



wwPDB EM Validation Summary Report ⓘ

Oct 21, 2024 – 11:50 AM JST

PDB ID : 5Z57
EMDB ID : EMD-6890
Title : Cryo-EM structure of the human activated spliceosome (late Bact) at 6.5 angstrom
Authors : Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on : 2018-01-17
Resolution : 6.50 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.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

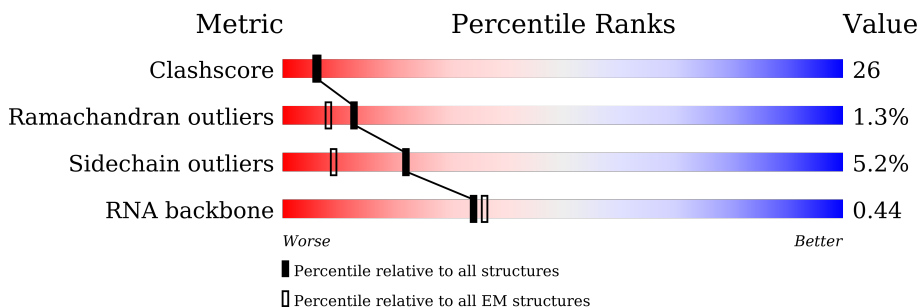
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.50 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	2335	<div> <div>18%</div> <div>48%</div> <div>33%</div> <div>15%</div> </div>
2	B	117	<div> <div>13%</div> <div>29%</div> <div>26%</div> <div>14%</div> <div>28%</div> </div>
3	C	972	<div> <div>8%</div> <div>49%</div> <div>31%</div> <div>7%</div> <div>12%</div> </div>
4	D	2136	<div> <div>78%</div> <div>79%</div> <div>19%</div> </div>
5	E	357	<div> <div>22%</div> <div>58%</div> <div>22%</div> <div>16%</div> </div>
6	a	126	<div> <div>57%</div> <div>64%</div> <div>36%</div> </div>
6	h	126	<div> <div>60%</div> <div>63%</div> <div>37%</div> </div>

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Mol	Chain	Length	Quality of chain
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	
22	2	895	
23	3	1217	
24	4	424	
25	5	125	

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Mol	Chain	Length	Quality of chain
26	6	110	
27	7	86	
28	J	848	
29	L	802	
30	q	504	
30	r	504	
30	s	504	
30	t	504	
31	K	225	
32	I	855	
33	Q	1485	
34	N	144	
35	O	420	
36	P	229	
37	R	540	
38	S	166	
39	T	514	
40	U	2752	
41	V	908	
42	W	579	
43	X	396	
44	Y	322	
45	Z	619	
46	x	1041	
47	y	301	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
48	IHP	A	2401	-	-	X	-
50	GTP	C	1500	-	-	X	-
52	ZN	O	502	-	-	X	-

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 113433 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1978	Total	C	N	O	S	0	0
			16399	10552	2875	2897	75		

- Molecule 2 is a RNA chain called U5 snRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	860	Total	C	N	O	S	0	0
			6716	4294	1120	1270	32		

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

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

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

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

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 13 is a RNA chain called U6 snRNA.

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

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

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

- Molecule 15 is a RNA chain called U2 snRNA.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	438	Total	C	N	O	S	0	0
			2373	1450	461	459	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	104	Total	C	N	O	0	0
			520	312	104	104		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	v	165	Total	C	N	O	S	0
			936	565	191	178	2	0

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	3	1177	Total	C	N	O	S	0
			9195	5834	1561	1755	45	0

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	342	Total	C	N	O	S	0	0
			2260	1430	406	420	4		

- Molecule 30 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	132	Total	C	N	O		0	0
			659	395	132	132			
30	r	131	Total	C	N	O		0	0
			654	392	131	131			
30	s	67	Total	C	N	O		0	0
			335	201	67	67			
30	t	67	Total	C	N	O		0	0
			335	201	67	67			

- Molecule 31 is a protein called Pre-mRNA-splicing factor SPF27.

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

- Molecule 32 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	I	564	Total	C	N	O	0	0
			2778	1650	564	564		

- Molecule 33 is a protein called Intron-binding protein aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	1317	Total	C	N	O	0	0
			6528	3894	1317	1317		

- Molecule 34 is a protein called Protein BUD31 homolog.

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

- Molecule 35 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O	285	Total	C	N	O	S	0	0
			2273	1428	401	424	20		

- Molecule 36 is a protein called Spliceosome-associated protein CWC15 homolog.

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

- Molecule 37 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R	288	Total	C	N	O	S	0	0
			2188	1375	392	409	12		

- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

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

- Molecule 39 is a protein called Pleiotropic regulator 1.

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

- Molecule 40 is a protein called Serine/arginine repetitive matrix protein 2.

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

- Molecule 41 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	V	452	Total	C	N	O		0	0
			2243	1339	452	452			

- Molecule 42 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	W	483	Total	C	N	O		0	0
			2384	1418	483	483			

- Molecule 43 is a protein called Smad nuclear-interacting protein 1.

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

- Molecule 44 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Y	105	Total	C	N	O	S	0	0
			743	470	127	144	2		

- Molecule 45 is a protein called BUD13 homolog.

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

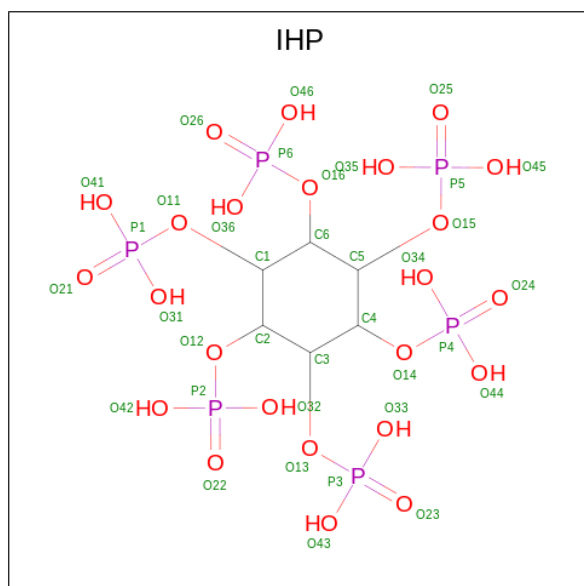
- Molecule 46 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

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

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase E.

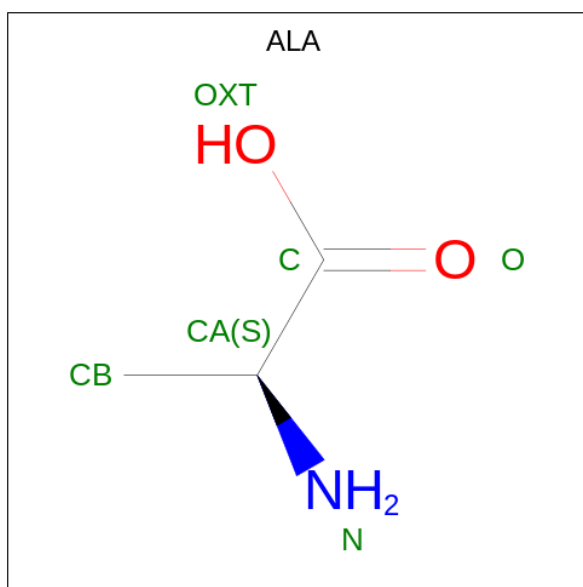
Mol	Chain	Residues	Atoms				AltConf	Trace
47	y	232	Total	C	N	O	0	0
			1133	669	232	232		

- Molecule 48 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



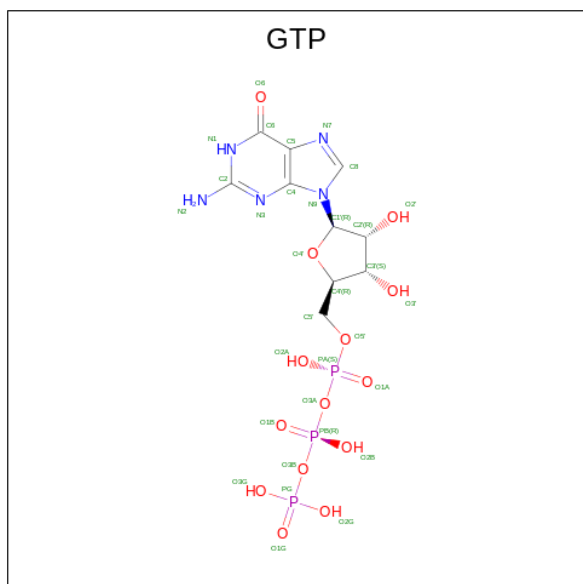
Mol	Chain	Residues	Atoms				AltConf
48	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 49 is ALANINE (three-letter code: ALA) (formula: $C_3H_7NO_2$).



Mol	Chain	Residues	Atoms				AltConf
49	A	1	Total	C	N	O	0
			5	3	1	1	

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

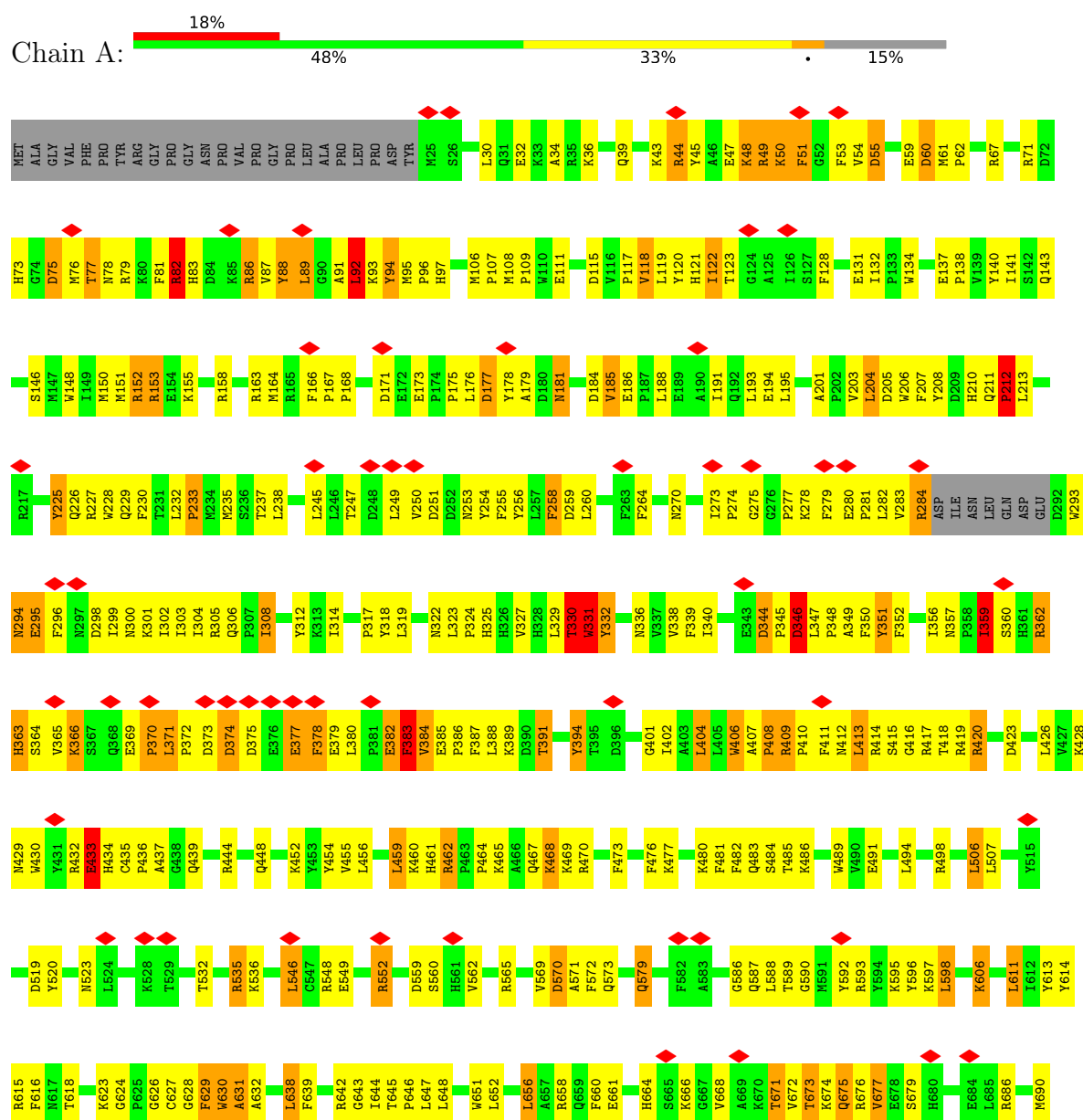
- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	v	1	Total 1	Zn 1	0
52	6	3	Total 3	Zn 3	0
52	N	3	Total 3	Zn 3	0
52	O	3	Total 3	Zn 3	0

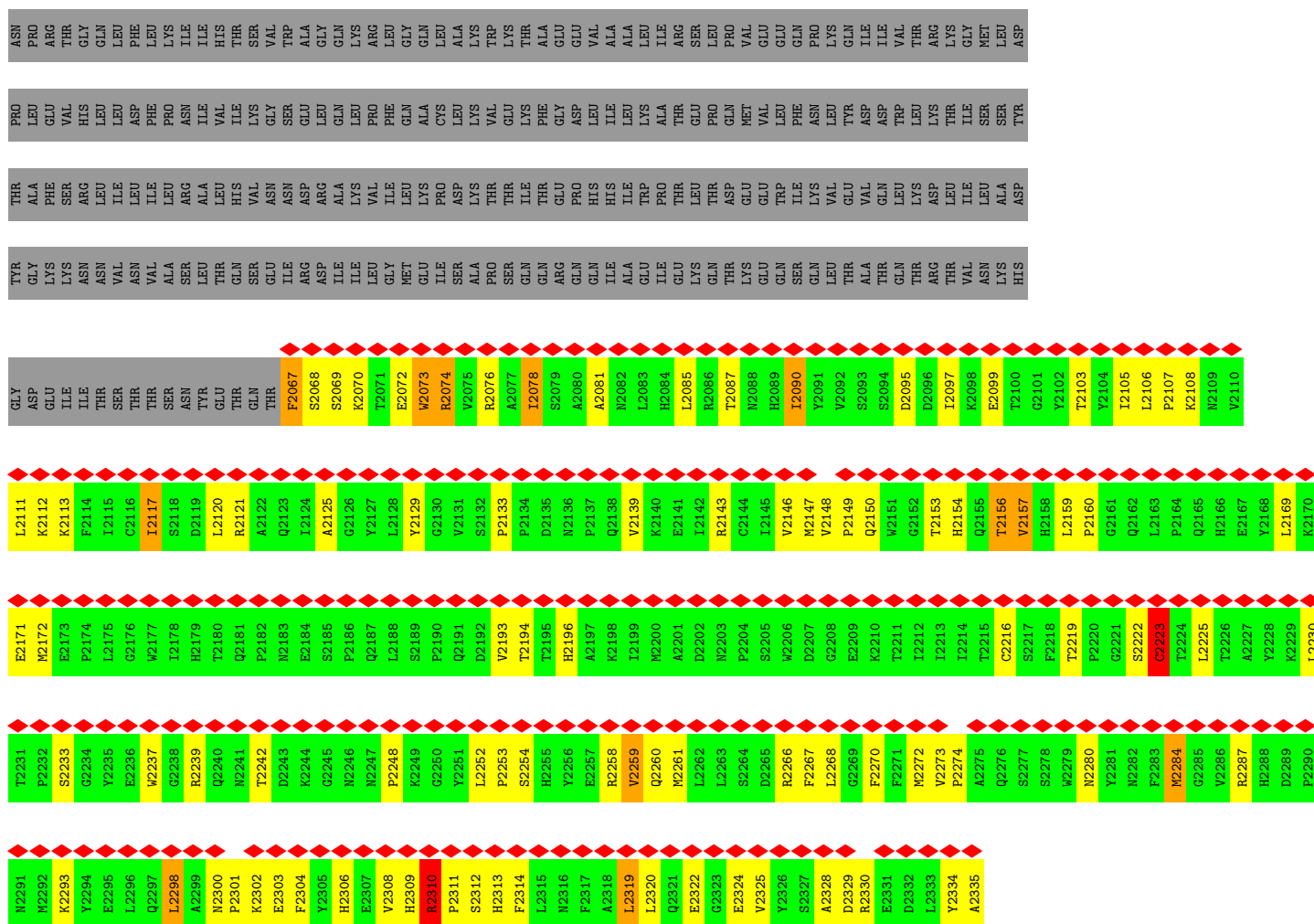
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

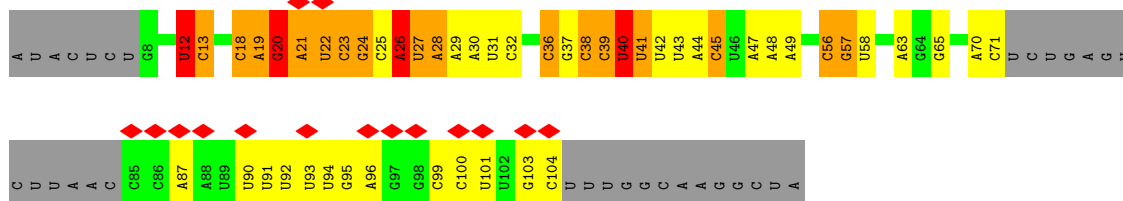
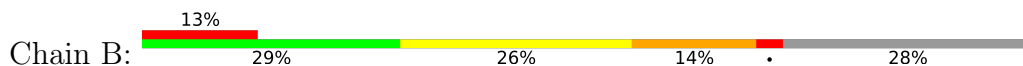
• Molecule 1: Pre-mRNA-processing-splicing factor 8



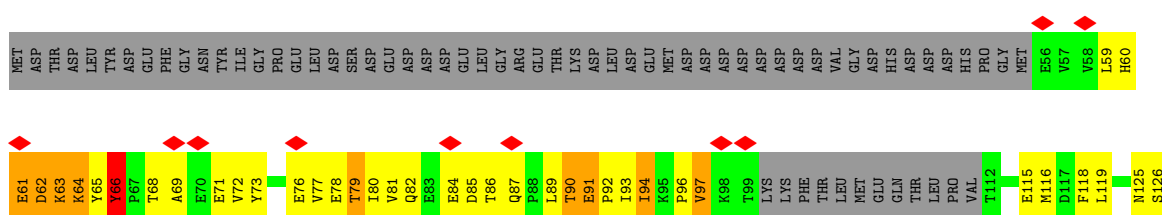


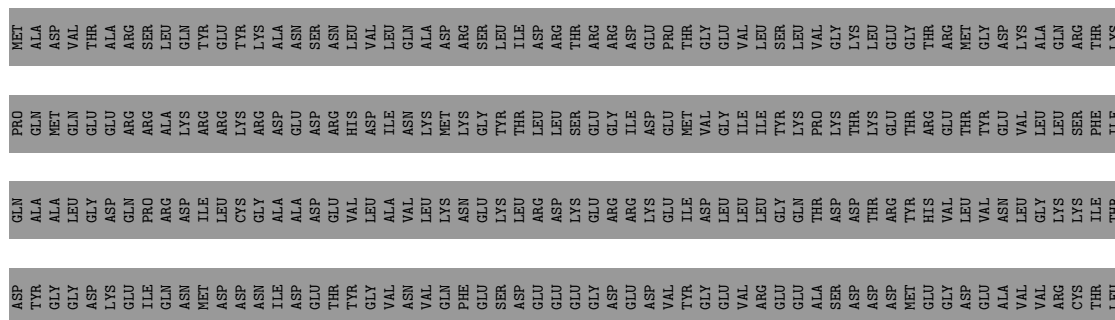
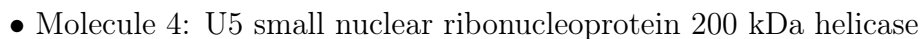


• Molecule 2: U5 snRNA



• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component



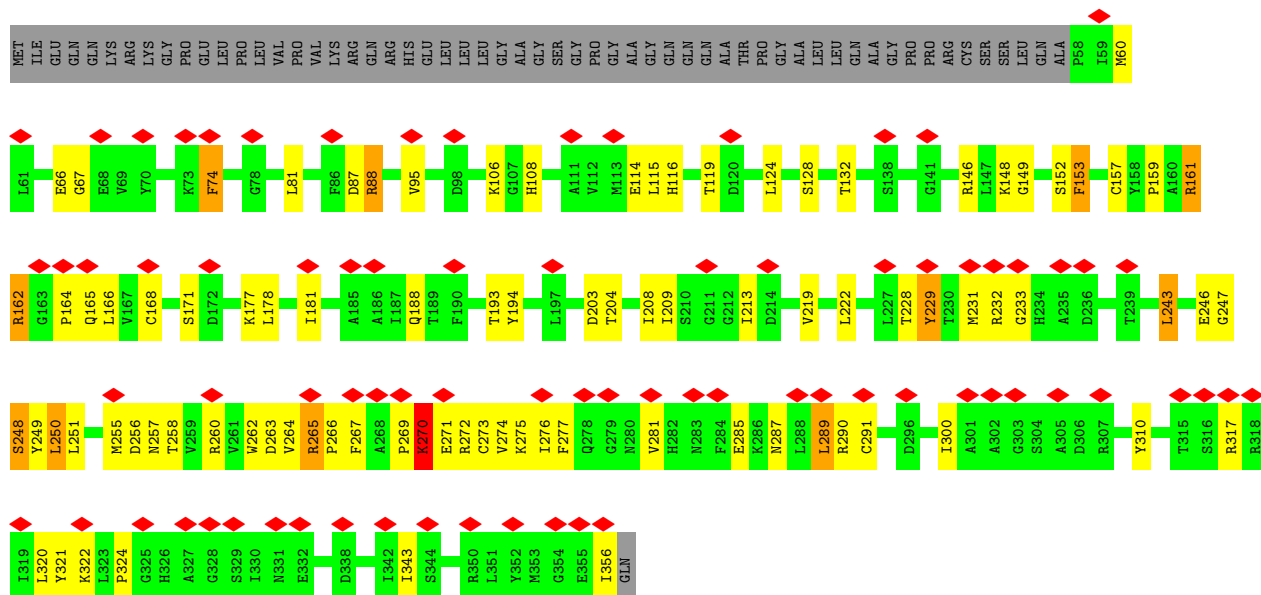


WORLDWIDE
PDB
PROTEIN DATA BANK

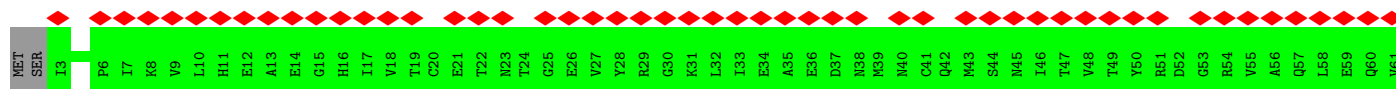
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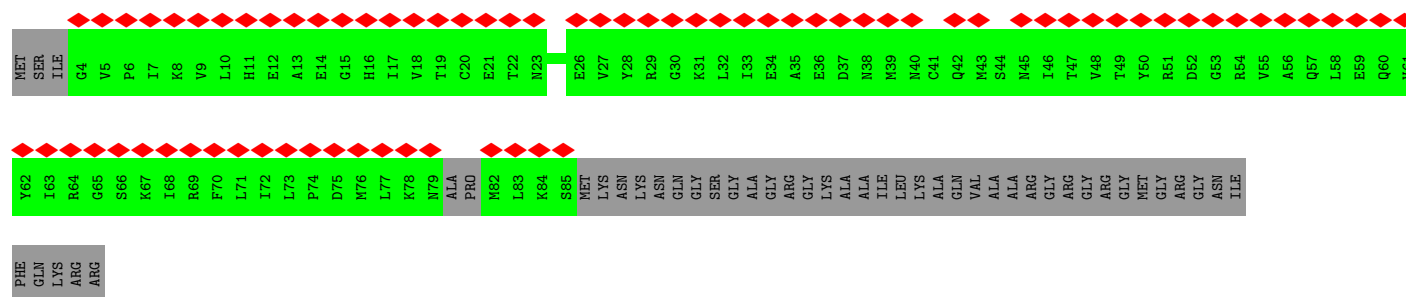
- Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein



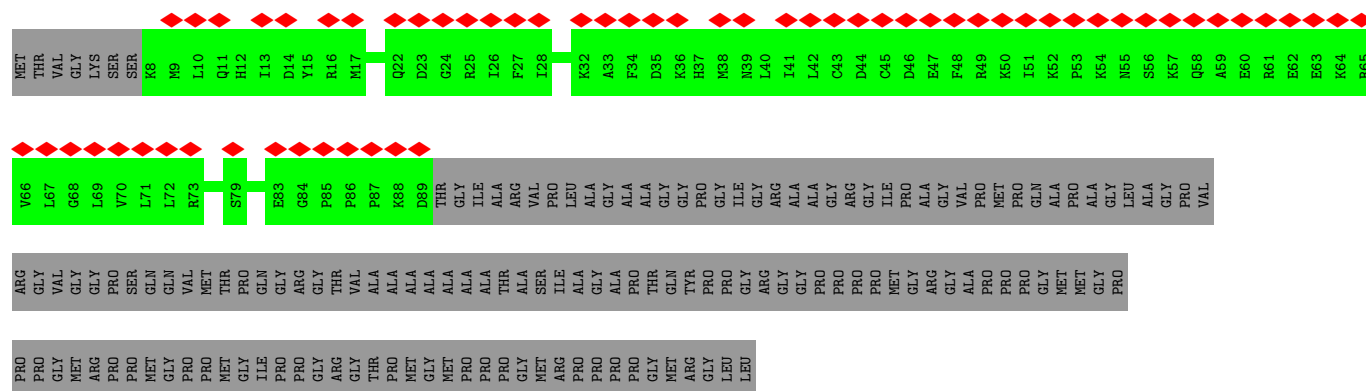
- Molecule 6: Small nuclear ribonucleoprotein Sm D3



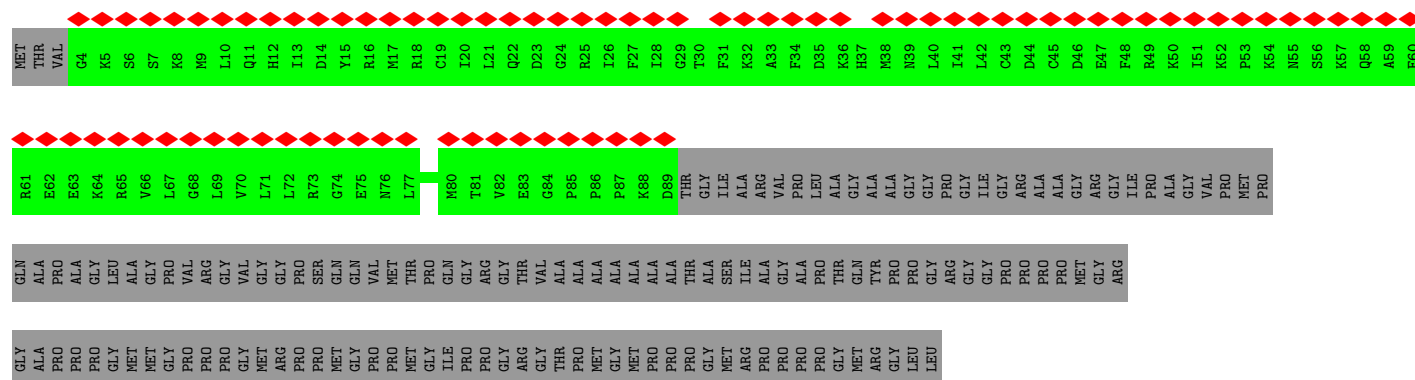
- Molecule 6: Small nuclear ribonucleoprotein Sm D3



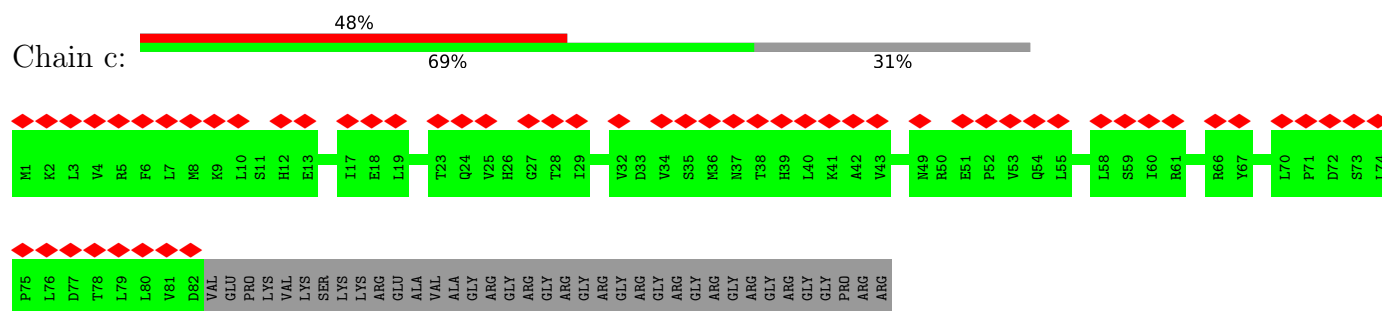
- Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



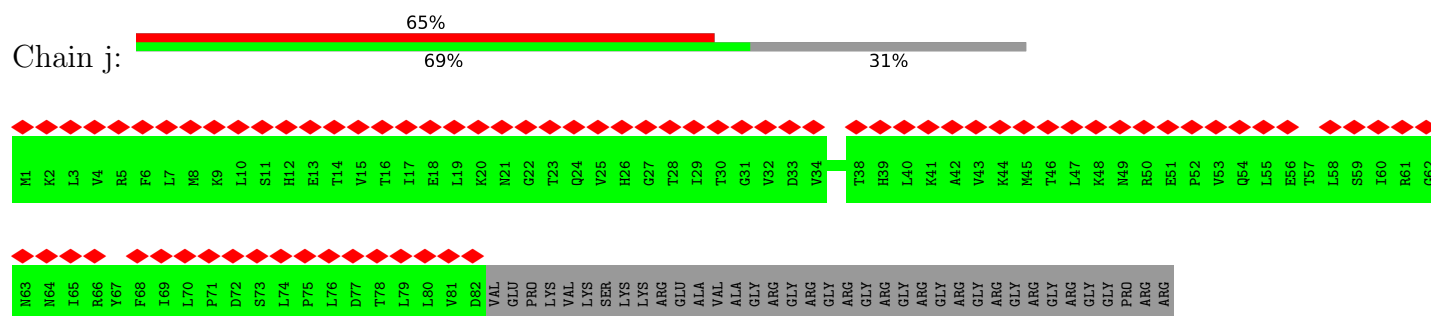
- Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



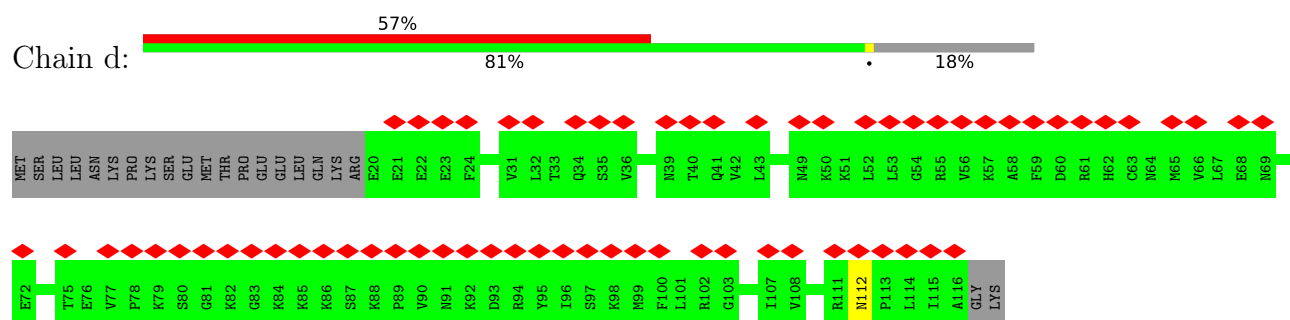
- Molecule 8: Small nuclear ribonucleoprotein Sm D1

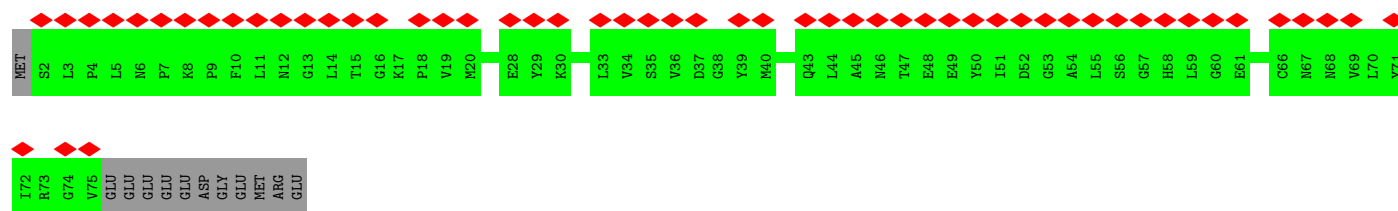


- Molecule 8: Small nuclear ribonucleoprotein Sm D1

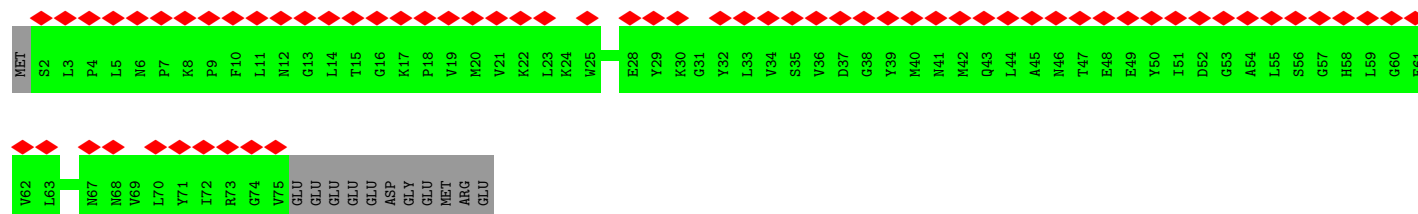
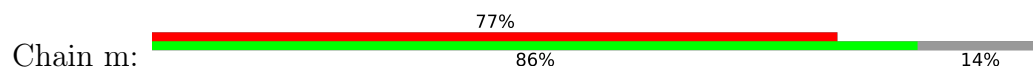


- Molecule 9: Small nuclear ribonucleoprotein Sm D2

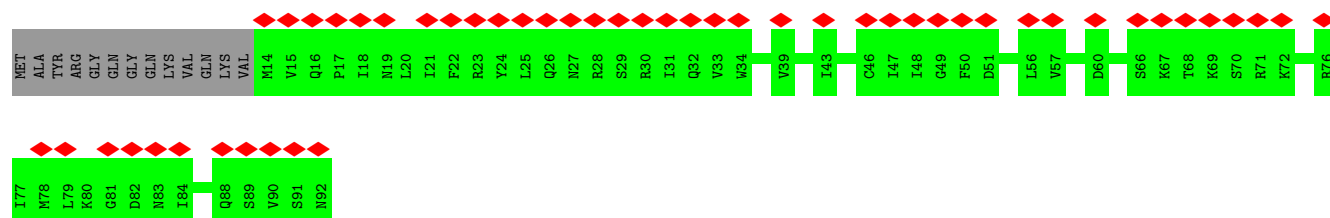
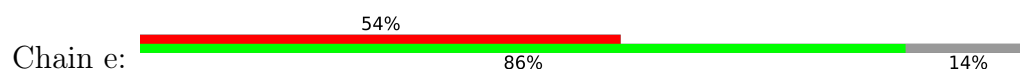




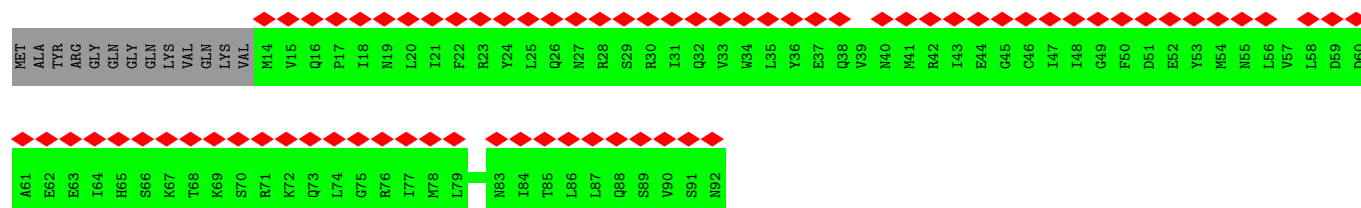
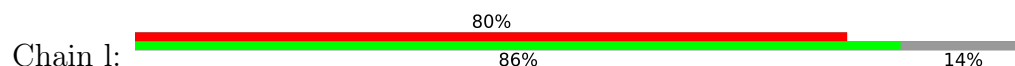
• Molecule 10: Small nuclear ribonucleoprotein F



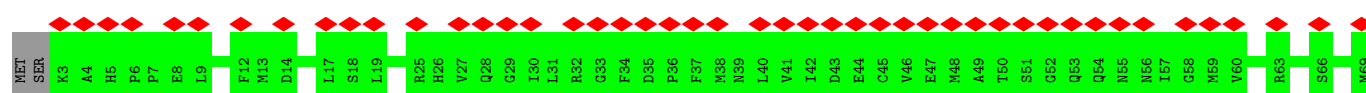
• Molecule 11: Small nuclear ribonucleoprotein E

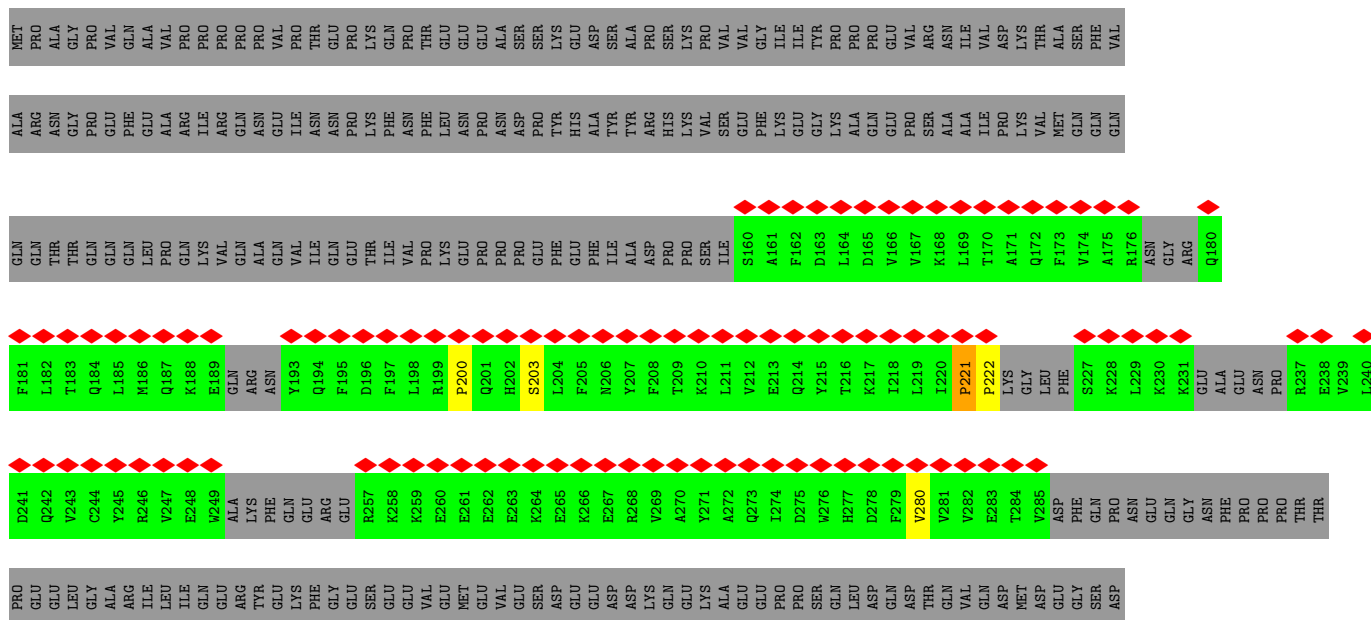


• Molecule 11: Small nuclear ribonucleoprotein E



• Molecule 12: Small nuclear ribonucleoprotein G





[illegible]

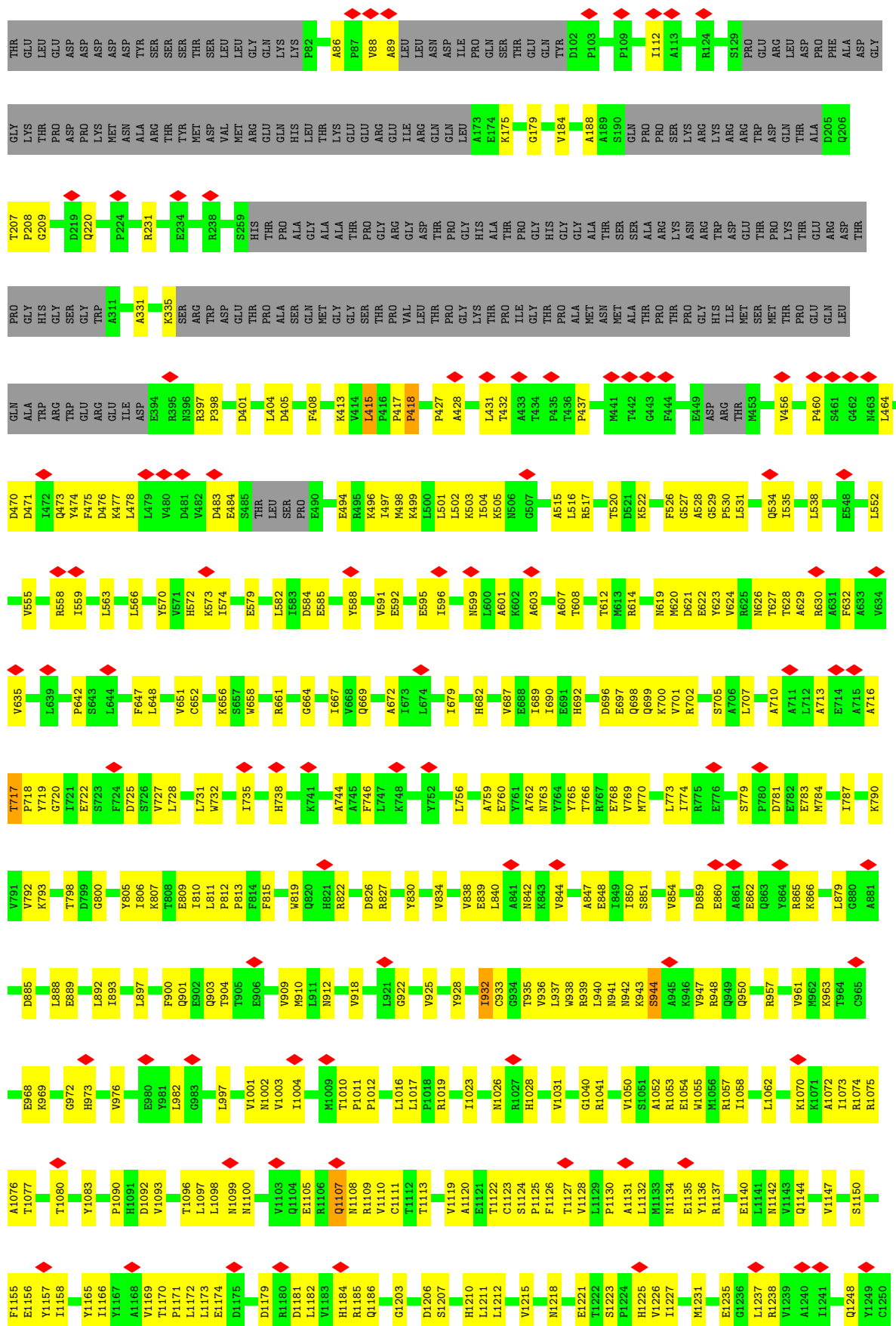
- Molecule 20: Splicing factor 3A subunit 2

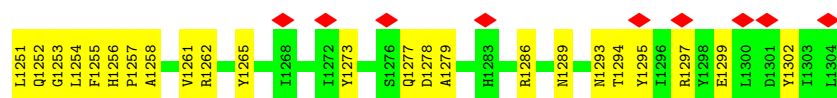
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- Molecule 21: Splicing factor 3B subunit 1

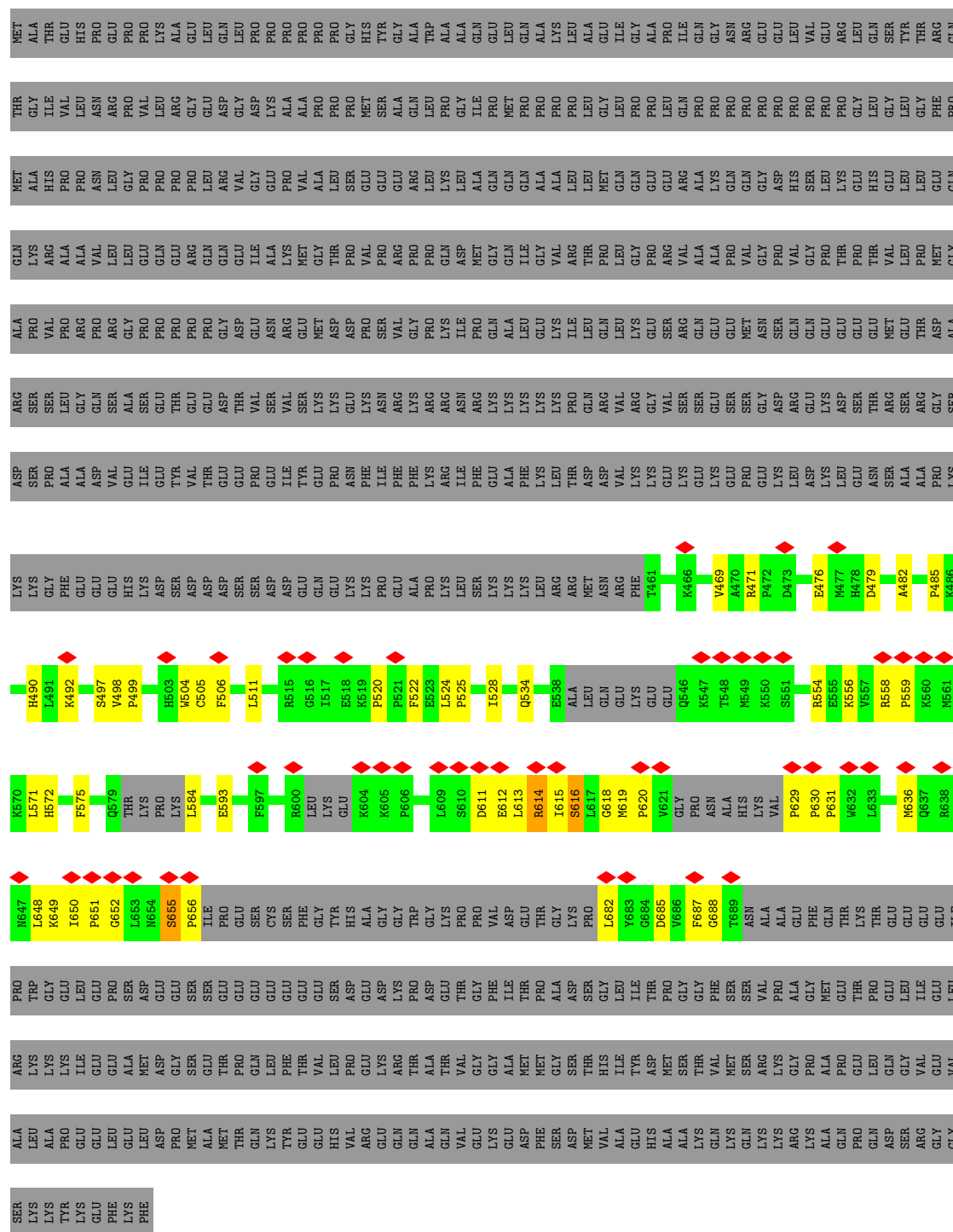


MET	ALA	ALA	LYS	ILE	ALA	LYS	THR	HIS	GLU	ASP	ILE	GLU	ALA	GLN	ILE	ARG	LYS	LYS	ILE	GLN	GLY	GLY	LYS	LEU	ASP	SER	THR	GLY	TYR	TYR	ASP	GLN	GLU	ILE	TYR	GLY	GLY	SER	SER	PHE	ARG	VAL	THR	SER	ILE	ALA	ALA	ALA
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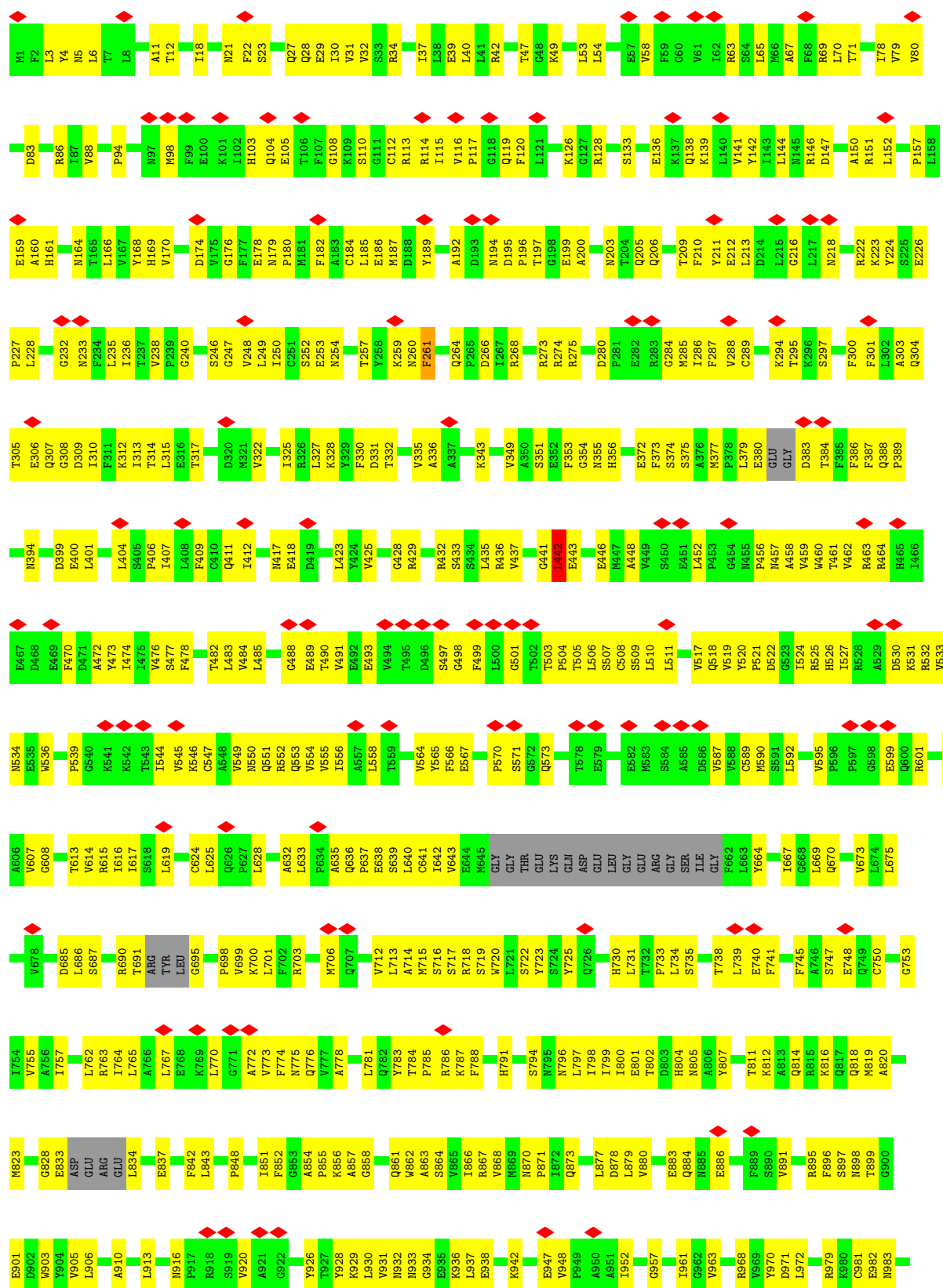


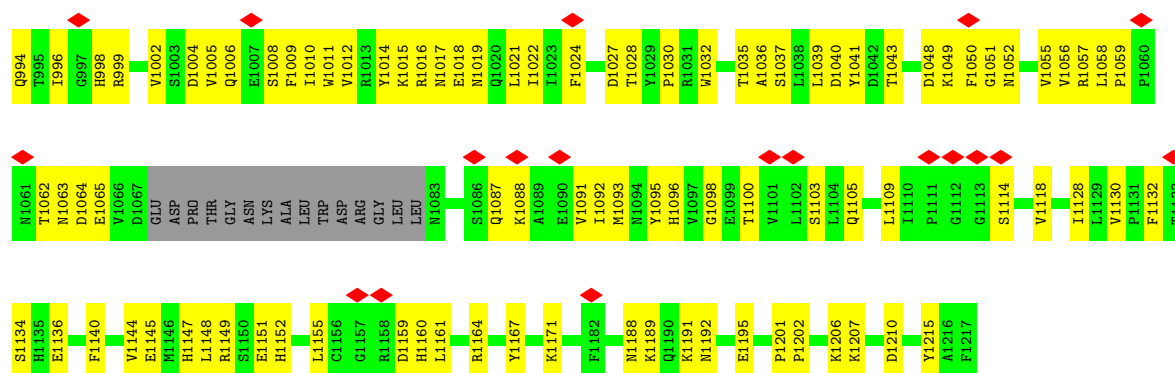
• Molecule 22: Splicing factor 3B subunit 2



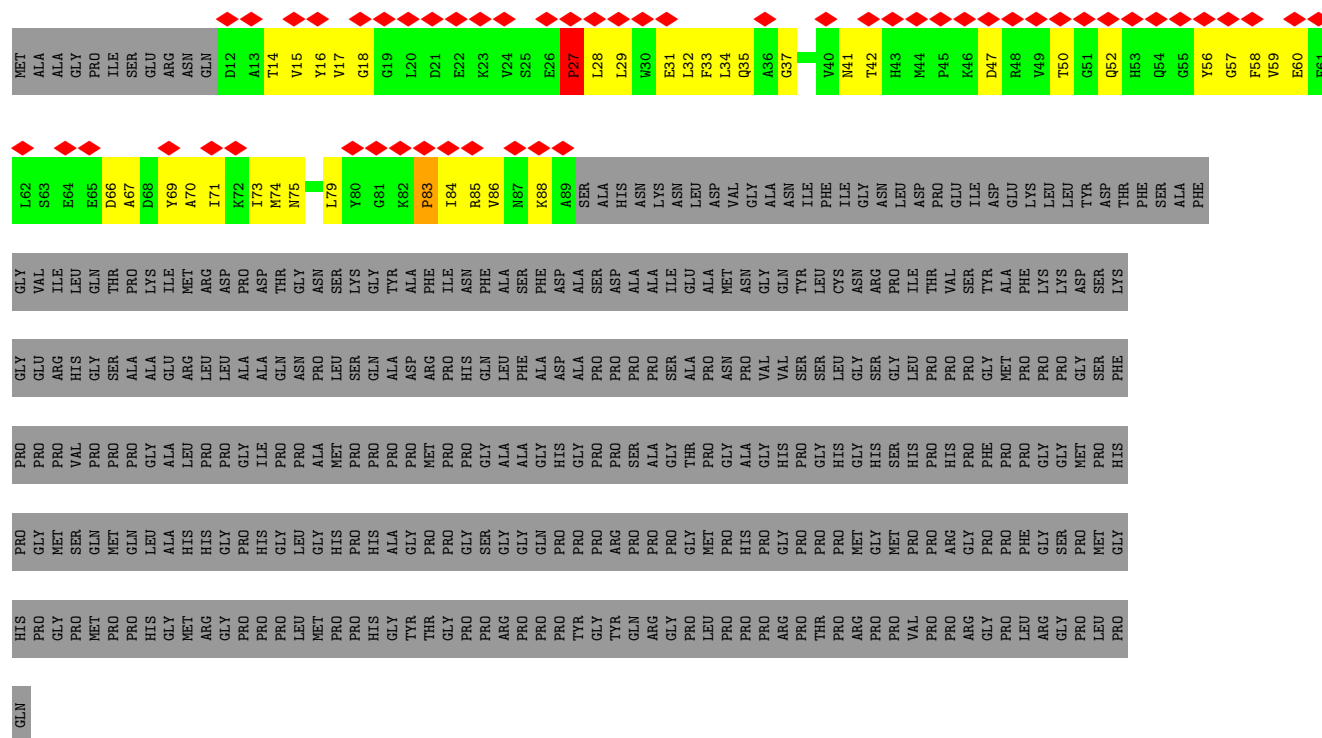
• Molecule 23: Splicing factor 3B subunit 3

Chain 3:  11% 50% 47%

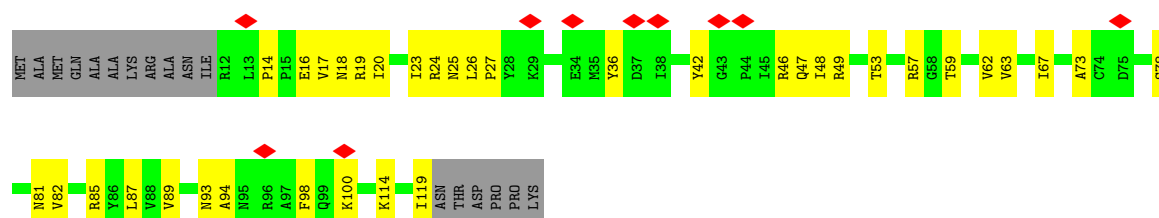




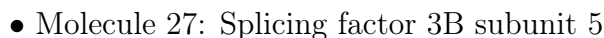
• Molecule 24: Splicing factor 3B subunit 4

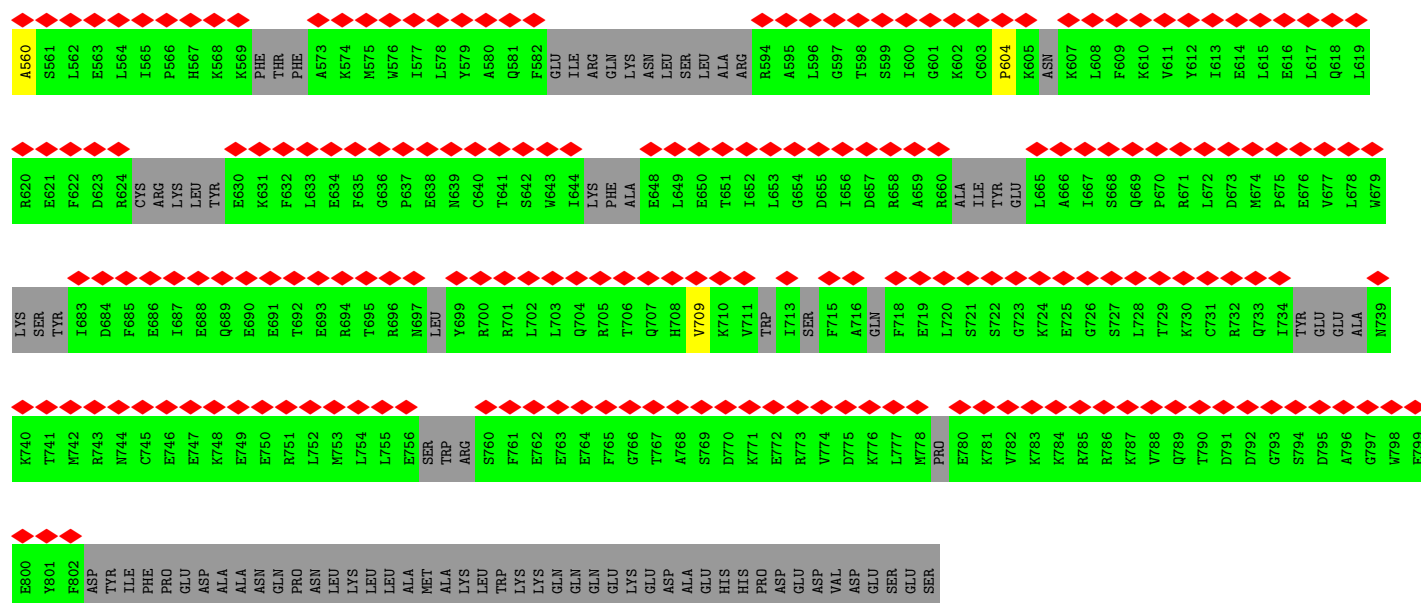


• Molecule 25: Splicing factor 3B subunit 6

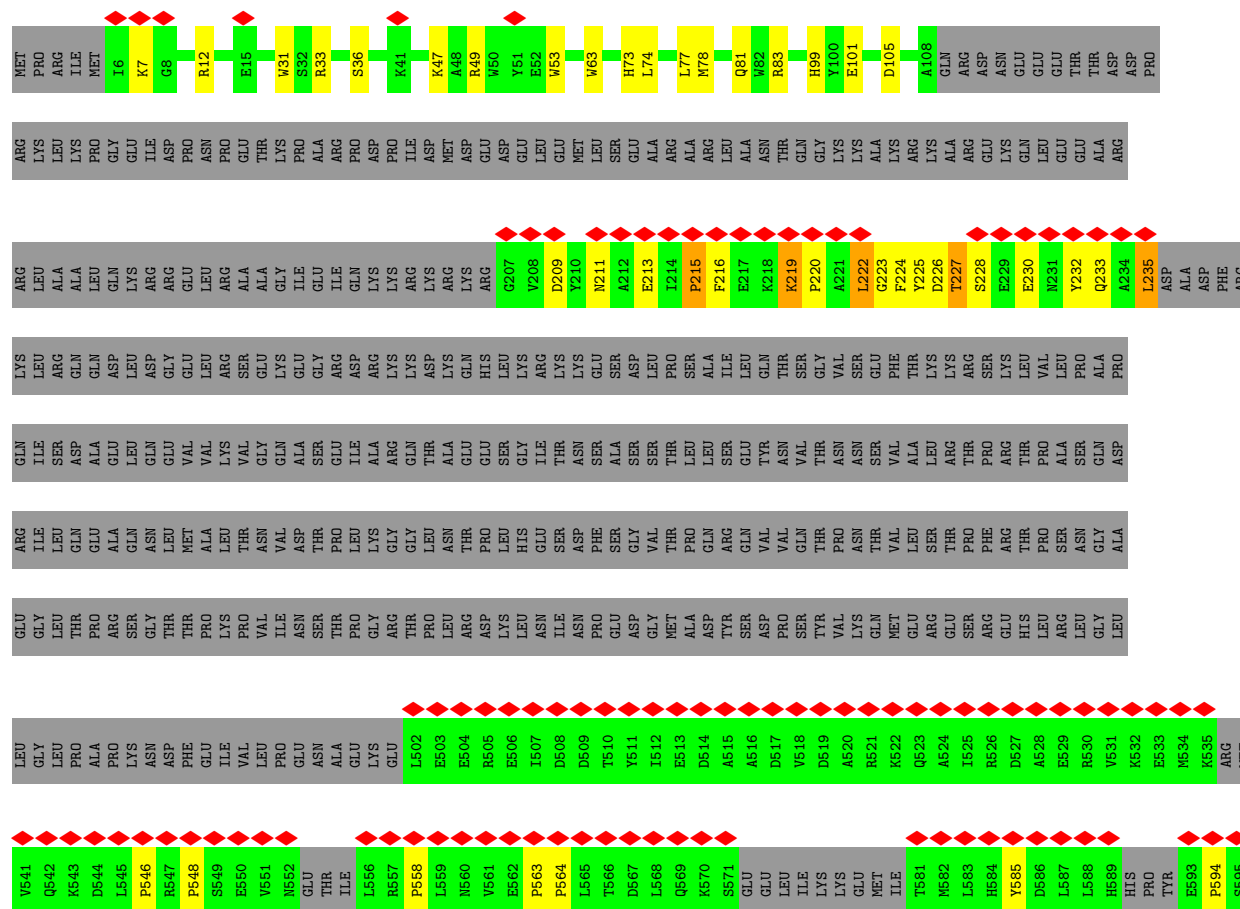
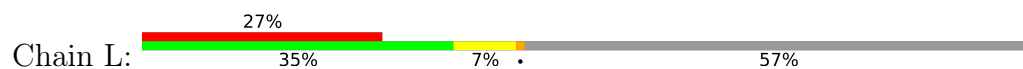


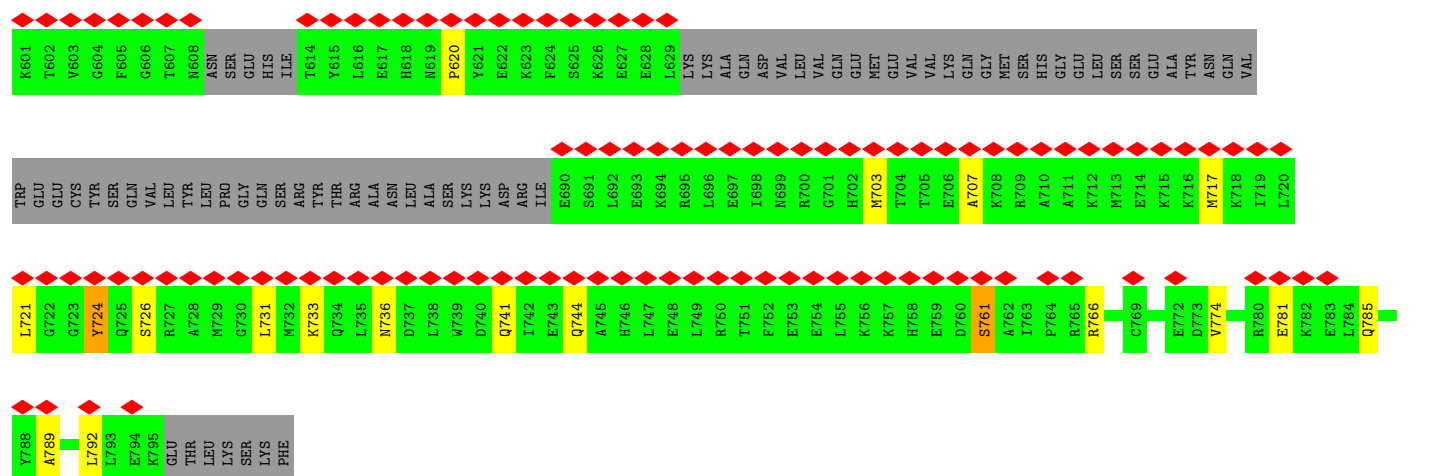
• Molecule 26: PHD finger-like domain-containing protein 5A



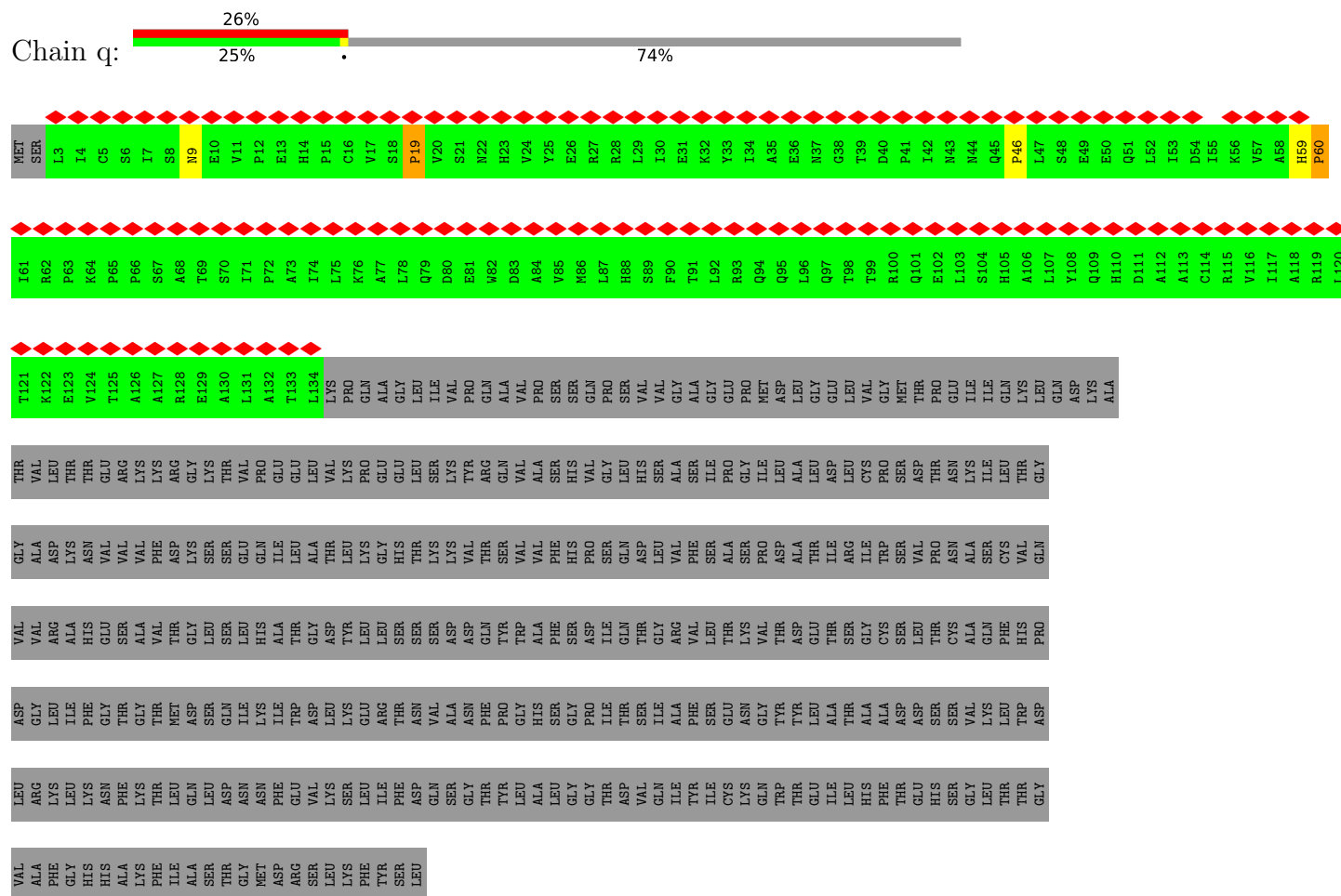


• Molecule 29: Cell division cycle 5-like protein

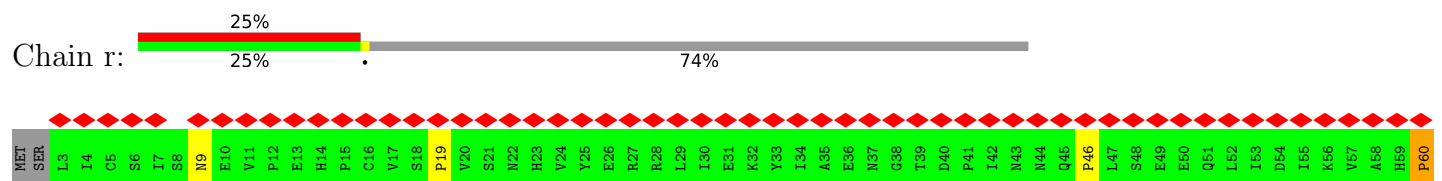




• Molecule 30: Pre-mRNA-processing factor 19



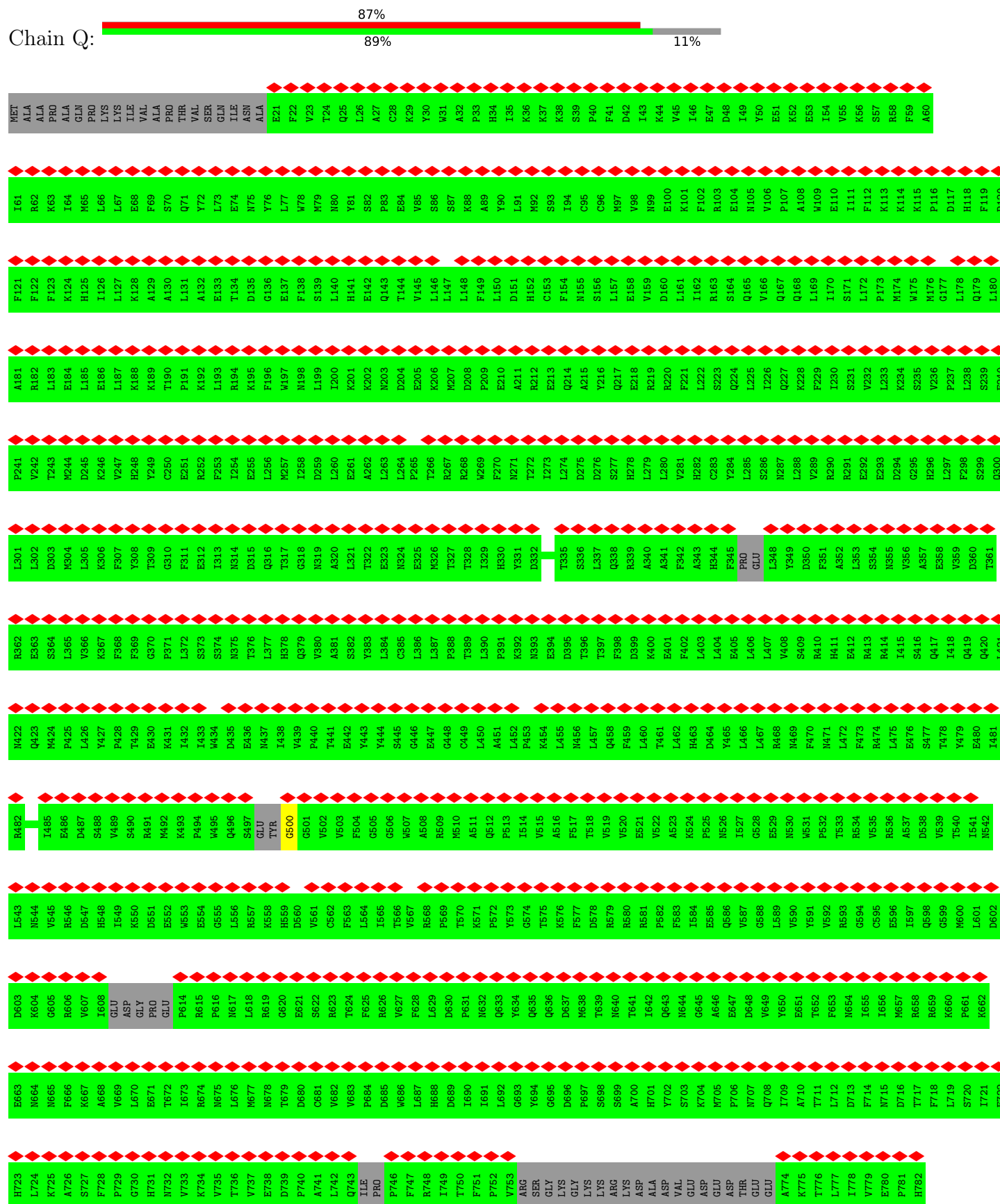
• Molecule 30: Pre-mRNA-processing factor 19





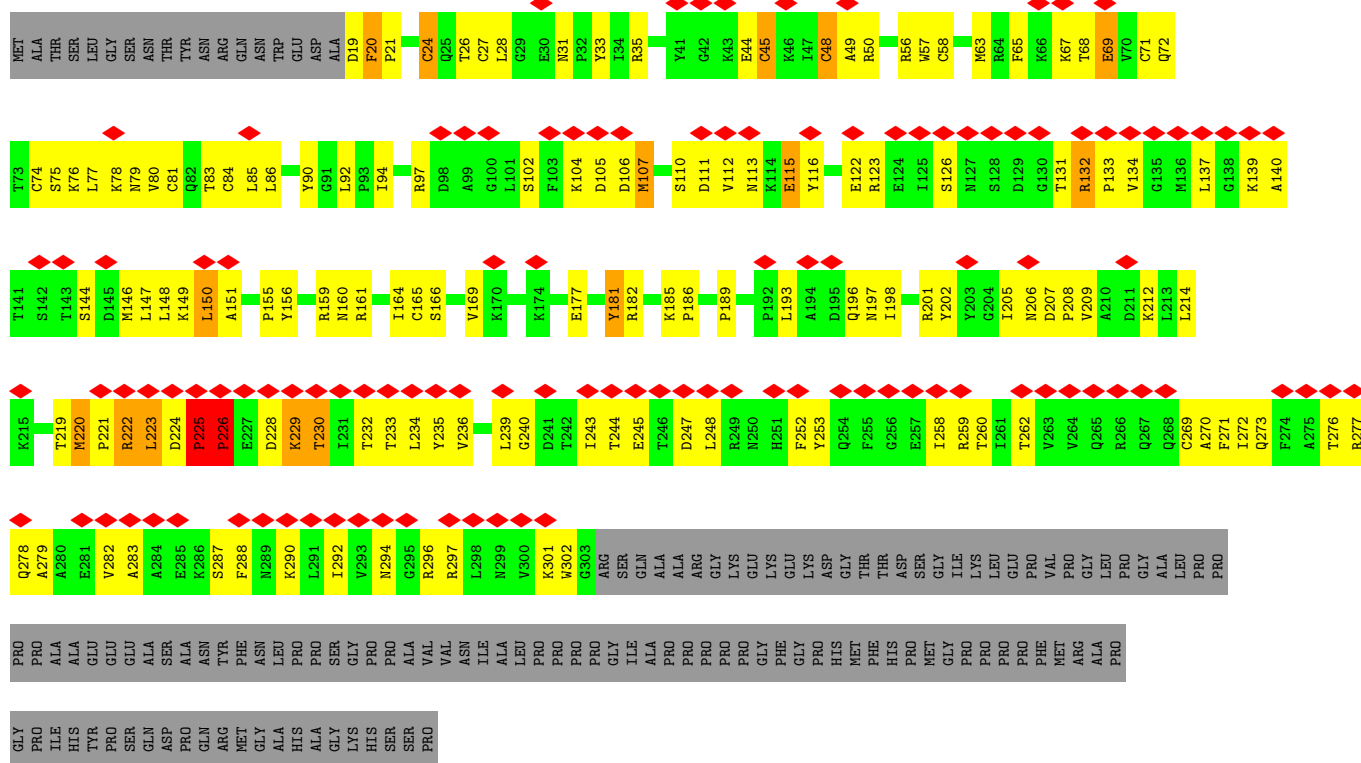
● Molecule 33: Intron-binding protein aquarius

Chain Q:

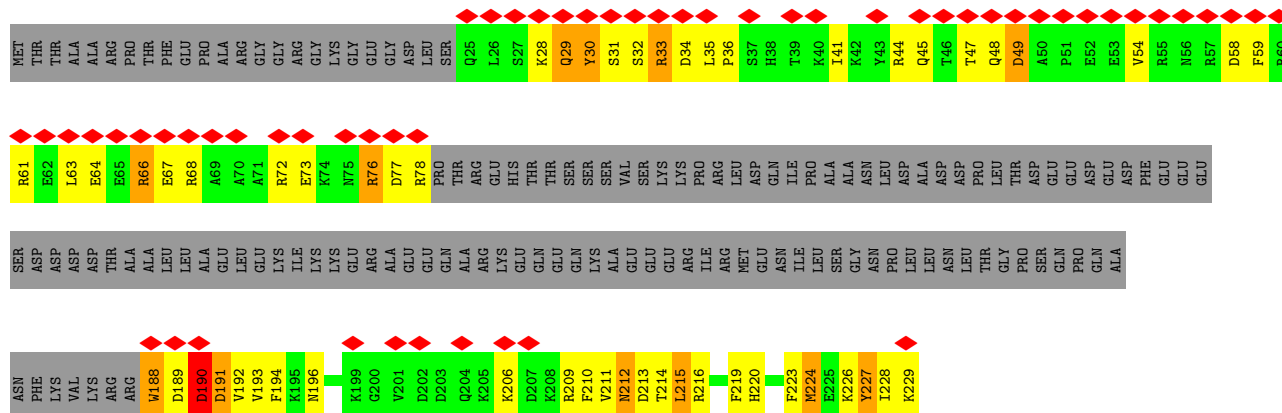
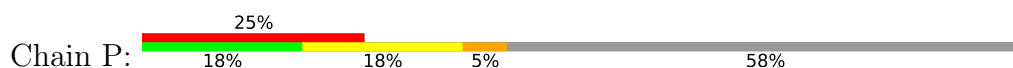




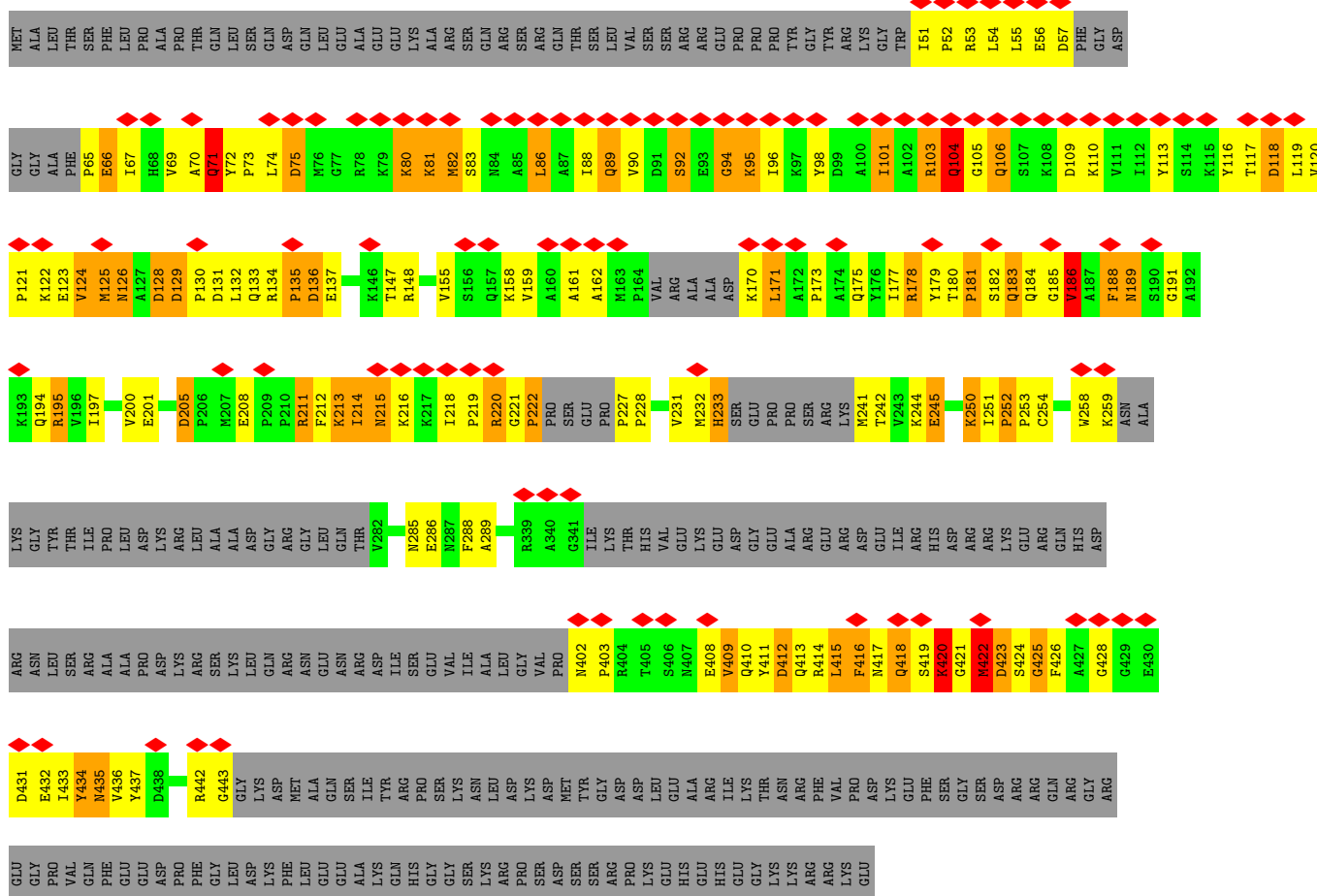
• Molecule 35: Pre-mRNA-splicing factor RBM22



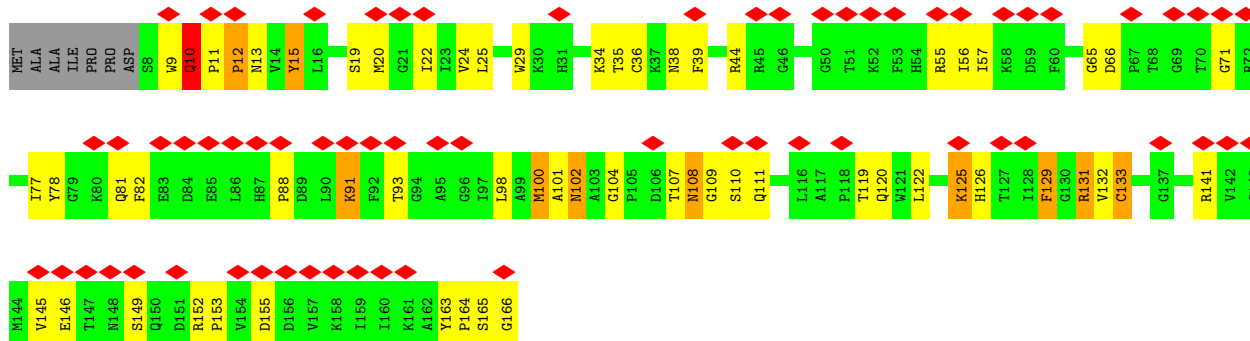
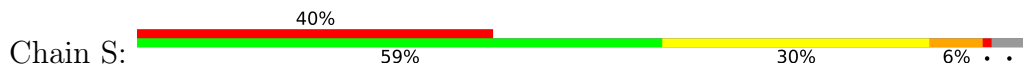
• Molecule 36: Spliceosome-associated protein CWC15 homolog



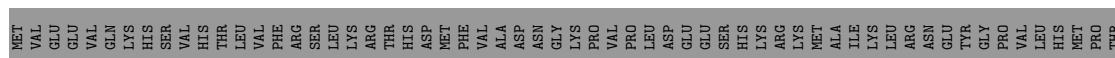
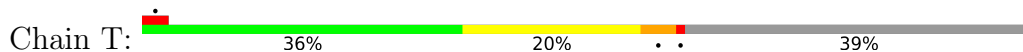
• Molecule 37: Skip

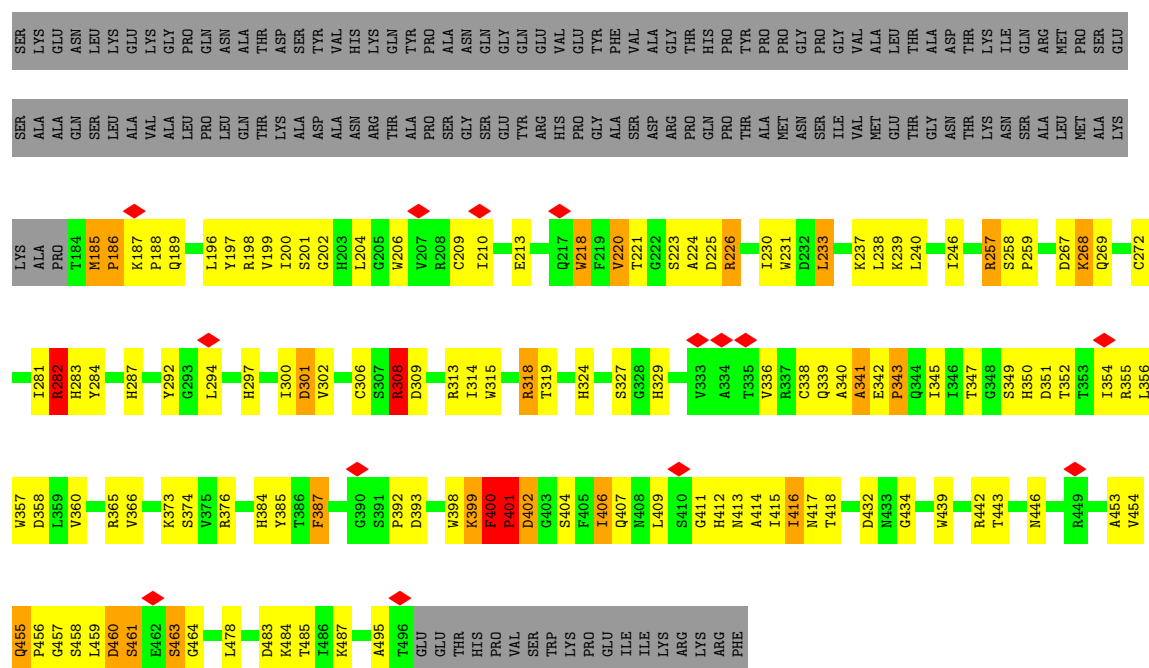


• Molecule 38: Peptidyl-prolyl cis-trans isomerase-like 1

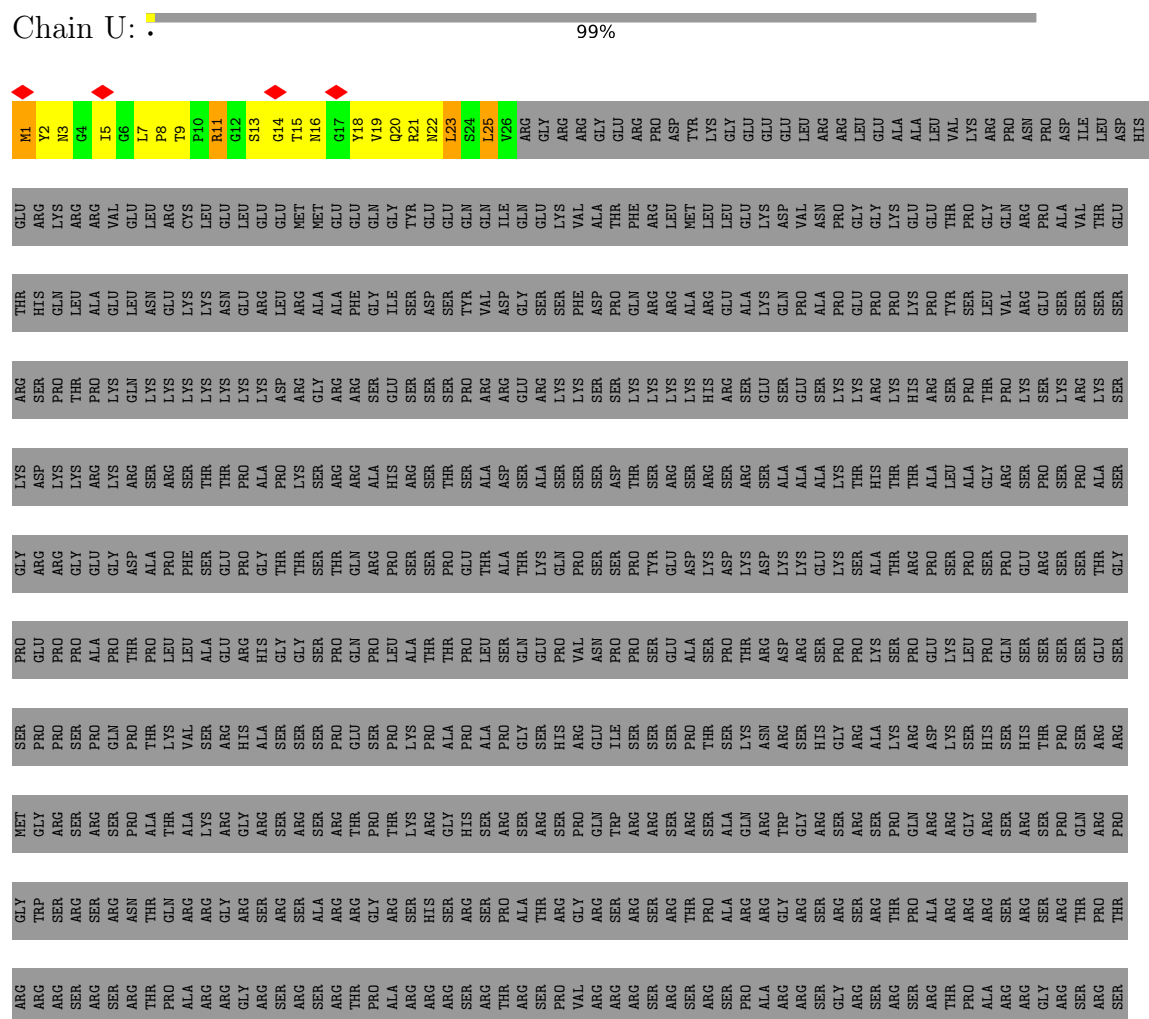


• Molecule 39: Pleiotropic regulator 1

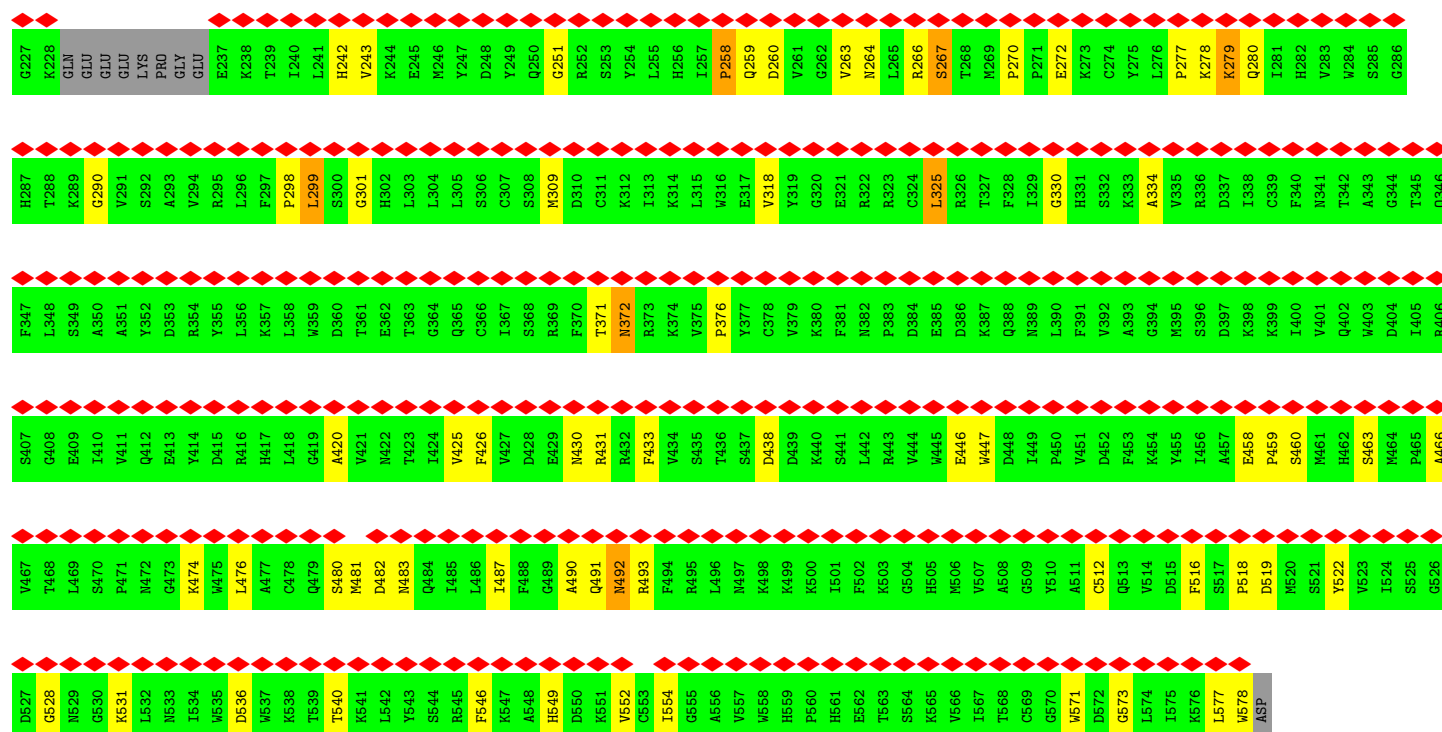




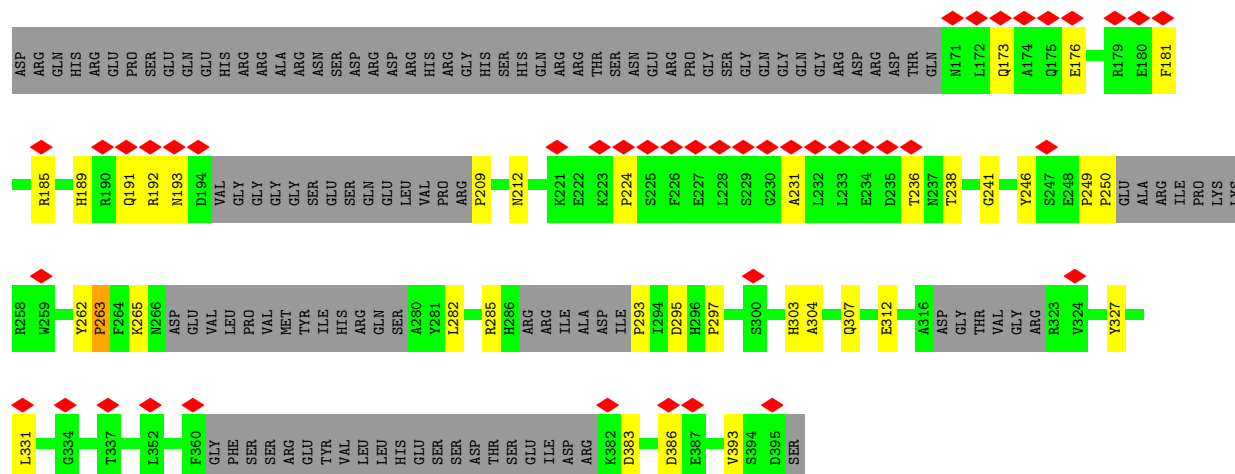
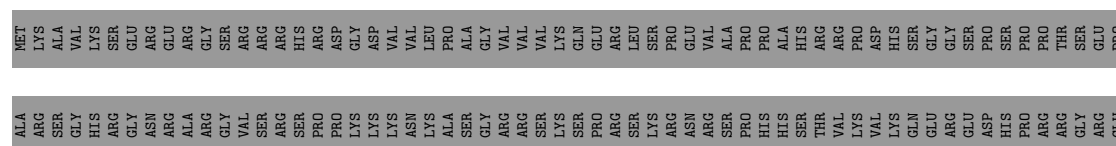
• Molecule 40: Serine/arginine repetitive matrix protein 2



WORLDWIDE
PDB
PROTEIN DATA BANK

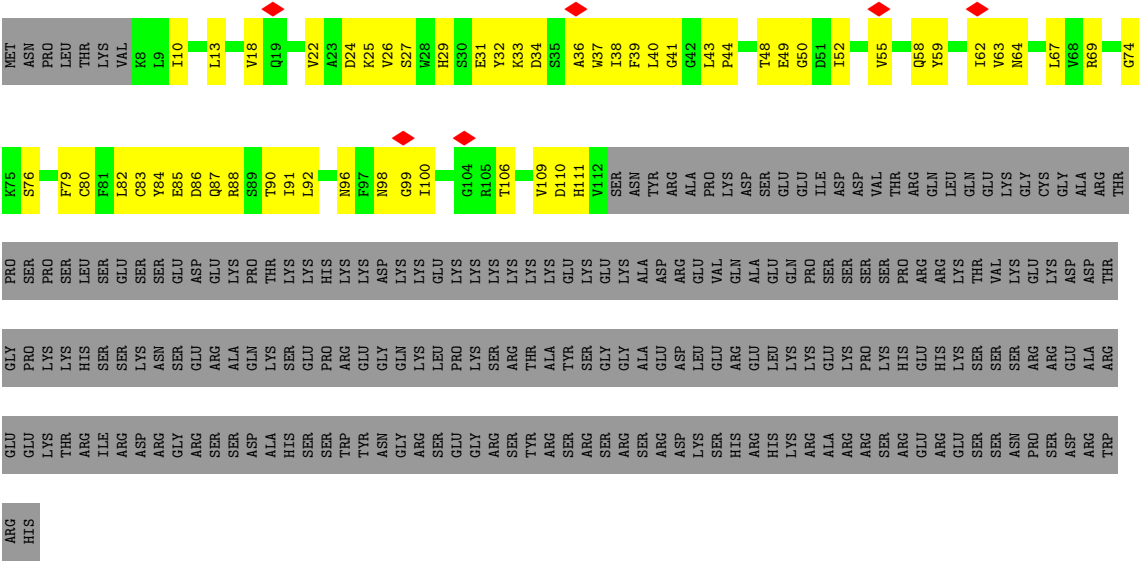


• Molecule 43: Smad nuclear-interacting protein 1

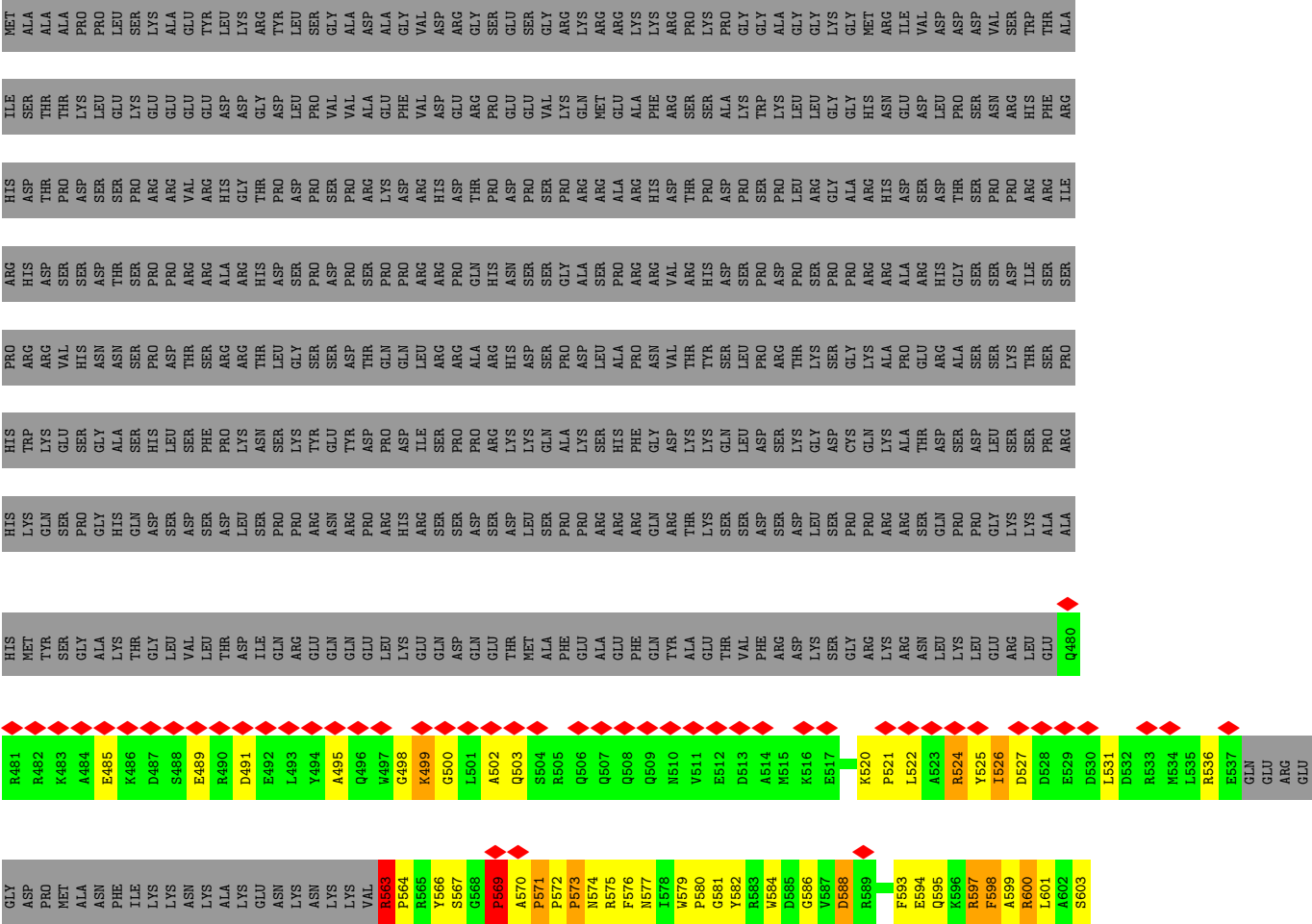


• Molecule 44: RNA-binding motif protein, X-linked 2

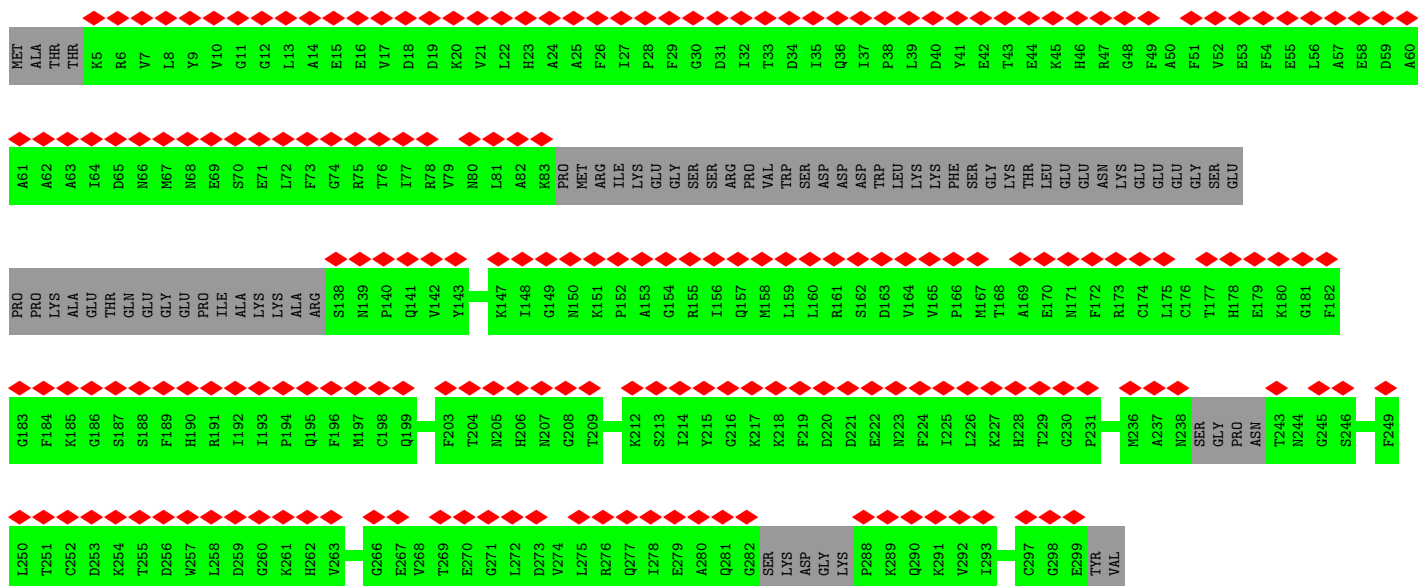
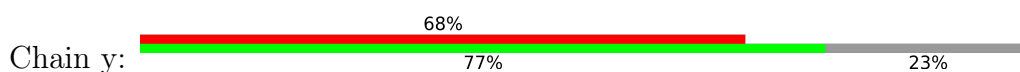




• Molecule 45: BUD13 homolog



- Molecule 47: Peptidyl-prolyl cis-trans isomerase E



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.142	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0323	Depositor
Map size (\AA)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.338, 1.338, 1.338	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.72	9/16867 (0.1%)	0.80	25/22888 (0.1%)
2	B	0.75	2/1970 (0.1%)	0.91	7/3060 (0.2%)
3	C	0.79	1/6864 (0.0%)	0.96	10/9334 (0.1%)
4	D	0.33	0/8527	0.59	0/11887
5	E	0.64	0/2392	0.79	0/3242
6	a	0.47	0/397	0.61	0/549
6	h	0.46	0/391	0.61	0/540
7	b	0.49	0/404	0.72	0/561
7	i	0.50	0/421	0.73	0/583
8	c	0.57	0/405	0.73	0/563
8	j	0.57	0/405	0.73	0/563
9	d	0.68	0/479	0.84	0/666
9	k	0.70	0/420	0.85	0/583
10	f	0.75	0/360	0.81	0/497
10	m	0.75	0/360	0.81	0/497
11	e	0.65	0/390	0.80	0/542
11	l	0.64	0/390	0.80	0/542
12	g	0.54	0/362	0.71	0/501
12	n	0.54	0/332	0.72	0/458
13	F	0.39	0/2224	0.86	0/3462
14	G	0.35	0/1717	0.95	1/2664 (0.0%)
15	H	0.59	7/3217 (0.2%)	1.06	18/4997 (0.4%)
16	o	0.61	0/803	1.41	2/1119 (0.2%)
17	p	1.01	1/810 (0.1%)	1.46	4/1122 (0.4%)
18	w	0.53	5/2380 (0.2%)	0.67	13/3274 (0.4%)
19	u	0.23	0/514	0.63	4/710 (0.6%)
20	v	0.73	4/935 (0.4%)	0.81	9/1266 (0.7%)
21	1	0.33	0/7826	0.51	0/10617
22	2	0.52	3/1277 (0.2%)	0.73	7/1724 (0.4%)
23	3	0.32	0/9381	0.52	0/12732
24	4	0.83	2/535 (0.4%)	0.98	4/724 (0.6%)
25	5	0.29	0/823	0.48	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	6	0.29	0/678	0.51	0/909
27	7	0.31	0/556	0.45	0/751
28	J	0.62	0/3500	0.73	0/4750
29	L	0.52	3/2283 (0.1%)	0.58	8/3088 (0.3%)
30	q	0.35	0/658	0.58	3/919 (0.3%)
30	r	0.32	0/653	0.59	3/912 (0.3%)
30	s	0.26	0/334	0.37	0/466
30	t	0.30	0/334	0.38	0/466
31	K	1.28	14/981 (1.4%)	0.69	5/1317 (0.4%)
32	I	0.39	0/2745	0.56	17/3765 (0.5%)
33	Q	0.21	0/6518	0.42	0/9075
34	N	0.88	1/1210 (0.1%)	1.00	3/1622 (0.2%)
35	O	0.80	3/2321 (0.1%)	0.94	6/3135 (0.2%)
36	P	0.83	1/841 (0.1%)	1.01	2/1117 (0.2%)
37	R	0.68	5/2224 (0.2%)	0.88	7/2992 (0.2%)
38	S	0.59	0/1268	0.80	1/1714 (0.1%)
39	T	1.05	1/2522 (0.0%)	1.11	4/3438 (0.1%)
40	U	1.03	0/196	1.09	1/265 (0.4%)
41	V	0.54	0/2239	0.67	1/3118 (0.0%)
42	W	0.55	0/2381	0.76	4/3310 (0.1%)
43	X	0.27	0/1012	0.48	0/1351
44	Y	0.31	0/753	0.48	0/1014
45	Z	0.57	2/772 (0.3%)	0.79	7/1056 (0.7%)
46	x	0.35	0/2871	0.53	3/3981 (0.1%)
47	y	0.35	0/1129	0.61	0/1558
All	All	0.58	64/115557 (0.1%)	0.75	179/159679 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	N	0	1
37	R	0	1
39	T	0	2
43	X	0	1
All	All	0	32

The worst 5 of 64 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	K	106	CYS	CB-SG	-23.13	1.43	1.82
31	K	132	CYS	CB-SG	-17.48	1.52	1.82
29	L	761	SER	CB-OG	8.91	1.53	1.42
31	K	128	SER	CB-OG	8.42	1.53	1.42
31	K	183	SER	CB-OG	8.28	1.53	1.42

The worst 5 of 179 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	4	83	PRO	CA-CB-CG	10.19	124.17	104.80
22	2	636	MET	CG-SD-CE	9.28	115.05	100.20
31	K	90	PRO	CA-CB-CG	8.66	121.26	104.80
45	Z	569	PRO	CA-N-CD	-8.56	99.52	111.50
45	Z	573	PRO	CA-N-CD	-8.45	99.67	111.50

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16399	0	16176	1407	0
2	B	1768	0	897	120	0
3	C	6716	0	6691	892	0
4	D	8528	0	3745	78	0
5	E	2338	0	2272	153	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	0	0
9	k	422	0	175	0	0
10	f	361	0	158	0	0
10	m	361	0	158	0	0
11	e	391	0	163	0	0
11	l	391	0	163	0	0
12	g	363	0	160	0	0
12	n	334	0	143	0	0
13	F	1988	0	1005	186	0
14	G	1545	0	786	197	0
15	H	2886	0	1463	239	0
16	o	804	0	350	0	0
17	p	813	0	365	0	0
18	w	2373	0	1301	0	0
19	u	520	0	214	0	0
20	v	936	0	591	0	0
21	1	7702	0	7389	309	0
22	2	1252	0	1040	57	0
23	3	9195	0	9091	465	0
24	4	527	0	438	40	0
25	5	807	0	729	26	0
26	6	670	0	654	21	0
27	7	540	0	509	25	0
28	J	3463	0	2544	107	0
29	L	2260	0	1776	92	0
30	q	659	0	296	0	0
30	r	654	0	294	0	0
30	s	335	0	168	0	0
30	t	335	0	168	0	0
31	K	979	0	739	11	0
32	I	2778	0	1238	21	0
33	Q	6528	0	2814	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	N	1184	0	1190	75	0
35	O	2273	0	2244	244	0
36	P	829	0	814	192	0
37	R	2188	0	2102	400	0
38	S	1236	0	1210	135	0
39	T	2457	0	2416	251	0
40	U	193	0	196	40	0
41	V	2243	0	971	48	0
42	W	2384	0	1055	126	0
43	X	1012	0	733	17	0
44	Y	743	0	613	67	0
45	Z	755	0	591	113	0
46	x	2882	0	1308	0	0
47	y	1133	0	519	0	0
48	A	36	0	6	10	0
49	A	5	0	4	2	0
50	C	32	0	12	11	0
51	C	1	0	0	0	0
51	F	5	0	0	0	0
52	6	3	0	0	0	0
52	N	3	0	0	0	0
52	O	3	0	0	3	0
52	v	1	0	0	0	0
All	All	113433	0	84077	4900	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 26.

The worst 5 of 4900 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)
44:Y:37:TRP:CH2	45:Z:498:GLY:HA2	1.23	1.65
1:A:1758:PRO:HA	21:1:938:TRP:CD1	1.28	1.59
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.54

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1970/2335 (84%)	1835 (93%)	108 (6%)	27 (1%)	9	41
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5	28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	44	78
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3	22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100	100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100	100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100	100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100	100
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	10	43
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	10
18	w	420/501 (84%)	380 (90%)	37 (9%)	3 (1%)	19	57
19	u	92/793 (12%)	86 (94%)	4 (4%)	2 (2%)	5	29
20	v	153/464 (33%)	124 (81%)	22 (14%)	7 (5%)	2	17
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	22	60
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	3	1165/1217 (96%)	1081 (93%)	80 (7%)	4 (0%)	37	73
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	10	43
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	41
29	L	324/802 (40%)	304 (94%)	18 (6%)	2 (1%)	22	60
30	q	130/504 (26%)	119 (92%)	7 (5%)	4 (3%)	3	22
30	r	129/504 (26%)	118 (92%)	9 (7%)	2 (2%)	8	38
30	s	65/504 (13%)	62 (95%)	2 (3%)	1 (2%)	8	40
30	t	65/504 (13%)	64 (98%)	0	1 (2%)	8	40
31	K	144/225 (64%)	134 (93%)	6 (4%)	4 (3%)	4	24
32	I	498/855 (58%)	479 (96%)	11 (2%)	8 (2%)	8	38
33	Q	1297/1485 (87%)	1271 (98%)	26 (2%)	0	100	100
34	N	141/144 (98%)	126 (89%)	12 (8%)	3 (2%)	5	30
35	O	283/420 (67%)	247 (87%)	26 (9%)	10 (4%)	3	20
36	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	29
37	R	274/540 (51%)	234 (85%)	25 (9%)	15 (6%)	1	14
38	S	157/166 (95%)	144 (92%)	10 (6%)	3 (2%)	6	32
39	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	19
40	U	24/2752 (1%)	20 (83%)	3 (12%)	1 (4%)	2	17
41	V	444/908 (49%)	412 (93%)	27 (6%)	5 (1%)	12	47
42	W	477/579 (82%)	421 (88%)	32 (7%)	24 (5%)	1	16
43	X	144/396 (36%)	134 (93%)	10 (7%)	0	100	100
44	Y	103/322 (32%)	92 (89%)	11 (11%)	0	100	100
45	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1	14
46	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	14	51
47	y	224/301 (74%)	217 (97%)	7 (3%)	0	100	100
All	All	16082/29057 (55%)	14914 (93%)	957 (6%)	211 (1%)	13	43

5 of 211 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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	1773/2108 (84%)	1675 (94%)	98 (6%)	18	39
3	C	745/866 (86%)	677 (91%)	68 (9%)	7	24
5	E	256/300 (85%)	244 (95%)	12 (5%)	22	44
18	w	49/446 (11%)	47 (96%)	2 (4%)	26	47
20	v	30/382 (8%)	28 (93%)	2 (7%)	13	34
21	1	735/1104 (67%)	735 (100%)	0	100	100
22	2	94/776 (12%)	90 (96%)	4 (4%)	25	46
23	3	1012/1051 (96%)	1011 (100%)	1 (0%)	92	95
24	4	39/336 (12%)	37 (95%)	2 (5%)	20	41
25	5	74/109 (68%)	74 (100%)	0	100	100
26	6	76/95 (80%)	76 (100%)	0	100	100
27	7	57/77 (74%)	57 (100%)	0	100	100
28	J	205/751 (27%)	194 (95%)	11 (5%)	18	40
29	L	131/709 (18%)	122 (93%)	9 (7%)	13	33
31	K	54/196 (28%)	49 (91%)	5 (9%)	7	23
34	N	130/130 (100%)	125 (96%)	5 (4%)	28	49
35	O	250/361 (69%)	239 (96%)	11 (4%)	24	45
36	P	90/203 (44%)	77 (86%)	13 (14%)	2	12
37	R	215/463 (46%)	165 (77%)	50 (23%)	0	4
38	S	129/134 (96%)	119 (92%)	10 (8%)	10	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	T	268/441 (61%)	251 (94%)	17 (6%)	15 36
40	U	21/2432 (1%)	16 (76%)	5 (24%)	0 4
43	X	51/349 (15%)	44 (86%)	7 (14%)	3 13
44	Y	57/291 (20%)	56 (98%)	1 (2%)	54 71
45	Z	47/545 (9%)	39 (83%)	8 (17%)	1 9
46	x	1/897 (0%)	1 (100%)	0	100 100
All	All	6589/15552 (42%)	6248 (95%)	341 (5%)	22 40

5 of 341 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	P	29	GLN
37	R	415	LEU
36	P	188	TRP
37	R	125	MET
38	S	129	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
23	3	97	ASN
28	J	351	ASN
39	T	413	ASN
23	3	254	ASN
23	3	775	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	37 (40%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	19 (23%)	10 (12%)
All	All	379/686 (55%)	137 (36%)	35 (9%)

5 of 137 RNA backbone outliers are listed below:

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

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	G	151	C
14	G	153	C
15	H	46	U
13	F	25	C
13	F	7	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 16 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	$\# Z > 2$
50	GTP	C	1500	51	26,34,34	1.18	1 (3%)	32,54,54	1.81	8 (25%)
48	IHP	A	2401	-	36,36,36	1.01	2 (5%)	54,60,60	1.62	12 (22%)
49	ALA	A	2402	-	3,4,5	0.65	0	2,4,6	0.83	0

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
50	GTP	C	1500	51	-	7/18/38/38	0/3/3/3
48	IHP	A	2401	-	-	6/30/54/54	0/1/1/1
49	ALA	A	2402	-	-	0/0/2/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	C	1500	GTP	C6-N1	-3.52	1.32	1.37
48	A	2401	IHP	P5-O45	-2.86	1.43	1.54
48	A	2401	IHP	P2-O12	2.65	1.64	1.59

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	A	2401	IHP	O45-P5-O35	4.10	123.30	107.64
48	A	2401	IHP	O35-P5-O15	-3.97	88.19	105.99
50	C	1500	GTP	C5-C6-N1	3.79	120.64	113.95
50	C	1500	GTP	PA-O3A-PB	-3.79	119.84	132.83
50	C	1500	GTP	O6-C6-C5	-3.73	117.08	124.37

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

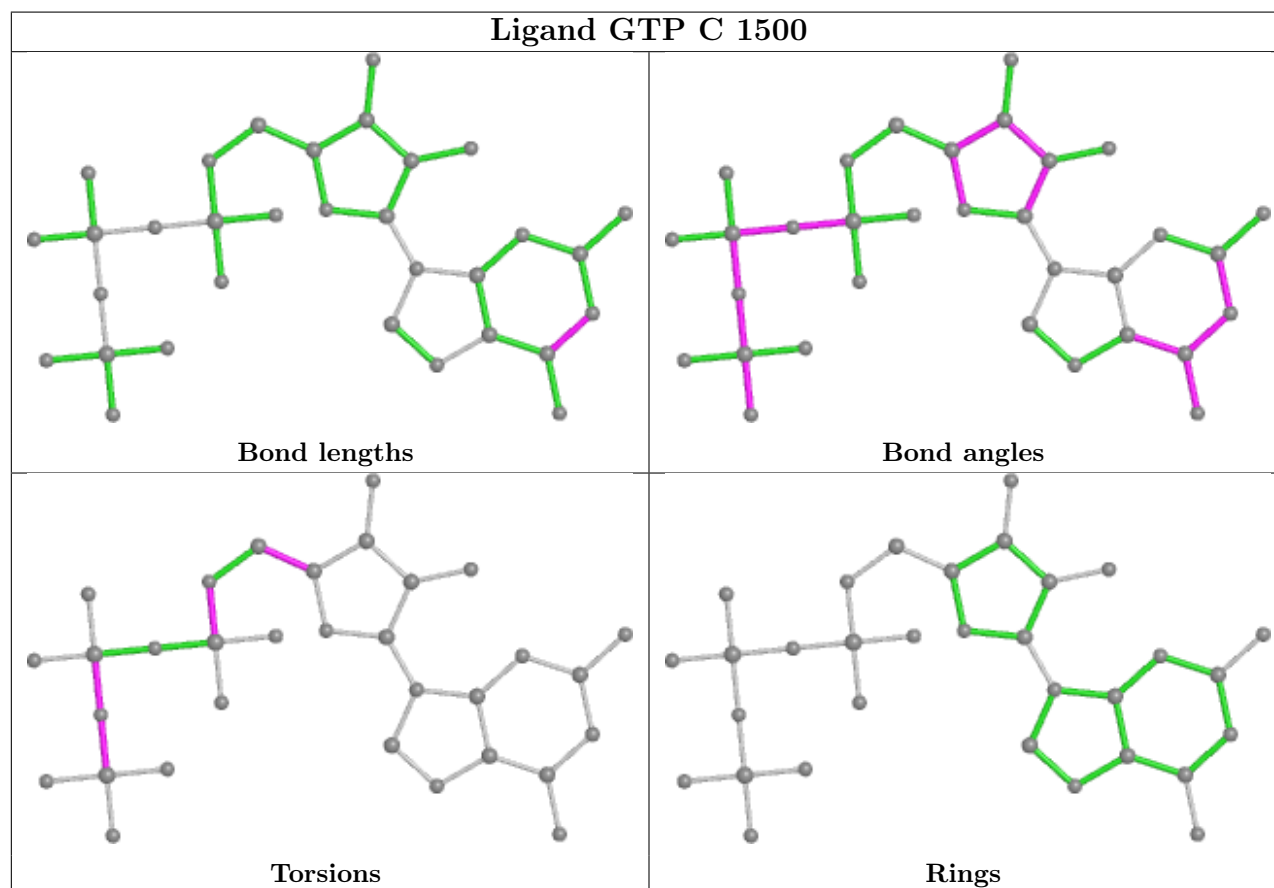
Mol	Chain	Res	Type	Atoms
48	A	2401	IHP	C4-C5-O15-P5
48	A	2401	IHP	C6-C5-O15-P5
50	C	1500	GTP	PB-O3B-PG-O3G
50	C	1500	GTP	C5'-O5'-PA-O3A
50	C	1500	GTP	C5'-O5'-PA-O1A

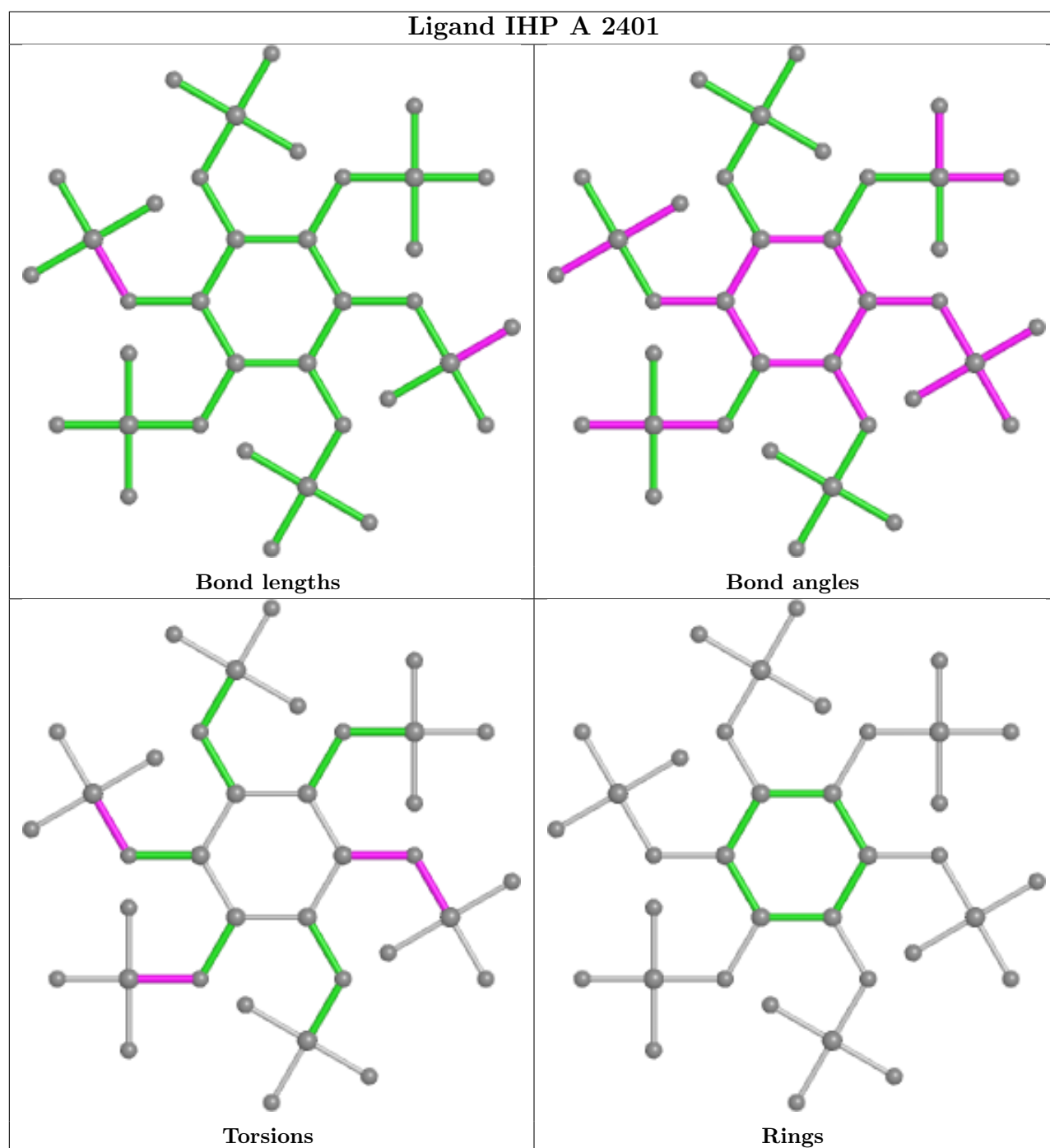
There are no ring outliers.

3 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	C	1500	GTP	11	0
48	A	2401	IHP	10	0
49	A	2402	ALA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

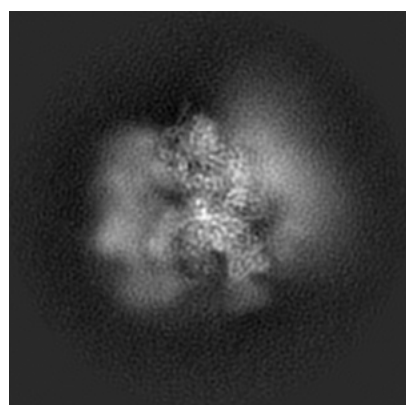
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6890. These allow visual inspection of the internal detail of the map and identification of artifacts.

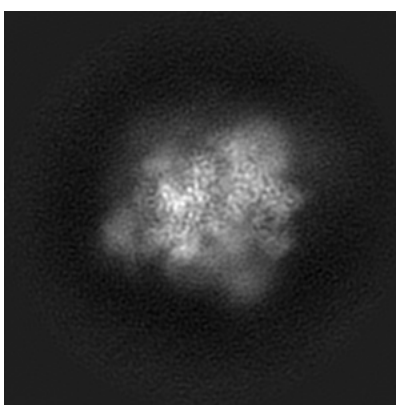
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

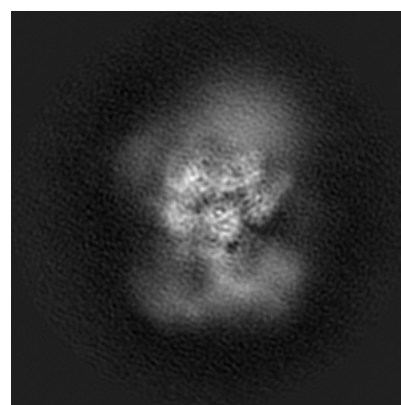
6.1.1 Primary map



X



Y

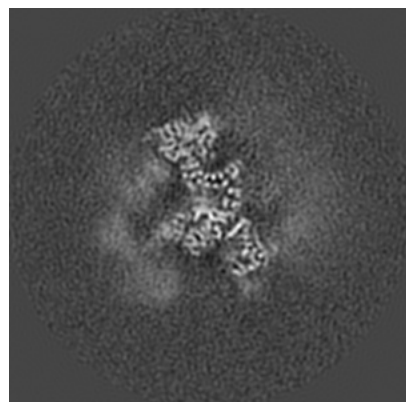


Z

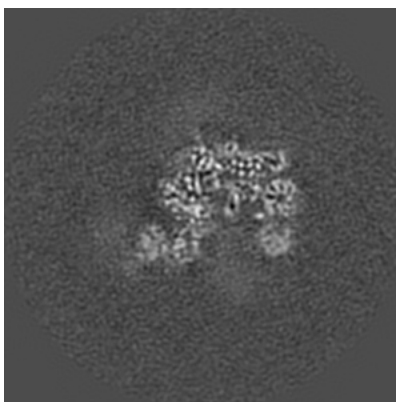
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

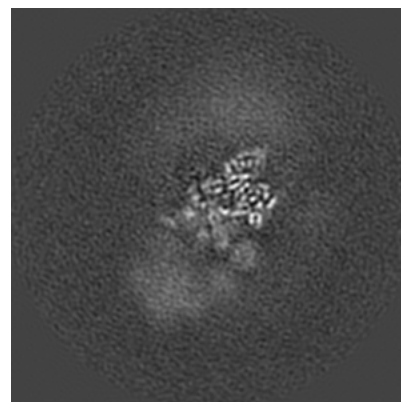
6.2.1 Primary map



X Index: 200



Y Index: 200

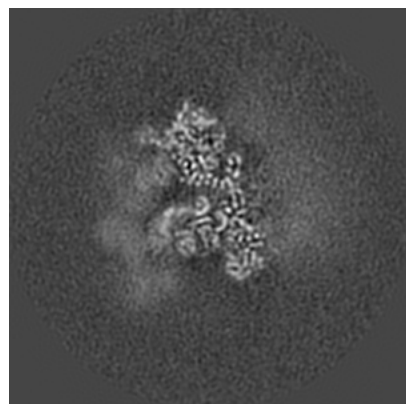


Z Index: 200

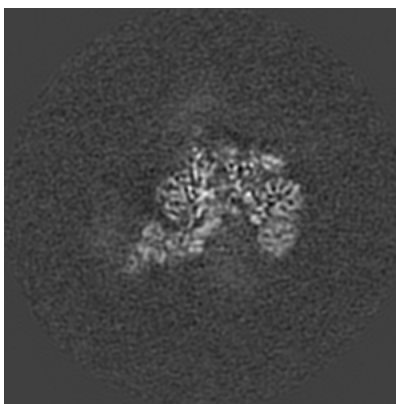
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

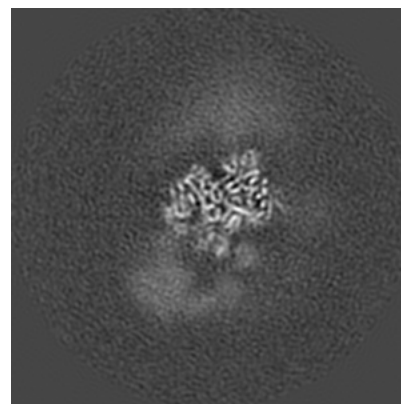
6.3.1 Primary map



X Index: 210



Y Index: 195

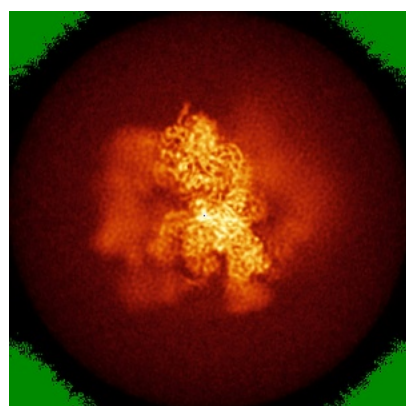


Z Index: 192

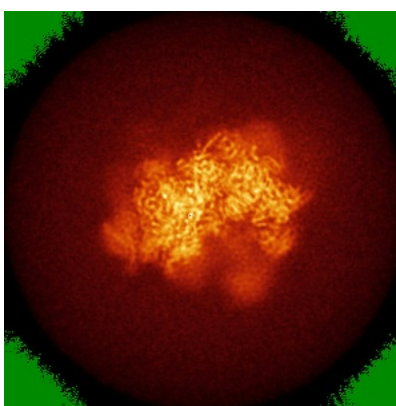
The images above show the largest variance slices of the map in three orthogonal directions.

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

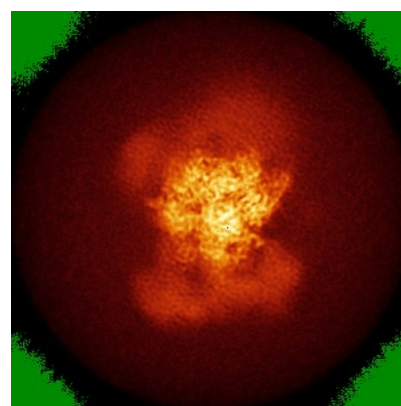
6.4.1 Primary map



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 0.0323. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

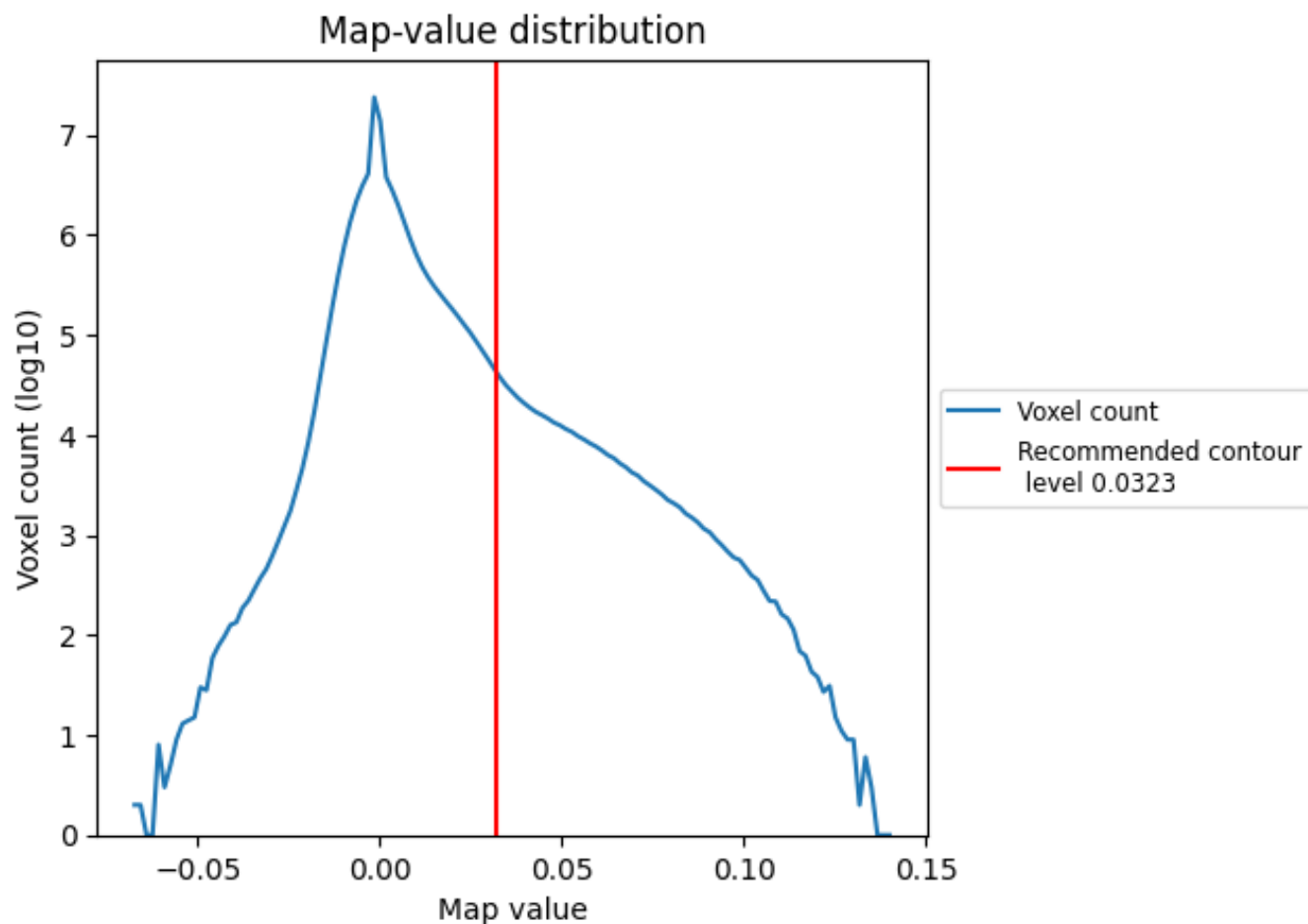
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

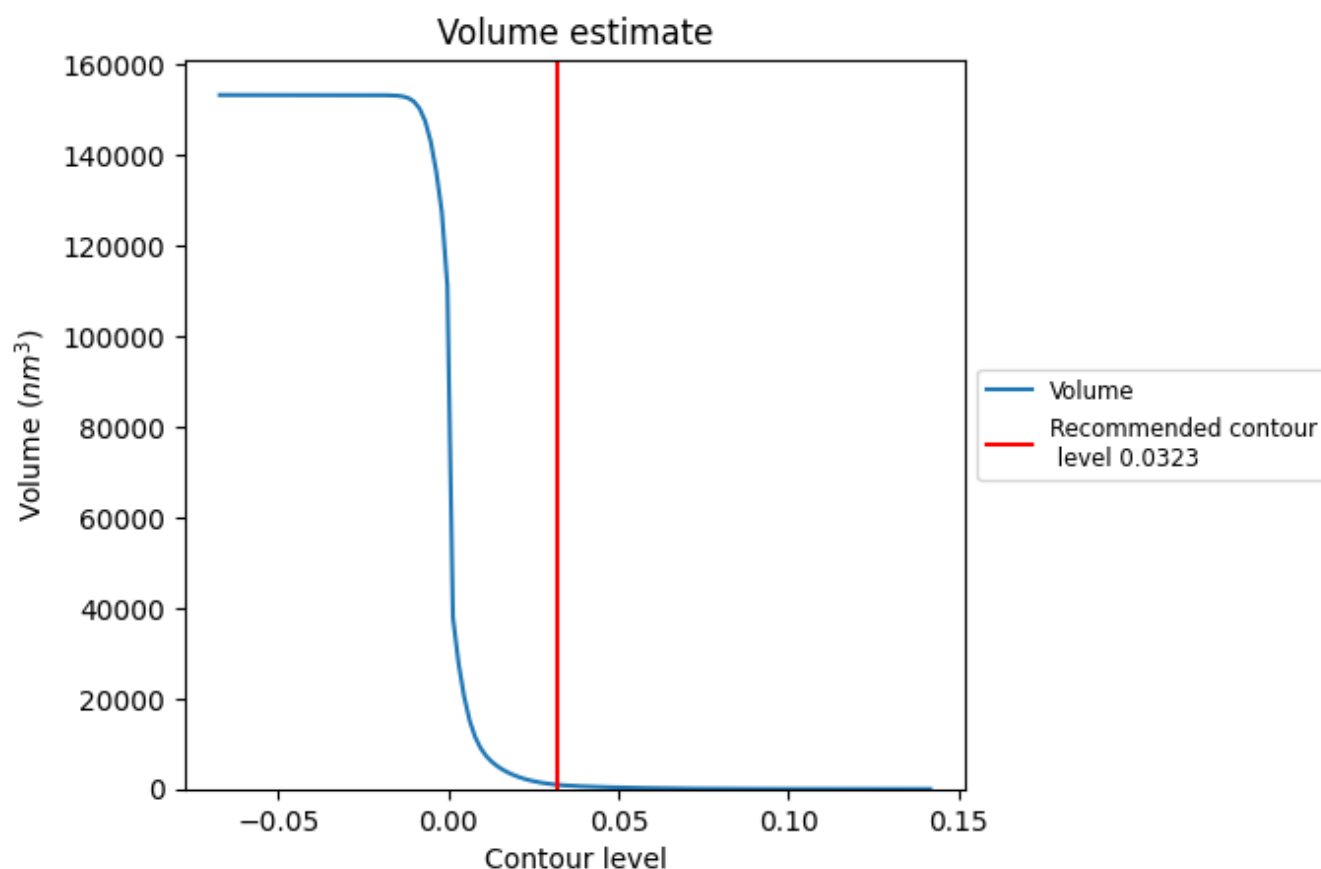
This section contains the results of statistical analysis of the map.

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.

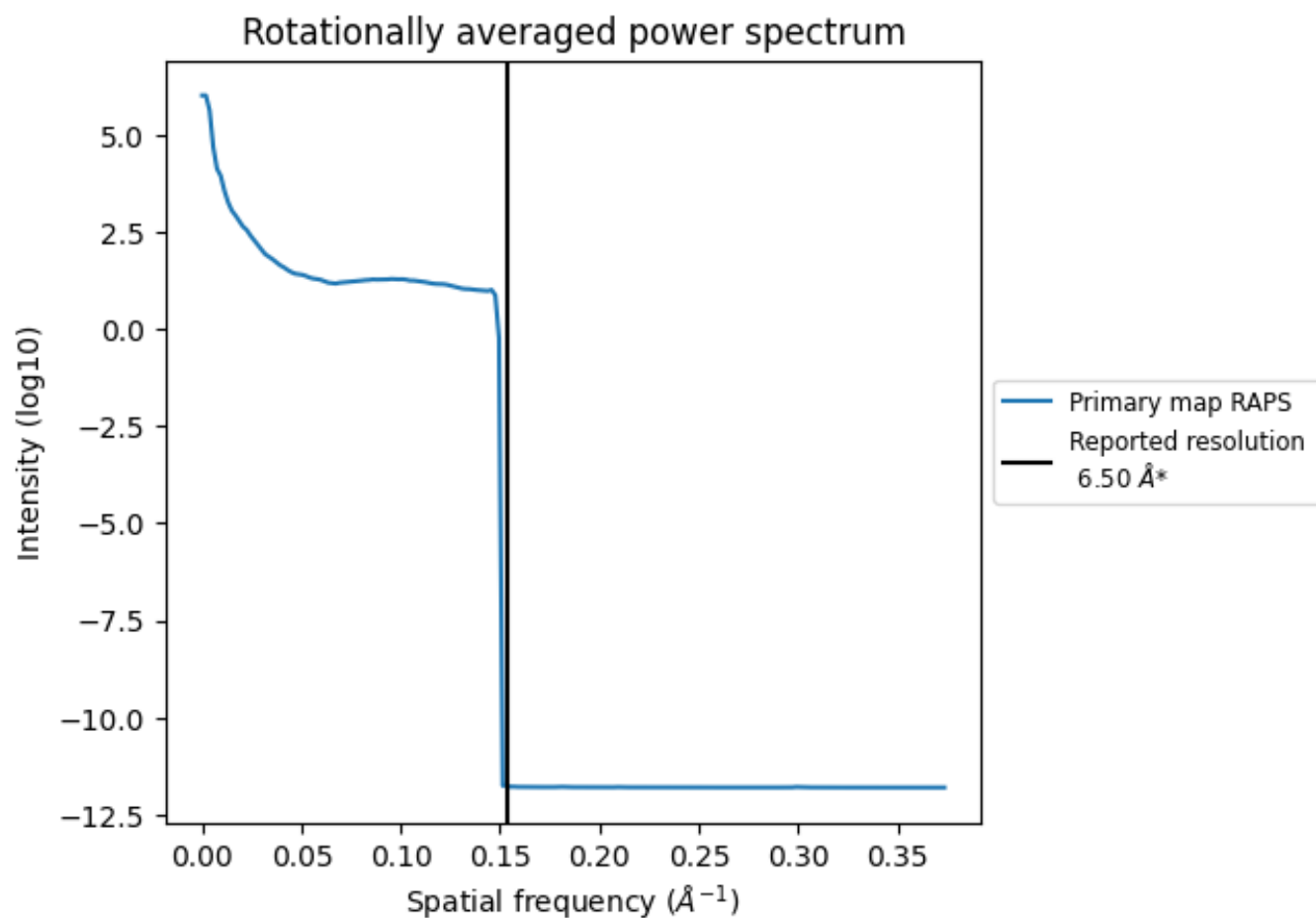
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 909 nm³; this corresponds to an approximate mass of 821 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 0.154 \AA^{-1}

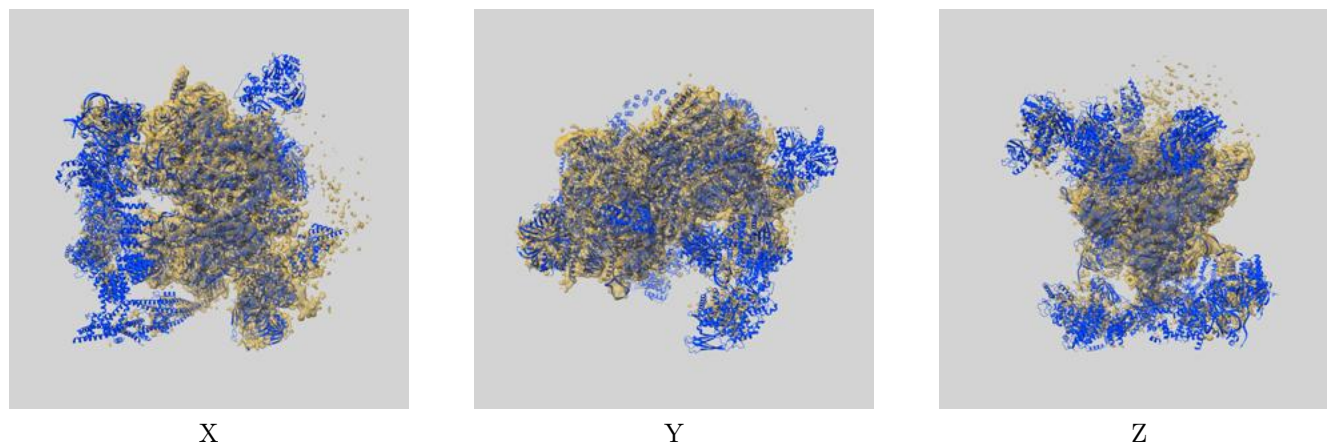
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

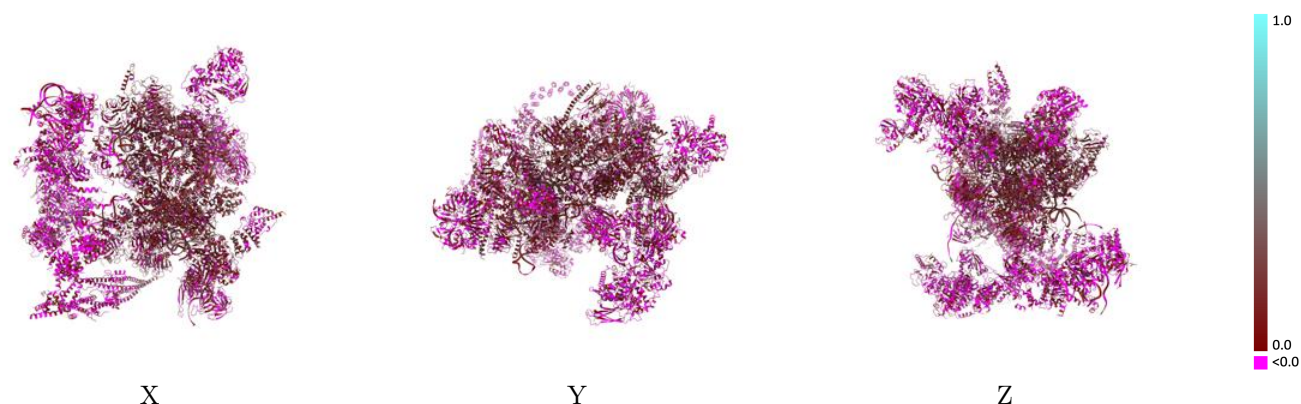
This section contains information regarding the fit between EMDB map EMD-6890 and PDB model 5Z57. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



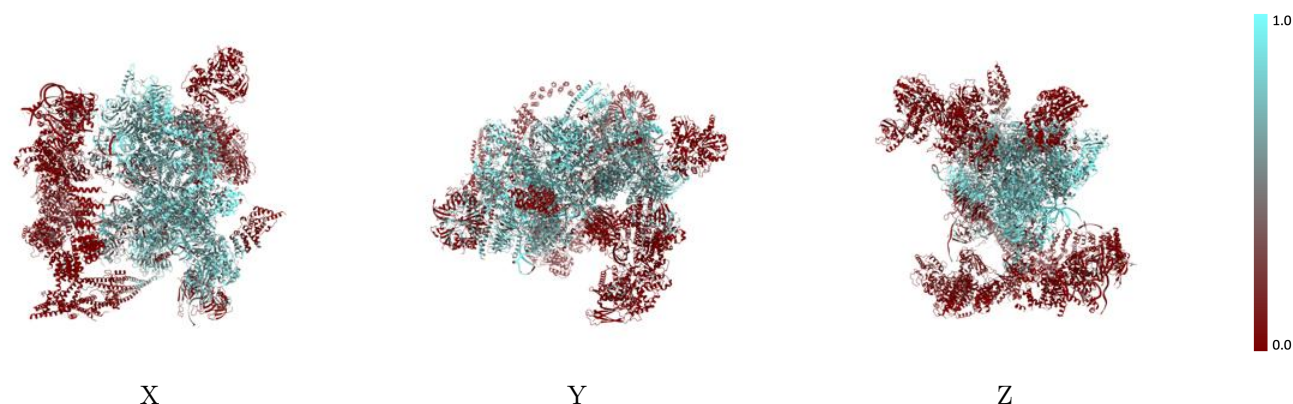
The images above show the 3D surface view of the map at the recommended contour level 0.0323 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



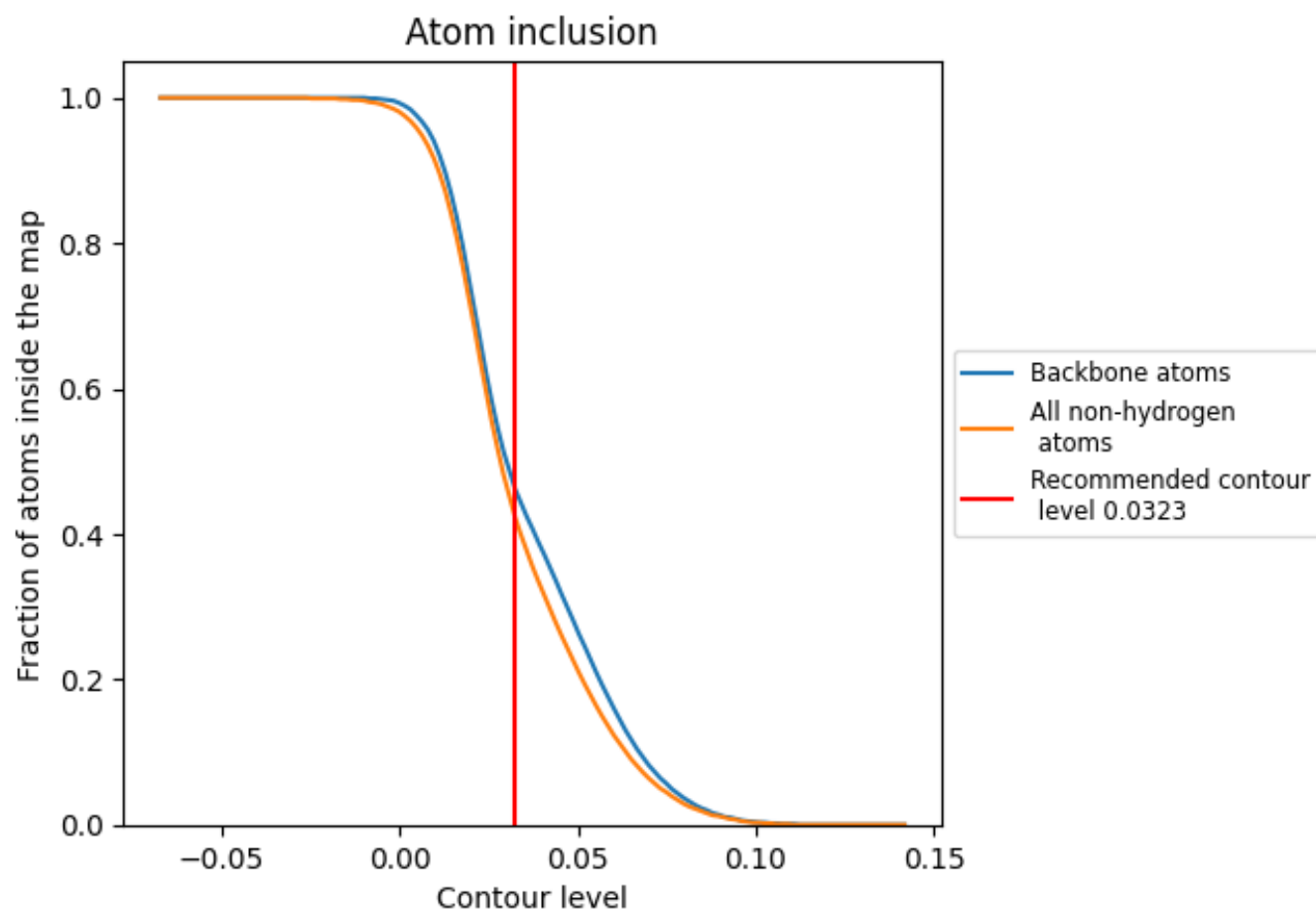
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0323).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 42% 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 (0.0323) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4240	 0.0970
1	 0.6630	 0.1660
2	 0.6030	 0.1390
3	 0.6990	 0.1390
4	 0.3290	 0.0210
5	 0.7030	 0.1570
6	 0.6660	 0.1340
7	 0.6700	 0.1450
A	 0.5700	 0.1360
B	 0.7770	 0.1670
C	 0.6930	 0.1510
D	 0.0490	 0.0190
E	 0.6060	 0.1060
F	 0.8090	 0.1690
G	 0.7570	 0.1610
H	 0.4220	 0.0840
I	 0.0380	 0.0050
J	 0.3450	 0.0650
K	 0.1220	 0.0430
L	 0.3250	 0.0880
N	 0.6690	 0.1380
O	 0.4910	 0.1160
P	 0.3290	 0.1440
Q	 0.0240	 0.0100
R	 0.4890	 0.1440
S	 0.4900	 0.1130
T	 0.7380	 0.1470
U	 0.6680	 0.1850
V	 0.4080	 0.1230
W	 0.1940	 0.0690
X	 0.6450	 0.1400
Y	 0.7100	 0.1780
Z	 0.4450	 0.1540
a	 0.1400	 0.0070
b	 0.2860	 0.0520



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Chain	Atom inclusion	Q-score
c	 0.3200	 0.0290
d	 0.3120	 0.0350
e	 0.3480	 0.0300
f	 0.2800	 0.0180
g	 0.2810	 0.0330
h	 0.0590	 -0.0130
i	 0.0690	 0.0440
j	 0.0910	 0.0080
k	 0.0640	 0.0180
l	 0.0790	 -0.0210
m	 0.1190	 -0.0100
n	 0.0870	 0.0230
o	 0.0310	 0.0290
p	 0.1010	 0.0230
q	 0.0210	 -0.0080
r	 0.0460	 0.0430
s	 0.1100	 0.0360
t	 0.0000	 0.0240
u	 0.0130	 0.0250
v	 0.3530	 0.0880
w	 0.2140	 0.0530
x	 0.0000	 0.0020
y	 0.1290	 0.0030