



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 06:38 PM UTC

PDB ID : 4UJE / pdb_00004uje
EMDB ID : EMD-2620
Title : Regulation of the mammalian elongation cycle by 40S subunit rolling: a eukaryotic-specific ribosome rearrangement
Authors : Budkevich, T.V.; Giesebrecht, J.; Behrmann, E.; Loerke, J.; Ramrath, D.J.F.; Mielke, T.; Ismer, J.; Hildebrand, P.; Tung, C.-S.; Nierhaus, K.H.; Sanbonmatsu, K.Y.; Spahn, C.M.T.
Deposited on : 2014-04-05
Resolution : 6.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
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

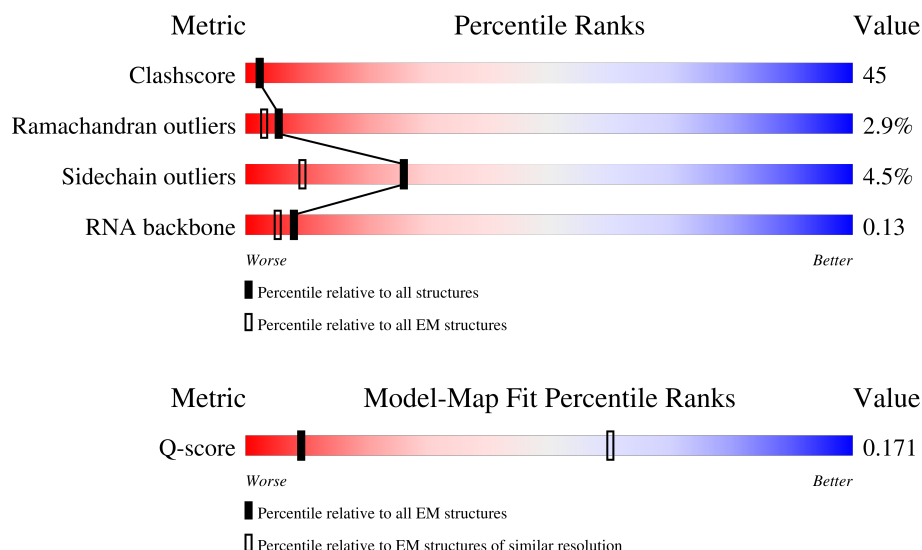
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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	479 (6.40 - 7.40)

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 ≥ 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	AV	76	
2	AW	76	
3	AX	28	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	B1	1869	
5	BA	295	
6	BB	264	
7	BC	293	
8	BD	243	
9	BE	263	
10	BF	204	
11	BG	249	
12	BH	194	
13	BI	208	
14	BJ	194	
15	BK	165	
16	BL	158	
17	BM	132	
18	BN	151	
19	BO	151	
20	BP	145	
21	BQ	146	
22	BR	135	
23	BS	152	
24	BT	145	
25	BU	119	
26	BV	83	
27	BW	130	
28	BX	143	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	BY	133	
30	BZ	125	
31	Ba	115	
32	Bb	84	
33	Bc	69	
34	Bd	56	
35	Be	59	
36	Bf	156	
37	Bg	317	
38	CA	257	
39	CB	403	
40	CC	427	
41	CD	297	
42	CE	288	
43	CF	248	
44	CG	266	
45	CH	192	
46	CI	214	
47	CJ	178	
48	CL	211	
49	CM	215	
50	CN	204	
51	CO	203	
52	CP	184	
53	CQ	188	

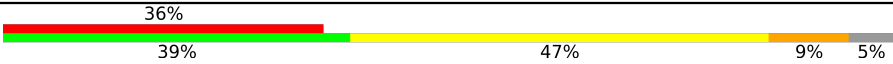
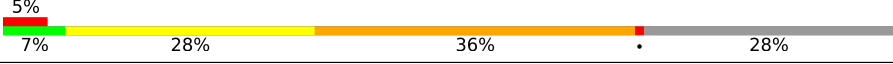
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	CR	196	
55	CS	176	
56	CT	160	
57	CU	128	
58	CV	140	
59	CW	157	
60	CX	156	
61	CY	145	
62	CZ	136	
63	Ca	148	
64	Cb	159	
65	Cc	115	
66	Cd	125	
67	Ce	135	
68	Cf	110	
69	Cg	117	
70	Ch	123	
71	Ci	105	
72	Cj	97	
73	Ck	70	
74	Cl	51	
75	Cm	128	
76	Cn	25	
77	Co	106	
78	Cp	92	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	Ct	137	
80	Cu	210	
81	A2	5025	
82	A3	194	
83	A4	121	

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
2	MIA	AW	37	-	-	X	-

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 215620 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called TRNA-LYS.

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

- Molecule 2 is a RNA chain called TRNA-PHE.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AW	76	Total	C	N	O	P	S	0	0
			1626	729	290	531	75	1		

- Molecule 3 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AX	28	Total	C	N	O	P	0	0
			560	252	56	224	28		

- Molecule 4 is a RNA chain called 18S Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	1742	Total	C	N	O	P	0	0
			37159	16589	6665	12164	1741		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN SA.

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

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S3A.

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

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S2.

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

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN S3.

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

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1.

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

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S5.

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

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S6.

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

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S7.

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

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S8.

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

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S9.

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

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S10.

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

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S11.

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

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S12.

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

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S13.

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

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S14.

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

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S15.

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

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S16.

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

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S17.

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

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S18.

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

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S19.

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

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S20.

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

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S21.

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

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S15A.

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

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S23.

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

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S24.

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

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S25.

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

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S26.

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

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S27.

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

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S28.

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

- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN S29.

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

- Molecule 35 is a protein called 40S RIBOSOMAL PROTEIN S30.

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

- Molecule 36 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

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

- Molecule 37 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

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

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L8.

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

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L3.

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

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L4.

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

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CD	290	Total	C	N	O	S	0	0
			2361	1489	431	427	14		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	CE	158	Total	C	N	O		
			1286	834	238	214	0	0

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CF	234	Total	C	N	O	S		
			1949	1252	376	312	9	0	0

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L7A.

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

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CH	192	Total	C	N	O	S		
			1535	965	286	278	6	0	0

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CI	196	Total	C	N	O	S		
			1604	1022	308	262	12	0	0

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CJ	170	Total	C	N	O	S		
			1362	861	254	241	6	0	0

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L13.

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

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L14.

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

- Molecule 50 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CN	204	Total	C	N	O	S	0	0
			1708	1077	360	266	5		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L13A.

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

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L17.

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

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CQ	184	Total	C	N	O	S	0	0
			1493	933	311	244	5		

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L19.

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

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CS	173	Total	C	N	O	S	0	0
			1438	916	280	232	10		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CT	159	Total	C	N	O	S	0	0
			1297	823	252	216	6		

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L22.

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

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CV	128	Total	C	N	O	S	0	0
			963	610	181	167	5		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L24.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CX	119	Total	C	N	O	S	0	0
			975	624	183	167	1		

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L26.

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

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CZ	136	Total	C	N	O	S	0	0
			1114	719	209	182	4		

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ca	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L29.

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

- Molecule 65 is a protein called 60S RIBOSOMAL PROTEIN L30.

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

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	109	Total	C	N	O	S	0	0
			904	570	174	158	2		

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L32.

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

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	107	Total	C	N	O	S	0	0
			865	550	172	140	3		

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L34.

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

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ch	122	Total	C	N	O	S	0	0
			1014	641	205	167	1		

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L36.

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

- Molecule 72 is a protein called 60S RIBOSOMAL PROTEIN L37.

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

- Molecule 73 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Ck	69	Total	C	N	O	S	0	0
			568	366	103	98	1		

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Cl	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 75 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 76 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 77 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Co	106	Total	C	N	O	S	0	0
			870	547	176	140	7		

- Molecule 78 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Cp	91	Total	C	N	O	S	0	0
			707	445	136	119	7		

- Molecule 79 is a protein called 60S RIBOSOMAL PROTEIN L28.

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

- Molecule 80 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cu	210	Total	C	N	O	S	0	0
			1621	990	278	347	6		

- Molecule 81 is a RNA chain called 28S Ribosomal RNA.

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

- Molecule 82 is a RNA chain called 5.8S Ribosomal RNA.

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

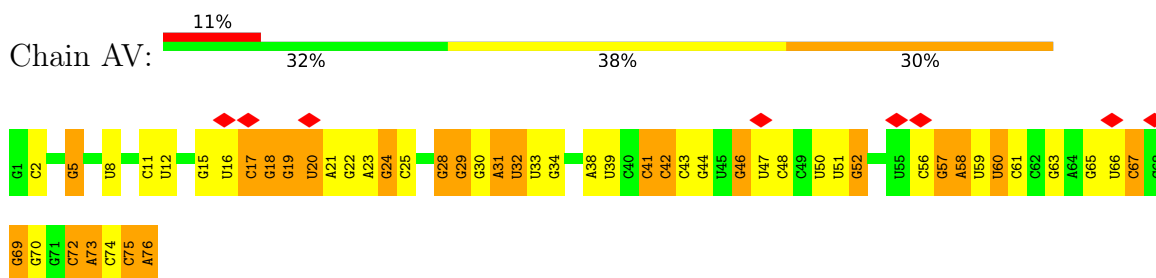
- Molecule 83 is a RNA chain called 5S Ribosomal RNA.

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

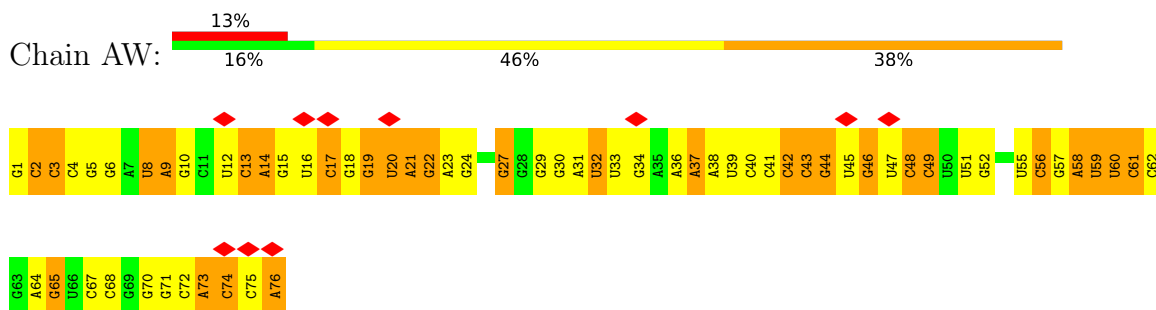
3 Residue-property plots [i](#)

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

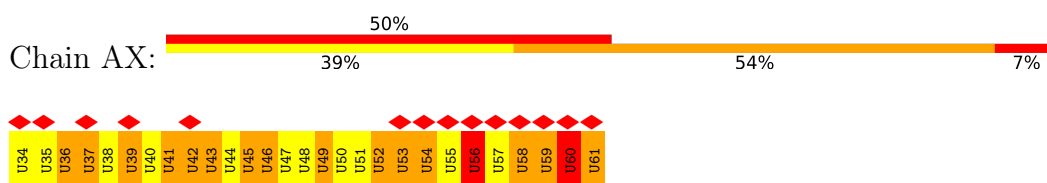
- Molecule 1: TRNA-LYS



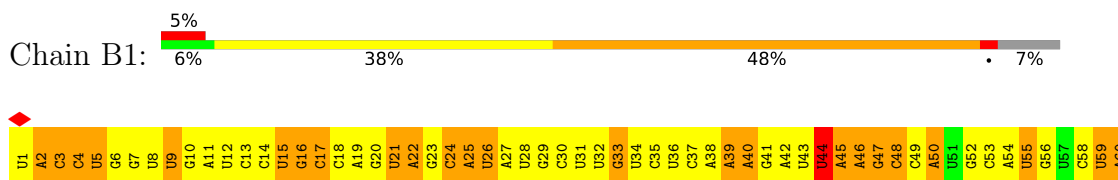
- Molecule 2: TRNA-PHE



- Molecule 3: Messenger RNA



- Molecule 4: 18S Ribosomal RNA

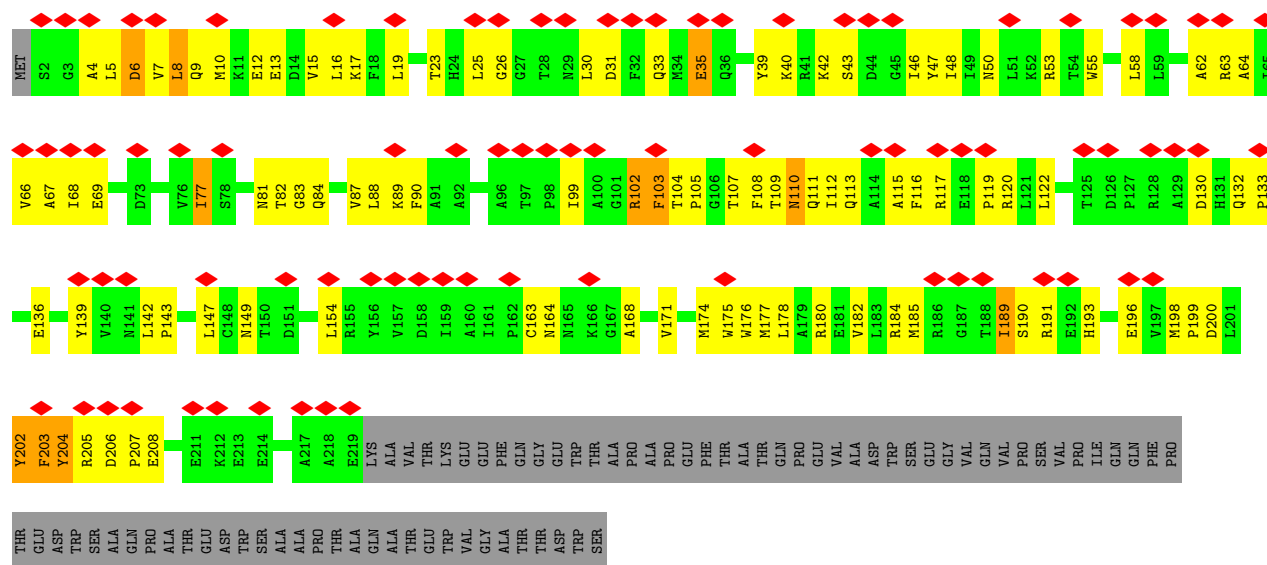


C905	U906	U844	G	A	G544	A484	C424	U361	A301	G	U	A181	U121	A61
G907	G845	G845	C	C	A445	A485	G425	C362	A302	U	C	C182	G122	G62
A908	G846	G846	C	C	G546	A486	A426	A364	C303	C	C	G183	U123	U63
G909	A847	U667	G	U	G547	U487	U427	G365	C304	A	A	G184	U124	A64
G910	U848	C508	C	C	C548	U488	U428	U366	U305	C	C	G185	C125	G65
G911	C850	U609	C	C	C549	A489	C429	U367	C306	C	C	G186	G126	G66
G912	C851	G610	C	C	C550	C490	G430	U368	C307	C	C	G187	C127	C67
A913	G852	G611	U	U	U551	C491	G431	U369	G308	C	C	C188	U128	A68
U914	C853	U612	U	C	U552	C492	G432	C369	G309	U	U	U189	C129	G70
U915	G854	C514	C	C	U553	A493	A433	G370	C310	C	C	G190	G130	G71
A916	A855	C515	C	C	A554	C494	G434	G371	C311	U	U	A191	C131	C72
U917	C855	C616	C	C	U555	U495	A435	U372	G312	C	C	C192	U132	C73
U918	G796	G617	U	U	U556	C496	G436	G373	A313	C	C	C193	U133	G74
A919	C797	G618	U	U	U557	C497	G437	G374	U314	G	G	C195	C134	G75
U920	G798	G558	U	U	G558	C498	G438	U375	C315	C	C	C196	U135	U76
G921	U799	G680	U	U	A560	A499	A439	A376	G316	C	C	U197	C136	A77
A922	U800	C621	U	U	A561	C501	C441	G377	C322	C	C	U198	C137	C78
G923	U801	G622	U	U	U562	C502	C442	U378	C321	G	G	C201	U138	A79
G924	A802	C523	U	U	G563	G503	U443	C379	G320	C	C	G200	C139	G80
G925	C803	G624	U	U	A564	C504	G444	G380	C321	G	G	C202	C140	U81
A926	U804	G625	U	U	G565	G505	A445	C381	C322	C	C	G203	C141	A84
U927	U805	G626	U	U	U566	G506	G446	C382	C323	C	C	G204	C142	A85
G928	C867	U627	U	U	C567	G507	A447	U384	C324	G	G	G205	U143	C86
G929	U806	A628	U	U	C568	A508	A448	G385	C325	C	C	G206	U144	U87
C930	A807	A629	U	U	A569	G509	A449	C386	G326	G	G	G207	G145	G88
C931	A808	U630	U	U	C570	G510	C450	C387	G327	G	G	G208	A146	C89
G932	A809	U631	U	U	U571	G511	G451	U388	G328	C	C	A209	C147	G90
G933	A810	C532	U	U	U572	G512	G452	C389	G329	C	C	U210	U148	A91
G934	A811	C533	U	U	U573	G513	C453	C390	G330	C	C	G211	A149	A92
G935	A812	A634	U	U	U574	U514	U454	U391	C331	G	G	C212	C331	U93
G936	G873	G635	U	U	A575	G515	A455	G394	G332	C	C	G213	C151	G94
G937	G874	C536	U	U	A576	A516	C456	G395	G333	C	C	U214	U152	G95
A938	A875	U637	U	U	U577	G517	A458	U396	G334	C	C	G215	G153	C96
C939	C876	C539	U	U	C578	G518	C459	G397	A335	C	C	C216	U154	U97
U940	C877	C540	U	U	C579	A519	A460	C398	A336	C	C	A217	G155	C98
C941	G878	A641	U	U	U580	A520	A461	C399	C337	G	G	U218	G156	U99
G942	G880	U642	U	U	U581	A521	C462	C400	A338	C	C	U219	U157	A99
U943	U883	U643	U	U	U582	A522	C463	A401	A339	C	C	U220	A158	U100
A944	C884	G644	U	U	A583	A523	A464	C402	C340	C	C	U221	A159	U101
U945	U885	C545	U	U	A584	A524	A465	G403	C341	C	C	U222	U160	A102
G946	A886	G646	U	U	C585	A525	G466	G404	C342	C	C	U223	U161	A103
C947	U887	U647	U	U	G586	C527	G467	G407	A343	C	C	A224	C162	A104
G948	U888	A648	U	U	A587	A528	A468	A408	U344	U	U	G225	U163	U105
G949	U889	U649	U	U	G588	A529	A469	C409	C345	U	U	U226	A164	C106
C950	U890	A650	U	U	G589	U530	G470	G410	C346	U	U	U227	G165	A107
G951	C829	U651	U	U	A590	A531	G471	G411	C347	G	G	U228	A166	U108
C952	G891	U652	U	U	U591	C532	C472	G412	A348	U	U	A229	C167	U109
G953	U892	A653	U	U	C592	A533	A473	G413	C349	C	C	A230	C168	U110
U954	U893	C593	U	U	C593	G534	G474	A414	C350	A	A	A231	A170	G111
A955	C894	A594	U	U	A594	G535	C475	A415	C351	U	U	A232	U171	G112
G956	G895	U595	U	U	U595	A536	A476	U416	U352	C	C	A233	C172	G113
A957	U896	U596	U	U	U596	C537	G477	U417	C353	U	U	C234	U173	G114
G958	U897	G597	U	U	G597	U538	C478	G418	U354	C	C	U235	A174	U115
U959	U898	U598	U	U	U598	C539	G479	A419	G355	U	U	A236	C175	U116
G960	U899	A599	U	U	A599	U540	G480	G420	C356	U	U	A237	A176	C117
G961	C900	G600	U	U	G600	U541	C481	G421	C357	U	U	A238	U177	U118
A962	G901	U661	U	U	G601	U542	G482	U422	C358	U	U	C239	G178	U119
G963	G902	G602	U	U	G602	U543	C483	U423	A360	C	C	G240	C179	U120
A964	A903	C563	C	C	C603								G180	

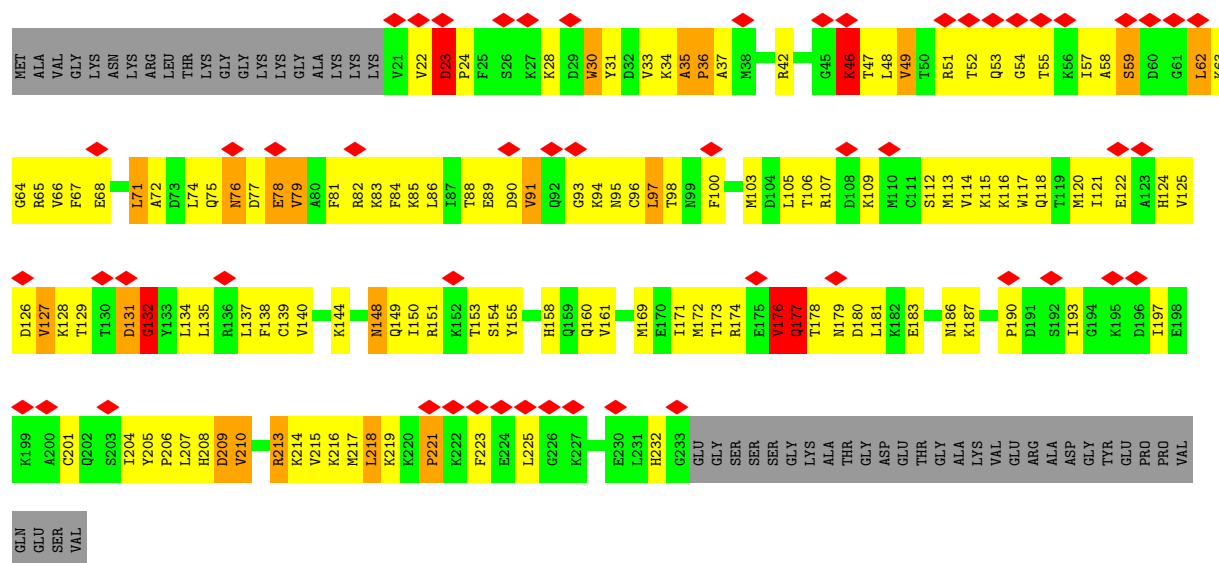
G1759	A1695	C1635	G1575	C1513	A1452	U1392	C1331	G1269	A1209	A1149	G1089	A1027	U965
G1760	C1696	G1636	G1576	G1514	C1453	G1393	A1332	G1270	G1210	A1150	C1090	A1028	U966
U1761	A1697	G1637	U1577	G1515	A1454	G1394	U1333	C1271	G1211	A1151	C1091	A1029	C967
G1762	C1698	G1638	U1578	G1516	A1455	G1395	U1334	C1272	G1212	U1152	G1092	A1030	U968
A1640	A1699	G1639	A1579	G1517	G1456	A1396	G1335	C1273	C1213	G1153	A1093	A1031	U969
G1763	C1700	G1640	A1580	C1518	U1457	G1397	G1336	G1274	A1214	U1154	C1094	C1032	G970
A1641	C1701	C1641	C1581	U1519	G1458	G1398	C1337	G1275	C1215	U1155	C1095	G1033	G971
U1642	G1702	U1643	C1582	G1520	G1461	C1399	U1338	A1276	C1216	U1156	G1096	G1034	G972
G1643	C1703	C1583	G1521	C1520	U1462	U1400	G1339	C1277	A1217	G1157	G1097	A1035	A973
C1644	C1704	U1644	A1584	A1522	U1463	A1401	U1340	A1278	C1218	G1158	C1098	A1036	C974
G1645	C1705	U1645	U1585	C1523	U1464	A1402	C1341	C1279	C1219	G1159	G1099	G1037	G975
C1646	U1706	C1647	U1586	C1527	A1465	A1403	U1342	G1280	A1220	U1160	A1100	U1038	G976
A1647	G1707	G1648	U1587	G1528	G1466	U1404	U1343	G1281	G1221	U1161	U1101	U1039	C977
G1648	C1708	A1649	A1588	G1529	C1467	A1405	A1344	A1282	G1222	C1162	G1102	G1040	C978
U1649	G1709	A1650	A1589	C1529	U1468	G1406	U1345	G1283	A1223	G1163	G1103	G1041	C979
A1651	C1710	C1650	U1590	U1530	U1469	A1407	U1346	A1284	G1224	G1164	G1104	A1042	A980
G1652	U1711	A1652	C1591	A1531	A1469	A1408	U1347	G1285	U1225	G1165	G1105	G1043	A981
A1712	G1712	C1653	C1592	C1532	C1470	A1409	G1348	G1286	G1226	G1166	C1106	G1044	G982
U1713	C1713	U1653	A1593	A1533	C1471	C1410	U1349	A1287	G1227	G1167	G1107	U1045	A983
U1714	U1714	G1654	C1594	C1534	C1472	G1411	U1350	U1288	A1228	G1168	G1108	U1046	C984
A1715	C1715	C1655	A1594	U1535	A1473	G1412	G1351	U1289	G1229	G1169	C1109	C1047	G985
C1775	C1775	U1656	U1595	G1536	U1474	A1413	G1352	G1290	C1230	A1170	G1110	G1048	G986
G1776	U1720	G1657	C1597	A1537	G1475	A1414	A1353	A1291	C1231	G1171	A1111	A1049	G987
C1777	U1721	G1658	U1598	C1538	U1476	C1415	G1354	C1292	U1232	U1172	U1112	G1051	C988
U1774	U1722	G1659	U1599	U1539	A1477	C1416	C1355	C1293	G1233	A1173	U1113	A1050	C989
C1778	G1723	C1660	G1600	G1540	U1478	C1417	G1356	U1296	C1234	U1174	U1114	A1052	A990
G1779	U1724	A1661	U1601	G1541	G1479	C1418	A1357	U1297	G1235	G1175	U1115	G1053	G991
G1780	C1725	U1662	U1602	C1542	A1480	C1419	U1358	G1298	G1236	G1176	C1116	G1054	A992
G1781	U1726	A1663	G1603	U1543	G1481	C1420	U1359	A1299	C1237	U1177	C1117	U1055	G993
C1783	G1727	A1664	G1604	C1544	C1482	A1421	U1360	U1300	U1238	U1178	C1118	C1057	C994
G1784	U1728	G1665	G1605	A1545	A1483	G1422	U1361	A1301	U1239	G1179	A1119	A1058	G995
C1785	U1729	C1666	U1606	G1546	A1484	C1423	U1362	G1302	A1240	C1180	U1120	G1059	C999
U1786	U1730	U1667	A1607	C1547	U1485	G1424	C1363	C1303	U1242	A1181	G1121	A1060	C1000
G1787	C1731	U1668	U1608	U1548	A1486	G1425	U1364	U1304	U1243	A1182	A1122	U1061	A1001
A1788	G1732	G1669	G1609	C1549	A1487	G1426	C1365	C1305	G1244	A1183	C1123	A1062	U1002
G1789	U1733	C1670	G1610	U1551	C1488	C1427	U1366	U1306	U1245	G1184	C1124	C1063	U1003
A1790	C1734	G1671	G1611	U1552	A1489	G1428	U1367	U1307	A1246	U1185	C1125	C1064	U1004
U1791	U1735	U1672	G1612	G1553	G1490	G1429	A1369	C1308	G1247	G1187	G1126	G1065	U1005
G1792	G1736	G1673	A1613	C1554	U1491	C1430	U1370	U1310	U1248	A1188	C1127	U1066	G1006
A1793	C1737	A1674	U1614	U1555	U1492	G1431	U1371	C1311	C1249	A1189	G1128	C1067	C1007
G1794	U1738	U1675	U1615	A1556	C1493	U1432	U1372	G1312	A1250	A1190	G1129	G1068	U1008
C1798	G1739	G1676	U1616	U1557	G1495	C1433	C1374	A1313	C1251	C1191	G1130	U1069	A1009
G1799	U1740	C1677	C1617	C1558	U1496	G1434	G1375	U1314	C1252	U1192	C1131	A1070	G1010
A1800	C1741	A1678	C1618	C1559	G1497	C1435	U1376	U1315	A1253	U1193	C1132	G1071	A1011
A1801	U1742	A1679	U1619	U1560	A1498	C1436	U1377	C1316	C1254	A1194	G1134	C1074	A1012
C1743	C1743	G1680	U1620	U1561	U1499	G1437	A1378	G1317	G1255	A1195	C1135	C1075	U1013
U1803	U1744	C1681	U1621	A1561	U1499	C1437	A1379	G1318	G1256	A1196	U1136	G1076	G1014
U1804	C1745	C1682	A1622	C1562	G1500	A1438	C1380	U1319	G1257	G1197	U1137	C1079	U1015
C1807	U1746	C1683	U1623	G1563	C1501	A1439	G1381	G1320	A1258	G1198	C1138	U1016	U1017
U1808	U1747	C1684	U1624	C1564	G1502	C1440	A1382	G1321	A1259	A1199	C1139	A1080	U1018
A1809	G1748	U1685	U1625	C1565	C1503	U1441	A1383	G1322	C1260	A1200	G1140	U1081	C1019
C1810	U1749	C1686	C1626	G1566	U1504	U1442	A1384	U1323	C1261	U1201	G1141	A1082	A1020
C1811	C1750	C1687	C1627	G1567	U1505	C1443	C1385	G1324	C1262	U1202	G1142	A1083	U1021
U1812	C1751	C1688	C1628	U1568	A1506	U1444	A1386	G1325	U1263	A1203	A1143	A1084	U1022
C1752	C1752	A1689	A1569	C1568	G1507	U1445	A1387	U1326	C1264	A1204	C1144	C1085	A1023
A1813	U1690	C1630	G1570	A1568	A1508	A1446	C1387	U1327	A1265	C1205	A1145	G1086	A1024
C1753	U1691	U1681	G1571	U1569	U1509	A1447	A1388	G1328	C1266	G1206	C1146	A1087	U1025
U1754	G1692	G1632	U1510	U1509	G1447	A1448	C1389	U1329	C1267	G1207	C1147	U1088	C1026
C1755	C1693	G1633	G1572	C1573	U1511	A1449	U1390	U1329	C1268	A1208	A1148		
C1756	U1694	A1634	C1574	C1574	C1512	G1450	C1391	G1330					



• Molecule 5: 40S RIBOSOMAL PROTEIN SA



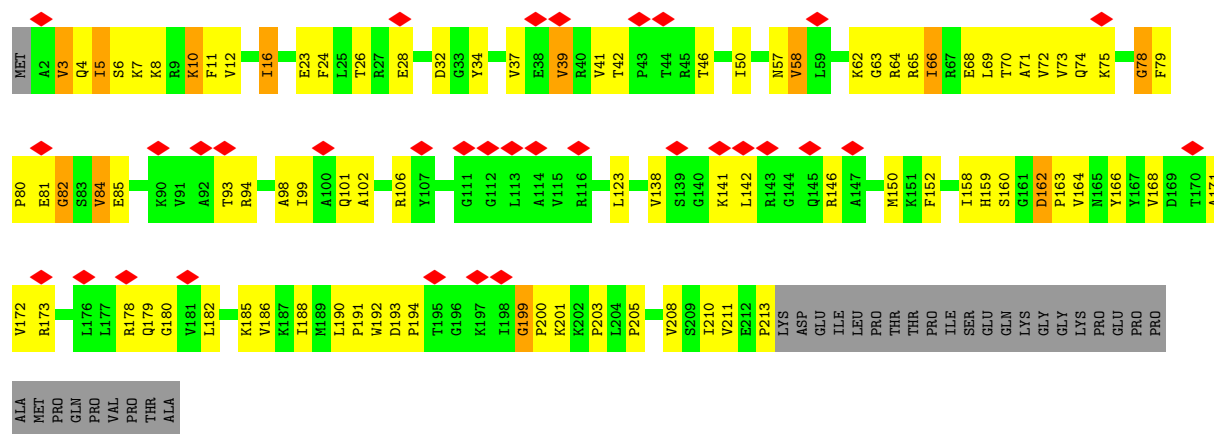
• Molecule 6: 40S RIBOSOMAL PROTEIN S3A



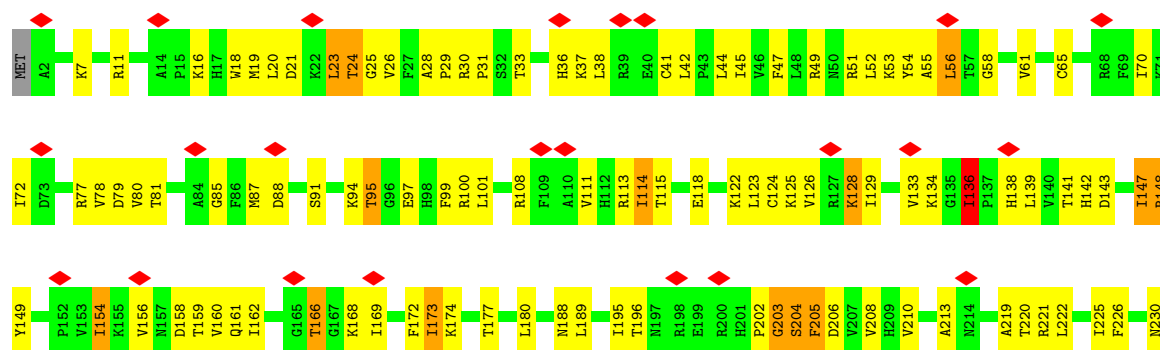
• Molecule 7: 40S RIBOSOMAL PROTEIN S2



- Molecule 8: 40S RIBOSOMAL PROTEIN S3

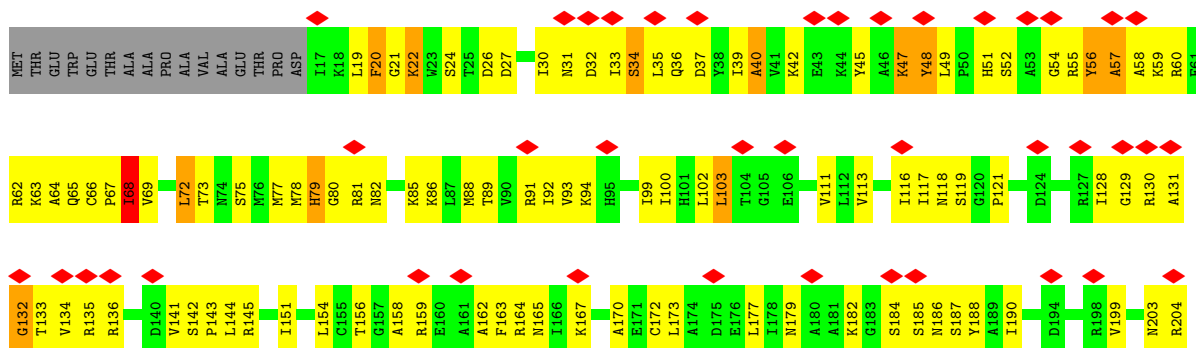
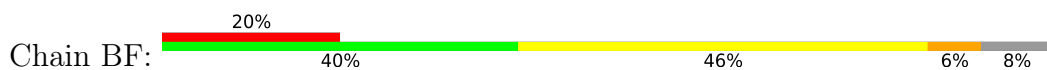


- Molecule 9: 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1

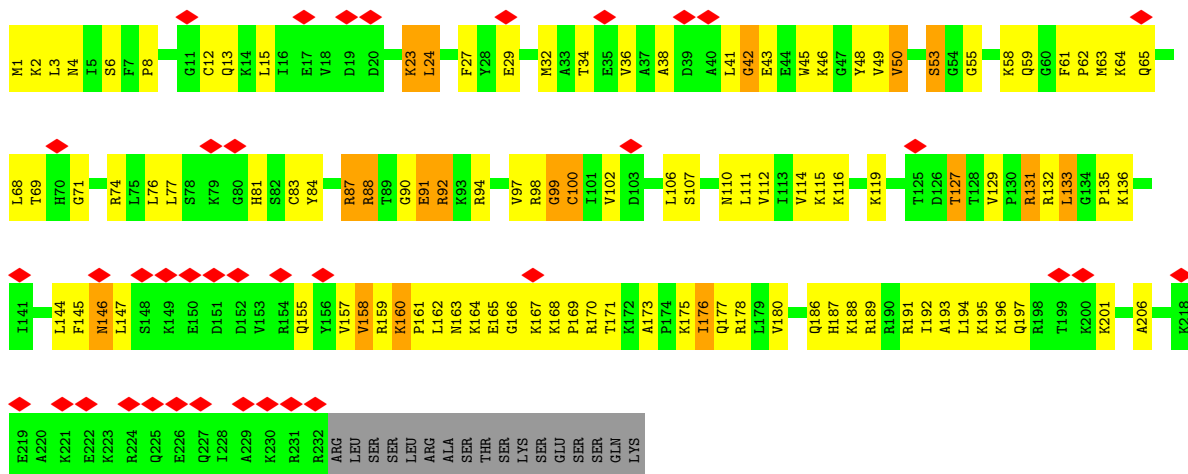




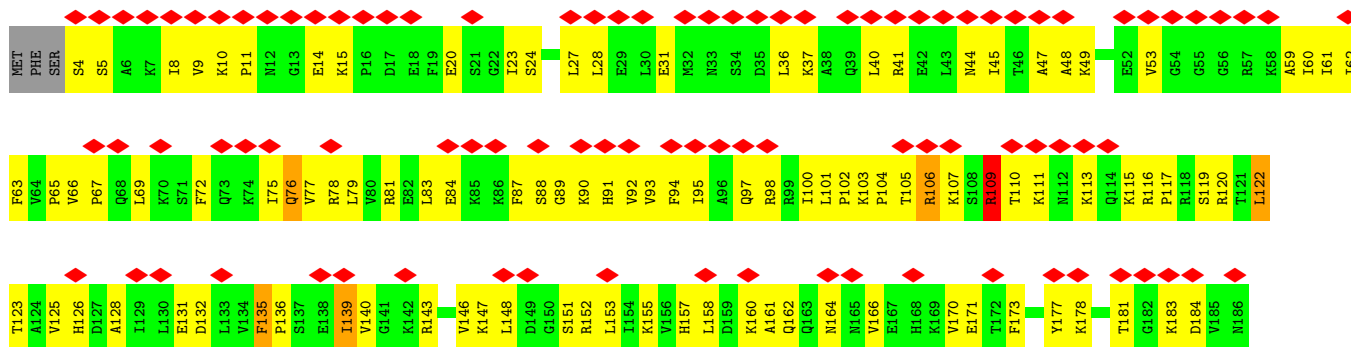
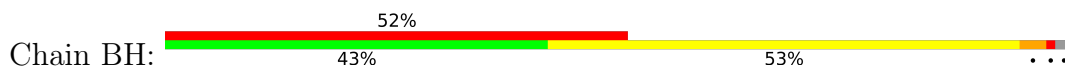
• Molecule 10: 40S RIBOSOMAL PROTEIN S5

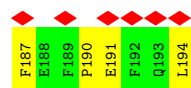


• Molecule 11: 40S RIBOSOMAL PROTEIN S6

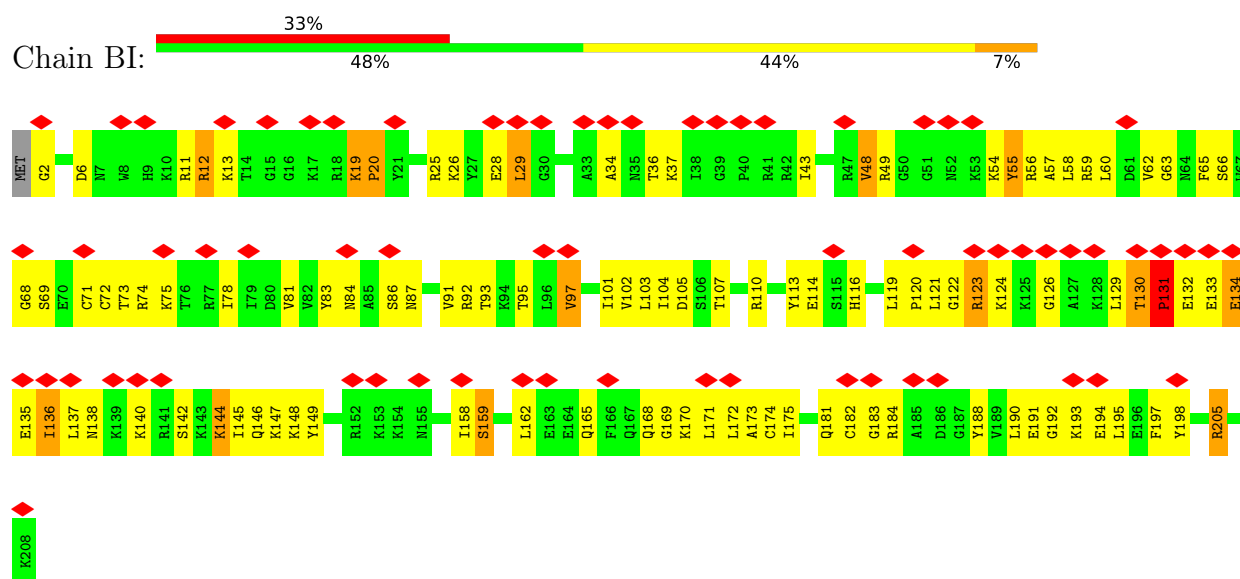


• Molecule 12: 40S RIBOSOMAL PROTEIN S7

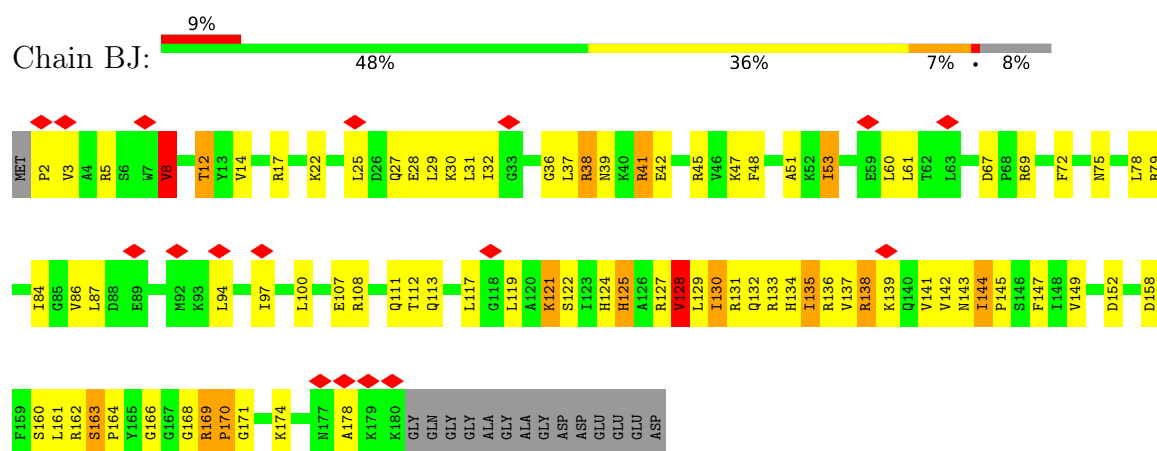




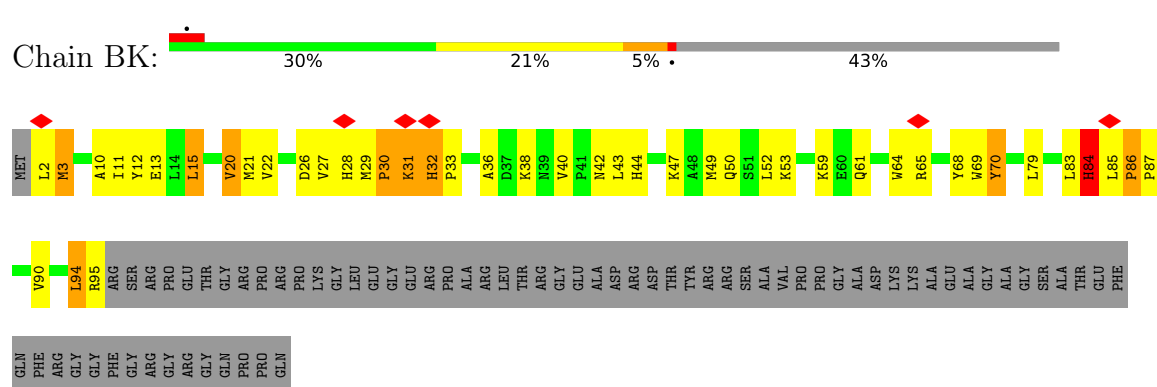
• Molecule 13: 40S RIBOSOMAL PROTEIN S8



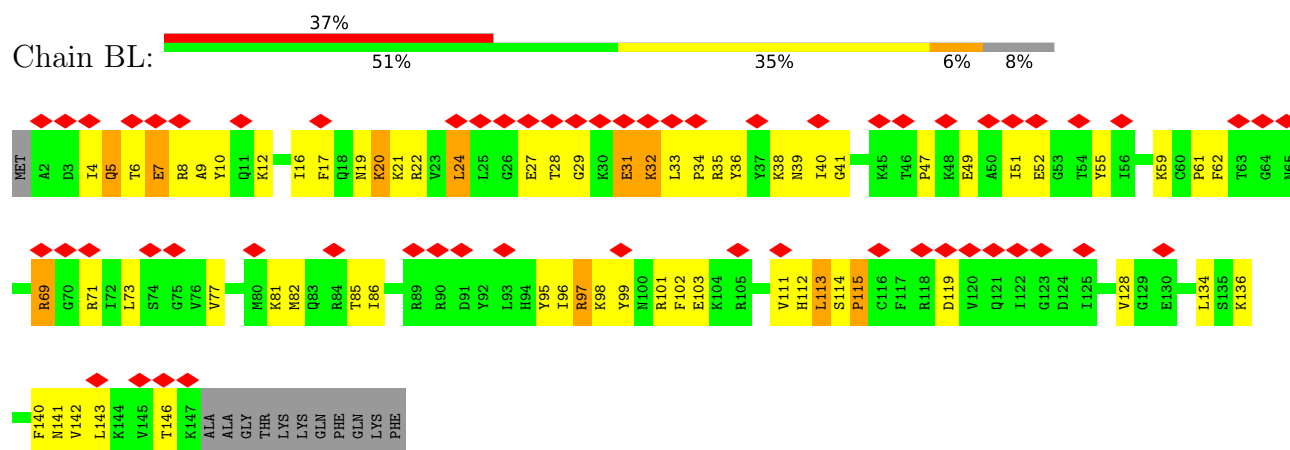
• Molecule 14: 40S RIBOSOMAL PROTEIN S9



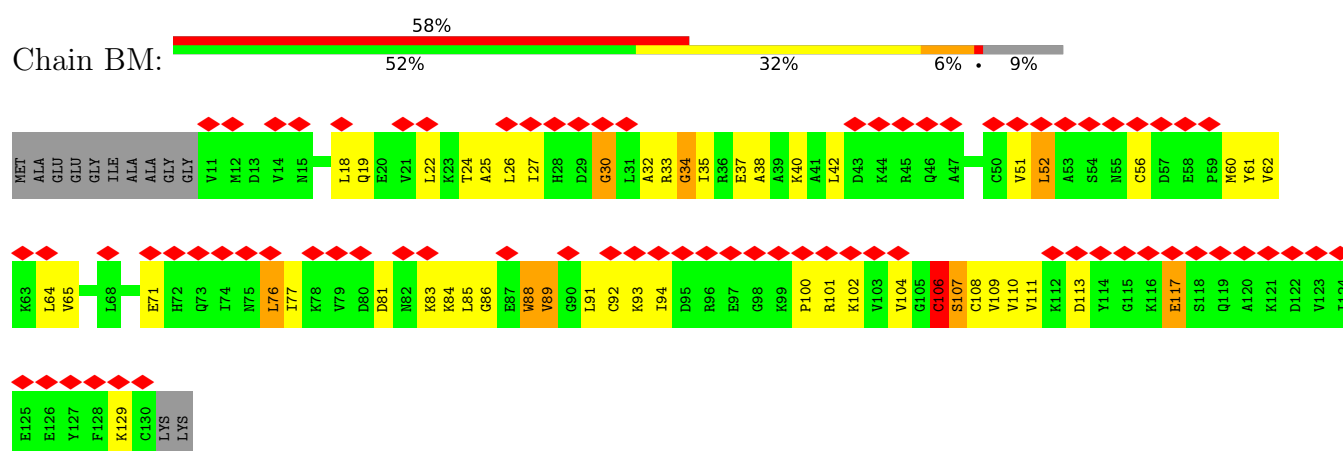
• Molecule 15: 40S RIBOSOMAL PROTEIN S10



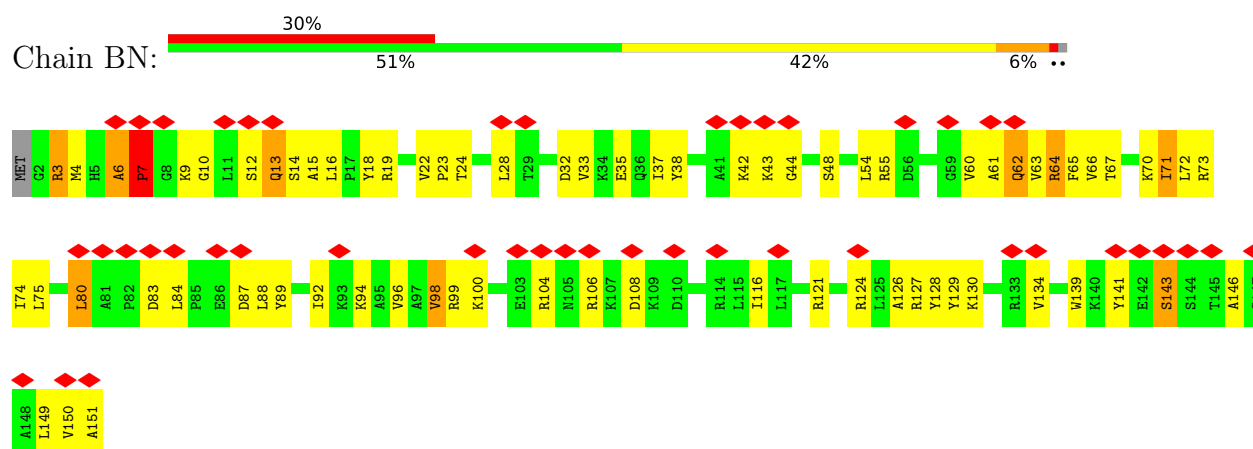
• Molecule 16: 40S RIBOSOMAL PROTEIN S11



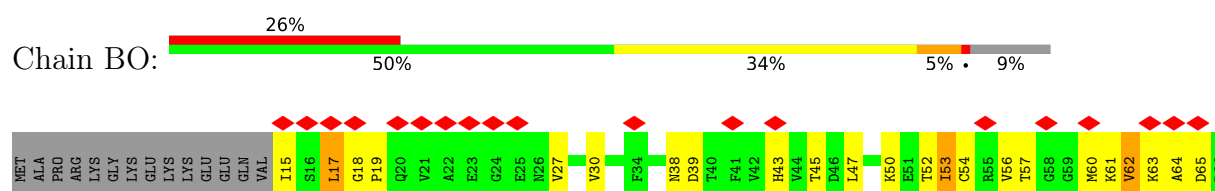
• Molecule 17: 40S RIBOSOMAL PROTEIN S12

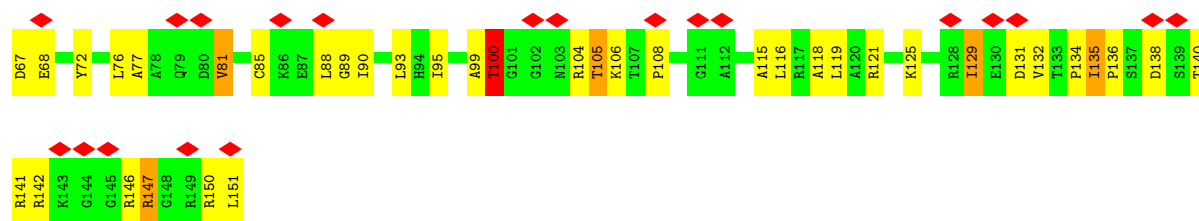


• Molecule 18: 40S RIBOSOMAL PROTEIN S13



• Molecule 19: 40S RIBOSOMAL PROTEIN S14

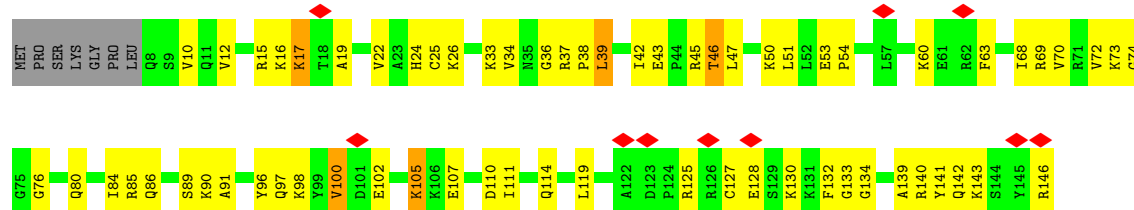




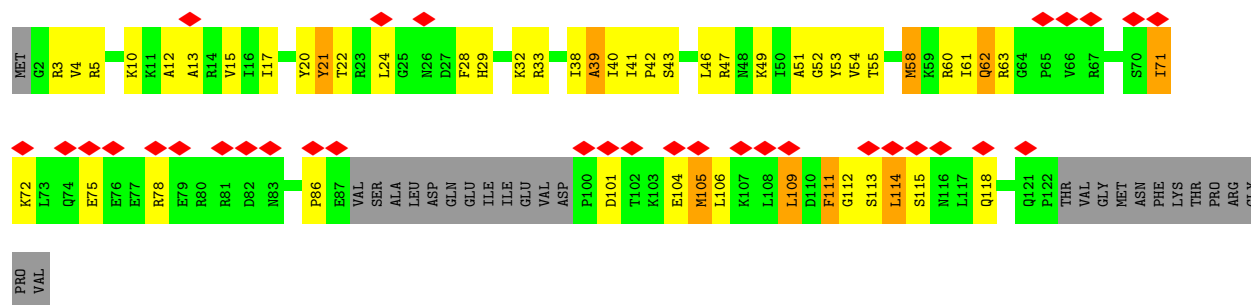
• Molecule 20: 40S RIBOSOMAL PROTEIN S15



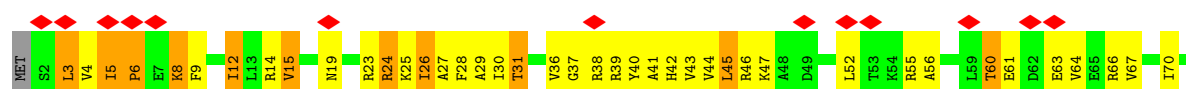
• Molecule 21: 40S RIBOSOMAL PROTEIN S16



• Molecule 22: 40S RIBOSOMAL PROTEIN S17



• Molecule 23: 40S RIBOSOMAL PROTEIN S18

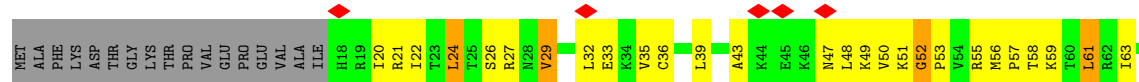




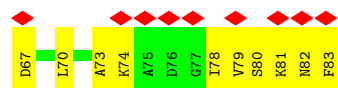
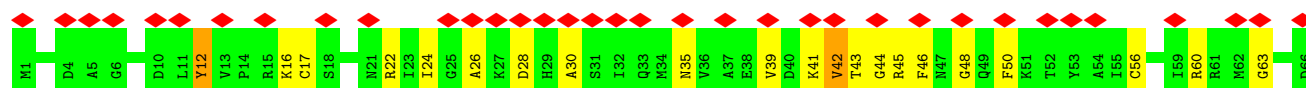
• Molecule 24: 40S RIBOSOMAL PROTEIN S19



• Molecule 25: 40S RIBOSOMAL PROTEIN S20



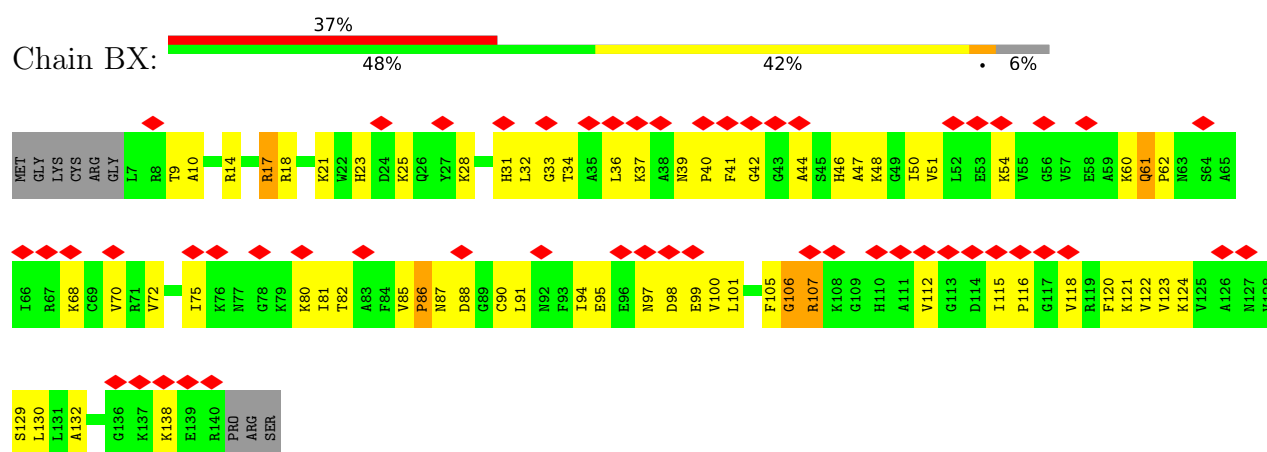
• Molecule 26: 40S RIBOSOMAL PROTEIN S21



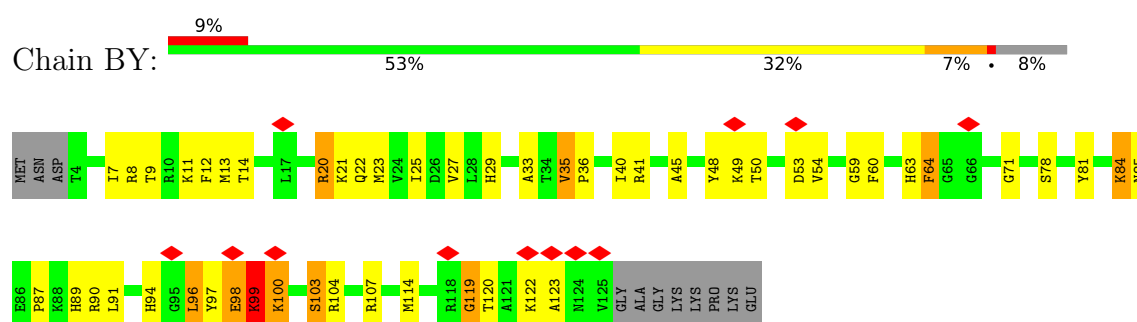
• Molecule 27: 40S RIBOSOMAL PROTEIN S15A



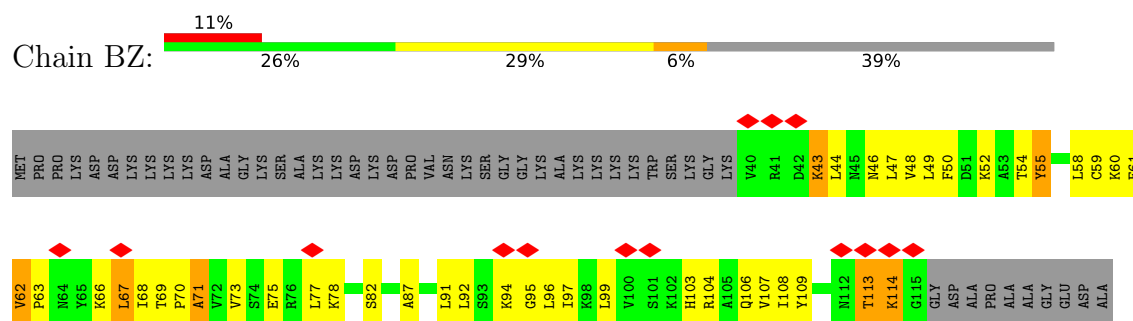
• Molecule 28: 40S RIBOSOMAL PROTEIN S23



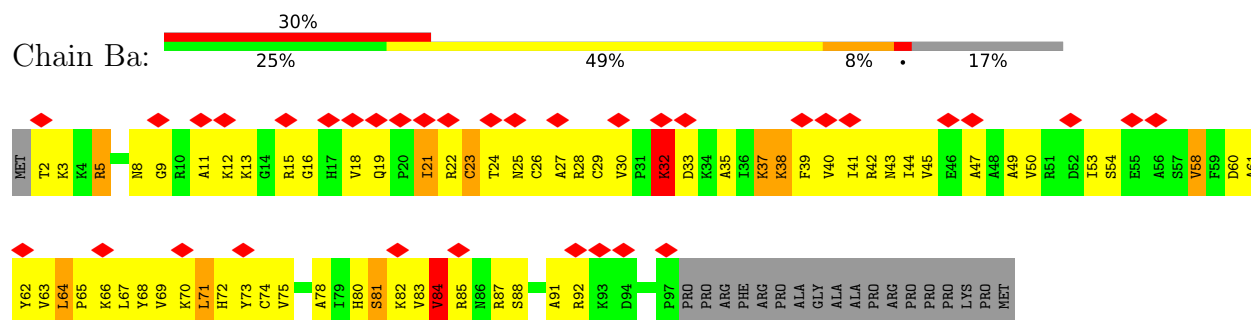
• Molecule 29: 40S RIBOSOMAL PROTEIN S24



• Molecule 30: 40S RIBOSOMAL PROTEIN S25

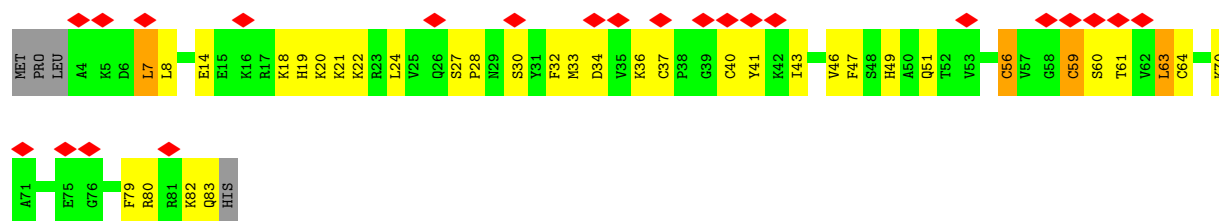


• Molecule 31: 40S RIBOSOMAL PROTEIN S26

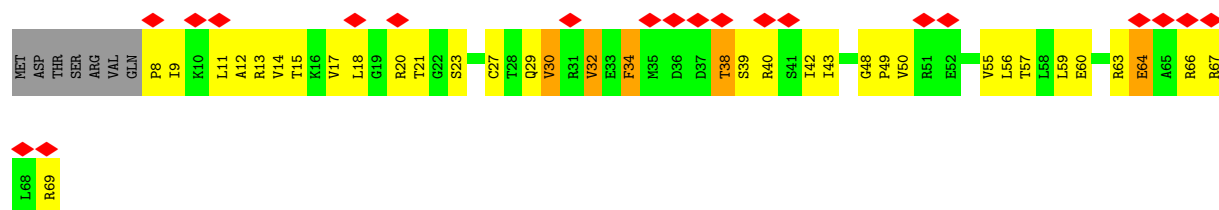


• Molecule 32: 40S RIBOSOMAL PROTEIN S27

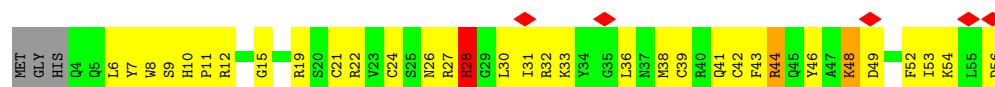




• Molecule 33: 40S RIBOSOMAL PROTEIN S28



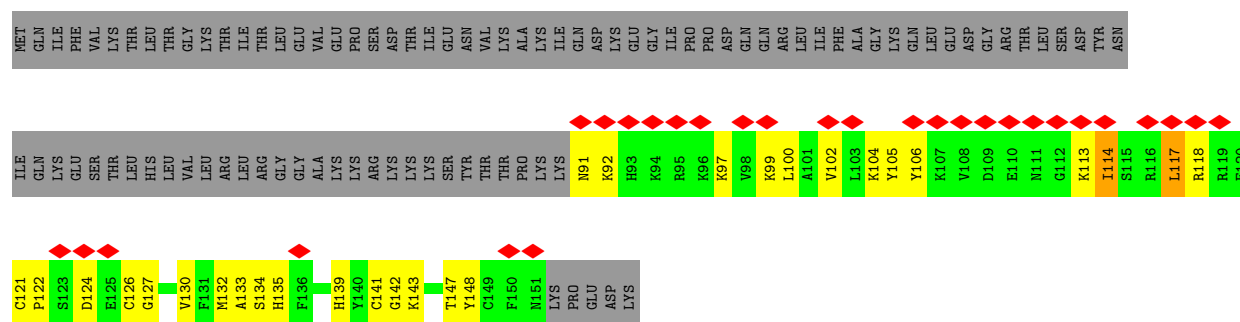
• Molecule 34: 40S RIBOSOMAL PROTEIN S29



• Molecule 35: 40S RIBOSOMAL PROTEIN S30

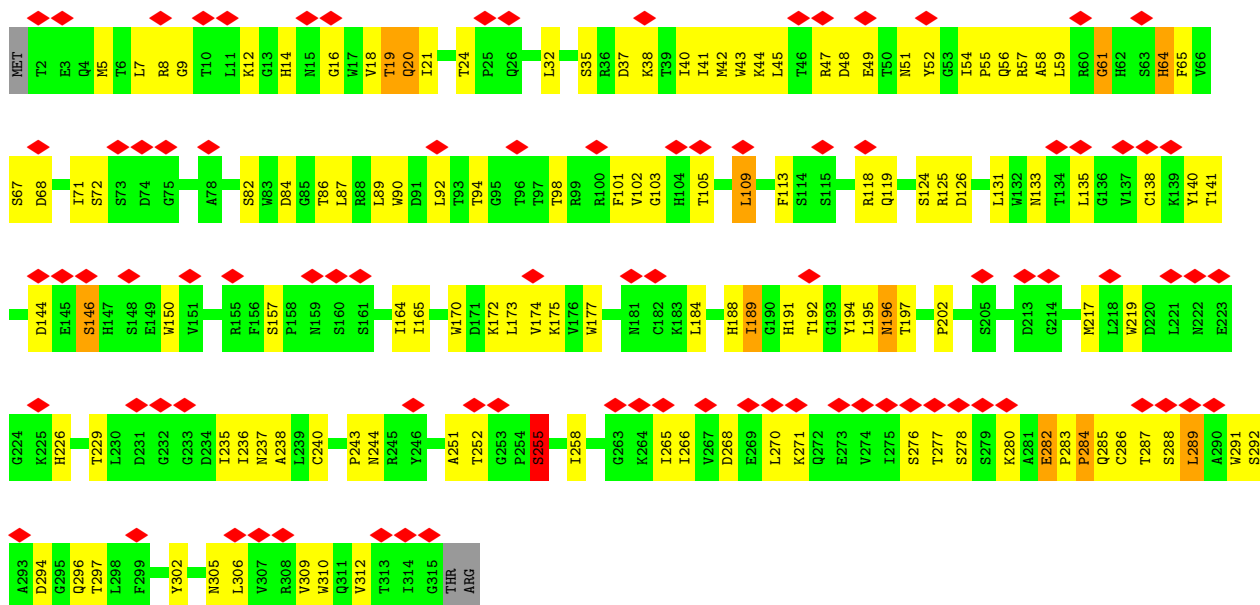


• Molecule 36: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

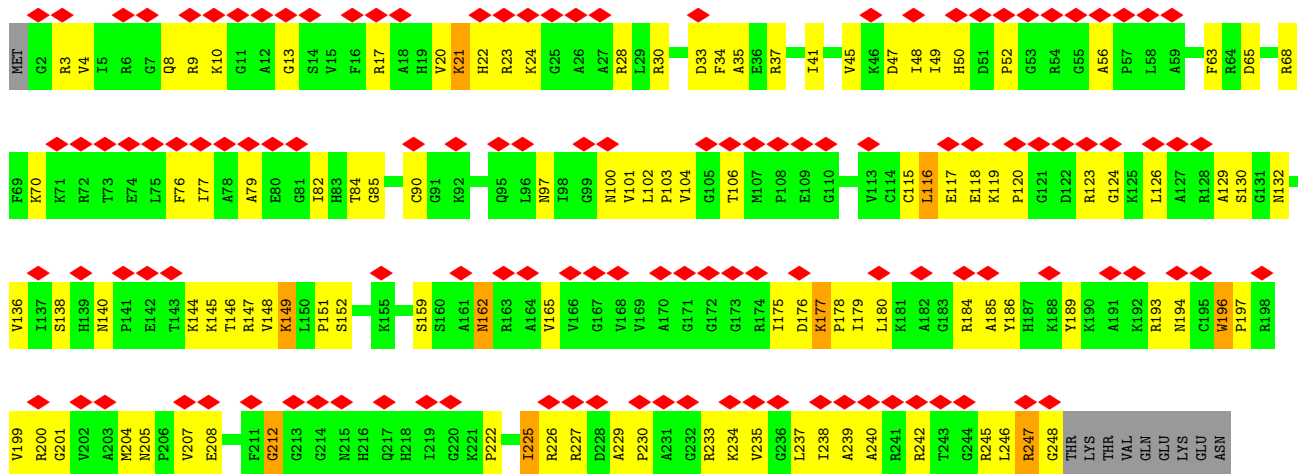


• Molecule 37: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1

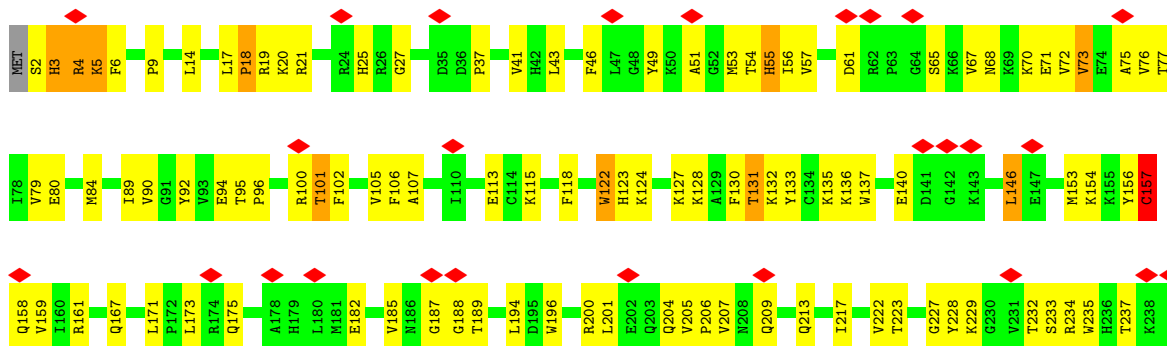


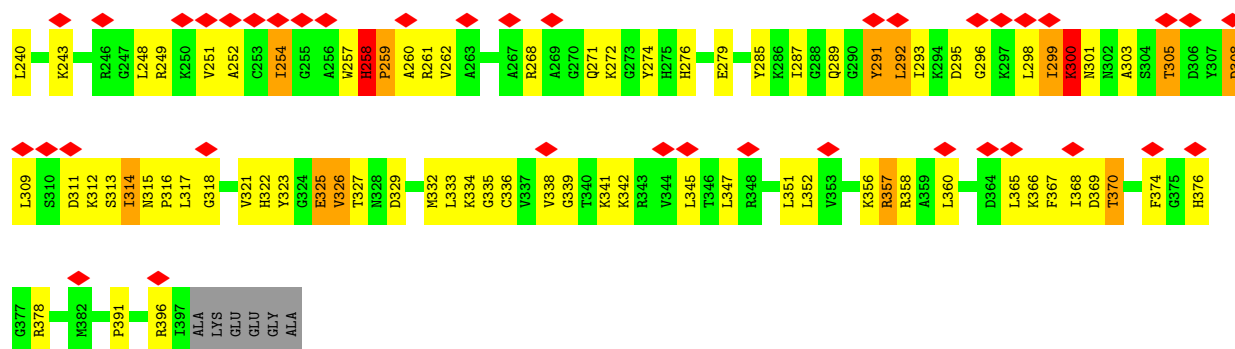


• Molecule 38: 60S RIBOSOMAL PROTEIN L8

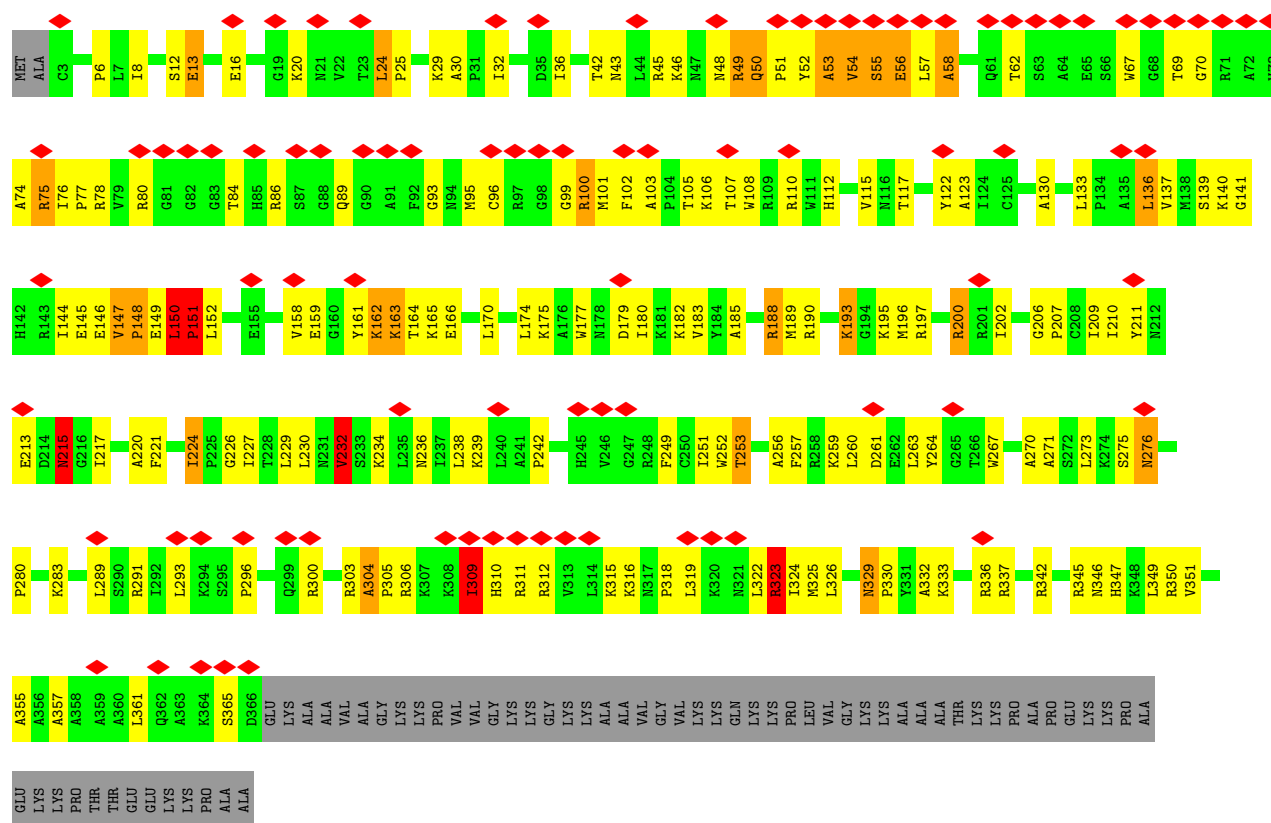
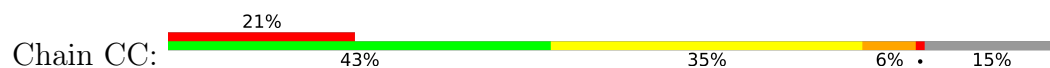


• Molecule 39: 60S RIBOSOMAL PROTEIN L3

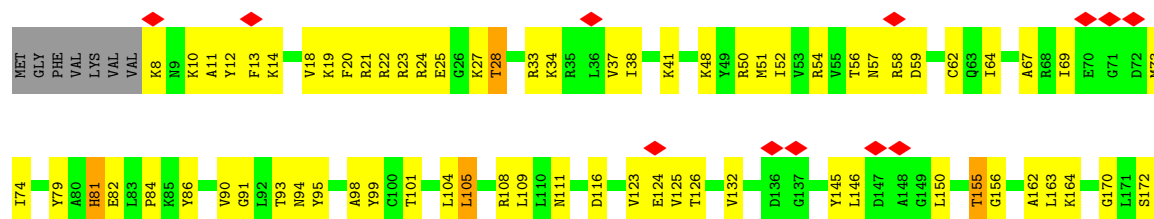


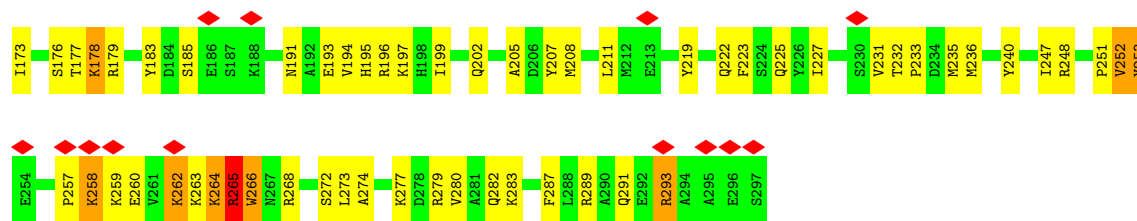


• Molecule 40: 60S RIBOSOMAL PROTEIN L4

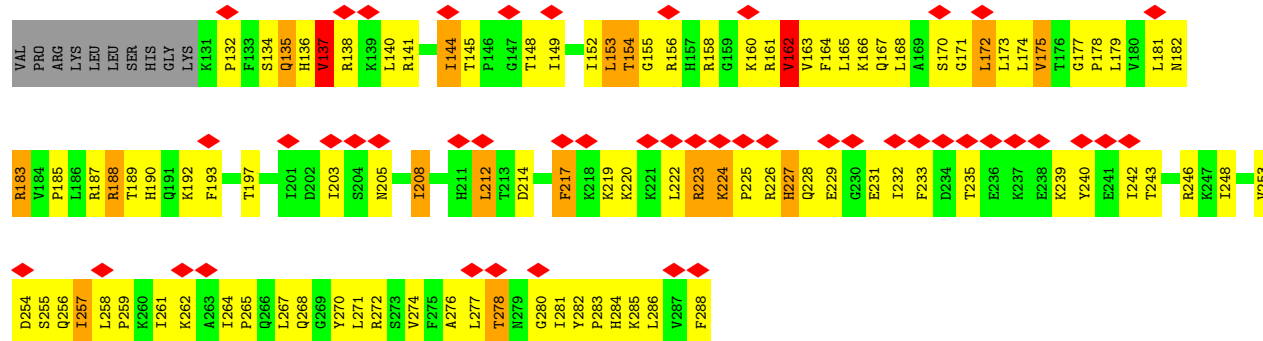
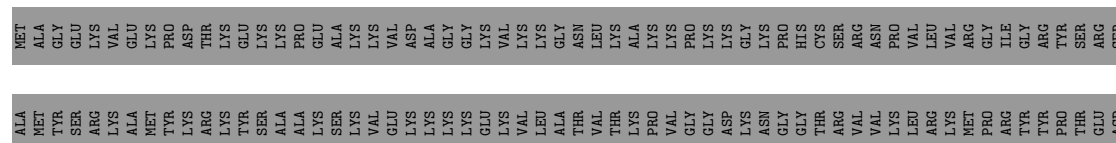


• Molecule 41: 60S RIBOSOMAL PROTEIN L5

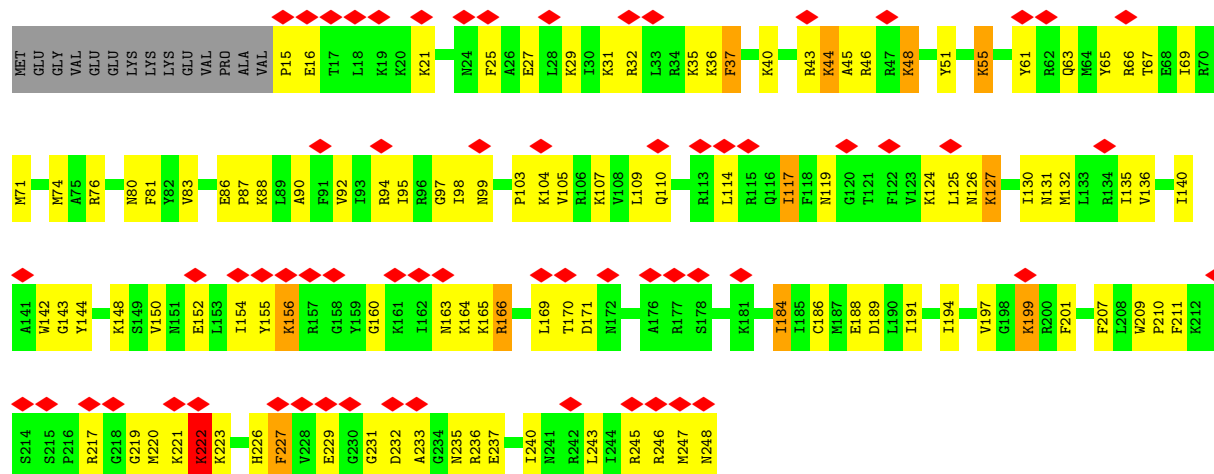




• Molecule 42: 60S RIBOSOMAL PROTEIN L6

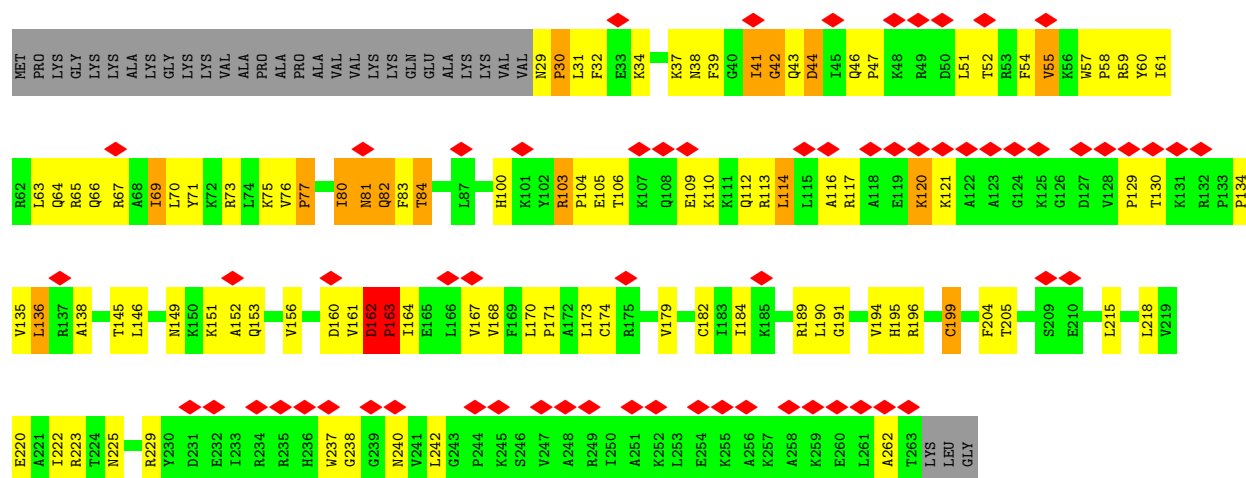


• Molecule 43: 60S RIBOSOMAL PROTEIN L7

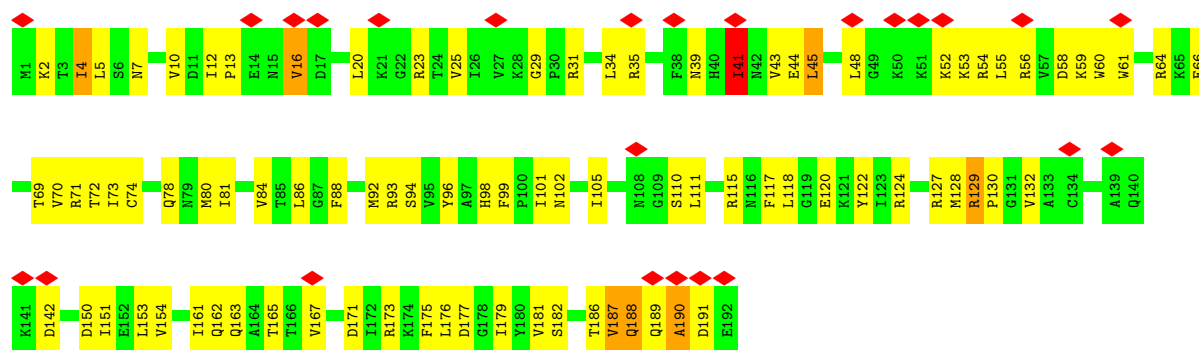


• Molecule 44: 60S RIBOSOMAL PROTEIN L7A

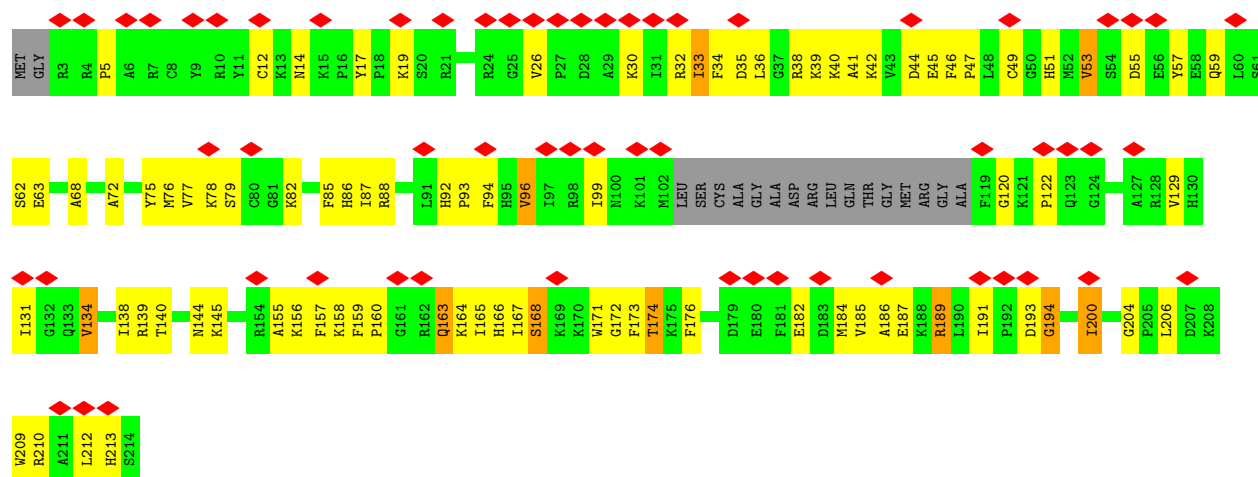




• Molecule 45: 60S RIBOSOMAL PROTEIN L9

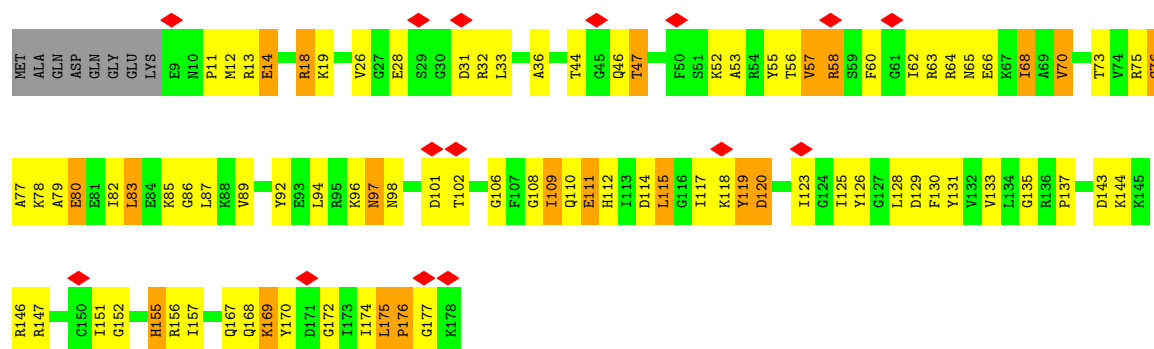


• Molecule 46: 60S RIBOSOMAL PROTEIN L10

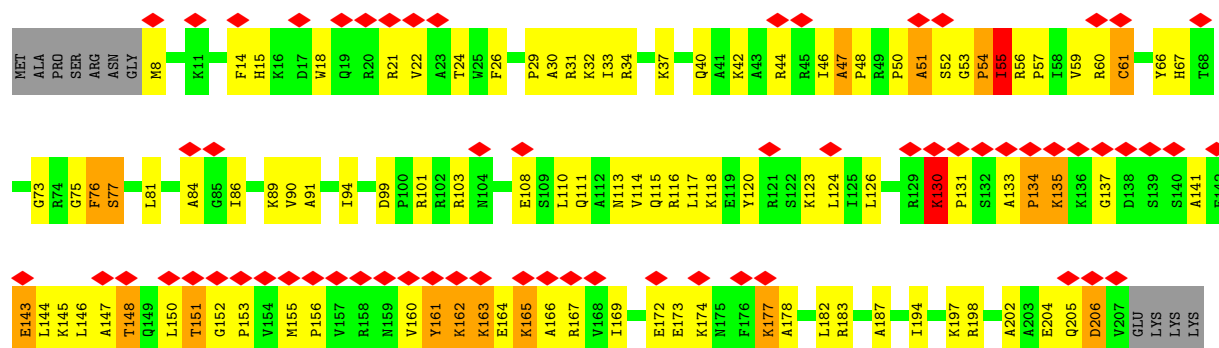


• Molecule 47: 60S RIBOSOMAL PROTEIN L11

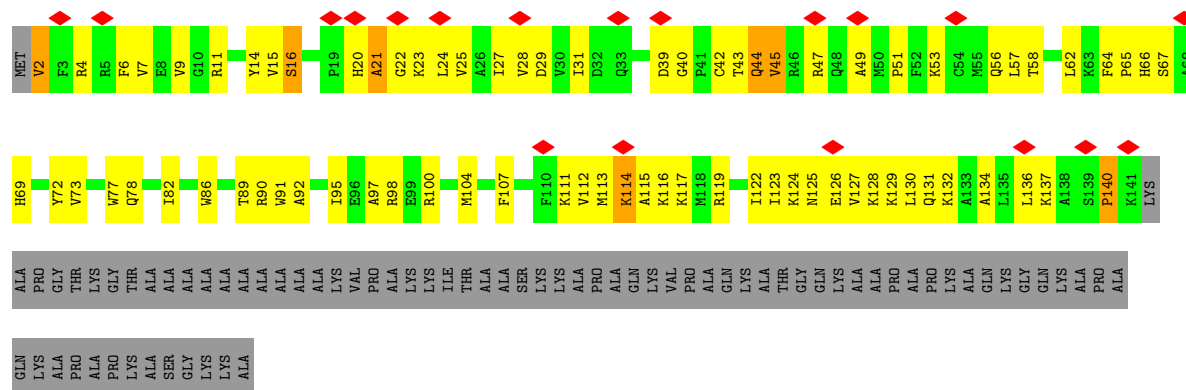




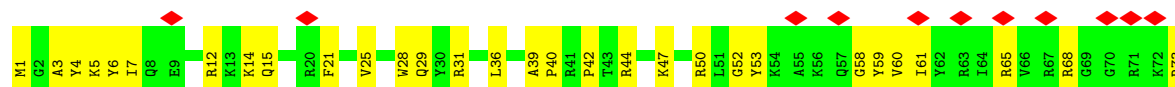
• Molecule 48: 60S RIBOSOMAL PROTEIN L13

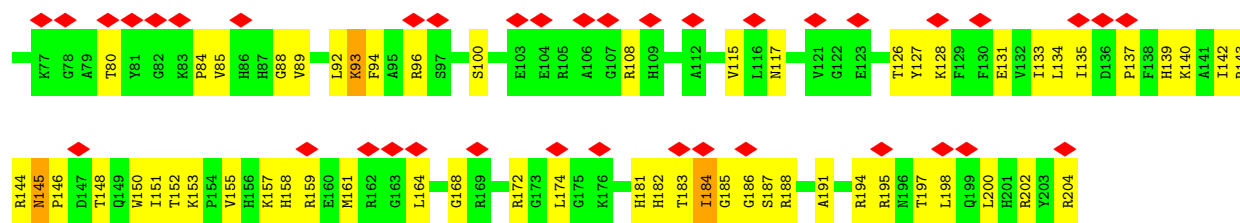


• Molecule 49: 60S RIBOSOMAL PROTEIN L14

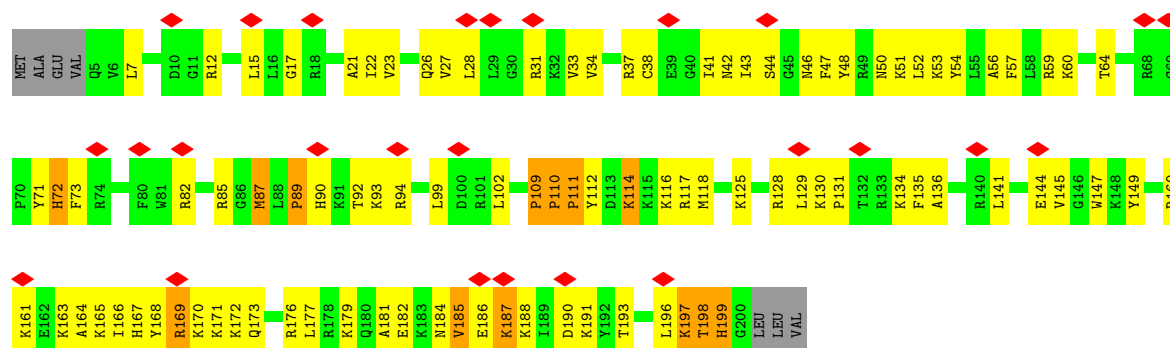


• Molecule 50: 60S RIBOSOMAL PROTEIN L15

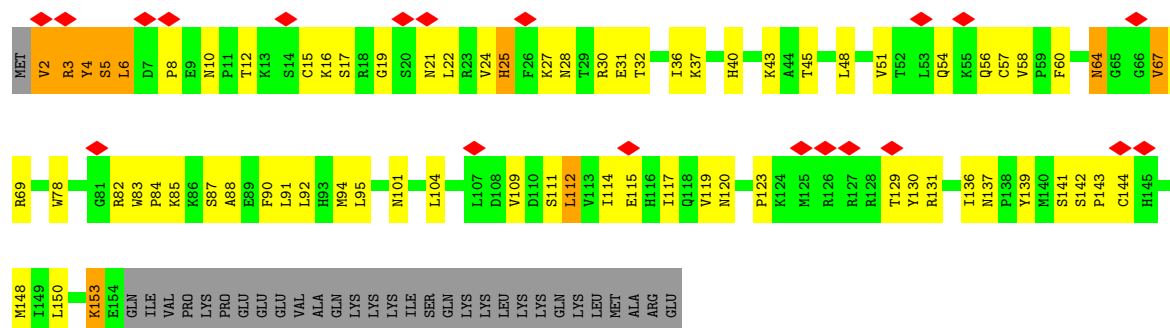
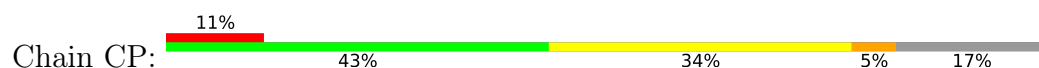




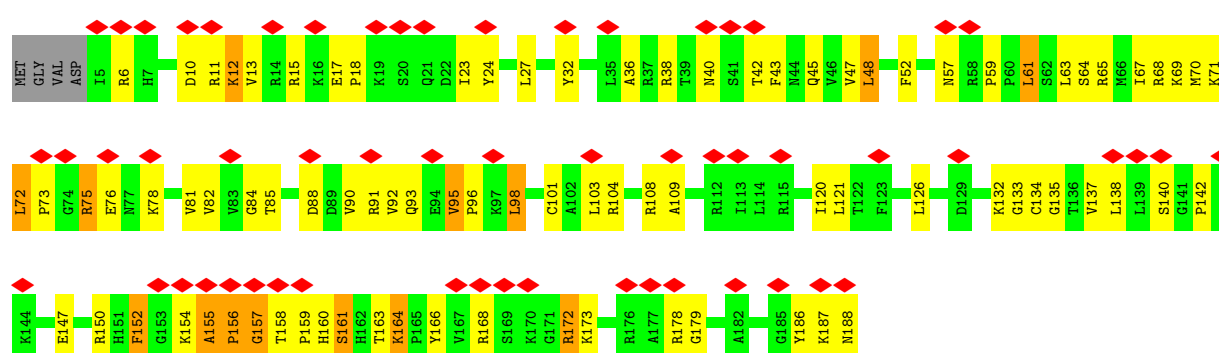
• Molecule 51: 60S RIBOSOMAL PROTEIN L13A



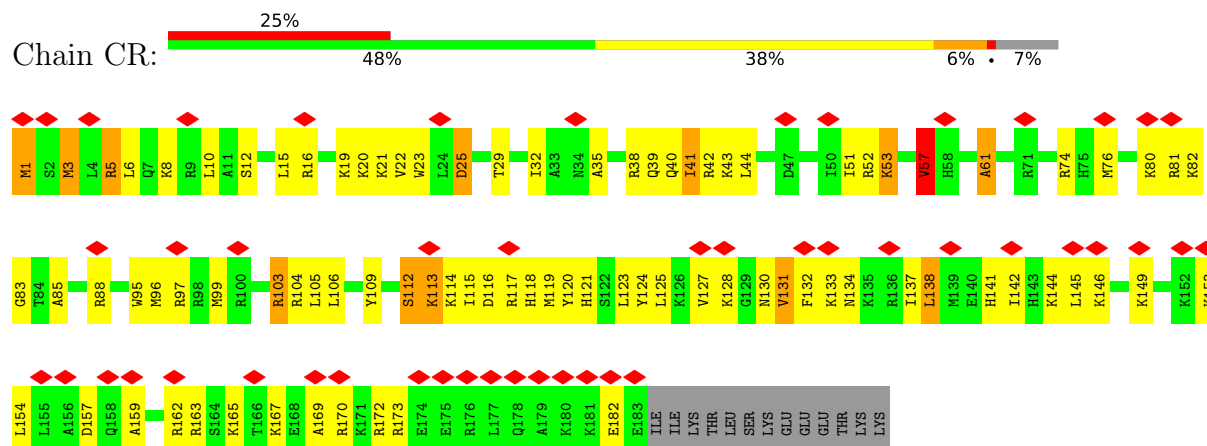
• Molecule 52: 60S RIBOSOMAL PROTEIN L17



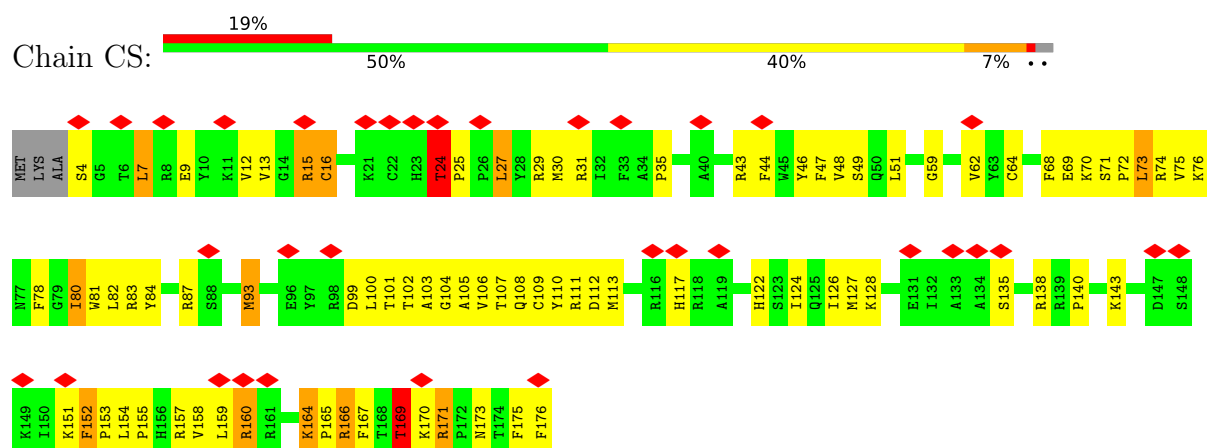
• Molecule 53: 60S RIBOSOMAL PROTEIN L18



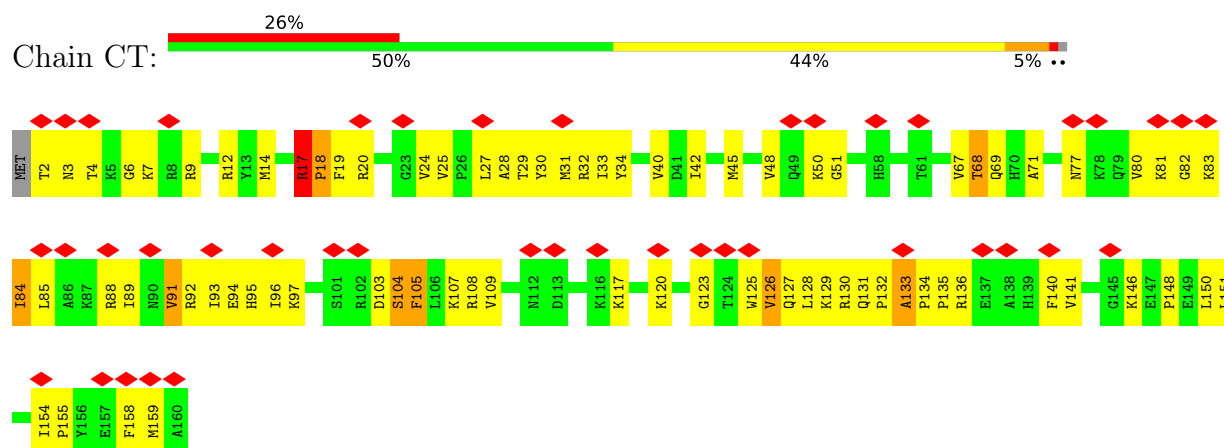
- Molecule 54: 60S RIBOSOMAL PROTEIN L19



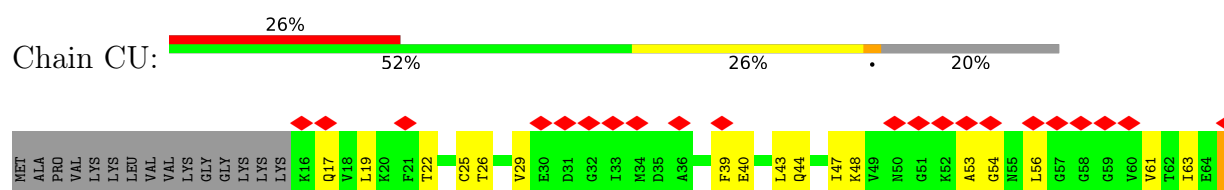
- Molecule 55: 60S RIBOSOMAL PROTEIN L18A

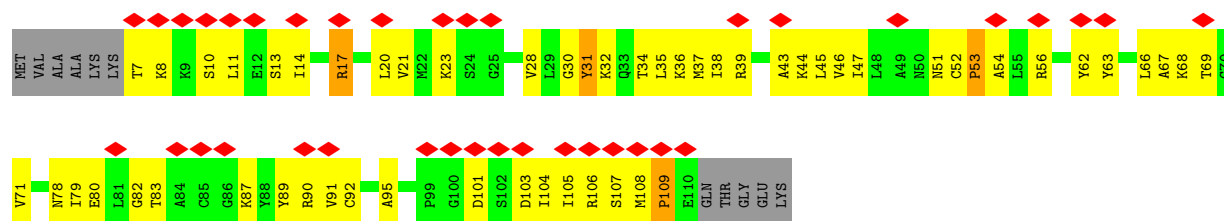


- Molecule 56: 60S RIBOSOMAL PROTEIN L21

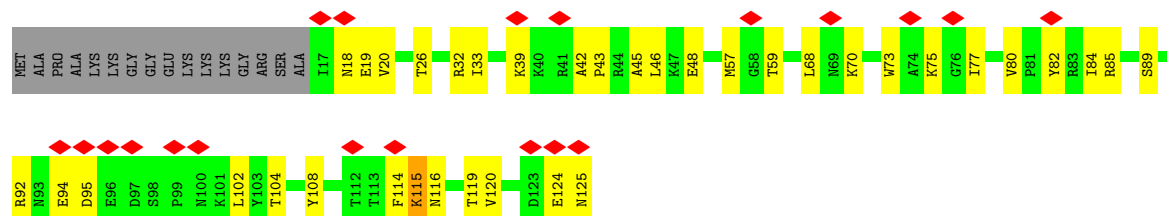


- Molecule 57: 60S RIBOSOMAL PROTEIN L22

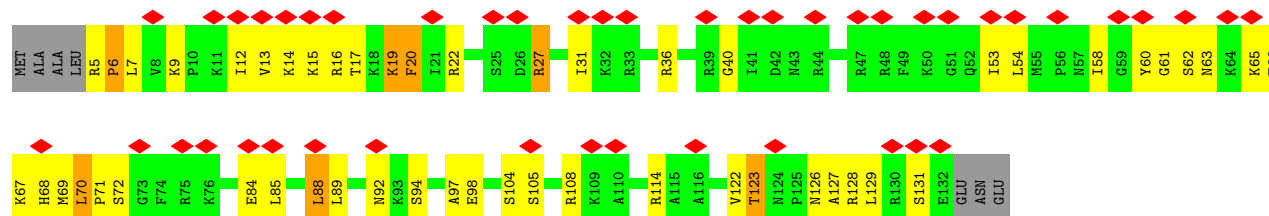




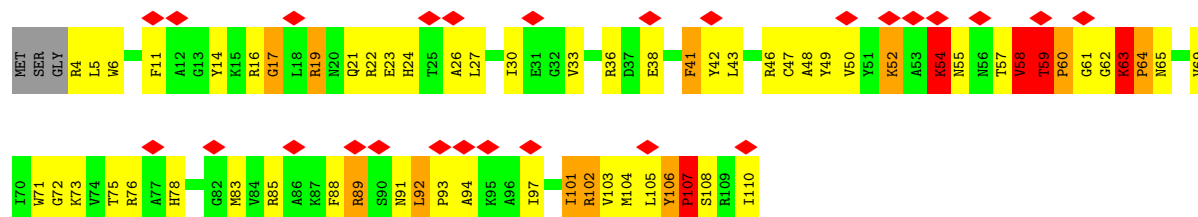
• Molecule 66: 60S RIBOSOMAL PROTEIN L31



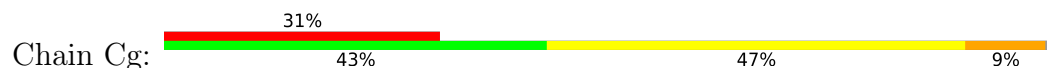
• Molecule 67: 60S RIBOSOMAL PROTEIN L32

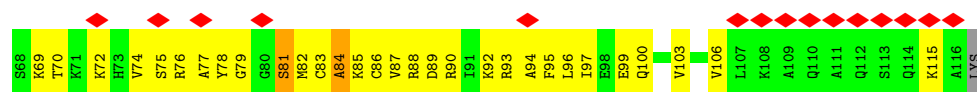


• Molecule 68: 60S RIBOSOMAL PROTEIN L35A

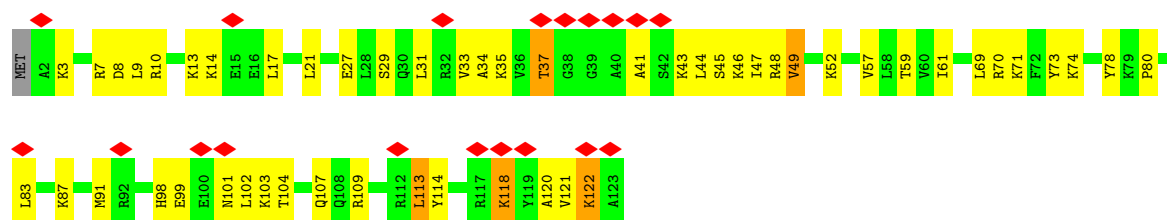


• Molecule 69: 60S RIBOSOMAL PROTEIN L34

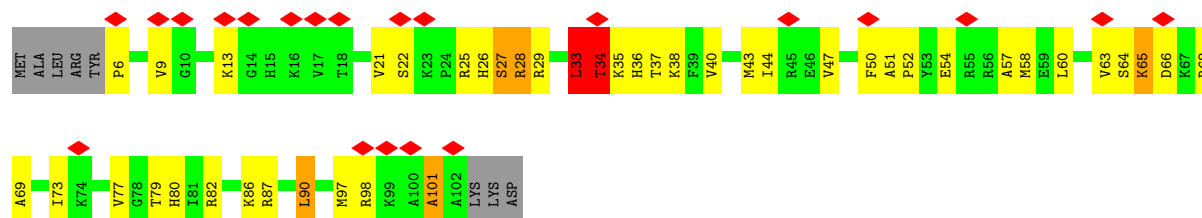




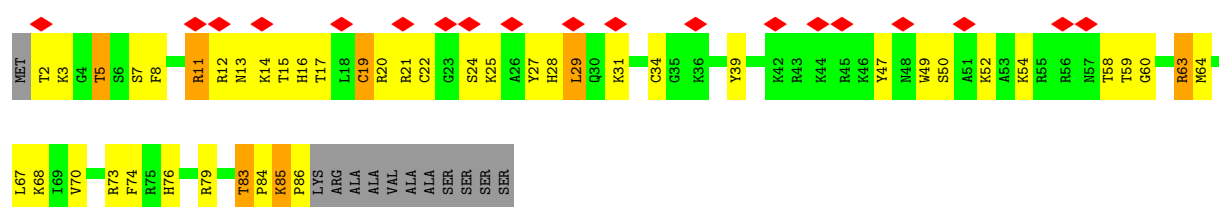
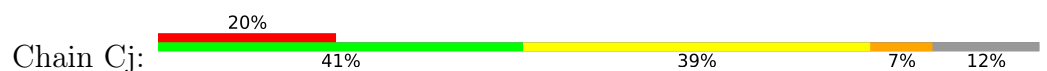
• Molecule 70: 60S RIBOSOMAL PROTEIN L35



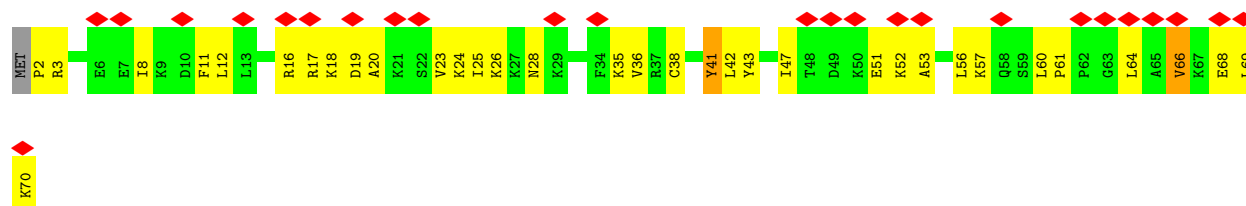
• Molecule 71: 60S RIBOSOMAL PROTEIN L36



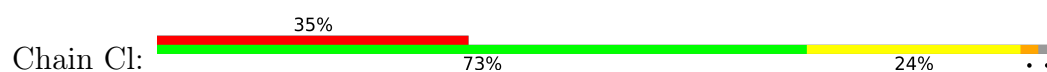
• Molecule 72: 60S RIBOSOMAL PROTEIN L37

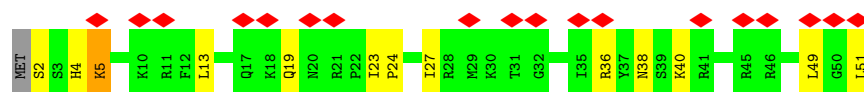


• Molecule 73: 60S RIBOSOMAL PROTEIN L38

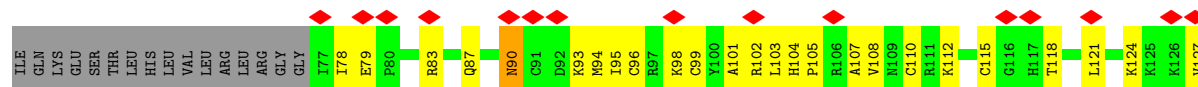
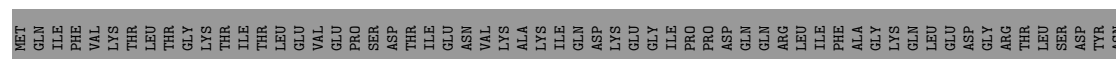


• Molecule 74: 60S RIBOSOMAL PROTEIN L39

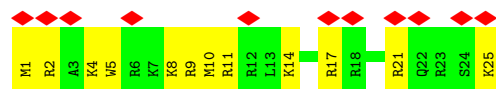




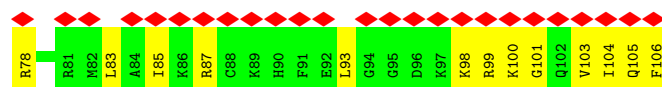
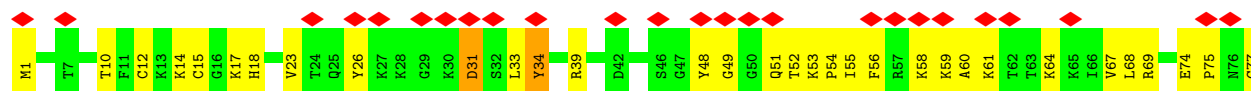
• Molecule 75: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



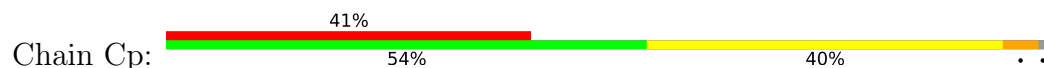
• Molecule 76: 60S RIBOSOMAL PROTEIN L41



• Molecule 77: 60S RIBOSOMAL PROTEIN L36A

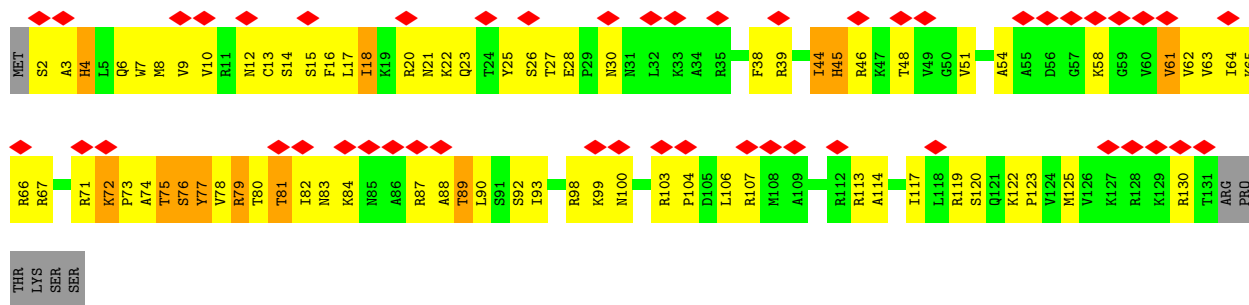


• Molecule 78: 60S RIBOSOMAL PROTEIN L37A

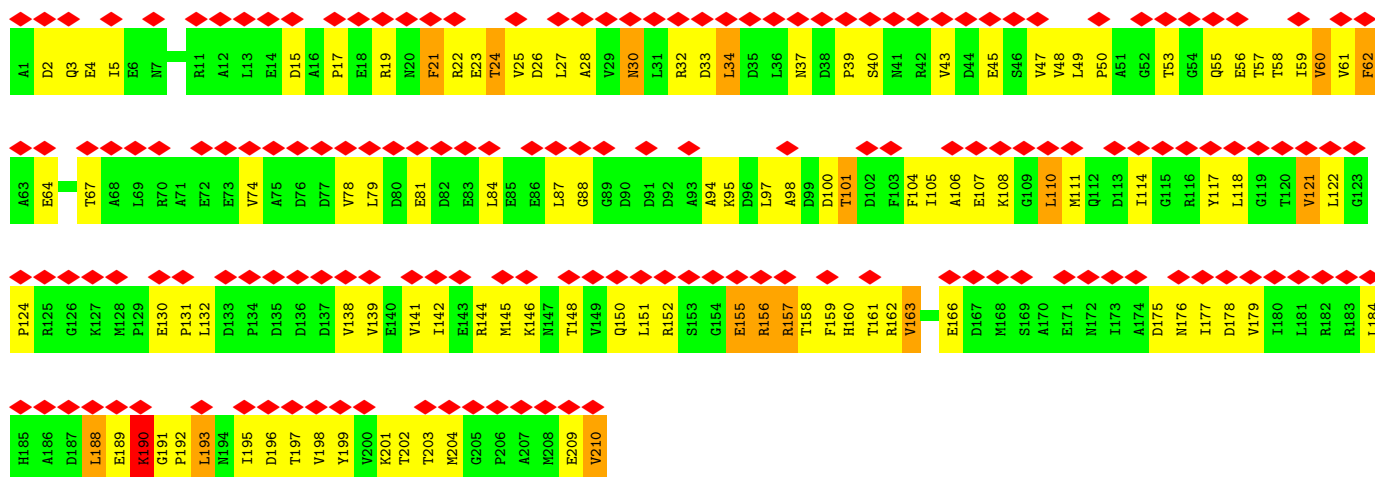
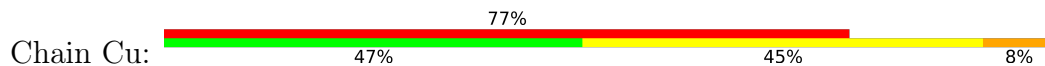


• Molecule 79: 60S RIBOSOMAL PROTEIN L28

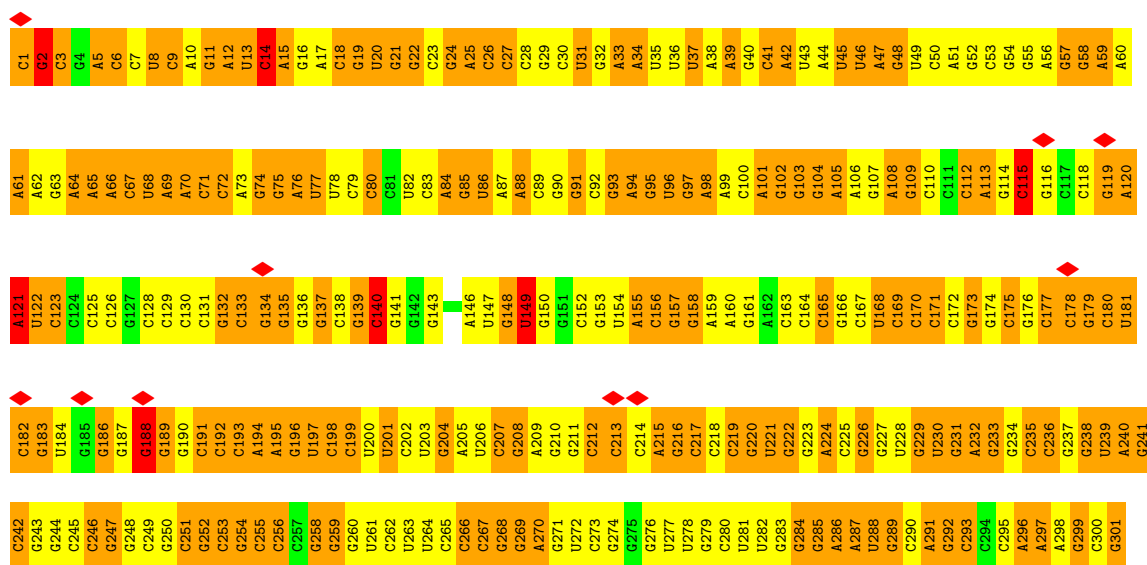




• Molecule 80: 60S RIBOSOMAL PROTEIN L10A



• Molecule 81: 28S Ribosomal RNA



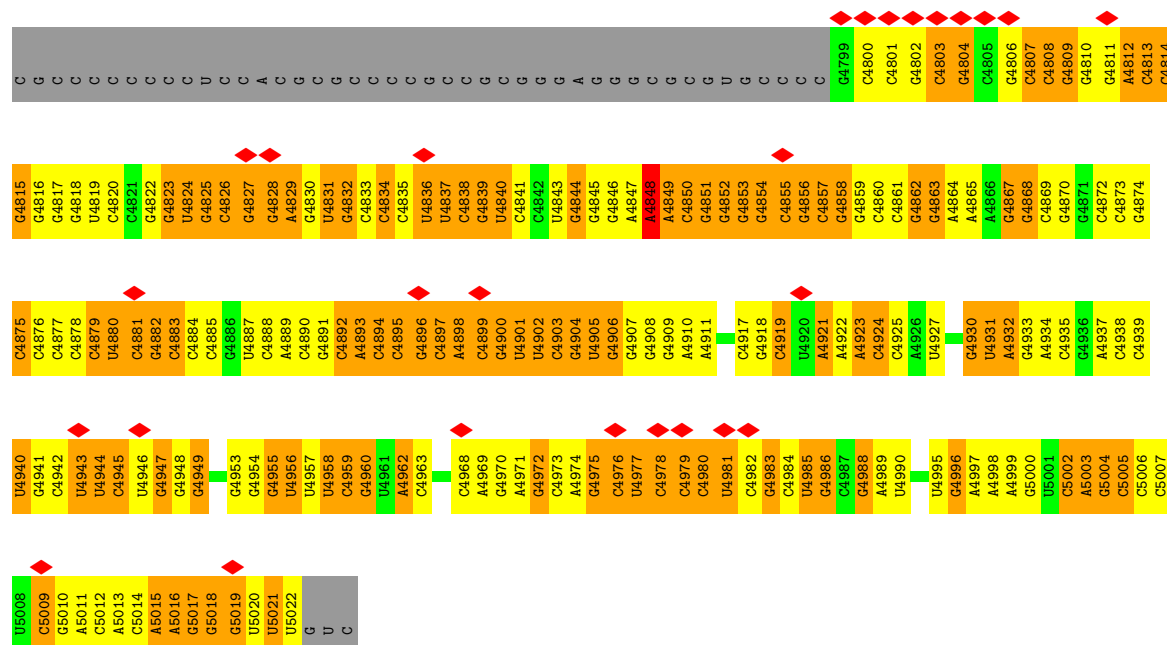




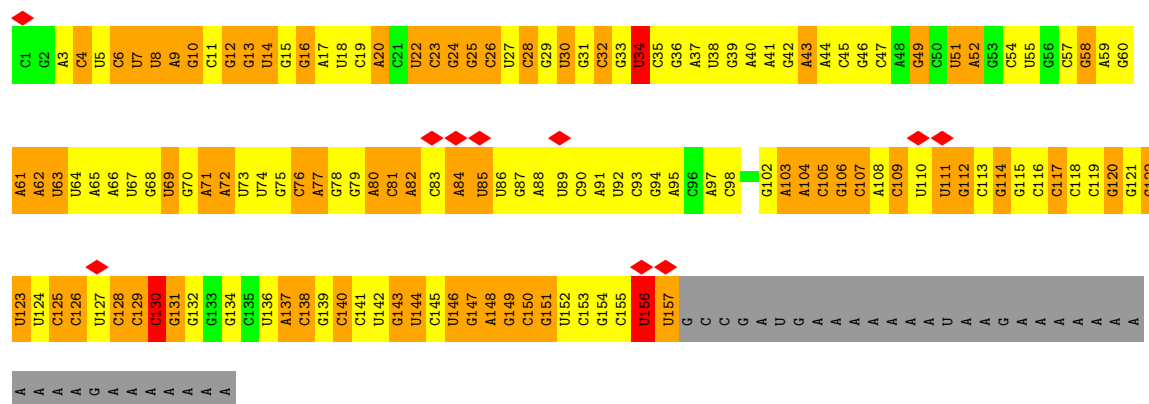




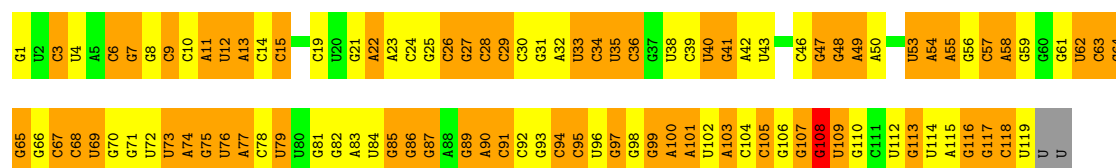




• Molecule 82: 5.8S Ribosomal RNA



• Molecule 83: 5S Ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	236113	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP	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)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	14.352	Depositor
Minimum map value	-4.787	Depositor
Average map value	0.195	Depositor
Map value standard deviation	0.958	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.26, 1.26, 1.26	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	AV	0.26	0/1809	0.57	0/2819
2	AW	0.29	0/1783	0.57	0/2776
3	AX	0.42	0/615	1.32	15/948 (1.6%)
4	B1	0.30	0/41550	0.66	11/64763 (0.0%)
5	BA	0.89	4/1756 (0.2%)	1.16	11/2386 (0.5%)
6	BB	0.83	0/1756	1.20	13/2350 (0.6%)
7	BC	0.69	0/1761	1.10	5/2379 (0.2%)
8	BD	0.63	0/1672	1.15	8/2250 (0.4%)
9	BE	0.72	0/2072	1.16	10/2793 (0.4%)
10	BF	0.68	0/1507	1.15	10/2026 (0.5%)
11	BG	0.77	1/1907 (0.1%)	1.22	11/2538 (0.4%)
12	BH	0.75	0/1558	1.26	12/2087 (0.6%)
13	BI	0.75	0/1724	1.12	6/2298 (0.3%)
14	BJ	0.74	0/1520	1.25	13/2030 (0.6%)
15	BK	0.76	0/815	1.10	5/1101 (0.5%)
16	BL	0.69	0/1220	1.16	8/1633 (0.5%)
17	BM	0.74	0/941	1.19	3/1264 (0.2%)
18	BN	0.68	0/1231	1.21	12/1656 (0.7%)
19	BO	0.73	0/1036	1.16	6/1391 (0.4%)
20	BP	0.66	0/1000	1.07	2/1335 (0.1%)
21	BQ	0.69	0/1125	1.10	3/1506 (0.2%)
22	BR	0.69	0/904	1.12	6/1208 (0.5%)
23	BS	0.69	0/1190	1.13	5/1594 (0.3%)
24	BT	0.68	0/1131	1.10	3/1515 (0.2%)
25	BU	0.75	0/813	1.17	3/1092 (0.3%)
26	BV	0.70	0/643	1.16	2/860 (0.2%)
27	BW	0.69	0/1050	1.12	6/1406 (0.4%)
28	BX	0.76	0/1063	1.11	1/1421 (0.1%)
29	BY	0.70	0/1019	1.12	5/1354 (0.4%)
30	BZ	0.68	0/611	1.14	3/820 (0.4%)
31	Ba	0.78	0/778	1.19	7/1041 (0.7%)
32	Bb	0.70	0/637	1.09	2/854 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bc	0.71	0/492	1.15	5/657 (0.8%)
34	Bd	0.74	0/454	1.10	1/603 (0.2%)
35	Be	0.70	0/417	1.09	0/548
36	Bf	0.76	0/507	1.33	5/673 (0.7%)
37	Bg	0.69	0/2497	1.06	7/3399 (0.2%)
38	CA	0.68	1/1926 (0.1%)	1.09	3/2583 (0.1%)
39	CB	0.72	2/3258 (0.1%)	1.12	10/4361 (0.2%)
40	CC	0.76	1/2943 (0.0%)	1.16	18/3953 (0.5%)
41	CD	0.78	6/2406 (0.2%)	1.11	12/3221 (0.4%)
42	CE	0.81	1/1311 (0.1%)	1.17	9/1763 (0.5%)
43	CF	0.68	0/1985	1.12	10/2644 (0.4%)
44	CG	0.75	1/1914 (0.1%)	1.19	14/2578 (0.5%)
45	CH	0.64	0/1554	1.10	4/2089 (0.2%)
46	CI	0.68	0/1642	1.15	13/2194 (0.6%)
47	CJ	0.78	0/1385	1.18	9/1852 (0.5%)
48	CL	0.82	6/1647 (0.4%)	1.18	14/2205 (0.6%)
49	CM	0.79	1/1162 (0.1%)	1.12	1/1556 (0.1%)
50	CN	0.68	0/1753	1.07	10/2348 (0.4%)
51	CO	0.72	2/1639 (0.1%)	1.15	11/2193 (0.5%)
52	CP	0.67	1/1260 (0.1%)	1.09	2/1691 (0.1%)
53	CQ	0.70	0/1517	1.15	8/2026 (0.4%)
54	CR	0.66	1/1542 (0.1%)	1.08	6/2037 (0.3%)
55	CS	0.70	0/1478	1.19	15/1985 (0.8%)
56	CT	0.74	0/1325	1.21	14/1770 (0.8%)
57	CU	0.74	1/841 (0.1%)	1.16	8/1128 (0.7%)
58	CV	0.69	1/977 (0.1%)	1.03	0/1312
59	CW	0.64	1/542 (0.2%)	0.98	2/722 (0.3%)
60	CX	0.65	0/992	1.12	3/1334 (0.2%)
61	CY	0.74	1/1082 (0.1%)	1.17	5/1441 (0.3%)
62	CZ	0.74	0/1137	1.25	5/1517 (0.3%)
63	Ca	0.72	0/1190	1.11	4/1591 (0.3%)
64	Cb	0.72	1/570 (0.2%)	1.10	1/752 (0.1%)
65	Cc	0.71	1/813 (0.1%)	1.05	3/1091 (0.3%)
66	Cd	0.70	0/919	1.06	2/1238 (0.2%)
67	Ce	0.71	1/1071 (0.1%)	1.12	5/1428 (0.4%)
68	Cf	0.75	1/884 (0.1%)	1.22	10/1185 (0.8%)
69	Cg	0.74	1/917 (0.1%)	1.15	4/1222 (0.3%)
70	Ch	0.63	0/1022	1.03	1/1351 (0.1%)
71	Ci	0.70	1/793 (0.1%)	1.18	6/1048 (0.6%)
72	Cj	0.77	1/704 (0.1%)	1.16	4/931 (0.4%)
73	Ck	0.72	0/574	1.18	4/761 (0.5%)
74	Cl	0.66	0/453	1.04	2/599 (0.3%)
75	Cm	0.68	0/434	1.22	3/575 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Cn	0.61	0/240	0.85	0/305
77	Co	0.70	0/884	1.14	4/1166 (0.3%)
78	Cp	0.63	0/717	0.97	1/953 (0.1%)
79	Ct	0.78	1/1058 (0.1%)	1.22	7/1416 (0.5%)
80	Cu	0.69	0/1638	1.12	6/2222 (0.3%)
81	A2	0.34	12/86672 (0.0%)	0.66	28/135198 (0.0%)
82	A3	0.30	0/3723	0.62	2/5800 (0.0%)
83	A4	0.31	0/2836	0.67	1/4421 (0.0%)
All	All	0.52	52/231894 (0.0%)	0.87	529/341130 (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
3	AX	1	0
4	B1	0	23
81	A2	0	35
82	A3	0	2
All	All	1	60

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	A2	1701	C	O5'-C5'	16.74	1.67	1.42
81	A2	1701	C	C5'-C4'	14.78	1.73	1.51
81	A2	1673	C	C3'-O3'	13.66	1.63	1.43
81	A2	1673	C	O3'-P	11.31	1.78	1.61
81	A2	1673	C	O5'-C5'	10.37	1.58	1.42

The worst 5 of 529 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	A2	1701	C	C2'-C3'-O3'	-18.42	86.07	113.70
81	A2	1701	C	C4'-C3'-O3'	16.21	137.32	113.00
81	A2	1701	C	O4'-C4'-C3'	-15.19	88.81	104.00
3	AX	58	U	P-O5'-C5'	13.52	141.18	120.90
3	AX	58	U	C4'-C3'-O3'	12.43	131.65	113.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	AX	58	U	C3'

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B1	111	A	Sidechain
4	B1	216	C	Sidechain
4	B1	44	U	Sidechain
4	B1	77	A	Sidechain
4	B1	84	A	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	AV	1619	0	820	143	0
2	AW	1626	0	826	194	0
3	AX	560	0	281	168	0
4	B1	37159	0	18778	4029	0
5	BA	1719	0	1717	135	0
6	BB	1729	0	1803	146	0
7	BC	1724	0	1808	74	0
8	BD	1646	0	1737	96	0
9	BE	2031	0	2138	119	0
10	BF	1486	0	1540	159	0
11	BG	1884	0	2044	155	0
12	BH	1535	0	1632	134	0
13	BI	1695	0	1785	168	0
14	BJ	1495	0	1615	95	0
15	BK	791	0	811	54	0
16	BL	1199	0	1269	73	0
17	BM	931	0	961	45	0
18	BN	1207	0	1292	87	0
19	BO	1023	0	1049	73	0
20	BP	981	0	1026	56	0
21	BQ	1108	0	1172	97	0
22	BR	893	0	946	65	0
23	BS	1172	0	1229	81	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	BT	1112	0	1146	114	0
25	BU	803	0	866	80	0
26	BV	636	0	637	45	0
27	BW	1033	0	1080	68	0
28	BX	1046	0	1110	69	0
29	BY	1002	0	1075	65	0
30	BZ	605	0	665	54	0
31	Ba	767	0	816	125	0
32	Bb	625	0	642	39	0
33	Bc	490	0	520	36	0
34	Bd	444	0	442	54	0
35	Be	412	0	463	34	0
36	Bf	497	0	497	33	0
37	Bg	2440	0	2396	118	0
38	CA	1888	0	1983	143	0
39	CB	3190	0	3327	189	0
40	CC	2889	0	3064	272	0
41	CD	2361	0	2385	141	0
42	CE	1286	0	1398	159	0
43	CF	1949	0	2093	140	0
44	CG	1881	0	2018	123	0
45	CH	1535	0	1611	105	0
46	CI	1604	0	1652	65	0
47	CJ	1362	0	1399	101	0
48	CL	1617	0	1725	117	0
49	CM	1139	0	1204	127	0
50	CN	1708	0	1761	89	0
51	CO	1607	0	1745	127	0
52	CP	1234	0	1263	72	0
53	CQ	1493	0	1612	100	0
54	CR	1526	0	1682	119	0
55	CS	1438	0	1472	88	0
56	CT	1297	0	1366	115	0
57	CU	827	0	852	22	0
58	CV	963	0	1026	42	0
59	CW	529	0	541	32	0
60	CX	975	0	1053	47	0
61	CY	1065	0	1145	87	0
62	CZ	1114	0	1194	102	0
63	Ca	1161	0	1213	82	0
64	Cb	560	0	590	42	0
65	Cc	802	0	844	77	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
66	Cd	904	0	947	28	0
67	Ce	1053	0	1144	50	0
68	Cf	865	0	904	99	0
69	Cg	907	0	1002	101	0
70	Ch	1014	0	1148	47	0
71	Ci	783	0	862	53	0
72	Cj	690	0	719	56	0
73	Ck	568	0	637	31	0
74	Cl	443	0	483	14	0
75	Cm	428	0	466	25	0
76	Cn	239	0	285	62	0
77	Co	870	0	943	62	0
78	Cp	707	0	760	44	0
79	Ct	1043	0	1120	124	0
80	Cu	1621	0	1563	158	0
81	A2	77488	0	39155	7802	0
82	A3	3334	0	1693	298	0
83	A4	2538	0	1286	250	0
All	All	215620	0	158969	16755	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 45.

The worst 5 of 16755 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)
4:B1:1183:A:H5'	76:Cn:11:ARG:CZ	1.29	1.62
3:AX:45:U:C2	4:B1:1207:G:C2	1.88	1.61
2:AW:19:G:C8	81:A2:3927:G:H1'	1.13	1.59
3:AX:45:U:C2	4:B1:1207:G:N2	1.69	1.58
13:BI:123:ARG:CZ	81:A2:4979:C:H5''	1.25	1.58

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
5	BA	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	14	51
6	BB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	9
7	BC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	5	28
8	BD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	4	27
9	BE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6	31
10	BF	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	1	15
11	BG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	2	19
12	BH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	5	30
13	BI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	21
14	BJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	7	36
15	BK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	10
16	BL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	2	17
17	BM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	1	15
18	BN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	21
19	BO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	5	29
20	BP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	17
21	BQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	8	40
22	BR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	6	32
23	BS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	14
24	BT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	9	40
25	BU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	12	48
26	BV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	4	26
27	BW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	7	38
28	BX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	1	15
29	BY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	3	21
30	BZ	74/125 (59%)	71 (96%)	0	3 (4%)	2	18
31	Ba	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	17
32	Bb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
33	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	21
34	Bd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Be	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	6	31
36	Bf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
37	Bg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	5	29
38	CA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	10	44
39	CB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	2	20
40	CC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	2	18
41	CD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	7	36
42	CE	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	2	17
43	CF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	7	36
44	CG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	2	19
45	CH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	7	38
46	CI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	7	38
47	CJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	11
48	CL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	1	14
49	CM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	9	40
50	CN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40
51	CO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	8	40
52	CP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	31
53	CQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	3	21
54	CR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	7	36
55	CS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	20
56	CT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	6	32
57	CU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
58	CV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	7	38
59	CW	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
60	CX	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
61	CY	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	4	27
62	CZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	3	23
63	Ca	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	21
64	Cb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	13
65	Cc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	6	31

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	Cd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	51
67	Ce	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	4	27
68	Cf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	16
69	Cg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	20
70	Ch	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	4	26
71	Ci	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	13
72	Cj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	4	27
73	Ck	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	8	40
74	Cl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	30
75	Cm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
76	Cn	23/25 (92%)	23 (100%)	0	0	100	100
77	Co	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	6	32
78	Cp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	21
79	Ct	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	1	14
80	Cu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	9	40
All	All	11190/12898 (87%)	10477 (94%)	390 (4%)	323 (3%)	5	23

5 of 323 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	BB	76	ASN
6	BB	132	GLY
6	BB	148	ASN
6	BB	154	SER
6	BB	176	VAL

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	
5	BA	181/243 (74%)	177 (98%)	4 (2%)	45	64

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	BB	194/231 (84%)	182 (94%)	12 (6%)	16	38
7	BC	188/225 (84%)	179 (95%)	9 (5%)	23	44
8	BD	175/202 (87%)	164 (94%)	11 (6%)	16	37
9	BE	220/225 (98%)	207 (94%)	13 (6%)	18	39
10	BF	158/170 (93%)	152 (96%)	6 (4%)	29	50
11	BG	202/218 (93%)	196 (97%)	6 (3%)	36	57
12	BH	171/174 (98%)	170 (99%)	1 (1%)	78	83
13	BI	179/180 (99%)	167 (93%)	12 (7%)	15	36
14	BJ	160/168 (95%)	152 (95%)	8 (5%)	22	43
15	BK	85/136 (62%)	81 (95%)	4 (5%)	23	45
16	BL	133/142 (94%)	130 (98%)	3 (2%)	44	64
17	BM	102/108 (94%)	96 (94%)	6 (6%)	18	39
18	BN	130/131 (99%)	128 (98%)	2 (2%)	57	72
19	BO	107/119 (90%)	99 (92%)	8 (8%)	12	33
20	BP	107/130 (82%)	103 (96%)	4 (4%)	30	51
21	BQ	115/121 (95%)	111 (96%)	4 (4%)	32	53
22	BR	99/122 (81%)	92 (93%)	7 (7%)	13	35
23	BS	123/132 (93%)	115 (94%)	8 (6%)	15	37
24	BT	113/115 (98%)	106 (94%)	7 (6%)	16	38
25	BU	93/107 (87%)	87 (94%)	6 (6%)	15	37
26	BV	67/67 (100%)	67 (100%)	0	100	100
27	BW	112/113 (99%)	108 (96%)	4 (4%)	31	52
28	BX	108/115 (94%)	104 (96%)	4 (4%)	30	51
29	BY	107/115 (93%)	100 (94%)	7 (6%)	15	37
30	BZ	67/103 (65%)	62 (92%)	5 (8%)	12	33
31	Ba	83/98 (85%)	76 (92%)	7 (8%)	10	30
32	Bb	72/76 (95%)	68 (94%)	4 (6%)	19	40
33	Bc	55/62 (89%)	52 (94%)	3 (6%)	19	41
34	Bd	47/49 (96%)	44 (94%)	3 (6%)	16	37
35	Be	42/48 (88%)	39 (93%)	3 (7%)	13	35
36	Bf	54/140 (39%)	51 (94%)	3 (6%)	19	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Bg	272/275 (99%)	260 (96%)	12 (4%)	25	47
38	CA	189/199 (95%)	182 (96%)	7 (4%)	30	51
39	CB	344/349 (99%)	322 (94%)	22 (6%)	16	37
40	CC	302/348 (87%)	283 (94%)	19 (6%)	16	37
41	CD	244/250 (98%)	237 (97%)	7 (3%)	37	58
42	CE	143/252 (57%)	133 (93%)	10 (7%)	14	35
43	CF	203/215 (94%)	195 (96%)	8 (4%)	28	49
44	CG	199/223 (89%)	190 (96%)	9 (4%)	24	46
45	CH	171/171 (100%)	165 (96%)	6 (4%)	32	53
46	CI	170/181 (94%)	161 (95%)	9 (5%)	20	41
47	CJ	143/149 (96%)	137 (96%)	6 (4%)	26	48
48	CL	167/177 (94%)	157 (94%)	10 (6%)	17	39
49	CM	118/161 (73%)	113 (96%)	5 (4%)	26	48
50	CN	172/172 (100%)	167 (97%)	5 (3%)	37	58
51	CO	168/174 (97%)	165 (98%)	3 (2%)	51	68
52	CP	133/163 (82%)	126 (95%)	7 (5%)	20	41
53	CQ	162/165 (98%)	157 (97%)	5 (3%)	35	56
54	CR	161/175 (92%)	151 (94%)	10 (6%)	16	38
55	CS	155/157 (99%)	149 (96%)	6 (4%)	28	49
56	CT	139/140 (99%)	135 (97%)	4 (3%)	37	58
57	CU	91/115 (79%)	91 (100%)	0	100	100
58	CV	100/107 (94%)	100 (100%)	0	100	100
59	CW	55/126 (44%)	52 (94%)	3 (6%)	19	41
60	CX	107/133 (80%)	105 (98%)	2 (2%)	50	67
61	CY	119/135 (88%)	114 (96%)	5 (4%)	26	48
62	CZ	118/118 (100%)	114 (97%)	4 (3%)	32	54
63	Ca	120/121 (99%)	115 (96%)	5 (4%)	26	48
64	Cb	58/126 (46%)	57 (98%)	1 (2%)	53	69
65	Cc	88/97 (91%)	87 (99%)	1 (1%)	65	76
66	Cd	100/110 (91%)	97 (97%)	3 (3%)	36	57
67	Ce	115/121 (95%)	111 (96%)	4 (4%)	32	53

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Cf	87/89 (98%)	77 (88%)	10 (12%)	5	18
69	Cg	98/100 (98%)	89 (91%)	9 (9%)	8	26
70	Ch	109/110 (99%)	105 (96%)	4 (4%)	30	51
71	Ci	82/89 (92%)	76 (93%)	6 (7%)	13	34
72	Cj	71/80 (89%)	69 (97%)	2 (3%)	38	60
73	Ck	64/65 (98%)	64 (100%)	0	100	100
74	Cl	47/48 (98%)	46 (98%)	1 (2%)	47	65
75	Cm	48/116 (41%)	45 (94%)	3 (6%)	16	37
76	Cn	24/24 (100%)	24 (100%)	0	100	100
77	Co	94/94 (100%)	90 (96%)	4 (4%)	26	47
78	Cp	74/75 (99%)	72 (97%)	2 (3%)	39	61
79	Ct	113/121 (93%)	108 (96%)	5 (4%)	25	47
80	Cu	177/177 (100%)	161 (91%)	16 (9%)	9	27
All	All	9763/10978 (89%)	9319 (96%)	444 (4%)	26	46

5 of 444 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	CC	150	LEU
80	Cu	210	VAL
46	CI	53	VAL
80	Cu	163	VAL
69	Cg	74	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 246 such sidechains are listed below:

Mol	Chain	Res	Type
40	CC	317	ASN
70	Ch	20	GLN
46	CI	177	ASN
69	Cg	3	GLN
77	Co	45	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AV	75/76 (98%)	37 (49%)	2 (2%)
2	AW	75/76 (98%)	33 (44%)	5 (6%)
3	AX	27/28 (96%)	15 (55%)	4 (14%)
4	B1	1738/1869 (92%)	1042 (59%)	152 (8%)
81	A2	3605/5025 (71%)	2052 (56%)	325 (9%)
82	A3	156/194 (80%)	81 (51%)	6 (3%)
83	A4	118/121 (97%)	69 (58%)	9 (7%)
All	All	5794/7389 (78%)	3329 (57%)	503 (8%)

5 of 3329 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AV	2	C
1	AV	5	G
1	AV	8	U
1	AV	11	C
1	AV	17	C

5 of 503 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	A2	947	G
81	A2	4596	U
81	A2	1619	C
81	A2	4533	G
81	A2	4848	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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$
2	MIA	AW	37	2	28,31,32	1.86	4 (14%)	38,44,47	2.41	8 (21%)

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
2	MIA	AW	37	2	-	6/15/33/34	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C13-C14	5.90	1.50	1.32
2	AW	37	MIA	C2-S10	4.42	1.79	1.75
2	AW	37	MIA	C12-C13	-2.87	1.33	1.47
2	AW	37	MIA	C5-C4	2.45	1.43	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AW	37	MIA	C11-S10-C2	11.37	110.78	102.25
2	AW	37	MIA	C12-C13-C14	-3.61	120.54	127.01
2	AW	37	MIA	C5-C6-N6	3.56	128.89	122.03
2	AW	37	MIA	C5-C4-N3	3.28	130.63	127.18
2	AW	37	MIA	C5-C4-N9	-2.87	102.69	105.81

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AW	37	MIA	N1-C2-S10-C11
2	AW	37	MIA	N3-C2-S10-C11
2	AW	37	MIA	O4'-C4'-C5'-O5'
2	AW	37	MIA	C3'-C4'-C5'-O5'
2	AW	37	MIA	N6-C12-C13-C14

There are no ring outliers.

1 monomer is involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AW	37	MIA	44	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

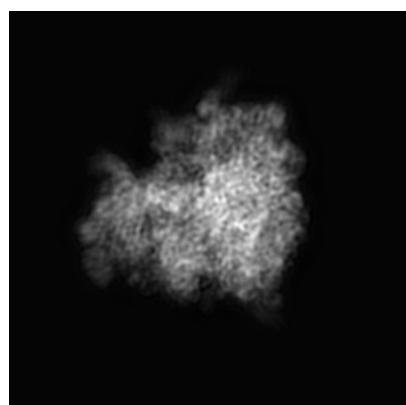
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2620. These allow visual inspection of the internal detail of the map and identification of artifacts.

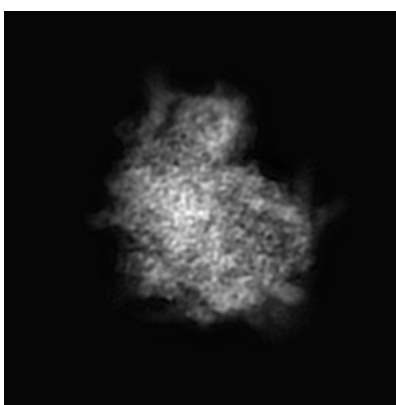
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

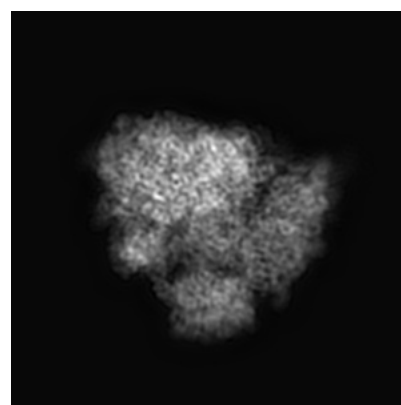
6.1.1 Primary map



X



Y

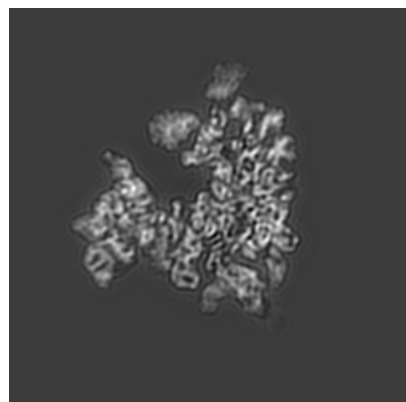


Z

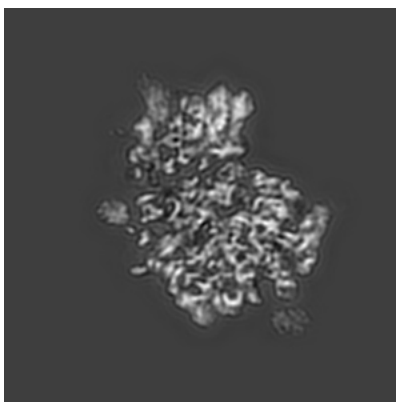
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

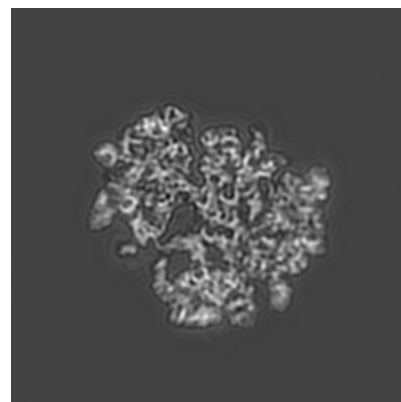
6.2.1 Primary map



X Index: 180



Y Index: 180

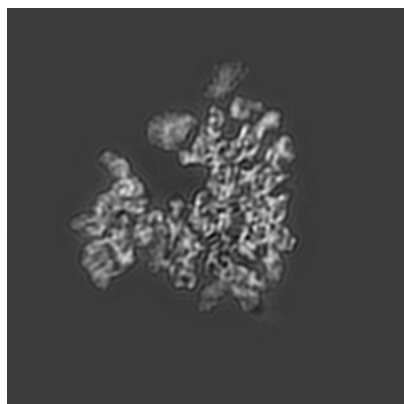


Z Index: 180

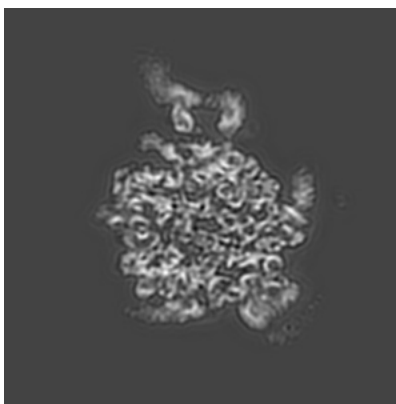
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

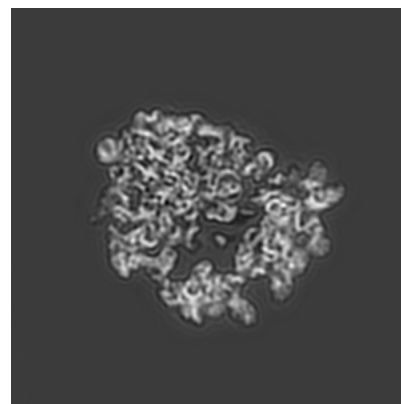
6.3.1 Primary map



X Index: 182



Y Index: 217

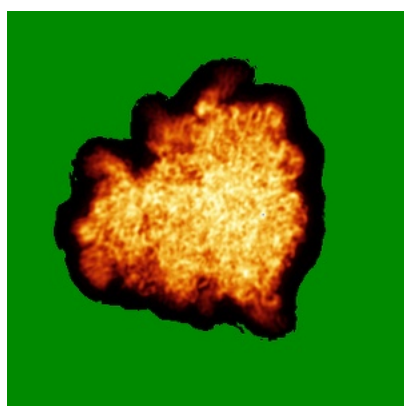


Z Index: 190

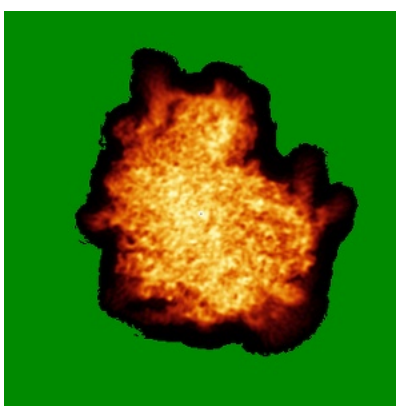
The images above show the largest variance slices of the map in three orthogonal directions.

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

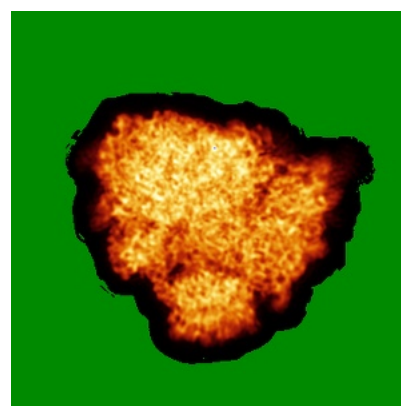
6.4.1 Primary map



X



Y

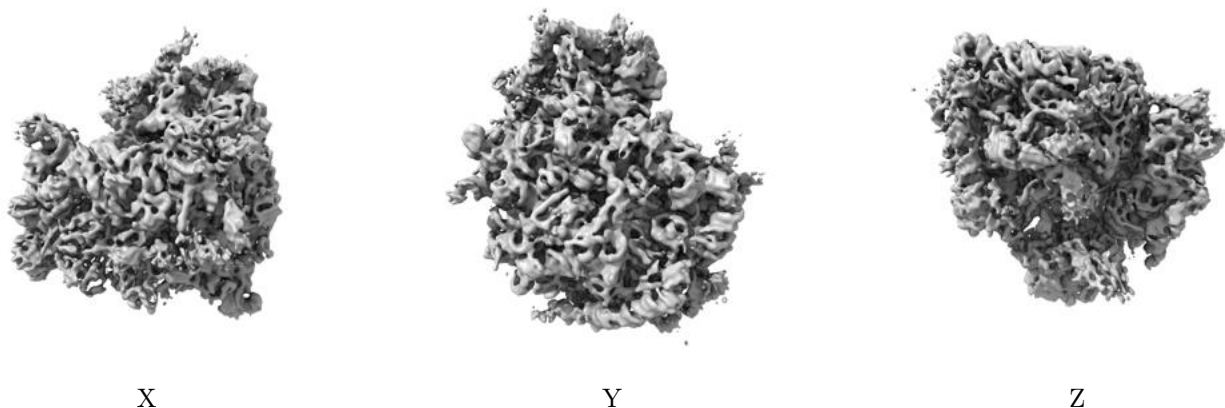


Z

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

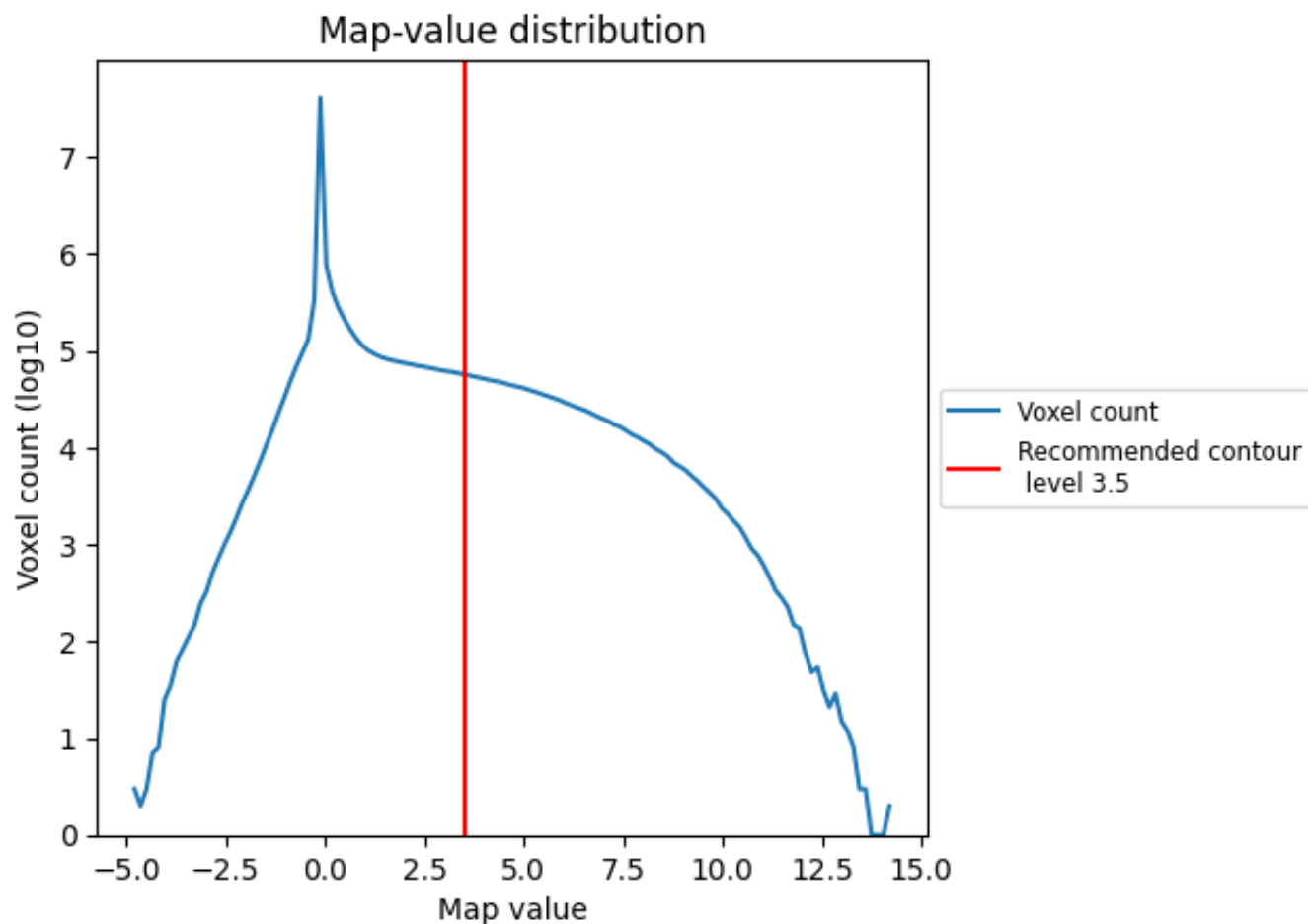
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

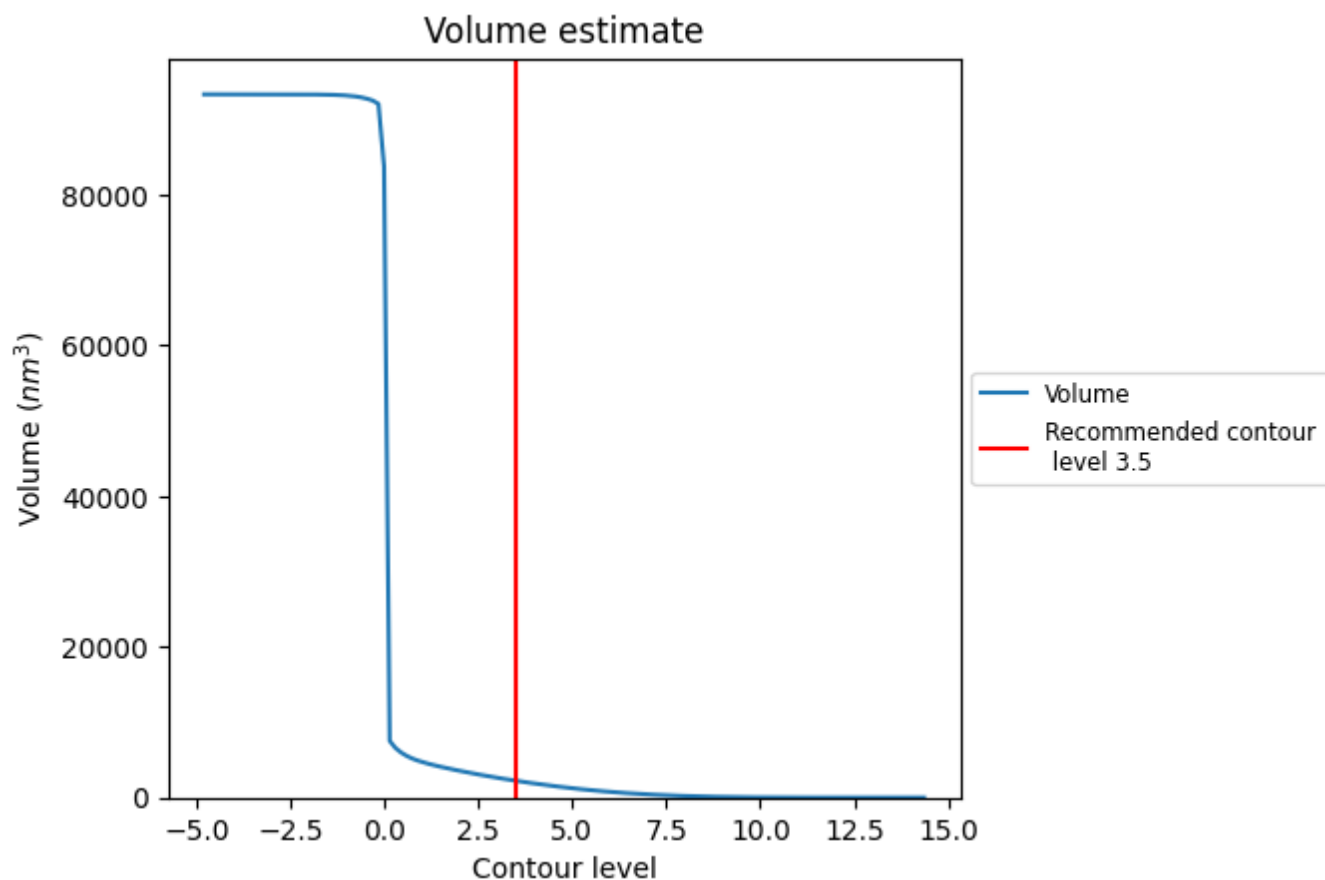
This section contains the results of statistical analysis of the map.

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.

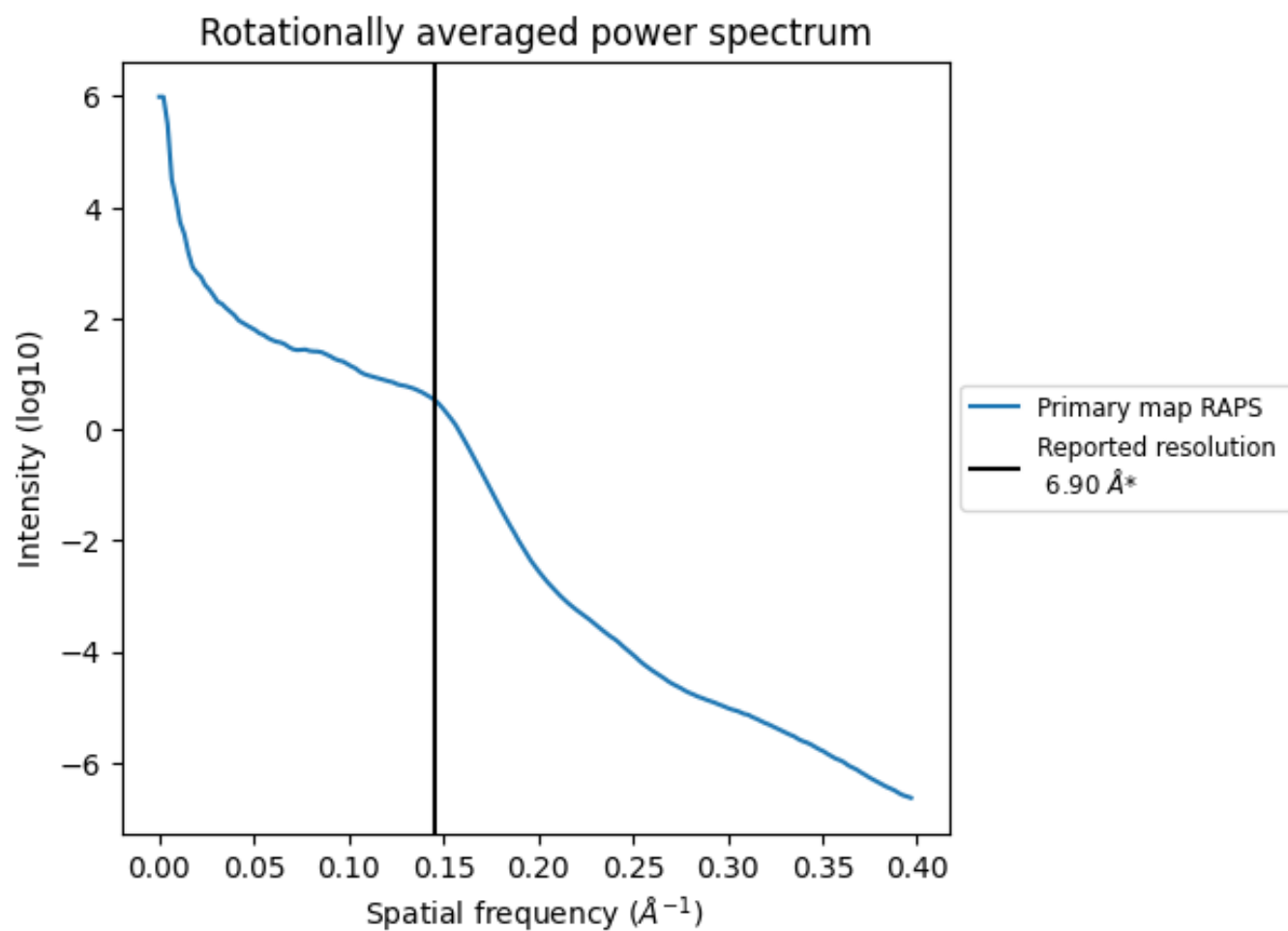
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2230 nm³; this corresponds to an approximate mass of 2014 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 0.145 Å⁻¹

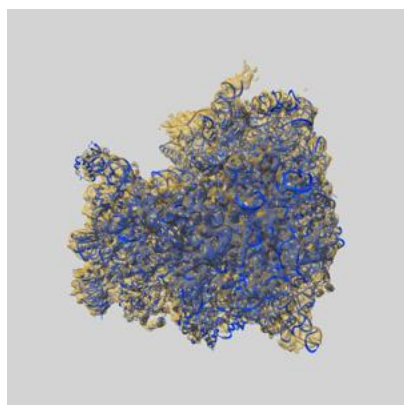
8 Fourier-Shell correlation

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

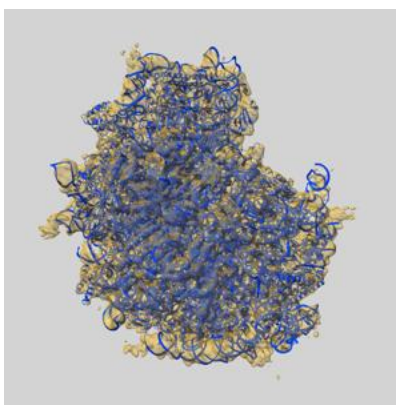
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2620 and PDB model 4UJE. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

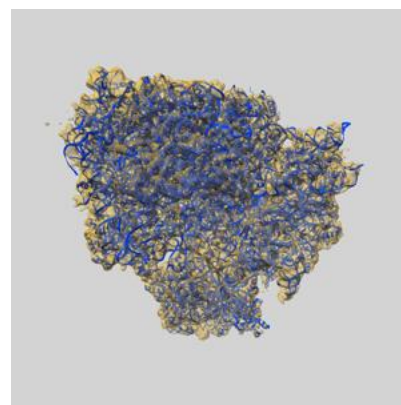
9.1 Map-model overlay [i](#)



X



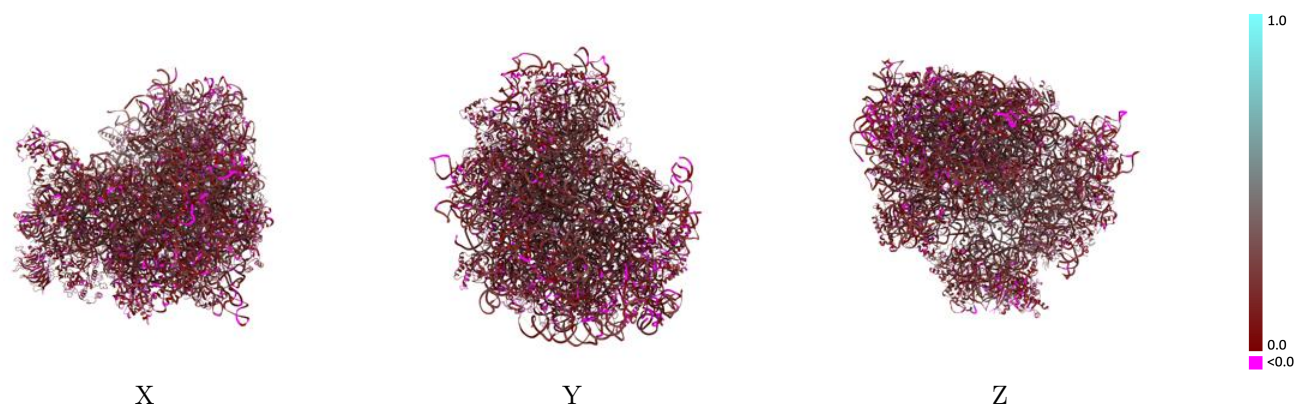
Y



Z

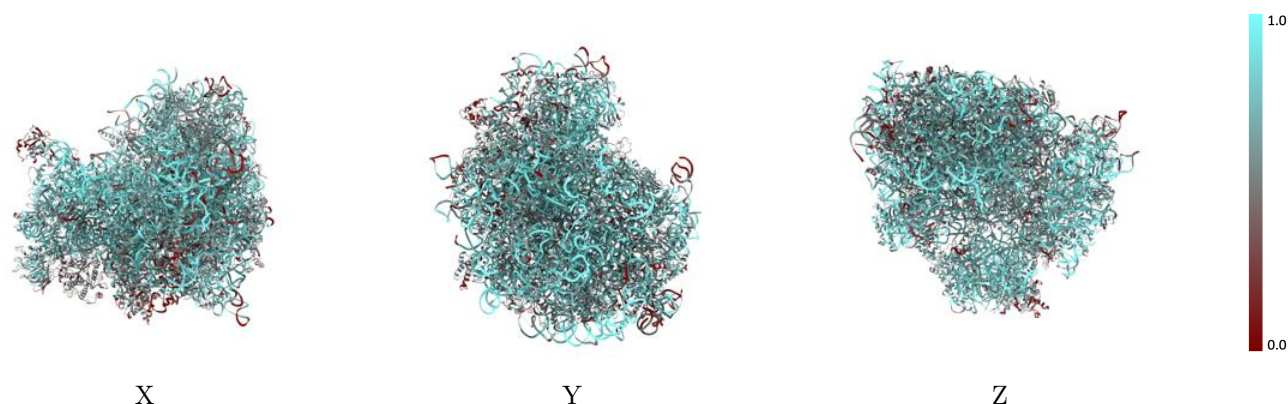
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



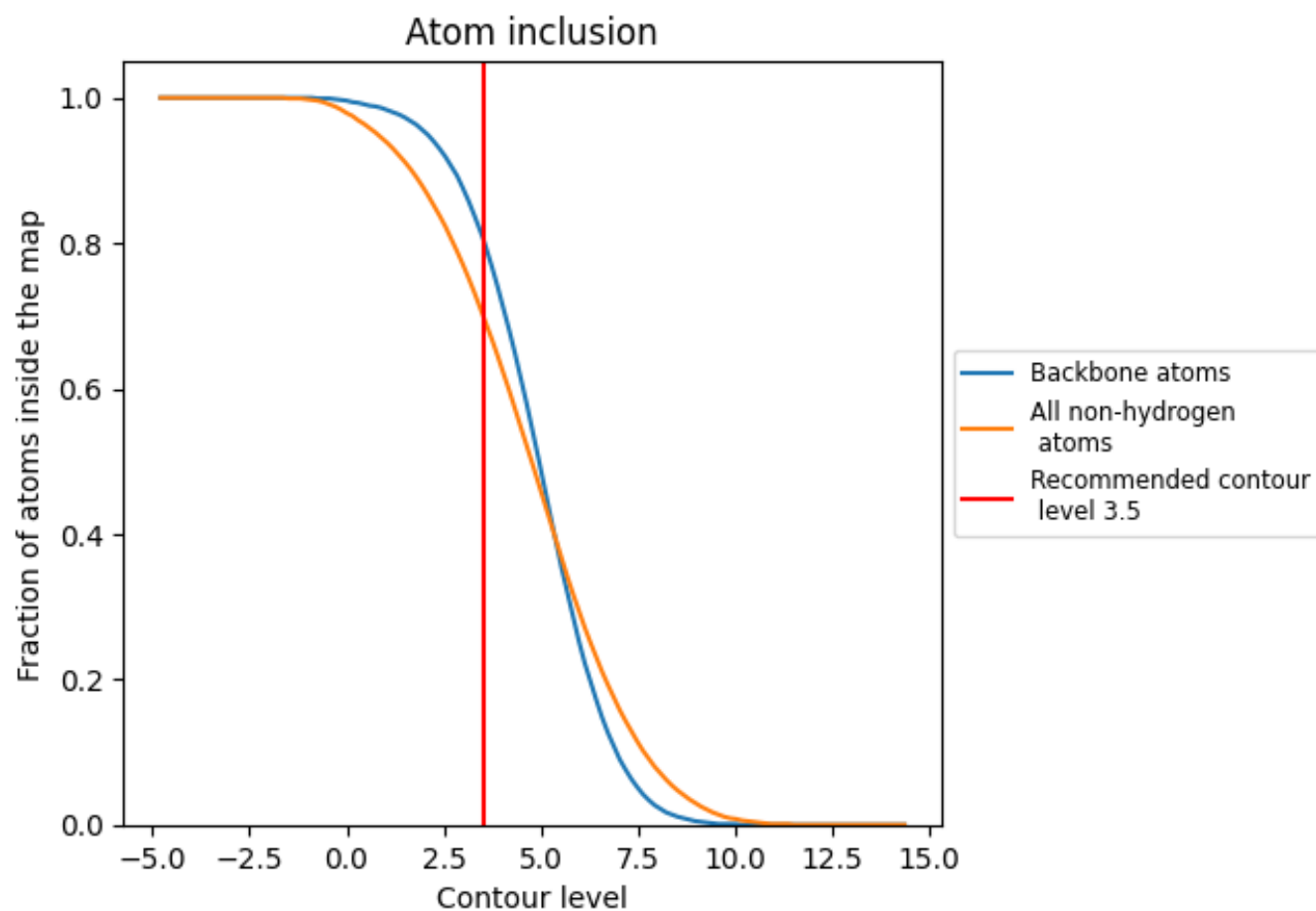
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 81% of all backbone atoms, 70% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7020	 0.1710
A2	 0.8020	 0.1990
A3	 0.8340	 0.2060
A4	 0.9340	 0.2240
AV	 0.6980	 0.1980
AW	 0.6540	 0.1800
AX	 0.4390	 0.1920
B1	 0.8420	 0.1980
BA	 0.4630	 0.1340
BB	 0.5470	 0.1440
BC	 0.5270	 0.1500
BD	 0.6230	 0.1450
BE	 0.6500	 0.1470
BF	 0.5930	 0.1430
BG	 0.6190	 0.1270
BH	 0.3620	 0.1240
BI	 0.4990	 0.1140
BJ	 0.6910	 0.1330
BK	 0.7040	 0.1420
BL	 0.4550	 0.1310
BM	 0.2750	 0.0910
BN	 0.5080	 0.1320
BO	 0.5350	 0.1440
BP	 0.6620	 0.1470
BQ	 0.6730	 0.1220
BR	 0.5190	 0.1350
BS	 0.6770	 0.1460
BT	 0.7490	 0.1450
BU	 0.6320	 0.1180
BV	 0.3920	 0.1150
BW	 0.5800	 0.1400
BX	 0.4420	 0.1450
BY	 0.6820	 0.1330
BZ	 0.5780	 0.1520
Ba	 0.4950	 0.0950



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bb	 0.5020	 0.1420
Bc	 0.4600	 0.1380
Bd	 0.7040	 0.1140
Be	 0.5570	 0.1360
Bf	 0.4330	 0.1020
Bg	 0.5610	 0.1360
CA	 0.4330	 0.1330
CB	 0.5870	 0.1480
CC	 0.5340	 0.1210
CD	 0.6800	 0.1550
CE	 0.5330	 0.1100
CF	 0.5170	 0.1280
CG	 0.5350	 0.1330
CH	 0.6210	 0.1420
CI	 0.5100	 0.1400
CJ	 0.6530	 0.1430
CL	 0.5210	 0.1100
CM	 0.6590	 0.1560
CN	 0.5560	 0.1340
CO	 0.5860	 0.1330
CP	 0.5710	 0.1350
CQ	 0.5110	 0.1140
CR	 0.5350	 0.1250
CS	 0.5890	 0.1320
CT	 0.5360	 0.1400
CU	 0.4760	 0.1410
CV	 0.4430	 0.1460
CW	 0.5120	 0.1220
CX	 0.5420	 0.1390
CY	 0.6350	 0.1300
CZ	 0.5900	 0.1460
Ca	 0.5490	 0.1380
Cb	 0.4760	 0.1260
Cc	 0.4840	 0.1410
Cd	 0.5750	 0.1500
Ce	 0.5050	 0.1580
Cf	 0.5560	 0.1140
Cg	 0.5160	 0.1320
Ch	 0.5660	 0.1230
Ci	 0.5600	 0.1380
Cj	 0.5560	 0.1160
Ck	 0.4860	 0.1230

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Cl	 0.4980	 0.1130
Cm	 0.5360	 0.1320
Cn	 0.4360	 0.1070
Co	 0.4360	 0.1130
Cp	 0.4440	 0.1140
Ct	 0.5290	 0.0840
Cu	 0.2250	 0.0560