



# wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:36 AM UTC

PDB ID : 4UJD / pdb\_00004ujd  
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](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:

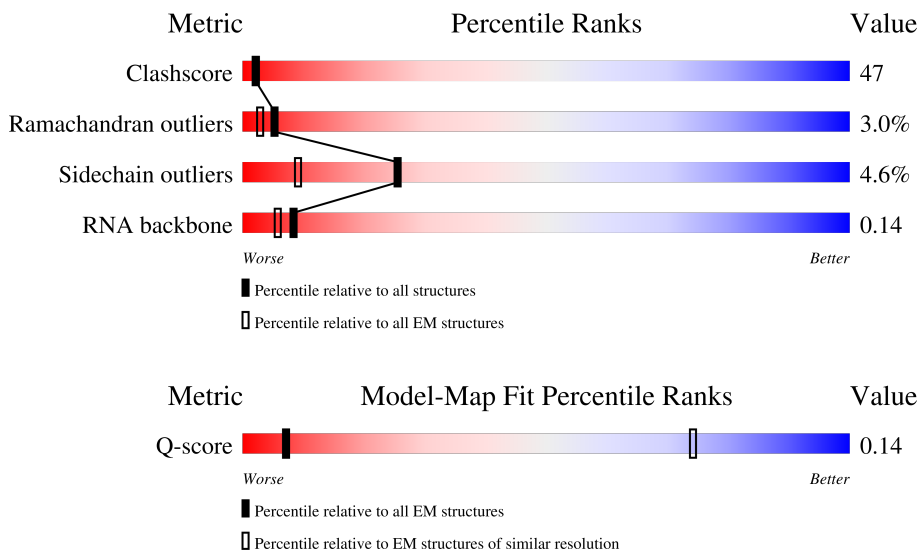
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	258 ( 8.40 - 9.40 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A2	5025	
2	A3	194	
3	A4	121	

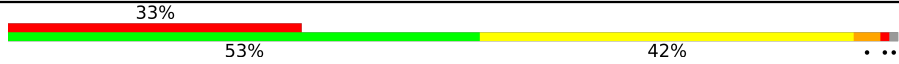

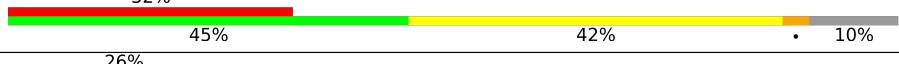



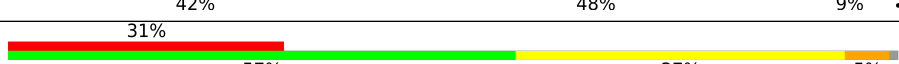

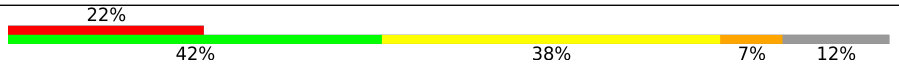
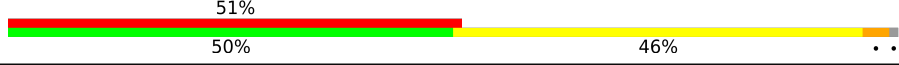


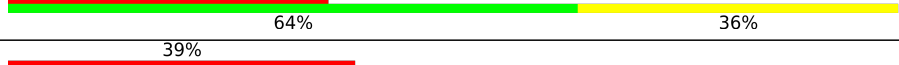

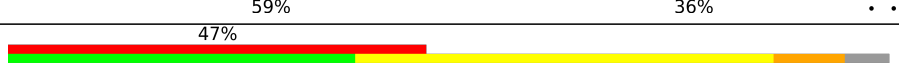
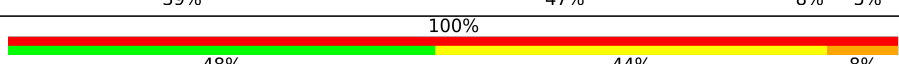
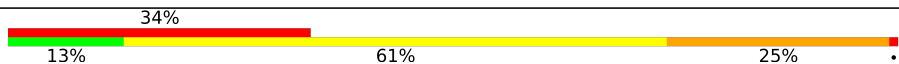

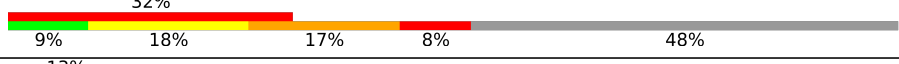


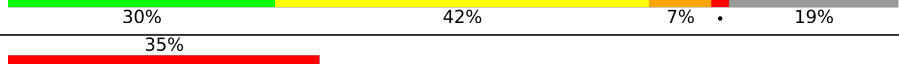



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Mol	Chain	Length	Quality of chain
4	AA	257	58% 54% 39% . .
5	AB	403	43% 54% 38% 5% . .
6	AC	427	35% 43% 35% 6% . 15%
7	AD	297	24% 54% 40% . .
8	AE	158	44% 35% 54% 10% .
9	AF	248	37% 52% 38% . 6%
10	AG	266	44% 50% 32% 6% . 12%
11	AH	192	48% 54% 42% . .
12	AI	214	33% 49% 38% 5% 8%
13	AJ	178	30% 45% 39% 11% .
14	AL	211	44% 45% 40% 9% . 5%
15	AM	215	22% 31% 32% . 35%
16	AN	204	46% 58% 41% .
17	AO	203	35% 50% 40% 6% .
18	AP	184	23% 45% 33% 5% 17%
19	AQ	188	39% 51% 39% 7% .
20	AR	196	31% 53% 33% 6% . 7%
21	AS	176	41% 51% 39% 7% . .
22	AT	160	45% 51% 43% 5% . .
23	AU	128	38% 51% 26% . 20%
24	AV	140	64% 60% 29% . 9%
25	AW	157	15% 28% 9% . 59%
26	AX	156	34% 46% 29% . 24%
27	AY	145	25% 40% 43% 6% 12%
28	AZ	136	45% 48% 48% . .

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Mol	Chain	Length	Quality of chain
29	Aa	148	
30	Ab	159	
31	Ac	115	
32	Ad	125	
33	Ae	135	
34	Af	110	
35	Ag	117	
36	Ah	123	
37	Ai	105	
38	Aj	97	
39	Ak	70	
40	Al	51	
41	Am	128	
42	An	25	
43	Ao	106	
44	Ap	92	
45	At	137	
46	Au	210	
47	BA	76	
48	BB	627	
49	BC	504	
50	C1	1869	
51	CA	295	
52	CB	264	
53	CC	293	

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Mol	Chain	Length	Quality of chain
54	CD	243	56% 51% 32% 5% 13%
55	CE	263	43% 52% 40% 5%
56	CF	204	47% 42% 44% 6% 8%
57	CG	249	45% 49% 37% 7% 7%
58	CH	194	65% 43% 52% ...
59	CI	208	47% 47% 45% 7%
60	CJ	194	27% 48% 37% 7% 8%
61	CK	165	43% 29% 22% 5% 43%
62	CL	158	55% 51% 36% 5% 8%
63	CM	132	91% 53% 32% 5% 9%
64	CN	151	49% 52% 40% 6% ..
65	CO	151	47% 51% 34% 5% 9%
66	CP	145	52% 40% 37% .. 19%
67	CQ	146	49% 51% 41% . 5%
68	CR	135	48% 42% 32% 7% 19%
69	CS	152	45% 47% 38% 9% 7%
70	CT	145	41% 43% 51% ..
71	CU	119	59% 34% 45% 5% 15%
72	CV	83	60% 63% 35% .
73	CW	130	49% 47% 48% ...
74	CX	143	54% 48% 41% . 6%
75	CY	133	29% 53% 31% 7% 8%
76	CZ	125	38% 28% 27% 6% 39%
77	Ca	115	61% 26% 48% 8% . 17%
78	Cb	84	60% 54% 38% . 5%

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

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
84	GNP	BB	2435	-	-	X	-

## 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
			Total	C	N	O	P		
1	A2	3616	77488	34508	14153	25212	3615	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
21	AS	173	1439	916	280	233	10	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	P		
49	BC	261	5574	2485	1001	1828	260	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
63	CM	120	931	584	164	174	9	0	0

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN ES15.

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

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN ES11.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

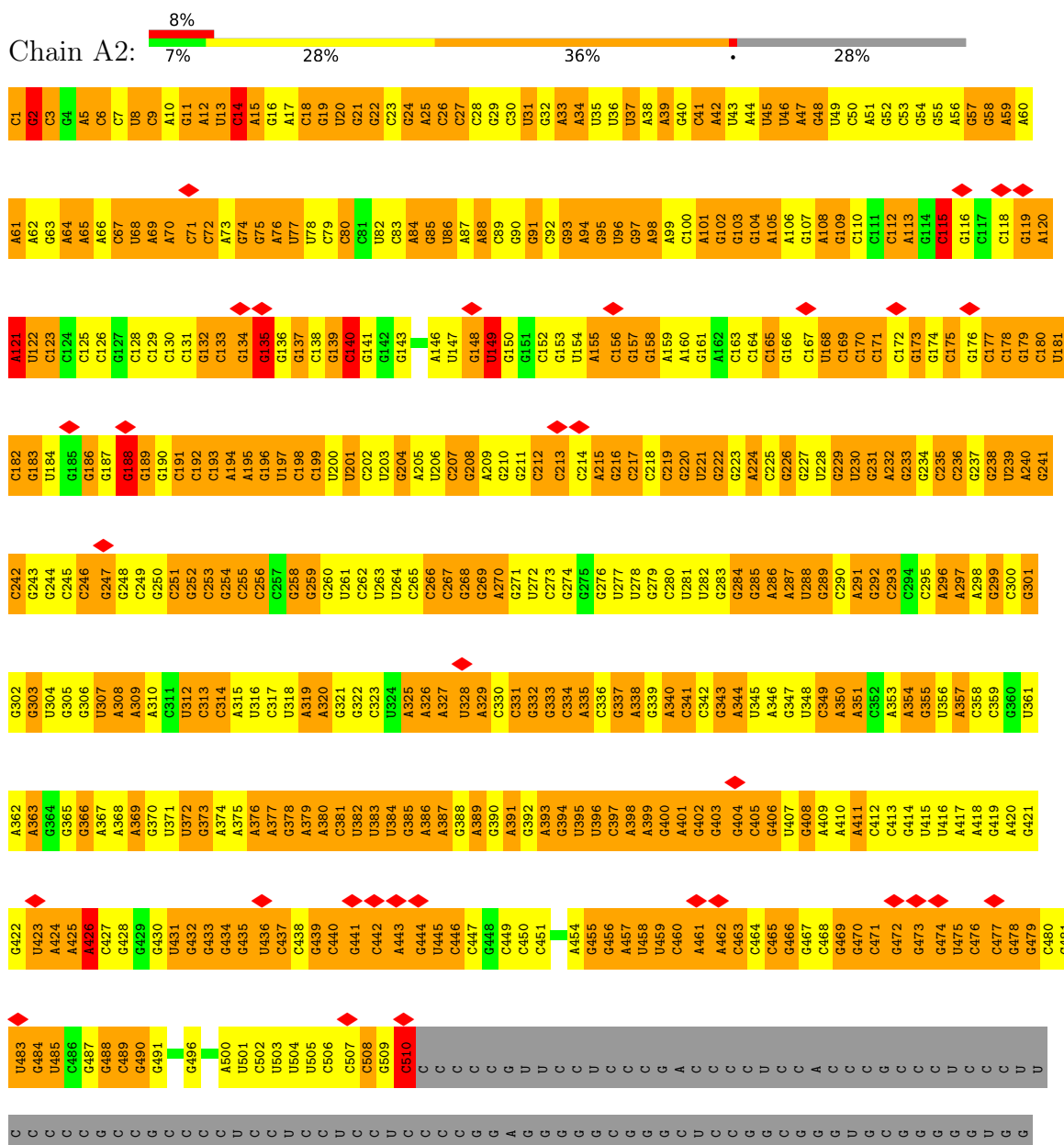
- Molecule 84 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>13</sub>P<sub>3</sub>).



### 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



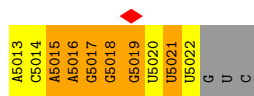
G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460																																																																							
G1341	G1342	G1343	G1344	G1345	G1346	G1347	G1348	G1349	G1350	G1351	G1352	G1353	G1354	G1355	G1356	G1357	G1358	G1359	G1360	G1361	G1362	G1363	G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	A1400																																																																							
G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320	G1321	G1322	G1323	G1324	G1325	G1326	G1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340																																																																				
G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260	G1261	G1262	G1263	G1264	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277																																																																							
U1157	U1158	U1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166	U1167	U1170	U1171	U1172	U1173	U1174	U1175	U1176	U1177	U1178	U1179	U1180	U1181	U1182	U1183	U1184	U1185	U1186	U1187	U1188	U1189	U1190	U1191	U1192	U1193	U1194	U1195	U1196	U1197	U1198	U1199	U1200	U1201	U1202	U1203	U1204	U1205	U1206	U1207	U1208	U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217																																																																								
C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155																																																																						
C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040																																																																
G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979																																																																	
C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999
G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724	G725	G726	G727	G728	G729	G730																																																																					
G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667																																																																																																





G4147	U4084	U4023	G3903	A3841	G3777	A3717	G3683	C3591	C
U4148	U4085	A4024	C3904	G3842	G3778	C3718	C3684	C3592	G
U4149	C4086	C4025	A3905	G3843	G3779	G3719	G3655	C3593	G
U4150	C4087	U4026	A3906	G3844	G3780	G3720	A3656	U3657	A
G4088	U4087	C4027	G3907	A3845	C3781	C3721	U3657	U3658	C
G4089	G4088	C4027	G3908	A3846	A3782	G3722	G3658	C3596	C
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G4091	G4090	G	G3910	G3848	G3784	G3724	G3660	C3598	C
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C4093	C4092	G	G3912	G3850	A3786	G3726	U3662	U3600	C
A4094	U4031	G	G3913	C3851	U3787	U3727	U3663	C3601	C
A4095	C4032	G	A3914	U3852	G3788	A3728	C3665	G3602	C
G4096	G4033	G	G3915	U3853	G3789	A3729	C3666	G3603	C
G4097	A3916	G	G3854	G3854	A3790	C3730	U3667	A3604	C
G4098	C3917	C	G3855	G3855	A3791	C3731	C3668	C3605	C
C4099	A3918	C	G3856	G3856	G3792	U3731	U3669	U3606	C
C4100	U4036	C	G3857	G3857	A3793	U3732	C3670	G3607	A
C4101	U4037	G	A3859	A3859	G3793	U3733	A3671	U3608	C
G4102	U4038	G	A3860	A3860	G3796	U3734	G3674	U3609	C
C4103	U4039	G	A3863	A3863	A3797	G3735	U3674	U3610	C
C4104	C4040	G	G3864	G3864	A3798	A3735	C3675	A3611	C
C4105	A4041	G	G3865	G3865	U3800	C3736	U3676	A3612	C
G4106	G4042	G	G3866	G3866	U3801	C3737	U3677	U3613	C
G4107	U4043	G	G3867	G3867	C3738	C3738	U3678	U3614	C
C4108	G4044	G	G3868	G3868	U3739	U3739	C3679	A3615	C
C4109	A4045	U	G3869	G3869	C3740	C3740	C3680	A3616	C
C4110	C4046	C	A3870	A3870	U3741	U3741	A3681	A3617	C
G4111	C4047	C	C3871	C3871	A3742	A3742	U3682	C3619	C
U4178	G4050	C	A3872	A3872	A3743	A3743	C3683	C3621	C
A4179	U4051	C	G3873	G3873	U3744	U3744	U3684	A3620	C
A4180	G4052	G	A3874	A3874	G3745	G3745	C3685	A3621	C
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C4183	G4055	C	A3877	A3877	A3749	A3749	A3688	A3625	C
A4184	C4056	U	C3878	C3878	C3750	C3750	A3689	U3626	C
G4185	G4057	G	G3879	G3879	C3751	C3751	U3690	C3627	C
C4186	G4058	C	C3880	C3880	A3752	A3752	G3691	G3630	C
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C4188	G4060	C	G3882	G3882	A3754	A3754	A3693	G3632	C
U4189	G4061	G	U3883	U3883	U3755	U3755	G3694	G3633	C
C4190	G4062	C	U3884	U3884	C3756	C3756	A3695	G3634	C
C4191	G4063	C	G3885	G3885	C3757	C3757	A3696	C3635	C
U4192	C4005	C	A3886	A3886	C3758	C3758	A3697	G3636	C
A4193	C4006	C	G3887	G3887	U3759	U3759	U3698	U3574	C
C4194	C4007	C	U3888	U3888	C3760	C3760	U3699	U3575	C
G4195	A4066	C	U3889	U3889	C3761	C3761	C3700	A3577	C
C4196	G4067	C	U3890	U3890	U3762	U3762	A3701	A3578	C
C4197	C4068	C	A3891	A3891	C3763	C3763	A3702	A3579	C
C4198	G4011	C	A3892	A3892	U3765	U3765	U3703	C3580	C
U4199	U4012	C	C3893	C3893	C3766	C3766	G3704	C3642	C
C4200	G4013	C	U3894	U3894	U3767	U3767	A3705	G3643	C
C4201	A4014	C	C3895	C3895	A3768	A3768	A3706	G3644	C
U4202	A4015	C	U3896	U3896	A3769	A3769	A3706	G3645	C
C4203	A4016	C	G3897	G3897	U3770	U3770	C3710	U3646	C
A4204	A4017	C	G3898	G3898	U3771	U3771	G3711	G3647	C
G4209	U4017	C	U3899	U3899	A3772	A3772	U3714	U3648	C
G4210	C4018	C	C3900	C3900	G3773	G3773	G3650	C3587	C
	A4019	C			U3774	U3774	A3651	G3589	C
	C4019	C			G3775	G3775	A3652	A3590	C
	C4020	C			A3776	A3776			C
	A4021	C							C
	U4078	C							C
	U4080	C							C
	C4081	C							C
	G4082	C							C
	C4083	U							C

U4944	C4945	U4946	G4947	C4948	C4949	G4954	G4955	U4956	U4957	U4958	C4959	C4960	U4961	C4962	C4963	C4964	C4965	C4966	C4967	C4968	C4969	C4970	C4971	C4972	C4973	C4974	C4975	C4976	U4977	C4978	C4979	C4980	U4981	C4982	G4983	C4984	C4985	C4986	C4987	C4988	C4989	C4990	C4991	C4992	C4993	C4994	C4995	C4996	C4997	C4998	C4999	U5000	C5001	A5002	G5003	C5004	C5005	C5006	C5007	U5008	C5009	G5010	A5011	C5012																							
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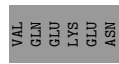
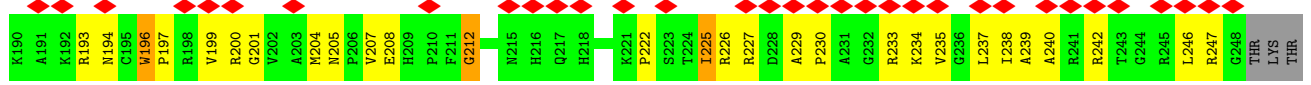
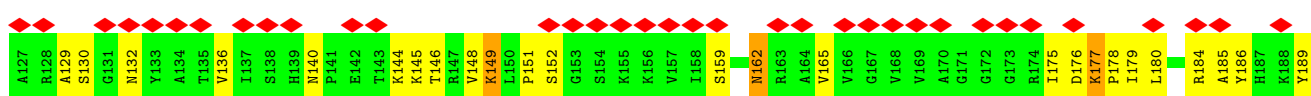
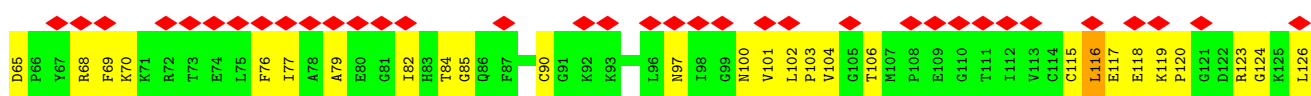
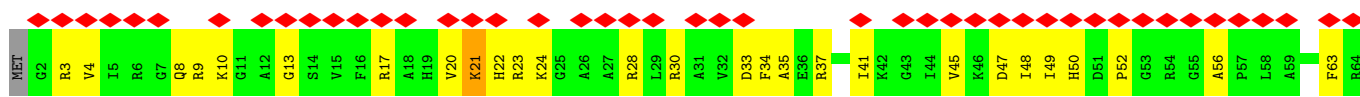
• Molecule 2: 5.8S Ribosomal RNA



• Molecule 3: 5S Ribosomal RNA



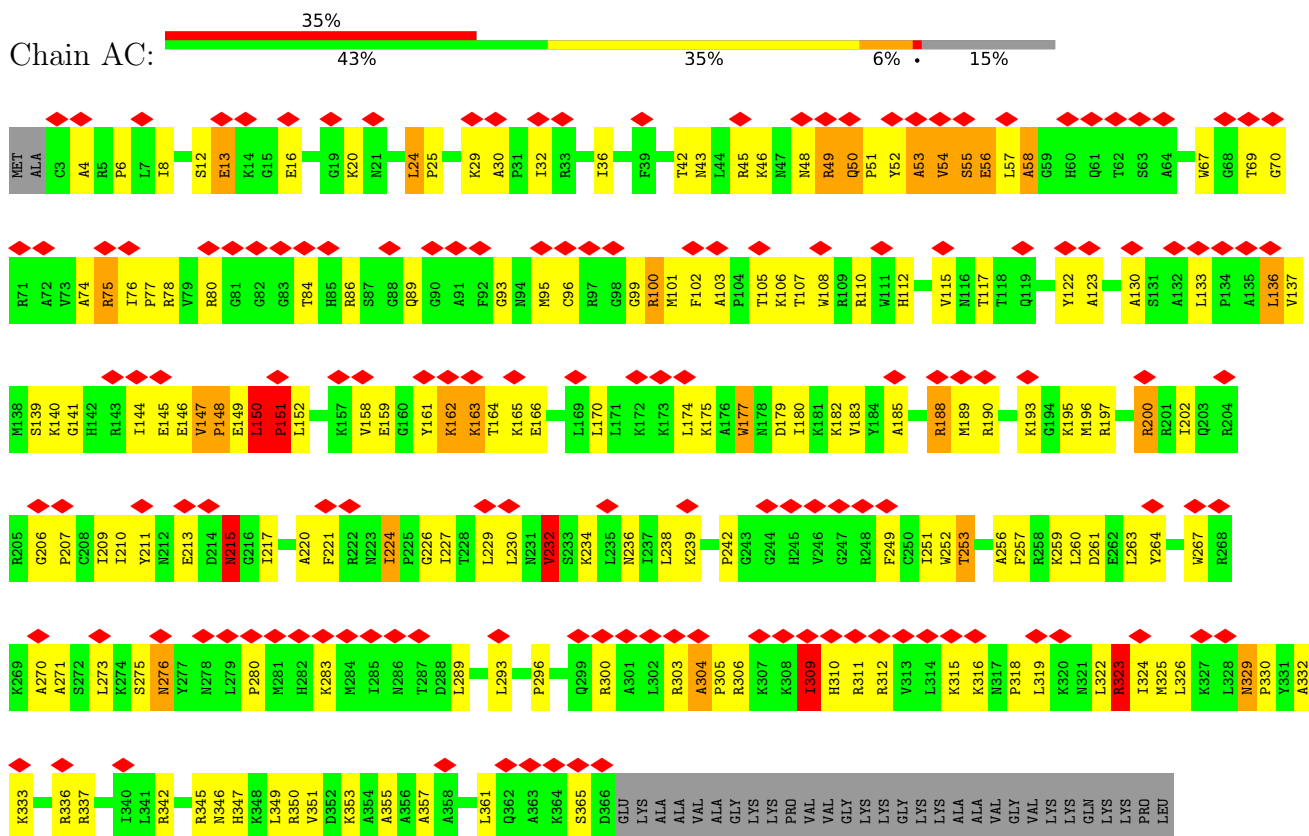
• Molecule 4: 60S RIBOSOMAL PROTEIN L8



- Molecule 5: 60S RIBOSOMAL PROTEIN L3

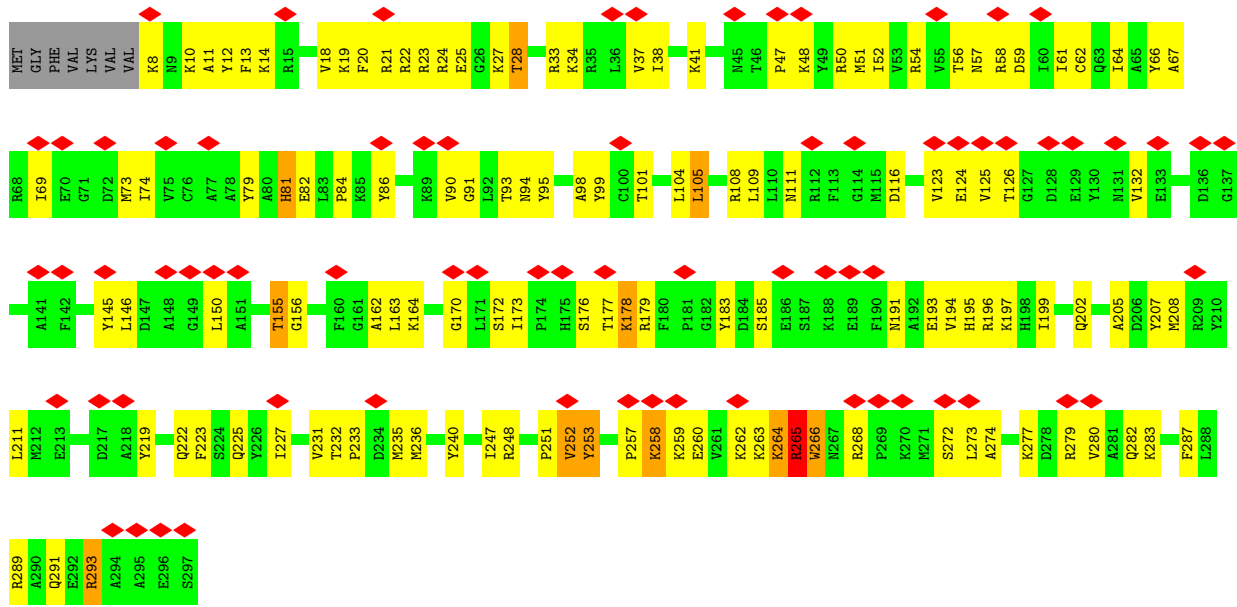


- Molecule 6: 60S RIBOSOMAL PROTEIN L4

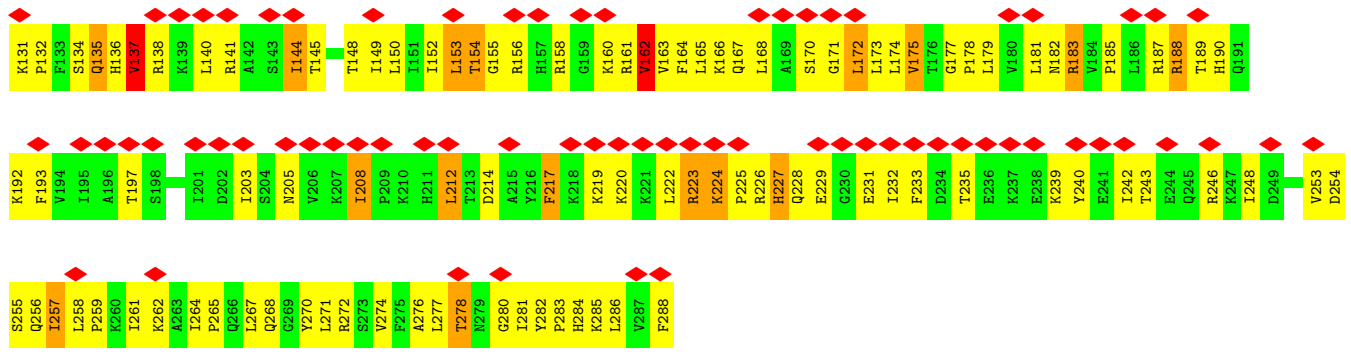


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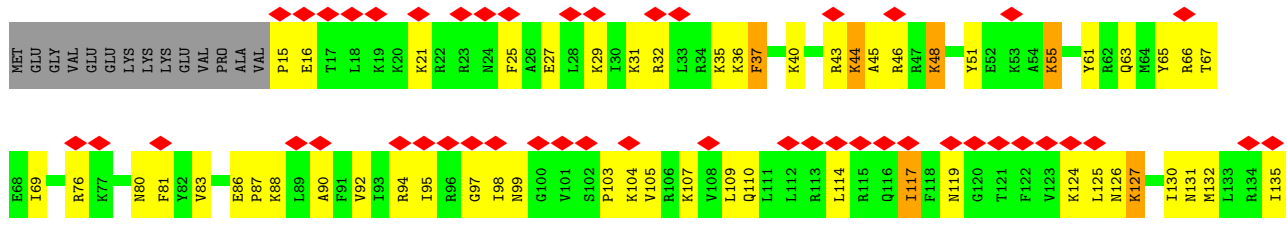
• Molecule 7: 60S RIBOSOMAL PROTEIN L5



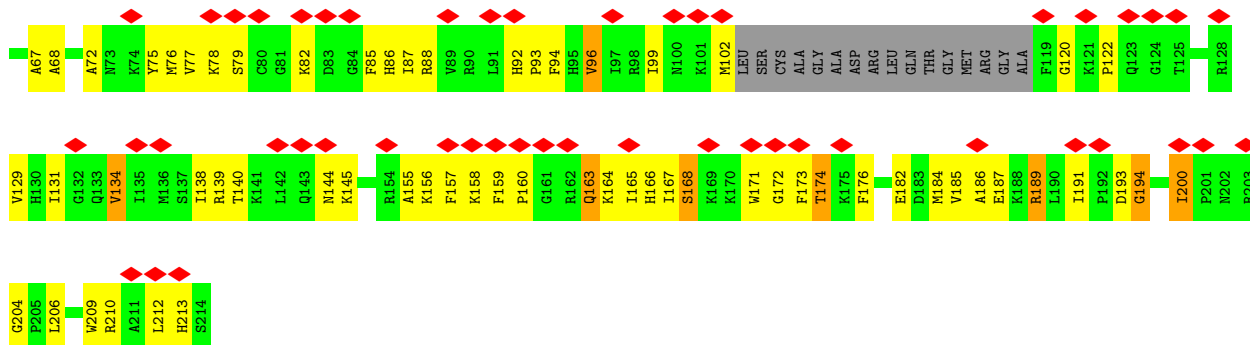
• Molecule 8: 60S RIBOSOMAL PROTEIN L6



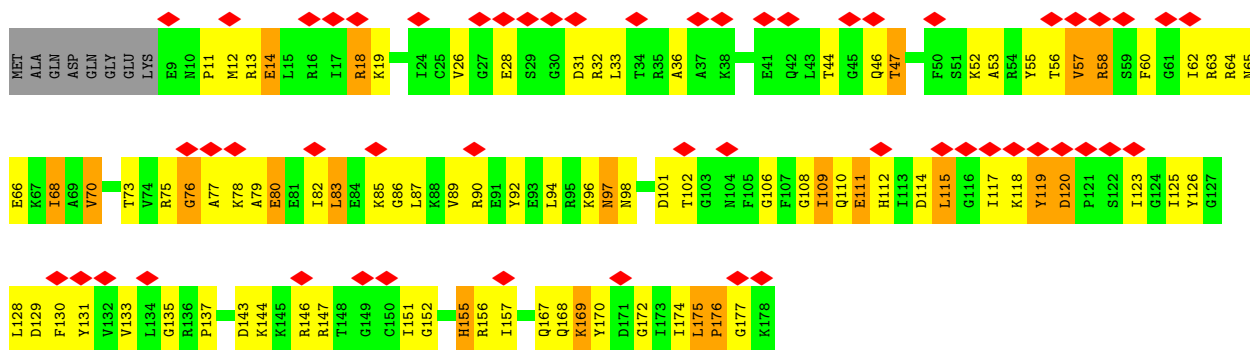
• Molecule 9: 60S RIBOSOMAL PROTEIN L7



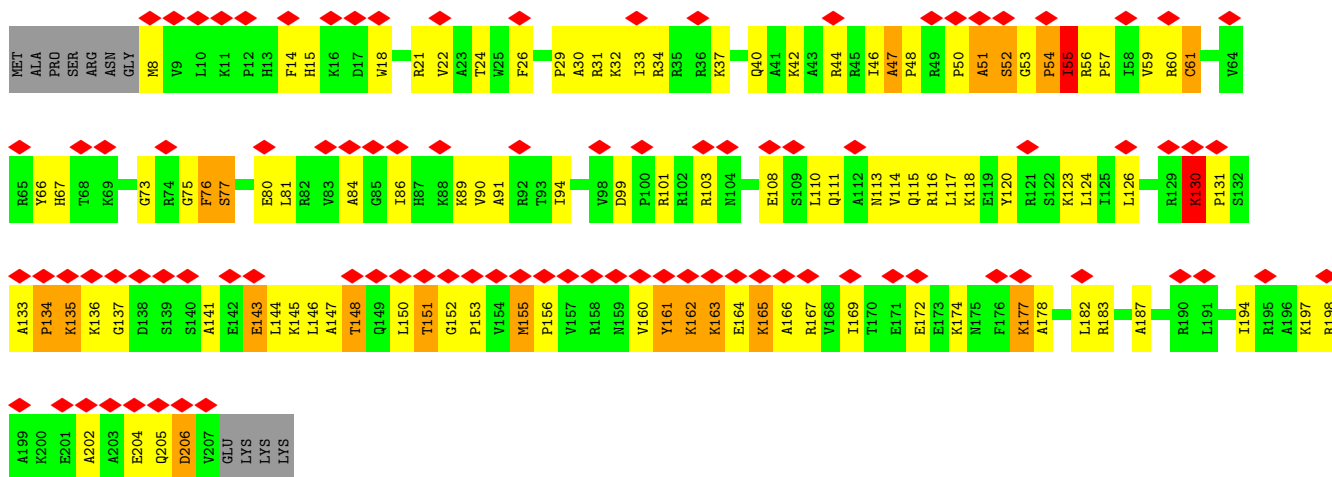




• Molecule 13: 60S RIBOSOMAL PROTEIN L11

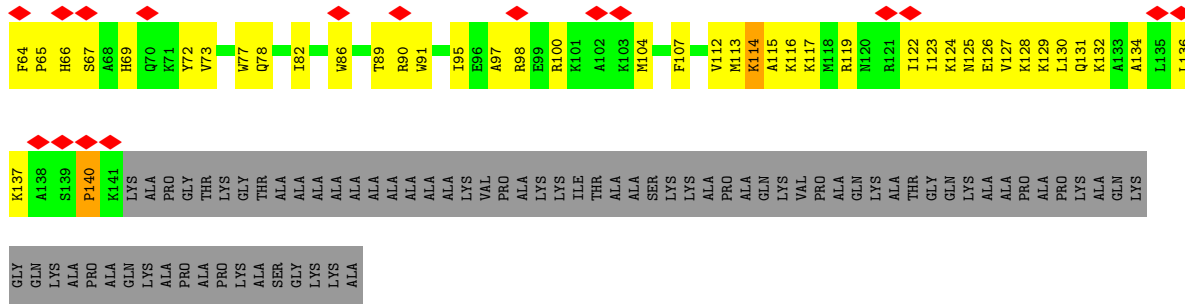


• Molecule 14: 60S RIBOSOMAL PROTEIN L13

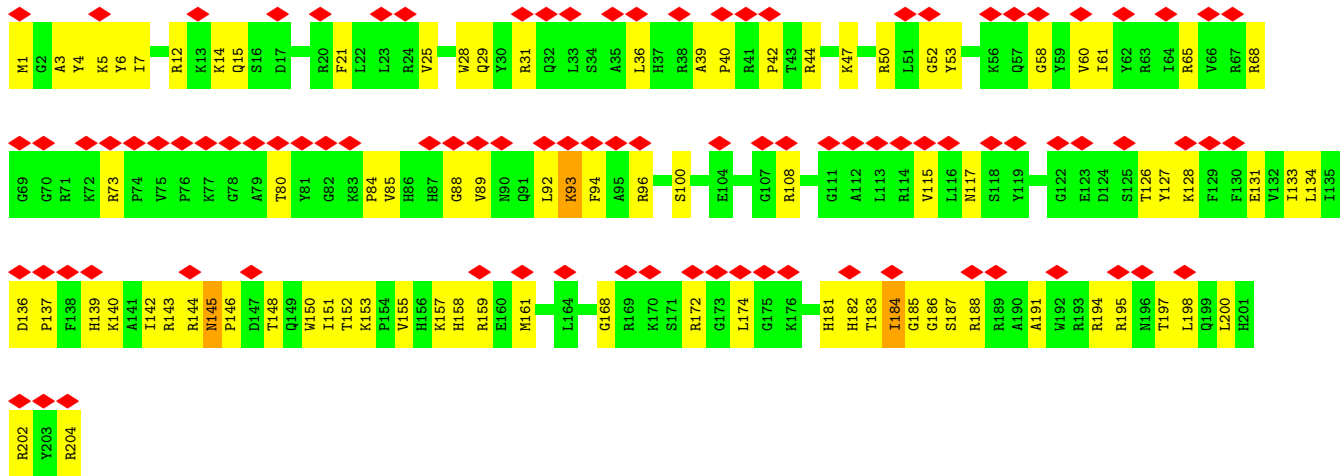


• Molecule 15: 60S RIBOSOMAL PROTEIN L14

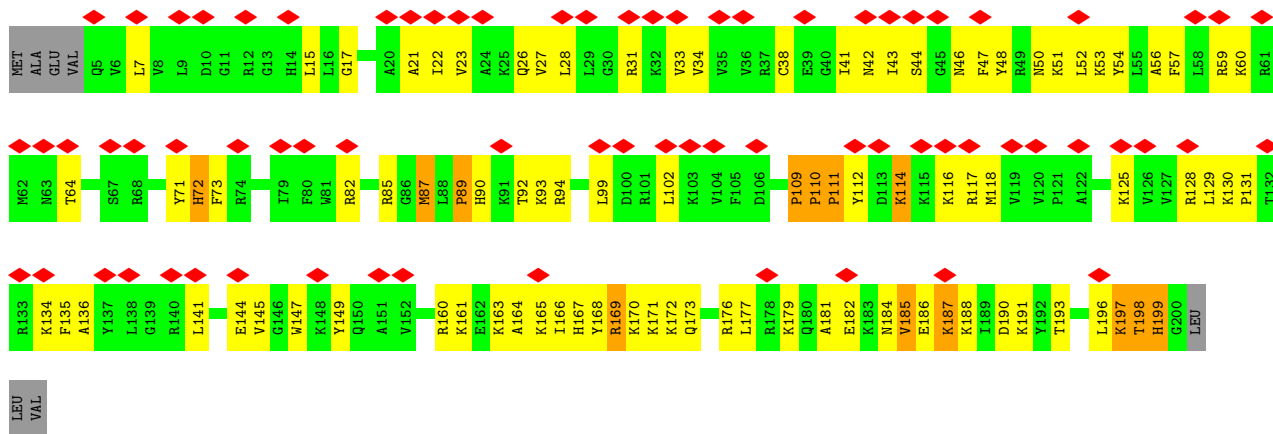




• Molecule 16: 60S RIBOSOMAL PROTEIN L15

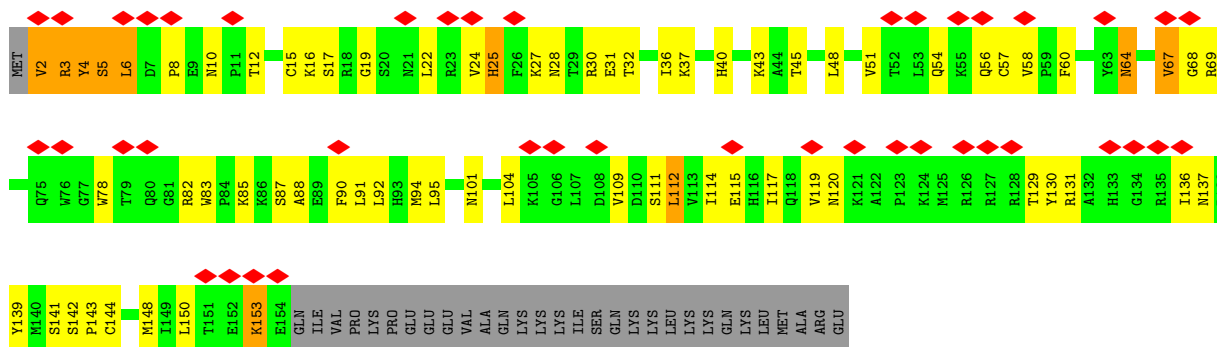


• Molecule 17: 60S RIBOSOMAL PROTEIN L13A

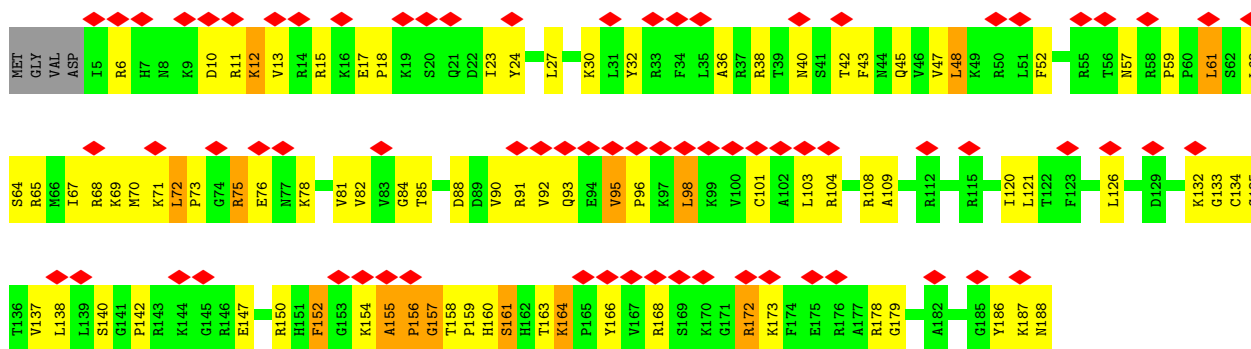
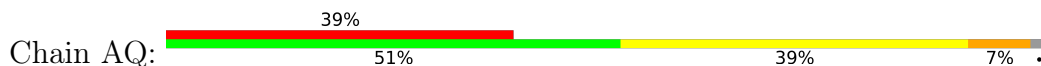


• Molecule 18: 60S RIBOSOMAL PROTEIN L17

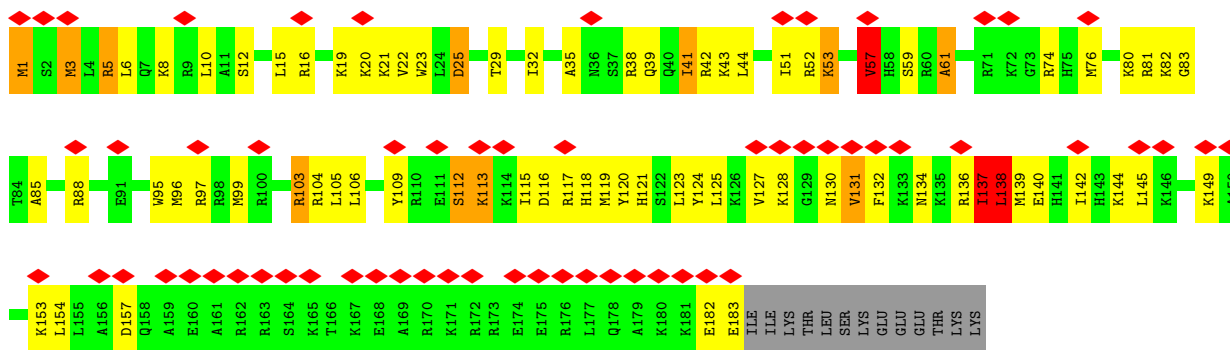




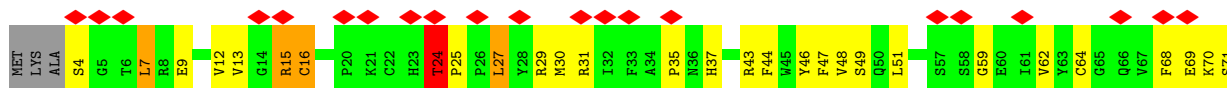
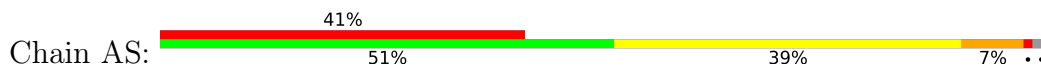
• Molecule 19: 60S RIBOSOMAL PROTEIN L18

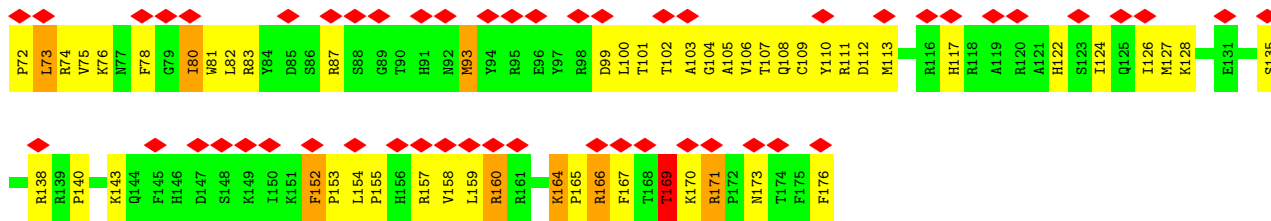


• Molecule 20: 60S RIBOSOMAL PROTEIN L19

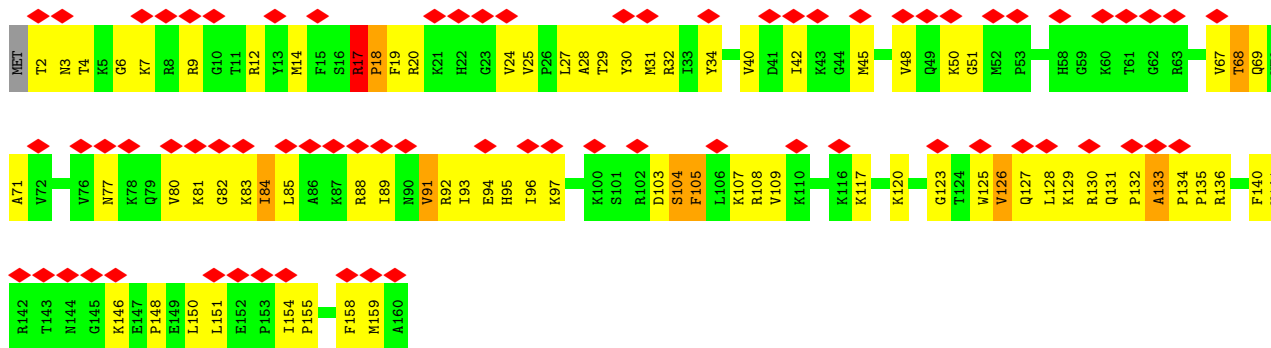


• Molecule 21: 60S RIBOSOMAL PROTEIN L18A

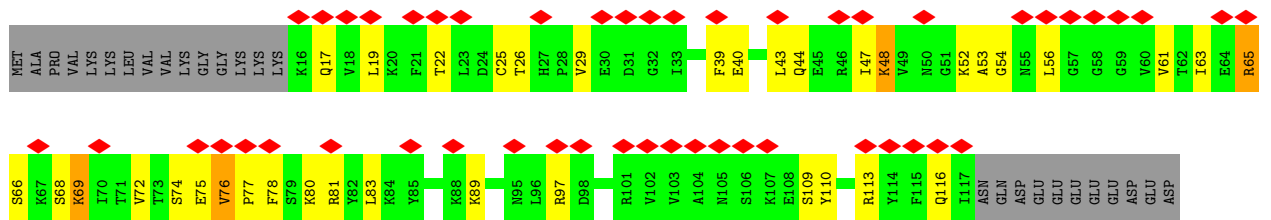
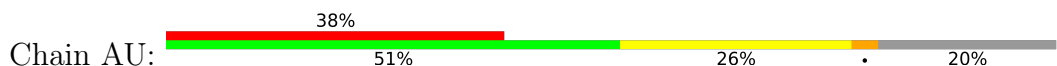




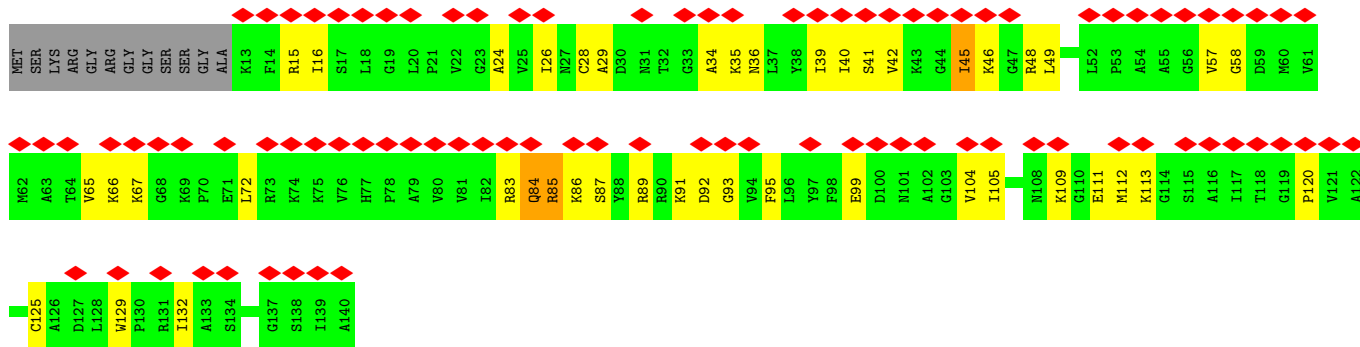
• Molecule 22: 60S RIBOSOMAL PROTEIN L21



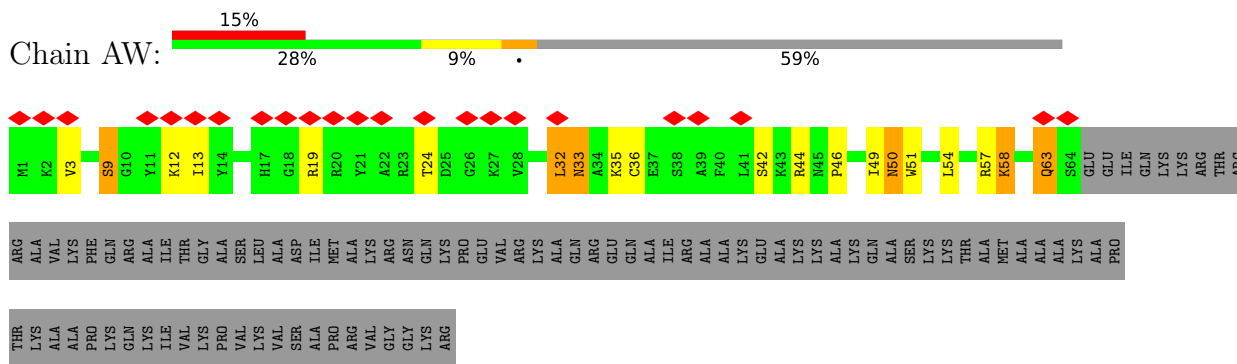
• Molecule 23: 60S RIBOSOMAL PROTEIN L22



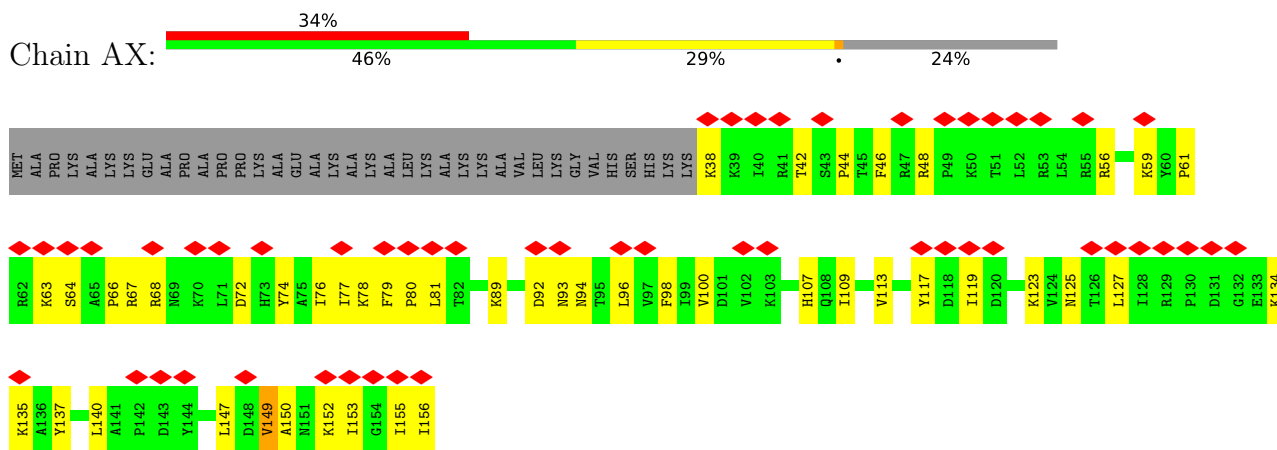
• Molecule 24: 60S RIBOSOMAL PROTEIN L23



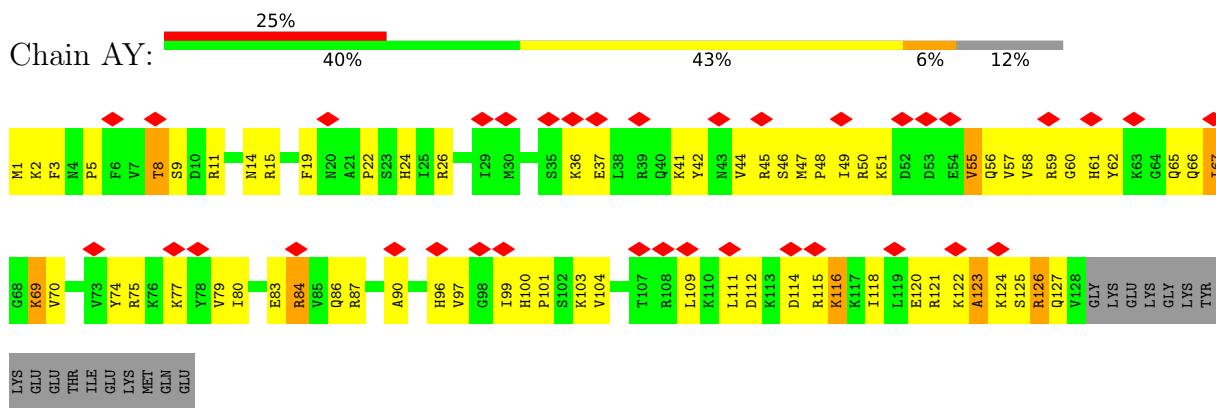
• Molecule 25: 60S RIBOSOMAL PROTEIN L24



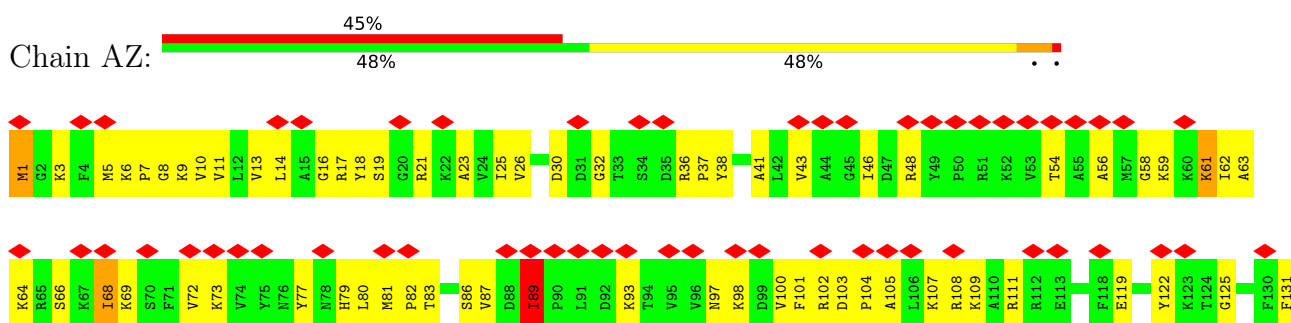
• Molecule 26: 60S RIBOSOMAL PROTEIN L23A



• Molecule 27: 60S RIBOSOMAL PROTEIN L26



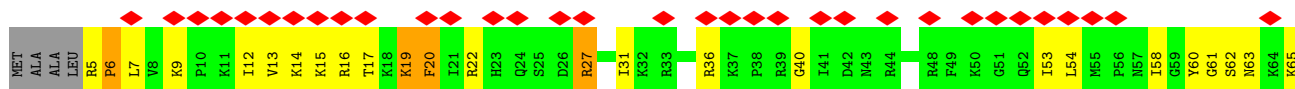
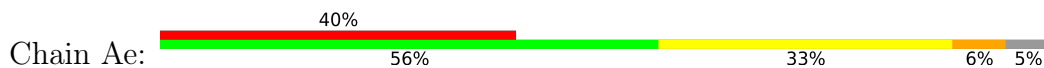
• Molecule 28: 60S RIBOSOMAL PROTEIN L27



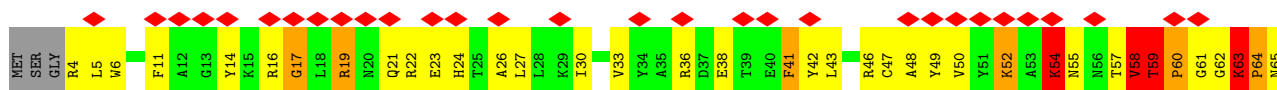




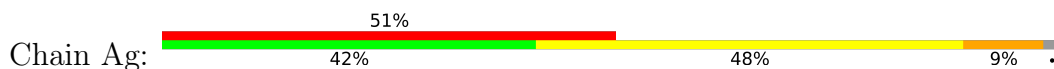
• Molecule 33: 60S RIBOSOMAL PROTEIN L32



• Molecule 34: 60S RIBOSOMAL PROTEIN L35A



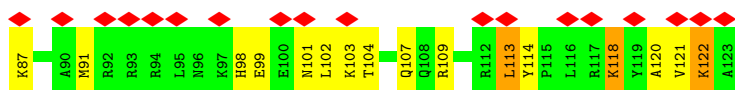
• Molecule 35: 60S RIBOSOMAL PROTEIN L34

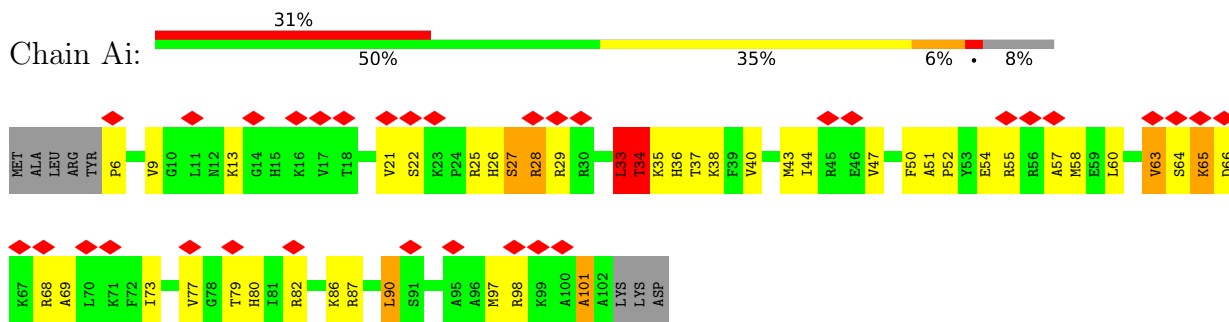


• Molecule 36: 60S RIBOSOMAL PROTEIN L35

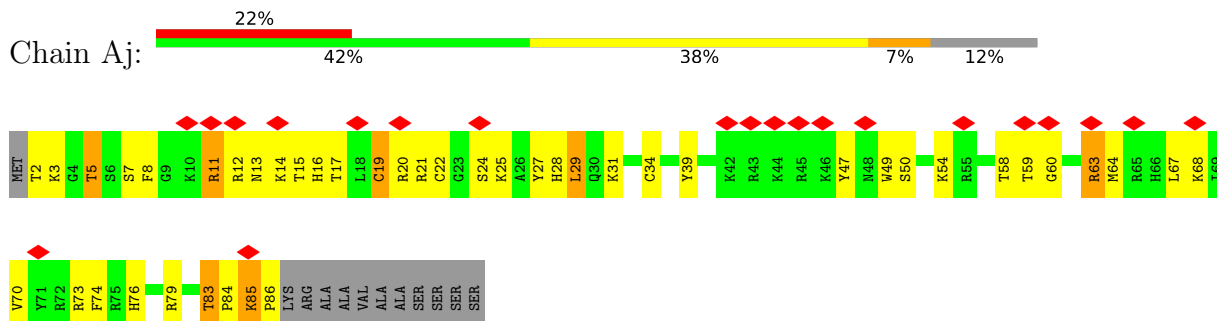


• Molecule 37: 60S RIBOSOMAL PROTEIN L36

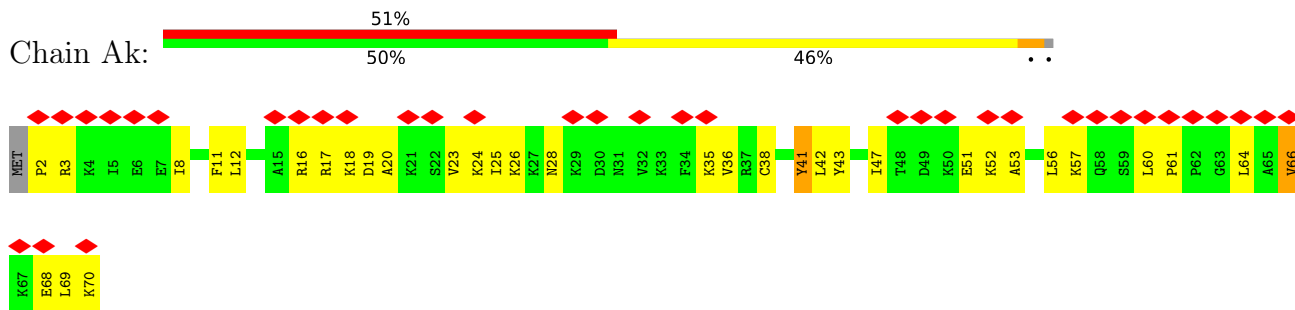




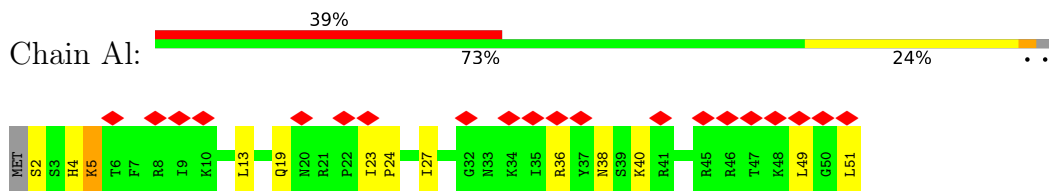
• Molecule 38: 60S RIBOSOMAL PROTEIN L37



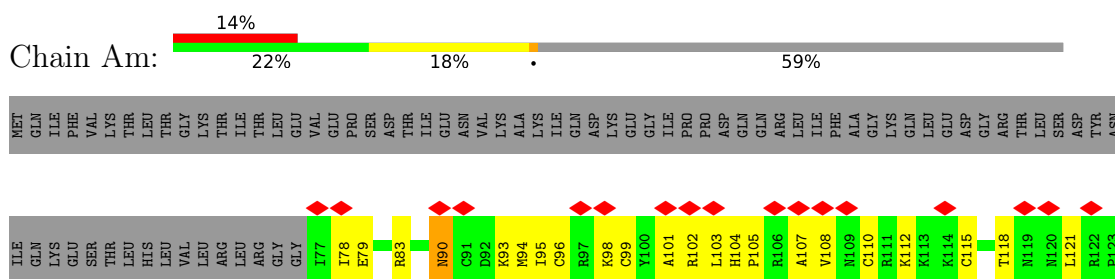
• Molecule 39: 60S RIBOSOMAL PROTEIN L38



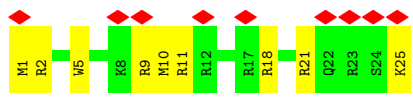
• Molecule 40: 60S RIBOSOMAL PROTEIN L39



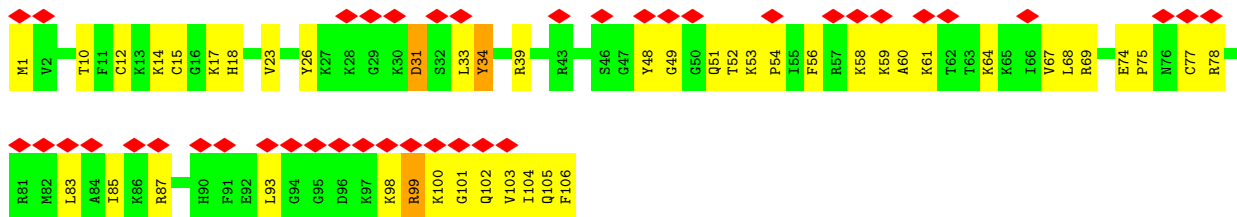
• Molecule 41: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



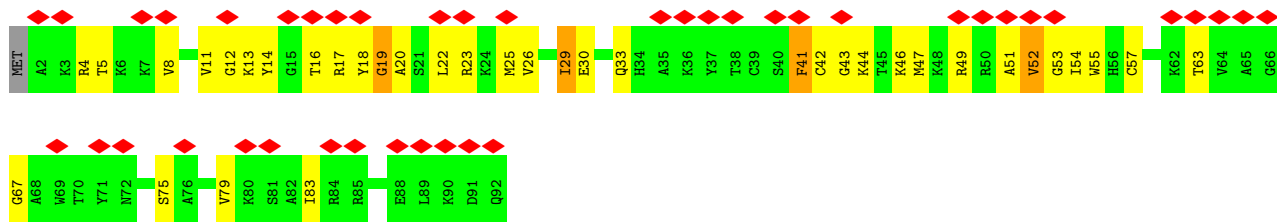
• Molecule 42: 60S RIBOSOMAL PROTEIN L41



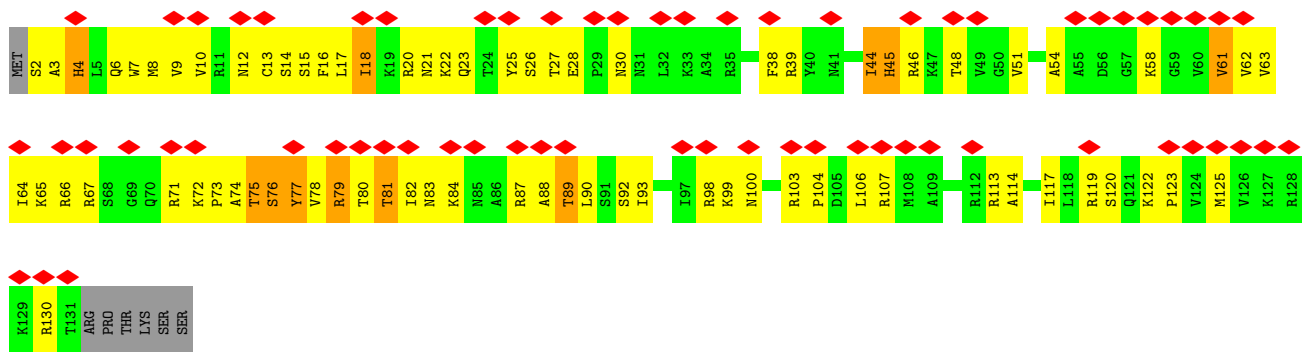
• Molecule 43: 60S RIBOSOMAL PROTEIN L36A



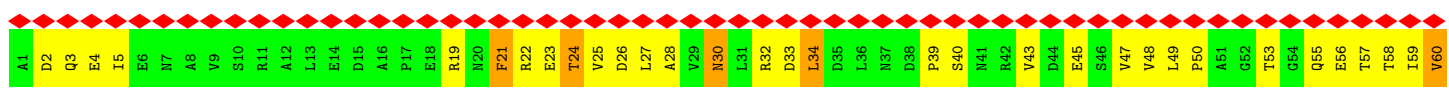
• Molecule 44: 60S RIBOSOMAL PROTEIN L37A

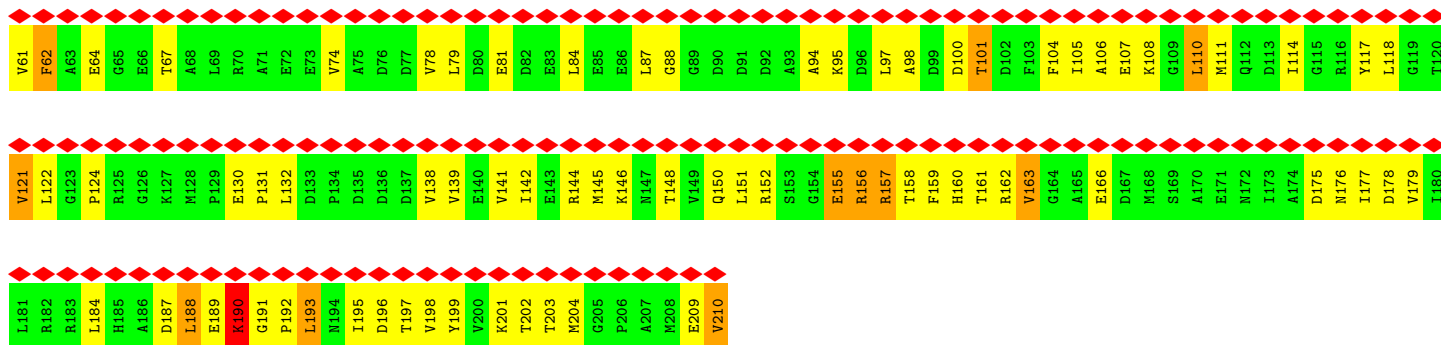


• Molecule 45: 60S RIBOSOMAL PROTEIN L28



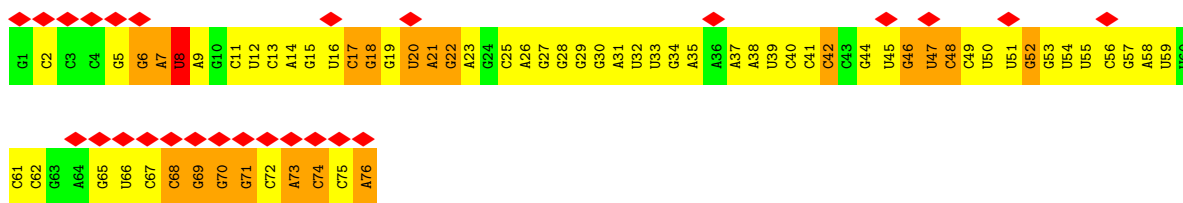
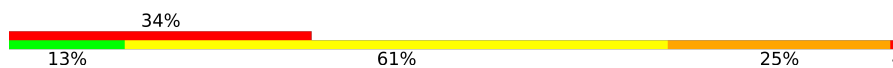
• Molecule 46: 60S RIBOSOMAL PROTEIN L10A





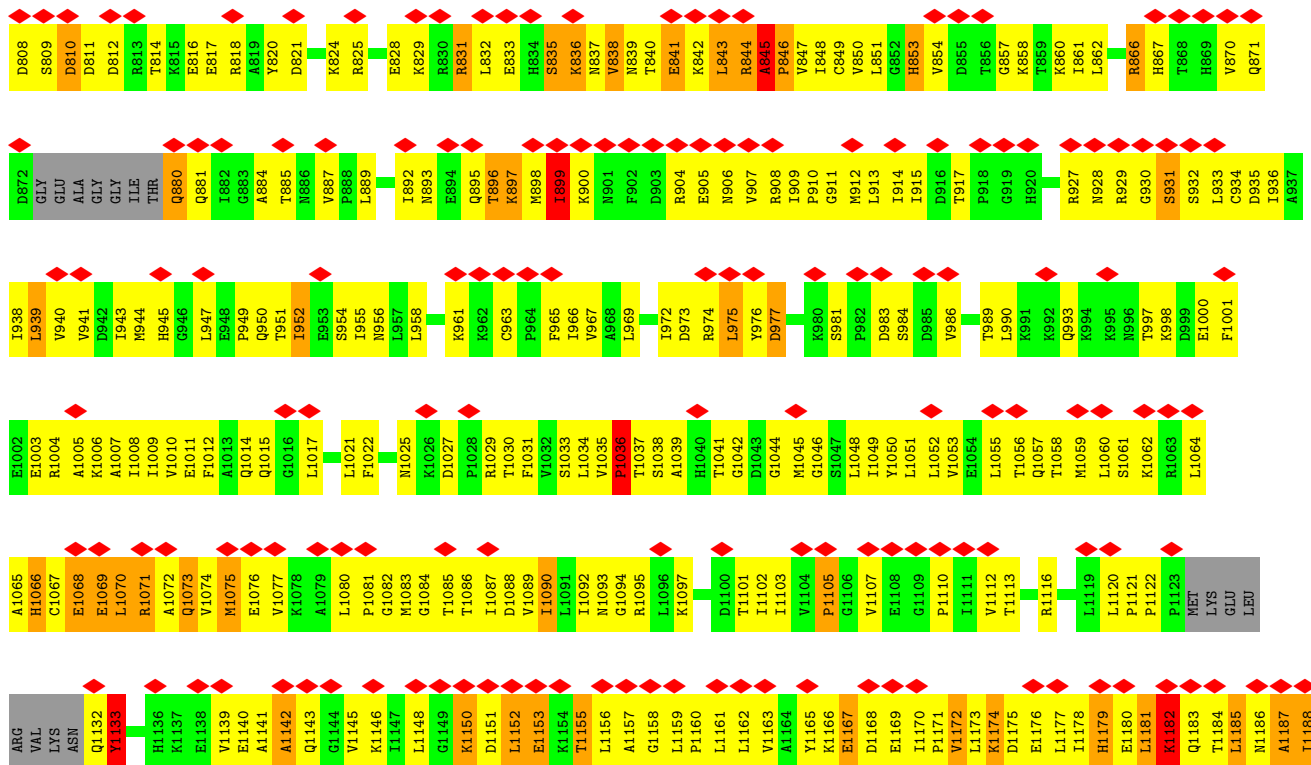
• Molecule 47: TRNA

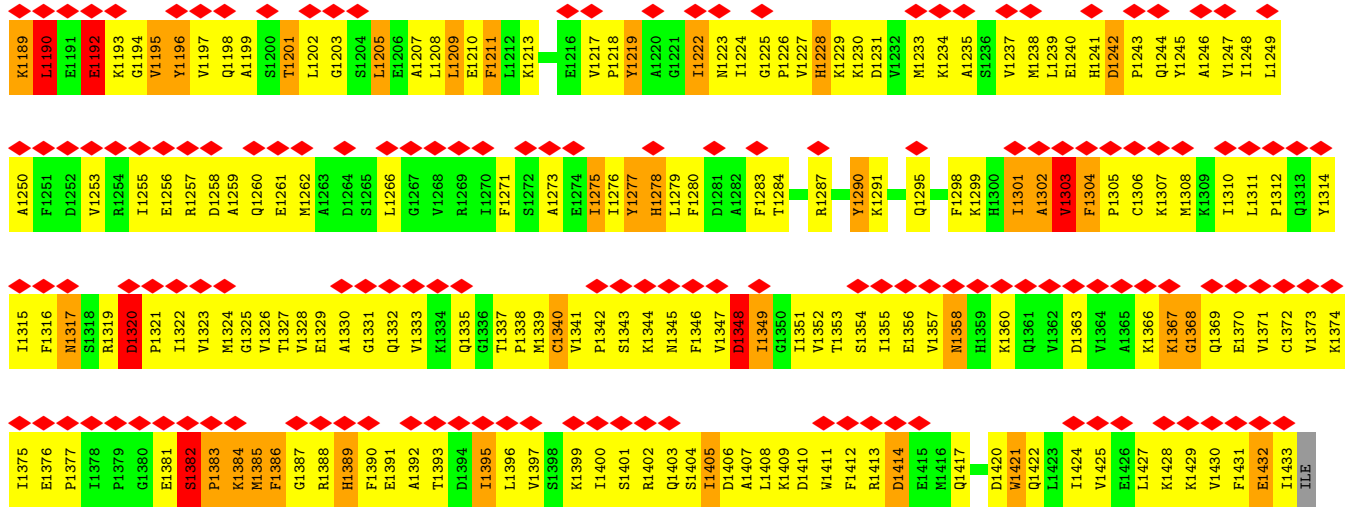
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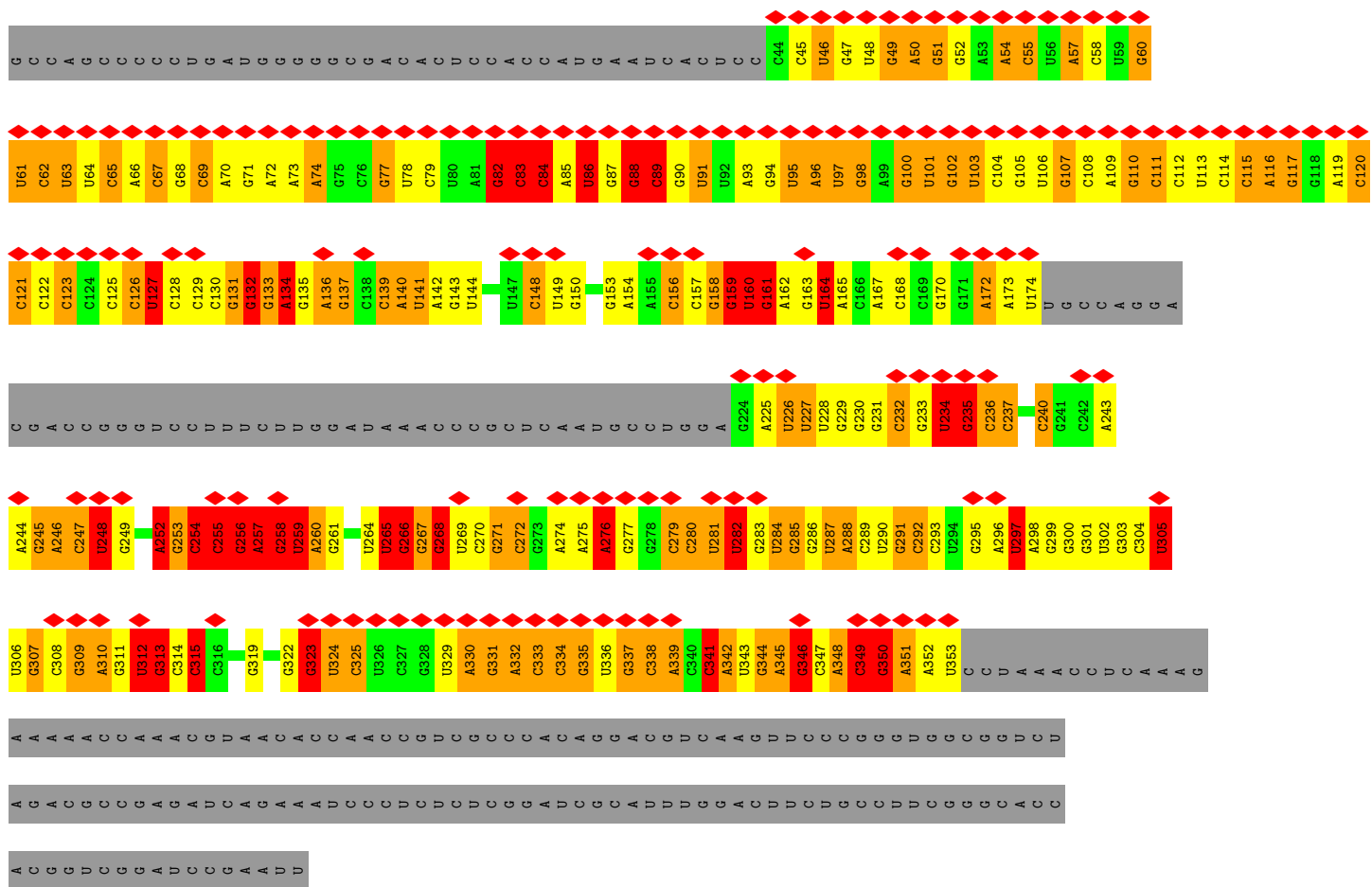
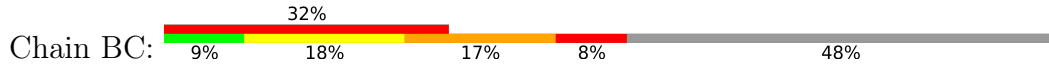
• Molecule 48: EIF5B

Chain BB:





● Molecule 49: HCV-IRES

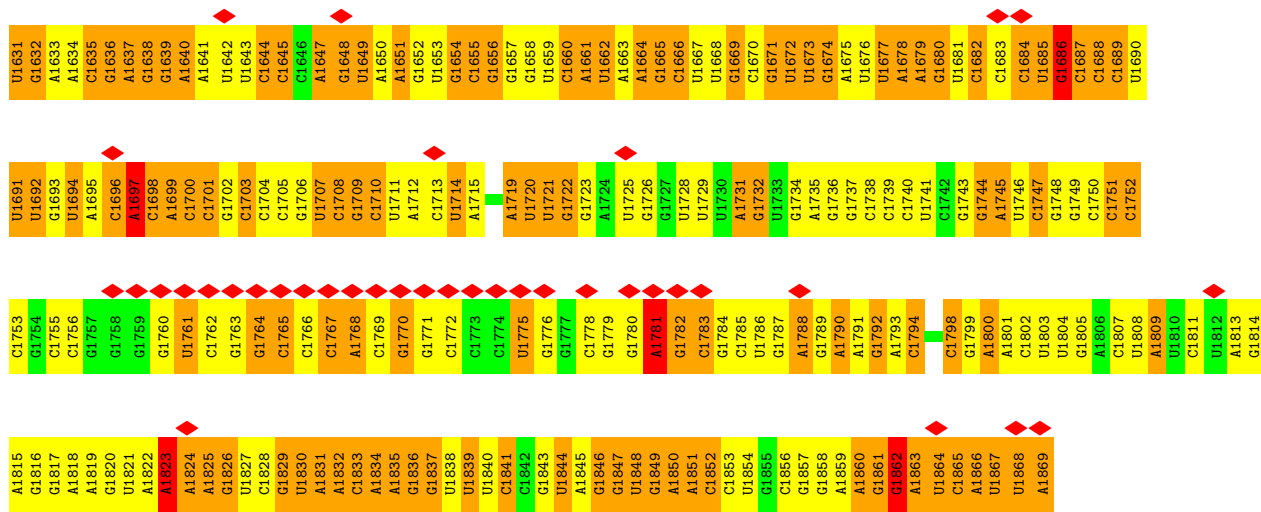


● Molecule 50: 18S Ribosomal RNA

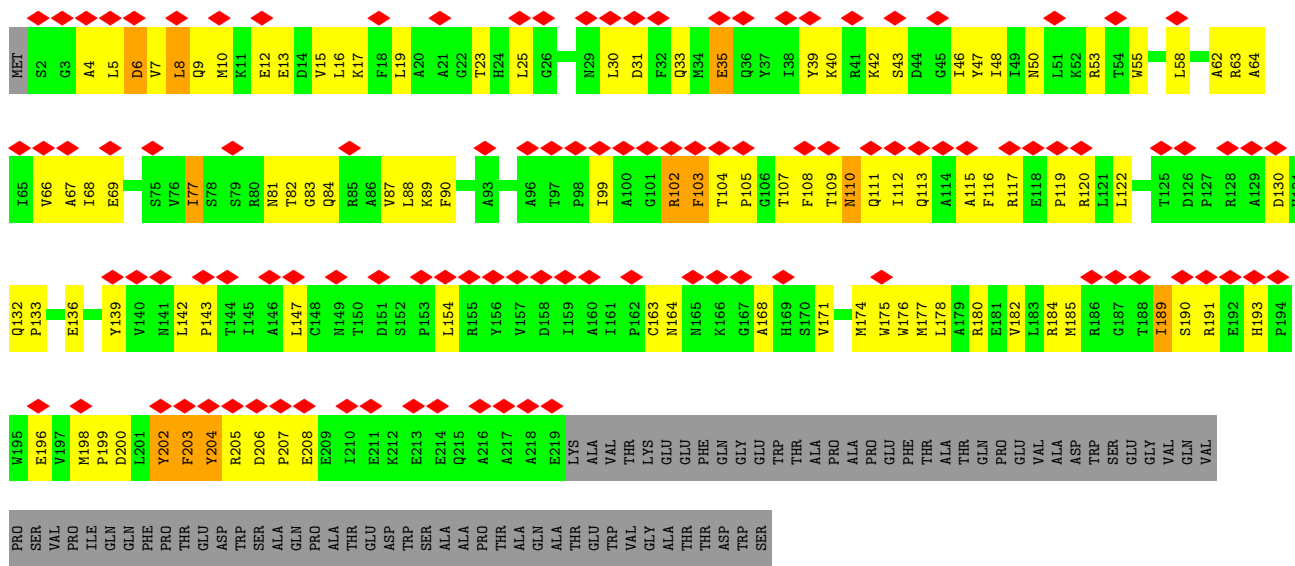


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C	C544	A545	G546	G547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603
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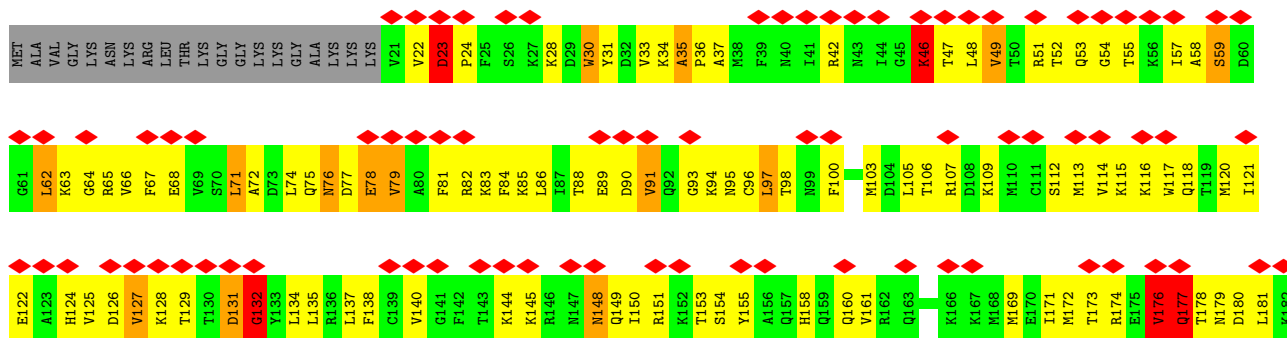
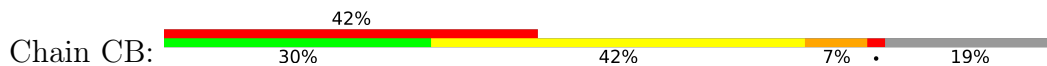
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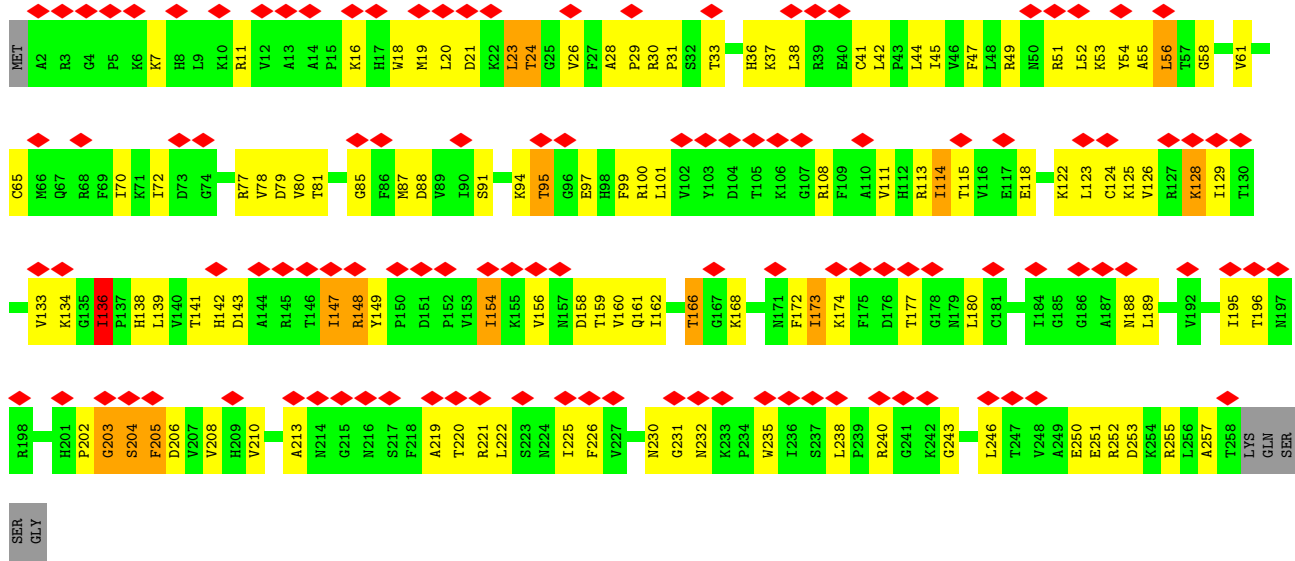
• Molecule 51: 40S RIBOSOMAL PROTEIN US2



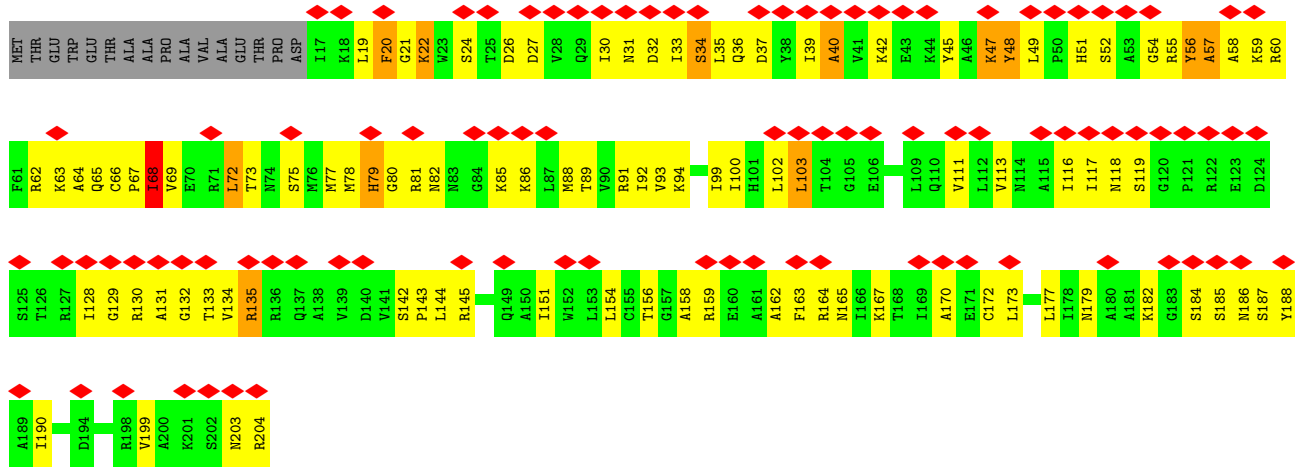
• Molecule 52: 40S RIBOSOMAL PROTEIN ES1



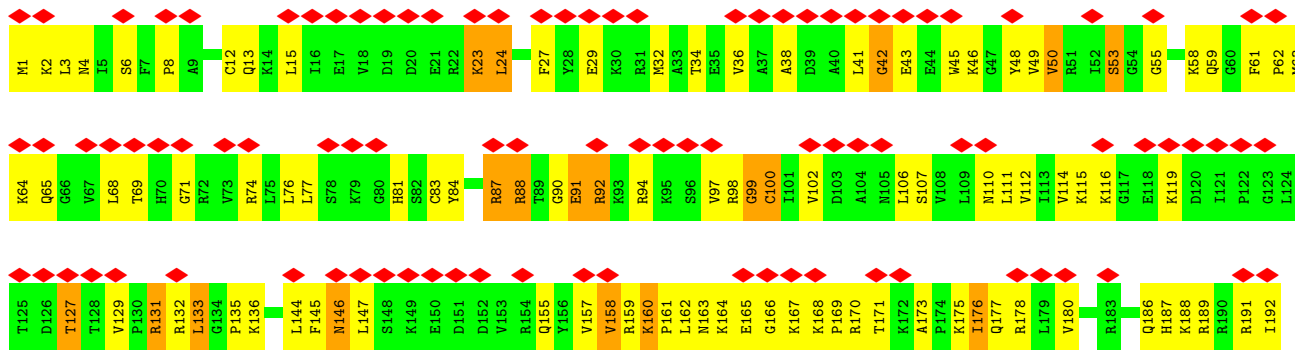


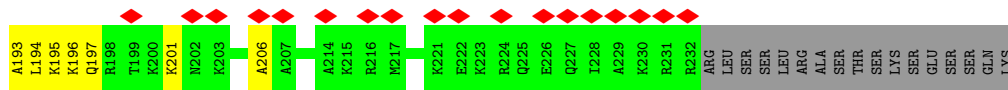


• Molecule 56: 40S RIBOSOMAL PROTEIN US7

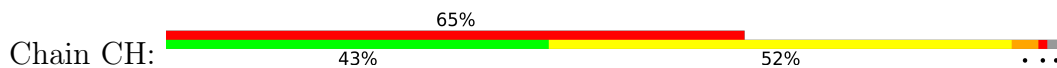


• Molecule 57: 40S RIBOSOMAL PROTEIN ES6

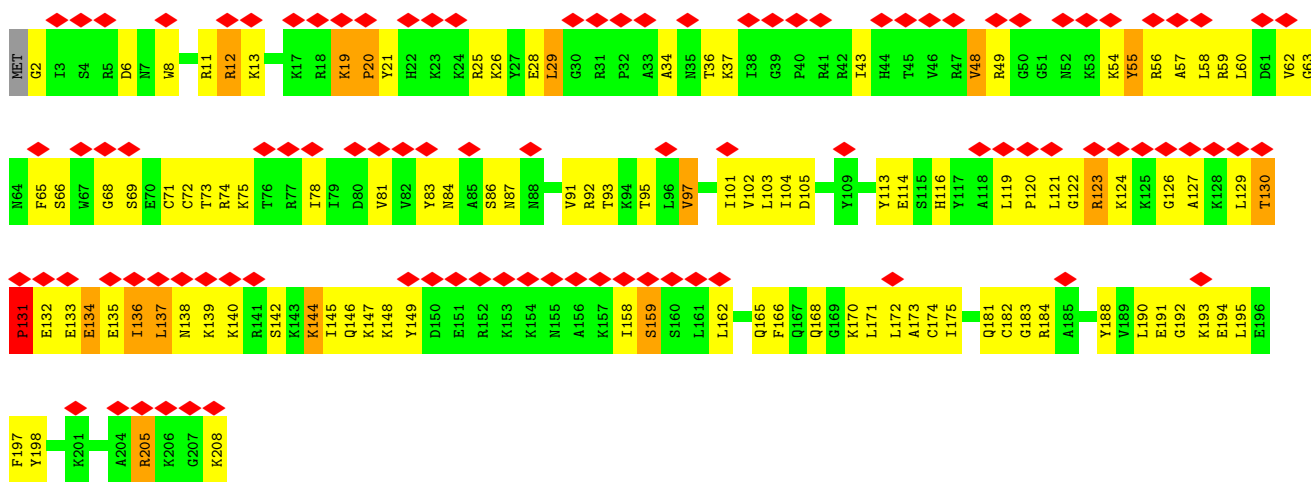




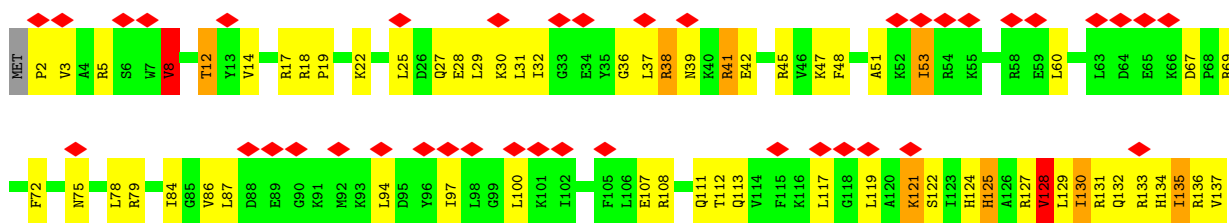
• Molecule 58: 40S RIBOSOMAL PROTEIN ES7

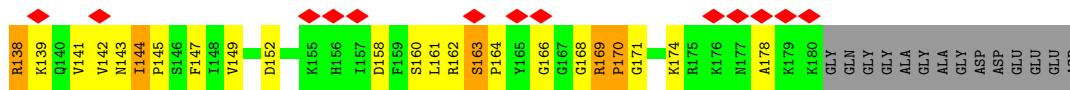


• Molecule 59: 40S RIBOSOMAL PROTEIN ES8

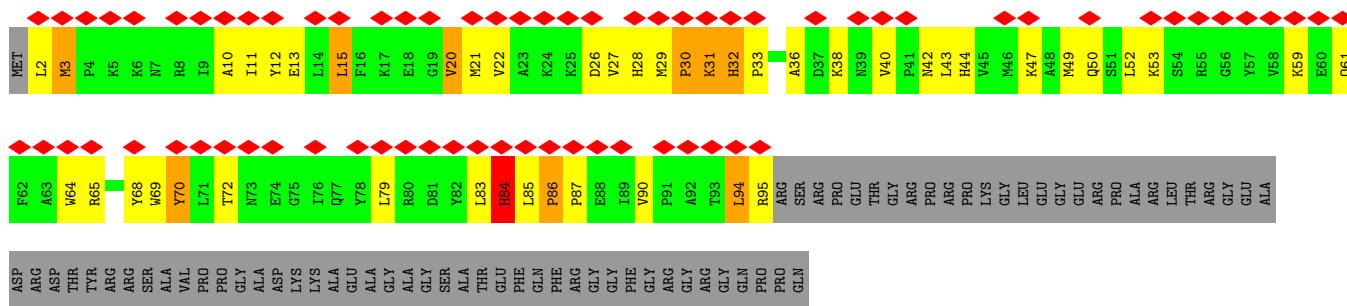
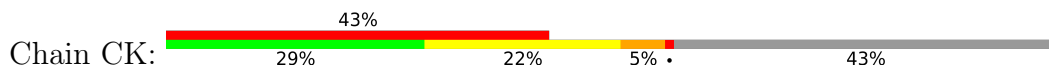


• Molecule 60: 40S RIBOSOMAL PROTEIN US4

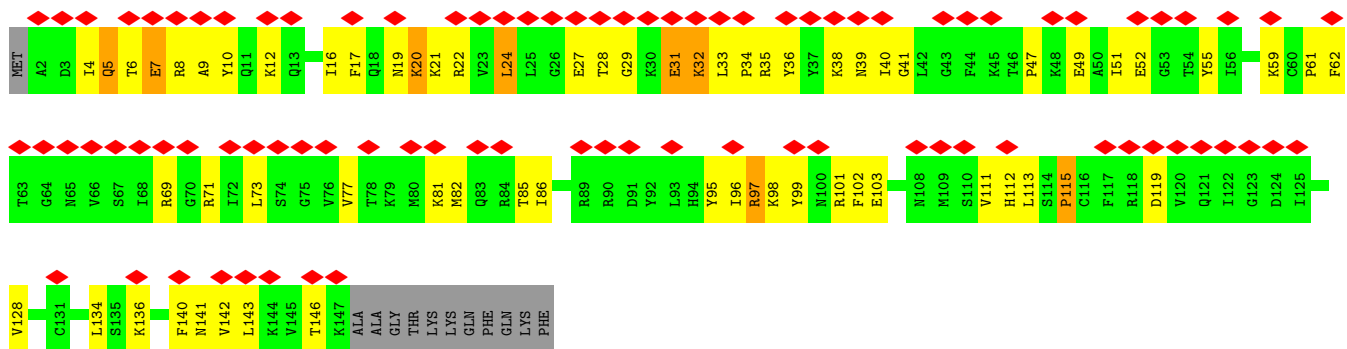




• Molecule 61: 40S RIBOSOMAL PROTEIN ES10



• Molecule 62: 40S RIBOSOMAL PROTEIN US17

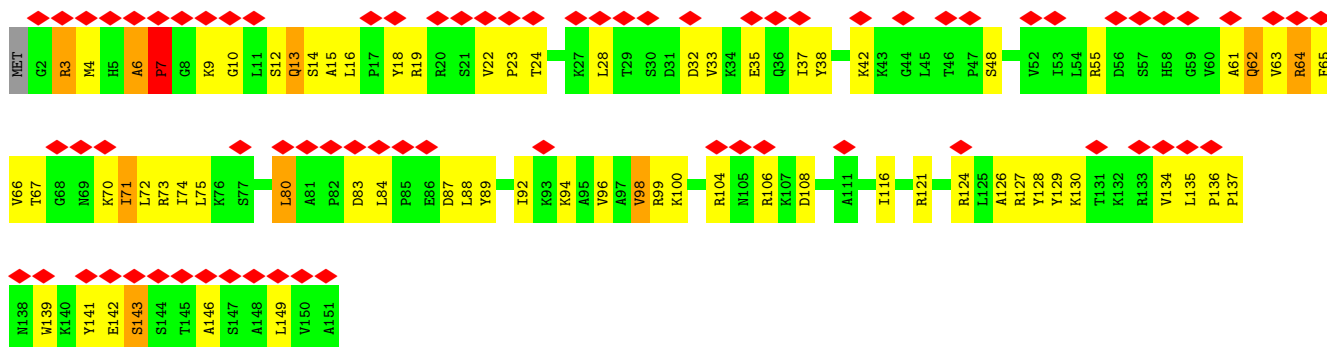


• Molecule 63: 40S RIBOSOMAL PROTEIN ES12

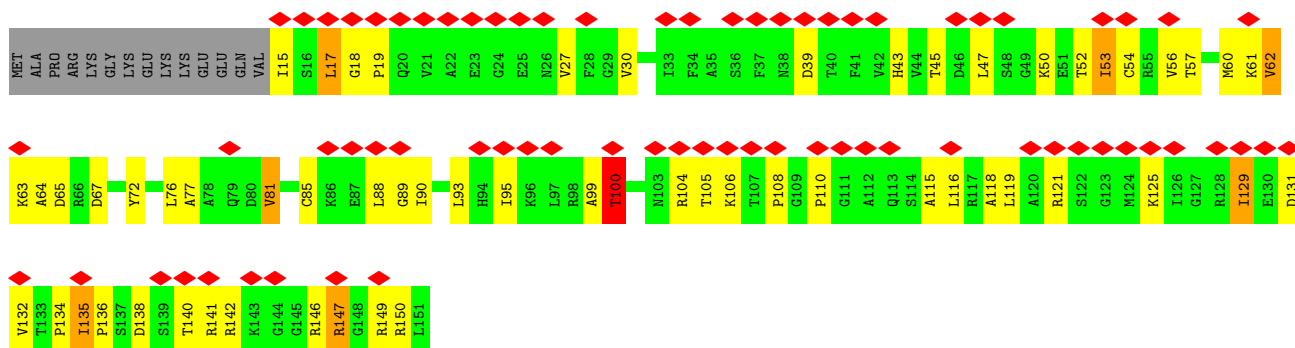


• Molecule 64: 40S RIBOSOMAL PROTEIN ES15

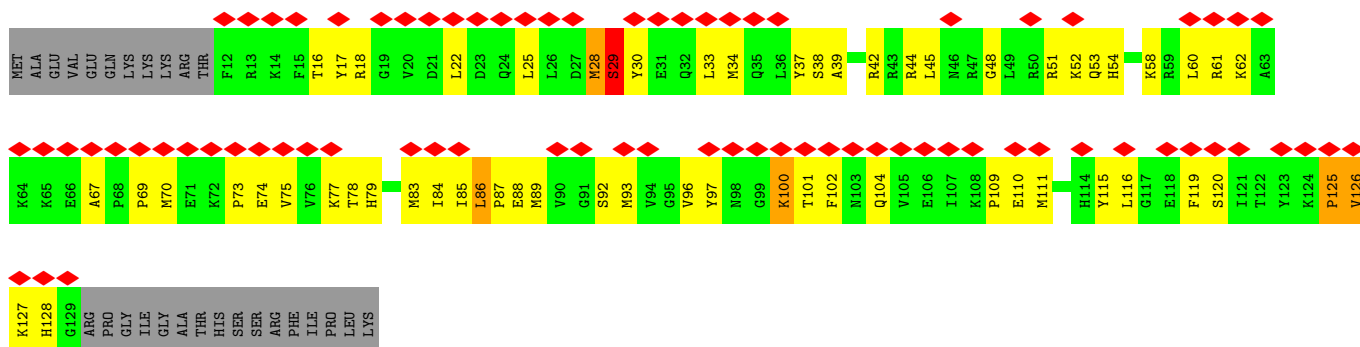




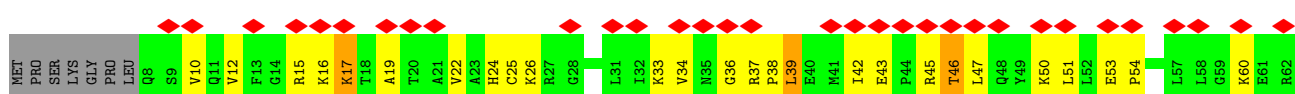
• Molecule 65: 40S RIBOSOMAL PROTEIN ES11

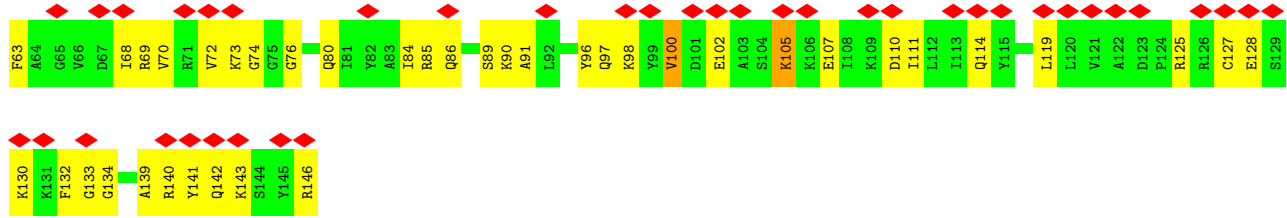


• Molecule 66: 40S RIBOSOMAL PROTEIN US19

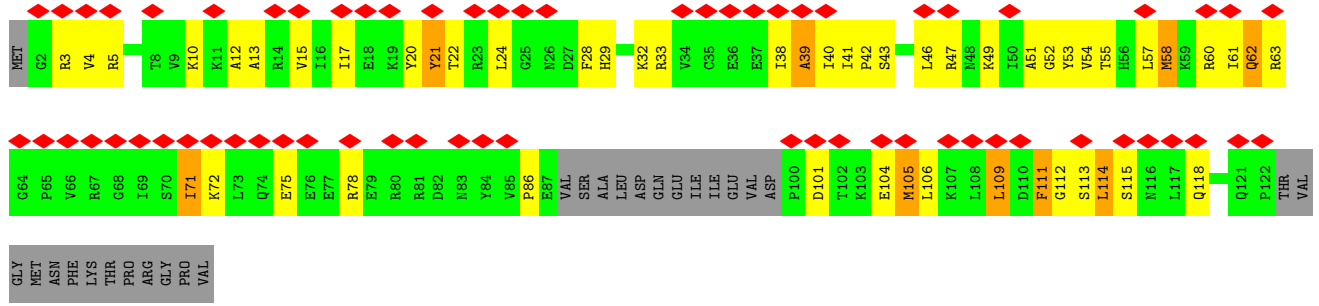


• Molecule 67: 40S RIBOSOMAL PROTEIN US9

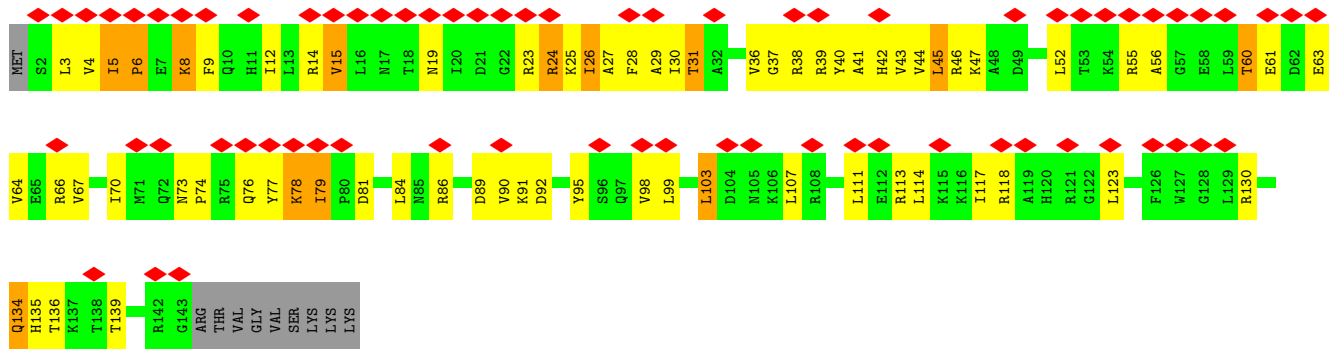




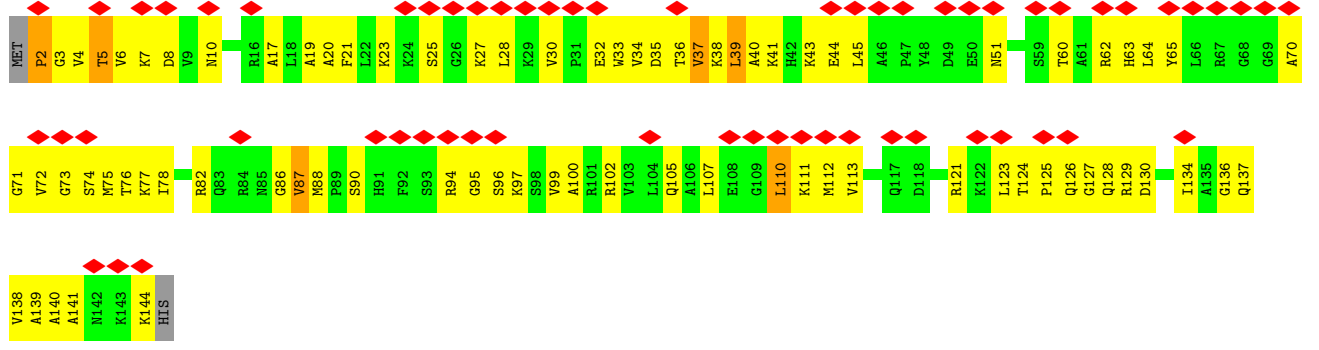
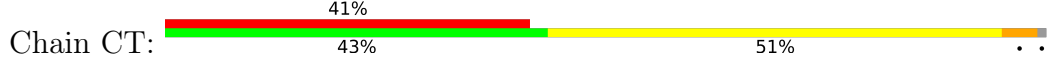
• Molecule 68: 40S RIBOSOMAL PROTEIN ES17



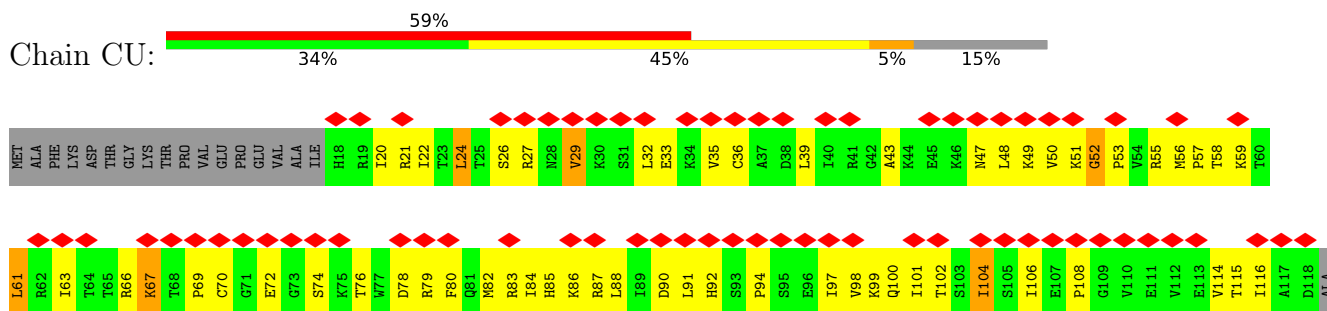
• Molecule 69: 40S RIBOSOMAL PROTEIN US13



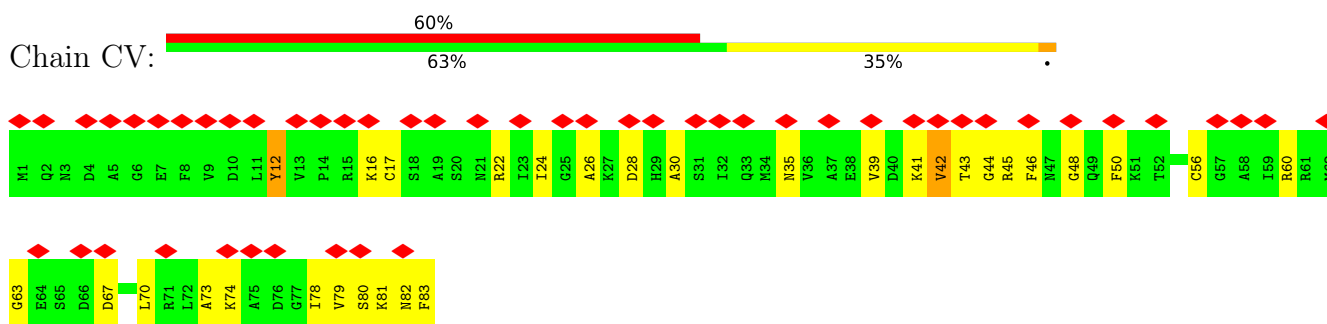
• Molecule 70: 40S RIBOSOMAL PROTEIN ES19



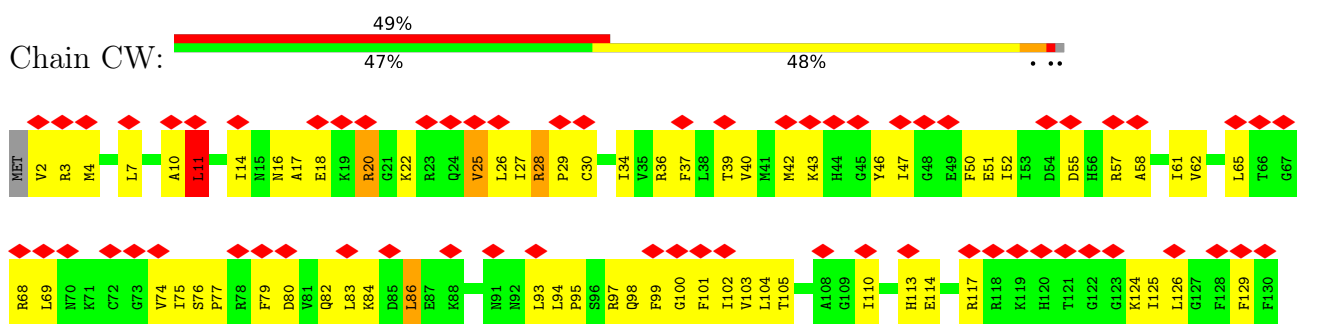
• Molecule 71: 40S RIBOSOMAL PROTEIN US10



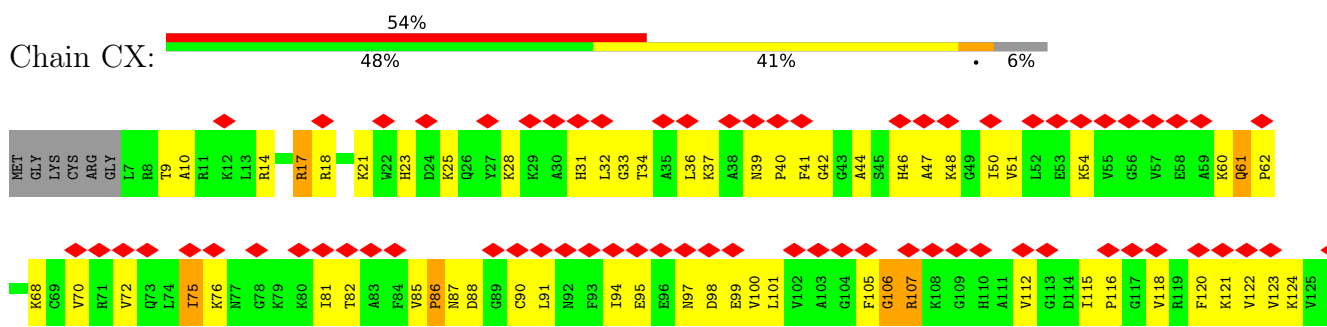
• Molecule 72: 40S RIBOSOMAL PROTEIN ES21



• Molecule 73: 40S RIBOSOMAL PROTEIN US8



• Molecule 74: 40S RIBOSOMAL PROTEIN US12

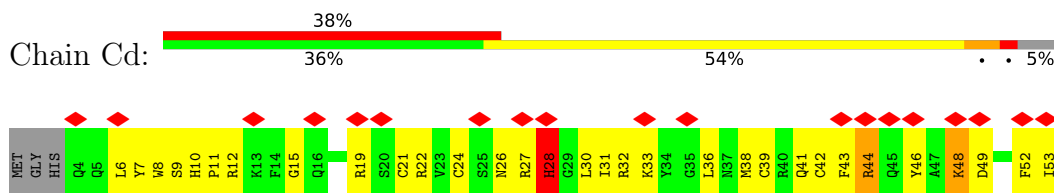


• Molecule 75: 40S RIBOSOMAL PROTEIN ES24

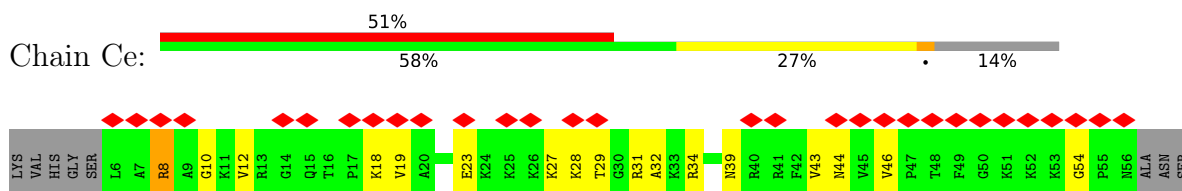




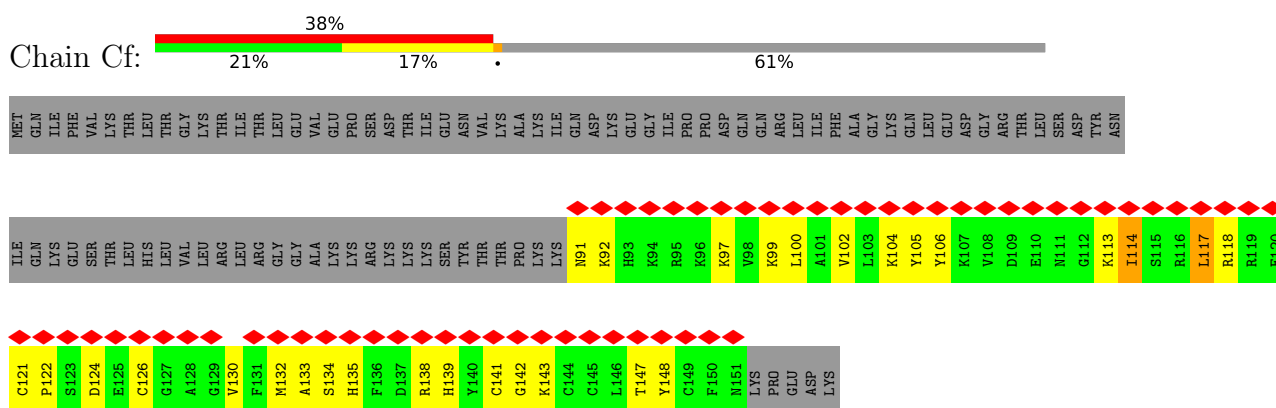
• Molecule 80: 40S RIBOSOMAL PROTEIN US14



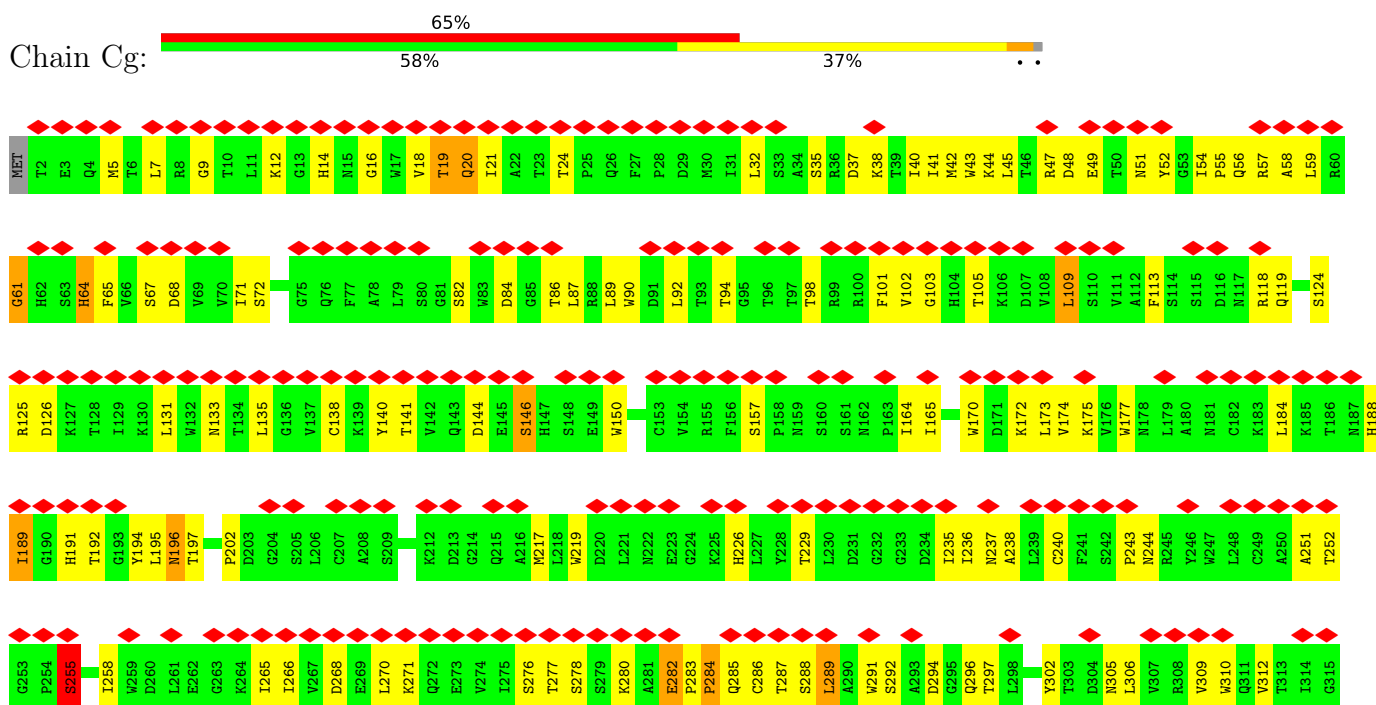
• Molecule 81: 40S RIBOSOMAL PROTEIN ES30



• Molecule 82: 40S RIBOSOMAL PROTEIN ES31



• Molecule 83: 40S RIBOSOMAL PROTEIN RACK1



THE  
ARC

## 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 ( $\text{\AA}$ )	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 i

### 5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A2	0.35	16/86671 (0.0%)	0.68	69/135194 (0.1%)
2	A3	0.30	0/3723	0.63	2/5800 (0.0%)
3	A4	0.31	0/2836	0.67	1/4421 (0.0%)
4	AA	0.68	1/1926 (0.1%)	1.09	3/2583 (0.1%)
5	AB	0.72	2/3258 (0.1%)	1.12	10/4361 (0.2%)
6	AC	0.76	1/2943 (0.0%)	1.16	19/3953 (0.5%)
7	AD	0.78	6/2407 (0.2%)	1.11	12/3221 (0.4%)
8	AE	0.81	1/1312 (0.1%)	1.17	9/1763 (0.5%)
9	AF	0.68	0/1986	1.12	10/2644 (0.4%)
10	AG	0.75	1/1914 (0.1%)	1.20	14/2578 (0.5%)
11	AH	0.64	0/1555	1.10	4/2089 (0.2%)
12	AI	0.68	0/1643	1.15	13/2194 (0.6%)
13	AJ	0.79	0/1386	1.18	9/1852 (0.5%)
14	AL	0.82	5/1647 (0.3%)	1.18	14/2205 (0.6%)
15	AM	0.79	1/1162 (0.1%)	1.12	1/1556 (0.1%)
16	AN	0.68	0/1754	1.08	10/2348 (0.4%)
17	AO	0.72	2/1639 (0.1%)	1.15	11/2193 (0.5%)
18	AP	0.67	1/1260 (0.1%)	1.09	2/1691 (0.1%)
19	AQ	0.70	0/1518	1.15	8/2026 (0.4%)
20	AR	0.64	0/1541	1.07	6/2035 (0.3%)
21	AS	0.71	0/1479	1.19	16/1985 (0.8%)
22	AT	0.74	0/1326	1.21	14/1770 (0.8%)
23	AU	0.74	1/841 (0.1%)	1.16	8/1128 (0.7%)
24	AV	0.69	1/978 (0.1%)	1.03	0/1312
25	AW	0.64	1/542 (0.2%)	0.98	2/722 (0.3%)
26	AX	0.66	0/993	1.12	3/1334 (0.2%)
27	AY	0.74	1/1082 (0.1%)	1.17	5/1441 (0.3%)
28	AZ	0.74	0/1138	1.25	5/1517 (0.3%)
29	Aa	0.72	0/1191	1.11	4/1591 (0.3%)
30	Ab	0.71	1/570 (0.2%)	1.10	1/752 (0.1%)
31	Ac	0.72	1/813 (0.1%)	1.05	3/1091 (0.3%)
32	Ad	0.70	0/920	1.06	2/1238 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Ae	0.71	1/1071 (0.1%)	1.12	5/1428 (0.4%)
34	Af	0.75	1/885 (0.1%)	1.22	10/1185 (0.8%)
35	Ag	0.74	1/917 (0.1%)	1.15	4/1222 (0.3%)
36	Ah	0.63	0/1023	1.03	1/1351 (0.1%)
37	Ai	0.70	1/793 (0.1%)	1.18	6/1048 (0.6%)
38	Aj	0.77	1/704 (0.1%)	1.16	4/931 (0.4%)
39	Ak	0.72	0/575	1.18	4/761 (0.5%)
40	Al	0.66	0/454	1.04	2/599 (0.3%)
41	Am	0.68	0/435	1.21	3/575 (0.5%)
42	An	0.62	0/241	0.85	0/305
43	Ao	0.70	0/885	1.14	4/1166 (0.3%)
44	Ap	0.63	0/718	0.97	1/953 (0.1%)
45	At	0.78	1/1058 (0.1%)	1.22	7/1416 (0.5%)
46	Au	0.69	0/1639	1.12	7/2222 (0.3%)
47	BA	0.50	1/1809 (0.1%)	1.11	22/2819 (0.8%)
48	BB	0.90	11/4926 (0.2%)	1.37	44/6641 (0.7%)
49	BC	0.96	4/6230 (0.1%)	1.51	109/9712 (1.1%)
50	C1	0.31	0/41550	0.66	11/64763 (0.0%)
51	CA	0.89	4/1756 (0.2%)	1.16	11/2386 (0.5%)
52	CB	0.83	0/1756	1.20	11/2350 (0.5%)
53	CC	0.69	0/1761	1.10	4/2379 (0.2%)
54	CD	0.63	0/1672	1.15	8/2250 (0.4%)
55	CE	0.72	0/2072	1.16	10/2793 (0.4%)
56	CF	0.68	0/1507	1.15	10/2026 (0.5%)
57	CG	0.77	1/1907 (0.1%)	1.23	11/2538 (0.4%)
58	CH	0.75	0/1558	1.26	12/2087 (0.6%)
59	CI	0.75	0/1724	1.12	6/2298 (0.3%)
60	CJ	0.74	0/1520	1.25	13/2030 (0.6%)
61	CK	0.77	0/815	1.10	5/1101 (0.5%)
62	CL	0.69	0/1220	1.16	8/1633 (0.5%)
63	CM	0.74	0/941	1.19	3/1264 (0.2%)
64	CN	0.69	0/1231	1.21	12/1656 (0.7%)
65	CO	0.73	0/1036	1.16	6/1391 (0.4%)
66	CP	0.66	0/1000	1.07	2/1335 (0.1%)
67	CQ	0.69	0/1125	1.10	3/1506 (0.2%)
68	CR	0.69	0/904	1.12	6/1208 (0.5%)
69	CS	0.69	0/1190	1.13	5/1594 (0.3%)
70	CT	0.68	0/1131	1.10	3/1515 (0.2%)
71	CU	0.76	0/813	1.17	3/1092 (0.3%)
72	CV	0.70	0/643	1.16	2/860 (0.2%)
73	CW	0.69	0/1050	1.12	6/1406 (0.4%)
74	CX	0.75	0/1063	1.11	1/1421 (0.1%)
75	CY	0.70	0/1019	1.12	5/1354 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	CZ	0.68	0/611	1.14	3/820 (0.4%)
77	Ca	0.78	0/778	1.19	7/1041 (0.7%)
78	Cb	0.70	0/637	1.09	2/854 (0.2%)
79	Cc	0.71	0/492	1.15	5/657 (0.8%)
80	Cd	0.74	0/454	1.10	1/603 (0.2%)
81	Ce	0.70	0/417	1.09	0/548
82	Cf	0.76	0/507	1.34	4/673 (0.6%)
83	Cg	0.69	0/2497	1.06	7/3399 (0.2%)
All	All	0.55	70/240674 (0.0%)	0.91	729/353753 (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 70 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A2	1701	C	O5'-C5'	16.80	1.67	1.42
1	A2	1701	C	C5'-C4'	14.79	1.73	1.51
1	A2	1673	C	C3'-O3'	13.66	1.63	1.43
1	A2	1673	C	O3'-P	11.27	1.78	1.61
1	A2	1673	C	O5'-C5'	10.36	1.58	1.42

The worst 5 of 729 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A2	1701	C	C2'-C3'-O3'	-18.44	86.04	113.70
47	BA	6	G	C4'-C3'-O3'	16.88	134.72	109.40
1	A2	3920	G	C4'-C3'-O3'	-16.37	88.44	113.00
1	A2	1701	C	C4'-C3'-O3'	16.15	137.22	113.00
49	BC	63	U	C4'-C3'-O3'	15.96	133.34	109.40

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A2	77488	0	39156	7714	0
2	A3	3334	0	1693	299	0
3	A4	2538	0	1286	247	0
4	AA	1888	0	1983	134	0
5	AB	3190	0	3327	187	0
6	AC	2889	0	3064	271	0
7	AD	2362	0	2385	142	0
8	AE	1287	0	1398	161	0
9	AF	1950	0	2093	140	0
10	AG	1881	0	2018	123	0
11	AH	1536	0	1611	119	0
12	AI	1605	0	1652	71	0
13	AJ	1363	0	1398	107	0
14	AL	1617	0	1725	122	0
15	AM	1139	0	1204	119	0
16	AN	1709	0	1761	90	0
17	AO	1607	0	1745	126	0
18	AP	1234	0	1263	71	0
19	AQ	1494	0	1612	105	0
20	AR	1526	0	1682	88	0
21	AS	1439	0	1472	86	0
22	AT	1298	0	1366	117	0
23	AU	827	0	852	23	0
24	AV	964	0	1026	45	0
25	AW	529	0	541	32	0
26	AX	976	0	1053	47	0
27	AY	1065	0	1145	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	AZ	1115	0	1194	99	0
29	Aa	1162	0	1213	83	0
30	Ab	560	0	590	43	0
31	Ac	802	0	845	64	0
32	Ad	905	0	947	27	0
33	Ae	1053	0	1144	51	0
34	Af	866	0	904	102	0
35	Ag	907	0	1002	103	0
36	Ah	1015	0	1148	46	0
37	Ai	783	0	862	57	0
38	Aj	690	0	719	54	0
39	Ak	569	0	637	32	0
40	Al	444	0	483	14	0
41	Am	429	0	466	24	0
42	An	240	0	287	46	0
43	Ao	871	0	940	128	0
44	Ap	708	0	760	40	0
45	At	1043	0	1120	122	0
46	Au	1622	0	1563	151	0
47	BA	1619	0	816	416	0
48	BB	4846	0	4954	1445	0
49	BC	5574	0	2803	302	0
50	C1	37159	0	18772	3999	0
51	CA	1719	0	1717	133	0
52	CB	1729	0	1803	151	0
53	CC	1724	0	1808	93	0
54	CD	1646	0	1737	115	0
55	CE	2031	0	2138	114	0
56	CF	1486	0	1543	112	0
57	CG	1884	0	2044	155	0
58	CH	1535	0	1632	132	0
59	CI	1695	0	1774	138	0
60	CJ	1495	0	1615	96	0
61	CK	791	0	811	56	0
62	CL	1199	0	1269	71	0
63	CM	931	0	961	45	0
64	CN	1207	0	1294	81	0
65	CO	1023	0	1050	67	0
66	CP	981	0	1026	56	0
67	CQ	1108	0	1172	98	0
68	CR	893	0	946	66	0
69	CS	1172	0	1229	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	CT	1112	0	1146	116	0
71	CU	803	0	866	80	0
72	CV	636	0	637	45	0
73	CW	1033	0	1080	67	0
74	CX	1046	0	1110	87	0
75	CY	1002	0	1075	65	0
76	CZ	605	0	665	68	0
77	Ca	767	0	816	108	0
78	Cb	625	0	642	57	0
79	Cc	490	0	519	44	0
80	Cd	444	0	442	51	0
81	Ce	412	0	463	35	0
82	Cf	497	0	497	35	0
83	Cg	2440	0	2396	120	0
84	BB	32	0	13	11	0
85	BB	1	0	0	0	0
All	All	223911	0	165616	18166	0

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

The worst 5 of 18166 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BB:1116:ARG:HB3	50:C1:488:U:C6	1.22	1.65
47:BA:75:C:H5	48:BB:1316:PHE:CD2	1.14	1.64
47:BA:34:G:H4'	50:C1:1248:U:C1'	1.19	1.63
42:An:10:MET:HE1	50:C1:1172:U:C5'	1.18	1.62
48:BB:1116:ARG:HB3	50:C1:488:U:C5	1.20	1.60

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	10	44
5	AB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	2	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	36
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	36
10	AG	233/266 (88%)	216 (93%)	8 (3%)	9 (4%)	2	19
11	AH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	7	38
12	AI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	7	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	40
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
18	AP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	31
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%)	7	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%)	4	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	31
32	Ad	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	51
33	Ae	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	4	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	31
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	40
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	51
52	CB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	9
53	CC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	5	28
54	CD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	4	27
55	CE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6	31
56	CF	186/204 (91%)	163 (88%)	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	36
61	CK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	10
62	CL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	2	17
63	CM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	1	15
64	CN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	21
65	CO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	5	29
66	CP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	17
67	CQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	8	40

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AA	189/199 (95%)	182 (96%)	7 (4%)	30	51
5	AB	344/349 (99%)	322 (94%)	22 (6%)	16	37
6	AC	302/348 (87%)	283 (94%)	19 (6%)	16	37
7	AD	244/250 (98%)	237 (97%)	7 (3%)	37	58
8	AE	143/143 (100%)	133 (93%)	10 (7%)	14	35
9	AF	203/215 (94%)	195 (96%)	8 (4%)	28	49
10	AG	199/223 (89%)	190 (96%)	9 (4%)	24	46
11	AH	171/171 (100%)	165 (96%)	6 (4%)	32	53
12	AI	170/181 (94%)	161 (95%)	9 (5%)	20	41
13	AJ	143/149 (96%)	137 (96%)	6 (4%)	26	48
14	AL	167/177 (94%)	156 (93%)	11 (7%)	15	37
15	AM	118/161 (73%)	113 (96%)	5 (4%)	26	48
16	AN	172/172 (100%)	167 (97%)	5 (3%)	37	58
17	AO	168/174 (97%)	165 (98%)	3 (2%)	51	68
18	AP	133/163 (82%)	126 (95%)	7 (5%)	20	41
19	AQ	162/165 (98%)	157 (97%)	5 (3%)	35	56
20	AR	161/175 (92%)	150 (93%)	11 (7%)	14	36
21	AS	155/157 (99%)	149 (96%)	6 (4%)	28	49
22	AT	139/140 (99%)	135 (97%)	4 (3%)	37	58
23	AU	91/115 (79%)	91 (100%)	0	100	100
24	AV	100/107 (94%)	100 (100%)	0	100	100
25	AW	55/126 (44%)	52 (94%)	3 (6%)	19	41
26	AX	107/133 (80%)	105 (98%)	2 (2%)	50	67
27	AY	119/135 (88%)	114 (96%)	5 (4%)	26	48
28	AZ	118/118 (100%)	114 (97%)	4 (3%)	32	54
29	Aa	120/121 (99%)	115 (96%)	5 (4%)	26	48
30	Ab	58/126 (46%)	57 (98%)	1 (2%)	53	69
31	Ac	88/97 (91%)	87 (99%)	1 (1%)	65	76
32	Ad	100/110 (91%)	97 (97%)	3 (3%)	36	57
33	Ae	115/121 (95%)	111 (96%)	4 (4%)	32	53
34	Af	87/89 (98%)	77 (88%)	10 (12%)	5	18
35	Ag	98/100 (98%)	89 (91%)	9 (9%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Ah	109/110 (99%)	105 (96%)	4 (4%)	30	51
37	Ai	82/89 (92%)	76 (93%)	6 (7%)	13	34
38	Aj	71/80 (89%)	69 (97%)	2 (3%)	38	60
39	Ak	64/65 (98%)	64 (100%)	0	100	100
40	Al	47/48 (98%)	46 (98%)	1 (2%)	47	65
41	Am	48/116 (41%)	45 (94%)	3 (6%)	16	37
42	An	24/24 (100%)	24 (100%)	0	100	100
43	Ao	94/94 (100%)	90 (96%)	4 (4%)	26	47
44	Ap	74/75 (99%)	72 (97%)	2 (3%)	39	61
45	At	113/121 (93%)	108 (96%)	5 (4%)	25	47
46	Au	177/177 (100%)	161 (91%)	16 (9%)	9	27
48	BB	540/552 (98%)	517 (96%)	23 (4%)	26	47
51	CA	181/243 (74%)	177 (98%)	4 (2%)	45	64
52	CB	194/231 (84%)	182 (94%)	12 (6%)	16	38
53	CC	188/225 (84%)	179 (95%)	9 (5%)	23	44
54	CD	175/202 (87%)	164 (94%)	11 (6%)	16	37
55	CE	220/225 (98%)	207 (94%)	13 (6%)	18	39
56	CF	158/170 (93%)	152 (96%)	6 (4%)	29	50
57	CG	202/218 (93%)	196 (97%)	6 (3%)	36	57
58	CH	171/174 (98%)	170 (99%)	1 (1%)	78	83
59	CI	179/180 (99%)	167 (93%)	12 (7%)	15	36
60	CJ	160/168 (95%)	152 (95%)	8 (5%)	22	43
61	CK	85/136 (62%)	81 (95%)	4 (5%)	23	45
62	CL	133/142 (94%)	130 (98%)	3 (2%)	44	64
63	CM	102/108 (94%)	96 (94%)	6 (6%)	18	39
64	CN	130/131 (99%)	128 (98%)	2 (2%)	57	72
65	CO	107/119 (90%)	99 (92%)	8 (8%)	12	33
66	CP	107/130 (82%)	103 (96%)	4 (4%)	30	51
67	CQ	115/121 (95%)	111 (96%)	4 (4%)	32	53
68	CR	99/122 (81%)	92 (93%)	7 (7%)	13	35
69	CS	123/132 (93%)	115 (94%)	8 (6%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	CT	113/115 (98%)	106 (94%)	7 (6%)	16	38
71	CU	93/107 (87%)	87 (94%)	6 (6%)	15	37
72	CV	67/67 (100%)	67 (100%)	0	100	100
73	CW	112/113 (99%)	108 (96%)	4 (4%)	31	52
74	CX	108/115 (94%)	104 (96%)	4 (4%)	30	51
75	CY	107/115 (93%)	100 (94%)	7 (6%)	15	37
76	CZ	67/103 (65%)	62 (92%)	5 (8%)	12	33
77	Ca	83/98 (85%)	76 (92%)	7 (8%)	10	30
78	Cb	72/76 (95%)	68 (94%)	4 (6%)	19	40
79	Cc	55/62 (89%)	52 (94%)	3 (6%)	19	41
80	Cd	47/49 (96%)	44 (94%)	3 (6%)	16	37
81	Ce	42/48 (88%)	39 (93%)	3 (7%)	13	35
82	Cf	54/140 (39%)	51 (94%)	3 (6%)	19	40
83	Cg	272/275 (99%)	260 (96%)	12 (4%)	25	47
All	All	10303/11421 (90%)	9834 (95%)	469 (5%)	25	45

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

Mol	Chain	Res	Type
45	At	61	VAL
78	Cb	59	CYS
52	CB	177	GLN
77	Ca	64	LEU
69	CS	99	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 271 such sidechains are listed below:

Mol	Chain	Res	Type
69	CS	87	GLN
71	CU	100	GLN
80	Cd	16	GLN
23	AU	116	GLN
22	AT	144	ASN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	3604/5025 (71%)	2050 (56%)	324 (8%)
2	A3	156/194 (80%)	82 (52%)	6 (3%)
3	A4	118/121 (97%)	69 (58%)	9 (7%)
47	BA	75/76 (98%)	14 (18%)	1 (1%)
49	BC	259/504 (51%)	142 (54%)	40 (15%)
50	C1	1738/1869 (92%)	1042 (59%)	152 (8%)
All	All	5950/7789 (76%)	3399 (57%)	532 (8%)

5 of 3399 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	34,34,34	1.78	6 (17%)	47,54,54	1.30	5 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	GNP	BB	2435	85	-	2/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	BB	2435	GNP	PA-O3A	-6.53	1.52	1.59
84	BB	2435	GNP	C2'-C1'	-3.03	1.44	1.53
84	BB	2435	GNP	PB-O3A	-2.66	1.55	1.59
84	BB	2435	GNP	C4-N3	2.58	1.40	1.34
84	BB	2435	GNP	PB-N3B	-2.47	1.56	1.63

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	BB	2435	GNP	O1B-PB-N3B	3.38	116.75	111.77
84	BB	2435	GNP	O2A-PA-O3A	3.07	115.58	107.27
84	BB	2435	GNP	O2G-PG-O1G	2.43	119.53	113.45
84	BB	2435	GNP	C1'-N9-C8	2.23	133.07	126.73
84	BB	2435	GNP	O3A-PB-N3B	2.21	112.73	106.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

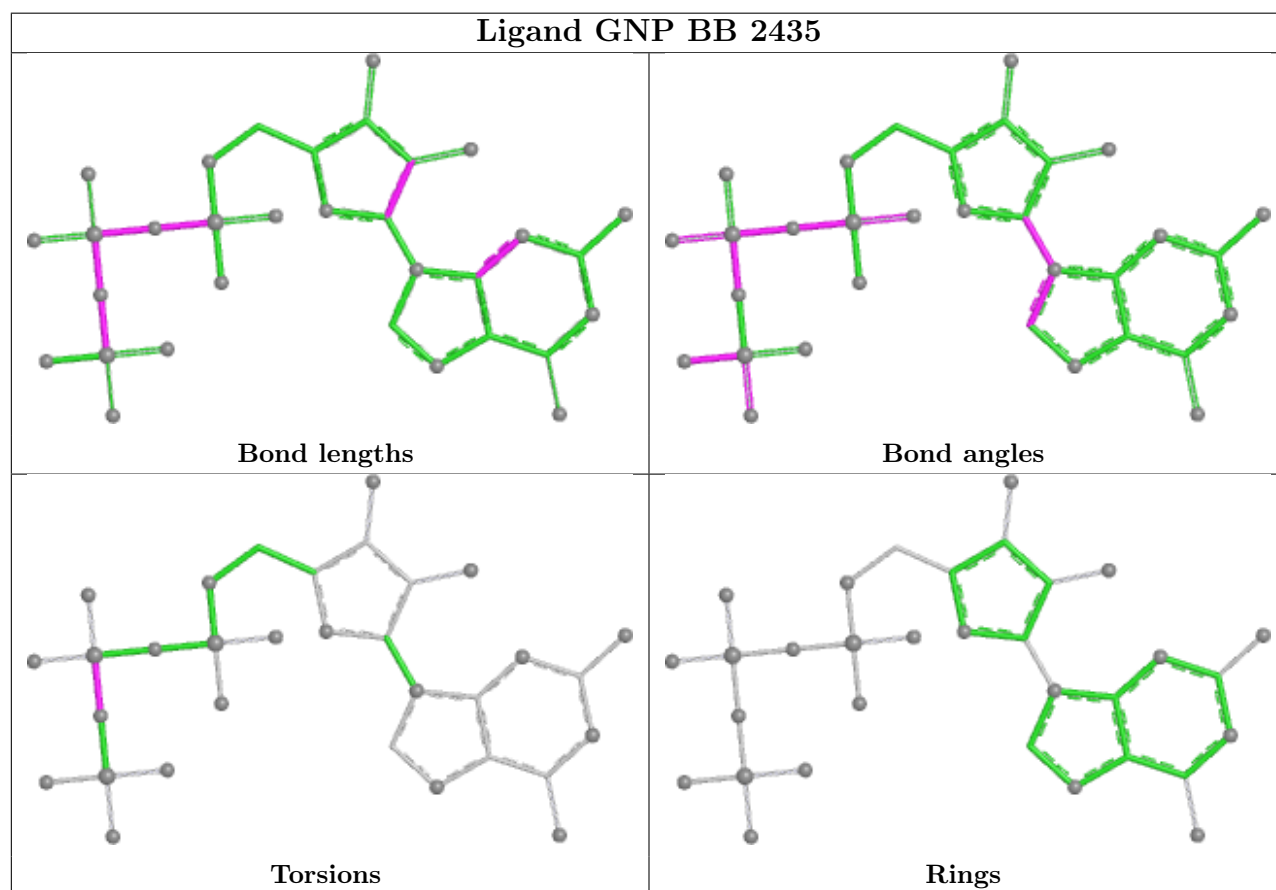
Mol	Chain	Res	Type	Atoms
84	BB	2435	GNP	PG-N3B-PB-O1B
84	BB	2435	GNP	PG-N3B-PB-O3A

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	BB	2435	GNP	11	0

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



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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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

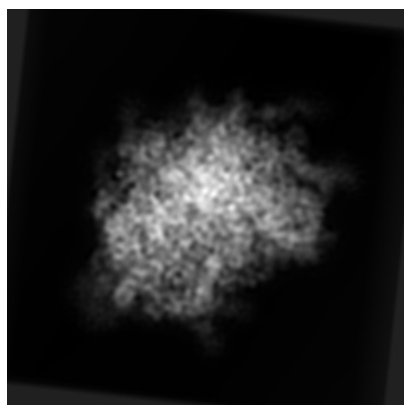
## 6 Map visualisation [i](#)

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.

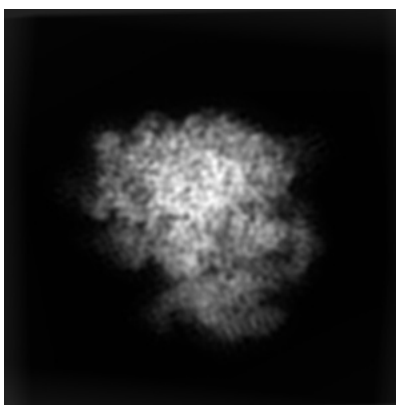
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

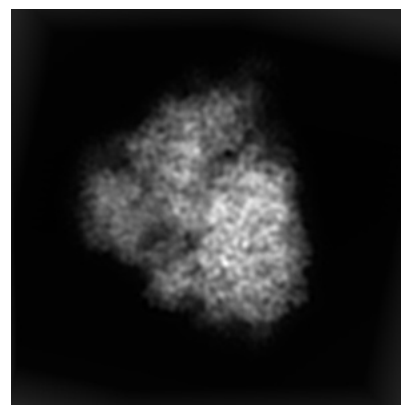
#### 6.1.1 Primary map



X



Y

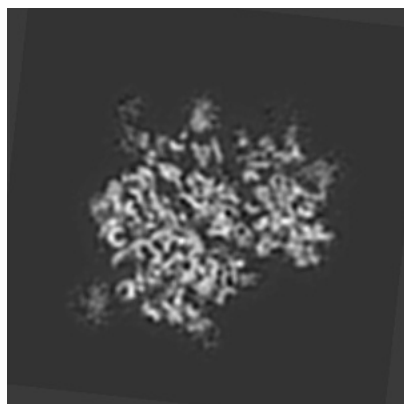


Z

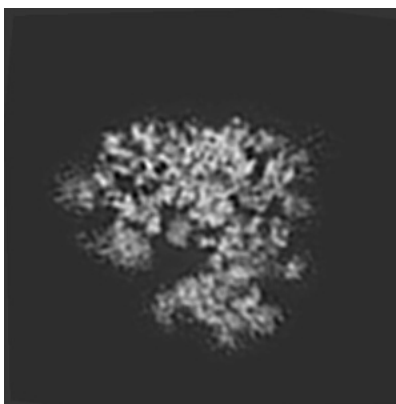
The images above show the map projected in three orthogonal directions.

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

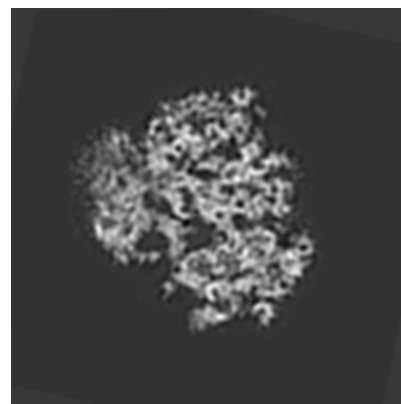
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

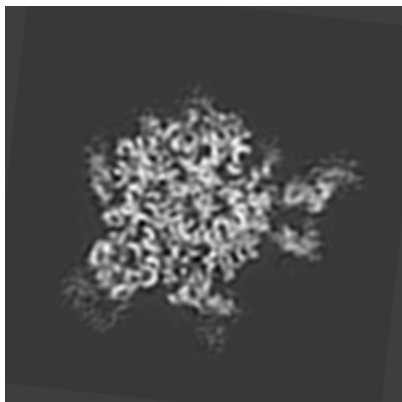


Z Index: 180

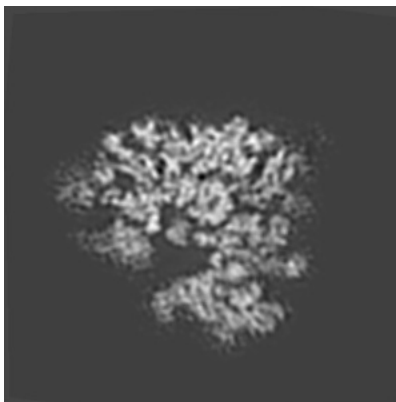
The images above show central slices of the map in three orthogonal directions.

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

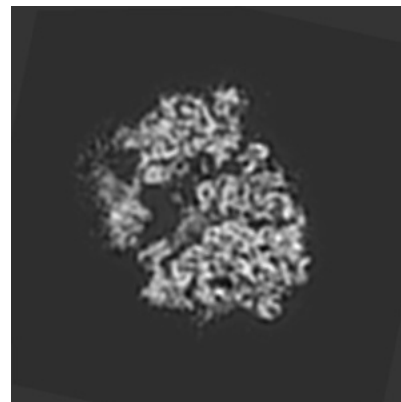
### 6.3.1 Primary map



X Index: 214



Y Index: 182

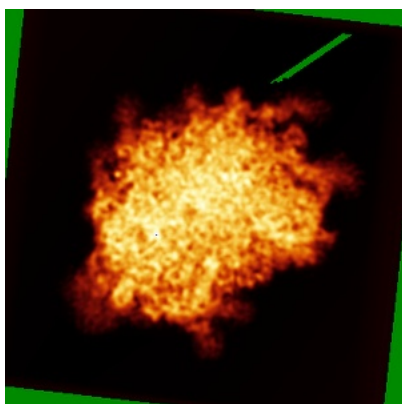


Z Index: 169

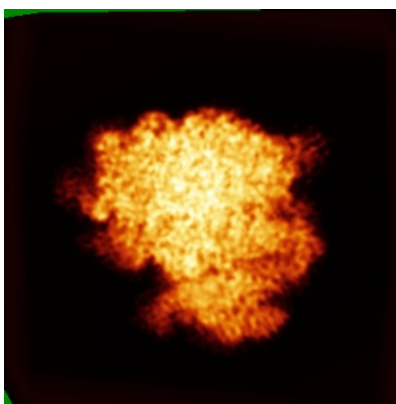
The images above show the largest variance slices of the map in three orthogonal directions.

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

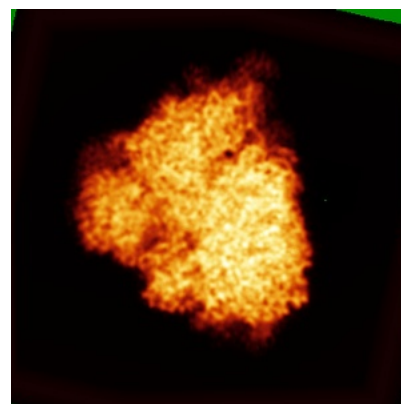
### 6.4.1 Primary map



X



Y

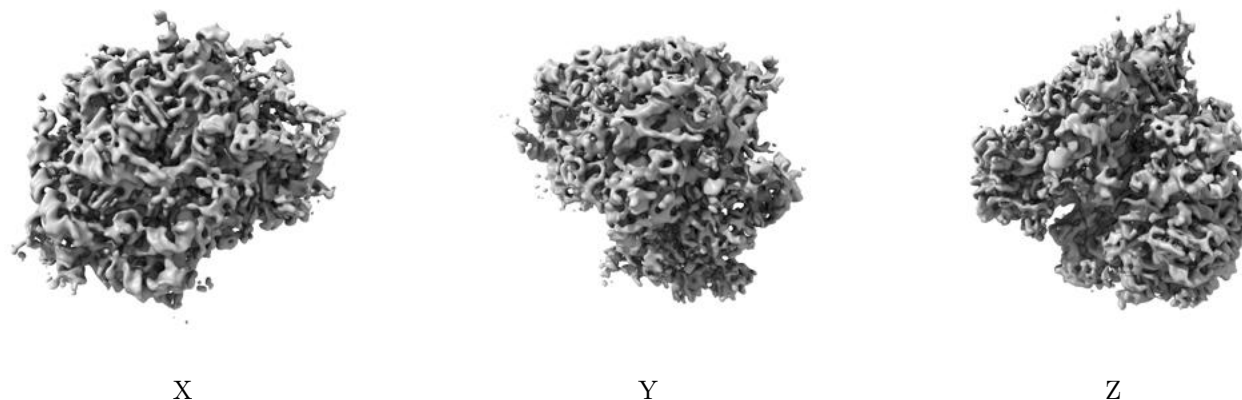


Z

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.

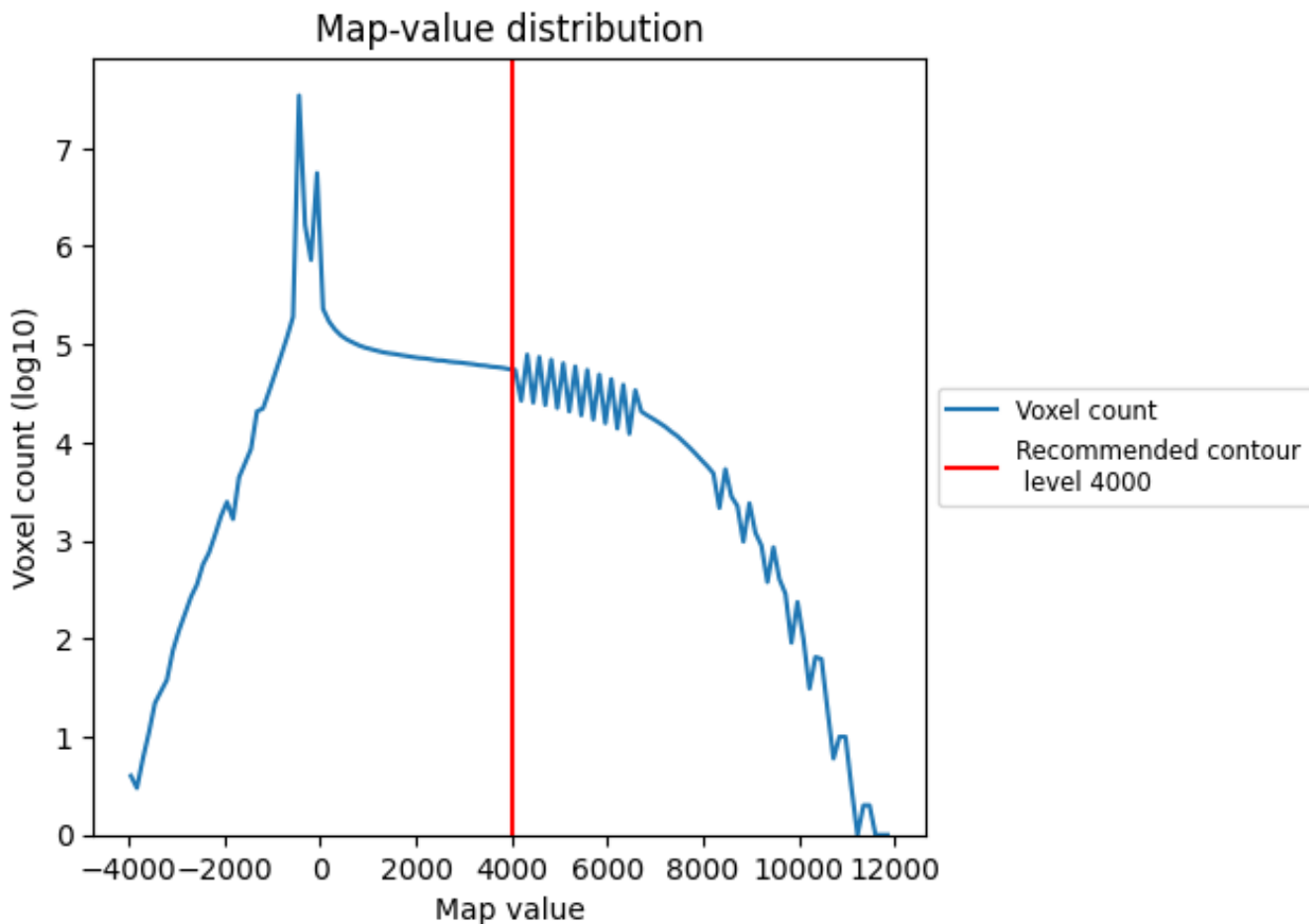
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

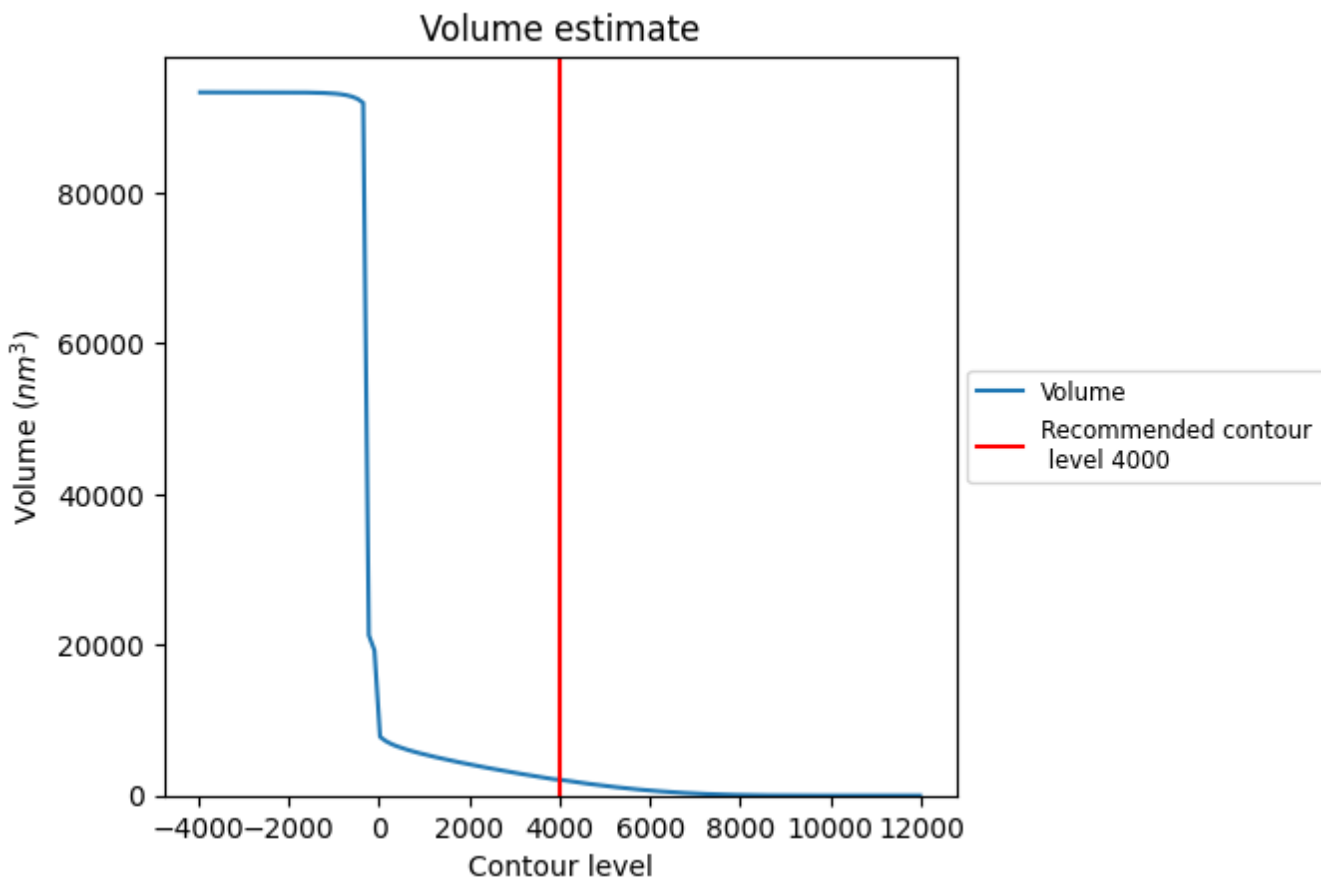
This section contains the results of statistical analysis of the map.

### 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.

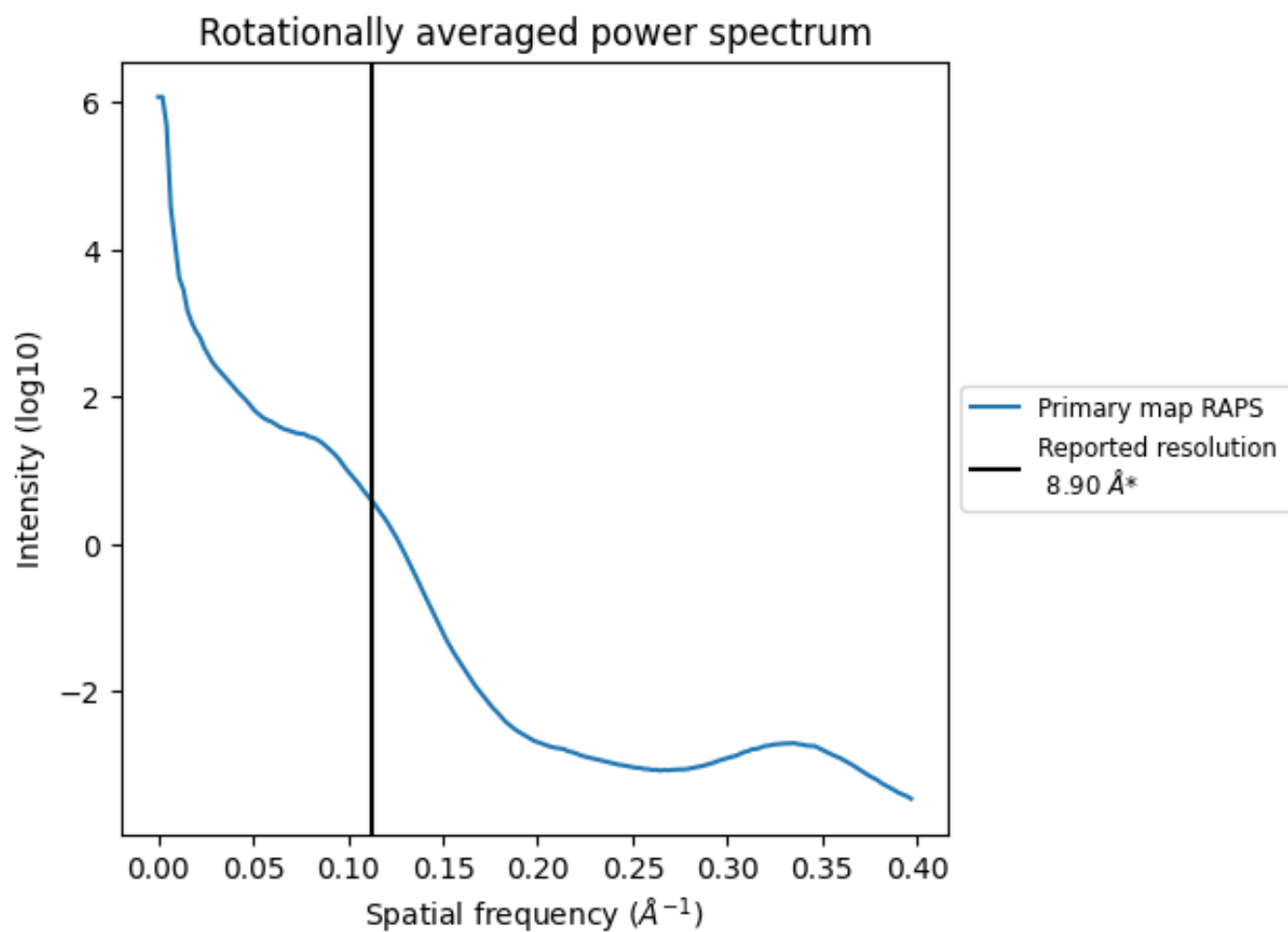
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2109  $\text{nm}^3$ ; 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 [i](#)



\*Reported resolution corresponds to spatial frequency of 0.112 Å<sup>-1</sup>

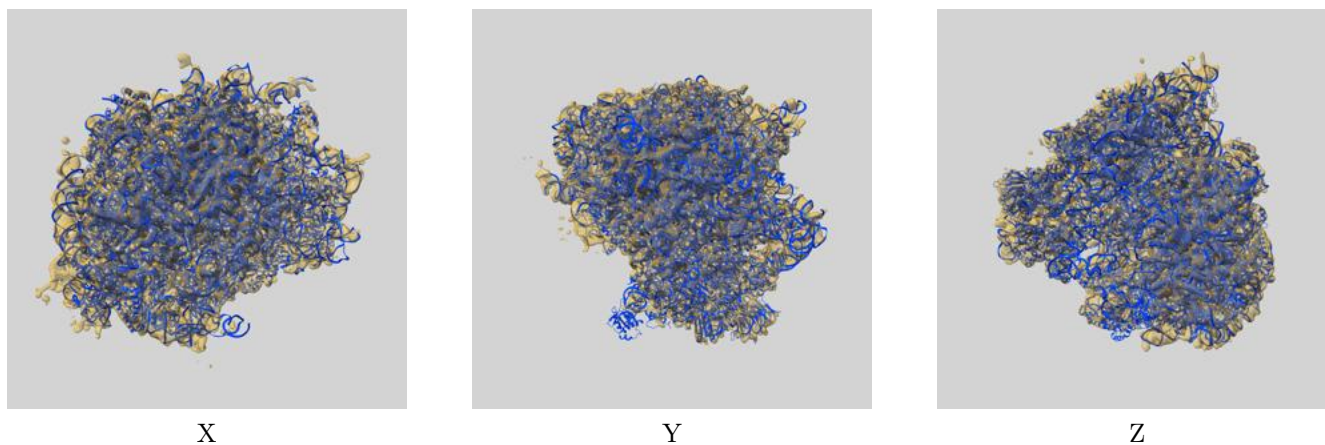
## 8 Fourier-Shell correlation

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

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

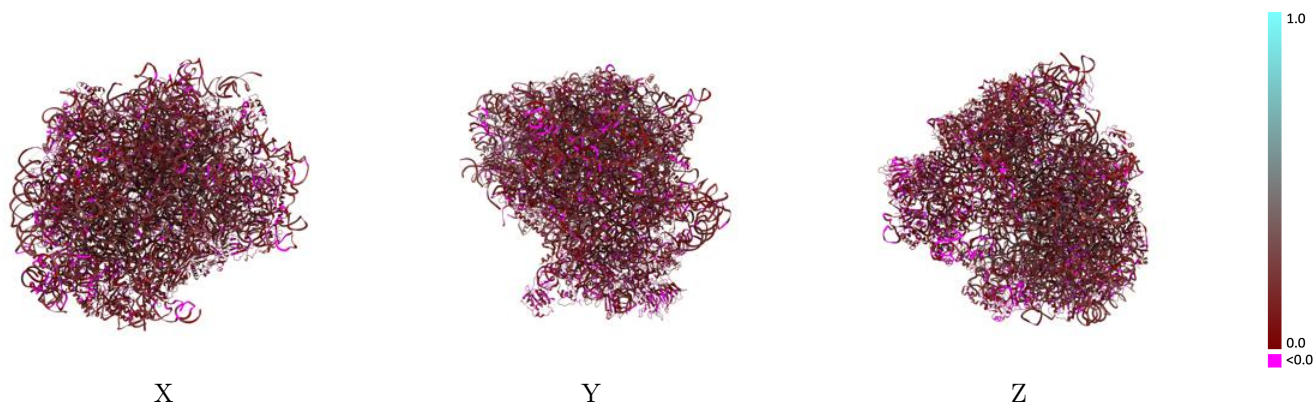
This section contains information regarding the fit between EMDB map EMD-2682 and PDB model 4UJD. Per-residue inclusion information can be found in section 3 on page 20.

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



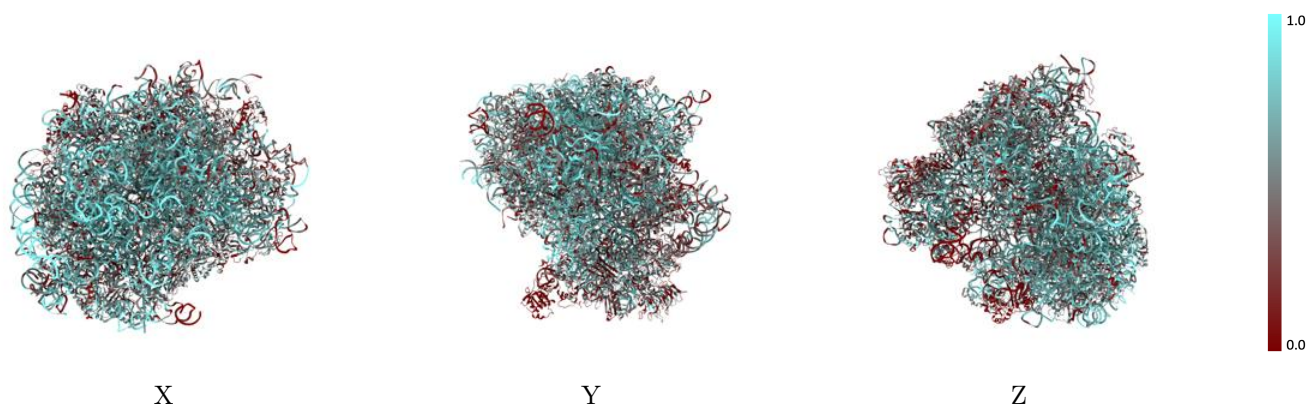
The images above show the 3D surface view of the map at the recommended contour level 4000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



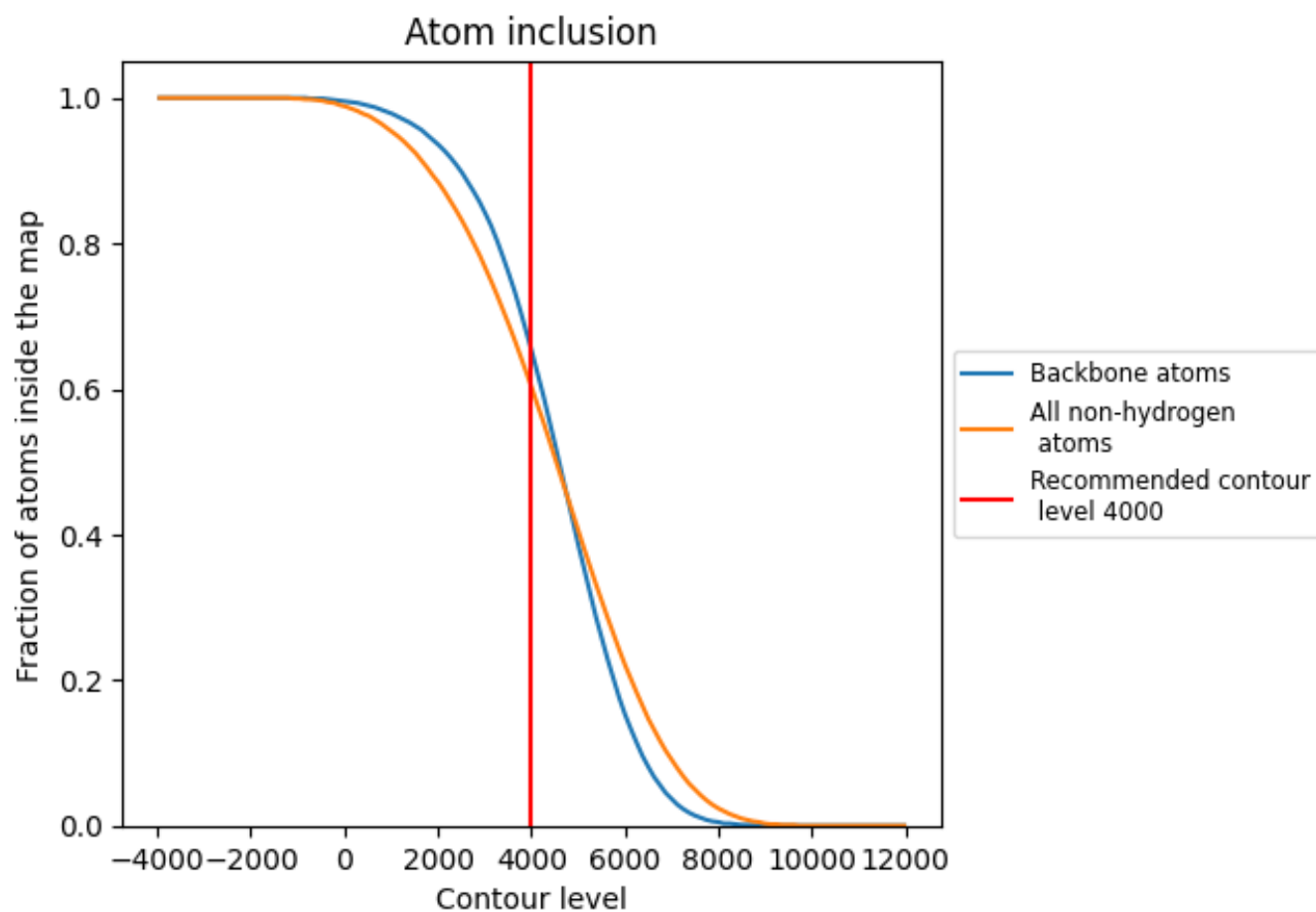
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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