



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 09:07 pm BST

PDB ID : 9FMD
EMDB ID : EMD-4525
Title : Integrative model of the human post-catalytic spliceosome (P-complex)
Authors : Rothe, P.; Plaschka, C.; Vorlaender, M.K.
Deposited on : 2024-06-05
Resolution : 3.30 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:

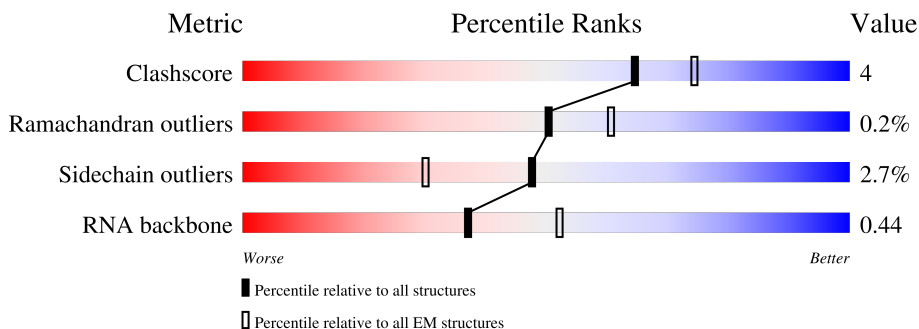
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

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 3.30 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)
Clashscore	158937	4297
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	1	184	
2	2	187	
3	3	476	
4	32	112	
5	5	116	
6	50	339	
7	56	222	

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Mol	Chain	Length	Quality of chain
8	6	106	
9	7	411	
10	8	174	
11	9	146	
12	A	2335	
13	B	2136	
14	C	972	
15	D	285	
16	E	357	
17	EX	14	
18	F	758	
19	H	908	
20	I	855	
21	IN	113	
22	J	848	
23	K	225	
24	L	802	
25	M	243	
26	N	144	
27	NO	301	
28	O	420	
29	P	229	
30	Q	1485	
31	R	536	
32	S	166	







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Mol	Chain	Length	Quality of chain
33	SR	2752	97%
34	T	514	57% 13% 29%
35	U	586	41% 9% 50%
36	V	1220	60% 40%
37	W	579	68% 20% 11%
38	X	451	85%
39	Z	166	31% 68%
40	a	126	67% 33%
40	h	126	66% 34%
41	b	240	64%
41	i	240	66%
42	c	119	67% 33%
42	j	119	67% 33%
43	d	118	75% 25%
43	k	118	81% 19%
44	e	92	86% 14%
44	l	92	88% 12%
45	f	86	81% 16%
45	m	86	84% 16%
46	g	76	93%
46	n	76	95%
47	o	255	63% 36%
48	p	225	41% 59%
49	q	504	20% 80%
49	r	504	24% 76%

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Mol	Chain	Length	Quality of chain
49	s	504	
49	t	504	
50	w	646	
51	x	289	
52	y	301	
53	z	415	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 120526 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 PRKR-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	123	1013	635	193	180	5	0	0

- Molecule 2 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	120	2535	1135	428	852	120	0	0

- Molecule 3 is a protein called Splicing factor ESS-2 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	3	82	408	244	82	82	0	0

- Molecule 4 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	32	60	504	314	96	92	2	0	0

- Molecule 5 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	5	92	1936	867	322	655	92	0	0

- Molecule 6 is a protein called Protein FAM50A.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	N			O
6	50	212	1053	629	212	212	0	0

- Molecule 7 is a protein called STING ER exit protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	56	101	Total	C	N	O	0	0
			498	296	101	101		

- Molecule 8 is a DNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	6	97	Total	C	N	O	P	0	0
			2075	928	381	669	97		

- Molecule 9 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	7	390	Total	C	N	O	0	0
			1928	1147	390	391		

- Molecule 10 is a protein called RNA-binding protein 8A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	8	91	Total	C	N	O	0	0
			445	263	91	91		

- Molecule 11 is a protein called Protein mago nashi homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	9	144	Total	C	N	O	0	0
			712	423	144	145		

- Molecule 12 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	2250	Total	C	N	O	S	0	0
			17802	11405	3151	3176	70		

- Molecule 13 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	1864	Total	C	N	O	S	0	0
			15004	9583	2569	2775	77		

- Molecule 14 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	C	899	7116	4553	1184	1345	34	0	0

- Molecule 15 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	D	72	358	214	72	72	0	0

- Molecule 16 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	E	306	2394	1501	422	457	14	0	0

- Molecule 17 is a RNA chain called Exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
17	EX	14	296	132	52	98	14	0	0

- Molecule 18 is a protein called Splicing factor Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	F	122	1085	712	197	174	2	0	0

- Molecule 19 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	H	459	2932	1827	533	560	12	0	0

- Molecule 20 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	I	727	3610	2156	727	727	0	0

- Molecule 21 is a RNA chain called INTRON.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	IN	42	893	400	158	293	42	0	0

- Molecule 22 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	J	602	2998	1794	602	602	0	0

- Molecule 23 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	K	189	941	563	189	189	0	0

- Molecule 24 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	L	555	3642	2233	706	695	8	0	0

- Molecule 25 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	M	224	1115	666	224	225	0	0

- Molecule 26 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	N	144	1189	748	218	211	12	0	0

- Molecule 27 is a protein called Nitric oxide synthase-interacting protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	NO	174	864	516	174	174	0	0

- Molecule 28 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	O	289	Total	C	N	O	S	0	0
			2318	1455	416	428	19		

- Molecule 29 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P	106	Total	C	N	O	S	0	0
			889	544	174	169	2		

- Molecule 30 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Q	1322	Total	C	N	O		0	0
			6554	3910	1322	1322			

- Molecule 31 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	R	328	Total	C	N	O	P	S	0	0
			2618	1634	479	489	2	14		

- Molecule 32 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	164	Total	C	N	O	S	0	0
			1271	810	220	234	7		

- Molecule 33 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SR	70	Total	C	N	O	S	0	0
			412	251	80	80	1		

- Molecule 34 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	T	363	Total	C	N	O	S	0	0
			2881	1820	525	526	10		

- Molecule 35 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	U	295	2425	1525	431	461	8	0	0

- Molecule 36 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	V	733	3629	2163	733	733	0	0

- Molecule 37 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	W	513	4158	2643	719	772	24	0	0

- Molecule 38 is a protein called Splicing regulator SDE2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	X	66	328	196	66	66	0	0

- Molecule 39 is a protein called Coiled-coil domain-containing protein 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	Z	53	265	159	53	53	0	0

- Molecule 40 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	a	84	658	412	116	124	6	0	0
40	h	83	652	409	115	122	6	0	0

- Molecule 41 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	b	87	654	412	120	115	7	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	82	Total	C	N	O	S	0	0
			664	419	121	117	7		

- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	c	80	Total	C	N	O	S	0	0
			634	404	111	115	4		
42	j	80	Total	C	N	O	S	0	0
			634	404	111	115	4		

- Molecule 43 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	89	Total	C	N	O	S	0	0
			723	454	133	131	5		
43	k	95	Total	C	N	O	S	0	0
			774	486	141	142	5		

- Molecule 44 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	e	79	Total	C	N	O	S	0	0
			651	413	115	118	5		
44	l	81	Total	C	N	O	S	0	0
			669	424	119	121	5		

- Molecule 45 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	f	72	Total	C	N	O	S	0	0
			562	364	93	100	5		
45	m	72	Total	C	N	O	S	0	0
			562	364	93	100	5		

- Molecule 46 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	73	Total	C	N	O	S	0	0
			568	358	102	102	6		
46	n	73	Total	C	N	O	S	0	0
			568	358	102	102	6		

- Molecule 47 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	o	162	1282	820	219	240	3	0	0

- Molecule 48 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	p	92	745	480	130	130	5	0	0

- Molecule 49 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	q	103	514	308	103	103	0	0
49	r	119	594	356	119	119	0	0
49	s	132	659	395	132	132	0	0
49	t	103	514	308	103	103	0	0

- Molecule 50 is a protein called Peptidylprolyl isomerase domain and WD repeat-containing protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	w	538	2655	1578	538	539	0	0

- Molecule 51 is a protein called Splicing factor C9orf78.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
51	x	128	636	379	128	129	0	0

- Molecule 52 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
52	y	79	318	160	79	79	0	0

- Molecule 53 is a protein called NF-kappa-B-activating protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	z	70	430	259	83	86	2	0	0

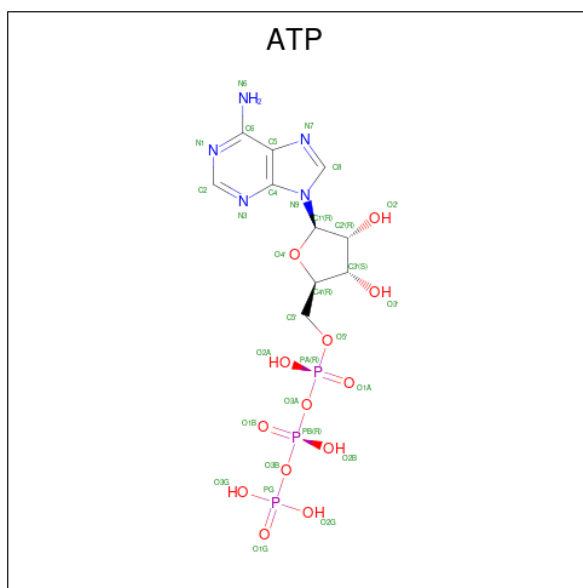
- Molecule 54 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
54	6	5	5	5	0
54	7	1	1	1	0

- Molecule 55 is POTASSIUM ION (three-letter code: K) (formula: K).

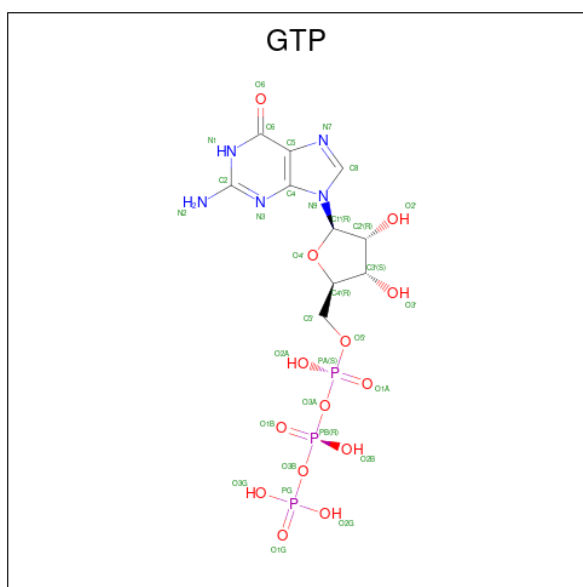
Mol	Chain	Residues	Atoms		AltConf
			Total	K	
55	6	1	1	1	0

- Molecule 56 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
56	7	1	31	10	5	13	3	0

- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

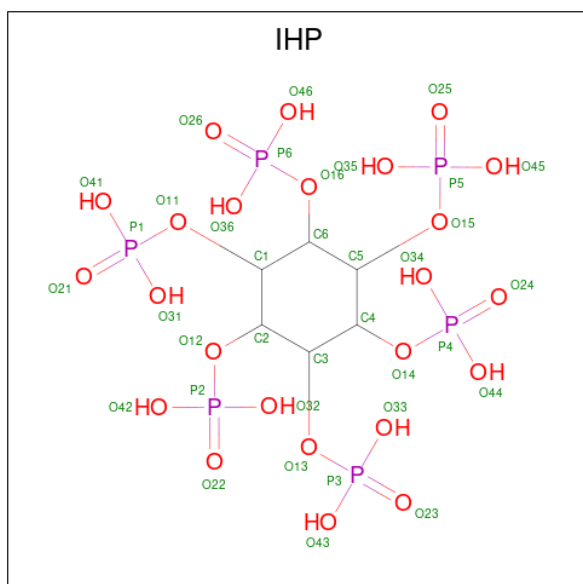


Mol	Chain	Residues	Atoms					AltConf
57	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	N	3	Total	Zn	0
			3	3	
58	O	3	Total	Zn	0
			3	3	

- Molecule 59 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: C₆H₁₈O₂₄P₆).

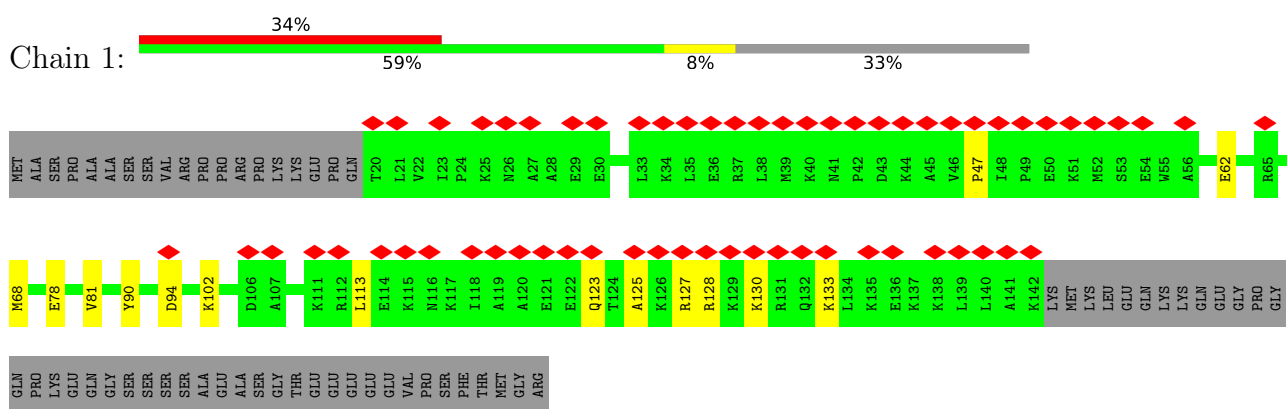


Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
59	U	1	36	6	24	6	0

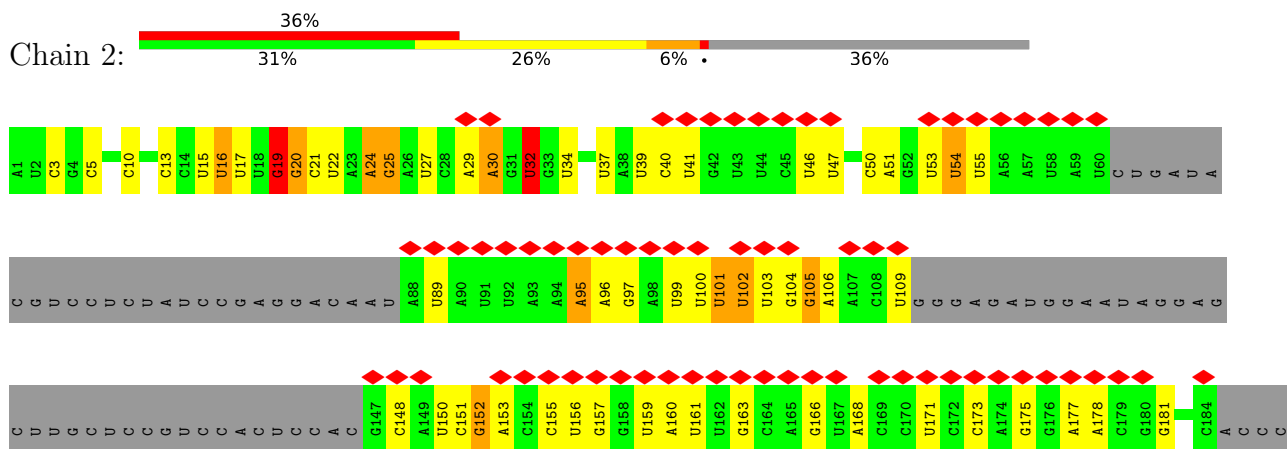
3 Residue-property plots [i](#)

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.

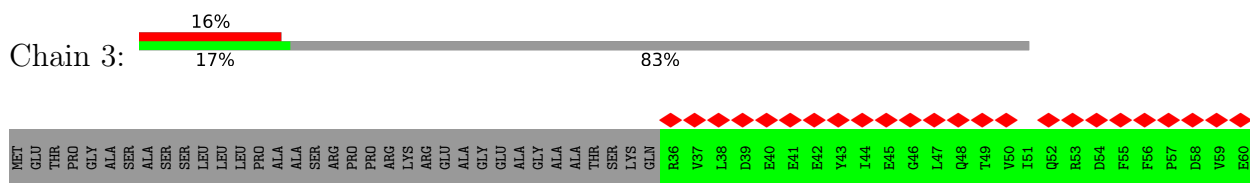
- Molecule 1: PRKR-interacting protein 1

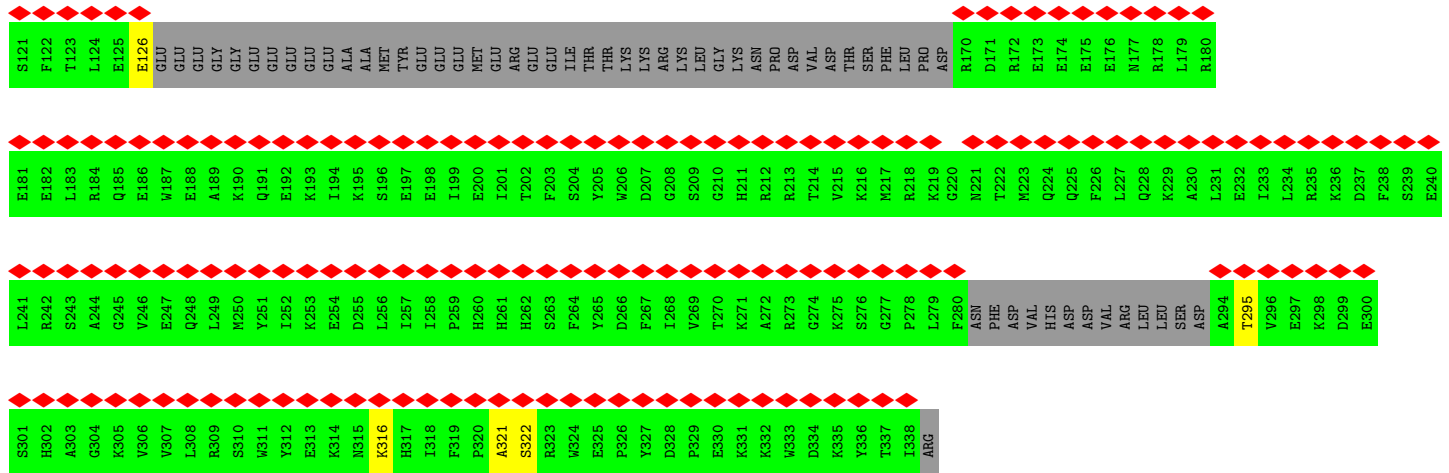


- Molecule 2: U2 snRNA

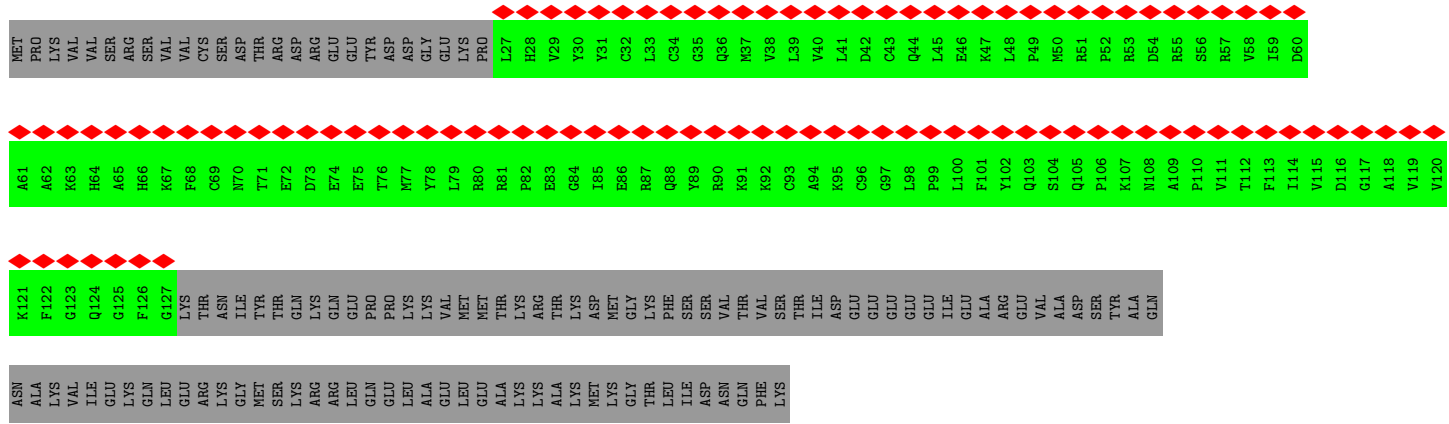


- Molecule 3: Splicing factor ESS-2 homolog

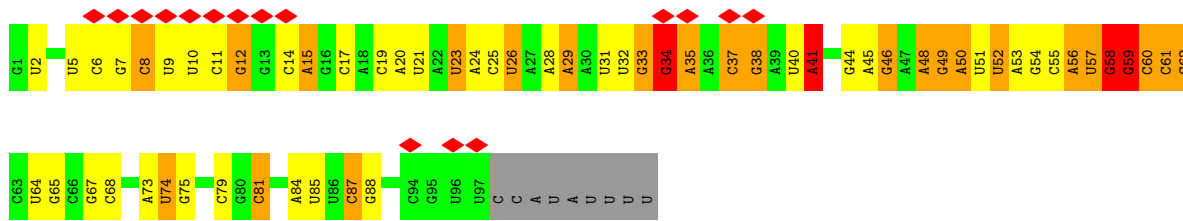




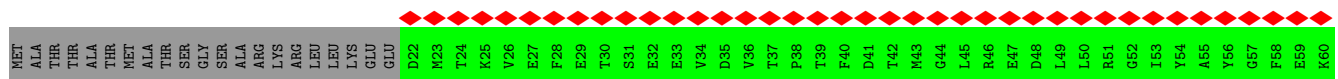
• Molecule 7: STING ER exit protein



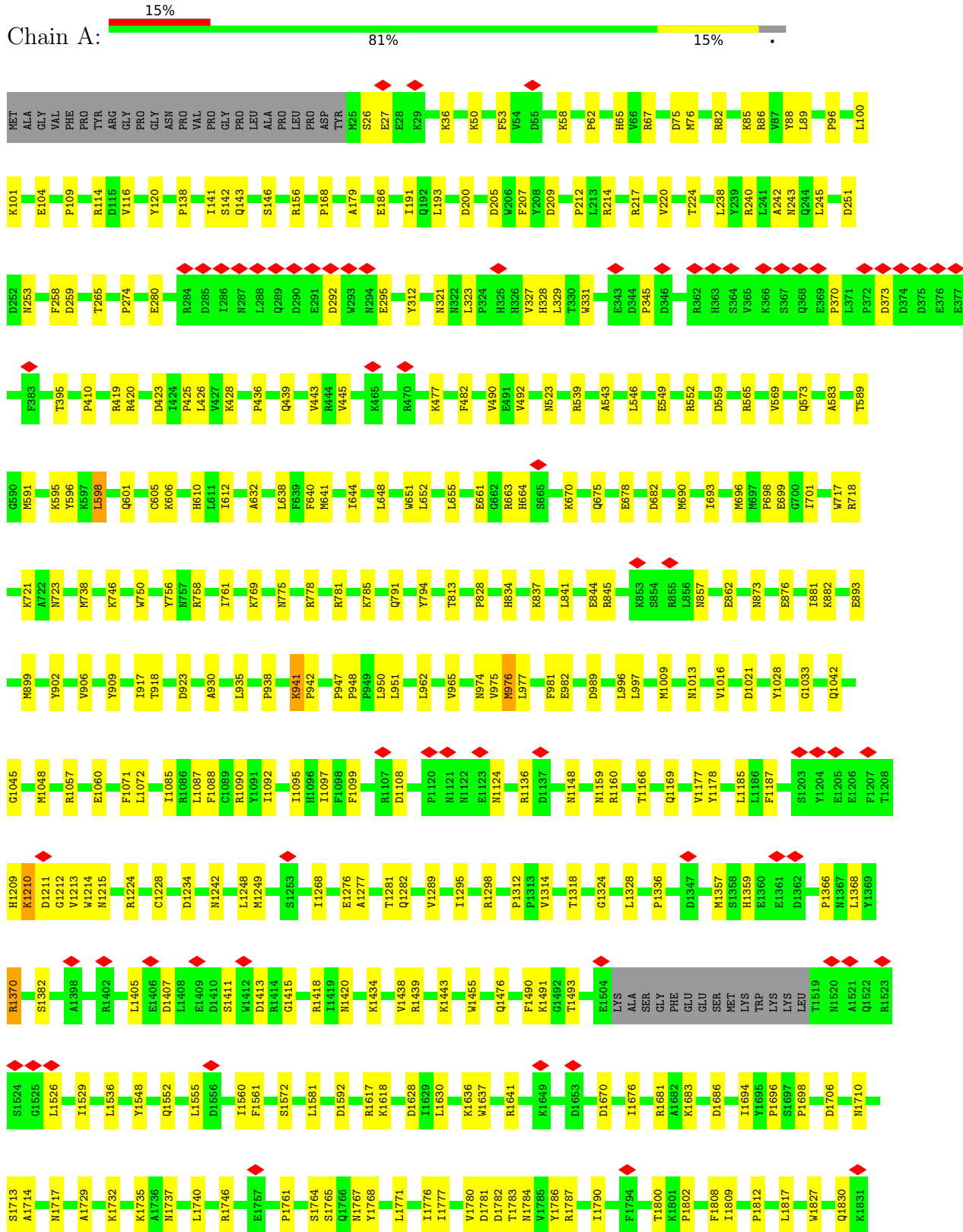
• Molecule 8: U6 snRNA

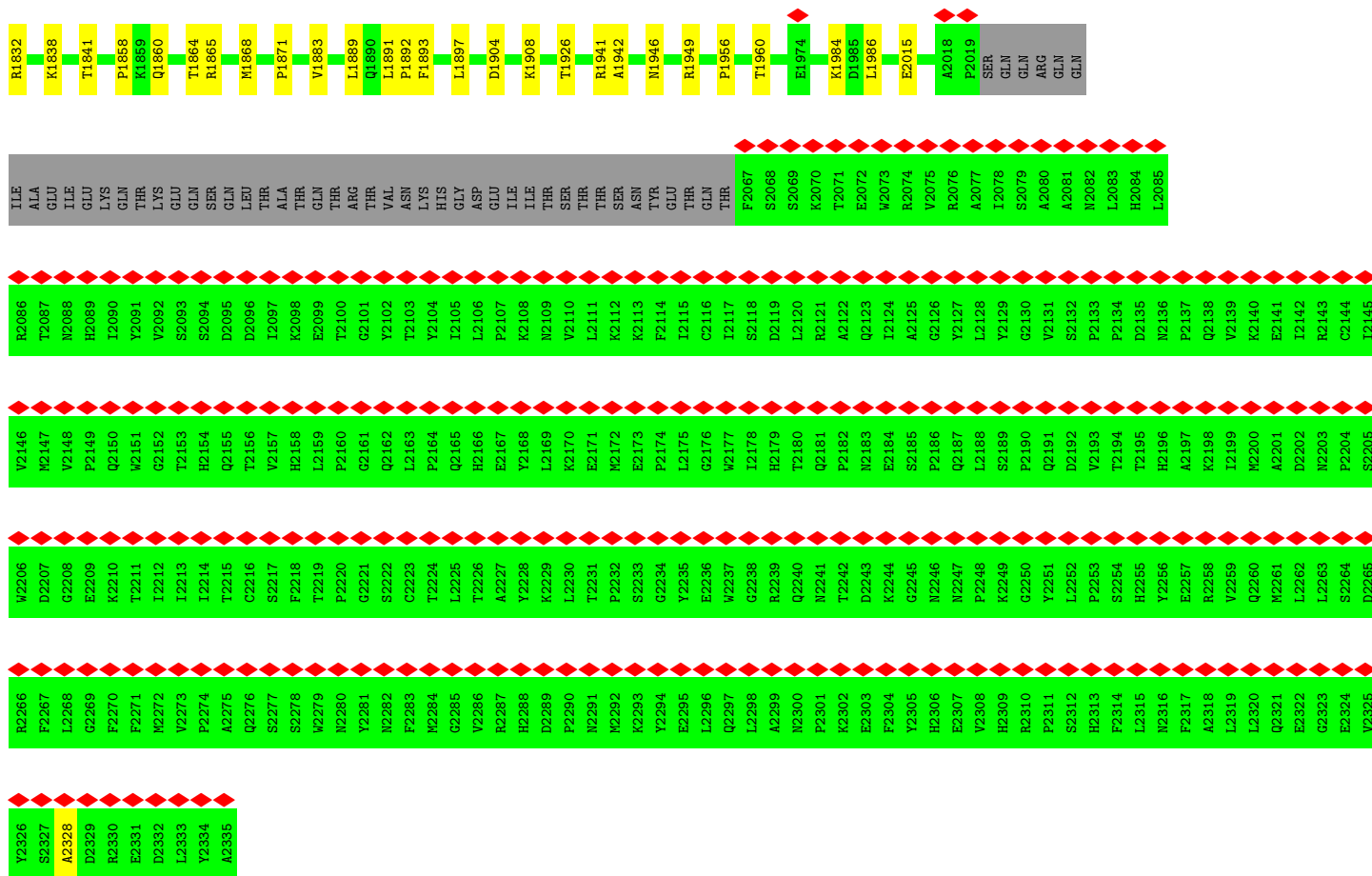


• Molecule 9: Eukaryotic initiation factor 4A-III

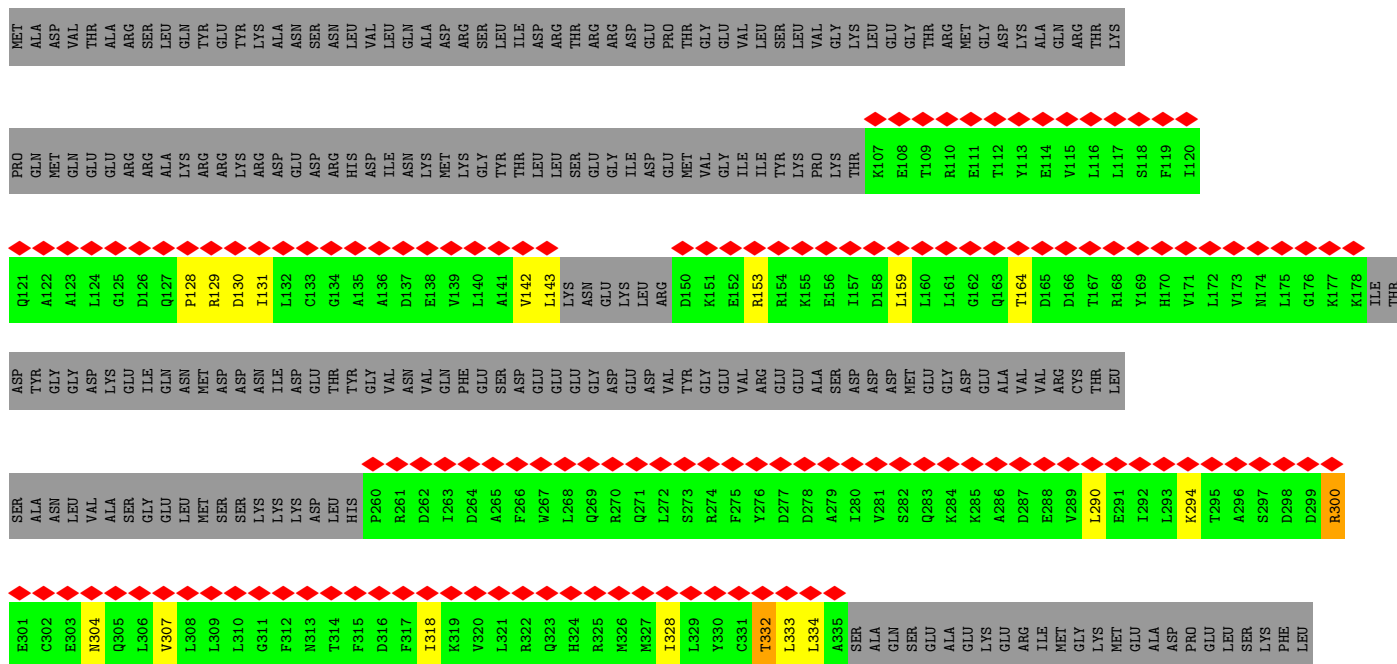
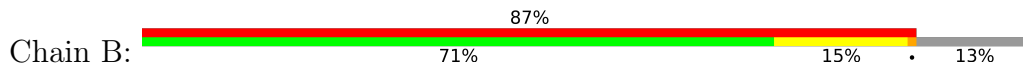


● Molecule 12: Pre-mRNA-processing-splicing factor 8

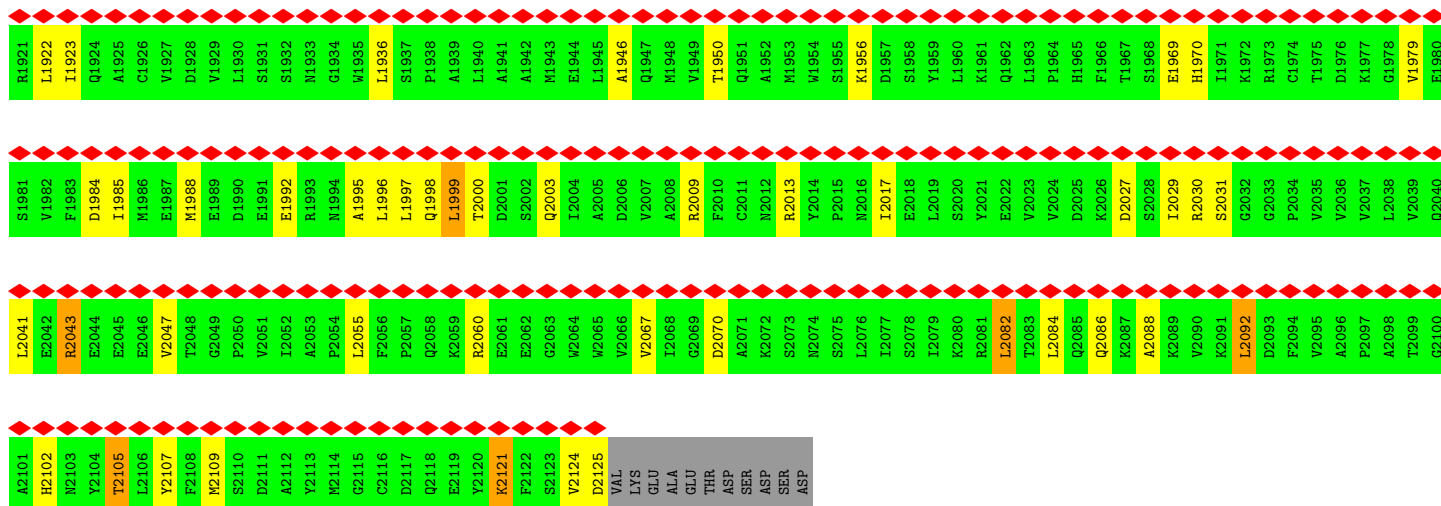




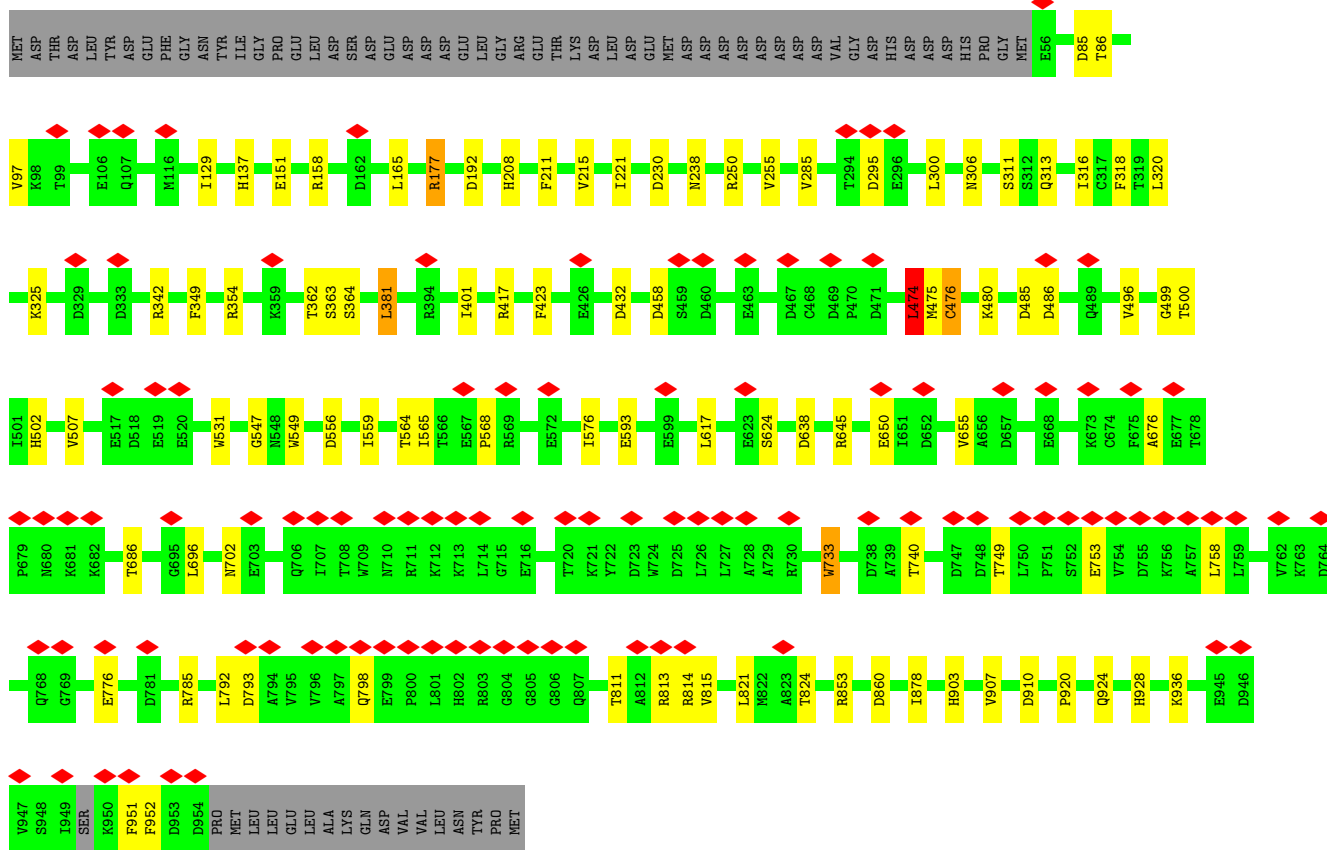
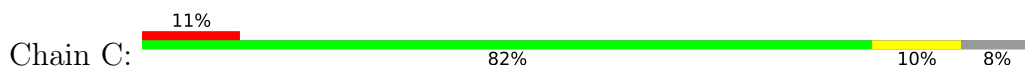
• Molecule 13: U5 small nuclear ribonucleoprotein 200 kDa helicase



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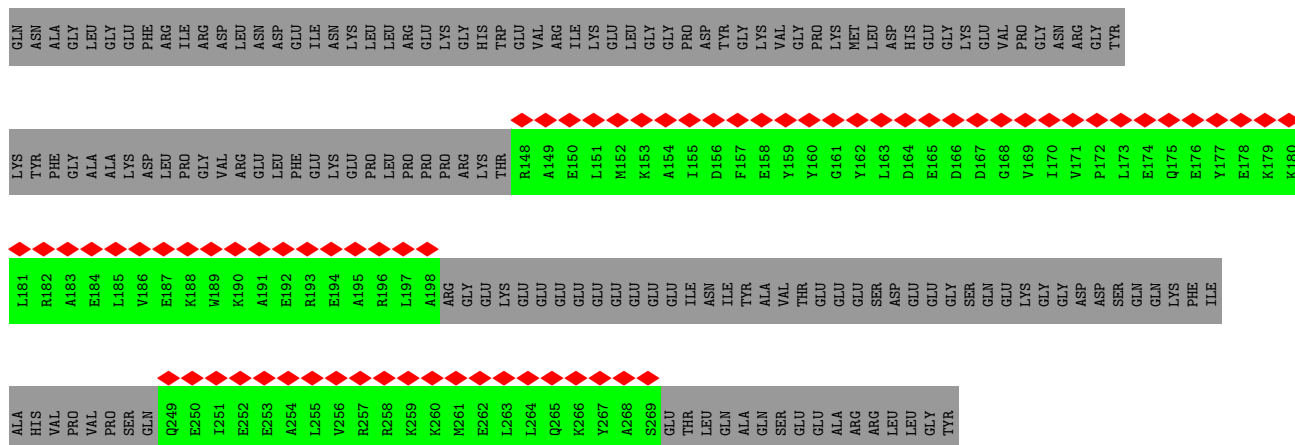


• Molecule 14: 116 kDa U5 small nuclear ribonucleoprotein component

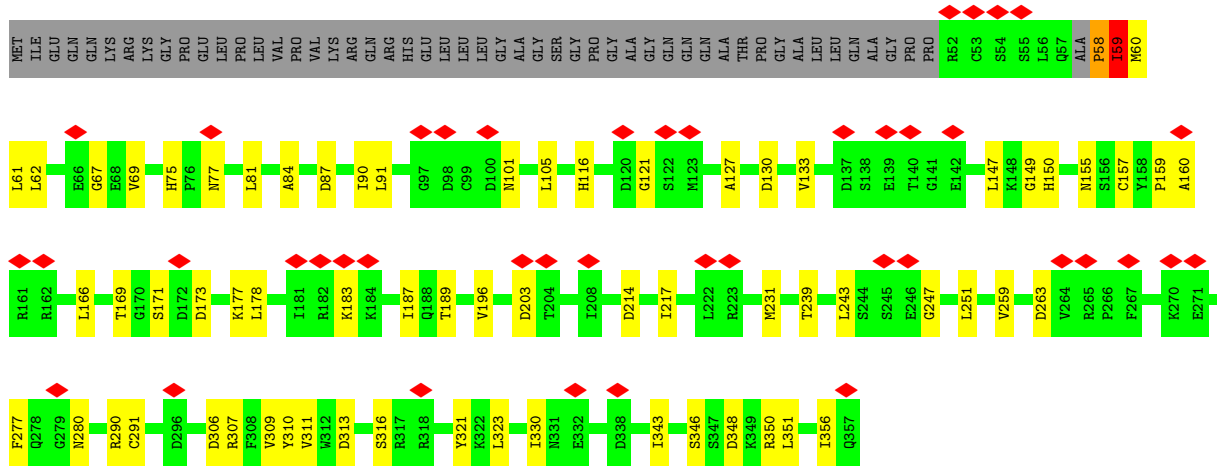


• Molecule 15: Pre-mRNA-splicing factor ISY1 homolog





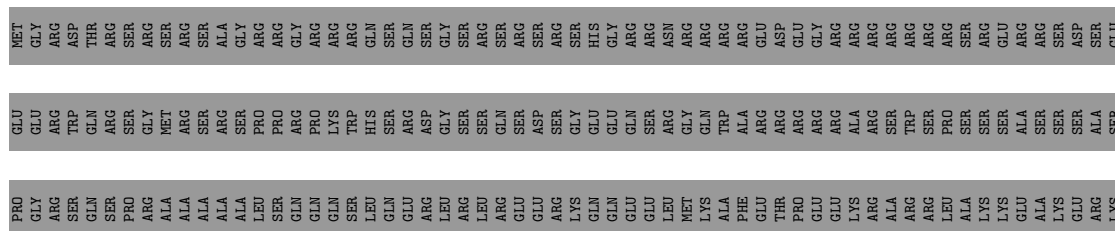
• Molecule 16: U5 small nuclear ribonucleoprotein 40 kDa protein

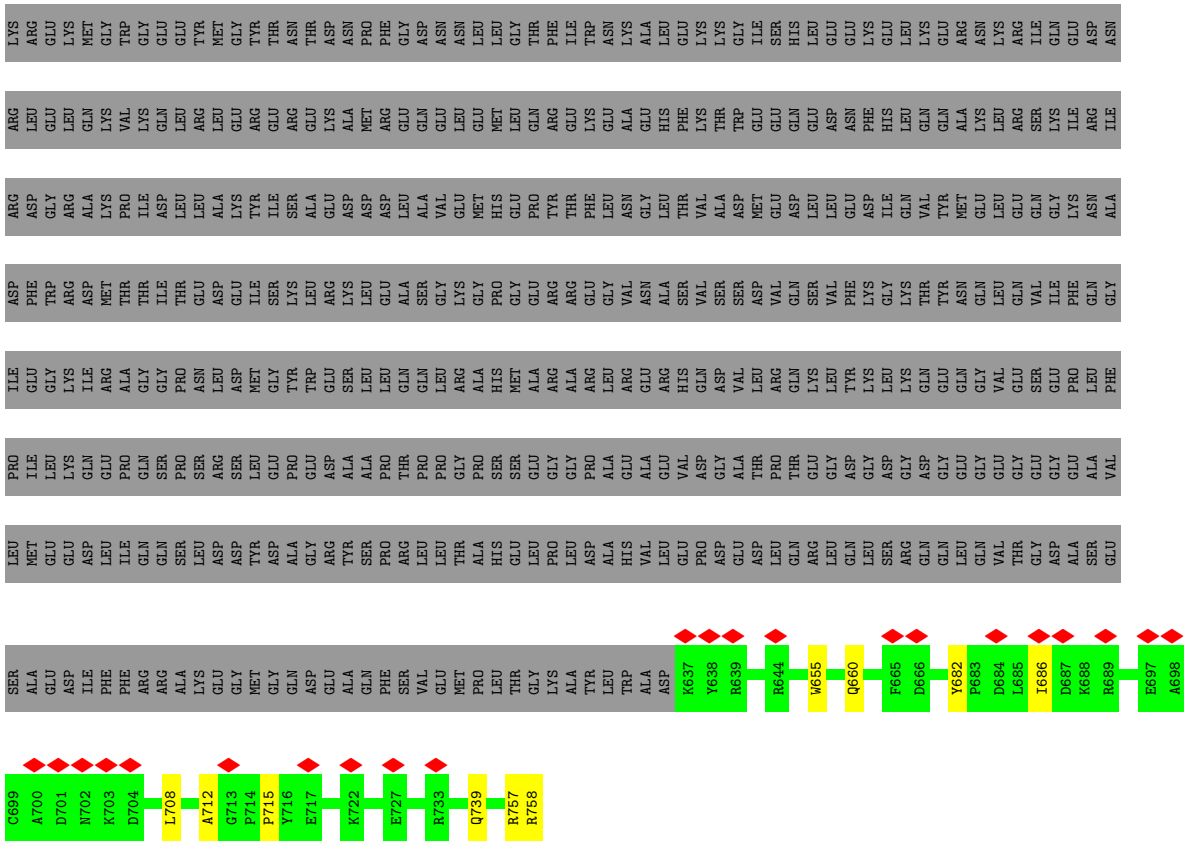


• Molecule 17: Exon

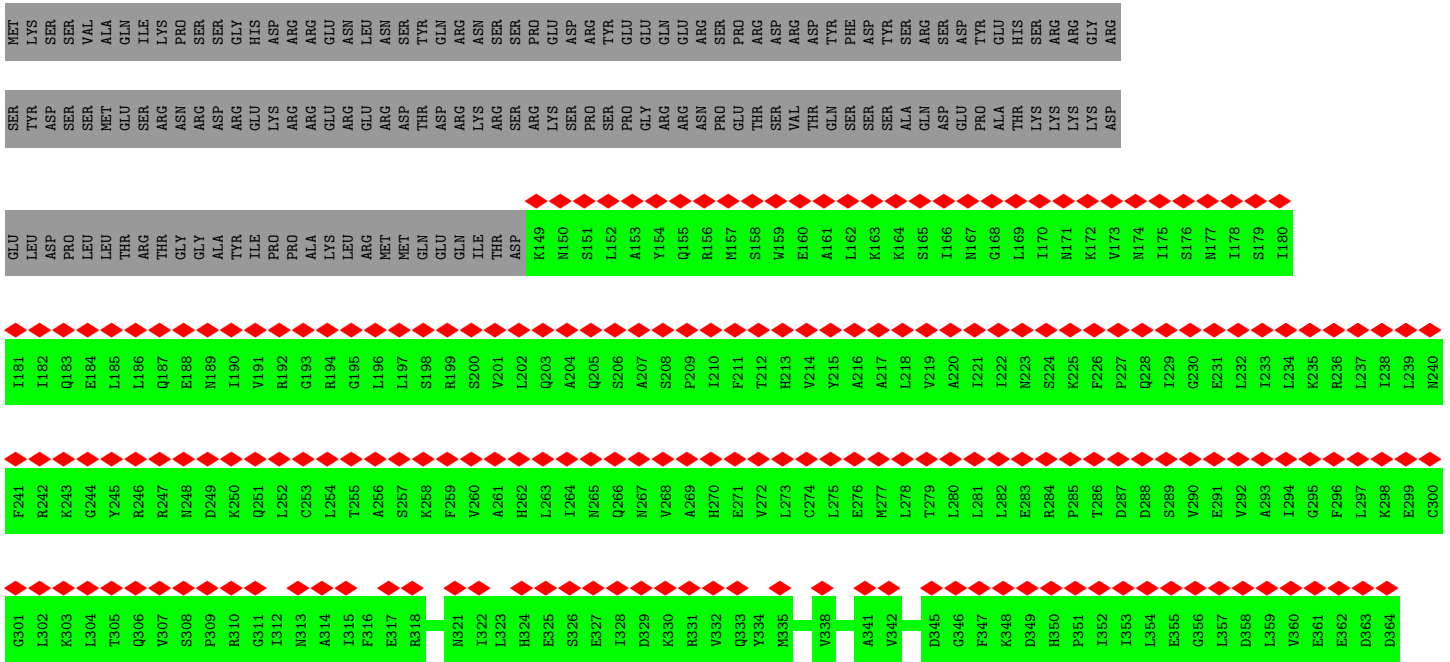


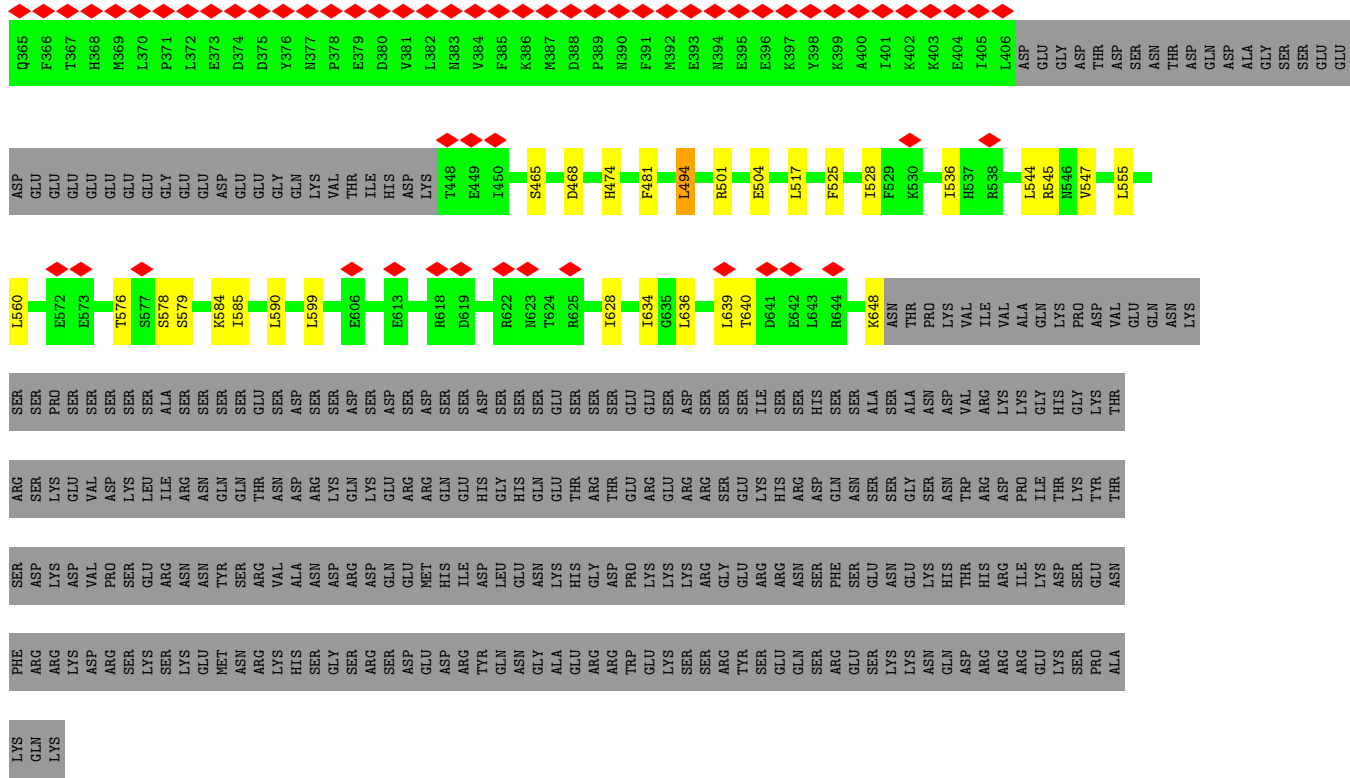
• Molecule 18: Splicing factor Cactin





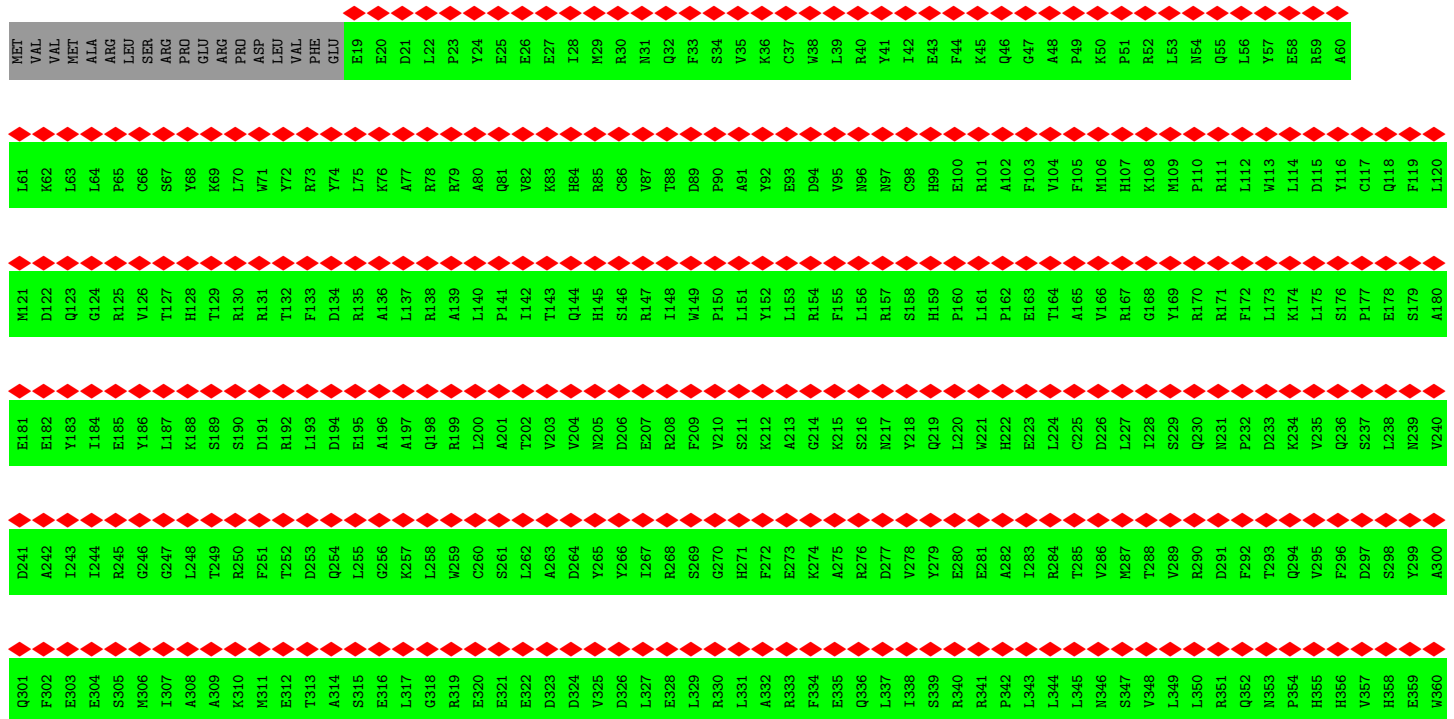
● Molecule 19: Pre-mRNA-splicing factor CWC22 homolog

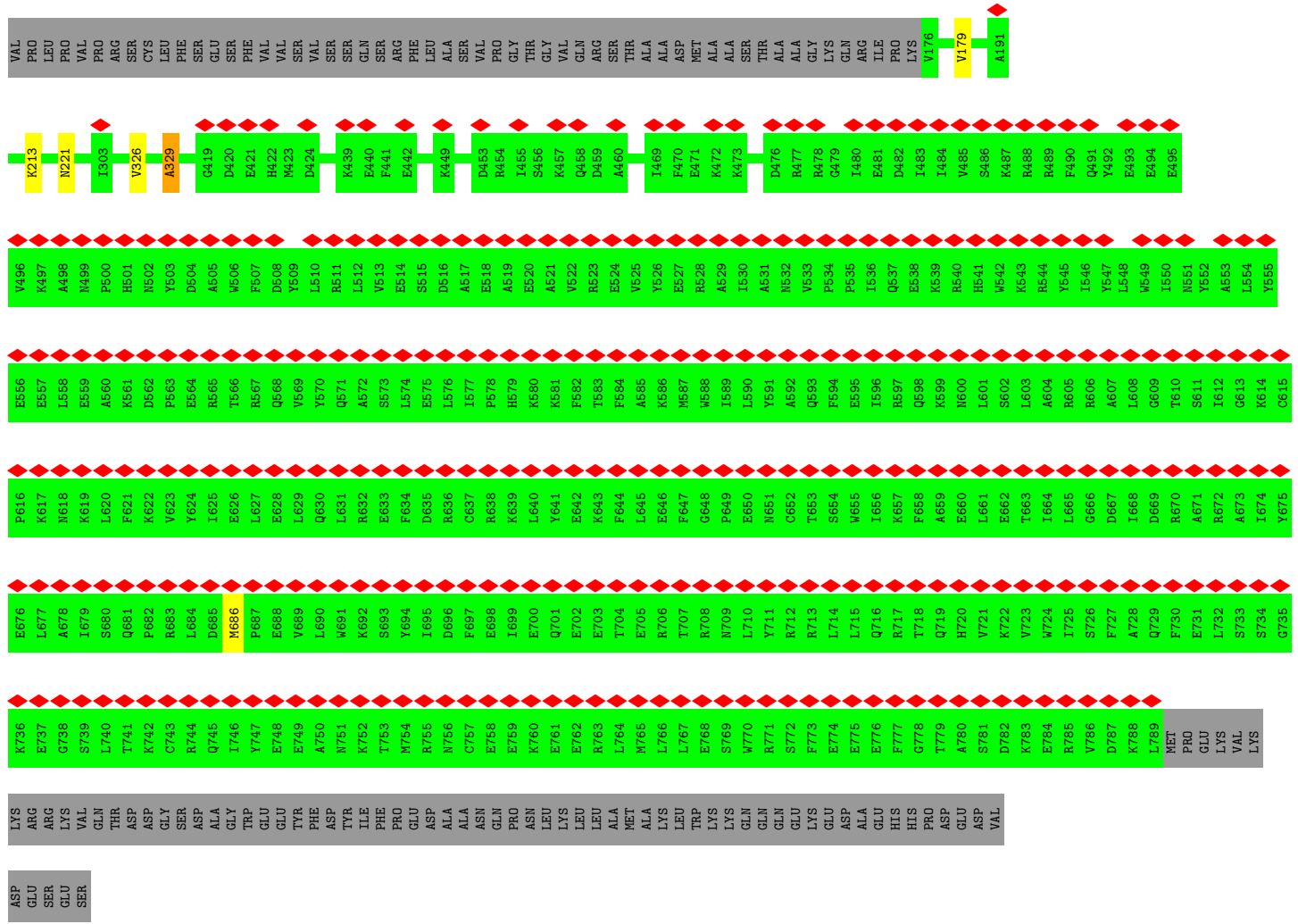




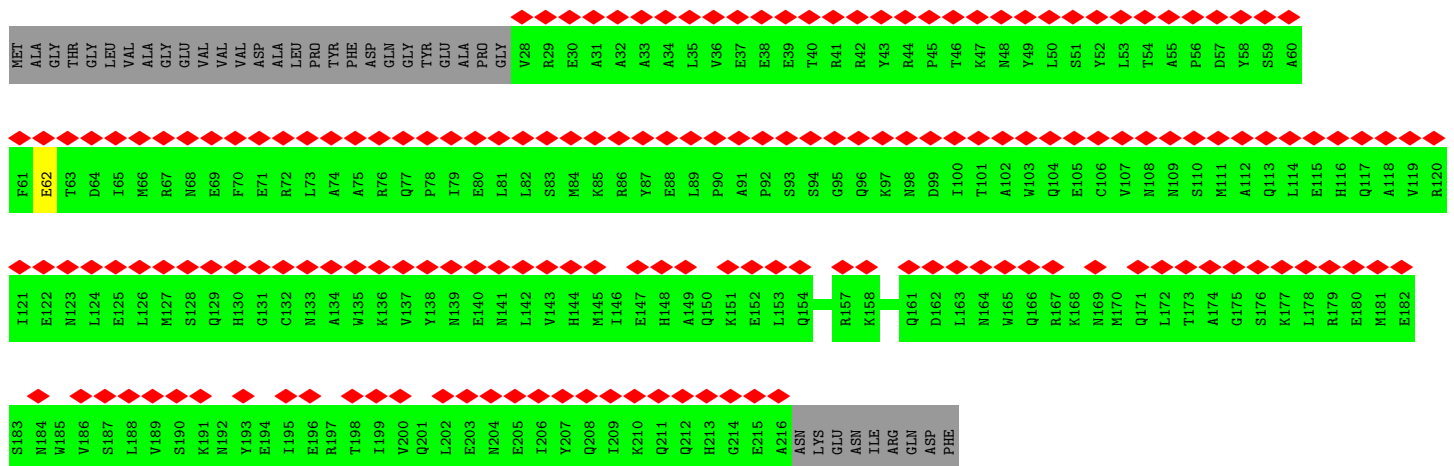
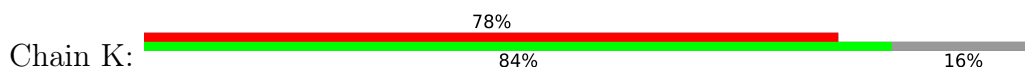
● Molecule 20: Pre-mRNA-splicing factor SYF1

Chain I:

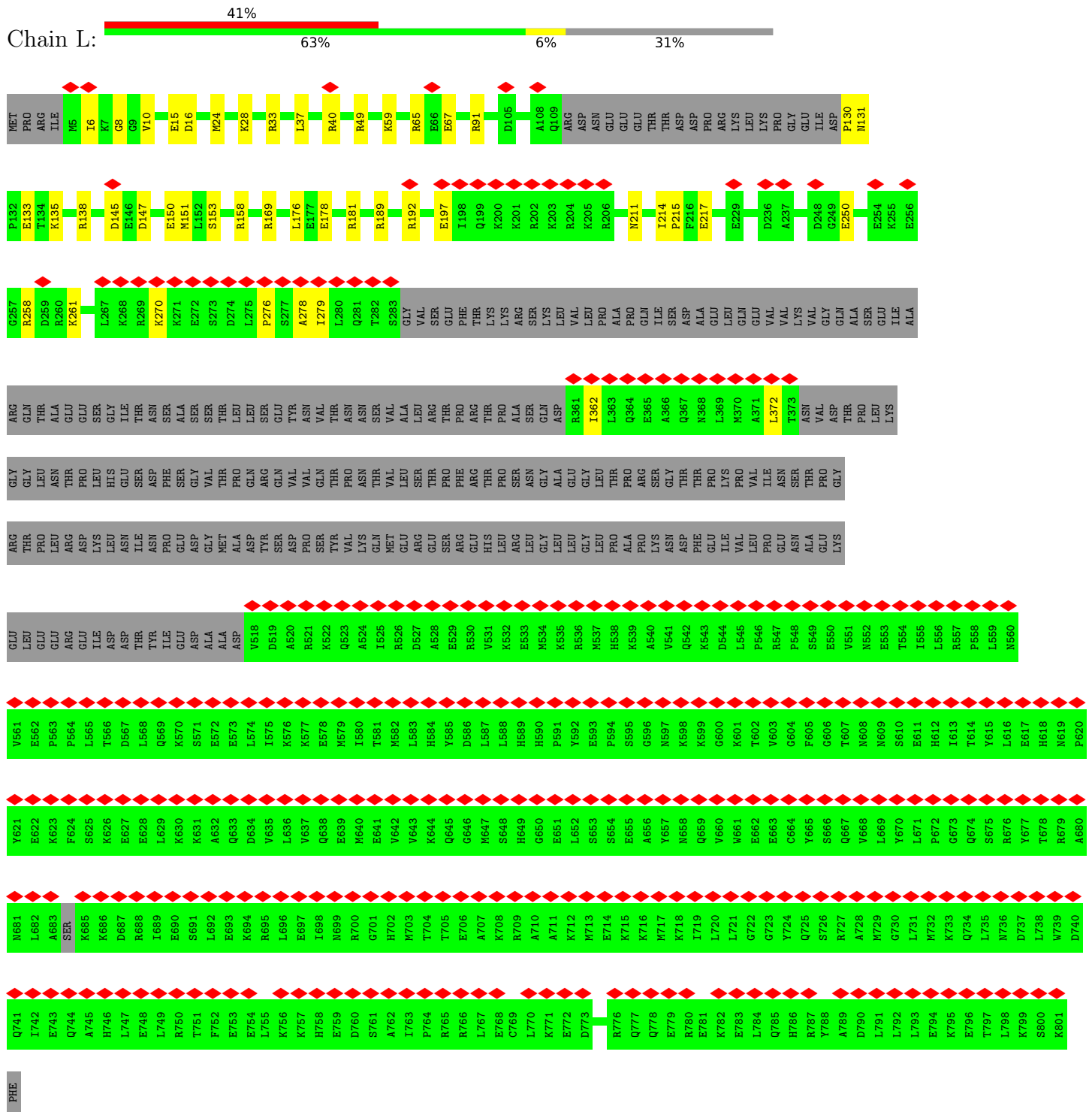




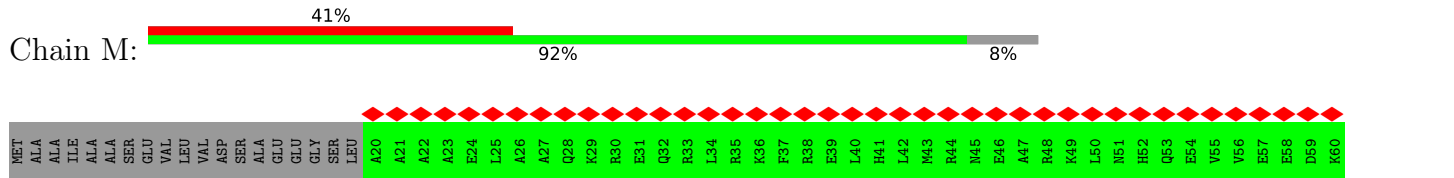
● Molecule 23: Pre-mRNA-splicing factor SPF27

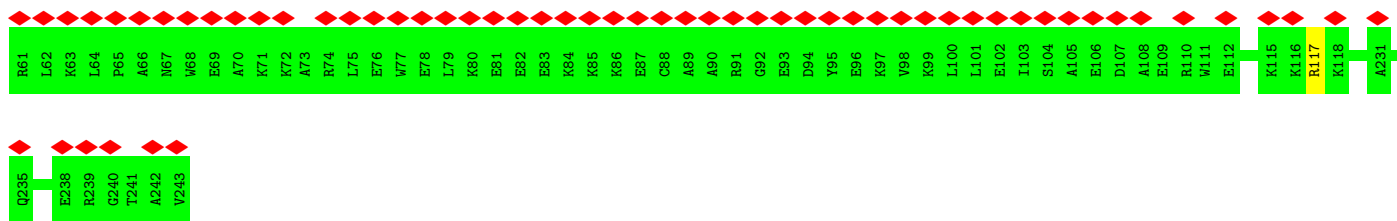


● Molecule 24: Cell division cycle 5-like protein

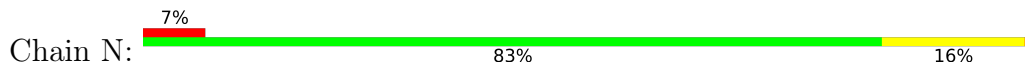


• Molecule 25: Pre-mRNA-splicing factor SYF2

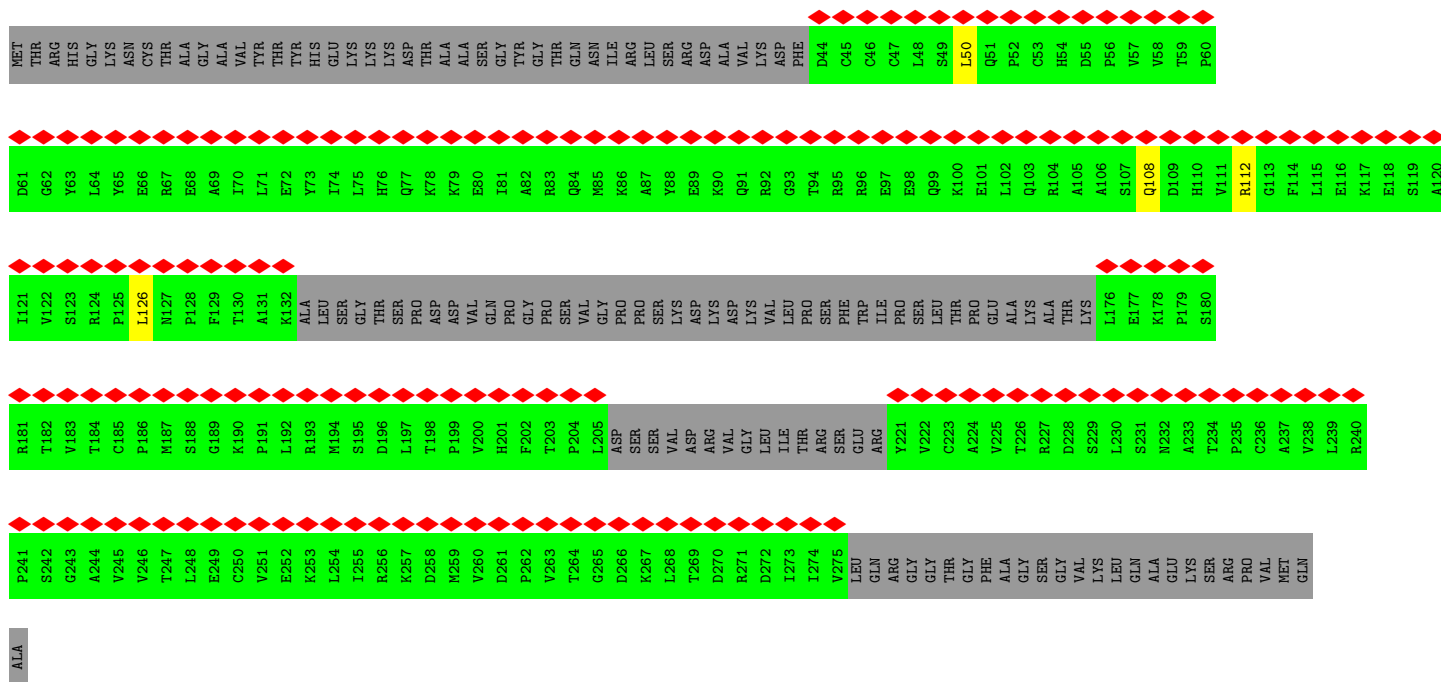




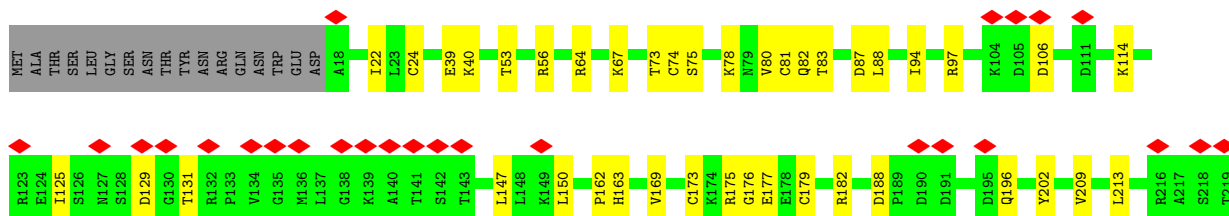
• Molecule 26: Protein BUD31 homolog

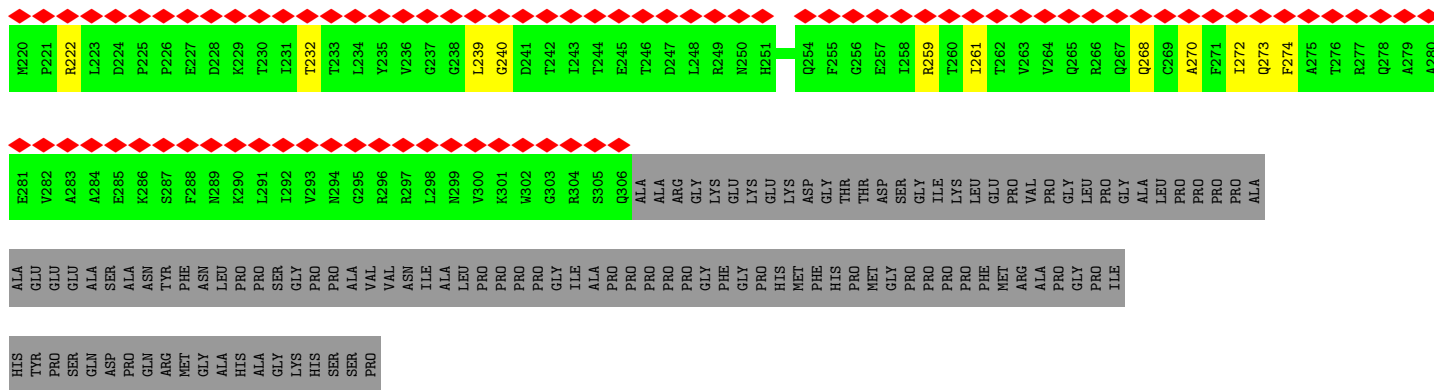


• Molecule 27: Nitric oxide synthase-interacting protein

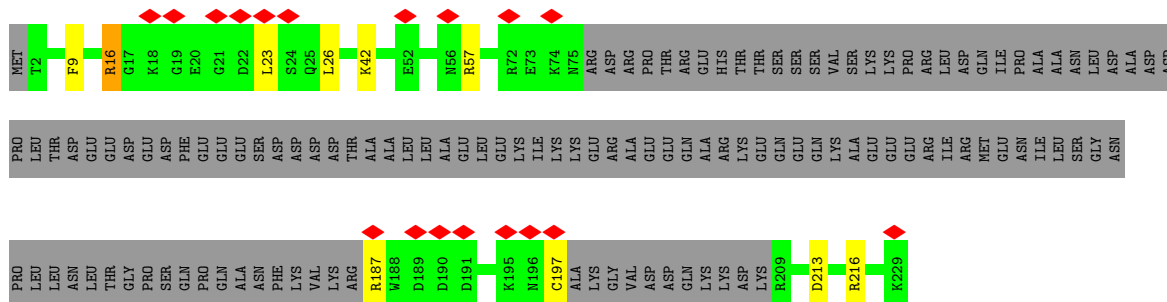
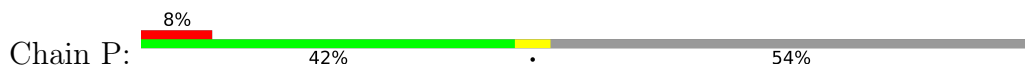


• Molecule 28: Pre-mRNA-splicing factor RBM22

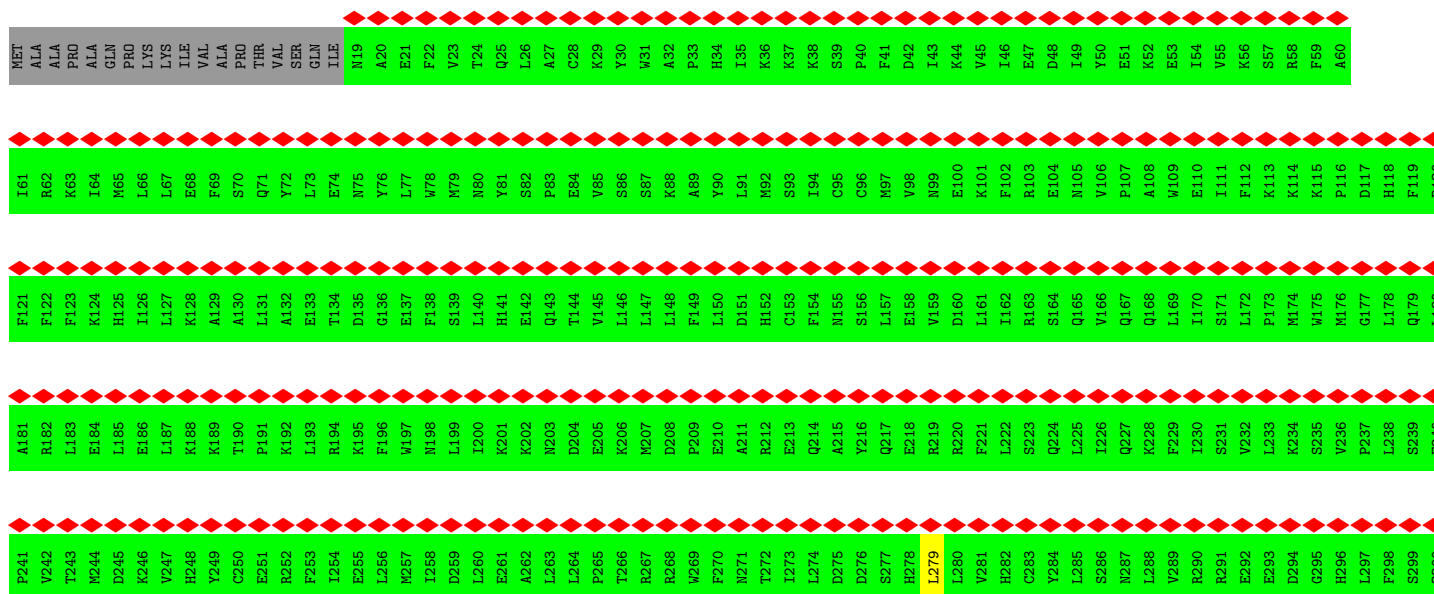
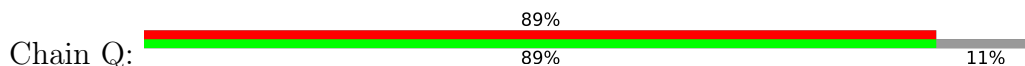




• Molecule 29: Spliceosome-associated protein CWC15 homolog



• Molecule 30: Intron-binding protein aquarius



L1021	L1022	R1023	S1024	K1025	Y1026	L1027	L1028	K1029	V1030	E1031	A1032	K1033	I1034	I1035	A1036	M1037	T1038	C1039	T1040	H1041	A1042	A1043	L1044	K1045	R1046	H1047	D1048	L1049	V1050	K1051	L1052	G1053	G1054	K1055	Y1056	D1057	M1058	I1059	L1060	M1061	E1062	E1063	A1064	A1065	Q1066	Q1067	I1067	L1068	E1069	I1070	E1071	T1072	I1073	F1074	P1075	L1076	L1077	L1078	Q1079	M1080
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L601	D602	D603	K604	G605	R606	V607	GLU	ASP	GLY	PRO	GLU	P614	R615	P616	N617	L618	R619	G620	E621	S622	C623	F624	F625	L626	I627	F628	L629	D630	P631	M632	Q633	Y634	Q635	Q636	D637	M638	T639	N640	T641	I642	Q643	M644	G645	A646	E647	D648	V649	Y650	E651	V652	F653	M654	I655	I656	M657	R658	R659	K660		
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I481	R482	Q483	D484	I485	E486	D487	S488	V489	S490	R491	M492	K493	P494	W495	Q496	GLU	TYR	G500	G501	V502	V503	F504	G505	G506	W507	A508	R509	M510	A511	Q512	P513	I514	V515	A516	F517	T518	V519	V520	E521	V522	A523	K524	P525	N526	I527	G528	E529	M530	M531	P532	T533	R534	V535	R536	A537	D538	V539	T540		
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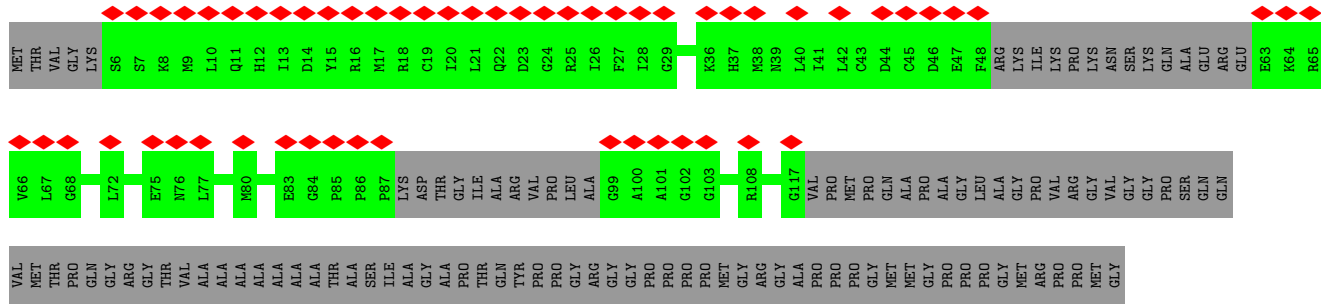
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S1321	Q1322	L1323	T1324	A1325	R1326	P1327	L1328	H1329	L1330	H1331	I1332	L1333	P1334	T1335	E1336	PRO	PHE	PRO	T1340	T1341	R1342	K1343	M1344	G1345	E1346	R1347	P1348	S1349	H1350	E1351	V1352	Q1353	I1354	L1355	K1356	M1357	M1358	P1359	Q1360	M1361	A1362	L1363	F1364	V1365	Y1366	M1367	M1368	Y1369	M1370	H1371	L1372	I1373	Q1374	T1375	T1376	H1377	H1378	H1380	
Q1381	THR	LEU	LEU	GLN	PRO	PRO	ALA	ALA	VAL	GLU	GLU	VAL	GLN	ASN	GLN	THR	GLU	LEU	GLU	THR	GLU	ALA	MET	THR	VAL	PRO	GLN	ALA	ASP	ILE	ALA	THR	THR	CYS	ARG	GLN	GLU	PRO	ALA	ALA	PHE	GLN	THR	ASP	THR	PRO	THR	SER											
GLU	THR	GLY	ALA	THR	SER	TRP	ARG	GLY	ILE	PRO	GLU	ALA	LEU	SER	VAL	VAL	GLY	ALA	VAL	SER	ALA	PRO	GLU	ALA	ASN	THR	PRO	GLN	ALA	ASP	ILE	ALA	THR	SER	ARG	GLN	GLU	THR	PHE	GLN	THR	ASP	THR	PRO	THR	SER													

• Molecule 31: SNW domain-containing protein 1

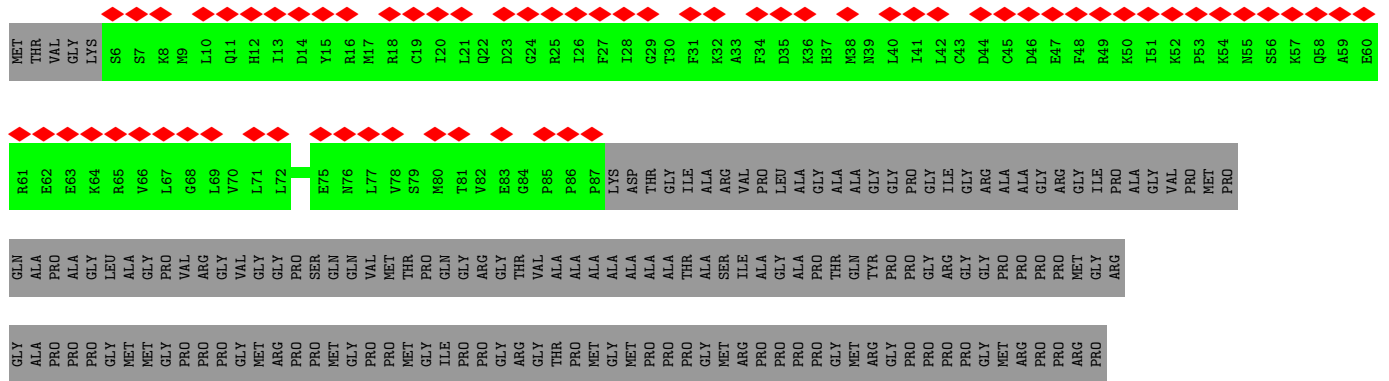


M1	A2	L3	T4	S5	F6	L7	P8	A9	P10	T11	Q12	L13	S14	Q15	D16	L18	E19	A20	E21	E22	K23	A24	R25	S26	Q27	R28	S29	R30	Q31	T32	S33	VAL	SER	SER	ARG	ARG	ARG	P41	Y44	G45	Y46	R47	K48	G49	W50	F51	P52	R53	L54	L55	E56	D57	F58	G59	D60	G61
G62	E66	V69	A70	Q71	D75	M76	G77	R78	K80	L86	D91	S92	E93	D99	R103	Q104	G105	Q106	S107	K108	D109	K110	K122	D128	D129	P130	D131	E137	E182	V185	K188	V189	A180	A181	A182	M183	P184	V185	R186	A187	A188	D189	K170	L171	A172											
P173	A174	I177	R178	Y179	S182	N189	A192	R195	D205	E208	K213	I214	I218	S224	S232	R235	K236	T238	E241	I251	S252	T261	T262	P130	D131	E137	E182	V185	K188	V189	A180	A181	A182	M183	P184	V185	R186	A187	A188	D189	K170	L171	A172													
M312	A313	Q314	K315	E316	K317	E318	K319	H320	E321	E322	K323	L324	R325	E326	M327	A328	Q329	K330	A331	R332	E333	R334	R335	ALA	GLY	ILE	LYS	HIS	THR	VAL	GLU	LYS	ARG	GLU	GLU	ASP	ASP	ILE	GLU	GLN	ARG	GLN	HIS	ASP	ARG	ASN	LEU	SER	ARG							
ALA	ALA	PRO	ASP	LYS	ARG	LYS	GLN	ARG	ASN	GLU	ASN	ASP	ILE	ARG	SER	VAL	ILE	LEU	GLY	VAL	PRO	ASN	THR	GLY	ALA	VAL	ARG	ILE	LYS	HIS	THR	VAL	GLU	LYS	ARG	GLU	GLU	ASP	ASP	ILE	GLU	GLN	ARG	GLN	HIS	ASP	ARG	ASN	LEU	SER	ARG					
VAL	TYR	ASP	GLN	ALA	TRP	ARG	GLY	GLY	LYS	ASP	ASP	MET	ALA	GLN	SER	ILE	TYR	ARG	SER	PRO	SER	LYS	ASN	LEU	LEU	GLY	VAL	ASP	ASP	MET	TYR	PRO	GLY	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		

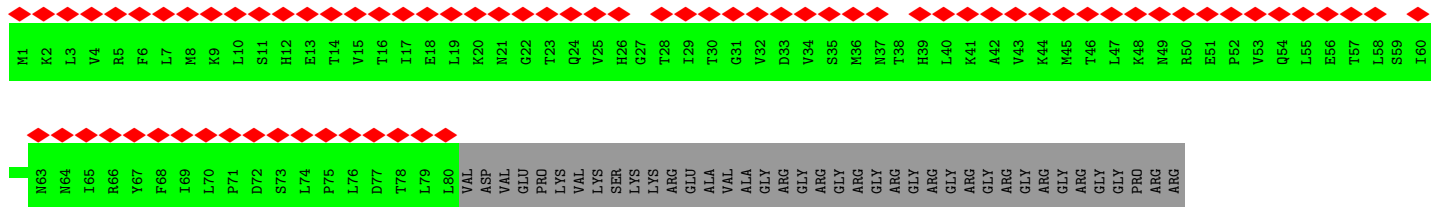
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K991	M992	L993	I994	M995	S996	V997	H998	L999	G1000	C1001	S1002	E1003	E1004	M1005	L1006	T1007	I1008	V1009	S1010	M1011	L1012	S1013	V1014	Q1015	M1016	V1017	F1018	Y1019	R1020	P1021	K1022	D1023	Q1025	A1026	L1027	R1028	D1029	Q1030	K1031	K1032	A1033	K1034	F1035	H1036	Q1037	T1038	E1039	D1041	H1042	L1043	T1044	L1045	L1046	I1047	V1048	Y1049	N1050				
S831	L832	K833	A834	M835	G836	I837	N838	D839	L840	L841	S842	F843	D844	F845	M846	D847	A848	P849	P850	M851	E852	T853	L854	I855	T856	A857	M858	E859	Q860	L861	Y862	T863	L864	G865	A866	L867	D868	D869	E870	M871	S872	L873	T874	R875	L876	G877	R878	R879	M880	Q881	R882	F883	P884	L885	L886	E887	N888	L889	C890		
I871	D872	Q873	L874	V875	V876	T877	P878	I879	S880	Q881	A882	Q883	A884	K885	Q886	R887	A888	G889	R890	A891	G892	R893	T894	G895	P896	G897	K898	C899	Y900	R901	L902	Y903	T904	E905	R906	A907	Y908	R909	D910	E911	M912	L913	T914	T915	N916	V917	P918	E919	I920	Q921	R922	T923	N924	L925	A926	S927	R928	V929	L930		
P811	V812	Y813	S814	A815	L816	V817	S818	E819	M820	Q821	T822	R823	I824	F825	D826	P827	A828	P829	P830	G831	S832	R833	K834	V835	V836	I837	A838	T839	N840	I841	A842	E843	T844	S845	L846	T847	I848	D849	G850	I851	Y852	Y853	V854	R855	D856	P857	G858	F859	V860	K861	Q862	K863	V864	Y865	N866	S867	T868	V869	G870		
E751	P752	E753	T754	D755	V756	L757	D758	A759	S760	L761	I762	T763	V764	M765	Q766	R767	H768	L769	T770	E771	P772	F773	G774	V775	I776	L777	V778	F779	L780	T781	G782	Q783	E784	E785	I786	D787	T788	A789	C790	E791	I792	L793	Y794	E795	D796	M797	K798	S799	L800	G801	P802	D803	V804	P805	E806	L807	I808	I809	L810		
T691	I692	H693	T694	D695	V696	L697	F698	G699	L700	L701	K702	T703	T704	V705	Q706	R707	R708	Q709	D710	M711	K712	L713	I714	V715	T716	S717	A718	T719	L720	D721	A722	V723	K724	F725	S726	Q727	V728	F729	Y730	E731	F732	P733	I734	F735	D736	I737	P738	Q739	R740	T741	V742	P743	V744	E745	I746	L747	V748	T749	K750		
S631	E632	E633	F634	G635	C636	C637	L638	G639	Q640	E641	V642	G643	Y644	T645	I646	R647	F648	E649	D650	C651	T652	S653	P654	E655	T656	V657	I658	K659	Q660	Y661	T662	D663	G664	M665	L666	L667	R668	E669	C670	L671	I672	D673	P674	D675	L676	T677	Q678	Y679	A680	I681	I682	M683	L684	D685	E686	A687	H688	E689	R690		
K571	E572	Q573	L574	V575	Q576	A577	V578	H579	D580	N581	Q582	L583	I584	I585	V586	R587	G588	E589	T590	G591	S592	G593	K594	T595	T596	Q597	I598	S599	Q600	Y601	L602	A603	E604	A605	G606	Y607	T608	S609	R610	G611	K612	I613	G614	C615	T616	Q617	P618	R619	R620	V621	A622	M623	M624	S625	V626	A627	K628	R629	V630		
G451	H452	T453	K454	Q455	S456	M457	D458	M459	S460	P461	I462	K463	I464	V465	K466	M467	P468	D469	Q470	S471	L472	S473	Q474	A475	A476	M477	M478	Q479	S480	A481	L482	A483	K484	E485	R486	R487	E488	L489	K490	Q491	A492	Q493	R494	E495	A496	E497	M498	D499	SER	I570	P571	M572	G573	A574	S575	H576	L577	N578	K579	L580	
GLU	THR	SER	MET	ASN	PRO	ASP	ARG	PRO	GLN	HIS	VAL	LEU	LEU	VAL	VAL	VAL	ASP	ASN	ASP	GLY	THR	THR	LYS	LEU	R393	I394	S395	P427	VAL	VAL	ASP	GLN	GLY	THR	VAL	GLY	GLY	GLY	ASP	GLU	GLU	LEU	LEU	ASN	PRO	ARG	ARG	TRP	ARG	GLU	GLY	ASN	LEU	VAL	VAL	GLY	THR	ASN	GLU	LEU	R450
ASP	PRO	LEU	ASP	ALA	GLU	GLY	ARG	ILE	ALA	ASN	MET	ARG	GLY	ILE	MET	MET	ASN	ASN	ILE	PRO	GLU	TRP	LYS	GLY	HIS	ALA	PHE	GLY	ASN	ALA	THR	LYS	GLY	THR	THR	THR	GLN	ILE	L559	E560	Q561	R562	E563	S564	L565	P566	I567	Y568	K569	L570	SER	ILE	PRO	MET	GLY	ASN	LYS	TRP	VAL		



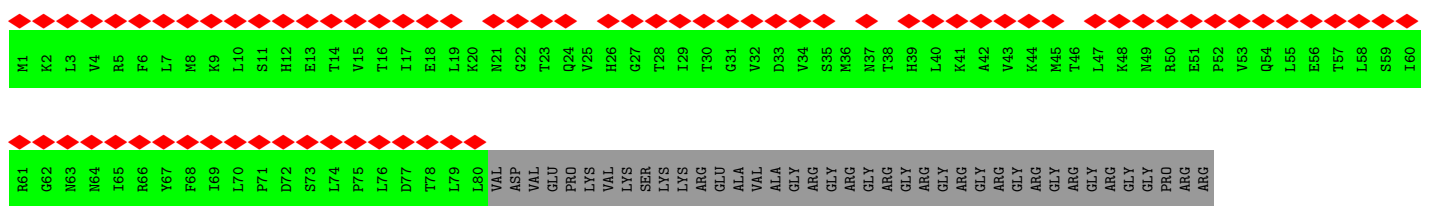
• Molecule 41: Small nuclear ribonucleoprotein-associated proteins B and B'



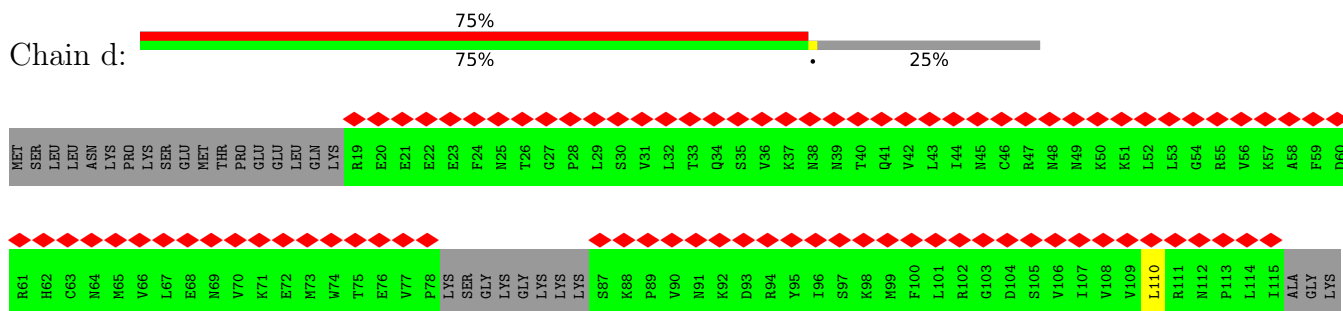
• Molecule 42: Small nuclear ribonucleoprotein Sm D1



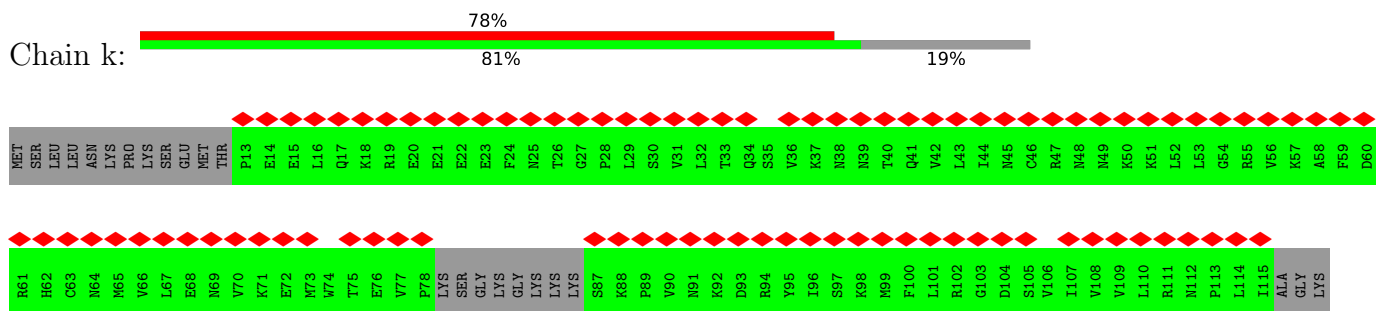
• Molecule 42: Small nuclear ribonucleoprotein Sm D1



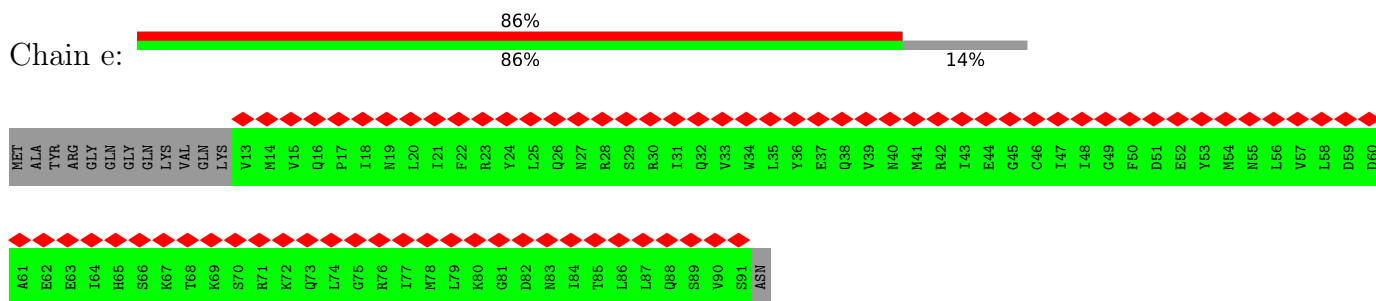
• Molecule 43: Small nuclear ribonucleoprotein Sm D2



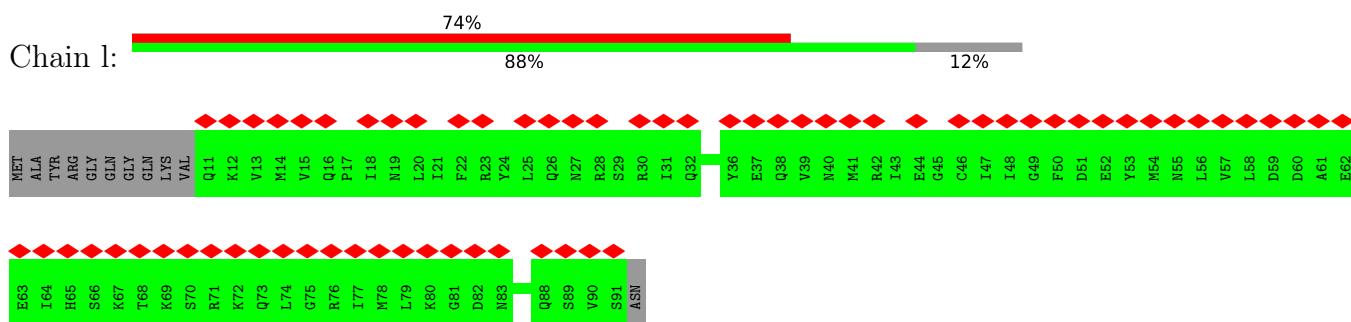
• Molecule 43: Small nuclear ribonucleoprotein Sm D2



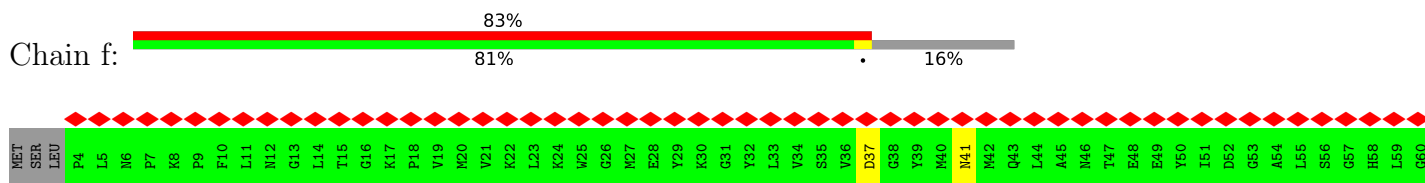
• Molecule 44: Small nuclear ribonucleoprotein E

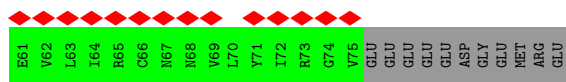


• Molecule 44: Small nuclear ribonucleoprotein E

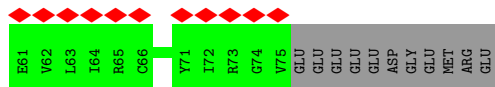
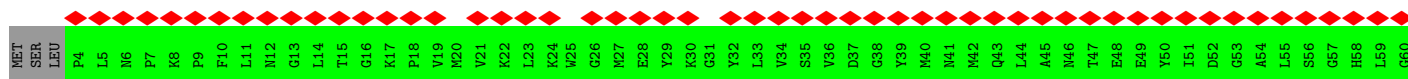
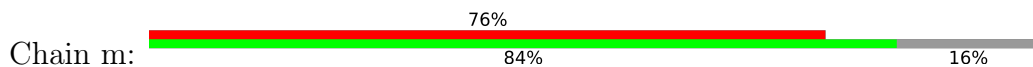


• Molecule 45: Small nuclear ribonucleoprotein F

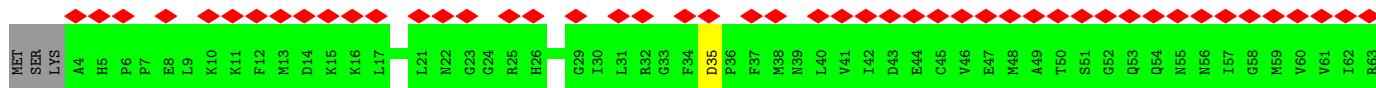
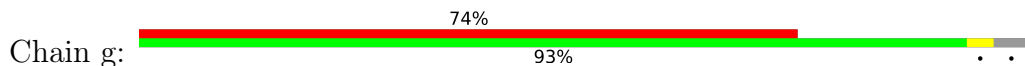




• Molecule 45: Small nuclear ribonucleoprotein F



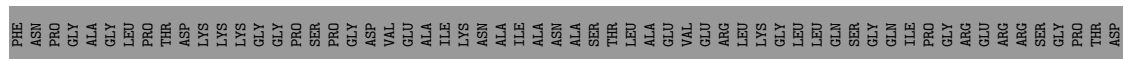
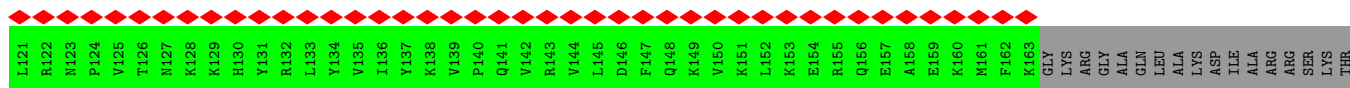
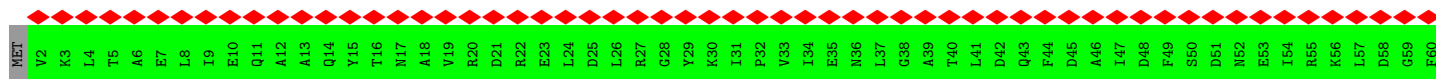
• Molecule 46: Small nuclear ribonucleoprotein G



• Molecule 46: Small nuclear ribonucleoprotein G

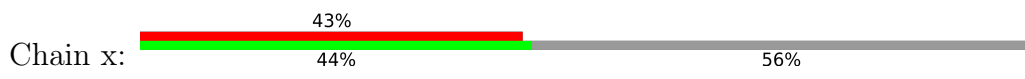


• Molecule 47: U2 small nuclear ribonucleoprotein A'



E181	E182	I183	Y184	C185	P186	G187	D188	A189	I190	S191	S192	V193	A194	A195	S196	E197	K198	S199	T200	K201	I203	F204	I205	Y206	D207	G208	R209	G210	D211	N212	Q213	Q214	L215	H216	L217	F218	D219	K220	L221	H222	T223	S224	P225	L226	T227	Q228	I229	R230	L231	N232	P233	V234	Y235	K236	A237	V238	V239	S240		
S241	D242	K243	S244	G245	M246	I247	E248	Y249	W250	T251	G252	P253	P254	H255	E256	Y257	K258	F259	P260	K261	N262	V263	N264	W265	E266	Y267	K268	T269	D270	T271	D272	L273	Y274	E275	F276	A277	K278	C279	K280	A281	Y282	P283	S284	S285	V286	C287	F288	S289	P290	D291	K292	K293	A294	I295	A296	T297	I298	G299	S300	
D301	R302	K303	V304	I306	F307	R308	F309	V310	T311	G312	K313	L314	M315	R316	F317	F318	D319	E320	S321	L322	S323	M324	F325	T326	E327	L328	Q329	Q330	M331	R332	Q333	Q334	L335	P336	D337	M338	E339	F340	G341	R342	R343	M344	A345	V346	E347	R348	E349	L350	E351	K352	V353	A354	A355	V356	R357	L358	I359	N360		
I361	V362	F363	D364	E365	T366	G367	H368	F369	V370	L371	Y372	G373	T374	M375	L376	G377	I378	K379	V380	I381	N382	V383	E384	T385	N386	R387	C388	V389	R390	I391	L392	G393	K394	Q395	E396	N397	I398	R399	V400	M401	Q402	L403	A404	L405	F406	GLN	GLY	ILE	ALA	LYS	LYS	HIS	ARG	ALA	ALA	THR	THR	ILE	GLU	
MET	LYS	ALA	SER	GLU	ASN	PRO	VAL	LEU	GLN	ASN	ASP	T437	I438	V439	C440	T441	S442	F443	K444	K445	N446	R447	F448	Y449	M450	F451	T452	K453	R454	E455	P456	E457	D458	T459	K460	S461	A462	D463	S464	D465	R466	D467	V468	F469	N470	E471	K472	P473	S474	K475	E476	E477	V478	M479	A480					
A481	T482	Q483	ALA	GLU	GLY	PRO	LYS	ARG	VAL	SER	ASP	S493	A494	I495	I496	H497	T498	S499	M500	G501	D502	I503	H504	T505	K506	L507	F508	P509	V510	E511	P512	P513	K514	T515	V516	E517	N518	F519	C520	V521	H522	S523	R524	N525	G526	Y527	E528	N529	G530	H531	P473	T532	F533	H534	R535	I536	I537	K538	G539	F540
M541	Q543	T544	G545	D546	F547	T548	G549	T550	G551	M552	G553	G554	E555	S556	I557	M558	G559	G560	E561	H562	E563	D564	E565	F566	H567	S568	T569	L570	R571	H572	D573	D574	P575	Y576	T577	L578	S579	M580	A581	N582	A583	G584	S585	N586	T587	N588	G589	S590	Q591	F592	F593	I594	T595	V596	V597	P598	T599	P600		
M601	L602	D603	N604	K605	H606	T607	V608	F609	G610	R611	V612	T613	K614	G615	M616	E617	V618	V619	Q620	R621	I622	S623	N624	V625	K626	V627	N628	P629	K630	T631	D632	P633	K634	Y635	E636	D637	V638	S639	I640	I641	N642	I643	T644	V645	K646															

• Molecule 51: Splicing factor C9orf78



MET	PRO	VAL	VAL	R5	K6	I7	F8	R9	R10	R11	R12	G13	D14	S15	E16	S17	E18	E19	D20	E21	Q22	D23	S24	E25	E26	V27	R28	L29	K30	L31	E32	E33	T34	R35	E36	V37	Q38	N39	L40	R41	K42	R43	P44	N45	G46	V47	S48	A49	V50	A51	L52	L53	V54	G55	GLU	LYS	VAL	GLN	GLU
GLU	THR	LEU	VAL	ASP	PRO	PHE	GLN	MET	LYS	THR	GLY	MET	VAL	LYS	MET	LYS	LEU	LYS	GLU	ARG	GLY	LYS	SER	GLU	GLU	GLU	ASN	ASP	LEU	VAL	HIS	THR	SER	ALA	GLU	THR	THR	THR	THR	ARG	ARG	ASP	E111	D112	A113	D114	M115	M116	K117	Y118	I119	E120							
T121	E122	L123	K124	K125	R126	LYS	GLY	ILE	VAL	GLU	HIS	GLU	GLN	LYS	VAL	LYS	LYS	ASN	ALA	GLU	ASP	CYS	LEU	LEU	PRO	GLU	ASN	ILE	ARG	VAL	VAL	SER	ALA	ALA	ASN	TYR	E36	M164	L165	S166	N167	Q168	M169	L170	S171	G172	D177	L178	G179	I180	D181	A182	K183						
I184	K185	N186	I187	I188	S189	T190	E191	D192	A193	K194	A195	R196	L197	L198	A199	E200	Q201	Q202	N203	K204	K205	K206	D207	SER	GLU	THR	PHE	VAL	PRO	THR	ASN	ALA	LYS	ALA	VAL	ASN	TYR	VAL	GLN	HIS	ASN	ARG	ARG	PHE	TYR	HIS	ARG	ASN	ASN	LYS	GLU	GLU	GLU	PRO					
LYS	ALA	ARG	ARG	LEU	ARG	GLY	ASP	THR	GLU	LYS	PRO	GLU	GLU	SER	PRO	ASN	ARG	ARG	PRO	ALA	ASN	LYS	ALA	THR	D275	D276	Y277	H278	Y279	E280	K281	F282	K283	K284	M285	M286	R287	R288	Y289																				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	103860	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.177	Depositor
Minimum map value	-0.101	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.024	Depositor
Map size (\AA)	492.00003, 492.00003, 492.00003	wwPDB
Map dimensions	410, 410, 410	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.2, 1.2, 1.2	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: IHP, MG, ZN, GTP, SEP, K, ATP

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	1	0.38	0/1030	0.74	1/1371 (0.1%)
2	2	0.73	1/2827 (0.0%)	1.40	46/4393 (1.0%)
3	3	0.28	0/406	0.43	0/564
4	32	0.37	0/513	0.66	0/683
5	5	1.00	2/2157 (0.1%)	1.79	85/3351 (2.5%)
6	50	0.33	0/1050	0.69	0/1461
7	56	0.28	0/497	0.57	0/690
8	6	1.06	2/2323 (0.1%)	1.44	34/3619 (0.9%)
9	7	0.31	0/1927	0.65	1/2681 (0.0%)
10	8	0.28	0/444	0.67	0/614
11	9	0.31	0/711	0.62	0/987
12	A	0.61	1/18250 (0.0%)	0.71	9/24798 (0.0%)
13	B	0.36	0/15311	0.76	17/20733 (0.1%)
14	C	0.58	0/7277	0.87	15/9887 (0.2%)
15	D	0.30	0/356	0.52	0/494
16	E	0.41	0/2448	0.70	1/3316 (0.0%)
17	EX	1.43	0/329	2.62	36/510 (7.1%)
18	F	0.46	0/1130	0.68	1/1525 (0.1%)
19	H	0.40	0/2965	0.65	1/4049 (0.0%)
20	I	0.31	0/3609	0.57	0/5036
21	IN	0.73	0/996	1.71	36/1544 (2.3%)
22	J	0.34	1/2997 (0.0%)	0.63	0/4187
23	K	0.30	0/940	0.52	0/1312
24	L	0.41	0/3674	0.64	1/4988 (0.0%)
25	M	0.29	0/1114	0.53	0/1553
26	N	0.58	1/1215 (0.1%)	0.74	1/1627 (0.1%)
27	NO	0.31	0/861	0.58	0/1197
28	O	0.50	0/2366	0.67	0/3193
29	P	0.47	0/903	0.70	0/1201
30	Q	0.30	0/6545	0.57	0/9115
31	R	0.48	1/2647 (0.0%)	0.73	4/3554 (0.1%)
32	S	0.38	0/1305	0.65	0/1767

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	SR	0.59	2/414 (0.5%)	0.56	0/568
34	T	0.70	1/2957 (0.0%)	0.77	1/4023 (0.0%)
35	U	0.50	0/2483	0.68	0/3341
36	V	0.30	0/3626	0.57	0/5050
37	W	0.53	1/4266 (0.0%)	0.71	4/5761 (0.1%)
38	X	0.28	0/326	0.49	0/452
39	Z	0.28	0/263	0.53	0/365
40	a	0.34	0/666	0.68	0/897
40	h	0.36	0/660	0.68	0/889
41	b	0.31	0/663	0.65	0/885
41	i	0.31	0/674	0.62	0/899
42	c	0.29	0/642	0.59	0/867
42	j	0.28	0/642	0.60	0/867
43	d	0.29	0/732	0.66	0/984
43	k	0.32	0/784	0.64	0/1053
44	e	0.28	0/659	0.67	0/885
44	l	0.31	0/677	0.68	0/908
45	f	0.35	0/574	0.75	1/775 (0.1%)
45	m	0.34	0/574	0.65	0/775
46	g	0.34	0/575	0.72	2/768 (0.3%)
46	n	0.32	0/575	0.66	0/768
47	o	0.30	0/1299	0.71	1/1761 (0.1%)
48	p	0.30	0/759	0.57	0/1016
49	q	0.29	0/512	0.48	0/713
49	r	0.35	0/592	0.56	0/825
49	s	0.35	0/658	0.58	0/919
49	t	0.32	0/512	0.54	0/713
50	w	0.30	0/2652	0.65	0/3685
51	x	0.30	0/632	0.50	0/874
52	y	0.28	0/317	0.62	0/396
53	z	0.37	0/431	0.57	0/582
All	All	0.50	13/122919 (0.0%)	0.80	298/169264 (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
12	A	0	2
13	B	0	20
14	C	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
16	E	0	1
29	P	0	1
31	R	0	2
All	All	0	29

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
37	W	307	CYS	CB-SG	-7.01	1.70	1.82
34	T	220	VAL	CB-CG2	-6.64	1.38	1.52
8	6	58	G	N7-C5	-6.24	1.35	1.39
5	5	57	G	C2-N3	-5.78	1.28	1.32
12	A	492	VAL	CB-CG2	-5.66	1.41	1.52

The worst 5 of 298 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	IN	145	U	O4'-C1'-N1	14.47	119.78	108.20
17	EX	-2	C	O4'-C1'-N1	14.36	119.69	108.20
5	5	24	G	O4'-C1'-N9	-12.82	97.94	108.20
5	5	86	C	N1-C2-O2	12.72	126.53	118.90
2	2	50	C	N1-C2-O2	11.88	126.03	118.90

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	A	1418	ARG	Sidechain
12	A	941	LYS	Peptide
13	B	129	ARG	Sidechain
13	B	728	ARG	Sidechain
13	B	739	ARG	Sidechain

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	1	1013	0	1058	9	0
2	2	2535	0	1281	19	0
3	3	408	0	181	0	0
4	32	504	0	509	11	0
5	5	1936	0	982	19	0
6	50	1053	0	456	2	0
7	56	498	0	220	0	0
8	6	2075	0	1048	28	0
9	7	1928	0	855	0	0
10	8	445	0	203	0	0
11	9	712	0	299	0	0
12	A	17802	0	17006	229	0
13	B	15004	0	15162	104	0
14	C	7116	0	7128	32	0
15	D	358	0	167	0	0
16	E	2394	0	2329	42	0
17	EX	296	0	153	2	0
18	F	1085	0	1019	5	0
19	H	2932	0	2204	17	0
20	I	3610	0	1639	0	0
21	IN	893	0	453	13	0
22	J	2998	0	1333	3	0
23	K	941	0	424	0	0
24	L	3642	0	2904	31	0
25	M	1115	0	513	0	0
26	N	1189	0	1192	17	0
27	NO	864	0	371	1	0
28	O	2318	0	2298	38	0
29	P	889	0	865	8	0
30	Q	6554	0	2828	1	0
31	R	2618	0	2663	35	0
32	S	1271	0	1244	19	0
33	SR	412	0	287	5	0
34	T	2881	0	2836	40	0
35	U	2425	0	2370	39	0
36	V	3629	0	1603	0	0
37	W	4158	0	4060	75	0
38	X	328	0	156	1	0
39	Z	265	0	114	1	0
40	a	658	0	675	0	0
40	h	652	0	670	0	0
41	b	654	0	667	0	0
41	i	664	0	690	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	c	634	0	680	0	0
42	j	634	0	680	0	0
43	d	723	0	750	0	0
43	k	774	0	802	0	0
44	e	651	0	671	0	0
44	l	669	0	692	0	0
45	f	562	0	574	0	0
45	m	562	0	574	0	0
46	g	568	0	590	0	0
46	n	568	0	590	0	0
47	o	1282	0	1305	0	0
48	p	745	0	767	0	0
49	q	514	0	236	0	0
49	r	594	0	270	0	0
49	s	659	0	299	0	0
49	t	514	0	236	0	0
50	w	2655	0	1150	0	0
51	x	636	0	276	0	0
52	y	318	0	88	0	0
53	z	430	0	321	0	0
54	6	5	0	0	0	0
54	7	1	0	0	0	0
55	6	1	0	0	0	0
56	7	31	0	12	0	0
57	C	32	0	12	0	0
58	N	3	0	0	0	0
58	O	3	0	0	0	0
59	U	36	0	6	1	0
All	All	120526	0	96696	730	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 4.

The worst 5 of 730 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)
5:5:36:C:H42	5:5:46:U:H3	1.09	0.90
2:2:25:G:N1	8:6:52:U:O2	2.15	0.76
2:2:153:A:H62	2:2:177:A:H2	1.32	0.75
2:2:153:A:N6	2:2:177:A:C2	2.57	0.73
5:5:36:C:N4	5:5:46:U:H3	1.85	0.73

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	1	121/184 (66%)	113 (93%)	7 (6%)	1 (1%)	19	51
3	3	78/476 (16%)	78 (100%)	0	0	100	100
4	32	58/112 (52%)	56 (97%)	2 (3%)	0	100	100
6	50	206/339 (61%)	194 (94%)	10 (5%)	2 (1%)	15	46
7	56	99/222 (45%)	98 (99%)	1 (1%)	0	100	100
9	7	388/411 (94%)	377 (97%)	10 (3%)	1 (0%)	41	71
10	8	89/174 (51%)	87 (98%)	1 (1%)	1 (1%)	14	45
11	9	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
12	A	2244/2335 (96%)	2109 (94%)	132 (6%)	3 (0%)	51	81
13	B	1856/2136 (87%)	1786 (96%)	67 (4%)	3 (0%)	47	77
14	C	897/972 (92%)	821 (92%)	72 (8%)	4 (0%)	34	66
15	D	68/285 (24%)	67 (98%)	1 (2%)	0	100	100
16	E	304/357 (85%)	281 (92%)	21 (7%)	2 (1%)	22	54
18	F	120/758 (16%)	109 (91%)	11 (9%)	0	100	100
19	H	455/908 (50%)	439 (96%)	15 (3%)	1 (0%)	47	77
20	I	725/855 (85%)	710 (98%)	15 (2%)	0	100	100
22	J	600/848 (71%)	572 (95%)	26 (4%)	2 (0%)	41	71
23	K	187/225 (83%)	174 (93%)	12 (6%)	1 (0%)	29	61
24	L	545/802 (68%)	524 (96%)	20 (4%)	1 (0%)	47	77
25	M	222/243 (91%)	215 (97%)	6 (3%)	1 (0%)	29	61
26	N	142/144 (99%)	131 (92%)	9 (6%)	2 (1%)	11	38
27	NO	168/301 (56%)	158 (94%)	8 (5%)	2 (1%)	13	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	O	287/420 (68%)	272 (95%)	15 (5%)	0	100	100
29	P	100/229 (44%)	94 (94%)	6 (6%)	0	100	100
30	Q	1304/1485 (88%)	1267 (97%)	34 (3%)	3 (0%)	47	77
31	R	322/536 (60%)	296 (92%)	25 (8%)	1 (0%)	41	71
32	S	162/166 (98%)	148 (91%)	14 (9%)	0	100	100
33	SR	66/2752 (2%)	59 (89%)	7 (11%)	0	100	100
34	T	359/514 (70%)	340 (95%)	16 (4%)	3 (1%)	19	51
35	U	291/586 (50%)	272 (94%)	18 (6%)	1 (0%)	41	71
36	V	727/1220 (60%)	708 (97%)	18 (2%)	1 (0%)	51	81
37	W	511/579 (88%)	460 (90%)	51 (10%)	0	100	100
38	X	62/451 (14%)	59 (95%)	3 (5%)	0	100	100
39	Z	49/166 (30%)	49 (100%)	0	0	100	100
40	a	82/126 (65%)	77 (94%)	5 (6%)	0	100	100
40	h	81/126 (64%)	75 (93%)	6 (7%)	0	100	100
41	b	81/240 (34%)	80 (99%)	1 (1%)	0	100	100
41	i	80/240 (33%)	74 (92%)	6 (8%)	0	100	100
42	c	78/119 (66%)	73 (94%)	5 (6%)	0	100	100
42	j	78/119 (66%)	76 (97%)	2 (3%)	0	100	100
43	d	85/118 (72%)	82 (96%)	3 (4%)	0	100	100
43	k	91/118 (77%)	88 (97%)	3 (3%)	0	100	100
44	e	77/92 (84%)	75 (97%)	2 (3%)	0	100	100
44	l	79/92 (86%)	77 (98%)	2 (2%)	0	100	100
45	f	70/86 (81%)	70 (100%)	0	0	100	100
45	m	70/86 (81%)	69 (99%)	1 (1%)	0	100	100
46	g	71/76 (93%)	67 (94%)	4 (6%)	0	100	100
46	n	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
47	o	160/255 (63%)	146 (91%)	14 (9%)	0	100	100
48	p	90/225 (40%)	88 (98%)	2 (2%)	0	100	100
49	q	99/504 (20%)	98 (99%)	1 (1%)	0	100	100
49	r	115/504 (23%)	111 (96%)	4 (4%)	0	100	100
49	s	130/504 (26%)	125 (96%)	4 (3%)	1 (1%)	19	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	t	99/504 (20%)	96 (97%)	2 (2%)	1 (1%)	15	46
50	w	532/646 (82%)	514 (97%)	18 (3%)	0	100	100
51	x	120/289 (42%)	118 (98%)	2 (2%)	0	100	100
52	y	77/301 (26%)	75 (97%)	2 (3%)	0	100	100
53	z	66/415 (16%)	64 (97%)	1 (2%)	1 (2%)	10	38
All	All	16536/28198 (59%)	15749 (95%)	748 (4%)	39 (0%)	50	77

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	B	1584	ILE
16	E	59	ILE
30	Q	1078	LEU
49	s	65	PRO
6	50	322	SER

5.3.2 Protein sidechains [i](#)

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	1	106/157 (68%)	105 (99%)	1 (1%)	78	87
4	32	54/99 (54%)	53 (98%)	1 (2%)	57	77
12	A	1792/2108 (85%)	1783 (100%)	9 (0%)	88	93
13	B	1668/1908 (87%)	1513 (91%)	155 (9%)	9	30
14	C	799/866 (92%)	770 (96%)	29 (4%)	35	63
16	E	263/300 (88%)	262 (100%)	1 (0%)	91	95
18	F	110/655 (17%)	109 (99%)	1 (1%)	78	87
19	H	182/838 (22%)	180 (99%)	2 (1%)	73	85
24	L	233/709 (33%)	232 (100%)	1 (0%)	91	95
26	N	130/130 (100%)	129 (99%)	1 (1%)	81	89
28	O	254/361 (70%)	253 (100%)	1 (0%)	91	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	P	94/203 (46%)	94 (100%)	0	100	100
31	R	275/457 (60%)	274 (100%)	1 (0%)	91	95
32	S	133/134 (99%)	132 (99%)	1 (1%)	81	89
33	SR	21/2432 (1%)	20 (95%)	1 (5%)	25	56
34	T	316/441 (72%)	312 (99%)	4 (1%)	69	82
35	U	258/520 (50%)	253 (98%)	5 (2%)	57	77
37	W	451/502 (90%)	445 (99%)	6 (1%)	69	82
40	a	74/101 (73%)	74 (100%)	0	100	100
40	h	73/101 (72%)	73 (100%)	0	100	100
41	b	68/177 (38%)	68 (100%)	0	100	100
41	i	75/177 (42%)	75 (100%)	0	100	100
42	c	75/101 (74%)	75 (100%)	0	100	100
42	j	75/101 (74%)	75 (100%)	0	100	100
43	d	85/110 (77%)	84 (99%)	1 (1%)	71	83
43	k	91/110 (83%)	91 (100%)	0	100	100
44	e	74/84 (88%)	74 (100%)	0	100	100
44	l	76/84 (90%)	76 (100%)	0	100	100
45	f	61/74 (82%)	60 (98%)	1 (2%)	62	79
45	m	61/74 (82%)	61 (100%)	0	100	100
46	g	63/66 (96%)	63 (100%)	0	100	100
46	n	63/66 (96%)	62 (98%)	1 (2%)	62	79
47	o	139/218 (64%)	138 (99%)	1 (1%)	84	90
48	p	81/195 (42%)	81 (100%)	0	100	100
53	z	25/366 (7%)	25 (100%)	0	100	100
All	All	8398/15025 (56%)	8174 (97%)	224 (3%)	48	71

5 of 224 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	B	1442	ARG
45	f	41	ASN
13	B	1956	LYS
37	W	552	VAL
24	L	261	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
34	T	269	GLN
37	W	402	GLN
34	T	446	ASN
35	U	154	HIS
41	b	76	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
17	EX	14/14 (100%)	5 (35%)	1 (7%)
2	2	117/187 (62%)	30 (25%)	5 (4%)
21	IN	39/113 (34%)	19 (48%)	3 (7%)
5	5	90/116 (77%)	23 (25%)	2 (2%)
All	All	260/430 (60%)	77 (29%)	11 (4%)

5 of 77 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	2	16	U
2	2	17	U
2	2	19	G
2	2	20	G
2	2	24	A

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	EX	-12	G
21	IN	137	C
21	IN	145	U
21	IN	142	U
2	2	105	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	SEP	R	232	31	8,9,10	1.58	1 (12%)	8,12,14	1.37	1 (12%)
31	SEP	R	224	31	8,9,10	1.45	1 (12%)	8,12,14	1.88	1 (12%)

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
31	SEP	R	232	31	-	3/5/8/10	-
31	SEP	R	224	31	-	1/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	R	232	SEP	P-O1P	3.39	1.61	1.50
31	R	224	SEP	P-O1P	3.07	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	R	224	SEP	P-OG-CB	-4.78	105.13	118.30
31	R	232	SEP	P-OG-CB	-2.74	110.76	118.30

There are no chirality outliers.

All (4) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 13 are monoatomic - leaving 3 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
59	IHP	U	601	-	36,36,36	1.33	6 (16%)	54,60,60	0.95	3 (5%)
57	GTP	C	1500	-	26,34,34	1.43	2 (7%)	32,54,54	1.68	8 (25%)
56	ATP	7	702	54	26,33,33	0.64	0	31,52,52	1.06	2 (6%)

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
59	IHP	U	601	-	-	6/30/54/54	0/1/1/1
57	GTP	C	1500	-	-	0/18/38/38	0/3/3/3
56	ATP	7	702	54	-	0/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	C	1500	GTP	C5-C6	-4.98	1.37	1.47
59	U	601	IHP	P3-O13	2.68	1.64	1.59
59	U	601	IHP	P6-O16	2.58	1.64	1.59
59	U	601	IHP	P2-O12	2.37	1.63	1.59
57	C	1500	GTP	C5-C4	-2.29	1.37	1.43

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	C	1500	GTP	C5-C6-N1	3.66	120.41	113.95
57	C	1500	GTP	PA-O3A-PB	-3.42	121.10	132.83
57	C	1500	GTP	C2-N1-C6	-3.24	119.14	125.10
57	C	1500	GTP	C8-N7-C5	3.07	108.84	102.99
59	U	601	IHP	C6-C1-C2	-3.02	103.80	110.41

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

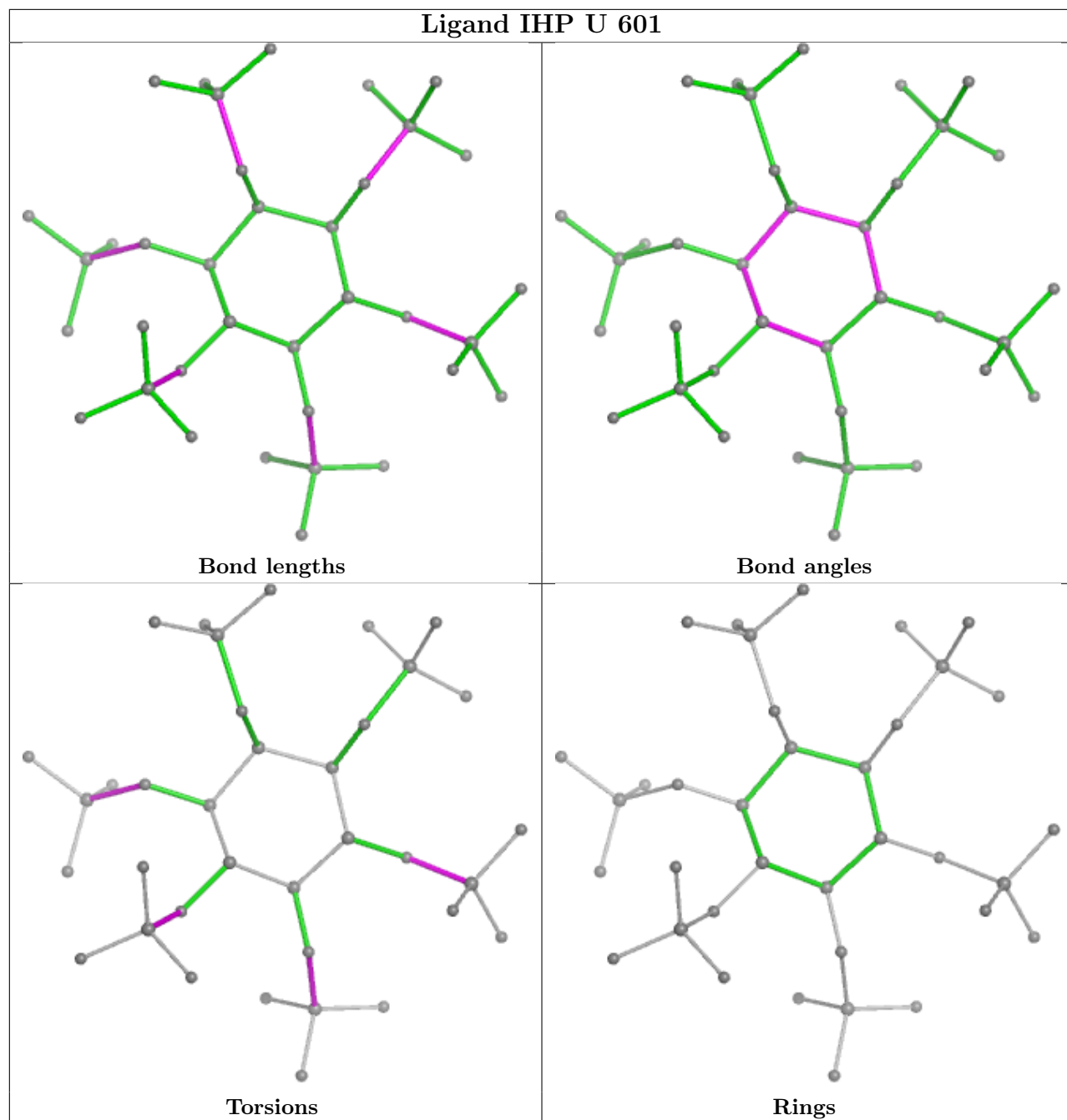
Mol	Chain	Res	Type	Atoms
59	U	601	IHP	C2-O12-P2-O42
59	U	601	IHP	C5-O15-P5-O25
59	U	601	IHP	C6-O16-P6-O26
59	U	601	IHP	C1-O11-P1-O31
59	U	601	IHP	C1-O11-P1-O41

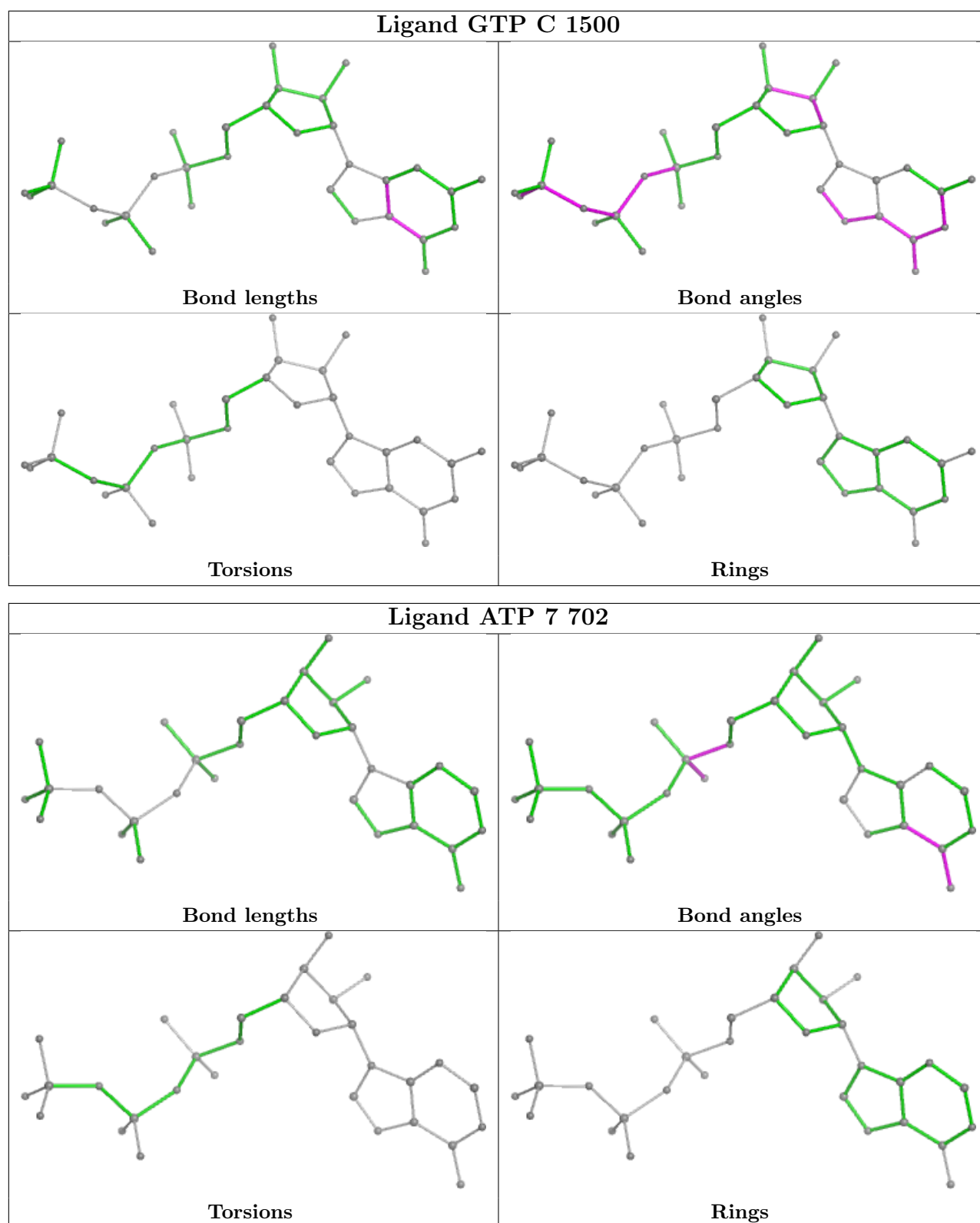
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	U	601	IHP	1	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

There are no chain breaks in this entry.

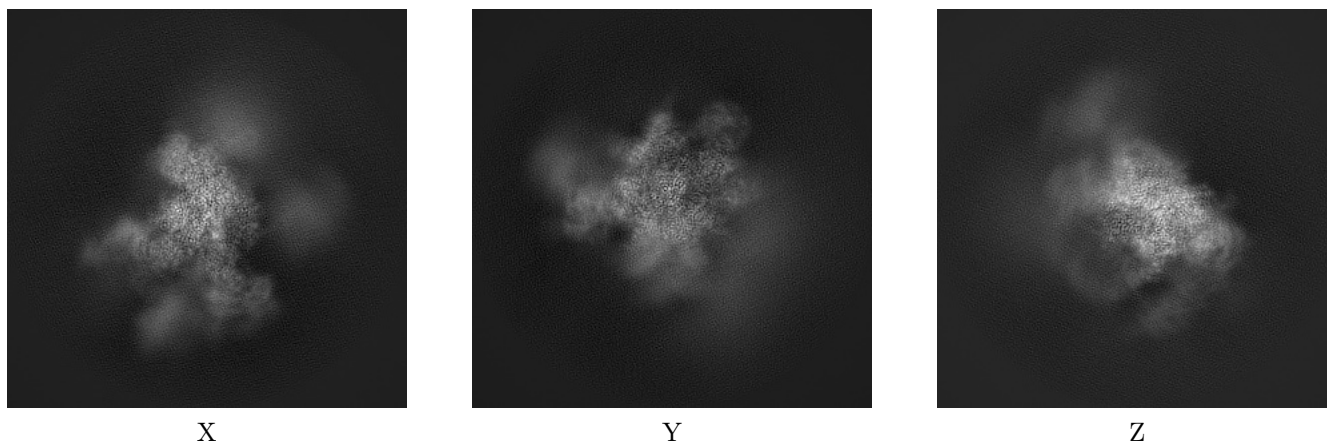
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4525. 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](#)

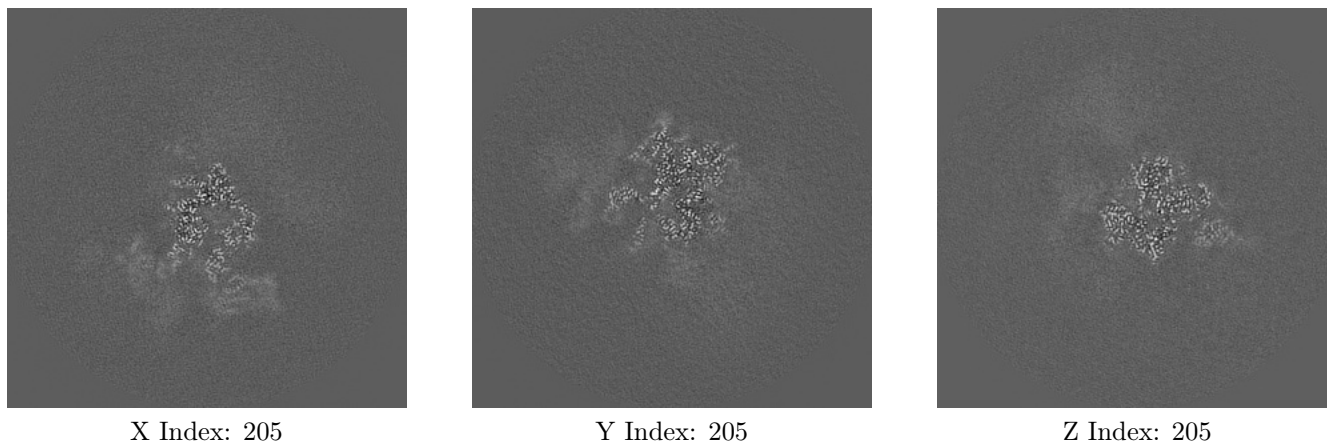
6.1.1 Primary map



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

6.2 Central slices [i](#)

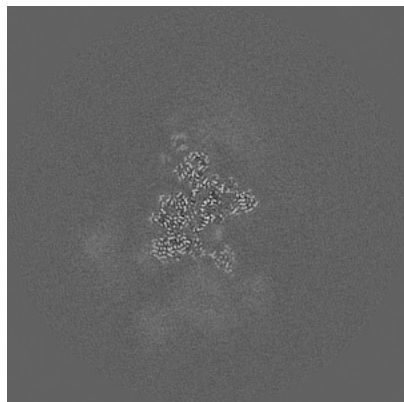
6.2.1 Primary map



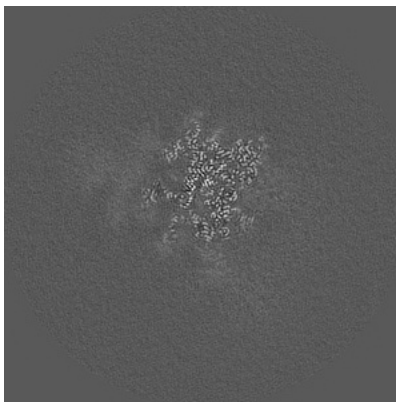
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

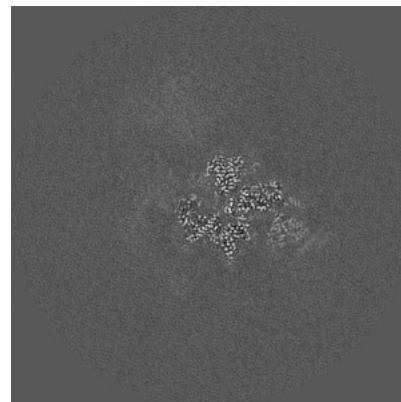
6.3.1 Primary map



X Index: 231



Y Index: 203

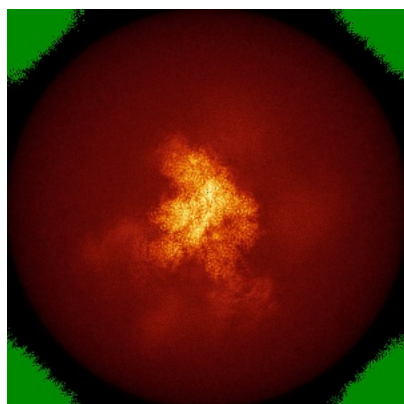


Z Index: 202

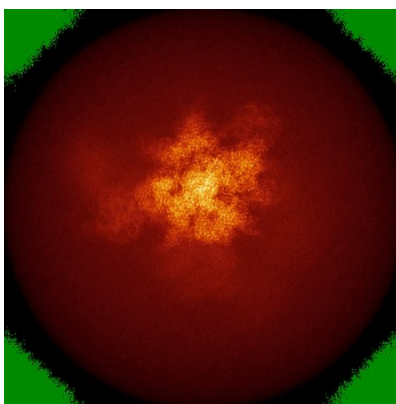
The images above show the largest variance slices of the map in three orthogonal directions.

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

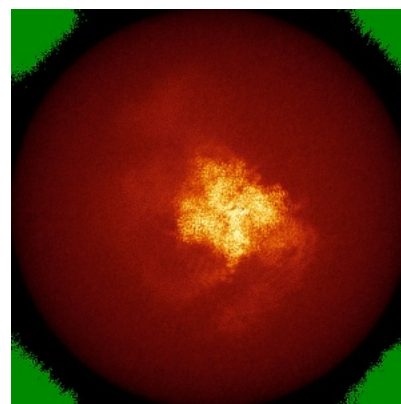
6.4.1 Primary map



X



Y

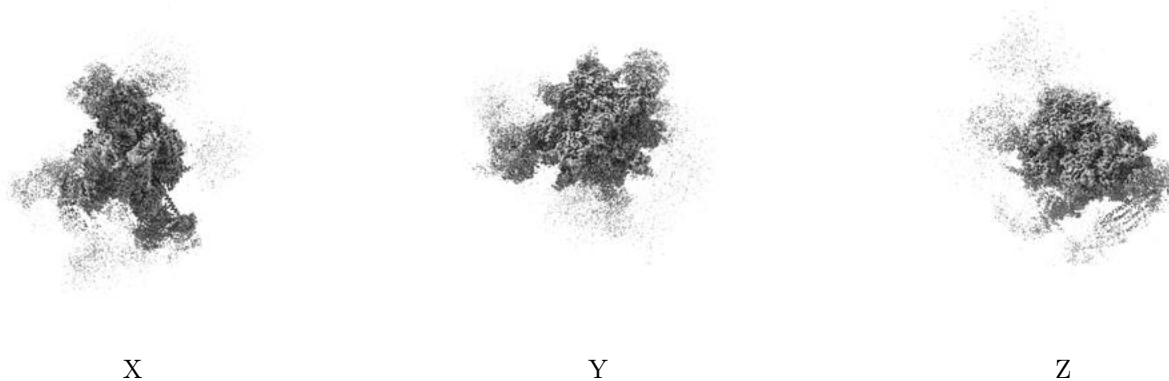


Z

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

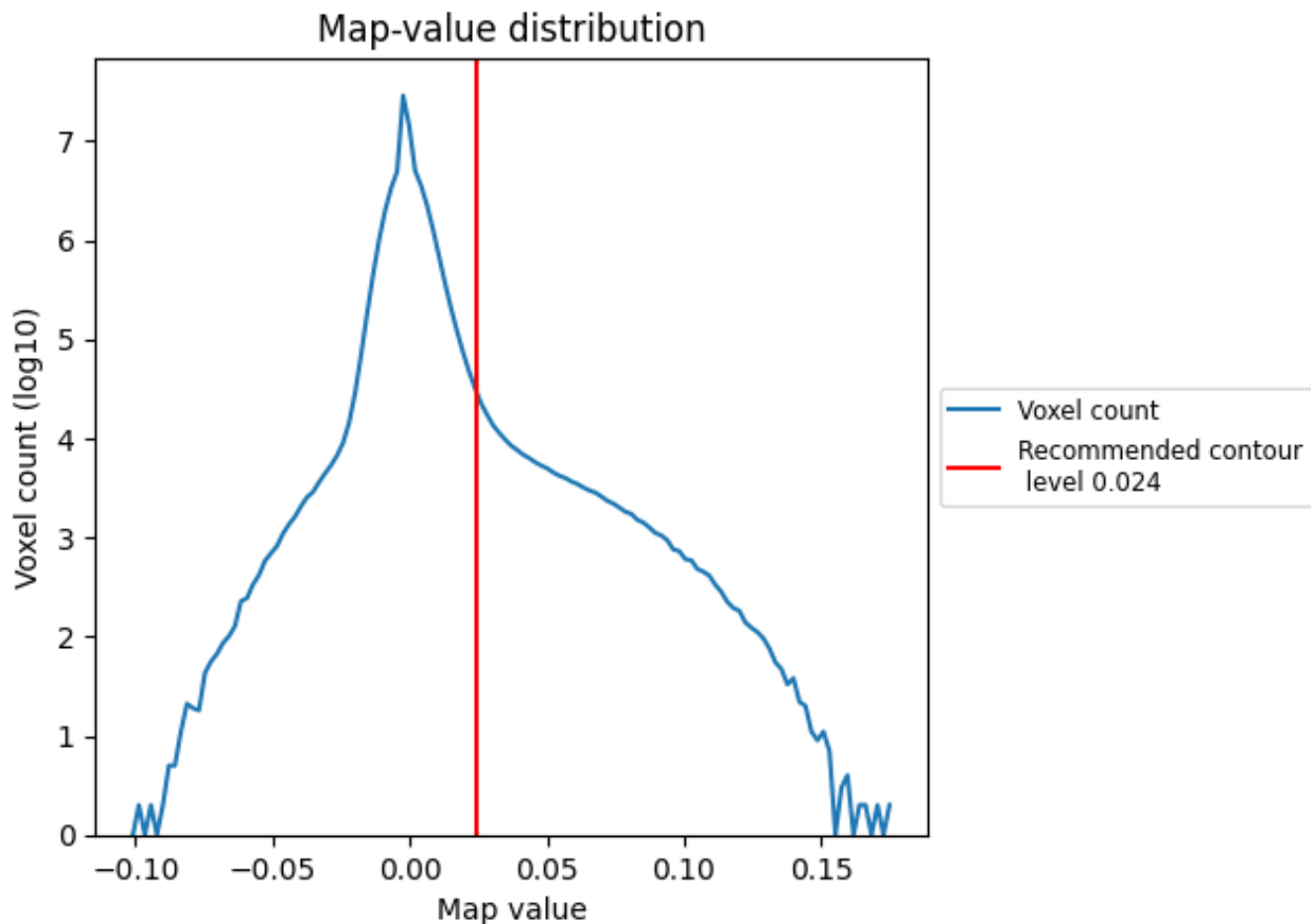
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

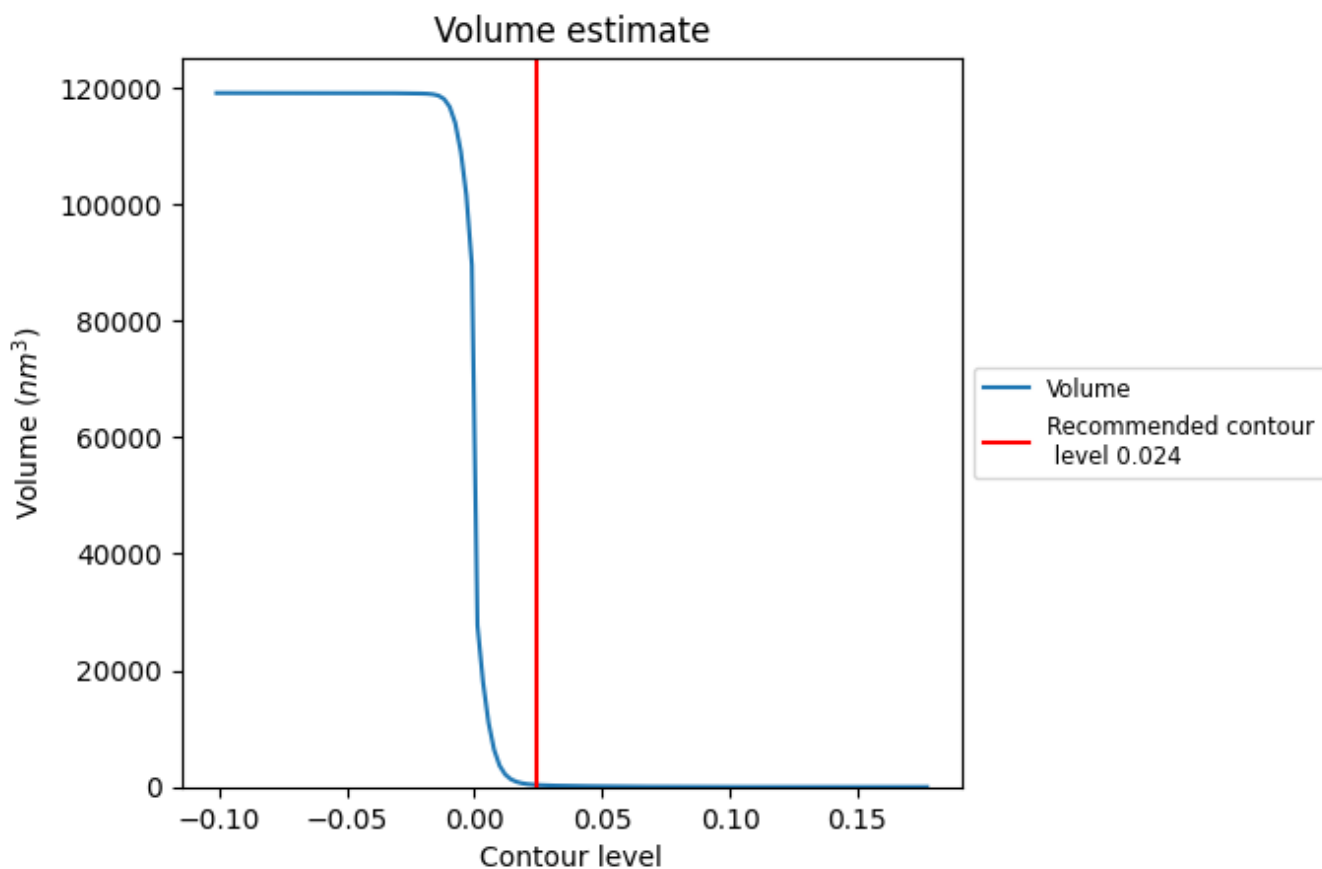
This section contains the results of statistical analysis of the map.

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.

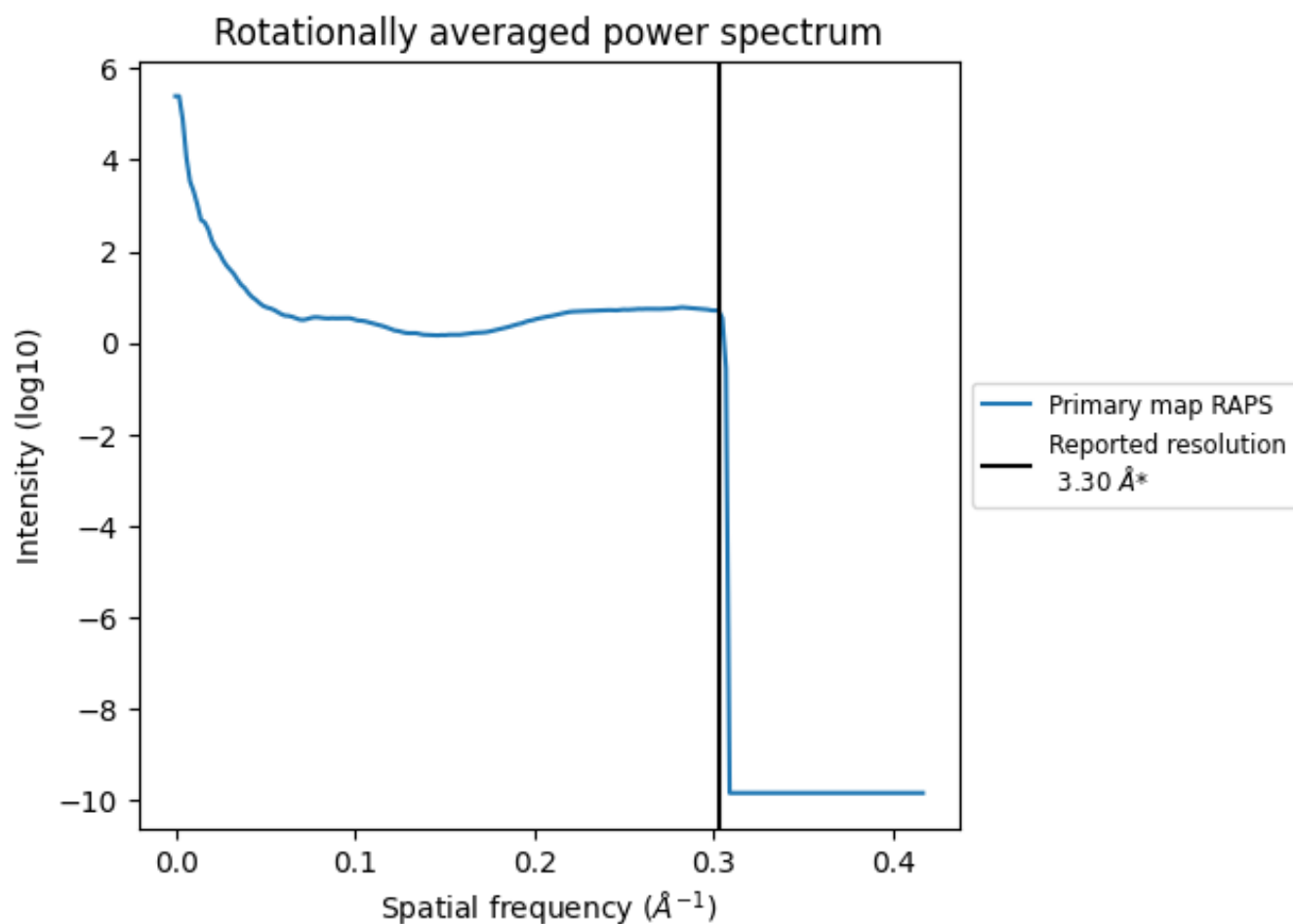
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 356 nm³; this corresponds to an approximate mass of 321 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 [\(i\)](#)

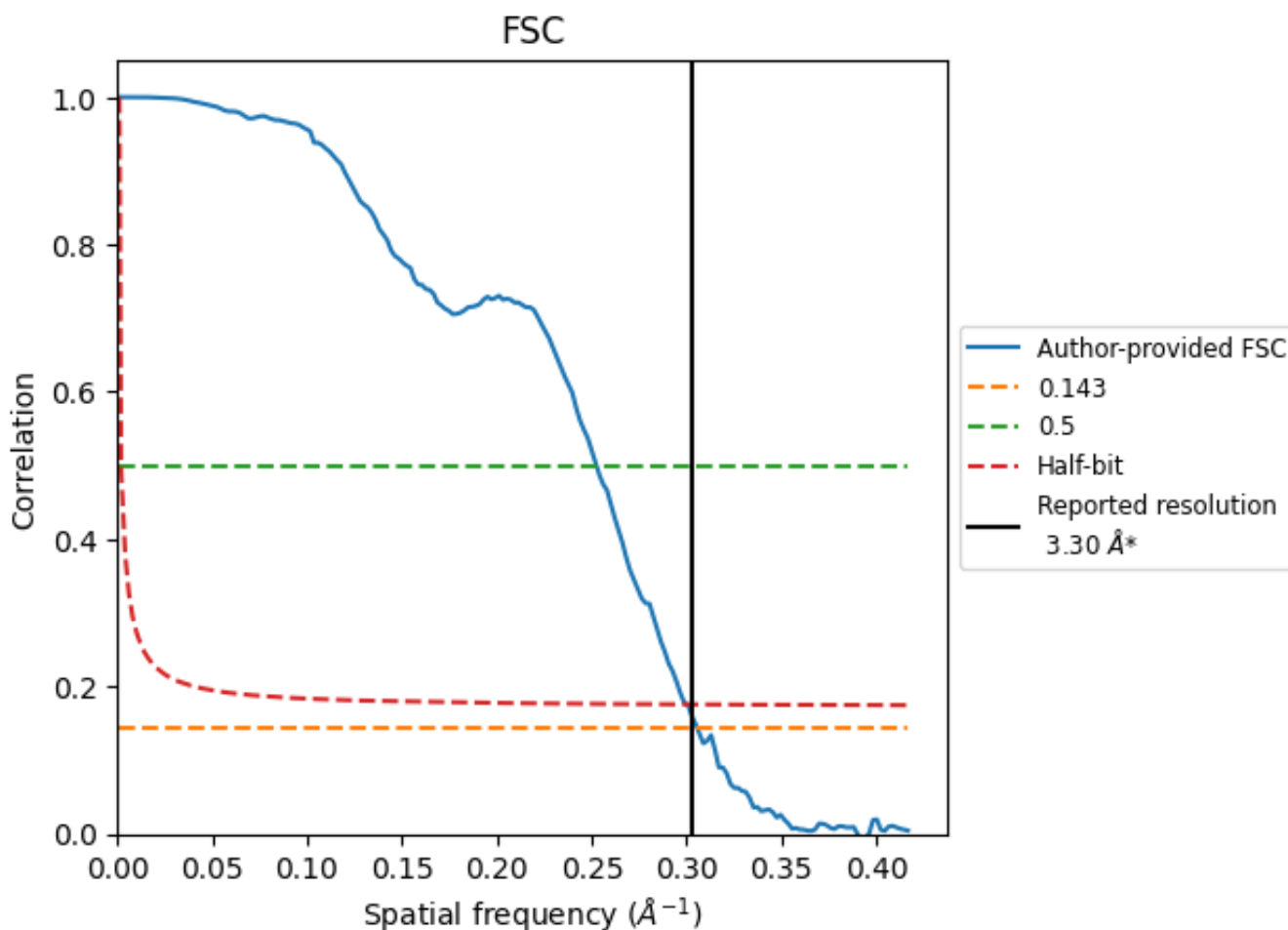


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

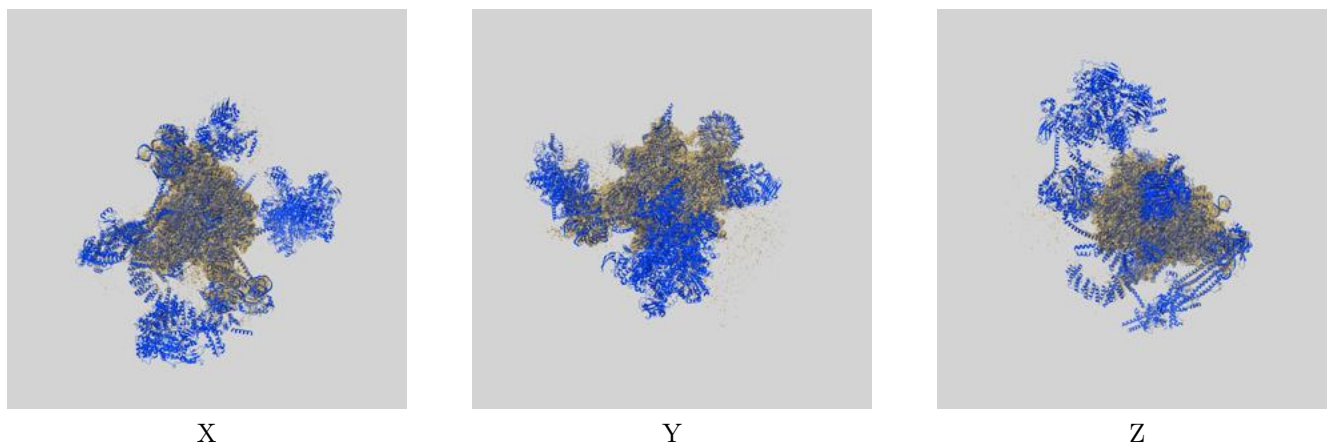
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.27	3.96	3.33
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

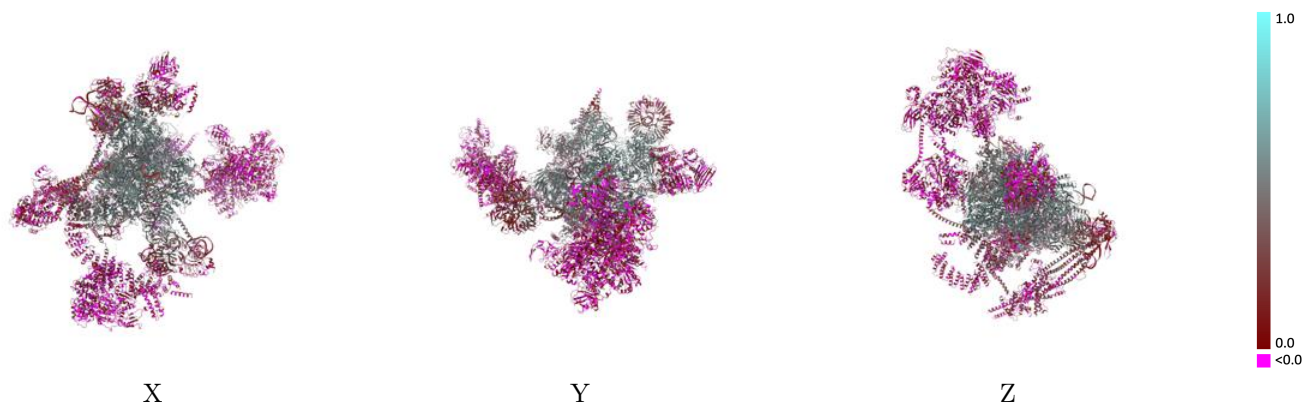
This section contains information regarding the fit between EMDB map EMD-4525 and PDB model 9FMD. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



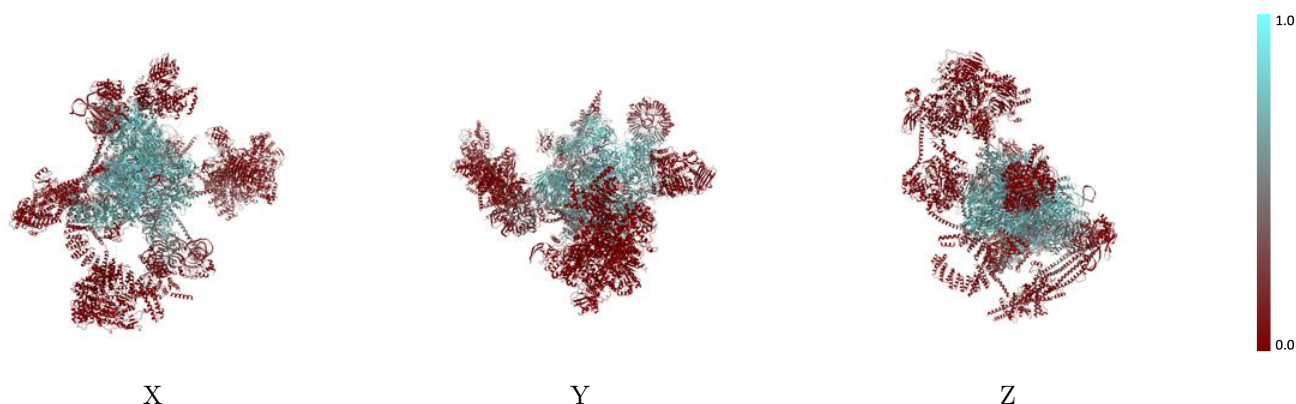
The images above show the 3D surface view of the map at the recommended contour level 0.024 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



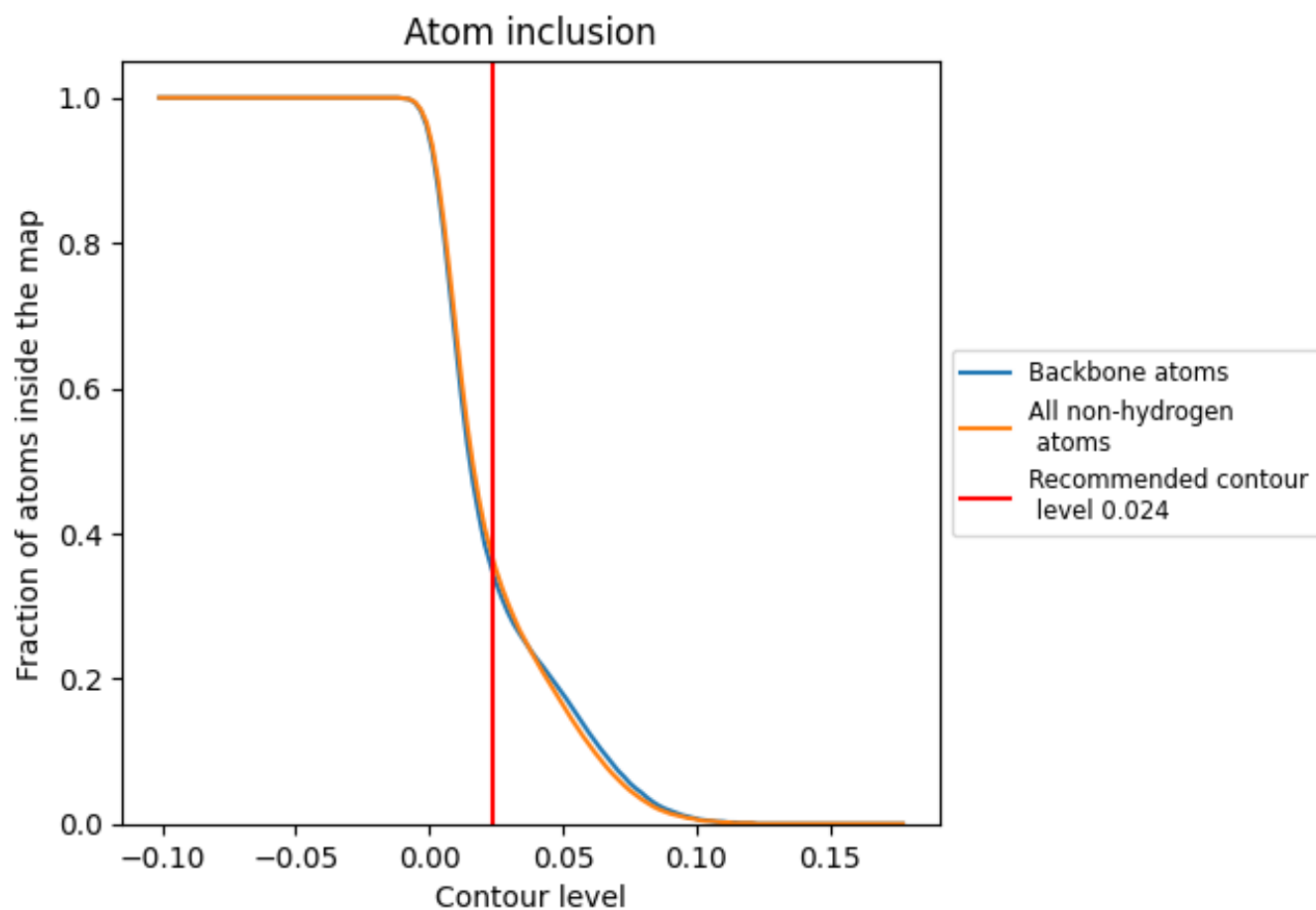
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.024).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 34% of all backbone atoms, 36% 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 (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3620	 0.2980
1	 0.4130	 0.3810
2	 0.4200	 0.3000
3	 0.1450	 0.2540
32	 0.5850	 0.5110
5	 0.6150	 0.3810
50	 0.0100	 0.1010
56	 0.0000	 -0.0090
6	 0.7350	 0.4580
7	 0.0070	 0.1140
8	 0.0000	 0.0490
9	 0.0000	 0.0430
A	 0.7240	 0.5090
B	 0.0010	 0.0500
C	 0.6900	 0.4910
D	 0.0000	 0.0950
E	 0.6280	 0.4780
EX	 0.8180	 0.5330
F	 0.6330	 0.4700
H	 0.4150	 0.3570
I	 0.0520	 0.1020
IN	 0.5710	 0.3790
J	 0.3960	 0.2850
K	 0.1190	 0.1860
L	 0.4040	 0.3650
M	 0.4970	 0.3810
N	 0.7490	 0.5370
NO	 0.0010	 0.1270
O	 0.5200	 0.4490
P	 0.6510	 0.5200
Q	 0.0020	 0.0530
R	 0.5330	 0.4400
S	 0.5800	 0.4560
SR	 0.4040	 0.3320
T	 0.7390	 0.5090



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Chain	Atom inclusion	Q-score
U	 0.5870	 0.4570
V	 0.0510	 0.0800
W	 0.6730	 0.5020
X	 0.0150	 0.1550
Z	 0.0150	 0.0570
a	 0.4310	 0.4160
b	 0.3380	 0.3350
c	 0.1330	 0.2070
d	 0.0620	 0.1480
e	 0.0850	 0.1950
f	 0.0470	 0.1550
g	 0.2210	 0.3340
h	 0.3960	 0.3520
i	 0.2430	 0.2910
j	 0.1220	 0.2030
k	 0.0780	 0.1560
l	 0.2420	 0.2790
m	 0.1360	 0.1820
n	 0.3660	 0.3690
o	 0.0260	 0.1130
p	 0.0600	 0.1370
q	 0.0410	 0.1150
r	 0.0200	 0.0850
s	 0.0290	 0.1460
t	 0.0100	 0.0890
w	 0.0000	 0.0380
x	 0.0300	 0.1330
y	 0.0030	 0.1230
z	 0.3510	 0.3010