



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 08:17 am BST

PDB ID : 4UJD
EMDB ID : EMD-2682
Title : mammalian 80S HCV-IRES initiation complex with eIF5B PRE-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 : 8.90 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:

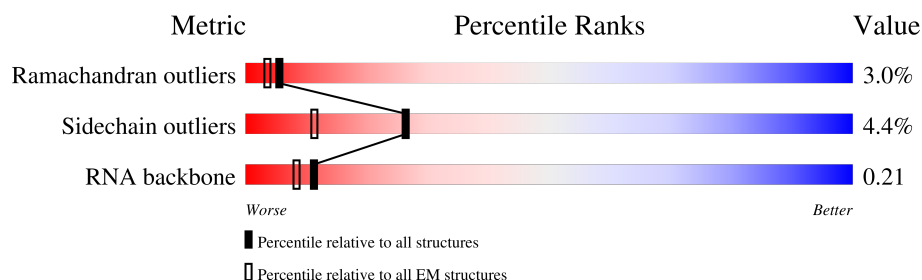
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : 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 8.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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 ≥ 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	A2	5025	
2	A3	194	
3	A4	121	
4	AA	257	
5	AB	403	
6	AC	427	
7	AD	297	
8	AE	158	

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Mol	Chain	Length	Quality of chain
9	AF	248	
10	AG	266	
11	AH	192	
12	AI	214	
13	AJ	178	
14	AL	211	
15	AM	215	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	159	
31	Ac	115	
32	Ad	125	
33	Ae	135	

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Mol	Chain	Length	Quality of chain
34	Af	110	<div> <div>45%</div> <div>86%</div> <div>10%</div> <div>..</div> </div>
35	Ag	117	<div> <div>51%</div> <div>87%</div> <div>10%</div> <div>..</div> </div>
36	Ah	123	<div> <div>31%</div> <div>94%</div> <div>5%</div> <div>.</div> </div>
37	Ai	105	<div> <div>31%</div> <div>83%</div> <div>8%</div> <div>.</div> <div>8%</div> </div>
38	Aj	97	<div> <div>22%</div> <div>84%</div> <div>.</div> <div>12%</div> </div>
39	Ak	70	<div> <div>51%</div> <div>97%</div> <div>..</div> </div>
40	Al	51	<div> <div>39%</div> <div>94%</div> <div>.</div> <div>.</div> </div>
41	Am	128	<div> <div>14%</div> <div>38%</div> <div>.</div> <div>59%</div> </div>
42	An	25	<div> <div>36%</div> <div>100%</div> </div>
43	Ao	106	<div> <div>39%</div> <div>93%</div> <div>7%</div> </div>
44	Ap	92	<div> <div>46%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
45	At	137	<div> <div>47%</div> <div>86%</div> <div>7%</div> <div>.</div> <div>5%</div> </div>
46	Au	210	<div> <div>100%</div> <div>92%</div> <div>8%</div> </div>
47	BA	76	<div> <div>34%</div> <div>67%</div> <div>32%</div> <div>.</div> </div>
48	BB	627	<div> <div>48%</div> <div>86%</div> <div>10%</div> <div>.</div> <div>..</div> </div>
49	BC	504	<div> <div>32%</div> <div>15%</div> <div>22%</div> <div>12%</div> <div>48%</div> </div>
50	C1	1869	<div> <div>13%</div> <div>36%</div> <div>55%</div> <div>.</div> <div>7%</div> </div>
51	CA	295	<div> <div>37%</div> <div>72%</div> <div>.</div> <div>26%</div> </div>
52	CB	264	<div> <div>42%</div> <div>71%</div> <div>8%</div> <div>.</div> <div>19%</div> </div>
53	CC	293	<div> <div>35%</div> <div>72%</div> <div>.</div> <div>24%</div> </div>
54	CD	243	<div> <div>56%</div> <div>81%</div> <div>6%</div> <div>13%</div> </div>
55	CE	263	<div> <div>43%</div> <div>92%</div> <div>6%</div> <div>.</div> </div>
56	CF	204	<div> <div>47%</div> <div>84%</div> <div>8%</div> <div>8%</div> </div>
57	CG	249	<div> <div>45%</div> <div>87%</div> <div>6%</div> <div>7%</div> </div>
58	CH	194	<div> <div>65%</div> <div>94%</div> <div>.</div> <div>..</div> </div>

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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 28S Ribosomal RNA.

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

- Molecule 2 is a RNA chain called 5.8S Ribosomal RNA.

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

- Molecule 3 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L8.

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

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L3.

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

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L4.

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

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L5.

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

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L6.

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

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L7.

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

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L7A.

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

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L9.

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

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L10.

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

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L11.

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

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L13.

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

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L14.

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

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L15.

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

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L13A.

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

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L17.

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

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L18.

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

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L19.

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

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L18A.

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

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L21.

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

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L22.

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

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L23.

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

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L24.

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

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L23A.

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

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L26.

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

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L27.

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

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L27A.

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

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L29.

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

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L30.

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

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L31.

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

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L32.

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

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L35A.

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

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L34.

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

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L35.

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

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L36.

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

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L37.

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

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L38.

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

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L39.

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

- Molecule 41 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

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

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L41.

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

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L36A.

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

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L37A.

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

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L28.

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

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10A.

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

- Molecule 47 is a RNA chain called TRNA.

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

- Molecule 48 is a protein called EIF5B.

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

- Molecule 49 is a RNA chain called HCV-IRES.

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

- 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 ES15.

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 ES11.

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		

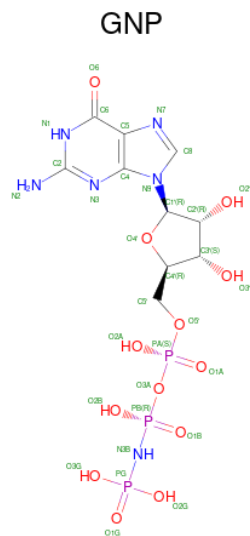
- Molecule 82 is a protein called 40S RIBOSOMAL PROTEIN ES31.

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: C₁₀H₁₇N₆O₁₃P₃).



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

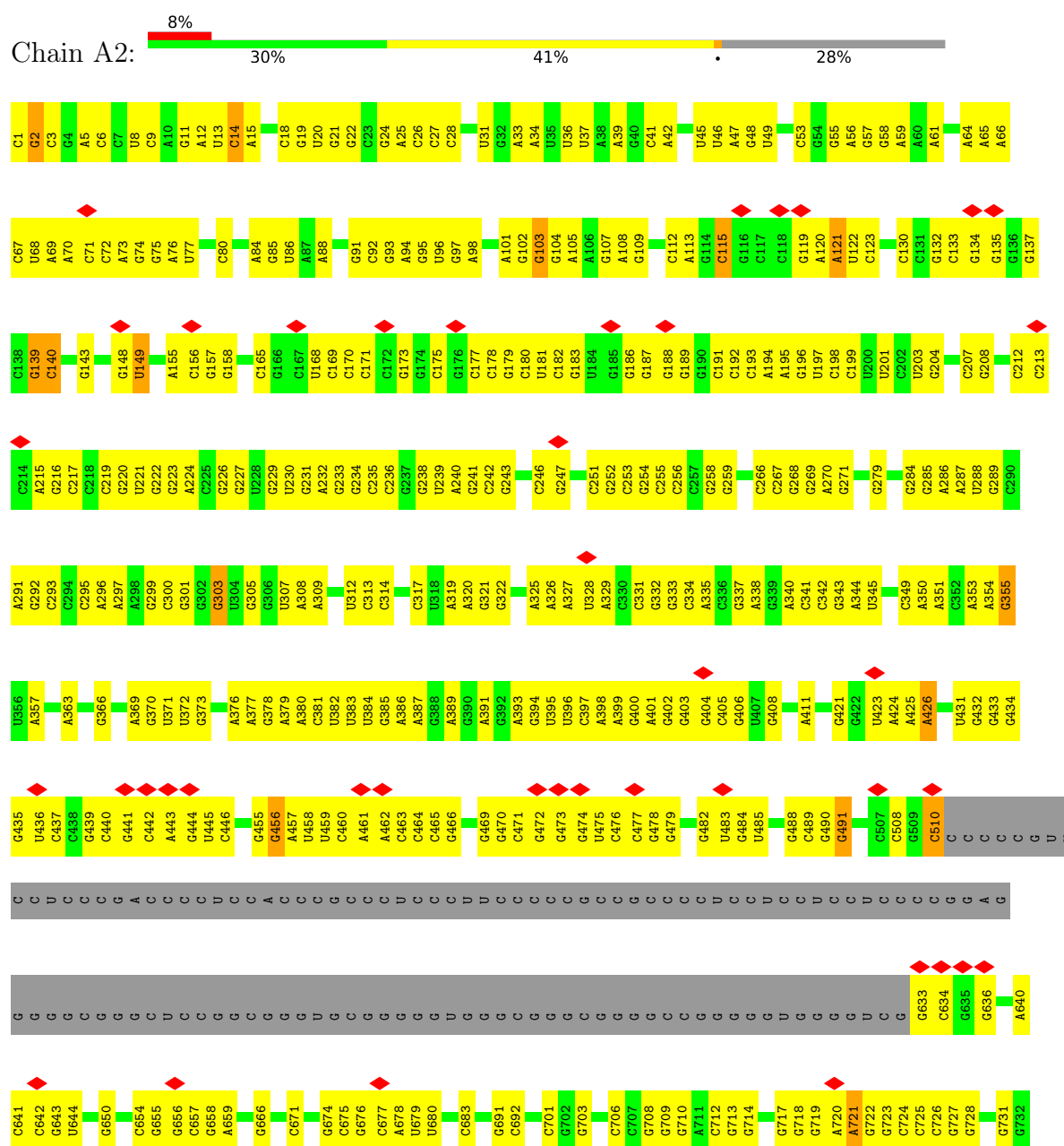
- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

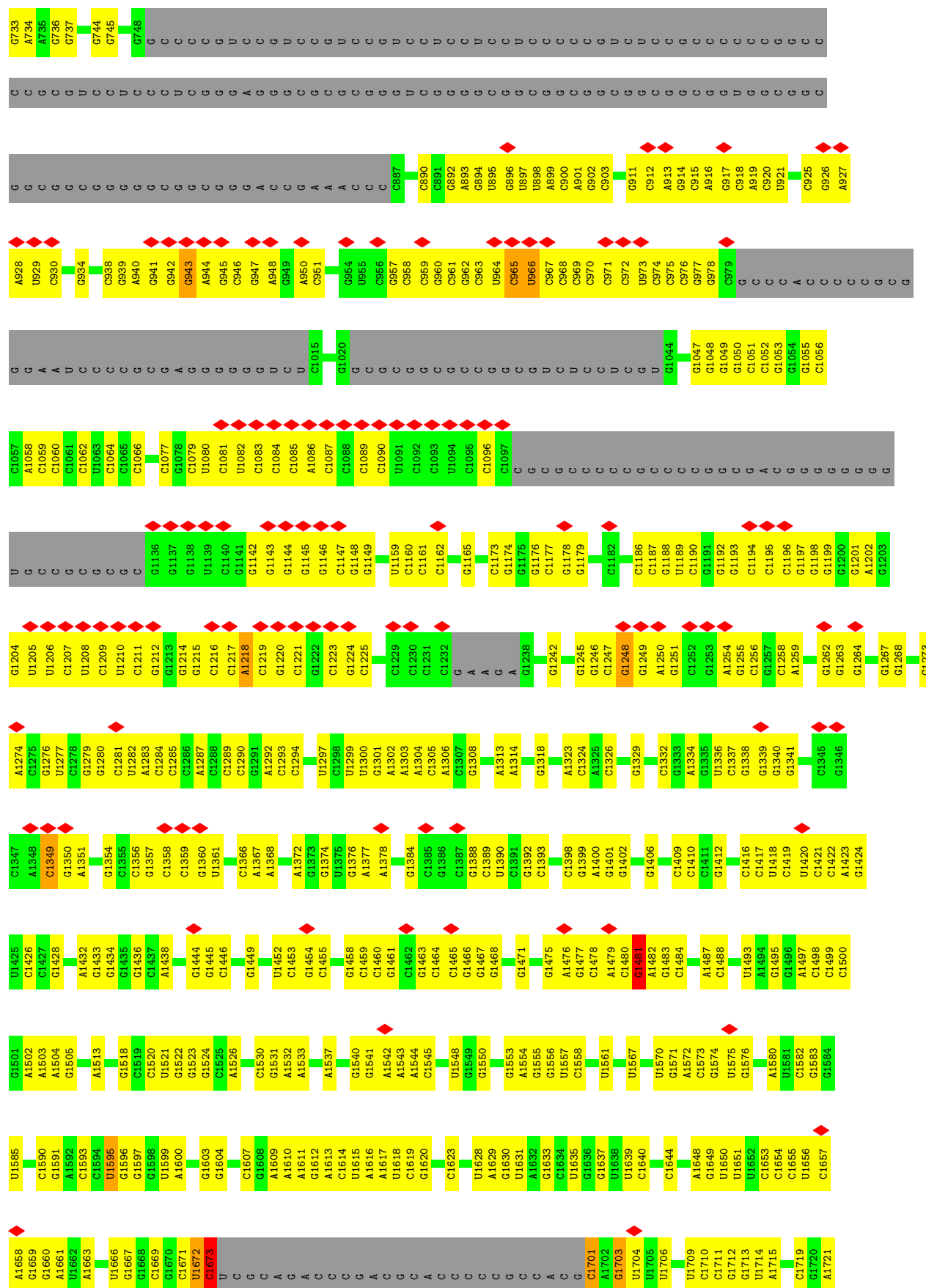
Mol	Chain	Residues	Atoms	AltConf
85	BB	1	Total Mg 1 1	0

3 Residue-property plots

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

• Molecule 1: 28S Ribosomal RNA

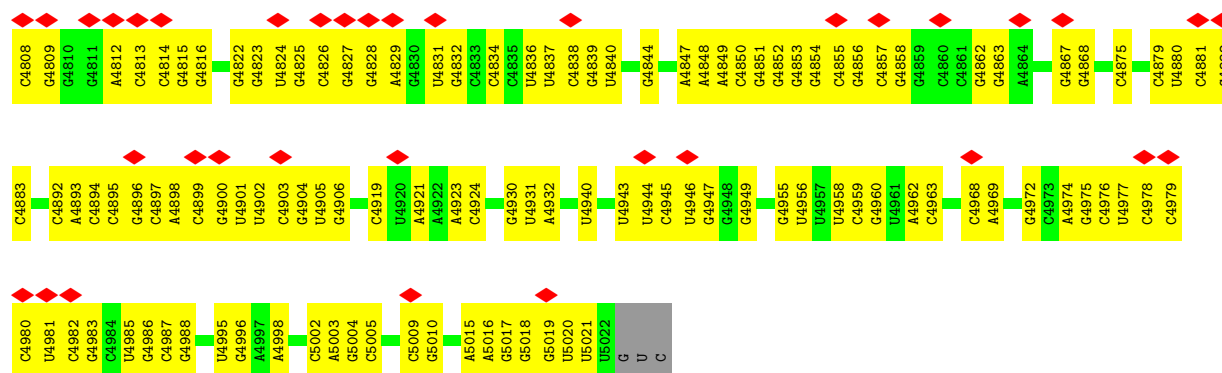




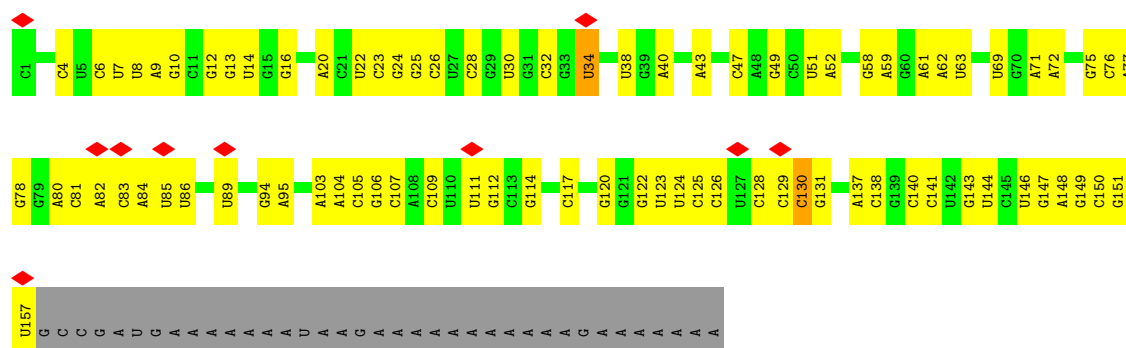


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A3799	G3726	U3646	G3586	G2839	C2762	U2685	◆
U3800	U3727	G3647	C3567	G2840	C2763	C2686	◆
U3801	A3728	U3648	A3568	C2843	A2764	U2765	
C3802	A3729	U3649	G3569	C2844	U2766	C2687	
C3803	C3730	G3650	C3570	U2846	U2767	U2689	
U3807	U3731	A3651	C3574	A2847			
G3808	C3652	G3652	U3575	A2848	C2771	C2692	
U3809	G3653	G3653	U3576		A2772		
A3814	U3733	G3654	G3578	C2852	G2773	C2696	
C3815	G3734	G3655	A3579	G2853	C2774	C2697	
U3819	U3735	A3656	G3583	G2854	A2775	C2698	
U3820	U3737	G3657	U3584			C2699	
A3821	U3741	G3658	U3585	U2857	U2778	U2700	
G3826	U3742	A3661	G3586	A2858	C2779	U2701	
U3830	A3743	U3662	U3587	A2859	U2780	A2702	
U3833	U3744	G3663	C3587	C2860	C2781	C2703	
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C3835	U3746	G3665	G3589	A2862	A2783	U2705	
A3836	G3749	U3666	A3590	U2863	U2789	C2706	
G3837	C3750	G3667	G3594	U2864	C2708	U2707	
C3838	C3751	C3668	G3595		C2709	C2710	
A3845	A3752	C3675	G3596	C2867	U2710	U2711	
A3846	A3753	U3676	G3597	U2868	C2791		
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G3856	U3765	A3686	A3612	C	U2805		
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G3858	C3767	G3694	G3617	C	A2810		
A3859	A3768	A3695	A3618	C	C2811		
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C3867	A3776	G3704	A3625	C	G2818		
G3868	C3777	A3705	U3626	C	G2823		
U3869	G3778	A3706	C3627	C	A2826		
A3870	C3779		A3631	C	A2827		
A3871	G3780		A3632	C	U2746		
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A3874	A3782		G3634	C	C2749		
G3875	U3787		C3635	C	C2750		
U3876	G3788		G3636	C	C2751		
A3877			G3641	C	C2752		
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				C	A2760		
				C			

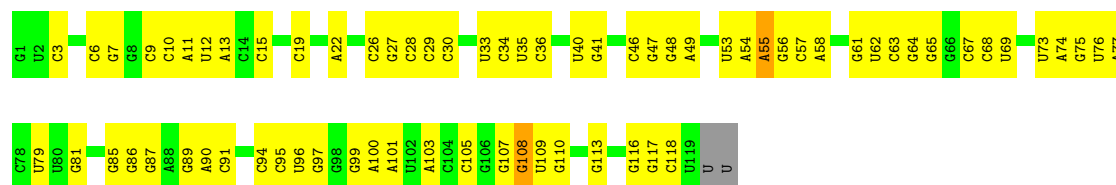
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C4750	A4677	G4600	G4527	U4457	U4379	U4314	A4240	G4151	G4071	C4009	U3883
G	G4678	U4601	U4458	U4458	C4381	G4315	A4242	G4155	A4072	G4010	U3884
G	C4679	U4602	U4459	U4460	A4382	G4316	U4245	G4156	G4073	C4011	G3885
G	G4680	G4603	G4530	U4461	U4383	G4317	G4246	U4159	G4074	U4012	U3886
C	A4682	A4531	A4532	C4465	A4384	U4318	G4247	C4159	G4077	G4013	G3887
C	A4683	U4532	C4466	C4466	C4385	U4319	C4248	C4159	C4078	G4014	C3888
C	C4684	G4533	A4467	A4467	C4387	U4320	U4249	A4163	C4079	A4015	U3889
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C	G4689	G4535	A4471	A4471	A4389	G4324	G4251	A4166	U4017	A4017	G3891
C	G4690	U4536	U4472	U4472	C4390	A4325	A4252	A4167	A4018	G4018	U3894
C	G4691	G4537	A4473	A4473	C4394	A4326	U4253	U4168	G4082	C4019	U3895
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C	A4693	U4539	G4475	G4475	C4396	C4328	U4255	U4168	U4084	A4021	A3897
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C	A4632	U4551	C4486	C4486	U4410	A4339	A4270	A4186	U4031	U4031	G3915
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C	A4641	U4561	A4493	A4493	C4416	A4348	G4279	U4193	C4109	G4040	G3924
C	U4642	A4562	G4494	G4494	U4420	C4349	G4280	A4194	C4110	U3926	U3927
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C	A4651	A4567	C4500	C4500	U4423	A4354	C4287	C4201	G4044	G4044	A3929
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C	U4657	G4578	C4504	C4504	U4431	C4358	G4291	G4216	U4051	U4051	U3933
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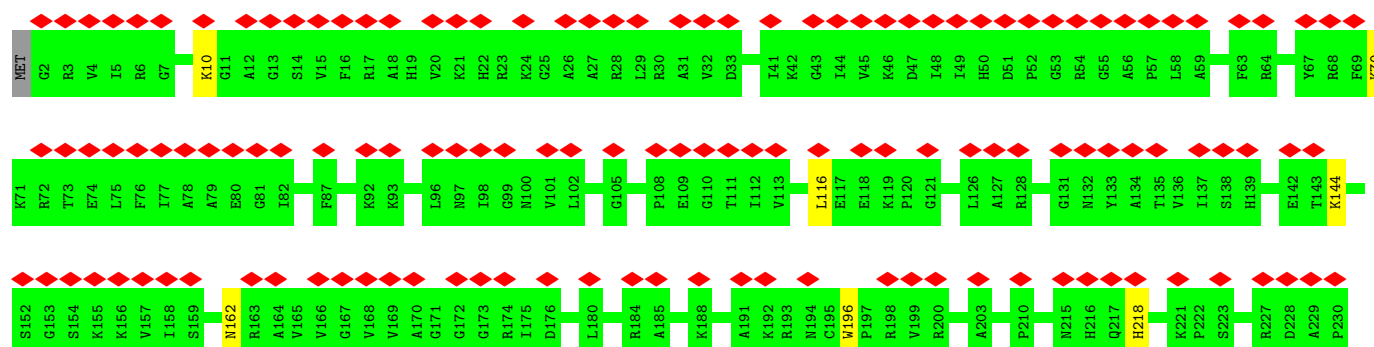
• Molecule 2: 5.8S Ribosomal RNA

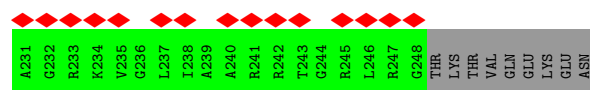


• Molecule 3: 5S Ribosomal RNA

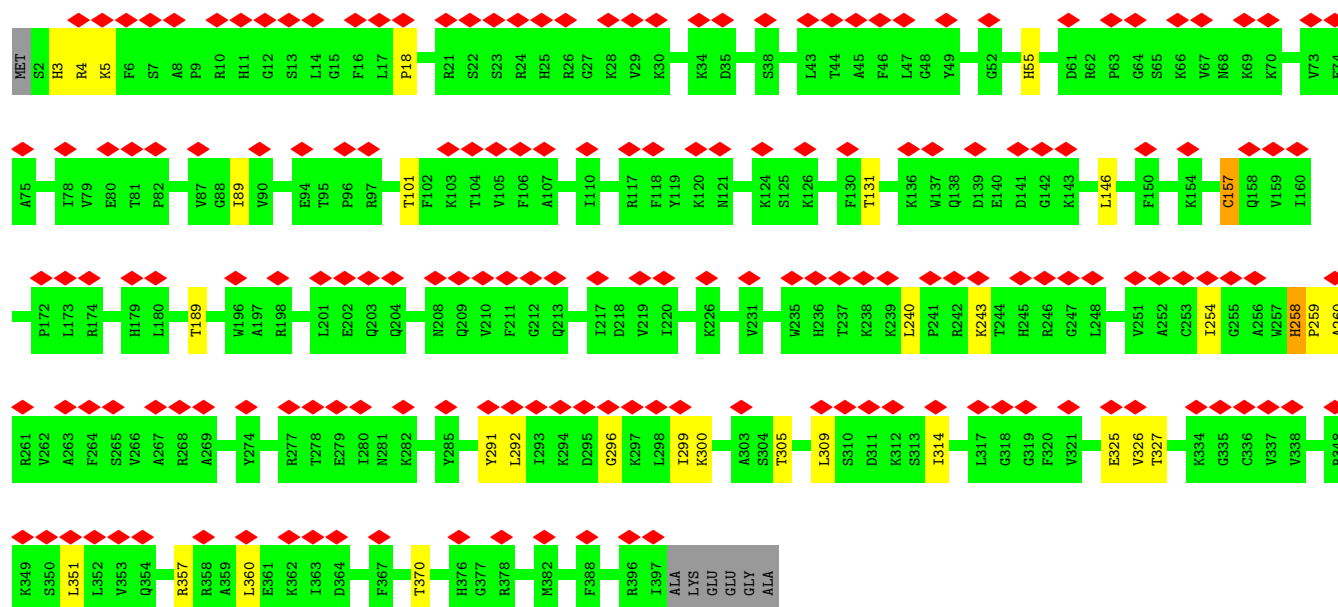
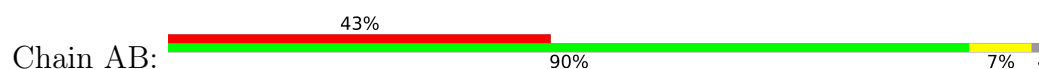


• Molecule 4: 60S RIBOSOMAL PROTEIN L8

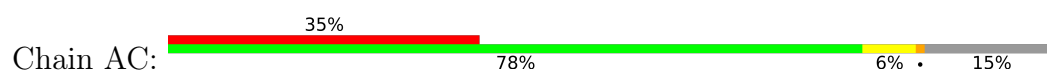




• Molecule 5: 60S RIBOSOMAL PROTEIN L3

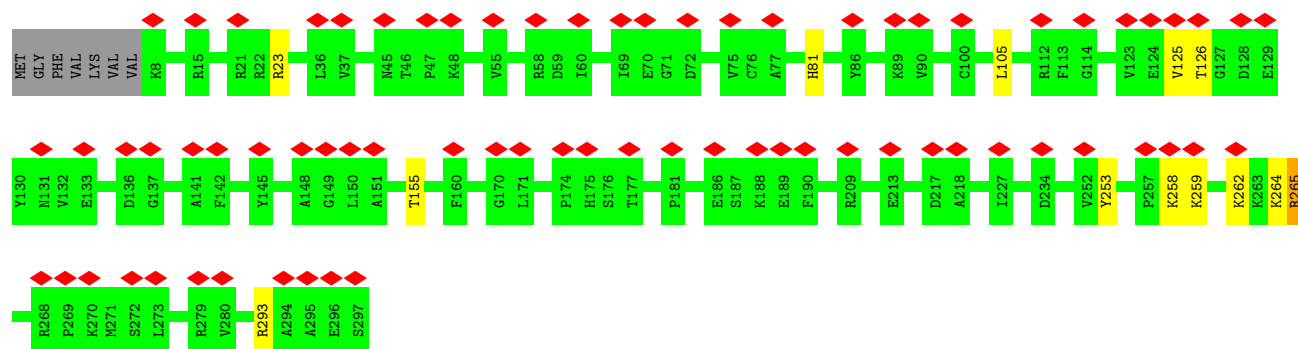


• Molecule 6: 60S RIBOSOMAL PROTEIN L4

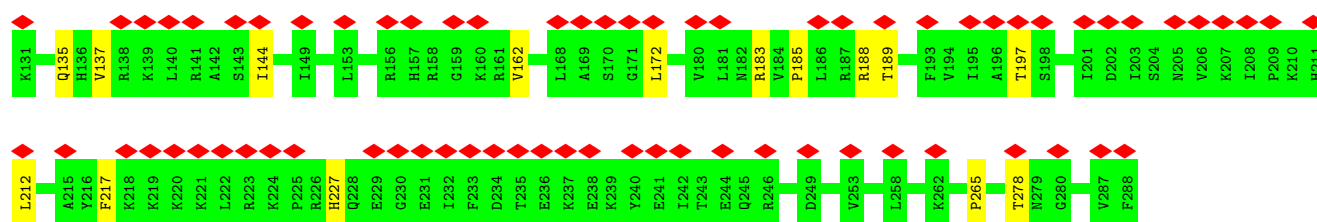


• Molecule 7: 60S RIBOSOMAL PROTEIN L5

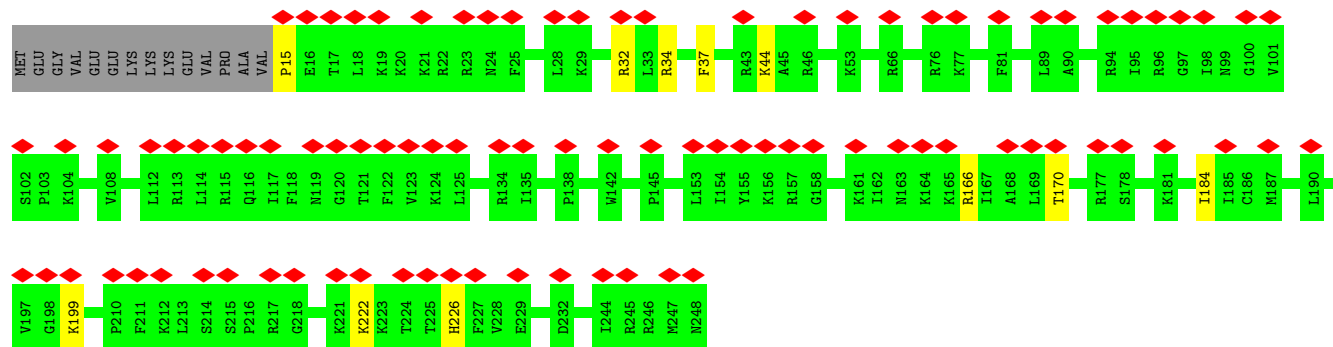
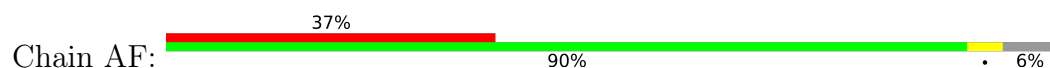




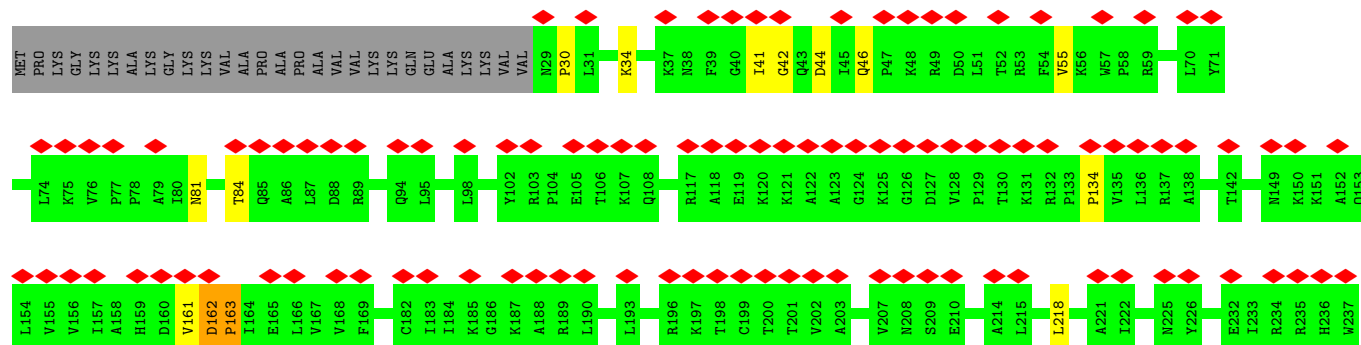
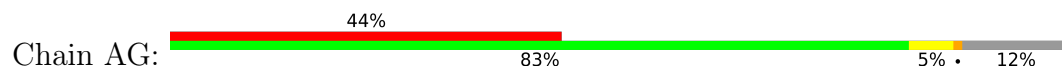
• Molecule 8: 60S RIBOSOMAL PROTEIN L6

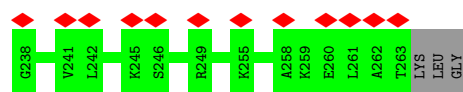


• Molecule 9: 60S RIBOSOMAL PROTEIN L7

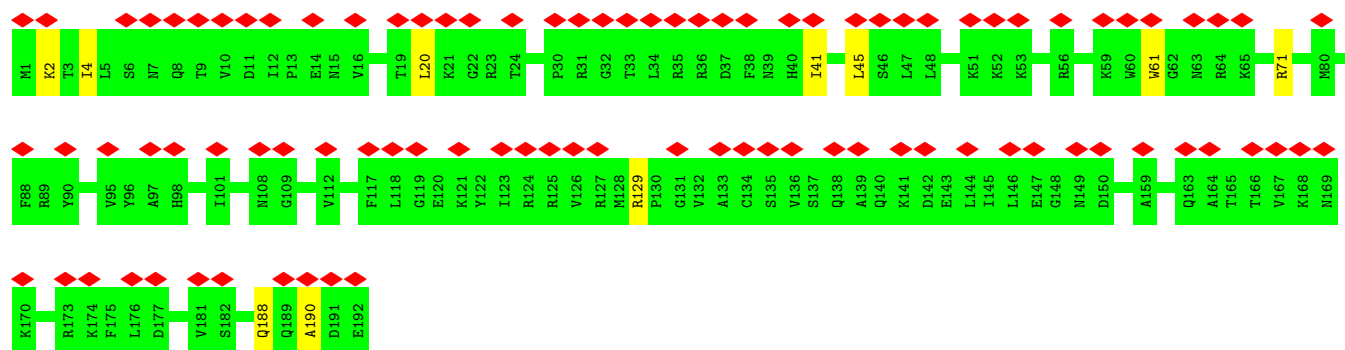


• Molecule 10: 60S RIBOSOMAL PROTEIN L7A

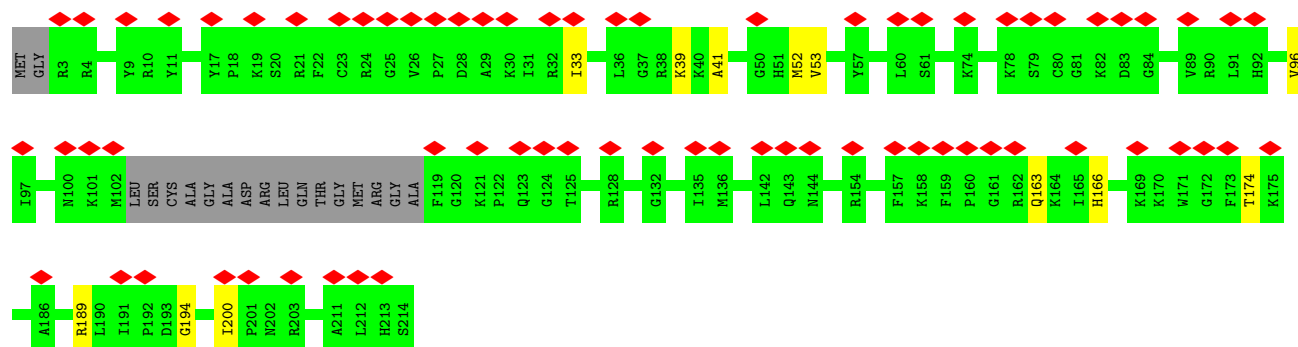
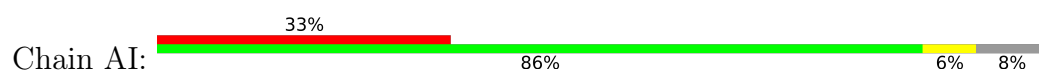




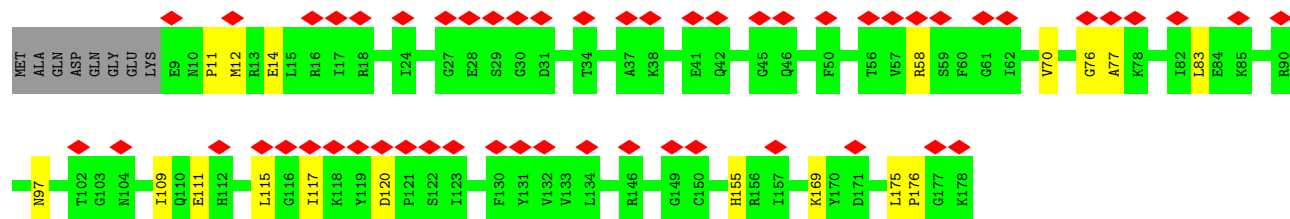
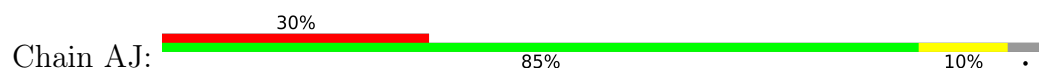
• Molecule 11: 60S RIBOSOMAL PROTEIN L9



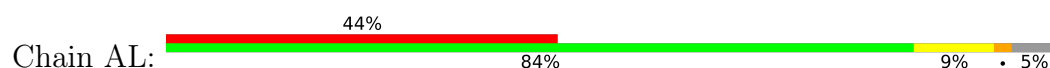
• Molecule 12: 60S RIBOSOMAL PROTEIN L10

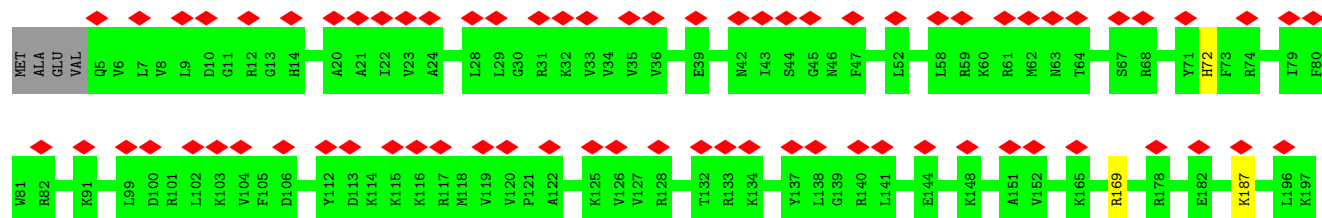


• Molecule 13: 60S RIBOSOMAL PROTEIN L11



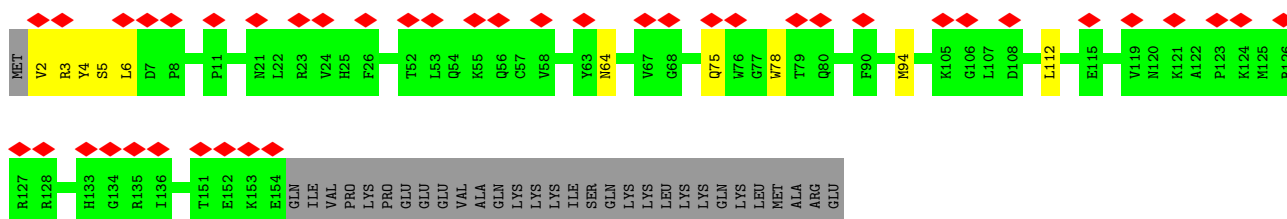
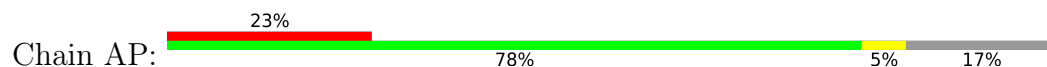
• Molecule 14: 60S RIBOSOMAL PROTEIN L13



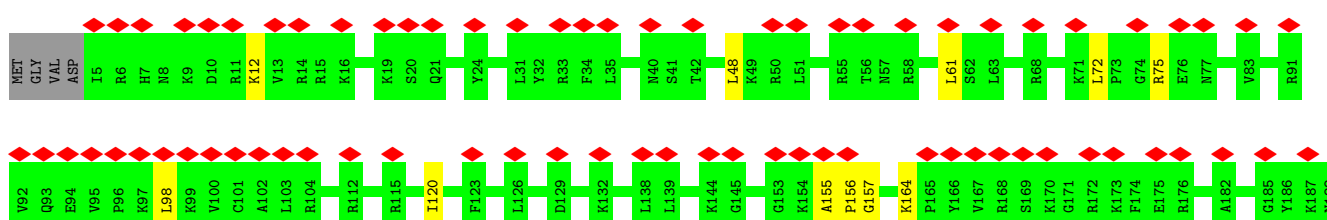
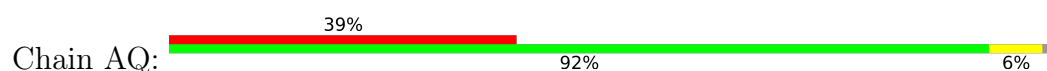




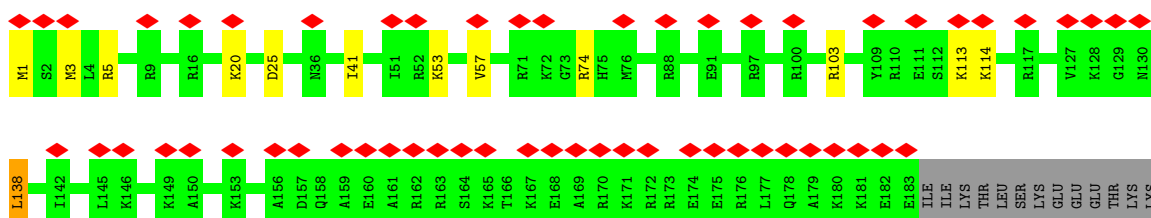
• Molecule 18: 60S RIBOSOMAL PROTEIN L17



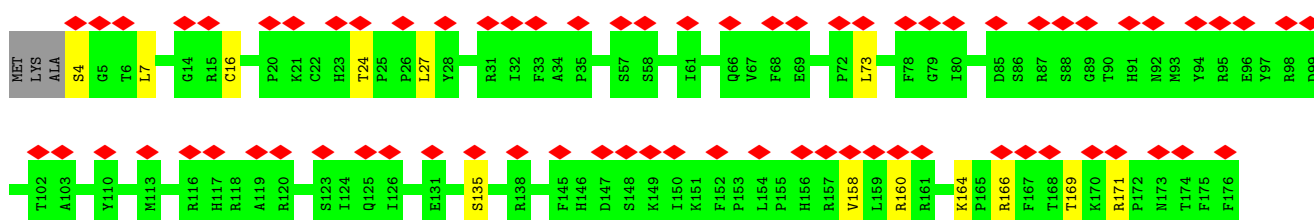
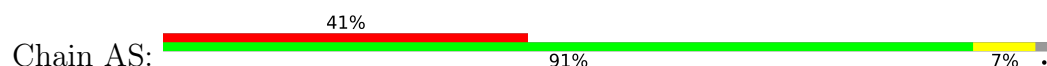
• Molecule 19: 60S RIBOSOMAL PROTEIN L18



• Molecule 20: 60S RIBOSOMAL PROTEIN L19



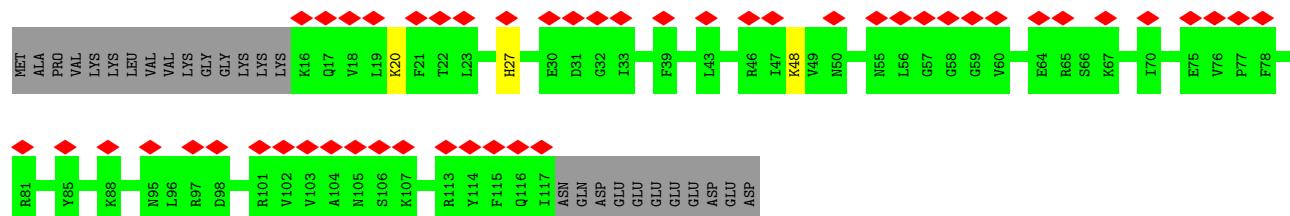
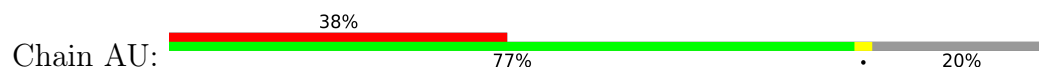
• Molecule 21: 60S RIBOSOMAL PROTEIN L18A



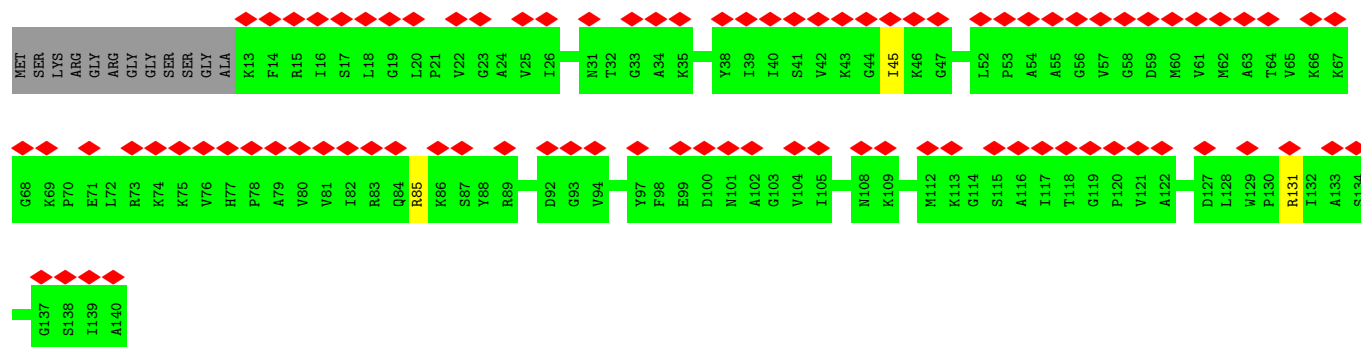
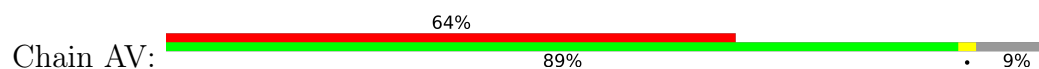
• Molecule 22: 60S RIBOSOMAL PROTEIN L21



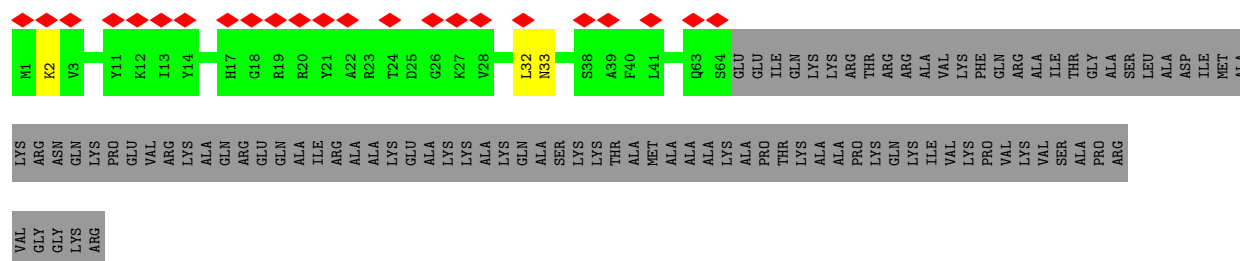
● Molecule 23: 60S RIBOSOMAL PROTEIN L22



- Molecule 24: 60S RIBOSOMAL PROTEIN L23

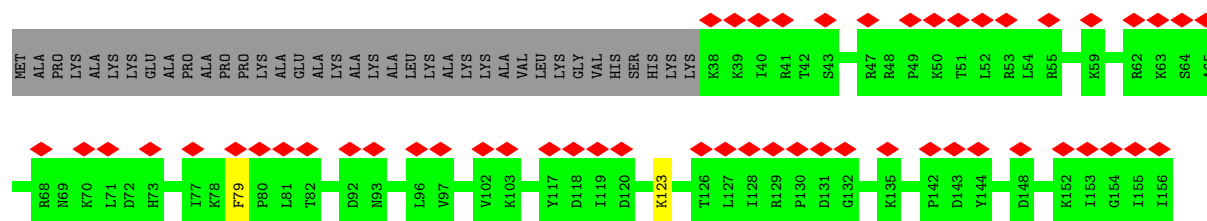


● Molecule 25: 60S RIBOSOMAL PROTEIN L24



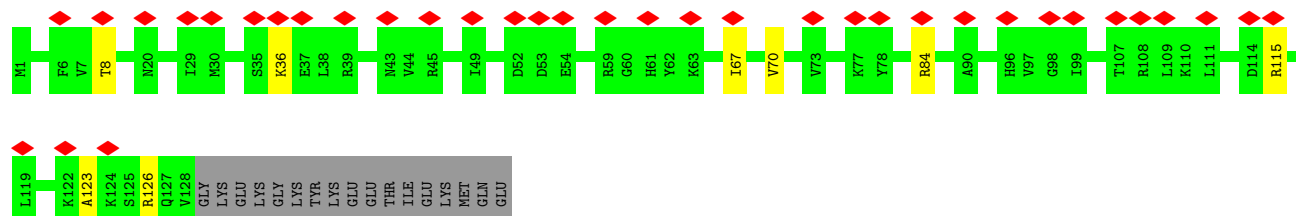
● Molecule 26: 60S RIBOSOMAL PROTEIN L23A





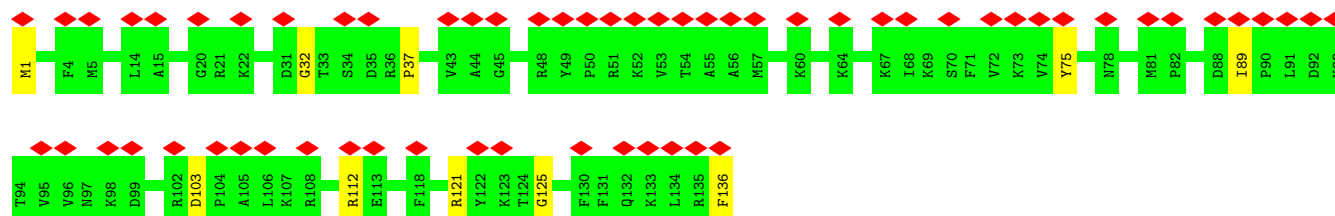
• Molecule 27: 60S RIBOSOMAL PROTEIN L26

Chain AY:



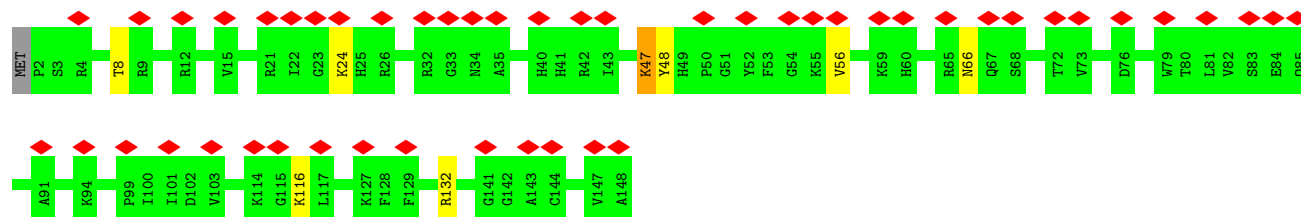
• Molecule 28: 60S RIBOSOMAL PROTEIN L27

Chain AZ:



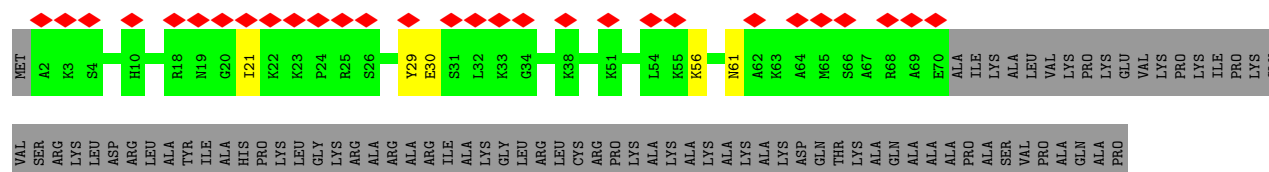
• Molecule 29: 60S RIBOSOMAL PROTEIN L27A

Chain Aa:




• Molecule 30: 60S RIBOSOMAL PROTEIN L29

Chain Ab:



LYS
ARG
THR
GLN
ALA
PRO
THR
LYS
ALA
SER
GLU


• Molecule 31: 60S RIBOSOMAL PROTEIN L30

Chain Ac: 

MET VAL ALA PRO ALA LYS T7 K8 K9 S10 L11 E12 R17 K23 L29 I47 L48 P53 A54 L55 R56 I60 Y63 G70 H73 I79 E80 L81 A84 C85 G86 K87 Y88 T93 L94 D98 P99 G100 D101 S102 D103 I104 I105 R106 S107 M108 P109

E110
GLN
THR
GLY
GLU
LYS

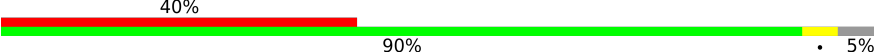
• Molecule 32: 60S RIBOSOMAL PROTEIN L31

Chain Ad: 

MET ALA PRO ALA LYS GLY GLY LYS LYS GLY ARG SER ALA I17 N18 E19 V20 Y25 R32 I33 H34 G35 K39 K40 K55 E56 M57 G58 T59 P60 I64 I77 V80 R83 R92 N93 E94 D95 E96 P99 V106 T107 Y108 V109 P110 V111

T112 T113 F114 K115 M116 L117 Q118 T119 D123 E124 M125


• Molecule 33: 60S RIBOSOMAL PROTEIN L32

Chain Ae: 

MET ALA PRO ALA LEU R5 P6 L7 W8 K9 P10 K11 K12 V13 K14 K15 R16 R17 T17 K18 K19 F20 I21 R22 H23 Q24 S25 D26 R27 R33 R36 K37 P38 R39 Q40 I41 D42 M43 R44 R48 F49 K50 Q51 Q52 I53 L54 M55 P56 K64 L70 P71 S72 K76 H80

R83 L83 N92 K93 S94 Y95 C96 A97 E98 I99 R108 K109 A110 R114 A119 R128 L129 R130 S131 E132 GLU ASN GLU


• Molecule 34: 60S RIBOSOMAL PROTEIN L35A

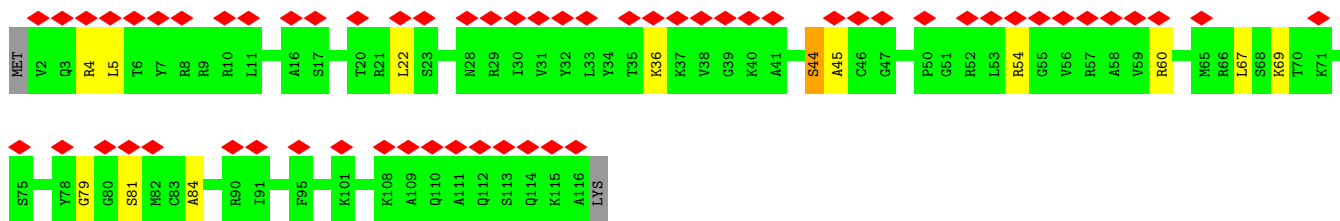
Chain Af: 

MET SER GLY R4 L5 F11 A12 G13 G14 K15 R16 G17 L18 R19 N20 Q21 E23 H24 A26 K29 Y34 A35 R36 T39 E40 F41 Y42 A48 Y49 V50 Y51 K52 K53 A54 N55 N56 T57 V58 T59 P60 G61 P64 N65 K66 W71 G72 K73 R76 A77

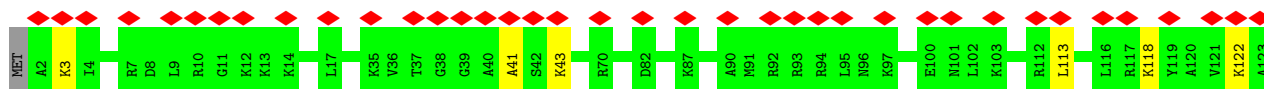
A86 R89 S90 N91 L92 P93 A94 K95 A96 I97 G98 H99 R100 I101 R102 L105 Y106 P107 S108 R109 I110

• Molecule 35: 60S RIBOSOMAL PROTEIN L34

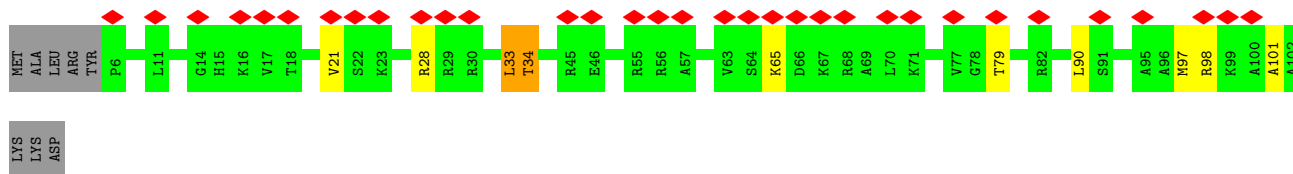
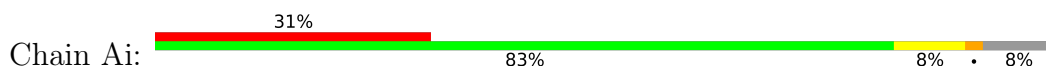
Chain Ag: 



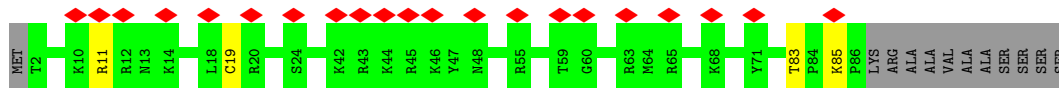
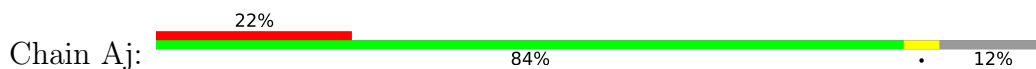
• Molecule 36: 60S RIBOSOMAL PROTEIN L35



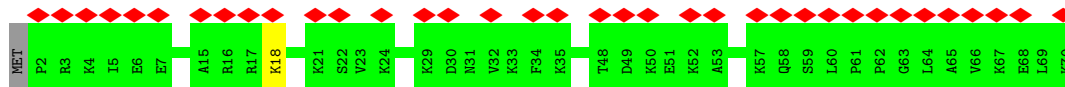
• Molecule 37: 60S RIBOSOMAL PROTEIN L36



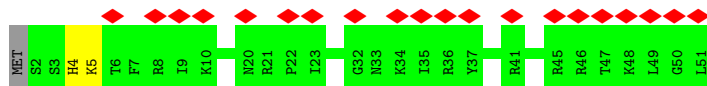
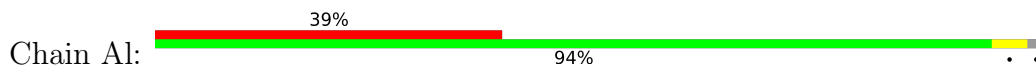
• Molecule 38: 60S RIBOSOMAL PROTEIN L37



• Molecule 39: 60S RIBOSOMAL PROTEIN L38

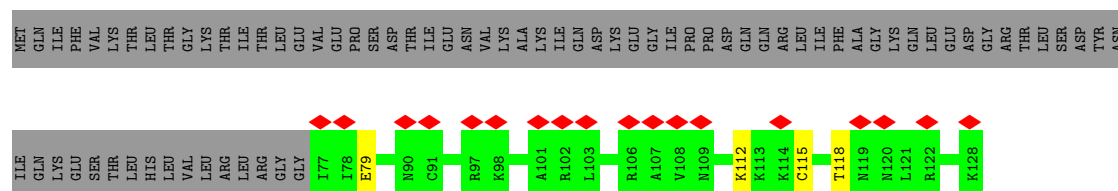


• Molecule 40: 60S RIBOSOMAL PROTEIN L39



• Molecule 41: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

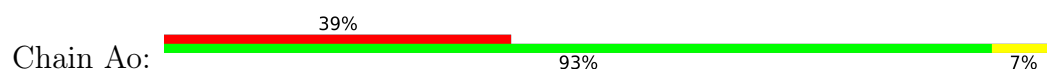




• Molecule 42: 60S RIBOSOMAL PROTEIN L41



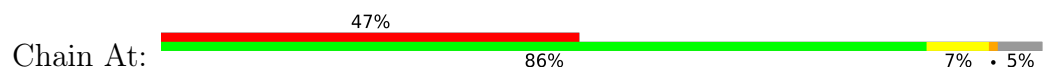
• Molecule 43: 60S RIBOSOMAL PROTEIN L36A



• Molecule 44: 60S RIBOSOMAL PROTEIN L28



• Molecule 45: 60S RIBOSOMAL PROTEIN L28



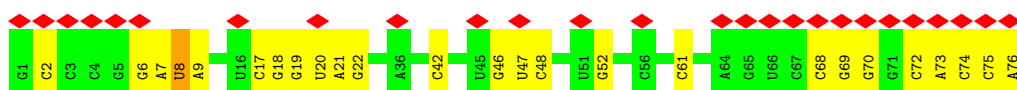
• Molecule 46: 60S RIBOSOMAL PROTEIN L10A





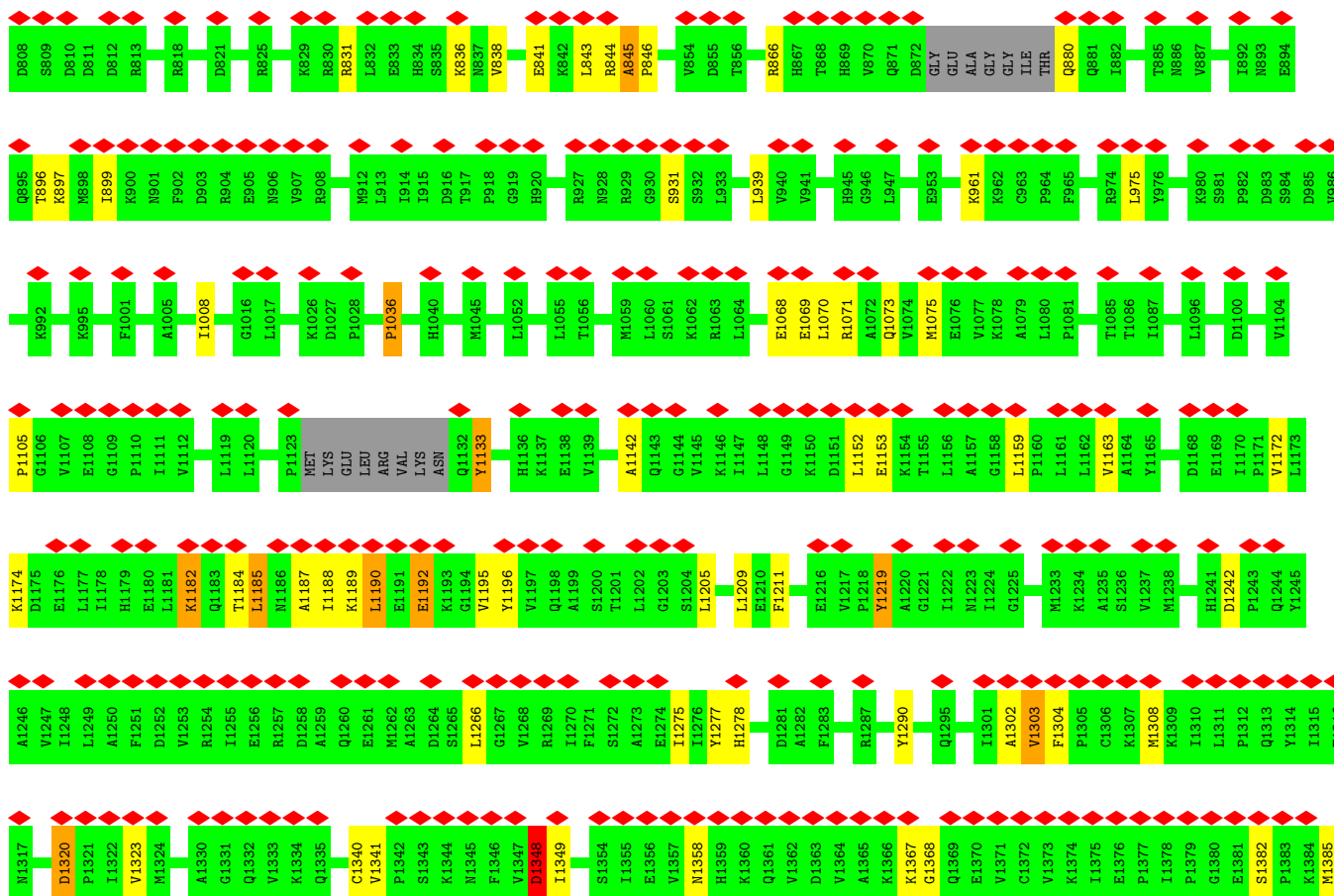
• Molecule 47: TRNA

Chain BA:

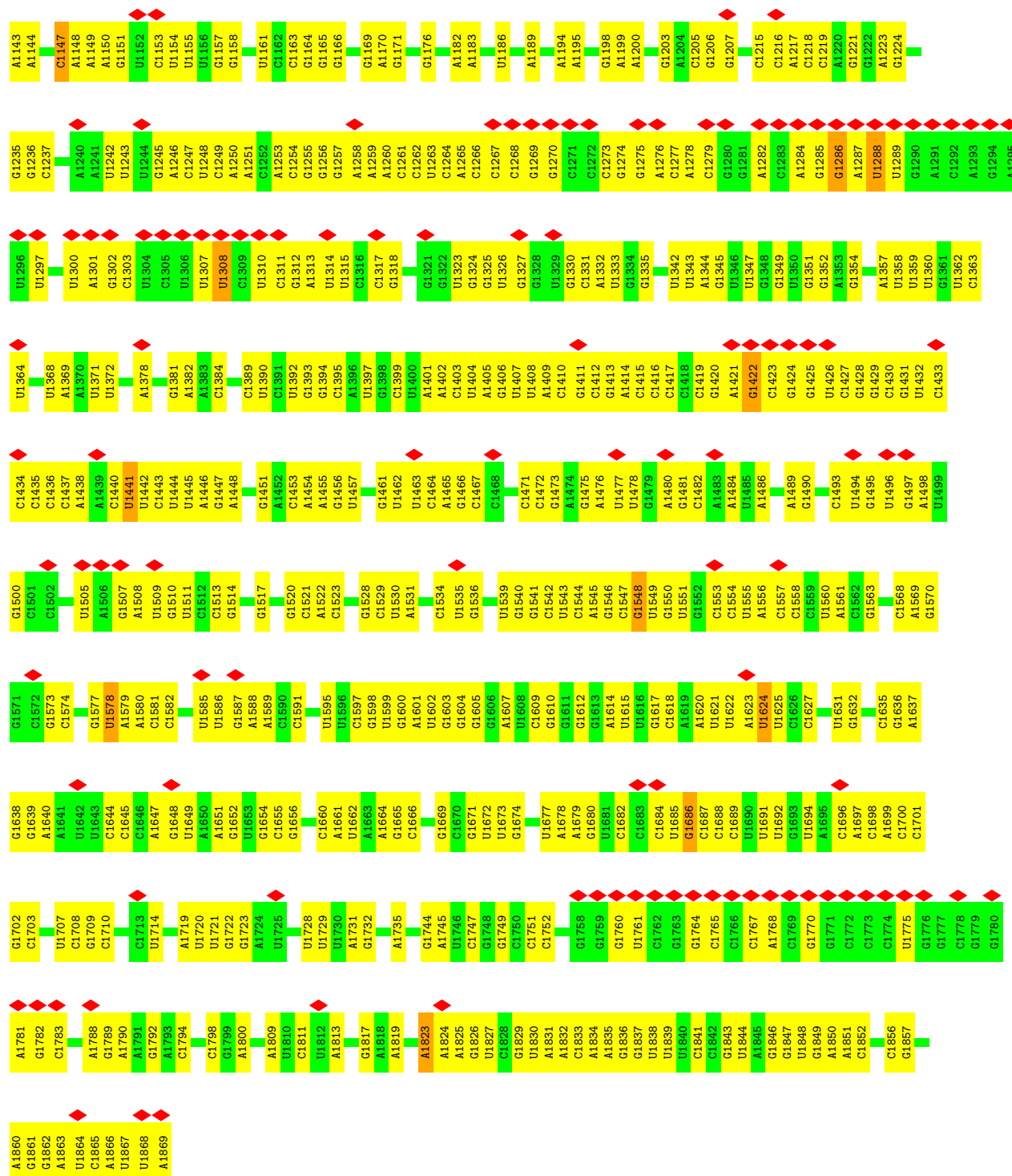


• Molecule 48: EIF5B

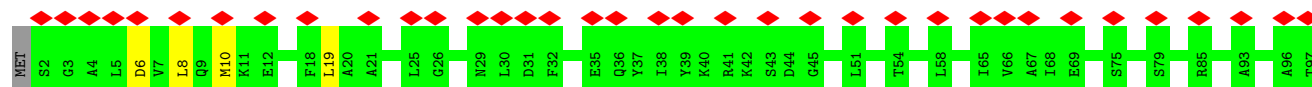
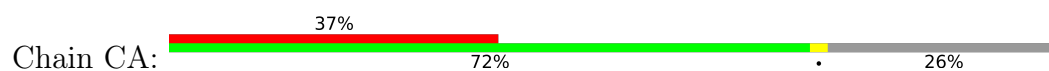
Chain BB:

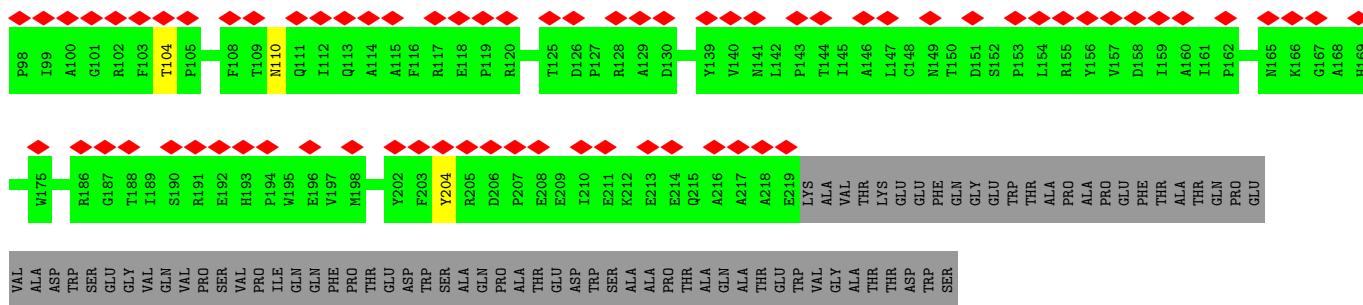




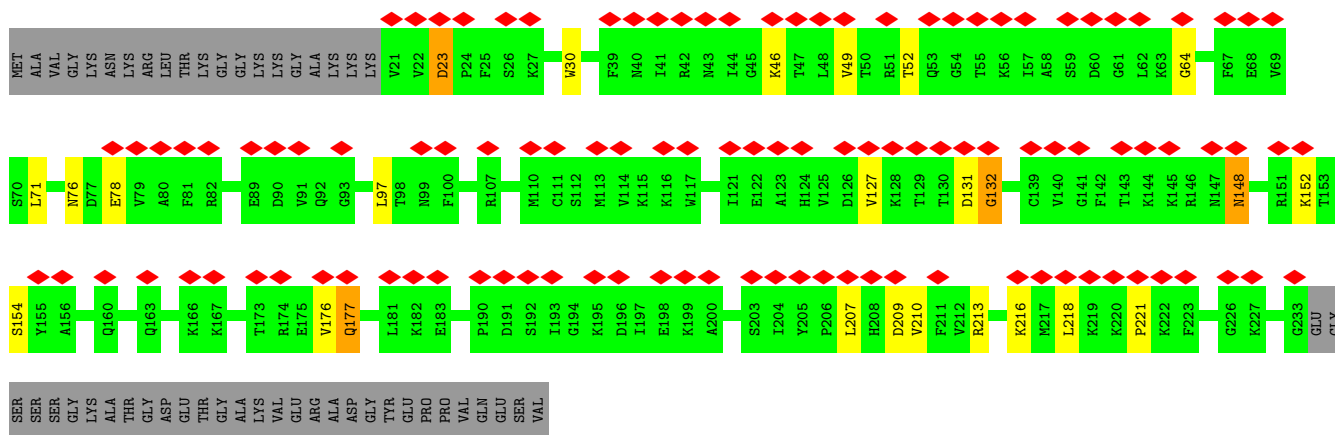
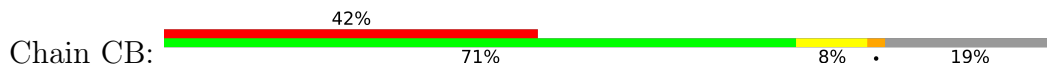


• Molecule 51: 40S RIBOSOMAL PROTEIN US2

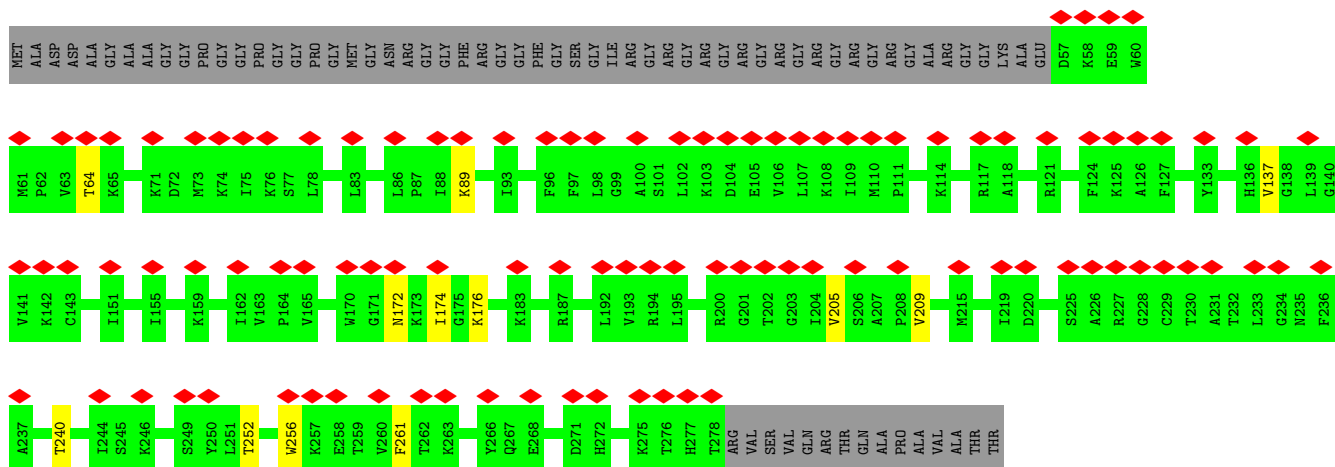




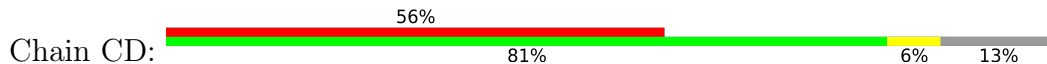
- Molecule 52: 40S RIBOSOMAL PROTEIN ES1

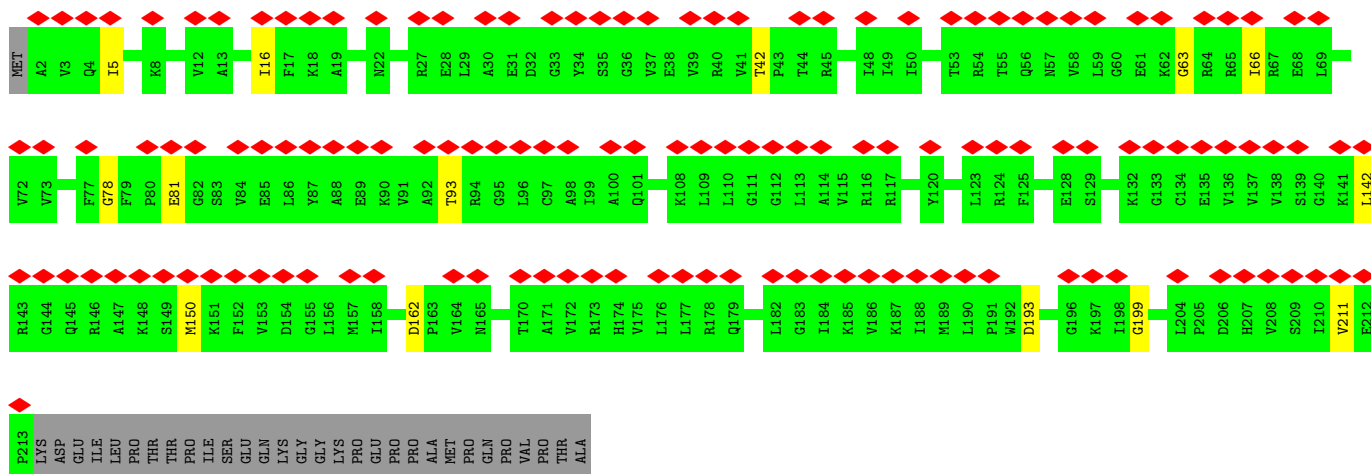


● Molecule 53: 40S RIBOSOMAL PROTEIN US5



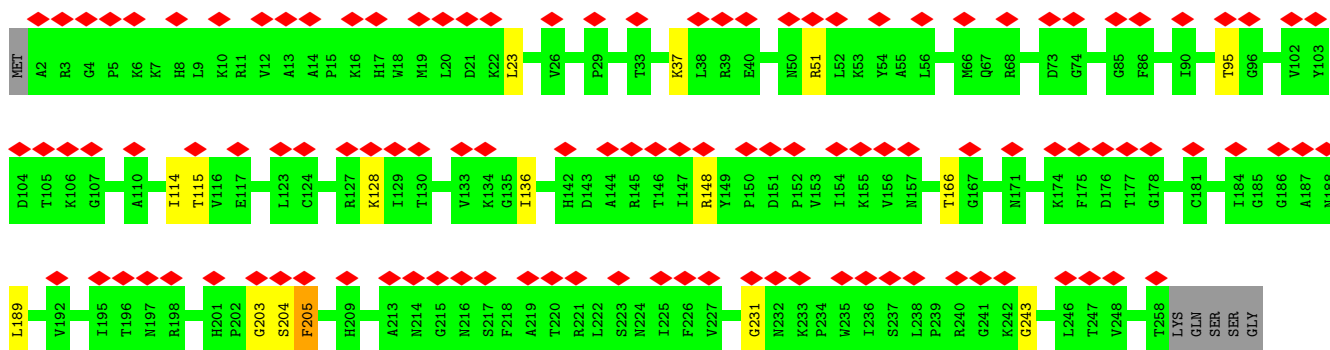
- Molecule 54: 40S RIBOSOMAL PROTEIN US3





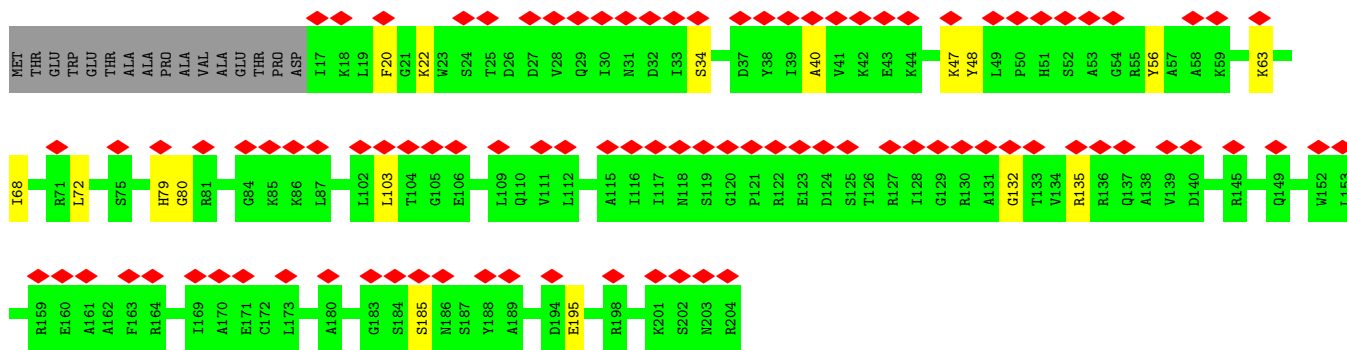
• Molecule 55: 40S RIBOSOMAL PROTEIN ES4

Chain CE: 43% 92% 6% •



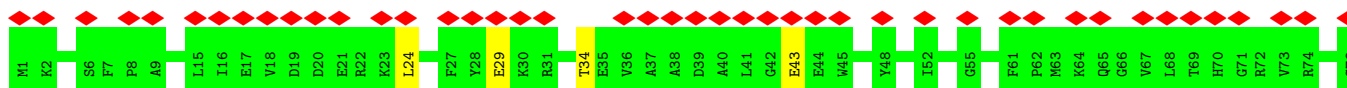
• Molecule 56: 40S RIBOSOMAL PROTEIN US7

Chain CF: 47% 84% 8% 8%

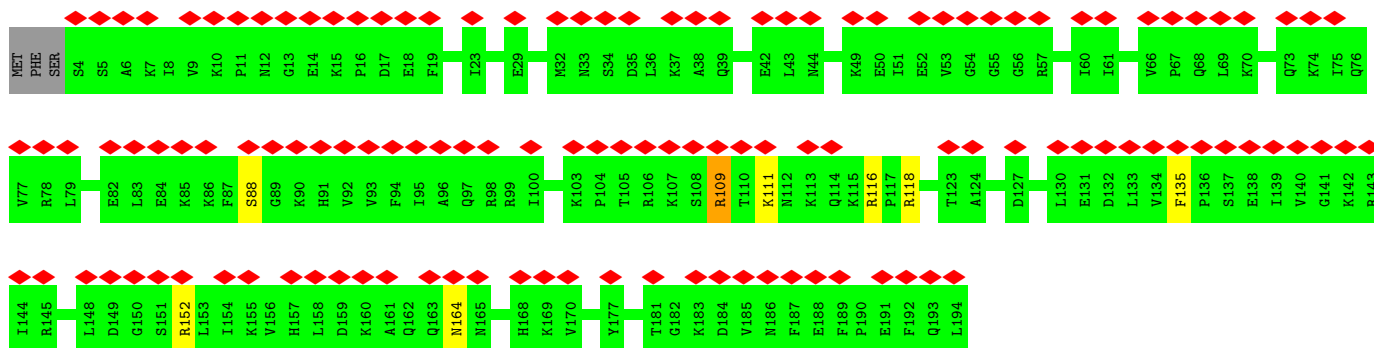


• Molecule 57: 40S RIBOSOMAL PROTEIN ES6

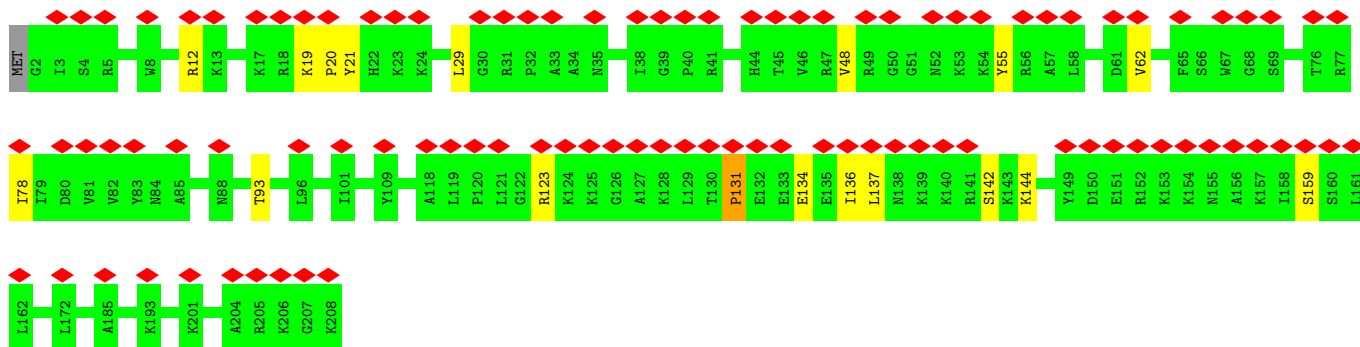
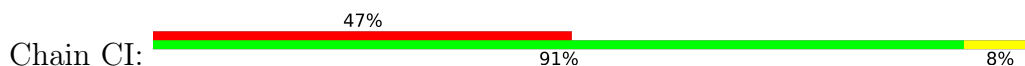
Chain CG: 45% 87% 6% 7%



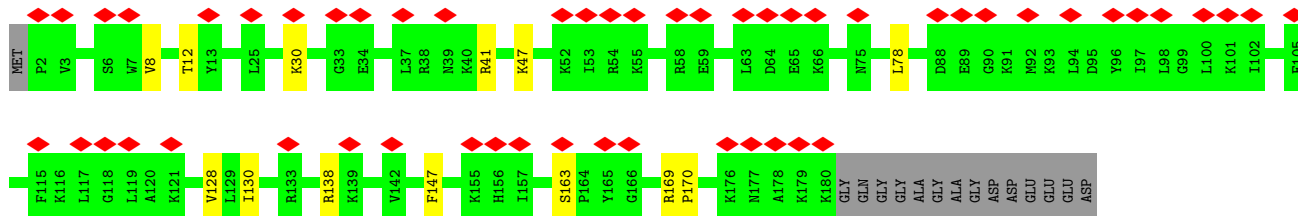
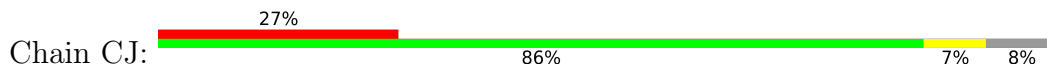
• Molecule 58: 40S RIBOSOMAL PROTEIN ES7



● Molecule 59: 40S RIBOSOMAL PROTEIN ES8

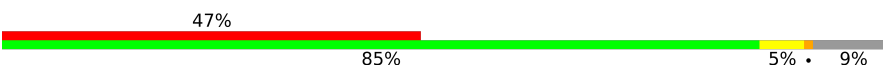


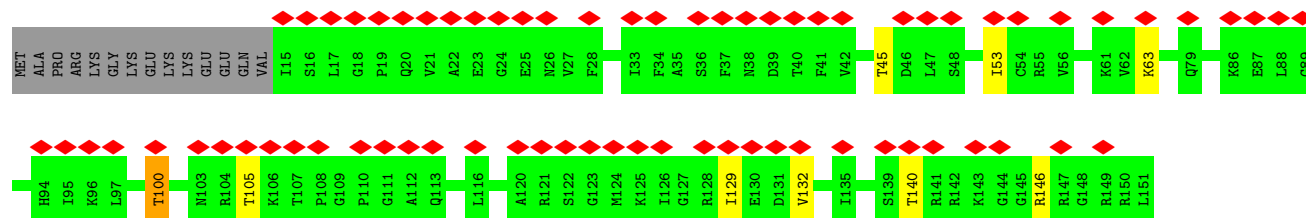
- Molecule 60: 40S RIBOSOMAL PROTEIN US4



- Molecule 61: 40S RIBOSOMAL PROTEIN ES10

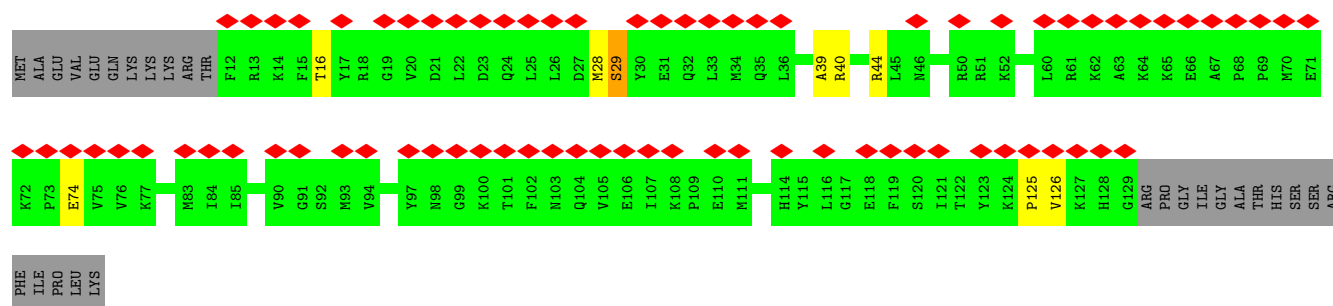
- Molecule 65: 40S RIBOSOMAL PROTEIN ES11

Chain CO: 



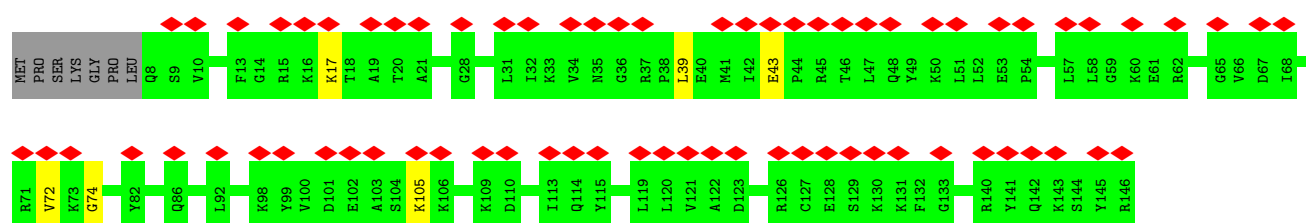
- Molecule 66: 40S RIBOSOMAL PROTEIN US19

Chain CP: 

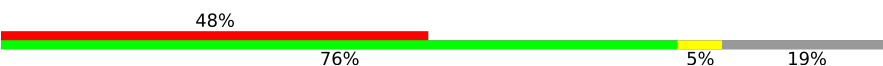


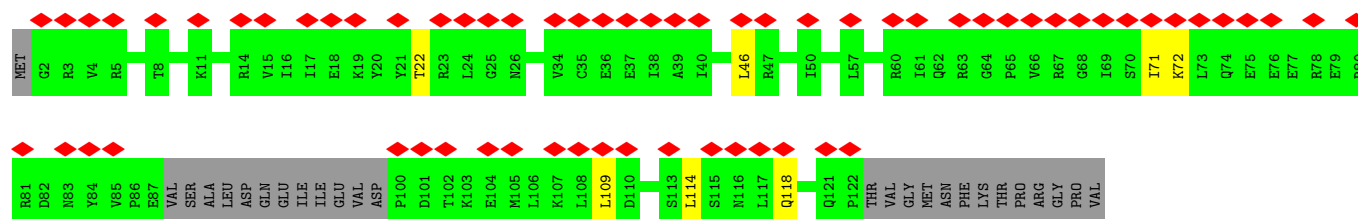
- Molecule 67: 40S RIBOSOMAL PROTEIN US9

Chain CQ: 




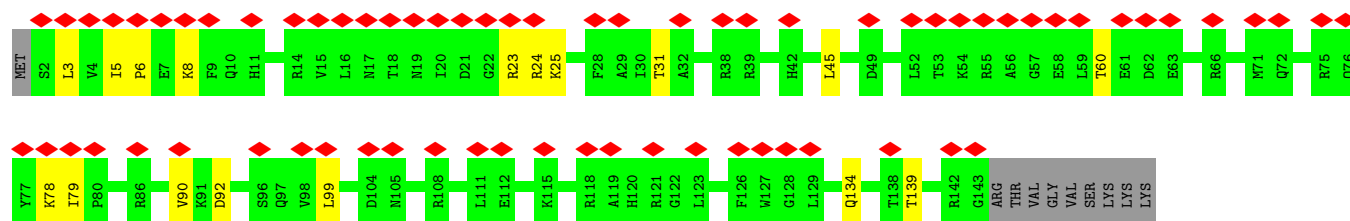
- Molecule 68: 40S RIBOSOMAL PROTEIN ES17

Chain CR: 

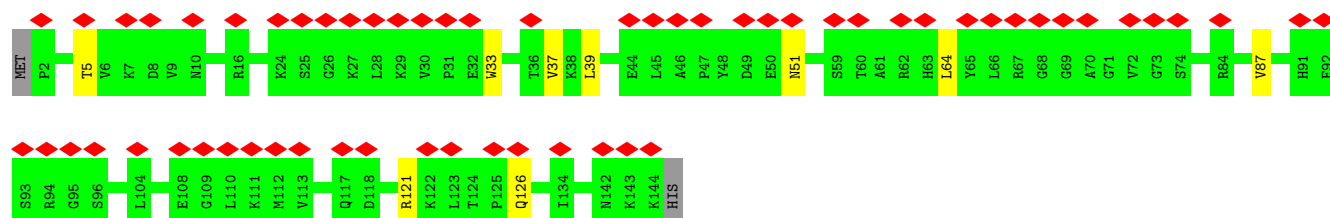
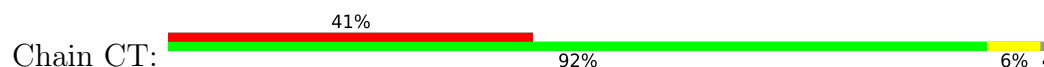


- Molecule 69: 40S RIBOSOMAL PROTEIN US13

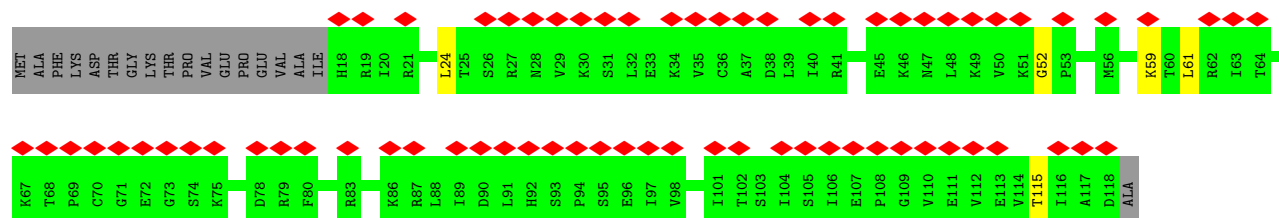
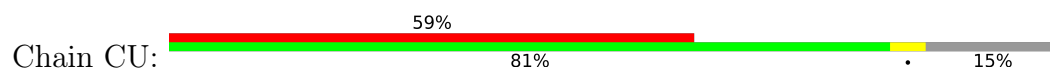
Chain CS: 



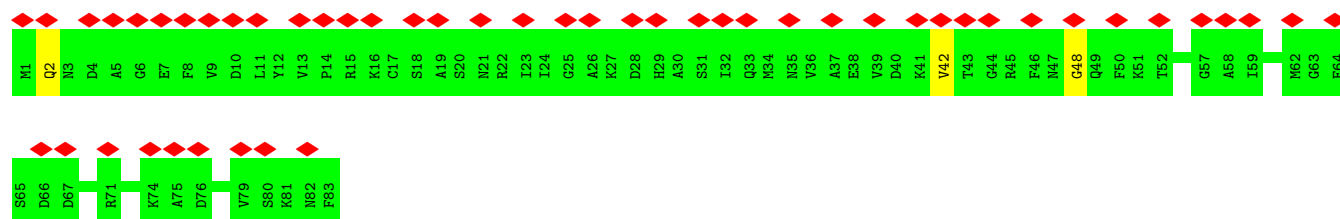
• Molecule 70: 40S RIBOSOMAL PROTEIN ES19



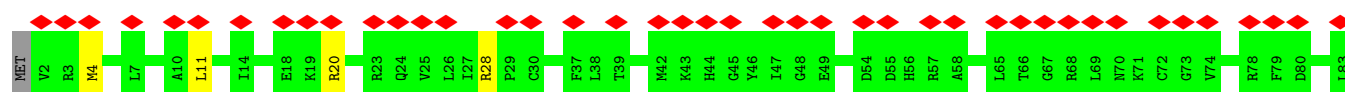
• Molecule 71: 40S RIBOSOMAL PROTEIN US10

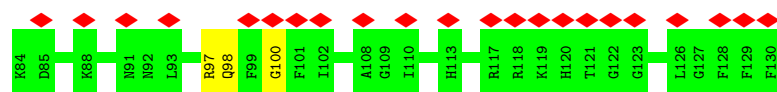


• Molecule 72: 40S RIBOSOMAL PROTEIN ES21

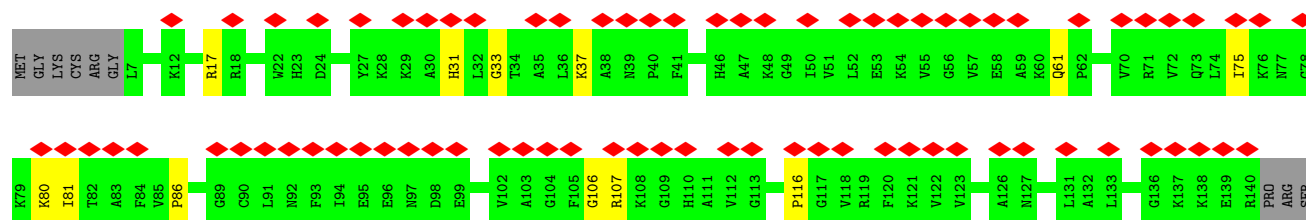
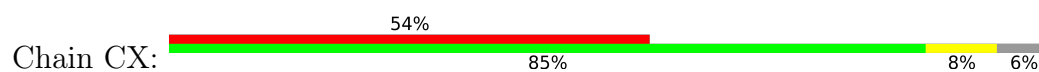


• Molecule 73: 40S RIBOSOMAL PROTEIN US8

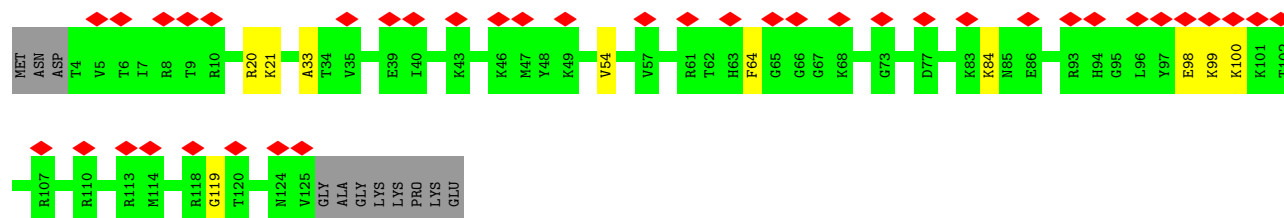
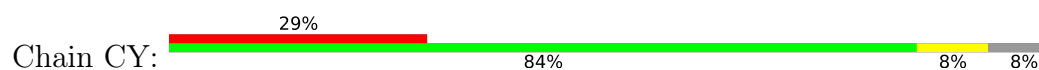




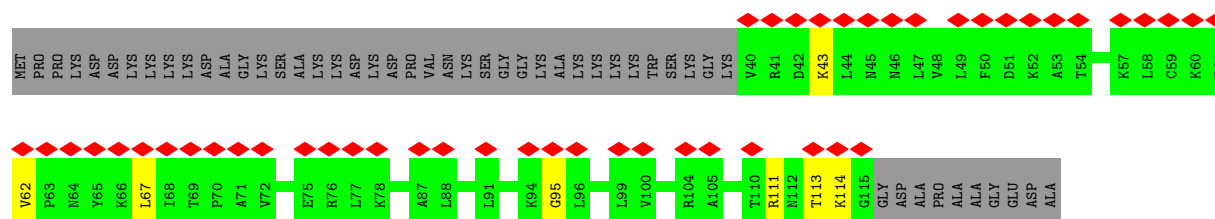
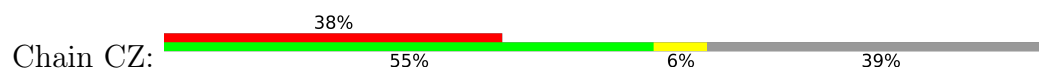
• Molecule 74: 40S RIBOSOMAL PROTEIN US12



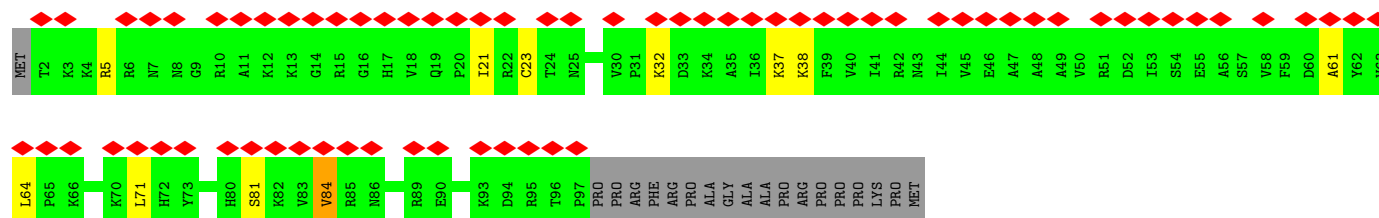
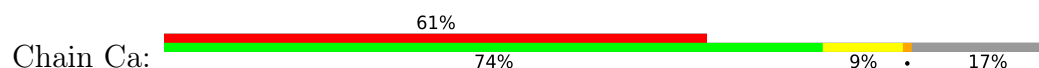
• Molecule 75: 40S RIBOSOMAL PROTEIN ES24



• Molecule 76: 40S RIBOSOMAL PROTEIN ES25

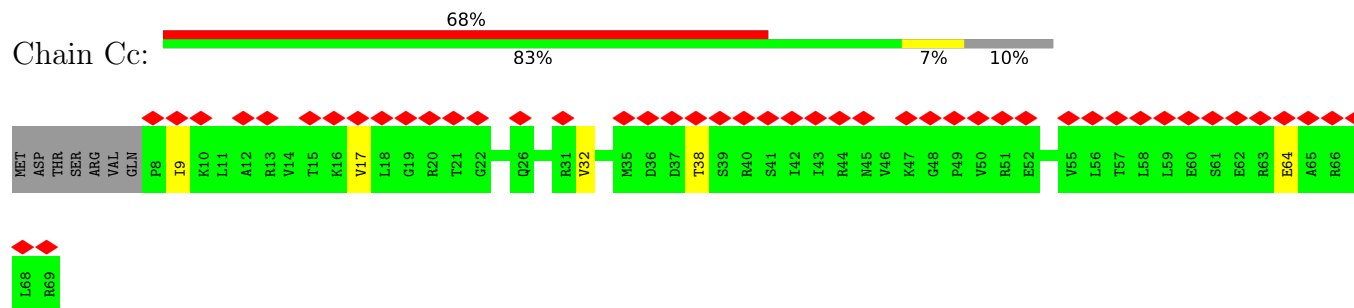


• Molecule 77: 40S RIBOSOMAL PROTEIN ES26

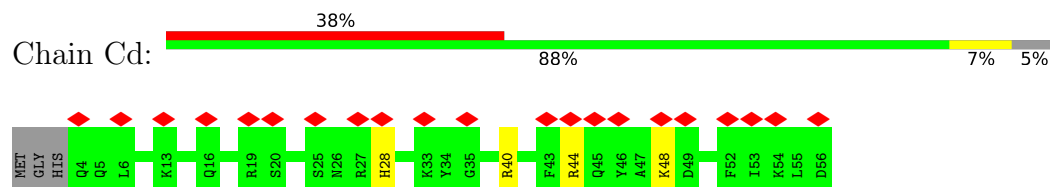


• Molecule 78: 40S RIBOSOMAL PROTEIN ES27

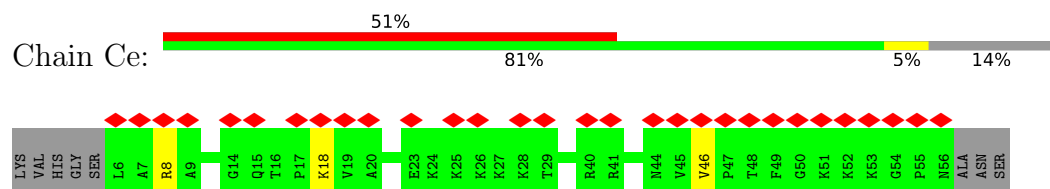
● Molecule 79: 40S RIBOSOMAL PROTEIN ES28



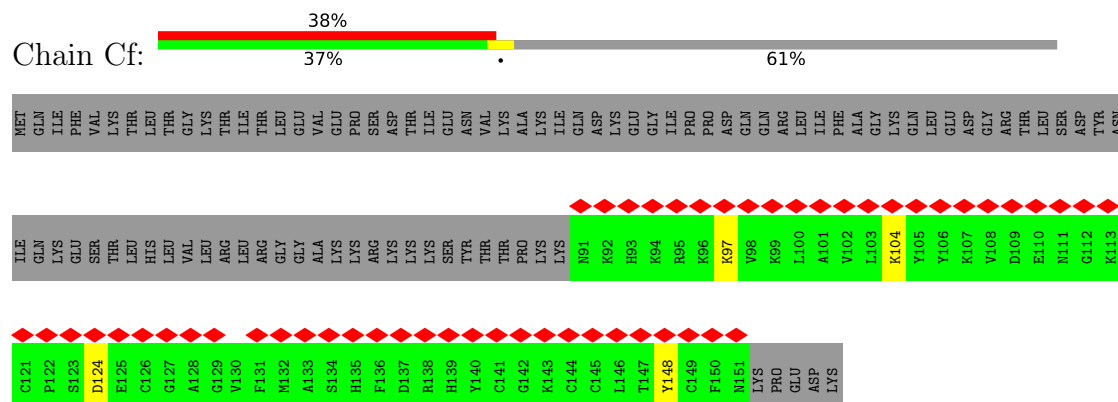
- Molecule 80: 40S RIBOSOMAL PROTEIN US14



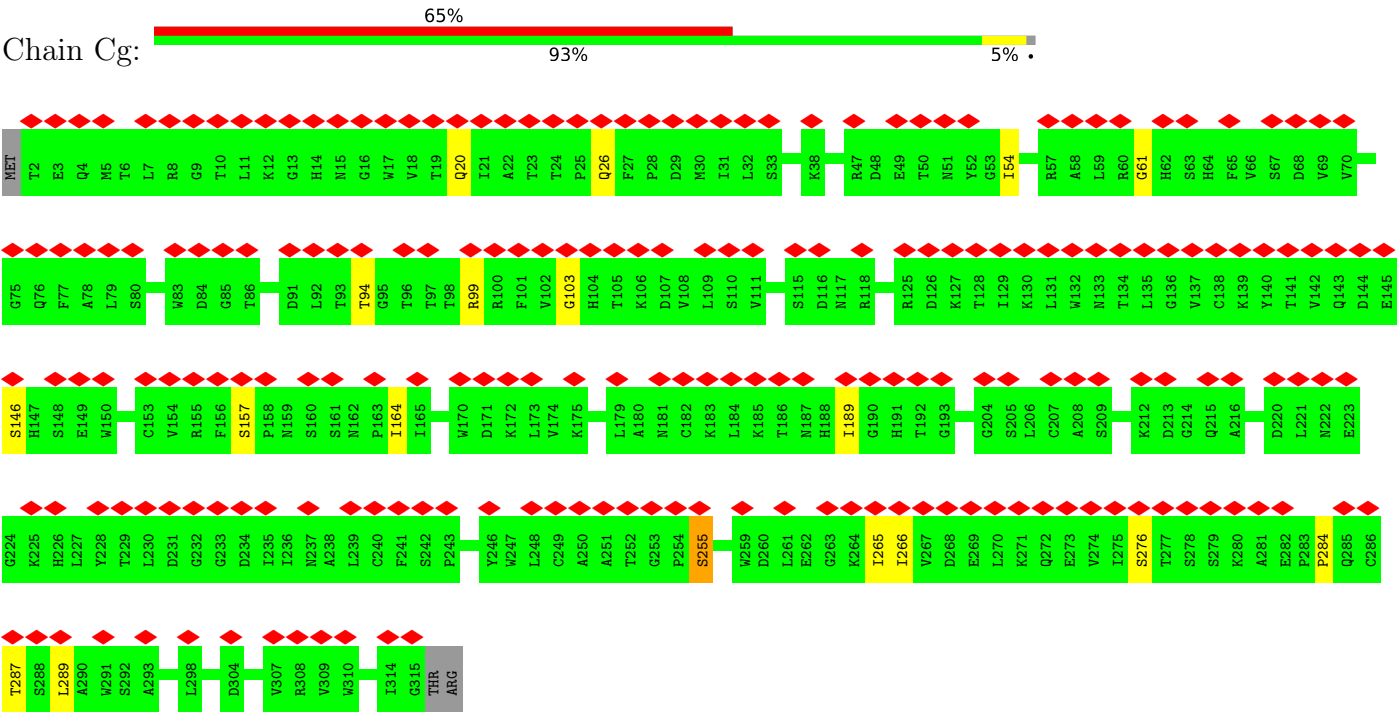
● Molecule 81: 40S RIBOSOMAL PROTEIN ES30



- 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	11974.922	Depositor
Minimum map value	-3949.843	Depositor
Average map value	-27.770	Depositor
Map value standard deviation	1021.781	Depositor
Recommended contour level	4000	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 ⓘ

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	A2	0.43	33/86671 (0.0%)	0.83	82/135194 (0.1%)
2	A3	0.36	0/3723	0.79	1/5800 (0.0%)
3	A4	0.38	0/2836	0.82	3/4421 (0.1%)
4	AA	0.44	0/1926	0.67	0/2583
5	AB	0.45	0/3258	0.73	2/4361 (0.0%)
6	AC	0.47	0/2943	0.73	0/3953
7	AD	0.49	2/2407 (0.1%)	0.70	1/3221 (0.0%)
8	AE	0.52	0/1312	0.73	0/1763
9	AF	0.44	0/1986	0.68	0/2644
10	AG	0.46	0/1914	0.72	0/2578
11	AH	0.43	0/1555	0.69	0/2089
12	AI	0.42	0/1643	0.67	0/2194
13	AJ	0.49	0/1386	0.71	0/1852
14	AL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
15	AM	0.49	0/1162	0.70	0/1556
16	AN	0.43	0/1754	0.65	0/2348
17	AO	0.44	0/1639	0.69	0/2193
18	AP	0.44	0/1260	0.70	0/1691
19	AQ	0.45	0/1518	0.74	0/2026
20	AR	0.39	0/1541	0.64	0/2035
21	AS	0.45	0/1479	0.73	0/1985
22	AT	0.46	0/1326	0.71	0/1770
23	AU	0.47	0/841	0.71	0/1128
24	AV	0.44	0/978	0.63	0/1312
25	AW	0.43	0/542	0.60	0/722
26	AX	0.42	0/993	0.67	0/1334
27	AY	0.47	0/1082	0.72	1/1441 (0.1%)
28	AZ	0.47	0/1138	0.79	0/1517
29	Aa	0.45	0/1191	0.71	0/1591
30	Ab	0.45	0/570	0.72	0/752
31	Ac	0.46	0/813	0.70	0/1091
32	Ad	0.45	0/920	0.67	0/1238

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ae	0.46	0/1071	0.68	0/1428
34	Af	0.50	0/885	0.81	0/1185
35	Ag	0.48	0/917	0.74	0/1222
36	Ah	0.38	0/1023	0.64	0/1351
37	Ai	0.43	0/793	0.75	0/1048
38	Aj	0.50	0/704	0.76	0/931
39	Ak	0.43	0/575	0.73	0/761
40	Al	0.41	0/454	0.61	0/599
41	Am	0.42	0/435	0.70	0/575
42	An	0.40	0/241	0.51	0/305
43	Ao	0.45	0/885	0.74	0/1166
44	Ap	0.40	0/718	0.61	0/953
45	At	0.48	0/1058	0.75	0/1416
46	Au	0.45	0/1639	0.69	1/2222 (0.0%)
47	BA	0.53	0/1809	1.02	17/2819 (0.6%)
48	BB	0.65	1/4926 (0.0%)	1.15	29/6641 (0.4%)
49	BC	1.53	11/6230 (0.2%)	2.37	540/9712 (5.6%)
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	0.45	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	0.77	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	51/240674 (0.0%)	0.87	691/353753 (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
1	A2	0	35
2	A3	0	2
48	BB	0	12
49	BC	0	105
50	C1	0	23
All	All	0	177

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	1701	C	C5'-C4'	18.41	1.73	1.51
1	A2	1673	C	C3'-O3'	15.36	1.63	1.42
1	A2	1701	C	O5'-C5'	14.50	1.67	1.44
1	A2	1673	C	O3'-P	14.08	1.78	1.61
1	A2	1701	C	P-O5'	13.46	1.73	1.59

The worst 5 of 691 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	3919	U	N1-C2-O2	-33.15	99.59	122.80
1	A2	3919	U	N3-C2-O2	32.84	145.19	122.20
1	A2	1701	C	O4'-C4'-C3'	-15.18	88.82	104.00
1	A2	3914	A	O4'-C1'-N9	15.11	120.28	108.20
48	BB	1133	TYR	CB-CG-CD2	-14.74	112.15	121.00

There are no chirality outliers.

5 of 177 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A2	1	C	Sidechain
1	A2	115	C	Sidechain
1	A2	121	A	Sidechain
1	A2	140	C	Sidechain
1	A2	2	G	Sidechain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	11	44
5	AB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	3	20
6	AC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	2	18
7	AD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	7	37
8	AE	156/158 (99%)	141 (90%)	8 (5%)	7 (4%)	2	17
9	AF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	7	37
10	AG	233/266 (88%)	216 (93%)	8 (3%)	9 (4%)	2	19
11	AH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	8	38
12	AI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	8	38
13	AJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	11
14	AL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	1	14
15	AM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	9	41
16	AN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40
17	AO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	AP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	32
19	AQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	3	21
20	AR	180/196 (92%)	172 (96%)	3 (2%)	5 (3%)	4	24
21	AS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	20
22	AT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	6	32
23	AU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
24	AV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	8	38
25	AW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
26	AX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
27	AY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	5	27
28	AZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	3	23
29	Aa	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	21
30	Ab	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	13
31	Ac	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	6	32
32	Ad	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	52
33	Ae	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	5	27
34	Af	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	16
35	Ag	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	20
36	Ah	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	4	26
37	Ai	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	13
38	Aj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	5	27
39	Ak	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	8	40
40	Al	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	30
41	Am	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	32
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	6	32
44	Ap	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	21
45	At	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	1	15
46	Au	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	9	41
48	BB	605/627 (96%)	523 (86%)	51 (8%)	31 (5%)	1	15
51	CA	216/295 (73%)	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%)	13 (7%)	10 (5%)	1	15
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	11794/13395 (88%)	10996 (93%)	442 (4%)	356 (3%)	5	23

5 of 356 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AA	144	LYS
4	AA	196	TRP
5	AB	4	ARG
5	AB	5	LYS
5	AB	157	CYS

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	
4	AA	189/199 (95%)	185 (98%)	4 (2%)	48	66
5	AB	344/349 (99%)	326 (95%)	18 (5%)	19	40
6	AC	302/348 (87%)	284 (94%)	18 (6%)	16	37
7	AD	244/250 (98%)	237 (97%)	7 (3%)	37	56
8	AE	143/143 (100%)	135 (94%)	8 (6%)	17	38
9	AF	203/215 (94%)	196 (97%)	7 (3%)	32	51
10	AG	199/223 (89%)	192 (96%)	7 (4%)	31	51
11	AH	171/171 (100%)	164 (96%)	7 (4%)	26	47
12	AI	170/181 (94%)	161 (95%)	9 (5%)	19	40
13	AJ	143/149 (96%)	137 (96%)	6 (4%)	25	46
14	AL	167/177 (94%)	156 (93%)	11 (7%)	14	34
15	AM	118/161 (73%)	114 (97%)	4 (3%)	32	51
16	AN	172/172 (100%)	170 (99%)	2 (1%)	67	78
17	AO	168/174 (97%)	166 (99%)	2 (1%)	67	78
18	AP	133/163 (82%)	126 (95%)	7 (5%)	19	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AQ	162/165 (98%)	157 (97%)	5 (3%)	35	54
20	AR	161/175 (92%)	149 (92%)	12 (8%)	11	31
21	AS	155/157 (99%)	148 (96%)	7 (4%)	23	45
22	AT	139/140 (99%)	134 (96%)	5 (4%)	30	50
23	AU	91/115 (79%)	88 (97%)	3 (3%)	33	52
24	AV	100/107 (94%)	99 (99%)	1 (1%)	73	82
25	AW	55/126 (44%)	52 (94%)	3 (6%)	18	39
26	AX	107/133 (80%)	105 (98%)	2 (2%)	52	69
27	AY	119/135 (88%)	115 (97%)	4 (3%)	32	51
28	AZ	118/118 (100%)	112 (95%)	6 (5%)	20	41
29	Aa	120/121 (99%)	116 (97%)	4 (3%)	33	52
30	Ab	58/126 (46%)	57 (98%)	1 (2%)	56	72
31	Ac	88/97 (91%)	87 (99%)	1 (1%)	70	80
32	Ad	100/110 (91%)	96 (96%)	4 (4%)	27	47
33	Ae	115/121 (95%)	112 (97%)	3 (3%)	41	59
34	Af	87/89 (98%)	79 (91%)	8 (9%)	7	23
35	Ag	98/100 (98%)	88 (90%)	10 (10%)	6	20
36	Ah	109/110 (99%)	106 (97%)	3 (3%)	38	57
37	Ai	82/89 (92%)	76 (93%)	6 (7%)	11	31
38	Aj	71/80 (89%)	69 (97%)	2 (3%)	38	57
39	Ak	64/65 (98%)	64 (100%)	0	100	100
40	Al	47/48 (98%)	46 (98%)	1 (2%)	48	66
41	Am	48/116 (41%)	45 (94%)	3 (6%)	15	36
42	An	24/24 (100%)	24 (100%)	0	100	100
43	Ao	94/94 (100%)	89 (95%)	5 (5%)	19	40
44	Ap	74/75 (99%)	72 (97%)	2 (3%)	40	58
45	At	113/121 (93%)	106 (94%)	7 (6%)	15	36
46	Au	177/177 (100%)	163 (92%)	14 (8%)	10	29
48	BB	540/552 (98%)	519 (96%)	21 (4%)	27	48
51	CA	181/243 (74%)	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	10303/11421 (90%)	9849 (96%)	454 (4%)	26 45

5 of 454 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	Au	101	THR
83	Cg	26	GLN
54	CD	66	ILE
81	Ce	46	VAL
73	CW	4	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 228 such sidechains are listed below:

Mol	Chain	Res	Type
41	Am	90	ASN
80	Cd	41	GLN
51	CA	215	GLN
80	Cd	16	GLN
69	CS	87	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	3604/5025 (71%)	2040 (56%)	324 (8%)
2	A3	156/194 (80%)	82 (52%)	6 (3%)
3	A4	118/121 (97%)	68 (57%)	9 (7%)
47	BA	75/76 (98%)	14 (18%)	1 (1%)
49	BC	259/504 (51%)	135 (52%)	40 (15%)
50	C1	1738/1869 (92%)	1038 (59%)	152 (8%)
All	All	5950/7789 (76%)	3377 (56%)	532 (8%)

5 of 3377 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	2	G
1	A2	3	C
1	A2	5	A
1	A2	6	C
1	A2	8	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
1	A2	2607	U

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	BB	2435	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	BB	2435	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	BB	2435	GNP	C2'-C1'	-6.46	1.44	1.53
84	BB	2435	GNP	C6-N1	5.34	1.42	1.33
84	BB	2435	GNP	C4-N3	2.86	1.40	1.35
84	BB	2435	GNP	PB-O3A	-2.61	1.55	1.59
84	BB	2435	GNP	PB-N3B	-2.47	1.56	1.63

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	BB	2435	GNP	C5-C6-N1	-7.05	113.79	123.43
84	BB	2435	GNP	C2-N1-C6	5.20	124.19	115.93
84	BB	2435	GNP	N3-C2-N1	-3.58	122.44	127.22
84	BB	2435	GNP	O1B-PB-N3B	3.38	116.75	111.77
84	BB	2435	GNP	C4-C5-C6	-2.99	117.95	120.80

There are no chirality outliers.

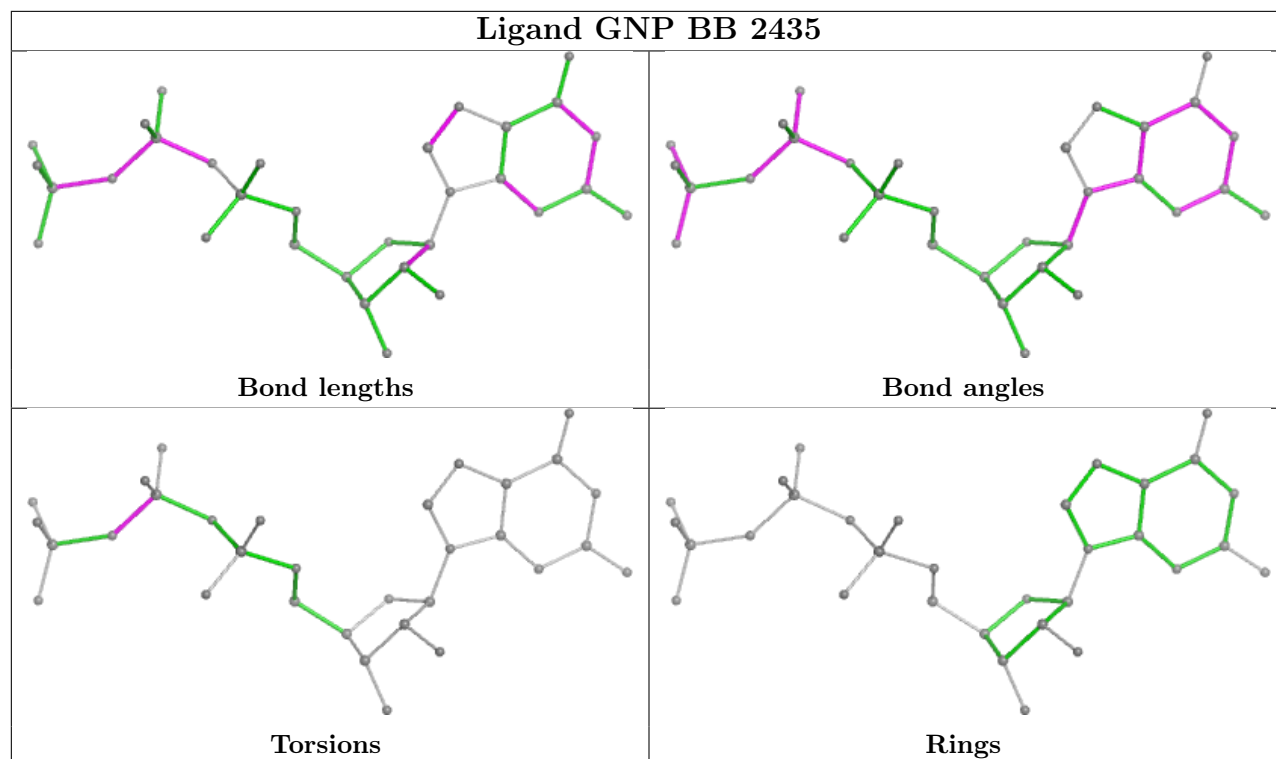
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	BB	2435	GNP	PG-N3B-PB-O1B
84	BB	2435	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	AR	1
1	A2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AR	182:GLU	C	183:GLU	N	5.96
1	A2	4036:U	O3'	4037:U	P	4.57

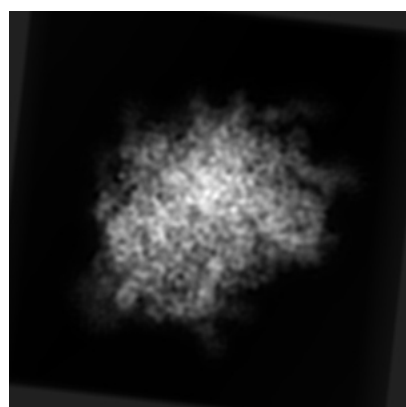
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2682. These allow visual inspection of the internal detail of the map and identification of artifacts.

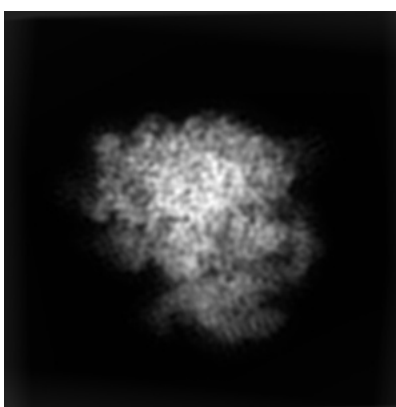
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

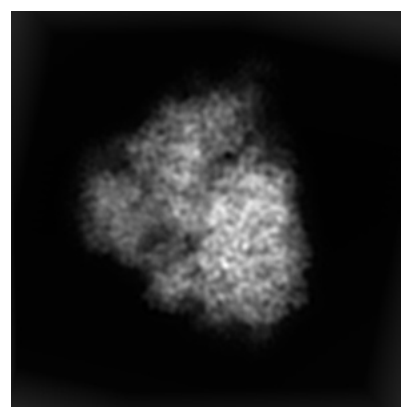
6.1.1 Primary map



X



Y

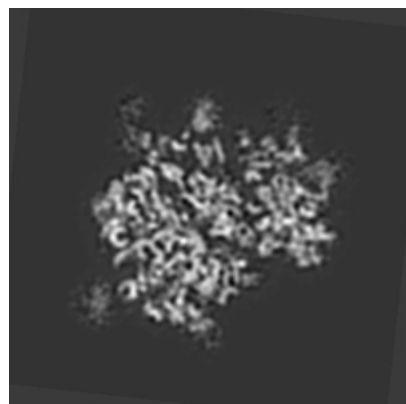


Z

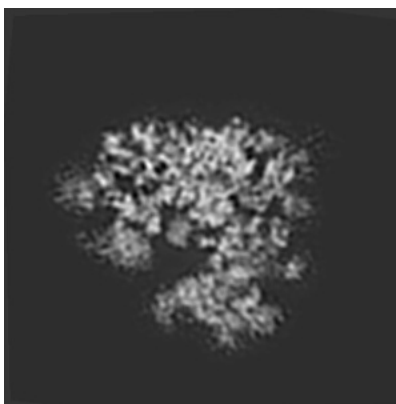
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

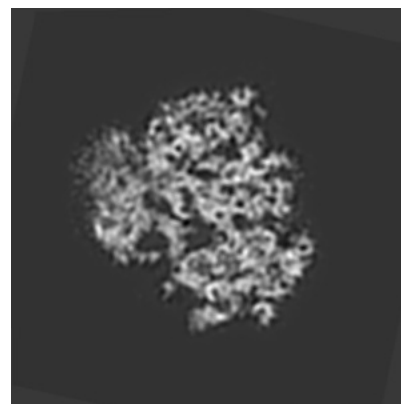
6.2.1 Primary map



X Index: 180



Y Index: 180

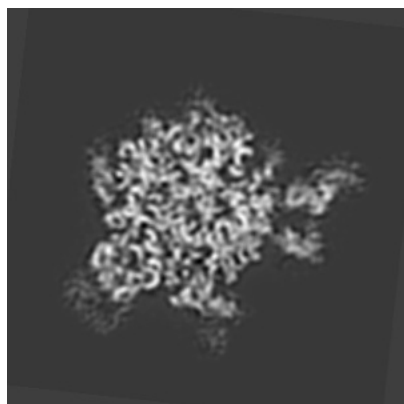


Z Index: 180

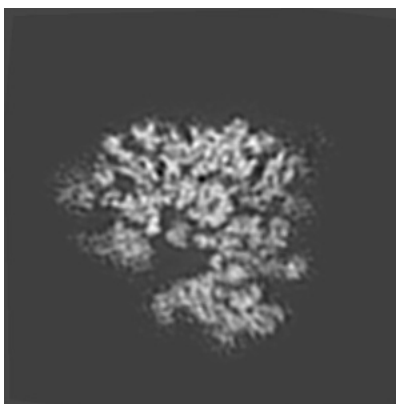
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

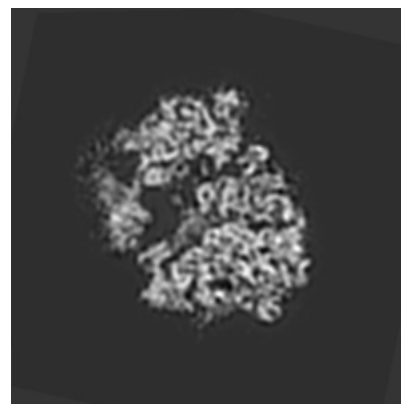
6.3.1 Primary map



X Index: 214



Y Index: 182

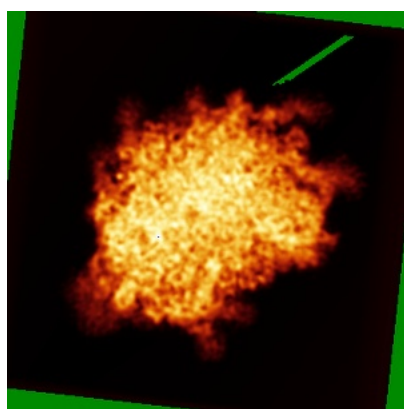


Z Index: 169

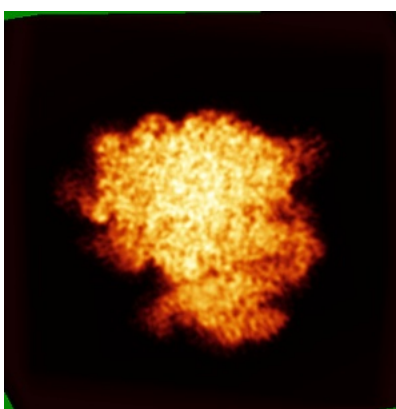
The images above show the largest variance slices of the map in three orthogonal directions.

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

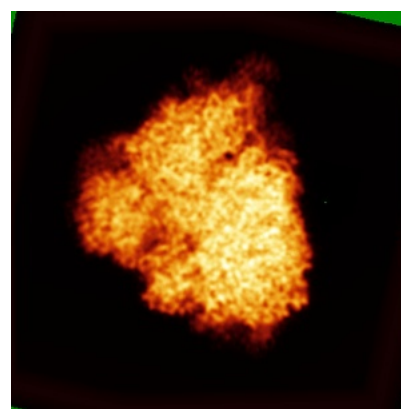
6.4.1 Primary map



X



Y

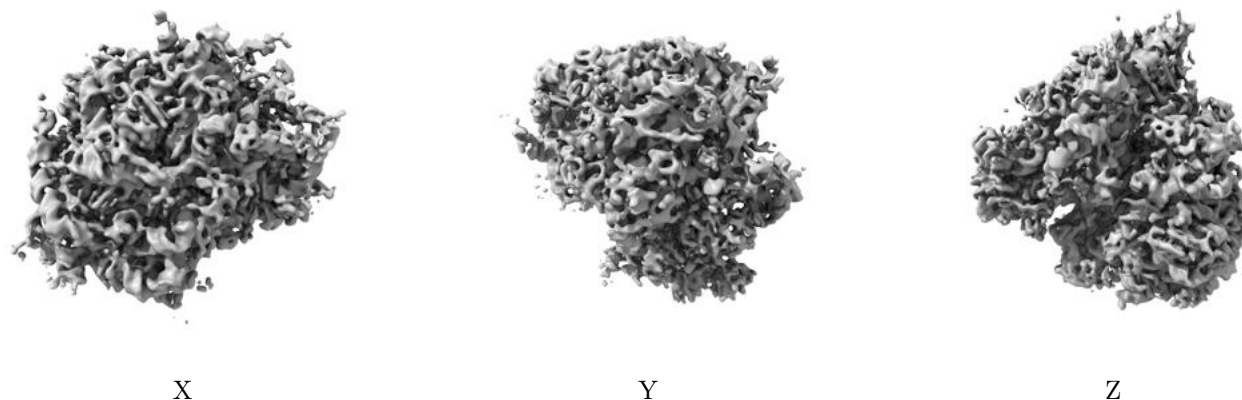


Z

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 4000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

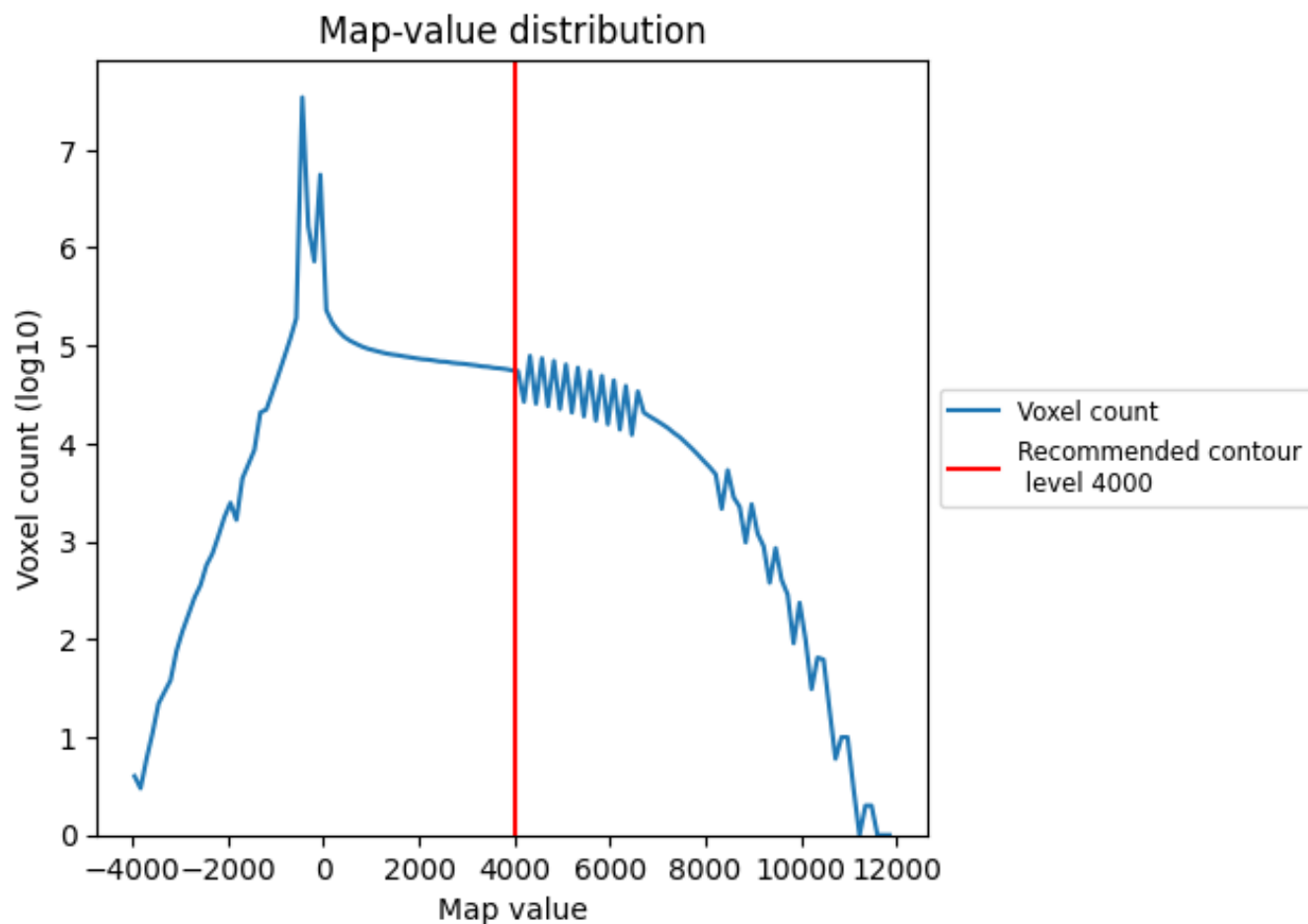
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

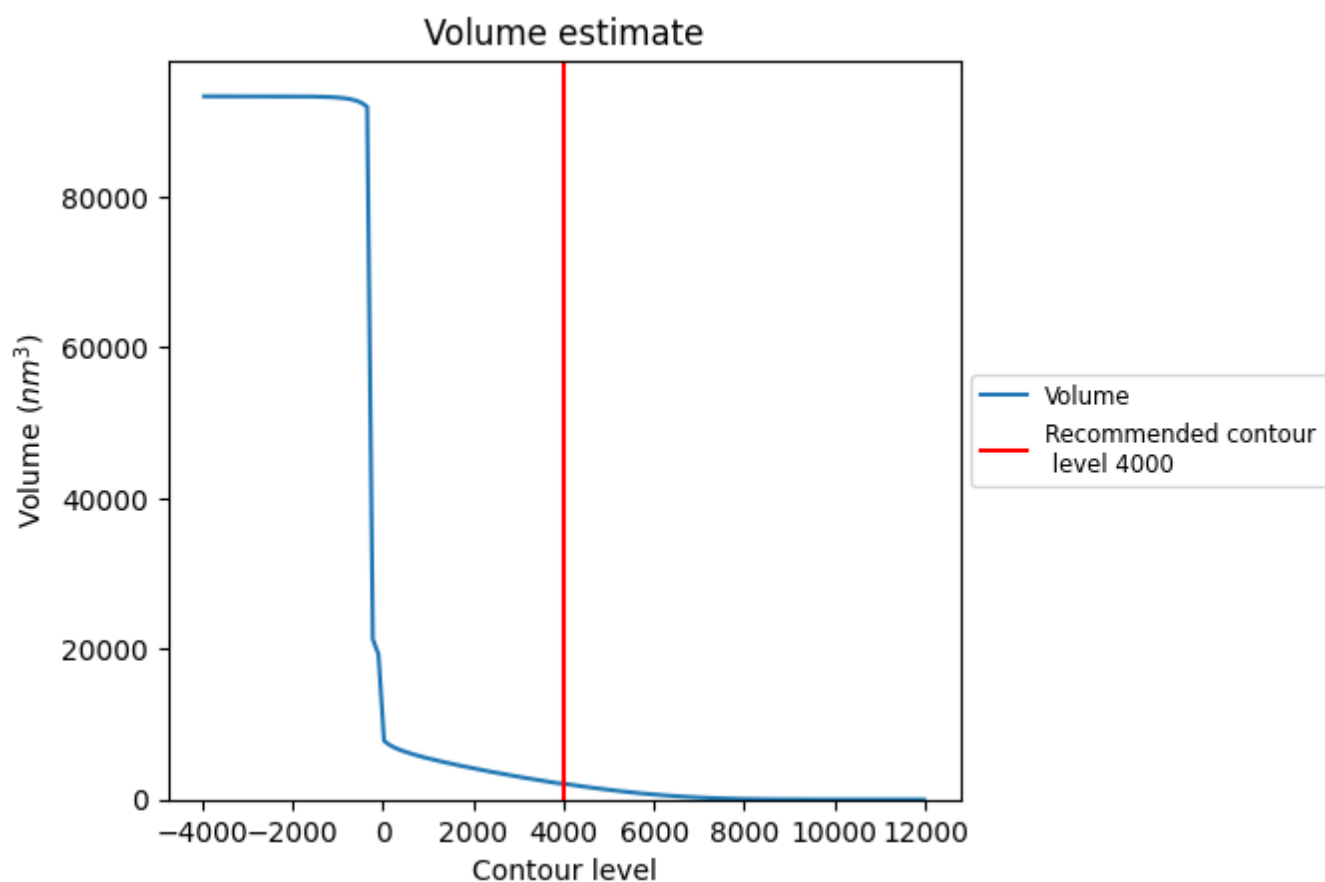
This section contains the results of statistical analysis of the map.

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.

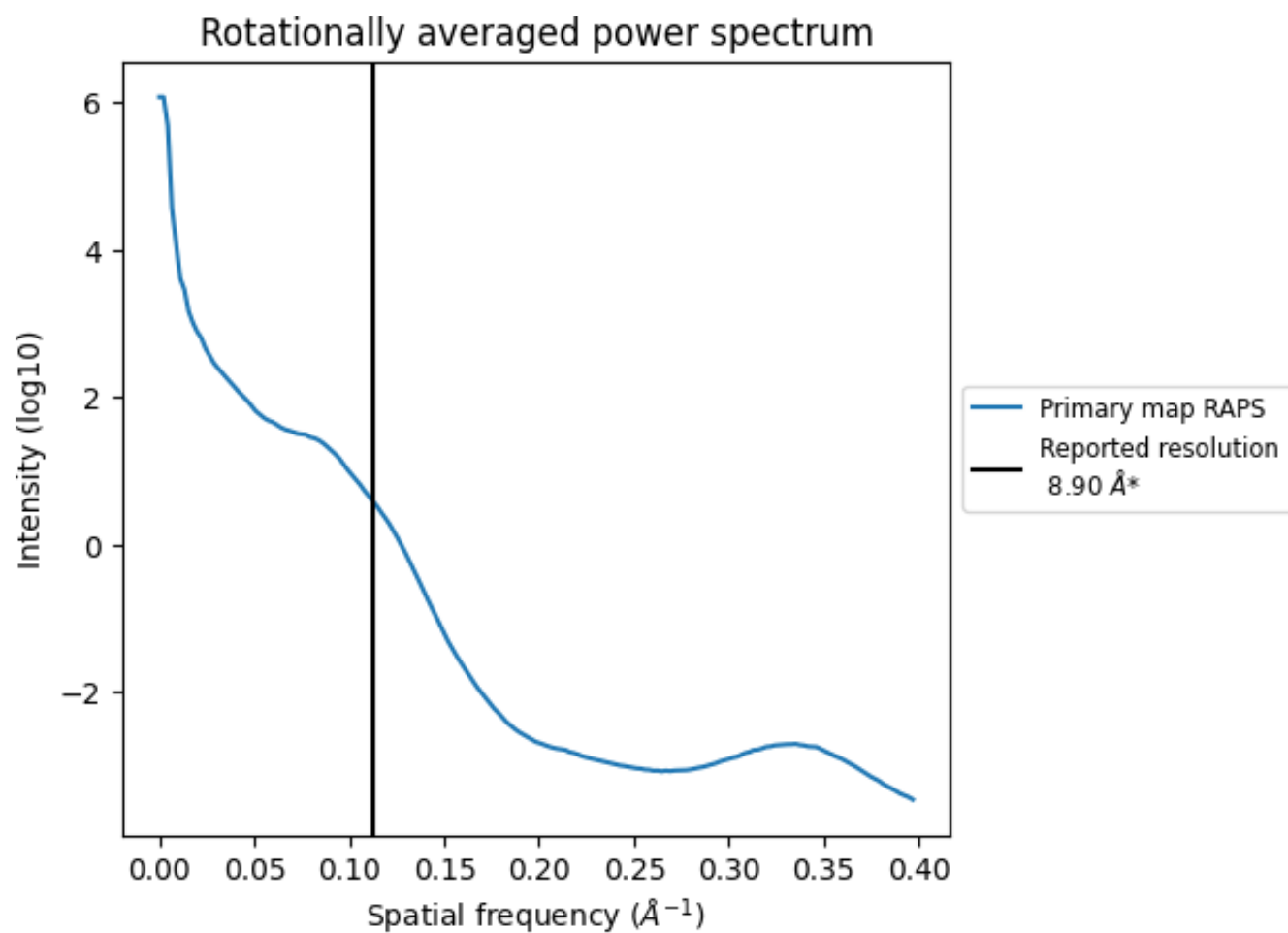
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2109 nm³; this corresponds to an approximate mass of 1905 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 0.112 Å⁻¹

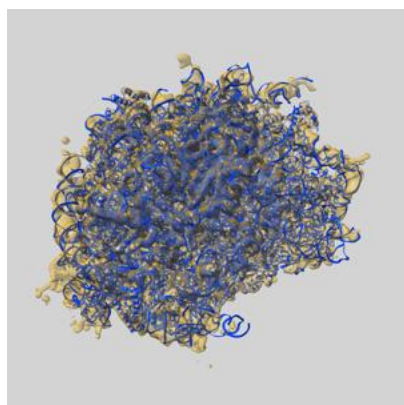
8 Fourier-Shell correlation

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

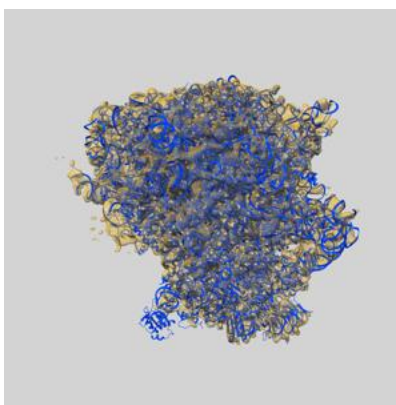
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2682 and PDB model 4UJD. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

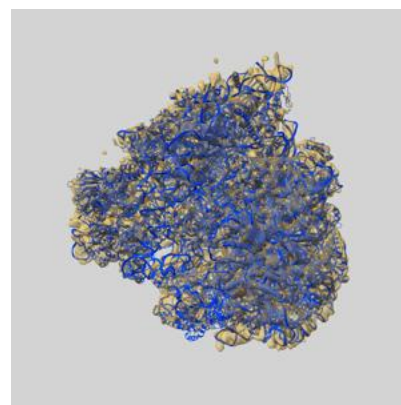
9.1 Map-model overlay [i](#)



X



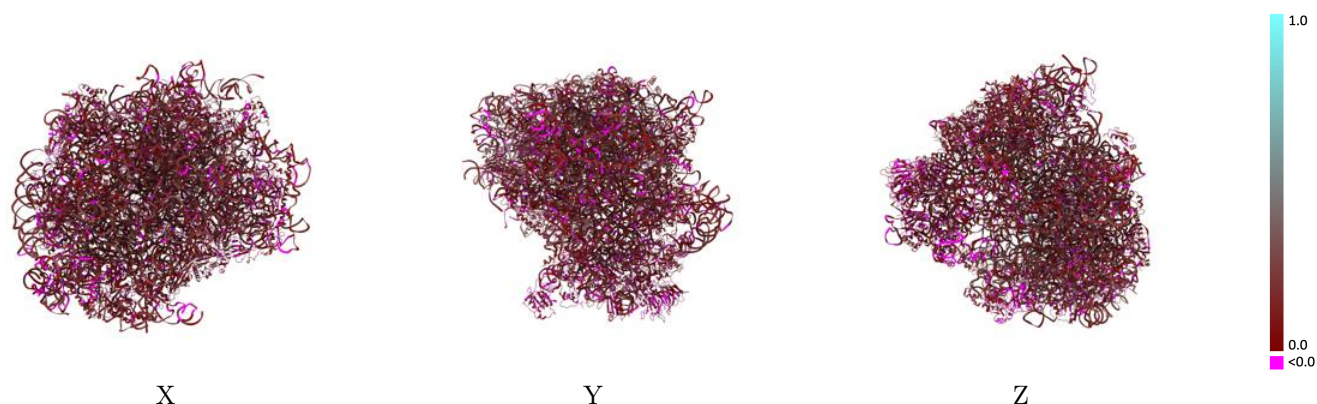
Y



Z

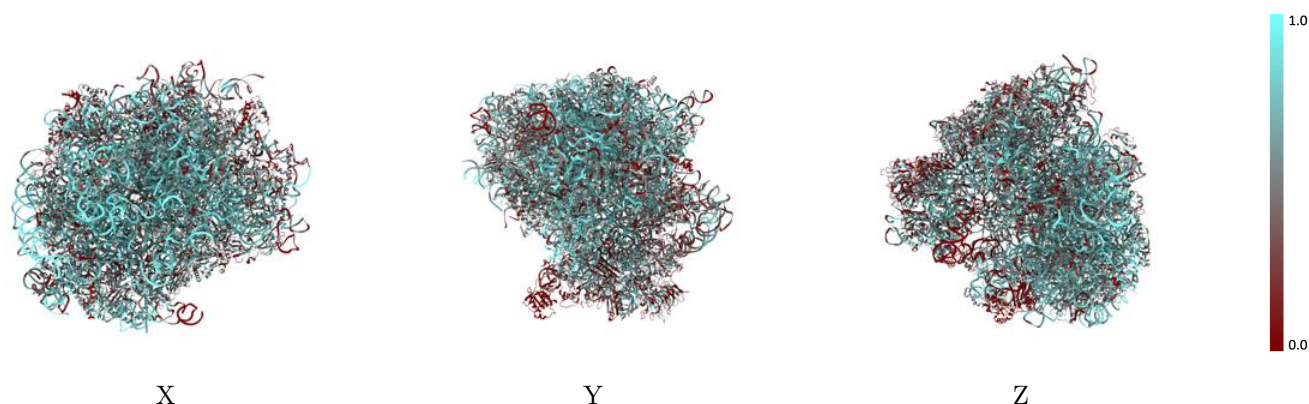
The images above show the 3D surface view of the map at the recommended contour level 4000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



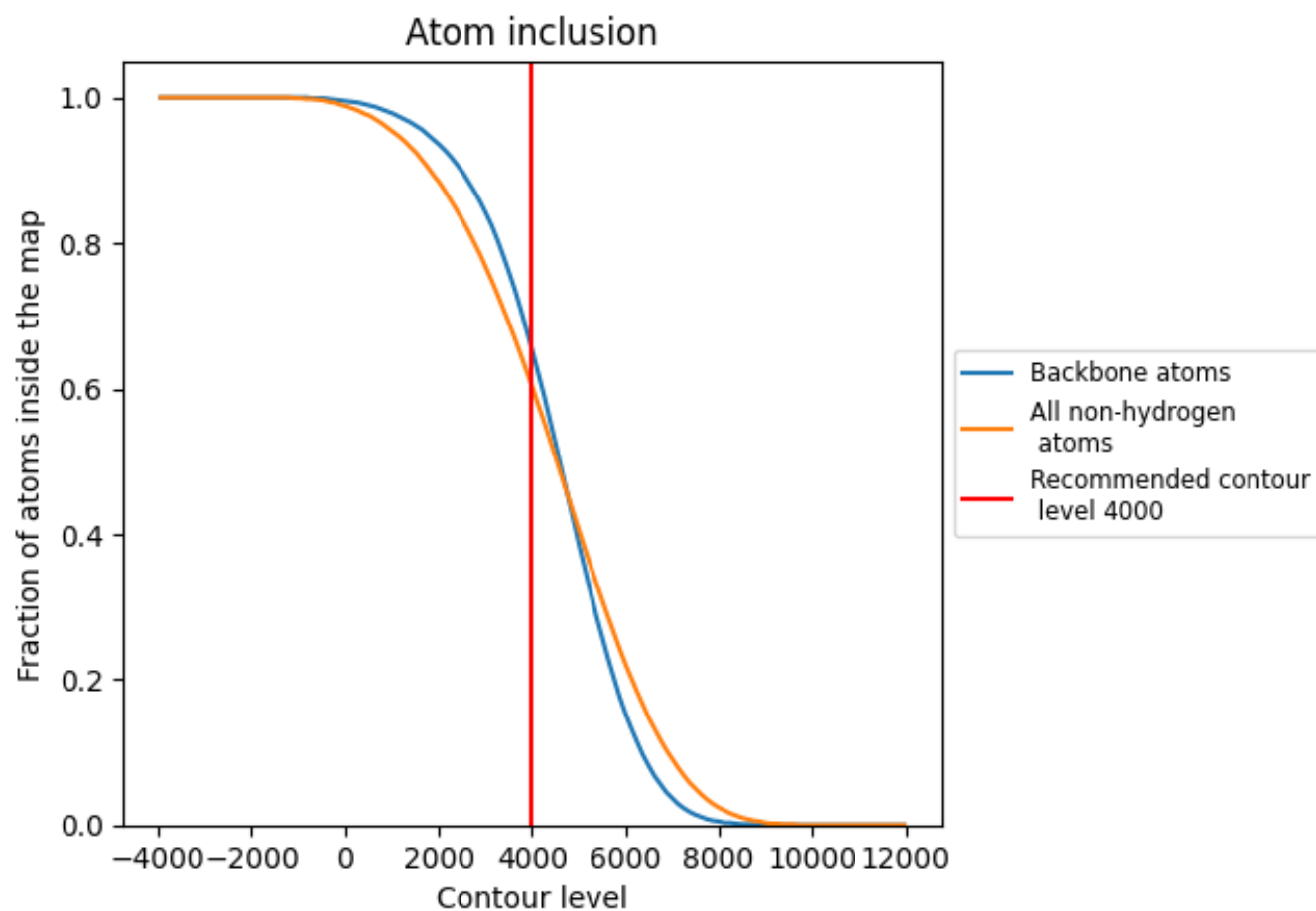
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4000).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 60% 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 (4000) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6030	 0.1400
A2	 0.7730	 0.1740
A3	 0.8110	 0.1810
A4	 0.8820	 0.1860
AA	 0.3690	 0.0980
AB	 0.4360	 0.1060
AC	 0.4690	 0.0950
AD	 0.5650	 0.1180
AE	 0.4260	 0.1110
AF	 0.4720	 0.1090
AG	 0.3940	 0.1190
AH	 0.4050	 0.1260
AI	 0.4690	 0.1190
AJ	 0.5450	 0.1210
AL	 0.4470	 0.1070
AM	 0.5300	 0.1270
AN	 0.4680	 0.0890
AO	 0.4750	 0.1200
AP	 0.5310	 0.0990
AQ	 0.4910	 0.1120
AR	 0.5060	 0.1100
AS	 0.4450	 0.1100
AT	 0.4350	 0.1120
AU	 0.4150	 0.1150
AV	 0.2600	 0.1050
AW	 0.5120	 0.1190
AX	 0.4560	 0.1250
AY	 0.5550	 0.1120
AZ	 0.4370	 0.1140
Aa	 0.5160	 0.1030
Ab	 0.4940	 0.0950
Ac	 0.5100	 0.1340
Ad	 0.5350	 0.1220
Ae	 0.4440	 0.1190
Af	 0.4340	 0.0890

















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Chain	Atom inclusion	Q-score
Ag	0.3810	0.0930
Ah	0.4980	0.1240
Ai	0.5050	0.1240
Aj	0.5890	0.0940
Ak	0.4040	0.1290
Al	0.4590	0.1280
Am	0.5110	0.1350
An	0.4570	0.0870
Ao	0.4630	0.1150
Ap	0.4360	0.1160
At	0.4660	0.0870
Au	0.0050	0.0190
BA	0.5500	0.1590
BB	0.4060	0.1210
BC	0.3360	0.0940
C1	0.7250	0.1580
CA	0.4020	0.1280
CB	0.3900	0.1300
CC	0.4200	0.1220
CD	0.2820	0.1000
CE	0.4550	0.0970
CF	0.3950	0.0940
CG	0.4270	0.0970
CH	0.2740	0.1210
CI	0.4110	0.0920
CJ	0.5180	0.1270
CK	0.2260	0.0740
CL	0.3600	0.1090
CM	0.0020	0.0180
CN	0.4080	0.1170
CO	0.4070	0.1010
CP	0.2880	0.0910
CQ	0.3980	0.0730
CR	0.3440	0.1000
CS	0.4260	0.0970
CT	0.4790	0.0800
CU	0.2860	0.0850
CV	0.3750	0.1200
CW	0.4130	0.1270
CX	0.3500	0.1280
CY	0.5460	0.0980
CZ	0.3170	0.1280

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Chain	Atom inclusion	Q-score
Ca	 0.2580	 0.0590
Cb	 0.3300	 0.1140
Cc	 0.2470	 0.0720
Cd	 0.5590	 0.0860
Ce	 0.3500	 0.1000
Cf	 0.0290	 0.0390
Cg	 0.2940	 0.0750