



wwPDB EM Validation Summary Report ⓘ

Nov 12, 2022 – 07:07 PM EST

PDB ID : 6UZ7
EMDB ID : EMD-20952
Title : K.lactis 80S ribosome with p/PE tRNA and eIF5B
Authors : Fernandez, I.S.; Huang, B.Y.
Deposited on : 2019-11-14
Resolution : 3.60 Å(reported)
Based on initial model : 3U5B

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:

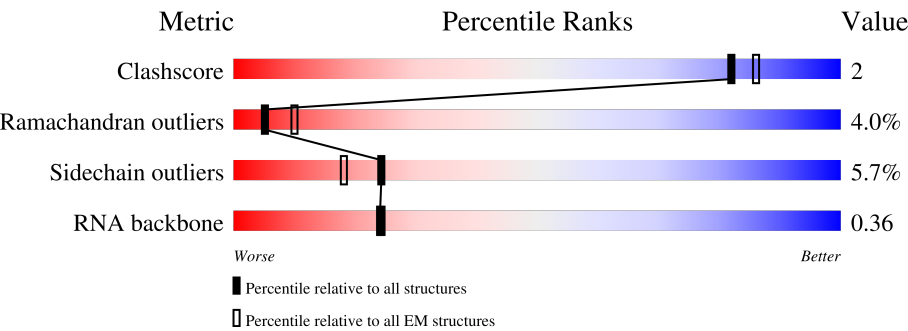
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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)
Clashscore	158937	4297
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	5	3364	<div><div>13%</div><div>66%</div><div>30%</div><div>..</div></div>
2	7	121	<div><div>75%</div><div>23%</div><div>.</div></div>
3	8	2825	<div><div>94%</div></div>
4	AA	254	<div><div>7%</div><div>91%</div><div>6%</div><div>..</div></div>
5	AB	387	<div><div>9%</div><div>87%</div><div>11%</div><div>..</div></div>
6	AC	363	<div><div>12%</div><div>84%</div><div>11%</div><div>...</div></div>
7	AD	297	<div><div>27%</div><div>92%</div><div>7%</div><div>.</div></div>

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Mol	Chain	Length	Quality of chain
8	AE	175	
9	AF	241	
10	AG	255	
11	AH	191	
12	AI	220	
13	AJ	174	
14	AL	199	
15	AM	138	
16	AN	204	
17	AO	199	
18	AP	184	
19	AQ	186	
20	AR	189	
21	AS	172	
22	AT	160	
23	AU	122	
24	AV	137	
25	AW	155	
26	AX	142	
27	AY	127	
28	AZ	136	
29	Ba	149	
30	Bb	62	
31	Bc	105	
32	Bd	114	

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Mol	Chain	Length	Quality of chain
33	Be	130	
34	Bf	107	
35	Bg	125	
36	Bh	120	
37	Bi	100	
38	Bj	88	
39	Bk	78	
40	Bl	51	
41	Bm	128	
42	Bn	23	
43	Bo	106	
44	Bp	92	
45	Bq	217	
46	Br	311	
47	AK	147	
48	A	254	
49	B	255	
50	C	259	
51	D	237	
52	E	261	
53	F	227	
54	G	236	
55	H	190	
56	I	201	
57	J	188	

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Mol	Chain	Length	Quality of chain
58	K	106	
59	L	156	
60	M	134	
61	N	151	
62	O	137	
63	P	142	
64	Q	143	
65	R	136	
66	S	146	
67	T	144	
68	U	117	
69	V	87	
70	W	130	
71	X	145	
72	Y	135	
73	Z	108	
74	a	119	
75	b	82	
76	c	67	
77	d	56	
78	e	63	
79	f	150	
80	g	326	
81	2	1798	
82	1	967	

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Mol	Chain	Length	Quality of chain
83	3	76	<div><div></div><div>92%</div><div>47%</div><div>50%</div><div></div></div>

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 211187 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3269	Total	C	N	O	P	0	0
			69874	31213	12576	22816	3269		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	1923	A	C	conflict	REF 1241923359
5	2021	U	C	conflict	REF 1241923359
5	2051	U	C	conflict	REF 1241923359

- Molecule 2 is a RNA chain called RNA (121-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	157	Total	C	N	O	P	0	0
			3326	1488	573	1108	157		

- Molecule 4 is a protein called KLLA0D16027p.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	249	Total	C	N	O	S	0	0
			1892	1176	385	330	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	384	Total	C	N	O	S	0	0
			3064	1946	580	533	5		

- Molecule 6 is a protein called KLLA0B07139p.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	360	Total	C	N	O	S	0	0
			2743	1725	522	493	3		

- Molecule 7 is a protein called KLLA0D06941p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	295	Total	C	N	O	S	0	0
			2384	1510	417	456	1		

- Molecule 8 is a protein called KLLA0B04686p.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	164	Total	C	N	O		0	0
			1321	847	247	227			

- Molecule 9 is a protein called KLLA0D03410p.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	222	Total	C	N	O	S	0	0
			1774	1138	319	316	1		

- Molecule 10 is a protein called KLLA0E00573p.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	233	Total	C	N	O	S	0	0
			1817	1160	324	330	3		

- Molecule 11 is a protein called KLLA0F04499p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AH	191	Total	C	N	O	S	0	0
			1528	965	277	284	2		

- Molecule 12 is a protein called KLLA0D05643p.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	207	Total	C	N	O	S	0	0
			1690	1074	319	292	5		

- Molecule 13 is a protein called KLLA0F08261p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	168	Total	C	N	O	S	0	0
			1349	845	255	245	4		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	197	Total	C	N	O		0	0
			1581	988	317	276			

- Molecule 15 is a protein called KLLA0B13409p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	136	Total	C	N	O		0	0
			1045	666	196	183			

- Molecule 16 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AN	202	Total	C	N	O	S	0	0
			1709	1069	359	280	1		

- Molecule 17 is a protein called KLLA0F04675p.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	198	Total	C	N	O	S	0	0
			1571	1013	290	267	1		

- Molecule 18 is a protein called KLLA0A06336p.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	180	Total	C	N	O		0	0
			1432	885	287	260			

- Molecule 19 is a protein called KLLA0A07227p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	184	Total	C	N	O		0	0
			1444	911	290	243			

- Molecule 20 is a protein called KLLA0E12453p.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	188	Total	C	N	O	S	0	0
			1522	933	328	259	2		

- Molecule 21 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	169	Total	C	N	O	S	0	0
			1422	916	265	238	3		

- Molecule 22 is a protein called KLLA0E23651p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	158	Total	C	N	O	S	0	0
			1262	797	240	220	5		

- Molecule 23 is a protein called KLLA0D05181p.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AU	100	Total	C	N	O	0	0
			807	524	131	152		

- Molecule 24 is a protein called KLLA0E06997p.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	132	Total	C	N	O	S	0	0
			976	612	182	174	8		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	AW	62	Total	C	N	O	0	0
			515	330	103	82		

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AX	121	Total	C	N	O	S	0	0
			964	620	169	174	1		

- Molecule 27 is a protein called KLLA0B05742p.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	AY	125	Total	C	N	O	0	0
			992	622	189	181		

- Molecule 28 is a protein called KLLA0E03455p.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	AZ	134	Total	C	N	O	0	0
			1089	708	199	182		

- Molecule 29 is a protein called RPL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ba	147	Total	C	N	O	S	0	0
			1156	740	225	189	2		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Bb	57	Total	C	N	O	0	0
			458	287	99	72		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bc	97	Total	C	N	O	S	0	0
			740	477	125	137	1		

- Molecule 32 is a protein called KLLA0B02937p.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bd	106	Total	C	N	O	S	0	0
			869	553	167	147	2		

- Molecule 33 is a protein called KLLA0E06843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Be	122	Total	C	N	O	S	0	0
			980	618	198	162	2		

- Molecule 34 is a protein called KLLA0D07405p.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bf	105	Total	C	N	O	S	0	0
			837	531	161	144	1		

- Molecule 35 is a protein called KLLA0C08371p.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bg	121	Total	C	N	O	S	0	0
			951	591	192	167	1		

- Molecule 36 is a protein called KLLA0F05247p.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bh	116	Total	C	N	O	S	0	0
			961	608	187	166			

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bi	98	Total	C	N	O	S	0	0
			766	479	155	131	1		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bj	85	Total	C	N	O	S	0	0
			675	410	148	111	6		

- Molecule 39 is a protein called KLLA0C18216p.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bk	76	Total	C	N	O	S	0	0
			619	398	114	107			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bl	49	Total	C	N	O	S	0	0
			428	266	96	64	2		

- Molecule 41 is a protein called Ubiquitin fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bm	51	Total	C	N	O	S	0	0
			410	254	85	66	5		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bn	23	Total	C	N	O	S	0	0
			218	133	60	24	1		

- Molecule 43 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bo	101	Total	C	N	O	S	0	0
			814	509	163	136	6		

- Molecule 44 is a protein called KLLA0E05941p.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Bp	87	Total	C	N	O	S	0	0
			660	404	133	117	6		

- Molecule 45 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bq	217	Total	C	N	O	S	0	0
			1716	1097	297	313	9		

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Br	195	Total	C	N	O	S	0	0
			1508	968	258	278	4		

- Molecule 47 is a protein called GDPCP.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AK	147	Total	C	N	O		0	0
			735	441	147	147			

- Molecule 48 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A	206	Total	C	N	O	S	0	0
			1616	1035	285	294	2		

- Molecule 49 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B	214	Total	C	N	O	S	0	0
			1722	1089	313	317	3		

- Molecule 50 is a protein called KLLA0F09812p.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C	217	Total	C	N	O	S	0	0
			1629	1041	287	297	4		

- Molecule 51 is a protein called KLLA0D08305p.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	D	223	Total	C	N	O	S	0	0
			1744	1108	313	318	5		

- Molecule 52 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 53 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	G	226	Total	C	N	O	S	0	0
			1812	1134	348	326	4		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	H	184	Total	C	N	O	0	0
			1483	950	270	263		

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	I	188	Total	C	N	O	S	0	0
			1493	926	301	265	1		

- Molecule 57 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 58 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 59 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	L	145	Total	C	N	O	S	0	0
			1168	745	222	198	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	M	122	Total	C	N	O	0	0
			922	575	167	180		

- Molecule 61 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 62 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 63 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	P	119	Total	C	N	O	S	0	0
			950	611	170	164	5		

- Molecule 64 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Q	141	Total	C	N	O		0	0
			1105	709	204	192			

- Molecule 65 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	R	123	Total	C	N	O	S	0	0
			983	614	181	185	3		

- Molecule 66 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	S	138	Total	C	N	O	S	0	0
			1138	707	231	198	2		

- Molecule 67 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	T	143	Total	C	N	O		0	0
			1110	693	210	207			

- Molecule 68 is a protein called KLLA0F25542p.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 69 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 70 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 71 is a protein called RPS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	X	143	Total	C	N	O	S	0	0
			1110	704	214	189	3		

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Y	134	Total	C	N	O		0	0
			1061	665	207	189			

- Molecule 73 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	a	100	Total	C	N	O	S	0	0
			798	491	170	131	6		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	b	82	Total	C	N	O	S	0	0
			617	384	113	114	6		

- Molecule 76 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	e	55	Total	C	N	O	S	0	0
			443	276	90	76	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	f	44	Total	C	N	O	S	0	0
			337	213	65	55	4		

- Molecule 80 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 81 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	676	G	U	conflict	GB 49642208
2	678	U	G	conflict	GB 49642208

- Molecule 82 is a protein called KLLA0F23265p.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	1	600	Total	C	N	O	S	0	0
			4702	2981	808	890	23		

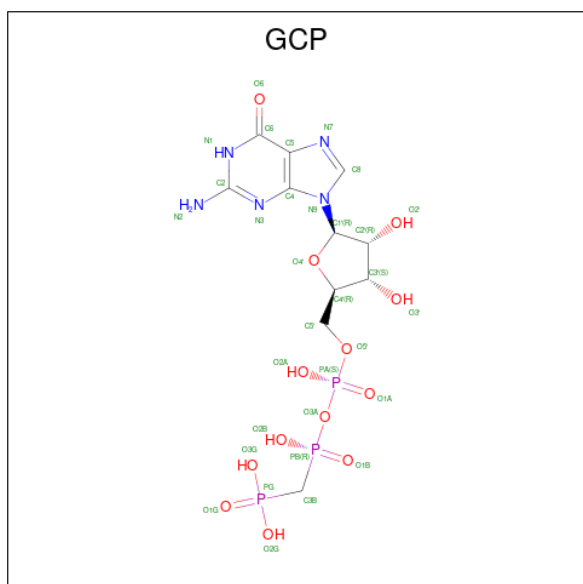
- Molecule 83 is a RNA chain called RNA (76-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	76	Total	C	N	O	P	0	0
			1623	725	295	528	75		

- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Bj	1	Total	Zn	0
			1	1	
84	Bm	1	Total	Zn	0
			1	1	
84	Bo	1	Total	Zn	0
			1	1	
84	a	1	Total	Zn	0
			1	1	
84	b	1	Total	Zn	0
			1	1	
84	f	1	Total	Zn	0
			1	1	

- Molecule 85 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

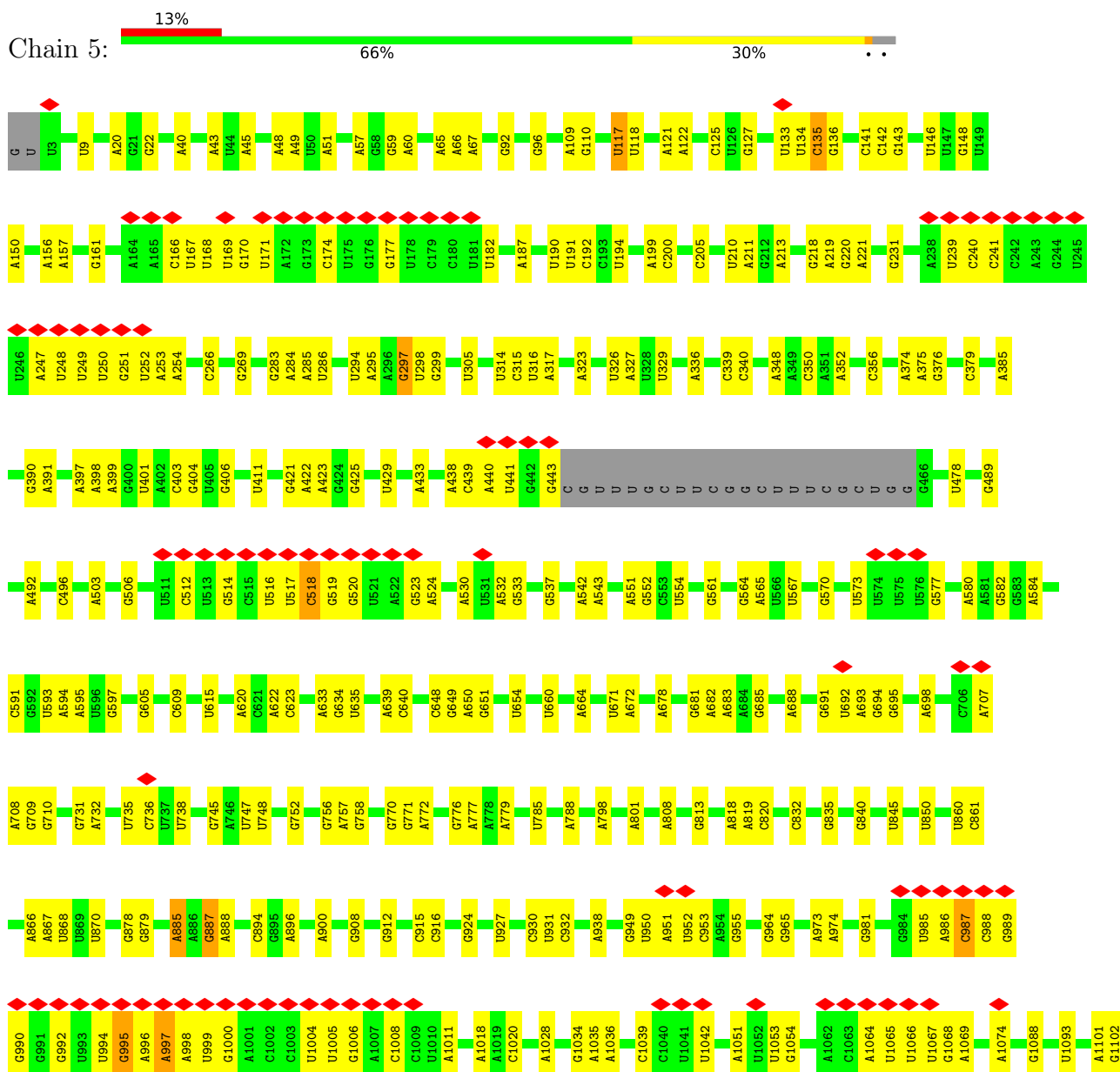


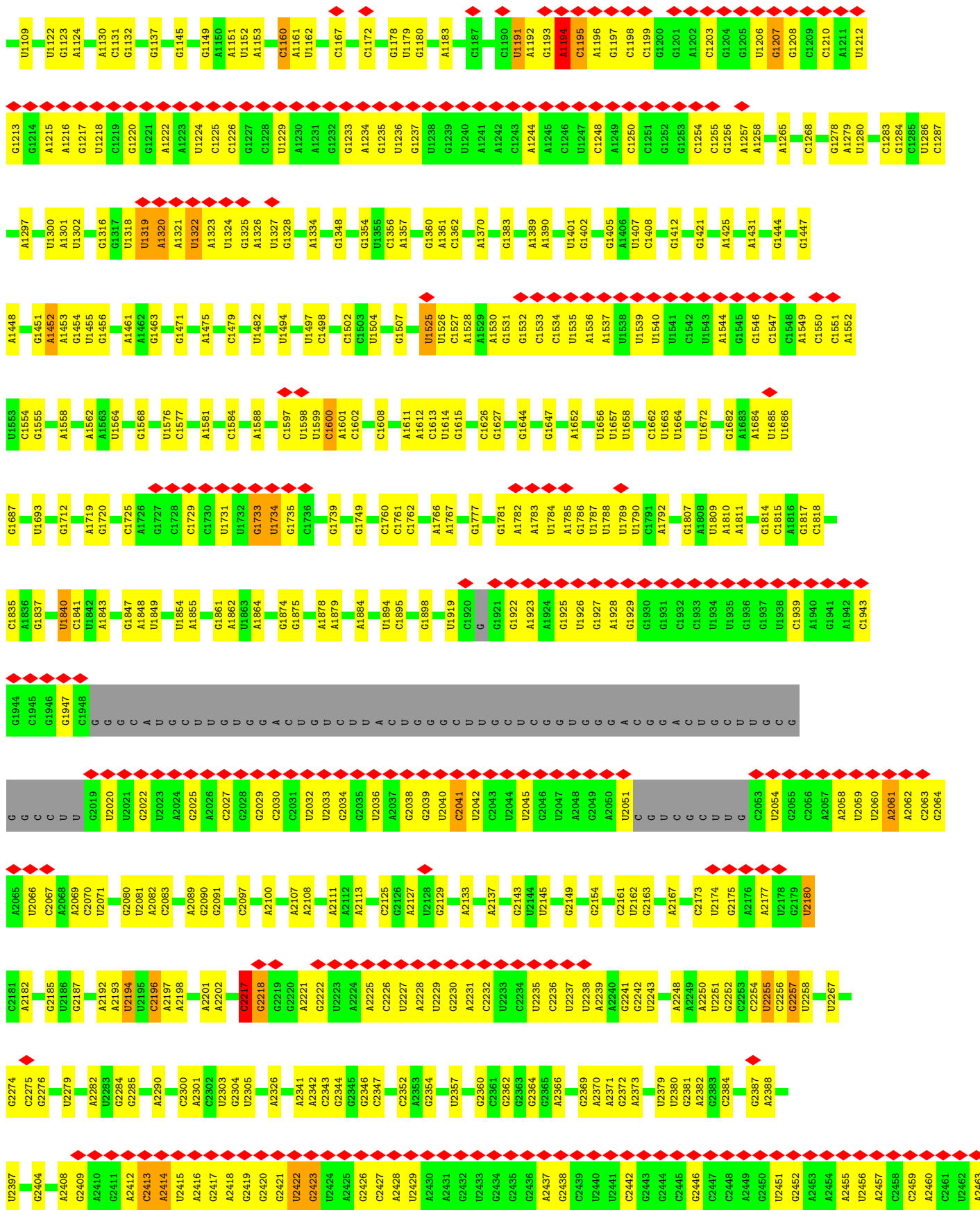
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
85	1	1	32	11	5	13	3	0

3 Residue-property plots

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

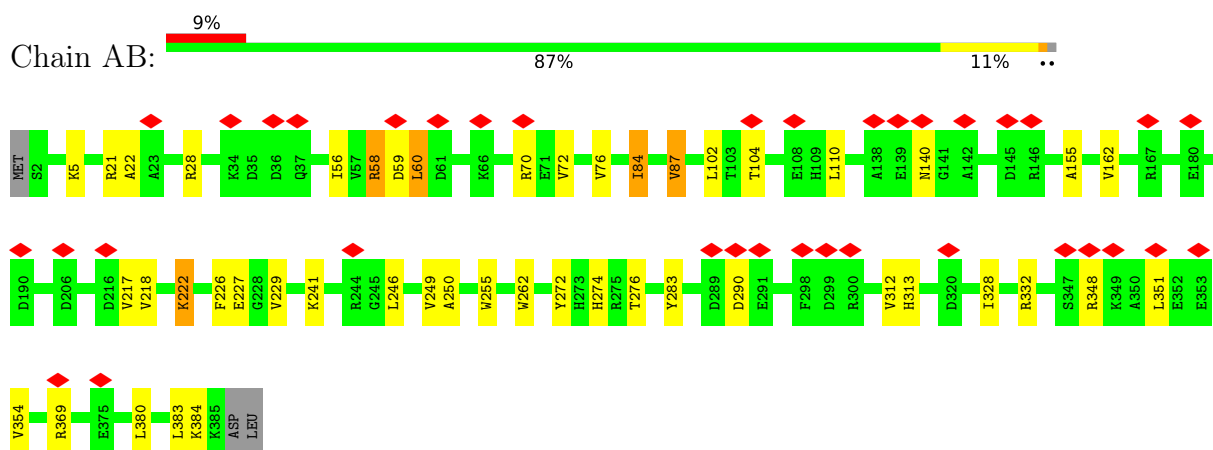
• Molecule 1: 25S ribosomal RNA



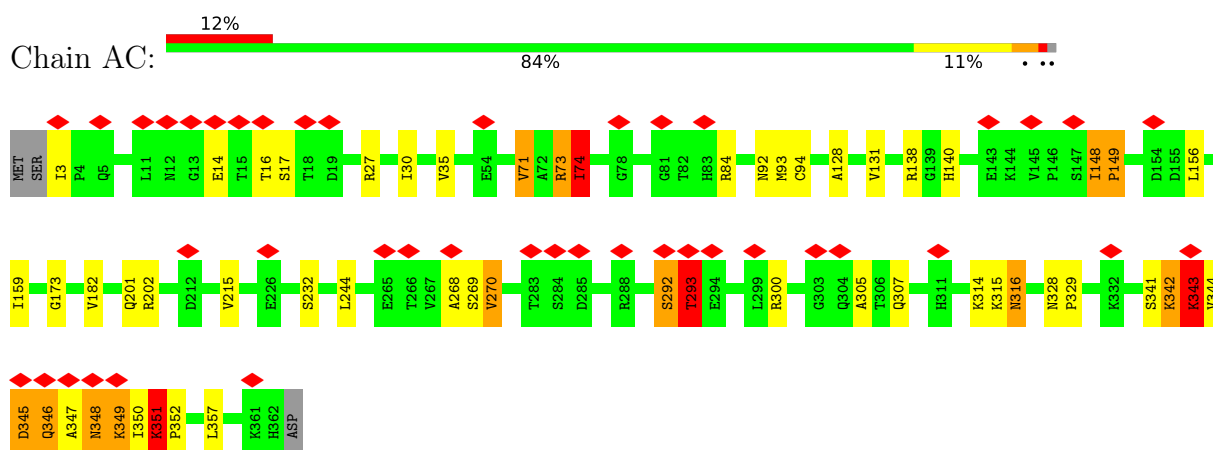




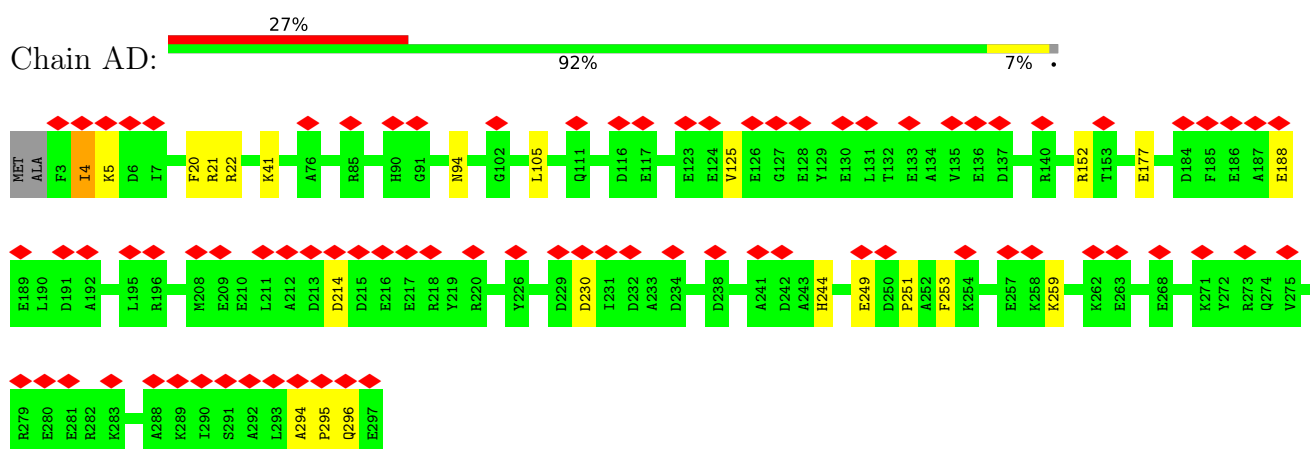




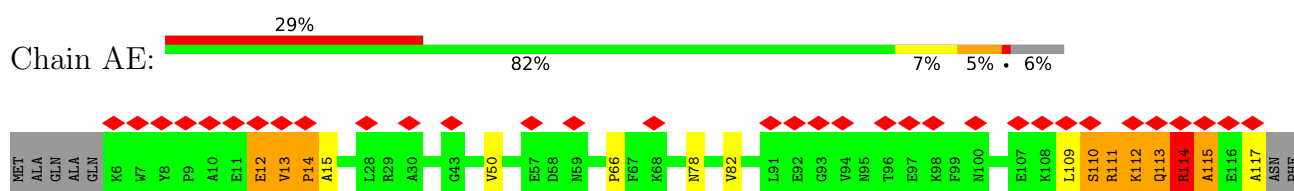
• Molecule 6: KLLA0B07139p

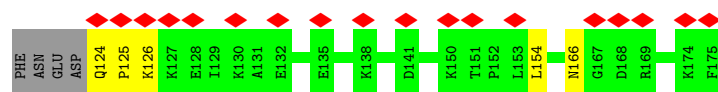


• Molecule 7: KLLA0D06941p

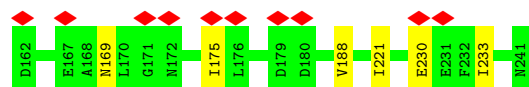
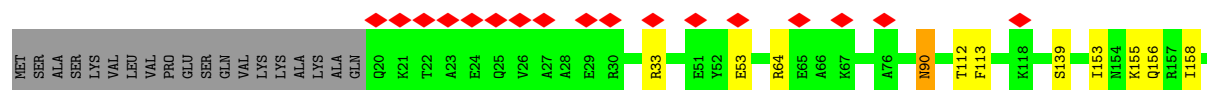
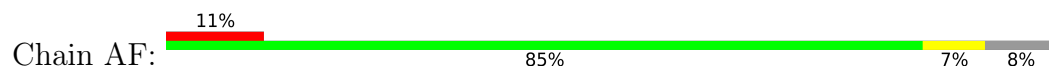


• Molecule 8: KLLA0B04686p

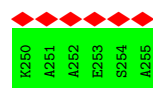
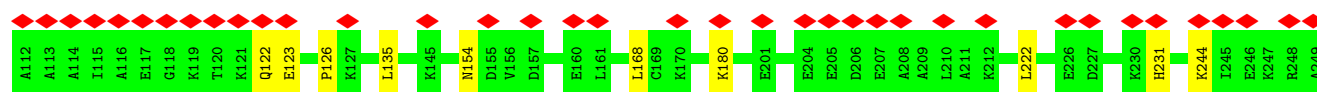
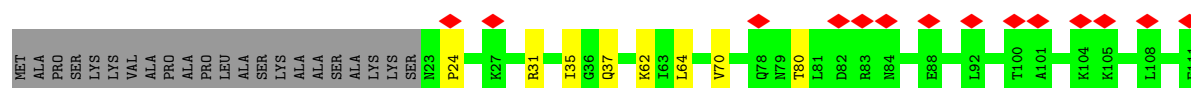
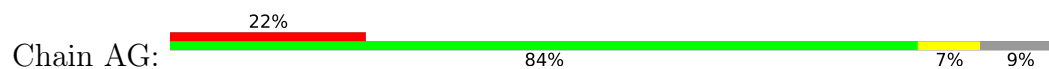




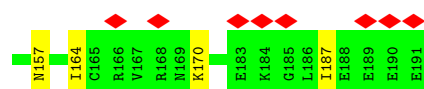
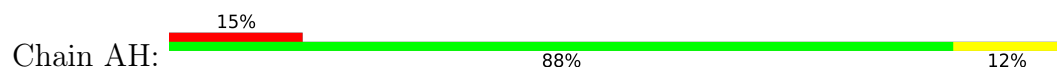
• Molecule 9: KLLA0D03410p



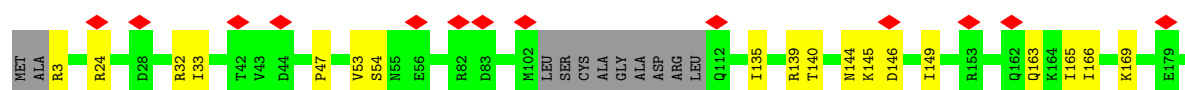
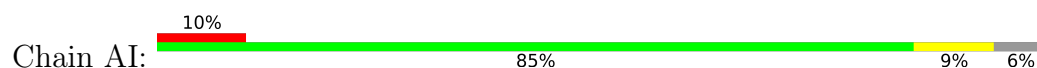
• Molecule 10: KLLA0E00573p

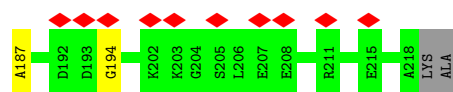


• Molecule 11: KLLA0F04499p

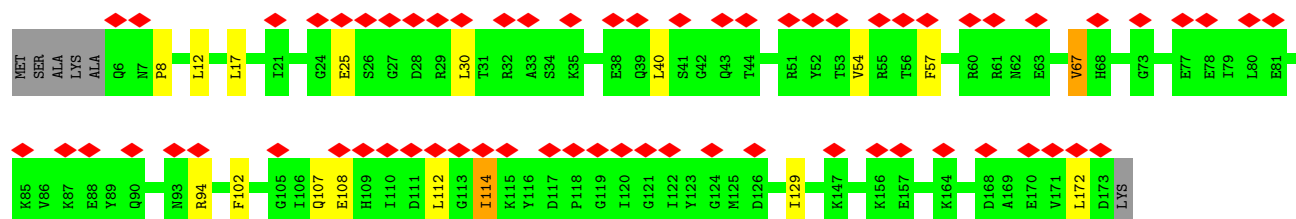
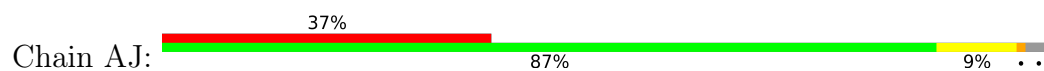


• Molecule 12: KLLA0D05643p

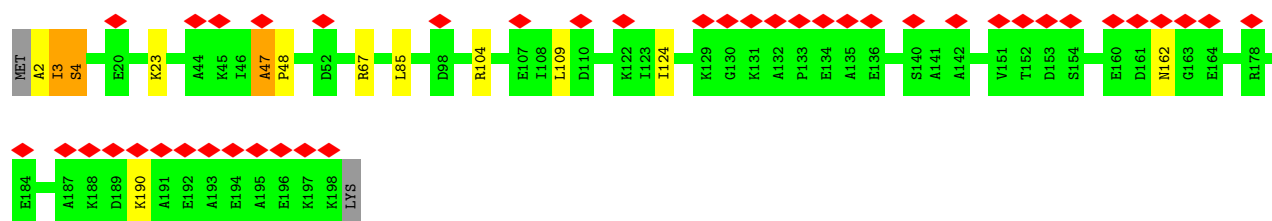
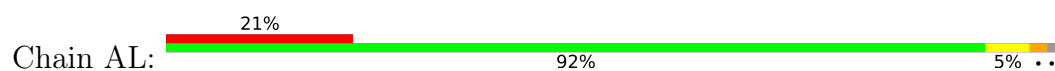




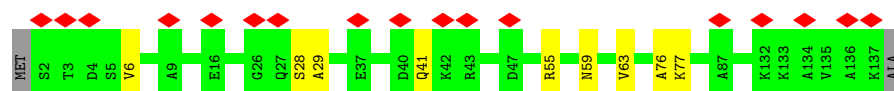
• Molecule 13: KLLA0F08261p



• Molecule 14: 60S ribosomal protein L13



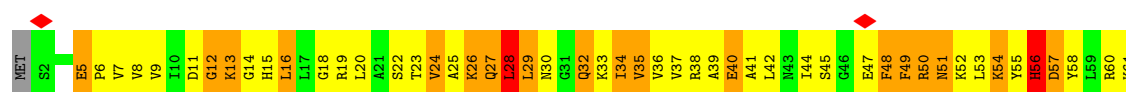
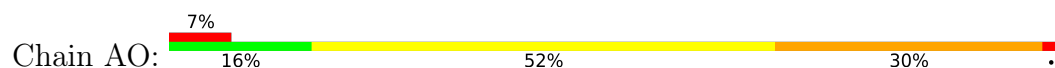
• Molecule 15: KLLA0B13409p

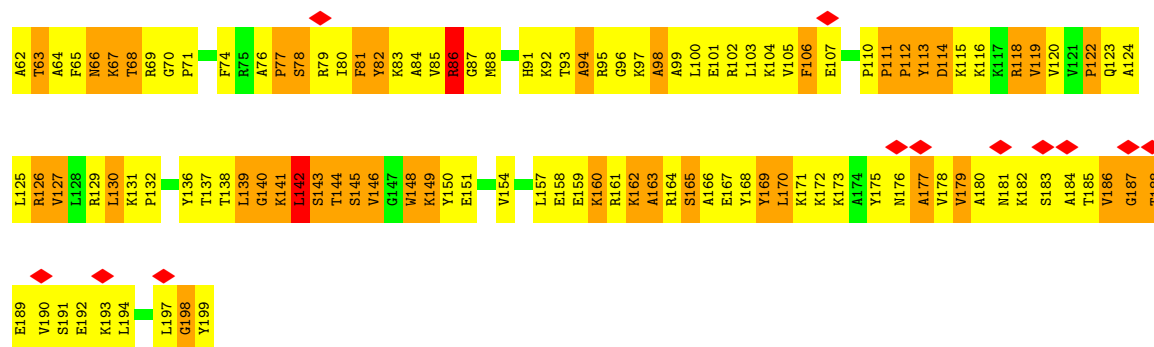


• Molecule 16: Ribosomal protein L15

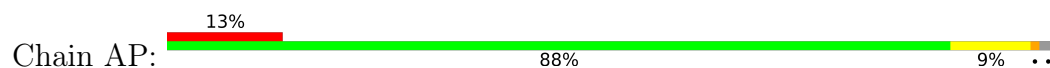


• Molecule 17: KLLA0F04675p

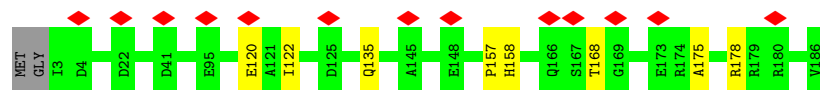




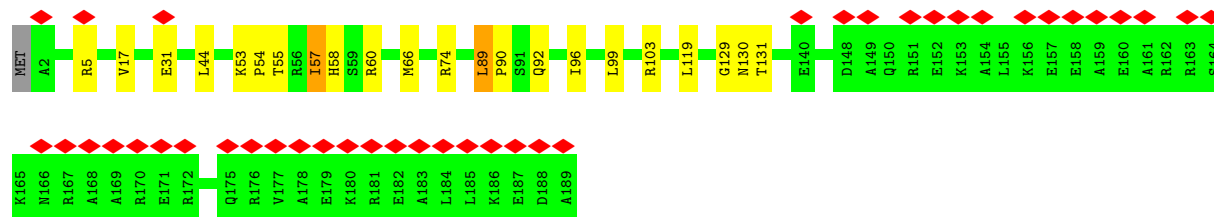
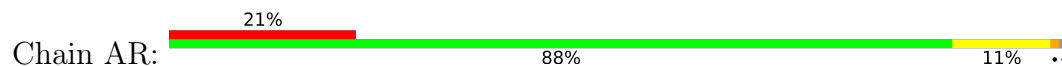
• Molecule 18: KLLA0A06336p



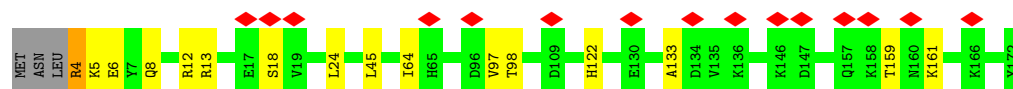
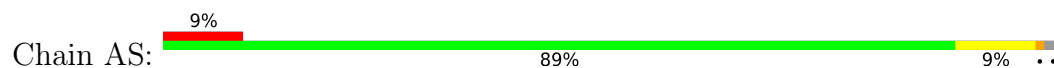
• Molecule 19: KLLA0A07227p



• Molecule 20: KLLA0E12453p



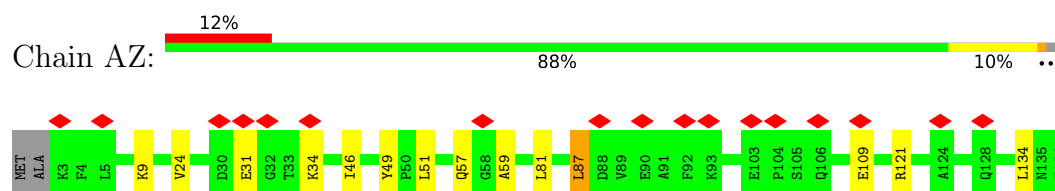
• Molecule 21: 60S ribosomal protein L20



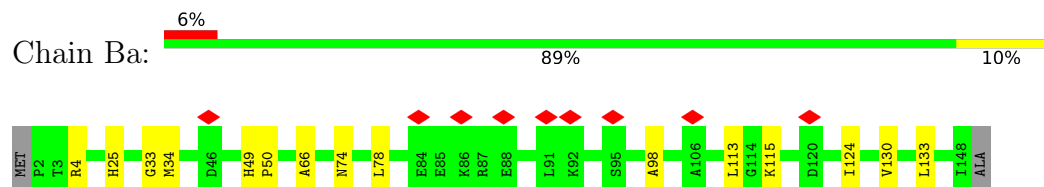
• Molecule 22: KLLA0E23651p



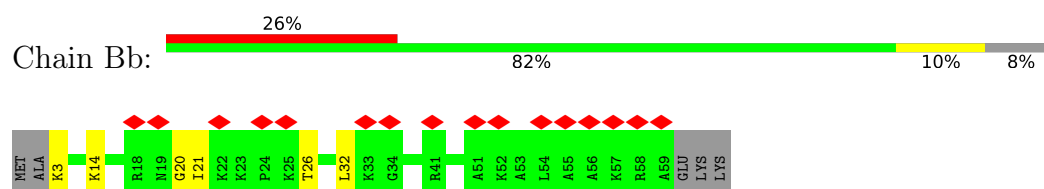
- Molecule 28: KLLA0E03455p



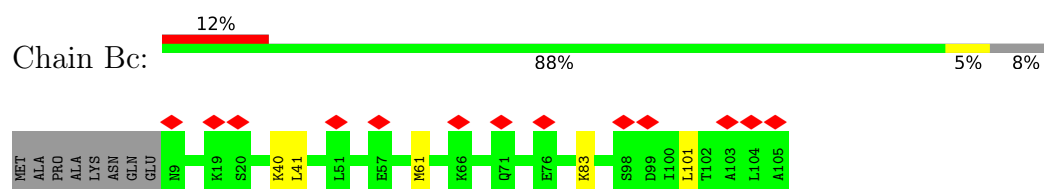
- Molecule 29: RPL28



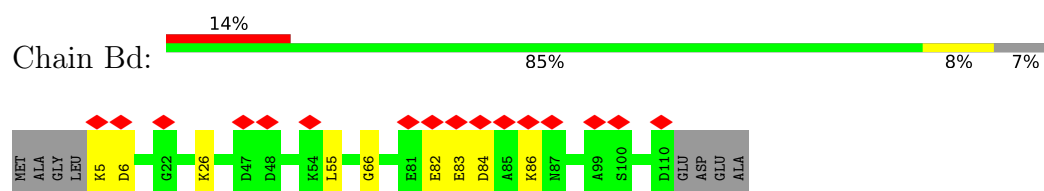
- Molecule 30: 60S ribosomal protein L29



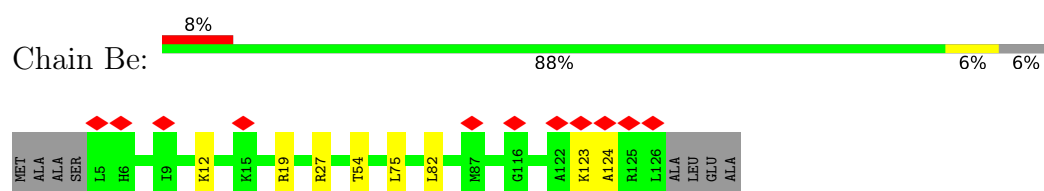
- Molecule 31: 60S ribosomal protein L30



- Molecule 32: KLLA0B02937p

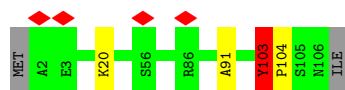


- Molecule 33: KLLA0E06843p

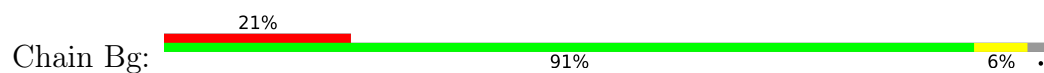


- Molecule 34: KLLA0D07405p

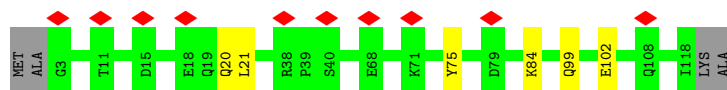




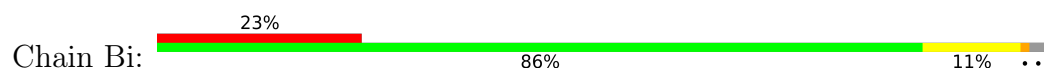
- Molecule 35: KLLA0C08371p



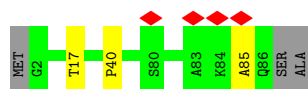
- Molecule 36: KLLA0F05247p



- Molecule 37: 60S ribosomal protein L36



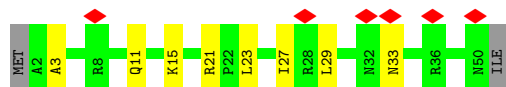
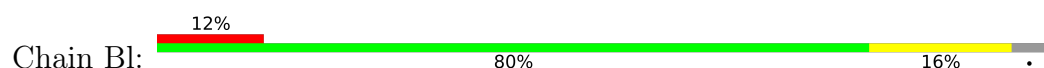
- Molecule 38: Ribosomal protein L37



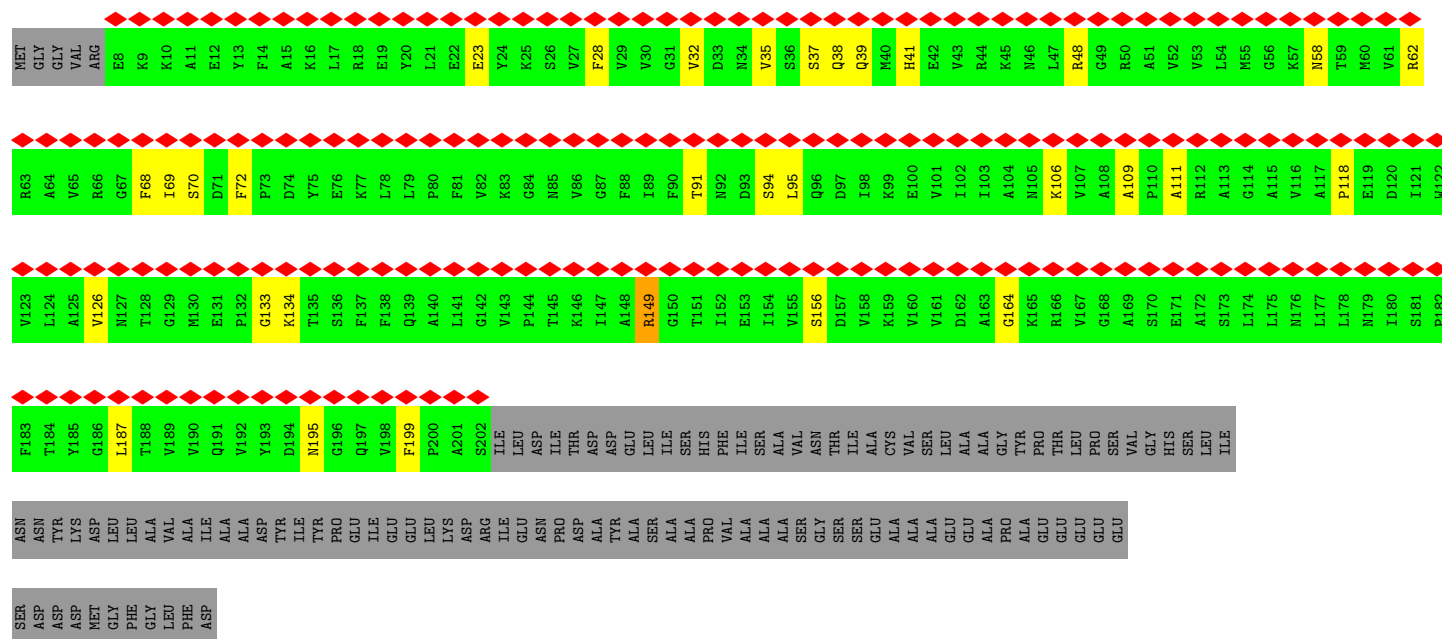
- Molecule 39: KLLA0C18216p



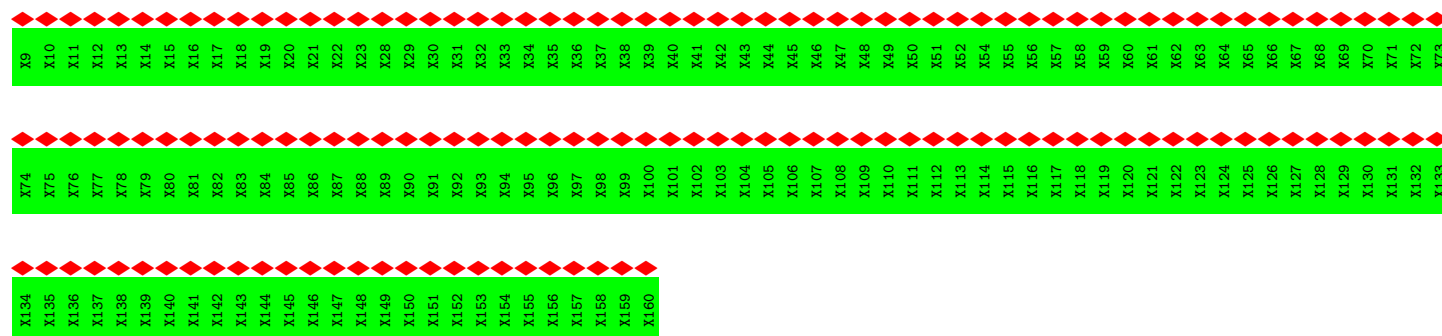
- Molecule 40: 60S ribosomal protein L39



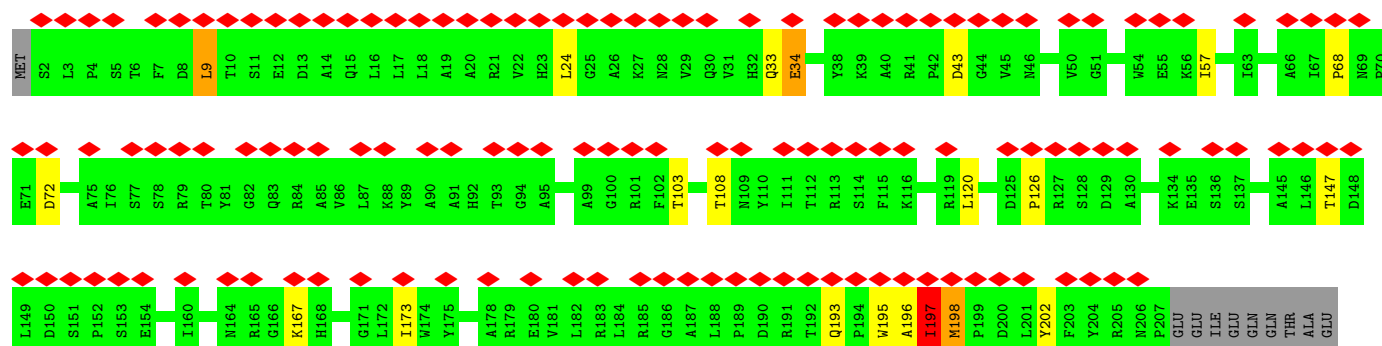
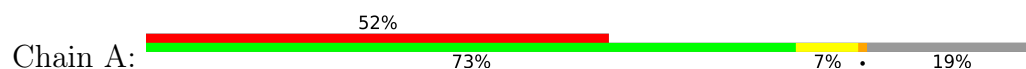
- Molecule 41: Ubiquitin fusion protein



• Molecule 47: GDPCP




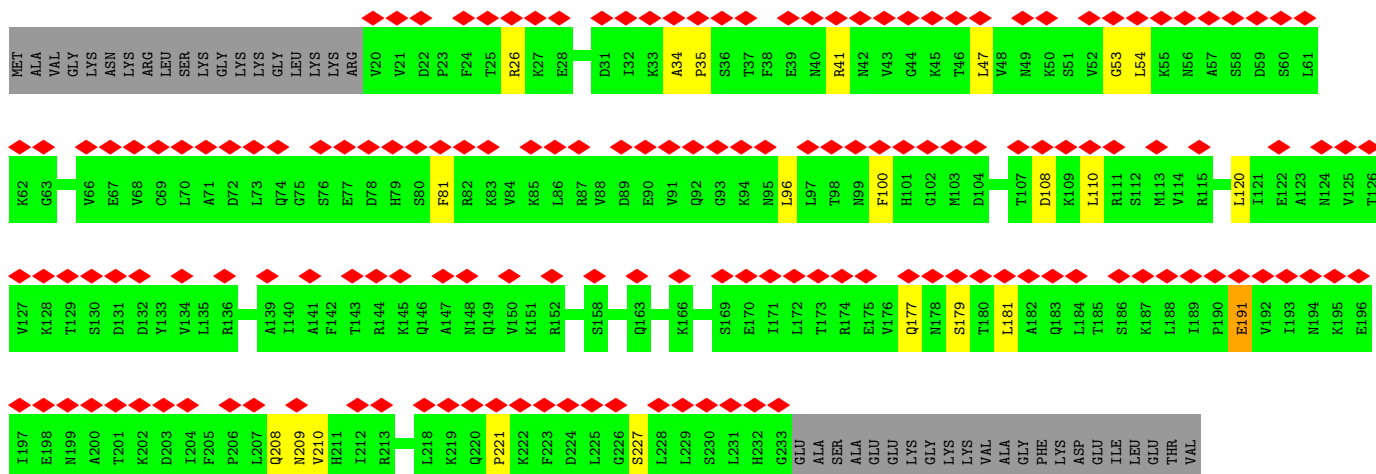
• Molecule 48: 40S ribosomal protein S0



GLU
GLU
VAL
VAL
SER
SER
GLY
GLU
GLN
THR
THR
GLU
GLU
ALA
VAL
ASP
ALA
THR
GLY
GLU
GLU
GLN
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ALA
GLU
GLY
GLN
ALA
GLN
GLU
TRP
ASN

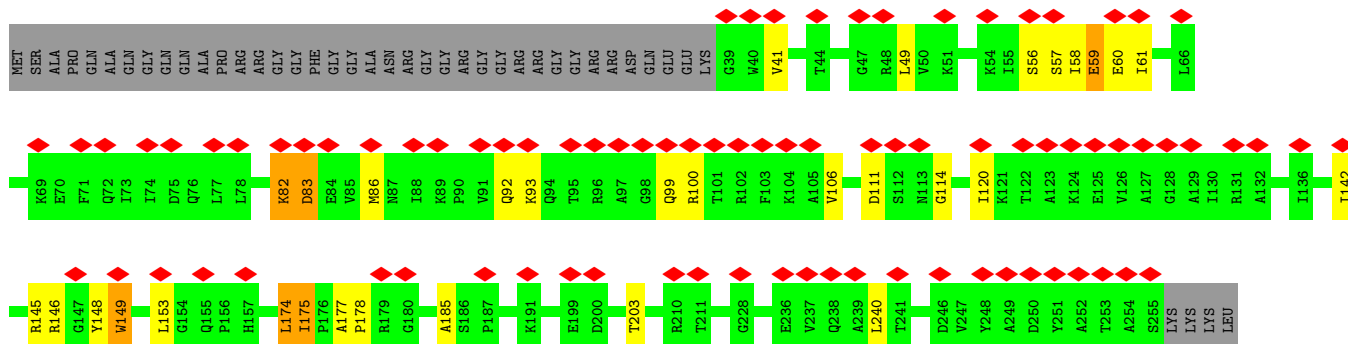
• Molecule 49: 40S ribosomal protein S1

Chain B: 

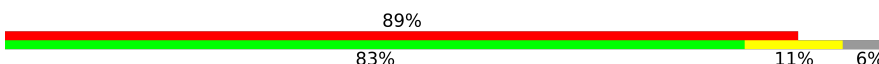


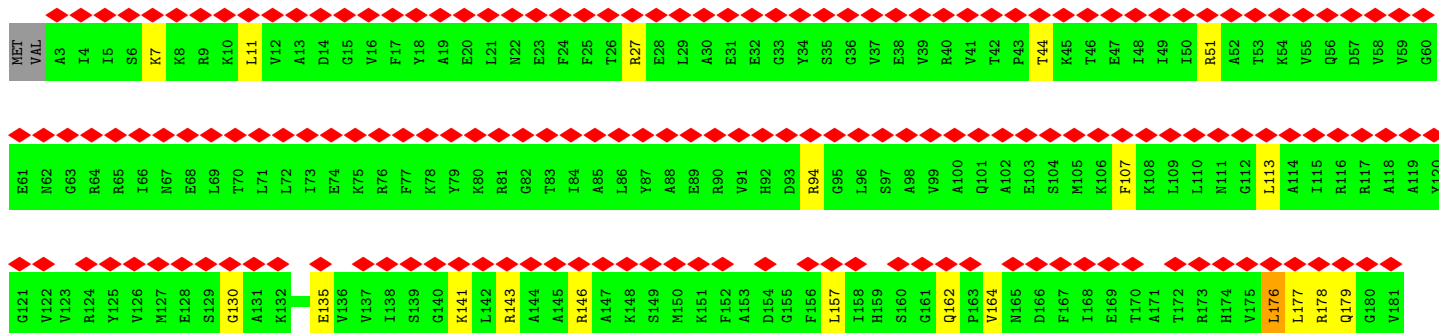
• Molecule 50: KLLA0F09812p

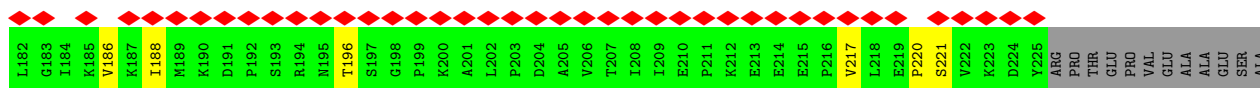
Chain C: 



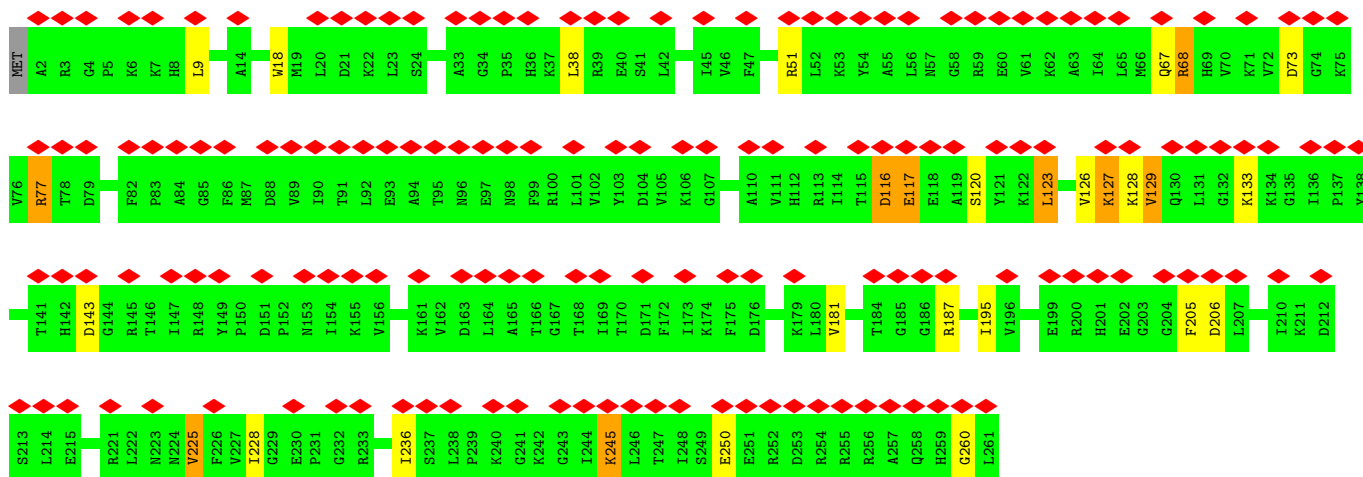
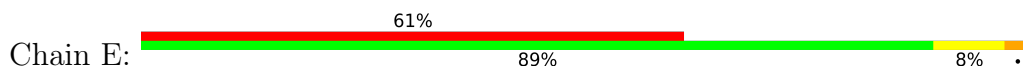
• Molecule 51: KLLA0D08305p

Chain D: 

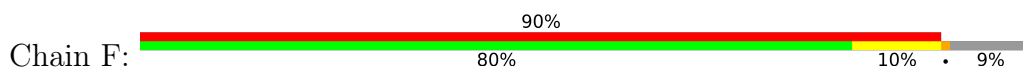




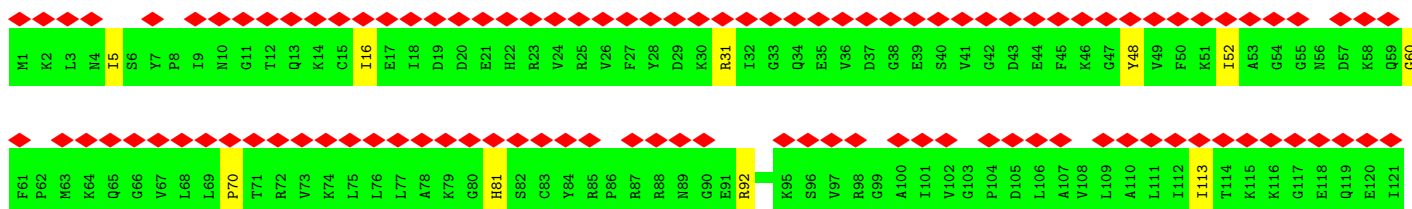
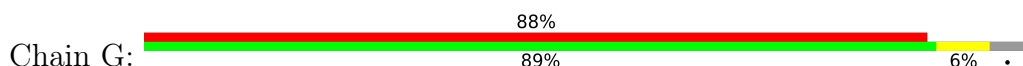
• Molecule 52: 40S ribosomal protein S4



• Molecule 53: KLLA0D10659p



• Molecule 54: 40S ribosomal protein S6





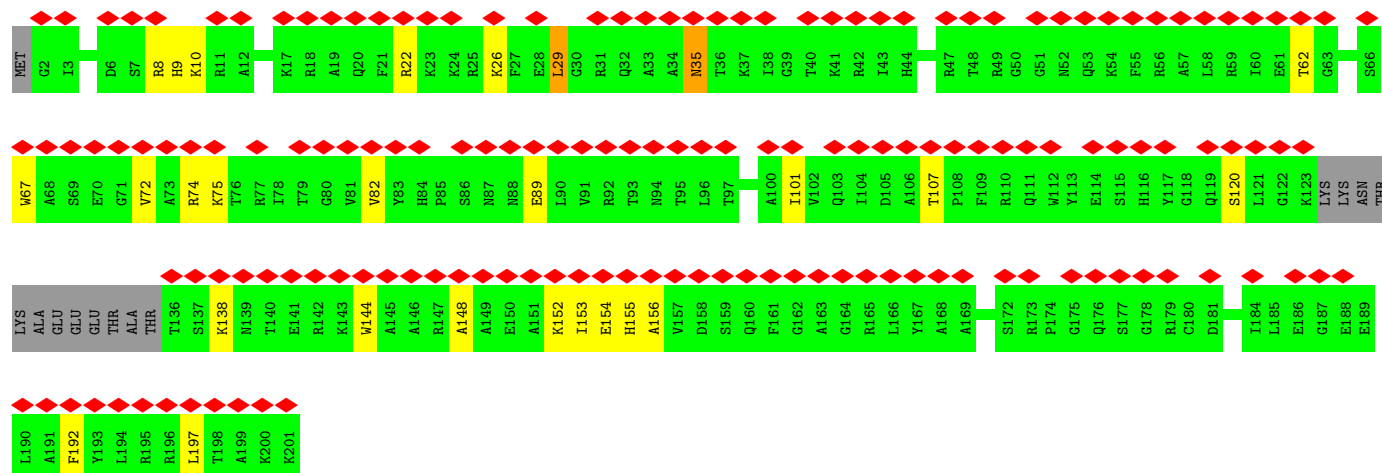
• Molecule 55: 40S ribosomal protein S7

Chain H: 68% 86% 11% .



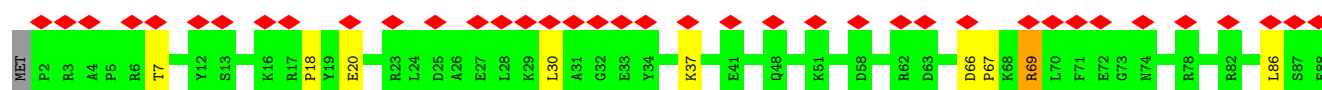
• Molecule 56: 40S ribosomal protein S8

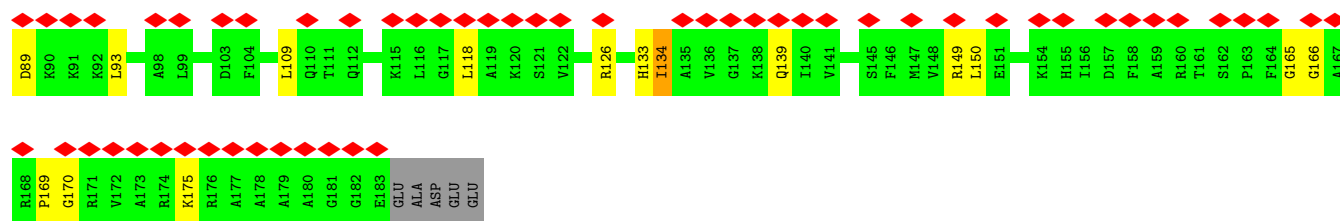
Chain I: 77% 80% 12% 6%



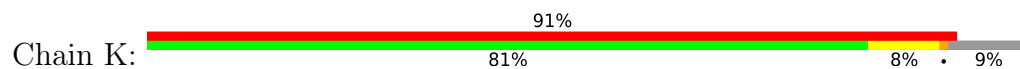
• Molecule 57: KLLA0E23673p

Chain J: 50% 84% 12% . .

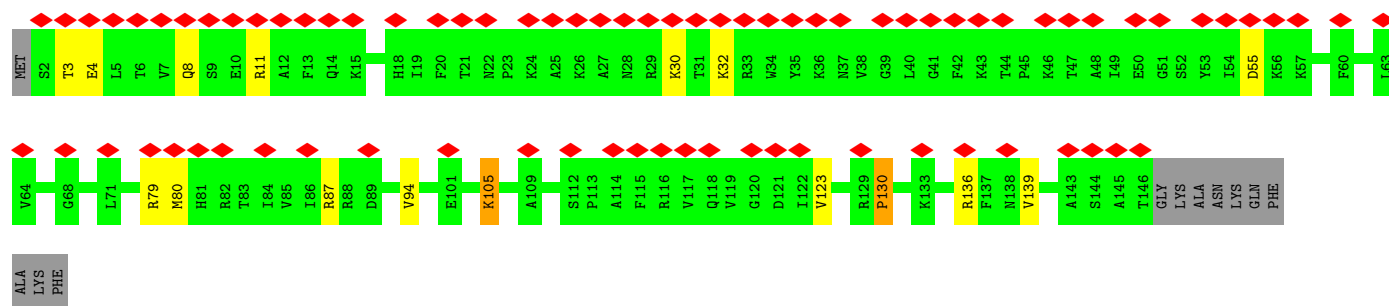
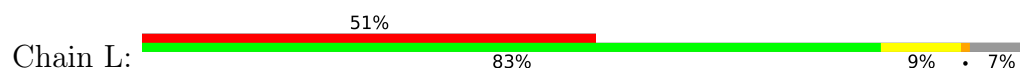




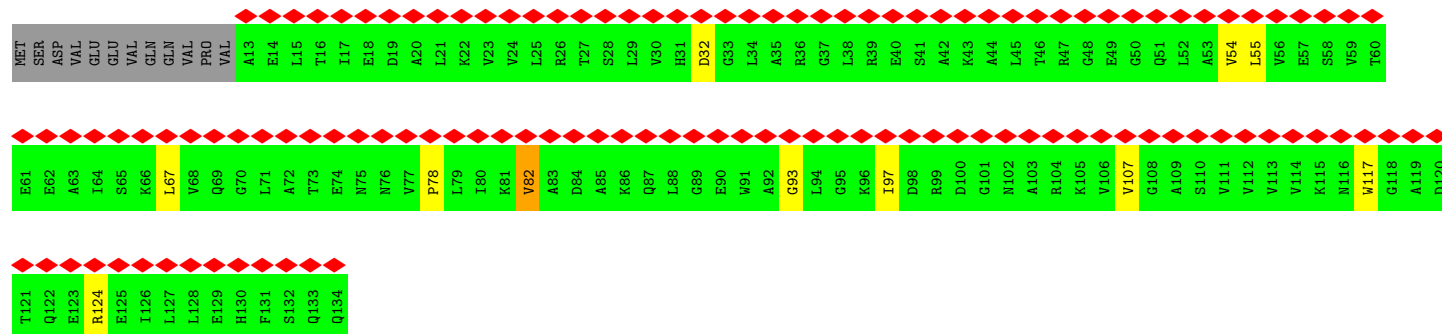
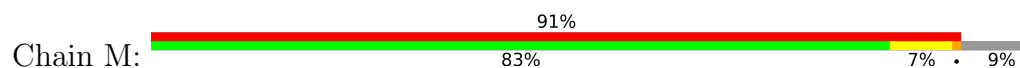
• Molecule 58: KLLA0B08173p



• Molecule 59: KLLA0A10483p

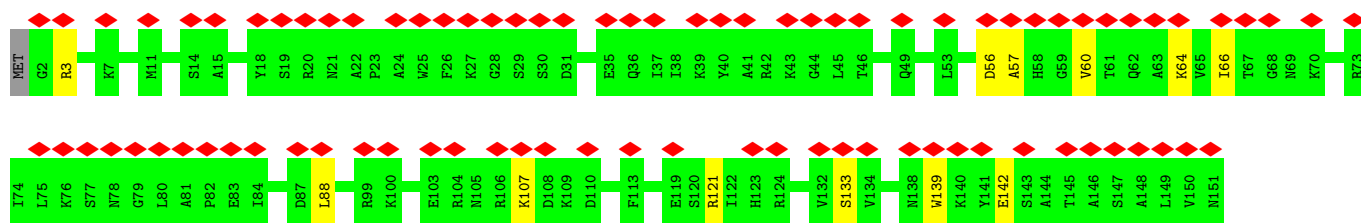


• Molecule 60: 40S ribosomal protein S12

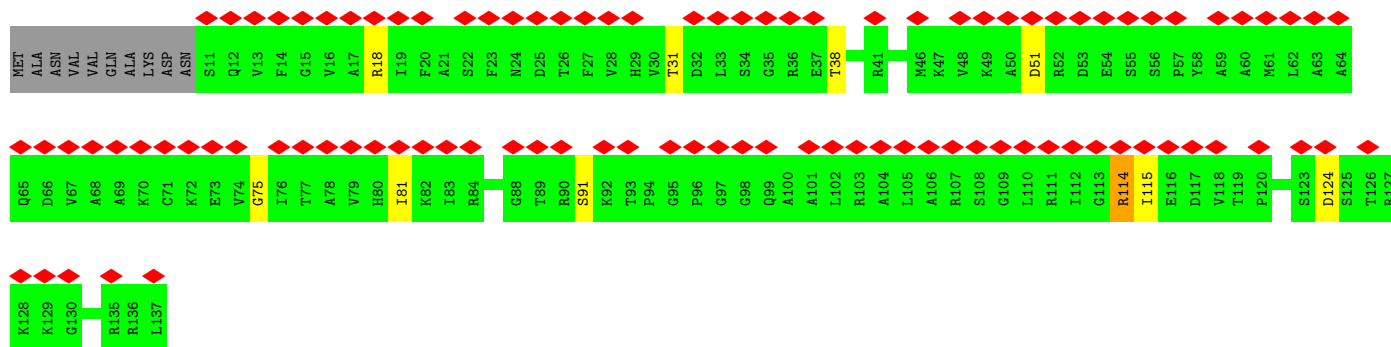
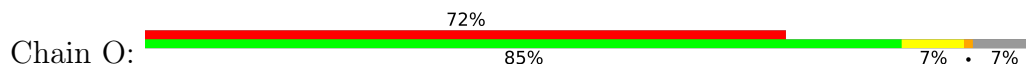


• Molecule 61: KLLA0F18040p

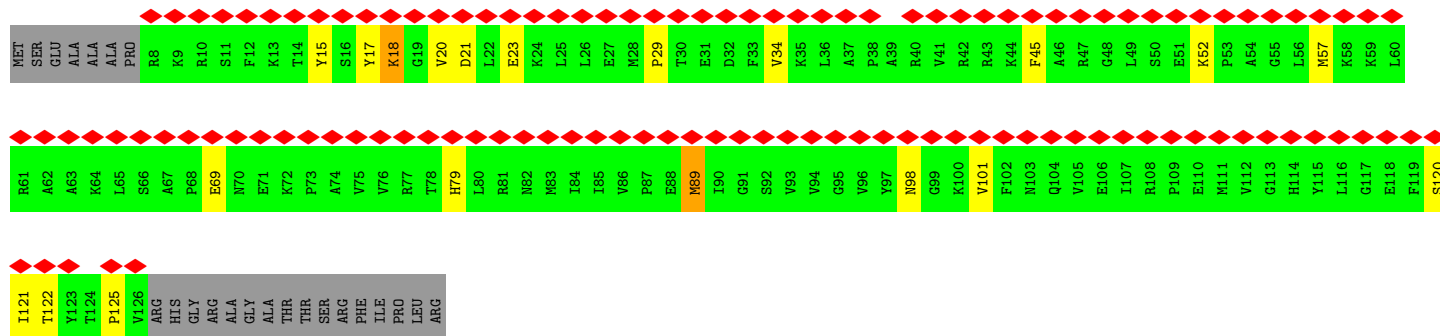
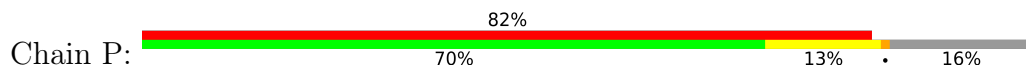




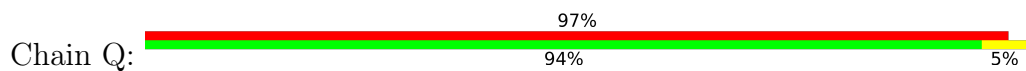
• Molecule 62: 40S ribosomal protein S14

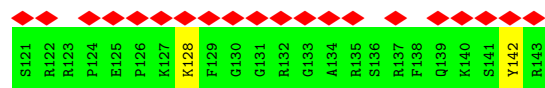


• Molecule 63: KLLA0F07843p

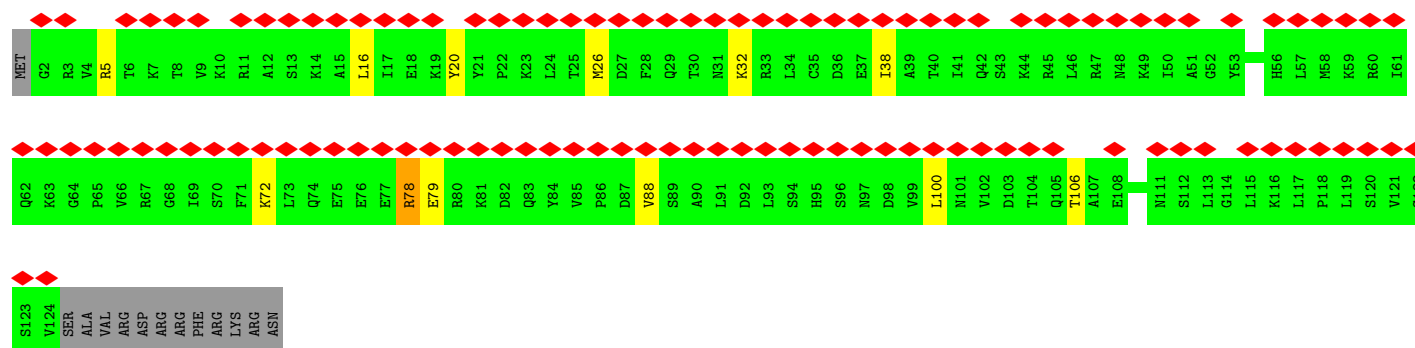
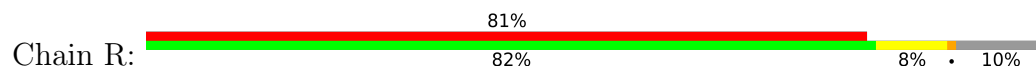


• Molecule 64: 40S ribosomal protein S16

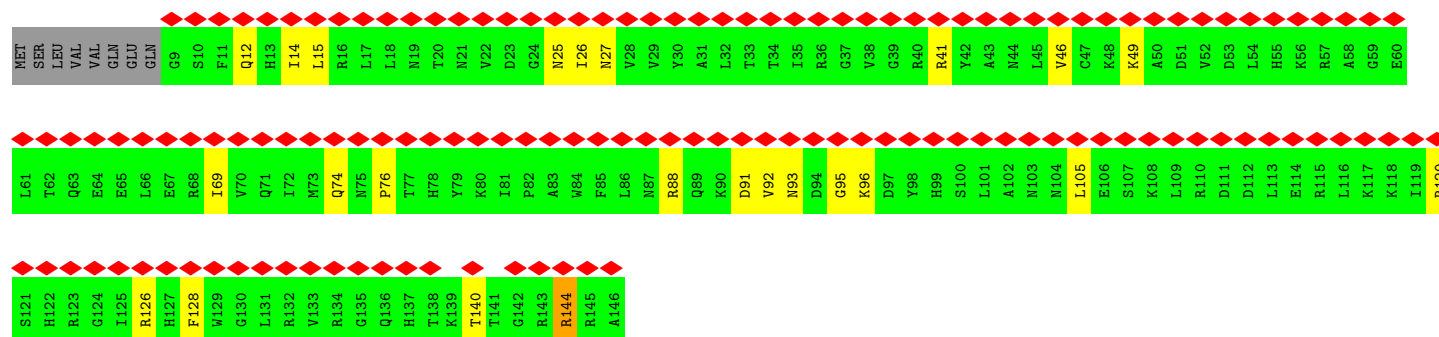
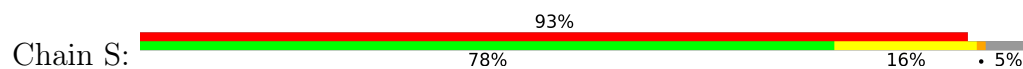




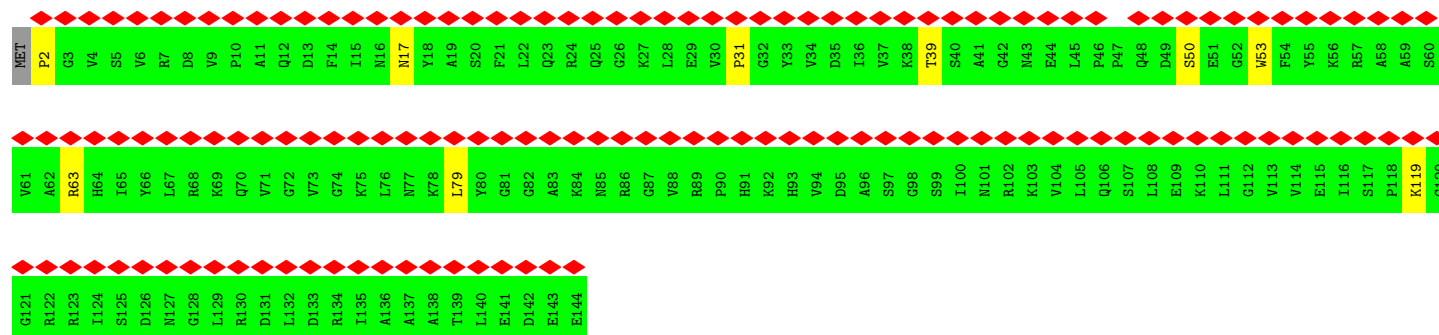
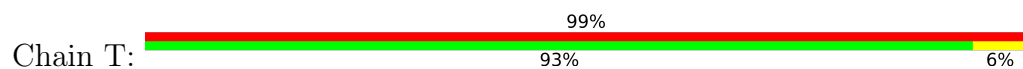
• Molecule 65: KLLA0B01474p



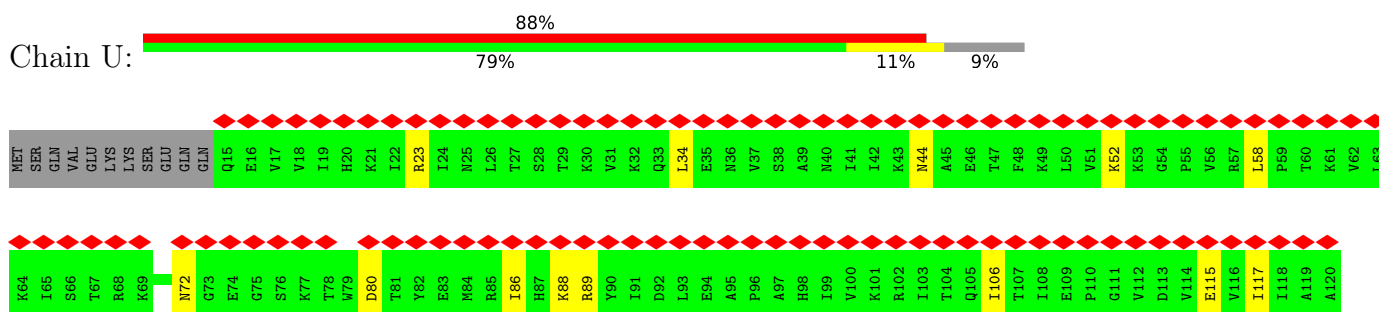
• Molecule 66: KLLA0B01562p



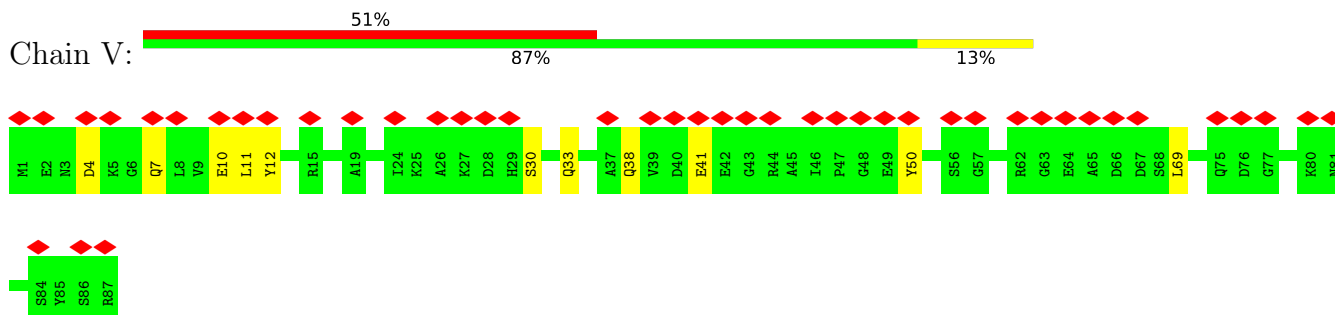
• Molecule 67: KLLA0A07194p



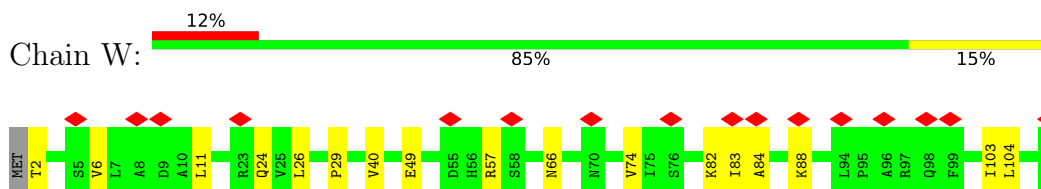
• Molecule 68: KLLA0F25542p



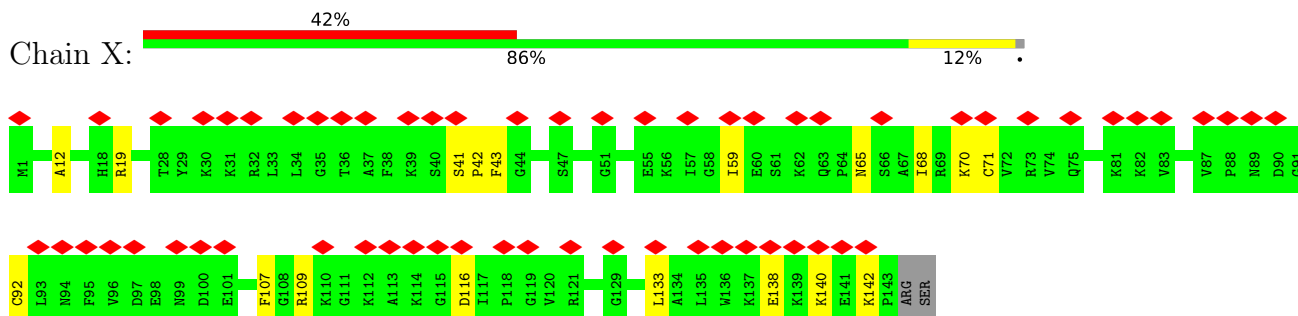
- Molecule 69: 40S ribosomal protein S21



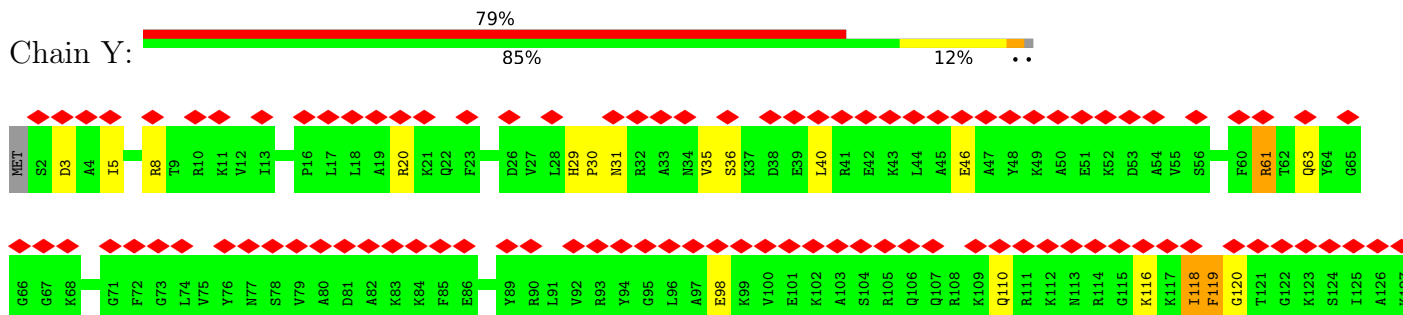
- Molecule 70: 40S ribosomal protein S22

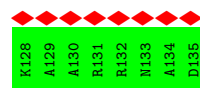


- Molecule 71: RPS23

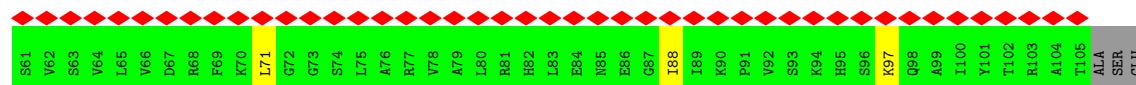
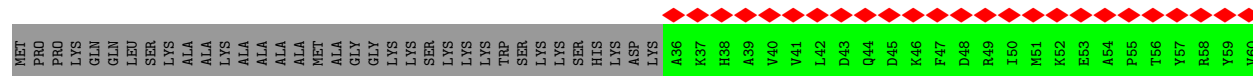


- Molecule 72: 40S ribosomal protein S24

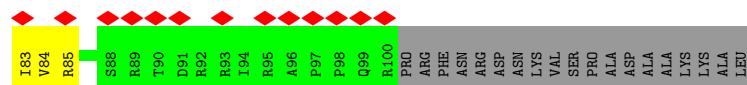
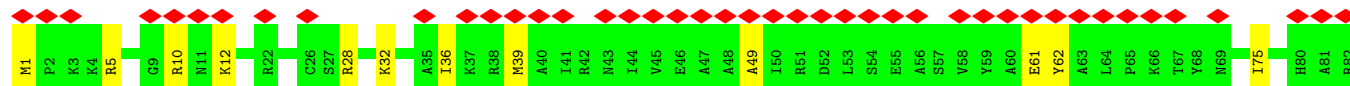




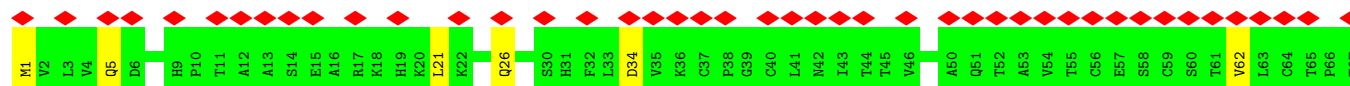
• Molecule 73: 40S ribosomal protein S25



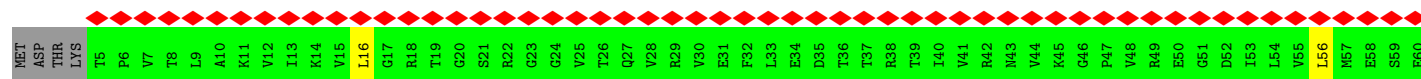
• Molecule 74: 40S ribosomal protein S26



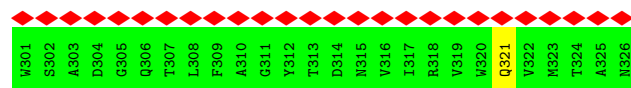
• Molecule 75: 40S ribosomal protein S27



• Molecule 76: 40S ribosomal protein S28

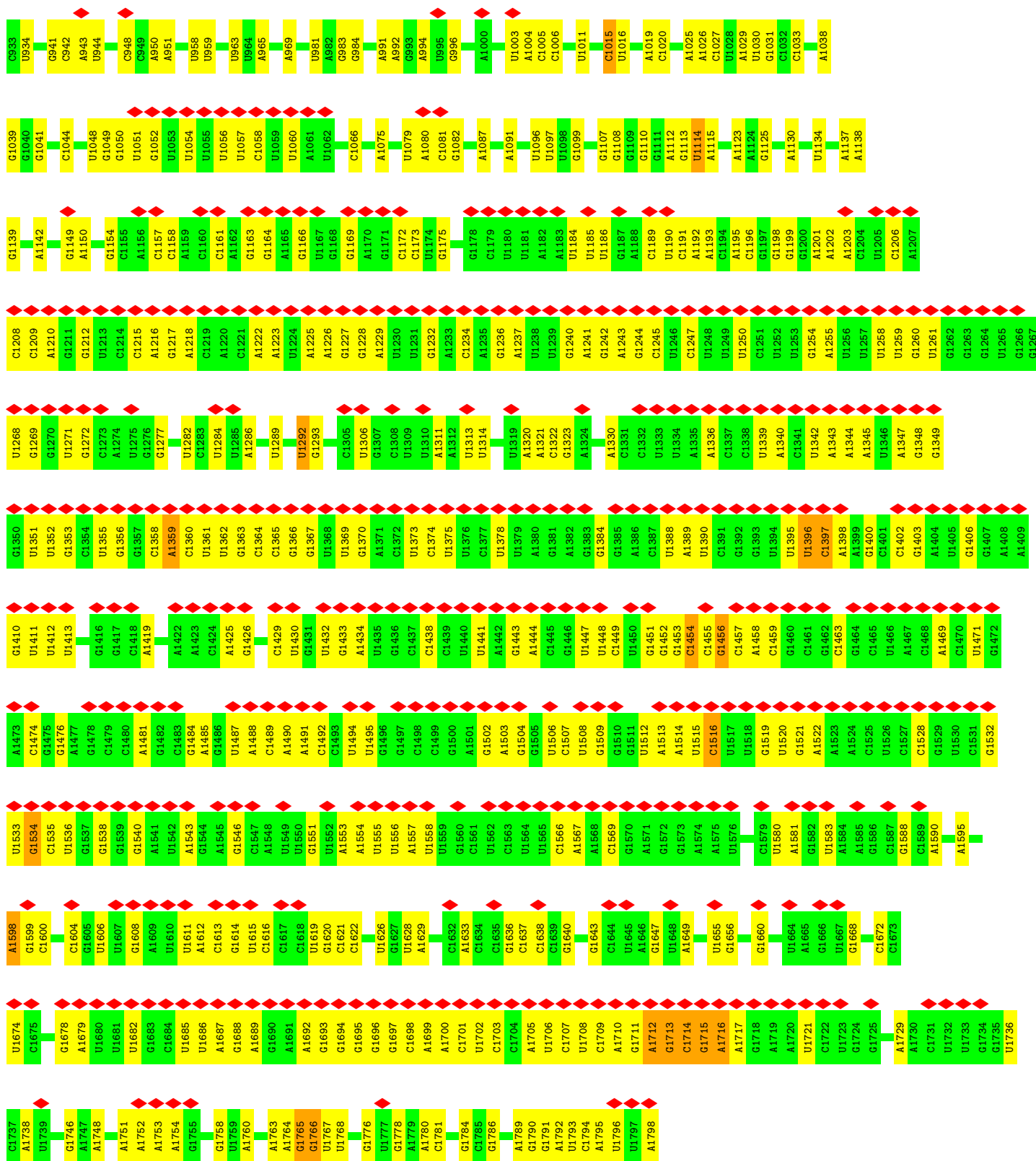


• Molecule 77: 40S ribosomal protein S29



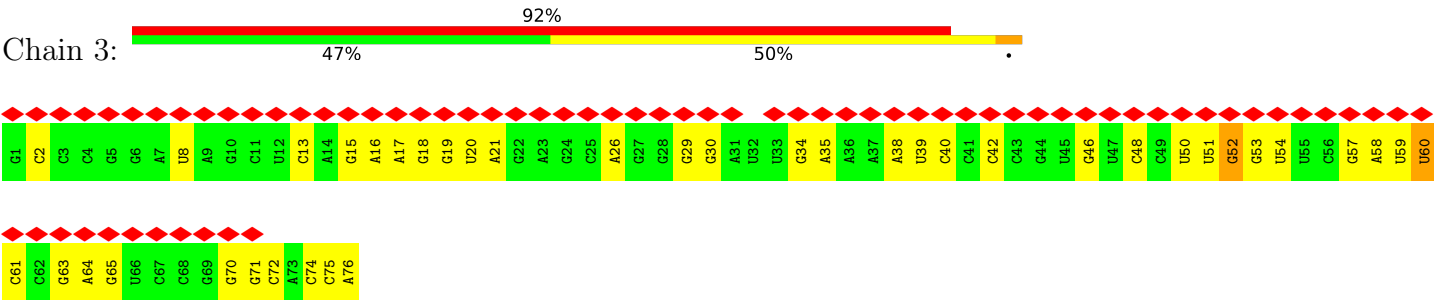
• Molecule 81: 18S ribosomal RNA





R920	H921	V922	D923	E924	K925	D926	T927	L928	P929	S930	H931	I932	T933	R934	R935	S936	I937	D938	T939	G940	K941	D942	P943	A944	F945	R946	D947	Q948	V949	P950	K951	S952	T953	S954	S955	L956	I957	R958	K959	L960	P961	A962	G963	F964	G965	ILE	GLU												
T860	P861	I862	C863	A864	V865	K866	D867	D868	P869	A870	T871	K872	E873	R874	I875	T876	L877	L878	L879	G880	R881	V882	T883	S884	L885	E886	A887	T888	F889	S890	C891	N892	T893	V894	K895	K896	K897	G898	Q899	T900	N901	A902	G903	V904	A905	M906	R907	L908	D909	P910	S911	S912	G913	Q914	Q915	P916	I917	W918	G919
L737	K738	D739	M740	K741	I742	P743	V744	M745	S746	V747	G750	P751	P752	Y753	K754	R755	I756	I757	M758	K759	A760	E761	T762	M763	L764	E765	K766	A767	P768	E769	L770	A771	V772	M773	L774	C775	F776	D777	V778	K779	V780	D781	G782	E783	A784	E785	Q786	Y787	A788	D789	E790	Q791	H792	I793	K794	I795	F796	N797	
A798	D799	I800	Y801	Y802	H803	L804	F805	D806	A807	A810	Y811	Q812	K813	E814	L815	L816	E817	K818	R819	R820	A821	E822	F823	I824	G825	D826	A827	T828	F829	P830	C831	N832	N833	L834	L835	L836	Q837	I838	I839	N840	K841	R842	G843	P844	M845	I846	I847	G848	V849	D850	V851	I852	E853	G854	S855	L856	K857	I858	G859
M675	D676	L677	E678	K679	A680	V681	S682	G683	S684	R685	L686	L687	V688	V689	G690	P691	D692	D693	D694	E695	E696	E697	T698	M699	D700	D701	V702	M703	E704	D705	L706	T707	G708	L709	L710	D711	S712	V713	D714	T715	T716	Q717	R718	Q719	V720	Q723	T726	G728	L727	G729	L730	A732	L733	L734	D735	F736			
I615	L616	S617	N618	G619	Y620	L621	R622	E623	G624	D625	L626	I627	V628	L629	C630	G631	M632	N633	G634	P635	I636	V637	T638	M639	L640	A642	L643	L644	T645	P646	Q647	P648	L649	R650	E651	L652	R653	L654	K655	S656	E657	V658	Q659	H660	H661	K662	E663	V664	K665	A666	A667	L668	G669	V670	K671	I672	A673	A674	
L553	A554	K555	Y556	V557	S558	I559	V560	P561	T562	S563	A564	V565	T566	G567	I568	G569	V570	D572	L573	L574	W575	L576	L577	L578	E579	L580	T581	Q582	K583	R584	M585	S586	K587	Q588	L589	K590	Y591	L592	S593	H594	V595	E596	A597	T598	I599	L600	E601	V602	K603	V604	V605	E606	T610	V611	I612	L613	V614		
R486	K487	A488	P489	F490	I491	V492	K496	R499	D502	W503	V504	I505	T506	P507	N508	N509	R512	D513	S514	F515	D516	K517	Q518	E519	R520	A521	V522	K523	Q524	E525	F526	Q527	A462	I463	L464	V465	I466	D467	I468	M469	H470	G471	L472	E473	Q474	Q475	T476	I477	E478	S479	I480	R481	L482	L483	R484	D485			
ALA	ALA	ALA	ALA	LYS	K366	D367	L368	R369	S370	P371	I372	C373	L376	D380	T381	G382	K383	T384	K385	L386	L387	D388	K389	I390	R391	Q392	T393	N394	V395	Q396	G397	C398	E399	A400	G401	G402	Q405	Q406	I407	G408	A409	T410	Y411	F412	P413	I414	D415	I417	E418	Q419	K420	T421	A422	V423	M424				
ASP	ASP	TRP	VAL	ASN	LEU	ALA	LEU	GLU	ASP	PRO	GLU	HIS	GLU	GLN	PRO	GLY	PRO	LYS	LYS	VAL	THR	SER	GLY	THR	GLN	VAL	TYR	GLN	ARG	GLY	LEU	THR	ALA	GLU	THR	ASN	GLN	GLU	THR	ASN	GLN	GLU	ALA	ASP	VAL	GLU	GLN	PRO	ILE	GLU	PRO	SER	LYS	ARG	SER				
THR	SER	LYS	LEU	LYS	LYS	ALA	GLU	LYS	LYS	THR	LYS	THR	LYS	THR	GLY	VAL	ALA	PRO	LYS	LYS	VAL	VAL	ALA	PRO	LYS	GLY	LEU	ALA	ALA	GLY	LEU	GLN	LYS	VAL	ALA	GLU	GLN	GLU	ALA	ALA	GLN	ASN	ASN	GLU	GLU	ALA	GLU	ARG	LEU	HIS	ALA	LYS	GLN						
GLU	GLU	GLU	GLU	LYS	LEU	ALA	LYS	GLN	GLY	ASP	GLU	HIS	GLU	GLU	GLY	ARG	ALA	LYS	LYS	ALA	LYS	ARG	ARG	GLY	GLY	LEU	LYS	ALA	GLY	LEU	GLN	LYS	LYS	GLU	GLU	GLU	LYS	LYS	GLU	LEU	ASN	ARG	ARG	GLU	GLU	ALA	GLU	ARG	LEU	ALA	GLY								
ASN	ILE	LYS	VAL	ALA	GLY	LEU	GLU	LYS	GLY	ASP	GLU	HIS	PRO	GLU	LYS	VAL	VAL	GLY	ARG	VAL	ARG	THR	SER	GLY	VAL	GLN	GLY	GLY	THR	LYS	LEU	GLU	ILE	GLU	GLU	GLU	GLU	THR	GLN	GLU	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ILE						

● Molecule 83: RNA (76-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29712	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.588	Depositor
Minimum map value	-0.380	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.11	Depositor
Map size (\AA)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	5	0.20	0/78206	0.67	9/121916 (0.0%)
2	7	0.19	0/2883	0.65	0/4491
3	8	0.20	0/3714	0.66	0/5781
4	AA	0.36	0/1926	0.58	0/2588
5	AB	0.36	0/3136	0.56	0/4225
6	AC	0.44	1/2792 (0.0%)	0.60	0/3777
7	AD	0.37	0/2436	0.56	0/3292
8	AE	0.41	0/1343	0.58	0/1804
9	AF	0.39	0/1810	0.53	0/2440
10	AG	0.37	0/1846	0.52	0/2486
11	AH	0.36	0/1547	0.54	0/2083
12	AI	0.37	0/1725	0.55	0/2310
13	AJ	0.38	0/1370	0.60	0/1835
14	AL	0.38	0/1607	0.62	0/2156
15	AM	0.38	0/1060	0.57	0/1430
16	AN	0.38	0/1746	0.61	0/2339
17	AO	0.23	0/1602	0.39	0/2151
18	AP	0.38	0/1455	0.60	0/1952
19	AQ	0.37	0/1469	0.61	0/1970
20	AR	0.40	0/1539	0.62	0/2047
21	AS	0.37	0/1458	0.56	0/1964
22	AT	0.37	0/1286	0.55	0/1722
23	AU	0.38	0/824	0.47	0/1113
24	AV	0.37	0/991	0.57	0/1331
25	AW	0.39	0/528	0.57	0/703
26	AX	0.36	0/979	0.55	0/1320
27	AY	0.37	0/1003	0.59	0/1339
28	AZ	0.39	0/1114	0.55	0/1493
29	Ba	0.37	0/1186	0.57	0/1590
30	Bb	0.37	0/468	0.53	0/621
31	Bc	0.38	0/748	0.50	0/1005
32	Bd	0.36	0/885	0.54	0/1186

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Be	0.37	0/998	0.56	0/1332
34	Bf	0.37	0/855	0.56	0/1150
35	Bg	0.37	0/961	0.59	0/1281
36	Bh	0.38	0/970	0.58	0/1291
37	Bi	0.41	0/773	0.62	0/1029
38	Bj	0.40	0/690	0.61	0/913
39	Bk	0.43	0/626	0.70	0/835
40	Bl	0.41	0/435	0.64	0/577
41	Bm	0.38	0/416	0.59	0/552
42	Bn	0.41	0/219	0.83	0/281
43	Bo	0.38	0/825	0.65	0/1086
44	Bp	0.42	0/667	0.70	0/891
45	Bq	0.45	1/1742 (0.1%)	0.59	1/2342 (0.0%)
46	Br	0.41	0/1535	0.62	0/2077
48	A	0.39	0/1656	0.57	0/2264
49	B	0.38	0/1747	0.56	0/2353
50	C	0.39	0/1659	0.60	0/2252
51	D	0.38	0/1769	0.57	0/2378
52	E	0.39	0/2122	0.62	1/2861 (0.0%)
53	F	0.39	0/1628	0.60	0/2198
54	G	0.37	0/1835	0.60	0/2451
55	H	0.37	0/1507	0.56	0/2028
56	I	0.40	0/1519	0.63	0/2033
57	J	0.40	0/1495	0.64	0/2001
58	K	0.40	0/831	0.50	0/1123
59	L	0.39	0/1194	0.63	0/1611
60	M	0.38	0/929	0.57	0/1255
61	N	0.38	0/1210	0.58	0/1628
62	O	0.38	0/953	0.61	0/1279
63	P	0.43	0/969	0.62	0/1302
64	Q	0.39	0/1125	0.58	0/1510
65	R	0.38	0/994	0.61	0/1335
66	S	0.42	0/1157	0.63	0/1554
67	T	0.38	0/1129	0.56	0/1520
68	U	0.36	0/857	0.54	0/1158
69	V	0.36	0/696	0.57	0/938
70	W	0.37	0/1039	0.58	0/1399
71	X	0.39	0/1128	0.62	0/1504
72	Y	0.40	0/1075	0.59	0/1433
73	Z	0.38	0/567	0.58	0/762
74	a	0.40	0/810	0.69	0/1084
75	b	0.35	0/627	0.55	0/847
76	c	0.37	0/496	0.63	0/666

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	d	0.39	0/457	0.55	0/607
78	e	0.37	0/450	0.53	0/599
79	f	0.39	0/344	0.54	0/458
80	g	0.37	0/2521	0.55	0/3431
81	2	0.21	0/42269	0.68	4/65862 (0.0%)
82	1	0.39	0/4776	0.67	0/6459
83	3	0.21	0/1815	0.67	0/2829
All	All	0.30	2/225749 (0.0%)	0.64	15/331069 (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
1	5	2	0
4	AA	0	1
6	AC	0	7
8	AE	0	8
29	Ba	0	1
34	Bf	0	1
37	Bi	0	4
39	Bk	0	1
45	Bq	0	6
65	R	0	1
72	Y	0	2
74	a	0	1
82	1	0	6
All	All	2	39

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	Bq	60	ARG	C-N	8.47	1.50	1.34
6	AC	74	ILE	C-N	8.46	1.50	1.34

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	1191	U	N1-C1'-C2'	10.70	127.90	114.00
1	5	2506	U	C5'-C4'-O4'	7.34	117.90	109.10
1	5	2506	U	C5'-C4'-C3'	7.24	127.58	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	2	1534	G	C2'-C3'-O3'	6.24	123.69	113.70
1	5	3257	A	C2'-C3'-O3'	5.95	123.22	113.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1191	U	C1'
1	5	2506	U	C4'

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AA	196	TRP	Peptide
6	AC	343	LYS	Peptide
6	AC	345	ASP	Peptide
6	AC	346	GLN	Peptide
6	AC	73	ARG	Peptide

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	5	69874	0	35111	118	0
2	7	2579	0	1304	3	0
3	8	3326	0	1680	0	0
4	AA	1892	0	1954	6	0
5	AB	3064	0	3140	13	0
6	AC	2743	0	2865	23	0
7	AD	2384	0	2337	1	0
8	AE	1321	0	1412	33	0
9	AF	1774	0	1832	4	0
10	AG	1817	0	1927	3	0
11	AH	1528	0	1596	7	0
12	AI	1690	0	1729	3	0
13	AJ	1349	0	1382	3	0
14	AL	1581	0	1661	4	0
15	AM	1045	0	1126	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	AN	1709	0	1763	1	0
17	AO	1571	0	1669	318	0
18	AP	1432	0	1465	4	0
19	AQ	1444	0	1541	2	0
20	AR	1522	0	1622	14	0
21	AS	1422	0	1466	8	0
22	AT	1262	0	1309	1	0
23	AU	807	0	821	0	0
24	AV	976	0	1021	2	0
25	AW	515	0	532	1	0
26	AX	964	0	1031	0	0
27	AY	992	0	1070	1	0
28	AZ	1089	0	1150	3	0
29	Ba	1156	0	1206	0	0
30	Bb	458	0	486	0	0
31	Bc	740	0	792	0	0
32	Bd	869	0	920	0	0
33	Be	980	0	1048	0	0
34	Bf	837	0	861	0	0
35	Bg	951	0	1036	0	0
36	Bh	961	0	1062	0	0
37	Bi	766	0	840	0	0
38	Bj	675	0	678	0	0
39	Bk	619	0	675	0	0
40	Bl	428	0	464	0	0
41	Bm	410	0	447	0	0
42	Bn	218	0	266	0	0
43	Bo	814	0	875	0	0
44	Bp	660	0	690	0	0
45	Bq	1716	0	1819	0	0
46	Br	1508	0	1542	0	0
47	AK	735	0	178	0	0
48	A	1616	0	1636	6	0
49	B	1722	0	1795	2	0
50	C	1629	0	1710	11	0
51	D	1744	0	1826	3	0
52	E	2078	0	2157	7	0
53	F	1609	0	1679	6	0
54	G	1812	0	1911	3	0
55	H	1483	0	1579	2	0
56	I	1493	0	1515	5	0
57	J	1471	0	1554	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	K	809	0	810	1	0
59	L	1168	0	1227	3	0
60	M	922	0	953	2	0
61	N	1187	0	1251	2	0
62	O	942	0	979	2	0
63	P	950	0	1001	7	0
64	Q	1105	0	1170	1	0
65	R	983	0	1033	3	0
66	S	1138	0	1161	4	0
67	T	1110	0	1124	1	0
68	U	845	0	913	4	0
69	V	687	0	682	0	0
70	W	1021	0	1056	6	0
71	X	1110	0	1192	4	0
72	Y	1061	0	1111	9	0
73	Z	558	0	585	0	0
74	a	798	0	854	0	0
75	b	617	0	643	0	0
76	c	494	0	534	0	0
77	d	446	0	436	0	0
78	e	443	0	481	0	0
79	f	337	0	333	0	0
80	g	2466	0	2406	0	0
81	2	37797	0	19016	89	0
82	1	4702	0	4822	59	0
83	3	1623	0	823	12	0
84	Bj	1	0	0	0	0
84	Bm	1	0	0	0	0
84	Bo	1	0	0	0	0
84	a	1	0	0	0	0
84	b	1	0	0	0	0
84	f	1	0	0	0	0
85	1	32	0	14	0	0
All	All	211187	0	157373	792	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 2.

The worst 5 of 792 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)
8:AE:113:GLN:HA	8:AE:117:ALA:CB	1.12	1.54
81:2:214:A:C6	81:2:241:U:C4	1.95	1.54
1:5:2502:G:N2	1:5:2516:A:C4	1.77	1.51
8:AE:113:GLN:CA	8:AE:117:ALA:HB3	1.33	1.51
81:2:214:A:C2	81:2:241:U:O4	1.63	1.50

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AA	247/254 (97%)	216 (87%)	24 (10%)	7 (3%)	5	34
5	AB	382/387 (99%)	321 (84%)	51 (13%)	10 (3%)	5	35
6	AC	358/363 (99%)	279 (78%)	54 (15%)	25 (7%)	1	14
7	AD	293/297 (99%)	266 (91%)	15 (5%)	12 (4%)	3	26
8	AE	159/175 (91%)	138 (87%)	16 (10%)	5 (3%)	4	32
9	AF	220/241 (91%)	196 (89%)	17 (8%)	7 (3%)	4	31
10	AG	231/255 (91%)	213 (92%)	14 (6%)	4 (2%)	9	45
11	AH	189/191 (99%)	162 (86%)	24 (13%)	3 (2%)	9	46
12	AI	203/220 (92%)	181 (89%)	16 (8%)	6 (3%)	4	33
13	AJ	166/174 (95%)	147 (89%)	12 (7%)	7 (4%)	3	25
14	AL	195/199 (98%)	172 (88%)	19 (10%)	4 (2%)	7	40
15	AM	134/138 (97%)	116 (87%)	14 (10%)	4 (3%)	4	33
16	AN	200/204 (98%)	189 (94%)	11 (6%)	0	100	100
17	AO	196/199 (98%)	94 (48%)	38 (19%)	64 (33%)	0	0
18	AP	178/184 (97%)	156 (88%)	17 (10%)	5 (3%)	5	34
19	AQ	182/186 (98%)	163 (90%)	18 (10%)	1 (0%)	29	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AR	186/189 (98%)	171 (92%)	12 (6%)	3 (2%)	9	46
21	AS	167/172 (97%)	152 (91%)	10 (6%)	5 (3%)	4	33
22	AT	156/160 (98%)	138 (88%)	16 (10%)	2 (1%)	12	50
23	AU	98/122 (80%)	89 (91%)	9 (9%)	0	100	100
24	AV	130/137 (95%)	118 (91%)	10 (8%)	2 (2%)	10	47
25	AW	60/155 (39%)	57 (95%)	3 (5%)	0	100	100
26	AX	119/142 (84%)	110 (92%)	9 (8%)	0	100	100
27	AY	123/127 (97%)	107 (87%)	14 (11%)	2 (2%)	9	46
28	AZ	132/136 (97%)	111 (84%)	17 (13%)	4 (3%)	4	33
29	Ba	145/149 (97%)	120 (83%)	19 (13%)	6 (4%)	3	26
30	Bb	55/62 (89%)	47 (86%)	6 (11%)	2 (4%)	3	29
31	Bc	95/105 (90%)	88 (93%)	7 (7%)	0	100	100
32	Bd	104/114 (91%)	94 (90%)	6 (6%)	4 (4%)	3	27
33	Be	120/130 (92%)	111 (92%)	6 (5%)	3 (2%)	5	36
34	Bf	103/107 (96%)	94 (91%)	6 (6%)	3 (3%)	4	33
35	Bg	119/125 (95%)	105 (88%)	9 (8%)	5 (4%)	3	25
36	Bh	114/120 (95%)	106 (93%)	5 (4%)	3 (3%)	5	35
37	Bi	96/100 (96%)	81 (84%)	10 (10%)	5 (5%)	2	20
38	Bj	83/88 (94%)	75 (90%)	6 (7%)	2 (2%)	6	37
39	Bk	74/78 (95%)	61 (82%)	11 (15%)	2 (3%)	5	35
40	Bl	47/51 (92%)	41 (87%)	4 (8%)	2 (4%)	2	24
41	Bm	49/128 (38%)	47 (96%)	2 (4%)	0	100	100
42	Bn	21/23 (91%)	19 (90%)	2 (10%)	0	100	100
43	Bo	99/106 (93%)	76 (77%)	15 (15%)	8 (8%)	1	11
44	Bp	85/92 (92%)	71 (84%)	8 (9%)	6 (7%)	1	14
45	Bq	215/217 (99%)	171 (80%)	29 (14%)	15 (7%)	1	14
46	Br	193/311 (62%)	140 (72%)	33 (17%)	20 (10%)	0	7
48	A	204/254 (80%)	174 (85%)	21 (10%)	9 (4%)	2	23
49	B	212/255 (83%)	181 (85%)	22 (10%)	9 (4%)	3	25
50	C	215/259 (83%)	178 (83%)	29 (14%)	8 (4%)	3	28
51	D	221/237 (93%)	193 (87%)	19 (9%)	9 (4%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	E	258/261 (99%)	225 (87%)	22 (8%)	11 (4%)	2	24
53	F	204/227 (90%)	166 (81%)	29 (14%)	9 (4%)	2	23
54	G	224/236 (95%)	196 (88%)	22 (10%)	6 (3%)	5	35
55	H	182/190 (96%)	155 (85%)	18 (10%)	9 (5%)	2	21
56	I	184/201 (92%)	158 (86%)	19 (10%)	7 (4%)	3	27
57	J	180/188 (96%)	146 (81%)	25 (14%)	9 (5%)	2	21
58	K	94/106 (89%)	81 (86%)	9 (10%)	4 (4%)	2	24
59	L	143/156 (92%)	127 (89%)	12 (8%)	4 (3%)	5	34
60	M	120/134 (90%)	99 (82%)	15 (12%)	6 (5%)	2	21
61	N	148/151 (98%)	137 (93%)	10 (7%)	1 (1%)	22	61
62	O	125/137 (91%)	106 (85%)	13 (10%)	6 (5%)	2	22
63	P	117/142 (82%)	90 (77%)	18 (15%)	9 (8%)	1	12
64	Q	139/143 (97%)	121 (87%)	14 (10%)	4 (3%)	4	33
65	R	121/136 (89%)	96 (79%)	22 (18%)	3 (2%)	5	36
66	S	136/146 (93%)	112 (82%)	17 (12%)	7 (5%)	2	20
67	T	141/144 (98%)	123 (87%)	14 (10%)	4 (3%)	5	34
68	U	104/117 (89%)	89 (86%)	13 (12%)	2 (2%)	8	42
69	V	85/87 (98%)	70 (82%)	11 (13%)	4 (5%)	2	22
70	W	127/130 (98%)	106 (84%)	19 (15%)	2 (2%)	9	46
71	X	141/145 (97%)	116 (82%)	21 (15%)	4 (3%)	5	34
72	Y	132/135 (98%)	112 (85%)	15 (11%)	5 (4%)	3	27
73	Z	68/108 (63%)	60 (88%)	6 (9%)	2 (3%)	4	33
74	a	98/119 (82%)	78 (80%)	12 (12%)	8 (8%)	1	10
75	b	80/82 (98%)	67 (84%)	10 (12%)	3 (4%)	3	27
76	c	61/67 (91%)	58 (95%)	3 (5%)	0	100	100
77	d	51/56 (91%)	42 (82%)	8 (16%)	1 (2%)	7	41
78	e	53/63 (84%)	50 (94%)	2 (4%)	1 (2%)	8	42
79	f	40/150 (27%)	28 (70%)	8 (20%)	4 (10%)	0	8
80	g	312/326 (96%)	250 (80%)	52 (17%)	10 (3%)	4	31
82	1	598/967 (62%)	465 (78%)	103 (17%)	30 (5%)	2	21
All	All	11839/13368 (89%)	10064 (85%)	1297 (11%)	478 (4%)	5	26

5 of 478 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AA	34	TYR
4	AA	196	TRP
4	AA	197	PRO
5	AB	5	LYS
5	AB	351	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AA	190/195 (97%)	183 (96%)	7 (4%)	34	66
5	AB	323/326 (99%)	303 (94%)	20 (6%)	18	53
6	AC	291/294 (99%)	271 (93%)	20 (7%)	15	49
7	AD	243/244 (100%)	234 (96%)	9 (4%)	34	66
8	AE	141/150 (94%)	133 (94%)	8 (6%)	20	55
9	AF	188/204 (92%)	182 (97%)	6 (3%)	39	70
10	AG	192/209 (92%)	182 (95%)	10 (5%)	23	58
11	AH	173/173 (100%)	162 (94%)	11 (6%)	17	52
12	AI	177/187 (95%)	169 (96%)	8 (4%)	27	62
13	AJ	144/148 (97%)	138 (96%)	6 (4%)	30	63
14	AL	162/164 (99%)	156 (96%)	6 (4%)	34	66
15	AM	109/110 (99%)	106 (97%)	3 (3%)	43	72
16	AN	175/177 (99%)	171 (98%)	4 (2%)	50	76
17	AO	163/164 (99%)	151 (93%)	12 (7%)	13	46
18	AP	148/150 (99%)	141 (95%)	7 (5%)	26	61
19	AQ	150/151 (99%)	147 (98%)	3 (2%)	55	79
20	AR	152/153 (99%)	141 (93%)	11 (7%)	14	47
21	AS	154/157 (98%)	150 (97%)	4 (3%)	46	74
22	AT	135/137 (98%)	125 (93%)	10 (7%)	13	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	AU	90/110 (82%)	89 (99%)	1 (1%)	73	88
24	AV	101/105 (96%)	97 (96%)	4 (4%)	31	65
25	AW	54/127 (42%)	52 (96%)	2 (4%)	34	66
26	AX	106/120 (88%)	95 (90%)	11 (10%)	7	33
27	AY	111/112 (99%)	105 (95%)	6 (5%)	22	57
28	AZ	115/116 (99%)	108 (94%)	7 (6%)	18	53
29	Ba	117/118 (99%)	109 (93%)	8 (7%)	16	50
30	Bb	45/49 (92%)	41 (91%)	4 (9%)	9	40
31	Bc	79/85 (93%)	74 (94%)	5 (6%)	18	53
32	Bd	95/100 (95%)	90 (95%)	5 (5%)	22	58
33	Be	106/110 (96%)	101 (95%)	5 (5%)	26	61
34	Bf	90/92 (98%)	88 (98%)	2 (2%)	52	77
35	Bg	102/106 (96%)	100 (98%)	2 (2%)	55	79
36	Bh	104/106 (98%)	101 (97%)	3 (3%)	42	72
37	Bi	79/80 (99%)	75 (95%)	4 (5%)	24	58
38	Bj	69/71 (97%)	68 (99%)	1 (1%)	67	85
39	Bk	68/69 (99%)	65 (96%)	3 (4%)	28	63
40	Bl	44/46 (96%)	38 (86%)	6 (14%)	3	22
41	Bm	46/116 (40%)	43 (94%)	3 (6%)	17	51
42	Bn	21/21 (100%)	18 (86%)	3 (14%)	3	21
43	Bo	86/90 (96%)	79 (92%)	7 (8%)	11	43
44	Bp	69/71 (97%)	64 (93%)	5 (7%)	14	47
45	Bq	198/198 (100%)	182 (92%)	16 (8%)	11	43
46	Br	162/251 (64%)	150 (93%)	12 (7%)	13	46
48	A	174/211 (82%)	167 (96%)	7 (4%)	31	65
49	B	196/228 (86%)	185 (94%)	11 (6%)	21	56
50	C	176/203 (87%)	161 (92%)	15 (8%)	10	41
51	D	185/196 (94%)	171 (92%)	14 (8%)	13	45
52	E	223/224 (100%)	209 (94%)	14 (6%)	18	53
53	F	174/194 (90%)	168 (97%)	6 (3%)	37	69
54	G	192/200 (96%)	187 (97%)	5 (3%)	46	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	H	164/170 (96%)	156 (95%)	8 (5%)	25	59
56	I	148/159 (93%)	134 (90%)	14 (10%)	8	37
57	J	153/158 (97%)	139 (91%)	14 (9%)	9	39
58	K	88/96 (92%)	83 (94%)	5 (6%)	20	55
59	L	129/137 (94%)	120 (93%)	9 (7%)	15	48
60	M	97/109 (89%)	94 (97%)	3 (3%)	40	71
61	N	127/128 (99%)	120 (94%)	7 (6%)	21	57
62	O	96/104 (92%)	95 (99%)	1 (1%)	76	88
63	P	103/119 (87%)	97 (94%)	6 (6%)	20	55
64	Q	117/119 (98%)	115 (98%)	2 (2%)	60	82
65	R	112/124 (90%)	108 (96%)	4 (4%)	35	67
66	S	121/129 (94%)	108 (89%)	13 (11%)	6	32
67	T	117/118 (99%)	113 (97%)	4 (3%)	37	69
68	U	96/107 (90%)	93 (97%)	3 (3%)	40	71
69	V	73/73 (100%)	66 (90%)	7 (10%)	8	37
70	W	110/111 (99%)	102 (93%)	8 (7%)	14	46
71	X	118/120 (98%)	111 (94%)	7 (6%)	19	55
72	Y	108/109 (99%)	97 (90%)	11 (10%)	7	34
73	Z	60/88 (68%)	59 (98%)	1 (2%)	60	82
74	a	85/100 (85%)	79 (93%)	6 (7%)	14	48
75	b	72/72 (100%)	68 (94%)	4 (6%)	21	56
76	c	55/59 (93%)	53 (96%)	2 (4%)	35	67
77	d	46/48 (96%)	42 (91%)	4 (9%)	10	41
78	e	49/55 (89%)	47 (96%)	2 (4%)	30	64
79	f	35/133 (26%)	33 (94%)	2 (6%)	20	55
80	g	265/272 (97%)	254 (96%)	11 (4%)	30	63
82	1	522/836 (62%)	465 (89%)	57 (11%)	6	32
All	All	10153/11271 (90%)	9576 (94%)	577 (6%)	24	55

5 of 577 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	W	26	LEU

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Mol	Chain	Res	Type
82	1	896	LYS
71	X	142	LYS
70	W	24	GLN
82	1	385	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
55	H	19	GLN
80	g	32	ASN
56	I	160	GLN
69	V	33	GLN
82	1	475	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3261/3364 (96%)	978 (29%)	153 (4%)
2	7	120/121 (99%)	27 (22%)	2 (1%)
3	8	156/2825 (5%)	41 (26%)	5 (3%)
81	2	1778/1798 (98%)	770 (43%)	94 (5%)
83	3	75/76 (98%)	35 (46%)	6 (8%)
All	All	5390/8184 (65%)	1851 (34%)	260 (4%)

5 of 1851 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	9	U
1	5	20	A
1	5	22	G
1	5	40	A
1	5	43	A

5 of 260 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
81	2	1491	A
81	2	1580	U
1	5	2422	U
1	5	2341	A

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Mol	Chain	Res	Type
81	2	1655	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
85	GCP	1	1001	-	27,34,34	1.60	6 (22%)	34,54,54	1.93	9 (26%)

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
85	GCP	1	1001	-	-	6/15/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	1	1001	GCP	C5-C6	4.48	1.49	1.41
85	1	1001	GCP	PB-O3A	3.01	1.61	1.58
85	1	1001	GCP	PG-O2G	2.85	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	1	1001	GCP	PG-O3G	2.80	1.61	1.54
85	1	1001	GCP	C5-C4	2.61	1.47	1.40

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	1	1001	GCP	C2-N3-C4	5.14	121.23	115.36
85	1	1001	GCP	C4-C5-C6	-3.99	116.99	120.80
85	1	1001	GCP	C2-N1-C6	3.87	122.07	115.93
85	1	1001	GCP	C5-C6-N1	-3.61	118.49	123.43
85	1	1001	GCP	N3-C2-N1	-3.49	122.57	127.22

There are no chirality outliers.

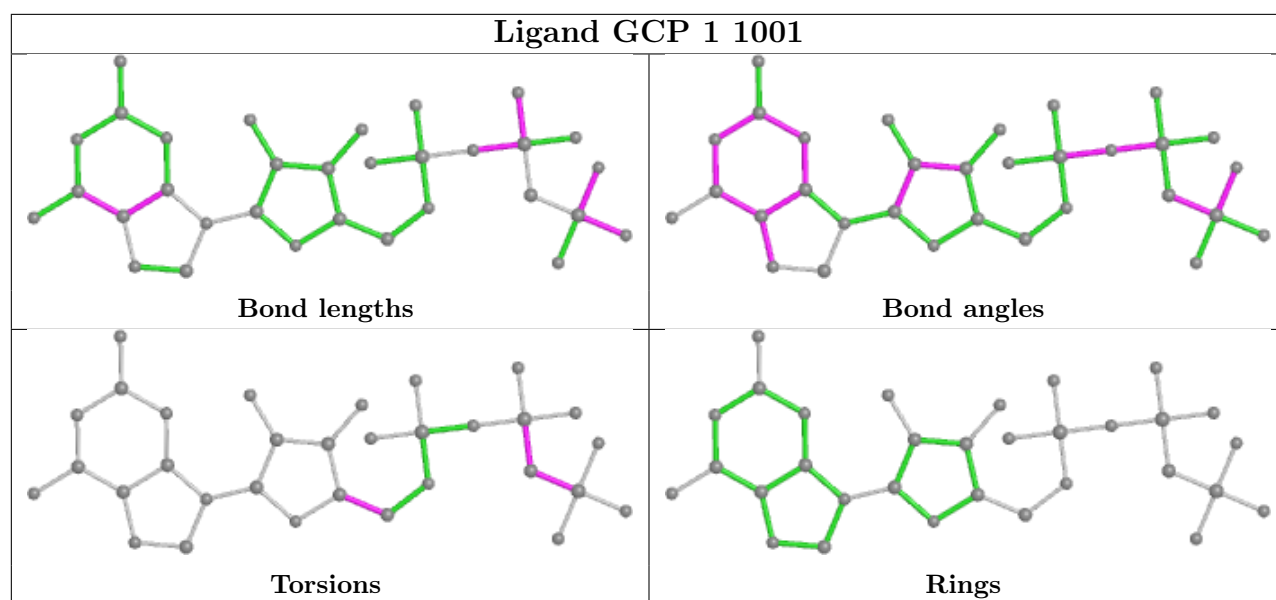
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	1	1001	GCP	PB-C3B-PG-O1G
85	1	1001	GCP	PB-C3B-PG-O2G
85	1	1001	GCP	PB-C3B-PG-O3G
85	1	1001	GCP	PG-C3B-PB-O3A
85	1	1001	GCP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	2
47	AK	2
8	AE	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AE	116:GLU	C	117:ALA	N	6.39
1	5	2049:G	O3'	2050:A	P	6.33
1	AK	52:UNK	C	54:UNK	N	5.65
1	AK	23:UNK	C	28:UNK	N	3.69
1	5	2196:C	O3'	2197:A	P	3.40

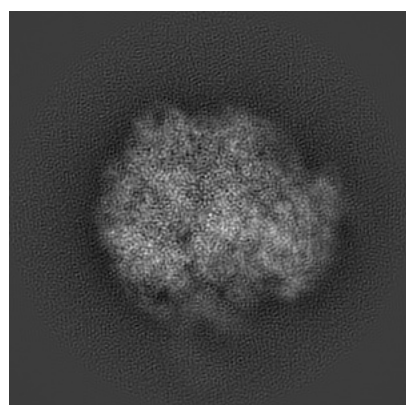
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20952. These allow visual inspection of the internal detail of the map and identification of artifacts.

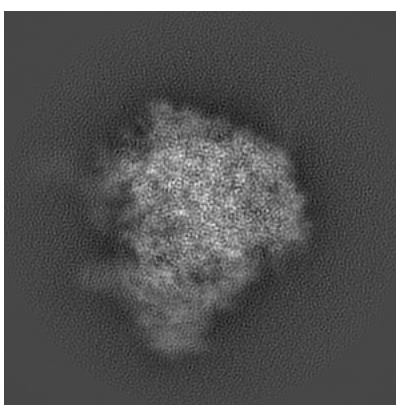
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

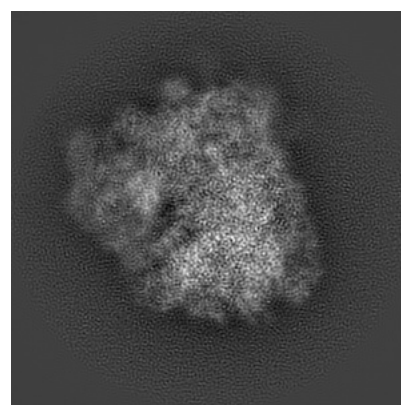
6.1.1 Primary map



X



Y

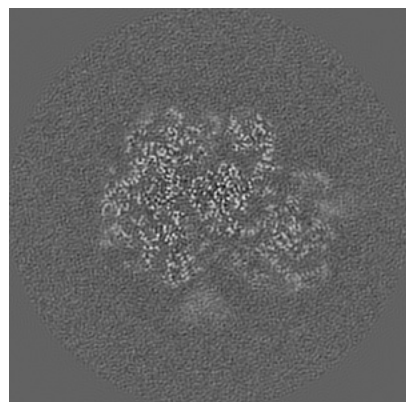


Z

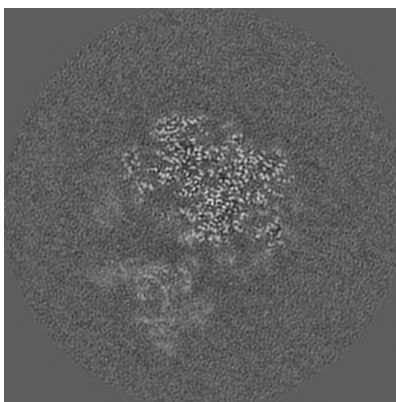
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

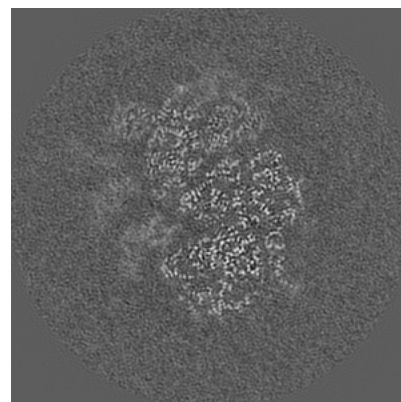
6.2.1 Primary map



X Index: 200



Y Index: 200

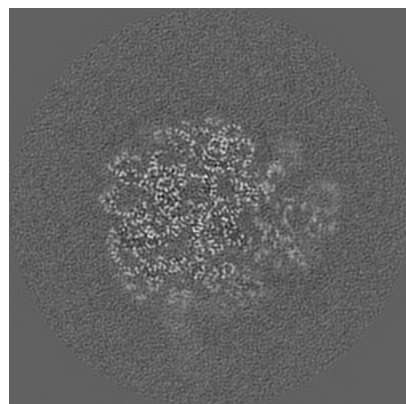


Z Index: 200

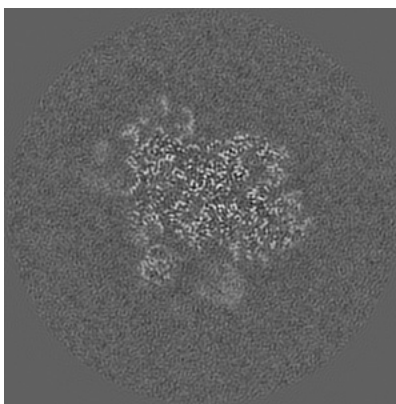
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

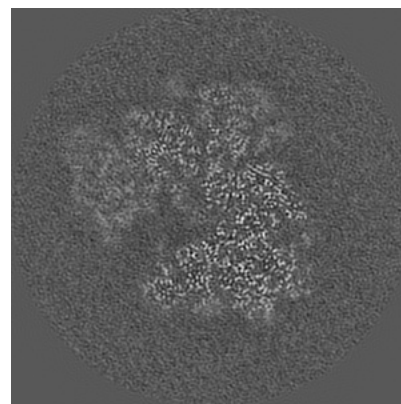
6.3.1 Primary map



X Index: 230



Y Index: 158



Z Index: 176

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

6.4 Orthogonal surface views [i](#)

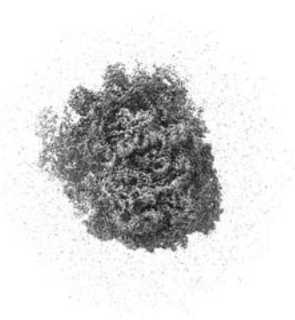
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

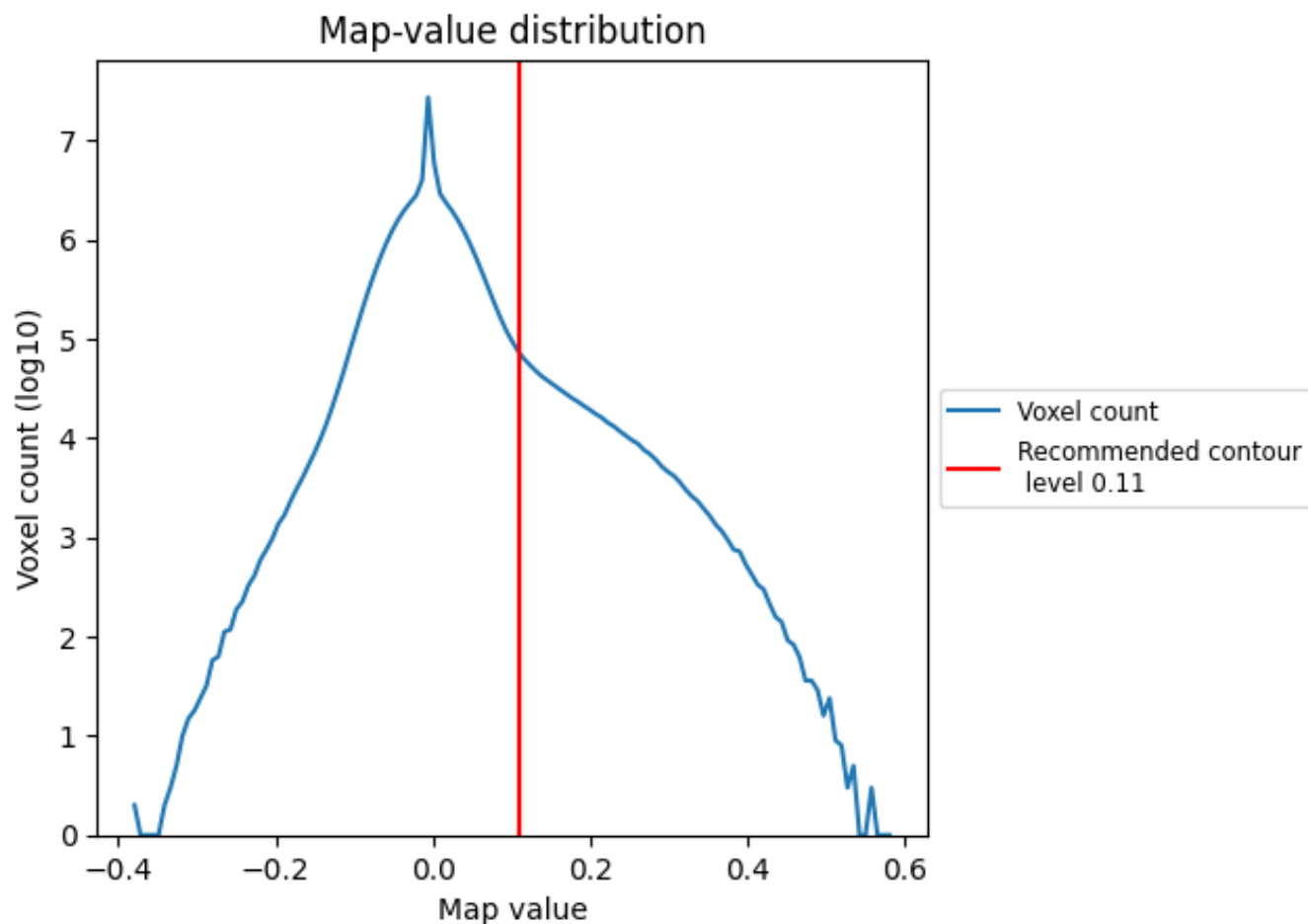
6.5 Mask visualisation

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

7 Map analysis [i](#)

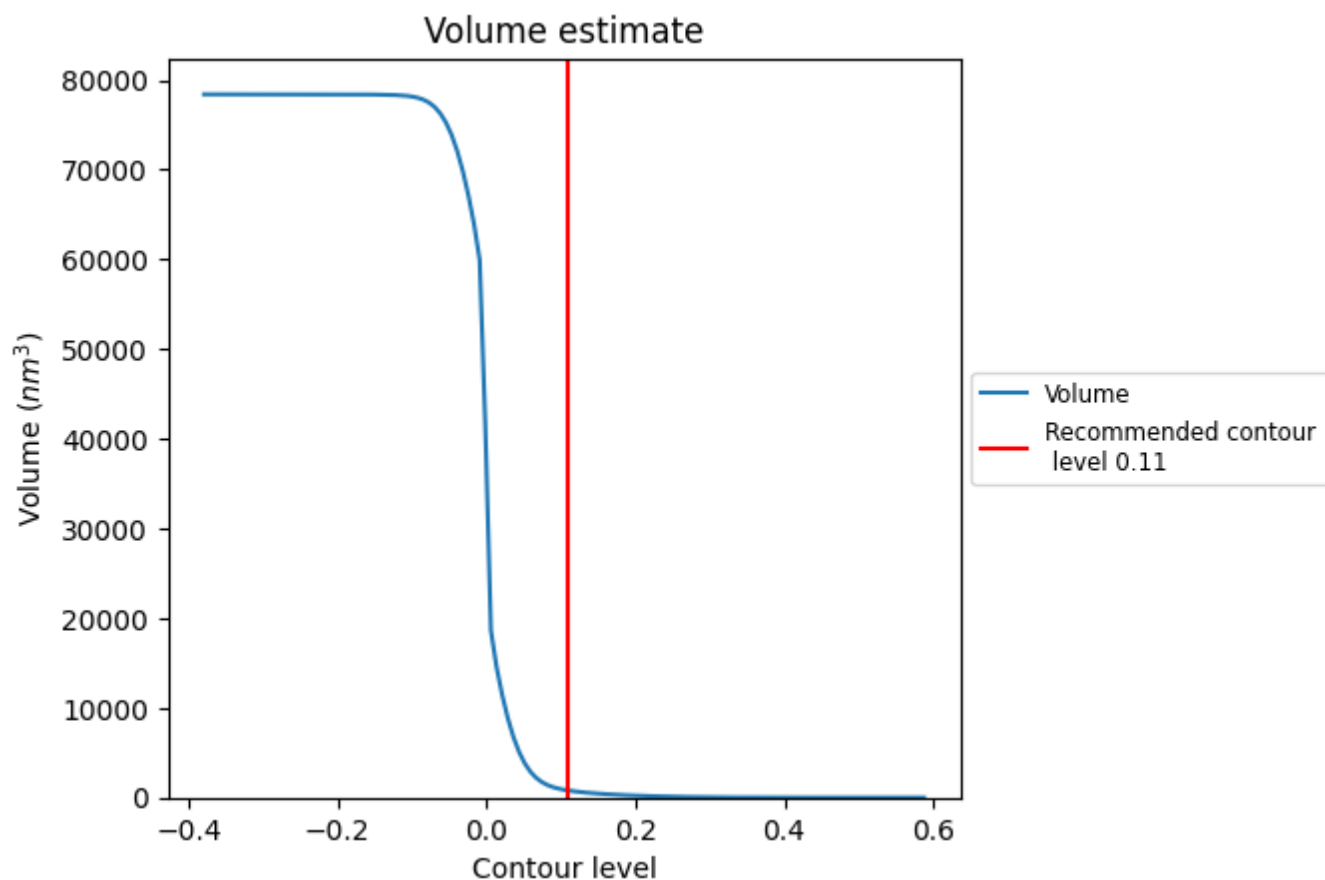
This section contains the results of statistical analysis of the map.

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.

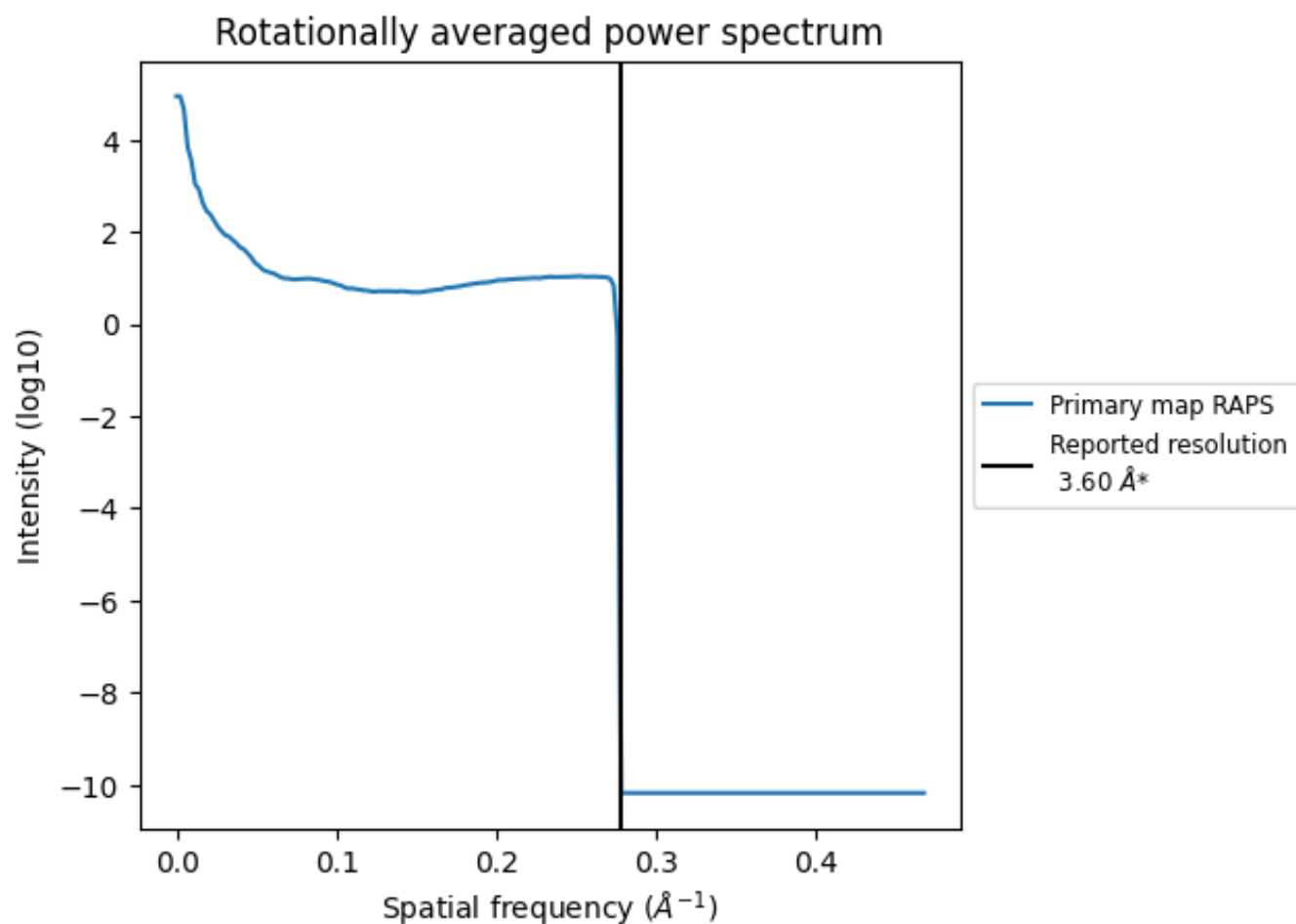
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 787 nm³; this corresponds to an approximate mass of 711 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 0.278 Å⁻¹

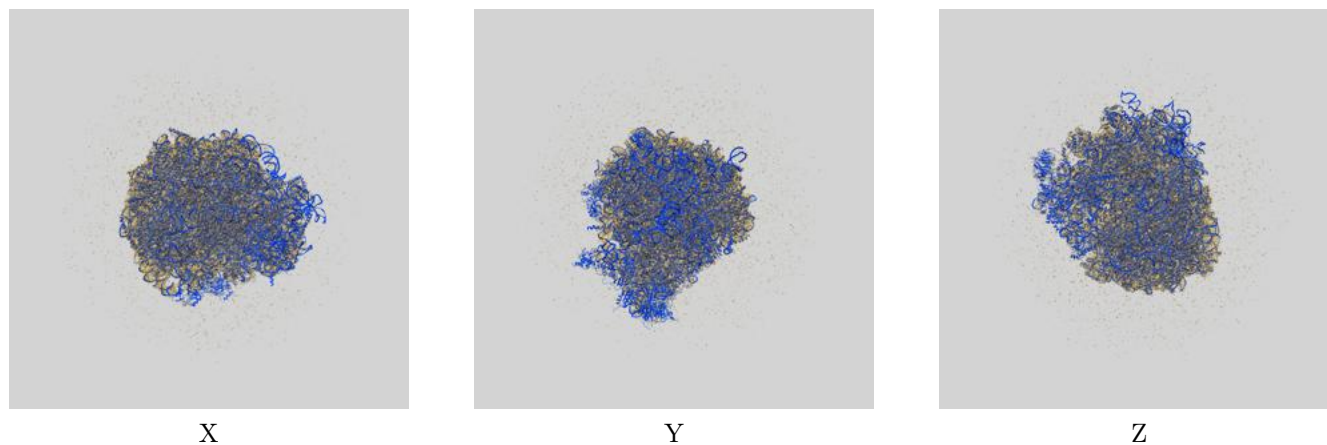
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

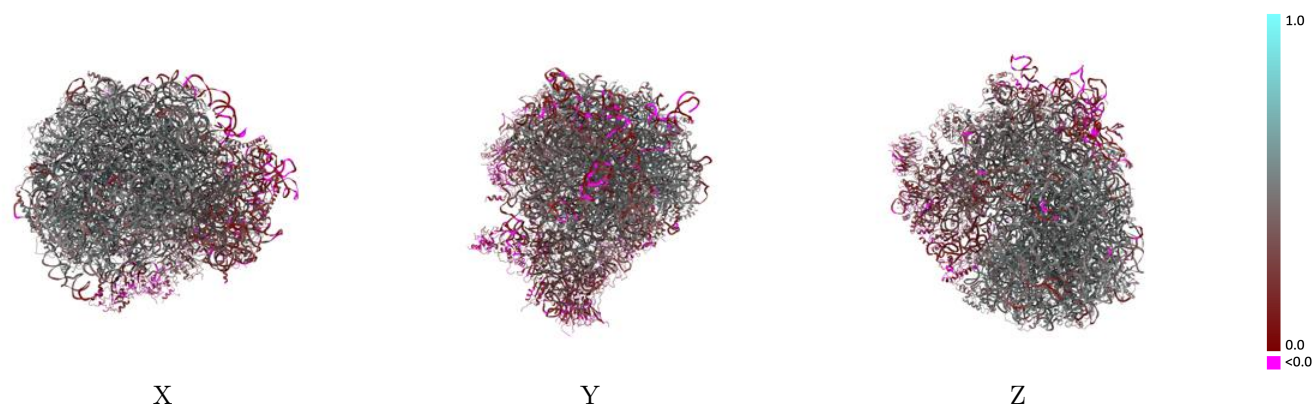
This section contains information regarding the fit between EMDB map EMD-20952 and PDB model 6UZ7. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



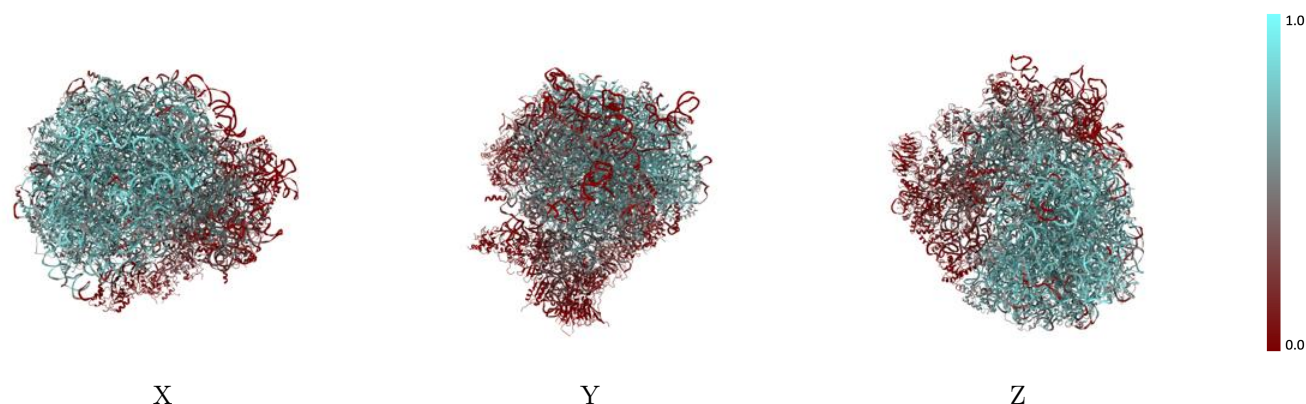
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



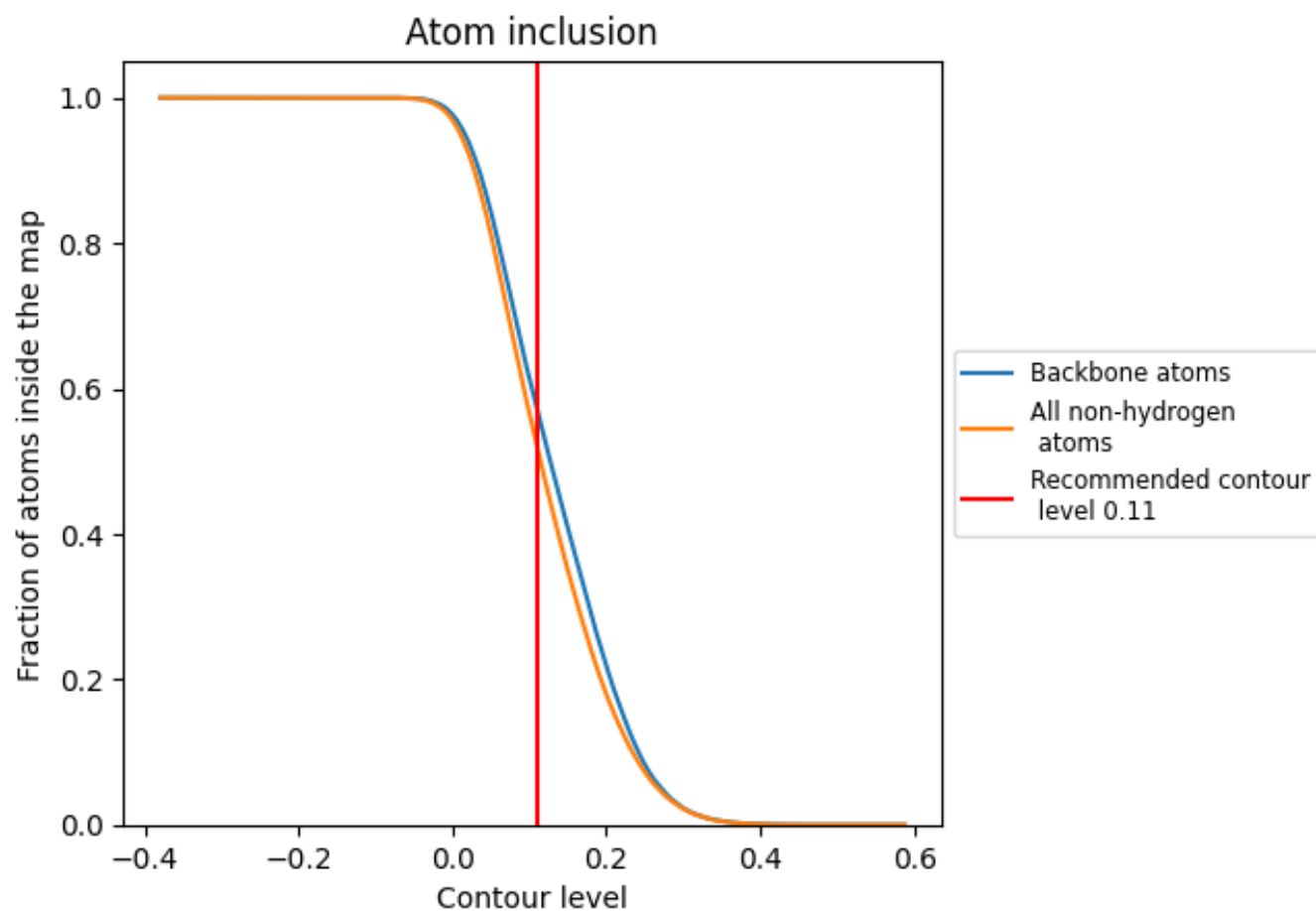
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 52% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5197	 0.3900
1	 0.2174	 0.3570
2	 0.4227	 0.3290
3	 0.2384	 0.2170
5	 0.7017	 0.4420
7	 0.7829	 0.4790
8	 0.7631	 0.4730
A	 0.3344	 0.3440
AA	 0.6578	 0.4920
AB	 0.6711	 0.4920
AC	 0.6327	 0.4730
AD	 0.5454	 0.4330
AE	 0.5097	 0.4230
AF	 0.6555	 0.4730
AG	 0.5507	 0.4400
AH	 0.5829	 0.4690
AI	 0.6298	 0.4810
AJ	 0.4717	 0.4040
AK	 0.0082	 0.0410
AL	 0.5730	 0.4520
AM	 0.5941	 0.4720
AN	 0.7242	 0.5110
AO	 0.6911	 0.5000
AP	 0.6409	 0.4700
AQ	 0.6474	 0.4950
AR	 0.5536	 0.4380
AS	 0.6533	 0.4920
AT	 0.6203	 0.4710
AU	 0.4239	 0.4050
AV	 0.6038	 0.4940
AW	 0.6190	 0.4790
AX	 0.5981	 0.4580
AY	 0.6184	 0.4580
AZ	 0.6011	 0.4430
B	 0.2848	 0.3630

















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Chain	Atom inclusion	Q-score
Ba	 0.7028	 0.5000
Bb	 0.5628	 0.4500
Bc	 0.5810	 0.4590
Bd	 0.6291	 0.4830
Be	 0.6168	 0.4760
Bf	 0.7074	 0.5080
Bg	 0.5672	 0.4440
Bh	 0.6152	 0.4740
Bi	 0.5270	 0.4310
Bj	 0.7323	 0.5150
Bk	 0.4300	 0.3690
Bl	 0.6339	 0.4810
Bm	 0.5819	 0.4800
Bn	 0.1726	 0.2430
Bo	 0.5885	 0.4680
Bp	 0.6173	 0.4680
Bq	 0.0254	 0.0860
Br	 0.0155	 0.1060
C	 0.4497	 0.4040
D	 0.1029	 0.2240
E	 0.3543	 0.3740
F	 0.0394	 0.1680
G	 0.1438	 0.2400
H	 0.2772	 0.3410
I	 0.2184	 0.2820
J	 0.3912	 0.3650
K	 0.0528	 0.1820
L	 0.3921	 0.3760
M	 0.0055	 0.0710
N	 0.3868	 0.3750
O	 0.2755	 0.3630
P	 0.0714	 0.1780
Q	 0.0694	 0.2130
R	 0.1366	 0.2480
S	 0.0610	 0.1430
T	 0.0685	 0.2050
U	 0.0747	 0.2000
V	 0.4318	 0.4250
W	 0.5880	 0.4640
X	 0.4470	 0.4300
Y	 0.2228	 0.3260
Z	 0.0055	 0.0990

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Chain	Atom inclusion	Q-score
a	 0.3657	 0.3450
b	 0.2918	 0.3310
c	 0.0443	 0.2110
d	 0.1920	 0.3010
e	 0.2214	 0.2980
f	 0.0090	 0.1220
g	 0.0269	 0.1600