



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:27 AM UTC

PDB ID : 7D63 / pdb_00007d63
EMDB ID : EMD-30588
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state C)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-29
Resolution : 12.30 Å (reported)
Based on initial model : 6LQR

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

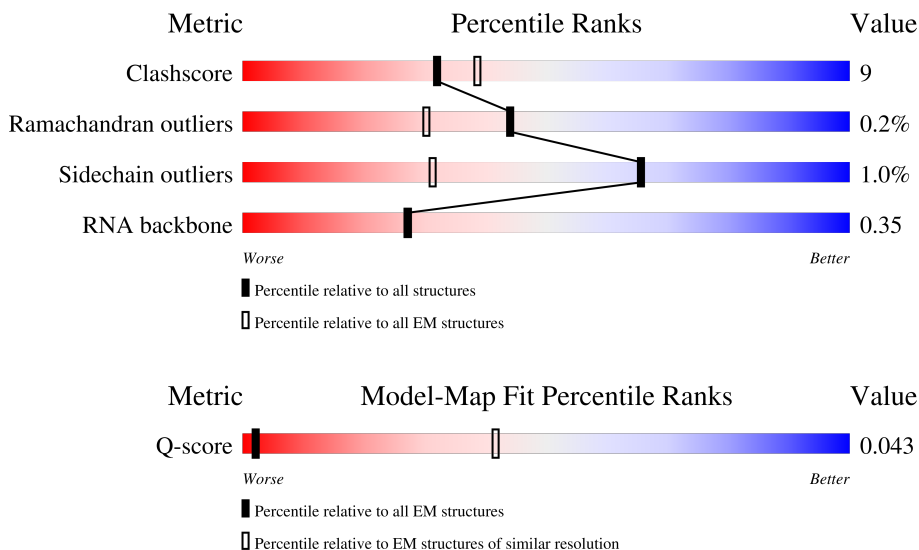
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 12.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	82 (11.80 - 12.80)

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	3A	333	
2	5A	700	
3	SA	1812	

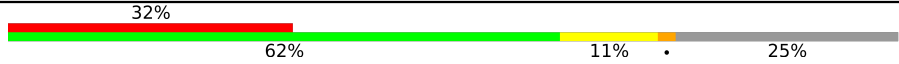

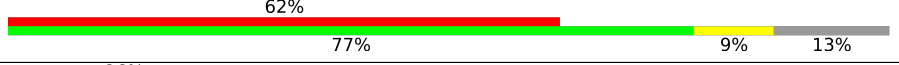

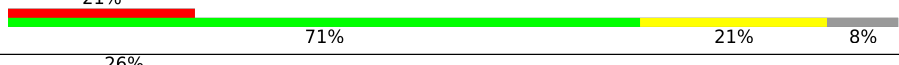
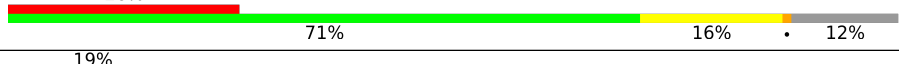
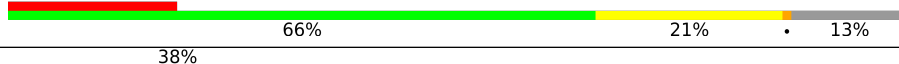

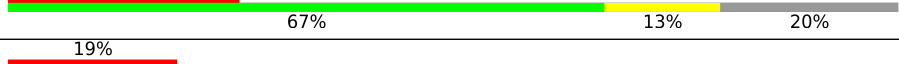


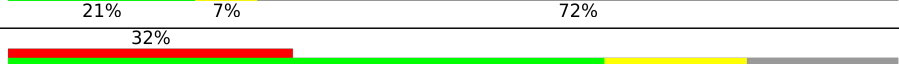
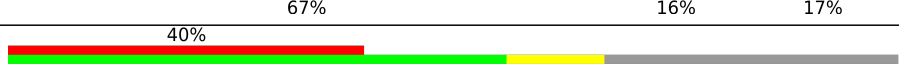


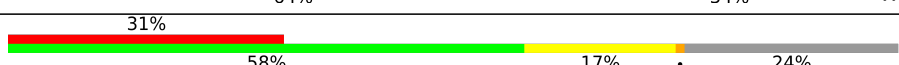

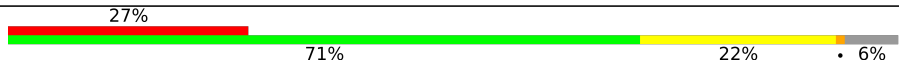
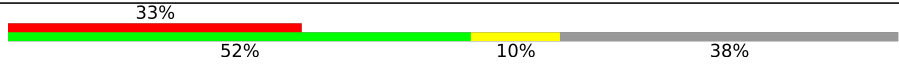
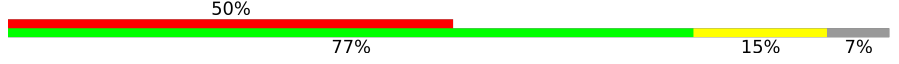


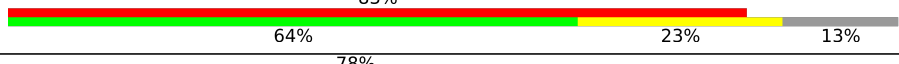


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Mol	Chain	Length	Quality of chain
4	SC	255	80% 71% 19% 10%
5	SF	261	37% 65% 21% 12%
6	SG	225	22% 81% 14% 5%
7	SH	236	32% 53% 17% 29%
8	SI	190	77% 67% 18% 13%
9	SJ	200	28% 56% 27% 17%
10	SK	197	30% 75% 12% 13%
11	SM	155	28% 52% 27% 21%
12	SO	151	72% 79% 8% 11%
13	SP	137	68% 64% 21% 14%
14	SR	143	26% 72% 15% 13%
15	SX	130	83% 82% 15% ..
16	SY	145	26% 63% 6% 29%
17	SZ	135	27% 59% 15% 24%
18	Sc	82	83% 83% 13% ..
19	Sd	67	24% 88% 6% 6%
20	3B	327	30% 60% 13% 27%
20	3C	327	28% 51% 17% 31%
21	3D	504	18% 61% 12% 27%
22	3E	511	35% 67% 17% 16%
23	3F	573	18% 61% 18% 21%
24	3G	126	16% 80% 16% .
24	3H	126	32% 75% 21% .
25	A4	776	19% 65% 20% 15%
26	A5	643	25% 64% 15% 20%

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Mol	Chain	Length	Quality of chain
27	A8	713	
28	A9	575	
29	AE	1769	
30	AF	513	
31	AG	896	
32	B1	900	
33	B2	943	
34	B3	817	
35	B8	594	
36	BE	939	
37	B6	440	
38	5B	214	
39	5C	554	
40	5D	250	
41	5E	593	
42	5F	183	
43	5G	290	
44	5H	610	
45	5I	489	
46	5J	217	
47	5K	189	
48	RA	707	
49	RB	357	
50	RE	1237	
51	RF	297	

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Mol	Chain	Length	Quality of chain
52	RG	252	
52	RH	252	
53	RJ	1183	
54	RK	367	
55	RL	1056	
55	RM	1056	
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RY	534	
62	X1	611	
63	RT	326	
64	ST	146	
65	SU	144	
66	RD	1729	
67	RZ	1267	

2 Entry composition

There are 71 unique types of molecules in this entry. The entry contains 225233 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 U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	3A	175	3711	1661	648	1227	175	0	0

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5A	192	4117	1838	746	1341	192	0	0

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	SA	1331	28383	12684	5049	9319	1331	0	0

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	SC	230	1830	1156	335	335	4	0	0

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	SF	229	1815	1161	331	320	3	0	0

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	SG	213	1669	1045	307	314	3	0	0

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	SH	167	1327	834	256	235	2	0	0

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	SI	165	1321	853	226	242		0	0

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	SJ	166	1324	824	262	236	2	0	0

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	SK	171	1388	879	268	240	1	0	0

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	SM	123	997	641	189	164	3	0	0

- Molecule 12 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	SO	134	1087	698	202	186	1	0	0

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	SP	118	868	536	164	165	3	0	0

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	SR	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SX	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	102	Total	C	N	O	0	0
			809	517	148	144		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	3D	369	2848	1811	489	540	8	0	0

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	3E	431	3028	1888	543	588	9	0	0

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	3F	454	3643	2315	638	680	10	0	0

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	3G	121	916	583	158	171	4	0	0
24	3H	121	916	583	158	171	4	0	0

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	A4	662	5226	3309	910	986	21	0	0

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	A5	514	3976	2520	688	755	13	0	0

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	A8	532	3229	2008	592	626	3	0	0

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	A9	128	939	594	173	170	2	0	0

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	AE	1534	9955	6242	1771	1923	19	0	0

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AF	493	3911	2462	702	735	12	0	0

- Molecule 31 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	AG	826	6570	4181	1111	1259	19	0	0

- Molecule 32 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	B1	793	6331	4046	1085	1182	18	0	0

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	B2	825	6502	4156	1096	1223	27	0	0

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	B3	757	5919	3769	993	1130	27	0	0

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	B8	477	3764	2387	662	705	10	0	0

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	BE	820	6450	4090	1114	1225	21	0	0

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	B6	374	2800	1782	501	505	12	0	0

- Molecule 38 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	5B	60	495	310	101	84	0	0

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	5C	458	3612	2276	636	689	11	0	0

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	5D	167	1396	862	266	263	5	0	0

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	5E	193	1564	970	280	310	4	0	0

- Molecule 42 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 43 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	219	Total	C	N	O	S	0	0
			1756	1107	325	318	6		

- Molecule 44 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	5H	74	Total	C	N	O	0	0
			596	373	122	101		

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 46 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	134	Total	C	N	O	S	0	0
			1131	715	206	207	3		

- Molecule 47 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 48 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 49 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 50 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 51 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 52 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
52	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 53 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 54 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RK	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 55 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
55	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 56 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	RN	607	4529	2861	820	837	11	0	0

- Molecule 57 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	RO	525	3766	2412	646	696	12	0	0

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	RP	2108	12171	7483	2291	2381	16	0	0

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	RQ	275	1853	1139	356	356	2	0	0

- Molecule 60 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	RS	251	2051	1340	349	359	3	0	0

- Molecule 61 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
61	RY	37	299	191	48	60	0	0

- Molecule 62 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	X1	22	110	66	22	22	0	0

- Molecule 63 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RT	212	Total	C	N	O	S	0	0
			1587	1010	290	283	4		

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	ST	110	Total	C	N	O	S	0	0
			896	565	170	159	2		

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SU	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 66 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RD	316	Total	C	N	O	S	0	0
			2412	1541	414	452	5		

- Molecule 67 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RZ	839	Total	C	N	O	S	1	0
			6604	4215	1146	1208	35		

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
68	Sc	1	Total	Zn	0
			1	1	
68	5K	1	Total	Zn	0
			1	1	

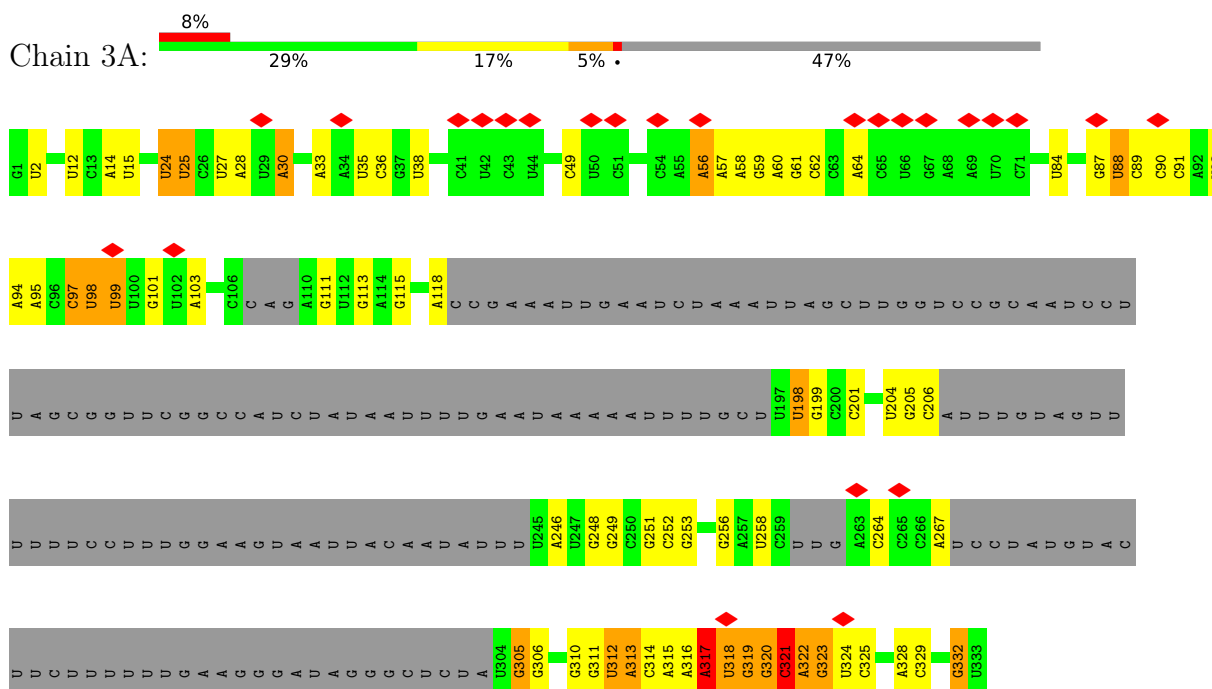
- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

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

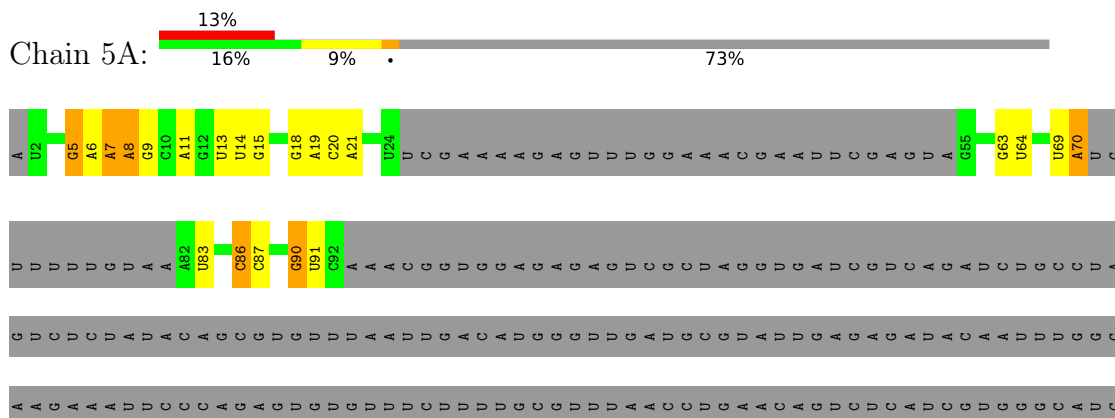
3 Residue-property plots [i](#)

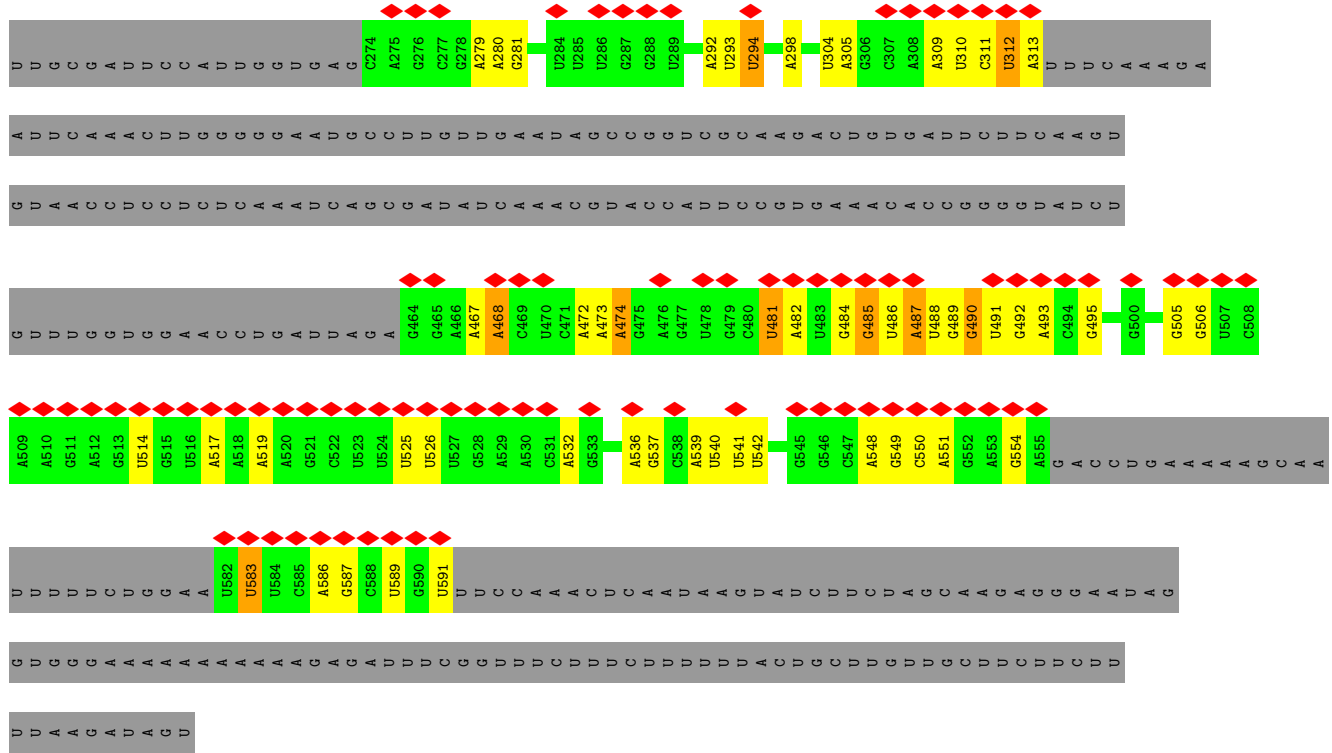
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: U3 snoRNA

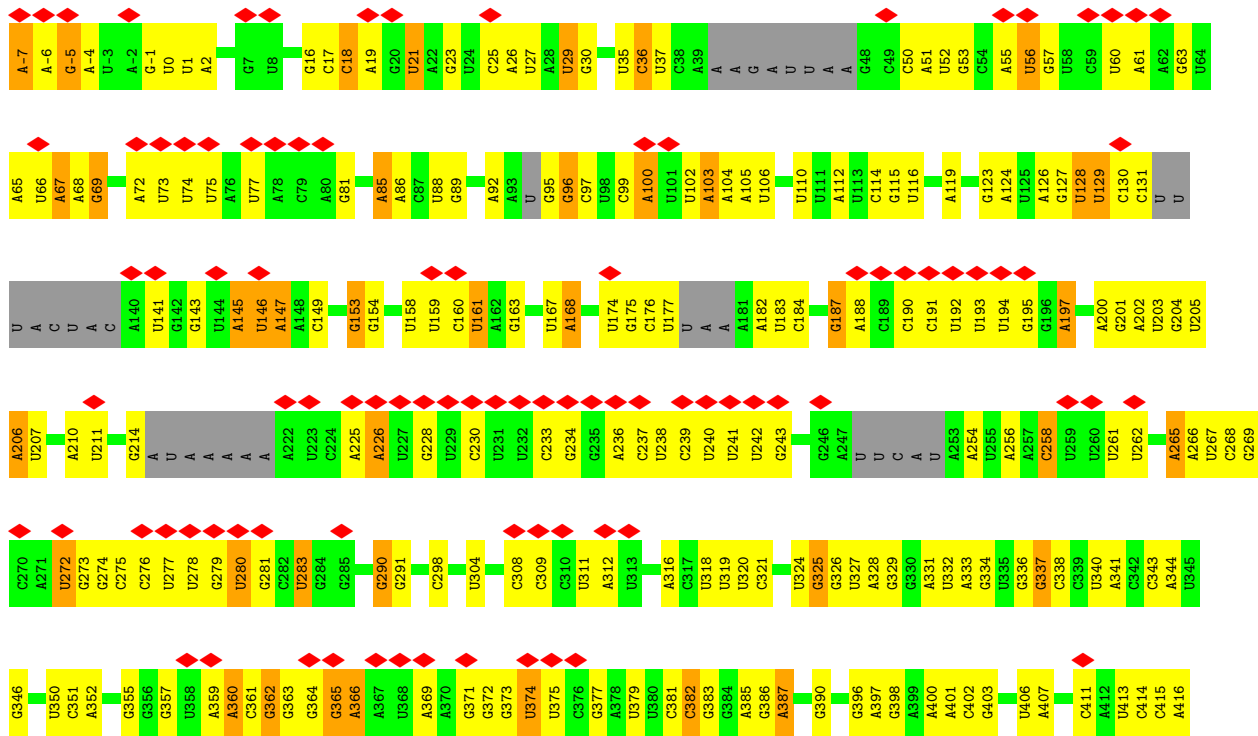


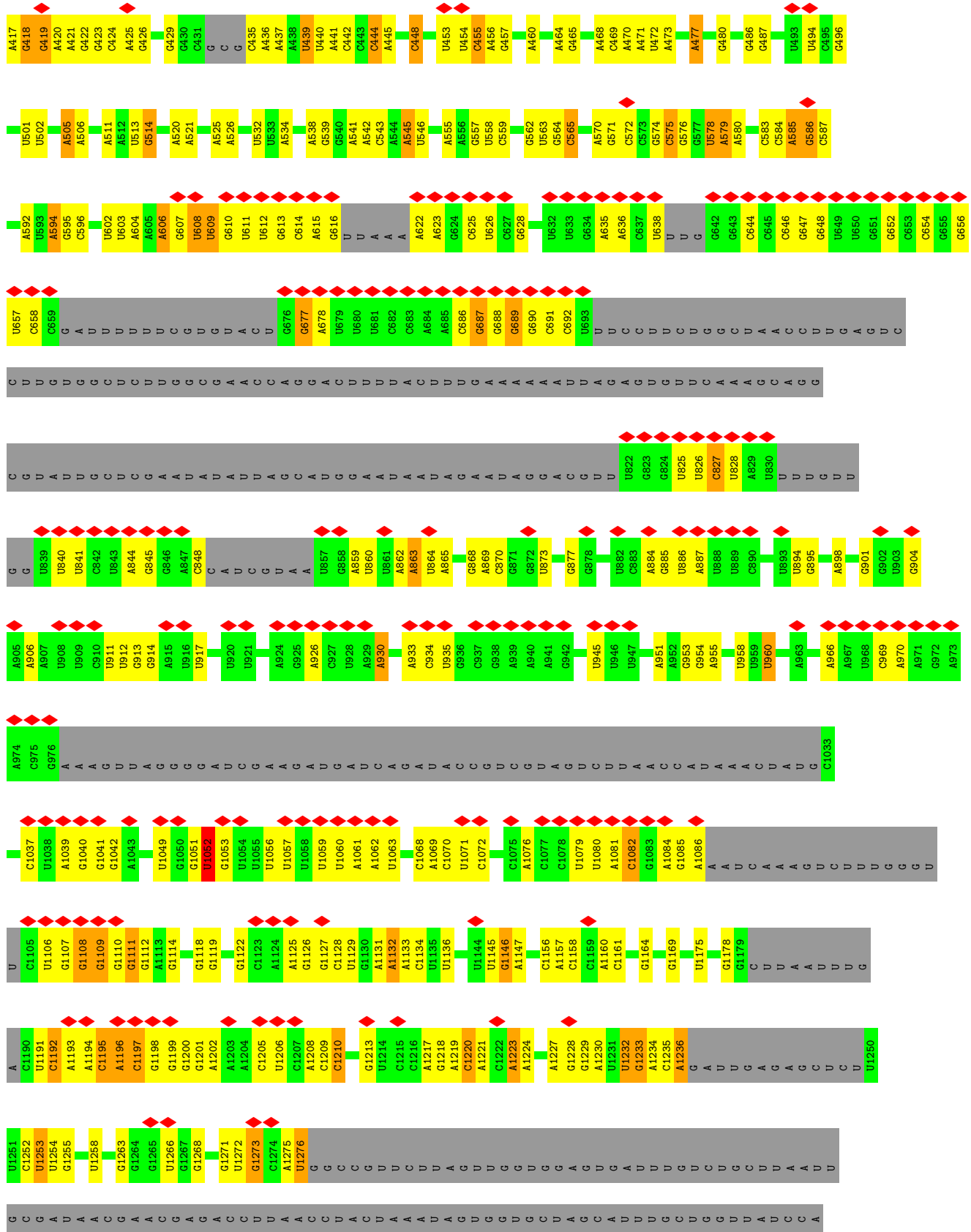
- Molecule 2: 5' ETS

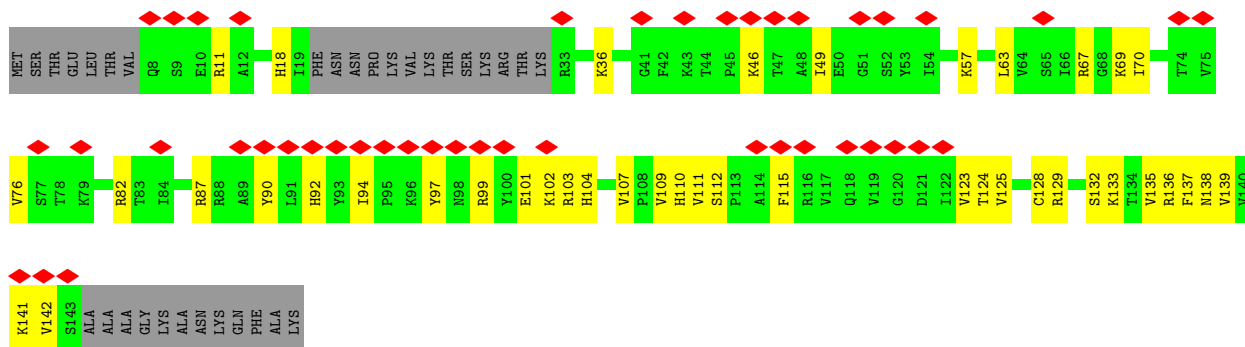




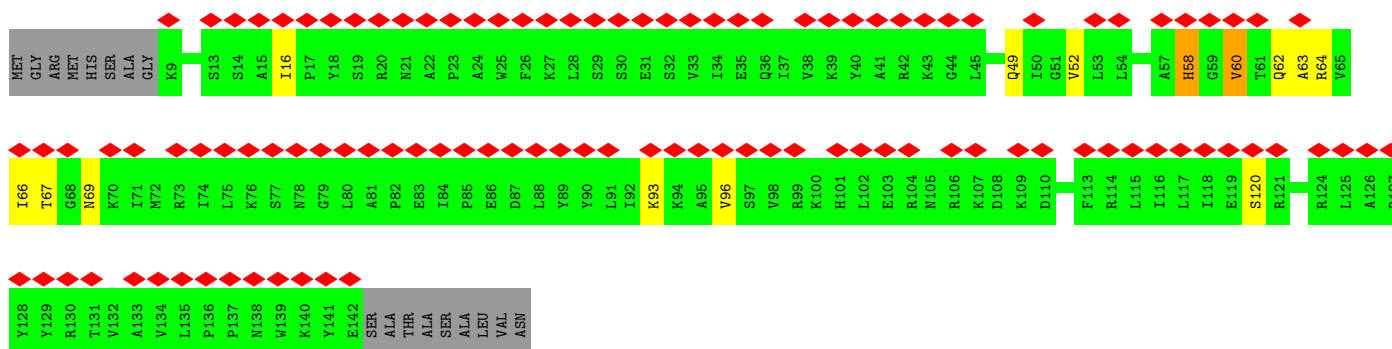
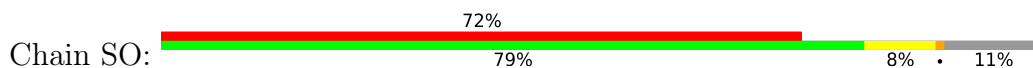
• Molecule 3: 18S rRNA







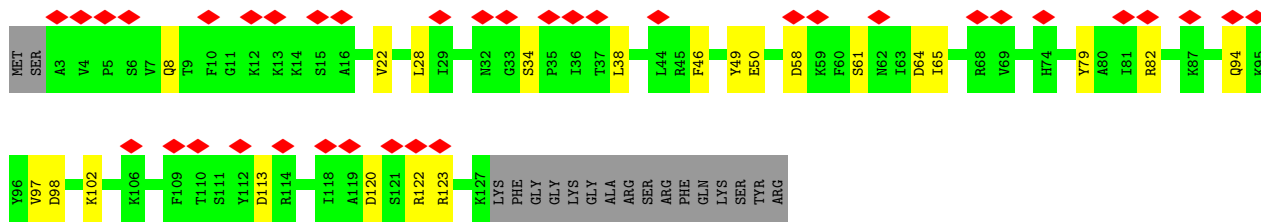
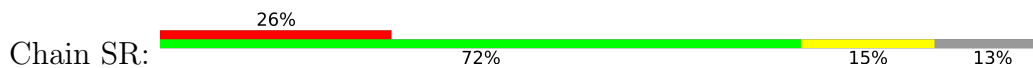
• Molecule 12: 40S ribosomal protein S13



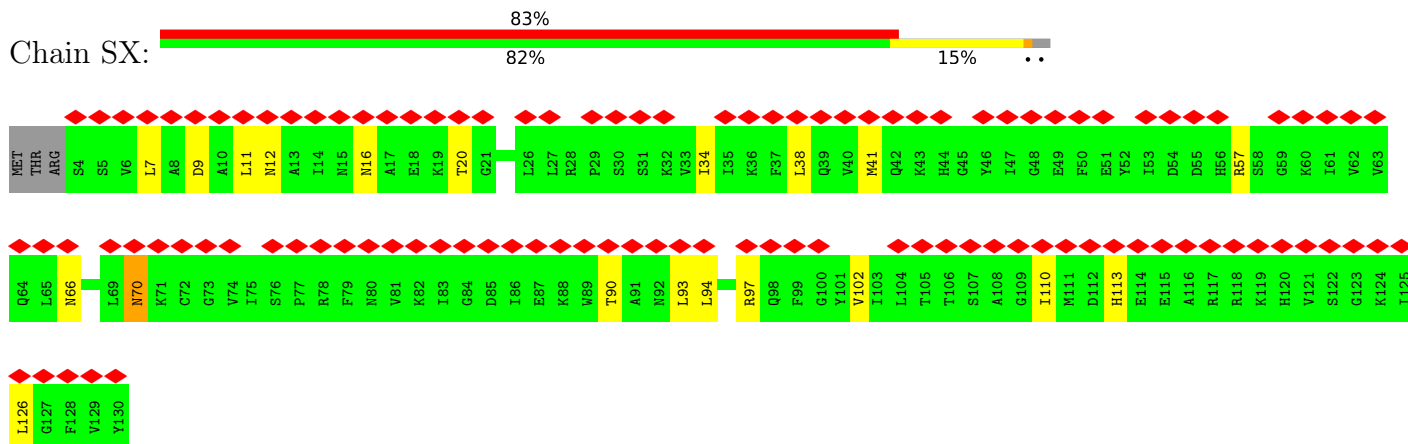
• Molecule 13: 40S ribosomal protein S14-A



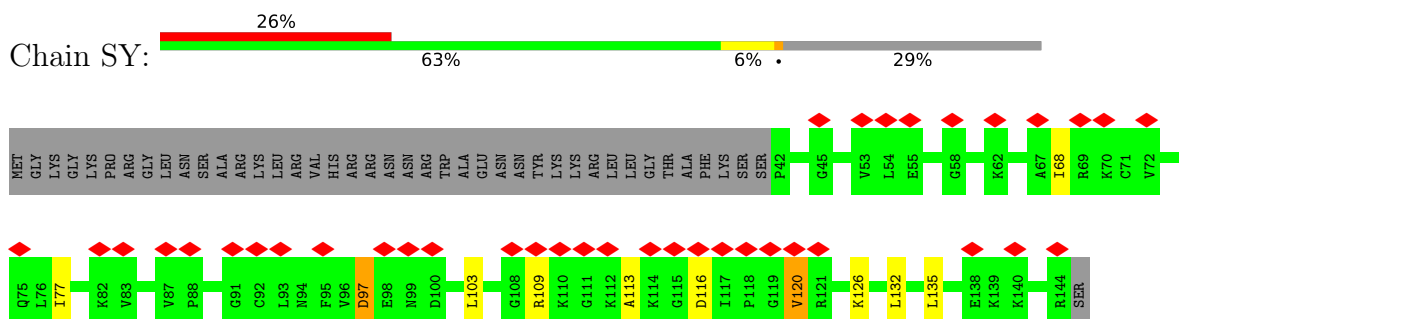
• Molecule 14: 40S ribosomal protein S16-A



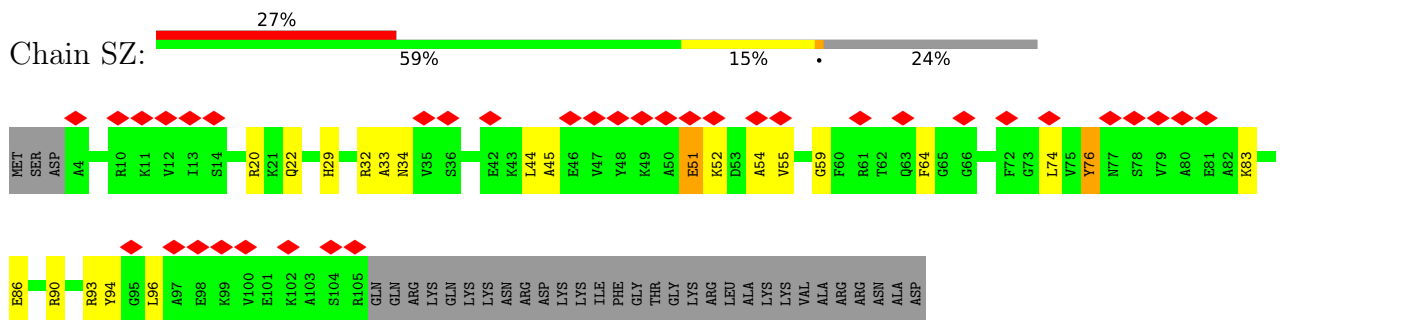
• Molecule 15: 40S ribosomal protein S22-B



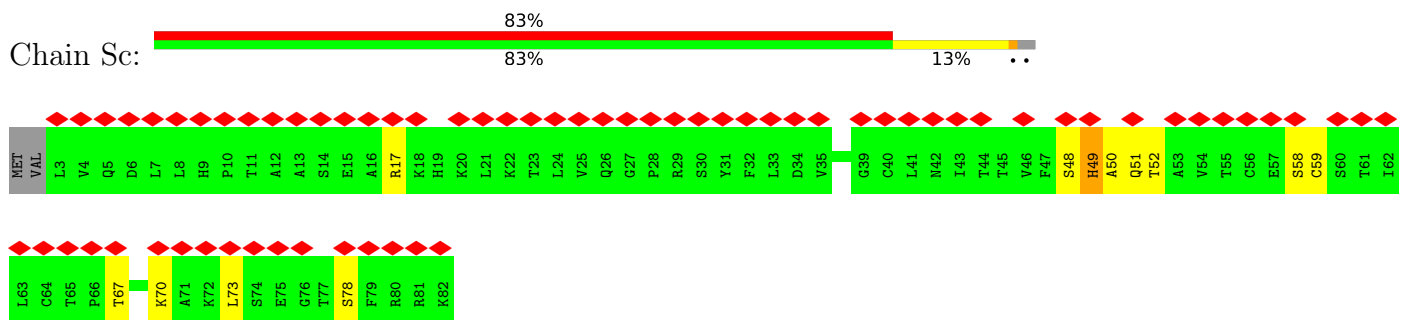
• Molecule 16: 40S ribosomal protein S23-A



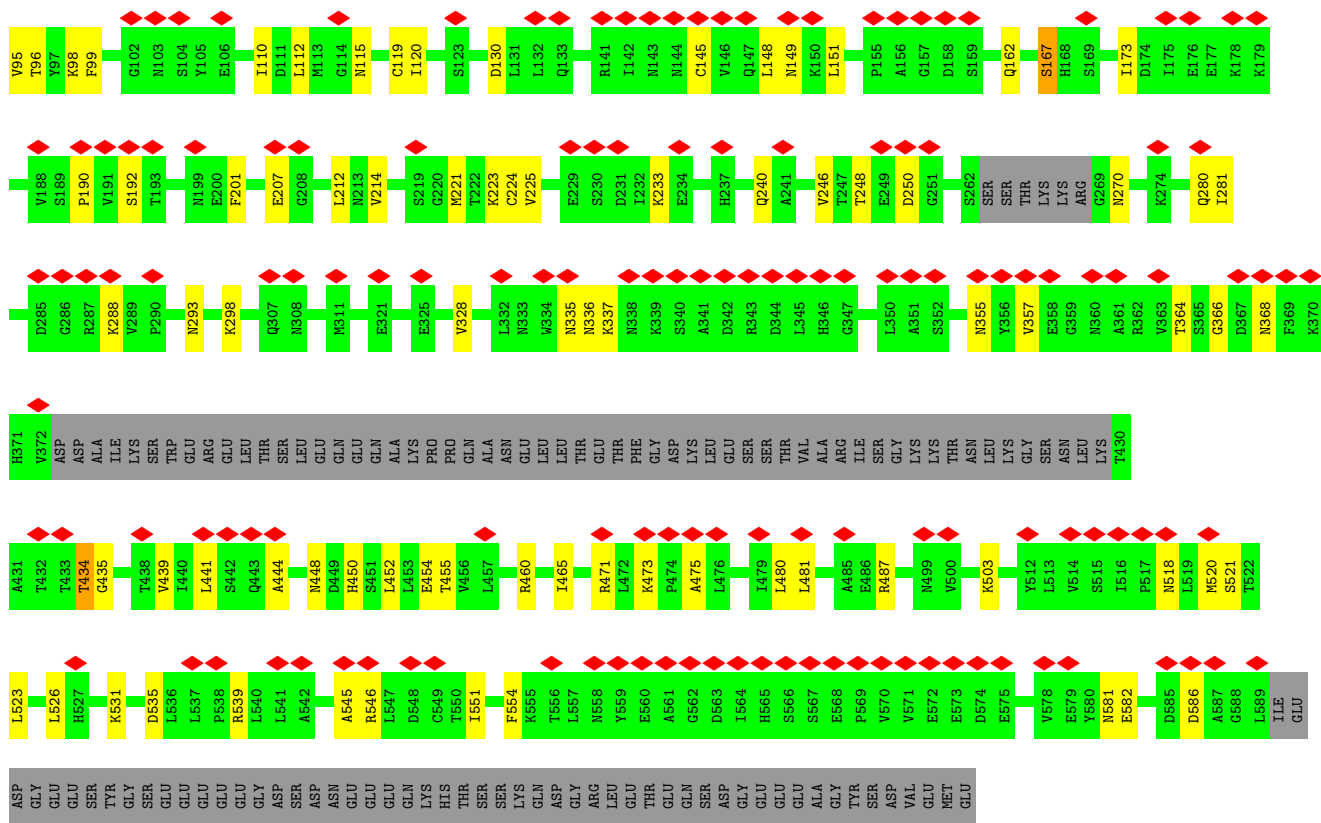
• Molecule 17: 40S ribosomal protein S24-A



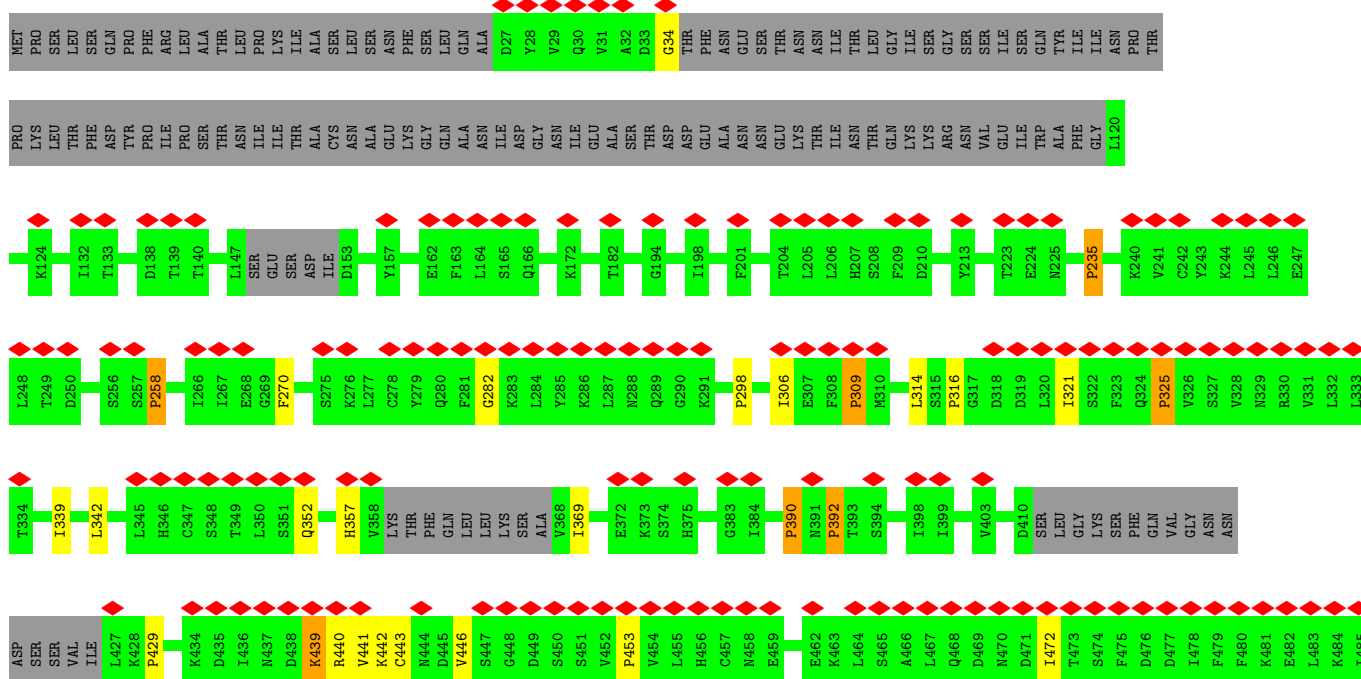
• Molecule 18: 40S ribosomal protein S27-A

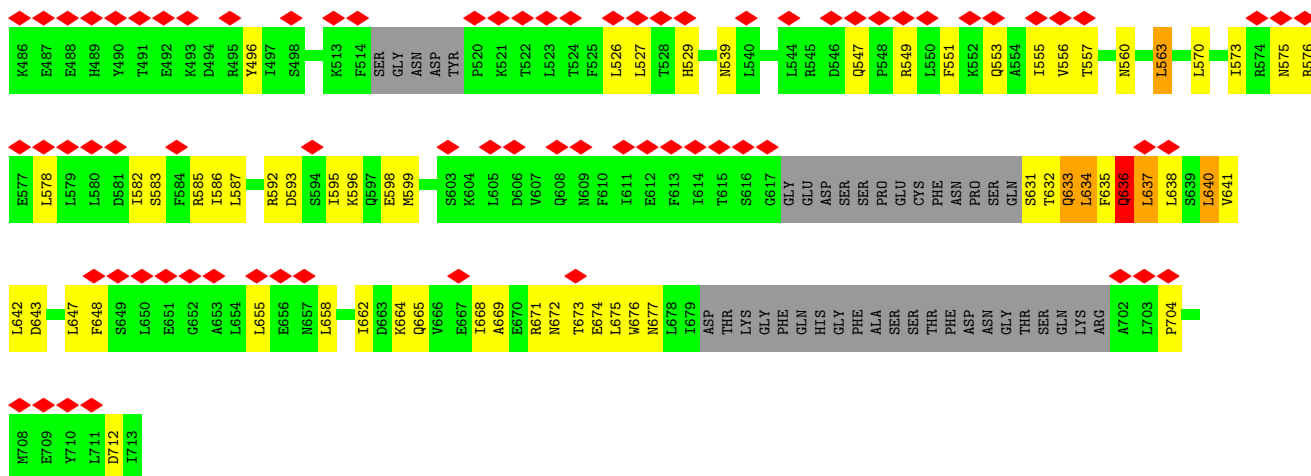


• Molecule 19: 40S ribosomal protein S28-A

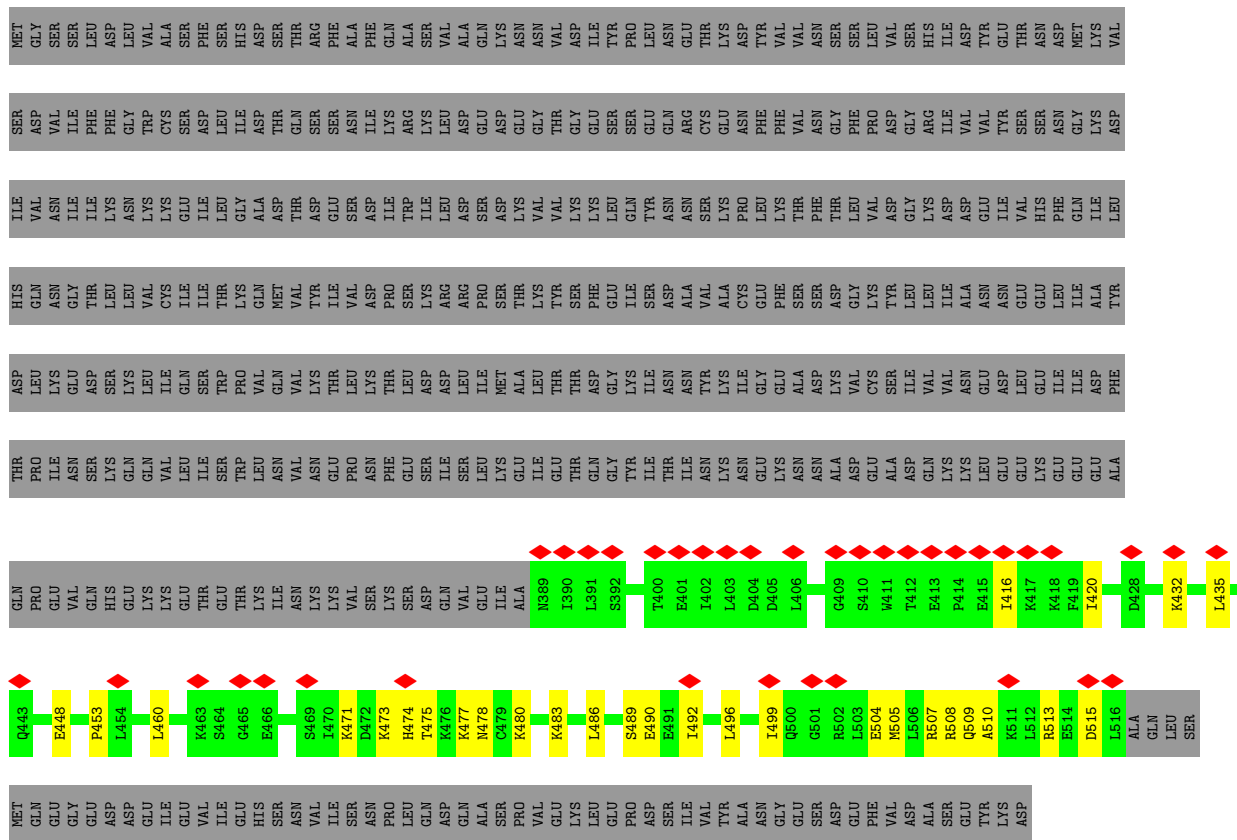


• Molecule 27: U3 small nucleolar RNA-associated protein 8

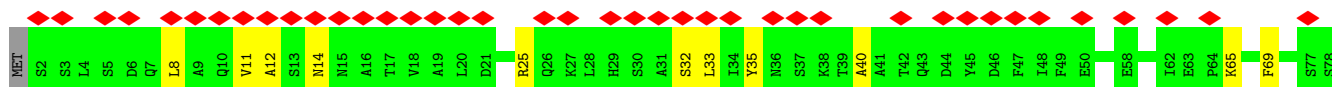
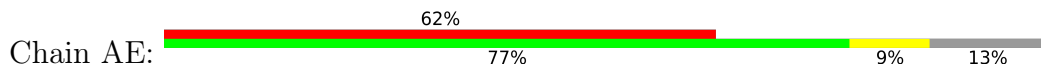


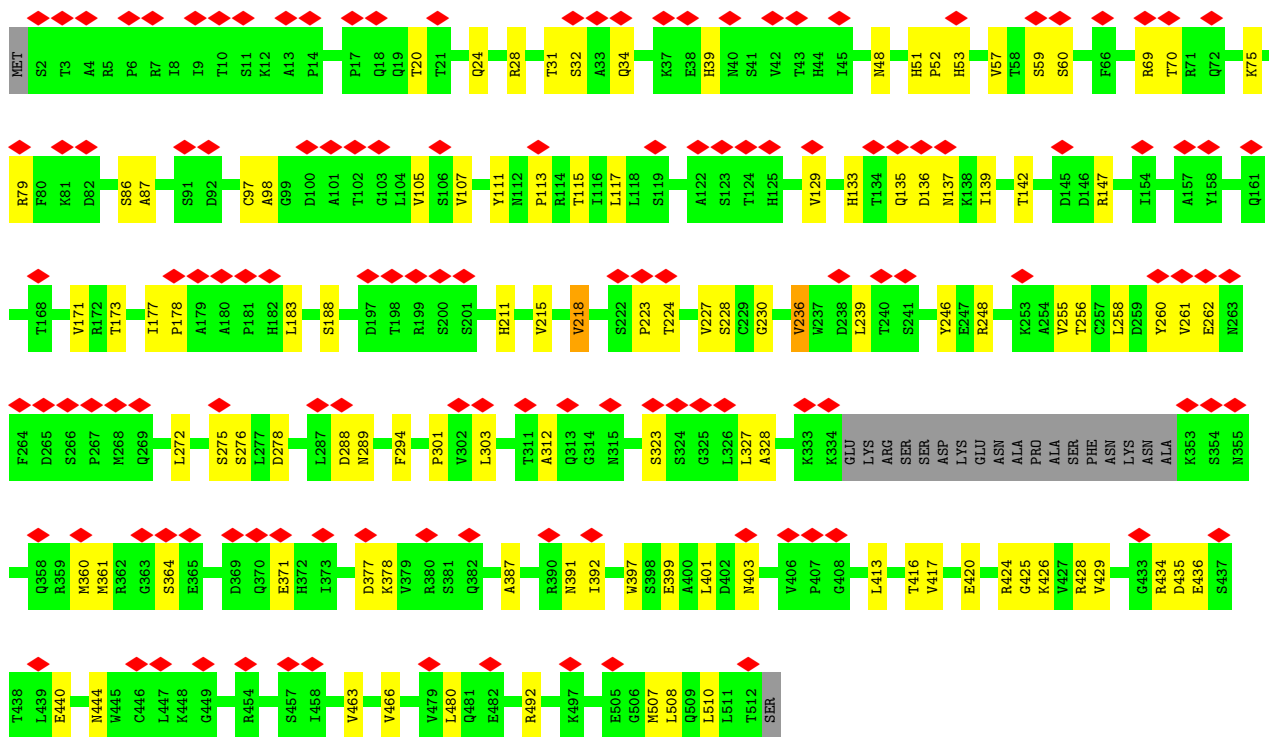


• Molecule 28: U3 small nucleolar RNA-associated protein 9

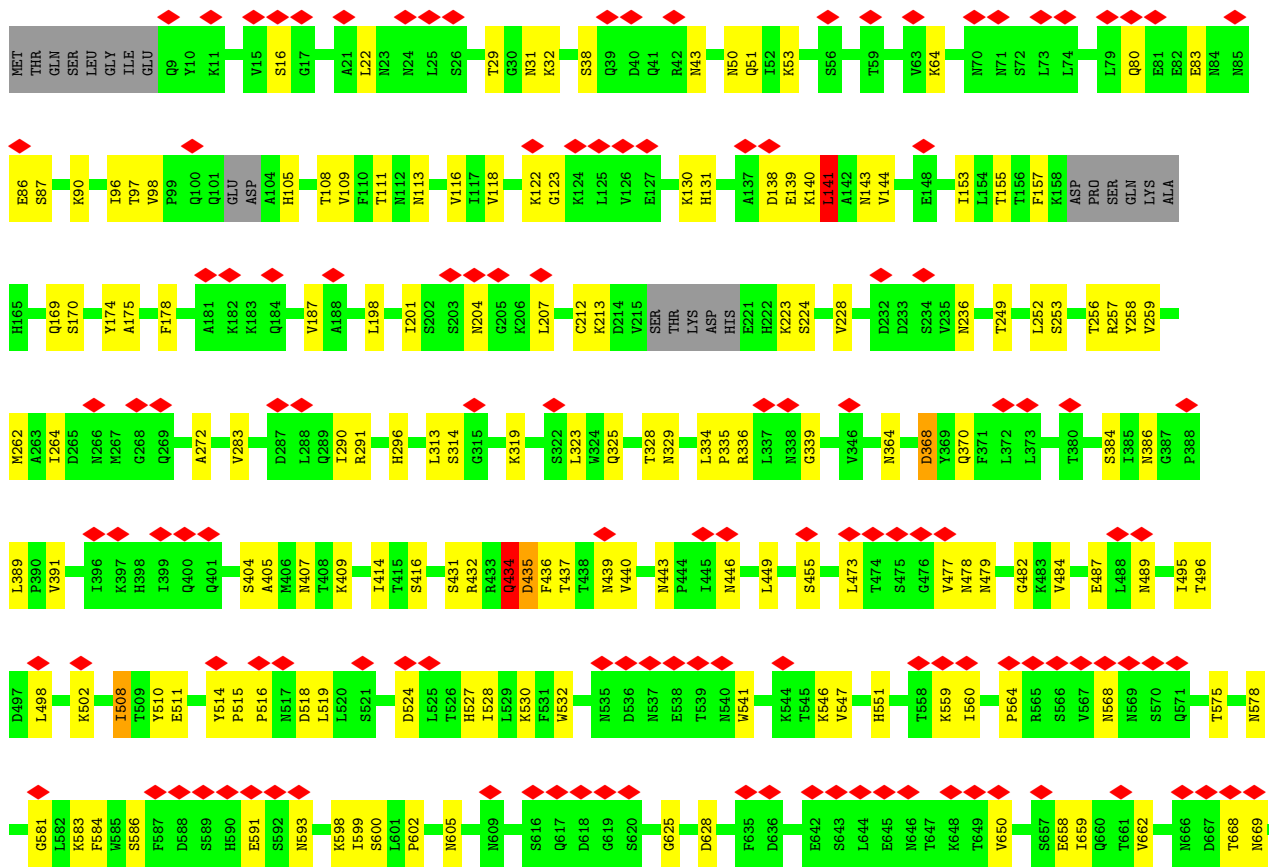
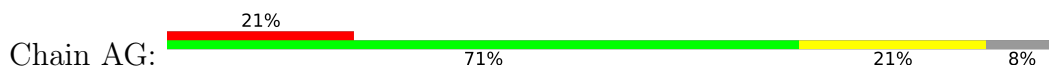


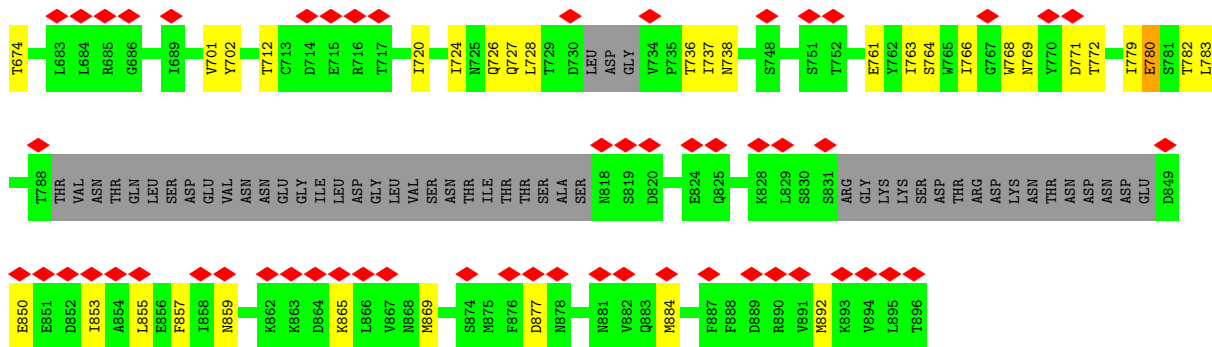
• Molecule 29: U3 small nucleolar RNA-associated protein 10



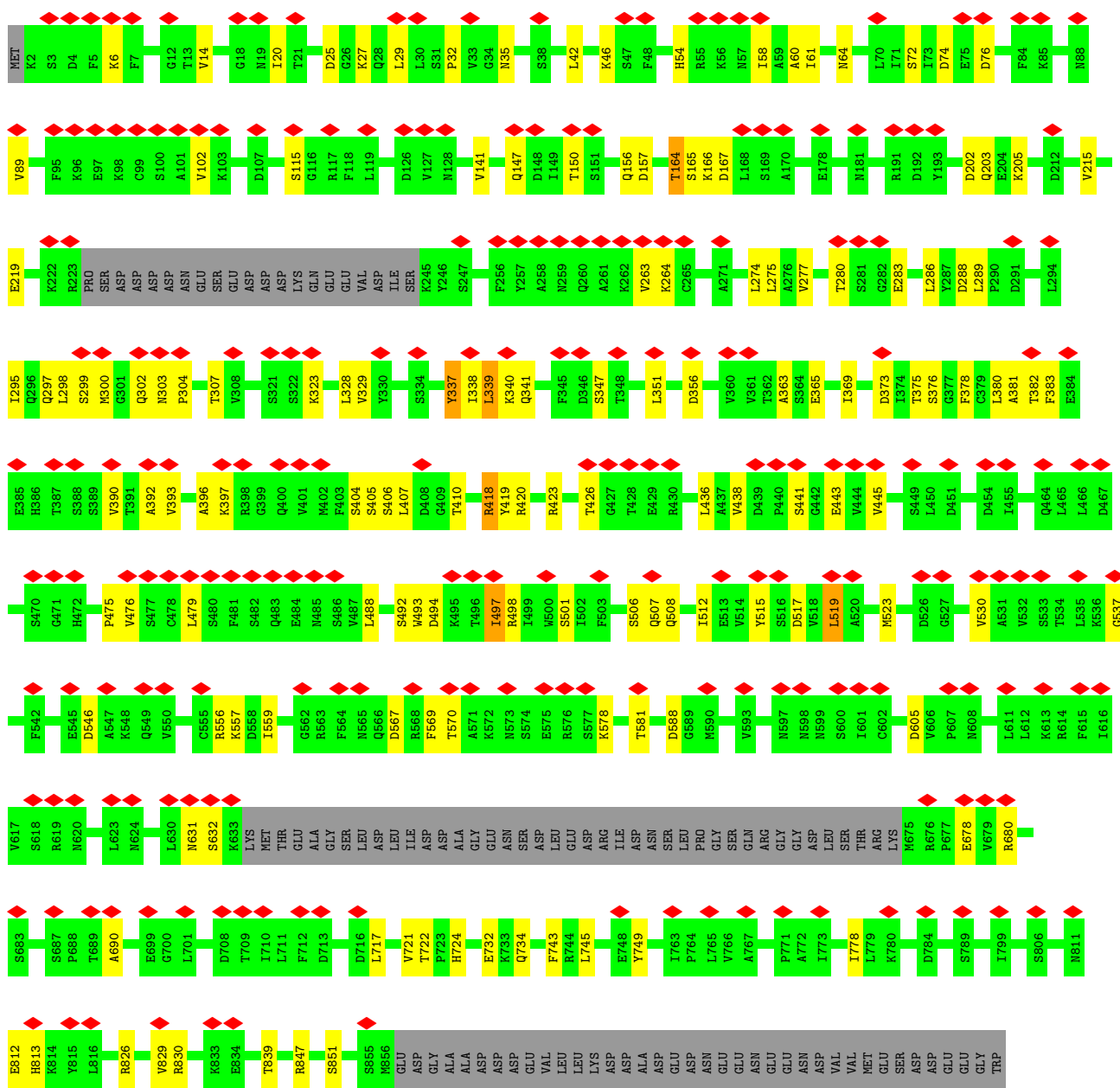
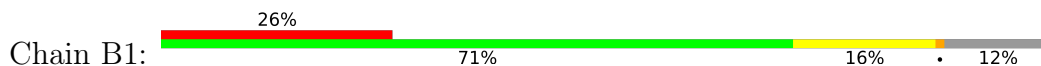


• Molecule 31: NET1-associated nuclear protein 1



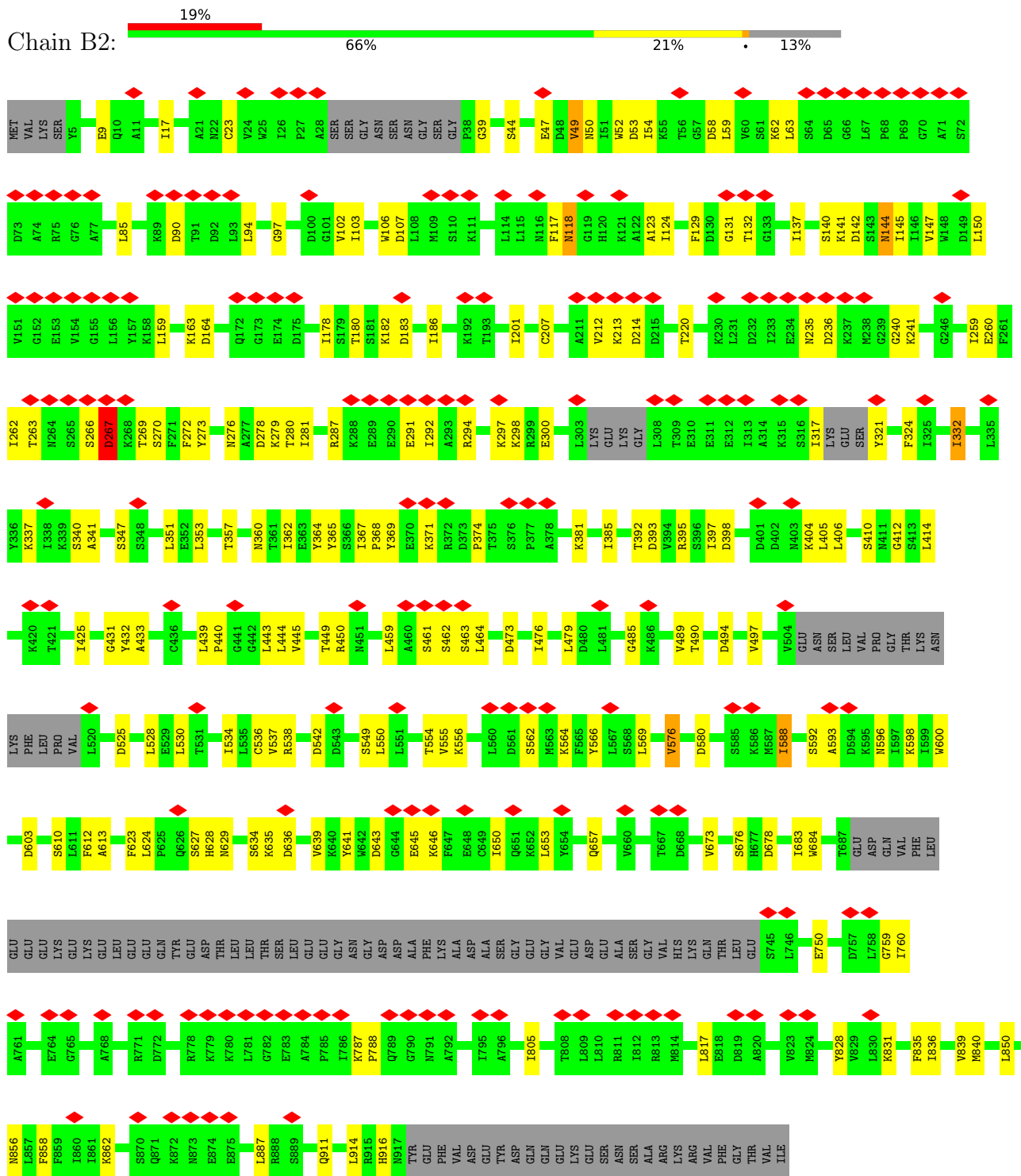


• Molecule 32: Periodic tryptophan protein 2



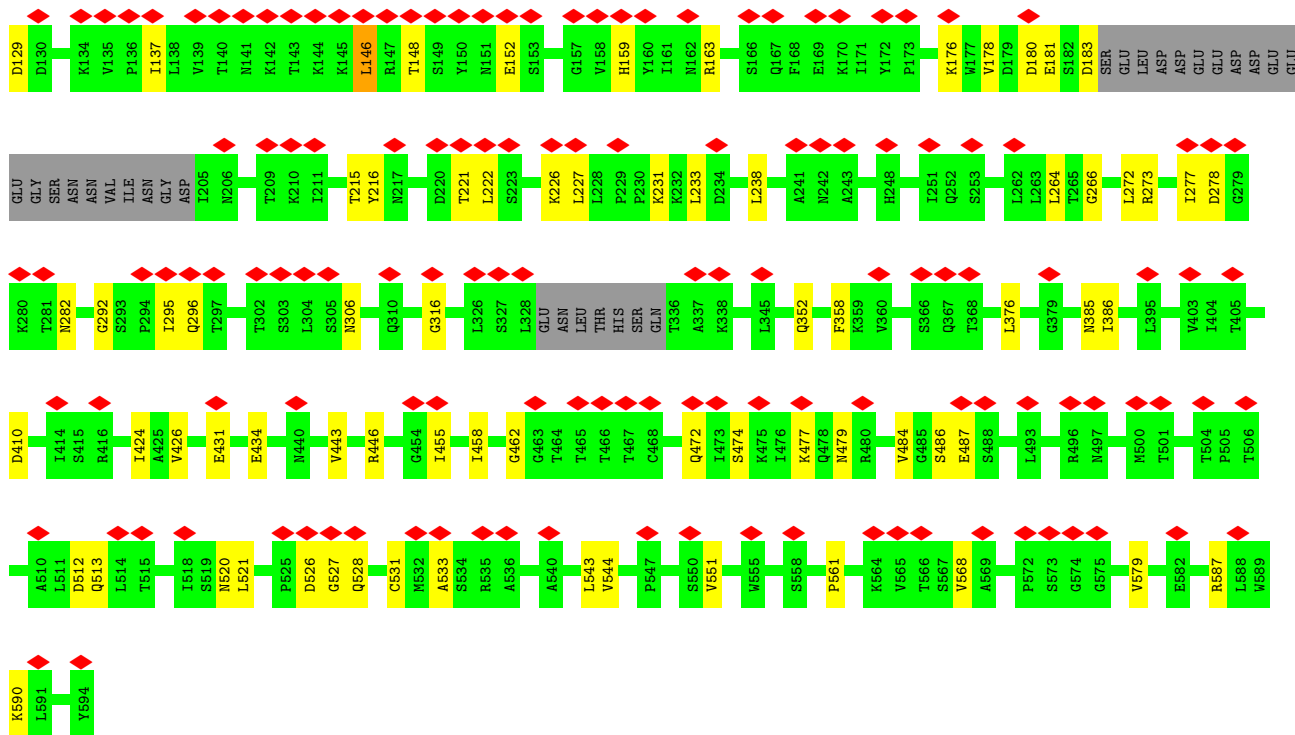
ILE
GLY
PHE
ASN
GLY
LYS

• Molecule 33: U3 small nucleolar RNA-associated protein 12

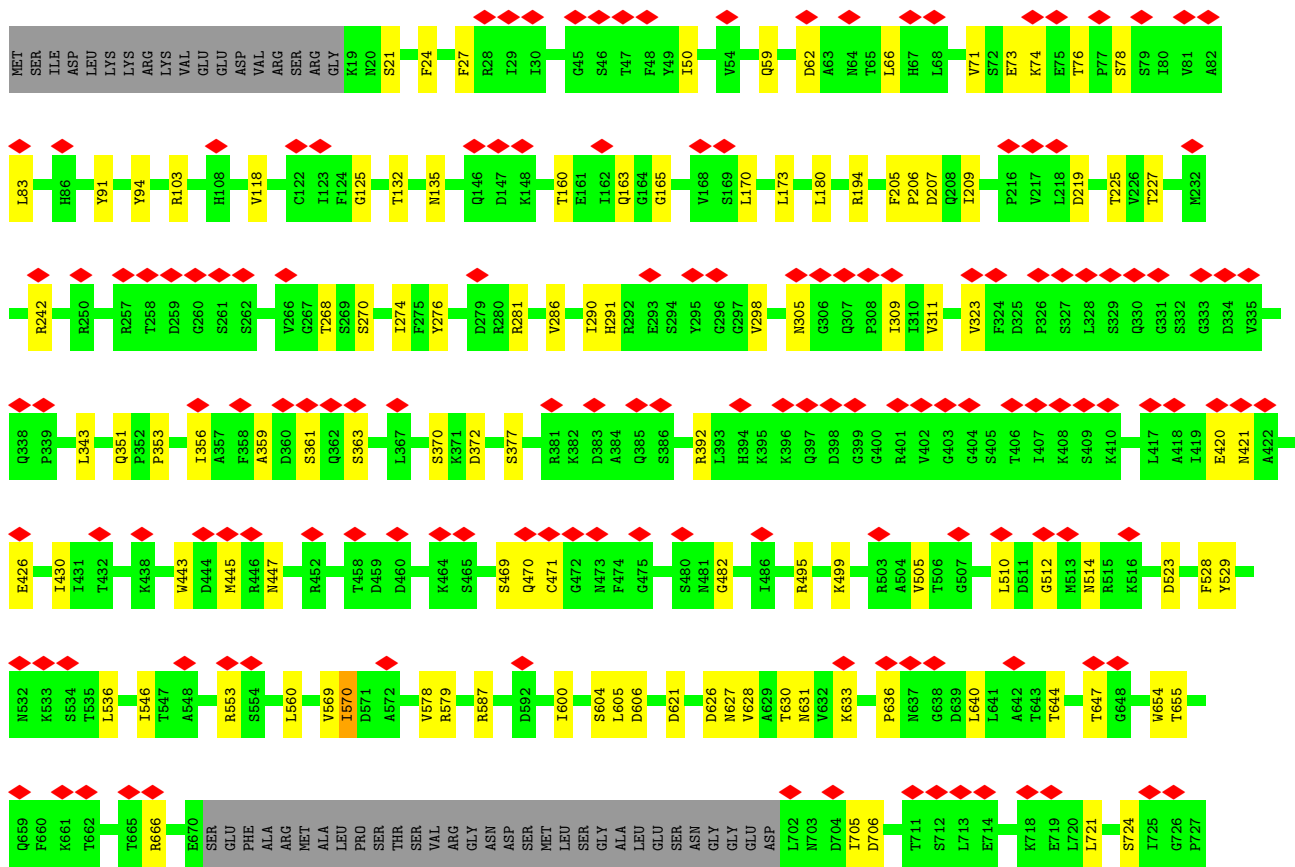
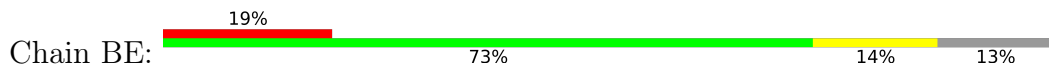


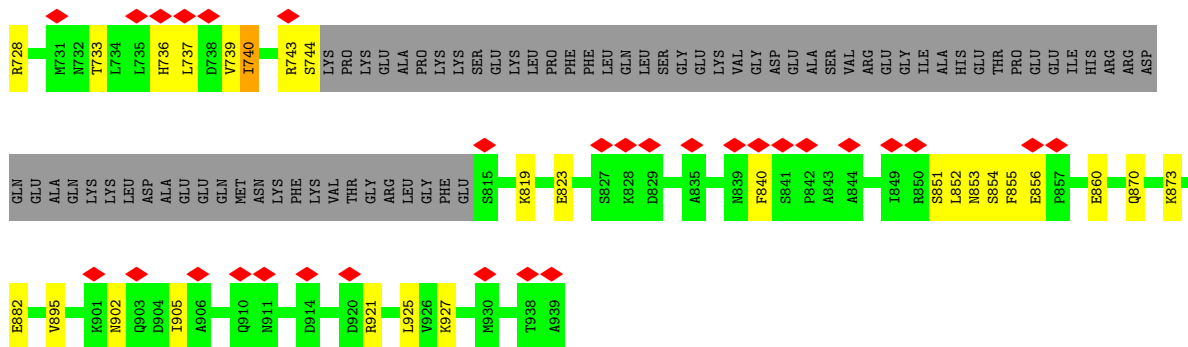
• Molecule 34: U3 small nucleolar RNA-associated protein 13



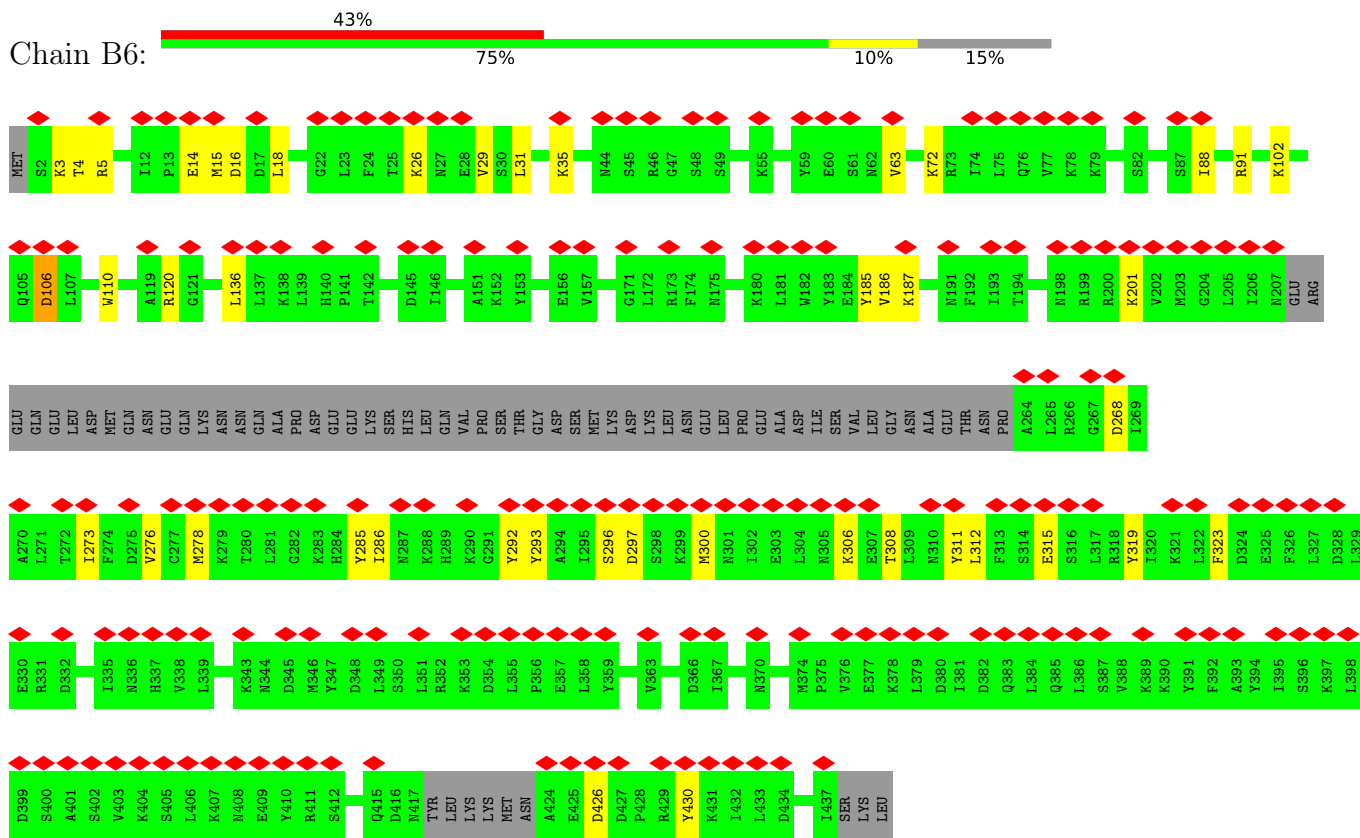


• Molecule 36: U3 small nucleolar RNA-associated protein 21

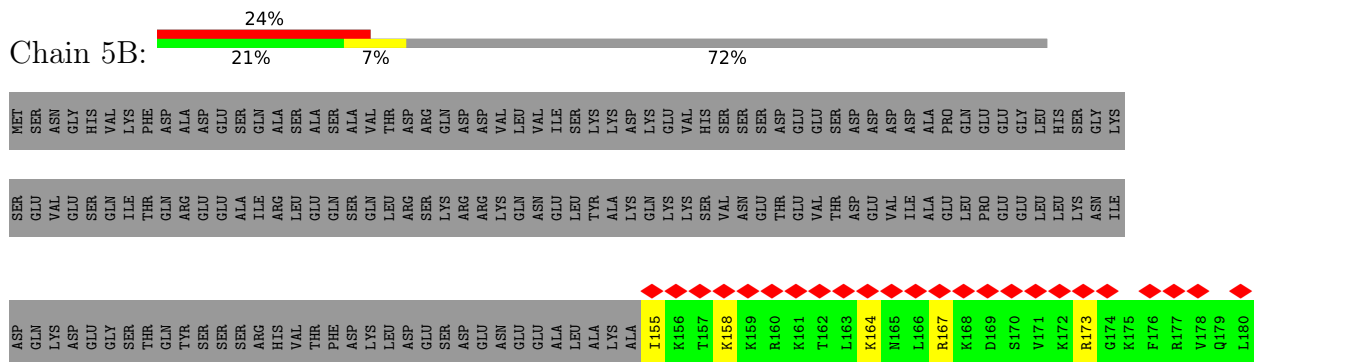


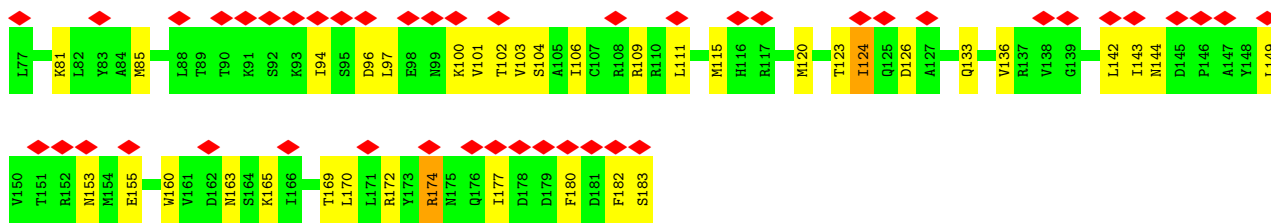


• Molecule 37: U3 small nucleolar RNA-associated protein 6

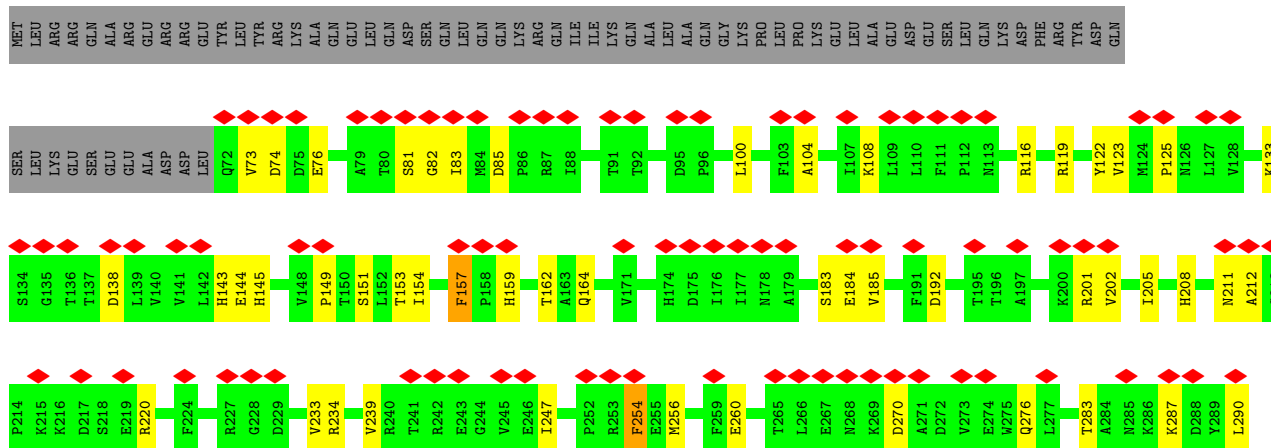


• Molecule 38: Bud site selection protein 21

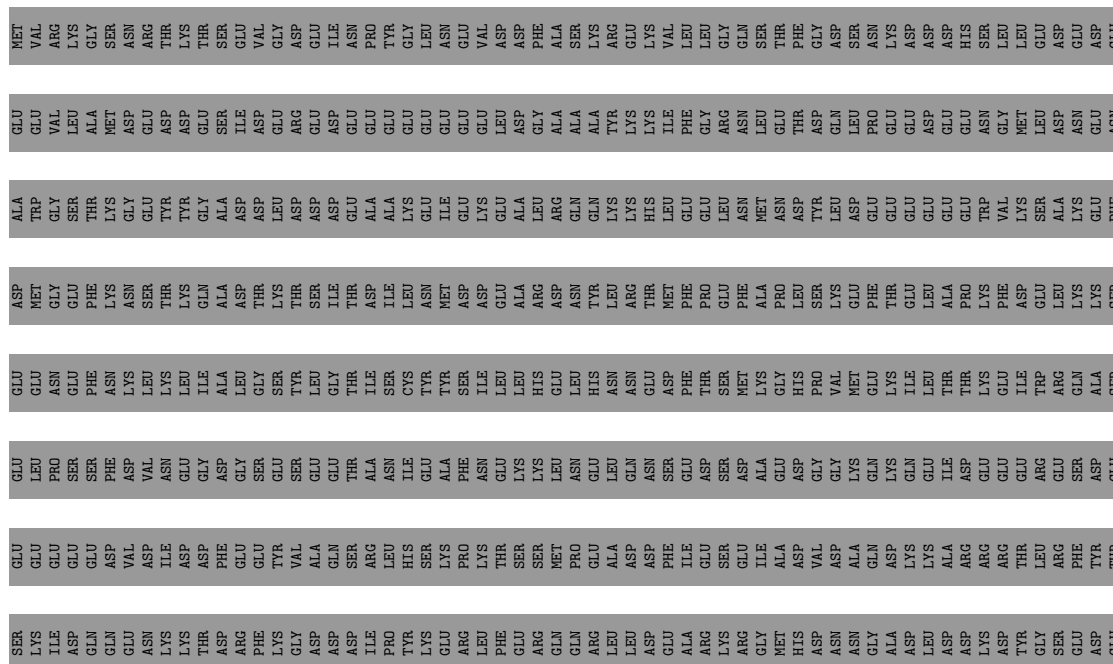




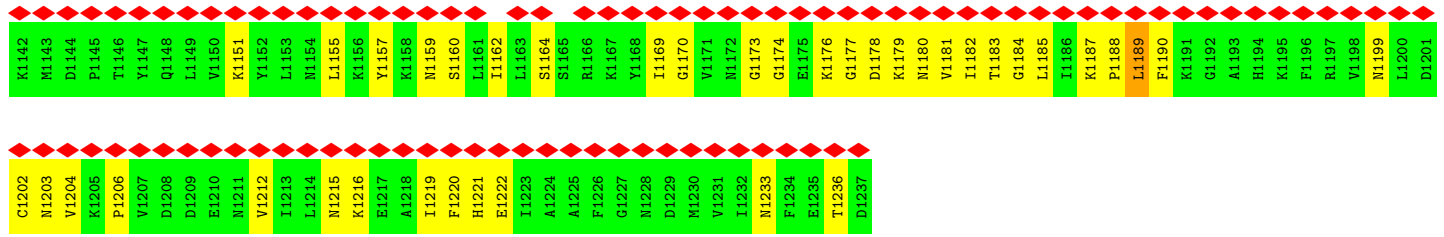
• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4



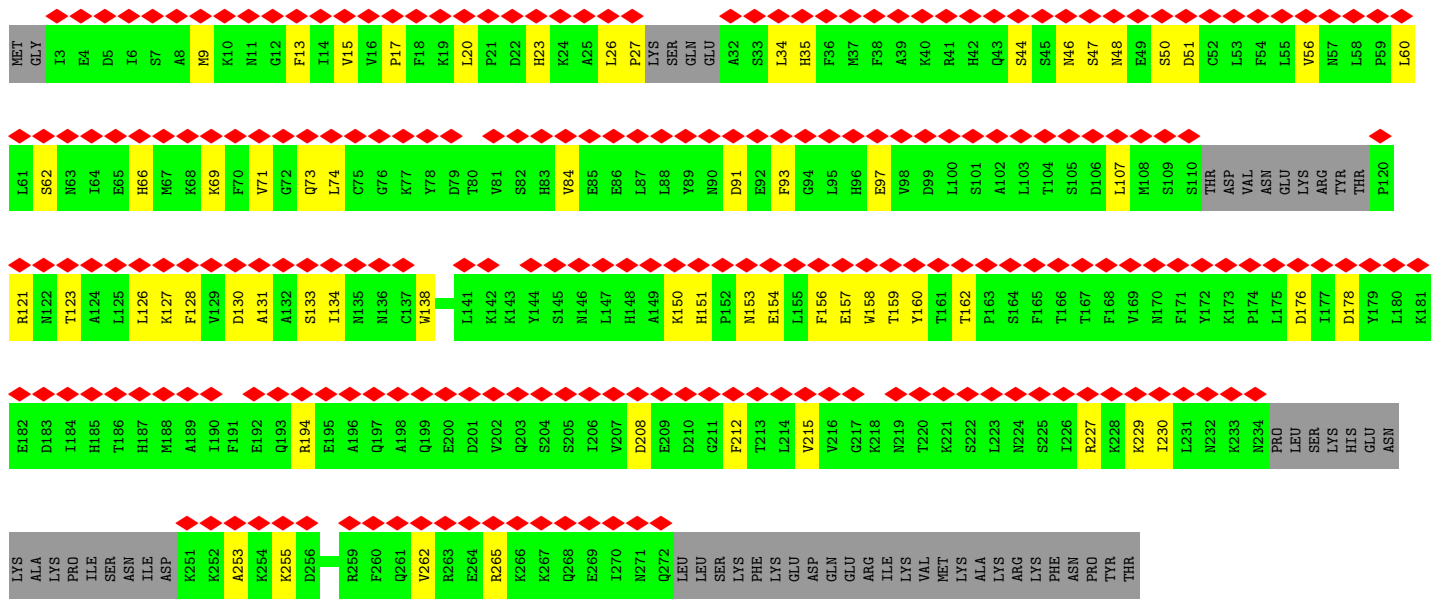
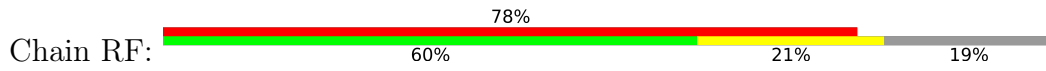
• Molecule 44: Something about silencing protein 10



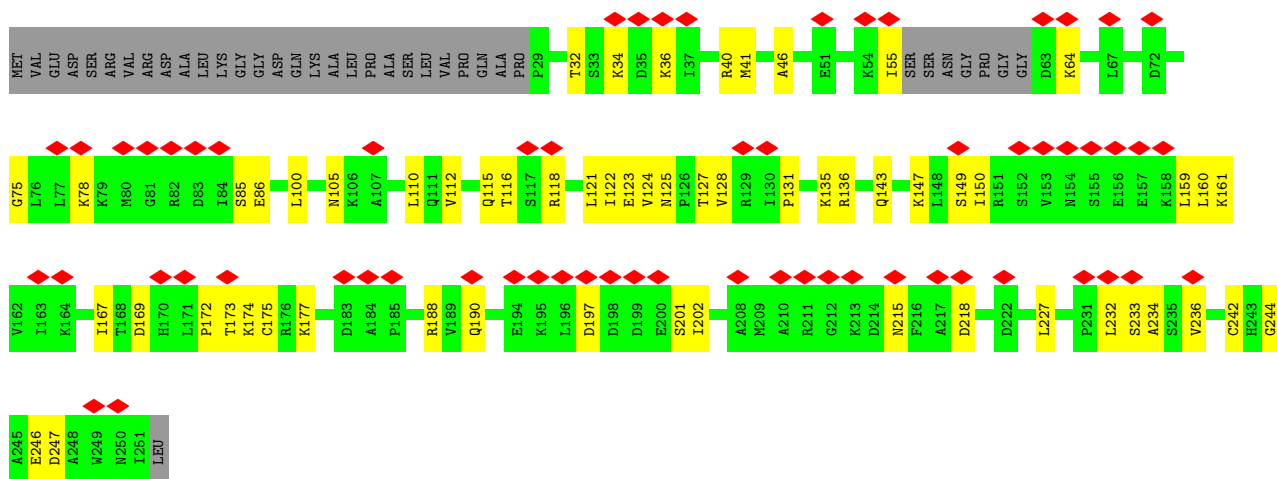
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L421	F422	K423	G424	Y425	I426	K427	Y428	L429	A430	Q431	M432	D433	L434	C435	H436	D437	G438	H439	L440	Q441	F442	H443	S444	M445	PRO	GLU	ASN	SER	SER	SER	P453	A454	S455	K456	Y457	I458	R459	E460	G461	F462	Q463	T464	P465	L466	F467	F468	D469	K470	S471	Q530	L531	P532	L533	G534	K535	Y536	N537	N538	L539	E540	
T481	S482	S483	S484	Y485	Q486	L487	L488	K489	M490	Y491	A492	G493	E494	T495	L496	R497	M498	L499	N500	N501	F502	V503	Q504	D505	Q506	F507	S508	N509	I510	F511	L512	T513	M514	I515	S516	R517	F518	D519	N520	L521	K522	Y523	D524	L525	C526	Y527	D528	Y529	L530	P531	L532	L533	G534	K535	Y536	N537	N538	L539	E540		
T541	S542	L543	A544	A545	T546	F547	G548	S549	M550	E551	R552	V553	K554	F555	I556	T557	L558	E559	N560	F561	L562	A563	H564	K565	I566	T567	N568	N569	I570	R571	Y572	A573	L574	G575	D576	R577	I578	K579	Y580	I581	Q582	I583	D584	M585	V586	Q588	K589	S590	D591	F592	F593	I594	T595	K596	R597	K598	V599	Y600			
S601	N602	T603	G604	N605	G606	H607	F608	N609	D610	D611	F612	V613	R614	F615	K616	L617	I618	V619	N620	R621	S622	E623	C624	D625	K626	L627	V628	T629	K630	G631	P632	A633	H634	S635	E636	T637	M638	S639	T640	E641	A642	A643	V644	F645	M646	K647	F648	W649	I650	K652	S653	S654	L655	R656	K657	F658	K659	D660			
G661	S662	I663	T664	H665	G666	C667	V668	W669	S670	T671	S672	S673	S674	E675	P676	I677	I678	S679	S680	I681	V682	N683	F684	A685	L686	Q687	K688	H689	V690	S691	K692	K693	A694	Q695	I696	S697	N698	E699	T700	I701	K702	H705	M706	F707	L708	F709	L710	P711	M712	L713	F714	S715	S716	A717	K718	T719	S720	V721			
L722	N723	L724	S725	F726	S727	F728	N729	L730	K731	K732	S733	F734	D735	D736	L737	Y738	Y739	I740	R741	F742	Q743	M744	K745	L746	L747	L748	S749	V750	K751	S752	I753	L754	F755	V756	G757	S758	A759	F760	R761	Y762	T763	S764	L765	Q766	Q767	F768	V769	F770	F771	A772	Y773	S774	D775	P776	D777	F778	F779	Q780	D781		
V782	I783	L784	E785	F786	E787	L788	S789	P790	K791	M792	P793	D794	L795	I796	T797	S798	L799	E800	K801	A802	K803	T804	A805	F806	L807	L808	K809	L810	Q811	E812	E813	L814	S815	A816	N817	S818	S819	T820	Y821	R822	S823	F824	F825	S826	R827	D828	E829	S830	L831	P832	Y833	N834	L835	E836	L837	R838	T839	L840	N841		
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I902	S903	H904	S905	Y906	Q907	F908	Y909	S910	P911	Y912	V913	R914	L915	F916	K917	R918	W919	L920	D921	T922	H923	L924	L925	L926	G927	H928	I929	T930	D931	E932	L933	S1053	A934	S1054	G1055	L936	L937	A938	L939	K940	P941	F942	V943	D944	P945	A946	P947	Y948	F949	I950	P951	G952	S953	L954	E955	N956	G957	F958	L959	K960	V961
L962	K963	F964	I965	S966	Q967	W968	N969	W970	K971	D972	D973	P974	L975	I976	L977	D978	L979	V980	K981	P982	E983	ASP	ASP	I984	ARG	THR	PHE	GLU	THR	SER	I988	G1103	A934	G1055	L936	L937	A938	L939	K940	P941	F942	V943	D944	P945	A946	P947	Y948	F949	I950	P951	G952	S953	L954	E955	N956	G957	F958	L959	K960	V961	
M1022	F1024	T1025	M1026	L1027	L1028	M1029	S1030	D1031	P1032	M1033	G1034	T1035	H1036	L1037	Q1038	F1039	F1040	V1041	A1042	S1043	K1044	M1045	D1046	P1047	S1048	G1049	I1050	L1051	Y1052	S1053	S1054	G1055	I1056	P1057	L1058	P1059	I1060	T1061	R1063	L1064	T1065	A1066	L1067	A1068	K1069	V1070	A1071	H1072	V1073	L1074	L1075	Q1076	T1077	H1078	G1079	L1080	M1081				
Q1082	Q1083	T1084	I1085	M1086	L1087	L1088	F1089	T1090	P1091	G1092	L1093	K1094	I1095	Y1096	D1097	F1098	V1099	V1100	D1101	L1102	R1103	T1104	P1105	I1106	G1107	L1108	K1109	S1110	S1111	C1112	G1113	I1114	L1115	S1116	ALA	THR	GLU	PHE	LYS	ASN	ILE	THR	ASN	ASP	GLN	A1128	P1129	S1130	M1131	F1132	P1133	E1134	L1135	L1136	M1137	D1138	L1139	S1140	G1079	L1080	M1081



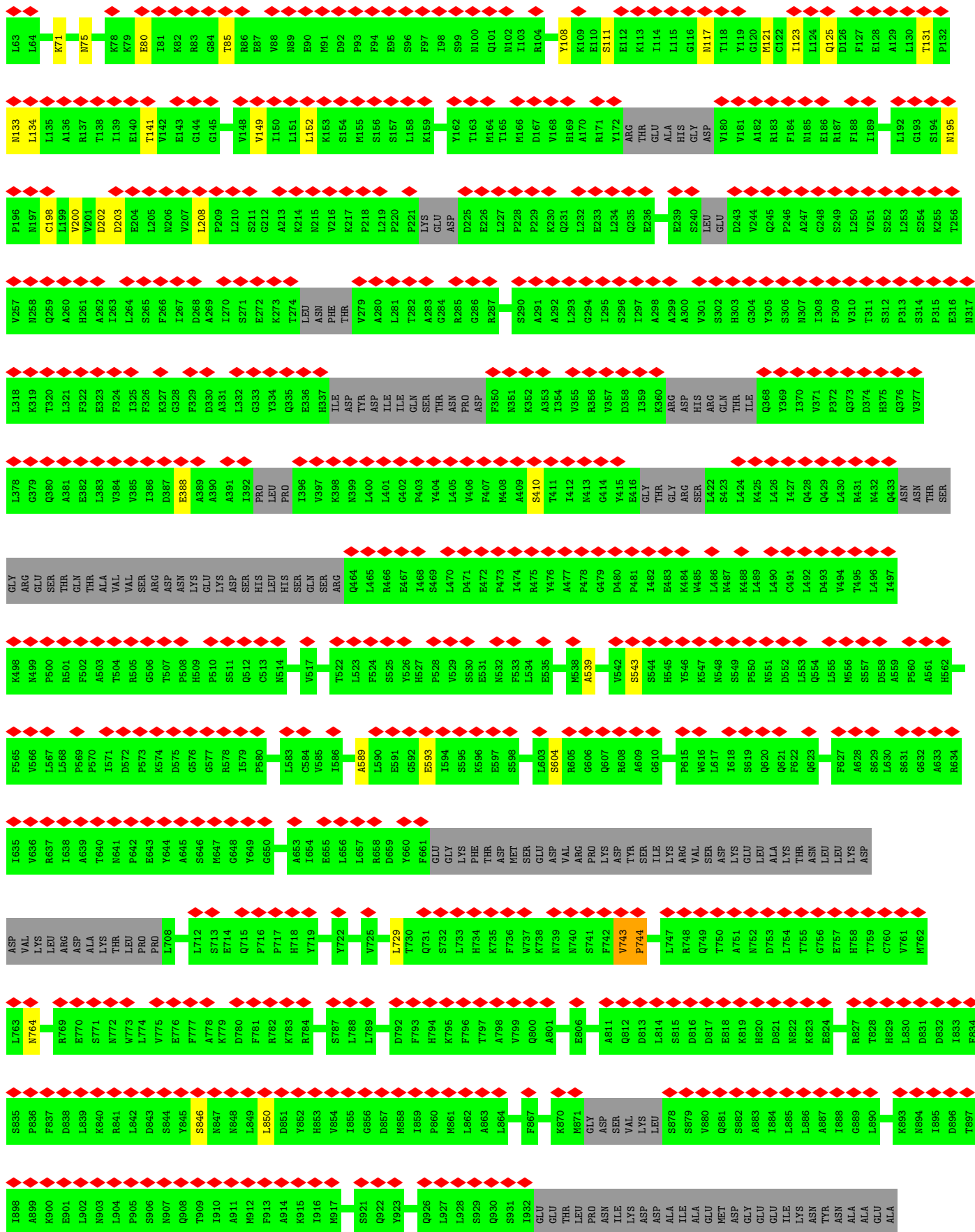
• Molecule 51: Ribosomal RNA-processing protein 7



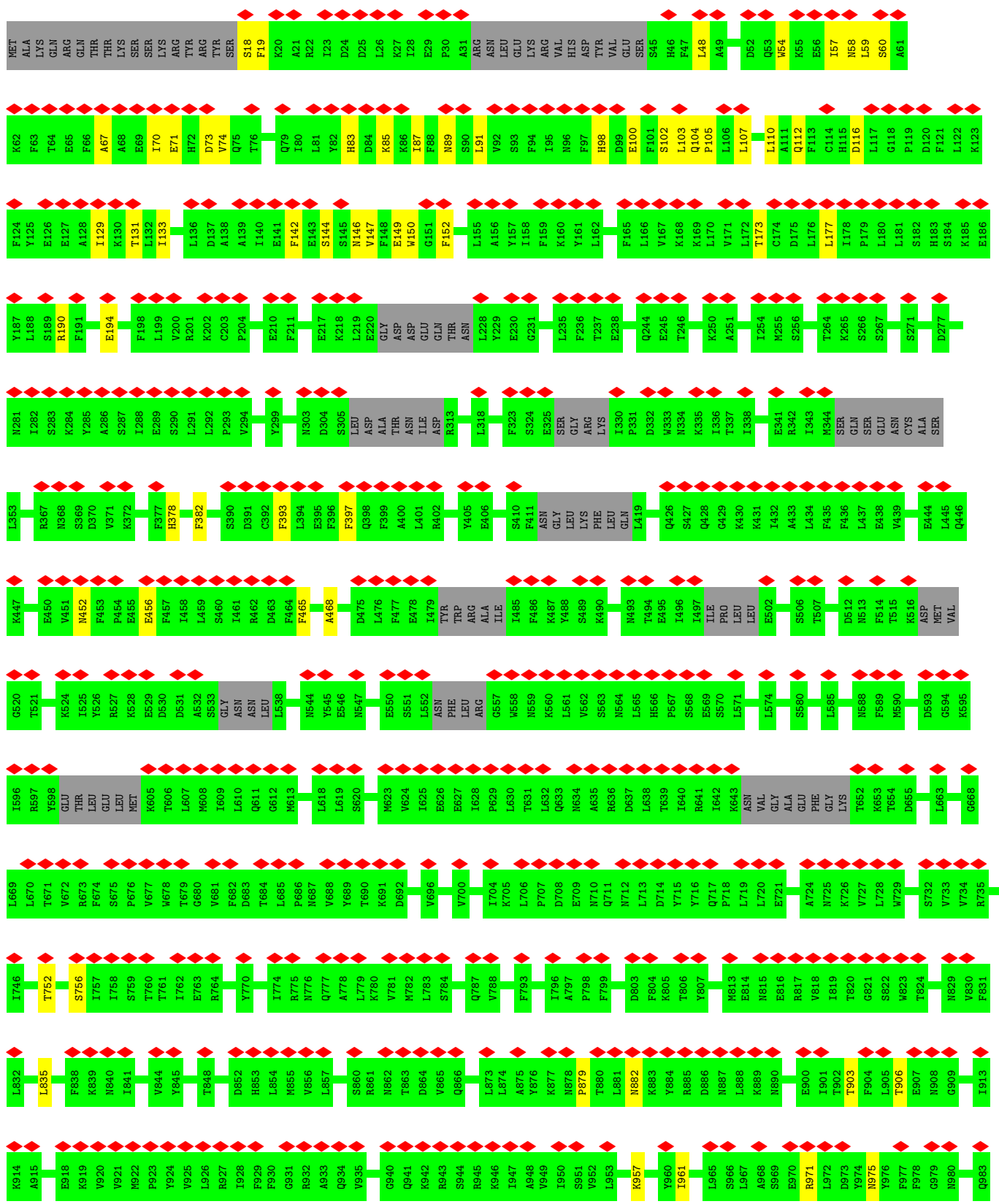
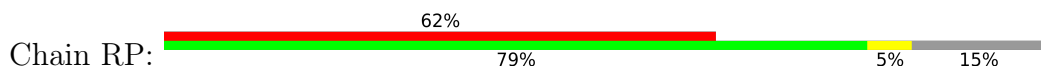
• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1



• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1



• Molecule 58: U3 small nucleolar RNA-associated protein 20



T1768	L1769	L1770	S1771	P1772	V1773	L1774	A1775	L1776	L1777	M1778	V1779	R1780	I1781	M1782	L1783	R1784	N1785	Q1786	E1787	K1788	S1789	E1791	L1792	L1793	R1794	R1795	Y1796	L1797	L1800	H1801	H1802	M1803	S1804	D1805	S1806	E1807	S1808	E1809	S1810	I1811	L1812	F1813	E1755	I1756	L1757	A1758	S1759	M1760	I1761	Q1820	E1821	S1822	E1823	MET	SER	ASN	SER	PRO																								
L1643	R1644	S1645	K1646	S1647	E1648	E1649	L1650	R1651	D1652	A1653	V1654	L1655	V1656	T1657	L1658	G1659	K1660	S1662	I1663	I1664	L1665	G1666	A1667	E1668	Y1669	L1670	L1671	F1672	V1673	I1674	K1675	L1676	L1677	M1678	A1679	L1680	L1681	K1682	R1683	G1684	S1685	Q1686	L1687	H1688	V1689	L1690	Y1691	Y1692	T1693	L1694	H1695	Y1696	L1697	L1698	K1699	H1702																										
L1705	K1706	H1707	S1708	D1709	L1710	D1711	L1712	S1713	S1714	S1715	M1716	L1718	K1719	I1721	M1722	E1723	M1724	I1725	F1726	G1727	F1728	A1729	G1730	K1733	D1734	S1735	E1736	H1739	T1740	K1741	V1742	K1743	E1744	K1745	K1746	S1747	M1748	Y1751	D1752	E1755	I1756	L1757	A1758	S1759	M1760	I1761	S1762	L1763	T1764	E1765	F1766	G1767																														
L1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	P1161	V1162	M1163	D1164	D1165	H1166	Y1167	Q1100	Q1101	P1102	S1103	S1104	L1105	F1109	L1110	N1115	P1116	S1117	L1118	Y1119	Q1120	F1121	L1122	Y1123	Y1124	K1049	M1050	A1051	S1052	M1053	L1054	G1058	L1059	K1060	C1061	V1069	G1070	M1071	T1072	S1076	T1077	S1078	M1079	E1080	L1081																												
F1210	I1211	D1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	L1220	I1221	S1222	S1223	L1224	I1225	S1226	I1227	L1228	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	S1176	S1177	C1178	L1179	I1181	L1182	P1183	S1184	L1185	Y1186	V1187	K1188	L1189	S1190	S1192	M1193	S1194	I1195	S1196	T1197	F1198	L1199	M1200	L1201	L1202	V1203	S1204	L1205	T1206	E1207	M1209																								
L1274	F1275	D1276	E1277	R1278	M1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	L1291	G1292	R1293	K1294	E1299	S1300	ASN	I1301	S1302	K1303	L1304	V1305	A1306	D1307	L1308	M1309	S1310	Y1311	S1312	S1313	S1314	R1315	M1316	H1317	E1318	Y1319	D1320	F1321	P1322	ARG	I1E	LEU	SER	THR	PHE	LYS	GLY	LEU	I1E	E1262	E1263	L1264	Y1265	L1266	T1267	I1268	S1269	S1270	L1271	F1272	K1273																	
SER	TYR	GLU	LEU	TRP	LEU	PRO	LEU	LEU	PHE	THR	PHE	LEU	HIS	PHE	LEU	ASN	ASN	LYS	GLU	GLU	LEU	ALA	LEU	ARG	THR	ASN	ALA	HIS	HIS	ALA	ILE	MET	LYS	PHE	ILE	D1376	F1377	M1379	E1380	K1381	P1382	M1383	L1438	L1439	L1440	L1441	E1386	A1387	S1388	K1389	S1390	I1391	S1392	M1393	L1394	K1395	D1396	I1397	THR	ASN	VAL	HIS	ILE	GLN	LEU	ASP	M1505	E1506	T1507	Q1508	L1509	A1510	I1511	G1512	L1513	L1514	A1515	Q1516	H1517	M1518	S1519	W1520
L1398	L1399	R1403	L1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	V1413	GLN	SER	TYR	VAL	V1420	L1421	S1422	Y1423	M1424	V1425	K1426	M1427	L1428	K1429	Y1430	F1431	L1432	D1433	F1434	E1435	D1436	M1437	A1438	L1439	L1440	L1441	Y1442	M1443	G1444	D1445	E1446	E1447	A1448	D1449	PHE	THR	ASN	ASN	VAL	HIS	ILE	GLN	LEU	M1505	E1506	T1507	Q1508	L1509	A1510	I1511	G1512	L1513	L1514	A1515	Q1516	H1517	M1518	S1519	W1520											
HIS	R1461	R1462	Q1463	R1464	A1465	L1466	K1467	L1469	G1470	E1471	H1472	A1473	H1474	Q1475	L1476	K1477	D1478	M1479	S1480	T1481	S1482	H1483	Y1484	L1485	I1486	P1487	M1488	I1489	E1490	H1491	Y1492	V1493	F1494	S1495	D1497	E1498	R1499	Y1500	R1501	M1502	M1505	E1506	T1507	Q1508	L1509	A1510	I1511	G1512	L1513	L1514	A1515	Q1516	H1517	M1518	S1519	W1520																										
M1521	Q1522	Y1523	K1524	A1525	L1526	L1527	R1528	R1529	Y1530	I1531	S1532	M1533	L1534	K1535	T1536	P1537	P1538	M1539	Q1540	M1541	K1542	Q1543	A1544	V1545	Q1546	L1547	I1548	VAL	GLN	LEU	SER	VAL	PRO	ARG	LEU	T1558	L1559	R1560	I1561	V1562	R1563	D1564	G1565	A1566	E1567	S1568	K1569	L1570	T1571	L1572	S1573	K1574	F1575	P1576	S1577	ASN	LEU	ASP																								
GLU	PRO	SER	ASN	PHE	ILE	LYS	GLN	LEU	TYR	PRO	THR	LEU	SER	LYS	ILE	GLY	THR	ARG	ASP	GLU	THR	ILE	E1608	R1609	M1610	P1611	I1612	A1613	E1614	A1615	L1616	V1617	F1672	V1673	I1674	K1675	L1676	L1677	M1678	A1679	L1680	L1681	L1682	D1627	I1628	T1629	M1630	F1631	L1632	P1633	S1634	I1635	L1636	T1637	M1638	I1639	C1640																									
L1643	R1644	S1645	K1646	S1647	E1648	E1649	L1650	R1651	D1652	A1653	V1654	L1655	V1656	T1657	L1658	G1659	K1660	S1662	I1663	I1664	L1665	G1666	A1667	E1668	Y1669	L1670	L1671	F1672	V1673	I1674	K1675	L1676	L1677	M1678	A1679	L1680	L1681	L1682	R1683	G1684	S1685	Q1686	L1687	H1688	V1689	L1690	Y1691	Y1692	T1693	L1694	H1695	Y1696	L1697	L1698	K1699	H1702																										
L1705	K1706	H1707	S1708	D1709	L1710	D1711	L1712	S1713	S1714	S1715	M1716	L1718	K1719	I1721	M1722	E1723	M1724	I1725	F1726	G1727	F1728	A1729	G1730	K1733	D1734	S1735	E1736	H1739	T1740	K1741	V1742	K1743	E1744	K1745	K1746	S1747	M1748	Y1751	D1752	E1755	I1756	L1757	A1758	S1759	M1760	I1761	S1762	L1763	T1764	E1765	F1766	G1767																														

GLN	ILE	PRO	LYS	LYS	LYS	VAL	ASP	GLN	VAL	ASP	GLU	LYS	ASP	PHE	LEU	ASN	VAL	GLU	SER	LYS	TYR	THR	ILE	ASN	SER	ASN	S1861	S1862	L1863	L1864	M1865	S1866	T1867	L1868	Q1869	K1870	L1873	D1874	R1877	M1878	V1879	I1880	T1881	R1882	H1883	H1884	S1885	F1886	L1887	T1888	V1889	S1890								
H1891	L1892	E1893	F1894	G1895	I1896	P1897	F1898	L1899	R1900	D1901	L1902	L1903	L1904	S1905	E1906	N1907	E1908	G1909	V1910	V1911	S1912	S1913	T1914	L1915	L1916	L1917	L1918	L1919	T1920	L1921	I1922	R1923	L1924	D1925	F1926	S1927	D1928	E1929	S1930	S1931	E1932	I1933	F1934	K1935	N1936	C1937	A1938	R1939	K1940	V1941	L1942	N1943	I1944	I1945	K1946	V1947	S1948	P1949	S1950	
T1951	S1952	E1953	E1954	L1955	C1956	Q1957	M1958	G1959	L1960	K1961	F1962	L1963	S1964	A1965	F1966	I1967	H1968	T1969	D1970	D1971	S1972	L1973	L1974	K1975	D1976	T1977	A1978	L1979	S1980	Y1981	V1982	L1983	G1984	R1985	V1986	L1987	P1988	D1989	L1990	N1991	E1992	P1993	S1994	R1995	Q1996	G1997	L1998	A1999	F2000	N2001	F2002	L2003	K2004	A2005	L2006	V2007	S2008	K2009	H2010	
I2011	M2012	L2013	P2014	E2015	L2016	Y2017	D2018	V2019	A2020	D2021	T2022	T2023	R2024	E2025	L2026	M2027	V2028	T2029	N2030	H2031	S2032	K2033	E2034	I2035	R2036	D2037	V2038	S2039	R2040	S2041	V2042	Y2043	Y2044	Q2045	F2046	L2047	M2048	E2049	Y2050	D2051	Q2052	S2053	K2054	G2055	G2056	L2057	E2058	K2059	Q2060	F2061	K2062	F2063	K2064	A2065	L2066	V2067	S2068	K2069	Q2069	Y2070
P2071	T2072	E2073	S2074	G2075	R2076	Q2077	S2078	V2079	M2080	E2081	L2082	L2083	N2084	L2085	I2086	T2087	T2088	K2089	ALA	ASN	P2092	A2093	L2094	L2095	S2096	K2097	L2098	S2099	S2100	S2101	F2102	F2103	L2104	A2105	L2106	V2107	N2108	V2109	S2110	F2111	N2112	D2113	D2114	A2115	P2116	R2117	C2118	R2119	E2120	M2121	A2122	S2123	V2124	L2125	I2126	S2127	T2128	M2129	L2130	
F2131	K2132	L2133	E2134	M2135	K2136	D2137	L2138	E2139	T2140	V2141	E2142	K2143	Y2144	I2145	A2146	A2147	TRP	LEU	LYS	GLN	VAL	D2153	N2154	A2155	S2156	F2157	L2158	N2159	L2160	G2161	L2162	K2163	T2164	Y2165	K2166	V2167	TRP	LEU	LYS	S2171	I2172	G2173	F2174	E2175	H2176	T2177	I2178	E2179	L2180	D2181	E2182	L2183	I2185	K2186	R2187	T2188	R2189	TRP		
ILE	LEU	ASP	THR	THR	VAL	GLY	SER	GLU	HIS	TRP	ASP	LEU	TYR	ALA	LEU	ASN	THR	F2213	S2214	S2215	Y2216	M2217	E2218	E2221	S2222	V2223	Y2224	K2225	H2226	G2227	PHE	LYS	ASP	ILE	V2232	D2233	G2234	I2235	I2236	T2237	C2238	L2239	L2240	Y2241	P2242	H2243	S2244	W2245	V2246	ARG	GLN	SER	ALA	A2251						
N2252	L2253	V2254	H2255	Q2256	L2257	I2258	A2259	N2260	K2261	D2262	K2263	L2264	E2265	I2266	S2267	L2268	T2269	ASN	LEU	GLU	ILE	GLN	T2275	L2276	A2277	T2278	R2279	L2280	L2281	H2282	Q2283	L2284	G2285	A2286	P2287	I2288	P2290	GLU	ASN	LEU	A2294	N2295	V2296	S2297	L2298	K2299	T2300	L2301	V2302	N2303	I2304	S2305	L2306	L2307	W2308	K2309	E2310	Q2311		
ARG	THR	PRO	PHE	ILE	MET	ASP	VAL	GLN	T2323	G2324	E2325	D2326	L2327	K2328	Y2329	T2330	T2331	A2332	I2333	D2334	V2337	T2338	R2339	ILE	G2342	I2343	T2344	R2345	S2346	D2347	E2348	H2349	R2350	M2351	F2354	M2355	S2356	K2357	LYS	ALA	CYS	ILE	GLN	LEU	A2365	L2366	L2367	V2368	Q2369	V2370	L2371	D2372	E2373							
D2374	E2375	V2376	I2377	A2378	E2379	G2380	E2381	LYS	ILE	LEU	LEU	PRO	VAL	TYR	GLY	Y2390	L2391	E2392	T2393	Y2395	S2396	R2397	A2398	V2399	D2400	E2401	Q2403	E2404	E2405	L2406	ARG	THR	LEU	SER	ASN	GLU	CYS	LYS	L2417	E2418	D2419	K2420	L2421	Q2422	V2423	S2424	D2425	F2426	T2427	K2428	I2429	Y2430	T2431	A2432	V2433					
K2434	Q2435	T2436	V2437	L2438	GLU	ARG	ARG	LYS	ARG	ARG	ARG	ARG	ARG	VAL	ALA	ILE	ALA	VAL	ALA	ASN	PRO	GLN	ILE	ILE	SER	ASN	ALA	ASP	LYS	LEU	ARG	LYS	HIS	ASP	ARG	LEU	GLU	ASP	GLY	THR	VAL	VAL	ASN	TRP	TYR	GLN	ARG	ARG	SER	SER	LYS	GLY	ASP	ARG	ALA					

• Molecule 59: U3 small nucleolar RNA-associated protein 14



MET	ALA	LYS	LYS	LYS	LYS	SER	SER	ARG	ARG	VAL	ASP	LEU	ALA	LEU	GLN	LEU	ALA	ALA	GLU	ARG	GLU	ILE	LYS	ASN	ALA	GLY	GLU	PHE	ASP	ASN	SER	SER	SER	ASP	ALA	ARG	ARG	ARG	ASN	GLY	THR	VAL	VAL	ASN	LEU	LEU	LEU	ARG	ARG	SER	SER	LYS	GLY	ASP	THR
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T1207	L1144	M1083	E1022	LEU	K901	E841	R781	E721	K661	M601
E1208	G1145	I1084	I1023	ASP	M902	I842	S782	G722	M662	Y602
R1209	E1146	C1085	F1024	ASP	S903	L843	K783	Q723	G663	T603
Y1210	M1147	A1086	M1025	ILE	L904	R844	E784	T724	I664	D604
C1211	P1148	G1087	K1026	ARC	F905	M845	R785	A725	N665	E605
V1212	P1149	F1088	K1027	GLU	P906	P846	K786	N726	S666	A606
V1213	L1153	V1089	M1028	HIS	L907	V847	V787	D727	K667	F607
V1214	Y1154	D1090	F1029	GLU	S908	E848	N788	P728	T668	R608
P1215	Y1155	H1091	L1030	SER	P909	S849	N789	L729	T669	K609
R1216	Y1156	V1092	L1031	THR	R910	I850	S790	Y730	D670	T610
F1217	S1156	A1093	G1032	PRO	F911	V851	G792	L732	L671	C611
G1218	L1157	V1094	K1033	GLY	S912	L852	G793	P733	E672	K612
S1219	H1158	R1095	L1034	ASP	K913	Q853	V794	L734	A673	I613
T1220	L1159	D1097	M1035	E978	M914	M854	Q794	L735	E674	H614
V1221	G1160	V1098	E1036	L979	L915	K855	S795	Y735	D675	Q615
D1222	G1161	L1099	I1037	K960	L916	S856	F796	S736	I676	K616
N1223	M1162	F1100	I1038	K961	V917	M857	E797	L737	D677	L617
D1224	M1163	P1101	V1039	K962	S918	A858	V798	L738	P618	P618
L1225	K1164	D1102	K1040	E982	D919	I859	G799	P739	S679	P619
K1226	T1165	D1103	L1041	L983	E920	H860	W800	T740	V680	G620
I1227	R1166	D1104	R1042	L984	K921	N861	W801	K741	Q881	A621
G1228	M1167	A1104	K1043	S985	A922	I862	S802	E742	E682	I622
W1229	M1168	K1105	Q1044	K986	C923	I863	K803	Q743	I683	L623
D1230	T1169	I1106	L1045	F987	C924	N864	A804	M744	D684	V624
L1231	D1172	M1108	M1046	K989	P925	F865	S805	R745	Q685	F625
N1232	L1173	T1107	Y1047	S990	Y926	P866	A806	V746	D686	L626
P1233	I1174	R1109	I1048	R991	I927	F867	N807	F747	K687	T627
I1234	A1174	T1110	I1049	S992	V928	P868	Q808	Q748	F688	G628
H1237	S1175	S1111	I1050	A929	A929	T869	R809	K749	K689	Q629
H1238	T1176	I1112	S1051	I930	P970	P871	S810	P750	Q630	Q630
K1239	P1177	I1113	M1052	F994	V931	D872	R812	P751	A691	E631
K1240	L1178	M1114	K1055	S995	S932	R873	A813	Q752	I692	I632
Q1241	A1179	N1117	L1056	K996	A933	V874	G814	G753	R693	T633
K1242	M1180	I1118	M1057	F1000	S935	A875	R815	S754	Y694	H634
W1245	I1181	P1119	N1058	F1000	V936	L876	R816	R755	E695	M635
T1246	A1182	F1120	A1059	S1001	G937	S877	G817	C757	ASP	V636
V1247	K1183	L1121	V1060	D1002	D938	K978	P818	I758	GLU	K637
K1249	G1185	A1122	M1061	V1003	P939	A879	G819	P759	GLY	R638
F1250	G1186	T1123	I1062	F1004	F940	I880	H820	A760	ASN	L639
I1251	L1187	T1125	M1063	R1005	I941	Q881	C821	A761	GLY	R640
T1252	L1188	P1126	E1065	L1006	N942	L882	Y822	N762	ASN	K641
R1253	L1189	M1127	D1066	L1007	E943	L883	R823	V763	GLY	R642
L1254	Y1190	I1128	L1067	S1008	E944	Q884	L824	A764	GLY	F643
L1255	S1191	E1129	K1068	V1009	E945	Y885	Y825	A765	ASP	P644
GLY	P1193	D1130	S1069	G947	L946	L886	S826	T766	GLU	F645
PHE	L1194	C1131	D1070	A1012	G947	G887	S827	S767	GLU	K646
THR	T1195	F1132	I1071	M1013	ILE	A888	A828	L768	ASP	K647
ILE	T1196	V1133	P1072	D1014	ASN	L889	V829	L769	GLY	N648
THR	G1196	Y1134	S1073	D1014	GLU	V890	E712	E712	GLY	S649
GLY	Q1197	I1135	V1074	V1015	ILE	D890	F830	I770	ASN	K650
GLU	H1136	H1136	V1074	V1016	SER	N891	E831	P771	GLY	Y651
GLU	P1137	P1137	I1075	P1017	ARG	K992	H832	G772	ASN	N652
LYS	L1139	T1138	Q1076	K1018	LYS	E993	D833	V773	GLY	F645
LYS	S1139	I1140	I1077	E1019	PRO	M994	F834	R774	GLY	K646
LYS	L1141	L1141	K1078	Q1020	ASN	I895	E835	E775	GLY	K647
LYS	L1142	L1142	L1079	K1021	PRO	T896	Q836	V776	GLY	N648
LYS	M1143	M1143	K1081		ASN	E997	F837	V777	GLY	S649
LYS	P1206	P1206			ASN	D898	S838	D778	GLY	K651
LYS						G899	K839	S779	ASP	N653
LYS						R900	P840	G780	ASP	K654
LYS									ASP	D654
LYS									ASP	L655
LYS									ASP	E656
LYS									ASP	L719
LYS									ASP	T720

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3841	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ADP, ZN, 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	3A	0.46	0/4141	0.62	3/6433 (0.0%)
2	5A	0.40	0/4605	0.46	1/7168 (0.0%)
3	SA	0.35	1/31727 (0.0%)	0.50	17/49393 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.27	0/1020	0.64	0/1374
12	SO	0.40	0/1109	0.63	0/1495
13	SP	0.48	0/879	0.83	0/1186
14	SR	0.52	0/990	0.77	3/1335 (0.2%)
15	SX	0.46	0/1020	0.63	0/1371
16	SY	0.48	0/798	0.65	0/1065
17	SZ	0.36	0/822	0.73	0/1103
18	Sc	0.40	0/613	0.63	0/828
19	Sd	0.50	0/499	0.72	2/670 (0.3%)
20	3B	0.51	0/1901	0.66	0/2567
20	3C	0.38	0/1796	0.69	2/2424 (0.1%)
21	3D	0.40	0/2891	0.62	0/3895
22	3E	0.38	0/3059	0.62	0/4153
23	3F	0.36	0/3715	0.64	0/5001
24	3G	0.51	0/928	0.72	1/1262 (0.1%)
24	3H	0.46	0/928	0.70	0/1262
25	A4	0.43	0/5321	0.66	0/7207
26	A5	0.44	0/4044	0.65	0/5493
27	A8	0.38	0/3249	0.86	12/4454 (0.3%)
28	A9	0.30	0/951	0.61	0/1287
29	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
30	AF	0.48	0/3993	0.68	0/5413

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.42	0/6699	0.64	3/9077 (0.0%)
32	B1	0.59	0/6474	0.70	3/8763 (0.0%)
33	B2	0.39	0/6628	0.69	2/8954 (0.0%)
34	B3	0.35	0/6014	0.70	0/8137
35	B8	0.55	0/3848	0.63	0/5218
36	BE	0.54	0/6580	0.65	2/8901 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.32	0/499	0.62	0/659
39	5C	0.58	0/3690	0.67	2/4991 (0.0%)
40	5D	0.47	0/1417	0.74	0/1885
41	5E	0.42	0/1580	0.87	1/2115 (0.0%)
42	5F	0.38	0/1559	0.81	2/2097 (0.1%)
43	5G	0.34	0/1792	0.76	3/2425 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.36	0/1151	0.56	0/1535
47	5K	0.52	0/1426	0.66	0/1917
48	RA	0.28	0/2769	0.66	2/3753 (0.1%)
49	RB	0.37	0/1121	0.79	0/1487
50	RE	0.33	0/8924	0.64	4/12070 (0.0%)
51	RF	0.28	0/2004	0.66	1/2697 (0.0%)
52	RG	0.32	0/1727	0.70	0/2329
52	RH	0.37	0/1828	0.59	0/2470
53	RJ	0.45	0/6514	0.62	0/8768
54	RK	0.39	0/2832	0.64	0/3825
55	RL	0.21	0/4549	0.51	1/6241 (0.0%)
55	RM	0.16	0/3765	0.44	1/5218 (0.0%)
56	RN	0.31	0/4591	0.63	1/6187 (0.0%)
57	RO	0.32	0/3849	0.63	0/5261
58	RP	0.21	0/12225	0.54	4/16812 (0.0%)
59	RQ	0.43	0/1879	0.73	3/2564 (0.1%)
60	RS	0.30	0/2104	0.70	1/2854 (0.0%)
61	RY	0.23	0/307	0.53	0/415
63	RT	0.43	0/1611	0.77	1/2174 (0.0%)
64	ST	0.35	0/908	0.74	2/1221 (0.2%)
65	SU	0.56	1/1130 (0.1%)	0.94	3/1517 (0.2%)
66	RD	0.26	0/2453	0.67	2/3308 (0.1%)
67	RZ	0.27	0/6737	0.60	3/9099 (0.0%)
All	All	0.39	3/232365 (0.0%)	0.63	97/322899 (0.0%)

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
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
50	RE	0	1
51	RF	0	1
53	RJ	0	2
54	RK	0	1
55	RL	0	1
55	RM	0	1
56	RN	0	1
57	RO	0	1
58	RP	0	3
59	RQ	0	4
67	RZ	0	2
All	All	0	75

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	SU	46	PRO	C-N	12.73	1.50	1.33
29	AE	564	VAL	C-N	5.40	1.40	1.34
3	SA	1572	G	O3'-P	-5.25	1.53	1.61

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	SU	46	PRO	CA-C-N	17.60	137.85	119.89
65	SU	46	PRO	C-N-CA	17.60	137.85	119.89
3	SA	1541	G	P-O5'-C5'	-10.70	104.84	120.90
27	A8	316	PRO	N-CA-CB	10.50	109.84	102.81
3	SA	1541	G	O5'-C5'-C4'	9.05	125.08	111.50

There are no chirality outliers.

5 of 75 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	58	0
2	5A	4117	0	2068	38	0
3	SA	28383	0	14310	307	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	43	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	31	0
8	SI	1321	0	1387	22	0
9	SJ	1324	0	1344	46	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	SO	1087	0	1152	9	0
13	SP	868	0	894	63	0
14	SR	973	0	1029	18	0
15	SX	1003	0	1040	15	0
16	SY	786	0	843	7	0
17	SZ	809	0	842	15	0
18	Sc	603	0	623	9	0
19	Sd	497	0	535	3	0
20	3B	1865	0	1910	30	0
20	3C	1763	0	1805	46	0
21	3D	2848	0	2815	43	0
22	3E	3028	0	2813	58	0
23	3F	3643	0	3654	78	0
24	3G	916	0	964	11	0
24	3H	916	0	964	25	0
25	A4	5226	0	5199	96	0
26	A5	3976	0	3919	62	0
27	A8	3229	0	2281	131	0
28	A9	939	0	898	47	0
29	AE	9955	0	7968	102	0
30	AF	3911	0	3906	77	0
31	AG	6570	0	6473	142	0
32	B1	6331	0	6236	140	0
33	B2	6502	0	6493	126	0
34	B3	5919	0	6007	147	0
35	B8	3764	0	3757	54	0
36	BE	6450	0	6420	102	0
37	B6	2800	0	2517	32	0
38	5B	495	0	561	12	0
39	5C	3612	0	3578	62	0
40	5D	1396	0	1407	49	0
41	5E	1564	0	1592	180	0
42	5F	1530	0	1572	84	0
43	5G	1756	0	1765	56	0
44	5H	596	0	661	7	0
45	5I	3765	0	3714	79	0
46	5J	1131	0	1161	19	0
47	5K	1403	0	1484	20	0
48	RA	2709	0	2622	61	0
49	RB	1108	0	1087	27	0
50	RE	8716	0	8828	236	0
51	RF	1963	0	1942	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	RG	1701	0	1767	39	0
52	RH	1799	0	1872	28	0
53	RJ	6379	0	6506	152	0
54	RK	2781	0	2878	53	0
55	RL	4539	0	2874	26	0
55	RM	3779	0	1650	9	0
56	RN	4529	0	4262	87	0
57	RO	3766	0	3269	58	0
58	RP	12171	0	7749	78	0
59	RQ	1853	0	1474	30	0
60	RS	2051	0	2096	53	0
61	RY	299	0	275	6	0
62	X1	110	0	29	4	0
63	RT	1587	0	1583	73	0
64	ST	896	0	930	60	0
65	SU	1112	0	1124	65	0
66	RD	2412	0	2263	42	0
67	RZ	6604	0	6637	120	0
68	5K	1	0	0	0	0
68	Sc	1	0	0	0	0
69	RJ	32	0	12	2	0
70	RJ	1	0	0	0	0
71	RZ	27	0	12	1	0
All	All	225233	0	195610	3575	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 9.

The worst 5 of 3575 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)
27:A8:596:LYS:HE3	27:A8:637:LEU:CD2	1.25	1.57
50:RE:1203:ASN:HD22	50:RE:1219:ILE:CG2	1.50	1.23
32:B1:382:THR:O	41:5E:481:PRO:HB3	1.40	1.21
3:SA:1478:G:OP1	65:SU:39:THR:HB	1.38	1.20
41:5E:366:GLU:OE2	43:5G:247:ILE:HG21	1.40	1.20

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	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	67
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/155 (77%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	51
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	49
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	78
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	54
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	5	28
28	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
29	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
30	AF	489/513 (95%)	443 (91%)	46 (9%)	0	100	100
31	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	48	83
32	B1	787/900 (87%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	723 (89%)	88 (11%)	2 (0%)	43	78
34	B3	733/817 (90%)	605 (82%)	126 (17%)	2 (0%)	36	72
35	B8	469/594 (79%)	440 (94%)	29 (6%)	0	100	100
36	BE	814/939 (87%)	764 (94%)	50 (6%)	0	100	100
37	B6	368/440 (84%)	342 (93%)	26 (7%)	0	100	100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
39	5C	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	43	78
40	5D	165/250 (66%)	146 (88%)	19 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	11	46
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
47	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
48	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
49	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	16	54
50	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
51	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
52	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
52	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
53	RJ	784/1183 (66%)	722 (92%)	61 (8%)	1 (0%)	48	83
54	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
55	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	72
55	RM	738/1056 (70%)	626 (85%)	108 (15%)	4 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	RN	593/810 (73%)	546 (92%)	46 (8%)	1 (0%)	43	78
57	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
58	RP	2042/2493 (82%)	1816 (89%)	226 (11%)	0	100	100
59	RQ	267/899 (30%)	227 (85%)	40 (15%)	0	100	100
60	RS	247/480 (52%)	225 (91%)	22 (9%)	0	100	100
61	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
63	RT	206/326 (63%)	178 (86%)	27 (13%)	1 (0%)	24	63
64	ST	106/146 (73%)	89 (84%)	17 (16%)	0	100	100
65	SU	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	18	56
66	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	12	49
67	RZ	834/1267 (66%)	739 (89%)	91 (11%)	4 (0%)	24	63
All	All	25032/35454 (71%)	22530 (90%)	2459 (10%)	43 (0%)	44	78

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	A8	258	PRO
27	A8	309	PRO
27	A8	325	PRO
27	A8	390	PRO
27	A8	392	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	78
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	72
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	83
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	64
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	72
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/136 (81%)	108 (98%)	2 (2%)	51	68
12	SO	117/128 (91%)	116 (99%)	1 (1%)	70	79
13	SP	90/105 (86%)	88 (98%)	2 (2%)	45	64
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	106 (98%)	2 (2%)	50	67
16	SY	85/120 (71%)	83 (98%)	2 (2%)	43	64
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	188 (99%)	2 (1%)	65	76
21	3D	296/435 (68%)	295 (100%)	1 (0%)	86	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	84	84
23	3F	396/503 (79%)	392 (99%)	4 (1%)	68	78
24	3G	100/104 (96%)	100 (100%)	0	100	100
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	591/713 (83%)	584 (99%)	7 (1%)	63	75
26	A5	433/574 (75%)	429 (99%)	4 (1%)	70	79
27	A8	174/657 (26%)	168 (97%)	6 (3%)	32	54
28	A9	89/533 (17%)	89 (100%)	0	100	100
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	84
30	AF	437/454 (96%)	431 (99%)	6 (1%)	59	72
31	AG	750/826 (91%)	739 (98%)	11 (2%)	57	72
32	B1	696/789 (88%)	685 (98%)	11 (2%)	55	70
33	B2	712/832 (86%)	705 (99%)	7 (1%)	68	78
34	B3	665/719 (92%)	656 (99%)	9 (1%)	59	72
35	B8	421/529 (80%)	417 (99%)	4 (1%)	68	78
36	BE	718/819 (88%)	712 (99%)	6 (1%)	73	80
37	B6	251/414 (61%)	249 (99%)	2 (1%)	73	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	5B	57/196 (29%)	56 (98%)	1 (2%)	51	68
39	5C	394/480 (82%)	392 (100%)	2 (0%)	81	83
40	5D	156/234 (67%)	156 (100%)	0	100	100
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	33
42	5F	171/172 (99%)	169 (99%)	2 (1%)	63	75
43	5G	194/258 (75%)	194 (100%)	0	100	100
44	5H	63/538 (12%)	63 (100%)	0	100	100
45	5I	416/443 (94%)	412 (99%)	4 (1%)	68	78
46	5J	125/200 (62%)	125 (100%)	0	100	100
47	5K	157/169 (93%)	157 (100%)	0	100	100
48	RA	303/636 (48%)	299 (99%)	4 (1%)	61	74
49	RB	117/315 (37%)	116 (99%)	1 (1%)	70	79
50	RE	984/1125 (88%)	976 (99%)	8 (1%)	73	80
51	RF	221/274 (81%)	221 (100%)	0	100	100
52	RG	195/222 (88%)	193 (99%)	2 (1%)	68	78
52	RH	206/222 (93%)	205 (100%)	1 (0%)	81	83
53	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	81
54	RK	307/312 (98%)	304 (99%)	3 (1%)	68	78
55	RL	164/934 (18%)	164 (100%)	0	100	100
56	RN	422/732 (58%)	421 (100%)	1 (0%)	87	87
57	RO	329/506 (65%)	326 (99%)	3 (1%)	70	79
58	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	83
59	RQ	136/808 (17%)	133 (98%)	3 (2%)	45	64
60	RS	225/421 (53%)	224 (100%)	1 (0%)	84	84
61	RY	31/482 (6%)	31 (100%)	0	100	100
63	RT	158/282 (56%)	155 (98%)	3 (2%)	50	67
64	ST	98/129 (76%)	96 (98%)	2 (2%)	48	66
65	SU	115/116 (99%)	113 (98%)	2 (2%)	53	69
66	RD	226/1544 (15%)	224 (99%)	2 (1%)	70	79
67	RZ	718/1140 (63%)	715 (100%)	3 (0%)	84	84
All	All	18207/30620 (60%)	18031 (99%)	176 (1%)	65	78

5 of 176 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	5E	451	LEU
52	RG	100	LEU
41	5E	517	LYS
48	RA	155	VAL
54	RK	26	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 431 such sidechains are listed below:

Mol	Chain	Res	Type
36	BE	877	ASN
45	5I	418	HIS
58	RP	1802	HIS
37	B6	166	ASN
41	5E	493	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)
3	SA	1311/1812 (72%)	501 (38%)	32 (2%)
All	All	1666/2845 (58%)	610 (36%)	44 (2%)

5 of 610 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1475	A
3	SA	1533	C
3	SA	1486	G
3	SA	1521	G

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Mol	Chain	Res	Type
3	SA	1540	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 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
69	GTP	RJ	1201	70	33,34,34	0.57	0	50,54,54	0.72	1 (2%)
71	ADP	RZ	1301	-	28,29,29	1.43	5 (17%)	43,45,45	1.84	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
69	GTP	RJ	1201	70	-	3/22/38/38	0/3/3/3
71	ADP	RZ	1301	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	RZ	1301	ADP	C5-C4	4.64	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	RZ	1301	ADP	C5-C6	2.81	1.48	1.41
71	RZ	1301	ADP	C8-N7	2.37	1.36	1.31
71	RZ	1301	ADP	C5-N7	-2.24	1.35	1.39
71	RZ	1301	ADP	PA-O3A	2.17	1.61	1.59

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RZ	1301	ADP	C5-C4-N3	-5.89	118.61	126.72
71	RZ	1301	ADP	N3-C4-N9	4.59	134.98	127.17
71	RZ	1301	ADP	C2-N3-C4	3.87	121.27	111.83
71	RZ	1301	ADP	C4-C5-N7	-3.68	106.37	110.58
71	RZ	1301	ADP	N3-C2-N1	-3.47	123.33	128.58

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RZ	1301	ADP	C5'-O5'-PA-O2A
71	RZ	1301	ADP	C5'-O5'-PA-O3A
69	RJ	1201	GTP	O4'-C4'-C5'-O5'
69	RJ	1201	GTP	C3'-C4'-C5'-O5'
69	RJ	1201	GTP	C4'-C5'-O5'-PA

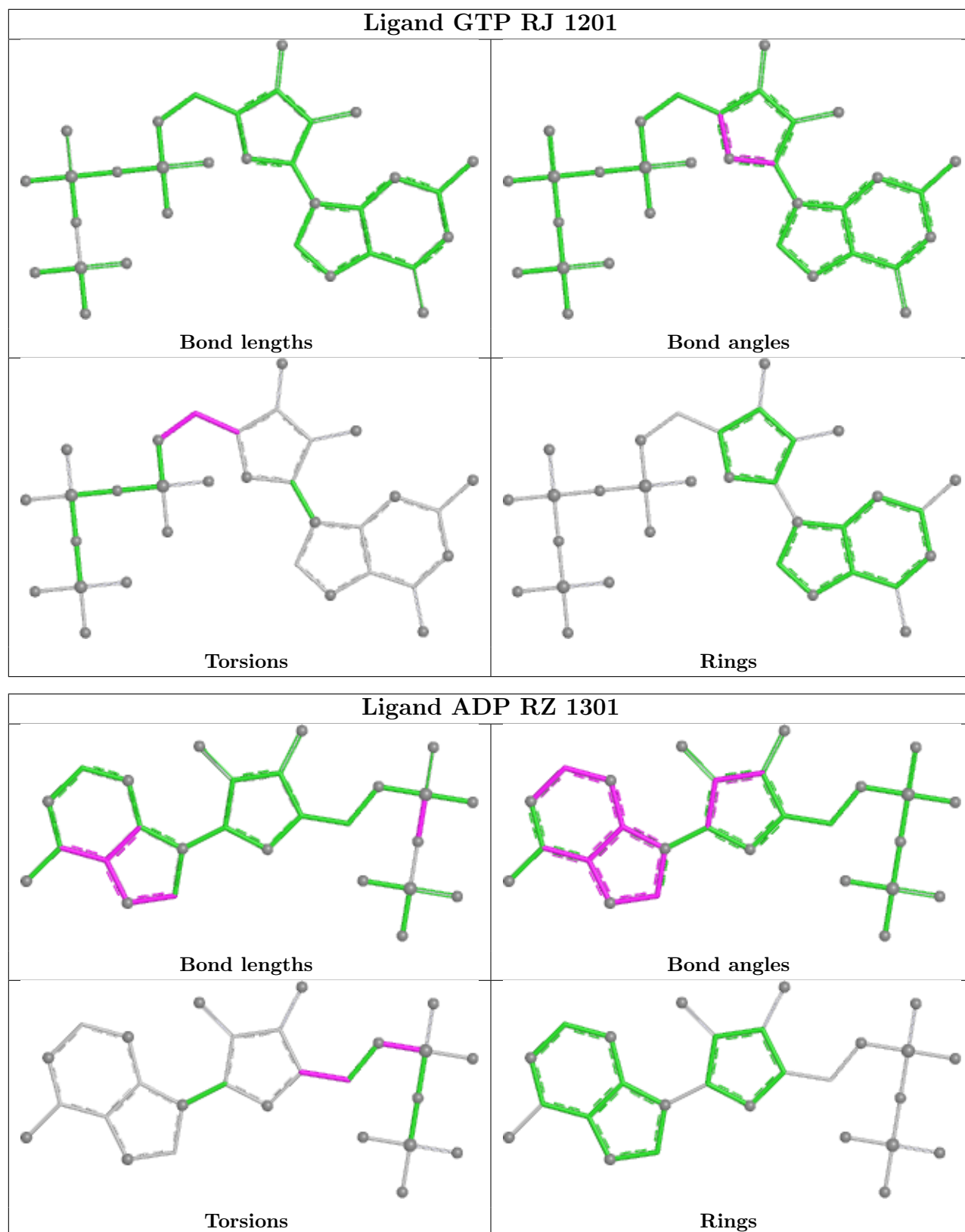
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	RJ	1201	GTP	2	0
71	RZ	1301	ADP	1	0

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

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

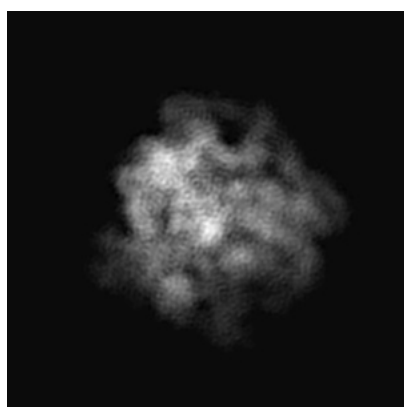
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30588. These allow visual inspection of the internal detail of the map and identification of artifacts.

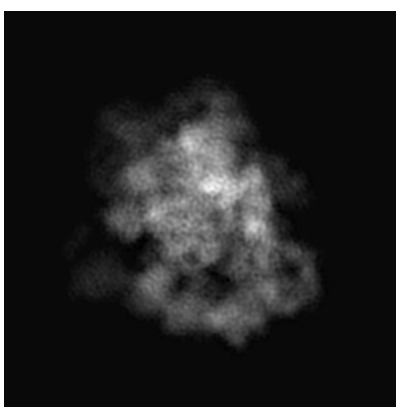
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

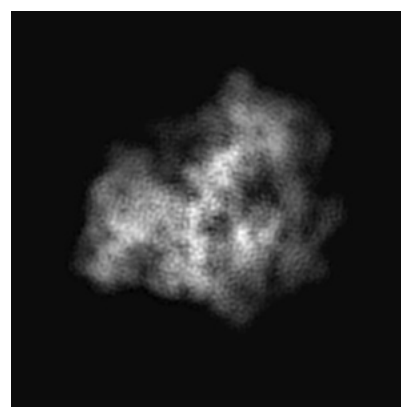
6.1.1 Primary map



X



Y

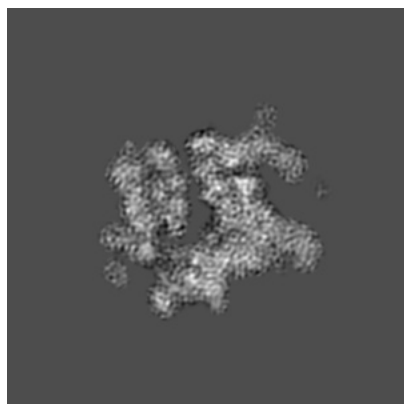


Z

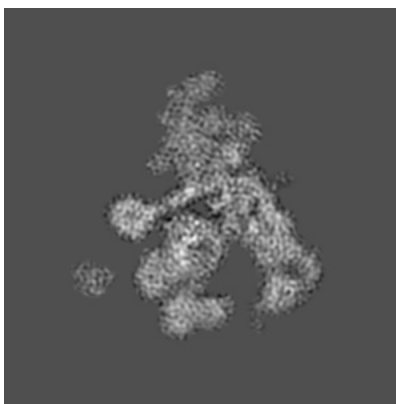
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

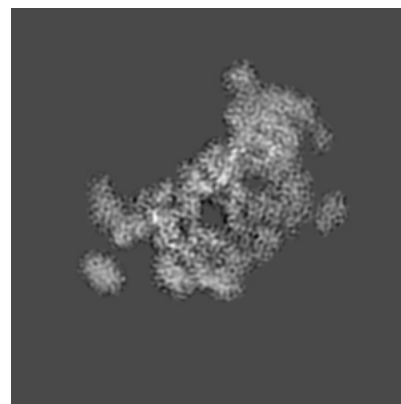
6.2.1 Primary map



X Index: 200



Y Index: 200

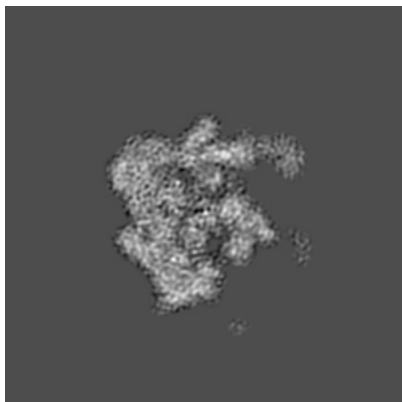


Z Index: 200

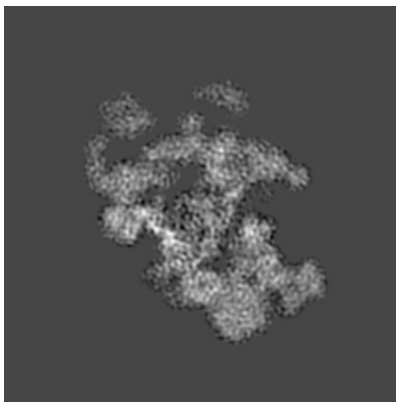
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

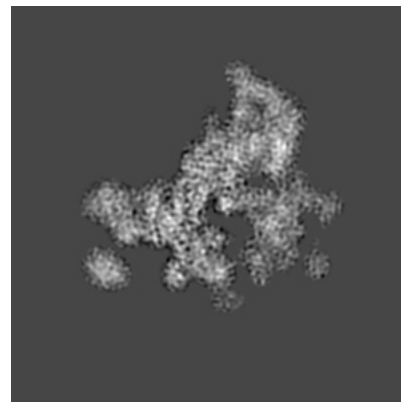
6.3.1 Primary map



X Index: 185



Y Index: 174

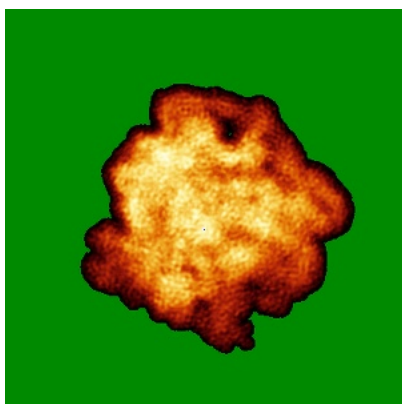


Z Index: 185

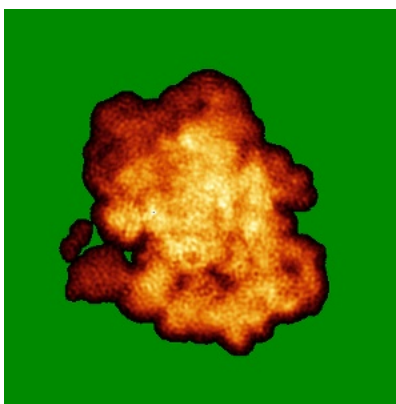
The images above show the largest variance slices of the map in three orthogonal directions.

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

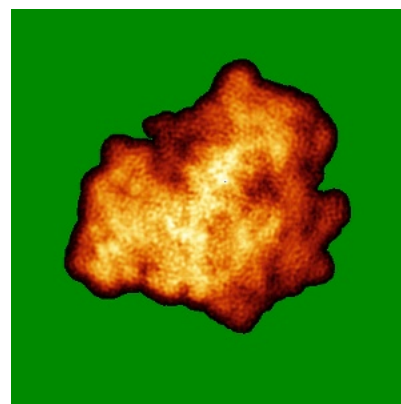
6.4.1 Primary map



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

This section was not generated.

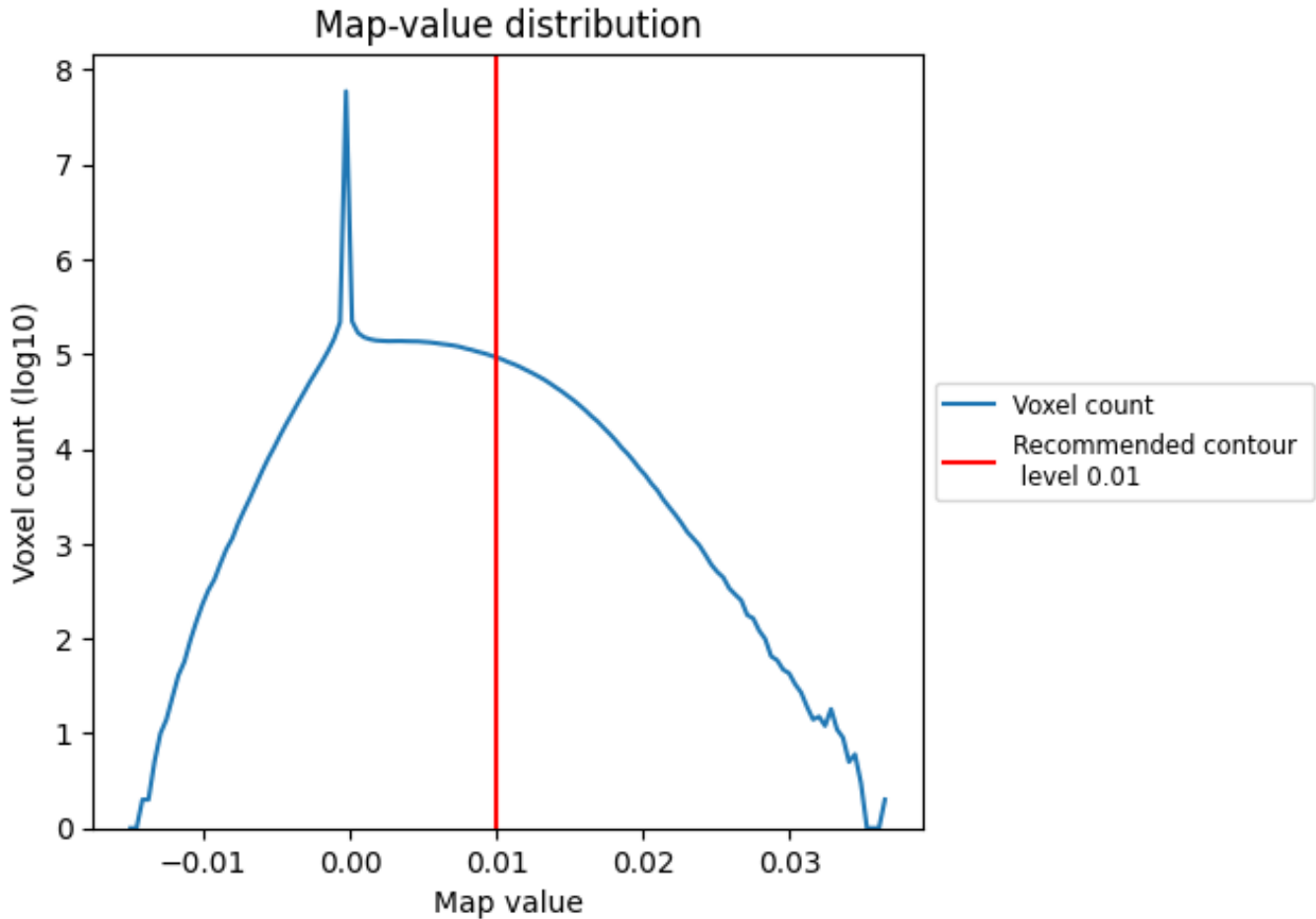
6.6 Mask visualisation

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

7 Map analysis [i](#)

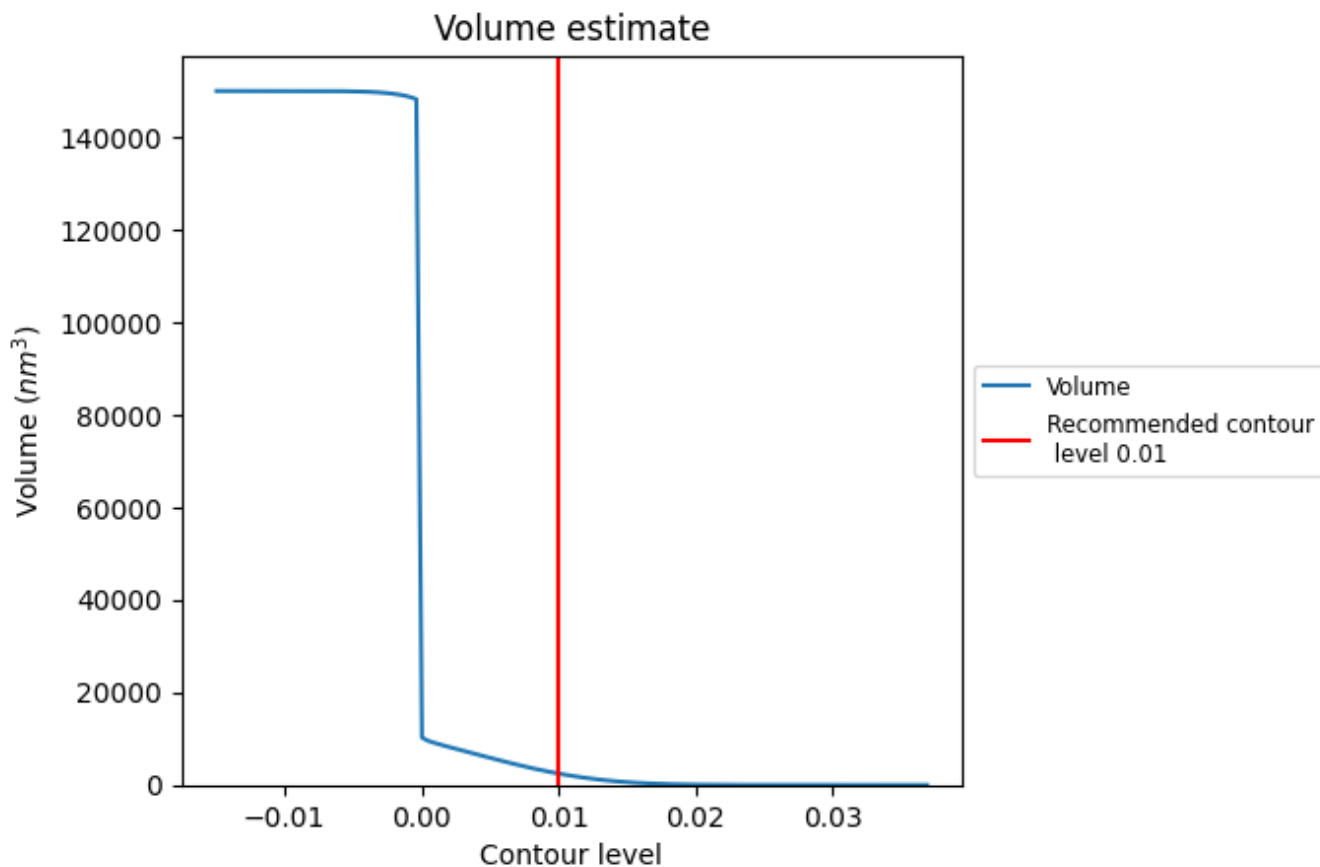
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

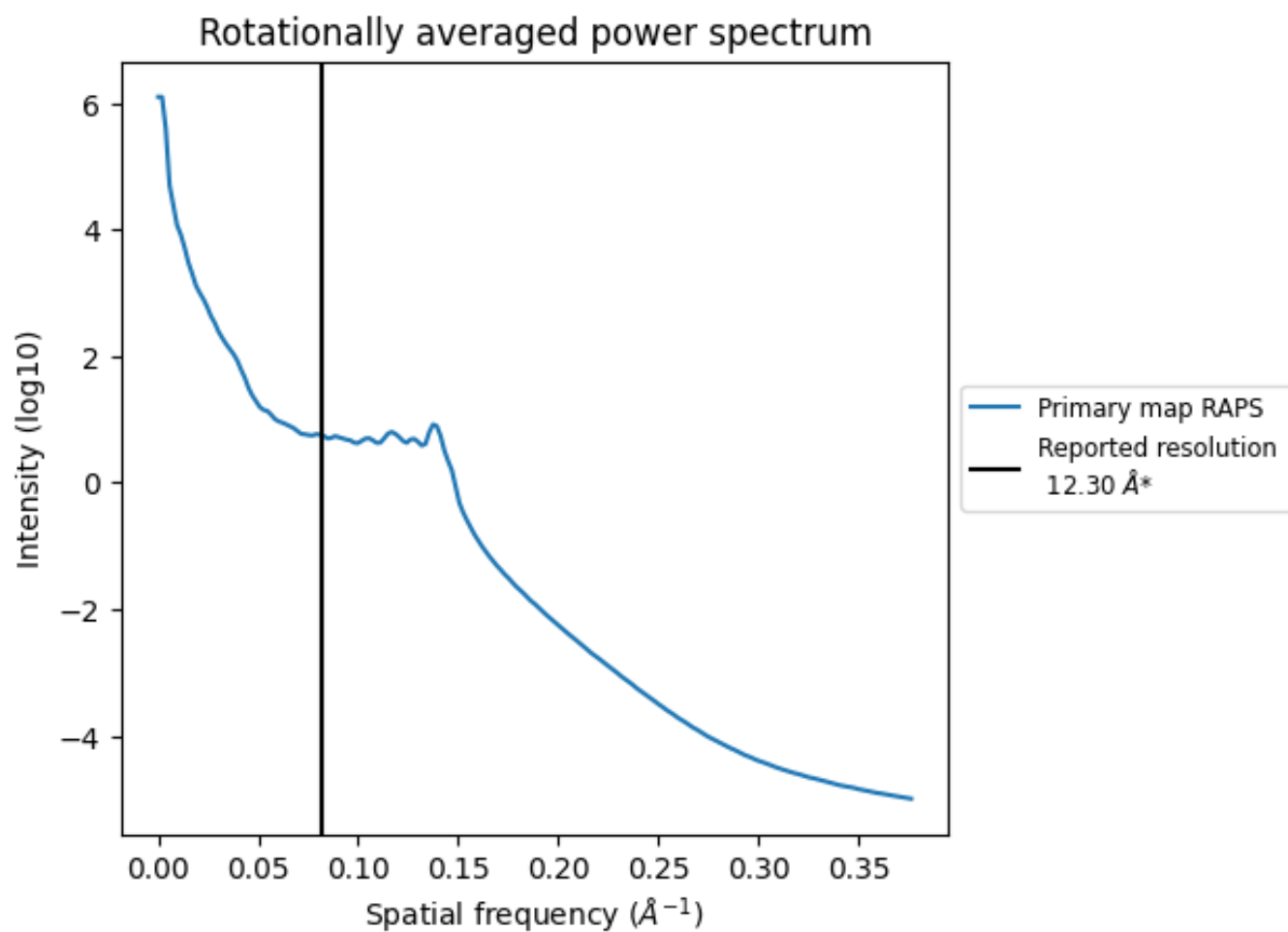
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2465 nm³; this corresponds to an approximate mass of 2227 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.081 Å⁻¹

8 Fourier-Shell correlation

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

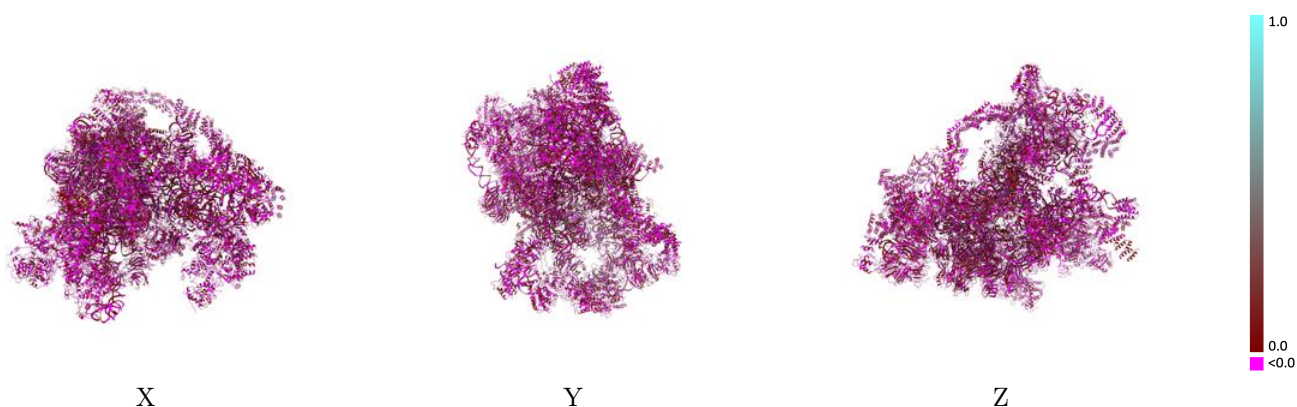
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30588 and PDB model 7D63. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

This section was not generated.

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

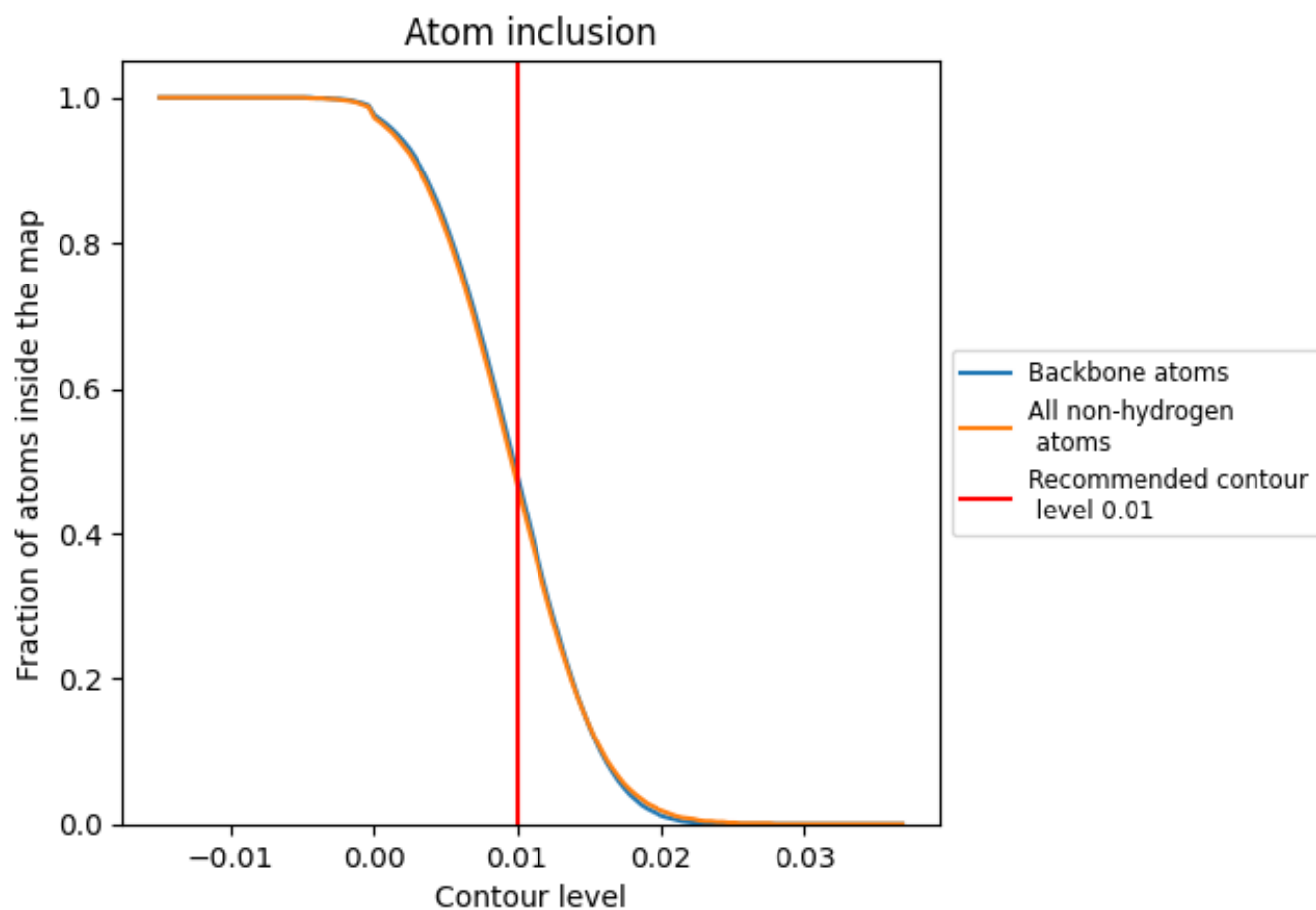


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 47% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4660	 0.0430
3A	 0.7300	 0.0750
3B	 0.4850	 0.0720
3C	 0.5050	 0.0300
3D	 0.6480	 0.0740
3E	 0.5400	 0.0530
3F	 0.6800	 0.0520
3G	 0.7000	 0.0700
3H	 0.5480	 0.0570
5A	 0.4620	 0.0410
5B	 0.1730	 0.0220
5C	 0.5190	 0.0420
5D	 0.3620	 0.0510
5E	 0.4860	 0.0690
5F	 0.4840	 0.0750
5G	 0.4940	 0.0710
5H	 0.5400	 0.0360
5I	 0.6100	 0.0490
5J	 0.3960	 0.0810
5K	 0.3810	 0.0530
A4	 0.6800	 0.0470
A5	 0.6300	 0.0460
A8	 0.5600	 0.0260
A9	 0.6910	 0.0700
AE	 0.3060	 0.0360
AF	 0.6460	 0.0650
AG	 0.7180	 0.0530
B1	 0.6050	 0.0590
B2	 0.7070	 0.0560
B3	 0.5320	 0.0300
B6	 0.4550	 0.0650
B8	 0.5910	 0.0510
BE	 0.6960	 0.0560
RA	 0.3730	 0.0180
RB	 0.3330	 0.0360



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Chain	Atom inclusion	Q-score
RD	 0.0000	 -0.0180
RE	 0.0600	 0.0080
RF	 0.0430	 0.0160
RG	 0.6280	 0.0530
RH	 0.4680	 0.0300
RJ	 0.5960	 0.0590
RK	 0.6340	 0.0620
RL	 0.2220	 0.0320
RM	 0.0710	 0.0130
RN	 0.4700	 0.0370
RO	 0.4470	 0.0330
RP	 0.2620	 0.0280
RQ	 0.2180	 0.0110
RS	 0.6410	 0.0240
RT	 0.0870	 -0.0040
RY	 0.1740	 -0.0020
RZ	 0.0700	 0.0220
SA	 0.5940	 0.0540
SC	 0.1120	 0.0220
SF	 0.5140	 0.0200
SG	 0.6420	 0.0910
SH	 0.4740	 0.0360
SI	 0.1110	 0.0190
SJ	 0.5740	 0.0260
SK	 0.5500	 0.0880
SM	 0.5310	 -0.0050
SO	 0.1890	 0.0210
SP	 0.1960	 0.0140
SR	 0.5560	 0.0800
ST	 0.1510	 0.0370
SU	 0.1310	 0.0350
SX	 0.1590	 0.0140
SY	 0.5430	 0.0730
SZ	 0.5910	 0.0530
Sc	 0.1360	 0.0130
Sd	 0.6440	 0.0760
X1	 0.2730	 0.0560