



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:10 AM UTC

PDB ID : 4UJC / pdb_00004ujc
EMDB ID : EMD-2683
Title : mammalian 80S HCV-IRES initiation complex with eIF5B POST-like state
Authors : Yamamoto, H.; Unbehaun, A.; Loerke, J.; Behrmann, E.; Marianne, C.;
Burger, J.; Mielke, T.; Spahn, C.M.T.
Deposited on : 2014-06-18
Resolution : 9.50 Å(reported)
Based on initial model : 4CXC

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

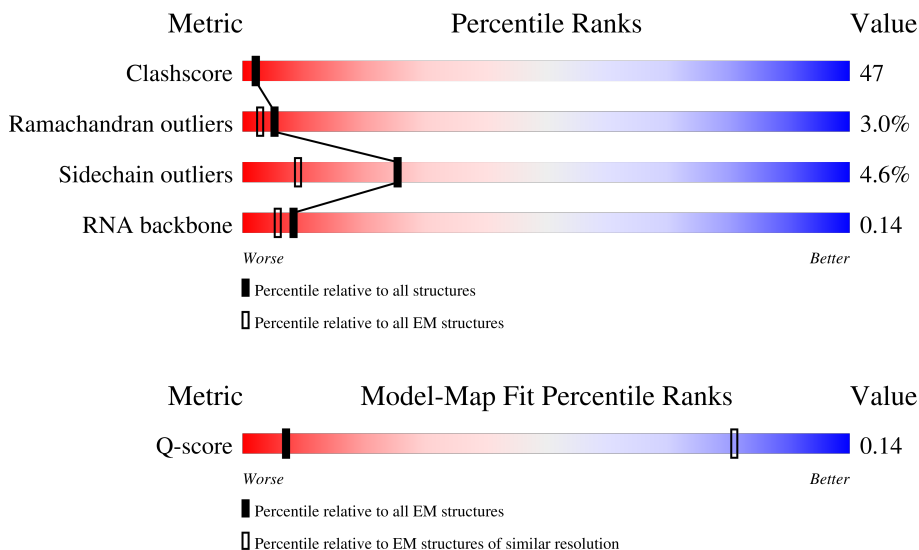
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	234 (9.00 - 10.00)

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

Mol	Chain	Length	Quality of chain
1	AA	76	12% (Upper red bar) 12% (Red) 64% (Yellow) 22% (Orange) . (Green)
2	AB	627	62% (Upper red bar) 27% (Red) 57% (Yellow) 11% (Orange) . . (Green)
3	AC	504	19% (Upper red bar) 8% (Red) 18% (Yellow) 18% (Orange) 7% (Green) 48% (Grey)

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Mol	Chain	Length	Quality of chain
4	A2	5025	7% 28% 36% 28%
5	A3	194	8% 37% 35% 19%
6	A4	121	12% 36% 50%
7	BA	257	12% 54% 39%
8	BB	403	8% 54% 38% 5%
9	BC	427	10% 43% 35% 5% 15%
10	BD	297	15% 54% 40%
11	BE	158	8% 35% 54% 10%
12	BF	248	14% 50% 32% 6% 12%
13	BG	266	11% 54% 42%
14	BH	192	6% 49% 38% 5% 8%
15	BI	214	8% 45% 40% 11%
16	BJ	178	17% 45% 40% 9% 5%
17	BL	211	7% 31% 32% 35%
18	BM	215	7% 58% 40%
19	BN	204	6% 50% 40% 6%
20	BO	203	10% 45% 33% 5% 17%
21	BP	184	7% 51% 40% 7%
22	BQ	188	7% 49% 37% 6% 7%
23	BR	196	7% 51% 39% 7%
24	BS	176	13% 51% 43% 5%
25	BT	160	21% 51% 27% 20%
26	BU	128	10% 61% 29% 9%
27	BV	140	28% 9% 59%
28	BW	157	28% 9% 59%

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Mol	Chain	Length	Quality of chain
29	BX	156	
30	BY	145	
31	BZ	136	
32	Ba	148	
33	Bb	159	
34	Bc	115	
35	Bd	125	
36	Be	135	
37	Bf	110	
38	Bg	117	
39	Bh	123	
40	Bi	105	
41	Bj	97	
42	Bk	70	
43	Bl	51	
44	Bm	128	
45	Bn	25	
46	Bo	106	
47	Bp	92	
48	Bt	137	
49	Bu	210	
50	C1	1869	
51	CA	263	
52	CB	264	
53	CC	293	

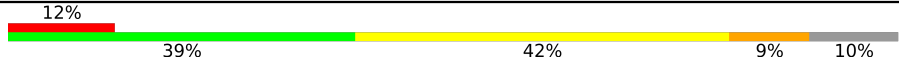

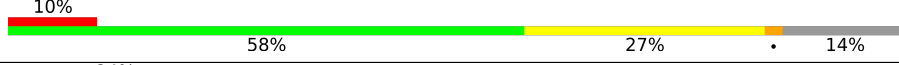


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Mol	Chain	Length	Quality of chain
54	CD	243	14% 50% 32% 5% 13%
55	CE	263	8% 51% 41% 5%
56	CF	204	6% 41% 45% 6% 8%
57	CG	249	6% 49% 37% 7% 7%
58	CH	194	21% 43% 52% ...
59	CI	208	13% 48% 45% 6%
60	CJ	194	• 47% 37% 7% • 8%
61	CK	165	7% 29% 22% 5% • 43%
62	CL	158	15% 51% 36% 5% 8%
63	CM	132	58% 52% 33% 5% • 9%
64	CN	151	13% 50% 42% 6% ••
65	CO	151	12% 46% 39% 5% • 9%
66	CP	145	12% 41% 37% •• 19%
67	CQ	146	5% 50% 42% • 5%
68	CR	135	15% 42% 32% 7% 19%
69	CS	152	9% 48% 37% 9% 7%
70	CT	145	8% 43% 51% ••
71	CU	119	9% 34% 45% 5% 15%
72	CV	83	10% 63% 35% •
73	CW	130	5% 47% 48% •••
74	CX	143	7% 49% 41% • 6%
75	CY	133	• 53% 31% 7% • 8%
76	CZ	125	6% 26% 29% 6% 39%
77	Ca	115	23% 28% 46% 8% • 17%
78	Cb	84	18% 55% 36% 5% 5%

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Mol	Chain	Length	Quality of chain
79	Cc	69	
80	Cd	56	
81	Ce	59	
82	Cf	156	
83	Cg	317	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 223911 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 TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	76	1619	723	290	531	75	0	0

- Molecule 2 is a protein called EIF5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AB	611	4846	3084	834	906	22	0	0

- Molecule 3 is a RNA chain called HCV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	AC	261	5574	2485	1001	1828	260	0	0

- Molecule 4 is a RNA chain called 28S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	A2	3616	77488	34508	14153	25212	3615	0	0

- Molecule 5 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	A3	157	3334	1489	587	1102	156	0	0

- Molecule 6 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	A4	119	2538	1132	454	834	118	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BA	247	1888	1183	388	311	6	0	1

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BB	396	3190	2030	601	545	14	0	1

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BC	364	2889	1817	578	480	14	0	1

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	BD	290	2362	1489	431	428	14	0	0

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BE	158	1287	834	238	215		0	0

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BF	234	1950	1252	376	313	9	0	0

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	BG	235	1881	1197	363	317	4	0	1

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BH	192	Total	C	N	O	S	0	0
			1536	965	286	279	6		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BI	196	Total	C	N	O	S	0	0
			1605	1022	308	263	12		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BJ	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BL	200	Total	C	N	O	S	0	1
			1617	1013	335	265	4		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BM	140	Total	C	N	O	S	0	1
			1139	730	219	183	7		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BN	204	Total	C	N	O	S	0	0
			1709	1077	360	267	5		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BO	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	BP	153	1234	771	241	213	9	0	1

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	BQ	184	1494	933	311	245	5	0	0

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	BR	183	1526	943	331	242	10	0	1

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	BS	173	1439	916	280	233	10	0	0

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	BT	159	1298	823	252	217	6	0	0

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	BU	102	827	529	146	150	2	0	1

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	BV	128	964	610	181	168	5	0	0

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BW	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BX	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BY	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BZ	136	Total	C	N	O	S	0	0
			1115	719	209	183	4		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ba	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Bb	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bc	104	Total	C	N	O	S	0	1
			802	508	142	145	7		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Bd	109	905	570	174	159	2	0	0

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Be	128	1053	664	219	165	5	0	1

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Bf	107	866	550	172	141	3	0	0

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Bg	115	907	566	188	147	6	0	1

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN UL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Bh	122	1015	641	205	168	1	0	0

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Bi	97	783	488	168	122	5	0	1

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Bj	85	690	423	153	109	5	0	1

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	Bk	69	569	366	103	99	1	0	0

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Bl	50	444	281	98	64	1	0	0

- Molecule 44 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Bm	52	429	266	90	67	6	0	0

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Bn	25	240	145	64	28	3	0	0

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Bo	106	871	547	176	141	7	0	0

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L37A.

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

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	Bt	130	1043	646	220	172	5	0	1

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Bu	210	Total	C	N	O	S	0	0
			1622	990	278	348	6		

- Molecule 50 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C1	1742	Total	C	N	O	P	0	0
			37159	16589	6665	12164	1741		

- Molecule 51 is a protein called 40S RIBOSOMAL PROTEIN US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	218	Total	C	N	O	S	0	0
			1719	1091	301	319	8		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN ES1.

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

- Molecule 53 is a protein called 40S RIBOSOMAL PROTEIN US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CC	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 54 is a protein called 40S RIBOSOMAL PROTEIN US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CD	212	Total	C	N	O	S	0	0
			1646	1050	299	290	7		

- Molecule 55 is a protein called 40S RIBOSOMAL PROTEIN ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CE	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	CF	188	1486	930	283	266	7	0	0

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	CG	232	1884	1176	379	322	7	0	0

- Molecule 58 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	CH	191	1535	978	282	274	1	0	0

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	CI	207	1695	1064	334	292	5	0	0

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	CJ	179	1495	953	299	241	2	0	0

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	CK	94	791	519	138	129	5	0	0

- Molecule 62 is a protein called 40S RIBOSOMAL PROTEIN US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	CL	146	1199	764	224	205	6	0	0

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CM	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CN	150	Total	C	N	O	S	0	0
			1207	773	229	204	1		

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CO	137	Total	C	N	O	S	0	0
			1023	627	200	190	6		

- Molecule 66 is a protein called 40S RIBOSOMAL PROTEIN US19.

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

- Molecule 67 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	CQ	139	Total	C	N	O	S	0	0
			1108	704	210	191	3		

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	CR	109	Total	C	N	O	S	0	0
			893	561	170	159	3		

- Molecule 69 is a protein called 40S RIBOSOMAL PROTEIN US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CS	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 70 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	CT	143	1112	697	214	198	3	0	0

- Molecule 71 is a protein called 40S RIBOSOMAL PROTEIN US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	CU	101	803	502	153	144	4	0	0

- Molecule 72 is a protein called 40S RIBOSOMAL PROTEIN ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	CV	83	636	393	117	121	5	0	0

- Molecule 73 is a protein called 40S RIBOSOMAL PROTEIN US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	CW	129	1033	659	193	175	6	0	0

- Molecule 74 is a protein called 40S RIBOSOMAL PROTEIN US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	CX	134	1046	663	205	176	2	0	0

- Molecule 75 is a protein called 40S RIBOSOMAL PROTEIN ES24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	CY	122	1002	635	196	166	5	0	0

- Molecule 76 is a protein called 40S RIBOSOMAL PROTEIN ES25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	CZ	76	605	387	112	105	1	0	0

- Molecule 77 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ca	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 78 is a protein called 40S RIBOSOMAL PROTEIN ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Cb	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Cc	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 80 is a protein called 40S RIBOSOMAL PROTEIN US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cd	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 81 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ce	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

- Molecule 82 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Cf	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

- Molecule 83 is a protein called 40S RIBOSOMAL PROTEIN RACK1.

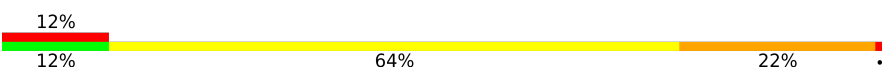
Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cg	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

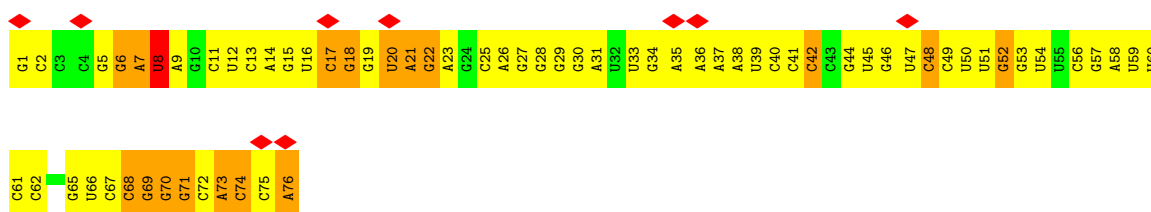
- Molecule 84 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).

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.

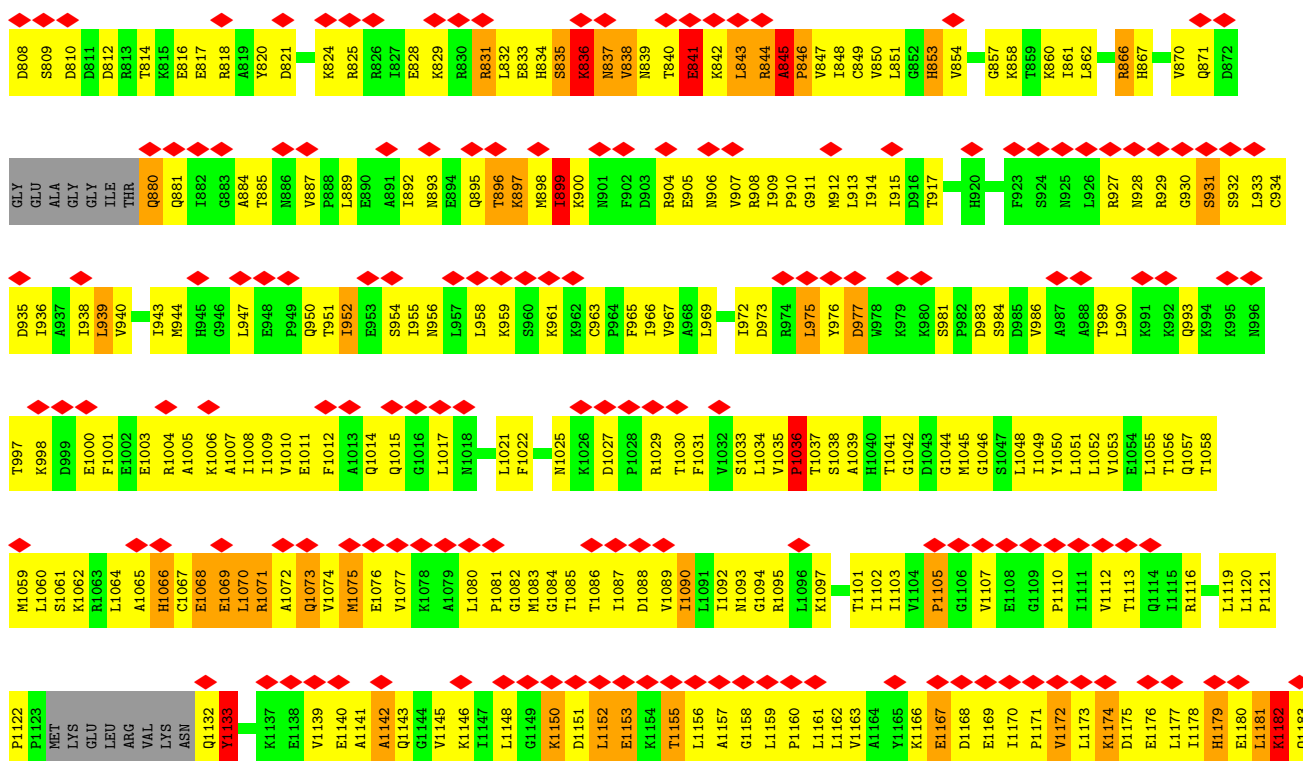
• Molecule 1: TRNA

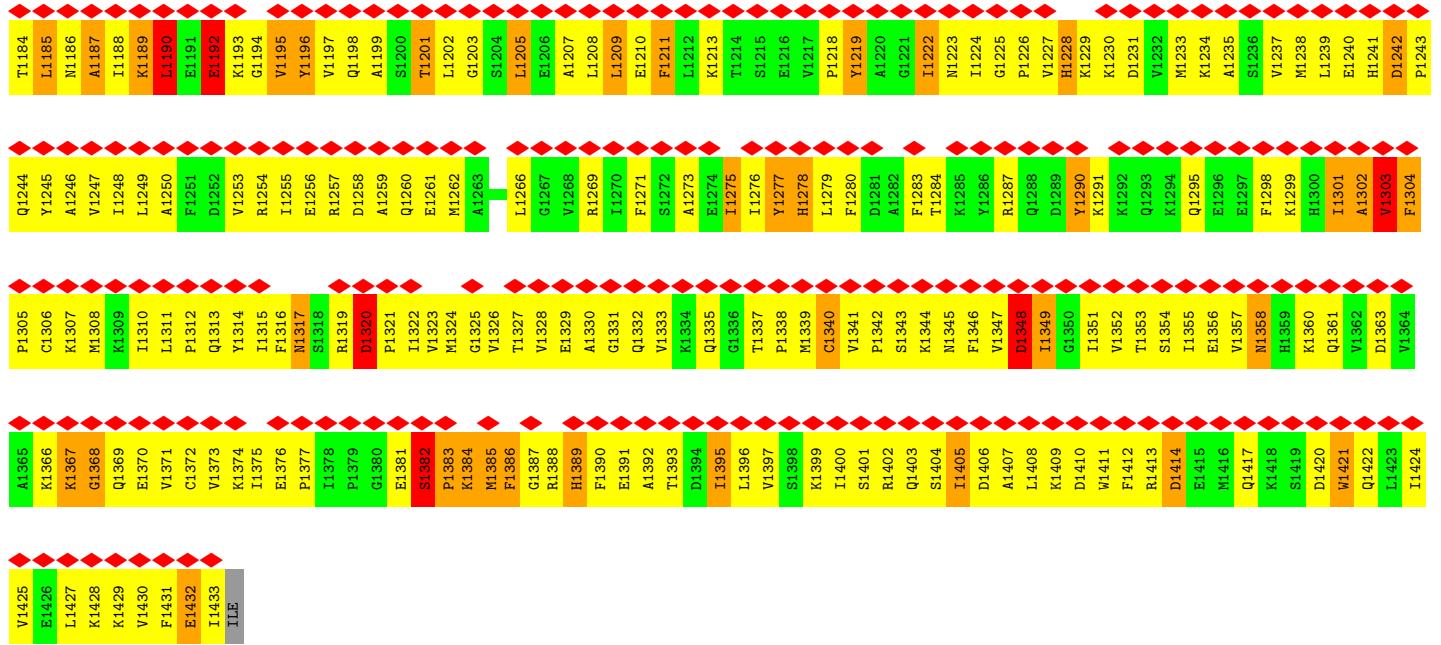
Chain AA: 



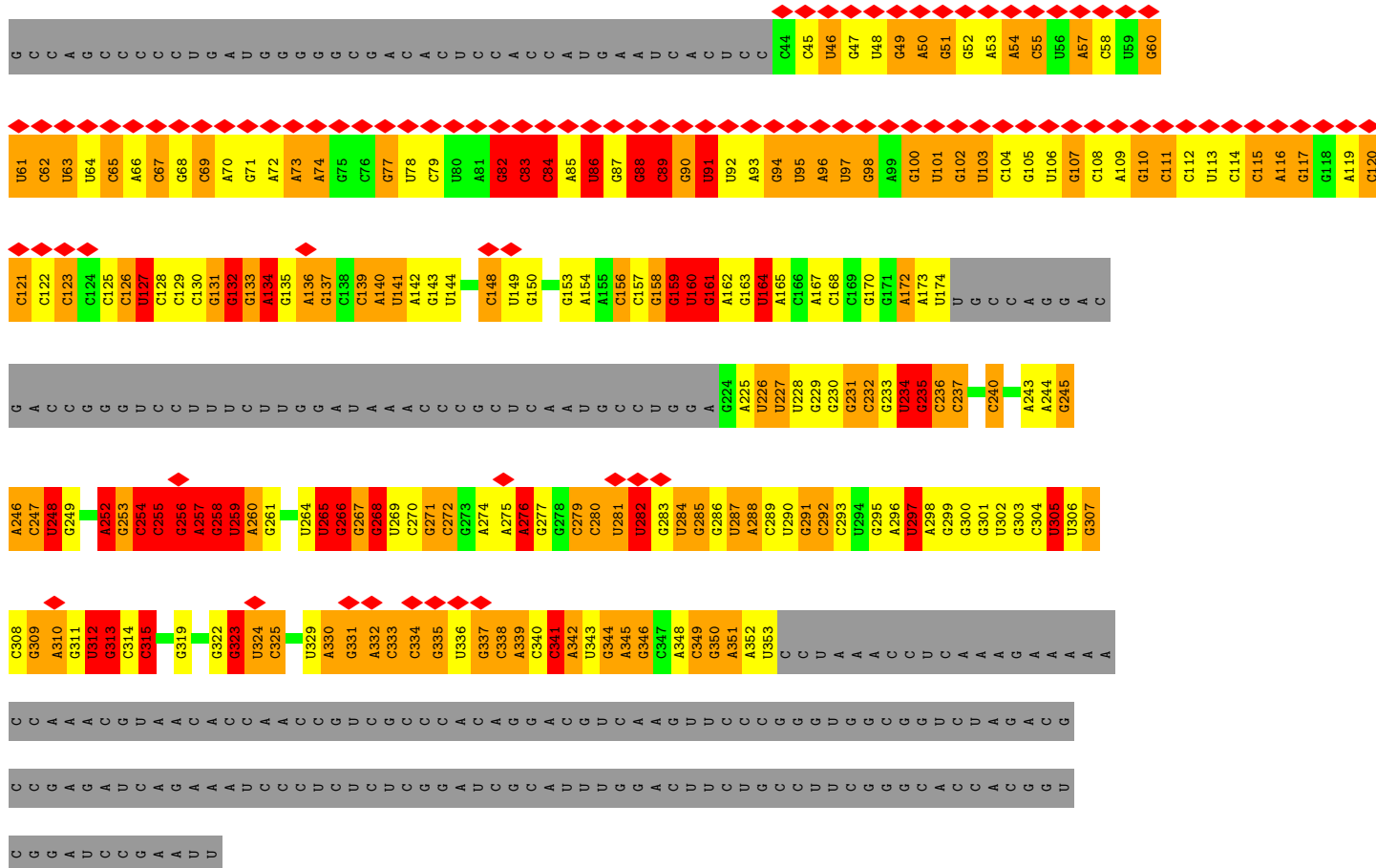
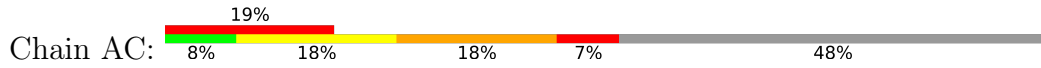
• Molecule 2: EIF5B

Chain AB: 

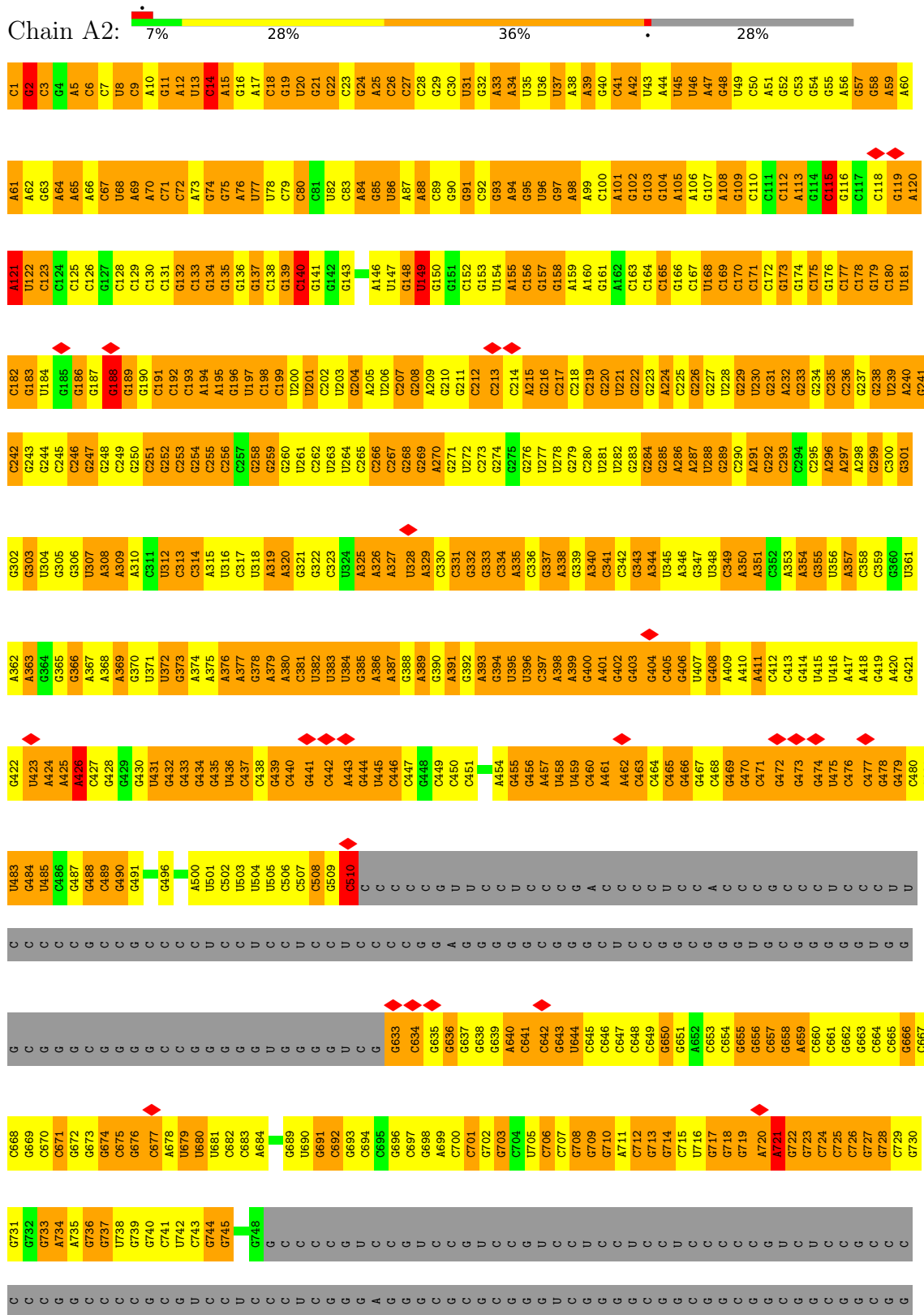




● Molecule 3: HCV-IRES



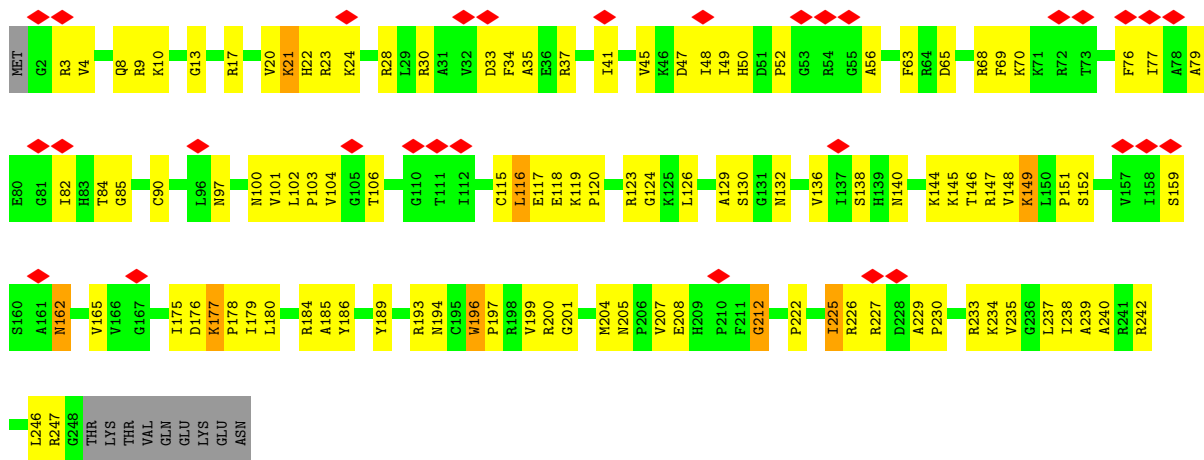
• Molecule 4: 28S RIBOSOMAL RNA



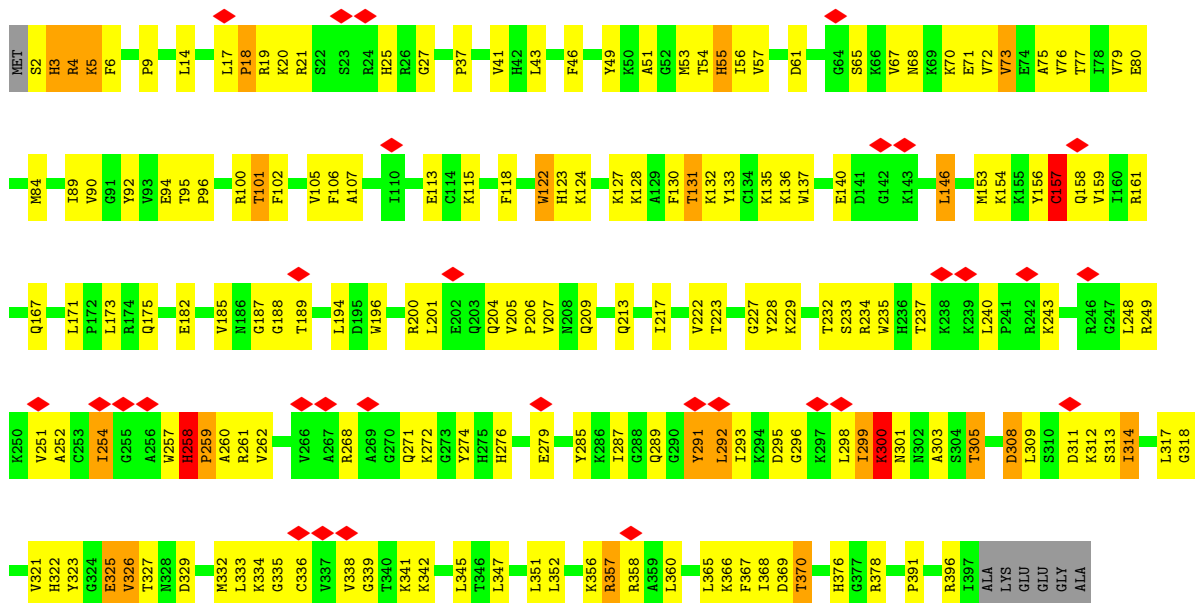
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G1646	U1585	G1523	C1462	G1402	G1342	G1279	C1219	G1158	C1096	U	C975	C915	G
A1647	G1586	G1524	G1463	U1403	U1343	G1280	G1220	U1159	C1097	U	C976	A916	G
G1648	G1587	G1525	G1464	G1404	U1344	C1281	G1221	C1160	C	U	C977	G917	C
U1649	U1588	A1526	C1345	G1405	U1282	U1282	G1222	C1161	C	C	C978	C918	C
U1650	G1589	G1466	G1346	G1406	A1283	A1283	C1223	C1162	C	C	C979	A919	C
U1651	G1590	G1467	C1347	A1407	C1284	C1284	C1224	C1163	C	U	G	C920	C
U1652	A1591	G1468	A1348	U1408	C1285	C1285	G1224	A1164	C	C	C	U921	C
C1653	G1592	G1471	C1349	C1409	C1286	C1286	C1225	G1165	C	C	C	C922	C
C1654	A1593	G1472	C1410	C1410	C1287	C1287	G1226	U1166	C	U	A	C923	C
C1655	G1594	U1473	A1351	C1411	C1288	C1288	U1227	G1167	C	C	C	G924	C
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C1657	U1596	G1475	A1353	A1413	C1290	C1290	U1229	C1171	C	C	C	G926	C
A1658	G1597	G1476	A1354	G1414	G1291	G1291	C1230	C1172	C	C	C	A927	C
G1659	U1598	A1476	C1355	G1415	C1292	C1292	C1231	C1173	C	C	C	G1044	C
G1660	G1599	C1477	C1356	C1416	C1293	C1293	C	C1174	C	C	C	G1045	C
A1661	A1600	A1478	C1357	C1417	C1294	C1294	A	G1175	C	C	C	G1046	C
U1662	G1601	A1479	C1358	C1419	C1295	C1295	G	C1176	C	C	C	G1047	C
A1663	G1602	C480	C1359	U1420	U1297	U1297	A	C1177	C	C	C	A928	C
G1664	A1542	G1481	G1360	C1421	C1298	C1298	A	G1178	C	C	C	U929	C
G1665	G1605	A1482	U1361	C1422	U1299	U1299	G	G1179	C	C	C	C930	C
U1666	G1606	G1483	U1362	C1423	U1300	U1300	G	U1180	C	C	C	C931	C
G1667	C1607	G1484	G1363	G1424	G1301	G1301	G	U1181	C	C	C	C932	C
G1668	G1608	G1485	G1364	U1425	G1302	A1302	G	C1182	C	C	C	G933	C
G1669	A1609	G1486	G1365	C1426	A1303	A1303	G	G1183	C	C	C	G934	C
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C1671	A1611	G1488	G1367	U1428	C1305	C1305	G	G1185	C	C	C	G936	C
U1672	G1612	G1489	C1368	C1429	A1306	A1306	G	C1186	C	C	C	C937	C
C1673	A1613	U1491	A1369	C1430	A1307	A1307	G	U1187	C	C	C	G938	C
U	G1614	G1491	G1370	G1431	G1308	G1308	G	C1188	C	C	C	G939	C
C	U1615	U1492	G1371	U1432	C1312	C1312	G	U1189	C	C	C	G940	C
C	A1616	U1493	A1372	G1433	A1313	A1313	G	C1190	C	C	C	A944	C
C	U1618	A1494	A1373	G1434	A1314	A1314	G	G1191	C	C	C	G945	C
A	G1619	G1495	G1374	G1435	G1315	G1315	G	U1192	C	C	C	G946	C
A	G1620	A1496	G1375	C1436	G1316	G1316	G	G1193	C	C	C	G947	C
C	A1621	A1497	U1376	C1437	A1317	A1317	G	C1194	C	C	C	G948	C
C	A1622	C1498	A1377	A1438	G1318	G1318	G	U1195	C	C	C	A949	C
C	C1623	C1499	A1378	C1439	U1319	U1319	G	G1196	C	C	C	A950	C
G	C1624	U1561	A1379	C1440	A1322	A1322	G	C1197	C	C	C	C951	C
A	A1625	A1562	G1380	C1441	C1323	C1323	G	U1198	C	C	C	C952	C
A	A1626	A1563	C1381	C1442	A1324	A1324	G	C1199	C	C	C	C953	C
C	C1627	G1564	C1382	C1443	A1325	A1325	G	G1200	C	C	C	G954	C
C	G1565	G1566	G1383	G1444	A1326	A1326	G	U1201	C	C	C	U955	C
A	U1567	U1567	G1384	G1445	A1327	A1327	G	C1202	C	C	C	C956	C
C	G1630	C1568	G1385	C1446	G1328	G1328	G	U1203	C	C	C	C957	C
C	G1631	C1569	C1386	C1447	U1329	U1329	G	U1204	C	C	C	C958	C
C	G1632	U1570	C1387	C1448	G1330	G1330	G	U1205	C	C	C	C959	C
C	G1633	G1571	G1388	G1449	C1331	C1331	G	U1206	C	C	C	C960	C
C	C1634	A1572	C1389	U1450	C1332	C1332	G	C1207	C	C	C	A901	C
G	U1635	A1512	U1390	C1451	C1333	C1333	G	U1208	C	C	C	C961	C
C	C1636	A1513	C1391	U1452	G1334	G1334	G	C1209	C	C	C	C962	C
C	G1637	C1514	C1392	G1453	A1335	A1335	G	U1210	C	C	C	C963	C
A	U1638	U1515	C1393	G1454	G1336	G1336	G	C1211	C	C	C	U964	C
A	U1639	A1516	C1394	C1455	U1337	U1337	G	U1212	C	C	C	C965	C
C	C1640	U1517	C1395	C1456	G1338	G1338	G	G1213	C	C	C	U966	C
C	G1641	U1518	G1396	C1457	G1339	G1339	G	U1214	C	C	C	C967	C
C1701	A1580	G1519	C1397	C1458	G1340	G1340	G	G1215	C	C	C	C968	C
A1702	G1581	C1519	C1398	C1459	G1341	G1341	G	U1216	C	C	C	C969	C
G1703	C1582	C1520	C1399	C1460	G1342	G1342	G	U1217	C	C	C	C970	C
U1704	C1644	U1521	A1400				G	G1154	C	C	C	C971	C
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							G	C1156	C	C	C	U973	C



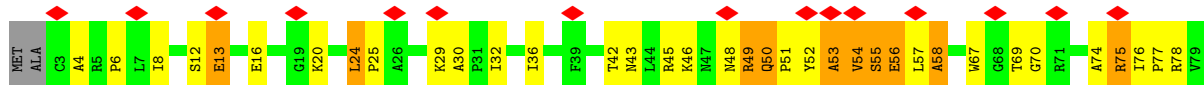
• Molecule 7: 60S RIBOSOMAL PROTEIN L8

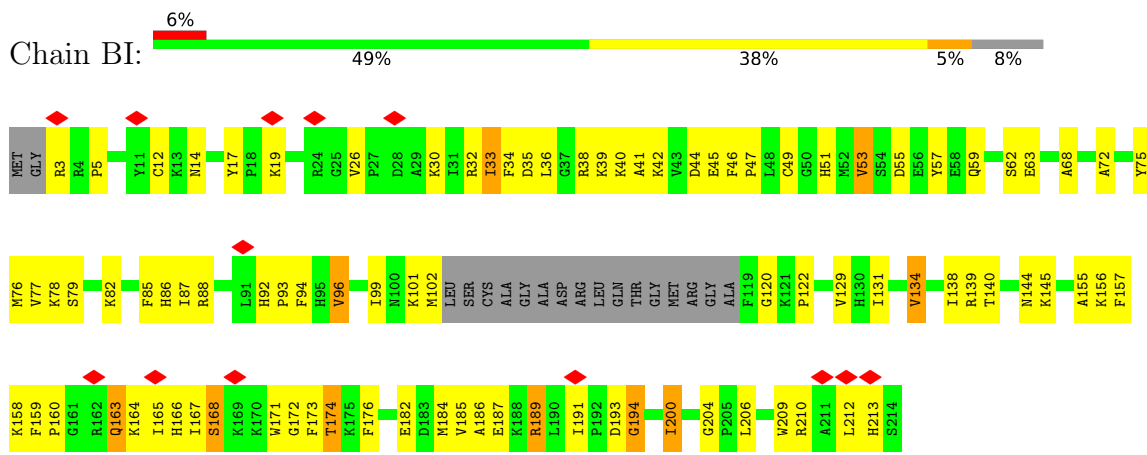


• Molecule 8: 60S RIBOSOMAL PROTEIN L3

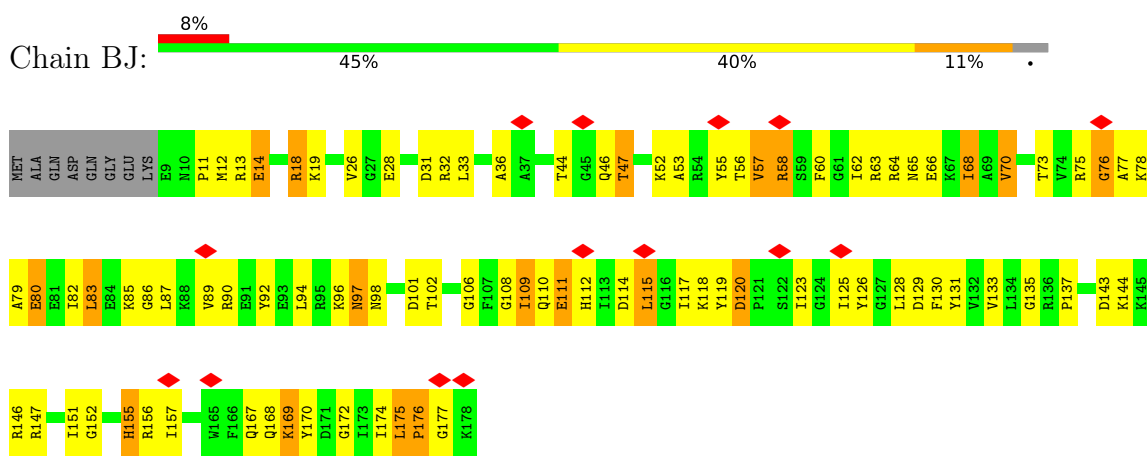


• Molecule 9: 60S RIBOSOMAL PROTEIN L4

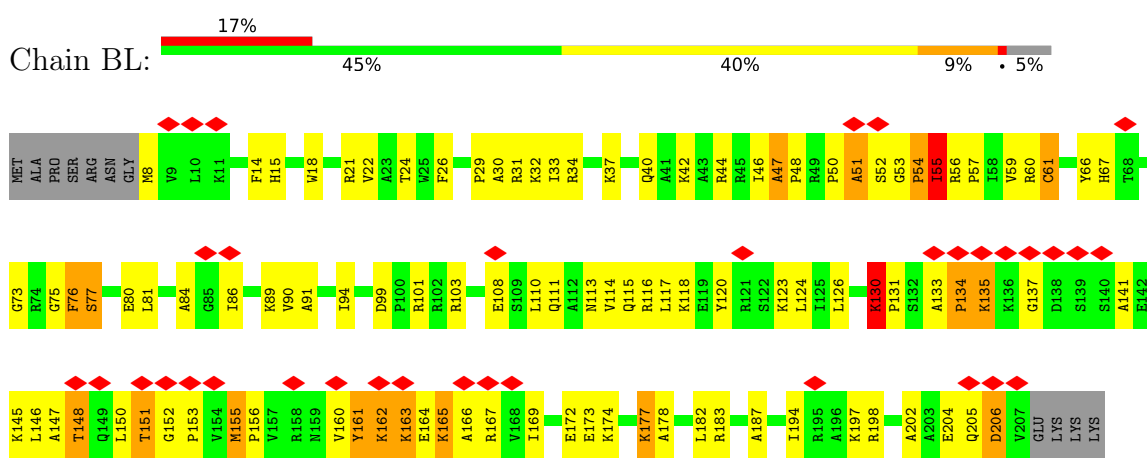




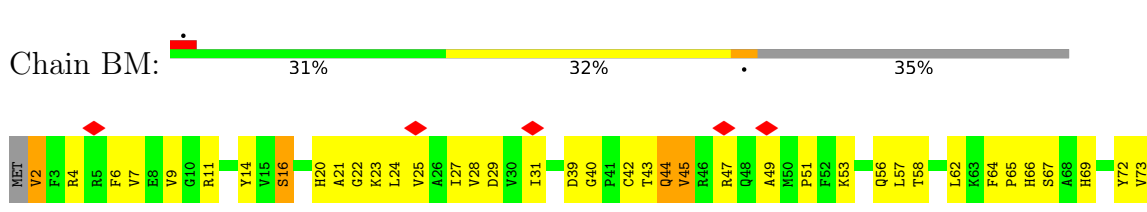
• Molecule 16: 60S RIBOSOMAL PROTEIN L11

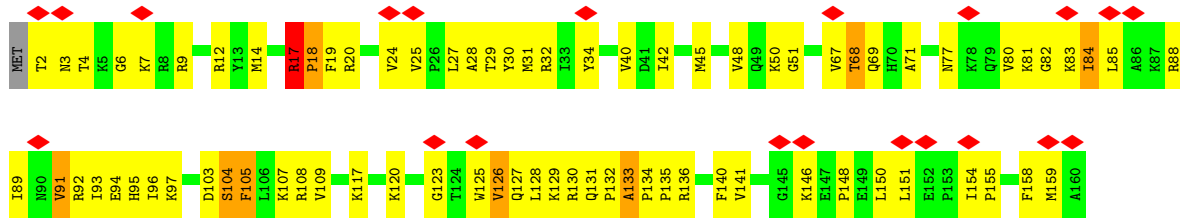


• Molecule 17: 60S RIBOSOMAL PROTEIN L13

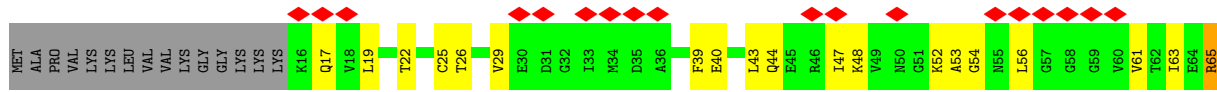


• Molecule 18: 60S RIBOSOMAL PROTEIN L14

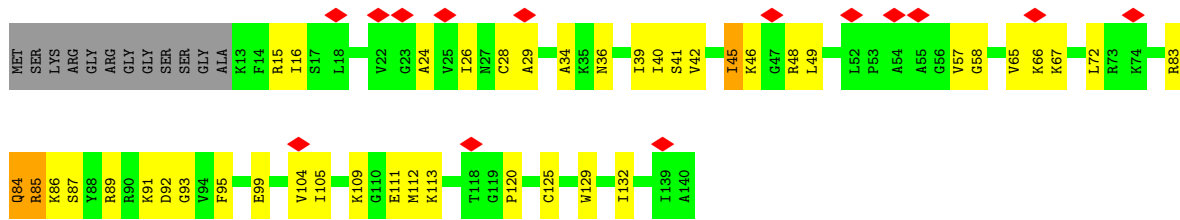




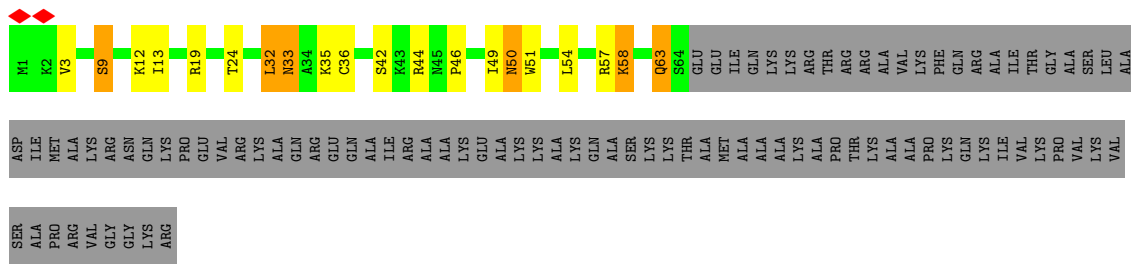
• Molecule 26: 60S RIBOSOMAL PROTEIN L22



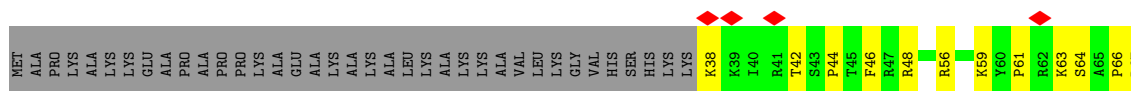
• Molecule 27: 60S RIBOSOMAL PROTEIN L23

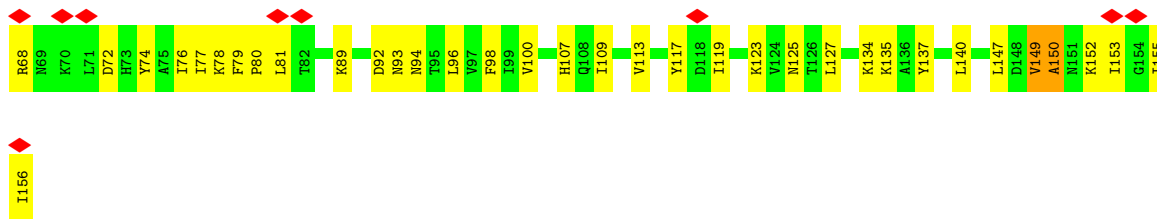


• Molecule 28: 60S RIBOSOMAL PROTEIN L24

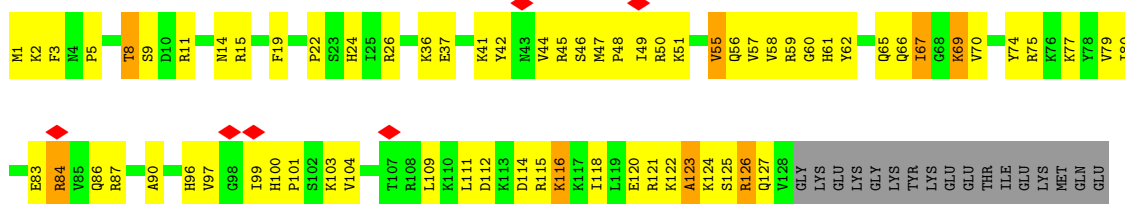


• Molecule 29: 60S RIBOSOMAL PROTEIN L23A

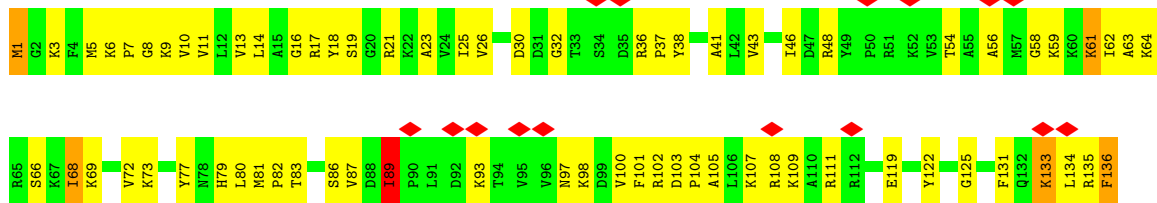




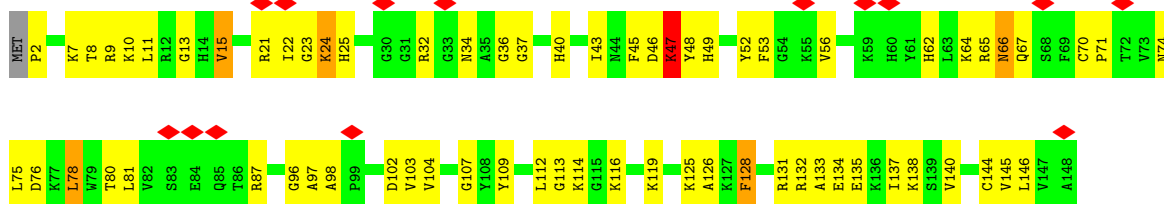
• Molecule 30: 60S RIBOSOMAL PROTEIN L26



• Molecule 31: 60S RIBOSOMAL PROTEIN L27



• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

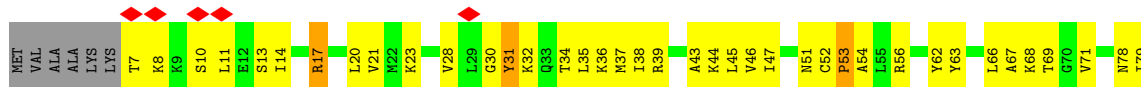


• Molecule 33: 60S RIBOSOMAL PROTEIN L29

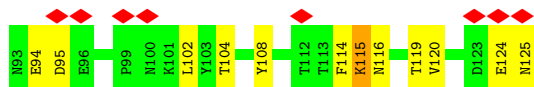
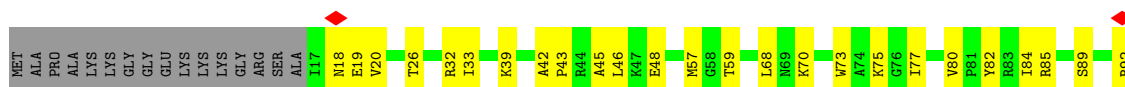


ALA GLN
ALA GLN
ALA ALA
ALA ALA
PRO PRO
ALA ALA
SER VAL
VAL
PRO PRO
ALA ALA
GLN GLN
ALA ALA
PRO PRO
LYS LYS
SER SER
GLU

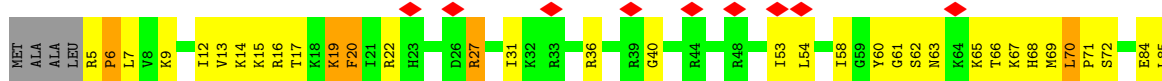
• Molecule 34: 60S RIBOSOMAL PROTEIN L30



• Molecule 35: 60S RIBOSOMAL PROTEIN L31



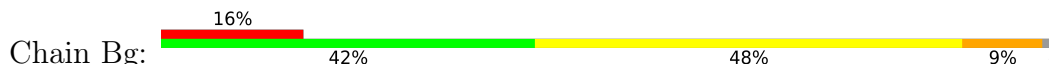
• Molecule 36: 60S RIBOSOMAL PROTEIN L32

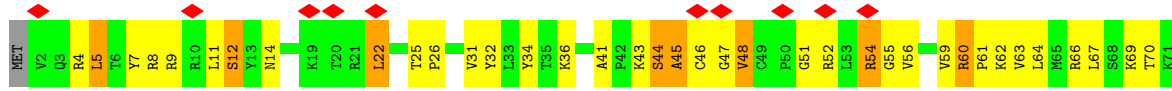


• Molecule 37: 60S RIBOSOMAL PROTEIN L35A

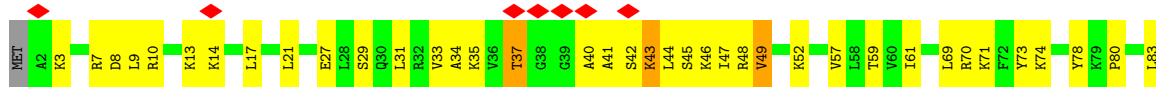


• Molecule 38: 60S RIBOSOMAL PROTEIN L34

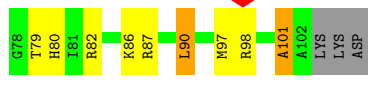
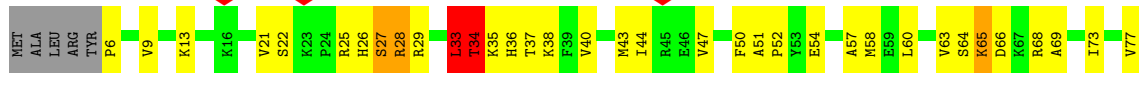




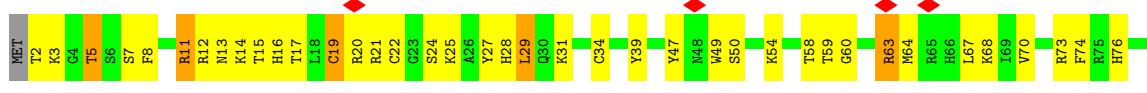
• Molecule 39: 60S RIBOSOMAL PROTEIN UL29



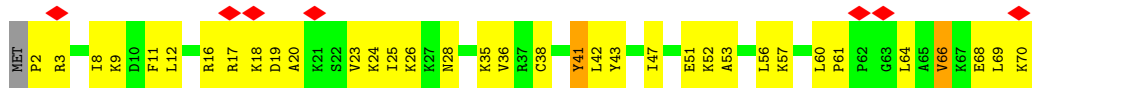
• Molecule 40: 60S RIBOSOMAL PROTEIN L36



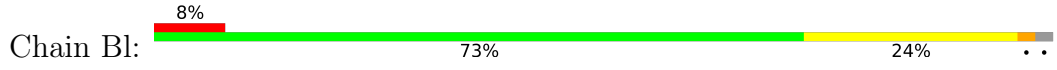
• Molecule 41: 60S RIBOSOMAL PROTEIN L37



• Molecule 42: 60S RIBOSOMAL PROTEIN L38

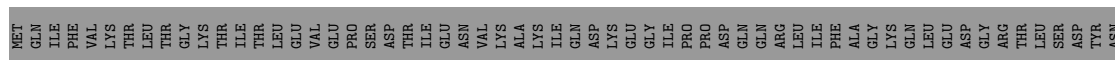


• Molecule 43: 60S RIBOSOMAL PROTEIN L39





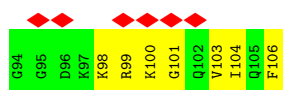
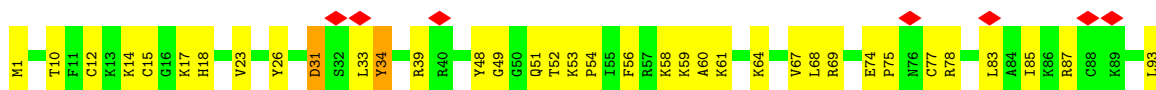
• Molecule 44: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



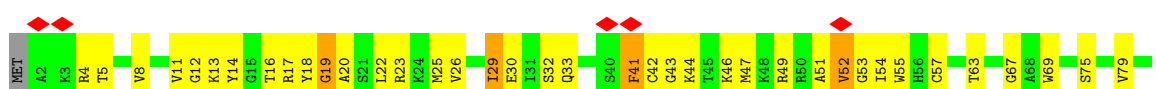
• Molecule 45: 60S RIBOSOMAL PROTEIN L41



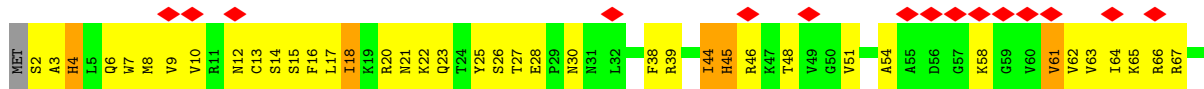
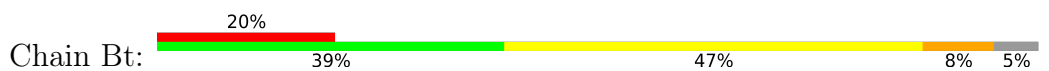
• Molecule 46: 60S RIBOSOMAL PROTEIN L36A

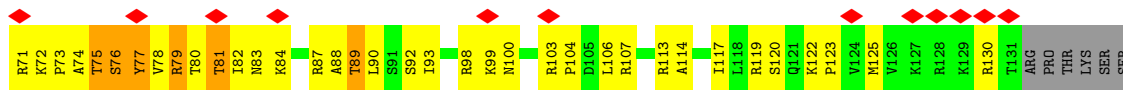


• Molecule 47: 60S RIBOSOMAL PROTEIN L37A

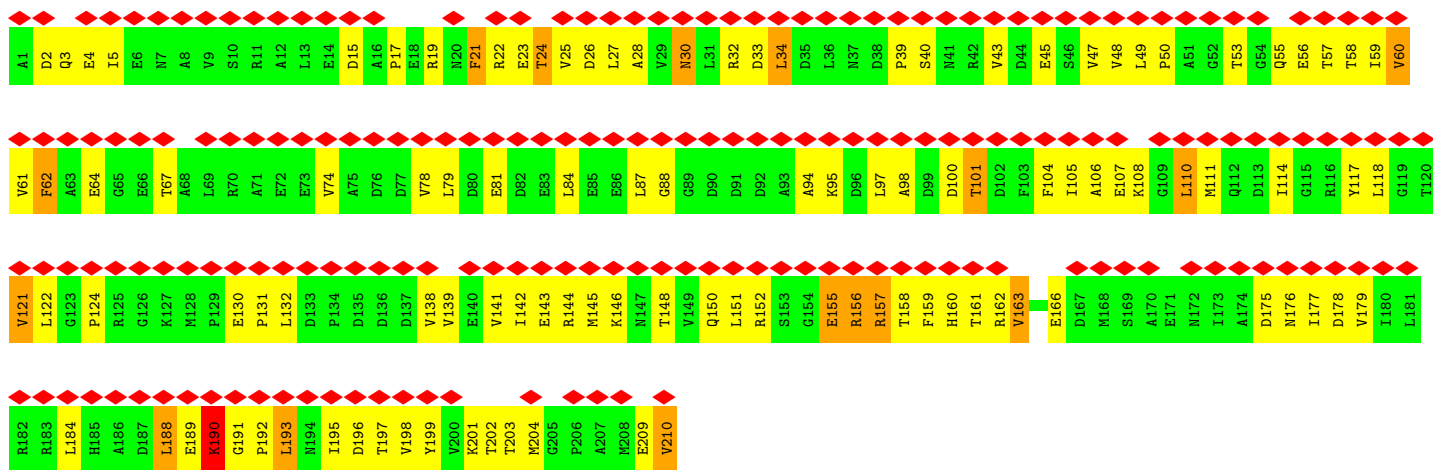


• Molecule 48: 60S RIBOSOMAL PROTEIN L28

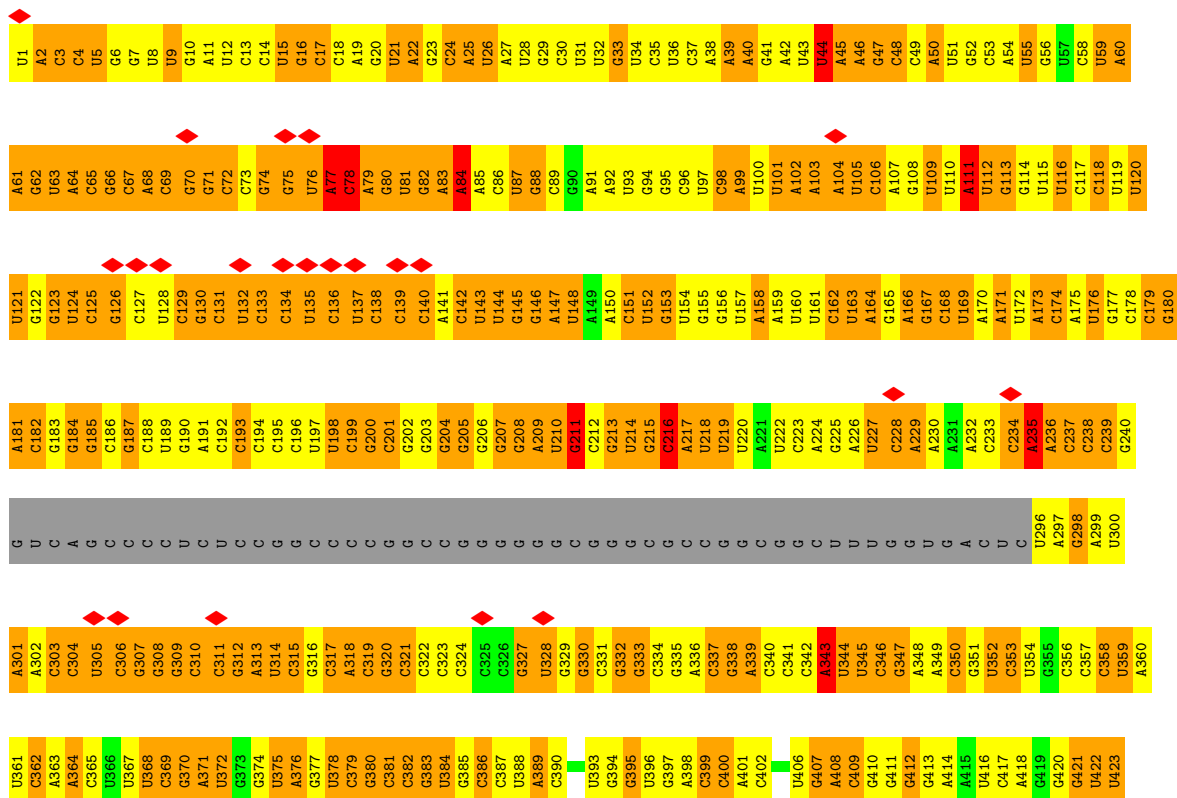


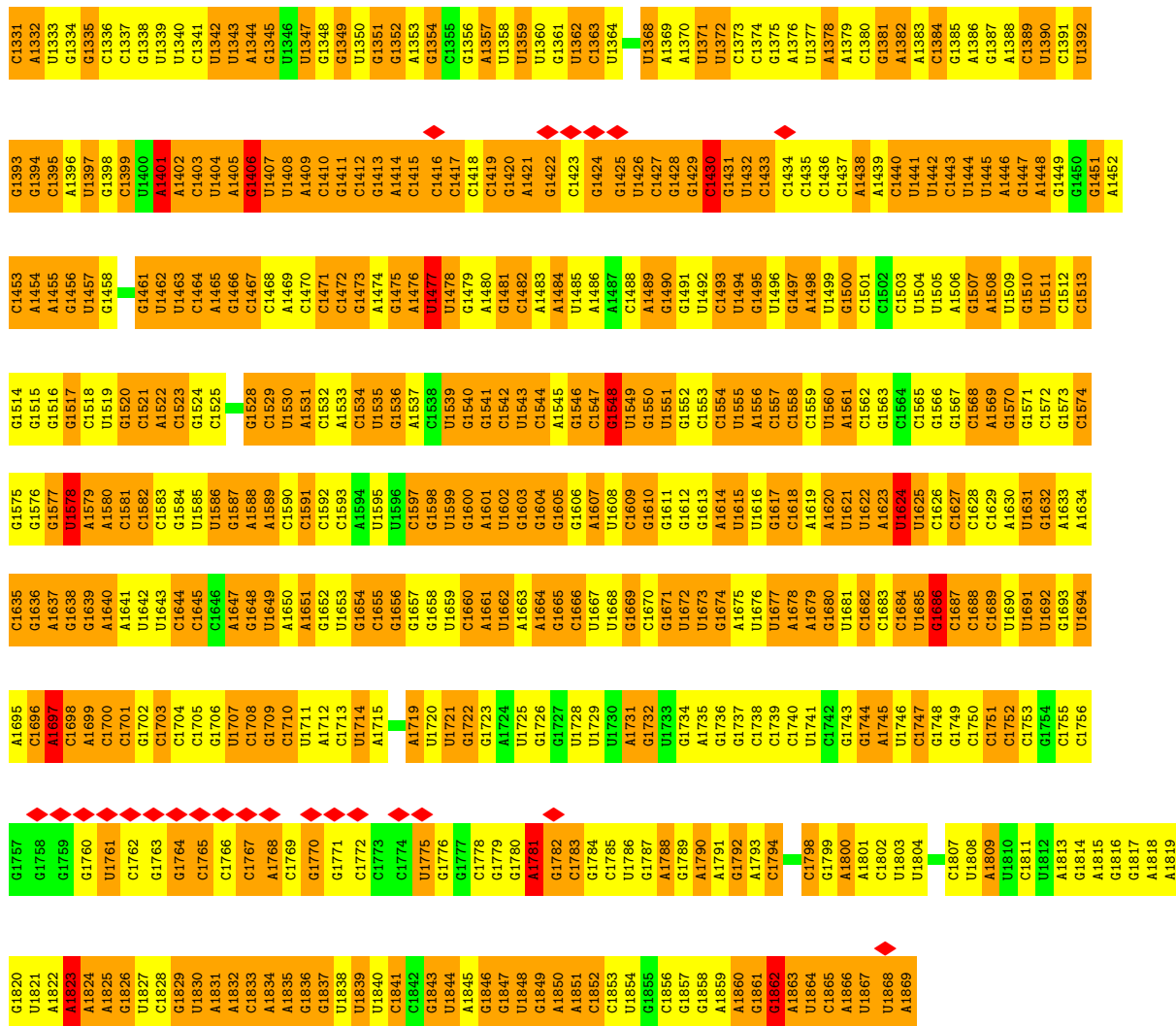


• Molecule 49: 60S RIBOSOMAL PROTEIN L10A

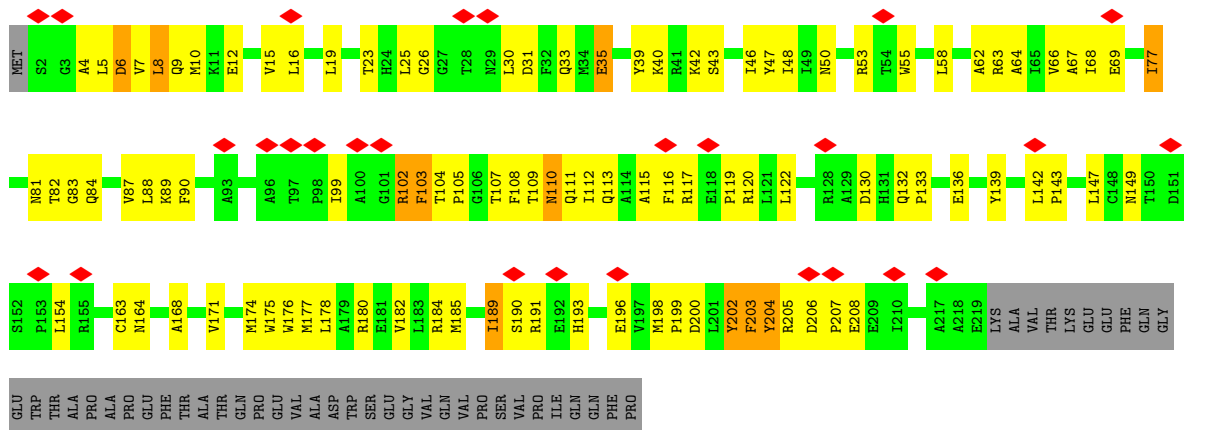


• Molecule 50: 18S RIBOSOMAL RNA





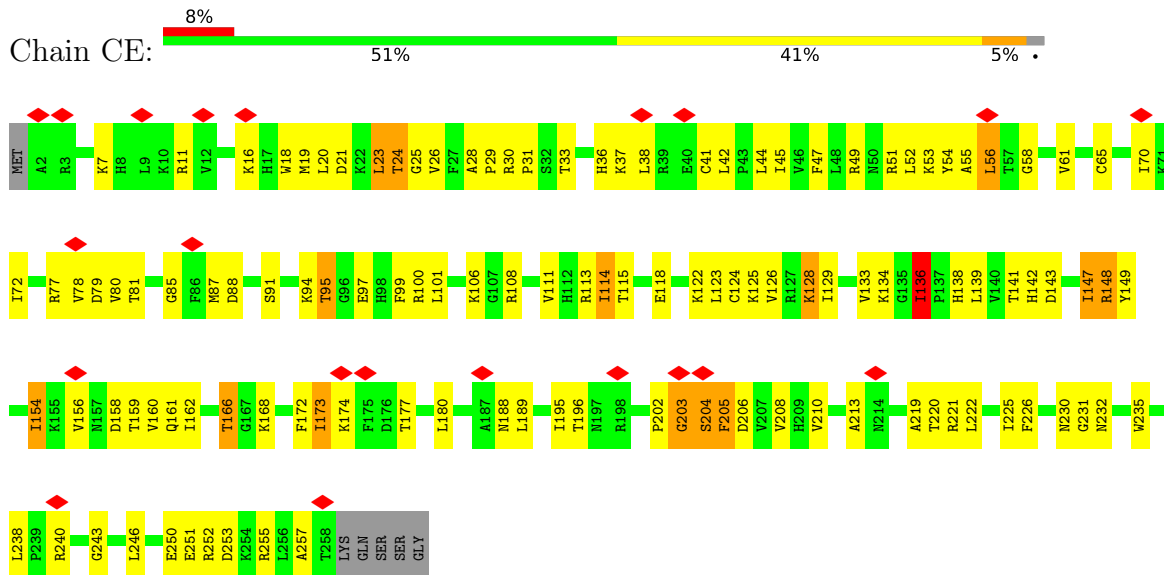
• Molecule 51: 40S RIBOSOMAL PROTEIN US2



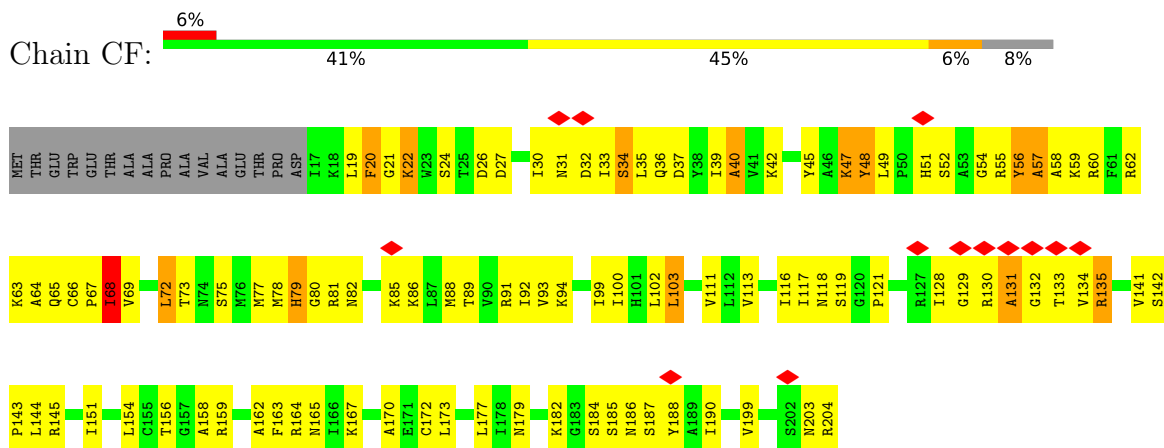
• Molecule 52: 40S RIBOSOMAL PROTEIN ES1

PRO
GLN
PRO
VAL
PRO
THR
ALA

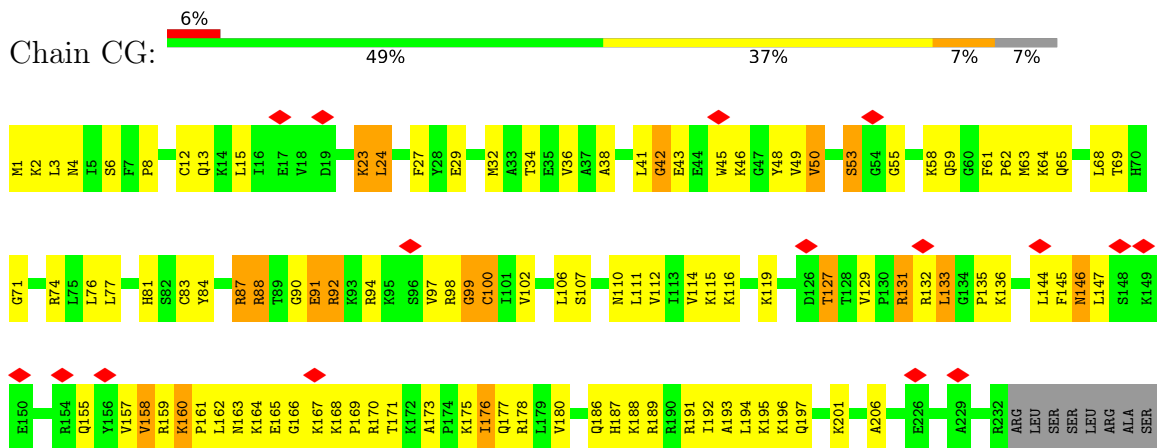
• Molecule 55: 40S RIBOSOMAL PROTEIN ES4



• Molecule 56: 40S RIBOSOMAL PROTEIN US7

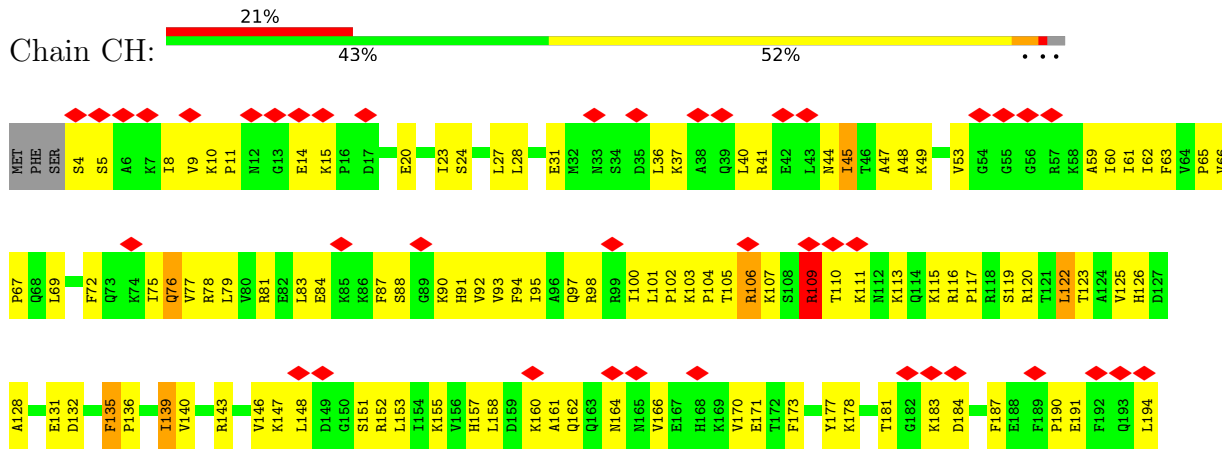


• Molecule 57: 40S RIBOSOMAL PROTEIN ES6

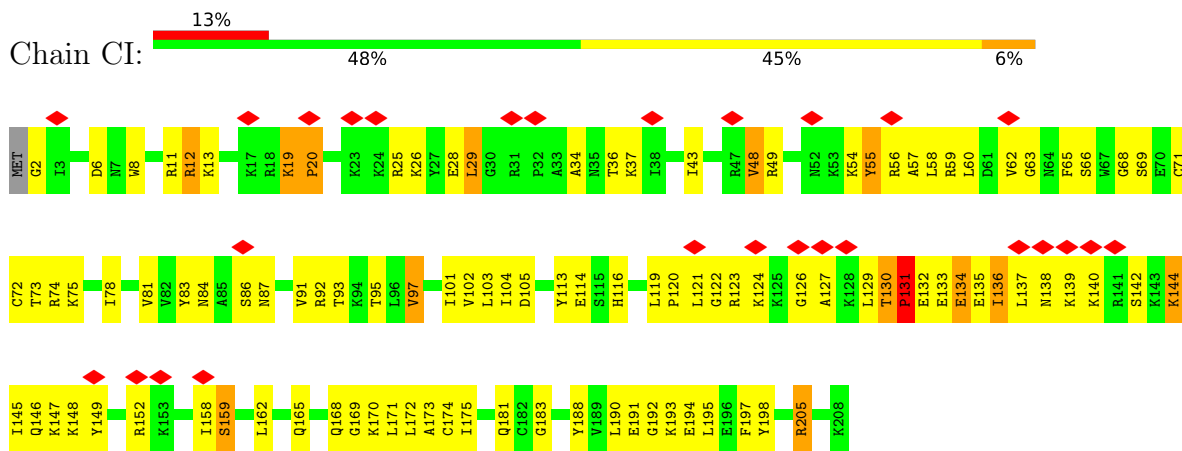


THR
SER
LYS
SER
GLU
SER
SER
GLN
LYS

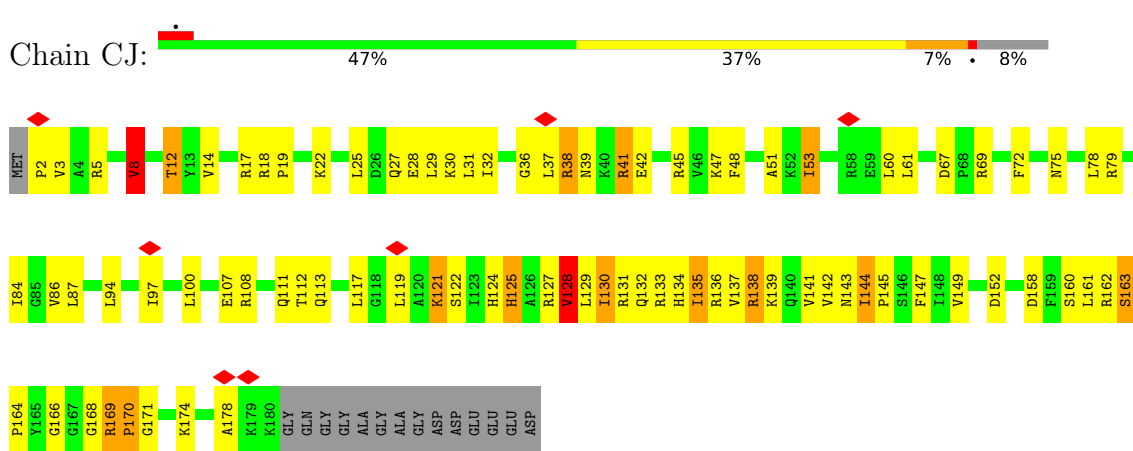
• Molecule 58: 40S RIBOSOMAL PROTEIN ES7



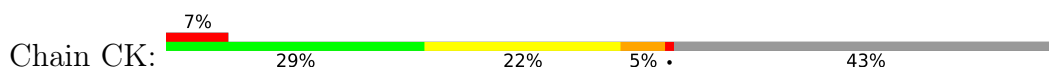
• Molecule 59: 40S RIBOSOMAL PROTEIN ES8

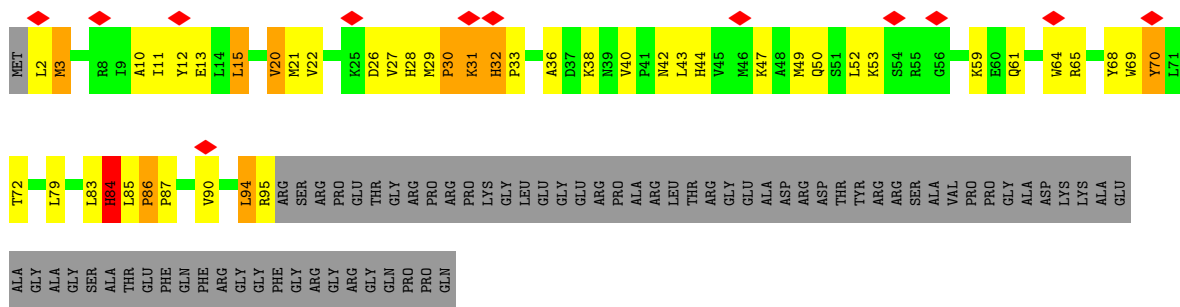


• Molecule 60: 40S RIBOSOMAL PROTEIN US4

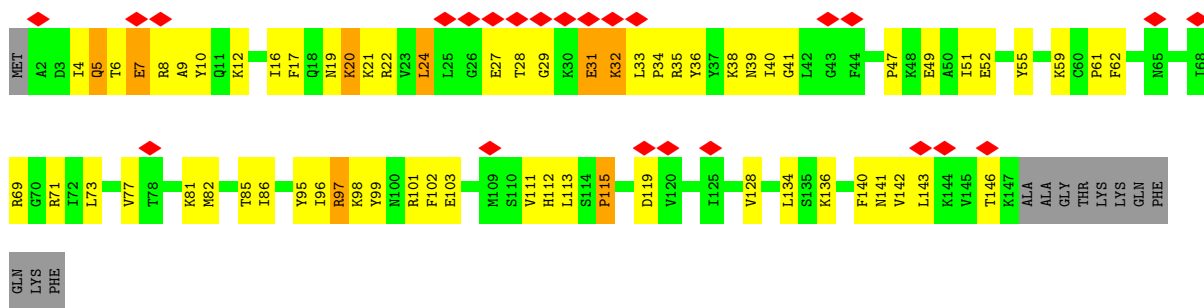


• Molecule 61: 40S RIBOSOMAL PROTEIN ES10

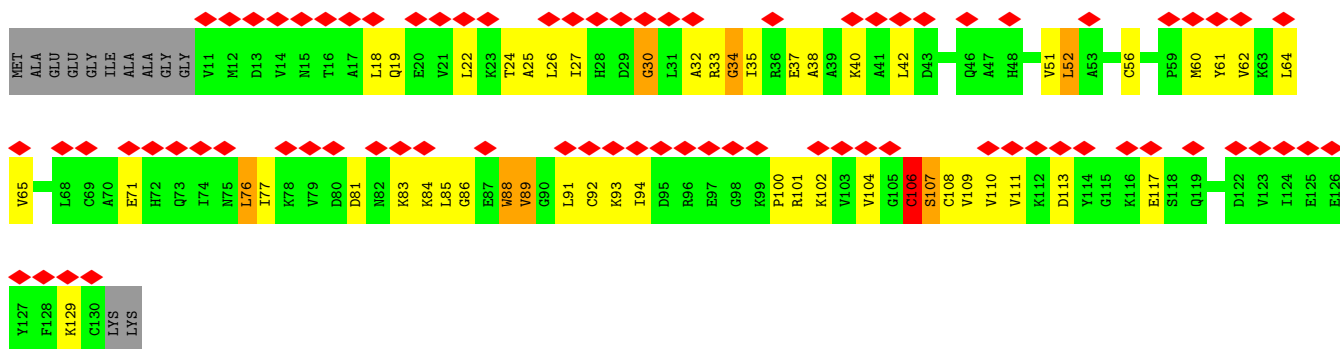




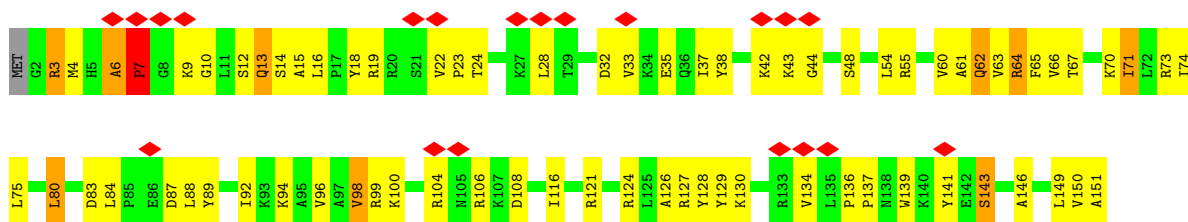
• Molecule 62: 40S RIBOSOMAL PROTEIN US17



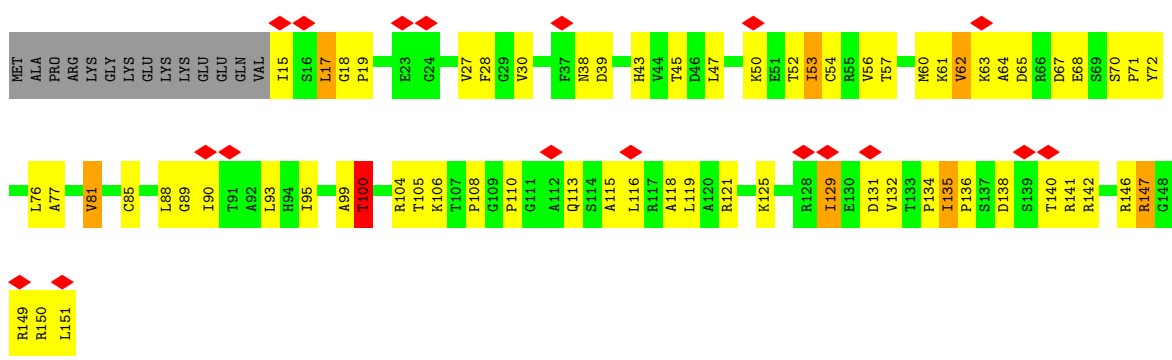
• Molecule 63: 40S RIBOSOMAL PROTEIN ES12



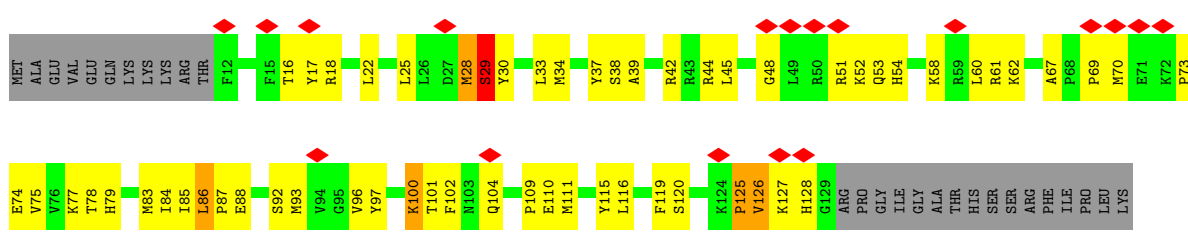
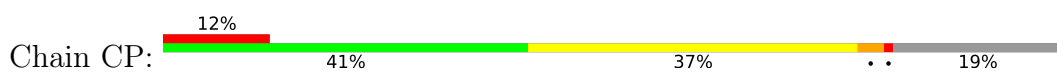
• Molecule 64: 40S RIBOSOMAL PROTEIN US15



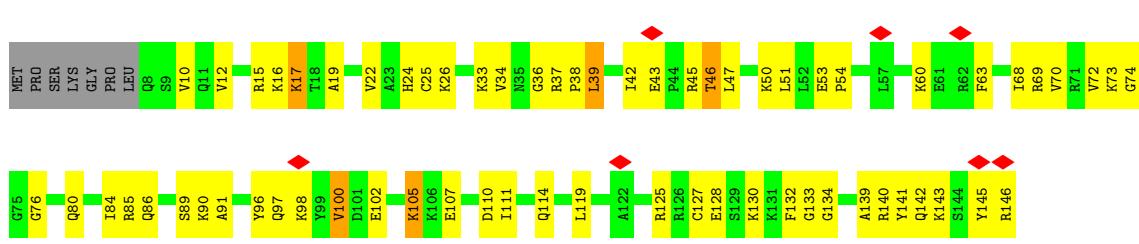
• Molecule 65: 40S RIBOSOMAL PROTEIN US11



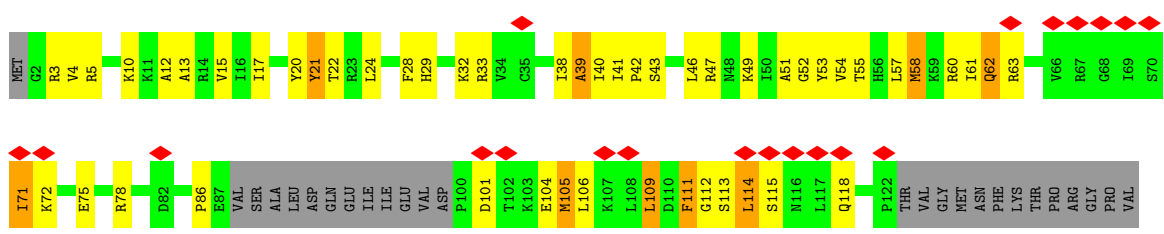
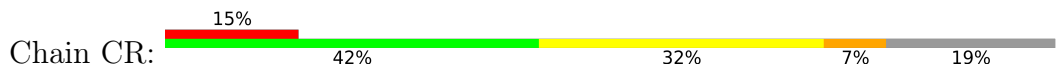
• Molecule 66: 40S RIBOSOMAL PROTEIN US19



• Molecule 67: 40S RIBOSOMAL PROTEIN US9

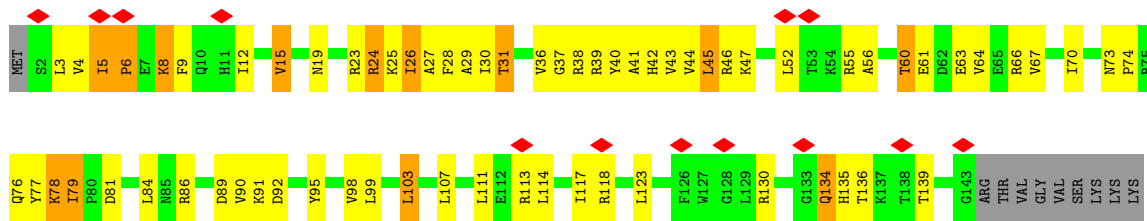


• Molecule 68: 40S RIBOSOMAL PROTEIN ES17

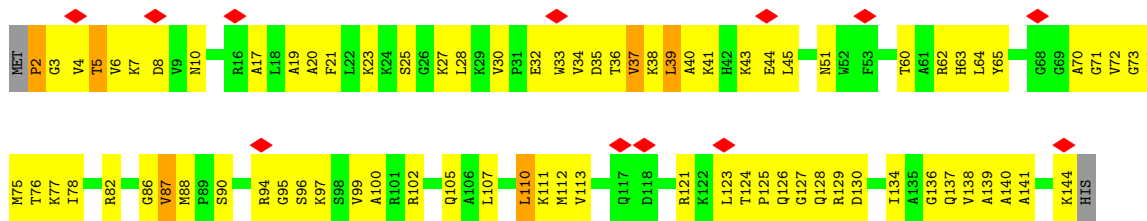
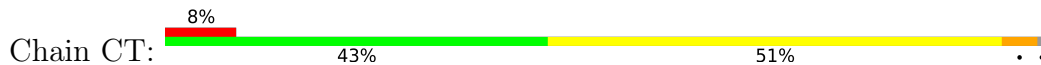


• Molecule 69: 40S RIBOSOMAL PROTEIN US13

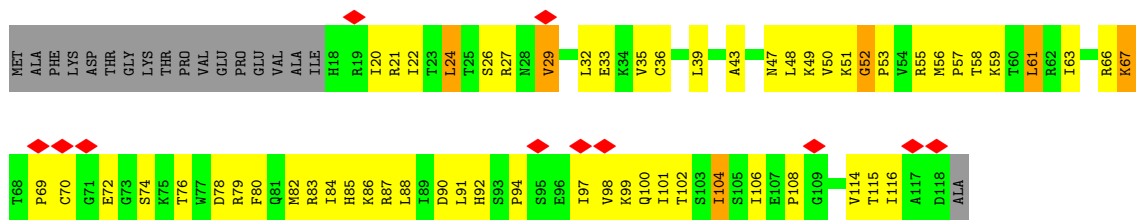




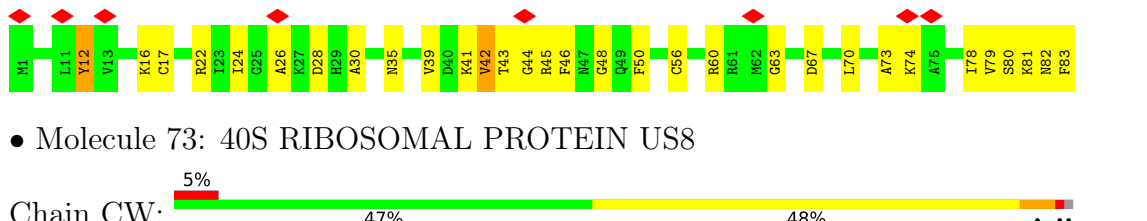
• Molecule 70: 40S RIBOSOMAL PROTEIN ES19



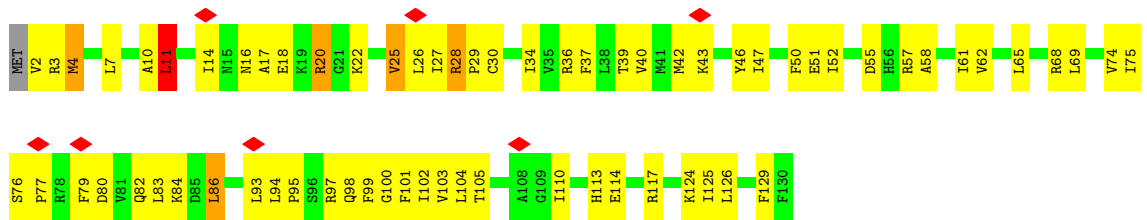
• Molecule 71: 40S RIBOSOMAL PROTEIN US10



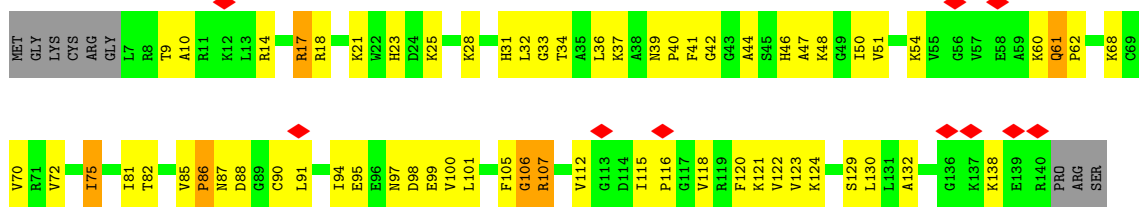
• Molecule 72: 40S RIBOSOMAL PROTEIN ES21



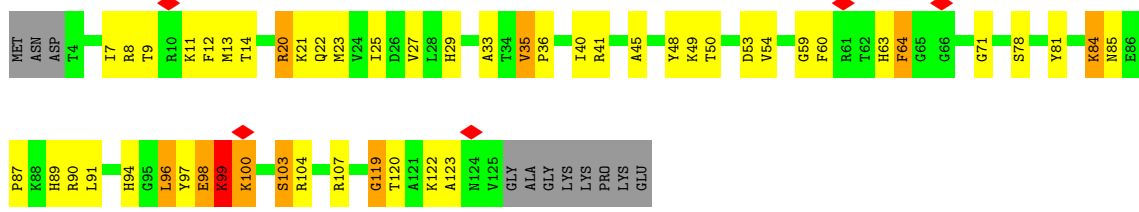
• Molecule 73: 40S RIBOSOMAL PROTEIN US8



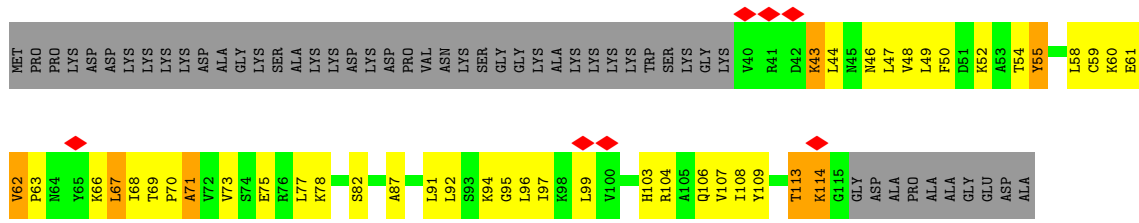
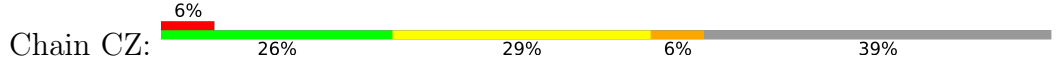
• Molecule 74: 40S RIBOSOMAL PROTEIN US12



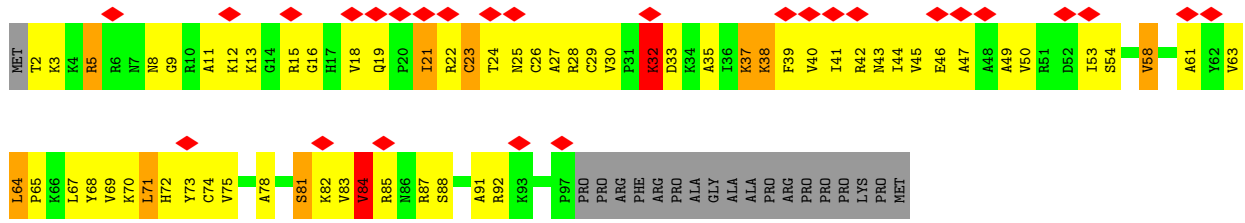
• Molecule 75: 40S RIBOSOMAL PROTEIN ES24



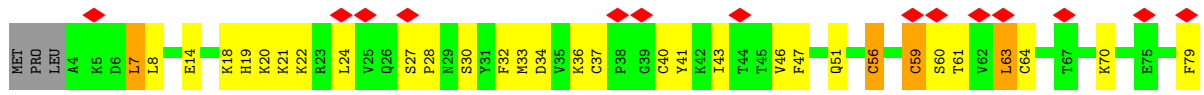
• Molecule 76: 40S RIBOSOMAL PROTEIN ES25

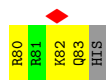


• Molecule 77: 40S RIBOSOMAL PROTEIN ES26

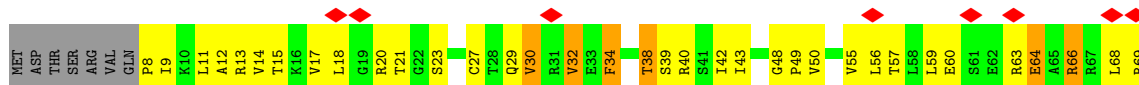


• Molecule 78: 40S RIBOSOMAL PROTEIN ES27

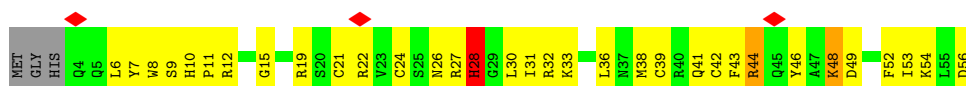




• Molecule 79: 40S RIBOSOMAL PROTEIN ES28



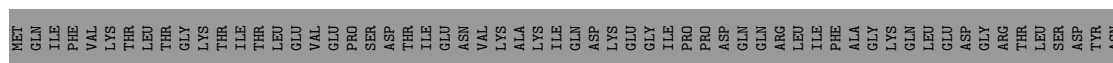
• Molecule 80: 40S RIBOSOMAL PROTEIN US14



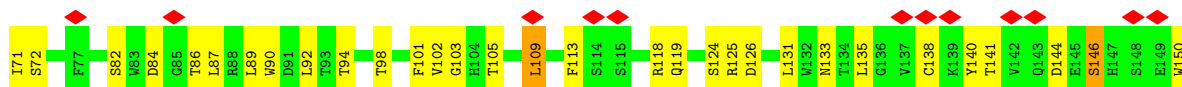
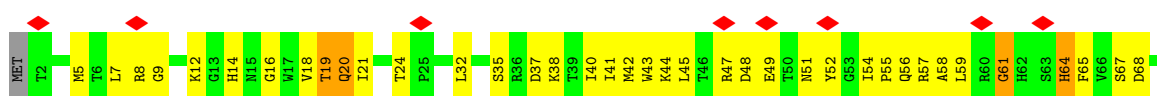
• Molecule 81: 40S RIBOSOMAL PROTEIN ES30

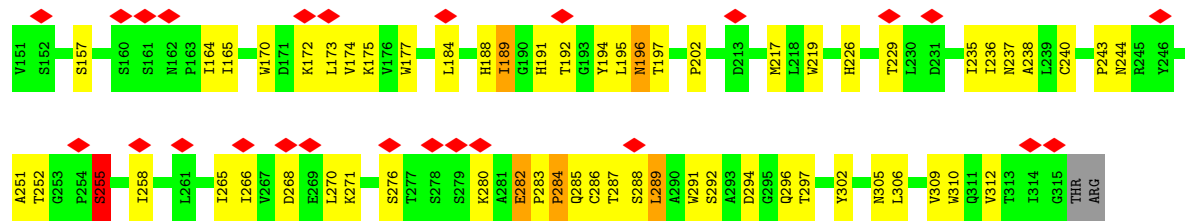


• Molecule 82: 40S RIBOSOMAL PROTEIN ES31



• Molecule 83: 40S RIBOSOMAL PROTEIN RACK1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	541570	Depositor
Resolution determination method	Not provided	
CTF correction method	CTFFIND3	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	194805	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	12450.331	Depositor
Minimum map value	-4370.861	Depositor
Average map value	-6.032	Depositor
Map value standard deviation	1022.400	Depositor
Recommended contour level	2700	Depositor
Map size (\AA)	453.6, 453.6, 453.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.26, 1.26, 1.26	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: GNP, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.50	1/1809 (0.1%)	1.11	22/2819 (0.8%)
2	AB	0.90	11/4926 (0.2%)	1.37	43/6641 (0.6%)
3	AC	0.94	2/6230 (0.0%)	1.49	102/9712 (1.1%)
4	A2	0.34	12/86672 (0.0%)	0.66	28/135198 (0.0%)
5	A3	0.30	0/3723	0.62	2/5800 (0.0%)
6	A4	0.31	0/2836	0.67	1/4421 (0.0%)
7	BA	0.68	1/1926 (0.1%)	1.09	3/2583 (0.1%)
8	BB	0.72	2/3258 (0.1%)	1.12	10/4361 (0.2%)
9	BC	0.76	1/2943 (0.0%)	1.16	18/3953 (0.5%)
10	BD	0.78	6/2407 (0.2%)	1.11	12/3221 (0.4%)
11	BE	0.82	1/1312 (0.1%)	1.18	9/1763 (0.5%)
12	BF	0.68	0/1986	1.12	10/2644 (0.4%)
13	BG	0.76	1/1914 (0.1%)	1.19	14/2578 (0.5%)
14	BH	0.64	0/1555	1.10	4/2089 (0.2%)
15	BI	0.68	0/1643	1.15	13/2194 (0.6%)
16	BJ	0.78	0/1386	1.18	9/1852 (0.5%)
17	BL	0.82	6/1647 (0.4%)	1.18	14/2205 (0.6%)
18	BM	0.79	1/1162 (0.1%)	1.12	1/1556 (0.1%)
19	BN	0.68	0/1754	1.07	10/2348 (0.4%)
20	BO	0.72	2/1639 (0.1%)	1.15	11/2193 (0.5%)
21	BP	0.67	1/1260 (0.1%)	1.09	2/1691 (0.1%)
22	BQ	0.70	0/1518	1.15	8/2026 (0.4%)
23	BR	0.67	1/1542 (0.1%)	1.08	6/2037 (0.3%)
24	BS	0.70	0/1479	1.19	15/1985 (0.8%)
25	BT	0.74	0/1326	1.21	14/1770 (0.8%)
26	BU	0.74	1/841 (0.1%)	1.16	7/1128 (0.6%)
27	BV	0.68	1/978 (0.1%)	1.03	0/1312
28	BW	0.64	1/542 (0.2%)	0.98	2/722 (0.3%)
29	BX	0.65	0/993	1.12	4/1334 (0.3%)
30	BY	0.74	1/1082 (0.1%)	1.17	5/1441 (0.3%)
31	BZ	0.74	0/1138	1.25	5/1517 (0.3%)
32	Ba	0.72	0/1191	1.11	4/1591 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bb	0.72	1/570 (0.2%)	1.10	1/752 (0.1%)
34	Bc	0.72	1/813 (0.1%)	1.05	3/1091 (0.3%)
35	Bd	0.70	0/920	1.06	2/1238 (0.2%)
36	Be	0.71	1/1071 (0.1%)	1.12	5/1428 (0.4%)
37	Bf	0.75	1/885 (0.1%)	1.22	10/1185 (0.8%)
38	Bg	0.74	1/917 (0.1%)	1.15	4/1222 (0.3%)
39	Bh	0.63	0/1023	1.03	1/1351 (0.1%)
40	Bi	0.70	1/793 (0.1%)	1.18	6/1048 (0.6%)
41	Bj	0.77	1/704 (0.1%)	1.16	4/931 (0.4%)
42	Bk	0.72	0/575	1.18	5/761 (0.7%)
43	Bl	0.66	0/454	1.04	2/599 (0.3%)
44	Bm	0.69	0/435	1.22	3/575 (0.5%)
45	Bn	0.62	0/241	0.85	0/305
46	Bo	0.70	0/885	1.14	4/1166 (0.3%)
47	Bp	0.64	0/718	0.97	1/953 (0.1%)
48	Bt	0.78	1/1058 (0.1%)	1.22	7/1416 (0.5%)
49	Bu	0.69	0/1639	1.12	6/2222 (0.3%)
50	C1	0.31	0/41550	0.66	11/64763 (0.0%)
51	CA	0.89	4/1756 (0.2%)	1.16	11/2386 (0.5%)
52	CB	0.83	0/1756	1.20	11/2350 (0.5%)
53	CC	0.69	0/1761	1.10	5/2379 (0.2%)
54	CD	0.63	0/1672	1.15	8/2250 (0.4%)
55	CE	0.72	0/2072	1.16	10/2793 (0.4%)
56	CF	0.68	0/1507	1.15	10/2026 (0.5%)
57	CG	0.77	1/1907 (0.1%)	1.22	11/2538 (0.4%)
58	CH	0.75	0/1558	1.26	12/2087 (0.6%)
59	CI	0.75	0/1724	1.12	6/2298 (0.3%)
60	CJ	0.74	0/1520	1.25	13/2030 (0.6%)
61	CK	0.77	0/815	1.10	5/1101 (0.5%)
62	CL	0.69	0/1220	1.16	8/1633 (0.5%)
63	CM	0.74	0/941	1.19	3/1264 (0.2%)
64	CN	0.69	0/1231	1.21	12/1656 (0.7%)
65	CO	0.73	0/1036	1.16	6/1391 (0.4%)
66	CP	0.66	0/1000	1.07	2/1335 (0.1%)
67	CQ	0.69	0/1125	1.10	3/1506 (0.2%)
68	CR	0.69	0/904	1.12	6/1208 (0.5%)
69	CS	0.69	0/1190	1.13	5/1594 (0.3%)
70	CT	0.69	0/1131	1.10	3/1515 (0.2%)
71	CU	0.75	0/813	1.17	3/1092 (0.3%)
72	CV	0.71	0/643	1.16	2/860 (0.2%)
73	CW	0.69	0/1050	1.12	6/1406 (0.4%)
74	CX	0.76	0/1063	1.11	1/1421 (0.1%)
75	CY	0.71	0/1019	1.12	5/1354 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	CZ	0.68	0/611	1.14	3/820 (0.4%)
77	Ca	0.78	0/778	1.19	7/1041 (0.7%)
78	Cb	0.70	0/637	1.09	2/854 (0.2%)
79	Cc	0.71	0/492	1.15	5/657 (0.8%)
80	Cd	0.73	0/454	1.10	1/603 (0.2%)
81	Ce	0.70	0/417	1.09	0/548
82	Cf	0.76	0/507	1.34	5/673 (0.7%)
83	Cg	0.69	0/2497	1.06	7/3399 (0.2%)
All	All	0.55	66/240676 (0.0%)	0.91	680/353759 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	14
3	AC	0	105
4	A2	0	35
5	A3	0	2
50	C1	0	24
All	All	0	180

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A2	1701	C	O5'-C5'	16.75	1.67	1.42
4	A2	1701	C	C5'-C4'	14.81	1.73	1.51
4	A2	1673	C	C3'-O3'	13.66	1.63	1.43
4	A2	1673	C	O3'-P	11.31	1.78	1.61
4	A2	1673	C	O5'-C5'	10.41	1.58	1.42

The worst 5 of 680 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A2	1701	C	C2'-C3'-O3'	-18.43	86.06	113.70
1	AA	6	G	C4'-C3'-O3'	16.86	134.69	109.40
4	A2	1701	C	C4'-C3'-O3'	16.23	137.35	113.00
3	AC	63	U	C4'-C3'-O3'	15.95	133.32	109.40
4	A2	1701	C	O4'-C4'-C3'	-15.17	88.83	104.00

There are no chirality outliers.

5 of 180 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	1105	PRO	Mainchain
2	AB	834	HIS	Peptide
2	AB	836	LYS	Peptide
2	AB	880	GLN	Mainchain
2	AB	899	ILE	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1619	0	814	330	0
2	AB	4846	0	4956	1452	0
3	AC	5574	0	2810	370	0
4	A2	77488	0	39154	7612	0
5	A3	3334	0	1693	299	0
6	A4	2538	0	1286	249	0
7	BA	1888	0	1983	135	0
8	BB	3190	0	3327	188	0
9	BC	2889	0	3064	272	0
10	BD	2362	0	2385	141	0
11	BE	1287	0	1398	161	0
12	BF	1950	0	2093	142	0
13	BG	1881	0	2018	123	0
14	BH	1536	0	1611	103	0
15	BI	1605	0	1651	80	0
16	BJ	1363	0	1397	123	0
17	BL	1617	0	1725	119	0
18	BM	1139	0	1204	119	0
19	BN	1709	0	1761	89	0
20	BO	1607	0	1745	126	0
21	BP	1234	0	1263	71	0
22	BQ	1494	0	1612	105	0
23	BR	1526	0	1681	103	0
24	BS	1439	0	1472	89	0
25	BT	1298	0	1366	118	0
26	BU	827	0	852	23	0
27	BV	964	0	1026	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	BW	529	0	541	31	0
29	BX	976	0	1053	47	0
30	BY	1065	0	1145	86	0
31	BZ	1115	0	1194	98	0
32	Ba	1162	0	1213	83	0
33	Bb	560	0	590	43	0
34	Bc	802	0	845	89	0
35	Bd	905	0	947	27	0
36	Be	1053	0	1144	51	0
37	Bf	866	0	904	103	0
38	Bg	907	0	1002	104	0
39	Bh	1015	0	1148	47	0
40	Bi	783	0	862	54	0
41	Bj	690	0	719	55	0
42	Bk	569	0	637	33	0
43	Bl	444	0	483	14	0
44	Bm	429	0	466	24	0
45	Bn	240	0	287	39	0
46	Bo	871	0	943	47	0
47	Bp	708	0	760	41	0
48	Bt	1043	0	1120	122	0
49	Bu	1622	0	1563	153	0
50	C1	37159	0	18774	4092	0
51	CA	1719	0	1717	130	0
52	CB	1729	0	1803	145	0
53	CC	1724	0	1808	118	0
54	CD	1646	0	1737	90	0
55	CE	2031	0	2138	116	0
56	CF	1486	0	1543	127	0
57	CG	1884	0	2044	160	0
58	CH	1535	0	1632	132	0
59	CI	1695	0	1783	126	0
60	CJ	1495	0	1615	96	0
61	CK	791	0	811	53	0
62	CL	1199	0	1269	72	0
63	CM	931	0	961	45	0
64	CN	1207	0	1292	96	0
65	CO	1023	0	1050	97	0
66	CP	981	0	1026	54	0
67	CQ	1108	0	1172	93	0
68	CR	893	0	946	66	0
69	CS	1172	0	1229	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	CT	1112	0	1146	116	0
71	CU	803	0	866	81	0
72	CV	636	0	637	43	0
73	CW	1033	0	1080	68	0
74	CX	1046	0	1110	78	0
75	CY	1002	0	1075	67	0
76	CZ	605	0	665	56	0
77	Ca	767	0	816	104	0
78	Cb	625	0	640	55	0
79	Cc	490	0	520	50	0
80	Cd	444	0	442	54	0
81	Ce	412	0	463	34	0
82	Cf	497	0	497	32	0
83	Cg	2440	0	2396	119	0
84	AB	32	0	13	7	0
85	AB	1	0	0	0	0
All	All	223911	0	165629	18148	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 47.

The worst 5 of 18148 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:1116:ARG:CD	50:C1:488:U:C6	1.76	1.69
2:AB:1116:ARG:CB	50:C1:488:U:C5	1.78	1.62
1:AA:75:C:H5	2:AB:1316:PHE:CD2	1.14	1.62
2:AB:817:GLU:CB	2:AB:1172:VAL:HG12	1.27	1.60
2:AB:927:ARG:HH12	2:AB:1158:GLY:CA	1.16	1.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	605/627 (96%)	523 (86%)	50 (8%)	32 (5%)	1	15
7	BA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	10	44
8	BB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	2	20
9	BC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	2	18
10	BD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	7	36
11	BE	156/158 (99%)	141 (90%)	8 (5%)	7 (4%)	2	17
12	BF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	7	36
13	BG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	2	19
14	BH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	7	38
15	BI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	7	38
16	BJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	11
17	BL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	1	14
18	BM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	9	40
19	BN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40
20	BO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	8	40
21	BP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	31
22	BQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	3	21
23	BR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	7	36
24	BS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	20
25	BT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	6	32
26	BU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
27	BV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	7	38
28	BW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
29	BX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
30	BY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	4	27
31	BZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	3	23
32	Ba	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	21
33	Bb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	13
34	Bc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	6	31
35	Bd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Be	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	4	27
37	Bf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	16
38	Bg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	20
39	Bh	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	4	26
40	Bi	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	13
41	Bj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	4	27
42	Bk	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	8	40
43	Bl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	30
44	Bm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
45	Bn	23/25 (92%)	23 (100%)	0	0	100	100
46	Bo	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	6	32
47	Bp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	21
48	Bt	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	1	15
49	Bu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	9	40
51	CA	216/263 (82%)	209 (97%)	5 (2%)	2 (1%)	14	51
52	CB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	9
53	CC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	5	28
54	CD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	4	27
55	CE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6	31
56	CF	186/204 (91%)	163 (88%)	12 (6%)	11 (6%)	1	13
57	CG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	2	19
58	CH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	5	30
59	CI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	21
60	CJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	7	36
61	CK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	10
62	CL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	2	17
63	CM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	1	15
64	CN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	21
65	CO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	5	29
66	CP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	17
67	CQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	CR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	6	32
69	CS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	14
70	CT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	9	40
71	CU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	12	49
72	CV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	4	26
73	CW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	7	38
74	CX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	1	15
75	CY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	3	21
76	CZ	74/125 (59%)	71 (96%)	0	3 (4%)	2	18
77	Ca	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	17
78	Cb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
79	Cc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	21
80	Cd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
81	Ce	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	6	31
82	Cf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
83	Cg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	5	29
All	All	11795/13363 (88%)	11000 (93%)	439 (4%)	356 (3%)	5	23

5 of 356 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	835	SER
2	AB	838	VAL
2	AB	843	LEU
2	AB	897	LYS
2	AB	931	SER

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	
2	AB	540/552 (98%)	515 (95%)	25 (5%)	24	45
7	BA	189/199 (95%)	182 (96%)	7 (4%)	30	51
8	BB	344/349 (99%)	322 (94%)	22 (6%)	16	37
9	BC	302/348 (87%)	283 (94%)	19 (6%)	16	37
10	BD	244/250 (98%)	237 (97%)	7 (3%)	37	58
11	BE	143/143 (100%)	133 (93%)	10 (7%)	14	35
12	BF	203/215 (94%)	195 (96%)	8 (4%)	28	49
13	BG	199/223 (89%)	190 (96%)	9 (4%)	24	46
14	BH	171/171 (100%)	165 (96%)	6 (4%)	32	53
15	BI	170/181 (94%)	161 (95%)	9 (5%)	20	41
16	BJ	143/149 (96%)	137 (96%)	6 (4%)	26	48
17	BL	167/177 (94%)	157 (94%)	10 (6%)	17	39
18	BM	118/161 (73%)	113 (96%)	5 (4%)	26	48
19	BN	172/172 (100%)	167 (97%)	5 (3%)	37	58
20	BO	168/174 (97%)	165 (98%)	3 (2%)	51	68
21	BP	133/163 (82%)	126 (95%)	7 (5%)	20	41
22	BQ	162/165 (98%)	157 (97%)	5 (3%)	35	56
23	BR	161/175 (92%)	151 (94%)	10 (6%)	16	38
24	BS	155/157 (99%)	149 (96%)	6 (4%)	28	49
25	BT	139/140 (99%)	135 (97%)	4 (3%)	37	58
26	BU	91/115 (79%)	91 (100%)	0	100	100
27	BV	100/107 (94%)	100 (100%)	0	100	100
28	BW	55/126 (44%)	52 (94%)	3 (6%)	19	41
29	BX	107/133 (80%)	105 (98%)	2 (2%)	50	67
30	BY	119/135 (88%)	114 (96%)	5 (4%)	26	48
31	BZ	118/118 (100%)	114 (97%)	4 (3%)	32	54
32	Ba	120/121 (99%)	115 (96%)	5 (4%)	26	48
33	Bb	58/126 (46%)	57 (98%)	1 (2%)	53	69
34	Bc	88/97 (91%)	87 (99%)	1 (1%)	65	76
35	Bd	100/110 (91%)	97 (97%)	3 (3%)	36	57
36	Be	115/121 (95%)	111 (96%)	4 (4%)	32	53
37	Bf	87/89 (98%)	77 (88%)	10 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Bg	98/100 (98%)	89 (91%)	9 (9%)	8	27
39	Bh	109/110 (99%)	105 (96%)	4 (4%)	30	51
40	Bi	82/89 (92%)	76 (93%)	6 (7%)	13	34
41	Bj	71/80 (89%)	69 (97%)	2 (3%)	38	60
42	Bk	64/65 (98%)	64 (100%)	0	100	100
43	Bl	47/48 (98%)	46 (98%)	1 (2%)	47	65
44	Bm	48/116 (41%)	45 (94%)	3 (6%)	16	37
45	Bn	24/24 (100%)	24 (100%)	0	100	100
46	Bo	94/94 (100%)	90 (96%)	4 (4%)	26	47
47	Bp	74/75 (99%)	72 (97%)	2 (3%)	39	61
48	Bt	113/121 (93%)	108 (96%)	5 (4%)	25	47
49	Bu	177/177 (100%)	161 (91%)	16 (9%)	9	27
51	CA	181/219 (83%)	177 (98%)	4 (2%)	45	64
52	CB	194/231 (84%)	182 (94%)	12 (6%)	16	38
53	CC	188/225 (84%)	179 (95%)	9 (5%)	23	44
54	CD	175/202 (87%)	164 (94%)	11 (6%)	16	37
55	CE	220/225 (98%)	207 (94%)	13 (6%)	18	39
56	CF	158/170 (93%)	152 (96%)	6 (4%)	29	50
57	CG	202/218 (93%)	196 (97%)	6 (3%)	36	57
58	CH	171/174 (98%)	170 (99%)	1 (1%)	78	83
59	CI	179/180 (99%)	167 (93%)	12 (7%)	15	36
60	CJ	160/168 (95%)	152 (95%)	8 (5%)	22	43
61	CK	85/136 (62%)	81 (95%)	4 (5%)	23	45
62	CL	133/142 (94%)	130 (98%)	3 (2%)	44	64
63	CM	102/108 (94%)	96 (94%)	6 (6%)	18	39
64	CN	130/131 (99%)	128 (98%)	2 (2%)	57	72
65	CO	107/119 (90%)	99 (92%)	8 (8%)	12	33
66	CP	107/130 (82%)	103 (96%)	4 (4%)	30	51
67	CQ	115/121 (95%)	111 (96%)	4 (4%)	32	53
68	CR	99/122 (81%)	92 (93%)	7 (7%)	13	35
69	CS	123/132 (93%)	115 (94%)	8 (6%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	CT	113/115 (98%)	106 (94%)	7 (6%)	16	38
71	CU	93/107 (87%)	87 (94%)	6 (6%)	15	37
72	CV	67/67 (100%)	67 (100%)	0	100	100
73	CW	112/113 (99%)	108 (96%)	4 (4%)	31	52
74	CX	108/115 (94%)	104 (96%)	4 (4%)	30	51
75	CY	107/115 (93%)	100 (94%)	7 (6%)	15	37
76	CZ	67/103 (65%)	62 (92%)	5 (8%)	12	33
77	Ca	83/98 (85%)	76 (92%)	7 (8%)	10	30
78	Cb	72/76 (95%)	68 (94%)	4 (6%)	19	40
79	Cc	55/62 (89%)	52 (94%)	3 (6%)	19	41
80	Cd	47/49 (96%)	44 (94%)	3 (6%)	16	37
81	Ce	42/48 (88%)	39 (93%)	3 (7%)	13	35
82	Cf	54/140 (39%)	51 (94%)	3 (6%)	19	40
83	Cg	272/275 (99%)	260 (96%)	12 (4%)	25	47
All	All	10303/11397 (90%)	9834 (95%)	469 (5%)	25	45

5 of 469 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	Bh	49	VAL
78	Cb	59	CYS
52	CB	177	GLN
77	Ca	64	LEU
69	CS	99	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 270 such sidechains are listed below:

Mol	Chain	Res	Type
70	CT	11	GLN
73	CW	56	HIS
80	Cd	26	ASN
21	BP	120	ASN
21	BP	64	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	14 (18%)	1 (1%)
3	AC	259/504 (51%)	142 (54%)	40 (15%)
4	A2	3605/5025 (71%)	2051 (56%)	325 (9%)
5	A3	156/194 (80%)	82 (52%)	6 (3%)
50	C1	1738/1869 (92%)	1042 (59%)	151 (8%)
6	A4	118/121 (97%)	69 (58%)	9 (7%)
All	All	5951/7789 (76%)	3400 (57%)	532 (8%)

5 of 3400 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	17	C
1	AA	18	G
1	AA	19	G
1	AA	20	U

5 of 532 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	C1	1115	U
50	C1	1264	C
50	C1	1114	U
50	C1	1721	U
4	A2	2003	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	GNP	AB	2434	85	34,34,34	1.78	6 (17%)	47,54,54	1.30	5 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	GNP	AB	2434	85	-	2/18/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	AB	2434	GNP	PA-O3A	-6.53	1.52	1.59
84	AB	2434	GNP	C2'-C1'	-3.04	1.43	1.53
84	AB	2434	GNP	PB-O3A	-2.67	1.55	1.59
84	AB	2434	GNP	C4-N3	2.60	1.40	1.34
84	AB	2434	GNP	PB-N3B	-2.48	1.56	1.63

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	AB	2434	GNP	O1B-PB-N3B	3.40	116.78	111.77
84	AB	2434	GNP	O2A-PA-O3A	3.08	115.59	107.27
84	AB	2434	GNP	O2G-PG-O1G	2.43	119.53	113.45
84	AB	2434	GNP	C1'-N9-C8	2.23	133.07	126.73
84	AB	2434	GNP	O3A-PB-N3B	2.21	112.71	106.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

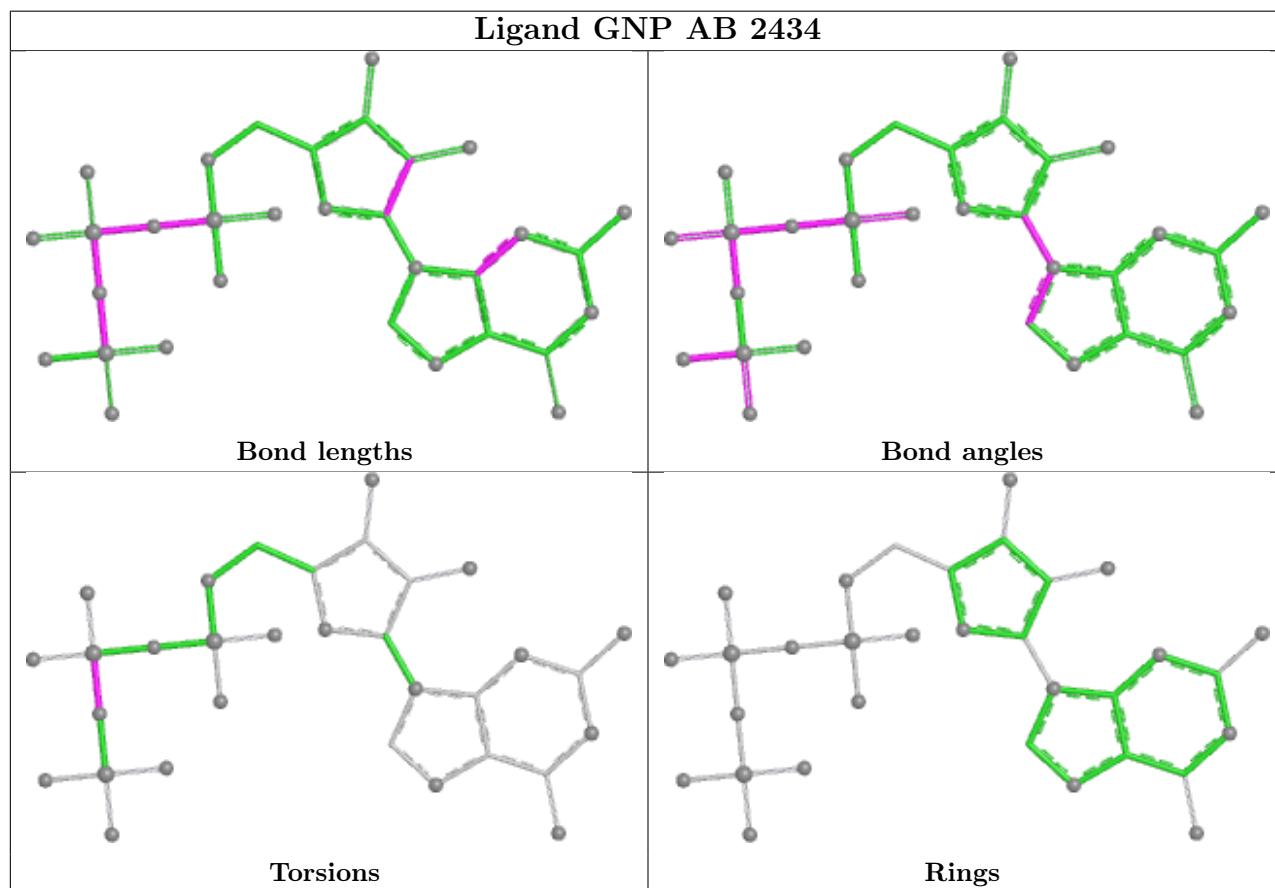
Mol	Chain	Res	Type	Atoms
84	AB	2434	GNP	PG-N3B-PB-O1B
84	AB	2434	GNP	PG-N3B-PB-O3A

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	AB	2434	GNP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

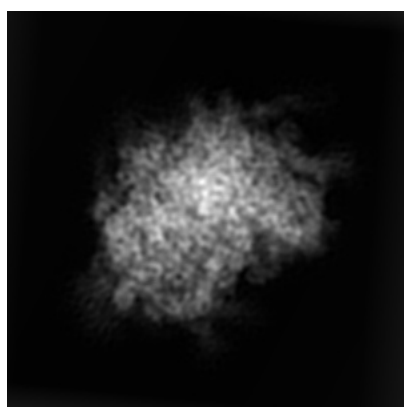
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2683. These allow visual inspection of the internal detail of the map and identification of artifacts.

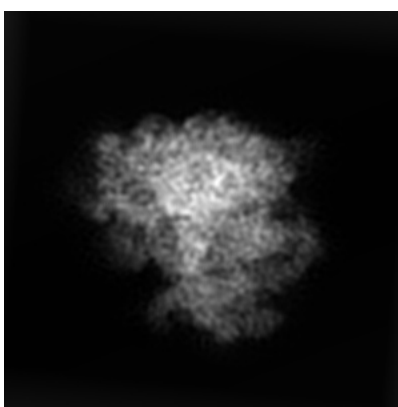
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

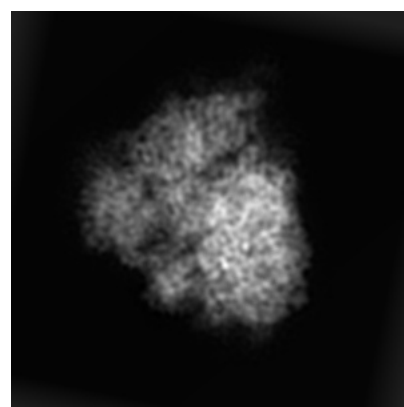
6.1.1 Primary map



X



Y

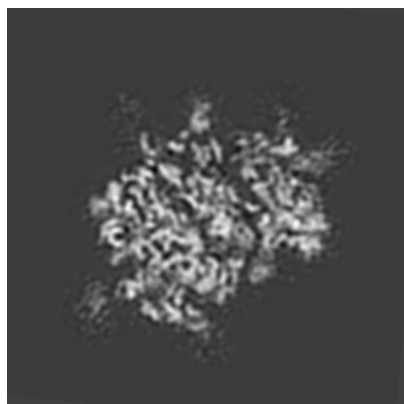


Z

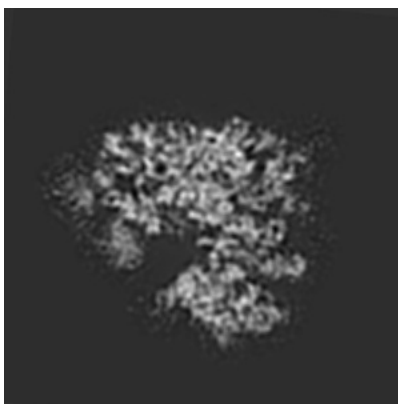
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

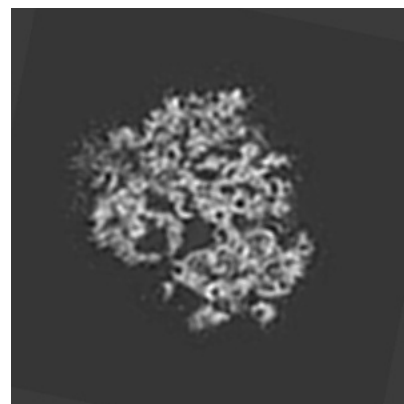
6.2.1 Primary map



X Index: 180



Y Index: 180

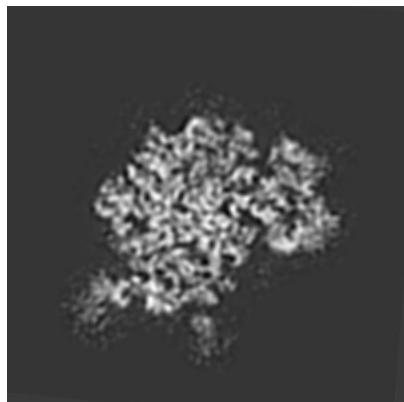


Z Index: 180

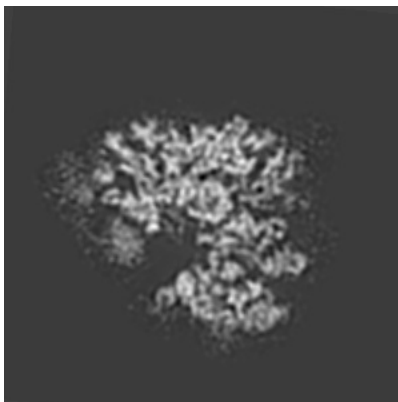
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

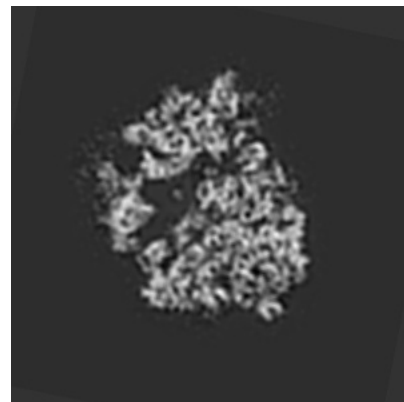
6.3.1 Primary map



X Index: 192



Y Index: 182

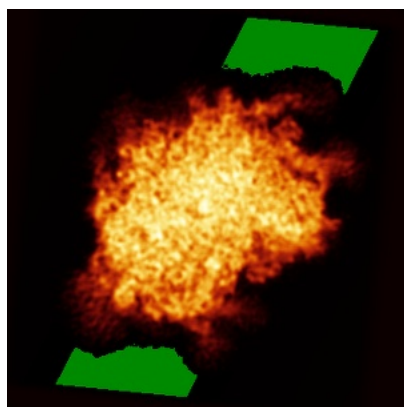


Z Index: 167

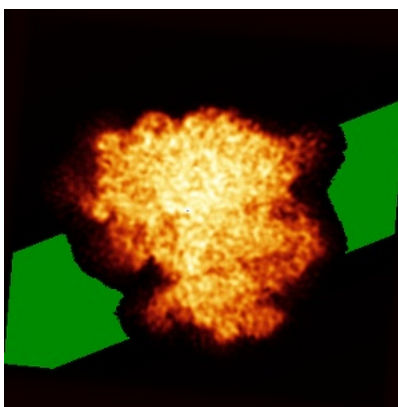
The images above show the largest variance slices of the map in three orthogonal directions.

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

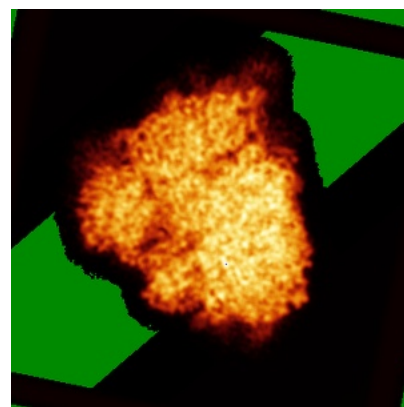
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2700.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

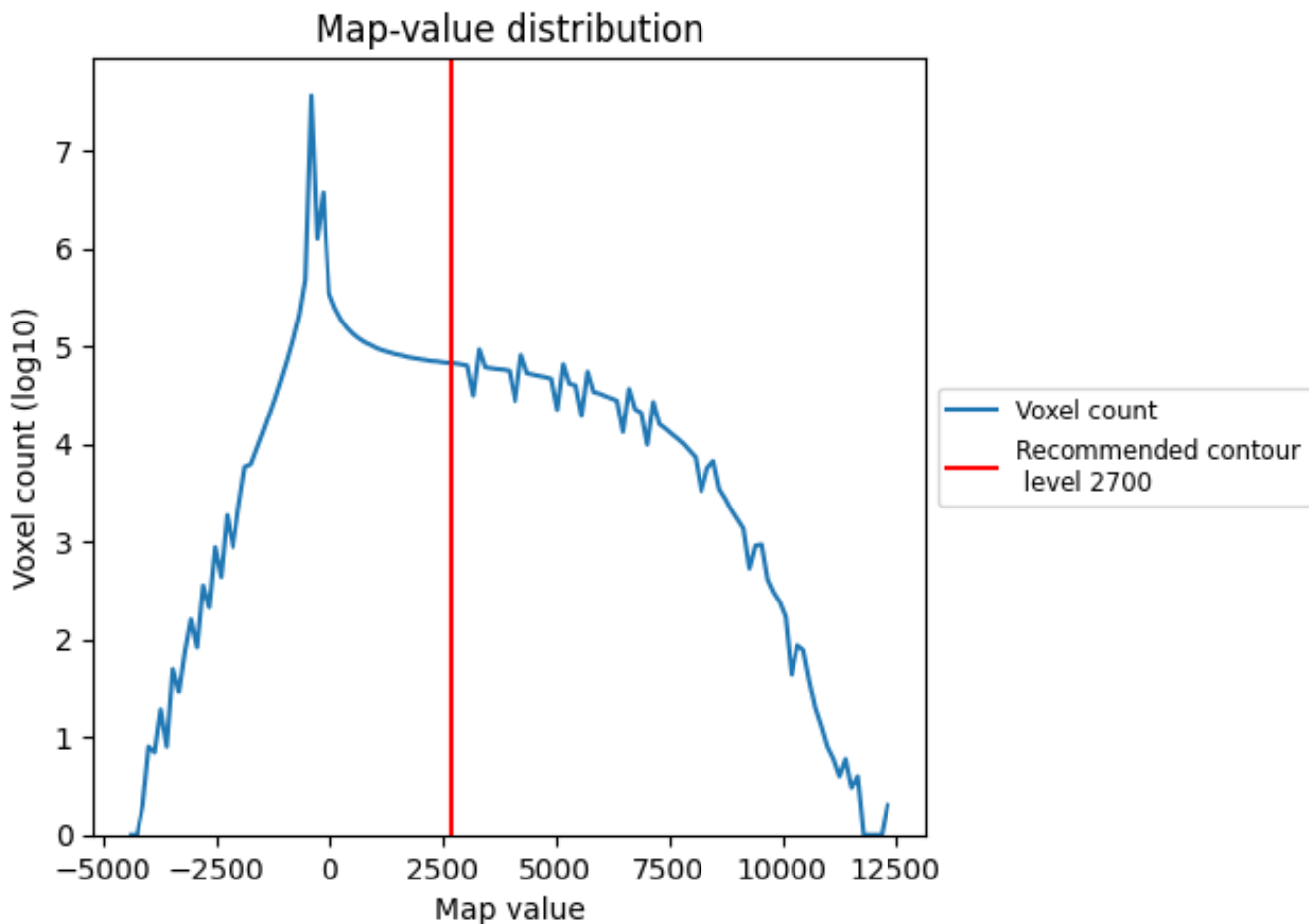
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

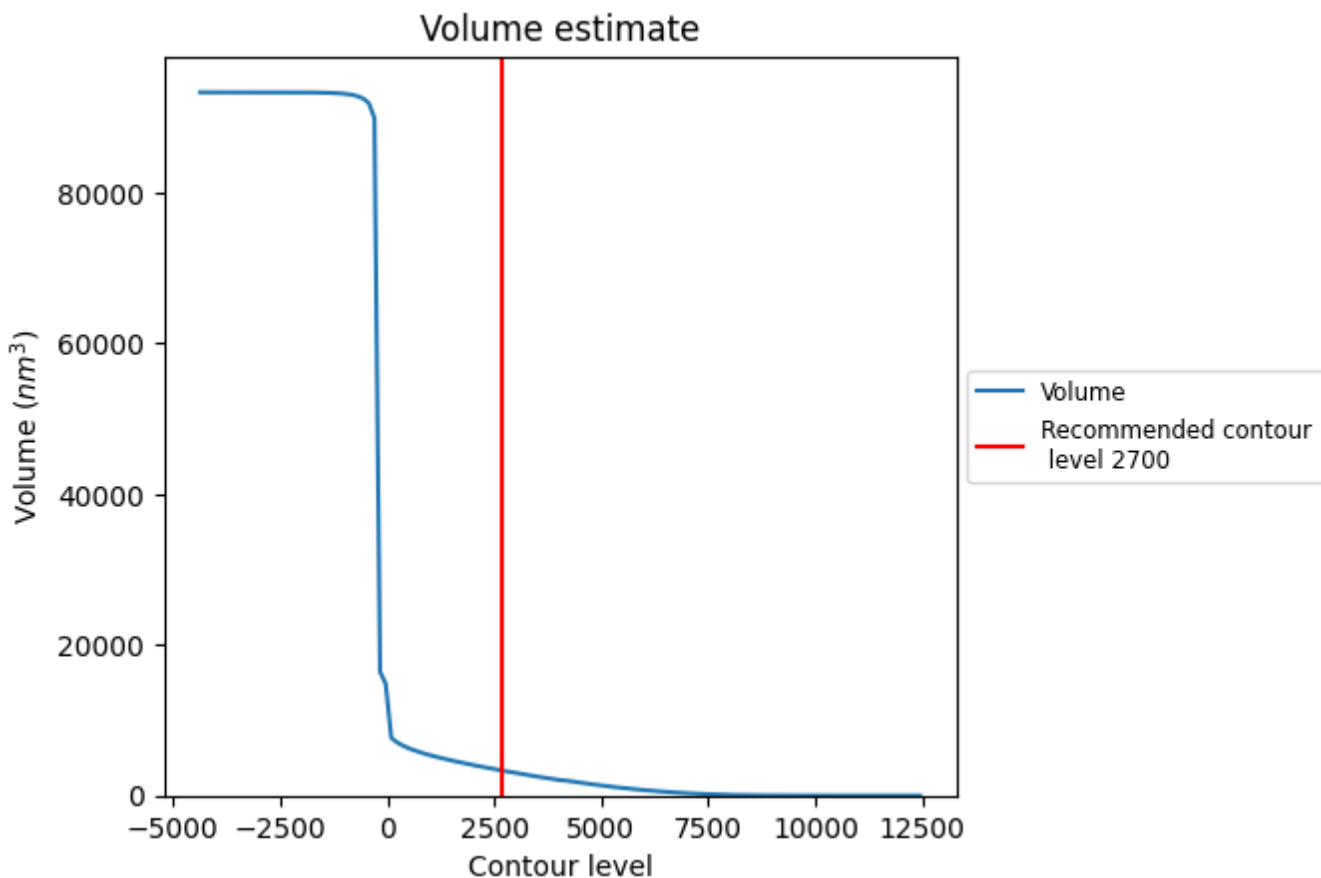
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

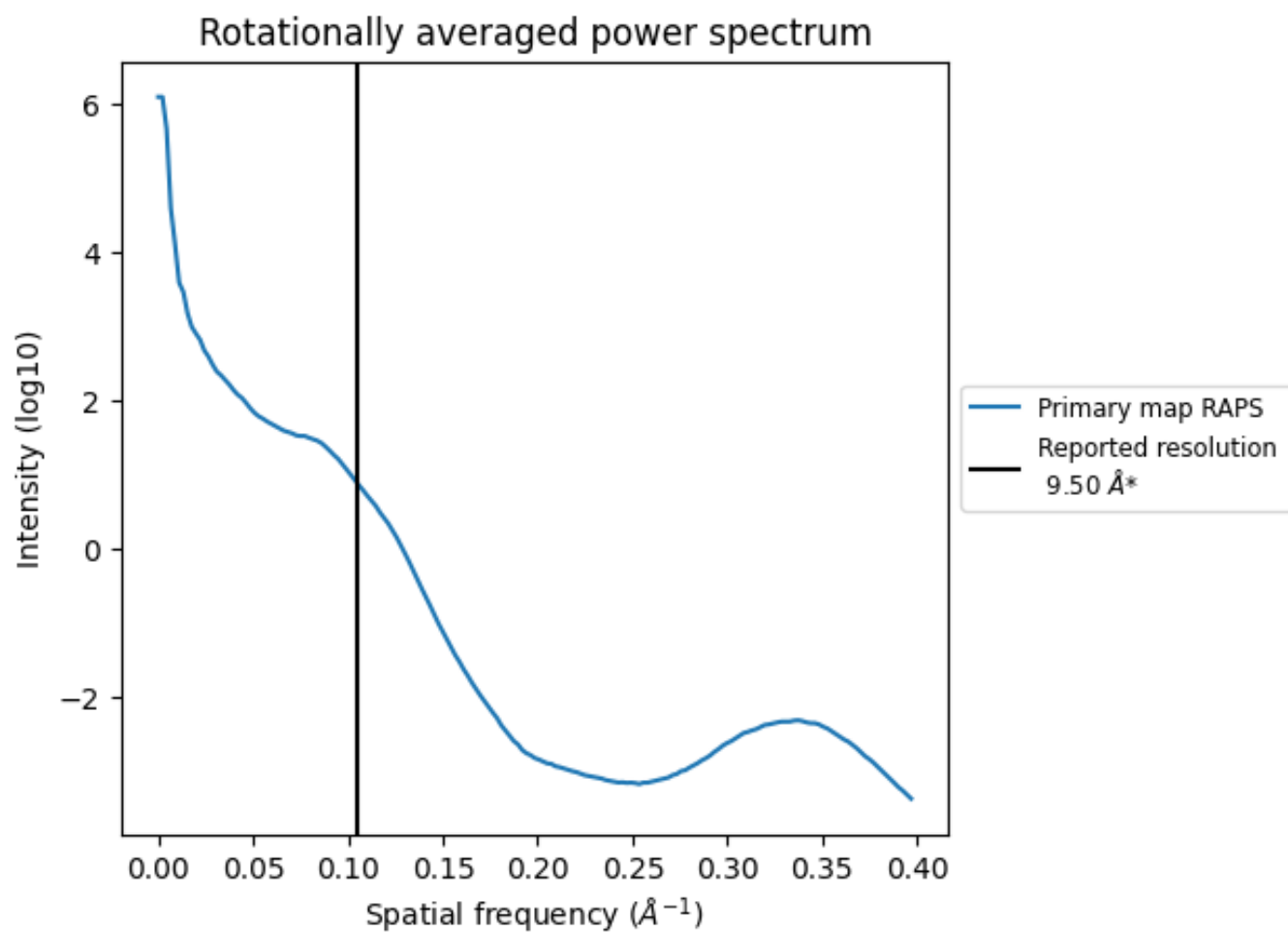
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3306 nm³; this corresponds to an approximate mass of 2986 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 0.105 Å⁻¹

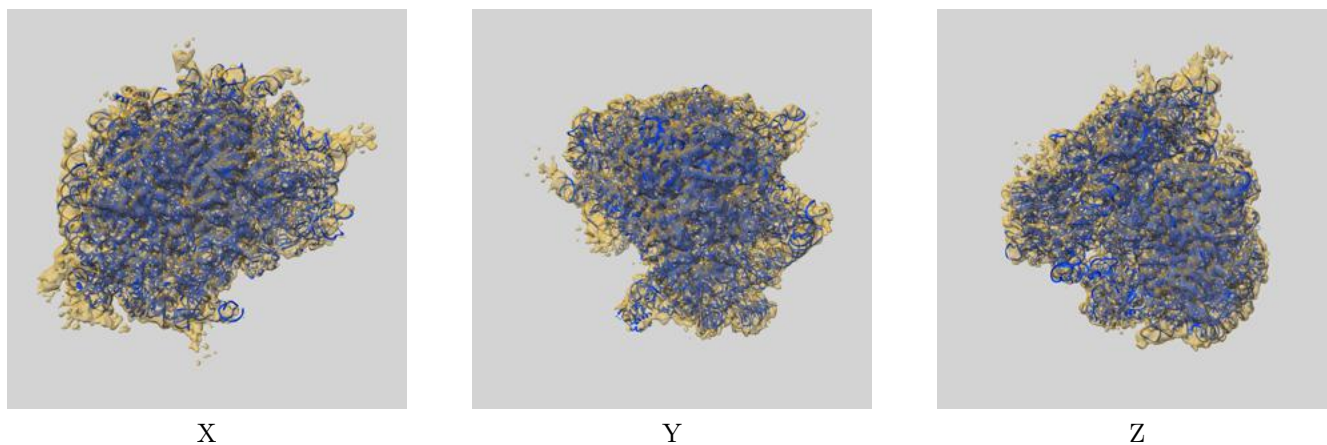
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

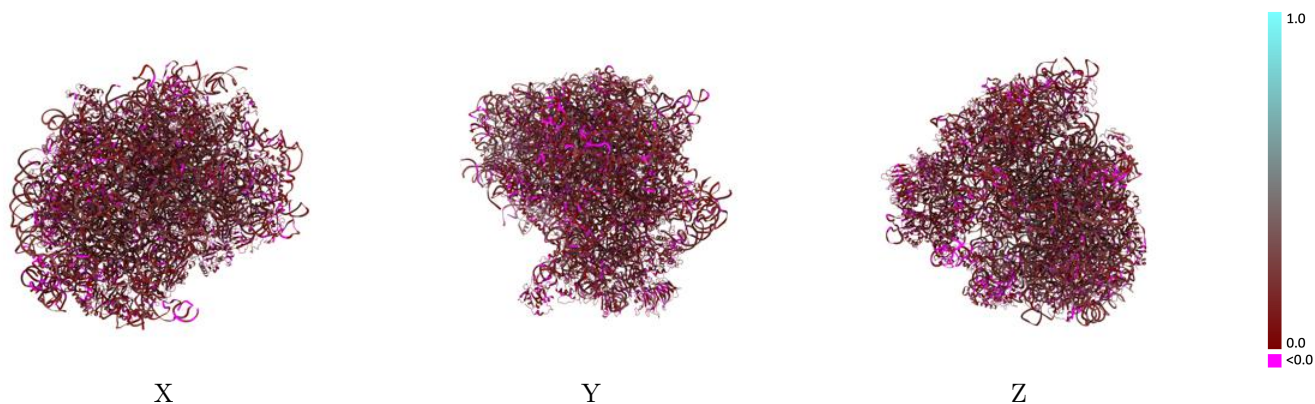
This section contains information regarding the fit between EMDB map EMD-2683 and PDB model 4UJC. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



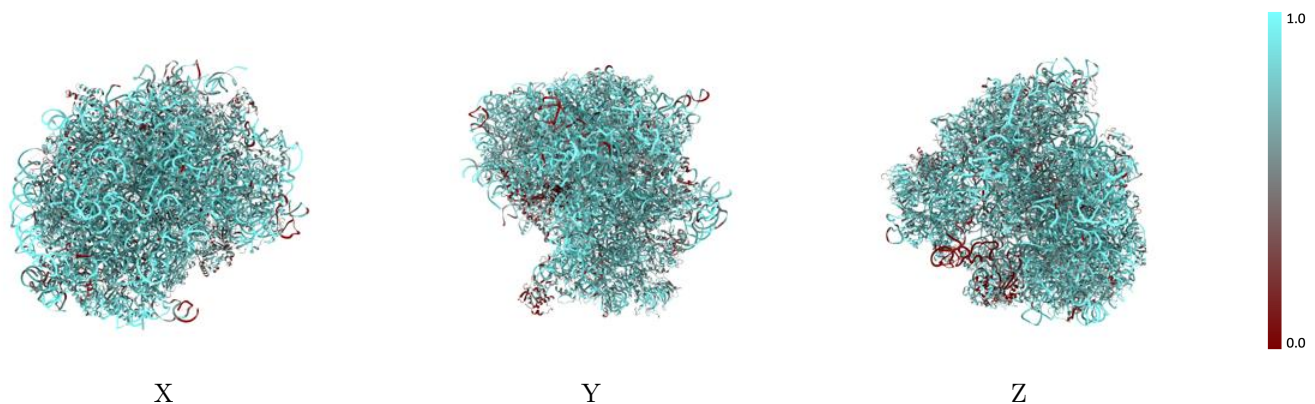
The images above show the 3D surface view of the map at the recommended contour level 2700.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



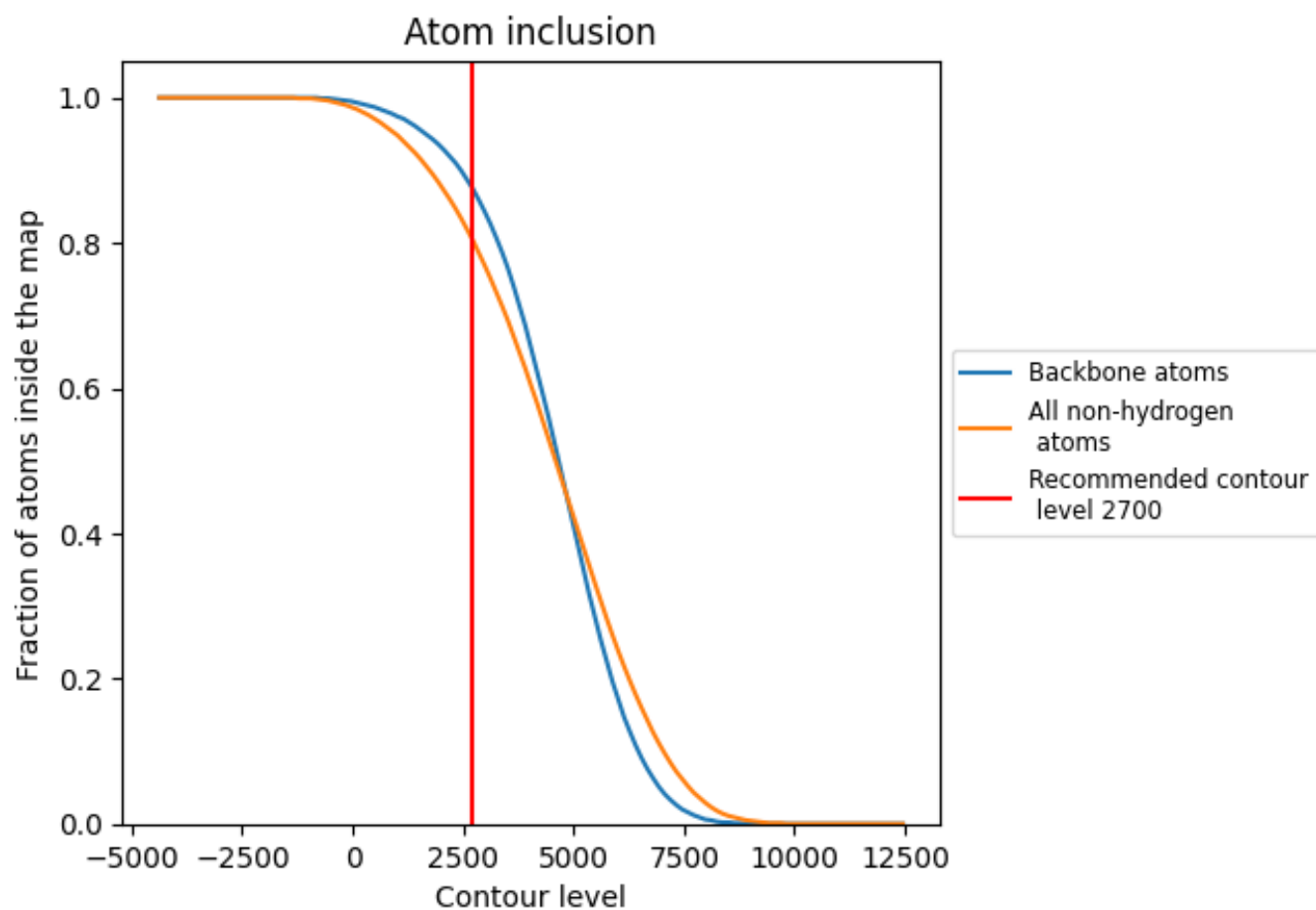
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2700).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% 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 (2700) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.1400
A2	 0.9060	 0.1710
A3	 0.9320	 0.1780
A4	 0.9680	 0.1840
AA	 0.7430	 0.1320
AB	 0.3160	 0.0780
AC	 0.5430	 0.0940
BA	 0.6920	 0.1010
BB	 0.7540	 0.1020
BC	 0.7240	 0.0950
BD	 0.8020	 0.1160
BE	 0.6890	 0.1040
BF	 0.7250	 0.1010
BG	 0.6740	 0.1210
BH	 0.7570	 0.1210
BI	 0.7440	 0.1220
BJ	 0.7560	 0.0980
BL	 0.6860	 0.1040
BM	 0.8050	 0.1400
BN	 0.7750	 0.0860
BO	 0.7240	 0.1160
BP	 0.7990	 0.0960
BQ	 0.7080	 0.1120
BR	 0.7490	 0.1200
BS	 0.7280	 0.1100
BT	 0.7080	 0.1100
BU	 0.6070	 0.1230
BV	 0.6880	 0.1100
BW	 0.7880	 0.1160
BX	 0.7170	 0.1160
BY	 0.7960	 0.1030
BZ	 0.7170	 0.1140
Ba	 0.7360	 0.0960
Bb	 0.7130	 0.1000
Bc	 0.7190	 0.1300

















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Chain	Atom inclusion	Q-score
Bd	 0.7670	 0.1100
Be	 0.7450	 0.1190
Bf	 0.7440	 0.0770
Bg	 0.7090	 0.0940
Bh	 0.7430	 0.1200
Bi	 0.7420	 0.1290
Bj	 0.8140	 0.0930
Bk	 0.6930	 0.1150
Bl	 0.7590	 0.1200
Bm	 0.8240	 0.1110
Bn	 0.7310	 0.1120
Bo	 0.6940	 0.1080
Bp	 0.6930	 0.1200
Bt	 0.7010	 0.0830
Bu	 0.0870	 0.0300
C1	 0.9070	 0.1630
CA	 0.7260	 0.1290
CB	 0.7160	 0.1370
CC	 0.7200	 0.1190
CD	 0.6710	 0.1230
CE	 0.7520	 0.1130
CF	 0.7560	 0.1170
CG	 0.7610	 0.0990
CH	 0.5940	 0.1170
CI	 0.7240	 0.0950
CJ	 0.7500	 0.1110
CK	 0.7220	 0.0950
CL	 0.6920	 0.1140
CM	 0.3020	 0.0620
CN	 0.6650	 0.1120
CO	 0.7080	 0.1080
CP	 0.7370	 0.1200
CQ	 0.7570	 0.0990
CR	 0.6400	 0.1030
CS	 0.7330	 0.1030
CT	 0.8030	 0.1020
CU	 0.6780	 0.1020
CV	 0.7120	 0.1300
CW	 0.7350	 0.1170
CX	 0.7330	 0.1230
CY	 0.7880	 0.1010
CZ	 0.7150	 0.1280

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Chain	Atom inclusion	Q-score
Ca	 0.5990	 0.0860
Cb	 0.6720	 0.1070
Cc	 0.6680	 0.1080
Cd	 0.8150	 0.0830
Ce	 0.7050	 0.1180
Cf	 0.3500	 0.0560
Cg	 0.7470	 0.1030