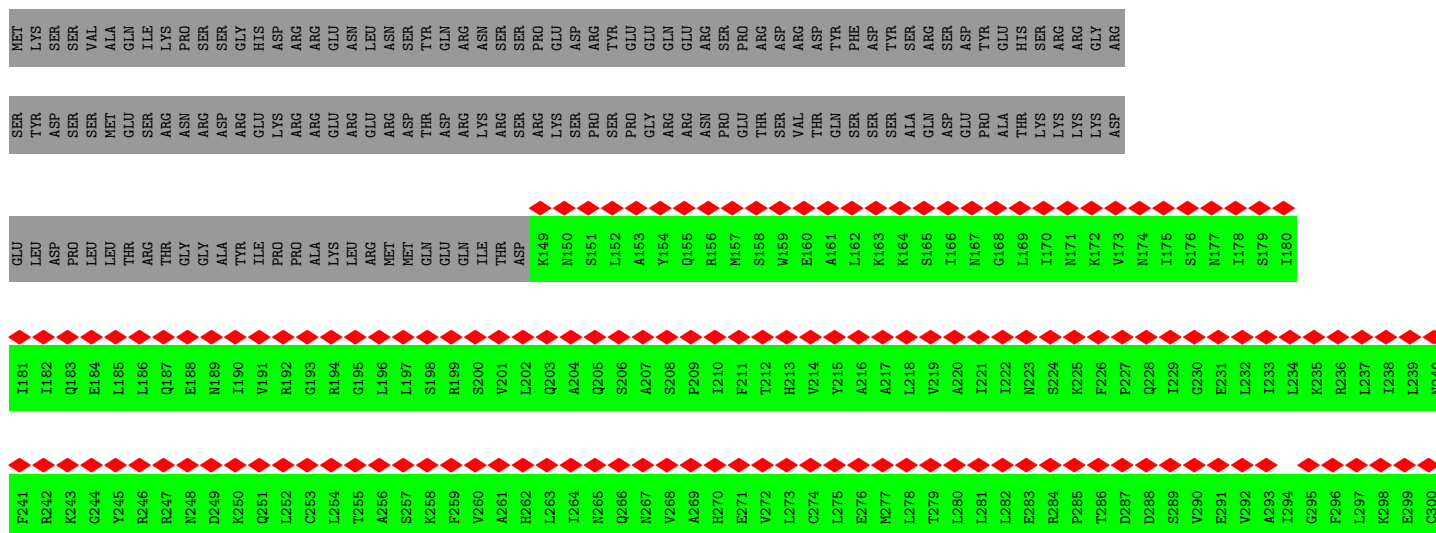
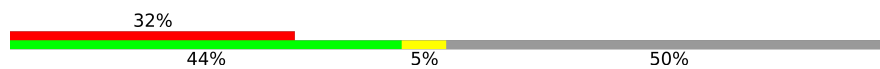
Chain R: 29% 31% 23% 43%



Chain T:

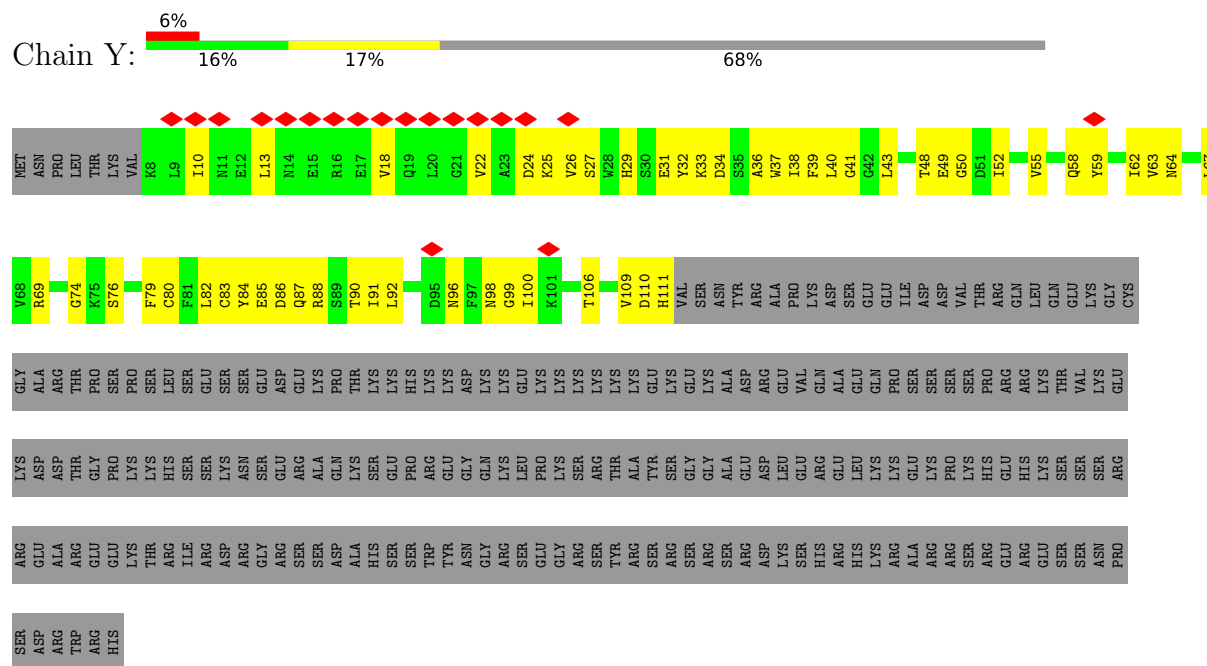


Chain V:

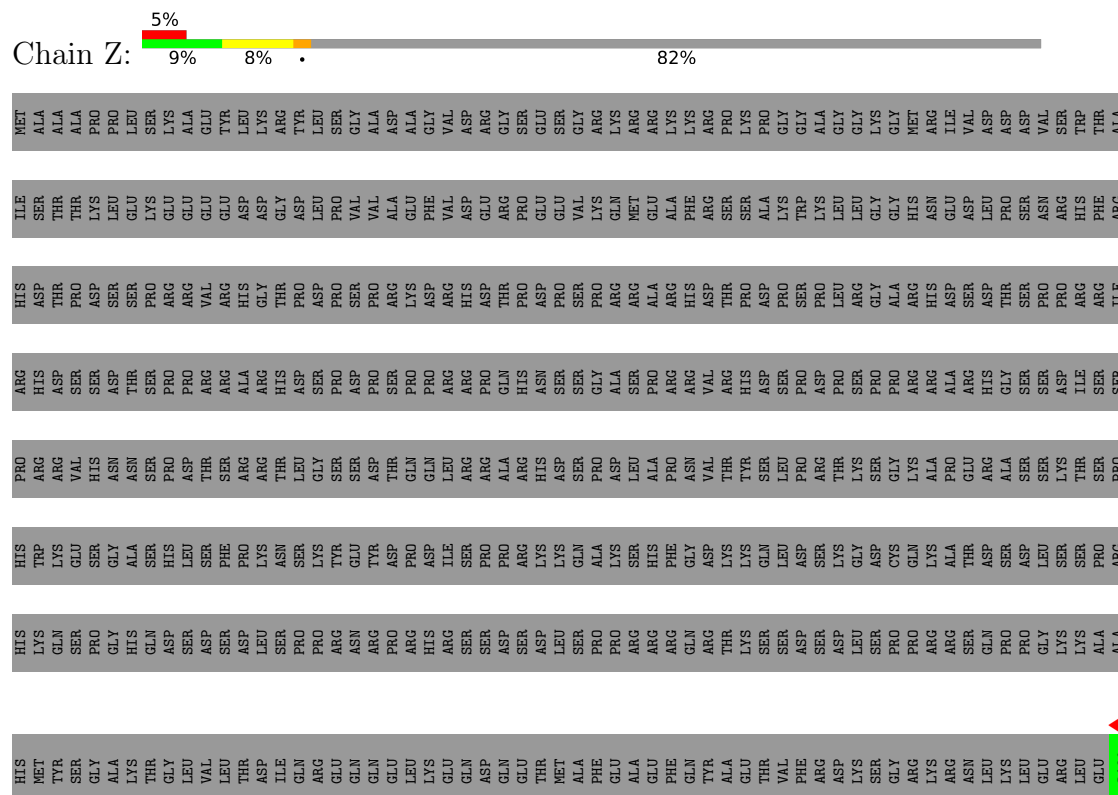




- Molecule 36: RNA-binding motif protein, X-linked 2

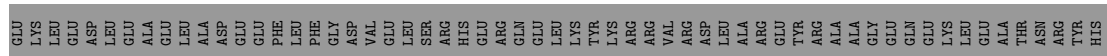


- Molecule 37: BUD13 homolog





Chain z: 13% 29% 9% 62%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96523	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 ($e^-/\text{\AA}^2$)	48	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	0.184	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0346	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: IHP, ZN, GTP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.84	40/18665 (0.2%)	0.96	56/25340 (0.2%)
2	B	0.66	1/1970 (0.1%)	0.93	6/3060 (0.2%)
3	C	1.08	13/6864 (0.2%)	1.27	40/9334 (0.4%)
4	D	0.55	0/8527	1.11	27/11887 (0.2%)
5	E	0.87	0/2392	1.00	6/3242 (0.2%)
6	a	0.77	0/397	0.99	0/549
6	h	0.77	0/391	0.99	0/540
7	b	0.83	0/404	1.12	2/561 (0.4%)
7	i	0.84	0/421	1.15	3/583 (0.5%)
8	c	0.88	0/405	1.11	0/563
8	j	0.87	0/405	1.11	0/563
9	d	1.12	0/479	1.25	1/666 (0.2%)
9	k	1.14	0/420	1.23	1/583 (0.2%)
10	f	1.20	0/360	1.25	0/497
10	m	1.21	1/360 (0.3%)	1.25	0/497
11	e	1.03	0/390	1.24	1/542 (0.2%)
11	l	1.02	0/390	1.23	0/542
12	g	0.86	0/362	1.08	1/501 (0.2%)
12	n	0.85	0/332	1.08	1/458 (0.2%)
13	F	0.35	0/2224	0.66	5/3462 (0.1%)
14	G	0.25	0/1717	0.54	0/2664
15	H	0.51	7/3217 (0.2%)	0.77	8/4997 (0.2%)
16	o	0.93	0/803	2.15	35/1119 (3.1%)
17	p	1.60	3/810 (0.4%)	2.10	25/1122 (2.2%)
18	w	0.62	6/2376 (0.3%)	0.99	14/3269 (0.4%)
19	u	0.36	0/519	0.95	3/717 (0.4%)
20	v	0.50	2/482 (0.4%)	1.16	8/666 (1.2%)
21	1	0.27	0/7826	0.61	3/10617 (0.0%)
22	2	0.59	4/1277 (0.3%)	0.92	9/1724 (0.5%)
23	3	0.23	0/9408	0.57	6/12767 (0.0%)
24	4	1.08	2/535 (0.4%)	1.28	5/724 (0.7%)
25	5	0.20	0/823	0.53	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	6	0.20	0/678	0.59	0/909
27	7	0.22	0/556	0.49	0/751
28	J	0.80	1/3500 (0.0%)	1.13	3/4750 (0.1%)
29	L	0.47	0/1103	0.71	0/1487
30	M	0.20	0/272	0.57	0/363
31	P	0.98	0/841	1.27	4/1117 (0.4%)
32	R	0.85	7/2351 (0.3%)	1.14	10/3163 (0.3%)
33	T	1.44	13/2522 (0.5%)	1.42	26/3438 (0.8%)
34	V	0.89	1/2234 (0.0%)	1.17	2/3111 (0.1%)
35	X	0.21	0/1011	0.57	0/1348
36	Y	0.24	0/747	0.58	0/1006
37	Z	0.65	6/772 (0.8%)	1.11	9/1056 (0.9%)
38	z	0.21	0/1414	0.54	0/1916
39	x	0.59	1/2871 (0.0%)	0.82	11/3981 (0.3%)
All	All	0.74	108/96823 (0.1%)	0.99	331/133875 (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	7
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1
30	M	0	1
32	R	0	1
33	T	0	2
35	X	0	1
All	All	0	33

The worst 5 of 108 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	387	ASP	CA-C	-8.61	1.48	1.52
17	p	156	ASN	C-N	-8.31	1.22	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	316	PHE	C-N	-8.15	1.25	1.34
1	A	483	GLN	CA-C	-7.71	1.43	1.52
33	T	353	THR	CA-C	-7.66	1.43	1.52

The worst 5 of 331 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	T	187	LYS	CA-C-N	13.13	132.89	119.76
33	T	187	LYS	C-N-CA	13.13	132.89	119.76
24	4	83	PRO	CA-CB-CG	10.35	124.17	104.50
2	B	104	C	C2'-C3'-O3'	-9.92	94.61	109.50
31	P	189	ASP	N-CA-C	-9.51	100.67	112.47

There are no chirality outliers.

5 of 33 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	697	MET	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18165	0	17930	1570	0
2	B	1768	0	897	124	0
3	C	6716	0	6691	991	0
4	D	8528	0	3745	72	0
5	E	2338	0	2272	138	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	10	0
8	c	406	0	170	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	j	406	0	170	0	0
9	d	480	0	200	2	0
9	k	422	0	175	2	0
10	f	361	0	158	1	0
10	m	361	0	158	0	0
11	e	391	0	163	3	0
11	l	391	0	163	1	0
12	g	363	0	160	1	0
12	n	334	0	143	3	0
13	F	1988	0	1005	132	0
14	G	1545	0	786	130	0
15	H	2886	0	1463	261	0
16	o	804	0	350	9	0
17	p	813	0	366	14	0
18	w	2369	0	1298	97	0
19	u	525	0	216	0	0
20	v	486	0	206	3	0
21	1	7702	0	7389	304	0
22	2	1252	0	1040	59	0
23	3	9220	0	9139	520	0
24	4	527	0	438	41	0
25	5	807	0	729	28	0
26	6	670	0	654	21	0
27	7	540	0	509	24	0
28	J	3463	0	2544	115	0
29	L	1077	0	1067	57	0
30	M	267	0	225	24	0
31	P	829	0	814	195	0
32	R	2314	0	2189	412	0
33	T	2457	0	2416	253	0
34	V	2238	0	969	51	0
35	X	1012	0	731	18	0
36	Y	737	0	608	67	0
37	Z	755	0	591	156	0
38	z	1381	0	1298	29	0
39	x	2882	0	1308	23	0
40	A	36	0	6	0	0
41	C	32	0	12	11	0
42	C	1	0	0	0	0
42	F	5	0	0	0	0
43	6	3	0	0	0	0
43	M	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	94673	0	74251	4761	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 28.

The worst 5 of 4761 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)
36:Y:37:TRP:CH2	37:Z:498:GLY:HA2	1.23	1.65
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.57
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
3:C:77:VAL:HG11	33:T:196:LEU:CG	1.39	1.52

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2186/2335 (94%)	2036 (93%)	117 (5%)	33 (2%)	8	38
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5	28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	43	77
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100	100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	9	41
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	10
18	w	419/501 (84%)	379 (90%)	37 (9%)	3 (1%)	18	55
19	u	93/793 (12%)	87 (94%)	4 (4%)	2 (2%)	5	28
20	v	90/464 (19%)	67 (74%)	16 (18%)	7 (8%)	1	10
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	21	58
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1086 (93%)	78 (7%)	1 (0%)	48	83
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	9	41
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	39
29	L	128/802 (16%)	119 (93%)	8 (6%)	1 (1%)	16	52
30	M	34/343 (10%)	30 (88%)	3 (9%)	1 (3%)	3	23
31	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	28
32	R	295/540 (55%)	249 (84%)	31 (10%)	15 (5%)	1	15
33	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	18
34	V	443/908 (49%)	412 (93%)	26 (6%)	5 (1%)	11	45
35	X	142/396 (36%)	131 (92%)	11 (8%)	0	100	100
36	Y	102/322 (32%)	91 (89%)	11 (11%)	0	100	100
37	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	z	176/472 (37%)	170 (97%)	6 (3%)	0	100	100
39	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	14	49
All	All	12632/20929 (60%)	11667 (92%)	812 (6%)	153 (1%)	13	42

5 of 153 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	38 (41%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	21 (25%)	10 (12%)
All	All	379/686 (55%)	140 (36%)	35 (9%)

5 of 140 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
14	G	151	C

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Mol	Chain	Res	Type
14	G	153	C
15	H	46	U
13	F	25	C
13	F	7	G

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 12 ligands modelled in this entry, 10 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	$\# Z > 2$
41	GTP	C	1500	42	33,34,34	1.45	5 (15%)	50,54,54	2.04	10 (20%)
40	IHP	A	3000	-	36,36,36	1.04	2 (5%)	60,60,60	1.74	15 (25%)

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
41	GTP	C	1500	42	-	8/22/38/38	0/3/3/3
40	IHP	A	3000	-	-	6/30/54/54	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	C	1500	GTP	C5-N7	-3.76	1.31	1.39
41	C	1500	GTP	C6-N1	-3.32	1.32	1.38
41	C	1500	GTP	PA-O3A	3.16	1.62	1.59
40	A	3000	IHP	P5-O45	-2.95	1.43	1.54
40	A	3000	IHP	P2-O12	2.73	1.64	1.59

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	C	1500	GTP	C5-C4-N3	-7.07	117.14	128.39
41	C	1500	GTP	C2-N3-C4	5.94	122.54	112.30
41	C	1500	GTP	N9-C4-N3	5.74	137.44	125.95
40	A	3000	IHP	O35-P5-O15	-4.53	88.19	105.85
40	A	3000	IHP	O45-P5-O35	4.13	123.30	107.80

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

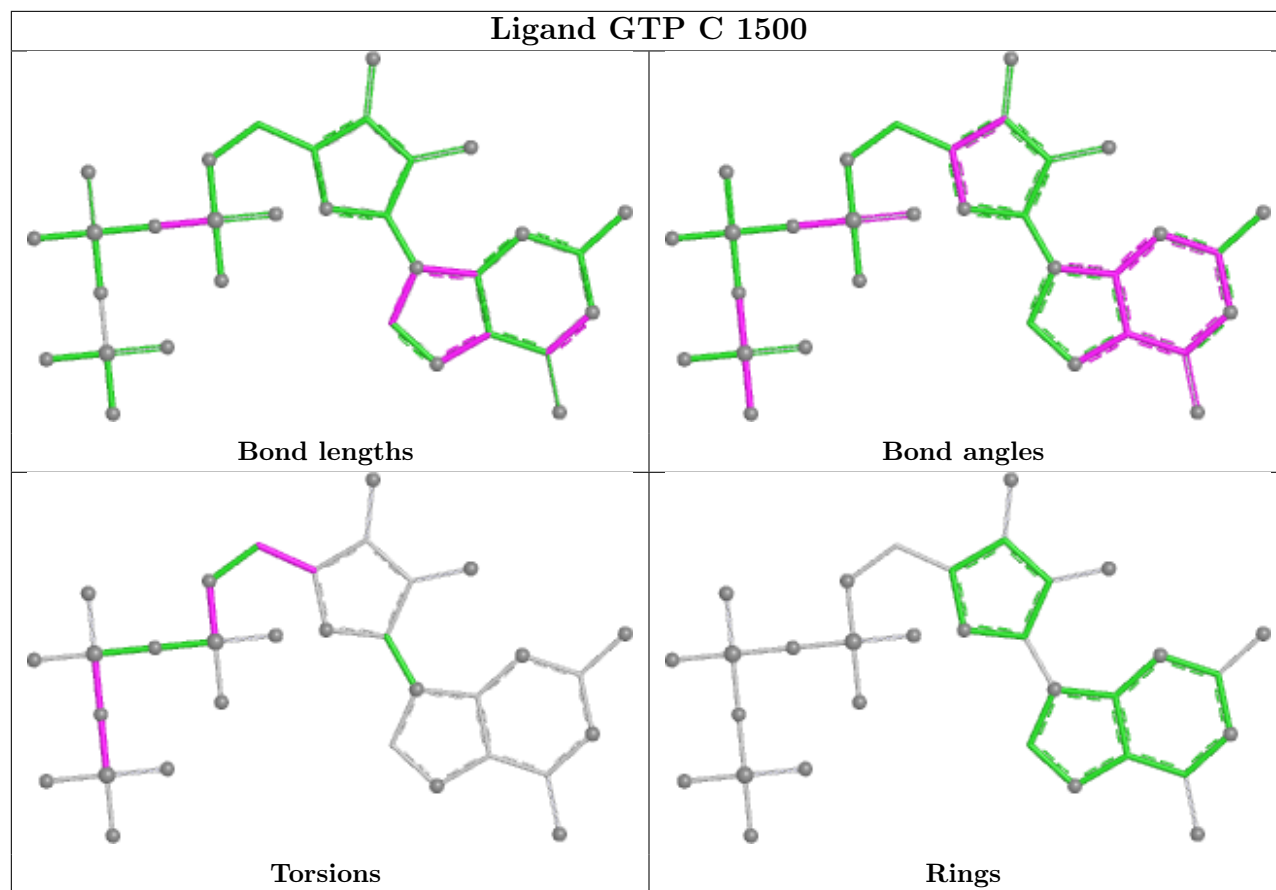
Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C4-C5-O15-P5
40	A	3000	IHP	C6-C5-O15-P5
41	C	1500	GTP	PB-O3B-PG-O3G
41	C	1500	GTP	C5'-O5'-PA-O1A
41	C	1500	GTP	C5'-O5'-PA-O2A

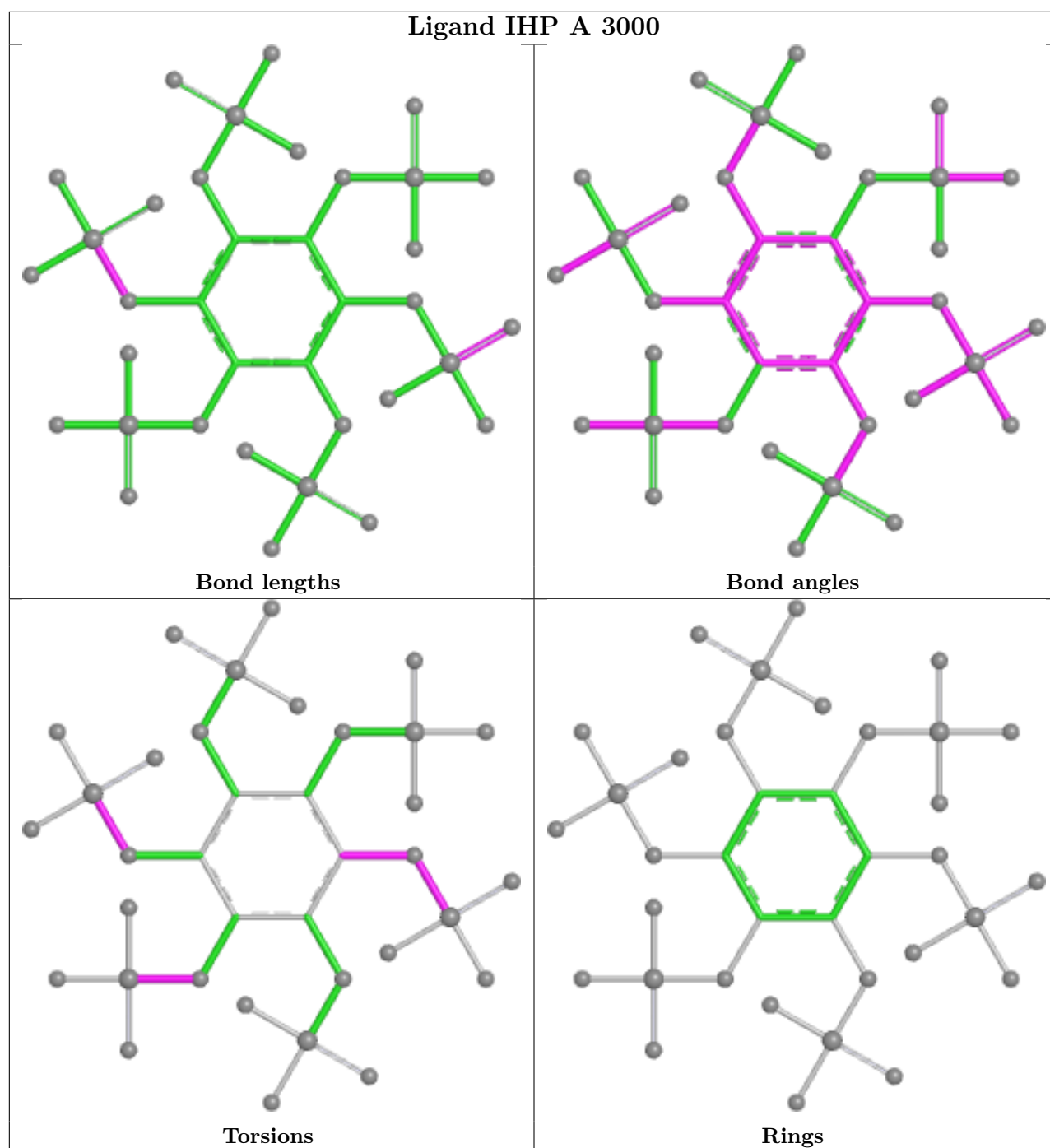
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	C	1500	GTP	11	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.

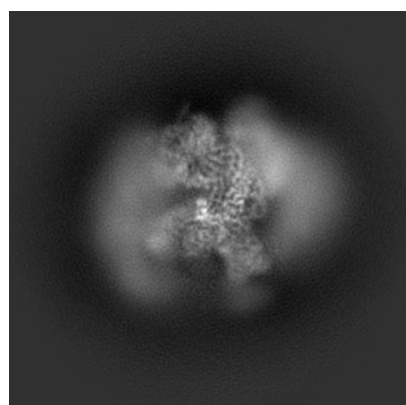
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6891. These allow visual inspection of the internal detail of the map and identification of artifacts.

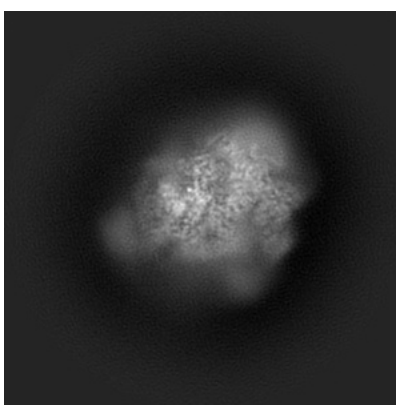
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

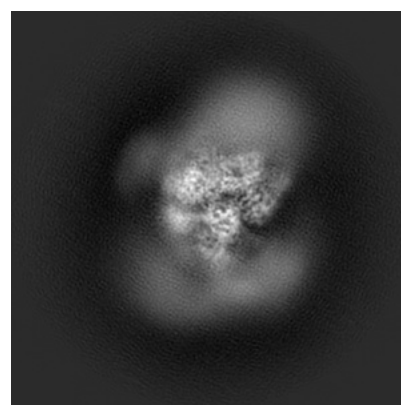
6.1.1 Primary map



X



Y

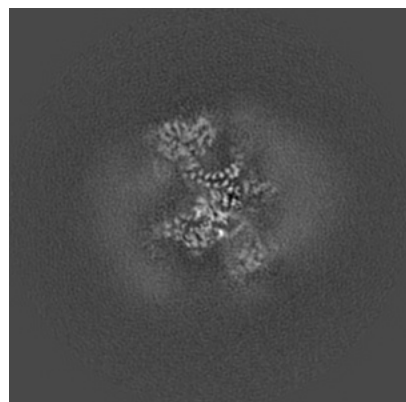


Z

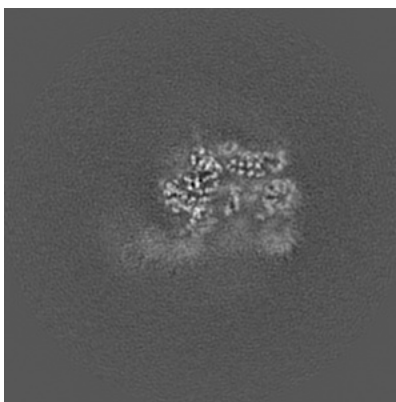
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

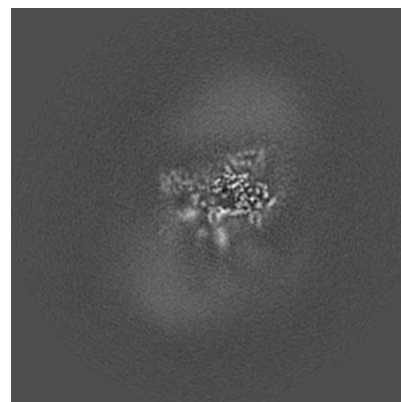
6.2.1 Primary map



X Index: 200



Y Index: 200

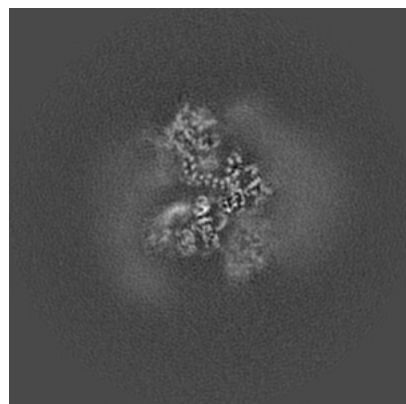


Z Index: 200

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

6.3 Largest variance slices [i](#)

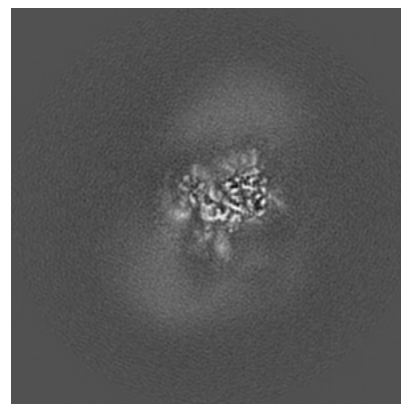
6.3.1 Primary map



X Index: 210



Y Index: 195

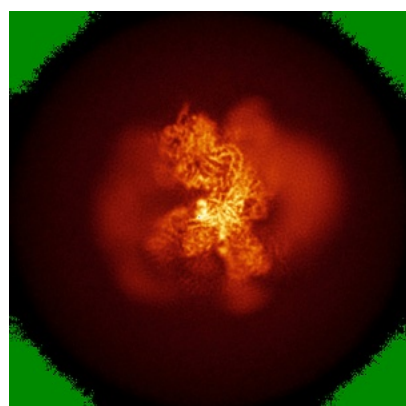


Z Index: 193

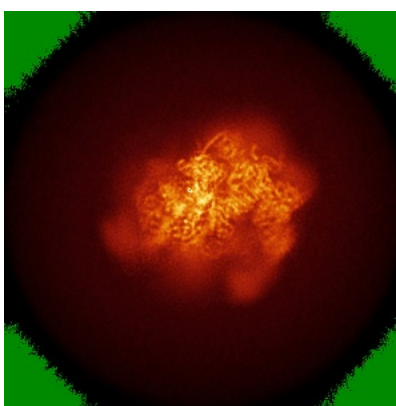
The images above show the largest variance slices of the map in three orthogonal directions.

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

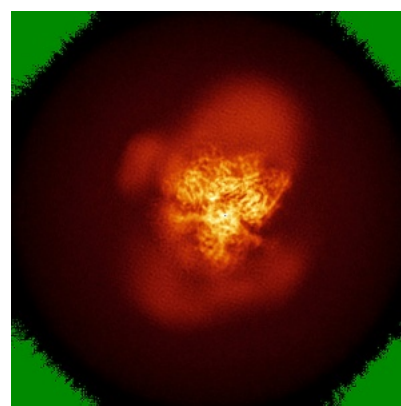
6.4.1 Primary map



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 0.0346. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

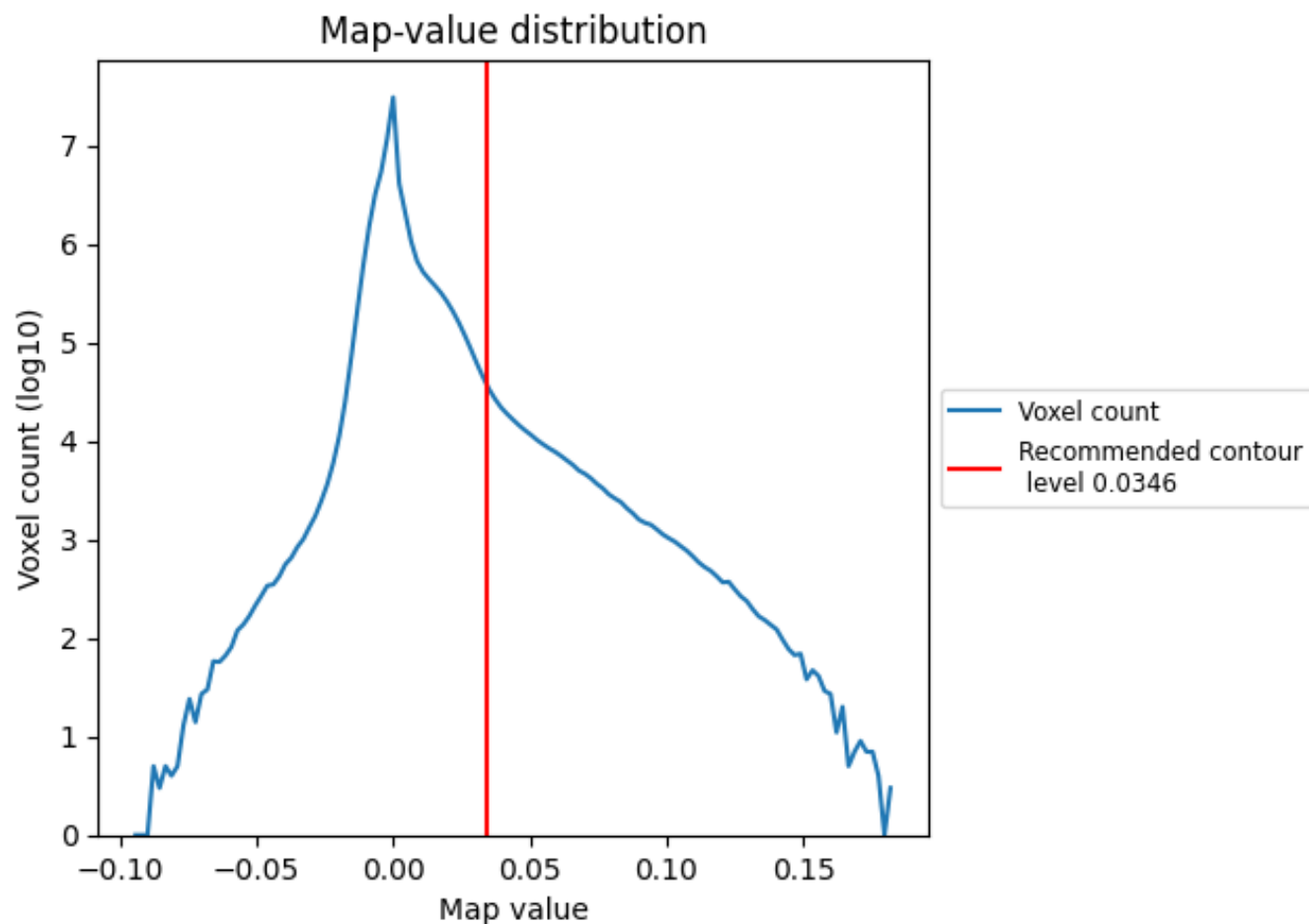
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

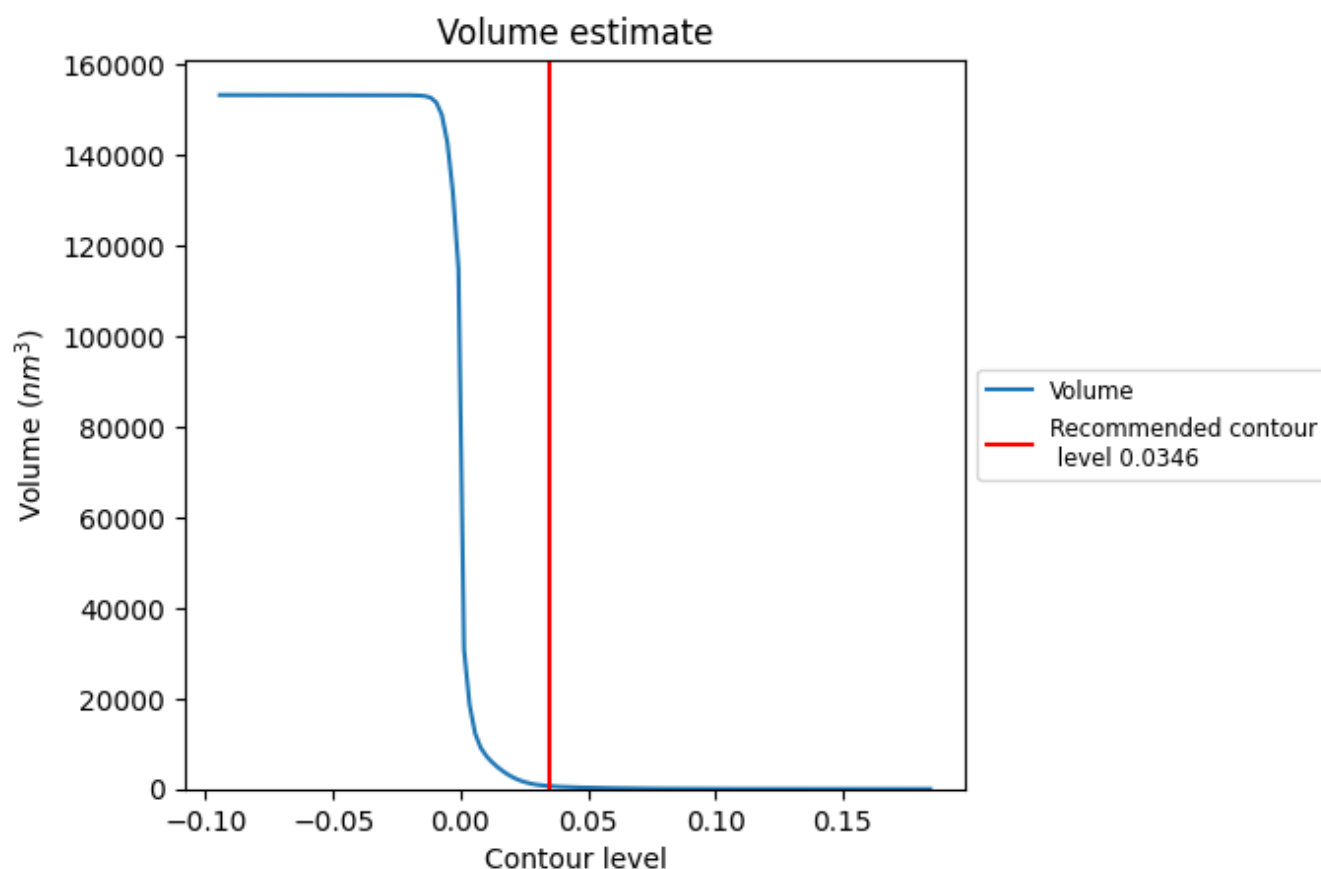
This section contains the results of statistical analysis of the map.

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.

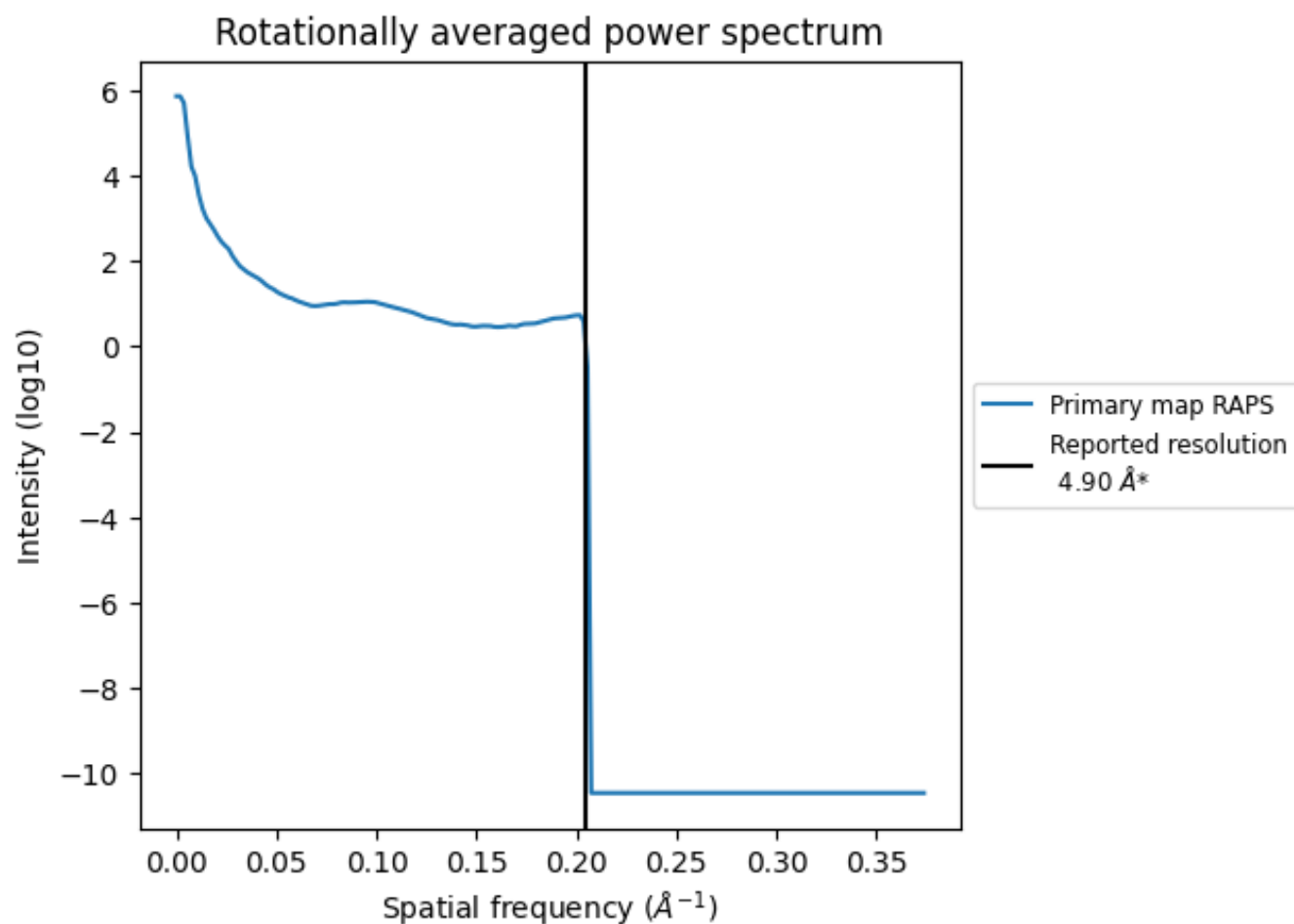
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 642 nm^3 ; this corresponds to an approximate mass of 580 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 0.204 Å⁻¹

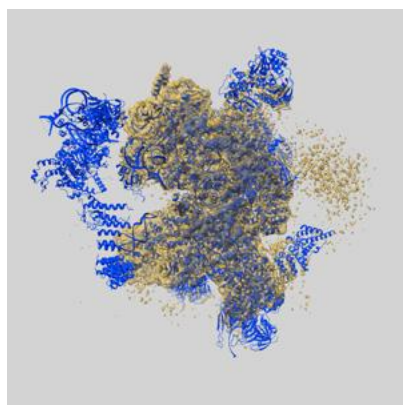
8 Fourier-Shell correlation

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

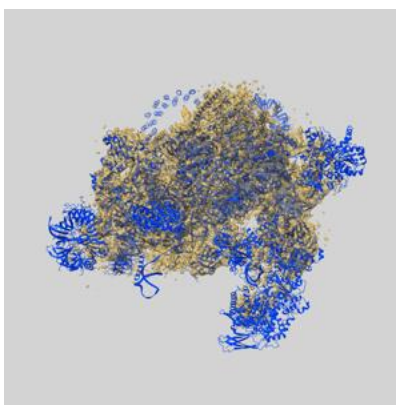
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6891 and PDB model 5Z58. Per-residue inclusion information can be found in section 3 on page 13.

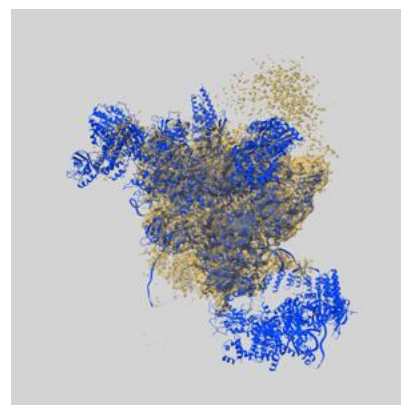
9.1 Map-model overlay [i](#)



X



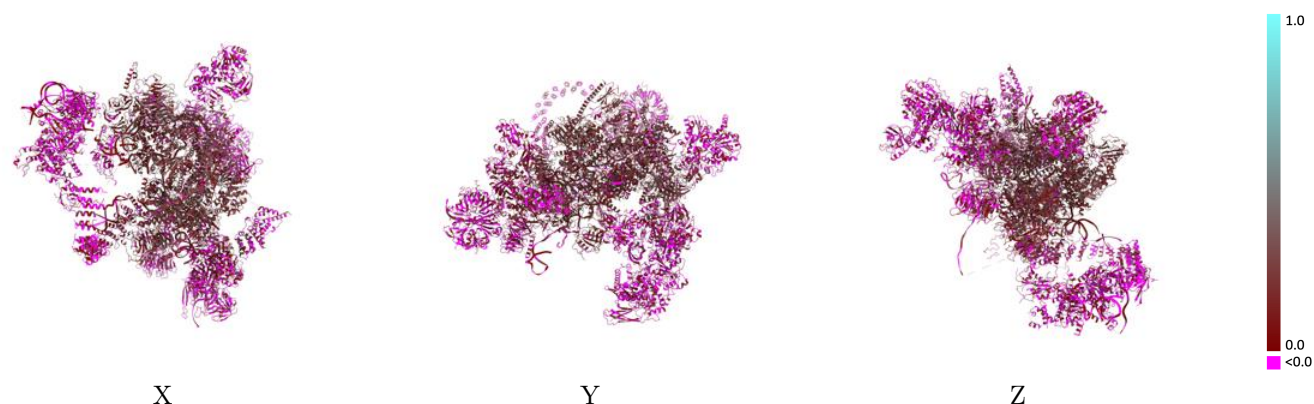
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0346 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](#)

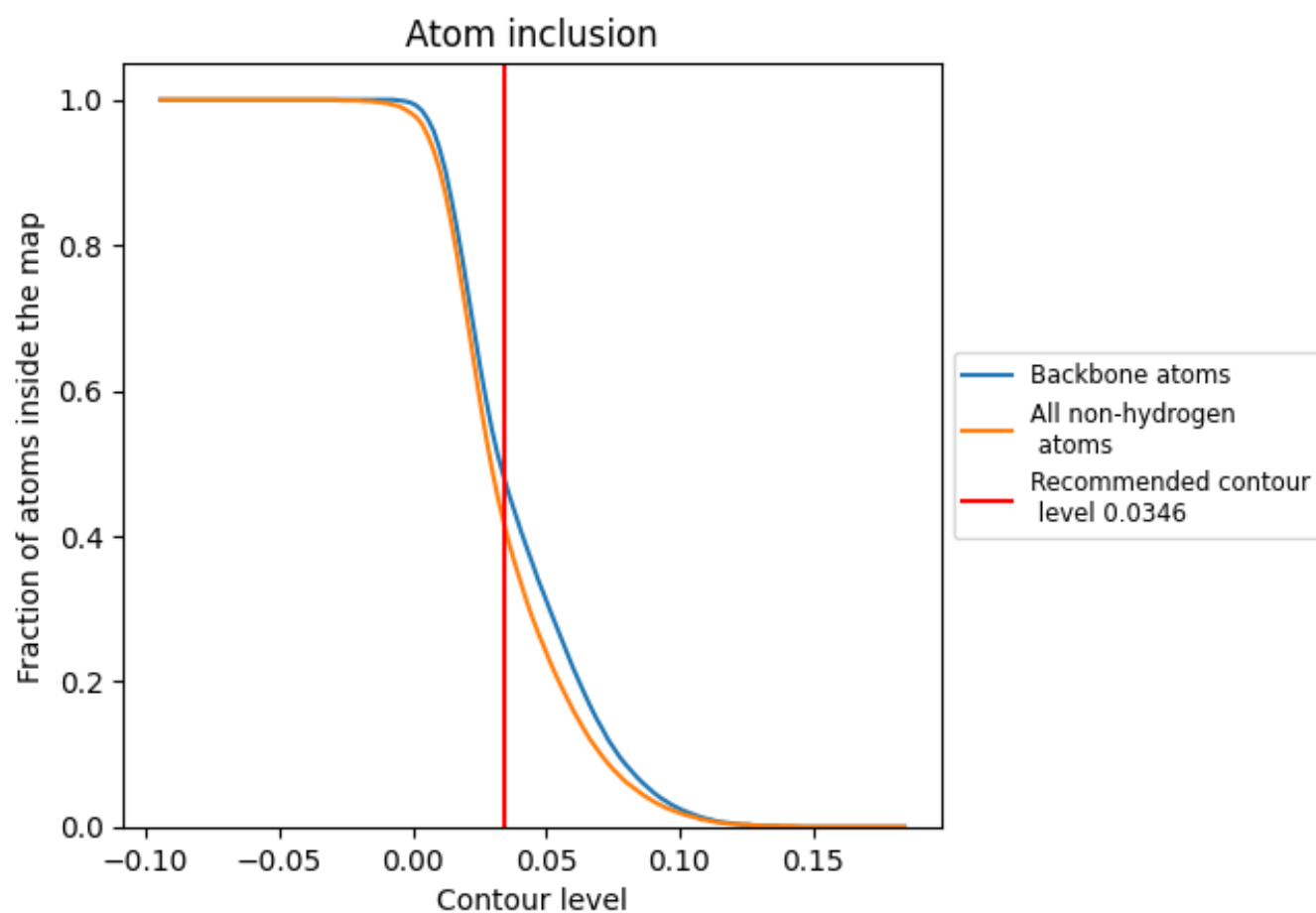


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 41% 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 (0.0346) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4120	 0.1310
1	 0.6670	 0.2300
2	 0.2970	 0.1480
3	 0.6080	 0.1670
4	 0.0730	 0.0080
5	 0.7300	 0.2390
6	 0.5060	 0.1590
7	 0.6800	 0.2240
A	 0.5570	 0.1970
B	 0.5980	 0.1040
C	 0.4530	 0.0950
D	 0.1160	 0.0400
E	 0.0260	 0.0260
F	 0.5990	 0.1470
G	 0.6230	 0.1490
H	 0.3420	 0.0880
J	 0.2790	 0.0660
L	 0.4750	 0.2070
M	 0.7170	 0.2530
P	 0.3090	 0.1160
R	 0.4080	 0.1660
T	 0.7530	 0.2280
V	 0.3420	 0.1200
X	 0.7090	 0.2160
Y	 0.6250	 0.2470
Z	 0.5950	 0.2670
a	 0.0000	 0.0170
b	 0.0050	 0.0410
c	 0.0220	 0.0060
d	 0.0940	 -0.0040
e	 0.0050	 0.0020
f	 0.0170	 -0.0230
g	 0.0000	 0.0030
h	 0.0000	 0.0340
i	 0.0000	 0.0210



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Chain	Atom inclusion	Q-score
j	 0.0000	 -0.0440
k	 0.0000	 0.0110
l	 0.0000	 0.0140
m	 0.0000	 -0.0500
n	 0.0000	 0.0110
o	 0.0000	 0.0280
p	 0.0000	 0.0160
u	 0.0000	 0.0040
v	 0.0000	 0.0460
w	 0.1150	 0.0420
x	 0.0290	 0.0110
z	 0.4980	 0.1870