



wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 07:02 AM JST

PDB ID : 5YLZ
EMDB ID : EMD-6839
Title : Cryo-EM Structure of the Post-catalytic Spliceosome from *Saccharomyces cerevisiae* at 3.6 angstrom
Authors : Wan, R.; Yan, C.; Bai, R.; Lei, J.; Shi, Y.
Deposited on : 2017-10-20
Resolution : 3.60 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:

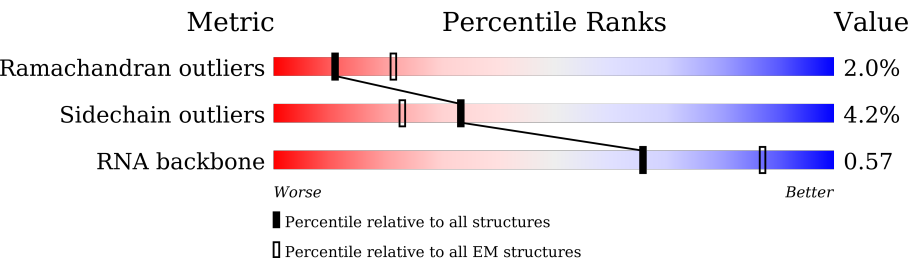
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	2413	
2	B	214	
3	C	1008	
4	D	112	
5	E	369	
6	F	1175	
7	G	175	
8	H	859	

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Mol	Chain	Length	Quality of chain
9	I	687	
10	J	590	
11	K	215	
12	L	157	
13	T	455	
14	M	364	
15	N	339	
16	O	451	
17	P	175	
18	Q	379	
19	R	135	
20	S	577	
21	U	251	
22	V	382	
23	W	1145	
24	a	196	
24	h	196	
25	b	94	
25	i	94	
26	c	86	
26	j	86	
27	d	77	
27	k	77	
28	e	101	
28	l	101	

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Mol	Chain	Length	Quality of chain
29	f	146	
29	m	146	
30	g	110	
30	n	110	
31	o	238	
32	p	111	
33	q	503	
33	r	503	
33	s	503	
33	t	503	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 76247 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1931	Total	C	N	O	S	0	0
			15931	10239	2737	2897	58		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 3 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	878	Total	C	N	O	S	0	0
			7019	4529	1166	1295	29		

- Molecule 4 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 5 is a RNA chain called mRNA/intron lariat.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	62	Total	C	N	O	P	0	0
			1310	590	224	434	62		

- Molecule 6 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	91	Total	C	N	O	P	0	0
			1909	854	309	655	91		

- Molecule 7 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	562	Total	C	N	O	S	0	0
			3012	1844	572	595	1		

- Molecule 9 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	517	Total	C	N	O	S	0	0
			3424	2130	643	643	8		

- Molecule 10 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	432	Total	C	N	O	S	0	0
			2949	1827	545	569	8		

- Molecule 11 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	96	Total	C	N	O	S	0	0
			777	476	143	157	1		

- Molecule 12 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 13 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	344	Total	C	N	O	S	0	0
			2357	1504	414	432	7		

- Molecule 14 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 15 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 16 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	69	Total	C	N	O	S	0	0
			560	351	112	96	1		

- Molecule 18 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 19 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	R	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 20 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	207	Total	C	N	O	S	0	0
			1701	1096	275	323	7		

- Molecule 21 is a protein called Pre-mRNA-splicing factor 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	148	Total	C	N	O	S	0	0
			1202	780	204	214	4		

- Molecule 22 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	88	Total	C	N	O		0	0
			554	350	100	104			

- Molecule 23 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	703	Total	C	N	O	S	0	0
			5553	3521	941	1060	31		

- Molecule 24 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
24	h	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 25 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
25	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 26 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
26	j	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
27	k	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	e	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
28	l	81	Total	C	N	O	S	0	0
			616	393	107	114	2		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	f	82	Total	C	N	O	S	0	0
			644	409	110	123	2		
29	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
30	n	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
31	o	135	Total	C	N	O	0	0
			841	538	142	161		

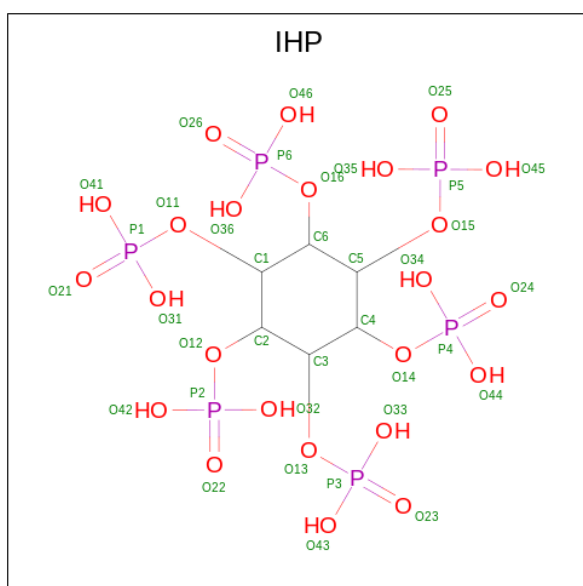
- Molecule 32 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	p	81	Total	C	N	O	0	0
			513	332	89	92		

- Molecule 33 is a protein called Pre-mRNA-processing factor 19.

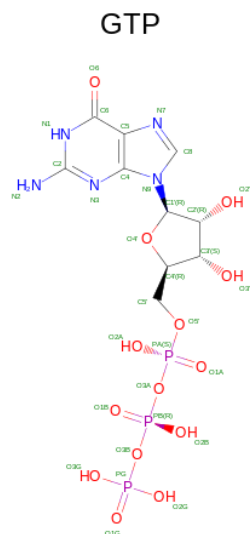
Mol	Chain	Residues	Atoms					AltConf	Trace
33	q	129	Total	C	N	O	S	0	0
			850	537	137	174	2		
33	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		
33	s	126	Total	C	N	O	S	0	0
			830	525	134	169	2		
33	t	128	Total	C	N	O	S	0	0
			843	532	136	173	2		

- Molecule 34 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



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

- Molecule 35 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
36	C	1	Total Mg 1 1	0
36	D	5	Total Mg 5 5	0

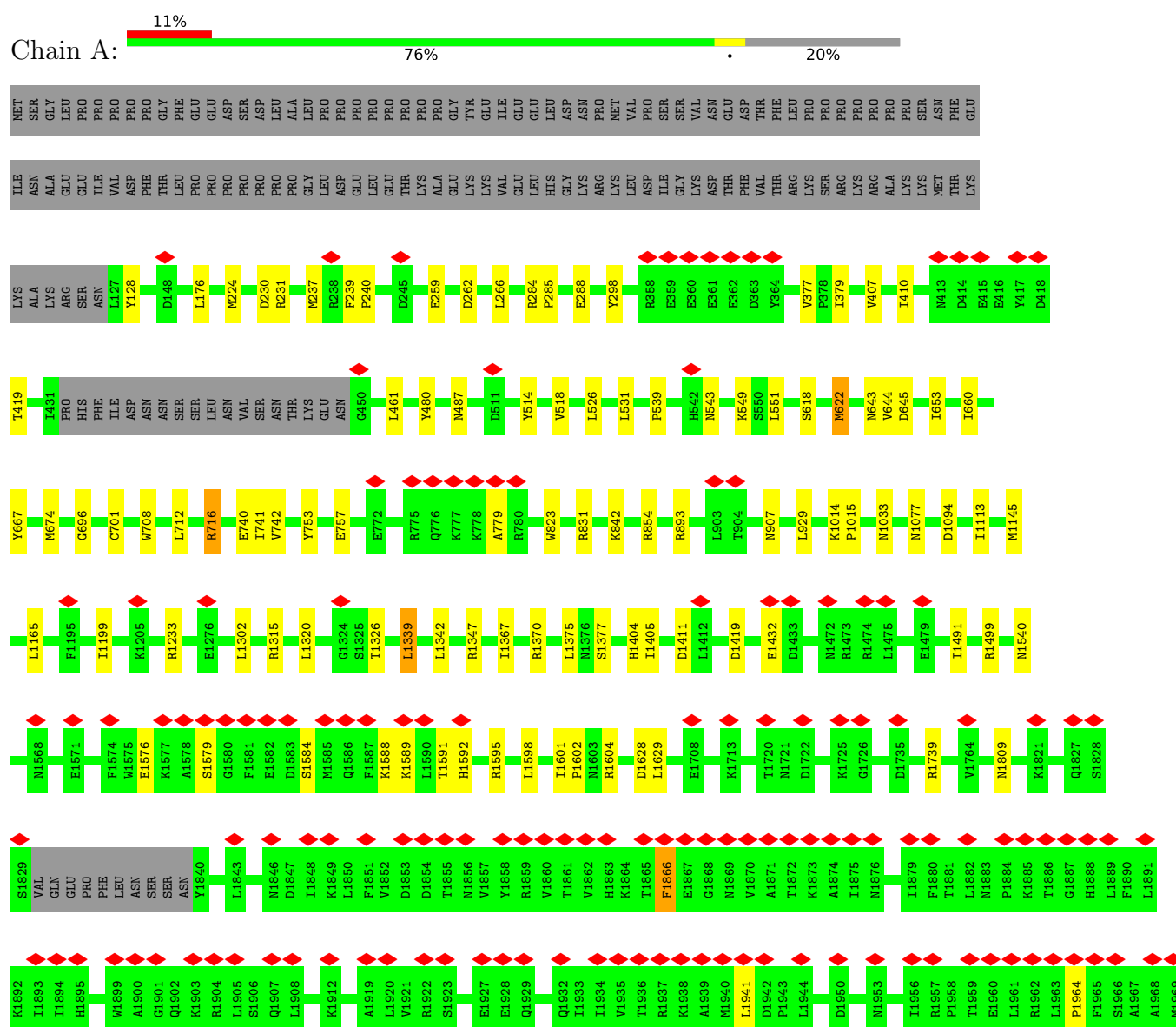
- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	L	3	Total 3	Zn 3	0
37	M	2	Total 2	Zn 2	0
37	N	1	Total 1	Zn 1	0

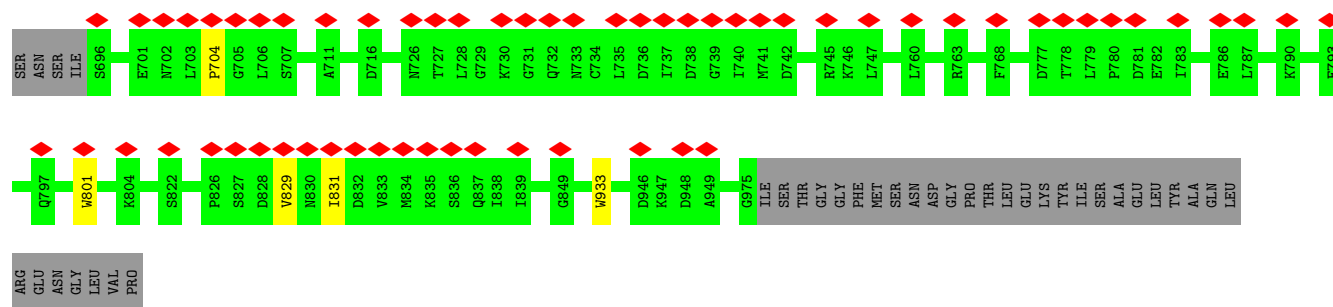
3 Residue-property plots

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.

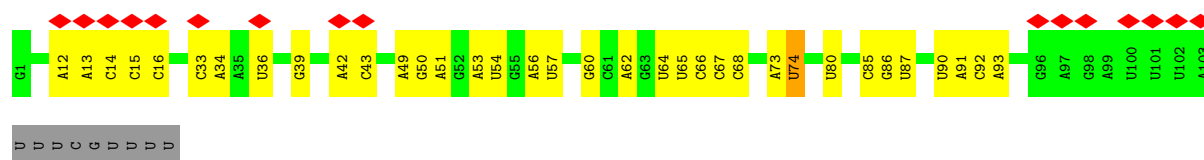
• Molecule 1: Pre-mRNA-splicing factor 8



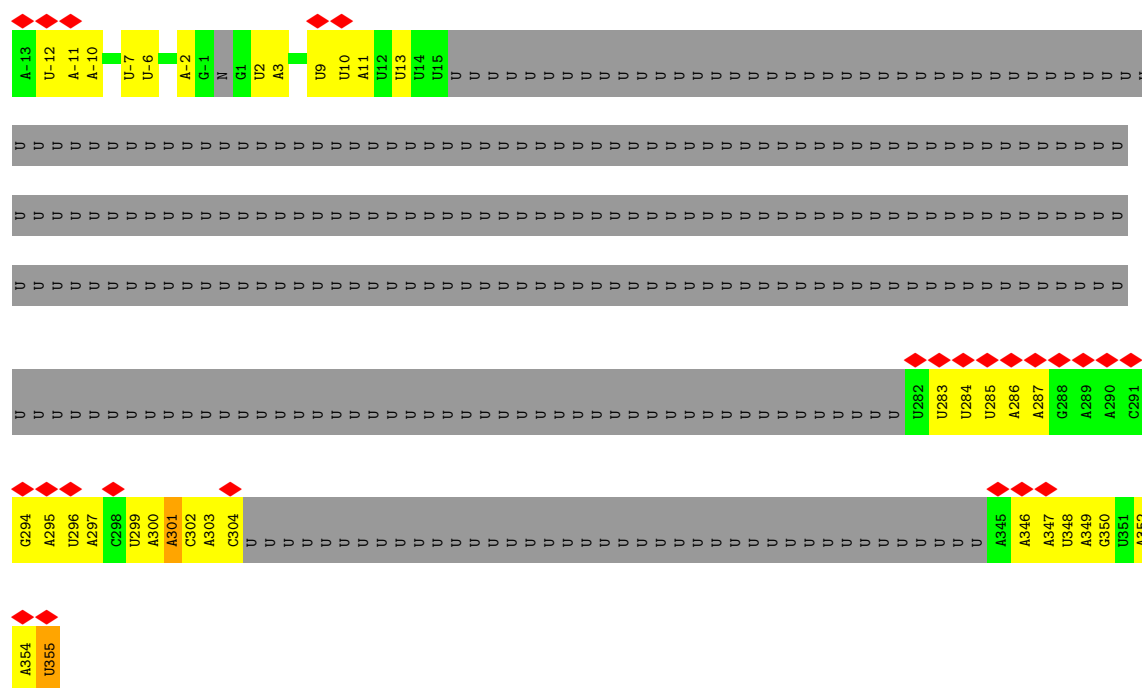




• Molecule 4: U6 snRNA

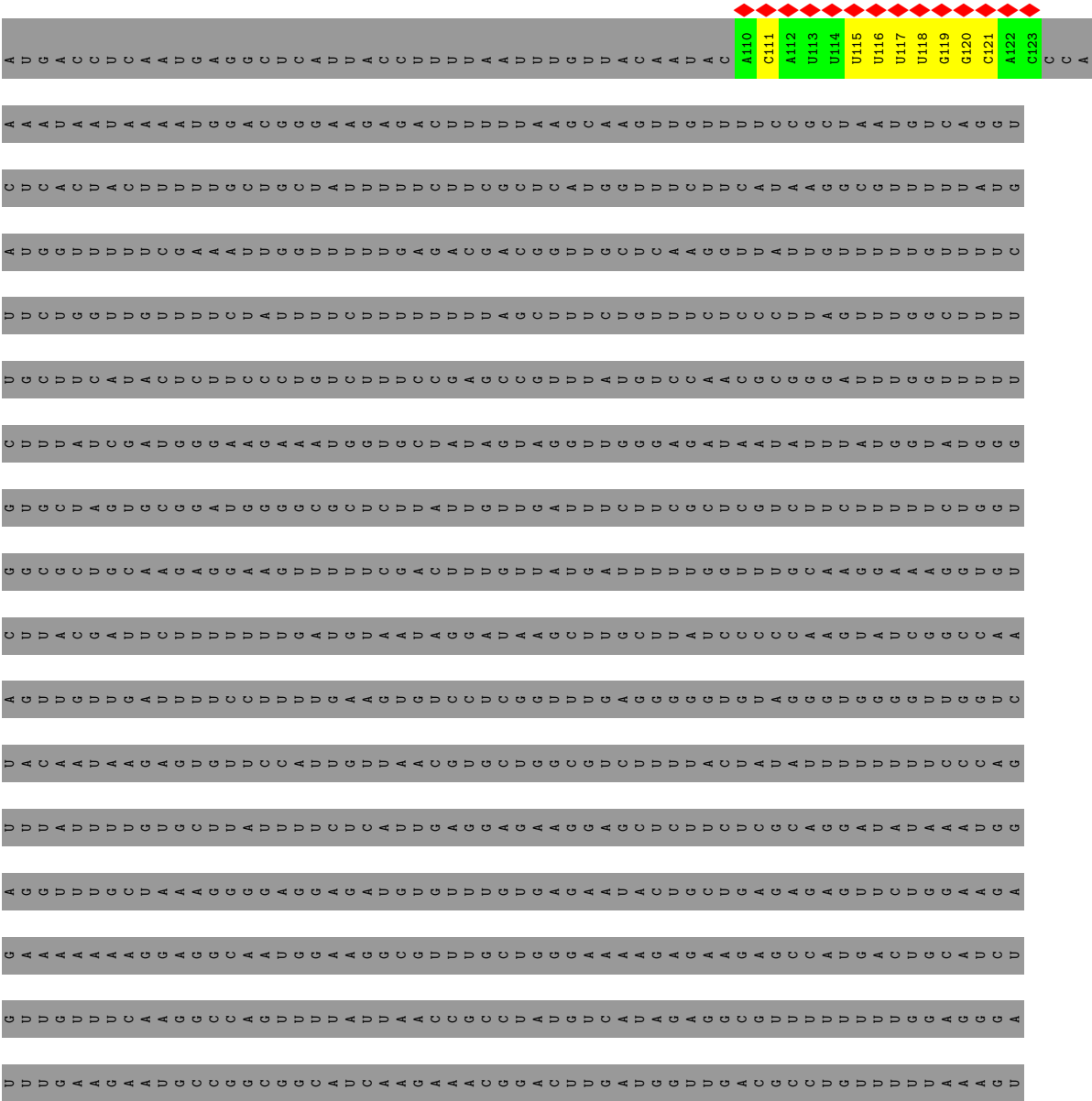


• Molecule 5: mRNA/intron lariat

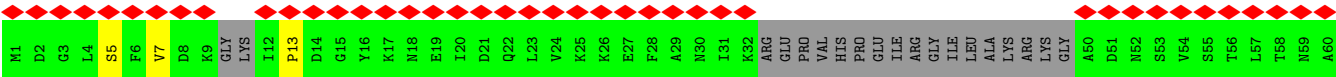
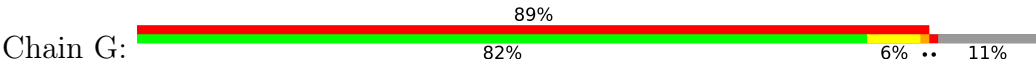


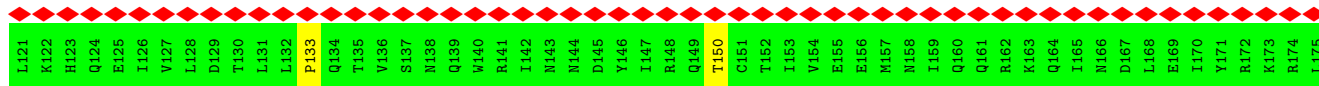
• Molecule 6: U2 snRNA



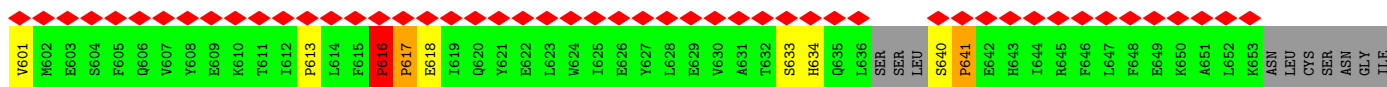
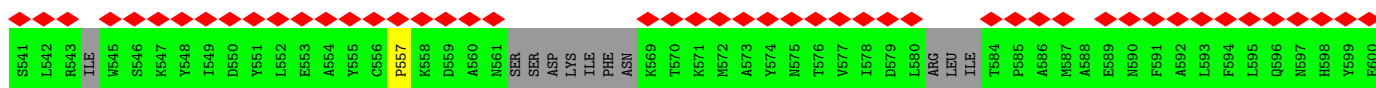
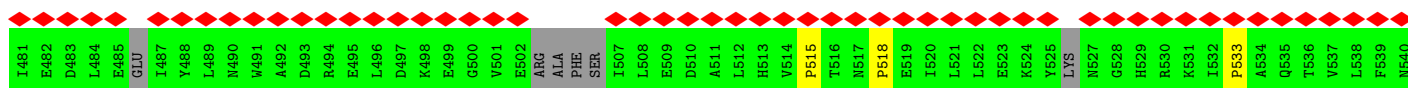
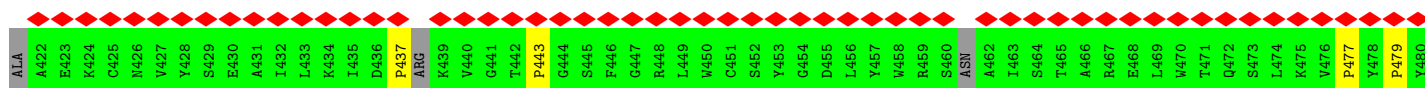
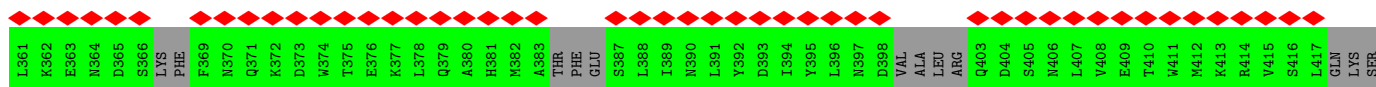
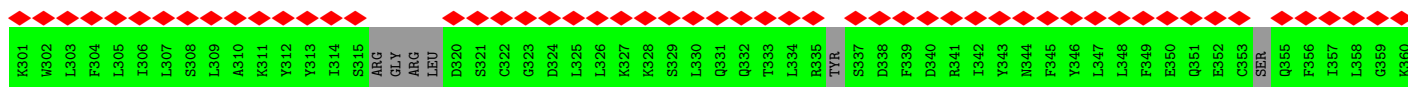
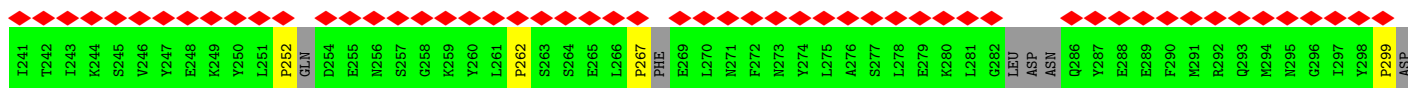
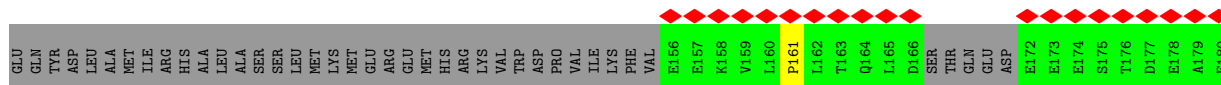
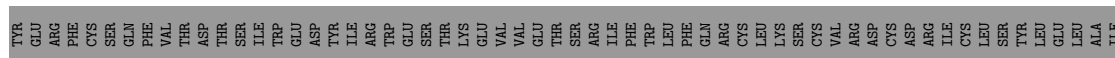
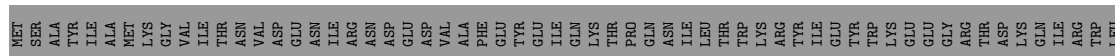


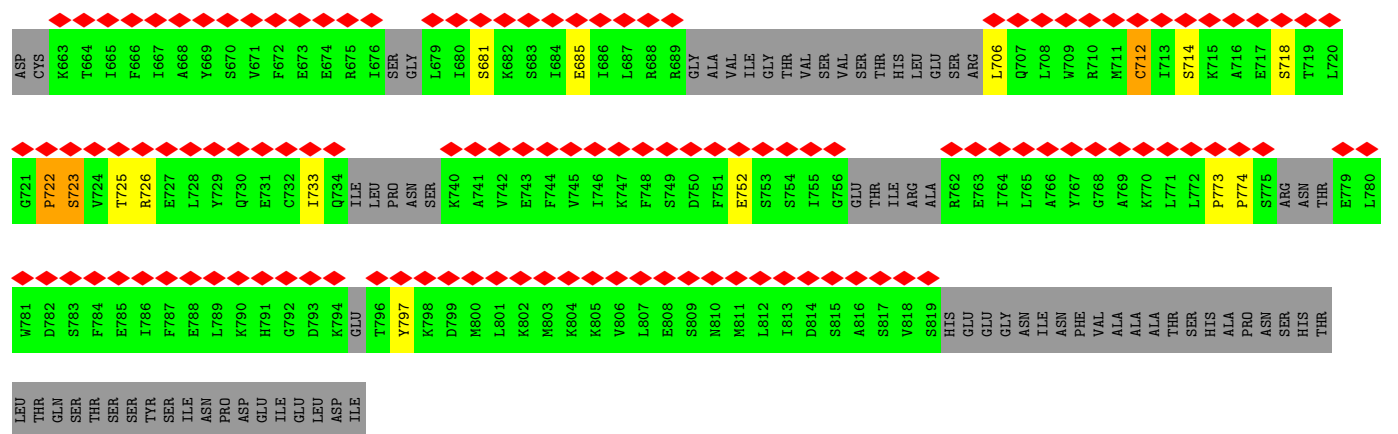
● Molecule 7: Pre-mRNA-splicing factor SNT309



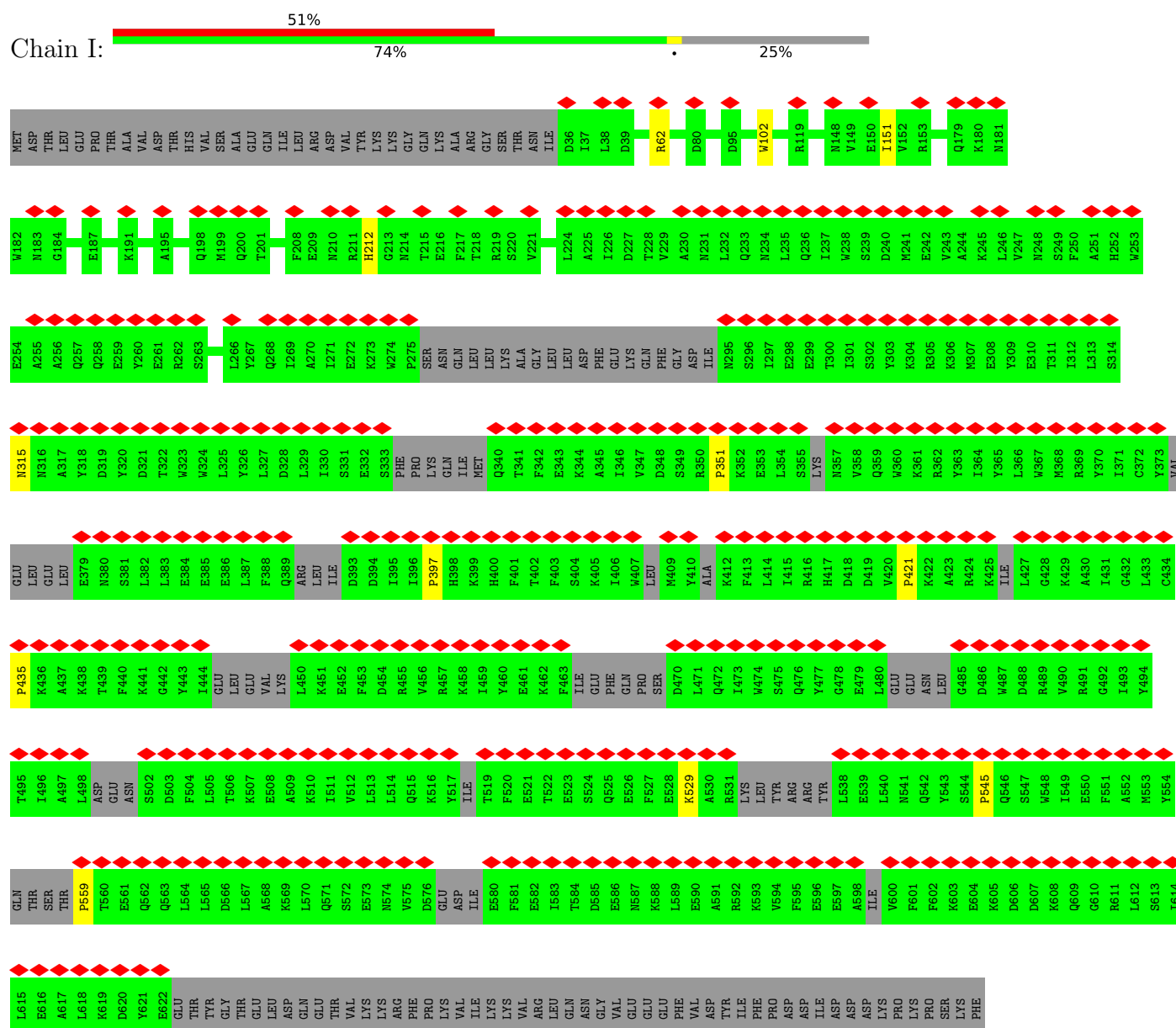


- Molecule 8: Pre-mRNA-splicing factor SYF1





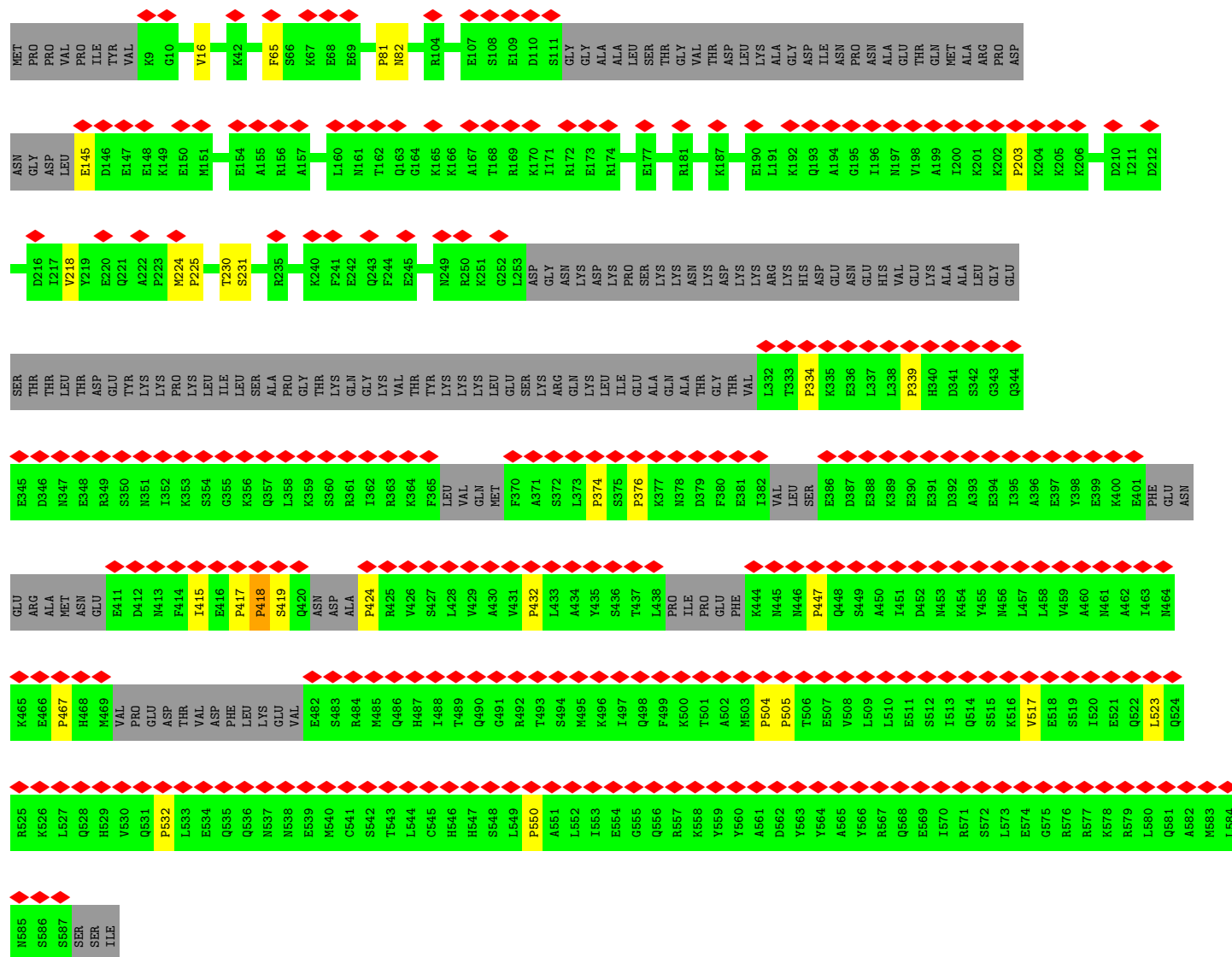
• Molecule 9: Pre-mRNA-splicing factor CLF1




LEU
GLU
LEU
ALA
LYS
LYS
TRP
LYS
GLN
GLU
GLN
ALA
LEU

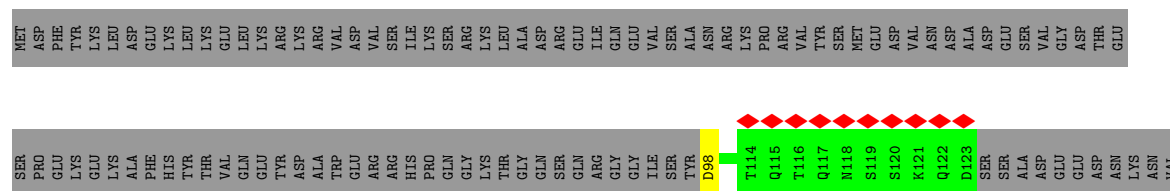
• Molecule 10: Pre-mRNA-splicing factor CEF1

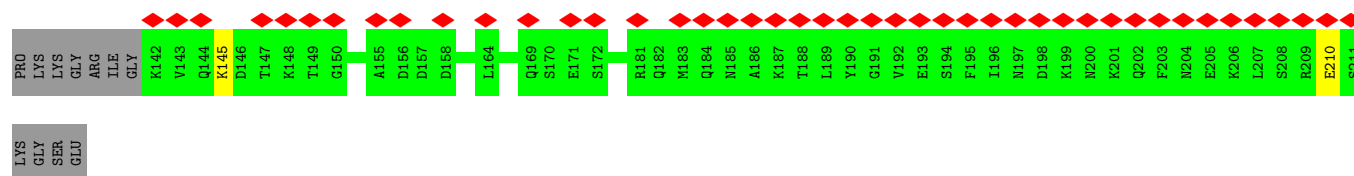
Chain J: 



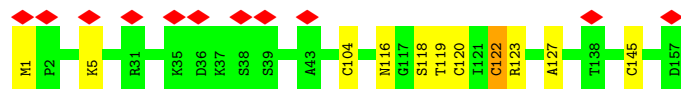
• Molecule 11: Pre-mRNA-splicing factor SYF2

Chain K: 

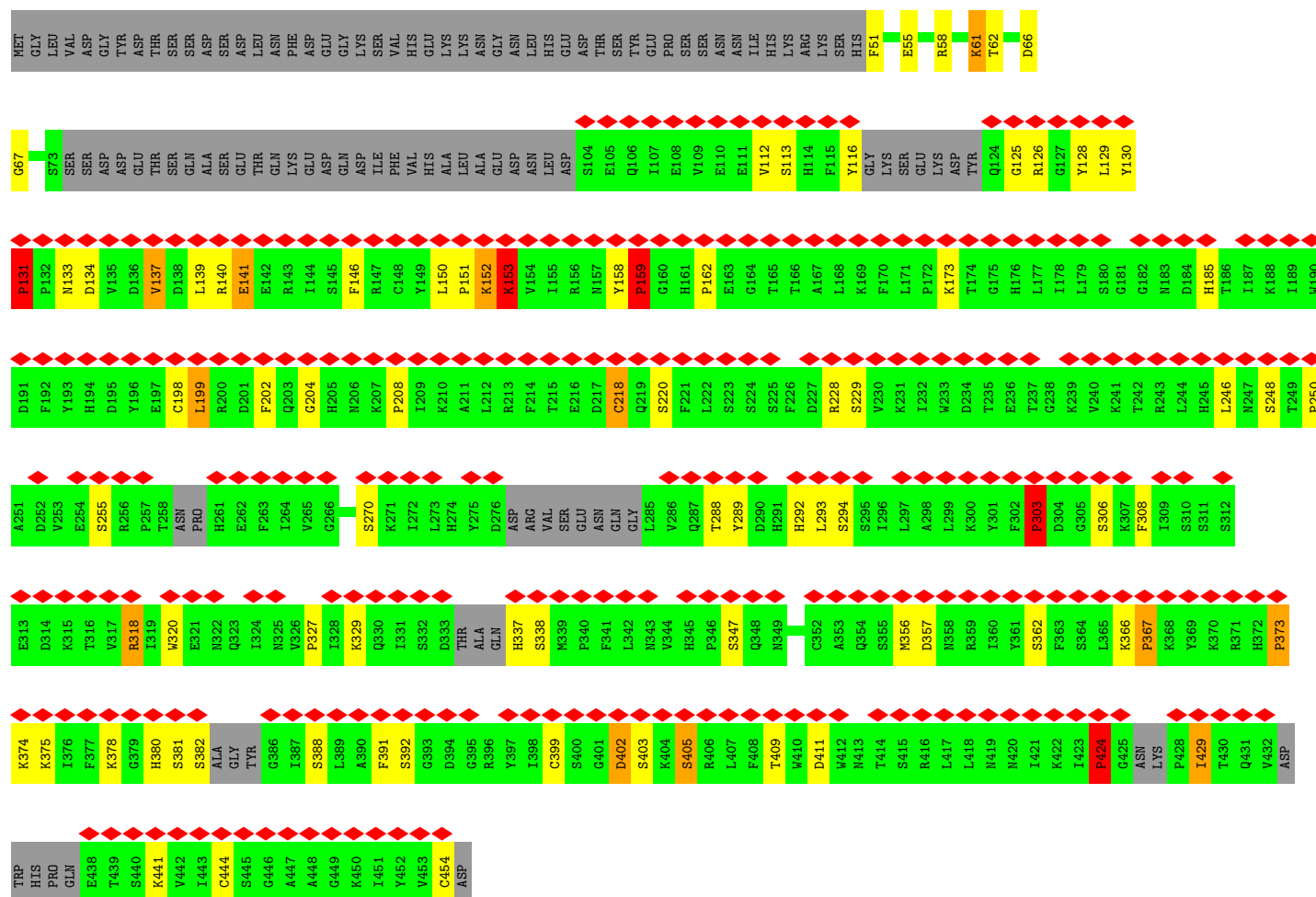




• Molecule 12: Pre-mRNA-splicing factor BUD31

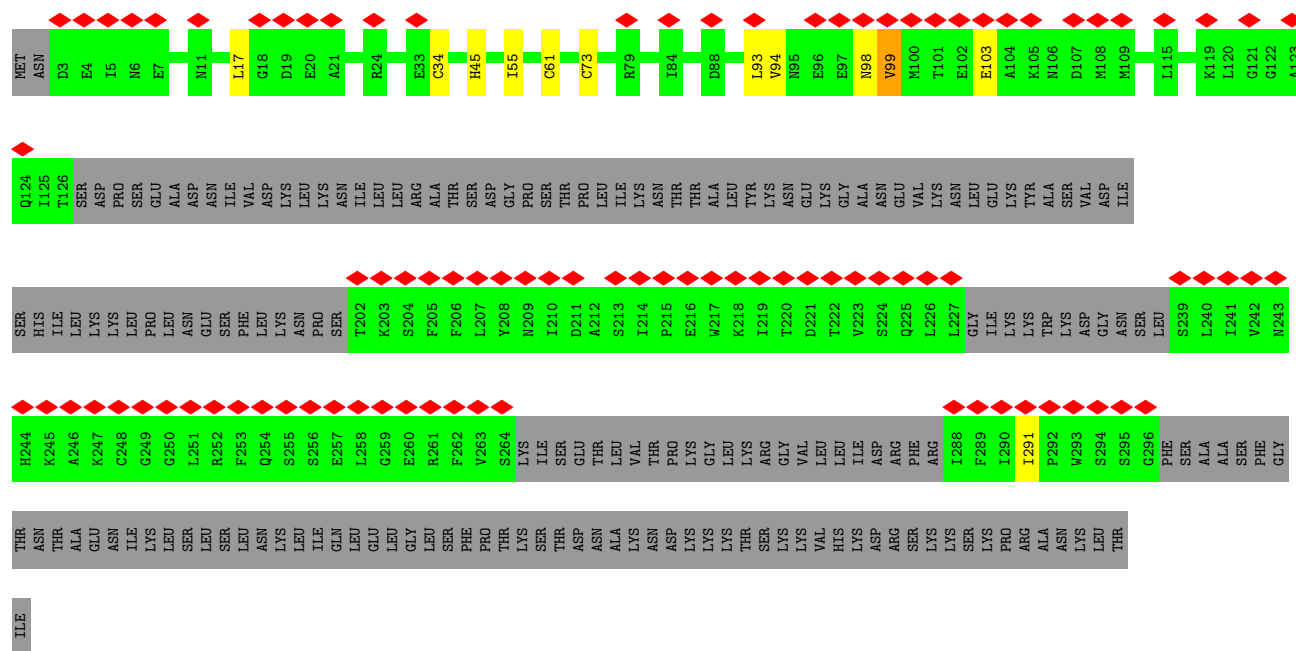


• Molecule 13: Pre-mRNA-processing factor 17

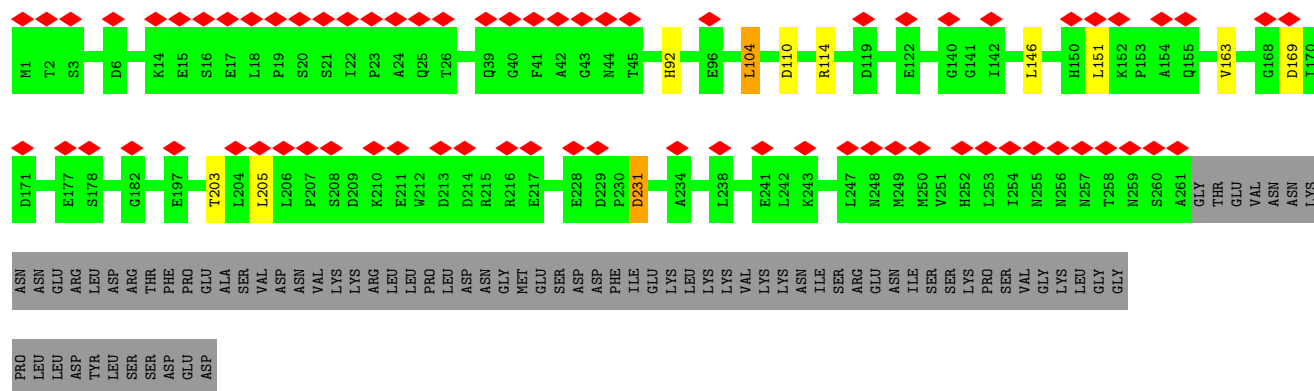


• Molecule 14: Pre-mRNA-splicing factor SLT11

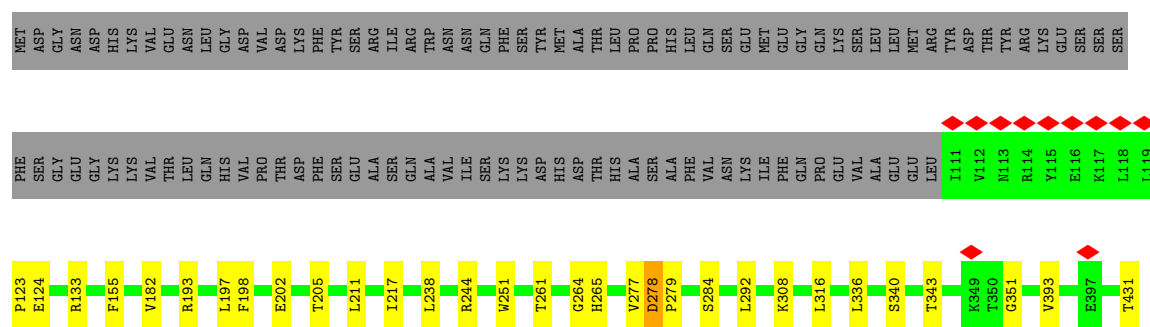




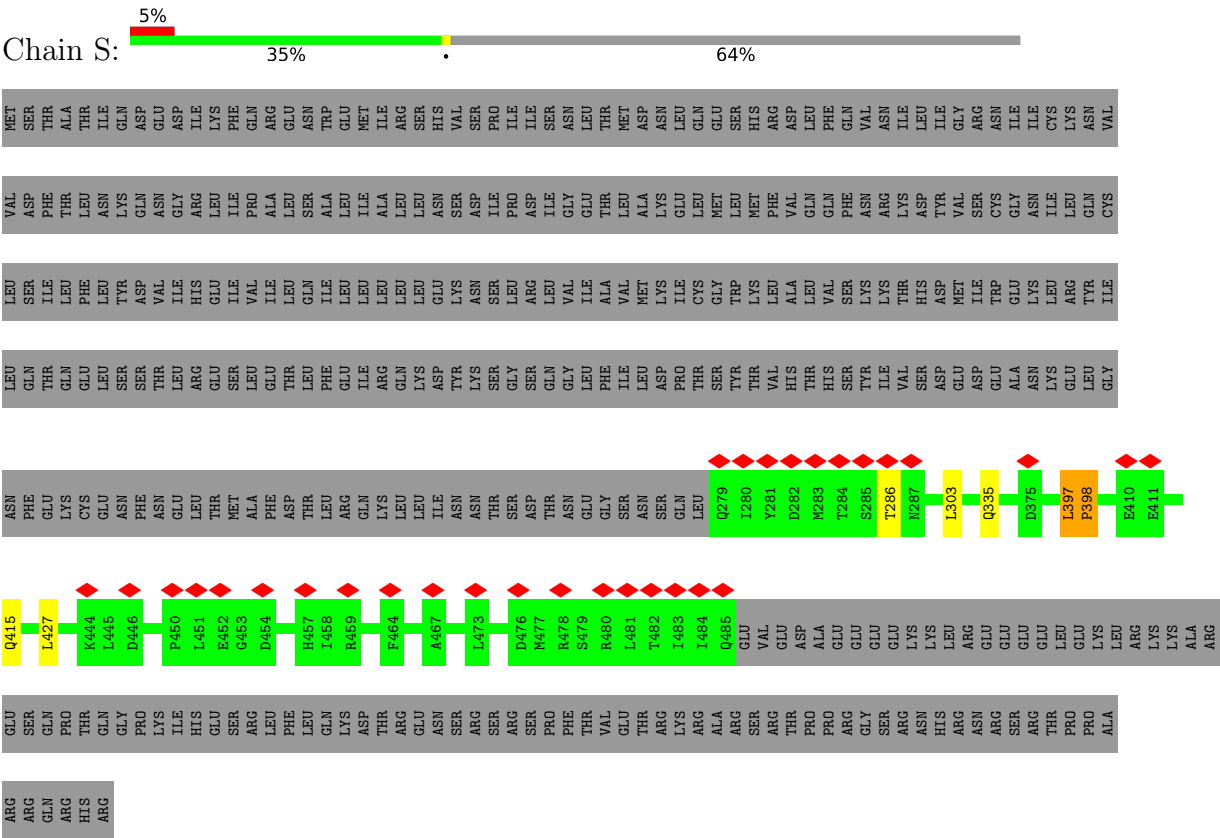
• Molecule 15: Pre-mRNA-splicing factor CWC2



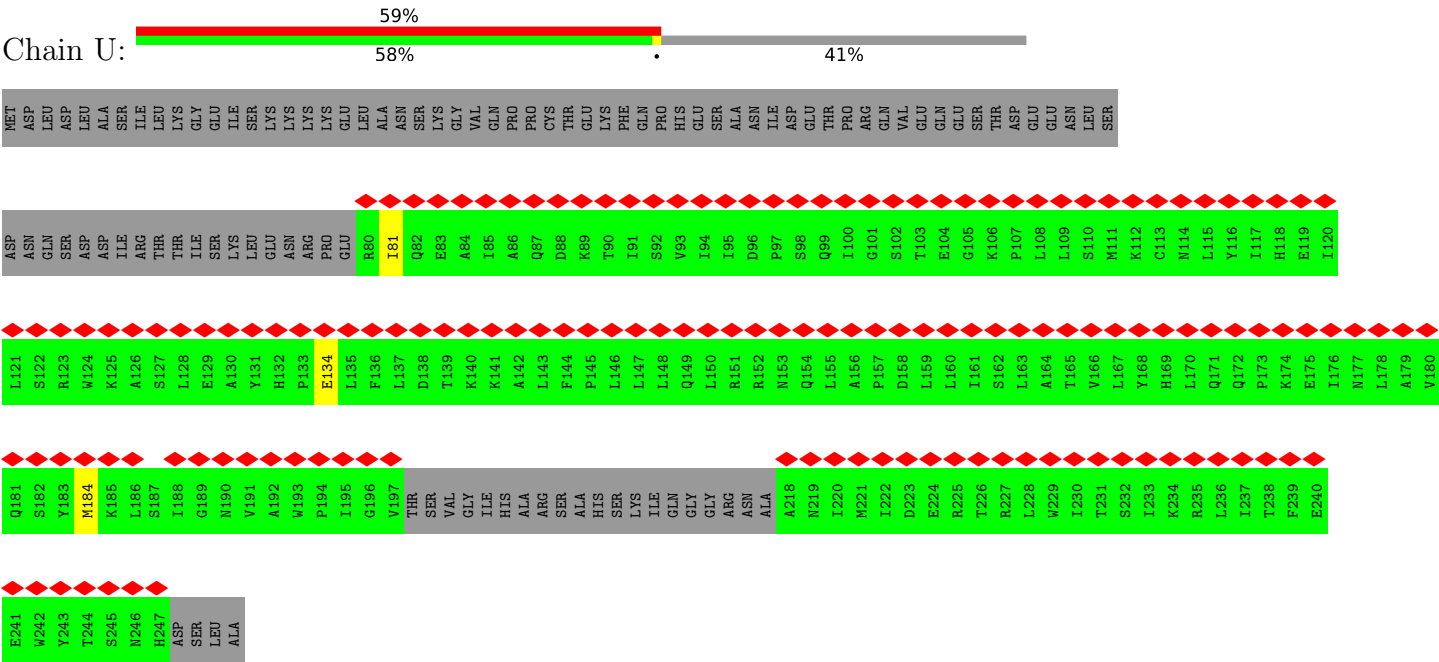
• Molecule 16: Pre-mRNA-splicing factor PRP46



• Molecule 20: Pre-mRNA-splicing factor CWC22



• Molecule 21: Pre-mRNA-splicing factor 18



• Molecule 22: Pre-mRNA-splicing factor SLU7



● Molecule 23: Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP22

Chain W:

60%

51%

8%

39%

GLN Q429 S430 F431 E491 D432 D433 D434 T435 K436 N437 K438 K439 K440 D441 S441 T442 T443 T444 T445 T446 T447 T448 T449 T450 T451 T452 T453 T454 T455 T456 T457 T458 T459 T460 T461 T462 T463 T464 T465 T466 T467 T468 T469 T470 T471 T472 T473 T474 T475 T476 T477 T478 T479 T480 Q481 T482 T483 T484 T485 T486 T487 T488 T489 T490 T491 T492 T493 T494 T495 T496 T497 T498 T499 T500 T501 T502 T503 T504 T505 T506 T507 T508 T509 T510 T511 T512 T513 T514 T515 T516 T517 T518 T519 T520 T521 T522 T523 T524 T525 T526 T527 T528 T529 T530 T531 T532 T533 T534 T535 T536 T537 T538 T539 T540 T541 T542 T543 T544 T545 T546 T547 T548 T549 T550 T551 T552 T553 T554 T555 T556 T557 T558 T559 T560 T561 T562 T563 T564 T565 T566 T567 T568 T569 T570 T571 T572 T573 T574 T575 T576 T577 T578 T579 T580 T581 T582 T583 T584 T585 T586 T587 T588 T589 T590 T591 T592 T593 T594 T595 T596 T597 T598 T599 T600 T601 T602 T603 T604 T605 T606 T607 T608 T609 T610 T611 T612 T613 T614 T615 T616 T617 T618 T619 T620 T621 T622 T623 T624 T625 T626 T627 T628 T629 T630 T631 T632 T633 T634 T635 T636 T637 T638 T639 T640 T641 T642 T643 T644 T645 T646 T647 T648 T649 T650 T651 T652 T653 T654 T655 T656 T657 T658 T659 T660 T661 T662 T663 T664 T665 T666 T667 T668 T669 T670 T671 T672 T673 T674 T675 T676 T677 T678 T679 T680 T681 T682 T683 T684 T685 T686 T687 T688 T689 T690 T691 T692 T693 T694 T695 T696 T697 T698 T699 T700 T701 T702 T703 T704 T705 T706 T707 T708 T709 T710 T711 T712 T713 T714 T715 T716 T717 T718 T719 T720 T721 T722 T723 T724 T725 T726 T727 T728 T729 T730 T731 T732 T733 T734 T735 T736 T737 T738 T739 T740 T741 T742 T743 T744 T745 T746 T747 T748 T749 T750 T751 T752 T753 T754 T755 T756 T757 T758 T759 T760 T761 T762 T763 T764 T765 T766 T767 T768 T769 T770 T771 T772 T773 T774 T775 T776 T777 T778 T779 T780 T781 T782 T783 T784 T785 T786 T787 T788 T789 T790 T791 T792 T793 T794 T795 T796 T797 T798 T799 T800 T801 T802 T803 T804 T805 T806 T807 T808 T809 T810 T811 T812 T813 T814 T815 T816 T817 T818 T819 T820 T821 T822 T823 T824 T825 T826 T827 T828 T829 T830 T831 T832 T833 T834 T835 T836 T837 T838 T839 T840 T841 T842 T843 T844 T845 T846 T847 T848 T849 T850 T851 T852 T853 T854 T855 T856 T857 T858 T859 T860 T861 T862 T863 T864 T865 T866 T867 T868 T869 T870 T871 T872 T873 T874 T875 T876 T877 T878 T879 T880 T881 T882 T883 T884 T885 T886 T887 T888 T889 T890 T891 T892 T893 T894 T895 T896 T897 T898 T899 T900 T901 T902 T903 T904 T905 T906 T907 T908 T909 T910 T911 T912 T913 T914 T915 T916 T917 T918 T919 T920 T921 T922 T923 T924 T925 T926 T927 T928 T929 T930 T931 T932 T933 T934 T935 T936 T937 T938 T939 T940 T941 T942 T943 T944 T945 T946 T947 T948 T949 T950 T951 T952 T953 T954 T955 T956 T957 T958 T959 T960 T961 T962 T963 T964 T965 T966 T967 T968 T969 T970 T971 T972 T973 T974 T975 T976 T977 T978 T979 T980 T981 T982 T983 T984 T985 T986 T987 T988 T989 T990 T991 T992 T993 T994 T995 T996 T997 T998 T999 T1000

P1088	Q1089	W1090	L1091	L1092	E1093	V1094	A1095	P1096	F1098	Y1099	K1100	A1101	G1102	D1103	A1104	E1105	S1106	Q1107	SER	ARG	LYS	LYS	ALA	LYS	ILE	ILE	PRO	LEU	HIS	ASN	LYS	PHE	ALA	LYS	ASP	GLN	ASN	SER	TRP	ARG	LEU	SER	SER	ILE	ARG	GLN	SER	ARG	GLU	ALA	LEU	GLY	ILE	LYS	ARG				
G1028	F1029	F1030	M1031	M1032	A1033	A1034	K1035	R1036	D1037	S1038	Q1039	V1040	G1041	Y1042	K1043	T1044	I1045	M1046	G1047	T1048	T1049	E1050	V1051	G1052	I1053	H1054	P1055	P1056	S1057	S1058	L1059	Y1060	G1061	K1062	E1063	Y1064	E1065	K1066	Y1067	M1068	Y1069	H1070	S1071	I1072	V1073	L1074	T1075	S1076	E1077	E1078	Y1079	M1080	S1081	Q1082	V1083	T1084	S1085	I1086	F1087
T968	R969	W970	Q971	Q972	A973	N974	Y975	S976	E977	Q978	Y979	C980	K981	T982	N983	F984	L985	H986	F987	R988	H989	L990	K991	R992	A993	R994	D995	V996	K997	S998	Q999	I1000	S1001	M1002	I1003	F1004	K1005	K1006	I1007	G1008	L1009	K1010	L1011	I1012	N1013	C1014	H1015	S1016	D1017	P1018	D1019	L1020	I1021	R1022	K1023	T1024	F1025	V1026	S1027
S908	R909	S910	L911	L912	S913	S914	V915	D916	N917	Q918	C919	S920	D921	E922	I923	V924	T925	I926	I927	S928	H929	L930	S931	V932	Q933	N934	V935	F936	R937	R938	Q939	K940	D941	R942	Q943	L944	E945	A946	D947	S948	K949	K950	A951	K952	F953	H954	H955	P956	Y957	Q958	D959	H960	L961	T962	L963	L964	N965	V966	Y967
L848	M849	L850	K851	A852	M853	G854	I855	N856	D857	L858	L859	K860	F861	D862	F863	M864	D865	P866	P867	P868	K869	N870	L871	M872	L873	N874	A875	L876	T877	E878	L879	Y880	H881	L882	Q883	S884	L885	D886	D887	E888	G889	K890	L891	T892	N893	L894	G895	K896	E897	M898	S899	L900	F901	P902	N903	D904	P905	T906	L907
G788	I789	E790	Q791	L792	I793	Y794	S795	P796	I797	S798	Q799	Q801	A802	N803	Q804	R805	K806	G807	R808	A809	G810	R811	T812	G813	P814	G815	K816	C817	Y818	R819	L820	Y821	T822	E823	S824	A825	F826	Y827	N828	E829	M830	L831	E832	N833	T834	V835	P836	E837	I838	Q839	R840	Q841	N842	L843	S844	H845	T846	I847	
L728	P729	V730	Y731	S732	A733	L734	P735	E736	E737	I738	Q739	S740	K741	I742	F743	E744	P745	THR	PRO	K748	G749	S750	R751	K752	V753	V754	F755	A756	T757	N758	I759	A760	E761	T762	S763	I764	T765	I766	D767	G768	I769	Y770	Y771	V772	V773	D774	F775	G776	F777	A778	K779	I780	N781	I782	Y783	N784	A785	R786	A787
Q668	T669	P670	Q671	M672	D673	Y674	I675	E676	A677	A678	L679	D680	C681	V682	I683	D684	I685	H686	I687	N688	E689	G690	P691	G692	D693	I694	L695	V696	F697	L698	T699	G700	Q701	E702	E703	I704	D705	S706	C707	C708	E709	I710	L711	Y712	D713	R714	V715	K716	T717	L718	G719	D720	S721	I722	G723	E724	L725	L726	I727
R608	T609	V610	A611	T612	D613	V614	L615	F616	A617	L618	L619	K620	K621	A622	A623	I624	K625	R626	P627	E628	L629	K630	V631	I632	V633	T634	S635	A636	T637	L638	N639	S640	A641	K642	F643	S644	E645	Y646	F647	L648	N649	C650	P651	I652	N653	M654	I655	P656	G657	K658	T659	F660	P661	V662	E663	V664	L665	Y666	S667
V548	A549	E550	E551	V552	G553	C554	K555	V556	G557	H558	D559	V560	G561	Y562	T563	I564	R565	F566	E567	D568	V569	T570	G571	P572	D573	T574	R575	I576	K577	Y578	M579	T580	D581	G582	M583	L584	Q585	R586	E587	A588	L589	L590	D591	P592	E593	M594	S595	K596	Y597	S598	V599	I600	M601	L602	D603	E604	A605	H606	E607

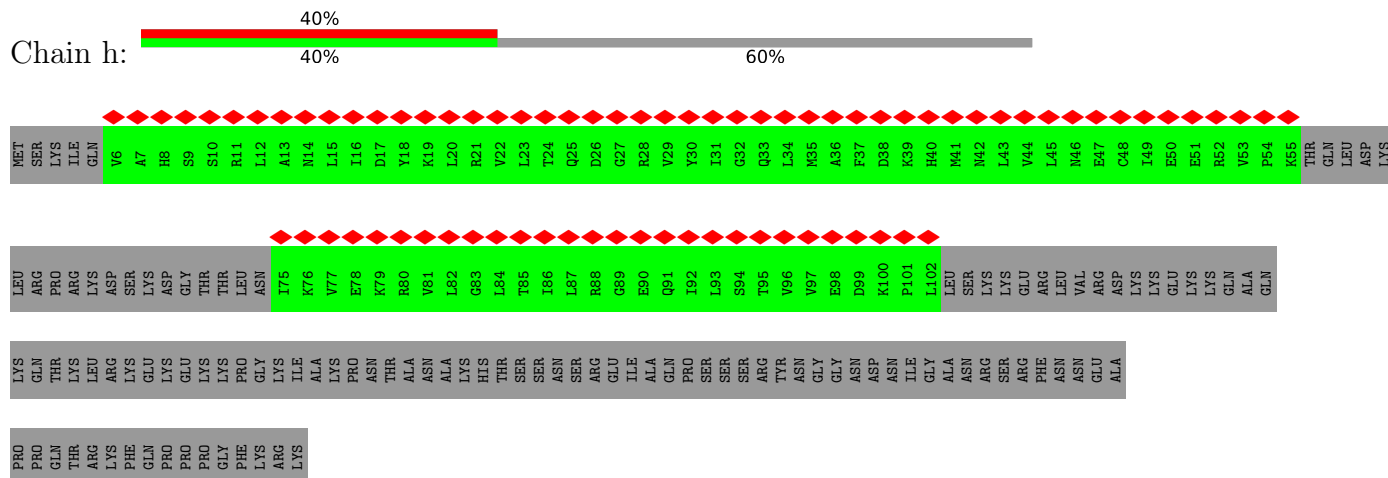
• Molecule 24: Small nuclear ribonucleoprotein-associated protein B



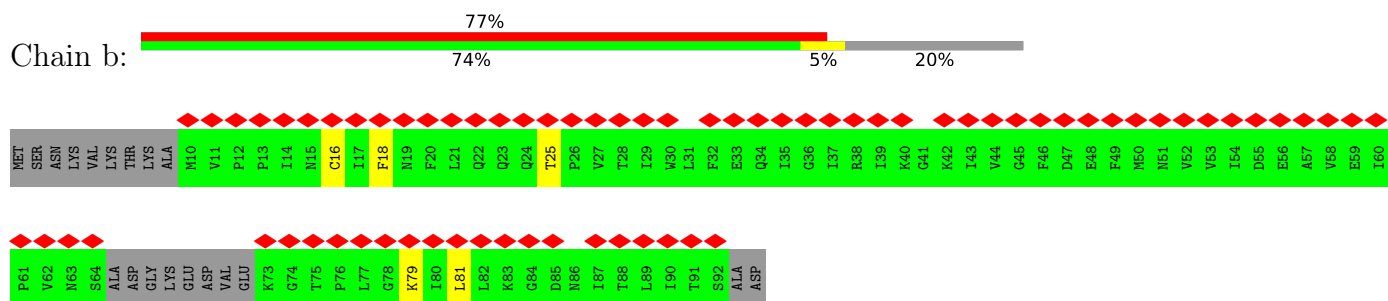
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LYS	ASP	THR	THR	ASN	I75	K76	V77	E78	K79	R80	V81	L82	G83	L84	T85	I86	L87	E90	Q91	I92	L93	S94	T95	V96	V97	E98	D99	K100	P101	L102	LEU	SER	LYS	LYS	GLU	ARG	LEU	VAL	ARG	ASP	LYS	GLU	LYS	LYS	GLN	ALA	LYS	GLN	LYS	THR	GLN	LYS	LEU	ASP	LEU	ARG	PRO	LYS	ASP	GLN	THR	K55	P54	V53	R52	E51	E50	I49	C48	E47	L43	K39	D38	L34	Q33	I31	Y30	R29	R28	G27	D26	Q25	V22	R21	L20	K19	Y18	D17	I16	L15	N14	A13	L12	R11	S10	S9	H8	A7	V6	Q5	I4	LYS	SER	MET

PRO
PRO
PRO
GLY
PHE
LYS
ARG
LYS

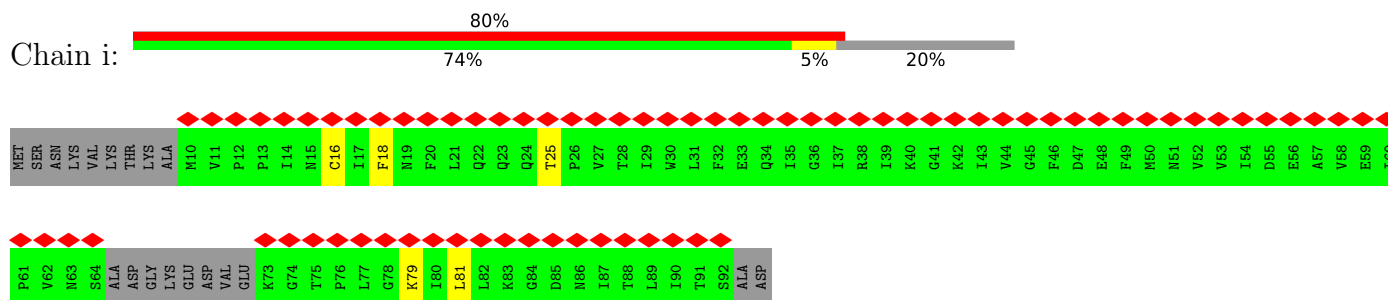
• Molecule 24: Small nuclear ribonucleoprotein-associated protein B



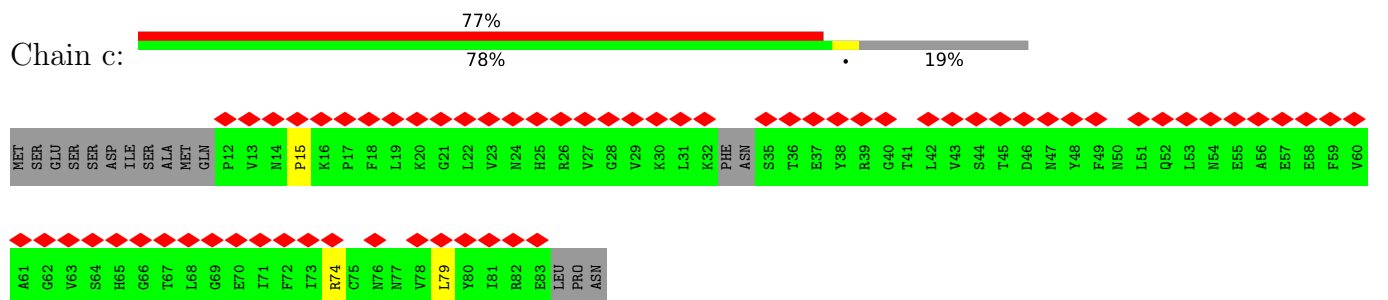
• Molecule 25: Small nuclear ribonucleoprotein E



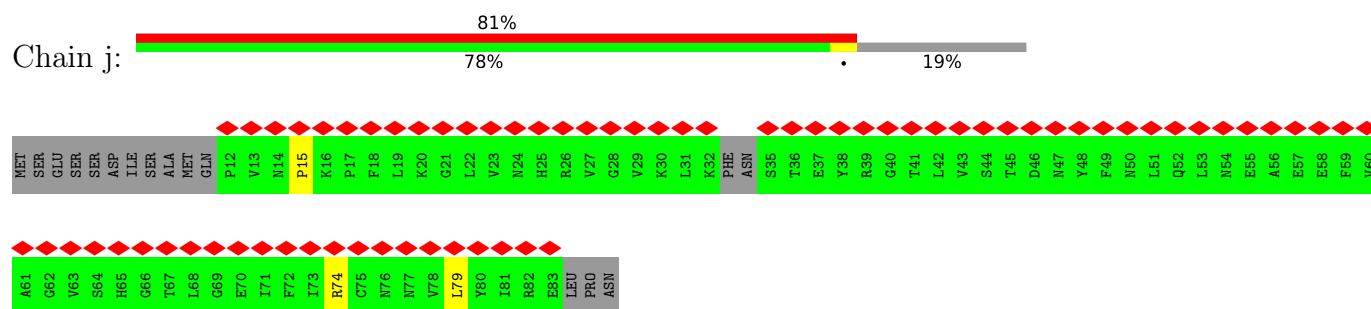
• Molecule 25: Small nuclear ribonucleoprotein E



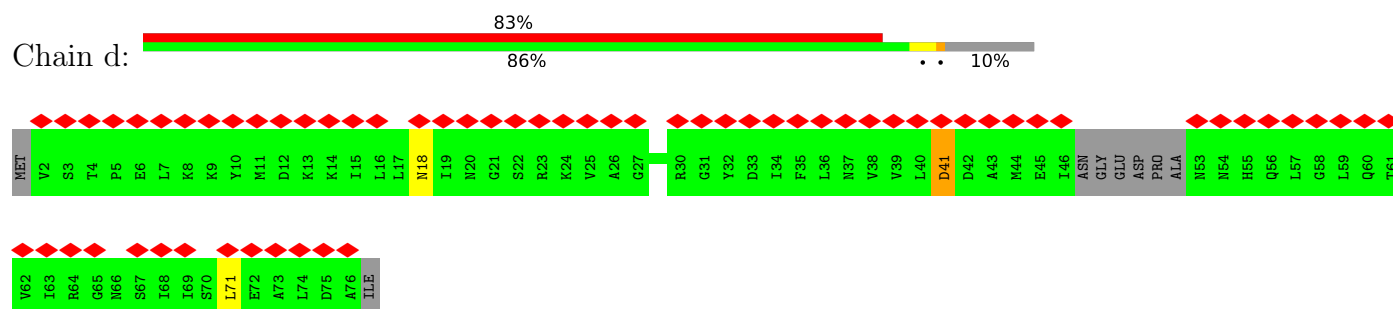
• Molecule 26: Small nuclear ribonucleoprotein F



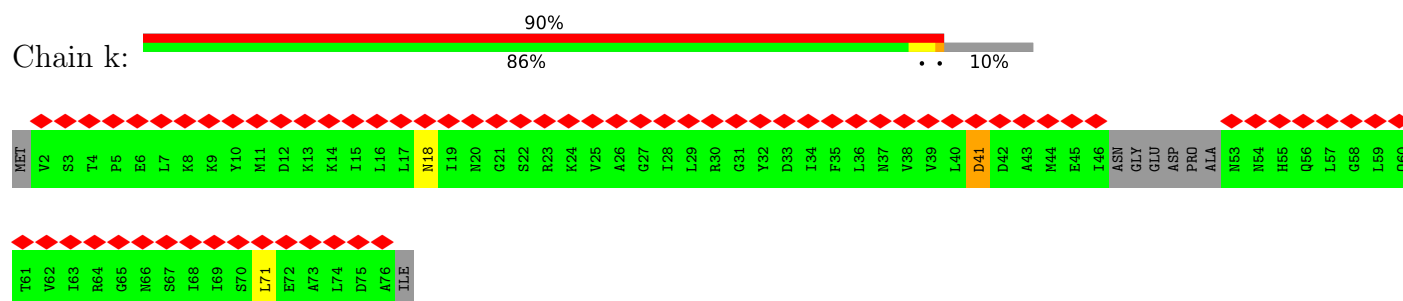
- Molecule 26: Small nuclear ribonucleoprotein F



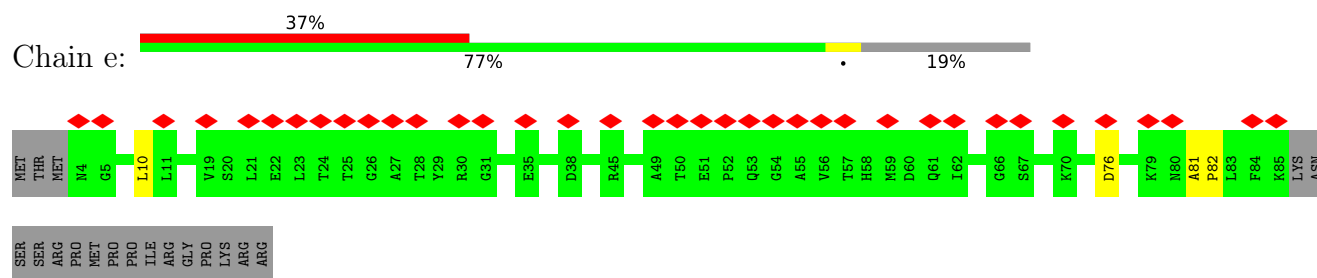
- Molecule 27: Small nuclear ribonucleoprotein G



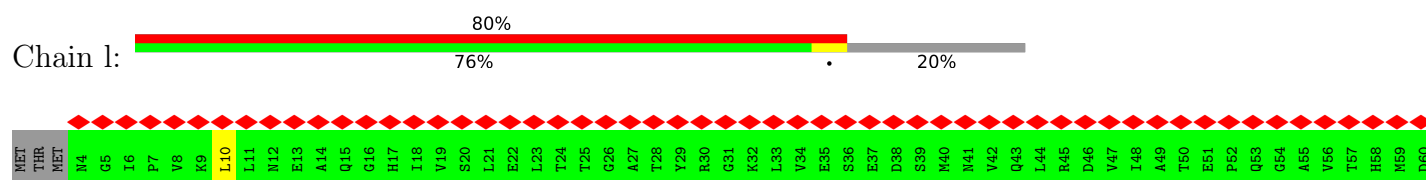
- Molecule 27: Small nuclear ribonucleoprotein G

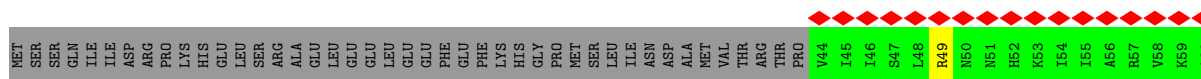


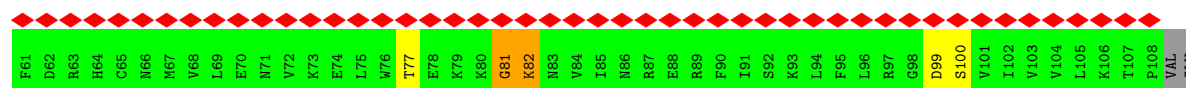
- Molecule 28: Small nuclear ribonucleoprotein Sm D3



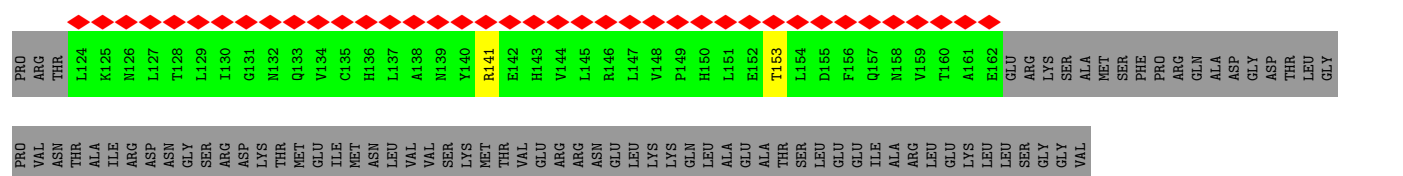
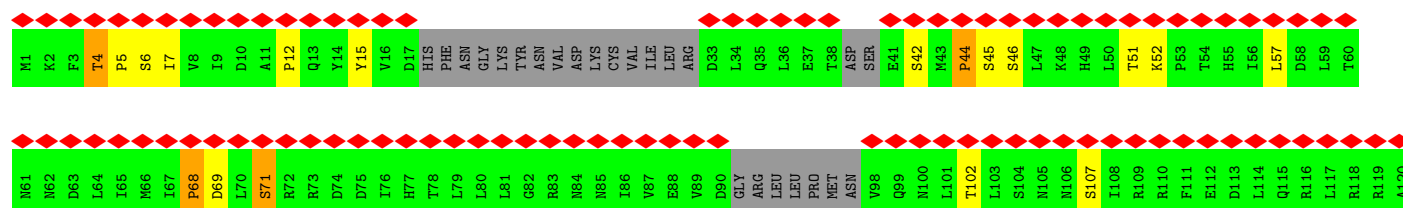
- Molecule 28: Small nuclear ribonucleoprotein Sm D3



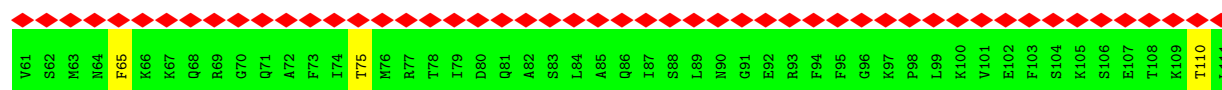
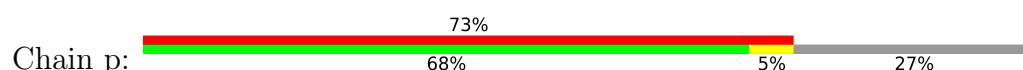




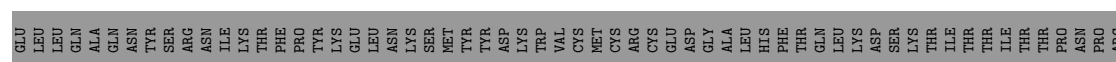
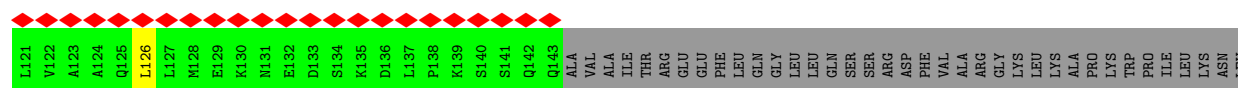
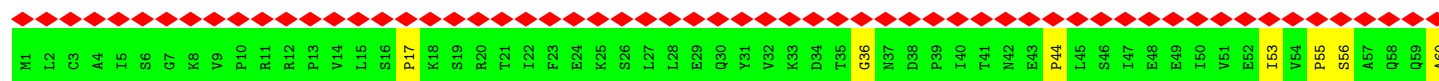
• Molecule 31: U2 small nuclear ribonucleoprotein A'

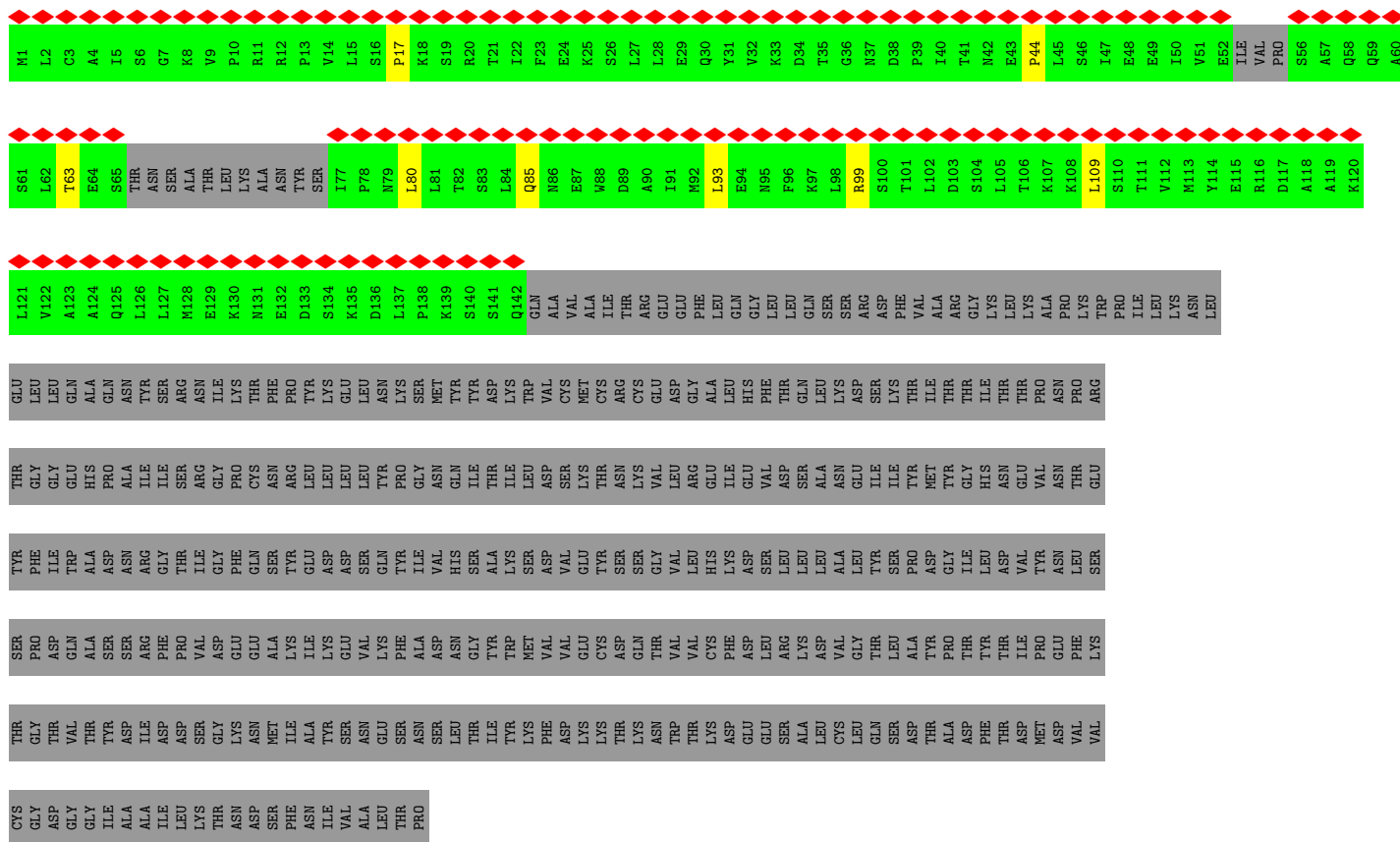


• Molecule 32: U2 small nuclear ribonucleoprotein B''



• Molecule 33: Pre-mRNA-processing factor 19





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134517	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	0.230	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.034	Depositor
Map size (\AA)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ZN, IHP, 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	0.82	7/16338 (0.0%)	0.94	27/22145 (0.1%)
2	B	0.37	0/2747	0.70	0/4267
3	C	0.67	1/7168 (0.0%)	0.85	3/9707 (0.0%)
4	D	0.46	3/2452 (0.1%)	0.69	0/3817
5	E	0.41	2/1461 (0.1%)	0.68	0/2260
6	F	0.73	11/2123 (0.5%)	1.09	19/3295 (0.6%)
7	G	0.42	0/924	0.56	2/1244 (0.2%)
8	H	0.66	8/2991 (0.3%)	0.63	22/4072 (0.5%)
9	I	0.48	1/3459 (0.0%)	0.61	6/4708 (0.1%)
10	J	0.49	1/2967 (0.0%)	0.68	9/3994 (0.2%)
11	K	0.42	0/780	0.63	0/1036
12	L	0.72	0/1315	0.89	2/1759 (0.1%)
13	T	1.25	24/2390 (1.0%)	1.10	20/3200 (0.6%)
14	M	0.57	0/1496	0.85	0/2014
15	N	0.57	0/2135	0.83	3/2871 (0.1%)
16	O	1.13	5/2704 (0.2%)	1.18	12/3676 (0.3%)
17	P	0.85	0/574	0.98	2/766 (0.3%)
18	Q	0.66	0/1604	0.87	1/2160 (0.0%)
19	R	0.41	0/191	0.73	0/254
20	S	0.60	0/1732	0.84	2/2330 (0.1%)
21	U	0.29	0/1227	0.50	0/1665
22	V	0.98	1/555 (0.2%)	0.90	2/742 (0.3%)
23	W	0.72	1/5660 (0.0%)	1.24	44/7653 (0.6%)
24	a	0.38	0/636	0.61	0/856
24	h	0.37	0/615	0.61	0/829
25	b	0.43	0/585	0.62	0/795
25	i	0.43	0/585	0.62	0/795
26	c	0.44	0/564	0.65	1/761 (0.1%)
26	j	0.44	0/564	0.66	1/761 (0.1%)
27	d	0.37	0/532	0.60	0/715
27	k	0.37	0/532	0.60	0/715
28	e	0.40	0/634	0.71	0/859

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	l	0.40	0/625	0.70	0/848
29	f	0.41	0/649	0.61	0/880
29	m	0.42	0/649	0.61	0/880
30	g	0.45	0/753	0.69	2/1013 (0.2%)
30	n	0.43	0/535	0.66	2/717 (0.3%)
31	o	1.03	9/839 (1.1%)	1.65	11/1127 (1.0%)
32	p	0.83	4/514 (0.8%)	1.32	2/686 (0.3%)
33	q	0.41	0/856	0.54	0/1155
33	r	0.39	0/828	0.54	1/1117 (0.1%)
33	s	0.40	0/835	0.53	0/1126
33	t	0.40	0/848	0.56	0/1143
All	All	0.69	78/78171 (0.1%)	0.88	196/107413 (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	8
3	C	0	3
9	I	0	1
10	J	0	3
12	L	0	5
13	T	0	2
14	M	0	5
15	N	0	1
16	O	0	11
18	Q	0	3
20	S	0	3
23	W	0	35
27	d	0	1
27	k	0	1
28	e	0	2
28	l	0	2
30	g	0	2
30	n	0	2
All	All	0	90

The worst 5 of 78 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	T	444	CYS	CB-SG	-22.89	1.43	1.82
13	T	454	CYS	CB-SG	-18.67	1.50	1.82
13	T	185	HIS	CB-CG	18.43	1.83	1.50
13	T	399	CYS	CB-SG	-17.51	1.52	1.82
8	H	712	CYS	CB-SG	-17.09	1.53	1.82

The worst 5 of 196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	T	130	TYR	N-CA-C	16.80	156.37	111.00
13	T	152	LYS	CB-CA-C	-16.28	77.83	110.40
13	T	153	LYS	N-CA-CB	12.84	133.71	110.60
6	F	1110	U	C5-C4-O4	11.77	132.96	125.90
1	A	284	ARG	NE-CZ-NH2	11.66	126.13	120.30

There are no chirality outliers.

5 of 90 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	239	PHE	Peptide
1	A	288	GLU	Peptide
1	A	539	PRO	Peptide
1	A	907	ASN	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1925/2413 (80%)	1558 (81%)	328 (17%)	39 (2%)	7	41
3	C	872/1008 (86%)	735 (84%)	121 (14%)	16 (2%)	8	43
7	G	150/175 (86%)	134 (89%)	13 (9%)	3 (2%)	7	41
8	H	496/859 (58%)	474 (96%)	16 (3%)	6 (1%)	13	51
9	I	481/687 (70%)	433 (90%)	45 (9%)	3 (1%)	25	64
10	J	414/590 (70%)	368 (89%)	35 (8%)	11 (3%)	5	35
11	K	92/215 (43%)	84 (91%)	7 (8%)	1 (1%)	14	53
12	L	155/157 (99%)	118 (76%)	34 (22%)	3 (2%)	8	42
13	T	326/455 (72%)	283 (87%)	21 (6%)	22 (7%)	1	15
14	M	177/364 (49%)	137 (77%)	36 (20%)	4 (2%)	6	38
15	N	259/339 (76%)	219 (85%)	35 (14%)	5 (2%)	8	42
16	O	335/451 (74%)	268 (80%)	58 (17%)	9 (3%)	5	35
17	P	63/175 (36%)	50 (79%)	10 (16%)	3 (5%)	2	22
18	Q	193/379 (51%)	156 (81%)	29 (15%)	8 (4%)	3	26
19	R	25/135 (18%)	20 (80%)	5 (20%)	0	100	100
20	S	205/577 (36%)	166 (81%)	36 (18%)	3 (2%)	10	47
21	U	144/251 (57%)	140 (97%)	4 (3%)	0	100	100
22	V	82/382 (22%)	71 (87%)	9 (11%)	2 (2%)	6	37
23	W	697/1145 (61%)	600 (86%)	72 (10%)	25 (4%)	3	29
24	a	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
24	h	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
25	b	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
25	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
26	c	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	10	47
26	j	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	10	47
27	d	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
27	k	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
28	e	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	12	50
28	l	79/101 (78%)	69 (87%)	9 (11%)	1 (1%)	12	50
29	f	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
29	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
30	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	14	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	n	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	9	46
31	o	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	9	46
32	p	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
33	q	125/503 (25%)	115 (92%)	6 (5%)	4 (3%)	4	31
33	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	5	36
33	s	120/503 (24%)	115 (96%)	4 (3%)	1 (1%)	19	59
33	t	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
All	All	8803/14738 (60%)	7603 (86%)	1021 (12%)	179 (2%)	11	41

5 of 179 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	487	ASN
1	A	645	ASP
1	A	1404	HIS
1	A	1405	ILE
1	A	1540	ASN

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	1751/2182 (80%)	1715 (98%)	36 (2%)	53	78
3	C	794/910 (87%)	785 (99%)	9 (1%)	73	88
7	G	36/165 (22%)	26 (72%)	10 (28%)	0	3
8	H	57/786 (7%)	47 (82%)	10 (18%)	2	12
9	I	219/633 (35%)	218 (100%)	1 (0%)	88	95
10	J	212/525 (40%)	206 (97%)	6 (3%)	43	72
11	K	88/193 (46%)	86 (98%)	2 (2%)	50	76
12	L	141/141 (100%)	139 (99%)	2 (1%)	67	85
13	T	177/413 (43%)	130 (73%)	47 (27%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	M	171/332 (52%)	167 (98%)	4 (2%)	50	76
15	N	224/296 (76%)	220 (98%)	4 (2%)	59	81
16	O	295/397 (74%)	290 (98%)	5 (2%)	60	82
17	P	56/151 (37%)	54 (96%)	2 (4%)	35	67
18	Q	173/328 (53%)	171 (99%)	2 (1%)	71	87
19	R	21/121 (17%)	20 (95%)	1 (5%)	25	60
20	S	192/538 (36%)	190 (99%)	2 (1%)	76	88
21	U	134/225 (60%)	131 (98%)	3 (2%)	52	77
22	V	24/346 (7%)	22 (92%)	2 (8%)	11	42
23	W	613/1029 (60%)	559 (91%)	54 (9%)	10	40
24	a	70/176 (40%)	70 (100%)	0	100	100
24	h	67/176 (38%)	67 (100%)	0	100	100
25	b	65/83 (78%)	60 (92%)	5 (8%)	13	45
25	i	65/83 (78%)	60 (92%)	5 (8%)	13	45
26	c	61/77 (79%)	60 (98%)	1 (2%)	62	83
26	j	61/77 (79%)	60 (98%)	1 (2%)	62	83
27	d	58/66 (88%)	55 (95%)	3 (5%)	23	58
27	k	58/66 (88%)	55 (95%)	3 (5%)	23	58
28	e	69/89 (78%)	67 (97%)	2 (3%)	42	72
28	l	68/89 (76%)	66 (97%)	2 (3%)	42	72
29	f	77/129 (60%)	71 (92%)	6 (8%)	12	44
29	m	77/129 (60%)	71 (92%)	6 (8%)	12	44
30	g	79/103 (77%)	74 (94%)	5 (6%)	18	53
30	n	59/103 (57%)	55 (93%)	4 (7%)	16	50
31	o	45/219 (20%)	42 (93%)	3 (7%)	16	50
32	p	26/100 (26%)	25 (96%)	1 (4%)	33	66
33	q	63/451 (14%)	56 (89%)	7 (11%)	6	31
33	r	60/451 (13%)	55 (92%)	5 (8%)	11	42
33	s	59/451 (13%)	52 (88%)	7 (12%)	5	27
33	t	62/451 (14%)	54 (87%)	8 (13%)	4	24
All	All	6627/13280 (50%)	6351 (96%)	276 (4%)	33	63

5 of 276 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	k	41	ASP
29	m	77	ASP
33	r	99	ARG
13	T	202	PHE
13	T	159	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
13	T	292	HIS
16	O	428	GLN
13	T	358	ASN
15	N	227	ASN
18	Q	37	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	114/214 (53%)	27 (23%)	3 (2%)
4	D	102/112 (91%)	31 (30%)	5 (4%)
5	E	57/369 (15%)	34 (59%)	6 (10%)
6	F	88/1175 (7%)	30 (34%)	8 (9%)
All	All	361/1870 (19%)	122 (33%)	22 (6%)

5 of 122 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	32	G
2	B	33	U
2	B	42	A
2	B	44	A
2	B	74	U

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	F	29	C
6	F	40	U
6	F	31	A

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Mol	Chain	Res	Type
6	F	41	C
4	D	56	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 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	$\# Z > 2$
34	IHP	A	3000	-	36,36,36	0.70	0	54,60,60	0.96	0
35	GTP	C	1500	36	26,34,34	1.35	3 (11%)	32,54,54	2.46	12 (37%)

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
34	IHP	A	3000	-	-	15/30/54/54	0/1/1/1
35	GTP	C	1500	36	-	5/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	C	1500	GTP	C6-N1	-3.52	1.32	1.37
35	C	1500	GTP	PB-O1B	-2.77	1.41	1.50
35	C	1500	GTP	C4-N3	-2.35	1.31	1.37

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	C	1500	GTP	PB-O3B-PG	-6.13	111.78	132.83
35	C	1500	GTP	PA-O3A-PB	-5.30	114.65	132.83
35	C	1500	GTP	O6-C6-N1	4.93	126.47	120.65
35	C	1500	GTP	O6-C6-C5	-4.54	115.51	124.37
35	C	1500	GTP	O4'-C1'-C2'	3.61	112.19	106.93

There are no chirality outliers.

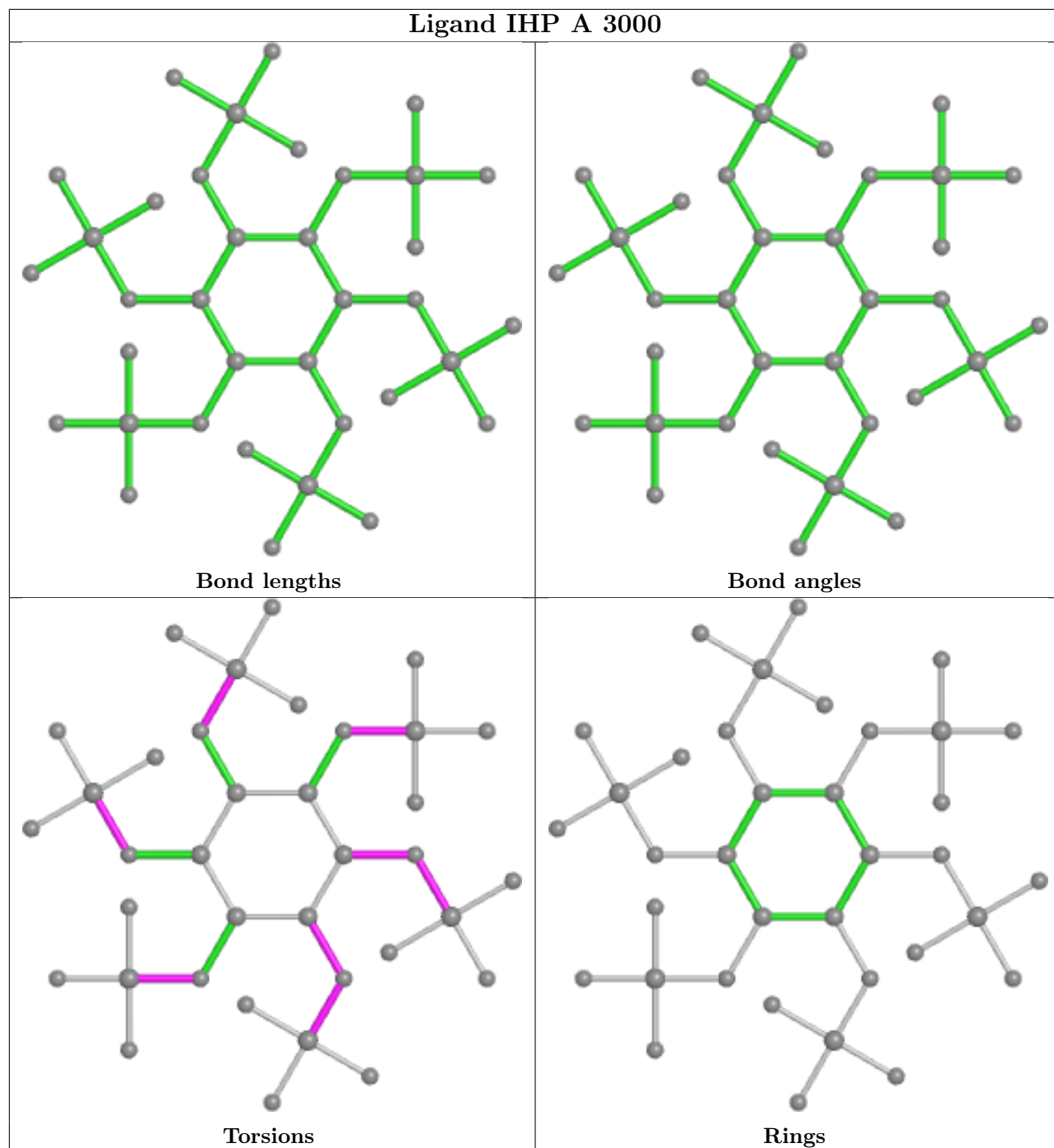
5 of 20 torsion outliers are listed below:

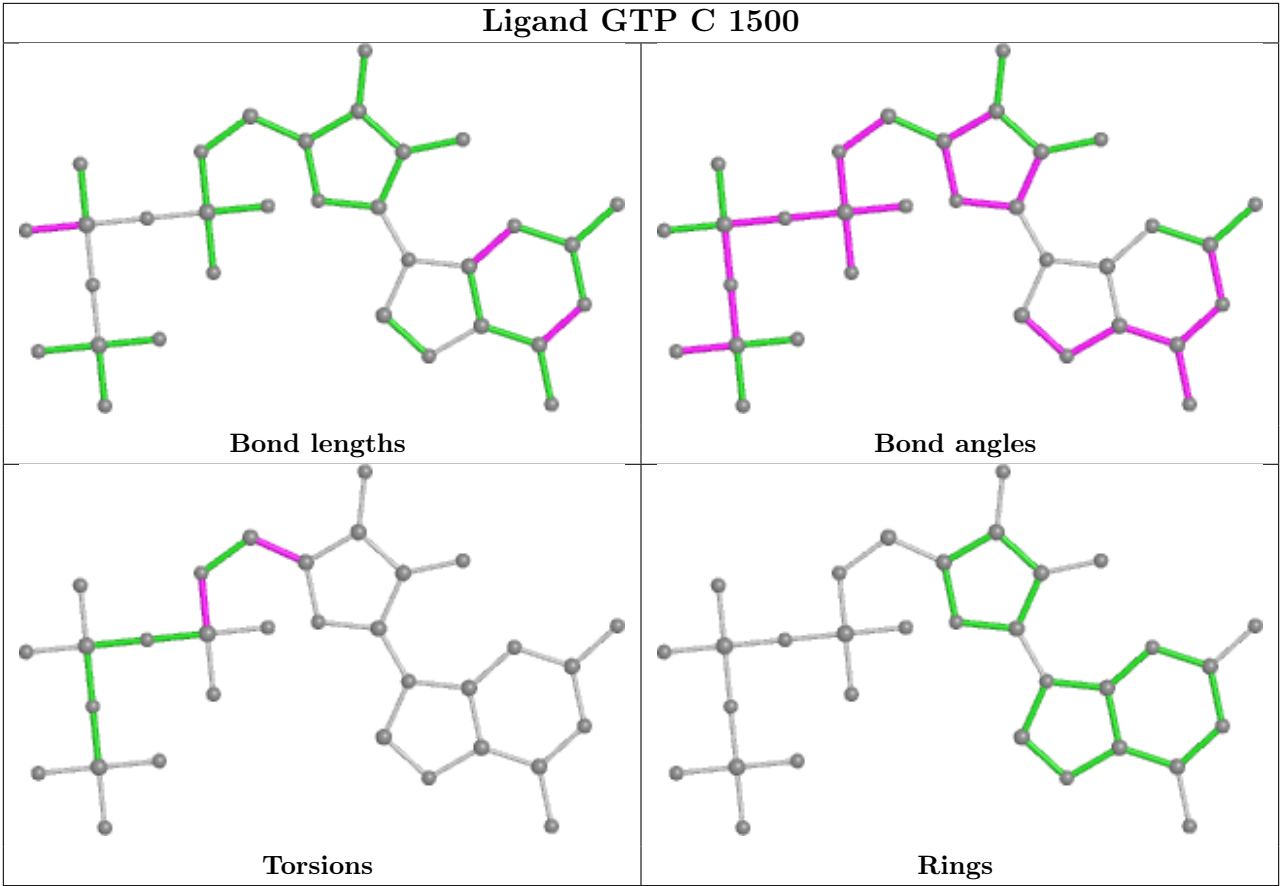
Mol	Chain	Res	Type	Atoms
34	A	3000	IHP	C1-C6-O16-P6
34	A	3000	IHP	C5-C6-O16-P6
34	A	3000	IHP	C2-O12-P2-O22
34	A	3000	IHP	C3-O13-P3-O43
35	C	1500	GTP	C5'-O5'-PA-O3A

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	350:G	O3'	351:U	P	3.39

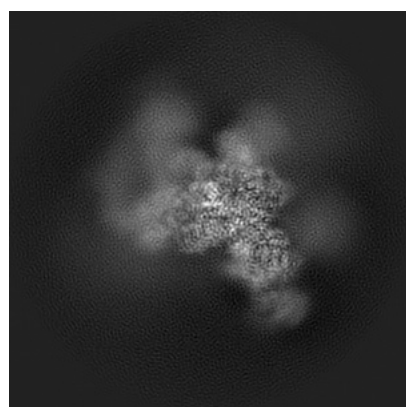
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6839. These allow visual inspection of the internal detail of the map and identification of artifacts.

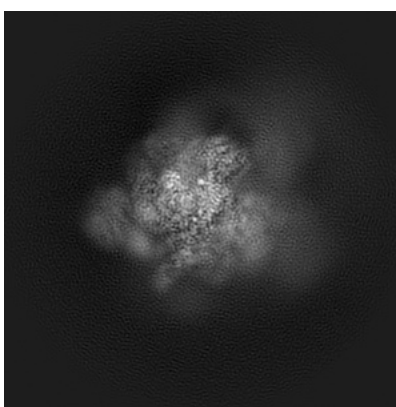
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

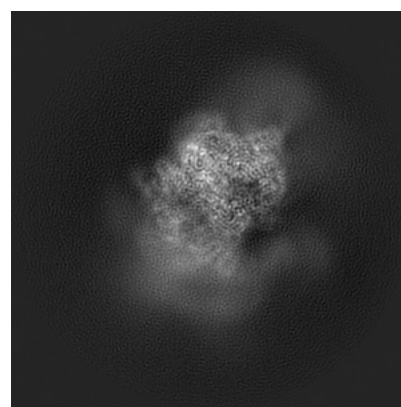
6.1.1 Primary map



X



Y

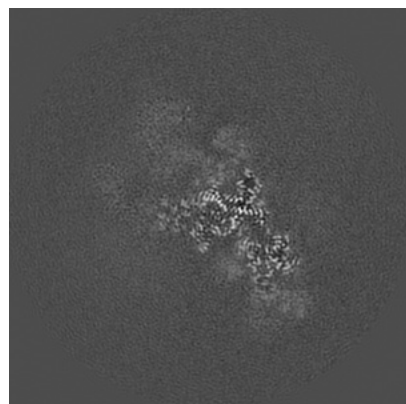


Z

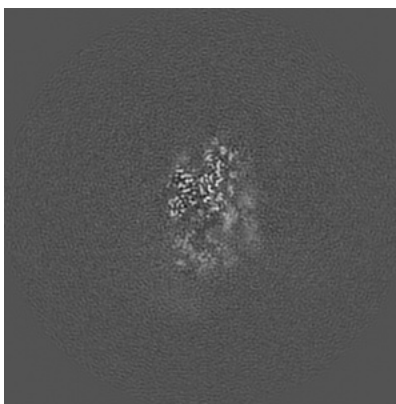
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

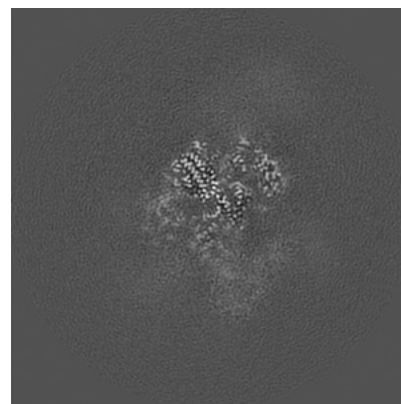
6.2.1 Primary map



X Index: 200



Y Index: 200

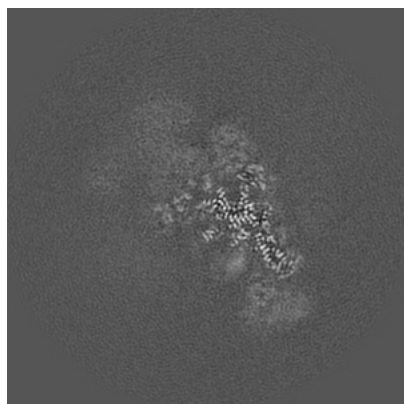


Z Index: 200

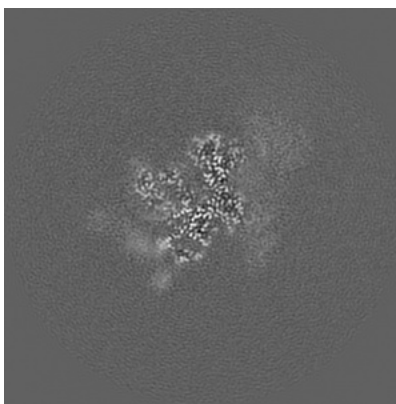
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

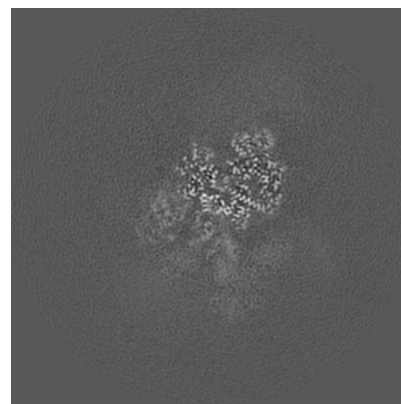
6.3.1 Primary map



X Index: 192



Y Index: 238



Z Index: 206

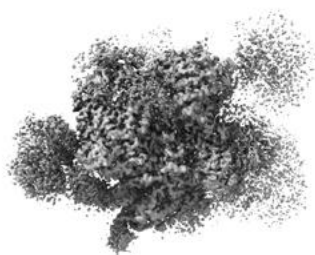
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.034. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

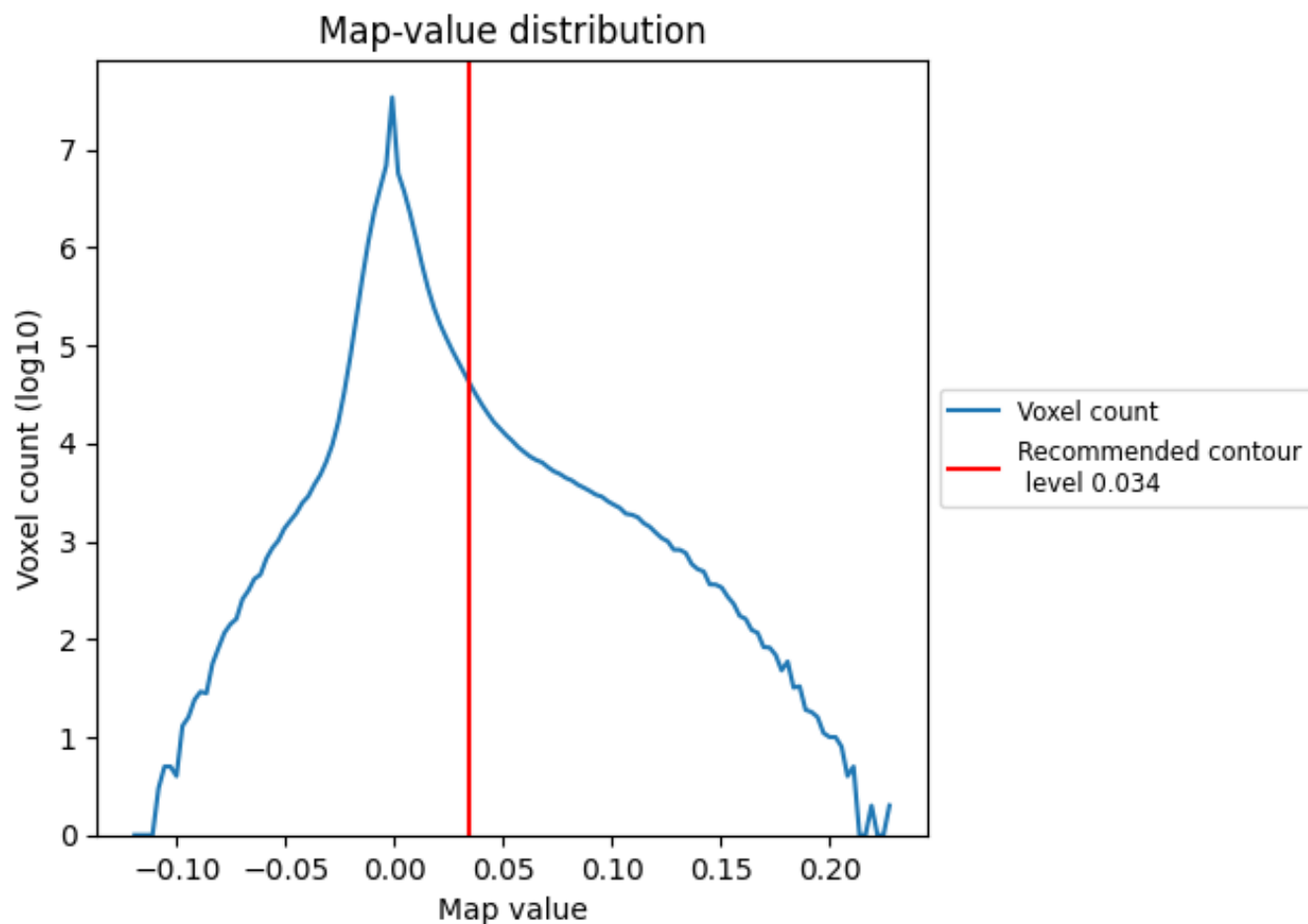
6.5 Mask visualisation

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

7 Map analysis [i](#)

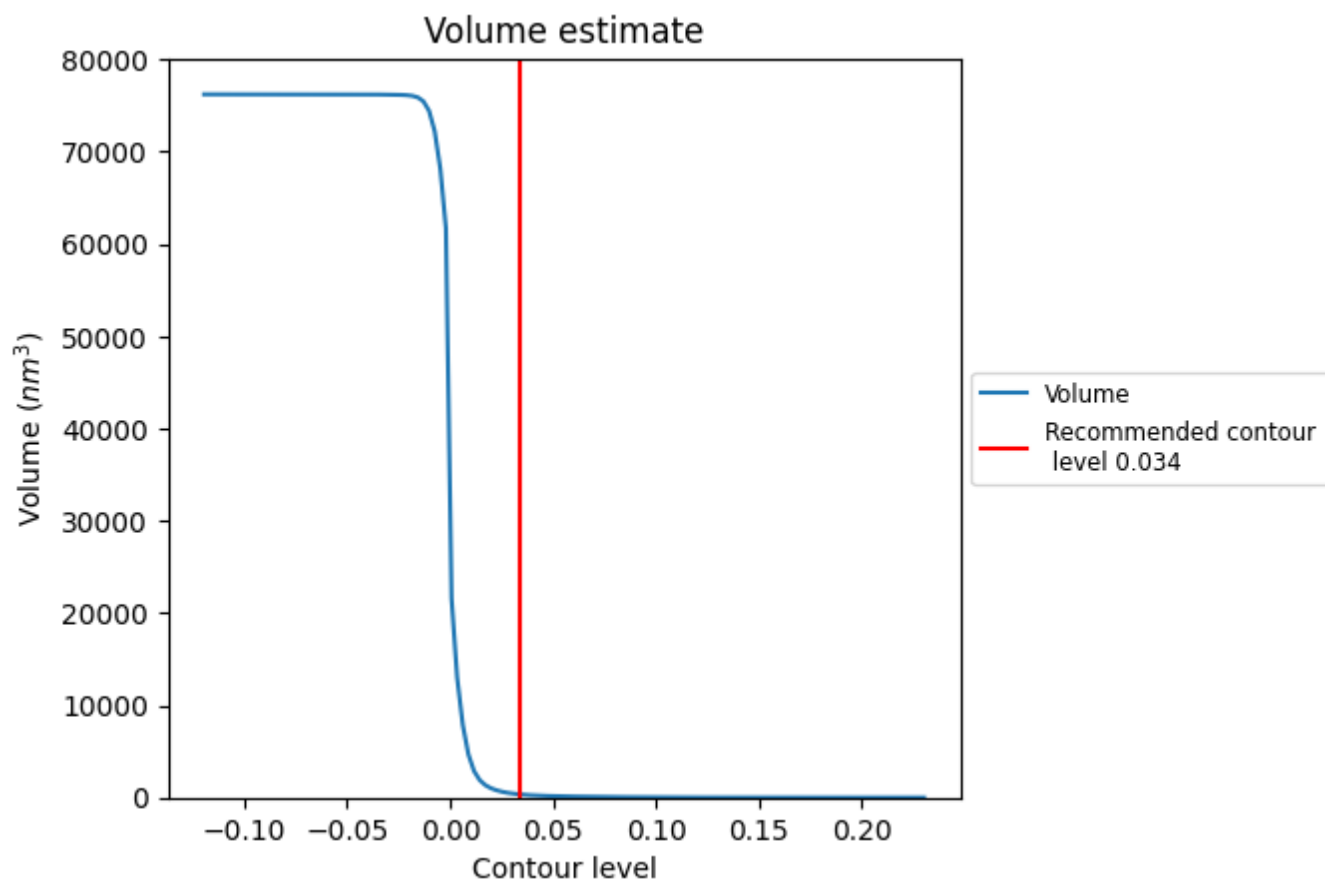
This section contains the results of statistical analysis of the map.

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.

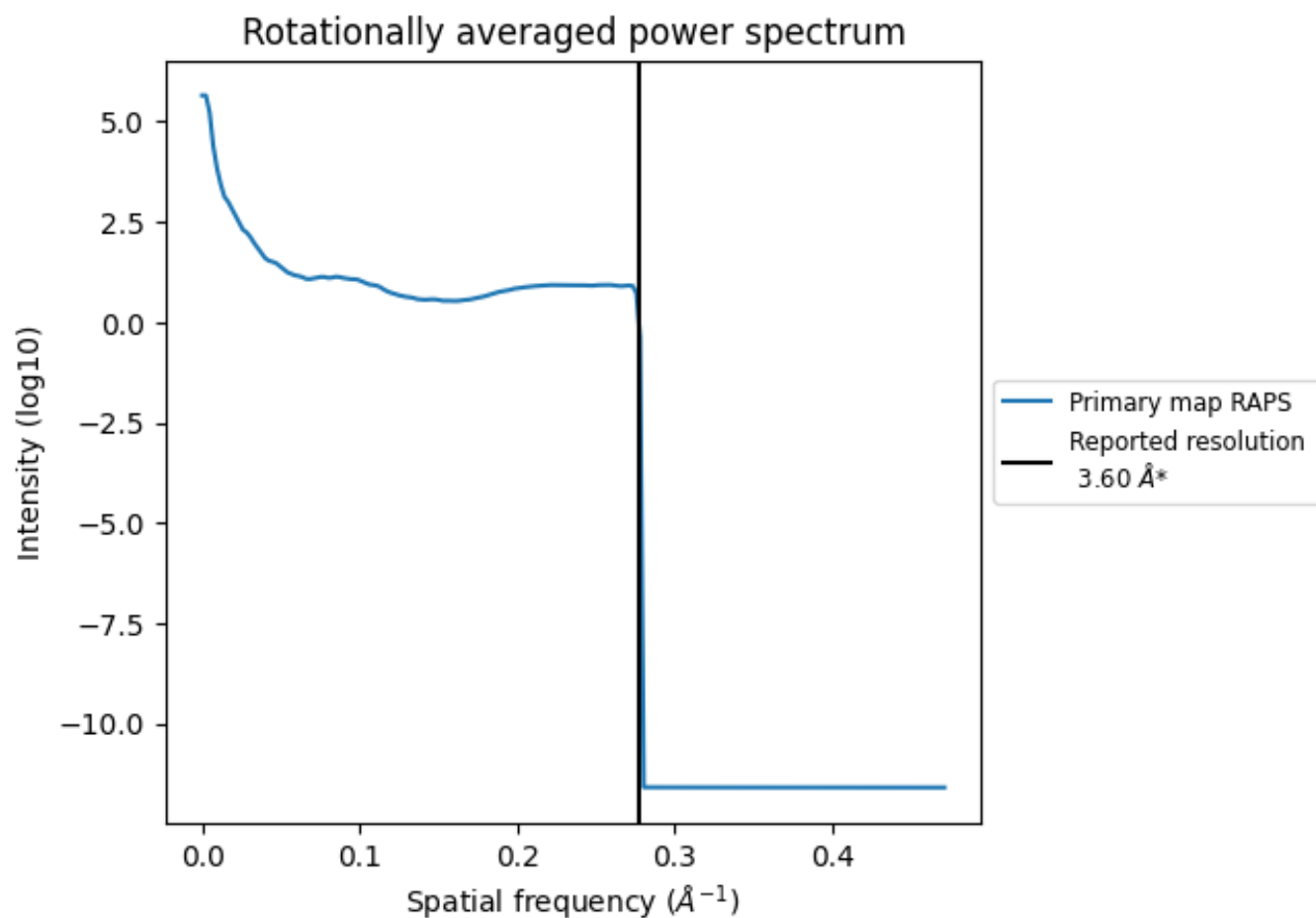
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 343 nm³; this corresponds to an approximate mass of 309 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.278 \AA^{-1}

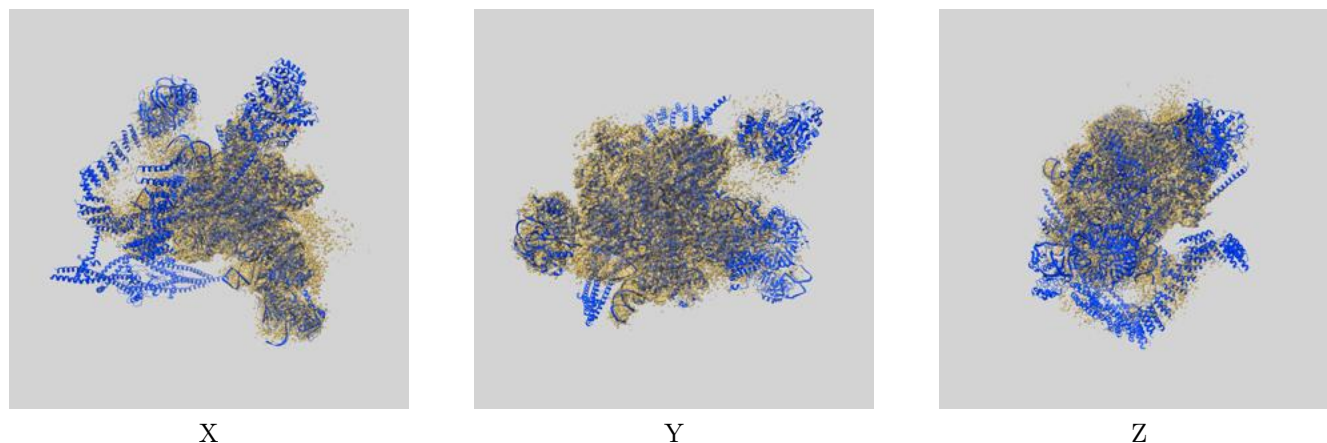
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

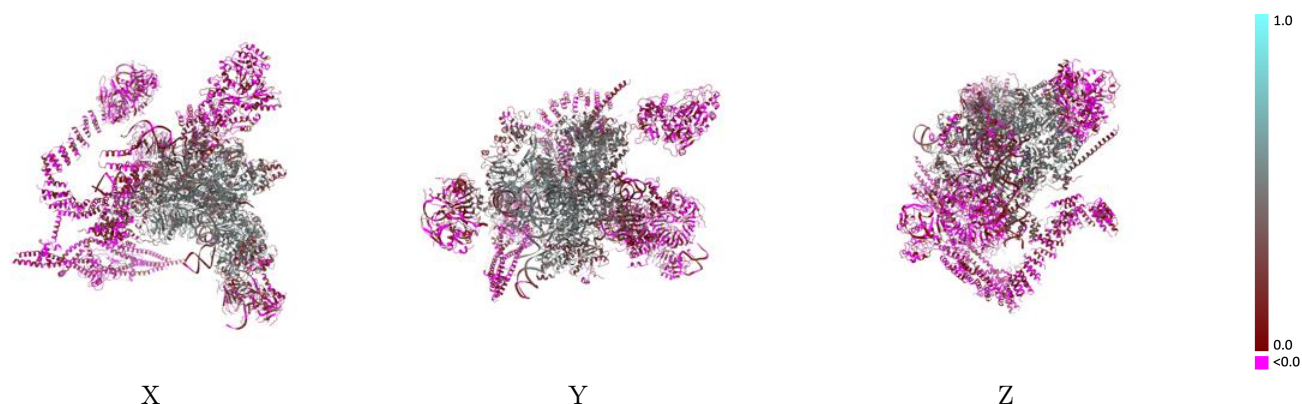
This section contains information regarding the fit between EMDB map EMD-6839 and PDB model 5YLZ. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



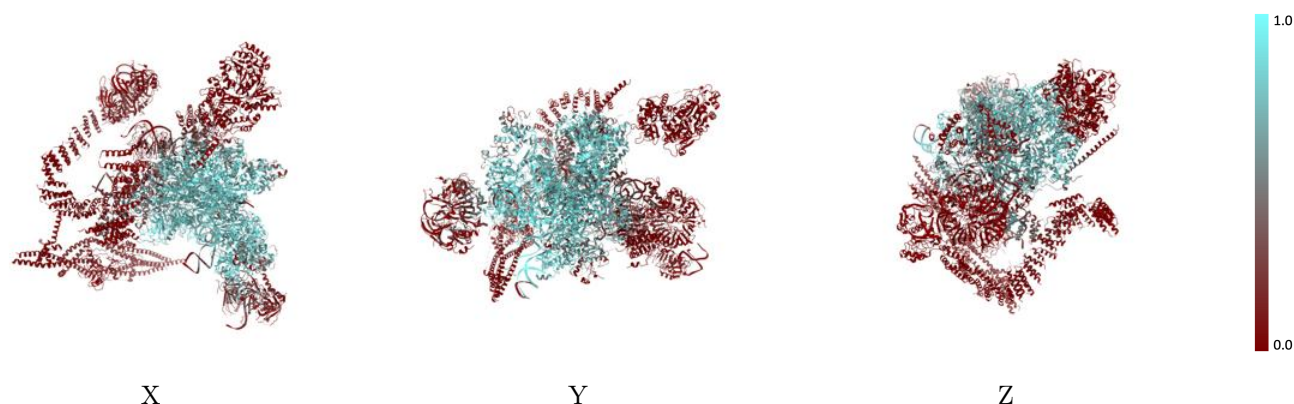
The images above show the 3D surface view of the map at the recommended contour level 0.034 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



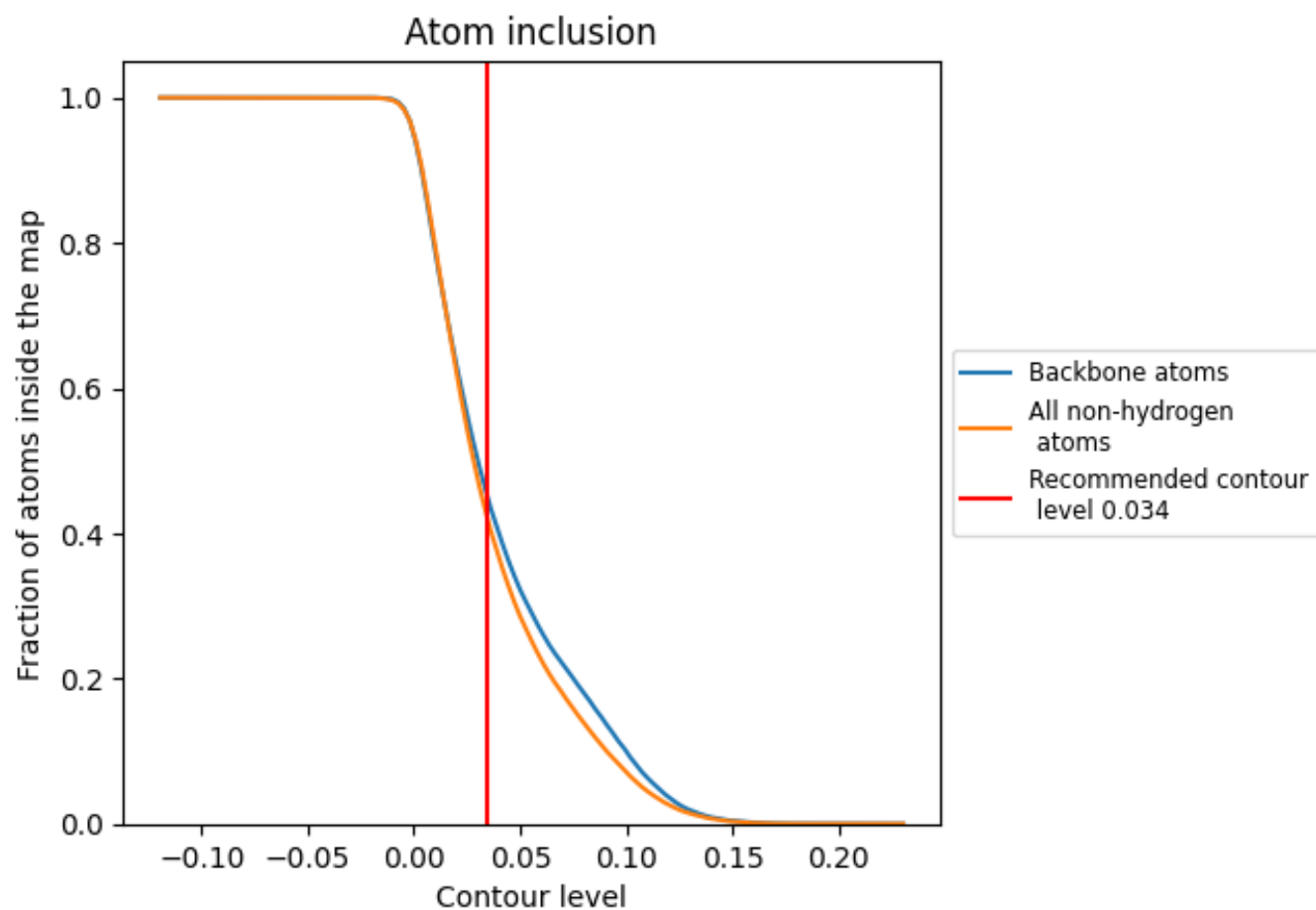
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.034).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 43% 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 (0.034) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4272	 0.2510
A	 0.7290	 0.4270
B	 0.7079	 0.3360
C	 0.7331	 0.4230
D	 0.7560	 0.3550
E	 0.4947	 0.2470
F	 0.2525	 0.1240
G	 0.0000	 0.0080
H	 0.0190	 0.0080
I	 0.3308	 0.2120
J	 0.3032	 0.1980
K	 0.3325	 0.2530
L	 0.7893	 0.4380
M	 0.4135	 0.3100
N	 0.5739	 0.3440
O	 0.8106	 0.4820
P	 0.6784	 0.4730
Q	 0.4653	 0.3650
R	 0.5401	 0.4360
S	 0.6812	 0.3860
T	 0.1841	 0.1280
U	 0.0204	 0.0470
V	 0.0238	 0.0620
W	 0.0314	 0.0290
a	 0.2707	 0.1470
b	 0.1136	 0.0690
c	 0.1160	 0.0480
d	 0.1862	 0.1130
e	 0.4256	 0.2570
f	 0.2311	 0.0990
g	 0.1257	 0.0380
h	 0.0067	 0.0070
i	 0.0052	 -0.0350
j	 0.0129	 -0.0110
k	 0.0038	 -0.0070



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Chain	Atom inclusion	Q-score
l	 0.0049	 0.0330
m	 0.0267	 -0.0240
n	 0.0194	 0.0030
o	 0.0024	 0.0180
p	 0.0000	 0.0110
q	 0.0000	 -0.0150
r	 0.0000	 0.0230
s	 0.0000	 -0.0180
t	 0.0000	 0.0140