



Full wwPDB EM Validation Report ⓘ

Jan 1, 2023 – 11:22 PM JST

PDB ID : 7CPV
EMDB ID : EMD-30433
Title : Cryo-EM structure of 80S ribosome from mouse testis
Authors : Huo, Y.G.; He, X.; Jiang, T.; Qin, Y.; Guo, X.J.; Sha, J.H.
Deposited on : 2020-08-08
Resolution : 3.03 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

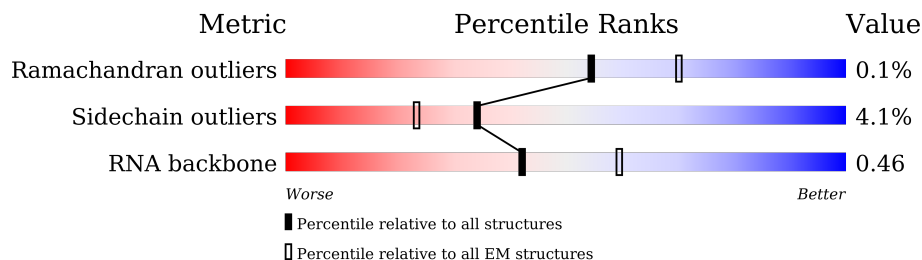
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.03 Å.

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




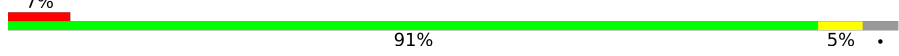
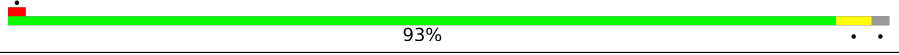
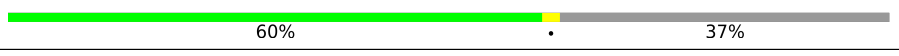
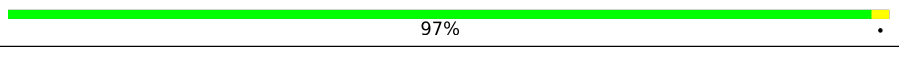
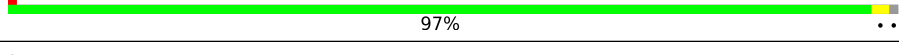

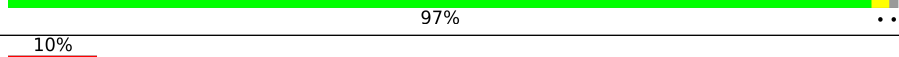
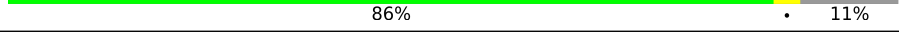
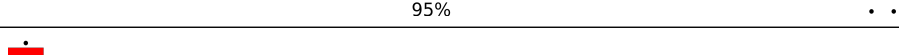
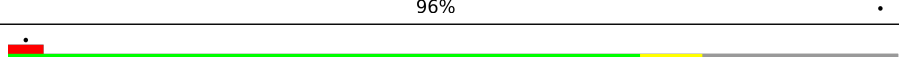
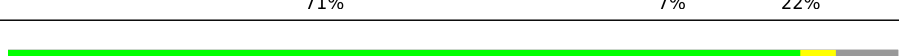

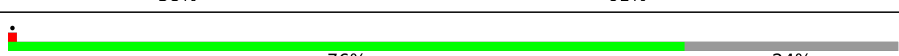
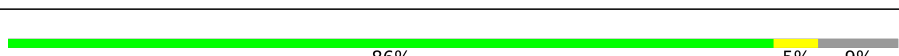
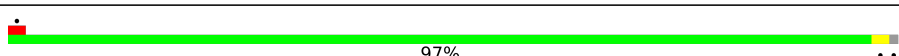
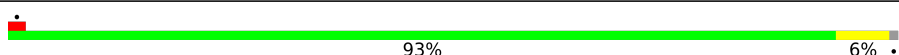



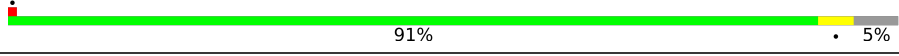
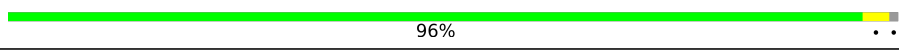
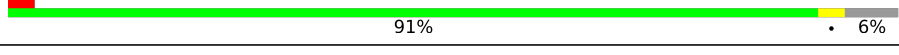
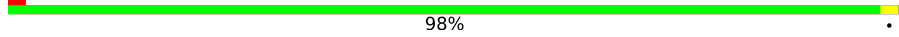

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	LA	257	
2	LB	403	
3	LC	419	
4	LD	297	
5	LE	296	
6	LF	270	
7	LG	266	
8	LH	192	

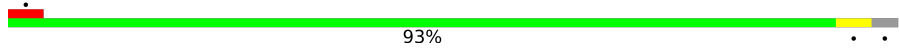

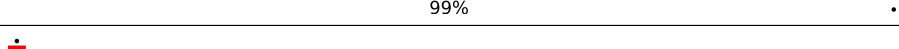
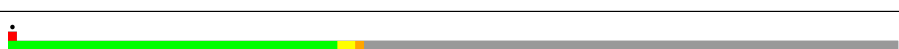

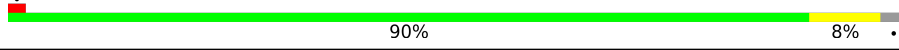
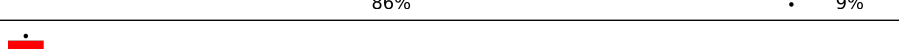



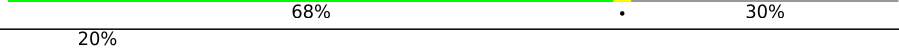

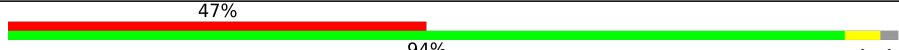


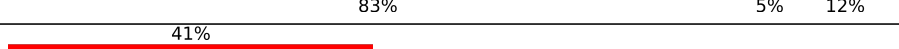


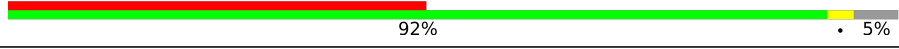
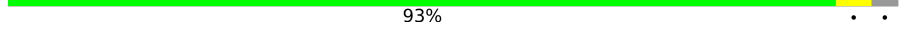


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Mol	Chain	Length	Quality of chain
9	LI	214	 90% 6%
10	LJ	178	 7% 91% 5%
11	LL	211	 93%
12	LM	217	 60% 37%
13	LN	204	 97%
14	LO	203	 97%
15	LP	184	 82% 16%
16	LQ	188	 97%
17	LR	196	 10% 86% 11%
18	LS	176	 95%
19	LT	160	 96%
20	LU	128	 71% 7% 22%
21	LV	140	 89% 7%
22	LW	157	 38% 61%
23	LX	156	 76% 24%
24	LY	145	 86% 5% 9%
25	LZ	136	 97%
26	La	148	 93% 6%
27	Lb	160	 59% 38%
28	Lc	115	 78% 18%
29	Ld	125	 6% 86% 14%
30	Le	135	 91% 5%
31	Lf	110	 96%
32	Lg	117	 91% 6%
33	Lh	123	 98%

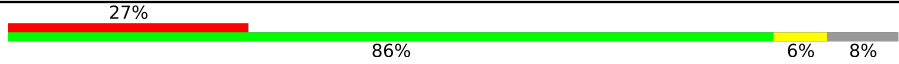
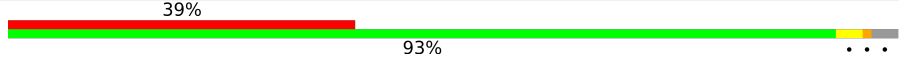
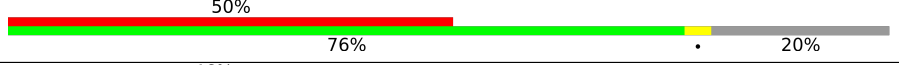
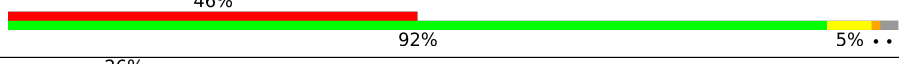
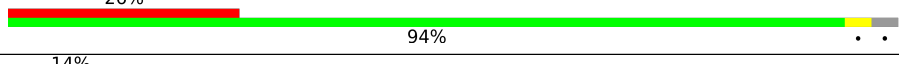

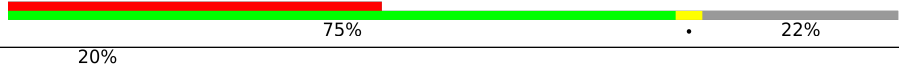
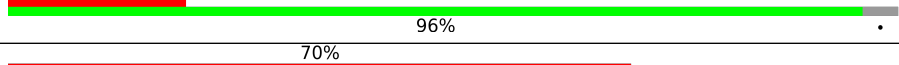
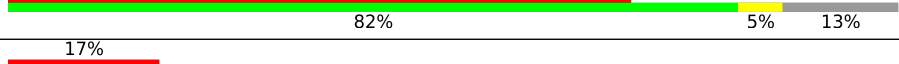


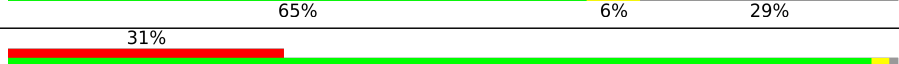
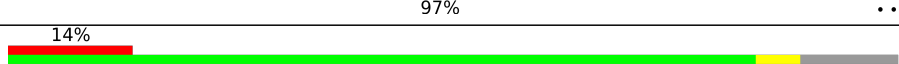
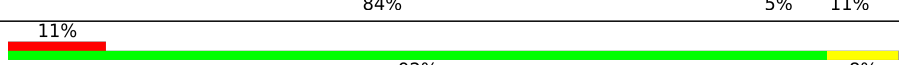
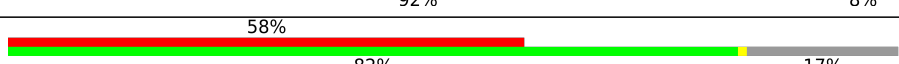
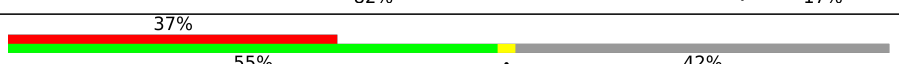
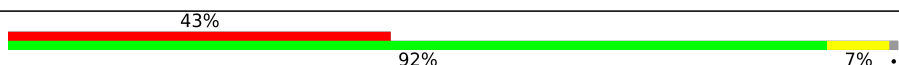
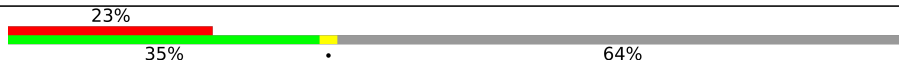


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Mol	Chain	Length	Quality of chain
34	Li	105	 93%
35	Lj	97	 88% 11%
36	Lk	70	 99% 7%
37	Ll	51	 84% 14%
38	Lm	128	 37% 60%
39	Ln	25	 96%
40	Lo	106	 90% 8%
41	Lp	92	 96%
42	Lr	137	 86% 9%
43	L5	4731	 55% 19% 25%
44	L7	120	 90% 10%
45	L8	158	 76% 22% 6%
46	S2	1870	 63% 24% 14%
47	SA	295	 68% 30% 31%
48	SB	264	 80% 19% 20%
49	SD	243	 90% 8% 61%
50	SE	263	 94% 47%
51	SF	204	 84% 12% 44%
52	SH	194	 89% 7% 73%
53	SI	208	 83% 5% 12% 34%
54	SK	165	 53% 45% 41%
55	SL	158	 82% 15% 22%
56	SP	145	 81% 19% 21%
57	SQ	146	 92% 5% 47%
58	SR	135	93% 70%

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Mol	Chain	Length	Quality of chain
59	SS	152	
60	ST	145	
61	SU	119	
62	SV	83	
63	SX	143	
64	Sa	115	
65	Sc	69	
66	Sd	56	
67	Sg	317	
68	SC	293	
69	SG	249	
70	SJ	194	
71	SN	151	
72	SO	151	
73	SW	130	
74	SY	133	
75	SZ	125	
76	Sb	84	
77	Se	133	
78	S6	75	

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 206030 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	LA	248	1898	1189	389	314	6	0	0

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	LB	397	3202	2039	603	546	14	0	0

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	LC	362	2891	1819	577	480	15	0	0

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LD	293	2385	1506	440	425	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LE	231	1874	1195	358	317	4	0	0

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LF	214	1771	1139	337	287	8	0	0

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	LG	229	1848	1179	354	311	4	0	0

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LH	190	1519	956	284	273	6	0	0

- Molecule 9 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LI	201	1631	1037	316	267	11	0	0

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LJ	171	1371	866	255	244	6	0	0

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LL	206	1667	1043	343	277	4	0	0

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LM	136	1125	721	218	179	7	0	0

- Molecule 13 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LN	203	1701	1072	359	266	4	0	0

- Molecule 14 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	LO	201	1640	1055	320	259	6	0	0

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LP	154	1251	782	243	217	9	0	0

- Molecule 16 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	LQ	187	1515	948	314	249	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LR	174	1457	901	316	231	9	0	0

- Molecule 18 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	LS	175	1451	924	283	234	10	0	0

- Molecule 19 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LT	160	1307	829	253	218	7	0	0

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	LU	100	817	523	143	149	2	0	0

- Molecule 21 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 23 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	La	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Lb	99	Total	C	N	O	S	0	0
			807	505	174	124	4		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ld	108	Total	C	N	O	S	0	0
			896	566	172	156	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lf	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lg	110	Total	C	N	O	S	0	0
			873	546	180	141	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 35 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 37 is a protein called Ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ll	50	Total	C	N	O	S	0	0
			438	279	93	64	2		

- Molecule 38 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 39 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lr	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

- Molecule 43 is a RNA chain called Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L5	3541	Total	C	N	O	P	0	0
			75913	33809	13873	24691	3540		

- Molecule 44 is a RNA chain called Mus musculus 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 46 is a RNA chain called Mus musculus 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1637	Total	C	N	O	P	0	0
			34941	15601	6275	11429	1636		

- Molecule 47 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	224	Total	C	N	O	S	0	0
			1744	1111	314	312	7		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SP	118	981	625	183	166	7	0	0

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SQ	139	1109	704	210	192	3	0	0

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SR	131	1064	668	198	194	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SS	140	1157	728	231	197	1	0	0

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	ST	140	1090	681	212	195	2	0	0

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SU	95	753	471	142	136	4	0	0

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SV	81	619	379	116	119	5	0	0

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SX	139	1080	682	214	181	3	0	0

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Sa	99	792	492	165	130	5	0	0

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Sc	54	416	257	80	77	2	0	0

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Sd	54	455	284	93	73	5	0	0

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Sg	276	2148	1357	378	401	12	0	0

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SC	215	1673	1085	288	291	9	1	0

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	SG	204	1645	1029	330	280	6	0	0

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	SJ	138	1162	743	230	187	2	0	0

- Molecule 71 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	SN	150	1208	773	229	205	1	0	0

- Molecule 72 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	SO	134	1002	612	197	187	6	0	0

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SW	129	1034	659	193	176	6	0	0

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SY	110	891	565	173	149	4	0	0

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	SZ	72	574	368	104	101	1	0	0

- Molecule 76 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Sb	83	651	408	121	115	7	0	0

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	48	Total	C	N	O	S	0	0
			384	234	86	63	1		

- Molecule 78 is a RNA chain called Met-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 79 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	LN	1	Total	Mg	0
			1	1	
79	LP	1	Total	Mg	0
			1	1	
79	LT	1	Total	Mg	0
			1	1	
79	LV	1	Total	Mg	0
			1	1	
79	Le	1	Total	Mg	0
			1	1	
79	Lf	1	Total	Mg	0
			1	1	
79	L5	173	Total	Mg	0
			173	173	
79	L7	3	Total	Mg	0
			3	3	
79	L8	5	Total	Mg	0
			5	5	
79	S2	59	Total	Mg	0
			59	59	
79	SF	1	Total	Mg	0
			1	1	

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	Lg	1	Total	Zn	0
			1	1	
80	Lj	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
80	Lm	1	Total 1	Zn 1	0
80	Lo	1	Total 1	Zn 1	0
80	Lp	1	Total 1	Zn 1	0
80	Sa	1	Total 1	Zn 1	0
80	Sd	1	Total 1	Zn 1	0

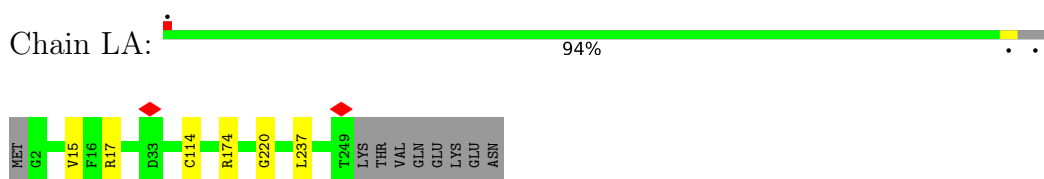
- Molecule 81 is water.

Mol	Chain	Residues	Atoms		AltConf
81	LB	1	Total 1	O 1	0
81	LH	1	Total 1	O 1	0
81	LI	2	Total 2	O 2	0
81	LN	1	Total 1	O 1	0
81	La	1	Total 1	O 1	0
81	L5	7	Total 7	O 7	0
81	S2	2	Total 2	O 2	0

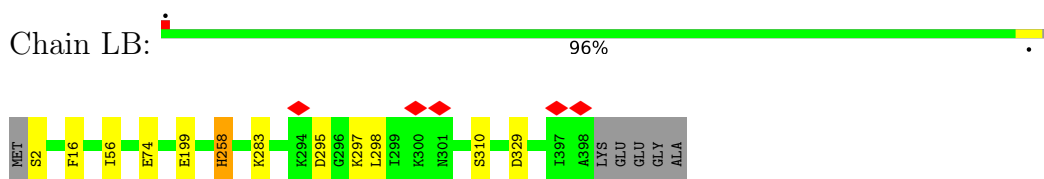
3 Residue-property plots [i](#)

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

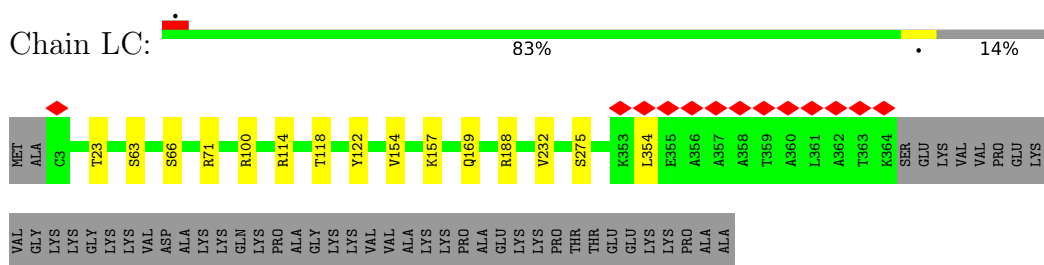
- Molecule 1: 60S ribosomal protein L8



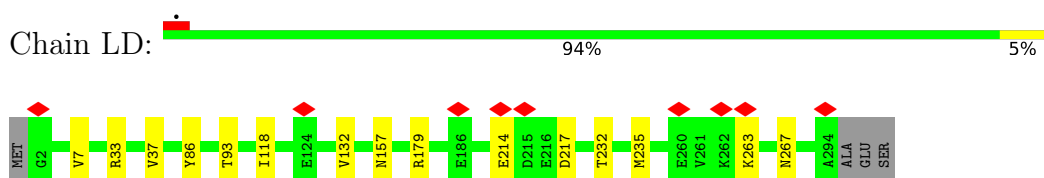
- Molecule 2: 60S ribosomal protein L3



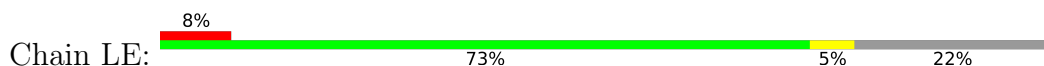
- Molecule 3: 60S ribosomal protein L4

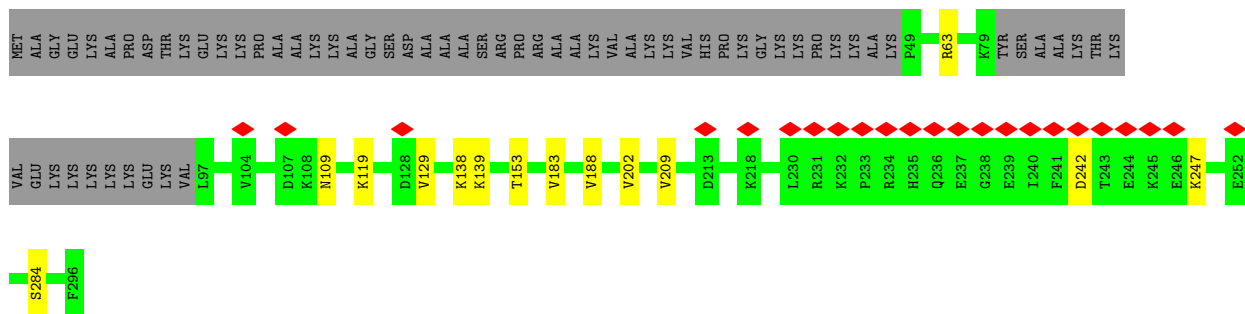


- Molecule 4: 60S ribosomal protein L5

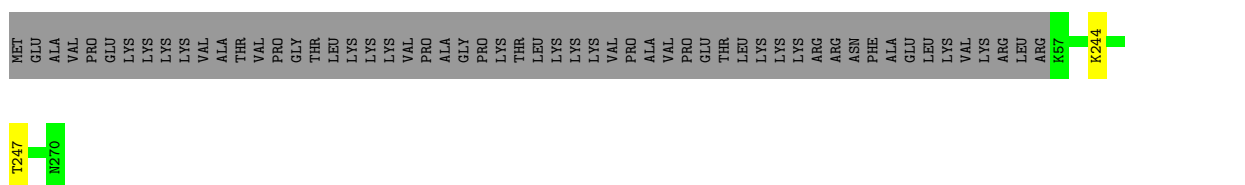
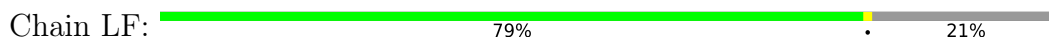


- Molecule 5: 60S ribosomal protein L6

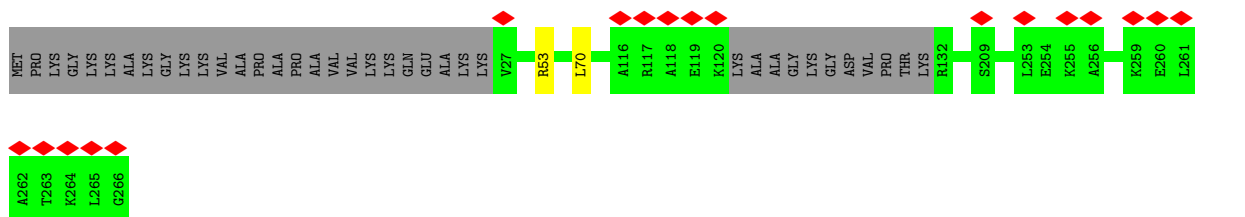
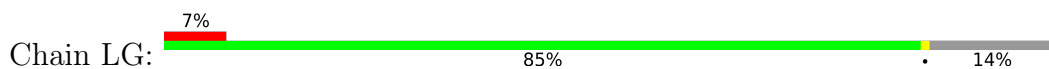




• Molecule 6: 60S ribosomal protein L7



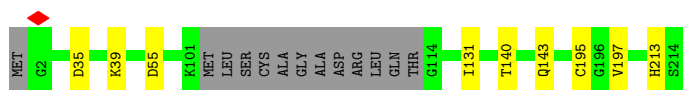
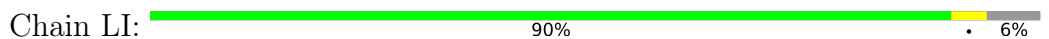
• Molecule 7: 60S ribosomal protein L7a



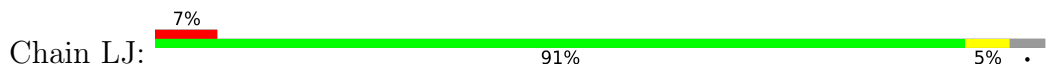
• Molecule 8: 60S ribosomal protein L9



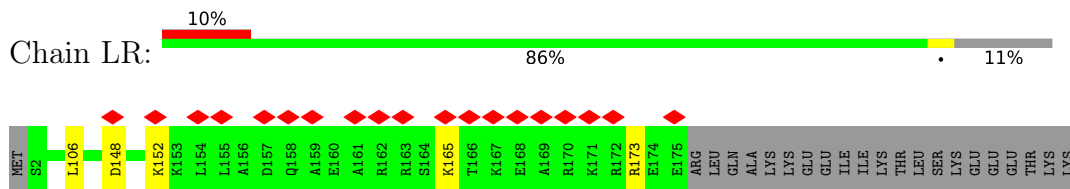
• Molecule 9: 60S ribosomal protein L10-like



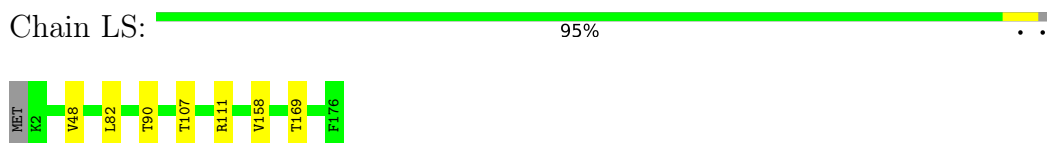
• Molecule 10: 60S ribosomal protein L11



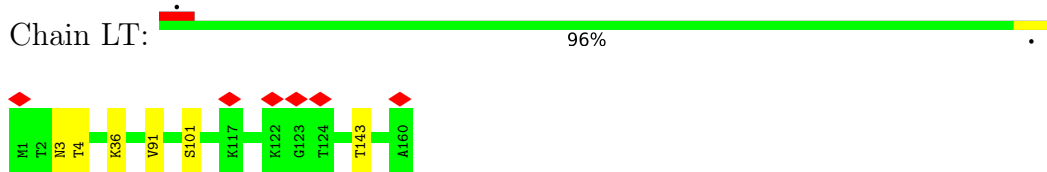
• Molecule 17: 60S ribosomal protein L19



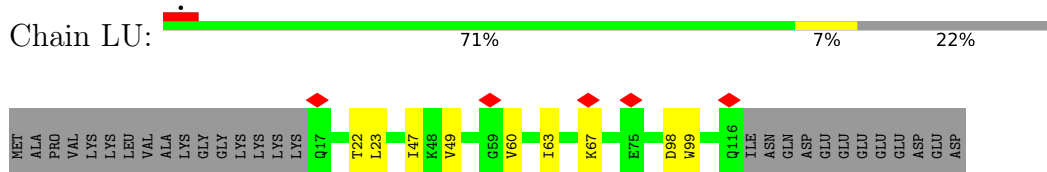
• Molecule 18: 60S ribosomal protein L18a



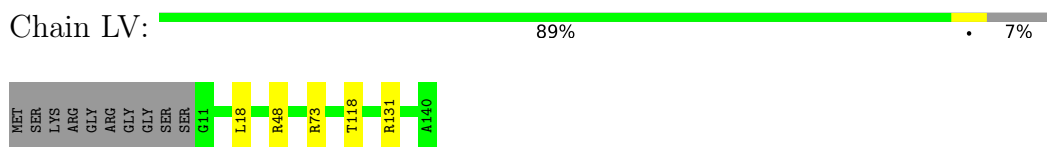
• Molecule 19: 60S ribosomal protein L21



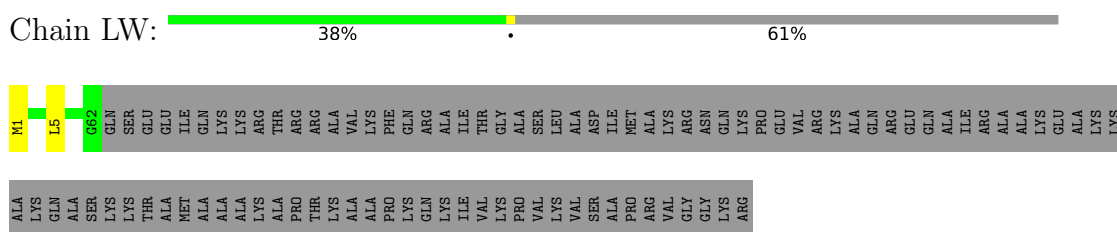
• Molecule 20: 60S ribosomal protein L22



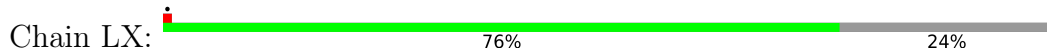
• Molecule 21: 60S ribosomal protein L23

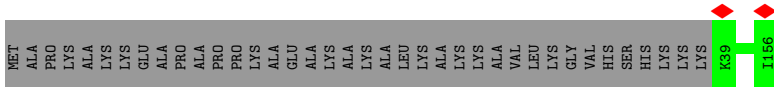


• Molecule 22: 60S ribosomal protein L24

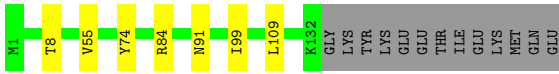
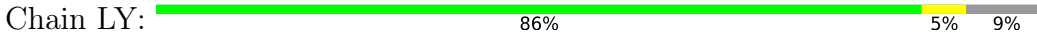


• Molecule 23: 60S ribosomal protein L23a

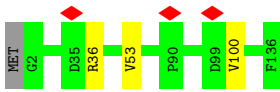




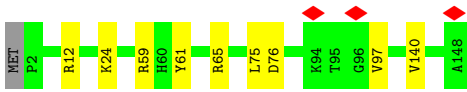
• Molecule 24: 60S ribosomal protein L26



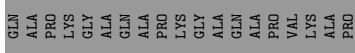
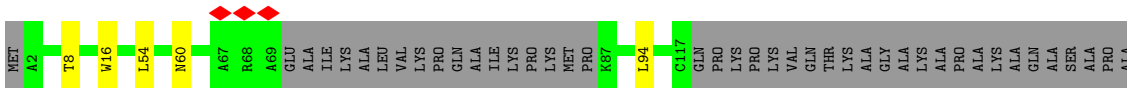
• Molecule 25: 60S ribosomal protein L27



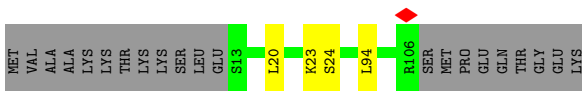
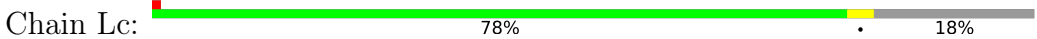
• Molecule 26: 60S ribosomal protein L27a



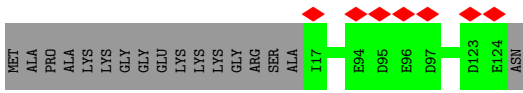
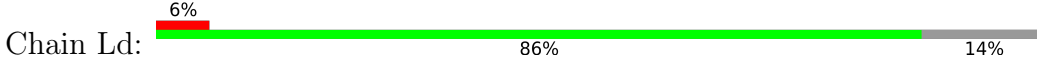
• Molecule 27: 60S ribosomal protein L29




• Molecule 28: 60S ribosomal protein L30



• Molecule 29: 60S ribosomal protein L31



- Molecule 30: 60S ribosomal protein L32

Chain Le:  91% 5%



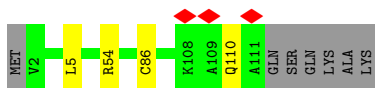
- Molecule 31: 60S ribosomal protein L35a

Chain Lf:  96%



- Molecule 32: 60S ribosomal protein L34

Chain Lg:  91% 6%



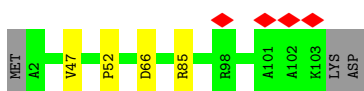
- Molecule 33: 60S ribosomal protein L35

Chain Lh:  98%




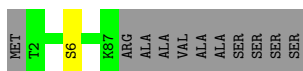
- Molecule 34: 60S ribosomal protein L36

Chain Li:  93%



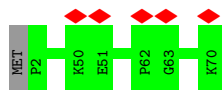
- Molecule 35: 60S ribosomal protein L37

Chain Lj:  88% 11%

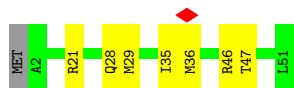
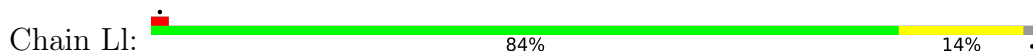


- Molecule 36: 60S ribosomal protein L38

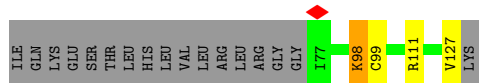
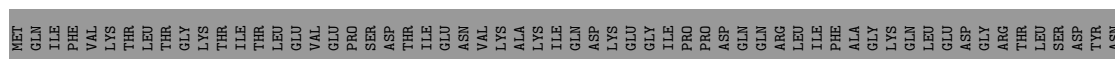
Chain Lk:  7% 99%



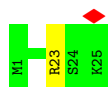
• Molecule 37: Ribosomal protein L39-like



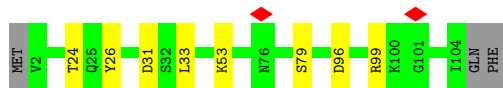
• Molecule 38: Ubiquitin-60S ribosomal protein L40



• Molecule 39: 60S ribosomal protein L41



• Molecule 40: 60S ribosomal protein L36a

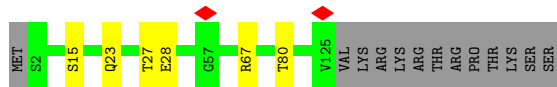


• Molecule 41: 60S ribosomal protein L37a

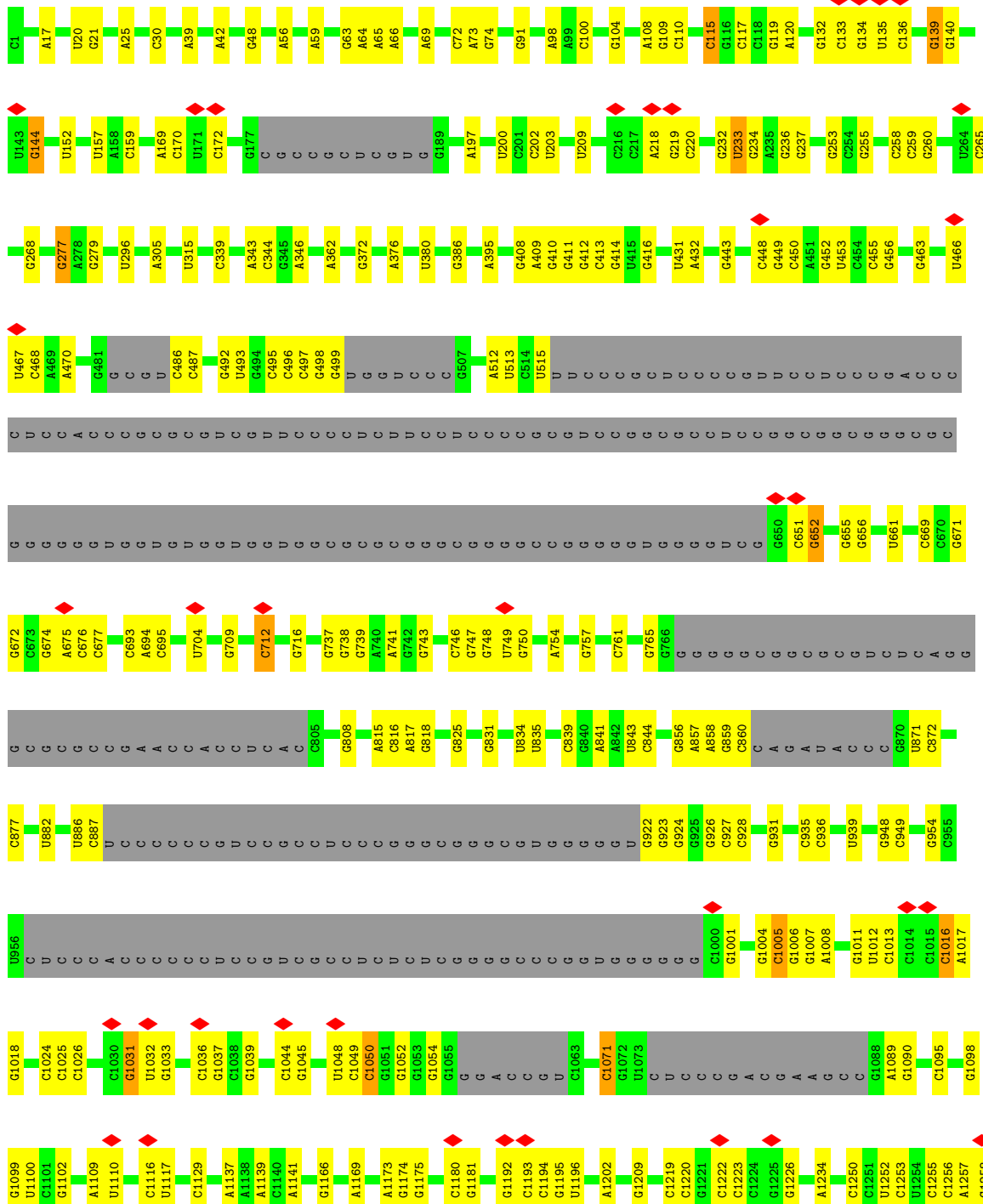


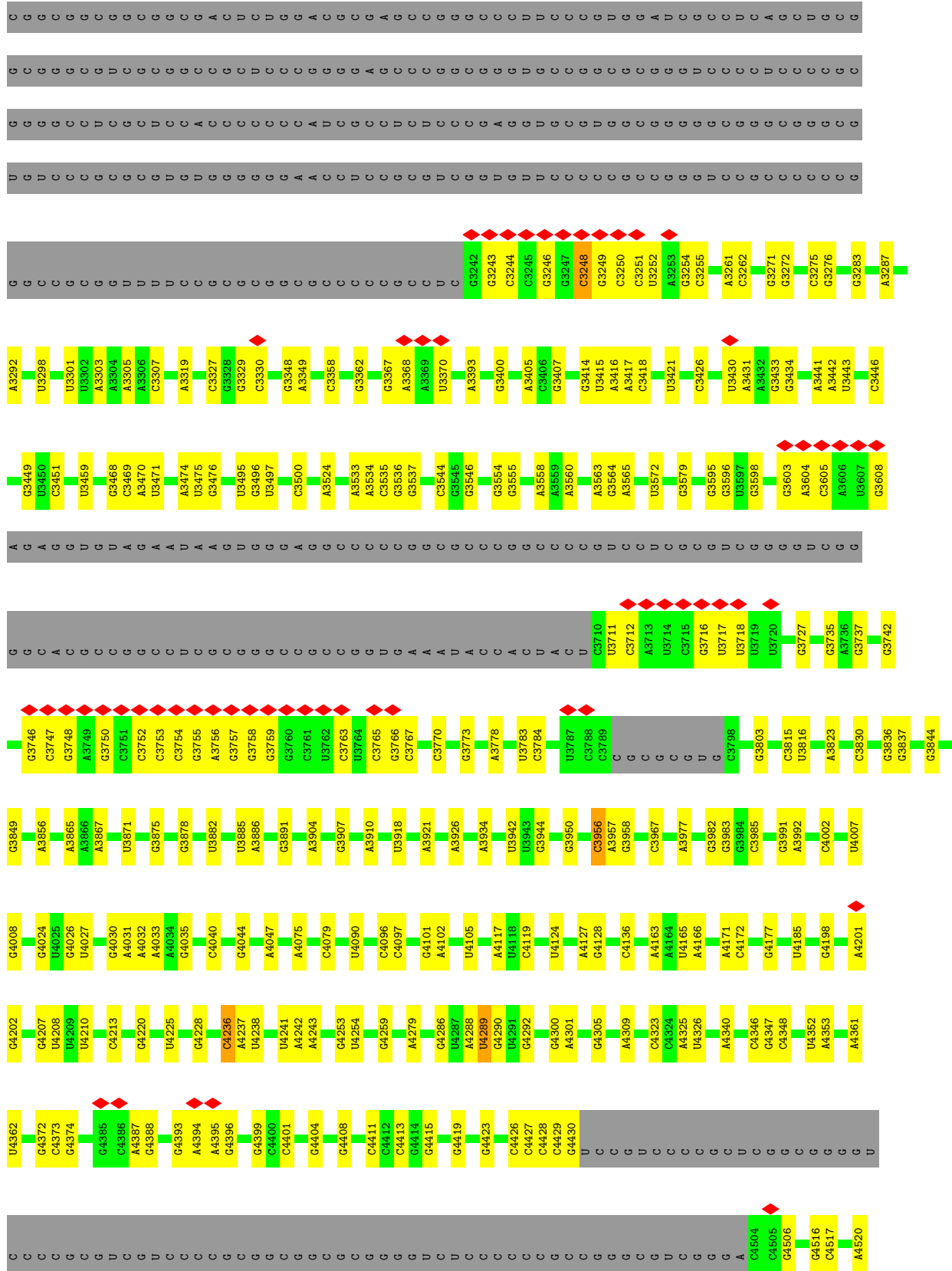
• Molecule 42: 60S ribosomal protein L28

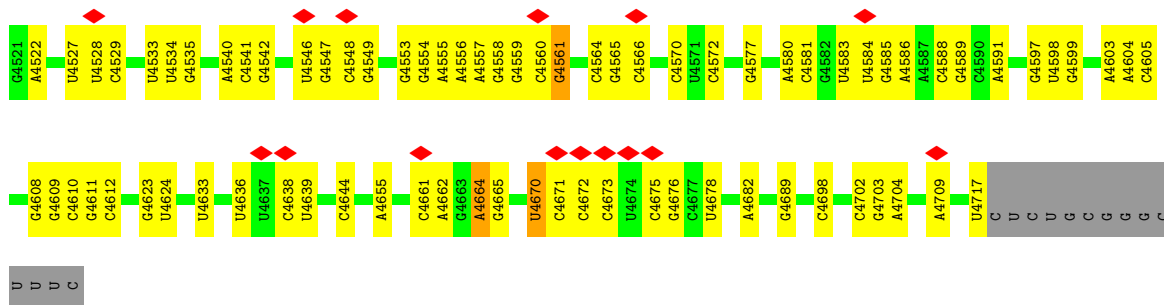




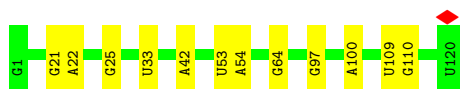
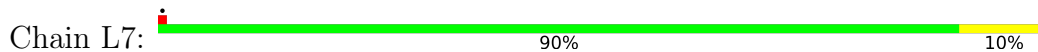
• Molecule 43: Mus musculus 28S ribosomal RNA



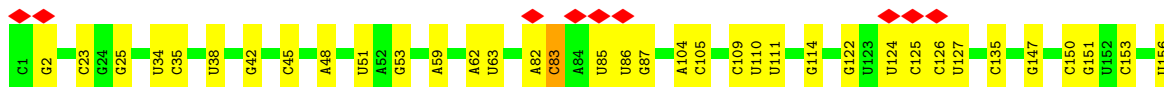
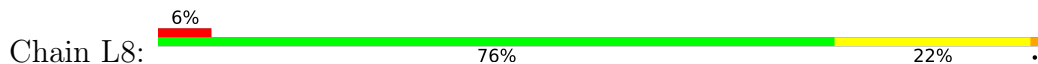




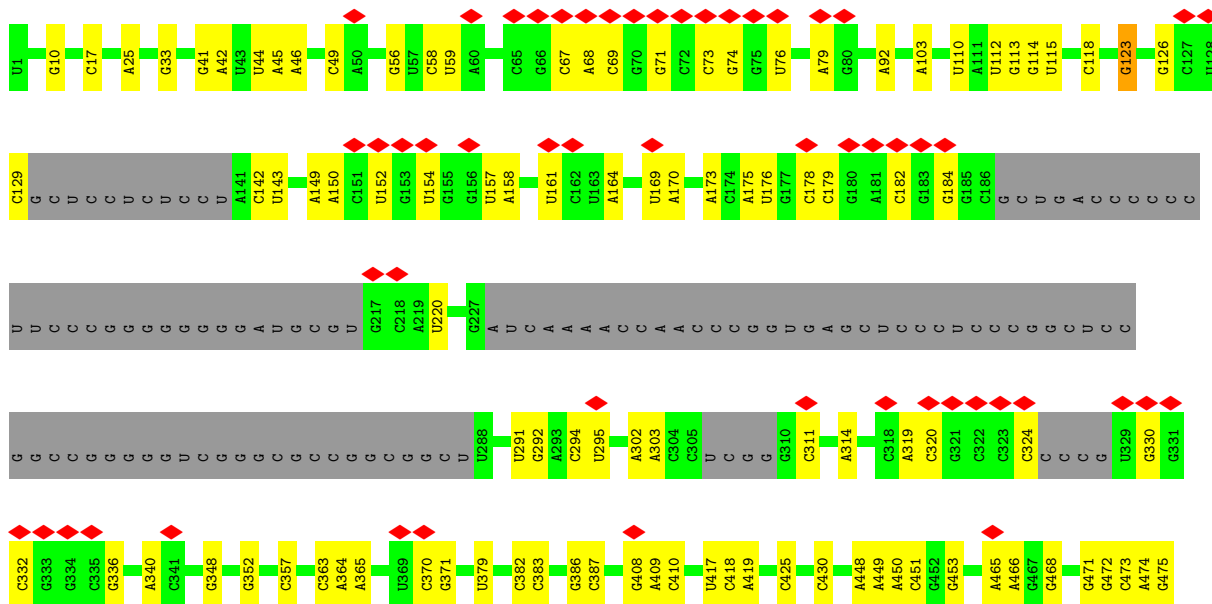
• Molecule 44: Mus musculus 5S ribosomal RNA



• Molecule 45: Mus musculus 5.8S ribosomal RNA



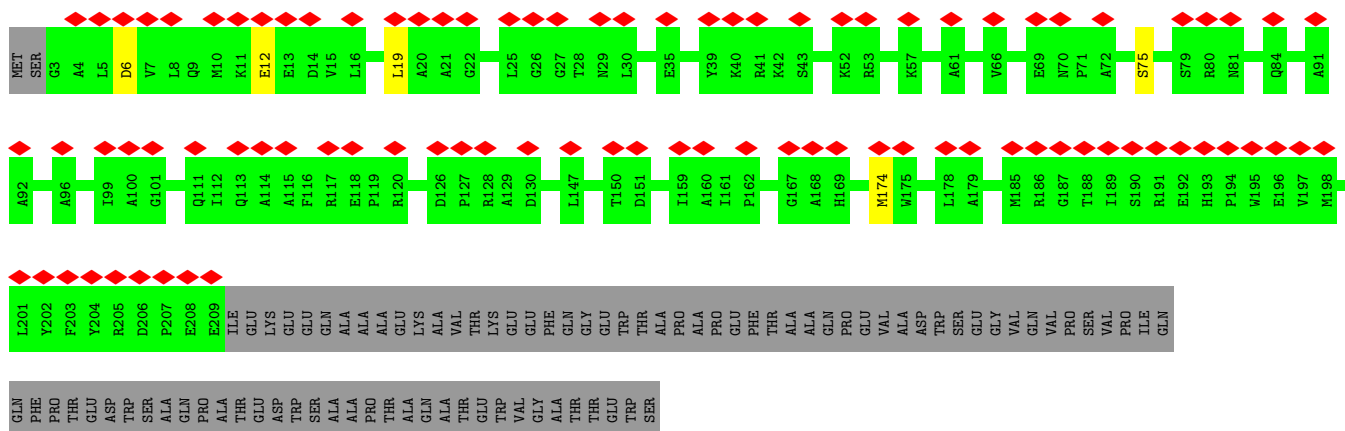
• Molecule 46: Mus musculus 18S ribosomal RNA



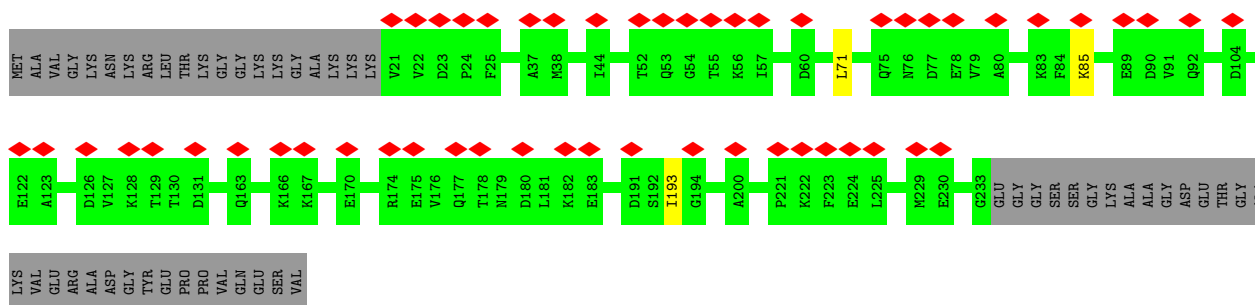
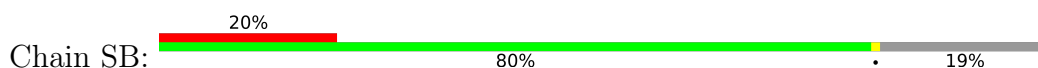




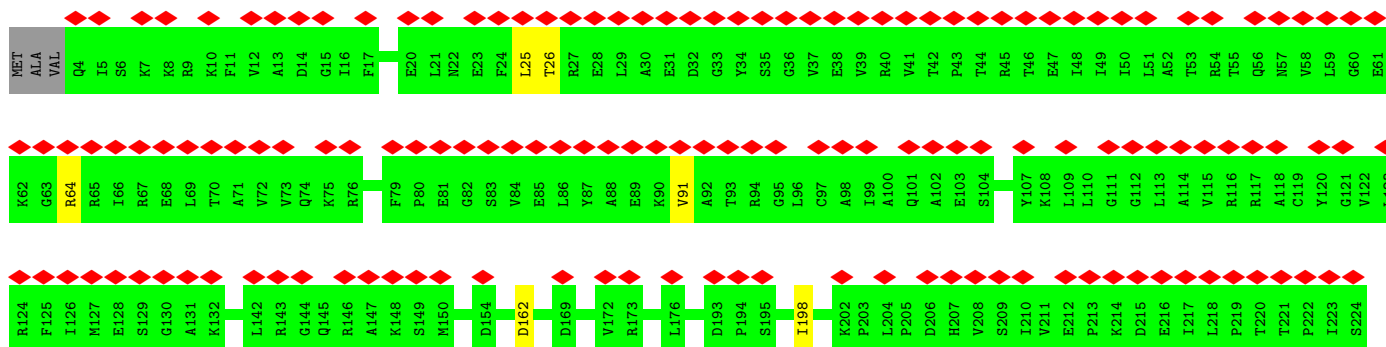
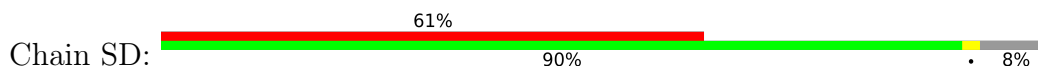
• Molecule 47: 40S ribosomal protein SA

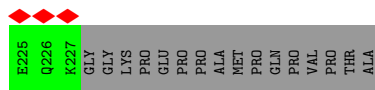


• Molecule 48: 40S ribosomal protein S3a

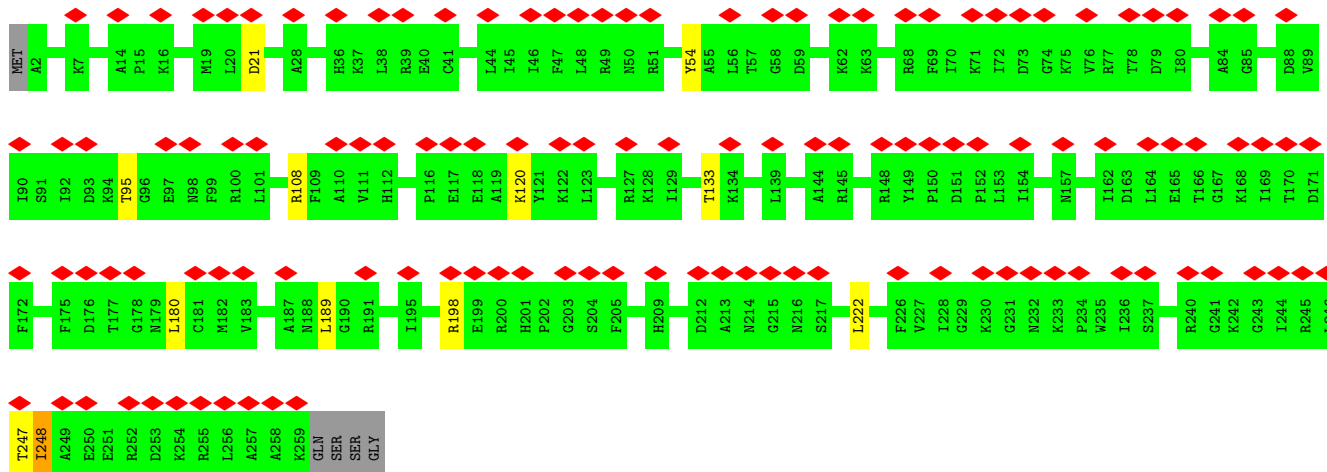


• Molecule 49: 40S ribosomal protein S3

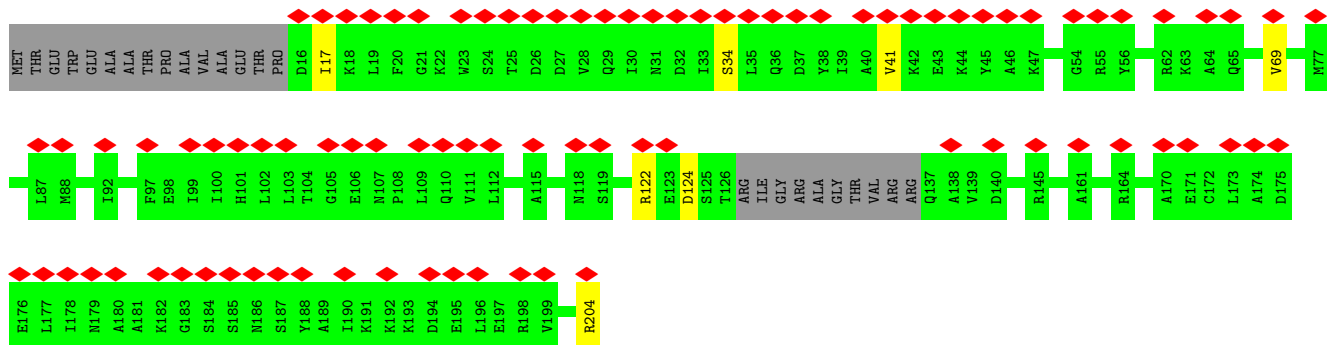
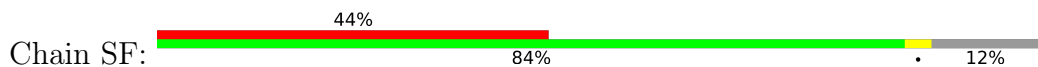




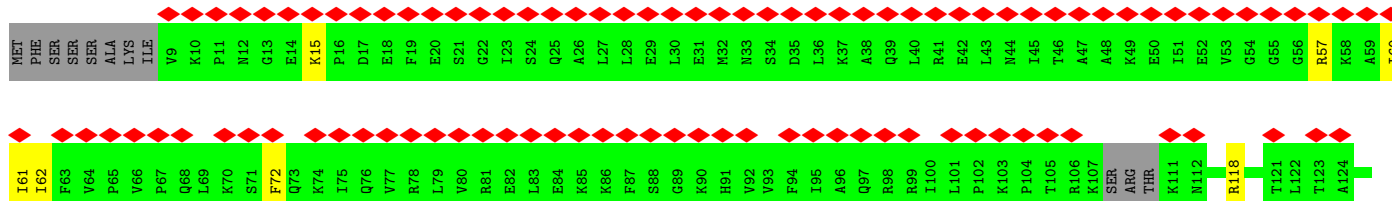
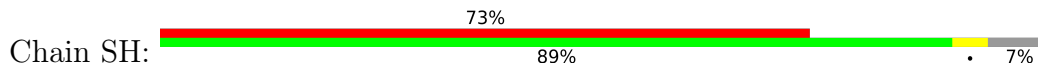
• Molecule 50: 40S ribosomal protein S4, X isoform

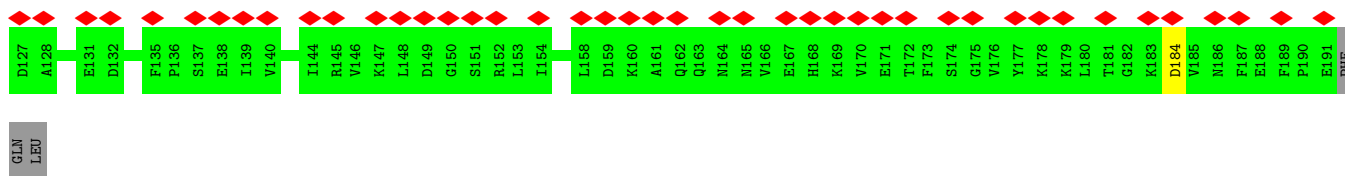


• Molecule 51: 40S ribosomal protein S5

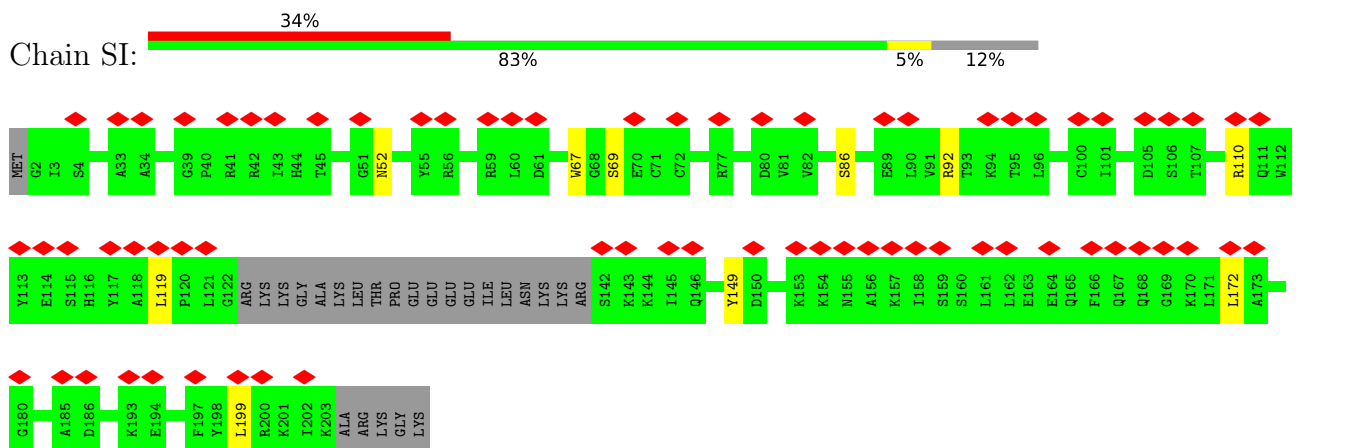


• Molecule 52: 40S ribosomal protein S7

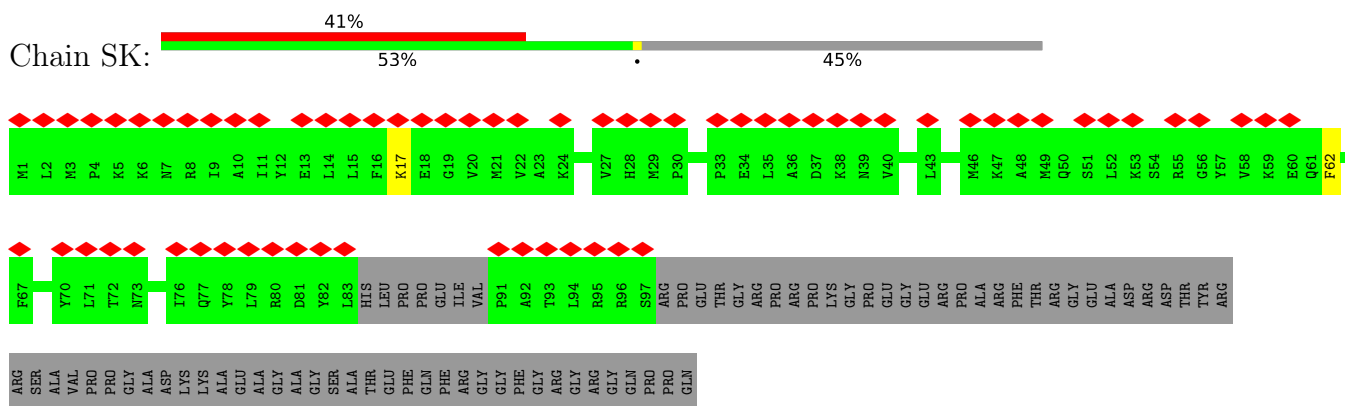




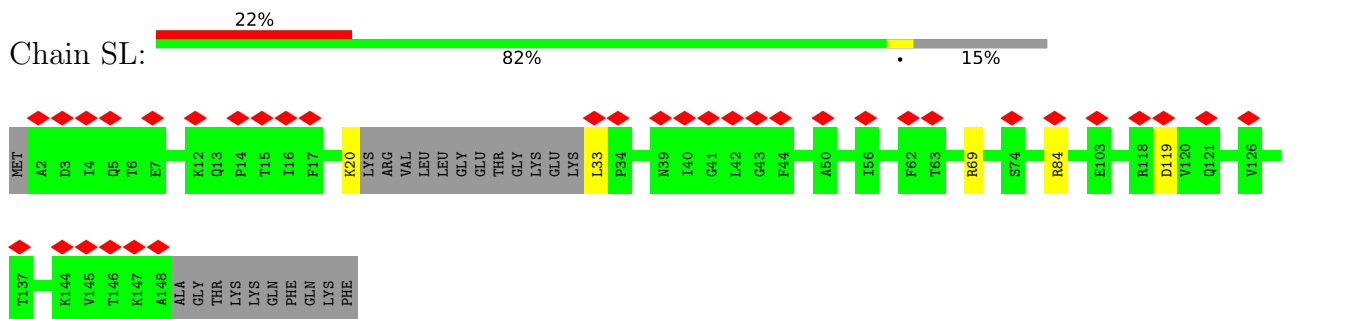
• Molecule 53: 40S ribosomal protein S8



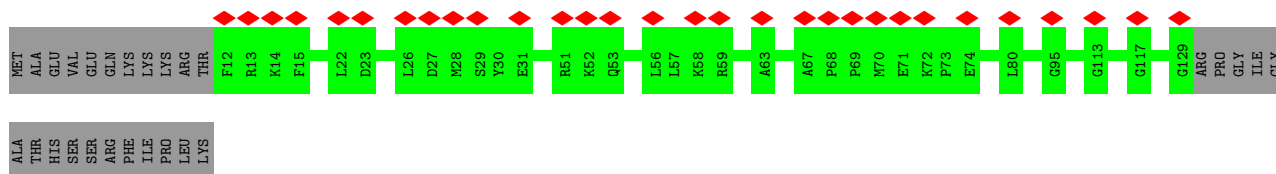
• Molecule 54: 40S ribosomal protein S10



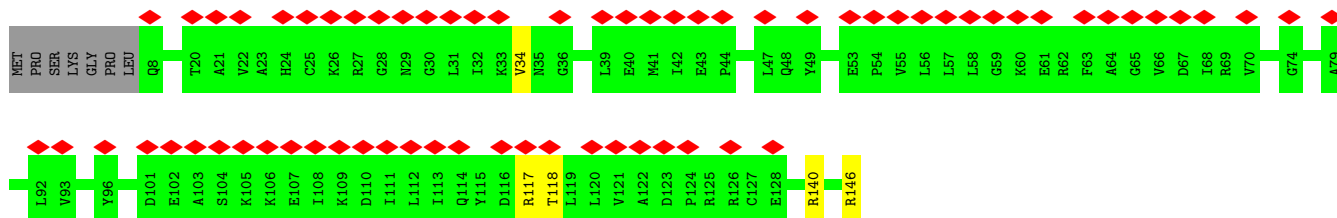
• Molecule 55: 40S ribosomal protein S11



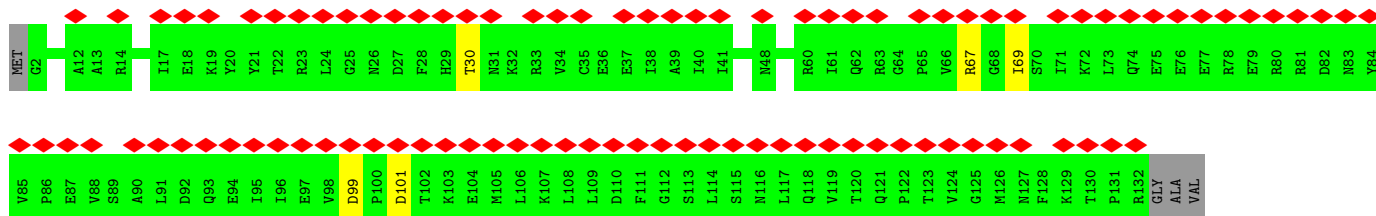
• Molecule 56: 40S ribosomal protein S15



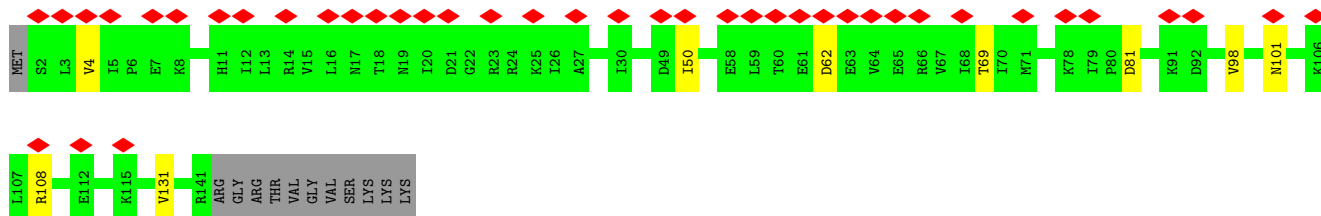
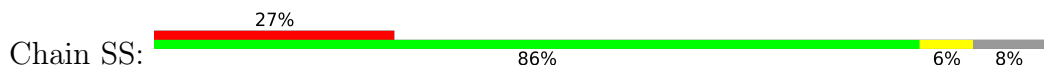
• Molecule 57: 40S ribosomal protein S16



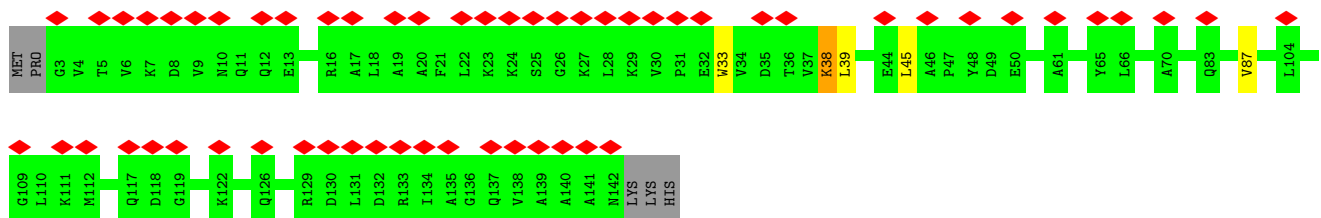
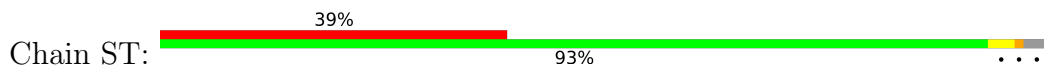
• Molecule 58: 40S ribosomal protein S17



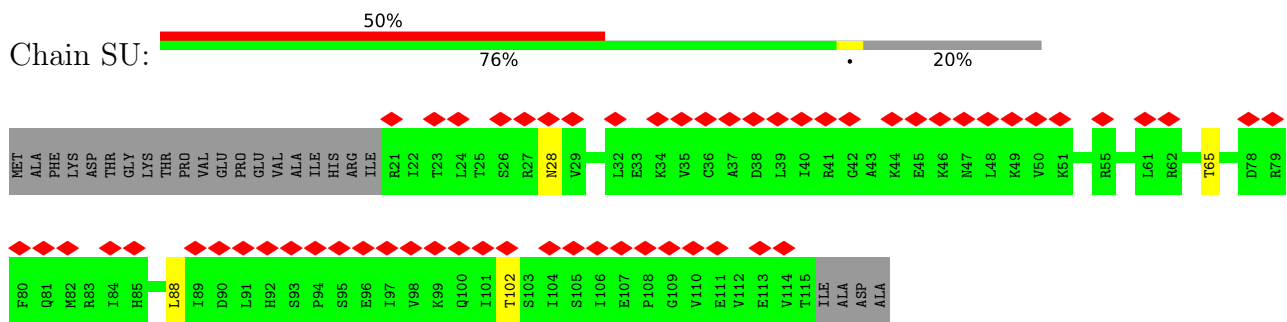
• Molecule 59: 40S ribosomal protein S18



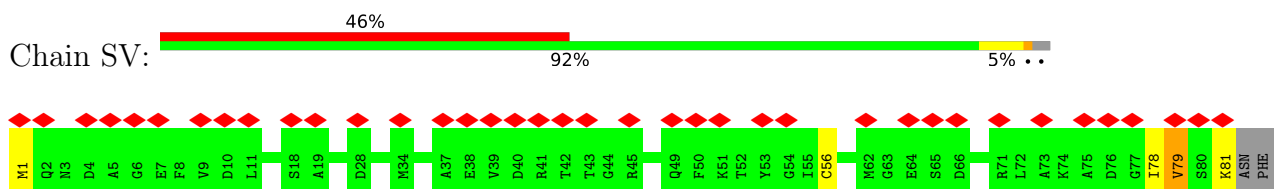
• Molecule 60: 40S ribosomal protein S19



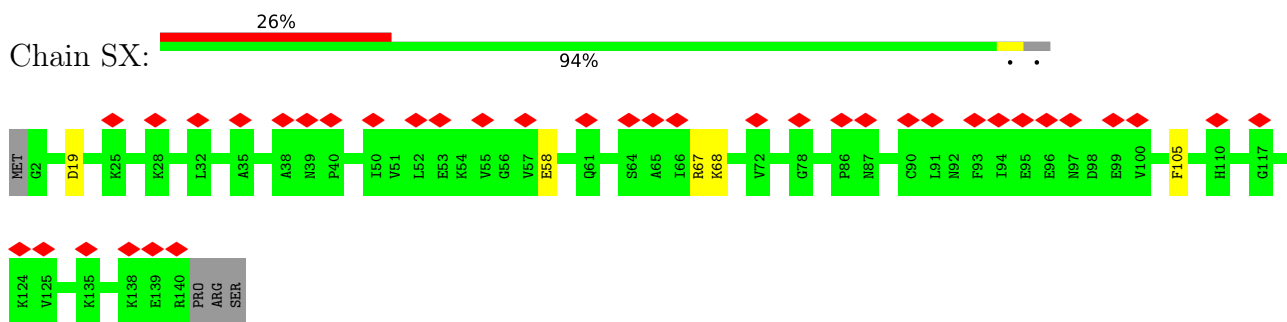
• Molecule 61: 40S ribosomal protein S20



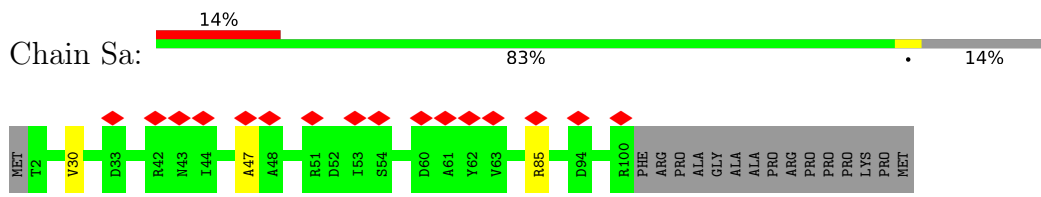
• Molecule 62: 40S ribosomal protein S21



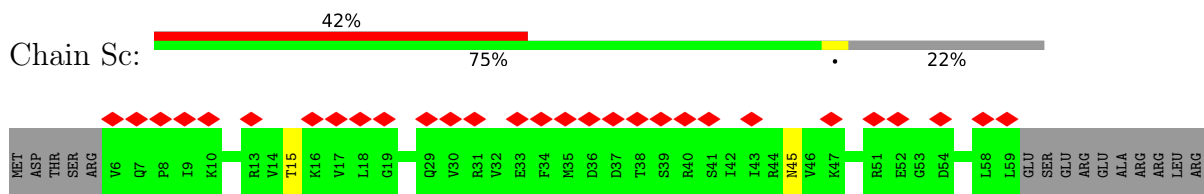
• Molecule 63: 40S ribosomal protein S23



• Molecule 64: 40S ribosomal protein S26

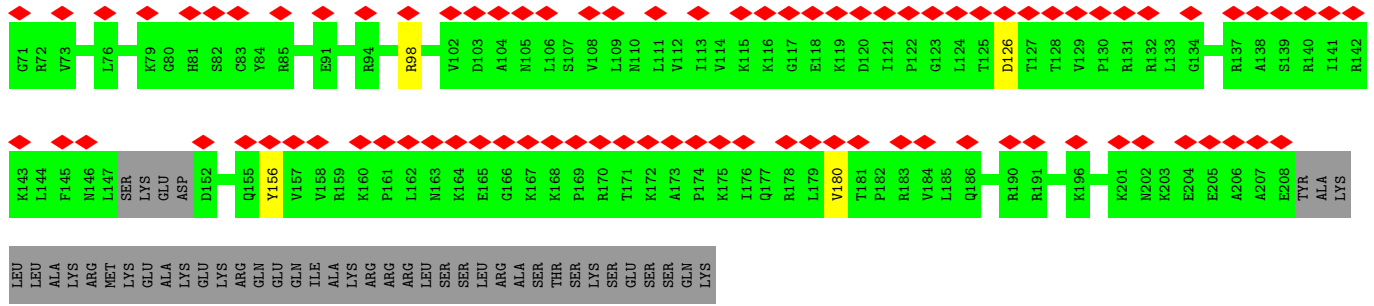


• Molecule 65: 40S ribosomal protein S28

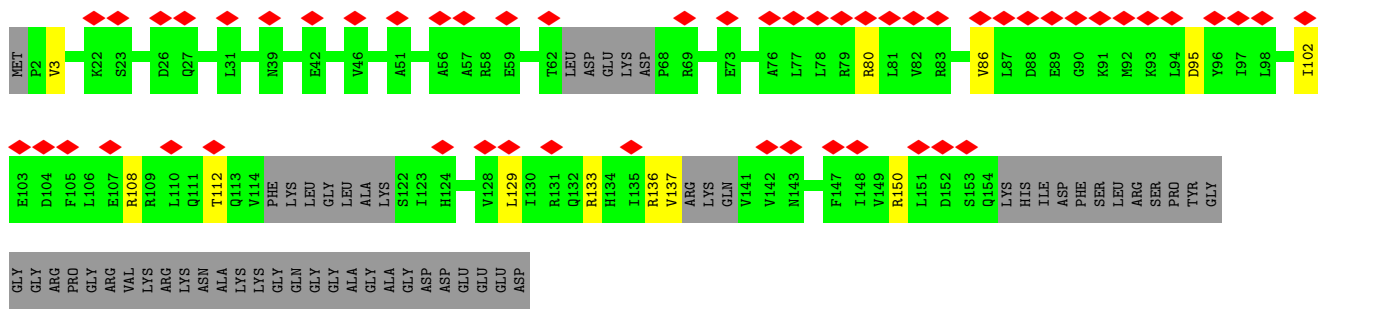


• Molecule 66: 40S ribosomal protein S29

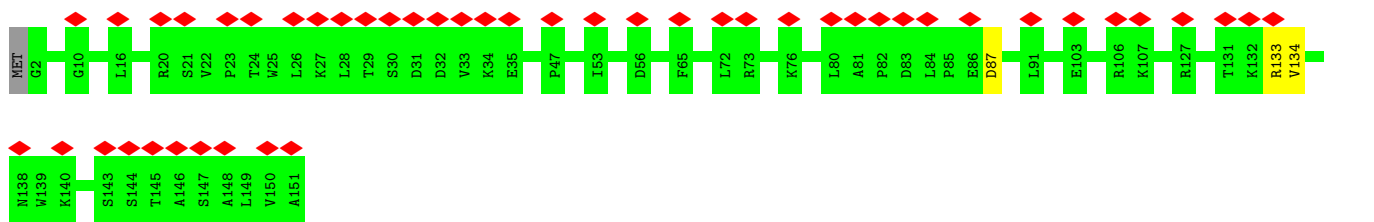




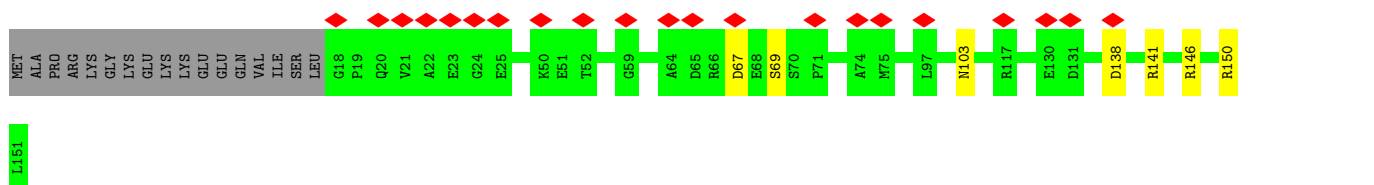
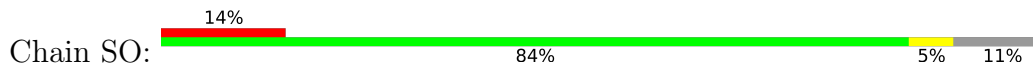
• Molecule 70: 40S ribosomal protein S9



• Molecule 71: 40S ribosomal protein S13

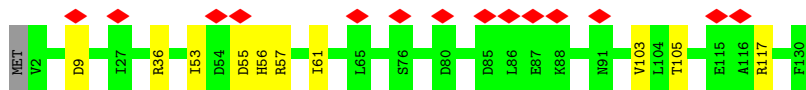


• Molecule 72: 40S ribosomal protein S14

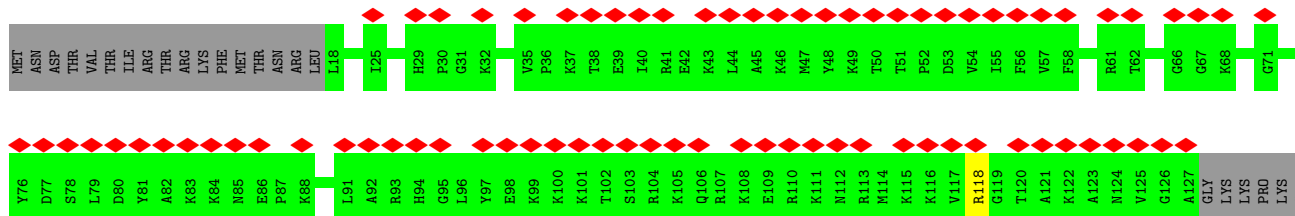
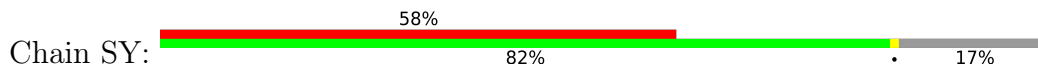


• Molecule 73: 40S ribosomal protein S15a

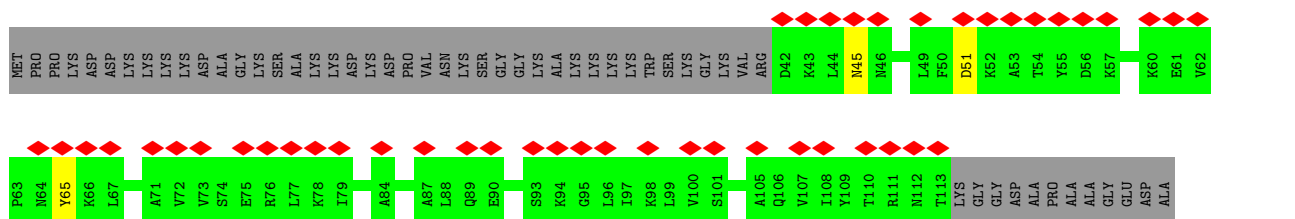
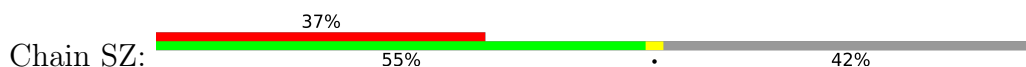




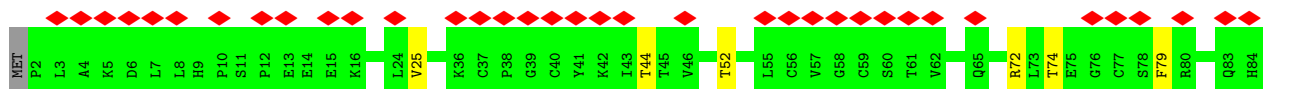
• Molecule 74: 40S ribosomal protein S24



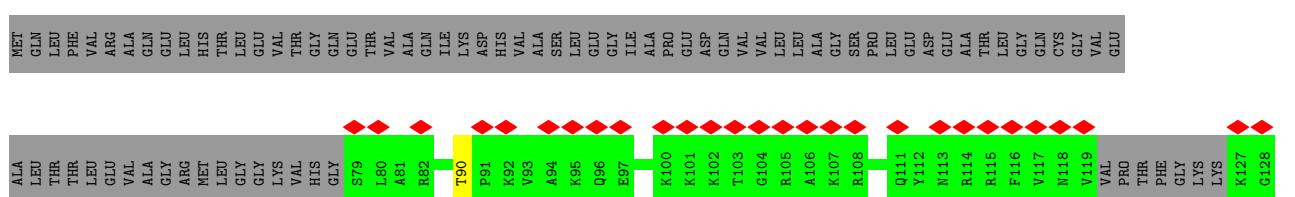
• Molecule 75: 40S ribosomal protein S25



• Molecule 76: 40S ribosomal protein S27



• Molecule 77: 40S ribosomal protein S30



• Molecule 78: Met-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	0.220	Depositor
Minimum map value	-0.102	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size (\AA)	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

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

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	LA	0.63	1/1936 (0.1%)	0.58	0/2596
2	LB	0.61	0/3269	0.56	0/4375
3	LC	0.61	0/2945	0.58	0/3953
4	LD	0.56	0/2431	0.52	0/3256
5	LE	0.52	0/1910	0.56	0/2562
6	LF	0.64	0/1805	0.56	0/2408
7	LG	0.51	0/1880	0.54	0/2531
8	LH	0.52	0/1537	0.57	0/2065
9	LI	0.57	0/1669	0.50	0/2227
10	LJ	0.43	0/1394	0.55	0/1864
11	LL	0.56	0/1698	0.53	0/2274
12	LM	0.60	0/1146	0.54	0/1531
13	LN	0.71	0/1746	0.55	0/2338
14	LO	0.61	0/1670	0.53	0/2232
15	LP	0.63	0/1277	0.53	0/1712
16	LQ	0.66	0/1539	0.59	0/2053
17	LR	0.52	0/1473	0.52	0/1947
18	LS	0.65	0/1491	0.55	0/2000
19	LT	0.60	0/1335	0.50	0/1781
20	LU	0.47	0/831	0.52	0/1115
21	LV	0.59	0/987	0.58	0/1324
22	LW	0.62	0/532	0.52	0/708
23	LX	0.55	0/984	0.49	0/1323
24	LY	0.59	0/1119	0.53	0/1488
25	LZ	0.58	0/1130	0.53	0/1507
26	La	0.63	0/1193	0.55	0/1593
27	Lb	0.49	0/821	0.50	0/1082
28	Lc	0.54	0/742	0.56	0/996
29	Ld	0.58	0/911	0.54	0/1227
30	Le	0.66	0/1071	0.56	0/1429
31	Lf	0.68	0/895	0.61	0/1198
32	Lg	0.59	0/883	0.55	0/1178

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lh	0.52	0/1023	0.53	0/1350
34	Li	0.48	0/843	0.53	0/1115
35	Lj	0.64	0/720	0.58	0/952
36	Lk	0.49	0/574	0.50	0/760
37	Ll	0.54	0/448	0.56	0/592
38	Lm	0.52	0/425	0.54	0/564
39	Ln	0.37	0/240	0.47	0/305
40	Lo	0.55	0/855	0.57	0/1128
41	Lp	0.59	0/718	0.55	0/953
42	Lr	0.61	0/1009	0.52	0/1353
43	L5	1.22	0/84917	0.97	116/132450 (0.1%)
44	L7	1.19	0/2858	0.89	0/4455
45	L8	1.26	0/3701	0.93	3/5766 (0.1%)
46	S2	0.65	0/39073	0.94	53/60890 (0.1%)
47	SA	0.35	0/1673	0.54	0/2275
48	SB	0.36	0/1756	0.53	0/2350
49	SD	0.35	0/1772	0.57	0/2385
50	SE	0.33	0/2092	0.55	0/2816
51	SF	0.33	0/1436	0.51	0/1930
52	SH	0.33	0/1470	0.53	0/1968
53	SI	0.38	0/1526	0.54	0/2038
54	SK	0.34	0/780	0.52	0/1046
55	SL	0.40	0/1130	0.54	0/1514
56	SP	0.37	0/1000	0.50	0/1335
57	SQ	0.36	0/1126	0.56	0/1506
58	SR	0.33	0/1078	0.52	0/1447
59	SS	0.36	0/1175	0.52	0/1575
60	ST	0.34	0/1108	0.49	0/1486
61	SU	0.30	0/762	0.54	0/1023
62	SV	0.38	0/625	0.52	0/836
63	SX	0.38	0/1097	0.56	0/1464
64	Sa	0.42	0/805	0.54	0/1079
65	Sc	0.31	0/418	0.57	0/562
66	Sd	0.38	0/466	0.49	0/618
67	Sg	0.32	0/2199	0.59	0/2989
68	SC	0.41	0/1712	0.55	0/2314
69	SG	0.32	0/1666	0.54	1/2222 (0.0%)
70	SJ	0.32	0/1178	0.55	0/1574
71	SN	0.39	1/1232 (0.1%)	0.51	0/1656
72	SO	0.38	0/1015	0.57	0/1361
73	SW	0.39	0/1051	0.53	0/1406
74	SY	0.31	0/907	0.53	0/1204
75	SZ	0.31	0/580	0.53	0/780

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sb	0.34	0/665	0.54	0/891
77	Se	0.34	0/386	0.53	0/504
78	S6	0.55	0/1795	1.10	8/2798 (0.3%)
All	All	0.89	2/221335 (0.0%)	0.83	181/325458 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	LB	0	2
3	LC	0	2
10	LJ	0	1
12	LM	0	1
31	Lf	0	1
50	SE	0	1
52	SH	0	1
60	ST	0	1
70	SJ	0	1
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	LA	220	GLY	C-N	-5.13	1.22	1.34
71	SN	134	VAL	C-N	-5.00	1.22	1.34

All (181) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	L5	923	G	N3-C4-N9	-10.16	119.90	126.00
43	L5	416	G	O4'-C1'-N9	9.74	115.99	108.20
43	L5	923	G	C5-C6-O6	9.31	134.19	128.60
78	S6	55	U	O5'-P-OP1	-8.86	97.73	105.70
43	L5	2464	C	C2-N1-C1'	8.61	128.27	118.80
46	S2	884	U	N1-C2-O2	8.54	128.78	122.80
43	L5	1565	C	N1-C2-O2	7.89	123.64	118.90
43	L5	652	G	O4'-C1'-N9	7.87	114.49	108.20
46	S2	884	U	C2-N1-C1'	7.64	126.86	117.70
46	S2	968	C	N3-C2-O2	-7.58	116.59	121.90
43	L5	2464	C	N1-C2-O2	7.54	123.42	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	294	C	C2-N1-C1'	7.51	127.07	118.80
69	SG	180	VAL	C-N-CA	7.50	140.45	121.70
43	L5	2659	C	C6-N1-C1'	7.45	129.74	120.80
43	L5	486	C	C2-N1-C1'	7.32	126.85	118.80
43	L5	3246	G	N3-C4-N9	-7.22	121.67	126.00
43	L5	3246	G	C6-C5-N7	7.17	134.70	130.40
43	L5	3421	U	N3-C2-O2	-7.14	117.20	122.20
46	S2	1454	C	N1-C2-O2	7.12	123.17	118.90
46	S2	1454	C	C2-N1-C1'	7.09	126.60	118.80
43	L5	923	G	N3-C4-C5	7.03	132.12	128.60
43	L5	923	G	N1-C6-O6	-6.95	115.73	119.90
43	L5	2659	C	C2-N1-C1'	-6.91	111.20	118.80
43	L5	4561	G	N3-C4-N9	6.88	130.13	126.00
43	L5	1005	C	C2-N1-C1'	-6.88	111.23	118.80
43	L5	4428	C	C6-N1-C2	6.80	123.02	120.30
43	L5	2464	C	N3-C2-O2	-6.72	117.19	121.90
43	L5	4561	G	N9-C4-C5	-6.70	102.72	105.40
43	L5	4561	G	C6-C5-N7	-6.65	126.41	130.40
43	L5	1366	G	O4'-C1'-N9	6.63	113.51	108.20
43	L5	3433	G	O4'-C1'-N9	6.59	113.47	108.20
46	S2	884	U	N3-C2-O2	-6.59	117.59	122.20
43	L5	1259	U	C2-N1-C1'	6.58	125.60	117.70
43	L5	1497	U	N3-C2-O2	-6.55	117.61	122.20
43	L5	2540	C	C6-N1-C2	-6.53	117.69	120.30
43	L5	3246	G	N3-C2-N2	-6.51	115.34	119.90
46	S2	1023	U	C2-N1-C1'	6.47	125.46	117.70
43	L5	923	G	N9-C4-C5	6.44	107.98	105.40
43	L5	923	G	C6-C5-N7	6.44	134.26	130.40
78	S6	66	C	N1-C2-O2	6.33	122.70	118.90
78	S6	66	C	N3-C2-O2	-6.31	117.48	121.90
43	L5	2429	G	P-O3'-C3'	6.31	127.27	119.70
43	L5	4428	C	C2-N1-C1'	-6.29	111.88	118.80
43	L5	2464	C	C6-N1-C1'	-6.27	113.28	120.80
43	L5	4561	G	C8-N9-C1'	-6.27	118.85	127.00
46	S2	294	C	N1-C2-O2	6.26	122.66	118.90
43	L5	233	U	N3-C2-O2	-6.26	117.82	122.20
43	L5	3298	U	C5-C6-N1	-6.25	119.58	122.70
43	L5	1016	C	C2-N1-C1'	6.24	125.67	118.80
46	S2	660	G	C4-N9-C1'	6.24	134.62	126.50
46	S2	1017	U	C2-N1-C1'	6.18	125.12	117.70
46	S2	571	C	C2-N1-C1'	6.16	125.57	118.80
43	L5	4664	A	O4'-C1'-N9	6.16	113.12	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	1521	G	C4-N9-C1'	6.15	134.49	126.50
45	L8	51	U	N3-C2-O2	-6.12	117.91	122.20
46	S2	1441	C	N1-C2-O2	6.10	122.56	118.90
46	S2	1808	C	C2-N1-C1'	6.10	125.51	118.80
43	L5	486	C	C6-N1-C1'	-6.09	113.49	120.80
46	S2	1521	G	C8-N9-C1'	-6.07	119.11	127.00
43	L5	2166	U	N3-C2-O2	-6.03	117.98	122.20
43	L5	4401	C	C2-N1-C1'	5.99	125.39	118.80
43	L5	1050	C	N1-C2-O2	5.99	122.49	118.90
43	L5	1565	C	N3-C2-O2	-5.98	117.71	121.90
46	S2	1454	C	N3-C2-O2	-5.96	117.72	121.90
46	S2	1441	C	N3-C2-O2	-5.96	117.73	121.90
43	L5	4210	U	N3-C2-O2	-5.94	118.04	122.20
43	L5	1772	G	N3-C4-C5	-5.94	125.63	128.60
46	S2	1061	A	O4'-C1'-N9	5.94	112.95	108.20
43	L5	4561	G	C4-C5-N7	5.90	113.16	110.80
46	S2	1390	C	C2-N1-C1'	5.89	125.28	118.80
43	L5	1259	U	N1-C2-O2	5.88	126.92	122.80
43	L5	712	C	N1-C2-O2	5.88	122.43	118.90
43	L5	923	G	C4-C5-N7	-5.87	108.45	110.80
46	S2	495	C	N1-C2-O2	5.87	122.42	118.90
43	L5	923	G	C8-N9-C1'	5.86	134.61	127.00
43	L5	4561	G	C4-N9-C1'	5.83	134.08	126.50
43	L5	1565	C	C2-N1-C1'	5.82	125.20	118.80
46	S2	1140	C	C2-N1-C1'	5.82	125.20	118.80
43	L5	922	G	C8-N9-C1'	-5.81	119.44	127.00
43	L5	3426	C	O4'-C1'-N1	5.81	112.85	108.20
43	L5	1259	U	N3-C2-O2	-5.81	118.14	122.20
43	L5	2659	C	C5-C4-N4	5.81	124.27	120.20
43	L5	2286	A	O4'-C1'-N9	5.80	112.84	108.20
46	S2	594	C	C2-N1-C1'	5.80	125.18	118.80
43	L5	923	G	C4-N9-C1'	-5.79	118.98	126.50
43	L5	1772	G	N3-C4-N9	5.79	129.47	126.00
46	S2	357	C	C2-N1-C1'	5.78	125.16	118.80
46	S2	968	C	C6-N1-C2	-5.77	117.99	120.30
43	L5	2222	C	C5-C6-N1	5.75	123.87	121.00
43	L5	2019	G	N3-C4-N9	5.74	129.44	126.00
43	L5	1255	C	C2-N3-C4	-5.73	117.03	119.90
43	L5	100	C	C2-N1-C1'	5.71	125.08	118.80
46	S2	332	C	C2-N1-C1'	5.71	125.08	118.80
43	L5	100	C	C6-N1-C2	-5.69	118.02	120.30
43	L5	1071	C	C2-N1-C1'	5.69	125.06	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	S6	54	A	O4'-C1'-N9	5.69	112.75	108.20
43	L5	100	C	N3-C2-O2	-5.67	117.93	121.90
46	S2	1284	C	N1-C2-O2	5.64	122.28	118.90
43	L5	2381	C	C2-N1-C1'	5.63	125.00	118.80
46	S2	533	C	C6-N1-C2	-5.62	118.05	120.30
43	L5	712	C	C2-N1-C1'	5.61	124.97	118.80
78	S6	71	C	C2-N1-C1'	5.59	124.95	118.80
43	L5	4210	U	C2-N1-C1'	5.58	124.40	117.70
43	L5	4289	U	C2-N1-C1'	5.58	124.40	117.70
46	S2	884	U	C6-N1-C1'	-5.58	113.39	121.20
43	L5	1388	G	P-O3'-C3'	5.57	126.39	119.70
43	L5	139	G	C8-N9-C1'	-5.57	119.76	127.00
43	L5	2568	C	C2-N1-C1'	5.57	124.93	118.80
46	S2	294	C	N3-C2-O2	-5.57	118.00	121.90
43	L5	139	G	C4-N9-C1'	5.57	133.74	126.50
43	L5	4664	A	C5-N7-C8	-5.56	101.12	103.90
78	S6	54	A	OP1-P-O3'	5.56	117.43	105.20
43	L5	1255	C	N1-C2-N3	5.56	123.09	119.20
43	L5	2568	C	N1-C2-O2	5.55	122.23	118.90
43	L5	3956	C	C2-N1-C1'	5.51	124.86	118.80
43	L5	3956	C	N3-C2-O2	-5.50	118.05	121.90
46	S2	660	G	C8-N9-C1'	-5.50	119.85	127.00
43	L5	277	G	O4'-C1'-N9	-5.49	103.81	108.20
43	L5	2226	C	C2-N1-C1'	5.48	124.83	118.80
43	L5	4279	A	O4'-C1'-N9	5.48	112.58	108.20
43	L5	1005	C	C6-N1-C1'	5.48	127.37	120.80
43	L5	3246	G	C4-N9-C1'	-5.46	119.40	126.50
43	L5	2104	A	O4'-C1'-N9	-5.46	103.83	108.20
43	L5	4236	C	O4'-C1'-N1	5.46	112.56	108.20
46	S2	123	G	N3-C4-N9	5.46	129.27	126.00
46	S2	357	C	N1-C2-O2	5.45	122.17	118.90
43	L5	3246	G	C8-N9-C1'	5.44	134.07	127.00
46	S2	518	C	C2-N1-C1'	5.43	124.78	118.80
43	L5	486	C	N1-C2-O2	5.41	122.15	118.90
43	L5	922	G	C4-N9-C1'	5.40	133.52	126.50
46	S2	1454	C	O4'-C1'-N1	5.38	112.51	108.20
78	S6	56	C	C2-N1-C1'	5.37	124.71	118.80
43	L5	115	C	C2-N1-C1'	5.37	124.70	118.80
43	L5	3246	G	N9-C4-C5	5.36	107.54	105.40
45	L8	83	C	C2-N1-C1'	5.34	124.68	118.80
46	S2	1521	G	N3-C4-N9	5.33	129.20	126.00
43	L5	1031	G	N9-C4-C5	-5.32	103.27	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	L8	51	U	N1-C2-O2	5.32	126.52	122.80
46	S2	1728	G	C6-C5-N7	-5.32	127.21	130.40
78	S6	41	C	C2-N1-C1'	5.32	124.65	118.80
43	L5	2222	C	C6-N1-C2	-5.31	118.17	120.30
46	S2	1808	C	C6-N1-C1'	-5.31	114.43	120.80
43	L5	1220	C	C5-C6-N1	5.30	123.65	121.00
46	S2	1273	C	N1-C2-O2	5.30	122.08	118.90
43	L5	1005	C	O4'-C1'-N1	5.28	112.43	108.20
43	L5	2429	G	OP2-P-O3'	5.28	116.83	105.20
43	L5	4572	C	C2-N1-C1'	5.28	124.61	118.80
43	L5	922	G	N3-C4-N9	5.28	129.17	126.00
46	S2	594	C	N1-C2-O2	5.27	122.06	118.90
46	S2	118	C	C2-N1-C1'	5.26	124.59	118.80
46	S2	633	C	C2-N1-C1'	5.26	124.59	118.80
46	S2	1140	C	N3-C2-O2	-5.25	118.23	121.90
46	S2	1023	U	C6-N1-C1'	-5.25	113.86	121.20
43	L5	233	U	O4'-C1'-N1	5.24	112.39	108.20
46	S2	968	C	N1-C2-O2	5.24	122.04	118.90
43	L5	954	G	N3-C4-N9	5.22	129.13	126.00
43	L5	3298	U	C4-C5-C6	5.20	122.82	119.70
46	S2	294	C	C6-N1-C1'	-5.19	114.58	120.80
46	S2	1295	G	C4-N9-C1'	5.18	133.24	126.50
43	L5	2568	C	N3-C2-O2	-5.17	118.28	121.90
46	S2	1284	C	C2-N1-C1'	5.15	124.47	118.80
43	L5	416	G	N1-C6-O6	-5.14	116.81	119.90
46	S2	332	C	N1-C2-O2	5.14	121.99	118.90
43	L5	1016	C	N1-C2-O2	5.13	121.98	118.90
43	L5	954	G	C4-N9-C1'	5.12	133.16	126.50
43	L5	4289	U	N1-C2-O2	5.11	126.38	122.80
43	L5	1685	U	C5-C4-O4	-5.09	122.84	125.90
43	L5	887	C	C6-N1-C2	-5.09	118.26	120.30
43	L5	2429	G	C4-N9-C1'	5.08	133.10	126.50
43	L5	4670	U	O4'-C1'-N1	5.07	112.25	108.20
43	L5	3248	C	N1-C2-O2	-5.06	115.86	118.90
46	S2	1661	C	C2-N1-C1'	5.05	124.36	118.80
46	S2	1023	U	N1-C2-O2	5.04	126.33	122.80
46	S2	1808	C	C5-C6-N1	5.04	123.52	121.00
43	L5	2166	U	N1-C2-N3	5.02	117.91	114.90
43	L5	144	G	N3-C4-N9	-5.02	122.99	126.00
43	L5	1016	C	C6-N1-C1'	-5.02	114.78	120.80
43	L5	1255	C	C6-N1-C1'	5.01	126.81	120.80
43	L5	2514	G	P-O3'-C3'	5.00	125.70	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	S2	1454	C	C6-N1-C2	-5.00	118.30	120.30
43	L5	1799	C	N1-C2-O2	5.00	121.90	118.90

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	LB	16	PHE	Peptide
2	LB	258	HIS	Peptide
3	LC	354	LEU	Peptide
3	LC	66	SER	Peptide
10	LJ	173	ILE	Peptide
12	LM	32	ASP	Peptide
31	Lf	103	VAL	Peptide
50	SE	247	THR	Peptide
52	SH	15	LYS	Peptide
70	SJ	108	ARG	Peptide
60	ST	38	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	LB	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
3	LC	360/419 (86%)	326 (91%)	33 (9%)	1 (0%)	41	74
4	LD	291/297 (98%)	270 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LE	227/296 (77%)	207 (91%)	20 (9%)	0	100	100
6	LF	212/270 (78%)	200 (94%)	12 (6%)	0	100	100
7	LG	225/266 (85%)	209 (93%)	16 (7%)	0	100	100
8	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
9	LI	197/214 (92%)	187 (95%)	10 (5%)	0	100	100
10	LJ	169/178 (95%)	147 (87%)	22 (13%)	0	100	100
11	LL	204/211 (97%)	186 (91%)	17 (8%)	1 (0%)	29	65
12	LM	134/217 (62%)	121 (90%)	13 (10%)	0	100	100
13	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	15	49
14	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
15	LP	152/184 (83%)	140 (92%)	12 (8%)	0	100	100
16	LQ	185/188 (98%)	173 (94%)	12 (6%)	0	100	100
17	LR	172/196 (88%)	166 (96%)	6 (4%)	0	100	100
18	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
19	LT	158/160 (99%)	150 (95%)	8 (5%)	0	100	100
20	LU	98/128 (77%)	85 (87%)	13 (13%)	0	100	100
21	LV	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
22	LW	60/157 (38%)	55 (92%)	5 (8%)	0	100	100
23	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
24	LY	130/145 (90%)	124 (95%)	6 (5%)	0	100	100
25	LZ	133/136 (98%)	116 (87%)	17 (13%)	0	100	100
26	La	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	Lb	95/160 (59%)	88 (93%)	7 (7%)	0	100	100
28	Lc	92/115 (80%)	85 (92%)	7 (8%)	0	100	100
29	Ld	106/125 (85%)	93 (88%)	13 (12%)	0	100	100
30	Le	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	19	54
31	Lf	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
32	Lg	108/117 (92%)	104 (96%)	4 (4%)	0	100	100
33	Lh	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	Li	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	Lj	84/97 (87%)	78 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	Lm	49/128 (38%)	46 (94%)	1 (2%)	2 (4%)	3	14
39	Ln	23/25 (92%)	23 (100%)	0	0	100	100
40	Lo	101/106 (95%)	93 (92%)	8 (8%)	0	100	100
41	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	Lr	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
47	SA	205/295 (70%)	179 (87%)	25 (12%)	1 (0%)	29	65
48	SB	211/264 (80%)	193 (92%)	18 (8%)	0	100	100
49	SD	222/243 (91%)	193 (87%)	29 (13%)	0	100	100
50	SE	256/263 (97%)	229 (90%)	26 (10%)	1 (0%)	34	69
51	SF	175/204 (86%)	156 (89%)	19 (11%)	0	100	100
52	SH	176/194 (91%)	155 (88%)	21 (12%)	0	100	100
53	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
54	SK	86/165 (52%)	73 (85%)	13 (15%)	0	100	100
55	SL	131/158 (83%)	124 (95%)	7 (5%)	0	100	100
56	SP	116/145 (80%)	110 (95%)	6 (5%)	0	100	100
57	SQ	137/146 (94%)	118 (86%)	18 (13%)	1 (1%)	22	57
58	SR	129/135 (96%)	116 (90%)	13 (10%)	0	100	100
59	SS	138/152 (91%)	125 (91%)	12 (9%)	1 (1%)	22	57
60	ST	138/145 (95%)	131 (95%)	7 (5%)	0	100	100
61	SU	93/119 (78%)	86 (92%)	7 (8%)	0	100	100
62	SV	79/83 (95%)	71 (90%)	7 (9%)	1 (1%)	12	42
63	SX	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
64	Sa	97/115 (84%)	87 (90%)	9 (9%)	1 (1%)	15	49
65	Sc	52/69 (75%)	42 (81%)	10 (19%)	0	100	100
66	Sd	52/56 (93%)	47 (90%)	5 (10%)	0	100	100
67	Sg	270/317 (85%)	218 (81%)	52 (19%)	0	100	100
68	SC	214/293 (73%)	199 (93%)	15 (7%)	0	100	100
69	SG	200/249 (80%)	184 (92%)	16 (8%)	0	100	100
70	SJ	130/194 (67%)	118 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	SN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
72	SO	132/151 (87%)	116 (88%)	15 (11%)	1 (1%)	19	54
73	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
74	SY	108/133 (81%)	93 (86%)	15 (14%)	0	100	100
75	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
76	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
77	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
All	All	10668/12499 (85%)	9753 (91%)	901 (8%)	14 (0%)	54	84

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
64	Sa	47	ALA
30	Le	92	ASN
47	SA	12	GLU
11	LL	51	ALA
13	LN	84	PRO
38	Lm	98	LYS
57	SQ	117	ARG
59	SS	101	ASN
62	SV	79	VAL
72	SO	141	ARG
38	Lm	99	CYS
3	LC	232	VAL
50	SE	248	ILE
13	LN	83	LYS

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/199 (96%)	185 (97%)	5 (3%)	46	76
2	LB	344/348 (99%)	333 (97%)	11 (3%)	39	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	LC	304/348 (87%)	292 (96%)	12 (4%)	32	66
4	LD	245/249 (98%)	230 (94%)	15 (6%)	18	50
5	LE	208/256 (81%)	194 (93%)	14 (7%)	16	46
6	LF	185/234 (79%)	183 (99%)	2 (1%)	73	90
7	LG	197/223 (88%)	195 (99%)	2 (1%)	76	91
8	LH	169/171 (99%)	161 (95%)	8 (5%)	26	61
9	LI	170/180 (94%)	161 (95%)	9 (5%)	22	56
10	LJ	144/149 (97%)	136 (94%)	8 (6%)	21	54
11	LL	173/178 (97%)	165 (95%)	8 (5%)	27	61
12	LM	116/157 (74%)	112 (97%)	4 (3%)	37	70
13	LN	171/172 (99%)	168 (98%)	3 (2%)	59	83
14	LO	172/173 (99%)	168 (98%)	4 (2%)	50	78
15	LP	135/163 (83%)	131 (97%)	4 (3%)	41	73
16	LQ	164/165 (99%)	160 (98%)	4 (2%)	49	78
17	LR	154/175 (88%)	149 (97%)	5 (3%)	39	72
18	LS	155/156 (99%)	148 (96%)	7 (4%)	27	62
19	LT	140/140 (100%)	134 (96%)	6 (4%)	29	63
20	LU	90/114 (79%)	81 (90%)	9 (10%)	7	27
21	LV	100/107 (94%)	95 (95%)	5 (5%)	24	58
22	LW	54/126 (43%)	52 (96%)	2 (4%)	34	68
23	LX	106/133 (80%)	106 (100%)	0	100	100
24	LY	123/135 (91%)	116 (94%)	7 (6%)	20	53
25	LZ	117/118 (99%)	114 (97%)	3 (3%)	46	76
26	La	120/121 (99%)	111 (92%)	9 (8%)	13	41
27	Lb	83/124 (67%)	78 (94%)	5 (6%)	19	51
28	Lc	79/97 (81%)	75 (95%)	4 (5%)	24	57
29	Ld	99/110 (90%)	99 (100%)	0	100	100
30	Le	114/121 (94%)	110 (96%)	4 (4%)	36	69
31	Lf	88/89 (99%)	86 (98%)	2 (2%)	50	78
32	Lg	94/100 (94%)	90 (96%)	4 (4%)	29	63
33	Lh	109/110 (99%)	107 (98%)	2 (2%)	59	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Li	86/89 (97%)	82 (95%)	4 (5%)	26	61
35	Lj	73/80 (91%)	72 (99%)	1 (1%)	67	86
36	Lk	64/65 (98%)	64 (100%)	0	100	100
37	Ll	46/47 (98%)	39 (85%)	7 (15%)	3	12
38	Lm	47/116 (40%)	44 (94%)	3 (6%)	17	48
39	Ln	24/24 (100%)	23 (96%)	1 (4%)	30	64
40	Lo	91/94 (97%)	83 (91%)	8 (9%)	10	34
41	Lp	74/75 (99%)	71 (96%)	3 (4%)	30	65
42	Lr	108/121 (89%)	102 (94%)	6 (6%)	21	54
47	SA	173/242 (72%)	169 (98%)	4 (2%)	50	78
48	SB	194/229 (85%)	191 (98%)	3 (2%)	65	86
49	SD	188/202 (93%)	182 (97%)	6 (3%)	39	72
50	SE	221/225 (98%)	210 (95%)	11 (5%)	24	58
51	SF	152/170 (89%)	145 (95%)	7 (5%)	27	61
52	SH	161/174 (92%)	154 (96%)	7 (4%)	29	63
53	SI	159/180 (88%)	149 (94%)	10 (6%)	18	49
54	SK	81/136 (60%)	79 (98%)	2 (2%)	47	77
55	SL	123/142 (87%)	118 (96%)	5 (4%)	30	65
56	SP	107/130 (82%)	107 (100%)	0	100	100
57	SQ	115/121 (95%)	111 (96%)	4 (4%)	36	69
58	SR	119/121 (98%)	114 (96%)	5 (4%)	30	64
59	SS	122/132 (92%)	114 (93%)	8 (7%)	16	47
60	ST	110/115 (96%)	105 (96%)	5 (4%)	27	62
61	SU	88/107 (82%)	84 (96%)	4 (4%)	27	62
62	SV	65/67 (97%)	60 (92%)	5 (8%)	13	40
63	SX	111/115 (96%)	106 (96%)	5 (4%)	27	62
64	Sa	86/98 (88%)	84 (98%)	2 (2%)	50	78
65	Sc	48/62 (77%)	46 (96%)	2 (4%)	30	64
66	Sd	48/49 (98%)	48 (100%)	0	100	100
67	Sg	237/275 (86%)	222 (94%)	15 (6%)	18	49
68	SC	182/224 (81%)	181 (100%)	1 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	SG	178/218 (82%)	171 (96%)	7 (4%)	32	66
70	SJ	126/168 (75%)	115 (91%)	11 (9%)	10	34
71	SN	130/131 (99%)	128 (98%)	2 (2%)	65	86
72	SO	104/119 (87%)	98 (94%)	6 (6%)	20	52
73	SW	112/113 (99%)	102 (91%)	10 (9%)	9	33
74	SY	93/115 (81%)	92 (99%)	1 (1%)	73	90
75	SZ	64/103 (62%)	61 (95%)	3 (5%)	26	61
76	Sb	75/76 (99%)	69 (92%)	6 (8%)	12	38
77	Se	39/106 (37%)	37 (95%)	2 (5%)	24	57
All	All	9336/10617 (88%)	8957 (96%)	379 (4%)	34	65

All (379) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	LA	15	VAL
1	LA	17	ARG
1	LA	114	CYS
1	LA	174	ARG
1	LA	237	LEU
2	LB	2	SER
2	LB	56	ILE
2	LB	74	GLU
2	LB	199	GLU
2	LB	258	HIS
2	LB	283	LYS
2	LB	295	ASP
2	LB	297	LYS
2	LB	298	LEU
2	LB	310	SER
2	LB	329	ASP
3	LC	23	THR
3	LC	63	SER
3	LC	71	ARG
3	LC	100	ARG
3	LC	114	ARG
3	LC	118	THR
3	LC	122	TYR
3	LC	154	VAL
3	LC	157	LYS

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Mol	Chain	Res	Type
3	LC	169	GLN
3	LC	188	ARG
3	LC	275	SER
4	LD	7	VAL
4	LD	33	ARG
4	LD	37	VAL
4	LD	86	TYR
4	LD	93	THR
4	LD	118	ILE
4	LD	132	VAL
4	LD	157	ASN
4	LD	179	ARG
4	LD	214	GLU
4	LD	217	ASP
4	LD	232	THR
4	LD	235	MET
4	LD	263	LYS
4	LD	267	ASN
5	LE	63	ARG
5	LE	109	ASN
5	LE	119	LYS
5	LE	129	VAL
5	LE	138	LYS
5	LE	139	LYS
5	LE	153	THR
5	LE	183	VAL
5	LE	188	VAL
5	LE	202	VAL
5	LE	209	VAL
5	LE	242	ASP
5	LE	247	LYS
5	LE	284	SER
6	LF	244	LYS
6	LF	247	THR
7	LG	53	ARG
7	LG	70	LEU
8	LH	3	THR
8	LH	14	GLU
8	LH	23	ARG
8	LH	24	THR
8	LH	37	ASP
8	LH	44	GLU

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Mol	Chain	Res	Type
8	LH	66	GLU
8	LH	111	LEU
9	LI	35	ASP
9	LI	39	LYS
9	LI	55	ASP
9	LI	131	ILE
9	LI	140	THR
9	LI	143	GLN
9	LI	195	CYS
9	LI	197	VAL
9	LI	213	HIS
10	LJ	24	ILE
10	LJ	56	THR
10	LJ	62	ILE
10	LJ	78	LYS
10	LJ	80	GLU
10	LJ	90	ARG
10	LJ	104	ASN
10	LJ	154	LYS
11	LL	23	ASP
11	LL	56	ARG
11	LL	63	THR
11	LL	64	VAL
11	LL	67	HIS
11	LL	70	VAL
11	LL	144	LEU
11	LL	162	LYS
12	LM	38	VAL
12	LM	59	ASP
12	LM	106	ASP
12	LM	124	LYS
13	LN	182	HIS
13	LN	183	THR
13	LN	187	SER
14	LO	31	ARG
14	LO	44	SER
14	LO	117	ARG
14	LO	175	LEU
15	LP	6	LEU
15	LP	24	VAL
15	LP	79	THR
15	LP	118	GLN

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Mol	Chain	Res	Type
16	LQ	5	ILE
16	LQ	14	ARG
16	LQ	121	LEU
16	LQ	170	LYS
17	LR	106	LEU
17	LR	148	ASP
17	LR	152	LYS
17	LR	165	LYS
17	LR	173	ARG
18	LS	48	VAL
18	LS	82	LEU
18	LS	90	THR
18	LS	107	THR
18	LS	111	ARG
18	LS	158	VAL
18	LS	169	THR
19	LT	3	ASN
19	LT	4	THR
19	LT	36	LYS
19	LT	91	VAL
19	LT	101	SER
19	LT	143	THR
20	LU	22	THR
20	LU	23	LEU
20	LU	47	ILE
20	LU	49	VAL
20	LU	60	VAL
20	LU	63	ILE
20	LU	67	LYS
20	LU	98	ASP
20	LU	99	TRP
21	LV	18	LEU
21	LV	48	ARG
21	LV	73	ARG
21	LV	118	THR
21	LV	131	ARG
22	LW	1	MET
22	LW	5	LEU
24	LY	8	THR
24	LY	55	VAL
24	LY	74	TYR
24	LY	84	ARG

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Mol	Chain	Res	Type
24	LY	91	ASN
24	LY	99	ILE
24	LY	109	LEU
25	LZ	36	ARG
25	LZ	53	VAL
25	LZ	100	VAL
26	La	12	ARG
26	La	24	LYS
26	La	59	ARG
26	La	61	TYR
26	La	65	ARG
26	La	75	LEU
26	La	76	ASP
26	La	97	VAL
26	La	140	VAL
27	Lb	8	THR
27	Lb	16	TRP
27	Lb	54	LEU
27	Lb	60	ASN
27	Lb	94	LEU
28	Lc	20	LEU
28	Lc	23	LYS
28	Lc	24	SER
28	Lc	94	LEU
30	Le	17	THR
30	Le	26	ASP
30	Le	45	VAL
30	Le	123	THR
31	Lf	37	ASP
31	Lf	39	THR
32	Lg	5	LEU
32	Lg	54	ARG
32	Lg	86	CYS
32	Lg	110	GLN
33	Lh	33	VAL
33	Lh	70	ARG
34	Li	47	VAL
34	Li	52	PRO
34	Li	66	ASP
34	Li	85	ARG
35	Lj	6	SER
37	Ll	21	ARG

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Mol	Chain	Res	Type
37	Ll	28	GLN
37	Ll	29	MET
37	Ll	35	ILE
37	Ll	36	MET
37	Ll	46	ARG
37	Ll	47	THR
38	Lm	98	LYS
38	Lm	111	ARG
38	Lm	127	VAL
39	Ln	23	ARG
40	Lo	24	THR
40	Lo	26	TYR
40	Lo	31	ASP
40	Lo	33	LEU
40	Lo	53	LYS
40	Lo	79	SER
40	Lo	96	ASP
40	Lo	99	ARG
41	Lp	73	THR
41	Lp	74	THR
41	Lp	92	GLN
42	Lr	15	SER
42	Lr	23	GLN
42	Lr	27	THR
42	Lr	28	GLU
42	Lr	67	ARG
42	Lr	80	THR
47	SA	6	ASP
47	SA	19	LEU
47	SA	75	SER
47	SA	174	MET
48	SB	71	LEU
48	SB	85	LYS
48	SB	193	ILE
49	SD	25	LEU
49	SD	26	THR
49	SD	64	ARG
49	SD	91	VAL
49	SD	162	ASP
49	SD	198	ILE
50	SE	21	ASP
50	SE	54	TYR

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Mol	Chain	Res	Type
50	SE	95	THR
50	SE	108	ARG
50	SE	120	LYS
50	SE	133	THR
50	SE	180	LEU
50	SE	189	LEU
50	SE	198	ARG
50	SE	222	LEU
50	SE	248	ILE
51	SF	17	ILE
51	SF	34	SER
51	SF	41	VAL
51	SF	69	VAL
51	SF	122	ARG
51	SF	124	ASP
51	SF	204	ARG
52	SH	57	ARG
52	SH	60	ILE
52	SH	61	ILE
52	SH	62	ILE
52	SH	72	PHE
52	SH	118	ARG
52	SH	184	ASP
53	SI	52	ASN
53	SI	67	TRP
53	SI	69	SER
53	SI	86	SER
53	SI	92	ARG
53	SI	110	ARG
53	SI	119	LEU
53	SI	149	TYR
53	SI	172	LEU
53	SI	199	LEU
54	SK	17	LYS
54	SK	62	PHE
55	SL	20	LYS
55	SL	33	LEU
55	SL	69	ARG
55	SL	84	ARG
55	SL	119	ASP
57	SQ	34	VAL
57	SQ	118	THR

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Mol	Chain	Res	Type
57	SQ	140	ARG
57	SQ	146	ARG
58	SR	30	THR
58	SR	67	ARG
58	SR	69	ILE
58	SR	99	ASP
58	SR	101	ASP
59	SS	4	VAL
59	SS	50	ILE
59	SS	62	ASP
59	SS	69	THR
59	SS	81	ASP
59	SS	98	VAL
59	SS	108	ARG
59	SS	131	VAL
60	ST	33	TRP
60	ST	38	LYS
60	ST	39	LEU
60	ST	45	LEU
60	ST	87	VAL
61	SU	28	ASN
61	SU	65	THR
61	SU	88	LEU
61	SU	102	THR
62	SV	1	MET
62	SV	56	CYS
62	SV	78	ILE
62	SV	79	VAL
62	SV	81	LYS
63	SX	19	ASP
63	SX	58	GLU
63	SX	67	ARG
63	SX	68	LYS
63	SX	105	PHE
64	Sa	30	VAL
64	Sa	85	ARG
65	Sc	15	THR
65	Sc	45	ASN
67	Sg	44	LYS
67	Sg	91	ASP
67	Sg	98	THR
67	Sg	109	LEU

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Mol	Chain	Res	Type
67	Sg	111	VAL
67	Sg	128	THR
67	Sg	134	THR
67	Sg	138	CYS
67	Sg	143	GLN
67	Sg	165	ILE
67	Sg	186	THR
67	Sg	203	ASP
67	Sg	227	LEU
67	Sg	247	TRP
67	Sg	297	THR
68	SC	98	LEU
69	SG	20	ASP
69	SG	27	PHE
69	SG	31	ARG
69	SG	50	VAL
69	SG	98	ARG
69	SG	126	ASP
69	SG	156	TYR
70	SJ	3	VAL
70	SJ	80	ARG
70	SJ	86	VAL
70	SJ	95	ASP
70	SJ	102	ILE
70	SJ	112	THR
70	SJ	129	LEU
70	SJ	133	ARG
70	SJ	136	ARG
70	SJ	137	VAL
70	SJ	150	ARG
71	SN	87	ASP
71	SN	133	ARG
72	SO	67	ASP
72	SO	69	SER
72	SO	103	ASN
72	SO	138	ASP
72	SO	146	ARG
72	SO	150	ARG
73	SW	9	ASP
73	SW	36	ARG
73	SW	53	ILE
73	SW	55	ASP

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Mol	Chain	Res	Type
73	SW	56	HIS
73	SW	57	ARG
73	SW	61	ILE
73	SW	103	VAL
73	SW	105	THR
73	SW	117	ARG
74	SY	118	ARG
75	SZ	45	ASN
75	SZ	51	ASP
75	SZ	65	TYR
76	Sb	25	VAL
76	Sb	44	THR
76	Sb	52	THR
76	Sb	72	ARG
76	Sb	74	THR
76	Sb	79	PHE
77	Se	90	THR
77	Se	132	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (145) such sidechains are listed below:

Mol	Chain	Res	Type
1	LA	97	ASN
1	LA	132	ASN
1	LA	162	ASN
1	LA	187	HIS
1	LA	194	ASN
2	LB	42	HIS
2	LB	151	ASN
2	LB	184	GLN
2	LB	213	GLN
2	LB	289	GLN
3	LC	38	ASN
3	LC	50	GLN
3	LC	119	GLN
3	LC	215	ASN
3	LC	276	ASN
3	LC	329	ASN
4	LD	9	ASN
4	LD	111	ASN
4	LD	225	GLN
4	LD	244	HIS

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Mol	Chain	Res	Type
5	LE	198	HIS
5	LE	219	HIS
5	LE	229	GLN
5	LE	274	GLN
6	LF	85	GLN
6	LF	173	ASN
6	LF	228	ASN
7	LG	43	GLN
7	LG	66	GLN
8	LH	116	ASN
8	LH	163	GLN
9	LI	14	ASN
10	LJ	65	ASN
10	LJ	112	HIS
11	LL	20	GLN
13	LN	145	ASN
13	LN	196	ASN
14	LO	42	ASN
14	LO	167	HIS
15	LP	75	GLN
15	LP	80	GLN
15	LP	97	ASN
15	LP	137	ASN
16	LQ	44	ASN
18	LS	37	HIS
18	LS	77	ASN
18	LS	122	HIS
20	LU	44	GLN
20	LU	94	ASN
22	LW	17	HIS
23	LX	57	GLN
23	LX	93	ASN
23	LX	107	HIS
23	LX	151	ASN
26	La	17	HIS
26	La	28	HIS
26	La	120	GLN
27	Lb	7	HIS
27	Lb	19	ASN
27	Lb	49	HIS
27	Lb	58	GLN
28	Lc	72	HIS

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Mol	Chain	Res	Type
28	Lc	73	HIS
29	Ld	69	ASN
30	Le	80	HIS
30	Le	107	ASN
30	Le	117	GLN
31	Lf	56	ASN
35	Lj	30	GLN
35	Lj	57	ASN
35	Lj	66	HIS
37	Ll	17	GLN
40	Lo	19	GLN
40	Lo	51	GLN
41	Lp	33	GLN
41	Lp	56	HIS
41	Lp	92	GLN
42	Lr	6	GLN
42	Lr	100	ASN
48	SB	75	GLN
48	SB	147	ASN
48	SB	202	GLN
49	SD	4	GLN
49	SD	56	GLN
49	SD	101	GLN
49	SD	165	ASN
50	SE	112	HIS
50	SE	138	HIS
50	SE	161	GLN
50	SE	188	ASN
50	SE	209	HIS
51	SF	148	ASN
51	SF	179	ASN
52	SH	44	ASN
52	SH	91	HIS
52	SH	112	ASN
53	SI	44	HIS
53	SI	52	ASN
54	SK	44	HIS
54	SK	61	GLN
55	SL	18	GLN
55	SL	100	ASN
56	SP	128	HIS
57	SQ	8	GLN

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Mol	Chain	Res	Type
57	SQ	77	HIS
57	SQ	80	GLN
57	SQ	86	GLN
58	SR	31	ASN
58	SR	93	GLN
60	ST	12	GLN
60	ST	128	GLN
61	SU	81	GLN
63	SX	23	HIS
63	SX	46	HIS
63	SX	92	ASN
63	SX	110	HIS
64	Sa	17	HIS
65	Sc	29	GLN
66	Sd	3	HIS
66	Sd	5	GLN
67	Sg	62	HIS
67	Sg	76	GLN
67	Sg	188	HIS
67	Sg	226	HIS
67	Sg	285	GLN
67	Sg	305	ASN
68	SC	120	GLN
69	SG	70	HIS
69	SG	146	ASN
69	SG	163	ASN
69	SG	186	GLN
70	SJ	75	ASN
70	SJ	113	GLN
71	SN	49	GLN
71	SN	69	ASN
72	SO	103	ASN
73	SW	82	GLN
73	SW	90	GLN
73	SW	98	GLN
74	SY	19	GLN
74	SY	63	HIS
74	SY	112	ASN
76	Sb	19	HIS
76	Sb	26	GLN
77	Se	111	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	L5	3523/4731 (74%)	905 (25%)	22 (0%)
44	L7	119/120 (99%)	12 (10%)	0
45	L8	155/158 (98%)	35 (22%)	0
46	S2	1627/1870 (87%)	448 (27%)	7 (0%)
78	S6	74/75 (98%)	35 (47%)	2 (2%)
All	All	5498/6954 (79%)	1435 (26%)	31 (0%)

All (1435) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	L5	17	A
43	L5	20	U
43	L5	21	G
43	L5	25	A
43	L5	30	C
43	L5	39	A
43	L5	42	A
43	L5	48	G
43	L5	56	A
43	L5	59	A
43	L5	63	G
43	L5	64	A
43	L5	65	A
43	L5	66	A
43	L5	69	A
43	L5	72	C
43	L5	73	A
43	L5	74	G
43	L5	91	G
43	L5	98	A
43	L5	104	G
43	L5	108	A
43	L5	109	G
43	L5	110	C
43	L5	115	C
43	L5	117	C
43	L5	119	G
43	L5	120	A
43	L5	132	G
43	L5	133	C
43	L5	134	G

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Mol	Chain	Res	Type
43	L5	135	U
43	L5	136	C
43	L5	139	G
43	L5	140	G
43	L5	144	G
43	L5	152	U
43	L5	157	U
43	L5	159	C
43	L5	169	A
43	L5	170	C
43	L5	172	C
43	L5	197	A
43	L5	200	U
43	L5	202	C
43	L5	203	U
43	L5	209	U
43	L5	218	A
43	L5	219	G
43	L5	220	C
43	L5	232	G
43	L5	233	U
43	L5	234	G
43	L5	237	G
43	L5	253	G
43	L5	255	G
43	L5	258	C
43	L5	259	C
43	L5	260	G
43	L5	265	C
43	L5	268	G
43	L5	279	G
43	L5	296	U
43	L5	305	A
43	L5	315	U
43	L5	339	C
43	L5	343	A
43	L5	344	C
43	L5	346	A
43	L5	362	A
43	L5	372	G
43	L5	376	A
43	L5	380	U

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Mol	Chain	Res	Type
43	L5	386	G
43	L5	395	A
43	L5	408	G
43	L5	409	A
43	L5	410	G
43	L5	411	G
43	L5	412	G
43	L5	413	C
43	L5	414	G
43	L5	431	U
43	L5	432	A
43	L5	443	G
43	L5	448	C
43	L5	449	G
43	L5	450	C
43	L5	452	G
43	L5	453	U
43	L5	455	C
43	L5	456	G
43	L5	463	G
43	L5	466	U
43	L5	467	U
43	L5	468	C
43	L5	470	A
43	L5	487	C
43	L5	493	U
43	L5	495	C
43	L5	496	C
43	L5	497	C
43	L5	498	G
43	L5	499	G
43	L5	512	A
43	L5	513	U
43	L5	515	U
43	L5	651	C
43	L5	652	G
43	L5	655	G
43	L5	656	G
43	L5	661	U
43	L5	669	C
43	L5	671	G
43	L5	672	G

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Mol	Chain	Res	Type
43	L5	674	G
43	L5	675	A
43	L5	676	C
43	L5	677	C
43	L5	693	C
43	L5	694	A
43	L5	695	C
43	L5	704	U
43	L5	709	G
43	L5	712	C
43	L5	716	G
43	L5	737	G
43	L5	738	G
43	L5	739	G
43	L5	741	A
43	L5	743	G
43	L5	746	C
43	L5	747	G
43	L5	748	G
43	L5	749	U
43	L5	750	G
43	L5	754	A
43	L5	757	G
43	L5	761	C
43	L5	765	G
43	L5	808	G
43	L5	815	A
43	L5	816	C
43	L5	817	A
43	L5	818	G
43	L5	825	G
43	L5	831	G
43	L5	834	U
43	L5	835	U
43	L5	839	C
43	L5	841	A
43	L5	843	U
43	L5	844	C
43	L5	856	G
43	L5	857	A
43	L5	858	A
43	L5	859	G

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Mol	Chain	Res	Type
43	L5	860	C
43	L5	871	U
43	L5	872	C
43	L5	877	C
43	L5	882	U
43	L5	886	U
43	L5	924	G
43	L5	926	G
43	L5	927	C
43	L5	928	C
43	L5	931	G
43	L5	935	C
43	L5	936	C
43	L5	939	U
43	L5	948	G
43	L5	949	C
43	L5	1001	G
43	L5	1004	G
43	L5	1005	C
43	L5	1006	G
43	L5	1007	G
43	L5	1008	A
43	L5	1011	G
43	L5	1012	U
43	L5	1013	C
43	L5	1016	C
43	L5	1017	A
43	L5	1018	G
43	L5	1024	C
43	L5	1025	C
43	L5	1026	C
43	L5	1031	G
43	L5	1032	U
43	L5	1033	G
43	L5	1036	C
43	L5	1037	G
43	L5	1039	G
43	L5	1044	C
43	L5	1045	G
43	L5	1048	U
43	L5	1049	C
43	L5	1050	C

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Mol	Chain	Res	Type
43	L5	1052	G
43	L5	1054	G
43	L5	1071	C
43	L5	1089	A
43	L5	1090	G
43	L5	1095	C
43	L5	1098	G
43	L5	1099	G
43	L5	1100	U
43	L5	1102	G
43	L5	1109	A
43	L5	1110	U
43	L5	1116	C
43	L5	1117	U
43	L5	1129	C
43	L5	1137	A
43	L5	1139	A
43	L5	1141	A
43	L5	1166	G
43	L5	1169	A
43	L5	1173	A
43	L5	1174	G
43	L5	1175	G
43	L5	1180	C
43	L5	1181	G
43	L5	1192	G
43	L5	1193	C
43	L5	1194	C
43	L5	1195	G
43	L5	1196	U
43	L5	1202	A
43	L5	1209	G
43	L5	1219	C
43	L5	1222	C
43	L5	1223	C
43	L5	1226	G
43	L5	1234	A
43	L5	1250	C
43	L5	1252	U
43	L5	1253	C
43	L5	1256	C
43	L5	1257	A

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Mol	Chain	Res	Type
43	L5	1258	G
43	L5	1259	U
43	L5	1260	C
43	L5	1264	C
43	L5	1272	C
43	L5	1296	G
43	L5	1297	C
43	L5	1298	G
43	L5	1308	U
43	L5	1311	A
43	L5	1312	G
43	L5	1316	G
43	L5	1319	C
43	L5	1329	A
43	L5	1338	A
43	L5	1348	A
43	L5	1361	A
43	L5	1363	G
43	L5	1375	G
43	L5	1376	G
43	L5	1377	A
43	L5	1378	A
43	L5	1380	C
43	L5	1388	G
43	L5	1389	A
43	L5	1392	U
43	L5	1405	U
43	L5	1407	A
43	L5	1410	U
43	L5	1414	A
43	L5	1415	A
43	L5	1427	A
43	L5	1438	G
43	L5	1439	G
43	L5	1445	A
43	L5	1447	G
43	L5	1448	A
43	L5	1450	U
43	L5	1452	A
43	L5	1454	C
43	L5	1455	G
43	L5	1456	A

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Mol	Chain	Res	Type
43	L5	1468	G
43	L5	1475	C
43	L5	1484	G
43	L5	1490	C
43	L5	1491	U
43	L5	1492	C
43	L5	1495	G
43	L5	1505	G
43	L5	1512	C
43	L5	1524	G
43	L5	1534	C
43	L5	1536	G
43	L5	1537	G
43	L5	1553	G
43	L5	1557	U
43	L5	1558	C
43	L5	1559	U
43	L5	1560	U
43	L5	1561	G
43	L5	1562	G
43	L5	1563	G
43	L5	1564	G
43	L5	1565	C
43	L5	1566	C
43	L5	1567	G
43	L5	1568	A
43	L5	1569	A
43	L5	1570	A
43	L5	1571	C
43	L5	1572	G
43	L5	1573	A
43	L5	1575	C
43	L5	1576	U
43	L5	1590	A
43	L5	1594	U
43	L5	1607	A
43	L5	1618	G
43	L5	1624	G
43	L5	1625	U
43	L5	1636	G
43	L5	1639	G
43	L5	1640	A

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Mol	Chain	Res	Type
43	L5	1645	G
43	L5	1658	G
43	L5	1672	G
43	L5	1678	C
43	L5	1683	G
43	L5	1684	C
43	L5	1685	U
43	L5	1692	U
43	L5	1695	A
43	L5	1696	C
43	L5	1700	A
43	L5	1714	C
43	L5	1716	C
43	L5	1720	A
43	L5	1721	U
43	L5	1722	G
43	L5	1723	C
43	L5	1724	C
43	L5	1725	G
43	L5	1727	C
43	L5	1728	G
43	L5	1729	C
43	L5	1734	C
43	L5	1735	A
43	L5	1738	C
43	L5	1739	C
43	L5	1741	C
43	L5	1743	G
43	L5	1749	G
43	L5	1750	U
43	L5	1751	G
43	L5	1752	U
43	L5	1754	G
43	L5	1758	G
43	L5	1763	A
43	L5	1764	G
43	L5	1765	A
43	L5	1768	G
43	L5	1769	C
43	L5	1770	A
43	L5	1771	G
43	L5	1776	G

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Mol	Chain	Res	Type
43	L5	1777	U
43	L5	1778	G
43	L5	1779	G
43	L5	1780	C
43	L5	1781	C
43	L5	1784	G
43	L5	1785	G
43	L5	1787	A
43	L5	1788	G
43	L5	1789	U
43	L5	1790	C
43	L5	1792	G
43	L5	1794	A
43	L5	1795	U
43	L5	1796	C
43	L5	1797	C
43	L5	1798	G
43	L5	1799	C
43	L5	1800	U
43	L5	1801	A
43	L5	1803	G
43	L5	1806	G
43	L5	1807	U
43	L5	1810	G
43	L5	1811	U
43	L5	1812	A
43	L5	1813	A
43	L5	1815	A
43	L5	1816	A
43	L5	1817	C
43	L5	1818	U
43	L5	1819	C
43	L5	1822	C
43	L5	1823	U
43	L5	1824	G
43	L5	1826	C
43	L5	1827	G
43	L5	1828	A
43	L5	1829	A
43	L5	1836	A
43	L5	1837	G
43	L5	1847	U

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Mol	Chain	Res	Type
43	L5	1849	G
43	L5	1851	U
43	L5	1853	G
43	L5	1858	G
43	L5	1859	G
43	L5	1872	A
43	L5	1873	U
43	L5	1874	A
43	L5	1887	C
43	L5	1891	A
43	L5	1892	G
43	L5	1902	A
43	L5	1904	C
43	L5	1905	G
43	L5	1912	G
43	L5	1913	A
43	L5	1914	G
43	L5	2013	C
43	L5	2015	C
43	L5	2016	G
43	L5	2017	C
43	L5	2018	G
43	L5	2019	G
43	L5	2033	A
43	L5	2046	C
43	L5	2057	A
43	L5	2058	G
43	L5	2063	G
43	L5	2070	A
43	L5	2079	G
43	L5	2084	G
43	L5	2089	A
43	L5	2090	G
43	L5	2098	A
43	L5	2102	G
43	L5	2103	C
43	L5	2105	G
43	L5	2107	U
43	L5	2108	C
43	L5	2117	A
43	L5	2127	A
43	L5	2138	A

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Mol	Chain	Res	Type
43	L5	2146	A
43	L5	2152	A
43	L5	2153	A
43	L5	2154	G
43	L5	2155	U
43	L5	2159	G
43	L5	2166	U
43	L5	2174	A
43	L5	2178	G
43	L5	2179	C
43	L5	2182	U
43	L5	2183	U
43	L5	2192	G
43	L5	2193	U
43	L5	2194	C
43	L5	2198	C
43	L5	2204	U
43	L5	2206	A
43	L5	2207	G
43	L5	2222	C
43	L5	2224	U
43	L5	2226	C
43	L5	2228	G
43	L5	2232	G
43	L5	2235	C
43	L5	2237	G
43	L5	2238	G
43	L5	2241	A
43	L5	2242	U
43	L5	2243	G
43	L5	2244	G
43	L5	2245	C
43	L5	2246	C
43	L5	2247	U
43	L5	2248	C
43	L5	2249	C
43	L5	2250	G
43	L5	2252	U
43	L5	2260	G
43	L5	2261	C
43	L5	2262	C
43	L5	2263	G

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Mol	Chain	Res	Type
43	L5	2264	A
43	L5	2269	A
43	L5	2270	A
43	L5	2271	G
43	L5	2277	C
43	L5	2286	A
43	L5	2301	G
43	L5	2302	U
43	L5	2303	G
43	L5	2304	G
43	L5	2311	U
43	L5	2313	G
43	L5	2318	C
43	L5	2319	G
43	L5	2320	C
43	L5	2321	G
43	L5	2324	G
43	L5	2327	A
43	L5	2337	C
43	L5	2341	A
43	L5	2372	G
43	L5	2381	C
43	L5	2395	A
43	L5	2406	G
43	L5	2407	C
43	L5	2415	U
43	L5	2416	G
43	L5	2423	C
43	L5	2427	G
43	L5	2430	A
43	L5	2441	U
43	L5	2448	G
43	L5	2449	A
43	L5	2450	A
43	L5	2457	G
43	L5	2460	G
43	L5	2462	U
43	L5	2463	C
43	L5	2465	G
43	L5	2467	C
43	L5	2479	A
43	L5	2480	G

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Mol	Chain	Res	Type
43	L5	2486	G
43	L5	2493	C
43	L5	2496	G
43	L5	2497	A
43	L5	2508	G
43	L5	2510	G
43	L5	2513	G
43	L5	2515	U
43	L5	2517	U
43	L5	2518	A
43	L5	2523	U
43	L5	2524	C
43	L5	2541	A
43	L5	2542	U
43	L5	2544	U
43	L5	2552	A
43	L5	2557	U
43	L5	2564	U
43	L5	2568	C
43	L5	2569	A
43	L5	2580	U
43	L5	2581	G
43	L5	2583	U
43	L5	2592	G
43	L5	2596	G
43	L5	2598	A
43	L5	2600	G
43	L5	2603	A
43	L5	2609	G
43	L5	2621	C
43	L5	2624	A
43	L5	2631	G
43	L5	2646	C
43	L5	2648	A
43	L5	2654	U
43	L5	2655	G
43	L5	2656	G
43	L5	2657	G
43	L5	2658	U
43	L5	2659	C
43	L5	2660	G
43	L5	2661	G

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Mol	Chain	Res	Type
43	L5	3243	G
43	L5	3244	C
43	L5	3248	C
43	L5	3249	G
43	L5	3250	C
43	L5	3251	C
43	L5	3252	U
43	L5	3254	G
43	L5	3255	C
43	L5	3261	A
43	L5	3262	C
43	L5	3271	G
43	L5	3272	G
43	L5	3275	C
43	L5	3276	G
43	L5	3283	G
43	L5	3287	A
43	L5	3292	A
43	L5	3301	U
43	L5	3303	A
43	L5	3305	A
43	L5	3307	C
43	L5	3319	A
43	L5	3327	C
43	L5	3329	G
43	L5	3330	C
43	L5	3348	G
43	L5	3349	A
43	L5	3358	C
43	L5	3362	G
43	L5	3367	G
43	L5	3368	A
43	L5	3370	U
43	L5	3393	A
43	L5	3400	G
43	L5	3405	A
43	L5	3407	G
43	L5	3414	G
43	L5	3415	U
43	L5	3416	A
43	L5	3417	A
43	L5	3418	C

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Mol	Chain	Res	Type
43	L5	3430	U
43	L5	3431	A
43	L5	3434	G
43	L5	3441	A
43	L5	3442	A
43	L5	3443	U
43	L5	3446	C
43	L5	3449	G
43	L5	3451	C
43	L5	3459	U
43	L5	3468	G
43	L5	3469	C
43	L5	3470	A
43	L5	3471	U
43	L5	3474	A
43	L5	3475	U
43	L5	3476	G
43	L5	3495	U
43	L5	3496	G
43	L5	3497	U
43	L5	3500	C
43	L5	3524	A
43	L5	3533	A
43	L5	3534	A
43	L5	3535	C
43	L5	3536	G
43	L5	3537	G
43	L5	3544	C
43	L5	3546	G
43	L5	3554	G
43	L5	3555	G
43	L5	3558	A
43	L5	3560	A
43	L5	3563	A
43	L5	3564	G
43	L5	3565	A
43	L5	3572	U
43	L5	3579	G
43	L5	3595	G
43	L5	3596	G
43	L5	3598	G
43	L5	3603	G

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Mol	Chain	Res	Type
43	L5	3604	A
43	L5	3605	C
43	L5	3608	G
43	L5	3711	U
43	L5	3712	C
43	L5	3716	G
43	L5	3717	U
43	L5	3718	U
43	L5	3727	G
43	L5	3735	G
43	L5	3737	G
43	L5	3742	G
43	L5	3746	G
43	L5	3747	C
43	L5	3748	G
43	L5	3750	G
43	L5	3752	C
43	L5	3753	C
43	L5	3754	C
43	L5	3755	G
43	L5	3756	A
43	L5	3757	G
43	L5	3758	G
43	L5	3759	G
43	L5	3763	C
43	L5	3765	C
43	L5	3766	G
43	L5	3767	C
43	L5	3770	C
43	L5	3773	G
43	L5	3778	A
43	L5	3783	U
43	L5	3784	C
43	L5	3803	G
43	L5	3815	C
43	L5	3816	U
43	L5	3823	A
43	L5	3830	C
43	L5	3836	G
43	L5	3837	G
43	L5	3844	G
43	L5	3849	G

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Mol	Chain	Res	Type
43	L5	3856	A
43	L5	3865	A
43	L5	3867	A
43	L5	3871	U
43	L5	3875	G
43	L5	3878	G
43	L5	3882	U
43	L5	3885	U
43	L5	3886	A
43	L5	3891	G
43	L5	3904	A
43	L5	3907	G
43	L5	3910	A
43	L5	3918	U
43	L5	3921	A
43	L5	3926	A
43	L5	3934	A
43	L5	3942	U
43	L5	3944	G
43	L5	3950	G
43	L5	3956	C
43	L5	3957	A
43	L5	3958	G
43	L5	3967	C
43	L5	3977	A
43	L5	3982	G
43	L5	3983	G
43	L5	3985	C
43	L5	3991	G
43	L5	3992	A
43	L5	4002	C
43	L5	4007	U
43	L5	4008	G
43	L5	4024	G
43	L5	4026	G
43	L5	4027	U
43	L5	4030	G
43	L5	4031	A
43	L5	4032	A
43	L5	4033	A
43	L5	4035	G
43	L5	4040	C

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Mol	Chain	Res	Type
43	L5	4044	G
43	L5	4047	A
43	L5	4075	A
43	L5	4079	C
43	L5	4090	U
43	L5	4096	C
43	L5	4097	C
43	L5	4101	G
43	L5	4102	A
43	L5	4105	U
43	L5	4117	A
43	L5	4119	C
43	L5	4124	U
43	L5	4127	A
43	L5	4128	G
43	L5	4136	C
43	L5	4163	A
43	L5	4165	U
43	L5	4166	A
43	L5	4171	A
43	L5	4172	C
43	L5	4177	G
43	L5	4185	U
43	L5	4198	G
43	L5	4201	A
43	L5	4202	G
43	L5	4207	G
43	L5	4208	U
43	L5	4213	C
43	L5	4220	G
43	L5	4225	U
43	L5	4228	G
43	L5	4236	C
43	L5	4237	A
43	L5	4238	U
43	L5	4241	U
43	L5	4242	A
43	L5	4243	A
43	L5	4253	G
43	L5	4254	U
43	L5	4259	G
43	L5	4286	G

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Mol	Chain	Res	Type
43	L5	4288	A
43	L5	4289	U
43	L5	4290	G
43	L5	4292	G
43	L5	4300	G
43	L5	4301	A
43	L5	4305	G
43	L5	4309	A
43	L5	4323	C
43	L5	4325	A
43	L5	4326	U
43	L5	4340	A
43	L5	4346	C
43	L5	4347	G
43	L5	4348	C
43	L5	4353	A
43	L5	4361	A
43	L5	4362	U
43	L5	4372	G
43	L5	4373	C
43	L5	4374	G
43	L5	4387	A
43	L5	4388	G
43	L5	4393	G
43	L5	4394	A
43	L5	4395	A
43	L5	4396	G
43	L5	4399	G
43	L5	4404	G
43	L5	4408	G
43	L5	4411	C
43	L5	4413	C
43	L5	4415	G
43	L5	4419	G
43	L5	4423	G
43	L5	4426	C
43	L5	4427	C
43	L5	4429	C
43	L5	4430	G
43	L5	4506	G
43	L5	4516	G
43	L5	4517	C

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Mol	Chain	Res	Type
43	L5	4520	A
43	L5	4522	A
43	L5	4527	U
43	L5	4528	U
43	L5	4529	C
43	L5	4533	U
43	L5	4534	U
43	L5	4535	G
43	L5	4540	A
43	L5	4541	C
43	L5	4542	G
43	L5	4546	U
43	L5	4547	G
43	L5	4548	C
43	L5	4549	G
43	L5	4553	G
43	L5	4554	G
43	L5	4555	A
43	L5	4556	A
43	L5	4557	A
43	L5	4558	G
43	L5	4559	G
43	L5	4560	C
43	L5	4561	G
43	L5	4564	C
43	L5	4565	G
43	L5	4566	C
43	L5	4570	C
43	L5	4577	G
43	L5	4580	A
43	L5	4581	C
43	L5	4583	U
43	L5	4584	U
43	L5	4585	G
43	L5	4586	A
43	L5	4588	C
43	L5	4589	G
43	L5	4591	A
43	L5	4597	G
43	L5	4598	U
43	L5	4599	G
43	L5	4603	A

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Mol	Chain	Res	Type
43	L5	4604	A
43	L5	4605	C
43	L5	4608	G
43	L5	4609	G
43	L5	4610	C
43	L5	4611	G
43	L5	4612	C
43	L5	4623	G
43	L5	4624	U
43	L5	4633	U
43	L5	4636	U
43	L5	4638	C
43	L5	4639	U
43	L5	4644	C
43	L5	4655	A
43	L5	4661	C
43	L5	4662	A
43	L5	4664	A
43	L5	4665	G
43	L5	4670	U
43	L5	4671	C
43	L5	4672	C
43	L5	4673	C
43	L5	4675	C
43	L5	4676	G
43	L5	4678	U
43	L5	4682	A
43	L5	4689	G
43	L5	4698	C
43	L5	4702	C
43	L5	4703	G
43	L5	4704	A
43	L5	4709	A
43	L5	4717	U
44	L7	21	G
44	L7	22	A
44	L7	25	G
44	L7	33	U
44	L7	42	A
44	L7	53	U
44	L7	54	A
44	L7	64	G

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Mol	Chain	Res	Type
44	L7	97	G
44	L7	100	A
44	L7	109	U
44	L7	110	G
45	L8	2	G
45	L8	23	C
45	L8	25	G
45	L8	34	U
45	L8	35	C
45	L8	38	U
45	L8	42	G
45	L8	45	C
45	L8	48	A
45	L8	53	G
45	L8	59	A
45	L8	62	A
45	L8	63	U
45	L8	82	A
45	L8	83	C
45	L8	85	U
45	L8	86	U
45	L8	87	G
45	L8	104	A
45	L8	105	C
45	L8	109	C
45	L8	110	U
45	L8	111	U
45	L8	114	G
45	L8	122	G
45	L8	124	U
45	L8	125	C
45	L8	126	C
45	L8	127	U
45	L8	135	C
45	L8	147	G
45	L8	150	C
45	L8	151	G
45	L8	153	C
45	L8	156	U
46	S2	10	G
46	S2	17	C
46	S2	25	A

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Mol	Chain	Res	Type
46	S2	33	G
46	S2	41	G
46	S2	42	A
46	S2	44	U
46	S2	45	A
46	S2	46	A
46	S2	49	C
46	S2	56	G
46	S2	58	C
46	S2	59	U
46	S2	67	C
46	S2	68	A
46	S2	69	C
46	S2	71	G
46	S2	73	C
46	S2	74	G
46	S2	76	U
46	S2	79	A
46	S2	92	A
46	S2	103	A
46	S2	110	U
46	S2	113	G
46	S2	114	G
46	S2	115	U
46	S2	123	G
46	S2	126	G
46	S2	129	C
46	S2	142	C
46	S2	143	U
46	S2	149	A
46	S2	150	A
46	S2	152	U
46	S2	154	U
46	S2	157	U
46	S2	158	A
46	S2	161	U
46	S2	164	A
46	S2	169	U
46	S2	170	A
46	S2	173	A
46	S2	175	A
46	S2	176	U

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Mol	Chain	Res	Type
46	S2	178	C
46	S2	179	C
46	S2	182	C
46	S2	184	G
46	S2	220	U
46	S2	291	U
46	S2	292	G
46	S2	295	U
46	S2	302	A
46	S2	303	A
46	S2	311	C
46	S2	314	A
46	S2	319	A
46	S2	320	C
46	S2	324	C
46	S2	330	G
46	S2	336	G
46	S2	340	A
46	S2	348	G
46	S2	352	G
46	S2	363	C
46	S2	364	A
46	S2	365	A
46	S2	370	C
46	S2	371	G
46	S2	379	U
46	S2	382	C
46	S2	383	C
46	S2	386	G
46	S2	387	C
46	S2	408	G
46	S2	409	A
46	S2	410	C
46	S2	417	U
46	S2	418	C
46	S2	419	A
46	S2	425	C
46	S2	430	C
46	S2	448	A
46	S2	449	A
46	S2	450	A
46	S2	451	C

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Mol	Chain	Res	Type
46	S2	453	G
46	S2	465	A
46	S2	466	A
46	S2	468	G
46	S2	471	G
46	S2	472	G
46	S2	473	C
46	S2	474	A
46	S2	475	G
46	S2	483	G
46	S2	484	C
46	S2	488	U
46	S2	493	C
46	S2	494	A
46	S2	496	U
46	S2	501	A
46	S2	517	A
46	S2	524	A
46	S2	526	A
46	S2	529	A
46	S2	532	A
46	S2	533	C
46	S2	535	G
46	S2	537	A
46	S2	538	C
46	S2	540	C
46	S2	541	U
46	S2	542	U
46	S2	543	U
46	S2	545	G
46	S2	547	G
46	S2	548	G
46	S2	549	C
46	S2	552	U
46	S2	555	A
46	S2	556	A
46	S2	558	U
46	S2	559	G
46	S2	560	G
46	S2	561	A
46	S2	562	A
46	S2	563	U

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Mol	Chain	Res	Type
46	S2	564	G
46	S2	565	A
46	S2	567	U
46	S2	571	C
46	S2	577	A
46	S2	584	A
46	S2	587	G
46	S2	590	G
46	S2	591	A
46	S2	592	U
46	S2	593	C
46	S2	594	C
46	S2	595	A
46	S2	597	U
46	S2	604	C
46	S2	605	A
46	S2	608	U
46	S2	609	C
46	S2	613	U
46	S2	615	C
46	S2	616	C
46	S2	624	G
46	S2	628	U
46	S2	629	A
46	S2	630	A
46	S2	632	U
46	S2	637	C
46	S2	638	U
46	S2	639	C
46	S2	644	A
46	S2	645	G
46	S2	646	C
46	S2	656	A
46	S2	661	C
46	S2	669	A
46	S2	670	A
46	S2	672	A
46	S2	673	A
46	S2	674	G
46	S2	678	G
46	S2	680	A
46	S2	685	G

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Mol	Chain	Res	Type
46	S2	688	C
46	S2	689	U
46	S2	750	U
46	S2	751	C
46	S2	799	G
46	S2	800	U
46	S2	801	U
46	S2	802	U
46	S2	812	A
46	S2	818	G
46	S2	822	G
46	S2	823	U
46	S2	827	A
46	S2	831	A
46	S2	832	G
46	S2	835	C
46	S2	836	C
46	S2	837	G
46	S2	838	A
46	S2	839	G
46	S2	840	C
46	S2	841	C
46	S2	842	G
46	S2	843	C
46	S2	844	C
46	S2	847	G
46	S2	848	A
46	S2	852	C
46	S2	854	C
46	S2	870	A
46	S2	871	A
46	S2	872	U
46	S2	873	A
46	S2	874	G
46	S2	878	C
46	S2	881	G
46	S2	884	U
46	S2	886	U
46	S2	889	U
46	S2	890	U
46	S2	892	G
46	S2	895	G

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Mol	Chain	Res	Type
46	S2	896	G
46	S2	897	U
46	S2	898	U
46	S2	899	U
46	S2	900	U
46	S2	901	C
46	S2	902	G
46	S2	903	G
46	S2	904	A
46	S2	905	A
46	S2	914	A
46	S2	915	U
46	S2	918	U
46	S2	920	A
46	S2	921	A
46	S2	934	G
46	S2	944	U
46	S2	952	C
46	S2	964	A
46	S2	969	U
46	S2	972	G
46	S2	991	A
46	S2	993	A
46	S2	1000	G
46	S2	1002	A
46	S2	1009	A
46	S2	1018	U
46	S2	1019	U
46	S2	1024	A
46	S2	1028	A
46	S2	1031	A
46	S2	1034	G
46	S2	1035	A
46	S2	1040	C
46	S2	1043	A
46	S2	1046	U
46	S2	1048	C
46	S2	1059	A
46	S2	1061	A
46	S2	1062	U
46	S2	1063	A
46	S2	1068	C

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Mol	Chain	Res	Type
46	S2	1072	G
46	S2	1084	A
46	S2	1085	A
46	S2	1086	C
46	S2	1088	A
46	S2	1090	G
46	S2	1102	U
46	S2	1107	C
46	S2	1110	C
46	S2	1115	U
46	S2	1117	C
46	S2	1127	G
46	S2	1133	C
46	S2	1139	C
46	S2	1149	A
46	S2	1152	G
46	S2	1154	C
46	S2	1155	U
46	S2	1158	G
46	S2	1173	U
46	S2	1181	C
46	S2	1196	A
46	S2	1200	A
46	S2	1201	A
46	S2	1208	G
46	S2	1209	A
46	S2	1216	C
46	S2	1217	C
46	S2	1218	A
46	S2	1225	G
46	S2	1228	G
46	S2	1235	C
46	S2	1243	U
46	S2	1244	U
46	S2	1248	C
46	S2	1249	U
46	S2	1252	A
46	S2	1254	A
46	S2	1257	G
46	S2	1258	G
46	S2	1260	A
46	S2	1261	A

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Mol	Chain	Res	Type
46	S2	1262	C
46	S2	1264	U
46	S2	1265	C
46	S2	1274	C
46	S2	1275	G
46	S2	1276	G
46	S2	1284	C
46	S2	1286	G
46	S2	1287	G
46	S2	1291	G
46	S2	1296	A
46	S2	1299	G
46	S2	1303	G
46	S2	1304	C
46	S2	1305	U
46	S2	1309	U
46	S2	1315	U
46	S2	1334	U
46	S2	1343	U
46	S2	1344	U
46	S2	1363	U
46	S2	1370	A
46	S2	1372	U
46	S2	1373	U
46	S2	1374	C
46	S2	1379	A
46	S2	1383	A
46	S2	1397	A
46	S2	1403	A
46	S2	1406	A
46	S2	1407	G
46	S2	1409	U
46	S2	1415	A
46	S2	1416	C
46	S2	1419	C
46	S2	1420	C
46	S2	1422	A
46	S2	1423	G
46	S2	1424	C
46	S2	1430	G
46	S2	1440	A
46	S2	1441	C

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Mol	Chain	Res	Type
46	S2	1447	A
46	S2	1449	A
46	S2	1453	A
46	S2	1455	A
46	S2	1456	A
46	S2	1463	U
46	S2	1464	U
46	S2	1466	A
46	S2	1475	A
46	S2	1481	A
46	S2	1485	A
46	S2	1488	A
46	S2	1489	C
46	S2	1490	A
46	S2	1491	G
46	S2	1496	G
46	S2	1498	G
46	S2	1499	A
46	S2	1507	A
46	S2	1508	G
46	S2	1509	A
46	S2	1510	U
46	S2	1511	G
46	S2	1521	G
46	S2	1522	C
46	S2	1523	A
46	S2	1535	C
46	S2	1545	C
46	S2	1547	G
46	S2	1552	U
46	S2	1553	G
46	S2	1556	U
46	S2	1557	A
46	S2	1561	U
46	S2	1571	G
46	S2	1574	G
46	S2	1575	C
46	S2	1580	A
46	S2	1581	A
46	S2	1585	G
46	S2	1586	U
46	S2	1587	U

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Mol	Chain	Res	Type
46	S2	1588	G
46	S2	1589	A
46	S2	1594	C
46	S2	1595	A
46	S2	1601	G
46	S2	1602	A
46	S2	1603	U
46	S2	1621	A
46	S2	1622	U
46	S2	1624	A
46	S2	1639	G
46	S2	1649	G
46	S2	1655	G
46	S2	1662	A
46	S2	1664	A
46	S2	1666	G
46	S2	1681	G
46	S2	1683	C
46	S2	1687	G
46	S2	1694	G
46	S2	1706	C
46	S2	1711	C
46	S2	1716	A
46	S2	1722	U
46	S2	1723	G
46	S2	1727	G
46	S2	1728	G
46	S2	1730	U
46	S2	1736	A
46	S2	1743	C
46	S2	1744	G
46	S2	1746	A
46	S2	1748	C
46	S2	1753	C
46	S2	1754	C
46	S2	1757	C
46	S2	1778	G
46	S2	1784	C
46	S2	1785	G
46	S2	1787	U
46	S2	1790	G
46	S2	1799	C

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Mol	Chain	Res	Type
46	S2	1801	A
46	S2	1806	G
46	S2	1807	A
46	S2	1808	C
46	S2	1809	U
46	S2	1812	C
46	S2	1814	A
46	S2	1817	G
46	S2	1823	A
46	S2	1825	A
46	S2	1832	A
46	S2	1836	A
46	S2	1838	G
46	S2	1839	U
46	S2	1844	G
46	S2	1850	G
46	S2	1852	A
46	S2	1853	C
46	S2	1862	G
46	S2	1863	G
46	S2	1864	A
46	S2	1865	U
46	S2	1866	C
46	S2	1868	U
46	S2	1869	U
78	S6	3	G
78	S6	4	C
78	S6	6	G
78	S6	7	A
78	S6	8	G
78	S6	11	G
78	S6	18	G
78	S6	20	A
78	S6	21	A
78	S6	22	G
78	S6	23	C
78	S6	24	G
78	S6	35	A
78	S6	36	U
78	S6	45	G
78	S6	46	G
78	S6	47	U

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Mol	Chain	Res	Type
78	S6	48	C
78	S6	53	G
78	S6	54	A
78	S6	55	U
78	S6	56	C
78	S6	57	G
78	S6	58	A
78	S6	60	A
78	S6	61	C
78	S6	62	C
78	S6	66	C
78	S6	67	U
78	S6	68	C
78	S6	69	U
78	S6	71	C
78	S6	72	U
78	S6	74	C
78	S6	76	A

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	L5	236	G
43	L5	277	G
43	L5	492	G
43	L5	676	C
43	L5	693	C
43	L5	1388	G
43	L5	1447	G
43	L5	1563	G
43	L5	1768	G
43	L5	1822	C
43	L5	1836	A
43	L5	2270	A
43	L5	2429	G
43	L5	2514	G
43	L5	2540	C
43	L5	2659	C
43	L5	3271	G
43	L5	3417	A
43	L5	4031	A
43	L5	4208	U

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Mol	Chain	Res	Type
43	L5	4253	G
43	L5	4352	U
46	S2	112	U
46	S2	532	A
46	S2	547	G
46	S2	564	G
46	S2	629	A
46	S2	1343	U
46	S2	1721	U
78	S6	53	G
78	S6	54	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 254 ligands modelled in this entry, 254 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

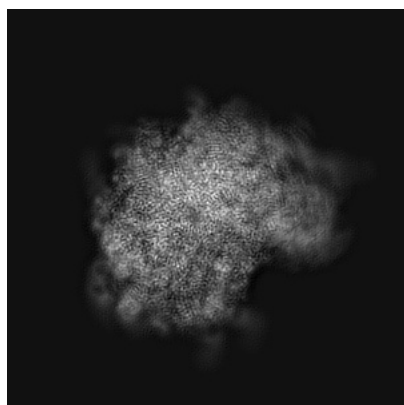
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30433. These allow visual inspection of the internal detail of the map and identification of artifacts.

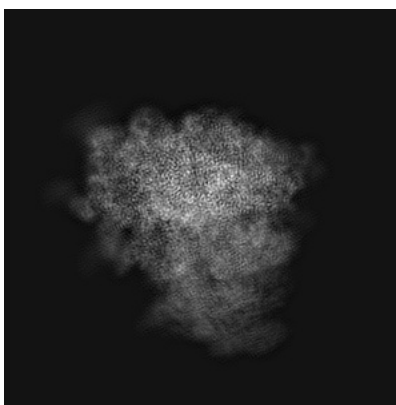
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

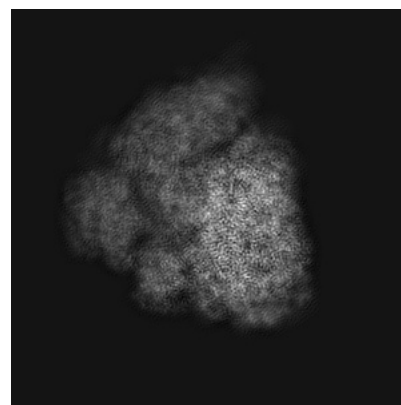
6.1.1 Primary map



X



Y

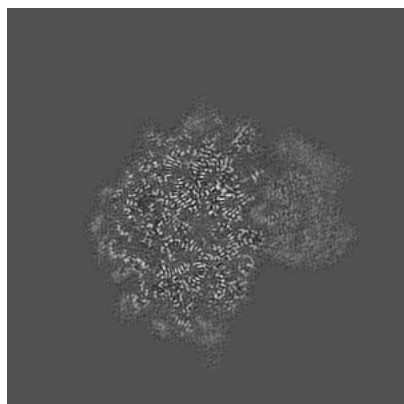


Z

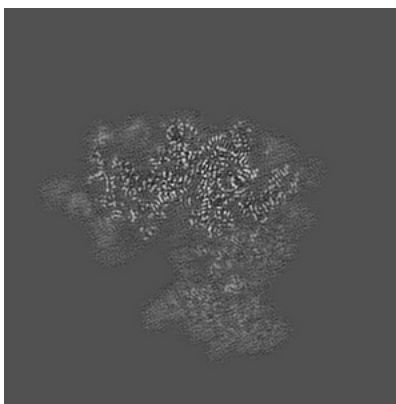
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

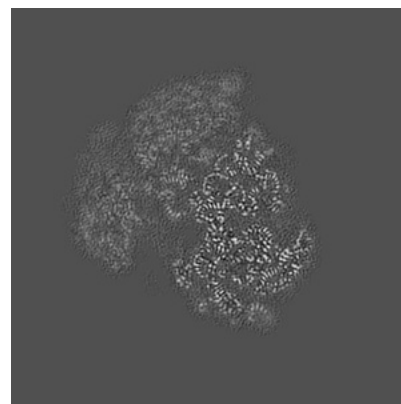
6.2.1 Primary map



X Index: 200



Y Index: 200

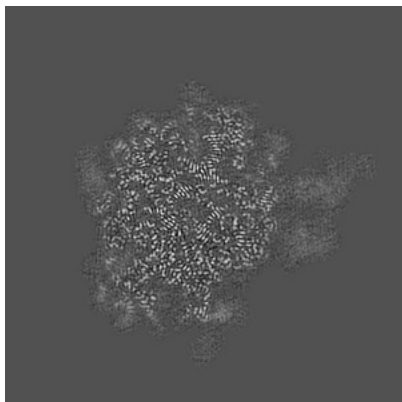


Z Index: 200

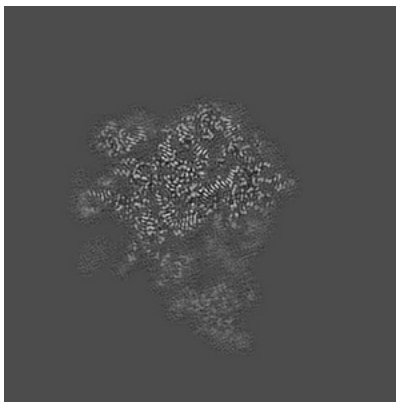
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

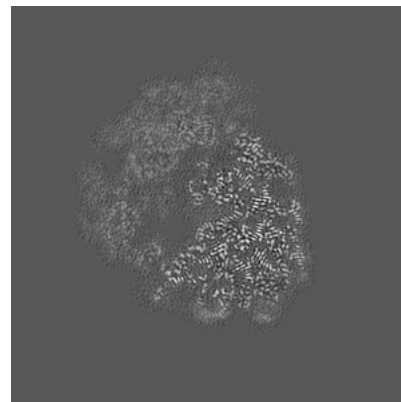
6.3.1 Primary map



X Index: 229



Y Index: 158



Z Index: 183

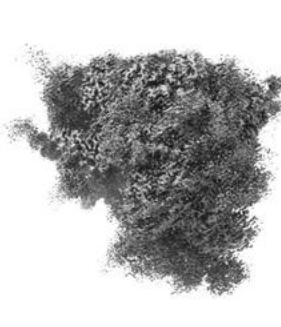
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

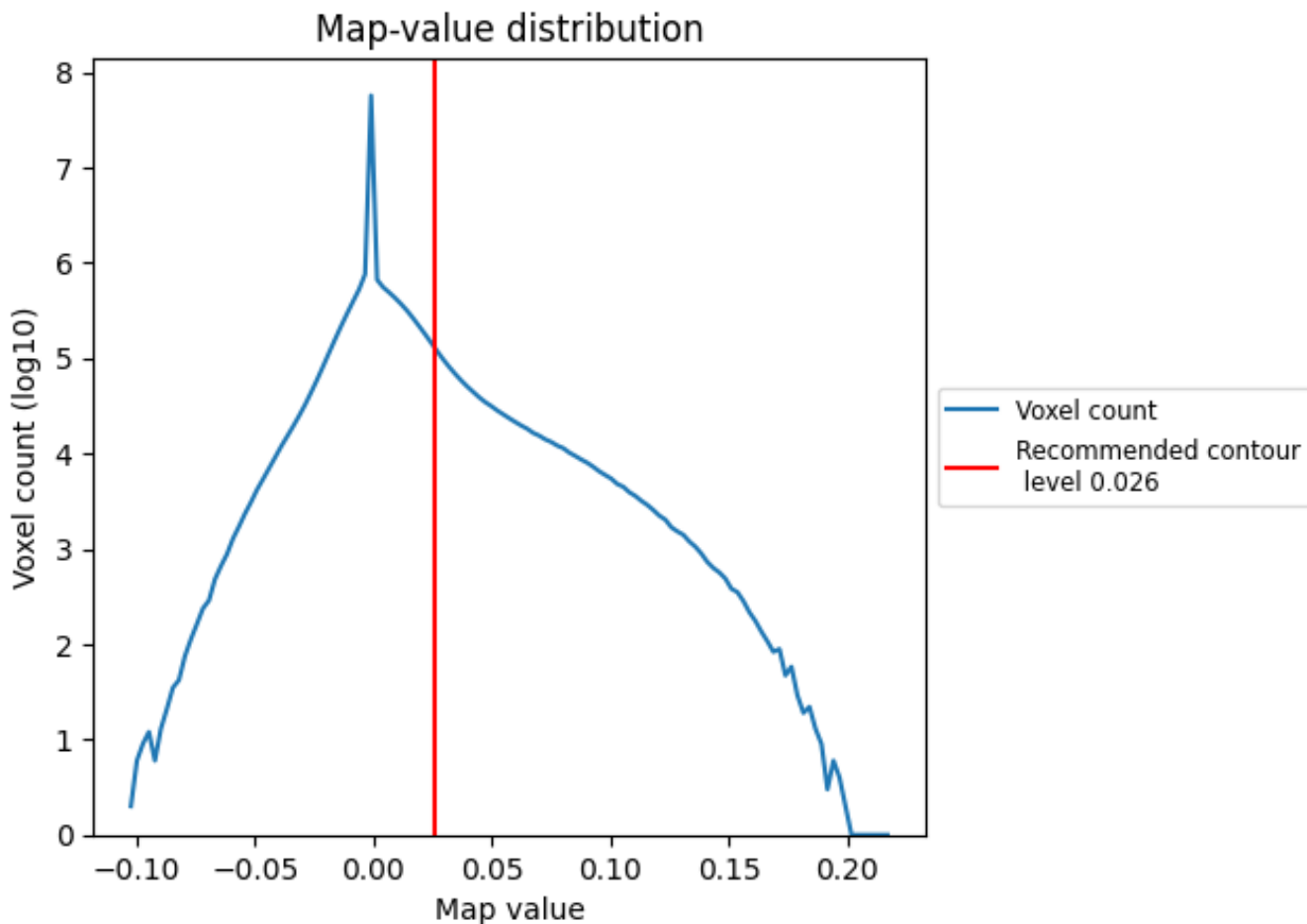
6.5 Mask visualisation

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

7 Map analysis [i](#)

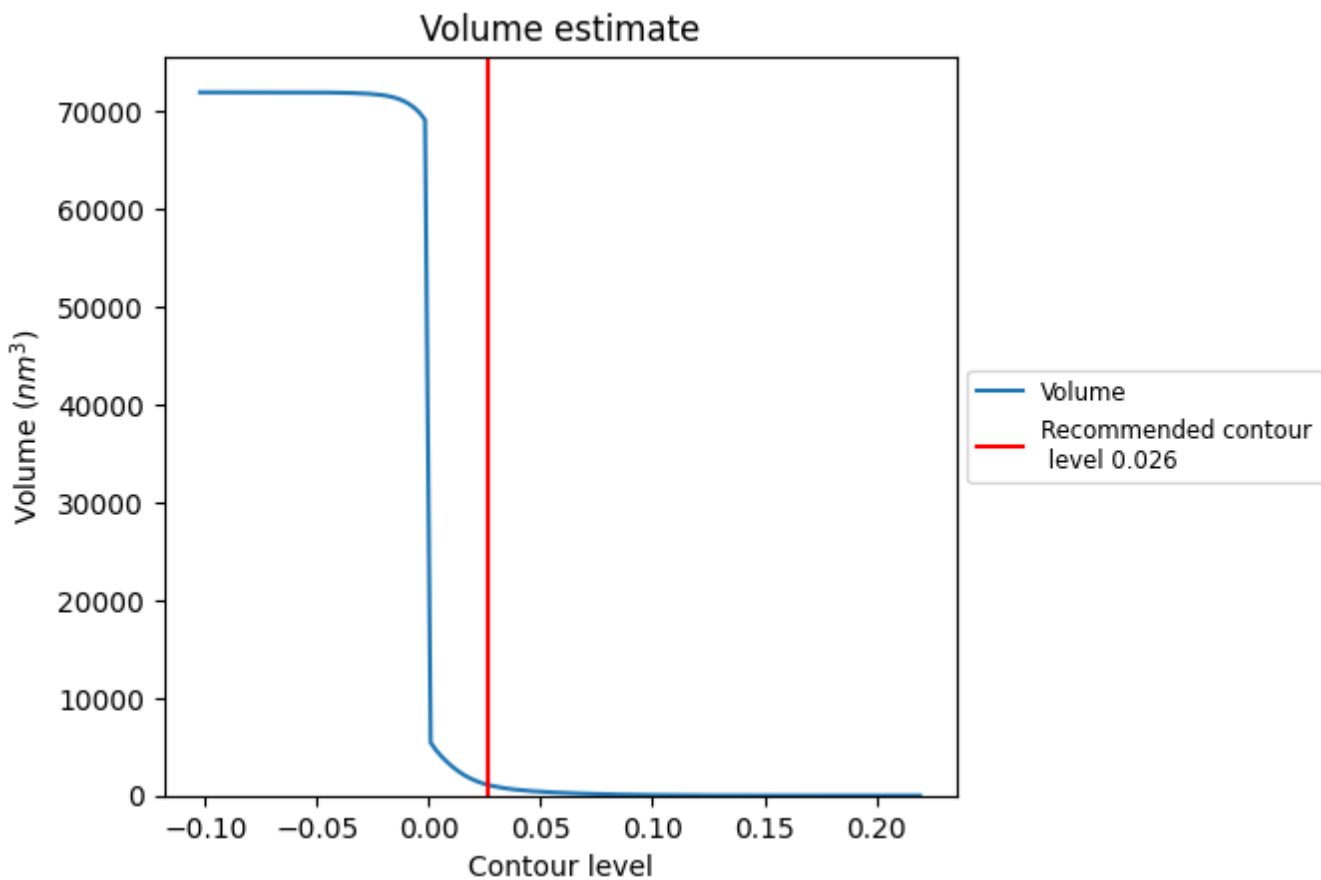
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

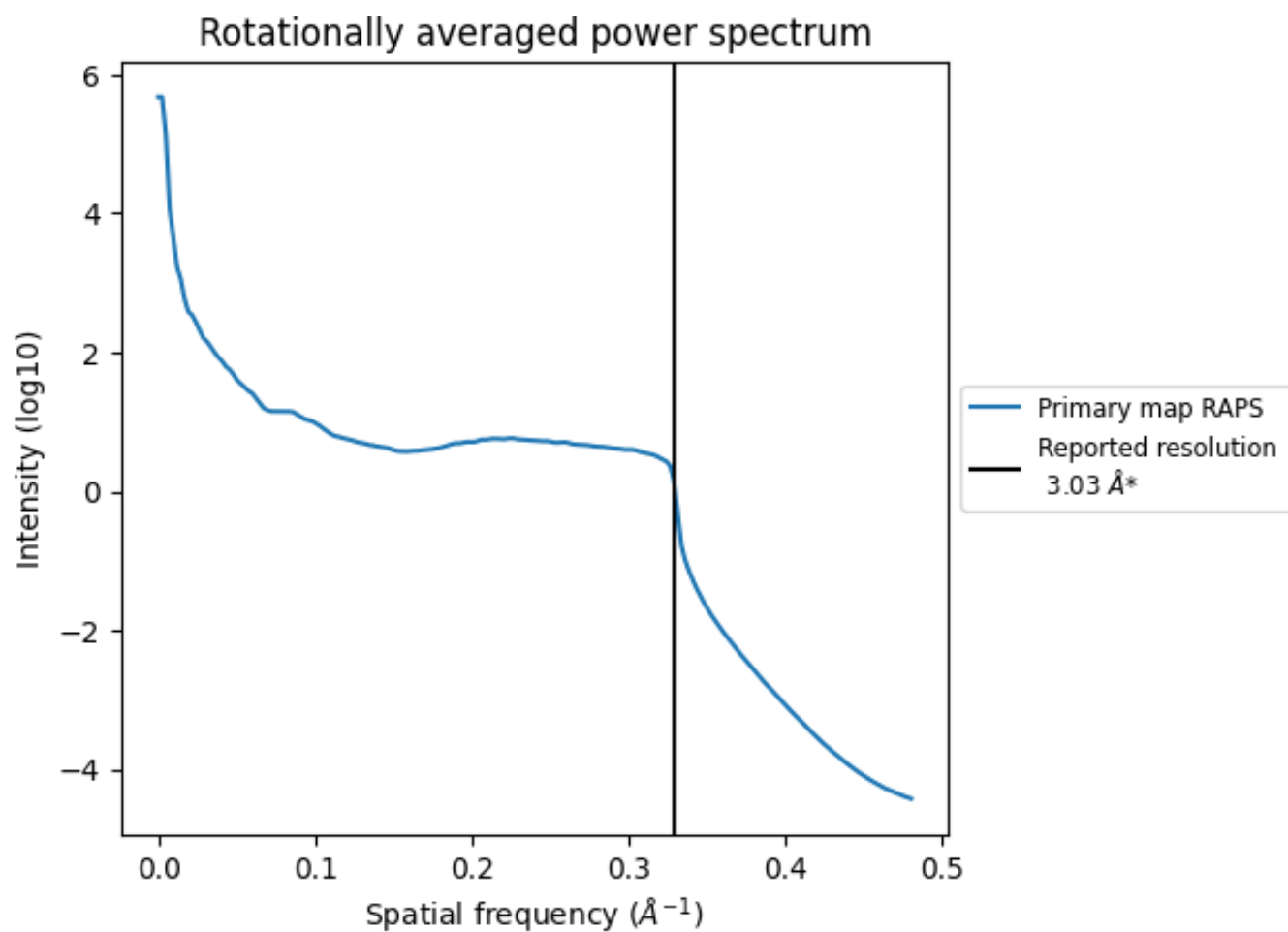
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1121 nm³; this corresponds to an approximate mass of 1013 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.330\AA^{-1}

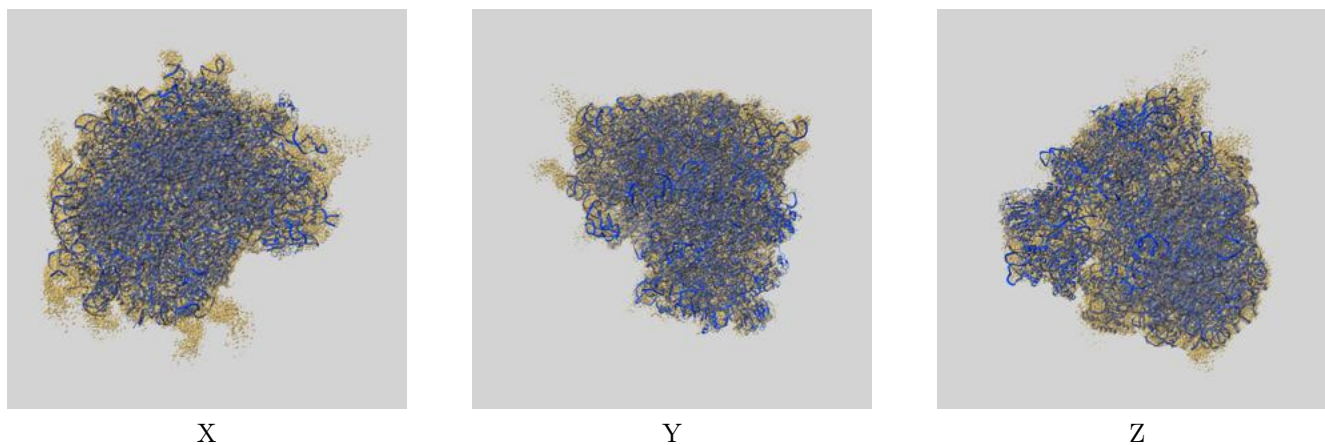
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

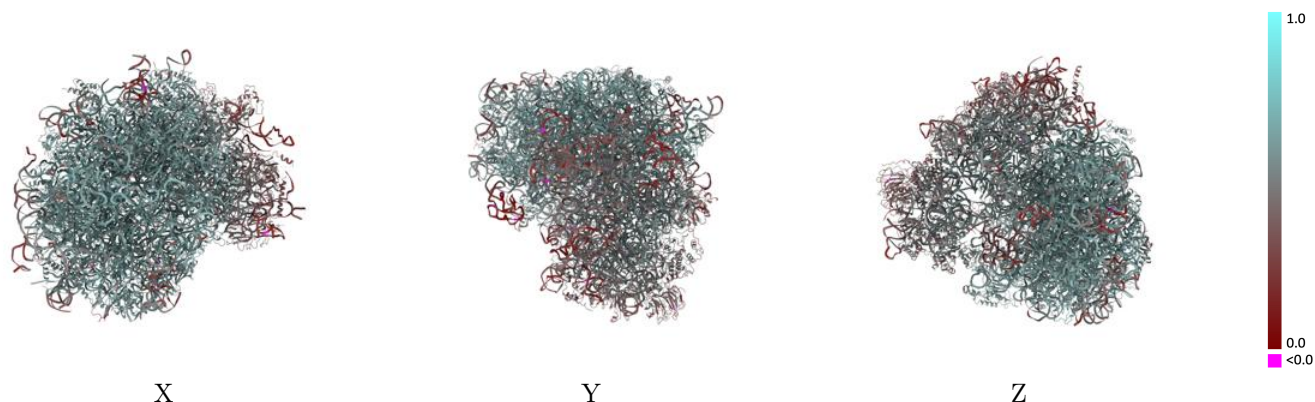
This section contains information regarding the fit between EMDB map EMD-30433 and PDB model 7CPV. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



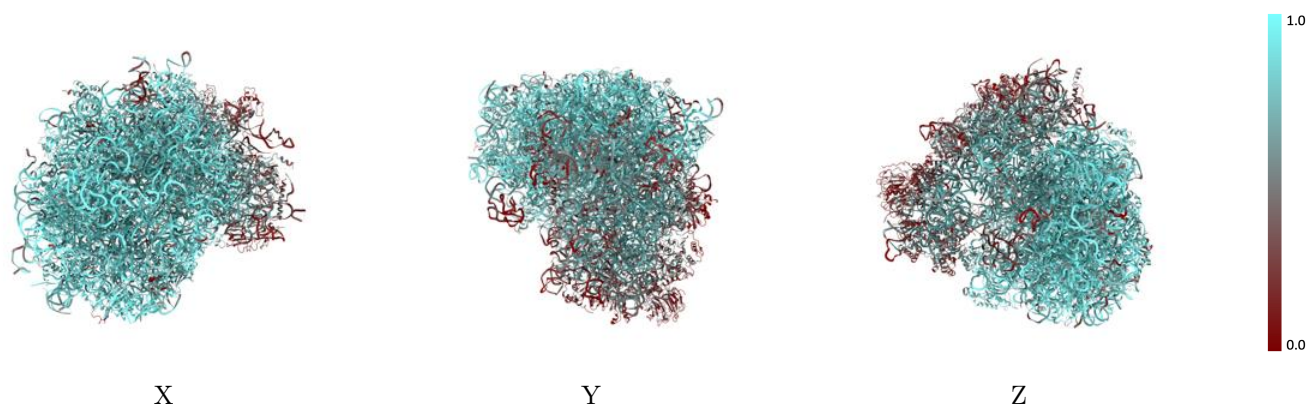
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



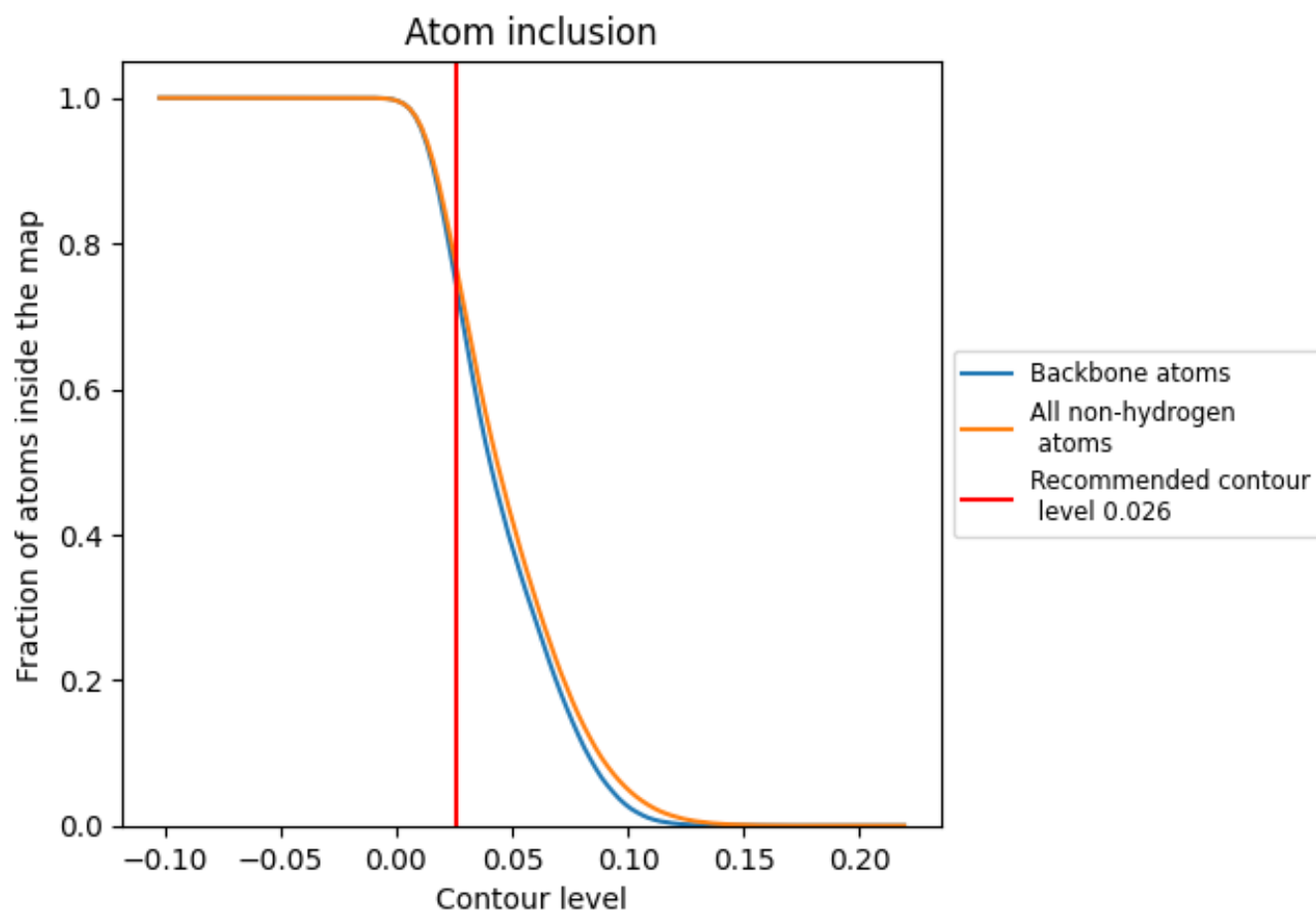
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 77% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7667	 0.5340
L5	 0.8905	 0.5640
L7	 0.9649	 0.6030
L8	 0.9135	 0.5840
LA	 0.8916	 0.6090
LB	 0.8743	 0.6030
LC	 0.8801	 0.5980
LD	 0.8429	 0.5780
LE	 0.7933	 0.5590
LF	 0.8996	 0.6140
LG	 0.7884	 0.5620
LH	 0.8488	 0.5800
LI	 0.8501	 0.5940
LJ	 0.7541	 0.5370
LL	 0.8489	 0.5880
LM	 0.8924	 0.5970
LN	 0.9334	 0.6220
LO	 0.8866	 0.6070
LP	 0.8865	 0.6100
LQ	 0.8972	 0.6160
LR	 0.7953	 0.5690
LS	 0.9114	 0.6180
LT	 0.8539	 0.5890
LU	 0.7584	 0.5440
LV	 0.8498	 0.5990
LW	 0.8660	 0.5990
LX	 0.8511	 0.5980
LY	 0.8695	 0.5980
LZ	 0.8350	 0.5760
La	 0.9150	 0.6210
Lb	 0.8261	 0.5870
Lc	 0.8294	 0.5700
Ld	 0.8254	 0.5880
Le	 0.8870	 0.6100
Lf	 0.9253	 0.6250







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Chain	Atom inclusion	Q-score
Lg	 0.8722	 0.5960
Lh	 0.8389	 0.5850
Li	 0.8246	 0.5760
Lj	 0.9198	 0.6140
Lk	 0.7266	 0.5590
Ll	 0.8694	 0.5980
Lm	 0.8916	 0.5950
Ln	 0.7294	 0.5580
Lo	 0.8397	 0.5970
Lp	 0.8229	 0.5980
Lr	 0.9026	 0.6060
S2	 0.6847	 0.4640
S6	 0.4327	 0.3540
SA	 0.4489	 0.4730
SB	 0.5821	 0.5100
SC	 0.5769	 0.4920
SD	 0.3151	 0.4170
SE	 0.4277	 0.4080
SF	 0.4184	 0.4670
SG	 0.3029	 0.4010
SH	 0.2560	 0.4030
SI	 0.5007	 0.4340
SJ	 0.4789	 0.3900
SK	 0.2770	 0.3950
SL	 0.6017	 0.4990
SN	 0.5333	 0.5020
SO	 0.6280	 0.5060
SP	 0.5699	 0.4750
SQ	 0.4203	 0.4580
SR	 0.2776	 0.4180
SS	 0.5484	 0.4830
ST	 0.4698	 0.4660
SU	 0.3202	 0.4240
SV	 0.4428	 0.4620
SW	 0.6366	 0.5280
SX	 0.5611	 0.4960
SY	 0.2953	 0.3490
SZ	 0.3476	 0.4350
Sa	 0.6496	 0.5190
Sb	 0.4570	 0.4450
Sc	 0.3688	 0.4500
Sd	 0.6393	 0.4780

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Chain	Atom inclusion	Q-score
Se	 0.3496	 0.4080
Sg	 0.2381	 0.3800