



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 03:29 AM UTC

PDB ID : 6ZQC / pdb_00006zqc
EMDB ID : EMD-11359
Title : Cryo-EM structure of the 90S pre-ribosome from *Saccharomyces cerevisiae*, state Pre-A1
Authors : Cheng, J.; Lau, B.; Venuta, G.L.; Berninghausen, O.; Hurt, E.; Beckmann, R.
Deposited on : 2020-07-09
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

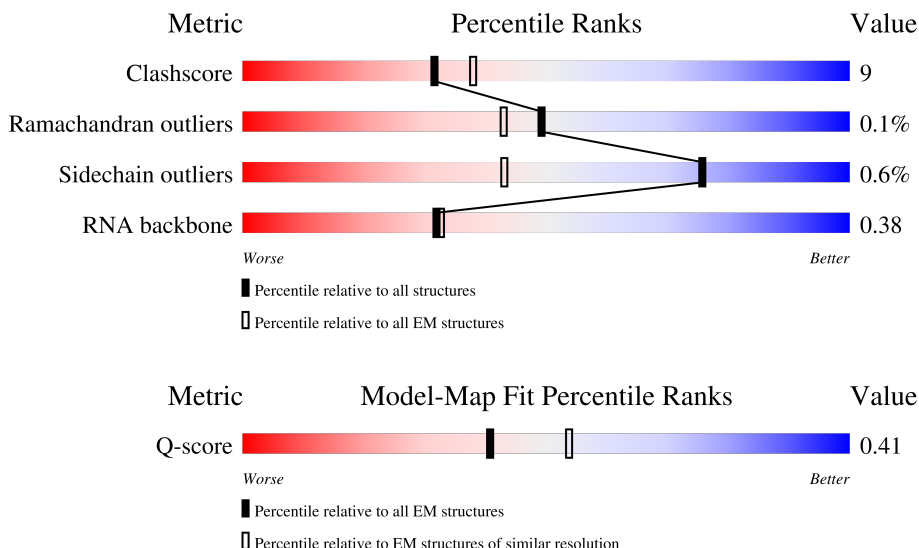
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



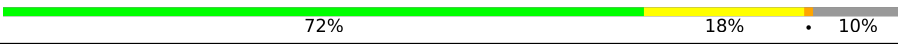
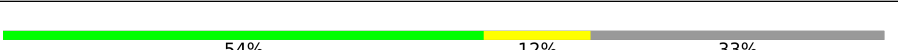
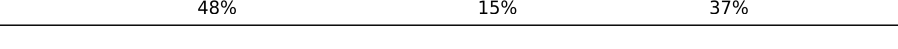
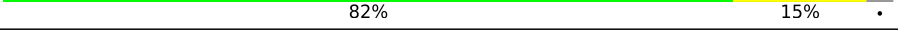
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	CA	327	
1	CB	327	
2	DA	255	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	JA	1056	
3	JB	1056	
4	UA	923	
5	UB	810	
6	UC	610	
7	UD	776	
8	UE	643	
9	UF	440	
10	UG	554	
11	UH	713	
12	UI	575	
13	UJ	1769	
14	UK	250	
15	UL	943	
16	UM	817	
17	UN	899	
18	UO	513	
19	UP	214	
20	UQ	896	
21	UR	594	
22	US	552	
23	UT	2493	
24	UU	939	
25	UV	1237	
26	UX	189	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	UZ	274	
28	CD	504	
29	CE	511	
30	CF	126	
30	CG	126	
31	CH	573	
32	CI	183	
33	CJ	290	
34	CK	593	
35	CL	1183	
36	CM	367	
37	CN	297	
38	JC	707	
39	JF	252	
39	JG	252	
40	JH	483	
41	JI	1729	
42	JJ	274	
43	JK	534	
44	JM	217	
45	JN	346	
46	JO	316	
47	JP	489	
48	JQ	206	
49	DE	261	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
50	DF	225	
51	DG	236	
52	DH	190	
53	DI	200	
54	DJ	197	
55	DL	156	
56	DN	151	
57	DO	137	
58	DQ	143	
59	DS	146	
60	DW	130	
61	DX	145	
62	DY	135	
63	Db	82	
64	Dc	67	
65	D2	700	
66	D3	1808	
67	D4	333	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
70	GTP	CL	2001	-	-	X	-

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 234757 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 rRNA 2'-O-methyltransferase fibrillarin.

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

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 3 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	JA	812	Total	C	N	O	S	0	0
			5916	3745	1044	1102	25		
3	JB	835	Total	C	N	O		0	0
			4132	2462	835	835			

- Molecule 4 is a protein called Periodic tryptophan protein 2.

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

- Molecule 5 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	UB	507	Total	C	N	O	S	0	0
			3734	2367	663	695	9		

- Molecule 6 is a protein called Something about silencing protein 10.

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

- Molecule 7 is a protein called U3 small nucleolar RNA-associated protein 4.

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

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 9 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 10 is a protein called U3 small nucleolar RNA-associated protein 7.

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

- Molecule 11 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UH	442	Total	C	N	O	S	0	0
			2701	1680	494	524	3		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	UI	104	Total	C	N	O	S	0	0
			860	556	152	150	2		

- Molecule 13 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	UJ	1116	Total	C	N	O	S	0	0
			8961	5802	1468	1666	25		

- Molecule 14 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UK	242	Total	C	N	O	S	0	0
			2021	1254	389	371	7		

- Molecule 15 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UL	842	Total	C	N	O	S	0	0
			6726	4303	1129	1267	27		

- Molecule 16 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UM	762	Total	C	N	O	S	0	0
			5969	3785	1007	1149	28		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UN	147	Total	C	N	O	S	0	0
			1227	765	233	227	2		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 19 is a protein called Bud site selection protein 21.

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

- Molecule 20 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	UR	482	Total	C	N	O	S	0	0
			3799	2405	669	715	10		

- Molecule 22 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	US	494	Total	C	N	O	S	0	0
			3622	2326	617	667	12		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	UT	2255	Total	C	N	O	S	0	0
			17290	11076	2927	3235	52		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 21.

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

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	UV	1081	Total	C	N	O	S	0	0
			8736	5681	1440	1591	24		

- Molecule 26 is a protein called rRNA-processing protein FCF1.

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

- Molecule 27 is a protein called Ribosome biogenesis protein UTP30.

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

- Molecule 28 is a protein called Nucleolar protein 56.

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

- Molecule 29 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CE	435	Total	C	N	O	S	0	0
			3325	2093	571	653	8		

- Molecule 30 is a protein called 13 kDa ribonucleoprotein-associated protein.

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

- Molecule 31 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CH	465	Total	C	N	O	S	0	0
			3725	2365	653	697	10		

- Molecule 32 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

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

- Molecule 33 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

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

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

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

- Molecule 35 is a protein called Ribosome biogenesis protein BMS1.

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

- Molecule 36 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 37 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 38 is a protein called Ribosome biogenesis protein ENP2.

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

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

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

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

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

- Molecule 41 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Jl	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 42 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	JJ	182	Total	C	N	O	S	0	0
			1442	923	259	256	4		

- Molecule 43 is a protein called Protein BFR2.

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

- Molecule 44 is a protein called rRNA-processing protein FCF2.

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

- Molecule 45 is a protein called Protein FAF1.

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

- Molecule 46 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	JO	230	Total	C	N	O	S	0	0
			1876	1203	330	332	11		

- Molecule 47 is a protein called Protein SOF1.

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

- Molecule 48 is a protein called Regulator of rDNA transcription protein 14.

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

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

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

- Molecule 50 is a protein called 40S ribosomal protein S5.

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
52	DH	184	Total	C	N	O	0	0
			1481	951	265	265		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
62	DY	134	Total	C	N	O	0	0
			1073	676	208	189		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	D2	446	Total	C	N	O	P	0	0
			9508	4250	1682	3130	446		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
66	D3	1327	Total	C	N	O	P	0	0
			28287	12644	5022	9294	1327		

- Molecule 67 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	D4	230	Total	C	N	O	P	0	0
			4872	2181	844	1617	230		

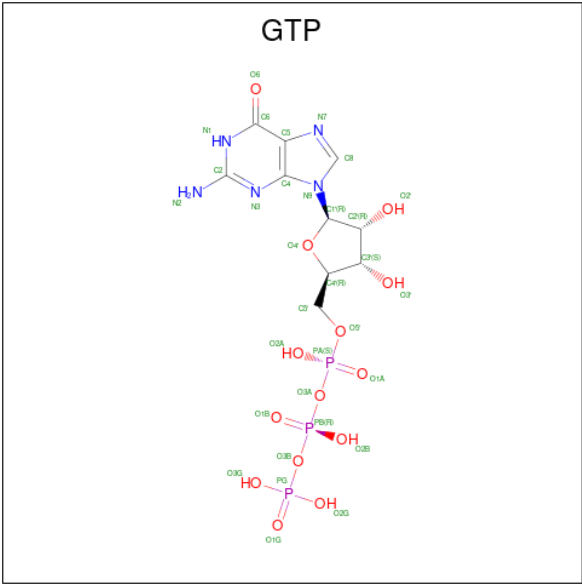
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 69 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
69	UX	1	Total	Mg	0
			1	1	
69	CL	1	Total	Mg	0
			1	1	

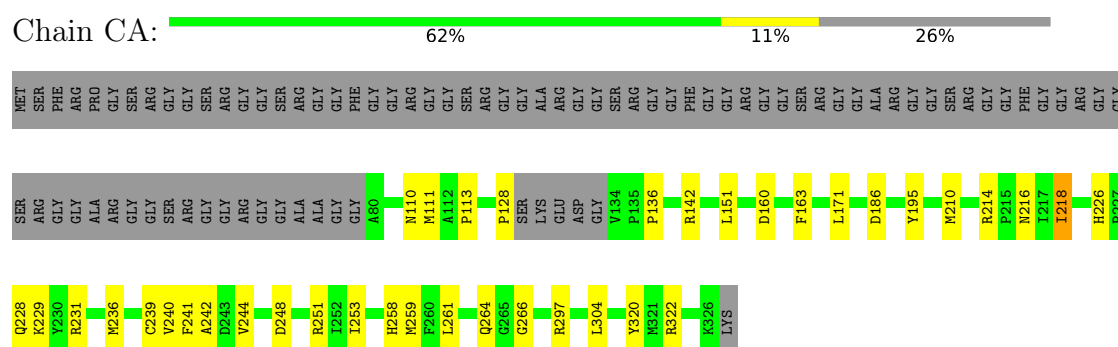
- Molecule 70 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



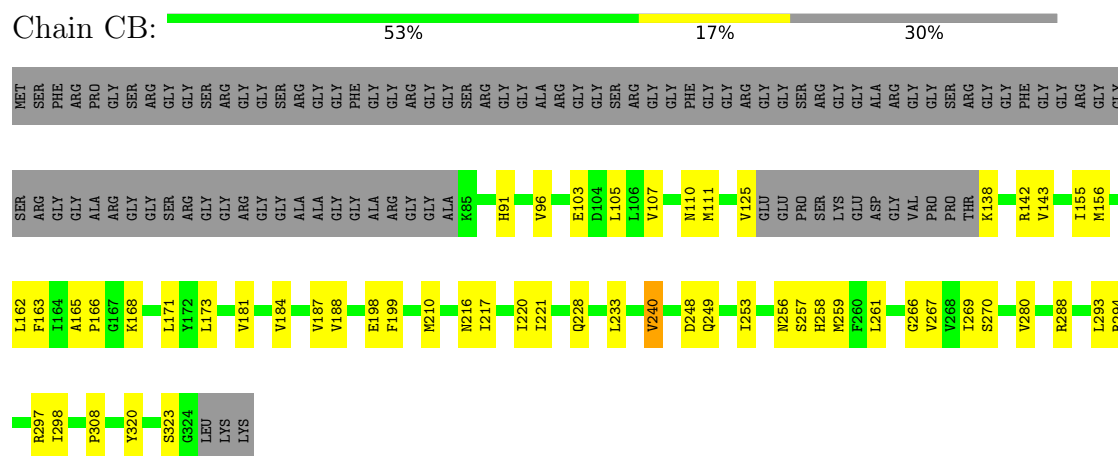
3 Residue-property plots

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

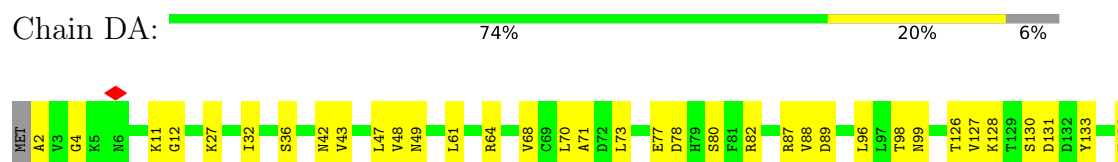
- Molecule 1: rRNA 2'-O-methyltransferase fibrillarin



- Molecule 1: rRNA 2'-O-methyltransferase fibrillarin

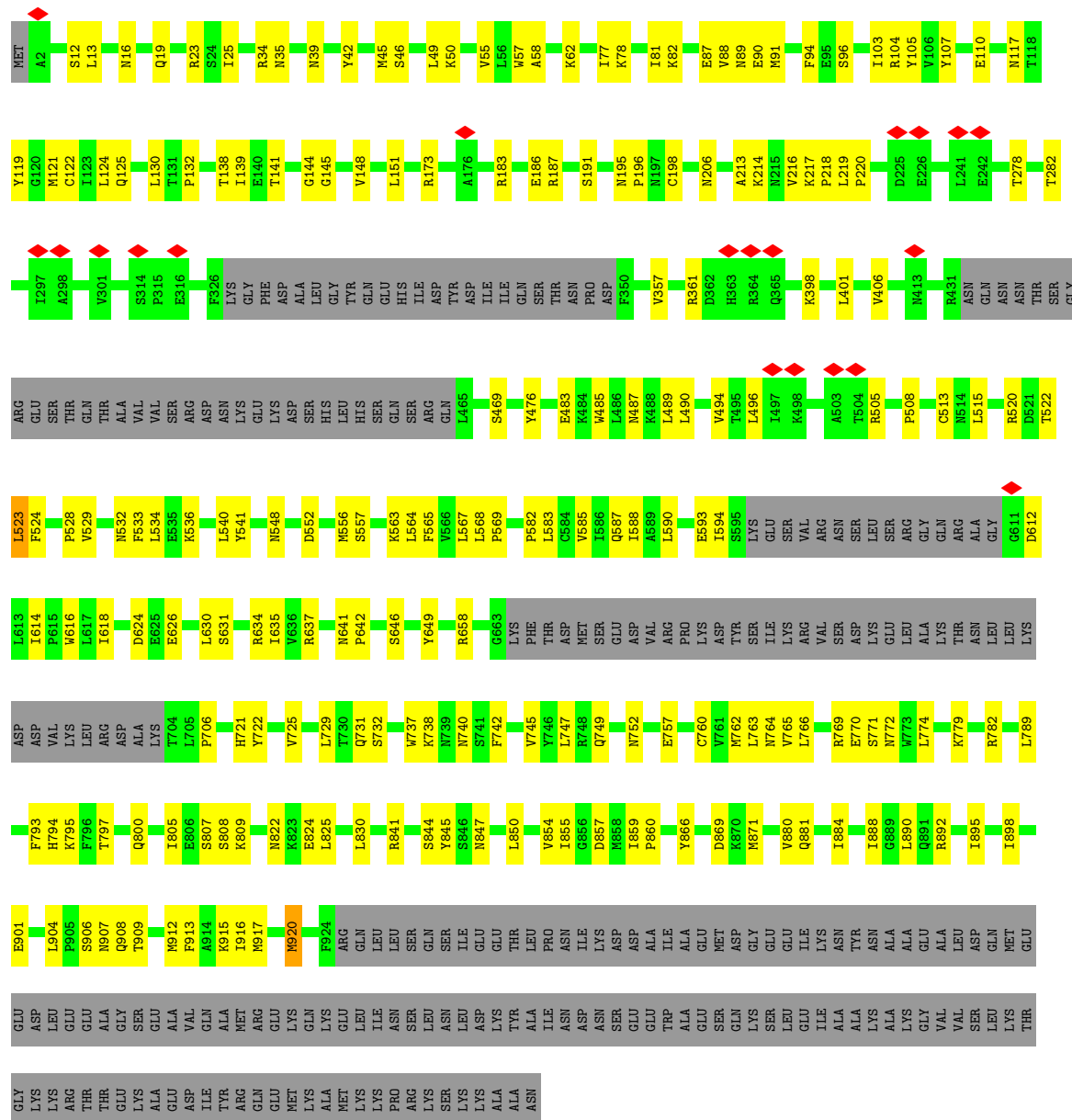


- Molecule 2: 40S ribosomal protein S1-A

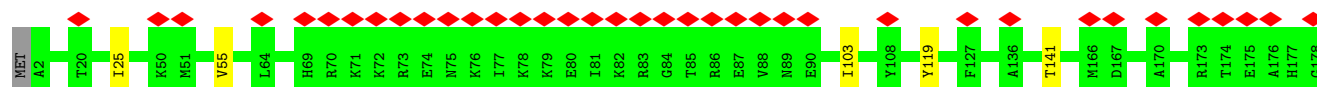
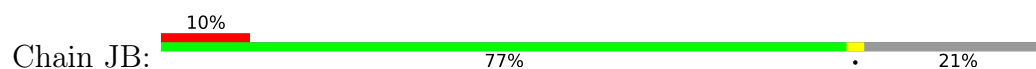


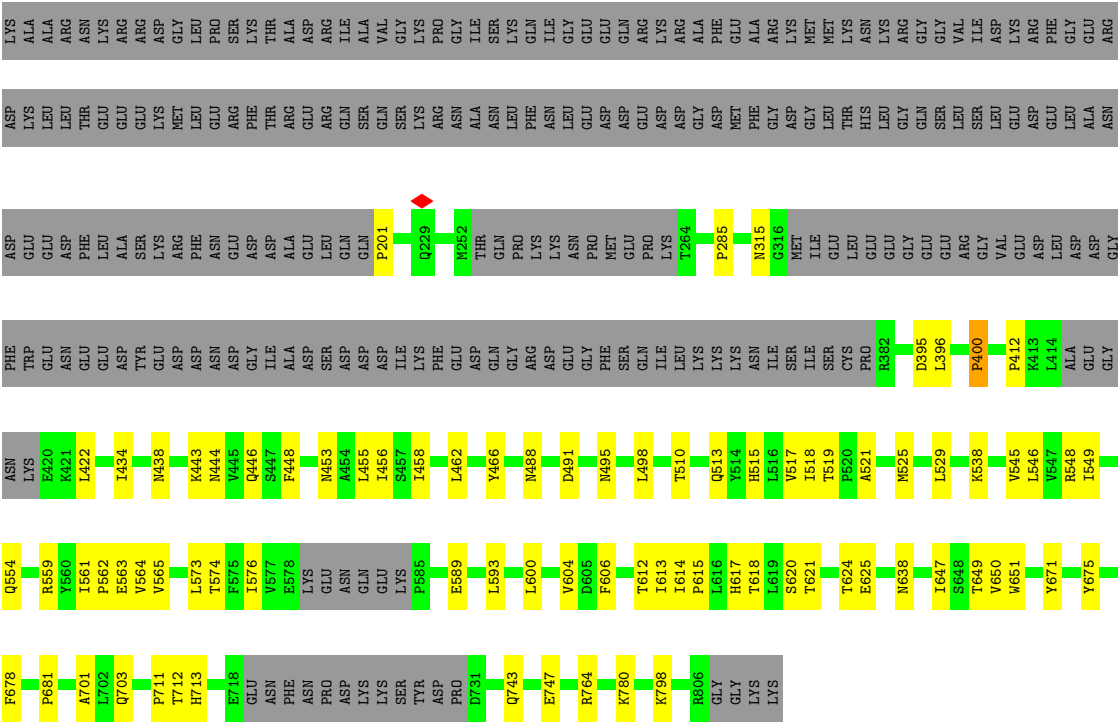


• Molecule 3: RNA cytidine acetyltransferase

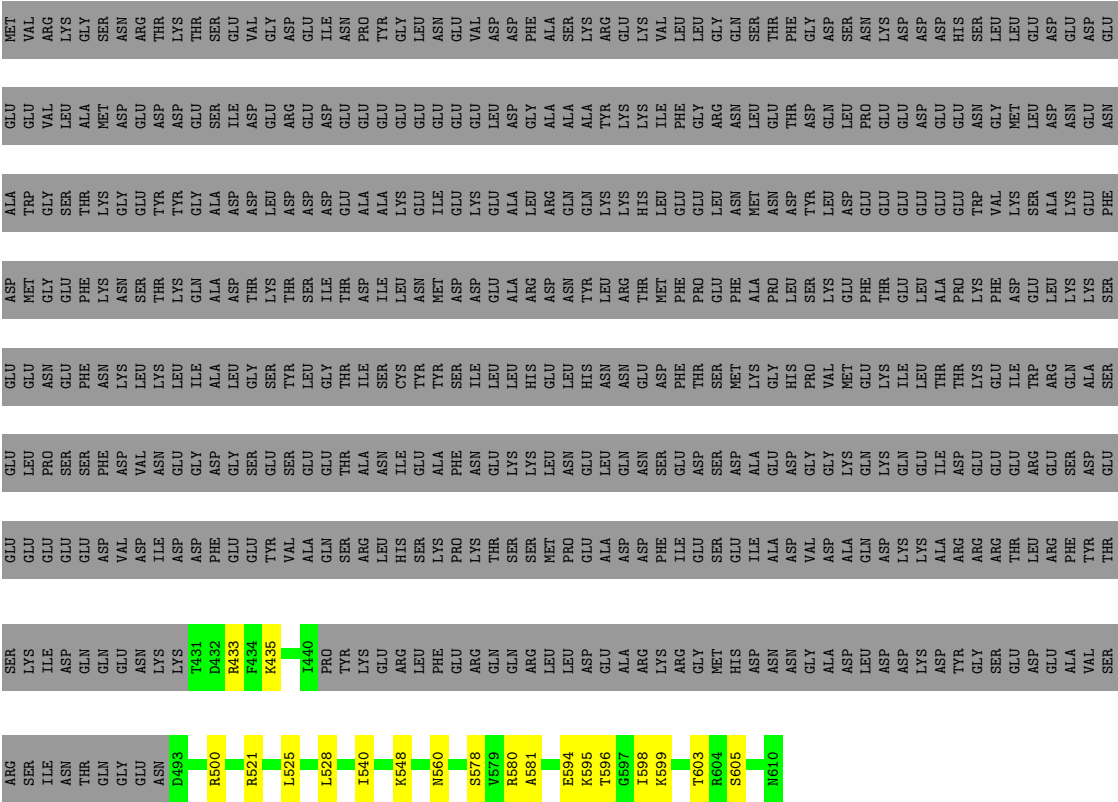


• Molecule 3: RNA cytidine acetyltransferase



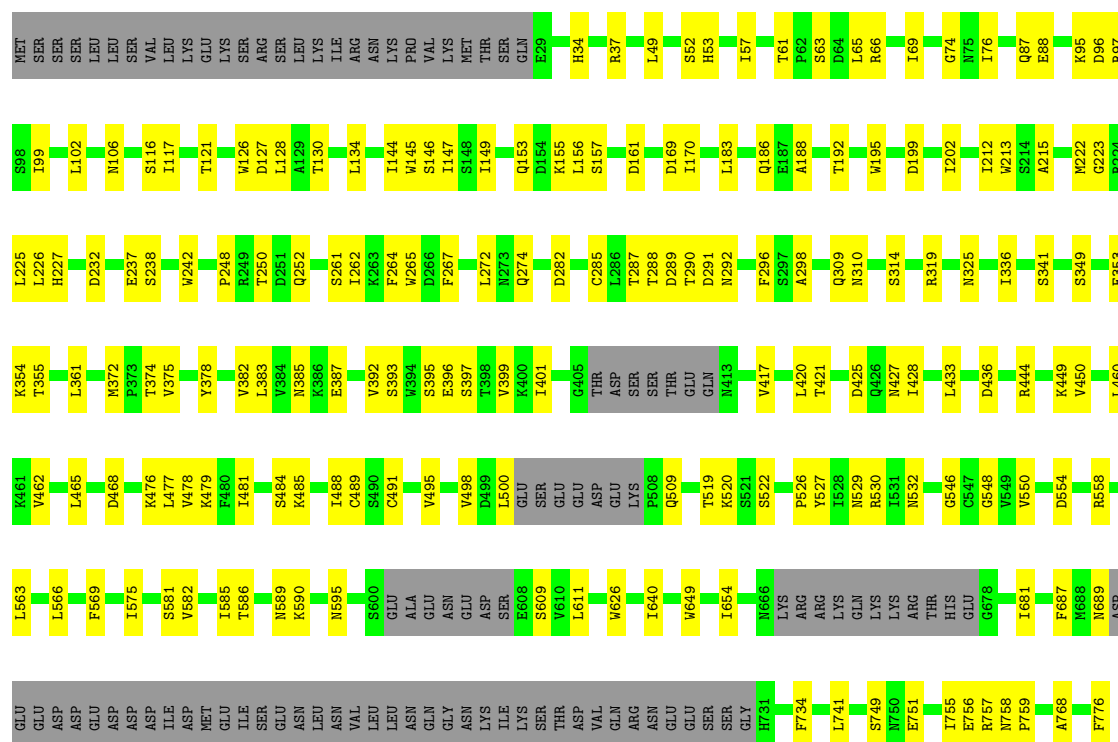


● Molecule 6: Something about silencing protein 10



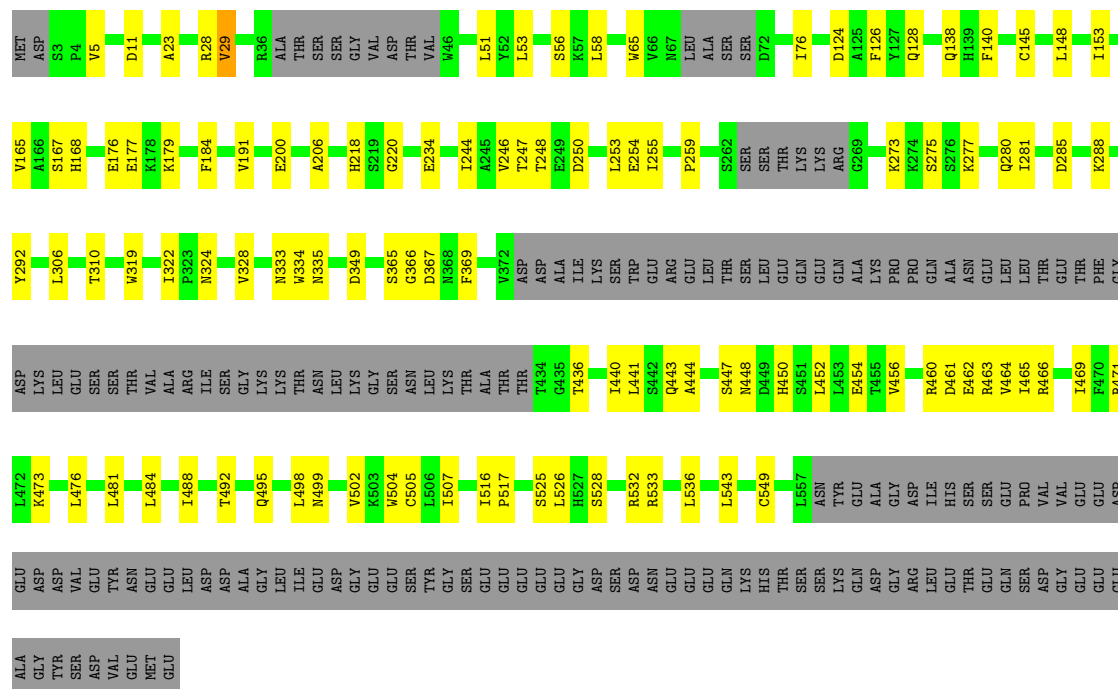
● Molecule 7: U3 small nucleolar RNA-associated protein 4

Chain UD:  64% 23% 13%



• Molecule 8: U3 small nucleolar RNA-associated protein 5

Chain UE:  57% 16% 26%



• Molecule 9: U3 small nucleolar RNA-associated protein 6

GLU	T362	THR	N198	MET
ASP	V363	ASN	K201	S2
PRO	I367	PRO	V202	R5
ARG	T368	A264	I265	E9
THR	I371	R266	I206	Q10
LYS	K372	L271	I207	C11
ILE	LEU	L271	ARG	G11
LEU	LEU	Y265	GLU	M15
ASP	PRO	Y265	GLN	Y29
LEU	VAL	H289	GLU	V29
ILE	GLU	K290	LEU	V29
SER	LYS	GLY	ASP	K34
LYS	LEU	TYR	MET	K35
LEU	ASP	TYR	GLN	R36
ILE	ASP	ALA	ASN	T37
ASP	ASP	ILE	GLU	D38
GLN	GLN	S296	GLN	H41
LEU	LEU	LEU	LYS	R42
LEU	LEU	I302	ASN	R42
SER	SER	K306	GLN	S49
VAL	VAL	E307	ALA	I50
LYS	LYS	T308	PRO	D85
LYS	LYS	Y319	ASP	D85
TYR	TYR	I320	GLU	Q105
PHE	PHE	I320	GLU	Q105
ALA	ALA	ALA	LYS	Q105
TYR	TYR	F323	SER	N122
ILE	ILE	ASP	HIS	N122
SER	SER	GLU	LEU	K128
SER	LYS	PHE	GLN	K128
LEU	LEU	LEU	VAL	N143
ASP	ASP	ASP	PRO	V144
SER	SER	LEU	SER	D145
ALA	ALA	E350	THR	D145
SER	SER	R331	GLY	I146
VAL	VAL	D332	ASP	I146
LYS	LYS	I335	ASP	R165
SER	SER	I335	SER	N166
LEU	LEU	VAL	MET	N167
ASN	ASN	V338	LYS	F168
ASN	ASN	ASN	ASP	Q169
GLU	GLU	N344	LEU	L172
TYR	TYR	ASP	ASN	R173
ARG	ARG	MET	GLU	R173
SER	SER	TYR	LEU	V178
TYR	TYR	ASP	PRO	V178
LEU	LEU	LEU	GLU	L181
GLN	GLN	SER	ALA	L181
ASN	ASN	LEU	ASP	Y185
ASN	ASN	ARG	ILE	V186
TYR	TYR	LYS	SER	V186
LEU	LEU	ASP	VAL	E189
LYS	LYS	LEU	LEU	L190
LYS	LYS	P356	GLY	N191
MET	MET	E357	ASN	F192
LYS	LYS	L358	ALA	I193
ASN	ASN	ALA	CTU	I193

- | | | |
|------|------|------|
| I324 | R140 | MET |
| T327 | E147 | GLY |
| L345 | L148 | HIS |
| S351 | F149 | LYS |
| G356 | L150 | ASN |
| S357 | H151 | GLY |
| R364 | E152 | HIS |
| L372 | T153 | ARG |
| E379 | L160 | ARG |
| F386 | Q161 | GLN |
| S387 | V168 | ILE |
| D388 | K171 | K13 |
| I398 | K172 | T25 |
| I402 | Y173 | Y26 |
| V403 | D178 | THR |
| P404 | E183 | ASN |
| G405 | L184 | ASN |
| A406 | H185 | ALA |
| A409 | R186 | LYS |
| M410 | L187 | ASN |
| L444 | G212 | ASN |
| D445 | L224 | THR |
| P446 | E227 | HIS |
| K464 | L228 | Q36 |
| M480 | R229 | T49 |
| D482 | T230 | Y53 |
| L483 | N241 | L67 |
| P484 | N244 | L74 |
| L497 | A245 | Q88 |
| R502 | V246 | D96 |
| R515 | N253 | L108 |
| D544 | L258 | P113 |
| R552 | M263 | I116 |
| F553 | P264 | N121 |
| G554 | L267 | G122 |
| | V268 | T123 |
| | T292 | H124 |
| | R296 | I127 |
| | S297 | T128 |
| | M298 | G29 |
| | L315 | R130 |
| | | K131 |
| | | G132 |
| | | H133 |
| | | V134 |
| | | A135 |

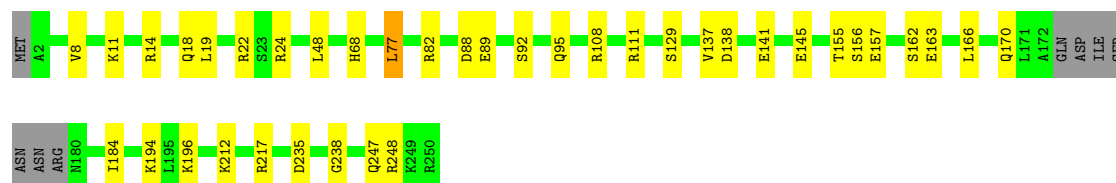
- | | | | | |
|-----|-----|------|------|-----|
| LEU | ALA | S185 | I69 | MET |
| LYS | VAL | F201 | P70 | PRO |
| PRO | ILE | K202 | S71 | SER |
| LEU | ASN | | | LEU |
| PHE | SER | | A77 | SER |
| ASP | GLU | D214 | | GLN |
| ASP | LYS | | A80 | PRO |
| LYS | SER | F231 | | PHE |
| ASP | HIS | | G83 | ARG |
| ILE | ASN | P235 | GLN | LEU |
| ASN | SER | | A85 | ALA |
| ASP | LYS | D238 | | THR |
| LYS | THR | | D88 | LEU |
| ARG | ILE | P258 | | PRO |
| VAL | ALA | | A93 | LYS |
| LYS | ILE | S264 | SER | ILE |
| CYS | GLY | | THR | ALA |
| ASN | ILE | I267 | ASP | SER |
| ASP | SER | | ASP | LEU |
| VAL | THR | F272 | GLU | SER |
| SER | LYS | F273 | ALA | LEU |
| GLY | ASN | N274 | ASN | ASN |
| ASP | GLY | | ASN | PHE |
| SER | PRO | Y279 | GLU | SER |
| ASN | ASN | | LYS | LEU |
| VAL | PRO | Y285 | THR | GLN |
| PRO | THR | | ILE | ALA |
| VAL | SER | Y293 | ASN | D27 |
| LEU | SER | | THR | Y28 |
| LEU | LEU | | GLN | Y29 |
| HIS | LEU | P298 | LYS | R30 |
| CYS | GLU | H299 | LYS | V31 |
| ASN | ILE | | ARG | A32 |
| GLU | ILE | Q304 | ASN | ASP |
| VAL | ASN | | GLY | GLY |
| ILE | ILE | F308 | VAL | THR |
| GLU | ASP | P309 | GLU | PHE |
| LYS | VAL | | ILE | ASN |
| LEU | GLY | P316 | TRP | GLU |
| SER | THR | | ALA | SER |
| ALA | ASN | P325 | PHE | THR |
| LEU | THR | | GLY | ASN |
| LEU | LEU | R330 | L120 | ASN |
| ASP | LYS | | | ILE |
| ASN | ASP | Y340 | Y127 | THR |
| ASP | SER | L341 | | LEU |
| ILE | LEU | | L147 | GLY |
| THR | GLY | L350 | SER | ILE |
| SER | LYS | | GLU | SER |
| PHE | SER | L355 | SER | GLY |
| ASP | PHE | T356 | ASP | |
| ASP | GLN | H357 | ILE | R50 |
| ILE | VAL | V358 | D153 | S51 |
| PHE | GLY | | | |
| PHE | ASN | LYS | Y167 | I56 |
| LYS | ASN | THR | K168 | I57 |
| GLU | ASN | PHE | | R58 |
| LEU | GLN | ASN | P59 | |
| LEU | SER | LEU | A173 | T60 |
| LYS | SER | LEU | | P61 |
| ILE | VAL | LYS | I180 | |
| R58 | THR | LYS | | R62 |



K1502	F1594	PHE	ALA	SER	ALA	THR	TYR	LEU	LEU	LEU	ILE	ARG	HIS	THR	L763	A681	C566	LEU
F1510	T1595	LEU	THR	PHE	THR	THR	ASP	ILE	ASP	ILE	GLN	CYS	THR	ILE	K768	S682	A570	ASN
L1598	L1598	SER	LEU	SER	LEU	GLU	ARG	LYS	ILE	THR	GLU	THR	THR	GLU	I771	S683	L571	THR
L1605	L1605	GLU	THR	GLU	THR	THR	ASN	LEU	ASP	LEU	GLU	LEU	LEU	ALA	I775	S684	S575	ASN
K1606	R1607	V1422	GLU	GLY	GLU	SER	LEU	LEU	PRO	THR	PHE	THR	THR	ASP	F688	S575	VAL	
F1608	F1607	L1423	VAL	GLU	LEU	SER	LEU	THR	VAL	VAL	THR	VAL	VAL	LEU	T788	I576	SER	
I1609	I1609	I1426	SER	GLU	SER	ASP	LYS	SER	ALA	LEU	ARG	ARG	ARG	VAL	L696	K577	LEU	
V1616	V1616	S1429	SER	ILE	SER	HIS	VAL	LYS	VAL	LEU	VAL	ALA	ALA	ASN	E697	R579	THR	
R1619	R1619	ARG	MET	THR	THR	THR	THR	SER	GLY	VAL	GLU	ILE	ASP	ASN	N698	V582	GLU	
V1528	V1528	GLU	THR	VAL	GLU	ILE	VAL	SER	PHE	LEU	THR	VAL	VAL	GLY	R699	I585	THR	
I1623	I1623	ASP	VAL	ASN	LYS	LYS	LEU	LYS	PHE	LEU	ILE	THR	THR	GLU	S701	V682	THR	
I1531	I1531	S1434	K1348	VAL	GLU	GLU	ASP	LYS	LEU	LEU	ALA	ALA	ALA	LYS	Q808	L588	G488	
S1532	S1532	ILE	ILE	MET	ILE	THR	GLU	LYS	ILE	THR	THR	ILE	ILE	LEU	K704	L589	Y491	
N1533	N1533	I1441	L1352	VAL	LEU	LEU	THR	SER	VAL	VAL	ARG	ASN	ASN	LEU	S705	A590	L495	
V1536	V1536	I1444	I1355	VAL	PHE	GLN	SER	GLU	GLN	VAL	VAL	ASN	PHE	THR	N709	K591	G503	
M1539	M1539	I1448	C1358	LEU	VAL	GLN	LYS	THR	ASN	ASP	GLN	ASN	ALA	LEU	H715	R592	LYS	
N1540	N1540	ASP	V1361	ASP	GLY	LEU	LYS	ARG	LEU	SER	LEU	PRO	ALA	GLU	F716	T595	TYR	
F1544	F1544	L1450	K1365	MET	ASN	GLN	ILE	VAL	ASN	LYS	ILE	GLN	PRO	MET	E717	L600	LYS	
L1547	L1547	K1452	LEU	PRO	VAL	VAL	ARG	PHE	LEU	ALA	ASN	VAL	GLN	ASP	R718	L603	ALA	
F1548	F1548	V1453	GLU	LEU	LEU	GLN	ILE	ASN	VAL	SER	GLN	VAL	GLN	THR	S719	K603	SER	
L1551	L1551	K1455	ILE	SER	ILE	GLN	ARG	PHE	GLY	LYS	LYS	LEU	PHE	LEU	V724	L604	PHE	
V1552	V1552	V1456	ALA	LYS	PRO	LEU	GLU	VAL	ASN	LYS	ILE	ASN	LEU	GLU	S725	P611	LEU	
R1554	R1554	ALA	F1369	SER	VAL	THR	GLU	THR	GLU	GLY	GLY	GLY	GLY	SER	P726	I611	THR	
A1555	A1555	THR	I1373	GLN	VAL	VAL	LEU	LEU	ARG	ILE	ILE	ILE	ILE	ARG	K727	P612	SER	
F1556	F1556	SER	L1380	VAL	ASN	ASN	GLU	GLU	GLU	THR	GLU	GLU	GLU	ARG	E728	N615	PHE	
D1557	D1557	ASN	A1383	VAL	ILE	ILE	GLY	PHE	LEU	ILE	LEU	LEU	GLY	ARG	K729	P616	THR	
I1686	I1686	GLY	S1384	LEU	ILE	ALA	VAL	GLY	THR	ILE	THR	THR	THR	ARG	Q730	K617	LEU	
K1689	K1689	VAL	L1388	THR	ASN	THR	PHE	PHE	THR	PHE	LEU	LEU	SER	LEU	M733	E620	GLU	
L1690	L1690	THR	SER	MET	THR	PRO	LEU	LEU	THR	LEU	THR	THR	THR	THR	I734	L623	SER	
I1691	I1691	L1476	N1390	ALA	LEU	LEU	ILE	ASN	THR	ASN	THR	THR	THR	ALA	A740	D636	B528	
V1692	V1692	GLY	P1391	THR	SER	THR	THR	ASN	ASN	ASN	THR	THR	THR	GLN	N742	I637	I531	
M1695	M1695	V1485	L1396	VAL	VAL	SER	GLU	PHE	PHE	PHE	LEU	ILE	VAL	LEU	S743	R639	L539	
K1696	K1696	I1487	Q1397	SER	THR	THR	VAL	THR	THR	THR	ASP	GLN	GLN	GLU	E746	N646	I542	
A1697	A1697	ILE	L1398	LYS	ASN	ASN	GLU	PHE	THR	THR	LEU	HIS	SER	GLU	L748	V649	I542	
K1704	K1704	ASP	Q1397	THR	GLU	GLU	THR	ILE	HIS	VAL	THR	THR	VAL	VAL	A749	N750	K549	
L1705	L1705	LYS	N1400	GLY	ASP	ASP	PHE	ASN	ASN	ASN	ARG	MET	CYS	GLN	I751	Q657	Y550	
Q1583	Q1583	LYS	I1492	LYS	ILE	THR	THR	ASN	THR	THR	GLU	PRO	THR	SER	A752	I661	S553	
R1709	R1709	ALA	S1493	LEU	ARG	THR	CYS	ILE	GLU	GLU	HIS	ILE	LEU	LEU	E753	P662	S553	
A1710	A1710	GLU	F1404	GLU	THR	THR	THR	THR	GLU	GLU	PHE	PHE	ASN	ALA	E754	R755	K556	
I1714	I1714	GLY	I1408	GLY	LEU	LEU	THR	THR	GLU	SER	THR	THR	THR	LEU	L756	L670	N559	
E1735	E1735	THR	K1409	SER	THR	THR	GLN	THR	THR	GLY	GLY	MET	GLY	THR	I759	L671	I560	
L1736	L1736	ILE	R1410	ILE	LEU	LEU	GLU	ASP	GLN	ASN	PHE	ALA	ALA	LEU	F760	F561	S562	
S1592	S1592	PRO	I1499	GLN	ILE	GLY	GLU	ASP	THR	THR	SER	HIS	SER	LYS	A761	L674	T562	
Y1593	Y1593	SER	THR	GLN	THR	THR	GLU	TYR	LEU	LEU	THR	THR	THR	GLU	N675	N675	RED	

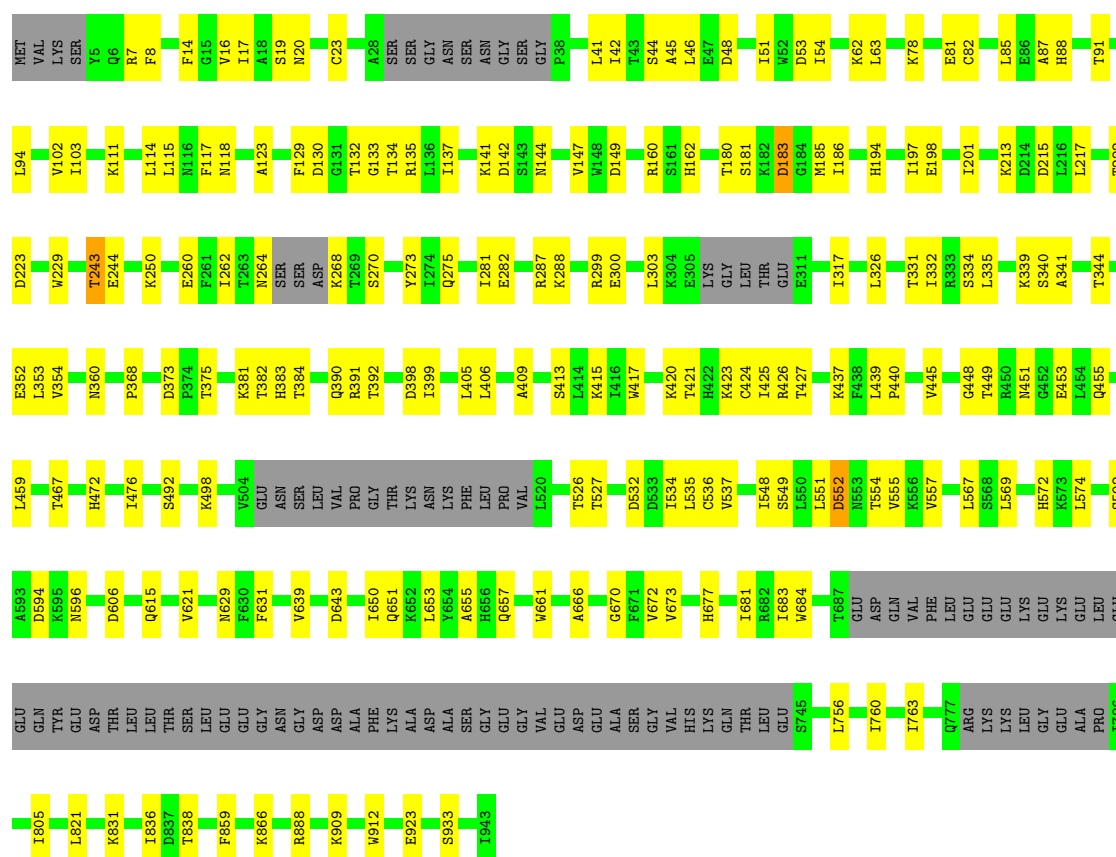
- Molecule 14: U3 small nucleolar RNA-associated protein 11

Chain UK:  82% 15%



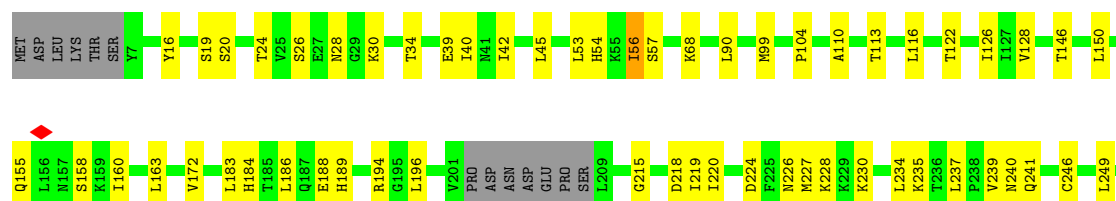
- Molecule 15: U3 small nucleolar RNA-associated protein 12

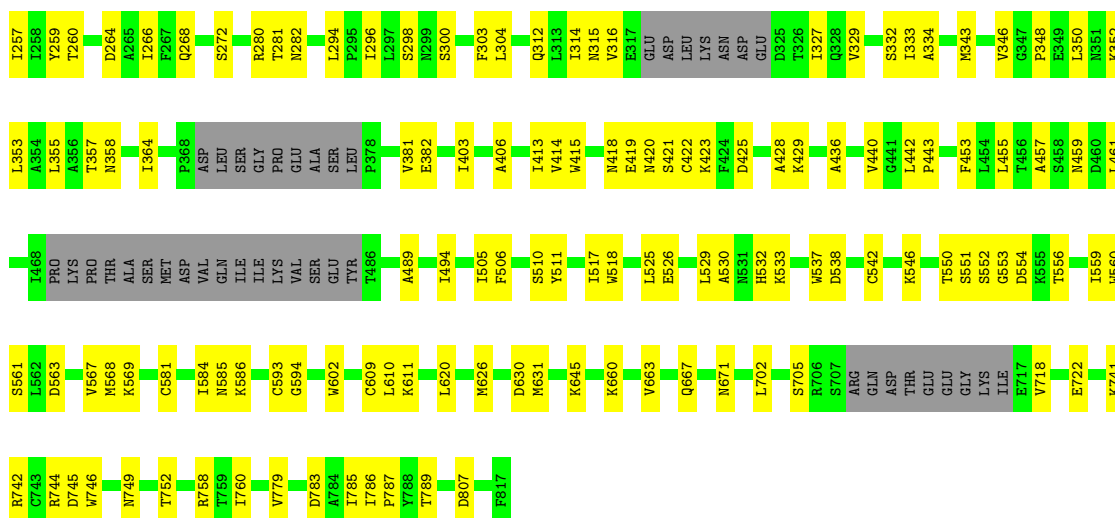
Chain UL:  69% 20% 11%



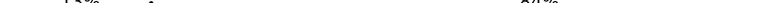
- Molecule 16: U3 small nucleolar RNA-associated protein 13

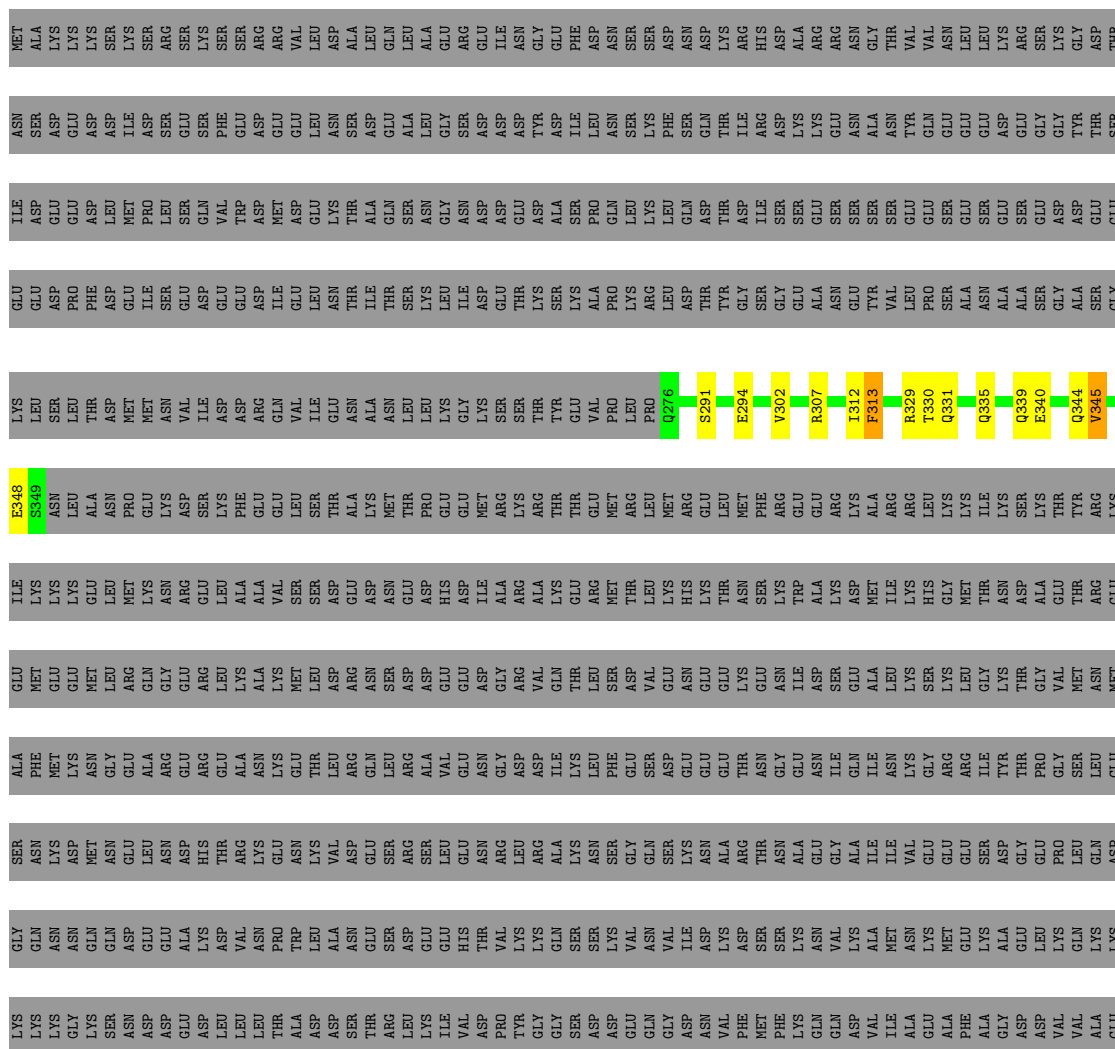
Chain UM:  70% 23% 7%





- Molecule 17: U3 small nucleolar RNA-associated protein 14

Chain UN:  13% 1% 84%



PHE
GLN
GLU
GLU
LYS
LYS
ARG
VAL
ILE
ASP
ASP
GLU
ASP
ASP
LYS
GLU
VAL
ASP
THR
THR
LEU
PRO
GLY
TRP
GLY
GLU
TRP
ALA
GLY
ALA
GLY
GLY
SER
LYS
LYS
PRO
LYS
ASN
LYS
LYS
ARG
LYS
PHE
ILE
LYS
LYS
VAL
VAL
GLY
VAL
ASN
LYS
ASP
LYS
ARG
ARG
ASP
LYS
ASN
LEU
Q827

K834
S845
A846
S860
R861
R862
M863
M864
I865
I879
I883
K886
V880
L894
K899

• Molecule 18: U3 small nucleolar RNA-associated protein 15

Chain UO:  74% 21%

MET
S2
T3
A4
R5
K12
P17
T20
R28
Q29
T31
S32
A33
Q34
M40
G166
V42
H51
P52
H53
S59
S60
T61
R62
R71
R79
S86
R90
L95
A98
V106
S106
Y107
Y108
L117
L118
I120
H125
P126
T127
H128
H133
T134
Q135
D136
N137
K138
I139
S144
D145
R147
R150
L151
A157
P160
T165
K166
A167
T168
R172
T173
P181
H182
S188
G191
D197
T198
R199
S200
S201
D212
L215
E216
C229
G230
N233
K244
E247
N252
C257
L258
N263
Q269
I273
G279
F298
P301
V302
L303
N315
S323
T331
K332
K333
K334
GLU
LYS
ARG
SER
SER
SER
LYS
ASP
LYS
ASN
ALA
PRO
ALA
ALA
SER
PHE
ASN
LYS
ASN
ALA
Y453
R454
S455
A456
V459
A460
Y470
L508
Q509
T512
SER

• Molecule 19: Bud site selection protein 21

Chain UP:  21% 7% 72%

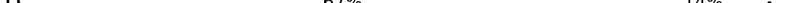
MET
SER
ASN
GLY
HIS
VAL
LYS
PHE
GLN
ASP
ALA
ASP
GLU
SER
GLN
ALA
SER
SER
VAL
VAL
THR
K333
K334
GLU
LYS
ARG
SER
ASP
ASP
VAL
VAL
LYS
ASN
VAL
ILE
SER
LYS
LYS
LYS
ASP
LYS
GLN
LYS
VAL
HIS
SER
SER
SER
ASP
SER
GLU
GLU
GLU
VAL
SER
SER
SER
ASP
ASP
ASP
ASP
ALA
PRO
GLN
GLU
GLU
GLY
HIS
LEU
SER
GLY
LYS
SER
GLU
VAL
THR
ASP
GLU
THR
GLU
VAL
SER
ASP
VAL
VAL
ASP
ILE
ALA
GLU
LEU
PRO
GLU
PRO
GLU
GLU
GLY
LEU
LEU
HIS
SER
ASN
ILE
ASP
GLN
LYS
ASP
GLN
LYS
VAL
SER
VAL
ASN
GLU
THR
GLU
VAL
S182
L190
K194
I199
R204
W205
L206
N207
R208
K209
A210
K213
G214
ASP
GLN
LYS
ASP
GLY
SER
THR
THR
TYR
SER
SER
SER
ARG
HIS
VAL
PHE
ASP
LYS
LEU
ASP
SER
SER
F48
M49
N50
T59
R60
Q61
L66
L73
K90
I96
Q101
GLU
ASP
A104
T108
N112
N113
V118
L119
N120
K124
L125
P129
K130
K133
G214
ASP
GLN
LYS
ASP
GLY
SER
THR
THR
TYR
SER
SER
SER
ARG
HIS
VAL
PHE
ASP
LYS
LEU
ASP
SER
SER
F48
M49
N50
T59
R60
Q61
L66
L73
K90
I96
Q101
GLU
ASP
A104
T108
N112
N113
V118
L119
N120
K124
L125
P129
K130
K133

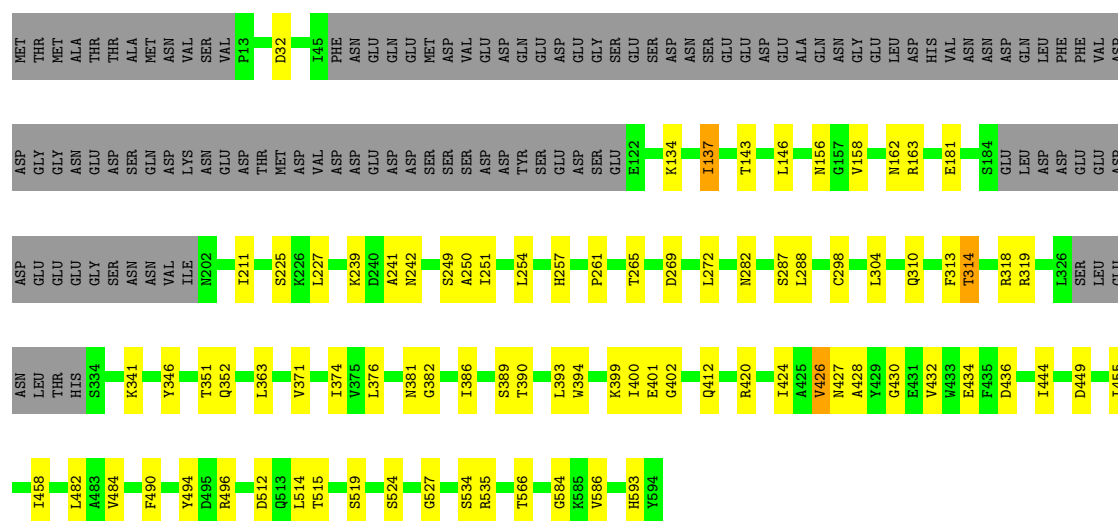
• Molecule 20: NET1-associated nuclear protein 1

Chain UQ:  72% 21% 7%

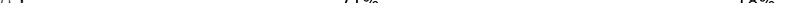
MET
THR
GLN
SER
LEU
GLY
ILE
GLU
Q9
G17
G18
K19
P20
N24
S38
Q39
D40
Q41
R42
F48
M49
N50
T59
R60
Q61
L66
L73
K90
I96
Q101
GLU
ASP
A104
T108
N112
N113
V118
L119
N120
K124
L125
P129
K130
K133
L141
V144
S147
E148
I153
L154
T155
D159
PRO
SER
GLN
LYS
ALA
HIS
M166
S167
Y171
R172
L173
Y174
K182
K183
N200
N204
L208
S226
L230
F231
D232
L237
P240
S243
I244
N255
M262
D265
N266
G278
V279
V283
Q289
I290
K294
V300
D308
Y311
L312
E318
K319
V320
M321
S322
L323
W324
Q325
L326
Q331
Q332
F333
L334
P335
R336
L337
N338
G339
I340
D343
I357
L358
Q359
E362
N363
N366
S367
D368
Y369
F370
F371
S377
D378
L379
T380
S381
I385
N386
G387
P388

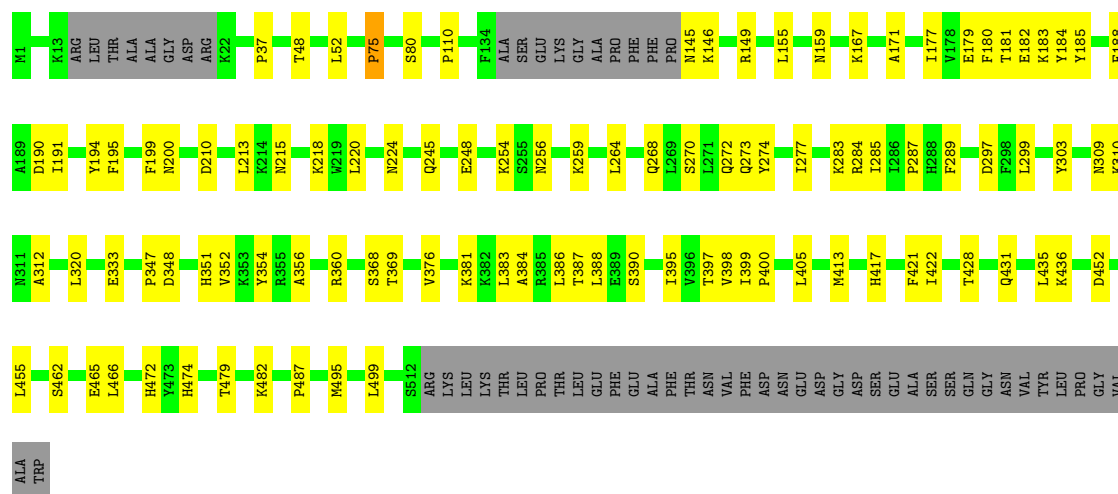
- Molecule 21: U3 small nucleolar RNA-associated protein 18

Chain UR:  67% 14% 1% 19%

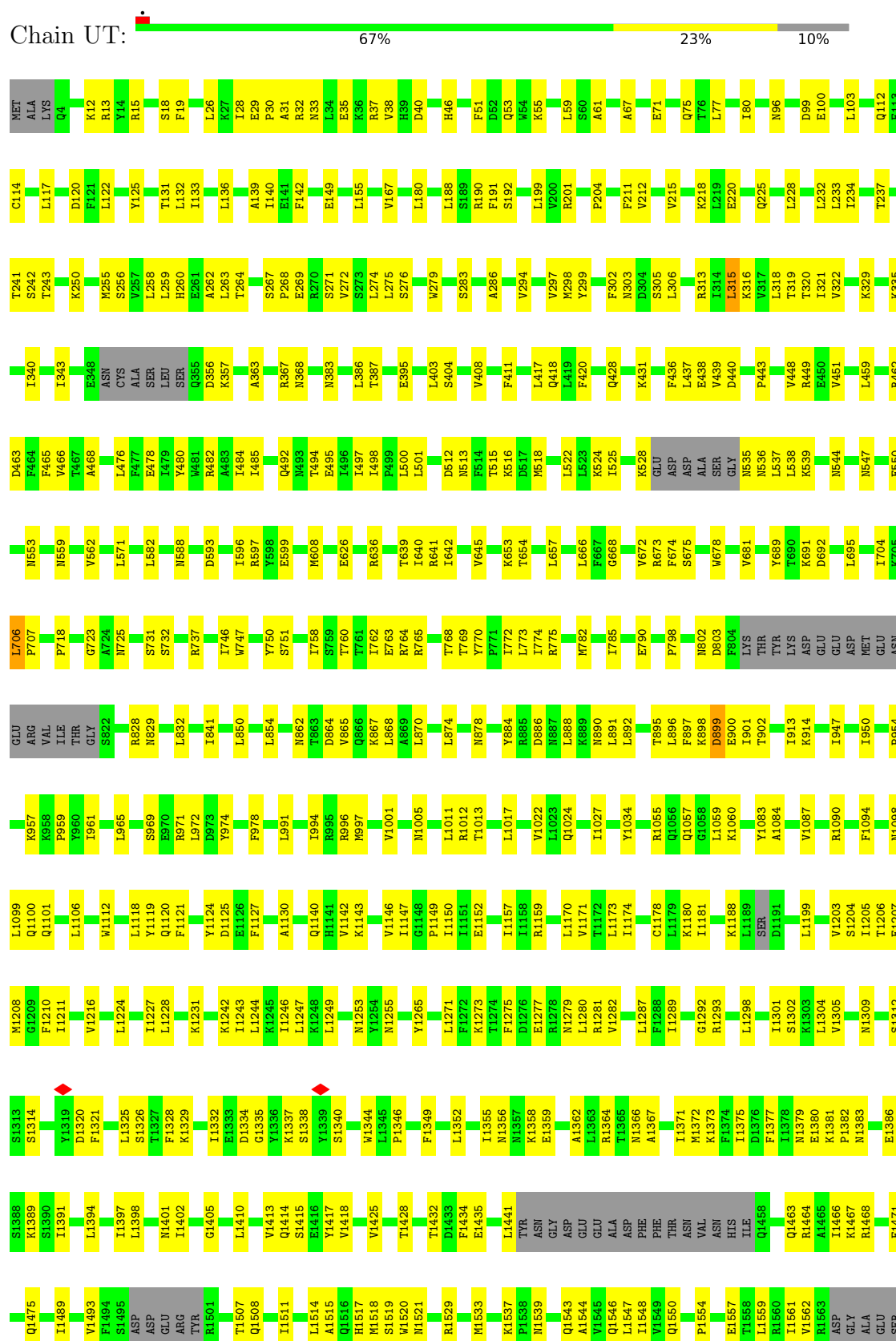


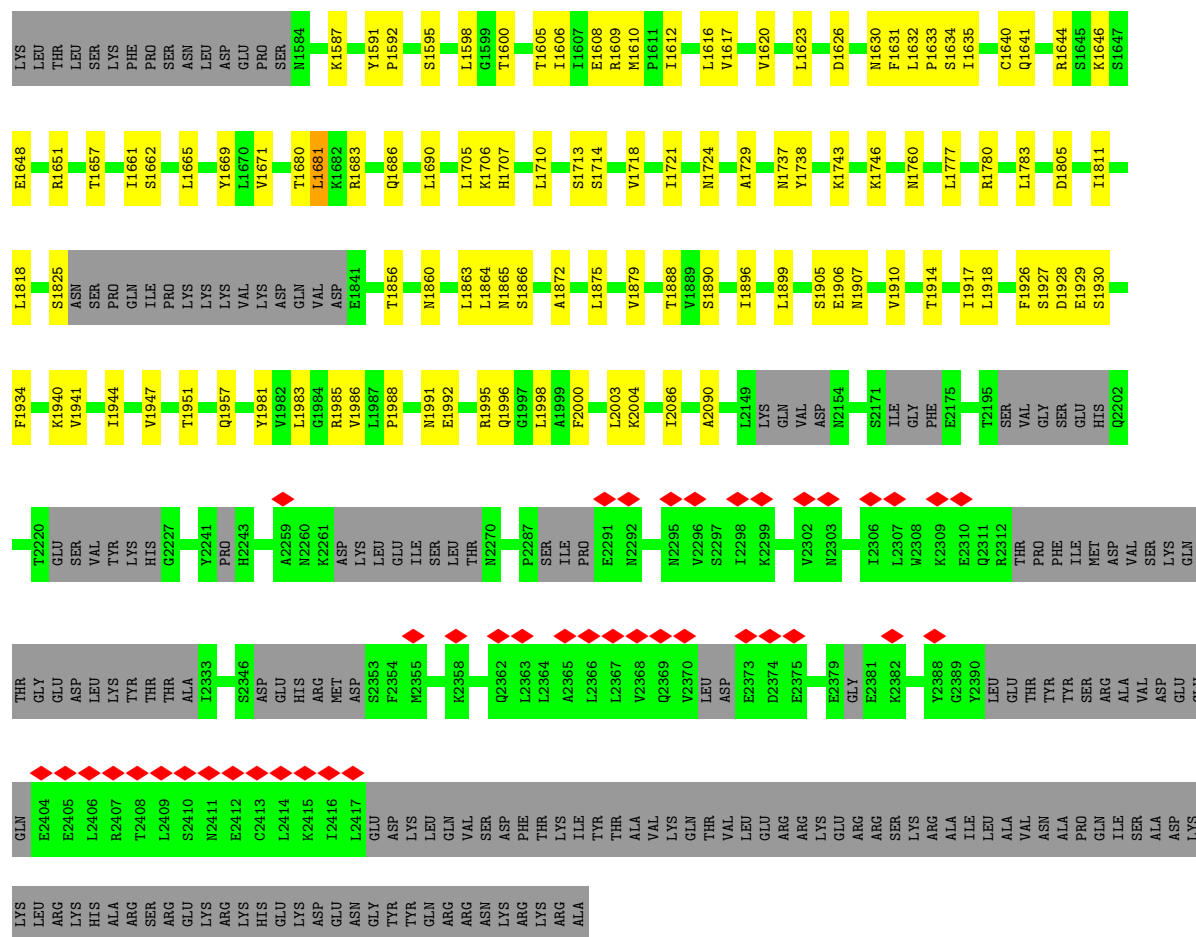
- Molecule 22: Nucleolar complex protein 4

Chain US:  71% 18% 11%



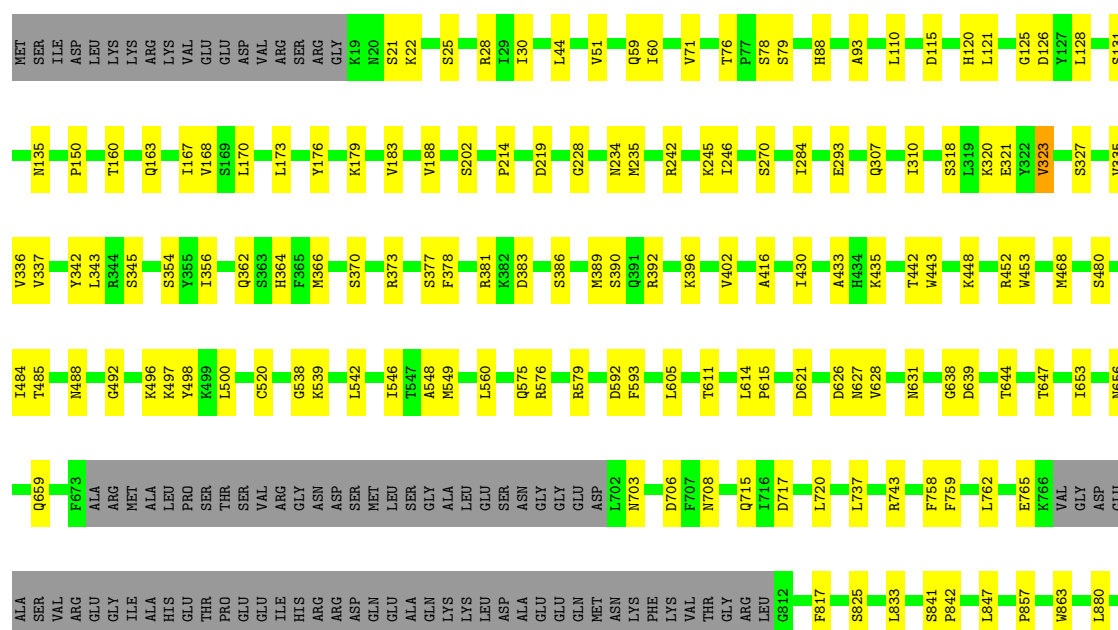
● Molecule 23: U3 small nucleolar RNA-associated protein 20



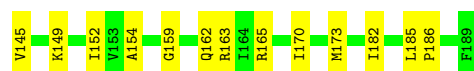


• Molecule 24: U3 small nucleolar RNA-associated protein 21

Chain UU: 74% 16% 10%

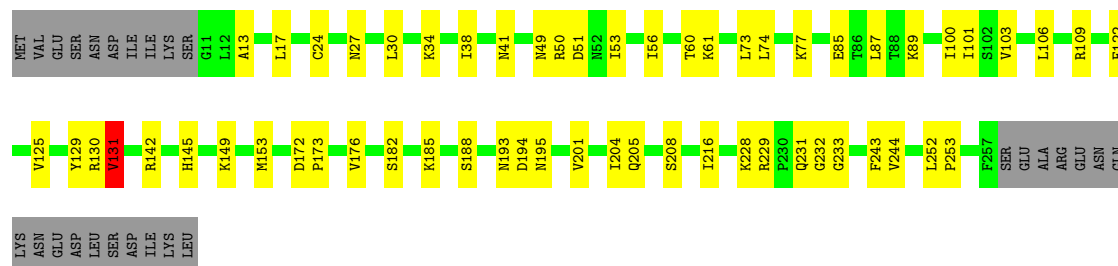






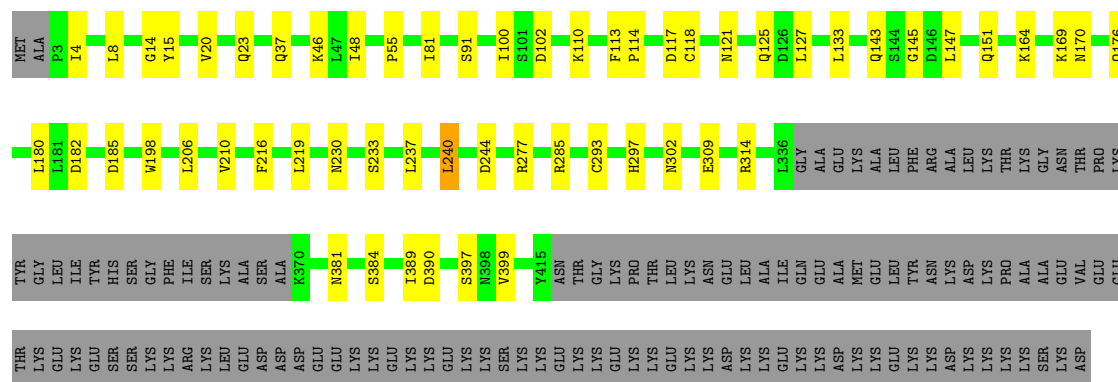
• Molecule 27: Ribosome biogenesis protein UTP30

Chain UZ: 69% 21% 10%



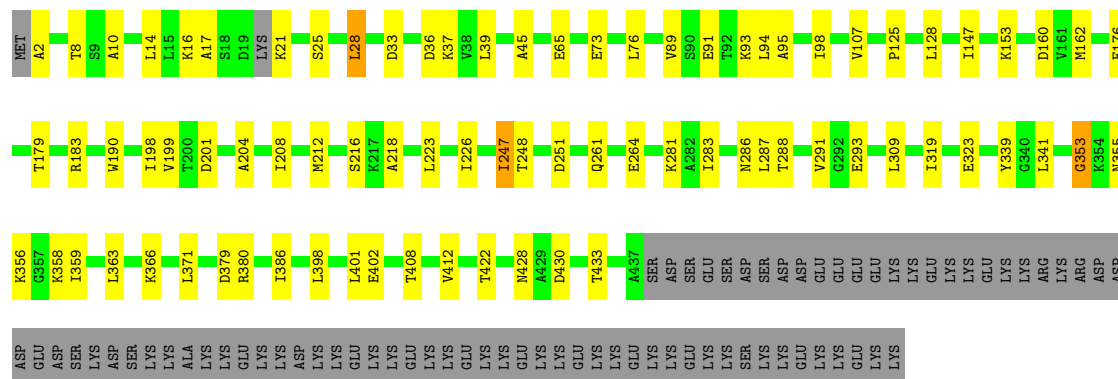
• Molecule 28: Nucleolar protein 56

Chain CD: 64% 11% 25%



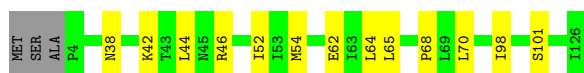
• Molecule 29: Nucleolar protein 58

Chain CE: 69% 15% 15%



• Molecule 30: 13 kDa ribonucleoprotein-associated protein

Chain CF: 87% 10%



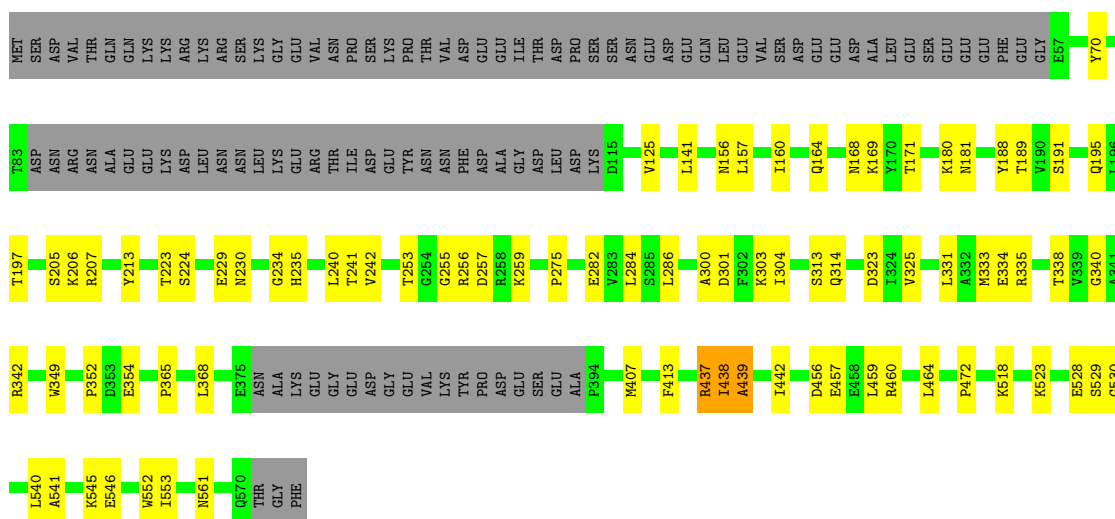
- Molecule 30: 13 kDa ribonucleoprotein-associated protein

Chain CG: 74% 24%



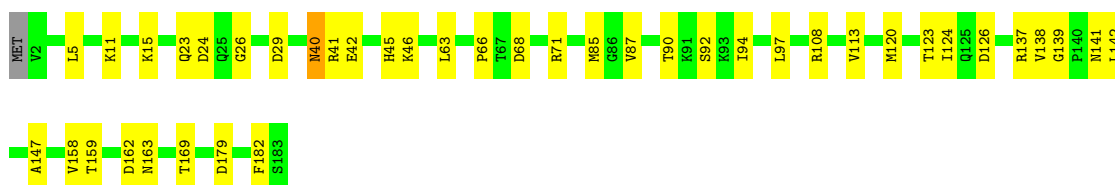
- Molecule 31: Ribosomal RNA-processing protein 9

Chain CH: 67% 14% 19%



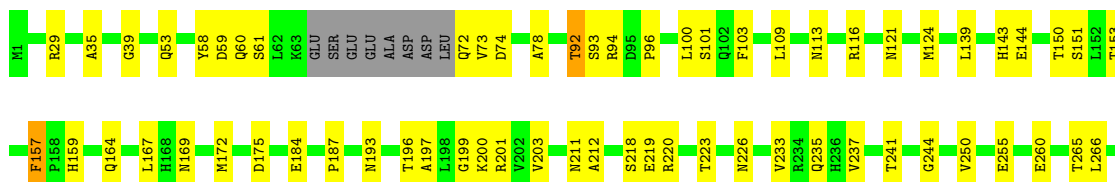
- Molecule 32: U3 small nucleolar ribonucleoprotein protein IMP3

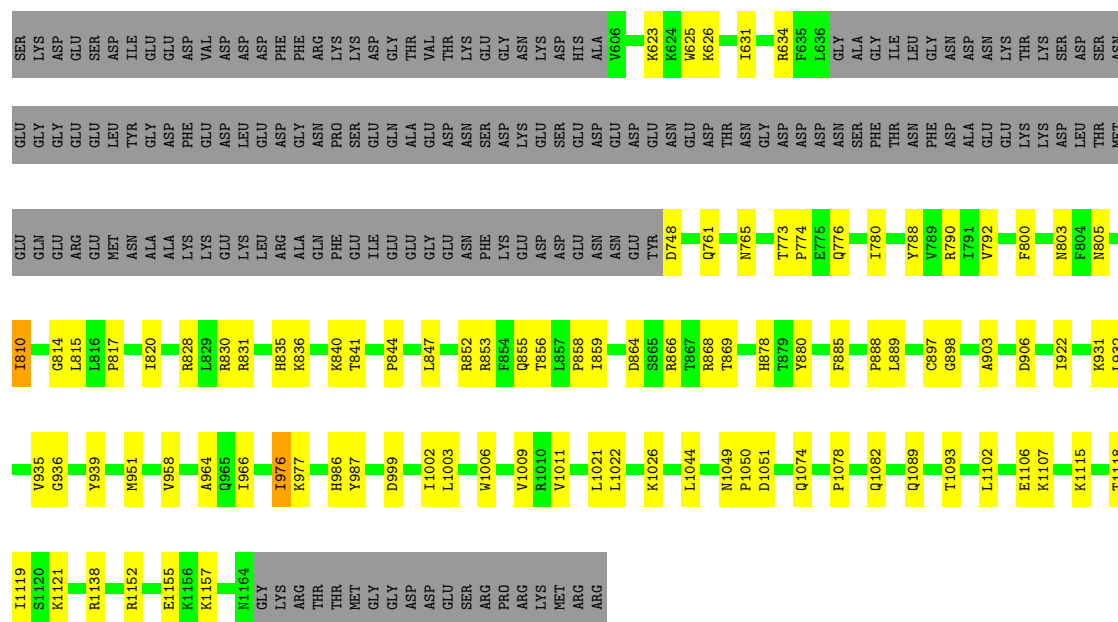
Chain CI: 77% 22%



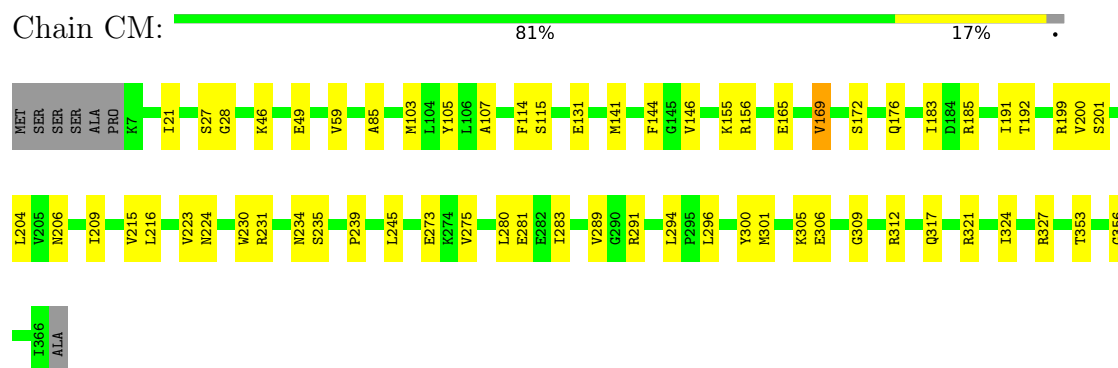
- Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP4

Chain CJ: 73% 23%

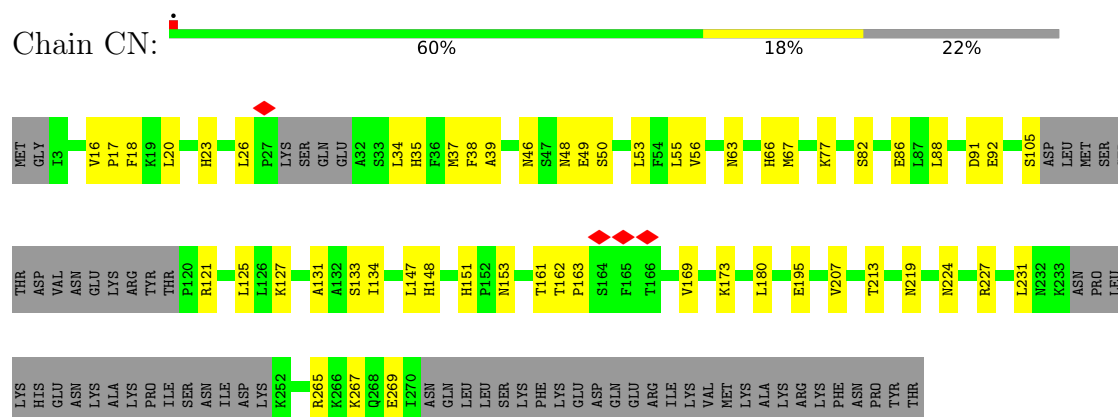




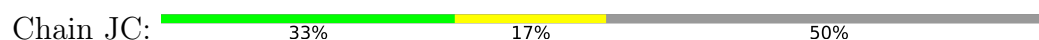
- Molecule 36: RNA 3'-terminal phosphate cyclase-like protein

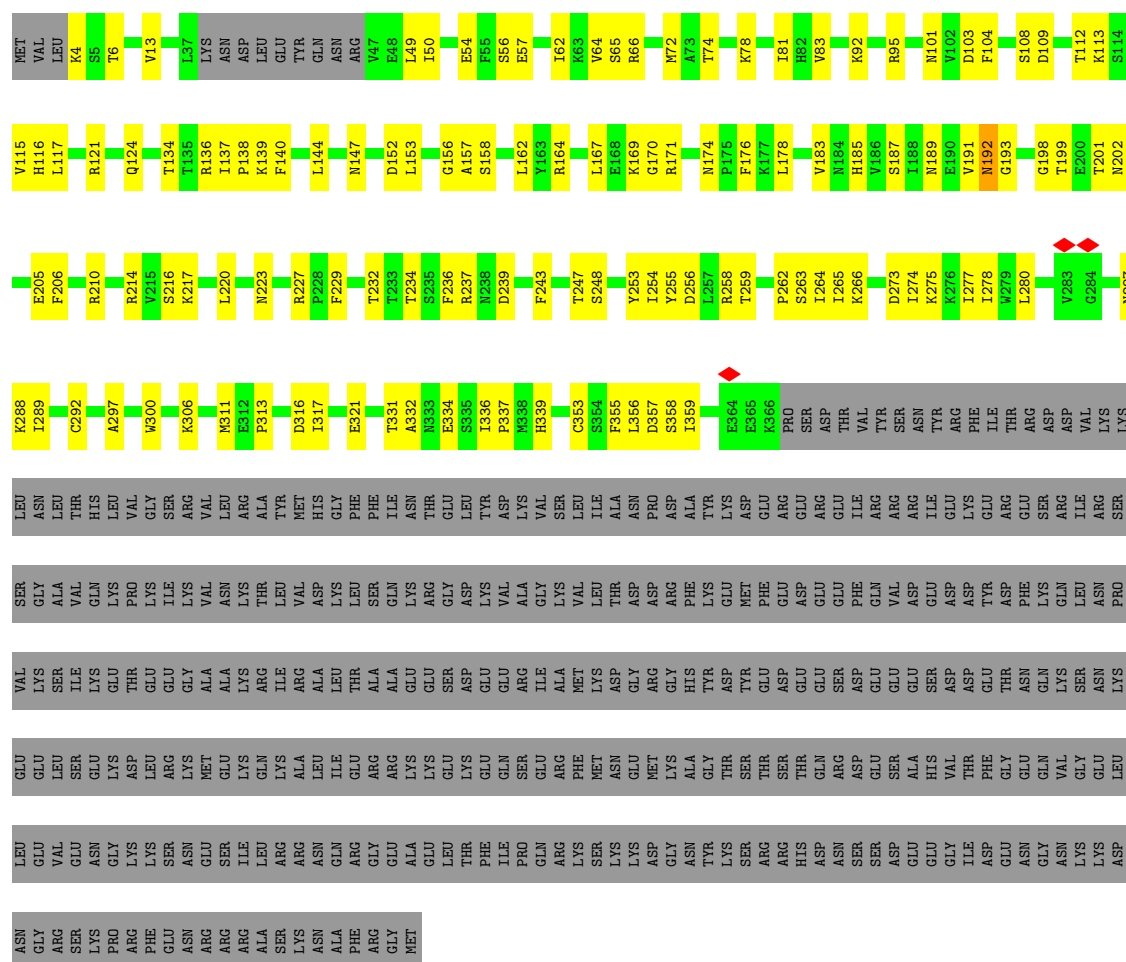


- Molecule 37: Ribosomal RNA-processing protein 7



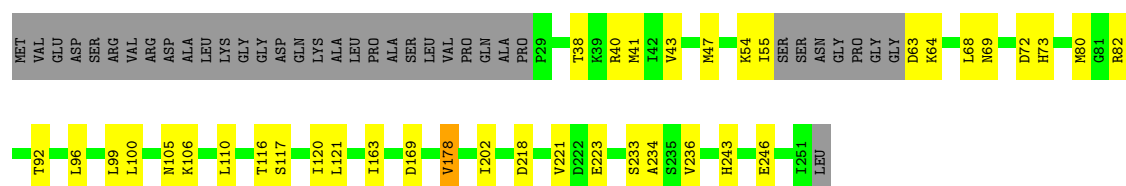
- Molecule 38: Ribosome biogenesis protein ENP2





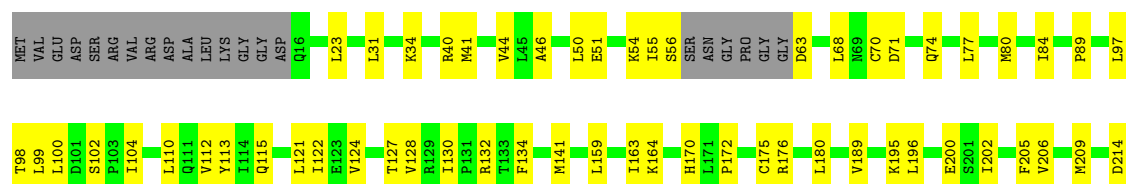
● Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain JF: 71% 15% 14%



● Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain JG: 66% 25% 9%

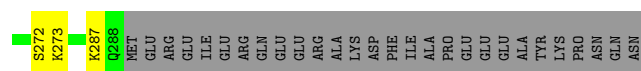




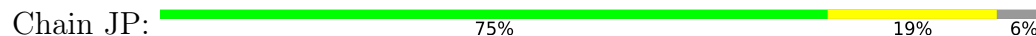
- Molecule 45: Protein FAF1



- Molecule 46: KRR1 small subunit processome component



- Molecule 47: Protein SOF1



GLY
ARG
ASP
ARG
LYS
ARG
ARG
LYS
GLY
ASP
ASP
LYS
LYS
ASP
THR
GLN
GLY
LYS

- Molecule 48: Regulator of rDNA transcription protein 14

Chain JQ:  27% 69%

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

ASN
ARG
ASP
VAL
HIS
LYS
ILE
ASP
LYS
LYS
LYS
CYS
TYR
LYS
ARG
LYS
LEU
VAL
PHE
LYS
LYS
HIS
ILE
LYS
LEU
ASP
LYS
GLY
GLN
LEU
GLN
GLY
VAL
LEU
LYS
HIS
HIS
GLN
HIS
GLY
LYS
THR
THR
THR
ASP
HIS
GLU
R112
R127
R131
R148
THR

VAL
THR
ALA
ASN
THR
ASP
ARG
SER
LYS
LYS
ARG
LYS
ARG
PHE
LYS
LYS
GLN
PHE
LYS
GLY
ASP
SER
ASP
F178
R183
Y184
L187
T188
P189
P193
S203
GLU
GLY
ASP

- Molecule 49: 40S ribosomal protein S4-A

Chain DE:  69% 25% 6%

MET
R2
R11
D21
S24
K37
E40
S41
L42
I45
L48
R49
R68
H69
V70
V76
R77
D79
T80
T81
Y82
P83
R87
T91
R96
E97
N98
F99
R100
L101
V105
F109
A110
V111
T114
T115
D116
E117
E118
K127
K133
K134

G135
V136
R148
D163
S166
G167
G178
V181
T182
V183
T184
G185
G186
R187
G190
I195
V196
H197
K198
E199
D202
H209
T210
K211
D212
S213
L214
D215
N216
V219
N224
V227
K233
P234
S237
L238
P239
K240
G241
K242
G243
T244
K245
L246
SER
ILE

ALA
GLU
ARG
ASP
ARG
ARG
ALA
GLN
GLY
LEU

- Molecule 50: 40S ribosomal protein S5

Chain DF:  79% 16% 5%

MET
SER
THR
GLU
ALA
PRO
VAL
GLU
VAL
GLN
GLU
D13
E18
L25
A26
I29
Q35
T38
E39
T40
K41
H72
R76
Y77
R80
R81
F82
R83
N89
M100
G101
R102
N103
L118
T125
D126
Q127
N128
P129
V133
P142
R143
R157
V162

Q170
L198
S206
T207
K212
K213
S223
N224
R225

- Molecule 51: 40S ribosomal protein S6-A

Chain DG:  66% 26% 8%

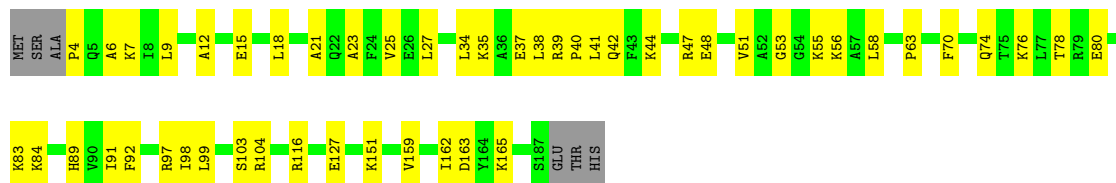
M1
K2
L3
M4
Y7
N10
G11
K14
T15
T24
F28
D29
K30
R31
G32
G33
Q34
Y48
K51
I52
D57
K58
Q59
L68
L69
P70
T78
K79
N80
V81
S82
C83
P86
R87
R92
K93
R98
T101
V102
D105
L106
A107
V108
L109
A110

E118
Q119
E120
L121
E122
G123
K131
R132
L133
A138
N139
I141
S148
K149
D155
R159
R160
K171
A172
P173
R183
L184
Q185
R186
K187
R188
R191
A192
L193
K194
N197
Q201
E218
ARG
LYS
ALA
GLU
LYS
ALA
GLU
ILE
ARG
LYS
ARG
ALA
SER

SER
LEU
LYS
ALA

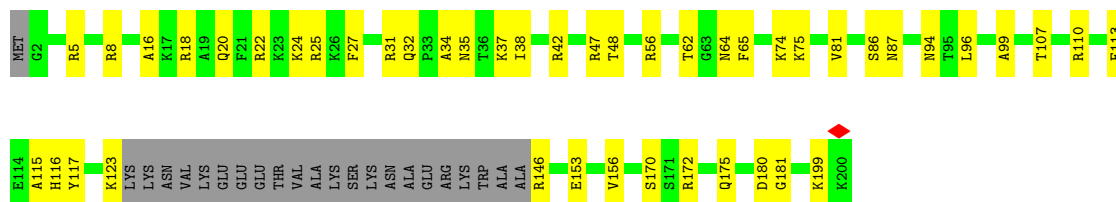
- Molecule 52: 40S ribosomal protein S7-A

Chain DH:  71% 26% .



- Molecule 53: 40S ribosomal protein S8-A

Chain DI:  66% 23% 12%



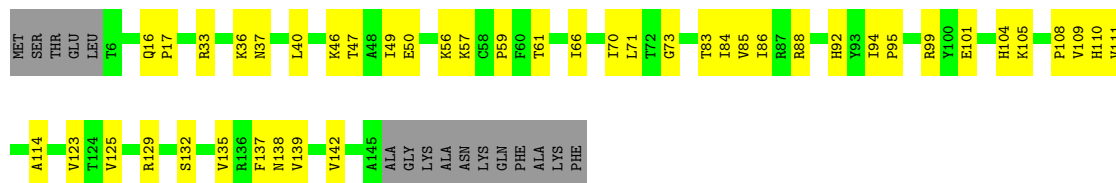
- Molecule 54: 40S ribosomal protein S9-A

Chain DJ:  81% 13% 6%



- Molecule 55: 40S ribosomal protein S11-A

Chain DL:  62% 28% 10%



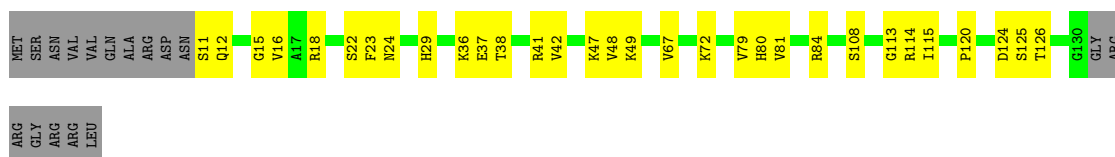
- Molecule 56: 40S ribosomal protein S13

Chain DN:  86% 13% .



- Molecule 57: 40S ribosomal protein S14-A

Chain DO:  65% 23% 12%



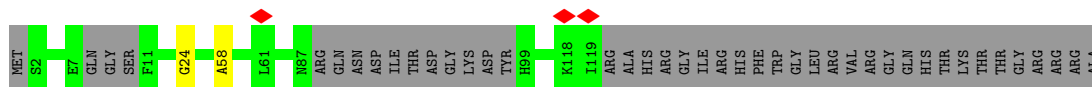
- Molecule 58: 40S ribosomal protein S16-A

Chain DQ: 75% 11% 13%



- Molecule 59: 40S ribosomal protein S18-A

Chain DS: 70% 29%



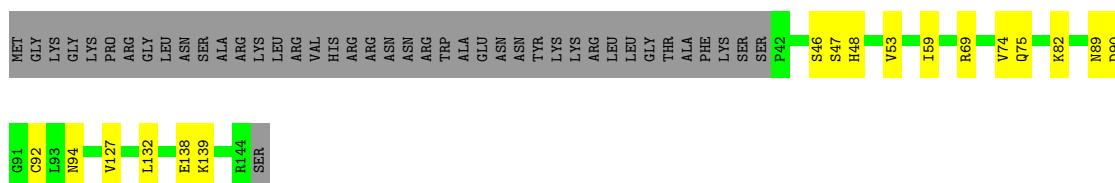
- Molecule 60: 40S ribosomal protein S22-A

Chain DW: 86% 13%



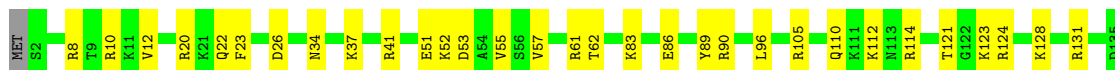
- Molecule 61: 40S ribosomal protein S23-A

Chain DX: 59% 12% 29%



- Molecule 62: 40S ribosomal protein S24-A

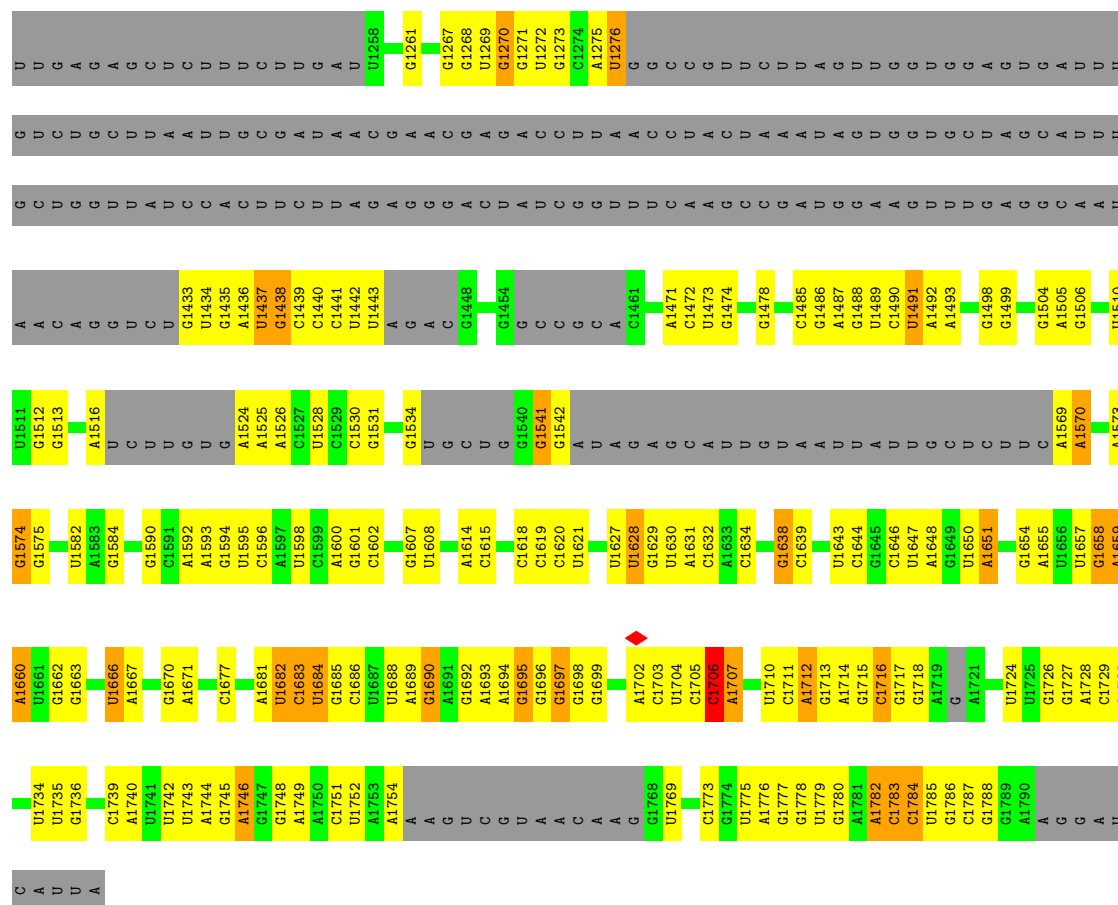
Chain DY: 76% 23%



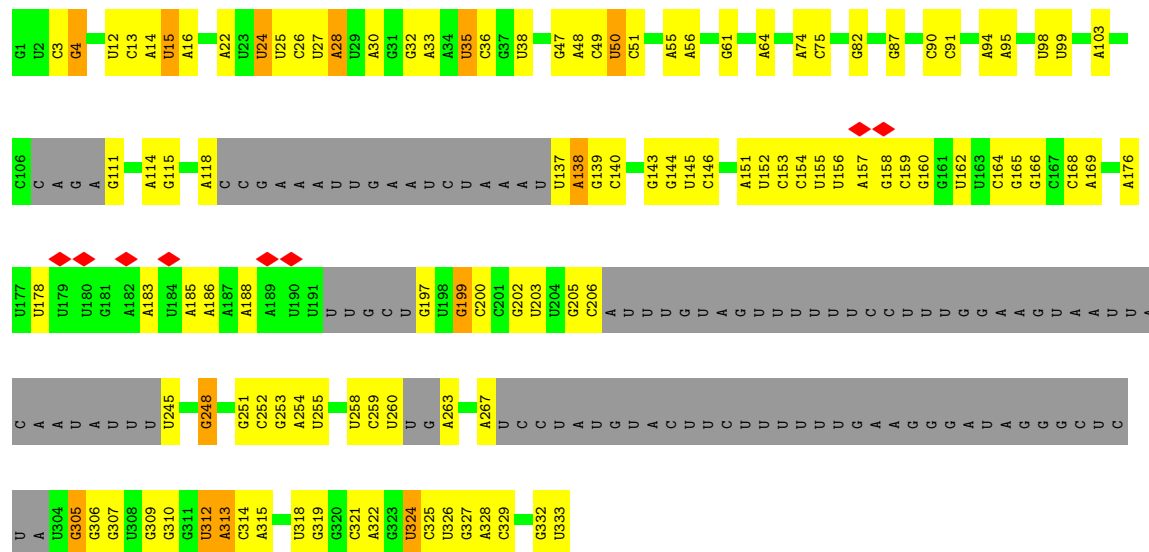
- Molecule 63: 40S ribosomal protein S27-A

Chain Db: 88% 11%





• Molecule 67: U3 snoRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43601	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	0.212	Depositor
Minimum map value	-0.128	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 ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CA	0.48	0/1917	0.61	0/2588
1	CB	0.30	0/1815	0.56	0/2448
2	DA	0.39	0/1937	0.59	0/2593
3	JA	0.22	0/6021	0.59	2/8176 (0.0%)
3	JB	0.24	0/4128	0.62	1/5747 (0.0%)
4	UA	0.56	0/6780	0.72	4/9175 (0.0%)
5	UB	0.26	0/3787	0.66	4/5126 (0.1%)
6	UC	0.39	0/1034	0.56	0/1365
7	UD	0.35	0/5461	0.60	0/7395
8	UE	0.38	0/3840	0.60	0/5208
9	UF	0.31	0/2538	0.51	0/3405
10	UG	0.55	0/4302	0.68	2/5805 (0.0%)
11	UH	0.30	1/2716 (0.0%)	0.76	7/3721 (0.2%)
12	UI	0.22	0/875	0.53	0/1176
13	UJ	0.30	0/9111	0.58	1/12323 (0.0%)
14	UK	0.39	0/2047	0.55	0/2711
15	UL	0.29	0/6857	0.58	0/9253
16	UM	0.28	0/6070	0.56	2/8216 (0.0%)
17	UN	0.41	0/1252	0.58	1/1688 (0.1%)
18	UO	0.37	0/3993	0.58	0/5413
19	UP	0.24	0/499	0.51	0/659
20	UQ	0.32	0/6794	0.56	0/9203
21	UR	0.51	0/3883	0.63	2/5265 (0.0%)
22	US	0.28	0/3703	0.66	3/5053 (0.1%)
23	UT	0.23	0/17584	0.57	2/23824 (0.0%)
24	UU	0.50	0/6815	0.63	0/9213
25	UV	0.23	0/8945	0.50	2/12097 (0.0%)
26	UX	0.51	0/1418	0.63	0/1906
27	UZ	0.27	0/2041	0.62	3/2745 (0.1%)
28	CD	0.35	0/3041	0.51	0/4098
29	CE	0.32	0/3362	0.54	1/4533 (0.0%)
30	CF	0.43	0/944	0.56	0/1284

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CG	0.44	0/941	0.63	0/1281
31	CH	0.34	0/3798	0.58	0/5113
32	CI	0.62	0/1559	0.74	0/2097
33	CJ	0.50	0/2337	0.69	1/3148 (0.0%)
34	CK	0.38	0/1685	0.59	1/2261 (0.0%)
35	CL	0.40	0/6471	0.58	0/8708
36	CM	0.30	0/2832	0.49	0/3825
37	CN	0.21	0/1934	0.46	0/2604
38	JC	0.22	0/2908	0.64	0/3938
39	JF	0.21	0/1727	0.49	0/2329
39	JG	0.30	0/1828	0.57	0/2470
40	JH	0.13	0/1293	0.38	0/1801
41	JI	0.24	0/1313	0.56	0/1830
42	JJ	0.27	0/1469	0.55	0/1980
43	JK	0.20	0/342	0.54	0/462
44	JM	0.33	0/1156	0.53	0/1536
45	JN	0.42	0/1435	0.68	1/1907 (0.1%)
46	JO	0.40	0/1910	0.61	0/2569
47	JP	0.56	0/3844	0.71	2/5174 (0.0%)
48	JQ	0.32	0/385	0.74	0/529
49	DE	0.27	0/1985	0.55	0/2675
50	DF	0.45	0/1690	0.64	2/2285 (0.1%)
51	DG	0.21	0/1779	0.51	0/2379
52	DH	0.28	0/1506	0.56	0/2028
53	DI	0.20	0/1422	0.50	0/1899
54	DJ	0.46	0/1519	0.61	2/2035 (0.1%)
55	DL	0.19	0/1155	0.51	0/1557
56	DN	0.34	0/1215	0.51	0/1638
57	DO	0.39	0/892	0.53	0/1202
58	DQ	0.55	0/990	0.69	0/1335
59	DS	0.22	0/513	0.53	0/711
60	DW	0.45	0/1038	0.58	0/1395
61	DX	0.45	0/798	0.63	0/1065
62	DY	0.37	0/1087	0.51	0/1449
63	Db	0.38	0/620	0.51	0/838
64	Dc	0.42	0/499	0.61	0/670
65	D2	0.37	0/10633	0.45	1/16564 (0.0%)
66	D3	0.34	0/31617	0.46	3/49213 (0.0%)
67	D4	0.37	0/5436	0.44	0/8446
All	All	0.36	1/243071 (0.0%)	0.56	50/338358 (0.0%)

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

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	JA	0	1
4	UA	0	1
11	UH	0	1
15	UL	0	2
16	UM	0	6
17	UN	0	1
23	UT	0	2
24	UU	0	1
25	UV	0	1
28	CD	0	1
31	CH	0	1
34	CK	0	1
46	JO	0	1
47	JP	0	2
58	DQ	0	1
All	All	0	23

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	UH	83	GLY	C-O	6.00	1.30	1.24

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	DF	162	VAL	CA-C-N	10.74	137.01	120.68
50	DF	162	VAL	C-N-CA	10.74	137.01	120.68
11	UH	520	PRO	CA-N-CD	-8.87	99.58	112.00
27	UZ	208	SER	CA-C-N	8.70	125.72	120.24
27	UZ	208	SER	C-N-CA	8.70	125.72	120.24

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	JA	46	SER	Peptide
4	UA	289	LEU	Peptide
11	UH	532	PHE	Peptide
15	UL	183	ASP	Peptide
15	UL	552	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	1881	0	1928	25	0
1	CB	1782	0	1826	32	0
2	DA	1912	0	2023	36	0
3	JA	5916	0	5463	137	0
3	JB	4132	0	1819	12	0
4	UA	6635	0	6525	108	0
5	UB	3734	0	3432	50	0
6	UC	1026	0	1080	17	0
7	UD	5361	0	5364	122	0
8	UE	3772	0	3806	72	0
9	UF	2487	0	2533	37	0
10	UG	4218	0	4223	60	0
11	UH	2701	0	1951	54	0
12	UI	860	0	922	15	0
13	UJ	8961	0	9273	182	0
14	UK	2021	0	2098	31	0
15	UL	6726	0	6764	121	0
16	UM	5969	0	6006	120	0
17	UN	1227	0	1223	21	0
18	UO	3911	0	3906	75	0
19	UP	495	0	561	13	0
20	UQ	6662	0	6588	141	0
21	UR	3799	0	3783	61	0
22	US	3622	0	3214	69	0
23	UT	17290	0	16616	387	0
24	UU	6678	0	6652	102	0
25	UV	8736	0	8850	162	0
26	UX	1395	0	1473	25	0
27	UZ	2006	0	2118	38	0
28	CD	2994	0	3018	43	0
29	CE	3325	0	3414	54	0
30	CF	931	0	983	8	0
30	CG	928	0	976	20	0
31	CH	3725	0	3746	51	0
32	CI	1530	0	1572	33	0
33	CJ	2296	0	2325	43	0
34	CK	1667	0	1701	30	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	CL	6332	0	6515	139	0
36	CM	2781	0	2878	36	0
37	CN	1893	0	1875	35	0
38	JC	2845	0	2761	87	0
39	JF	1701	0	1767	23	0
39	JG	1799	0	1872	48	0
40	JH	1295	0	570	3	0
41	JI	1314	0	610	0	0
42	JJ	1442	0	1513	29	0
43	JK	334	0	313	11	0
44	JM	1137	0	1188	23	0
45	JN	1428	0	1425	18	0
46	JO	1876	0	1968	23	0
47	JP	3765	0	3714	67	0
48	JQ	381	0	255	5	0
49	DE	1944	0	2030	44	0
50	DF	1669	0	1724	24	0
51	DG	1755	0	1846	48	0
52	DH	1481	0	1572	42	0
53	DI	1399	0	1431	42	0
54	DJ	1494	0	1573	18	0
55	DL	1129	0	1196	32	0
56	DN	1192	0	1255	17	0
57	DO	881	0	910	24	0
58	DQ	973	0	1029	14	0
59	DS	516	0	222	1	0
60	DW	1021	0	1060	15	0
61	DX	786	0	843	13	0
62	DY	1073	0	1132	24	0
63	Db	610	0	631	7	0
64	Dc	497	0	535	6	0
65	D2	9508	0	4781	120	0
66	D3	28287	0	14259	499	0
67	D4	4872	0	2469	66	0
68	Db	1	0	0	0	0
68	UX	1	0	0	0	0
69	CL	1	0	0	0	0
69	UX	1	0	0	0	0
70	CL	32	0	12	25	0
All	All	234757	0	209489	3802	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 3802 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)
35:CL:210:VAL:HG21	70:CL:2001:GTP:C5	1.53	1.43
35:CL:210:VAL:CG2	70:CL:2001:GTP:C5	2.05	1.39
52:DH:27:LEU:CD2	52:DH:84:LYS:HZ2	1.38	1.36
52:DH:27:LEU:CD2	52:DH:84:LYS:NZ	1.88	1.35
4:UA:77:GLY:HA3	4:UA:95:PHE:O	1.30	1.32

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	CA	238/327 (73%)	220 (92%)	18 (8%)	0	100	100
1	CB	224/327 (68%)	208 (93%)	16 (7%)	0	100	100
2	DA	236/255 (92%)	217 (92%)	19 (8%)	0	100	100
3	JA	802/1056 (76%)	735 (92%)	67 (8%)	0	100	100
3	JB	827/1056 (78%)	758 (92%)	69 (8%)	0	100	100
4	UA	830/923 (90%)	758 (91%)	72 (9%)	0	100	100
5	UB	495/810 (61%)	470 (95%)	24 (5%)	1 (0%)	43	73
6	UC	124/610 (20%)	112 (90%)	12 (10%)	0	100	100
7	UD	663/776 (85%)	599 (90%)	64 (10%)	0	100	100
8	UE	465/643 (72%)	412 (89%)	53 (11%)	0	100	100
9	UF	283/440 (64%)	276 (98%)	7 (2%)	0	100	100
10	UG	529/554 (96%)	481 (91%)	48 (9%)	0	100	100
11	UH	426/713 (60%)	345 (81%)	58 (14%)	23 (5%)	1	16
12	UI	100/575 (17%)	97 (97%)	3 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	UJ	1092/1769 (62%)	1030 (94%)	62 (6%)	0	100	100
14	UK	238/250 (95%)	219 (92%)	19 (8%)	0	100	100
15	UL	828/943 (88%)	752 (91%)	75 (9%)	1 (0%)	48	79
16	UM	750/817 (92%)	674 (90%)	74 (10%)	2 (0%)	36	67
17	UN	143/899 (16%)	132 (92%)	11 (8%)	0	100	100
18	UO	489/513 (95%)	446 (91%)	43 (9%)	0	100	100
19	UP	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
20	UQ	820/896 (92%)	750 (92%)	70 (8%)	0	100	100
21	UR	474/594 (80%)	434 (92%)	40 (8%)	0	100	100
22	US	488/552 (88%)	445 (91%)	41 (8%)	2 (0%)	30	62
23	UT	2213/2493 (89%)	2086 (94%)	127 (6%)	0	100	100
24	UU	842/939 (90%)	776 (92%)	66 (8%)	0	100	100
25	UV	1069/1237 (86%)	1020 (95%)	49 (5%)	0	100	100
26	UX	170/189 (90%)	161 (95%)	9 (5%)	0	100	100
27	UZ	245/274 (89%)	225 (92%)	20 (8%)	0	100	100
28	CD	376/504 (75%)	358 (95%)	18 (5%)	0	100	100
29	CE	431/511 (84%)	397 (92%)	34 (8%)	0	100	100
30	CF	121/126 (96%)	115 (95%)	6 (5%)	0	100	100
30	CG	121/126 (96%)	116 (96%)	5 (4%)	0	100	100
31	CH	459/573 (80%)	419 (91%)	37 (8%)	3 (1%)	18	51
32	CI	180/183 (98%)	167 (93%)	13 (7%)	0	100	100
33	CJ	278/290 (96%)	249 (90%)	29 (10%)	0	100	100
34	CK	203/593 (34%)	186 (92%)	16 (8%)	1 (0%)	24	57
35	CL	771/1183 (65%)	731 (95%)	40 (5%)	0	100	100
36	CM	358/367 (98%)	342 (96%)	16 (4%)	0	100	100
37	CN	224/297 (75%)	204 (91%)	20 (9%)	0	100	100
38	JC	350/707 (50%)	313 (89%)	37 (11%)	0	100	100
39	JF	212/252 (84%)	203 (96%)	9 (4%)	0	100	100
39	JG	226/252 (90%)	217 (96%)	9 (4%)	0	100	100
40	JH	257/483 (53%)	248 (96%)	9 (4%)	0	100	100
41	JI	263/1729 (15%)	255 (97%)	8 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	JJ	180/274 (66%)	171 (95%)	9 (5%)	0	100	100
43	JK	40/534 (8%)	33 (82%)	7 (18%)	0	100	100
44	JM	129/217 (59%)	122 (95%)	7 (5%)	0	100	100
45	JN	178/346 (51%)	162 (91%)	14 (8%)	2 (1%)	11	41
46	JO	226/316 (72%)	212 (94%)	14 (6%)	0	100	100
47	JP	457/489 (94%)	427 (93%)	30 (7%)	0	100	100
48	JQ	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
49	DE	243/261 (93%)	227 (93%)	16 (7%)	0	100	100
50	DF	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
51	DG	216/236 (92%)	205 (95%)	11 (5%)	0	100	100
52	DH	182/190 (96%)	171 (94%)	11 (6%)	0	100	100
53	DI	173/200 (86%)	162 (94%)	11 (6%)	0	100	100
54	DJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
55	DL	138/156 (88%)	129 (94%)	9 (6%)	0	100	100
56	DN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
57	DO	118/137 (86%)	111 (94%)	7 (6%)	0	100	100
58	DQ	123/143 (86%)	115 (94%)	8 (6%)	0	100	100
59	DS	98/146 (67%)	89 (91%)	9 (9%)	0	100	100
60	DW	127/130 (98%)	111 (87%)	16 (13%)	0	100	100
61	DX	101/145 (70%)	89 (88%)	11 (11%)	1 (1%)	12	43
62	DY	132/135 (98%)	129 (98%)	3 (2%)	0	100	100
63	Db	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
64	Dc	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
All	All	24593/34803 (71%)	22770 (93%)	1787 (7%)	36 (0%)	49	79

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	UH	59	PRO
11	UH	61	PRO
11	UH	68	PRO
11	UH	70	PRO
11	UH	235	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CA	202/240 (84%)	200 (99%)	2 (1%)	68	74
1	CB	192/240 (80%)	189 (98%)	3 (2%)	55	68
2	DA	212/224 (95%)	211 (100%)	1 (0%)	81	81
3	JA	555/934 (59%)	552 (100%)	3 (0%)	81	81
4	UA	730/812 (90%)	721 (99%)	9 (1%)	63	72
5	UB	344/732 (47%)	344 (100%)	0	100	100
6	UC	107/538 (20%)	107 (100%)	0	100	100
7	UD	615/713 (86%)	614 (100%)	1 (0%)	87	87
8	UE	428/574 (75%)	423 (99%)	5 (1%)	63	72
9	UF	277/414 (67%)	275 (99%)	2 (1%)	76	77
10	UG	462/480 (96%)	452 (98%)	10 (2%)	45	63
11	UH	152/657 (23%)	150 (99%)	2 (1%)	61	71
12	UI	99/533 (19%)	99 (100%)	0	100	100
13	UJ	1031/1633 (63%)	1023 (99%)	8 (1%)	73	76
14	UK	226/234 (97%)	225 (100%)	1 (0%)	84	83
15	UL	747/832 (90%)	741 (99%)	6 (1%)	73	76
16	UM	668/719 (93%)	663 (99%)	5 (1%)	76	77
17	UN	137/808 (17%)	136 (99%)	1 (1%)	76	77
18	UO	437/454 (96%)	431 (99%)	6 (1%)	59	70
19	UP	57/196 (29%)	57 (100%)	0	100	100
20	UQ	769/826 (93%)	767 (100%)	2 (0%)	86	84
21	UR	425/529 (80%)	422 (99%)	3 (1%)	76	77
22	US	332/506 (66%)	332 (100%)	0	100	100
23	UT	1787/2307 (78%)	1779 (100%)	8 (0%)	84	83
24	UU	743/819 (91%)	738 (99%)	5 (1%)	76	77
25	UV	986/1125 (88%)	985 (100%)	1 (0%)	88	89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	UX	156/169 (92%)	153 (98%)	3 (2%)	50	66
27	UZ	230/256 (90%)	229 (100%)	1 (0%)	84	83
28	CD	326/435 (75%)	325 (100%)	1 (0%)	86	84
29	CE	353/433 (82%)	348 (99%)	5 (1%)	59	70
30	CF	102/104 (98%)	102 (100%)	0	100	100
30	CG	101/104 (97%)	100 (99%)	1 (1%)	68	74
31	CH	406/503 (81%)	404 (100%)	2 (0%)	81	81
32	CI	171/172 (99%)	168 (98%)	3 (2%)	51	67
33	CJ	251/258 (97%)	248 (99%)	3 (1%)	63	72
34	CK	187/535 (35%)	186 (100%)	1 (0%)	81	81
35	CL	690/1039 (66%)	687 (100%)	3 (0%)	84	83
36	CM	307/312 (98%)	305 (99%)	2 (1%)	76	77
37	CN	212/274 (77%)	212 (100%)	0	100	100
38	JC	318/636 (50%)	316 (99%)	2 (1%)	78	79
39	JF	195/222 (88%)	194 (100%)	1 (0%)	81	81
39	JG	206/222 (93%)	206 (100%)	0	100	100
42	JJ	158/238 (66%)	158 (100%)	0	100	100
43	JK	35/482 (7%)	35 (100%)	0	100	100
44	JM	124/200 (62%)	122 (98%)	2 (2%)	55	68
45	JN	141/304 (46%)	141 (100%)	0	100	100
46	JO	210/289 (73%)	209 (100%)	1 (0%)	81	81
47	JP	416/443 (94%)	413 (99%)	3 (1%)	76	77
48	JQ	22/192 (12%)	22 (100%)	0	100	100
49	DE	209/222 (94%)	208 (100%)	1 (0%)	81	81
50	DF	180/191 (94%)	180 (100%)	0	100	100
51	DG	187/201 (93%)	187 (100%)	0	100	100
52	DH	165/170 (97%)	165 (100%)	0	100	100
53	DI	142/161 (88%)	142 (100%)	0	100	100
54	DJ	158/166 (95%)	158 (100%)	0	100	100
55	DL	125/137 (91%)	125 (100%)	0	100	100
56	DN	127/128 (99%)	127 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	DO	91/105 (87%)	91 (100%)	0	100	100
58	DQ	105/119 (88%)	104 (99%)	1 (1%)	68	74
60	DW	110/111 (99%)	110 (100%)	0	100	100
61	DX	85/120 (71%)	84 (99%)	1 (1%)	63	72
62	DY	112/113 (99%)	112 (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	19959/27976 (71%)	19838 (99%)	121 (1%)	76	79

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	UM	333	ILE
38	JC	192	ASN
23	UT	315	LEU
38	JC	50	ILE
49	DE	78	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 384 such sidechains are listed below:

Mol	Chain	Res	Type
23	UT	1630	ASN
30	CG	113	GLN
24	UU	291	HIS
25	UV	841	ASN
35	CL	157	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
65	D2	443/700 (63%)	121 (27%)	6 (1%)
66	D3	1303/1808 (72%)	442 (33%)	22 (1%)
67	D4	223/333 (66%)	63 (28%)	4 (1%)
All	All	1969/2841 (69%)	626 (31%)	32 (1%)

5 of 626 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
65	D2	6	A
65	D2	8	A
65	D2	14	U
65	D2	15	G
65	D2	58	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
67	D4	143	G
67	D4	151	A
66	D3	278	U
66	D3	139	C
67	D4	157	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 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
70	GTP	CL	2001	69	33,34,34	1.16	3 (9%)	50,54,54	1.74	7 (14%)

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
70	GTP	CL	2001	69	-	4/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
70	CL	2001	GTP	C5-C4	3.13	1.47	1.38
70	CL	2001	GTP	C6-N1	-2.51	1.34	1.38
70	CL	2001	GTP	C5-N7	-2.12	1.34	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	CL	2001	GTP	C5-C4-N3	-6.21	118.51	128.39
70	CL	2001	GTP	C2-N3-C4	5.08	121.05	112.30
70	CL	2001	GTP	N9-C4-N3	4.59	135.14	125.95
70	CL	2001	GTP	C6-C5-N7	3.22	136.14	130.29
70	CL	2001	GTP	C4-C5-N7	-2.56	106.61	110.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
70	CL	2001	GTP	C5'-O5'-PA-O3A
70	CL	2001	GTP	C5'-O5'-PA-O2A
70	CL	2001	GTP	C3'-C4'-C5'-O5'
70	CL	2001	GTP	O4'-C4'-C5'-O5'

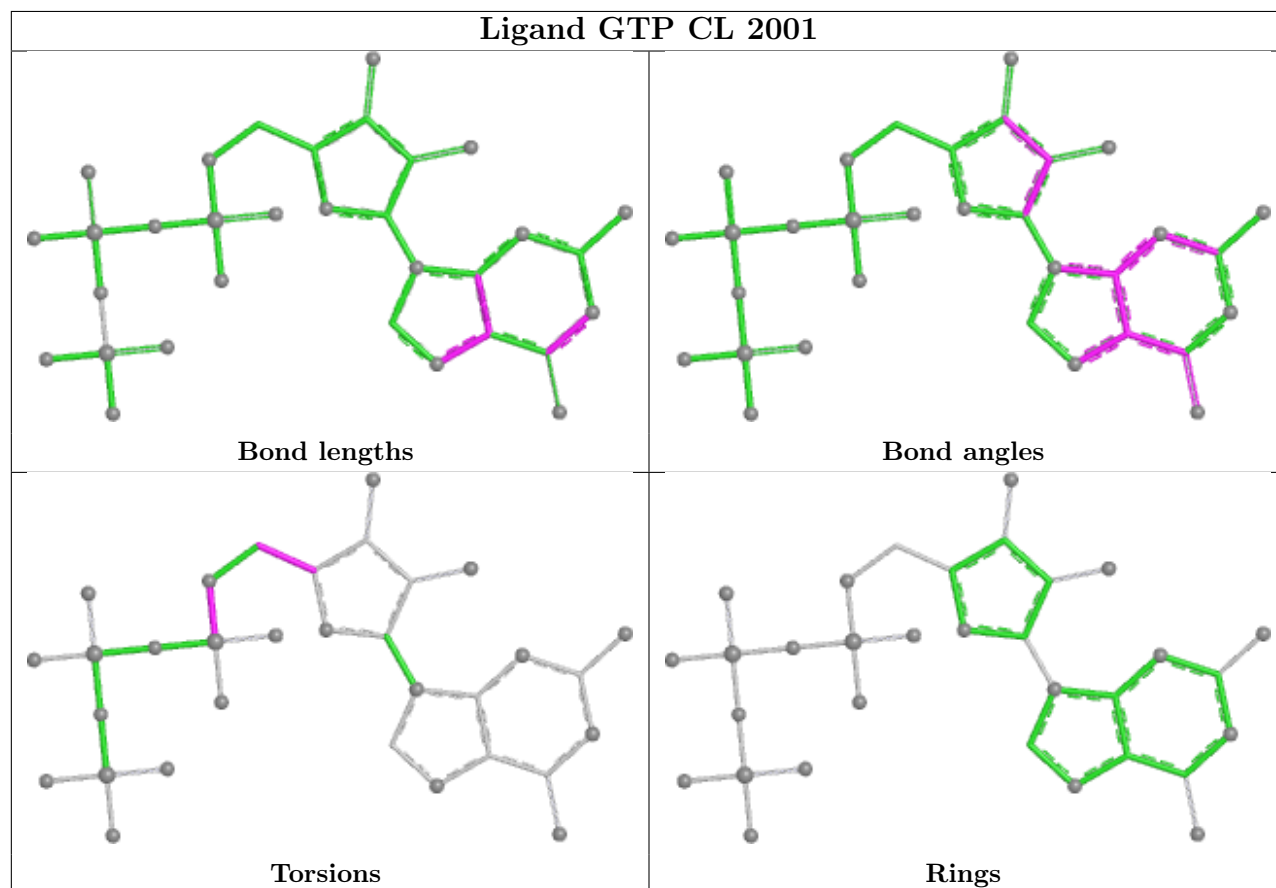
There are no ring outliers.

1 monomer is involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
70	CL	2001	GTP	25	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

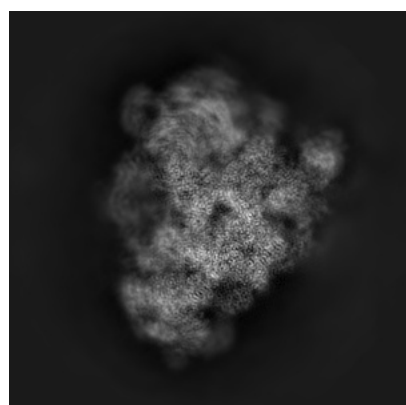
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11359. These allow visual inspection of the internal detail of the map and identification of artifacts.

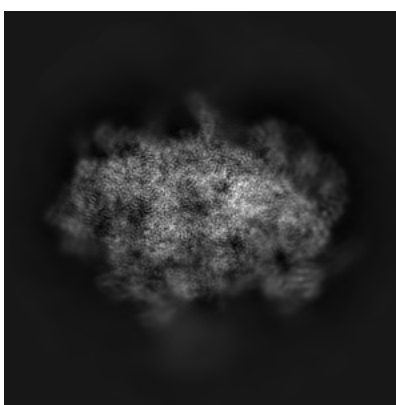
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

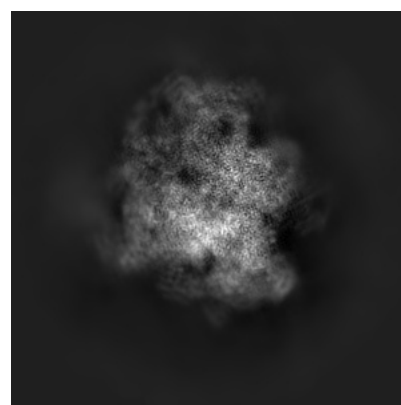
6.1.1 Primary map



X



Y

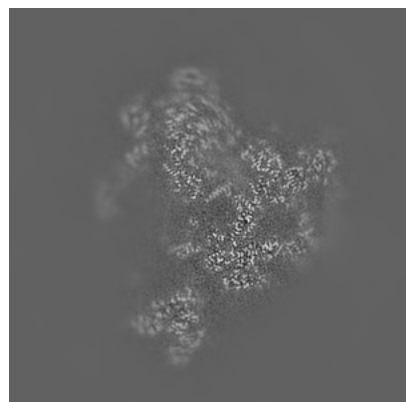


Z

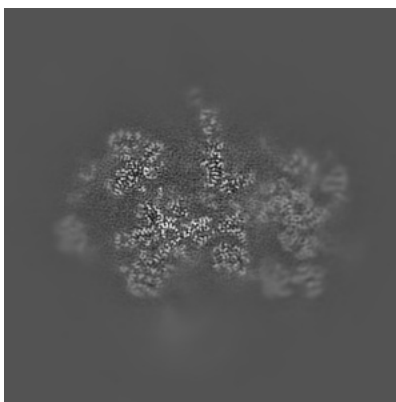
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

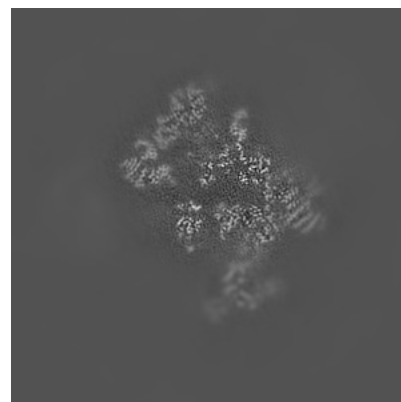
6.2.1 Primary map



X Index: 240



Y Index: 240

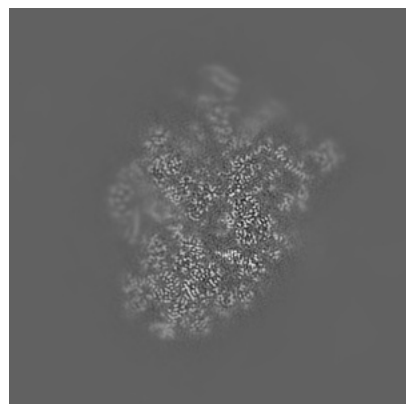


Z Index: 240

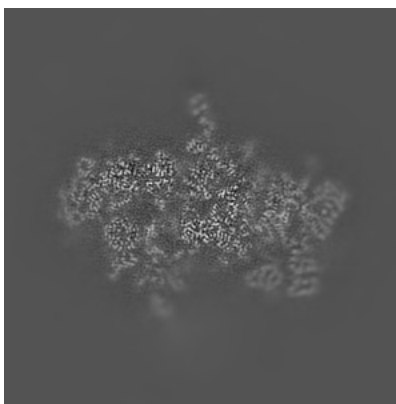
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

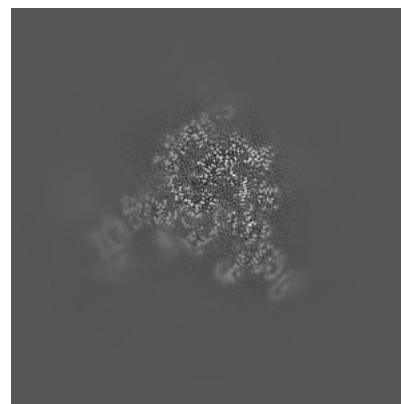
6.3.1 Primary map



X Index: 281



Y Index: 221

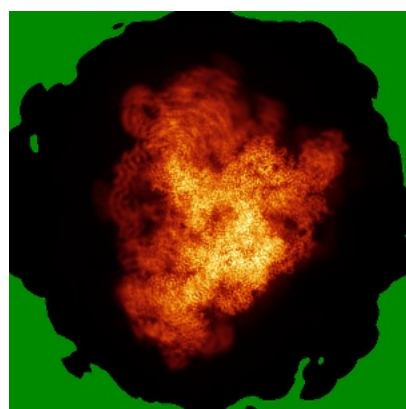


Z Index: 183

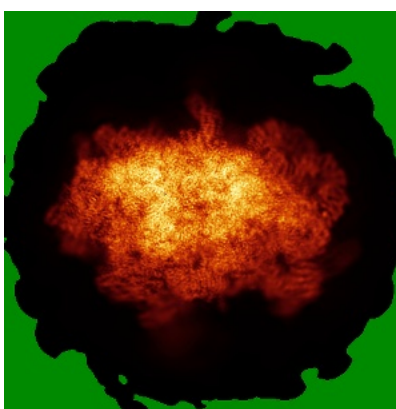
The images above show the largest variance slices of the map in three orthogonal directions.

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

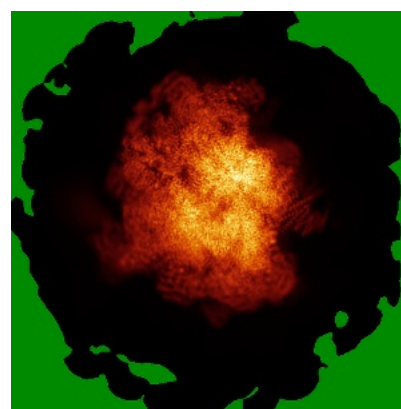
6.4.1 Primary map



X



Y

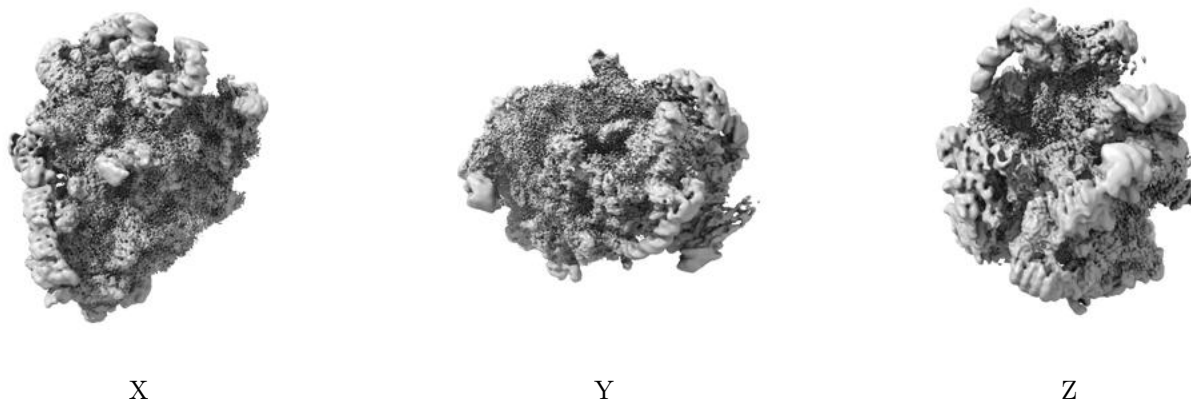


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

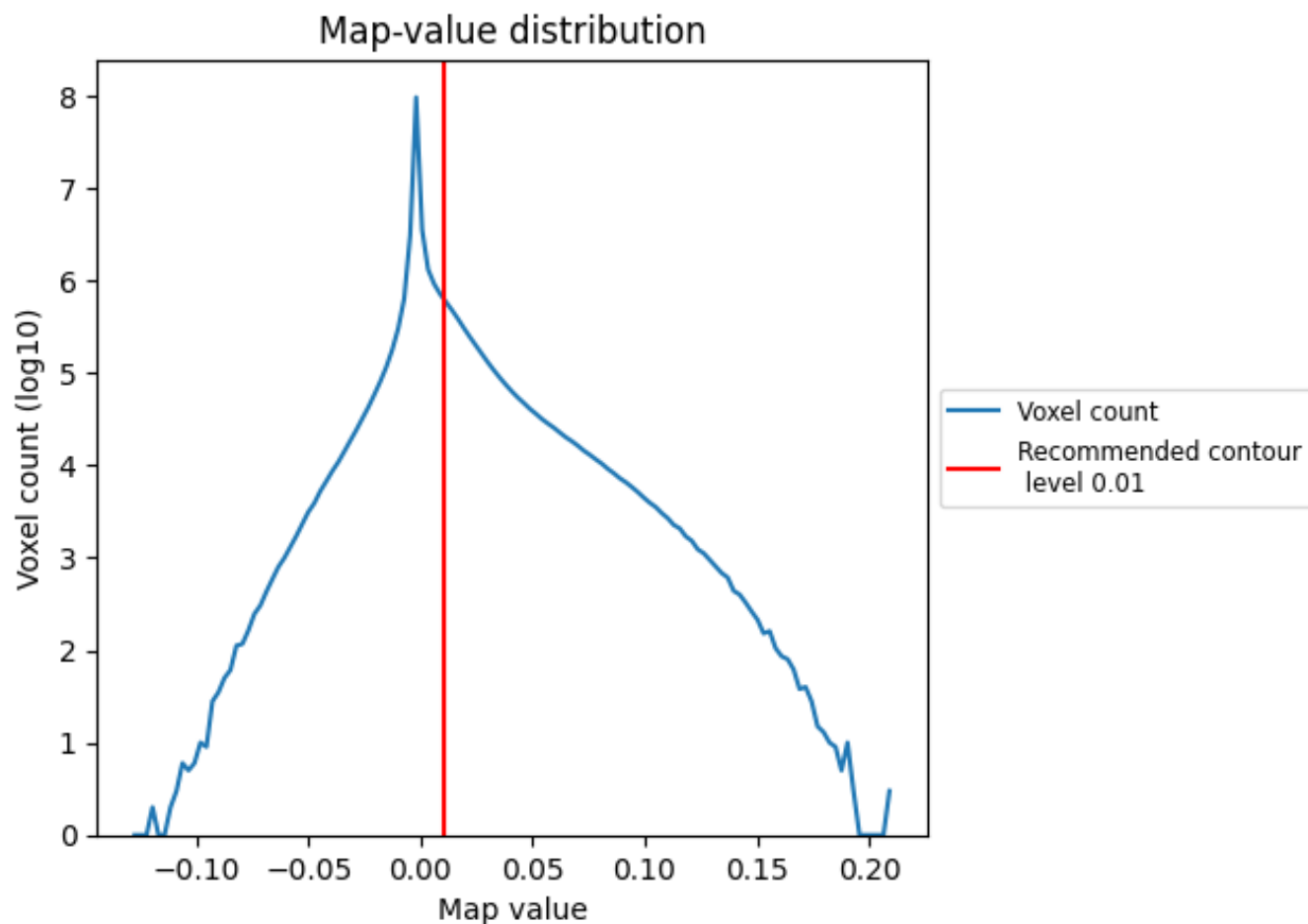
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

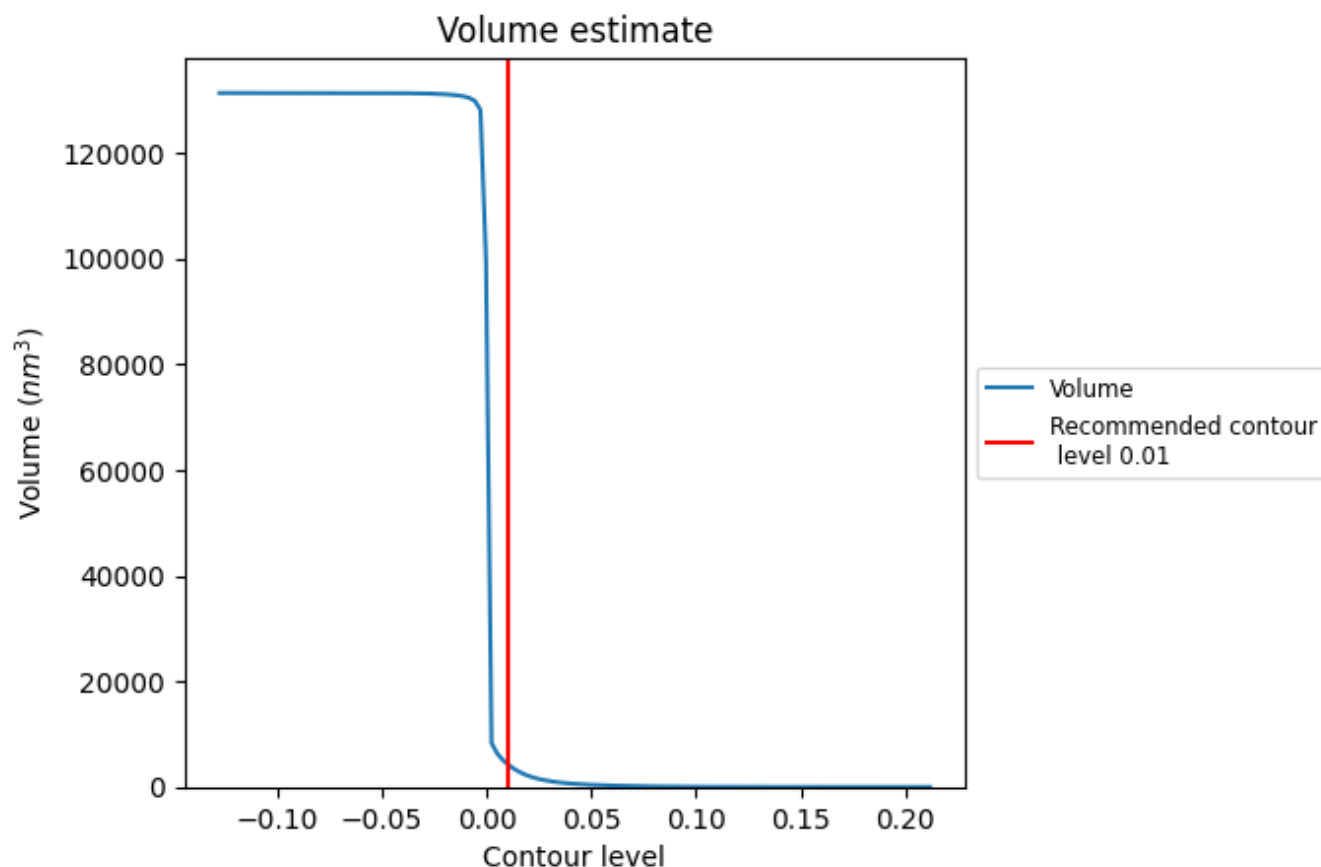
This section contains the results of statistical analysis of the map.

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.

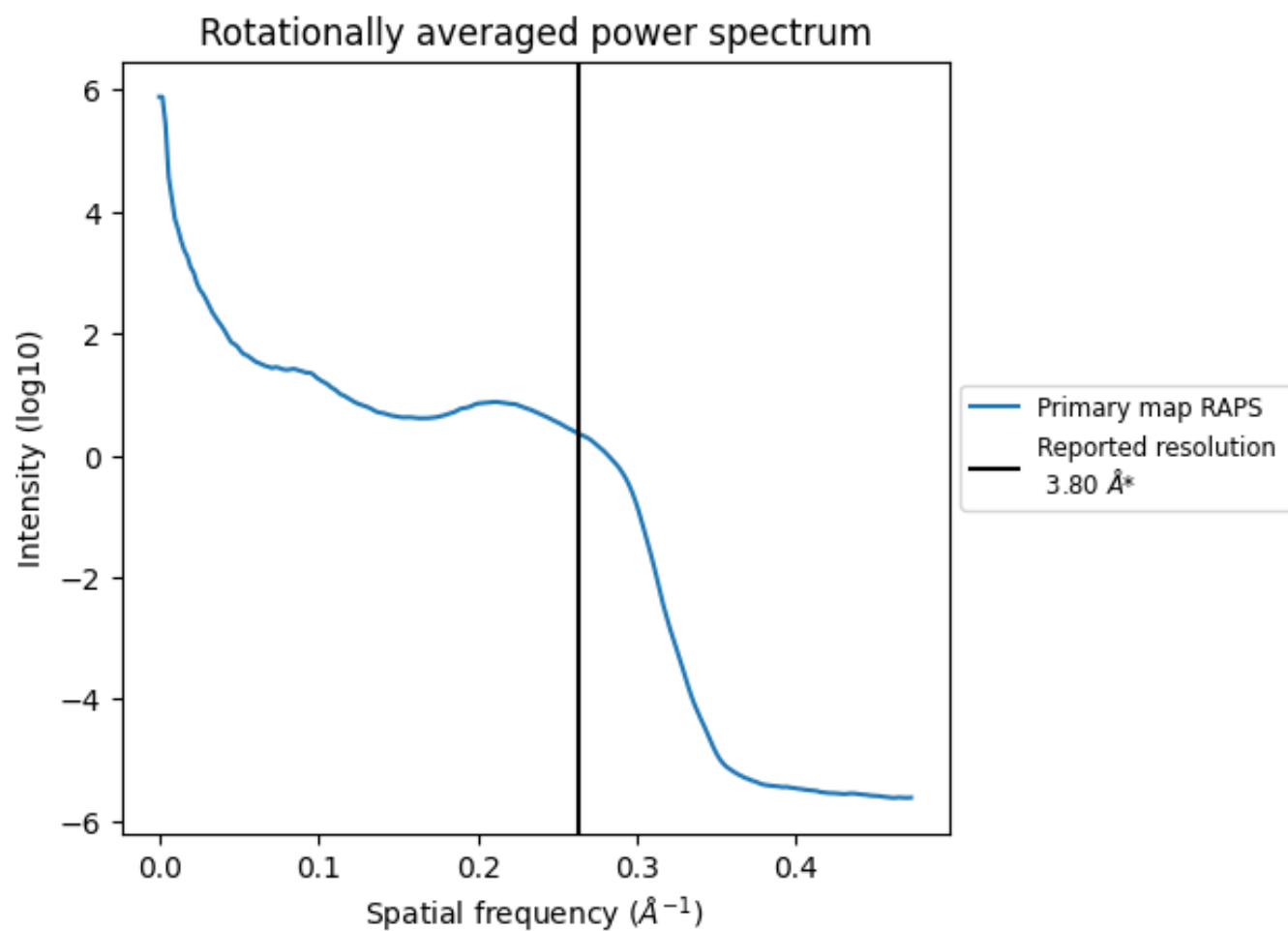
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4324 nm^3 ; this corresponds to an approximate mass of 3906 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

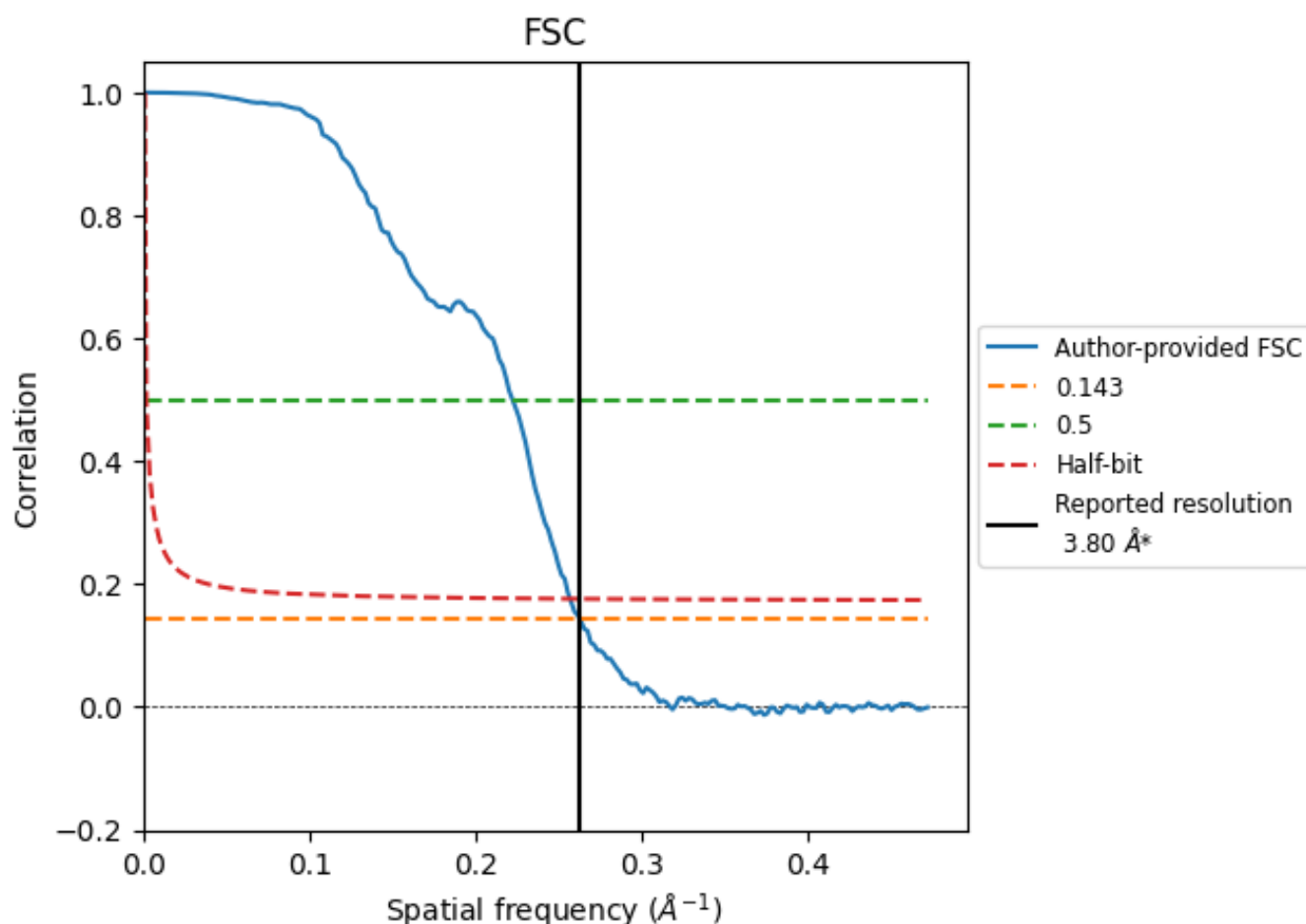


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

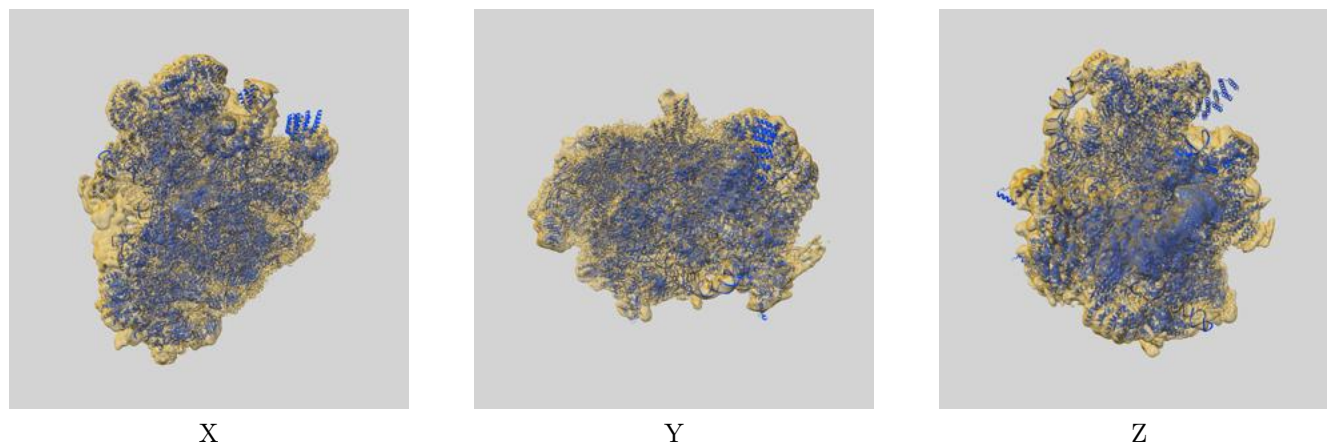
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.80	4.49	3.89
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

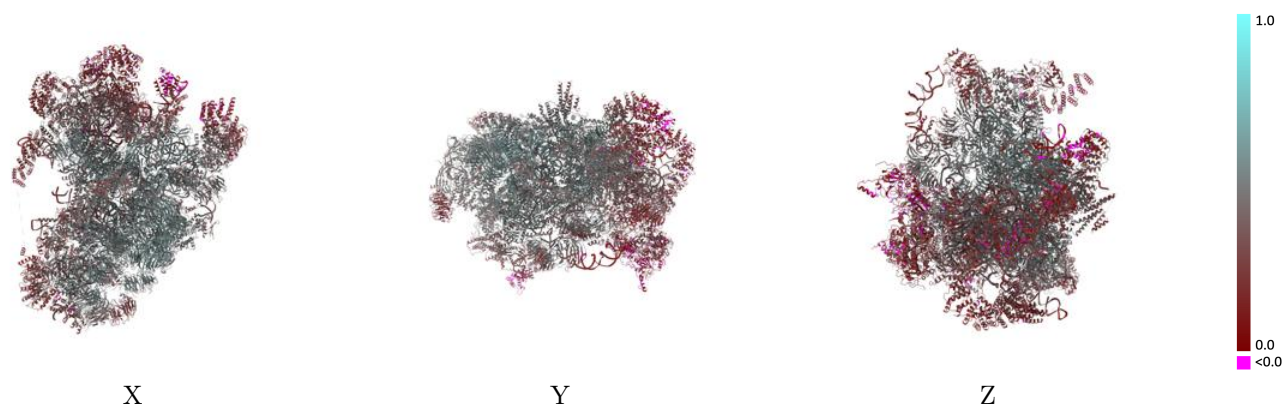
This section contains information regarding the fit between EMDB map EMD-11359 and PDB model 6ZQC. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



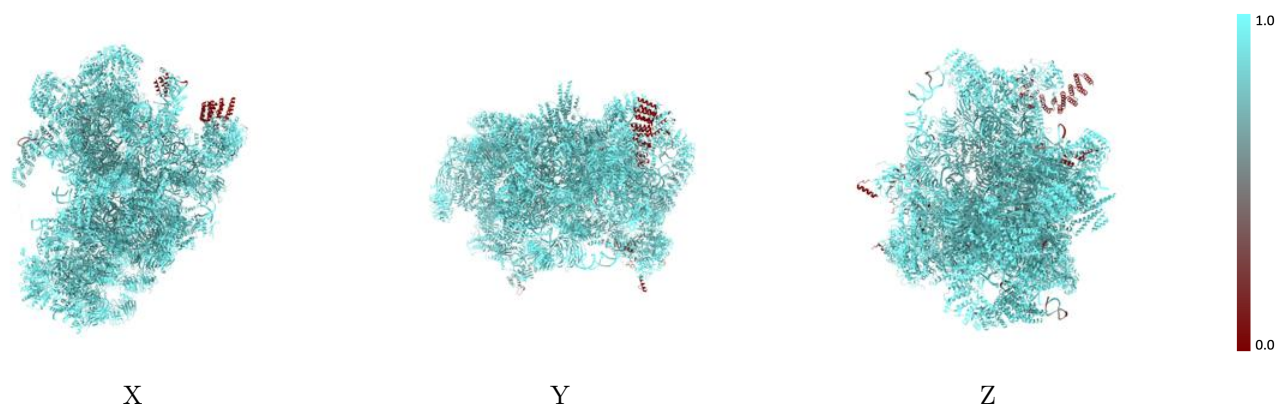
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



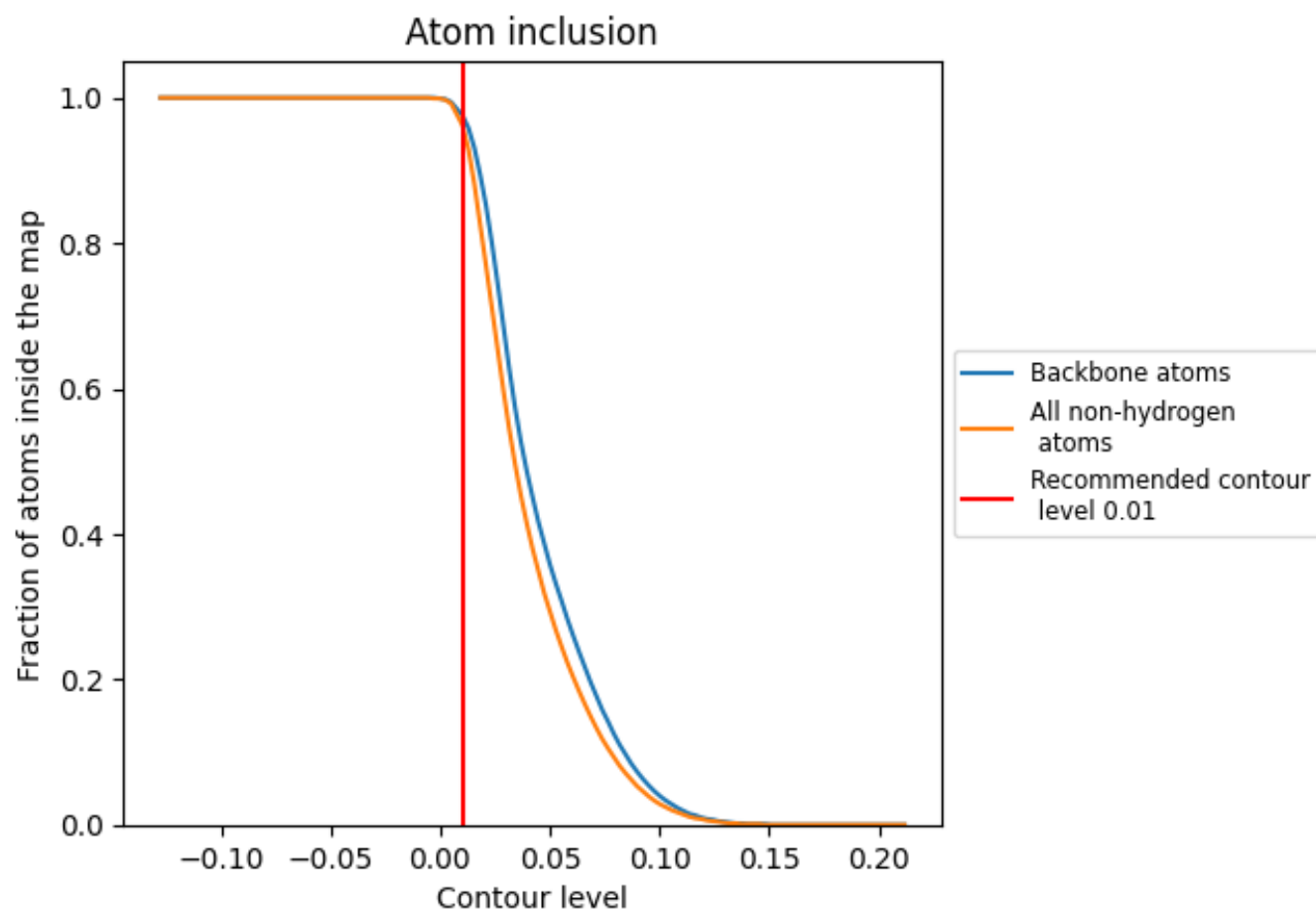
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9630	 0.4100
CA	 0.9800	 0.5280
CB	 0.9720	 0.4530
CD	 0.9790	 0.4550
CE	 0.9690	 0.4250
CF	 0.9880	 0.5300
CG	 0.9790	 0.5190
CH	 0.9840	 0.4790
CI	 0.9790	 0.5590
CJ	 0.9760	 0.5240
CK	 0.9690	 0.4920
CL	 0.9790	 0.4900
CM	 0.9750	 0.4690
CN	 0.9520	 0.3260
D2	 0.9820	 0.4330
D3	 0.9730	 0.3830
D4	 0.9420	 0.4140
DA	 0.9650	 0.4940
DE	 0.9680	 0.4160
DF	 0.9790	 0.5210
DG	 0.9450	 0.3320
DH	 0.9390	 0.3600
DI	 0.9620	 0.2980
DJ	 0.9740	 0.5200
DL	 0.9570	 0.3380
DN	 0.9680	 0.4820
DO	 0.9790	 0.5000
DQ	 0.9730	 0.5490
DS	 0.9380	 0.3330
DW	 0.9750	 0.5320
DX	 0.9760	 0.5200
DY	 0.9860	 0.5030
Db	 0.9870	 0.5290
Dc	 0.9810	 0.5220
JA	 0.9270	 0.2550



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
JB	 0.8650	 0.1600
JC	 0.9410	 0.2480
JF	 0.9660	 0.3720
JG	 0.9690	 0.4620
JH	 0.8600	 0.1180
JI	 0.2280	 0.1810
JJ	 0.9770	 0.4310
JK	 0.9420	 0.2260
JM	 0.9640	 0.4550
JN	 0.9710	 0.5090
JO	 0.9730	 0.4970
JP	 0.9820	 0.5460
JQ	 0.9840	 0.4020
UA	 0.9860	 0.5560
UB	 0.9650	 0.3190
UC	 0.9730	 0.4750
UD	 0.9800	 0.4500
UE	 0.9810	 0.4820
UF	 0.9750	 0.4240
UG	 0.9840	 0.5410
UH	 0.9800	 0.2630
UI	 0.9670	 0.3210
UJ	 0.9570	 0.3340
UK	 0.9790	 0.4920
UL	 0.9770	 0.4350
UM	 0.9700	 0.4210
UN	 0.9550	 0.4720
UO	 0.9810	 0.4900
UP	 0.9630	 0.4240
UQ	 0.9830	 0.4610
UR	 0.9810	 0.5350
US	 0.9710	 0.3450
UT	 0.9490	 0.2540
UU	 0.9870	 0.5400
UV	 0.9690	 0.3510
UX	 0.9820	 0.5500
UZ	 0.9780	 0.4170