



wwPDB EM Validation Summary Report ⓘ

Dec 10, 2022 – 12:35 pm GMT

PDB ID : 4UJE
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:

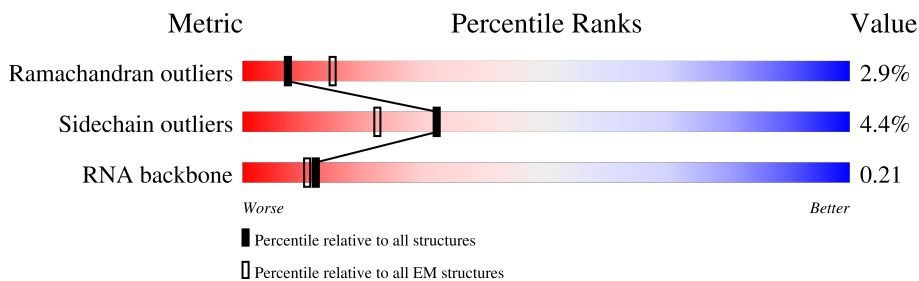
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
4	B1	1869	
5	BA	295	
6	BB	264	
7	BC	293	
8	BD	243	

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Mol	Chain	Length	Quality of chain
9	BE	263	10% 92% 6%
10	BF	204	20% 84% 8% 8%
11	BG	249	15% 87% 6% 7%
12	BH	194	52% 94% ...
13	BI	208	33% 91% 8%
14	BJ	194	9% 86% 7% 8%
15	BK	165	52% 5% 43%
16	BL	158	37% 87% 5% 8%
17	BM	132	58% 83% 7% 9%
18	BN	151	30% 95% ...
19	BO	151	26% 85% 5% 9%
20	BP	145	8% 75% 6% 19%
21	BQ	146	7% 91% 5%
22	BR	135	24% 76% 5% 19%
23	BS	152	9% 82% 11% 7%
24	BT	145	6% 92% 6%
25	BU	119	15% 81% 15%
26	BV	83	53% 96% .
27	BW	130	17% 94% 5%
28	BX	143	37% 85% 8% 6%
29	BY	133	9% 84% 8% 8%
30	BZ	125	11% 55% 6% 39%
31	Ba	115	30% 74% 9% 17%
32	Bb	84	27% 90% 5% 5%
33	Bc	69	29% 83% 7% 10%



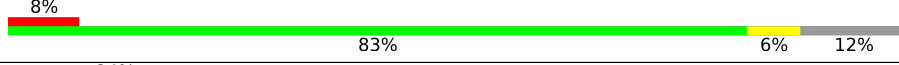
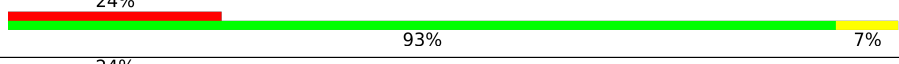
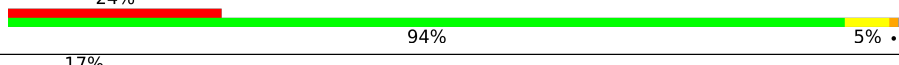

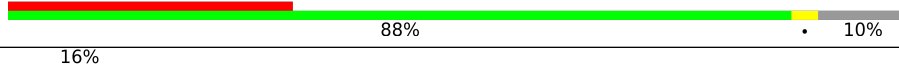

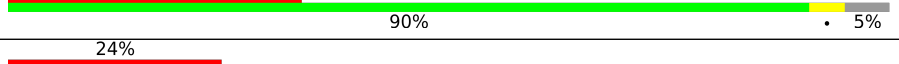


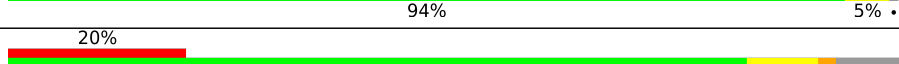
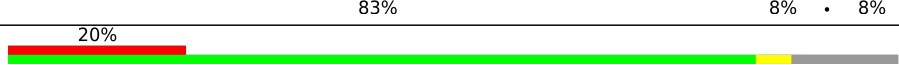
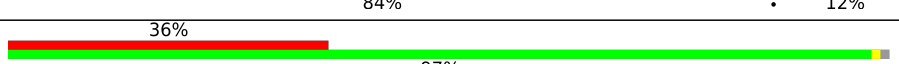
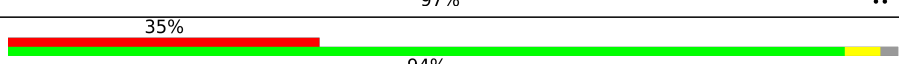
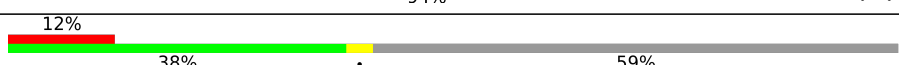
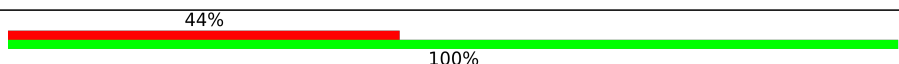
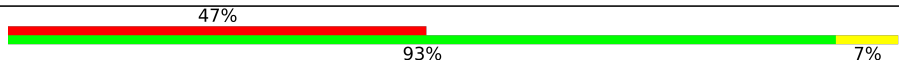
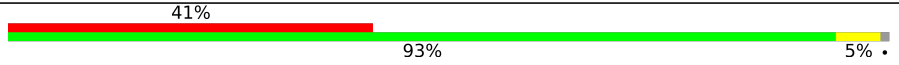

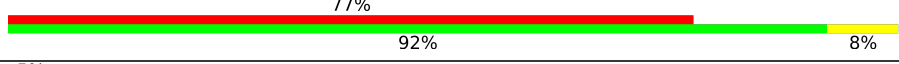
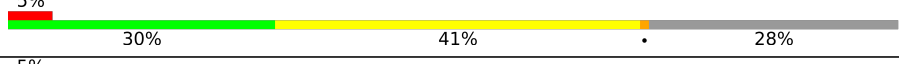

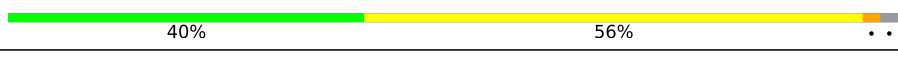

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Mol	Chain	Length	Quality of chain
34	Bd	56	9% 88% 7% 5%
35	Be	59	20% 81% 5% 14%
36	Bf	156	19% 37% 61%
37	Bg	317	28% 93% 5%
38	CA	257	48% 93% • •
39	CB	403	16% 90% 7% •
40	CC	427	21% 78% 6% • 15%
41	CD	297	8% 93% • •
42	CE	288	16% 50% 5% 45%
43	CF	248	26% 90% • 6%
44	CG	266	24% 83% 5% • 12%
45	CH	192	13% 95% 5%
46	CI	214	28% 86% 6% 8%
47	CJ	178	8% 85% 10% •
48	CL	211	30% 84% 9% • 5%
49	CM	215	9% 62% • 35%
50	CN	204	24% 98% •
51	CO	203	13% 94% • •
52	CP	184	11% 78% 5% 17%
53	CQ	188	30% 92% 6% •
54	CR	196	25% 86% 7% 7%
55	CS	176	19% 91% 7% •
56	CT	160	26% 95% • • •
57	CU	128	26% 77% • 20%
58	CV	140	36% 89% • 9%

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

2 Entry composition [i](#)

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
			Total	C	N	O	P		
1	AV	76	1619	723	290	531	75	0	0

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

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

- Molecule 3 is a RNA chain called Messenger RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
35	Be	51	412	258	90	63	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

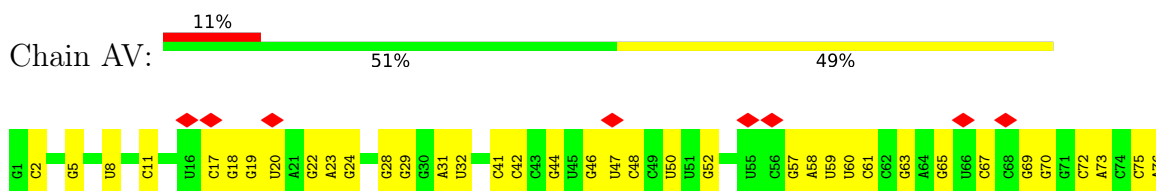
- Molecule 83 is a RNA chain called 5S Ribosomal RNA.

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

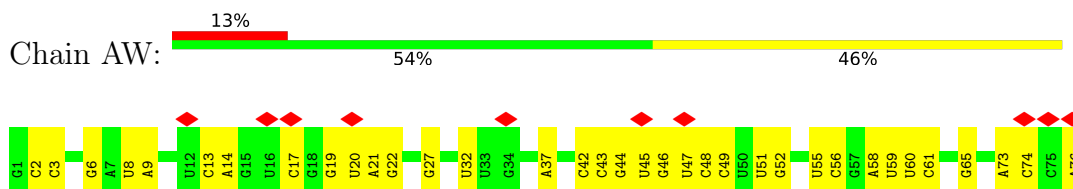
3 Residue-property plots [i](#)

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.

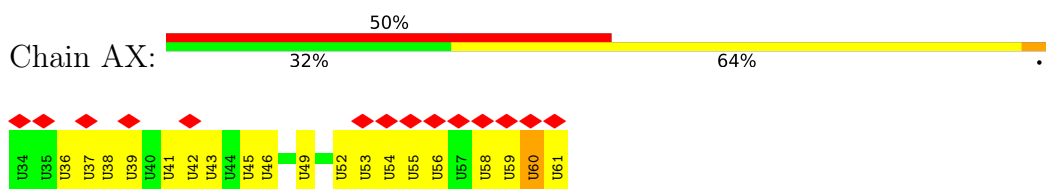
- Molecule 1: TRNA-LYS



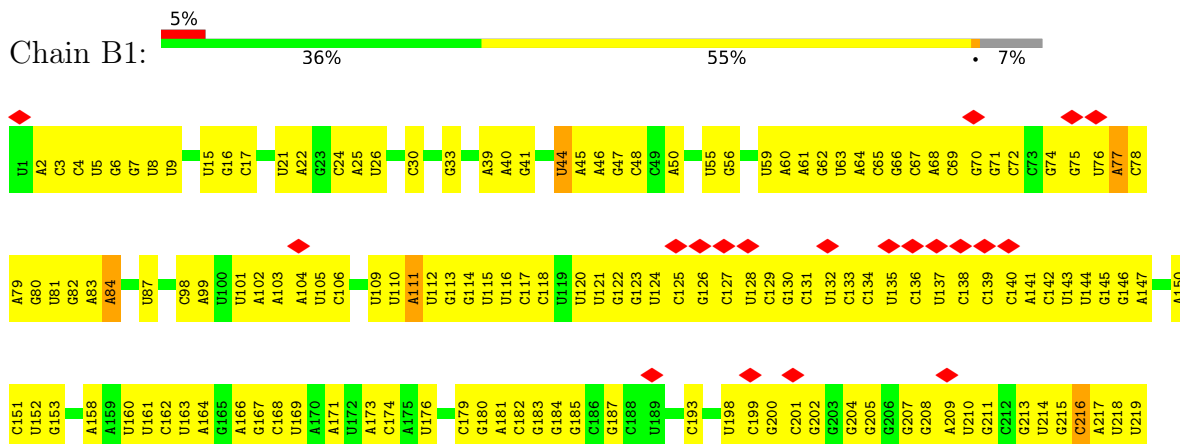
- Molecule 2: TRNA-PHE

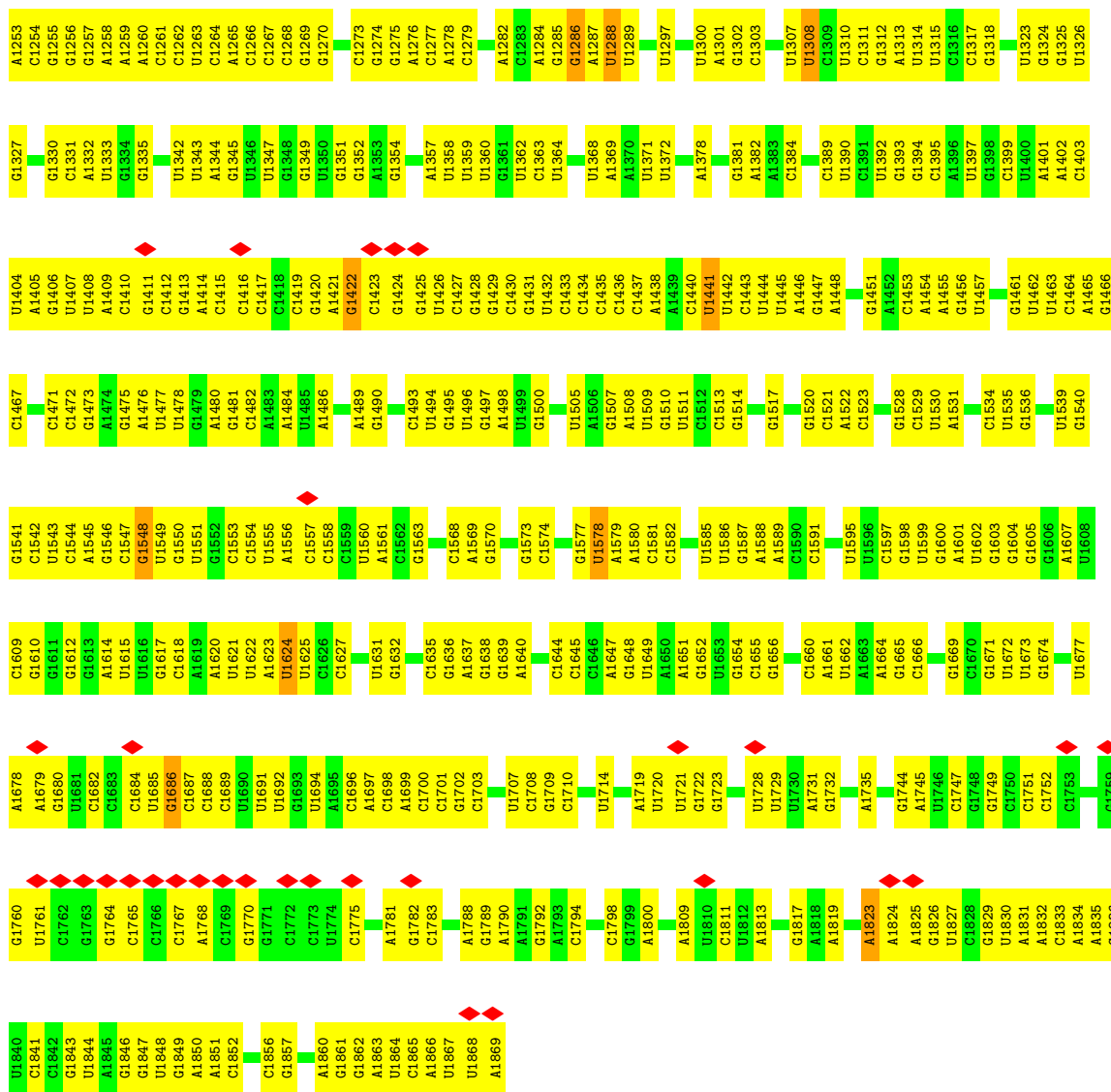


- Molecule 3: Messenger RNA

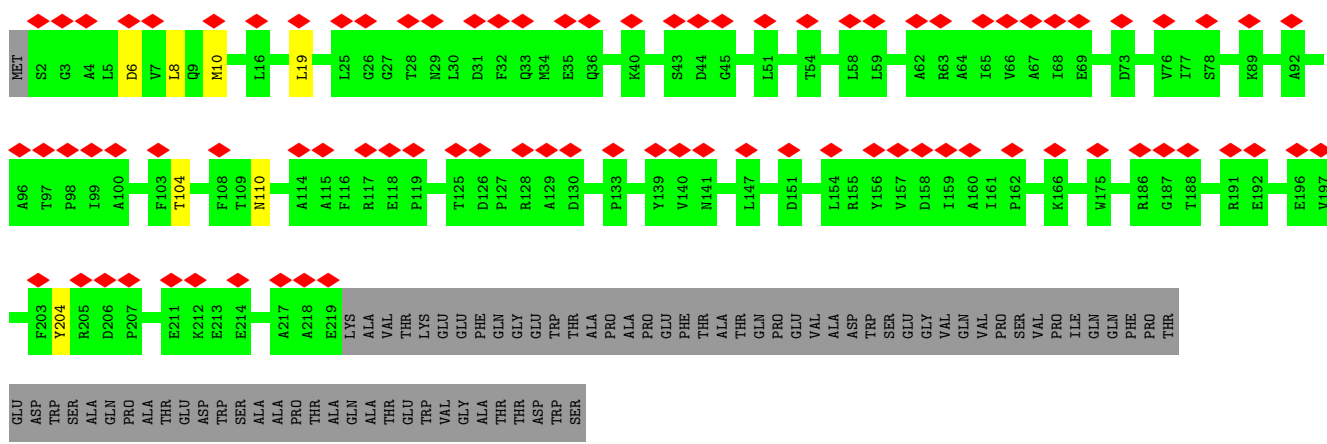
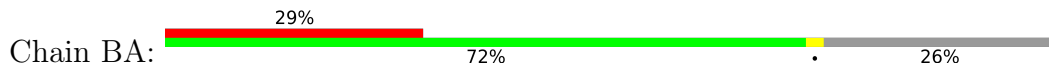


- Molecule 4: 18S Ribosomal RNA

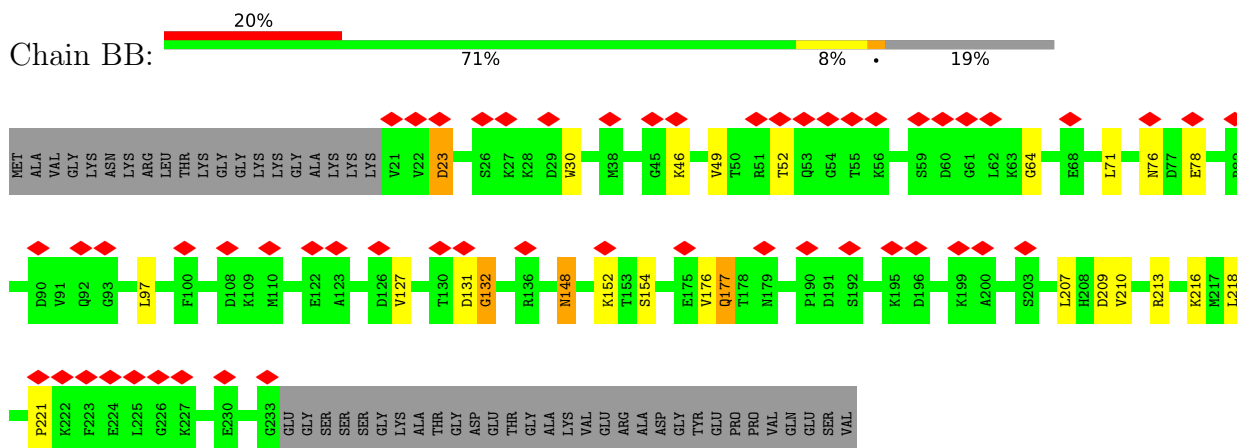




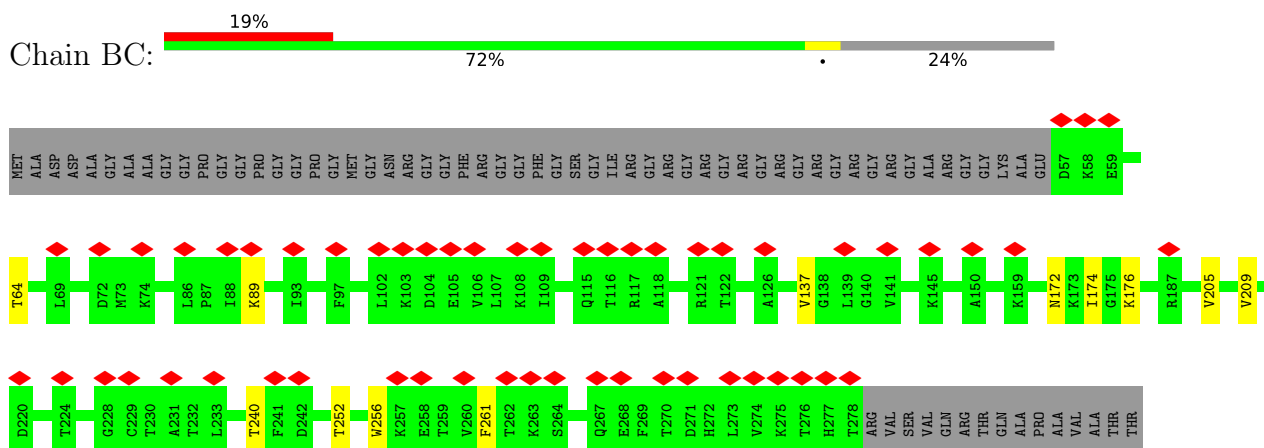
• Molecule 5: 40S RIBOSOMAL PROTEIN SA



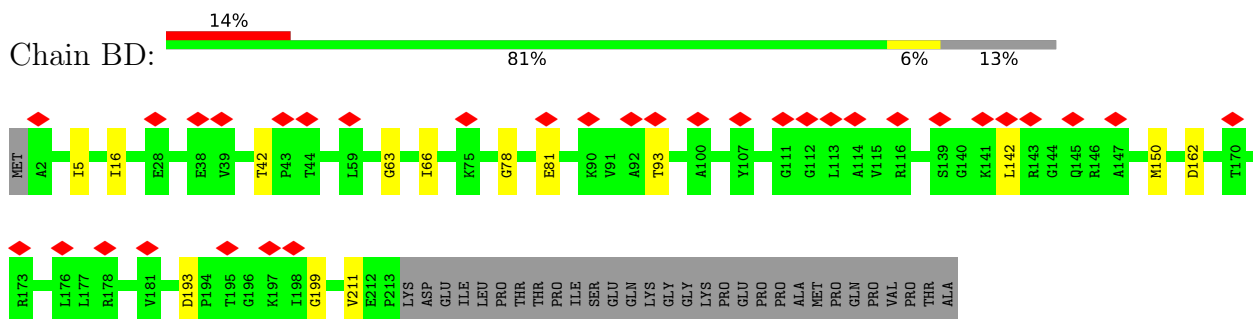
- Molecule 6: 40S RIBOSOMAL PROTEIN S3A



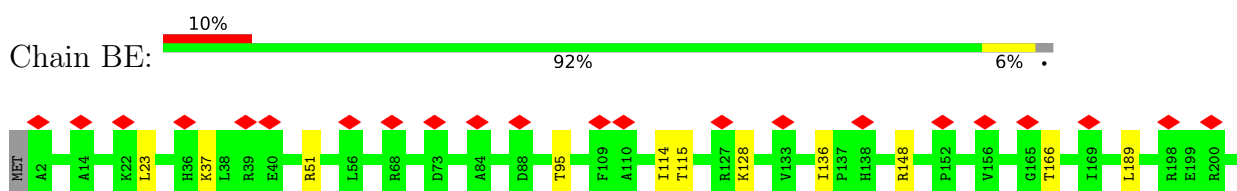
- Molecule 7: 40S RIBOSOMAL PROTEIN S2

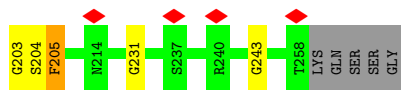


- Molecule 8: 40S RIBOSOMAL PROTEIN S3

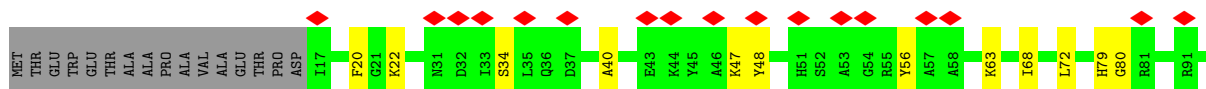
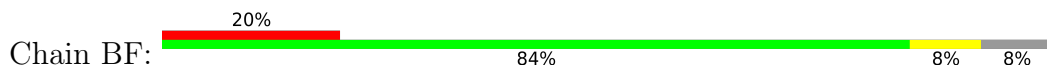


- Molecule 9: 40S RIBOSOMAL PROTEIN S4, Y ISOFORM 1

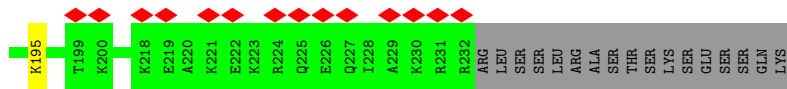
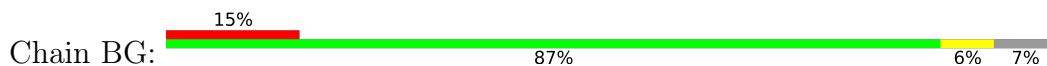




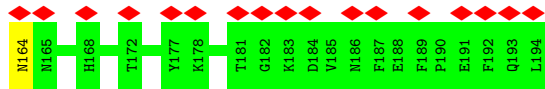
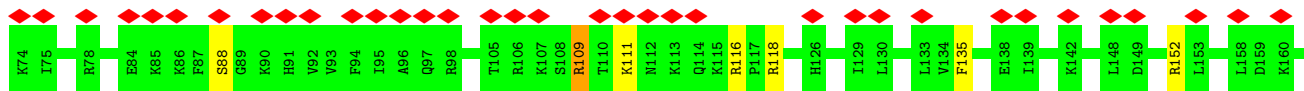
• Molecule 10: 40S RIBOSOMAL PROTEIN S5



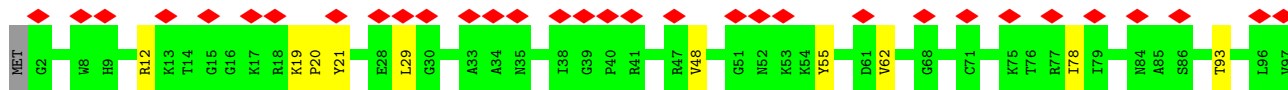
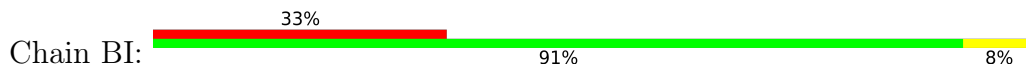
• Molecule 11: 40S RIBOSOMAL PROTEIN S6

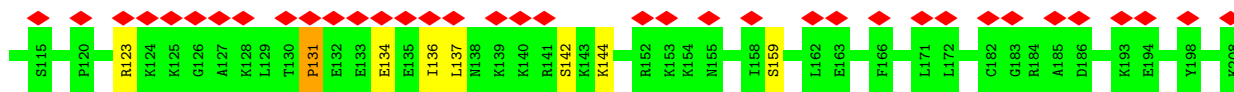


• Molecule 12: 40S RIBOSOMAL PROTEIN S7

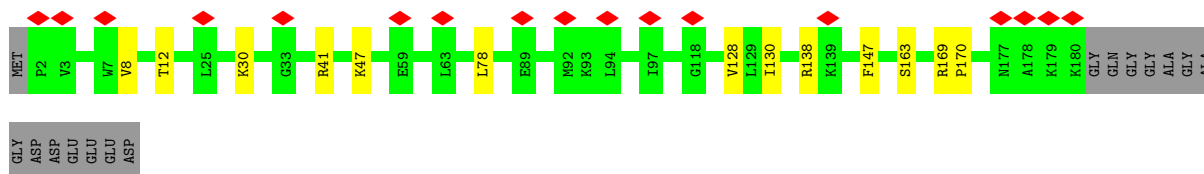
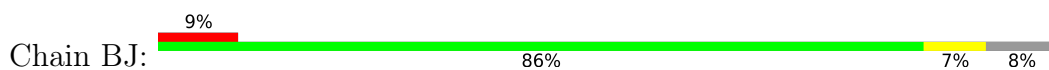


• Molecule 13: 40S RIBOSOMAL PROTEIN S8

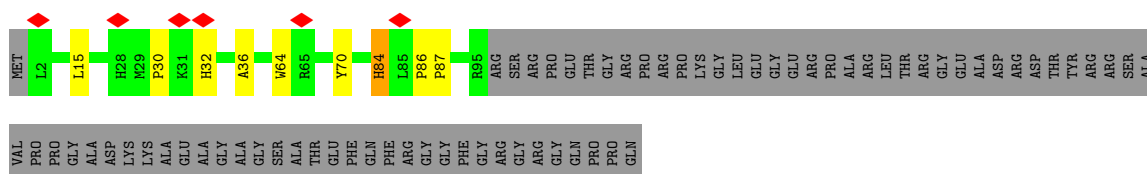




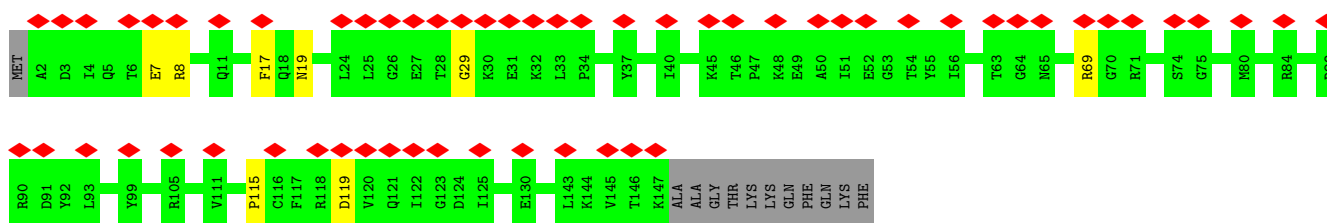
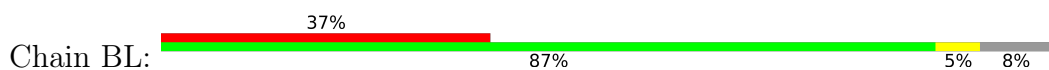
• Molecule 14: 40S RIBOSOMAL PROTEIN S9



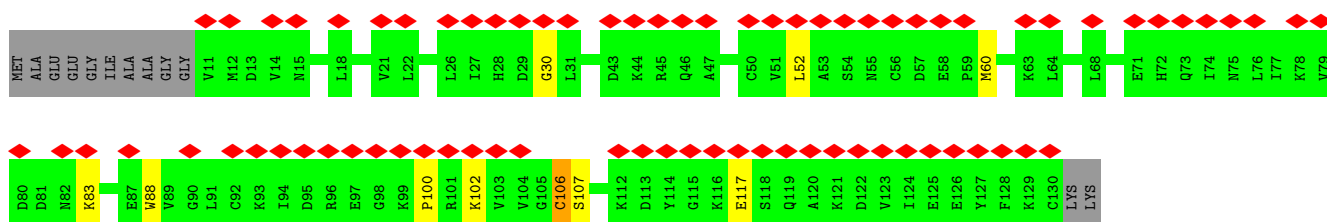
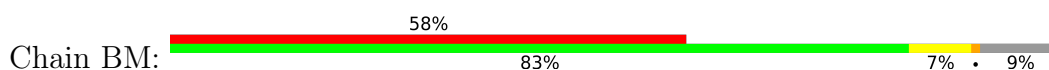
• Molecule 15: 40S RIBOSOMAL PROTEIN S10



• Molecule 16: 40S RIBOSOMAL PROTEIN S11

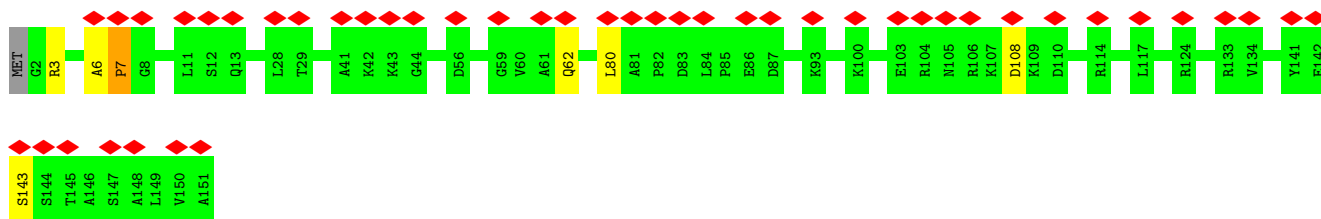


• Molecule 17: 40S RIBOSOMAL PROTEIN S12

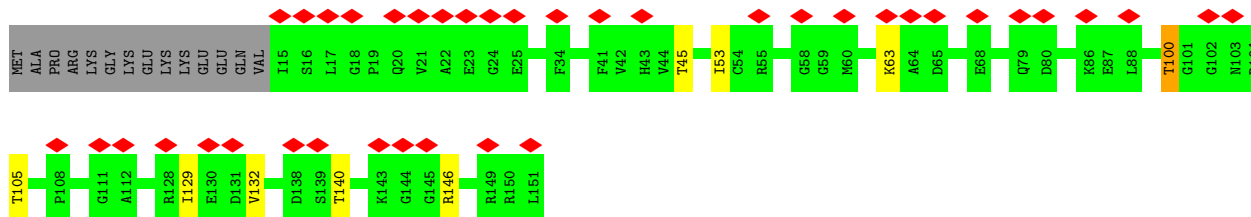
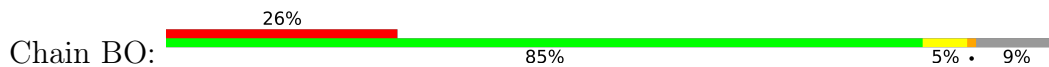


• Molecule 18: 40S RIBOSOMAL PROTEIN S13

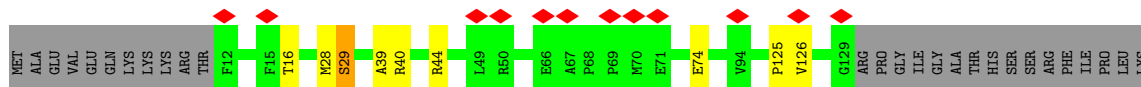
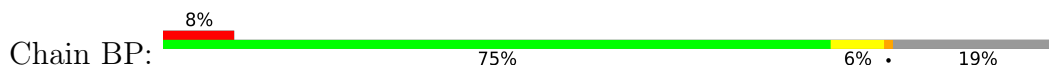




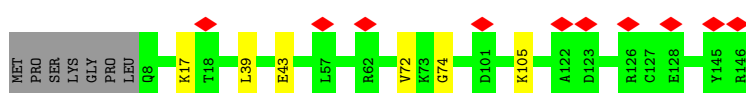
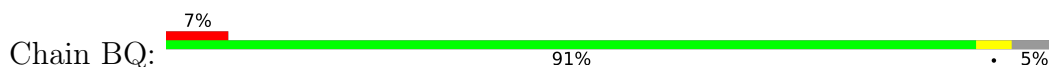
• Molecule 19: 40S RIBOSOMAL PROTEIN S14



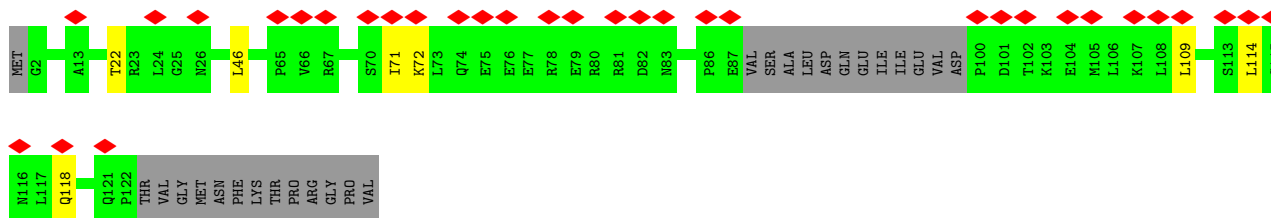
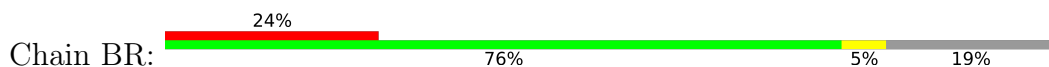
• Molecule 20: 40S RIBOSOMAL PROTEIN S15



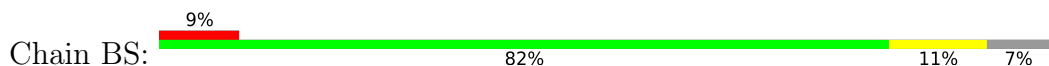
• Molecule 21: 40S RIBOSOMAL PROTEIN S16



• Molecule 22: 40S RIBOSOMAL PROTEIN S17

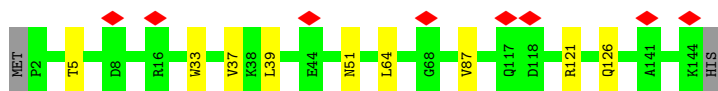


• Molecule 23: 40S RIBOSOMAL PROTEIN S18

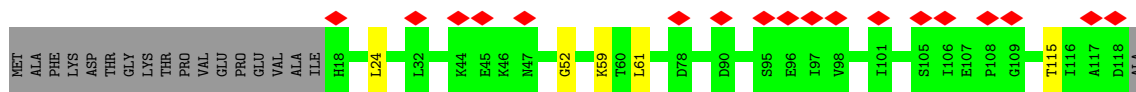
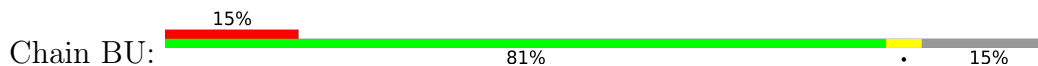




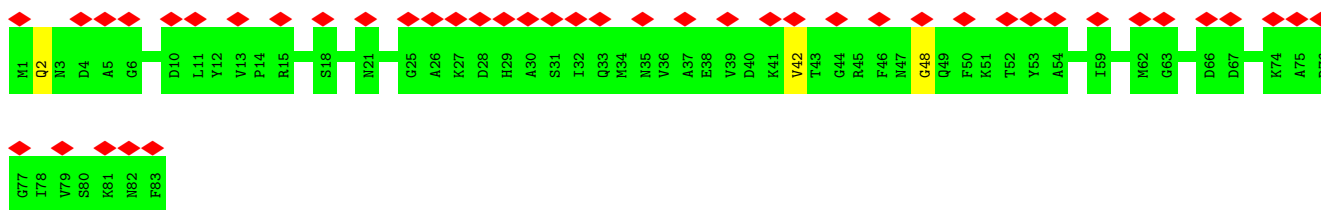
• Molecule 24: 40S RIBOSOMAL PROTEIN S19



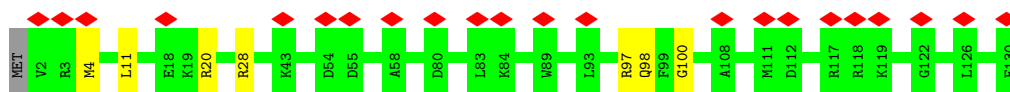
• Molecule 25: 40S RIBOSOMAL PROTEIN S20



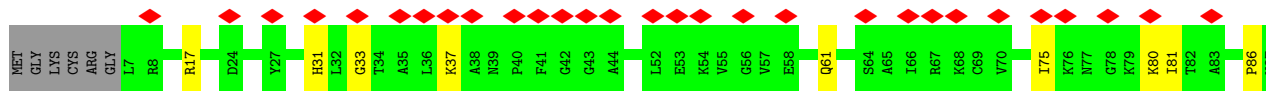
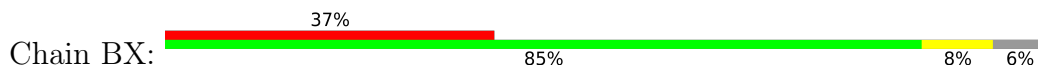
• Molecule 26: 40S RIBOSOMAL PROTEIN S21



• Molecule 27: 40S RIBOSOMAL PROTEIN S15A

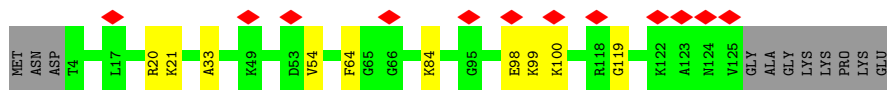
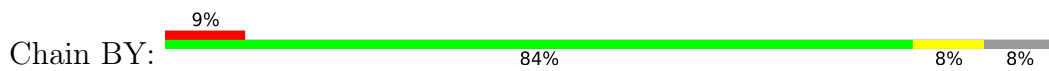


• Molecule 28: 40S RIBOSOMAL PROTEIN S23

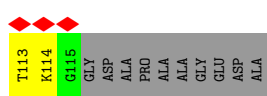
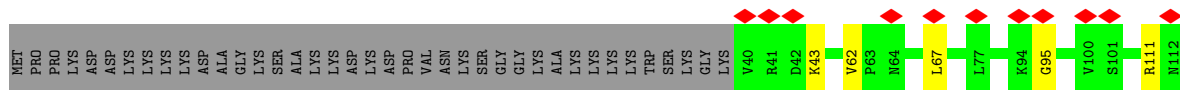


• Molecule 29: 40S RIBOSOMAL PROTEIN S24

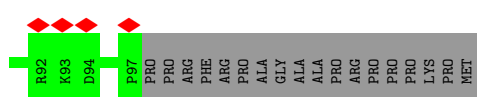
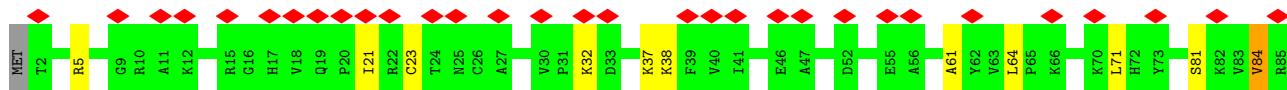
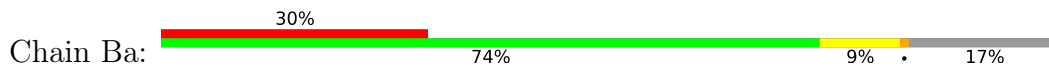




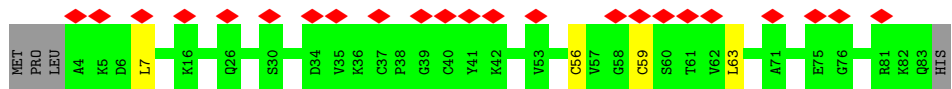
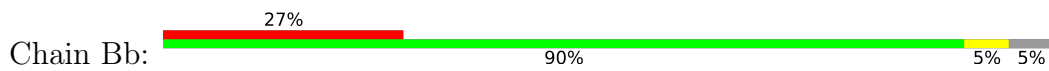
• Molecule 30: 40S RIBOSOMAL PROTEIN S25



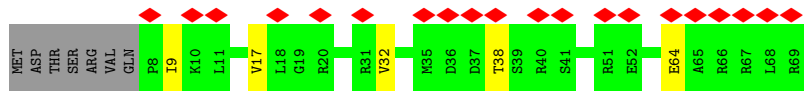
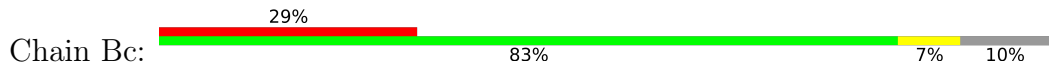
• Molecule 31: 40S RIBOSOMAL PROTEIN S26



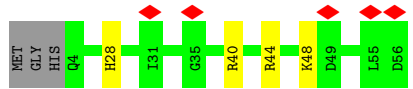
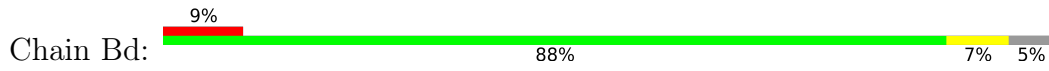
• Molecule 32: 40S RIBOSOMAL PROTEIN S27



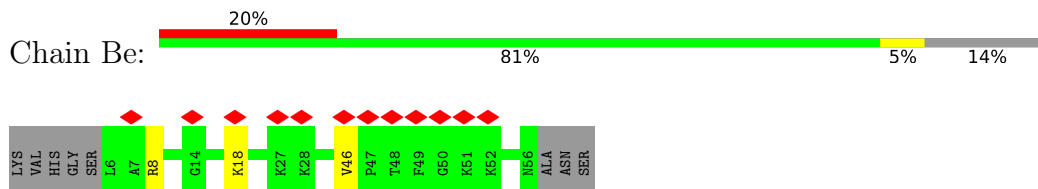
• Molecule 33: 40S RIBOSOMAL PROTEIN S28



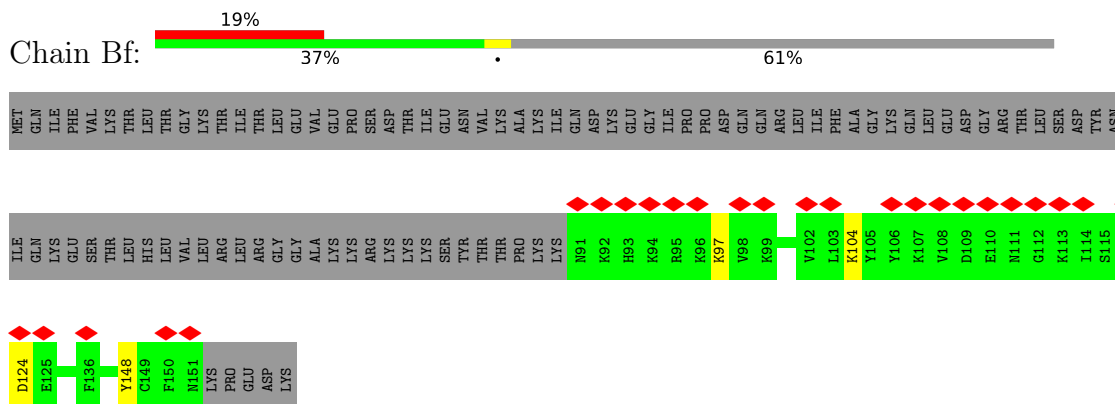
• Molecule 34: 40S RIBOSOMAL PROTEIN S29



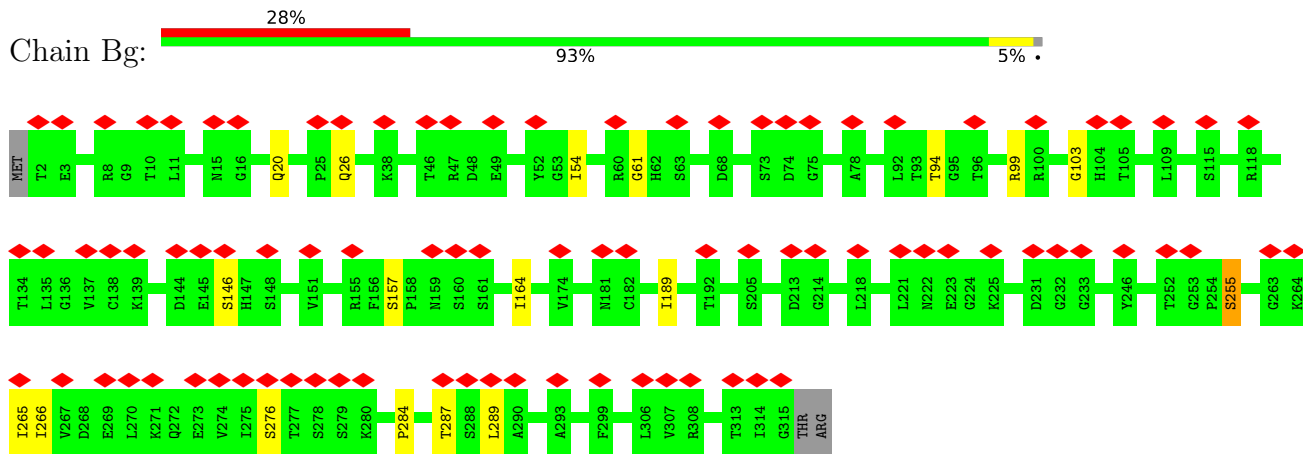
• Molecule 35: 40S RIBOSOMAL PROTEIN S30



• Molecule 36: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A



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

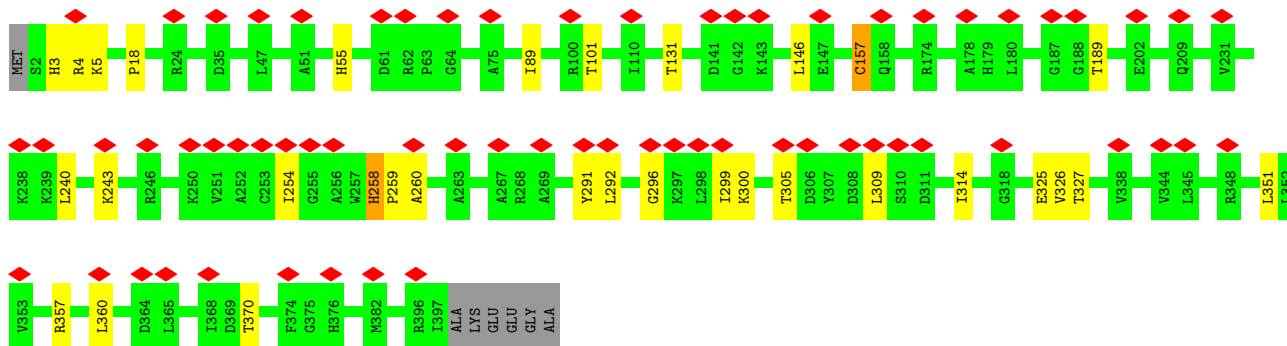


• Molecule 38: 60S RIBOSOMAL PROTEIN L8

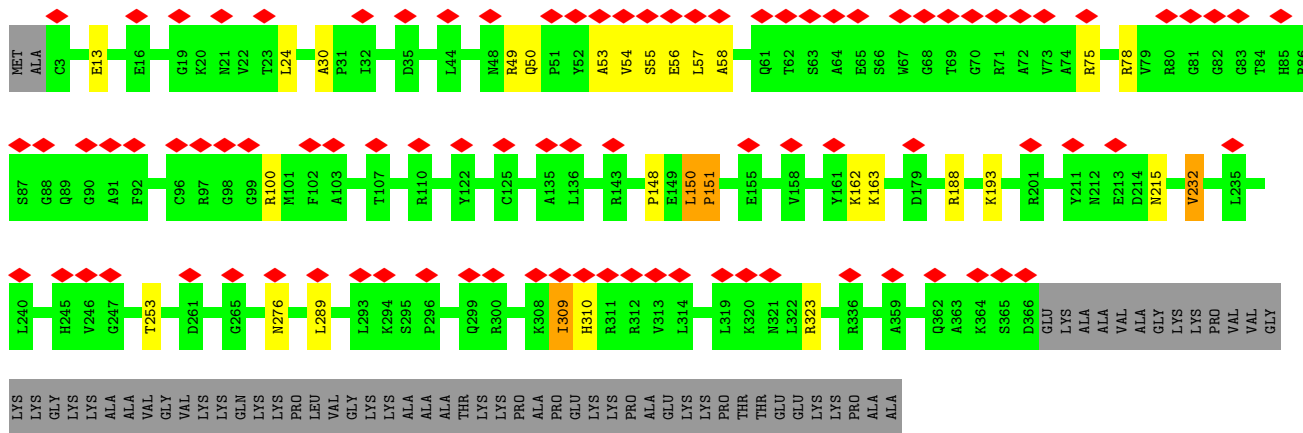
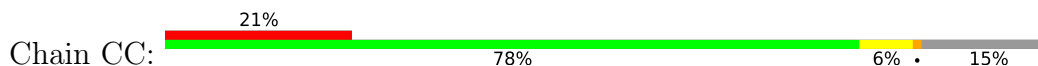


GLU
LYS
GLU
ASN

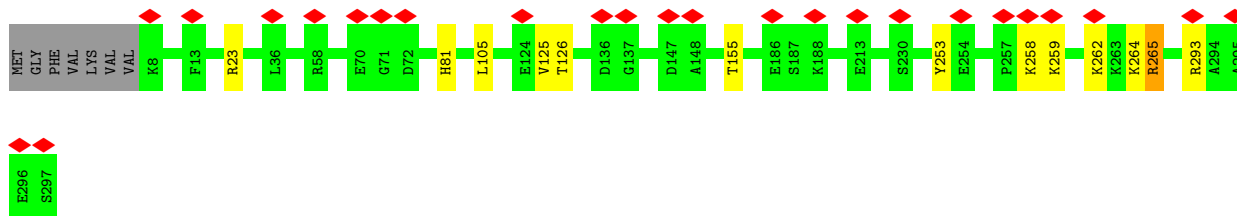
• Molecule 39: 60S RIBOSOMAL PROTEIN L3



• Molecule 40: 60S RIBOSOMAL PROTEIN L4

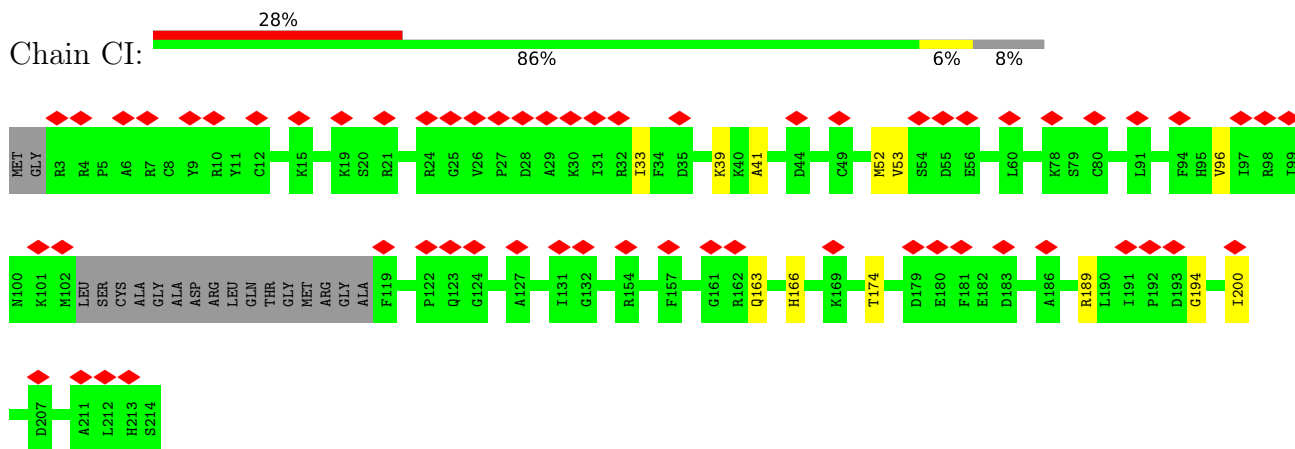


• Molecule 41: 60S RIBOSOMAL PROTEIN L5

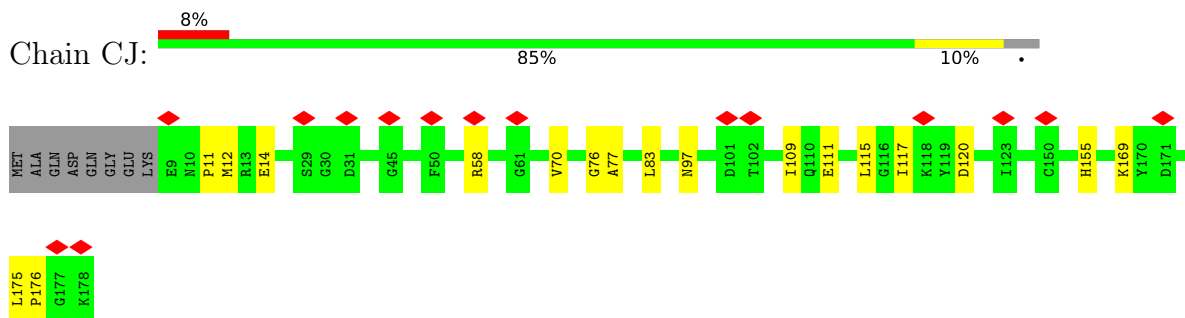


• Molecule 42: 60S RIBOSOMAL PROTEIN L6

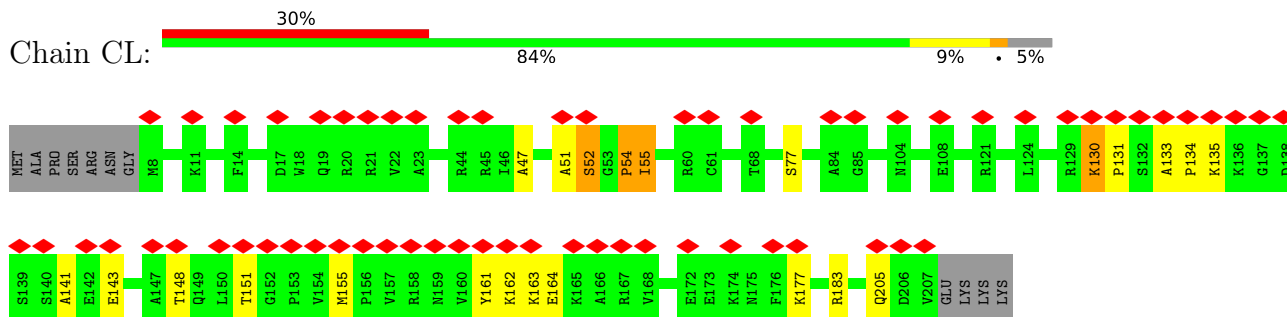




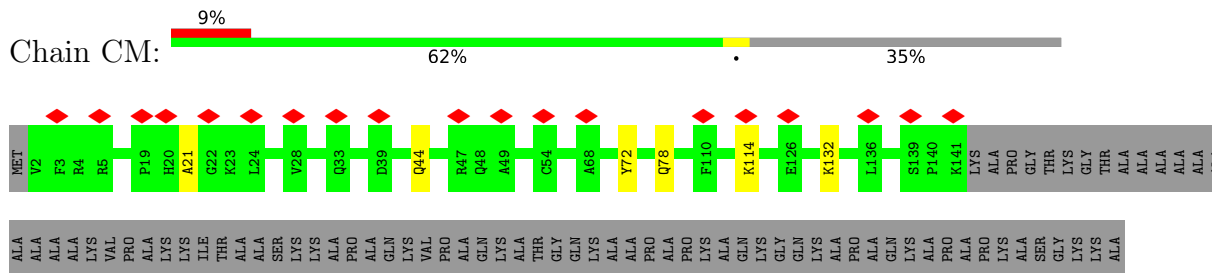
• Molecule 47: 60S RIBOSOMAL PROTEIN L11



• Molecule 48: 60S RIBOSOMAL PROTEIN L13

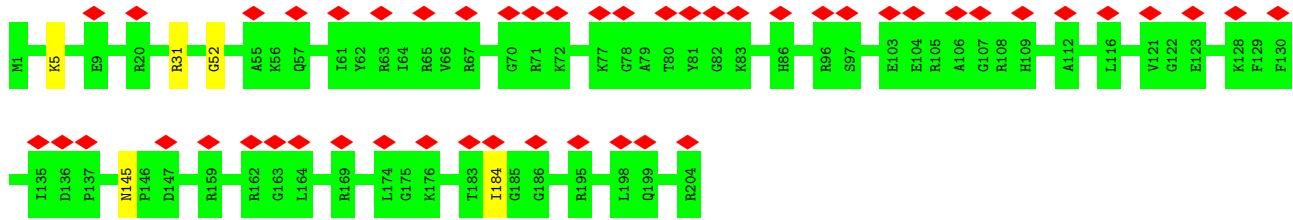


• Molecule 49: 60S RIBOSOMAL PROTEIN L14

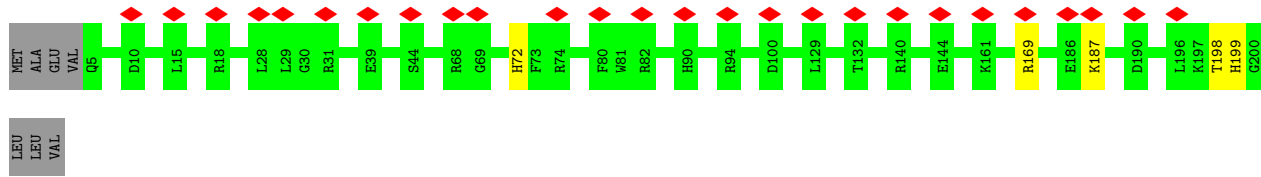


• Molecule 50: 60S RIBOSOMAL PROTEIN L15

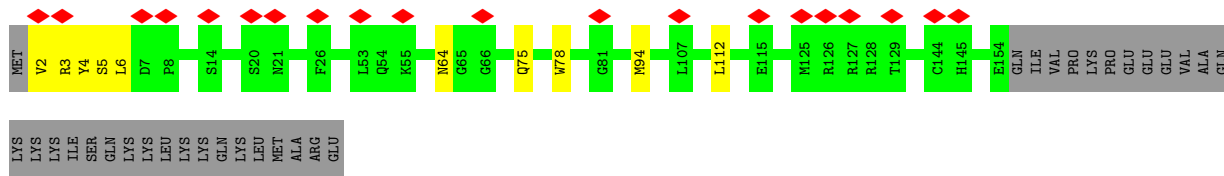
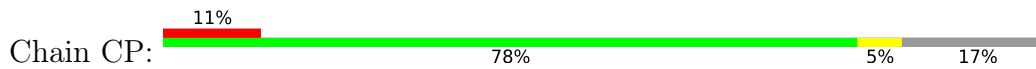




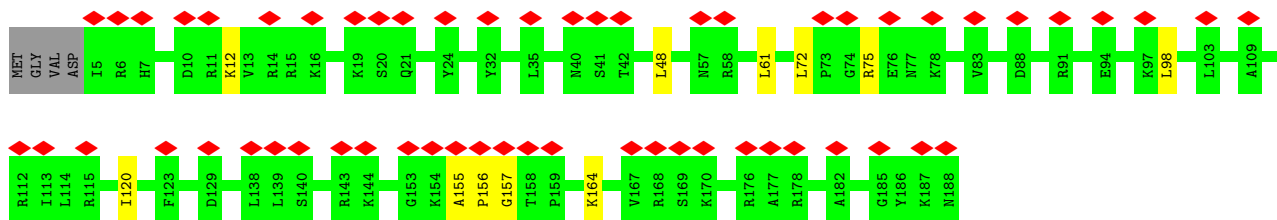
• Molecule 51: 60S RIBOSOMAL PROTEIN L13A



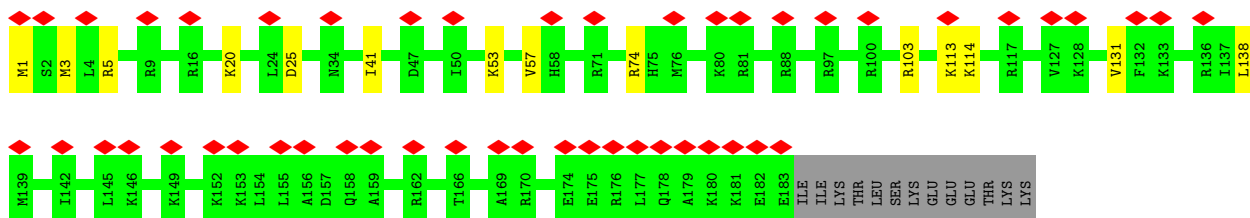
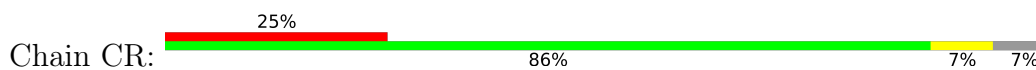
• Molecule 52: 60S RIBOSOMAL PROTEIN L17



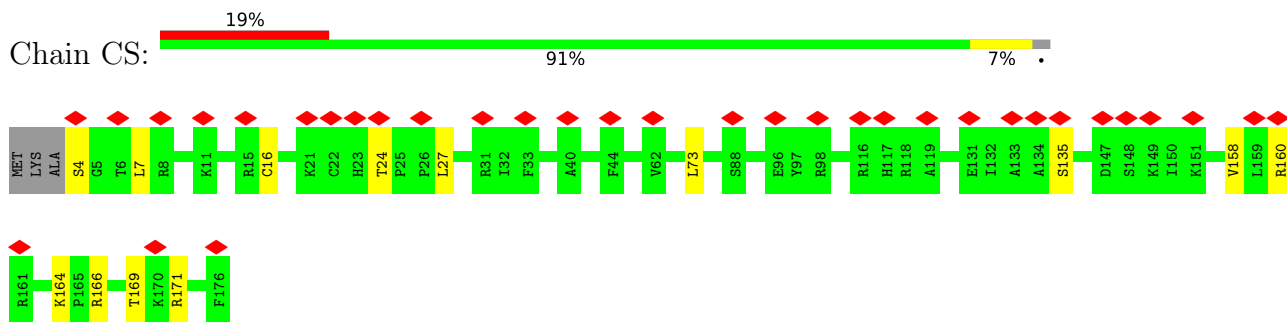
• Molecule 53: 60S RIBOSOMAL PROTEIN L18



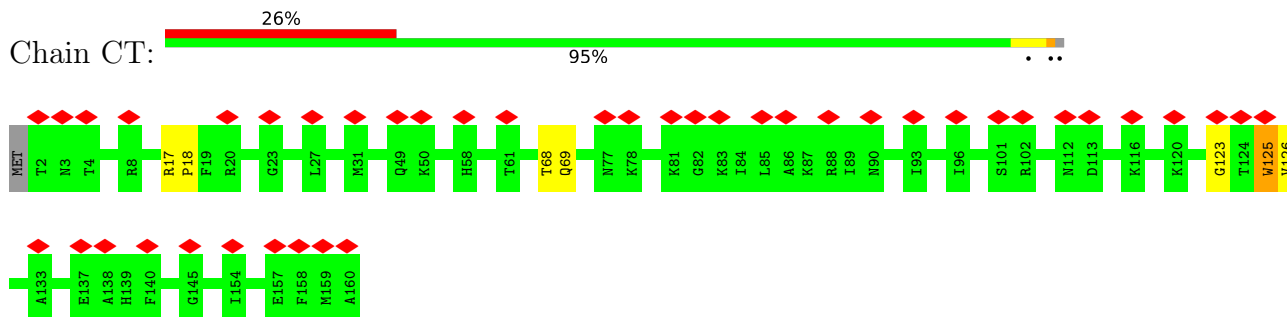
• Molecule 54: 60S RIBOSOMAL PROTEIN L19



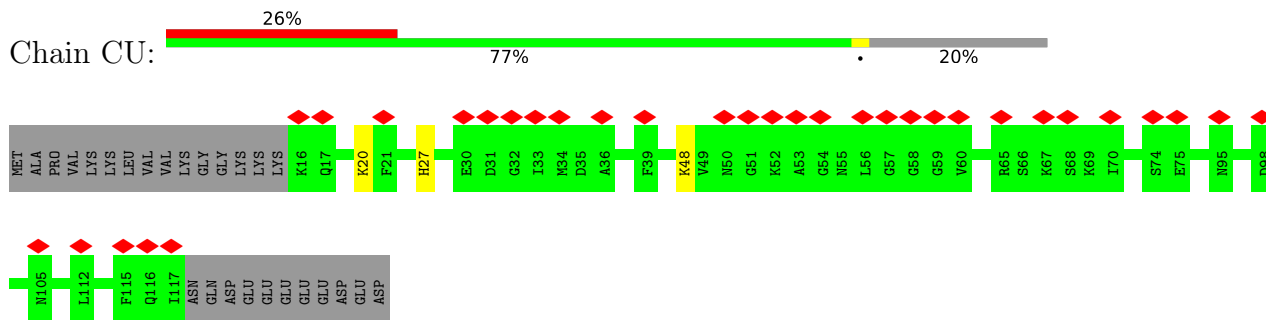
• Molecule 55: 60S RIBOSOMAL PROTEIN L18A



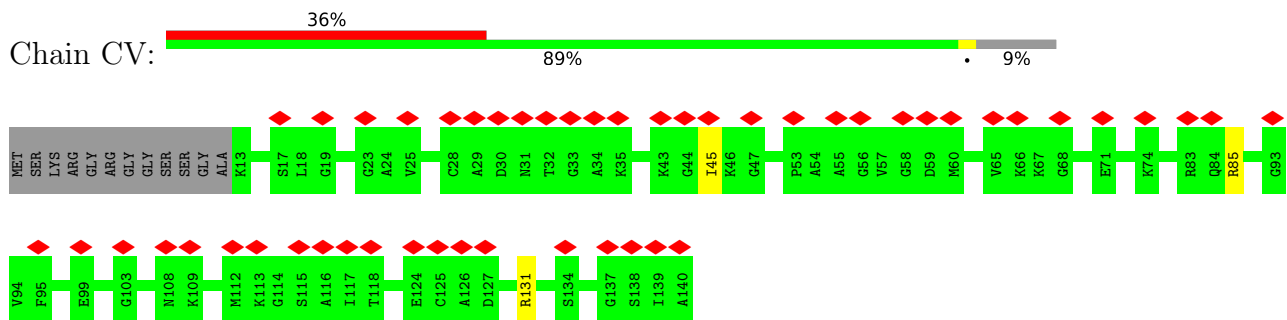
• Molecule 56: 60S RIBOSOMAL PROTEIN L21



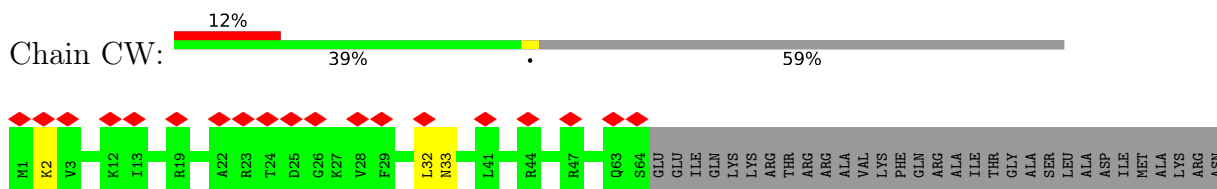
• Molecule 57: 60S RIBOSOMAL PROTEIN L22



• Molecule 58: 60S RIBOSOMAL PROTEIN L23



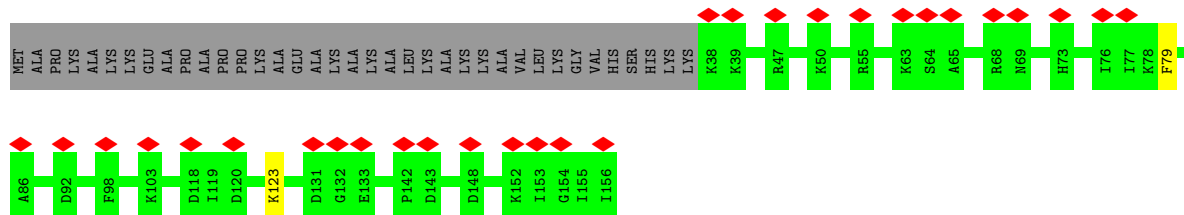
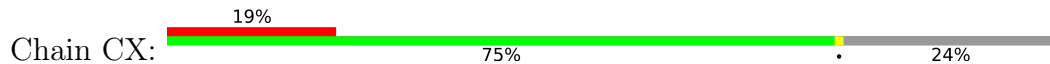
• Molecule 59: 60S RIBOSOMAL PROTEIN L24



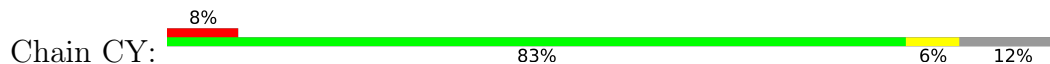
GLN
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ARG
ALA
ALA
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LYS
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LYS
THR
ALA
MET
ALA
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PRO
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VAL
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GLY

LYS
ARG

• Molecule 60: 60S RIBOSOMAL PROTEIN L23A



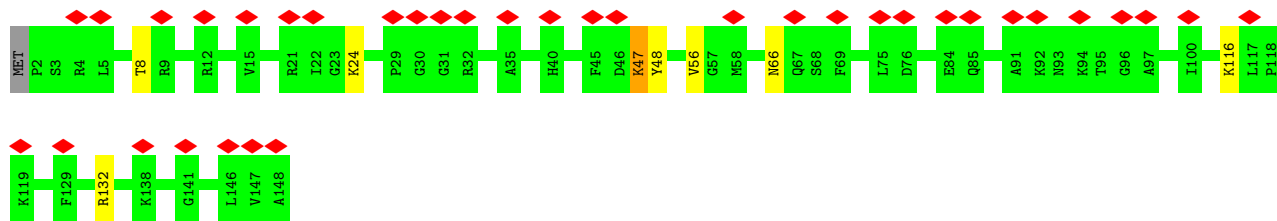
• Molecule 61: 60S RIBOSOMAL PROTEIN L26



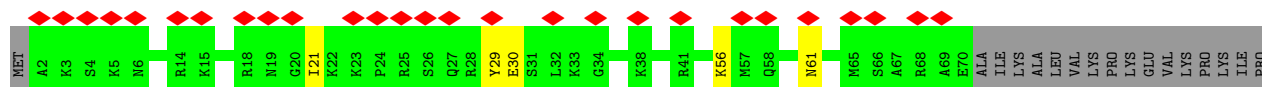
• Molecule 62: 60S RIBOSOMAL PROTEIN L27

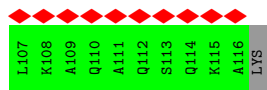


• Molecule 63: 60S RIBOSOMAL PROTEIN L27A

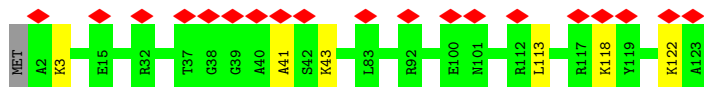


• Molecule 64: 60S RIBOSOMAL PROTEIN L29

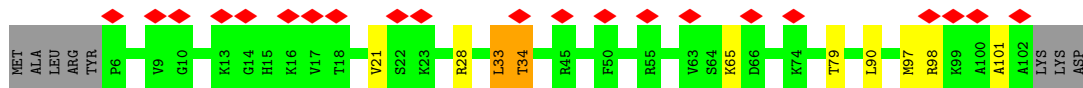
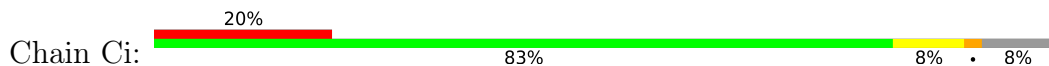




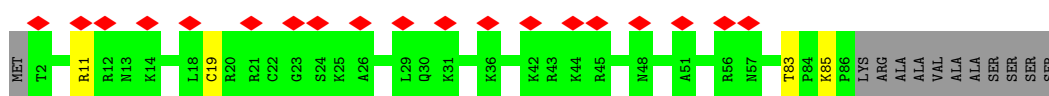
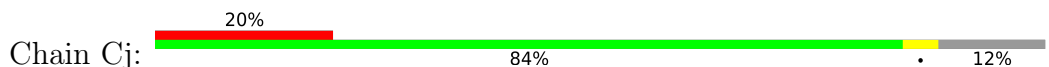
• Molecule 70: 60S RIBOSOMAL PROTEIN L35



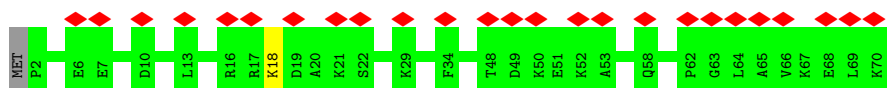
• Molecule 71: 60S RIBOSOMAL PROTEIN L36



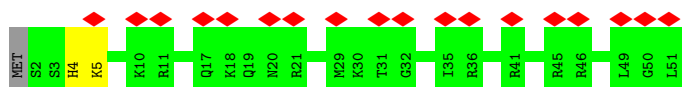
• Molecule 72: 60S RIBOSOMAL PROTEIN L37



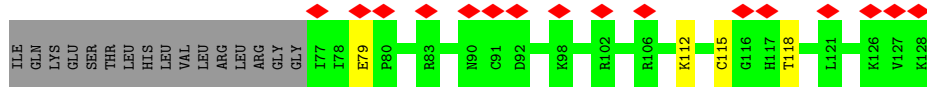
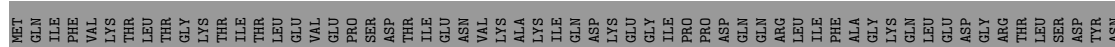
• Molecule 73: 60S RIBOSOMAL PROTEIN L38



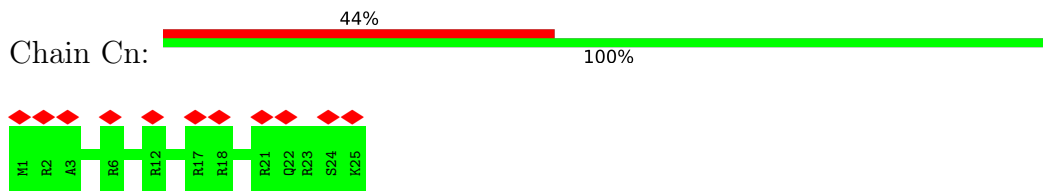
• Molecule 74: 60S RIBOSOMAL PROTEIN L39



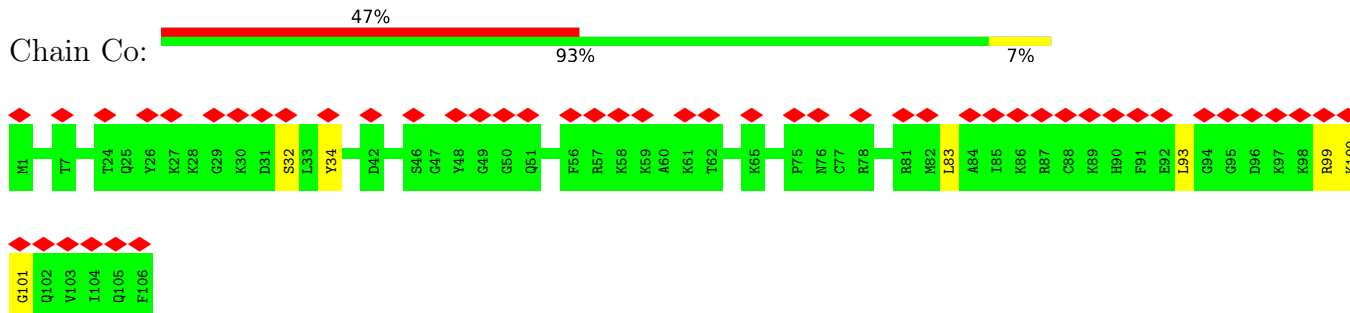
• Molecule 75: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



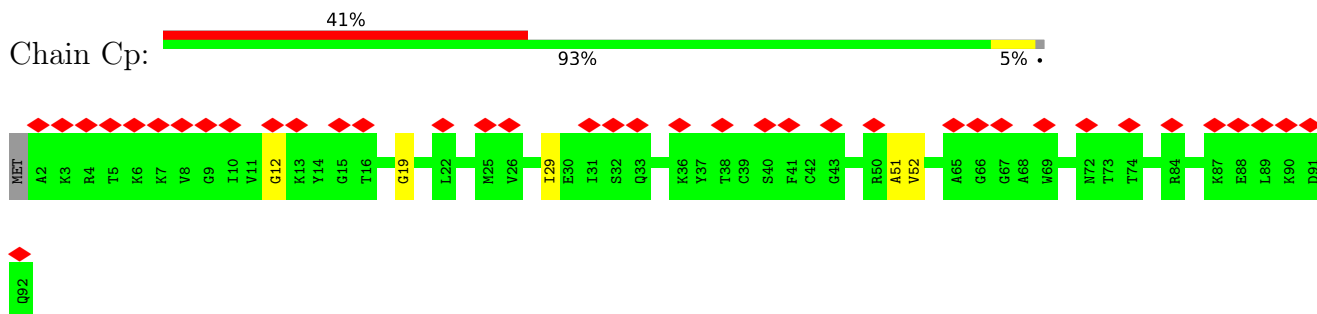
• Molecule 76: 60S RIBOSOMAL PROTEIN L41



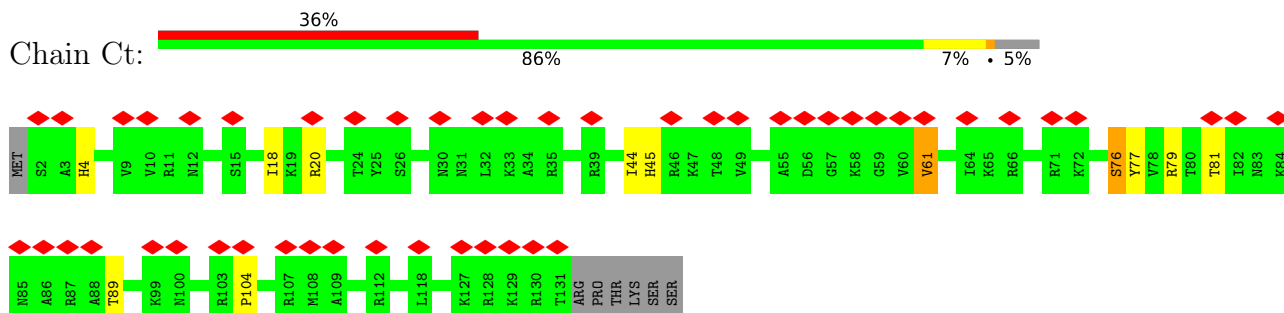
• Molecule 77: 60S RIBOSOMAL PROTEIN L36A



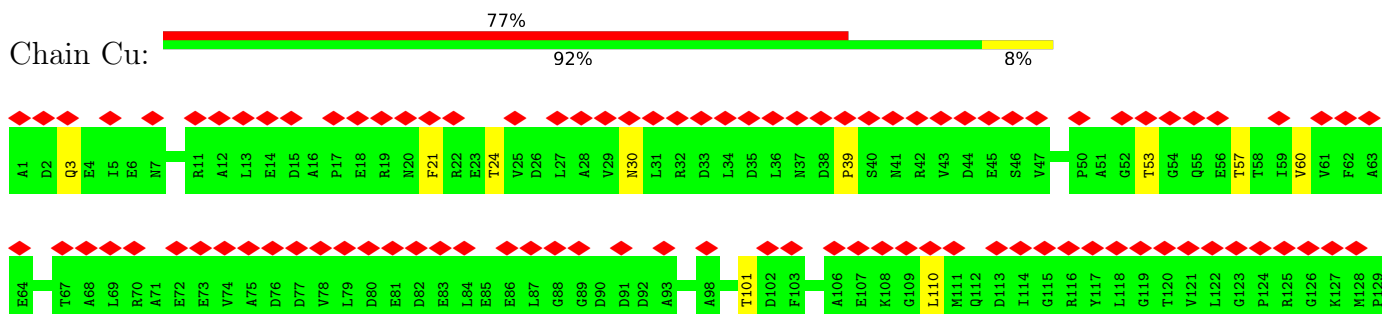
• Molecule 78: 60S RIBOSOMAL PROTEIN L37A

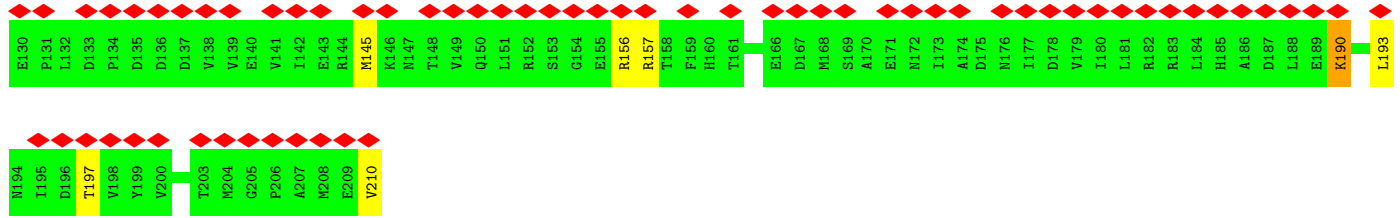


• Molecule 79: 60S RIBOSOMAL PROTEIN L28

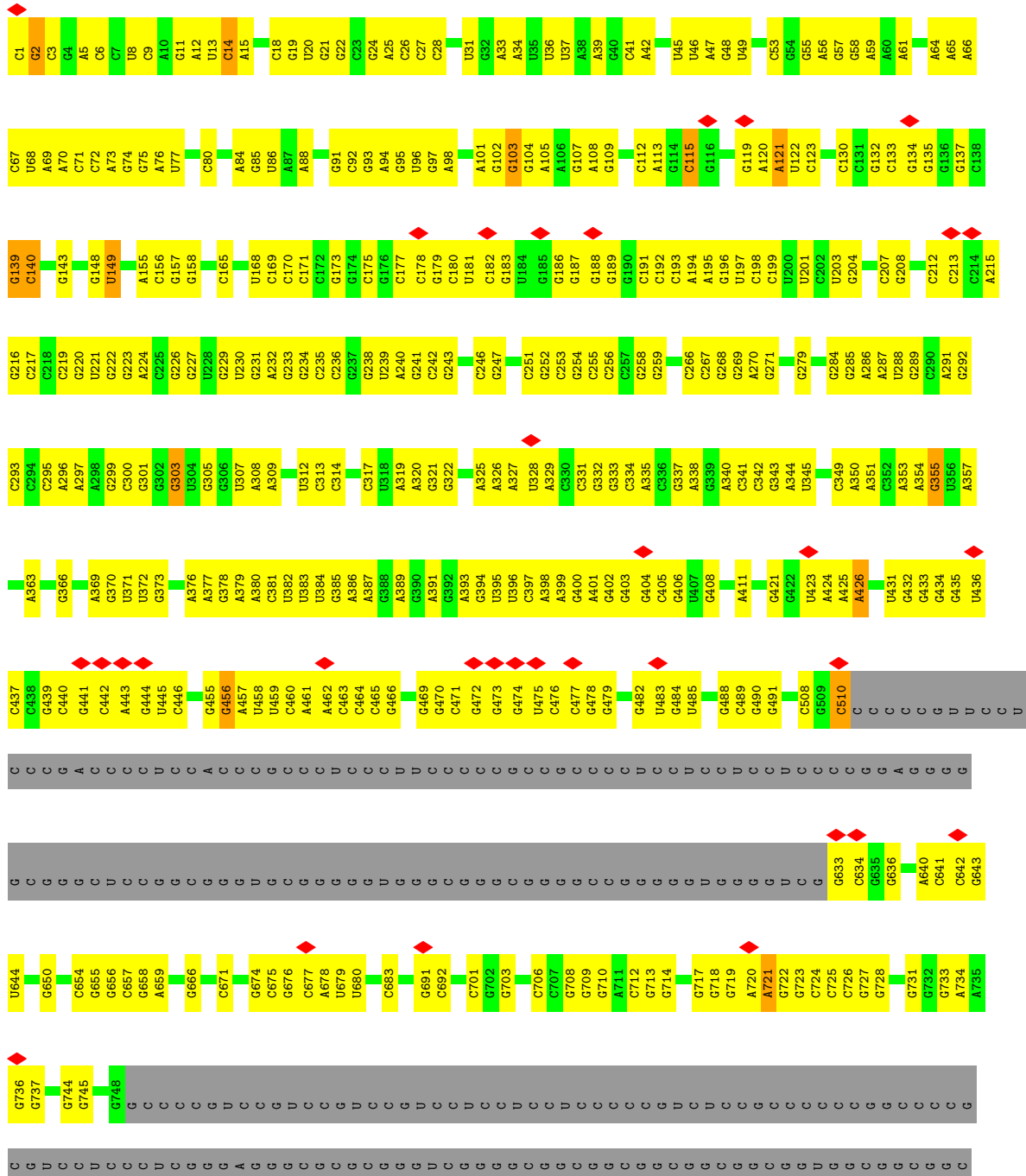


• Molecule 80: 60S RIBOSOMAL PROTEIN L10A

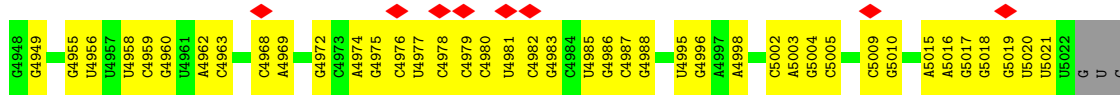




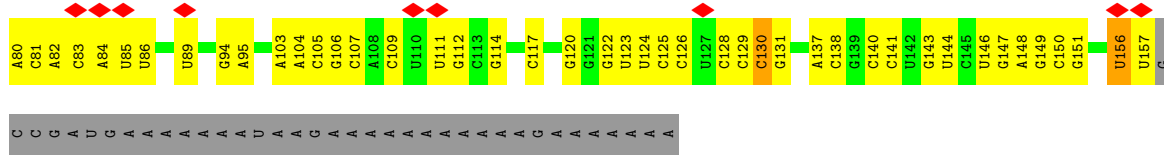
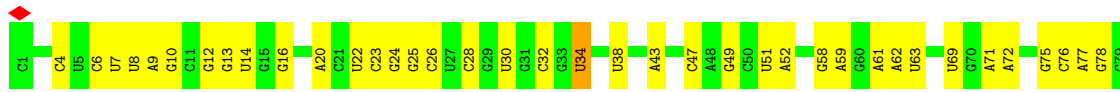
• Molecule 81: 28S Ribosomal RNA



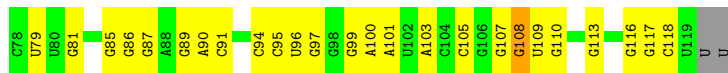
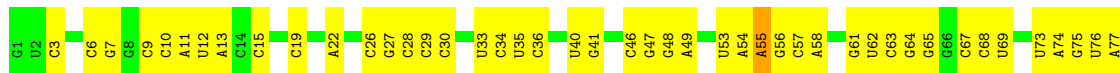
G2699	U2700	G2628	G2551	U2403	U2329	G2259	C2009	C1871	G1800
G2700	G2701	G2629	U2477	G2404	U2330	G2260	U2010	C1872	U1801
G2701	G2630	G2630	C2478	A2405	G2331	G2263	G2011	G1873	G1802
G2702	G2631	G2631	G2479	A2406	G2332	G2264	A2012	A1874	G1803
G2703	G2632	G2632	G2480	C2407	U2333	G2265	C2013	A1875	A1804
G2704	U2633	U2633	C2481	G2411	G2334	G2266	C2014	A1876	G1805
G2705	G2634	G2634	C2482	G2412	A2337	G2267	C2015	G1877	C1806
G2706	G2635	G2635	G2483	U2413	G2338	G2268	U2016	C1878	G1809
G2707	A2636	A2636	G2484	A2414	A2344	U2269	A2020	G1880	G1810
G2708	A2637	A2637	A2485	A2415	A2345	G2270	U2022	G1881	G1811
G2709	U2638	U2638	C2486	G2416	U2346	G2271	G2023	U1882	U1812
G2710	G2639	G2639	A2489	U2417	A2347	G2272	G2024	U1883	G1813
G2711	G2640	G2640	A2489	C2418	A2348	G2273	A2025	G1814	G1814
G2715	U2642	U2642	G2490	U2421	U2348	G2274	U2026	A1885	A1815
C2716	C2646	C2646	G2491	U2422	A2351	A2276	G2027	A1886	A1816
U2717	C2647	C2647	G2492	U2423	A2352	G2277	C2028	U1817	U1817
U2718	C2648	C2648	G2493	U2424	A2353	G2278	C2029	C1889	G1818
G2719	C2649	C2649	A2494	G2425	A2354	G2279	G2030	C1890	C1889
A2720	C2650	C2650	U2496	A2426	C2355	U2280	G2031	G1900	G1829
G2723	G2651	G2651	G2499	G2427	G2356	U2281	G2032	A1901	G1832
G2729	A2651	A2651	G2502	A2428	A2358	G2282	G2033	G1902	G1833
G2730	G2652	G2652	C2503	G2429	A2359	G2283	G2034	G1903	G1834
G2731	A2653	A2653	A2504	A2430	C2360	A2284	G2035	G1911	C1825
A2732	G2654	G2654	A2504	U2431	U2361	U2288	G2036	A1912	G1825
A2734	G2655	G2655	G2504	G2432	U2362	G2289	C2037	G1918	G1829
G2736	G2656	G2656	U2507	G2433	G2367	G2290	G2038	U1917	U1844
G2737	G2657	G2657	C2507	A2434	G2368	G2291	C2039	G1918	A1845
U2738	C2658	C2658	C2510	A2435	C2369	G2292	G2040	A1919	A1846
G2739	C2661	C2661	C2511	A2436	C2370	G2293	G2041	A1920	G1847
U2740	G2662	G2662	G2519	G2437	G2371	G2294	G2042	G1924	C1848
U2741	G2663	G2663	G2520	U2441	G2372	G2295	C2043	G1925	A1849
A2742	U2664	U2664	G2521	U2442	A2373	G2296	C2044	U1926	A1852
C2745	C2665	C2665	G2524	U2443	A2374	G2297	G2045	G1929	C1853
U2746	G2666	G2666	G2525	U2444	U2375	G2298	C2046	G1930	U1854
C2749	U2667	U2667	G2526	U2445	G2376	G2299	A2047	U1931	G1855
G2750	C2668	C2668	G2527	C2446	G2377	G2300	A2048	G1936	G1856
G2751	G2669	G2669	G2528	U2446	G2378	G2301	U2049	U1937	G1857
C2752	C2670	C2670	G2529	U2447	G2379	G2302	G2051	A1935	G1858
G2755	U2671	U2671	G2530	U2448	A2380	G2303	C2052	A1936	C1859
U2759	G2672	G2672	G2531	U2449	A2381	G2304	G2053	U1937	C1859
A2760	C2673	C2673	G2532	U2450	A2382	G2305	C2054	G1938	U1860
C2761	U2674	U2674	C2533	G2451	G2383	G2306	G2055	G1939	G1861
C2762	G2675	G2675	C2534	G2452	U2384	G2307	C2056	G1940	G1865
G2763	G2676	G2676	G2535	G2453	U2385	G2308	G2057	A1941	G1866
A2764	U2677	U2677	G2536	G2454	U2386	A2309	C2061	C1942	U1867
U2765	C2678	C2678	G2537	A2454	C2387	G2310	G2062	A1945	G1868
A2766	G2679	G2679	C2538	U2455	C2388	G2311	G2063	G1945	A1869
U2767	U2680	U2680	G2539	G2456	U2389	C2315	G2064	G1945	A1870
C2771	C2681	C2681	G2540	G2457	G2390	G2320	C2065	G1936	G
A2772	G2682	G2682	C2640	U2458	A2391	U2321	A	U1937	C2000
G2773	U2683	U2683	U2639	U2462	A2395	G2322	G	G1938	C2001
C2774	G2684	G2684	C2640	G2463	C2396	G2323	U	G1939	G2002
	U2685	U2685	U2640	G2464	A2397	C2324	C	A2003	C2003
	C2686	C2686	G2541	G2465	A2398	A2324	G	A2004	A2004
	G2687	G2687	G2542	C2466	C2399	G2255	A	U2005	U2005
	U2688	U2688	G2543	U2467	A2400	U2257	G	C2006	C2006
	G2689	G2689	G2544	C2468	G2401	G2258	G	A2007	A2007
	U2692	U2692	U2547	C2469	A2258	A2258	C	G	A2008
	C2696	C2696	C2548						
	G2697	G2697	C2549						
	C2774	C2774	A2550						



• 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 (\AA)	453.6, 453.6, 453.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.26, 1.26, 1.26	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.29	0/1809	0.75	0/2819
2	AW	0.31	0/1783	0.76	0/2776
3	AX	0.42	1/615 (0.2%)	1.25	11/948 (1.2%)
4	B1	0.37	2/41550 (0.0%)	0.79	6/64763 (0.0%)
5	BA	0.51	0/1756	0.68	0/2386
6	BB	0.51	0/1756	0.75	1/2350 (0.0%)
7	BC	0.42	0/1761	0.65	0/2379
8	BD	0.40	0/1672	0.66	0/2250
9	BE	0.47	0/2072	0.70	0/2793
10	BF	0.43	0/1507	0.74	0/2026
11	BG	0.47	0/1907	0.74	0/2538
12	BH	0.46	0/1558	0.74	1/2087 (0.0%)
13	BI	0.47	0/1724	0.72	0/2298
14	BJ	0.45	0/1520	0.77	0/2030
15	BK	0.48	0/815	0.68	0/1101
16	BL	0.45	0/1220	0.72	0/1633
17	BM	0.48	0/941	0.72	0/1264
18	BN	0.43	0/1231	0.73	1/1656 (0.1%)
19	BO	0.46	0/1036	0.71	0/1391
20	BP	0.43	0/1000	0.67	0/1335
21	BQ	0.43	0/1125	0.66	0/1506
22	BR	0.42	0/904	0.67	0/1208
23	BS	0.42	0/1190	0.68	0/1594
24	BT	0.44	0/1131	0.69	0/1515
25	BU	0.50	0/813	0.70	0/1092
26	BV	0.47	0/643	0.71	0/860
27	BW	0.44	0/1050	0.69	0/1406
28	BX	0.46	0/1063	0.70	0/1421
29	BY	0.45	0/1019	0.70	0/1354
30	BZ	0.46	0/611	0.71	0/820
31	Ba	0.48	0/778	0.75	1/1041 (0.1%)
32	Bb	0.48	0/637	0.68	0/854

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bc	0.46	0/492	0.74	0/657
34	Bd	0.51	0/454	0.76	0/603
35	Be	0.45	0/417	0.69	0/548
36	Bf	0.53	0/507	0.84	1/673 (0.1%)
37	Bg	0.45	0/2497	0.67	0/3399
38	CA	0.44	0/1926	0.67	0/2583
39	CB	0.45	0/3258	0.73	2/4361 (0.0%)
40	CC	0.47	0/2943	0.73	0/3953
41	CD	0.49	1/2406 (0.0%)	0.70	1/3221 (0.0%)
42	CE	0.52	0/1311	0.73	0/1763
43	CF	0.45	0/1985	0.68	0/2644
44	CG	0.46	0/1914	0.72	0/2578
45	CH	0.43	0/1554	0.69	0/2089
46	CI	0.42	0/1642	0.67	0/2194
47	CJ	0.49	0/1385	0.71	0/1852
48	CL	0.53	2/1647 (0.1%)	0.73	3/2205 (0.1%)
49	CM	0.49	0/1162	0.70	0/1556
50	CN	0.43	0/1753	0.65	0/2348
51	CO	0.44	0/1639	0.69	0/2193
52	CP	0.44	0/1260	0.70	0/1691
53	CQ	0.45	0/1517	0.74	0/2026
54	CR	0.40	0/1542	0.64	0/2037
55	CS	0.44	0/1478	0.73	0/1985
56	CT	0.46	0/1325	0.71	0/1770
57	CU	0.47	0/841	0.71	0/1128
58	CV	0.43	0/977	0.63	0/1312
59	CW	0.43	0/542	0.59	0/722
60	CX	0.41	0/992	0.67	0/1334
61	CY	0.47	0/1082	0.72	1/1441 (0.1%)
62	CZ	0.47	0/1137	0.79	0/1517
63	Ca	0.44	0/1190	0.71	0/1591
64	Cb	0.45	0/570	0.72	0/752
65	Cc	0.46	0/813	0.70	0/1091
66	Cd	0.44	0/919	0.67	0/1238
67	Ce	0.45	0/1071	0.68	0/1428
68	Cf	0.50	0/884	0.81	0/1185
69	Cg	0.48	0/917	0.74	0/1222
70	Ch	0.38	0/1022	0.64	0/1351
71	Ci	0.43	0/793	0.75	0/1048
72	Cj	0.49	0/704	0.76	0/931
73	Ck	0.43	0/574	0.73	0/761
74	Cl	0.41	0/453	0.61	0/599
75	Cm	0.42	0/434	0.70	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Cn	0.39	0/240	0.50	0/305
77	Co	0.45	0/884	0.74	0/1166
78	Cp	0.40	0/717	0.61	0/953
79	Ct	0.48	0/1058	0.75	0/1416
80	Cu	0.45	0/1638	0.69	1/2222 (0.0%)
81	A2	0.41	23/86672 (0.0%)	0.80	40/135198 (0.0%)
82	A3	0.35	0/3723	0.79	1/5800 (0.0%)
83	A4	0.37	0/2836	0.81	3/4421 (0.1%)
All	All	0.42	29/231894 (0.0%)	0.77	74/341130 (0.0%)

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 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	A2	1701	C	C5'-C4'	18.39	1.73	1.51
81	A2	1673	C	C3'-O3'	15.36	1.63	1.42
81	A2	1701	C	O5'-C5'	14.45	1.67	1.44
81	A2	1673	C	O3'-P	14.13	1.78	1.61
81	A2	1701	C	P-O5'	13.52	1.73	1.59

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	A2	1701	C	O4'-C4'-C3'	-15.19	88.81	104.00
39	CB	258	HIS	C-N-CD	-13.96	89.88	120.60
3	AX	58	U	P-O5'-C5'	12.68	141.18	120.90
81	A2	1701	C	O4'-C1'-N1	12.30	118.04	108.20
81	A2	1701	C	C4'-C3'-O3'	12.16	137.32	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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	BA	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	17	57
6	BB	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	12
7	BC	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	6	34
8	BD	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	6	33
9	BE	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	7	38
10	BF	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	2	19
11	BG	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	3	23
12	BH	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	7	36
13	BI	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	26
14	BJ	177/194 (91%)	169 (96%)	5 (3%)	3 (2%)	9	42
15	BK	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	BL	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	3	22
17	BM	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	2	19
18	BN	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	26
19	BO	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	6	35
20	BP	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	22
21	BQ	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	10	46
22	BR	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	8	38
23	BS	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	18
24	BT	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	11	46
25	BU	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	15	54
26	BV	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	5	32
27	BW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	9	44
28	BX	132/143 (92%)	120 (91%)	5 (4%)	7 (5%)	2	19
29	BY	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	4	26
30	BZ	74/125 (59%)	71 (96%)	0	3 (4%)	3	22
31	Ba	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	22
32	Bb	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
33	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	4	26
34	Bd	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
35	Be	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	7	38
36	Bf	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
37	Bg	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	6	35
38	CA	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	13	50
39	CB	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	3	25
40	CC	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	3	22
41	CD	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	9	42
42	CE	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	2	22
43	CF	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	9	42
44	CG	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	3	23
45	CH	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	9	44
46	CI	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	9	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	CJ	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	14
48	CL	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	2	18
49	CM	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	11	46
50	CN	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	10	46
51	CO	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	10	46
52	CP	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	7	38
53	CQ	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	4	26
54	CR	181/196 (92%)	175 (97%)	3 (2%)	3 (2%)	9	42
55	CS	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	25
56	CT	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	8	38
57	CU	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
58	CV	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	9	44
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%)	6	33
62	CZ	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	4	28
63	Ca	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	26
64	Cb	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	17
65	Cc	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	7	38
66	Cd	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	17	57
67	Ce	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	6	33
68	Cf	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	21
69	Cg	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	25
70	Ch	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	5	32
71	Ci	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	17
72	Cj	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	6	33
73	Ck	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	10	46
74	Cl	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	7	36
75	Cm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	7	38
76	Cn	23/25 (92%)	23 (100%)	0	0	100	100
77	Co	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	8	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
78	Cp	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	26
79	Ct	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	2	19
80	Cu	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	11	46
All	All	11190/12898 (87%)	10477 (94%)	390 (4%)	323 (3%)	7	29

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 [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	
5	BA	181/243 (74%)	176 (97%)	5 (3%)	43	65
6	BB	194/231 (84%)	183 (94%)	11 (6%)	20	45
7	BC	188/225 (84%)	181 (96%)	7 (4%)	34	58
8	BD	175/202 (87%)	166 (95%)	9 (5%)	24	48
9	BE	220/225 (98%)	208 (94%)	12 (6%)	21	47
10	BF	158/170 (93%)	151 (96%)	7 (4%)	28	53
11	BG	202/218 (93%)	195 (96%)	7 (4%)	36	59
12	BH	171/174 (98%)	167 (98%)	4 (2%)	50	70
13	BI	179/180 (99%)	167 (93%)	12 (7%)	16	41
14	BJ	160/168 (95%)	150 (94%)	10 (6%)	18	43
15	BK	85/136 (62%)	82 (96%)	3 (4%)	36	59
16	BL	133/142 (94%)	131 (98%)	2 (2%)	65	80
17	BM	102/108 (94%)	97 (95%)	5 (5%)	25	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	BN	130/131 (99%)	128 (98%)	2 (2%)	65	80
19	BO	107/119 (90%)	100 (94%)	7 (6%)	17	42
20	BP	107/130 (82%)	102 (95%)	5 (5%)	26	51
21	BQ	115/121 (95%)	111 (96%)	4 (4%)	36	59
22	BR	99/122 (81%)	94 (95%)	5 (5%)	24	48
23	BS	123/132 (93%)	114 (93%)	9 (7%)	14	39
24	BT	113/115 (98%)	106 (94%)	7 (6%)	18	43
25	BU	93/107 (87%)	89 (96%)	4 (4%)	29	53
26	BV	67/67 (100%)	66 (98%)	1 (2%)	65	80
27	BW	112/113 (99%)	107 (96%)	5 (4%)	27	52
28	BX	108/115 (94%)	103 (95%)	5 (5%)	27	52
29	BY	107/115 (93%)	101 (94%)	6 (6%)	21	46
30	BZ	67/103 (65%)	63 (94%)	4 (6%)	19	44
31	Ba	83/98 (85%)	76 (92%)	7 (8%)	11	33
32	Bb	72/76 (95%)	68 (94%)	4 (6%)	21	46
33	Bc	55/62 (89%)	52 (94%)	3 (6%)	21	47
34	Bd	47/49 (96%)	43 (92%)	4 (8%)	10	33
35	Be	42/48 (88%)	40 (95%)	2 (5%)	25	51
36	Bf	54/140 (39%)	51 (94%)	3 (6%)	21	46
37	Bg	272/275 (99%)	260 (96%)	12 (4%)	28	53
38	CA	189/199 (95%)	185 (98%)	4 (2%)	53	72
39	CB	344/349 (99%)	326 (95%)	18 (5%)	23	48
40	CC	302/348 (87%)	284 (94%)	18 (6%)	19	44
41	CD	244/250 (98%)	237 (97%)	7 (3%)	42	64
42	CE	143/252 (57%)	135 (94%)	8 (6%)	21	46
43	CF	203/215 (94%)	196 (97%)	7 (3%)	37	60
44	CG	199/223 (89%)	192 (96%)	7 (4%)	36	59
45	CH	171/171 (100%)	164 (96%)	7 (4%)	30	55
46	CI	170/181 (94%)	161 (95%)	9 (5%)	22	47
47	CJ	143/149 (96%)	137 (96%)	6 (4%)	30	54
48	CL	167/177 (94%)	156 (93%)	11 (7%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	CM	118/161 (73%)	114 (97%)	4 (3%)	37	60
50	CN	172/172 (100%)	170 (99%)	2 (1%)	71	83
51	CO	168/174 (97%)	166 (99%)	2 (1%)	71	83
52	CP	133/163 (82%)	126 (95%)	7 (5%)	22	47
53	CQ	162/165 (98%)	157 (97%)	5 (3%)	40	62
54	CR	161/175 (92%)	150 (93%)	11 (7%)	16	41
55	CS	155/157 (99%)	148 (96%)	7 (4%)	27	52
56	CT	139/140 (99%)	134 (96%)	5 (4%)	35	59
57	CU	91/115 (79%)	88 (97%)	3 (3%)	38	61
58	CV	100/107 (94%)	99 (99%)	1 (1%)	76	86
59	CW	55/126 (44%)	52 (94%)	3 (6%)	21	47
60	CX	107/133 (80%)	105 (98%)	2 (2%)	57	75
61	CY	119/135 (88%)	115 (97%)	4 (3%)	37	60
62	CZ	118/118 (100%)	112 (95%)	6 (5%)	24	48
63	Ca	120/121 (99%)	116 (97%)	4 (3%)	38	61
64	Cb	58/126 (46%)	57 (98%)	1 (2%)	60	78
65	Cc	88/97 (91%)	87 (99%)	1 (1%)	73	84
66	Cd	100/110 (91%)	96 (96%)	4 (4%)	31	55
67	Ce	115/121 (95%)	112 (97%)	3 (3%)	46	66
68	Cf	87/89 (98%)	79 (91%)	8 (9%)	9	29
69	Cg	98/100 (98%)	88 (90%)	10 (10%)	7	25
70	Ch	109/110 (99%)	106 (97%)	3 (3%)	43	65
71	Ci	82/89 (92%)	76 (93%)	6 (7%)	14	39
72	Cj	71/80 (89%)	69 (97%)	2 (3%)	43	65
73	Ck	64/65 (98%)	64 (100%)	0	100	100
74	Cl	47/48 (98%)	46 (98%)	1 (2%)	53	72
75	Cm	48/116 (41%)	45 (94%)	3 (6%)	18	43
76	Cn	24/24 (100%)	24 (100%)	0	100	100
77	Co	94/94 (100%)	89 (95%)	5 (5%)	22	47
78	Cp	74/75 (99%)	72 (97%)	2 (3%)	44	65
79	Ct	113/121 (93%)	106 (94%)	7 (6%)	18	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Cu	177/177 (100%)	163 (92%)	14 (8%)	12	35
All	All	9763/10978 (89%)	9332 (96%)	431 (4%)	32	53

5 of 431 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	CC	310	HIS
48	CL	55	ILE
74	Cl	5	LYS
41	CD	262	LYS
44	CG	163	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 210 such sidechains are listed below:

Mol	Chain	Res	Type
43	CF	116	GLN
52	CP	54	GLN
75	Cm	87	GLN
44	CG	108	GLN
47	CJ	168	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AV	75/76 (98%)	37 (49%)	2 (2%)
2	AW	74/76 (97%)	33 (44%)	5 (6%)
3	AX	27/28 (96%)	15 (55%)	4 (14%)
4	B1	1738/1869 (92%)	1038 (59%)	152 (8%)
81	A2	3605/5025 (71%)	2042 (56%)	325 (9%)
82	A3	156/194 (80%)	81 (51%)	6 (3%)
83	A4	118/121 (97%)	68 (57%)	9 (7%)
All	All	5793/7389 (78%)	3314 (57%)	503 (8%)

5 of 3314 RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
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 [i](#)

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	24,31,32	2.05	5 (20%)	26,44,47	3.30	8 (30%)

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	-	6/11/33/34	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C13-C14	6.16	1.50	1.32
2	AW	37	MIA	C2-S10	4.30	1.79	1.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AW	37	MIA	C12-C13	-3.27	1.33	1.48
2	AW	37	MIA	C6-N1	2.71	1.36	1.32
2	AW	37	MIA	C4-N3	-2.46	1.31	1.35

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	11.40	110.78	102.27
2	AW	37	MIA	C2-N3-C4	-6.18	106.80	115.32
2	AW	37	MIA	C12-N6-C6	-6.02	113.64	122.55
2	AW	37	MIA	C5-C6-N1	-5.98	115.84	120.81
2	AW	37	MIA	C12-C13-C14	-3.39	120.54	127.14

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.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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

There are no chain breaks in this entry.

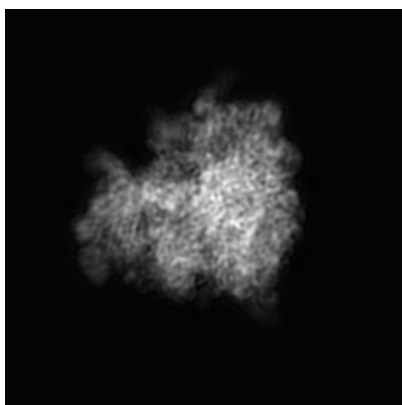
6 Map visualisation [i](#)

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.

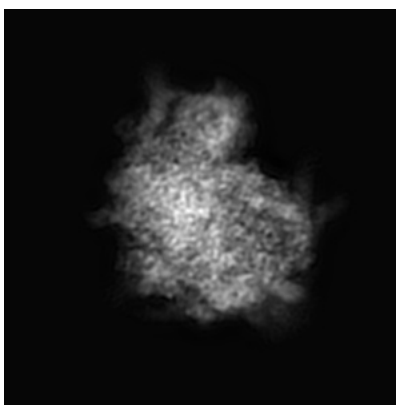
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

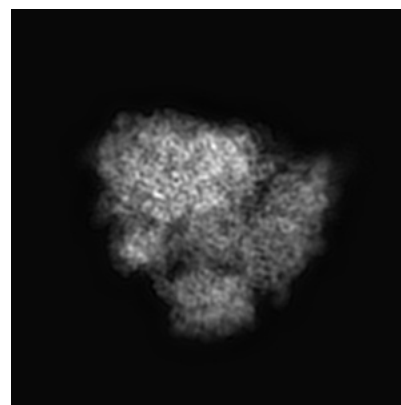
6.1.1 Primary map



X



Y

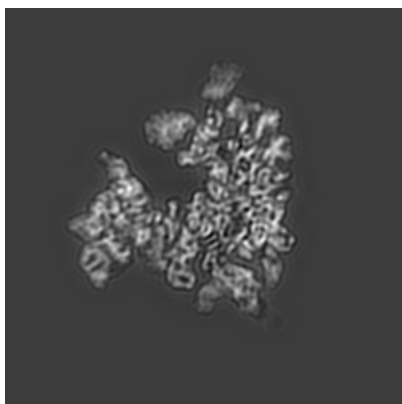


Z

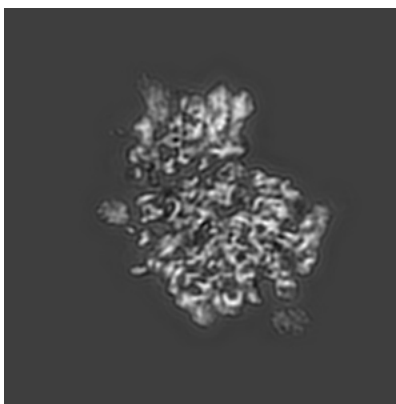
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

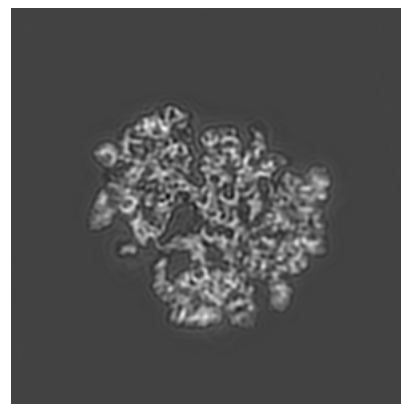
6.2.1 Primary map



X Index: 180



Y Index: 180

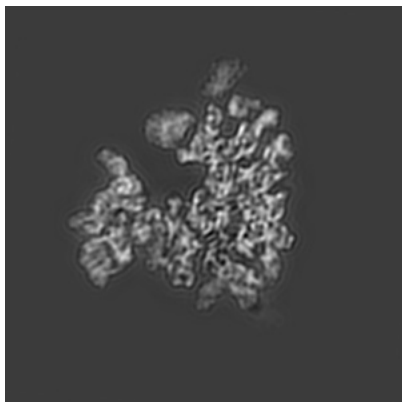


Z Index: 180

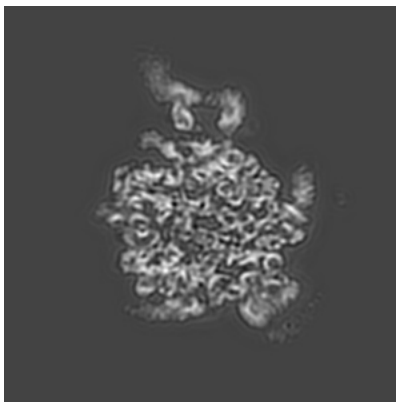
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

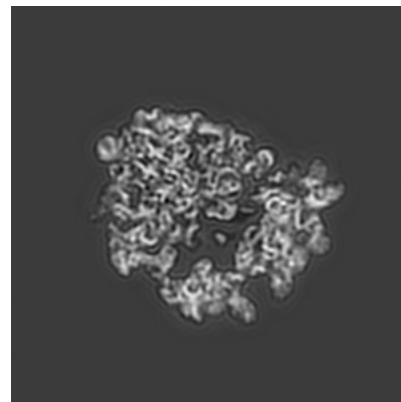
6.3.1 Primary map



X Index: 182



Y Index: 217



Z Index: 190

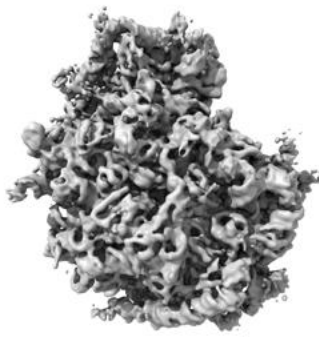
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

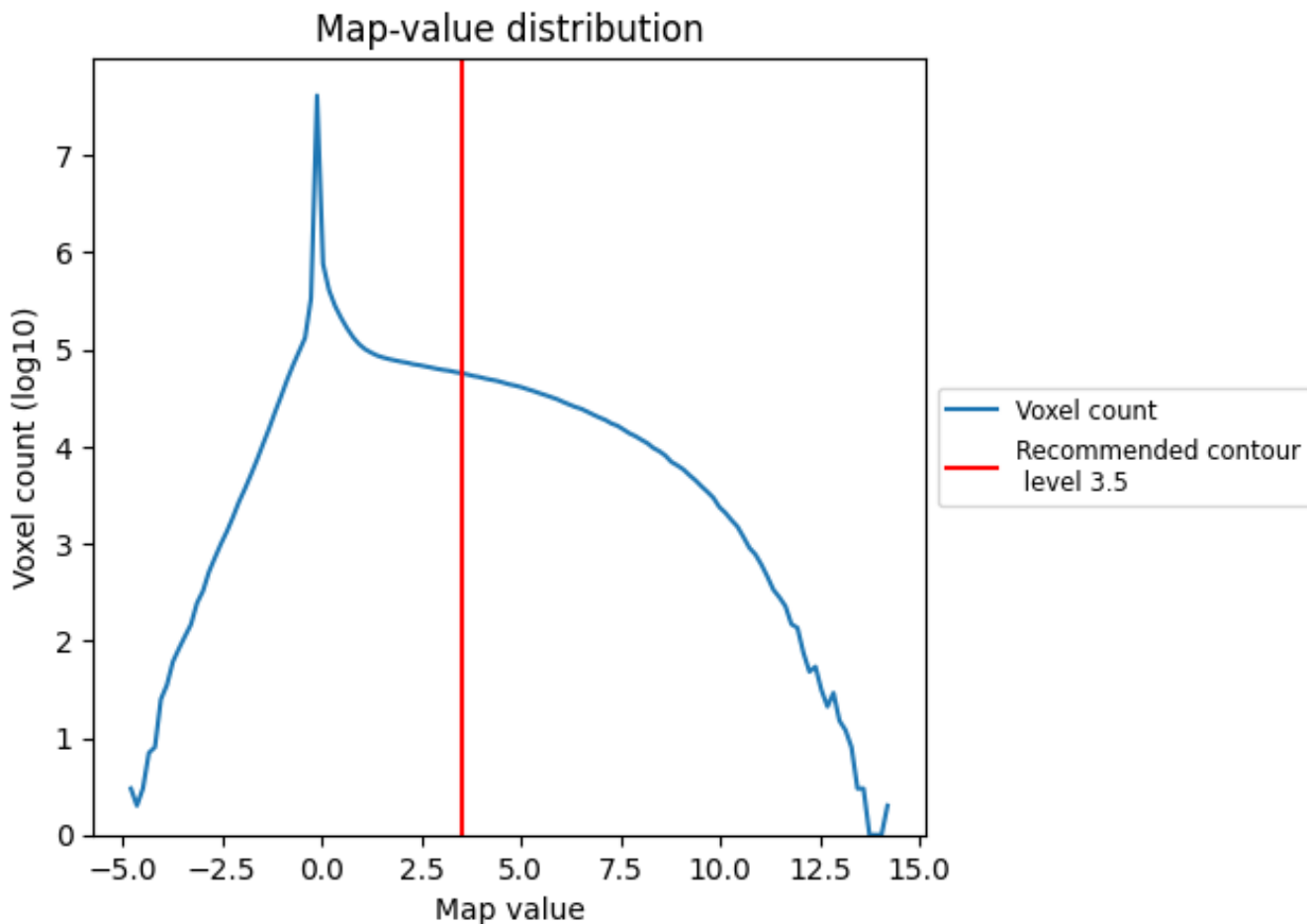
6.5 Mask visualisation

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

7 Map analysis [i](#)

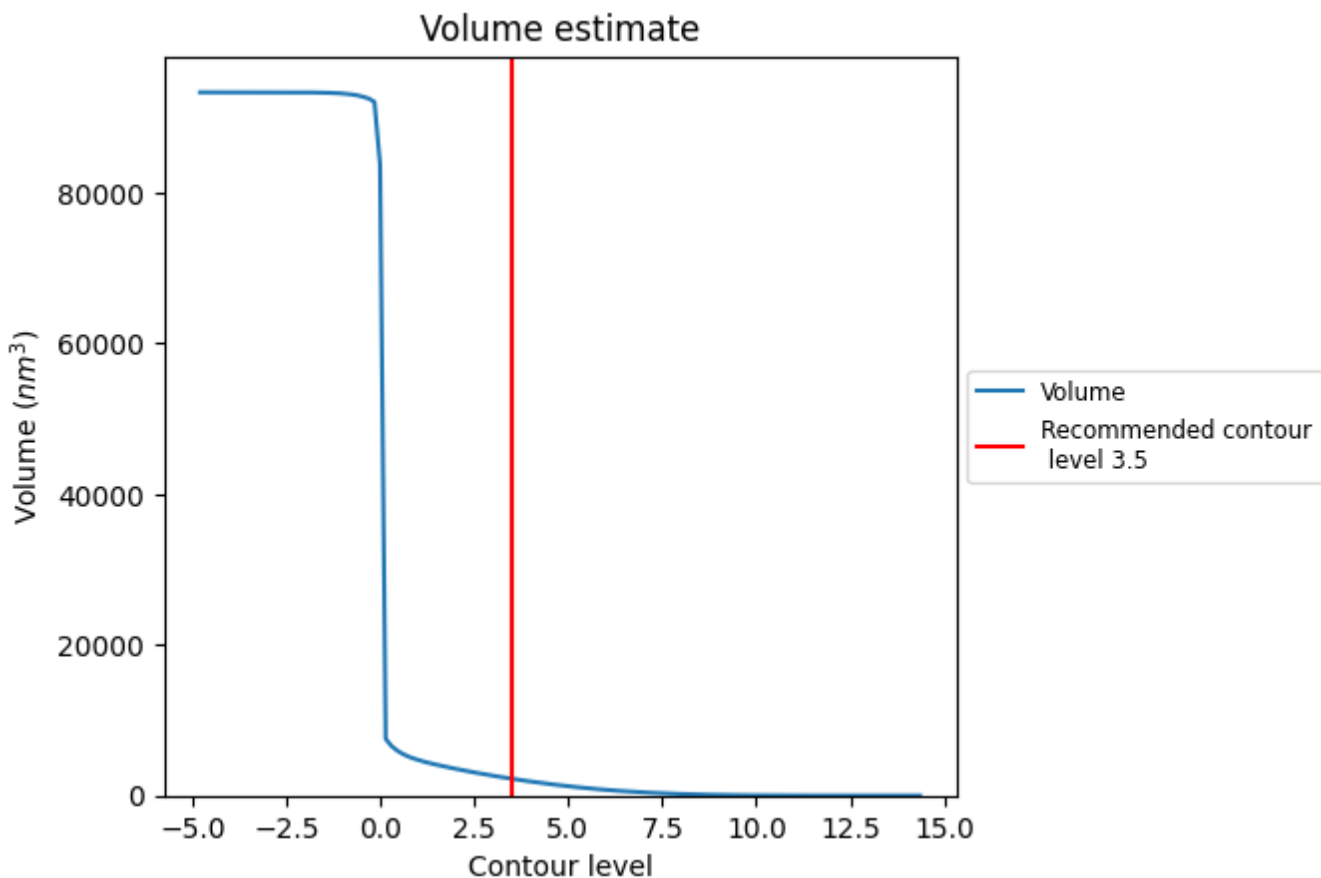
This section contains the results of statistical analysis of the map.

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.

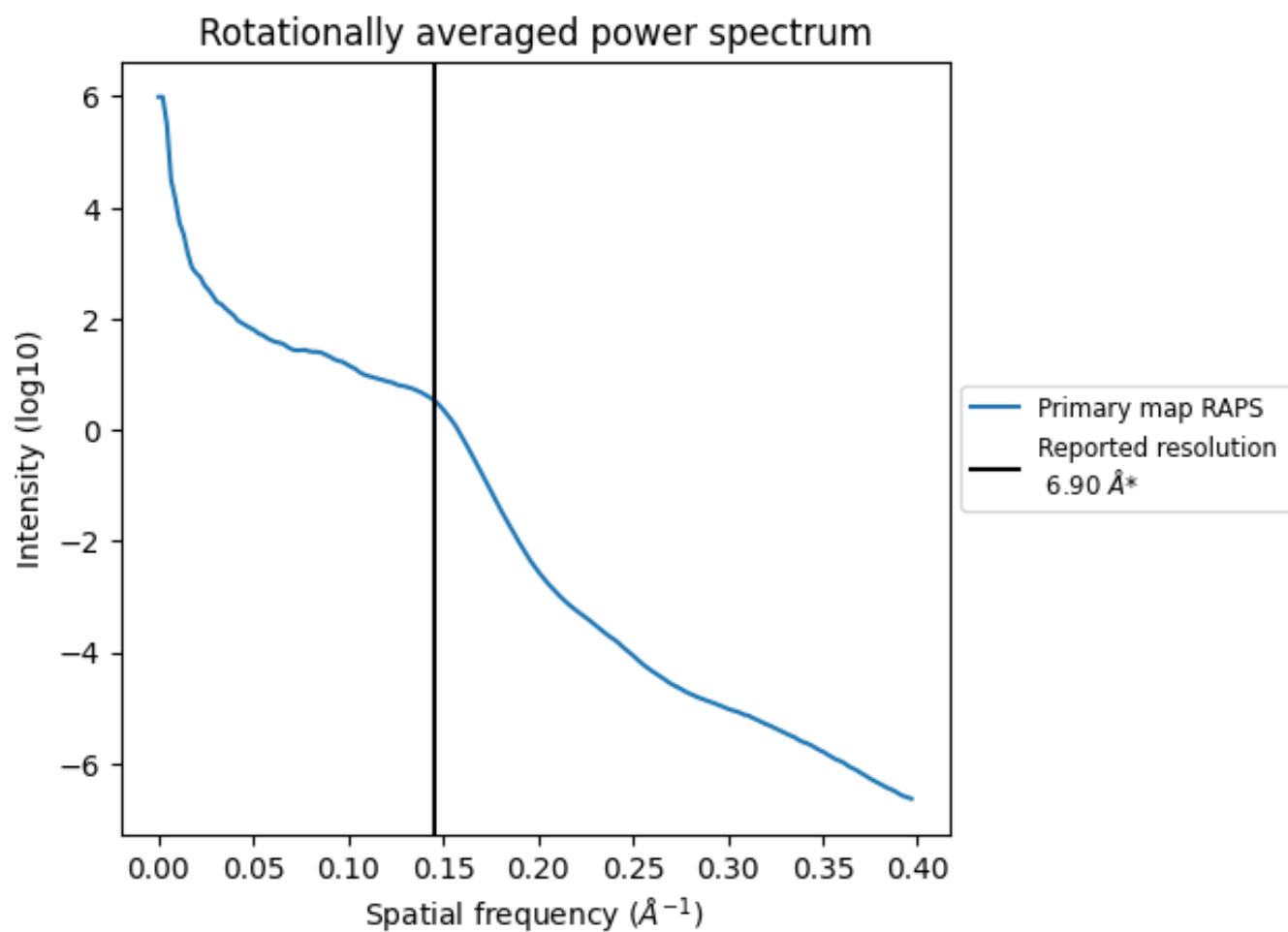
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2230 nm^3 ; 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 i



*Reported resolution corresponds to spatial frequency of 0.145 Å⁻¹

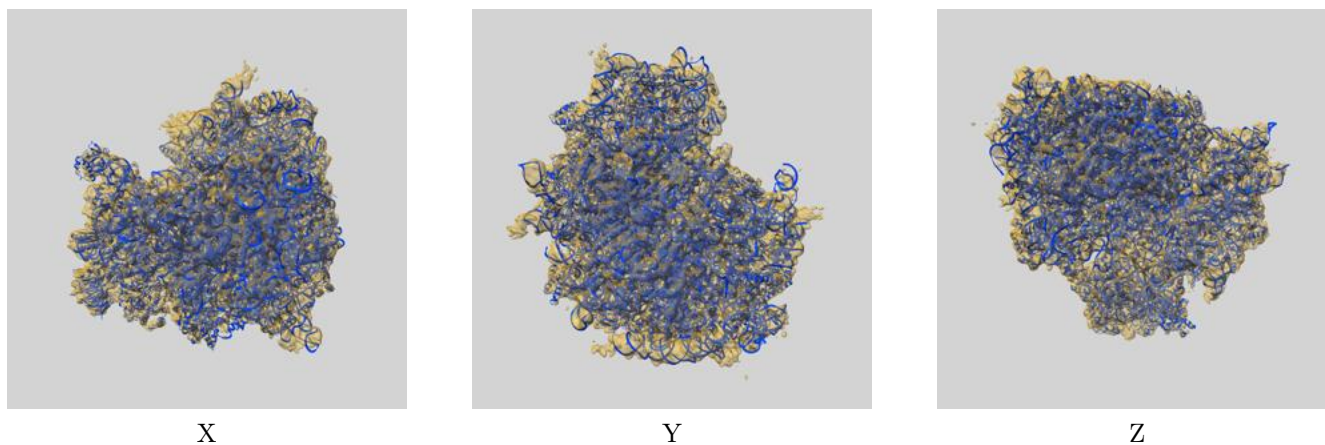
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

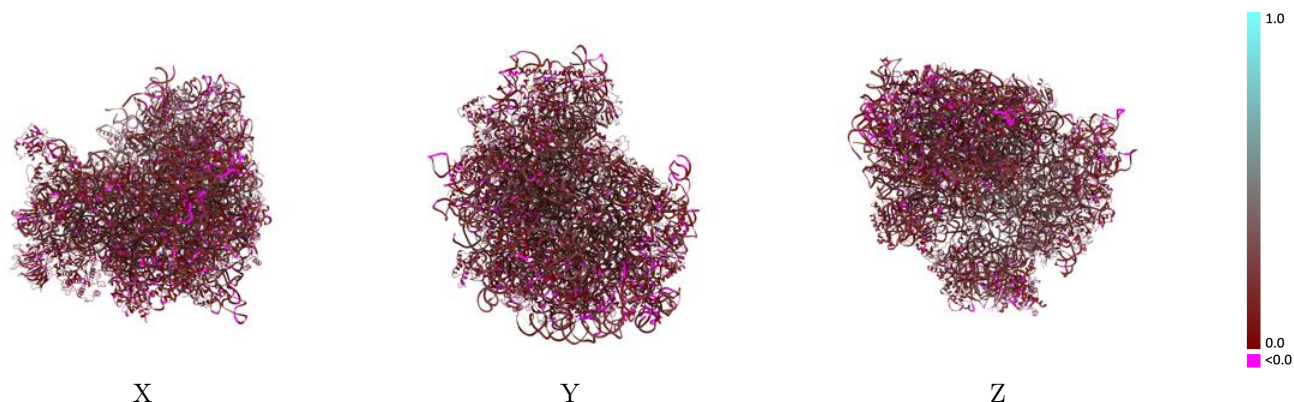
This section contains information regarding the fit between EMDB map EMD-2620 and PDB model 4UJE. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



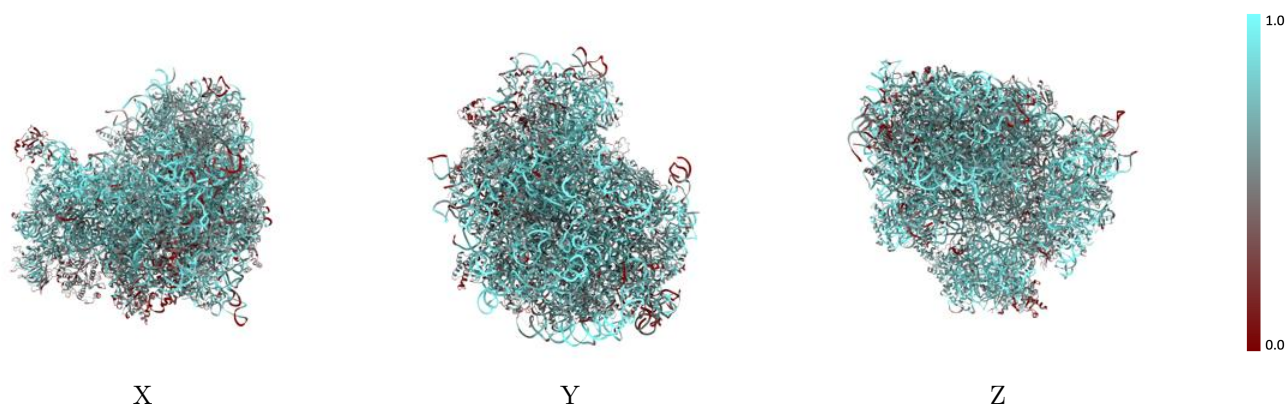
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



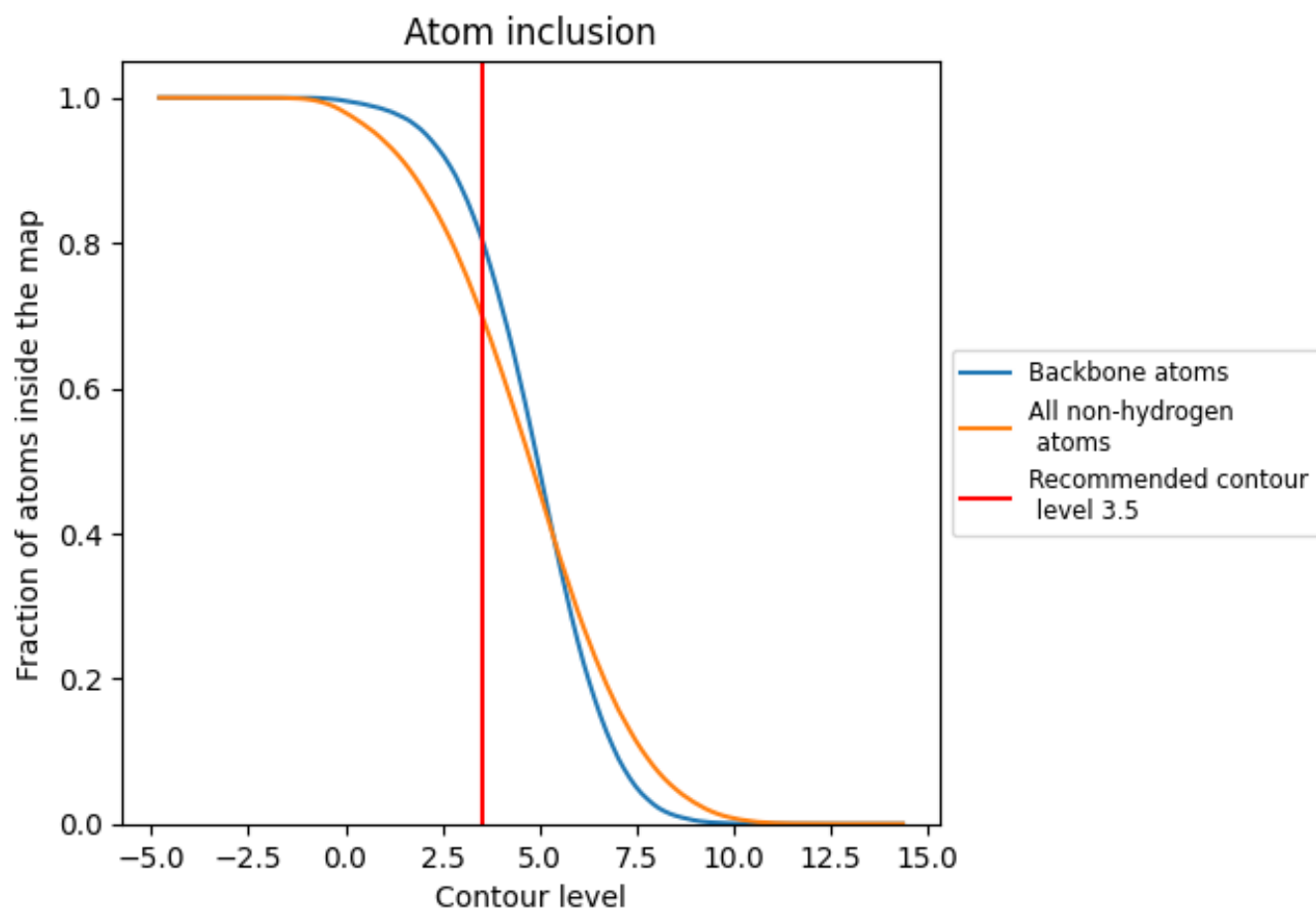
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.7022	 0.1710
A2	 0.8020	 0.1990
A3	 0.8335	 0.2060
A4	 0.9338	 0.2240
AV	 0.6980	 0.1980
AW	 0.6538	 0.1800
AX	 0.4393	 0.1920
B1	 0.8421	 0.1980
BA	 0.4631	 0.1340
BB	 0.5468	 0.1440
BC	 0.5272	 0.1500
BD	 0.6232	 0.1450
BE	 0.6505	 0.1470
BF	 0.5931	 0.1430
BG	 0.6194	 0.1270
BH	 0.3625	 0.1240
BI	 0.4994	 0.1140
BJ	 0.6913	 0.1330
BK	 0.7038	 0.1420
BL	 0.4553	 0.1310
BM	 0.2748	 0.0910
BN	 0.5081	 0.1320
BO	 0.5352	 0.1440
BP	 0.6625	 0.1470
BQ	 0.6735	 0.1220
BR	 0.5191	 0.1350
BS	 0.6767	 0.1460
BT	 0.7486	 0.1450
BU	 0.6317	 0.1180
BV	 0.3923	 0.1150
BW	 0.5798	 0.1400
BX	 0.4418	 0.1450
BY	 0.6821	 0.1330
BZ	 0.5780	 0.1520
Ba	 0.4946	 0.0950

















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Chain	Atom inclusion	Q-score
Bb	0.5024	0.1420
Bc	0.4596	0.1380
Bd	0.7042	0.1140
Be	0.5567	0.1360
Bf	0.4327	0.1020
Bg	0.5612	0.1360
CA	0.4329	0.1330
CB	0.5867	0.1480
CC	0.5340	0.1210
CD	0.6805	0.1550
CE	0.5334	0.1100
CF	0.5175	0.1280
CG	0.5348	0.1330
CH	0.6206	0.1420
CI	0.5103	0.1400
CJ	0.6533	0.1430
CL	0.5206	0.1100
CM	0.6588	0.1560
CN	0.5556	0.1340
CO	0.5860	0.1330
CP	0.5710	0.1350
CQ	0.5112	0.1140
CR	0.5353	0.1250
CS	0.5887	0.1320
CT	0.5357	0.1400
CU	0.4759	0.1410
CV	0.4431	0.1460
CW	0.5118	0.1220
CX	0.5422	0.1390
CY	0.6352	0.1300
CZ	0.5898	0.1460
Ca	0.5492	0.1380
Cb	0.4761	0.1260
Cc	0.4841	0.1410
Cd	0.5750	0.1500
Ce	0.5054	0.1580
Cf	0.5560	0.1140
Cg	0.5161	0.1320
Ch	0.5663	0.1230
Ci	0.5598	0.1380
Cj	0.5556	0.1160
Ck	0.4856	0.1230

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Chain	Atom inclusion	Q-score
Cl	 0.4976	 0.1130
Cm	 0.5362	 0.1320
Cn	 0.4358	 0.1070
Co	 0.4360	 0.1130
Cp	 0.4440	 0.1140
Ct	 0.5290	 0.0840
Cu	 0.2247	 0.0560