wwPDB EM Validation Summary Report

Oct 19, 2026 – 04:46 pm BST

PDB ID	:	9T0I / pdb_00009t0i
EMDB ID	:	EMD-55401
Title	:	Spraguea lophii ribosome dimer, conformation 1.
Authors	:	McLaren, M.; Isupov, M.N.; Daum, B.; Conners, R.
Deposited on	:	2025-10-17
Resolution	:	9.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

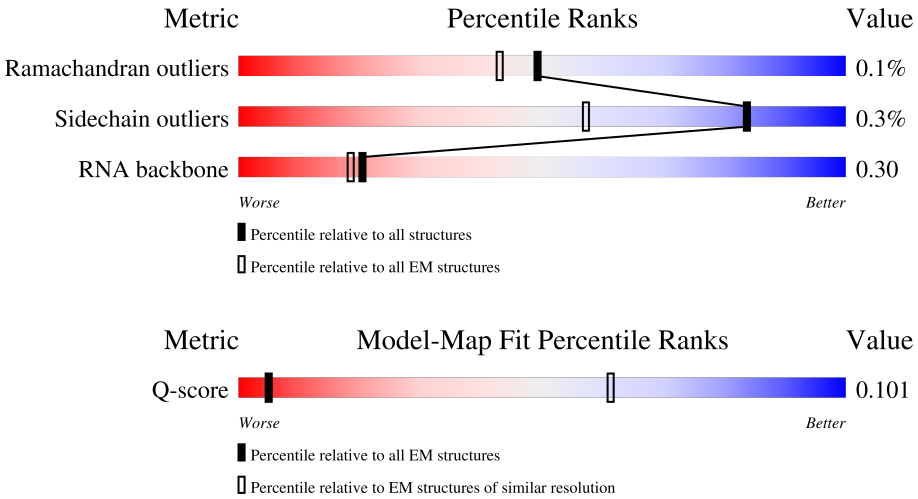
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 9.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	157 (9.30 - 10.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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%

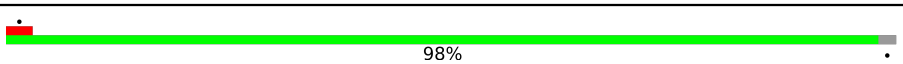
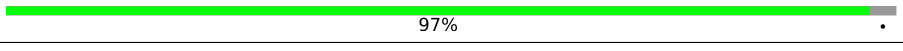
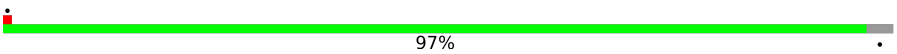
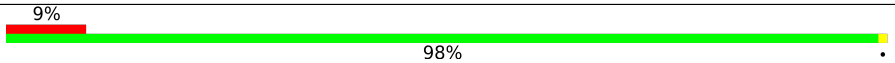
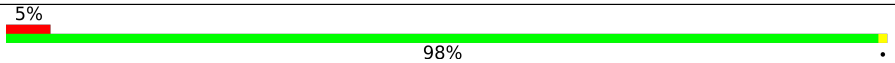
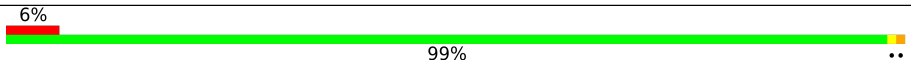
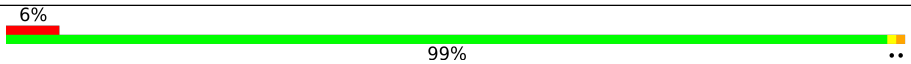
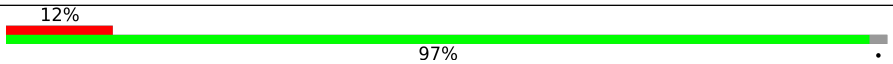
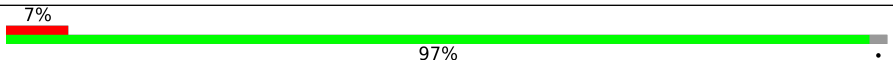
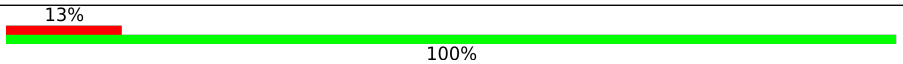
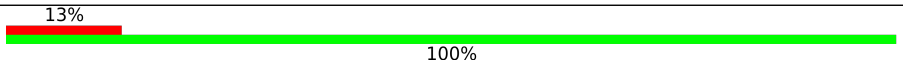
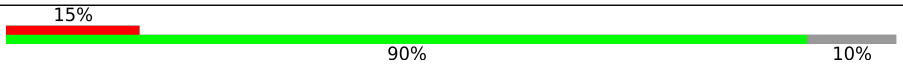
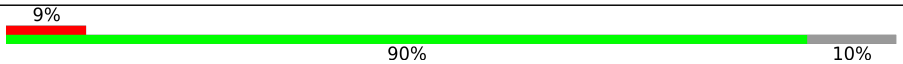
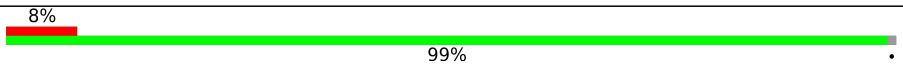
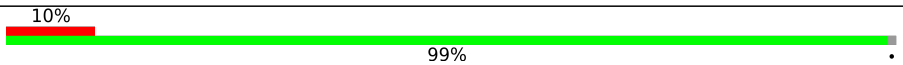
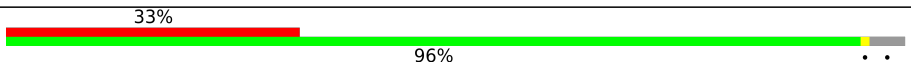
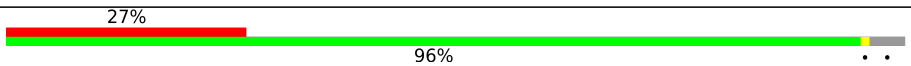
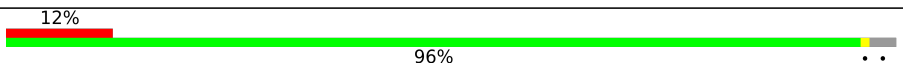
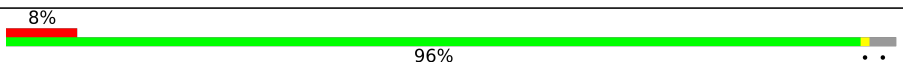
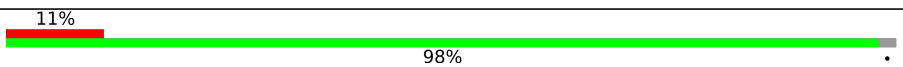
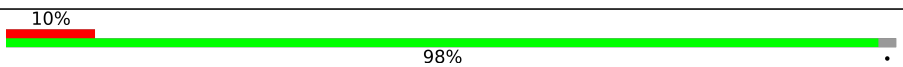
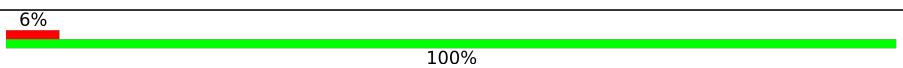
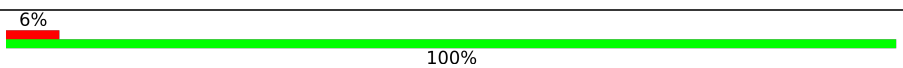
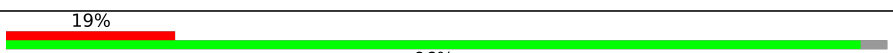
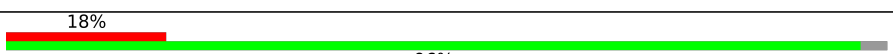
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Mol	Chain	Length	Quality of chain
3	D	164	16% 100%
3	E	164	18% 100%
4	KGG	106	97%
4	LGG	106	97%
5	RB0	230	13% 88% 11%
5	SB0	230	10% 88% 11%
6	RC0	248	14% 91% 9%
6	SC0	248	12% 91% 9%
7	K70	119	74% 25%
7	L70	119	74% 25%
8	A	847	10% 99%
8	B	847	15% 99%
9	K	210	16% 100%
9	L	210	13% 100%
10	M	269	20% 100%
10	N	269	20% 100%
11	KMM	127	6% 37% 59%
11	LMM	127	5% 37% 59%
12	RBB	82	21% 98%
12	SBB	82	29% 98%
13	RAA	102	11% 99%
13	SAA	102	10% 99%
14	KOO	104	9% 96%
14	LOO	104	5% 96%
15	KPP	89	98%

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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	12% 97%
28	LH0	187	11% 97%
29	KHH	119	9% 98%
29	LHH	119	8% 98%
30	KI0	218	11% 100%
30	LI0	218	6% 100%
31	KII	98	22% 98%
31	LII	98	15% 98%
32	KJ0	171	12% 96%
32	LJ0	171	9% 96%
33	KL0	165	12% 96%
33	LL0	165	8% 96%
34	KLL	52	98%
34	LLL	52	98%
35	KM0	122	22% 93% 6%
35	LM0	122	18% 93% 6%
36	KN0	204	100%
36	LN0	204	100%
37	KO0	198	15% 99%
37	LO0	198	11% 99%
38	KP0	167	6% 92% 8%
38	LP0	167	7% 92% 8%
39	KQ0	183	13% 99%
39	LQ0	183	12% 99%
40	KR0	168	15% 98%

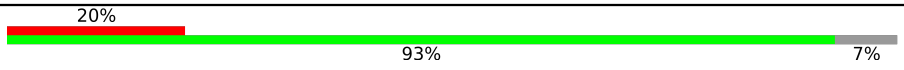
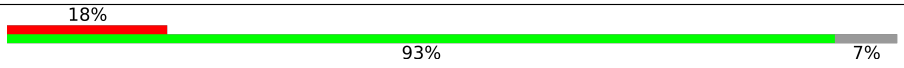
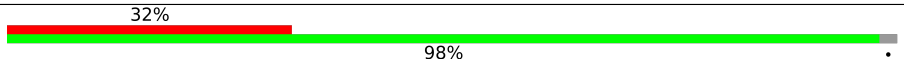
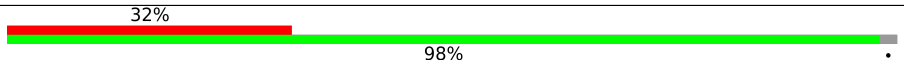
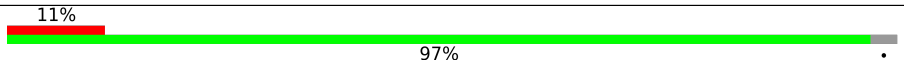
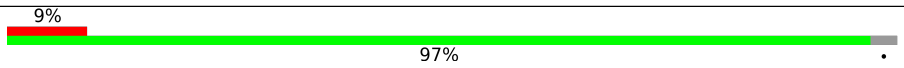
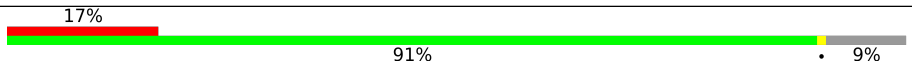
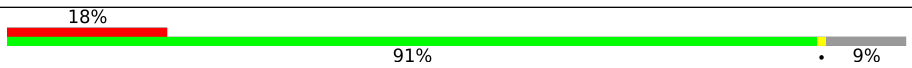
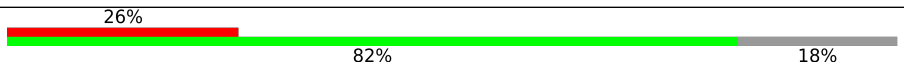
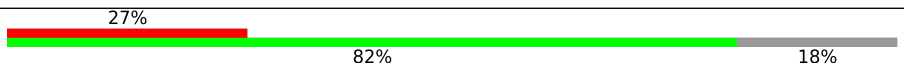
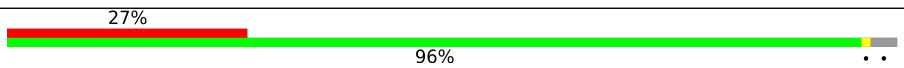
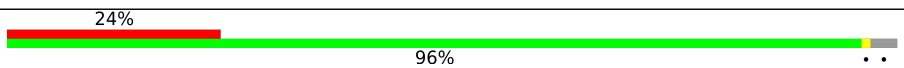
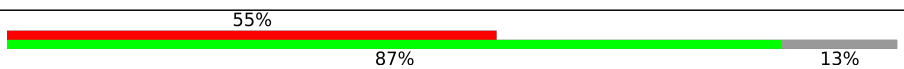
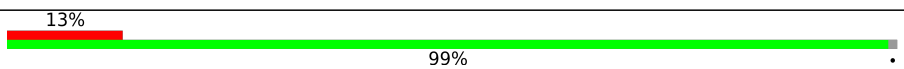
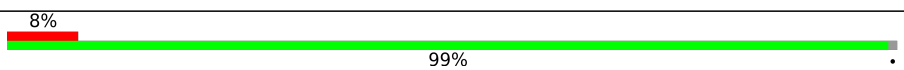
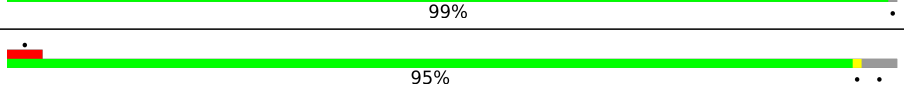
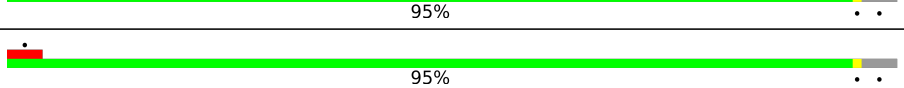
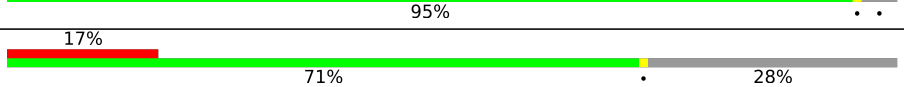
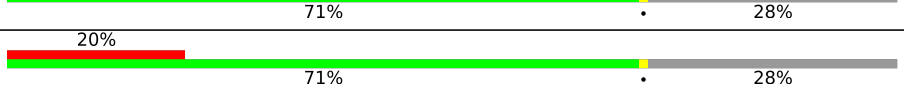
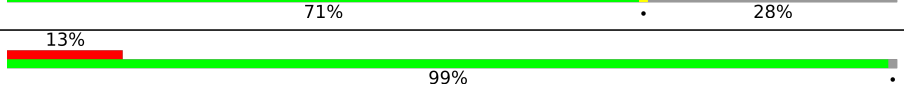
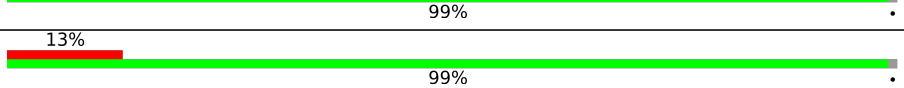
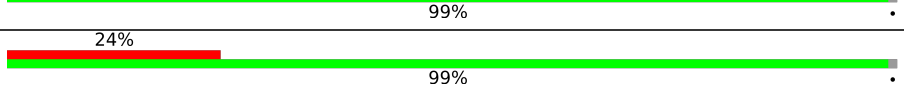
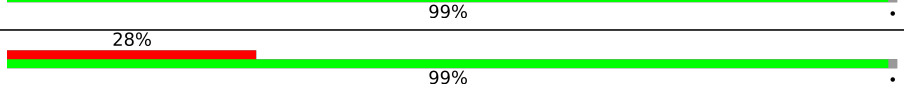
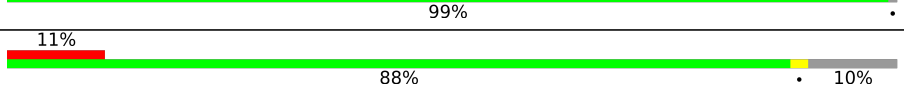
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Mol	Chain	Length	Quality of chain
40	LR0	168	11% 98%
41	KS0	171	19% 98%
41	LS0	171	14% 98%
42	KT0	158	20% 98%
42	LT0	158	16% 98%
43	KU0	113	17% 88% 12%
43	LU0	113	14% 88% 12%
44	KV0	142	9% 99%
44	LV0	142	99%
45	KW0	131	23% 78% 22%
45	LW0	131	21% 78% 22%
46	KX0	113	7% 99%
46	LX0	113	99%
47	KY0	131	9% 100%
47	LY0	131	8% 100%
48	KZ0	153	22% 76% 23%
48	LZ0	153	18% 76% 23%
49	MD1	151	5% 94% 6%
49	ND1	151	11% 94% 6%
50	RA0	233	21% 94% 6%
50	SA0	233	17% 94% 6%
51	RCC	65	17% 94% 5%
51	SCC	65	17% 94% 5%
52	RE0	280	26% 93% 7%
52	SE0	280	24% 93% 7%

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Mol	Chain	Length	Quality of chain
53	REE	60	
53	SEE	60	
54	RGG	326	
54	SGG	326	
55	RI0	173	
55	SI0	173	
56	RJ0	184	
56	SJ0	184	
57	RK0	107	
57	SK0	107	
58	RL0	155	
58	SL0	155	
59	RM0	130	
59	SM0	130	
60	RN0	143	
60	SN0	143	
61	RO0	135	
61	SO0	135	
62	RP0	163	
62	SP0	163	
63	RQ0	143	
63	SQ0	143	
64	RR0	120	
64	SR0	120	
65	RS0	160	

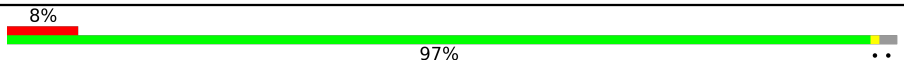
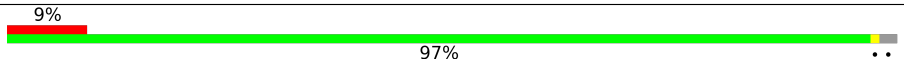
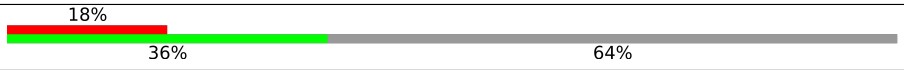
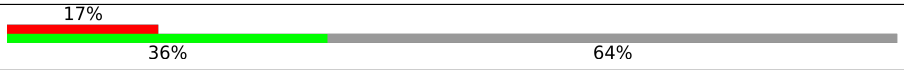
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Mol	Chain	Length	Quality of chain
65	SS0	160	11% 88% 10%
66	RT0	143	22% 98%
66	ST0	143	26% 98%
67	RU0	119	30% 82% 16%
67	SU0	119	27% 82% 16%
68	RV0	67	15% 94%
68	SV0	67	12% 94%
69	RX0	141	5% 99%
69	SX0	141	99%
70	RY0	146	29% 91% 7%
70	SY0	146	28% 91% 7%
71	RZ0	128	8% 59% 41%
71	SZ0	128	9% 59% 41%
72	KD0	291	18% 97%
72	LD0	291	21% 97%
73	RDD	65	17% 97%
73	SDD	65	17% 97%
74	RD0	242	39% 89% 11%
74	SD0	242	36% 89% 11%
75	RG0	230	33% 98%
75	SG0	230	32% 98%
76	RH0	164	39% 99%
76	SH0	164	35% 99%
77	RW0	128	11% 99%
77	SW0	128	5% 99%

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Mol	Chain	Length	Quality of chain
78	RF0	195	
78	SF0	195	
79	RFF	150	
79	SFF	150	

2 Entry composition (i)

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	K50	2605	Total 55952	C 24974	N 10318	O 18055	P 2605	0	0
1	L50	2605	Total 55952	C 24974	N 10318	O 18055	P 2605	0	0

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

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

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

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

- Molecule 4 is a protein called Ribosomal protein L34.

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

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

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

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	RC0	226	Total	C	N	O	S	0	0
			1729	1101	300	321	7		
6	SC0	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	K70	119	Total	C	N	O	P	0	0
			2541	1136	459	827	119		
7	L70	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	B	847	Total	C	N	O	S	0	0
			6606	4175	1125	1264	42		
8	A	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	K	210	Total	C	N	O	S	0	0
			1718	1109	291	312	6		
9	L	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	N	269	Total	C	N	O	S	0	0
			2113	1348	345	407	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	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	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
11	LMM	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	RBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		
12	SBB	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	RAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		
13	SAA	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	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
14	LOO	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	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
15	LPP	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	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
16	LJJ	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	KAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		
18	LAA	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	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
19	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 20 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
20	LC0	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	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
21	LCC	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	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
22	LDD	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	KE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		
23	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	KEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		
24	LEE	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	KF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		
25	LF0	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	KFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
32	LJ0	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	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
33	LL0	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	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
34	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 35 is a protein called eL14 LM0.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
35	LM0	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	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		
36	LN0	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	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
37	LO0	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	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
38	LP0	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	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
39	LQ0	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	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
40	LR0	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	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
41	LS0	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	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

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

- Molecule 43 is a protein called 60S ribosomal protein L22.

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

- Molecule 44 is a protein called Ribosomal protein L23.

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

- Molecule 45 is a protein called Ribosomal protein L24E.

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

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

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

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

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

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

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

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

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

- Molecule 50 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		
50	SA0	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	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
51	SCC	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	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
52	SE0	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	REE	56	Total 447	C 284	N 89	O 74	0	0
53	SEE	56	Total 447	C 284	N 89	O 74	0	0

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

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

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

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

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

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

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

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

- Molecule 58 is a protein called 40S ribosomal protein S11.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL0	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	RM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		
59	SM0	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	RN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		
60	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 61 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
61	SO0	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	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
62	SP0	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	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
63	SQ0	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	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
64	SR0	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	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
65	SS0	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	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
66	ST0	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	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
67	SU0	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	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
68	SV0	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	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
69	SX0	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	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
70	SY0	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	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		
71	SZ0	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	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
72	LD0	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	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
73	SDD	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	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	SD0	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	RG0	229	Total	C	N	O	S	0	0
			1835	1178	325	328	4		
75	SG0	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	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
76	SH0	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	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
77	SW0	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	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
78	SF0	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	RFF	54	Total	C	N	O	S	0	0
			413	256	74	78	5		
79	SFF	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).

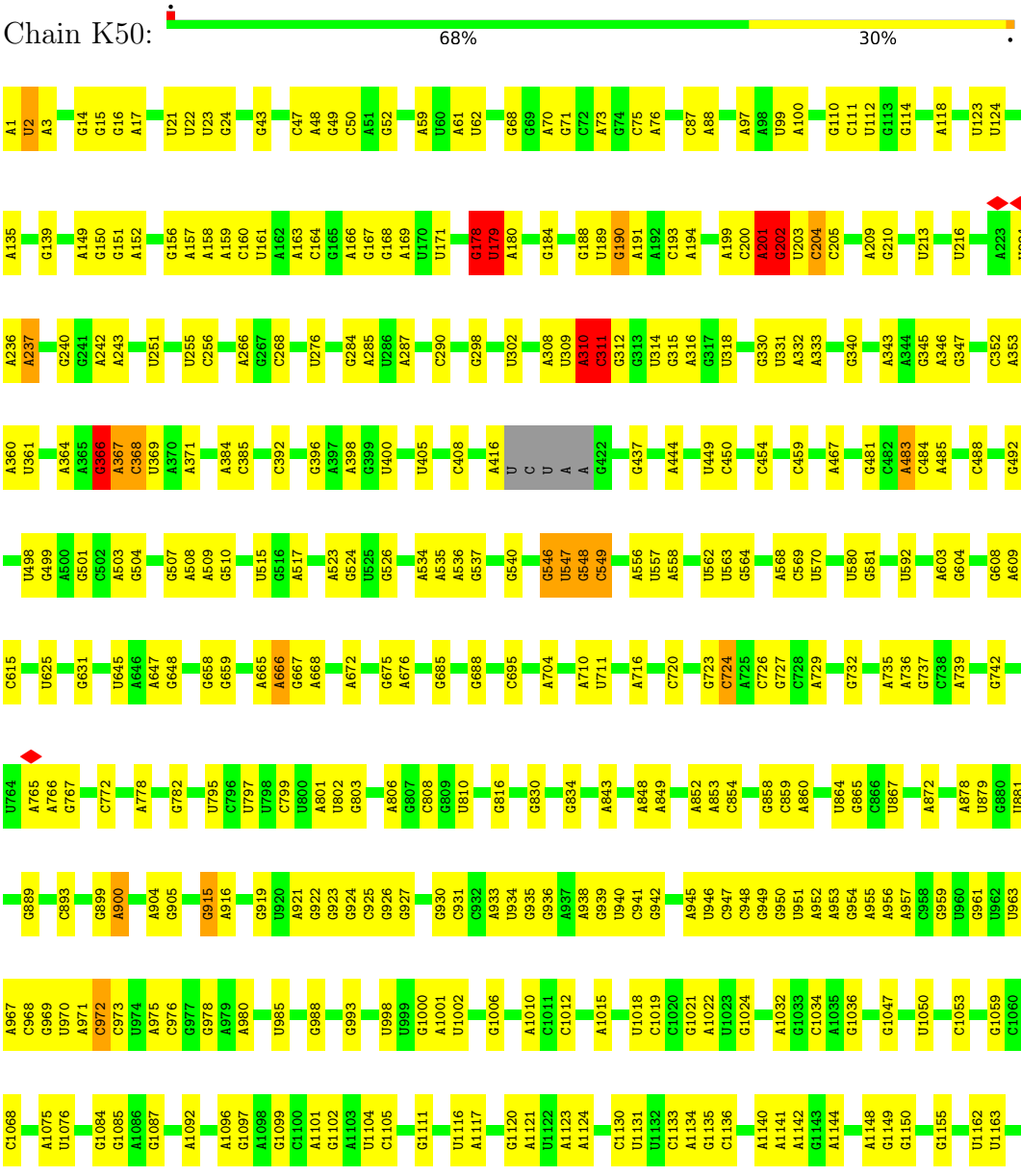
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80	KMM	1	Total Zn 1 1	0
80	RBB	1	Total Zn 1 1	0
80	RAA	1	Total Zn 1 1	0
80	KOO	1	Total Zn 1 1	0
80	KPP	1	Total Zn 1 1	0
80	KJJ	1	Total Zn 1 1	0
80	ND1	1	Total Zn 1 1	0
80	RFF	1	Total Zn 1 1	0
80	LGG	1	Total Zn 1 1	0
80	LMM	1	Total Zn 1 1	0
80	SBB	1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

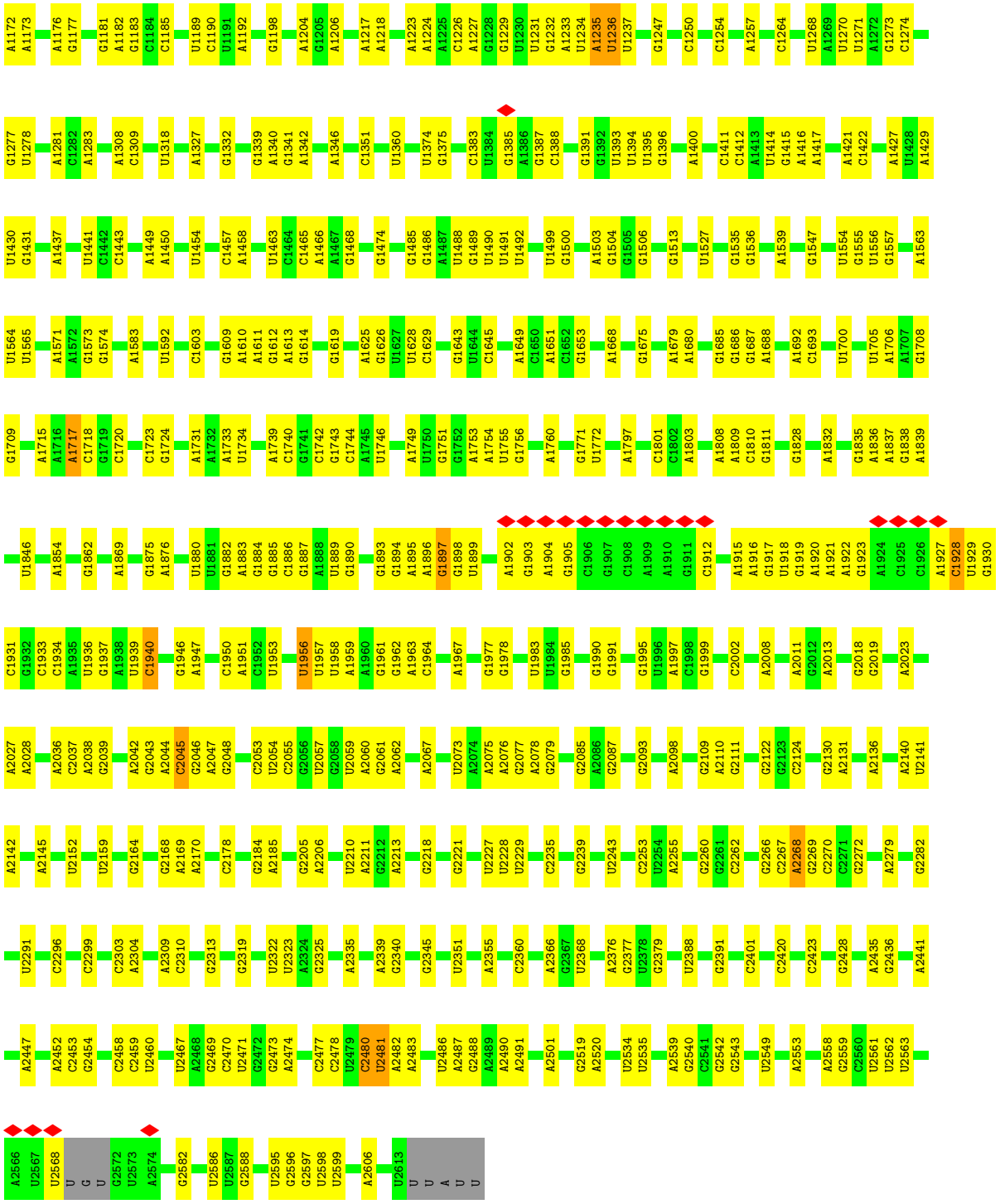
3 Residue-property plots (i)

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

- Molecule 1: RNA 23S

Chain K50:

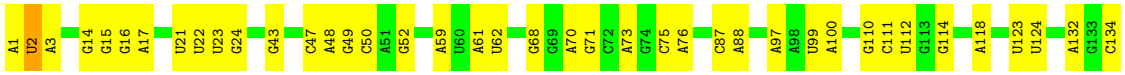


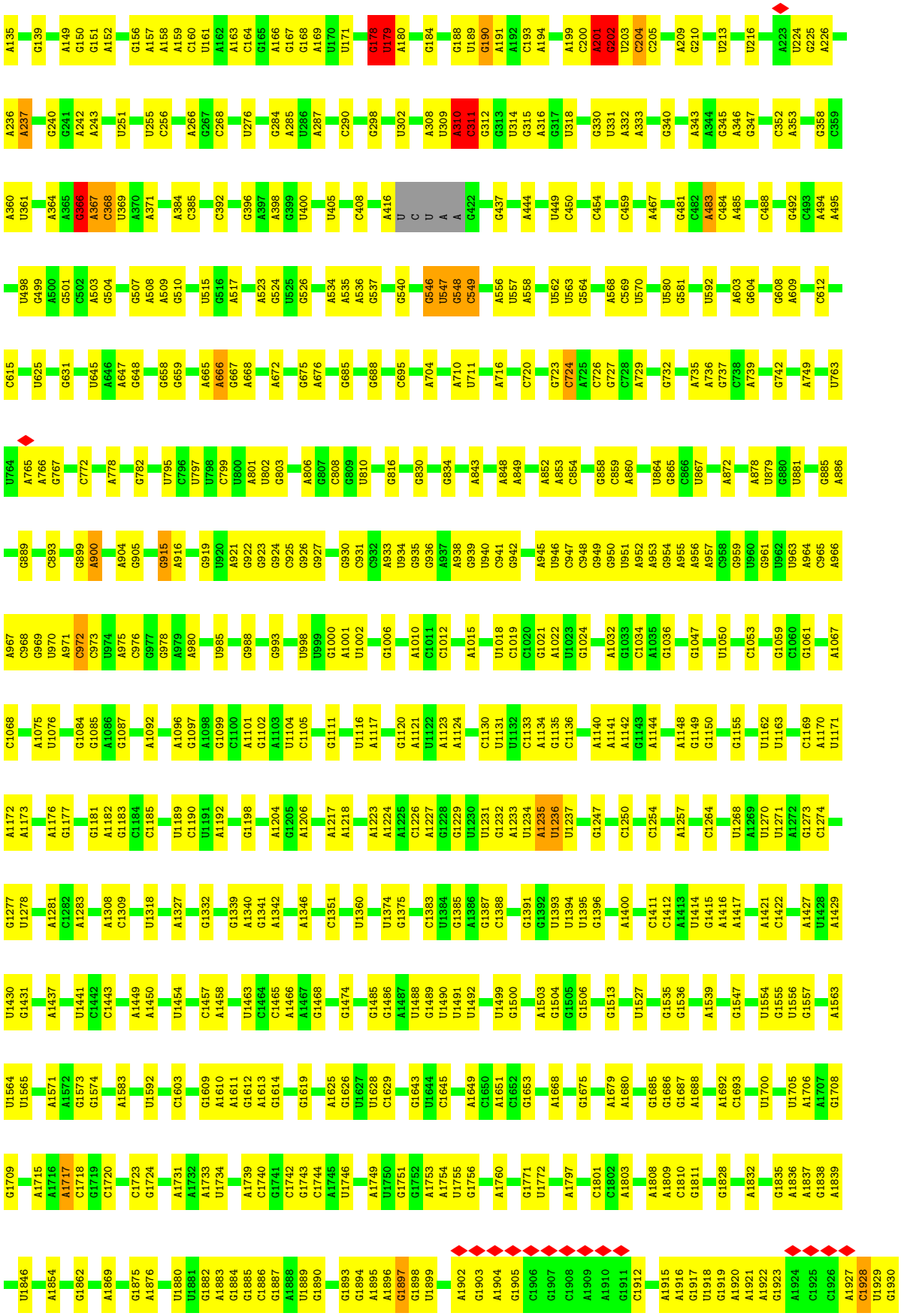


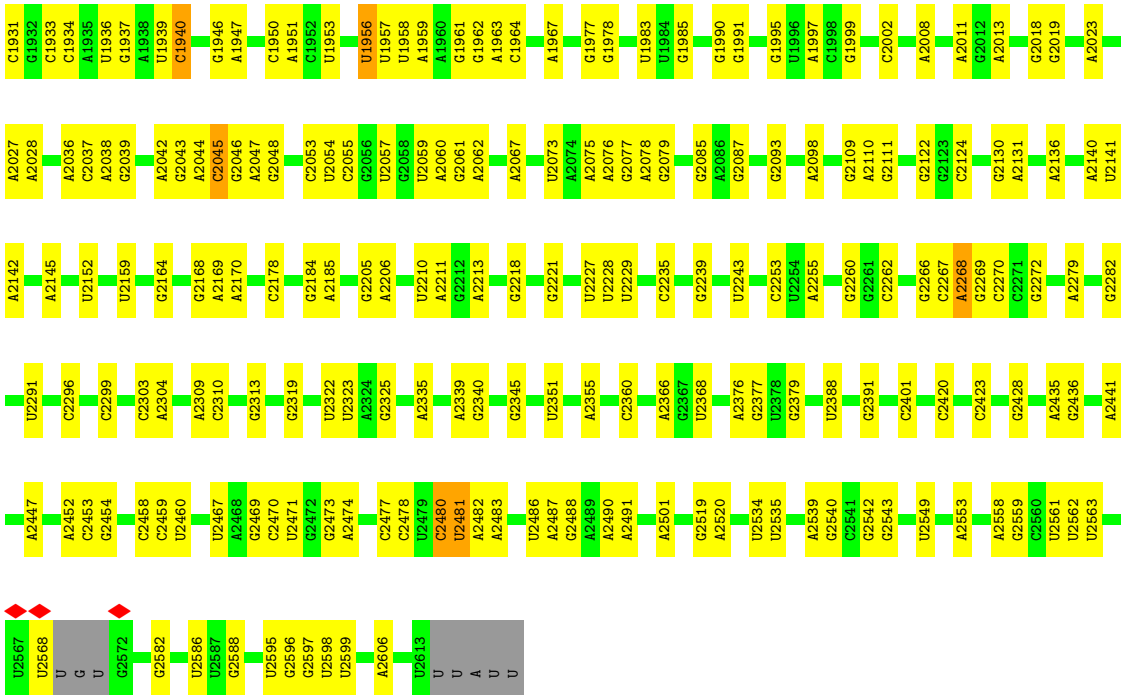
• Molecule 1: RNA 23S

Chain L50:





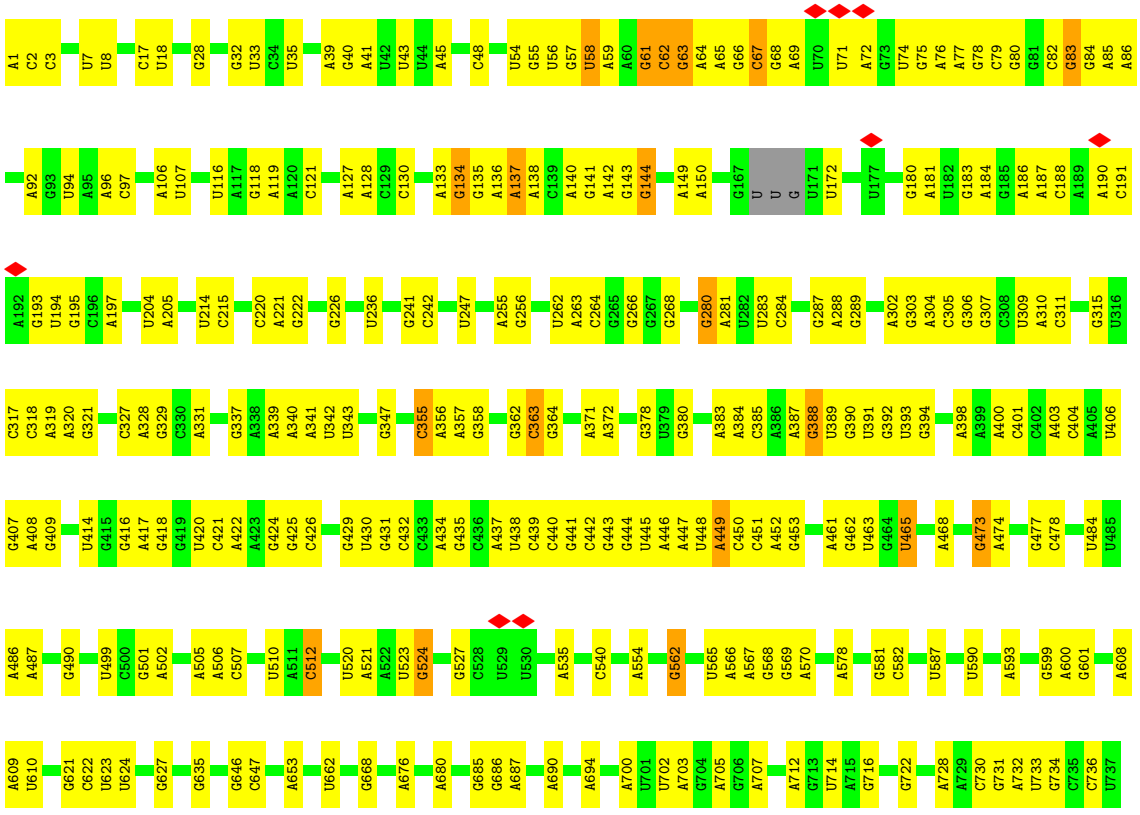

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A236 A237 G240 G241 A242 A243 U251 U255 C256 A266 G267 C268 U276 G284 A285 U286 A287 C290 G298 U302 A308 U309 A310 C311 G312 G313 U314 G315 A316 G317 U318 G330 U331 A332 A333 G340 A343 A344 G345 A346 G347 C352 A353 G358 C359
A360 U361 A364 A365 G366 A367 C368 U369 A370 A371 A384 C385 C392 G396 A397 A398 G399 U400 U405 C408 A416 U C U A A G422 G437 A444 U449 C450 C454 C459 A467 G481 C482 A483 C484 A485 C488 G492 C493 A494 A495
U498 G499 A500 G501 C502 A503 G504 G507 A508 A509 G510 U515 G516 A517 A523 G524 U525 G526 A534 A535 A536 G537 G540 G546 U547 G548 C549 A556 U557 A558 U562 U563 G564 A568 C569 U570 U580 G581 U592 A603 G604 G608 A609 C612
C615 U625 G631 U645 A646 A647 G648 G658 G659 A665 A666 G667 A668 A672 G675 A676 G685 G688 C695 A704 A710 U711 A716 C720 G723 C724 A725 C726 G727 C728 A729 G732 A735 A736 G737 C738 A739 G742 A749 U763
U764 A765 A766 G767 C772 A778 G782 U795 C796 U797 U798 C799 U800 A801 U802 G803 A806 G807 C808 G809 U810 G816 G830 G834 A843 A848 A849 A852 A853 C854 G858 C859 A860 U864 G865 C866 U867 A872 A878 U879 G880 U881 G885 A886
G889 C893 G899 A900 A904 G905 G915 A916 G919 U920 A921 G922 G923 G924 C925 G926 G927 G930 C931 C932 A933 U934 G935 G936 A937 A938 G939 U940 C941 G942 A945 U946 C947 C948 G949 G950 U951 A952 A953 G954 A955 A956 A957 C958 G959 U960 G961 U962 U963 A964 C965 A966
A967 C968 G969 U970 A971 C972 C973 U974 A975 C976 G977 G978 A979 A980 U985 G988 G993 U998 U999 G1000 A1001 U1002 G1006 A1010 C1011 C1012 A1015 U1018 C1019 C1020 G1021 A1022 U1023 G1024 A1032 G1033 C1034 A1035 G1036 G1047 U1050 C1053 G1059 C1060 G1061 A1067
C1068 A1075 U1076 G1084 G1085 A1086 G1087 A1092 A1096 G1097 A1098 G1099 C1100 A1101 G1102 A1103 U1104 C1105 G1111 U1116 A1117 G1120 A1121 U1122 A1123 A1124 C1130 U1131 U1132 C1133 A1134 G1135 C1136 A1140 A1141 A1142 G1143 A1144 A1148 G1149 G1150 G1155 U1162 U1163 C1169 A1170 U1171
A1172 A1173 A1176 G1177 G1181 A1182 G1183 C1184 C1185 U1189 C1190 U1191 A1192 G1198 A1204 G1205 A1206 A1217 A1218 A1223 A1224 A1225 C1226 A1227 G1228 G1229 U1230 U1231 G1232 A1233 U1234 A1235 U1236 U1237 G1247 C1250 C1254 A1257 C1264 U1268 A1269 U1270 U1271 A1272 G1273 C1274
G1277 U1278 A1281 C1282 A1283 A1308 C1309 U1318 A1327 G1332 G1339 A1340 G1341 A1342 A1346 C1351 U1360 U1374 G1375 C1383 U1384 G1385 A1386 G1387 C1388 G1391 C1392 U1393 U1394 U1395 G1396 A1400 C1411 C1412 A1413 U1414 G1415 A1416 A1417 A1421 C1422 A1427 U1428 A1429
U1430 G1431 A1437 U1441 C1442 C1443 A1449 A1450 U1454 C1457 A1458 U1463 C1464 C1465 A1466 A1467 G1468 G1474 G1485 G1486 A1487 U1488 G1489 U1490 U1491 U1492 U1499 G1500 A1503 G1504 G1505 G1506 G1513 U1527 G1535 G1536 A1539 G1547 U1554 G1555 U1556 G1557 A1563
U1564 U1565 A1571 A1572 G1573 G1574 A1583 U1592 C1603 G1609 A1610 A1611 G1612 A1613 G1614 G1619 A1625 G1626 U1627 U1628 C1629 G1643 U1644 C1645 A1649 C1650 A1651 C1652 G1653 A1668 G1675 A1679 A1680 G1685 G1686 G1687 A1688 A1692 C1693 U1700 U1705 A1706 A1707 G1708
G1709 A1715 A1716 A1717 C1718 G1719 C1720 C1723 G1724 A1731 A1732 A1733 U1734 A1739 C1740 G1741 C1742 G1743 C1744 A1745 U1746 A1749 U1750 G1751 G1752 A1753 A1754 U1755 G1756 A1760 G1771 U1772 A1797 C1801 C1802 A1803 A1808 A1809 C1810 G1811 G1828 A1832 G1835 A1836 A1837 A1838 A1839
U1846 A1854 G1862 A1869 G1875 A1876 U1880 U1881 G1882 A1883 G1884 G1885 C1886 G1887 A1888 U1889 G1890 G1893 G1894 A1895 A1896 G1897 G1898 U1899 A1902 G1903 A1904 G1905 C1906 G1907 C1908 A1909 A1910 G1911 C1912 A1915 A1916 G1917 U1918 G1919 A1920 A1921 A1922 G1923 A1924 C1925 C1926 A1927 C1928 U1929 G1930

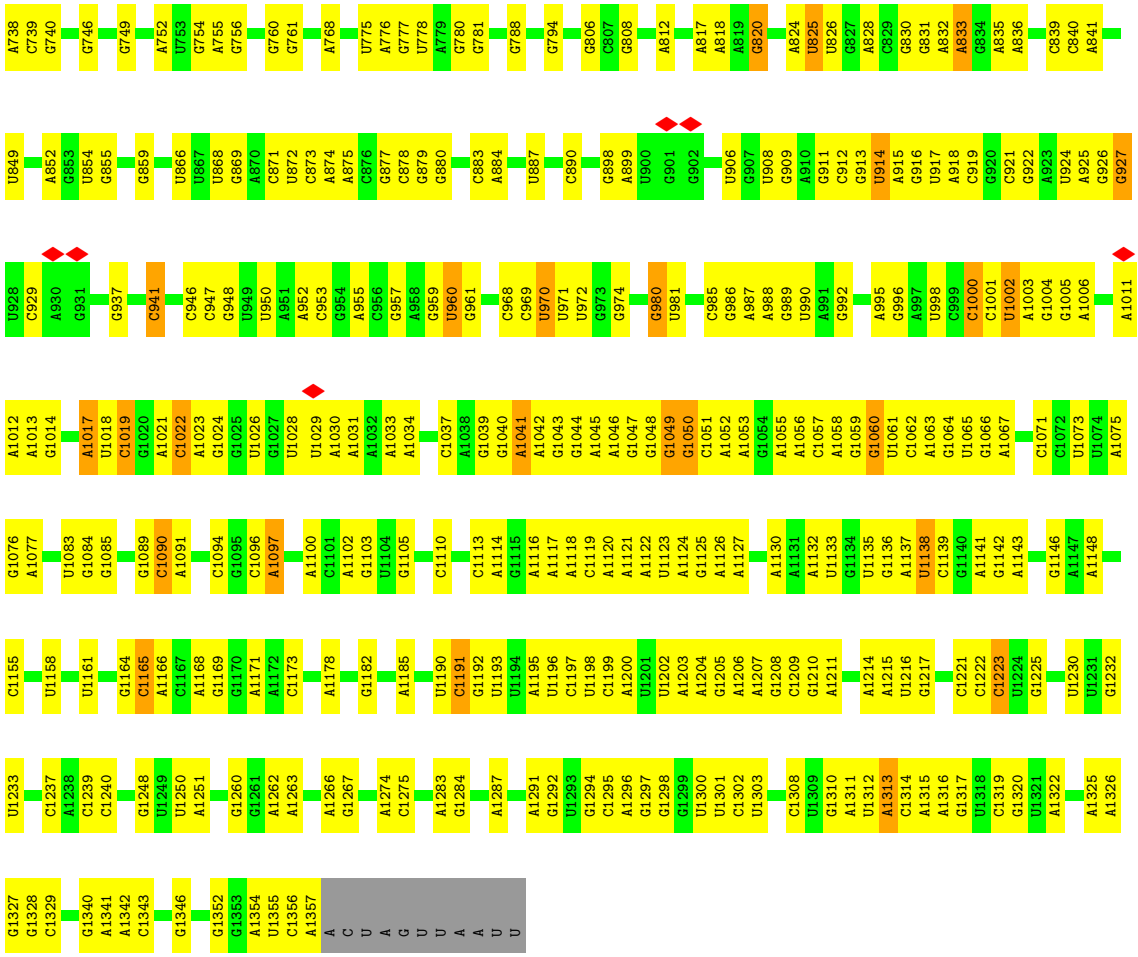


• Molecule 2: RNA 16S

Chain R60:



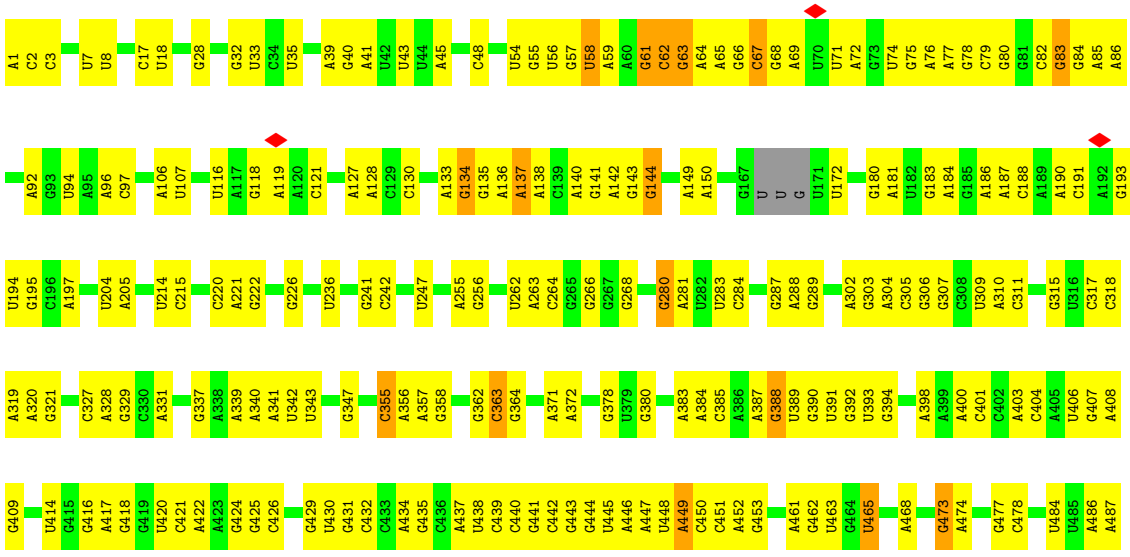


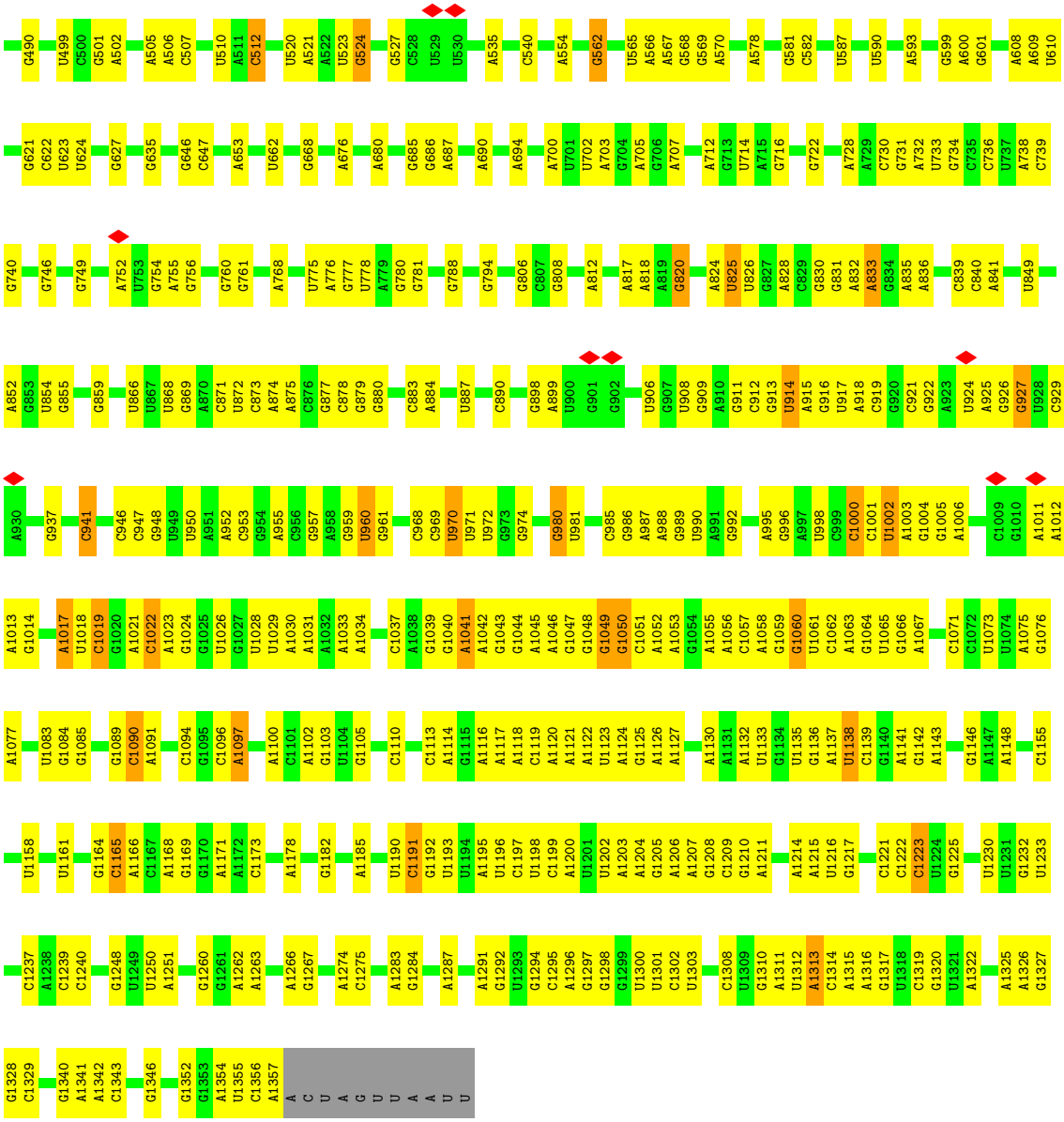


• Molecule 2: RNA 16S

Chain S60:

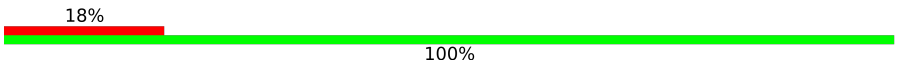


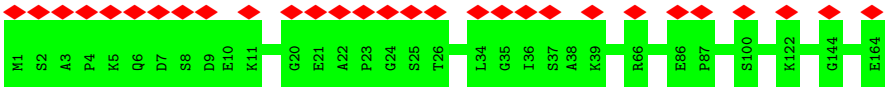




• Molecule 3: 60S ribosomal protein L12

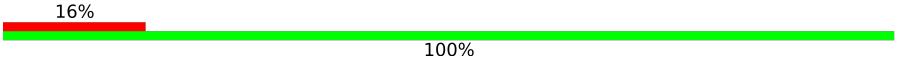
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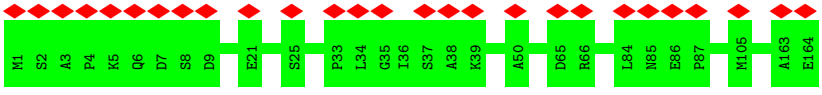




• Molecule 3: 60S ribosomal protein L12

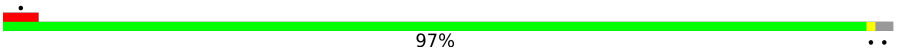
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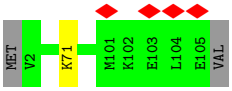




• Molecule 4: Ribosomal protein L34

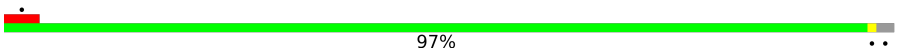
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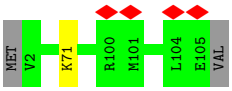




• Molecule 4: Ribosomal protein L34

Chain LGG:

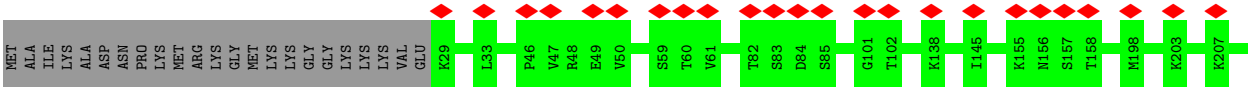


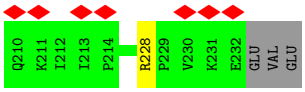


• Molecule 5: 40S ribosomal protein S1

Chain RB0:



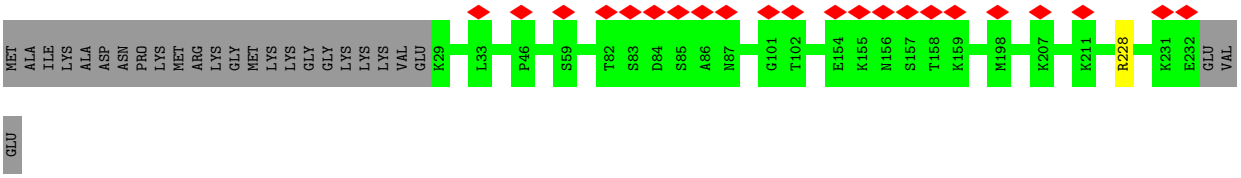




• Molecule 5: 40S ribosomal protein S1

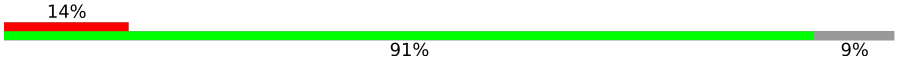
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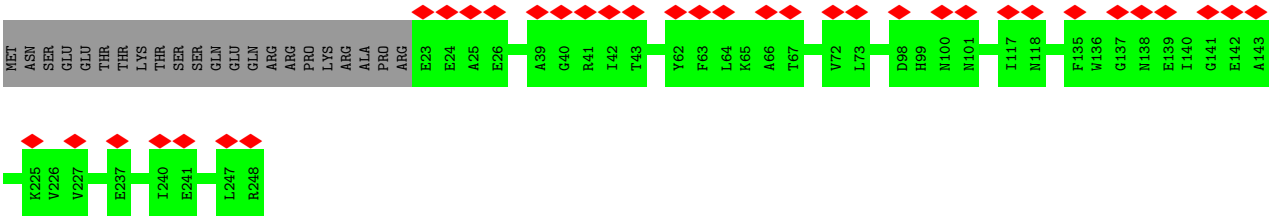




• Molecule 6: 40S ribosomal protein S2

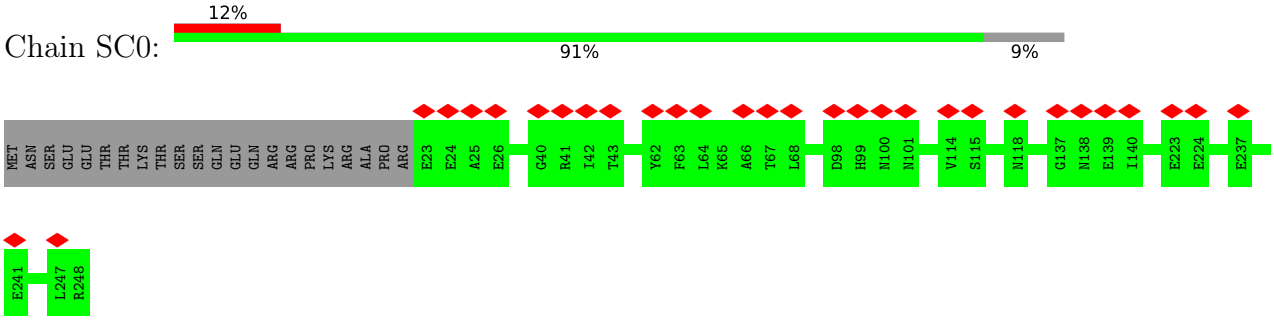
Chain RC0:





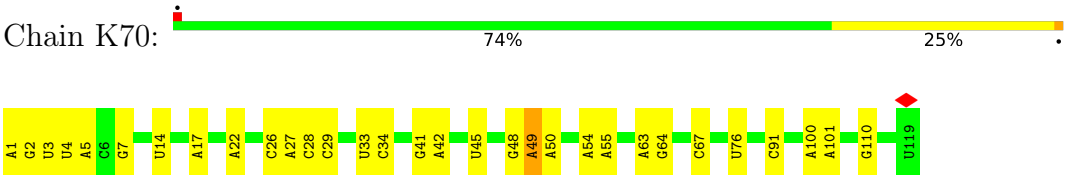
• Molecule 6: 40S ribosomal protein S2

Chain SC0:



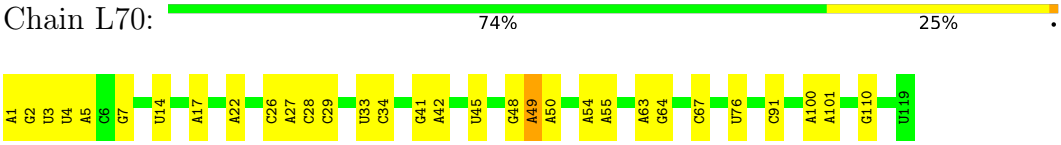
• Molecule 7: RNA 5S

Chain K70:



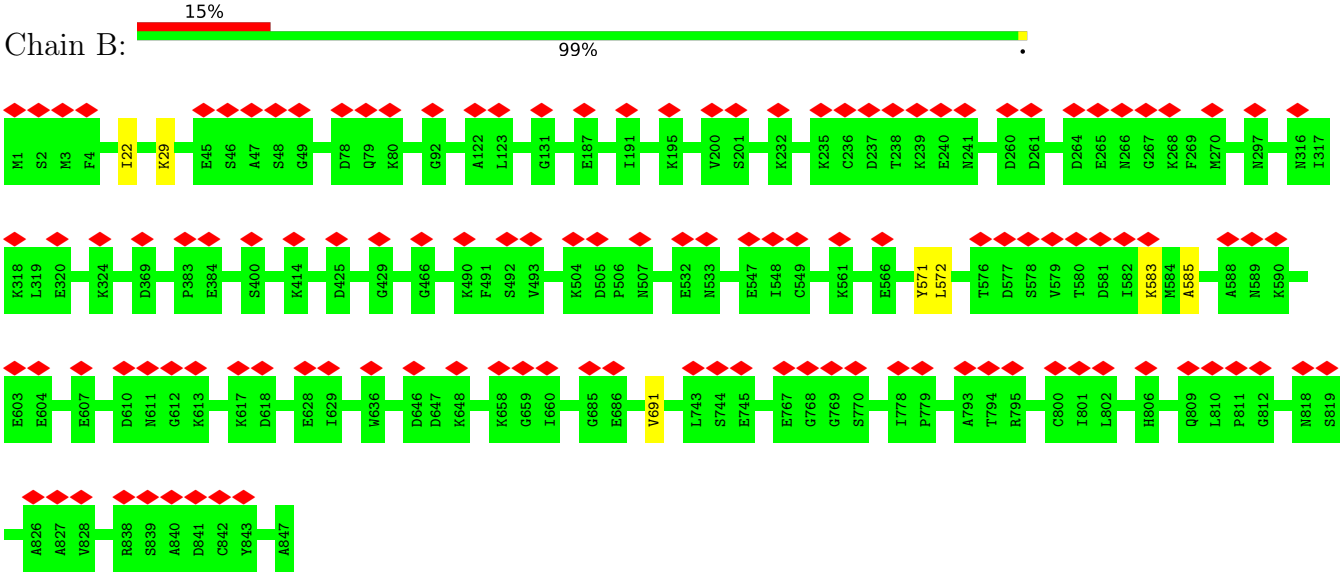
• Molecule 7: RNA 5S

Chain L70:



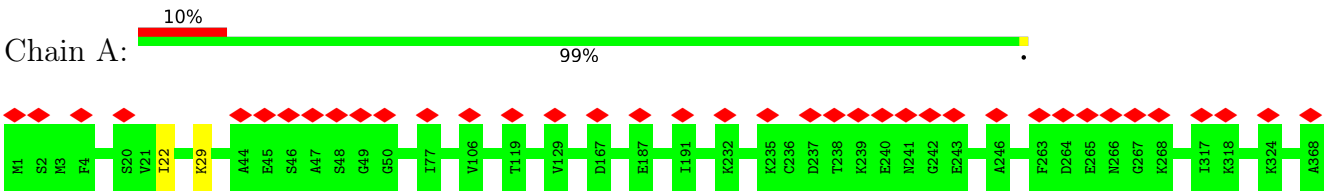
• Molecule 8: Elongation factor 2

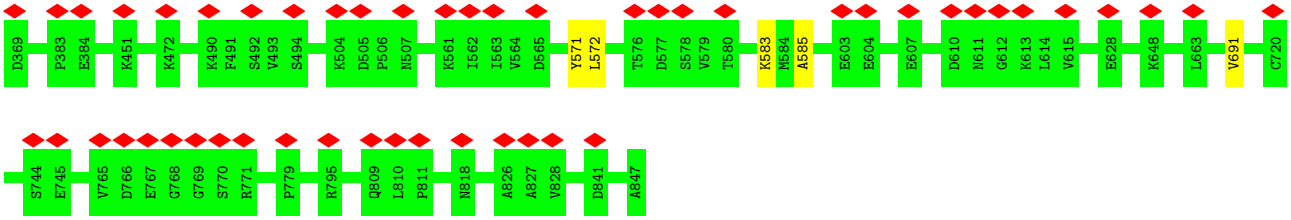
Chain B:



• Molecule 8: Elongation factor 2

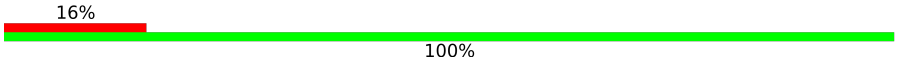
Chain A:

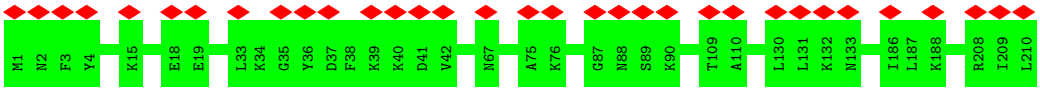




• Molecule 9: 60S ribosomal protein L10a

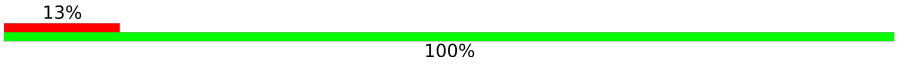
Chain K:

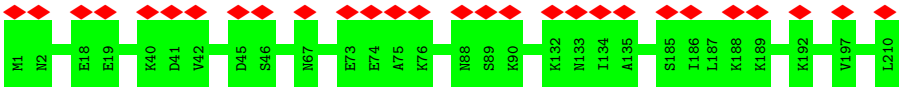




• Molecule 9: 60S ribosomal protein L10a

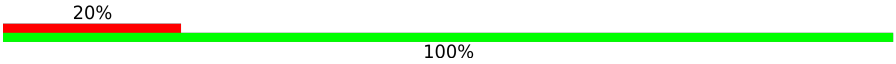
Chain L:

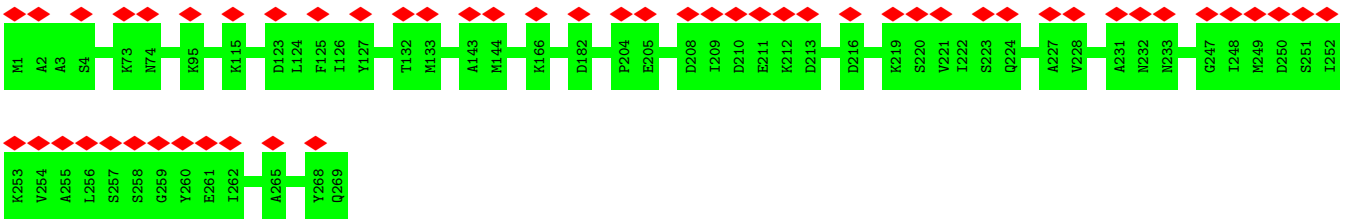




• Molecule 10: Large ribosomal subunit protein uL10

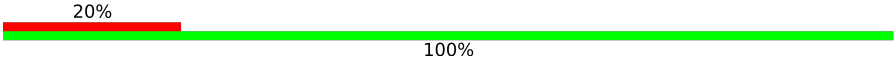
Chain N:

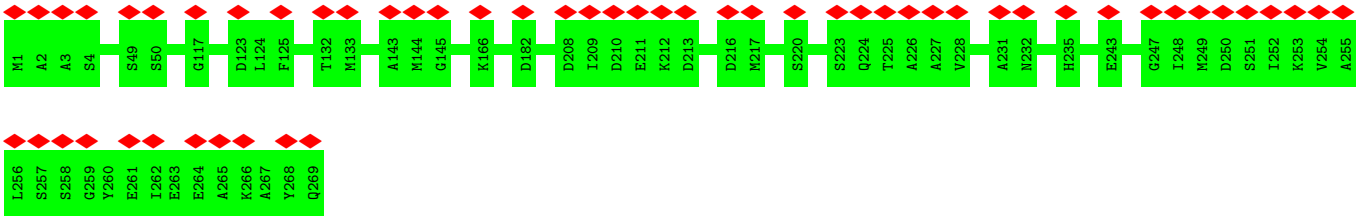




• Molecule 10: Large ribosomal subunit protein uL10

Chain M:



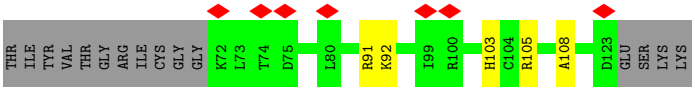


• Molecule 11: Ubiquitin

Chain KMM:

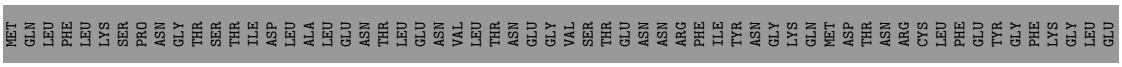


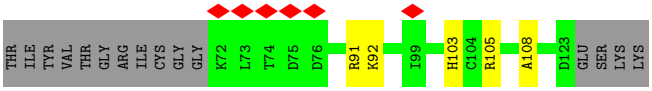




• Molecule 11: Ubiquitin

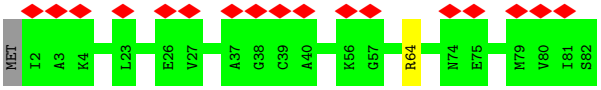






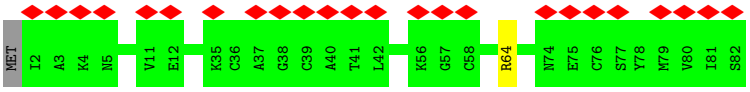
• Molecule 12: 40S ribosomal protein S27





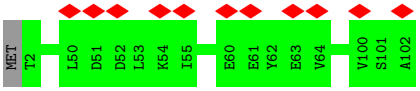
• Molecule 12: 40S ribosomal protein S27





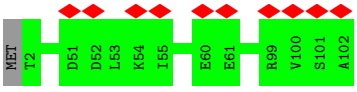
• Molecule 13: 40S ribosomal protein S26





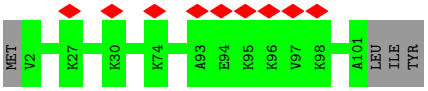
• Molecule 13: 40S ribosomal protein S26





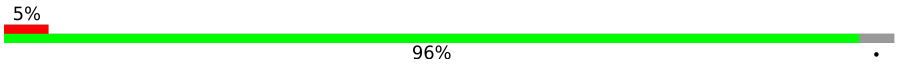
• Molecule 14: 60S ribosomal protein L44

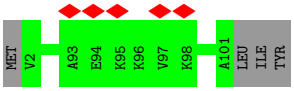




• Molecule 14: 60S ribosomal protein L44

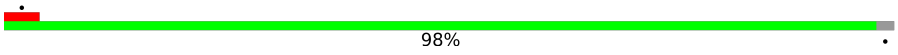
Chain LOO:

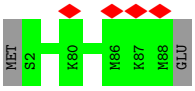




• Molecule 15: 60S ribosomal protein L37a.

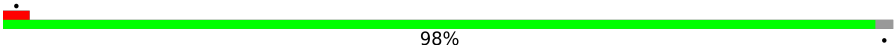
Chain KPP:

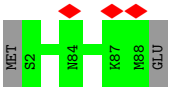




• Molecule 15: 60S ribosomal protein L37a.

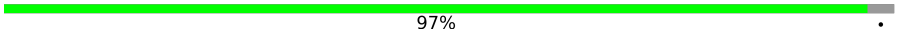
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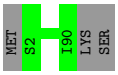




• Molecule 16: 60S ribosomal protein L37

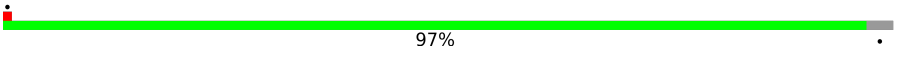
Chain KJJ:

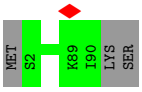




• Molecule 16: 60S ribosomal protein L37

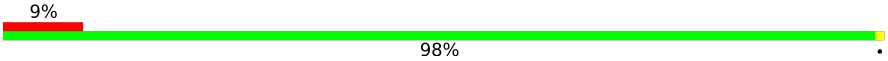
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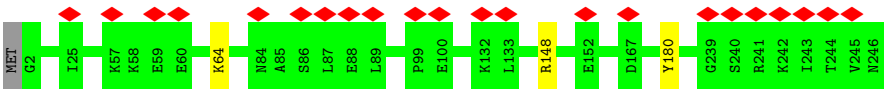




• Molecule 17: 60S ribosomal protein L8

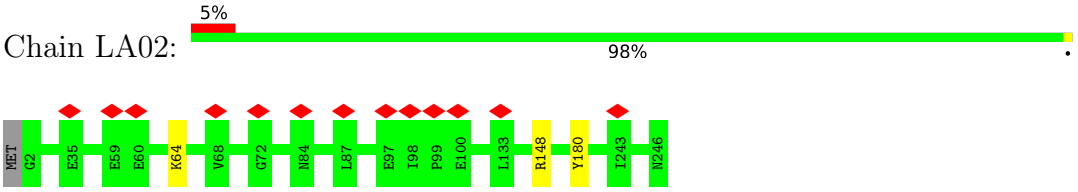
Chain LA0:





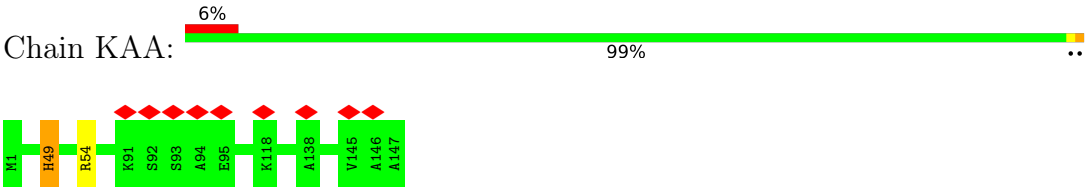
• Molecule 17: 60S ribosomal protein L8

Chain LA02:



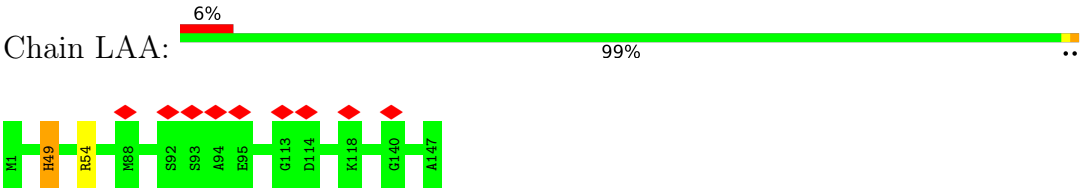
• Molecule 18: 60S ribosomal protein L15

Chain KAA:



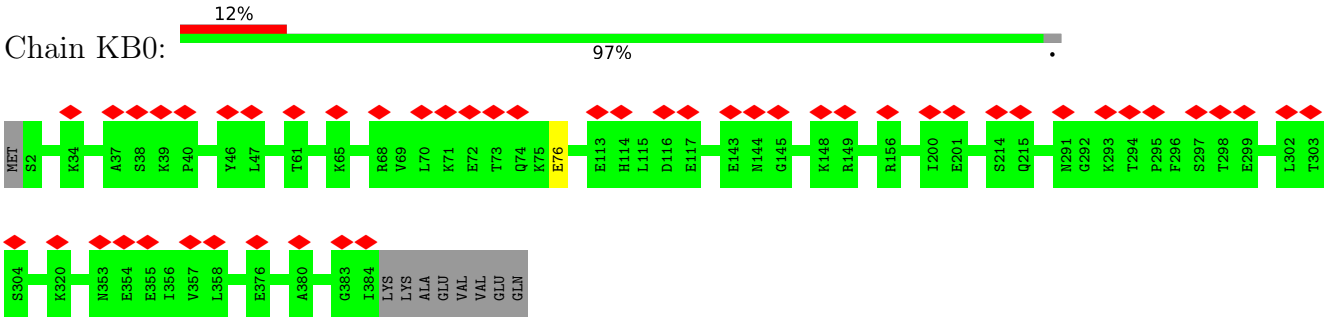
• Molecule 18: 60S ribosomal protein L15

Chain LAA:



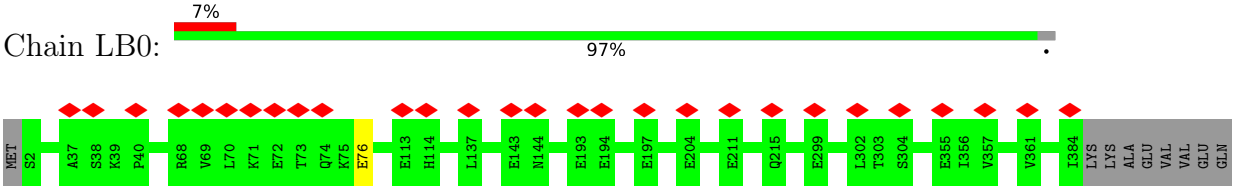
• Molecule 19: 60S ribosomal protein L3

Chain KB0:



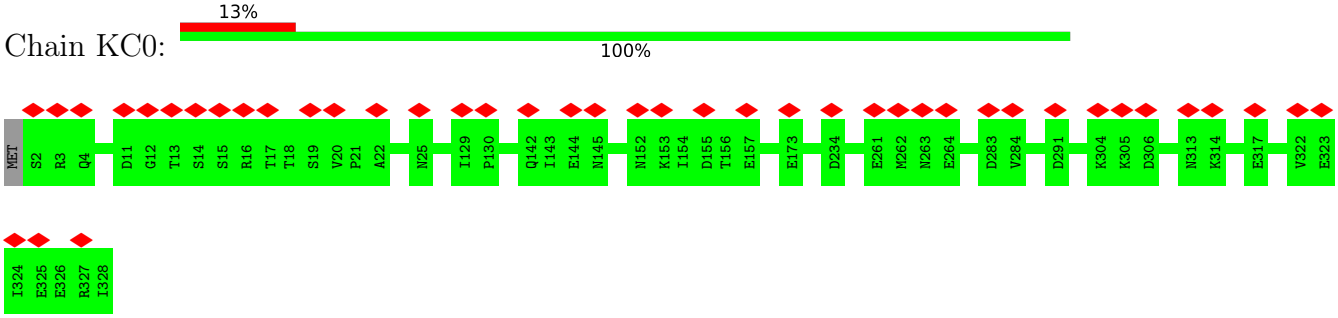
• Molecule 19: 60S ribosomal protein L3

Chain LB0:



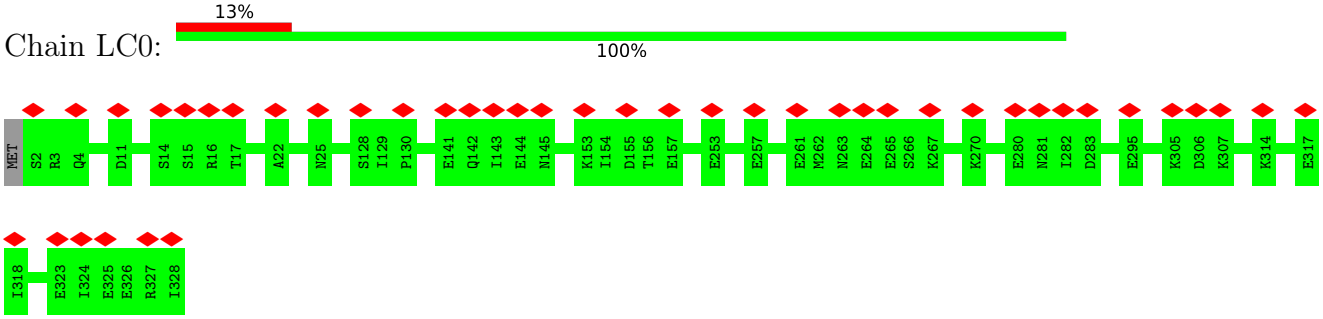
• Molecule 20: 60S ribosomal protein L4

Chain KC0:



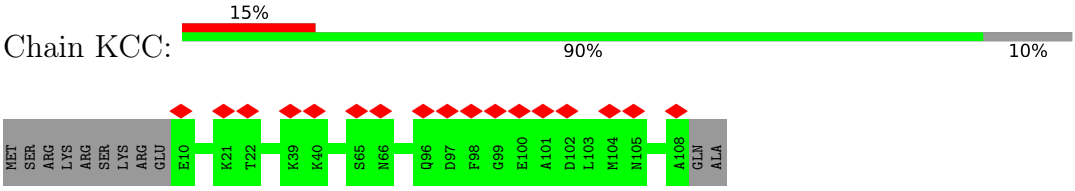
• Molecule 20: 60S ribosomal protein L4

Chain LC0:



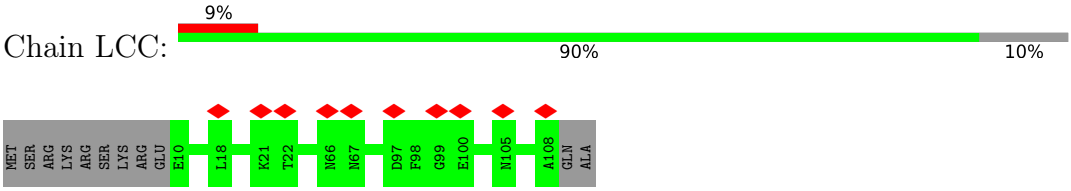
• Molecule 21: 60S ribosomal protein L3

Chain KCC:



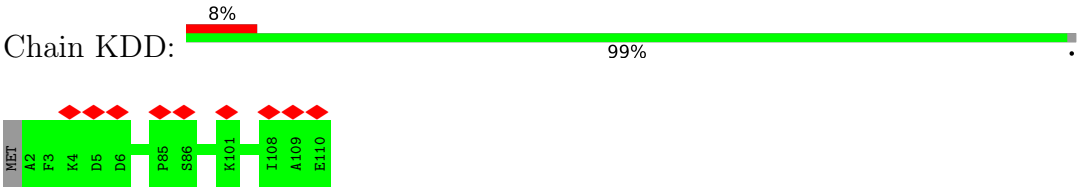
• Molecule 21: 60S ribosomal protein L3

Chain LCC:



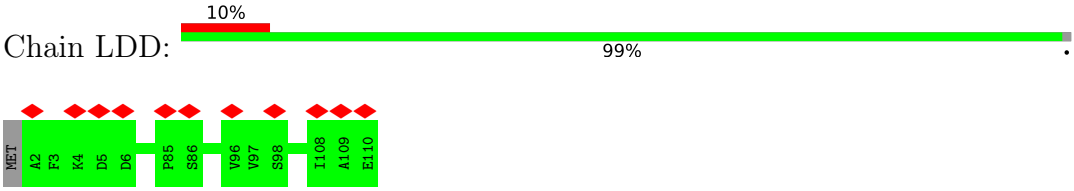
• Molecule 22: 60S ribosomal protein L31

Chain KDD:



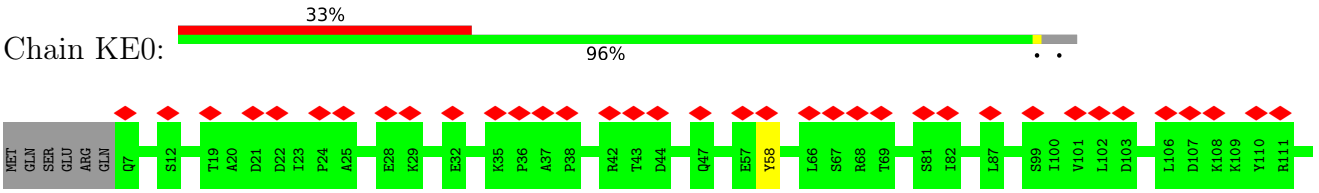
• Molecule 22: 60S ribosomal protein L31

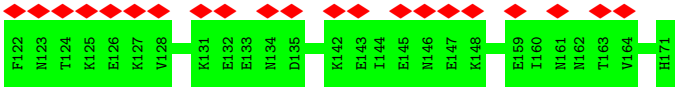
Chain LDD:



• Molecule 23: 60S ribosomal protein L6

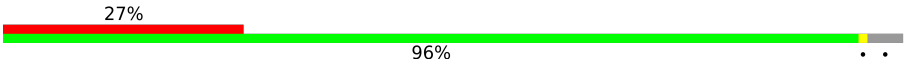
Chain KE0:

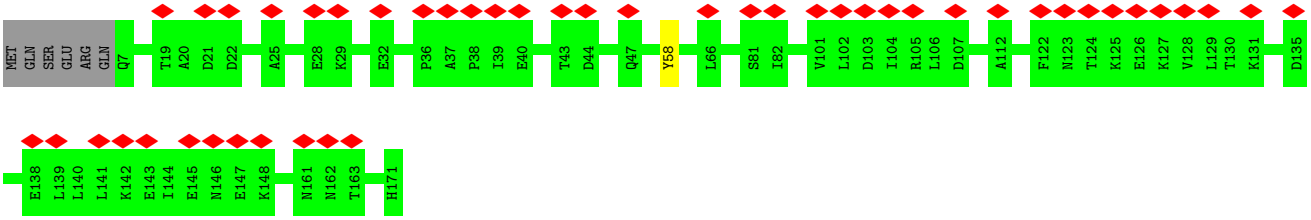




• Molecule 23: 60S ribosomal protein L6

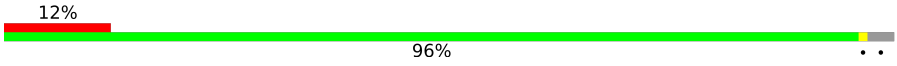
Chain LE0:

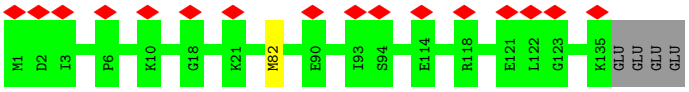




• Molecule 24: 60S ribosomal protein L32

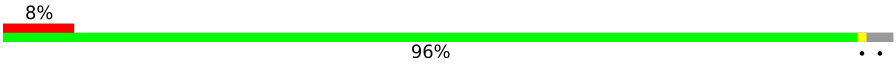
Chain KEE:

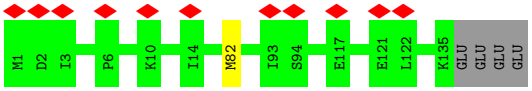




• Molecule 24: 60S ribosomal protein L32

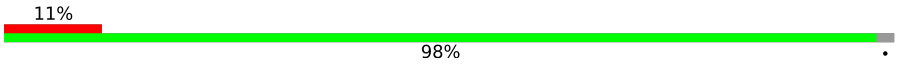
Chain LEE:

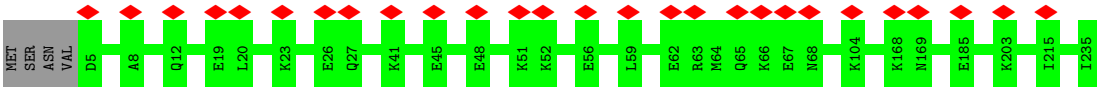




• Molecule 25: 60S ribosomal protein L7

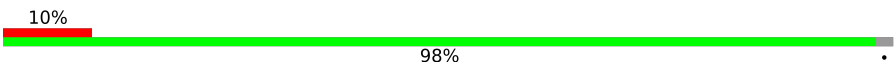
Chain KF0:

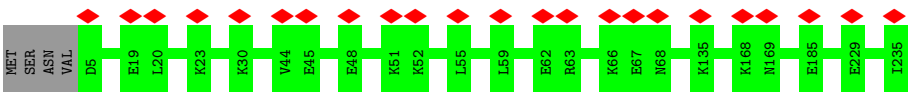




• Molecule 25: 60S ribosomal protein L7

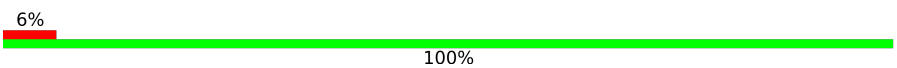
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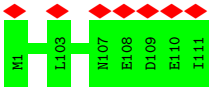




• Molecule 26: 60S ribosomal protein L35a

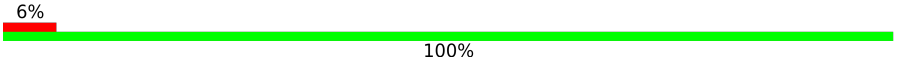
Chain KFF:

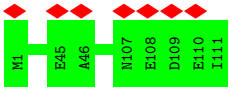




• Molecule 26: 60S ribosomal protein L35a

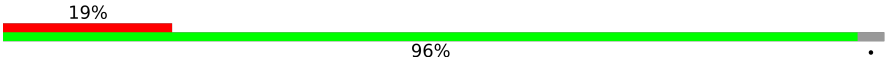
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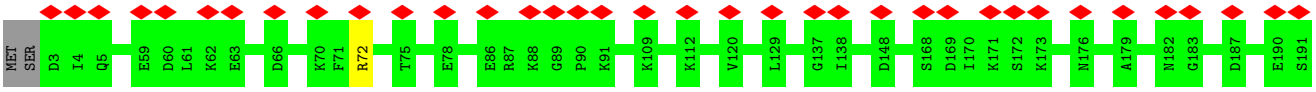


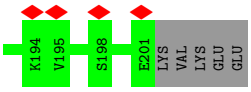


• Molecule 27: 60S ribosomal protein L8

Chain KG0:

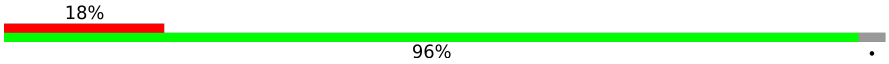


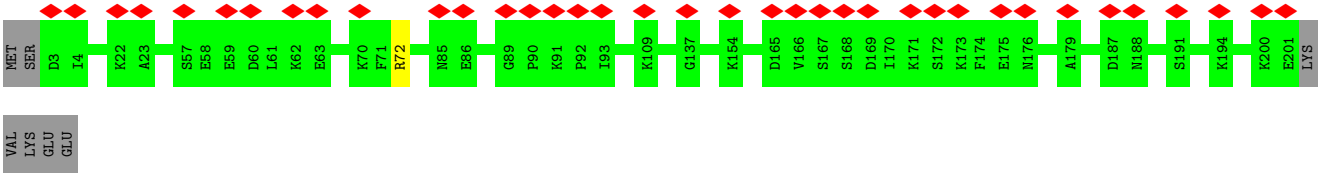




• Molecule 27: 60S ribosomal protein L8

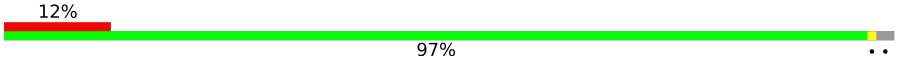
Chain LG0:

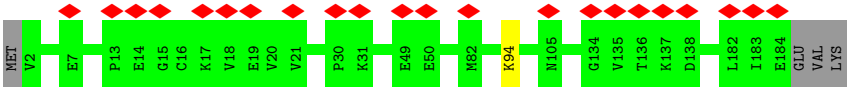




• Molecule 28: 60S ribosomal protein L9

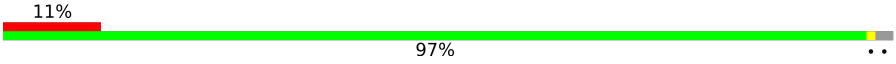
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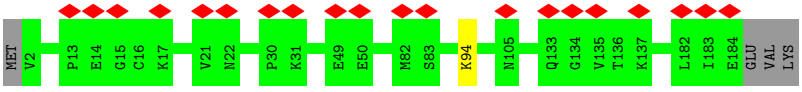




• Molecule 28: 60S ribosomal protein L9

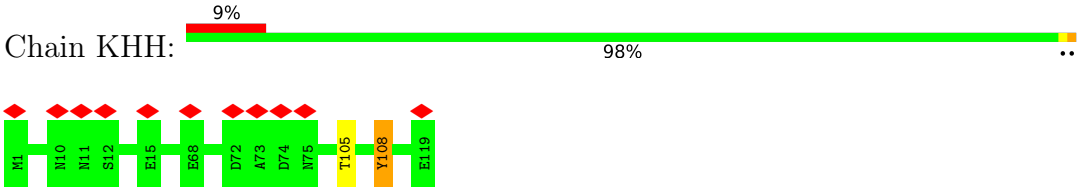
Chain LH0:





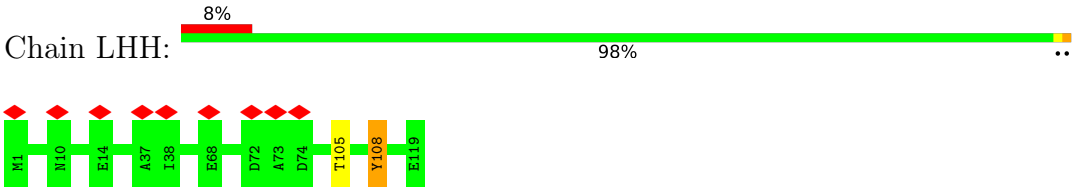
• Molecule 29: 60S Ribosomal L29 protein

Chain KHH:



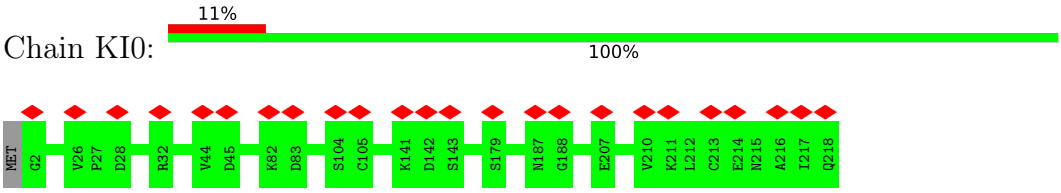
• Molecule 29: 60S Ribosomal L29 protein

Chain LHH:



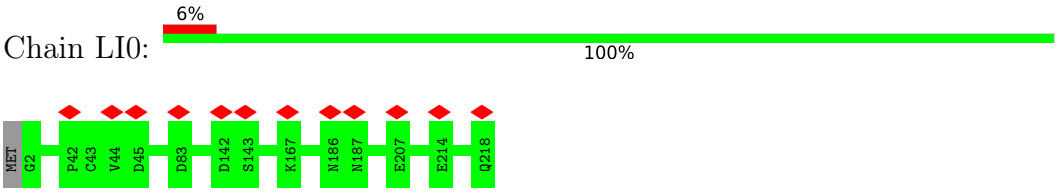
• Molecule 30: S60 ribosomal protein L10

Chain KI0:



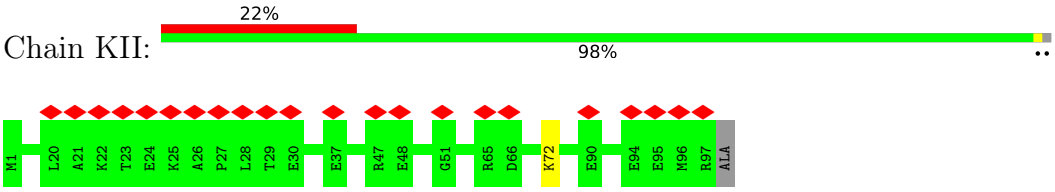
• Molecule 30: S60 ribosomal protein L10

Chain LI0:



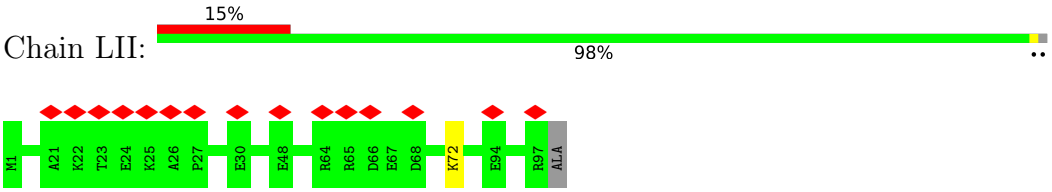
• Molecule 31: 60S ribosomal protein L36

Chain KII:



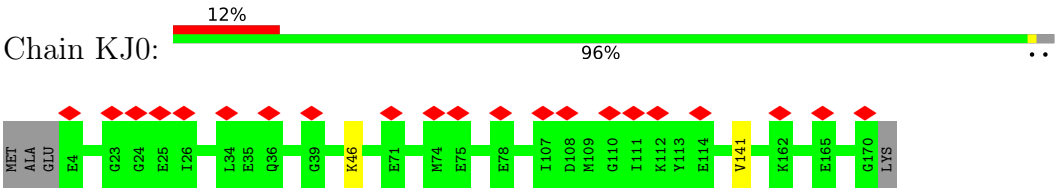
• Molecule 31: 60S ribosomal protein L36

Chain LII:



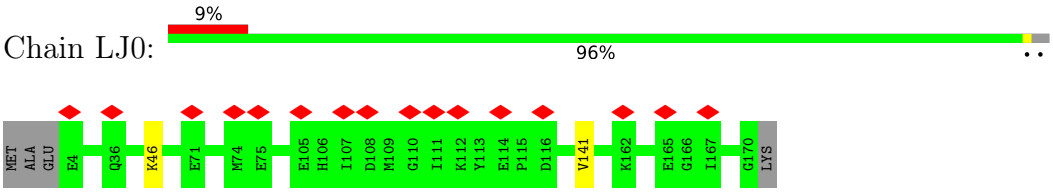
• Molecule 32: 60S ribosomal protein L11

Chain KJ0:



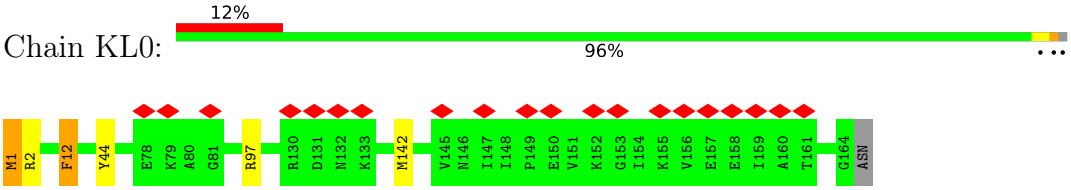
• Molecule 32: 60S ribosomal protein L11

Chain LJ0:



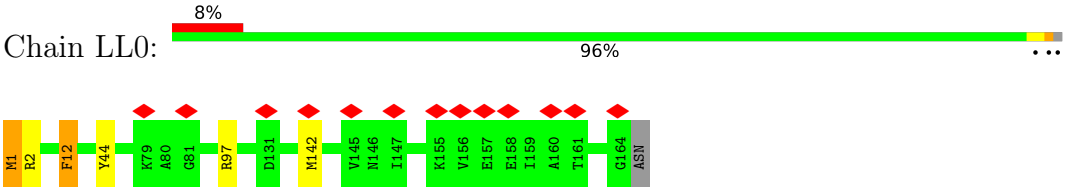
• Molecule 33: 60S ribosomal protein L13

Chain KL0:



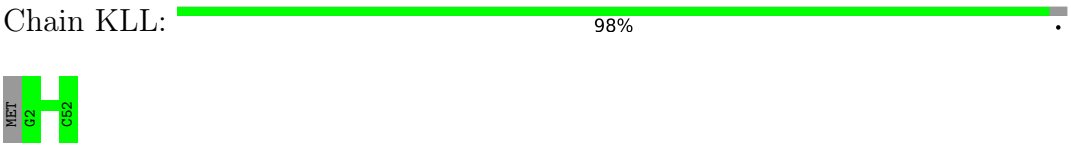
• Molecule 33: 60S ribosomal protein L13

Chain LL0:



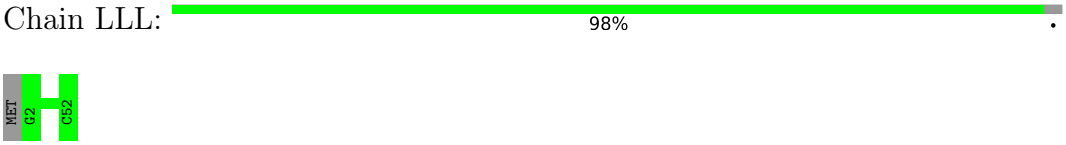
• Molecule 34: 60S ribosomal protein L39

Chain KLL:



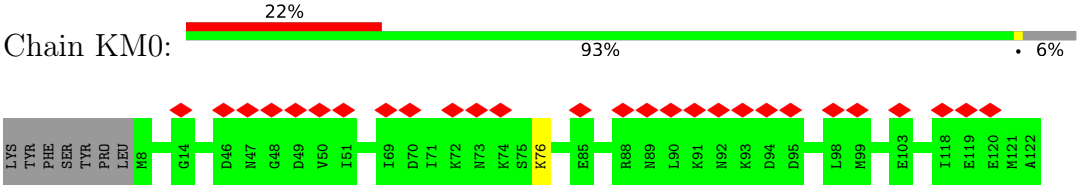
• Molecule 34: 60S ribosomal protein L39

Chain LLL:



• Molecule 35: eL14 LM0

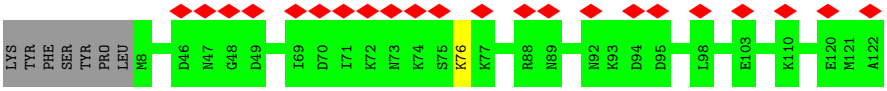
Chain KM0:



• Molecule 35: eL14 LM0

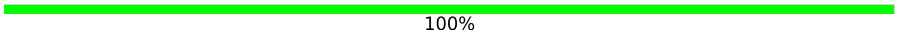
Chain LM0:

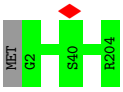




• Molecule 36: Ribosomal protein L15

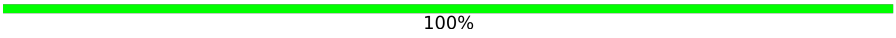
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• Molecule 36: Ribosomal protein L15

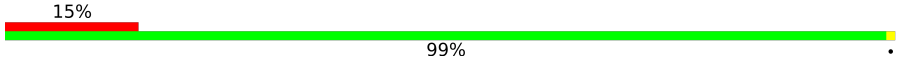
Chain LN0:

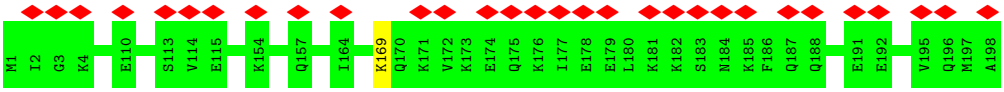




• Molecule 37: Ribosomal protein L13A

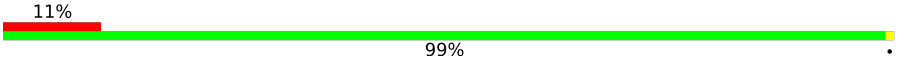
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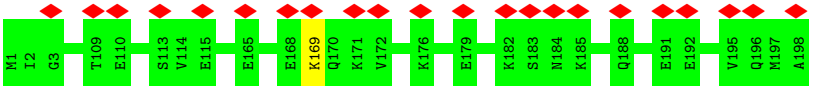




• Molecule 37: Ribosomal protein L13A

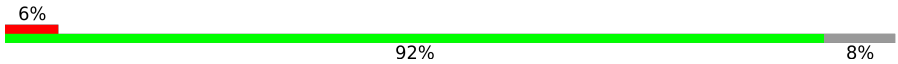
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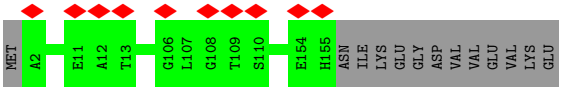




• Molecule 38: 60S ribosomal protein L17

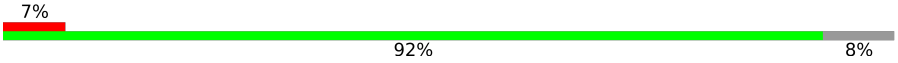
Chain KP0:

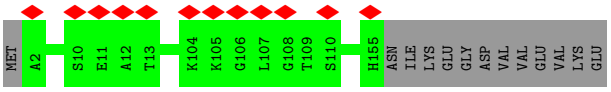




• Molecule 38: 60S ribosomal protein L17

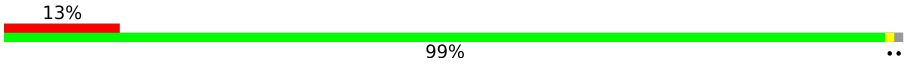
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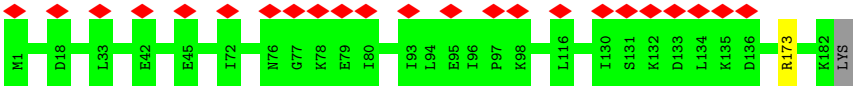




• Molecule 39: 60S ribosomal protein L18

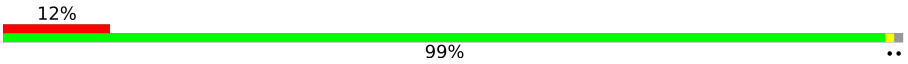
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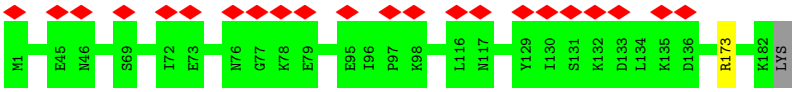




• Molecule 39: 60S ribosomal protein L18

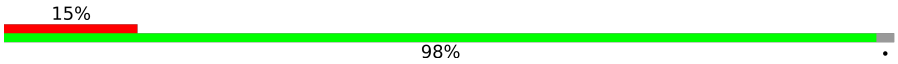
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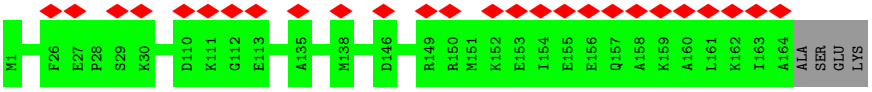




• Molecule 40: 60S ribosomal protein L19

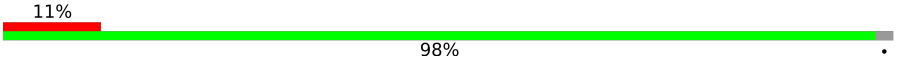
Chain KR0:

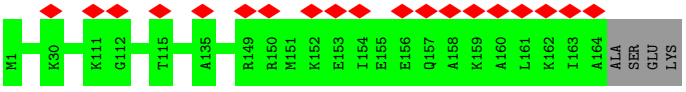




• Molecule 40: 60S ribosomal protein L19

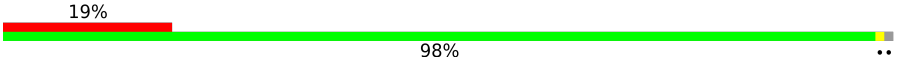
Chain LR0:

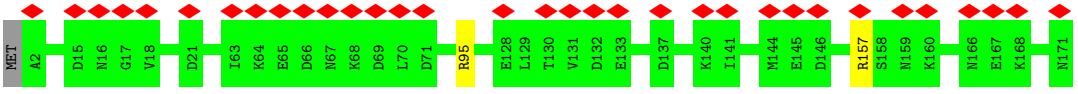




• Molecule 41: 60S ribosomal protein L20

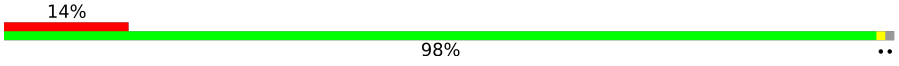
Chain KS0:

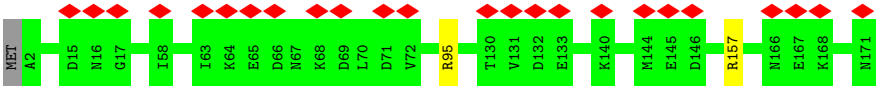




• Molecule 41: 60S ribosomal protein L20

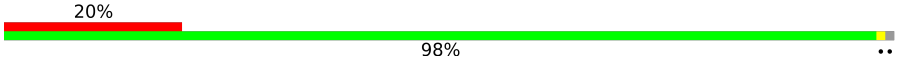
Chain LS0:

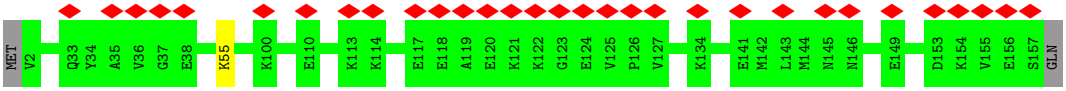




• Molecule 42: 60s ribosomal protein L21

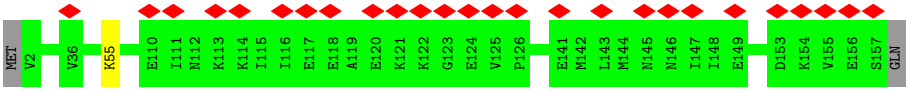
Chain KT0:



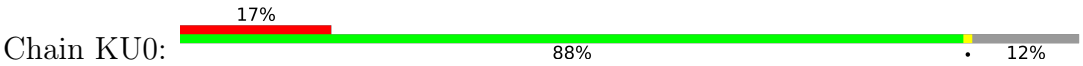


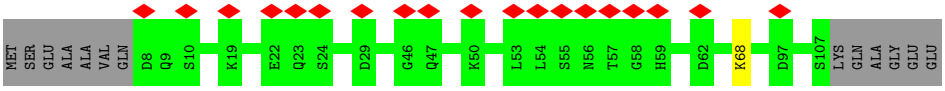
• Molecule 42: 60s ribosomal protein L21



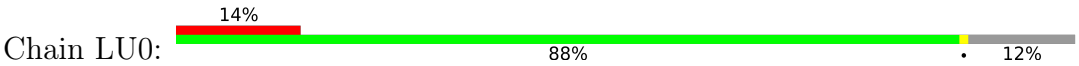


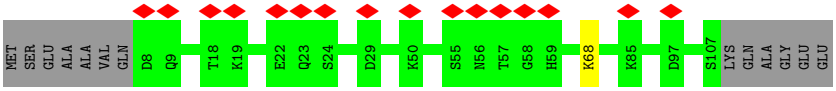
• Molecule 43: 60S ribosomal protein L22





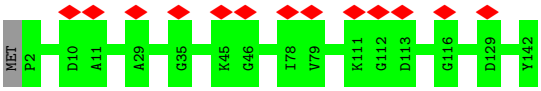
• Molecule 43: 60S ribosomal protein L22





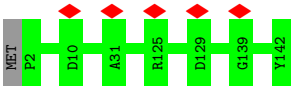
• Molecule 44: Ribosomal protein L23



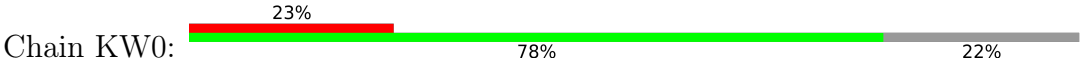


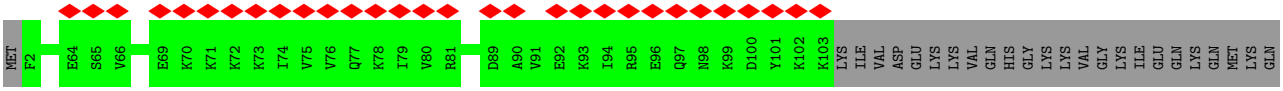
• Molecule 44: Ribosomal protein L23





• Molecule 45: Ribosomal protein L24E



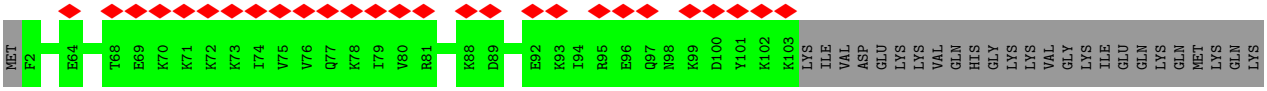




• Molecule 45: Ribosomal protein L24E

Chain LW0:

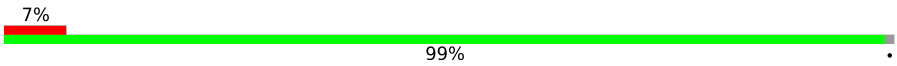


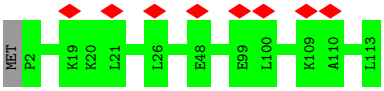




• Molecule 46: 60S ribosomal protein L23a

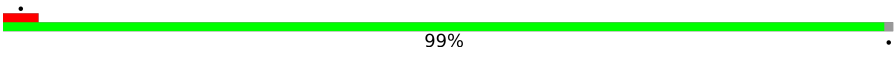
Chain KX0:

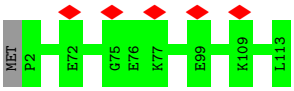




• Molecule 46: 60S ribosomal protein L23a

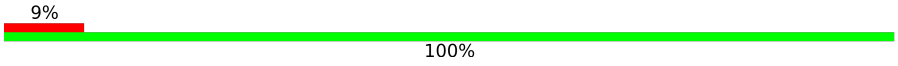
Chain LX0:

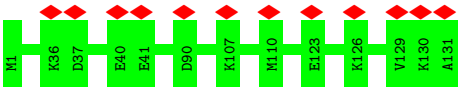




• Molecule 47: 60S ribosomal protein L26

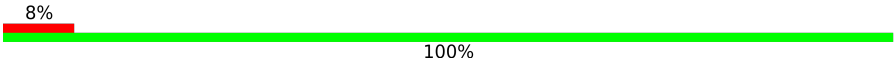
Chain KY0:

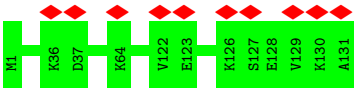




• Molecule 47: 60S ribosomal protein L26

Chain LY0:

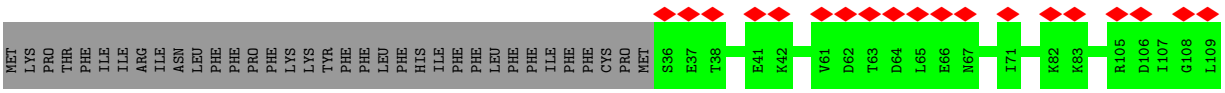


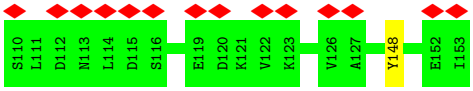


• Molecule 48: 60S ribosomal protein L27

Chain KZ0:



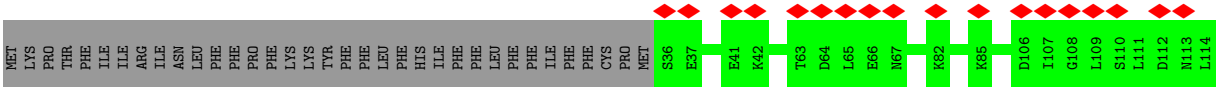


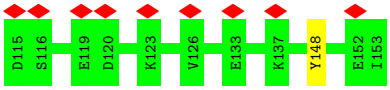


• Molecule 48: 60S ribosomal protein L27

Chain LZ0:

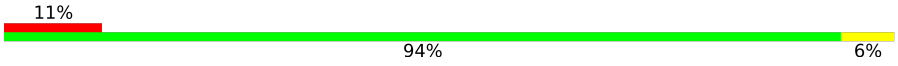


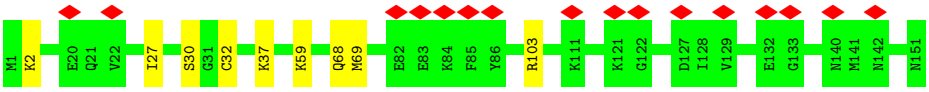




• Molecule 49: DNL-type domain-containing protein

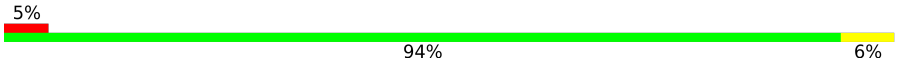
Chain ND1:

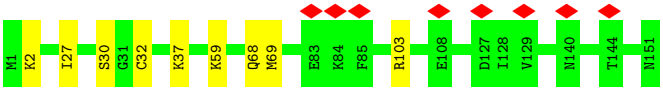




• Molecule 49: DNL-type domain-containing protein

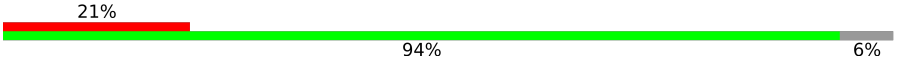
Chain MD1:

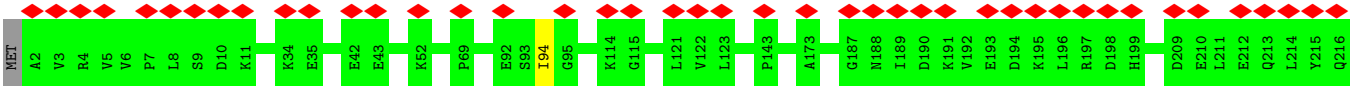


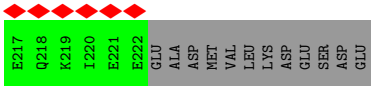


• Molecule 50: 40S ribosomal protein S0

Chain RA0:

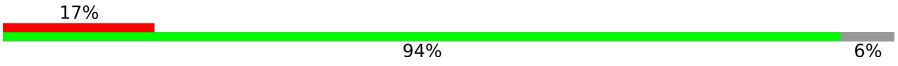


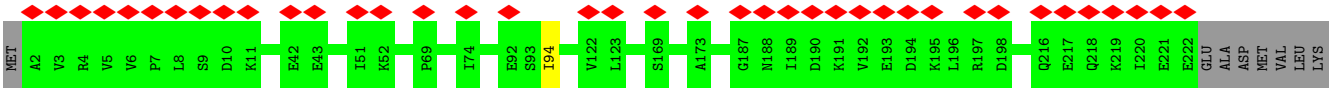




• Molecule 50: 40S ribosomal protein S0

Chain SA0:

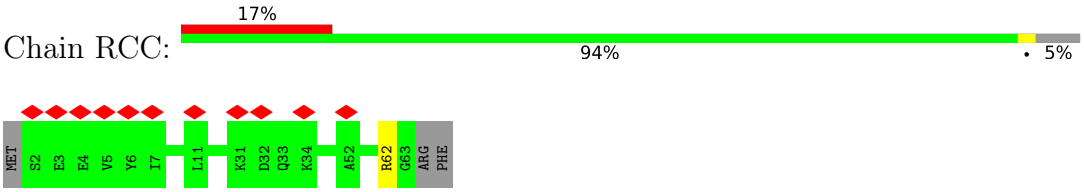






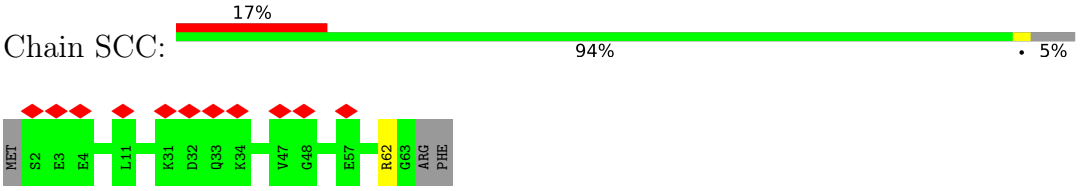
• Molecule 51: 40S ribosomal protein S28

Chain RCC:



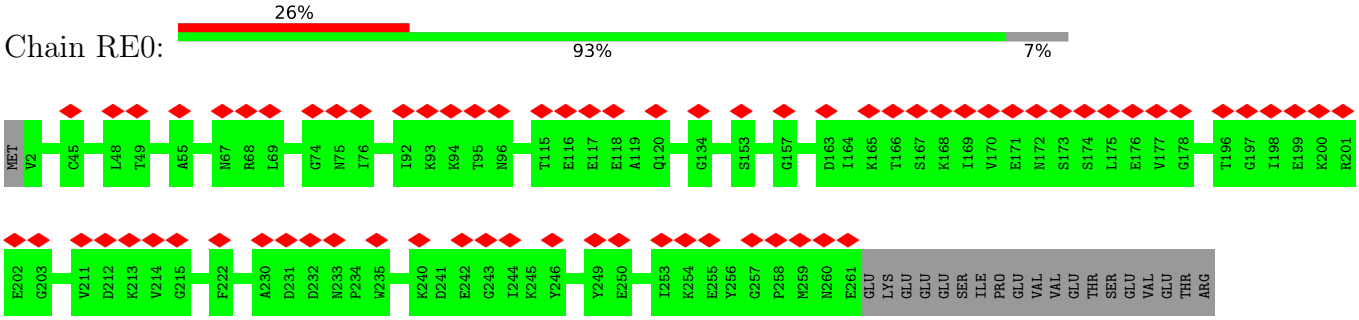
• Molecule 51: 40S ribosomal protein S28

Chain SCC:



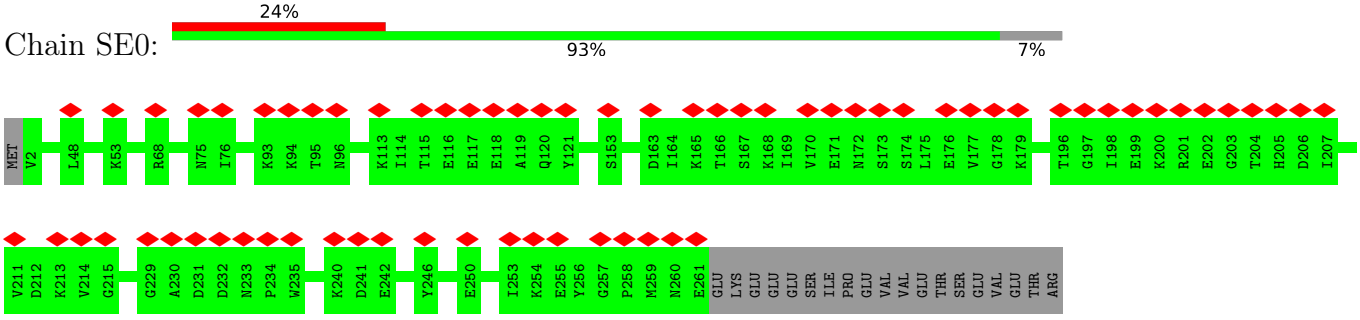
• Molecule 52: 40S ribosomal protein S4

Chain RE0:



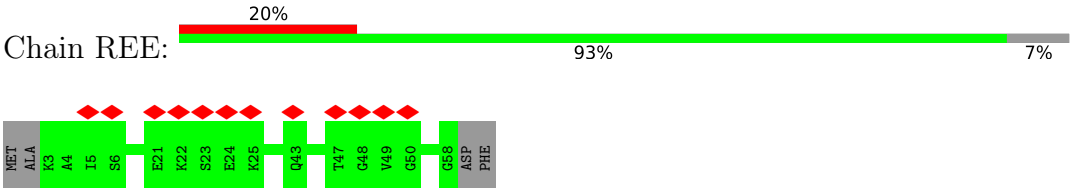
• Molecule 52: 40S ribosomal protein S4

Chain SE0:



• Molecule 53: 40S ribosomal protein S30

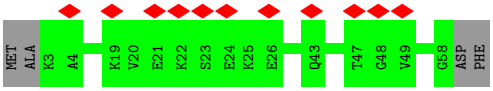
Chain REE:



• Molecule 53: 40S ribosomal protein S30

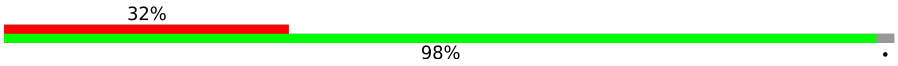
Chain SEE:

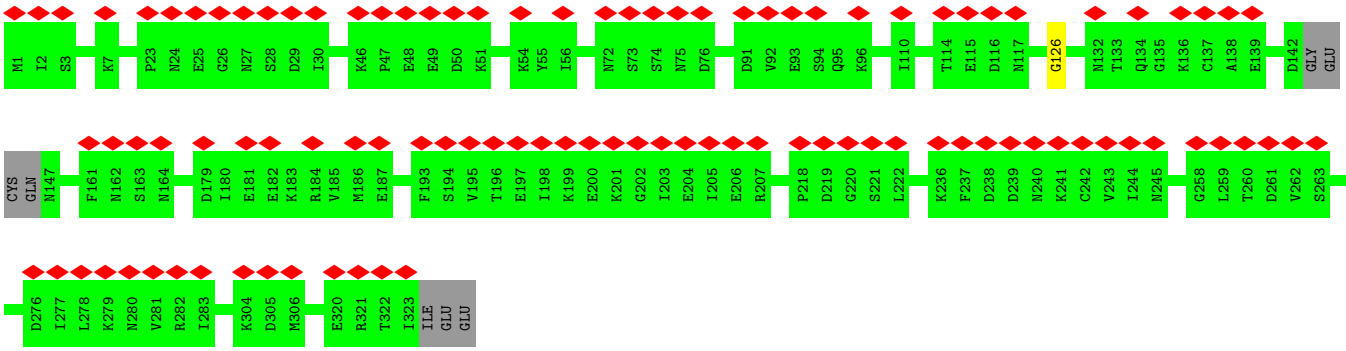




• Molecule 54: Guanine nucleotide binding protein beta subunit

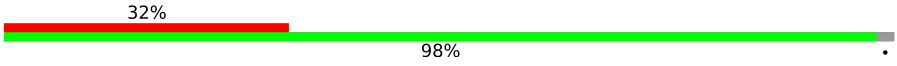
Chain RGG:

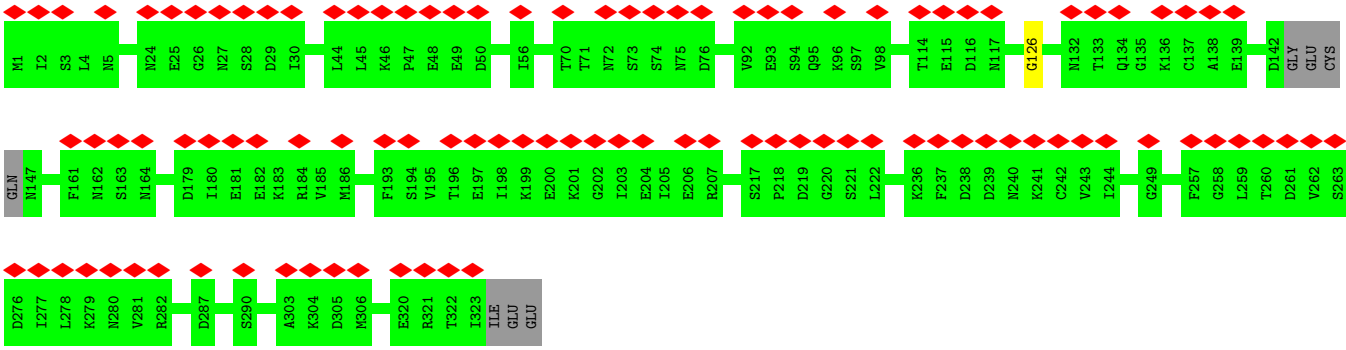




• Molecule 54: Guanine nucleotide binding protein beta subunit

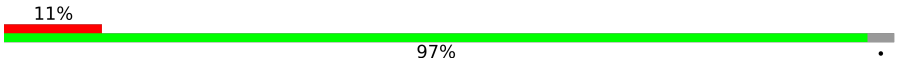
Chain SGG:

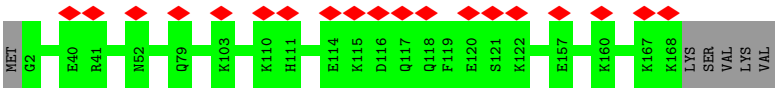




• Molecule 55: 40S ribosomal protein S8

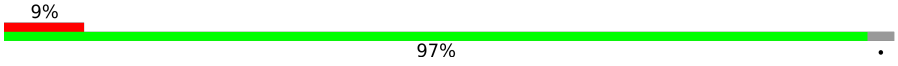
Chain RI0:

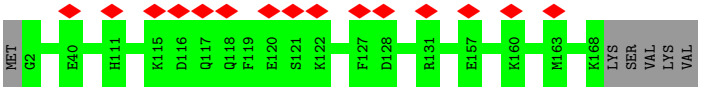




• Molecule 55: 40S ribosomal protein S8

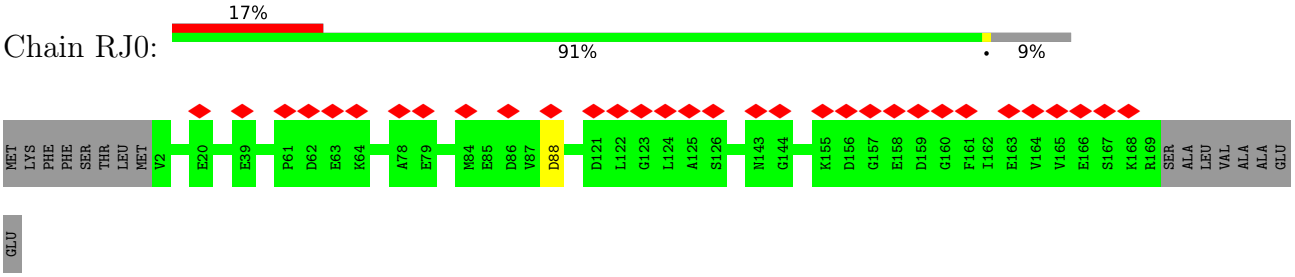
Chain SI0:





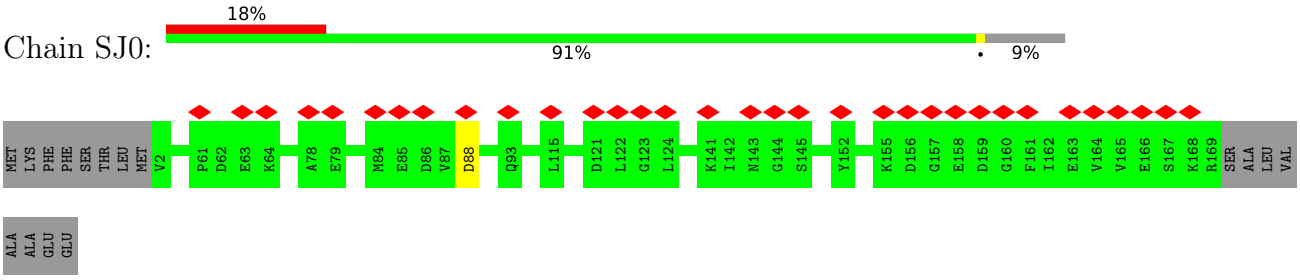
• Molecule 56: 40S ribosomal protein S9

Chain RJ0:



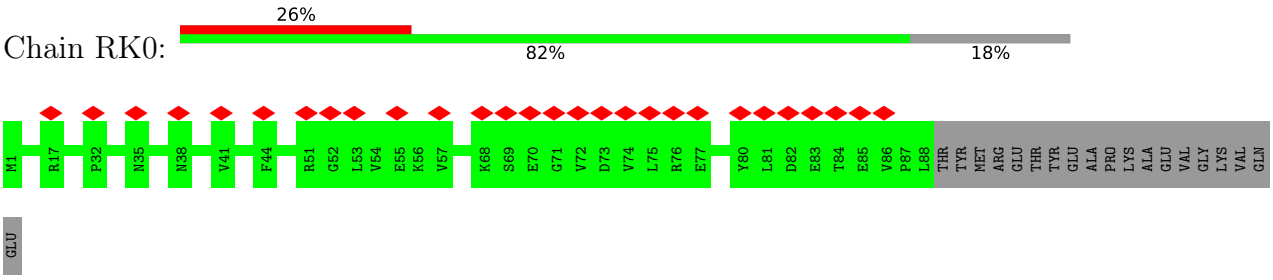
• Molecule 56: 40S ribosomal protein S9

Chain SJ0:



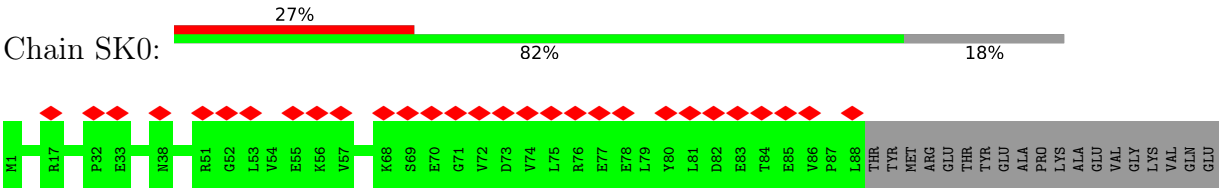
• Molecule 57: 40S ribosomal protein S10

Chain RK0:



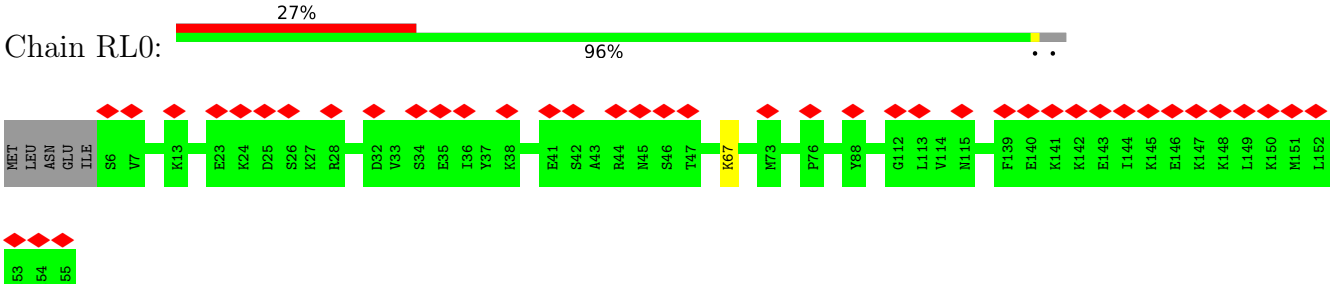
• Molecule 57: 40S ribosomal protein S10

Chain SK0:



• Molecule 58: 40S ribosomal protein S11

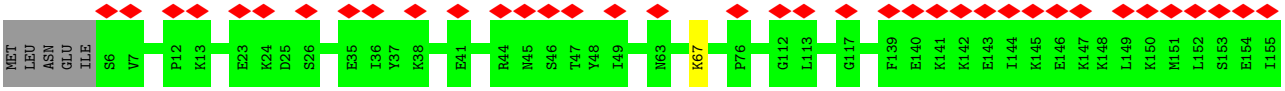
Chain RL0:



• Molecule 58: 40S ribosomal protein S11

Chain SL0:

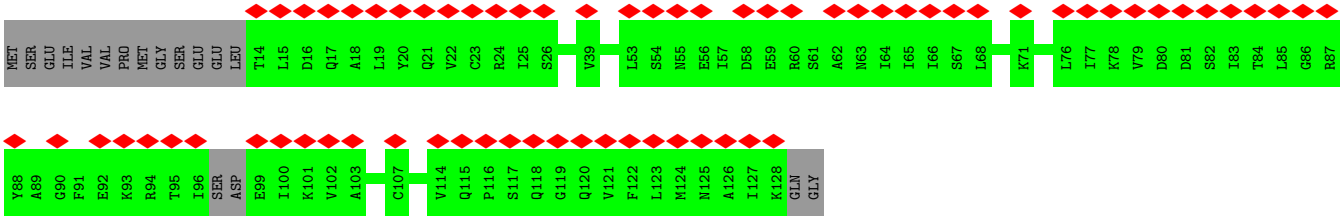




• Molecule 59: 40S ribosomal protein S12

Chain RM0:

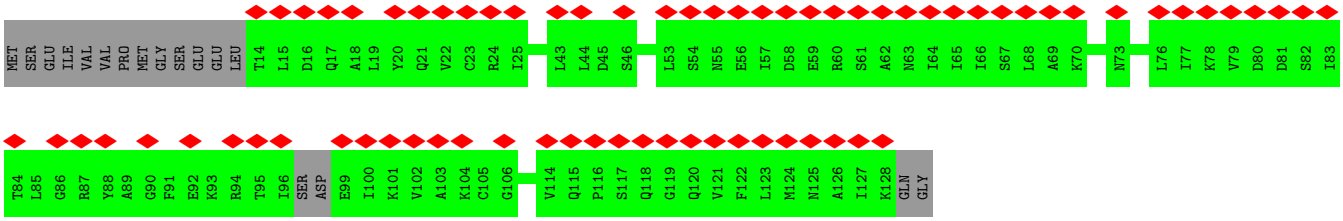




• Molecule 59: 40S ribosomal protein S12

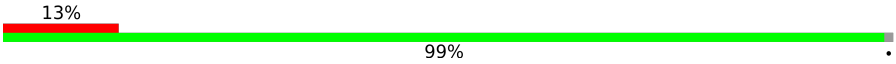
Chain SM0:

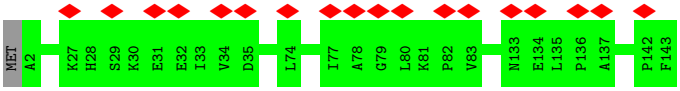




• Molecule 60: 40S ribosomal protein S13

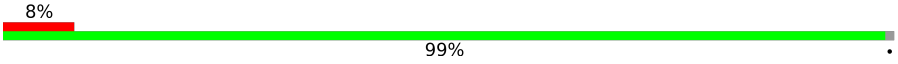
Chain RN0:

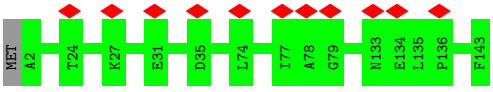




• Molecule 60: 40S ribosomal protein S13

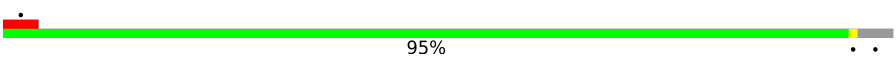
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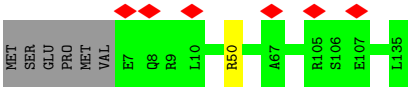




• Molecule 61: 40S ribosomal protein S14

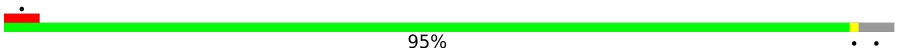
Chain RO0:

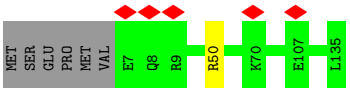




• Molecule 61: 40S ribosomal protein S14

Chain SO0:

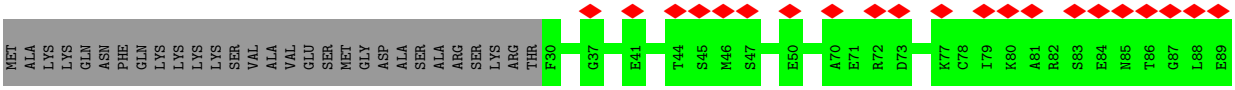


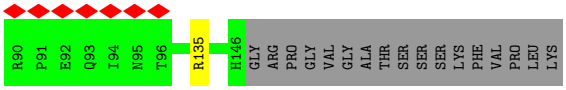


• Molecule 62: Ribosomal protein S19

Chain RP0:



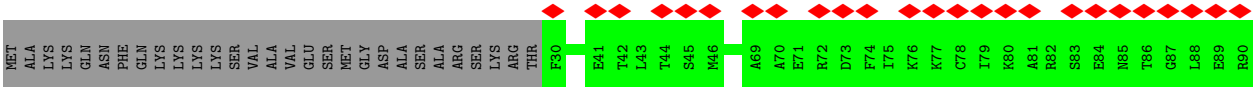


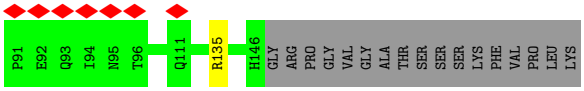


• Molecule 62: Ribosomal protein S19

Chain SP0:

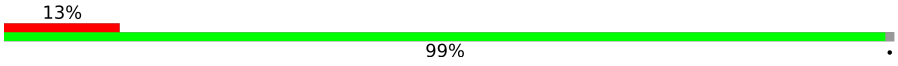


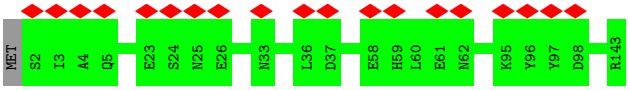




• Molecule 63: 40S ribosomal protein S16

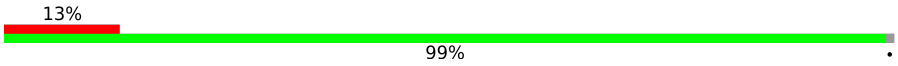
Chain RQ0:

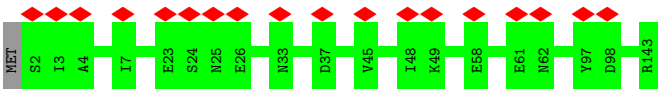




• Molecule 63: 40S ribosomal protein S16

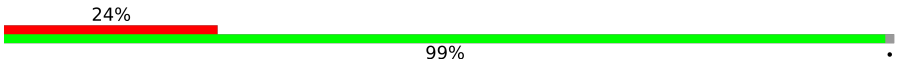
Chain SQ0:

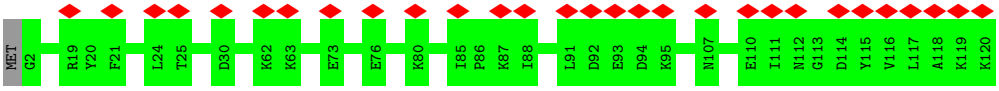




• Molecule 64: 40S ribosomal protein S17

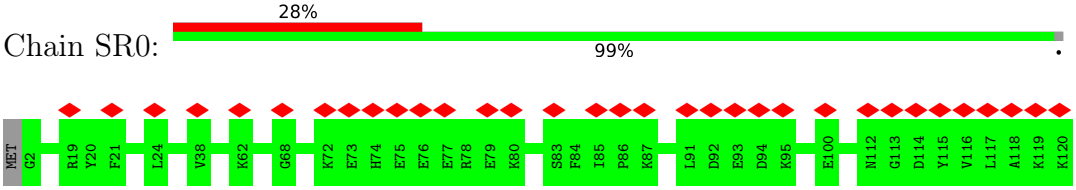
Chain RR0:





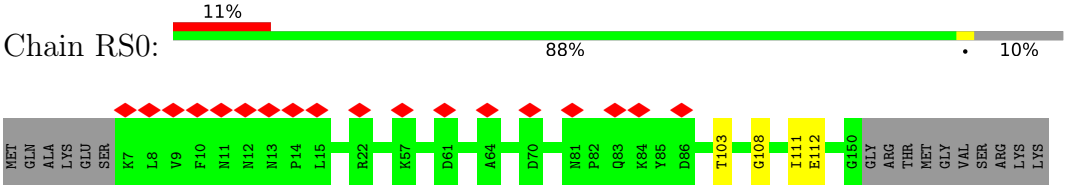
• Molecule 64: 40S ribosomal protein S17

Chain SR0:



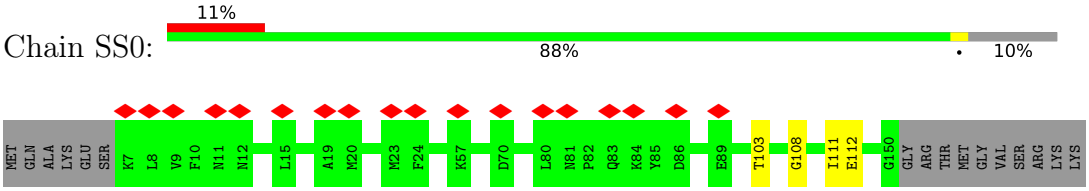
• Molecule 65: 40S ribosomal protein S18

Chain RS0:



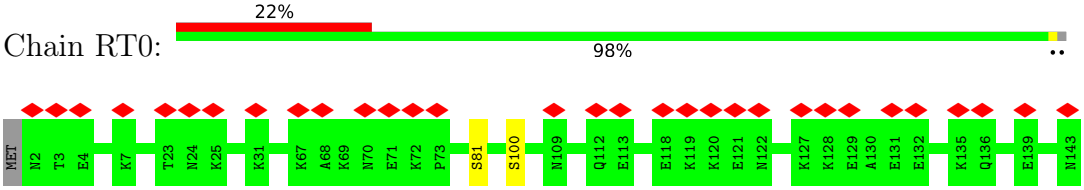
• Molecule 65: 40S ribosomal protein S18

Chain SS0:



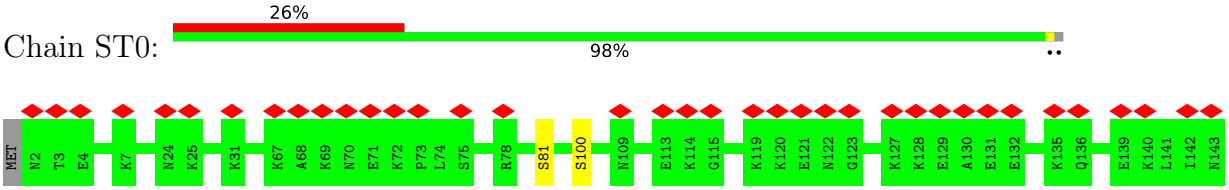
• Molecule 66: 40S Ribosomal protein S19

Chain RT0:



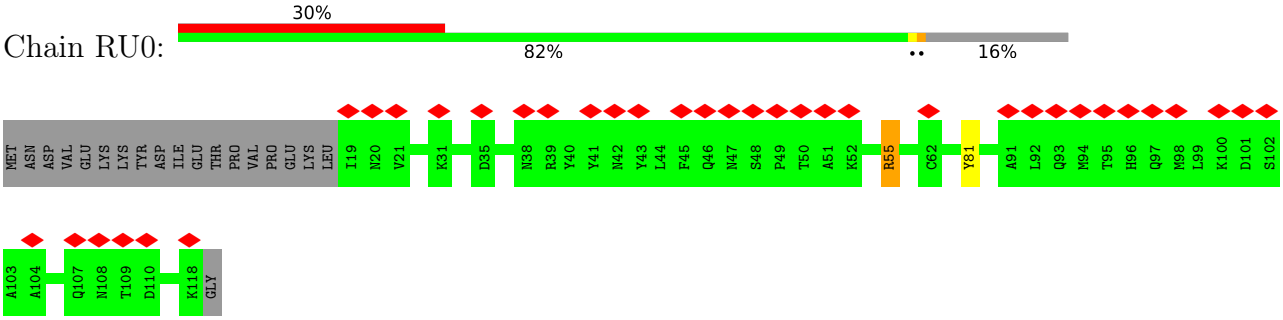
• Molecule 66: 40S Ribosomal protein S19

Chain ST0:



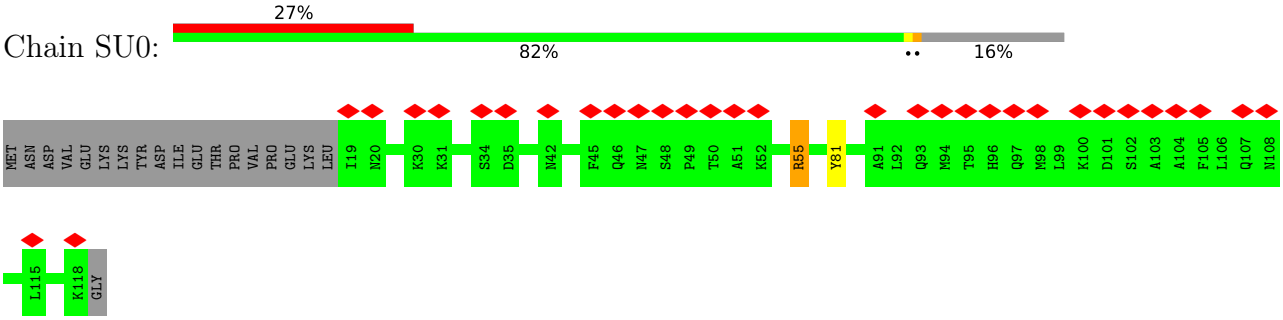
• Molecule 67: 40S ribosomal protein S20

Chain RU0:



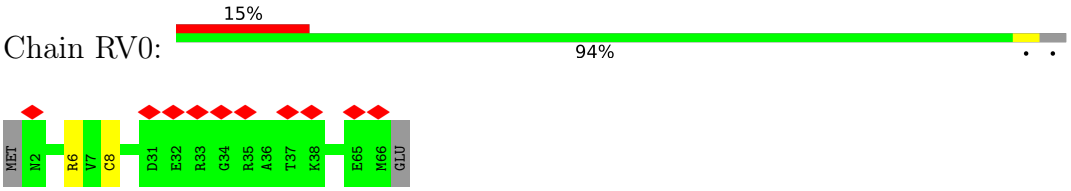
• Molecule 67: 40S ribosomal protein S20

Chain SU0:



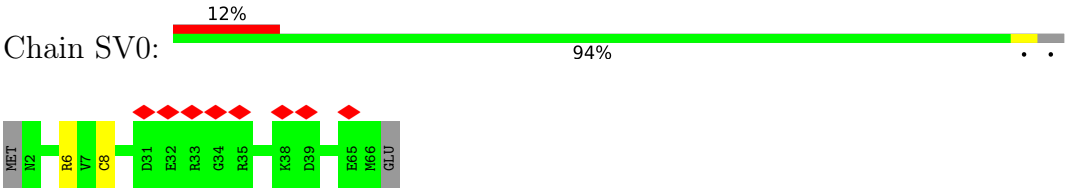
• Molecule 68: Ribosomal protein S21E

Chain RV0:



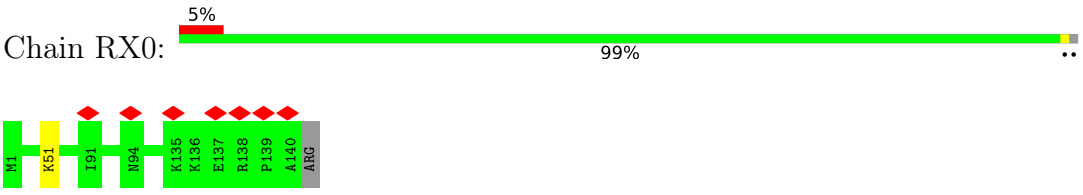
• Molecule 68: Ribosomal protein S21E

Chain SV0:



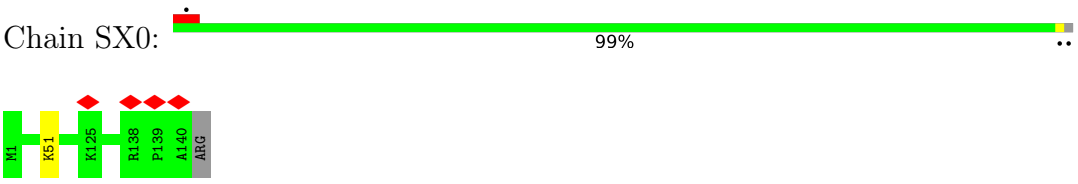
• Molecule 69: 40S ribosomal protein uS12

Chain RX0:



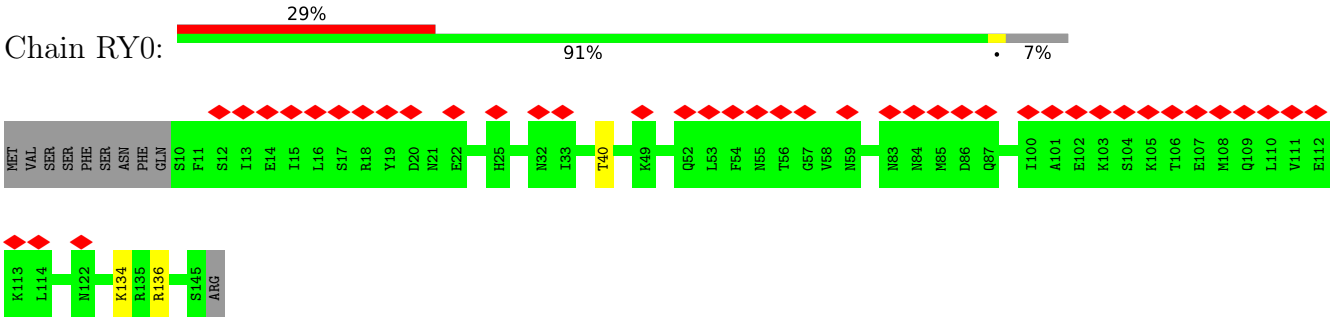
• Molecule 69: 40S ribosomal protein uS12

Chain SX0:



• Molecule 70: 40s ribosomal protein s24

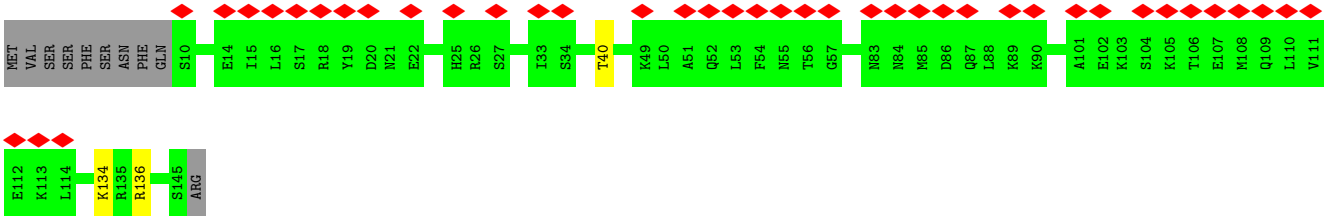
Chain RY0:



• Molecule 70: 40s ribosomal protein s24

Chain SY0:

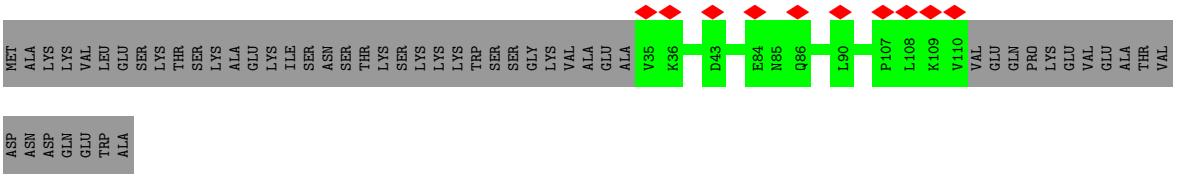




• Molecule 71: 40S ribosomal protein S25

Chain RZ0:

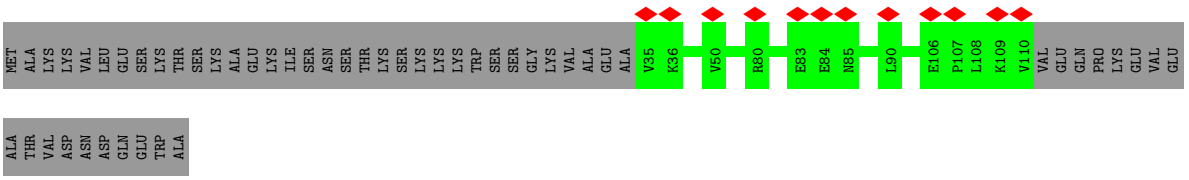




• Molecule 71: 40S ribosomal protein S25

Chain SZ0:

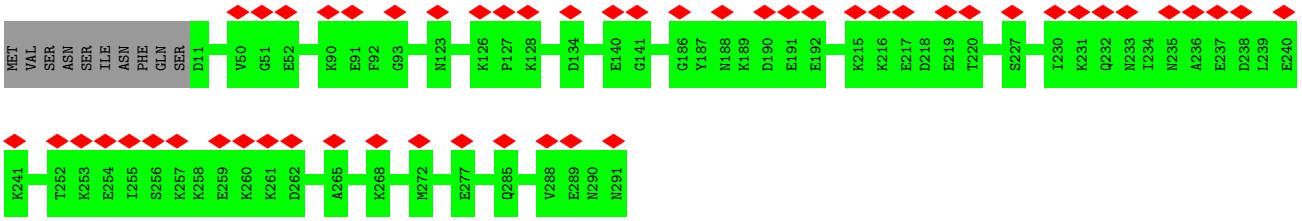




• Molecule 72: 60S ribosomal protein L5

Chain KD0:

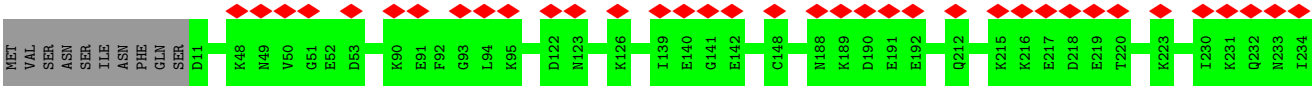


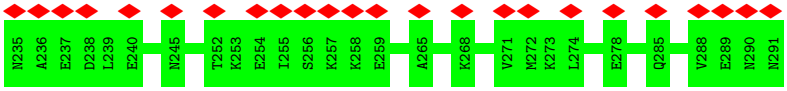


• Molecule 72: 60S ribosomal protein L5

Chain LD0:

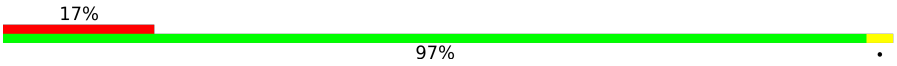


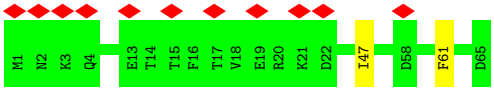




• Molecule 73: 40S ribosomal protein S29

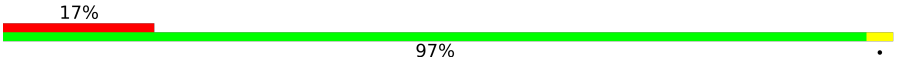
Chain RDD:

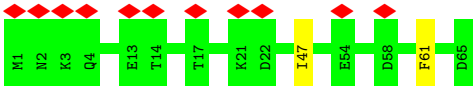




• Molecule 73: 40S ribosomal protein S29

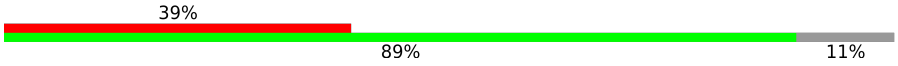
Chain SDD:

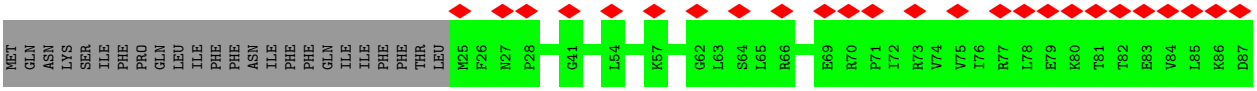


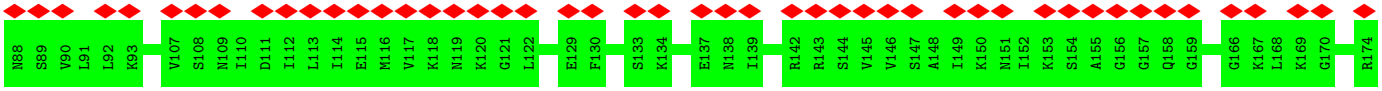


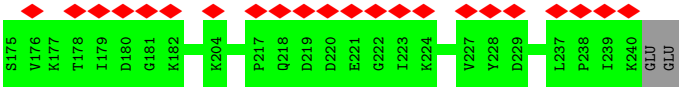
• Molecule 74: 40S ribosomal protein S3

Chain RD0:





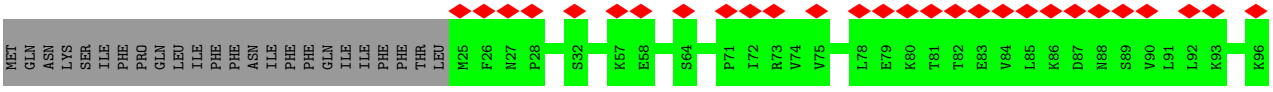


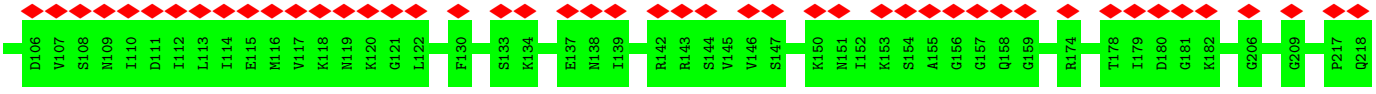


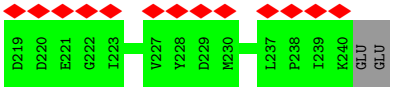
• Molecule 74: 40S ribosomal protein S3

Chain SD0:



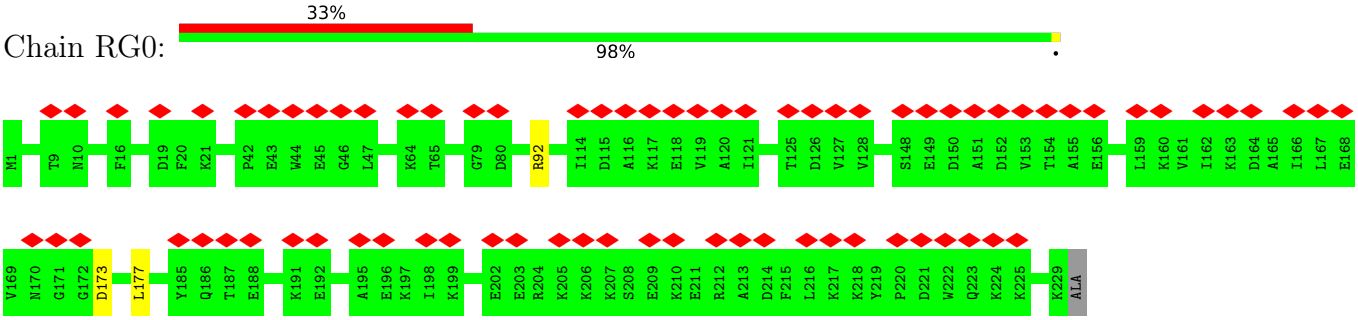






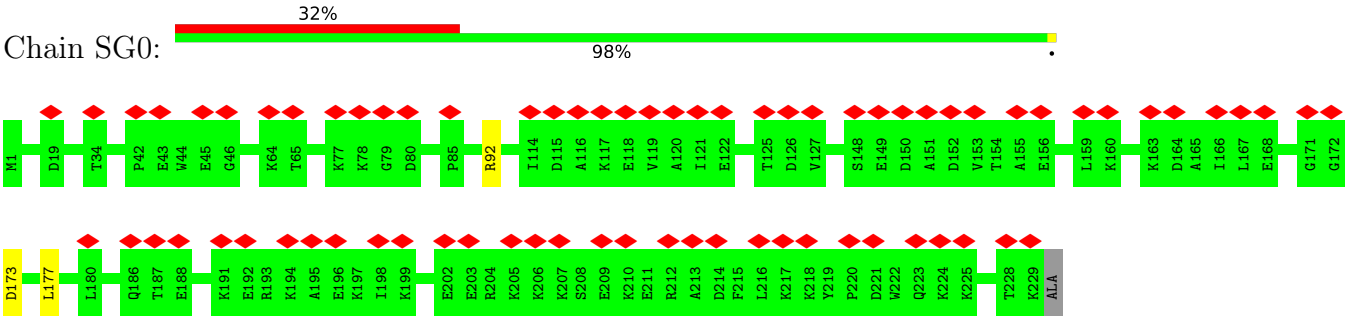
• Molecule 75: 40S ribosomal protein S6

Chain RG0:



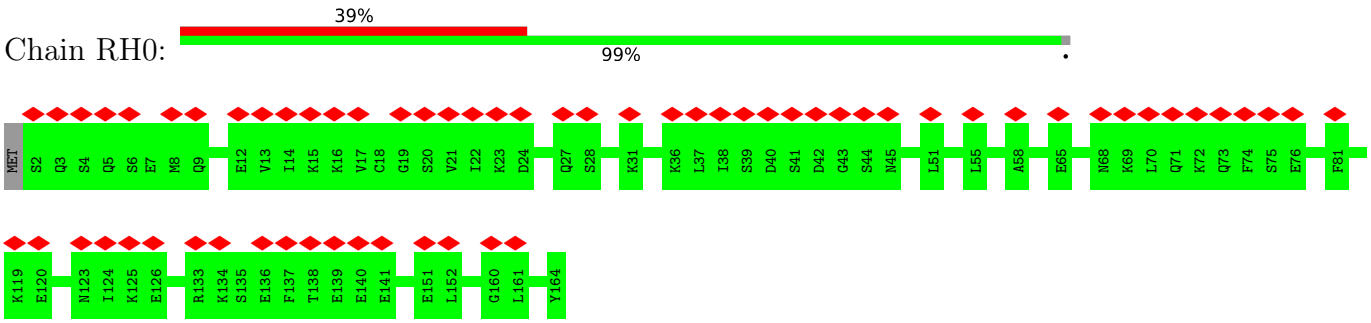
• Molecule 75: 40S ribosomal protein S6

Chain SG0:



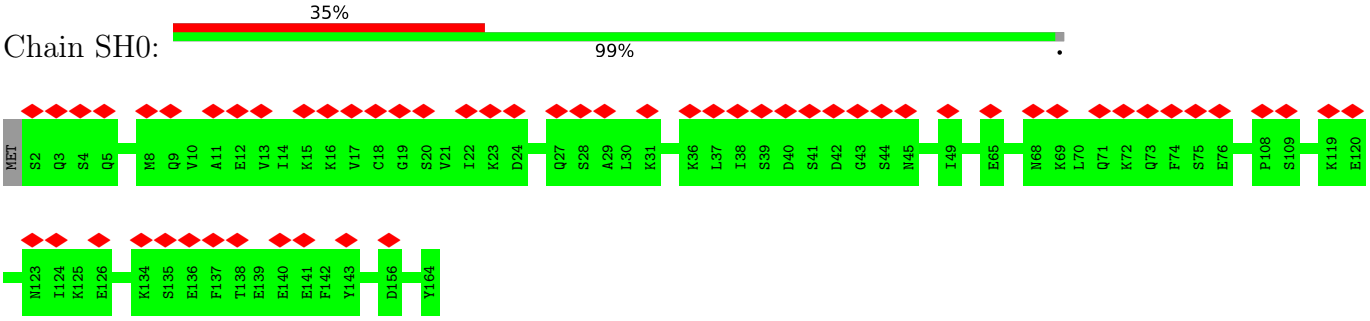
• Molecule 76: 40S ribosomal protein S7

Chain RH0:



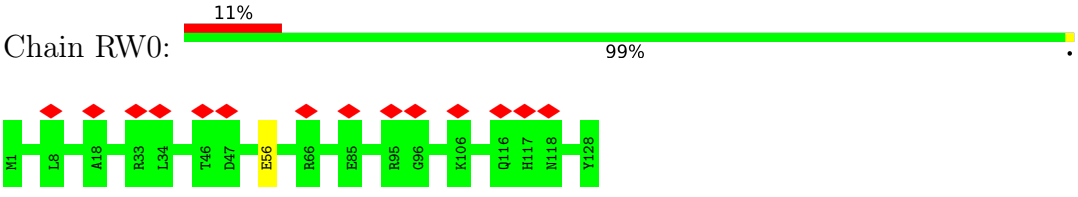
• Molecule 76: 40S ribosomal protein S7

Chain SH0:



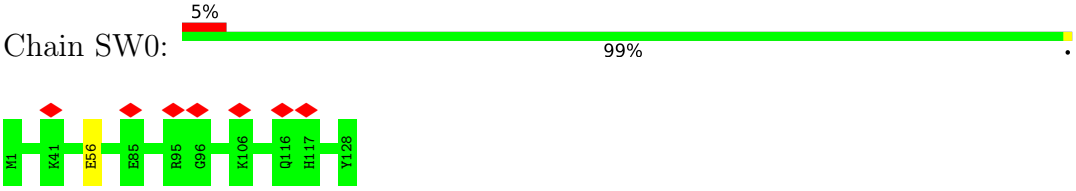
• Molecule 77: 40S ribosomal protein S15A

Chain RW0:



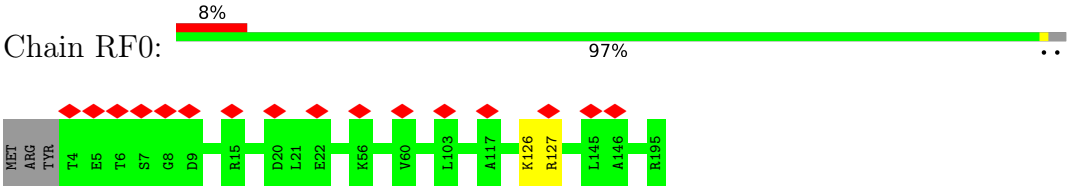
• Molecule 77: 40S ribosomal protein S15A

Chain SW0:



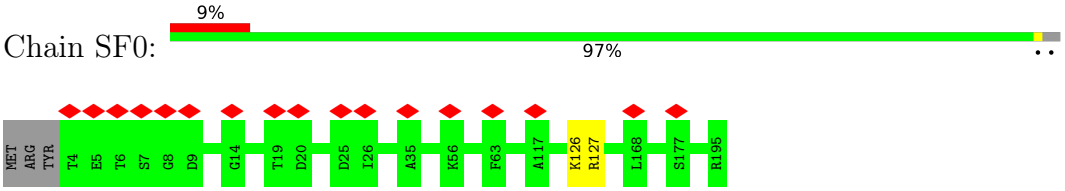
• Molecule 78: 40S ribosomal protein S5

Chain RF0:



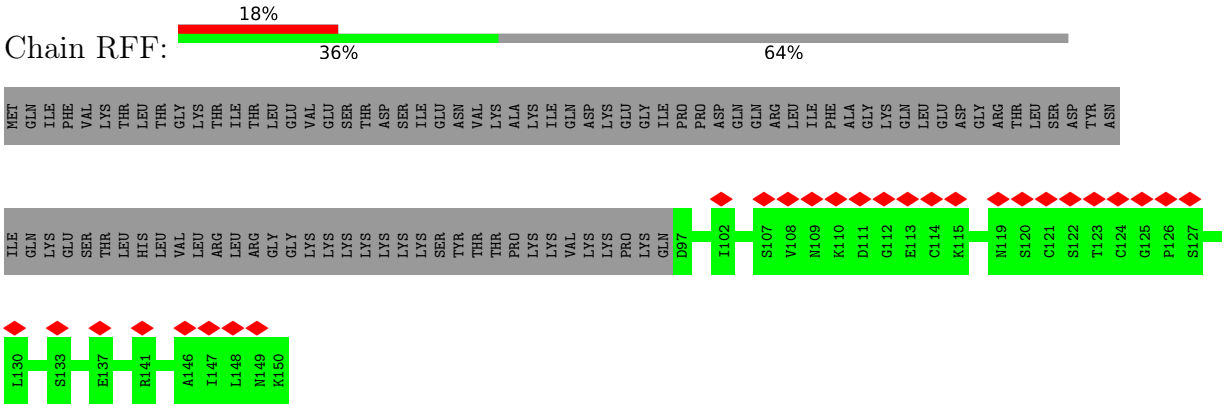
• Molecule 78: 40S ribosomal protein S5

Chain SF0:



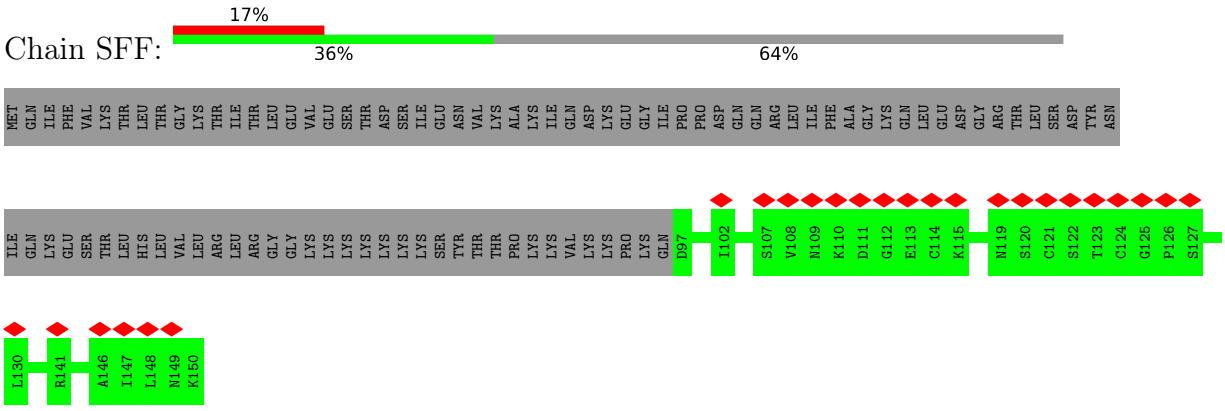
• Molecule 79: Ubiquitin/40s ribosomal protein S27a fusion

Chain RFF:



• Molecule 79: Ubiquitin/40s ribosomal protein S27a fusion

Chain SFF:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	3109	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 ($e^-/Å^2$)	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	2.637	Depositor
Minimum map value	-1.019	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.197	Depositor
Recommended contour level	0.25	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 (i)

5.1 Standard geometry (i)

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

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	KL0	1	MET	CG-SD	-7.84	1.61	1.80
33	LL0	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	K50	311	C	C3'-O3'	6.12	1.50	1.42

The worst 5 of 520 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	R60	355	C	N1-C2-O2	11.55	125.83	118.90
2	S60	355	C	N1-C2-O2	11.55	125.83	118.90
1	K50	366	G	O4'-C1'-N9	11.54	116.58	108.50
1	L50	366	G	O4'-C1'-N9	11.54	116.58	108.50
1	K50	202	G	O4'-C1'-N9	11.34	116.44	108.50

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
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

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	162/164 (99%)	145 (90%)	17 (10%)	0	100	100
3	E	162/164 (99%)	145 (90%)	17 (10%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	767 (91%)	77 (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%)	254 (95%)	13 (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%)	81 (93%)	6 (7%)	0	100	100
16	LJJ	87/92 (95%)	80 (92%)	7 (8%)	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%)	365 (96%)	16 (4%)	0	100	100
19	LB0	381/392 (97%)	365 (96%)	16 (4%)	0	100	100
20	KC0	325/328 (99%)	307 (94%)	18 (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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	98 (90%)	11 (10%)	0	100	100
26	LFF	109/111 (98%)	97 (89%)	12 (11%)	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%)	168 (93%)	13 (7%)	0	100	100
28	LH0	181/187 (97%)	168 (93%)	13 (7%)	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
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%)	96 (85%)	17 (15%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	KP0	152/167 (91%)	143 (94%)	9 (6%)	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%)	168 (93%)	12 (7%)	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%)	157 (94%)	11 (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%)	141 (92%)	13 (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
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%)	233 (90%)	25 (10%)	0	100	100
53	REE	54/60 (90%)	51 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	143 (97%)	5 (3%)	0	100	100
58	SL0	148/155 (96%)	144 (97%)	4 (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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	118 (88%)	16 (12%)	0	100	100
70	SY0	134/146 (92%)	119 (89%)	15 (11%)	0	100	100
71	RZ0	74/128 (58%)	66 (89%)	8 (11%)	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%)	50 (79%)	13 (21%)	0	100	100
73	SDD	63/65 (97%)	50 (79%)	13 (21%)	0	100	100
74	RD0	214/242 (88%)	208 (97%)	6 (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
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%)	22465 (93%)	1729 (7%)	20 (0%)	49	83

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	KL0	44	TYR
75	RG0	173	ASP
33	LL0	44	TYR
75	SG0	173	ASP
11	KMM	108	ALA

5.3.2 Protein sidechains (i)

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

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	LO0	169	LYS
70	SY0	136	ARG
41	LS0	157	ARG
51	SCC	62	ARG
43	KU0	68	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

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

5.3.3 RNA (i)

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%)	54 (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%)	224 (2%)

5 of 2690 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	K50	2	U
1	K50	3	A
1	K50	14	G

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Mol	Chain	Res	Type
1	K50	15	G
1	K50	16	G

5 of 224 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L50	75	C
2	S60	1314	C
1	L50	1394	U
2	S60	1311	A
2	S60	873	C

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

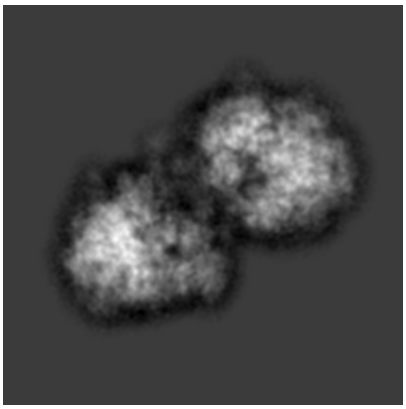
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55401. These allow visual inspection of the internal detail of the map and identification of artifacts.

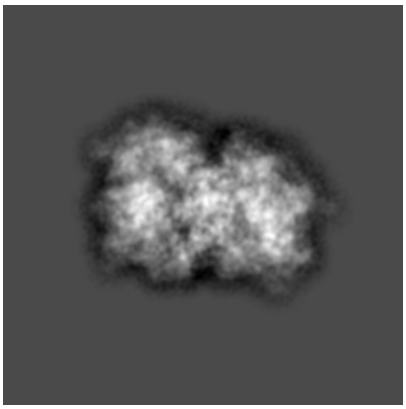
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

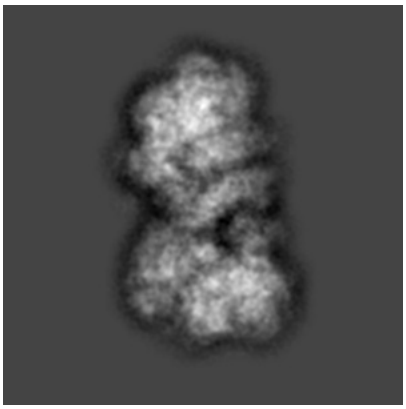
6.1.1 Primary map



X

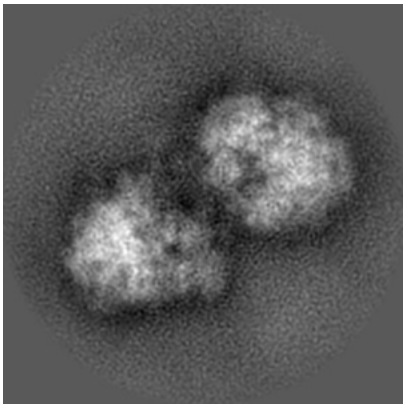


Y

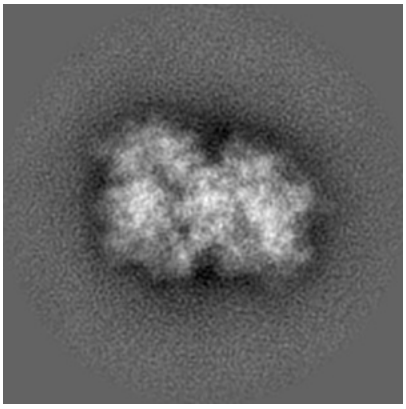


Z

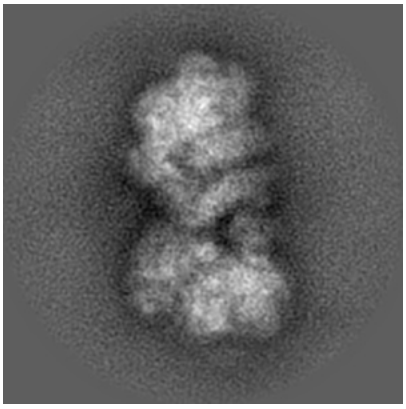
6.1.2 Raw map



X



Y

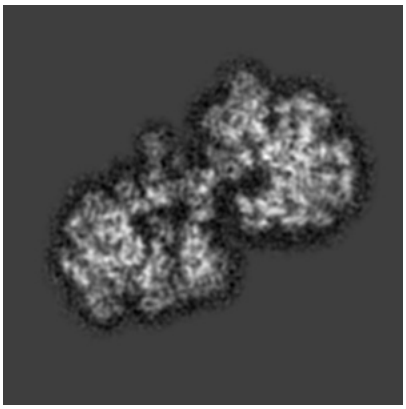


Z

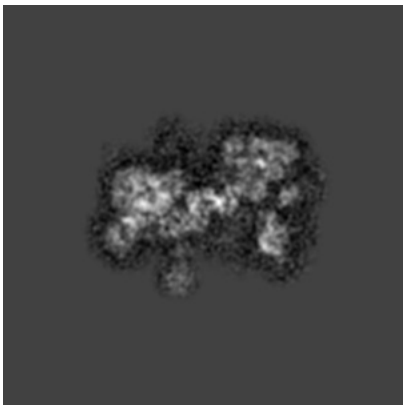
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

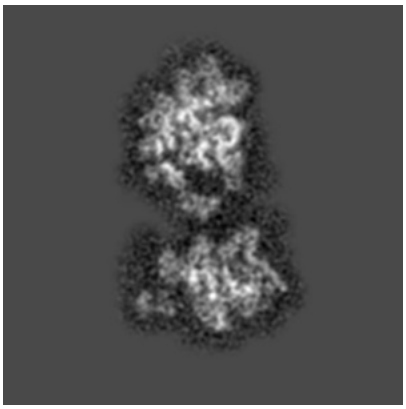
6.2.1 Primary map



X Index: 84

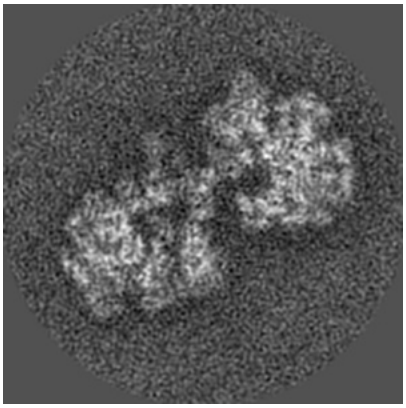


Y Index: 84

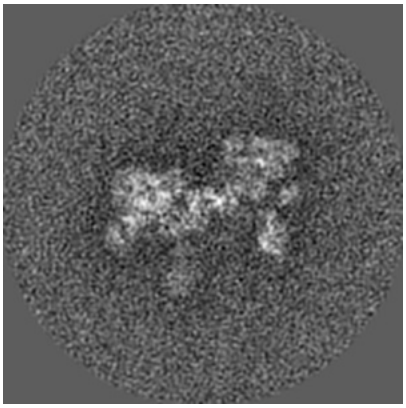


Z Index: 84

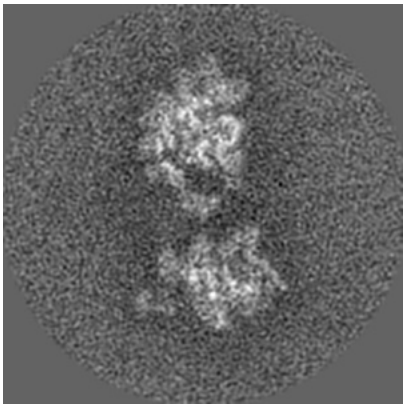
6.2.2 Raw map



X Index: 84



Y Index: 84

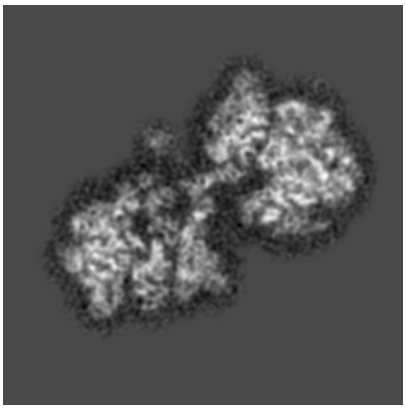


Z Index: 84

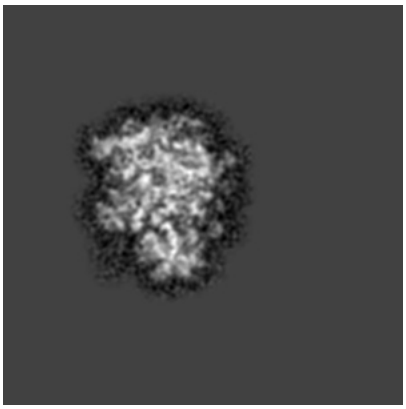
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

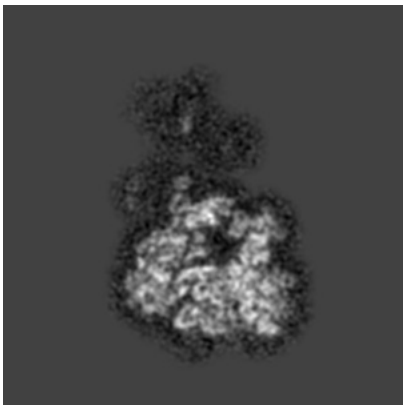
6.3.1 Primary map



X Index: 81

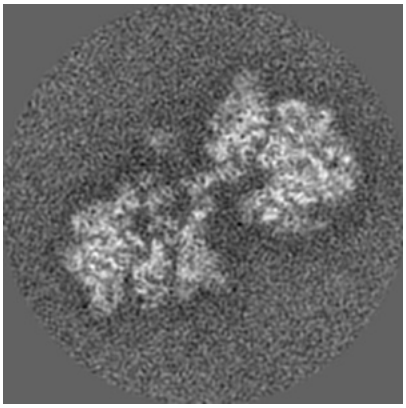


Y Index: 47

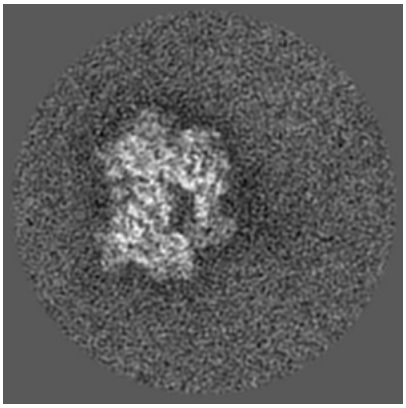


Z Index: 68

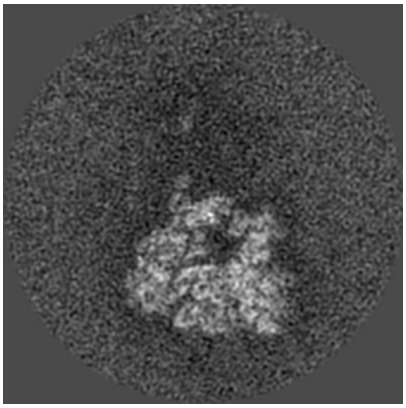
6.3.2 Raw map



X Index: 81



Y Index: 55

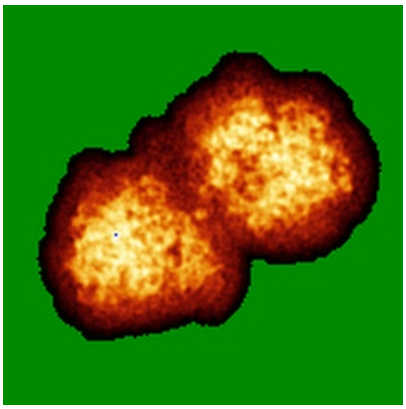


Z Index: 68

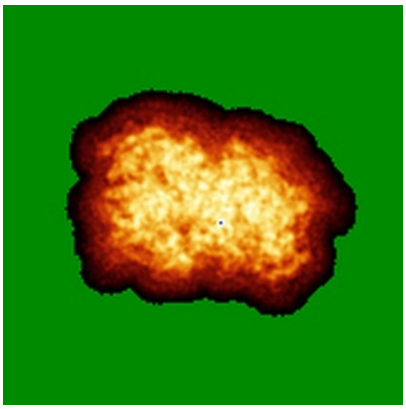
The images above show the largest variance slices of the map in three orthogonal directions.

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

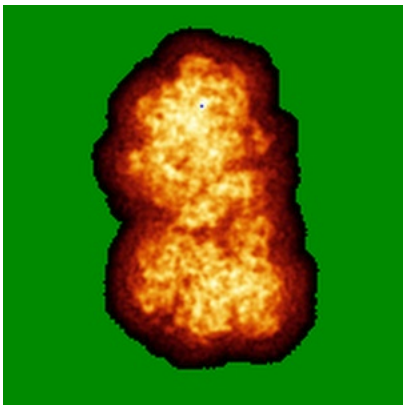
6.4.1 Primary map



X

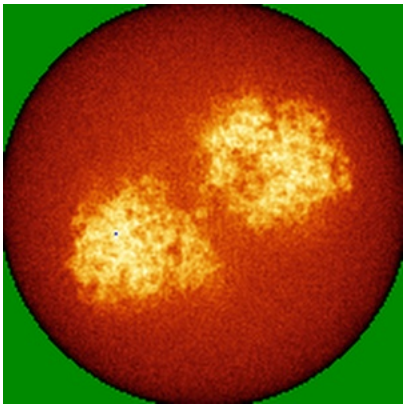


Y

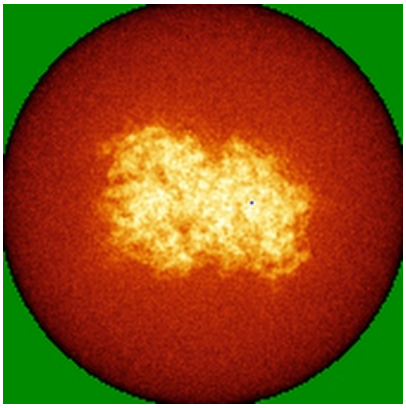


Z

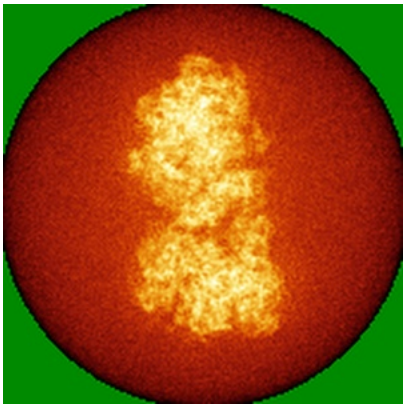
6.4.2 Raw map



X



Y

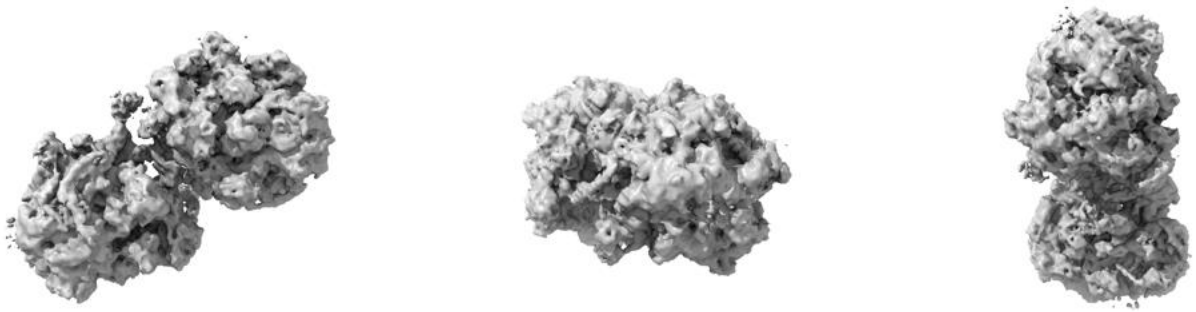


Z

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)

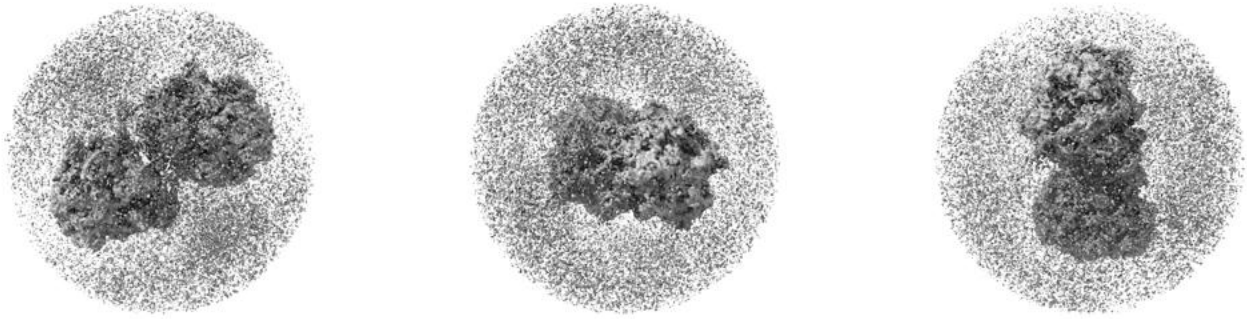
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. 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



X Y Z

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.

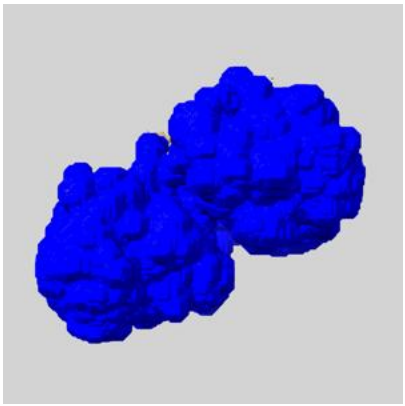
6.6 Mask visualisation (i)

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

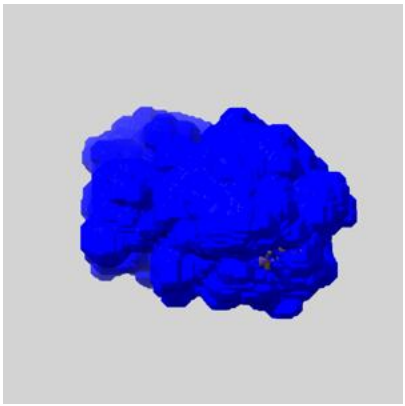
A mask typically either:

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

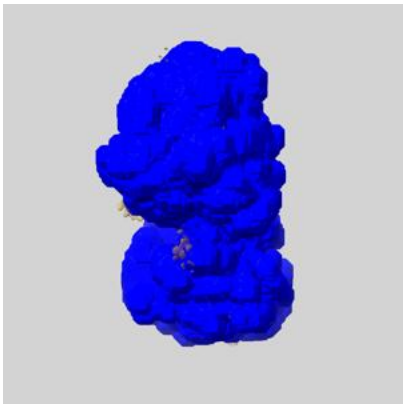
6.6.1 emd_55401_msk_1.map (i)



X



Y

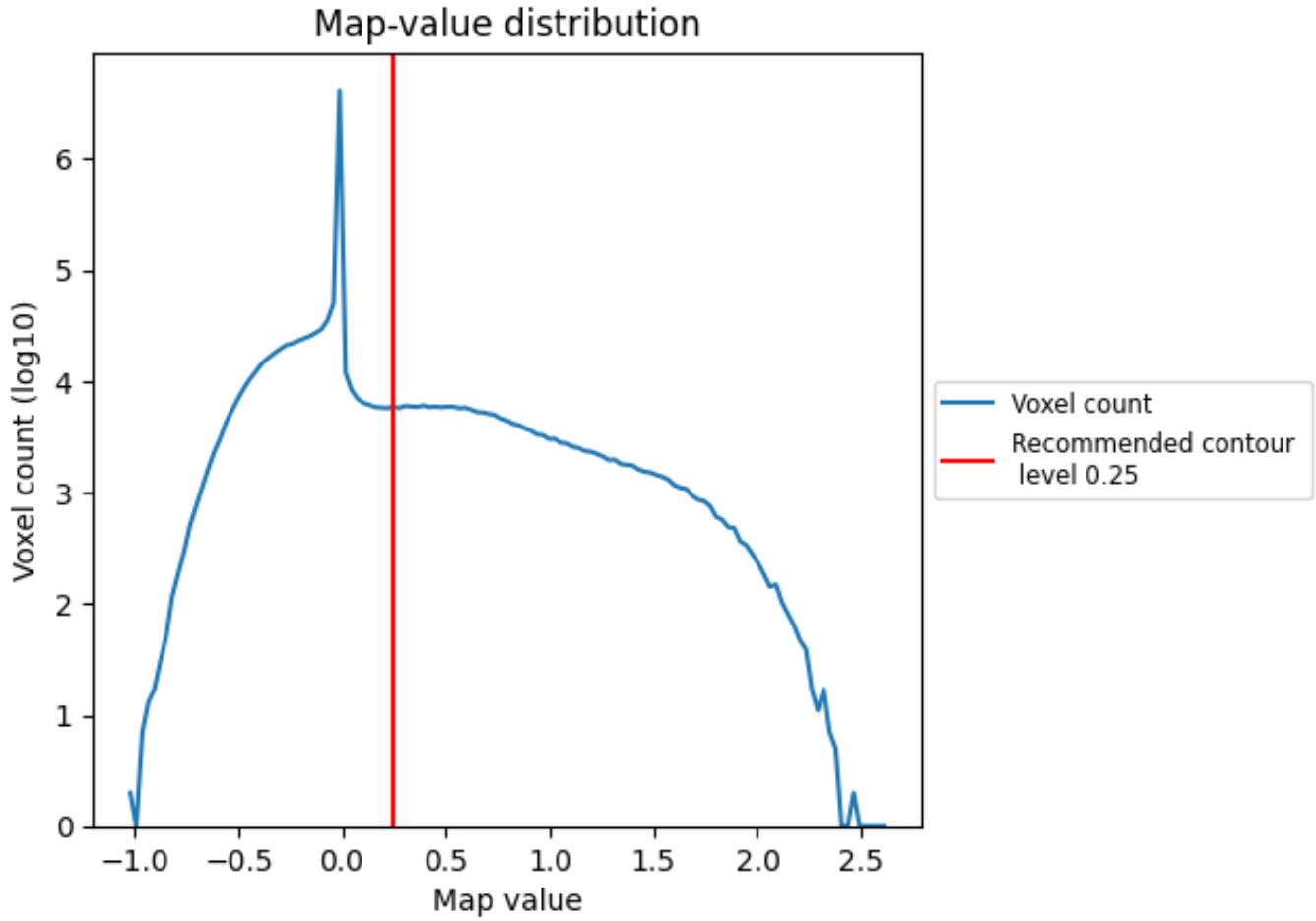


Z

7 Map analysis

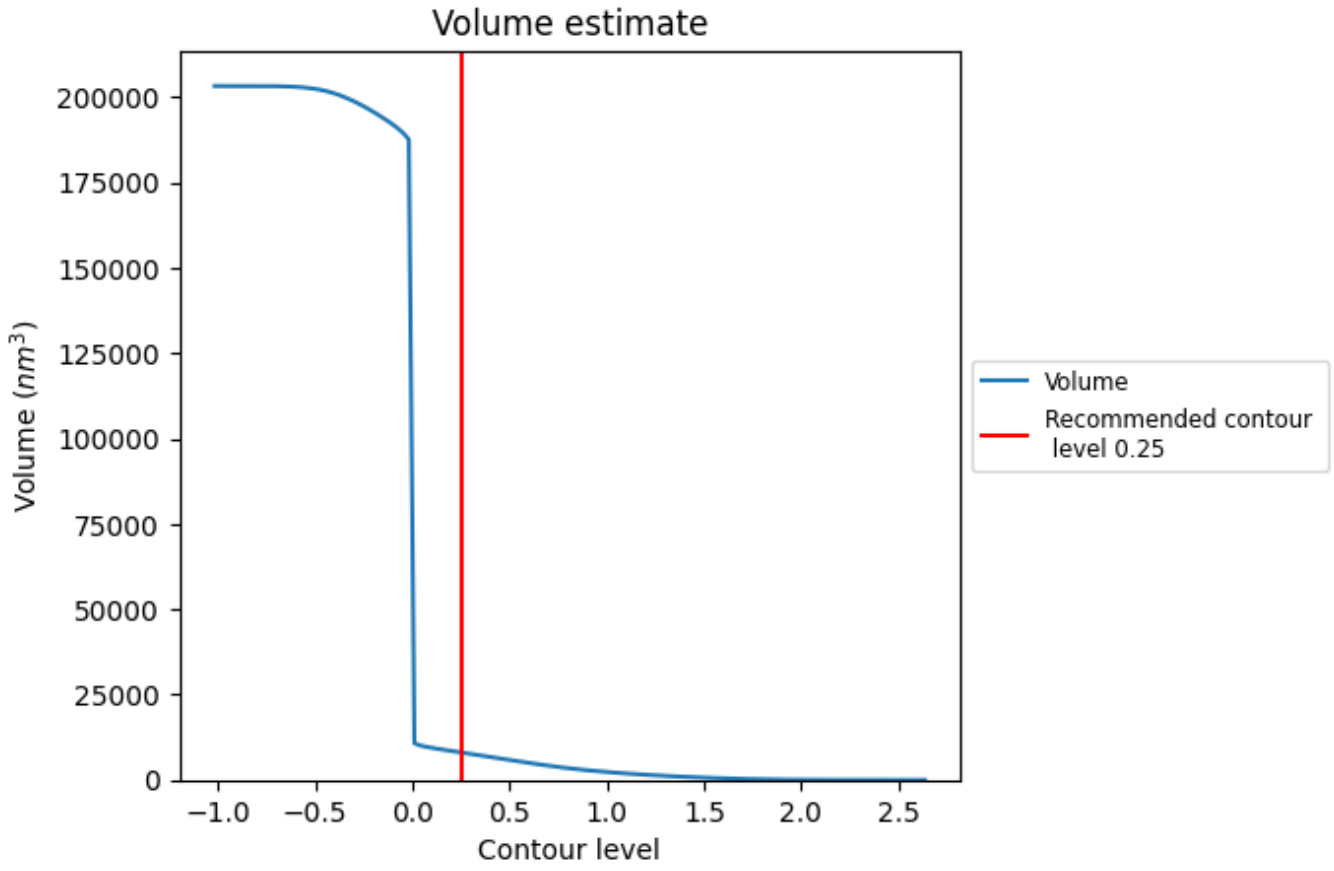
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

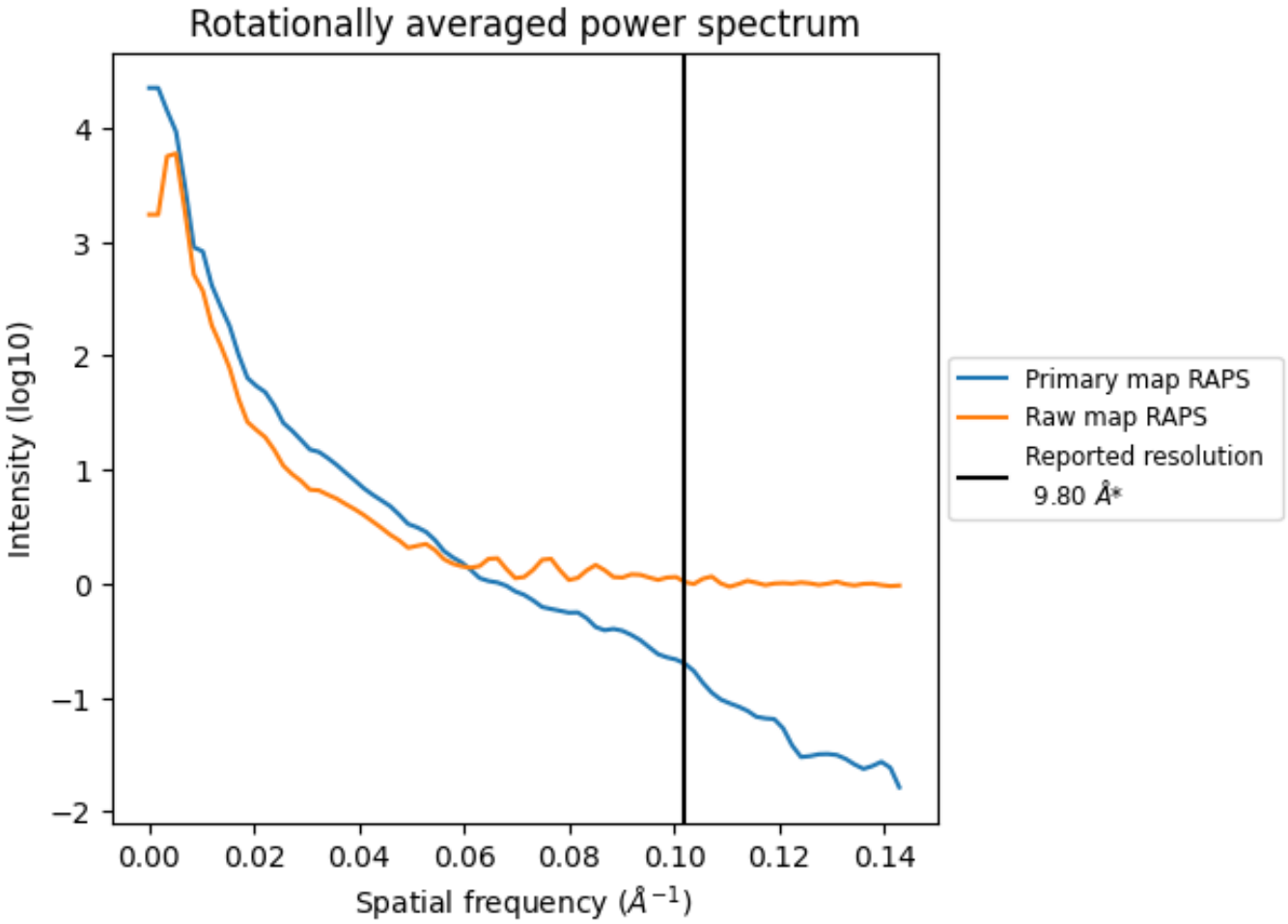
7.2 Volume estimate (i)



The volume at the recommended contour level is 8050 nm^3; this corresponds to an approximate mass of 7272 kDa.

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

7.3 Rotationally averaged power spectrum (i)

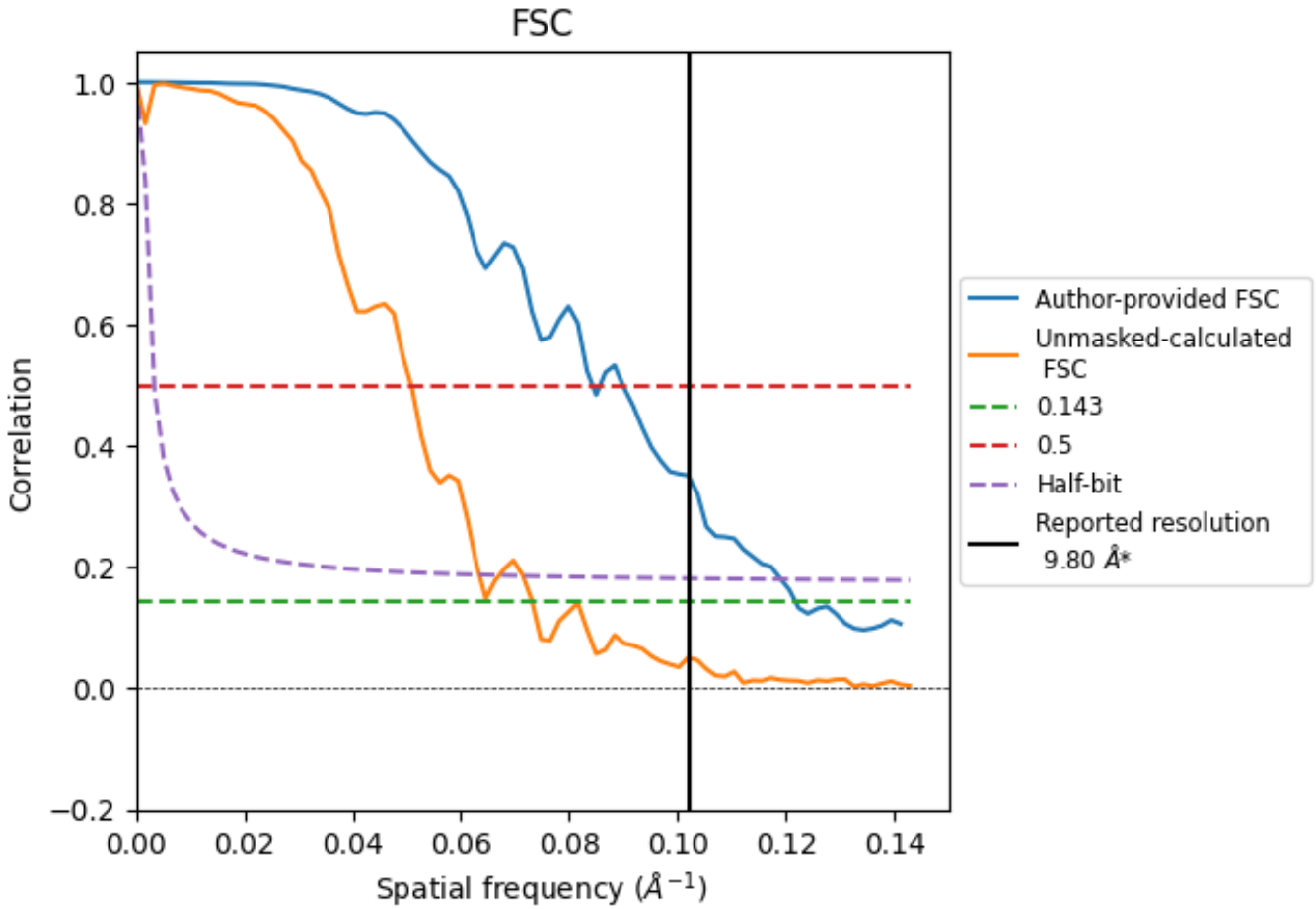


*Reported resolution corresponds to spatial frequency of 0.102 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.102 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.80	-	-
Author-provided FSC curve	8.20	11.85	8.39
Unmasked-calculated*	13.66	19.69	15.77

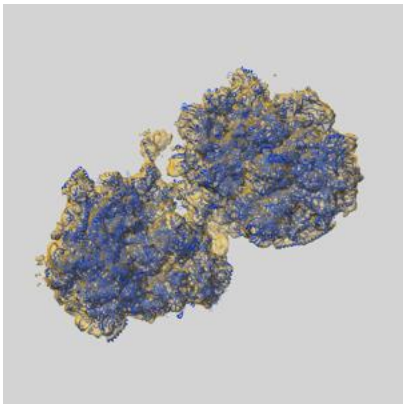
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.20 differs from the reported value 9.8 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.66 differs from the reported value 9.8 by more than 10 %

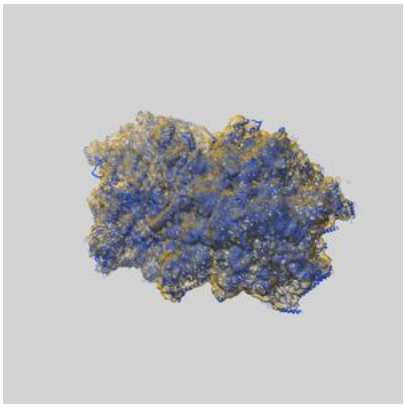
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55401 and PDB model 9T0I. Per-residue inclusion information can be found in section 3 on page 26.

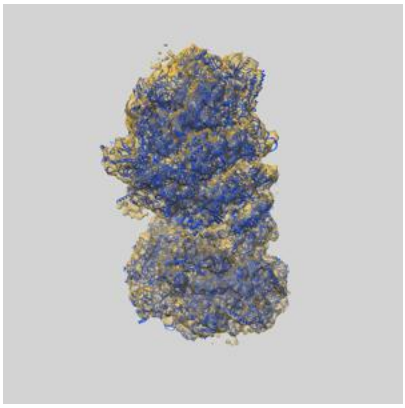
9.1 Map-model overlay



X



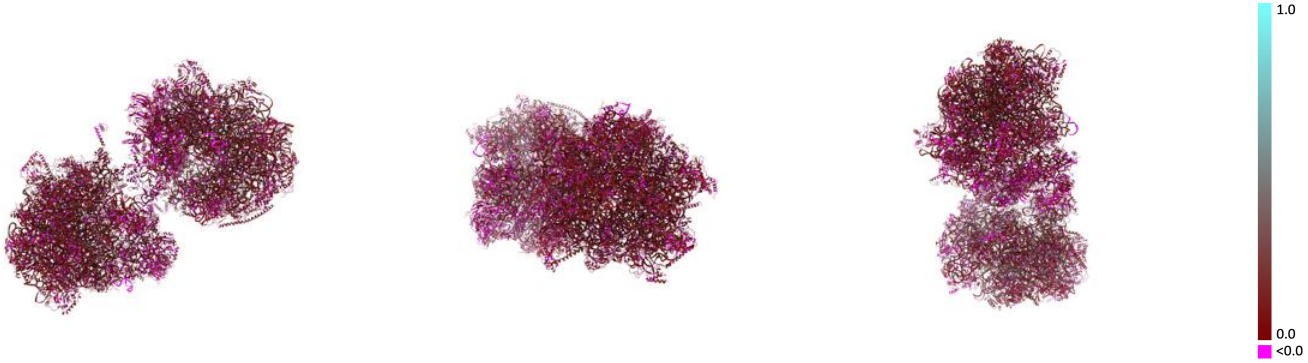
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

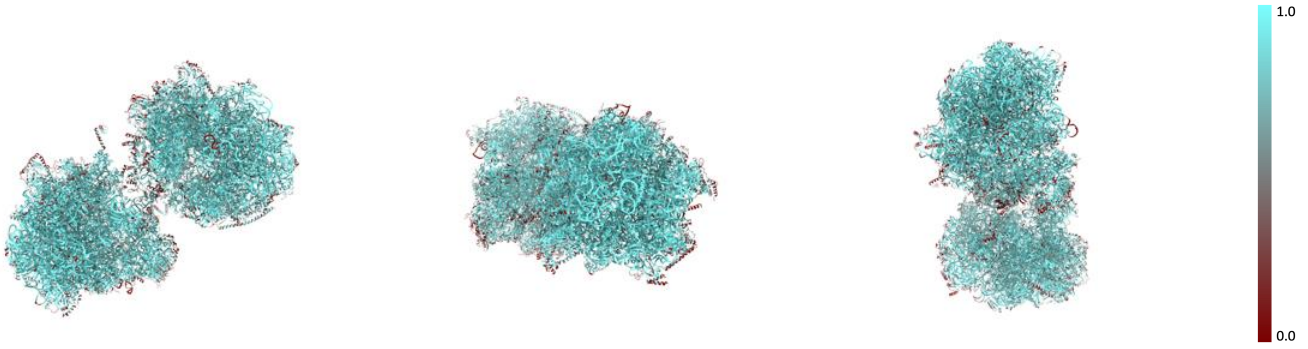
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

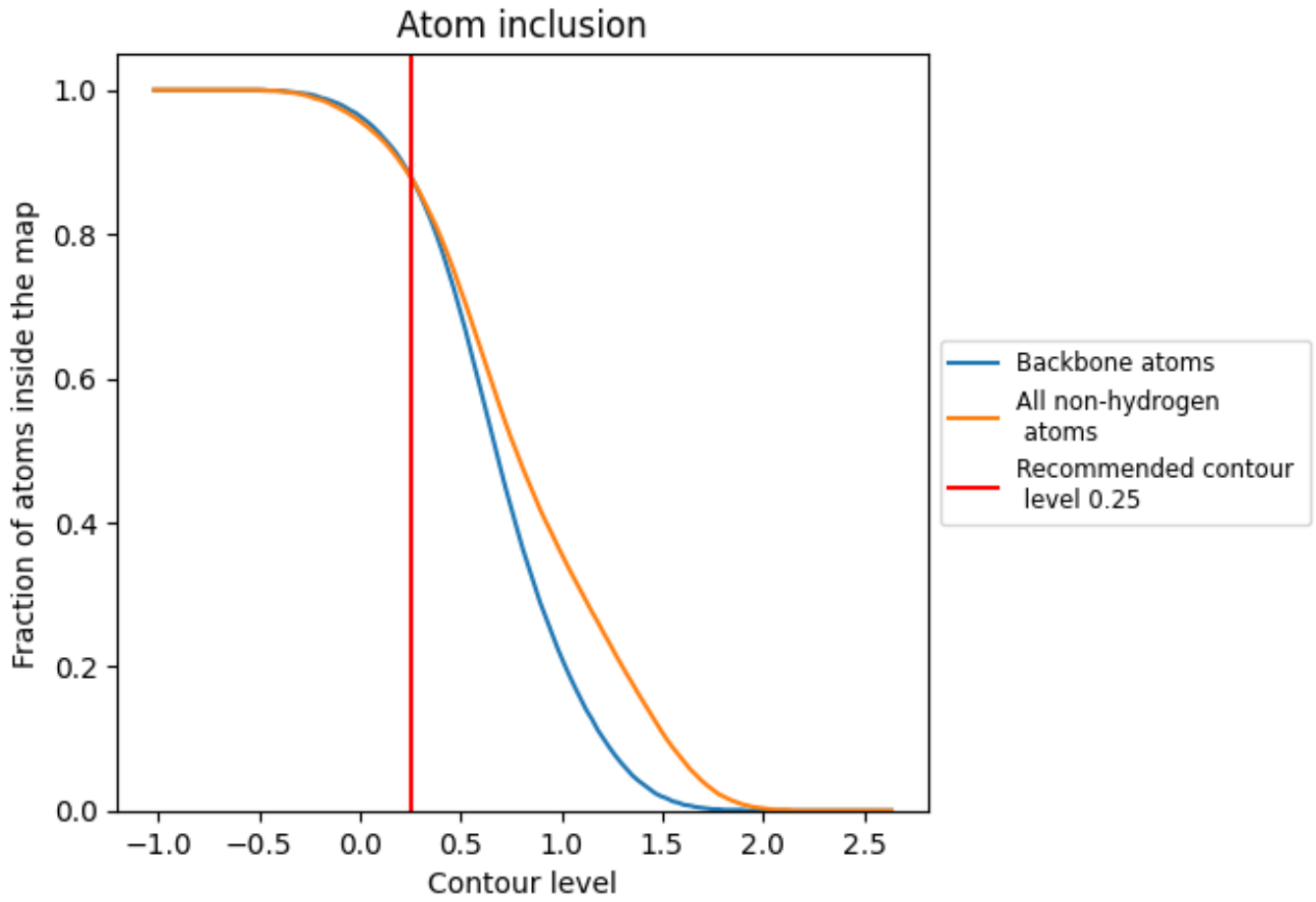
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8800	0.1010
A	0.8330	0.1060
B	0.7730	0.1040
D	0.7540	0.1350
E	0.7450	0.1180
K	0.7740	0.0850
K50	0.9840	0.1380
K70	0.9720	0.1290
KAA	0.9010	0.0550
KB0	0.8260	0.0710
KC0	0.8140	0.0570
KCC	0.7890	0.1120
KD0	0.7750	0.0540
KDD	0.8740	0.0920
KE0	0.5890	0.0720
KEE	0.8380	0.0570
KF0	0.7980	0.1010
KFF	0.8880	0.0860
KG0	0.7330	0.0890
KGG	0.9260	0.0580
KH0	0.8050	0.0960
KHH	0.8330	0.1240
KI0	0.8380	0.0910
KII	0.7490	0.0860
KJ0	0.8610	0.0660
KJJ	0.9750	0.0720
KL0	0.8260	0.0640
KLL	0.9850	0.0700
KM0	0.7140	0.1270
KMM	0.7730	0.0710
KN0	0.9820	0.0500
KO0	0.7890	0.1110
KOO	0.8380	0.0630
KP0	0.8990	0.1000
KPP	0.8970	0.0950



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Chain	Atom inclusion	Q-score
KQ0	0.8170	0.0910
KR0	0.8230	0.1050
KS0	0.7590	0.0980
KT0	0.7690	0.0690
KU0	0.7770	0.1030
KV0	0.8520	0.0830
KW0	0.6530	0.0660
KX0	0.8560	0.0750
KY0	0.8570	0.0750
KZ0	0.6950	0.0830
L	0.8250	0.0790
L50	0.9870	0.1400
L70	0.9820	0.1150
LA0	0.8730	0.0730
LA02	0.9070	0.0850
LAA	0.8940	0.0550
LB0	0.8800	0.0730
LC0	0.8270	0.0660
LCC	0.8330	0.1230
LD0	0.7350	0.0540
LDD	0.8720	0.0900
LE0	0.6550	0.0800
LEE	0.8690	0.0660
LF0	0.8210	0.1020
LFF	0.8820	0.0960
LG0	0.7740	0.1060
LGG	0.9420	0.0540
LH0	0.8280	0.1080
LHH	0.8640	0.1130
LI0	0.8800	0.0930
LII	0.7730	0.1130
LJ0	0.8510	0.0550
LJJ	0.9620	0.0890
LL0	0.8700	0.0800
LLL	1.0000	0.0900
LM0	0.7460	0.1190
LMM	0.8390	0.0770
LN0	0.9970	0.0520
LO0	0.8380	0.1200
LOO	0.8780	0.0760
LP0	0.9190	0.0920
LPP	0.9220	0.1110

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Chain	Atom inclusion	Q-score
LQ0	0.8290	0.0890
LR0	0.8600	0.1040
LS0	0.8010	0.0940
LT0	0.7890	0.0700
LU0	0.7840	0.0920
LV0	0.9200	0.0720
LW0	0.6720	0.0810
LX0	0.8960	0.0730
LY0	0.8730	0.0860
LZ0	0.7390	0.0910
M	0.7390	0.0950
MD1	0.8650	0.1070
N	0.7360	0.1110
ND1	0.7870	0.1090
R60	0.9740	0.1080
RA0	0.7270	0.0400
RAA	0.8320	0.0800
RB0	0.7850	0.1130
RBB	0.7100	0.0660
RC0	0.7930	0.0710
RCC	0.7090	0.0740
RD0	0.5250	0.0250
RDD	0.7820	0.0720
RE0	0.7000	0.0430
REE	0.7320	0.0540
RF0	0.8580	0.0460
RFF	0.5070	-0.0030
RG0	0.6240	0.0500
RGG	0.6400	0.0260
RH0	0.5990	0.0660
RI0	0.8430	0.0430
RJ0	0.7690	0.0480
RK0	0.6180	0.0200
RL0	0.6860	0.0600
RM0	0.3540	0.0260
RN0	0.8400	0.0650
RO0	0.8810	0.0780
RP0	0.7210	0.0530
RQ0	0.8040	0.0520
RR0	0.6730	0.0390
RS0	0.8390	0.0560
RT0	0.7340	0.0700

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Chain	Atom inclusion	Q-score
RU0	0.6260	0.0510
RV0	0.7890	0.0840
RW0	0.8510	0.0600
RX0	0.9110	0.0810
RY0	0.6390	0.0380
RZ0	0.8070	0.0730
S60	0.9770	0.1120
SA0	0.7680	0.0480
SAA	0.8710	0.0790
SB0	0.8360	0.1250
SBB	0.6870	0.0760
SC0	0.8110	0.0790
SCC	0.7370	0.0930
SD0	0.5490	0.0300
SDD	0.8060	0.0890
SE0	0.6990	0.0470
SEE	0.7610	0.0630
SF0	0.8670	0.0510
SFF	0.5420	0.0240
SG0	0.6510	0.0580
SGG	0.6330	0.0410
SH0	0.6220	0.0700
SI0	0.8800	0.0540
SJ0	0.7730	0.0570
SK0	0.6810	0.0550
SL0	0.7230	0.0820
SM0	0.3150	0.0060
SN0	0.8680	0.0840
SO0	0.9100	0.0560
SP0	0.6930	0.0460
SQ0	0.8120	0.0510
SR0	0.6700	0.0630
SS0	0.8360	0.0480
ST0	0.7070	0.0380
SU0	0.6430	0.0310
SV0	0.8230	0.1130
SW0	0.8980	0.0590
SX0	0.9410	0.0640
SY0	0.6360	0.0480
SZ0	0.7820	0.0580