



## wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 02:09 am GMT

PDB ID : 4UJC  
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](mailto: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>.

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

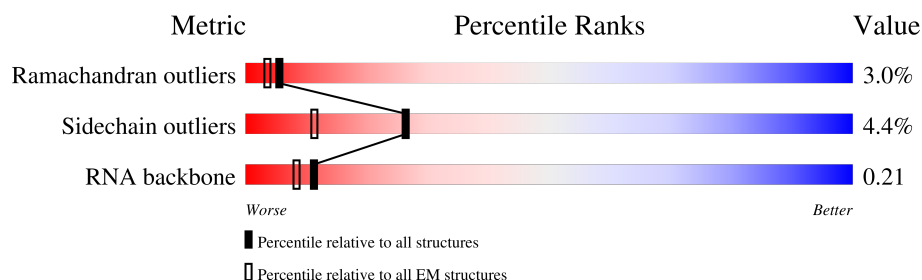
EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 1 Overall quality at a glance

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

The reported resolution of this entry is 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	<div> <div>12%</div> <div>67%</div> <div>32%</div> <div>.</div> </div>
2	AB	627	<div> <div>62%</div> <div>85%</div> <div>10%</div> <div>..</div> </div>
3	AC	504	<div> <div>19%</div> <div>15%</div> <div>21%</div> <div>12%</div> <div>48%</div> </div>
4	A2	5025	<div> <div>30%</div> <div>41%</div> <div>.</div> <div>28%</div> </div>
5	A3	194	<div> <div>38%</div> <div>41%</div> <div>.</div> <div>19%</div> </div>
6	A4	121	<div> <div>40%</div> <div>56%</div> <div>..</div> </div>
7	BA	257	<div> <div>12%</div> <div>93%</div> <div>..</div> </div>
8	BB	403	<div> <div>8%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	BC	427	
10	BD	297	
11	BE	158	
12	BF	248	
13	BG	266	
14	BH	192	
15	BI	214	
16	BJ	178	
17	BL	211	
18	BM	215	
19	BN	204	
20	BO	203	
21	BP	184	
22	BQ	188	
23	BR	196	
24	BS	176	
25	BT	160	
26	BU	128	
27	BV	140	
28	BW	157	
29	BX	156	
30	BY	145	
31	BZ	136	
32	Ba	148	
33	Bb	159	

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Mol	Chain	Length	Quality of chain
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	
54	CD	243	
55	CE	263	
56	CF	204	
57	CG	249	
58	CH	194	

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Mol	Chain	Length	Quality of chain
59	CI	208	
60	CJ	194	
61	CK	165	
62	CL	158	
63	CM	132	
64	CN	151	
65	CO	151	
66	CP	145	
67	CQ	146	
68	CR	135	
69	CS	152	
70	CT	145	
71	CU	119	
72	CV	83	
73	CW	130	
74	CX	143	
75	CY	133	
76	CZ	125	
77	Ca	115	
78	Cb	84	
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
1	AA	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 2 is a protein called EIF5B.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
21	BP	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
35	Bd	109	Total	C	N	O	S	0	0
			905	570	174	159	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
56	CF	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
70	CT	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

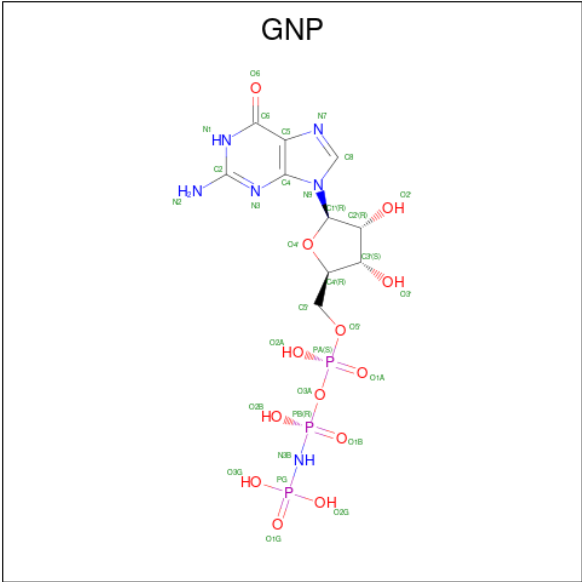
- Molecule 82 is a protein called 40S RIBOSOMAL PROTEIN ES31.

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 (three-letter code: GNP) (formula:  $C_{10}H_{17}N_6O_{13}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
84	AB	1	Total	C	N	O	P	0
			32	10	6	13	3	

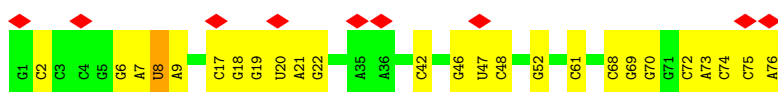
- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	AB	1	Total	Mg	0
			1	1	

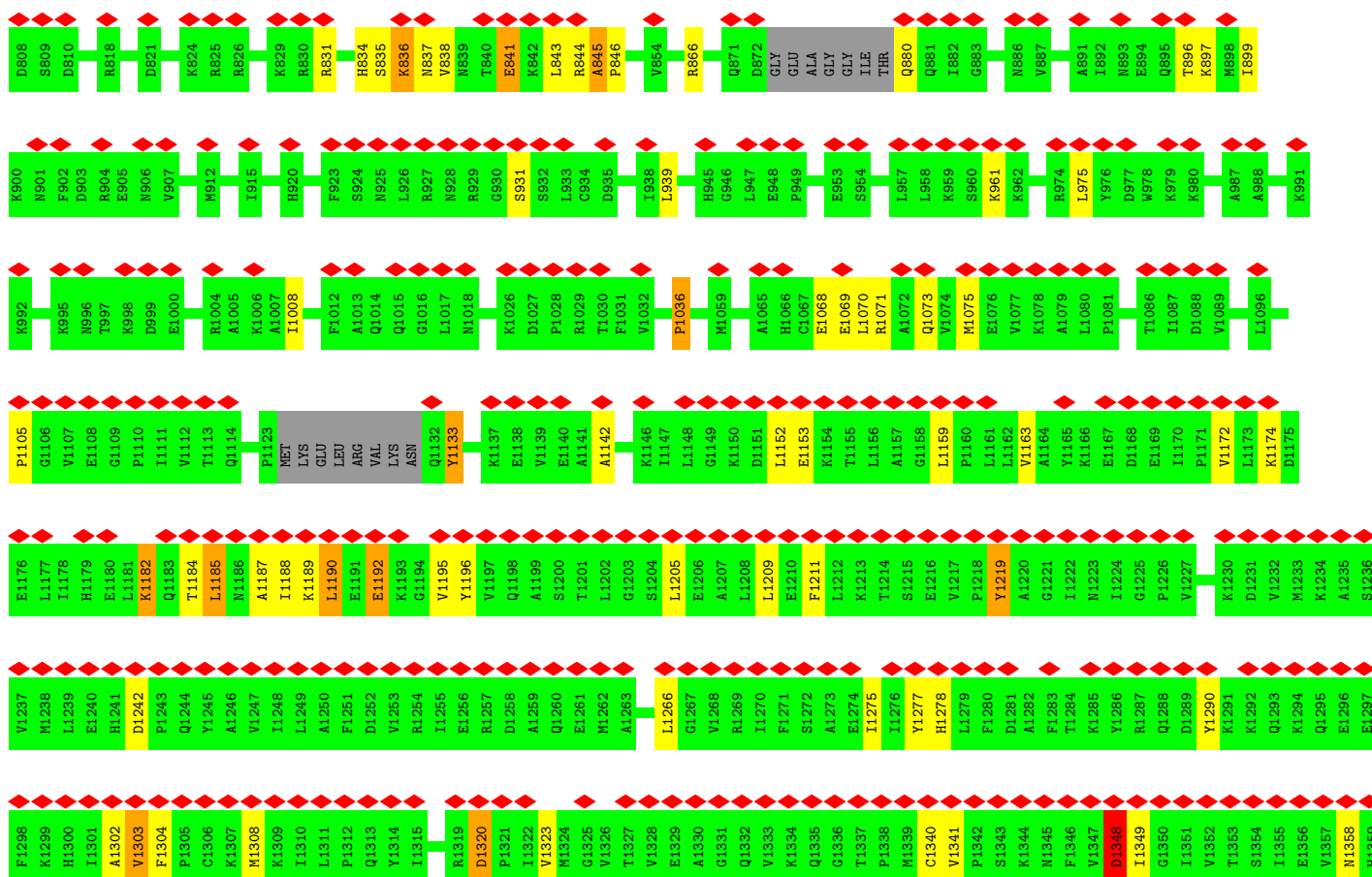
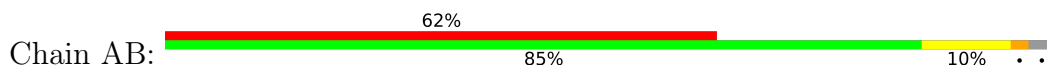
### 3 Residue-property plots

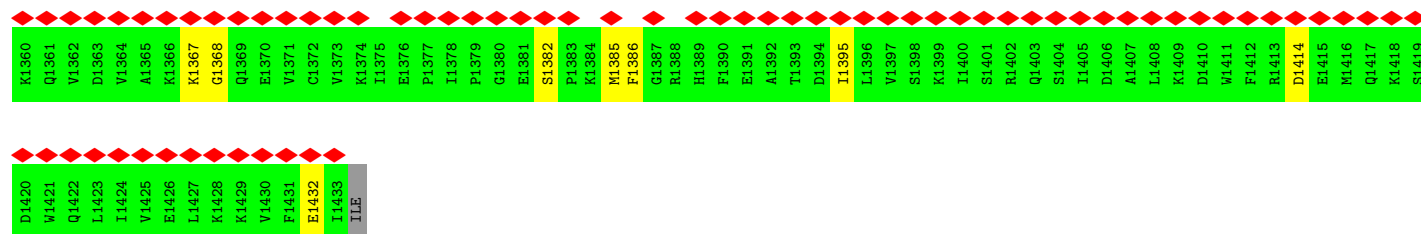
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

#### • Molecule 1: TRNA

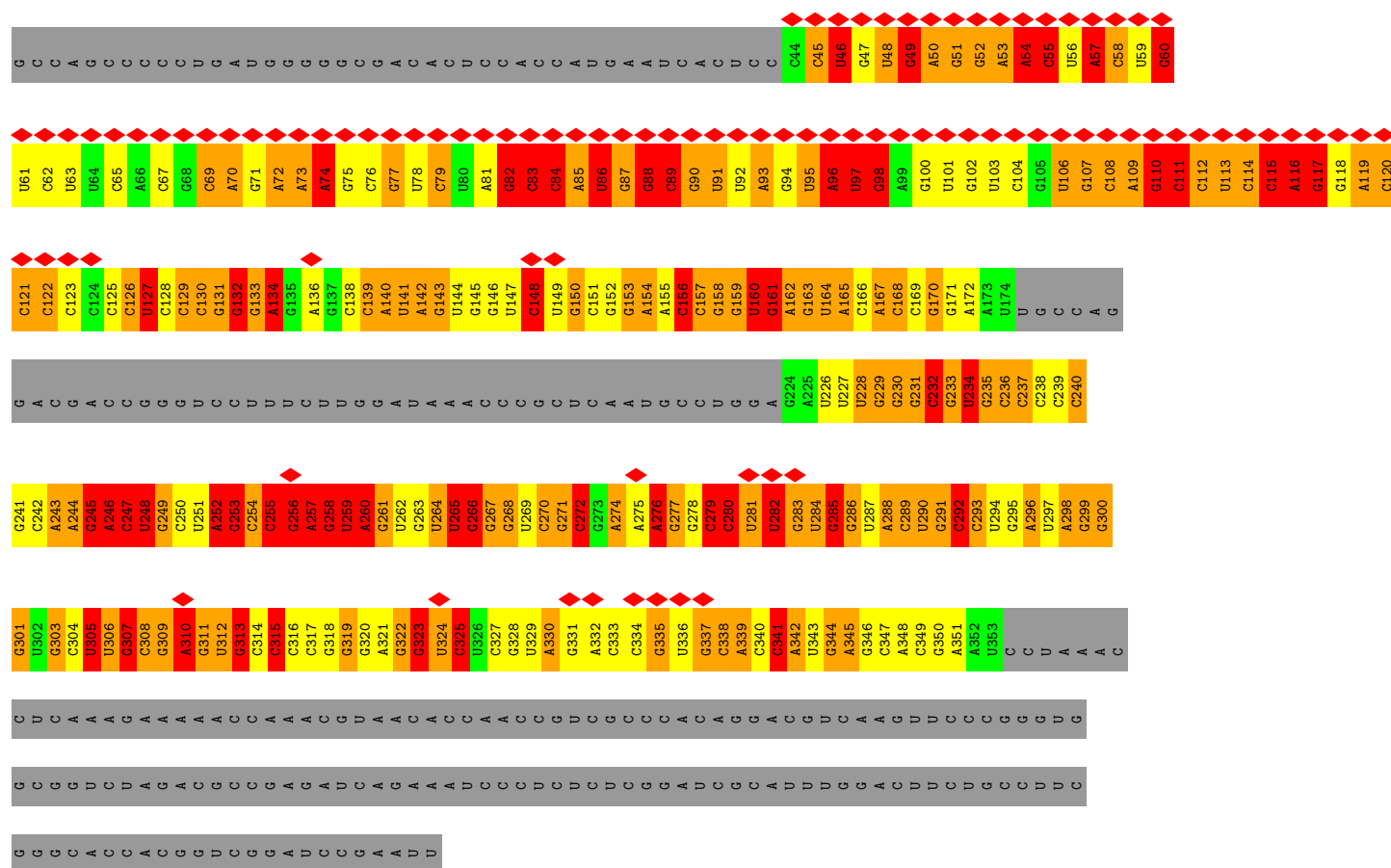


#### • Molecule 2: EIF5B

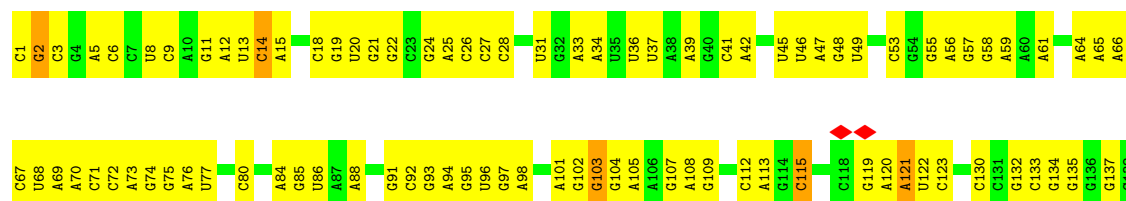
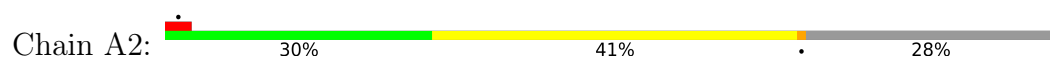


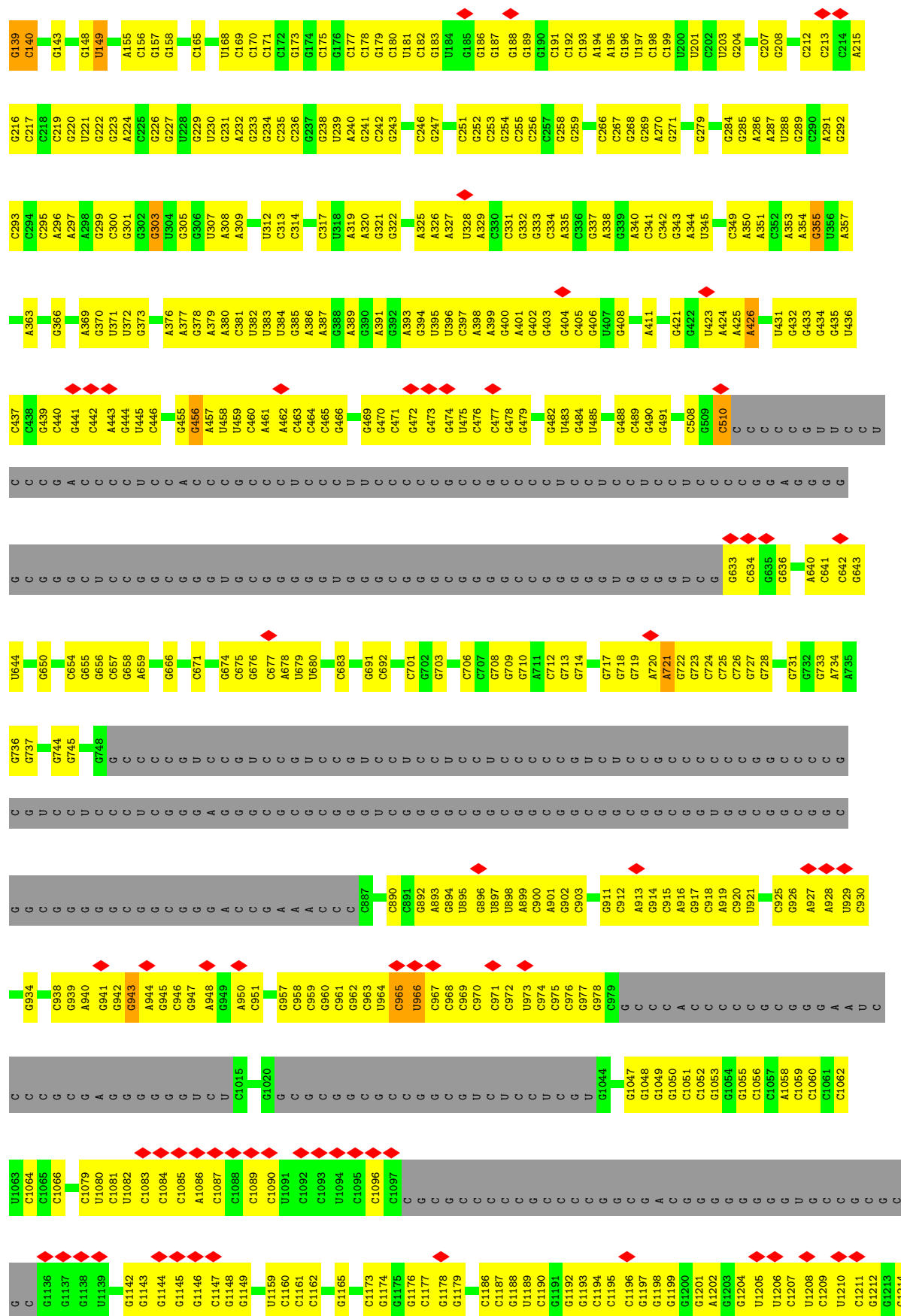


• Molecule 3: HCV-IRES



• Molecule 4: 28S RIBOSOMAL RNA



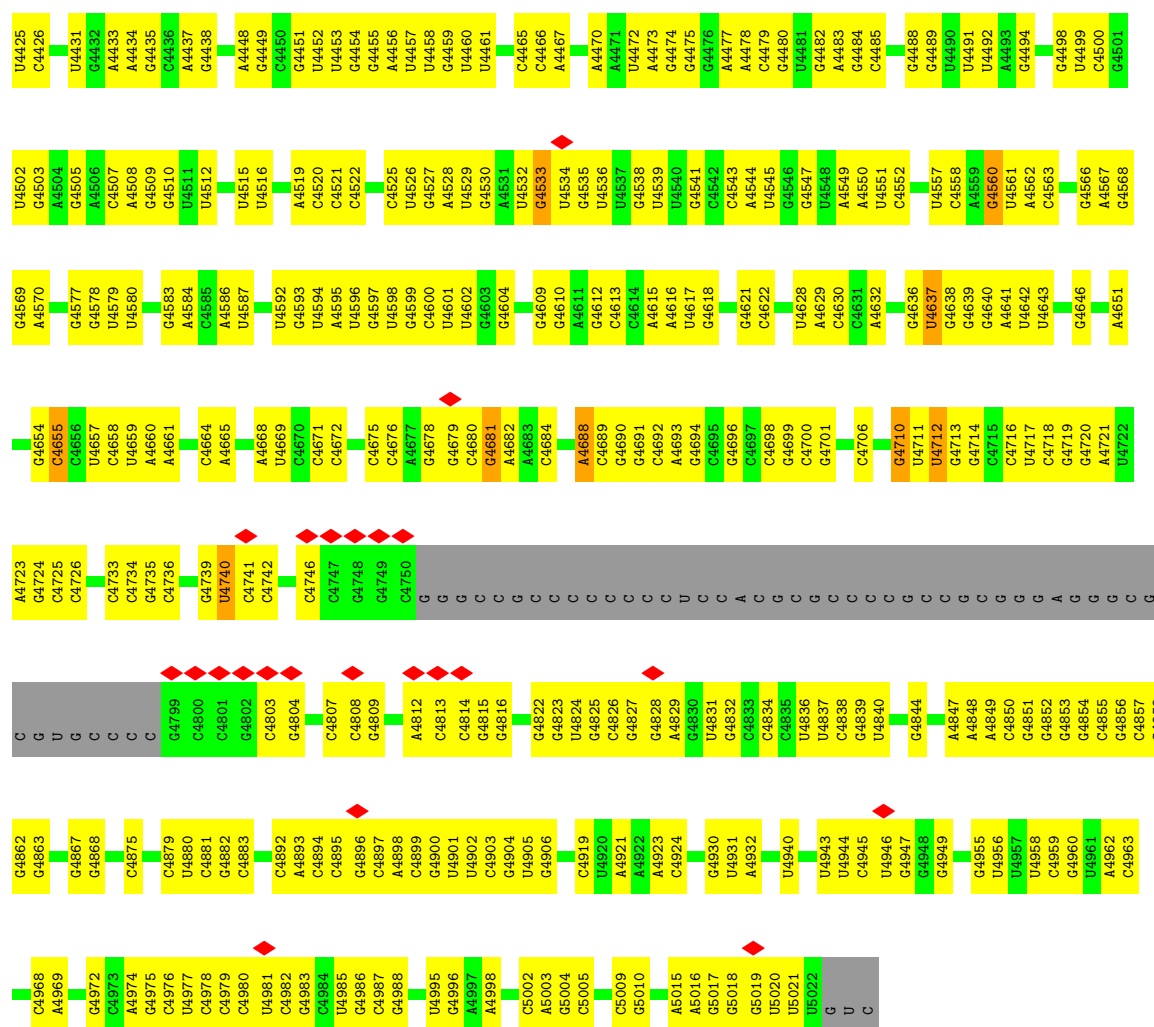






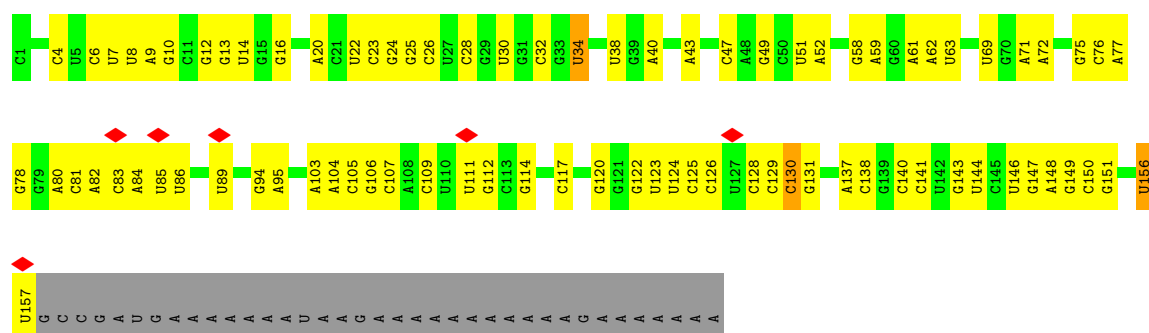






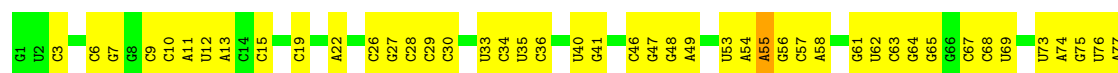
### • Molecule 5: 5.8S RIBOSOMAL RNA

Chain A3: 38% 41% 19%



### • Molecule 6: 5S RIBOSOMAL RNA

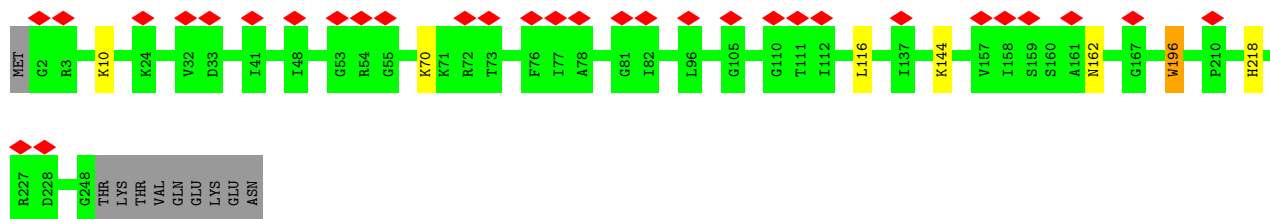
Chain A4: 40% 56%





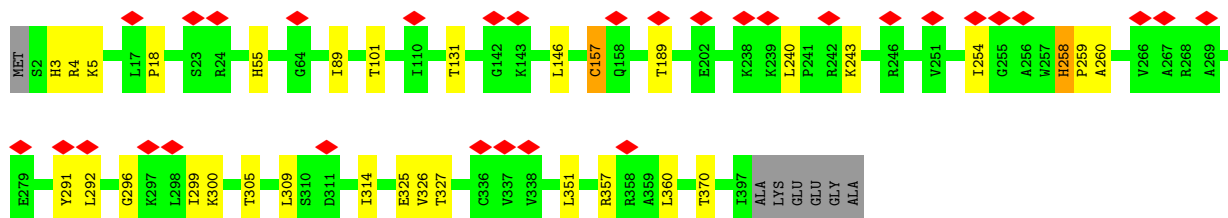
• Molecule 7: 60S RIBOSOMAL PROTEIN L8

Chain BA: 12% 93%



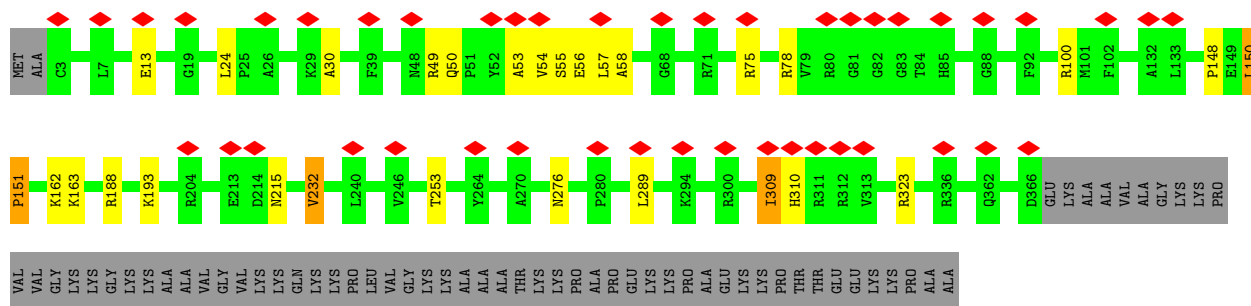
• Molecule 8: 60S RIBOSOMAL PROTEIN L3

Chain BB: 8% 90% 7%



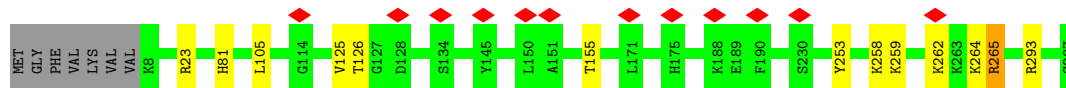
• Molecule 9: 60S RIBOSOMAL PROTEIN L4

Chain BC: 10% 78% 6% 15%



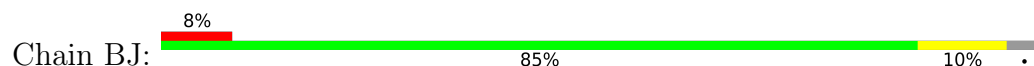
• Molecule 10: 60S RIBOSOMAL PROTEIN L5

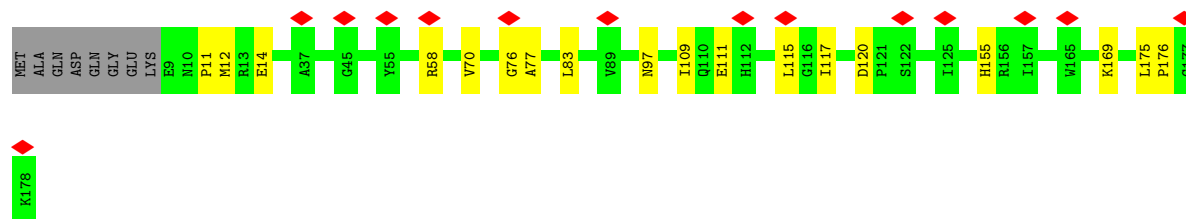
Chain BD: 93%



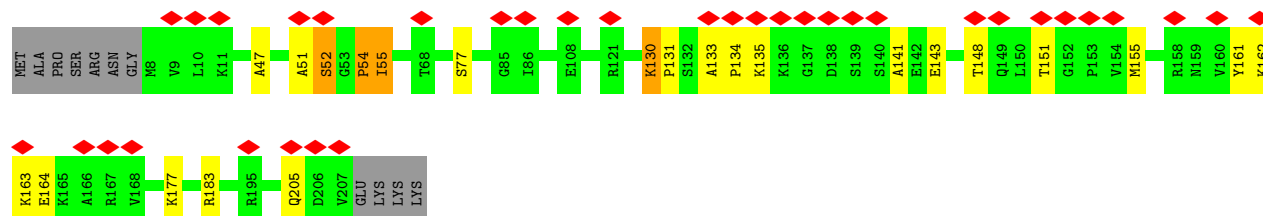
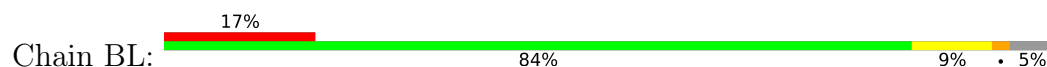
• Molecule 11: 60S RIBOSOMAL PROTEIN L6

Chain BE: 15% 91% 9%

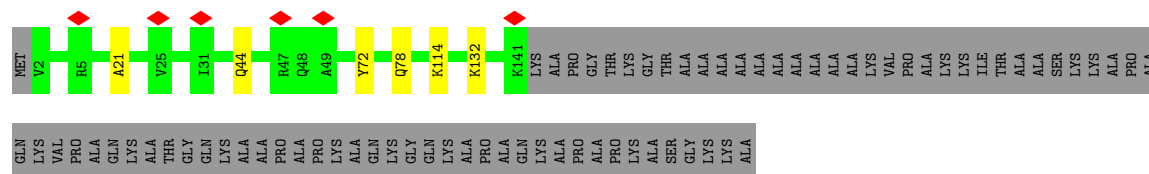




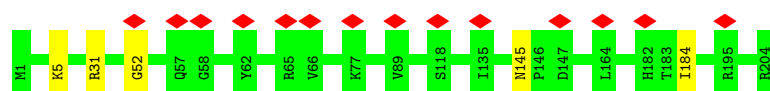
• Molecule 17: 60S RIBOSOMAL PROTEIN L13



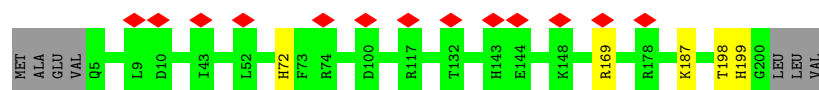
• Molecule 18: 60S RIBOSOMAL PROTEIN L14



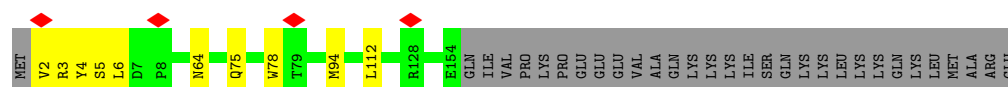
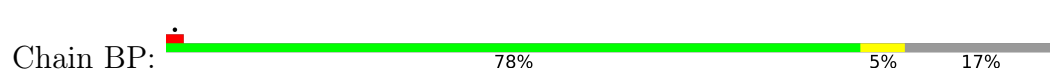
• Molecule 19: 60S RIBOSOMAL PROTEIN L15



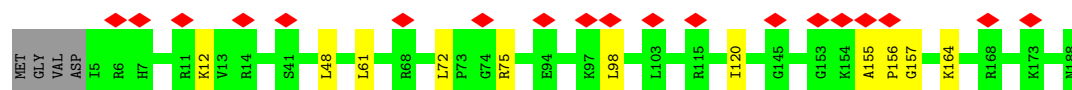
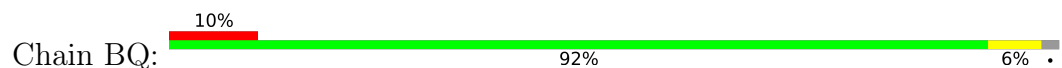
• Molecule 20: 60S RIBOSOMAL PROTEIN L13A



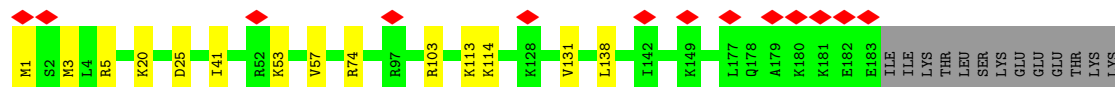
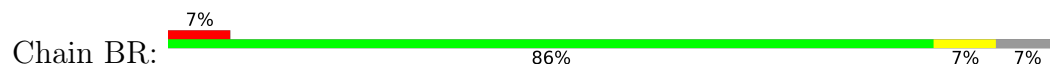
• Molecule 21: 60S RIBOSOMAL PROTEIN L17



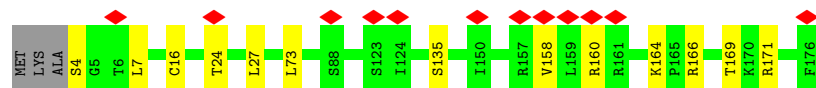
- Molecule 22: 60S RIBOSOMAL PROTEIN L18



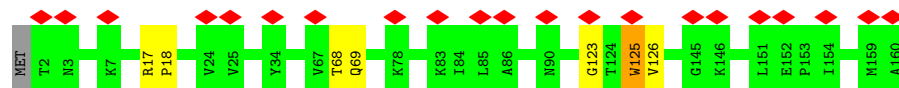
- Molecule 23: 60S RIBOSOMAL PROTEIN L19



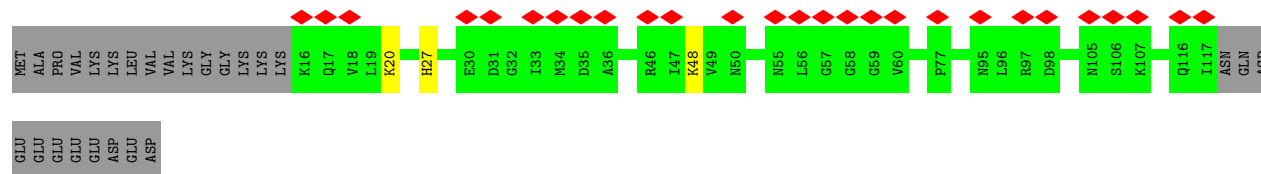
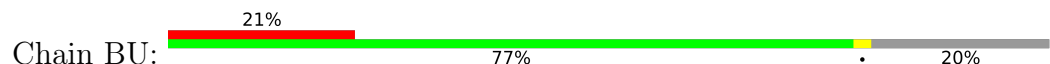
- Molecule 24: 60S RIBOSOMAL PROTEIN L18A



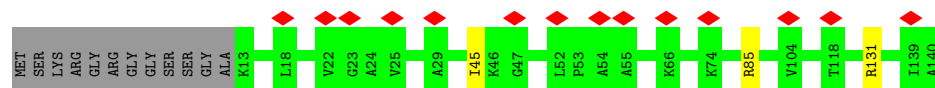
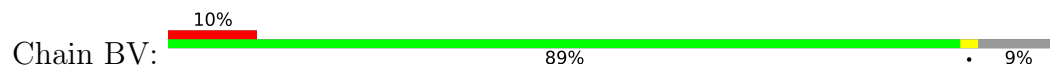
- Molecule 25: 60S RIBOSOMAL PROTEIN L21



- Molecule 26: 60S RIBOSOMAL PROTEIN L22

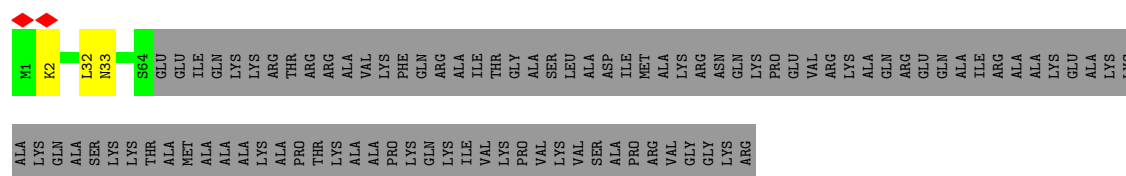


- Molecule 27: 60S RIBOSOMAL PROTEIN L23

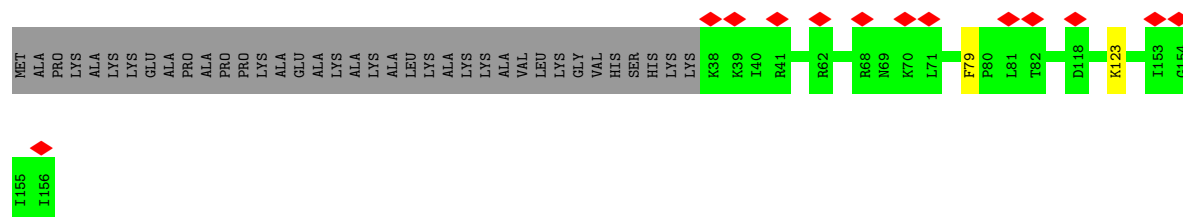
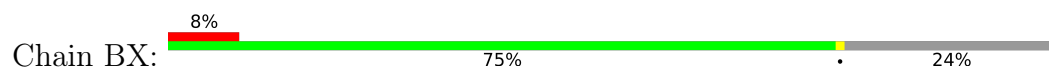


- Molecule 28: 60S RIBOSOMAL PROTEIN L24

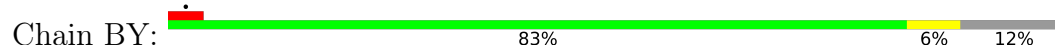




• Molecule 29: 60S RIBOSOMAL PROTEIN L23A



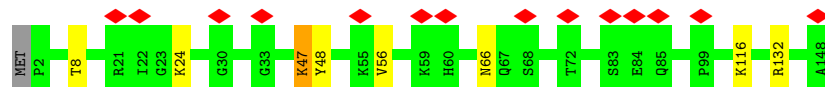
• Molecule 30: 60S RIBOSOMAL PROTEIN L26



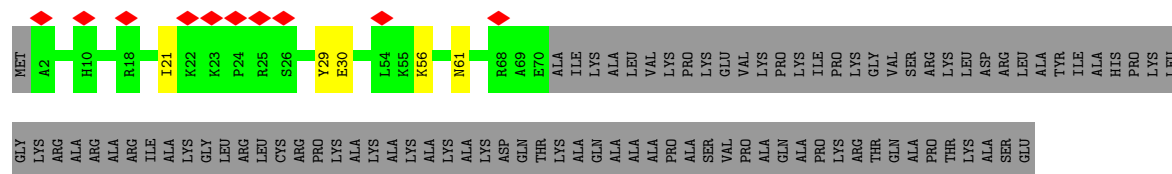
• Molecule 31: 60S RIBOSOMAL PROTEIN L27

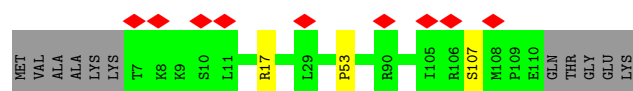
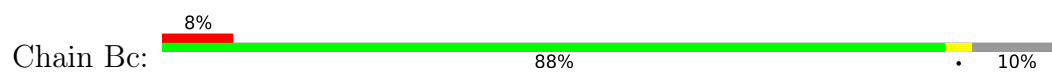


• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

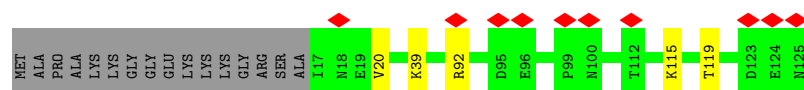
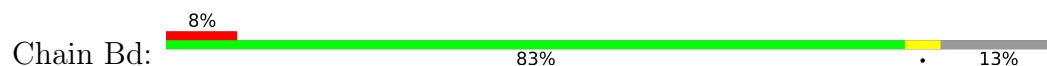


• Molecule 33: 60S RIBOSOMAL PROTEIN L29

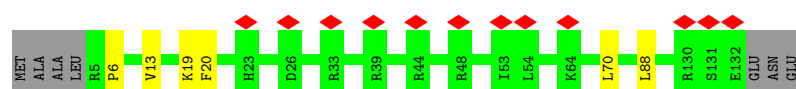
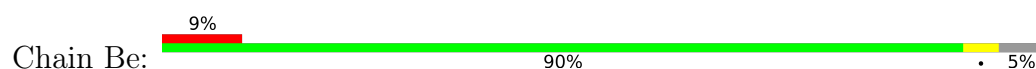




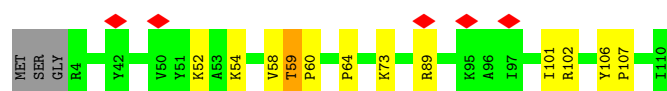
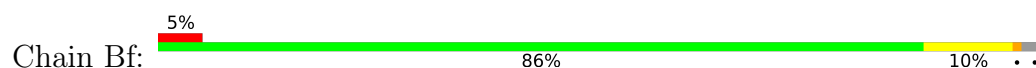
• Molecule 35: 60S RIBOSOMAL PROTEIN L31



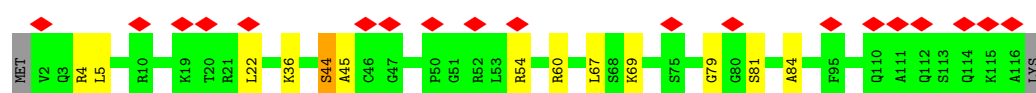
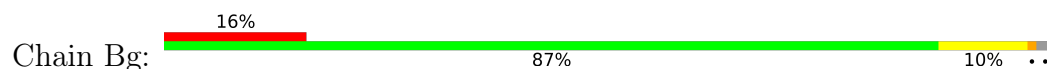
• Molecule 36: 60S RIBOSOMAL PROTEIN L32



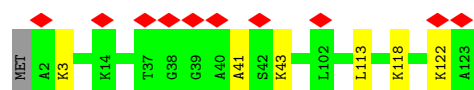
• Molecule 37: 60S RIBOSOMAL PROTEIN L35A



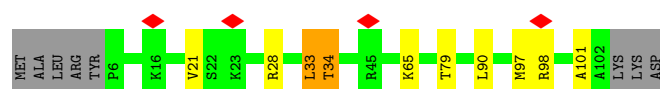
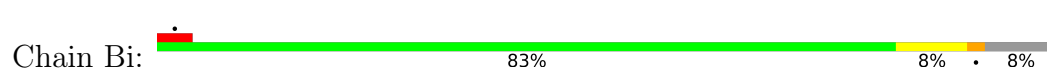
• Molecule 38: 60S RIBOSOMAL PROTEIN L34




• Molecule 39: 60S RIBOSOMAL PROTEIN UL29

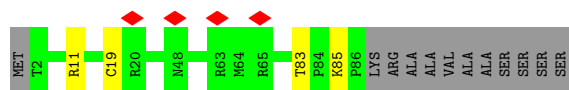


• Molecule 40: 60S RIBOSOMAL PROTEIN L36



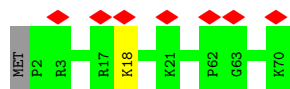
- Molecule 41: 60S RIBOSOMAL PROTEIN L37

Chain Bj:  84% 12%



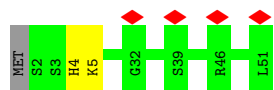
- Molecule 42: 60S RIBOSOMAL PROTEIN L38

Chain Bk:  10% 97%



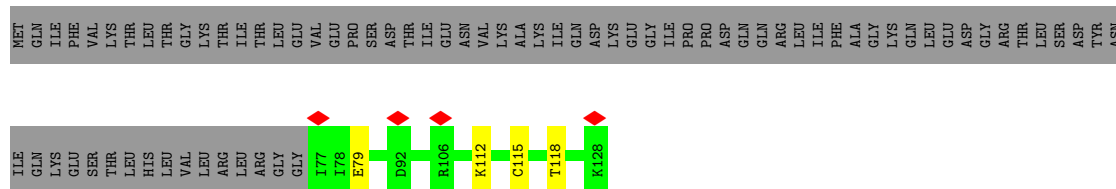
- Molecule 43: 60S RIBOSOMAL PROTEIN L39

Chain Bl:  8% 94%



- Molecule 44: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Bm:  38% 59%



- Molecule 45: 60S RIBOSOMAL PROTEIN L41

Chain Bn:  100%

There are no outlier residues recorded for this chain.

- Molecule 46: 60S RIBOSOMAL PROTEIN L36A

Chain Bo:  12% 93% 7%

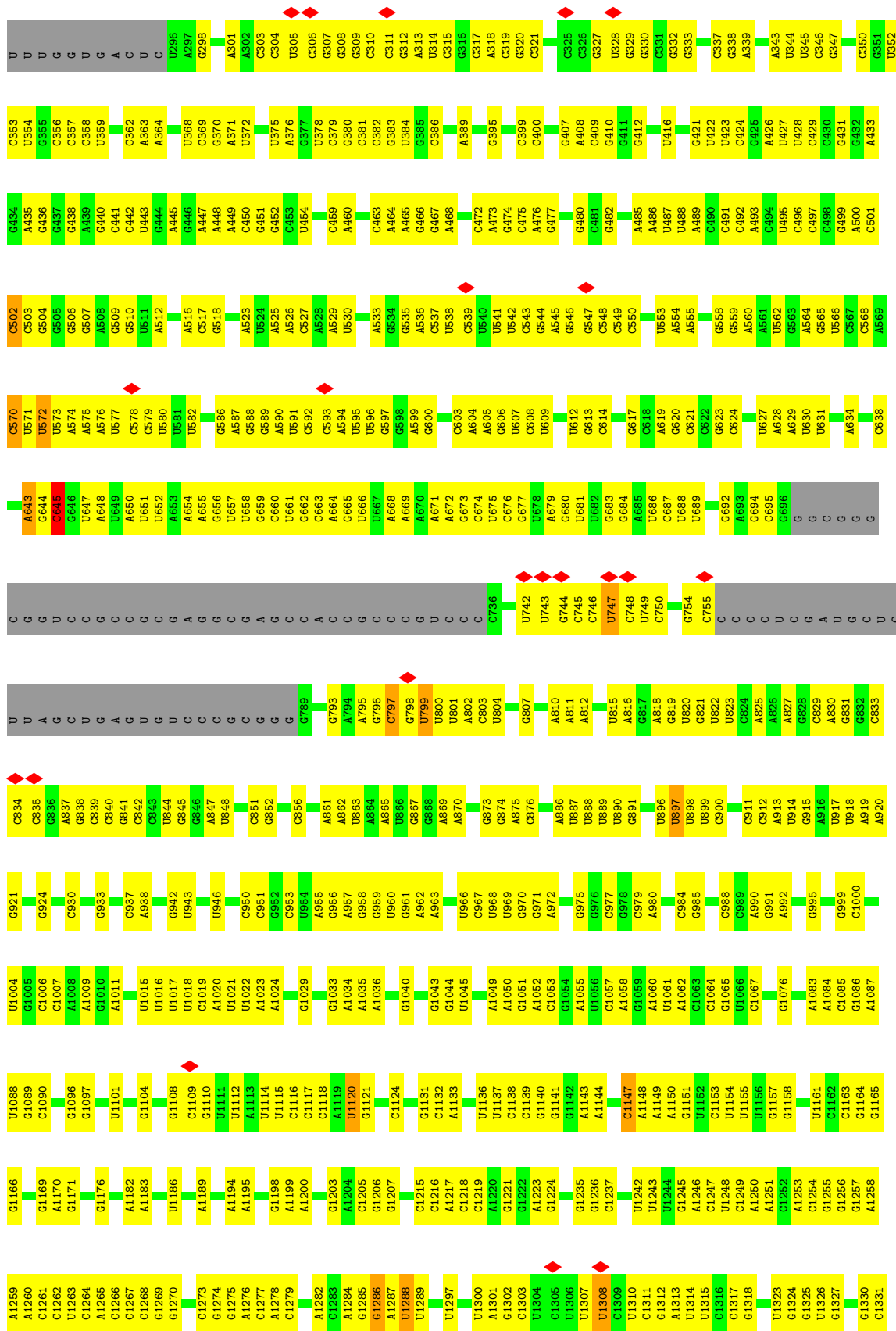


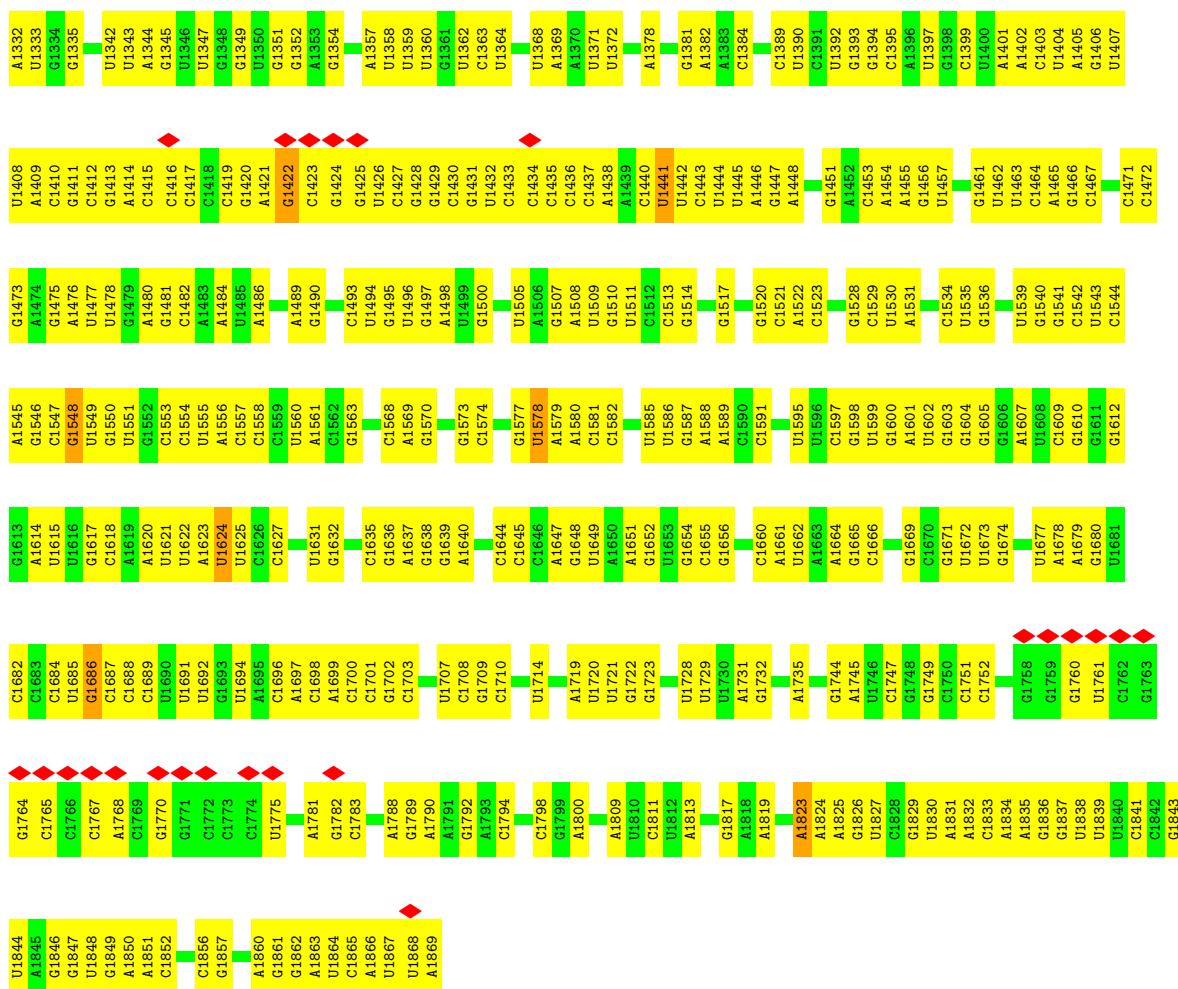
- Molecule 47: 60S RIBOSOMAL PROTEIN L37A

Chain Bp:  8% 93% 5%

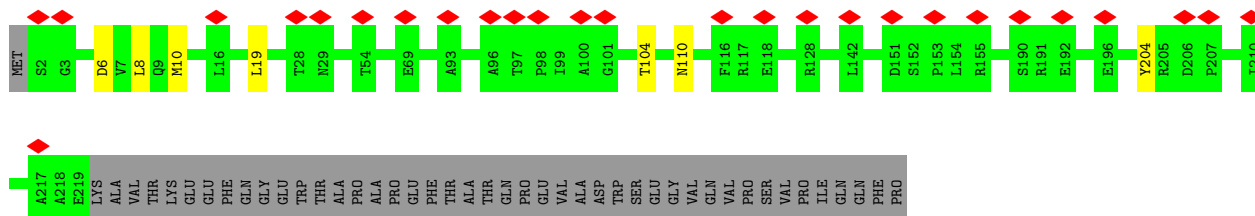
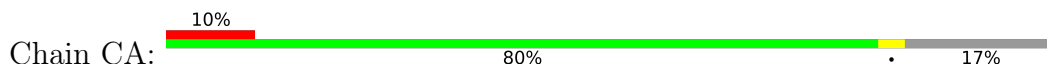




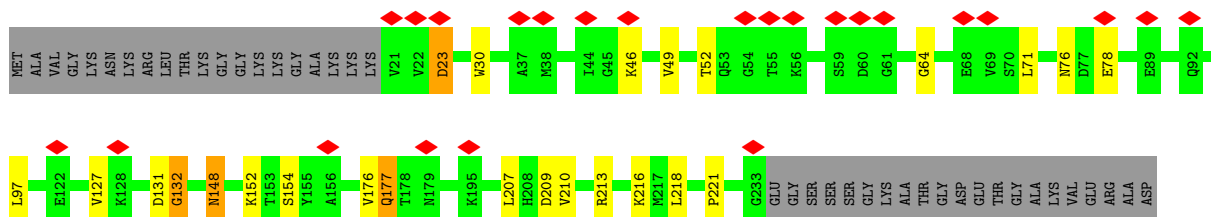
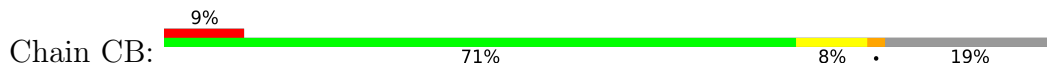




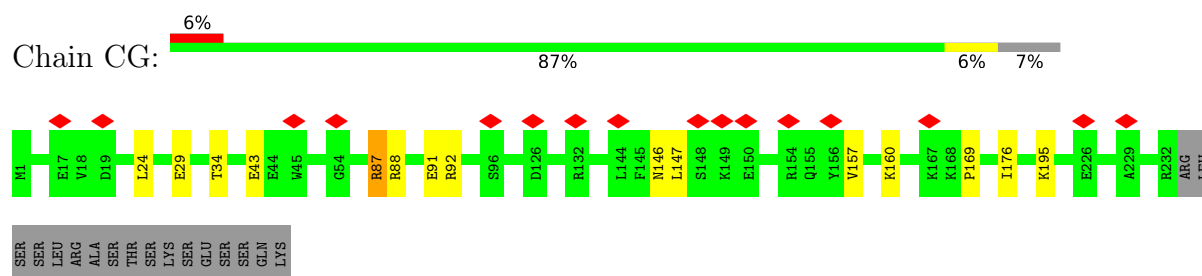
• Molecule 51: 40S RIBOSOMAL PROTEIN US2



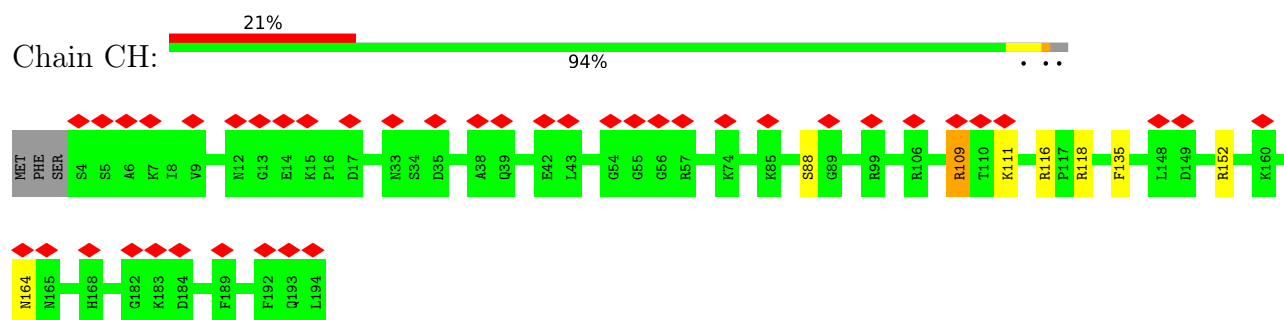
• Molecule 52: 40S RIBOSOMAL PROTEIN ES1



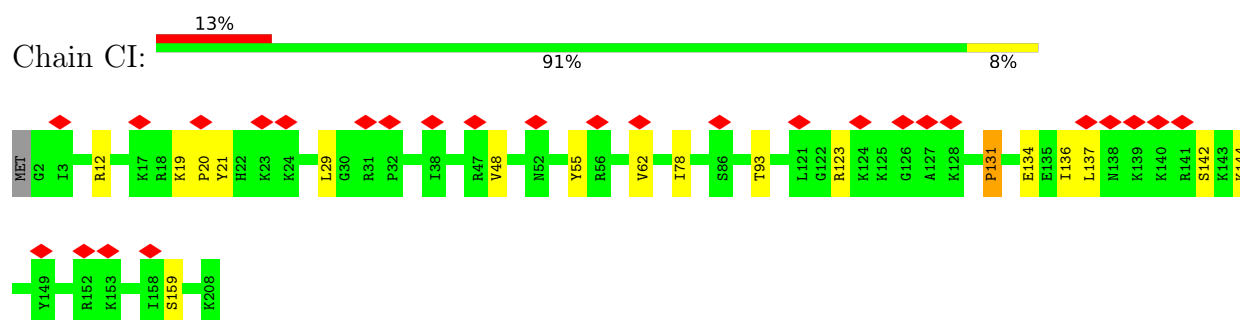




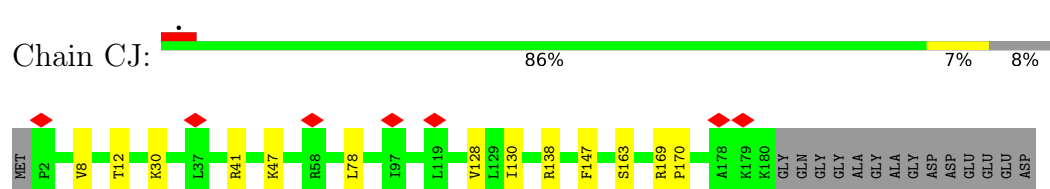
- Molecule 58: 40S RIBOSOMAL PROTEIN ES7



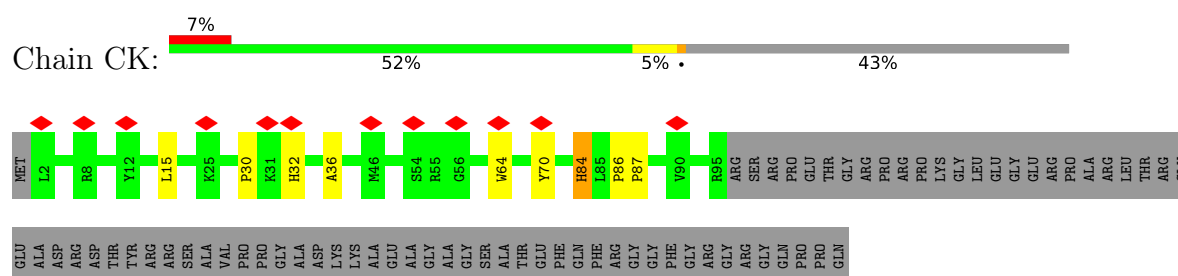
- Molecule 59: 40S RIBOSOMAL PROTEIN ES8



- Molecule 60: 40S RIBOSOMAL PROTEIN US4

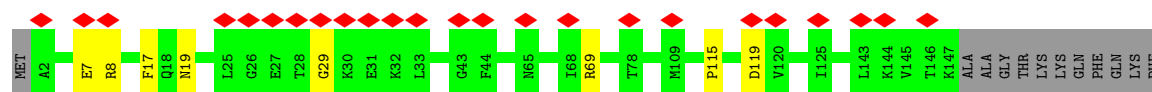


- Molecule 61: 40S RIBOSOMAL PROTEIN ES10

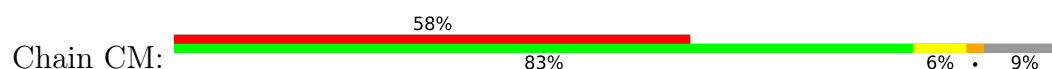


- Molecule 62: 40S RIBOSOMAL PROTEIN US17

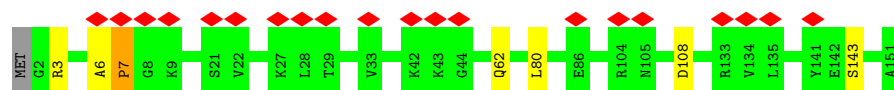




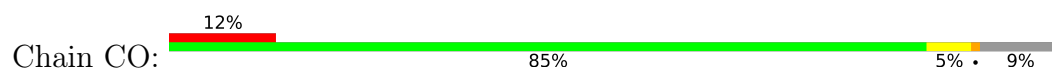
• Molecule 63: 40S RIBOSOMAL PROTEIN ES12



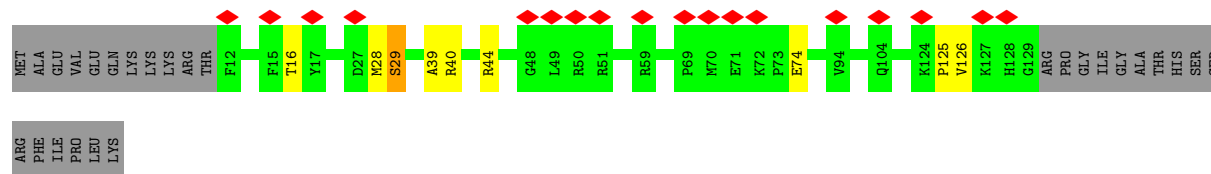
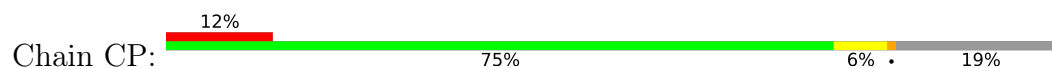
• Molecule 64: 40S RIBOSOMAL PROTEIN US15



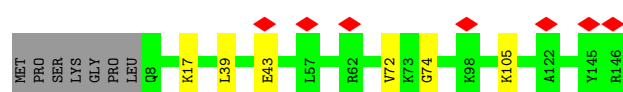
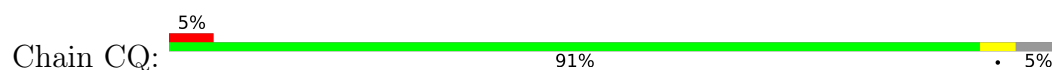
• Molecule 65: 40S RIBOSOMAL PROTEIN US11



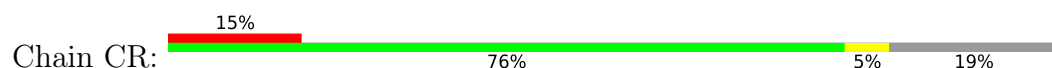
• Molecule 66: 40S RIBOSOMAL PROTEIN US19

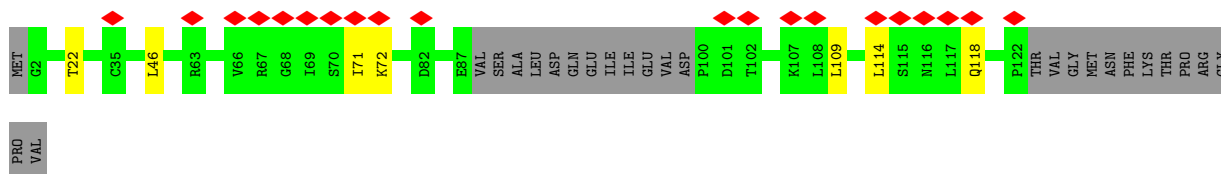


• Molecule 67: 40S RIBOSOMAL PROTEIN US9

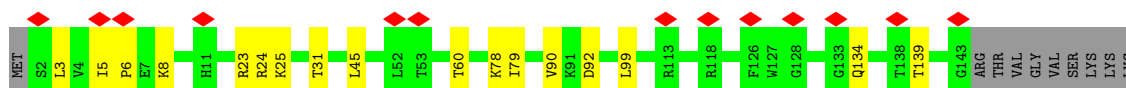
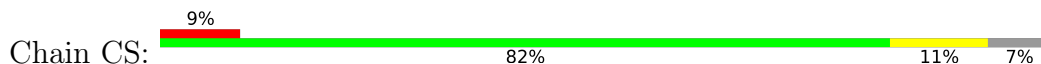


• Molecule 68: 40S RIBOSOMAL PROTEIN ES17

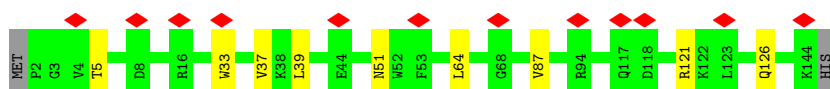




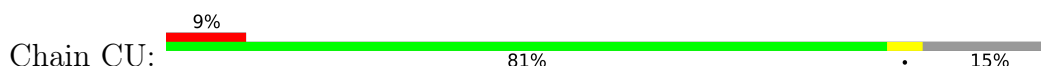
- Molecule 69: 40S RIBOSOMAL PROTEIN US13



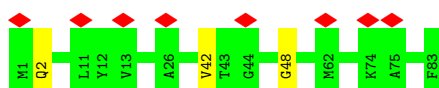
- Molecule 70: 40S RIBOSOMAL PROTEIN ES19



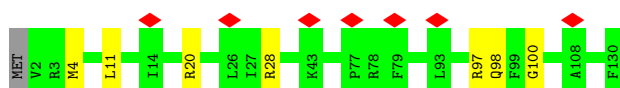
- Molecule 71: 40S RIBOSOMAL PROTEIN US10



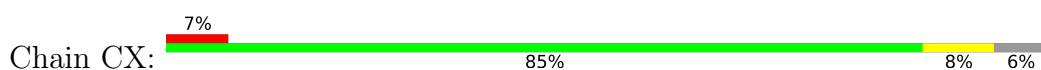
- Molecule 72: 40S RIBOSOMAL PROTEIN ES21




- Molecule 73: 40S RIBOSOMAL PROTEIN US8

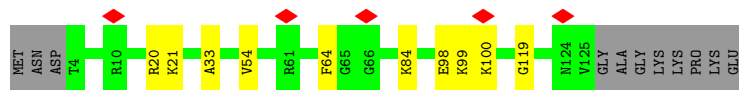


- Molecule 74: 40S RIBOSOMAL PROTEIN US12



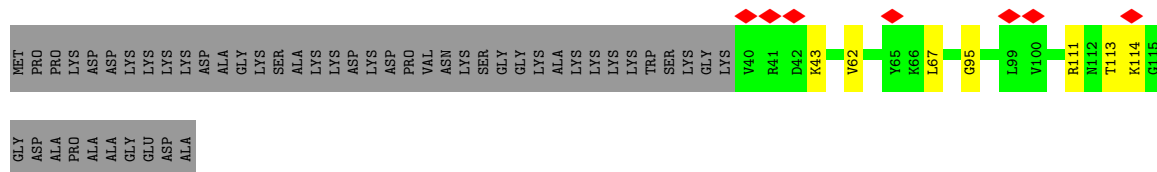
- Molecule 75: 40S RIBOSOMAL PROTEIN ES24

Chain CY: 




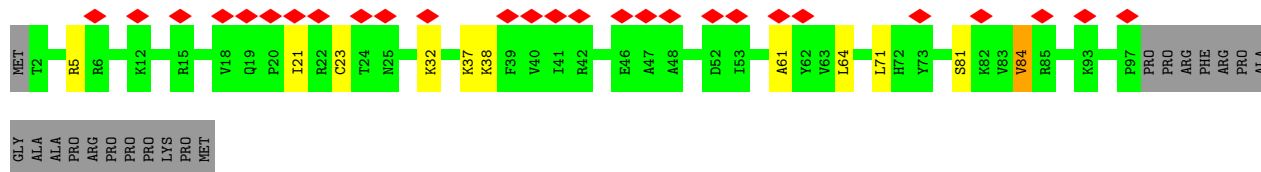
- Molecule 76: 40S RIBOSOMAL PROTEIN ES25

Chain CZ: 



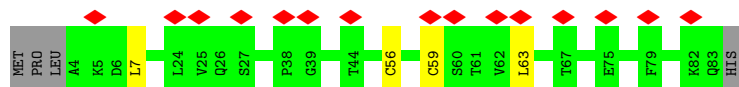
- Molecule 77: 40S RIBOSOMAL PROTEIN ES26

Chain Ca: 




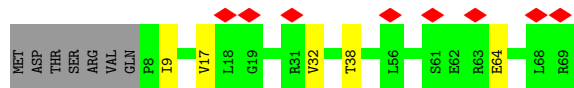
- Molecule 78: 40S RIBOSOMAL PROTEIN ES27

Chain Cb: 




- Molecule 79: 40S RIBOSOMAL PROTEIN ES28

Chain Cc: 



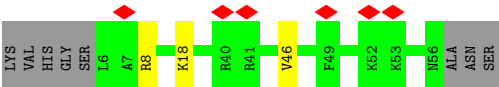
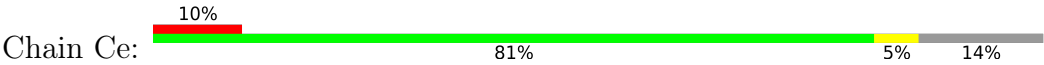
- Molecule 80: 40S RIBOSOMAL PROTEIN US14

Chain Cd: 

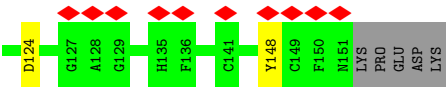
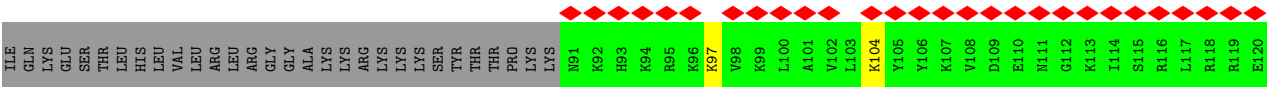
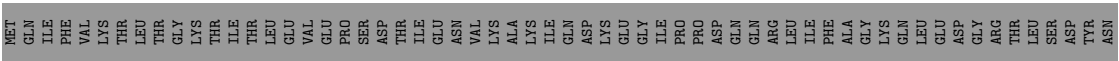


- Molecule 81: 40S RIBOSOMAL PROTEIN ES30

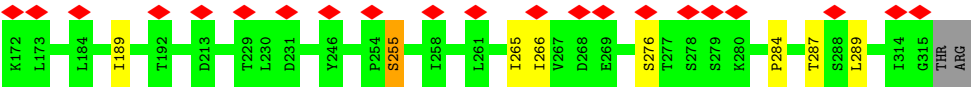
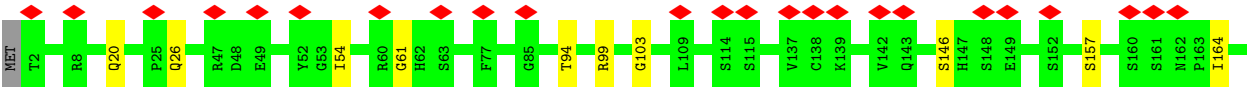




• Molecule 82: 40S RIBOSOMAL PROTEIN ES31



• 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 ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	1.26, 1.26, 1.26	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.53	0/1809	1.02	17/2819 (0.6%)
2	AB	0.65	1/4926 (0.0%)	1.15	29/6641 (0.4%)
3	AC	1.52	10/6230 (0.2%)	2.37	535/9712 (5.5%)
4	A2	0.41	23/86672 (0.0%)	0.81	40/135198 (0.0%)
5	A3	0.36	0/3723	0.79	1/5800 (0.0%)
6	A4	0.38	0/2836	0.81	3/4421 (0.1%)
7	BA	0.44	0/1926	0.67	0/2583
8	BB	0.45	0/3258	0.73	2/4361 (0.0%)
9	BC	0.47	0/2943	0.73	0/3953
10	BD	0.49	2/2407 (0.1%)	0.70	1/3221 (0.0%)
11	BE	0.52	0/1312	0.73	0/1763
12	BF	0.45	0/1986	0.68	0/2644
13	BG	0.46	0/1914	0.72	0/2578
14	BH	0.43	0/1555	0.69	0/2089
15	BI	0.42	0/1643	0.67	0/2194
16	BJ	0.49	0/1386	0.71	0/1852
17	BL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
18	BM	0.49	0/1162	0.70	0/1556
19	BN	0.43	0/1754	0.65	0/2348
20	BO	0.44	0/1639	0.69	0/2193
21	BP	0.44	0/1260	0.70	0/1691
22	BQ	0.45	0/1518	0.74	0/2026
23	BR	0.41	0/1542	0.64	0/2037
24	BS	0.44	0/1479	0.73	0/1985
25	BT	0.46	0/1326	0.71	0/1770
26	BU	0.47	0/841	0.71	0/1128
27	BV	0.43	0/978	0.63	0/1312
28	BW	0.43	0/542	0.59	0/722
29	BX	0.41	0/993	0.67	0/1334
30	BY	0.47	0/1082	0.72	1/1441 (0.1%)
31	BZ	0.47	0/1138	0.79	0/1517
32	Ba	0.45	0/1191	0.71	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Bb	0.45	0/570	0.72	0/752
34	Bc	0.46	0/813	0.70	0/1091
35	Bd	0.45	0/920	0.67	0/1238
36	Be	0.45	0/1071	0.68	0/1428
37	Bf	0.50	0/885	0.81	0/1185
38	Bg	0.48	0/917	0.74	0/1222
39	Bh	0.38	0/1023	0.64	0/1351
40	Bi	0.43	0/793	0.75	0/1048
41	Bj	0.49	0/704	0.76	0/931
42	Bk	0.43	0/575	0.73	0/761
43	Bl	0.41	0/454	0.61	0/599
44	Bm	0.42	0/435	0.70	0/575
45	Bn	0.40	0/241	0.51	0/305
46	Bo	0.45	0/885	0.74	0/1166
47	Bp	0.40	0/718	0.61	0/953
48	Bt	0.48	0/1058	0.75	0/1416
49	Bu	0.45	0/1639	0.69	1/2222 (0.0%)
50	C1	0.37	2/41550 (0.0%)	0.80	6/64763 (0.0%)
51	CA	0.51	0/1756	0.68	0/2386
52	CB	0.51	0/1756	0.75	1/2350 (0.0%)
53	CC	0.42	0/1761	0.65	0/2379
54	CD	0.40	0/1672	0.66	0/2250
55	CE	0.47	0/2072	0.70	0/2793
56	CF	0.43	0/1507	0.74	0/2026
57	CG	0.48	0/1907	0.74	0/2538
58	CH	0.46	0/1558	0.74	1/2087 (0.0%)
59	CI	0.47	0/1724	0.72	0/2298
60	CJ	0.46	0/1520	0.77	0/2030
61	CK	0.48	0/815	0.68	0/1101
62	CL	0.45	0/1220	0.72	0/1633
63	CM	0.48	0/941	0.72	0/1264
64	CN	0.43	0/1231	0.73	1/1656 (0.1%)
65	CO	0.46	0/1036	0.71	0/1391
66	CP	0.43	0/1000	0.67	0/1335
67	CQ	0.43	0/1125	0.66	0/1506
68	CR	0.42	0/904	0.67	0/1208
69	CS	0.42	0/1190	0.68	0/1594
70	CT	0.44	0/1131	0.69	0/1515
71	CU	0.50	0/813	0.70	0/1092
72	CV	0.47	0/643	0.71	0/860
73	CW	0.44	0/1050	0.69	0/1406
74	CX	0.46	0/1063	0.70	0/1421
75	CY	0.45	0/1019	0.70	0/1354

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	CZ	0.46	0/611	0.71	0/820
77	Ca	0.48	0/778	0.75	1/1041 (0.1%)
78	Cb	0.48	0/637	0.68	0/854
79	Cc	0.46	0/492	0.74	0/657
80	Cd	0.51	0/454	0.76	0/603
81	Ce	0.45	0/417	0.69	0/548
82	Cf	0.53	0/507	0.84	1/673 (0.1%)
83	Cg	0.45	0/2497	0.67	0/3399
All	All	0.49	40/240676 (0.0%)	0.86	644/353759 (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 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A2	1701	C	C5'-C4'	18.44	1.73	1.51
4	A2	1673	C	C3'-O3'	15.36	1.63	1.42
4	A2	1701	C	O5'-C5'	14.46	1.67	1.44
4	A2	1673	C	O3'-P	14.13	1.78	1.61
4	A2	1701	C	P-O5'	13.49	1.73	1.59

The worst 5 of 644 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A2	1701	C	O4'-C4'-C3'	-15.17	88.83	104.00
2	AB	1133	TYR	CB-CG-CD2	-14.76	112.14	121.00
8	BB	258	HIS	C-N-CD	-13.97	89.87	120.60
1	AA	8	U	C5'-C4'-C3'	13.49	137.58	116.00
4	A2	1701	C	O4'-C1'-N1	12.28	118.02	108.20

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](#)

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	
2	AB	605/627 (96%)	523 (86%)	50 (8%)	32 (5%)	1	15
7	BA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	11	44
8	BB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	3	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	37
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	37
13	BG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	2	19
14	BH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	8	38
15	BI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	8	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	41
19	BN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	32
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	37
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%)	8	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%)	5	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	32
35	Bd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	52
36	Be	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	5	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%)	5	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	32
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	41
51	CA	216/263 (82%)	209 (97%)	5 (2%)	2 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	5	27
55	CE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6	32
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	37
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
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	41
71	CU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	13	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%)	8	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	32
82	Cf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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%)	517 (96%)	23 (4%)	25	46
7	BA	189/199 (95%)	184 (97%)	5 (3%)	41	59
8	BB	344/349 (99%)	326 (95%)	18 (5%)	19	40
9	BC	302/348 (87%)	284 (94%)	18 (6%)	16	37
10	BD	244/250 (98%)	237 (97%)	7 (3%)	37	56
11	BE	143/143 (100%)	135 (94%)	8 (6%)	17	38
12	BF	203/215 (94%)	196 (97%)	7 (3%)	32	51
13	BG	199/223 (89%)	192 (96%)	7 (4%)	31	51
14	BH	171/171 (100%)	164 (96%)	7 (4%)	26	47
15	BI	170/181 (94%)	161 (95%)	9 (5%)	19	40
16	BJ	143/149 (96%)	137 (96%)	6 (4%)	25	46
17	BL	167/177 (94%)	156 (93%)	11 (7%)	14	34
18	BM	118/161 (73%)	114 (97%)	4 (3%)	32	51
19	BN	172/172 (100%)	170 (99%)	2 (1%)	67	78
20	BO	168/174 (97%)	166 (99%)	2 (1%)	67	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	BP	133/163 (82%)	126 (95%)	7 (5%)	19	40
22	BQ	162/165 (98%)	157 (97%)	5 (3%)	35	54
23	BR	161/175 (92%)	150 (93%)	11 (7%)	13	34
24	BS	155/157 (99%)	148 (96%)	7 (4%)	23	45
25	BT	139/140 (99%)	134 (96%)	5 (4%)	30	50
26	BU	91/115 (79%)	88 (97%)	3 (3%)	33	52
27	BV	100/107 (94%)	99 (99%)	1 (1%)	73	82
28	BW	55/126 (44%)	52 (94%)	3 (6%)	18	39
29	BX	107/133 (80%)	105 (98%)	2 (2%)	52	69
30	BY	119/135 (88%)	115 (97%)	4 (3%)	32	51
31	BZ	118/118 (100%)	112 (95%)	6 (5%)	20	41
32	Ba	120/121 (99%)	116 (97%)	4 (3%)	33	52
33	Bb	58/126 (46%)	57 (98%)	1 (2%)	56	72
34	Bc	88/97 (91%)	87 (99%)	1 (1%)	70	80
35	Bd	100/110 (91%)	96 (96%)	4 (4%)	27	47
36	Be	115/121 (95%)	112 (97%)	3 (3%)	41	59
37	Bf	87/89 (98%)	79 (91%)	8 (9%)	7	23
38	Bg	98/100 (98%)	88 (90%)	10 (10%)	6	20
39	Bh	109/110 (99%)	106 (97%)	3 (3%)	38	57
40	Bi	82/89 (92%)	76 (93%)	6 (7%)	11	31
41	Bj	71/80 (89%)	69 (97%)	2 (3%)	38	57
42	Bk	64/65 (98%)	64 (100%)	0	100	100
43	Bl	47/48 (98%)	46 (98%)	1 (2%)	48	66
44	Bm	48/116 (41%)	45 (94%)	3 (6%)	15	36
45	Bn	24/24 (100%)	24 (100%)	0	100	100
46	Bo	94/94 (100%)	89 (95%)	5 (5%)	19	40
47	Bp	74/75 (99%)	72 (97%)	2 (3%)	40	58
48	Bt	113/121 (93%)	106 (94%)	7 (6%)	15	36
49	Bu	177/177 (100%)	163 (92%)	14 (8%)	10	29
51	CA	181/219 (83%)	176 (97%)	5 (3%)	38	57
52	CB	194/231 (84%)	183 (94%)	11 (6%)	17	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	CC	188/225 (84%)	181 (96%)	7 (4%)	29	49
54	CD	175/202 (87%)	166 (95%)	9 (5%)	20	41
55	CE	220/225 (98%)	208 (94%)	12 (6%)	18	39
56	CF	158/170 (93%)	151 (96%)	7 (4%)	24	45
57	CG	202/218 (93%)	195 (96%)	7 (4%)	31	51
58	CH	171/174 (98%)	167 (98%)	4 (2%)	45	64
59	CI	179/180 (99%)	167 (93%)	12 (7%)	13	34
60	CJ	160/168 (95%)	150 (94%)	10 (6%)	15	36
61	CK	85/136 (62%)	82 (96%)	3 (4%)	31	51
62	CL	133/142 (94%)	131 (98%)	2 (2%)	60	75
63	CM	102/108 (94%)	96 (94%)	6 (6%)	16	37
64	CN	130/131 (99%)	128 (98%)	2 (2%)	60	75
65	CO	107/119 (90%)	100 (94%)	7 (6%)	14	35
66	CP	107/130 (82%)	102 (95%)	5 (5%)	22	44
67	CQ	115/121 (95%)	111 (96%)	4 (4%)	31	51
68	CR	99/122 (81%)	94 (95%)	5 (5%)	20	41
69	CS	123/132 (93%)	114 (93%)	9 (7%)	11	31
70	CT	113/115 (98%)	106 (94%)	7 (6%)	15	36
71	CU	93/107 (87%)	89 (96%)	4 (4%)	25	46
72	CV	67/67 (100%)	66 (98%)	1 (2%)	60	75
73	CW	112/113 (99%)	107 (96%)	5 (4%)	23	45
74	CX	108/115 (94%)	103 (95%)	5 (5%)	23	44
75	CY	107/115 (93%)	101 (94%)	6 (6%)	17	38
76	CZ	67/103 (65%)	63 (94%)	4 (6%)	16	37
77	Ca	83/98 (85%)	76 (92%)	7 (8%)	9	27
78	Cb	72/76 (95%)	68 (94%)	4 (6%)	17	38
79	Cc	55/62 (89%)	52 (94%)	3 (6%)	18	39
80	Cd	47/49 (96%)	43 (92%)	4 (8%)	8	27
81	Ce	42/48 (88%)	40 (95%)	2 (5%)	21	43
82	Cf	54/140 (39%)	51 (94%)	3 (6%)	17	38
83	Cg	272/275 (99%)	260 (96%)	12 (4%)	24	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10303/11397 (90%)	9847 (96%)	456 (4%)	26 45

5 of 456 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	Bm	112	LYS
82	Cf	148	TYR
54	CD	16	ILE
80	Cd	48	LYS
71	CU	115	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 227 such sidechains are listed below:

Mol	Chain	Res	Type
33	Bb	50	ASN
81	Ce	44	ASN
52	CB	40	ASN
80	Cd	41	GLN
70	CT	126	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	14 (18%)	1 (1%)
3	AC	259/504 (51%)	135 (52%)	40 (15%)
4	A2	3605/5025 (71%)	2041 (56%)	325 (9%)
5	A3	156/194 (80%)	82 (52%)	6 (3%)
50	C1	1738/1869 (92%)	1038 (59%)	151 (8%)
6	A4	118/121 (97%)	68 (57%)	9 (7%)
All	All	5951/7789 (76%)	3378 (56%)	532 (8%)

5 of 3378 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	29,34,34	2.16	8 (27%)	33,54,54	2.26	8 (24%)

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	-	2/14/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	AB	2434	GNP	C2'-C1'	-6.47	1.43	1.53
84	AB	2434	GNP	C6-N1	5.33	1.42	1.33
84	AB	2434	GNP	C4-N3	2.90	1.40	1.35
84	AB	2434	GNP	PB-O3A	-2.62	1.55	1.59
84	AB	2434	GNP	PB-N3B	-2.48	1.56	1.63

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	AB	2434	GNP	C5-C6-N1	-7.04	113.81	123.43
84	AB	2434	GNP	C2-N1-C6	5.18	124.16	115.93
84	AB	2434	GNP	N3-C2-N1	-3.57	122.46	127.22
84	AB	2434	GNP	O1B-PB-N3B	3.40	116.78	111.77
84	AB	2434	GNP	C4-C5-C6	-2.99	117.94	120.80

There are no chirality outliers.

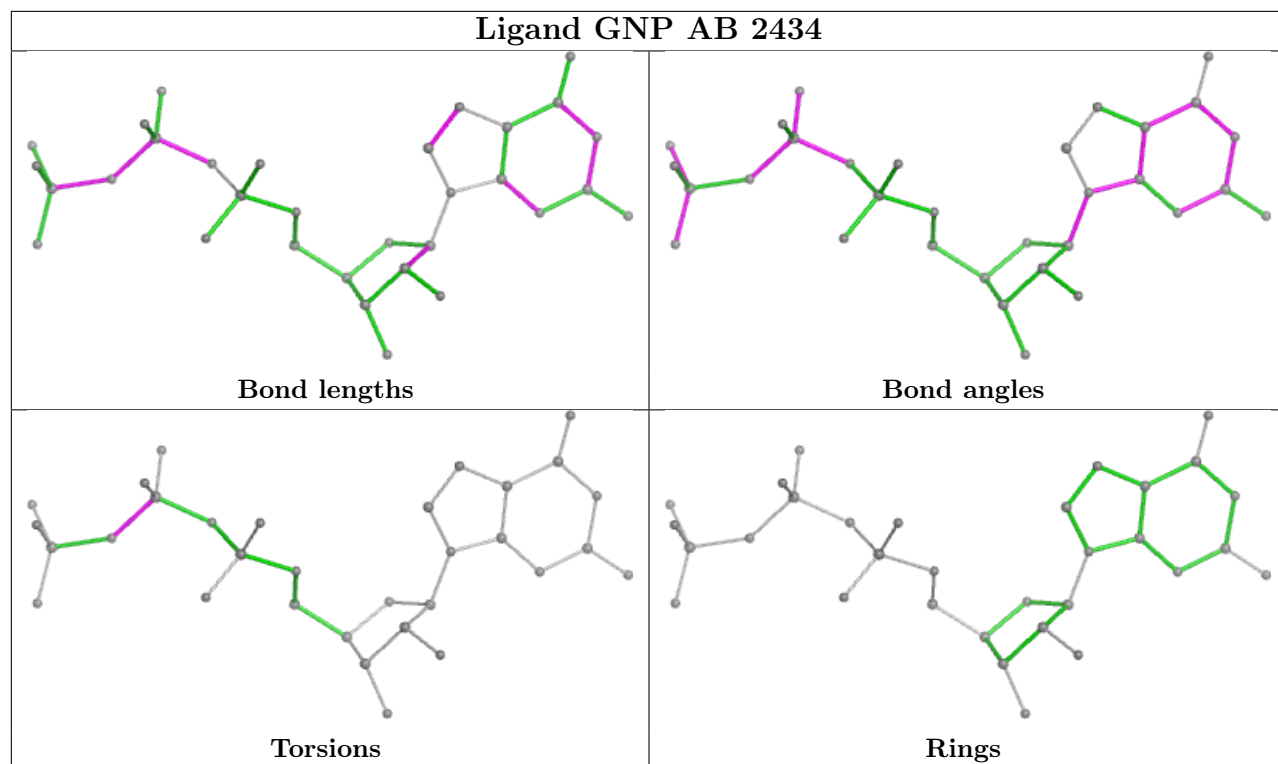
All (2) torsion outliers are listed below:

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.

No monomer is involved in short contacts.

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 [i](#)

There are no chain breaks in this entry.

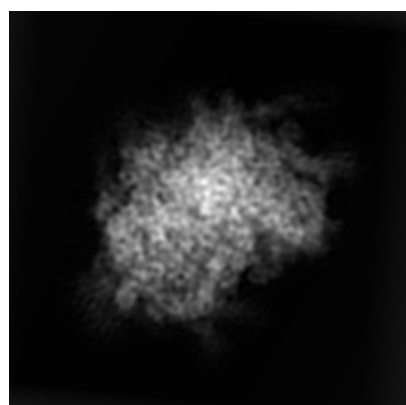
## 6 Map visualisation [i](#)

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.

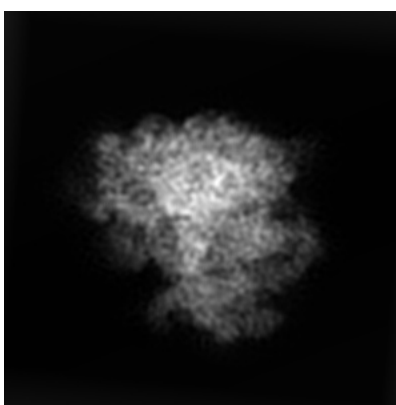
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

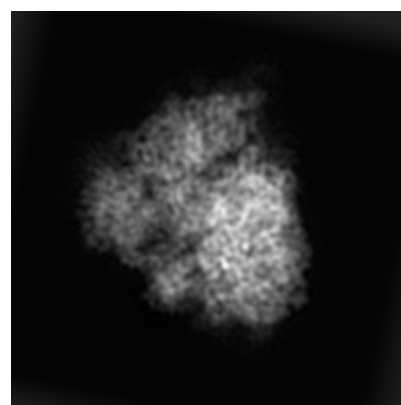
#### 6.1.1 Primary map



X



Y

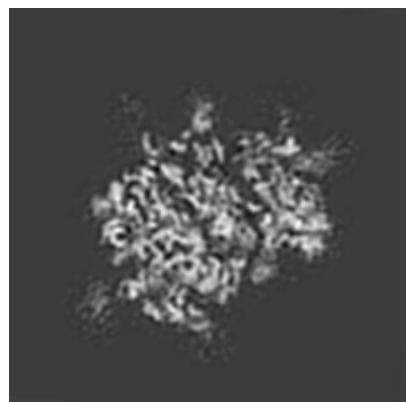


Z

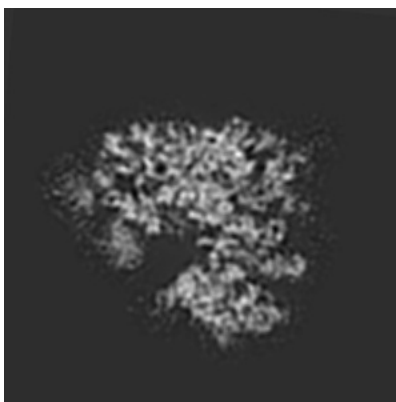
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

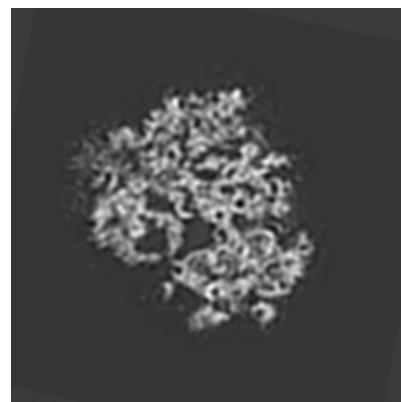
#### 6.2.1 Primary map



X Index: 180



Y Index: 180



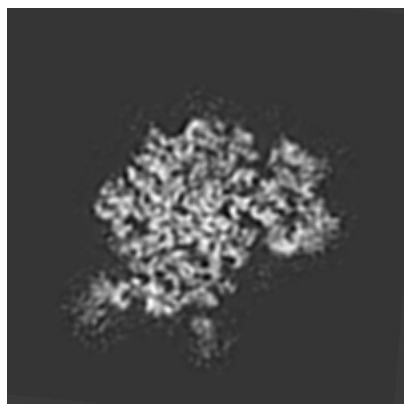
Z Index: 180



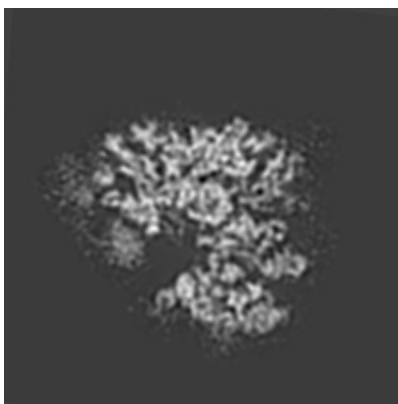
The images above show central slices of the map in three orthogonal directions.

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

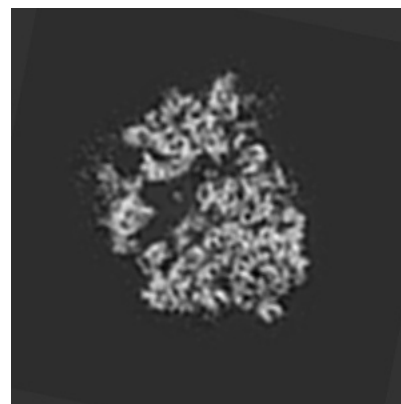
### 6.3.1 Primary map



X Index: 192



Y Index: 182

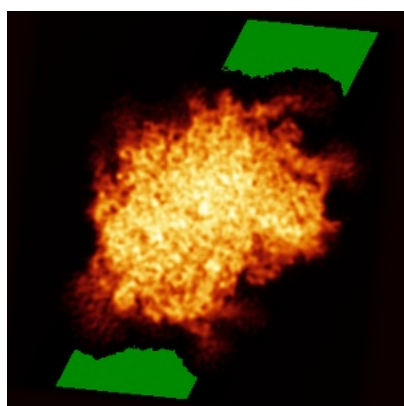


Z Index: 167

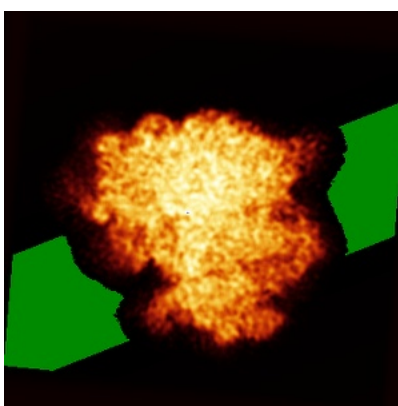
The images above show the largest variance slices of the map in three orthogonal directions.

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

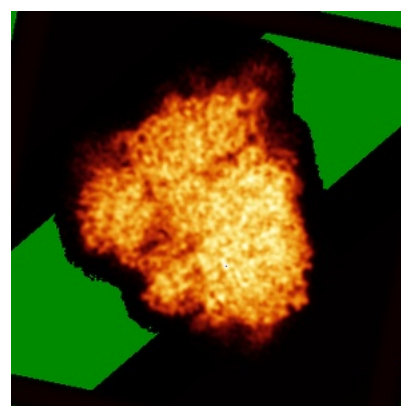
### 6.4.1 Primary map



X



Y

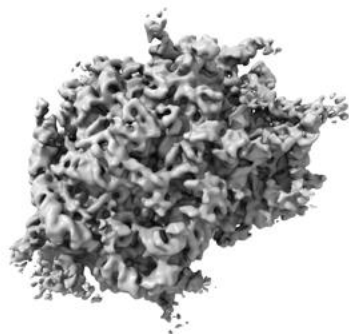


Z

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](#)

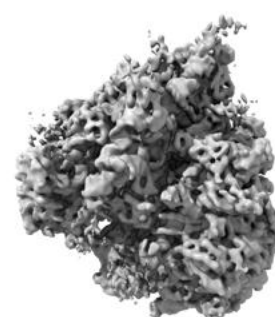
### 6.5.1 Primary map



X



Y



Z

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.

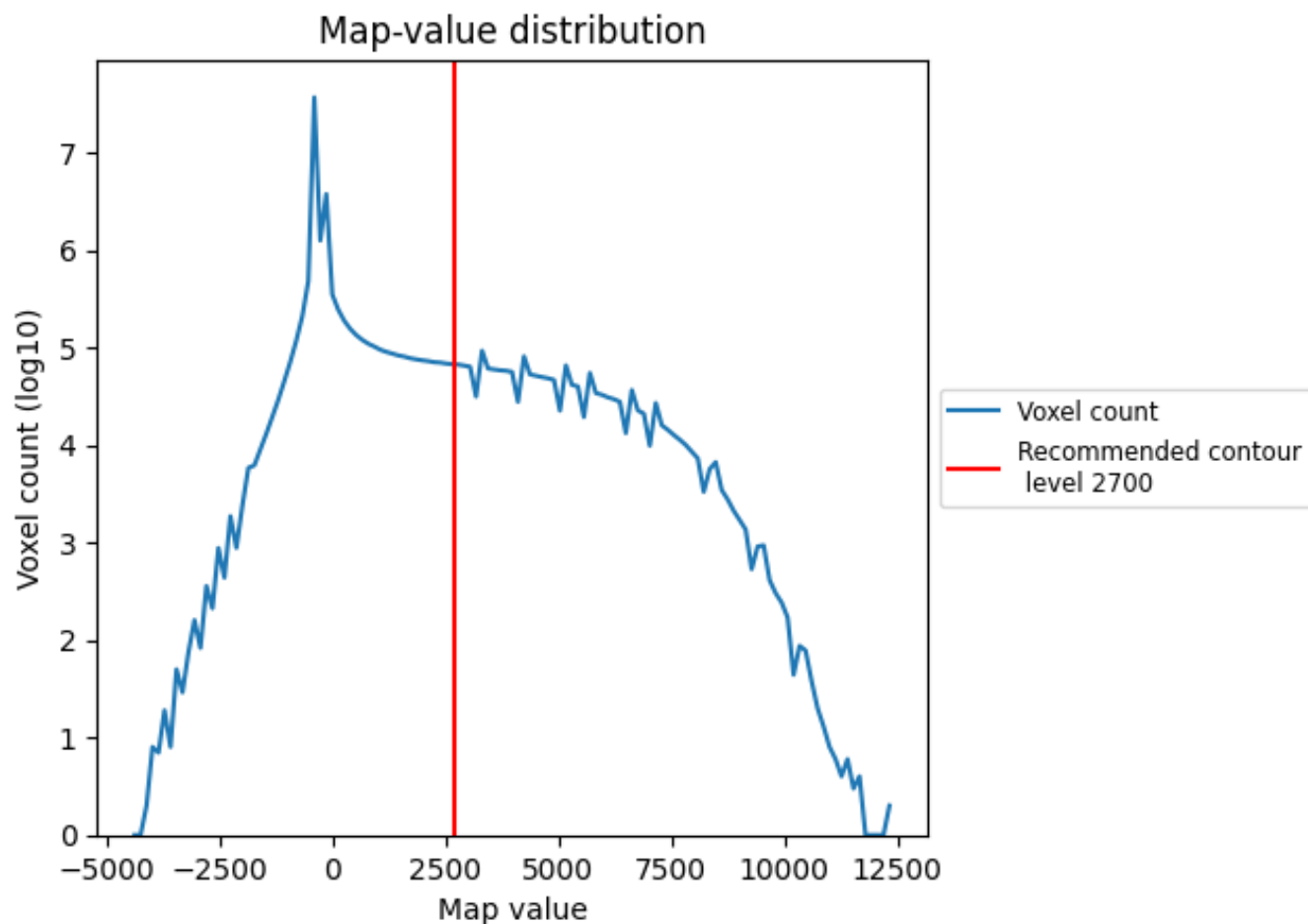
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

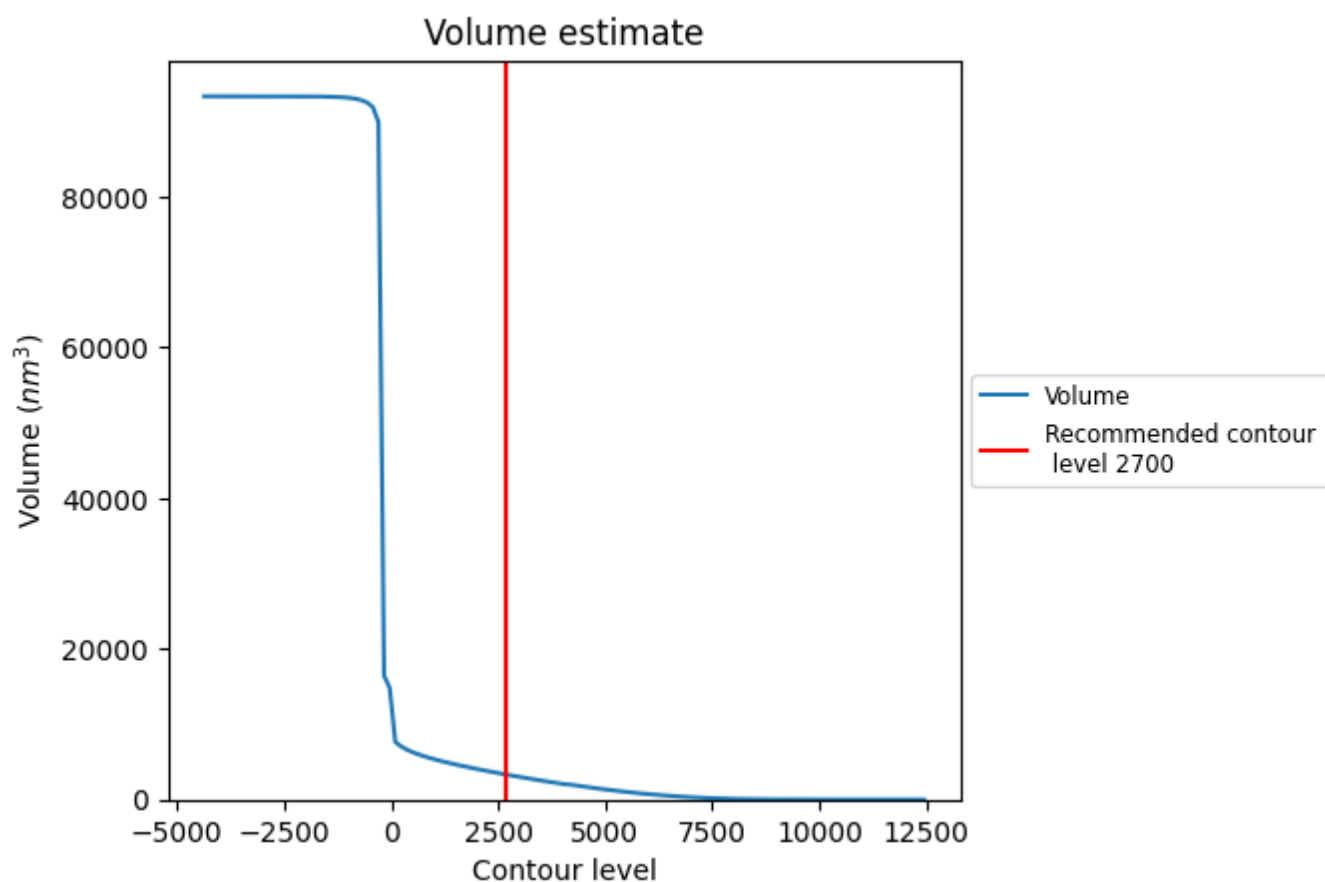
This section contains the results of statistical analysis of the map.

### 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.

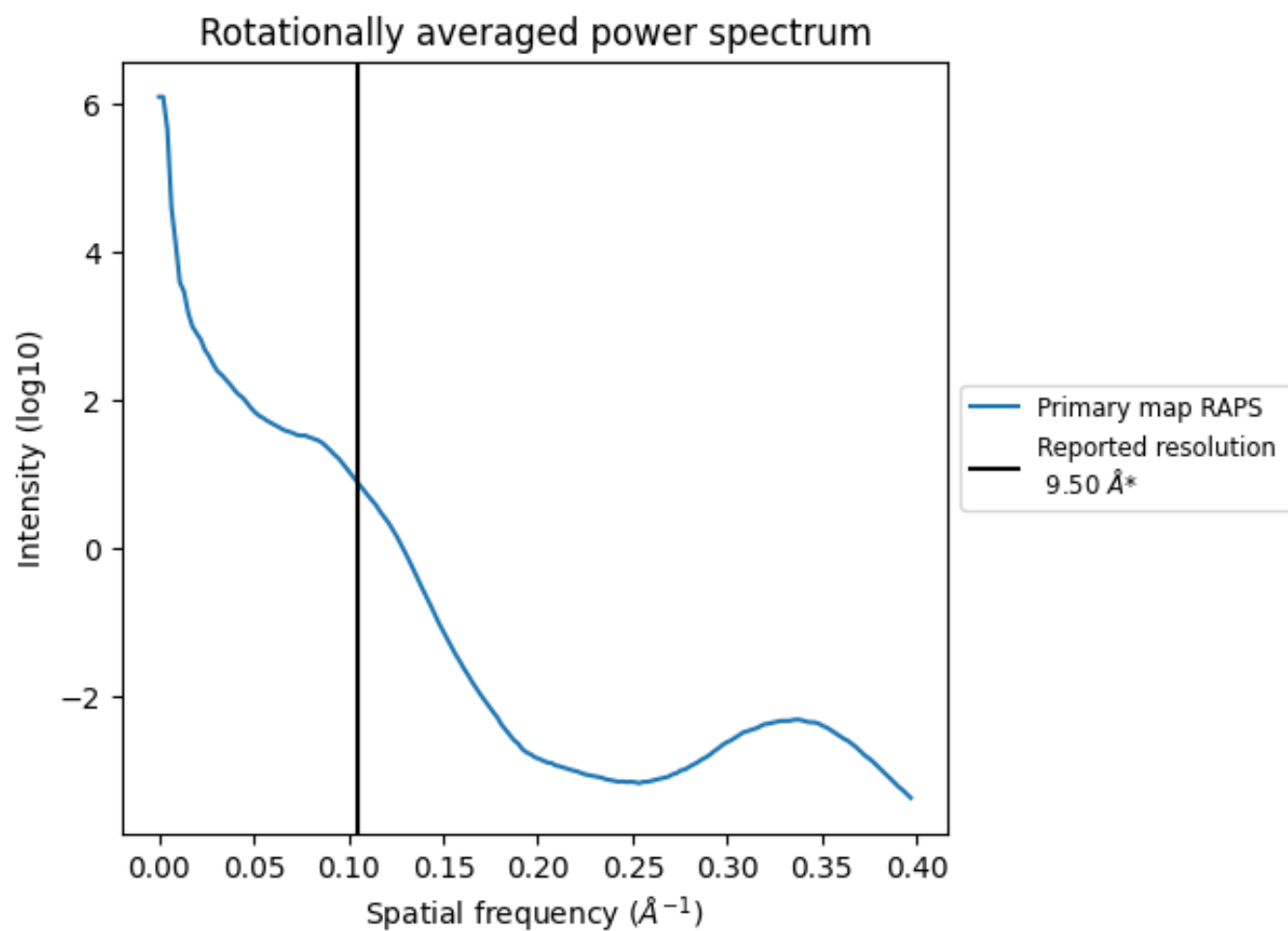
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3306 nm<sup>3</sup>; 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 ⓘ



\*Reported resolution corresponds to spatial frequency of 0.105 Å<sup>-1</sup>

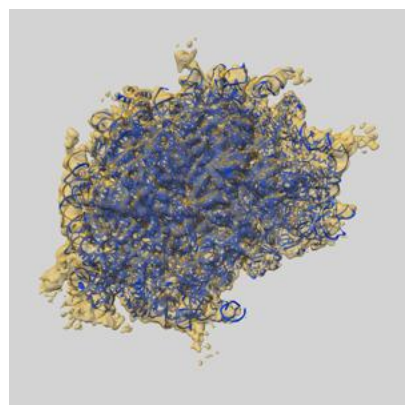
## 8 Fourier-Shell correlation

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

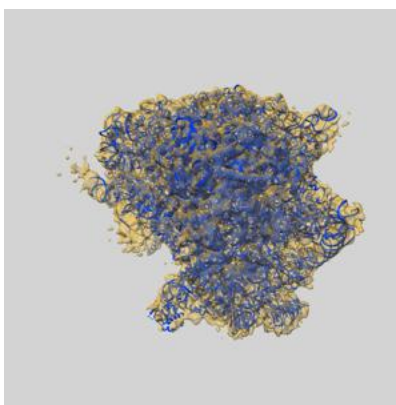
## 9 Map-model fit [i](#)

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 19](#).

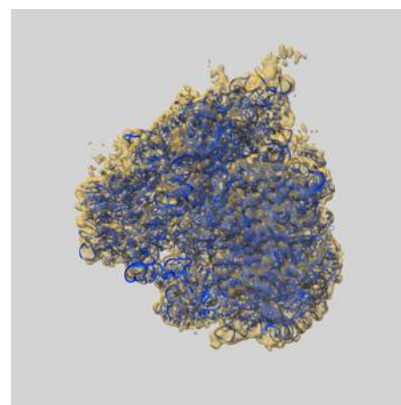
### 9.1 Map-model overlay [i](#)



X



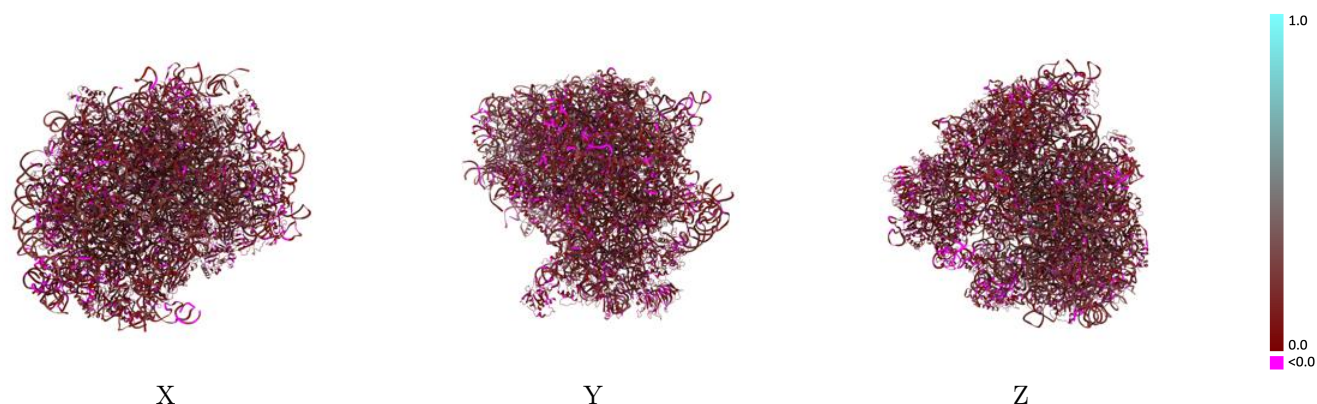
Y



Z

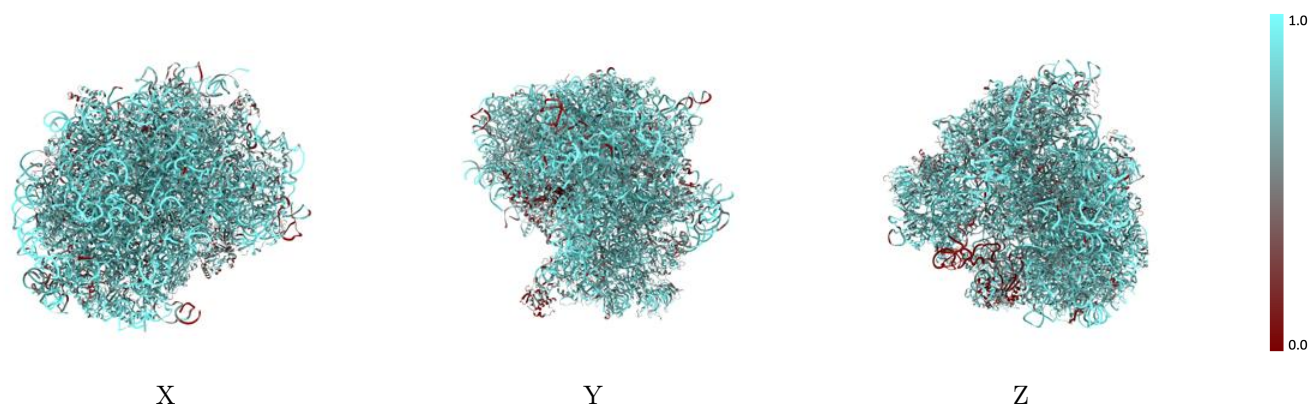
The images above show the 3D surface view of the map at the recommended contour level 2700.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

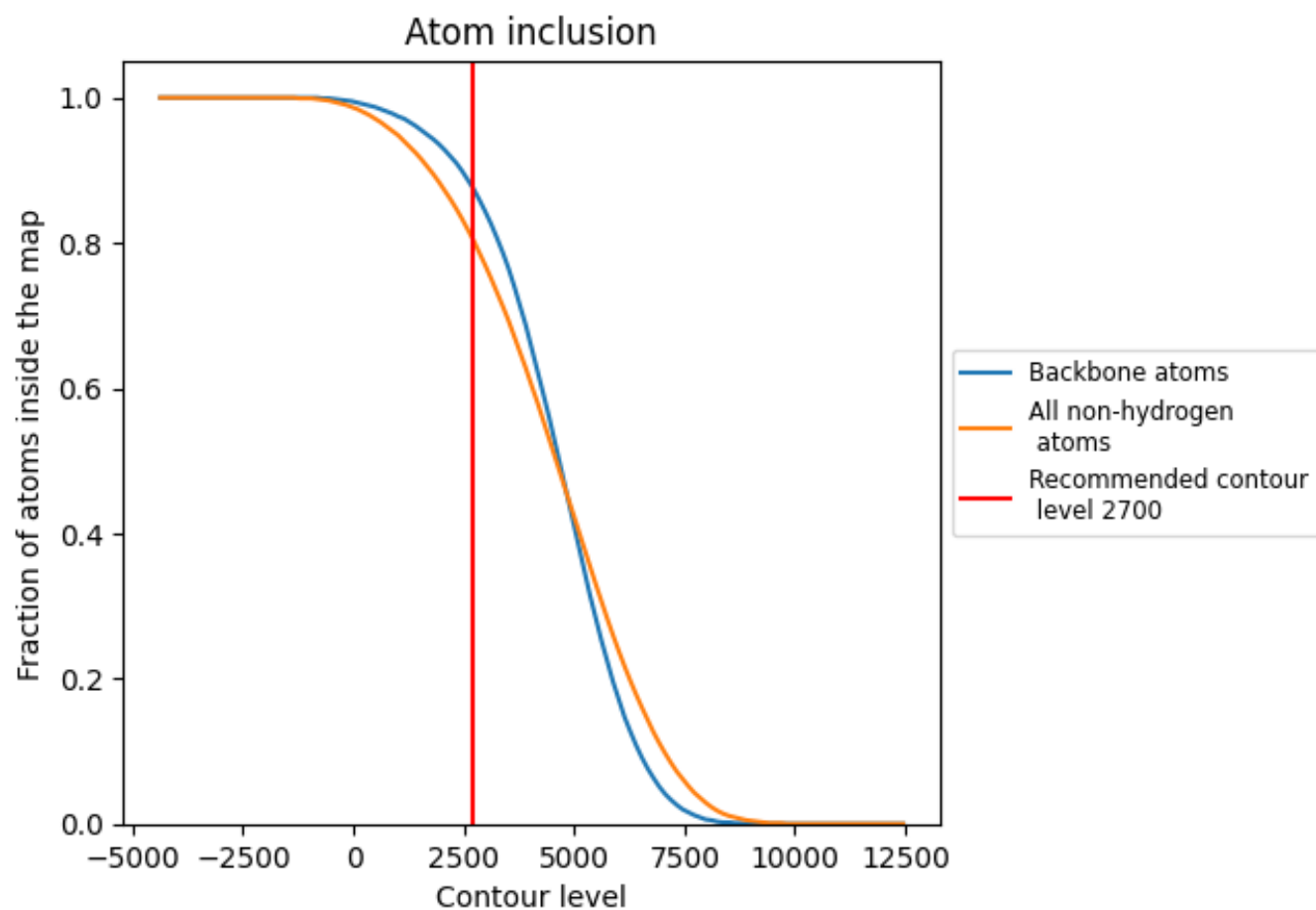
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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

*Continued on next page...*

*Continued from previous page...*

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