



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 06:52 AM JST

PDB ID : 6LQP
EMDB ID : EMD-0949
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State A)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 3.20 Å(reported)
Based on initial model : 6KE6

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

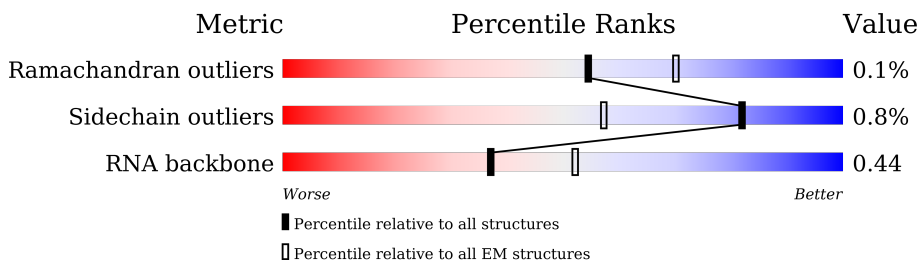
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



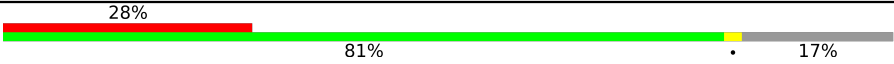
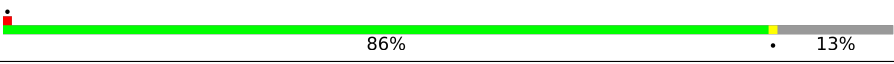
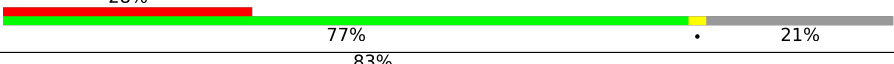


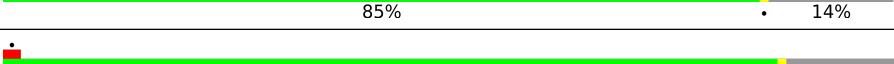
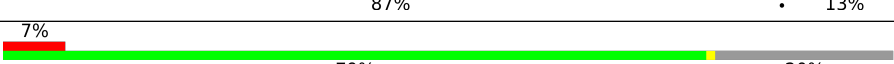
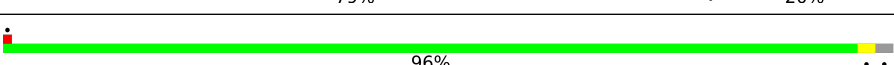
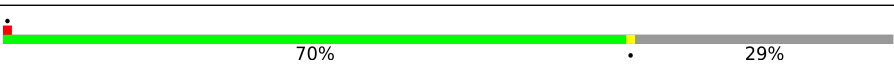

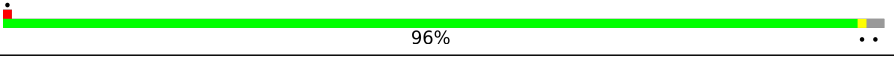
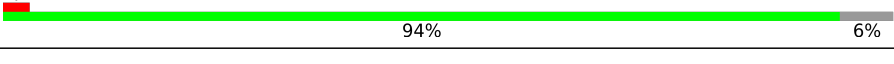
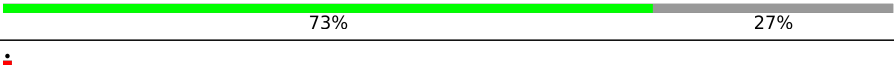

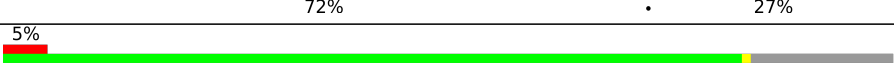

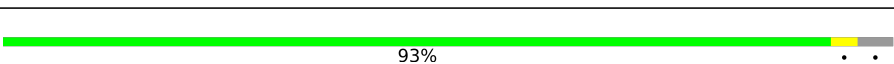
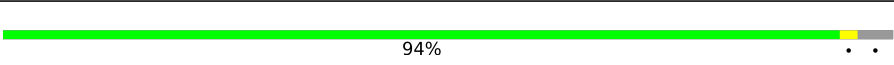







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1808	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	

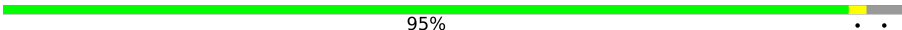









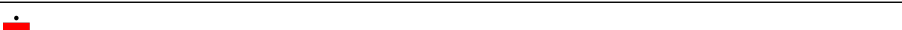

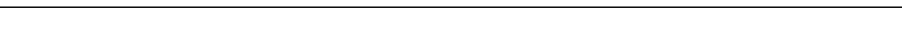
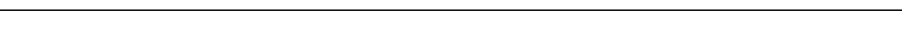
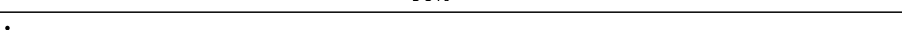

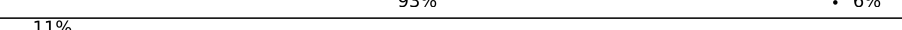








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Mol	Chain	Length	Quality of chain
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	

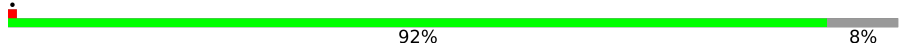

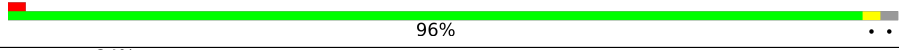



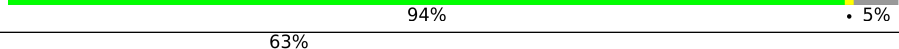
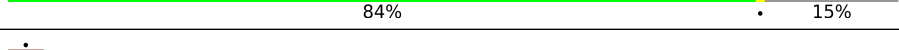
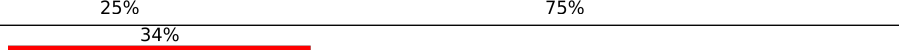
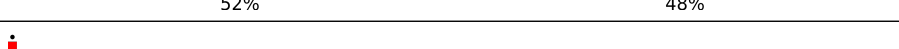

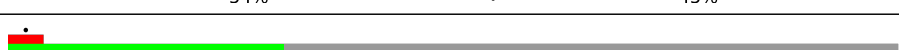


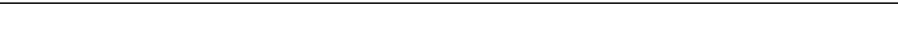
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Mol	Chain	Length	Quality of chain
32	AF	513	 95%
33	AG	896	 91% 8%
34	B1	923	 89% 10%
35	B2	943	 88% 10%
36	B3	817	 89% 7%
37	B8	594	 80% 20%
38	BE	939	 91% 8%
39	B6	440	 14% 84% 15%
40	5B	214	 27% 72%
41	5C	554	 95%
42	5D	250	 92% 6%
43	5E	593	 34% 66%
44	5F	183	 97%
45	5G	290	 96%
46	5H	610	 22% 78%
47	5I	489	 93% 6%
48	5J	217	 11% 70% 30%
49	5K	189	 92% 7%
50	RA	707	 12% 47% 52%
51	RB	357	 6% 36% 62%
52	RC	316	 14% 88% 12%
53	RE	1237	 11% 86% 13%
54	RF	297	 27% 79% 19%
55	RG	252	 9% 84% 14%
55	RH	252	 90% 9%

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Mol	Chain	Length	Quality of chain
56	RI	274	
57	RJ	1183	
58	RK	367	
59	RL	1056	
59	RM	1056	
60	RN	810	
61	RO	552	
62	RP	2493	
63	RQ	899	
64	RS	483	
65	RT	326	
66	RV	346	
67	RW	206	
68	RY	534	
69	X1	347	

2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 232186 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
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	523	Total	C	N	O	P	0	0
			11163	4988	1984	3668	523		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1325	Total	C	N	O	P	0	0
			28258	12629	5035	9269	1325		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- Molecule 13 is a protein called 40S ribosomal protein S13.

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

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	117	Total	C	N	O	S	0	0
			964	610	184	168	2		

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
22	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
26	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

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

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A8	548	Total	C	N	O	S	0	0
			3307	2054	608	642	3		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

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

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

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

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5C	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5H	136	Total	C	N	O		0	0
			1065	658	211	196			

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 50 is a protein called Ribosome biogenesis protein ENP2.

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

- Molecule 51 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

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

- Molecule 52 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RC	278	Total	C	N	O	S	0	0
			2207	1408	391	395	13		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 54 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 56 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1.

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

- Molecule 58 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 60 is a protein called Nucleolar complex protein 14.

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

- Molecule 61 is a protein called Nucleolar complex protein 4.

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

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RP	2109	Total	C	N	O	S	0	0
			12176	7486	2292	2382	16		

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 64 is a protein called Essential nuclear protein 1.

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

- Molecule 65 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 66 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RV	190	Total	C	N	O	S	0	0
			1448	891	290	264	3		

- Molecule 67 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	RW	63	Total	C	N	O	0	0
			381	234	69	78		

- Molecule 68 is a protein called Protein BFR2.

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

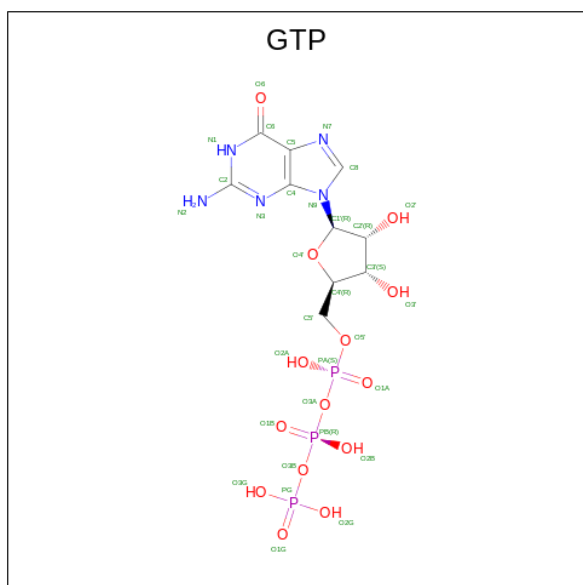
- Molecule 69 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 70 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
70	Sc	1	Total	Zn	0
			1	1	
70	5K	1	Total	Zn	0
			1	1	

- Molecule 71 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

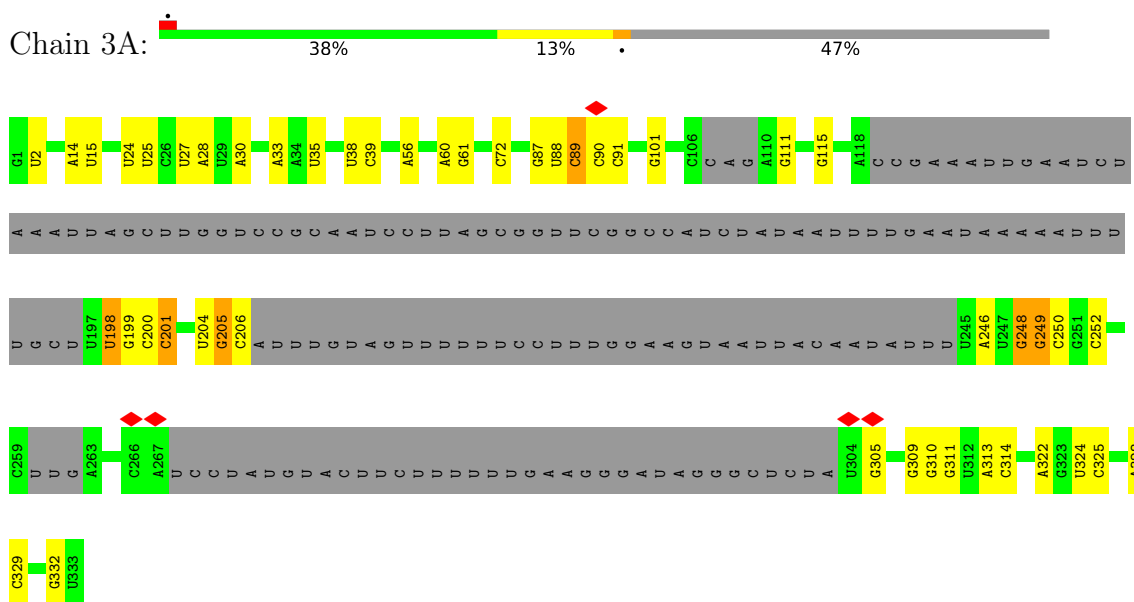
- Molecule 72 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	RJ	1	Total	Mg	0
			1	1	

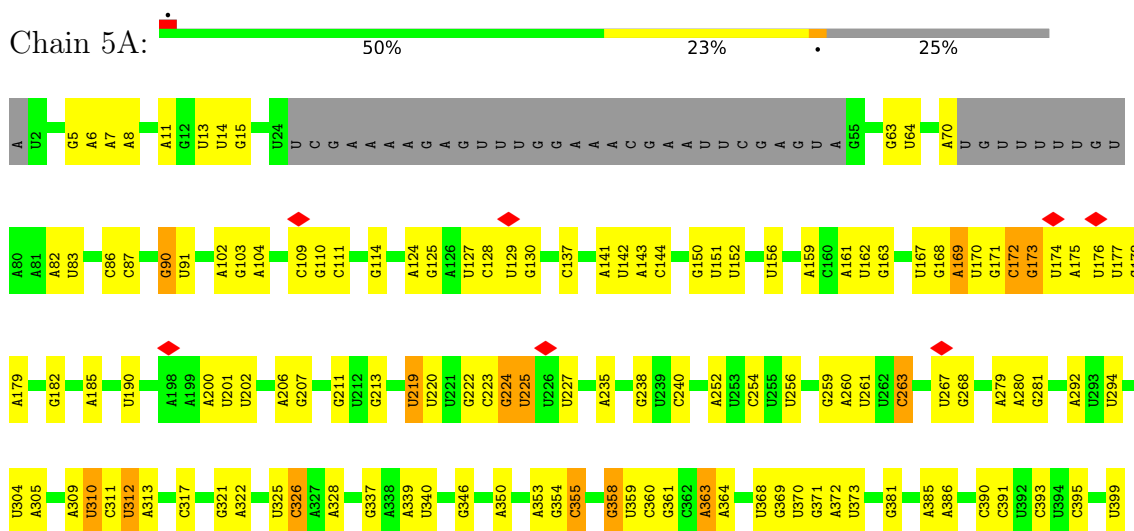
3 Residue-property plots [i](#)

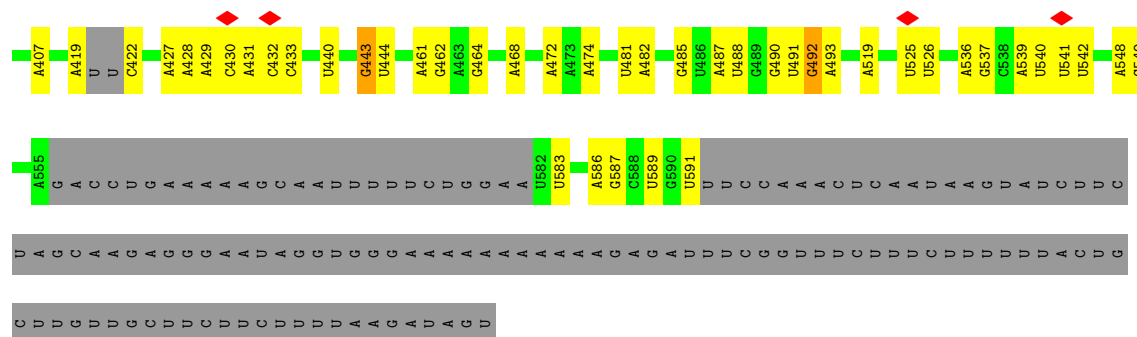
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U3 snoRNA

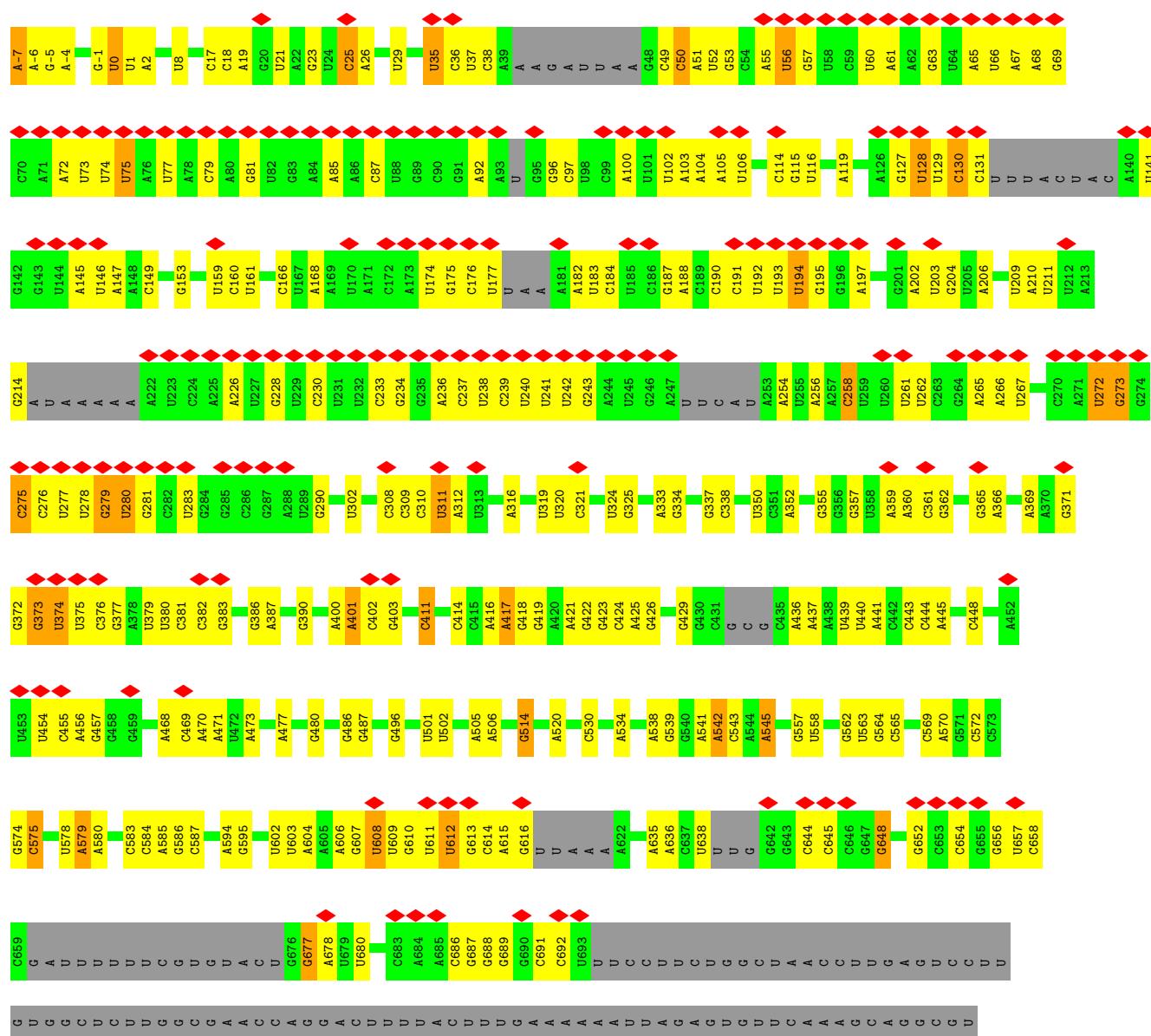
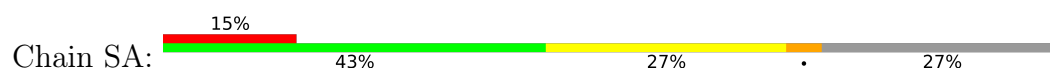


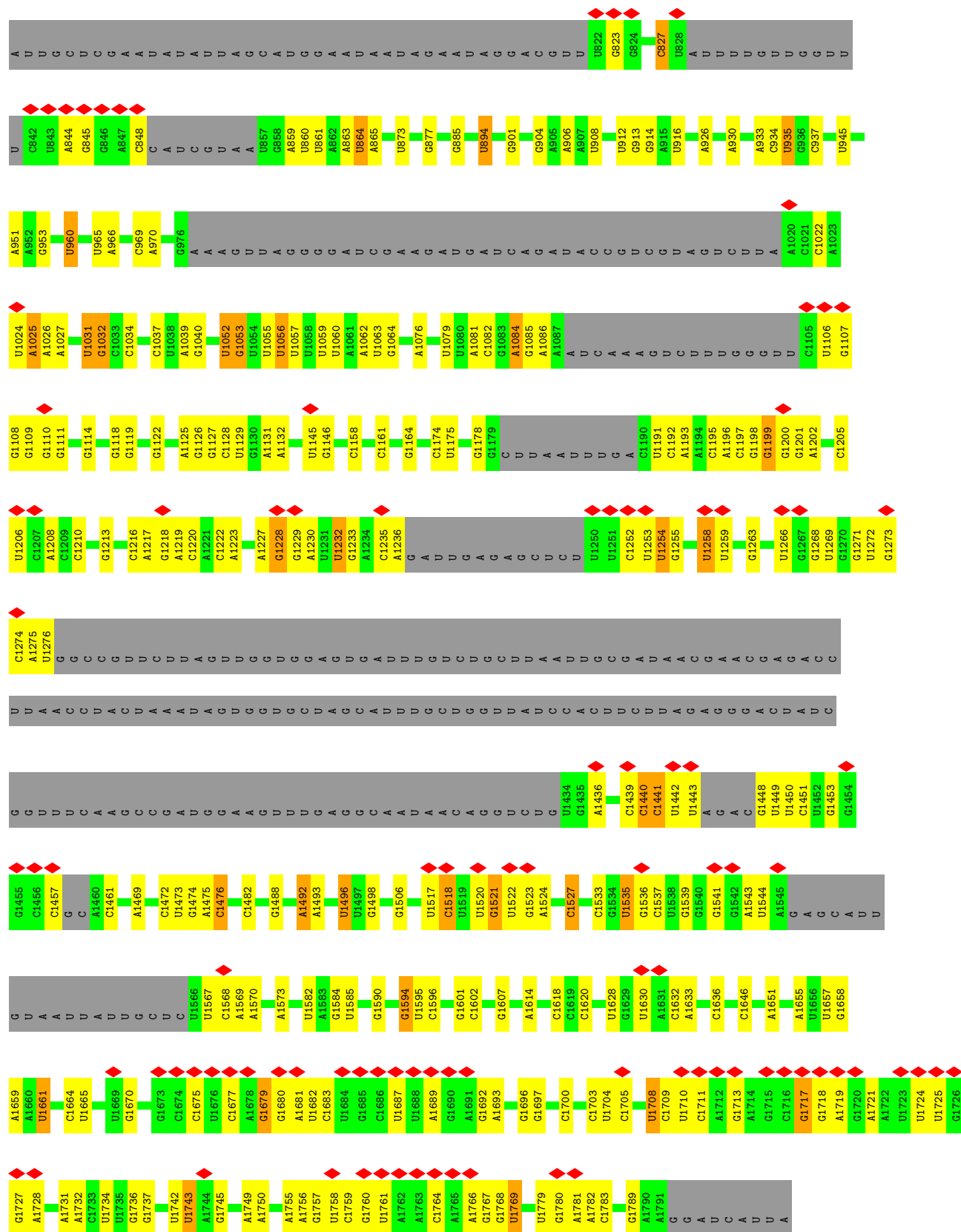
• Molecule 2: 5' ETS





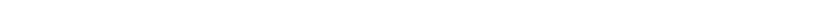
• Molecule 3: 18S pre-rRNA

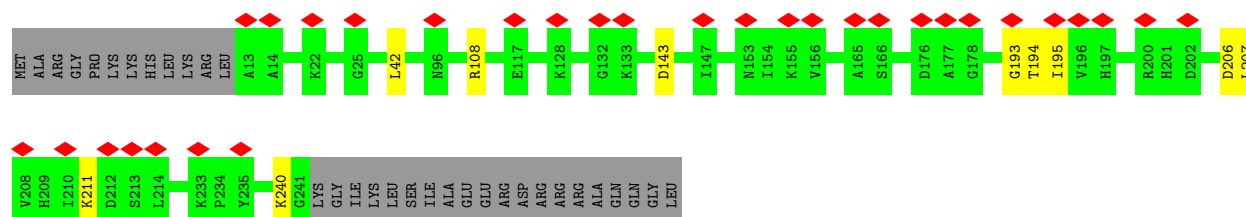


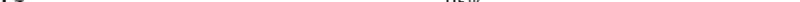


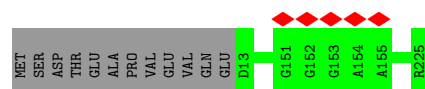
- Molecule 4: 40S ribosomal protein S1-A

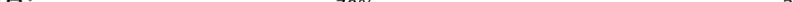
MET	ALA	VAL	GLY	LYS	ASN	ARG	LEU	SER	LYS	GLY	LYS	LYS	G15	L54	L110	L120	D132	A147	L172	F205	E234	G235	E238	V244	THR	GLY	PHE	LYS	ASP	GLU	VAL	LEU	GLU	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

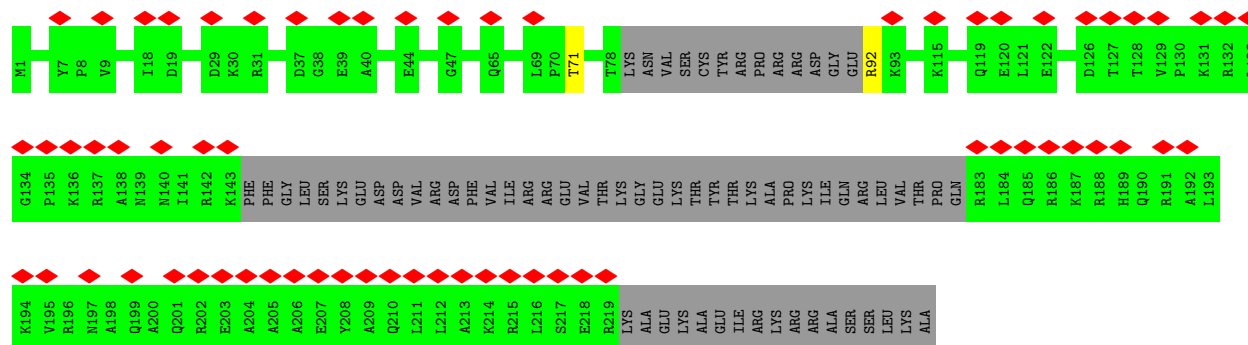
Chain SF: 



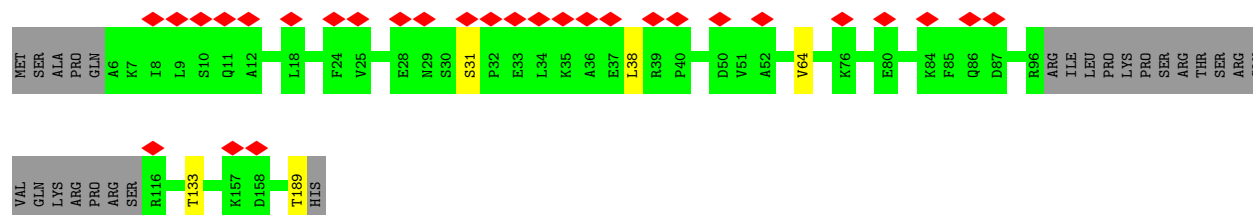
Chain SG:  95% 5%



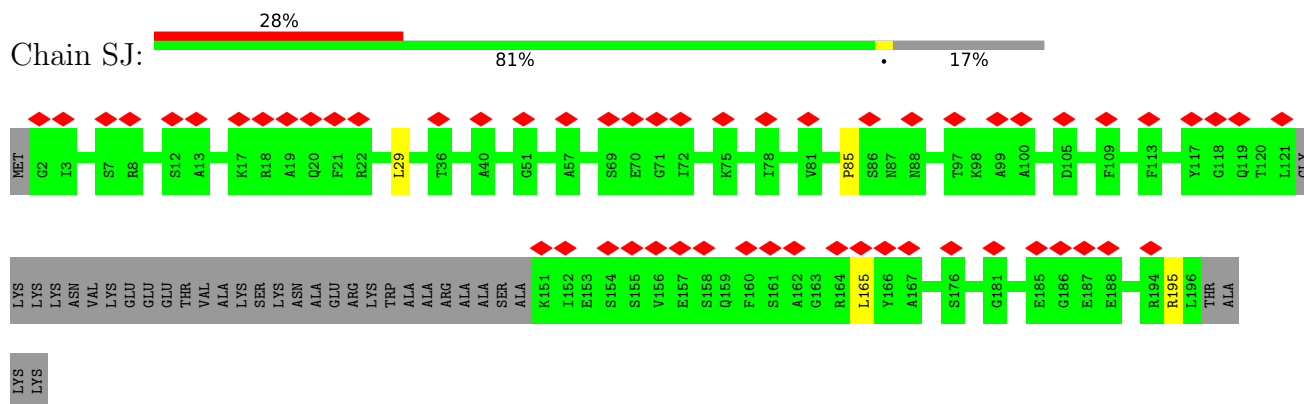
Chain SH:  28% 70% 2%



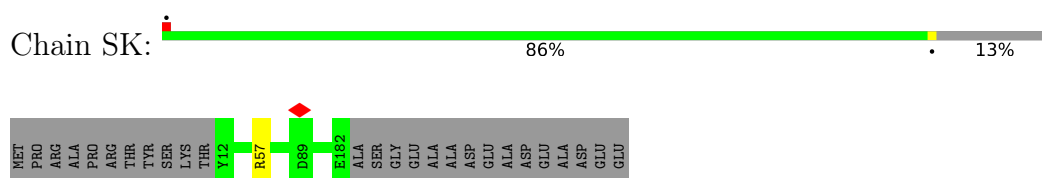
Chain SI:  15% 84% 1% 1% 1%



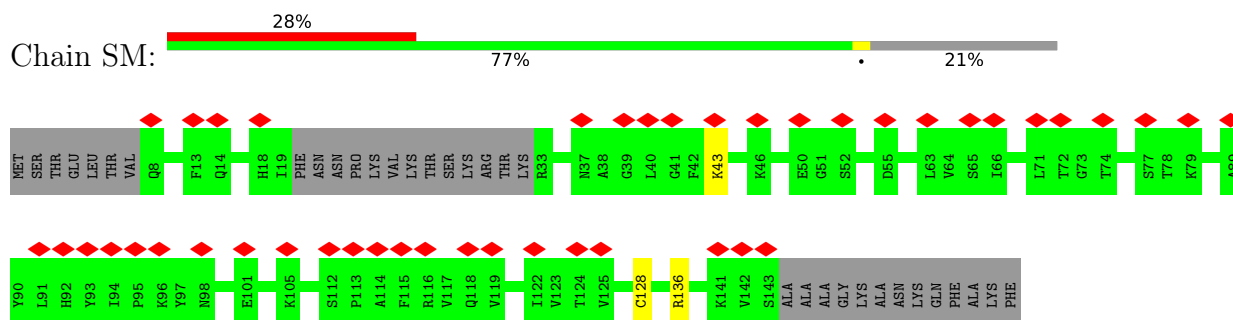
- Molecule 9: 40S ribosomal protein S8-A



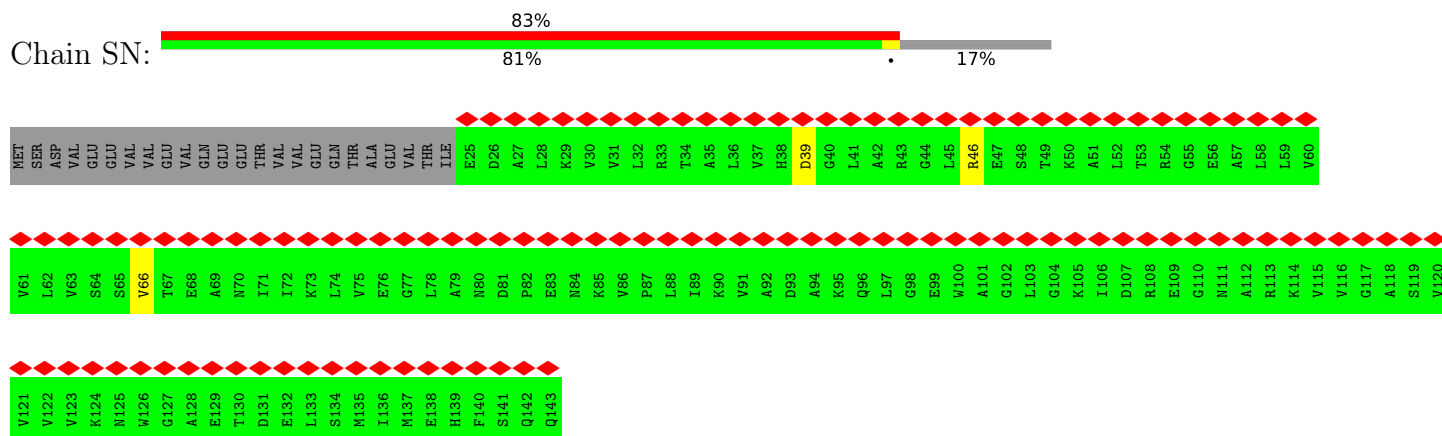
- Molecule 10: 40S ribosomal protein S9-A



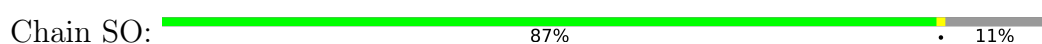
- Molecule 11: 40S ribosomal protein S11-A



- Molecule 12: 40S ribosomal protein S12

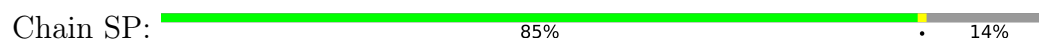


- Molecule 13: 40S ribosomal protein S13

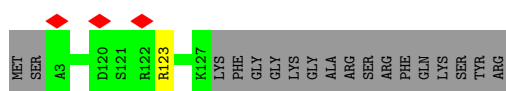




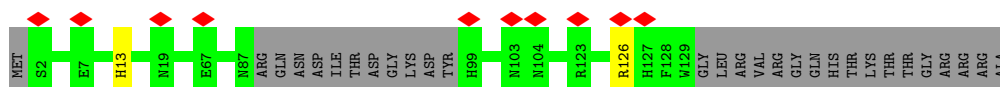
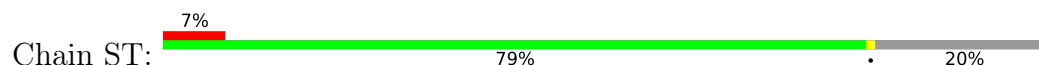
- Molecule 14: 40S ribosomal protein S14-A



- Molecule 15: 40S ribosomal protein S16-A



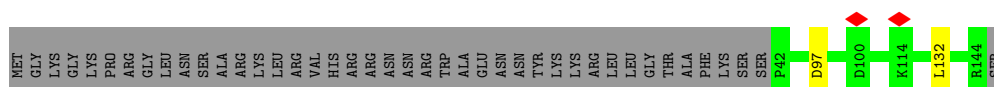
- Molecule 16: 40S ribosomal protein S18-A



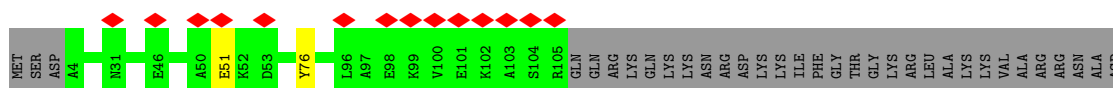
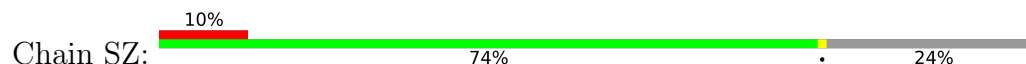
- Molecule 17: 40S ribosomal protein S22-B



- Molecule 18: 40S ribosomal protein S23-A



- Molecule 19: 40S ribosomal protein S24-A



- Molecule 20: 40S ribosomal protein S27-A

A diagram of a protein structure with four vertical bars representing different regions: MET VAL (grey), L3 (green), H49 (yellow), and K82 (green). A red diamond is positioned above the L3 bar, indicating a specific site of interest.

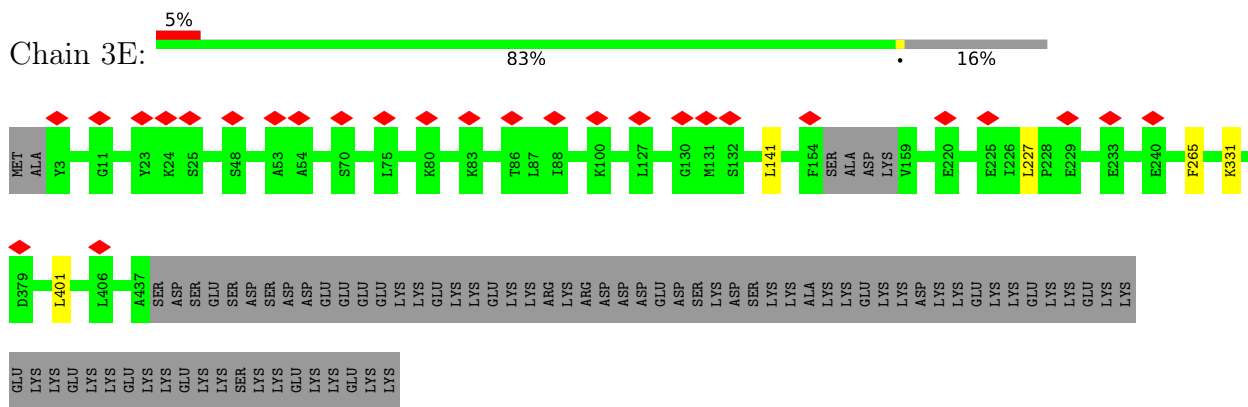
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- Diagram illustrating the structure of the T5-E34-R67 protein. The structure is shown as a grey box containing the residues MET, ASP, ASN, and LYS, and a green box containing the residues T5, E34, and R67. Red diamonds are positioned above the T5 and E34 residues.

- [illegible]

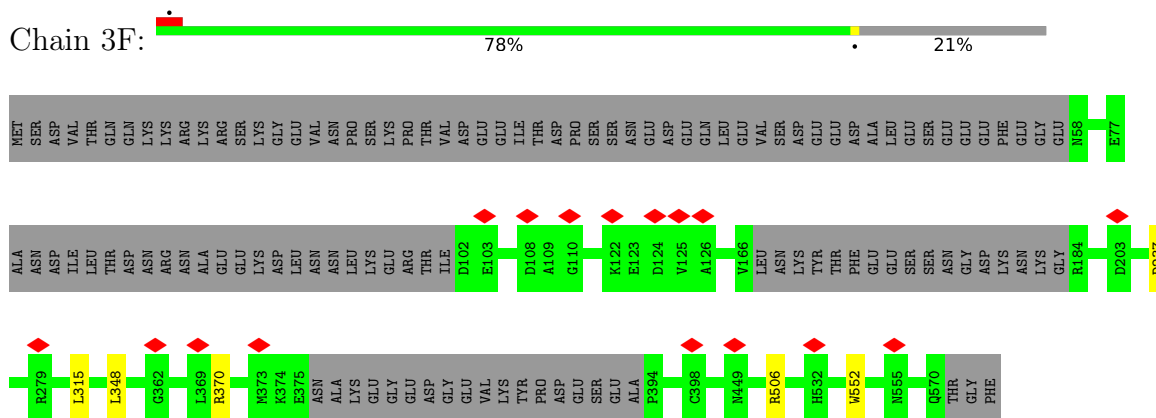
- [illegible]

- [illegible]

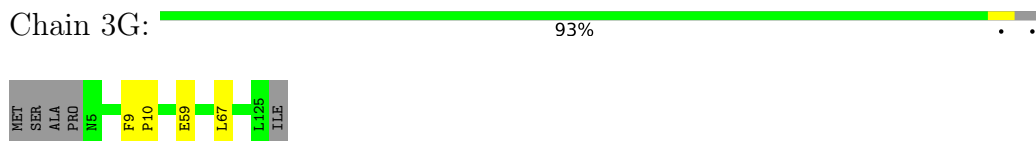
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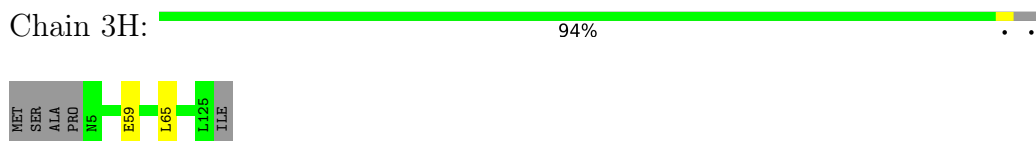
- Molecule 25: Ribosomal RNA-processing protein 9



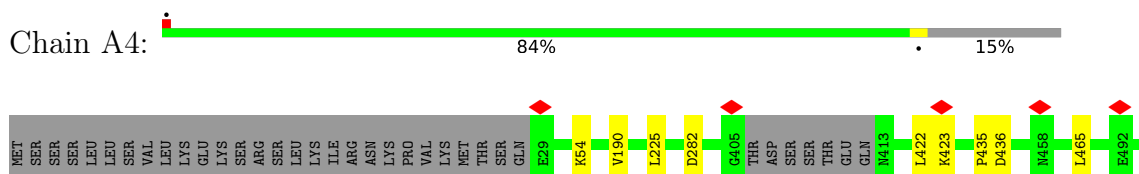
- Molecule 26: 13 kDa ribonucleoprotein-associated protein

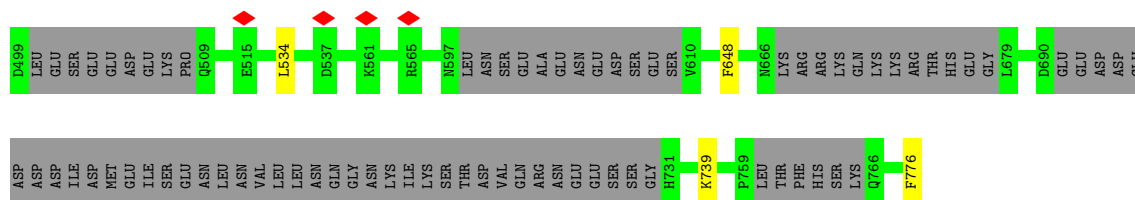


- Molecule 26: 13 kDa ribonucleoprotein-associated protein

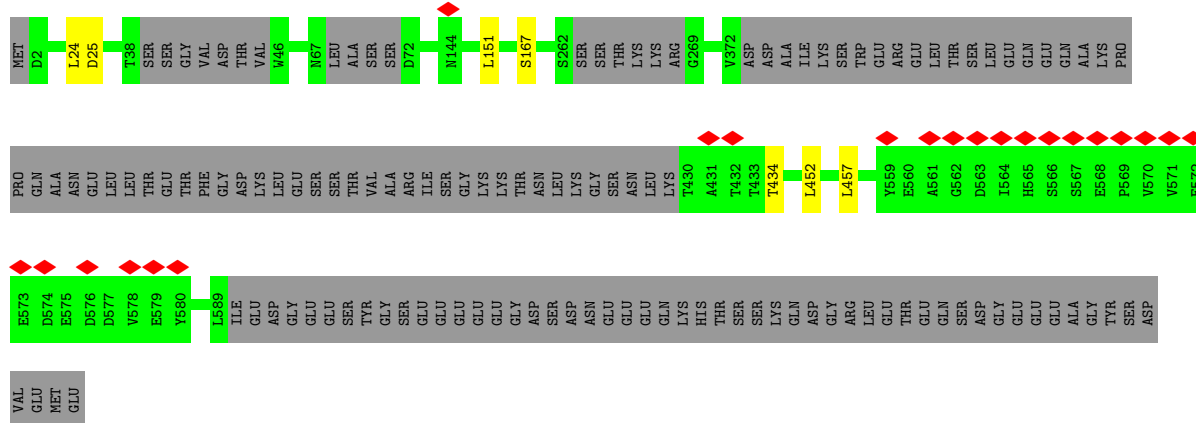
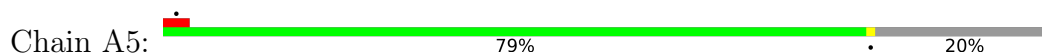


- Molecule 27: U3 small nucleolar RNA-associated protein 4

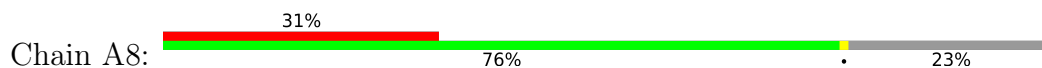


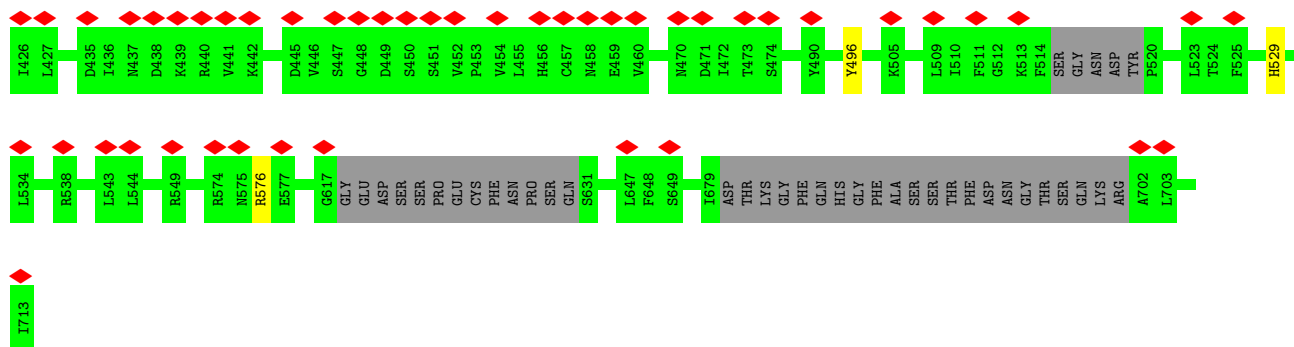


• Molecule 28: U3 small nucleolar RNA-associated protein 5



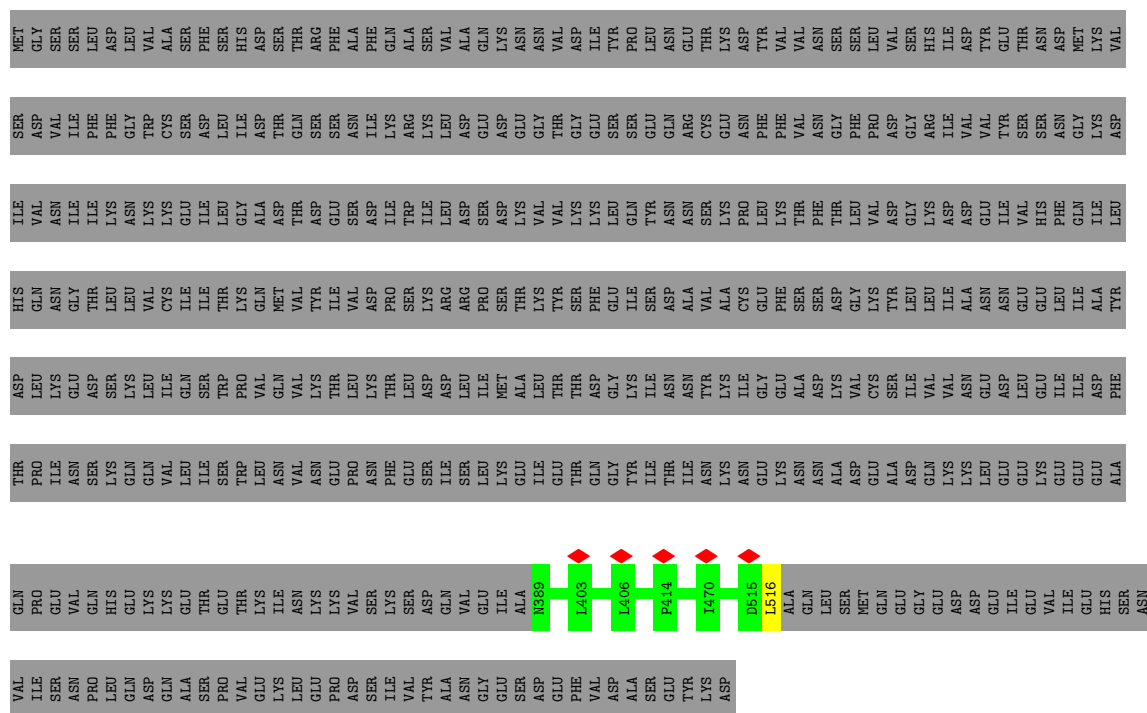
• Molecule 29: U3 small nucleolar RNA-associated protein 8





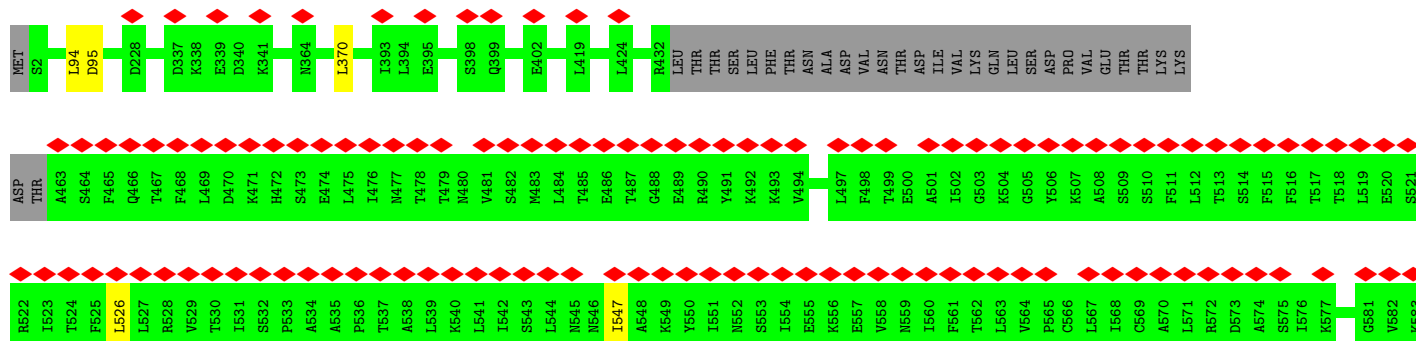
- Molecule 30: U3 small nucleolar RNA-associated protein 9

Chain A9: 22% 78%



- Molecule 31: U3 small nucleolar RNA-associated protein 10

Chain AE: 61% 86% 13%

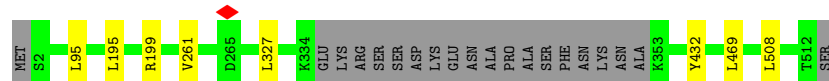


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E1245	F1246	V1247	N1248	A1249	V1250	P1251	P1252	L1253	L1254	S1255	T1256	S1257	T1258	N1259	E1260	D1261	I1262	R1263	Y1264	H1265	L1266	T1267	L1268	V1269	I1270	G1271	S1272	K1273	F1274	E1275	L1276	E1277	G1278	S1279	E1280	A1281	I1282	P1283	L1284	V1285	N1286	L1287	V1288	M1289	K1290	V1291	L1292	L1293	D1294	R1295	M1296	P1297	L1298	E1299	K1300	L1301	S1302	V1303	V1304	
THR	LEU	LEU	GLY	VAL	LEU	PHE	PHE	ILE	ASN	SER	V1197	E1198	L1199	T1200	F1201	S1202	G1203	I1204	T1205	S1206	Q1207	E1208	N1209	E1210	E1211	A1212	D1214	S1215	E1216	T1217	SER	LEU	SER	ASP	H1222	T1223	T1224	E1225	K1227	E1228	I1229	L1230	F1231	K1232	V1233	L1234	G1235	N1236	V1237	LEU	GLN	ILE	PRO	V1243	D1244					
SER	GLU	SER	PHE	LEU	PHE	THR	ASN	ASN	THR	LYS	H1080	V1081	N1082	E1083	E1084	L1085	S1086	G1087	Y1151	Y1152	D1153	V1154	R1155	R1156	N1157	L1158	R1159	L1160	K1161	V1162	Y1163	S1164	V1165	L1166	LEU	ASP	GLU	THR	SER	D1172	K1173	K1174	L1175	I1176	R1177	N1178	I1179	R1180	GLU	PHE	GLY	LEU	GLN	ILE	PRO	V1243	D1244			
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E1005	M1006	GLU	PHE	LEU	LEU	SER	PHE	THR	THR	GLN	H1019	V1020	P1021	R1022	R1023	R1024	R1025	V1026	K1027	L1028	F1029	S1030	T1031	L1032	LYS	THR	LEU	ASP	PRO	V1039	K1040	A1041	L1042	G1043	S1044	F1045	L1046	F1047	L1048	I1049	ALA	GLN	TYR	SER	SER	ALA	L1057	V1058	N1059	F1060	K1061	I1062	G1063	E1064						
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GLN	ASP	Q887	G888	L889	P890	V891	L892	Y893	A894	Q895	E896	T897	L898	I899	SER	CYS	THR	LEU	ASN	ALA	GLU	LEU	HIS	LEU	ARG	LYS	THR	ILE	LEU	GLU	A857	L858	D859	K860	V861	R862	N863	V864	G865	S866	E867	K868	LEU	LEU	PHE	THR	LEU	SER	LEU	SER	LEU	ASP	GLU	THR	LEU	ASP				
N765	A766	Q767	K768	L769	K770	I771	V772	Q773	N774	I775	V776	D777	S778	S779	S780	V781	N782	E783	S784	S785	Y786	D787	T788	V789	G790	V791	L792	M793	I794	D795	F796	L797	D798	S799	D800	I801	F802	V803	S804	I805	L806	N807	Q808	ASN	ILE	ASN	GLU	ASP	GLN	ASP	THR	ASP	ARG							
S705	C706	I707	A708	N709	K710	T711	N712	F713	E714	H715	F716	E717	R718	S719	L720	I661	P662	S663	P664	Y665	A666	K667	T668	V669	L670	L671	D672	M673	I734	D735	F736	V737	L738	S739	A740	L741	N742	S882	S883	S884	S885	S886	L887	F888	E889	E890	F691	I692	A752	E754	R755	L756	I757	S758	I759	F760	A761	S762	L763	N764
R645	M646	E647	K648	V649	F650	L651	M652	F653	W654	A655	M656	Q657	A658	L659	L660	I661	P662	S663	P664	Y665	A666	K667	T668	V669	L670	L671	D672	M673	I734	D735	F736	V737	L738	S739	A740	L741	N742	S882	S883	S884	S885	S886	L887	F888	E889	E890	F691	I692	A752	E754	R755	L756	I757	S758	I759	F760	A761	S762	L763	N764
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K1365	I1426	V1485	R1545	L1605	Y1665	L1726
S1366	I1427	E1486	P1546	K1606	L1666	P1726
I1367	Y1428	M1487	L1547	R1607	V1667	Q1728
A1368	F1429	I1488	F1548	F1608	K1668	L1729
F1369	R1430	D1489	I1549	S1610	I1669	V1730
Y1370	E1431	K1490	I1550	S1611	I1670	P1731
P1371	V1432	K1491	L1551	D1612	G1671	V1732
K1372	I1373	S1492	V1552	M1613	A1672	I1733
I1373	D1433	I1493	R1553	M1614	L1673	I1734
V1374	S1434	T1494	W1554	M1615	A1674	E1735
P1375	S1435	S1495	A1555	V1616	S1675	L1736
P1376	I1436	Q1496	F1556	M1617	N1676	L1737
S1377	R1437	D1497	D1557	L1618	M1677	L1738
I1378	L1438	P1498	G1558	R1619	S1678	D1739
K1379	S1439	I1499	E1559	R1620	G1679	D1740
L1380	V1440	F1500	G1560	R1621	V1680	L1741
F1381	I1441	F1501	V1561	L1622	D1681	E1742
D1382	S1442	K1502	T1562	I1623	E1682	E1743
A1383	L1443	L1503	M1563	N1624	H1683	I1744
S1384	I1444	L1504	A1564	M1625	N1684	E1745
L1385	I1445	L1505	G1565	L1626	Q1685	R1746
L1386	E1446	S1506	I1566	T1627	L1687	E1747
D1387	N1447	L1507	T1567	S1628	L1688	V1748
S1388	I1448	F1508	E1568	S1629	K1689	R1749
S1389	D1449	E1509	T1569	L1630	L1690	T1750
N1390	L1450	F1510	E1570	K1631	L1691	G1751
P1391	K1451	R1511	R1571	D1632	V1692	L1752
L1392	E1452	S1512	L1572	D1633	E1693	V1753
K1393	L1453	I1513	A1573	R1634	H1694	K1754
E1394	L1454	S1514	A1574	D1635	M1695	V1755
Q1395	K1455	S1515	F1575	E1636	L1696	V1756
L1396	V1456	F1516	F1576	Y1637	A1697	E1757
Q1397	L1457	D1517	K1577	W1638	S1698	N1758
V1398	F1458	M1518	F1578	K1639	C1699	V1759
A1399	R1459	M1519	F1579	S1640	S1700	L1760
I1400	I1460	T1520	N1580	T1641	S1701	G1761
L1401	W1461	I1521	K1581	S1642	N1702	E1762
L1402	S1462	S1522	L1582	R1643	E1703	P1763
L1403	T1463	R1523	Q1583	F1644	K1704	F1764
F1404	E1464	I1524	E1584	E1645	L1705	D1765
A1405	I1465	E1525	N1585	L1646	W1706	R1766
G1406	A1466	A1526	L1586	I1647	A1707	Y1767
L1407	T1467	S1527	R1587	V1648	I1708	LEU
I1408	S1468	V1528	G1588	V1649	R1709	ASP
K1409	N1469	H1529	I1589	L1651	A1710	
R1410	D1470	E1530	T1590	L1652	M1711	
I1411	T1471	I1531	T1591	N1653	K1712	
P1412	V1472	S1532	S1592	Q1654	L1713	
S1413	A1473	M1533	F1593	L1655	I1714	
F1414	V1474	S1534	T1595	S1656	Y1715	
L1415	S1475	Y1535	Y1596	M1657	S1716	
M1416	L1476	V1536	L1597	I1658	T1717	
S1417	F1477	L1537	L1598	E1659	K1718	
N1418	L1478	K1538	E1599	N1660	G1719	
I1419	S1479	M1539	P1600	S1661	E1720	
L1420	T1480	N1540	V1601	I1662	S1721	
D1421	L1481	D1541	D1602	G1663	L1723	
V1422	E1482	S1542	M1603	K1664	V1724	
L1423	S1483	F1543				
H1424	T1484					

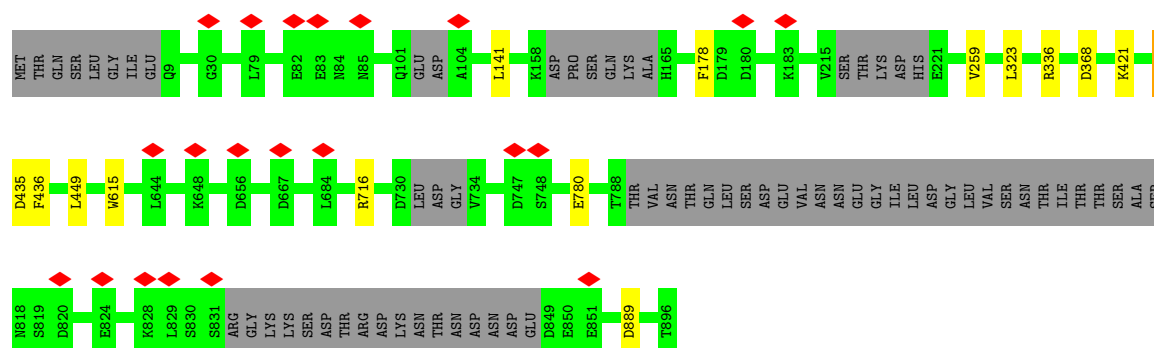
- Molecule 32: U3 small nucleolar RNA-associated protein 15

Chain AF:  95%

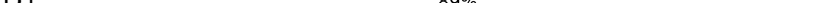


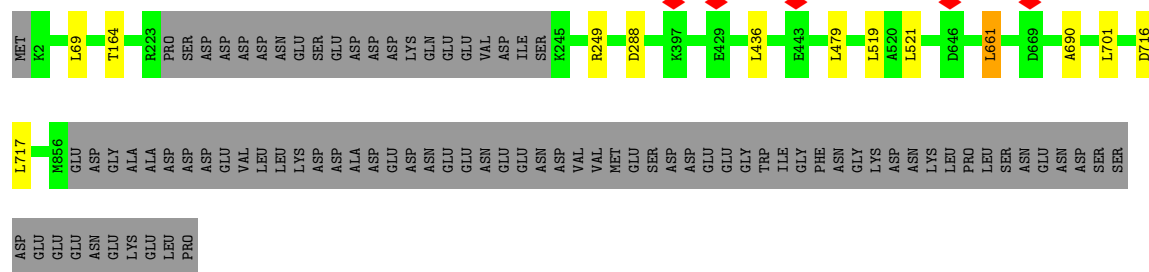
- Molecule 33: NET1-associated nuclear protein 1

Chain AG:  91%



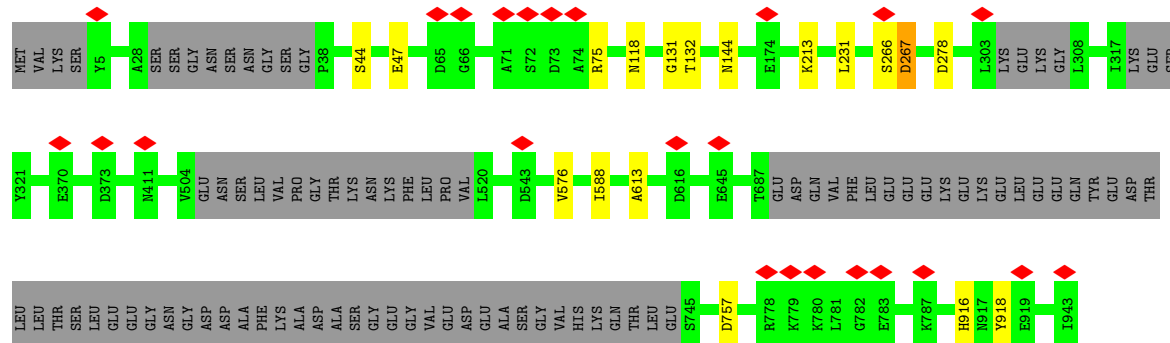
- Molecule 34: Periodic tryptophan protein 2

Chain B1:  89% 10%



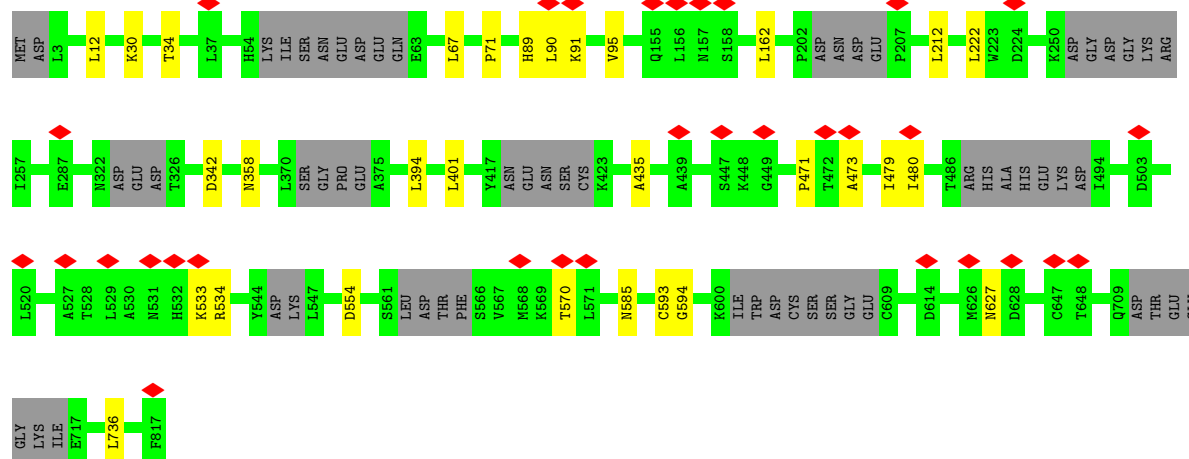
- Molecule 35: U3 small nucleolar RNA-associated protein 12

Chain B2: 88% 10%

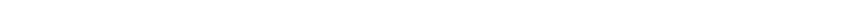


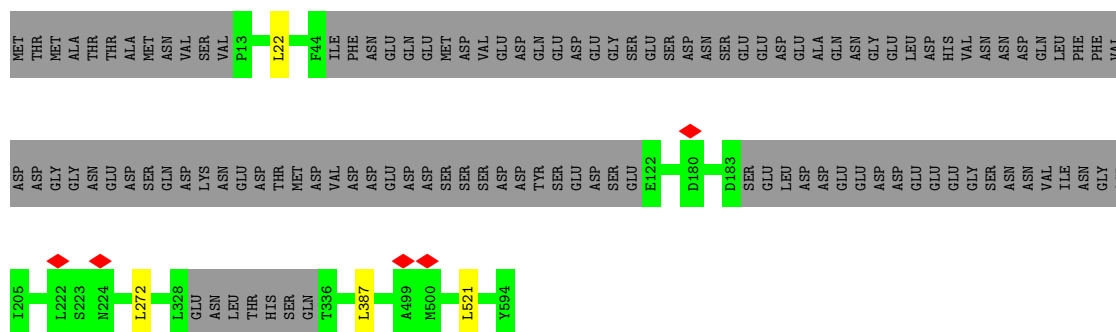
- Molecule 36: U3 small nucleolar RNA-associated protein 13

Chain B3:  89% 7%



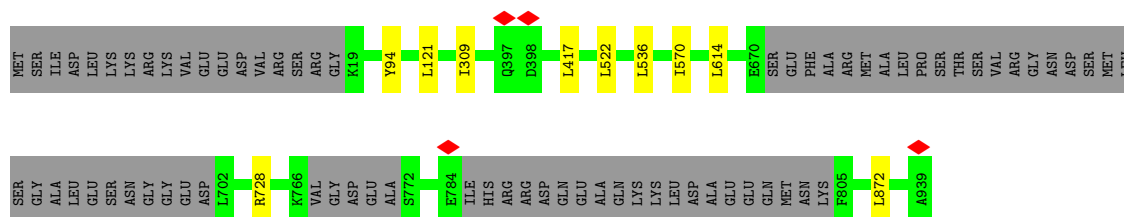
- Molecule 37: U3 small nucleolar RNA-associated protein 18

Chain B8: 



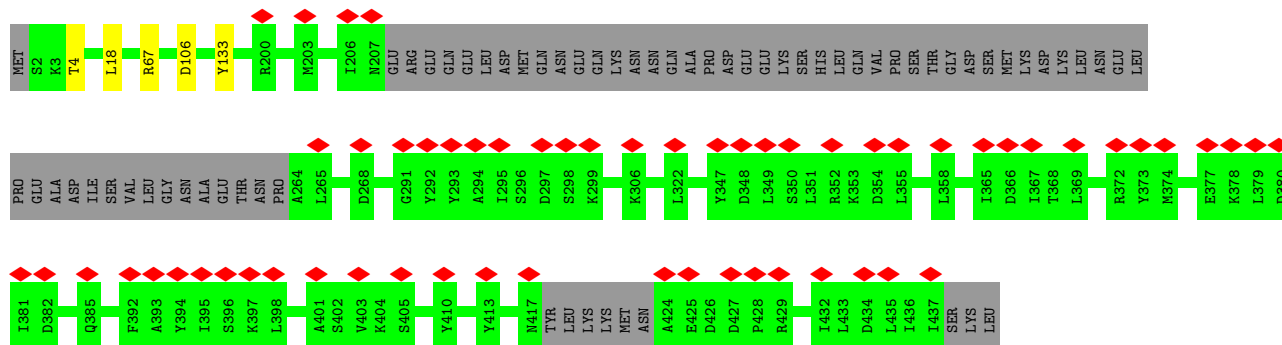
- Molecule 38: U3 small nucleolar RNA-associated protein 21

Chain BE: 91% 8%



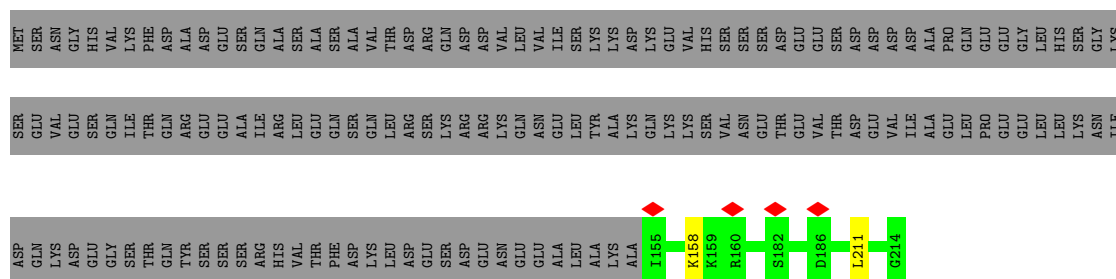
- Molecule 39: U3 small nucleolar RNA-associated protein 6

Chain B6: 14% 84% 15%



- Molecule 40: Bud site selection protein 21

Chain 5B: 27% 72%



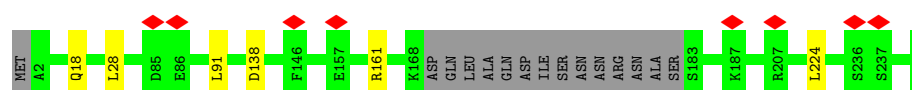
- Molecule 41: U3 small nucleolar RNA-associated protein 7

Chain 5C:  95%



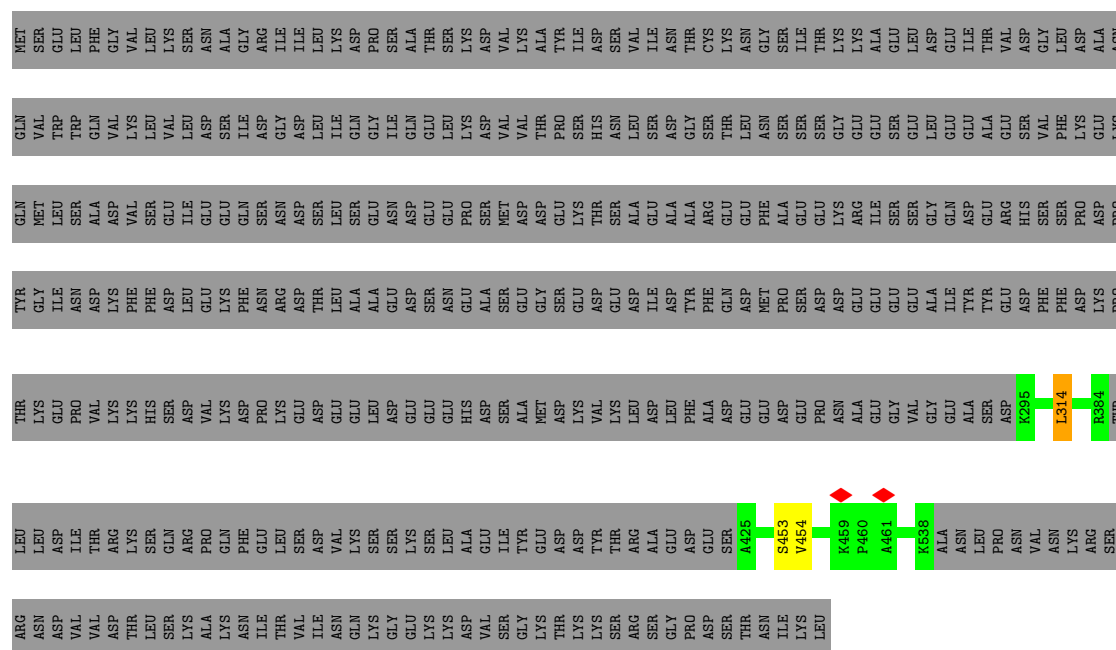
- Molecule 42: U3 small nucleolar RNA-associated protein 11

Chain 5D:  92%



- Molecule 43: U3 small nucleolar RNA-associated protein MPP10

Chain 5E:  34% 66%



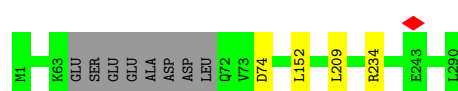
- Molecule 44: U3 small nucleolar ribonucleoprotein protein IMP3

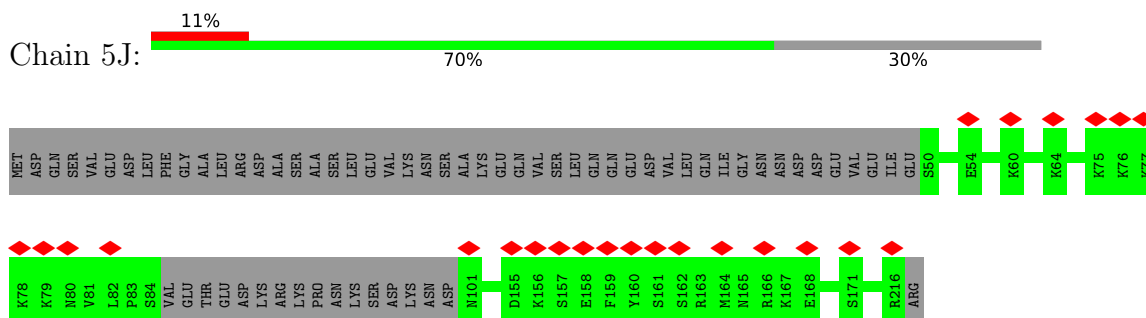
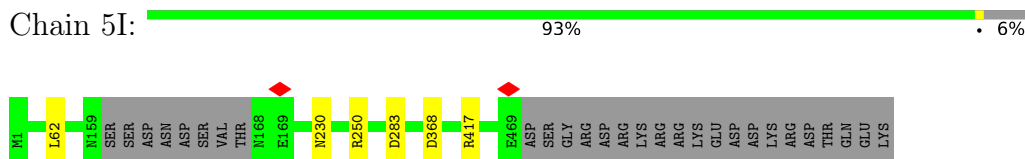
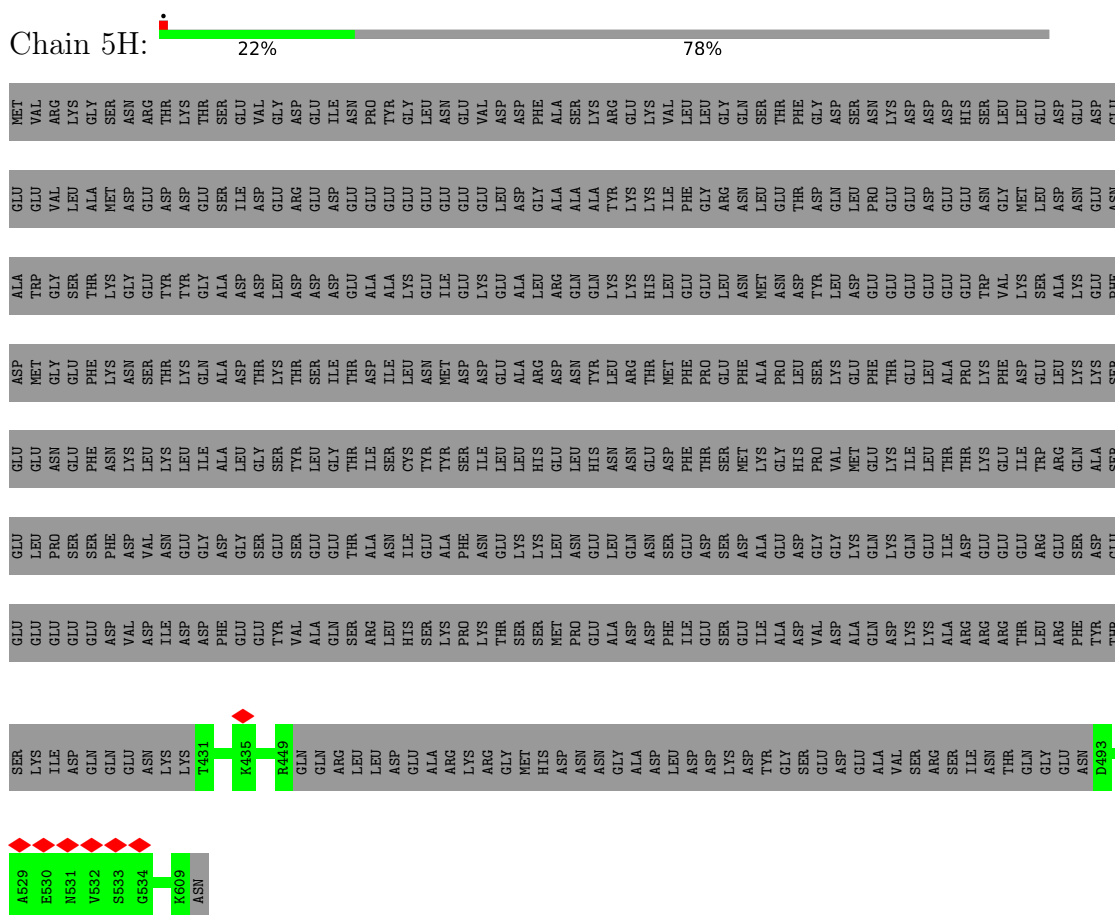
Chain 5F:  97%

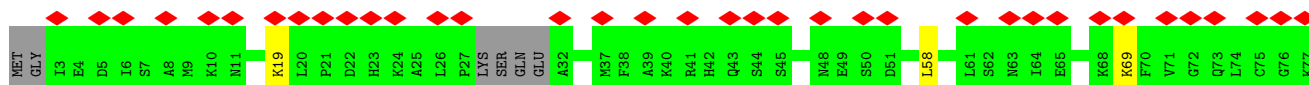


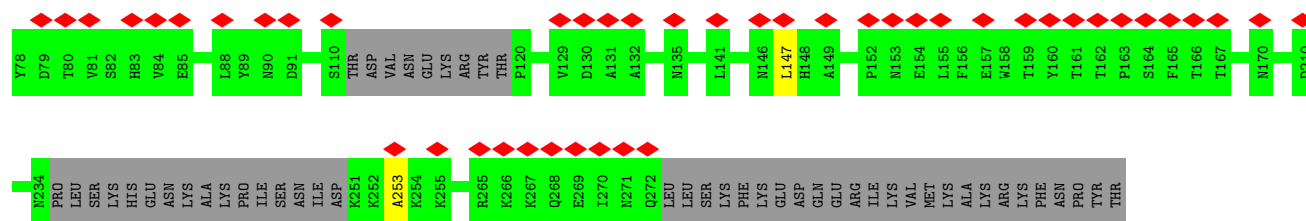
- Molecule 45: U3 small nucleolar ribonucleoprotein protein IMP4

Chain 5G:  96%

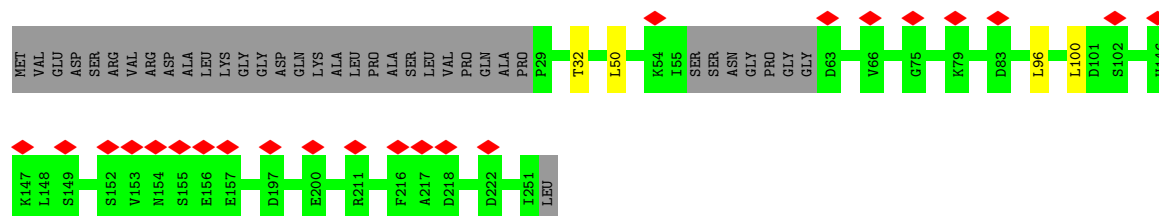
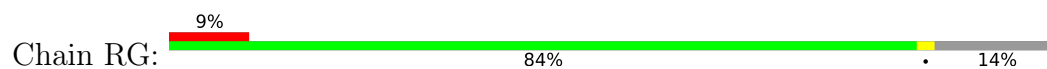




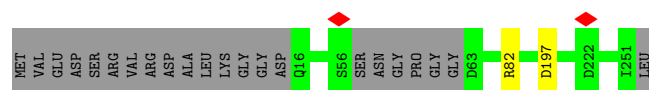




- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1



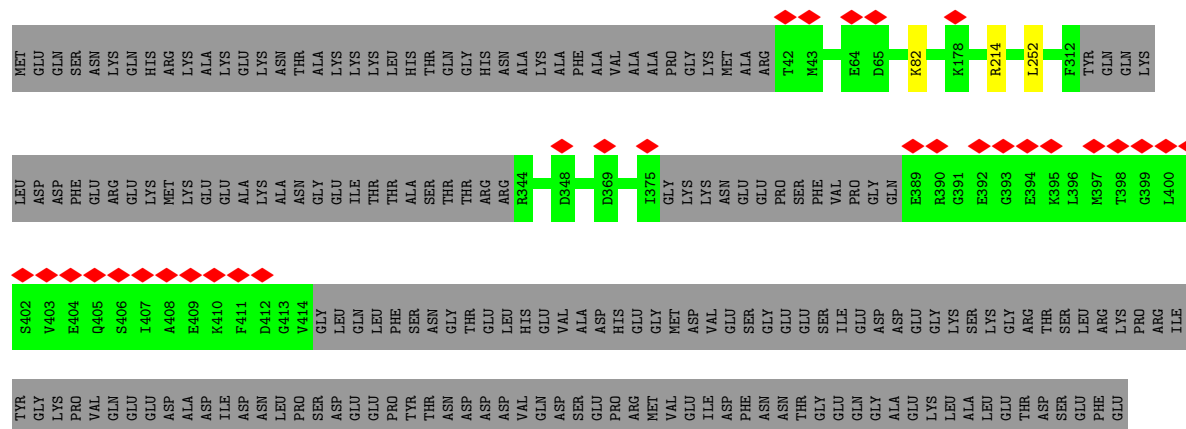
- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

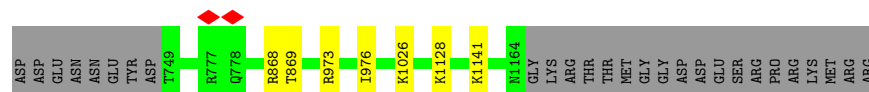


- Molecule 56: Ribosome biogenesis protein UTP30

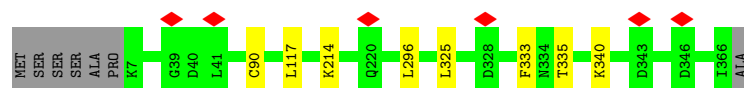


- Molecule 57: Ribosome biogenesis protein BMS1

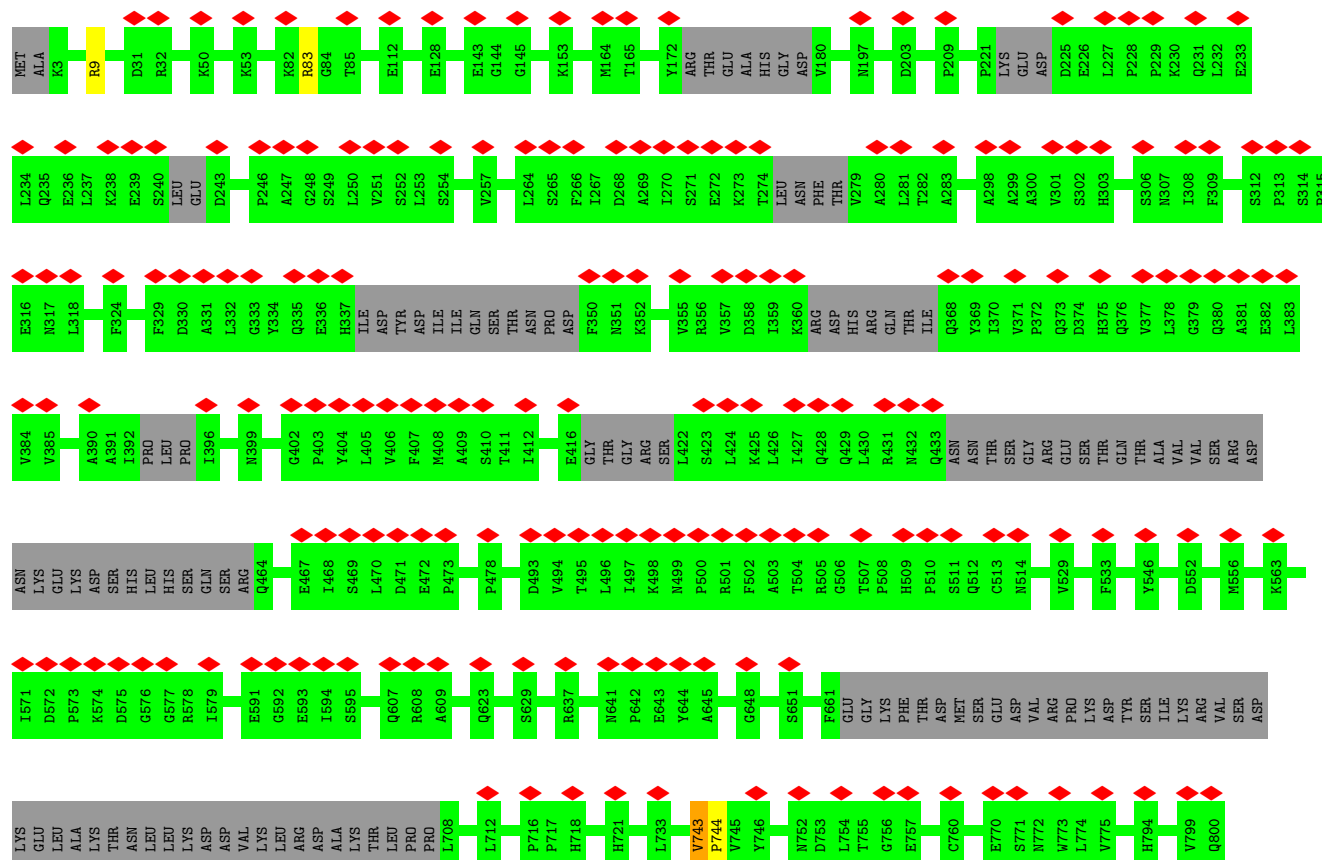
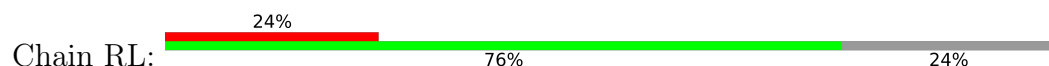




- Molecule 58: RNA 3'-terminal phosphate cyclase-like protein.

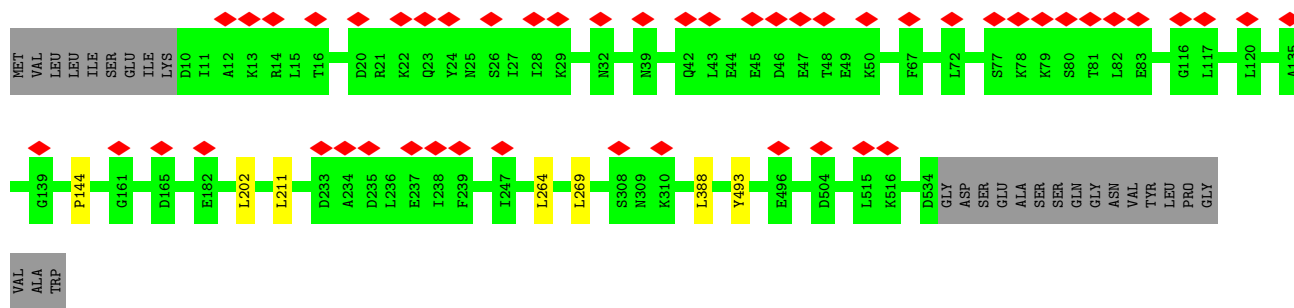


- Molecule 59: RNA cytidine acetyltransferase




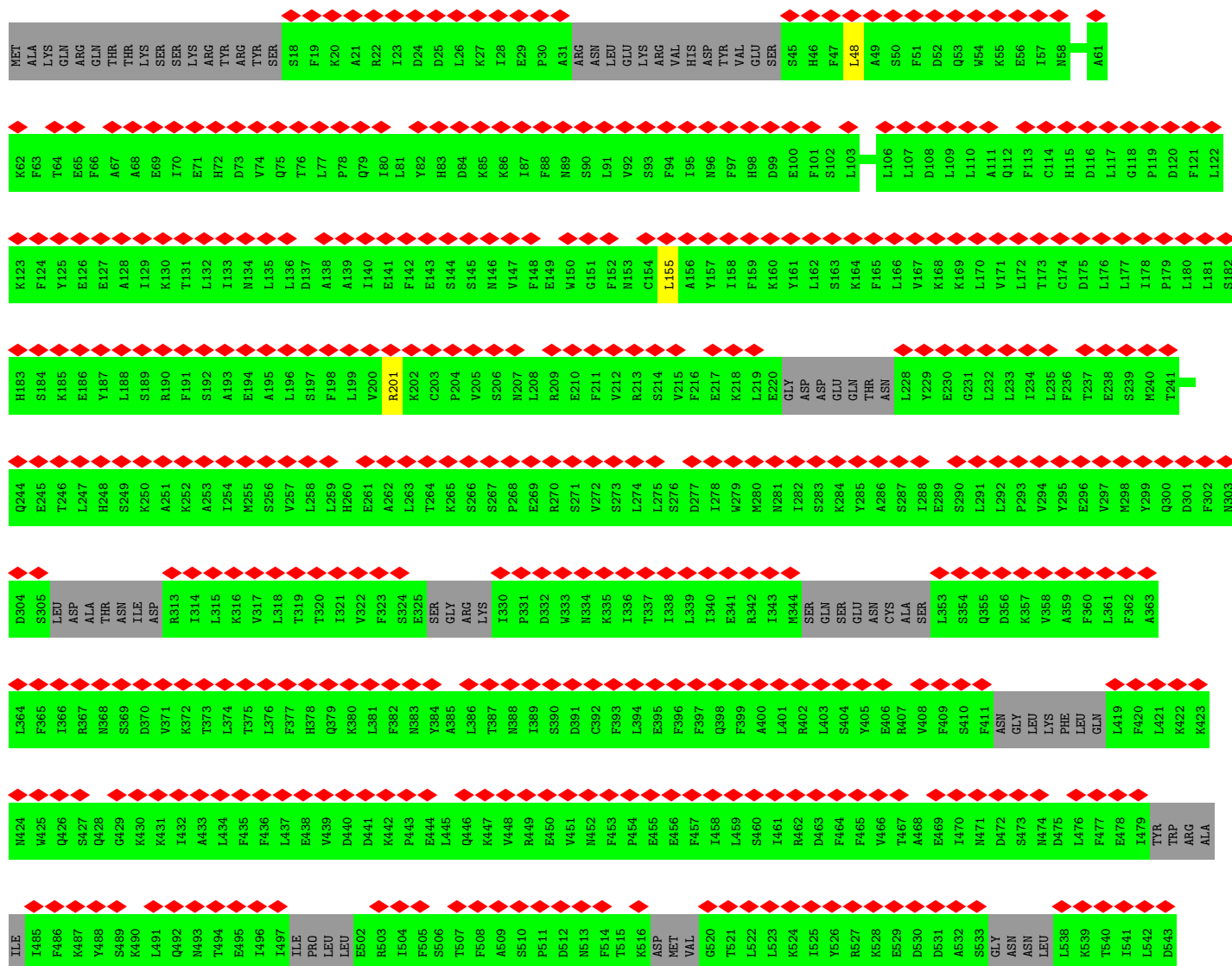


Chain RO: 



• Molecule 62: U3 small nucleolar RNA-associated protein 20

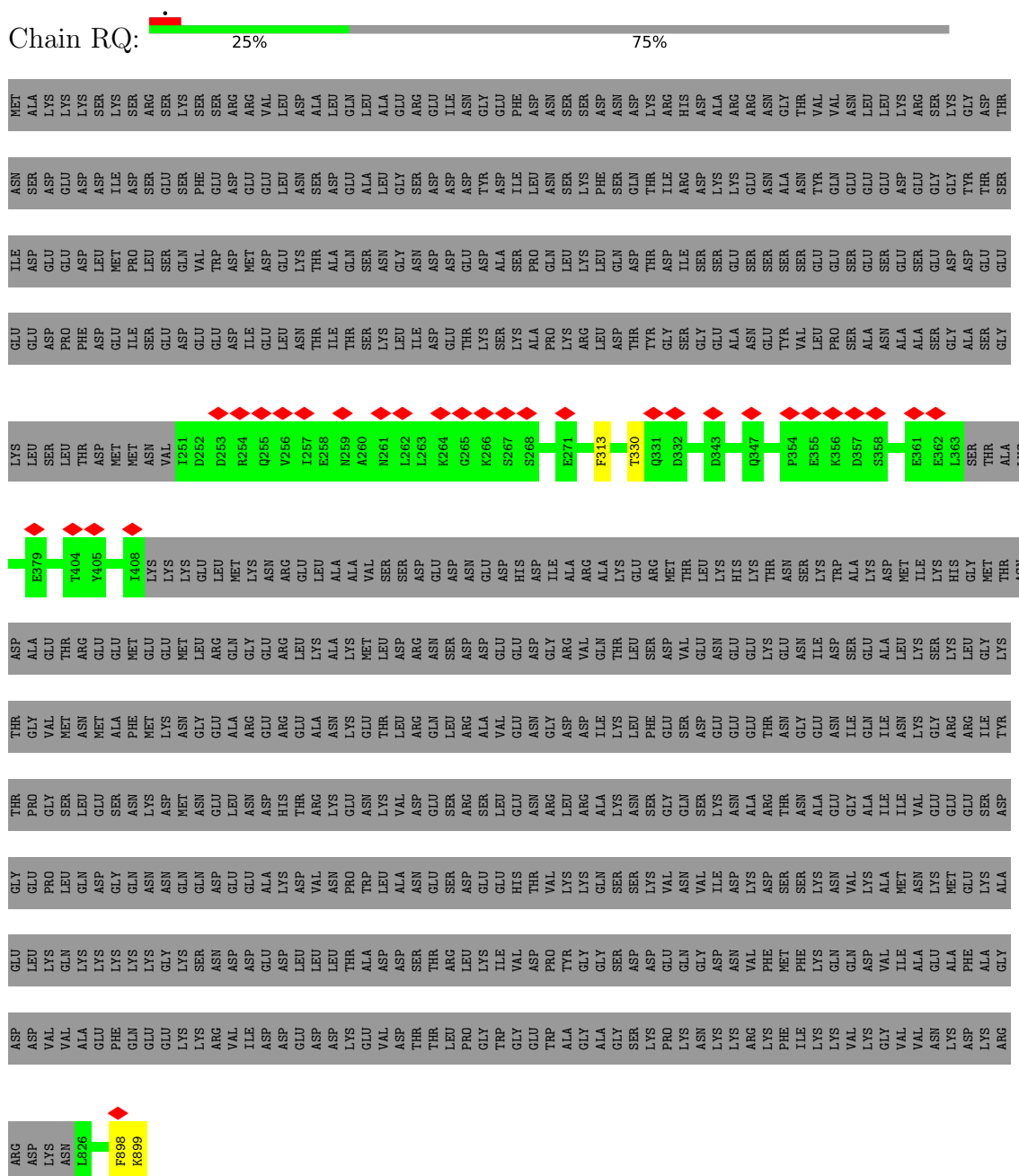
Chain RP: 





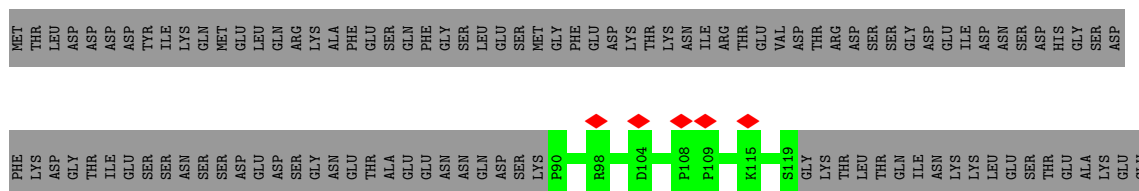
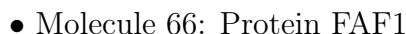
ASP	VAL	SER	LYS	T2323	K2261	D2262	Q2324	E2325	D2326	L2327	K2328	Y2329	T2330	T2331	A2332	L2333	D2334	Y2335	M2336	V2337	T2338	R2339	ILE	GLY	Q2342	L2343	I2344	R2345	S2346	D2347	E2348	H2349	K2350	M2351	D2352	S2353	F2354	M2355	S2356	K2357	LYS	ALA	CYS	ILE	GLN	LEU	LEU	A2365	L2366	L2367	V2368	K2369	V2370	L2371	D2372	E2373	D2374	E2375	V2376	I2377			
L2257	T2258	A2259	N2260	K2261	D2262	Q2324	E2325	D2326	L2327	K2328	Y2329	T2330	T2331	ASN	LEU	LEU	ILE	G1275	T2275	I2276	A2277	T2278	R2279	L2280	L2281	H2282	Q2283	L2284	G2285	A2286	P2287	I2288	I2289	P2290	GLU	ASN	A2294	N2295	V2296	S2297	K2298	L2299	T2300	L2301	V2302	S2305	L2306	L2307	W2308	K2309	E2310	Q2311	ARG	THR	PRO	PHE	ILE	MET					
SER	ASP	THR	SER	VAL	GLY	SER	GLU	HIS	GLN	TRP	ASP	LEU	VAL	TYR	SER	ALA	ASN	THR	F2213	S2214	S2215	Y2216	S2222	V2223	Y2224	K2225	H2226	G2227	PHE	LYS	ASP	ILE	W2232	D2233	K2234	L2235	I2236	T2237	C2238	L2239	L2240	Y2241	P2242	H2243	S2244	W2245	W2246	ARG	GLN	SER	ALA	A2251	N2252	L2253	H2254	Q2256							
S2123	V2124	L2125	I2126	L2130	L2133	E2134	N2135	K2136	D2137	L2138	E2139	I2140	V2141	E2142	K2143	A2147	TRP	LEU	GLN	D2153	M2154	A2155	S2156	F2157	L2162	R2163	T2164	Y2165	K2166	T2167	TYR	LEU	LYS	L2162	R2163	T2164	Y2165	K2166	T2167	TYR	LEU	LYS	S2171	I2172	G2173	F2174	E2175	H2176	T2177	I2178	E2179	L2180	L2183	K2186	R2187	I2188	R2189	TYR	ILE	LEU			
E1992	R1995	I2011	M2012	L2013	P2014	E2015	L2016	Y2017	D2018	K2033	Y2044	L2047	M2048	E2049	Y2050	D2051	Q2052	S2053	K2054	L2057	E2058	Q2059	Q2060	F2061	Y2065	L2082	L2085	I2086	K2089	ALA	ASN	P2092	A2093	S2096	K2097	L2098	S2099	F2103	L2104	A2105	N2112	D2113	D2114	A2115	A2122																		
E1765	F1766	G1767	T1768	L1769	L1770	R1780	I1781	N1782	L1783	R1784	N1785	L1792	L1793	R1794	L1797	H1802	N1803	S1804	E1809	K1813	F1814	G1815	E1821	S1822	MET	SER	ASN	ASN	PRO	GLN	ILE	PRO	LYS	LYS	VAL	ASP	GLN	VAL	ASP	GLU	LYS	GLU	ASP	PHE	THR	LEU	VAL	ASN	LEU														
K1682	R1683	G1684	S1685	Q1686	I1687	H1688	Y1692	Y1696	K1706	H1707	S1708	D1709	L1710	S1713	M1716	I1717	E1723	G1727	F1728	A1729	G1730	E1731	L1732	K1733	D1734	S1735	C1736	N1737	Y1738	H1739	T1740	K1741	V1742	K1743	E1744	I1745	K1746	K1749	S1750	Y1751	D1752	A1753	G1754	L1757	N1760	I1761	S1762	L1763	T1764														
ILE	E1608	R1609	M1610	P1611	I1612	A1613	E1614	A1615	L1616	V1617	N1618	I1619	V1620	L1621	G1622	L1623	T1624	N1625	D1626	D1627	I1628	T1629	N1630	F1631	L1632	P1633	S1634	I1635	L1636	T1637	N1638	I1639	C1640	Q1641	V1642	L1643	R1644	S1645	E1648	E1649	L1650	R1651	D1652	A1653	V1654	G1659	S1662	L1670	V1671	F1672	E1676	A1679											
V1545	Q1546	I1547	VAL	GLN	LEU	SER	VAL	PRO	LEU	ARG	GLU	T1558	I1561	V1562	G1565	A1566	E1567	S1568	K1569	L1570	T1571	L1572	S1573	K1574	F1575	P1576	S1577	ASN	LEU	ASP	GLU	PRO	ASN	PHE	ILE	LYS	GLN	GLU	LEU	TYR	PRO	THR	LEU	LYS	ILE	GLY	THR	ARG	ASP	ASP	GLU	THR	ILE										
Y1484	L1485	I1486	P1487	M1488	I1489	E1490	H1491	Y1492	V1493	F1494	S1495	D1496	D1497	E1498	R1499	Y1500	R1501	M1502	I1503	G1504	M1505	E1506	T1507	Q1508	I1509	A1510	I1511	G1512	G1513	L1514	Q1515	Q1516	H1517	M1518	S1519	M1520	M1521	K1524	A1525	L1526	L1527	R1528	R1529	Y1530	I1531	S1532	M1533	L1534	K1535	T1536	K1537	P1538	N1539	Q1540	M1541	K1542	Q1543	A1544					
Y1423	M1424	V1425	K1426	N1427	T1428	K1429	F1430	T1431	T1432	F1433	F1434	E1435	E1436	I1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1386	E1446	E1447	A1448	K1389	S1390	I1391	S1392	THR	PHE	ASN	VAL	ASN	HIS	ILE	GLN	LEU	HIS	R1461	R1462	Q1463	R1464	A1465	I1466	K1467	R1468	L1469	D1408	S1409	L1410	E1411	E1412	V1413	GLN	SER	GLU	TYR	VAL	SER	V1420	L1421	S1482	H1483

- Molecule 63: U3 small nucleolar RNA-associated protein 14



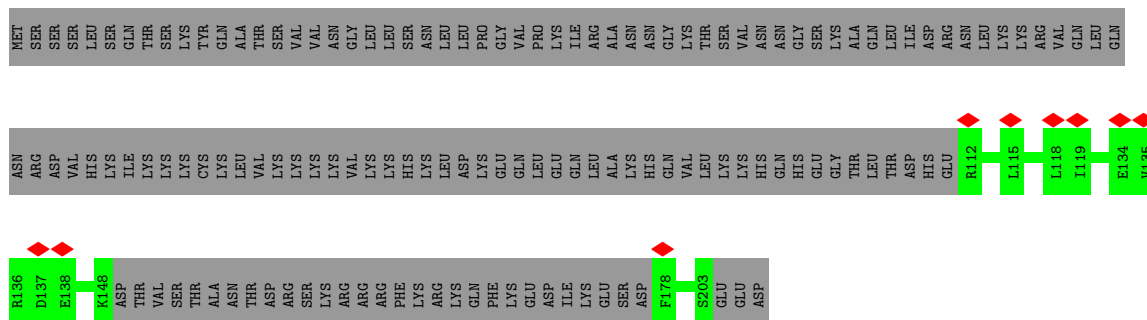
- Molecule 64: Essential nuclear protein 1





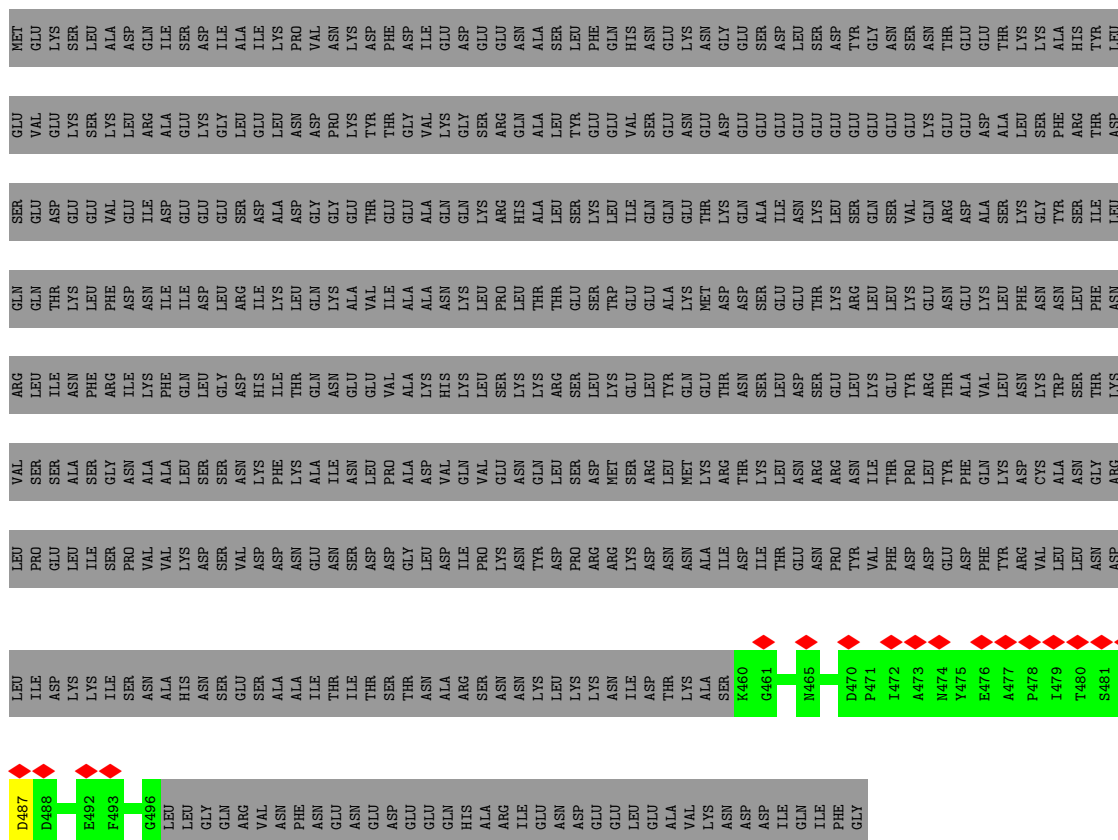
- Molecule 67: Regulator of rDNA transcription protein 14

Chain RW: 31% 69%



- Molecule 68: Protein BFR2

Chain RY: 7% 93%



- Molecule 69: Unassigned helices



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	71230	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	0.246	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.92	0/4141	1.17	24/6433 (0.4%)
2	5A	0.84	0/12485	1.11	48/19449 (0.2%)
3	SA	0.71	0/31590	1.16	247/49182 (0.5%)
4	SC	0.47	0/1856	0.73	5/2490 (0.2%)
5	SF	0.35	0/1854	0.66	1/2504 (0.0%)
6	SG	0.53	0/1690	0.64	0/2285
7	SH	0.31	0/1341	0.60	0/1789
8	SI	0.38	0/1341	0.67	1/1806 (0.1%)
9	SJ	0.31	0/1347	0.59	1/1801 (0.1%)
10	SK	0.47	0/1410	0.60	0/1888
11	SM	0.31	0/1020	0.58	0/1374
12	SN	0.32	0/873	0.73	1/1185 (0.1%)
13	SO	0.45	0/1109	0.62	0/1495
14	SP	0.49	0/879	0.68	0/1186
15	SR	0.58	0/990	0.73	1/1335 (0.1%)
16	ST	0.38	0/980	0.63	0/1319
17	SX	0.51	0/1020	0.66	1/1371 (0.1%)
18	SY	0.54	0/798	0.67	1/1065 (0.1%)
19	SZ	0.43	0/822	0.64	0/1103
20	Sc	0.44	0/613	0.65	0/828
21	Sd	0.54	0/499	0.66	0/670
22	3B	0.59	0/1901	0.66	1/2567 (0.0%)
22	3C	0.44	0/1796	0.62	1/2424 (0.0%)
23	3D	0.44	0/2891	0.63	3/3895 (0.1%)
24	3E	0.41	0/3059	0.62	3/4153 (0.1%)
25	3F	0.42	0/3715	0.64	2/5001 (0.0%)
26	3G	0.52	0/928	0.76	1/1262 (0.1%)
26	3H	0.47	0/928	0.69	2/1262 (0.2%)
27	A4	0.47	0/5321	0.66	5/7207 (0.1%)
28	A5	0.48	0/4044	0.68	5/5493 (0.1%)
29	A8	0.30	0/3328	0.61	0/4565
30	A9	0.31	0/951	0.58	1/1287 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.37	0/10049	0.56	6/13737 (0.0%)
32	AF	0.53	0/3993	0.67	4/5413 (0.1%)
33	AG	0.47	0/6699	0.65	3/9077 (0.0%)
34	B1	0.64	0/6780	0.68	7/9175 (0.1%)
35	B2	0.43	0/6853	0.67	3/9256 (0.0%)
36	B3	0.39	0/6014	0.69	7/8137 (0.1%)
37	B8	0.58	0/3848	0.66	4/5218 (0.1%)
38	BE	0.57	0/6948	0.66	7/9391 (0.1%)
39	B6	0.45	0/2849	0.58	1/3853 (0.0%)
40	5B	0.34	0/499	0.62	0/659
41	5C	0.58	0/4321	0.68	5/5832 (0.1%)
42	5D	0.50	0/1998	0.66	3/2644 (0.1%)
43	5E	0.47	0/1665	0.64	1/2233 (0.0%)
44	5F	0.66	0/1559	0.73	2/2097 (0.1%)
45	5G	0.56	0/2337	0.66	1/3148 (0.0%)
46	5H	0.45	0/1074	0.56	0/1422
47	5I	0.61	0/3844	0.66	2/5174 (0.0%)
48	5J	0.42	0/1302	0.54	0/1728
49	5K	0.56	0/1426	0.66	1/1917 (0.1%)
50	RA	0.34	0/2769	0.67	1/3753 (0.0%)
51	RB	0.38	0/1121	0.62	0/1487
52	RC	0.46	0/2245	0.60	0/3021
53	RE	0.38	0/8924	0.62	6/12070 (0.0%)
54	RF	0.34	0/2004	0.63	2/2697 (0.1%)
55	RG	0.39	0/1727	0.68	2/2329 (0.1%)
55	RH	0.42	0/1828	0.61	0/2470
56	RI	0.46	0/2080	0.65	0/2797
57	RJ	0.50	0/6514	0.60	1/8768 (0.0%)
58	RK	0.44	0/2832	0.65	3/3825 (0.1%)
59	RL	0.29	0/4549	0.50	0/6241
59	RM	0.25	0/3765	0.47	0/5218
60	RN	0.36	0/4591	0.58	2/6187 (0.0%)
61	RO	0.38	0/3849	0.62	5/5261 (0.1%)
62	RP	0.28	0/12230	0.51	5/16819 (0.0%)
63	RQ	0.46	0/1678	0.58	0/2282
64	RS	0.33	0/2104	0.67	1/2854 (0.0%)
65	RT	0.42	0/1379	0.63	1/1853 (0.1%)
66	RV	0.47	0/1456	0.63	2/1937 (0.1%)
67	RW	0.34	0/385	0.50	0/529
68	RY	0.29	0/307	0.51	0/415
All	All	0.53	0/239915	0.77	443/334598 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
13	SO	0	1
14	SP	0	1
16	ST	0	1
19	SZ	0	1
20	Sc	0	1
23	3D	0	3
24	3E	0	1
25	3F	0	1
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	1
29	A8	0	4
33	AG	0	2
34	B1	0	3
35	B2	0	9
36	B3	0	11
38	BE	0	1
41	5C	0	2
42	5D	0	1
43	5E	0	1
44	5F	0	1
45	5G	0	1
47	5I	0	2
50	RA	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
57	RJ	0	2
58	RK	0	1
59	RL	0	1
59	RM	0	1
60	RN	0	1
61	RO	0	1
62	RP	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
63	RQ	0	1
66	RV	0	2
All	All	0	79

There are no bond length outliers.

The worst 5 of 443 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	861	U	C2-N1-C1'	10.60	130.42	117.70
3	SA	376	C	N1-C2-O2	10.43	125.16	118.90
3	SA	1174	C	N1-C2-O2	10.35	125.11	118.90
44	5F	13	LEU	CA-CB-CG	10.29	138.96	115.30
3	SA	1034	C	C5-C6-N1	10.00	126.00	121.00

There are no chirality outliers.

5 of 79 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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	34	69
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	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
13	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
14	SP	116/137 (85%)	99 (85%)	16 (14%)	1 (1%)	17	56
15	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
16	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
17	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
18	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
19	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	15	54
20	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
21	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
23	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
24	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
25	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	47	79
26	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	19	58
26	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
27	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
28	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
29	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	34	69
30	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
31	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
32	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
33	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	51	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
35	B2	839/943 (89%)	749 (89%)	88 (10%)	2 (0%)	47	79
36	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	41	74
37	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
38	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
39	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	487 (92%)	43 (8%)	1 (0%)	47	79
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	29	67
44	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
45	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
46	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
47	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
48	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
49	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
50	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
51	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	19	58
52	RC	276/316 (87%)	259 (94%)	17 (6%)	0	100	100
53	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
54	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
55	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
55	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
56	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
57	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	51	83
58	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
59	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	41	74
59	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	29	67
60	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	47	79
61	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
62	RP	2043/2493 (82%)	1815 (89%)	227 (11%)	1 (0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
64	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
65	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
66	RV	184/346 (53%)	165 (90%)	19 (10%)	0	100	100
67	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
68	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	24979/33626 (74%)	22503 (90%)	2452 (10%)	24 (0%)	54	83

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
59	RM	905	PRO
19	SZ	51	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	SC	203/224 (91%)	201 (99%)	2 (1%)	76	90
5	SF	196/222 (88%)	190 (97%)	6 (3%)	40	72
6	SG	180/191 (94%)	180 (100%)	0	100	100
7	SH	139/201 (69%)	137 (99%)	2 (1%)	67	86
8	SI	146/170 (86%)	145 (99%)	1 (1%)	84	94
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	65	85
10	SK	147/166 (89%)	146 (99%)	1 (1%)	84	94
11	SM	110/137 (80%)	108 (98%)	2 (2%)	59	82
12	SN	88/119 (74%)	86 (98%)	2 (2%)	50	78
13	SO	117/128 (91%)	116 (99%)	1 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	SP	90/105 (86%)	90 (100%)	0	100	100
15	SR	105/119 (88%)	105 (100%)	0	100	100
16	ST	105/129 (81%)	104 (99%)	1 (1%)	76	90
17	SX	108/111 (97%)	107 (99%)	1 (1%)	78	91
18	SY	85/120 (71%)	84 (99%)	1 (1%)	71	88
19	SZ	85/113 (75%)	85 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	201 (100%)	0	100	100
22	3C	190/240 (79%)	187 (98%)	3 (2%)	62	84
23	3D	296/435 (68%)	293 (99%)	3 (1%)	76	90
24	3E	262/433 (60%)	261 (100%)	1 (0%)	91	95
25	3F	396/503 (79%)	394 (100%)	2 (0%)	88	95
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	591/713 (83%)	584 (99%)	7 (1%)	71	88
28	A5	433/574 (75%)	432 (100%)	1 (0%)	93	98
29	A8	174/657 (26%)	173 (99%)	1 (1%)	86	94
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	705 (100%)	3 (0%)	91	95
32	AF	437/454 (96%)	433 (99%)	4 (1%)	78	91
33	AG	750/826 (91%)	740 (99%)	10 (1%)	69	87
34	B1	730/812 (90%)	726 (100%)	4 (0%)	88	95
35	B2	736/832 (88%)	731 (99%)	5 (1%)	84	94
36	B3	665/719 (92%)	655 (98%)	10 (2%)	65	85
37	B8	421/529 (80%)	420 (100%)	1 (0%)	93	98
38	BE	757/819 (92%)	754 (100%)	3 (0%)	91	95
39	B6	251/414 (61%)	247 (98%)	4 (2%)	62	84
40	5B	57/196 (29%)	55 (96%)	2 (4%)	36	69
41	5C	465/480 (97%)	463 (100%)	2 (0%)	91	95
42	5D	221/234 (94%)	219 (99%)	2 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	5E	185/535 (35%)	184 (100%)	1 (0%)	88	95
44	5F	171/172 (99%)	170 (99%)	1 (1%)	86	94
45	5G	251/258 (97%)	249 (99%)	2 (1%)	81	93
46	5H	107/538 (20%)	107 (100%)	0	100	100
47	5I	416/443 (94%)	414 (100%)	2 (0%)	88	95
48	5J	140/200 (70%)	140 (100%)	0	100	100
49	5K	157/169 (93%)	157 (100%)	0	100	100
50	RA	303/636 (48%)	300 (99%)	3 (1%)	76	90
51	RB	117/315 (37%)	114 (97%)	3 (3%)	46	76
52	RC	231/289 (80%)	230 (100%)	1 (0%)	91	95
53	RE	984/1125 (88%)	979 (100%)	5 (0%)	88	95
54	RF	221/274 (81%)	219 (99%)	2 (1%)	78	91
55	RG	195/222 (88%)	193 (99%)	2 (1%)	76	90
55	RH	206/222 (93%)	204 (99%)	2 (1%)	76	90
56	RI	235/256 (92%)	235 (100%)	0	100	100
57	RJ	683/1039 (66%)	676 (99%)	7 (1%)	76	90
58	RK	307/312 (98%)	303 (99%)	4 (1%)	69	87
59	RL	164/934 (18%)	162 (99%)	2 (1%)	71	88
60	RN	422/732 (58%)	422 (100%)	0	100	100
61	RO	329/506 (65%)	328 (100%)	1 (0%)	92	96
62	RP	499/2307 (22%)	493 (99%)	6 (1%)	71	88
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	55	80
64	RS	225/424 (53%)	225 (100%)	0	100	100
65	RT	148/282 (52%)	146 (99%)	2 (1%)	67	86
66	RV	141/304 (46%)	141 (100%)	0	100	100
67	RW	22/192 (12%)	22 (100%)	0	100	100
68	RY	31/482 (6%)	30 (97%)	1 (3%)	39	71
All	All	18233/29007 (63%)	18093 (99%)	140 (1%)	82	93

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	RJ	566	ARG

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Mol	Chain	Res	Type
57	RJ	1128	LYS
62	RP	1770	LEU
33	AG	259	VAL
33	AG	141	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 304 such sidechains are listed below:

Mol	Chain	Res	Type
53	RE	537	ASN
62	RP	1686	GLN
53	RE	1033	ASN
57	RJ	289	HIS
65	RT	218	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	1304/1808 (72%)	498 (38%)	19 (1%)
All	All	1991/2841 (70%)	703 (35%)	32 (1%)

5 of 703 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 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1197	C
3	SA	1521	G
2	5A	536	A
2	5A	492	G
3	SA	1594	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\# Z > 2$
71	GTP	RJ	1201	72	26,34,34	0.94	2 (7%)	32,54,54	0.92	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
71	GTP	RJ	1201	72	-	3/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	RJ	1201	GTP	C5-C6	-2.47	1.42	1.47
71	RJ	1201	GTP	C8-N7	-2.05	1.31	1.35

There are no bond angle outliers.

There are no chirality outliers.

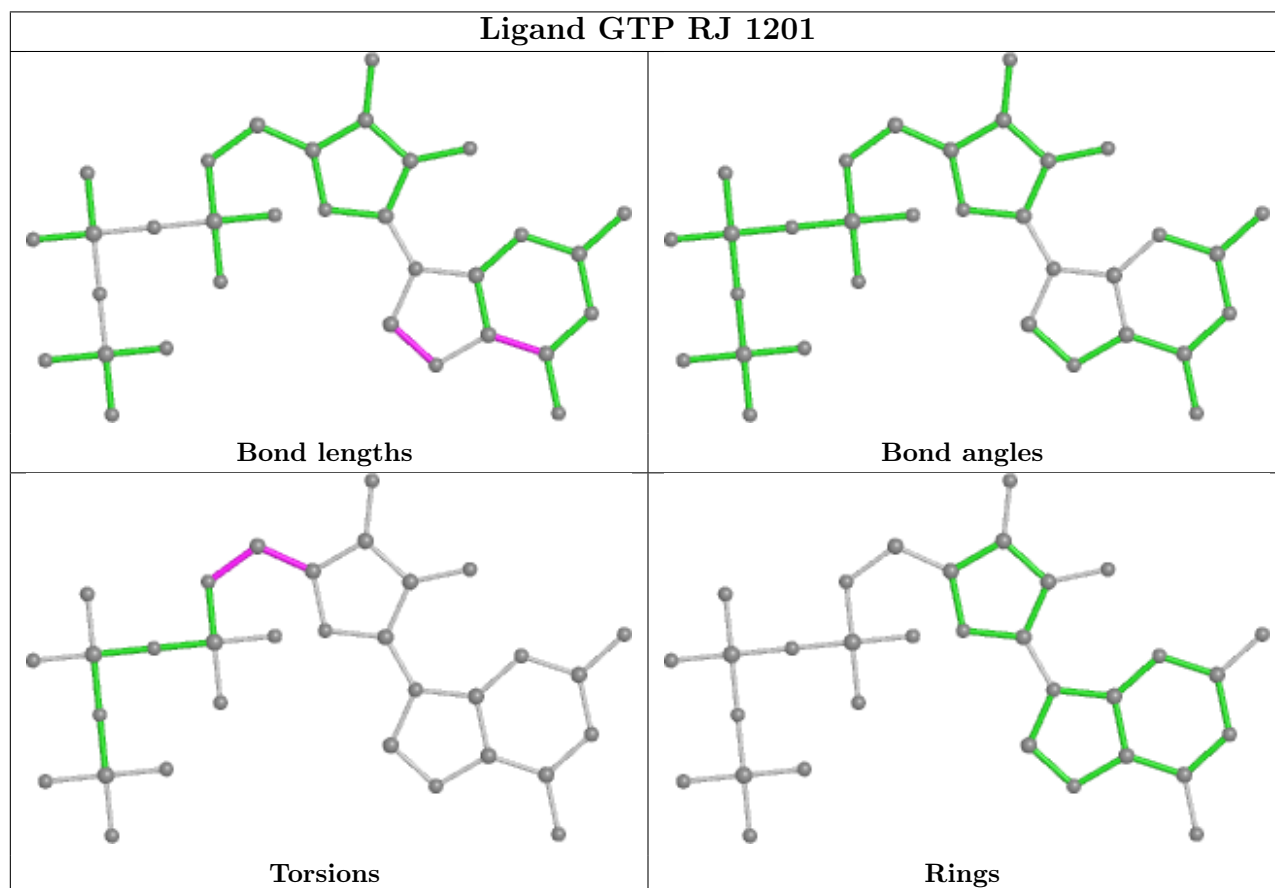
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RJ	1201	GTP	O4'-C4'-C5'-O5'
71	RJ	1201	GTP	C3'-C4'-C5'-O5'
71	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

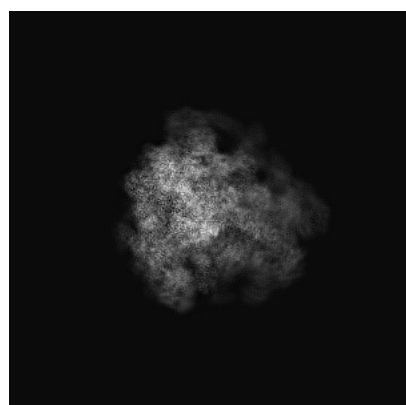
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0949. These allow visual inspection of the internal detail of the map and identification of artifacts.

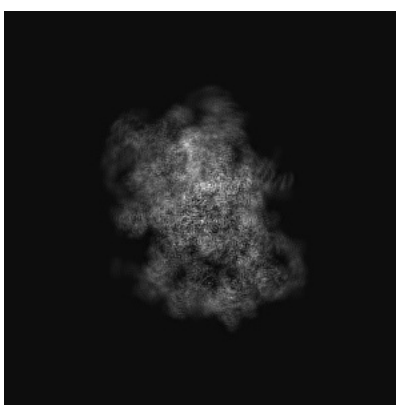
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

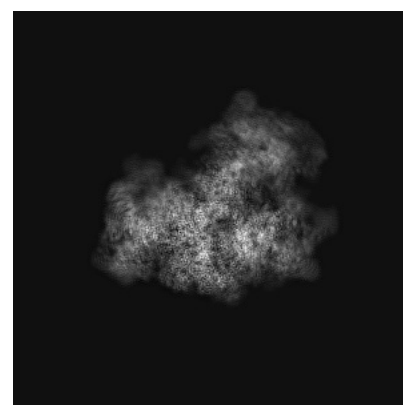
6.1.1 Primary map



X



Y

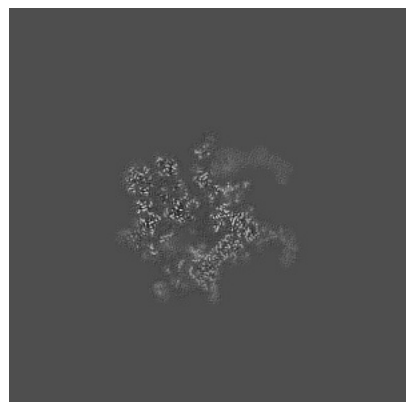


Z

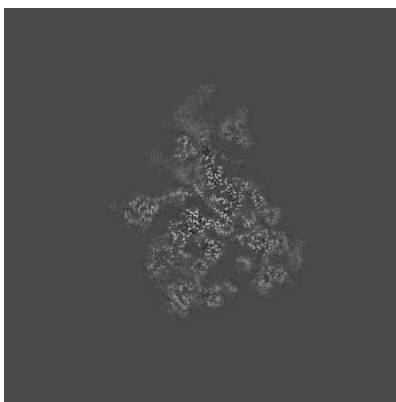
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

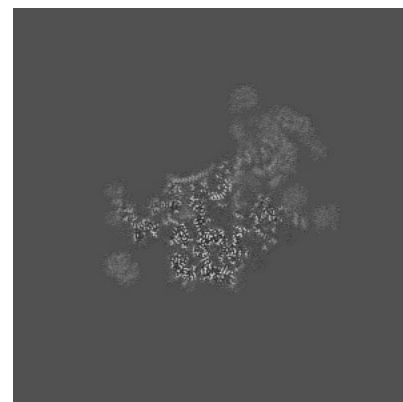
6.2.1 Primary map



X Index: 224



Y Index: 224



Z Index: 224

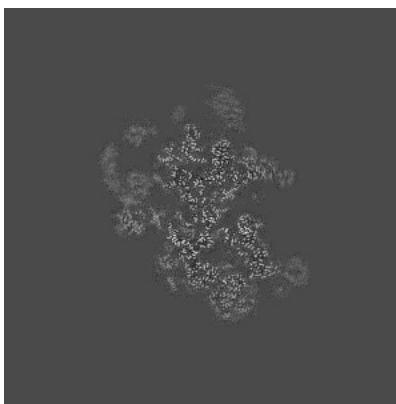
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

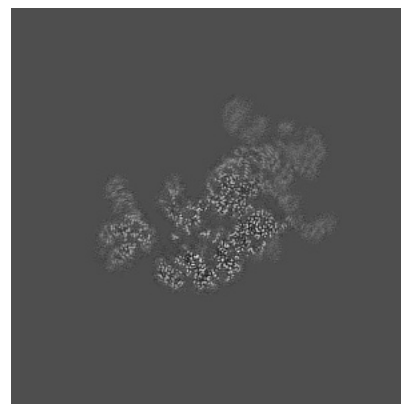
6.3.1 Primary map



X Index: 212



Y Index: 196



Z Index: 242

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

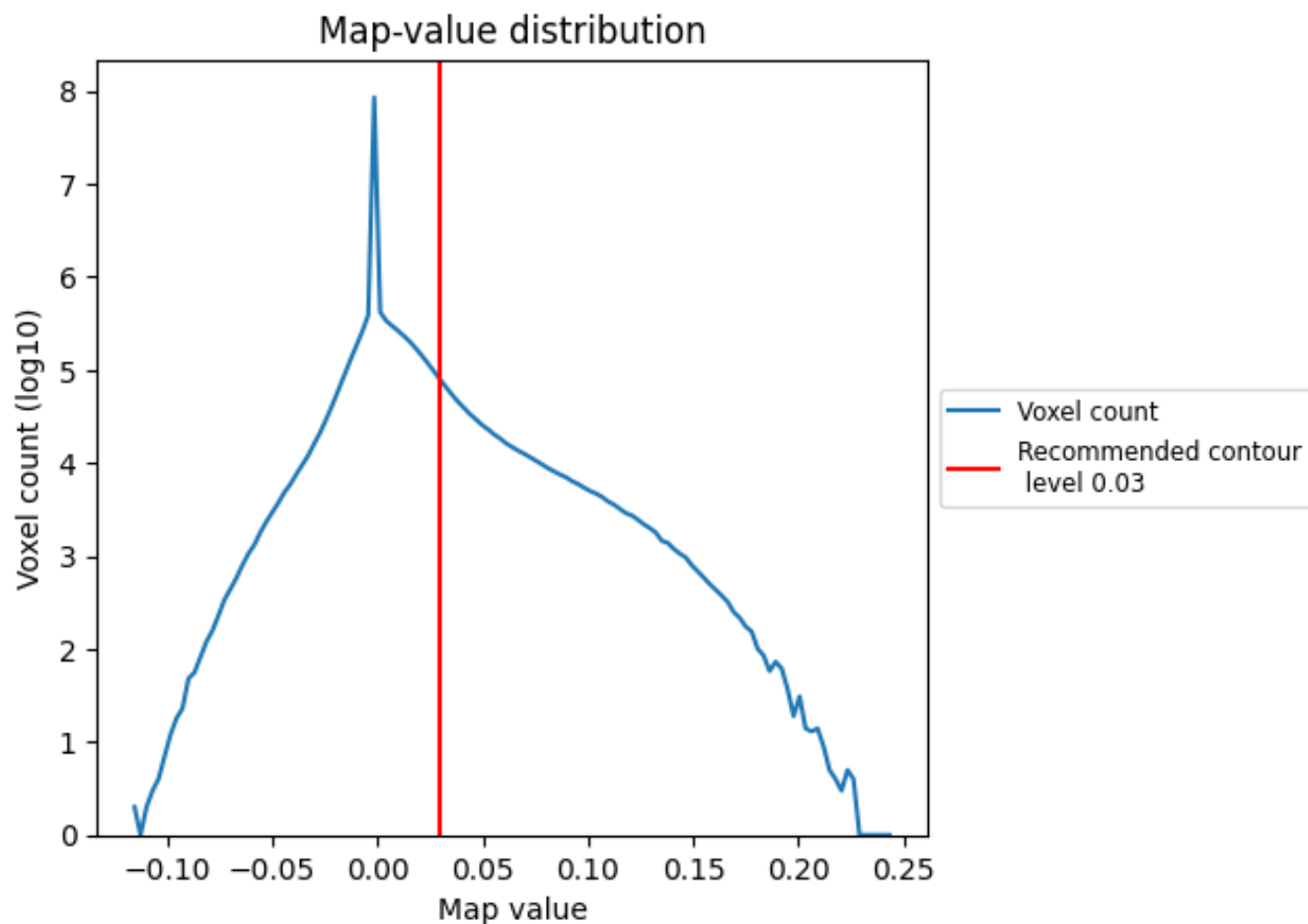
6.5 Mask visualisation

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

7 Map analysis [i](#)

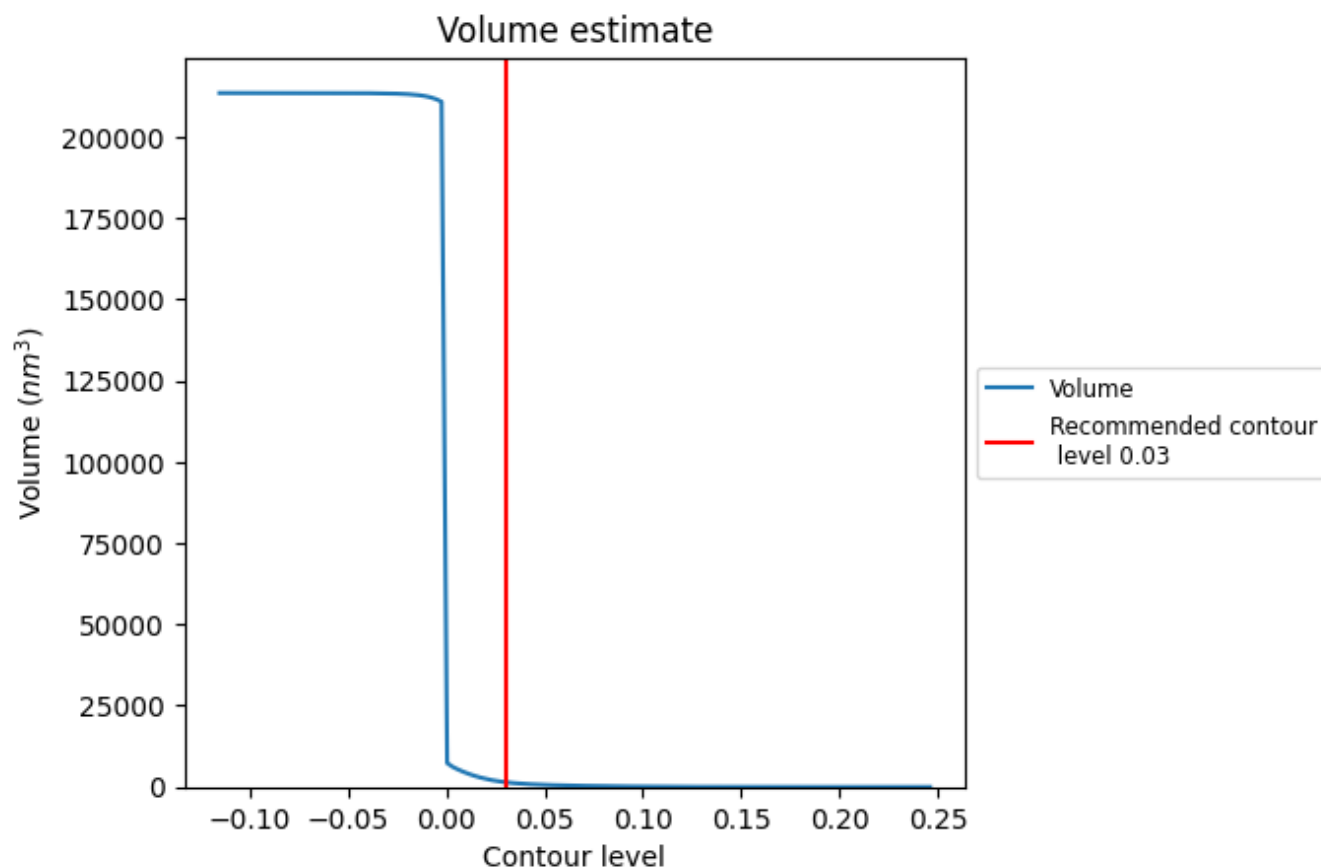
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

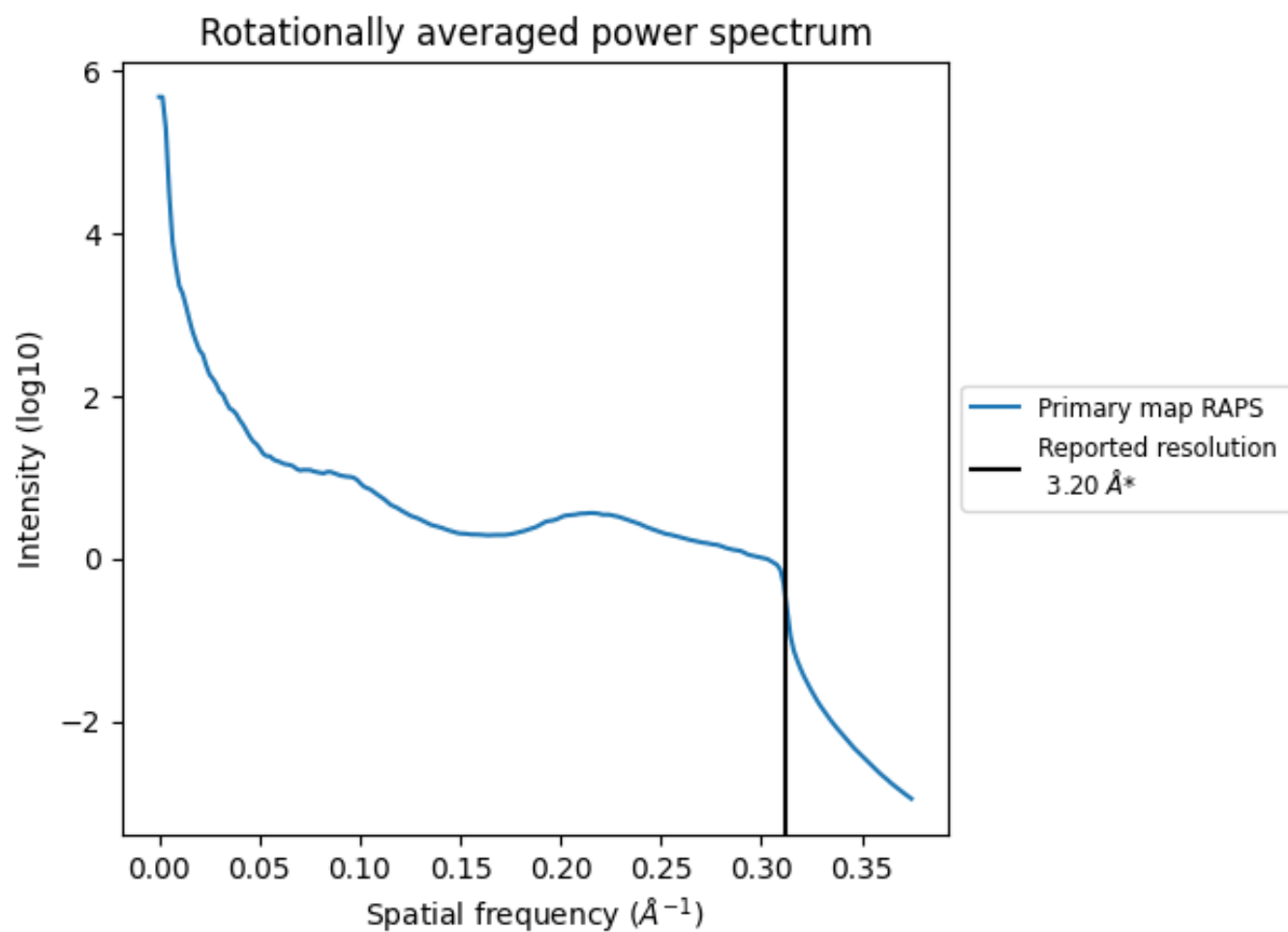
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1466 nm^3 ; this corresponds to an approximate mass of 1324 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 ⓘ

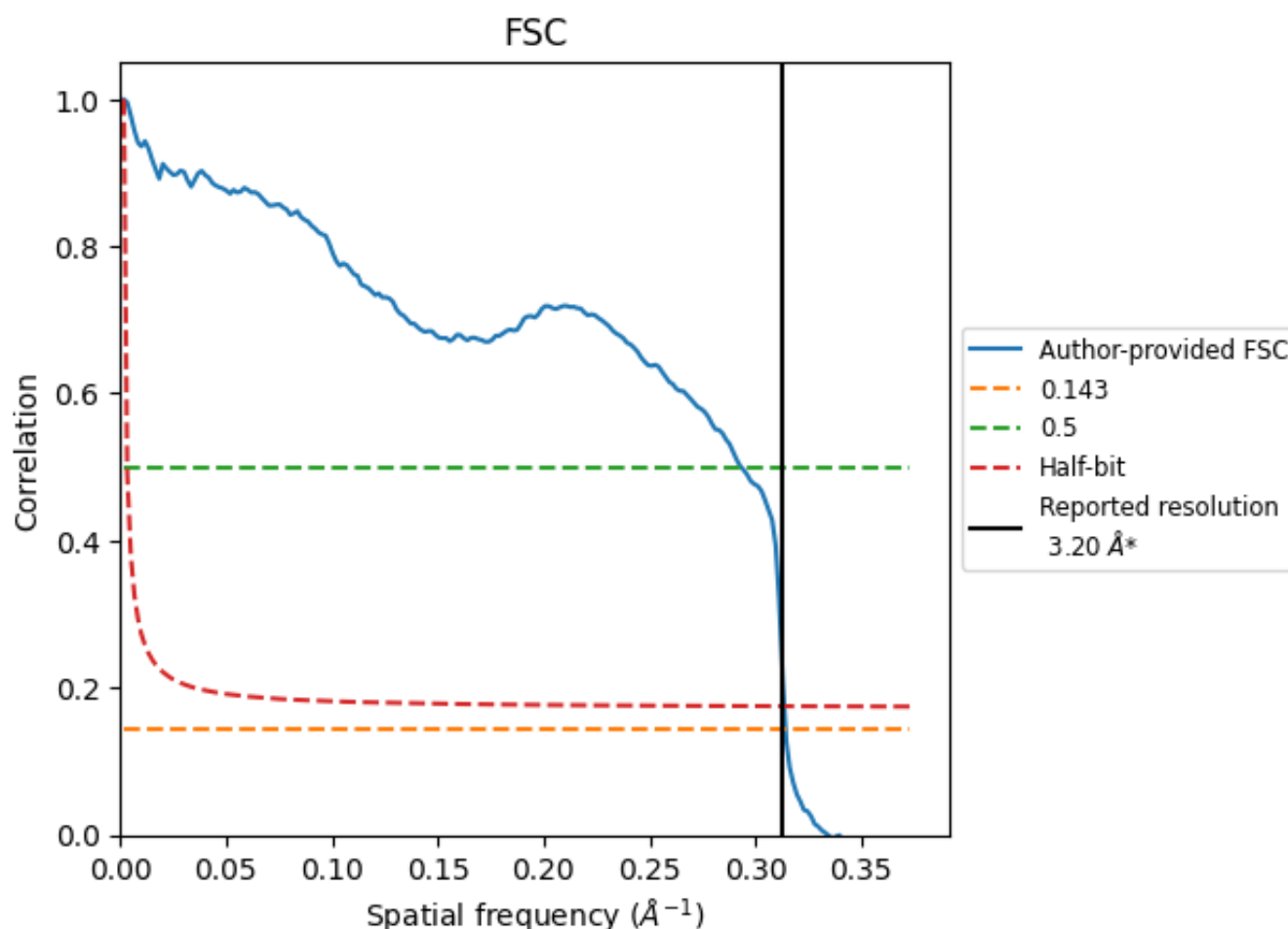


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

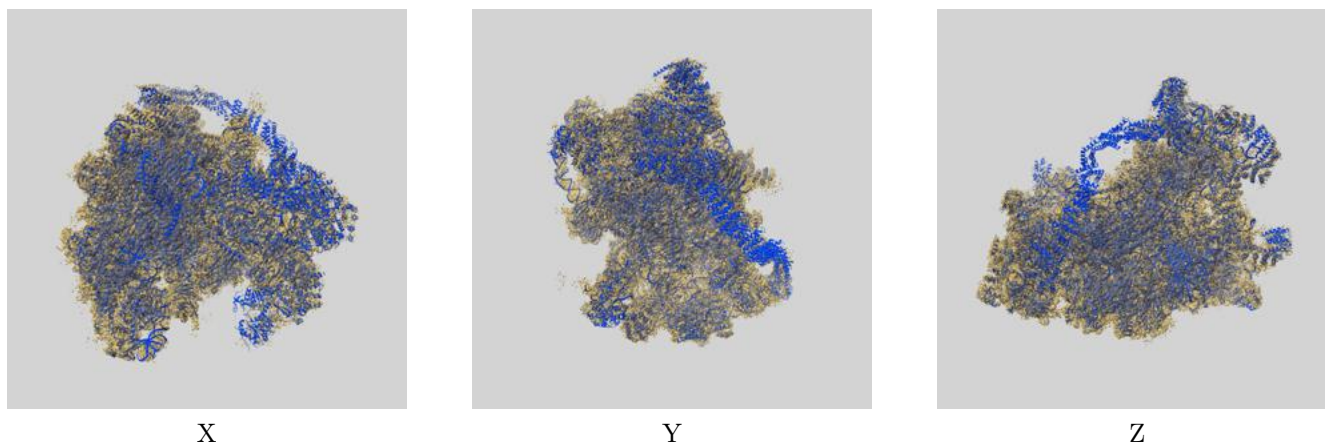
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.41	3.19
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

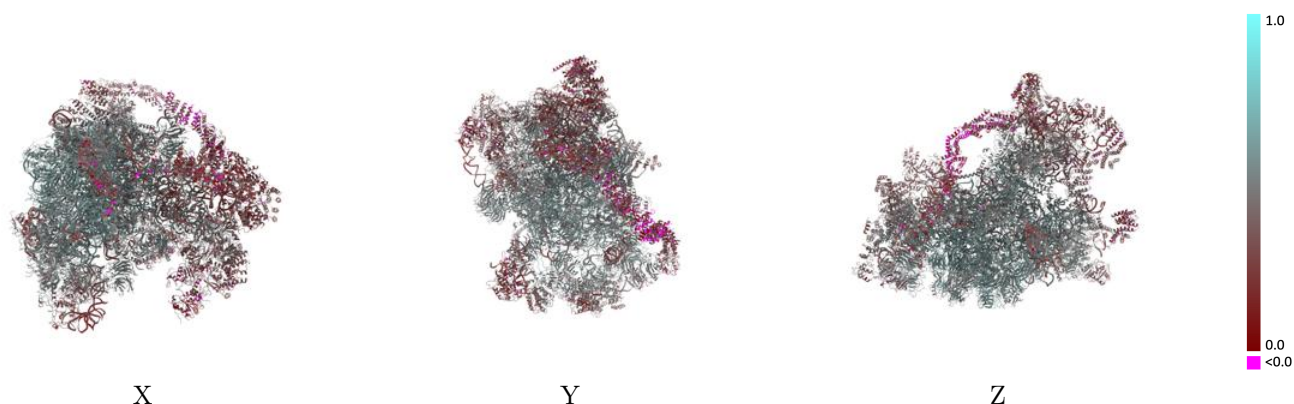
This section contains information regarding the fit between EMDB map EMD-0949 and PDB model 6LQP. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



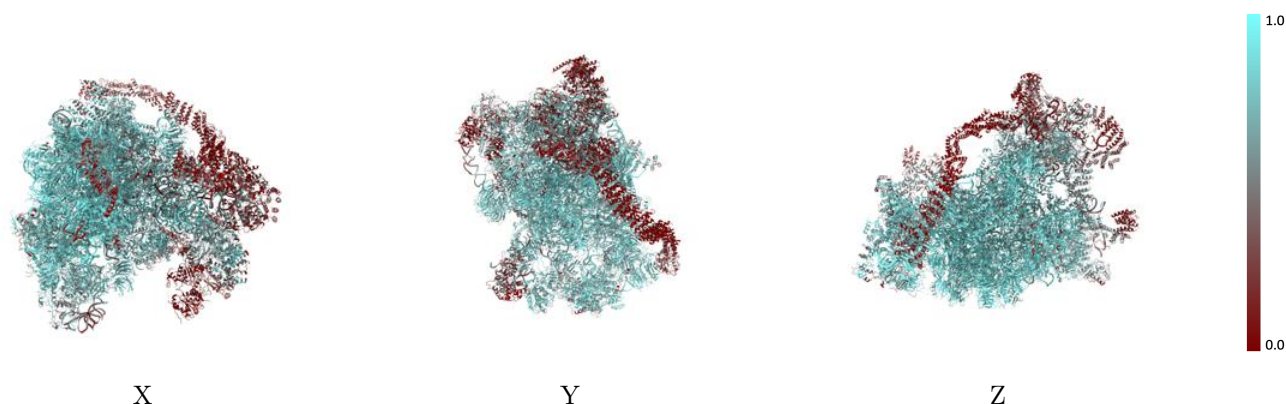
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



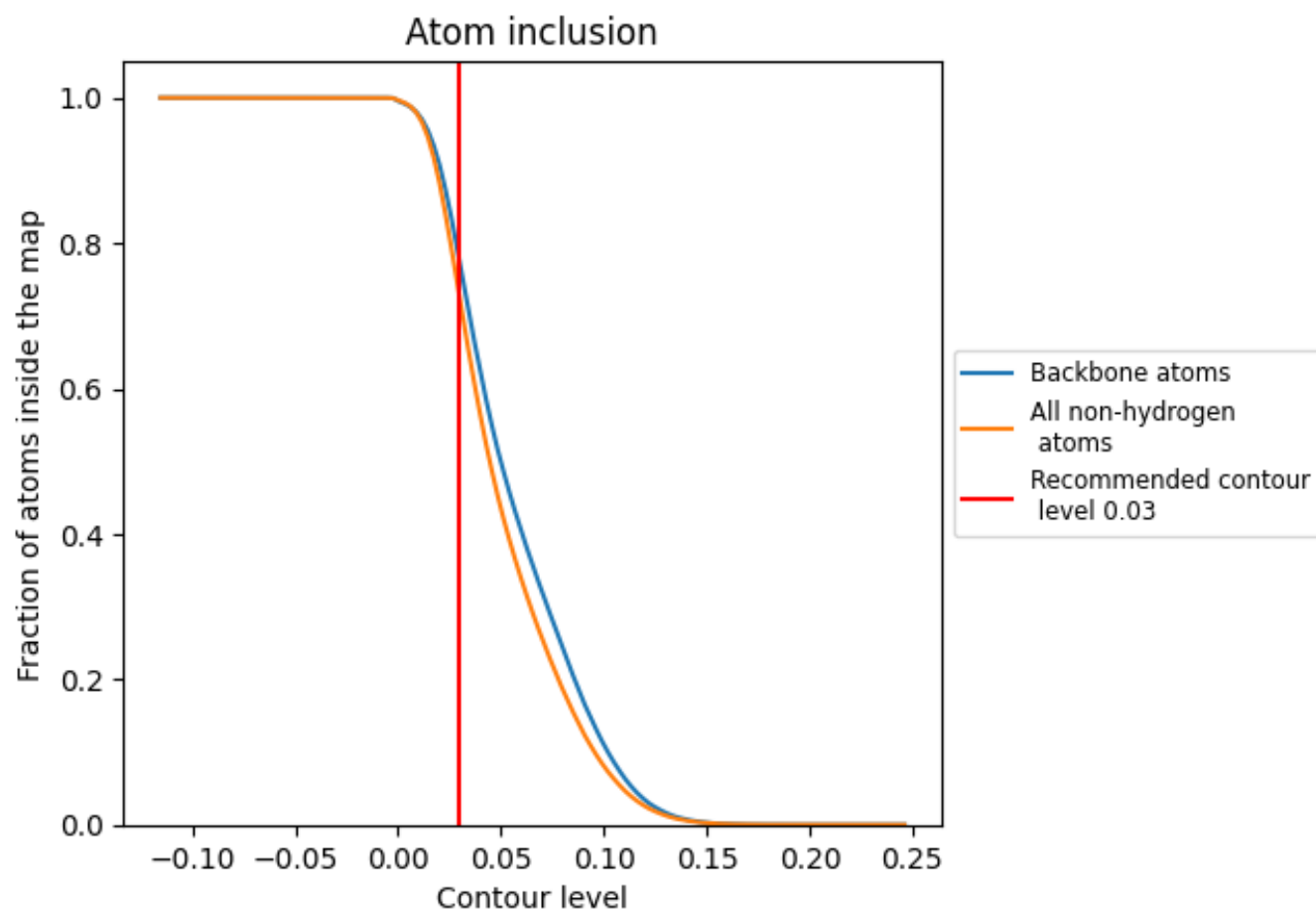
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7237	 0.4710
3A	 0.9049	 0.5090
3B	 0.8847	 0.5680
3C	 0.7983	 0.5000
3D	 0.8133	 0.5140
3E	 0.7924	 0.4870
3F	 0.7814	 0.4970
3G	 0.8706	 0.5540
3H	 0.8274	 0.5340
5A	 0.8942	 0.4880
5B	 0.7229	 0.4830
5C	 0.8962	 0.5750
5D	 0.8255	 0.5310
5E	 0.8193	 0.5440
5F	 0.9227	 0.5830
5G	 0.8715	 0.5680
5H	 0.8168	 0.5270
5I	 0.8995	 0.5770
5J	 0.7060	 0.5110
5K	 0.8814	 0.5670
A4	 0.8400	 0.5160
A5	 0.8531	 0.5350
A8	 0.5488	 0.3710
A9	 0.7581	 0.4200
AE	 0.3278	 0.3250
AF	 0.8918	 0.5540
AG	 0.8334	 0.5210
B1	 0.9099	 0.5770
B2	 0.8169	 0.5040
B3	 0.7658	 0.4720
B6	 0.7454	 0.4690
B8	 0.8984	 0.5670
BE	 0.9112	 0.5760
RA	 0.5413	 0.4120
RB	 0.6397	 0.4590



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Chain	Atom inclusion	Q-score
RC	 0.7472	 0.5120
RE	 0.6646	 0.4410
RF	 0.5402	 0.4040
RG	 0.6892	 0.4530
RH	 0.8227	 0.5330
RI	 0.8464	 0.5290
RJ	 0.8368	 0.5370
RK	 0.8315	 0.5310
RL	 0.5794	 0.4100
RM	 0.2390	 0.3000
RN	 0.6804	 0.4410
RO	 0.7592	 0.4580
RP	 0.3009	 0.3170
RQ	 0.7452	 0.5040
RS	 0.3357	 0.2730
RT	 0.8268	 0.5200
RV	 0.8294	 0.5350
RW	 0.7037	 0.4960
RY	 0.4403	 0.3860
SA	 0.7268	 0.4210
SC	 0.8165	 0.5370
SF	 0.6232	 0.4190
SG	 0.8590	 0.5590
SH	 0.4574	 0.4220
SI	 0.6406	 0.4510
SJ	 0.5165	 0.3740
SK	 0.8576	 0.5550
SM	 0.4928	 0.3660
SN	 0.0398	 0.2760
SO	 0.8527	 0.5380
SP	 0.8676	 0.5470
SR	 0.8983	 0.5690
ST	 0.6954	 0.4700
SX	 0.8401	 0.5470
SY	 0.8748	 0.5630
SZ	 0.6747	 0.4650
Sc	 0.8622	 0.5520
Sd	 0.8595	 0.5610
X1	 0.6557	 0.4480