



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:01 PM UTC

PDB ID : 7SUK / pdb_00007suk
EMDB ID : EMD-25441
Title : Structure of Bfr2-Lcp5 Complex Observed in the Small Subunit Processome
Isolated from R2TP-depleted Yeast Cells
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-11-17
Resolution : 3.99 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:

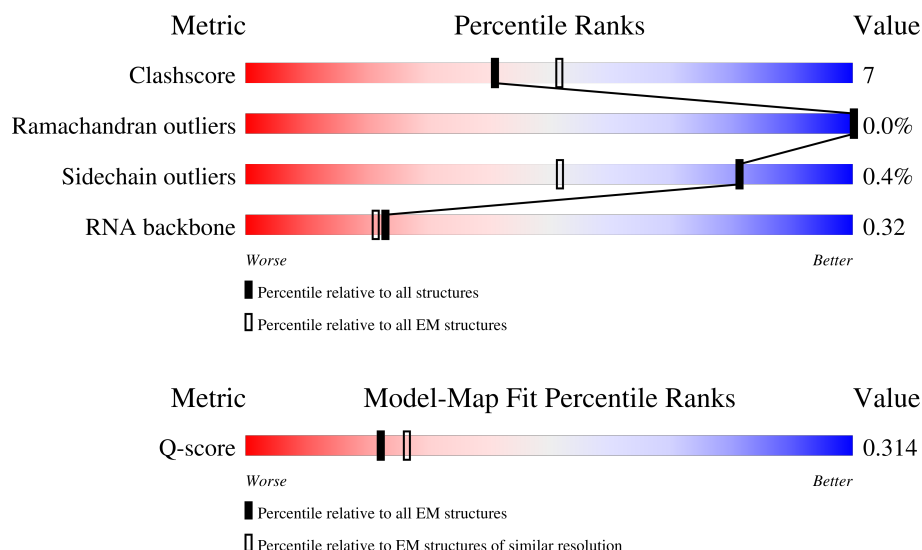
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.99 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.



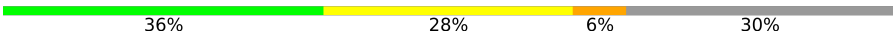
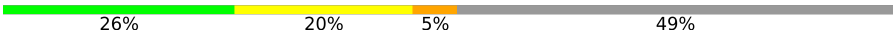
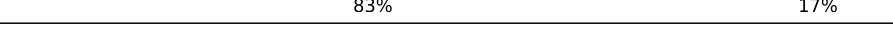
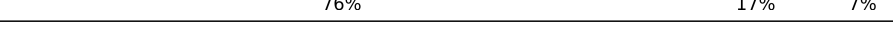
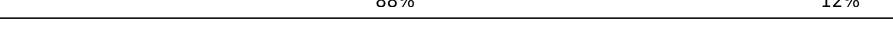
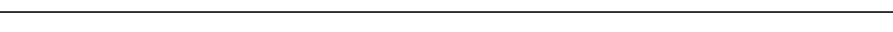
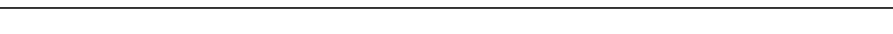
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7463 (3.49 - 4.49)

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	NA	245	
2	SA	413	
3	NB	180	

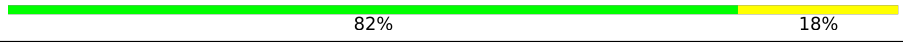
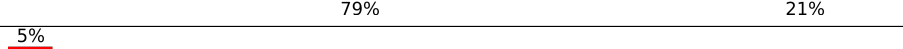
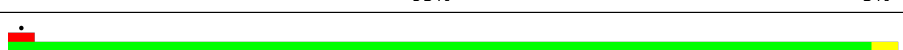
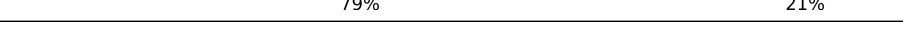
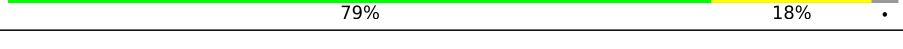
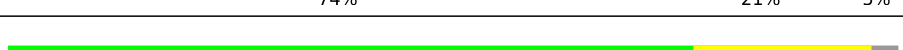
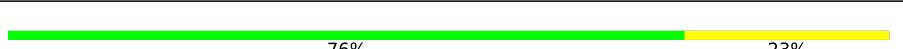
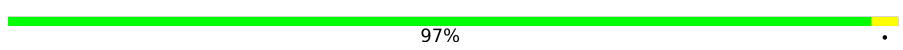
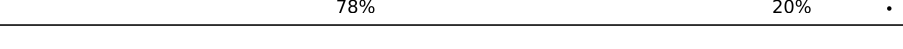
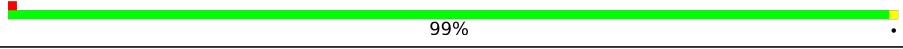
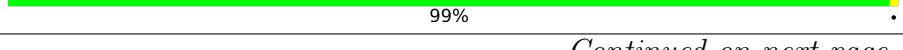
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	L0	700	
5	L2	333	
6	L3	127	
7	L4	228	
8	L5	213	
9	L7	190	
10	L8	200	
11	L9	175	
12	LC	125	
13	LD	156	
14	LE	127	
15	LF	90	
16	LG	63	
17	LH	896	
18	LJ	513	
19	LK	123	
20	LL	555	
21	LM	431	
22	LN	748	
23	LO	855	
24	LP	420	
25	LQ	939	
26	LS	594	
27	LT	921	
28	LU	465	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LV	362	
30	LW	438	
31	LZ	182	
32	NG	111	
33	NK	175	
34	SC	247	
34	SD	247	
35	SE	121	
35	SF	121	
36	SG	464	
37	SH	360	
38	SI	1123	
39	SJ	236	
39	SK	236	
40	SL	183	
41	SM	290	
42	SN	247	
43	SO	179	
44	SQ	167	
45	SR	104	
46	SS	197	
47	ST	806	
48	SY	248	
49	SZ	261	
50	NJ	265	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
51	NH	1141	
52	NI	187	
53	8	1807	
54	SU	513	
55	LI	687	
56	ND	60	
57	LR	811	
58	NE	240	
59	SB	436	
60	SV	92	
61	SP	2418	
62	LX	923	
62	LY	923	
63	L6	219	
64	NF	124	
65	5	534	
66	6	357	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 213241 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 U3 small nucleolar RNA-associated protein MPP10.

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

- Molecule 2 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	370	Total	C	N	O	S	0	0
			2854	1815	490	541	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	NB	142	Total	C	N	O		0	0
			1098	677	218	203			

- Molecule 4 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L0	488	Total	C	N	O	P	0	0
			10405	4650	1838	3429	488		

- Molecule 5 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L2	169	Total	C	N	O	P	0	0
			3585	1605	629	1182	169		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	200	C	G	conflict	GB 751247007

- Molecule 6 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L3	113	Total	C	N	O	S	0	0
			901	569	168	162	2		

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	228	Total	C	N	O	S	0	0
			1810	1158	330	319	3		

- Molecule 8 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L7	165	Total	C	N	O	S	0	0
			1321	854	227	240			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L8	170	Total	C	N	O	S	0	0
			1349	839	267	241	2		

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L9	175	Total	C	N	O	S	0	0
			1415	895	273	246	1		

- Molecule 12 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LC	125	Total	C	N	O	S	0	0
			973	625	174	174			

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	127	Total	C	N	O	S	0	0
			1027	660	194	170	3		

- Molecule 14 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LF	90	Total	C	N	O	S	0	0
			715	458	131	126			

- Molecule 16 is a protein called 40S ribosomal protein S28-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LH	834	Total	C	N	O	S	0	0
			6633	4215	1121	1278	19		

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

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

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	123	Total	C	N	O	S	0	0
			898	567	166	163	2		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	431	Total	C	N	O	S	0	0
			3443	2224	566	641	12		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	678	Total	C	N	O	S	0	0
			5344	3384	930	1009	21		

- Molecule 23 is a protein called Periodic tryptophan protein 2.

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

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	359	Total	C	N	O	S	0	0
			2709	1723	486	488	12		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	848	Total	C	N	O	S	0	0
			6640	4244	1116	1253	27		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LT	850	Total	C	N	O	S	0	0
			6697	4253	1154	1269	21		

- Molecule 28 is a protein called Protein SOF1.

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

- Molecule 29 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	362	Total	C	N	O	S	0	0
			2840	1789	487	555	9		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LW	438	Total	C	N	O	S	0	0
			3428	2163	601	652	12		

- Molecule 31 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

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

- Molecule 32 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	NG	111	Total	C	N	O		0	0
			543	321	111	111			

- Molecule 33 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	NK	175	Total	C	N	O		0	0
			868	518	175	175			

- Molecule 34 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SC	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
34	SD	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 35 is a protein called Ribonucloprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
35	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 36 is a protein called RRP9 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SG	429	Total	C	N	O	S	0	0
			3428	2185	596	637	10		

- Molecule 37 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 38 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SI	802	Total	C	N	O	S	0	0
			6412	4108	1142	1133	29		

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

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

- Molecule 40 is a protein called rRNA-processing protein FCF1.

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

- Molecule 41 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

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

- Molecule 42 is a protein called Ribosome biogenesis protein UTP30.

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

- Molecule 43 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SO	179	Total	C	N	O	S	0	0
			998	606	199	192	1		

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

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

- Molecule 45 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 46 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SS	197	Total	C	N	O	S	0	0
			1466	905	282	277	2		

- Molecule 47 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	ST	599	Total	C	N	O	S	0	0
			4473	2830	809	823	11		

- Molecule 48 is a protein called U3 small nucleolar RNA-associated protein 11.

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

- Molecule 49 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	SZ	261	Total	C	N	O	0	0
			1295	773	261	261		

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	NJ	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	NH	1082	Total	C	N	O	0	0
			5362	3198	1082	1082		

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	NI	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 53 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	1192	Total	C	N	O	P	0	0
			25439	11367	4542	8338	1192		

- Molecule 54 is a protein called Nucleolar complex protein 4.

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

- Molecule 55 is a protein called U3 small nucleolar RNA-associated protein 8.

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

- Molecule 56 is a protein called Bud site selection protein 21.

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

- Molecule 57 is a protein called U3 small nucleolar RNA-associated protein 13.

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

- Molecule 58 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	NE	163	Total	C	N	O	S	0	0
			1235	759	252	221	3		

- Molecule 59 is a protein called Nucleolar protein 58.

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

- Molecule 60 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 61 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	SP	2234	Total	C	N	O	0	0
			11108	6640	2234	2234		

- Molecule 62 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace	
62	LY	835	Total	C	N	O	0	0	
			4132	2462	835	835			
62	LX	812	Total	C	N	O	S	0	0
			5892	3727	1041	1099	25		

- Molecule 63 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	L6	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

- Molecule 64 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	NF	124	Total	C	N	O	0	0
			614	367	123	124		

- Molecule 65 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	5	296	Total	C	N	O	S	0	0
			2389	1496	422	467	4		

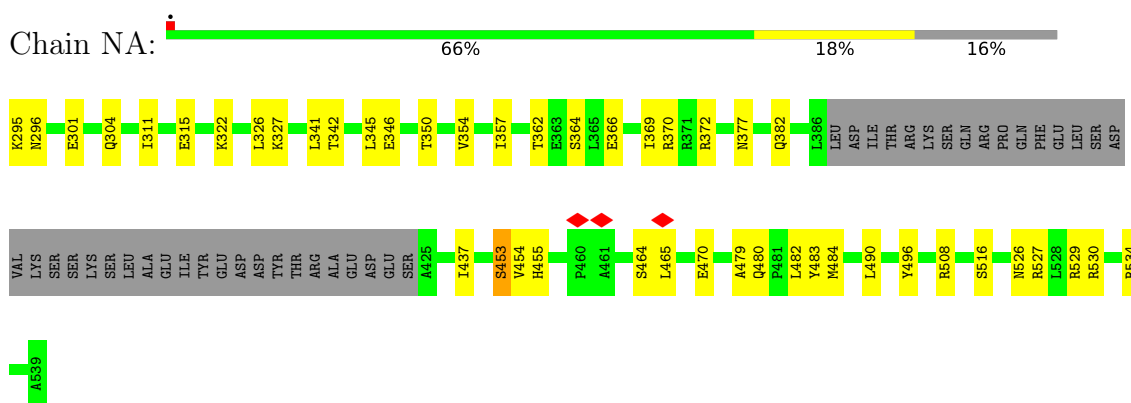
- Molecule 66 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	6	277	Total	C	N	O	S	0	0
			2244	1371	426	438	9		

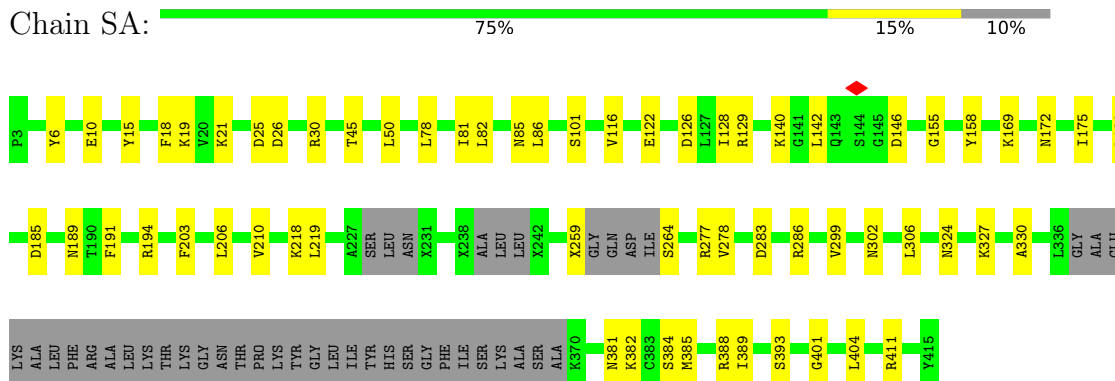
3 Residue-property plots

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.

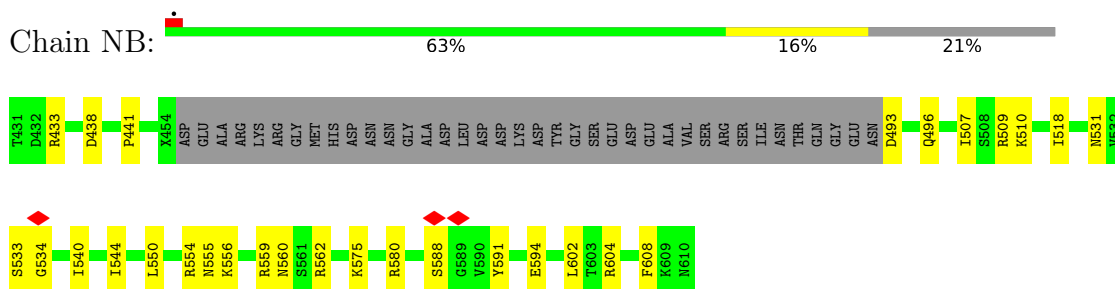
- Molecule 1: U3 small nucleolar RNA-associated protein MPP10



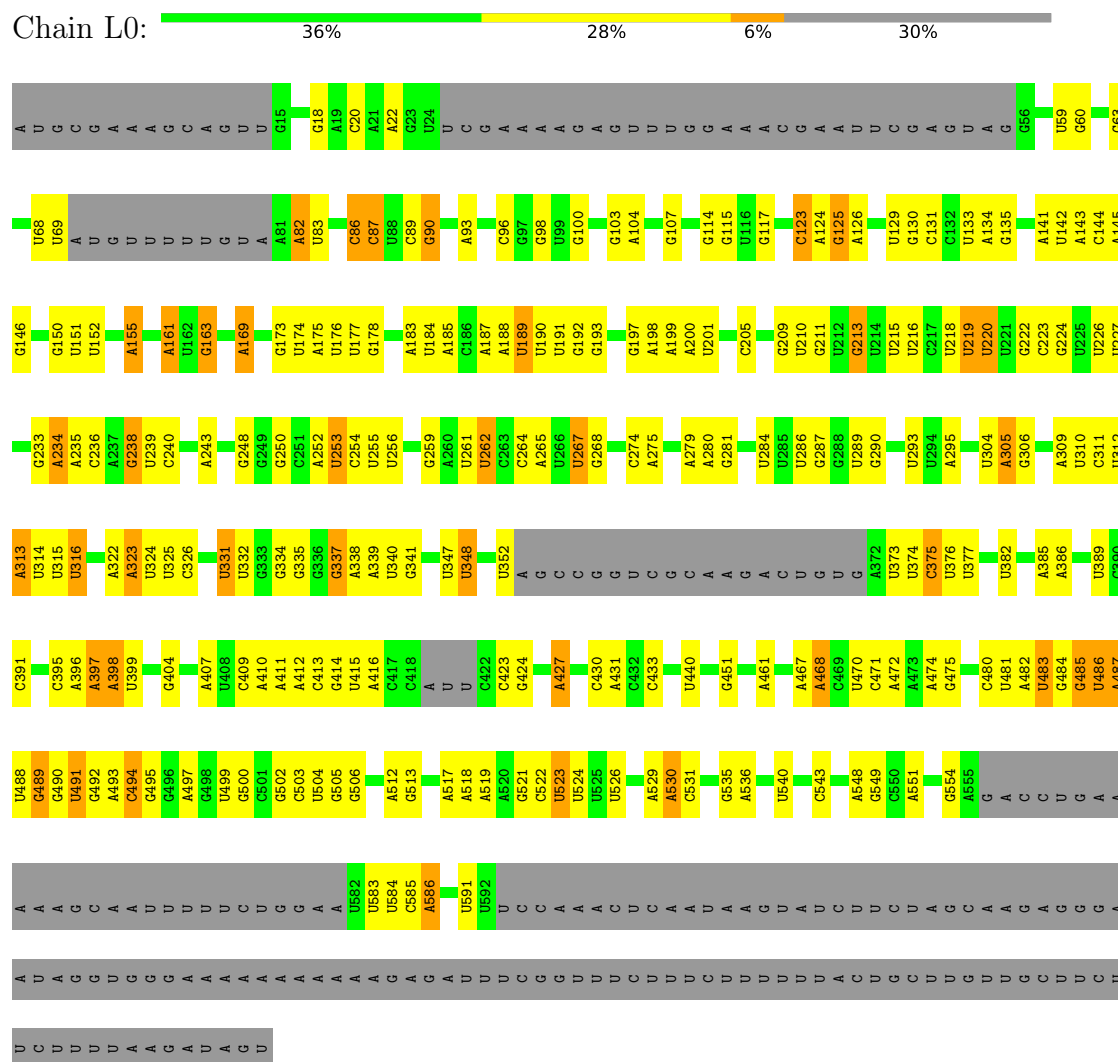
- Molecule 2: Nucleolar protein 56



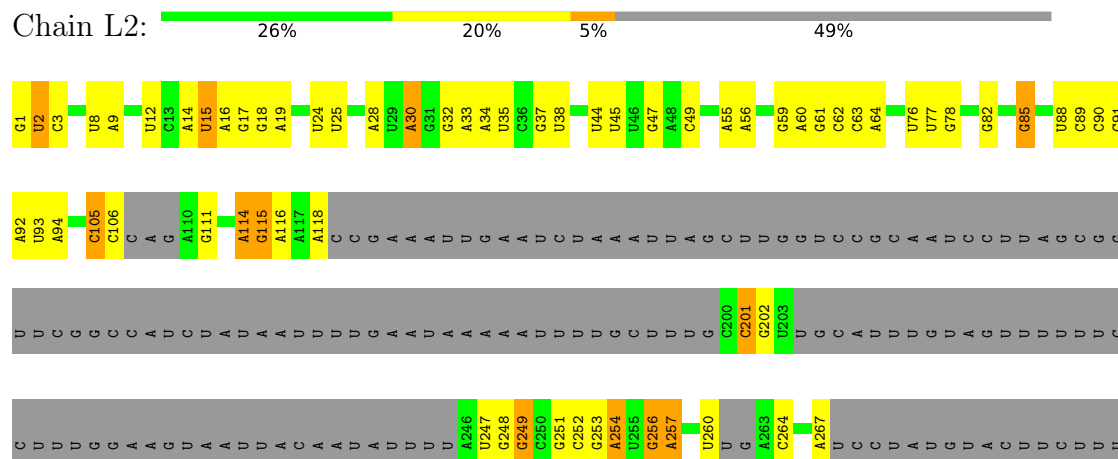
- Molecule 3: Something about silencing protein 10

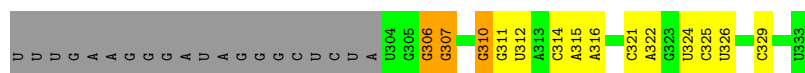


● Molecule 4: 5' ETS



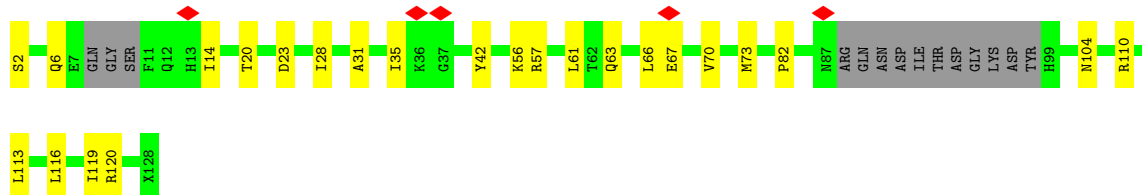
● Molecule 5: U3 snoRNA





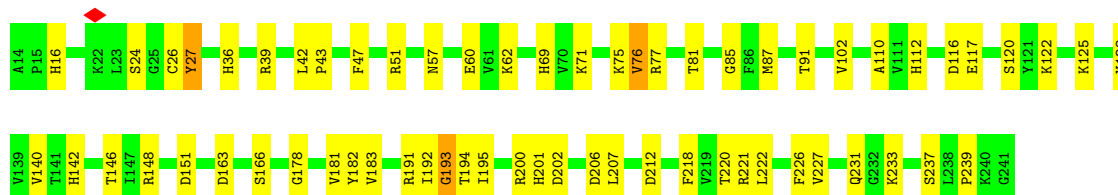
- Molecule 6: 40S ribosomal protein S18-A

Chain L3: 70% 19% 11%



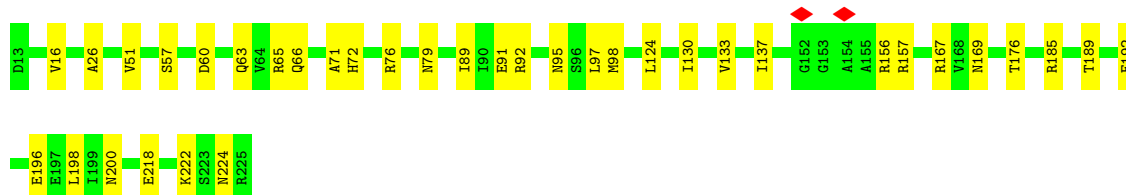
- Molecule 7: 40S ribosomal protein S4-A

Chain L4: 72% 26%



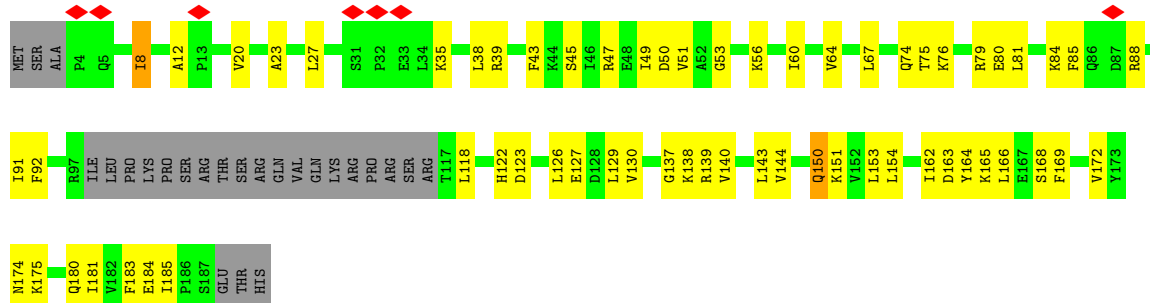
- Molecule 8: 40S ribosomal protein S5

Chain L5: 83% 17%



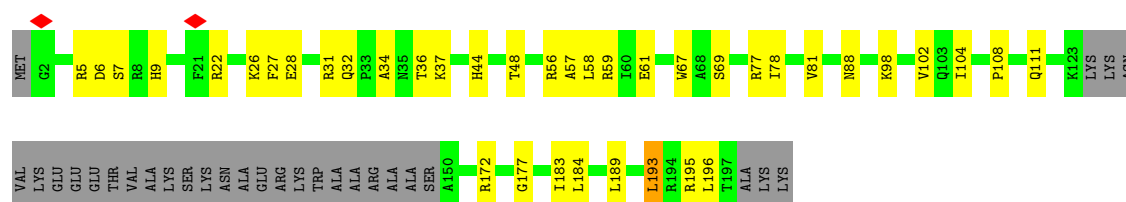
- Molecule 9: 40S ribosomal protein S7-A

Chain L7: 54% 32% 13%



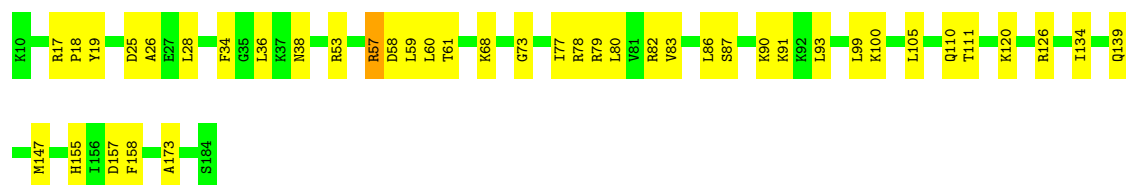
- Molecule 10: 40S ribosomal protein S8-A

Chain L8: 



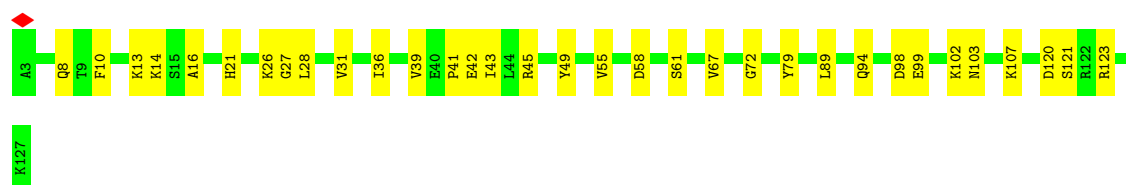
- Molecule 11: 40S ribosomal protein S9-A

Chain L9: 



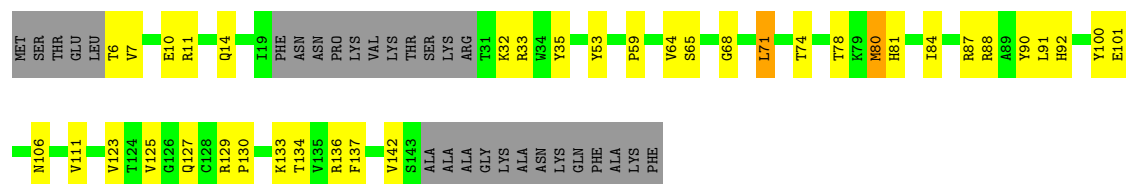
- Molecule 12: 40S ribosomal protein S16-A

Chain LC: 



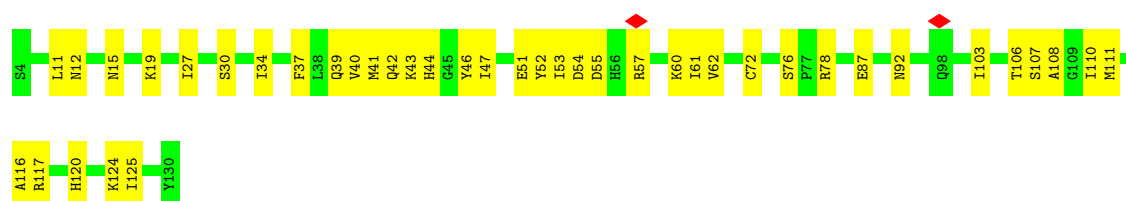
- Molecule 13: 40S ribosomal protein S11-A

Chain LD: 



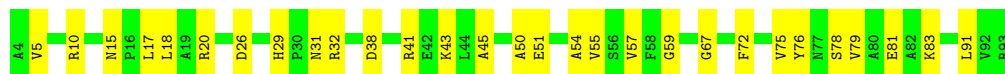
- Molecule 14: 40S ribosomal protein S22-A

Chain LE: 



- Molecule 15: 40S ribosomal protein S24-A

Chain LF:  68% 32%



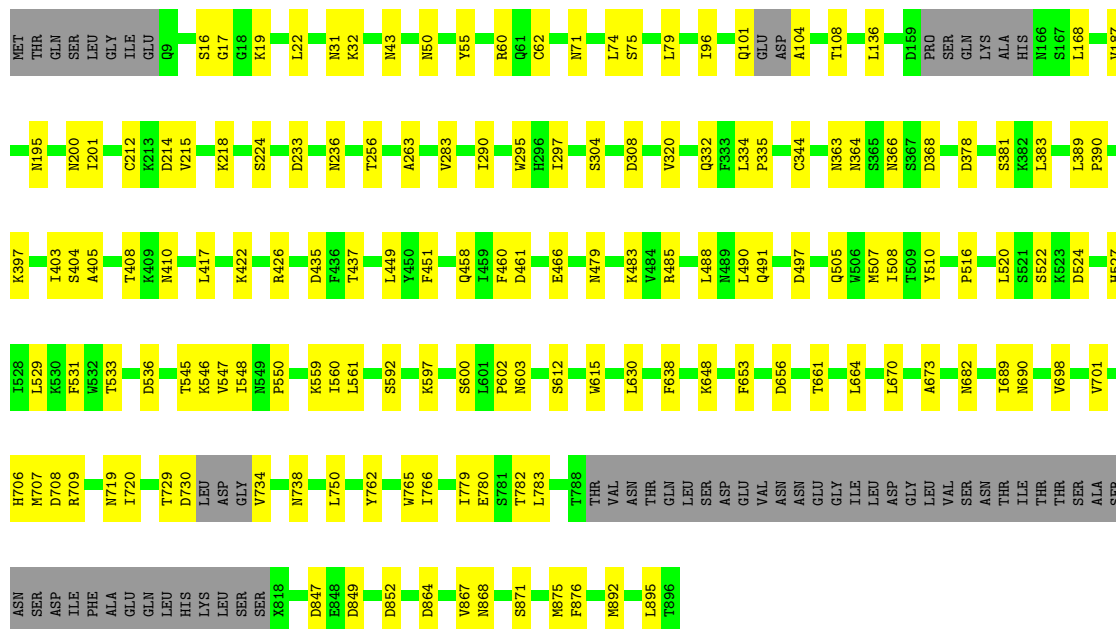
- Molecule 16: 40S ribosomal protein S28-A

Chain LG:  83% 17%



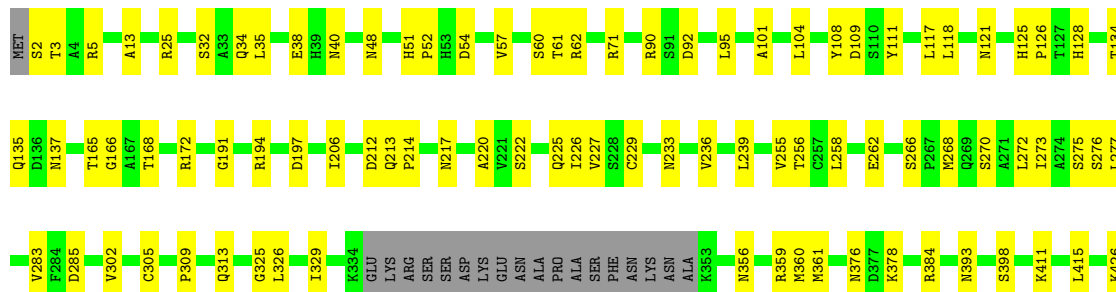
- Molecule 17: NET1-associated nuclear protein 1

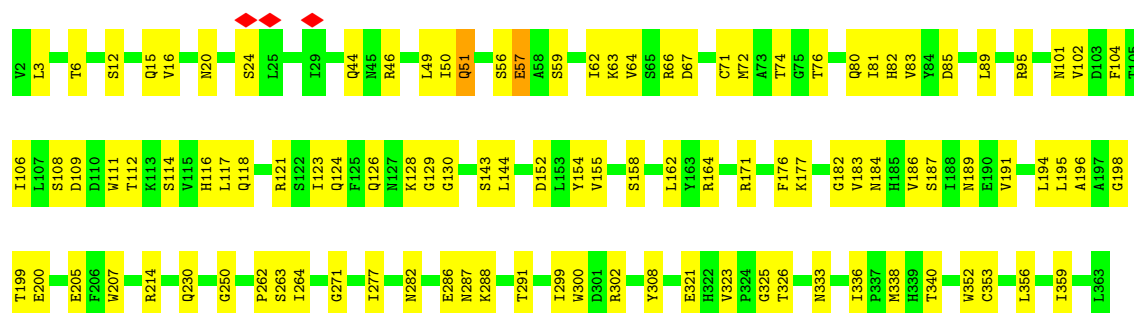
Chain LH:  76% 17% 7%



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

Chain LJ:  75% 21% .





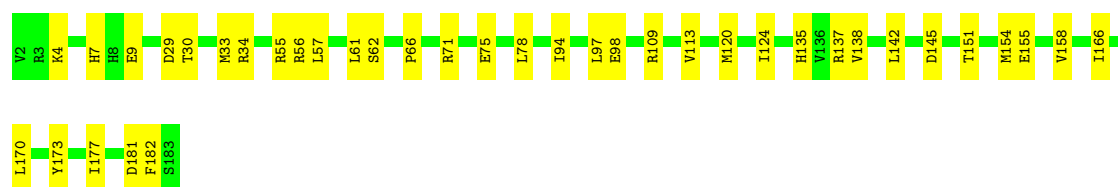
- Molecule 30: U3 small nucleolar RNA-associated protein 7

Chain LW: 82% 18%



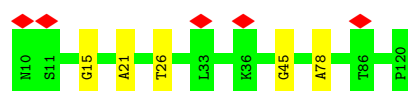
- Molecule 31: U3 small nucleolar ribonucleoprotein protein IMP3

Chain LZ: 79% 21%



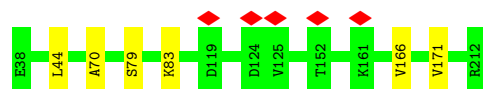
- Molecule 32: 40S ribosomal protein S14-B

Chain NG: 5% 95% 5%



- Molecule 33: KRR1 small subunit processome component

Chain NK: 97%



- Molecule 34: rRNA 2'-O-methyltransferase fibrillarin

K272	K273	N274	C275	T284	V285	Q291	K292	L293	T298	Q303	L306	E310	H313	C314	I315	V316	V317	R322	K326	A80	E89	D104	K109	N110	M111	A112	P128	SER	LYS	GLU	ASP	GLY	V134	S149	I155	L162	A165	K168	L171	G178	T179	S180	V181	L207	P219	E222	M232	L233	V237	A242	D243	V244	A245	Q246	T253	L261	V268	T269
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	------	------	------	------	------	------	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Y320	F199	ALA
M321	R202	ARG
R322		GLY
S323	L208	GLY
G324	D223	ALA
LEU	A224	R85
LYS	R225	R86
	H226	H91
	P227	R100
	Q228	L105
	R231	T108
	M232	K109
	M236	N110
	V237	K121
	F241	R122
	A242	I123
	D243	S124
	V244	V125
	Q249	GLU
	I252	GLU
	I253	PRO
	N256	SER
	S257	LYS
	L261	GLU
	G266	ASP
	V267	GLY
	T269	VAL
	S270	PRO
	I271	PRO
	D281	THR
	T284	K138
	E289	V139
	L301	E140
	E302	E141
	Q303	Y141
	L304	R142
	T305	V143
	L306	V144
	E307	N145
	P308	R148
	Y309	M156
	C314	F163
	I315	P166
		L171
		Y172
		L173
		S177
		V188

N5 P6 F9 P10 L11 A12 D13 T17 L21 D22 V23 V24 Q25 Q26 R31 K35 N38 R46 E50 C58 E62 I63 D73 F80 V81 R84 V85 C91 R95 I102 L125

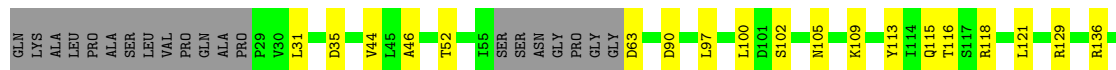
L368	L260	L107
R371	V262	L112
E375	W263	D113
ASN		K114
ALA	L268	R131
LYS	S269	G137
GLU	P270	
GLY	V271	
GLU	K272	Q164
ASP	V273	F165
GLY	I274	V166
GLU	P275	LEU
VAL		ASN
LYS	E282	LYS
TYR		TVR
PRO	S285	THR
ASP	L286	PHE
GLU		GLU
SER	S292	GLU
GLU	D293	SER
ALA	Q294	SER
P394	L295	ASN
		GLY
I402	S298	ASP
D410	R305	LYS
F411		ASN
S417	S308	GLY
D418	I309	R184
M421	N310	L185
	L315	F186
K430	F316	K198
I442	I317	
L443	H321	D203
S447	H322	K206
F448	D323	L211
N449	M333	K212
E457	E334	K225
	R335	E229
R460	R342	W230
K461	D343	T231
R462	A346	H235
Q463	M347	T241
L464	L348	V242
Q465	W349	
G466	K350	V252
K467	R356	T253
L470	L357	R256
Q471	T358	D257
P472	F359	W259
	P362	





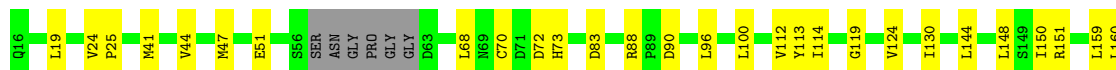
- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain SJ: 75% 17% 8%



- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1

Chain SK: 79% 18% 3%



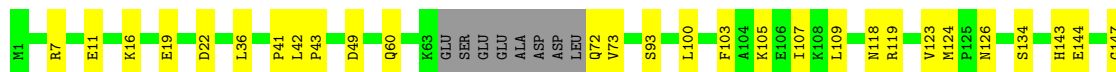
- Molecule 40: rRNA-processing protein FCF1

Chain SL: 74% 21% 5%



- Molecule 41: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM: 77% 20% 3%



- Molecule 42: Ribosome biogenesis protein UTP30

Chain SN: 76% 23% 1%





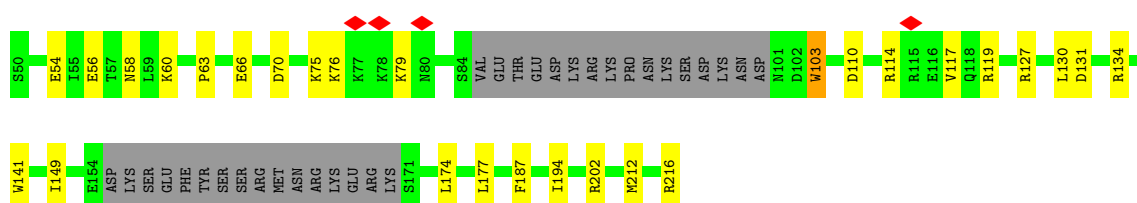
- Molecule 43: Pre-rRNA-processing protein PNO1

Chain SO: 97%



- Molecule 44: rRNA-processing protein FCF2

Chain SQ: 64% 16% 19%



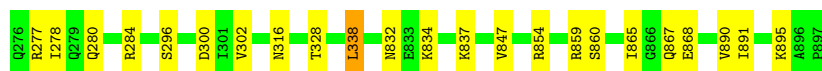
- Molecule 45: 40S ribosomal protein S23-A

Chain SR: 78% 20%



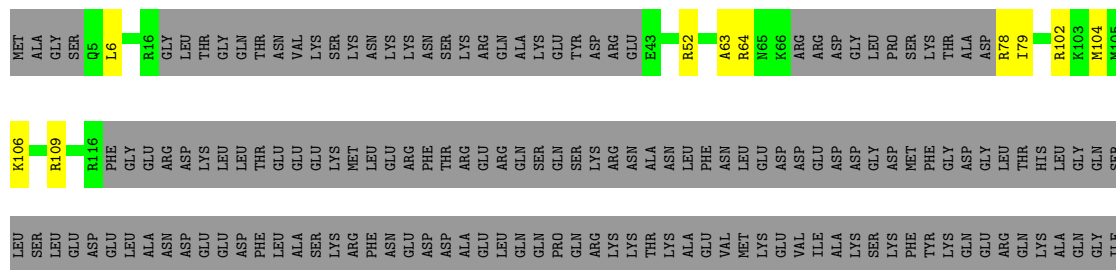
- Molecule 46: U3 small nucleolar RNA-associated protein 14

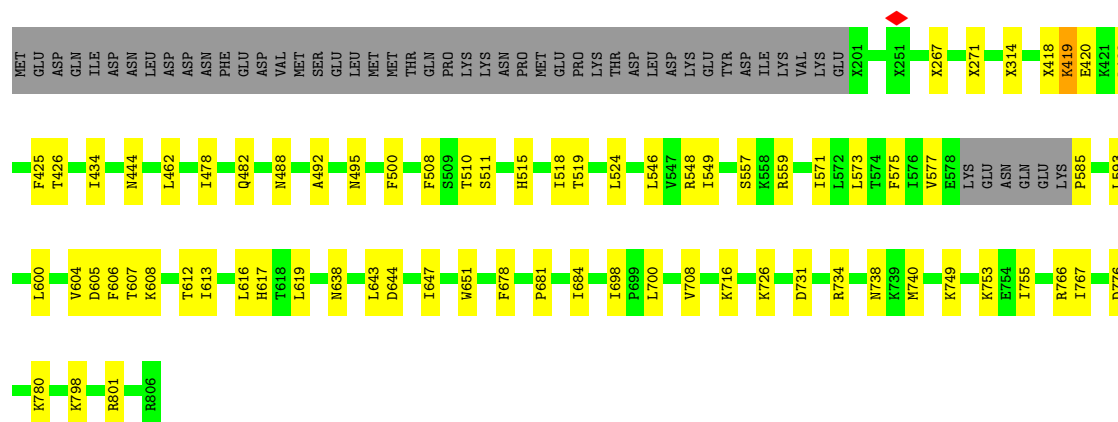
Chain SS: 88% 11%



- Molecule 47: Nucleolar complex protein 14

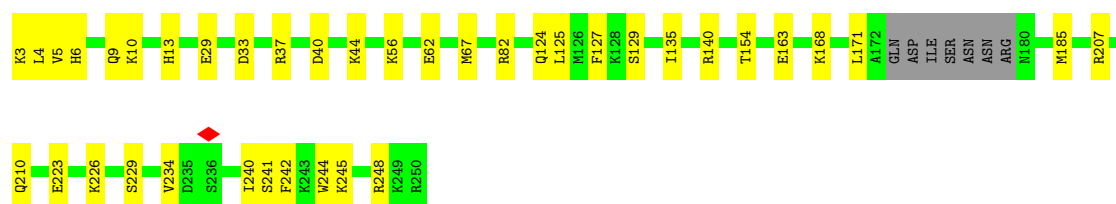
Chain ST: 64% 10% 26%





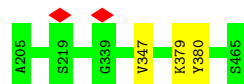
- Molecule 48: U3 small nucleolar RNA-associated protein 11

Chain SY: 81% 16% .



- Molecule 49: Essential nuclear protein 1

Chain SZ: 99% .



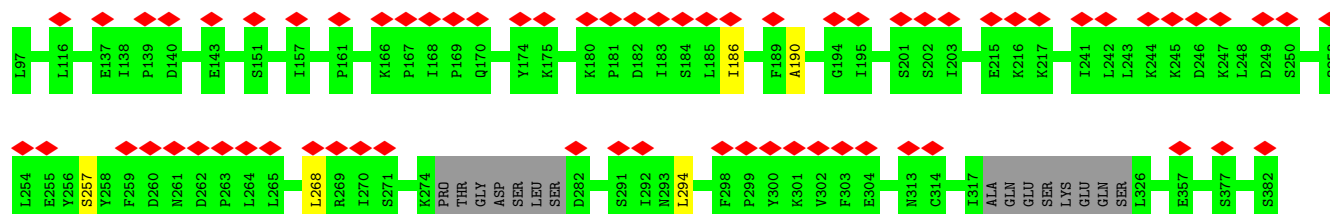
- Molecule 50: rRNA biogenesis protein RRP5

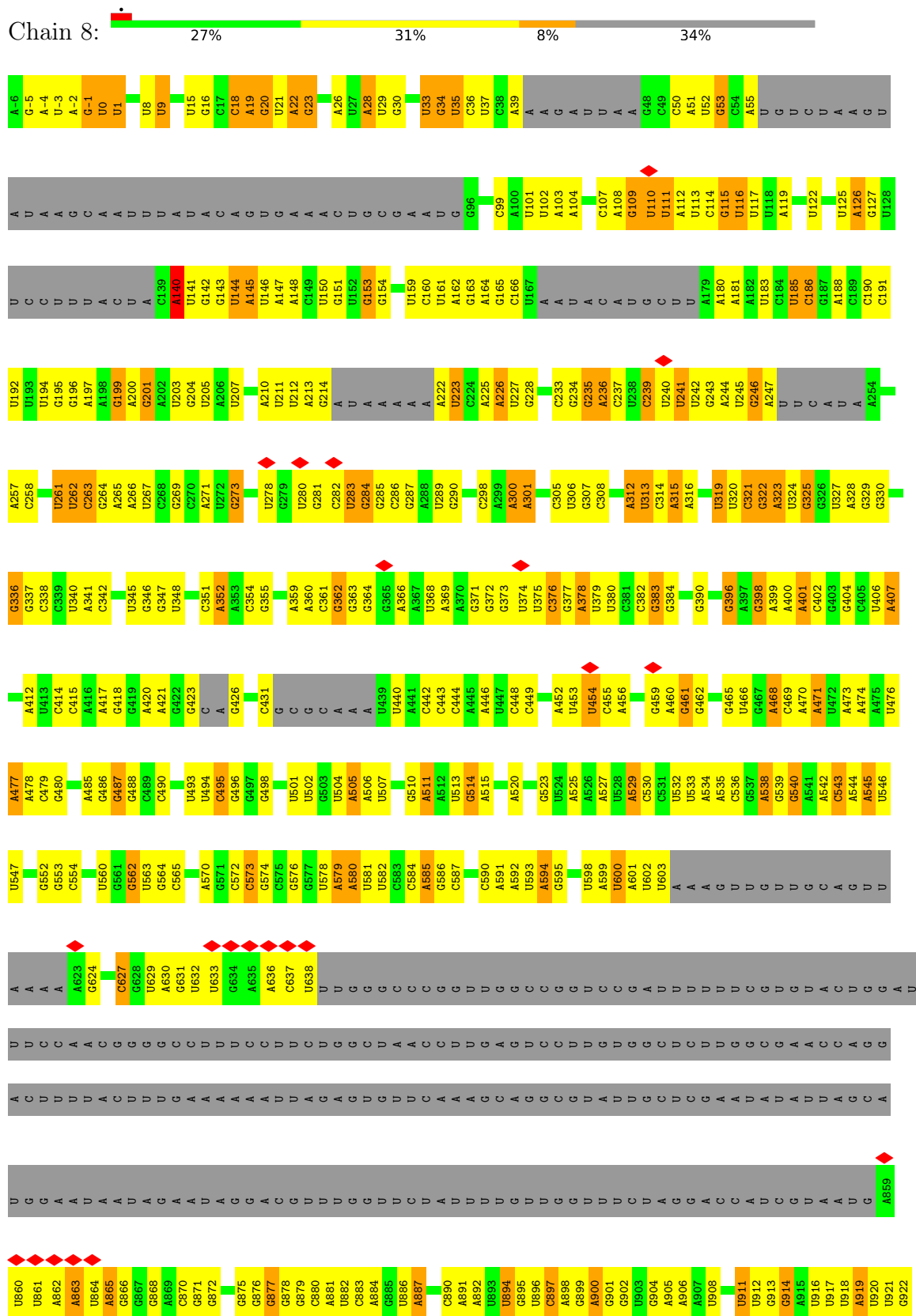
Chain NJ: 99% .

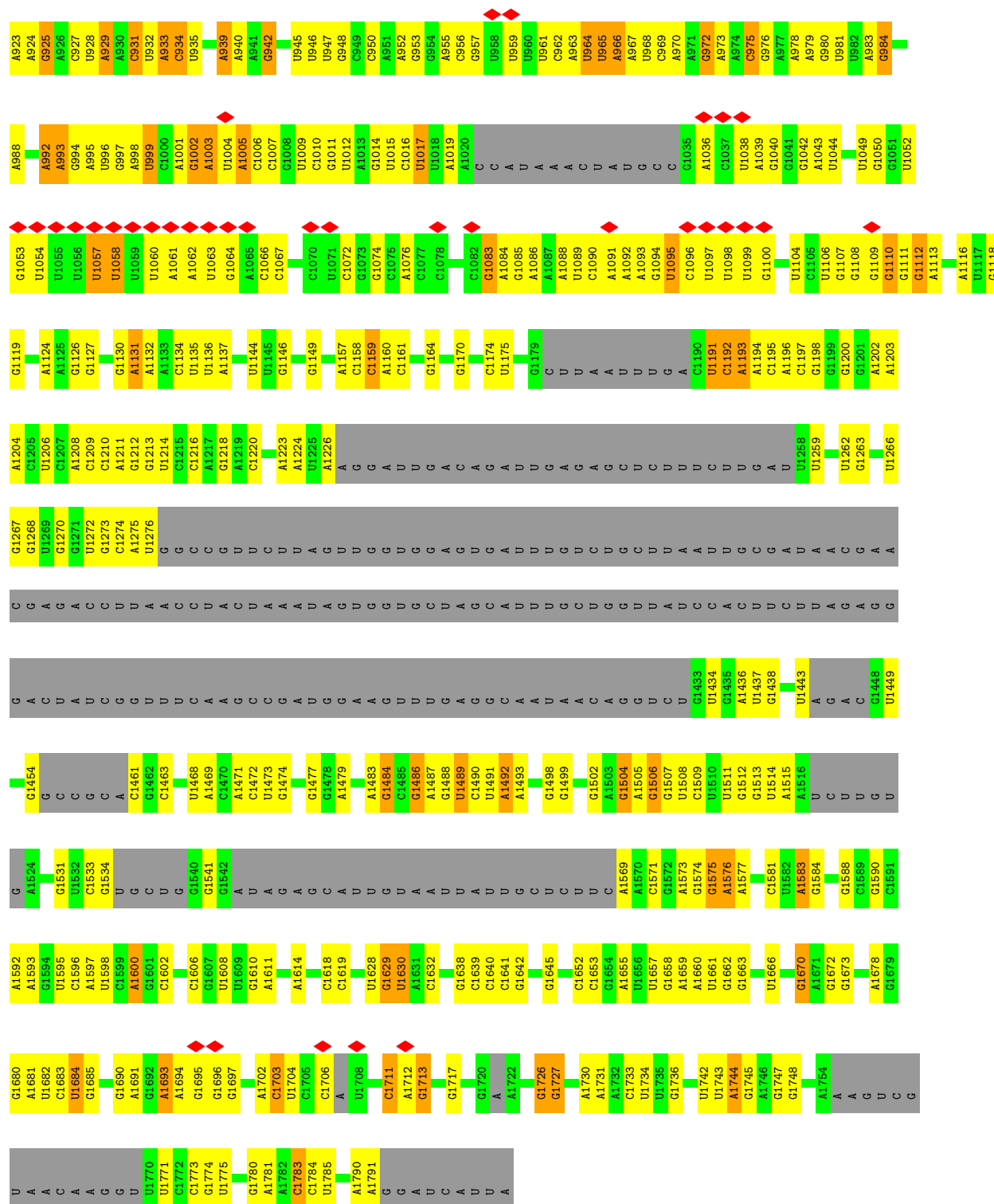


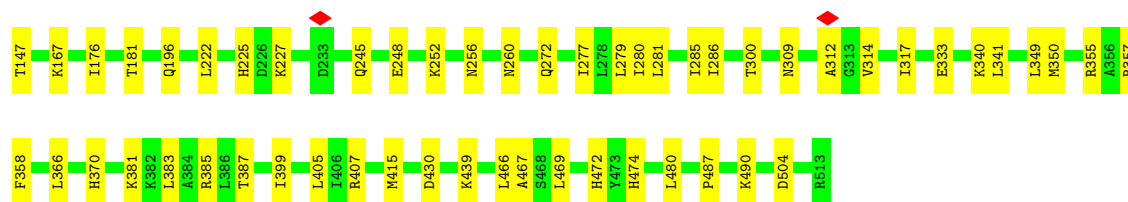
- Molecule 51: U3 small nucleolar RNA-associated protein 22

Chain NH: 33% 92% 5% .

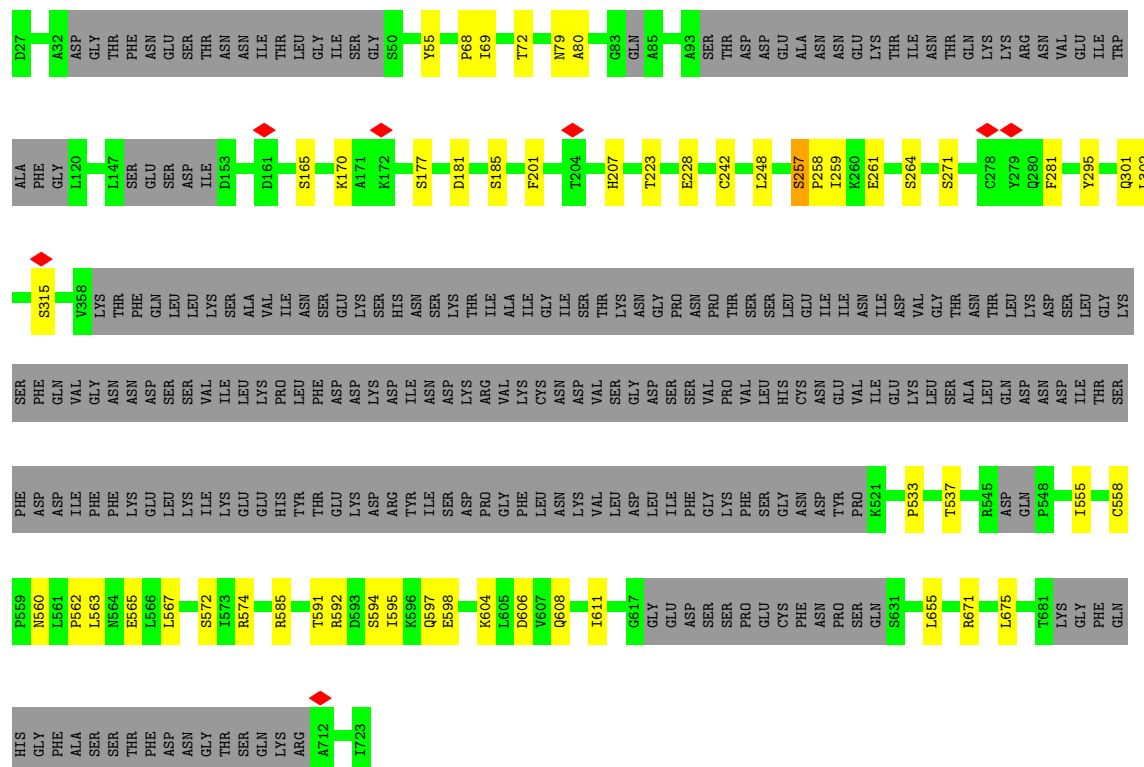




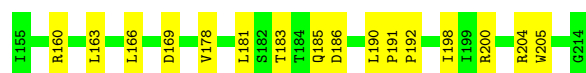




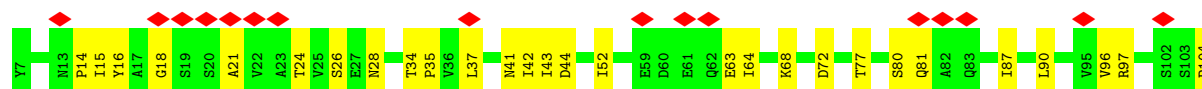
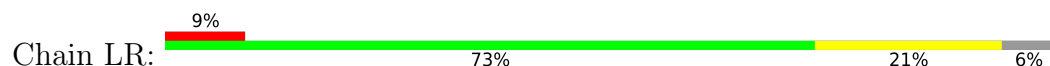
• Molecule 55: U3 small nucleolar RNA-associated protein 8

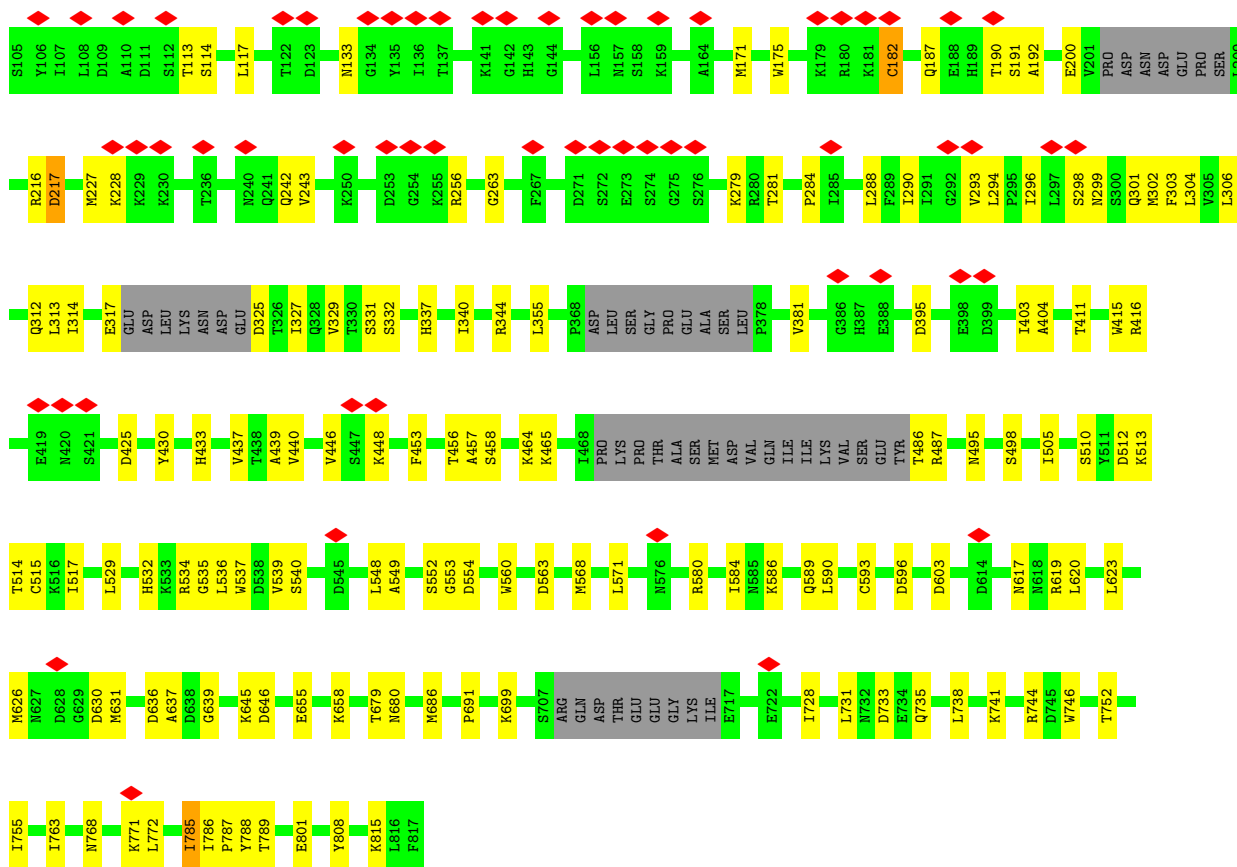


• Molecule 56: Bud site selection protein 21

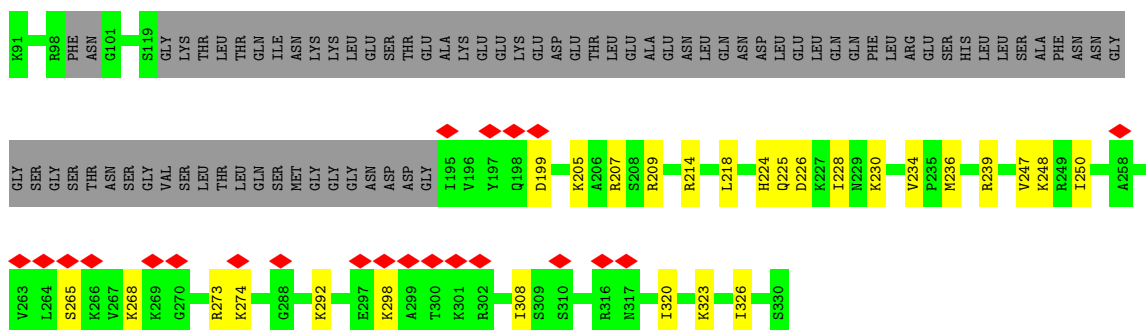


• Molecule 57: U3 small nucleolar RNA-associated protein 13

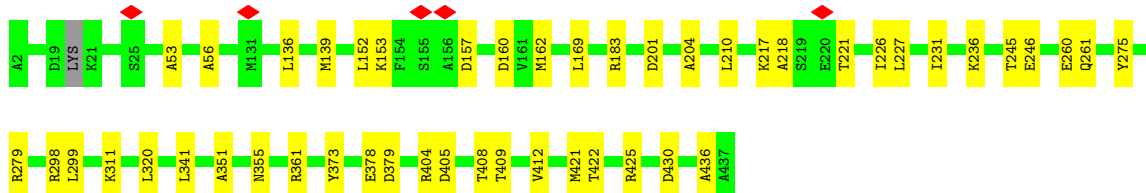
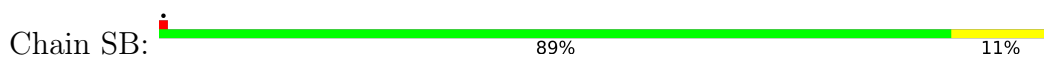




• Molecule 58: Protein FAF1

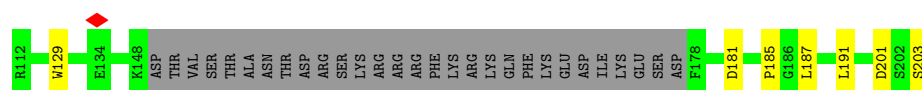


• Molecule 59: Nucleolar protein 58



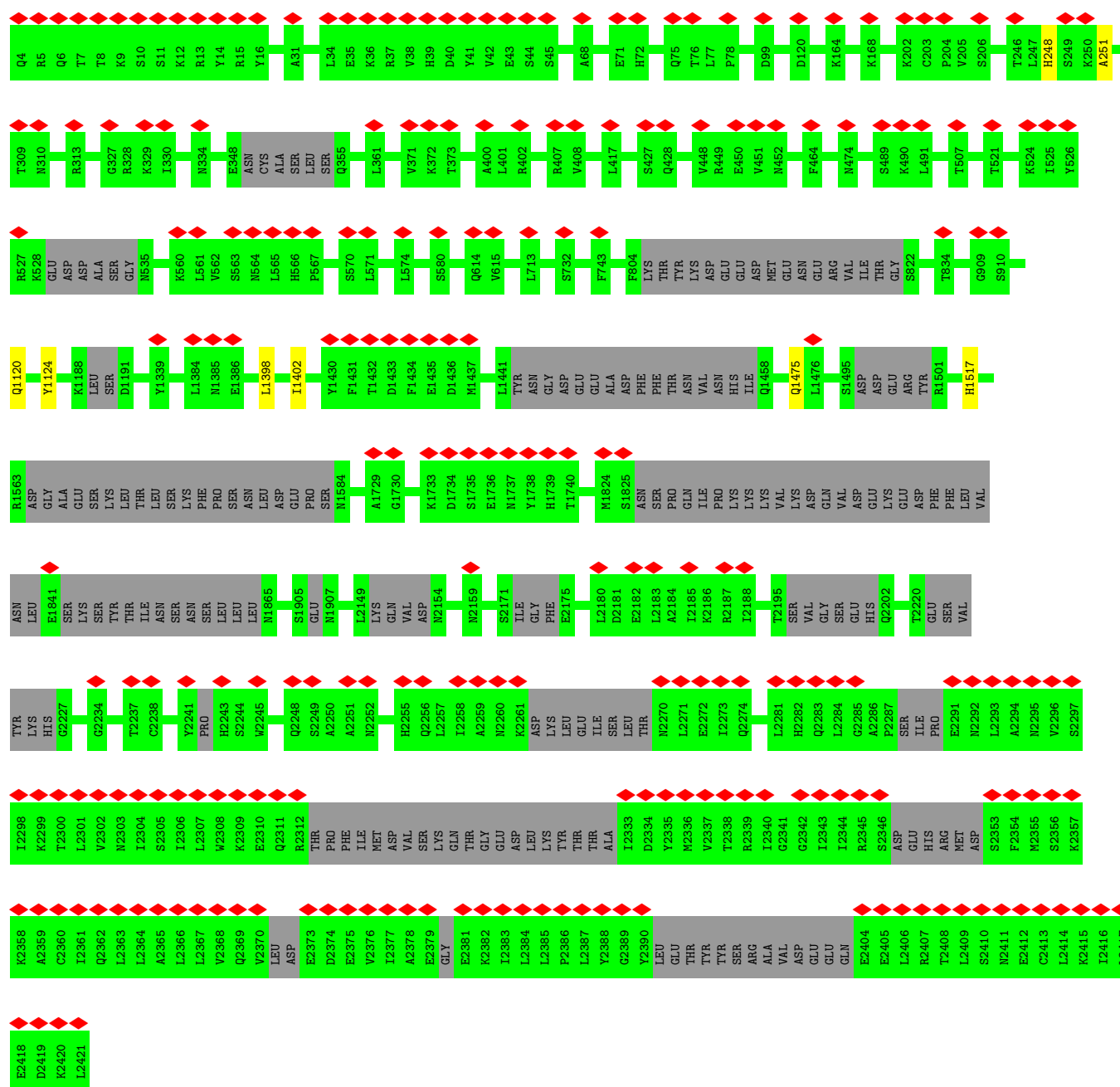
- Molecule 60: Regulator of rDNA transcription protein 14

Chain SV:  61% 8% 32%

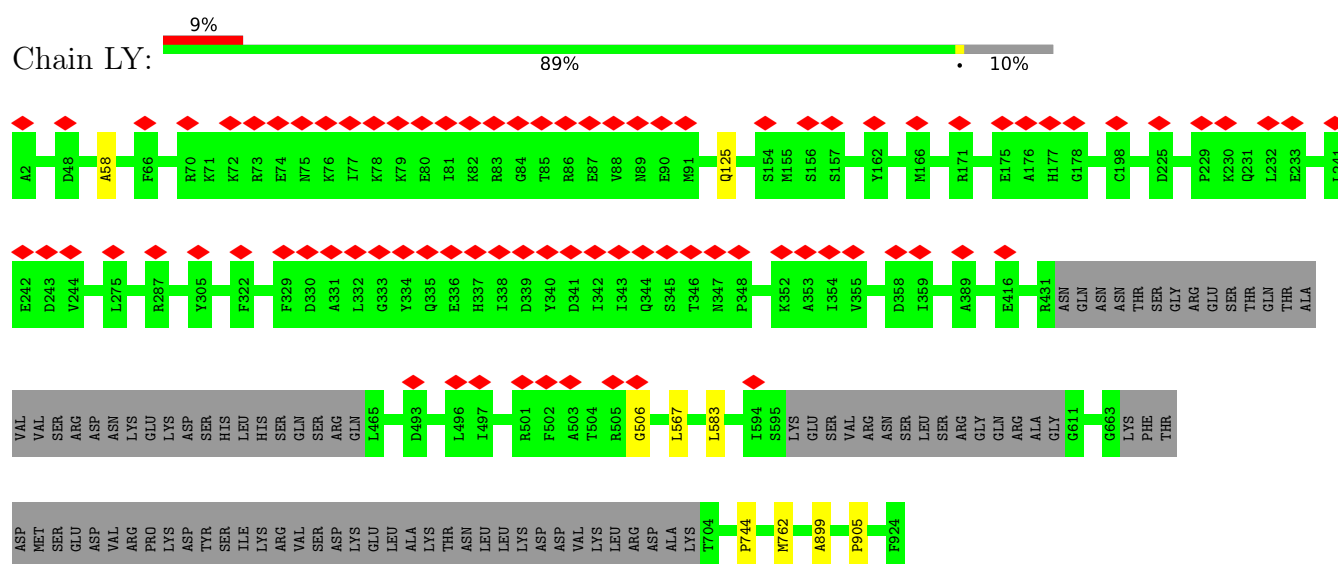


- Molecule 61: U3 small nucleolar RNA-associated protein 20

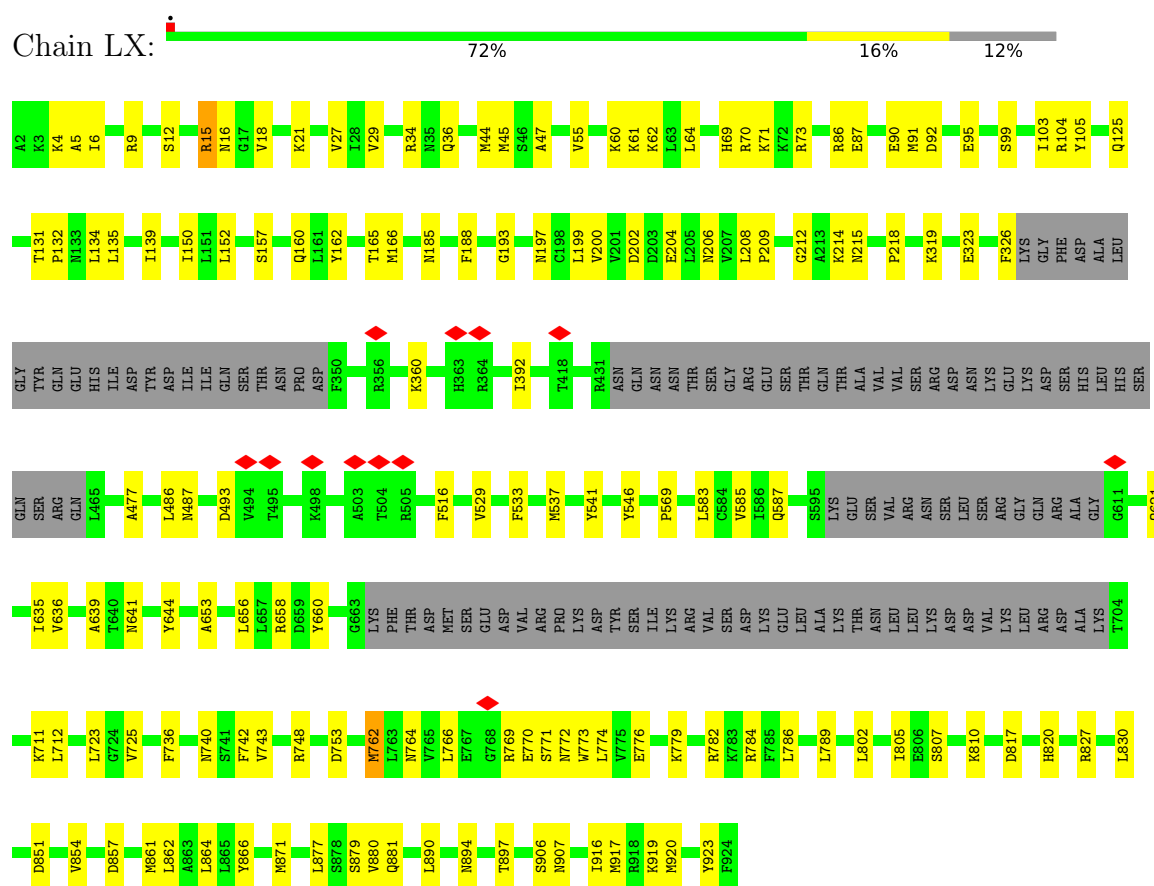
Chain SP:  10% 92% 8%



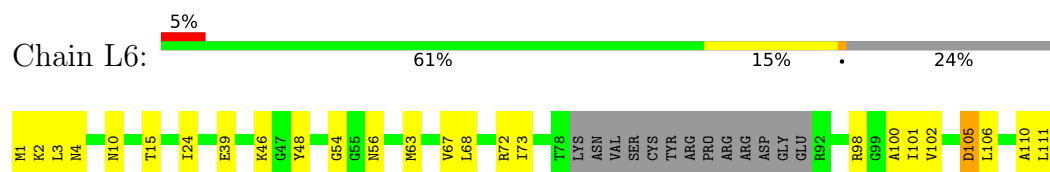
- Molecule 62: RNA cytidine acetyltransferase



• Molecule 62: RNA cytidine acetyltransferase



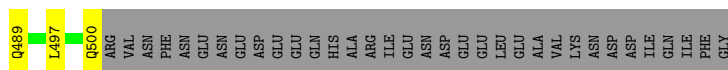
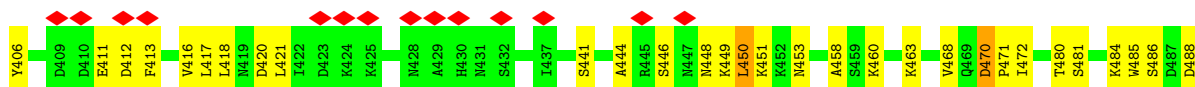
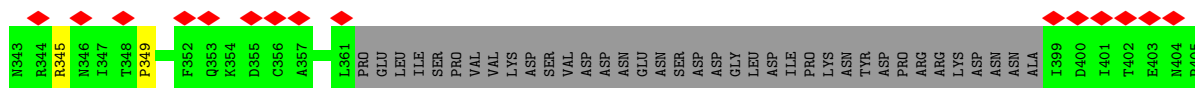
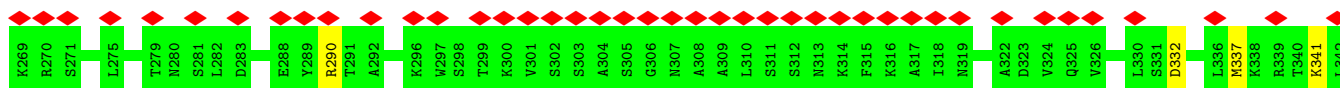
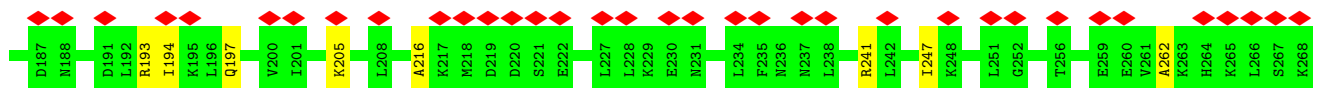
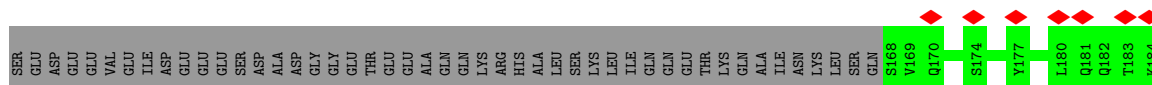
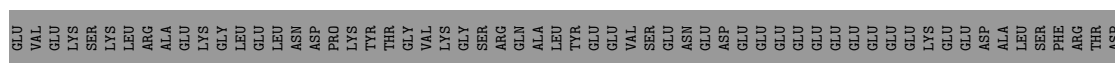
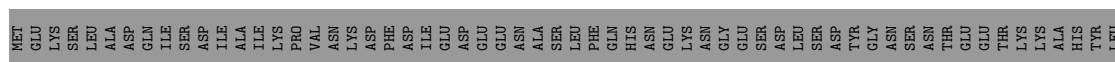
• Molecule 63: 40S ribosomal protein S6-A



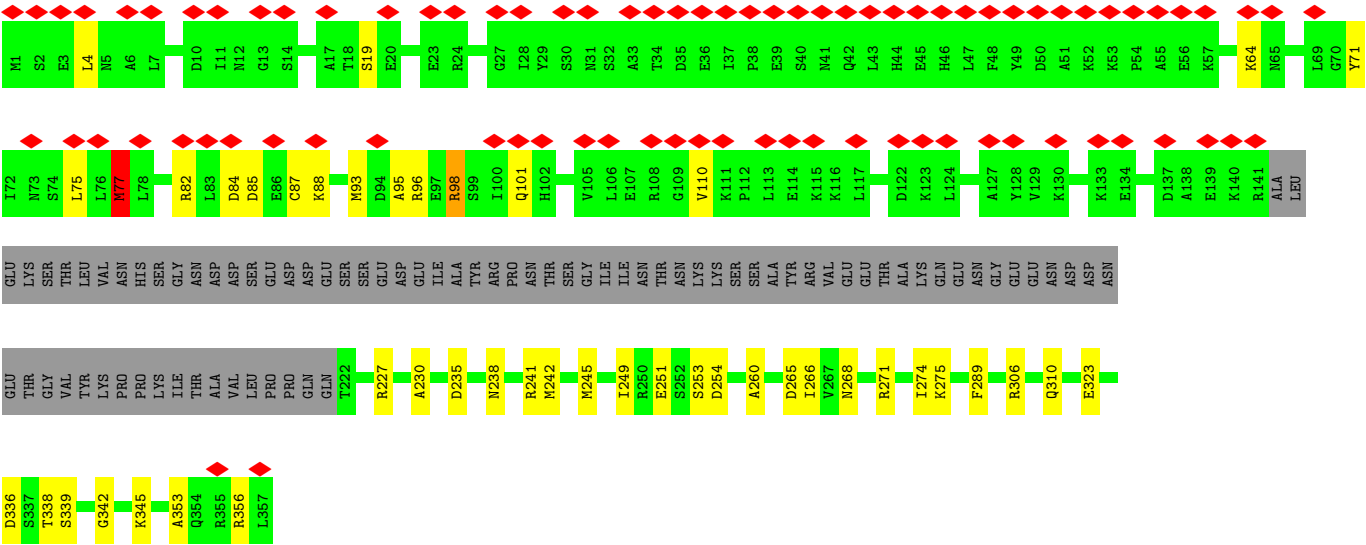
- Molecule 64: 40S ribosomal protein S13



- Molecule 65: Protein BFR2



- Molecule 66: U3 small nucleolar ribonucleoprotein protein LCP5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	199534	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 ($e^-/\text{\AA}^2$)	1.074	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	463.968, 463.968, 463.968	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	NA	0.20	0/1685	0.53	1/2261 (0.0%)
2	SA	0.17	0/2769	0.42	0/3728
3	NB	0.22	0/1042	0.56	1/1377 (0.1%)
4	L0	0.19	0/11634	0.39	0/18120
5	L2	0.20	0/4001	0.38	0/6215
6	L3	0.18	0/871	0.55	0/1171
7	L4	0.23	0/1849	0.62	0/2497
8	L5	0.21	0/1690	0.54	0/2285
9	L7	0.28	0/1342	0.77	1/1807 (0.1%)
10	L8	0.25	0/1372	0.67	2/1834 (0.1%)
11	L9	0.28	0/1437	0.71	2/1924 (0.1%)
12	LC	0.30	0/990	0.80	2/1335 (0.1%)
13	LD	0.24	0/1050	0.68	2/1415 (0.1%)
14	LE	0.24	0/1020	0.68	0/1371
15	LF	0.29	0/727	0.79	1/977 (0.1%)
16	LG	0.34	0/499	0.89	2/670 (0.3%)
17	LH	0.18	0/6694	0.48	1/9070 (0.0%)
18	LJ	0.20	0/3993	0.49	1/5413 (0.0%)
19	LK	0.17	0/735	0.46	0/987
20	LL	0.19	0/3840	0.46	0/5208
21	LM	0.19	0/3470	0.44	0/4694
22	LN	0.19	0/5369	0.48	0/7272
23	LO	0.23	0/6780	0.49	1/9175 (0.0%)
24	LP	0.19	0/2281	0.45	0/3059
25	LQ	0.18	0/6574	0.49	1/8881 (0.0%)
26	LS	0.21	0/3875	0.43	0/5254
27	LT	0.21	0/6834	0.47	1/9238 (0.0%)
28	LU	0.21	0/3802	0.52	0/5118
29	LV	0.24	0/2902	0.65	2/3941 (0.1%)
30	LW	0.21	0/3505	0.44	0/4748
31	LZ	0.29	0/1559	0.72	2/2097 (0.1%)
32	NG	0.13	0/542	0.41	0/750
33	NK	0.11	0/867	0.33	0/1208
34	SC	0.23	0/1917	0.53	0/2588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	SD	0.23	0/1815	0.60	0/2448
35	SE	0.30	0/928	0.69	0/1262
35	SF	0.32	0/928	0.75	2/1262 (0.2%)
36	SG	0.17	0/3498	0.49	1/4712 (0.0%)
37	SH	0.20	0/2832	0.46	1/3825 (0.0%)
38	SI	0.22	0/6403	0.55	4/8616 (0.0%)
39	SJ	0.17	0/1727	0.47	0/2329
39	SK	0.20	0/1828	0.50	0/2470
40	SL	0.23	0/1418	0.59	0/1906
41	SM	0.24	0/2337	0.61	6/3148 (0.2%)
42	SN	0.24	0/2041	0.59	1/2745 (0.0%)
43	SO	0.15	0/1003	0.45	0/1381
44	SQ	0.22	0/1156	0.56	1/1536 (0.1%)
45	SR	0.29	0/804	0.80	2/1074 (0.2%)
46	SS	0.22	0/1230	0.61	0/1660
47	ST	0.16	0/3826	0.48	2/5125 (0.0%)
48	SY	0.20	0/2042	0.49	0/2704
49	SZ	0.11	0/1294	0.33	0/1804
50	NJ	0.08	0/1313	0.29	0/1830
51	NH	0.10	0/5357	0.31	1/7463 (0.0%)
52	NI	0.11	0/838	0.32	0/1166
53	8	0.75	5/28439 (0.0%)	0.39	0/44273
54	SU	0.19	1/3736 (0.0%)	0.50	3/5086 (0.1%)
55	LI	0.17	0/2703	0.50	0/3703
56	ND	0.23	0/499	0.60	0/659
57	LR	0.19	1/6058 (0.0%)	0.51	4/8201 (0.0%)
58	NE	0.19	0/1240	0.50	0/1645
59	SB	0.18	0/3012	0.47	1/4091 (0.0%)
60	SV	0.32	0/385	0.67	2/529 (0.4%)
61	SP	0.09	0/11085	0.32	0/15445
62	LX	0.19	0/5994	0.52	4/8139 (0.0%)
62	LY	0.11	0/4128	0.34	0/5747
63	L6	2.81	1/1341 (0.1%)	0.80	5/1789 (0.3%)
64	NF	0.15	0/613	0.48	1/853 (0.1%)
65	5	0.19	0/2422	0.55	1/3257 (0.0%)
66	6	0.21	0/2271	0.59	2/3029 (0.1%)
All	All	0.39	8/218061 (0.0%)	0.48	67/304600 (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
1	NA	0	1
7	L4	0	2
9	L7	0	1
11	L9	0	1
15	LF	0	2
22	LN	0	1
29	LV	0	2
34	SD	0	1
35	SE	0	2
35	SF	0	1
38	SI	0	1
55	LI	0	1
57	LR	0	1
63	L6	0	1
65	5	0	1
66	6	0	1
All	All	0	20

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	L6	184	LEU	CA-CB	102.58	3.16	1.53
53	8	140	A	N9-C8	60.03	2.57	1.37
53	8	140	A	N7-C5	56.11	2.51	1.39
53	8	140	A	N9-C4	55.70	2.49	1.37
53	8	140	A	C8-N7	54.60	2.40	1.31

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	LR	104	PRO	CA-N-CD	-12.17	94.96	112.00
63	L6	184	LEU	CA-CB-CG	10.93	154.55	116.30
16	LG	6	PRO	CA-N-CD	-10.75	96.95	112.00
11	L9	18	PRO	CA-N-CD	-9.90	98.14	112.00
57	LR	104	PRO	N-CD-CG	-9.21	89.38	103.20

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	L4	193	GLY	Peptide
7	L4	195	ILE	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
9	L7	12	ALA	Peptide
11	L9	57	ARG	Sidechain
1	NA	453	SER	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	NA	1667	0	1701	37	0
2	SA	2854	0	2792	43	0
3	NB	1098	0	1102	24	0
4	L0	10405	0	5231	97	0
5	L2	3585	0	1819	34	0
6	L3	901	0	907	16	0
7	L4	1810	0	1865	42	0
8	L5	1669	0	1724	24	0
9	L7	1321	0	1390	43	0
10	L8	1349	0	1372	25	0
11	L9	1415	0	1497	30	0
12	LC	973	0	1029	25	0
13	LD	1027	0	1084	25	0
14	LE	1003	0	1040	28	0
15	LF	715	0	744	14	0
16	LG	497	0	535	6	0
17	LH	6633	0	6510	103	0
18	LJ	3911	0	3906	70	0
19	LK	898	0	811	11	0
20	LL	3772	0	3806	55	0
21	LM	3443	0	3559	42	0
22	LN	5344	0	5301	101	0
23	LO	6635	0	6525	119	0
24	LP	2709	0	2371	30	0
25	LQ	6640	0	6503	109	0
26	LS	3791	0	3772	59	0
27	LT	6697	0	6676	105	0
28	LU	3725	0	3679	94	0
29	LV	2840	0	2685	71	0
30	LW	3428	0	3407	55	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	LZ	1530	0	1572	26	0
32	NG	543	0	277	3	0
33	NK	868	0	379	3	0
34	SC	1881	0	1928	29	0
34	SD	1782	0	1826	37	0
35	SE	916	0	964	19	0
35	SF	916	0	964	20	0
36	SG	3428	0	3446	76	0
37	SH	2781	0	2878	62	0
38	SI	6412	0	6498	128	0
39	SJ	1701	0	1767	29	0
39	SK	1799	0	1872	33	0
40	SL	1395	0	1476	29	0
41	SM	2296	0	2325	44	0
42	SN	2006	0	2118	40	0
43	SO	998	0	631	5	0
44	SQ	1137	0	1188	20	0
45	SR	792	0	847	22	0
46	SS	1466	0	1257	23	0
47	ST	4473	0	4057	54	0
48	SY	2016	0	2093	32	0
49	SZ	1295	0	571	3	0
50	NJ	1314	0	610	1	0
51	NH	5362	0	2295	13	0
52	NI	841	0	365	4	0
53	8	25439	0	12823	274	0
54	SU	3650	0	3365	41	0
55	LI	2690	0	1931	33	0
56	ND	495	0	561	13	0
57	LR	5957	0	5992	112	0
58	NE	1235	0	1243	21	0
59	SB	2985	0	2703	34	0
60	SV	381	0	255	6	0
61	SP	11108	0	4748	4	0
62	LX	5892	0	5420	92	0
62	LY	4132	0	1819	5	0
63	L6	1327	0	1403	39	0
64	NF	614	0	279	7	0
65	5	2389	0	2411	36	0
66	6	2244	0	2245	39	0
All	All	213241	0	176745	2615	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 7.

The worst 5 of 2615 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)
53:8:140:A:C4	53:8:140:A:C5	2.33	1.17
53:8:140:A:C4	63:L6:184:LEU:HA	1.94	1.02
45:SR:41:SER:N	53:8:600:U:HO2'	1.68	0.91
53:8:140:A:C8	53:8:140:A:N7	2.40	0.88
53:8:140:A:C8	63:L6:184:LEU:CB	2.59	0.86

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	NA	203/245 (83%)	194 (96%)	8 (4%)	1 (0%)	24	60
2	SA	338/413 (82%)	332 (98%)	6 (2%)	0	100	100
3	NB	126/180 (70%)	118 (94%)	7 (6%)	1 (1%)	16	52
6	L3	100/127 (79%)	91 (91%)	9 (9%)	0	100	100
7	L4	226/228 (99%)	202 (89%)	24 (11%)	0	100	100
8	L5	211/213 (99%)	194 (92%)	17 (8%)	0	100	100
9	L7	161/190 (85%)	142 (88%)	19 (12%)	0	100	100
10	L8	166/200 (83%)	156 (94%)	10 (6%)	0	100	100
11	L9	173/175 (99%)	159 (92%)	14 (8%)	0	100	100
12	LC	123/125 (98%)	113 (92%)	10 (8%)	0	100	100
13	LD	123/156 (79%)	109 (89%)	14 (11%)	0	100	100
14	LE	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
15	LF	88/90 (98%)	74 (84%)	13 (15%)	1 (1%)	11	44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LG	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
17	LH	810/896 (90%)	754 (93%)	56 (7%)	0	100	100
18	LJ	489/513 (95%)	461 (94%)	28 (6%)	0	100	100
19	LK	86/123 (70%)	84 (98%)	2 (2%)	0	100	100
20	LL	465/555 (84%)	435 (94%)	30 (6%)	0	100	100
21	LM	424/431 (98%)	407 (96%)	17 (4%)	0	100	100
22	LN	654/748 (87%)	610 (93%)	43 (7%)	1 (0%)	43	75
23	LO	830/855 (97%)	777 (94%)	53 (6%)	0	100	100
24	LP	259/420 (62%)	257 (99%)	2 (1%)	0	100	100
25	LQ	798/939 (85%)	739 (93%)	58 (7%)	1 (0%)	48	81
26	LS	473/594 (80%)	448 (95%)	25 (5%)	0	100	100
27	LT	844/921 (92%)	805 (95%)	39 (5%)	0	100	100
28	LU	453/465 (97%)	415 (92%)	38 (8%)	0	100	100
29	LV	360/362 (99%)	324 (90%)	36 (10%)	0	100	100
30	LW	436/438 (100%)	409 (94%)	27 (6%)	0	100	100
31	LZ	180/182 (99%)	170 (94%)	10 (6%)	0	100	100
32	NG	109/111 (98%)	97 (89%)	12 (11%)	0	100	100
33	NK	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
34	SC	238/247 (96%)	227 (95%)	11 (5%)	0	100	100
34	SD	224/247 (91%)	207 (92%)	17 (8%)	0	100	100
35	SE	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
35	SF	119/121 (98%)	107 (90%)	12 (10%)	0	100	100
36	SG	423/464 (91%)	401 (95%)	22 (5%)	0	100	100
37	SH	358/360 (99%)	342 (96%)	16 (4%)	0	100	100
38	SI	763/1123 (68%)	727 (95%)	36 (5%)	0	100	100
39	SJ	212/236 (90%)	205 (97%)	7 (3%)	0	100	100
39	SK	226/236 (96%)	221 (98%)	5 (2%)	0	100	100
40	SL	170/183 (93%)	160 (94%)	10 (6%)	0	100	100
41	SM	278/290 (96%)	260 (94%)	18 (6%)	0	100	100
42	SN	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
43	SO	177/179 (99%)	163 (92%)	14 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	SQ	129/167 (77%)	124 (96%)	5 (4%)	0	100	100
45	SR	102/104 (98%)	91 (89%)	10 (10%)	1 (1%)	12	45
46	SS	142/197 (72%)	132 (93%)	10 (7%)	0	100	100
47	ST	448/806 (56%)	425 (95%)	22 (5%)	1 (0%)	43	75
48	SY	237/248 (96%)	222 (94%)	15 (6%)	0	100	100
49	SZ	259/261 (99%)	237 (92%)	22 (8%)	0	100	100
50	NJ	263/265 (99%)	259 (98%)	4 (2%)	0	100	100
51	NH	1072/1141 (94%)	1025 (96%)	47 (4%)	0	100	100
52	NI	163/187 (87%)	157 (96%)	6 (4%)	0	100	100
54	SU	471/513 (92%)	447 (95%)	24 (5%)	0	100	100
55	LI	423/687 (62%)	376 (89%)	45 (11%)	2 (0%)	24	60
56	ND	58/60 (97%)	58 (100%)	0	0	100	100
57	LR	750/811 (92%)	693 (92%)	57 (8%)	0	100	100
58	NE	157/240 (65%)	139 (88%)	18 (12%)	0	100	100
59	SB	431/436 (99%)	401 (93%)	30 (7%)	0	100	100
60	SV	59/92 (64%)	56 (95%)	3 (5%)	0	100	100
61	SP	2189/2418 (90%)	2132 (97%)	57 (3%)	0	100	100
62	LX	802/923 (87%)	745 (93%)	57 (7%)	0	100	100
62	LY	827/923 (90%)	774 (94%)	53 (6%)	0	100	100
63	L6	161/219 (74%)	150 (93%)	11 (7%)	0	100	100
64	NF	122/124 (98%)	112 (92%)	10 (8%)	0	100	100
65	5	292/534 (55%)	269 (92%)	22 (8%)	1 (0%)	36	70
66	6	273/357 (76%)	259 (95%)	14 (5%)	0	100	100
All	All	23449/27027 (87%)	22060 (94%)	1379 (6%)	10 (0%)	100	100

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	NA	454	VAL
3	NB	441	PRO
45	SR	90	ASP
65	5	451	LYS
22	LN	666	ASN

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	NA	187/223 (84%)	187 (100%)	0	100	100
2	SA	296/328 (90%)	296 (100%)	0	100	100
3	NB	108/139 (78%)	108 (100%)	0	100	100
6	L3	96/108 (89%)	96 (100%)	0	100	100
7	L4	196/196 (100%)	193 (98%)	3 (2%)	57	70
8	L5	180/180 (100%)	179 (99%)	1 (1%)	78	81
9	L7	146/170 (86%)	145 (99%)	1 (1%)	76	79
10	L8	138/161 (86%)	138 (100%)	0	100	100
11	L9	150/150 (100%)	150 (100%)	0	100	100
12	LC	105/105 (100%)	105 (100%)	0	100	100
13	LD	114/137 (83%)	114 (100%)	0	100	100
14	LE	108/108 (100%)	108 (100%)	0	100	100
15	LF	76/76 (100%)	75 (99%)	1 (1%)	61	72
16	LG	56/56 (100%)	55 (98%)	1 (2%)	51	68
17	LH	758/813 (93%)	758 (100%)	0	100	100
18	LJ	437/454 (96%)	435 (100%)	2 (0%)	81	82
19	LK	83/83 (100%)	83 (100%)	0	100	100
20	LL	428/497 (86%)	426 (100%)	2 (0%)	81	82
21	LM	391/391 (100%)	391 (100%)	0	100	100
22	LN	604/671 (90%)	601 (100%)	3 (0%)	81	82
23	LO	730/751 (97%)	727 (100%)	3 (0%)	84	84
24	LP	248/302 (82%)	247 (100%)	1 (0%)	84	84
25	LQ	717/794 (90%)	714 (100%)	3 (0%)	84	84
26	LS	424/529 (80%)	423 (100%)	1 (0%)	87	87
27	LT	745/802 (93%)	741 (100%)	4 (0%)	81	82
28	LU	412/420 (98%)	411 (100%)	1 (0%)	87	87

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	LV	307/326 (94%)	307 (100%)	0	100	100
30	LW	373/373 (100%)	371 (100%)	2 (0%)	81	82
31	LZ	171/171 (100%)	170 (99%)	1 (1%)	78	81
34	SC	202/206 (98%)	200 (99%)	2 (1%)	68	76
34	SD	192/206 (93%)	192 (100%)	0	100	100
35	SE	100/100 (100%)	100 (100%)	0	100	100
35	SF	100/100 (100%)	99 (99%)	1 (1%)	68	76
36	SG	373/402 (93%)	373 (100%)	0	100	100
37	SH	307/307 (100%)	307 (100%)	0	100	100
38	SI	684/965 (71%)	681 (100%)	3 (0%)	84	84
39	SJ	195/209 (93%)	195 (100%)	0	100	100
39	SK	206/209 (99%)	204 (99%)	2 (1%)	68	76
40	SL	156/165 (94%)	155 (99%)	1 (1%)	78	81
41	SM	251/258 (97%)	250 (100%)	1 (0%)	84	84
42	SN	230/230 (100%)	226 (98%)	4 (2%)	53	68
43	SO	33/156 (21%)	33 (100%)	0	100	100
44	SQ	124/156 (80%)	122 (98%)	2 (2%)	55	70
45	SR	86/86 (100%)	86 (100%)	0	100	100
46	SS	135/135 (100%)	134 (99%)	1 (1%)	76	79
47	ST	417/604 (69%)	416 (100%)	1 (0%)	87	87
48	SY	226/233 (97%)	226 (100%)	0	100	100
54	SU	360/473 (76%)	358 (99%)	2 (1%)	78	81
55	LI	150/634 (24%)	150 (100%)	0	100	100
56	ND	57/57 (100%)	57 (100%)	0	100	100
57	LR	665/713 (93%)	662 (100%)	3 (0%)	81	82
58	NE	119/210 (57%)	117 (98%)	2 (2%)	53	68
59	SB	244/359 (68%)	244 (100%)	0	100	100
60	SV	22/87 (25%)	22 (100%)	0	100	100
62	LX	549/822 (67%)	549 (100%)	0	100	100
63	L6	139/188 (74%)	138 (99%)	1 (1%)	76	79
65	5	267/482 (55%)	267 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
66	6	244/315 (78%)	242 (99%)	2 (1%)	73 77
All	All	15617/18581 (84%)	15559 (100%)	58 (0%)	81 84

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	LW	444	LEU
63	L6	105	ASP
38	SI	997	MET
58	NE	308	ILE
54	SU	176	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
38	SI	909	ASN
54	SU	245	GLN
39	SK	250	ASN
47	ST	5	GLN
58	NE	216	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	L0	483/700 (69%)	164 (33%)	3 (0%)
5	L2	163/333 (48%)	56 (34%)	0
53	8	1169/1807 (64%)	527 (45%)	17 (1%)
All	All	1815/2840 (63%)	747 (41%)	20 (1%)

5 of 747 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	L0	18	G
4	L0	20	C
4	L0	22	A
4	L0	59	U
4	L0	60	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	8	997	G
53	8	1573	A
53	8	1790	A
53	8	1638	G
53	8	199	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
46	SS	2
22	LN	2
47	ST	2
24	LP	2
19	LK	2
38	SI	1
17	LH	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SS	408:UNK	C	828:ASN	N	85.72
1	SI	417:UNK	C	548:ASN	N	63.03

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	LN	730:UNK	C	731:HIS	N	39.41
1	ST	316:UNK	C	382:UNK	N	38.49
1	LH	831:UNK	C	846:ASN	N	26.10

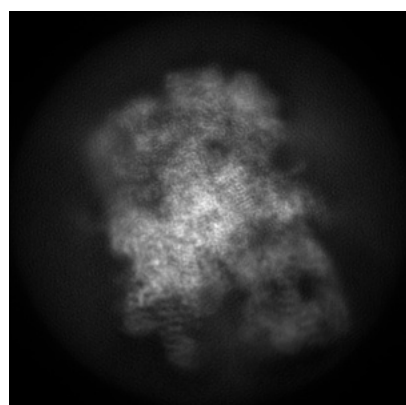
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25441. These allow visual inspection of the internal detail of the map and identification of artifacts.

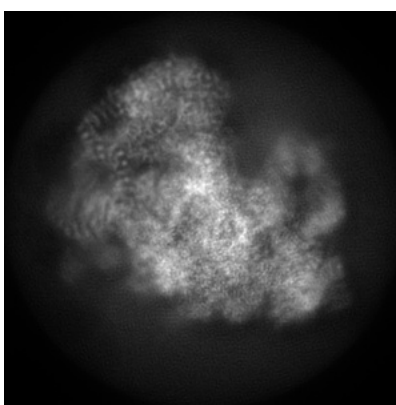
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

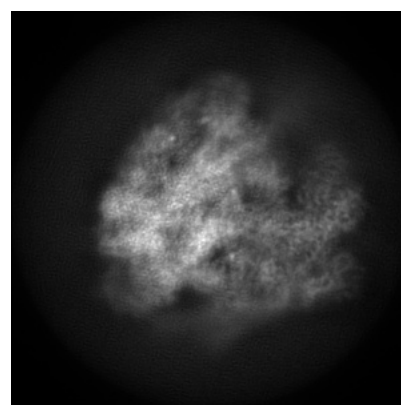
6.1.1 Primary map



X



Y

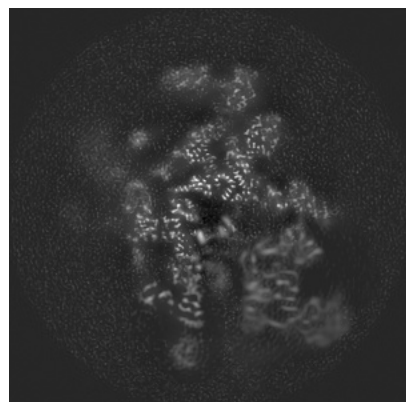


Z

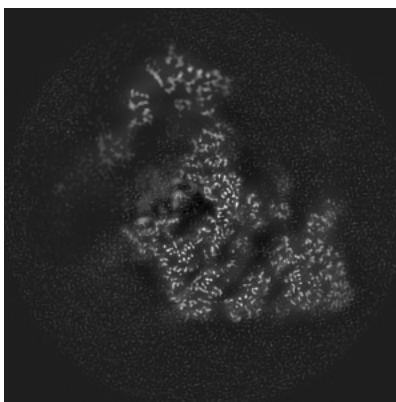
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

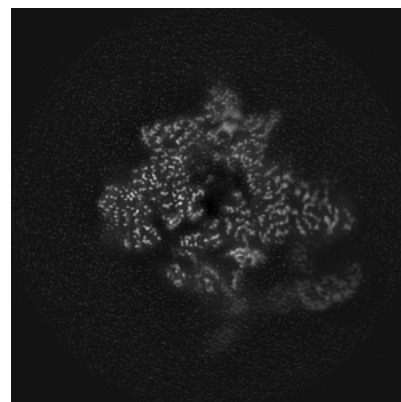
6.2.1 Primary map



X Index: 216



Y Index: 216

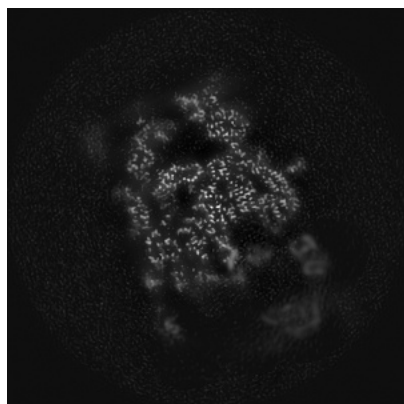


Z Index: 216

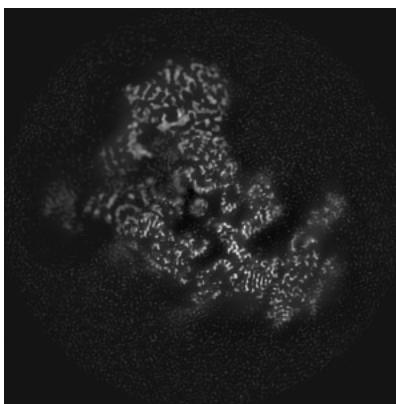
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

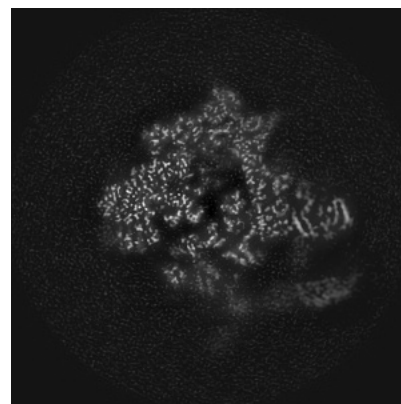
6.3.1 Primary map



X Index: 182



Y Index: 199

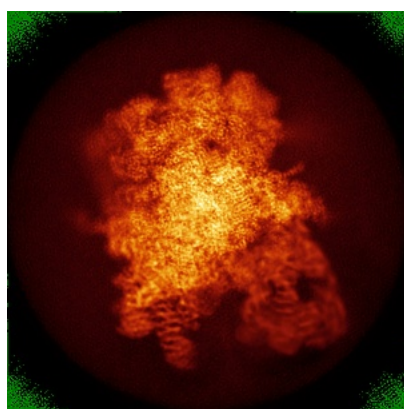


Z Index: 219

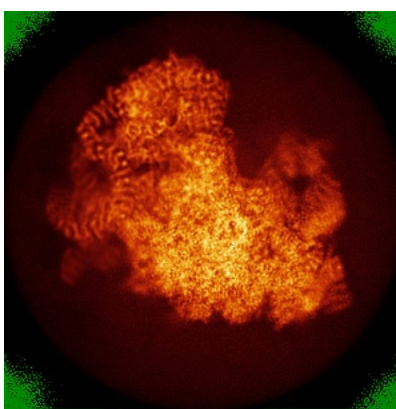
The images above show the largest variance slices of the map in three orthogonal directions.

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

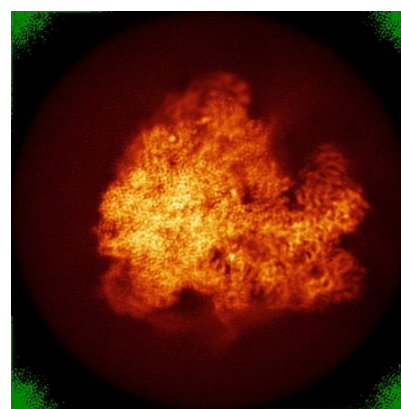
6.4.1 Primary map



X



Y

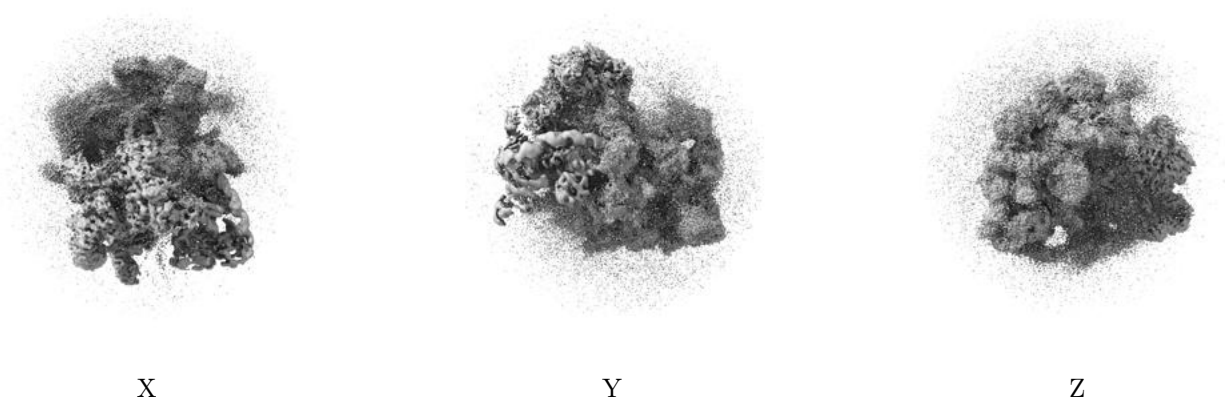


Z

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 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

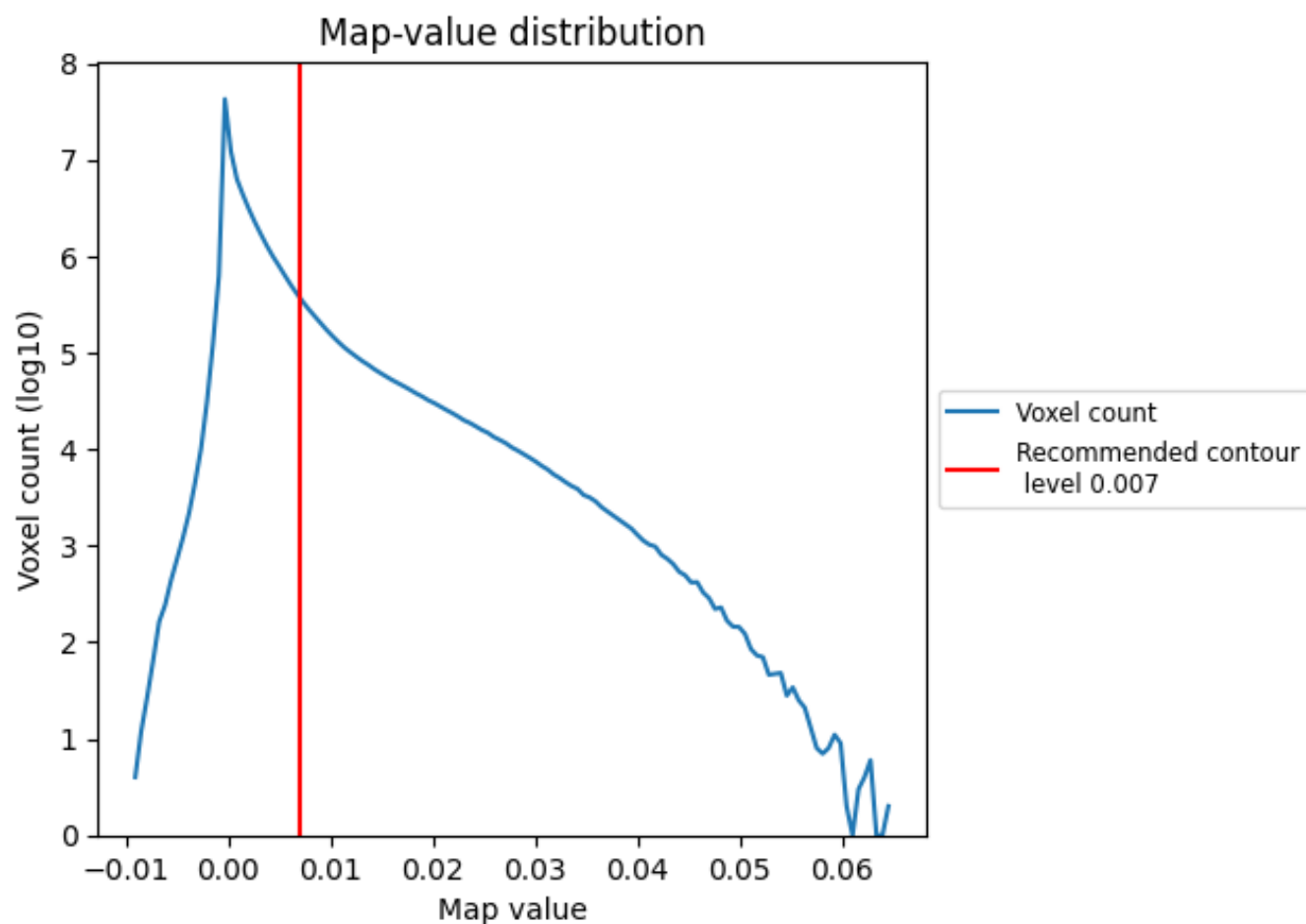
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

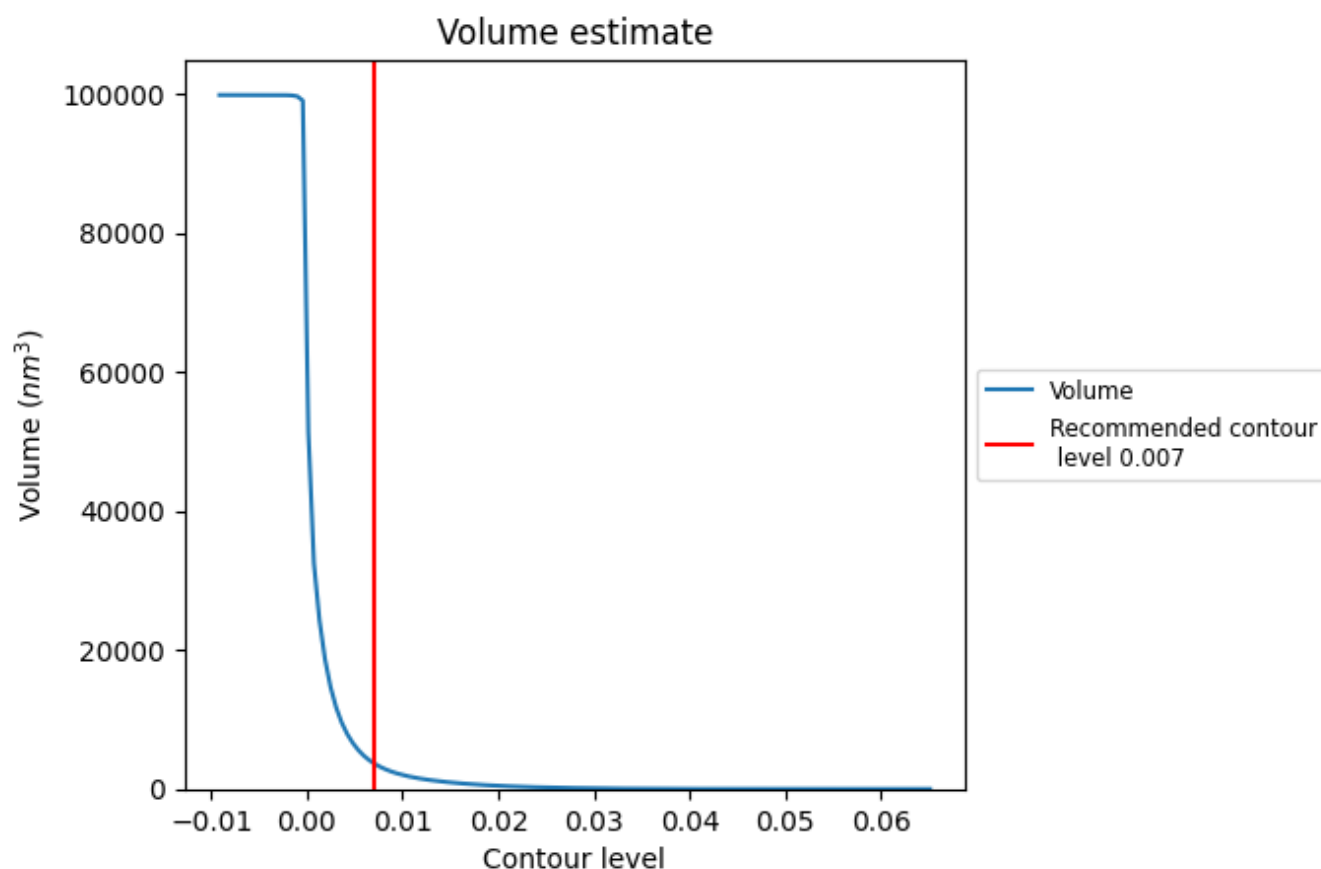
This section contains the results of statistical analysis of the map.

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.

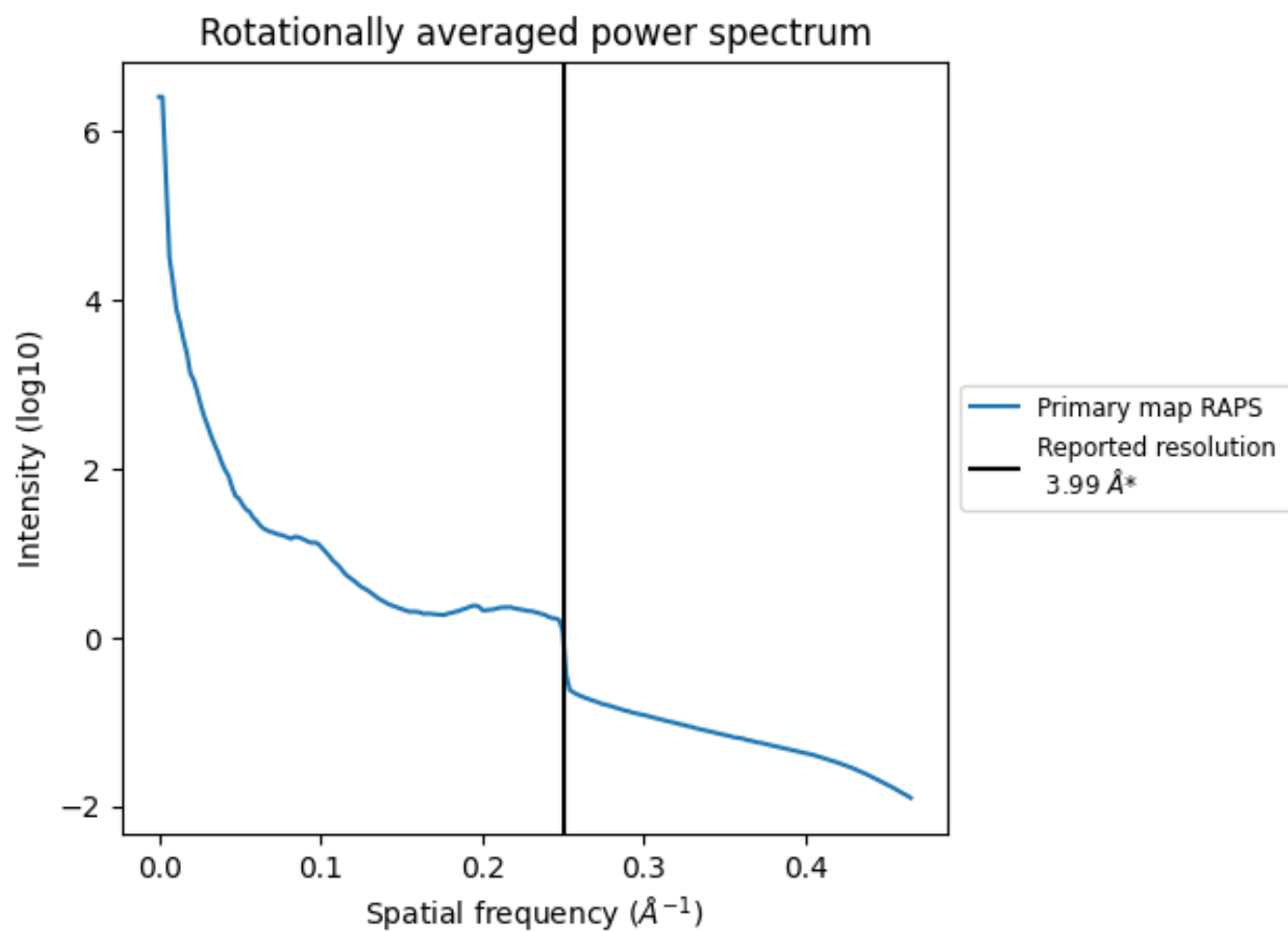
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3693 nm³; this corresponds to an approximate mass of 3336 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 0.251 Å⁻¹

8 Fourier-Shell correlation

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

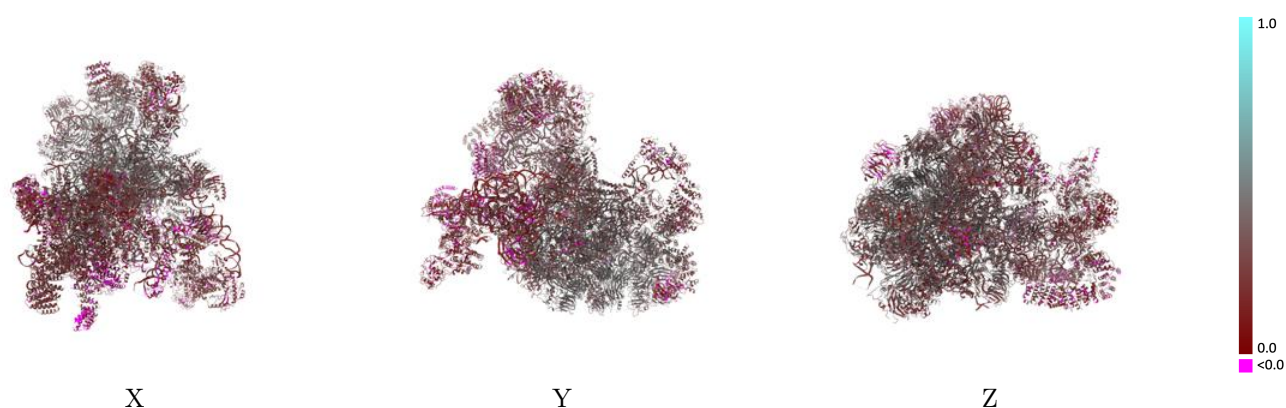
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25441 and PDB model 7SUK. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

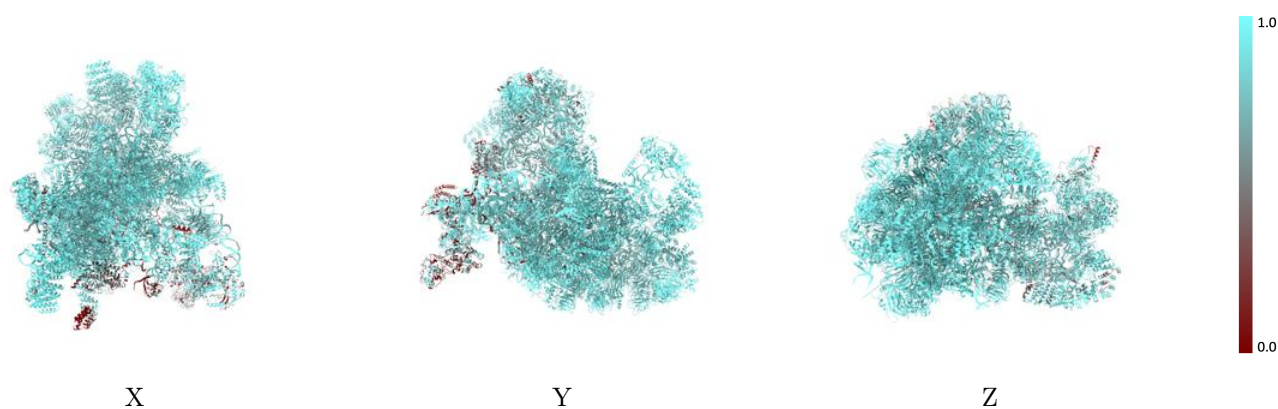
This section was not generated.

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



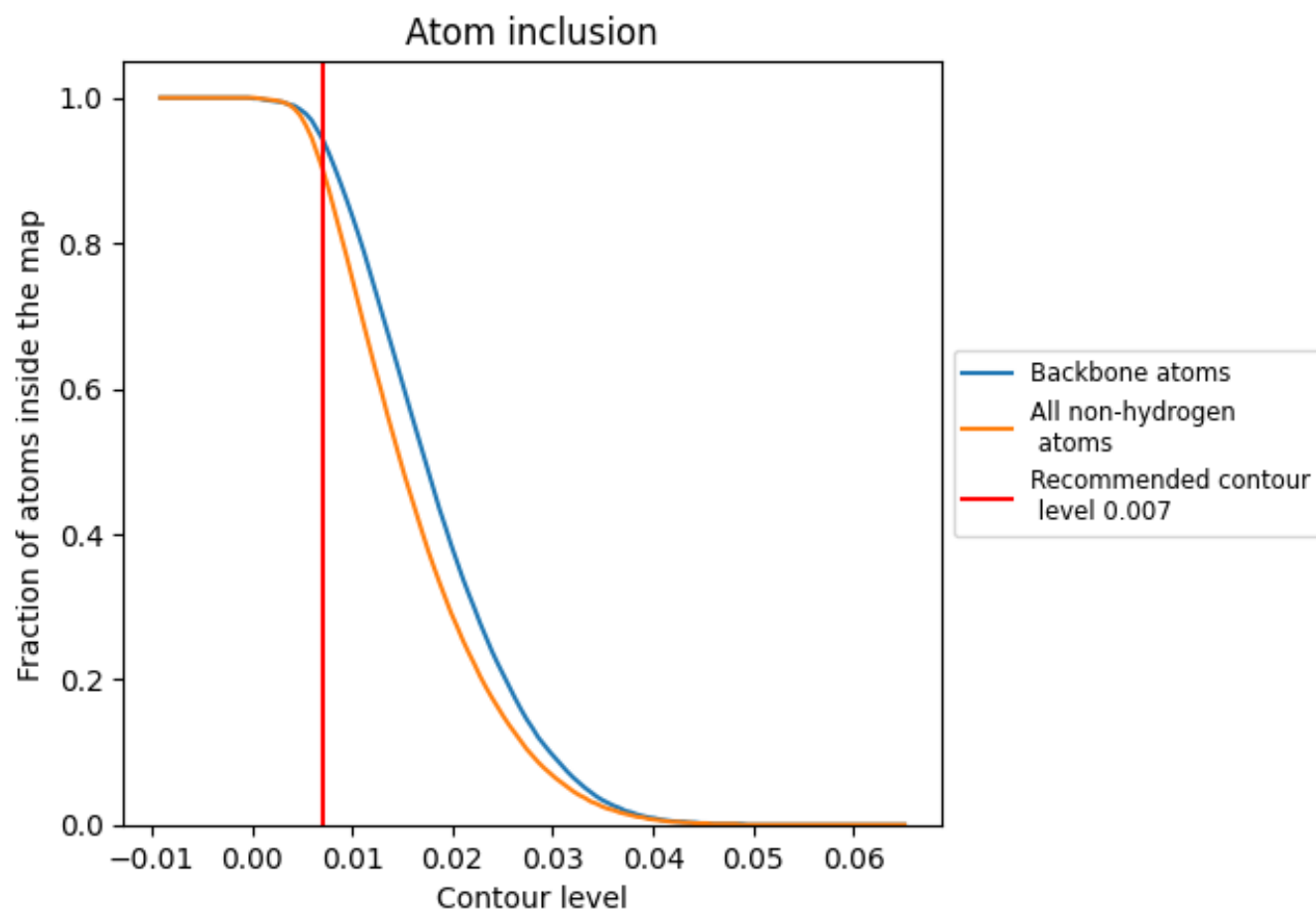
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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 (0.007).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.3140
5	 0.5200	 0.1000
6	 0.6050	 0.1570
8	 0.9090	 0.2630
L0	 0.9890	 0.3530
L2	 0.9880	 0.3600
L3	 0.8400	 0.3230
L4	 0.8350	 0.2260
L5	 0.9450	 0.4070
L6	 0.7430	 0.1750
L7	 0.7720	 0.2040
L8	 0.8670	 0.2410
L9	 0.9360	 0.3690
LC	 0.9570	 0.4350
LD	 0.8710	 0.2350
LE	 0.8460	 0.2520
LF	 0.9020	 0.2620
LG	 0.9810	 0.4260
LH	 0.9480	 0.3750
LI	 0.9290	 0.2260
LJ	 0.9540	 0.3970
LK	 0.9810	 0.3210
LL	 0.9530	 0.3990
LM	 0.9460	 0.3870
LN	 0.9490	 0.3700
LO	 0.9520	 0.4190
LP	 0.9710	 0.3330
LQ	 0.9530	 0.3300
LR	 0.8190	 0.1640
LS	 0.9550	 0.4190
LT	 0.9600	 0.4180
LU	 0.9370	 0.3700
LV	 0.8430	 0.2340
LW	 0.9490	 0.4130
LX	 0.8470	 0.2280



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LY	 0.8620	 0.2620
LZ	 0.9480	 0.4160
NA	 0.9010	 0.3710
NB	 0.9340	 0.3810
ND	 0.9270	 0.3450
NE	 0.7280	 0.2910
NF	 0.4850	 0.0300
NG	 0.9010	 0.2330
NH	 0.6270	 0.1930
NI	 0.3470	 0.1710
NJ	 0.9320	 0.2520
NK	 0.9510	 0.2180
SA	 0.9440	 0.3620
SB	 0.9440	 0.3510
SC	 0.9430	 0.4130
SD	 0.9390	 0.3550
SE	 0.9240	 0.3920
SF	 0.9500	 0.3550
SG	 0.9530	 0.3100
SH	 0.9470	 0.3710
SI	 0.9330	 0.3620
SJ	 0.9480	 0.3210
SK	 0.9610	 0.3840
SL	 0.9550	 0.4140
SM	 0.9260	 0.4050
SN	 0.9590	 0.3740
SO	 0.9890	 0.3240
SP	 0.8630	 0.2240
SQ	 0.8950	 0.3950
SR	 0.9210	 0.3730
SS	 0.9320	 0.3350
ST	 0.9440	 0.3160
SU	 0.9440	 0.2940
SV	 0.9070	 0.3540
SY	 0.9420	 0.3970
SZ	 0.9610	 0.2440