



Full wwPDB EM Validation Report ⓘ

Oct 19, 2026 – 04:52 pm BST

PDB ID : 9T0J / pdb_00009t0j
EMDB ID : EMD-55402
Title : Spraguea lophii ribosome dimer, conformation 2.
Authors : McLaren, M.; Isupov, M.N.; Daum, B.; Conners, R.
Deposited on : 2025-10-17
Resolution : 10.90 Å (reported)
Based on initial models : 9SWP, .

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:

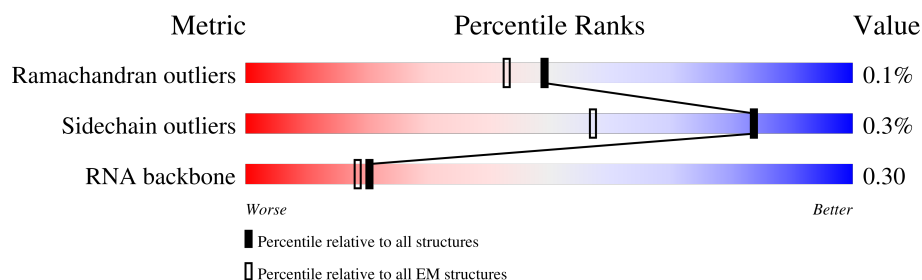
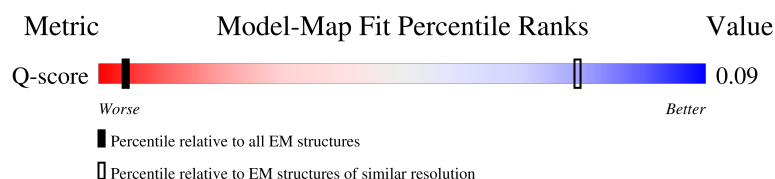
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 10.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	94 (10.40 - 11.40)

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	K50	2618	 68% 30% .
1	L50	2618	 68% 30% .
2	R60	1368	 56% 40% ..
2	S60	1368	 56% 40% ..

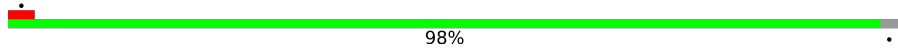
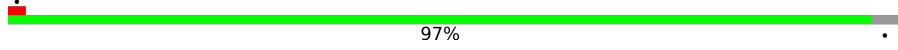
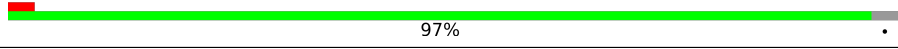
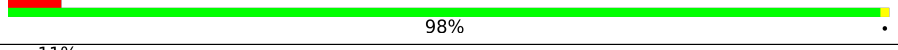
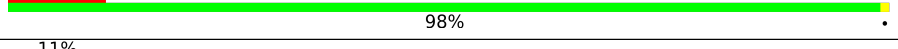
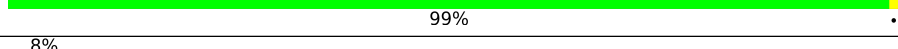
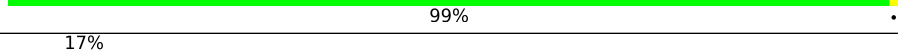
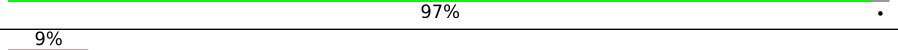
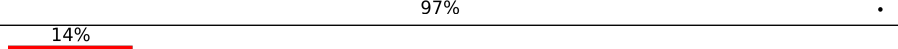
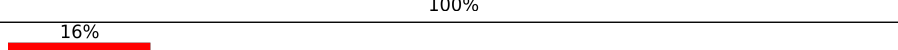
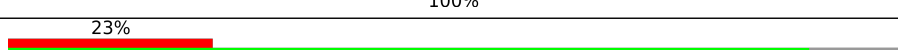
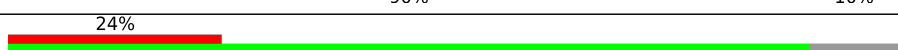
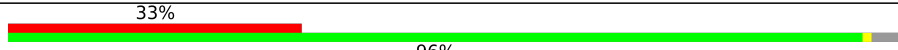
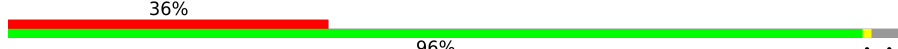
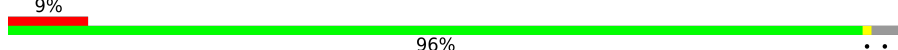
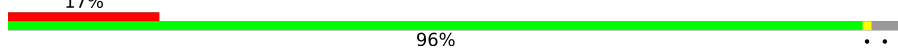
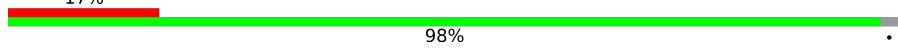
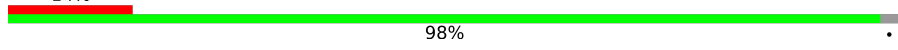
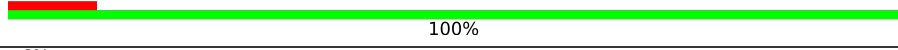
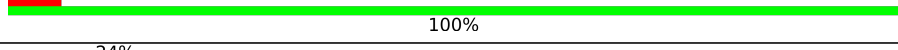
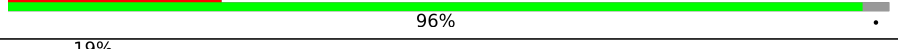
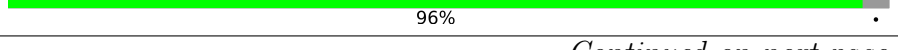
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Mol	Chain	Length	Quality of chain
3	D	164	<div> <div>29%</div> <div>100%</div> </div>
3	E	164	<div> <div>38%</div> <div>100%</div> </div>
4	KGG	106	<div> <div>8%</div> <div>97%</div> </div>
4	LGG	106	<div> <div>•</div> <div>97%</div> </div>
5	RB0	230	<div> <div>22%</div> <div>88%</div> <div>11%</div> </div>
5	SB0	230	<div> <div>14%</div> <div>88%</div> <div>11%</div> </div>
6	RC0	248	<div> <div>23%</div> <div>91%</div> <div>9%</div> </div>
6	SC0	248	<div> <div>20%</div> <div>91%</div> <div>9%</div> </div>
7	K70	119	<div> <div>•</div> <div>74%</div> <div>25%</div> <div>•</div> </div>
7	L70	119	<div> <div>•</div> <div>74%</div> <div>25%</div> <div>•</div> </div>
8	A	847	<div> <div>15%</div> <div>99%</div> <div>•</div> </div>
8	B	847	<div> <div>22%</div> <div>99%</div> <div>•</div> </div>
9	K	210	<div> <div>21%</div> <div>100%</div> </div>
9	L	210	<div> <div>18%</div> <div>100%</div> </div>
10	M	269	<div> <div>28%</div> <div>100%</div> </div>
10	N	269	<div> <div>28%</div> <div>100%</div> </div>
11	KMM	127	<div> <div>6%</div> <div>37%</div> <div>•</div> <div>59%</div> </div>
11	LMM	127	<div> <div>5%</div> <div>37%</div> <div>•</div> <div>59%</div> </div>
12	RBB	82	<div> <div>29%</div> <div>98%</div> <div>•</div> </div>
12	SBB	82	<div> <div>24%</div> <div>98%</div> <div>•</div> </div>
13	RAA	102	<div> <div>21%</div> <div>99%</div> <div>•</div> </div>
13	SAA	102	<div> <div>18%</div> <div>99%</div> <div>•</div> </div>
14	KOO	104	<div> <div>8%</div> <div>96%</div> <div>•</div> </div>
14	LOO	104	<div> <div>10%</div> <div>96%</div> <div>•</div> </div>
15	KPP	89	<div> <div>7%</div> <div>98%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
15	LPP	89	
16	KJJ	92	
16	LJJ	92	
17	LA0	246	
17	LA02	246	
18	KAA	147	
18	LAA	147	
19	KB0	392	
19	LB0	392	
20	KC0	328	
20	LC0	328	
21	KCC	110	
21	LCC	110	
22	KDD	110	
22	LDD	110	
23	KE0	171	
23	LE0	171	
24	KEE	139	
24	LEE	139	
25	KF0	235	
25	LF0	235	
26	KFF	111	
26	LFF	111	
27	KG0	206	
27	LG0	206	

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Mol	Chain	Length	Quality of chain
28	KH0	187	19% 97% ..
28	LH0	187	13% 97% ..
29	KHH	119	11% 98% ..
29	LHH	119	12% 98% ..
30	KI0	218	14% 100%
30	LI0	218	8% 100%
31	KII	98	19% 98% ..
31	LII	98	15% 98% ..
32	KJ0	171	18% 96% ..
32	LJ0	171	14% 96% ..
33	KL0	165	20% 96% ...
33	LL0	165	15% 96% ...
34	KLL	52	98% .
34	LLL	52	98% .
35	KM0	122	28% 93% 6%
35	LM0	122	25% 93% 6%
36	KN0	204	100%
36	LN0	204	100%
37	KO0	198	19% 99% .
37	LO0	198	13% 99% .
38	KP0	167	10% 92% 8%
38	LP0	167	10% 92% 8%
39	KQ0	183	17% 99% ..
39	LQ0	183	19% 99% ..
40	KR0	168	17% 98% .

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Mol	Chain	Length	Quality of chain
40	LR0	168	
41	KS0	171	
41	LS0	171	
42	KT0	158	
42	LT0	158	
43	KU0	113	
43	LU0	113	
44	KV0	142	
44	LV0	142	
45	KW0	131	
45	LW0	131	
46	KX0	113	
46	LX0	113	
47	KY0	131	
47	LY0	131	
48	KZ0	153	
48	LZ0	153	
49	MD1	151	
49	ND1	151	
50	RA0	233	
50	SA0	233	
51	RCC	65	
51	SCC	65	
52	RE0	280	
52	SE0	280	

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Mol	Chain	Length	Quality of chain
53	REE	60	<div> <div>25%</div> <div>93%</div> <div>7%</div> </div>
53	SEE	60	<div> <div>20%</div> <div>93%</div> <div>7%</div> </div>
54	RGG	326	<div> <div>35%</div> <div>98%</div> <div>.</div> </div>
54	SGG	326	<div> <div>34%</div> <div>98%</div> <div>.</div> </div>
55	RI0	173	<div> <div>11%</div> <div>97%</div> <div>.</div> </div>
55	SI0	173	<div> <div>13%</div> <div>97%</div> <div>.</div> </div>
56	RJ0	184	<div> <div>22%</div> <div>91%</div> <div>9%</div> </div>
56	SJ0	184	<div> <div>21%</div> <div>91%</div> <div>9%</div> </div>
57	RK0	107	<div> <div>28%</div> <div>82%</div> <div>18%</div> </div>
57	SK0	107	<div> <div>29%</div> <div>82%</div> <div>18%</div> </div>
58	RL0	155	<div> <div>28%</div> <div>96%</div> <div>..</div> </div>
58	SL0	155	<div> <div>23%</div> <div>96%</div> <div>..</div> </div>
59	RM0	130	<div> <div>52%</div> <div>87%</div> <div>13%</div> </div>
59	SM0	130	<div> <div>56%</div> <div>87%</div> <div>13%</div> </div>
60	RN0	143	<div> <div>14%</div> <div>99%</div> <div>.</div> </div>
60	SN0	143	<div> <div>11%</div> <div>99%</div> <div>.</div> </div>
61	RO0	135	<div> <div>10%</div> <div>95%</div> <div>..</div> </div>
61	SO0	135	<div> <div>.</div> <div>95%</div> <div>..</div> </div>
62	RP0	163	<div> <div>21%</div> <div>71%</div> <div>28%</div> </div>
62	SP0	163	<div> <div>19%</div> <div>71%</div> <div>28%</div> </div>
63	RQ0	143	<div> <div>22%</div> <div>99%</div> <div>.</div> </div>
63	SQ0	143	<div> <div>12%</div> <div>99%</div> <div>.</div> </div>
64	RR0	120	<div> <div>35%</div> <div>99%</div> <div>.</div> </div>
64	SR0	120	<div> <div>30%</div> <div>99%</div> <div>.</div> </div>
65	RS0	160	<div> <div>15%</div> <div>88%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
65	SS0	160	
66	RT0	143	
66	ST0	143	
67	RU0	119	
67	SU0	119	
68	RV0	67	
68	SV0	67	
69	RX0	141	
69	SX0	141	
70	RY0	146	
70	SY0	146	
71	RZ0	128	
71	SZ0	128	
72	KD0	291	
72	LD0	291	
73	RDD	65	
73	SDD	65	
74	RD0	242	
74	SD0	242	
75	RG0	230	
75	SG0	230	
76	RH0	164	
76	SH0	164	
77	RW0	128	
77	SW0	128	

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Mol	Chain	Length	Quality of chain
78	RF0	195	<div><div></div><div>12%</div><div>97%</div><div></div></div>
78	SF0	195	<div><div></div><div>10%</div><div>97%</div><div></div></div>
79	RFF	150	<div><div></div><div>17%</div><div>36%</div><div>64%</div><div></div></div>
79	SFF	150	<div><div></div><div>16%</div><div>36%</div><div>64%</div><div></div></div>

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 371532 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2605	Total	C	N	O	P	0	0
			55952	24974	10318	18055	2605		
1	K50	2605	Total	C	N	O	P	0	0
			55952	24974	10318	18055	2605		

- Molecule 2 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S60	1354	Total	C	N	O	P	0	0
			29180	13024	5463	9339	1354		
2	R60	1354	Total	C	N	O	P	0	0
			29180	13024	5463	9339	1354		

- Molecule 3 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	164	Total	C	N	O	S	0	0
			1224	769	218	231	6		
3	E	164	Total	C	N	O	S	0	0
			1224	769	218	231	6		

- Molecule 4 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		
4	KGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 5 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		
5	RB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 6 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SC0	226	Total	C	N	O	S	0	0
			1729	1101	300	321	7		
6	RC0	226	Total	C	N	O	S	0	0
			1729	1101	300	321	7		

- Molecule 7 is a RNA chain called RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L70	119	Total	C	N	O	P	0	0
			2541	1136	459	827	119		
7	K70	119	Total	C	N	O	P	0	0
			2541	1136	459	827	119		

- Molecule 8 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	847	Total	C	N	O	S	0	0
			6606	4175	1125	1264	42		
8	B	847	Total	C	N	O	S	0	0
			6606	4175	1125	1264	42		

- Molecule 9 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	210	Total	C	N	O	S	0	0
			1718	1109	291	312	6		
9	K	210	Total	C	N	O	S	0	0
			1718	1109	291	312	6		

- Molecule 10 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	269	Total	C	N	O	S	0	0
			2113	1348	345	407	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	269	Total	C	N	O	S	0	0
			2113	1348	345	407	13		

- Molecule 11 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
11	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 12 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		
12	RBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 13 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		
13	RAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 14 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
14	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 15 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
15	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 16 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
16	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 17 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		
17	LA02	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		
18	KAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		

- Molecule 19 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
19	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 20 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
20	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 21 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
21	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 22 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
22	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 23 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		
23	KE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 24 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		
24	KEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 25 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		
25	KF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 26 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	KFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 27 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		
27	KG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 28 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		
28	KH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 29 is a protein called 60S Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LHH	119	Total	C	N	O	S	0	0
			993	626	188	176	3		
29	KHH	119	Total	C	N	O	S	0	0
			993	626	188	176	3		

- Molecule 30 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		
30	KI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 31 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		
31	KII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 32 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
32	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
33	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 34 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
34	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 35 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
35	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 36 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		
36	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 37 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
37	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 38 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
38	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 39 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
39	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
40	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 41 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
41	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 42 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 43 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		
43	KU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 44 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		
44	KV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 45 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		
45	KW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 46 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		
46	KX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 47 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		
47	KY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		
48	KZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 49 is a protein called DNL-type domain-containing protein MD1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		
49	ND1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 50 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		
50	RA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 51 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
51	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 52 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
52	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 53 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	SEE	56	Total	C	N	O	0	0
			447	284	89	74		
53	REE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 54 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		
54	RGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		
55	RI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		
56	RJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		
57	RK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		

- Molecule 58 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	RL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		
59	RM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		
60	RN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 61 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
61	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 62 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
62	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
63	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
64	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 65 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
65	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 66 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
66	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
67	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 68 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
68	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 69 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
69	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 70 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
70	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		
71	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 72 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
72	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 73 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
73	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

- Molecule 74 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 75 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SG0	229	Total	C	N	O	S	0	0
			1835	1178	325	328	4		
75	RG0	229	Total	C	N	O	S	0	0
			1835	1178	325	328	4		

- Molecule 76 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
76	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 77 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
77	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 78 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
78	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 79 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SFF	54	Total	C	N	O	S	0	0
			413	256	74	78	5		
79	RFF	54	Total	C	N	O	S	0	0
			413	256	74	78	5		

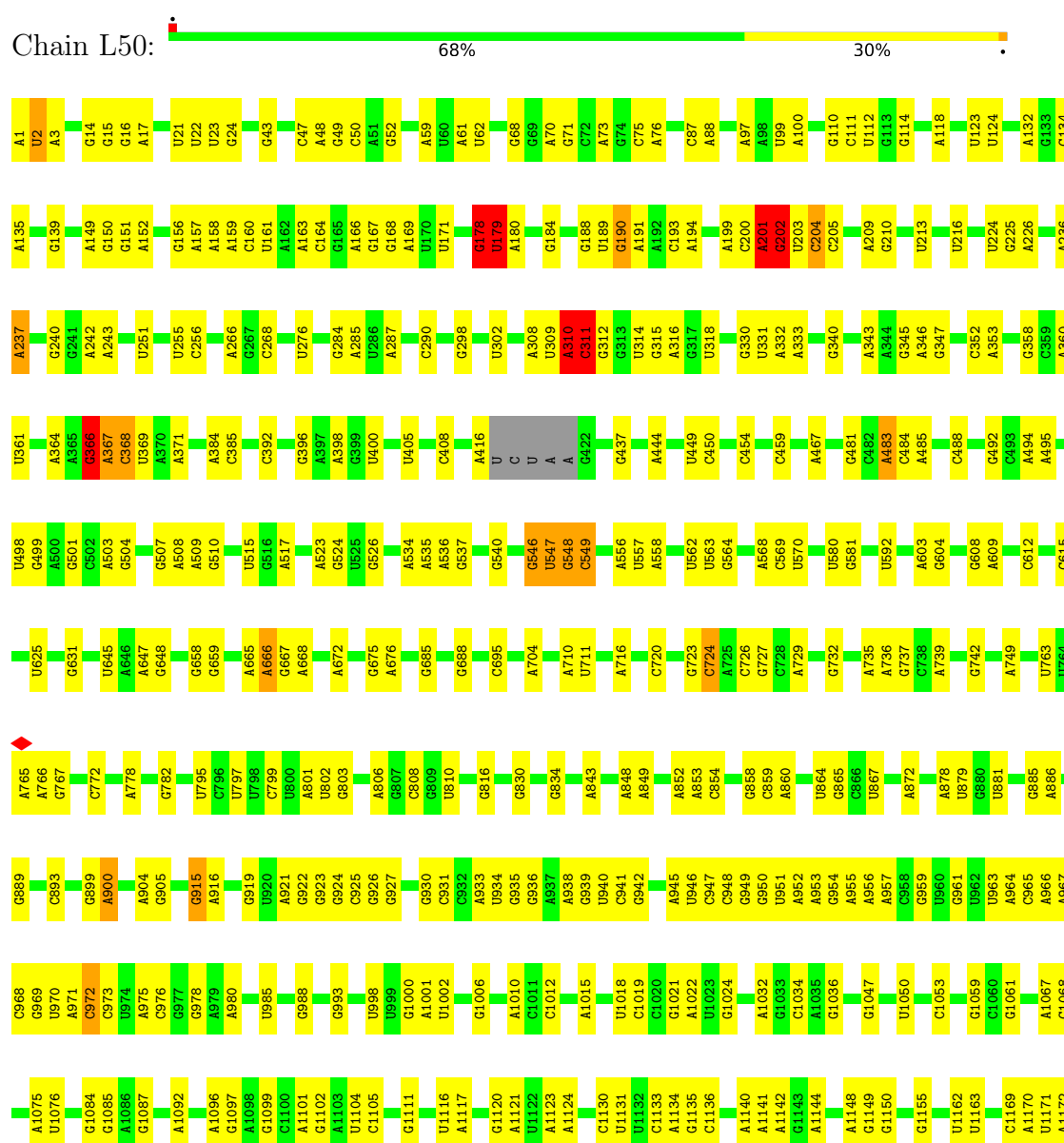
- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

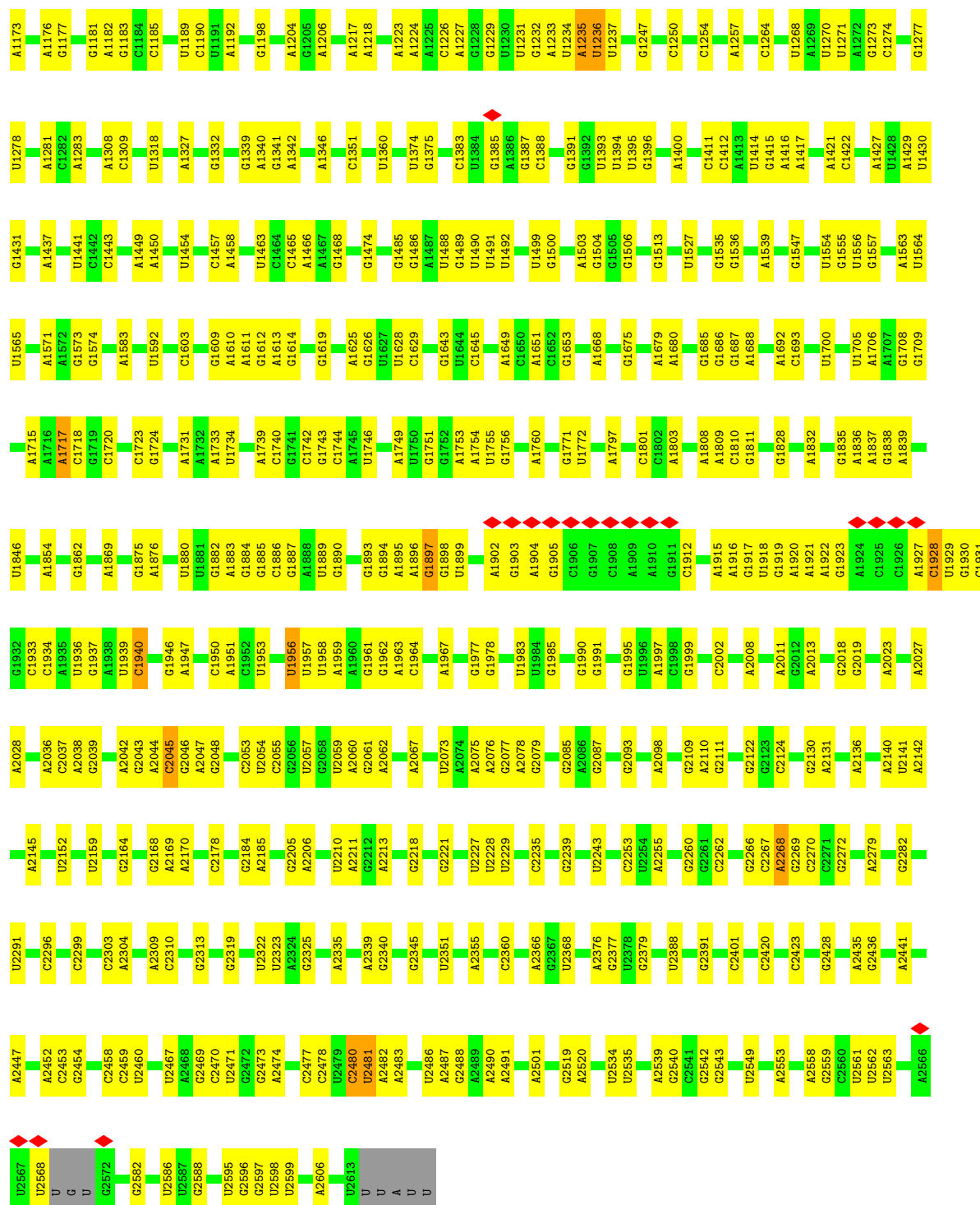
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80	LMM	1	Total 1	Zn 1	0
80	SBB	1	Total 1	Zn 1	0
80	SAA	1	Total 1	Zn 1	0
80	LOO	1	Total 1	Zn 1	0
80	LPP	1	Total 1	Zn 1	0
80	LJJ	1	Total 1	Zn 1	0
80	MD1	1	Total 1	Zn 1	0
80	SFF	1	Total 1	Zn 1	0
80	KGG	1	Total 1	Zn 1	0
80	KMM	1	Total 1	Zn 1	0
80	RBB	1	Total 1	Zn 1	0
80	RAA	1	Total 1	Zn 1	0
80	KOO	1	Total 1	Zn 1	0
80	KPP	1	Total 1	Zn 1	0
80	KJJ	1	Total 1	Zn 1	0
80	ND1	1	Total 1	Zn 1	0
80	RFF	1	Total 1	Zn 1	0

3 Residue-property plots

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

• Molecule 1: RNA 23S



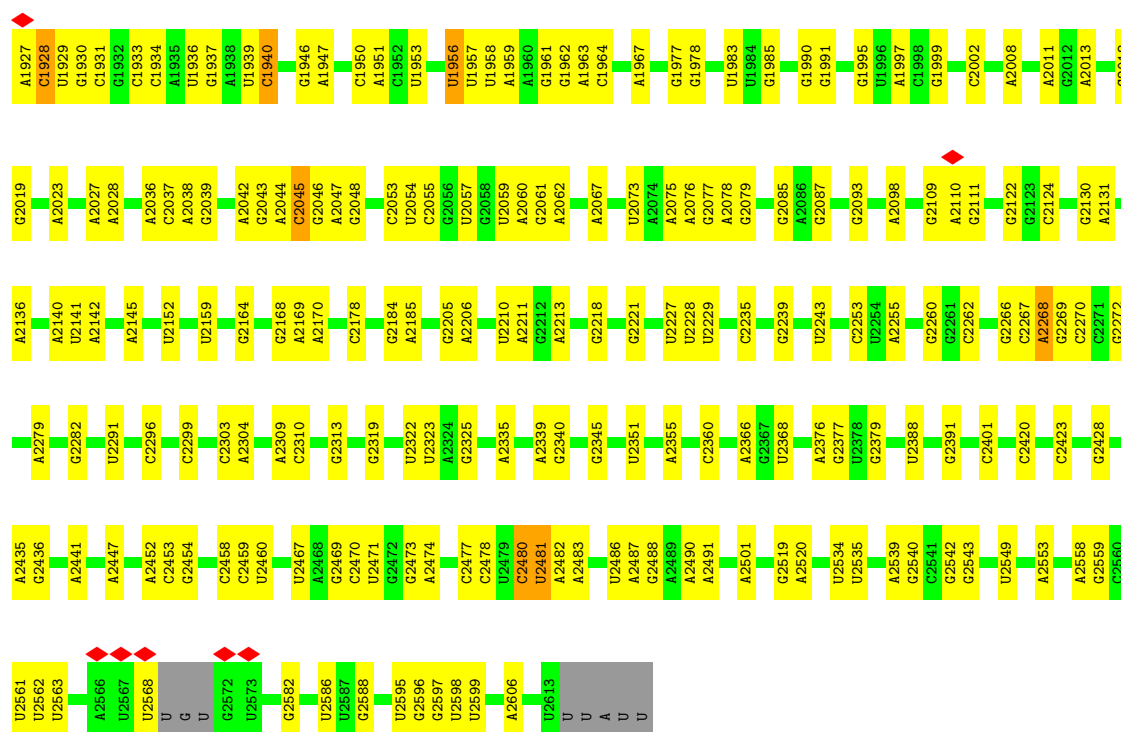


• Molecule 1: RNA 23S

Chain K50:

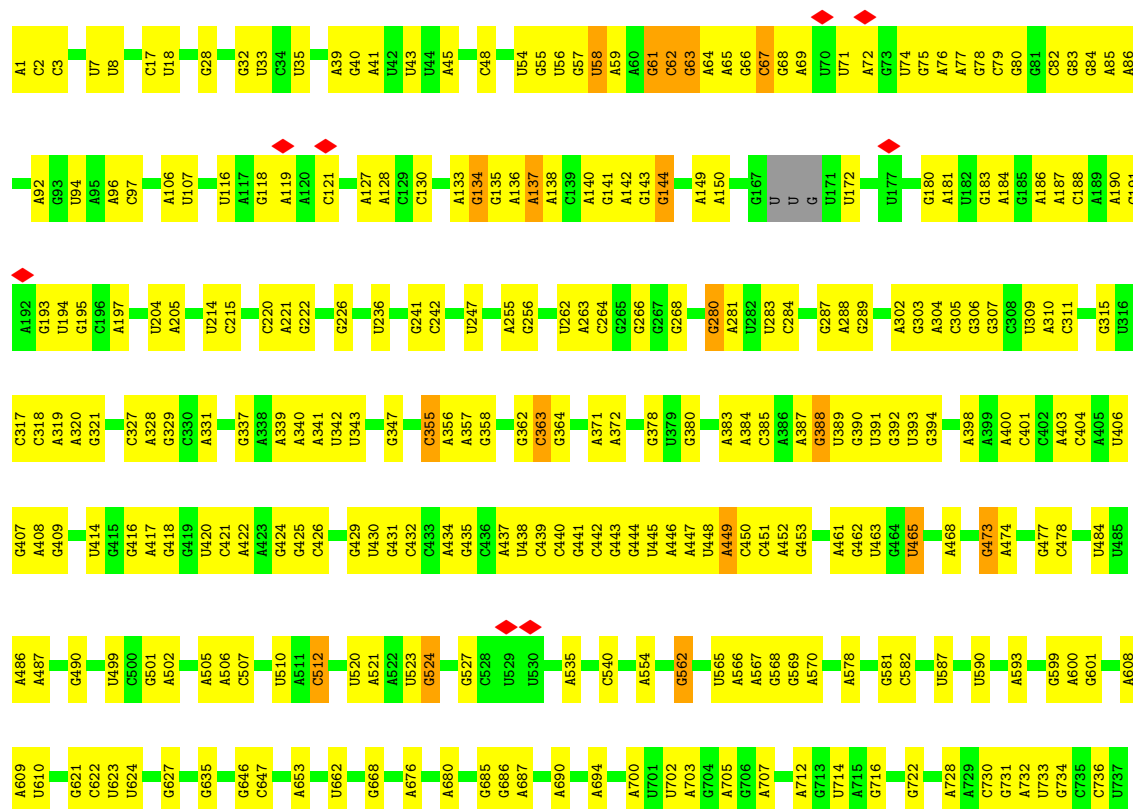


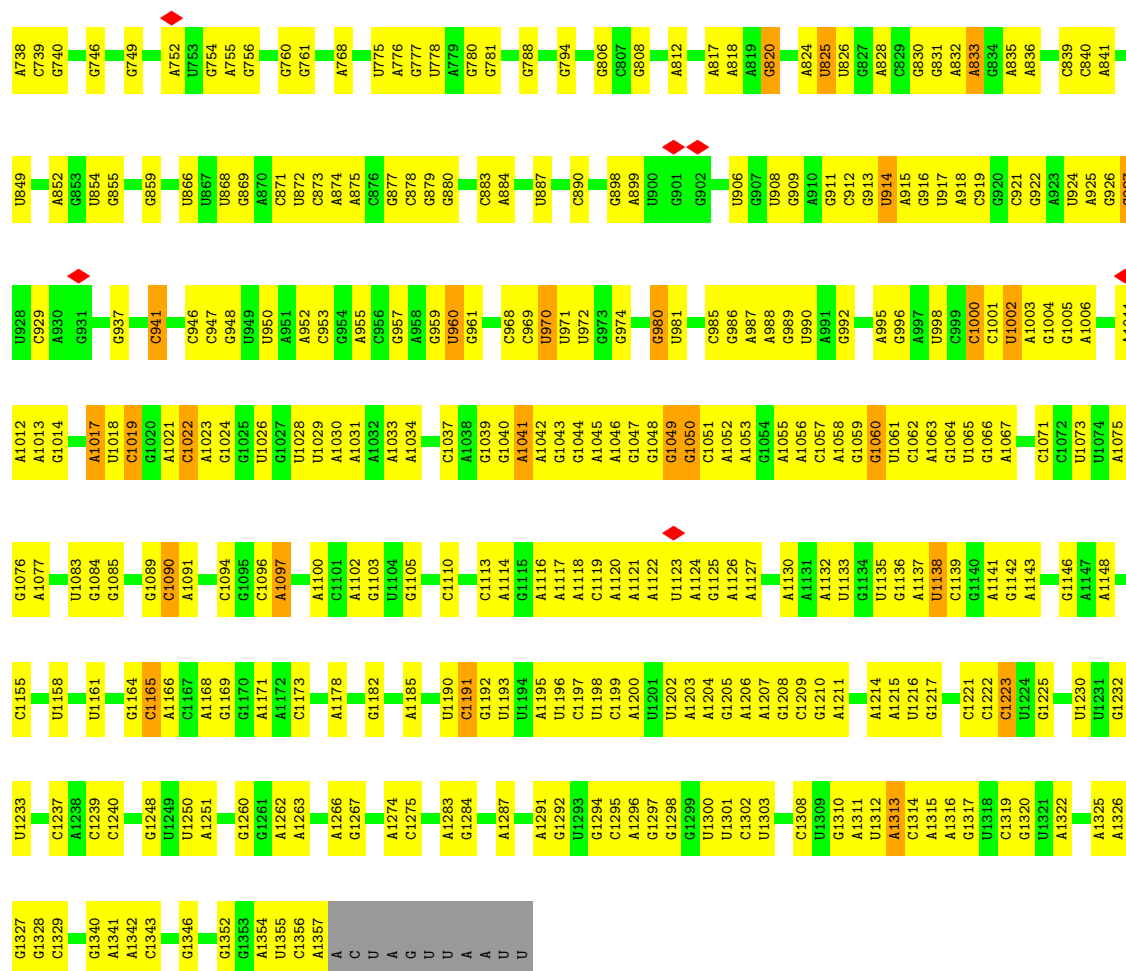
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• Molecule 2: RNA 16S

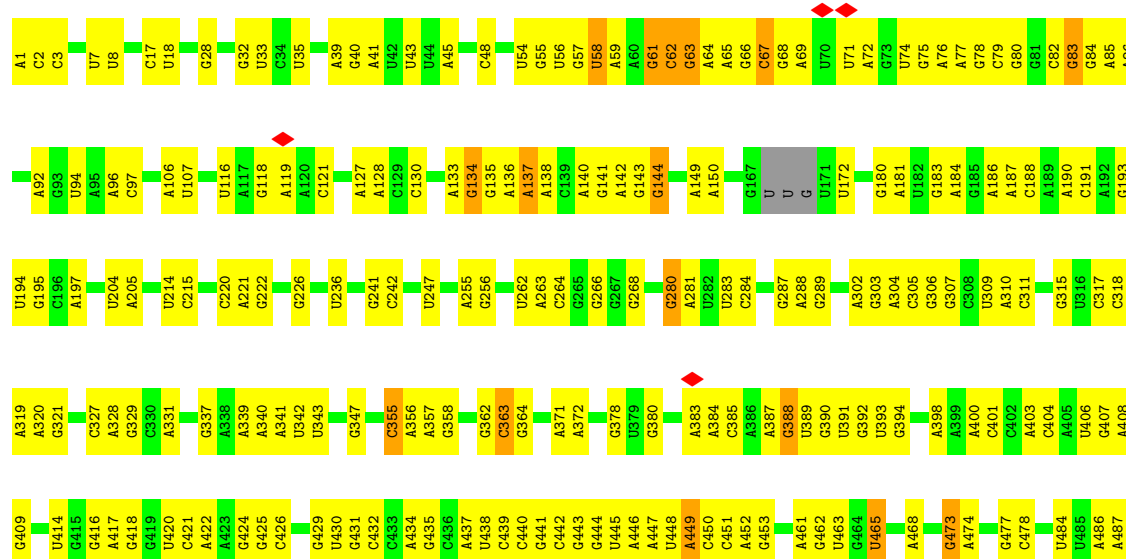
Chain S60: 56% 40%

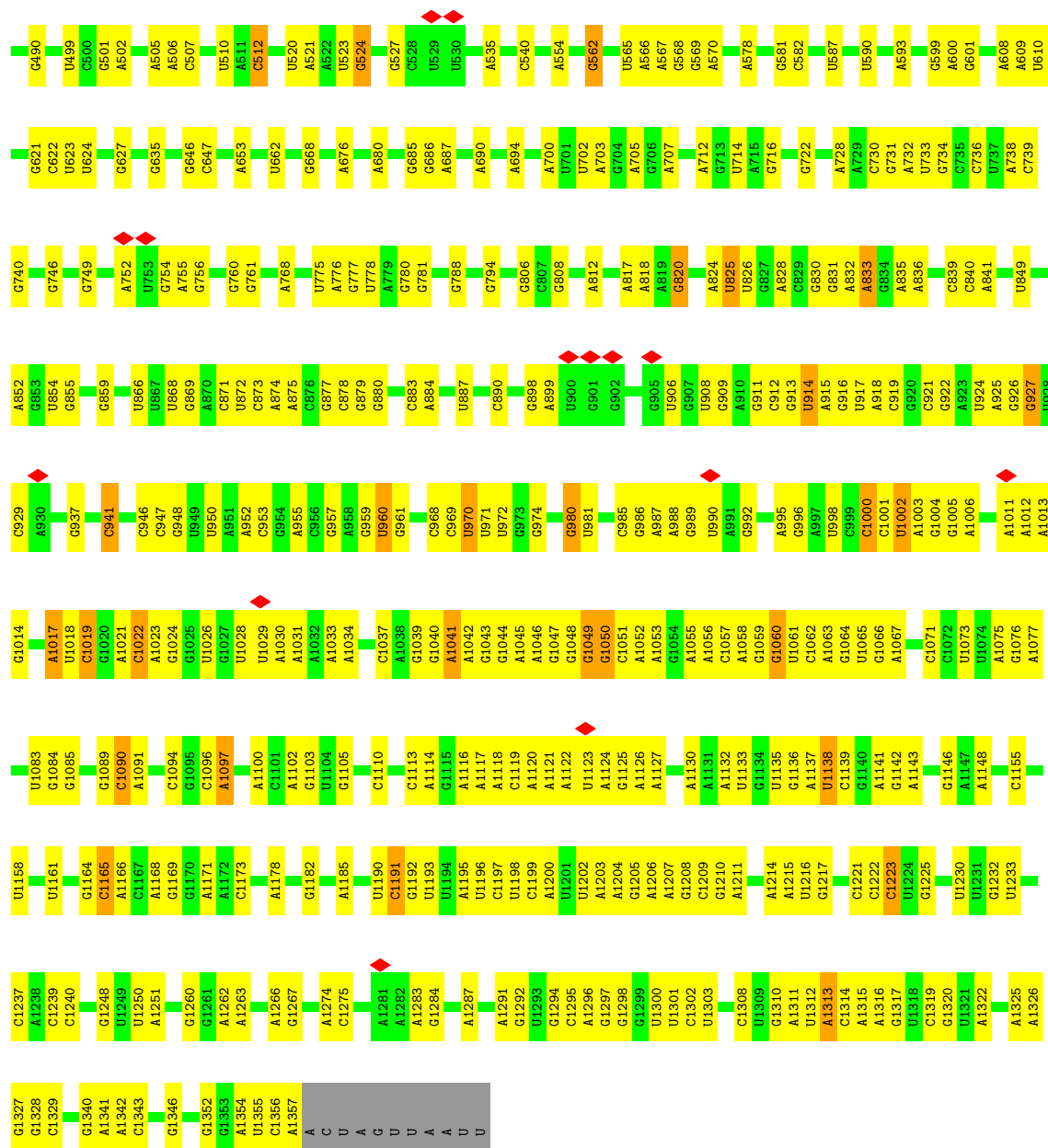




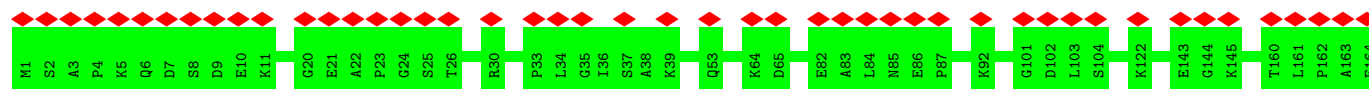
• Molecule 2: RNA 16S

Chain R60: 56% 40%

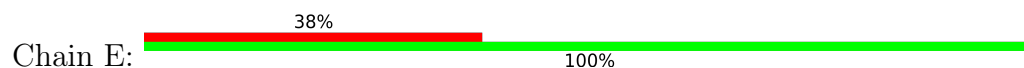


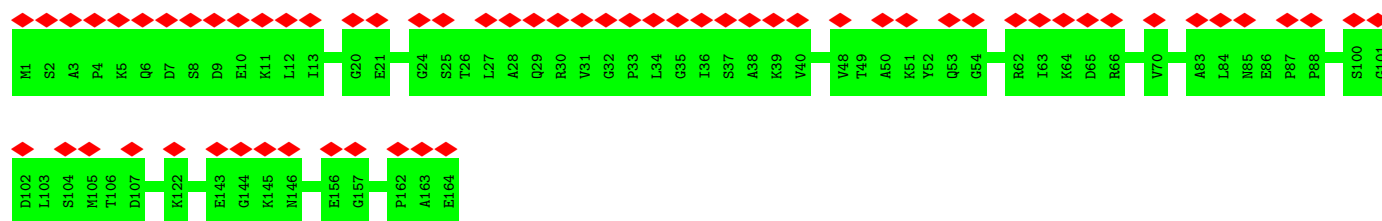


• Molecule 3: 60S ribosomal protein L12

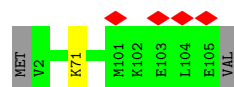


• Molecule 3: 60S ribosomal protein L12

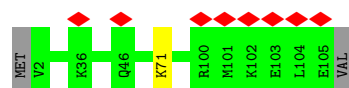




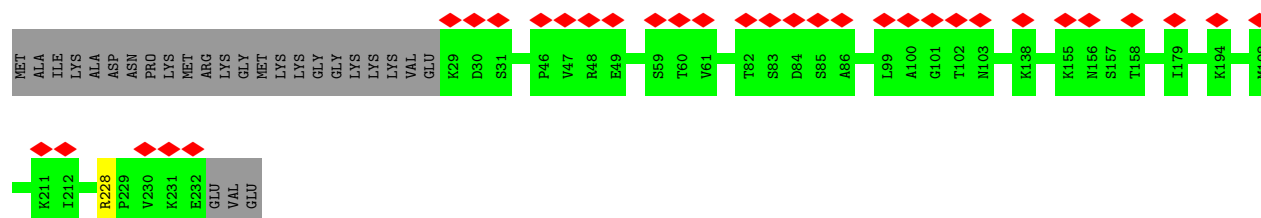
• Molecule 4: Ribosomal protein L34



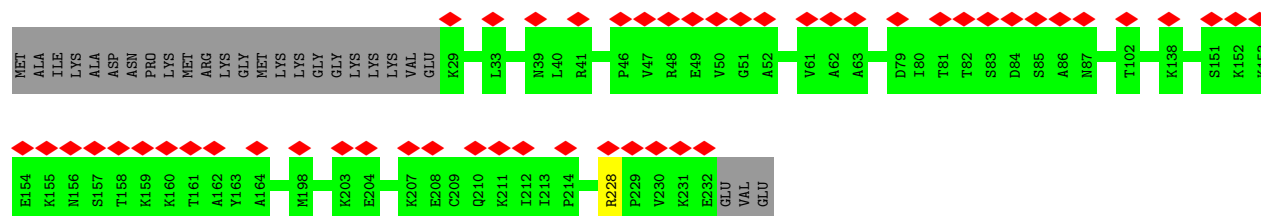
• Molecule 4: Ribosomal protein L34



• Molecule 5: 40S ribosomal protein S1

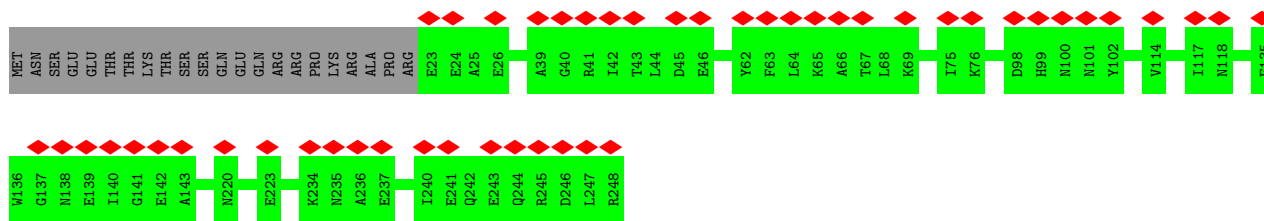


• Molecule 5: 40S ribosomal protein S1

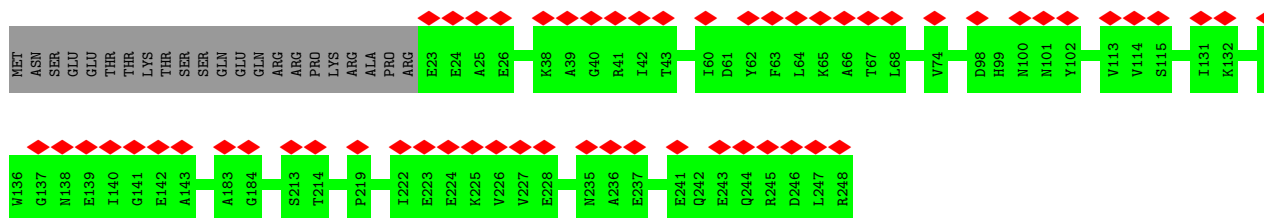


• Molecule 6: Small ribosomal subunit protein uS5

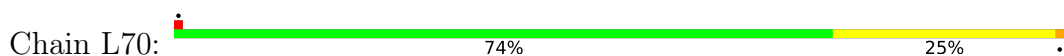




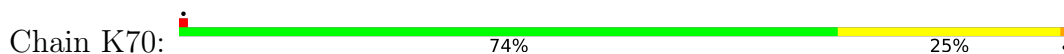
- Molecule 6: Small ribosomal subunit protein uS5



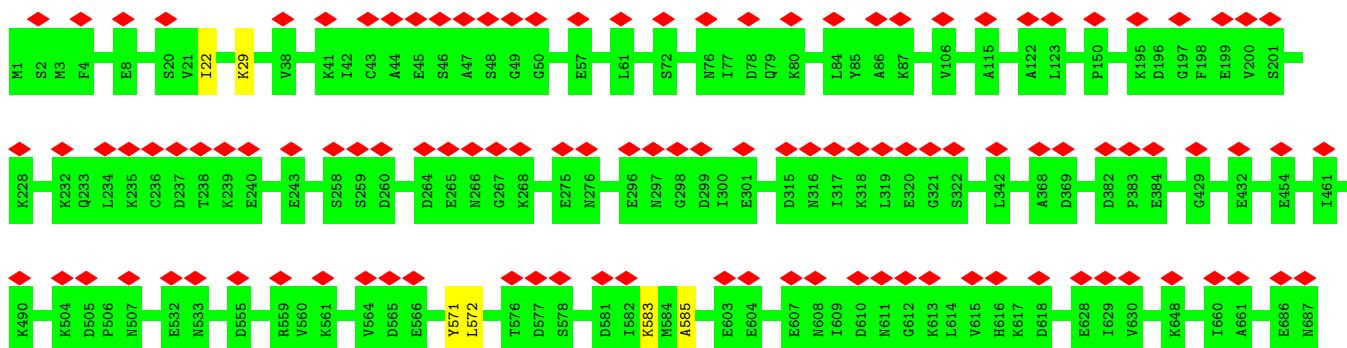
- Molecule 7: RNA 5S

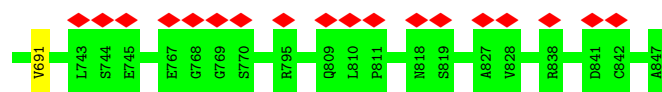


- Molecule 7: RNA 5S

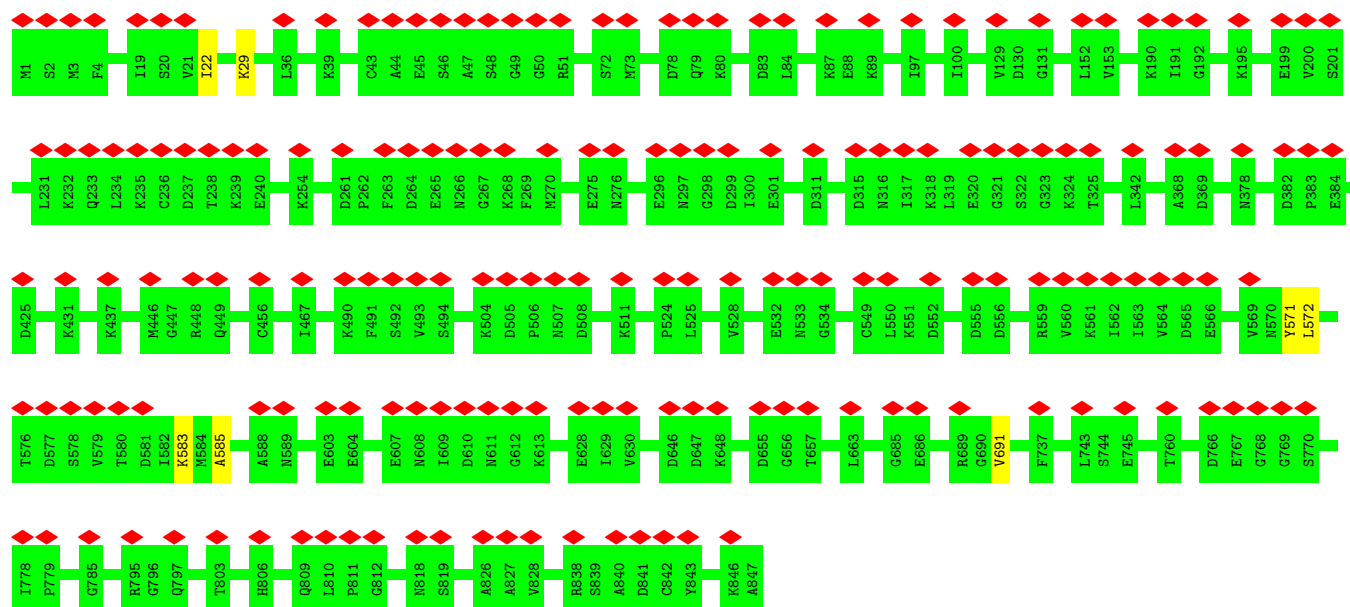


- Molecule 8: Elongation factor 2

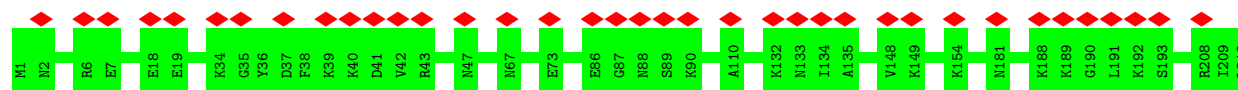




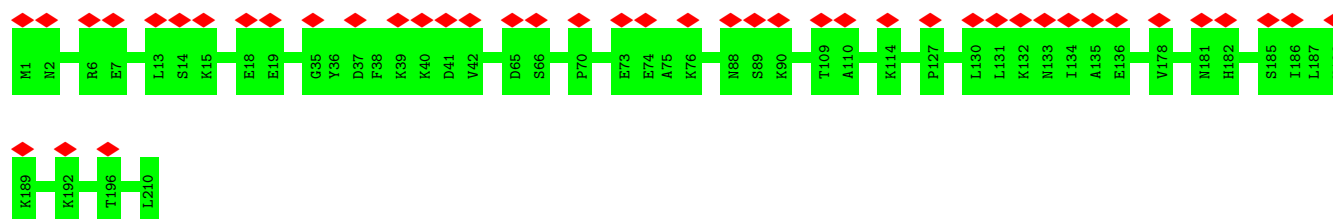
• Molecule 8: Elongation factor 2



• Molecule 9: 60S ribosomal protein L10a

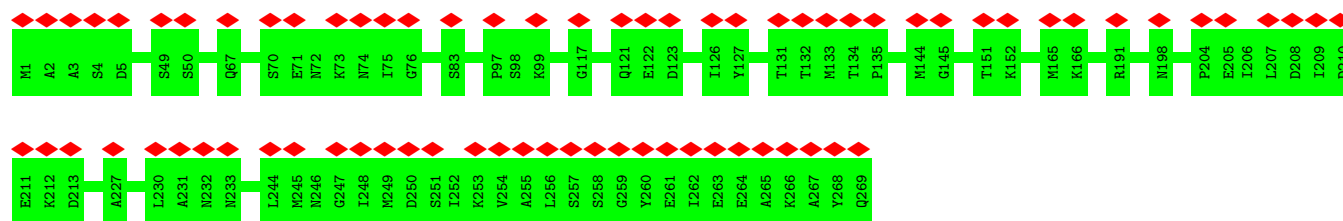


• Molecule 9: 60S ribosomal protein L10a

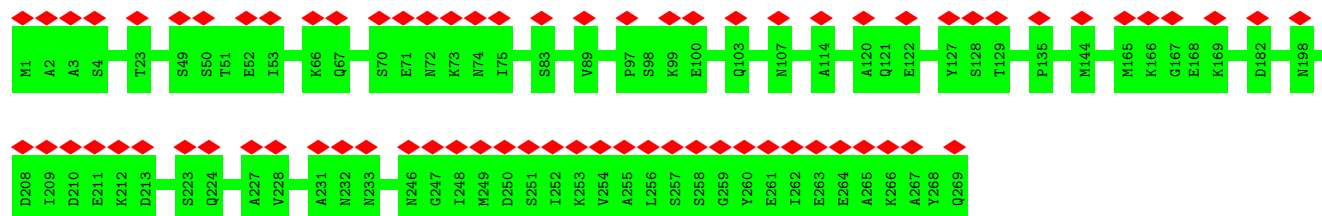


• Molecule 10: Large ribosomal subunit protein uL10

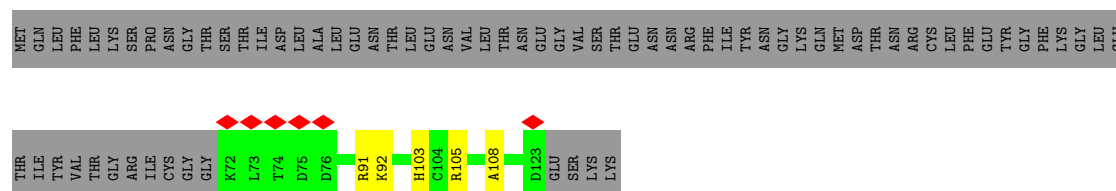




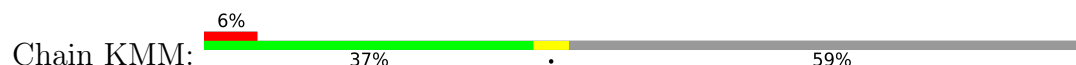
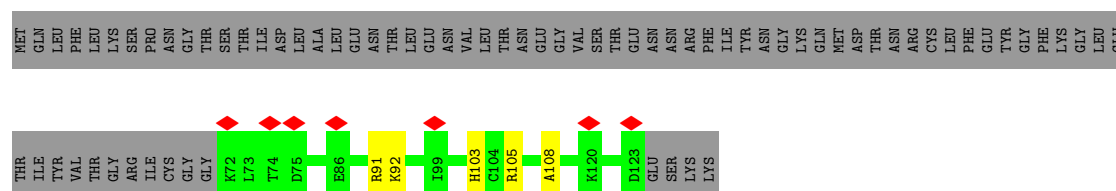
- Molecule 10: Large ribosomal subunit protein uL10



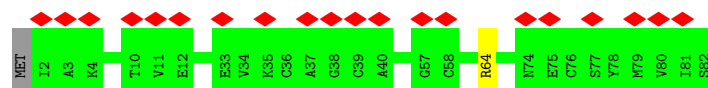
- Molecule 11: Ubiquitin



- Molecule 11: Ubiquitin

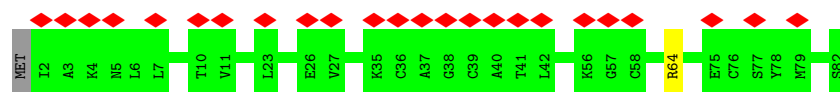


- Molecule 12: 40S ribosomal protein S27

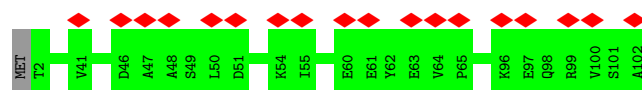


- Molecule 12: 40S ribosomal protein S27

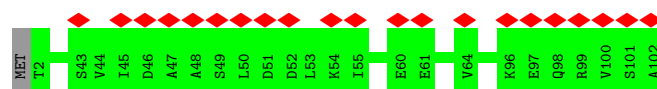




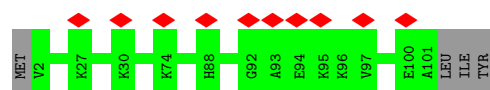
- Molecule 13: 40S ribosomal protein S26



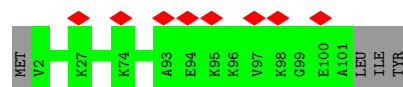
- Molecule 13: 40S ribosomal protein S26



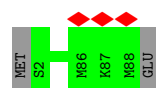
- Molecule 14: 60S ribosomal protein L44



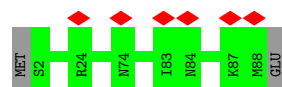
- Molecule 14: 60S ribosomal protein L44



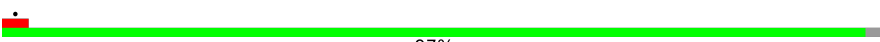
- Molecule 15: 60S ribosomal protein L37a

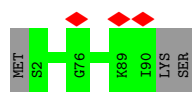


- Molecule 15: 60S ribosomal protein L37a

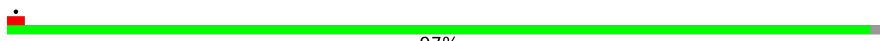


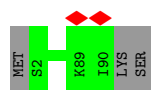
- Molecule 16: 60S ribosomal protein L37

Chain LJJ:  97%



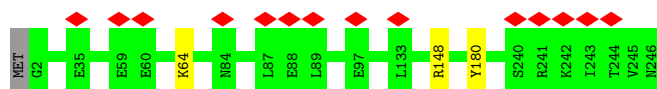
- Molecule 16: 60S ribosomal protein L37

Chain KJJ:  97%



- Molecule 17: 60S ribosomal protein L8

Chain LA0:  98%



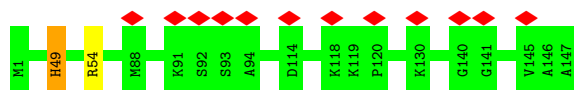
- Molecule 17: 60S ribosomal protein L8

Chain LA02:  98%



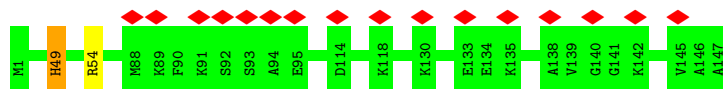
- Molecule 18: 60S ribosomal protein L15

Chain LAA:  99%



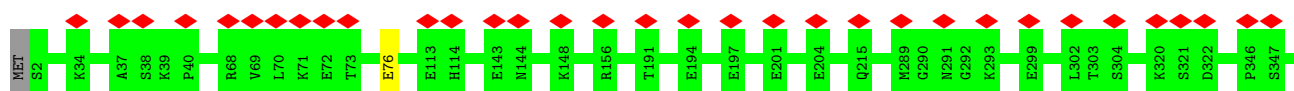
- Molecule 18: 60S ribosomal protein L15

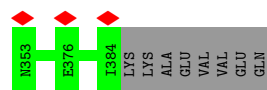
Chain KAA:  99%



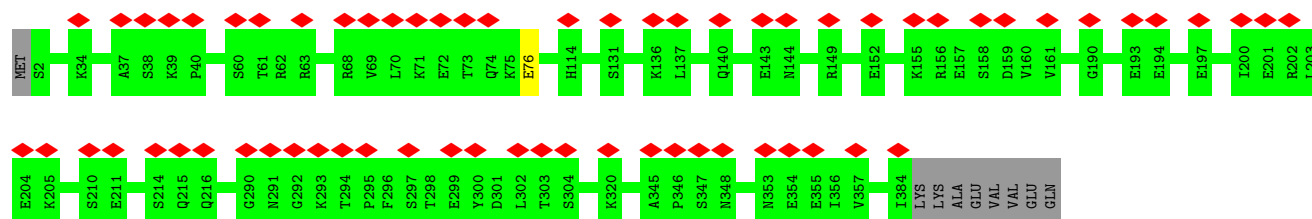
- Molecule 19: 60S ribosomal protein L3

Chain LB0:  97%

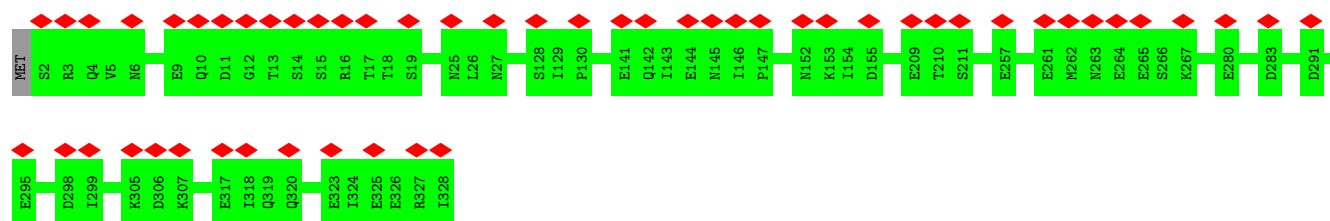




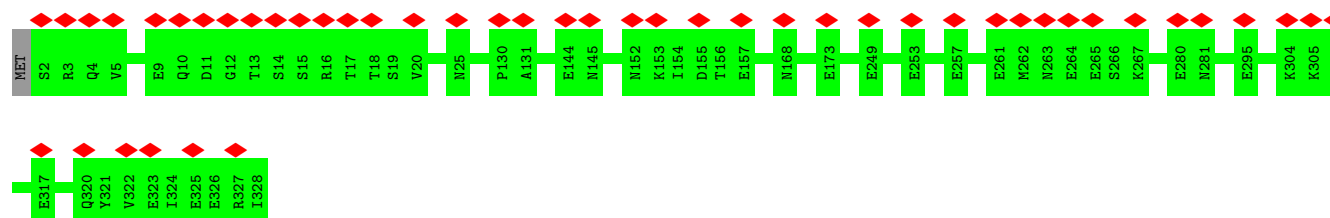
- Molecule 19: 60S ribosomal protein L3



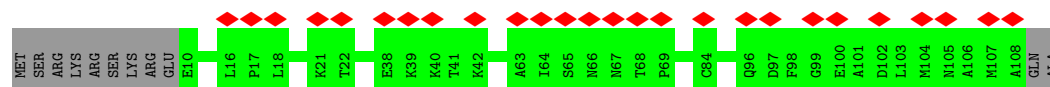
- Molecule 20: Large ribosomal subunit protein uL4



- Molecule 20: Large ribosomal subunit protein uL4

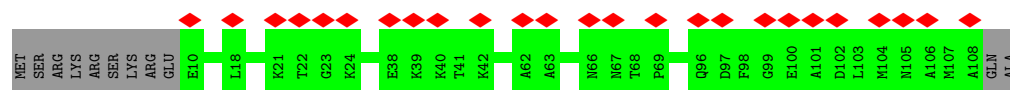


- Molecule 21: 60S ribosomal protein L3

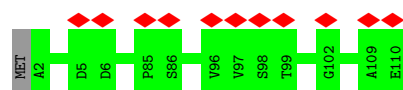


- Molecule 21: 60S ribosomal protein L3

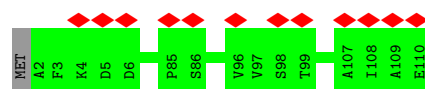




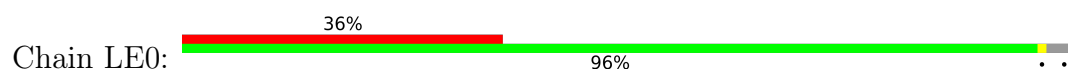
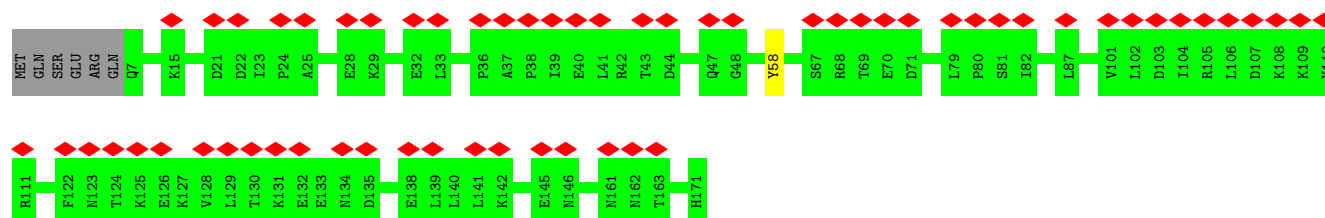
- Molecule 22: 60S ribosomal protein L31



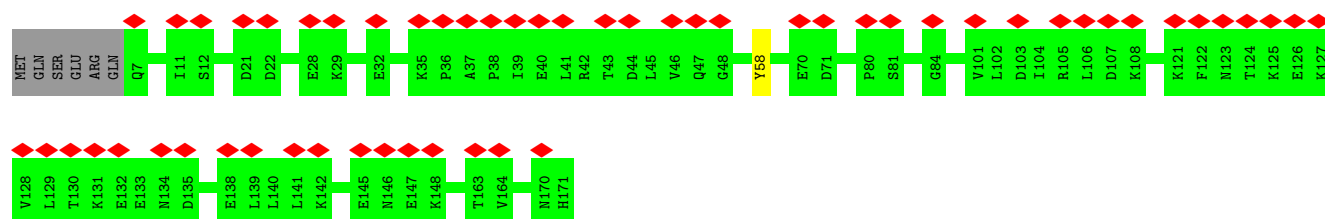
- Molecule 22: 60S ribosomal protein L31



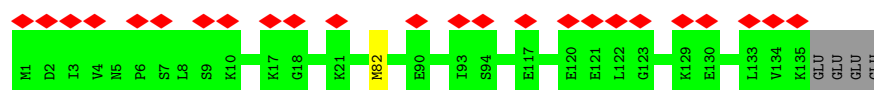
- Molecule 23: 60S ribosomal protein L6



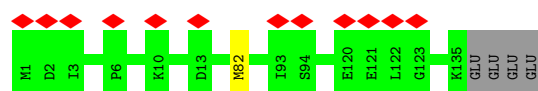
- Molecule 23: 60S ribosomal protein L6



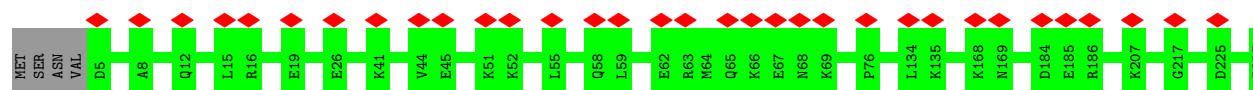
- Molecule 24: Large ribosomal subunit protein eL32



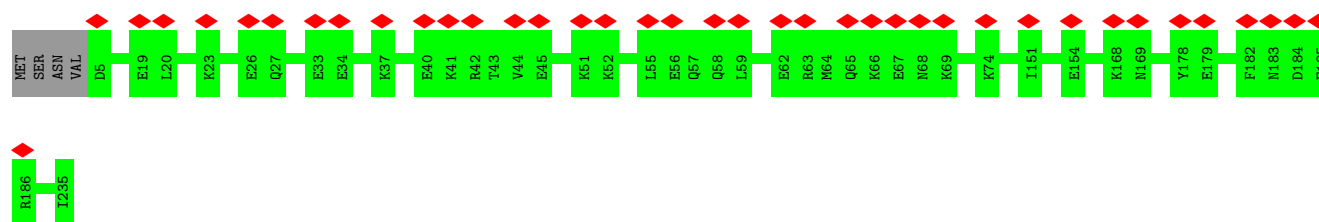
- Molecule 24: Large ribosomal subunit protein eL32



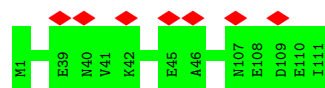
- Molecule 25: 60S ribosomal protein L7



- Molecule 25: 60S ribosomal protein L7



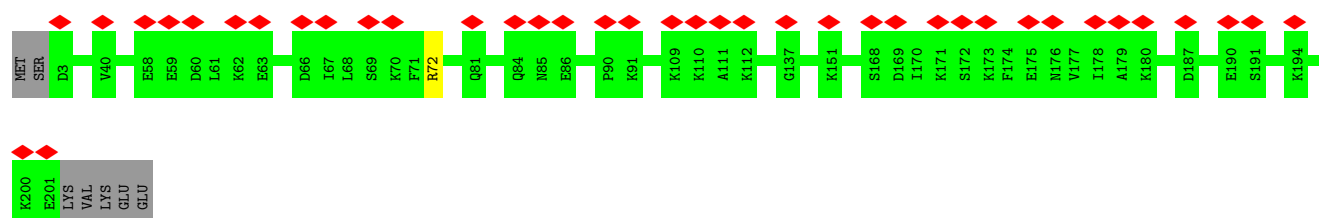
- Molecule 26: 60S ribosomal protein L35a



- Molecule 26: 60S ribosomal protein L35a



- Molecule 27: 60S ribosomal protein L8



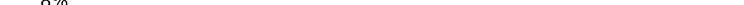
- Chain KG0: 

- Chain LH0: 

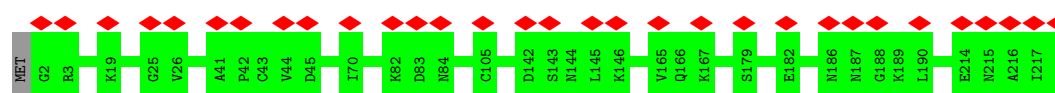
- Chain KH0: 

- Chain LHH: 

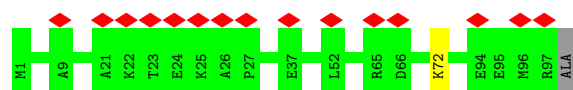
- Chain KHH: 
- 

- Chain LI0: 
- 
- | Category | Value |
|----------|-------|
| NET | 100% |
| G2 | 100% |
| D23 | 100% |
| V44 | 100% |
| M79 | 100% |
| D83 | 100% |
| M84 | 100% |
| K141 | 100% |
| D142 | 100% |
| S143 | 100% |
| K167 | 100% |
| M186 | 100% |
| M187 | 100% |
| G188 | 100% |
| E207 | 100% |
| V210 | 100% |
| K211 | 100% |
| E214 | 100% |
| G218 | 100% |

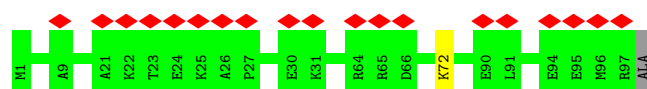
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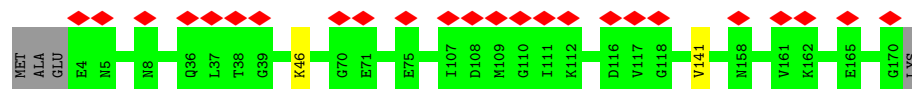
- Molecule 31: 60S ribosomal protein L36



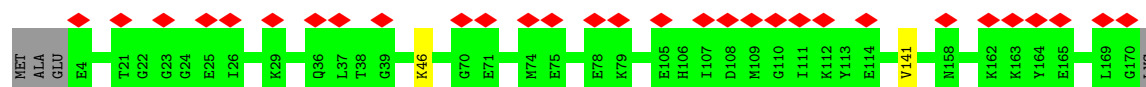
- Molecule 31: 60S ribosomal protein L36



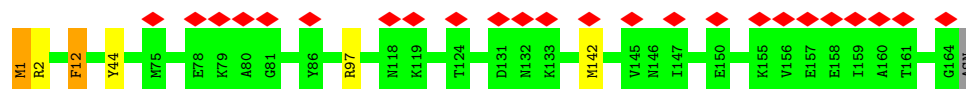
- Molecule 32: 60S ribosomal protein L11



- Molecule 32: 60S ribosomal protein L11



- Molecule 33: 60S ribosomal protein L13



- Molecule 33: 60S ribosomal protein L13

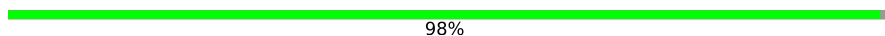


- Molecule 34: 60S ribosomal protein L39

Chain LLL:  98%

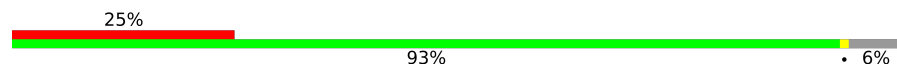


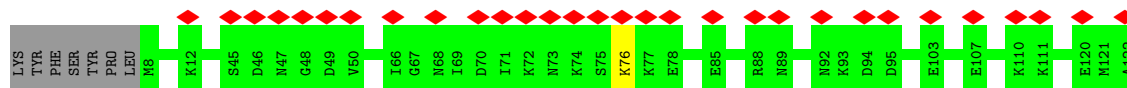
- Molecule 34: 60S ribosomal protein L39

Chain KLL:  98%

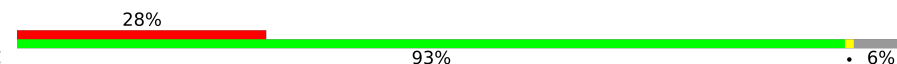


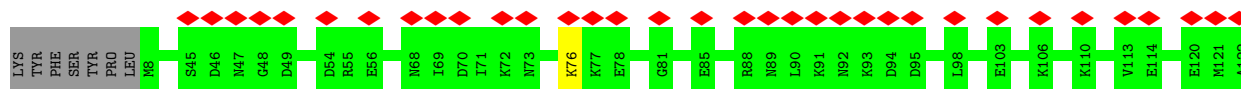
- Molecule 35: 60S ribosomal protein L14

Chain LM0:  25% 93% 6%

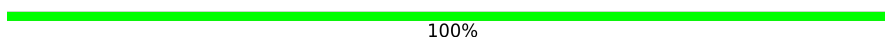


- Molecule 35: 60S ribosomal protein L14

Chain KM0:  28% 93% 6%

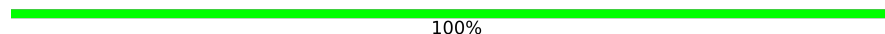


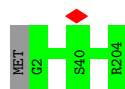
- Molecule 36: Ribosomal protein L15

Chain LN0:  100%

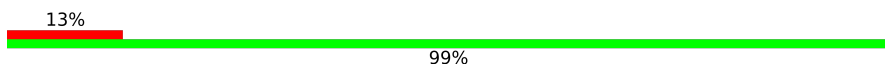


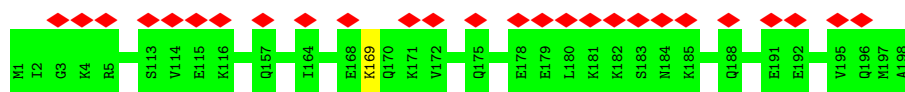
- Molecule 36: Ribosomal protein L15

Chain KN0:  100%

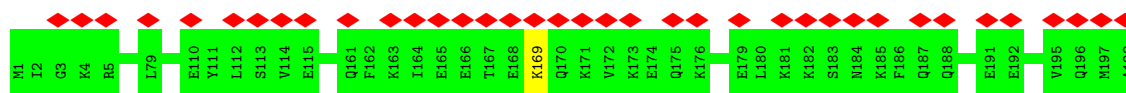


- Molecule 37: Ribosomal protein L13A

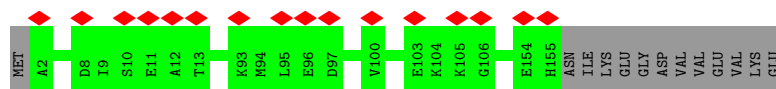
Chain LO0:  13% 99%



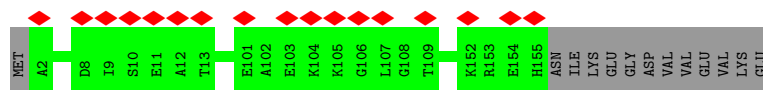
- Molecule 37: Ribosomal protein L13A



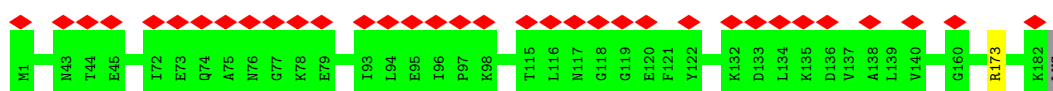
- Molecule 38: 60S ribosomal protein L17



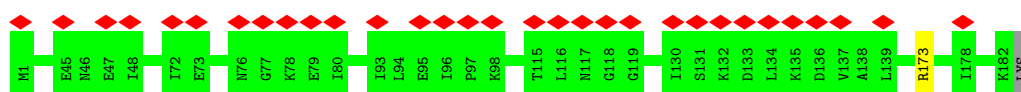
- Molecule 38: 60S ribosomal protein L17



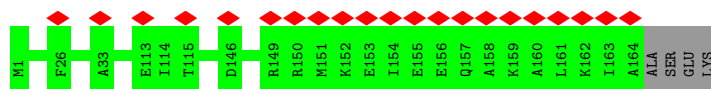
- Molecule 39: 60S ribosomal protein L18



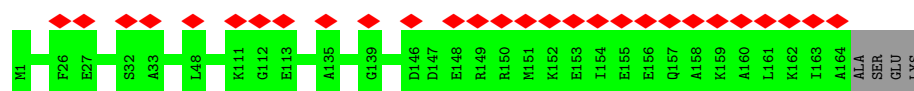
- Molecule 39: 60S ribosomal protein L18



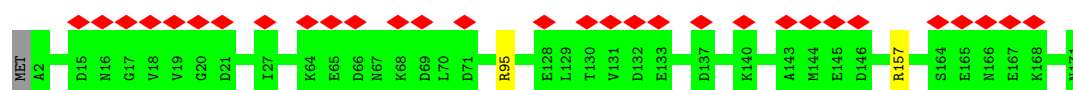
- Molecule 40: 60S ribosomal protein L19



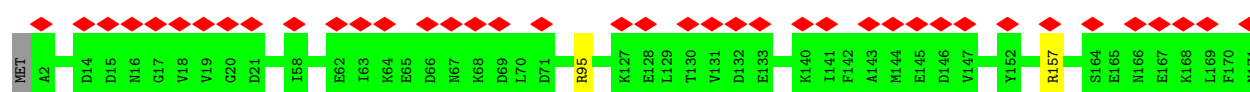
- Molecule 40: 60S ribosomal protein L19



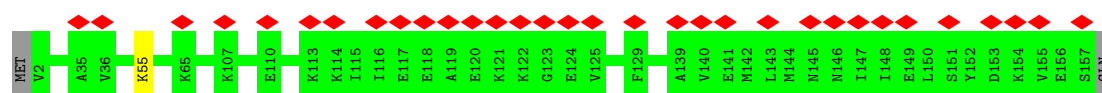
- Molecule 41: 60S ribosomal protein L20



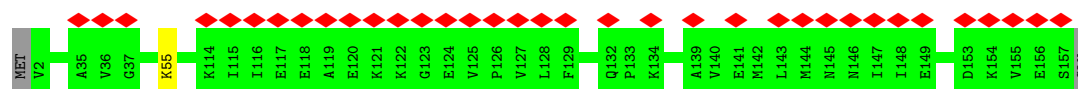
- Molecule 41: 60S ribosomal protein L20



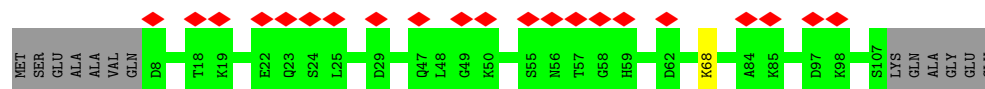
- Molecule 42: 60s ribosomal protein L21



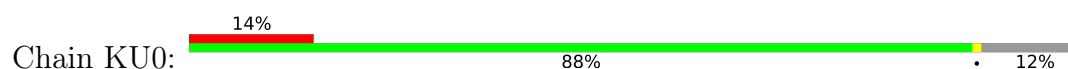
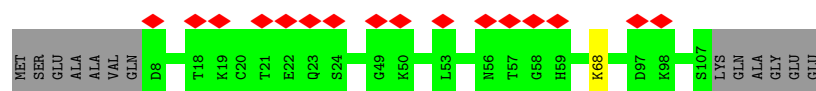
- Molecule 42: 60s ribosomal protein L21



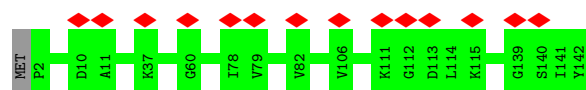
- Molecule 43: Large ribosomal subunit protein eL22



- Molecule 43: Large ribosomal subunit protein eL22



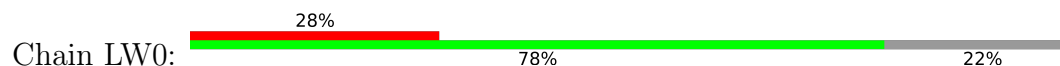
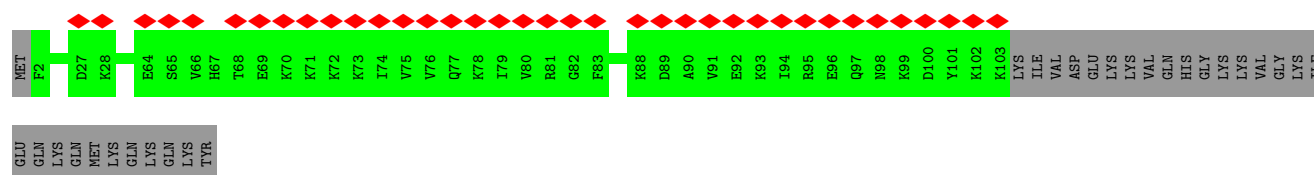
• Molecule 44: Ribosomal protein L23



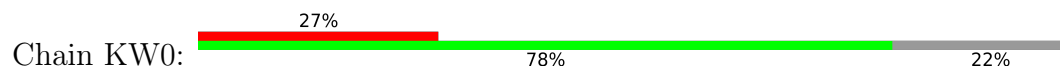
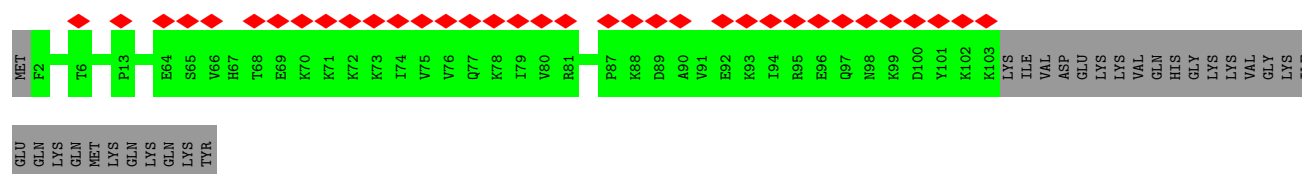
• Molecule 44: Ribosomal protein L23



• Molecule 45: Ribosomal protein L24E



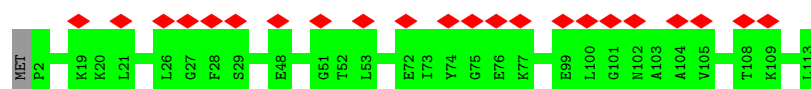
• Molecule 45: Ribosomal protein L24E



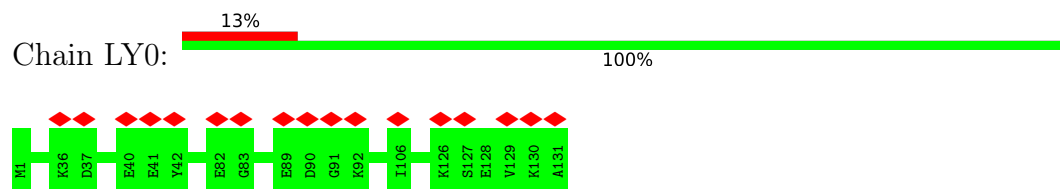
• Molecule 46: 60S ribosomal protein L23a



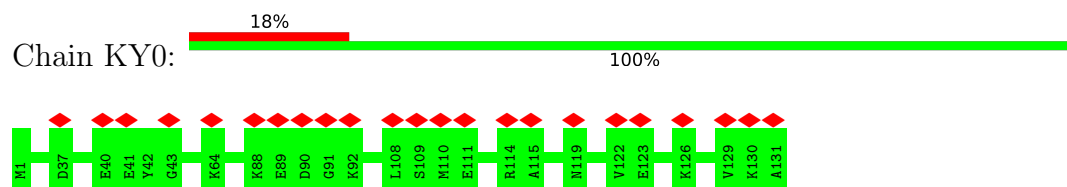
• Molecule 46: 60S ribosomal protein L23a



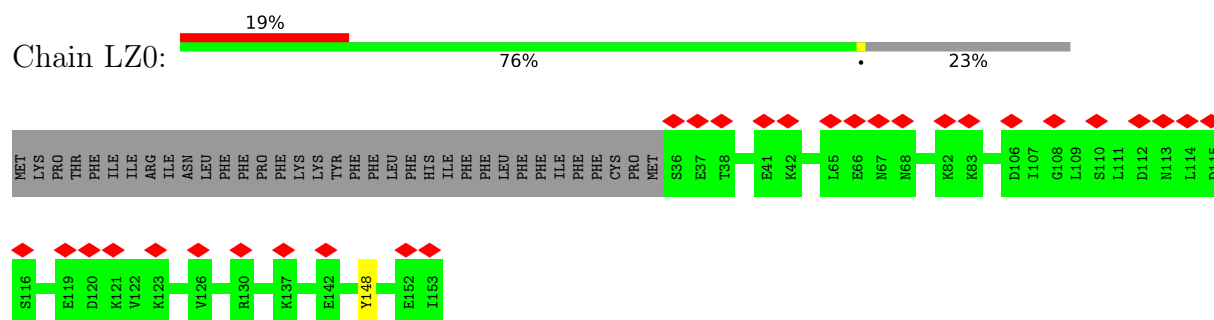
- Molecule 47: 60S ribosomal protein L26



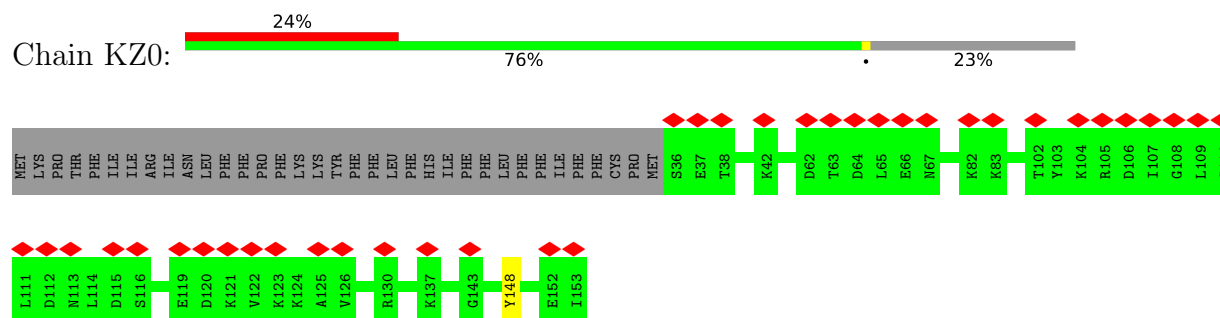
- Molecule 47: 60S ribosomal protein L26



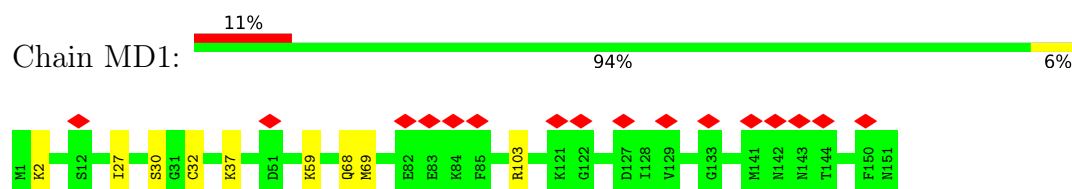
- Molecule 48: 60S ribosomal protein L27



- Molecule 48: 60S ribosomal protein L27



- Molecule 49: DNL-type domain-containing protein MD1

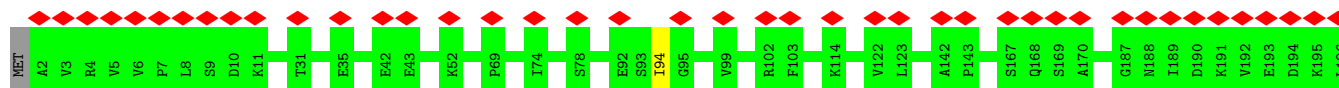
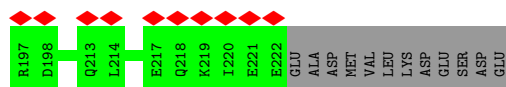


- Molecule 49: DNL-type domain-containing protein MD1

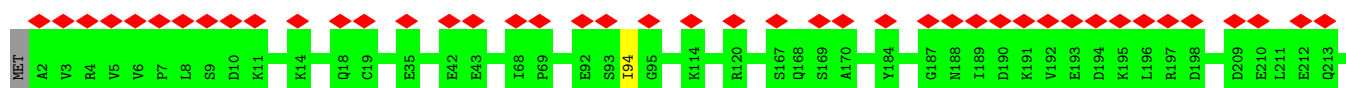
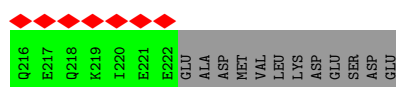




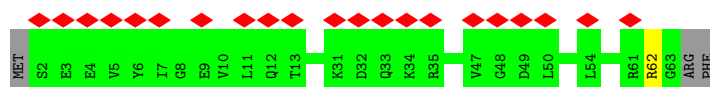
- Molecule 50: Small ribosomal subunit protein uS2



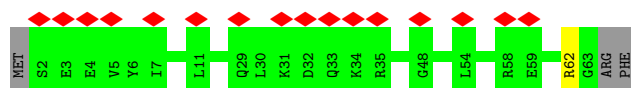
- Molecule 50: Small ribosomal subunit protein uS2



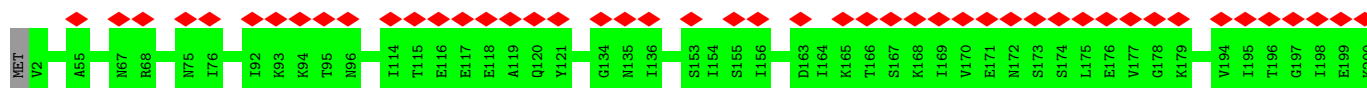
- Molecule 51: 40S ribosomal protein S28

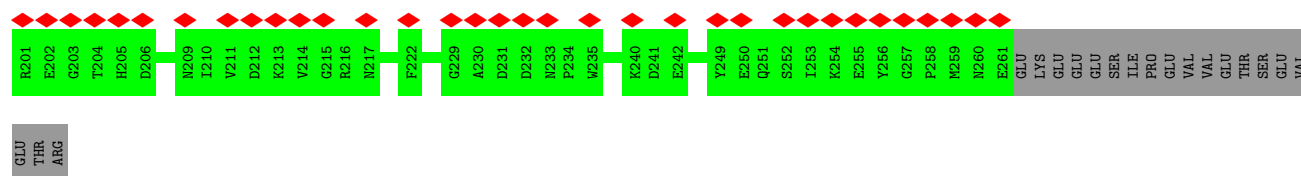


- Molecule 51: 40S ribosomal protein S28

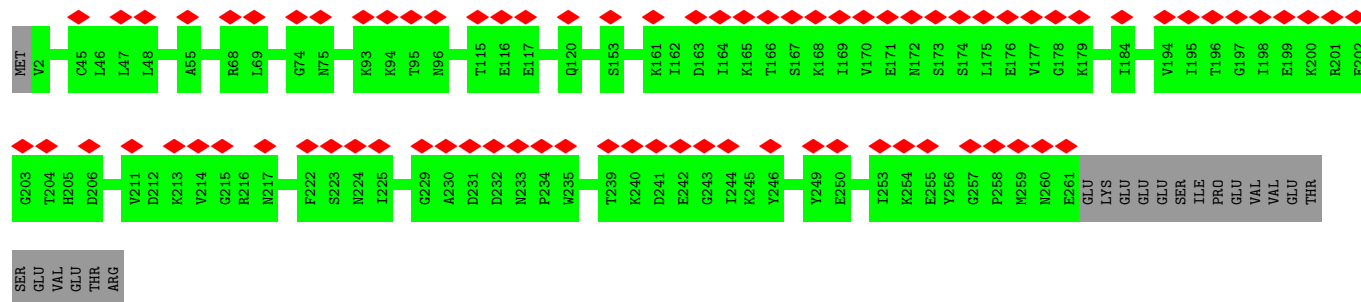


- Molecule 52: 40S ribosomal protein S4

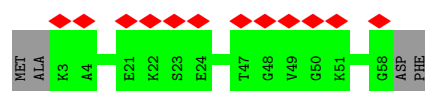




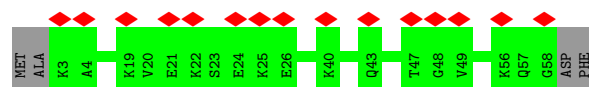
• Molecule 52: 40S ribosomal protein S4



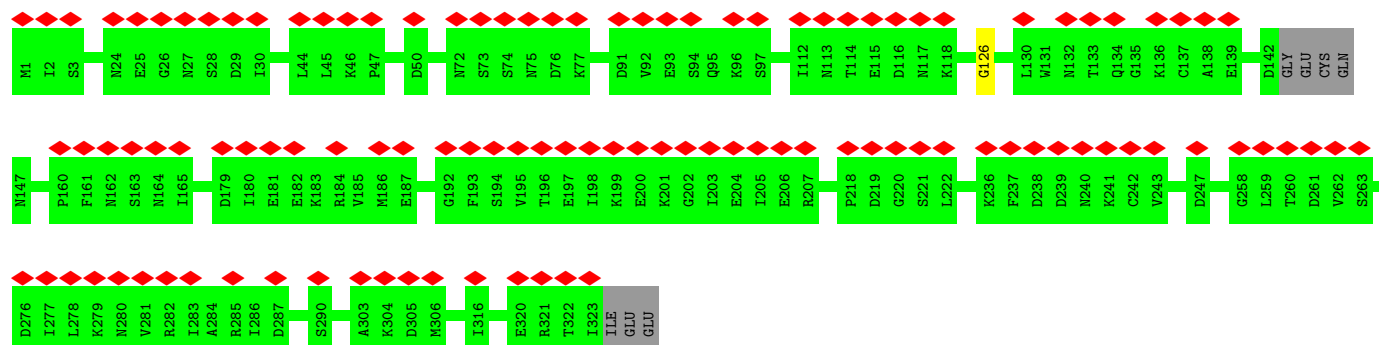
• Molecule 53: 40S ribosomal protein S30



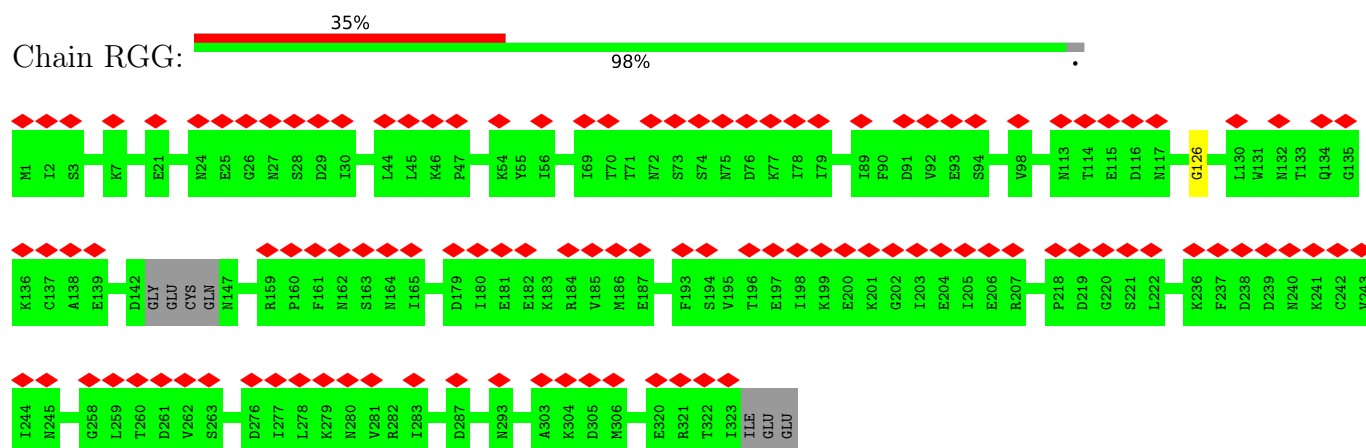
• Molecule 53: 40S ribosomal protein S30



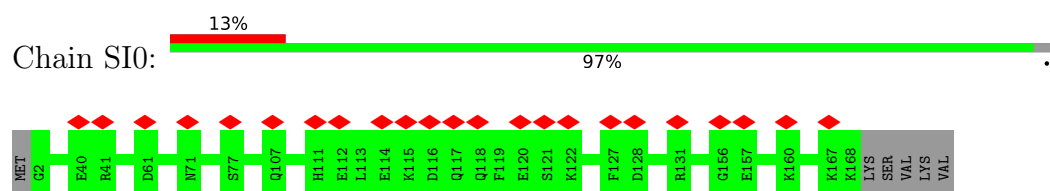
• Molecule 54: Guanine nucleotide binding protein beta subunit



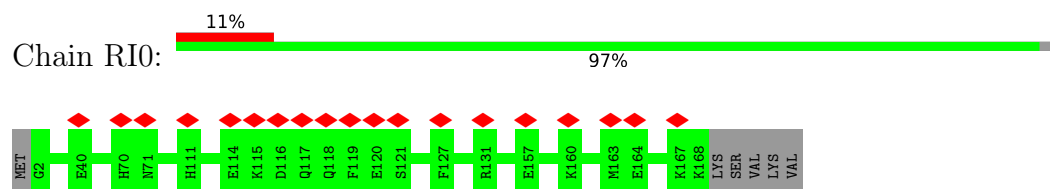
- Molecule 54: Guanine nucleotide binding protein beta subunit



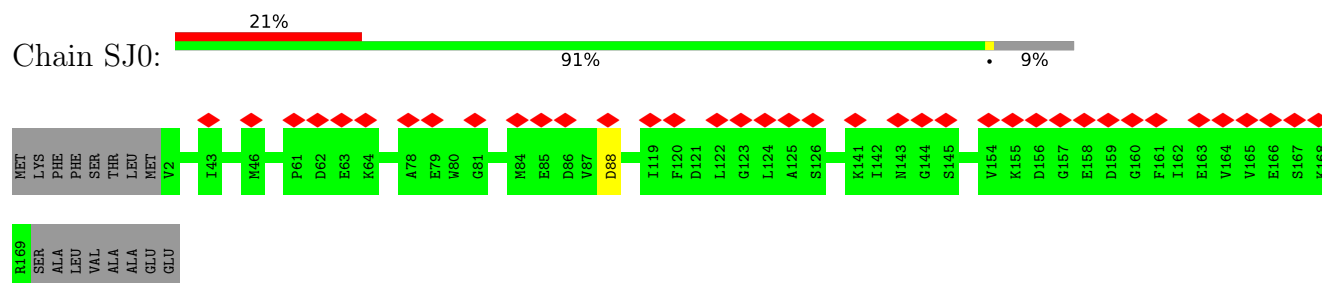
- Molecule 55: 40S ribosomal protein S8



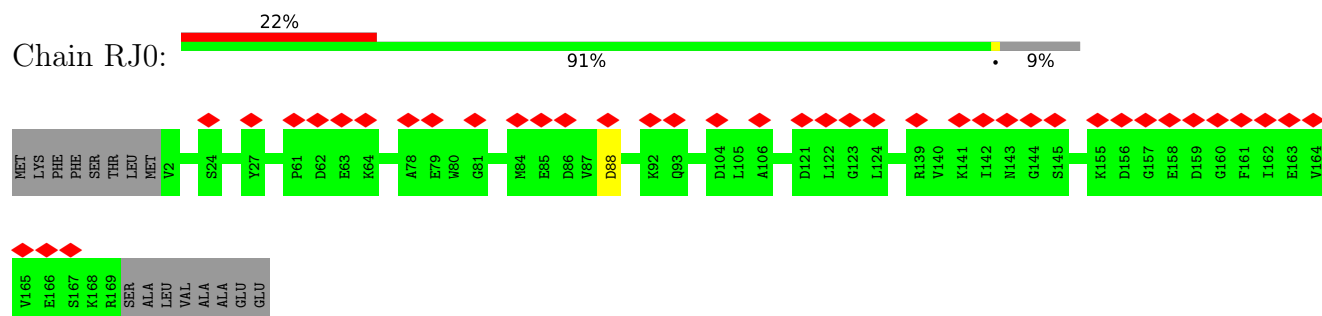
- Molecule 55: 40S ribosomal protein S8



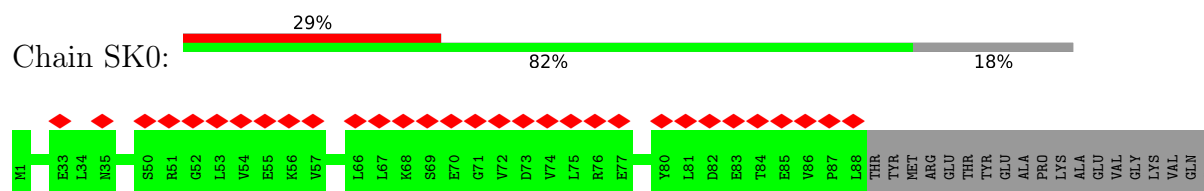
- Molecule 56: 40S ribosomal protein S9



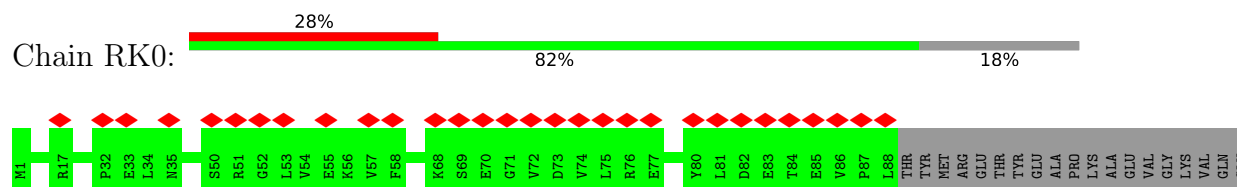
- Molecule 56: 40S ribosomal protein S9



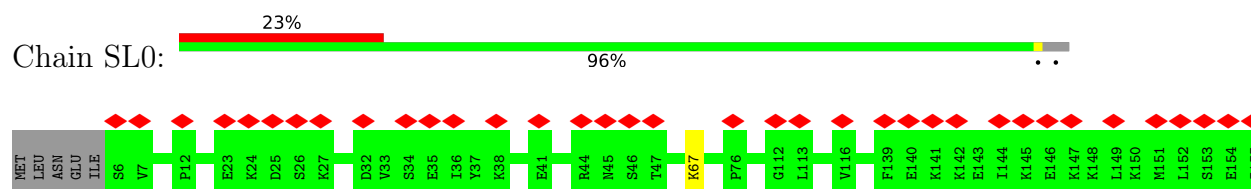
- Molecule 57: 40S ribosomal protein S10



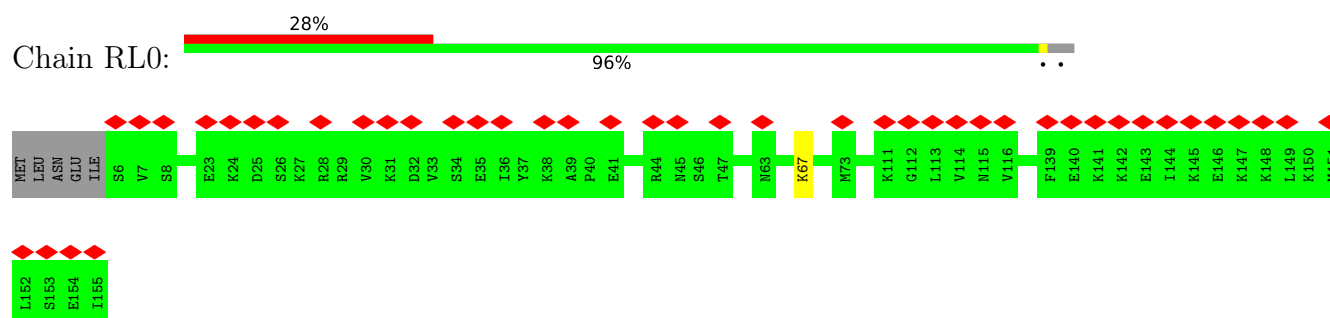
- Molecule 57: 40S ribosomal protein S10



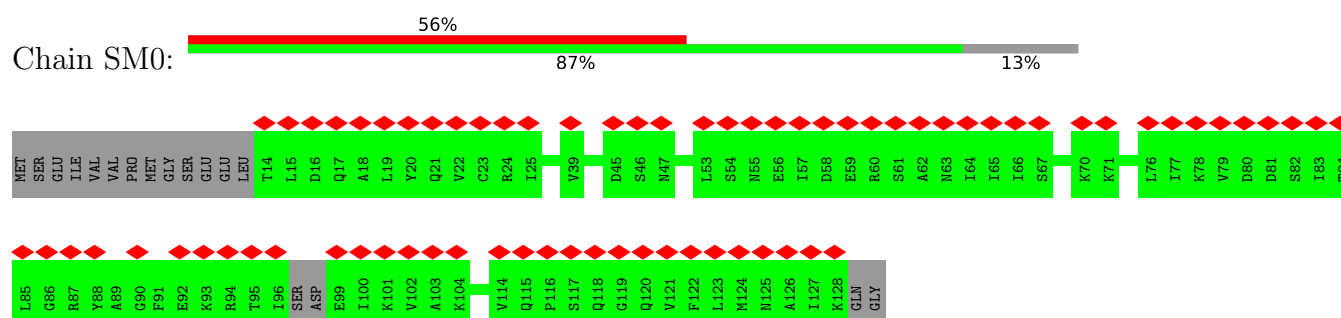
- Molecule 58: Small ribosomal subunit protein uS17



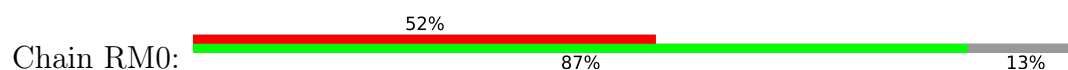
- Molecule 58: Small ribosomal subunit protein uS17

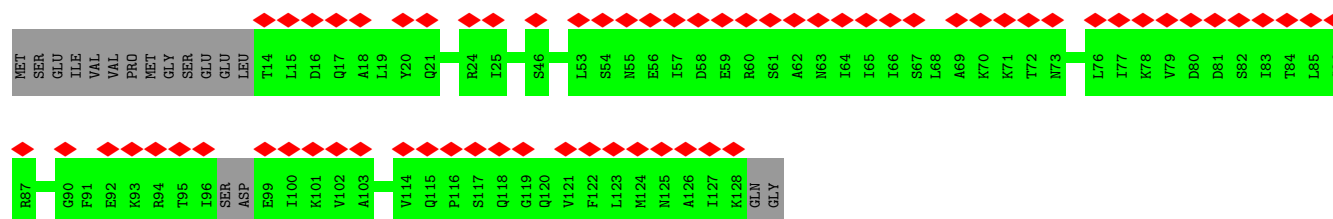


- Molecule 59: 40S ribosomal protein S12

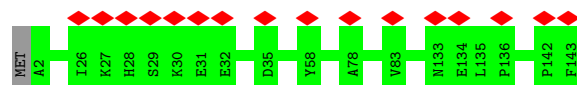


- Molecule 59: 40S ribosomal protein S12

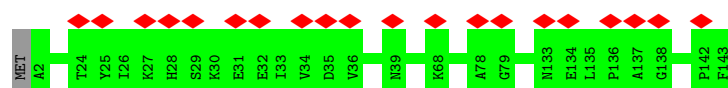




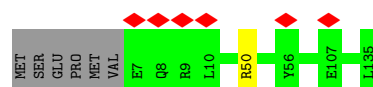
- Molecule 60: 40S ribosomal protein S13



- Molecule 60: 40S ribosomal protein S13



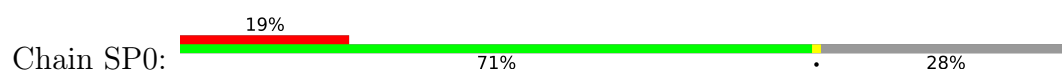
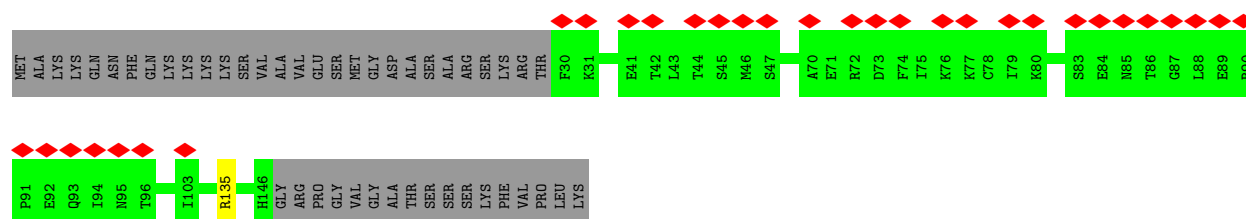
- Molecule 61: Small ribosomal subunit protein uS11



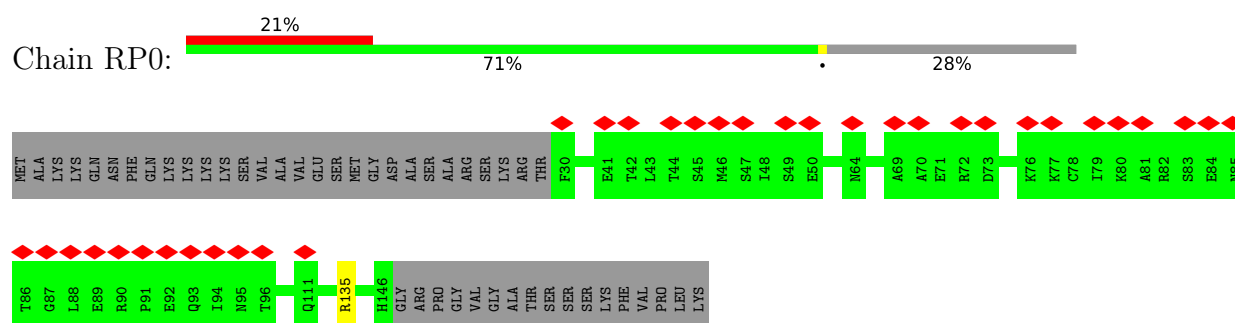
- Molecule 61: Small ribosomal subunit protein uS11



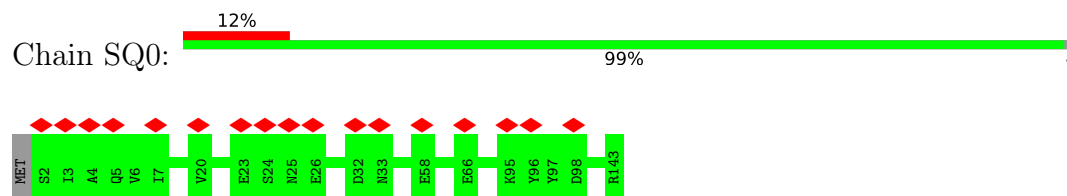
- Molecule 62: Ribosomal protein S19



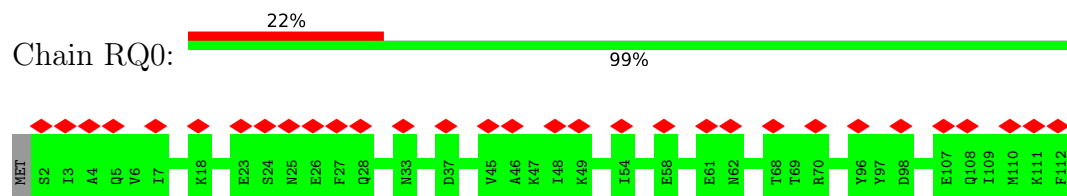
- Molecule 62: Ribosomal protein S19



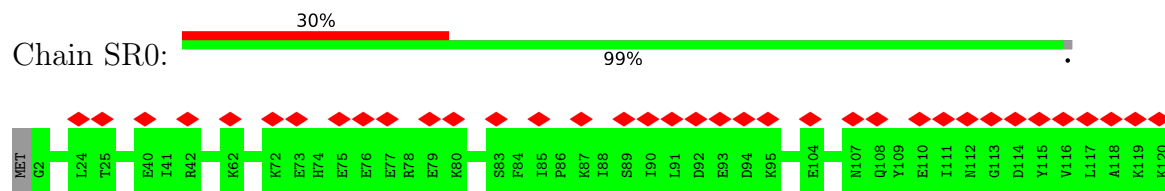
- Molecule 63: 40S ribosomal protein S16



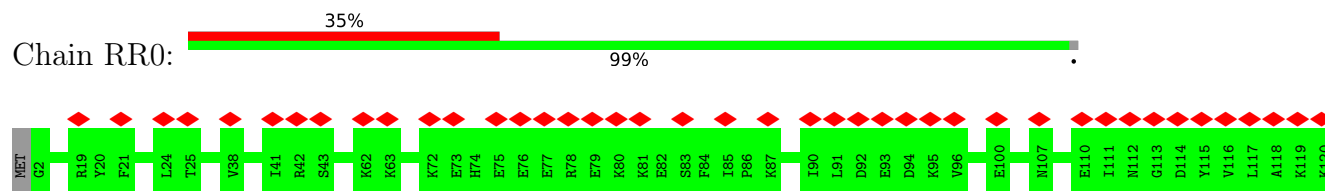
- Molecule 63: 40S ribosomal protein S16



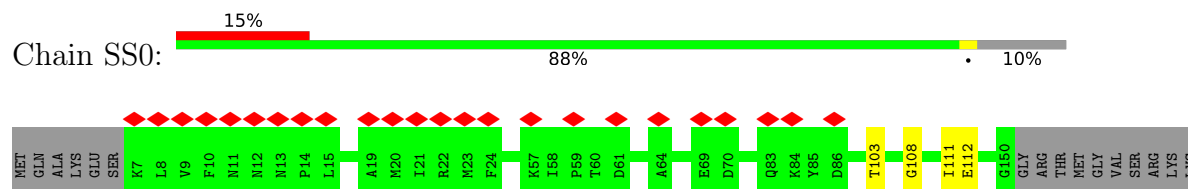
- Molecule 64: 40S ribosomal protein S17



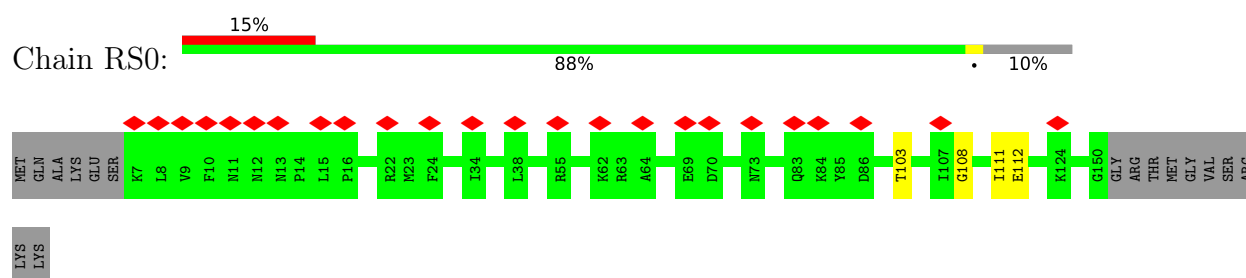
- Molecule 64: 40S ribosomal protein S17



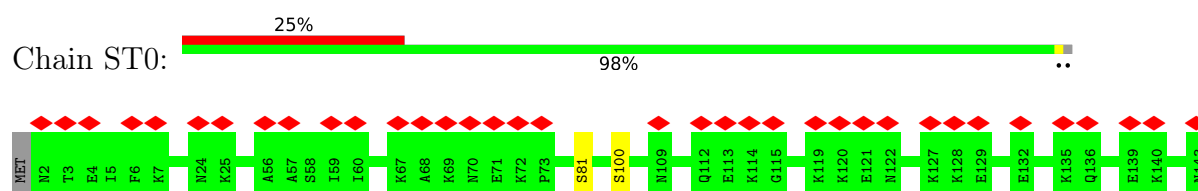
- Molecule 65: 40S ribosomal protein S18



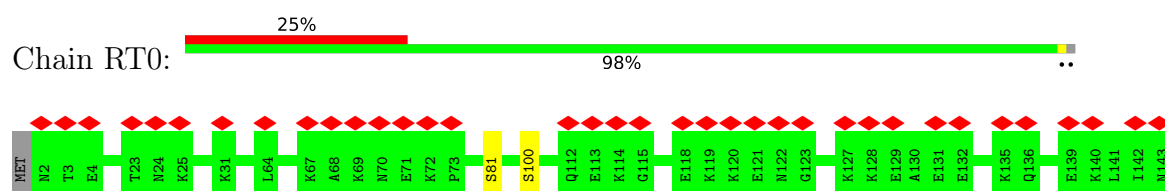
- Molecule 65: 40S ribosomal protein S18



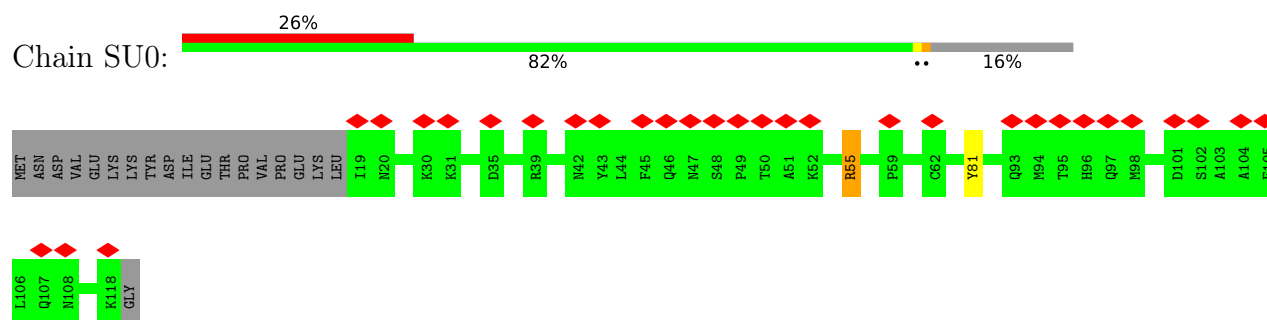
- Molecule 66: 40S Ribosomal protein S19



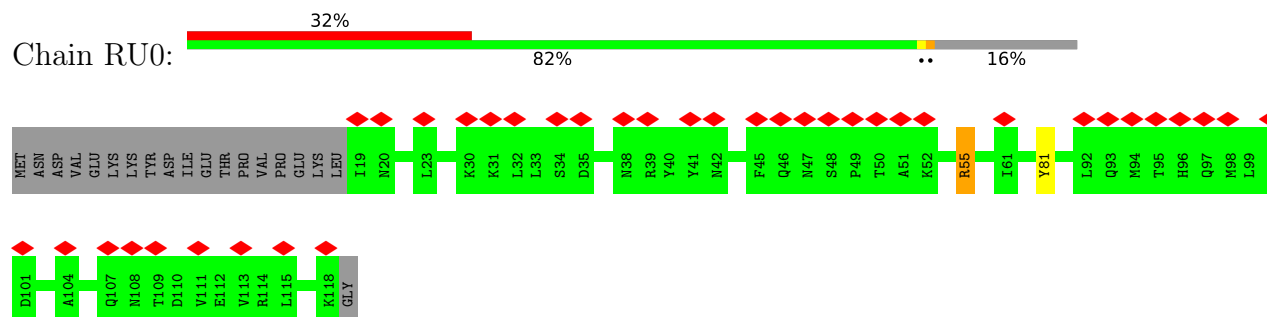
- Molecule 66: 40S Ribosomal protein S19



- Molecule 67: 40S ribosomal protein S20

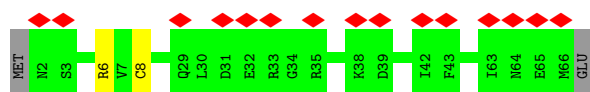


- Molecule 67: 40S ribosomal protein S20



- Molecule 68: Ribosomal protein S21E

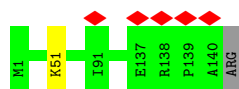




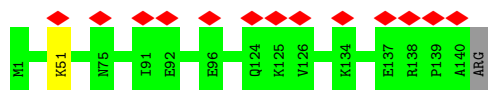
- Molecule 68: Ribosomal protein S21E



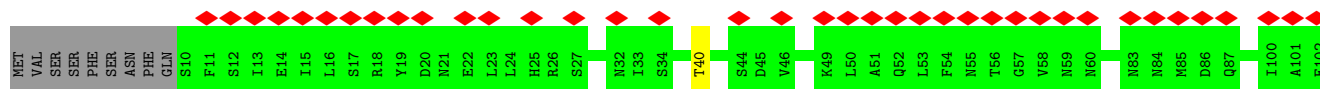
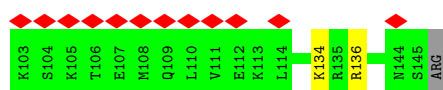
- Molecule 69: 40S ribosomal protein uS12



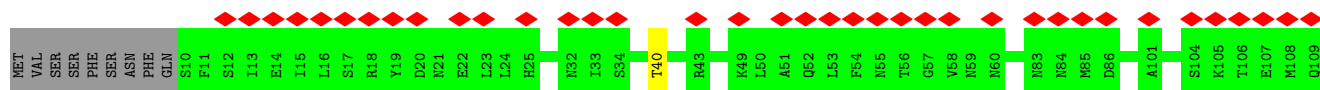
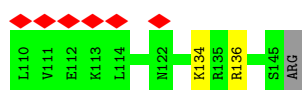
- Molecule 69: 40S ribosomal protein uS12



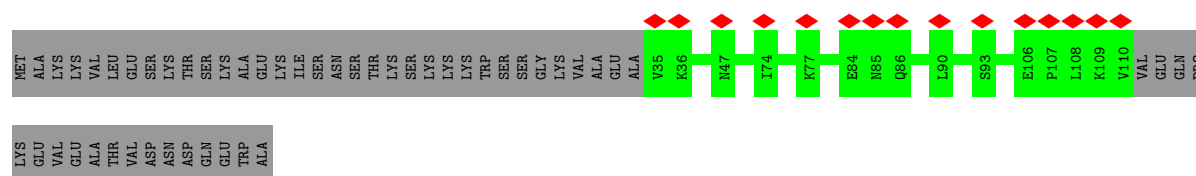
- Molecule 70: 40s ribosomal protein s24



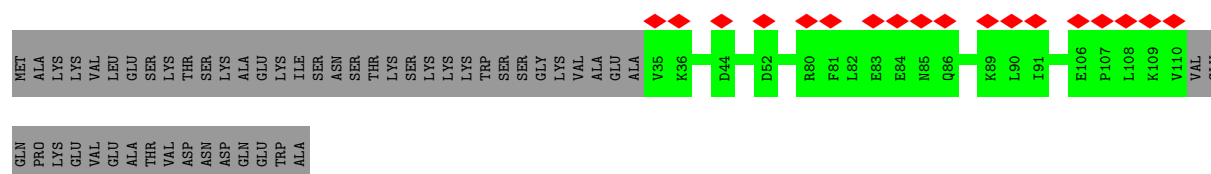
- Molecule 70: 40s ribosomal protein s24



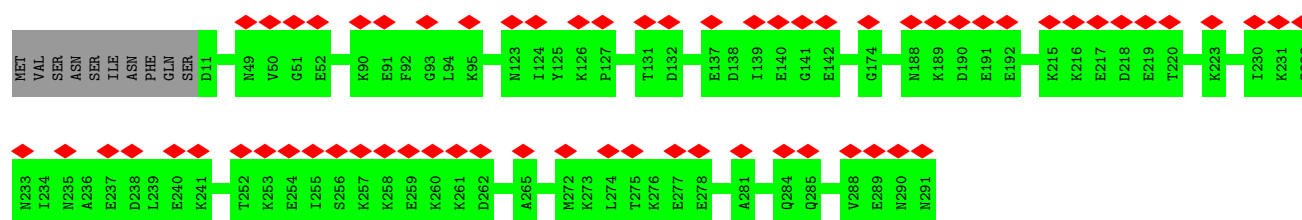
- Molecule 71: 40S ribosomal protein S25



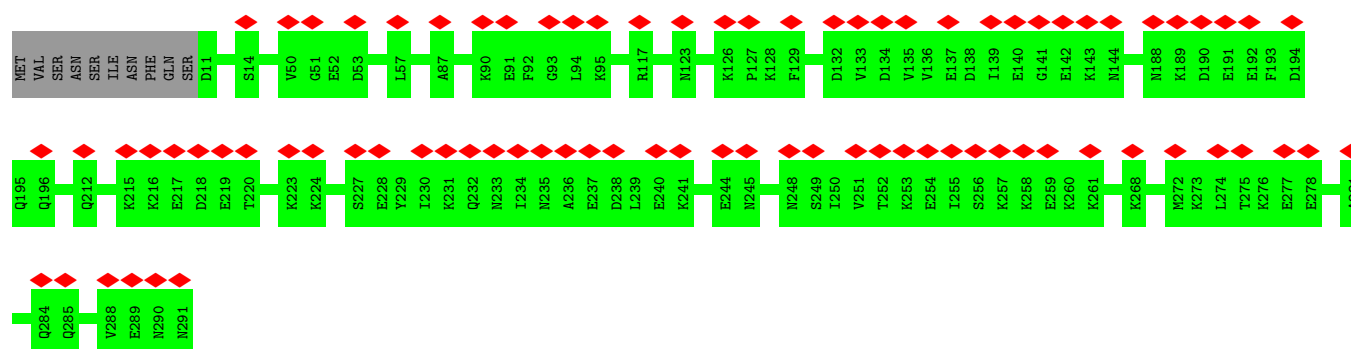
- Molecule 71: 40S ribosomal protein S25



- Molecule 72: 60S ribosomal protein L5

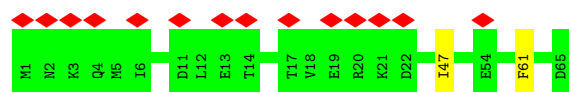


- Molecule 72: 60S ribosomal protein L5

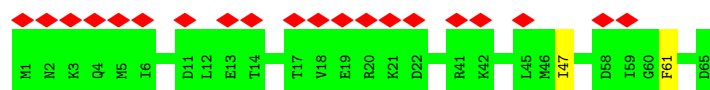


- Molecule 73: 40S ribosomal protein S29

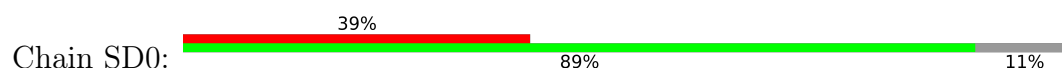
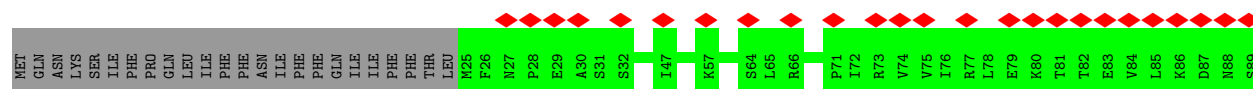
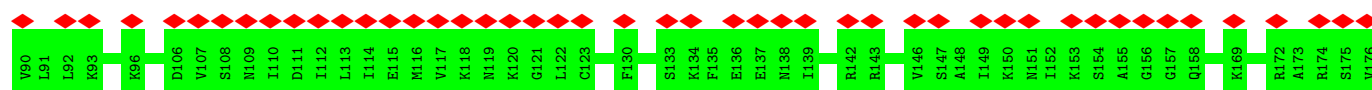
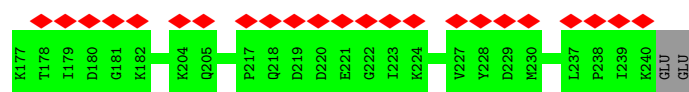




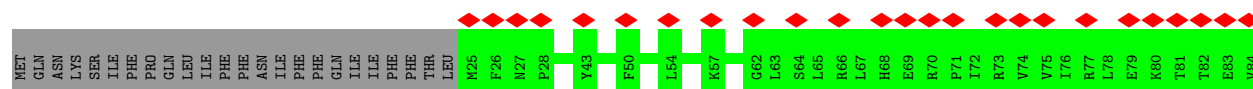
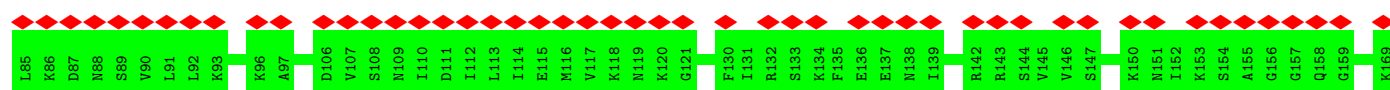
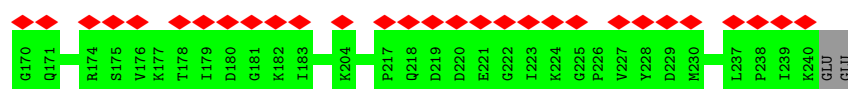
- Molecule 73: 40S ribosomal protein S29



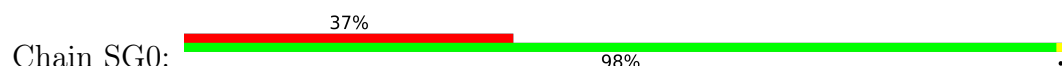
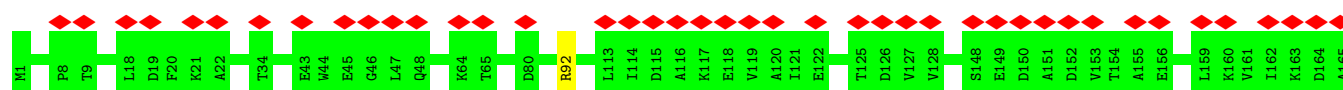
- Molecule 74: 40S ribosomal protein S3

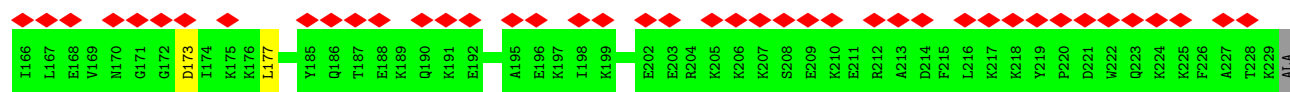


- Molecule 74: 40S ribosomal protein S3



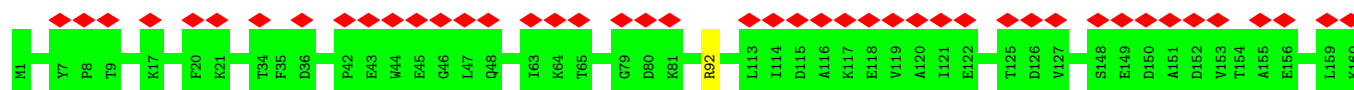
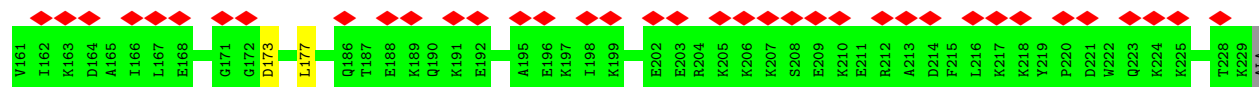
- Molecule 75: 40S ribosomal protein S6





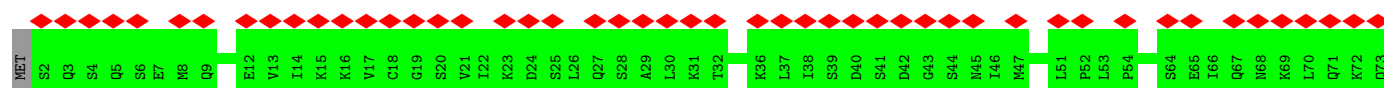
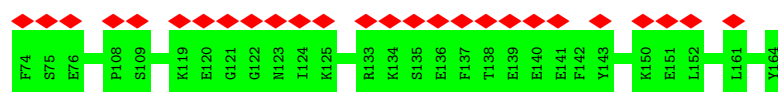
- Molecule 75: 40S ribosomal protein S6

Chain RG0: 35% 98%



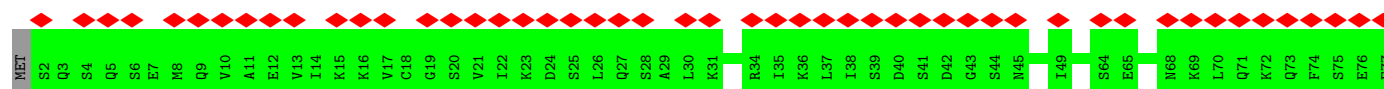
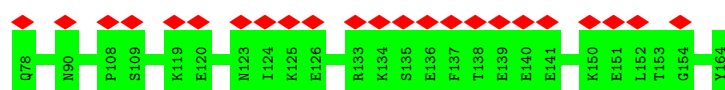
- Molecule 76: 40S ribosomal protein S7

Chain SH0: 46% 99%



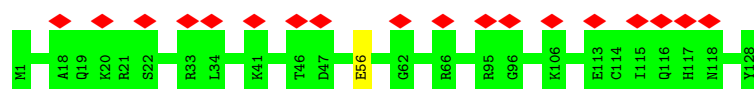
- Molecule 76: 40S ribosomal protein S7

Chain RH0: 45% 99%



- Molecule 77: 40S ribosomal protein S15A

Chain SW0: 14% 99%



- Molecule 77: 40S ribosomal protein S15A

Chain RW0: 11% 99%

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	2389	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.345	Depositor
Minimum map value	-0.974	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.188	Depositor
Recommended contour level	0.28	Depositor
Map size (Å)	588.0, 588.0, 588.0	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.5, 3.5, 3.5	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

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	K50	0.47	7/62688 (0.0%)	0.92	143/97791 (0.1%)
1	L50	0.47	7/62688 (0.0%)	0.92	143/97791 (0.1%)
2	R60	0.42	0/32724	1.01	96/51066 (0.2%)
2	S60	0.42	0/32724	1.01	96/51066 (0.2%)
3	D	0.24	0/1234	0.61	0/1662
3	E	0.24	0/1234	0.61	0/1662
4	KGG	0.29	0/825	0.61	0/1090
4	LGG	0.29	0/825	0.61	0/1090
5	RB0	0.21	0/1623	0.47	0/2169
5	SB0	0.21	0/1623	0.47	0/2169
6	RC0	0.21	0/1755	0.52	0/2364
6	SC0	0.21	0/1755	0.52	0/2364
7	K70	0.41	0/2843	0.86	2/4429 (0.0%)
7	L70	0.41	0/2843	0.86	2/4429 (0.0%)
8	A	0.32	0/6717	0.67	2/9049 (0.0%)
8	B	0.32	0/6717	0.67	2/9049 (0.0%)
9	K	0.19	0/1747	0.47	0/2333
9	L	0.19	0/1747	0.47	0/2333
10	M	0.23	0/2138	0.50	0/2865
10	N	0.23	0/2138	0.50	0/2865
11	KMM	0.55	0/431	0.78	0/568
11	LMM	0.55	0/431	0.78	0/568
12	RBB	0.18	0/634	0.45	0/844
12	SBB	0.18	0/634	0.45	0/844
13	RAA	0.20	0/839	0.54	0/1120
13	SAA	0.20	0/839	0.54	0/1120
14	KOO	0.22	0/811	0.57	0/1071
14	LOO	0.22	0/811	0.57	0/1071
15	KPP	0.24	0/693	0.65	0/918
15	LPP	0.24	0/693	0.65	0/918
16	KJJ	0.23	0/710	0.53	0/932
16	LJJ	0.23	0/710	0.53	0/932

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	LA0	0.31	1/1926 (0.1%)	0.51	1/2590 (0.0%)
17	LA02	0.31	1/1926 (0.1%)	0.51	1/2590 (0.0%)
18	KAA	0.27	0/1191	0.66	1/1586 (0.1%)
18	LAA	0.27	0/1191	0.66	1/1586 (0.1%)
19	KB0	0.25	0/3092	0.54	1/4144 (0.0%)
19	LB0	0.25	0/3092	0.54	1/4144 (0.0%)
20	KC0	0.22	0/2646	0.54	0/3555
20	LC0	0.22	0/2646	0.54	0/3555
21	KCC	0.21	0/794	0.45	0/1067
21	LCC	0.21	0/794	0.45	0/1067
22	KDD	0.21	0/913	0.49	0/1223
22	LDD	0.21	0/913	0.49	0/1223
23	KE0	0.21	0/1394	0.52	1/1875 (0.1%)
23	LE0	0.21	0/1394	0.52	1/1875 (0.1%)
24	KEE	0.36	0/1108	0.72	2/1477 (0.1%)
24	LEE	0.36	0/1108	0.72	2/1477 (0.1%)
25	KF0	0.23	0/1963	0.51	0/2618
25	LF0	0.23	0/1963	0.51	0/2618
26	KFF	0.23	0/906	0.53	0/1207
26	LFF	0.23	0/906	0.53	0/1207
27	KG0	0.23	0/1612	0.52	0/2163
27	LG0	0.23	0/1612	0.52	0/2163
28	KH0	0.26	0/1503	0.52	0/2018
28	LH0	0.26	0/1503	0.52	0/2018
29	KHH	0.34	0/1000	0.69	1/1324 (0.1%)
29	LHH	0.34	0/1000	0.69	1/1324 (0.1%)
30	KI0	0.22	0/1781	0.53	0/2382
30	LI0	0.22	0/1781	0.53	0/2382
31	KII	0.20	0/790	0.50	0/1041
31	LII	0.20	0/790	0.50	0/1041
32	KJ0	0.21	0/1350	0.56	0/1797
32	LJ0	0.21	0/1350	0.56	0/1797
33	KL0	0.45	2/1374 (0.1%)	0.77	2/1827 (0.1%)
33	LL0	0.45	2/1374 (0.1%)	0.77	2/1827 (0.1%)
34	KLL	0.24	0/435	0.55	0/576
34	LLL	0.24	0/435	0.55	0/576
35	KM0	0.20	0/935	0.50	0/1251
35	LM0	0.20	0/935	0.50	0/1251
36	KN0	0.26	0/1722	0.65	0/2297
36	LN0	0.26	0/1722	0.65	0/2297
37	KO0	0.23	0/1626	0.53	0/2168
37	LO0	0.23	0/1626	0.53	0/2168
38	KP0	0.22	0/1262	0.51	0/1689

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	LP0	0.22	0/1262	0.51	0/1689
39	KQ0	0.29	0/1512	0.61	1/2014 (0.0%)
39	LQ0	0.29	0/1512	0.61	1/2014 (0.0%)
40	KR0	0.24	0/1352	0.55	0/1790
40	LR0	0.24	0/1352	0.55	0/1790
41	KS0	0.25	0/1422	0.53	0/1898
41	LS0	0.25	0/1422	0.53	0/1898
42	KT0	0.22	0/1294	0.52	0/1736
42	LT0	0.22	0/1294	0.52	0/1736
43	KU0	0.20	0/826	0.45	0/1104
43	LU0	0.20	0/826	0.45	0/1104
44	KV0	0.22	0/1068	0.56	0/1429
44	LV0	0.22	0/1068	0.56	0/1429
45	KW0	0.18	0/849	0.45	0/1129
45	LW0	0.18	0/849	0.45	0/1129
46	KX0	0.20	0/883	0.45	0/1175
46	LX0	0.20	0/883	0.45	0/1175
47	KY0	0.23	0/1058	0.53	0/1399
47	LY0	0.23	0/1058	0.53	0/1399
48	KZ0	0.36	0/976	0.59	0/1302
48	LZ0	0.36	0/976	0.59	0/1302
49	MD1	0.52	0/1249	0.97	4/1677 (0.2%)
49	ND1	0.52	0/1249	0.97	4/1677 (0.2%)
50	RA0	0.21	0/1751	0.53	1/2358 (0.0%)
50	SA0	0.21	0/1751	0.53	1/2358 (0.0%)
51	RCC	0.19	0/480	0.48	0/644
51	SCC	0.19	0/480	0.48	0/644
52	RE0	0.20	0/2080	0.52	0/2804
52	SE0	0.20	0/2080	0.52	0/2804
53	REE	0.20	0/453	0.51	0/596
53	SEE	0.20	0/453	0.51	0/596
54	RGG	0.19	0/2517	0.51	0/3397
54	SGG	0.19	0/2517	0.51	0/3397
55	RI0	0.23	0/1369	0.54	0/1825
55	SI0	0.23	0/1369	0.54	0/1825
56	RJ0	0.22	0/1403	0.56	0/1880
56	SJ0	0.22	0/1403	0.56	0/1880
57	RK0	0.25	0/750	0.59	0/1009
57	SK0	0.25	0/750	0.59	0/1009
58	RL0	0.19	0/1252	0.45	0/1672
58	SL0	0.19	0/1252	0.45	0/1672
59	RM0	0.16	0/881	0.40	0/1182
59	SM0	0.16	0/881	0.40	0/1182

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	RN0	0.25	0/1154	0.47	0/1557
60	SN0	0.25	0/1154	0.47	0/1557
61	RO0	0.23	0/993	0.58	0/1326
61	SO0	0.23	0/993	0.58	0/1326
62	RP0	0.25	0/964	0.61	0/1289
62	SP0	0.25	0/964	0.61	0/1289
63	RQ0	0.23	0/1163	0.54	0/1556
63	SQ0	0.23	0/1163	0.54	0/1556
64	RR0	0.24	0/985	0.60	0/1315
64	SR0	0.24	0/985	0.60	0/1315
65	RS0	0.23	0/1165	0.64	0/1566
65	SS0	0.23	0/1165	0.64	0/1566
66	RT0	0.21	0/1181	0.56	0/1585
66	ST0	0.21	0/1181	0.56	0/1585
67	RU0	0.24	0/824	0.58	0/1110
67	SU0	0.24	0/824	0.58	0/1110
68	RV0	0.25	0/525	0.74	0/700
68	SV0	0.25	0/525	0.74	0/700
69	RX0	0.23	0/1113	0.62	0/1486
69	SX0	0.23	0/1113	0.62	0/1486
70	RY0	0.19	0/1131	0.58	0/1503
70	SY0	0.19	0/1131	0.58	0/1503
71	RZ0	0.22	0/640	0.58	0/855
71	SZ0	0.22	0/640	0.58	0/855
72	KD0	0.18	0/2328	0.46	0/3098
72	LD0	0.18	0/2328	0.46	0/3098
73	RDD	0.28	0/559	0.71	0/742
73	SDD	0.28	0/559	0.71	0/742
74	RD0	0.18	0/1721	0.46	0/2304
74	SD0	0.18	0/1721	0.46	0/2304
75	RG0	0.20	0/1863	0.53	0/2483
75	SG0	0.20	0/1863	0.53	0/2483
76	RH0	0.19	0/1356	0.49	0/1820
76	SH0	0.19	0/1356	0.49	0/1820
77	RW0	0.23	0/1037	0.60	0/1389
77	SW0	0.23	0/1037	0.60	0/1389
78	RF0	0.25	0/1527	0.61	2/2045 (0.1%)
78	SF0	0.25	0/1527	0.61	2/2045 (0.1%)
79	RFF	0.58	0/418	0.98	0/560
79	SFF	0.58	0/418	0.98	0/560
All	All	0.36	20/395614 (0.0%)	0.79	520/572910 (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
1	K50	0	13
1	L50	0	13
8	A	0	5
8	B	0	5
29	KHH	0	1
29	LHH	0	1
32	KJ0	0	1
32	LJ0	0	1
48	KZ0	0	1
48	LZ0	0	1
54	RGG	0	1
54	SGG	0	1
56	RJ0	0	1
56	SJ0	0	1
61	RO0	0	1
61	SO0	0	1
65	RS0	0	4
65	SS0	0	4
66	RT0	0	2
66	ST0	0	2
67	RU0	0	2
67	SU0	0	2
68	RV0	0	2
68	SV0	0	2
70	RY0	0	1
70	SY0	0	1
73	RDD	0	2
73	SDD	0	2
75	RG0	0	1
75	SG0	0	1
All	All	0	76

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	LL0	1	MET	CG-SD	-7.84	1.61	1.80
33	KL0	1	MET	CG-SD	-7.84	1.61	1.80
17	LA0	180	TYR	CD1-CE1	7.22	1.60	1.38
17	LA02	180	TYR	CD1-CE1	7.22	1.60	1.38
1	L50	311	C	C3'-O3'	6.12	1.50	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K50	311	C	C3'-O3'	6.12	1.50	1.42
1	K50	179	U	C5'-C4'	5.69	1.55	1.51
1	L50	179	U	C5'-C4'	5.69	1.55	1.51
33	LL0	1	MET	SD-CE	-5.57	1.65	1.79
33	KL0	1	MET	SD-CE	-5.57	1.65	1.79
1	L50	178	G	C4'-O4'	-5.53	1.40	1.45
1	K50	178	G	C4'-O4'	-5.53	1.40	1.45
1	K50	367	A	C5-C4	-5.51	1.34	1.38
1	L50	367	A	C5-C4	-5.50	1.34	1.38
1	K50	310	A	C5-C4	-5.11	1.35	1.38
1	L50	310	A	C5-C4	-5.11	1.35	1.38
1	L50	483	A	C5-C4	-5.07	1.35	1.38
1	K50	483	A	C5-C4	-5.07	1.35	1.38
1	L50	311	C	C5'-C4'	5.03	1.54	1.51
1	K50	311	C	C5'-C4'	5.03	1.54	1.51

All (520) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S60	355	C	N1-C2-O2	11.55	125.83	118.90
2	R60	355	C	N1-C2-O2	11.55	125.83	118.90
1	L50	366	G	O4'-C1'-N9	11.54	116.58	108.50
1	K50	366	G	O4'-C1'-N9	11.54	116.58	108.50
1	L50	202	G	O4'-C1'-N9	11.34	116.44	108.50
1	K50	202	G	O4'-C1'-N9	11.34	116.44	108.50
1	L50	485	A	N1-C6-N6	-10.86	112.08	118.60
1	K50	485	A	N1-C6-N6	-10.86	112.08	118.60
1	L50	1928	C	P-O3'-C3'	10.85	132.71	119.70
1	K50	1928	C	P-O3'-C3'	10.85	132.72	119.70
1	L50	236	A	N1-C6-N6	-9.33	113.00	118.60
1	K50	236	A	N1-C6-N6	-9.33	113.00	118.60
2	S60	980	G	O4'-C1'-N9	9.22	115.58	108.20
2	R60	980	G	O4'-C1'-N9	9.22	115.58	108.20
2	S60	1341	A	P-O3'-C3'	-9.18	108.68	119.70
2	R60	1341	A	P-O3'-C3'	-9.18	108.68	119.70
1	L50	201	A	N1-C6-N6	-8.96	113.22	118.60
1	K50	201	A	N1-C6-N6	-8.96	113.22	118.60
1	L50	311	C	N1-C1'-C2'	8.87	121.75	112.00
1	K50	311	C	N1-C1'-C2'	8.87	121.75	112.00
1	L50	366	G	N9-C1'-C2'	-8.84	102.28	112.00
1	K50	366	G	N9-C1'-C2'	-8.84	102.28	112.00
1	L50	483	A	C5-C6-N1	8.71	122.06	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	483	A	C5-C6-N1	8.71	122.06	117.70
1	L50	310	A	C5-C6-N1	8.66	122.03	117.70
1	K50	310	A	C5-C6-N1	8.66	122.03	117.70
1	L50	204	C	O4'-C1'-N1	8.58	114.50	108.50
1	K50	204	C	O4'-C1'-N1	8.58	114.50	108.50
1	L50	190	G	O5'-C5'-C4'	8.52	116.22	109.40
1	K50	190	G	O5'-C5'-C4'	8.52	116.22	109.40
1	K50	310	A	C4-C5-C6	-8.30	112.85	117.00
1	L50	310	A	C4-C5-C6	-8.30	112.85	117.00
1	K50	368	C	N3-C2-O2	-8.30	116.09	121.90
1	L50	368	C	N3-C2-O2	-8.30	116.09	121.90
1	K50	178	G	C1'-O4'-C4'	-8.27	103.92	109.70
1	L50	178	G	C1'-O4'-C4'	-8.26	103.92	109.70
2	S60	63	G	P-O3'-C3'	-8.22	109.83	119.70
2	R60	63	G	P-O3'-C3'	-8.22	109.83	119.70
2	S60	442	C	C2-N1-C1'	8.18	127.80	118.80
2	R60	442	C	C2-N1-C1'	8.18	127.80	118.80
1	L50	179	U	O4'-C1'-N1	8.16	114.21	108.50
1	K50	179	U	O4'-C1'-N1	8.16	114.21	108.50
1	L50	237	A	O5'-C5'-C4'	8.05	115.84	109.40
1	K50	237	A	O5'-C5'-C4'	8.05	115.84	109.40
1	L50	310	A	N1-C6-N6	-7.99	113.81	118.60
1	K50	310	A	N1-C6-N6	-7.99	113.81	118.60
1	L50	1235	A	P-O3'-C3'	-7.93	110.19	119.70
1	K50	1235	A	P-O3'-C3'	-7.93	110.19	119.70
1	L50	237	A	N1-C6-N6	-7.86	113.88	118.60
1	K50	237	A	N1-C6-N6	-7.86	113.88	118.60
1	L50	201	A	C5-C6-N1	7.83	121.62	117.70
1	K50	201	A	C5-C6-N1	7.83	121.62	117.70
1	L50	484	C	C3'-C2'-C1'	7.77	106.74	101.30
1	K50	484	C	C3'-C2'-C1'	7.77	106.74	101.30
2	S60	355	C	N3-C2-O2	-7.76	116.47	121.90
2	R60	355	C	N3-C2-O2	-7.76	116.47	121.90
49	ND1	103	ARG	NE-CZ-NH2	7.73	126.15	119.20
49	MD1	103	ARG	NE-CZ-NH2	7.72	126.15	119.20
1	L50	205	C	C5'-C4'-C3'	-7.71	103.66	116.00
1	K50	205	C	C5'-C4'-C3'	-7.71	103.66	116.00
2	S60	1049	G	O5'-C5'-C4'	7.70	115.56	109.40
2	R60	1049	G	O5'-C5'-C4'	7.70	115.56	109.40
1	L50	484	C	N3-C2-O2	-7.69	116.52	121.90
1	K50	484	C	N3-C2-O2	-7.69	116.52	121.90
1	K50	368	C	N1-C2-O2	7.68	123.51	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L50	368	C	N1-C2-O2	7.68	123.51	118.90
1	L50	178	G	O3'-P-O5'	7.67	118.58	104.00
1	K50	178	G	O3'-P-O5'	7.67	118.58	104.00
1	L50	915	G	C3'-C2'-C1'	-7.65	95.38	101.50
1	K50	915	G	C3'-C2'-C1'	-7.65	95.38	101.50
1	L50	2	U	O5'-C5'-C4'	7.64	115.52	109.40
1	K50	2	U	O5'-C5'-C4'	7.64	115.52	109.40
2	S60	1041	A	O4'-C1'-N9	7.55	114.24	108.20
2	R60	1041	A	O4'-C1'-N9	7.55	114.24	108.20
1	K50	202	G	O5'-C5'-C4'	7.53	115.42	109.40
1	L50	202	G	O5'-C5'-C4'	7.52	115.42	109.40
1	L50	1922	A	O4'-C1'-N9	7.52	114.22	108.20
1	K50	1922	A	O4'-C1'-N9	7.52	114.22	108.20
1	L50	367	A	C3'-C2'-C1'	7.50	106.55	101.30
1	K50	367	A	C3'-C2'-C1'	7.50	106.55	101.30
2	R60	67	C	C2-N1-C1'	7.50	127.04	118.80
2	S60	67	C	C2-N1-C1'	7.49	127.04	118.80
1	L50	188	G	N1-C6-O6	-7.49	115.41	119.90
1	K50	188	G	N1-C6-O6	-7.49	115.41	119.90
1	L50	311	C	C3'-C2'-C1'	7.45	106.52	101.30
1	K50	311	C	C3'-C2'-C1'	7.45	106.52	101.30
1	L50	547	U	O4'-C1'-N1	7.43	113.70	108.50
1	K50	547	U	O4'-C1'-N1	7.43	113.70	108.50
2	S60	83	G	O4'-C1'-N9	-7.41	103.32	108.50
2	R60	83	G	O4'-C1'-N9	-7.41	103.32	108.50
1	L50	367	A	C4-C5-C6	-7.35	113.33	117.00
1	K50	367	A	C4-C5-C6	-7.35	113.33	117.00
2	R60	1097	A	N9-C4-C5	-7.35	102.86	105.80
2	S60	1097	A	N9-C4-C5	-7.34	102.86	105.80
1	L50	1956	U	C2-N1-C1'	7.34	126.51	117.70
1	K50	1956	U	C2-N1-C1'	7.34	126.51	117.70
1	L50	485	A	C5-C6-N1	7.30	121.35	117.70
2	S60	62	C	N1-C2-O2	7.29	123.28	118.90
1	K50	485	A	C5-C6-N1	7.29	121.35	117.70
2	R60	62	C	N1-C2-O2	7.29	123.28	118.90
1	L50	367	A	C5-C6-N1	7.27	121.34	117.70
1	K50	367	A	C5-C6-N1	7.27	121.34	117.70
1	L50	189	U	N3-C2-O2	-7.25	117.13	122.20
1	K50	189	U	N3-C2-O2	-7.25	117.13	122.20
1	L50	547	U	O5'-C5'-C4'	7.22	115.18	109.40
1	K50	547	U	O5'-C5'-C4'	7.22	115.18	109.40
1	L50	237	A	C5-C6-N1	7.18	121.29	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	237	A	C5-C6-N1	7.18	121.29	117.70
1	L50	236	A	C5-C6-N1	7.17	121.29	117.70
1	K50	236	A	C5-C6-N1	7.17	121.29	117.70
1	L50	483	A	C3'-C2'-C1'	7.08	106.25	101.30
1	K50	483	A	C3'-C2'-C1'	7.08	106.25	101.30
1	L50	367	A	N1-C6-N6	-7.06	114.37	118.60
1	K50	367	A	N1-C6-N6	-7.06	114.37	118.60
1	K50	547	U	C5'-C4'-O4'	7.04	116.14	109.80
1	L50	547	U	C5'-C4'-O4'	7.04	116.14	109.80
1	L50	1422	C	C2-N1-C1'	7.01	126.51	118.80
1	K50	1422	C	C2-N1-C1'	7.01	126.52	118.80
1	L50	311	C	O5'-C5'-C4'	7.00	115.00	109.40
1	K50	311	C	O5'-C5'-C4'	7.00	115.00	109.40
1	K50	1717	A	P-O3'-C3'	-6.94	111.38	119.70
1	L50	1717	A	P-O3'-C3'	-6.94	111.38	119.70
1	L50	205	C	N3-C2-O2	-6.82	117.13	121.90
1	K50	205	C	N3-C2-O2	-6.82	117.13	121.90
2	S60	794	G	P-O3'-C3'	-6.80	111.54	119.70
2	R60	794	G	P-O3'-C3'	-6.80	111.54	119.70
1	L50	2268	A	P-O3'-C3'	-6.74	111.61	119.70
1	K50	2268	A	P-O3'-C3'	-6.74	111.61	119.70
2	R60	1097	A	C8-N9-C1'	-6.73	115.59	127.70
2	S60	1097	A	C8-N9-C1'	-6.73	115.59	127.70
1	L50	366	G	C4-N9-C1'	-6.71	117.78	126.50
1	K50	366	G	C4-N9-C1'	-6.71	117.78	126.50
2	S60	1097	A	C4-N9-C1'	6.67	138.30	126.30
2	R60	1097	A	C4-N9-C1'	6.67	138.30	126.30
2	R60	62	C	C2-N1-C1'	6.65	126.11	118.80
2	S60	62	C	C2-N1-C1'	6.65	126.11	118.80
2	R60	869	G	N9-C4-C5	-6.64	102.74	105.40
2	S60	869	G	N9-C4-C5	-6.64	102.75	105.40
1	L50	976	C	N3-C2-O2	-6.63	117.26	121.90
1	K50	976	C	N3-C2-O2	-6.63	117.26	121.90
1	L50	179	U	O4'-C1'-C2'	-6.61	101.66	107.60
1	K50	179	U	O4'-C1'-C2'	-6.61	101.65	107.60
1	L50	1922	A	C3'-C2'-C1'	-6.59	96.23	101.50
1	K50	1922	A	C3'-C2'-C1'	-6.59	96.23	101.50
2	S60	1097	A	C6-C5-N7	-6.57	127.70	132.30
2	R60	1097	A	C6-C5-N7	-6.57	127.70	132.30
1	L50	1224	A	P-O3'-C3'	-6.57	111.82	119.70
1	K50	1224	A	P-O3'-C3'	-6.57	111.82	119.70
2	S60	449	A	O4'-C1'-N9	6.56	113.09	108.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R60	449	A	O4'-C1'-N9	6.56	113.09	108.50
1	L50	202	G	C5'-C4'-C3'	-6.50	105.61	116.00
1	K50	202	G	C5'-C4'-C3'	-6.50	105.61	116.00
1	L50	547	U	C3'-C2'-C1'	6.48	105.84	101.30
1	K50	547	U	C3'-C2'-C1'	6.48	105.84	101.30
1	L50	237	A	C4-C5-C6	-6.48	113.76	117.00
1	K50	237	A	C4-C5-C6	-6.48	113.76	117.00
1	L50	724	C	O4'-C1'-N1	6.43	113.00	108.50
1	K50	724	C	O4'-C1'-N1	6.43	113.00	108.50
1	L50	368	C	N3-C4-N4	-6.41	113.51	118.00
1	K50	368	C	N3-C4-N4	-6.41	113.51	118.00
1	K50	311	C	N3-C2-O2	-6.38	117.44	121.90
1	L50	311	C	N3-C2-O2	-6.38	117.44	121.90
2	R60	869	G	C4-C5-N7	6.34	113.33	110.80
1	L50	205	C	O5'-C5'-C4'	-6.33	104.33	109.40
2	S60	869	G	C4-C5-N7	6.33	113.33	110.80
1	K50	205	C	O5'-C5'-C4'	-6.33	104.34	109.40
2	S60	970	U	C2-N1-C1'	6.31	125.28	117.70
2	R60	970	U	C2-N1-C1'	6.31	125.28	117.70
1	L50	1918	U	O5'-C5'-C4'	6.31	114.45	109.40
1	K50	1918	U	O5'-C5'-C4'	6.31	114.44	109.40
2	S60	1002	U	O5'-C5'-C4'	6.29	114.43	109.40
2	R60	1002	U	O5'-C5'-C4'	6.29	114.43	109.40
1	L50	547	U	C1'-O4'-C4'	-6.27	104.89	109.90
1	K50	547	U	C1'-O4'-C4'	-6.27	104.89	109.90
1	K50	204	C	N3-C2-O2	-6.26	117.52	121.90
1	L50	204	C	N3-C2-O2	-6.26	117.52	121.90
1	L50	2480	C	C2-N1-C1'	6.25	125.67	118.80
1	K50	2480	C	C2-N1-C1'	6.25	125.67	118.80
2	R60	62	C	N3-C2-O2	-6.24	117.53	121.90
2	S60	62	C	N3-C2-O2	-6.24	117.53	121.90
2	S60	825	U	C2-N1-C1'	6.23	125.17	117.70
2	R60	825	U	C2-N1-C1'	6.23	125.17	117.70
1	L50	201	A	C4-C5-C6	-6.22	113.89	117.00
1	K50	201	A	C4-C5-C6	-6.22	113.89	117.00
24	LEE	82	MET	CB-CG-SD	6.21	131.31	112.70
24	KEE	82	MET	CB-CG-SD	6.21	131.31	112.70
2	S60	562	G	O5'-C5'-C4'	6.20	114.36	109.40
2	R60	562	G	O5'-C5'-C4'	6.20	114.36	109.40
2	R60	855	G	N9-C1'-C2'	6.16	118.77	112.00
2	S60	144	G	C4-N9-C1'	6.16	134.50	126.50
2	S60	442	C	C6-N1-C1'	-6.16	113.41	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S60	855	G	N9-C1'-C2'	6.16	118.77	112.00
2	R60	144	G	C4-N9-C1'	6.16	134.50	126.50
2	R60	442	C	C6-N1-C1'	-6.16	113.41	120.80
2	S60	1097	A	N3-C4-N9	6.15	132.32	127.40
2	R60	1097	A	N3-C4-N9	6.15	132.32	127.40
1	L50	367	A	N9-C1'-C2'	-6.14	105.24	112.00
1	K50	367	A	N9-C1'-C2'	-6.14	105.25	112.00
1	L50	484	C	N3-C4-C5	6.12	124.35	121.90
1	K50	484	C	N3-C4-C5	6.12	124.35	121.90
2	S60	1313	A	O5'-C5'-C4'	6.10	114.28	109.40
2	R60	1313	A	O5'-C5'-C4'	6.10	114.28	109.40
2	S60	363	C	O5'-C5'-C4'	6.09	114.28	109.40
2	R60	363	C	O5'-C5'-C4'	6.09	114.28	109.40
2	S60	1275	C	C2-N1-C1'	-6.06	112.13	118.80
2	R60	1275	C	C2-N1-C1'	-6.06	112.13	118.80
2	S60	1222	C	O5'-C5'-C4'	6.05	114.24	109.40
2	R60	1222	C	O5'-C5'-C4'	6.05	114.24	109.40
1	L50	188	G	O4'-C1'-N9	6.01	112.70	108.50
1	K50	188	G	O4'-C1'-N9	6.01	112.71	108.50
2	S60	960	U	C5-C4-O4	-6.01	122.30	125.90
2	R60	960	U	C5-C4-O4	-6.01	122.30	125.90
2	R60	1097	A	O4'-C1'-N9	-5.97	104.32	108.50
2	S60	1097	A	O4'-C1'-N9	-5.97	104.32	108.50
39	KQ0	173	ARG	NE-CZ-NH2	5.96	124.57	119.20
39	LQ0	173	ARG	NE-CZ-NH2	5.96	124.57	119.20
2	S60	859	G	O5'-C5'-C4'	5.96	114.17	109.40
2	R60	859	G	O5'-C5'-C4'	5.96	114.17	109.40
2	S60	134	G	N3-C4-N9	5.94	129.57	126.00
2	R60	134	G	N3-C4-N9	5.94	129.57	126.00
1	L50	311	C	C2'-C3'-O3'	5.92	123.17	113.70
1	K50	311	C	C2'-C3'-O3'	5.92	123.17	113.70
2	S60	388	G	O4'-C1'-N9	-5.91	104.36	108.50
2	R60	388	G	O4'-C1'-N9	-5.91	104.36	108.50
1	L50	2480	C	C6-N1-C2	-5.88	117.95	120.30
1	K50	2480	C	C6-N1-C2	-5.88	117.95	120.30
2	S60	67	C	N1-C2-O2	5.87	122.42	118.90
1	K50	666	A	P-O3'-C3'	-5.87	112.65	119.70
1	L50	666	A	P-O3'-C3'	-5.87	112.65	119.70
2	S60	1017	A	O4'-C1'-N9	5.87	112.61	108.50
2	R60	67	C	N1-C2-O2	5.87	122.42	118.90
2	R60	1017	A	O4'-C1'-N9	5.87	112.61	108.50
18	LAA	49	HIS	CB-CG-CD2	-5.87	123.57	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	KAA	49	HIS	CB-CG-CD2	-5.87	123.57	131.20
1	K50	546	G	N1-C6-O6	-5.86	116.38	119.90
1	L50	546	G	N1-C6-O6	-5.86	116.38	119.90
1	L50	369	U	N1-C2-N3	5.86	118.41	114.90
1	K50	369	U	N1-C2-N3	5.86	118.42	114.90
1	L50	368	C	O4'-C1'-N1	5.85	112.60	108.50
1	K50	368	C	O4'-C1'-N1	5.85	112.60	108.50
1	L50	201	A	C3'-C2'-C1'	-5.85	96.82	101.50
1	K50	201	A	C3'-C2'-C1'	-5.85	96.82	101.50
1	L50	2586	U	O4'-C1'-N1	-5.84	104.42	108.50
1	K50	2586	U	O4'-C1'-N1	-5.84	104.42	108.50
2	S60	83	G	C8-N9-C1'	-5.83	119.43	127.00
2	S60	970	U	O4'-C1'-N1	-5.83	104.42	108.50
2	R60	970	U	O4'-C1'-N1	-5.83	104.42	108.50
2	R60	83	G	C8-N9-C1'	-5.82	119.43	127.00
2	S60	442	C	N1-C2-O2	5.82	122.39	118.90
2	R60	442	C	N1-C2-O2	5.82	122.39	118.90
1	K50	1936	U	O4'-C1'-N1	5.80	112.56	108.50
1	L50	1936	U	O4'-C1'-N1	5.80	112.56	108.50
1	L50	205	C	O4'-C4'-C3'	5.80	109.80	104.00
1	K50	205	C	O4'-C4'-C3'	5.80	109.80	104.00
2	R60	941	C	C2-N1-C1'	5.80	125.18	118.80
2	S60	941	C	C2-N1-C1'	5.80	125.18	118.80
2	R60	83	G	N9-C4-C5	-5.80	103.08	105.40
2	S60	83	G	N9-C4-C5	-5.79	103.08	105.40
1	L50	900	A	O5'-C5'-C4'	5.77	114.01	109.40
1	K50	900	A	O5'-C5'-C4'	5.77	114.01	109.40
1	K50	2299	C	P-O3'-C3'	-5.76	112.79	119.70
1	L50	236	A	C4-C5-C6	-5.76	114.12	117.00
1	L50	2299	C	P-O3'-C3'	-5.76	112.79	119.70
1	L50	2559	G	P-O3'-C3'	-5.76	112.79	119.70
2	S60	144	G	C8-N9-C1'	-5.76	119.52	127.00
1	K50	236	A	C4-C5-C6	-5.76	114.12	117.00
2	R60	144	G	C8-N9-C1'	-5.76	119.52	127.00
1	K50	2559	G	P-O3'-C3'	-5.75	112.79	119.70
1	L50	205	C	C3'-C2'-C1'	5.75	105.32	101.30
1	K50	205	C	C3'-C2'-C1'	5.75	105.32	101.30
1	L50	202	G	C5'-C4'-O4'	5.74	114.96	109.80
49	MD1	27	ILE	CA-C-N	5.74	130.56	120.87
49	MD1	27	ILE	C-N-CA	5.74	130.56	120.87
1	K50	202	G	C5'-C4'-O4'	5.74	114.96	109.80
49	ND1	27	ILE	CA-C-N	5.74	130.57	120.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	ND1	27	ILE	C-N-CA	5.74	130.57	120.87
1	K50	2480	C	N1-C2-O2	5.74	122.34	118.90
1	L50	2480	C	N1-C2-O2	5.73	122.34	118.90
1	L50	485	A	C4-C5-C6	-5.73	114.13	117.00
1	K50	485	A	C4-C5-C6	-5.73	114.14	117.00
1	L50	1234	U	C2-N1-C1'	5.72	124.57	117.70
1	K50	1234	U	C2-N1-C1'	5.72	124.57	117.70
2	R60	524	G	O5'-C5'-C4'	5.72	113.97	109.40
2	S60	524	G	O5'-C5'-C4'	5.72	113.97	109.40
78	SF0	127	ARG	NE-CZ-NH2	5.72	124.34	119.20
78	RF0	127	ARG	NE-CZ-NH2	5.72	124.34	119.20
2	S60	137	A	N9-C1'-C2'	5.71	118.29	112.00
2	R60	137	A	N9-C1'-C2'	5.71	118.29	112.00
2	S60	1223	C	O5'-C5'-C4'	5.70	113.96	109.40
2	R60	1223	C	O5'-C5'-C4'	5.70	113.96	109.40
1	L50	483	A	C4-C5-C6	-5.69	114.15	117.00
1	K50	483	A	C4-C5-C6	-5.69	114.16	117.00
2	S60	761	G	O5'-C5'-C4'	5.69	113.95	109.40
2	R60	761	G	O5'-C5'-C4'	5.69	113.95	109.40
1	L50	204	C	N1-C2-O2	5.69	122.31	118.90
1	K50	204	C	N1-C2-O2	5.69	122.31	118.90
1	L50	2558	A	P-O3'-C3'	-5.66	112.91	119.70
1	K50	2558	A	P-O3'-C3'	-5.66	112.91	119.70
1	L50	1443	C	P-O3'-C3'	-5.64	112.93	119.70
1	K50	1443	C	P-O3'-C3'	-5.64	112.93	119.70
33	LL0	12	PHE	CA-C-N	5.63	127.83	120.28
33	LL0	12	PHE	C-N-CA	5.63	127.83	120.28
33	KL0	12	PHE	CA-C-N	5.63	127.83	120.28
33	KL0	12	PHE	C-N-CA	5.63	127.83	120.28
1	L50	484	C	C2-N3-C4	-5.63	117.08	119.90
1	K50	484	C	C2-N3-C4	-5.63	117.08	119.90
2	S60	355	C	C2-N1-C1'	5.63	124.99	118.80
2	R60	355	C	C2-N1-C1'	5.63	124.99	118.80
1	L50	1236	U	P-O3'-C3'	-5.62	112.95	119.70
1	K50	1236	U	P-O3'-C3'	-5.62	112.95	119.70
1	L50	923	G	C4-N9-C1'	5.62	133.80	126.50
1	K50	923	G	C4-N9-C1'	5.62	133.80	126.50
2	S60	512	C	O5'-C5'-C4'	5.61	113.89	109.40
2	R60	512	C	O5'-C5'-C4'	5.61	113.89	109.40
2	S60	1026	U	C2-N1-C1'	-5.61	110.97	117.70
2	R60	1026	U	C2-N1-C1'	-5.61	110.97	117.70
2	S60	1090	C	O5'-C5'-C4'	5.60	113.88	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K50	923	G	C8-N9-C1'	-5.60	119.72	127.00
1	L50	923	G	C8-N9-C1'	-5.60	119.72	127.00
2	R60	1090	C	O5'-C5'-C4'	5.60	113.88	109.40
1	L50	548	G	C4'-C3'-C2'	-5.60	97.00	102.60
1	K50	548	G	C4'-C3'-C2'	-5.60	97.00	102.60
2	S60	1060	G	C5-C6-N1	5.57	114.29	111.50
2	R60	1060	G	C5-C6-N1	5.57	114.28	111.50
2	S60	1019	C	N3-C2-O2	-5.56	118.01	121.90
1	L50	547	U	N3-C2-O2	-5.56	118.31	122.20
2	R60	1019	C	N3-C2-O2	-5.56	118.01	121.90
1	L50	2018	G	N3-C4-N9	-5.56	122.67	126.00
1	K50	547	U	N3-C2-O2	-5.56	118.31	122.20
1	K50	2018	G	N3-C4-N9	-5.55	122.67	126.00
2	S60	473	G	C4-N9-C1'	5.55	133.71	126.50
2	R60	473	G	C4-N9-C1'	5.55	133.71	126.50
2	S60	1165	C	N1-C2-O2	5.54	122.23	118.90
2	R60	1165	C	N1-C2-O2	5.54	122.22	118.90
2	S60	569	G	C4-N9-C1'	-5.54	119.30	126.50
2	R60	569	G	C4-N9-C1'	-5.54	119.30	126.50
2	S60	820	G	C4-N9-C1'	5.53	133.69	126.50
2	R60	820	G	C4-N9-C1'	5.53	133.69	126.50
2	S60	61	G	N1-C2-N2	-5.53	111.23	116.20
2	R60	61	G	N1-C2-N2	-5.52	111.23	116.20
1	L50	1897	G	O5'-C5'-C4'	5.51	113.81	109.40
1	K50	1897	G	O5'-C5'-C4'	5.51	113.81	109.40
2	S60	833	A	O5'-C5'-C4'	5.50	113.80	109.40
8	A	22	ILE	CB-CA-C	5.50	116.68	110.41
2	R60	833	A	O5'-C5'-C4'	5.50	113.80	109.40
8	B	22	ILE	CB-CA-C	5.50	116.68	110.41
1	L50	202	G	N9-C1'-C2'	-5.49	105.96	112.00
1	K50	202	G	N9-C1'-C2'	-5.49	105.96	112.00
2	S60	1138	U	C2-N1-C1'	5.48	124.27	117.70
2	R60	1138	U	C2-N1-C1'	5.48	124.27	117.70
2	S60	83	G	N3-C4-N9	5.48	129.28	126.00
1	L50	203	U	N3-C2-O2	-5.47	118.37	122.20
1	K50	203	U	N3-C2-O2	-5.47	118.37	122.20
2	R60	83	G	N3-C4-N9	5.47	129.28	126.00
1	K50	2480	C	N3-C2-O2	-5.46	118.08	121.90
1	L50	2480	C	N3-C2-O2	-5.46	118.08	121.90
1	L50	1422	C	C6-N1-C1'	-5.45	114.27	120.80
1	K50	1422	C	C6-N1-C1'	-5.45	114.27	120.80
2	S60	280	G	O5'-C5'-C4'	5.44	113.75	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R60	280	G	O5'-C5'-C4'	5.44	113.75	109.40
2	S60	1060	G	N3-C4-N9	5.43	129.26	126.00
2	R60	1060	G	N3-C4-N9	5.43	129.26	126.00
7	L70	49	A	O4'-C1'-N9	5.43	112.30	108.50
7	K70	49	A	O4'-C1'-N9	5.43	112.30	108.50
2	S60	746	G	O5'-C5'-C4'	5.42	113.73	109.40
2	R60	746	G	O5'-C5'-C4'	5.42	113.73	109.40
2	S60	871	C	P-O3'-C3'	-5.42	113.20	119.70
1	K50	2002	C	N1-C2-O2	-5.42	115.65	118.90
2	R60	871	C	P-O3'-C3'	-5.42	113.20	119.70
1	L50	2002	C	N1-C2-O2	-5.42	115.65	118.90
49	MD1	59	LYS	N-CA-CB	-5.40	104.09	111.65
49	ND1	59	LYS	N-CA-CB	-5.40	104.09	111.65
2	S60	1000	C	N3-C2-O2	-5.39	118.12	121.90
2	R60	1000	C	N3-C2-O2	-5.39	118.12	121.90
2	S60	1191	C	O5'-C5'-C4'	5.37	113.70	109.40
2	R60	1191	C	O5'-C5'-C4'	5.37	113.70	109.40
19	LB0	76	GLU	OE1-CD-OE2	5.36	135.77	122.90
19	KB0	76	GLU	OE1-CD-OE2	5.36	135.77	122.90
1	L50	549	C	N3-C2-O2	-5.36	118.15	121.90
1	K50	549	C	N3-C2-O2	-5.36	118.15	121.90
1	L50	923	G	N3-C4-N9	5.36	129.22	126.00
1	K50	923	G	N3-C4-N9	5.36	129.22	126.00
1	L50	178	G	O4'-C4'-C3'	5.35	110.38	106.10
24	LEE	82	MET	N-CA-C	-5.35	100.68	109.40
1	K50	178	G	O4'-C4'-C3'	5.35	110.38	106.10
24	KEE	82	MET	N-CA-C	-5.35	100.68	109.40
1	L50	178	G	C4'-C3'-C2'	-5.35	97.25	102.60
1	K50	178	G	C4'-C3'-C2'	-5.35	97.25	102.60
1	L50	237	A	C5'-C4'-O4'	5.35	114.61	109.80
2	S60	67	C	C6-N1-C1'	-5.35	114.38	120.80
1	K50	237	A	C5'-C4'-O4'	5.35	114.61	109.80
2	R60	67	C	C6-N1-C1'	-5.35	114.38	120.80
1	L50	1922	A	C1'-O4'-C4'	-5.34	105.96	109.70
23	LE0	58	TYR	N-CA-C	-5.34	106.95	112.93
1	K50	1922	A	C1'-O4'-C4'	-5.34	105.96	109.70
23	KE0	58	TYR	N-CA-C	-5.34	106.95	112.93
8	A	22	ILE	N-CA-C	5.33	116.41	107.18
8	B	22	ILE	N-CA-C	5.33	116.41	107.18
17	LA0	180	TYR	CB-CG-CD2	-5.32	112.82	120.80
17	LA02	180	TYR	CB-CG-CD2	-5.32	112.81	120.80
2	S60	82	C	N3-C2-O2	-5.32	118.17	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R60	82	C	N3-C2-O2	-5.32	118.17	121.90
1	K50	976	C	N1-C2-O2	5.32	122.09	118.90
1	L50	976	C	N1-C2-O2	5.31	122.09	118.90
1	L50	368	C	O5'-C5'-C4'	-5.31	105.15	109.40
1	K50	368	C	O5'-C5'-C4'	-5.31	105.15	109.40
1	L50	1162	U	C2-N1-C1'	5.31	124.07	117.70
2	S60	961	G	O4'-C1'-N9	5.31	112.22	108.50
1	K50	1162	U	C2-N1-C1'	5.31	124.07	117.70
2	R60	961	G	O4'-C1'-N9	5.31	112.22	108.50
50	SA0	94	ILE	N-CA-C	-5.31	107.65	112.96
50	RA0	94	ILE	N-CA-C	-5.31	107.65	112.96
1	L50	1894	G	O4'-C1'-N9	-5.29	104.80	108.50
1	K50	1894	G	O4'-C1'-N9	-5.29	104.80	108.50
1	L50	2481	U	N3-C4-O4	-5.29	115.70	119.40
1	K50	2481	U	N3-C4-O4	-5.29	115.70	119.40
1	K50	204	C	C5'-C4'-O4'	5.28	114.55	109.80
1	L50	204	C	C5'-C4'-O4'	5.27	114.55	109.80
1	L50	190	G	C8-N9-C4	-5.27	104.29	106.40
1	K50	190	G	C8-N9-C4	-5.27	104.29	106.40
1	L50	972	C	O5'-C5'-C4'	5.26	113.61	109.40
1	K50	972	C	O5'-C5'-C4'	5.26	113.61	109.40
2	S60	67	C	O4'-C1'-N1	-5.25	104.82	108.50
2	R60	67	C	O4'-C1'-N1	-5.25	104.82	108.50
2	S60	927	G	C5-C6-O6	5.25	131.75	128.60
2	R60	927	G	C5-C6-O6	5.25	131.75	128.60
1	K50	205	C	N3-C4-C5	5.24	124.00	121.90
1	L50	205	C	N3-C4-C5	5.24	124.00	121.90
1	K50	188	G	O5'-C5'-C4'	-5.23	105.22	109.40
1	L50	188	G	N9-C1'-C2'	-5.23	106.25	112.00
1	L50	188	G	O5'-C5'-C4'	-5.23	105.22	109.40
2	S60	569	G	C8-N9-C1'	5.23	133.80	127.00
1	K50	188	G	N9-C1'-C2'	-5.23	106.25	112.00
2	R60	569	G	C8-N9-C1'	5.23	133.80	127.00
1	L50	808	C	N3-C2-O2	-5.22	118.24	121.90
1	K50	808	C	N3-C2-O2	-5.22	118.24	121.90
1	L50	923	G	C6-C5-N7	-5.21	127.27	130.40
1	K50	923	G	C6-C5-N7	-5.21	127.27	130.40
2	R60	869	G	C6-C5-N7	-5.21	127.27	130.40
2	S60	869	G	C6-C5-N7	-5.21	127.28	130.40
1	K50	369	U	N3-C2-O2	-5.21	118.56	122.20
1	L50	369	U	N3-C2-O2	-5.20	118.56	122.20
2	S60	1275	C	C6-N1-C1'	5.20	127.04	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R60	1275	C	C6-N1-C1'	5.20	127.04	120.80
1	L50	190	G	N7-C8-N9	5.19	115.69	113.10
1	L50	2038	A	N9-C1'-C2'	5.18	117.70	112.00
1	K50	190	G	N7-C8-N9	5.18	115.69	113.10
1	K50	2038	A	N9-C1'-C2'	5.18	117.70	112.00
1	L50	189	U	O4'-C1'-C2'	-5.17	102.95	107.60
1	K50	189	U	O4'-C1'-C2'	-5.17	102.95	107.60
2	S60	980	G	N1-C6-O6	-5.15	116.81	119.90
2	R60	980	G	N1-C6-O6	-5.15	116.81	119.90
2	S60	970	U	C6-N1-C1'	-5.15	113.99	121.20
1	K50	547	U	C5-C6-N1	-5.15	120.13	122.70
2	R60	970	U	C6-N1-C1'	-5.15	114.00	121.20
1	L50	547	U	C5-C6-N1	-5.14	120.13	122.70
1	K50	203	U	C5-C6-N1	-5.14	120.13	122.70
2	R60	58	U	O4'-C1'-N1	-5.14	104.90	108.50
1	L50	203	U	C5-C6-N1	-5.14	120.13	122.70
1	L50	310	A	C5'-C4'-O4'	5.14	114.43	109.80
2	S60	58	U	O4'-C1'-N1	-5.14	104.90	108.50
1	K50	310	A	C5'-C4'-O4'	5.14	114.43	109.80
1	L50	450	C	C6-N1-C2	-5.13	118.25	120.30
1	K50	450	C	C6-N1-C2	-5.13	118.25	120.30
2	S60	28	G	O5'-C5'-C4'	5.13	113.50	109.40
2	S60	465	U	O5'-C5'-C4'	5.13	113.50	109.40
2	R60	28	G	O5'-C5'-C4'	5.13	113.50	109.40
2	R60	465	U	O5'-C5'-C4'	5.13	113.50	109.40
1	L50	1940	C	C2-N1-C1'	-5.12	113.17	118.80
1	K50	188	G	C5-C6-N1	5.12	114.06	111.50
1	K50	1940	C	C2-N1-C1'	-5.12	113.17	118.80
1	L50	188	G	C5-C6-N1	5.12	114.06	111.50
1	K50	484	C	N1-C2-O2	5.12	121.97	118.90
1	L50	484	C	N1-C2-O2	5.12	121.97	118.90
1	L50	1956	U	C6-N1-C1'	-5.11	114.04	121.20
1	K50	1956	U	C6-N1-C1'	-5.11	114.04	121.20
2	S60	914	U	O5'-C5'-C4'	5.11	113.49	109.40
2	R60	914	U	O5'-C5'-C4'	5.11	113.49	109.40
29	LHH	108	TYR	CB-CA-C	5.10	119.67	111.36
29	KHH	108	TYR	CB-CA-C	5.10	119.67	111.36
2	S60	1097	A	O5'-C5'-C4'	5.09	113.47	109.40
2	R60	1097	A	O5'-C5'-C4'	5.09	113.47	109.40
1	L50	1190	C	C2-N1-C1'	5.07	124.38	118.80
1	K50	1190	C	C2-N1-C1'	5.07	124.38	118.80
2	S60	172	U	O4'-C1'-N1	5.07	112.26	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R60	172	U	O4'-C1'-N1	5.07	112.26	108.20
2	S60	927	G	N1-C6-O6	-5.07	116.86	119.90
2	R60	927	G	N1-C6-O6	-5.07	116.86	119.90
2	R60	1148	A	O5'-C5'-C4'	5.07	113.45	109.40
2	S60	1148	A	O5'-C5'-C4'	5.07	113.45	109.40
2	S60	67	C	N3-C2-O2	-5.07	118.35	121.90
2	S60	1022	C	O5'-C5'-C4'	5.07	113.45	109.40
2	R60	67	C	N3-C2-O2	-5.07	118.35	121.90
2	R60	1022	C	O5'-C5'-C4'	5.07	113.45	109.40
2	S60	62	C	C6-N1-C1'	-5.06	114.73	120.80
2	R60	62	C	C6-N1-C1'	-5.06	114.73	120.80
1	K50	810	U	O5'-C5'-C4'	-5.05	105.36	109.40
1	L50	810	U	O5'-C5'-C4'	-5.05	105.36	109.40
2	S60	946	C	N3-C4-C5	5.04	123.92	121.90
78	SF0	127	ARG	CD-NE-CZ	5.04	131.46	124.40
2	R60	946	C	N3-C4-C5	5.04	123.92	121.90
7	L70	1	A	N9-C1'-C2'	5.04	117.55	112.00
78	RF0	127	ARG	CD-NE-CZ	5.04	131.46	124.40
2	S60	1050	G	O4'-C1'-N9	5.04	112.03	108.50
2	R60	1050	G	O4'-C1'-N9	5.04	112.03	108.50
7	K70	1	A	N9-C1'-C2'	5.04	117.54	112.00
1	L50	179	U	N3-C2-O2	-5.04	118.67	122.20
1	L50	2045	C	O5'-C5'-C4'	5.04	113.43	109.40
1	K50	179	U	N3-C2-O2	-5.04	118.67	122.20
1	K50	2045	C	O5'-C5'-C4'	5.04	113.43	109.40
2	S60	236	U	N3-C4-O4	5.03	122.92	119.40
2	R60	236	U	N3-C4-O4	5.03	122.92	119.40
1	L50	368	C	N3-C4-C5	5.03	123.91	121.90
1	K50	368	C	N3-C4-C5	5.03	123.91	121.90
2	S60	1026	U	C6-N1-C1'	5.02	128.23	121.20
2	R60	1026	U	C6-N1-C1'	5.02	128.23	121.20
2	S60	820	G	C8-N9-C1'	-5.01	120.49	127.00
2	R60	820	G	C8-N9-C1'	-5.01	120.49	127.00
1	K50	366	G	C1'-O4'-C4'	-5.00	105.90	109.90
1	L50	366	G	C1'-O4'-C4'	-5.00	105.90	109.90

There are no chirality outliers.

All (76) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	A	571	TYR	Peptide
8	A	572	LEU	Peptide

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Mol	Chain	Res	Type	Group
8	A	583	LYS	Peptide
8	A	585	ALA	Peptide
8	A	691	VAL	Peptide
8	B	571	TYR	Peptide
8	B	572	LEU	Peptide
8	B	583	LYS	Peptide
8	B	585	ALA	Peptide
8	B	691	VAL	Peptide
1	K50	178	G	Sidechain
1	K50	179	U	Sidechain
1	K50	190	G	Sidechain
1	K50	201	A	Sidechain
1	K50	202	G	Sidechain
1	K50	204	C	Sidechain
1	K50	310	A	Sidechain
1	K50	311	C	Sidechain
1	K50	366	G	Sidechain
1	K50	367	A	Sidechain
1	K50	368	C	Sidechain
1	K50	483	A	Sidechain
1	K50	546	G	Sidechain
29	KHH	108	TYR	Sidechain
32	KJ0	46	LYS	Peptide
48	KZ0	148	TYR	Peptide
1	L50	178	G	Sidechain
1	L50	179	U	Sidechain
1	L50	190	G	Sidechain
1	L50	201	A	Sidechain
1	L50	202	G	Sidechain
1	L50	204	C	Sidechain
1	L50	310	A	Sidechain
1	L50	311	C	Sidechain
1	L50	366	G	Sidechain
1	L50	367	A	Sidechain
1	L50	368	C	Sidechain
1	L50	483	A	Sidechain
1	L50	546	G	Sidechain
29	LHH	108	TYR	Sidechain
32	LJ0	46	LYS	Peptide
48	LZ0	148	TYR	Peptide
73	RDD	47	ILE	Peptide
73	RDD	61	PHE	Peptide

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Mol	Chain	Res	Type	Group
75	RG0	177	LEU	Peptide
54	RGG	126	GLY	Peptide
56	RJ0	88	ASP	Peptide
61	RO0	50	ARG	Sidechain
65	RS0	103	THR	Peptide
65	RS0	108	GLY	Peptide
65	RS0	111	ILE	Peptide
65	RS0	112	GLU	Peptide
66	RT0	100	SER	Peptide
66	RT0	81	SER	Peptide
67	RU0	55	ARG	Peptide
67	RU0	81	TYR	Peptide
68	RV0	6	ARG	Peptide
68	RV0	8	CYS	Peptide
70	RY0	40	THR	Peptide
73	SDD	47	ILE	Peptide
73	SDD	61	PHE	Peptide
75	SG0	177	LEU	Peptide
54	SGG	126	GLY	Peptide
56	SJ0	88	ASP	Peptide
61	SO0	50	ARG	Sidechain
65	SS0	103	THR	Peptide
65	SS0	108	GLY	Peptide
65	SS0	111	ILE	Peptide
65	SS0	112	GLU	Peptide
66	ST0	100	SER	Peptide
66	ST0	81	SER	Peptide
67	SU0	55	ARG	Peptide
67	SU0	81	TYR	Peptide
68	SV0	6	ARG	Peptide
68	SV0	8	CYS	Peptide
70	SY0	40	THR	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	D	162/164 (99%)	145 (90%)	17 (10%)	0	100	100
3	E	162/164 (99%)	147 (91%)	15 (9%)	0	100	100
4	KGG	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
4	LGG	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
5	RB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
5	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
6	RC0	224/248 (90%)	203 (91%)	21 (9%)	0	100	100
6	SC0	224/248 (90%)	203 (91%)	21 (9%)	0	100	100
8	A	845/847 (100%)	765 (90%)	79 (9%)	1 (0%)	48	83
8	B	845/847 (100%)	767 (91%)	77 (9%)	1 (0%)	48	83
9	K	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
9	L	208/210 (99%)	199 (96%)	9 (4%)	0	100	100
10	M	267/269 (99%)	254 (95%)	13 (5%)	0	100	100
10	N	267/269 (99%)	253 (95%)	14 (5%)	0	100	100
11	KMM	50/127 (39%)	36 (72%)	13 (26%)	1 (2%)	6	31
11	LMM	50/127 (39%)	36 (72%)	13 (26%)	1 (2%)	6	31
12	RBB	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
12	SBB	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
13	RAA	99/102 (97%)	93 (94%)	6 (6%)	0	100	100
13	SAA	99/102 (97%)	93 (94%)	6 (6%)	0	100	100
14	KOO	98/104 (94%)	91 (93%)	7 (7%)	0	100	100
14	LOO	98/104 (94%)	91 (93%)	7 (7%)	0	100	100
15	KPP	85/89 (96%)	79 (93%)	6 (7%)	0	100	100
15	LPP	85/89 (96%)	79 (93%)	6 (7%)	0	100	100
16	KJJ	87/92 (95%)	80 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	LJJ	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
17	LA0	243/246 (99%)	227 (93%)	16 (7%)	0	100	100
17	LA02	243/246 (99%)	227 (93%)	16 (7%)	0	100	100
18	KAA	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
18	LAA	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
19	KB0	381/392 (97%)	364 (96%)	17 (4%)	0	100	100
19	LB0	381/392 (97%)	365 (96%)	16 (4%)	0	100	100
20	KC0	325/328 (99%)	306 (94%)	19 (6%)	0	100	100
20	LC0	325/328 (99%)	306 (94%)	19 (6%)	0	100	100
21	KCC	97/110 (88%)	95 (98%)	2 (2%)	0	100	100
21	LCC	97/110 (88%)	95 (98%)	2 (2%)	0	100	100
22	KDD	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
22	LDD	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
23	KE0	163/171 (95%)	153 (94%)	10 (6%)	0	100	100
23	LE0	163/171 (95%)	153 (94%)	10 (6%)	0	100	100
24	KEE	133/139 (96%)	125 (94%)	8 (6%)	0	100	100
24	LEE	133/139 (96%)	125 (94%)	8 (6%)	0	100	100
25	KF0	229/235 (97%)	216 (94%)	13 (6%)	0	100	100
25	LF0	229/235 (97%)	216 (94%)	13 (6%)	0	100	100
26	KFF	109/111 (98%)	97 (89%)	12 (11%)	0	100	100
26	LFF	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
27	KG0	197/206 (96%)	187 (95%)	10 (5%)	0	100	100
27	LG0	197/206 (96%)	187 (95%)	10 (5%)	0	100	100
28	KH0	181/187 (97%)	167 (92%)	14 (8%)	0	100	100
28	LH0	181/187 (97%)	167 (92%)	14 (8%)	0	100	100
29	KHH	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
29	LHH	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
30	KI0	215/218 (99%)	205 (95%)	10 (5%)	0	100	100
30	LI0	215/218 (99%)	205 (95%)	10 (5%)	0	100	100
31	KII	95/98 (97%)	92 (97%)	3 (3%)	0	100	100
31	LII	95/98 (97%)	92 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	KJ0	165/171 (96%)	143 (87%)	21 (13%)	1 (1%)	21	59
32	LJ0	165/171 (96%)	143 (87%)	21 (13%)	1 (1%)	21	59
33	KL0	162/165 (98%)	151 (93%)	9 (6%)	2 (1%)	10	44
33	LL0	162/165 (98%)	151 (93%)	9 (6%)	2 (1%)	10	44
34	KLL	49/52 (94%)	47 (96%)	2 (4%)	0	100	100
34	LLL	49/52 (94%)	47 (96%)	2 (4%)	0	100	100
35	KM0	113/122 (93%)	95 (84%)	18 (16%)	0	100	100
35	LM0	113/122 (93%)	95 (84%)	18 (16%)	0	100	100
36	KN0	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
36	LN0	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
37	KO0	196/198 (99%)	191 (97%)	5 (3%)	0	100	100
37	LO0	196/198 (99%)	191 (97%)	5 (3%)	0	100	100
38	KP0	152/167 (91%)	144 (95%)	8 (5%)	0	100	100
38	LP0	152/167 (91%)	143 (94%)	9 (6%)	0	100	100
39	KQ0	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
39	LQ0	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
40	KR0	162/168 (96%)	155 (96%)	7 (4%)	0	100	100
40	LR0	162/168 (96%)	155 (96%)	7 (4%)	0	100	100
41	KS0	168/171 (98%)	158 (94%)	10 (6%)	0	100	100
41	LS0	168/171 (98%)	158 (94%)	10 (6%)	0	100	100
42	KT0	154/158 (98%)	141 (92%)	13 (8%)	0	100	100
42	LT0	154/158 (98%)	142 (92%)	12 (8%)	0	100	100
43	KU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
43	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
44	KV0	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
44	LV0	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
45	KW0	100/131 (76%)	93 (93%)	7 (7%)	0	100	100
45	LW0	100/131 (76%)	93 (93%)	7 (7%)	0	100	100
46	KX0	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
46	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
47	KY0	129/131 (98%)	119 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	LY0	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
48	KZ0	116/153 (76%)	110 (95%)	6 (5%)	0	100	100
48	LZ0	116/153 (76%)	110 (95%)	6 (5%)	0	100	100
49	MD1	149/151 (99%)	124 (83%)	22 (15%)	3 (2%)	6	31
49	ND1	149/151 (99%)	124 (83%)	22 (15%)	3 (2%)	6	31
50	RA0	218/233 (94%)	201 (92%)	17 (8%)	0	100	100
50	SA0	218/233 (94%)	201 (92%)	17 (8%)	0	100	100
51	RCC	60/65 (92%)	60 (100%)	0	0	100	100
51	SCC	60/65 (92%)	60 (100%)	0	0	100	100
52	RE0	258/280 (92%)	233 (90%)	25 (10%)	0	100	100
52	SE0	258/280 (92%)	234 (91%)	24 (9%)	0	100	100
53	REE	54/60 (90%)	51 (94%)	3 (6%)	0	100	100
53	SEE	54/60 (90%)	51 (94%)	3 (6%)	0	100	100
54	RGG	315/326 (97%)	285 (90%)	30 (10%)	0	100	100
54	SGG	315/326 (97%)	285 (90%)	30 (10%)	0	100	100
55	RI0	165/173 (95%)	157 (95%)	8 (5%)	0	100	100
55	SI0	165/173 (95%)	157 (95%)	8 (5%)	0	100	100
56	RJ0	166/184 (90%)	150 (90%)	16 (10%)	0	100	100
56	SJ0	166/184 (90%)	150 (90%)	16 (10%)	0	100	100
57	RK0	86/107 (80%)	74 (86%)	12 (14%)	0	100	100
57	SK0	86/107 (80%)	74 (86%)	12 (14%)	0	100	100
58	RL0	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
58	SL0	148/155 (96%)	143 (97%)	5 (3%)	0	100	100
59	RM0	109/130 (84%)	109 (100%)	0	0	100	100
59	SM0	109/130 (84%)	109 (100%)	0	0	100	100
60	RN0	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
60	SN0	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
61	RO0	127/135 (94%)	126 (99%)	1 (1%)	0	100	100
61	SO0	127/135 (94%)	126 (99%)	1 (1%)	0	100	100
62	RP0	115/163 (71%)	105 (91%)	10 (9%)	0	100	100
62	SP0	115/163 (71%)	105 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RQ0	140/143 (98%)	135 (96%)	5 (4%)	0	100	100
63	SQ0	140/143 (98%)	135 (96%)	5 (4%)	0	100	100
64	RR0	117/120 (98%)	95 (81%)	22 (19%)	0	100	100
64	SR0	117/120 (98%)	95 (81%)	22 (19%)	0	100	100
65	RS0	142/160 (89%)	121 (85%)	21 (15%)	0	100	100
65	SS0	142/160 (89%)	121 (85%)	21 (15%)	0	100	100
66	RT0	140/143 (98%)	125 (89%)	15 (11%)	0	100	100
66	ST0	140/143 (98%)	125 (89%)	15 (11%)	0	100	100
67	RU0	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
67	SU0	98/119 (82%)	89 (91%)	9 (9%)	0	100	100
68	RV0	63/67 (94%)	51 (81%)	12 (19%)	0	100	100
68	SV0	63/67 (94%)	51 (81%)	12 (19%)	0	100	100
69	RX0	138/141 (98%)	117 (85%)	21 (15%)	0	100	100
69	SX0	138/141 (98%)	117 (85%)	21 (15%)	0	100	100
70	RY0	134/146 (92%)	119 (89%)	15 (11%)	0	100	100
70	SY0	134/146 (92%)	118 (88%)	16 (12%)	0	100	100
71	RZ0	74/128 (58%)	65 (88%)	9 (12%)	0	100	100
71	SZ0	74/128 (58%)	66 (89%)	8 (11%)	0	100	100
72	KD0	279/291 (96%)	269 (96%)	10 (4%)	0	100	100
72	LD0	279/291 (96%)	268 (96%)	11 (4%)	0	100	100
73	RDD	63/65 (97%)	49 (78%)	14 (22%)	0	100	100
73	SDD	63/65 (97%)	49 (78%)	14 (22%)	0	100	100
74	RD0	214/242 (88%)	207 (97%)	7 (3%)	0	100	100
74	SD0	214/242 (88%)	207 (97%)	7 (3%)	0	100	100
75	RG0	227/230 (99%)	209 (92%)	17 (8%)	1 (0%)	30	67
75	SG0	227/230 (99%)	209 (92%)	17 (8%)	1 (0%)	30	67
76	RH0	161/164 (98%)	152 (94%)	9 (6%)	0	100	100
76	SH0	161/164 (98%)	152 (94%)	9 (6%)	0	100	100
77	RW0	126/128 (98%)	117 (93%)	8 (6%)	1 (1%)	16	54
77	SW0	126/128 (98%)	117 (93%)	8 (6%)	1 (1%)	16	54
78	RF0	190/195 (97%)	173 (91%)	17 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	SF0	190/195 (97%)	173 (91%)	17 (9%)	0	100	100
79	RFF	52/150 (35%)	48 (92%)	4 (8%)	0	100	100
79	SFF	52/150 (35%)	48 (92%)	4 (8%)	0	100	100
All	All	24214/25932 (93%)	22460 (93%)	1734 (7%)	20 (0%)	49	83

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	LL0	44	TYR
75	SG0	173	ASP
33	KL0	44	TYR
75	RG0	173	ASP
11	LMM	108	ALA
33	LL0	142	MET
49	MD1	37	LYS
11	KMM	108	ALA
33	KL0	142	MET
49	ND1	37	LYS
49	MD1	30	SER
49	MD1	69	MET
49	ND1	30	SER
49	ND1	69	MET
77	SW0	56	GLU
77	RW0	56	GLU
8	A	29	LYS
8	B	29	LYS
32	LJ0	141	VAL
32	KJ0	141	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	137/137 (100%)	137 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	137/137 (100%)	137 (100%)	0	100	100
4	KGG	88/90 (98%)	87 (99%)	1 (1%)	65	76
4	LGG	88/90 (98%)	87 (99%)	1 (1%)	65	76
5	RB0	182/203 (90%)	181 (100%)	1 (0%)	81	83
5	SB0	182/203 (90%)	181 (100%)	1 (0%)	81	83
6	RC0	188/209 (90%)	188 (100%)	0	100	100
6	SC0	188/209 (90%)	188 (100%)	0	100	100
8	A	732/732 (100%)	732 (100%)	0	100	100
8	B	732/732 (100%)	732 (100%)	0	100	100
9	K	194/194 (100%)	194 (100%)	0	100	100
9	L	194/194 (100%)	194 (100%)	0	100	100
10	M	241/241 (100%)	241 (100%)	0	100	100
10	N	241/241 (100%)	241 (100%)	0	100	100
11	KMM	46/112 (41%)	42 (91%)	4 (9%)	9	29
11	LMM	46/112 (41%)	42 (91%)	4 (9%)	9	29
12	RBB	72/73 (99%)	71 (99%)	1 (1%)	59	72
12	SBB	72/73 (99%)	71 (99%)	1 (1%)	59	72
13	RAA	92/93 (99%)	92 (100%)	0	100	100
13	SAA	92/93 (99%)	92 (100%)	0	100	100
14	KOO	85/89 (96%)	85 (100%)	0	100	100
14	LOO	85/89 (96%)	85 (100%)	0	100	100
15	KPP	75/77 (97%)	75 (100%)	0	100	100
15	LPP	75/77 (97%)	75 (100%)	0	100	100
16	KJJ	78/81 (96%)	78 (100%)	0	100	100
16	LJJ	78/81 (96%)	78 (100%)	0	100	100
17	LA0	202/203 (100%)	200 (99%)	2 (1%)	68	78
17	LA02	202/203 (100%)	200 (99%)	2 (1%)	68	78
18	KAA	123/123 (100%)	121 (98%)	2 (2%)	55	70
18	LAA	123/123 (100%)	121 (98%)	2 (2%)	55	70
19	KB0	328/336 (98%)	328 (100%)	0	100	100
19	LB0	328/336 (98%)	328 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	KC0	277/278 (100%)	277 (100%)	0	100	100
20	LC0	277/278 (100%)	277 (100%)	0	100	100
21	KCC	87/97 (90%)	87 (100%)	0	100	100
21	LCC	87/97 (90%)	87 (100%)	0	100	100
22	KDD	99/100 (99%)	99 (100%)	0	100	100
22	LDD	99/100 (99%)	99 (100%)	0	100	100
23	KE0	153/159 (96%)	153 (100%)	0	100	100
23	LE0	153/159 (96%)	153 (100%)	0	100	100
24	KEE	118/122 (97%)	118 (100%)	0	100	100
24	LEE	118/122 (97%)	118 (100%)	0	100	100
25	KF0	212/216 (98%)	212 (100%)	0	100	100
25	LF0	212/216 (98%)	212 (100%)	0	100	100
26	KFF	98/98 (100%)	98 (100%)	0	100	100
26	LFF	98/98 (100%)	98 (100%)	0	100	100
27	KG0	183/190 (96%)	182 (100%)	1 (0%)	81	83
27	LG0	183/190 (96%)	182 (100%)	1 (0%)	81	83
28	KH0	165/169 (98%)	164 (99%)	1 (1%)	78	83
28	LH0	165/169 (98%)	164 (99%)	1 (1%)	78	83
29	KHH	110/110 (100%)	109 (99%)	1 (1%)	70	79
29	LHH	110/110 (100%)	109 (99%)	1 (1%)	70	79
30	KI0	188/189 (100%)	188 (100%)	0	100	100
30	LI0	188/189 (100%)	188 (100%)	0	100	100
31	KII	84/84 (100%)	83 (99%)	1 (1%)	63	75
31	LII	84/84 (100%)	83 (99%)	1 (1%)	63	75
32	KJ0	146/149 (98%)	146 (100%)	0	100	100
32	LJ0	146/149 (98%)	146 (100%)	0	100	100
33	KL0	148/149 (99%)	144 (97%)	4 (3%)	39	61
33	LL0	148/149 (99%)	144 (97%)	4 (3%)	39	61
34	KLL	46/47 (98%)	46 (100%)	0	100	100
34	LLL	46/47 (98%)	46 (100%)	0	100	100
35	KM0	110/117 (94%)	109 (99%)	1 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	LM0	110/117 (94%)	109 (99%)	1 (1%)	70	79
36	KN0	175/176 (99%)	175 (100%)	0	100	100
36	LN0	175/176 (99%)	175 (100%)	0	100	100
37	KO0	178/178 (100%)	177 (99%)	1 (1%)	78	83
37	LO0	178/178 (100%)	177 (99%)	1 (1%)	78	83
38	KP0	135/147 (92%)	135 (100%)	0	100	100
38	LP0	135/147 (92%)	135 (100%)	0	100	100
39	KQ0	165/166 (99%)	165 (100%)	0	100	100
39	LQ0	165/166 (99%)	165 (100%)	0	100	100
40	KR0	142/145 (98%)	142 (100%)	0	100	100
40	LR0	142/145 (98%)	142 (100%)	0	100	100
41	KS0	155/156 (99%)	153 (99%)	2 (1%)	61	74
41	LS0	155/156 (99%)	153 (99%)	2 (1%)	61	74
42	KT0	140/142 (99%)	139 (99%)	1 (1%)	76	81
42	LT0	140/142 (99%)	139 (99%)	1 (1%)	76	81
43	KU0	89/98 (91%)	88 (99%)	1 (1%)	65	76
43	LU0	89/98 (91%)	88 (99%)	1 (1%)	65	76
44	KV0	113/114 (99%)	113 (100%)	0	100	100
44	LV0	113/114 (99%)	113 (100%)	0	100	100
45	KW0	93/120 (78%)	93 (100%)	0	100	100
45	LW0	93/120 (78%)	93 (100%)	0	100	100
46	KX0	92/93 (99%)	92 (100%)	0	100	100
46	LX0	92/93 (99%)	92 (100%)	0	100	100
47	KY0	116/116 (100%)	116 (100%)	0	100	100
47	LY0	116/116 (100%)	116 (100%)	0	100	100
48	KZ0	106/141 (75%)	106 (100%)	0	100	100
48	LZ0	106/141 (75%)	106 (100%)	0	100	100
49	MD1	139/139 (100%)	136 (98%)	3 (2%)	45	64
49	ND1	139/139 (100%)	136 (98%)	3 (2%)	45	64
50	RA0	194/206 (94%)	194 (100%)	0	100	100
50	SA0	194/206 (94%)	194 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	RCC	51/54 (94%)	50 (98%)	1 (2%)	48	66
51	SCC	51/54 (94%)	50 (98%)	1 (2%)	48	66
52	RE0	231/251 (92%)	231 (100%)	0	100	100
52	SE0	231/251 (92%)	231 (100%)	0	100	100
53	REE	44/47 (94%)	44 (100%)	0	100	100
53	SEE	44/47 (94%)	44 (100%)	0	100	100
54	RGG	282/288 (98%)	282 (100%)	0	100	100
54	SGG	282/288 (98%)	282 (100%)	0	100	100
55	RI0	147/153 (96%)	147 (100%)	0	100	100
55	SI0	147/153 (96%)	147 (100%)	0	100	100
56	RJ0	152/165 (92%)	152 (100%)	0	100	100
56	SJ0	152/165 (92%)	152 (100%)	0	100	100
57	RK0	83/99 (84%)	83 (100%)	0	100	100
57	SK0	83/99 (84%)	83 (100%)	0	100	100
58	RL0	140/145 (97%)	139 (99%)	1 (1%)	76	81
58	SL0	140/145 (97%)	139 (99%)	1 (1%)	76	81
59	RM0	99/114 (87%)	99 (100%)	0	100	100
59	SM0	99/114 (87%)	99 (100%)	0	100	100
60	RN0	126/127 (99%)	126 (100%)	0	100	100
60	SN0	126/127 (99%)	126 (100%)	0	100	100
61	RO0	102/108 (94%)	102 (100%)	0	100	100
61	SO0	102/108 (94%)	102 (100%)	0	100	100
62	RP0	107/144 (74%)	106 (99%)	1 (1%)	70	79
62	SP0	107/144 (74%)	106 (99%)	1 (1%)	70	79
63	RQ0	120/121 (99%)	120 (100%)	0	100	100
63	SQ0	120/121 (99%)	120 (100%)	0	100	100
64	RR0	109/111 (98%)	109 (100%)	0	100	100
64	SR0	109/111 (98%)	109 (100%)	0	100	100
65	RS0	125/138 (91%)	125 (100%)	0	100	100
65	SS0	125/138 (91%)	125 (100%)	0	100	100
66	RT0	129/130 (99%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	ST0	129/130 (99%)	129 (100%)	0	100	100
67	RU0	92/110 (84%)	91 (99%)	1 (1%)	65	76
67	SU0	92/110 (84%)	91 (99%)	1 (1%)	65	76
68	RV0	61/63 (97%)	61 (100%)	0	100	100
68	SV0	61/63 (97%)	61 (100%)	0	100	100
69	RX0	115/116 (99%)	114 (99%)	1 (1%)	70	79
69	SX0	115/116 (99%)	114 (99%)	1 (1%)	70	79
70	RY0	126/136 (93%)	124 (98%)	2 (2%)	55	70
70	SY0	126/136 (93%)	124 (98%)	2 (2%)	55	70
71	RZ0	73/118 (62%)	73 (100%)	0	100	100
71	SZ0	73/118 (62%)	73 (100%)	0	100	100
72	KD0	251/261 (96%)	251 (100%)	0	100	100
72	LD0	251/261 (96%)	251 (100%)	0	100	100
73	RDD	57/57 (100%)	57 (100%)	0	100	100
73	SDD	57/57 (100%)	57 (100%)	0	100	100
74	RD0	189/215 (88%)	189 (100%)	0	100	100
74	SD0	189/215 (88%)	189 (100%)	0	100	100
75	RG0	199/200 (100%)	198 (100%)	1 (0%)	81	83
75	SG0	199/200 (100%)	198 (100%)	1 (0%)	81	83
76	RH0	153/154 (99%)	153 (100%)	0	100	100
76	SH0	153/154 (99%)	153 (100%)	0	100	100
77	RW0	111/111 (100%)	111 (100%)	0	100	100
77	SW0	111/111 (100%)	111 (100%)	0	100	100
78	RF0	167/170 (98%)	166 (99%)	1 (1%)	78	83
78	SF0	167/170 (98%)	166 (99%)	1 (1%)	78	83
79	RFF	48/136 (35%)	48 (100%)	0	100	100
79	SFF	48/136 (35%)	48 (100%)	0	100	100
All	All	21616/22892 (94%)	21542 (100%)	74 (0%)	84	86

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LGG	71	LYS

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Mol	Chain	Res	Type
5	SB0	228	ARG
11	LMM	91	ARG
11	LMM	92	LYS
11	LMM	103	HIS
11	LMM	105	ARG
12	SBB	64	ARG
17	LA0	64	LYS
17	LA0	148	ARG
18	LAA	49	HIS
18	LAA	54	ARG
27	LG0	72	ARG
28	LH0	94	LYS
29	LHH	105	THR
31	LII	72	LYS
33	LL0	1	MET
33	LL0	2	ARG
33	LL0	12	PHE
33	LL0	97	ARG
35	LM0	76	LYS
37	LO0	169	LYS
41	LS0	95	ARG
41	LS0	157	ARG
42	LT0	55	LYS
43	LU0	68	LYS
49	MD1	2	LYS
49	MD1	32	CYS
49	MD1	68	GLN
51	SCC	62	ARG
58	SL0	67	LYS
62	SP0	135	ARG
67	SU0	55	ARG
69	SX0	51	LYS
70	SY0	134	LYS
70	SY0	136	ARG
75	SG0	92	ARG
78	SF0	126	LYS
4	KG0	71	LYS
5	RB0	228	ARG
11	KMM	91	ARG
11	KMM	92	LYS
11	KMM	103	HIS
11	KMM	105	ARG

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Mol	Chain	Res	Type
12	RBB	64	ARG
17	LA02	64	LYS
17	LA02	148	ARG
18	KAA	49	HIS
18	KAA	54	ARG
27	KG0	72	ARG
28	KH0	94	LYS
29	KHH	105	THR
31	KII	72	LYS
33	KL0	1	MET
33	KL0	2	ARG
33	KL0	12	PHE
33	KL0	97	ARG
35	KM0	76	LYS
37	KO0	169	LYS
41	KS0	95	ARG
41	KS0	157	ARG
42	KT0	55	LYS
43	KU0	68	LYS
49	ND1	2	LYS
49	ND1	32	CYS
49	ND1	68	GLN
51	RCC	62	ARG
58	RL0	67	LYS
62	RP0	135	ARG
67	RU0	55	ARG
69	RX0	51	LYS
70	RY0	134	LYS
70	RY0	136	ARG
75	RG0	92	ARG
78	RF0	126	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
8	A	165	HIS
8	A	316	ASN
8	A	460	ASN
8	A	651	ASN
8	A	746	GLN
8	A	809	GLN
9	L	30	GLN

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Mol	Chain	Res	Type
9	L	53	GLN
9	L	139	ASN
9	L	164	HIS
8	B	165	HIS
8	B	460	ASN
8	B	651	ASN
9	K	30	GLN
9	K	53	GLN
9	K	139	ASN
9	K	164	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	K50	2603/2618 (99%)	755 (29%)	56 (2%)
1	L50	2603/2618 (99%)	755 (29%)	56 (2%)
2	R60	1353/1368 (98%)	561 (41%)	54 (3%)
2	S60	1353/1368 (98%)	561 (41%)	53 (3%)
7	K70	118/119 (99%)	29 (24%)	2 (1%)
7	L70	118/119 (99%)	29 (24%)	2 (1%)
All	All	8148/8210 (99%)	2690 (33%)	223 (2%)

All (2690) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	14	G
1	L50	15	G
1	L50	16	G
1	L50	17	A
1	L50	22	U
1	L50	23	U
1	L50	24	G
1	L50	43	G
1	L50	47	C
1	L50	48	A
1	L50	49	G
1	L50	50	C
1	L50	52	G
1	L50	59	A

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Mol	Chain	Res	Type
1	L50	61	A
1	L50	62	U
1	L50	68	G
1	L50	70	A
1	L50	71	G
1	L50	73	A
1	L50	75	C
1	L50	76	A
1	L50	87	C
1	L50	88	A
1	L50	97	A
1	L50	99	U
1	L50	100	A
1	L50	110	G
1	L50	111	C
1	L50	112	U
1	L50	114	G
1	L50	118	A
1	L50	123	U
1	L50	124	U
1	L50	132	A
1	L50	134	C
1	L50	135	A
1	L50	139	G
1	L50	149	A
1	L50	151	G
1	L50	152	A
1	L50	156	G
1	L50	157	A
1	L50	158	A
1	L50	159	A
1	L50	160	C
1	L50	161	U
1	L50	163	A
1	L50	164	C
1	L50	166	A
1	L50	167	G
1	L50	168	G
1	L50	169	A
1	L50	171	U
1	L50	178	G
1	L50	179	U

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Mol	Chain	Res	Type
1	L50	180	A
1	L50	184	G
1	L50	191	A
1	L50	193	C
1	L50	194	A
1	L50	199	A
1	L50	200	C
1	L50	202	G
1	L50	209	A
1	L50	210	G
1	L50	213	U
1	L50	216	U
1	L50	224	U
1	L50	225	G
1	L50	226	A
1	L50	237	A
1	L50	240	G
1	L50	243	A
1	L50	251	U
1	L50	255	U
1	L50	256	C
1	L50	266	A
1	L50	268	C
1	L50	276	U
1	L50	284	G
1	L50	285	A
1	L50	287	A
1	L50	290	C
1	L50	298	G
1	L50	302	U
1	L50	308	A
1	L50	309	U
1	L50	310	A
1	L50	311	C
1	L50	312	G
1	L50	314	U
1	L50	315	G
1	L50	316	A
1	L50	318	U
1	L50	331	U
1	L50	332	A
1	L50	333	A

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Mol	Chain	Res	Type
1	L50	340	G
1	L50	343	A
1	L50	345	G
1	L50	346	A
1	L50	347	G
1	L50	352	C
1	L50	353	A
1	L50	358	G
1	L50	360	A
1	L50	361	U
1	L50	364	A
1	L50	366	G
1	L50	371	A
1	L50	384	A
1	L50	385	C
1	L50	392	C
1	L50	396	G
1	L50	398	A
1	L50	400	U
1	L50	405	U
1	L50	408	C
1	L50	416	A
1	L50	437	G
1	L50	444	A
1	L50	449	U
1	L50	454	C
1	L50	459	C
1	L50	467	A
1	L50	481	G
1	L50	488	C
1	L50	492	G
1	L50	494	A
1	L50	495	A
1	L50	498	U
1	L50	499	G
1	L50	501	G
1	L50	503	A
1	L50	504	G
1	L50	507	G
1	L50	508	A
1	L50	509	A
1	L50	510	G

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Mol	Chain	Res	Type
1	L50	515	U
1	L50	517	A
1	L50	523	A
1	L50	524	G
1	L50	526	G
1	L50	534	A
1	L50	535	A
1	L50	537	G
1	L50	540	G
1	L50	547	U
1	L50	549	C
1	L50	556	A
1	L50	557	U
1	L50	558	A
1	L50	563	U
1	L50	564	G
1	L50	568	A
1	L50	569	C
1	L50	570	U
1	L50	580	U
1	L50	581	G
1	L50	592	U
1	L50	603	A
1	L50	604	G
1	L50	608	G
1	L50	609	A
1	L50	612	C
1	L50	615	C
1	L50	625	U
1	L50	631	G
1	L50	645	U
1	L50	647	A
1	L50	648	G
1	L50	658	G
1	L50	659	G
1	L50	665	A
1	L50	666	A
1	L50	667	G
1	L50	668	A
1	L50	672	A
1	L50	675	G
1	L50	676	A

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Mol	Chain	Res	Type
1	L50	685	G
1	L50	688	G
1	L50	695	C
1	L50	704	A
1	L50	710	A
1	L50	711	U
1	L50	716	A
1	L50	720	C
1	L50	724	C
1	L50	726	C
1	L50	727	G
1	L50	729	A
1	L50	732	G
1	L50	735	A
1	L50	736	A
1	L50	737	G
1	L50	739	A
1	L50	742	G
1	L50	749	A
1	L50	763	U
1	L50	765	A
1	L50	766	A
1	L50	767	G
1	L50	772	C
1	L50	778	A
1	L50	782	G
1	L50	795	U
1	L50	797	U
1	L50	799	C
1	L50	801	A
1	L50	802	U
1	L50	803	G
1	L50	806	A
1	L50	816	G
1	L50	830	G
1	L50	834	G
1	L50	843	A
1	L50	848	A
1	L50	849	A
1	L50	852	A
1	L50	853	A
1	L50	854	C

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Mol	Chain	Res	Type
1	L50	858	G
1	L50	859	C
1	L50	860	A
1	L50	864	U
1	L50	865	G
1	L50	867	U
1	L50	872	A
1	L50	878	A
1	L50	879	U
1	L50	881	U
1	L50	885	G
1	L50	886	A
1	L50	889	G
1	L50	893	C
1	L50	899	G
1	L50	900	A
1	L50	905	G
1	L50	915	G
1	L50	916	A
1	L50	919	G
1	L50	921	A
1	L50	922	G
1	L50	925	C
1	L50	926	G
1	L50	927	G
1	L50	930	G
1	L50	931	C
1	L50	933	A
1	L50	934	U
1	L50	935	G
1	L50	936	G
1	L50	938	A
1	L50	939	G
1	L50	940	U
1	L50	941	C
1	L50	942	G
1	L50	945	A
1	L50	946	U
1	L50	947	C
1	L50	948	C
1	L50	949	G
1	L50	950	G

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Mol	Chain	Res	Type
1	L50	951	U
1	L50	953	A
1	L50	954	G
1	L50	955	A
1	L50	956	A
1	L50	957	A
1	L50	959	G
1	L50	961	G
1	L50	963	U
1	L50	964	A
1	L50	965	C
1	L50	966	A
1	L50	967	A
1	L50	968	C
1	L50	969	G
1	L50	970	U
1	L50	971	A
1	L50	972	C
1	L50	973	C
1	L50	975	A
1	L50	978	G
1	L50	980	A
1	L50	985	U
1	L50	988	G
1	L50	993	G
1	L50	998	U
1	L50	1000	G
1	L50	1001	A
1	L50	1002	U
1	L50	1006	G
1	L50	1010	A
1	L50	1012	C
1	L50	1015	A
1	L50	1018	U
1	L50	1019	C
1	L50	1021	G
1	L50	1022	A
1	L50	1024	G
1	L50	1032	A
1	L50	1034	C
1	L50	1036	G
1	L50	1047	G

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Mol	Chain	Res	Type
1	L50	1050	U
1	L50	1053	C
1	L50	1059	G
1	L50	1061	G
1	L50	1067	A
1	L50	1068	C
1	L50	1075	A
1	L50	1076	U
1	L50	1084	G
1	L50	1085	G
1	L50	1087	G
1	L50	1092	A
1	L50	1096	A
1	L50	1097	G
1	L50	1099	G
1	L50	1101	A
1	L50	1102	G
1	L50	1104	U
1	L50	1105	C
1	L50	1111	G
1	L50	1116	U
1	L50	1117	A
1	L50	1120	G
1	L50	1121	A
1	L50	1123	A
1	L50	1124	A
1	L50	1130	C
1	L50	1131	U
1	L50	1133	C
1	L50	1135	G
1	L50	1136	C
1	L50	1140	A
1	L50	1141	A
1	L50	1142	A
1	L50	1144	A
1	L50	1148	A
1	L50	1149	G
1	L50	1150	G
1	L50	1155	G
1	L50	1163	U
1	L50	1169	C
1	L50	1170	A

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Mol	Chain	Res	Type
1	L50	1171	U
1	L50	1172	A
1	L50	1173	A
1	L50	1176	A
1	L50	1177	G
1	L50	1181	G
1	L50	1182	A
1	L50	1183	G
1	L50	1185	C
1	L50	1189	U
1	L50	1192	A
1	L50	1198	G
1	L50	1204	A
1	L50	1206	A
1	L50	1217	A
1	L50	1218	A
1	L50	1223	A
1	L50	1226	C
1	L50	1227	A
1	L50	1229	G
1	L50	1231	U
1	L50	1232	G
1	L50	1233	A
1	L50	1235	A
1	L50	1236	U
1	L50	1237	U
1	L50	1247	G
1	L50	1250	C
1	L50	1254	C
1	L50	1257	A
1	L50	1264	C
1	L50	1268	U
1	L50	1270	U
1	L50	1271	U
1	L50	1273	G
1	L50	1274	C
1	L50	1278	U
1	L50	1281	A
1	L50	1283	A
1	L50	1308	A
1	L50	1309	C
1	L50	1318	U

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Mol	Chain	Res	Type
1	L50	1327	A
1	L50	1332	G
1	L50	1339	G
1	L50	1340	A
1	L50	1341	G
1	L50	1342	A
1	L50	1346	A
1	L50	1351	C
1	L50	1360	U
1	L50	1374	U
1	L50	1375	G
1	L50	1383	C
1	L50	1385	G
1	L50	1387	G
1	L50	1388	C
1	L50	1391	G
1	L50	1393	U
1	L50	1395	U
1	L50	1396	G
1	L50	1400	A
1	L50	1411	C
1	L50	1412	C
1	L50	1414	U
1	L50	1415	G
1	L50	1416	A
1	L50	1417	A
1	L50	1421	A
1	L50	1427	A
1	L50	1429	A
1	L50	1430	U
1	L50	1431	G
1	L50	1437	A
1	L50	1441	U
1	L50	1449	A
1	L50	1450	A
1	L50	1454	U
1	L50	1457	C
1	L50	1458	A
1	L50	1463	U
1	L50	1465	C
1	L50	1466	A
1	L50	1468	G

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Mol	Chain	Res	Type
1	L50	1474	G
1	L50	1485	G
1	L50	1486	G
1	L50	1488	U
1	L50	1489	G
1	L50	1490	U
1	L50	1491	U
1	L50	1492	U
1	L50	1499	U
1	L50	1500	G
1	L50	1503	A
1	L50	1504	G
1	L50	1506	G
1	L50	1513	G
1	L50	1527	U
1	L50	1535	G
1	L50	1536	G
1	L50	1539	A
1	L50	1547	G
1	L50	1554	U
1	L50	1555	G
1	L50	1556	U
1	L50	1557	G
1	L50	1563	A
1	L50	1564	U
1	L50	1565	U
1	L50	1571	A
1	L50	1573	G
1	L50	1574	G
1	L50	1583	A
1	L50	1592	U
1	L50	1603	C
1	L50	1609	G
1	L50	1610	A
1	L50	1611	A
1	L50	1612	G
1	L50	1613	A
1	L50	1614	G
1	L50	1619	G
1	L50	1625	A
1	L50	1626	G
1	L50	1628	U

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Mol	Chain	Res	Type
1	L50	1629	C
1	L50	1643	G
1	L50	1645	C
1	L50	1649	A
1	L50	1651	A
1	L50	1653	G
1	L50	1668	A
1	L50	1675	G
1	L50	1679	A
1	L50	1680	A
1	L50	1685	G
1	L50	1687	G
1	L50	1688	A
1	L50	1692	A
1	L50	1693	C
1	L50	1700	U
1	L50	1705	U
1	L50	1706	A
1	L50	1708	G
1	L50	1709	G
1	L50	1715	A
1	L50	1717	A
1	L50	1718	C
1	L50	1720	C
1	L50	1723	C
1	L50	1724	G
1	L50	1731	A
1	L50	1733	A
1	L50	1734	U
1	L50	1739	A
1	L50	1740	C
1	L50	1742	C
1	L50	1743	G
1	L50	1744	C
1	L50	1746	U
1	L50	1749	A
1	L50	1751	G
1	L50	1753	A
1	L50	1754	A
1	L50	1755	U
1	L50	1756	G
1	L50	1760	A

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Mol	Chain	Res	Type
1	L50	1771	G
1	L50	1772	U
1	L50	1797	A
1	L50	1801	C
1	L50	1803	A
1	L50	1808	A
1	L50	1809	A
1	L50	1810	C
1	L50	1811	G
1	L50	1828	G
1	L50	1832	A
1	L50	1836	A
1	L50	1837	A
1	L50	1838	G
1	L50	1839	A
1	L50	1846	U
1	L50	1854	A
1	L50	1862	G
1	L50	1869	A
1	L50	1876	A
1	L50	1880	U
1	L50	1882	G
1	L50	1883	A
1	L50	1884	G
1	L50	1885	G
1	L50	1886	C
1	L50	1887	G
1	L50	1889	U
1	L50	1890	G
1	L50	1893	G
1	L50	1895	A
1	L50	1896	A
1	L50	1897	G
1	L50	1898	G
1	L50	1899	U
1	L50	1902	A
1	L50	1903	G
1	L50	1905	G
1	L50	1912	C
1	L50	1915	A
1	L50	1916	A
1	L50	1917	G

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Mol	Chain	Res	Type
1	L50	1919	G
1	L50	1920	A
1	L50	1921	A
1	L50	1923	G
1	L50	1927	A
1	L50	1928	C
1	L50	1929	U
1	L50	1930	G
1	L50	1931	C
1	L50	1933	C
1	L50	1934	C
1	L50	1937	G
1	L50	1939	U
1	L50	1940	C
1	L50	1947	A
1	L50	1950	C
1	L50	1951	A
1	L50	1953	U
1	L50	1956	U
1	L50	1957	U
1	L50	1958	U
1	L50	1959	A
1	L50	1961	G
1	L50	1962	G
1	L50	1963	A
1	L50	1964	C
1	L50	1967	A
1	L50	1977	G
1	L50	1978	G
1	L50	1983	U
1	L50	1985	G
1	L50	1990	G
1	L50	1991	G
1	L50	1995	G
1	L50	1997	A
1	L50	1999	G
1	L50	2008	A
1	L50	2011	A
1	L50	2013	A
1	L50	2019	G
1	L50	2023	A
1	L50	2027	A

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Mol	Chain	Res	Type
1	L50	2028	A
1	L50	2036	A
1	L50	2037	C
1	L50	2039	G
1	L50	2042	A
1	L50	2043	G
1	L50	2044	A
1	L50	2045	C
1	L50	2046	G
1	L50	2047	A
1	L50	2048	G
1	L50	2053	C
1	L50	2054	U
1	L50	2055	C
1	L50	2057	U
1	L50	2059	U
1	L50	2060	A
1	L50	2061	G
1	L50	2062	A
1	L50	2067	A
1	L50	2073	U
1	L50	2075	A
1	L50	2076	A
1	L50	2077	G
1	L50	2078	A
1	L50	2079	G
1	L50	2085	G
1	L50	2087	G
1	L50	2093	G
1	L50	2098	A
1	L50	2109	G
1	L50	2110	A
1	L50	2111	G
1	L50	2122	G
1	L50	2124	C
1	L50	2130	G
1	L50	2131	A
1	L50	2136	A
1	L50	2140	A
1	L50	2141	U
1	L50	2142	A
1	L50	2145	A

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Mol	Chain	Res	Type
1	L50	2152	U
1	L50	2159	U
1	L50	2164	G
1	L50	2168	G
1	L50	2169	A
1	L50	2170	A
1	L50	2178	C
1	L50	2184	G
1	L50	2185	A
1	L50	2206	A
1	L50	2210	U
1	L50	2211	A
1	L50	2213	A
1	L50	2218	G
1	L50	2221	G
1	L50	2227	U
1	L50	2228	U
1	L50	2229	U
1	L50	2235	C
1	L50	2239	G
1	L50	2243	U
1	L50	2253	C
1	L50	2255	A
1	L50	2260	G
1	L50	2262	C
1	L50	2266	G
1	L50	2267	C
1	L50	2268	A
1	L50	2269	G
1	L50	2270	C
1	L50	2272	G
1	L50	2279	A
1	L50	2282	G
1	L50	2291	U
1	L50	2296	C
1	L50	2303	C
1	L50	2304	A
1	L50	2309	A
1	L50	2310	C
1	L50	2313	G
1	L50	2319	G
1	L50	2322	U

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Mol	Chain	Res	Type
1	L50	2323	U
1	L50	2325	G
1	L50	2335	A
1	L50	2339	A
1	L50	2340	G
1	L50	2345	G
1	L50	2351	U
1	L50	2355	A
1	L50	2360	C
1	L50	2366	A
1	L50	2368	U
1	L50	2376	A
1	L50	2377	G
1	L50	2379	G
1	L50	2388	U
1	L50	2391	G
1	L50	2401	C
1	L50	2420	C
1	L50	2423	C
1	L50	2428	G
1	L50	2435	A
1	L50	2436	G
1	L50	2441	A
1	L50	2447	A
1	L50	2453	C
1	L50	2454	G
1	L50	2458	C
1	L50	2459	C
1	L50	2460	U
1	L50	2467	U
1	L50	2469	G
1	L50	2470	C
1	L50	2471	U
1	L50	2473	G
1	L50	2474	A
1	L50	2477	C
1	L50	2478	C
1	L50	2480	C
1	L50	2481	U
1	L50	2482	A
1	L50	2483	A
1	L50	2487	A

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Mol	Chain	Res	Type
1	L50	2488	G
1	L50	2490	A
1	L50	2491	A
1	L50	2501	A
1	L50	2519	G
1	L50	2520	A
1	L50	2534	U
1	L50	2535	U
1	L50	2539	A
1	L50	2540	G
1	L50	2542	G
1	L50	2543	G
1	L50	2549	U
1	L50	2553	A
1	L50	2561	U
1	L50	2562	U
1	L50	2563	U
1	L50	2568	U
1	L50	2582	G
1	L50	2588	G
1	L50	2595	U
1	L50	2596	G
1	L50	2598	U
1	L50	2599	U
1	L50	2606	A
2	S60	2	C
2	S60	3	C
2	S60	7	U
2	S60	8	U
2	S60	18	U
2	S60	32	G
2	S60	33	U
2	S60	35	U
2	S60	39	A
2	S60	40	G
2	S60	41	A
2	S60	43	U
2	S60	45	A
2	S60	48	C
2	S60	54	U
2	S60	55	G
2	S60	56	U

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Mol	Chain	Res	Type
2	S60	57	G
2	S60	58	U
2	S60	59	A
2	S60	61	G
2	S60	62	C
2	S60	63	G
2	S60	64	A
2	S60	65	A
2	S60	66	G
2	S60	68	G
2	S60	69	A
2	S60	71	U
2	S60	72	A
2	S60	74	U
2	S60	75	G
2	S60	76	A
2	S60	77	A
2	S60	78	G
2	S60	79	C
2	S60	80	G
2	S60	84	G
2	S60	85	A
2	S60	86	A
2	S60	92	A
2	S60	94	U
2	S60	96	A
2	S60	97	C
2	S60	106	A
2	S60	107	U
2	S60	116	U
2	S60	118	G
2	S60	119	A
2	S60	121	C
2	S60	127	A
2	S60	128	A
2	S60	130	C
2	S60	133	A
2	S60	134	G
2	S60	135	G
2	S60	136	A
2	S60	137	A
2	S60	138	A

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Mol	Chain	Res	Type
2	S60	140	A
2	S60	141	G
2	S60	142	A
2	S60	143	G
2	S60	144	G
2	S60	149	A
2	S60	150	A
2	S60	181	A
2	S60	183	G
2	S60	184	A
2	S60	186	A
2	S60	187	A
2	S60	188	C
2	S60	190	A
2	S60	191	C
2	S60	193	G
2	S60	194	U
2	S60	195	G
2	S60	197	A
2	S60	204	U
2	S60	205	A
2	S60	214	U
2	S60	215	C
2	S60	220	C
2	S60	221	A
2	S60	222	G
2	S60	226	G
2	S60	241	G
2	S60	242	C
2	S60	247	U
2	S60	255	A
2	S60	256	G
2	S60	263	A
2	S60	264	C
2	S60	266	G
2	S60	268	G
2	S60	280	G
2	S60	281	A
2	S60	283	U
2	S60	284	C
2	S60	287	G
2	S60	288	A

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Mol	Chain	Res	Type
2	S60	289	G
2	S60	302	A
2	S60	303	G
2	S60	304	A
2	S60	305	C
2	S60	306	G
2	S60	307	G
2	S60	309	U
2	S60	310	A
2	S60	311	C
2	S60	315	G
2	S60	317	C
2	S60	318	C
2	S60	319	A
2	S60	320	A
2	S60	321	G
2	S60	327	C
2	S60	328	A
2	S60	329	G
2	S60	331	A
2	S60	337	G
2	S60	339	A
2	S60	340	A
2	S60	341	A
2	S60	342	U
2	S60	343	U
2	S60	347	G
2	S60	355	C
2	S60	356	A
2	S60	357	A
2	S60	358	G
2	S60	362	G
2	S60	363	C
2	S60	364	G
2	S60	371	A
2	S60	372	A
2	S60	378	G
2	S60	380	G
2	S60	383	A
2	S60	384	A
2	S60	385	C
2	S60	387	A

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Mol	Chain	Res	Type
2	S60	388	G
2	S60	389	U
2	S60	390	G
2	S60	391	U
2	S60	392	G
2	S60	393	U
2	S60	394	G
2	S60	398	A
2	S60	400	A
2	S60	401	C
2	S60	403	A
2	S60	404	C
2	S60	406	U
2	S60	407	G
2	S60	408	A
2	S60	409	G
2	S60	414	U
2	S60	416	G
2	S60	418	G
2	S60	420	U
2	S60	421	C
2	S60	422	A
2	S60	424	G
2	S60	425	G
2	S60	426	C
2	S60	429	G
2	S60	430	U
2	S60	431	G
2	S60	432	C
2	S60	434	A
2	S60	435	G
2	S60	437	A
2	S60	438	U
2	S60	439	C
2	S60	440	C
2	S60	441	G
2	S60	443	G
2	S60	444	G
2	S60	445	U
2	S60	446	A
2	S60	447	A
2	S60	448	U

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Mol	Chain	Res	Type
2	S60	449	A
2	S60	450	C
2	S60	451	C
2	S60	452	A
2	S60	453	G
2	S60	461	A
2	S60	462	G
2	S60	463	U
2	S60	465	U
2	S60	468	A
2	S60	474	A
2	S60	477	G
2	S60	478	C
2	S60	484	U
2	S60	486	A
2	S60	487	A
2	S60	490	G
2	S60	499	U
2	S60	501	G
2	S60	502	A
2	S60	505	A
2	S60	506	A
2	S60	507	C
2	S60	510	U
2	S60	512	C
2	S60	520	U
2	S60	521	A
2	S60	523	U
2	S60	524	G
2	S60	527	G
2	S60	535	A
2	S60	540	C
2	S60	554	A
2	S60	562	G
2	S60	565	U
2	S60	566	A
2	S60	567	A
2	S60	568	G
2	S60	570	A
2	S60	578	A
2	S60	581	G
2	S60	582	C

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Mol	Chain	Res	Type
2	S60	587	U
2	S60	590	U
2	S60	593	A
2	S60	599	G
2	S60	600	A
2	S60	601	G
2	S60	608	A
2	S60	609	A
2	S60	610	U
2	S60	621	G
2	S60	622	C
2	S60	623	U
2	S60	624	U
2	S60	627	G
2	S60	635	G
2	S60	646	G
2	S60	647	C
2	S60	653	A
2	S60	662	U
2	S60	668	G
2	S60	676	A
2	S60	680	A
2	S60	685	G
2	S60	686	G
2	S60	687	A
2	S60	690	A
2	S60	694	A
2	S60	700	A
2	S60	702	U
2	S60	703	A
2	S60	705	A
2	S60	707	A
2	S60	712	A
2	S60	714	U
2	S60	716	G
2	S60	722	G
2	S60	728	A
2	S60	730	C
2	S60	731	G
2	S60	732	A
2	S60	733	U
2	S60	734	G

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Mol	Chain	Res	Type
2	S60	736	C
2	S60	738	A
2	S60	739	C
2	S60	740	G
2	S60	749	G
2	S60	752	A
2	S60	754	G
2	S60	755	A
2	S60	756	G
2	S60	760	G
2	S60	768	A
2	S60	775	U
2	S60	776	A
2	S60	777	G
2	S60	778	U
2	S60	780	G
2	S60	781	G
2	S60	788	G
2	S60	806	G
2	S60	808	G
2	S60	812	A
2	S60	817	A
2	S60	818	A
2	S60	820	G
2	S60	824	A
2	S60	826	U
2	S60	828	A
2	S60	830	G
2	S60	831	G
2	S60	832	A
2	S60	833	A
2	S60	835	A
2	S60	836	A
2	S60	839	C
2	S60	840	C
2	S60	841	A
2	S60	849	U
2	S60	852	A
2	S60	854	U
2	S60	866	U
2	S60	868	U
2	S60	872	U

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Mol	Chain	Res	Type
2	S60	873	C
2	S60	874	A
2	S60	875	A
2	S60	877	G
2	S60	878	C
2	S60	879	G
2	S60	880	G
2	S60	883	C
2	S60	884	A
2	S60	887	U
2	S60	890	C
2	S60	898	G
2	S60	899	A
2	S60	906	U
2	S60	908	U
2	S60	909	G
2	S60	911	G
2	S60	912	C
2	S60	913	G
2	S60	914	U
2	S60	915	A
2	S60	916	G
2	S60	917	U
2	S60	918	A
2	S60	919	C
2	S60	921	C
2	S60	922	G
2	S60	924	U
2	S60	925	A
2	S60	926	G
2	S60	927	G
2	S60	929	C
2	S60	937	G
2	S60	941	C
2	S60	947	C
2	S60	948	G
2	S60	950	U
2	S60	952	A
2	S60	953	C
2	S60	955	A
2	S60	957	G
2	S60	959	G

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Mol	Chain	Res	Type
2	S60	960	U
2	S60	968	C
2	S60	969	C
2	S60	970	U
2	S60	971	U
2	S60	972	U
2	S60	974	G
2	S60	980	G
2	S60	981	U
2	S60	985	C
2	S60	986	G
2	S60	987	A
2	S60	988	A
2	S60	989	G
2	S60	990	U
2	S60	992	G
2	S60	995	A
2	S60	996	G
2	S60	998	U
2	S60	1000	C
2	S60	1001	C
2	S60	1003	A
2	S60	1004	G
2	S60	1005	G
2	S60	1006	A
2	S60	1011	A
2	S60	1012	A
2	S60	1013	A
2	S60	1014	G
2	S60	1017	A
2	S60	1018	U
2	S60	1019	C
2	S60	1021	A
2	S60	1022	C
2	S60	1023	A
2	S60	1024	G
2	S60	1028	U
2	S60	1029	U
2	S60	1030	A
2	S60	1031	A
2	S60	1033	A
2	S60	1034	A

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Mol	Chain	Res	Type
2	S60	1037	C
2	S60	1039	G
2	S60	1040	G
2	S60	1041	A
2	S60	1042	A
2	S60	1043	G
2	S60	1044	G
2	S60	1045	A
2	S60	1046	A
2	S60	1047	G
2	S60	1048	G
2	S60	1049	G
2	S60	1050	G
2	S60	1051	C
2	S60	1052	A
2	S60	1053	A
2	S60	1055	A
2	S60	1056	A
2	S60	1057	C
2	S60	1058	A
2	S60	1059	G
2	S60	1060	G
2	S60	1061	U
2	S60	1062	C
2	S60	1063	A
2	S60	1064	G
2	S60	1065	U
2	S60	1066	G
2	S60	1067	A
2	S60	1071	C
2	S60	1073	U
2	S60	1075	A
2	S60	1076	G
2	S60	1077	A
2	S60	1083	U
2	S60	1084	G
2	S60	1085	G
2	S60	1089	G
2	S60	1090	C
2	S60	1091	A
2	S60	1094	C
2	S60	1096	C

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Mol	Chain	Res	Type
2	S60	1097	A
2	S60	1100	A
2	S60	1102	A
2	S60	1103	G
2	S60	1105	G
2	S60	1110	C
2	S60	1113	C
2	S60	1114	A
2	S60	1116	A
2	S60	1117	A
2	S60	1118	A
2	S60	1119	C
2	S60	1120	A
2	S60	1121	A
2	S60	1122	A
2	S60	1123	U
2	S60	1124	A
2	S60	1125	G
2	S60	1126	A
2	S60	1127	A
2	S60	1130	A
2	S60	1132	A
2	S60	1133	U
2	S60	1136	G
2	S60	1137	A
2	S60	1138	U
2	S60	1139	C
2	S60	1141	A
2	S60	1142	G
2	S60	1143	A
2	S60	1146	G
2	S60	1155	C
2	S60	1158	U
2	S60	1161	U
2	S60	1164	G
2	S60	1165	C
2	S60	1166	A
2	S60	1168	A
2	S60	1169	G
2	S60	1171	A
2	S60	1173	C
2	S60	1178	A

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Mol	Chain	Res	Type
2	S60	1182	G
2	S60	1185	A
2	S60	1190	U
2	S60	1191	C
2	S60	1192	G
2	S60	1193	U
2	S60	1195	A
2	S60	1197	C
2	S60	1198	U
2	S60	1199	C
2	S60	1200	A
2	S60	1202	U
2	S60	1203	A
2	S60	1204	A
2	S60	1205	G
2	S60	1206	A
2	S60	1207	A
2	S60	1208	G
2	S60	1209	C
2	S60	1210	G
2	S60	1211	A
2	S60	1214	A
2	S60	1215	A
2	S60	1216	U
2	S60	1217	G
2	S60	1221	C
2	S60	1223	C
2	S60	1225	G
2	S60	1230	U
2	S60	1232	G
2	S60	1233	U
2	S60	1237	C
2	S60	1239	C
2	S60	1240	C
2	S60	1248	G
2	S60	1250	U
2	S60	1251	A
2	S60	1260	G
2	S60	1262	A
2	S60	1263	A
2	S60	1266	A
2	S60	1267	G

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Mol	Chain	Res	Type
2	S60	1274	A
2	S60	1283	A
2	S60	1284	G
2	S60	1287	A
2	S60	1291	A
2	S60	1292	G
2	S60	1294	G
2	S60	1295	C
2	S60	1296	A
2	S60	1297	G
2	S60	1298	G
2	S60	1300	U
2	S60	1301	U
2	S60	1302	C
2	S60	1303	U
2	S60	1308	C
2	S60	1310	G
2	S60	1312	U
2	S60	1313	A
2	S60	1314	C
2	S60	1315	A
2	S60	1316	A
2	S60	1317	G
2	S60	1319	C
2	S60	1320	G
2	S60	1322	A
2	S60	1325	A
2	S60	1326	A
2	S60	1327	G
2	S60	1328	G
2	S60	1329	C
2	S60	1340	G
2	S60	1342	A
2	S60	1343	C
2	S60	1346	G
2	S60	1352	G
2	S60	1354	A
2	S60	1355	U
2	S60	1356	C
2	S60	1357	A
7	L70	2	G
7	L70	3	U

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Mol	Chain	Res	Type
7	L70	4	U
7	L70	5	A
7	L70	7	G
7	L70	14	U
7	L70	17	A
7	L70	22	A
7	L70	26	C
7	L70	27	A
7	L70	28	C
7	L70	29	C
7	L70	33	U
7	L70	34	C
7	L70	41	G
7	L70	42	A
7	L70	45	U
7	L70	49	A
7	L70	50	A
7	L70	54	A
7	L70	55	A
7	L70	63	A
7	L70	64	G
7	L70	67	C
7	L70	76	U
7	L70	91	C
7	L70	100	A
7	L70	101	A
7	L70	110	G
1	K50	2	U
1	K50	3	A
1	K50	14	G
1	K50	15	G
1	K50	16	G
1	K50	17	A
1	K50	22	U
1	K50	23	U
1	K50	24	G
1	K50	43	G
1	K50	47	C
1	K50	48	A
1	K50	49	G
1	K50	50	C
1	K50	52	G

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Mol	Chain	Res	Type
1	K50	59	A
1	K50	61	A
1	K50	62	U
1	K50	68	G
1	K50	70	A
1	K50	71	G
1	K50	73	A
1	K50	75	C
1	K50	76	A
1	K50	87	C
1	K50	88	A
1	K50	97	A
1	K50	99	U
1	K50	100	A
1	K50	110	G
1	K50	111	C
1	K50	112	U
1	K50	114	G
1	K50	118	A
1	K50	123	U
1	K50	124	U
1	K50	132	A
1	K50	134	C
1	K50	135	A
1	K50	139	G
1	K50	149	A
1	K50	151	G
1	K50	152	A
1	K50	156	G
1	K50	157	A
1	K50	158	A
1	K50	159	A
1	K50	160	C
1	K50	161	U
1	K50	163	A
1	K50	164	C
1	K50	166	A
1	K50	167	G
1	K50	168	G
1	K50	169	A
1	K50	171	U
1	K50	178	G

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Mol	Chain	Res	Type
1	K50	179	U
1	K50	180	A
1	K50	184	G
1	K50	191	A
1	K50	193	C
1	K50	194	A
1	K50	199	A
1	K50	200	C
1	K50	202	G
1	K50	209	A
1	K50	210	G
1	K50	213	U
1	K50	216	U
1	K50	224	U
1	K50	225	G
1	K50	226	A
1	K50	237	A
1	K50	240	G
1	K50	243	A
1	K50	251	U
1	K50	255	U
1	K50	256	C
1	K50	266	A
1	K50	268	C
1	K50	276	U
1	K50	284	G
1	K50	285	A
1	K50	287	A
1	K50	290	C
1	K50	298	G
1	K50	302	U
1	K50	308	A
1	K50	309	U
1	K50	310	A
1	K50	311	C
1	K50	312	G
1	K50	314	U
1	K50	315	G
1	K50	316	A
1	K50	318	U
1	K50	331	U
1	K50	332	A

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Mol	Chain	Res	Type
1	K50	333	A
1	K50	340	G
1	K50	343	A
1	K50	345	G
1	K50	346	A
1	K50	347	G
1	K50	352	C
1	K50	353	A
1	K50	358	G
1	K50	360	A
1	K50	361	U
1	K50	364	A
1	K50	366	G
1	K50	371	A
1	K50	384	A
1	K50	385	C
1	K50	392	C
1	K50	396	G
1	K50	398	A
1	K50	400	U
1	K50	405	U
1	K50	408	C
1	K50	416	A
1	K50	437	G
1	K50	444	A
1	K50	449	U
1	K50	454	C
1	K50	459	C
1	K50	467	A
1	K50	481	G
1	K50	488	C
1	K50	492	G
1	K50	494	A
1	K50	495	A
1	K50	498	U
1	K50	499	G
1	K50	501	G
1	K50	503	A
1	K50	504	G
1	K50	507	G
1	K50	508	A
1	K50	509	A

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Mol	Chain	Res	Type
1	K50	510	G
1	K50	515	U
1	K50	517	A
1	K50	523	A
1	K50	524	G
1	K50	526	G
1	K50	534	A
1	K50	535	A
1	K50	537	G
1	K50	540	G
1	K50	547	U
1	K50	549	C
1	K50	556	A
1	K50	557	U
1	K50	558	A
1	K50	563	U
1	K50	564	G
1	K50	568	A
1	K50	569	C
1	K50	570	U
1	K50	580	U
1	K50	581	G
1	K50	592	U
1	K50	603	A
1	K50	604	G
1	K50	608	G
1	K50	609	A
1	K50	612	C
1	K50	615	C
1	K50	625	U
1	K50	631	G
1	K50	645	U
1	K50	647	A
1	K50	648	G
1	K50	658	G
1	K50	659	G
1	K50	665	A
1	K50	666	A
1	K50	667	G
1	K50	668	A
1	K50	672	A
1	K50	675	G

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Mol	Chain	Res	Type
1	K50	676	A
1	K50	685	G
1	K50	688	G
1	K50	695	C
1	K50	704	A
1	K50	710	A
1	K50	711	U
1	K50	716	A
1	K50	720	C
1	K50	724	C
1	K50	726	C
1	K50	727	G
1	K50	729	A
1	K50	732	G
1	K50	735	A
1	K50	736	A
1	K50	737	G
1	K50	739	A
1	K50	742	G
1	K50	749	A
1	K50	763	U
1	K50	765	A
1	K50	766	A
1	K50	767	G
1	K50	772	C
1	K50	778	A
1	K50	782	G
1	K50	795	U
1	K50	797	U
1	K50	799	C
1	K50	801	A
1	K50	802	U
1	K50	803	G
1	K50	806	A
1	K50	816	G
1	K50	830	G
1	K50	834	G
1	K50	843	A
1	K50	848	A
1	K50	849	A
1	K50	852	A
1	K50	853	A

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Mol	Chain	Res	Type
1	K50	854	C
1	K50	858	G
1	K50	859	C
1	K50	860	A
1	K50	864	U
1	K50	865	G
1	K50	867	U
1	K50	872	A
1	K50	878	A
1	K50	879	U
1	K50	881	U
1	K50	885	G
1	K50	886	A
1	K50	889	G
1	K50	893	C
1	K50	899	G
1	K50	900	A
1	K50	905	G
1	K50	915	G
1	K50	916	A
1	K50	919	G
1	K50	921	A
1	K50	922	G
1	K50	925	C
1	K50	926	G
1	K50	927	G
1	K50	930	G
1	K50	931	C
1	K50	933	A
1	K50	934	U
1	K50	935	G
1	K50	936	G
1	K50	938	A
1	K50	939	G
1	K50	940	U
1	K50	941	C
1	K50	942	G
1	K50	945	A
1	K50	946	U
1	K50	947	C
1	K50	948	C
1	K50	949	G

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Mol	Chain	Res	Type
1	K50	950	G
1	K50	951	U
1	K50	953	A
1	K50	954	G
1	K50	955	A
1	K50	956	A
1	K50	957	A
1	K50	959	G
1	K50	961	G
1	K50	963	U
1	K50	964	A
1	K50	965	C
1	K50	966	A
1	K50	967	A
1	K50	968	C
1	K50	969	G
1	K50	970	U
1	K50	971	A
1	K50	972	C
1	K50	973	C
1	K50	975	A
1	K50	978	G
1	K50	980	A
1	K50	985	U
1	K50	988	G
1	K50	993	G
1	K50	998	U
1	K50	1000	G
1	K50	1001	A
1	K50	1002	U
1	K50	1006	G
1	K50	1010	A
1	K50	1012	C
1	K50	1015	A
1	K50	1018	U
1	K50	1019	C
1	K50	1021	G
1	K50	1022	A
1	K50	1024	G
1	K50	1032	A
1	K50	1034	C
1	K50	1036	G

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Mol	Chain	Res	Type
1	K50	1047	G
1	K50	1050	U
1	K50	1053	C
1	K50	1059	G
1	K50	1061	G
1	K50	1067	A
1	K50	1068	C
1	K50	1075	A
1	K50	1076	U
1	K50	1084	G
1	K50	1085	G
1	K50	1087	G
1	K50	1092	A
1	K50	1096	A
1	K50	1097	G
1	K50	1099	G
1	K50	1101	A
1	K50	1102	G
1	K50	1104	U
1	K50	1105	C
1	K50	1111	G
1	K50	1116	U
1	K50	1117	A
1	K50	1120	G
1	K50	1121	A
1	K50	1123	A
1	K50	1124	A
1	K50	1130	C
1	K50	1131	U
1	K50	1133	C
1	K50	1135	G
1	K50	1136	C
1	K50	1140	A
1	K50	1141	A
1	K50	1142	A
1	K50	1144	A
1	K50	1148	A
1	K50	1149	G
1	K50	1150	G
1	K50	1155	G
1	K50	1163	U
1	K50	1169	C

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Mol	Chain	Res	Type
1	K50	1170	A
1	K50	1171	U
1	K50	1172	A
1	K50	1173	A
1	K50	1176	A
1	K50	1177	G
1	K50	1181	G
1	K50	1182	A
1	K50	1183	G
1	K50	1185	C
1	K50	1189	U
1	K50	1192	A
1	K50	1198	G
1	K50	1204	A
1	K50	1206	A
1	K50	1217	A
1	K50	1218	A
1	K50	1223	A
1	K50	1226	C
1	K50	1227	A
1	K50	1229	G
1	K50	1231	U
1	K50	1232	G
1	K50	1233	A
1	K50	1235	A
1	K50	1236	U
1	K50	1237	U
1	K50	1247	G
1	K50	1250	C
1	K50	1254	C
1	K50	1257	A
1	K50	1264	C
1	K50	1268	U
1	K50	1270	U
1	K50	1271	U
1	K50	1273	G
1	K50	1274	C
1	K50	1278	U
1	K50	1281	A
1	K50	1283	A
1	K50	1308	A
1	K50	1309	C

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Mol	Chain	Res	Type
1	K50	1318	U
1	K50	1327	A
1	K50	1332	G
1	K50	1339	G
1	K50	1340	A
1	K50	1341	G
1	K50	1342	A
1	K50	1346	A
1	K50	1351	C
1	K50	1360	U
1	K50	1374	U
1	K50	1375	G
1	K50	1383	C
1	K50	1385	G
1	K50	1387	G
1	K50	1388	C
1	K50	1391	G
1	K50	1393	U
1	K50	1395	U
1	K50	1396	G
1	K50	1400	A
1	K50	1411	C
1	K50	1412	C
1	K50	1414	U
1	K50	1415	G
1	K50	1416	A
1	K50	1417	A
1	K50	1421	A
1	K50	1427	A
1	K50	1429	A
1	K50	1430	U
1	K50	1431	G
1	K50	1437	A
1	K50	1441	U
1	K50	1449	A
1	K50	1450	A
1	K50	1454	U
1	K50	1457	C
1	K50	1458	A
1	K50	1463	U
1	K50	1465	C
1	K50	1466	A

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Mol	Chain	Res	Type
1	K50	1468	G
1	K50	1474	G
1	K50	1485	G
1	K50	1486	G
1	K50	1488	U
1	K50	1489	G
1	K50	1490	U
1	K50	1491	U
1	K50	1492	U
1	K50	1499	U
1	K50	1500	G
1	K50	1503	A
1	K50	1504	G
1	K50	1506	G
1	K50	1513	G
1	K50	1527	U
1	K50	1535	G
1	K50	1536	G
1	K50	1539	A
1	K50	1547	G
1	K50	1554	U
1	K50	1555	G
1	K50	1556	U
1	K50	1557	G
1	K50	1563	A
1	K50	1564	U
1	K50	1565	U
1	K50	1571	A
1	K50	1573	G
1	K50	1574	G
1	K50	1583	A
1	K50	1592	U
1	K50	1603	C
1	K50	1609	G
1	K50	1610	A
1	K50	1611	A
1	K50	1612	G
1	K50	1613	A
1	K50	1614	G
1	K50	1619	G
1	K50	1625	A
1	K50	1626	G

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Mol	Chain	Res	Type
1	K50	1628	U
1	K50	1629	C
1	K50	1643	G
1	K50	1645	C
1	K50	1649	A
1	K50	1651	A
1	K50	1653	G
1	K50	1668	A
1	K50	1675	G
1	K50	1679	A
1	K50	1680	A
1	K50	1685	G
1	K50	1687	G
1	K50	1688	A
1	K50	1692	A
1	K50	1693	C
1	K50	1700	U
1	K50	1705	U
1	K50	1706	A
1	K50	1708	G
1	K50	1709	G
1	K50	1715	A
1	K50	1717	A
1	K50	1718	C
1	K50	1720	C
1	K50	1723	C
1	K50	1724	G
1	K50	1731	A
1	K50	1733	A
1	K50	1734	U
1	K50	1739	A
1	K50	1740	C
1	K50	1742	C
1	K50	1743	G
1	K50	1744	C
1	K50	1746	U
1	K50	1749	A
1	K50	1751	G
1	K50	1753	A
1	K50	1754	A
1	K50	1755	U
1	K50	1756	G

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Mol	Chain	Res	Type
1	K50	1760	A
1	K50	1771	G
1	K50	1772	U
1	K50	1797	A
1	K50	1801	C
1	K50	1803	A
1	K50	1808	A
1	K50	1809	A
1	K50	1810	C
1	K50	1811	G
1	K50	1828	G
1	K50	1832	A
1	K50	1836	A
1	K50	1837	A
1	K50	1838	G
1	K50	1839	A
1	K50	1846	U
1	K50	1854	A
1	K50	1862	G
1	K50	1869	A
1	K50	1876	A
1	K50	1880	U
1	K50	1882	G
1	K50	1883	A
1	K50	1884	G
1	K50	1885	G
1	K50	1886	C
1	K50	1887	G
1	K50	1889	U
1	K50	1890	G
1	K50	1893	G
1	K50	1895	A
1	K50	1896	A
1	K50	1897	G
1	K50	1898	G
1	K50	1899	U
1	K50	1902	A
1	K50	1903	G
1	K50	1905	G
1	K50	1912	C
1	K50	1915	A
1	K50	1916	A

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Mol	Chain	Res	Type
1	K50	1917	G
1	K50	1919	G
1	K50	1920	A
1	K50	1921	A
1	K50	1923	G
1	K50	1927	A
1	K50	1928	C
1	K50	1929	U
1	K50	1930	G
1	K50	1931	C
1	K50	1933	C
1	K50	1934	C
1	K50	1937	G
1	K50	1939	U
1	K50	1940	C
1	K50	1947	A
1	K50	1950	C
1	K50	1951	A
1	K50	1953	U
1	K50	1956	U
1	K50	1957	U
1	K50	1958	U
1	K50	1959	A
1	K50	1961	G
1	K50	1962	G
1	K50	1963	A
1	K50	1964	C
1	K50	1967	A
1	K50	1977	G
1	K50	1978	G
1	K50	1983	U
1	K50	1985	G
1	K50	1990	G
1	K50	1991	G
1	K50	1995	G
1	K50	1997	A
1	K50	1999	G
1	K50	2008	A
1	K50	2011	A
1	K50	2013	A
1	K50	2019	G
1	K50	2023	A

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Mol	Chain	Res	Type
1	K50	2027	A
1	K50	2028	A
1	K50	2036	A
1	K50	2037	C
1	K50	2039	G
1	K50	2042	A
1	K50	2043	G
1	K50	2044	A
1	K50	2045	C
1	K50	2046	G
1	K50	2047	A
1	K50	2048	G
1	K50	2053	C
1	K50	2054	U
1	K50	2055	C
1	K50	2057	U
1	K50	2059	U
1	K50	2060	A
1	K50	2061	G
1	K50	2062	A
1	K50	2067	A
1	K50	2073	U
1	K50	2075	A
1	K50	2076	A
1	K50	2077	G
1	K50	2078	A
1	K50	2079	G
1	K50	2085	G
1	K50	2087	G
1	K50	2093	G
1	K50	2098	A
1	K50	2109	G
1	K50	2110	A
1	K50	2111	G
1	K50	2122	G
1	K50	2124	C
1	K50	2130	G
1	K50	2131	A
1	K50	2136	A
1	K50	2140	A
1	K50	2141	U
1	K50	2142	A

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Mol	Chain	Res	Type
1	K50	2145	A
1	K50	2152	U
1	K50	2159	U
1	K50	2164	G
1	K50	2168	G
1	K50	2169	A
1	K50	2170	A
1	K50	2178	C
1	K50	2184	G
1	K50	2185	A
1	K50	2206	A
1	K50	2210	U
1	K50	2211	A
1	K50	2213	A
1	K50	2218	G
1	K50	2221	G
1	K50	2227	U
1	K50	2228	U
1	K50	2229	U
1	K50	2235	C
1	K50	2239	G
1	K50	2243	U
1	K50	2253	C
1	K50	2255	A
1	K50	2260	G
1	K50	2262	C
1	K50	2266	G
1	K50	2267	C
1	K50	2268	A
1	K50	2269	G
1	K50	2270	C
1	K50	2272	G
1	K50	2279	A
1	K50	2282	G
1	K50	2291	U
1	K50	2296	C
1	K50	2303	C
1	K50	2304	A
1	K50	2309	A
1	K50	2310	C
1	K50	2313	G
1	K50	2319	G

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Mol	Chain	Res	Type
1	K50	2322	U
1	K50	2323	U
1	K50	2325	G
1	K50	2335	A
1	K50	2339	A
1	K50	2340	G
1	K50	2345	G
1	K50	2351	U
1	K50	2355	A
1	K50	2360	C
1	K50	2366	A
1	K50	2368	U
1	K50	2376	A
1	K50	2377	G
1	K50	2379	G
1	K50	2388	U
1	K50	2391	G
1	K50	2401	C
1	K50	2420	C
1	K50	2423	C
1	K50	2428	G
1	K50	2435	A
1	K50	2436	G
1	K50	2441	A
1	K50	2447	A
1	K50	2453	C
1	K50	2454	G
1	K50	2458	C
1	K50	2459	C
1	K50	2460	U
1	K50	2467	U
1	K50	2469	G
1	K50	2470	C
1	K50	2471	U
1	K50	2473	G
1	K50	2474	A
1	K50	2477	C
1	K50	2478	C
1	K50	2480	C
1	K50	2481	U
1	K50	2482	A
1	K50	2483	A

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Mol	Chain	Res	Type
1	K50	2487	A
1	K50	2488	G
1	K50	2490	A
1	K50	2491	A
1	K50	2501	A
1	K50	2519	G
1	K50	2520	A
1	K50	2534	U
1	K50	2535	U
1	K50	2539	A
1	K50	2540	G
1	K50	2542	G
1	K50	2543	G
1	K50	2549	U
1	K50	2553	A
1	K50	2561	U
1	K50	2562	U
1	K50	2563	U
1	K50	2568	U
1	K50	2582	G
1	K50	2588	G
1	K50	2595	U
1	K50	2596	G
1	K50	2598	U
1	K50	2599	U
1	K50	2606	A
2	R60	2	C
2	R60	3	C
2	R60	7	U
2	R60	8	U
2	R60	18	U
2	R60	32	G
2	R60	33	U
2	R60	35	U
2	R60	39	A
2	R60	40	G
2	R60	41	A
2	R60	43	U
2	R60	45	A
2	R60	48	C
2	R60	54	U
2	R60	55	G

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Mol	Chain	Res	Type
2	R60	56	U
2	R60	57	G
2	R60	58	U
2	R60	59	A
2	R60	61	G
2	R60	62	C
2	R60	63	G
2	R60	64	A
2	R60	65	A
2	R60	66	G
2	R60	68	G
2	R60	69	A
2	R60	71	U
2	R60	72	A
2	R60	74	U
2	R60	75	G
2	R60	76	A
2	R60	77	A
2	R60	78	G
2	R60	79	C
2	R60	80	G
2	R60	84	G
2	R60	85	A
2	R60	86	A
2	R60	92	A
2	R60	94	U
2	R60	96	A
2	R60	97	C
2	R60	106	A
2	R60	107	U
2	R60	116	U
2	R60	118	G
2	R60	119	A
2	R60	121	C
2	R60	127	A
2	R60	128	A
2	R60	130	C
2	R60	133	A
2	R60	134	G
2	R60	135	G
2	R60	136	A
2	R60	137	A

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Mol	Chain	Res	Type
2	R60	138	A
2	R60	140	A
2	R60	141	G
2	R60	142	A
2	R60	143	G
2	R60	144	G
2	R60	149	A
2	R60	150	A
2	R60	181	A
2	R60	183	G
2	R60	184	A
2	R60	186	A
2	R60	187	A
2	R60	188	C
2	R60	190	A
2	R60	191	C
2	R60	193	G
2	R60	194	U
2	R60	195	G
2	R60	197	A
2	R60	204	U
2	R60	205	A
2	R60	214	U
2	R60	215	C
2	R60	220	C
2	R60	221	A
2	R60	222	G
2	R60	226	G
2	R60	241	G
2	R60	242	C
2	R60	247	U
2	R60	255	A
2	R60	256	G
2	R60	263	A
2	R60	264	C
2	R60	266	G
2	R60	268	G
2	R60	280	G
2	R60	281	A
2	R60	283	U
2	R60	284	C
2	R60	287	G

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Mol	Chain	Res	Type
2	R60	288	A
2	R60	289	G
2	R60	302	A
2	R60	303	G
2	R60	304	A
2	R60	305	C
2	R60	306	G
2	R60	307	G
2	R60	309	U
2	R60	310	A
2	R60	311	C
2	R60	315	G
2	R60	317	C
2	R60	318	C
2	R60	319	A
2	R60	320	A
2	R60	321	G
2	R60	327	C
2	R60	328	A
2	R60	329	G
2	R60	331	A
2	R60	337	G
2	R60	339	A
2	R60	340	A
2	R60	341	A
2	R60	342	U
2	R60	343	U
2	R60	347	G
2	R60	355	C
2	R60	356	A
2	R60	357	A
2	R60	358	G
2	R60	362	G
2	R60	363	C
2	R60	364	G
2	R60	371	A
2	R60	372	A
2	R60	378	G
2	R60	380	G
2	R60	383	A
2	R60	384	A
2	R60	385	C

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Mol	Chain	Res	Type
2	R60	387	A
2	R60	388	G
2	R60	389	U
2	R60	390	G
2	R60	391	U
2	R60	392	G
2	R60	393	U
2	R60	394	G
2	R60	398	A
2	R60	400	A
2	R60	401	C
2	R60	403	A
2	R60	404	C
2	R60	406	U
2	R60	407	G
2	R60	408	A
2	R60	409	G
2	R60	414	U
2	R60	416	G
2	R60	418	G
2	R60	420	U
2	R60	421	C
2	R60	422	A
2	R60	424	G
2	R60	425	G
2	R60	426	C
2	R60	429	G
2	R60	430	U
2	R60	431	G
2	R60	432	C
2	R60	434	A
2	R60	435	G
2	R60	437	A
2	R60	438	U
2	R60	439	C
2	R60	440	C
2	R60	441	G
2	R60	443	G
2	R60	444	G
2	R60	445	U
2	R60	446	A
2	R60	447	A

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Mol	Chain	Res	Type
2	R60	448	U
2	R60	449	A
2	R60	450	C
2	R60	451	C
2	R60	452	A
2	R60	453	G
2	R60	461	A
2	R60	462	G
2	R60	463	U
2	R60	465	U
2	R60	468	A
2	R60	474	A
2	R60	477	G
2	R60	478	C
2	R60	484	U
2	R60	486	A
2	R60	487	A
2	R60	490	G
2	R60	499	U
2	R60	501	G
2	R60	502	A
2	R60	505	A
2	R60	506	A
2	R60	507	C
2	R60	510	U
2	R60	512	C
2	R60	520	U
2	R60	521	A
2	R60	523	U
2	R60	524	G
2	R60	527	G
2	R60	535	A
2	R60	540	C
2	R60	554	A
2	R60	562	G
2	R60	565	U
2	R60	566	A
2	R60	567	A
2	R60	568	G
2	R60	570	A
2	R60	578	A
2	R60	581	G

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Mol	Chain	Res	Type
2	R60	582	C
2	R60	587	U
2	R60	590	U
2	R60	593	A
2	R60	599	G
2	R60	600	A
2	R60	601	G
2	R60	608	A
2	R60	609	A
2	R60	610	U
2	R60	621	G
2	R60	622	C
2	R60	623	U
2	R60	624	U
2	R60	627	G
2	R60	635	G
2	R60	646	G
2	R60	647	C
2	R60	653	A
2	R60	662	U
2	R60	668	G
2	R60	676	A
2	R60	680	A
2	R60	685	G
2	R60	686	G
2	R60	687	A
2	R60	690	A
2	R60	694	A
2	R60	700	A
2	R60	702	U
2	R60	703	A
2	R60	705	A
2	R60	707	A
2	R60	712	A
2	R60	714	U
2	R60	716	G
2	R60	722	G
2	R60	728	A
2	R60	730	C
2	R60	731	G
2	R60	732	A
2	R60	733	U

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Mol	Chain	Res	Type
2	R60	734	G
2	R60	736	C
2	R60	738	A
2	R60	739	C
2	R60	740	G
2	R60	749	G
2	R60	752	A
2	R60	754	G
2	R60	755	A
2	R60	756	G
2	R60	760	G
2	R60	768	A
2	R60	775	U
2	R60	776	A
2	R60	777	G
2	R60	778	U
2	R60	780	G
2	R60	781	G
2	R60	788	G
2	R60	806	G
2	R60	808	G
2	R60	812	A
2	R60	817	A
2	R60	818	A
2	R60	820	G
2	R60	824	A
2	R60	826	U
2	R60	828	A
2	R60	830	G
2	R60	831	G
2	R60	832	A
2	R60	833	A
2	R60	835	A
2	R60	836	A
2	R60	839	C
2	R60	840	C
2	R60	841	A
2	R60	849	U
2	R60	852	A
2	R60	854	U
2	R60	866	U
2	R60	868	U

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Mol	Chain	Res	Type
2	R60	872	U
2	R60	873	C
2	R60	874	A
2	R60	875	A
2	R60	877	G
2	R60	878	C
2	R60	879	G
2	R60	880	G
2	R60	883	C
2	R60	884	A
2	R60	887	U
2	R60	890	C
2	R60	898	G
2	R60	899	A
2	R60	906	U
2	R60	908	U
2	R60	909	G
2	R60	911	G
2	R60	912	C
2	R60	913	G
2	R60	914	U
2	R60	915	A
2	R60	916	G
2	R60	917	U
2	R60	918	A
2	R60	919	C
2	R60	921	C
2	R60	922	G
2	R60	924	U
2	R60	925	A
2	R60	926	G
2	R60	927	G
2	R60	929	C
2	R60	937	G
2	R60	941	C
2	R60	947	C
2	R60	948	G
2	R60	950	U
2	R60	952	A
2	R60	953	C
2	R60	955	A
2	R60	957	G

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Mol	Chain	Res	Type
2	R60	959	G
2	R60	960	U
2	R60	968	C
2	R60	969	C
2	R60	970	U
2	R60	971	U
2	R60	972	U
2	R60	974	G
2	R60	980	G
2	R60	981	U
2	R60	985	C
2	R60	986	G
2	R60	987	A
2	R60	988	A
2	R60	989	G
2	R60	990	U
2	R60	992	G
2	R60	995	A
2	R60	996	G
2	R60	998	U
2	R60	1000	C
2	R60	1001	C
2	R60	1003	A
2	R60	1004	G
2	R60	1005	G
2	R60	1006	A
2	R60	1011	A
2	R60	1012	A
2	R60	1013	A
2	R60	1014	G
2	R60	1017	A
2	R60	1018	U
2	R60	1019	C
2	R60	1021	A
2	R60	1022	C
2	R60	1023	A
2	R60	1024	G
2	R60	1028	U
2	R60	1029	U
2	R60	1030	A
2	R60	1031	A
2	R60	1033	A

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Mol	Chain	Res	Type
2	R60	1034	A
2	R60	1037	C
2	R60	1039	G
2	R60	1040	G
2	R60	1041	A
2	R60	1042	A
2	R60	1043	G
2	R60	1044	G
2	R60	1045	A
2	R60	1046	A
2	R60	1047	G
2	R60	1048	G
2	R60	1049	G
2	R60	1050	G
2	R60	1051	C
2	R60	1052	A
2	R60	1053	A
2	R60	1055	A
2	R60	1056	A
2	R60	1057	C
2	R60	1058	A
2	R60	1059	G
2	R60	1060	G
2	R60	1061	U
2	R60	1062	C
2	R60	1063	A
2	R60	1064	G
2	R60	1065	U
2	R60	1066	G
2	R60	1067	A
2	R60	1071	C
2	R60	1073	U
2	R60	1075	A
2	R60	1076	G
2	R60	1077	A
2	R60	1083	U
2	R60	1084	G
2	R60	1085	G
2	R60	1089	G
2	R60	1090	C
2	R60	1091	A
2	R60	1094	C

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Mol	Chain	Res	Type
2	R60	1096	C
2	R60	1097	A
2	R60	1100	A
2	R60	1102	A
2	R60	1103	G
2	R60	1105	G
2	R60	1110	C
2	R60	1113	C
2	R60	1114	A
2	R60	1116	A
2	R60	1117	A
2	R60	1118	A
2	R60	1119	C
2	R60	1120	A
2	R60	1121	A
2	R60	1122	A
2	R60	1123	U
2	R60	1124	A
2	R60	1125	G
2	R60	1126	A
2	R60	1127	A
2	R60	1130	A
2	R60	1132	A
2	R60	1133	U
2	R60	1136	G
2	R60	1137	A
2	R60	1138	U
2	R60	1139	C
2	R60	1141	A
2	R60	1142	G
2	R60	1143	A
2	R60	1146	G
2	R60	1155	C
2	R60	1158	U
2	R60	1161	U
2	R60	1164	G
2	R60	1165	C
2	R60	1166	A
2	R60	1168	A
2	R60	1169	G
2	R60	1171	A
2	R60	1173	C

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Mol	Chain	Res	Type
2	R60	1178	A
2	R60	1182	G
2	R60	1185	A
2	R60	1190	U
2	R60	1191	C
2	R60	1192	G
2	R60	1193	U
2	R60	1195	A
2	R60	1197	C
2	R60	1198	U
2	R60	1199	C
2	R60	1200	A
2	R60	1202	U
2	R60	1203	A
2	R60	1204	A
2	R60	1205	G
2	R60	1206	A
2	R60	1207	A
2	R60	1208	G
2	R60	1209	C
2	R60	1210	G
2	R60	1211	A
2	R60	1214	A
2	R60	1215	A
2	R60	1216	U
2	R60	1217	G
2	R60	1221	C
2	R60	1223	C
2	R60	1225	G
2	R60	1230	U
2	R60	1232	G
2	R60	1233	U
2	R60	1237	C
2	R60	1239	C
2	R60	1240	C
2	R60	1248	G
2	R60	1250	U
2	R60	1251	A
2	R60	1260	G
2	R60	1262	A
2	R60	1263	A
2	R60	1266	A

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Mol	Chain	Res	Type
2	R60	1267	G
2	R60	1274	A
2	R60	1283	A
2	R60	1284	G
2	R60	1287	A
2	R60	1291	A
2	R60	1292	G
2	R60	1294	G
2	R60	1295	C
2	R60	1296	A
2	R60	1297	G
2	R60	1298	G
2	R60	1300	U
2	R60	1301	U
2	R60	1302	C
2	R60	1303	U
2	R60	1308	C
2	R60	1310	G
2	R60	1312	U
2	R60	1313	A
2	R60	1314	C
2	R60	1315	A
2	R60	1316	A
2	R60	1317	G
2	R60	1319	C
2	R60	1320	G
2	R60	1322	A
2	R60	1325	A
2	R60	1326	A
2	R60	1327	G
2	R60	1328	G
2	R60	1329	C
2	R60	1340	G
2	R60	1342	A
2	R60	1343	C
2	R60	1346	G
2	R60	1352	G
2	R60	1354	A
2	R60	1355	U
2	R60	1356	C
2	R60	1357	A
7	K70	2	G

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Mol	Chain	Res	Type
7	K70	3	U
7	K70	4	U
7	K70	5	A
7	K70	7	G
7	K70	14	U
7	K70	17	A
7	K70	22	A
7	K70	26	C
7	K70	27	A
7	K70	28	C
7	K70	29	C
7	K70	33	U
7	K70	34	C
7	K70	41	G
7	K70	42	A
7	K70	45	U
7	K70	49	A
7	K70	50	A
7	K70	54	A
7	K70	55	A
7	K70	63	A
7	K70	64	G
7	K70	67	C
7	K70	76	U
7	K70	91	C
7	K70	100	A
7	K70	101	A
7	K70	110	G

All (223) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L50	1	A
1	L50	14	G
1	L50	21	U
1	L50	75	C
1	L50	150	G
1	L50	156	G
1	L50	166	A
1	L50	201	A
1	L50	225	G
1	L50	242	A

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Mol	Chain	Res	Type
1	L50	308	A
1	L50	311	C
1	L50	330	G
1	L50	494	A
1	L50	536	A
1	L50	548	G
1	L50	562	U
1	L50	667	G
1	L50	723	G
1	L50	904	A
1	L50	921	A
1	L50	924	G
1	L50	934	U
1	L50	952	A
1	L50	956	A
1	L50	970	U
1	L50	971	A
1	L50	972	C
1	L50	1134	A
1	L50	1148	A
1	L50	1277	G
1	L50	1394	U
1	L50	1395	U
1	L50	1415	G
1	L50	1491	U
1	L50	1686	G
1	L50	1733	A
1	L50	1835	G
1	L50	1875	G
1	L50	1883	A
1	L50	1898	G
1	L50	1904	A
1	L50	1928	C
1	L50	1929	U
1	L50	1946	G
1	L50	1950	C
1	L50	2109	G
1	L50	2205	G
1	L50	2267	C
1	L50	2268	A
1	L50	2269	G
1	L50	2452	A

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Mol	Chain	Res	Type
1	L50	2470	C
1	L50	2481	U
1	L50	2486	U
1	L50	2597	G
2	S60	1	A
2	S60	17	C
2	S60	56	U
2	S60	67	C
2	S60	74	U
2	S60	78	G
2	S60	141	G
2	S60	149	A
2	S60	180	G
2	S60	193	G
2	S60	262	U
2	S60	319	A
2	S60	355	C
2	S60	362	G
2	S60	363	C
2	S60	383	A
2	S60	391	U
2	S60	408	A
2	S60	417	A
2	S60	420	U
2	S60	421	C
2	S60	425	G
2	S60	447	A
2	S60	448	U
2	S60	473	G
2	S60	565	U
2	S60	738	A
2	S60	780	G
2	S60	825	U
2	S60	872	U
2	S60	873	C
2	S60	874	A
2	S60	877	G
2	S60	911	G
2	S60	913	G
2	S60	915	A
2	S60	989	G
2	S60	1002	U

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Mol	Chain	Res	Type
2	S60	1018	U
2	S60	1021	A
2	S60	1023	A
2	S60	1033	A
2	S60	1041	A
2	S60	1044	G
2	S60	1132	A
2	S60	1135	U
2	S60	1191	C
2	S60	1196	U
2	S60	1203	A
2	S60	1210	G
2	S60	1311	A
2	S60	1313	A
2	S60	1314	C
7	L70	48	G
7	L70	49	A
1	K50	1	A
1	K50	14	G
1	K50	21	U
1	K50	75	C
1	K50	150	G
1	K50	156	G
1	K50	166	A
1	K50	201	A
1	K50	225	G
1	K50	242	A
1	K50	308	A
1	K50	311	C
1	K50	330	G
1	K50	494	A
1	K50	536	A
1	K50	548	G
1	K50	562	U
1	K50	667	G
1	K50	723	G
1	K50	904	A
1	K50	921	A
1	K50	924	G
1	K50	934	U
1	K50	952	A
1	K50	956	A

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Mol	Chain	Res	Type
1	K50	970	U
1	K50	971	A
1	K50	972	C
1	K50	1134	A
1	K50	1148	A
1	K50	1277	G
1	K50	1394	U
1	K50	1395	U
1	K50	1415	G
1	K50	1491	U
1	K50	1686	G
1	K50	1733	A
1	K50	1835	G
1	K50	1875	G
1	K50	1883	A
1	K50	1898	G
1	K50	1904	A
1	K50	1928	C
1	K50	1929	U
1	K50	1946	G
1	K50	1950	C
1	K50	2109	G
1	K50	2205	G
1	K50	2267	C
1	K50	2268	A
1	K50	2269	G
1	K50	2452	A
1	K50	2470	C
1	K50	2481	U
1	K50	2486	U
1	K50	2597	G
2	R60	1	A
2	R60	17	C
2	R60	56	U
2	R60	67	C
2	R60	74	U
2	R60	78	G
2	R60	83	G
2	R60	141	G
2	R60	149	A
2	R60	180	G
2	R60	193	G

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Mol	Chain	Res	Type
2	R60	262	U
2	R60	319	A
2	R60	355	C
2	R60	362	G
2	R60	363	C
2	R60	383	A
2	R60	391	U
2	R60	408	A
2	R60	417	A
2	R60	420	U
2	R60	421	C
2	R60	425	G
2	R60	447	A
2	R60	448	U
2	R60	473	G
2	R60	565	U
2	R60	738	A
2	R60	780	G
2	R60	825	U
2	R60	872	U
2	R60	873	C
2	R60	874	A
2	R60	877	G
2	R60	911	G
2	R60	913	G
2	R60	915	A
2	R60	989	G
2	R60	1002	U
2	R60	1018	U
2	R60	1021	A
2	R60	1023	A
2	R60	1033	A
2	R60	1041	A
2	R60	1044	G
2	R60	1132	A
2	R60	1135	U
2	R60	1191	C
2	R60	1196	U
2	R60	1203	A
2	R60	1210	G
2	R60	1311	A
2	R60	1313	A

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Mol	Chain	Res	Type
2	R60	1314	C
7	K70	48	G
7	K70	49	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 18 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 [i](#)

There are no chain breaks in this entry.

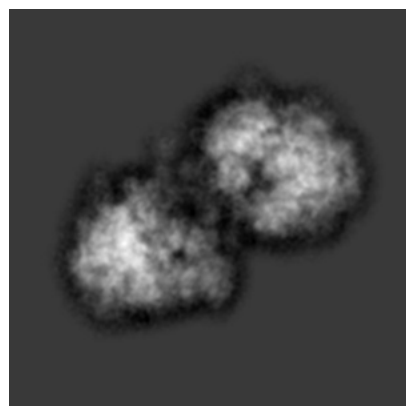
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55402. These allow visual inspection of the internal detail of the map and identification of artifacts.

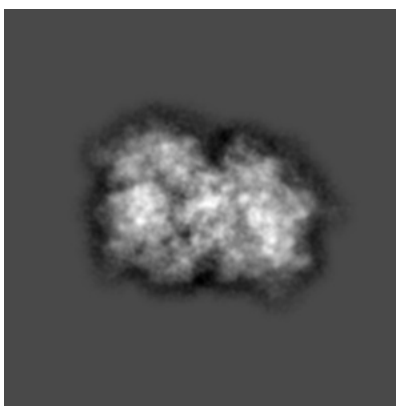
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

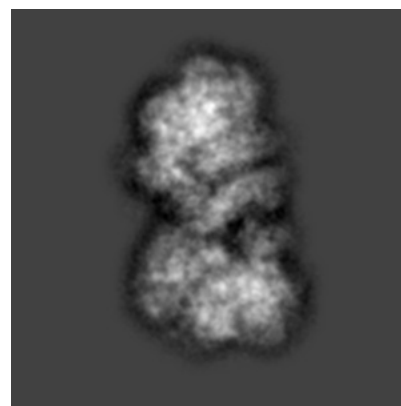
6.1.1 Primary map



X

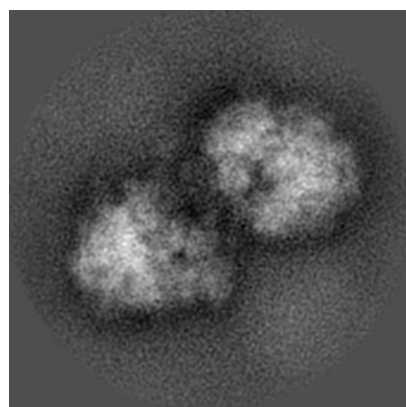


Y

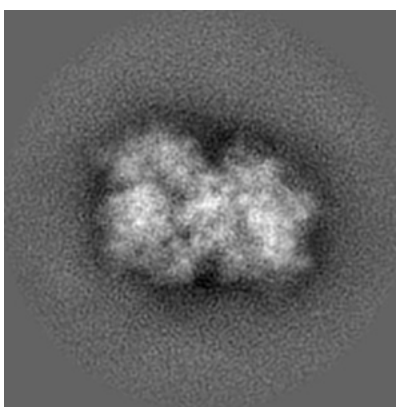


Z

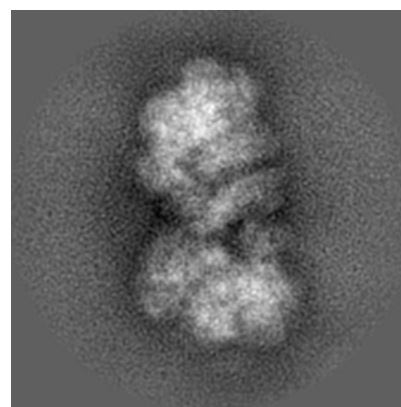
6.1.2 Raw map



X



Y

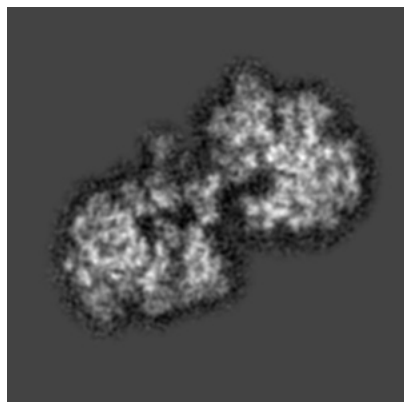


Z

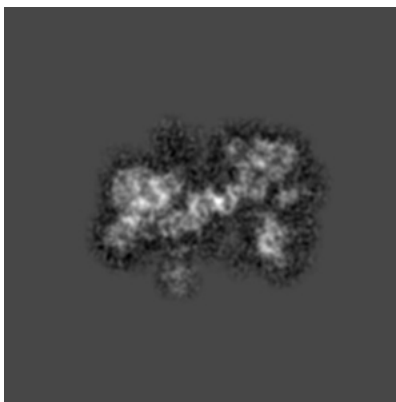
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

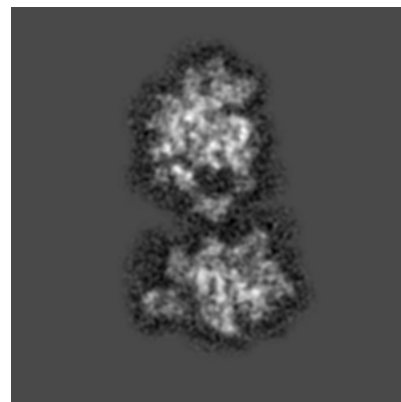
6.2.1 Primary map



X Index: 84

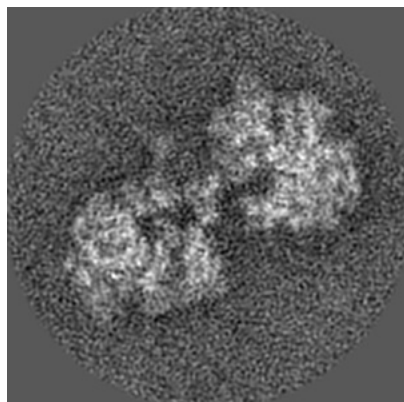


Y Index: 84

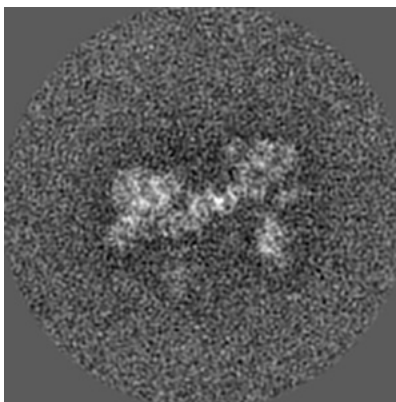


Z Index: 84

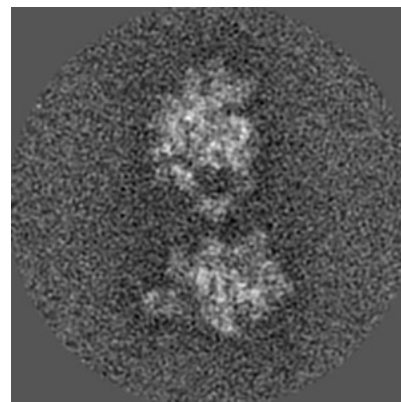
6.2.2 Raw map



X Index: 84



Y Index: 84

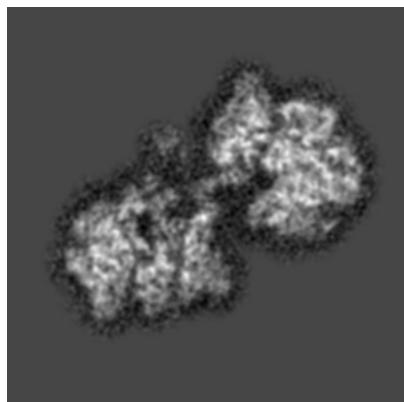


Z Index: 84

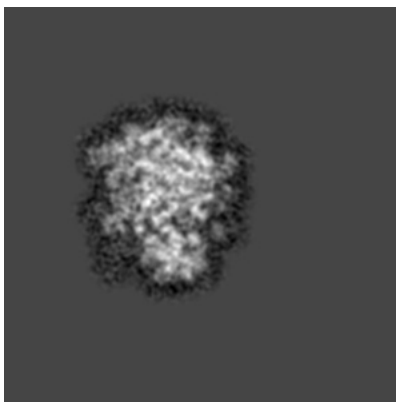
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

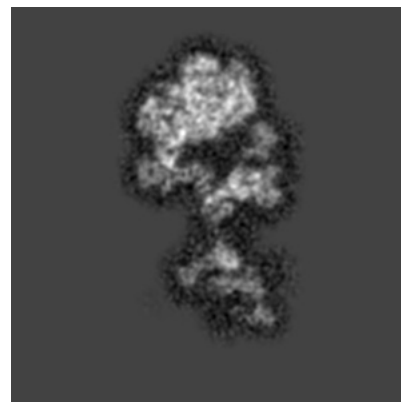
6.3.1 Primary map



X Index: 81

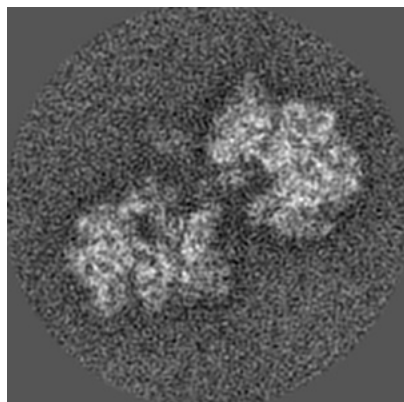


Y Index: 48

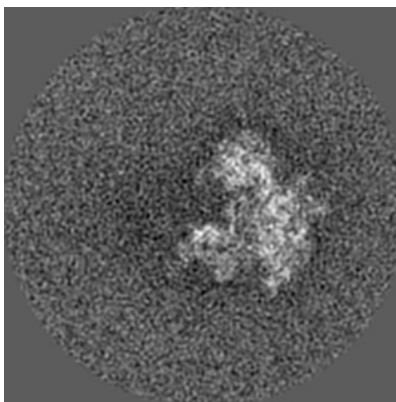


Z Index: 94

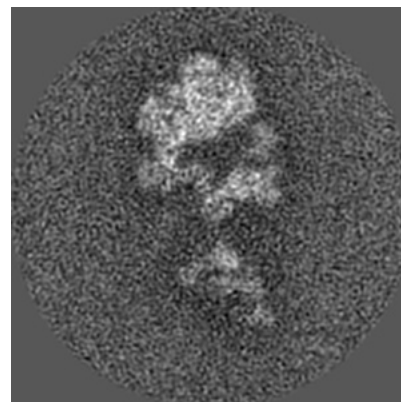
6.3.2 Raw map



X Index: 80



Y Index: 96



Z Index: 94

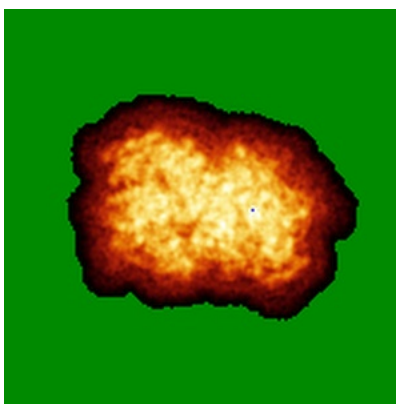
The images above show the largest variance slices of the map in three orthogonal directions.

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

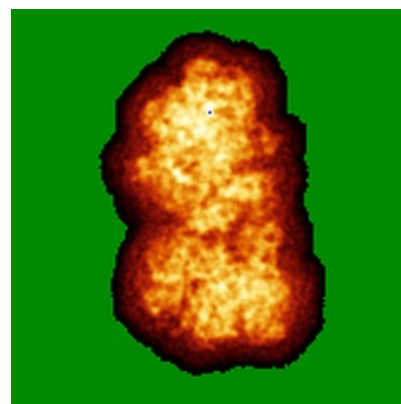
6.4.1 Primary map



X

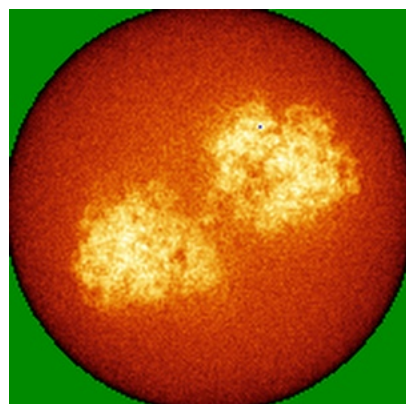


Y

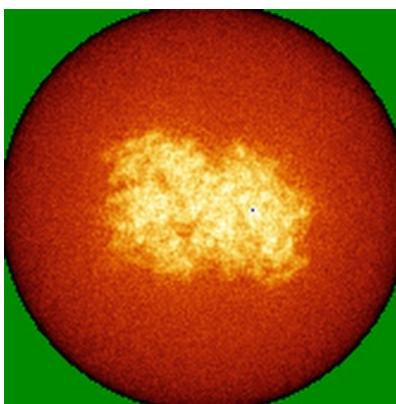


Z

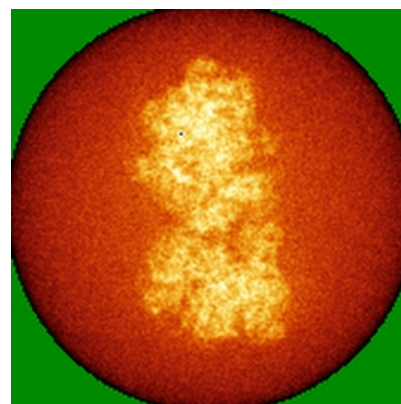
6.4.2 Raw map



X



Y

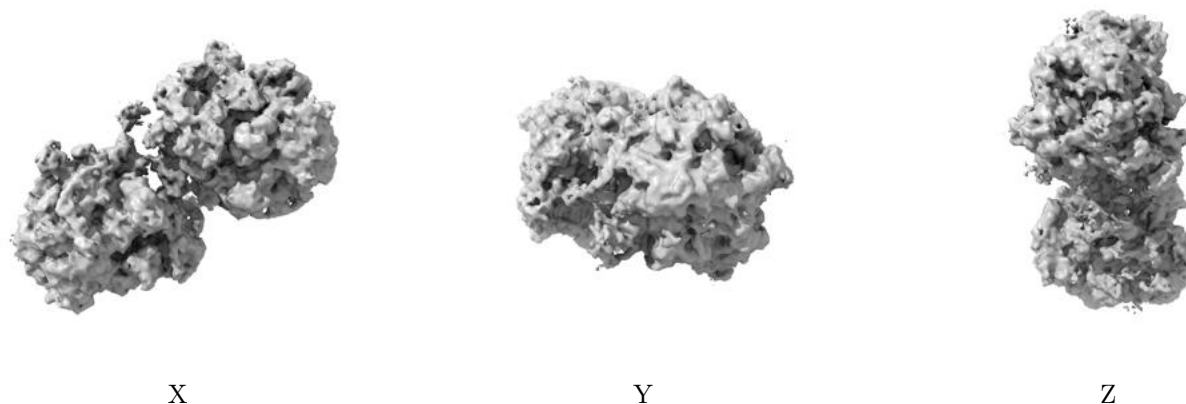


Z

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

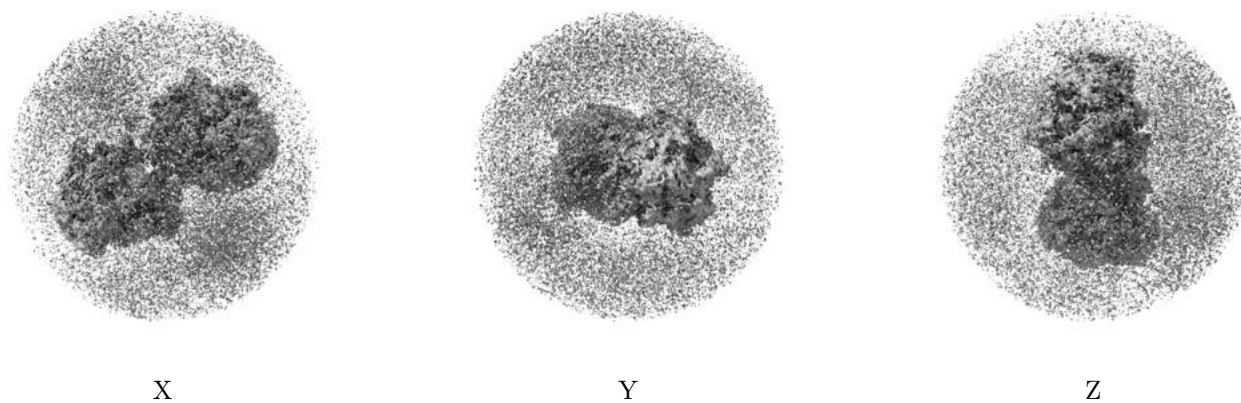
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.28. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

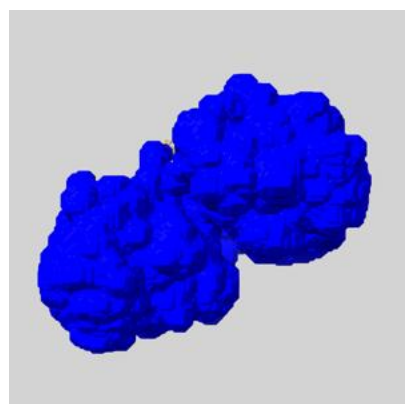
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

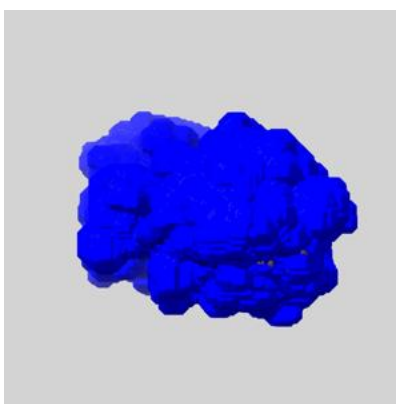
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

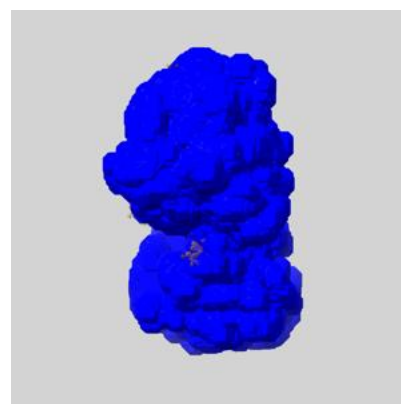
6.6.1 emd_55402_msk_1.map [i](#)



X



Y

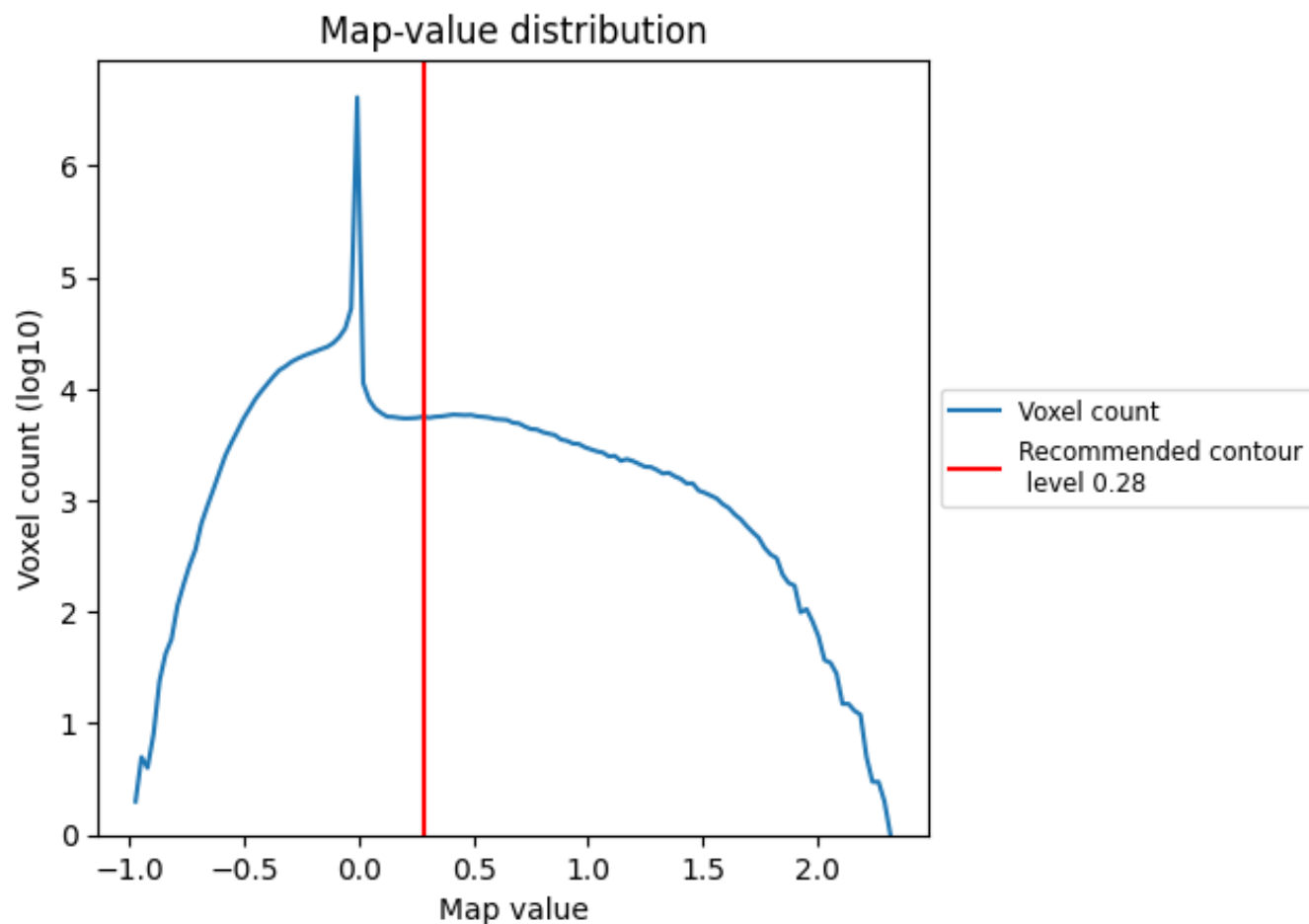


Z

7 Map analysis [i](#)

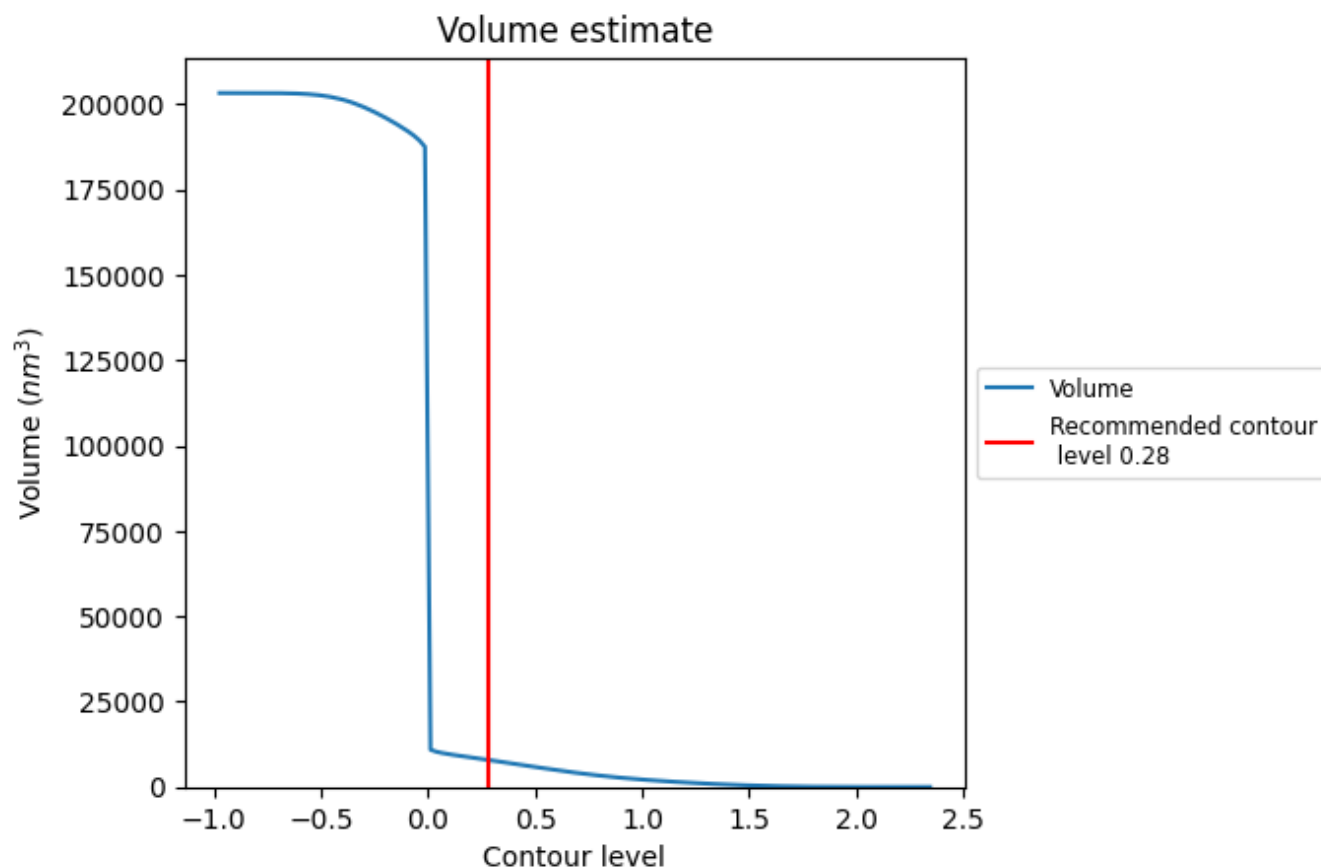
This section contains the results of statistical analysis of the map.

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.

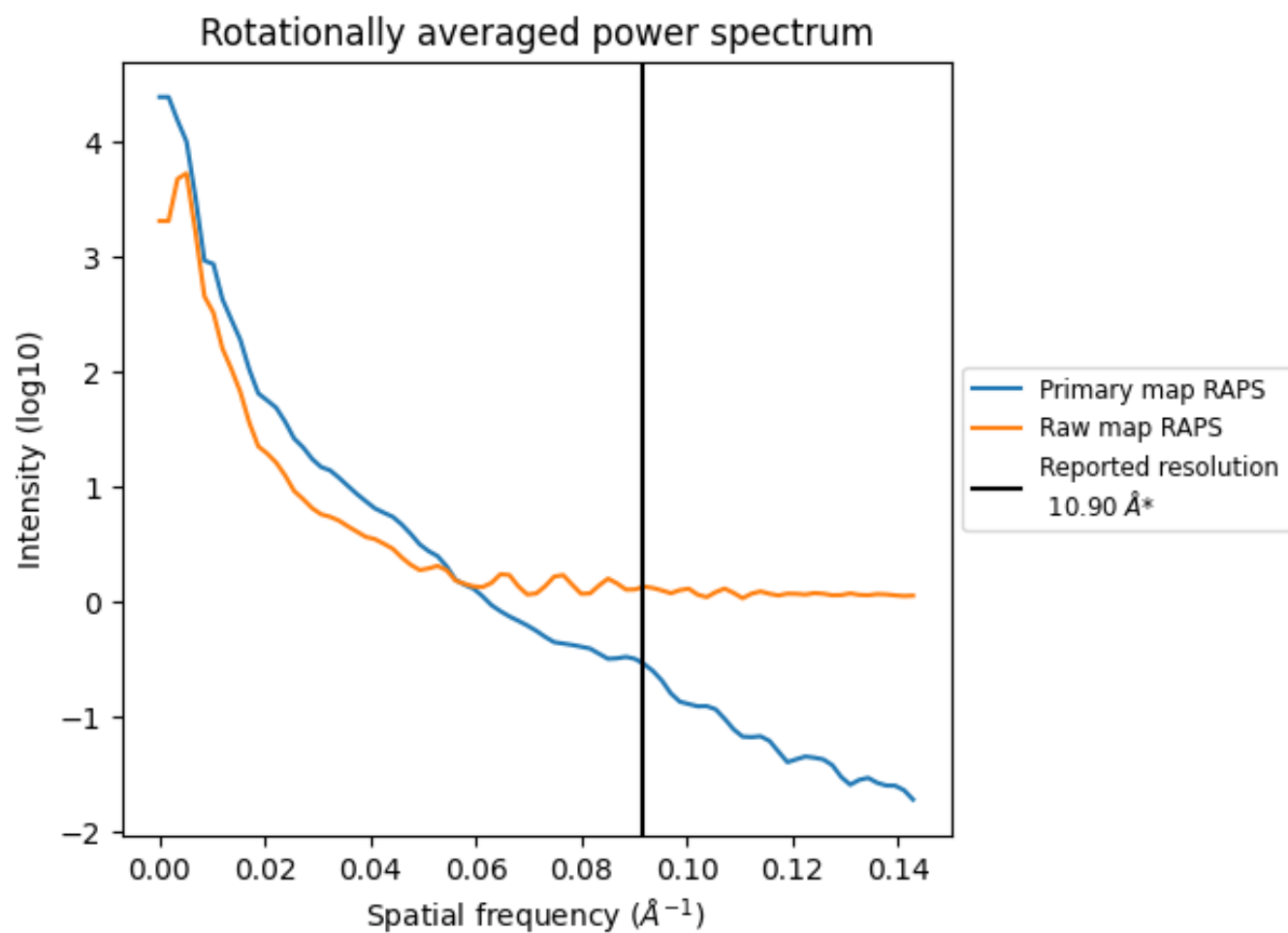
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7921 nm^3 ; this corresponds to an approximate mass of 7156 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

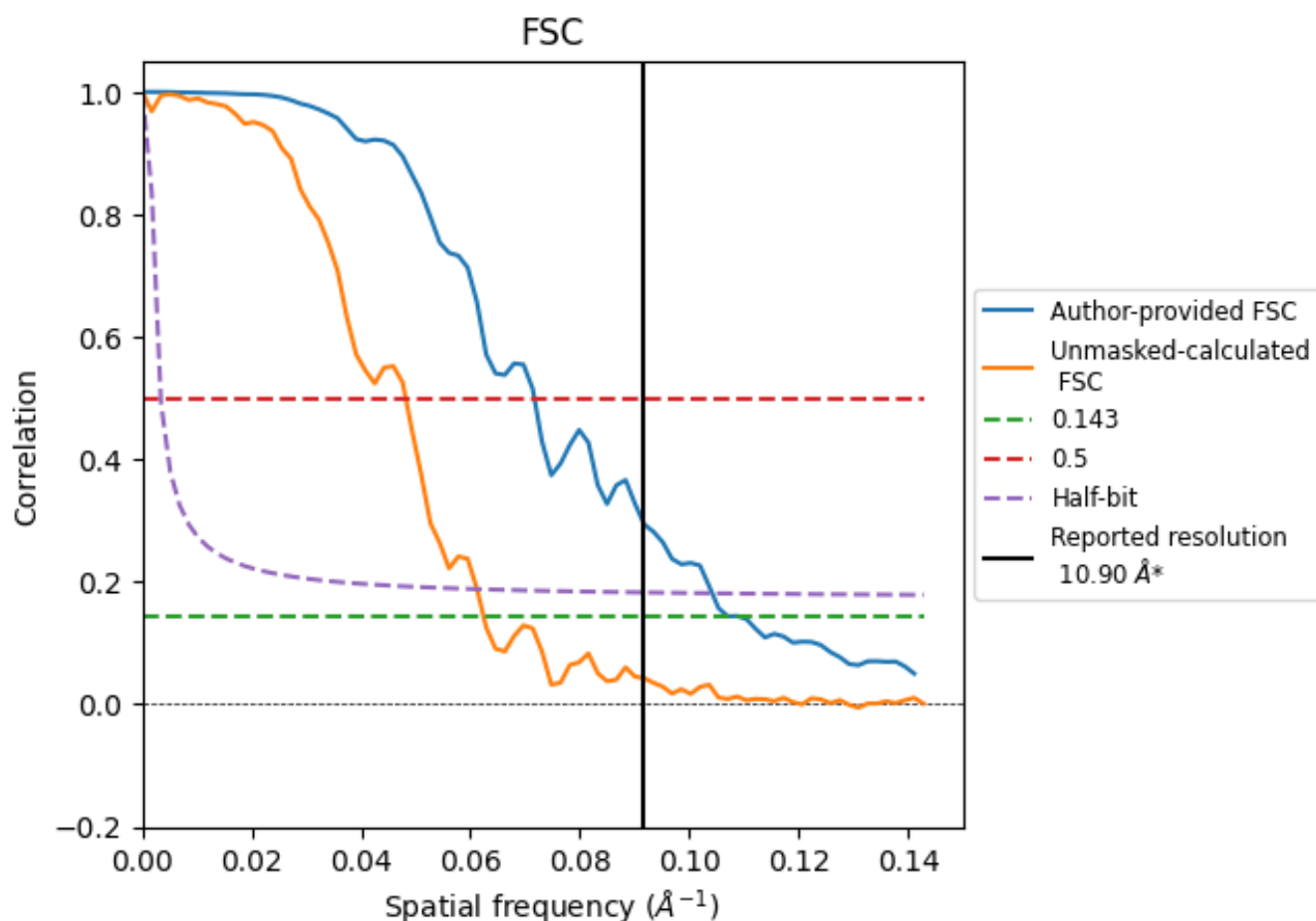


*Reported resolution corresponds to spatial frequency of 0.092 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.092 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.90	-	-
Author-provided FSC curve	9.16	13.95	9.59
Unmasked-calculated*	16.03	20.75	16.34

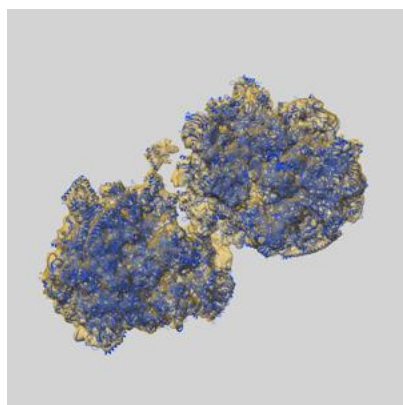
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 9.16 differs from the reported value 10.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 16.03 differs from the reported value 10.9 by more than 10 %

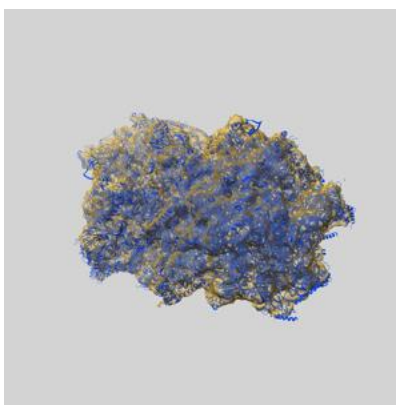
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55402 and PDB model 9T0J. Per-residue inclusion information can be found in [section 3](#) on [page 26](#).

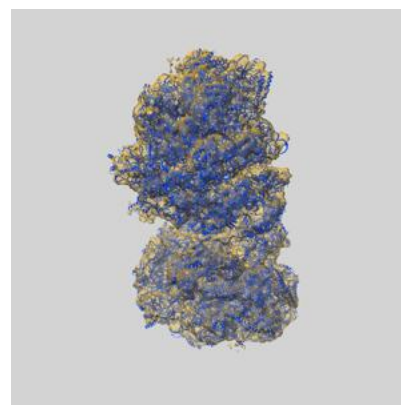
9.1 Map-model overlay [i](#)



X



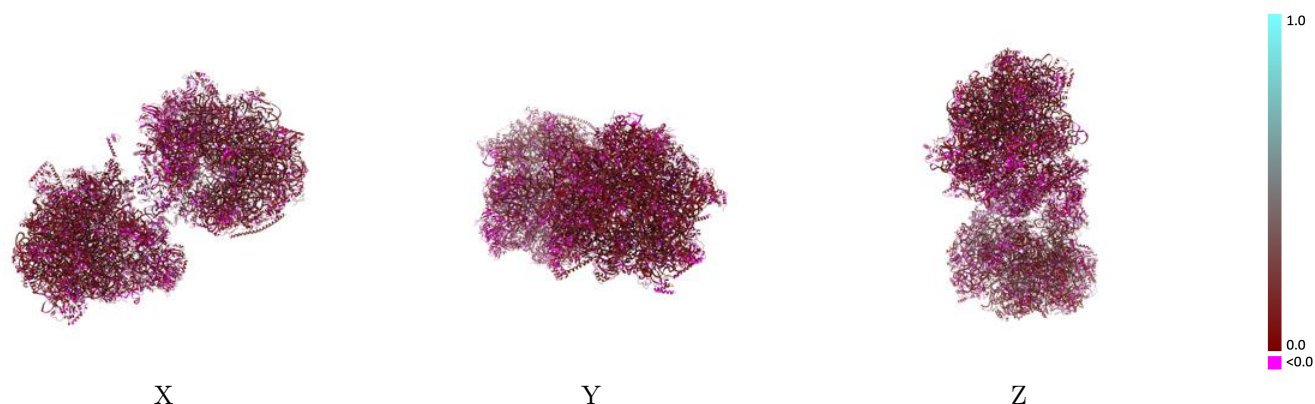
Y



Z

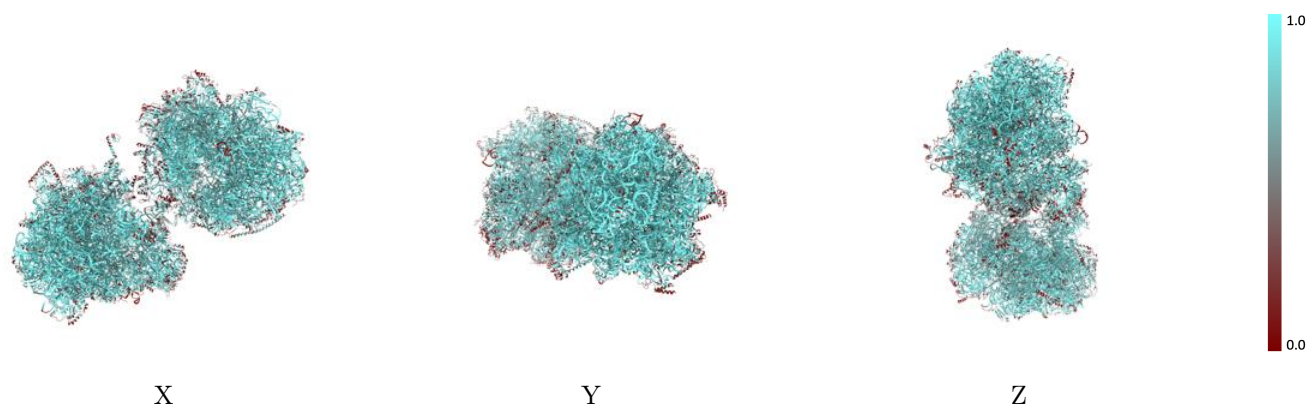
The images above show the 3D surface view of the map at the recommended contour level 0.28 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



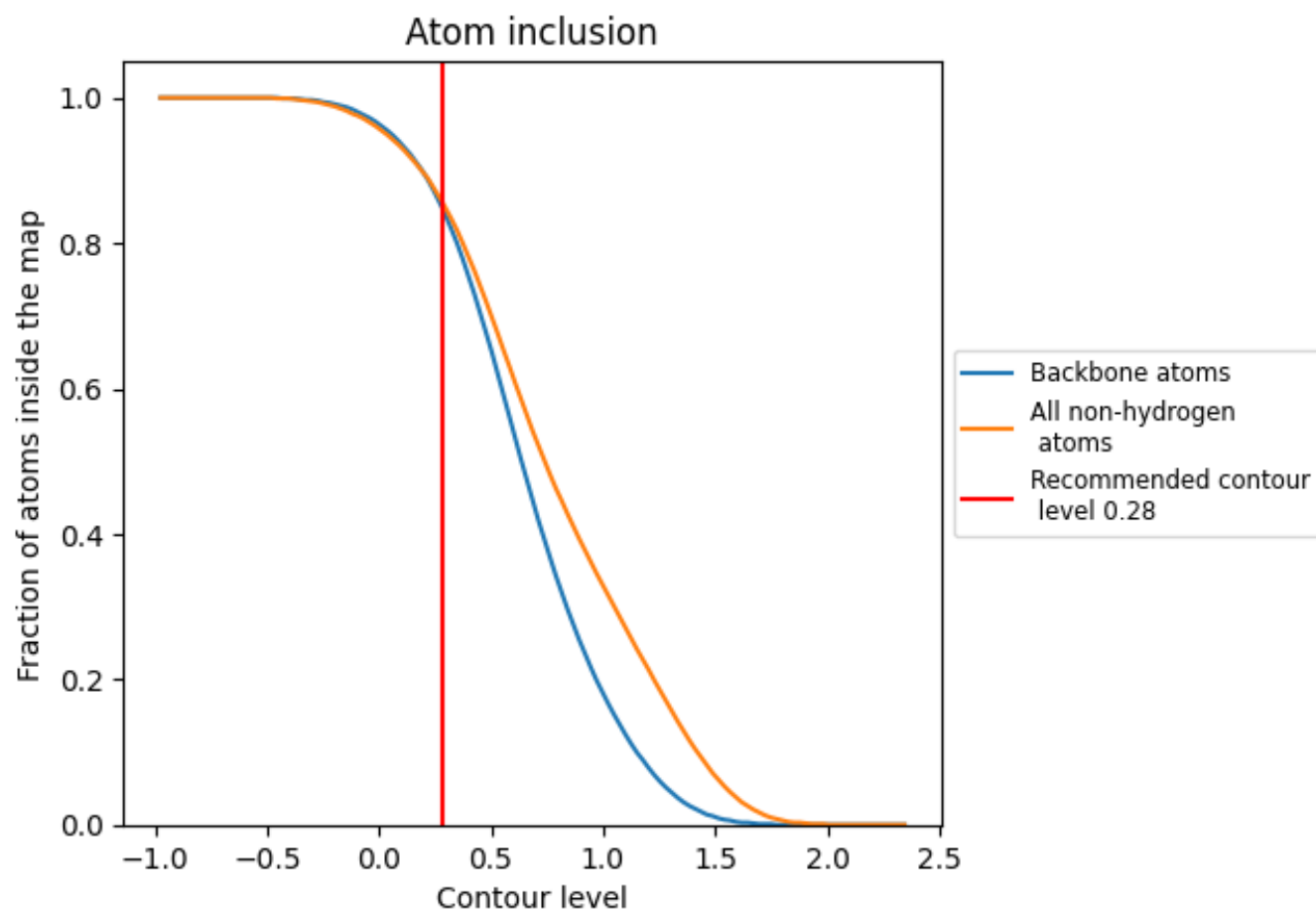
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.28).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 86% 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 (0.28) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.0900
A	 0.7950	 0.0950
B	 0.7120	 0.0790
D	 0.6560	 0.1020
E	 0.5760	 0.0990
K	 0.7240	 0.0800
K50	 0.9820	 0.1270
K70	 0.9670	 0.1240
KAA	 0.8700	 0.0340
KB0	 0.7990	 0.0610
KC0	 0.8120	 0.0480
KCC	 0.7130	 0.0900
KD0	 0.6760	 0.0390
KDD	 0.8560	 0.0800
KE0	 0.6180	 0.0790
KEE	 0.8470	 0.0610
KF0	 0.7620	 0.0880
KFF	 0.8640	 0.0830
KG0	 0.6880	 0.0720
KGG	 0.8780	 0.0540
KH0	 0.7570	 0.0880
KHH	 0.8300	 0.1090
KI0	 0.7980	 0.0780
KII	 0.7170	 0.0710
KJ0	 0.7590	 0.0580
KJJ	 0.9620	 0.0680
KL0	 0.7760	 0.0690
KLL	 0.9980	 0.0620
KM0	 0.6580	 0.0910
KMM	 0.7900	 0.0900
KN0	 0.9800	 0.0310
KO0	 0.7550	 0.1030
KOO	 0.8520	 0.0330
KP0	 0.8580	 0.0760
KPP	 0.8960	 0.0620



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Chain	Atom inclusion	Q-score
KQ0	 0.7830	 0.0660
KR0	 0.7840	 0.0870
KS0	 0.7300	 0.0690
KT0	 0.7320	 0.0580
KU0	 0.7650	 0.0730
KV0	 0.7690	 0.0560
KW0	 0.6170	 0.0630
KX0	 0.7620	 0.0690
KY0	 0.7880	 0.0820
KZ0	 0.6470	 0.0620
L	 0.7660	 0.0760
L50	 0.9850	 0.1290
L70	 0.9670	 0.1160
LA0	 0.9030	 0.0590
LA02	 0.8460	 0.0630
LAA	 0.8920	 0.0460
LB0	 0.8610	 0.0490
LC0	 0.8110	 0.0570
LCC	 0.7160	 0.1040
LD0	 0.7380	 0.0520
LDD	 0.8830	 0.0870
LE0	 0.5620	 0.0750
LEE	 0.8080	 0.0480
LF0	 0.7890	 0.0900
LFF	 0.8720	 0.0670
LG0	 0.7430	 0.0740
LGG	 0.9410	 0.0580
LH0	 0.8150	 0.0900
LHH	 0.8270	 0.1010
LI0	 0.8610	 0.0830
LII	 0.7870	 0.0930
LJ0	 0.7940	 0.0640
LJJ	 0.9520	 0.0460
LL0	 0.8250	 0.0720
LLL	 1.0000	 0.0510
LM0	 0.6800	 0.1070
LMM	 0.8170	 0.0730
LN0	 0.9960	 0.0540
LO0	 0.8160	 0.1050
LOO	 0.8520	 0.0610
LP0	 0.8750	 0.0800
LPP	 0.9140	 0.0630

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Chain	Atom inclusion	Q-score
LQ0	 0.7800	 0.0680
LR0	 0.8340	 0.1040
LS0	 0.7700	 0.0820
LT0	 0.7710	 0.0540
LU0	 0.7330	 0.0850
LV0	 0.8520	 0.0550
LW0	 0.6170	 0.0520
LX0	 0.8290	 0.0520
LY0	 0.8290	 0.0770
LZ0	 0.7000	 0.0540
M	 0.6710	 0.0720
MD1	 0.8200	 0.1050
N	 0.6690	 0.0930
ND1	 0.8060	 0.1010
R60	 0.9700	 0.1020
RA0	 0.7140	 0.0380
RAA	 0.7670	 0.0490
RB0	 0.7030	 0.0820
RBB	 0.6840	 0.0290
RC0	 0.6830	 0.0550
RCC	 0.6400	 0.0650
RD0	 0.4870	 0.0260
RDD	 0.6850	 0.0830
RE0	 0.6510	 0.0440
REE	 0.6930	 0.0460
RF0	 0.8310	 0.0590
RFF	 0.5000	 0.0010
RG0	 0.5830	 0.0570
RGG	 0.5940	 0.0340
RH0	 0.5430	 0.0500
RI0	 0.8440	 0.0490
RJ0	 0.7250	 0.0580
RK0	 0.6400	 0.0500
RL0	 0.6580	 0.0540
RM0	 0.3700	 0.0230
RN0	 0.8240	 0.0560
RO0	 0.8410	 0.0530
RP0	 0.6630	 0.0280
RQ0	 0.7380	 0.0500
RR0	 0.5890	 0.0300
RS0	 0.7810	 0.0540
RT0	 0.7250	 0.0440

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Chain	Atom inclusion	Q-score
RU0	 0.5830	 0.0410
RV0	 0.6990	 0.0820
RW0	 0.8380	 0.0460
RX0	 0.8690	 0.0690
RY0	 0.6450	 0.0720
RZ0	 0.7110	 0.0550
S60	 0.9710	 0.1040
SA0	 0.6910	 0.0490
SAA	 0.8070	 0.0490
SB0	 0.7580	 0.0960
SBB	 0.7080	 0.0620
SC0	 0.7510	 0.0630
SCC	 0.6230	 0.0700
SD0	 0.5180	 0.0430
SDD	 0.7530	 0.0770
SE0	 0.6660	 0.0380
SEE	 0.7340	 0.0410
SF0	 0.8610	 0.0620
SFF	 0.5490	 0.0040
SG0	 0.5950	 0.0500
SGG	 0.6070	 0.0430
SH0	 0.5010	 0.0490
SI0	 0.8310	 0.0540
SJ0	 0.7230	 0.0290
SK0	 0.6240	 0.0540
SL0	 0.7000	 0.0540
SM0	 0.3280	 0.0210
SN0	 0.8490	 0.0710
SO0	 0.8800	 0.0570
SP0	 0.7110	 0.0330
SQ0	 0.8220	 0.0490
SR0	 0.6330	 0.0640
SS0	 0.7960	 0.0510
ST0	 0.7030	 0.0330
SU0	 0.6240	 0.0320
SV0	 0.7170	 0.1000
SW0	 0.8460	 0.0410
SX0	 0.9220	 0.0540
SY0	 0.5870	 0.0400
SZ0	 0.7600	 0.0680