



wwPDB EM Validation Summary Report ⓘ

Aug 9, 2026 – 06:49 AM JST

PDB ID : 9XU3 / pdb_00009xu3
EMDB ID : EMD-67263
Title : Human minor spliceosome exon-ligation-ready C* complex (prior to step-II)
Authors : Wan, R.; Bai, R.
Deposited on : 2025-11-24
Resolution : 3.00 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

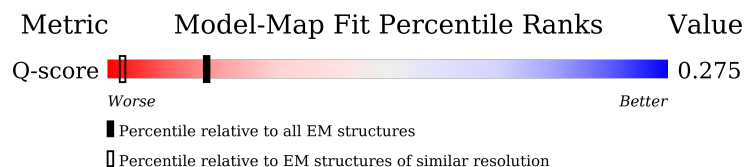
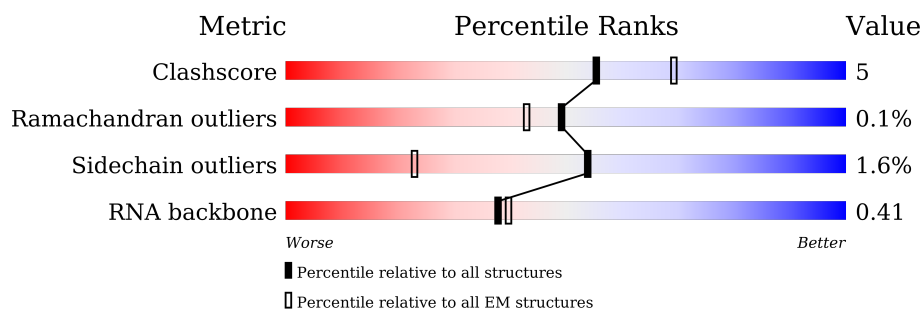
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	0	57	
2	1	277	
3	2	150	

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Mol	Chain	Length	Quality of chain
4	4	646	
5	5	117	
6	6	125	
7	A	2335	
8	B	972	
9	C	2136	
10	D	357	
11	E	802	
12	F	855	
13	G	848	
14	H	166	
15	I	285	
16	J	536	
17	K	514	
18	L	367	
19	L2	95	
20	L3	102	
21	L4	139	
22	L5	91	
23	L6	80	
24	L7	103	
25	L8	96	
26	M	198	
27	N	229	
28	O	166	

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Mol	Chain	Length	Quality of chain
29	P	301	
30	Q	1485	
31	R	161	
32	S	586	
33	T	1220	
34	U	2752	
35	V	908	
36	W	544	
37	X	758	
38	Y	112	
39	Z	415	
40	a	240	
40	h	240	
41	b	119	
41	i	119	
42	c	118	
42	j	118	
43	d	126	
43	k	126	
44	e	92	
44	l	92	
45	f	86	
45	m	86	
46	g	76	
46	n	76	

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Mol	Chain	Length	Quality of chain
47	p	476	
48	q	504	
48	r	504	
48	s	504	
48	t	504	
49	u	225	
50	v	411	
51	w	146	
52	x	174	
53	y	413	
54	z	233	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 123688 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 RNA chain called MSE-U12_5 exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	25	Total	C	N	O	P	0	0
			533	238	98	172	25		

- Molecule 2 is a RNA chain called MSE-U12_intron-3 exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	55	Total	C	N	O	P	0	0
			1155	518	190	392	55		

- Molecule 3 is a RNA chain called U12 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	42	Total	C	N	O	P	0	0
			898	403	163	290	42		

- Molecule 4 is a protein called Peptidylprolyl isomerase domain and WD repeat-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	407	Total	C	N	O	S	0	0
			3283	2095	559	606	23		

- Molecule 5 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	109	Total	C	N	O	P	0	0
			2296	1028	383	776	109		

- Molecule 6 is a RNA chain called U6atac snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	115	Total	C	N	O	P	0	0
			2439	1085	432	805	117		

- Molecule 7 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2283	Total	C	N	O	S	0	0
			18932	12179	3305	3366	82		

- Molecule 8 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	900	Total	C	N	O	S	0	0
			7122	4556	1185	1347	34		

- Molecule 9 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	1923	Total	C	N	O	S	0	0
			15118	9637	2604	2804	73		

- Molecule 10 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	308	Total	C	N	O	S	0	0
			2406	1509	424	459	14		

- Molecule 11 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	608	Total	C	N	O	S	0	0
			3925	2408	752	757	8		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	741	Total	C	N	O	S	0	0
			4897	3044	900	935	18		

- Molecule 13 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	639	Total	C	N	O	S	0	0
			4412	2762	819	825	6		

- Molecule 14 is a protein called Coiled-coil domain-containing protein 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	H	44	Total	C	N	O	0	0
			320	201	65	54		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	I	48	Total	C	N	O	0	0
			238	142	48	48		

- Molecule 16 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	J	245	Total	C	N	O	P	S	0	0
			1815	1133	322	348	2	10		

- Molecule 17 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	406	Total	C	N	O	S	0	0
			3014	1897	550	558	9		

- Molecule 18 is a protein called RNA-binding protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	141	Total	C	N	O	S	0	0
			1139	727	197	210	5		

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	L2	95	Total	C	N	O	0	0
			472	282	95	95		

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	L3	85	Total	C	N	O	0	0
			421	251	85	85		

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	L4	80	Total	C	N	O	0	0
			396	236	80	80		

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	L5	82	Total	C	N	O	0	0
			402	238	82	82		

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L6	75	Total	C	N	O	0	0
			368	218	75	75		

- Molecule 24 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	L7	89	Total	C	N	O	0	0
			437	259	89	89		

- Molecule 25 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	L8	96	Total	C	N	O	0	0
			472	280	96	96		

- Molecule 26 is a protein called Armadillo repeat-containing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	173	Total	C	N	O	S	0	0
			1292	815	218	253	6		

- Molecule 27 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	98	Total	C	N	O	S	0	0
			845	517	167	159	2		

- Molecule 28 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	O	159	Total	C	N	O	0	0
			776	457	159	160		

- Molecule 29 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	P	79	Total	C	N	O	0	0
			390	232	79	79		

- Molecule 30 is a protein called RNA helicase aquarius.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Q	1327	Total	C	N	O	0	0
			6579	3925	1327	1327		

- Molecule 31 is a protein called Peptidyl-prolyl cis-trans isomerase-like 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	R	161	Total	C	N	O	0	0
			791	468	161	162		

- Molecule 32 is a protein called Pre-mRNA-splicing factor SLU7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S	272	Total	C	N	O	S	0	0
			2249	1413	402	426	8		

- Molecule 33 is a protein called ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	780	Total	C	N	O	S	0	0
			6236	3955	1058	1182	41		

- Molecule 34 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	U	132	Total	C	N	O	S	0	0
			874	530	174	169	1		

- Molecule 35 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	V	464	Total	C	N	O	S	0	0
			3768	2415	642	689	22		

- Molecule 36 is a protein called WD repeat-containing protein 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	W	348	Total	C	N	O	S	0	0
			2764	1753	500	493	18		

- Molecule 37 is a protein called Splicing factor Cactin.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	X	142	Total	C	N	O	S	0	0
			1243	815	220	205	3		

- Molecule 38 is a protein called Protein FAM32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Y	59	Total	C	N	O	S	0	0
			494	308	94	90	2		

- Molecule 39 is a protein called NF-kappa-B-activating protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	31	Total	C	N	O	S	0	0
			234	142	44	46	2		

- Molecule 40 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	a	73	Total	C	N	O	S	0	0
			591	376	105	103	7		
40	h	73	Total	C	N	O		0	0
			360	214	73	73			

- Molecule 41 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	b	82	Total	C	N	O	S	0	0
			649	413	113	119	4		

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Mol	Chain	Residues	Atoms				AltConf	Trace
41	i	81	Total	C	N	O	0	0
			401	239	81	81		

- Molecule 42 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	c	98	Total	C	N	O	S	0	0
			796	498	144	148	6		
42	j	98	Total	C	N	O		0	0
			487	291	98	98			

- Molecule 43 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	85	Total	C	N	O	S	0	0
			663	415	117	125	6		
43	k	81	Total	C	N	O		0	0
			399	237	81	81			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	e	77	Total	C	N	O	S	0	0
			638	405	113	115	5		
44	l	77	Total	C	N	O		0	0
			381	227	77	77			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	f	73	Total	C	N	O	S	0	0
			567	367	94	101	5		
45	m	73	Total	C	N	O		0	0
			356	210	73	73			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	74	Total	C	N	O	S	0	0
			577	364	104	103	6		
46	n	74	Total	C	N	O		0	0
			364	215	74	75			

- Molecule 47 is a protein called Splicing factor ESS-2 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	p	52	Total	C	N	O	0	0
			265	161	52	52		

- Molecule 48 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	q	137	Total	C	N	O	0	0
			684	410	137	137		
48	r	135	Total	C	N	O	0	0
			674	404	135	135		
48	s	138	Total	C	N	O	0	0
			689	413	138	138		
48	t	136	Total	C	N	O	0	0
			679	407	136	136		

- Molecule 49 is a protein called Pre-mRNA-splicing factor SPF27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	u	225	Total	C	N	O	0	0
			1117	666	225	226		

- Molecule 50 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	390	Total	C	N	O	S	0	0
			3130	1976	546	589	19		

- Molecule 51 is a protein called Protein mago nashi homolog.

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

- Molecule 52 is a protein called RNA-binding protein 8A.

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

- Molecule 53 is a protein called RNA-binding protein 41.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	y	147	Total	C	N	O	0	0
			751	452	149	150		

- Molecule 54 is a protein called Protein FAM204A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	114	Total	C	N	O	S	0	0
			933	588	169	173	3		

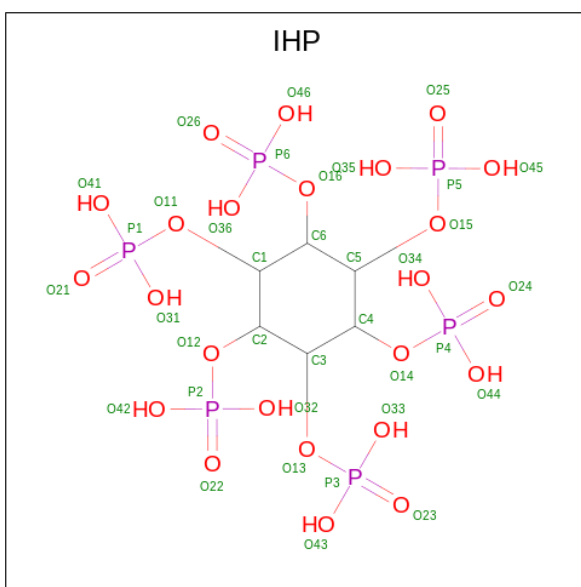
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
55	1	2	Total	Mg	0
			2	2	
55	6	4	Total	Mg	0
			4	4	
55	B	1	Total	Mg	0
			1	1	
55	C	1	Total	Mg	0
			1	1	
55	v	1	Total	Mg	0
			1	1	

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

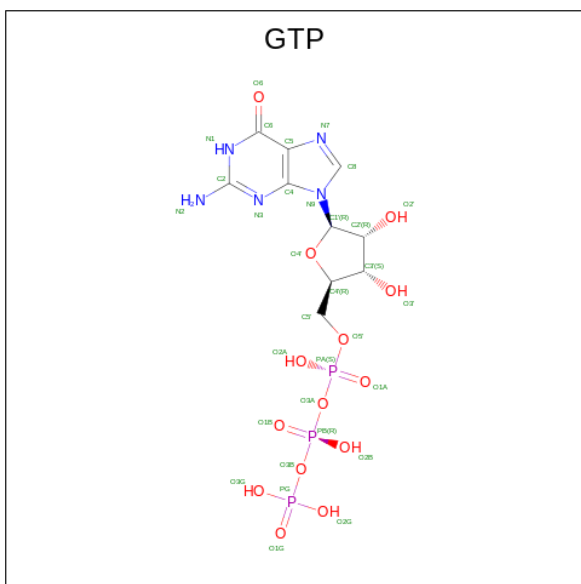
Mol	Chain	Residues	Atoms		AltConf
56	6	2	Total	K	0
			2	2	

- Molecule 57 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C₆H₁₈O₂₄P₆) (labeled as "Ligand of Interest" by depositor).



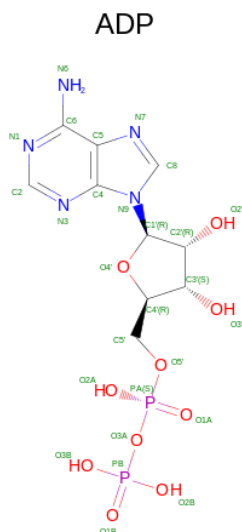
Mol	Chain	Residues	Atoms				AltConf
57	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 58 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 59 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

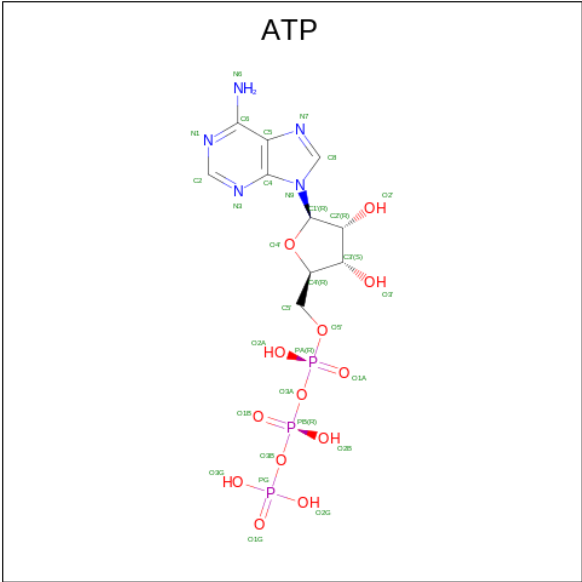


Mol	Chain	Residues	Atoms					AltConf
59	C	1	Total 27	C 10	N 5	O 10	P 2	0
59	C	1	Total 27	C 10	N 5	O 10	P 2	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
60	S	1	Total Zn 1 1	0

- Molecule 61 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).



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

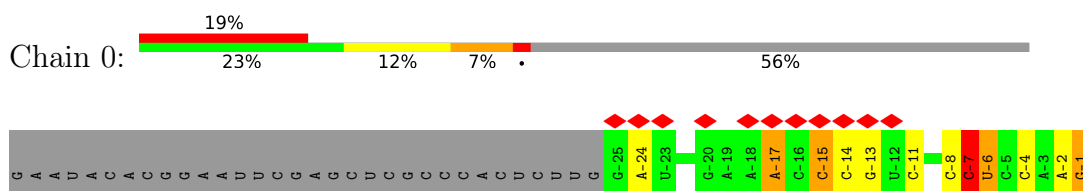
- Molecule 62 is water.

Mol	Chain	Residues	Atoms		AltConf
62	6	1	Total	O	0
			1	1	

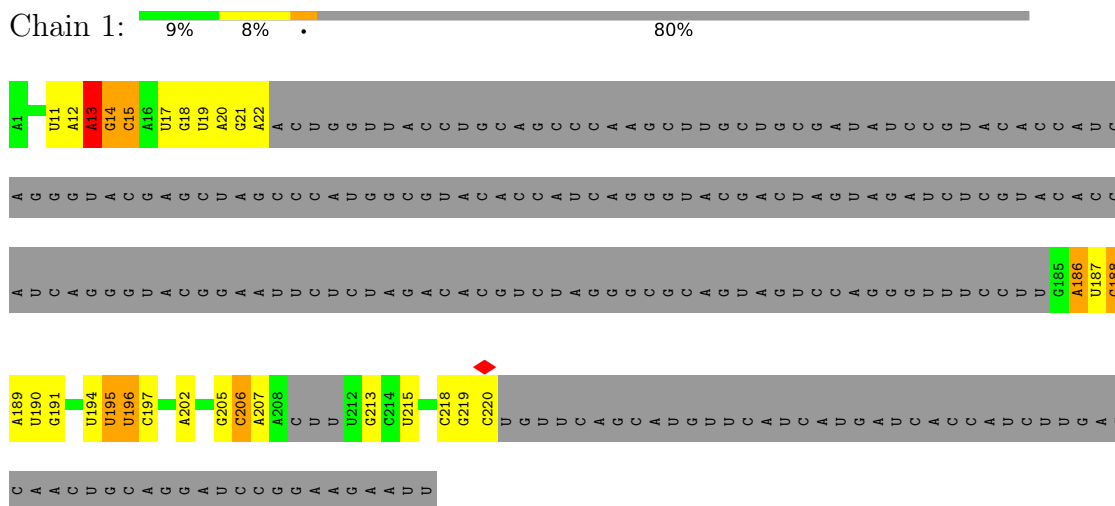
3 Residue-property plots [i](#)

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.

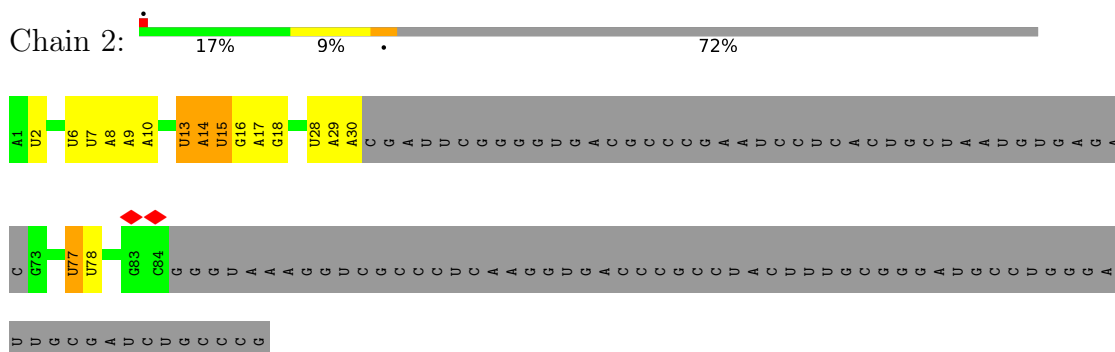
• Molecule 1: MSE-U12_5 exon



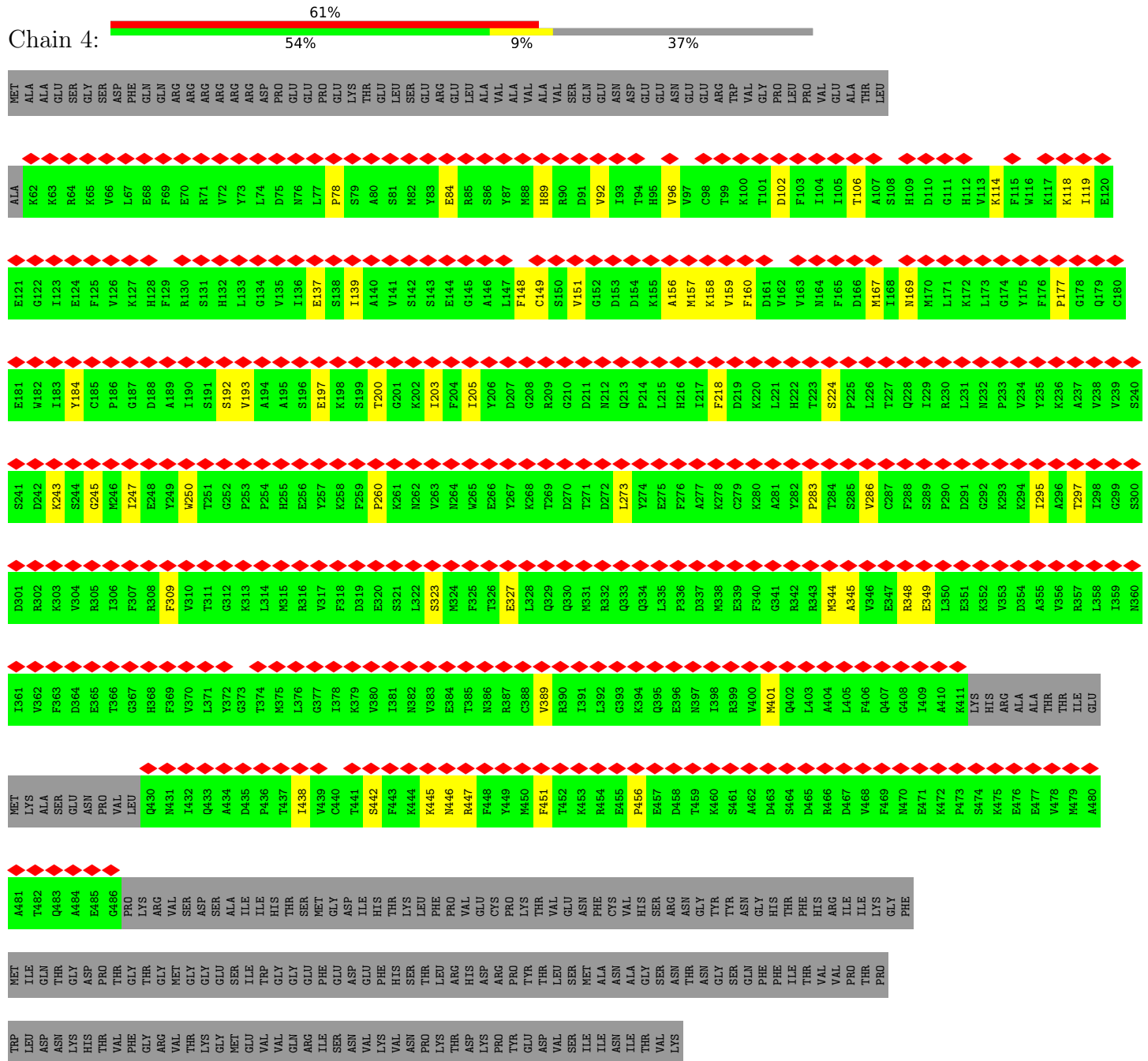
• Molecule 2: MSE-U12_intron-3 exon



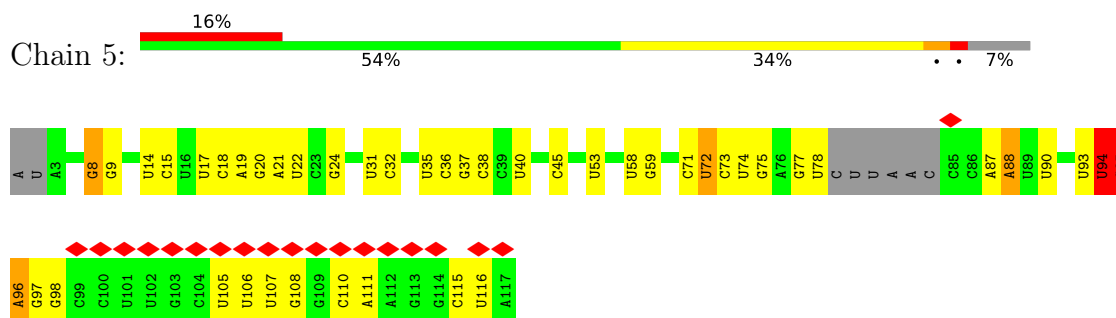
• Molecule 3: U12 snRNA



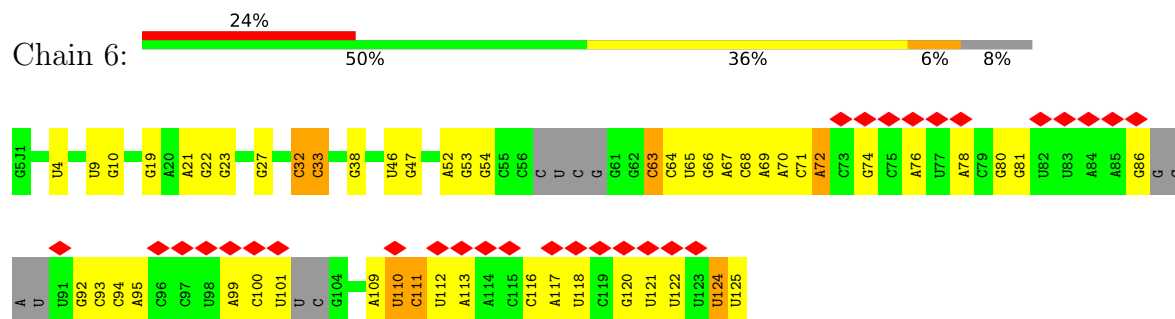
• Molecule 4: Peptidylprolyl isomerase domain and WD repeat-containing protein 1



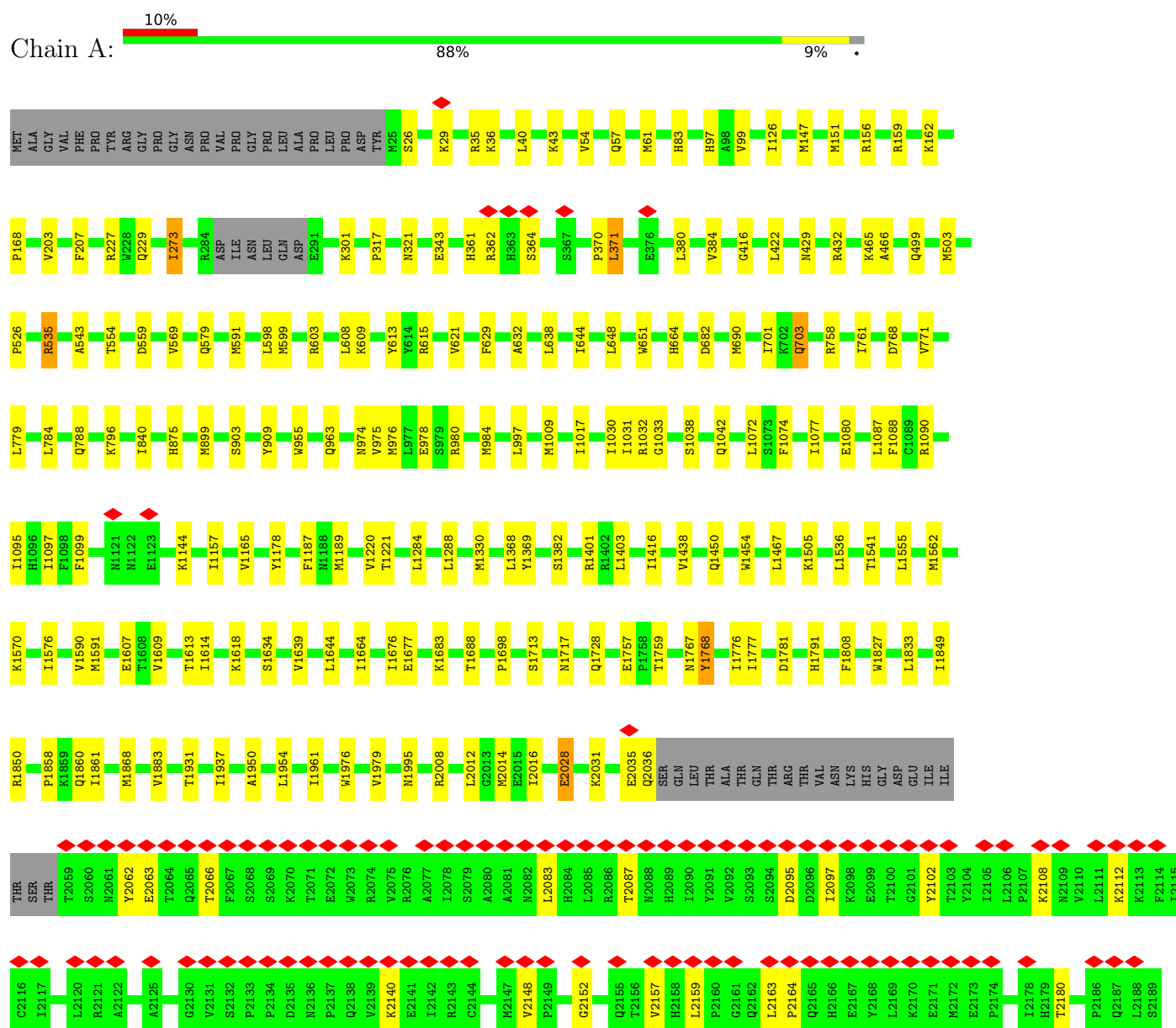
• Molecule 5: U5 snRNA

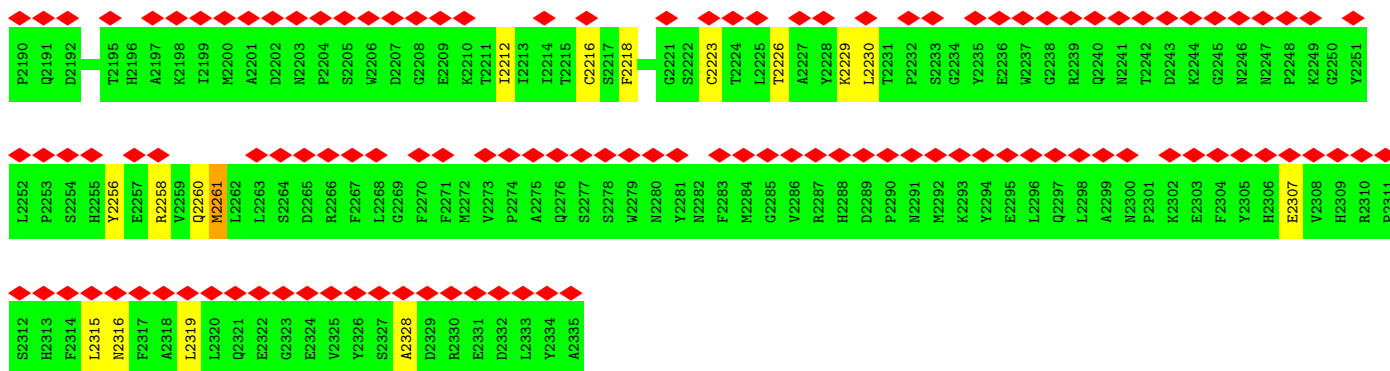


- Molecule 6: U6atac snRNA

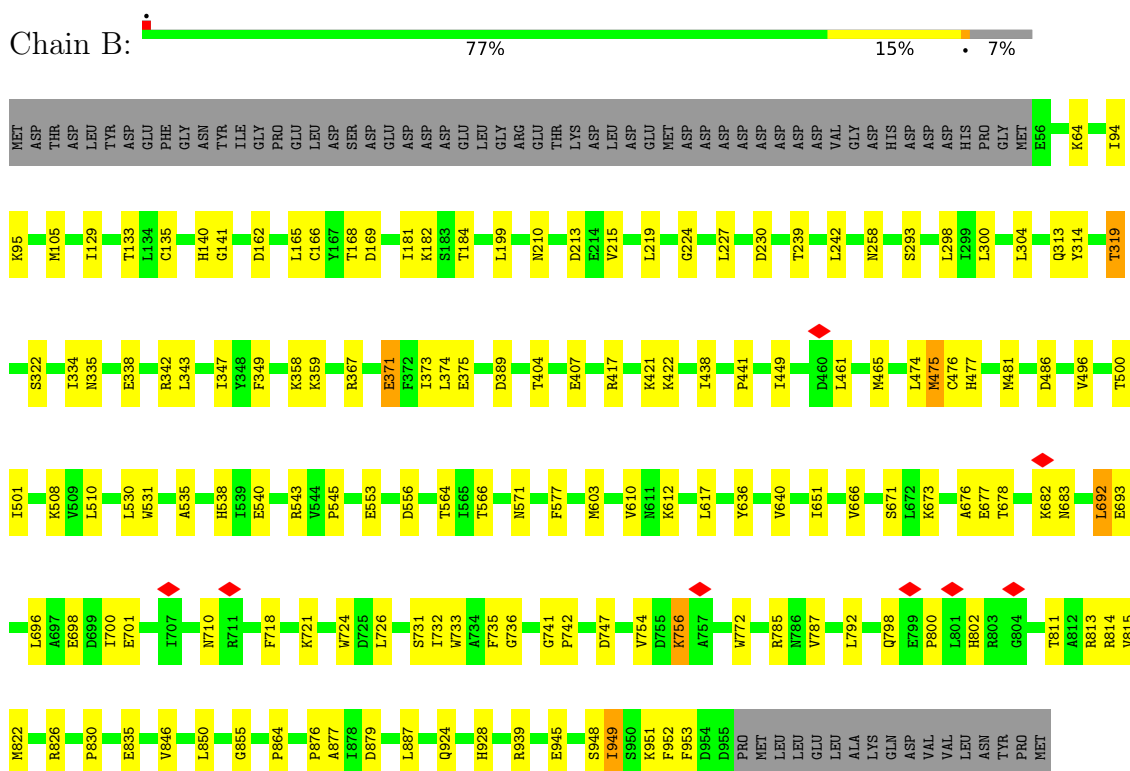


- Molecule 7: Pre-mRNA-processing-splicing factor 8

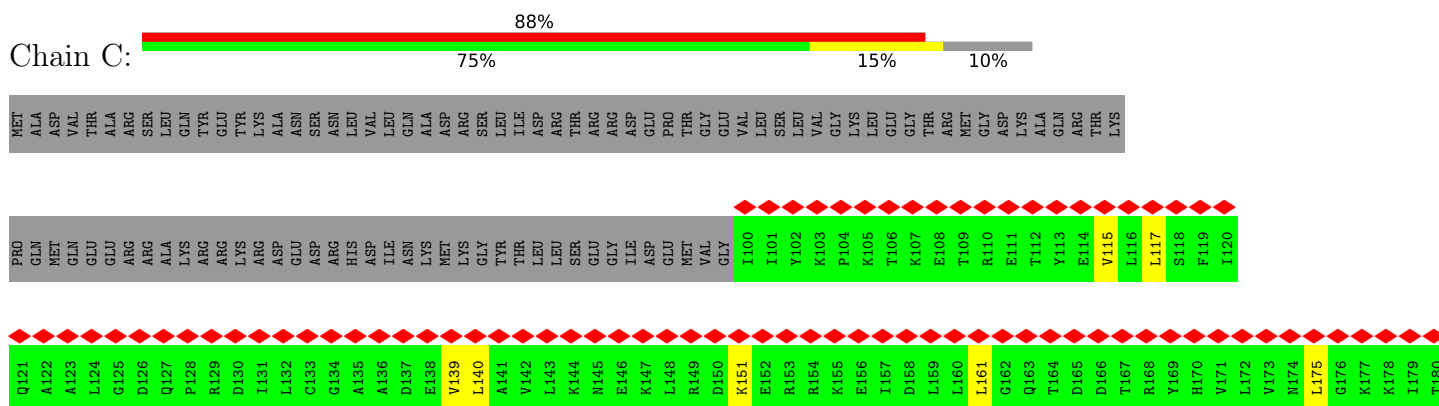




- Molecule 8: 116 kDa U5 small nuclear ribonucleoprotein component

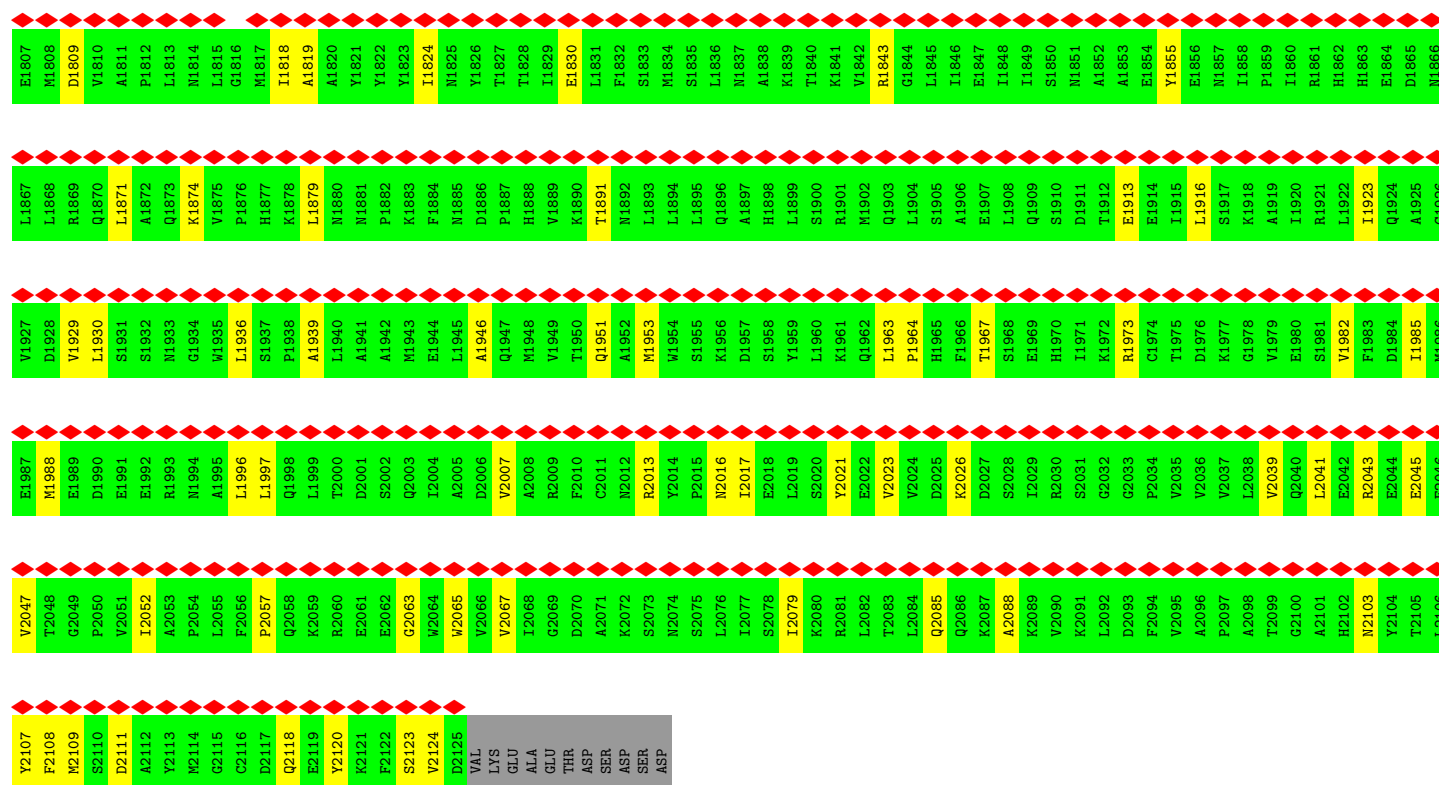


- Molecule 9: U5 small nuclear ribonucleoprotein 200 kDa helicase

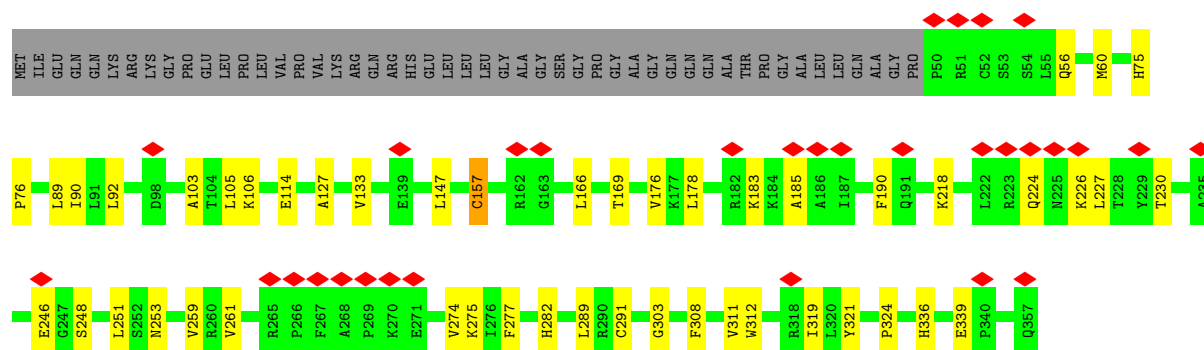
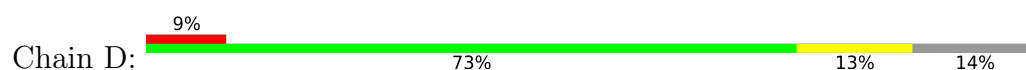




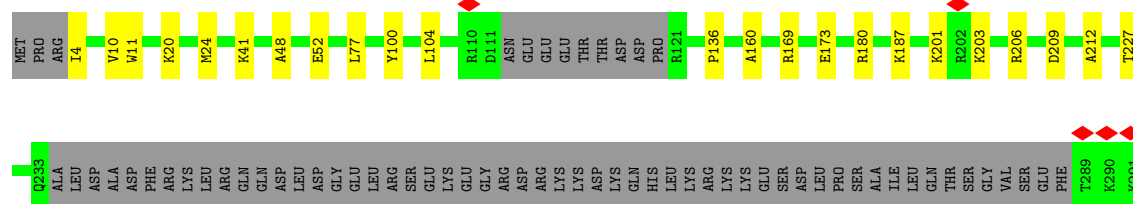
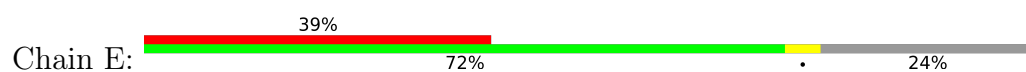
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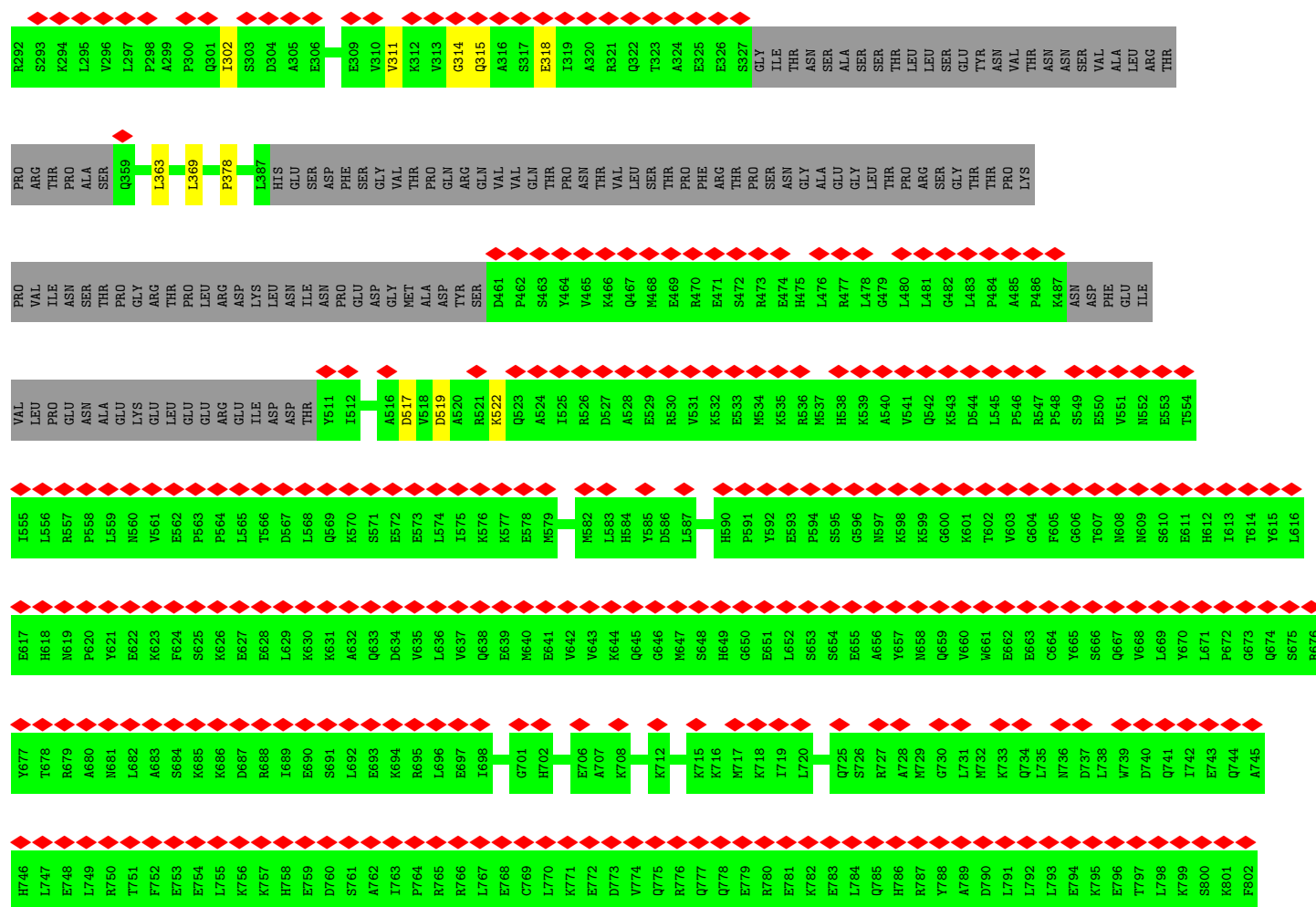


• Molecule 10: U5 small nuclear ribonucleoprotein 40 kDa protein

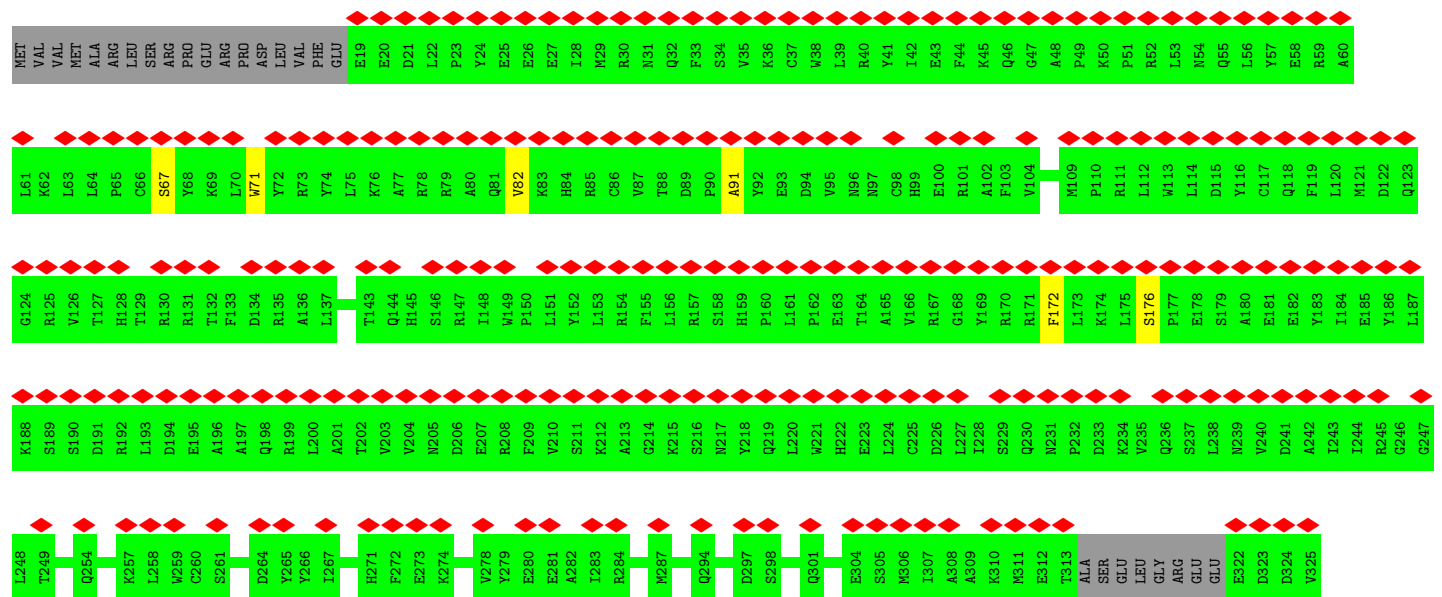
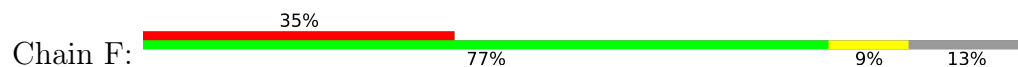


• Molecule 11: Cell division cycle 5-like protein



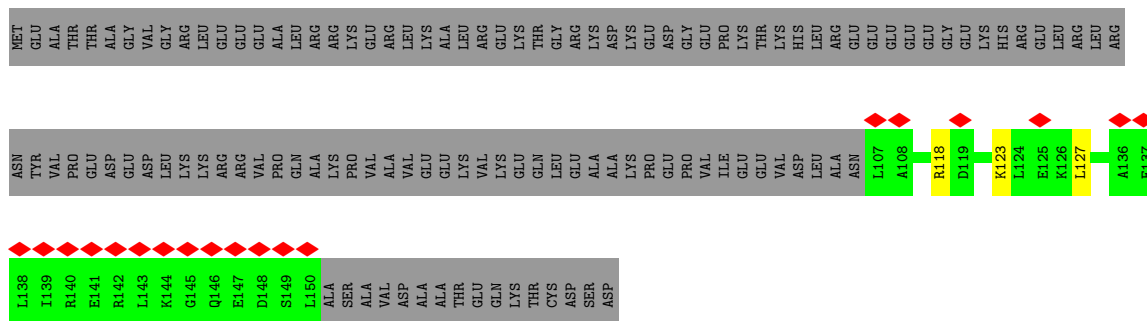


• Molecule 12: Pre-mRNA-splicing factor SYF1

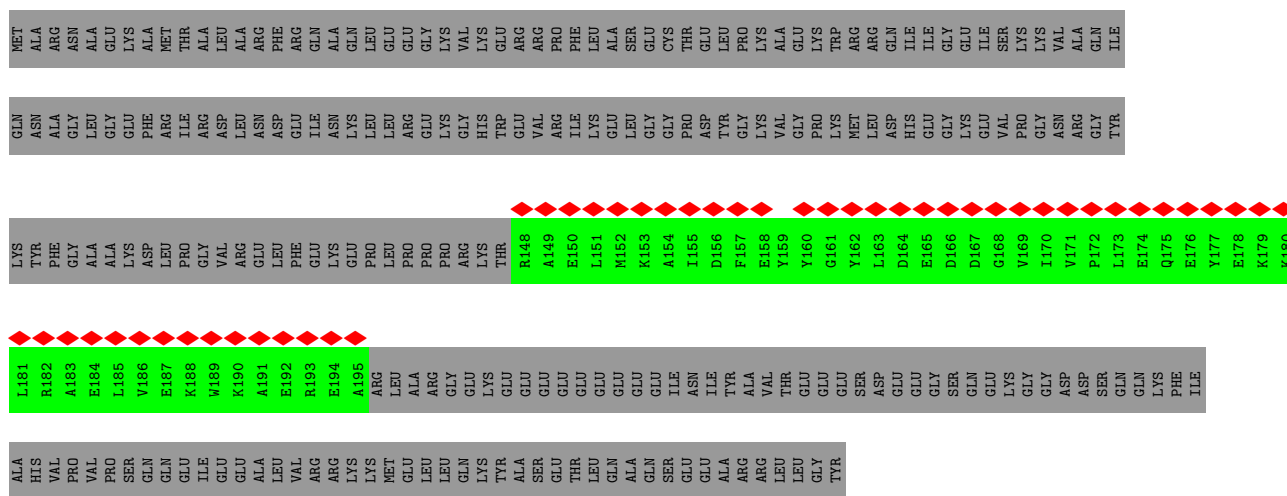




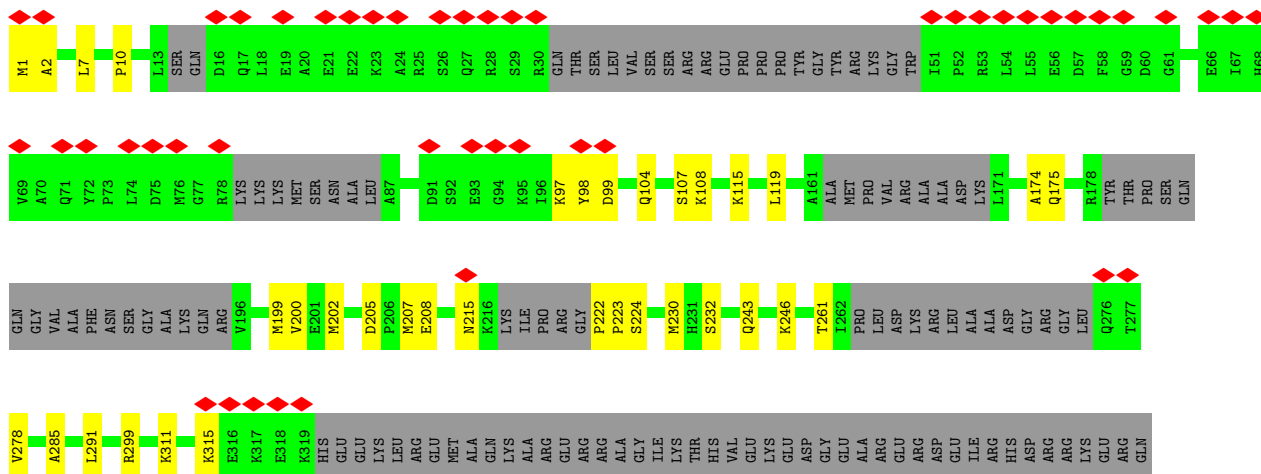
Chain H: 11% 25% 73%



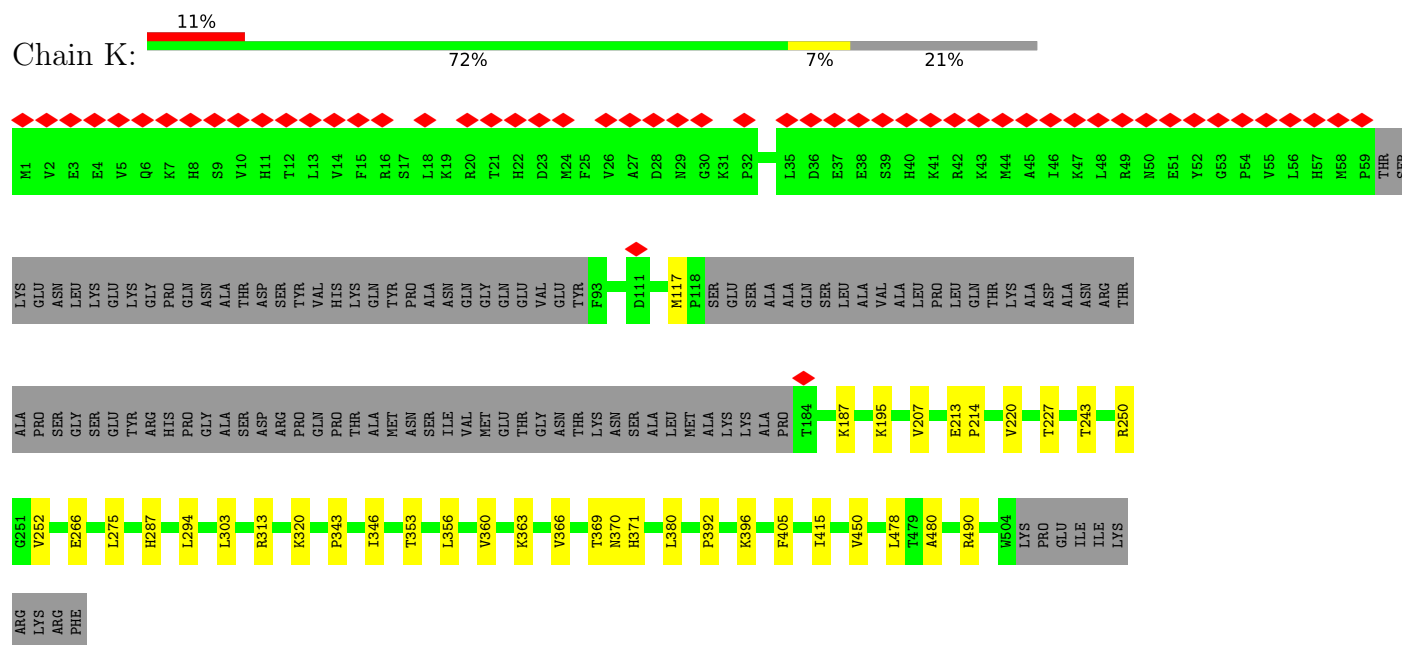
Chain I:



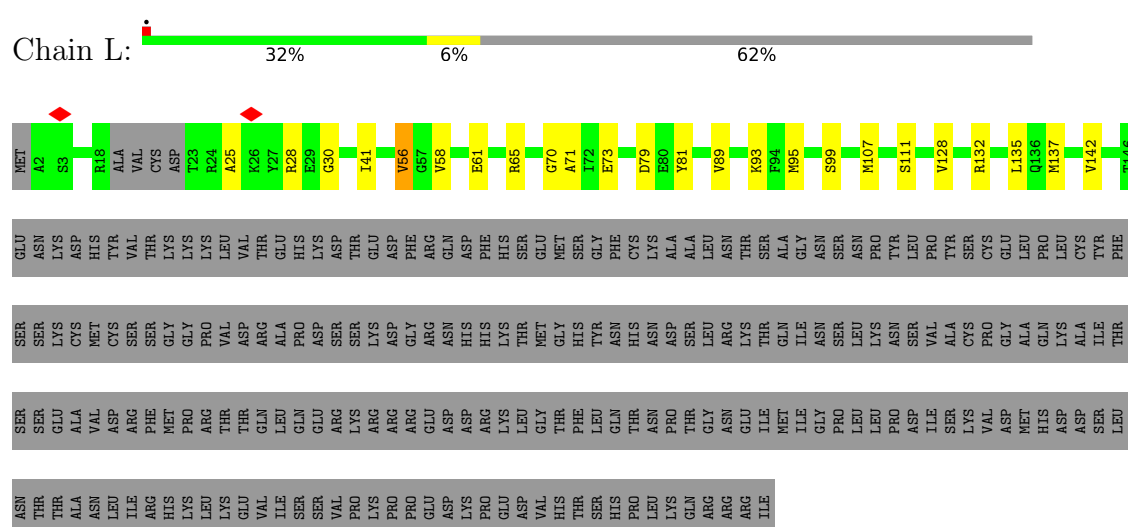
Chain J: 9% 39% 7% 45%



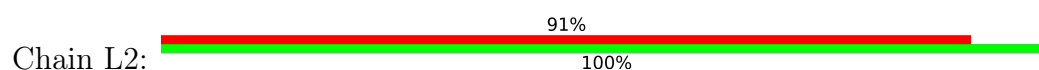
- Molecule 17: Pleiotropic regulator 1

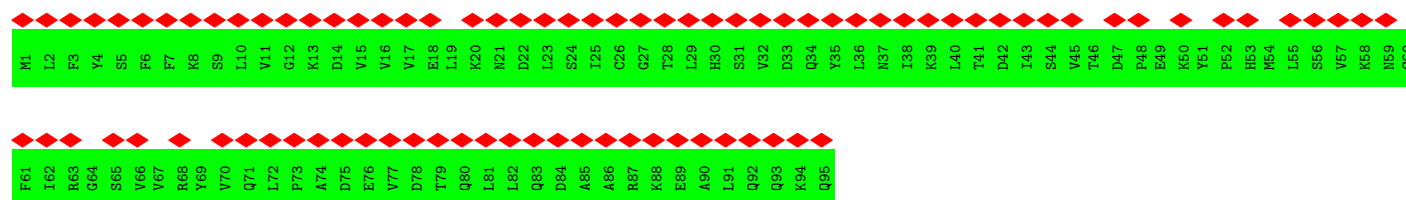


- Molecule 18: RNA-binding protein 48

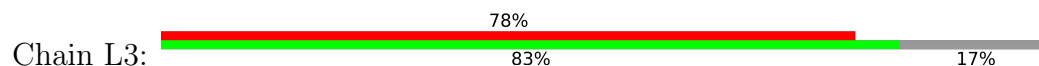


- Molecule 19: U6 snRNA-associated Sm-like protein LSm2

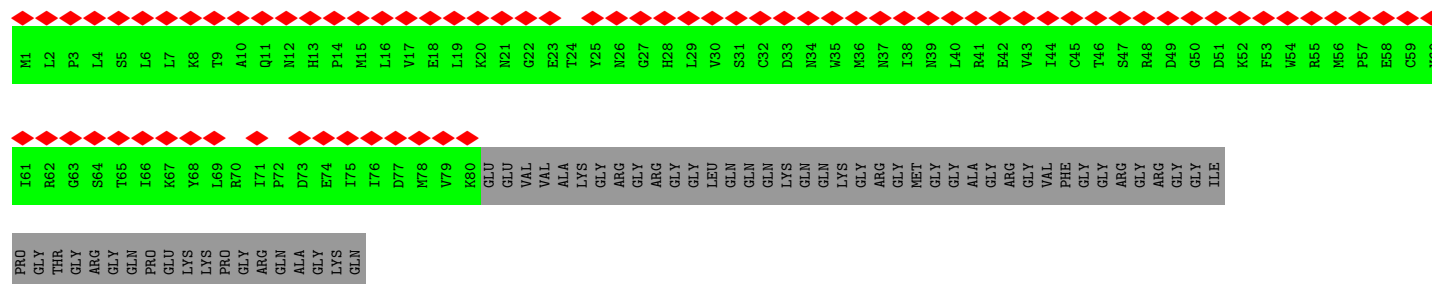




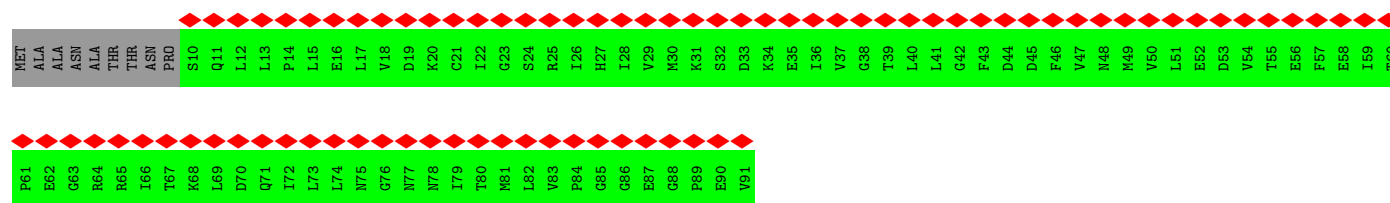
• Molecule 20: U6 snRNA-associated Sm-like protein LSm3



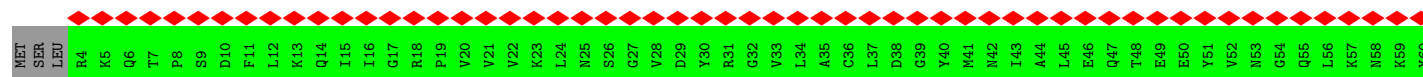
• Molecule 21: U6 snRNA-associated Sm-like protein LSm4



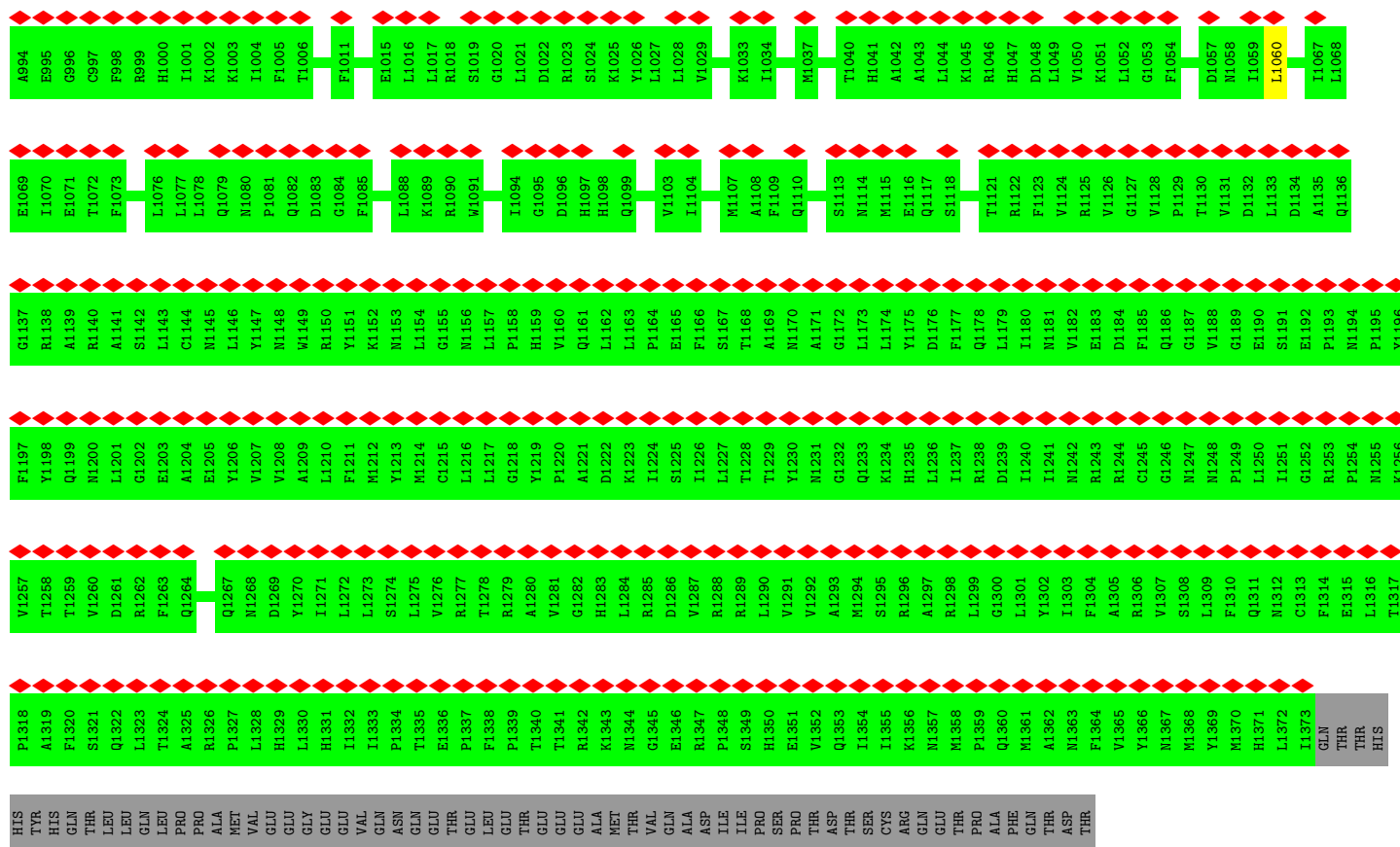
• Molecule 22: U6 snRNA-associated Sm-like protein LSm5



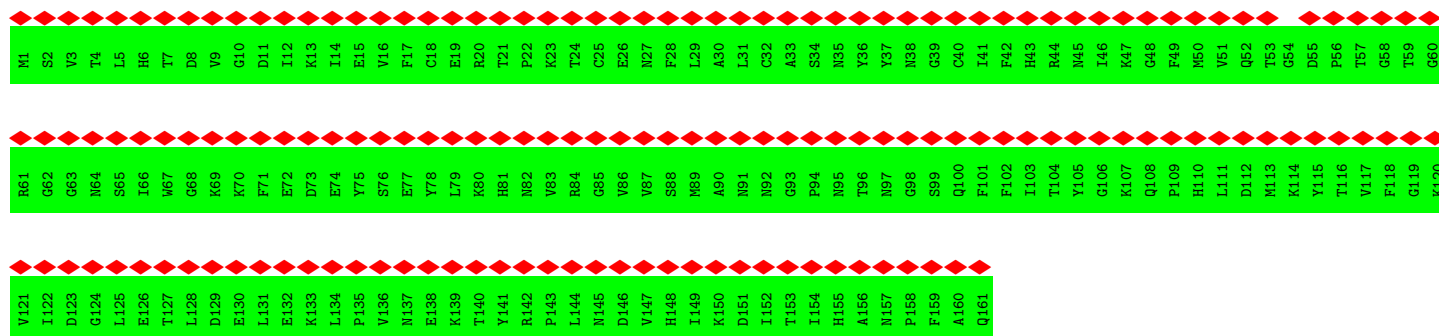
• Molecule 23: U6 snRNA-associated Sm-like protein LSm6



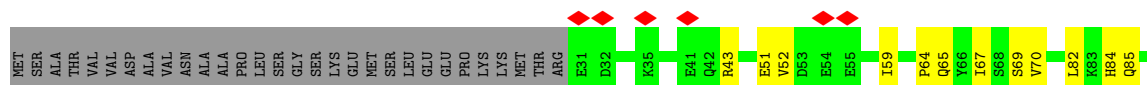
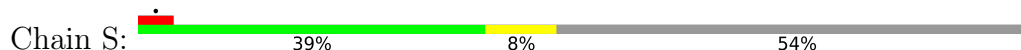
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F123	L183	T243	M304	S364	M424	D487	D547	F614	M677	V737	K797	E865	L937
K124	E184	M244	L305	L365	P425	S488	H548	R615	N678	E738	N798	I866	Y938
H125	L185	K245	K306	V366	L426	V489	I549	R616	T679	D739	T800	M867	Q939
I126	E186	K246	F307	K367	Y427	S490	K550	N617	D680	P740	L801	A868	V940
L127	L187	V247	Y308	F368	P428	R491	D551	L618	C681	A741	F802	L869	M941
K128	K188	H248	T309	F369	T429	M492	E552	R619	V682	L742	F803	D870	S942
A129	K189	Y249	G310	G370	E430	K493	E553	G620	V683	Q743	T804	L871	R943
A130	T190	C250	F311	P371	E431	K494	E554	E621	V684	I744	H804	D872	R944
L131	P191	E251	E312	L372	I432	W495	C562	S622	D685	F745	T805	E873	W944
A132	K192	R252	I313	S373	I433	Q496	F563	R623	V686	P746	Q806	E874	E945
E133	L193	F253	N314	S374	V434	S497	L564	T624	L687	F747	L807	R874	E946
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D135	K195	M257	Q316	T376	E436	TVR	T566	L629	D689	I749	A809	E884	I948
G136	F196	I258	T317	L377	M437	GLY	V567	L630	T690	T750	I810	E885	S949
E137	W197	D259	G318	H378	I438	GLY	R568	D630	L691	F751	R811	E886	K950
F138	N198	L260	N319	Q379	V439	V502	P569	F631	L692	G752	A812	L886	V951
S139	L199	E261	A320	V380	P440	F503	T570	N632	C693	VAL	G813	E887	K952
L140	I200	A262	L321	A381	T441	G505	K571	D633	Y694	ARG	M814	T888	N953
H141	K201	L263	T322	S382	E442	G506	F572	G634	C695	SER	Q815	E889	K954
E142	K202	L264	E323	Y383	Y443	W507	Y573	D635	D696	GLY	L816	K890	V955
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T144	D204	T266	E325	C385	S445	R509	T575	D637	S698	LYS	L818	F893	T957
V145	E205	R267	M326	L386	G446	N510	K576	H638	S699	ARG	T819	R894	L958
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D151	A211	I273	R333	N393	L452	A516	P582	N644	N705	ASP	P825	Y900	V964
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C153	E213	D275	T335	E394	K454	T518	L584	G646	N707	THR	T827	L902	T966
F154	Q214	D276	S336	D395	L455	V519	E585	E647	Q708	GLU	G828	A903	F967
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S156	Y216	H278	Q338	T397	L457	E521	V587	V649	A710	K775	T830	R905	P969
N157	Q217	L279	R339	F398	Q458	V522	G588	G650	T711	T776	V832	L906	F970
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I162	L222	Y284	H344	L403	H463	ILE	R593	L655	D716	F781	L836	E911	A975
R163	S223	L285	F345	L404	Y465	GLY	G594	L656	T717	H782	R837	N912	N976
S164	Q224	S286	P346	E405	L466	E529	C595	M657	F718	W783	K838	R913	A977
Q165	N287	N287	E347	L406	F470	N530	E596	R658	L719	L784	L840	L915	P978
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L172	V232	D294	S354	R413	Y479	D538	P603	K667	K726	Y790	Q847	P922	S986
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M174	K234	H296	A357	Q416	T481	T540	R606	V669	F728	Y792	L850	D924	E988
W175	S235	L297	A358	Q417	I481	I541	V607	L670	P729	W793	T849	A925	E989
M176	V236	F298	V359	I418	R482	N542	V607	E671	G730	N793	L851	S926	D990
G177	P237	S299	D360	I419	Q483	L543	L608	T672	H731	L732	Q861	Y927	E991
L178	L238	Q300	T361	Q420	D484	N544	D610	L674	V733	K734	L862	T928	E992
Q179	S239	L301		L421			G611						I993



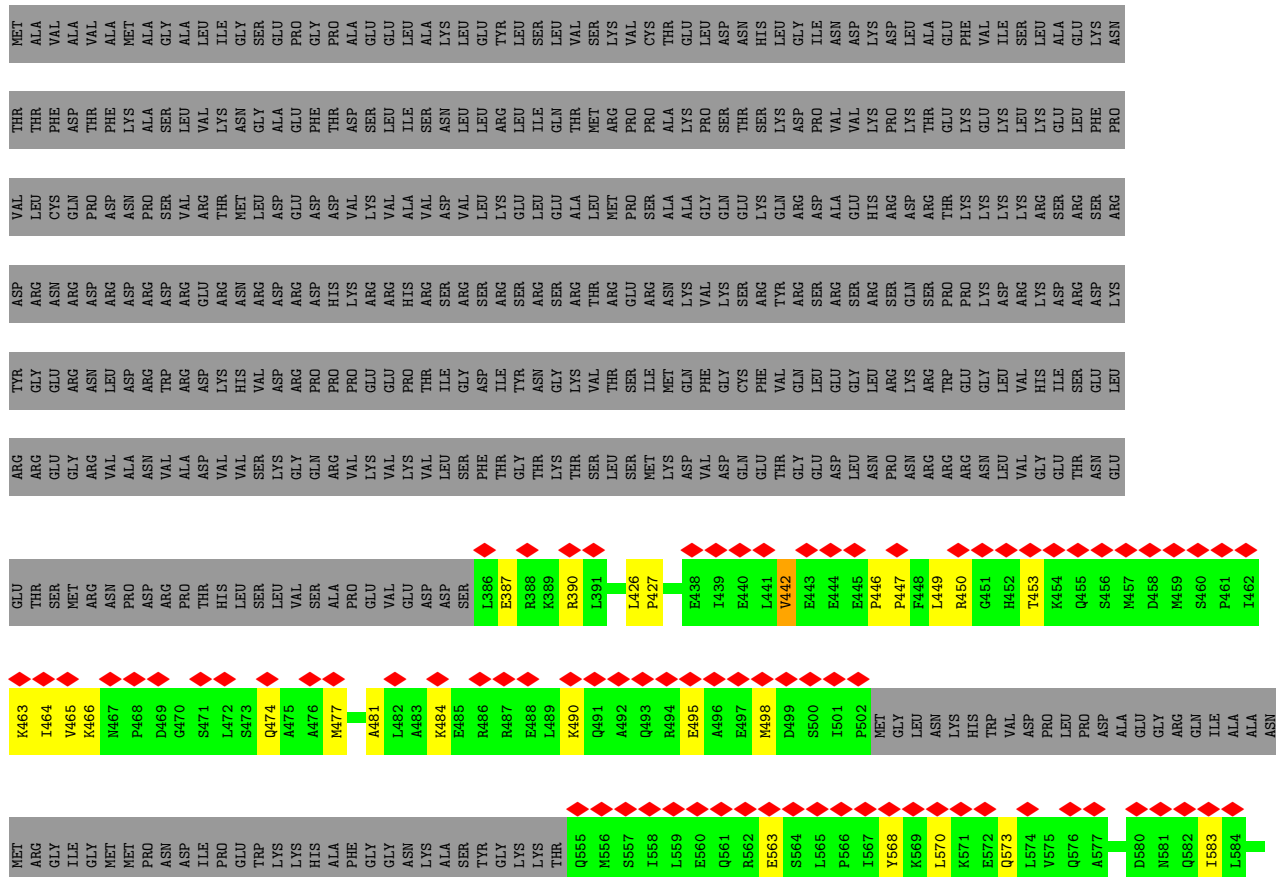
• Molecule 31: Peptidyl-prolyl cis-trans isomerase-like 3

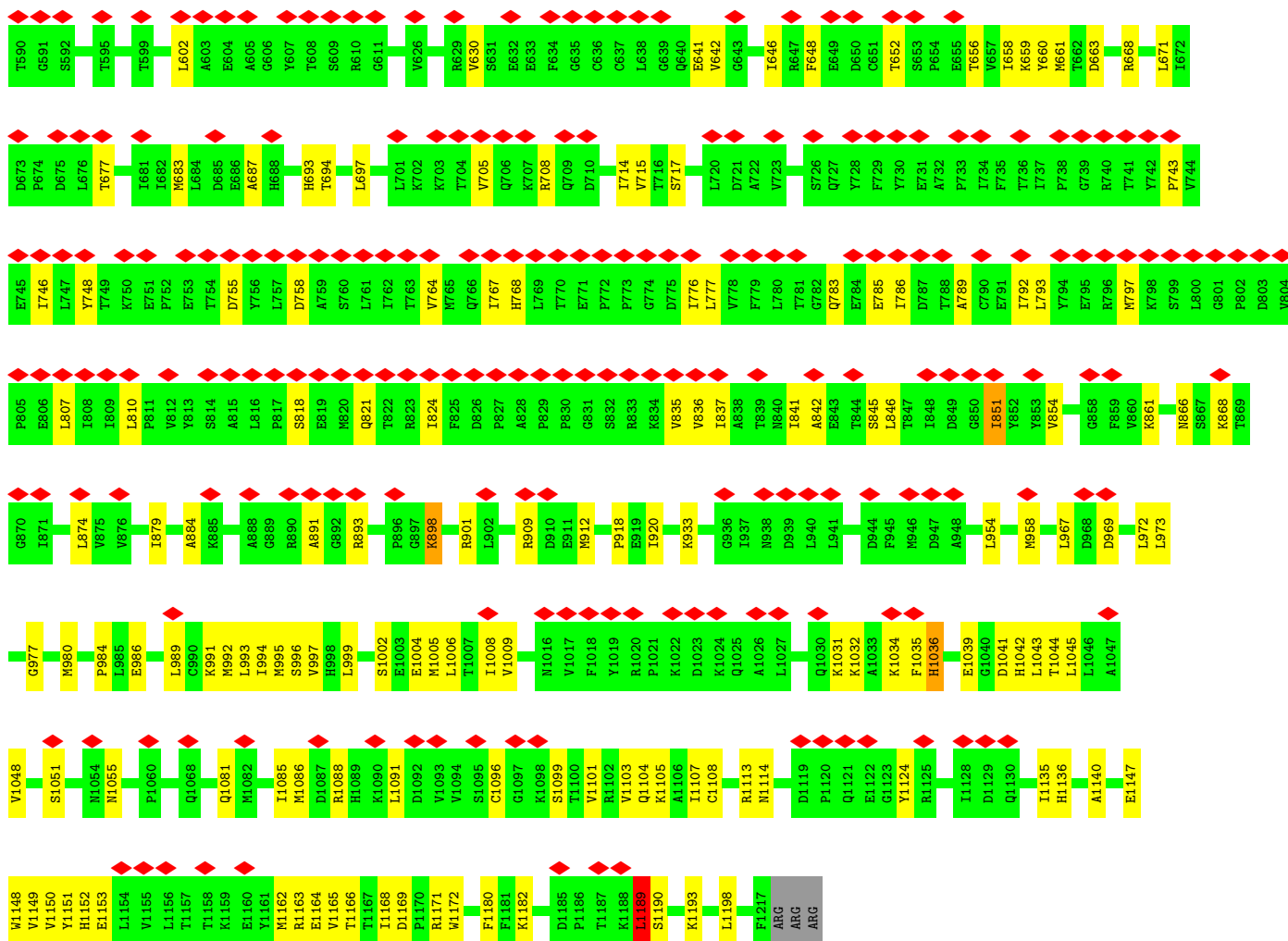


• Molecule 32: Pre-mRNA-splicing factor SLU7



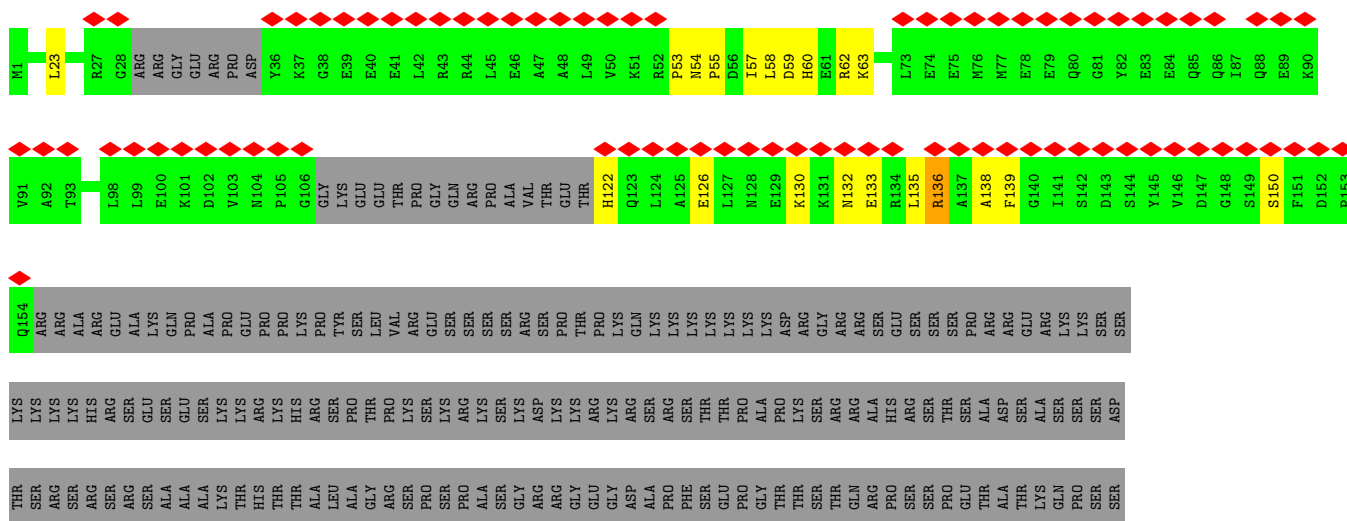
- Molecule 33: ATP-dependent RNA helicase DHX8





• Molecule 34: Serine/arginine repetitive matrix protein 2

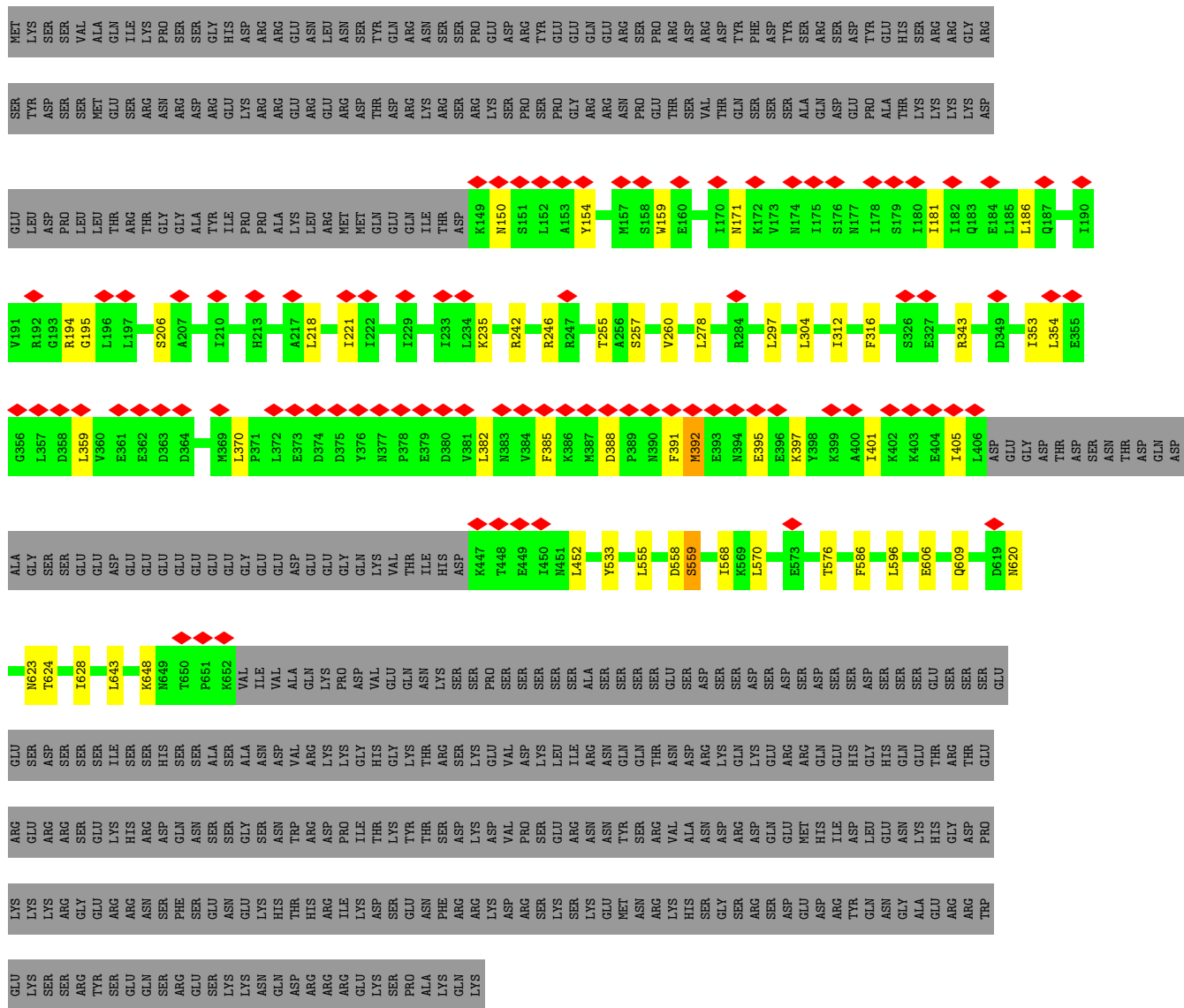
Chain U: 95%



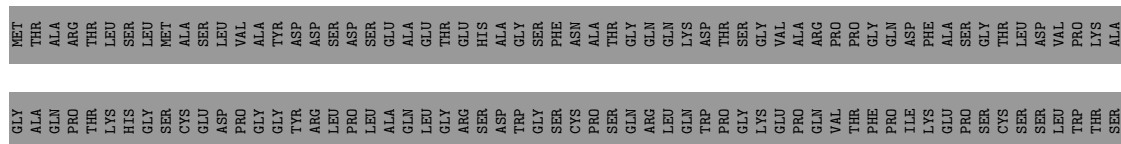


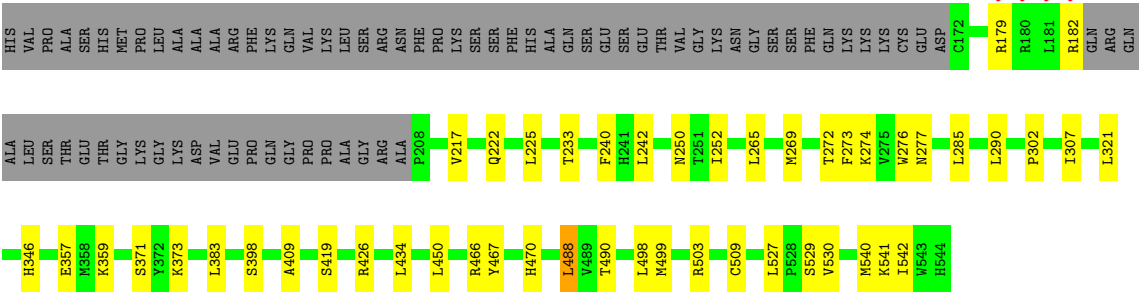


Chain V:

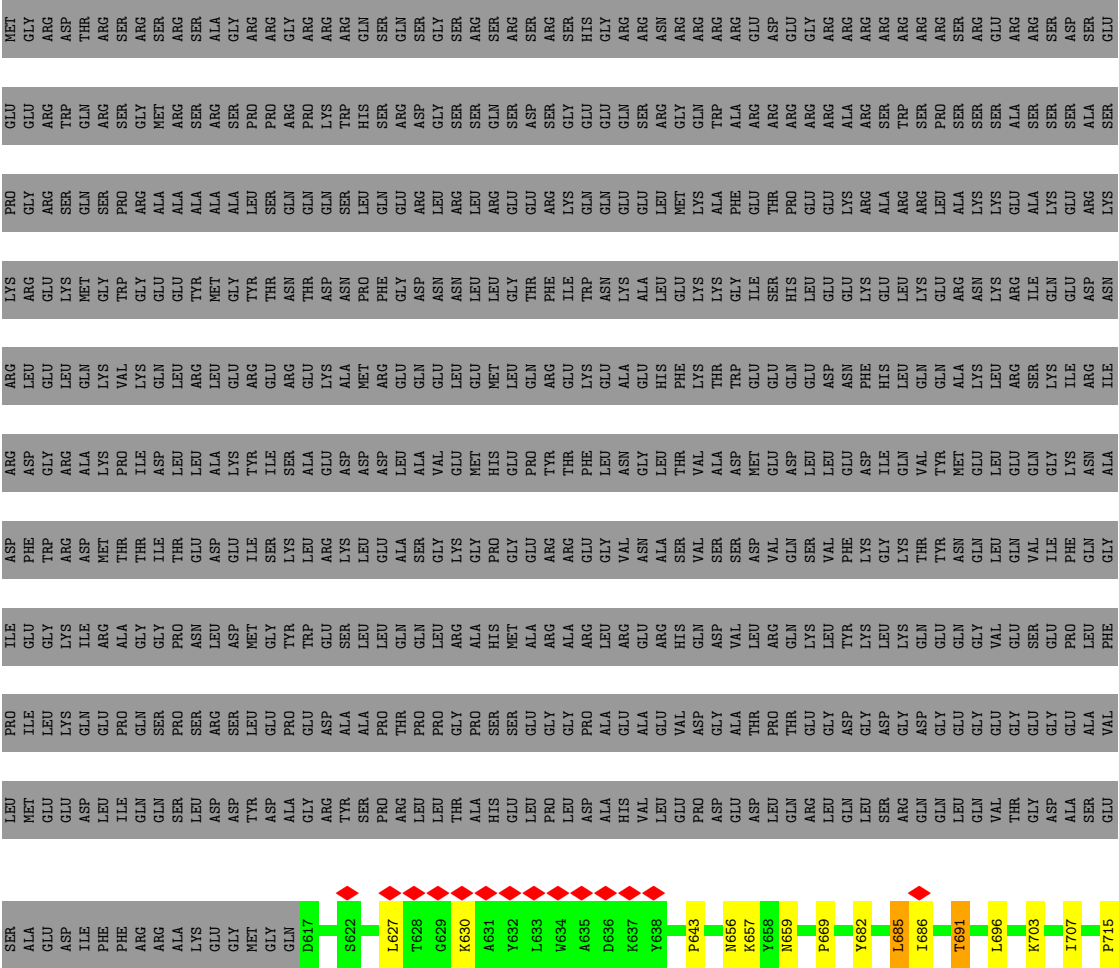


Chain W: 55% 9% 36%





• Molecule 37: Splicing factor Cactin

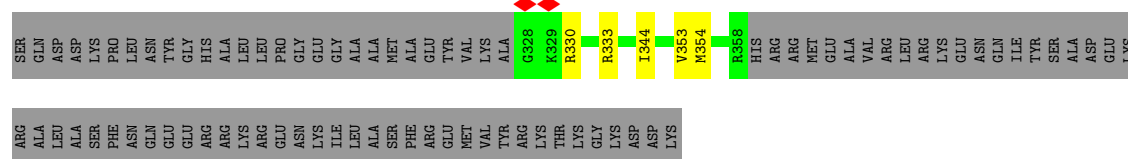


• Molecule 38: Protein FAM32A

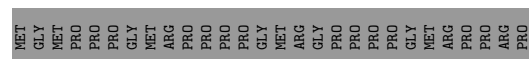




Chain Z: 6% 93%

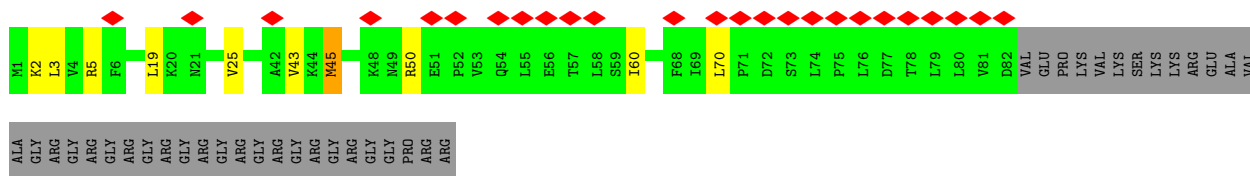


Chain a: 8% 26% 5% 61%

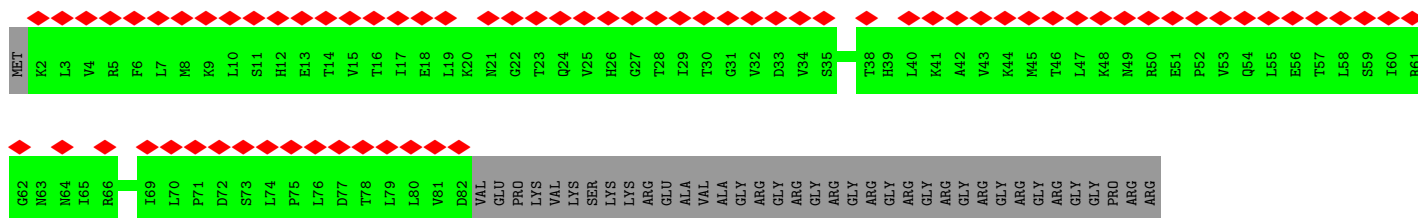


Chain h: 26% 30% 70%

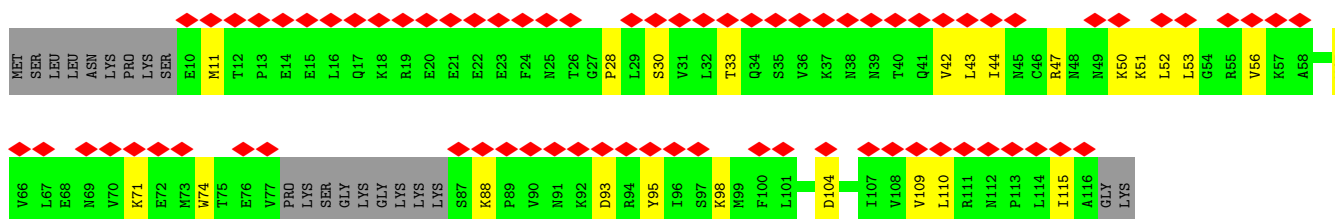
- Molecule 41: Small nuclear ribonucleoprotein Sm D1



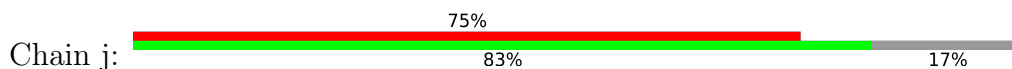
- Molecule 41: Small nuclear ribonucleoprotein Sm D1

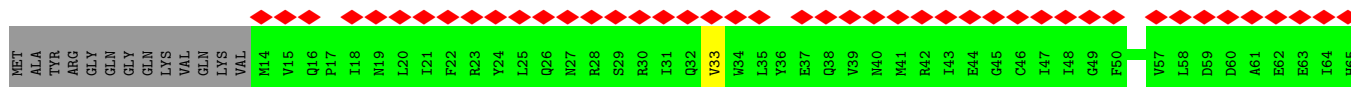


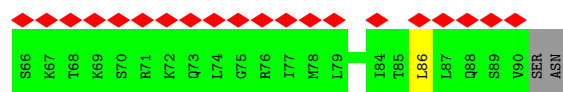
- Molecule 42: Small nuclear ribonucleoprotein Sm D2



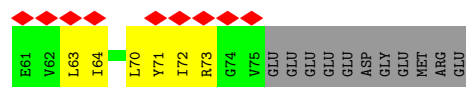
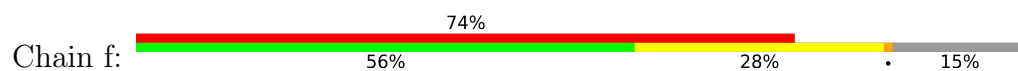
- Molecule 42: Small nuclear ribonucleoprotein Sm D2



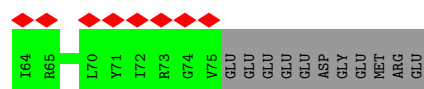
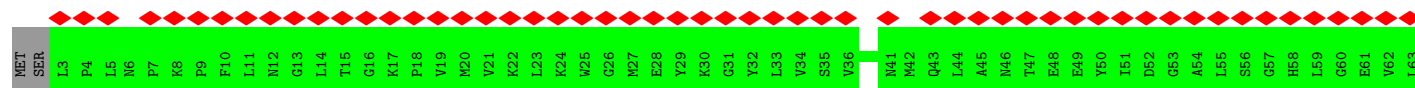
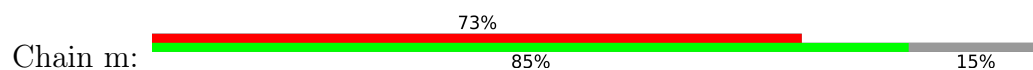




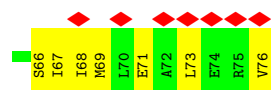
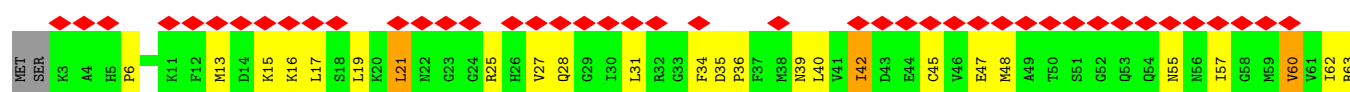
- Molecule 45: Small nuclear ribonucleoprotein F



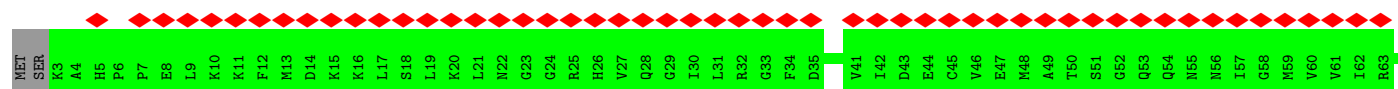
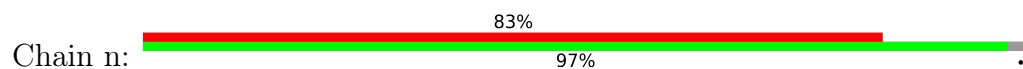
- Molecule 45: Small nuclear ribonucleoprotein F



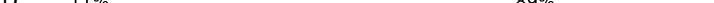
- Molecule 46: Small nuclear ribonucleoprotein G

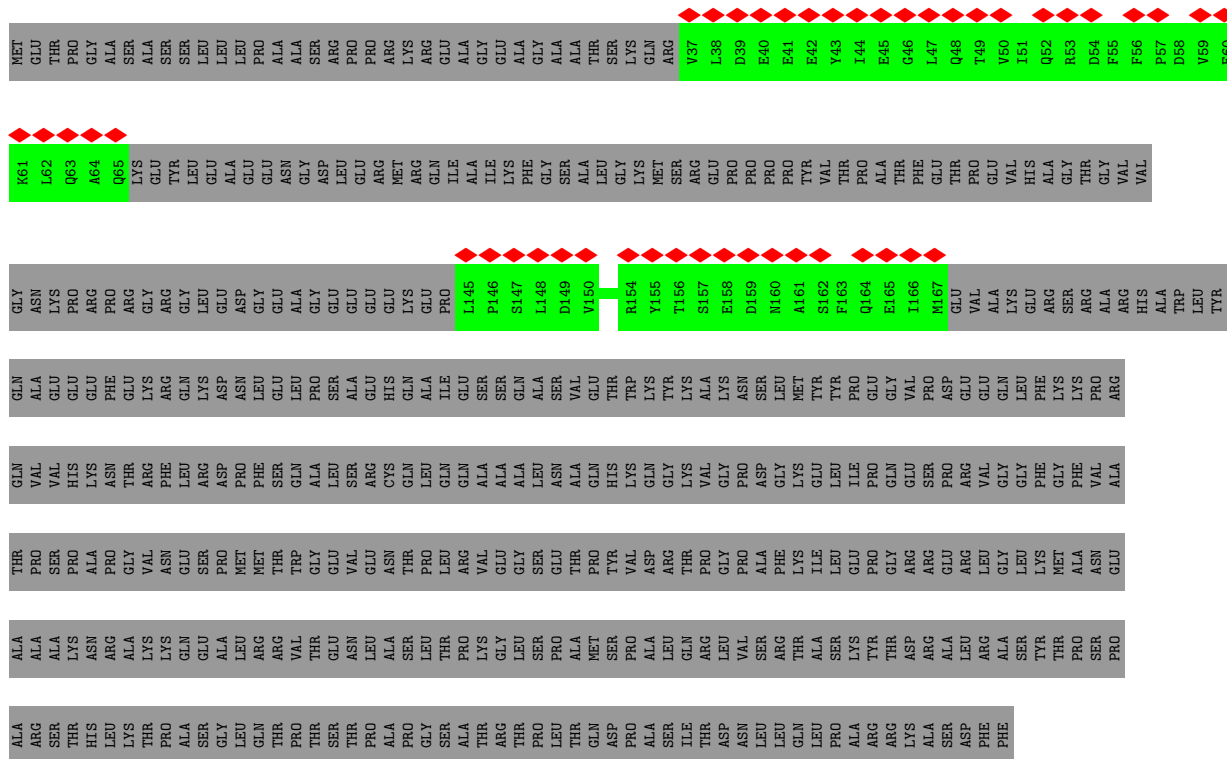


- Molecule 46: Small nuclear ribonucleoprotein G

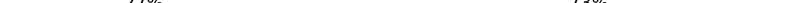


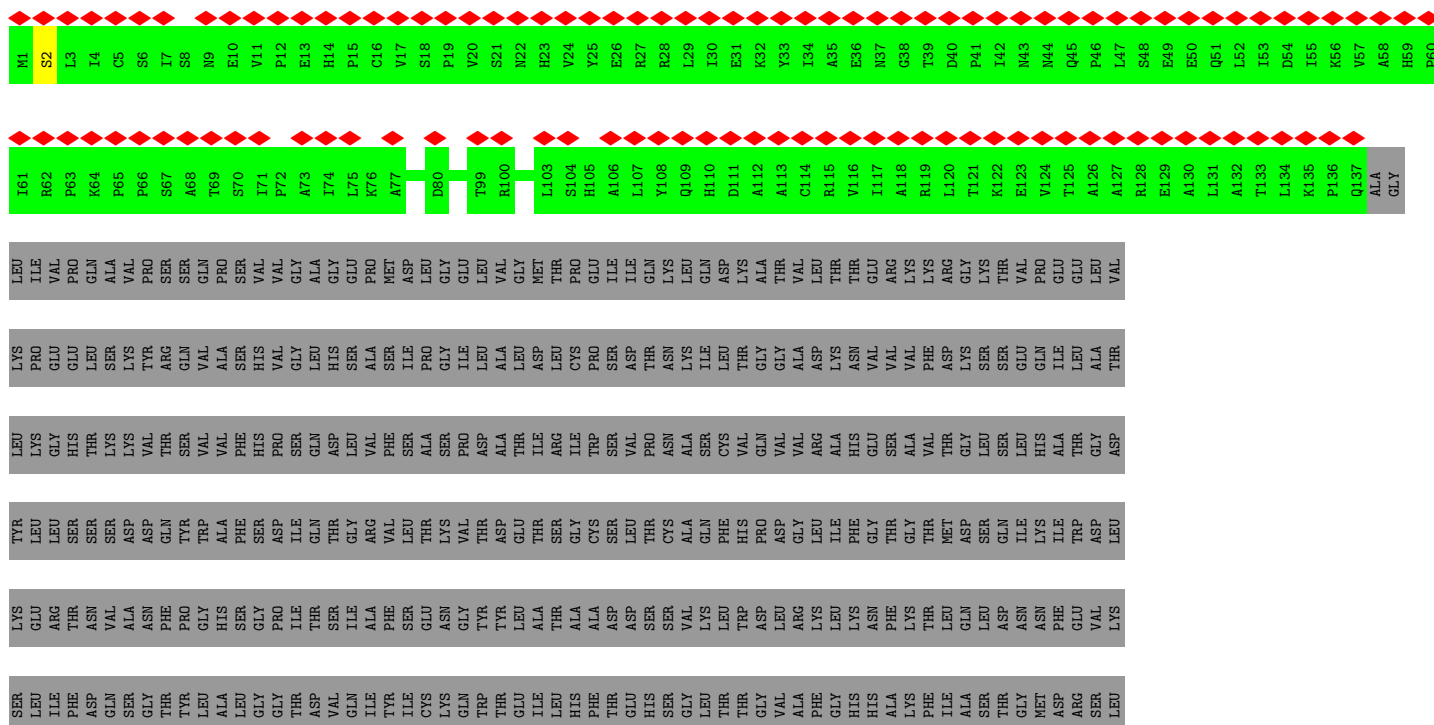
- Molecule 47: Splicing factor ESS-2 homolog

Chain p: 



- Molecule 48: Pre-mRNA-processing factor 19

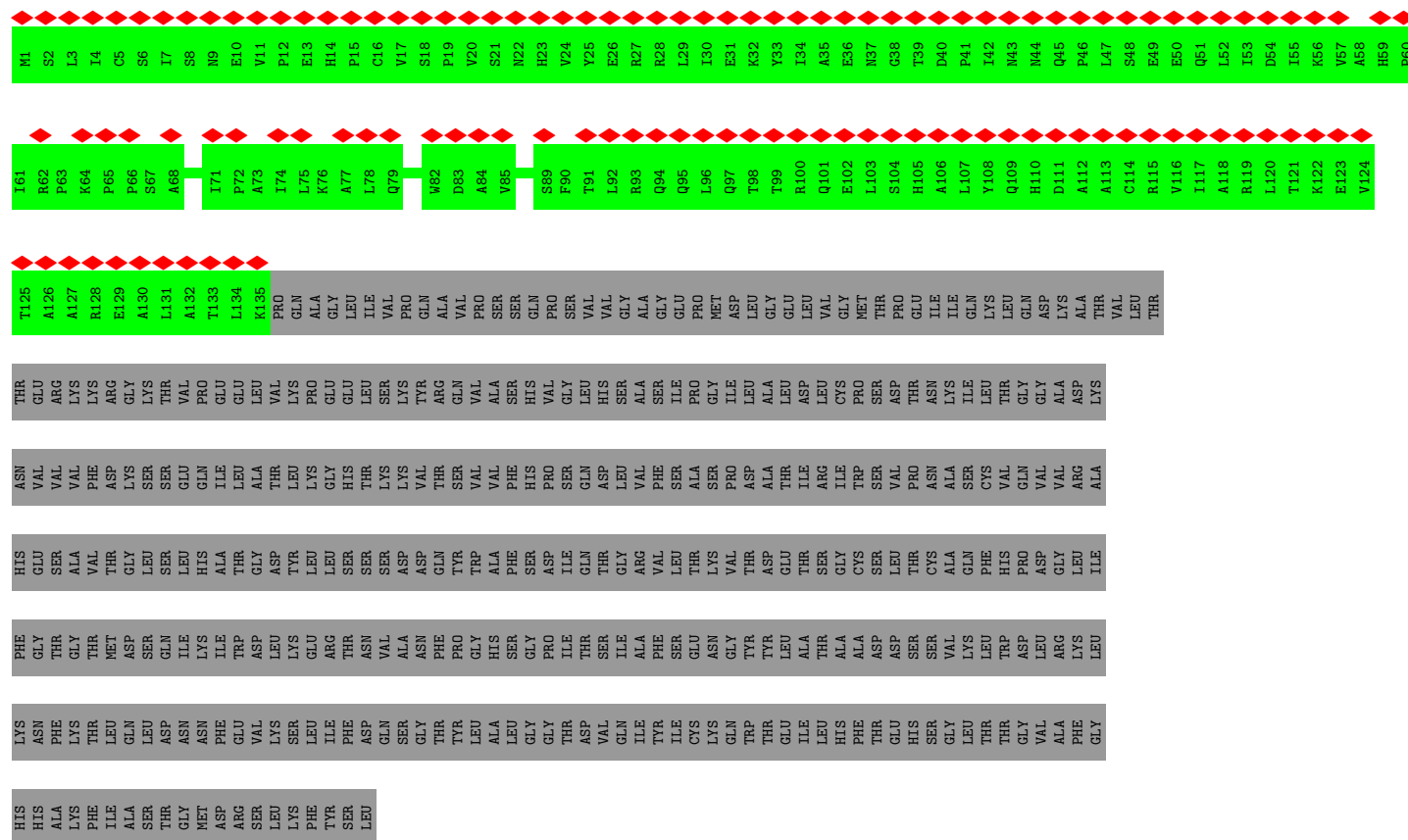
Chain q: 



LYS
PHE
TYR
SER
LEU

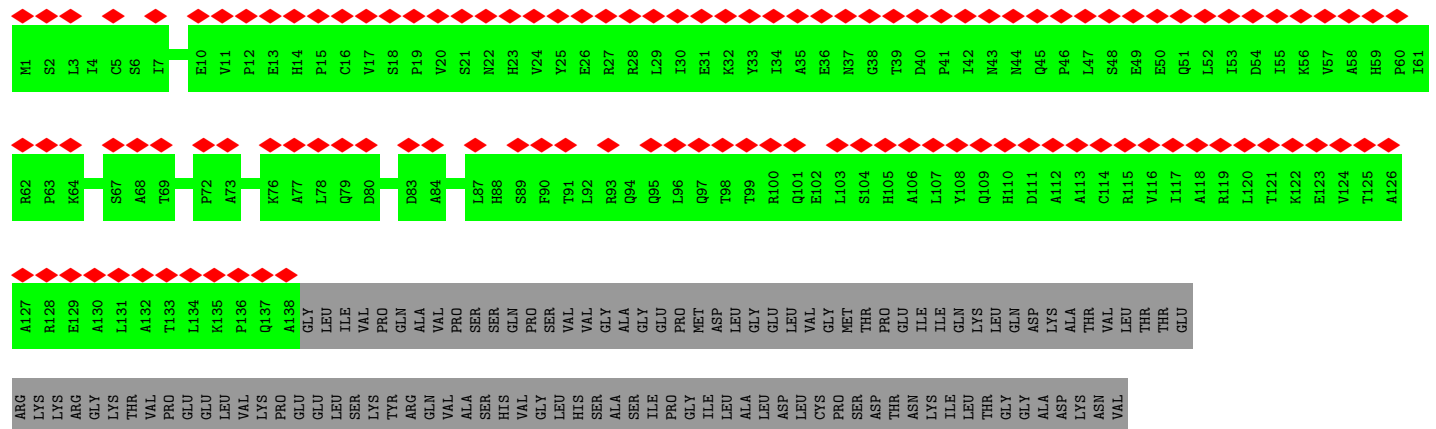
• Molecule 48: Pre-mRNA-processing factor 19

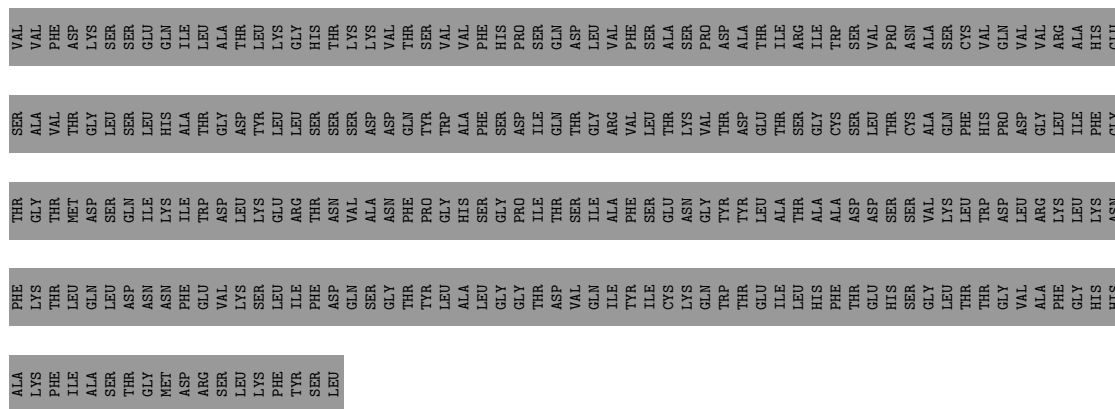
Chain r:  24%
27% 73%



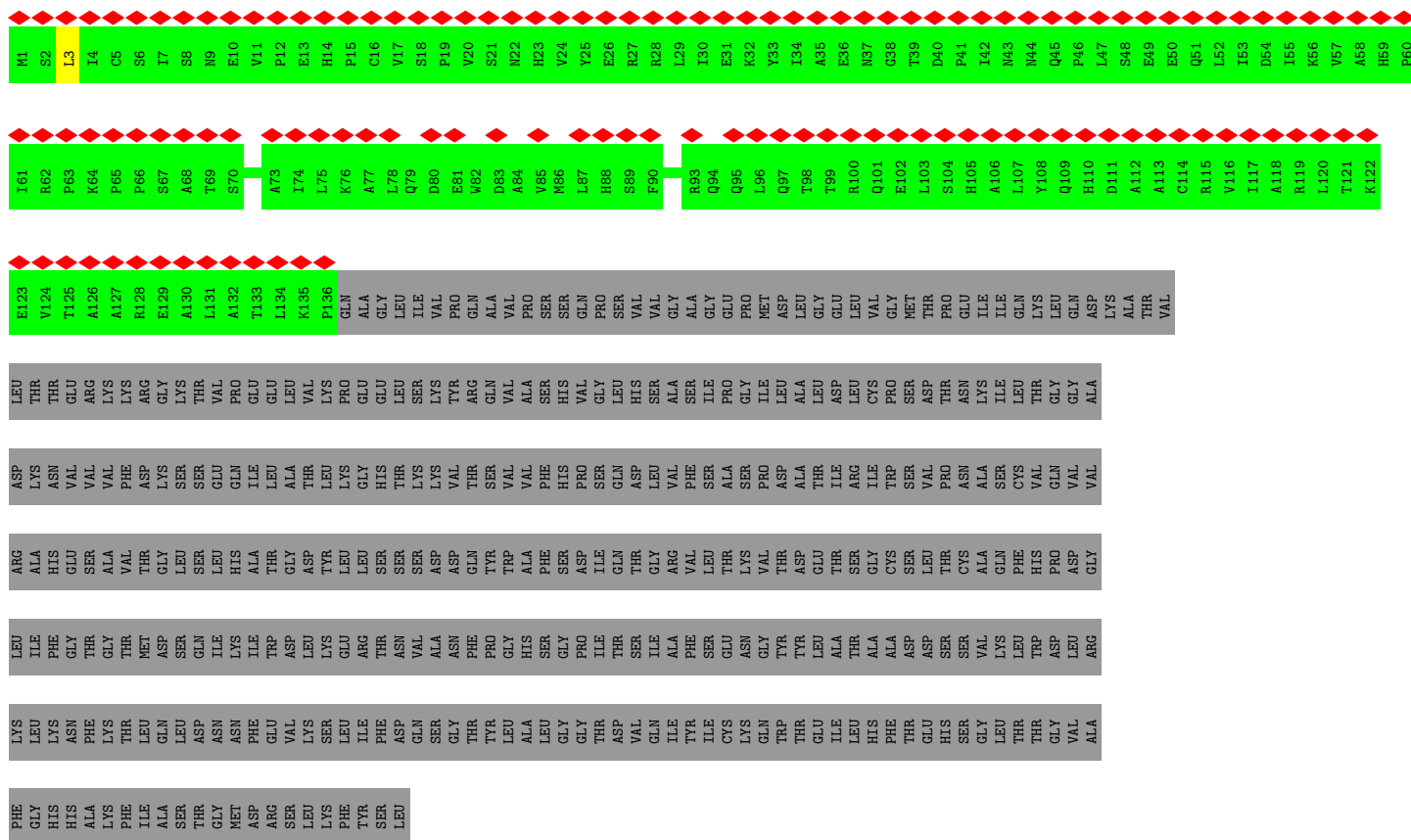
• Molecule 48: Pre-mRNA-processing factor 19

Chain s:  24%
27% 73%

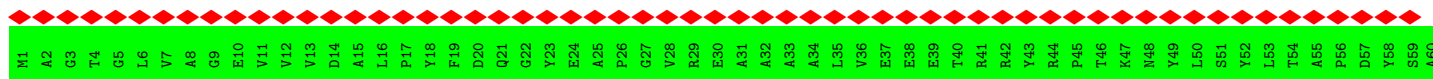


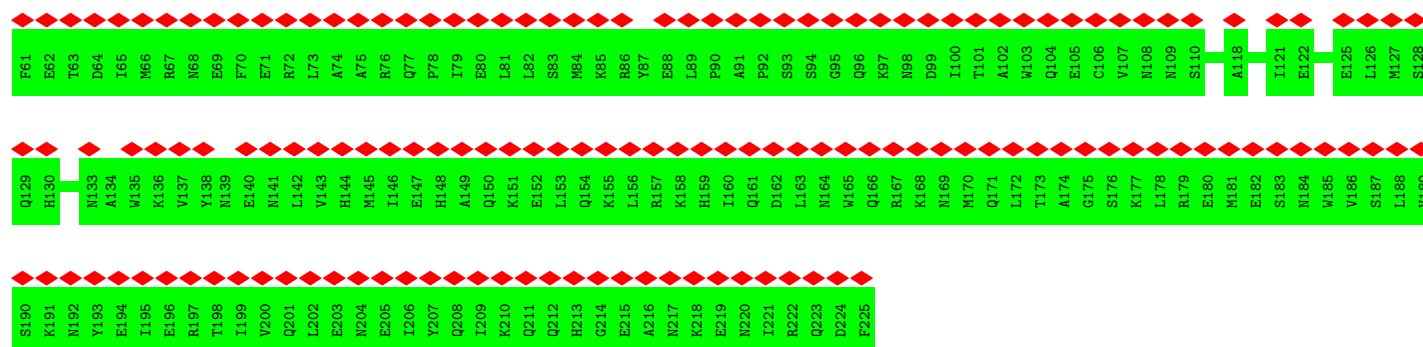


- Molecule 48: Pre-mRNA-processing factor 19



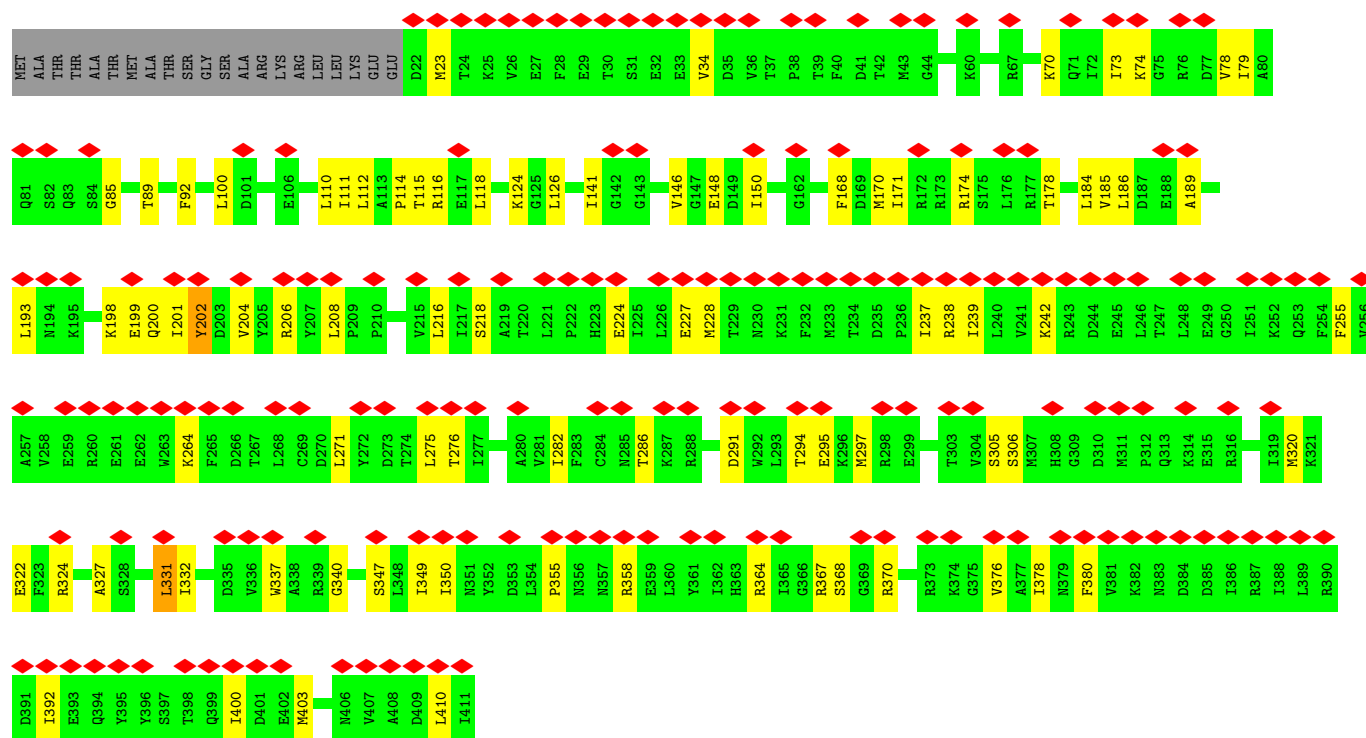
- Molecule 49: Pre-mRNA-splicing factor SPF27





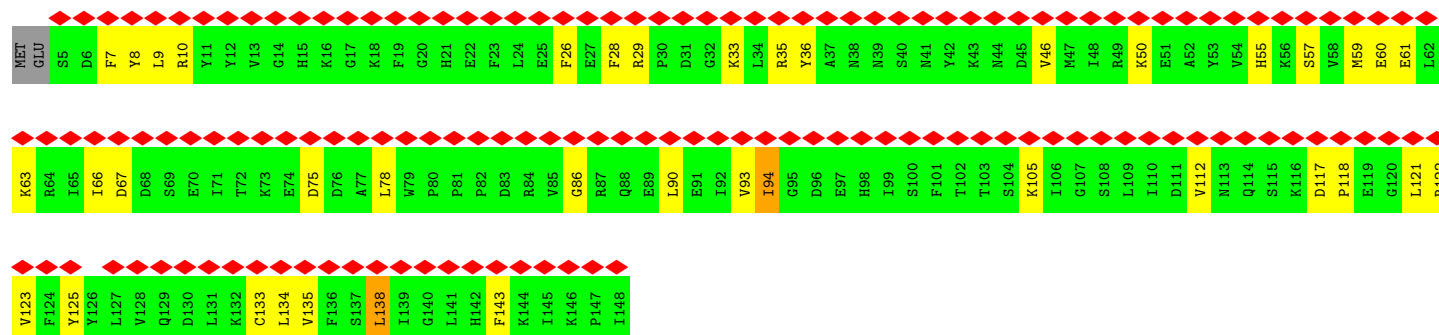
• Molecule 50: Eukaryotic initiation factor 4A-III

Chain v:



• Molecule 51: Protein mago nashi homolog

Chain w:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	145908	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.879	Depositor
Minimum map value	-1.241	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.36	Depositor
Map size (Å)	689.472, 689.472, 689.472	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0773, 1.0773, 1.0773	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G5J, GTP, ZN, ATP, IHP, SEP, ADP, K, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.27	0/595	0.58	2/925 (0.2%)
2	1	0.29	0/1285	0.50	2/1991 (0.1%)
3	2	0.24	0/1005	0.29	0/1561
4	4	0.16	0/3354	0.39	0/4515
5	5	0.31	0/2559	0.45	4/3977 (0.1%)
6	6	0.27	0/2687	0.38	1/4178 (0.0%)
7	A	0.31	0/19453	0.42	1/26385 (0.0%)
8	B	0.32	0/7283	0.49	0/9895
9	C	0.16	0/15420	0.41	0/20908
10	D	0.14	0/2461	0.35	0/3334
11	E	0.21	0/3959	0.39	0/5392
12	F	0.17	0/4968	0.45	0/6796
13	G	0.19	0/4487	0.42	0/6122
14	H	0.18	0/323	0.59	0/433
15	I	0.14	0/237	0.53	0/329
16	J	0.28	0/1817	0.55	0/2446
17	K	0.35	0/3089	0.47	0/4223
18	L	0.24	0/1160	0.39	1/1559 (0.1%)
19	L2	0.15	0/471	0.51	0/656
20	L3	0.15	0/420	0.40	0/584
21	L4	0.14	0/395	0.38	0/549
22	L5	0.12	0/401	0.40	0/555
23	L6	0.12	0/367	0.37	0/508
24	L7	0.13	0/436	0.38	0/604
25	L8	0.13	0/471	0.37	0/653
26	M	0.21	0/1314	0.56	0/1793
27	N	0.25	0/857	0.41	0/1138
28	O	0.15	0/775	0.37	0/1070
29	P	0.13	0/389	0.41	0/540
30	Q	0.14	0/6575	0.38	0/9165
31	R	0.12	0/790	0.35	0/1094
32	S	0.26	0/2303	0.48	0/3097

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	T	0.23	0/6355	0.54	0/8596
34	U	0.29	0/883	0.53	0/1198
35	V	0.22	0/3835	0.46	0/5164
36	W	0.26	0/2841	0.47	0/3851
37	X	0.20	0/1293	0.46	0/1749
38	Y	0.22	0/503	0.38	0/672
39	Z	0.21	0/236	0.39	0/312
40	a	0.16	0/599	0.49	0/798
40	h	0.14	0/358	0.44	0/495
41	b	0.24	0/657	0.54	0/888
41	i	0.19	0/400	0.48	0/556
42	c	0.19	0/805	0.48	0/1081
42	j	0.15	0/485	0.49	0/674
43	d	0.22	0/671	0.55	0/904
43	k	0.13	0/398	0.35	0/552
44	e	0.29	0/646	0.77	0/867
44	l	0.15	0/380	0.47	0/528
45	f	0.28	0/579	0.71	0/783
45	m	0.14	0/355	0.41	0/490
46	g	0.35	0/584	0.73	0/779
46	n	0.16	0/363	0.42	0/501
47	p	0.12	0/264	0.37	0/365
48	q	0.14	0/683	0.32	0/954
48	r	0.18	0/673	0.33	0/940
48	s	0.15	0/688	0.39	0/961
48	t	0.15	0/678	0.35	0/947
49	u	0.15	0/1116	0.33	0/1554
50	v	0.23	0/3179	0.48	0/4291
51	w	0.26	0/1225	0.61	1/1648 (0.1%)
52	x	0.28	0/748	0.55	0/1012
53	y	0.11	0/752	0.36	0/1044
54	z	0.21	0/950	0.48	0/1267
All	All	0.24	0/126288	0.45	12/173396 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	14	G	P-O3'-C3'	-7.64	108.74	120.20
5	5	95	G	P-O3'-C3'	-6.89	109.87	120.20
5	5	96	A	P-O3'-C3'	-6.64	110.23	120.20
1	0	-8	C	P-O3'-C3'	-6.34	110.69	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	w	94	ILE	N-CA-C	-6.24	106.24	112.17

There are no chirality outliers.

There are no planarity outliers.

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	0	533	0	272	6	0
2	1	1155	0	586	13	0
3	2	898	0	451	9	0
4	4	3283	0	3269	33	0
5	5	2296	0	1163	25	0
6	6	2439	0	1216	21	0
7	A	18932	0	18817	138	0
8	B	7122	0	7132	84	0
9	C	15118	0	14962	195	0
10	D	2406	0	2342	27	0
11	E	3925	0	3079	18	0
12	F	4897	0	3855	56	0
13	G	4412	0	3489	24	0
14	H	320	0	312	2	0
15	I	238	0	111	0	0
16	J	1815	0	1723	21	0
17	K	3014	0	2792	20	0
18	L	1139	0	1136	18	0
19	L2	472	0	204	0	0
20	L3	421	0	175	0	0
21	L4	396	0	165	0	0
22	L5	402	0	167	0	0
23	L6	368	0	163	0	0
24	L7	437	0	186	1	0
25	L8	472	0	219	0	0
26	M	1292	0	1233	32	0
27	N	845	0	829	5	0
28	O	776	0	358	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P	390	0	190	2	0
30	Q	6579	0	2831	1	0
31	R	791	0	347	0	0
32	S	2249	0	2193	27	0
33	T	6236	0	6292	125	0
34	U	874	0	702	31	0
35	V	3768	0	3833	34	0
36	W	2764	0	2717	29	0
37	X	1243	0	1165	14	0
38	Y	494	0	496	6	0
39	Z	234	0	232	2	0
40	a	591	0	613	7	0
40	h	360	0	149	0	0
41	b	649	0	693	8	0
41	i	401	0	165	0	0
42	c	796	0	821	25	0
42	j	487	0	199	0	0
43	d	663	0	680	11	0
43	k	399	0	176	0	0
44	e	638	0	657	19	0
44	l	381	0	159	1	0
45	f	567	0	575	25	0
45	m	356	0	156	0	0
46	g	577	0	603	23	0
46	n	364	0	160	0	0
47	p	265	0	114	0	0
48	q	684	0	308	1	0
48	r	674	0	305	0	0
48	s	689	0	313	0	0
48	t	679	0	306	1	0
49	u	1117	0	514	0	0
50	v	3130	0	3173	67	0
51	w	1196	0	1182	26	0
52	x	730	0	690	18	0
53	y	751	0	350	2	0
54	z	933	0	947	15	0
55	1	2	0	0	0	0
55	6	4	0	0	0	0
55	B	1	0	0	0	0
55	C	1	0	0	0	0
55	v	1	0	0	0	0
56	6	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	A	36	0	6	0	0
58	B	32	0	12	1	0
59	C	54	0	24	0	0
60	S	1	0	0	0	0
61	v	31	0	12	0	0
62	6	1	0	0	0	0
All	All	123688	0	105466	1152	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 5.

The worst 5 of 1152 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)
32:S:65:GLN:O	32:S:69:SER:HB2	1.61	0.99
33:T:1151:TYR:HB3	33:T:1162:MET:HG2	1.44	0.97
9:C:1001:TYR:O	9:C:1005:LEU:HB2	1.70	0.91
46:g:45:CYS:HB3	46:g:57:ILE:HG13	1.59	0.84
7:A:362:ARG:HG3	7:A:364:SER:H	1.45	0.81

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	
4	4	403/646 (62%)	396 (98%)	7 (2%)	0	100	100
7	A	2277/2335 (98%)	2203 (97%)	74 (3%)	0	100	100
8	B	898/972 (92%)	832 (93%)	62 (7%)	4 (0%)	30	65
9	C	1917/2136 (90%)	1824 (95%)	87 (4%)	6 (0%)	36	70
10	D	306/357 (86%)	298 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	E	596/802 (74%)	583 (98%)	13 (2%)	0	100	100
12	F	733/855 (86%)	695 (95%)	36 (5%)	2 (0%)	36	70
13	G	637/848 (75%)	611 (96%)	26 (4%)	0	100	100
14	H	42/166 (25%)	38 (90%)	4 (10%)	0	100	100
15	I	46/285 (16%)	45 (98%)	1 (2%)	0	100	100
16	J	227/536 (42%)	206 (91%)	18 (8%)	3 (1%)	9	38
17	K	400/514 (78%)	382 (96%)	18 (4%)	0	100	100
18	L	137/367 (37%)	133 (97%)	4 (3%)	0	100	100
19	L2	93/95 (98%)	88 (95%)	5 (5%)	0	100	100
20	L3	83/102 (81%)	82 (99%)	1 (1%)	0	100	100
21	L4	78/139 (56%)	75 (96%)	3 (4%)	0	100	100
22	L5	80/91 (88%)	74 (92%)	6 (8%)	0	100	100
23	L6	73/80 (91%)	70 (96%)	3 (4%)	0	100	100
24	L7	87/103 (84%)	85 (98%)	2 (2%)	0	100	100
25	L8	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
26	M	171/198 (86%)	163 (95%)	7 (4%)	1 (1%)	21	56
27	N	94/229 (41%)	85 (90%)	9 (10%)	0	100	100
28	O	157/166 (95%)	149 (95%)	8 (5%)	0	100	100
29	P	77/301 (26%)	76 (99%)	1 (1%)	0	100	100
30	Q	1319/1485 (89%)	1289 (98%)	30 (2%)	0	100	100
31	R	159/161 (99%)	157 (99%)	2 (1%)	0	100	100
32	S	268/586 (46%)	253 (94%)	15 (6%)	0	100	100
33	T	776/1220 (64%)	714 (92%)	61 (8%)	1 (0%)	48	80
34	U	126/2752 (5%)	123 (98%)	2 (2%)	1 (1%)	16	50
35	V	460/908 (51%)	452 (98%)	6 (1%)	2 (0%)	30	65
36	W	344/544 (63%)	314 (91%)	30 (9%)	0	100	100
37	X	140/758 (18%)	133 (95%)	7 (5%)	0	100	100
38	Y	57/112 (51%)	56 (98%)	1 (2%)	0	100	100
39	Z	29/415 (7%)	21 (72%)	8 (28%)	0	100	100
40	a	69/240 (29%)	69 (100%)	0	0	100	100
40	h	69/240 (29%)	69 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	b	80/119 (67%)	78 (98%)	2 (2%)	0	100	100
41	i	79/119 (66%)	76 (96%)	3 (4%)	0	100	100
42	c	94/118 (80%)	92 (98%)	2 (2%)	0	100	100
42	j	94/118 (80%)	90 (96%)	4 (4%)	0	100	100
43	d	83/126 (66%)	81 (98%)	2 (2%)	0	100	100
43	k	79/126 (63%)	74 (94%)	5 (6%)	0	100	100
44	e	75/92 (82%)	72 (96%)	3 (4%)	0	100	100
44	l	75/92 (82%)	75 (100%)	0	0	100	100
45	f	71/86 (83%)	69 (97%)	2 (3%)	0	100	100
45	m	71/86 (83%)	71 (100%)	0	0	100	100
46	g	72/76 (95%)	66 (92%)	5 (7%)	1 (1%)	9	36
46	n	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
47	p	48/476 (10%)	47 (98%)	1 (2%)	0	100	100
48	q	135/504 (27%)	133 (98%)	2 (2%)	0	100	100
48	r	133/504 (26%)	130 (98%)	3 (2%)	0	100	100
48	s	136/504 (27%)	134 (98%)	2 (2%)	0	100	100
48	t	134/504 (27%)	131 (98%)	3 (2%)	0	100	100
49	u	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
50	v	388/411 (94%)	373 (96%)	15 (4%)	0	100	100
51	w	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
52	x	89/174 (51%)	84 (94%)	5 (6%)	0	100	100
53	y	143/413 (35%)	141 (99%)	2 (1%)	0	100	100
54	z	112/233 (48%)	105 (94%)	7 (6%)	0	100	100
All	All	16150/27168 (59%)	15479 (96%)	650 (4%)	21 (0%)	49	80

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	480	THR
9	C	1996	LEU
12	F	354	PRO
35	V	559	SER
8	B	371	GLU

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	
4	4	363/572 (64%)	362 (100%)	1 (0%)	86	91
7	A	2063/2108 (98%)	2032 (98%)	31 (2%)	57	80
8	B	800/866 (92%)	776 (97%)	24 (3%)	36	69
9	C	1617/1908 (85%)	1605 (99%)	12 (1%)	76	86
10	D	264/300 (88%)	263 (100%)	1 (0%)	84	90
11	E	245/709 (35%)	238 (97%)	7 (3%)	37	70
12	F	327/749 (44%)	324 (99%)	3 (1%)	70	85
13	G	299/751 (40%)	296 (99%)	3 (1%)	68	84
14	H	26/143 (18%)	26 (100%)	0	100	100
16	J	171/457 (37%)	170 (99%)	1 (1%)	78	88
17	K	297/441 (67%)	292 (98%)	5 (2%)	53	78
18	L	119/326 (36%)	119 (100%)	0	100	100
26	M	135/171 (79%)	132 (98%)	3 (2%)	45	74
27	N	91/203 (45%)	88 (97%)	3 (3%)	33	67
32	S	240/520 (46%)	232 (97%)	8 (3%)	33	67
33	T	692/1085 (64%)	682 (99%)	10 (1%)	59	80
34	U	63/2432 (3%)	63 (100%)	0	100	100
35	V	420/838 (50%)	415 (99%)	5 (1%)	63	82
36	W	301/460 (65%)	296 (98%)	5 (2%)	53	78
37	X	126/655 (19%)	123 (98%)	3 (2%)	43	73
38	Y	53/99 (54%)	48 (91%)	5 (9%)	8	32
39	Z	25/366 (7%)	24 (96%)	1 (4%)	28	62
40	a	67/177 (38%)	66 (98%)	1 (2%)	57	80
41	b	77/101 (76%)	76 (99%)	1 (1%)	61	81
42	c	93/110 (84%)	91 (98%)	2 (2%)	45	74
43	d	74/101 (73%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	e	72/84 (86%)	68 (94%)	4 (6%)	19	52
45	f	61/74 (82%)	60 (98%)	1 (2%)	55	79
46	g	64/66 (97%)	62 (97%)	2 (3%)	35	68
47	p	1/395 (0%)	1 (100%)	0	100	100
50	v	345/361 (96%)	340 (99%)	5 (1%)	59	80
51	w	132/134 (98%)	126 (96%)	6 (4%)	24	59
52	x	76/143 (53%)	75 (99%)	1 (1%)	61	81
53	y	5/368 (1%)	5 (100%)	0	100	100
54	z	98/209 (47%)	96 (98%)	2 (2%)	48	76
All	All	9902/18482 (54%)	9746 (98%)	156 (2%)	54	79

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	V	452	LEU
50	v	186	LEU
36	W	290	LEU
39	Z	353	VAL
51	w	67	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
33	T	1054	ASN
40	a	22	GLN
33	T	1152	HIS
35	V	270	HIS
42	c	49	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	24/57 (42%)	10 (41%)	2 (8%)
2	1	52/277 (18%)	26 (50%)	3 (5%)
3	2	40/150 (26%)	9 (22%)	0
5	5	107/117 (91%)	25 (23%)	1 (0%)
6	6	110/125 (88%)	31 (28%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	333/726 (45%)	101 (30%)	8 (2%)

5 of 101 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	-24	A
1	0	-17	A
1	0	-15	C
1	0	-14	C
1	0	-13	G

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	6	121	U
6	6	65	U
2	1	195	U
2	1	186	A
5	5	105	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	SEP	J	224	16	8,9,10	1.51	1 (12%)	8,12,14	1.68	2 (25%)
16	SEP	J	232	16	8,9,10	1.54	1 (12%)	8,12,14	1.72	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	SEP	J	224	16	-	0/5/8/10	-
16	SEP	J	232	16	-	3/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	J	232	SEP	P-O1P	3.30	1.61	1.50
16	J	224	SEP	P-O1P	3.29	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	J	232	SEP	P-OG-CB	-3.37	109.00	118.30
16	J	224	SEP	P-OG-CB	-3.19	109.50	118.30
16	J	232	SEP	OG-CB-CA	3.01	111.07	108.14
16	J	224	SEP	OG-CB-CA	2.97	111.03	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	J	232	SEP	CB-OG-P-O2P
16	J	232	SEP	CB-OG-P-O3P
16	J	232	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 12 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	ADP	C	2202	55	27,29,29	1.35	4 (14%)	42,45,45	1.96	11 (26%)
57	IHP	A	3000	-	36,36,36	1.82	6 (16%)	54,60,60	1.36	5 (9%)
61	ATP	v	702	55	29,33,33	0.31	0	44,52,52	0.52	1 (2%)
58	GTP	B	1501	55	30,34,34	0.97	1 (3%)	46,54,54	1.75	10 (21%)
59	ADP	C	2201	-	27,29,29	1.36	4 (14%)	42,45,45	1.95	10 (23%)

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	ADP	C	2202	55	-	3/16/32/32	0/3/3/3
57	IHP	A	3000	-	-	3/30/54/54	0/1/1/1
61	ATP	v	702	55	-	1/22/38/38	0/3/3/3
58	GTP	B	1501	55	-	4/22/38/38	0/3/3/3
59	ADP	C	2201	-	-	3/16/32/32	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	A	3000	IHP	P2-O12	4.94	1.68	1.59
59	C	2201	ADP	C5-C4	4.57	1.47	1.39
59	C	2202	ADP	C5-C4	4.52	1.47	1.39
57	A	3000	IHP	P5-O15	4.17	1.67	1.59
57	A	3000	IHP	P6-O16	3.99	1.66	1.59

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	C	2201	ADP	C5-C4-N3	-6.16	118.72	126.75
59	C	2202	ADP	C5-C4-N3	-6.11	118.77	126.75
57	A	3000	IHP	O13-C3-C2	4.82	120.05	108.69
59	C	2202	ADP	N3-C4-N9	4.78	134.96	127.08
59	C	2201	ADP	N3-C4-N9	4.76	134.93	127.08

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

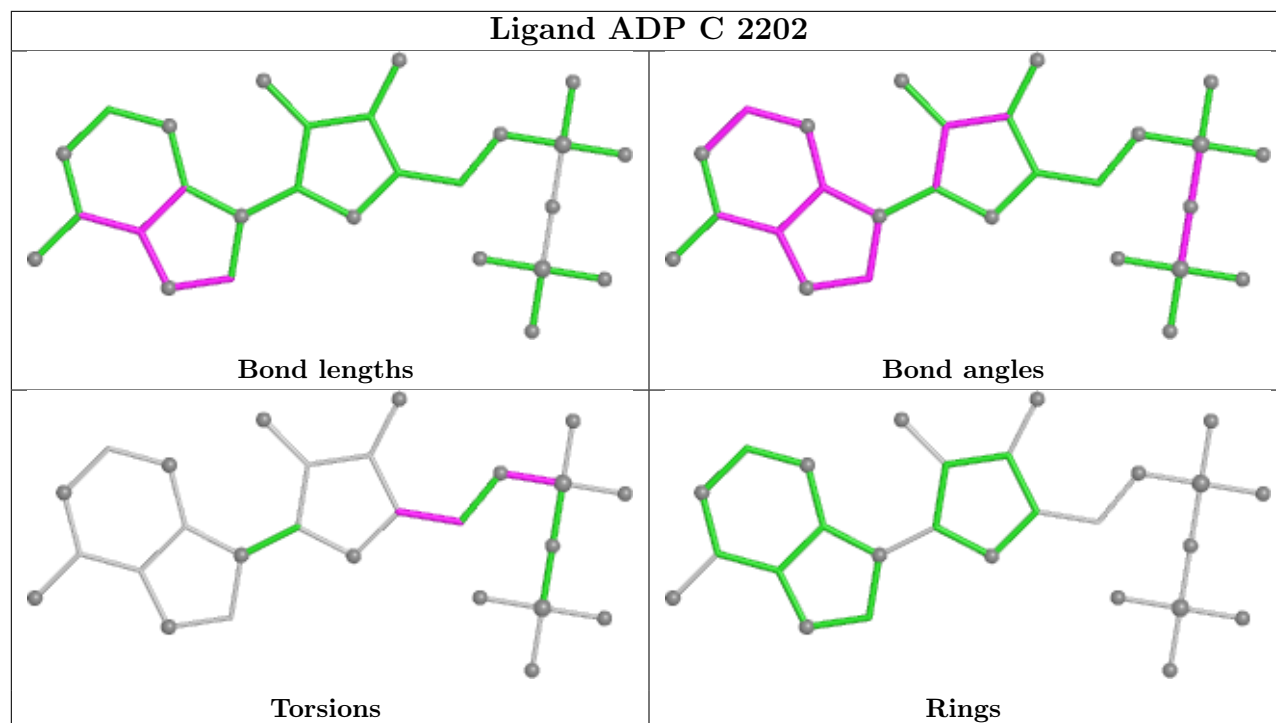
Mol	Chain	Res	Type	Atoms
57	A	3000	IHP	C2-C3-O13-P3
57	A	3000	IHP	C3-O13-P3-O33
57	A	3000	IHP	C6-O16-P6-O46
58	B	1501	GTP	C5'-O5'-PA-O1A
59	C	2201	ADP	C5'-O5'-PA-O1A

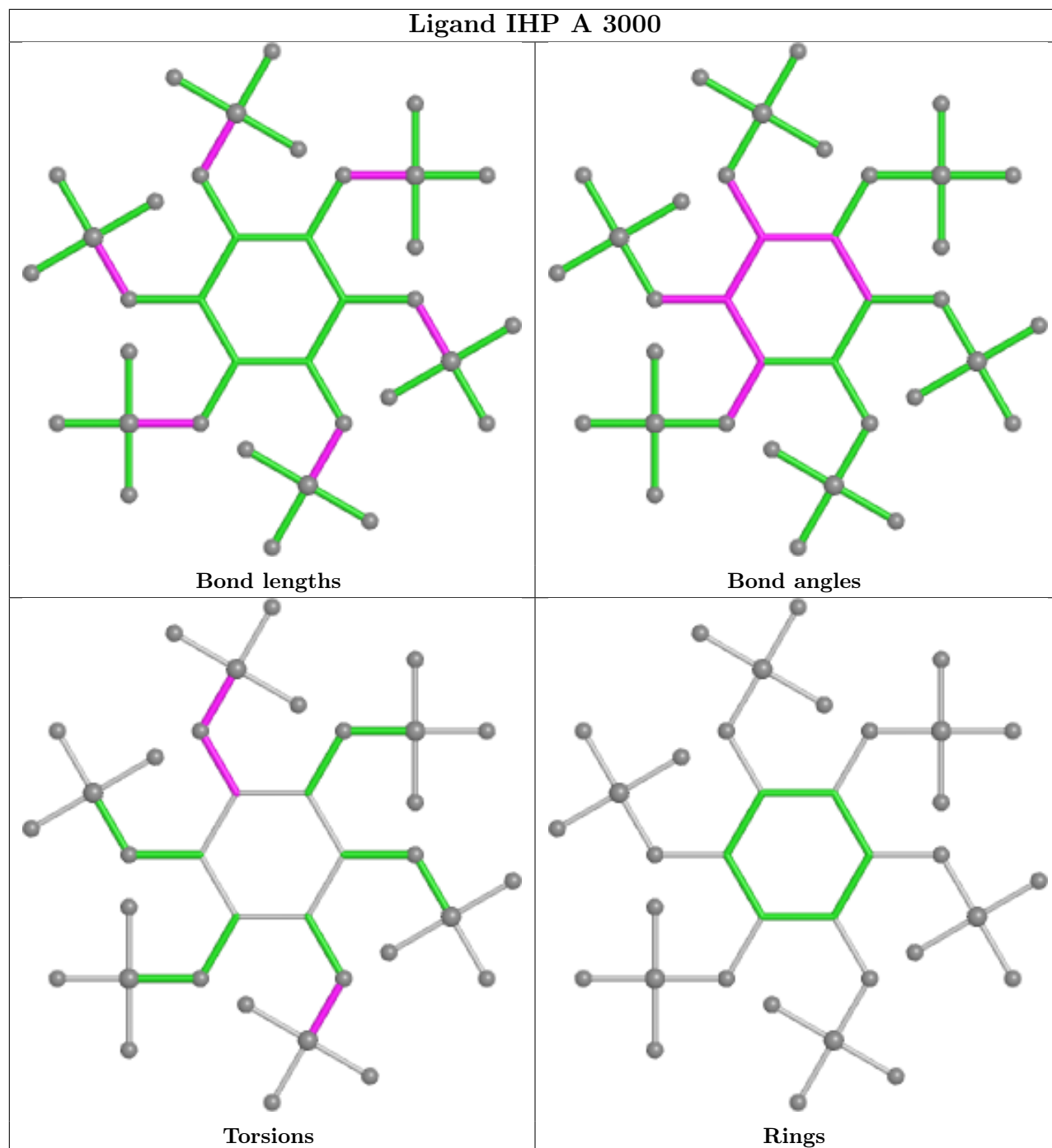
There are no ring outliers.

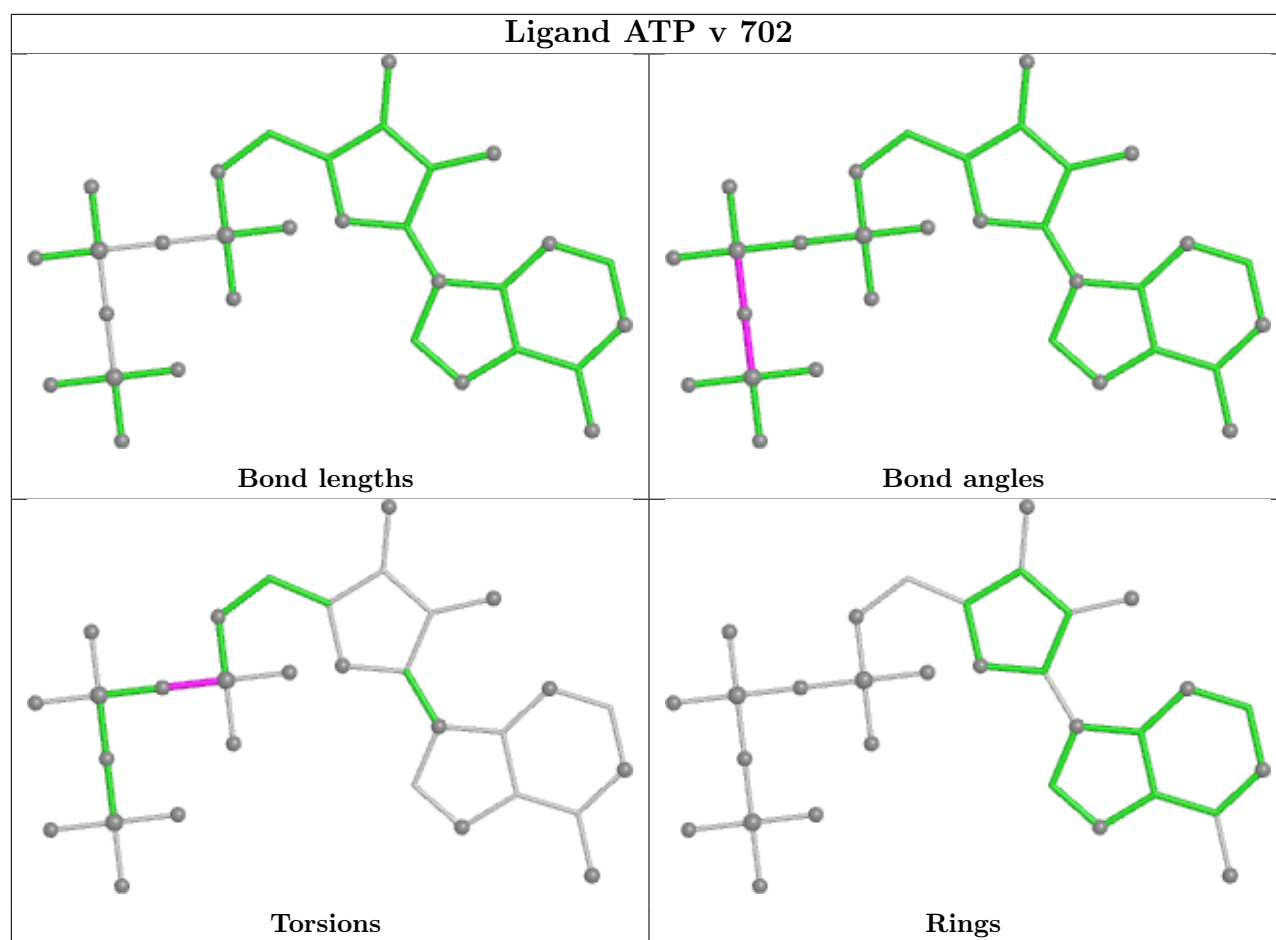
1 monomer is involved in 1 short contact:

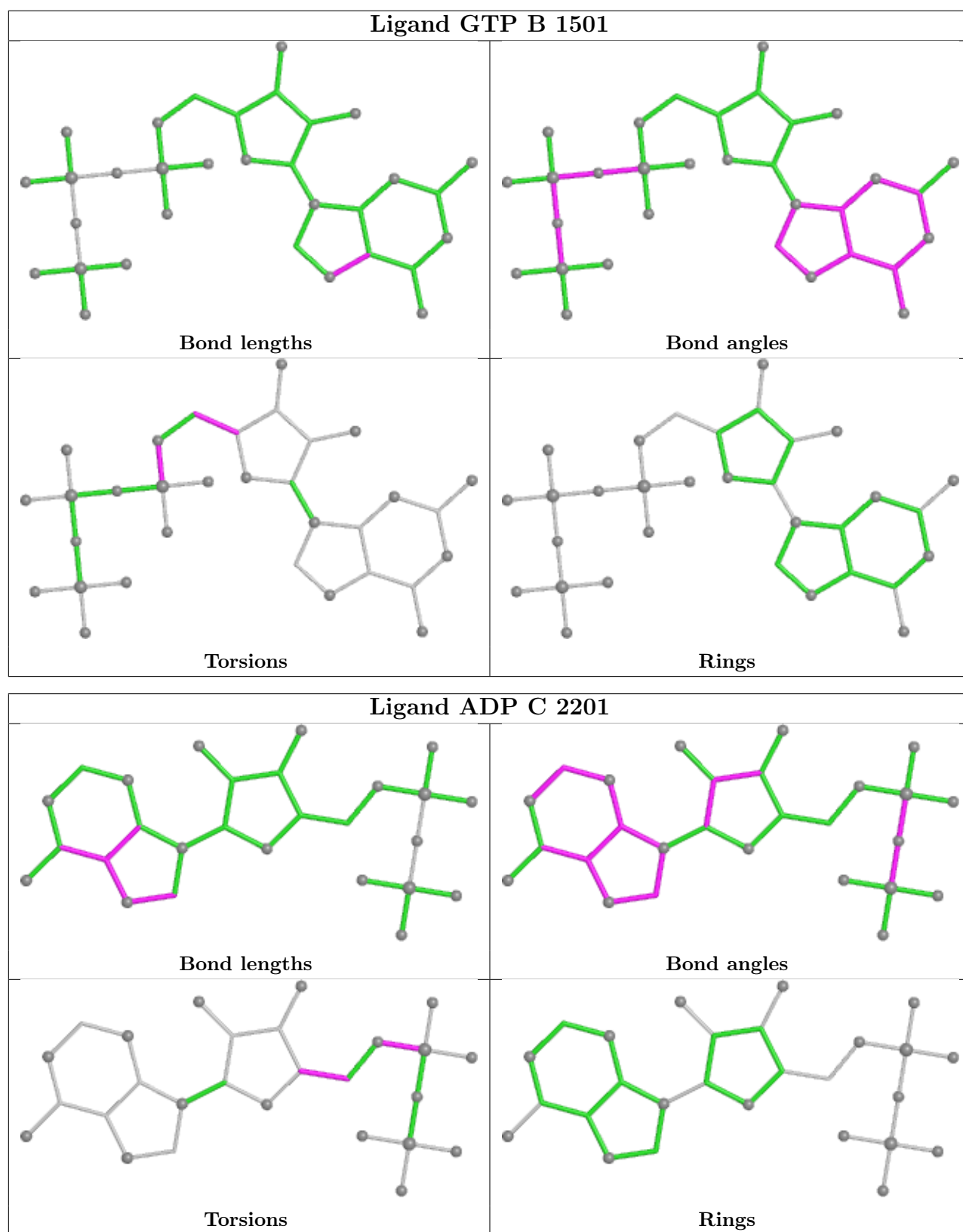
Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	B	1501	GTP	1	0

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

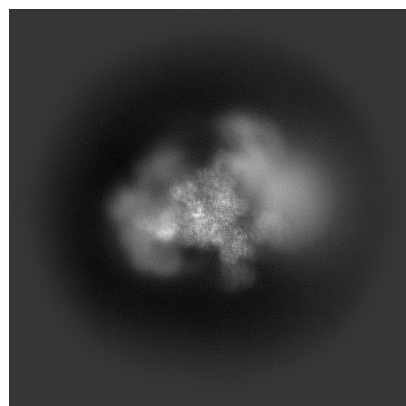
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-67263. These allow visual inspection of the internal detail of the map and identification of artifacts.

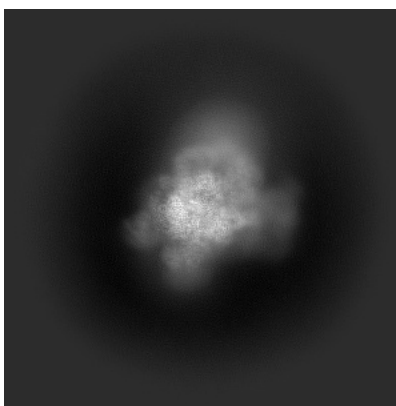
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

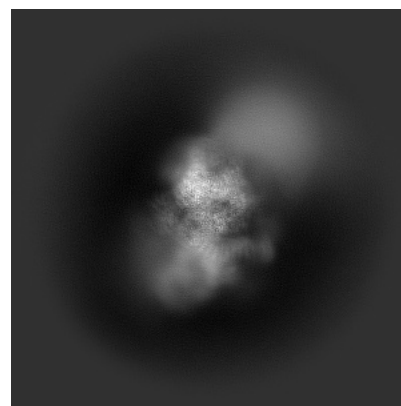
6.1.1 Primary map



X

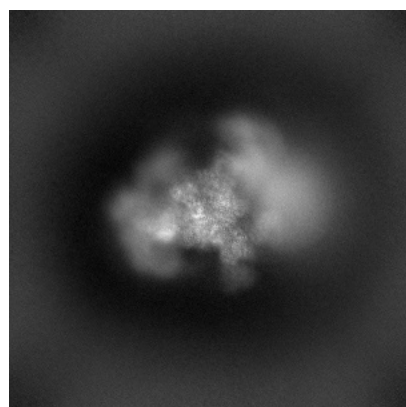


Y

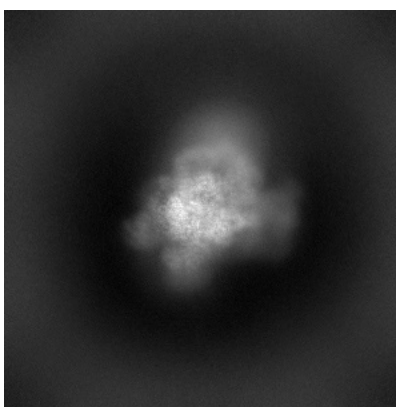


Z

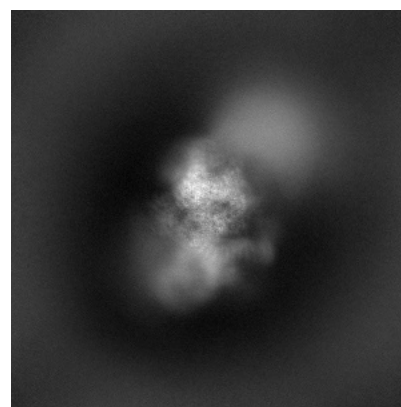
6.1.2 Raw map



X



Y

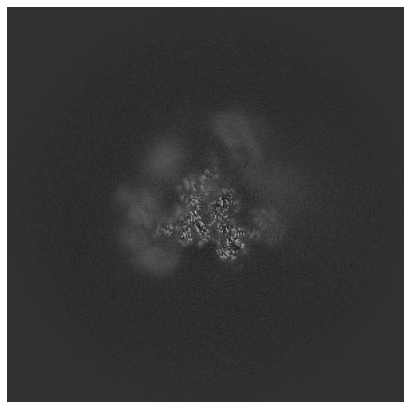


Z

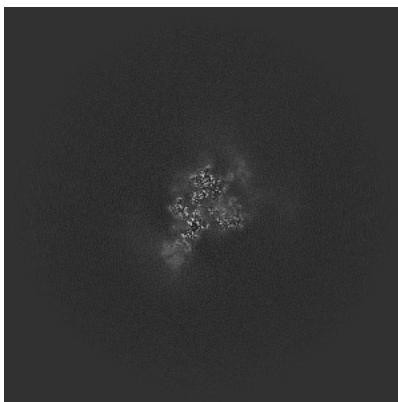
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

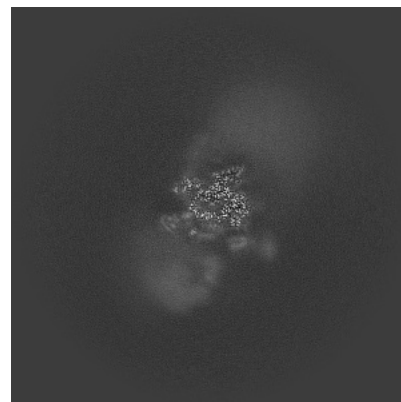
6.2.1 Primary map



X Index: 320

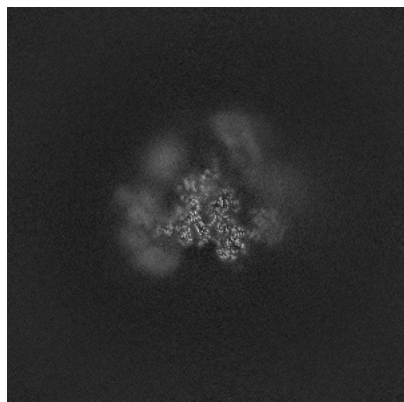


Y Index: 320

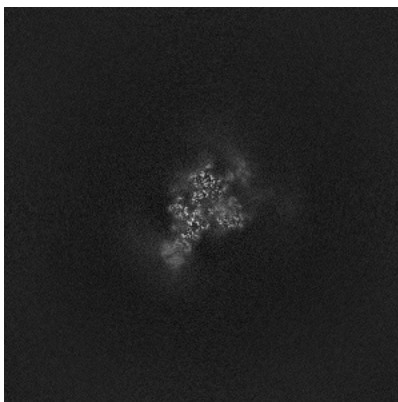


Z Index: 320

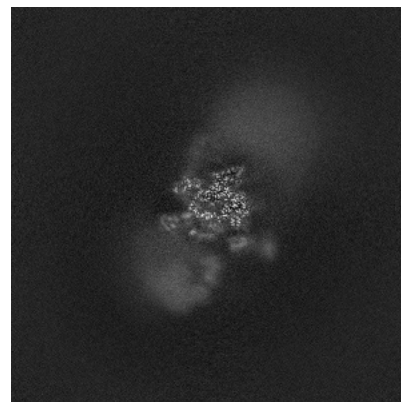
6.2.2 Raw map



X Index: 320



Y Index: 320

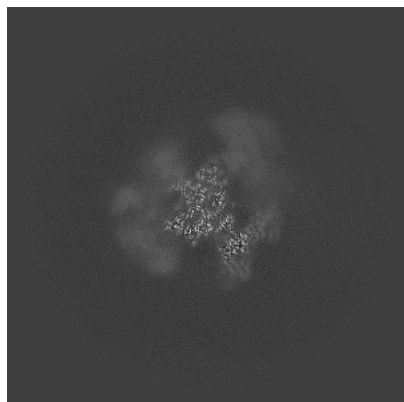


Z Index: 320

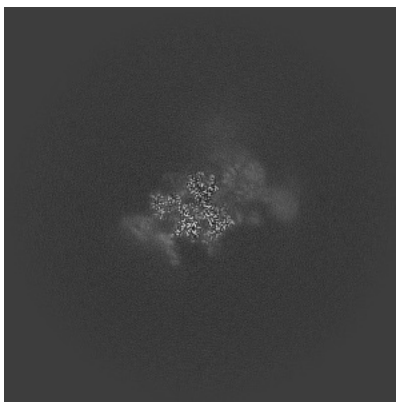
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

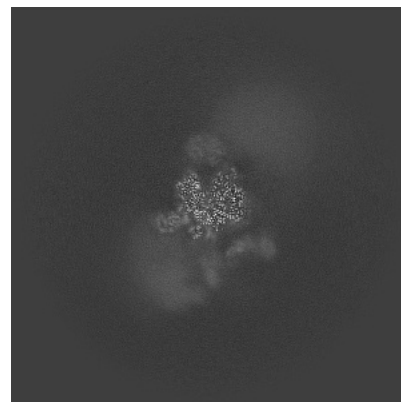
6.3.1 Primary map



X Index: 306

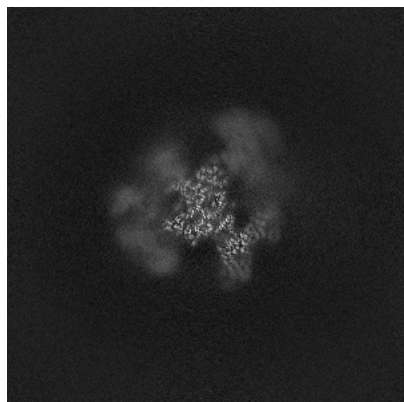


Y Index: 343

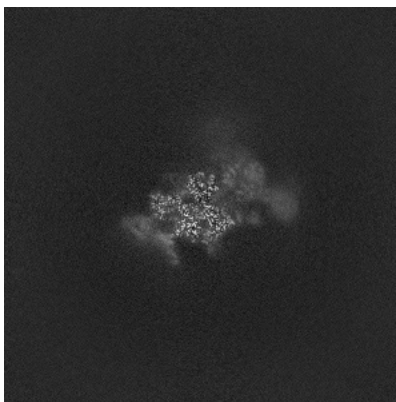


Z Index: 310

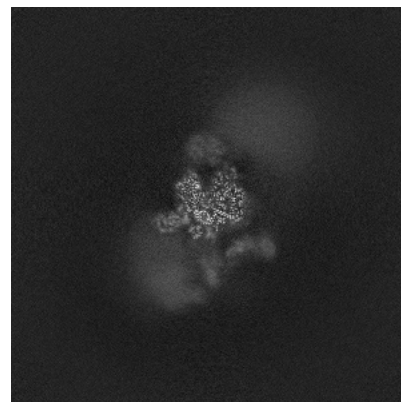
6.3.2 Raw map



X Index: 306



Y Index: 343

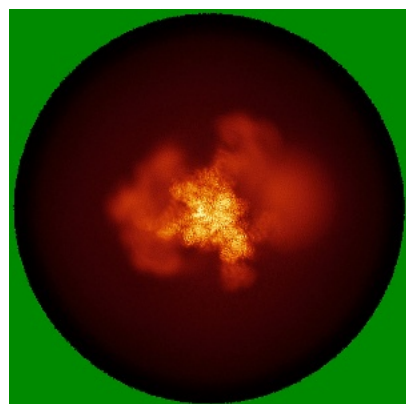


Z Index: 310

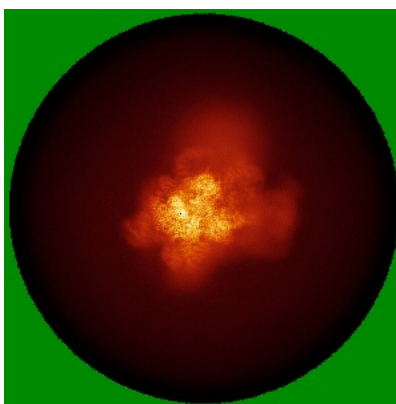
The images above show the largest variance slices of the map in three orthogonal directions.

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

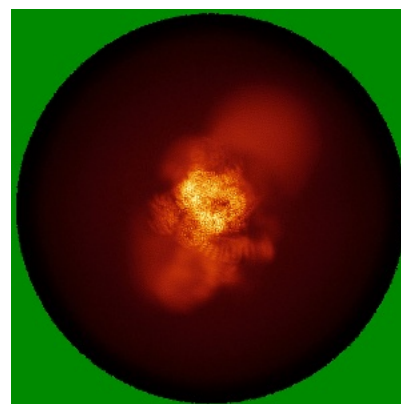
6.4.1 Primary map



X

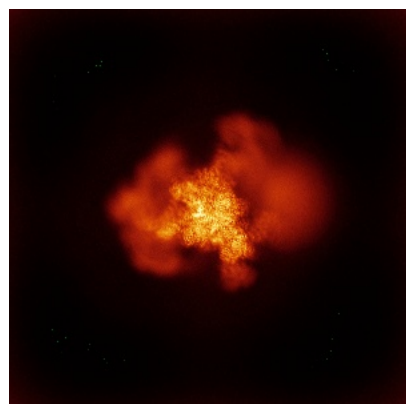


Y

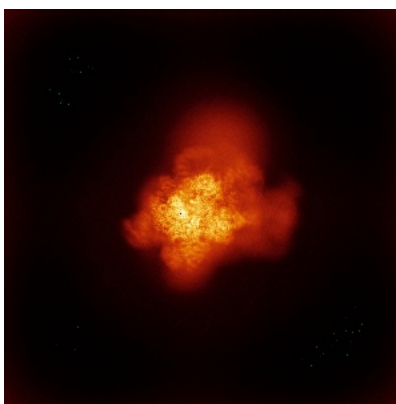


Z

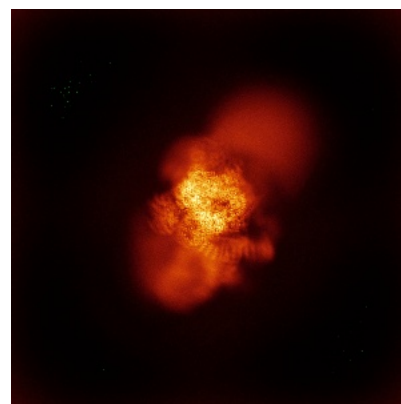
6.4.2 Raw map



X



Y

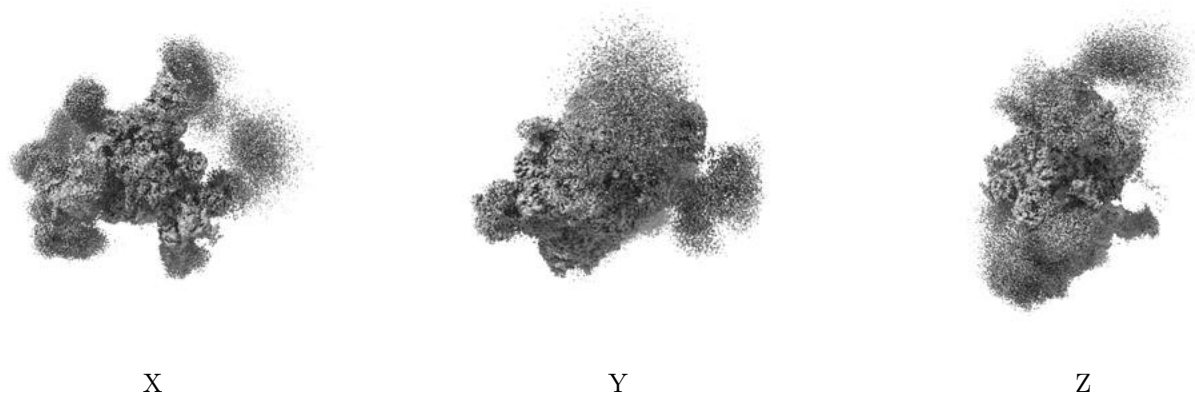


Z

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.

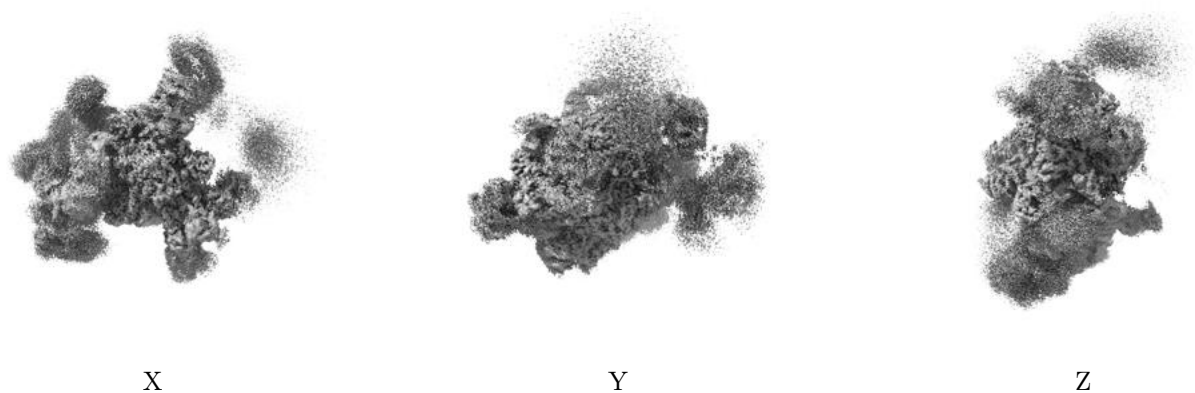
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.36. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

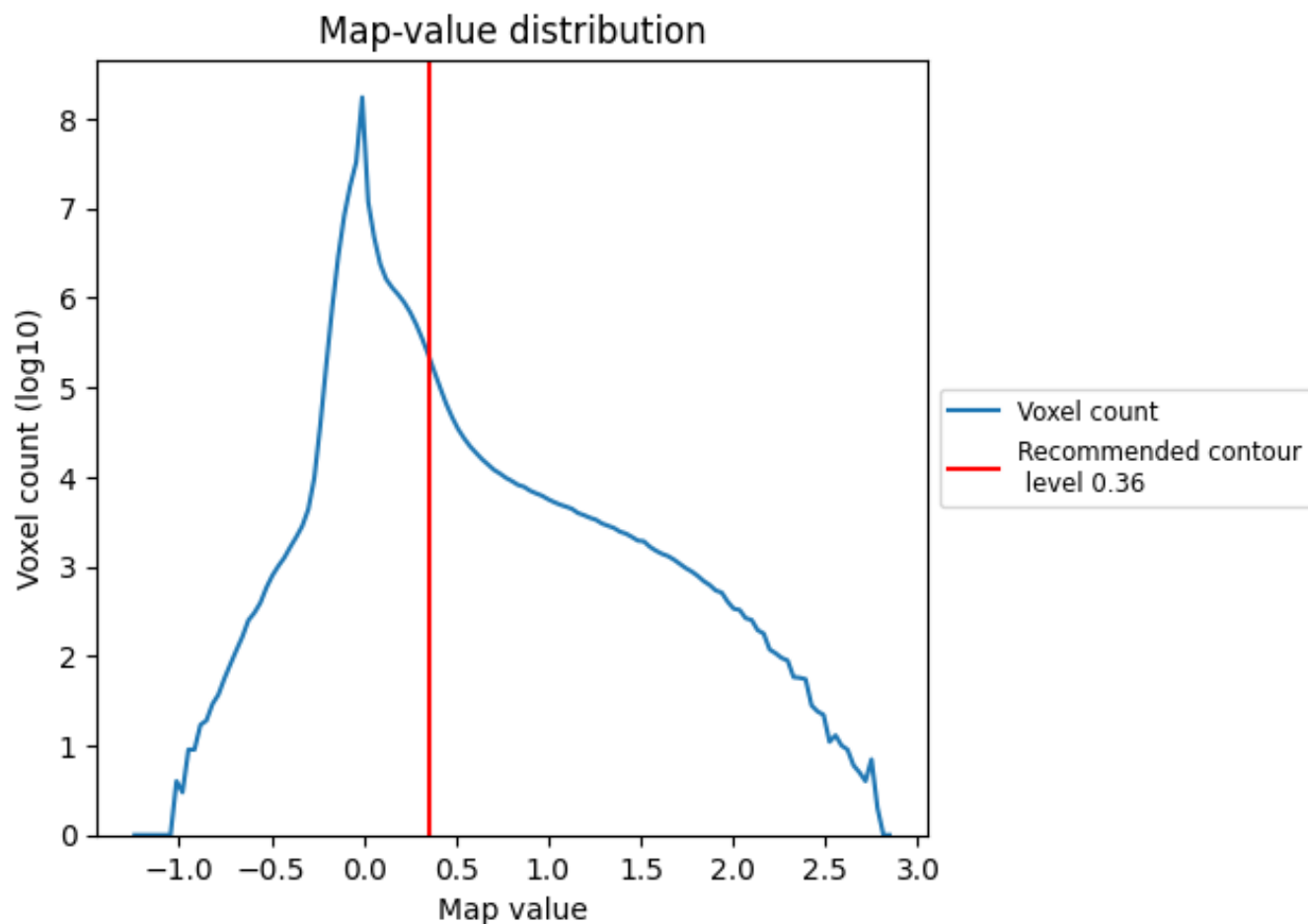
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

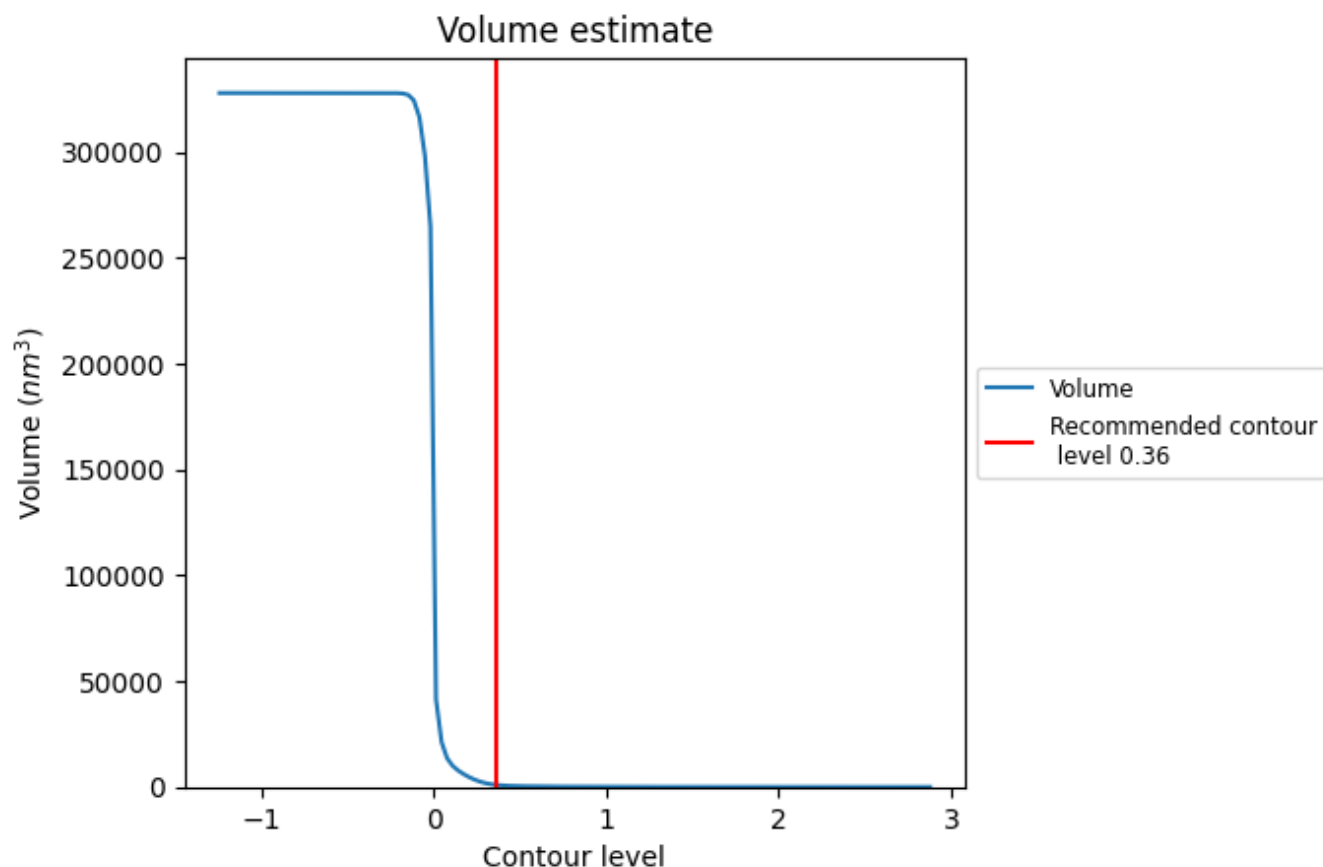
This section contains the results of statistical analysis of the map.

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.

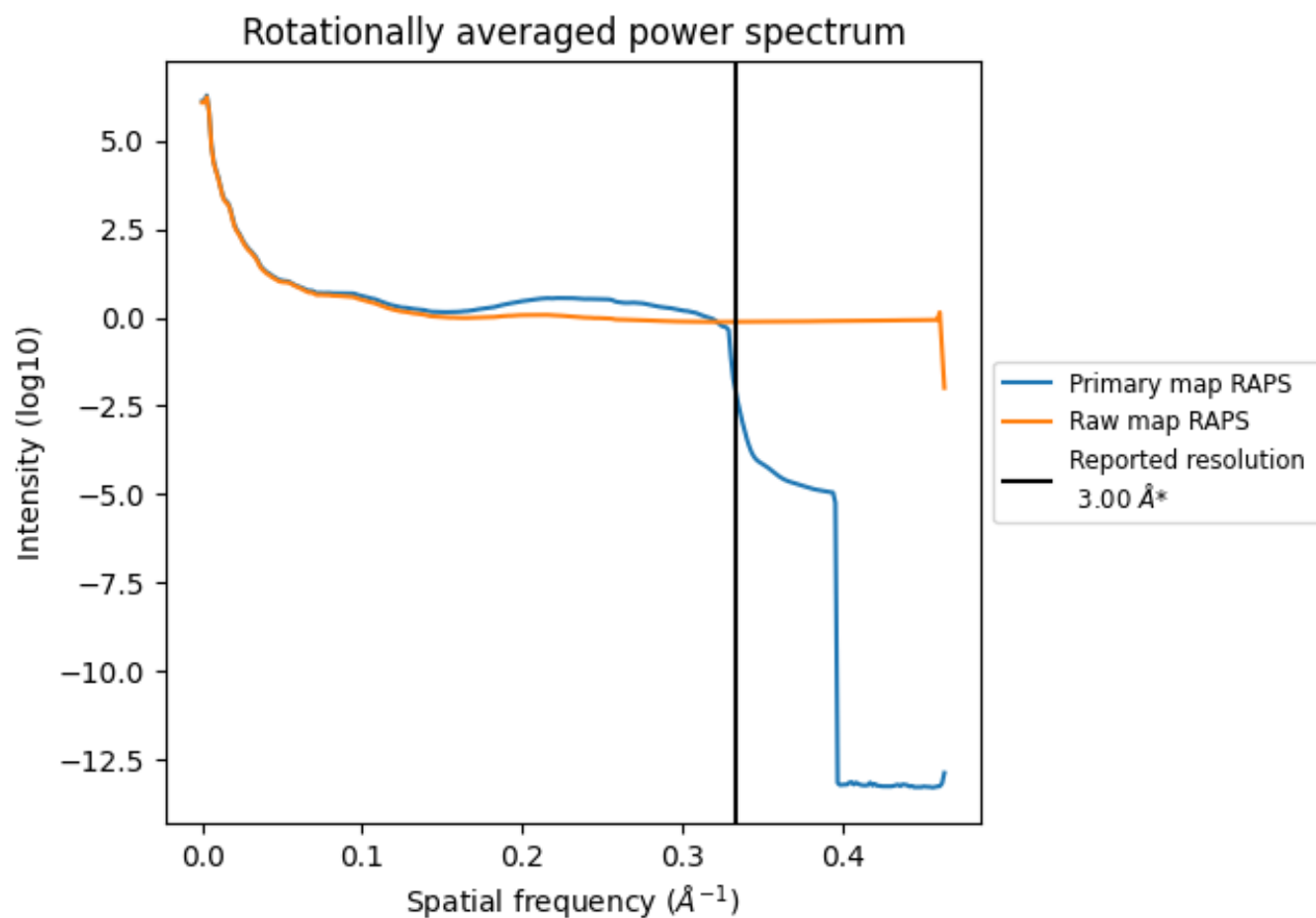
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 998 nm^3 ; this corresponds to an approximate mass of 902 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 ⓘ

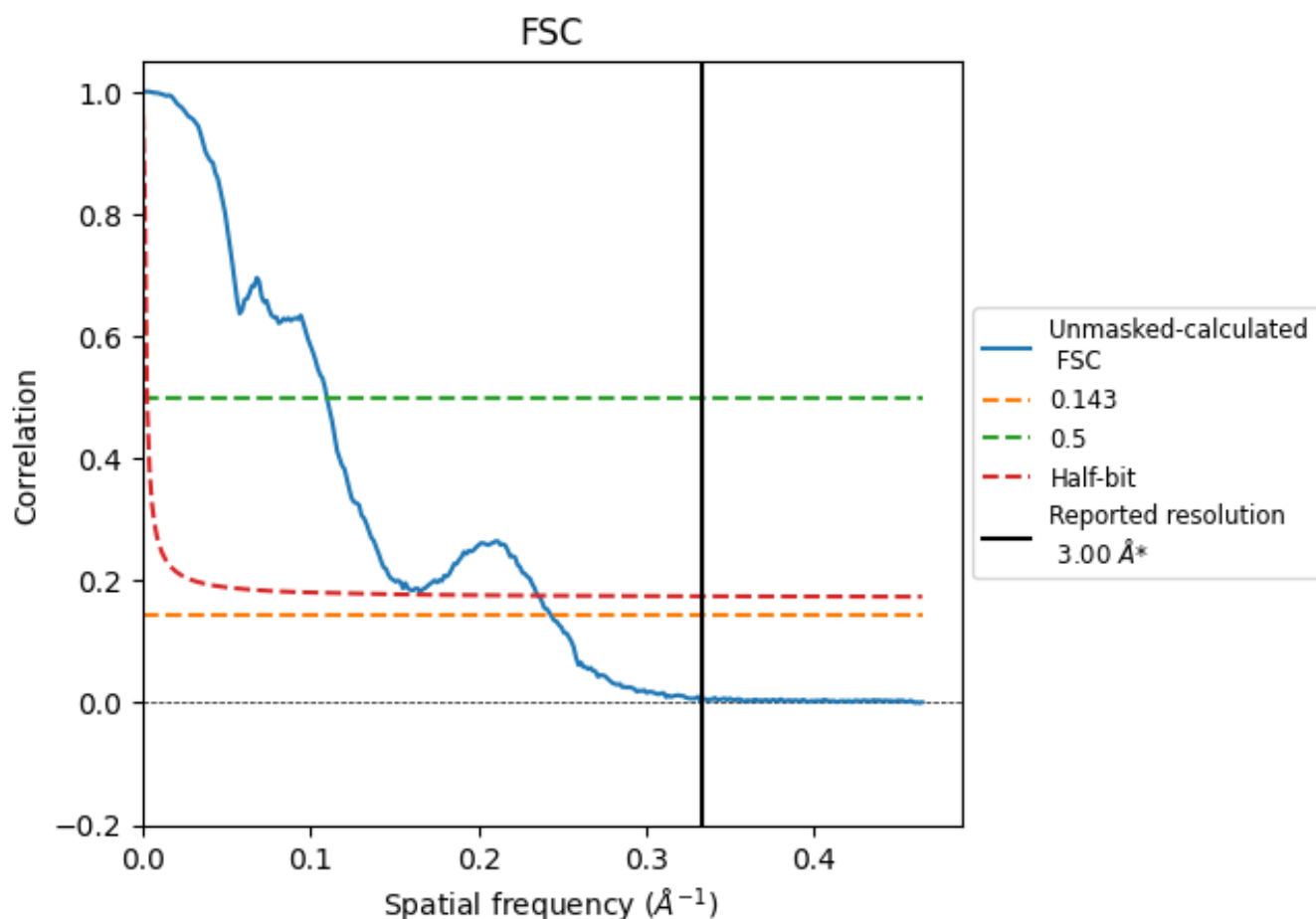


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

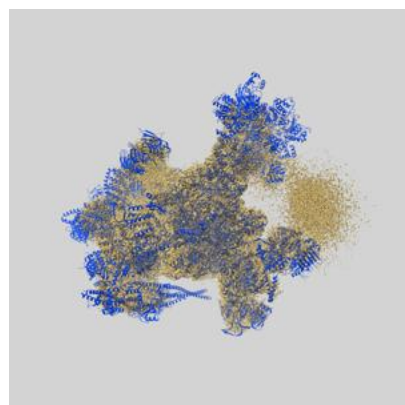
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.11	9.10	4.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.11 differs from the reported value 3.0 by more than 10 %

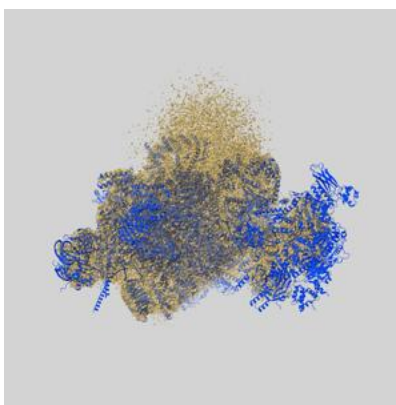
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-67263 and PDB model 9XU3. Per-residue inclusion information can be found in section [3](#) on page [18](#).

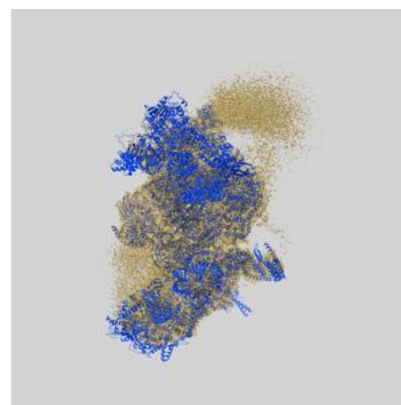
9.1 Map-model overlay [i](#)



X



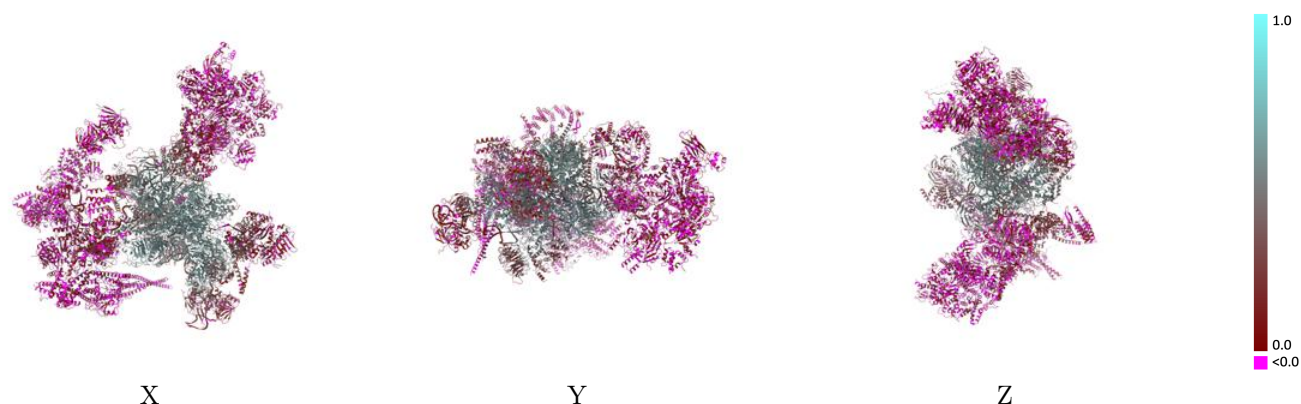
Y



Z

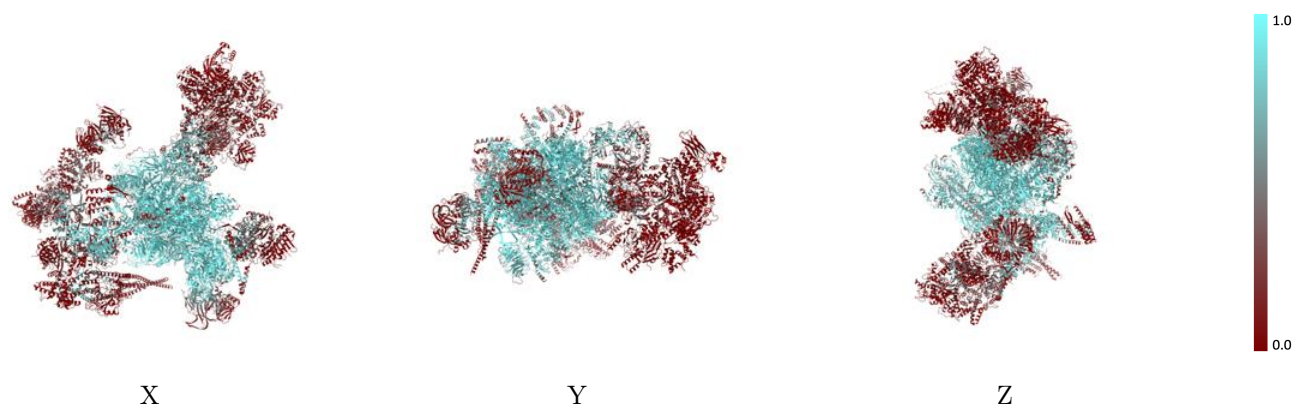
The images above show the 3D surface view of the map at the recommended contour level 0.36 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



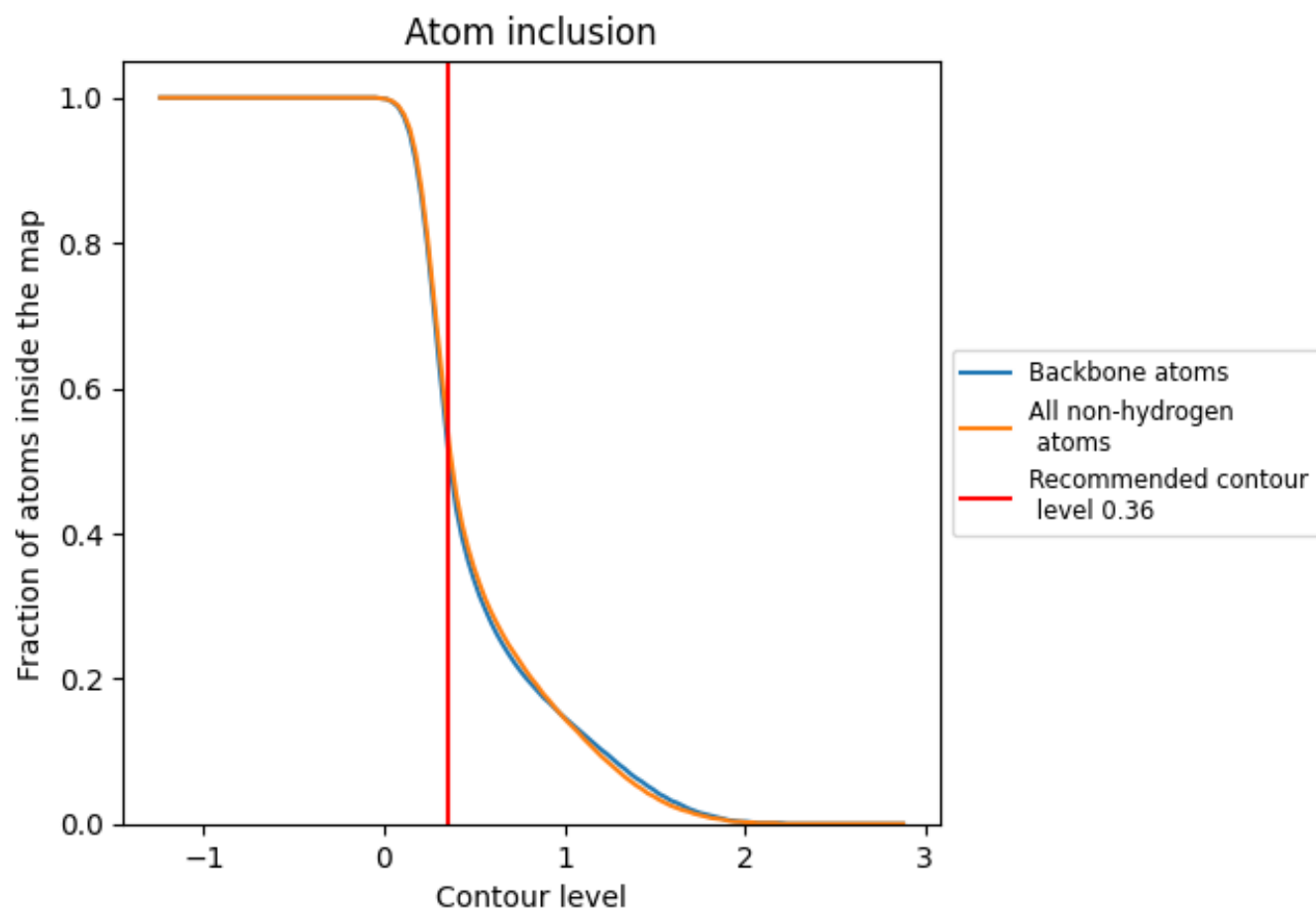
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.36).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 53% 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 (0.36) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5260	 0.2750
0	 0.5740	 0.3350
1	 0.9420	 0.4260
2	 0.8820	 0.3670
4	 0.0530	 0.0490
5	 0.7850	 0.3600
6	 0.7110	 0.3010
A	 0.8710	 0.5000
B	 0.9320	 0.5170
C	 0.0410	 0.0570
D	 0.7790	 0.3230
E	 0.5370	 0.2940
F	 0.5980	 0.1350
G	 0.7200	 0.3080
H	 0.5180	 0.1260
I	 0.0840	 0.0670
J	 0.7540	 0.3990
K	 0.8920	 0.5220
L	 0.9250	 0.4360
L2	 0.1630	 0.0580
L3	 0.1280	 0.0560
L4	 0.1160	 0.0210
L5	 0.0200	 0.0770
L6	 0.0410	 0.0850
L7	 0.0500	 0.0740
L8	 0.1800	 0.0620
M	 0.7410	 0.2690
N	 0.8620	 0.4780
O	 0.2640	 0.0410
P	 0.1410	 0.0620
Q	 0.1300	 0.0340
R	 0.0290	 0.0420
S	 0.8200	 0.4840
T	 0.5050	 0.2040
U	 0.4310	 0.2860



Continued on next page...

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Chain	Atom inclusion	Q-score
V	 0.6840	 0.3960
W	 0.9480	 0.4940
X	 0.8020	 0.3980
Y	 0.9070	 0.5200
Z	 0.7290	 0.4830
a	 0.6020	 0.2600
b	 0.4910	 0.1460
c	 0.2450	 0.1470
d	 0.6380	 0.3550
e	 0.1300	 0.1430
f	 0.1290	 0.1570
g	 0.3110	 0.2380
h	 0.1860	 0.0410
i	 0.1770	 0.0510
j	 0.1170	 0.0660
k	 0.1800	 0.0470
l	 0.1940	 0.0680
m	 0.1350	 0.0550
n	 0.1590	 0.0230
p	 0.2870	 0.3670
q	 0.1940	 0.0700
r	 0.1290	 0.0420
s	 0.1710	 0.0080
t	 0.0990	 0.0660
u	 0.1030	 0.0500
v	 0.4370	 0.2410
w	 0.0560	 0.1360
x	 0.0360	 0.1500
y	 0.1750	 0.1800
z	 0.8130	 0.3820