wwPDB EM Validation Summary Report (i)

Apr 23, 2024 – 03:17 pm BST

PDB ID	:	6ZQB
EMDB ID	:	EMD-11358
Title	:	Cryo-EM structure of the 90S pre-ribosome from Saccharomyces cerevisiae, state B2
Authors	:	Cheng, J.; Lau, B.; Venuta, G.L.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on	:	2020-07-09
Resolution	:	3.90 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

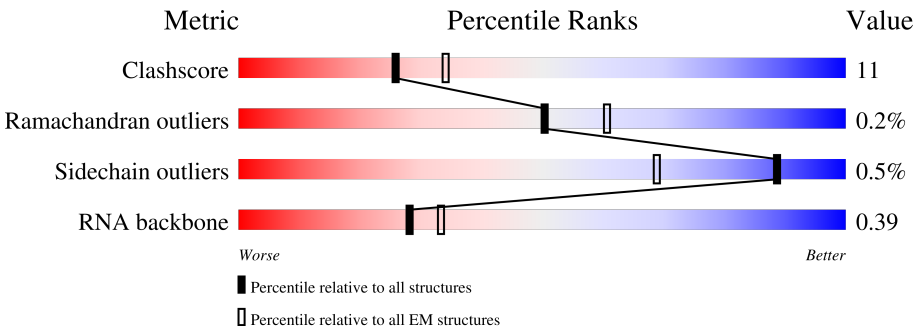
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	UA	923	60% 27% • 10%
2	UB	810	• 49% 13% 37%
3	UC	610	15% 6% 79%
4	UD	776	57% 29% • 13%
5	UE	643	53% 20% • 26%
6	UF	440	48% 18% • 33%
7	UG	554	65% 29% • •

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Mol	Chain	Length	Quality of chain
8	UH	713	44% 17% 38%
9	UI	575	11% 6% 82%
10	UJ	1769	55% 7% 37%
11	UK	250	64% 30%
12	UL	943	59% 30% 11%
13	UM	817	62% 30% 7%
14	UN	145	73% 25%
15	UO	513	68% 26%
16	UP	214	19% 9% 72%
17	UQ	896	62% 29% 7%
18	UR	594	58% 20% 19%
19	US	552	63% 23% 13%
20	UT	2493	5% 88% 10%
21	UU	939	67% 21% 10%
22	UV	1237	64% 24% 13%
23	UX	189	61% 28% 8%
24	UZ	274	62% 28% 10%
25	CA	327	57% 14% 26%
25	CB	327	47% 22% 30%
26	CD	504	55% 19% 25%
27	CE	511	72% 13% 15%
28	CF	126	73% 21%
28	CG	126	64% 32%
29	CH	573	51% 27% 21%
30	CI	183	62% 32% 5%

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Mol	Chain	Length	Quality of chain
31	CJ	290	66% 27%
32	CK	593	26% 8% 65%
33	CL	1183	46% 19% 34%
34	CM	367	70% 28%
35	CN	297	57% 21% 22%
36	JA	1056	57% 20% 23%
36	JB	1056	15% 76% 21%
37	JC	707	31% 19% 50%
38	JE	357	24% 14% 62%
39	JF	252	62% 24% 14%
39	JG	252	65% 25% 9%
40	JH	483	8% 53% 46%
41	JJ	274	47% 18% 34%
42	JK	534	5% 92%
43	JM	217	46% 17% 38%
44	JN	346	42% 11% 46%
45	JO	316	59% 15% 25%
46	JP	489	59% 30% 7%
47	JQ	206	28% 69%
48	DA	255	69% 24% 6%
49	DE	261	59% 34% 6%
50	DF	225	75% 19% 5%
51	DG	236	56% 36% 8%
52	DH	190	65% 31%
53	DI	200	64% 24% 12%

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Mol	Chain	Length	Quality of chain
54	DJ	197	61% 27% 10%
55	DL	156	57% 33% 10%
56	DN	151	75% 23%
57	DO	137	69% 19% 12%
58	DQ	143	61% 24% 13%
59	DS	147	67% 29%
60	DW	130	74% 25%
61	DX	145	49% 19% 29%
62	DY	135	38% 33% 28%
63	Db	82	96%
64	Dc	67	90% 6%
65	D2	700	20% 33% 17% 25%
66	D3	1808	18% 29% 16% 34%
67	D4	175	26% 39% 27% 8%

2 Entry composition (i)

There are 69 unique types of molecules in this entry. The entry contains 223151 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Periodic tryptophan protein 2.

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

- Molecule 2 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	UB	508	3743	2373	665	696	9	0	0

- Molecule 3 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	UC	128	1026	633	204	189	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	UD	675	5361	3395	929	1015	22	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	UE	475	3772	2400	649	710	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	UF	293	2487	1605	435	434	13	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	UG	533	4218	2646	758	802	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	UH	441	2690	1672	492	523	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	UI	102	846	547	149	148	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	UJ	1117	6857	4267	1252	1326	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	UK	241	2016	1251	388	370	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	UL	842	6720	4300	1126	1267	27	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	UM	762	5957	3779	1006	1144	28	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	UN	145	1207	750	230	225	2	0	0

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

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

- Molecule 16 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	UP	60	495	310	101	84	0	0

- Molecule 17 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	UQ	832	6662	4236	1124	1283	19	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	UR	481	3791	2399	668	714	10	0	0

- Molecule 19 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	US	481	3650	2355	611	672	12	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	UT	2234	11108	6640	2234	2234	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	UU	848	6678	4241	1149	1267	21	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	UV	1080	8725	5672	1439	1590	24	0	0

- Molecule 23 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	UX	174	1395	890	255	240	10	0	0

- Molecule 24 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	UZ	247	2006	1284	356	358	8	0	0

- Molecule 25 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	CA	242	1881	1193	338	340	10	0	0
25	CB	228	1782	1131	320	321	10	0	0

- Molecule 26 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	CD	380	2994	1898	513	574	9	0	0

- Molecule 27 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	CE	435	2985	1852	543	582	8	0	0

- Molecule 28 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	CF	123	931	594	160	173	4	0	0
28	CG	123	928	591	160	173	4	0	0

- Molecule 29 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	CH	454	3634	2311	638	675	10	0	0

- Molecule 30 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	CI	182	1530	967	287	269	7	0	0

- Molecule 31 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	CJ	282	2296	1441	430	418	7	0	0

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	CK	207	1667	1034	297	332	4	0	0

- Molecule 33 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	CL	781	6332	4063	1122	1117	30	0	0

- Molecule 34 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 35 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	CN	232	1893	1213	322	351	7	0	0

- Molecule 36 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	JA	812	5892	3727	1041	1099	25	0	0
			Total	C	N	O			
36	JB	835	4132	2462	835	835		0	0

- Molecule 37 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	JC	354	2845	1795	489	552	9	0	0

- Molecule 38 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	JE	136	1125	674	231	217	3	0	0

- Molecule 39 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	JF	216	1701	1079	296	315	11	0	0
			Total	C	N	O	S		
39	JG	230	1799	1142	313	333	11	0	0

- Molecule 40 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	JH	261	1295	773	261	261	0	0

- Molecule 41 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	JJ	182	1448	926	262	256	4	0	0

- Molecule 42 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	JK	42	334	213	54	67	0	0

- Molecule 43 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	JM	135	1137	721	211	201	4	0	0

- Molecule 44 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	JN	186	1428	879	287	259	3	0	0

- Molecule 45 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	JO	236	1930	1231	342	345	12	0	0

- Molecule 46 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	JP	457	3725	2328	679	702	16	0	0

- Molecule 47 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 48 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	DA	240	1912	1209	354	345	4	0	0

- Molecule 49 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	DE	245	1944	1245	360	336	3	0	0

- Molecule 50 is a protein called Rps5p.

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

- Molecule 51 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	DG	218	1755	1102	337	313	3	0	0

- Molecule 52 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
52	DH	184	1477	949	265	263	0	0

- Molecule 53 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	DI	177	1399	869	279	249	2	0	0

- Molecule 54 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	DJ	177	1428	902	275	250	1	0	0

- Molecule 55 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	DL	140	1129	724	215	187	3	0	0

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	DN	150	1192	759	224	207	2	0	0

- Molecule 57 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	DO	120	881	544	167	167	3	0	0

- Molecule 58 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
58	DQ	125	973	625	174	174	0	0

- Molecule 59 is a protein called 40S ribosomal protein S18-A,40S ribosomal protein S18-A,Rps18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
59	DS	104	516	308	104	104	0	0

- Molecule 60 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	DW	129	1021	650	188	180	3	0	0

- Molecule 61 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 62 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	DY	97	767	490	138	139	0	0

- Molecule 63 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Db	81	610	382	110	113	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 65 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
65	D2	522	11138	4977	1976	3663	522	0	0

- Molecule 66 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
66	D3	1198	25549	11417	4548	8386	1198	0	0

- Molecule 67 is a RNA chain called U3 snoRNA.

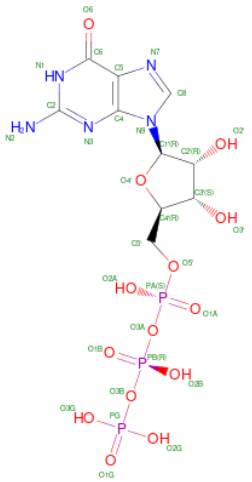
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
67	D4	175	3712	1661	648	1228	175	0	0

- Molecule 68 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
68	UX	1	1	1	0
68	Db	1	1	1	0

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

GTP



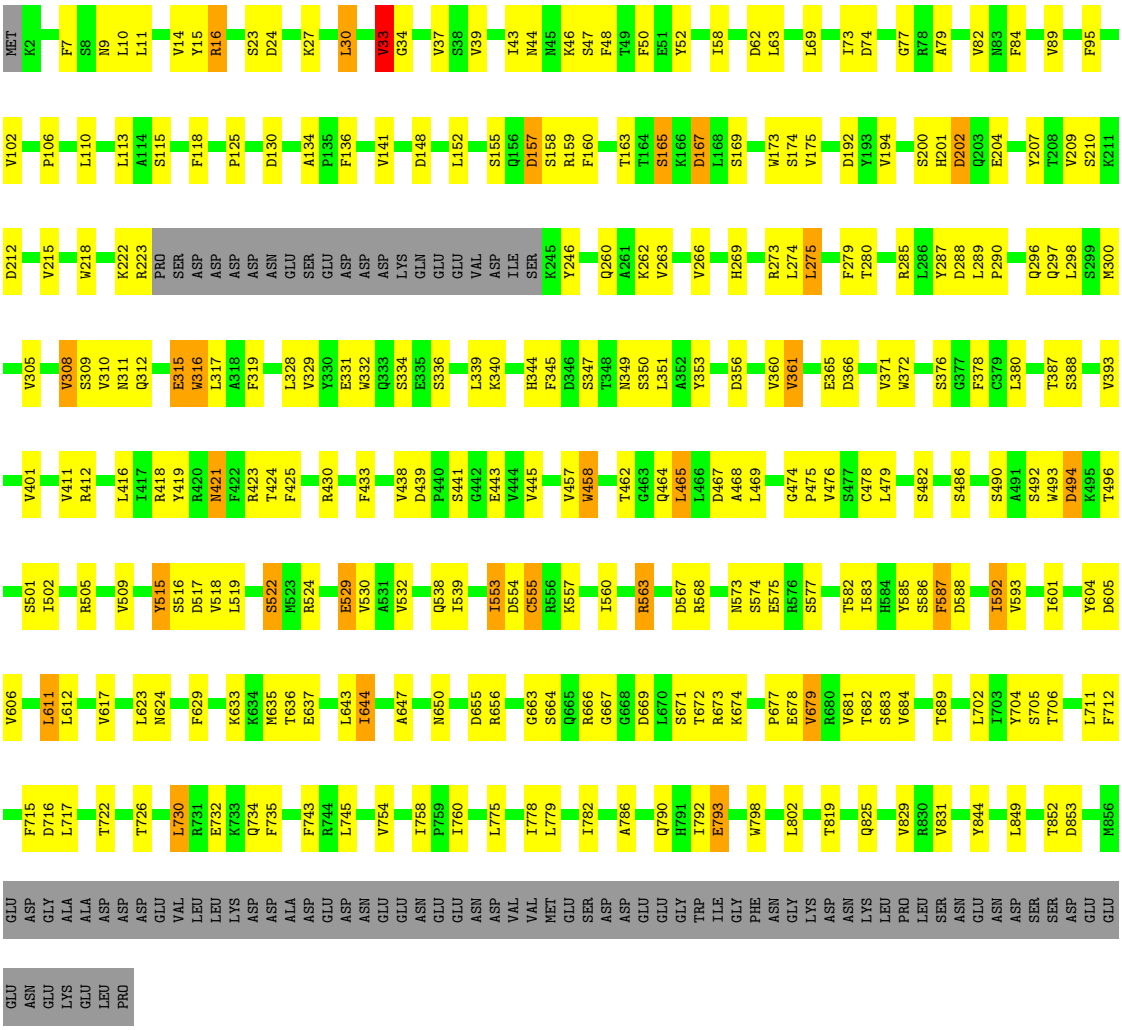
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
69	CL	1	32	10	5	14	3	0

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.

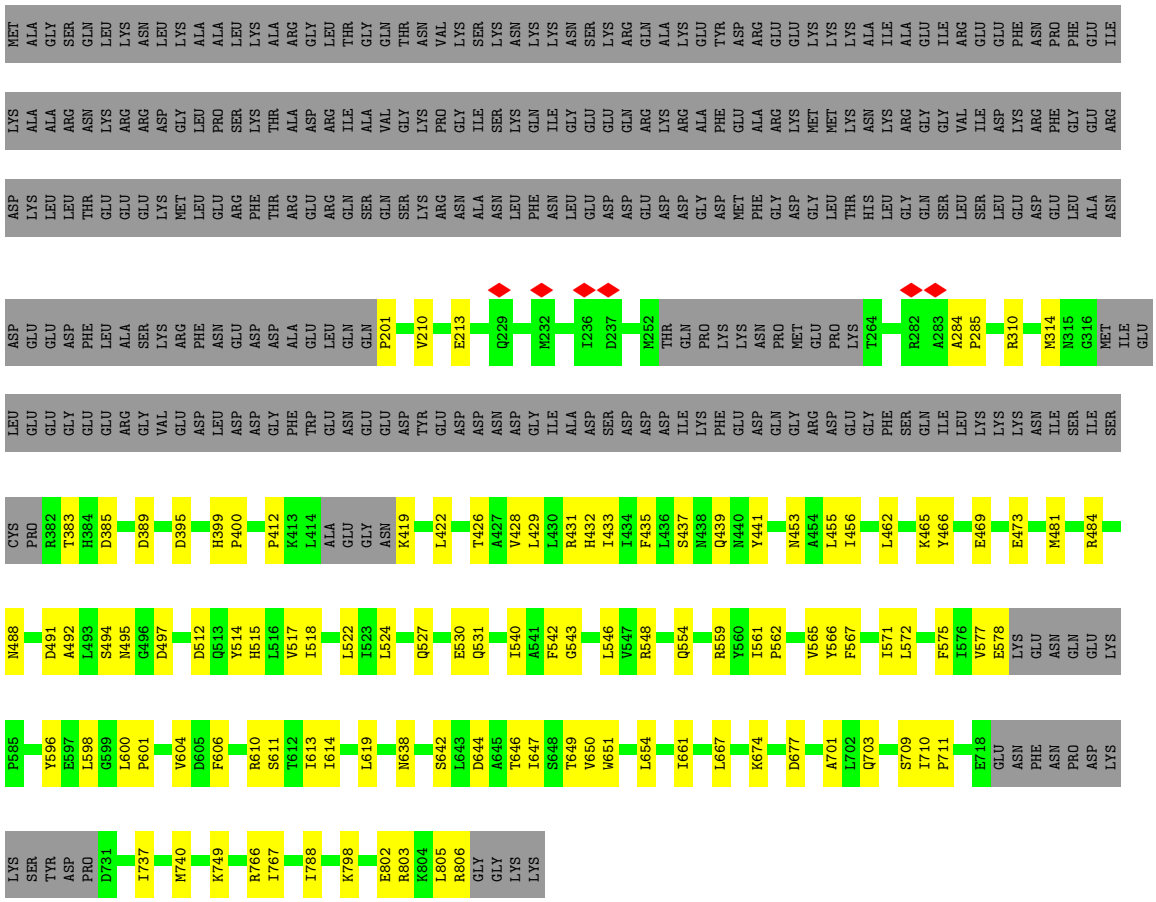
• Molecule 1: Periodic tryptophan protein 2

Chain UA: 60% 27% • 10%



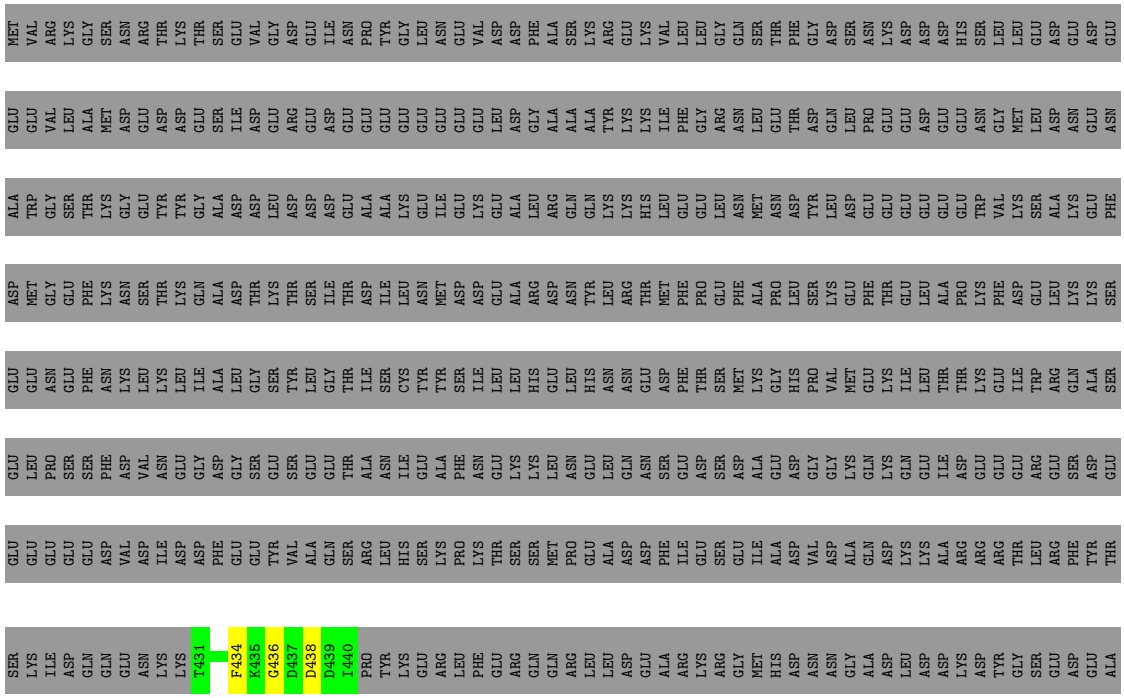
• Molecule 2: Nucleolar complex protein 14

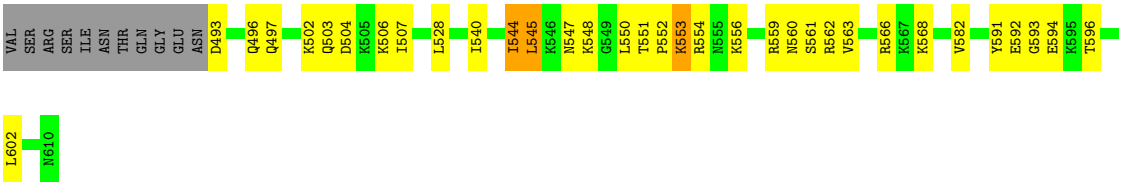
Chain UB: 49% 13% 37%



• Molecule 3: Something about silencing protein 10

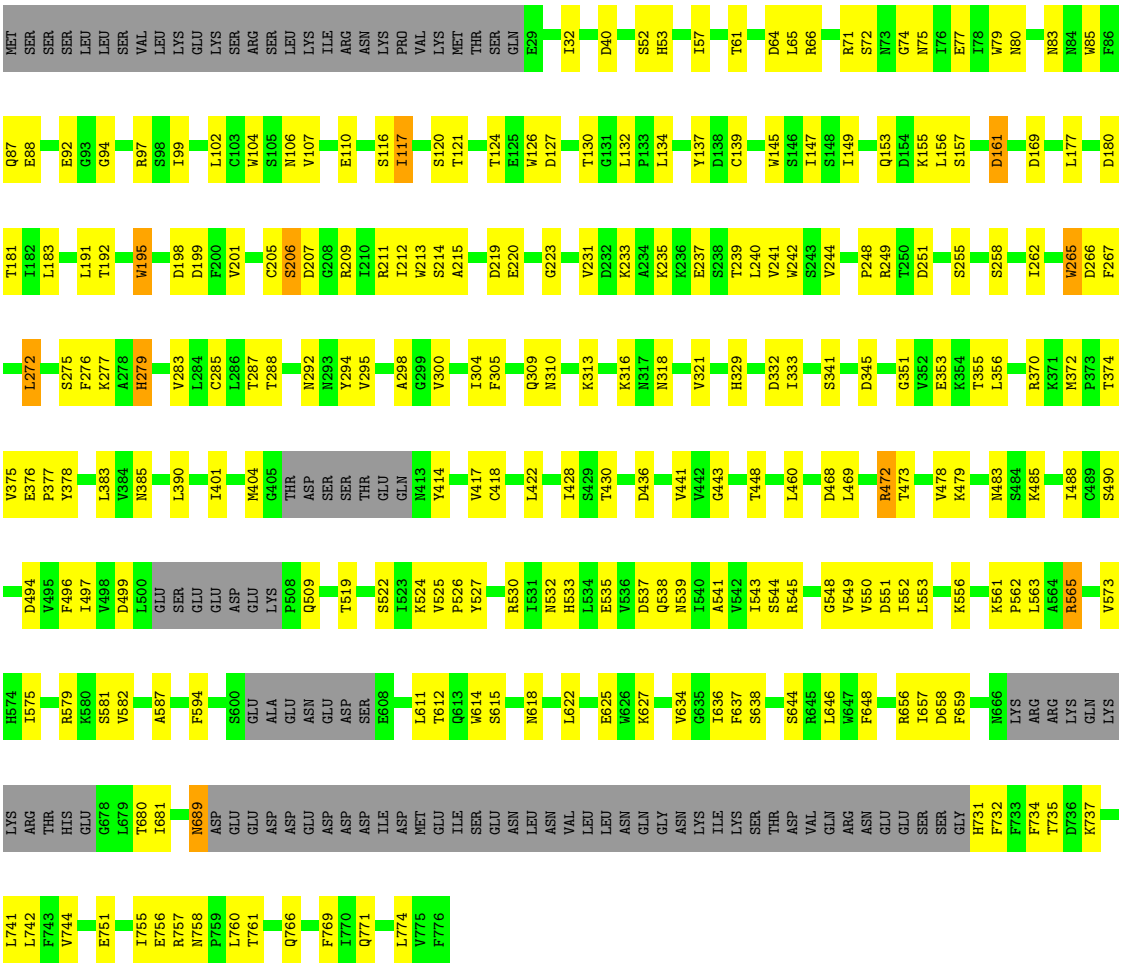
Chain UC: 15% 6% 79%





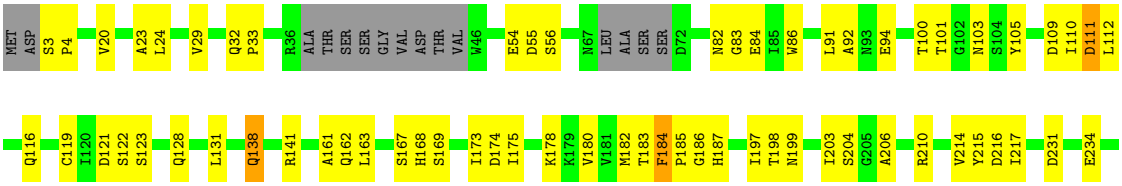
• Molecule 4: U3 small nucleolar RNA-associated protein 4

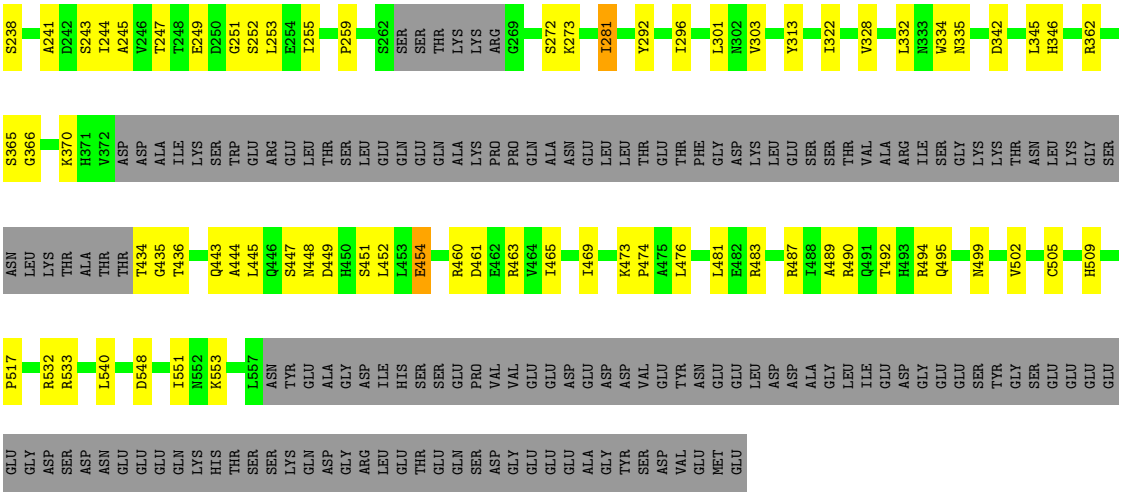
Chain UD: 57% 29% • 13%



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

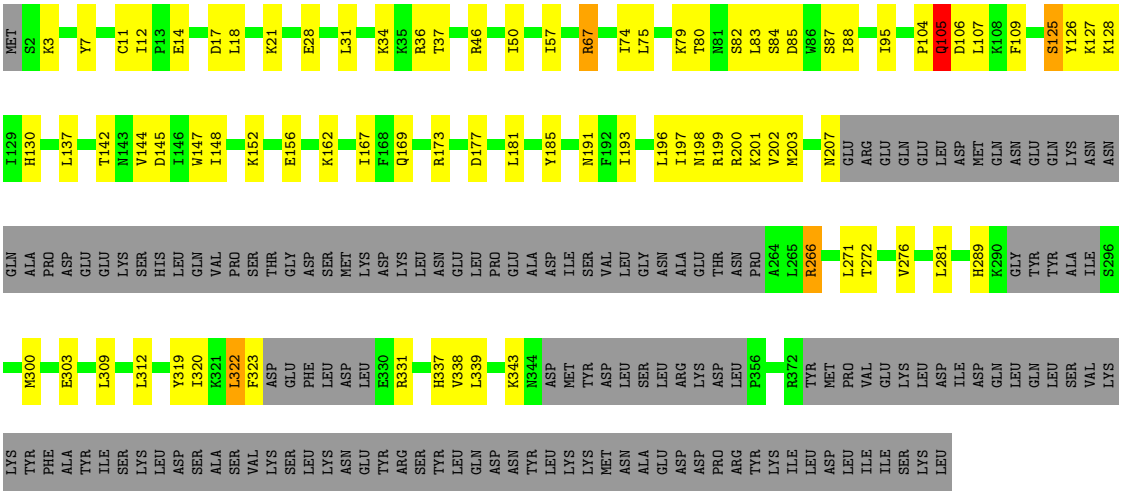
Chain UE: 53% 20% • 26%





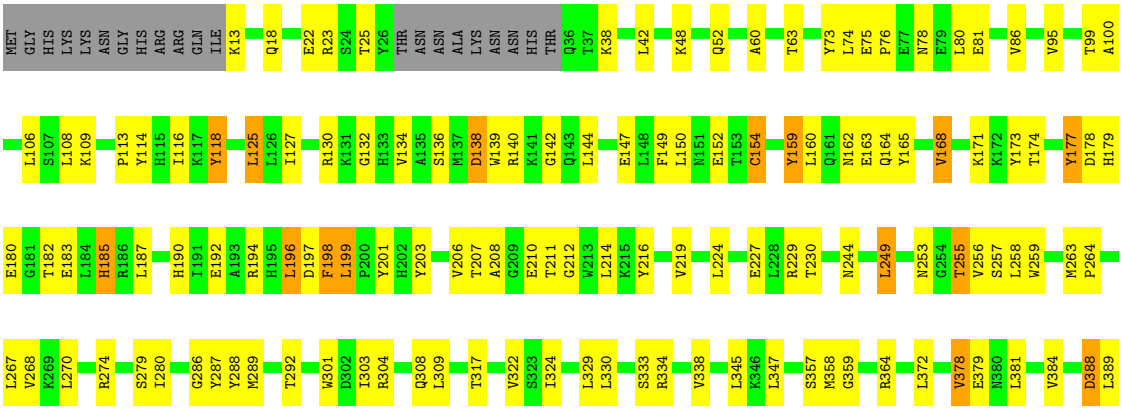
- Molecule 6: U3 small nucleolar RNA-associated protein 6

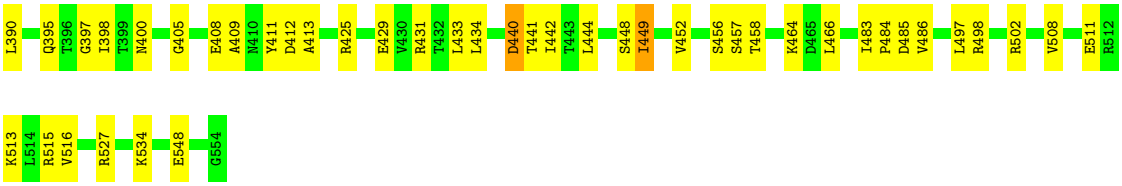
Chain UF:



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

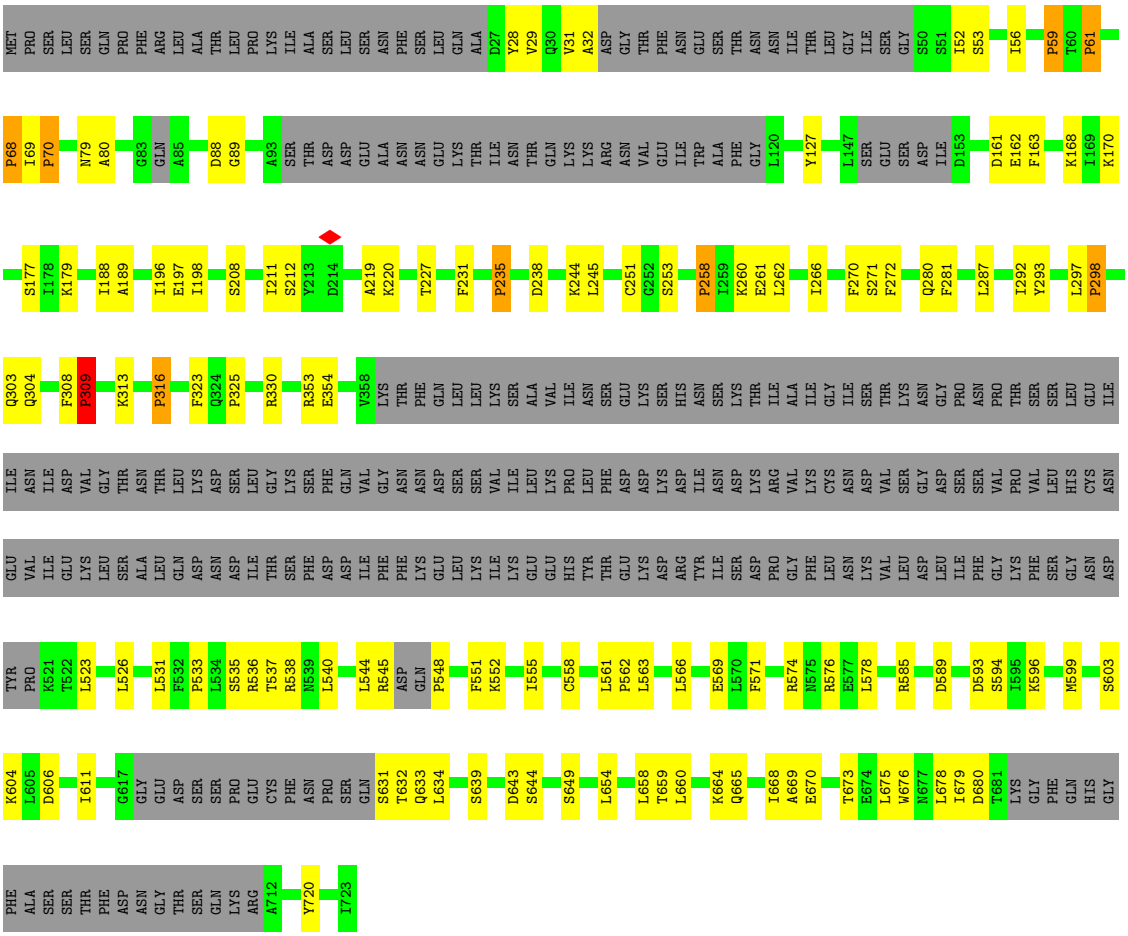
Chain UG:





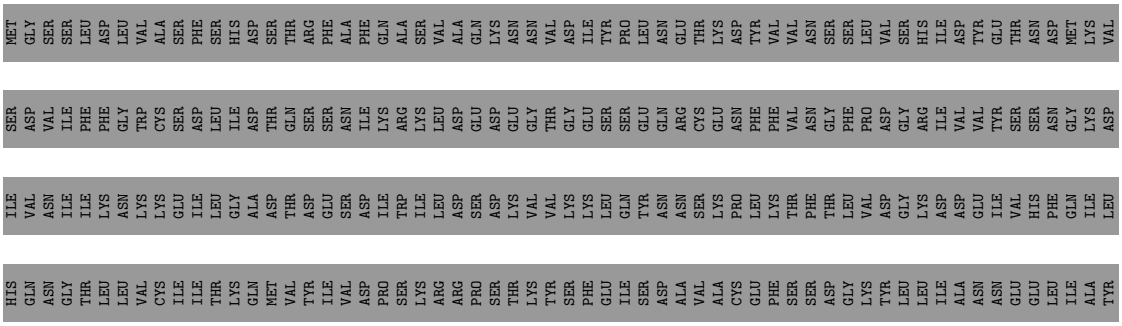
• Molecule 8: U3 small nucleolar RNA-associated protein 8

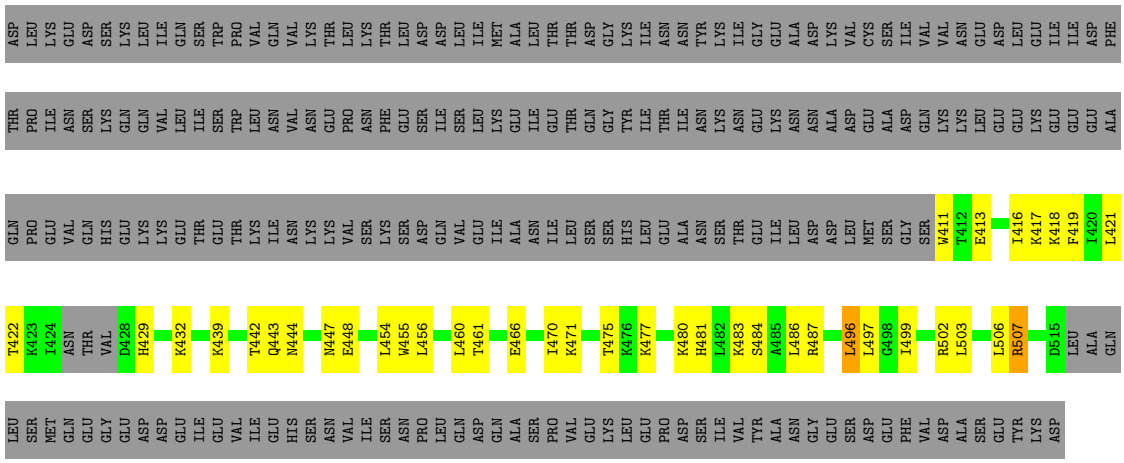
Chain UH: 44% 17% • 38%



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

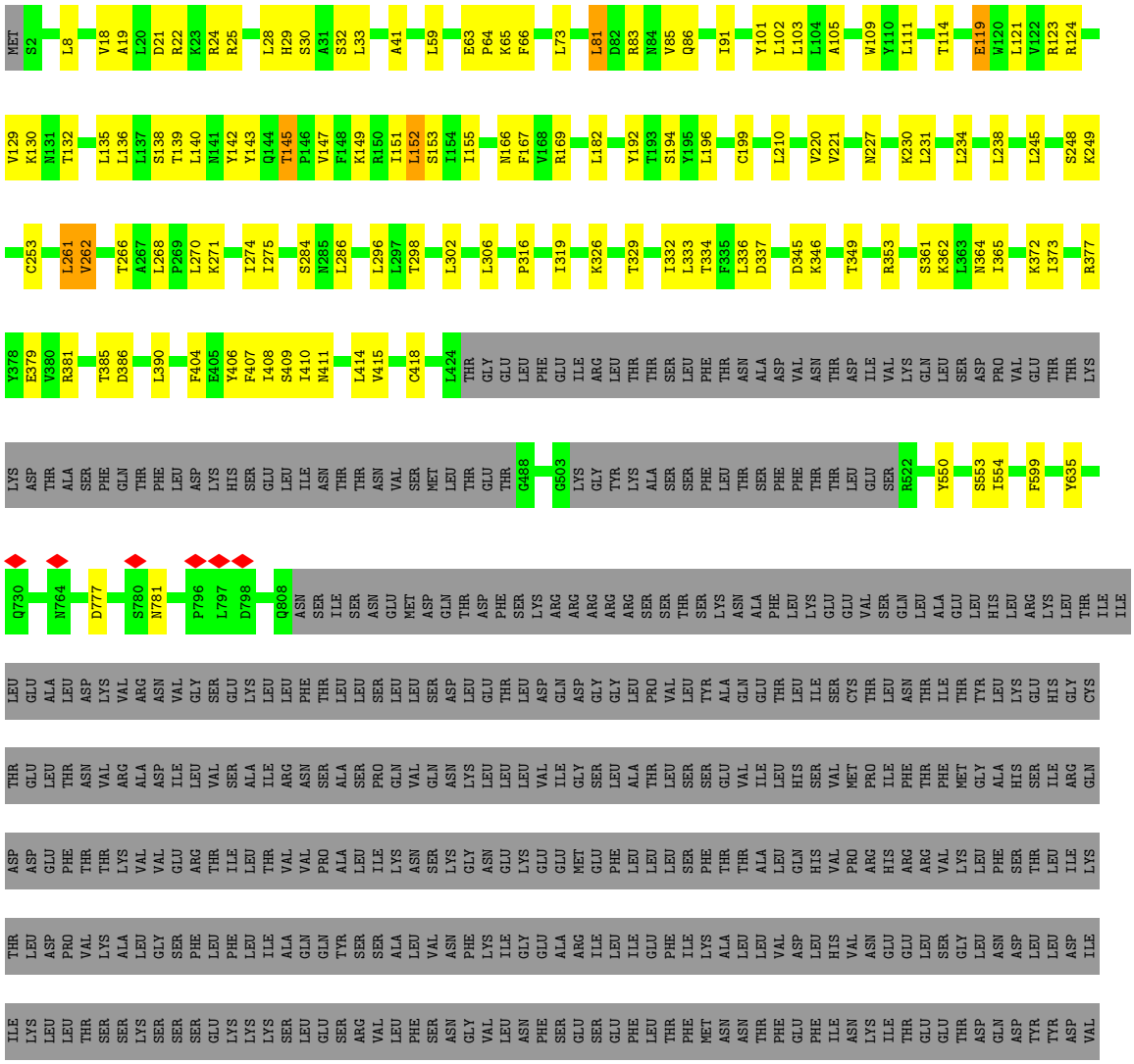
Chain UI: 11% 6% 82%

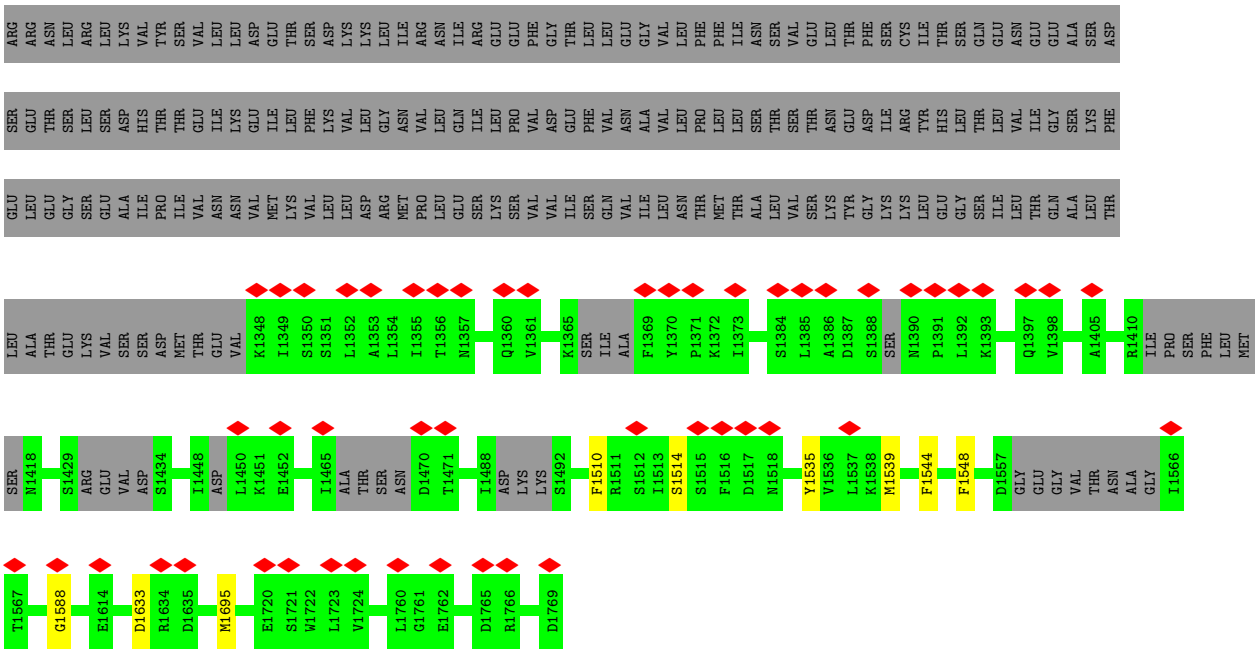




• Molecule 10: U3 small nucleolar RNA-associated protein 10

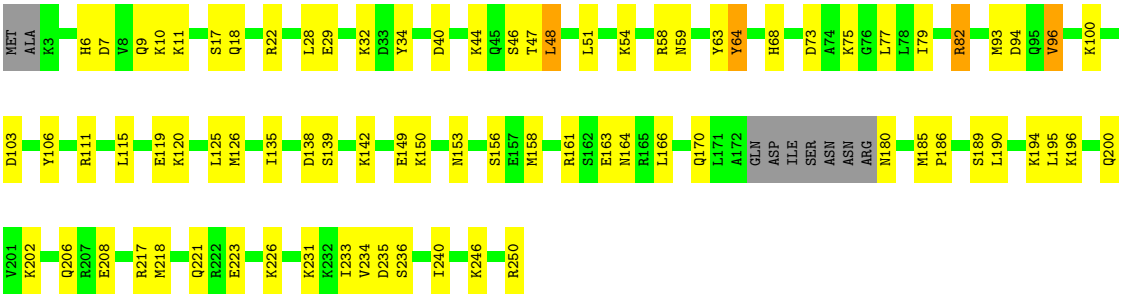
Chain UJ: 55% 7% 37%





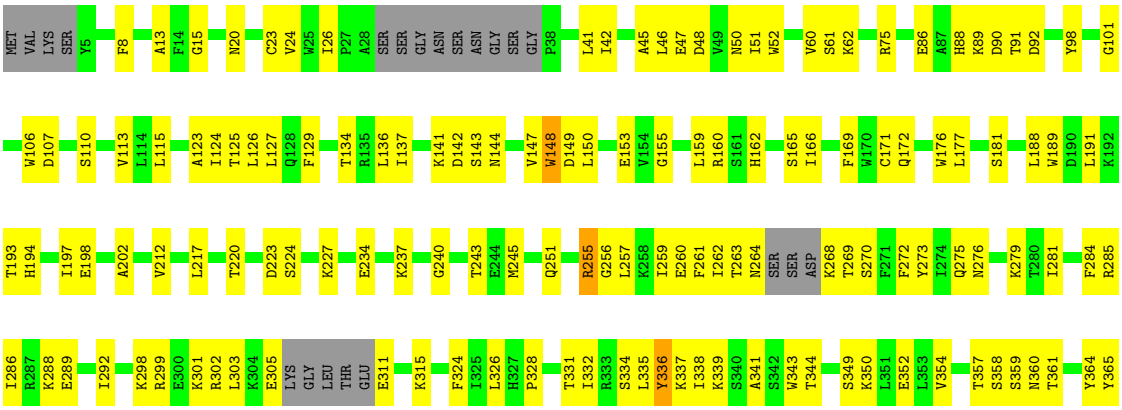
- Molecule 11: U3 small nucleolar RNA-associated protein 11

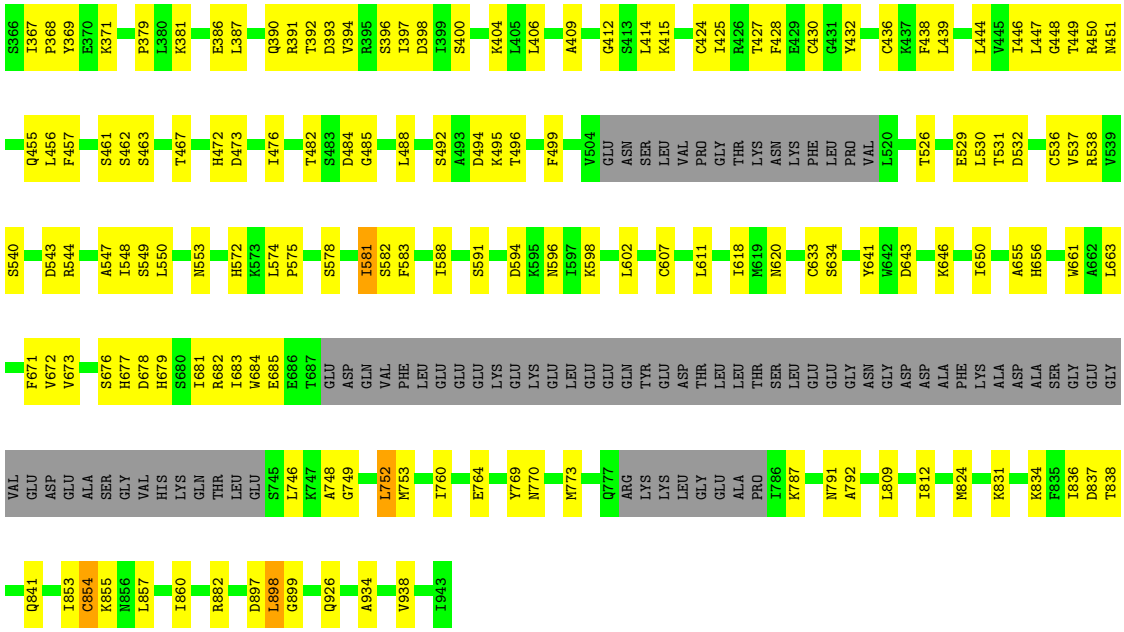
Chain UK: 64% 30%



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

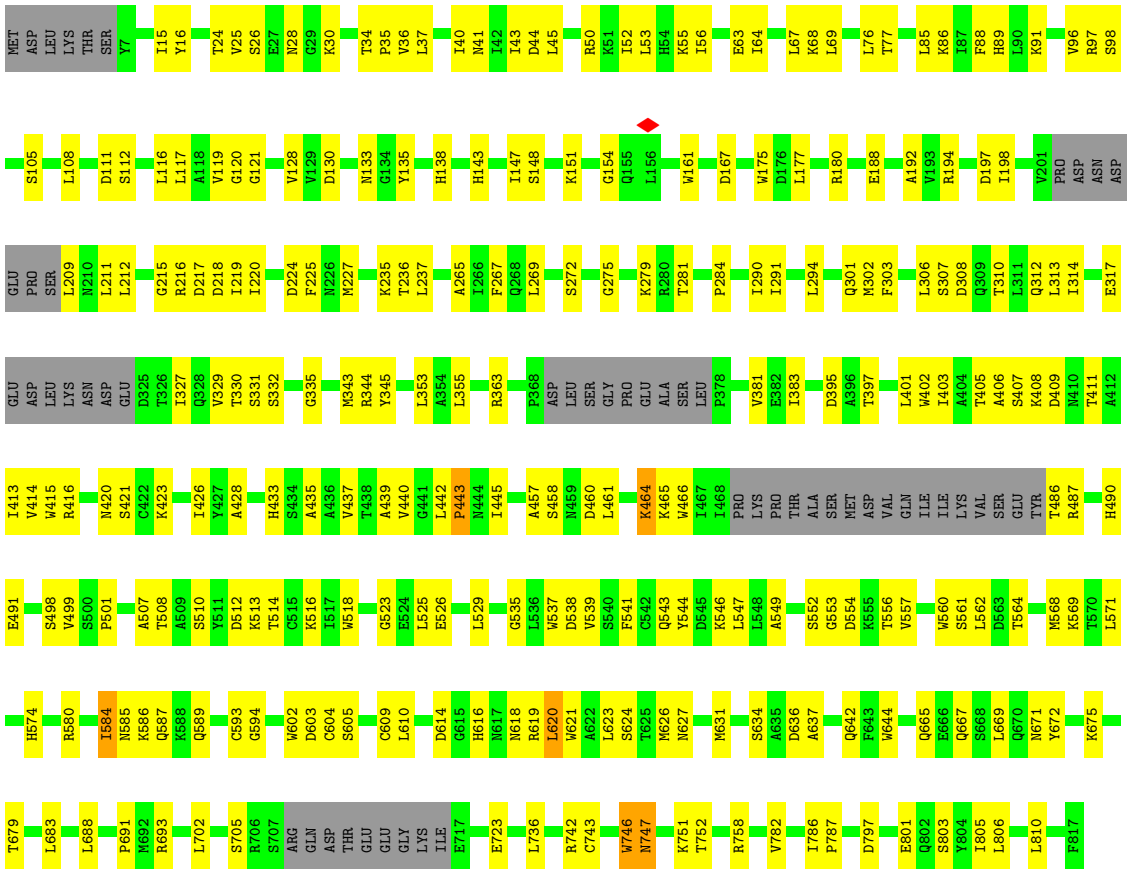
Chain UL: 59% 30% 11%





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

Chain UM: 62% 30% • 7%



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

Chain UN: 73% 25% •

Q276 R277 Q280 E294 K297 W298 Q303 R306 R307 A308 D309 F313 K317 E320 H323 F327 Q331 K837 K838 N839 L840 K841 Y842 Q843 S844 S845 A846 V847 R854 L861 R862 M863 P864 E868 R872 Q876 I879 K880 P881 M884 T885

K886 V890 I891 L894 K895 A896 P897

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

Chain UO: 68% 26% • •

MET S2 T3 S11 L16 Q19 T20 T21 P22 E23 Q24 R25 Y26 W27 R28 Q29 Y30 T31 S32 A33 Q34 T43 H44 H51 P52 H53 S60 S67 S68 R69 T70 R71 K75 T76 F77 V83 V84 Y85 S86 R90 S91 D92 G93 K94 L95 L96 C97 A98 A101

Y108 D109 S110 Y111 R114 L117 P126 T127 H128 K131 F132 H133 D136 N137 K138 I139 T142 A143 S144 D145 T149 L164 R172 S175 F176 I177 P178 G191 S200 S201 I206 H211 D212 N217 A220 V221 I226 C229 F234 K235

V236 W237 D238 L239 K244 E247 V255 T256 C257 L258 D259 Y260 V261 E262 M268 I273 S276 L277 D278 G279 H280 V283 F284 D285 P286 L287 V292 K293 F298 P301 V302 L303 N315 V319 S323 I329 R330 K334 GLU LYS ARG SER SER ASP LYS

GLU ASN ALA PRO ALA SER PHE ASN LYS ASN ALA K353 N356 M361 Y366 D369 I373 I374 H375 N376 D377 K378 M385 N393 A404 F405 E412 L413 V417 E420 L421 R422 K423 L431 R434 D435 T438 L439 L442 K448 G449 I450 E451 D452

V453 R454 I495 H496 K497 S498 K499 E500 Q509 T512 SER

• Molecule 16: Bud site selection protein 21

Chain UP: 19% 9% 72%

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

SER GLU VAL GLU SER GLN ILE THR GLN ARG GLU GLU ALA ILE ARG LEU GLU GLN SER GLN LEU ARG SER LYS ARG ARG LYS GLN ASN GLU LEU TYR ALA LYS GLN LYS LYS SER VAL ASN GLU THR GLU VAL THR ASP GLU VAL ILE ALA ALA GLU LEU PRO GLU GLU LEU LEU LYS ASN ILE

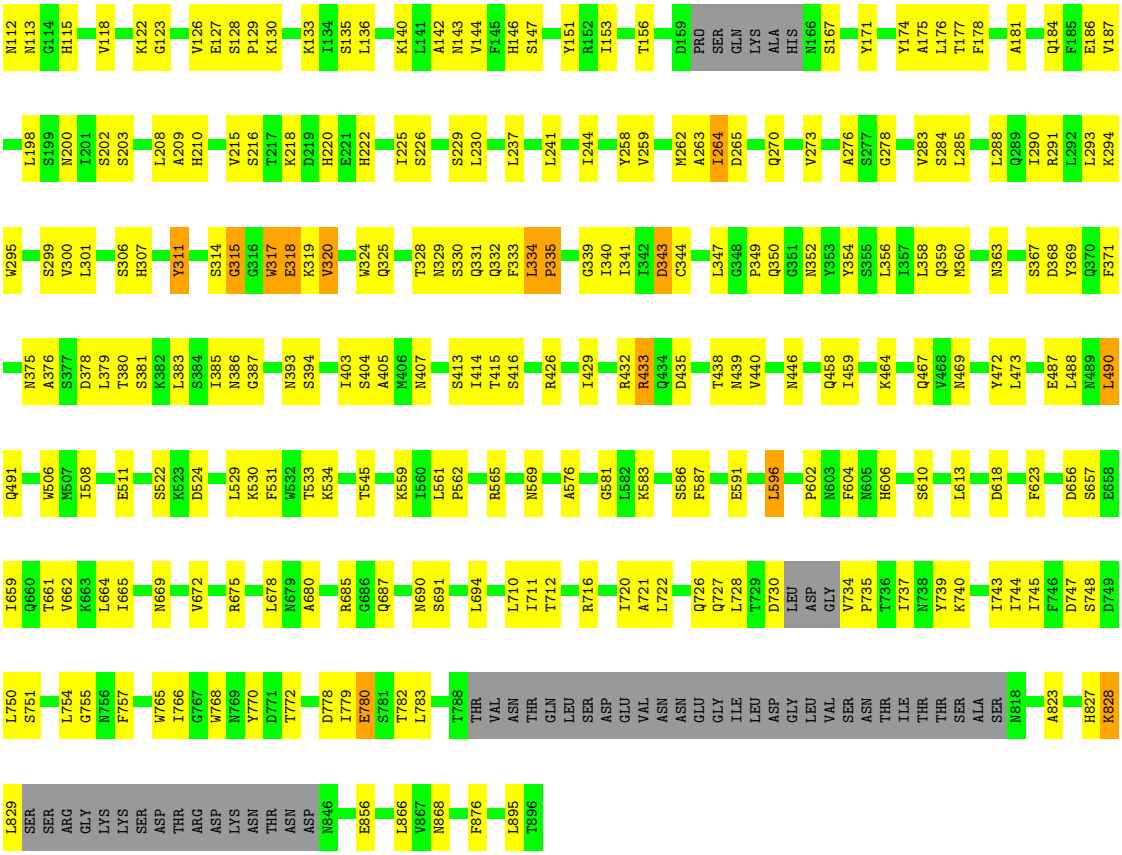
ASP GLN LYS ASP GLU GLY SER THR GLN TYR SER SER SER ARG HIS VAL THR PHE ASP LYS LEU ASP GLU SER ASP GLU ASN GLU GLU ALA LEU ALA LYS ALA I155 K159 R160 K161 T162 L163 R167 L181 S182 T183 D186 T189 L190 P191 P192 K193 K194 E195 S196 I199

R200 R208 L211 G214

• Molecule 17: NET1-associated nuclear protein 1

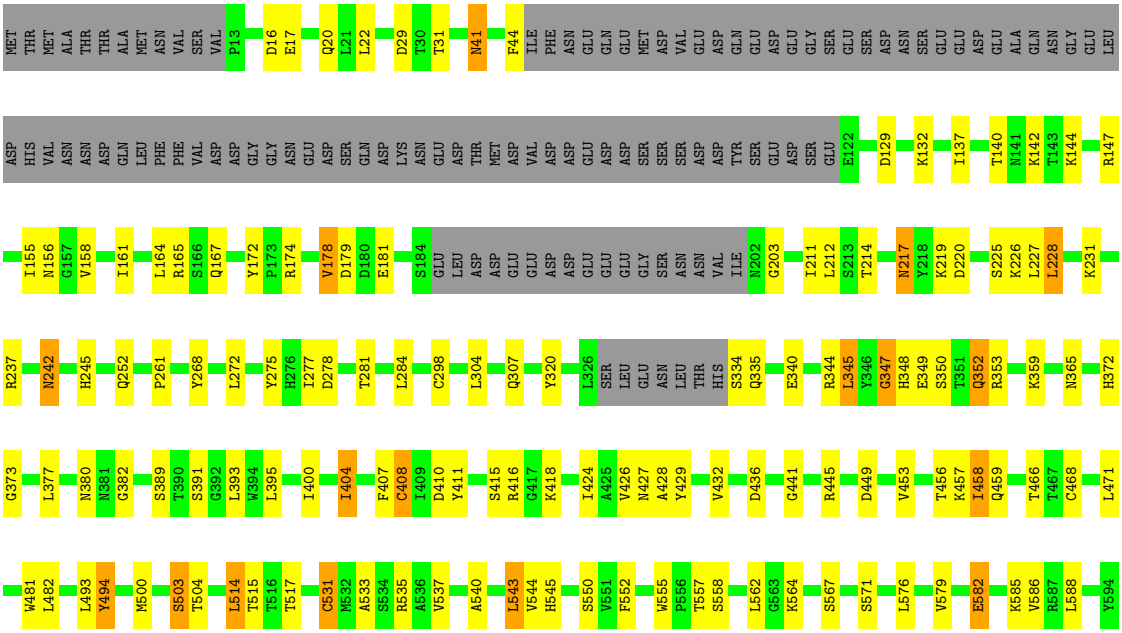
Chain UQ: 62% 29% • 7%

MET THR GLN SER LEU GLY ILE GLU Q9 S16 K19 L22 N23 N24 L25 S26 S27 K32 A35 R36 L37 S38 Q39 D40 Q41 R42 N43 I46 V57 K64 N71 S72 L73 S87 I88 L92 I96 Q101 GLU ASP A104 H105 T108 V109 F110 T111



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

Chain UR: 58% 20% • 19%



- Molecule 19: Nucleolar complex protein 4

Chain US: 63% 23% • 13%

M1 V2 L3 L4 I5 S6 E7 K13 ARG LEU THR ALA ALA GLY ASP ARG K22 P37 E44 GLU ASP GLU THR GLU LYS ASN LEU ARG F54 T73 LEU PRO SER SER LYS LYS SER THR LEU GLU K84 E85 F98 L102 S107 ASP ILE PRO PHE GLU T113 L124

E130 F134 P144 F148 I152 L155 W156 K167 E179 F180 K183 Y184 A189 D190 I191 Q192 Y193 Y194 F195 Q196 S197 E198 F199 N200 Q201 E204 D210 L211 L212 L213 K214 N215 K218 L222 V223 N224 H225 D226 S230 Q245 E248 S251

K252 F253 K254 S255 N256 N260 W261 L262 S263 S270 L271 Q272 Q273 Y274 K275 S276 I280 L281 R284 I285 H288 K294 L295 M296 D297 Y303 V314 L320 N321 F324 E325 L326 M327 F330 N331 L332 E333 Y334 K340 L341 I344 I345 N346 P347 D348 L349 M350

H351 V352 A356 R357 F365 L366 L371 F379 I380 K381 K382 R385 L386 T387 L388 E389 S390 T397 V398 I399 P400 F401 I402 R407 H417 N418 P419 I422 F446 D447 V448 H449 E450 S451 D452 P453 T456 H457 A458 L459 D460 S461 S462 E465 L466 A467 S468 L469

M470 E471 H472 Y473 L480 P487 L491 S492 Y493 N494 M495 L499 L507 R513 LYS LEU LYS THR LEU PRO THR LEU GLU PHE GLU ALA PHE THR ASN VAL PHE ASP ASN GLU ASP GLY ASP SER GLU ALA SER SER GLN GLY ASN VAL TYR LEU PRO GLY VAL ALA TRP

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

Chain UT: 5% 88% • 10%

MET ALA LYS Q4 D40 A139 F142 A156 K160 H248 A251 F323 E348 ASN CYS ALA SER LEU SER Q355 F464 A468 E469 I470 N471 D472 K528 GLU ASP ASP ALA SER GLY N535 L706 P707 F804 LYS THR TYR LYS ASP GLU GLU ASP MET

GLU ASN GLU ARG VAL ILE THR GLY S822 L896 E900 S969 L972 K1188 LEU SER D1191 E1297 D1334 G1335 Y1336 K1337 S1338 Y1339 S1340 W1344 N1357 K1358 N1383 L1384 N1385 E1386 A1387 S1388 K1389 S1390 I1391 S1392 Q1414 K1429 Y1430 F1431 T1432 D1433 F1434 E1435 D1436 M1437

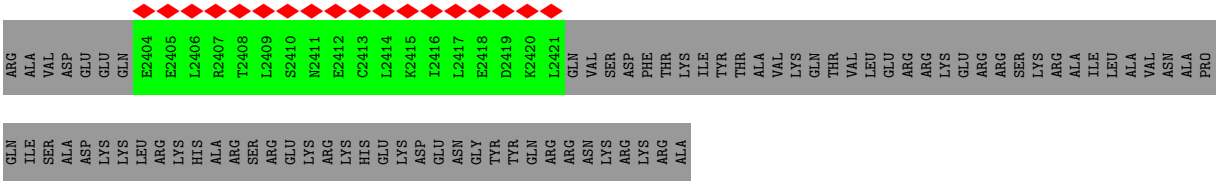
A1438 I1439 L1440 L1441 TYR ASN GLY ASP GLU GLU ALA ASP PHE PHE THR ASN VAL ASN HIS ILE Q1458 K1467 H1472 A1473 S1495 ASP ASP GLU ARG TYR R1501 R1563 ASP GLY ALA GLU SER LYS LEU THR LEU SER LYS PHE PRO SER ASN LEU ASP GLU PRO SER N1584 I1661 S1662

L1665 S1714 G1730 K1733 E1736 N1737 A1775 N1787 M1824 S1825 ASN SER PRO GLN ILE PRO LYS LYS LYS VAL LYS ASP GLN VAL ASP GLU LYS GLU ASP PHE PHE LEU VAL ASN LEU E1841 SER LYS SER TYR THR ILE ASN SER ASN SER LEU LEU LEU N1865 S1905

GLU N1907 E1908 L1921 L1924 D1925 N2091 L2095 M2121 L2149 LYS GLN VAL ASP N2154 A2155 S2156 S2171 ILE GLY PHE E2175 T2195 SER VAL GLY SER GLU HIS Q2202 E2218 A2219 T2220 GLU SER VAL TYR LYS HIS G2227 Y2241 PRO H2243 S2244 W2245 Q2248 S2249 N2252

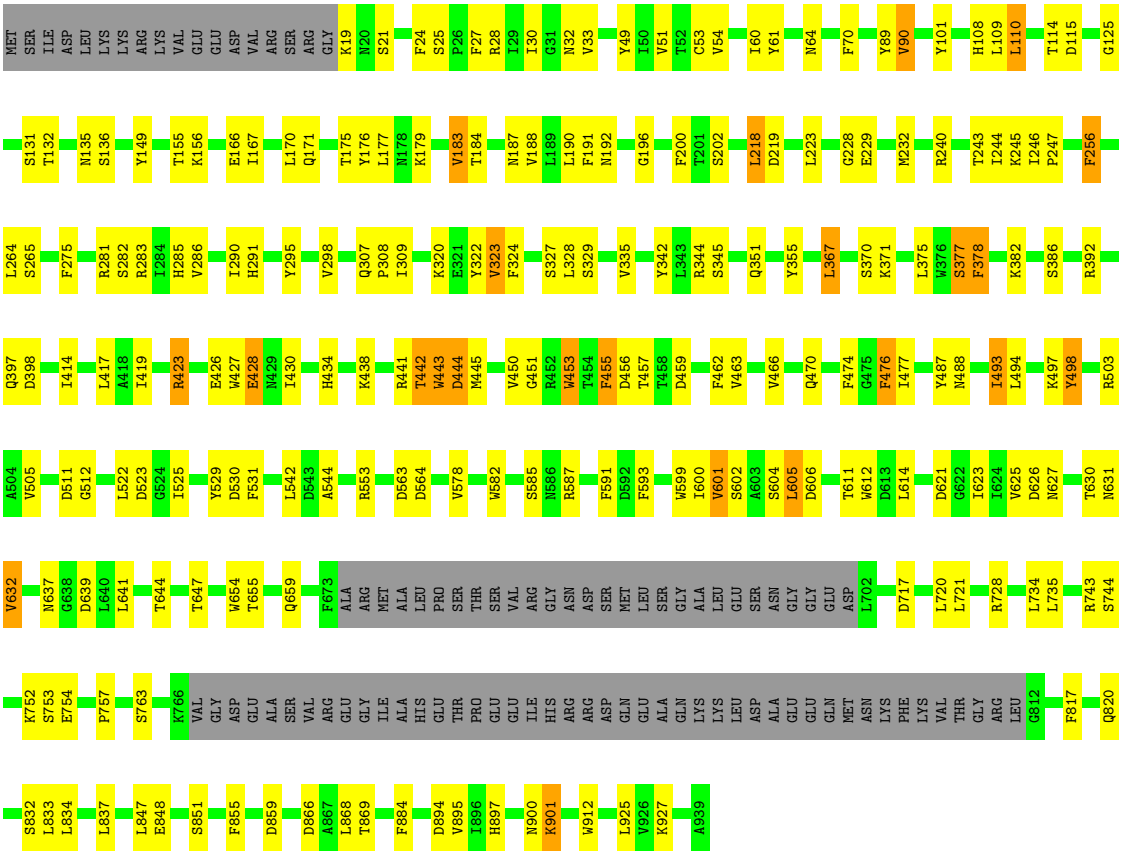
H2255 Q2256 L2257 I2258 A2259 N2260 K2261 ASP LYS LEU GLU ILE SER LEU THR N2270 L2271 P2287 SER ILE PRO E2291 N2292 L2293 A2294 N2295 V2296 S2297 I2298 K2299 T2300 L2301 V2302 N2303 I2304 S2305 I2306 L2307 W2308 K2309 E2310 Q2311 R2312 THR PRO PHE ILE MET ASP VAL SER LYS GLN THR GLY GLU ASP LEU

LYS TYR THR THR ALA I2333 D2334 R2345 S2346 ASP GLU HIS ARG MET ASP S2353 F2354 M2355 S2356 K2357 K2358 A2359 C2360 I2361 Q2362 L2363 L2364 A2365 L2366 L2367 V2368 Q2369 V2370 LEU ASP E2373 D2374 E2375 V2376 I2377 A2378 E2379 GLY E2381 K2382 I2383 L2384 L2385 P2386 L2387 Y2388 G2389 Y2390 LEU GLU THR TYR TYR SER



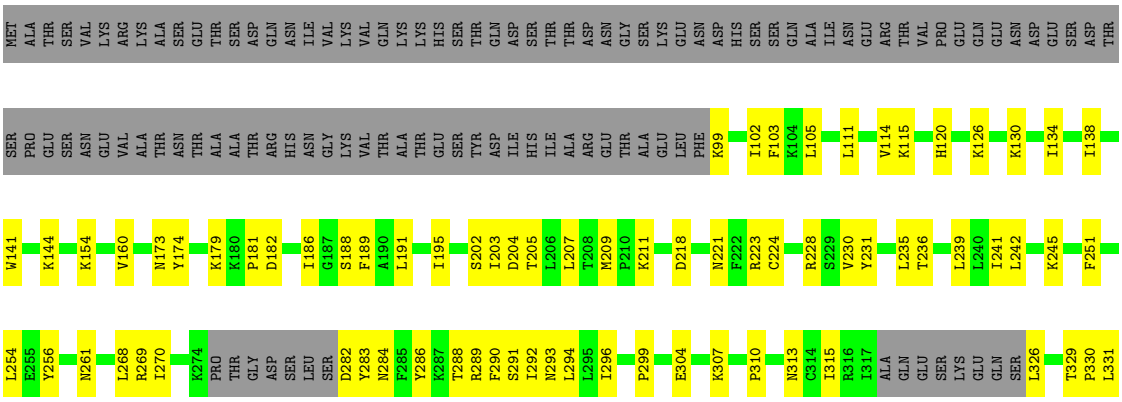
- Molecule 21: U3 small nucleolar RNA-associated protein 21

Chain UU:



- Molecule 22: U3 small nucleolar RNA-associated protein 22

Chain UV:



Y332 N333 L337 S338 S339 S340 T341 H342 Y345 L346 S358 Q372 R373 N378 M379 S380 G403 S408 N409 K410 I411 L412 L421 Y428 M432 D433 L434 C435 H436 D437 G438 H439 L440 Q441 F442 H443 S444 N445 PRO GLU ASN SER SER SER SER P453 K456 Y457 I458

D459 T464 P465 T466 L467 F468 D469 K470 S471 T472 K479 V482 E490 L499 F511 I515 F518 D519 N520 Y523 C526 V529 Q530 L533 L539 M550 V553 L574 R577 I578 K579 Y580 E584 M585 V586 G587 Q588 D591 F592 K596

V599 T603 N606 H607 F608 N609 F610 D611 F612 V613 R614 V615 K616 L617 I618 V619 N620 E623 K626 S635 E636 W649 K652 R656 R657 D660 V668 I681 V682 N683 Q695 I696 S697 N698 I701 F707 L708 N712 S716 T719 S726

K731 D735 Y738 I741 F742 Q743 M744 T763 S764 L765 P768 D777 E795 L799 E800 K801 A802 K803 T804 L807 I810 L814 S818 R827 D828 I831 N834 L835 E836 T839 R853 D859 L864 R865 A870 R871 N872 E873

L878 L883 K884 A887 K888 Y889 S892 R897 K917 R918 W919 L920 D921 T922 L925 L926 L933 A934 E935 L936 I937 F949 I950 P951 K960 K971 L975 E983 ASP ASP ILE ARG ASP THR PHE GLU THR SER ILE GLY ALA GLY SER GLU LEU ASP SER LYS

THR MET LYS LYS LEU SER E1010 R1011 L1012 T1013 Q1016 D1031 P1032 T1035 H1036 L1037 Q1038 V1041 K1044 I1050 S1054 L1058 R1063 L1075 L1087 T1090 K1094 D1095 Y1096 D1097 F1098 V1099 V1100 D1101 L1102 R1103 L1108 S1111 C1112 S1116 ALA THR GLU PHE

LYS ASN ILE THR ASN ASP GLN A1128 P1129 L1136 L1139 L1149 V1150 N1154 L1155 K1158 N1159 S1160 S1165 R1166 K1167 G1173 G1174 E1175 K1176 G1177 G1184 L1185 P1188 L1189 F1190 K1191 K1195 F1196 R1197 I1213 L1214 N1215 K1216 I1219 F1220 H1221 E1222 I1223 D1229 M1230 V1231

I1232 N1233 D1237

- Molecule 23: rRNA-processing protein FCF1

Chain UX: 61% 28% • 8%

MET GLY LYS ALA LYS LYS T7 R8 K9 F10 G11 L12 V13 T19 K27 N28 Q29 E30 N31 ILE LYS THR LYS GLU ASP PRO GLU LEU T41 F52 F53 Q54 Y55 N56 K60 V65 D68 T69 N70 F71 I72 I76 K79 V80 D81 I82 V83 R84 G85 M86 M87 D88

C89 A92 K93 C94 N95 P96 D100 M103 L106 L109 K112 Y113 L117 K118 L119 A120 R121 I125 K126 R127 S131 H132 K133 G134 T135 Y136 L141 V145 K149 I152 D157 G169 I170 P171 I182 L185 F189

- Molecule 24: Ribosome biogenesis protein UTP30

Chain UZ: 62% 28% 10%

MET VAL GLU SER ASN ASP ILE ILE LYS SER G11 N27 L30 K31 N32 D33 K34 I38 I39 I40 K45 R50 K63 L64 F65 K66 D69 L70 N71 I72 L73 K77 D78 P79 S80 Y83 R84 E85 T86 E91 S94 E99 I100 I101 S102 V103 K104 N105

L106 R109 L115 T116 Q117 K120 D123 R130 V131 L134 L135 L139 G140 S141 R142 K148 K149 R155 K163 E169 D172 P173 V176 Q179 I180 R181 K185 N186 T187 S188 N192 N193 D194 S198 I204 S208 I209 I212 L223

T224 D225 K226 S227 K228 R229 G232 I235 I242 F243 V244 K245 S251 L252 P253 Q256 F257 SER GLU ALA ARG GLU ASN GLN LYS ASN GLU ASP LEU SER ASP ILE LYS LEU

- Molecule 25: rRNA 2'-O-methyltransferase fibrillarin

Chain CA: 57% 14% • 26%

MET SER PHE ARG PRO GLY SER ARG GLY GLY SER ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY SER ARG GLY GLY ALA ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY

SER ARG GLY GLY ALA ARG GLY GLY SER ARG GLY GLY ARG GLY GLY ALA ALA GLY GLY A80 V96 G101 K102 E103 N110 M111 G114 R122 V125 P128 SER LYS GLU ASP GLY V134 P135 P136 T137 K138 R142 V143 I155 L162 K168 L171 Y172 L173

G174 A175 A176 S177 G178 V181 G192 V193 V194 E198 F199 S200 K212 D223 A224 R225 Q228 K229 Y230 R231 M236 V237 D238 C239 V240 Q246 R251 I252 I253 Q264 I269 S270 L301 T305 L306 E307 P308 Y309 H313 C314 I315 Y320 K326 LYS

- Molecule 25: rRNA 2'-O-methyltransferase fibrillarin

Chain CB: 47% 22% 30%

MET SER PHE ARG PRO GLY SER ARG GLY GLY SER ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY SER ARG GLY GLY ALA ARG GLY GLY SER ARG GLY GLY PHE GLY GLY ARG GLY GLY

SER ARG GLY GLY ALA ARG GLY GLY SER ARG GLY GLY ARG GLY GLY ALA ALA GLY GLY ALA ARG GLY GLY ALA K85 H91 R92 H93 V96 Y97 I98 K109 N110 M111 S116 V117 Y118 R122 V125 GLU GLU PRO SER LYS GLU ASP GLY VAL PRO PRO THR K138 V139 E140

Y141 W144 N145 P146 F147 R148 A152 L159 L162 F163 I164 G167 V170 L171 Y172 A175 H183 V184 V187 E191 V197 E198 F199 S200 H201 G204 M210 A211 K212 K213 R214 P215 N216 I217 I220 I221 P227 Y230 R231 C239 V240 F241

V244 Q249 H258 K262 D263 Q264 V267 V268 K272 C275 V280 D281 E289 K292 L293 R294 I298 E302 H313 C314 I315 V316 V317 G318 R319 Y320 S323 G324 LEU LYS LYS

- Molecule 26: Nucleolar protein 56

Chain CD: 55% 19% • 25%

MET ALA P3 I4 L7 L8 F9 E10 V20 Q23 S29 R30 V34 Q35 I38 N39 D40 I48 S52 F53 N67 S70 V74 L78 L82 D83 K88 N95 I96 S101 D102 K103 K110 D117 D126 L127 I128 V131 R132 L133

H134 K137 L138 L142 Q143 L147 E148 R149 L154 S166 K169 N170 D171 L180 D185 K186 D187 I188 N189 R194 W198 Y199 H202 F203 P204 E205 L206 L221 D225 D231 L234 L237 L240 S245 A248 Q249 R250 V251 I252 D253 N254

A255 R256 I257 S258 M259 I263 T266 D267 M268 E269 N270 V271 F274 A275 Q276 R277 L281 R285 S321 L322 Q328 A329 T332 L336 GLY ALA GLU LYS ALA LEU PHE ARG ALA LEU LYS THR LYS GLY ASN THR PRO LYS TYR GLY LEU ILE TYR HIS SER GLY PHE

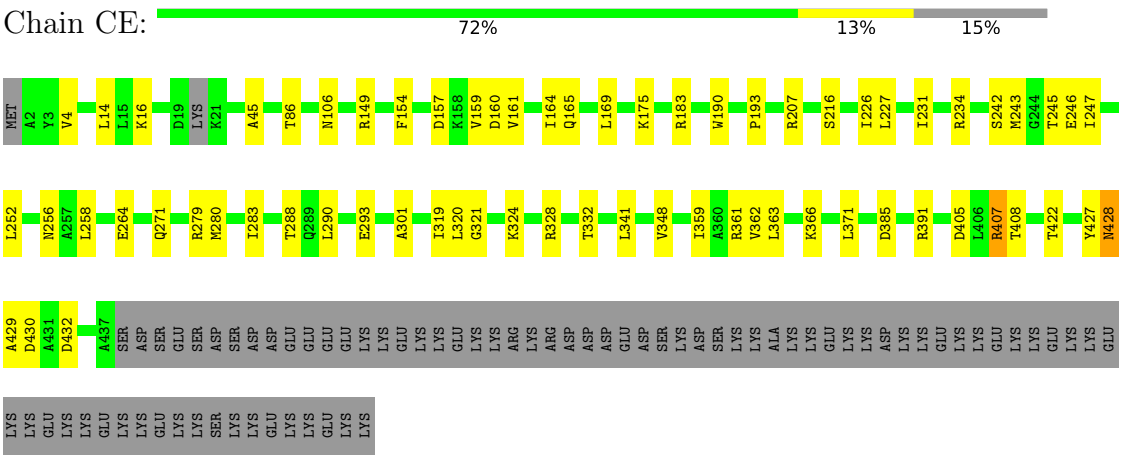
ILE SER LYS ALA SER ALA K370 N371 K372 R377 N381 K382 C383 S384 M385 A386 S387 R388 N391 Y392 S393 E394 V399 S402 V403 L404 R411 Y415 ASN THR GLY LYS PRO THR LEU LYS ASN GLU LEU ALA ILE GLN GLU ALA MET GLU LEU TYR ASN LYS ASP LYS PRO

ALA ALA GLU VAL GLU GLU THR LYS GLU LYS GLU SER SER LYS LYS ARG LYS LEU GLU ASP ASP ASP GLU GLU LYS LYS GLU LYS LYS LYS LYS LYS SER LYS LYS GLU LYS LYS GLU LYS LYS GLU LYS LYS ASP LYS LYS GLU LYS LYS ASP LYS LYS LYS

LYS SER LYS ASP

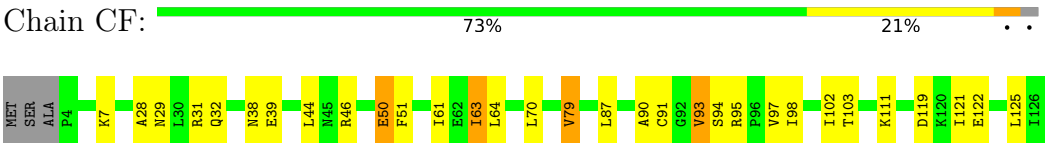
- Molecule 27: Nucleolar protein 58

Chain CE:



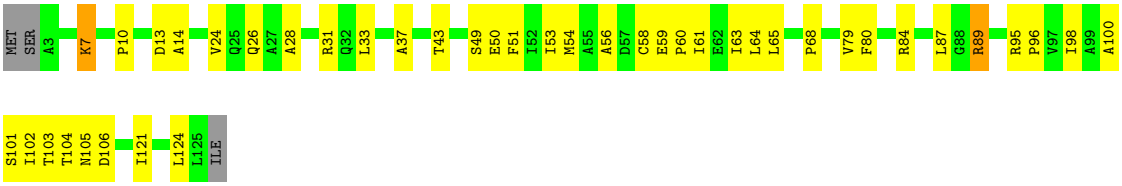
- Molecule 28: 13 kDa ribonucleoprotein-associated protein

Chain CF:



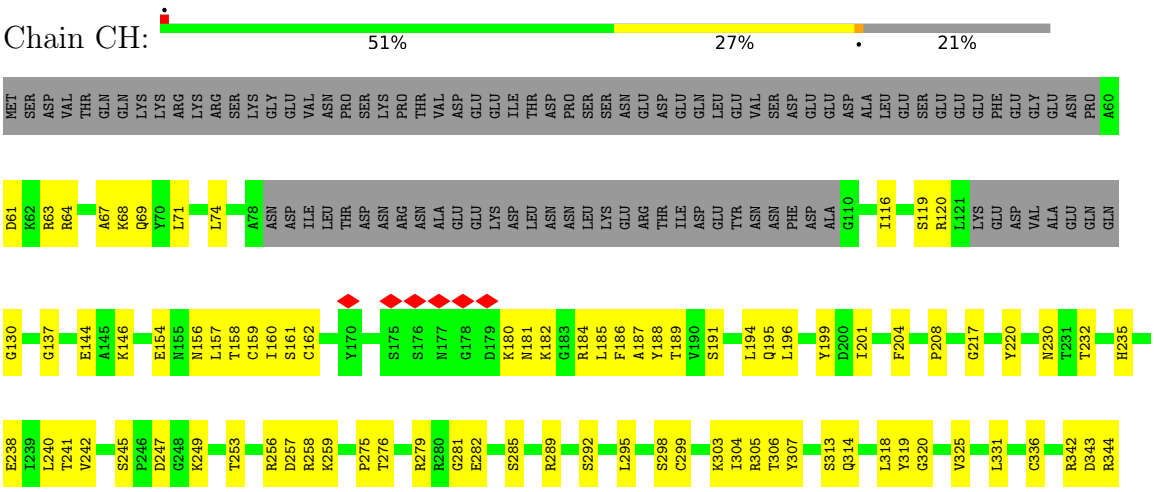
- Molecule 28: 13 kDa ribonucleoprotein-associated protein

Chain CG:



- Molecule 29: Ribosomal RNA-processing protein 9

Chain CH:



T345 W349 K350 D353 R356 L357 G361 E364 P365 Q366 K367 L368 L369 R370 R371 E375 ASN ALA LYS GLU GLY GLU ASP GLY GLU VAL LYS TYR PRO ASP GLU SER GLU ALA P394 C398 I402 V405 D409 D410 F411 H412 T415 N421 I422 C423 L424 W425

S426 L427 K430 K431 P432 I433 F434 T435 E436 R437 I438 A439 H440 G441 P444 F448 N449 D450 E457 R460 K461 R462 Q463 W474 I475 T476 Y483 S484 N485 V486 F487 I488 S489 G490 S491 W492 V498 W499 K500 I501 N504 L505 R506 V520 V521 T522 K523 I524 Q525 V526

V527 A541 A544 K545 R548 L549 G550 R551 W552 I553 S557 G558 A559 R560 N561 A566 Q570 THR GLY PHE

- Molecule 30: U3 small nucleolar ribonucleoprotein protein IMP3

Chain CI: 62% 32% 5% •

MET V2 R3 K4 L5 E9 Q10 K11 L12 L13 K14 K15 V16 L19 E20 W21 D24 Q25 G26 D29 T30 Q31 V32 M33 Y36 H37 I38 Q39 N40 R41 E42 D43 Y44 H45 K46 Y47 C51 R56 L57 L61 L64 R71 L77 L78 L79 D80 K81 L82

M85 G86 V87 L88 K91 I94 L97 E98 V103 V113 L118 V128 V136 R137 V138 G139 L142 I143 N144 D145 P146 A147 Y148 L149 V150 T151 R152 D156 Y157 W160 V161 D162 K165 I166 K167 K168 T169 L170 L171 R172 Y173 S183

- Molecule 31: U3 small nucleolar ribonucleoprotein protein IMP4

Chain CJ: 66% 27% • •

M1 R7 E8 R9 R10 E11 Y12 L13 L20 S23 Q26 Q27 K28 L42 P43 L46 S51 L52 Y58 S61 L62 K63 GLU SER GLU GLU ALA ASP ASP LEU Q72 R87 I88 I89 V90 S93 R94 S97 L100 P112 V115 R116 L117 N118 R119

G120 N121 Y122 V123 M124 P125 N126 L127 V128 D129 A130 C131 G135 T136 L139 V140 V141 E144 T150 S151 L152 F157 P158 H159 T162 L167 V171 M172 R173 I176 I177 E184 V185 N186 P187 H188 L189 D192 T195 K200 R201 V202 V203 C204 L209 F210

N211 A212 G213 P214 K215 E219 R220 V221 I222 T223 N226 R227 G228 D229 V233 R234 Q235 H236 V237 G244 V250 G251 P252 R253 E260 L266 V273 Q276 R279 F280 I281 R282 N285 Y289 L290

- Molecule 32: U3 small nucleolar RNA-associated protein MPP10

Chain CK: 26% 8% • 65%

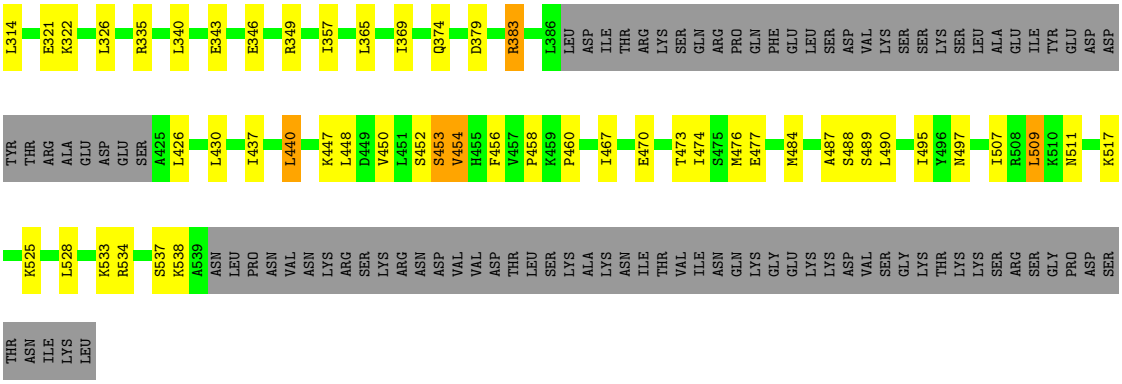
MET SER GLU LEU PHE GLY VAL LEU LYS SER ASN ALA GLY ARG ILE ILE LEU LYS ASP PRO SER ALA THR SER LYS ASP VAL LYS ALA TYR ILE ASP SER VAL ILE ASN THR CYS LYS ASN GLY SER ILE THR LYS LYS ALA GLU LEU ASP GLU ILE THR VAL ASP GLY LEU ASP ALA ASN

GLN VAL TRP TRP GLN VAL LYS LEU VAL LEU ASP SER ILE ASP GLY ASP LEU ILE GLN GLY ILE GLN GLU LEU LYS ASP VAL VAL THR PRO SER HIS ASN LEU SER ASP GLY SER THR LEU ASN SER SER SER GLY GLU GLU SER GLU LEU GLU GLU ALA GLU SER VAL PHE LYS GLU LYS

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

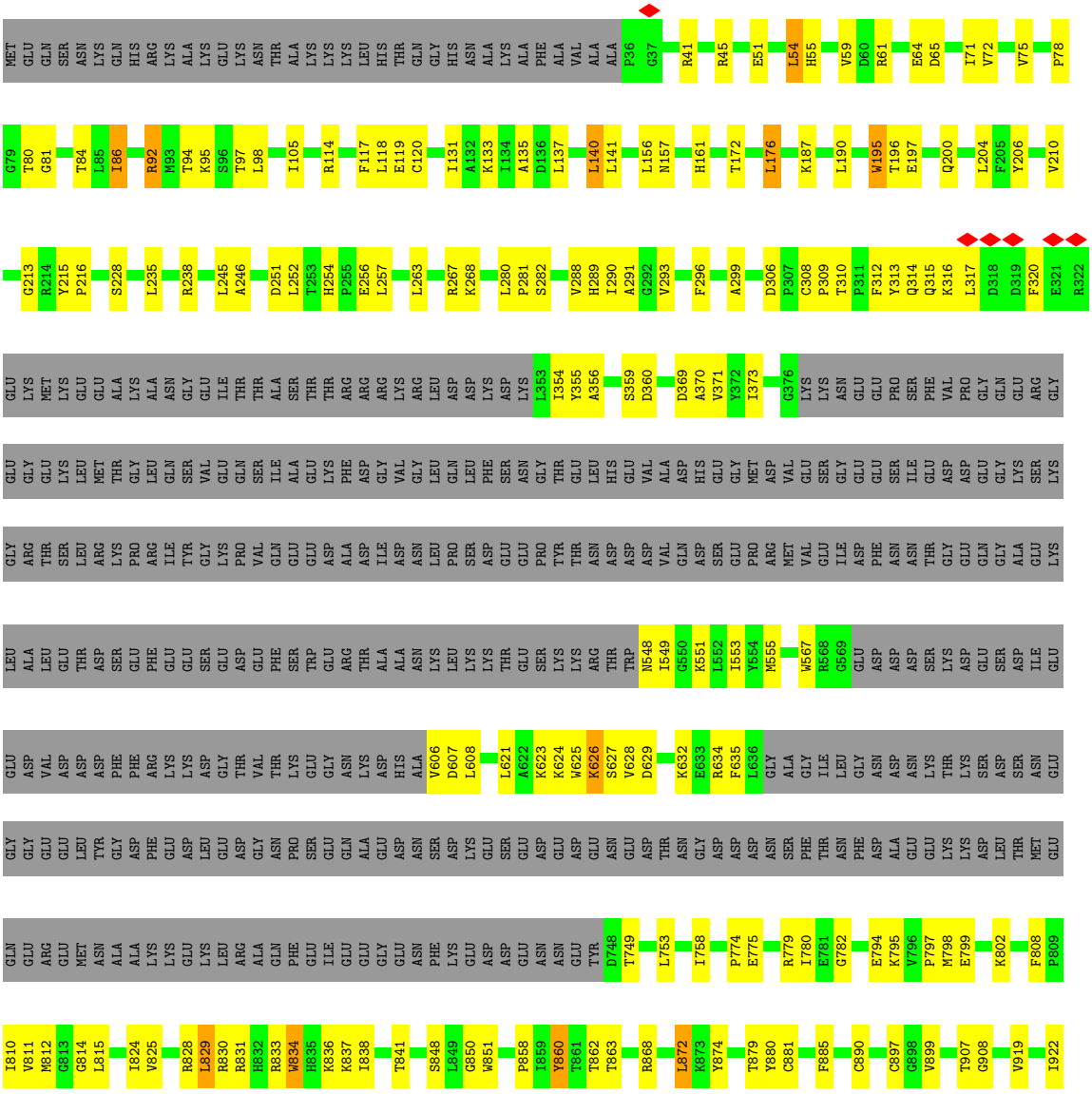
TYR GLY ILE ASN ASP LYS PHE PHE ASP LEU LEU LYS PHE ASN ARG ASP THR LEU ALA ALA GLU ASP SER ASN GLU ALA SER GLU GLY SER GLU ASP GLU ASP ASP ILE ASP TYR PHE GLN ASP MET PRO SER ASP ASP GLU GLU GLU GLU GLU ALA ILE TYR TYR GLU ASP PHE PHE ASP LYS PRO

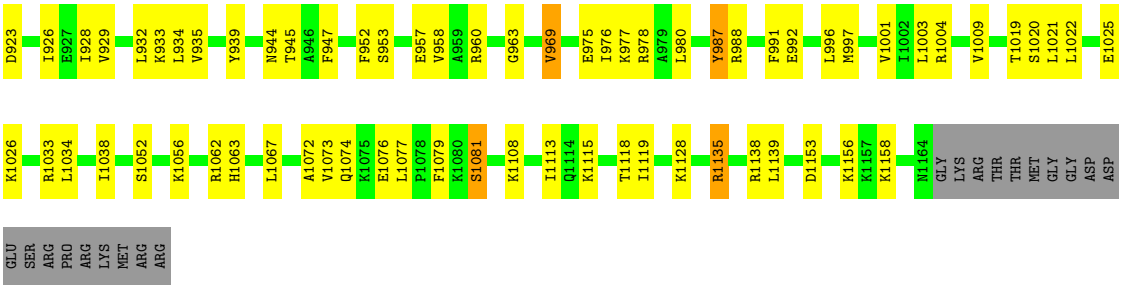
THR LYS GLU PRO VAL LYS LYS HIS SER ASP VAL LYS ASP PRO LYS GLU ASP GLU GLU LEU ASP GLU GLU GLU HIS ASP SER ALA MET ASP LYS VAL LYS LEU ASP LEU PHE ALA ASP GLU GLU ASP GLU PRO ASN ALA GLU GLY VAL GLY GLU ALA SER ASP K295 N296 L297 I305



• Molecule 33: Ribosome biogenesis protein BMS1

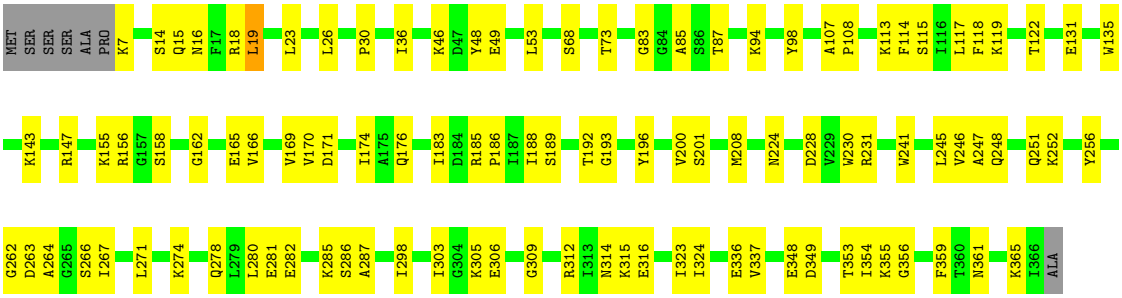
Chain CL:





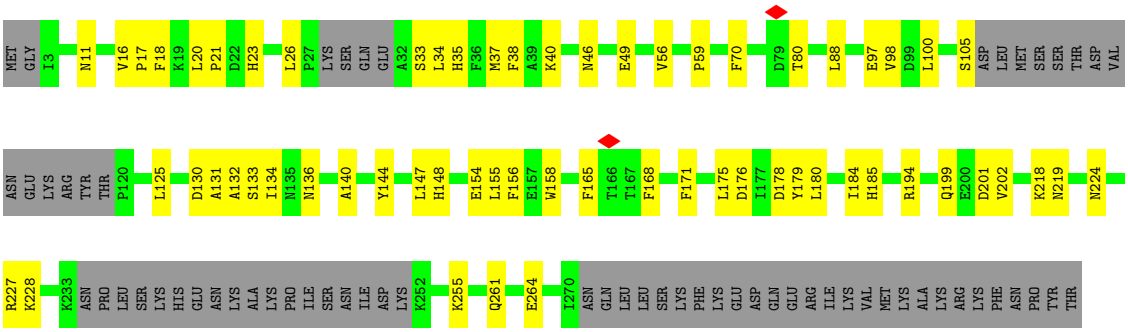
• Molecule 34: RNA 3'-terminal phosphate cyclase-like protein

Chain CM:



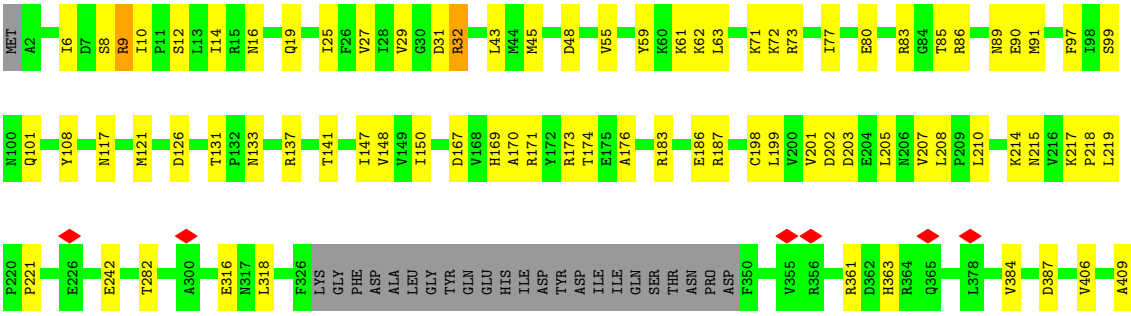
• Molecule 35: Ribosomal RNA-processing protein 7

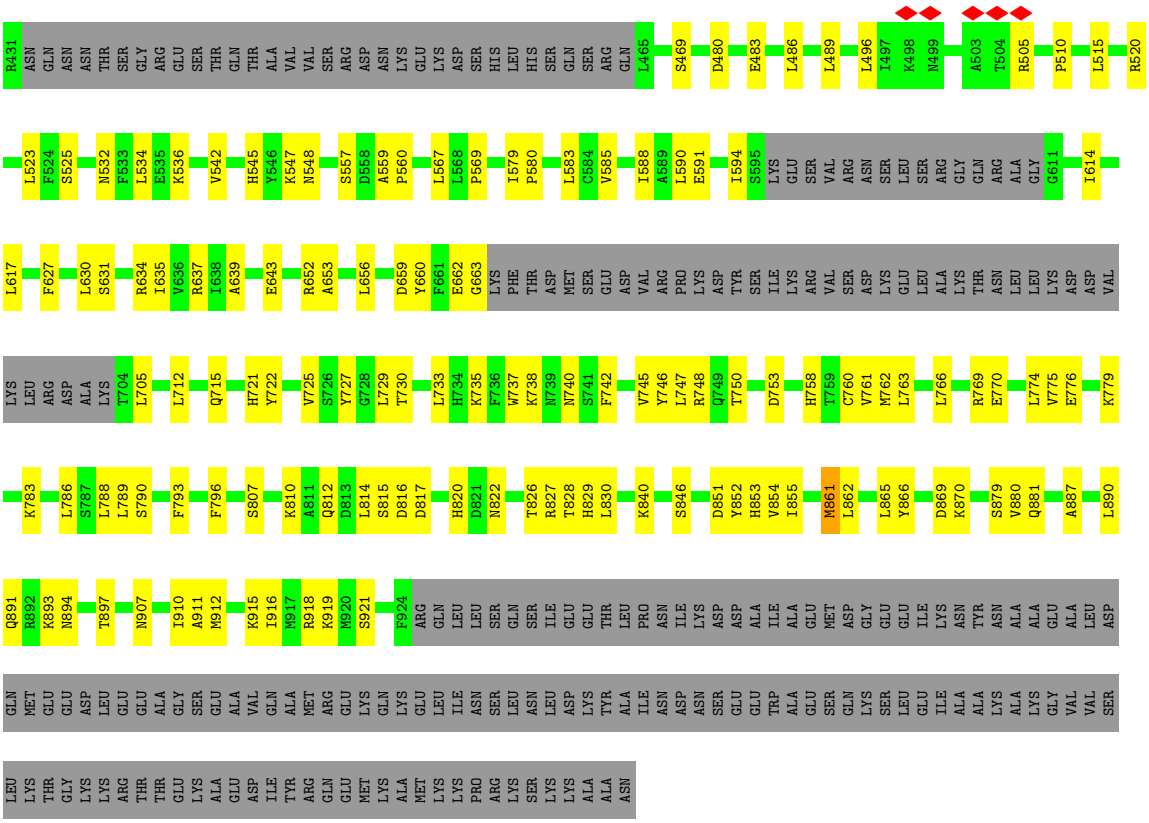
Chain CN:



• Molecule 36: RNA cytidine acetyltransferase

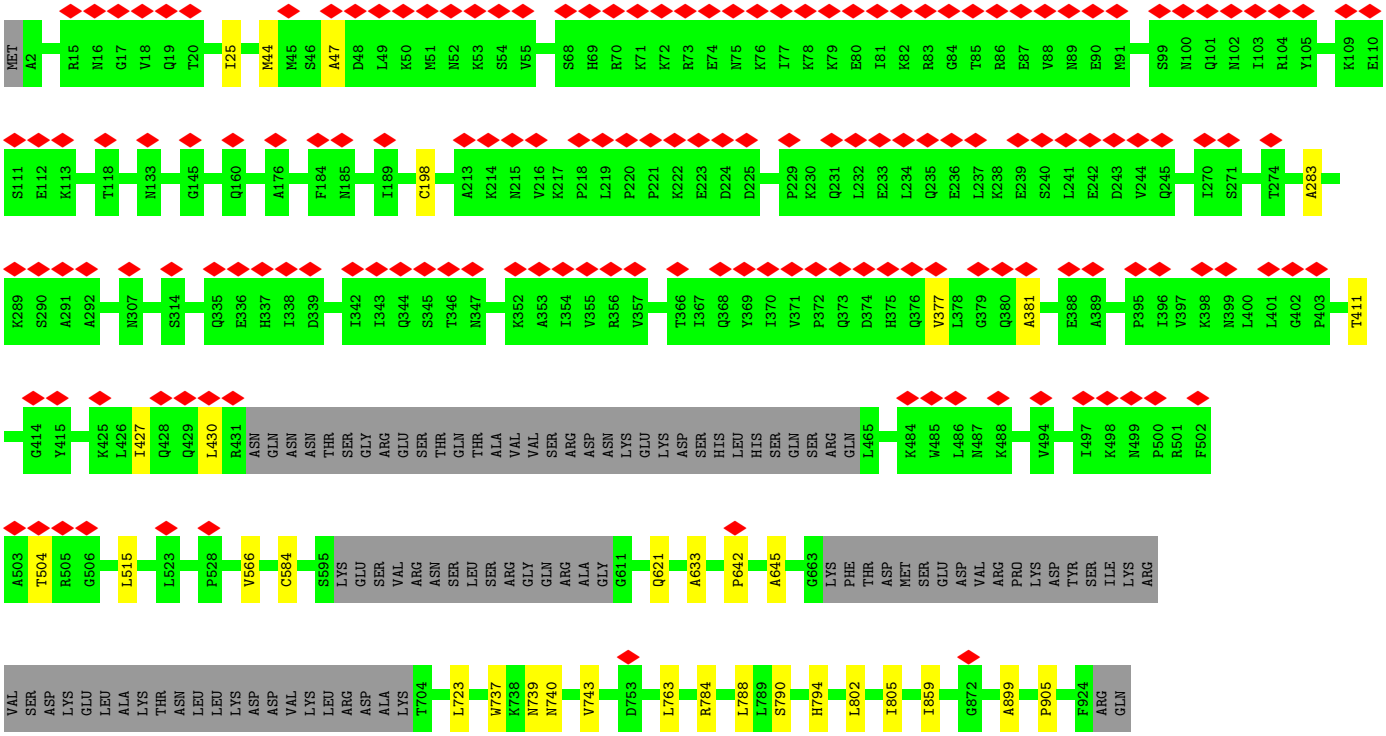
Chain JA:

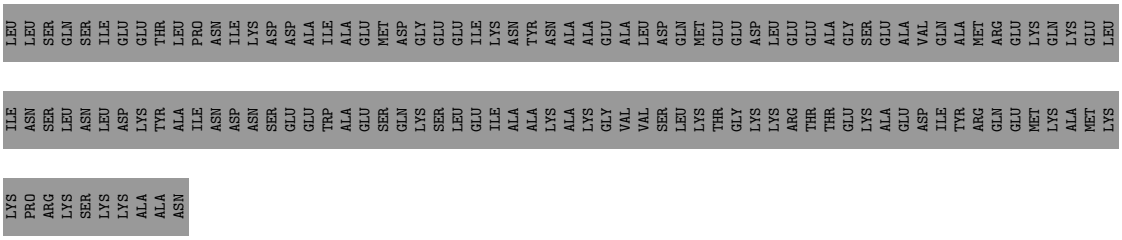




- Molecule 36: RNA cytidine acetyltransferase

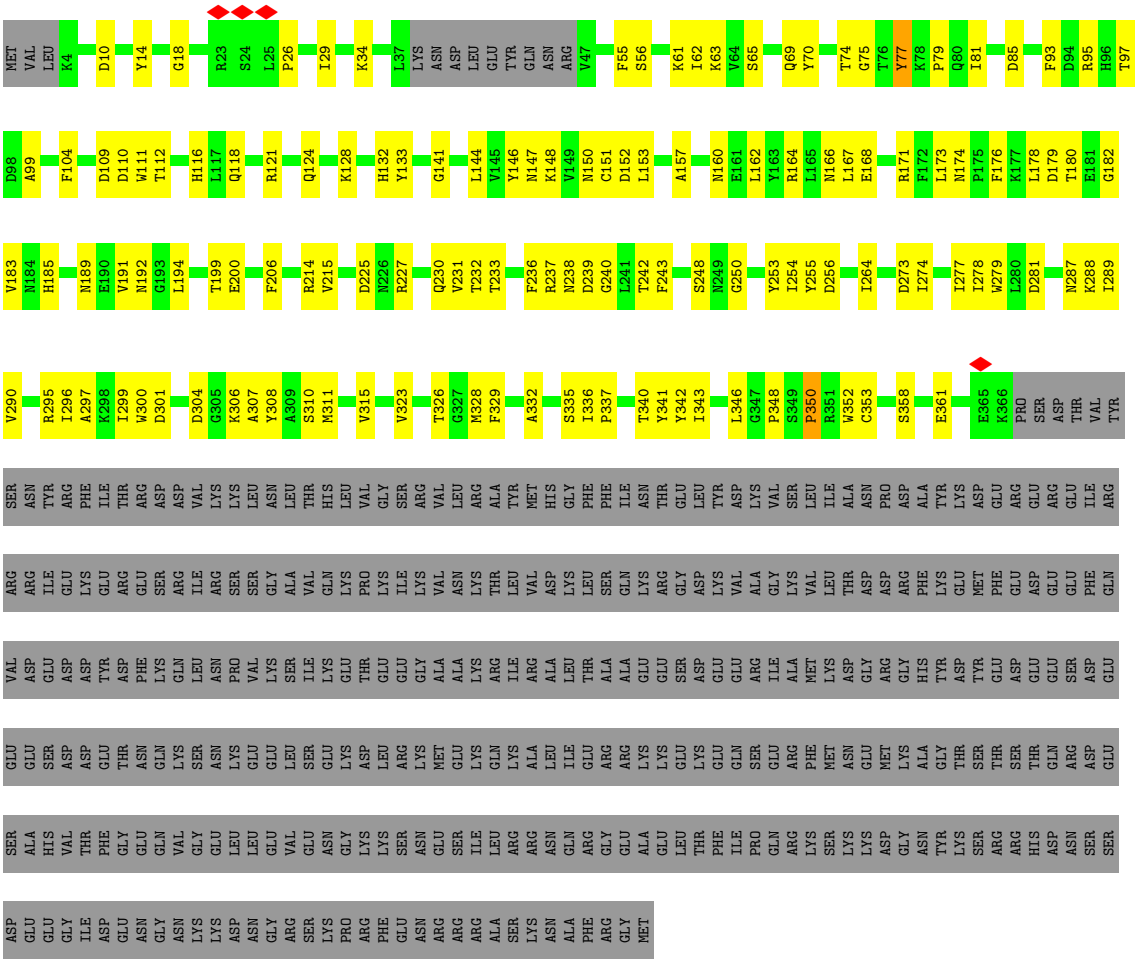
Chain JB:





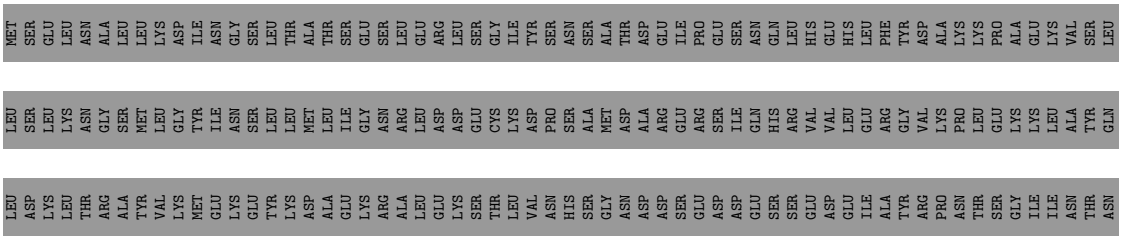
• Molecule 37: Ribosome biogenesis protein ENP2

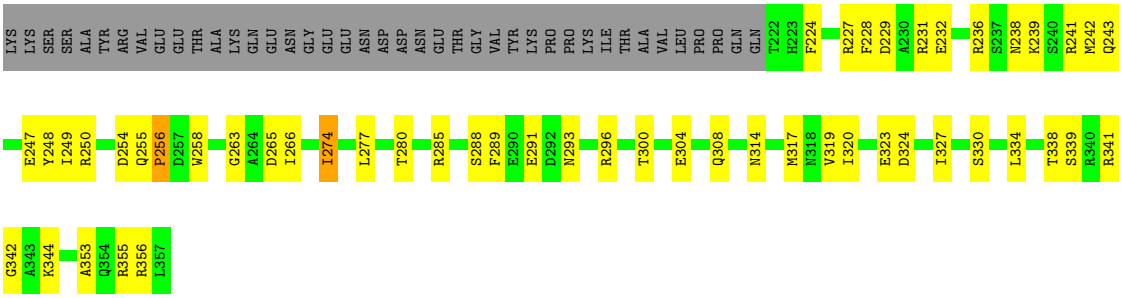
Chain JC:



• Molecule 38: U3 small nucleolar ribonucleoprotein protein LCP5

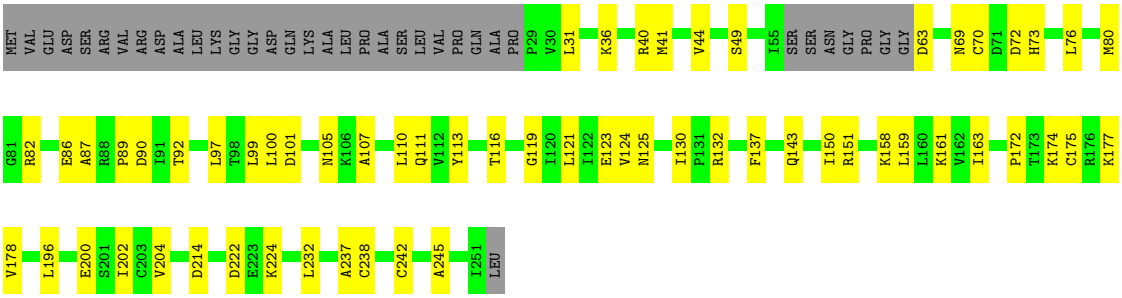
Chain JE:





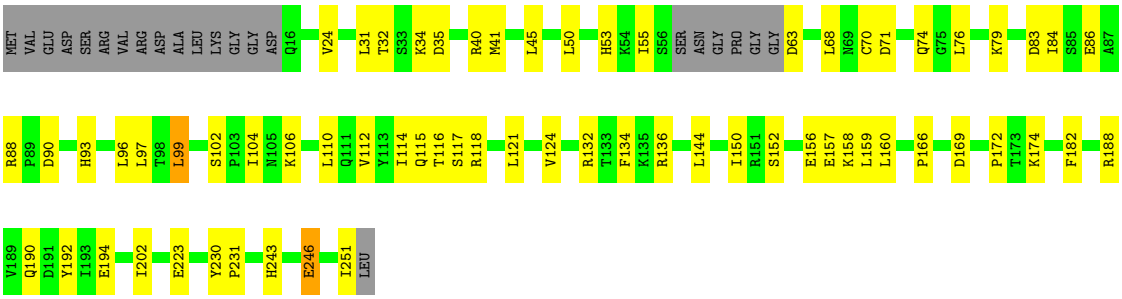
- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain JF:



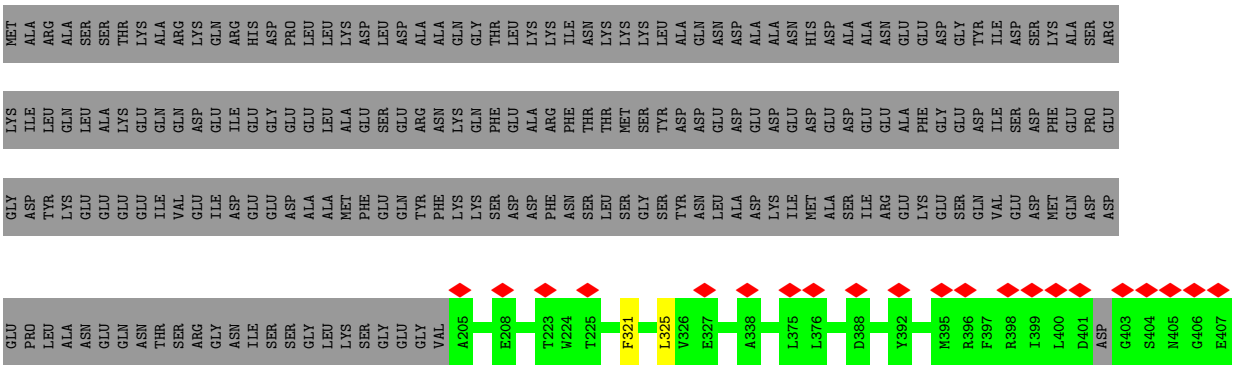
- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

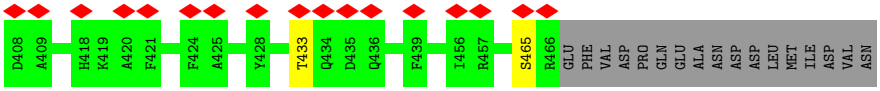
Chain JG:



- Molecule 40: Essential nuclear protein 1

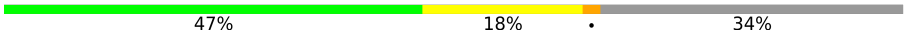
Chain JH:

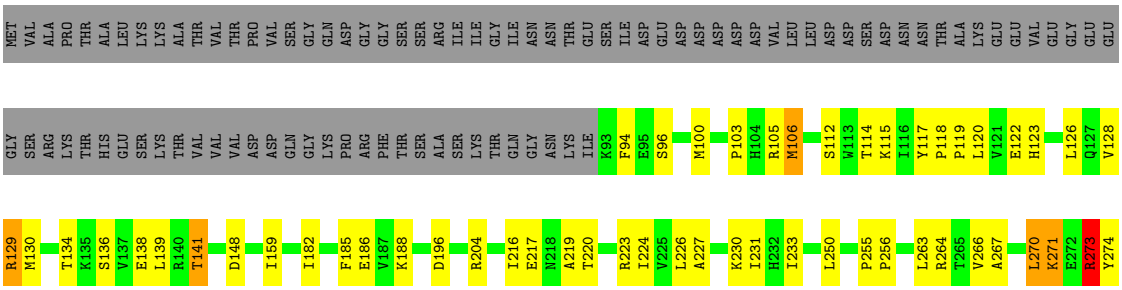




• Molecule 41: Pre-rRNA-processing protein PNO1

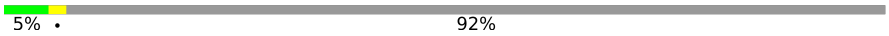
Chain JJ:

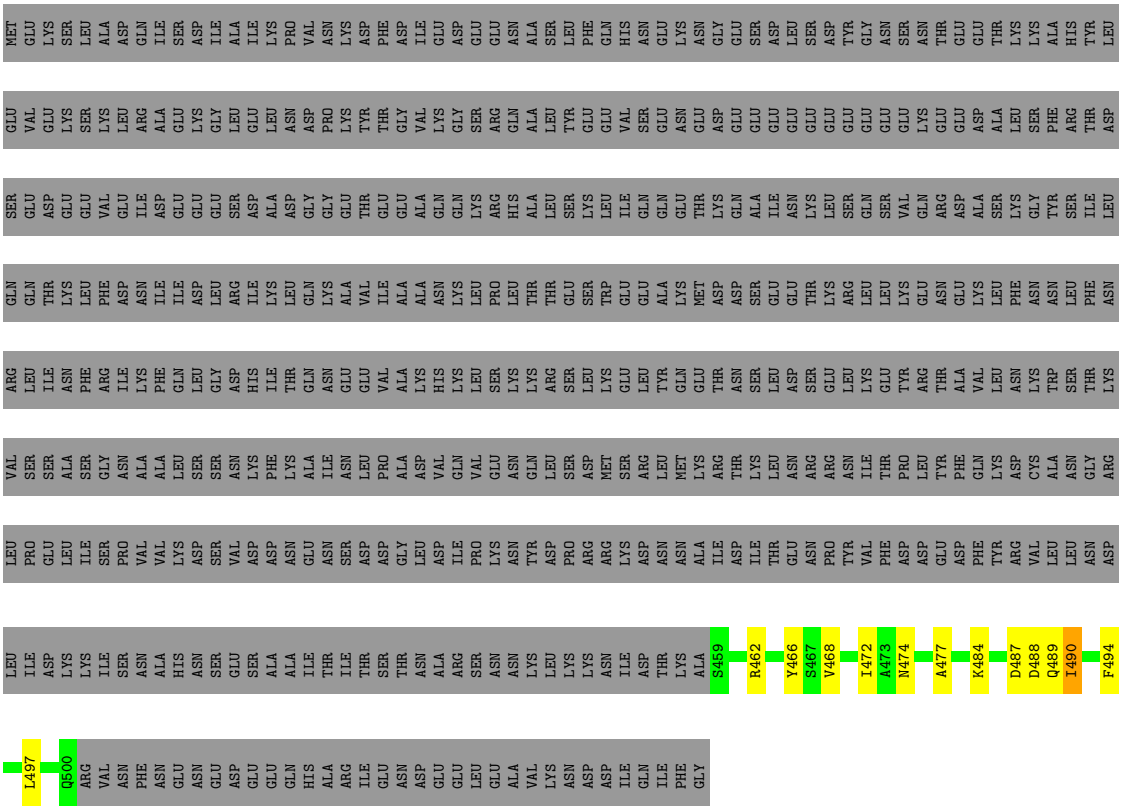




• Molecule 42: Protein BFR2

Chain JK:





• Molecule 43: rRNA-processing protein FCF2

Chain JM:

K77 K78 K79 N80 V81 S84 VAL GLU THR GLU ASP LYS ARG LYS PRO ASN LYS SER ASP LYS ASN ASP N101 L106 P107 K108 P109 N112 M113 R114 R115 E116 V117 Q118 L122 R127 L130 R134 H135 Y136 K137 R146 G150 E154 ASP LYS SER GLU PHE

TYR SER SER ARG MET ASN ARG LYS GLU ARG LYS S171 L177 G201 R202 K203 E211 M212 R213 K214 K215 R216 ARG

- Molecule 44: Protein FAF1

Chain JN: 42% 11% • 46%

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

PHE LYS ASP GLY THR ILE GLU SER SER ASN SER SER ASP GLU ASP SER GLY ASN GLU THR ALA GLU GLU ASN ASN GLN ASP SER LYS PRO K91 T92 Q93 P94 I97 R98 PHE ASN G101 P102 Y106 V107 P108 P109 S110 K111 K112 T113 Q114 S119 GLY LYS THR LEU THR GLN ILE

ASN LYS LYS LEU GLU SER THR GLU ALA LYS GLU GLU LYS GLU ASP GLU THR LEU GLU ALA GLU N148 S166 N170 GLY GLY SER GLY SER THR ASN SER GLY VAL SER LEU THR LEU GLN SER MET GLY GLY GLY ASN ASP ASP GLY I195 V196 I203 L215 V221 H224

Q225 D226 K227 V234 P235 I238 D244 K248 Y253 V263 L264 K268 K269 G270 K298 E303 L306 K307 I308 T315 R316 N317 I320 K323 R324 D325 R328 I329 S330 GLY GLY GLU ARG SER GLY LYS PHE ASN GLY LYS LYS LYS SER ARG ARG

- Molecule 45: KRR1 small subunit processome component

Chain JO: 59% 15% 25%

MET VAL SER THR HIS ASN ARG ASP LYS PRO TRP ASP THR ASP ASP ILE ASP LYS TRP LYS ILE GLU GLU PHE LYS GLU GLU ASP ASN ALA SER GLY GLN PRO PHE ALA GLU E38 F41 L53 W57 L64 L73 T85 R86 K87 D90 I93 I94 L95 K96 A97

R98 I101 K102 L103 L104 A113 I116 L117 N130 L145 V146 T152 L158 L159 Q167 T170 L180 K201 I205 R212 PRO GLU LEU ALA ASN GLU ASP TRP SER ARG PHE LEU PRO MET PHE LYS LYS ARG ASN VAL ALA ARG LYS LYS LYS PRO LYS LYS

ILE ARG ASN VAL GLU LYS LYS V247 K273 R274 E275 K276 K280 L281 N282 E283 Q284 K285 E286 K287 Q288 M289 E290 R291 E294 R295 E298 K301 A305 P306 E307 GLU GLU ALA TYR LYS PRO ASN GLN ASN

- Molecule 46: Protein SOF1

Chain JP: 59% 30% • 7%

M1 K2 I3 K7 R8 S9 A10 D11 D12 Y13 V14 Q20 E21 S22 Q23 R26 L32 F35 E36 E40 Y41 T48 K49 L50 F54 P57 F58 V59 G60 Q61 L62 H66 R67 D68 G69 V70 Y71 N81 K82 L83 A84 T85 G86 S87 V91 I92 K93 Y94

W95 N96 M97 S98 T99 F106 H109 L112 V113 L116 C117 Q120 M136 L137 S138 C139 S140 D141 T144 V145 K146 L147 K158 N159 SER SER ASP ASN ASP SER VAL THR N168 Q183 G184 I185 D186 S187 H188 R189 E190 N191 S192 T193 T196 I201 H202 L203 W204

K210 P211 L215 S216 W217 N221 S224 L225 N228 Q229 N230 E231 T232 D233 I234 L235 A236 S237 T238 I244 V245 L246 Y247 D248 T251 P254 T255 Q256 K257 I258 V259 Q260 R263 T264 W269 N270 P271 M272 V278 T279 A280 N281 Y287 Y288 Y289 D290 M291

S297 L298 N299 V300 F301 V308 V311 D312 F313 S314 P315 T316 G317 D318 E319 I320 V321 T322 G323 S324 Y325 D326 K327 S328 I329 Y332 R340 E341 I342 Y343 H344 T345 K346 H350 V351 Y356 S357 M358 Y362 S365 G366 S367 D368 D369 G370 N371 V372 R373 L374 W375 R382

V385 K399 L400 H416 R417 H418 V419 P420 I423 S436 R440 K449 D450 I454 S455 E456 K459 V465 HIS LYS TYR GLU ASP SER GLY ARG ASP ARG LYS ARG ARG LYS GLU ASP ASP LYS ARG ASP THR GLN GLU LYS

- Molecule 47: Regulator of rDNA transcription protein 14

Chain JQ: 28% • 69%

MET SER SER SER LEU SER GLN THR SER LYS TYR GLN ALA THR SER VAL VAL ASN GLY LEU LEU LEU SER ASN LEU LEU PRO GLY VAL PRO LYS ILE ARG ALA ASN ASN GLY LYS THR SER VAL ASN ASN GLY SER LYS ALA GLN LEU ILE ASP ARG ASN LEU LYS LYS ARG VAL GLN LEU GLN

ASN ARG ASP VAL HIS LYS ILE LYS LYS LYS CYS LYS LEU VAL LYS LYS LYS LYS VAL LYS LYS HIS LYS LEU ASP LYS GLU GLN LEU GLU GLN LEU ALA LYS HIS GLN VAL LEU LYS LYS HIS GLN HIS GLU GLY THR LEU THR ASP HIS GLU R112 I146 L147 K148 ASP THR VAL SER

THR ALA ASN THR ASP ARG SER LYS ARG ARG ARG PHE LYS ARG LYS GLN PHE LYS GLU ASP ILE LYS GLU SER ASP F178 V179 R183 Y184 A192 D201 S202 S203 GLU GLU ASP

- Molecule 48: 40S ribosomal protein S1-A

Chain DA: 69% 24% • 6%

MET A2 R8 K11 K14 G15 Q16 K17 K18 R19 D22 P23 F24 T25 R26 I32 N49 G53 L54 K55 S56 L61 K62 G63 R64 A71 H79 S80 F81 R82 K83 V88 D89 G93 L96 L97 T98 D104 F105 T106 R111 L120 V127

K128 T129 S130 D131 D132 Y133 V134 A141 Q149 V150 S154 Y155 A156 Q157 K166 E170 I171 L172 V176 Q177 G178 S179 T180 L181 L184 K187 P190 E191 V192 Q208 N209 K214 V215 K216 K219 H232 G233 GLU GLY SER GLY E238 E239 K240 G241 K242 K243

V244 T245 GLY PHE LYS ASP GLU VAL LEU GLU THR VAL

- Molecule 49: 40S ribosomal protein S4-A

Chain DE: 59% 34% • 6%

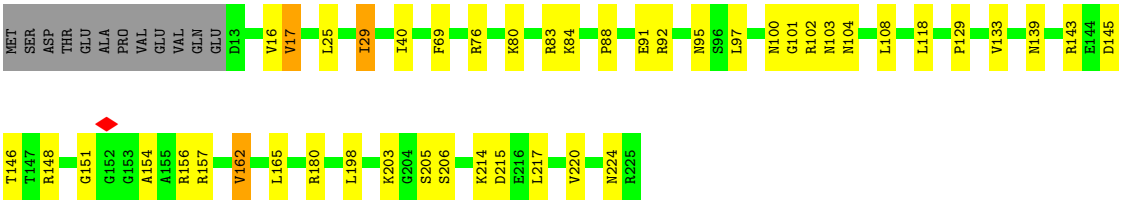
MET A2 R3 K6 R11 L19 Y27 R30 K37 S41 L42 P43 L44 I45 V46 F47 L48 R49 K53 Y54 R59 E60 V61 M66 K71 V76 D79 Y82 P83 A84 M87 D88 T91 L92 N98 F99 R100 L101 V102 Y103 D104 V105 K106

G107 R108 H112 R113 I114 Y121 K122 K125 V126 K127 K128 V129 Q130 L131 Y138 V139 V140 T141 H142 D143 G144 R145 Y149 P150 D151 P152 N153 I154 K155 V156 N157 D158 L164 K174 K179 L180 V181 Y182 V183 T184 G185 G186 R187 N188 L189 G190 R191 I192 G193 T194 I195 V196

R200 H201 F205 D206 L207 V208 H209 I210 K211 D212 D215 N216 T217 F218 V219 T220 R221 L222 N223 N224 V225 F226 K233 L246 SER ILE ALA GLU GLU ARG ASP ARG ARG ARG ALA GLN GLN GLY LEU

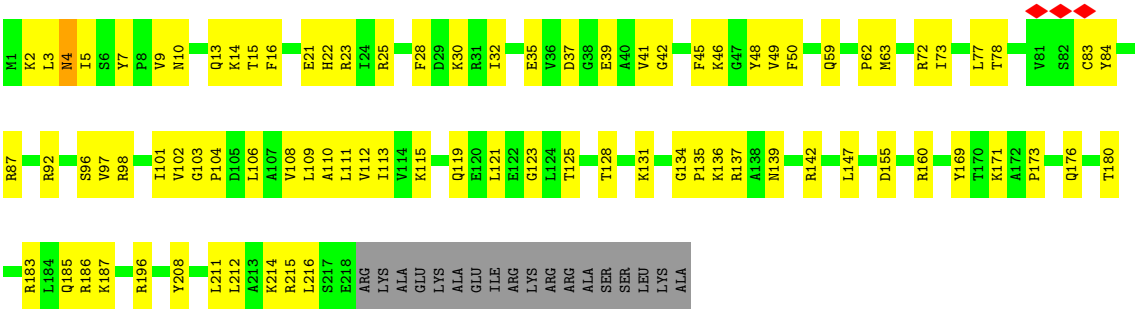
- Molecule 50: Rps5p

Chain DF: 75% 19% • 5%



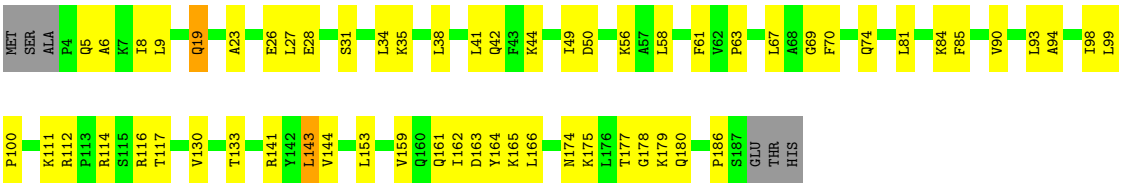
- Molecule 51: 40S ribosomal protein S6-A

Chain DG:



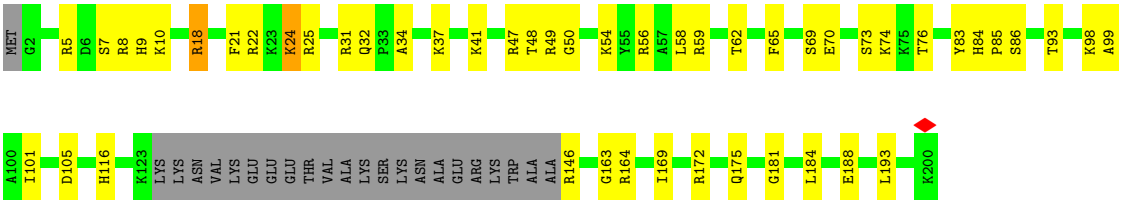
- Molecule 52: 40S ribosomal protein S7-A

Chain DH:



- Molecule 53: 40S ribosomal protein S8-A

Chain DI:



- Molecule 54: 40S ribosomal protein S9-A

Chain DJ:

R108 L109 Q110 V113 Y114 K115 V122 V127 L128 Q131 R132 H133 I134 A135 V136 G137 K138 Q139 F146 D151 S152 E153 K154 H155 I156 S162 P169 G170 R171 R174 R175 N176 E186 ALA ALA ASP GLU ALA ASP GLU ALA ASP GLU GLU

• Molecule 55: 40S ribosomal protein S11-A

Chain DL: 57% 33% 10%

MET SER THR GLU LEU T6 V7 Q8 S9 E10 R11 Q14 K26 T27 S28 K29 R30 R33 P45 K46 T47 Y53 I54 D55 K56 K57 C58 R67 G68 T72 G73 T74 V75 V85 I86 R87 R88 A89 Y90 I94 N98 R99 R103 H104 K105 P108 A114

F115 V119 T124 V125 G126 Q127 C128 R129 P130 I131 S132 K133 T134 V135 R136 V139 V140 K141 V142 A145 ALA GLY LYS ALA ASN LYS GLN PHE ALA LYS PHE

• Molecule 56: 40S ribosomal protein S13

Chain DN: 75% 23%

MET G2 R3 A7 R20 S29 S32 E35 V38 K43 T46 P47 S48 Q49 I50 G51 V52 L53 L54 T61 Q62 A63 R64 N69 K70 I71 M72 R73 I74 L75 I84 P85 E86 D87 V96 K100 K112 F113 R114 S120 L125 Y128

A146 S147 A148 L149 V150 N151

• Molecule 57: 40S ribosomal protein S14-A

Chain DO: 69% 19% 12%

MET SER ASN VAL VAL GLN ALA ARG ASP ASN S11 G15 Y20 A21 S22 F23 N24 D25 T26 E37 R41 V42 T43 M46 K47 V48 K49 A50 D53 E54 L62 D66 I76 V79 I112 G113 E116 D117 D124 R127 K128 K129 G130 GLY ARG ARG

GLY ARG ARG LEU

• Molecule 58: 40S ribosomal protein S16-A

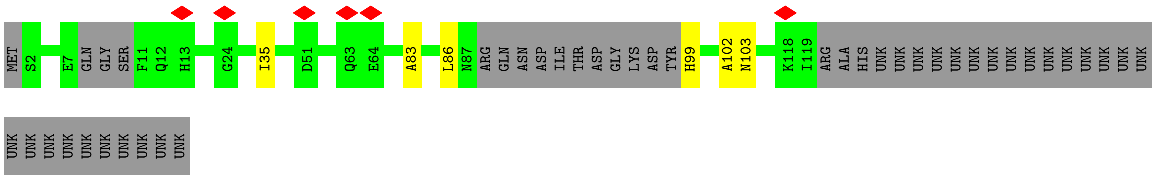
Chain DQ: 61% 24% 13%

MET SER A3 V7 K13 K14 S15 V19 V22 G25 L28 V31 T37 L38 V39 R45 E50 D58 K59 F60 S61 D64 I65 R66 V69 Y79 R82 L89 V90 A91 Y92 H93 Q94 K95 Y96 V97 D98 K102 K106 T110 S111

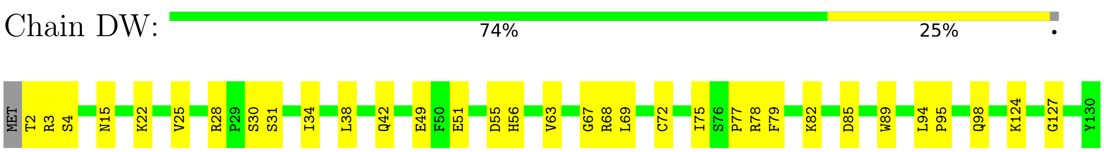
Y112 D113 R114 L117 I118 R122 K127 LYS PHE GLY GLY LYS GLY ALA ARG SER ARG PHE GLN LYS SER TYR ARG

• Molecule 59: 40S ribosomal protein S18-A,40S ribosomal protein S18-A,Rps18

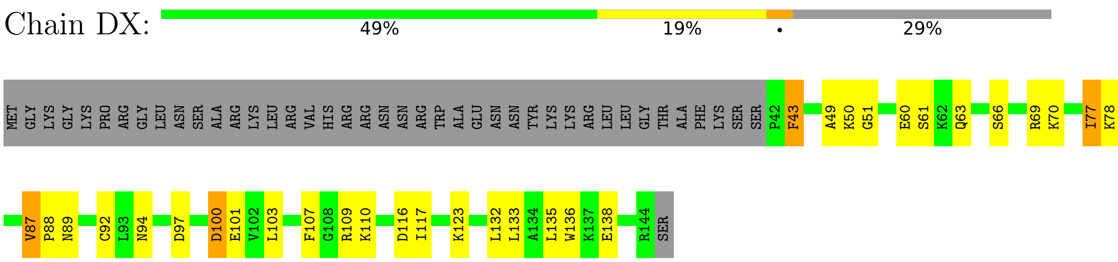
Chain DS: 67% 29%



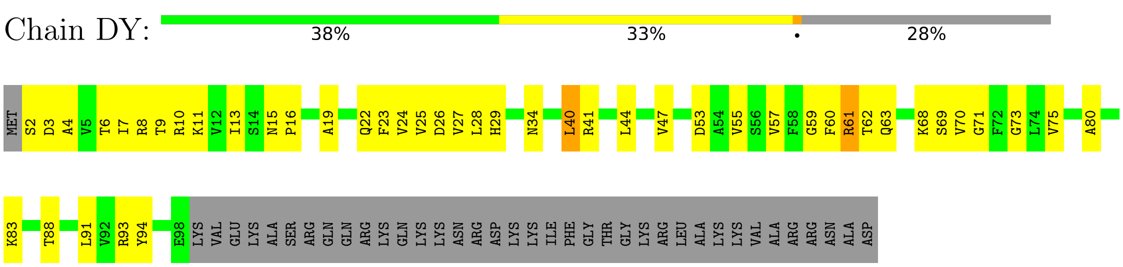
• Molecule 60: 40S ribosomal protein S22-A



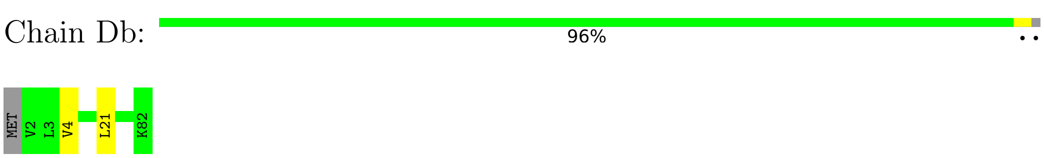
• Molecule 61: 40S ribosomal protein S23-A



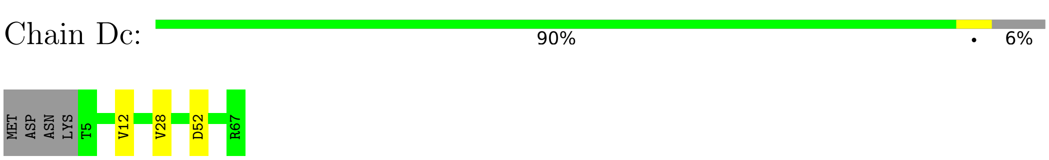
• Molecule 62: 40S ribosomal protein S24-A



• Molecule 63: 40S ribosomal protein S27-A

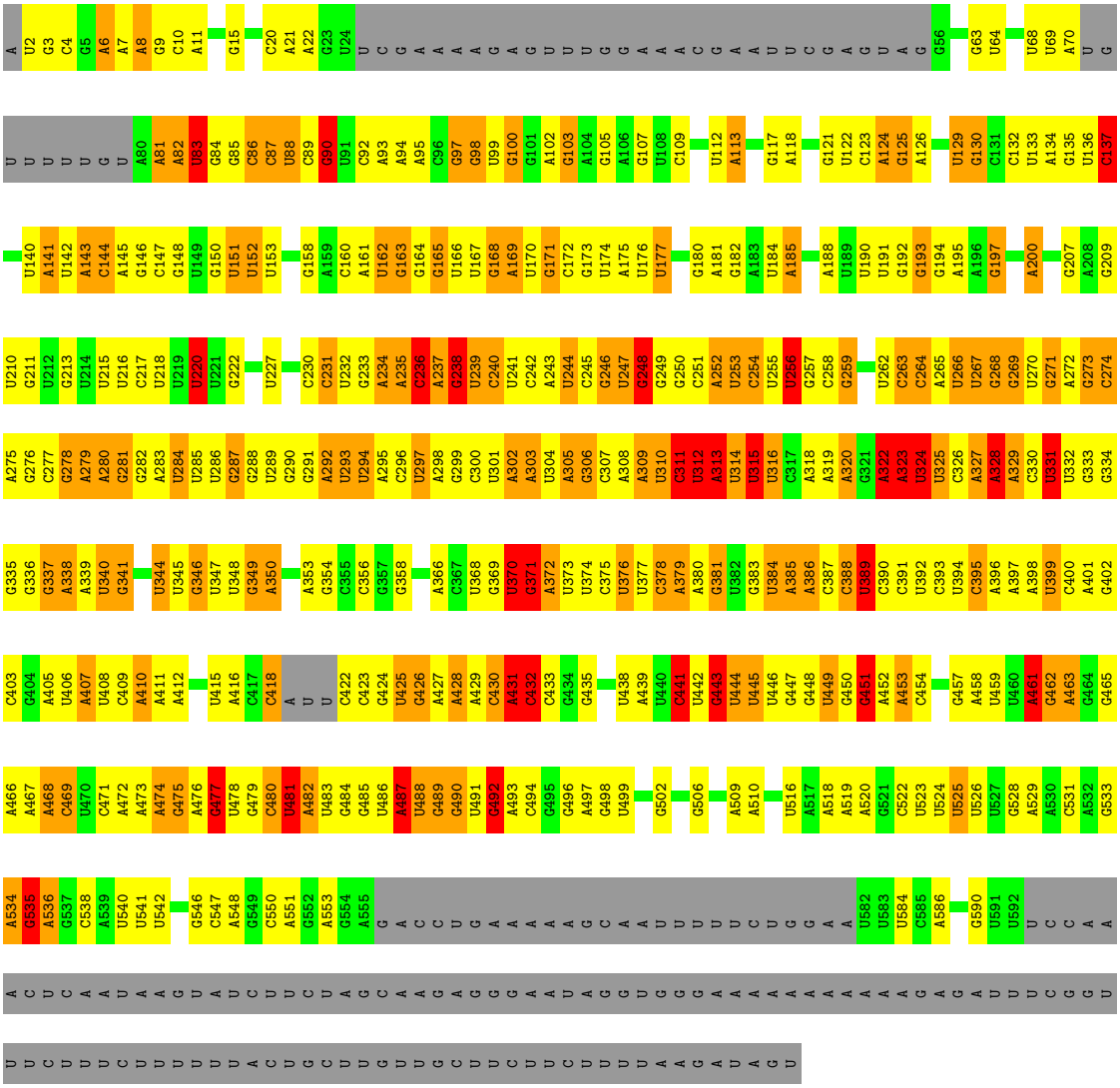


• Molecule 64: 40S ribosomal protein S28-A



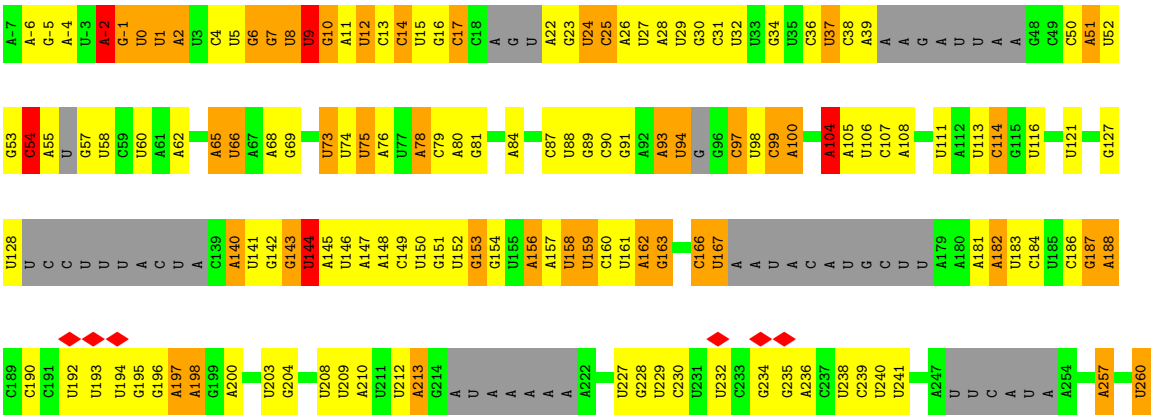
• Molecule 65: 5ETS RNA

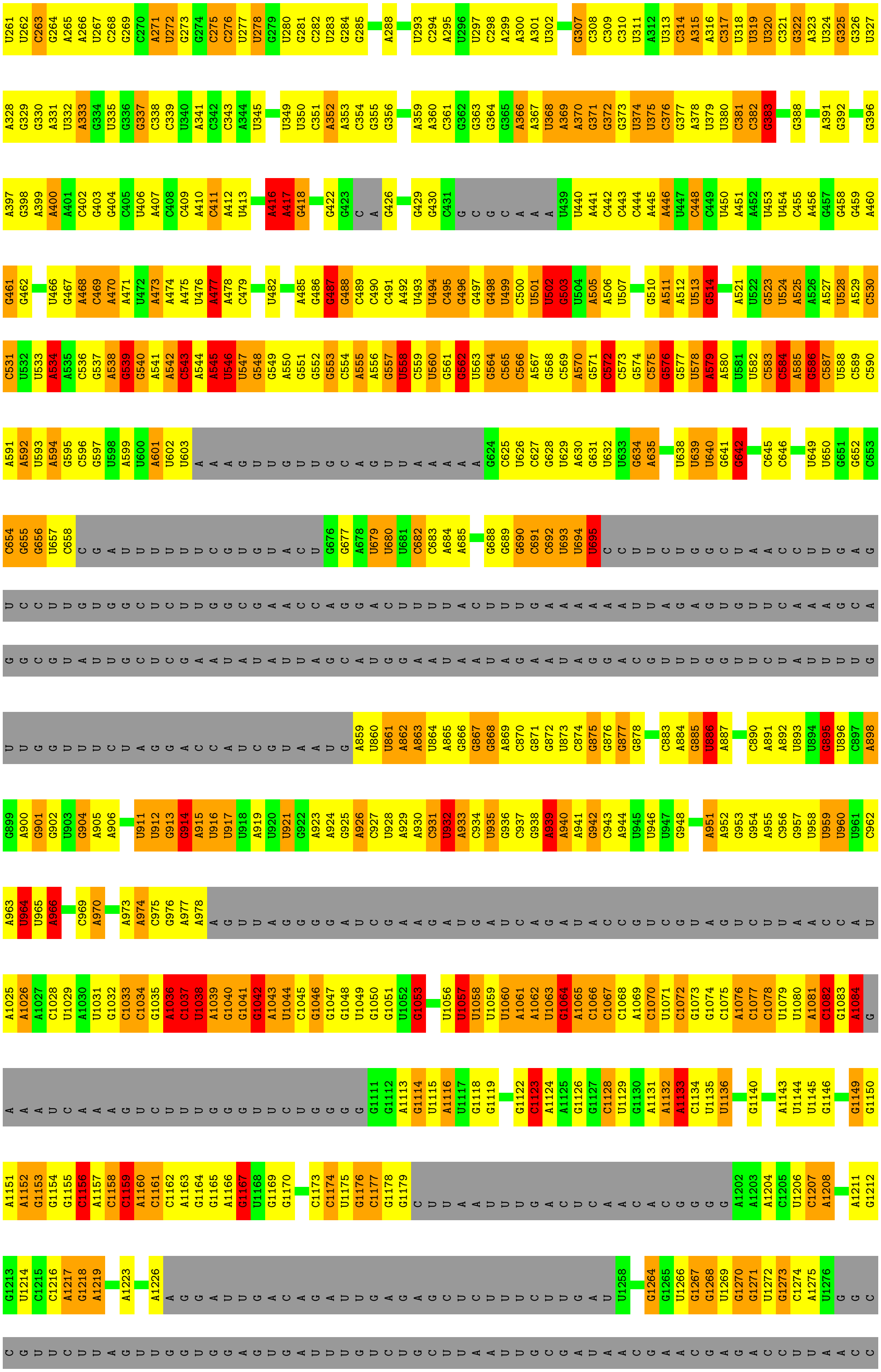
Chain D2: 20% 33% 17% • 25%

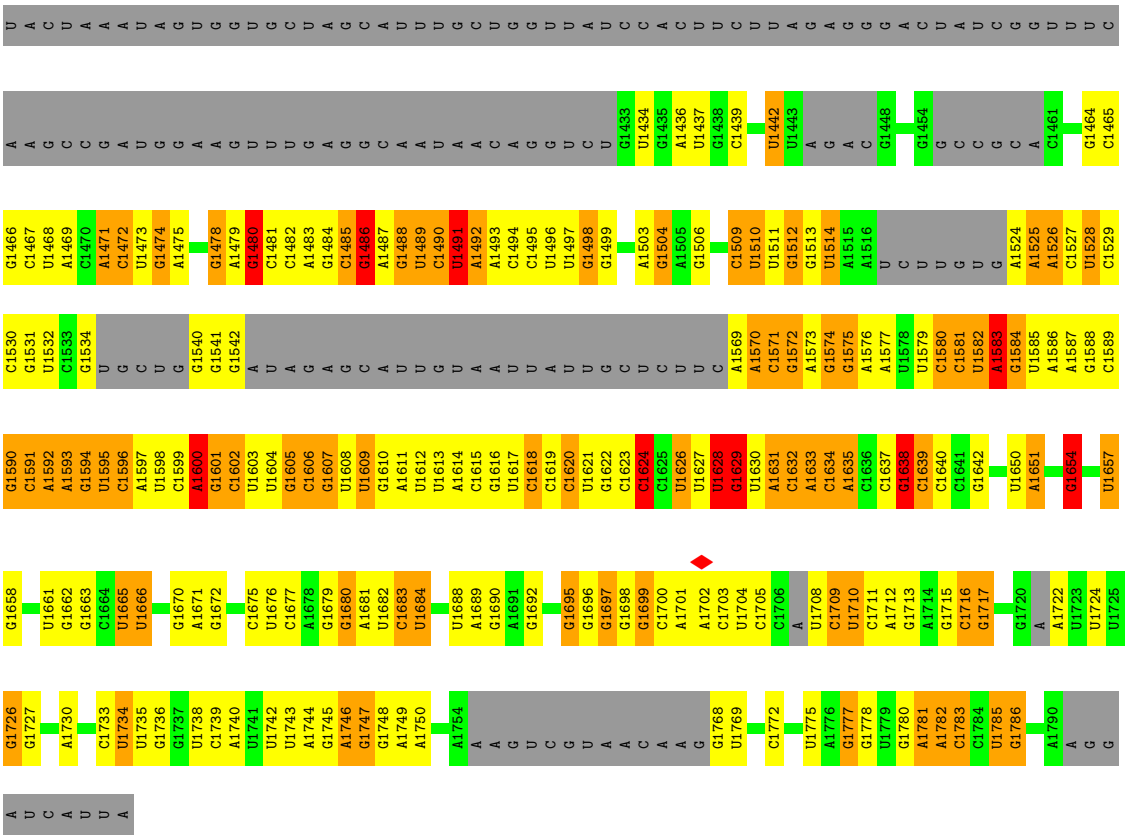


• Molecule 66: 18S rRNA

Chain D3: 18% 29% 16% • 34%

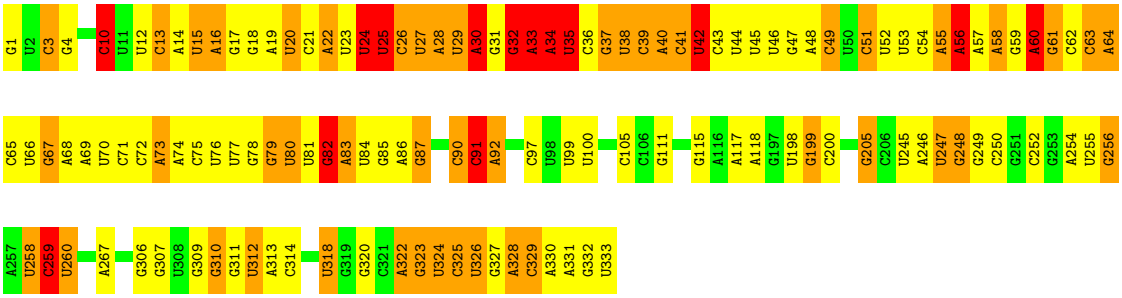



U261 U262 C263 G264 A265 A266 U267 C268 G269 C270 A271 U272 G273 G274 C275 C276 U277 U278 G279 U280 G281 C282 U283 G284 G285 A288 U293 C294 A295 U296 U297 C298 A299 A300 A301 U302 G307 C308 C309 C310 U311 A312 U313 C314 A315 A316 C317 U318 U319 U320 C321 G322 A323 U324 G325 G326 U327
A328 G329 G330 A331 U332 A333 G334 U335 G336 G337 C338 C339 U340 A341 C342 C343 A344 U345 U349 U350 C351 A352 A353 C354 G355 G356 A359 A360 C361 G362 G363 G364 G365 A366 A367 U368 A369 A370 G371 C372 G373 U374 U375 C376 G377 A378 U379 U380 C381 C382 G383 G388 A391 G392 G396
A397 G398 A399 A400 A401 C402 G403 G404 C405 U406 A407 C408 C409 A410 C411 A412 U413 A416 A417 G418 G422 G423 C A G426 G429 G430 C431 G C G C A A A U439 U440 A441 C442 C443 C444 A445 A446 U447 C448 C449 U450 A451 A452 U453 U454 C455 A456 G457 G458 G459 A460
G461 G462 U466 G467 A468 C469 A470 A471 U472 A473 A474 A475 U476 A477 A478 C479 U482 A485 G486 G487 G488 C489 C490 C491 A492 U493 U494 C495 G496 G497 G498 U499 C500 U501 U502 G503 U504 A505 A506 U507 G510 A511 A512 U513 G514 A521 U522 G523 U524 A525 A526 A527 U528 A529 C530
C531 U532 U533 A534 A535 C536 G537 A538 G539 G540 A541 A542 C543 A544 A545 U546 U547 G548 G549 A550 G551 G552 G553 C554 A555 A556 G557 U558 C559 U560 G561 G562 U563 G564 C565 C566 A567 G568 C569 A570 G571 C572 C573 G574 C575 G576 G577 U578 A579 A580 U581 U582 C583 C584 A585 G586 C587 U588 C589 C590
A591 A592 U593 A594 G595 C596 G597 U598 A599 U600 A601 U602 U603 A A A G U U G U U G C A G U U A A A A A G624 C625 U626 C627 G628 U629 A630 G631 U632 U633 G634 A635 U638 U639 U640 G641 G642 C645 C646 U649 U650 G651 G652 C653
C654 G655 G656 U657 C658 C G A U U U U U C G U G U A C U G676 G677 A678 U679 U680 U681 C682 C683 A684 A685 G688 G689 G690 C691 C692 U693 U694 U695 C C U U C U G G G C U A A C C U U G A G
U C C U U G U G G C U C U U G G C G A A C C A G G A C U U U U A C U U U G A A A A A A U U A G A G U G U U C A A A G C A
G G C G U A U U G C U C G A A U A U A U U A G C A U G G A A U A A U A G A A U A G G A C G U U U G G U U C U A U U U U G
U U G G U U U C U A G G A C C A U C G U A A U G A859 U860 U861 A862 A863 U864 A865 G866 G867 G868 A869 C870 G871 G872 U873 C874 G875 G876 G877 G878 C883 A884 G885 U886 A887 C890 A891 A892 U893 U894 G895 U896 C897 A898
G899 A900 G901 G902 U903 G904 A905 A906 U911 U912 G913 G914 A915 U916 U917 U918 A919 U920 U921 G922 A923 A924 G925 A926 C927 U928 A929 A930 C931 U932 A933 C934 U935 G936 C937 G938 A939 A940 A941 G942 C943 A944 G945 U946 U947 G948 A951 A952 G953 G954 A955 C956 G957 U958 U959 U960 U961 C962
A963 U964 U965 A966 C969 A970 A973 A974 C975 G976 A977 A978 A G U U A G G G G A U C G A A G A U G A U C A G A U A C C C G U C G U A G U C U U A A C C A U
A1025 A1026 A1027 C1028 U1029 A1030 U1031 G1032 C1033 C1034 G1035 A1036 C1037 U1038 A1039 G1040 G1041 G1042 A1043 U1044 C1045 G1046 G1047 G1048 U1049 G1050 G1051 U1052 G1053 U1056 U1057 U1058 U1059 U1060 A1061 A1062 U1063 G1064 A1065 C1066 C1067 C1068 A1069 C1070 U1071 C1072 G1073 G1074 C1075 A1076 C1077 C1078 U1079 U1080 A1081 C1082 G1083 A1084 G
A A A U C A A A G U C U U U G G G U U C U G G G G G1111 G1112 A1113 G1114 U1115 A1116 U1117 G1118 G1119 G1122 C1123 A1124 A1125 G1126 G1127 C1128 U1129 G1130 A1131 A1132 A1133 C1134 U1135 U1136 G1140 A1143 U1144 U1145 G1146 G1149 G1150
A1151 A1152 G1153 G1154 G1155 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1165 A1166 G1167 U1168 G1169 G1170 C1173 C1174 U1175 G1176 C1177 G1178 G1179 C U U A A U U U G A C U U C A A C A C G G G G A1202 A1203 A1204 C1205 U1206 C1207 A1208 A1211 G1212
G1213 U1214 C1215 C1216 A1217 G1218 A1219 A1223 A1226 A G G A U U G A C A G A U U G A G A G C U C U U U C U U G A U U1258 G1264 G1265 U1266 G1267 G1268 U1269 G1270 C1271 U1272 G1273 C1274 A1275 U1276 G G C
C G U U C U U A G U U G G U G G A G U G A U U U G U C U G G U U A A U U C C G A U A A C G A A C G A G A C C U U A A C C



• Molecule 67: U3 snoRNA

Chain D4: 26% 39% 27% 8%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32213	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 ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.206	Depositor
Minimum map value	-0.126	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	508.32, 508.32, 508.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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: ZN, 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	UA	1.71	109/6780 (1.6%)	1.08	35/9175 (0.4%)
2	UB	0.51	0/3796	0.61	6/5137 (0.1%)
3	UC	1.03	1/1034 (0.1%)	0.86	2/1365 (0.1%)
4	UD	0.95	15/5461 (0.3%)	0.82	6/7395 (0.1%)
5	UE	1.07	8/3840 (0.2%)	0.88	6/5208 (0.1%)
6	UF	1.03	4/2538 (0.2%)	0.84	5/3405 (0.1%)
7	UG	1.60	70/4302 (1.6%)	1.11	26/5805 (0.4%)
8	UH	0.39	0/2703	0.68	11/3703 (0.3%)
9	UI	0.50	0/861	0.80	2/1156 (0.2%)
10	UJ	0.85	11/6903 (0.2%)	0.75	14/9474 (0.1%)
11	UK	1.26	14/2042 (0.7%)	0.96	1/2704 (0.0%)
12	UL	0.76	2/6851 (0.0%)	0.79	6/9246 (0.1%)
13	UM	0.71	5/6058 (0.1%)	0.80	6/8201 (0.1%)
14	UN	1.22	8/1231 (0.6%)	0.93	6/1661 (0.4%)
15	UO	1.10	12/3993 (0.3%)	0.90	10/5413 (0.2%)
16	UP	0.56	0/499	0.84	0/659
17	UQ	0.96	10/6794 (0.1%)	0.86	12/9203 (0.1%)
18	UR	1.50	36/3875 (0.9%)	1.02	17/5254 (0.3%)
19	US	0.61	0/3736	0.75	7/5086 (0.1%)
20	UT	0.28	0/11085	0.52	0/15445
21	UU	1.49	68/6815 (1.0%)	0.98	17/9213 (0.2%)
22	UV	0.50	0/8933	0.60	3/12081 (0.0%)
23	UX	1.50	16/1418 (1.1%)	1.07	5/1906 (0.3%)
24	UZ	0.70	1/2041 (0.0%)	0.74	1/2745 (0.0%)
25	CA	1.43	14/1917 (0.7%)	1.00	6/2588 (0.2%)
25	CB	0.73	0/1815	0.77	1/2448 (0.0%)
26	CD	0.96	3/3041 (0.1%)	0.85	7/4098 (0.2%)
27	CE	0.88	4/3012 (0.1%)	0.79	0/4091
28	CF	1.33	6/944 (0.6%)	0.97	5/1284 (0.4%)
28	CG	0.93	0/941	1.00	5/1281 (0.4%)
29	CH	0.61	1/3705 (0.0%)	0.68	1/4983 (0.0%)
30	CI	1.84	39/1559 (2.5%)	1.21	19/2097 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	CJ	1.36	21/2337 (0.9%)	1.04	13/3148 (0.4%)
32	CK	1.06	2/1685 (0.1%)	0.98	6/2261 (0.3%)
33	CL	1.18	27/6471 (0.4%)	0.92	19/8708 (0.2%)
34	CM	0.85	0/2832	0.78	3/3825 (0.1%)
35	CN	0.44	0/1934	0.59	1/2604 (0.0%)
36	JA	0.48	0/5994	0.65	1/8139 (0.0%)
36	JB	0.30	0/4128	0.57	0/5747
37	JC	0.51	0/2908	0.71	1/3938 (0.0%)
38	JE	0.55	0/1139	0.75	2/1512 (0.1%)
39	JF	0.51	0/1727	0.70	1/2329 (0.0%)
39	JG	0.82	0/1828	0.83	3/2470 (0.1%)
40	JH	0.24	0/1293	0.37	0/1801
41	JJ	0.65	1/1475 (0.1%)	0.77	4/1987 (0.2%)
42	JK	0.49	0/342	0.71	1/462 (0.2%)
43	JM	1.02	2/1156 (0.2%)	0.88	2/1536 (0.1%)
44	JN	1.15	4/1435 (0.3%)	0.96	4/1907 (0.2%)
45	JO	1.01	3/1961 (0.2%)	0.89	3/2631 (0.1%)
46	JP	1.64	70/3802 (1.8%)	1.06	17/5118 (0.3%)
47	JQ	0.41	0/385	0.57	0/529
48	DA	1.00	2/1937 (0.1%)	0.90	2/2593 (0.1%)
49	DE	0.46	0/1985	0.63	1/2675 (0.0%)
50	DF	1.23	4/1690 (0.2%)	0.93	7/2285 (0.3%)
51	DG	0.45	0/1779	0.62	0/2379
52	DH	0.58	0/1502	0.74	2/2023 (0.1%)
53	DI	0.46	0/1422	0.63	1/1899 (0.1%)
54	DJ	1.14	5/1450 (0.3%)	0.92	1/1941 (0.1%)
55	DL	0.40	0/1155	0.60	0/1557
56	DN	0.82	0/1215	0.70	1/1638 (0.1%)
57	DO	0.98	0/892	0.79	0/1202
58	DQ	1.70	18/990 (1.8%)	1.04	2/1335 (0.1%)
59	DS	0.31	0/513	0.59	0/711
60	DW	1.18	3/1038 (0.3%)	0.93	1/1395 (0.1%)
61	DX	1.27	1/798 (0.1%)	0.99	2/1065 (0.2%)
62	DY	0.60	0/780	0.88	2/1049 (0.2%)
63	Db	0.91	0/620	0.84	2/838 (0.2%)
64	Dc	1.26	2/499 (0.4%)	1.05	2/670 (0.3%)
65	D2	2.24	658/12457 (5.3%)	1.69	374/19407 (1.9%)
66	D3	1.84	889/28553 (3.1%)	1.49	518/44437 (1.2%)
67	D4	2.61	329/4142 (7.9%)	1.84	155/6435 (2.4%)
All	All	1.26	2498/230772 (1.1%)	1.04	1402/321696 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	UA	0	4
4	UD	0	7
5	UE	0	1
6	UF	0	3
7	UG	0	4
10	UJ	0	3
12	UL	0	4
13	UM	0	2
14	UN	0	1
15	UO	0	1
17	UQ	0	4
18	UR	0	3
20	UT	0	7
21	UU	0	4
23	UX	0	1
26	CD	0	1
27	CE	0	1
30	CI	0	1
31	CJ	0	2
32	CK	0	1
34	CM	0	1
36	JA	0	1
36	JB	0	3
37	JC	0	2
38	JE	0	2
43	JM	0	1
44	JN	0	1
46	JP	0	4
48	DA	0	3
49	DE	0	1
52	DH	0	1
58	DQ	0	2
59	DS	0	1
60	DW	0	1
61	DX	0	3
All	All	0	82

The worst 5 of 2498 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	CL	1081	SER	CA-CB	-16.22	1.28	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	D2	280	A	N9-C4	-13.97	1.29	1.37
67	D4	61	G	C5-C4	-12.91	1.29	1.38
66	D3	584	C	N1-C6	-12.87	1.29	1.37
67	D4	61	G	N7-C5	-12.51	1.31	1.39

The worst 5 of 1402 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
65	D2	312	U	O4'-C1'-N1	19.10	123.48	108.20
13	UM	443	PRO	N-CD-CG	-16.65	78.23	103.20
67	D4	27	U	N3-C2-O2	-15.30	111.49	122.20
65	D2	233	G	N3-C4-C5	14.71	135.96	128.60
21	UU	494	LEU	CB-CG-CD2	-14.58	86.21	111.00

There are no chirality outliers.

5 of 82 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	157	ASP	Peptide
1	UA	202	ASP	Peptide
1	UA	288	ASP	Peptide
1	UA	516	SER	Peptide
4	UD	117	ILE	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	UA	6635	0	6524	147	0
2	UB	3743	0	3445	80	0
3	UC	1026	0	1080	40	0
4	UD	5361	0	5364	141	0
5	UE	3772	0	3806	99	0
6	UF	2487	0	2533	59	0
7	UG	4218	0	4223	94	0
8	UH	2690	0	1931	69	0
9	UI	846	0	904	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	UJ	6857	0	5023	85	0
11	UK	2016	0	2093	59	0
12	UL	6720	0	6753	196	0
13	UM	5957	0	5992	182	0
14	UN	1207	0	1201	26	0
15	UO	3911	0	3906	119	0
16	UP	495	0	561	13	0
17	UQ	6662	0	6588	173	0
18	UR	3791	0	3772	89	0
19	US	3650	0	3365	102	0
20	UT	11108	0	4748	16	0
21	UU	6678	0	6652	131	0
22	UV	8725	0	8841	190	0
23	UX	1395	0	1474	40	0
24	UZ	2006	0	2118	54	0
25	CA	1881	0	1928	31	0
25	CB	1782	0	1826	54	0
26	CD	2994	0	3018	81	0
27	CE	2985	0	2703	59	0
28	CF	931	0	983	18	0
28	CG	928	0	976	34	0
29	CH	3634	0	3662	112	0
30	CI	1530	0	1572	36	0
31	CJ	2296	0	2325	64	0
32	CK	1667	0	1701	50	0
33	CL	6332	0	6516	190	0
34	CM	2781	0	2878	73	0
35	CN	1893	0	1875	37	0
36	JA	5892	0	5420	146	0
36	JB	4132	0	1819	17	0
37	JC	2845	0	2761	91	0
38	JE	1125	0	1101	46	0
39	JF	1701	0	1767	42	0
39	JG	1799	0	1872	48	0
40	JH	1295	0	570	2	0
41	JJ	1448	0	1524	43	0
42	JK	334	0	313	12	0
43	JM	1137	0	1187	28	0
44	JN	1428	0	1425	25	0
45	JO	1930	0	2025	38	0
46	JP	3725	0	3679	100	0
47	JQ	381	0	255	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	DA	1912	0	2023	53	0
49	DE	1944	0	2030	69	0
50	DF	1669	0	1724	31	0
51	DG	1755	0	1846	68	0
52	DH	1477	0	1568	49	0
53	DI	1399	0	1431	47	0
54	DJ	1428	0	1506	48	0
55	DL	1129	0	1196	35	0
56	DN	1192	0	1255	27	0
57	DO	881	0	910	21	0
58	DQ	973	0	1029	23	0
59	DS	516	0	222	12	0
60	DW	1021	0	1060	24	0
61	DX	786	0	843	20	0
62	DY	767	0	787	53	0
63	Db	610	0	629	0	0
64	Dc	497	0	535	0	0
65	D2	11138	0	5569	138	0
66	D3	25549	0	12882	423	0
67	D4	3712	0	1876	51	0
68	Db	1	0	0	0	0
68	UX	1	0	0	0	0
69	CL	32	0	12	3	0
All	All	223151	0	191511	4355	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 11.

The worst 5 of 4355 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)
33:CL:80:THR:CG2	33:CL:141:LEU:CD2	2.05	1.33
12:UL:349:SER:HA	12:UL:369:TYR:O	1.21	1.30
1:UA:315:GLU:OE1	41:JJ:273:ARG:HG3	1.34	1.28
7:UG:132:GLY:HA3	7:UG:150:LEU:O	1.24	1.26
13:UM:30:LYS:HA	13:UM:45:LEU:O	1.37	1.21

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	UA	830/923 (90%)	730 (88%)	99 (12%)	1 (0%)	51	84
2	UB	496/810 (61%)	458 (92%)	35 (7%)	3 (1%)	25	63
3	UC	124/610 (20%)	113 (91%)	10 (8%)	1 (1%)	19	57
4	UD	663/776 (85%)	585 (88%)	78 (12%)	0	100	100
5	UE	465/643 (72%)	401 (86%)	63 (14%)	1 (0%)	47	79
6	UF	283/440 (64%)	273 (96%)	10 (4%)	0	100	100
7	UG	529/554 (96%)	471 (89%)	58 (11%)	0	100	100
8	UH	423/713 (59%)	305 (72%)	94 (22%)	24 (6%)	1	21
9	UI	98/575 (17%)	92 (94%)	6 (6%)	0	100	100
10	UJ	1093/1769 (62%)	1038 (95%)	55 (5%)	0	100	100
11	UK	237/250 (95%)	217 (92%)	19 (8%)	1 (0%)	34	71
12	UL	828/943 (88%)	733 (88%)	94 (11%)	1 (0%)	51	84
13	UM	750/817 (92%)	666 (89%)	84 (11%)	0	100	100
14	UN	141/145 (97%)	124 (88%)	16 (11%)	1 (1%)	22	60
15	UO	489/513 (95%)	433 (88%)	55 (11%)	1 (0%)	47	79
16	UP	58/214 (27%)	57 (98%)	1 (2%)	0	100	100
17	UQ	820/896 (92%)	720 (88%)	98 (12%)	2 (0%)	47	79
18	UR	473/594 (80%)	432 (91%)	40 (8%)	1 (0%)	47	79
19	US	471/552 (85%)	421 (89%)	49 (10%)	1 (0%)	47	79
20	UT	2189/2493 (88%)	2067 (94%)	122 (6%)	0	100	100
21	UU	842/939 (90%)	737 (88%)	105 (12%)	0	100	100
22	UV	1068/1237 (86%)	1006 (94%)	62 (6%)	0	100	100
23	UX	170/189 (90%)	151 (89%)	18 (11%)	1 (1%)	25	63
24	UZ	245/274 (89%)	217 (89%)	28 (11%)	0	100	100
25	CA	238/327 (73%)	220 (92%)	18 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	CB	224/327 (68%)	197 (88%)	27 (12%)	0	100	100
26	CD	376/504 (75%)	351 (93%)	25 (7%)	0	100	100
27	CE	431/511 (84%)	394 (91%)	37 (9%)	0	100	100
28	CF	121/126 (96%)	112 (93%)	9 (7%)	0	100	100
28	CG	121/126 (96%)	111 (92%)	10 (8%)	0	100	100
29	CH	446/573 (78%)	399 (90%)	45 (10%)	2 (0%)	34	71
30	CI	180/183 (98%)	162 (90%)	18 (10%)	0	100	100
31	CJ	278/290 (96%)	247 (89%)	30 (11%)	1 (0%)	34	71
32	CK	203/593 (34%)	177 (87%)	25 (12%)	1 (0%)	29	67
33	CL	771/1183 (65%)	704 (91%)	63 (8%)	4 (0%)	29	67
34	CM	358/367 (98%)	334 (93%)	24 (7%)	0	100	100
35	CN	224/297 (75%)	210 (94%)	14 (6%)	0	100	100
36	JA	802/1056 (76%)	717 (89%)	85 (11%)	0	100	100
36	JB	827/1056 (78%)	736 (89%)	91 (11%)	0	100	100
37	JC	350/707 (50%)	308 (88%)	42 (12%)	0	100	100
38	JE	134/357 (38%)	119 (89%)	14 (10%)	1 (1%)	22	60
39	JF	212/252 (84%)	201 (95%)	11 (5%)	0	100	100
39	JG	226/252 (90%)	215 (95%)	11 (5%)	0	100	100
40	JH	257/483 (53%)	244 (95%)	13 (5%)	0	100	100
41	JJ	180/274 (66%)	166 (92%)	13 (7%)	1 (1%)	25	63
42	JK	40/534 (8%)	30 (75%)	10 (25%)	0	100	100
43	JM	129/217 (59%)	113 (88%)	15 (12%)	1 (1%)	19	57
44	JN	178/346 (51%)	154 (86%)	19 (11%)	5 (3%)	5	34
45	JO	232/316 (73%)	215 (93%)	17 (7%)	0	100	100
46	JP	453/489 (93%)	412 (91%)	41 (9%)	0	100	100
47	JQ	59/206 (29%)	49 (83%)	9 (15%)	1 (2%)	9	43
48	DA	236/255 (92%)	207 (88%)	29 (12%)	0	100	100
49	DE	243/261 (93%)	224 (92%)	19 (8%)	0	100	100
50	DF	211/225 (94%)	188 (89%)	23 (11%)	0	100	100
51	DG	216/236 (92%)	203 (94%)	13 (6%)	0	100	100
52	DH	182/190 (96%)	160 (88%)	22 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	DI	173/200 (86%)	160 (92%)	13 (8%)	0	100	100
54	DJ	175/197 (89%)	160 (91%)	15 (9%)	0	100	100
55	DL	138/156 (88%)	125 (91%)	13 (9%)	0	100	100
56	DN	148/151 (98%)	127 (86%)	21 (14%)	0	100	100
57	DO	118/137 (86%)	107 (91%)	10 (8%)	1 (1%)	19	57
58	DQ	123/143 (86%)	114 (93%)	9 (7%)	0	100	100
59	DS	98/147 (67%)	89 (91%)	9 (9%)	0	100	100
60	DW	127/130 (98%)	106 (84%)	21 (16%)	0	100	100
61	DX	101/145 (70%)	89 (88%)	12 (12%)	0	100	100
62	DY	95/135 (70%)	79 (83%)	16 (17%)	0	100	100
63	Db	79/82 (96%)	66 (84%)	13 (16%)	0	100	100
64	Dc	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
All	All	24359/32678 (74%)	22000 (90%)	2302 (10%)	57 (0%)	50	79

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	UB	399	HIS
8	UH	59	PRO
8	UH	61	PRO
8	UH	68	PRO
8	UH	127	TYR

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	UA	730/812 (90%)	729 (100%)	1 (0%)	93	97
2	UB	345/732 (47%)	345 (100%)	0	100	100
3	UC	107/538 (20%)	103 (96%)	4 (4%)	34	60
4	UD	615/713 (86%)	612 (100%)	3 (0%)	88	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	UE	428/574 (75%)	426 (100%)	2 (0%)	88	93
6	UF	277/414 (67%)	275 (99%)	2 (1%)	84	90
7	UG	462/480 (96%)	462 (100%)	0	100	100
8	UH	150/657 (23%)	149 (99%)	1 (1%)	84	90
9	UI	97/533 (18%)	97 (100%)	0	100	100
10	UJ	390/1633 (24%)	388 (100%)	2 (0%)	88	93
11	UK	226/234 (97%)	223 (99%)	3 (1%)	69	82
12	UL	746/832 (90%)	745 (100%)	1 (0%)	93	97
13	UM	665/719 (92%)	663 (100%)	2 (0%)	92	95
14	UN	135/135 (100%)	135 (100%)	0	100	100
15	UO	437/454 (96%)	435 (100%)	2 (0%)	88	93
16	UP	57/196 (29%)	56 (98%)	1 (2%)	59	77
17	UQ	769/826 (93%)	763 (99%)	6 (1%)	81	89
18	UR	424/529 (80%)	421 (99%)	3 (1%)	84	90
19	US	360/506 (71%)	360 (100%)	0	100	100
21	UU	743/819 (91%)	740 (100%)	3 (0%)	91	94
22	UV	985/1125 (88%)	980 (100%)	5 (0%)	88	93
23	UX	156/169 (92%)	155 (99%)	1 (1%)	86	91
24	UZ	230/256 (90%)	228 (99%)	2 (1%)	78	87
25	CA	202/240 (84%)	200 (99%)	2 (1%)	76	86
25	CB	192/240 (80%)	191 (100%)	1 (0%)	88	93
26	CD	326/435 (75%)	325 (100%)	1 (0%)	92	95
27	CE	244/433 (56%)	244 (100%)	0	100	100
28	CF	102/104 (98%)	102 (100%)	0	100	100
28	CG	101/104 (97%)	100 (99%)	1 (1%)	76	86
29	CH	395/503 (78%)	393 (100%)	2 (0%)	88	93
30	CI	171/172 (99%)	170 (99%)	1 (1%)	86	91
31	CJ	251/258 (97%)	249 (99%)	2 (1%)	81	89
32	CK	187/535 (35%)	187 (100%)	0	100	100
33	CL	690/1039 (66%)	684 (99%)	6 (1%)	78	87
34	CM	307/312 (98%)	306 (100%)	1 (0%)	92	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	CN	212/274 (77%)	212 (100%)	0	100	100
36	JA	549/934 (59%)	545 (99%)	4 (1%)	84	90
37	JC	318/636 (50%)	318 (100%)	0	100	100
38	JE	119/315 (38%)	118 (99%)	1 (1%)	81	89
39	JF	195/222 (88%)	195 (100%)	0	100	100
39	JG	206/222 (93%)	206 (100%)	0	100	100
41	JJ	159/238 (67%)	156 (98%)	3 (2%)	57	75
42	JK	35/482 (7%)	35 (100%)	0	100	100
43	JM	124/200 (62%)	123 (99%)	1 (1%)	81	89
44	JN	141/304 (46%)	141 (100%)	0	100	100
45	JO	215/289 (74%)	213 (99%)	2 (1%)	78	87
46	JP	412/443 (93%)	412 (100%)	0	100	100
47	JQ	22/192 (12%)	21 (96%)	1 (4%)	27	56
48	DA	212/224 (95%)	209 (99%)	3 (1%)	67	81
49	DE	209/222 (94%)	206 (99%)	3 (1%)	67	81
50	DF	180/191 (94%)	180 (100%)	0	100	100
51	DG	187/201 (93%)	186 (100%)	1 (0%)	88	93
52	DH	164/170 (96%)	162 (99%)	2 (1%)	71	83
53	DI	142/161 (88%)	141 (99%)	1 (1%)	84	90
54	DJ	151/166 (91%)	150 (99%)	1 (1%)	84	90
55	DL	125/137 (91%)	125 (100%)	0	100	100
56	DN	127/128 (99%)	127 (100%)	0	100	100
57	DO	91/105 (87%)	91 (100%)	0	100	100
58	DQ	105/119 (88%)	105 (100%)	0	100	100
60	DW	110/111 (99%)	110 (100%)	0	100	100
61	DX	85/120 (71%)	83 (98%)	2 (2%)	49	69
62	DY	81/113 (72%)	81 (100%)	0	100	100
63	Db	70/71 (99%)	70 (100%)	0	100	100
64	Dc	56/60 (93%)	56 (100%)	0	100	100
All	All	17504/25311 (69%)	17418 (100%)	86 (0%)	89	93

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	CL	119	GLU
45	JO	280	LYS
33	CL	960	ARG
38	JE	356	ARG
48	DA	19	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
19	US	200	ASN
26	CD	23	GLN
52	DH	170	GLN
19	US	256	ASN
24	UZ	117	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
65	D2	518/700 (74%)	166 (32%)	9 (1%)
66	D3	1172/1808 (64%)	423 (36%)	28 (2%)
67	D4	169/175 (96%)	62 (36%)	2 (1%)
All	All	1859/2683 (69%)	651 (35%)	39 (2%)

5 of 651 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
65	D2	6	A
65	D2	7	A
65	D2	8	A
65	D2	9	G
65	D2	15	G

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
66	D3	1572	G
66	D3	1746	A
66	D3	1573	A
66	D3	1620	C
67	D4	24	U

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 3 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
69	GTP	CL	2001	-	26,34,34	0.93	1 (3%)	32,54,54	1.49	5 (15%)

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	CL	2001	-	-	4/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	CL	2001	GTP	C6-N1	-2.56	1.34	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
69	CL	2001	GTP	PA-O3A-PB	-3.97	119.20	132.83
69	CL	2001	GTP	PB-O3B-PG	-3.56	120.62	132.83
69	CL	2001	GTP	C3'-C2'-C1'	3.11	105.67	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
69	CL	2001	GTP	C5-C6-N1	2.35	118.11	113.95
69	CL	2001	GTP	C8-N7-C5	2.26	107.29	102.99

There are no chirality outliers.

All (4) torsion outliers are listed below:

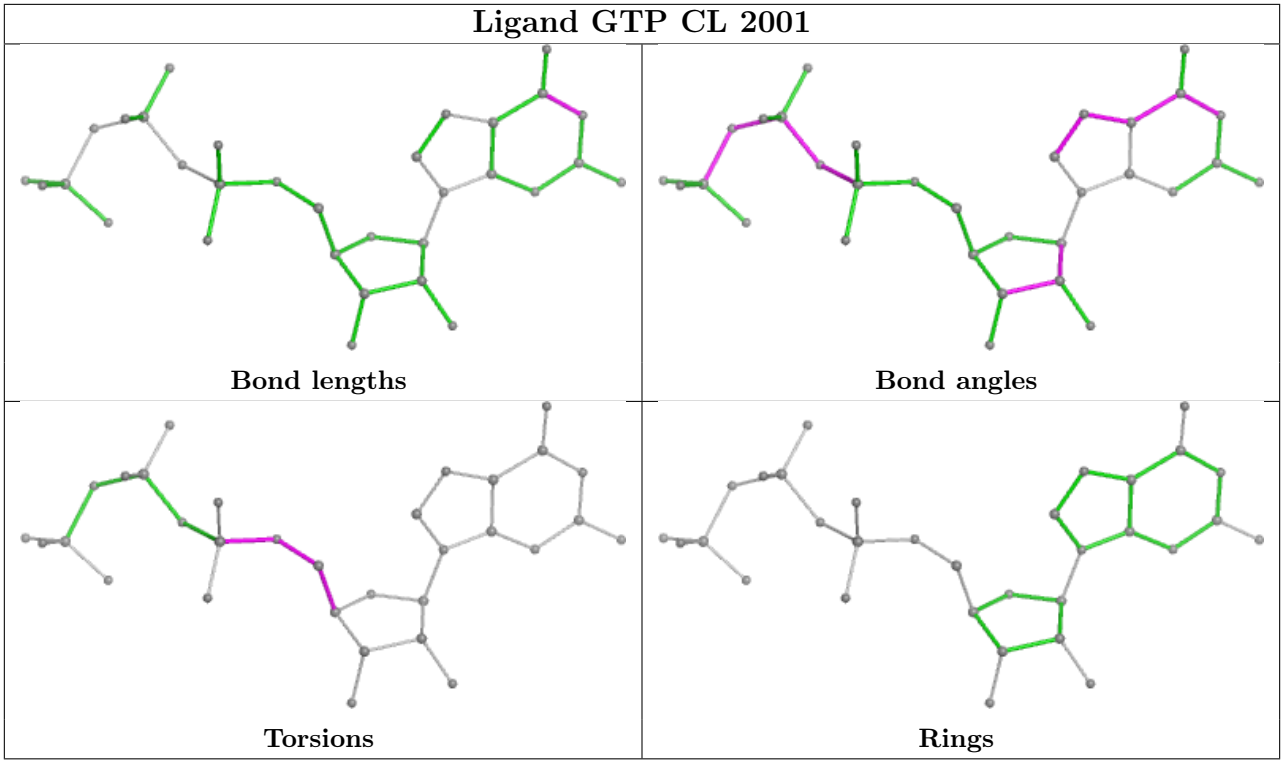
Mol	Chain	Res	Type	Atoms
69	CL	2001	GTP	C5'-O5'-PA-O1A
69	CL	2001	GTP	C3'-C4'-C5'-O5'
69	CL	2001	GTP	C4'-C5'-O5'-PA
69	CL	2001	GTP	C5'-O5'-PA-O3A

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	CL	2001	GTP	3	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 then 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
67	D4	5
14	UN	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	UN	349:SER	C	827:GLN	N	110.52
1	D4	118:A	O3'	197:G	P	24.98
1	D4	267:A	O3'	304:U	P	18.78
1	D4	106:C	O3'	111:G	P	16.51
1	D4	206:C	O3'	245:U	P	14.23

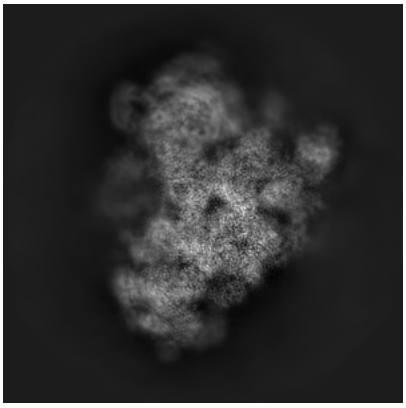
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11358. These allow visual inspection of the internal detail of the map and identification of artifacts.

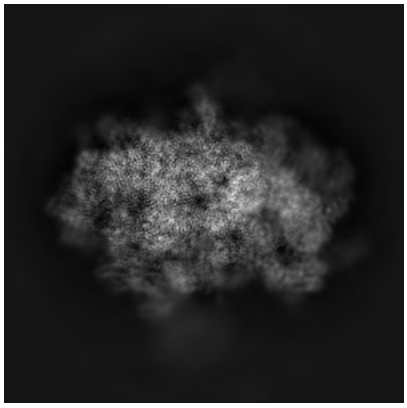
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

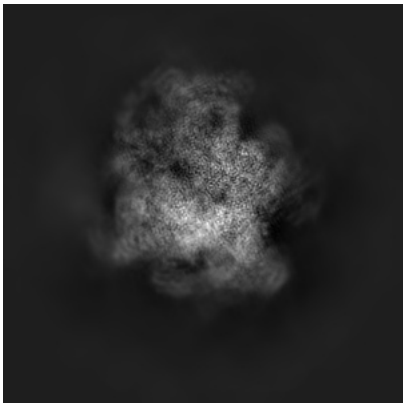
6.1.1 Primary map



X



Y

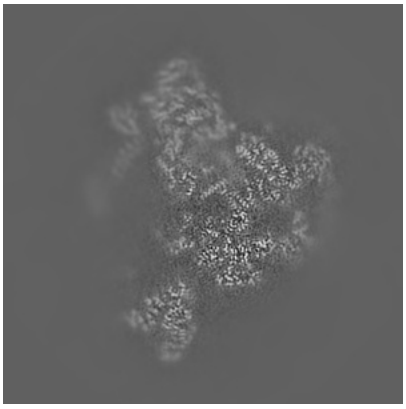


Z

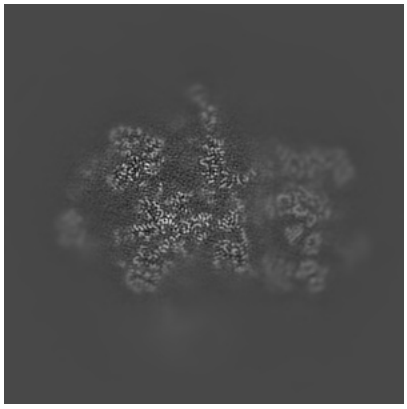
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

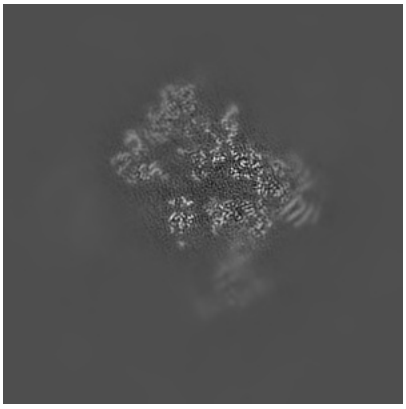
6.2.1 Primary map



X Index: 240



Y Index: 240

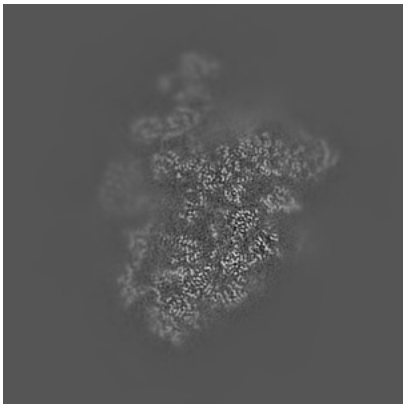


Z Index: 240

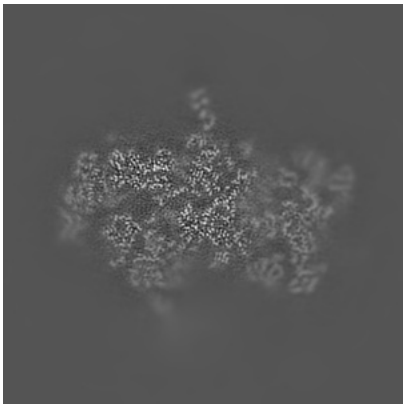
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

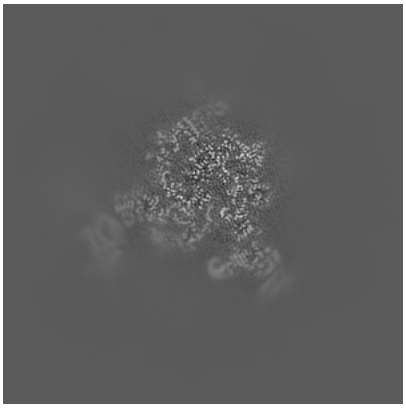
6.3.1 Primary map



X Index: 270



Y Index: 225

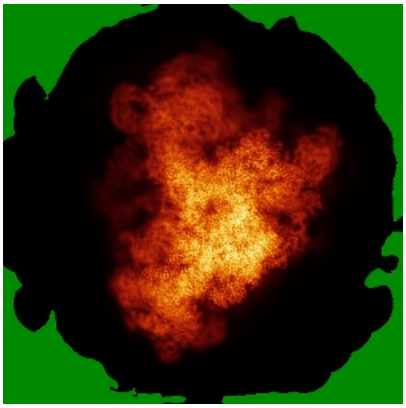


Z Index: 182

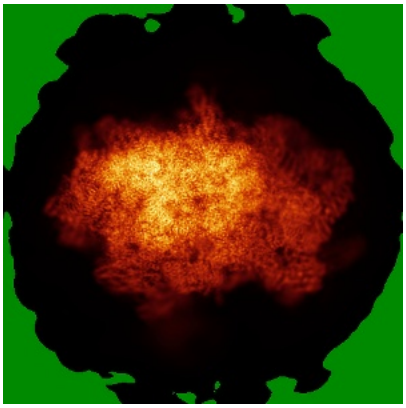
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

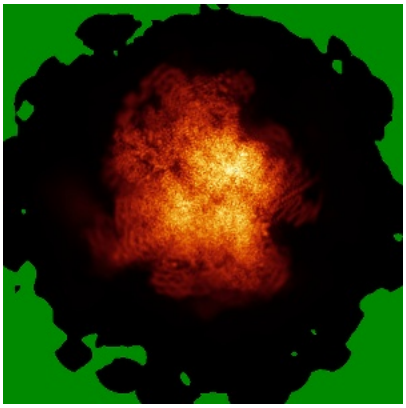
6.4.1 Primary map



X



Y

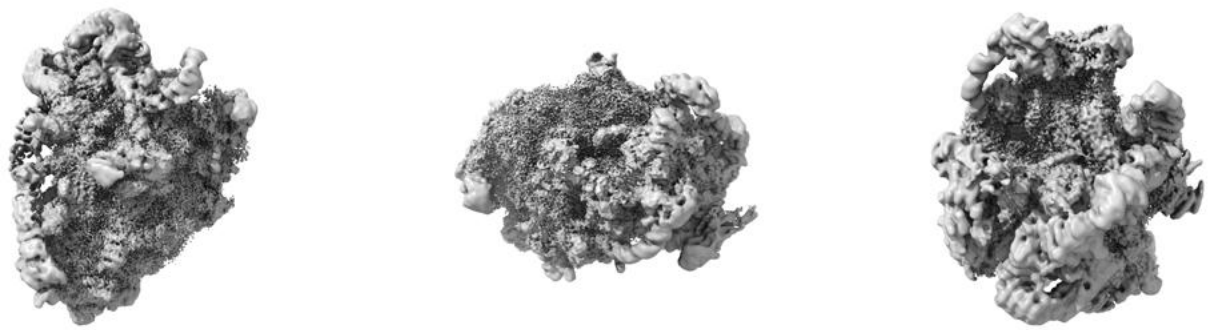


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

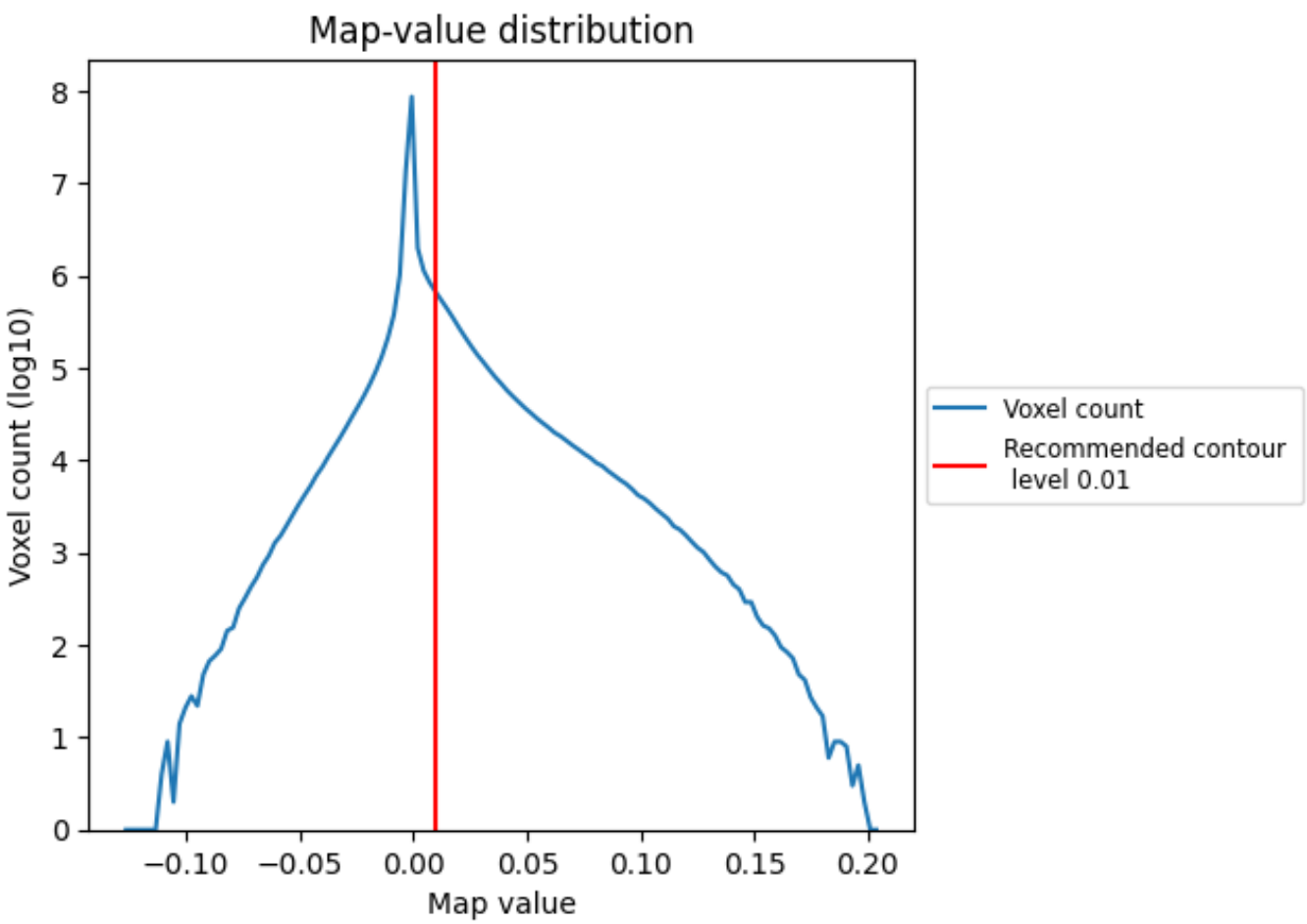
6.6 Mask visualisation (i)

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

7 Map analysis (i)

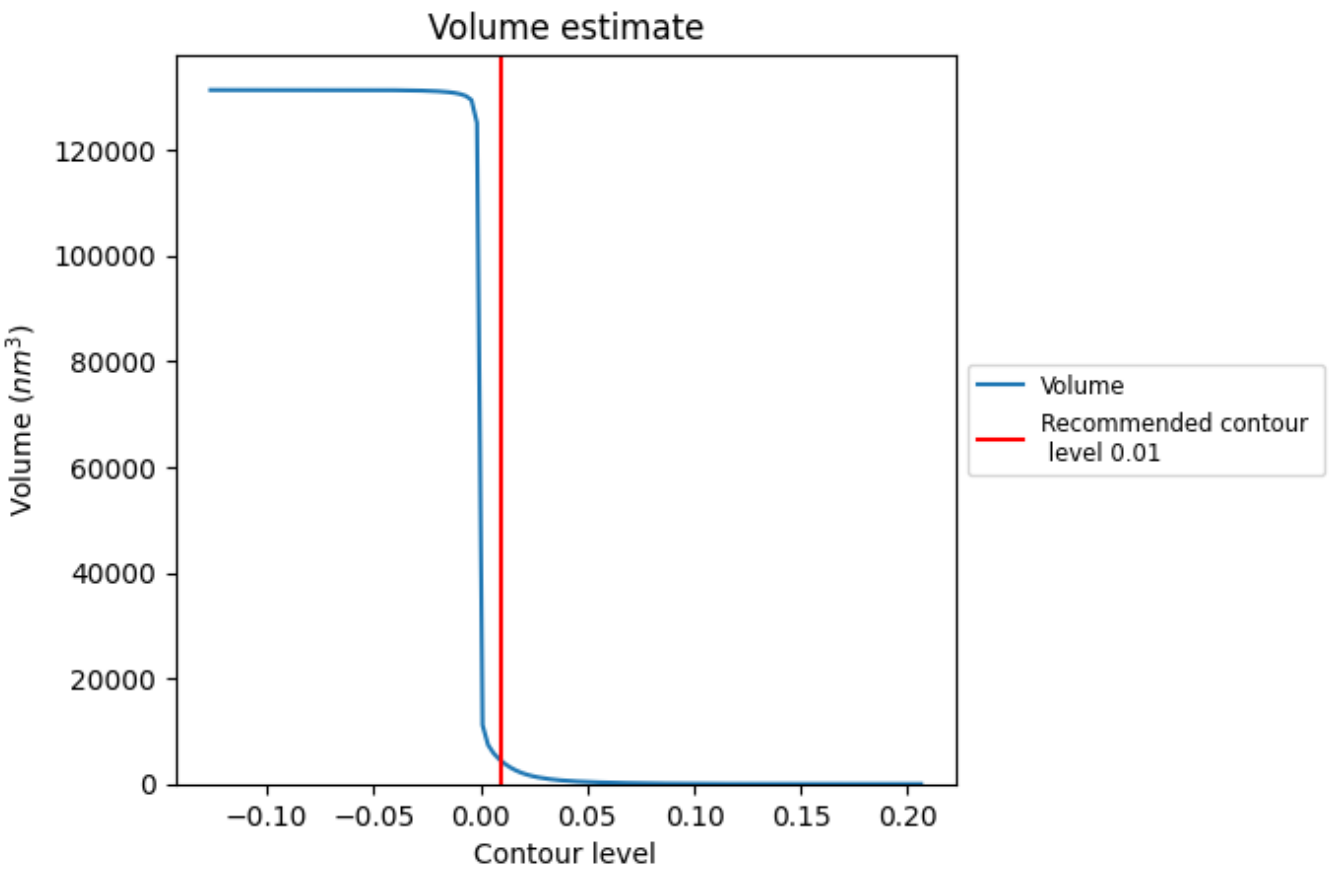
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

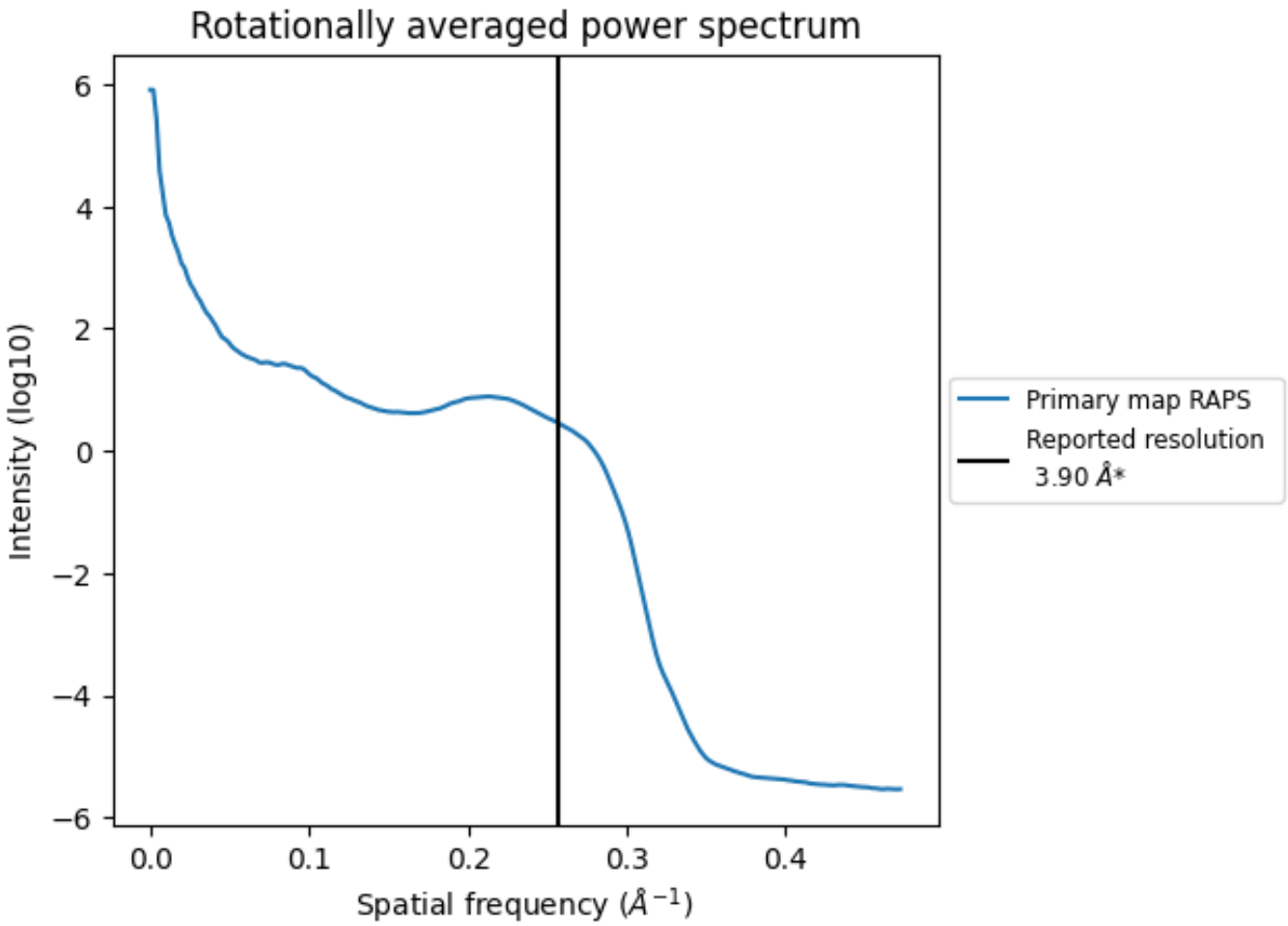
7.2 Volume estimate (i)



The volume at the recommended contour level is 4278 nm^3; this corresponds to an approximate mass of 3864 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)

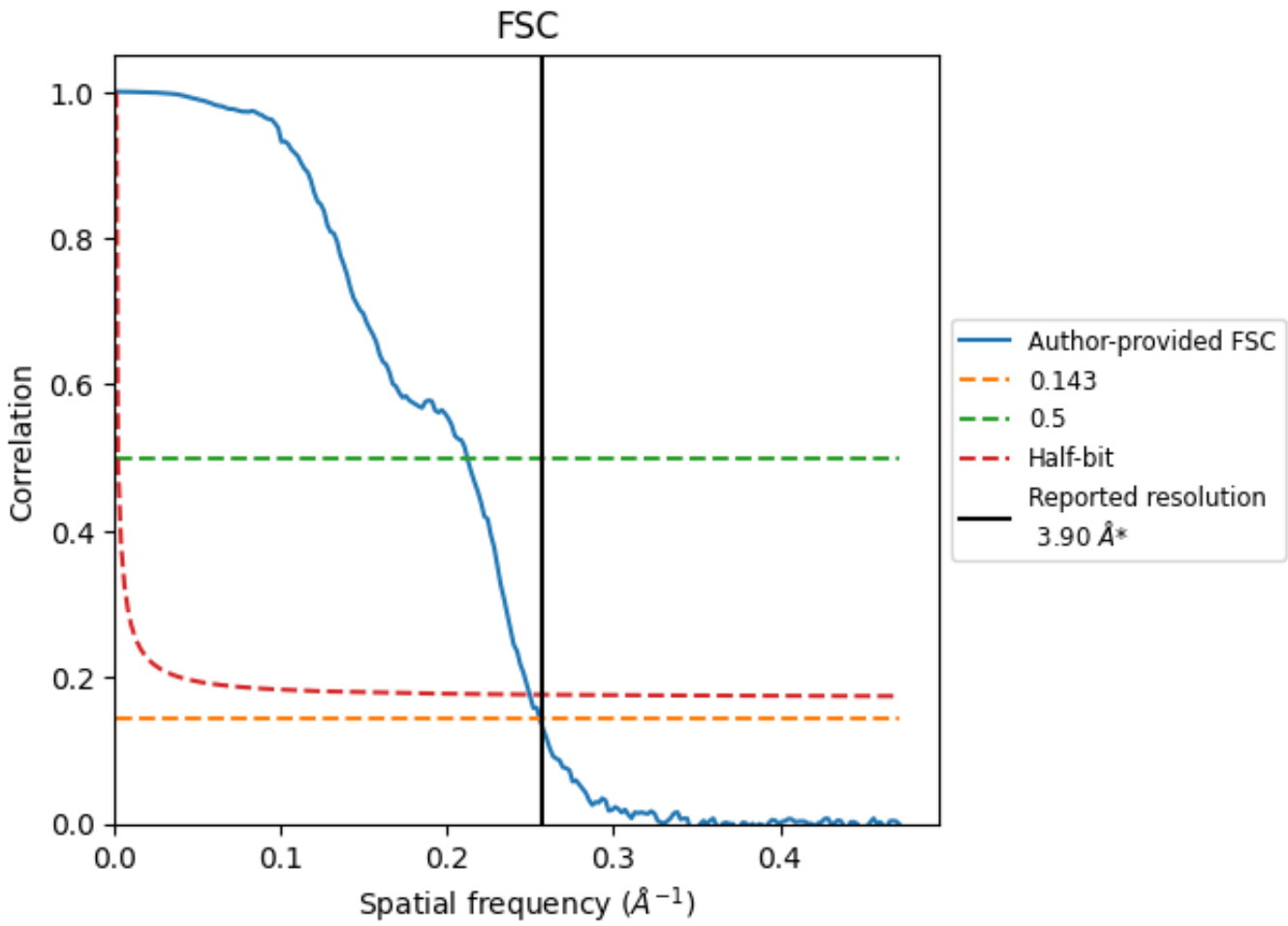


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

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 0.256 Å^{-1}

8.2 Resolution estimates (i)

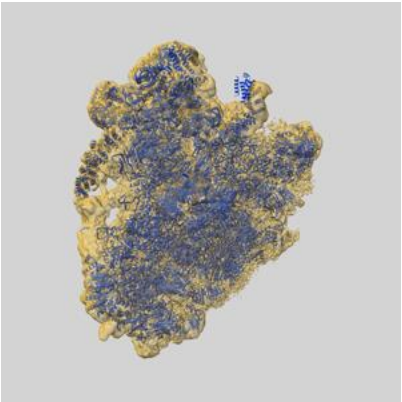
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.91	4.72	4.01
Unmasked-calculated*	-	-	-

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

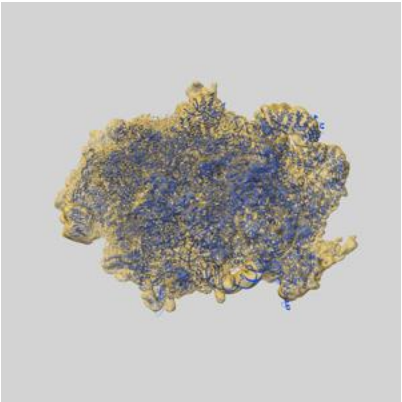
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11358 and PDB model 6ZQB. Per-residue inclusion information can be found in section 3 on page 17.

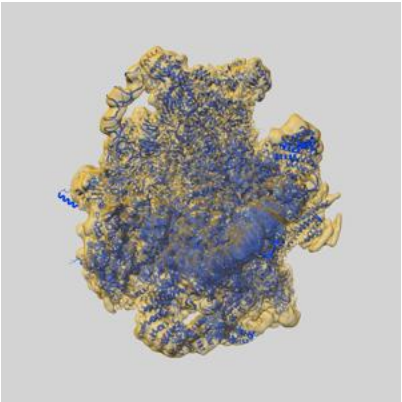
9.1 Map-model overlay (i)



X



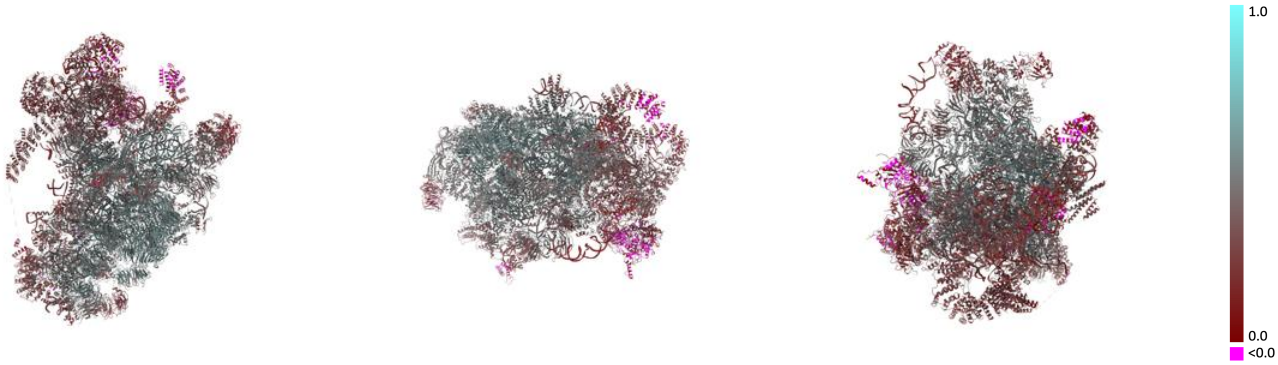
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

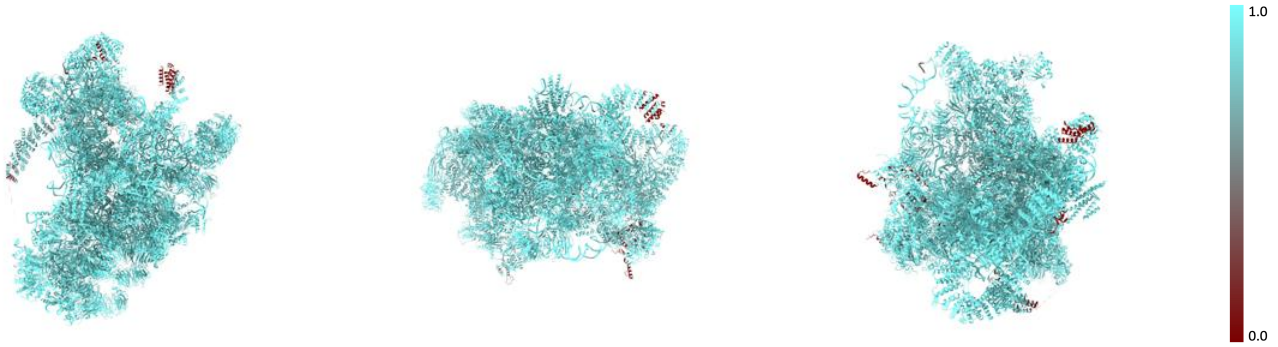
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

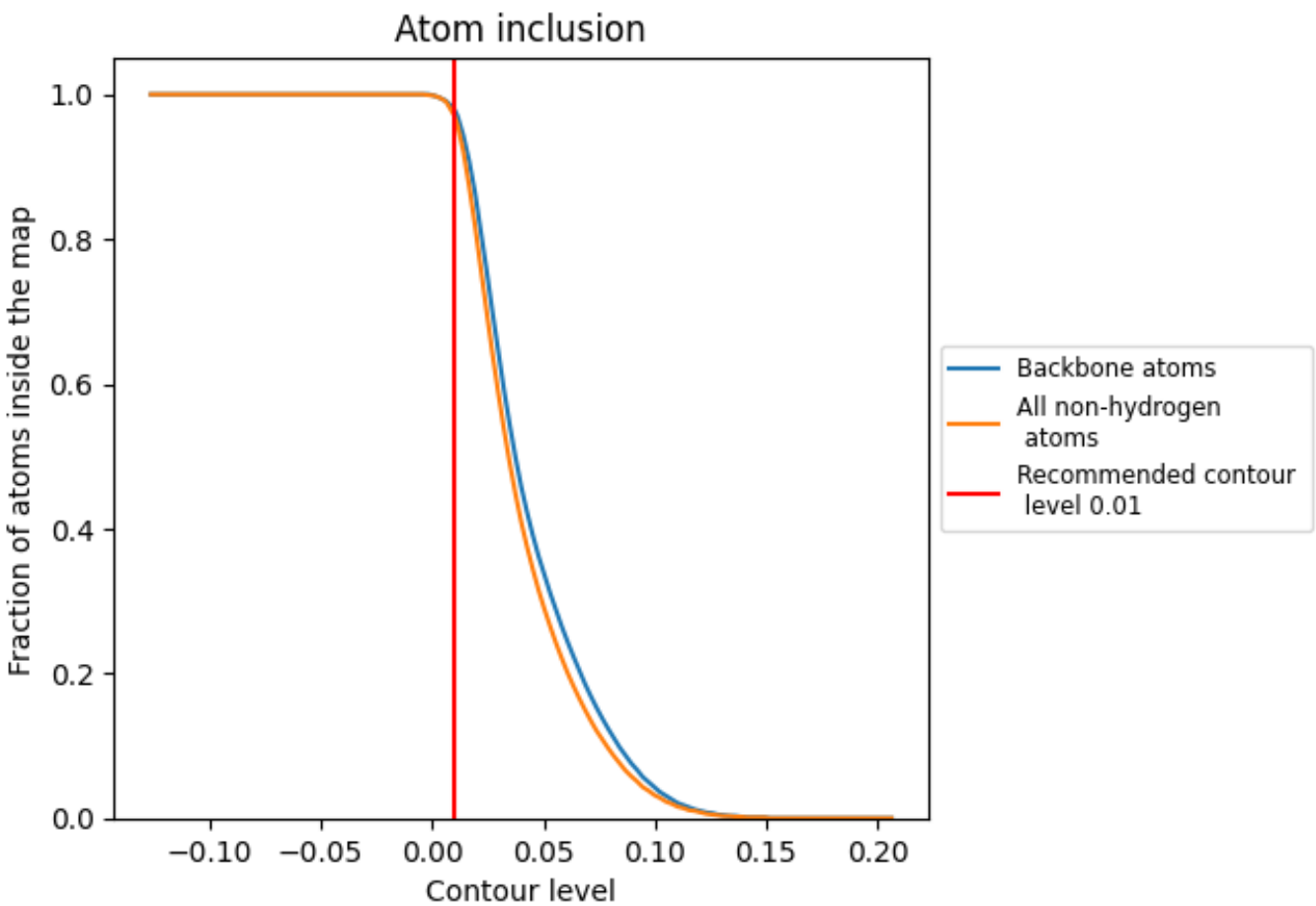
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.9700	0.4180
CA	0.9850	0.5400
CB	0.9790	0.4490
CD	0.9810	0.4390
CE	0.9870	0.4440
CF	0.9880	0.5340
CG	0.9830	0.4950
CH	0.9690	0.4040
CI	0.9870	0.5690
CJ	0.9840	0.5330
CK	0.9830	0.4980
CL	0.9800	0.4960
CM	0.9880	0.4760
CN	0.9400	0.2930
D2	0.9930	0.4430
D3	0.9800	0.3870
D4	0.9970	0.4560
DA	0.9620	0.4930
DE	0.9710	0.3350
DF	0.9870	0.5290
DG	0.9460	0.2890
DH	0.9570	0.3480
DI	0.9700	0.3140
DJ	0.9820	0.5030
DL	0.9690	0.3070
DN	0.9610	0.4690
DO	0.9940	0.5030
DQ	0.9920	0.5580
DS	0.8970	0.2850
DW	0.9810	0.5160
DX	0.9850	0.5290
DY	0.9410	0.2750
Db	0.9820	0.5160
Dc	0.9900	0.5280
JA	0.9490	0.2970

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
JB	0.7950	0.1190
JC	0.9370	0.3250
JE	0.9340	0.3590
JF	0.9640	0.3740
JG	0.9800	0.4690
JH	0.8460	0.1060
JJ	0.9770	0.4150
JK	0.9670	0.2650
JM	0.9750	0.4760
JN	0.9810	0.5150
JO	0.9840	0.4700
JP	0.9900	0.5540
JQ	0.9290	0.3940
UA	0.9910	0.5600
UB	0.9620	0.3210
UC	0.9800	0.4710
UD	0.9850	0.4520
UE	0.9900	0.4920
UF	0.9750	0.4290
UG	0.9890	0.5480
UH	0.9820	0.2700
UI	0.9810	0.3370
UJ	0.9280	0.3780
UK	0.9840	0.4860
UL	0.9820	0.4370
UM	0.9760	0.4100
UN	0.9850	0.5020
UO	0.9900	0.5010
UP	0.9650	0.4030
UQ	0.9900	0.4770
UR	0.9930	0.5470
US	0.9700	0.3530
UT	0.9300	0.2440
UU	0.9950	0.5490
UV	0.9510	0.3270
UX	0.9880	0.5520
UZ	0.9840	0.4270