



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:39 AM UTC

PDB ID : 5AJ0 / pdb_00005aj0
EMDB ID : EMD-2875
Title : Cryo electron microscopy of actively translating human polysomes (POST state).
Authors : Behrmann, E.; Loerke, J.; Budkevich, T.V.; Yamamoto, K.; Schmidt, A.; Penczek, P.A.; Vos, M.R.; Burger, J.; Mielke, T.; Scheerer, P.; Spahn, C.M.T.
Deposited on : 2015-02-19
Resolution : 3.50 Å (reported)
Based on initial model : 4UJE

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

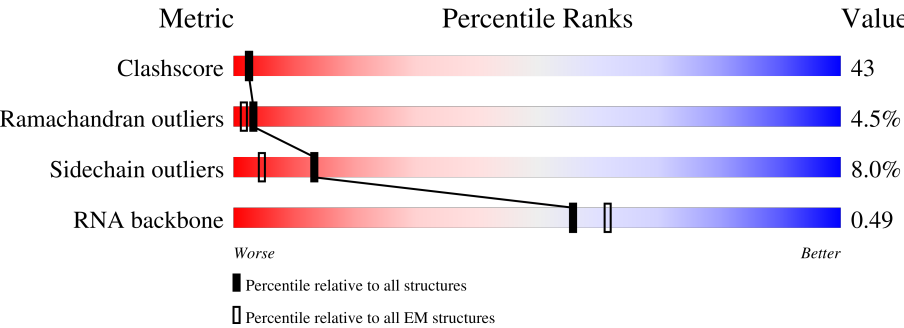
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.50 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	A3	194	81% 26% 28% 21% 6% 19%
2	A4	121	98% 26% 41% 31%
3	AA	257	98% 52% 39% 7%
4	AB	403	98% 41% 50% 6%
5	AC	427	85% 40% 37% 7% 15%
6	AD	297	99% 53% 36% 9%
7	AE	288	67% 19% 27% 17% 33%

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Mol	Chain	Length	Quality of chain
8	AF	248	
9	AG	266	
10	AH	192	
11	AI	214	
12	AJ	178	
13	AK	317	
14	AL	211	
15	AM	215	
16	AN	204	
17	AO	203	
18	AP	184	
19	AQ	188	
20	AR	196	
21	AS	176	
22	AT	160	
23	AU	128	
24	AV	140	
25	AW	157	
26	AX	156	
27	AY	145	
28	AZ	136	
29	Aa	148	
30	Ab	159	
31	Ac	115	
32	Ad	125	

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Mol	Chain	Length	Quality of chain
33	Ae	135	
34	Af	110	
35	Ag	117	
36	Ah	123	
37	Ai	105	
38	Aj	97	
39	Ak	70	
40	Al	51	
41	Am	128	
42	An	25	
43	Ao	106	
44	Ap	92	
45	Aq	165	
46	At	137	
47	Au	217	
48	A2	5029	
49	B1	1869	
50	BA	295	
51	BB	264	
52	BC	293	
53	BD	243	
54	BE	263	
55	BF	204	
56	BG	249	
57	BH	194	

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Mol	Chain	Length	Quality of chain
58	BI	208	
59	BJ	194	
60	BK	165	
61	BL	158	
62	BM	132	
63	BN	151	
64	BO	151	
65	BP	145	
66	BQ	146	
67	BR	135	
68	BS	152	
69	BT	145	
70	BU	119	
71	BV	83	
72	BW	130	
73	BX	143	
74	BY	133	
75	BZ	125	
76	Ba	115	
77	Bb	84	
78	Bc	69	
79	Bd	56	
80	Be	59	
81	Bf	156	
82	Bg	317	

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Mol	Chain	Length	Quality of chain
83	Bv	76	
83	Bw	76	
84	Bx	28	
85	By	24	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
86	MG	B1	1941	-	-	X	-

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 218559 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 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A3	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A4	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AA	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	394	Total	C	N	O	S	0	0
			3178	2024	596	544	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	363	Total	C	N	O	S	0	0
			2888	1817	577	480	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	294	Total	C	N	O	S	0	0
			2392	1510	436	432	14		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AE	194	Total	C	N	O	S	0	0
			1571	1013	294	263	1		

- Molecule 8 is a protein called 60S ribosomal protein L7.

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

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AG	234	Total	C	N	O	S	0	0
			1880	1197	362	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AH	191	Total	C	N	O	S	0	0
			1526	960	285	275	6		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AI	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AJ	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 13 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AK	109	Total	C	N	O	S	0	0
			872	554	159	151	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AL	205	Total	C	N	O	S	0	0
			1657	1036	344	273	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	195	Total	C	N	O	S	0	0
			1606	1034	315	252	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AR	181	Total	C	N	O	S	0	0
			1517	938	329	241	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	175	Total	C	N	O	S	0	0
			1449	921	283	234	11		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	157	Total	C	N	O	S	0	0
			1284	815	250	214	5		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AU	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	121	Total	C	N	O	S	0	0
			989	617	202	167	3		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AX	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AY	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AZ	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ab	68	Total	C	N	O	S	0	0
			559	344	122	90	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	103	Total	C	N	O	S	0	0
			801	508	141	145	7		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ag	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ai	97	Total	C	N	O	S	0	0
			794	497	168	124	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aj	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

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

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Am	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

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

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Aq	138	Total	C	N	O	S	0	0
			1046	654	196	193	3		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	At	122	Total	C	N	O	S	0	0
			980	607	204	165	4		

- Molecule 47 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Au	217	Total	C	N	O	S	0	0
			1744	1114	314	307	9		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A2	3612	Total	C	N	O	P	0	0
			77427	34482	14158	25175	3612		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	245	C	-	insertion	GB 337381
A2	246	C	-	insertion	GB 337381
A2	247	C	-	insertion	GB 337381
A2	4684	G	-	insertion	GB 337381

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B1	1708	Total	C	N	O	P	0	0
			36456	16274	6546	11928	1708		

- Molecule 50 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BA	215	Total	C	N	O	S	0	0
			1704	1083	298	315	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 52 is a protein called 40S ribosomal protein S2.

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

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	220	Total	C	N	O	S	0	0
			1709	1090	308	304	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, Y isoform 1.

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

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	190	Total	C	N	O	S	0	0
			1502	939	285	271	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BH	183	Total	C	N	O	S	0	0
			1479	941	272	265	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BI	207	Total	C	N	O	S	0	0
			1696	1064	334	293	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

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

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BL	153	Total	C	N	O	S	0	0
			1258	804	235	213	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

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

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BP	120	Total	C	N	O	S	0	0
			999	636	188	168	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 67 is a protein called 40S ribosomal protein S17-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BR	125	Total	C	N	O	S	0	0
			1011	634	187	186	4		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BS	139	Total	C	N	O	S	0	0
			1154	725	233	195	1		

- Molecule 69 is a protein called 40S ribosomal protein S19.

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

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BU	97	Total	C	N	O	S	0	0
			769	483	144	138	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BV	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BZ	86	Total	C	N	O	S	0	0
			688	442	129	116	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ba	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Bd	51	Total	C	N	O	S	0	0
			427	269	87	66	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Be	55	Total	C	N	O	S	0	0
			437	272	96	68	1		

- Molecule 81 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Bf	73	Total	C	N	O	S	0	0
			601	379	115	100	7		

- Molecule 82 is a protein called Guanine nucleotide-binding protein subunit beta-2-like 1.

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

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
83	Bw	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Bx	28	Total	C	N	O	P	0	0
			561	252	56	225	28		

- Molecule 85 is a protein called Nascent protein chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	By	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A3	8	Total	Mg	0
			8	8	
86	A4	9	Total	Mg	0
			9	9	
86	AA	1	Total	Mg	0
			1	1	
86	AB	2	Total	Mg	0
			2	2	
86	AN	2	Total	Mg	0
			2	2	
86	AY	1	Total	Mg	0
			1	1	
86	Aa	3	Total	Mg	0
			3	3	
86	Ae	2	Total	Mg	0
			2	2	
86	An	1	Total	Mg	0
			1	1	
86	A2	220	Total	Mg	0
			220	220	
86	B1	72	Total	Mg	0
			72	72	

Continued on next page...

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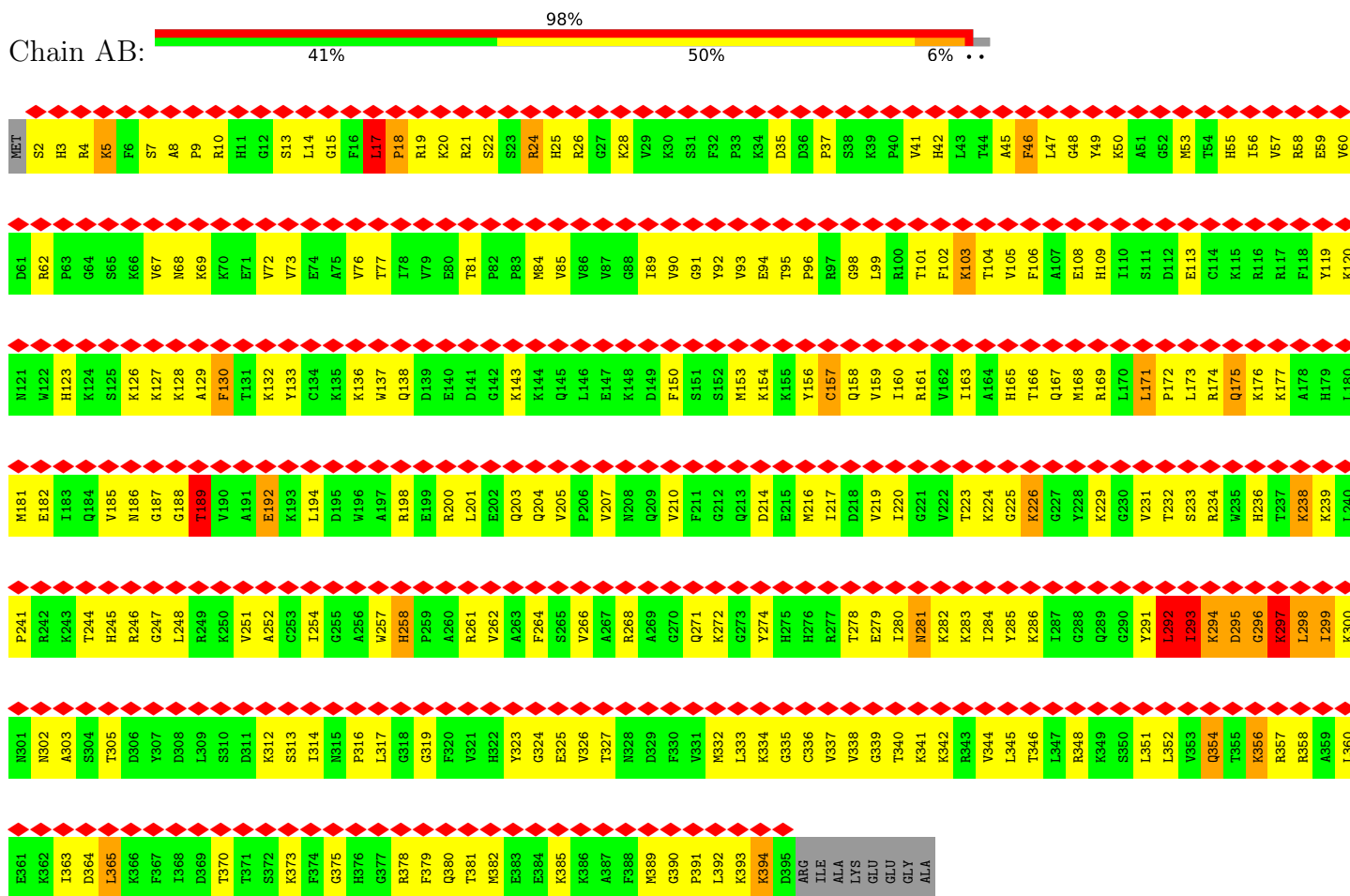
Mol	Chain	Residues	Atoms		AltConf
86	BD	1	Total 1	Mg 1	0
86	BX	1	Total 1	Mg 1	0
86	Bv	2	Total 2	Mg 2	0
86	Bx	1	Total 1	Mg 1	0

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

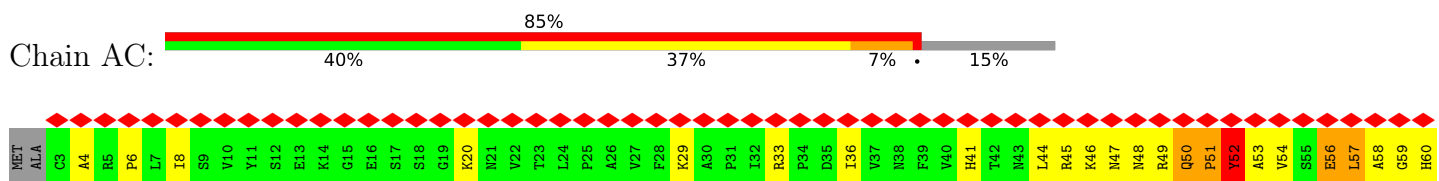
Mol	Chain	Residues	Atoms		AltConf
87	Aj	1	Total 1	Zn 1	0
87	Ao	1	Total 1	Zn 1	0
87	Ap	1	Total 1	Zn 1	0
87	Ba	1	Total 1	Zn 1	0
87	Bd	1	Total 1	Zn 1	0

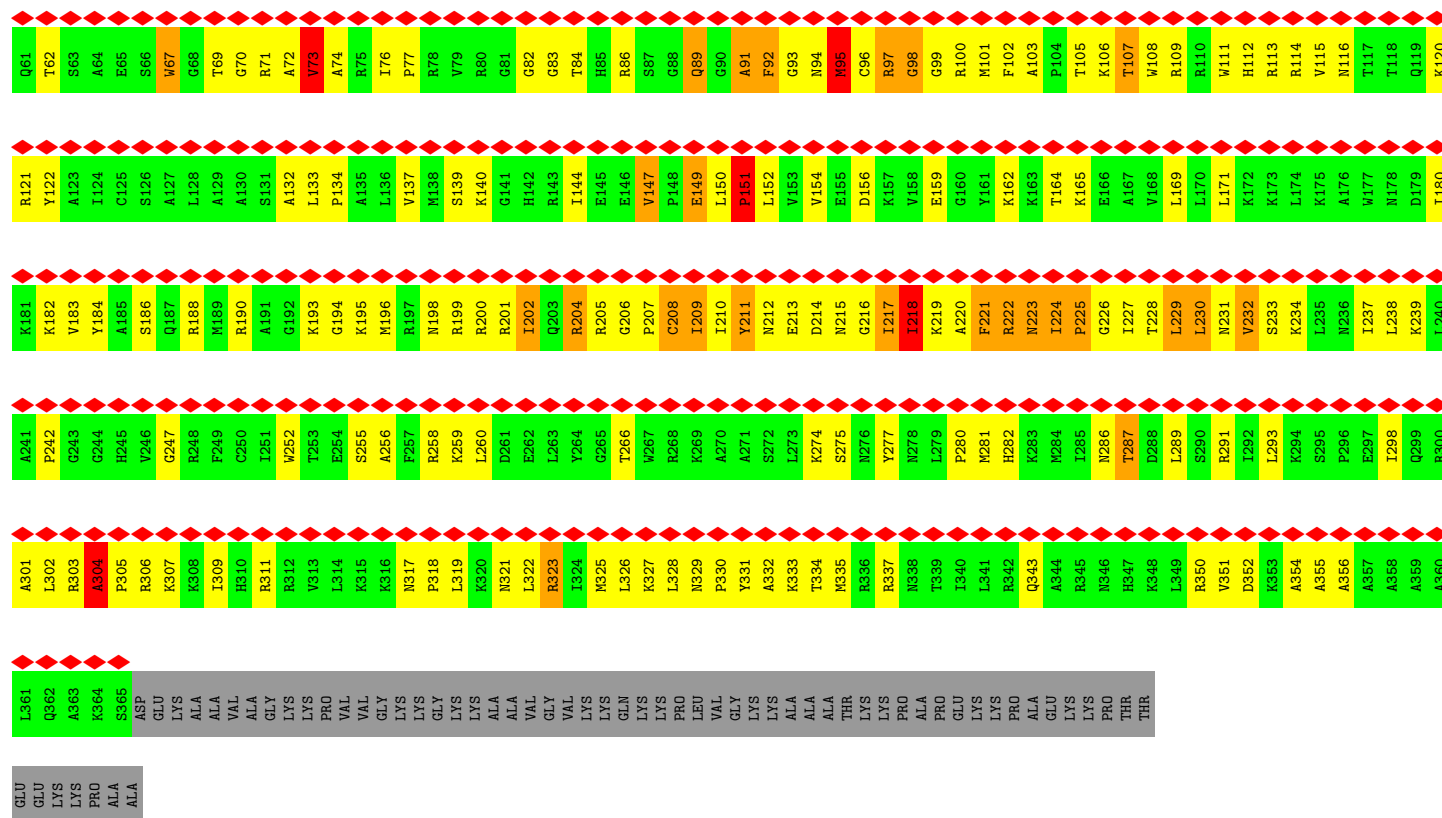


• Molecule 4: 60S ribosomal protein L3

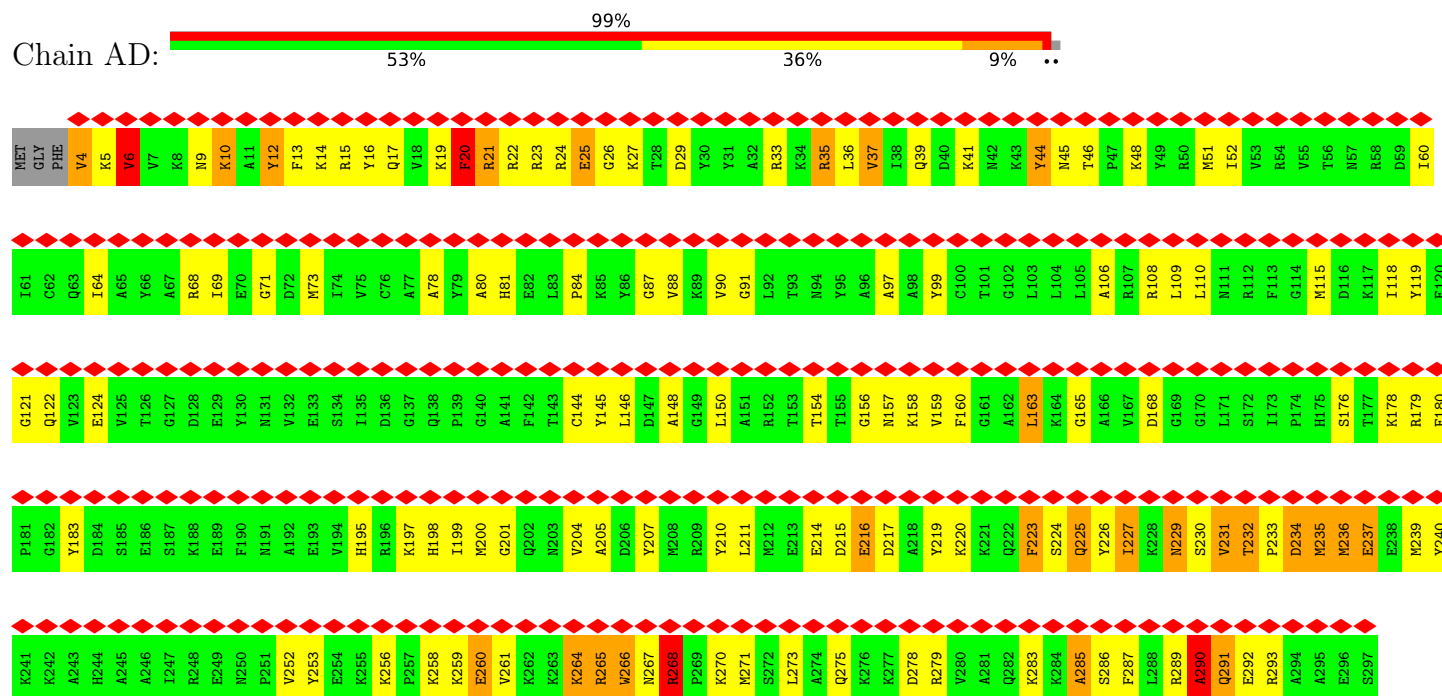


• Molecule 5: 60S ribosomal protein L4





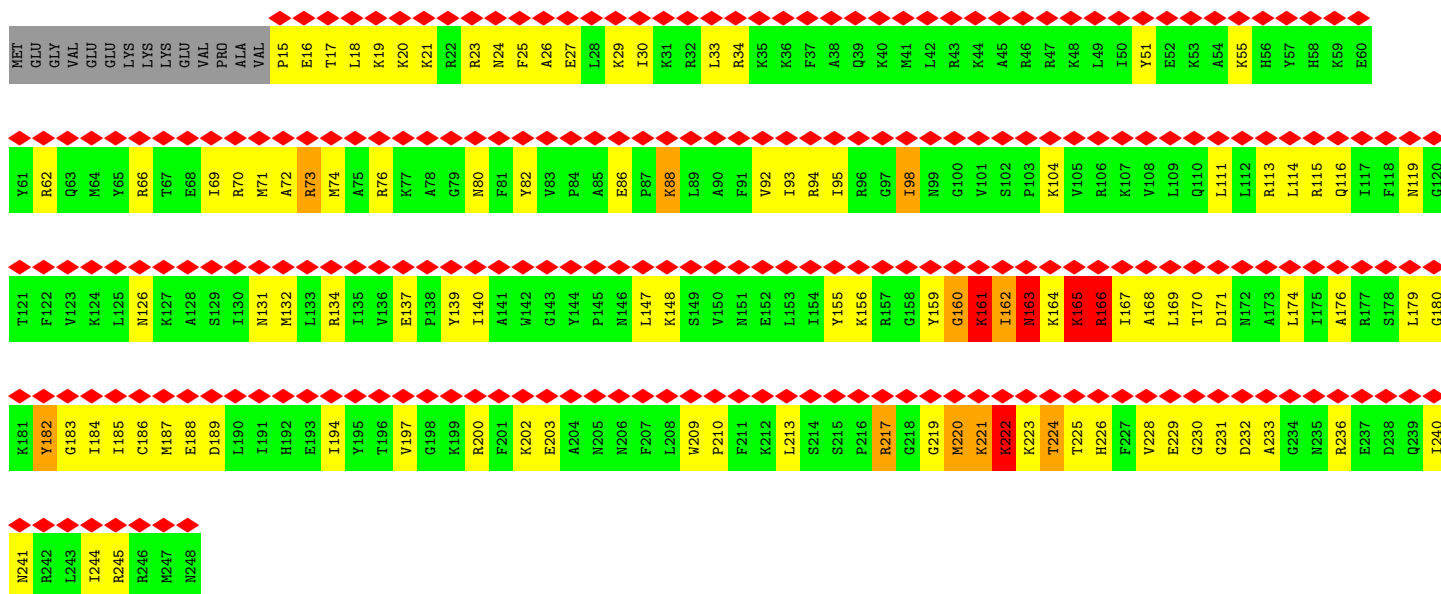
• Molecule 6: 60S ribosomal protein L5



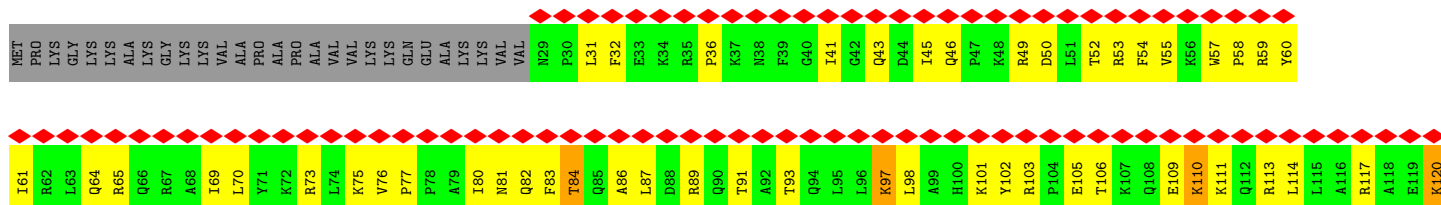
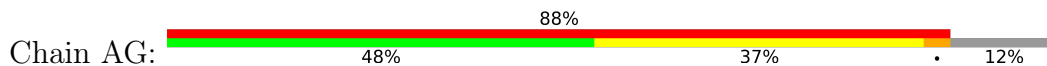
• Molecule 7: 60S ribosomal protein L6

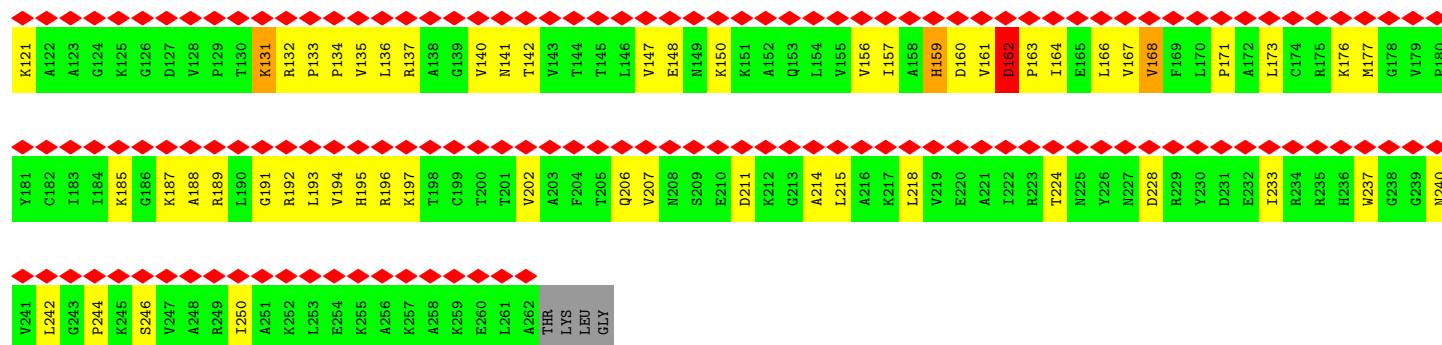


- Molecule 8: 60S ribosomal protein L7



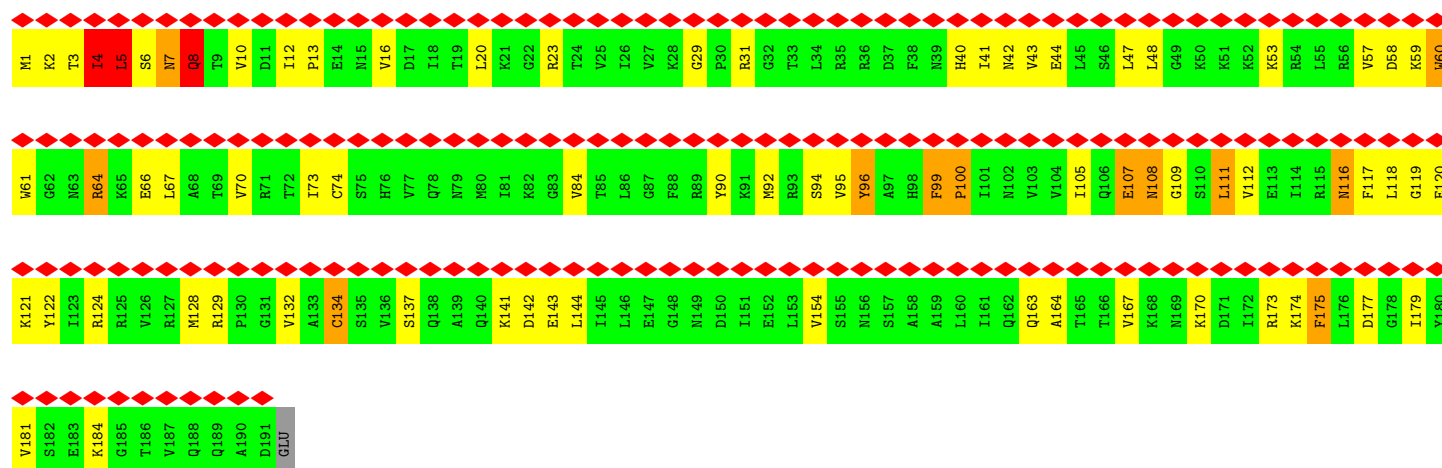
- Molecule 9: 60S ribosomal protein L7a





• Molecule 10: 60S ribosomal protein L9

Chain AH: 99% 59% 33% 6% ..



• Molecule 11: 60S ribosomal protein L10

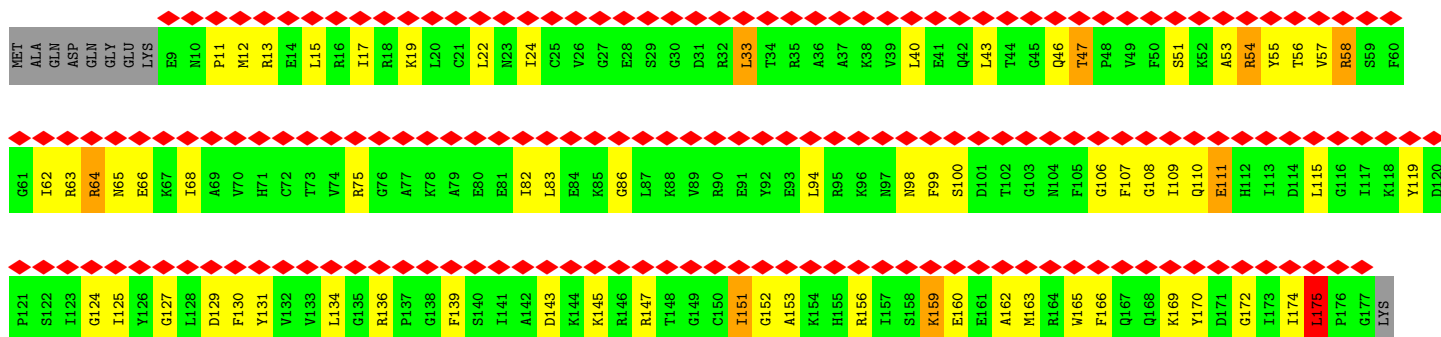
Chain AI: 97% 61% 31% 5% .



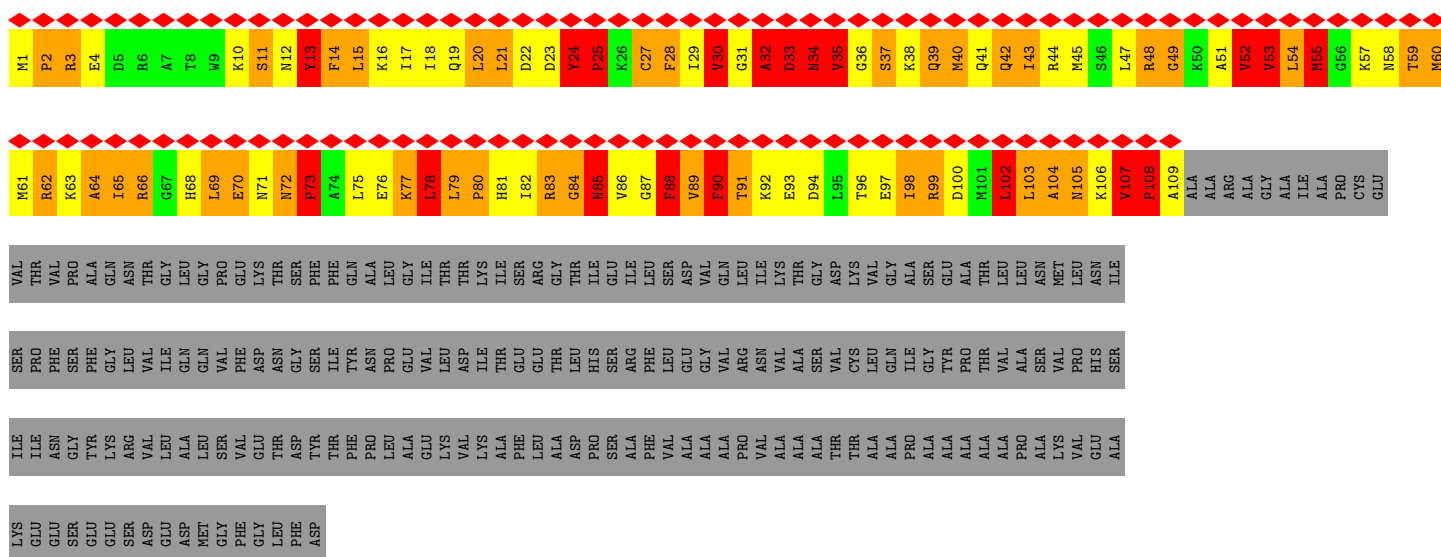
• Molecule 12: 60S ribosomal protein L11

Chain AJ: 95% 56% 34% . . 5%

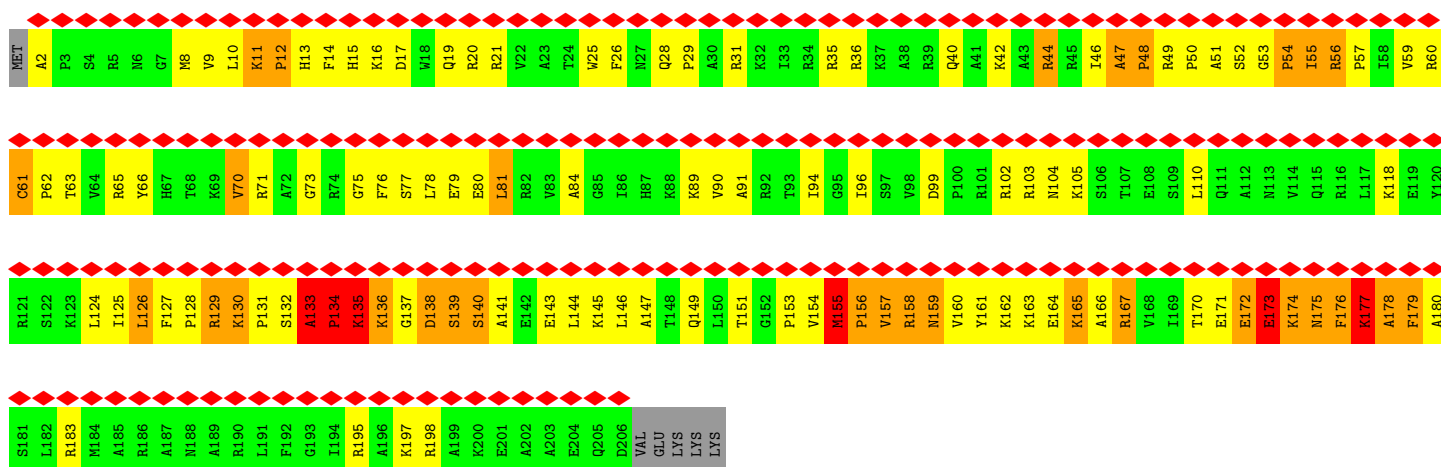




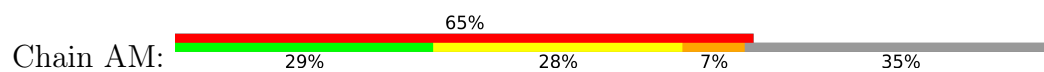
• Molecule 13: 60S acidic ribosomal protein P0



• Molecule 14: 60S ribosomal protein L13



• Molecule 15: 60S ribosomal protein L14



GLN	R121	I61	GLN	MET
	LYS	L62		
ALA	I122	K63	THR	F3
THR	I123	F64	GLY	R4
GLN	K124	P65	GLN	R5
LYS	N125	H66	ALA	F6
ALA	E126	S67	ALA	V7
ALA	V127	A68	ALA	E8
PRO	K128	H69	PRO	V9
ALA	K129	Q70	ALA	G10
PRO	L130	K71	PRO	R11
ALA	Q131	Y72	ALA	V12
GLN	K132	V73	GLN	A13
GLY	A133	R74	GLY	Y14
GLN	A134	Q75	GLN	V15
LYS	L135	A76	LYS	S16
ALA	L136	W77	ALA	V16
PRO	K137	Q78	PRO	F17
ALA	ALA	K79	ALA	G18
GLN	A138	A80	GLN	P19
LYS	S139	D81	LYS	H20
ALA	P140	I82	ALA	A21
PRO	LYS	N83	PRO	G22
PRO	ALA	T84	PRO	K23
LYS	LYS	K85	LYS	L24
LYS	GLY	W86	LYS	V25
LYS	THR	A87	LYS	A26
ALA	ALA	A88	ALA	I27
ALA	ALA	T89	ALA	V28
ALA	ALA	R90	ALA	D29
ALA	ALA	W91	ALA	V30
ALA	ALA	A92	ALA	I31
ALA	ALA	K93	ALA	D32
ALA	ALA	K94	ALA	Q33
ALA	ALA	I95	ALA	N34
LYS	LYS	E96	LYS	R35
VAL	VAL	A97	VAL	A36
PRO	PRO	R98	PRO	L37
ALA	ALA	E99	ALA	V38
LYS	LYS	R100	LYS	D39
LYS	ILE	K101	LYS	G40
THR	THR	A102	THR	P41
ALA	ALA	K103	ALA	C42
ALA	ALA	M104	ALA	T43
SER	SER	T105	SER	Q44
LYS	LYS	D106	LYS	V45
ALA	ALA	F107	ALA	R46
PRO	PRO	D108	PRO	R47
ALA	ALA	R109	ALA	Q48
GLN	GLN	F110	GLN	A49
LYS	LYS	K111	LYS	M50
VAL	VAL	V112	VAL	P51
PRO	PRO	M113	PRO	F52
ALA	ALA	K114	ALA	K53
		A115		C54
		K116		M55
		K117		Q56
		M118		L57
		R119		T58
		N120		D59
				F60

• Molecule 16: 60S ribosomal protein L15



MET	G2	A3	Y4	K5	Y6	I7	Q8	E9	L10	W11	K12	K13	K14	Q15	S16	D17	V18	M19	F20	L21	L22	L23	R24	V25	R26	C27	W28	Q29	Y30	R31	Q32	L33	S34	A35	L36	H37	R38	A39	P40	R41	P42	T43	R44	P45	D46	K47	A48	R49	R50	L51	G52	Y53	K54	A55	K56	Q57	G58	Y59	V60
I61	Y62	R63	I64	R65	V66	R67	R68	G69	G70	R71	K72	R73	P74	V75	P76	K77	G78	A79	T80	Y81	G82	K83	P84	V85	H86	H87	G88	V89	N90	Q91	L92	K93	F94	A95	R96	S97	L98	Q99	S100	V101	A102	E103	E104	R105	A106	G107	R108	H109	C110	G111	A112	L113	L114	V115	L116	N117	Y118	Y119	W120
V121	G122	E123	D124	S125	T126	V127	K128	F129	F130	E131	V132	L133	L134	L135	D136	P137	F138	H139	K140	A141	I142	R143	R144	N145	P146	D147	T148	Q149	W150	I151	T152	K153	P154	V155	H156	K157	H158	R159	E160	M161	R162	G163	L164	T165	S166	A167	G168	R169	K170	S171	R172	G173	L174	G175	K176	G177	H178	K179	F180
H181	H182	T183	I184	G185	G186	S187	R188	R189	A190	A191	W192	R193	R194	R195	N196	T197	L198	Q199	L200	H201	R202	Y203	R204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240

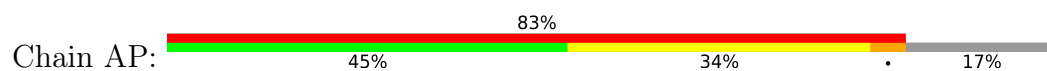
• Molecule 17: 60S ribosomal protein L13a



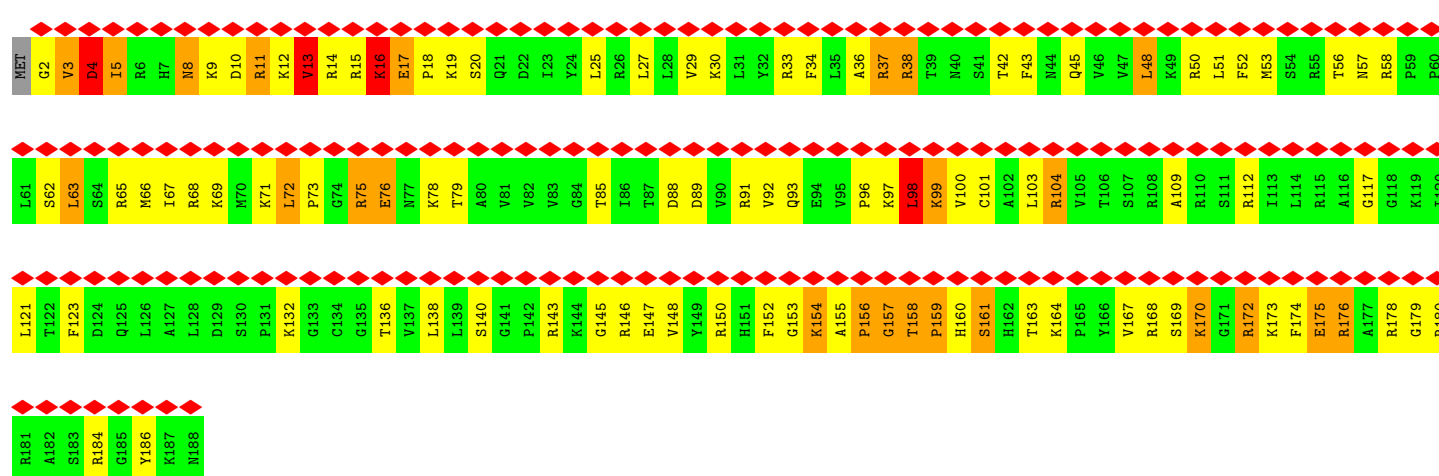
MET	ALA	GLU	VAL	Q5	V6	L7	V8	L9	D10	G11	R12	G13	H14	L15	L16	G17	R18	L19	A20	A21	I22	V23	A24	K25	Q26	V27	L28	L29	G30	R31	K32	V33	V34	V35	V36	R37	C38	E39	G40	I41	N42	L43	S44	G45	M46	F47	Y48	R49	N50	K51	L52	K53	Y54	L55	A56	F57	R58	K59	K60
R61	W62	R63	T64	R65	P66	S67	R68	G69	P70	Y71	H72	F73	R74	A75	P76	S77	I78	F79	F80	W81	R82	T83	V84	R85	G86	H87	L88	P89	H90	K91	T92	R93	R94	G95	Q96	A97	A98	L99	D100	R101	L102	K103	V104	F105	D106	G107	I108	P109	P110	P111	Y112	D113	K114	K115	L116	R117	M118	V119	V120
P121	A122	A123	L124	K125	V126	V127	R128	L129	K130	P131	T132	R133	K134	F135	A136	Y137	L138	G139	R140	L141	A142	H143	E144	V145	G146	W147	K148	Y149	Q150	A151	V152	T153	A154	T155	L156	E157	E158	K159	R160	K161	E162	K163	A164	K165	I166	H167	Y168	R169	K170	K171	K172	Q173	L174	M175	R176	L177	R178	K179	Q180



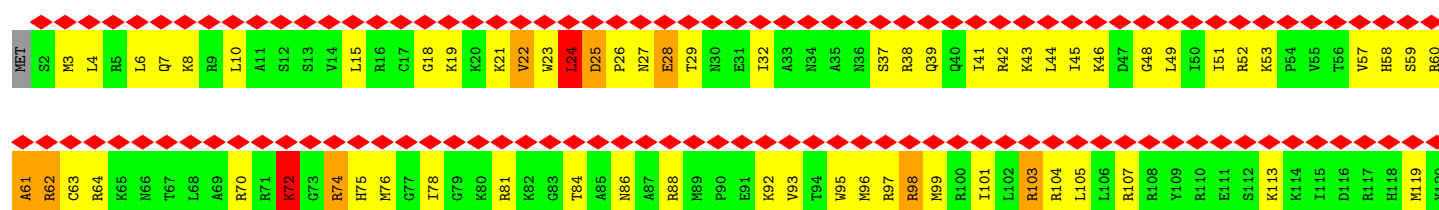
• Molecule 18: 60S ribosomal protein L17

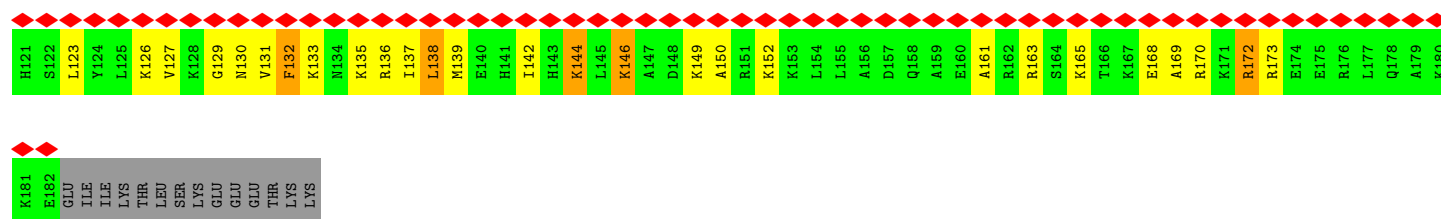


• Molecule 19: 60S ribosomal protein L18



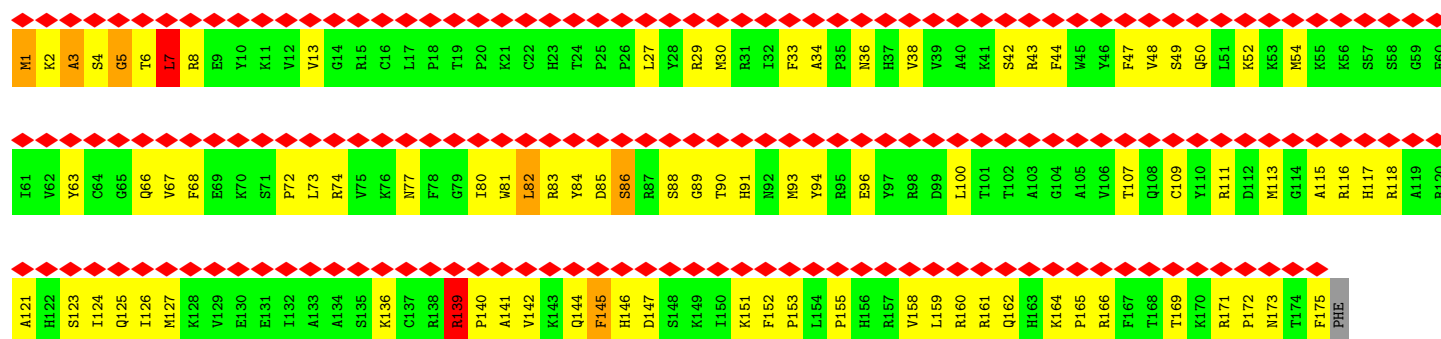
• Molecule 20: 60S ribosomal protein L19





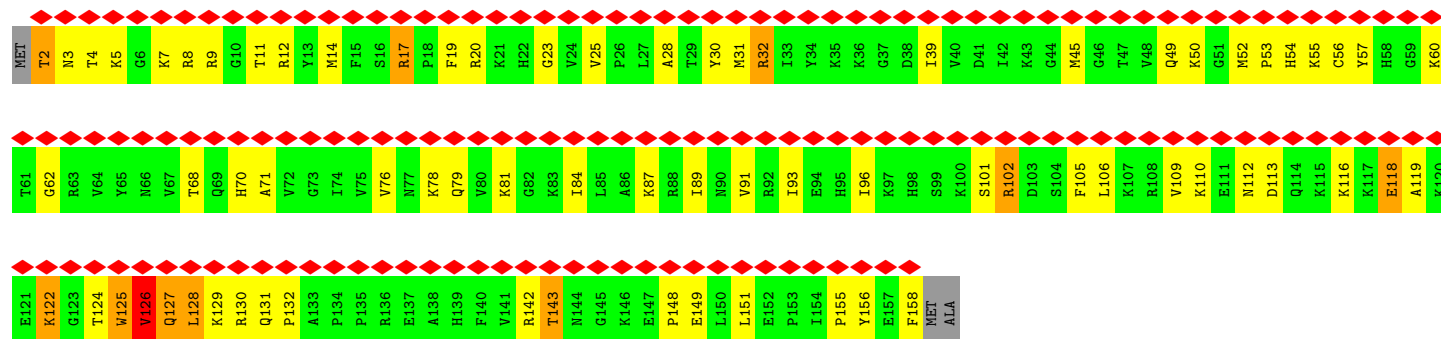
• Molecule 21: 60S ribosomal protein L18a

Chain AS: 99% 49% 45% ..



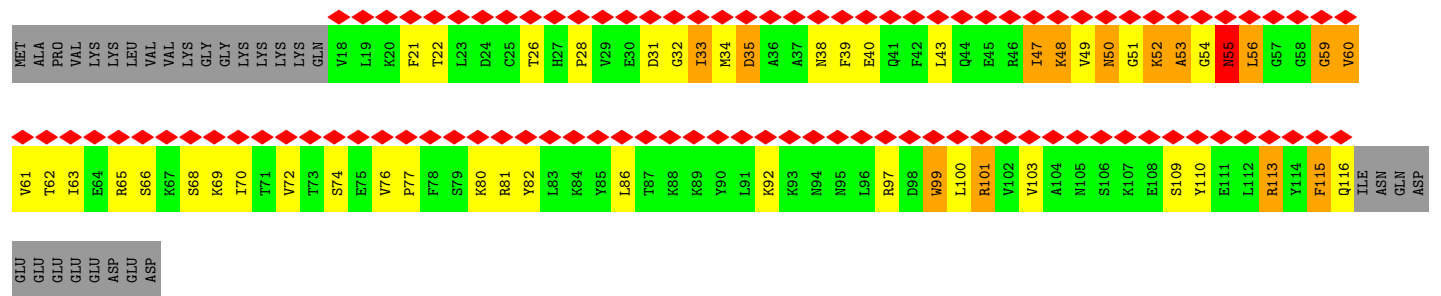
• Molecule 22: 60S ribosomal protein L21

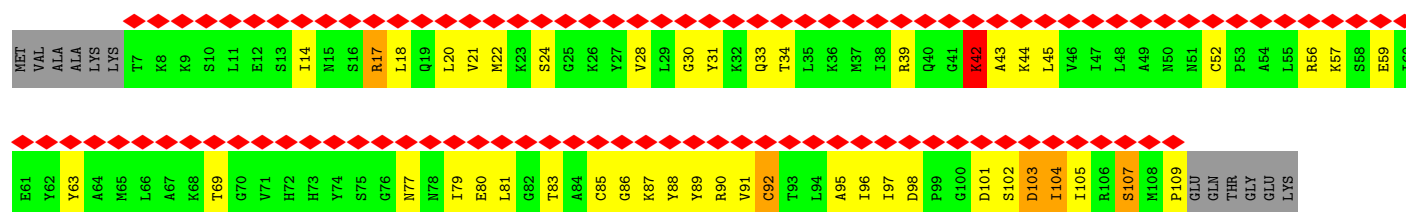
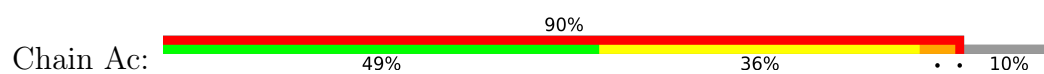
Chain AT: 98% 52% 39% 6% ..



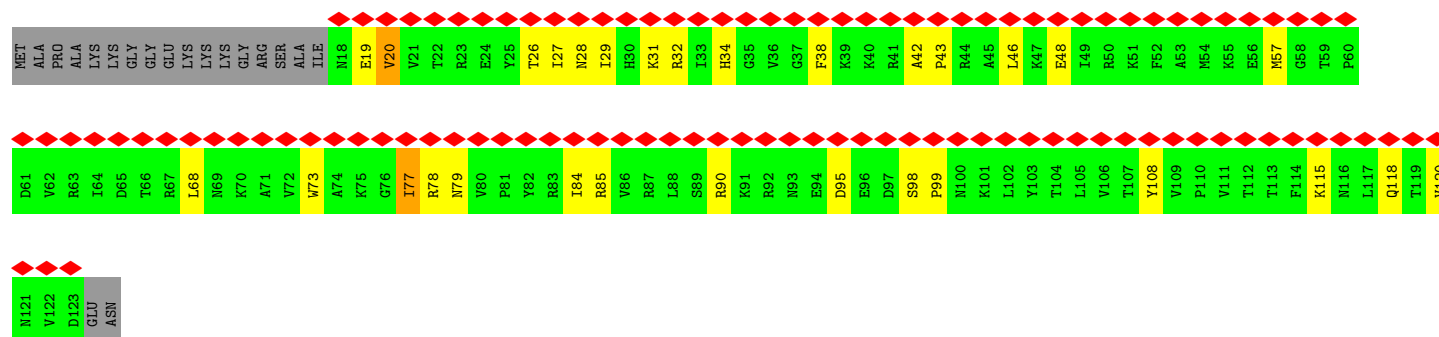
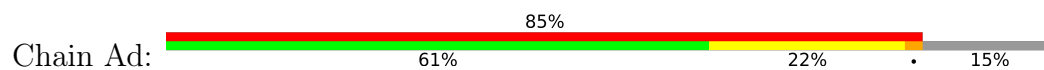
• Molecule 23: 60S ribosomal protein L22

Chain AU: 77% 37% 29% 11% 23%

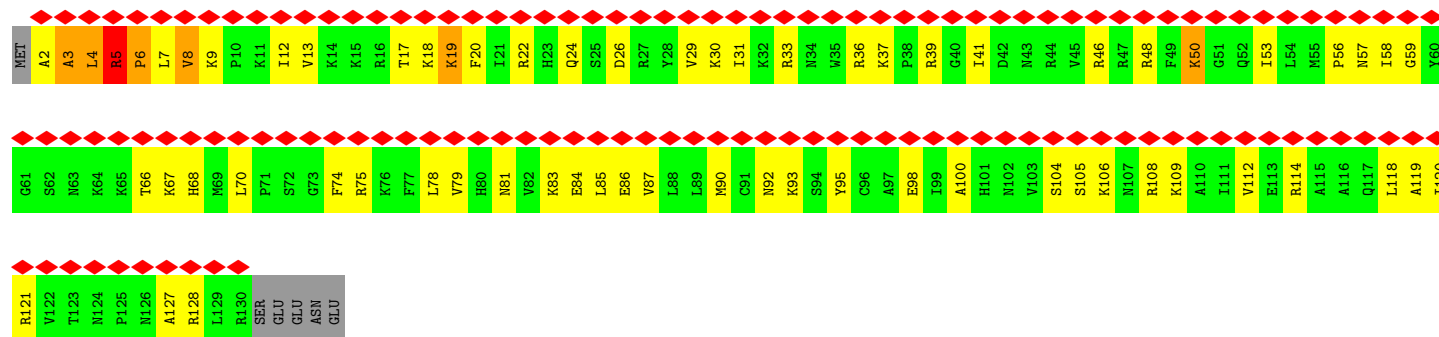




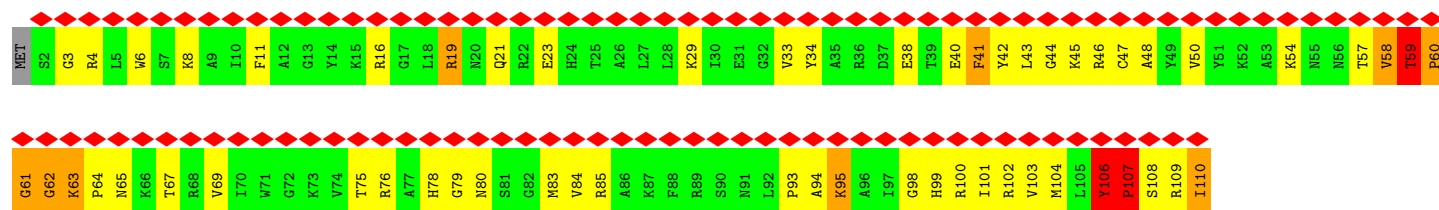
- Molecule 32: 60S ribosomal protein L31



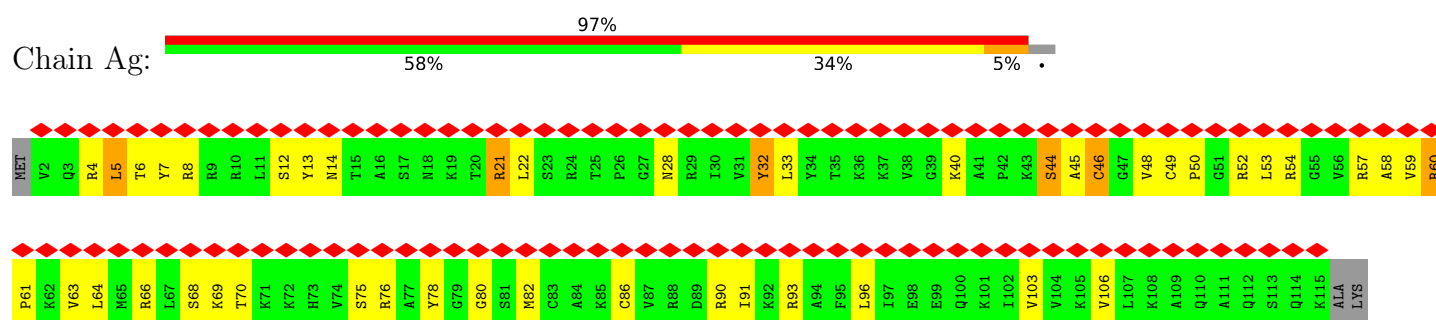
- Molecule 33: 60S ribosomal protein L32



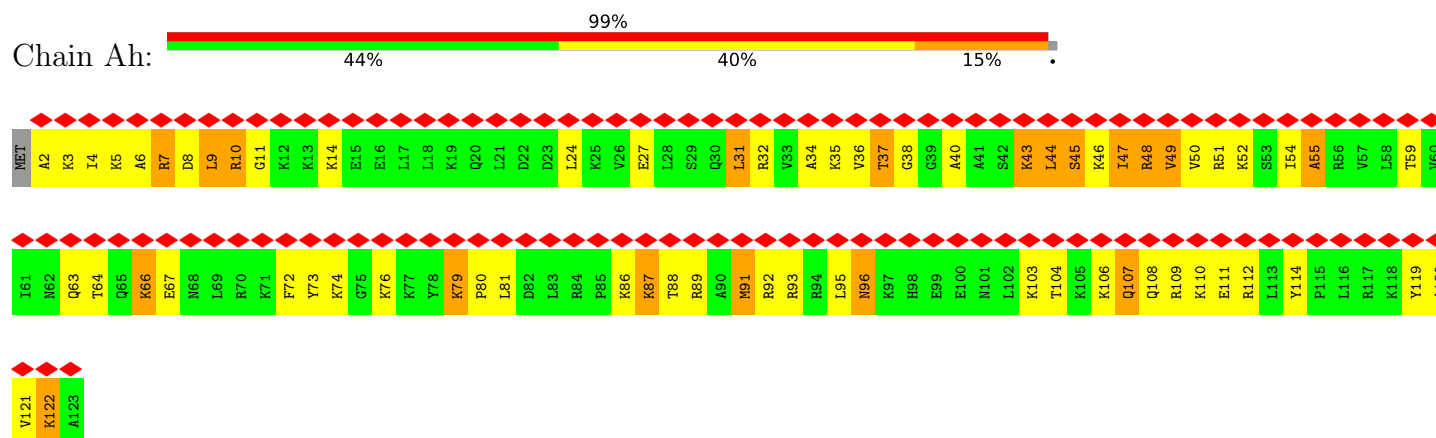
- Molecule 34: 60S ribosomal protein L35a



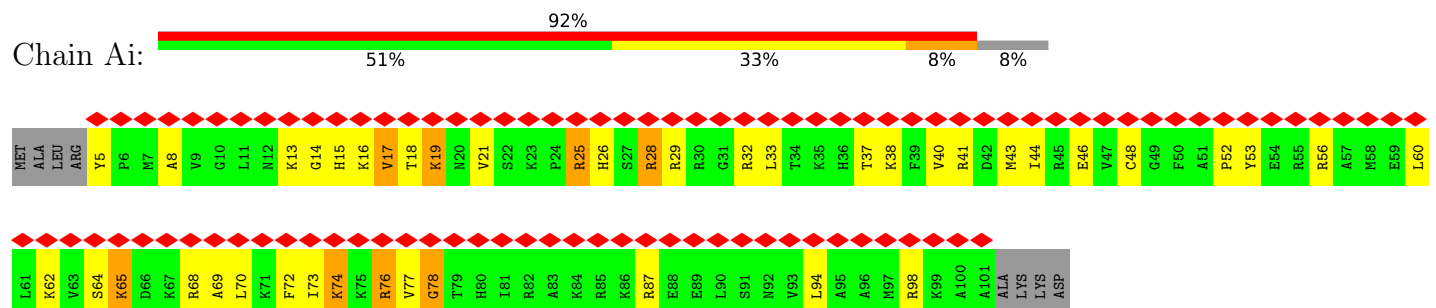
- Molecule 35: 60S ribosomal protein L34



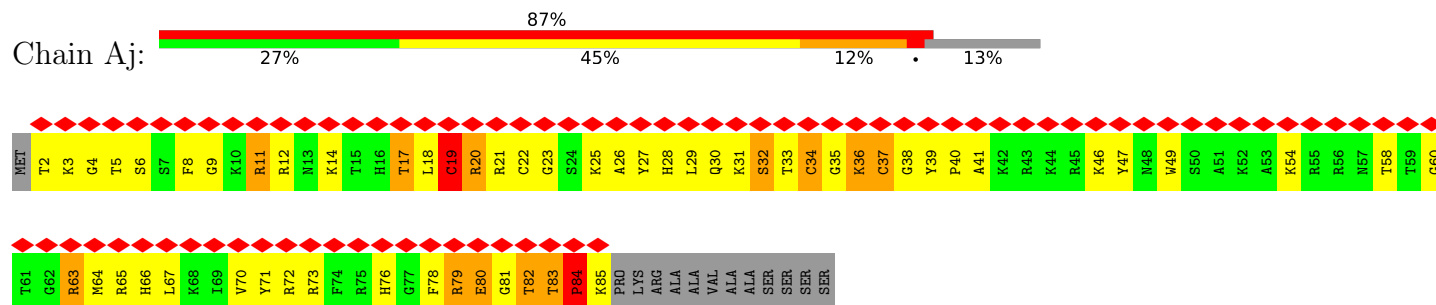
- Molecule 36: 60S ribosomal protein L35



- Molecule 37: 60S ribosomal protein L36

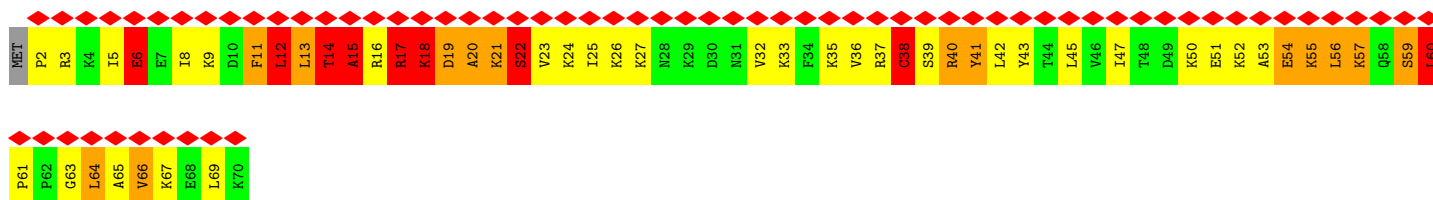


- Molecule 38: 60S ribosomal protein L37



- Molecule 39: 60S ribosomal protein L38

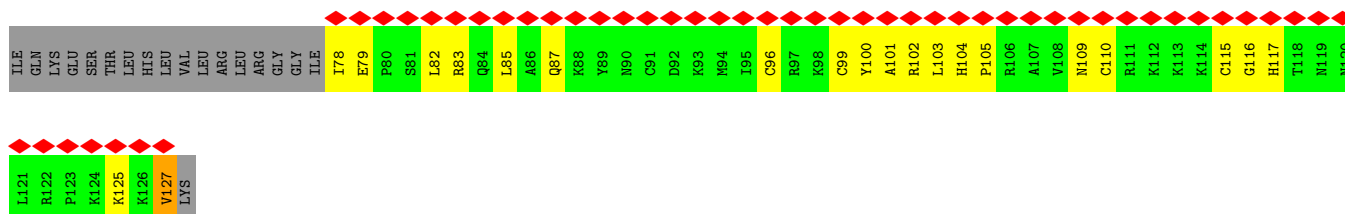




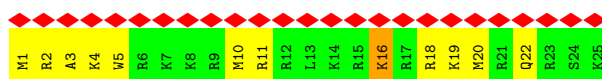
• Molecule 40: 60S ribosomal protein L39



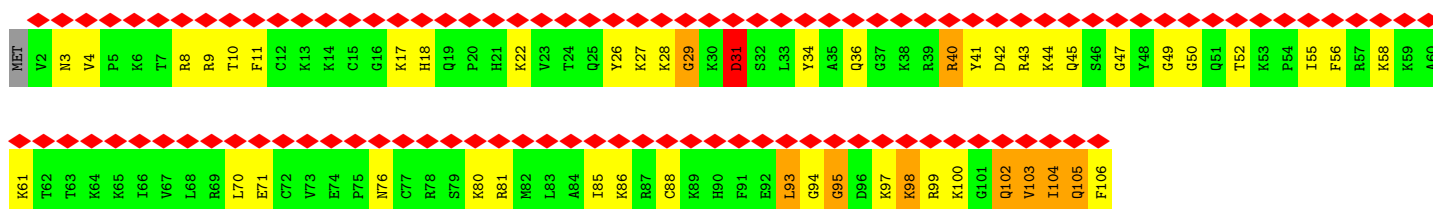
• Molecule 41: Ubiquitin-60S ribosomal protein L40



• Molecule 42: 60S ribosomal protein L41

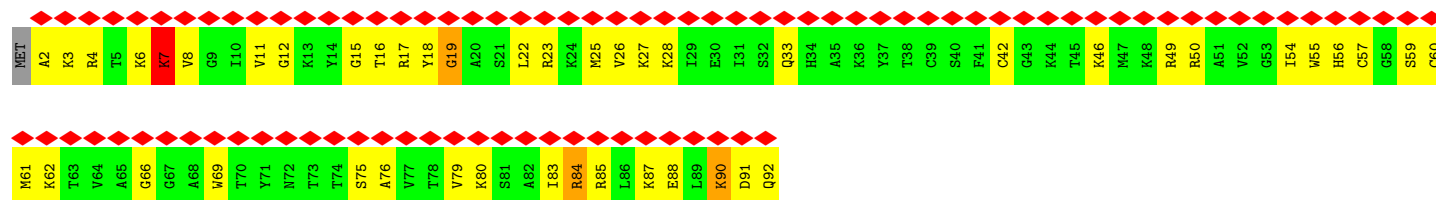


• Molecule 43: 60S ribosomal protein L36a

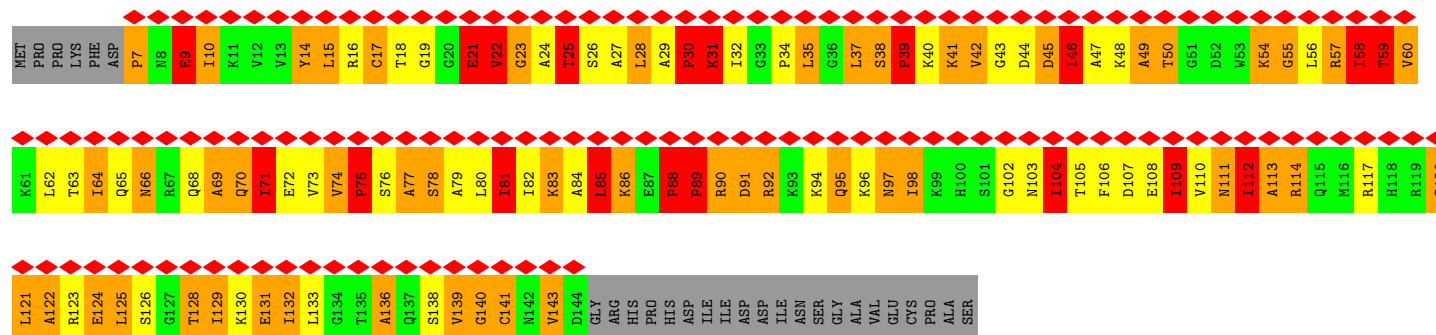
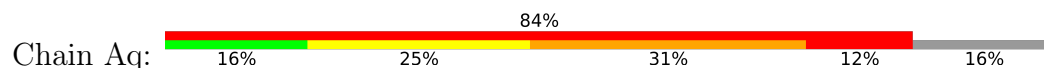


• Molecule 44: 60S ribosomal protein L37a

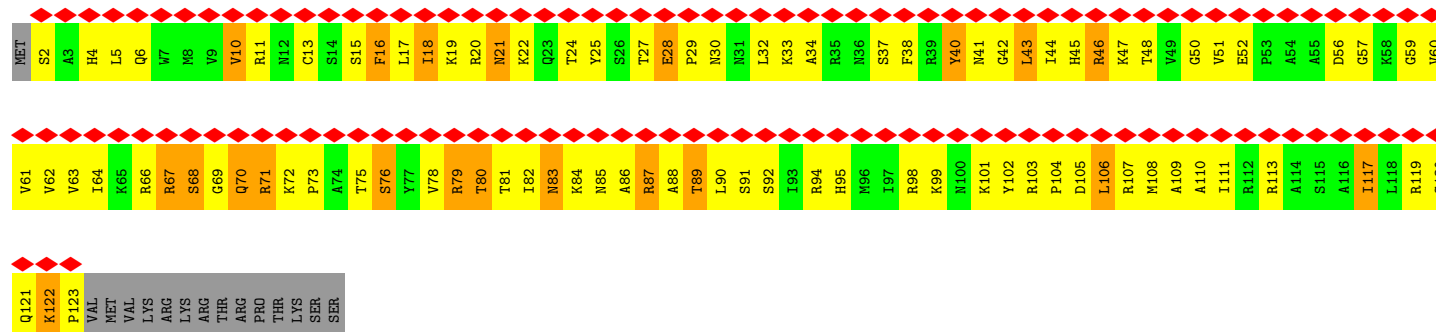
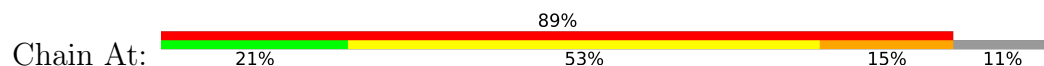




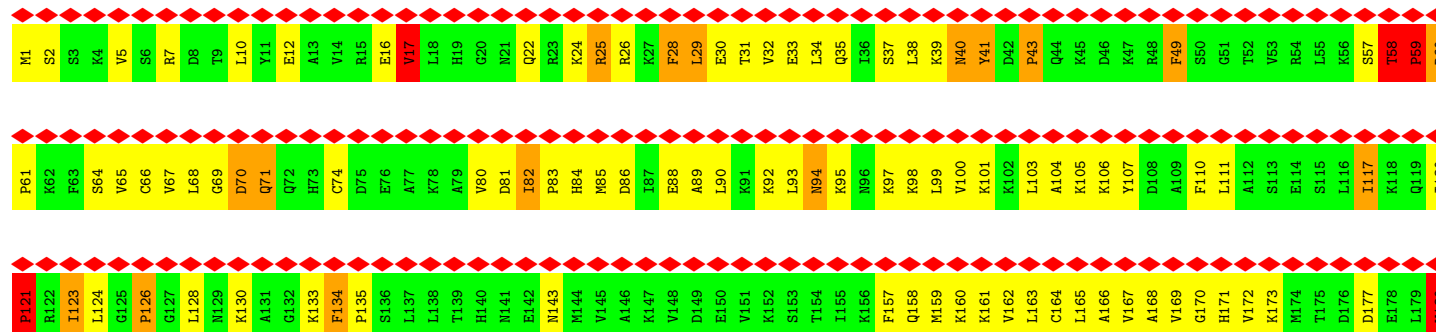
• Molecule 45: 60S ribosomal protein L12



• Molecule 46: 60S ribosomal protein L28



• Molecule 47: 60S ribosomal protein L10a



Chain A2: 72%







WORLDWIDE
PDB
PROTEIN DATA BANK

A4140	U4080	A4020	C	G3900	C3840	G3780	C3720	G3660	A3600	G
G4141	C4081	C4021	C	U3901	C3841	C3781	G3721	U3661	A3601	C
G4142	U4082	C4022	G	C3902	A3842	G3782	G3722	G3662	C3602	G
U4143	C4083	A4023	U	U3903	A3843	G3783	C3723	C3663	C3603	G
G4144	G4084	C4024	G	G3904	G3844	A3784	G3724	U3664	C3604	C
G4145	C4085	U4025	U	G3905	G3845	U3785	G3725	U3665	G3605	G
G4146	U4086	A4026	C	C3906	G3846	G3786	G3726	U3666	A3606	C
U4147	U4087	C4027	C	A3907	A3847	A3787	A3727	C3667	C3607	U
G4148	C4088	U4028	G	C3908	A3848	A3788	G3728	U3668	U3608	C
G4149	U4089	C4029	C	G3909	C3849	U3789	U3729	G3669	G3609	G
G4150	G4090	U4030	G	G3910	G3850	G3790	A3730	C3670	U3610	C
U4151	G4091	C4031	A	U3911	G3851	G3791	A3731	C3671	U3611	U
G4152	C4092	A4032	G	G3912	G3852	A3792	C3732	C3672	U3612	G
G4153	G4093	U4033	G	A3913	C3853	U3793	U3733	A3673	A3613	G
A4154	C4094	C4034	C	A3914	U3854	G3794	A3734	G3674	A3614	C
C4155	C4095	G4035	C	G3915	U3855	A3795	U3735	U3675	U3615	G
U4156	C4096	U4036	C	A3916	G3856	A3796	G3736	G3676	U3616	G
G4157	A4097	U4037	G	G3917	G3857	C3797	A3737	C3677	A3617	C
G4158	G4098	U4038	G	A3918	C3858	G3798	C3738	U3678	A3618	C
G4159	C4099	U4039	G	C3919	G3859	A3799	U3739	C3679	A3619	C
G4160	G4100	U4040	C	A3920	G3860	G3800	C3740	U3680	A3620	U
C4161	C4101	U4041	G	U3921	A3861	A3801	U3741	G3681	C3621	A
G4162	C4102	C4042	G	C3922	A3862	U3802	C3742	A3682	A3622	C
G4163	C4103	A4043	G	A3923	U3863	U3803	U3743	A3683	A3623	C
U4164	G4104	C4044	U	G3924	C3864	C3804	U3744	U3684	A3624	G
A4165	C4105	U4045	C	A3925	A3865	C3805	A3745	G3685	G3625	C
C4166	C4106	G4046	C	G3926	G3866	C3806	A3746	U3686	C3626	C
U4167	G4107	A4047	G	G3927	C3867	A3807	G3747	C3687	A3627	G
G4168	C4108	C4048	G	U3928	G3868	C3808	G3748	U3688	U3628	G
C4169	G4109	C4049	C	G3929	G3869	U3809	U3749	A3689	C3629	U
U4170	C4110	U4050	C	U3930	G3870	G3810	A3750	A3690	G3630	C
G4171	C4111	C4051	C	A3931	G3871	U3811	C3751	C3691	C3631	U
C4172	G4112	G4052	U	C3932	A3872	C3812	C3752	U3692	G3632	C
G4173	U4113	U4053	C	A3933	A3873	C3813	C3753	G3693	A3633	C
A4174	G4114	G4054	G4004	A3934	A3874	C3814	A3754	A3694	A3634	C
U4175	C4115	A4055	G4005	U3935	G3875	U3815	A3755	A3695	G3635	C
G4176	U4116	G4056	G4006	A3936	A3876	A3816	A3756	G3696	G3636	C
C4177	C4117	C4057	C4007	A3937	A3877	C3817	U3757	A3697	C3637	G
U4178	G4118	U4058	C4008	G3938	G3878	C3818	G3758	A3698	C3638	G
G4179	C4119	G4059	G4009	U3939	A3879	U3819	C3759	A3699	C3639	C
C4120	U4120	C4060	G4010	G3940	C3880	A3820	C3760	U3700	G3640	C
A4121	C4121	G4061	C4011	G3941	C3881	C3821	U3761	U3701	C3641	G
G4122	A4122	G4062	G4012	C3942	C3882	U3822	C3762	C3702	G3642	C
C4123	G4123	G4063	A4013	A3943	U3883	A3823	G3763	A3703	G3643	G
G4124	U4124	G4064	U4014	G3944	G3884	U3824	U3764	A3704	C3644	C
A4125	U4125	G4065	C4015	G3945	U3885	C3825	C3765	U3705	G3645	C
C4126	C4126	C4066	A4016	C3946	U3886	C3826	A3766	G3706	G3646	G
U4127	C4127	G4067	A4017	C3947	G3887	A3827	U3767	A3707	C3647	C
G4128	U4128	A4068	A4018	C3948	A3888	G3828	C3768	A3708	U3648	C
U4129	G4129	G4069	C	C	G3889	C3829	U3769	G3709	G3649	C
C4130	G4130	C4070	C	C	C3890	G3830	A3770	C3710	U3650	C
G4131	G4131	C4071	C	C	U3891	A3831	C3771	G3711	U3651	C
A4132	A4132	C4072	C	C	U3892	A3832	U3772	C3712	G3652	C
C4133	G4133	G4073	C	C	G3893	A3833	U3773	G3713	A3653	C
A4134	A4134	A4074	C	C	A3894	C3834	A3774	G3714	C3654	C
G4135	G4135	G4075	C	C	C3895	C3835	G3775	G3715	G3655	C
A4136	U4136	G4076	C	C	U3896	A3836	U3776	U3716	C3656	C
G4137	G4137	C4077	C	C	C3897	C3837	G3777	A3717	G3657	C
C4138	C4138	G4078	C	C	U3898	A3838	A3778	A3718	A3658	C
U4139	U4139	C4079	C	C	C3899	G3839	C3779	A3719	U3659	C
A4140	U4140	C4080	C	C	C3900	G3780	C3720	G3660	A3600	C
G4141	C4081	C4021	C	U3901	C3781	G3721	G3661	U3661	A3601	C
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G4144	G4084	C4024	G	G3904	A3784	G3724	U3664	G3664	C3604	C
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G4146	U4086	A4026	C	C3906	G3786	G3726	U3666	U3666	A3606	C
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G4148	C4088	U4028	G	C3908	A3788	G3728	U3668	U3668	U3608	C
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G4150	G4090	U4030	G	G3910	G3790	A3730	C3670	C3670	U3610	C
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G4153	G4093	U4033	G	A3913	U3793	U3733	A3673	A3673	A3613	G
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C4155	C4095	G4035	C	G3915	A3795	U3735	U3675	U3675	U3615	G
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G4162	C4102	C4042	G	C3922	A3802	C3742	A3682	A3682	A3622	C
G4163	C4103	A4043	G	A3923	U3803	U3743	A3683	A3683	A3623	C
U4164	G4104	C4044	U	G3924	C3804	U3744	U3684	U3684	A3624	G
A4165	C4105	U4045	C	A3925	C3805	A3745	G3685	G3685	G3625	C
C4166	C4106	G4046	C	G3926	G3806	A3746	U3686	U3686	C3626	C
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A4174	G4114	G4054	G4004	A3934	C3814	A3754	A3694	A3694	A3634	C
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G4176	U4116	G4056	G4006	A3936	A3816	A3756	G3696	G3696	G3636	C
C4177	C4117	C4057	C4007	A3937	A3817	U3757	A3697	A3697	C3637	G
U4178	G4118	U4058	C4008	G3938	G3818	G3758	A3698	A3698	C3638	G
G4179	C4119	G4059	G4009	U3939	A3819	C3759	A3699	A3699	C3639	C
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U4129	G4129	G4069	C	C	C3829	U3769	G3709	G3709	G3649	C
C4130	G4130	C4070	C	C	G3830	A3770	C3710	U3650	U3651	C
G4131	G4131	C4071	C	C	A3831	C3771	G3711	G3651	U3651	C
A4132	A4132	C4072	C	C	U3832	U3772	C3712	G3652	G3652	C
C4133	G4133	G4073	C	C	A3833	U3773	G3713	A3653	A3653	C
A4134	A4134	A4074	C	C	C3834	A3774	G3714	C3654	G3654	C
G4135	G4135	G4075	C	C	C3835	G3775	G3715	G3655	G3655	C
A4136	U4136	G4076	C	C	U3836	U3776	U3716	C3656	C3656	C
G4137	G4137	C4077	C	C	C3837	G3777	A3717	G3657	G3657	C
C4138	C4138	G4078	C	C	A3838	A3778	A3718	A3658	U3658	C
U4139	U4139	C4079	C	C	G3839	C3779	A3719	U3659	U3659	C
A4140	U4140	C4080	C	C	C3900	G3780	C3720	G3660	A3600	C
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G4142	U4082	C4022	G	C3902	G3782	G3722	G3662	C3662	C3602	G
U4143	C4083	A4023	U	U3903	G3783	C3723	C3663	A3663	C3603	G
G4144	G4084	C4024	G	G3904	A3784	G3724	U3664	U3664	C3604	C
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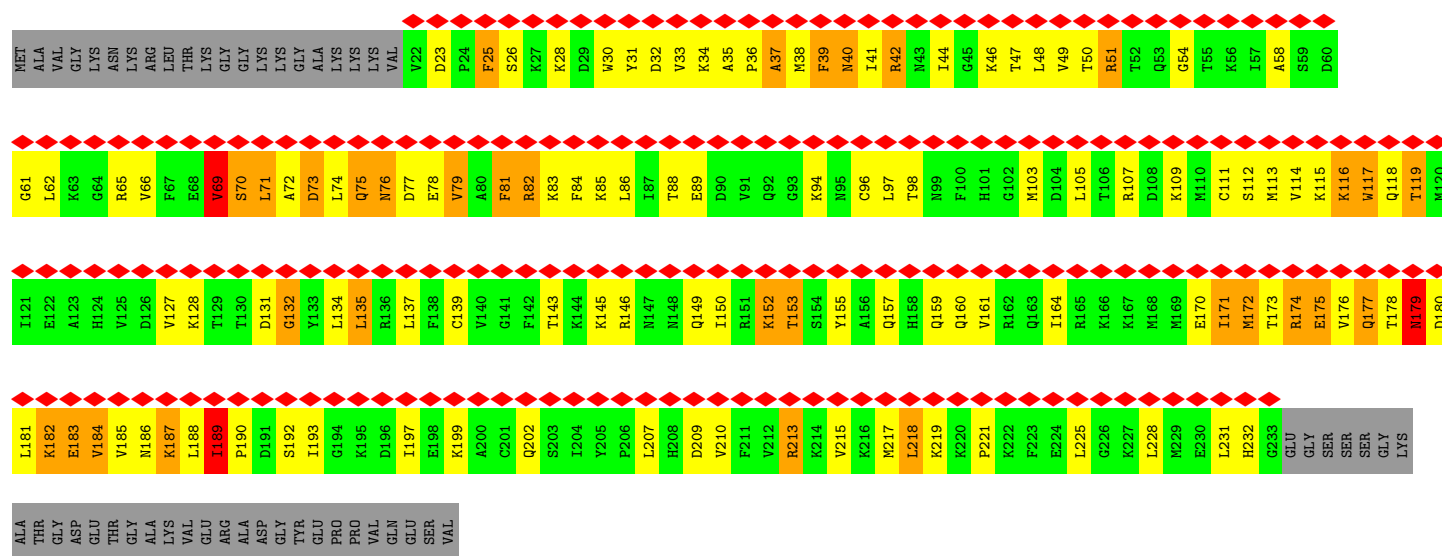
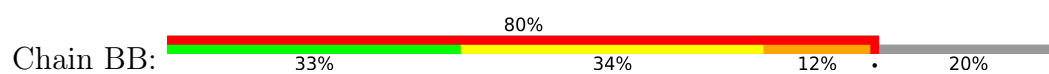


Chain B1:

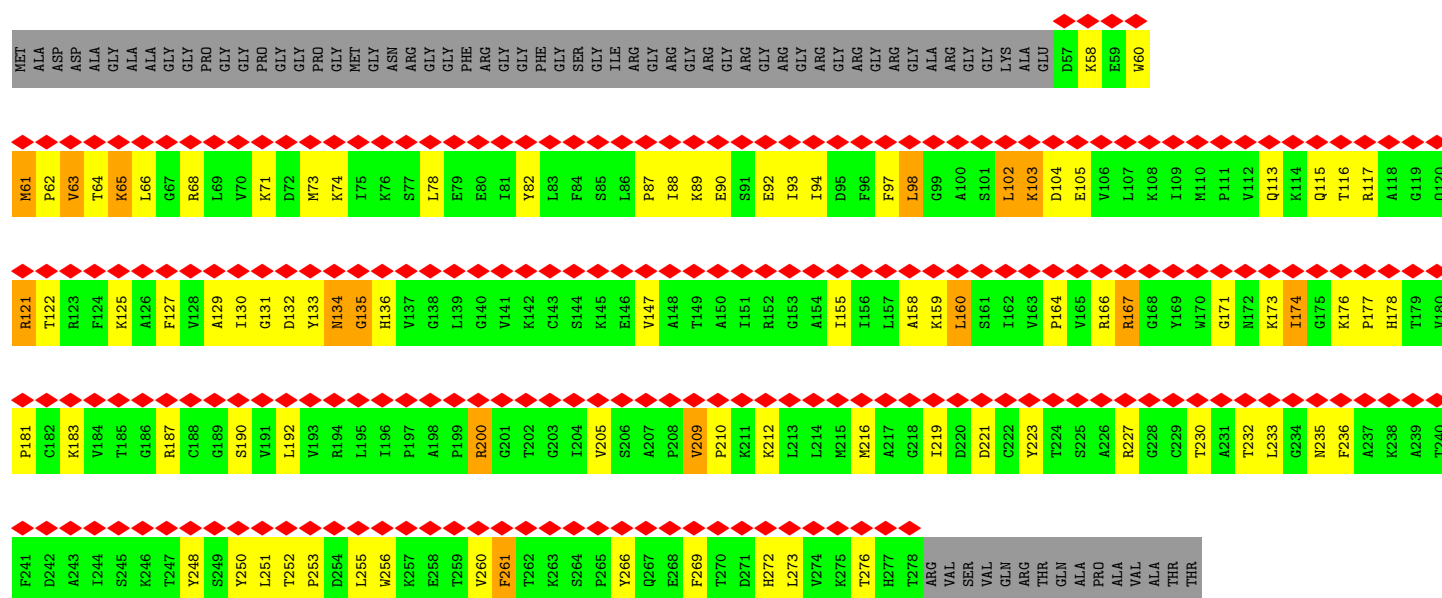
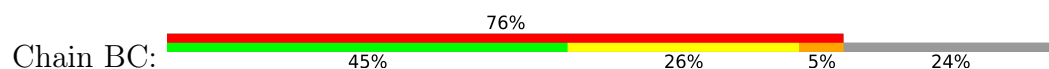


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U1442	A1382	G1322	C1262	U1202	G1142	A1082	U1022	A962	G902	C842	C
C1443	A1383	U1323	U1263	G1203	A1143	A1083	A1023	A963	A903	C843	C
U1444	G1384	G1324	C1264	A1204	A1144	A1084	A1024	A964	A904	U844	A
U1445	G1385	G1325	A1265	C1205	A1145	G1085	U1025	U965	C905	G845	C
A1446	A1386	U1326	C1266	G1206	C1146	G1086	U1026	U966	U906	G846	C
G1447	G1387	G1327	C1267	G1207	C1147	A1087	A1027	C967	G907	A847	C
A1448	A1388	G1328	C1268	A1208	A1148	U1088	G1028	U968	A908	U848	C
G1449	C1389	U1329	G1269	A1209	A1149	G1089	G1029	U969	G909	C791	C
G1450	U1390	G1270	G1270	G1210	A1150	C1090	A1030	G970	G910	C792	C
G1451	C1391	C1271	C1271	G1211	G1151	C1091	A1031	G971	C911	G793	C
A1452	U1392	A1332	C1272	G1212	U1152	G1092	G1032	A972	C912	A794	C
C1453	G1393	G1273	C1273	G1213	C1153	A1093	G1033	C973	A913	A795	C
A1454	G1394	G1274	C1274	A1214	U1154	C1094	A1034	C974	U914	G796	C
A1455	C1395	G1335	G1275	G1215	U1155	G1095	A1035	G975	G915	C797	C
G1456	A1396	C1336	A1276	G1216	U1156	G1096	A1036	G976	A916	C798	C
U1457	U1397	C1337	C1277	A1217	G1157	G1097	G1037	C977	U917	U799	C
G1458	G1398	G1338	A1278	G1218	G1158	C1098	U1038	G978	U918	U800	C
G1459	C1399	U1339	C1279	C1219	G1159	G1099	C1039	C979	A919	U801	C
C1460	U1400	U1340	G1280	A1220	U1160	A1100	G1040	A980	A920	A802	C
G1461	A1401	C1341	G1281	G1221	U1161	U1101	G1041	A981	G921	A861	C
U1462	A1402	C1342	C1282	A1222	C1162	G1102	A1042	G982	A922	A862	C
U1463	G1403	U1343	C1283	A1223	C1163	C1103	G1043	A983	G923	U863	C
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C1467	U1407	U1347	A1287	G1227	G1167	G1107	C1047	A987	C927	A807	C
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A1469	A1409	G1349	U1289	G1229	G1169	C1109	A1049	C989	G929	A810	C
C1470	C1410	U1350	G1290	C1230	A1170	G1110	A1050	A990	C930	A811	C
C1471	G1411	G1351	A1291	C1231	G1171	U1111	G1051	G991	C931	A813	C
G1472	C1412	G1352	C1292	U1232	U1172	U1112	A1052	A992	G932	U814	C
A1473	G1413	A1353	G1293	G1233	A1173	A1113	C1053	G993	G933	U815	C
A1474	A1414	G1354	C1294	C1234	U1174	U1114	G1054	C994	G934	A816	C
G1475	C1415	C1355	A1295	G1235	G1175	U1115	A1055	G995	G935	G817	C
A1476	C1416	G1356	U1296	G1236	G1176	C1116	U1056	G996	G936	A818	C
U1477	C1417	U1297	U1297	C1237	U1177	C1117	C1057	A997	C937	G819	C
U1478	C1418	U1357	U1298	C1238	U1178	C1118	U1058	A998	A938	U820	C
G1479	C1419	U1358	A1299	U1239	G1179	A1119	G1059	G999	U939	G821	C
A1480	G1420	U1359	U1300	A1240	C1180	U1120	A1060	C1000	U940	U822	C
G1481	A1421	G1361	A1301	A1241	A1181	G1121	U1061	A1001	C941	U823	C
C1482	G1422	U1362	G1302	U1242	A1182	A1122	A1062	U1002	G942	C824	C
A1483	C1423	C1363	C1303	U1243	A1183	G1123	C1063	U1003	U943	A825	C
A1484	G1424	U1364	U1304	U1244	G1184	C1124	C1064	A1004	A944	C884	C
U1485	G1425	G1365	C1305	G1245	C1185	C1125	G1065	U1005	U945	A826	C
A1486	U1426	G1366	U1306	A1246	U1186	G1126	U1066	C1006	U946	A827	C
A1487	C	U1367	U1307	C1247	G1187	C1127	C1067	C1007	G947	G828	C
C1488	G	U1368	U1308	U1248	A1188	C1128	U1068	A1008	C948	C829	C
A1489	C	A1369	C1309	C1249	A1189	G1129	U1069	G1009	G949	A830	C
G1490	C	U1370	U1310	A1250	A1190	G1130	A1070	G1010	C950	G832	C
G1491	U	U1371	C1311	A1251	C1191	G1131	G1071	A1011	C951	C833	C
U1492	C	U1372	G1312	C1252	U1192	U1132	U1072	A1012	G952	U892	C
C1493	C	C1373	A1313	A1253	U1193	A1133	U1073	U1013	C953	C835	C
U1494	C	G1374	U1314	C1254	A1194	G1134	C1074	G1014	U954	G836	C
G1495	A1438	G1375	U1315	G1255	A1195	C1135	C1075	U1015	A955	A837	C
A1496	A1439	A1376	C1316	G1256	A1196	U1136	G1076	U1016	G956	G838	C
G1497	C1440	U1377	G1317	G1257	G1197	U1137	A1077	U1017	A957	U897	C
A1498		A1378	C1318	G1258	G1198	C1138	U1078	U1018	G958	G839	C
U1499		A1379	U1319	A1259	A1199	C1139	C1079	C1019	G959	U899	C
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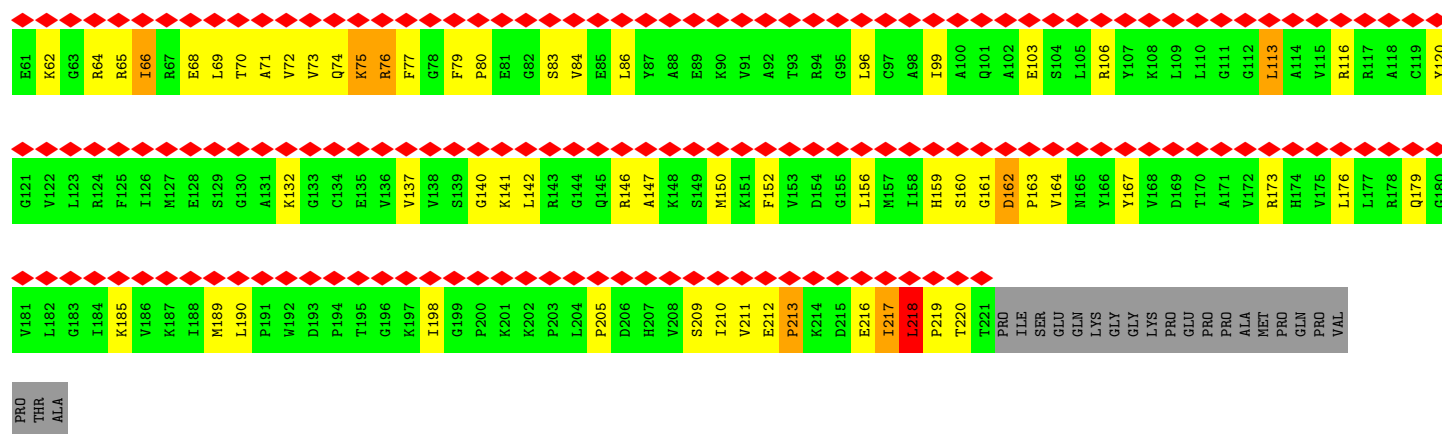


• Molecule 52: 40S ribosomal protein S2

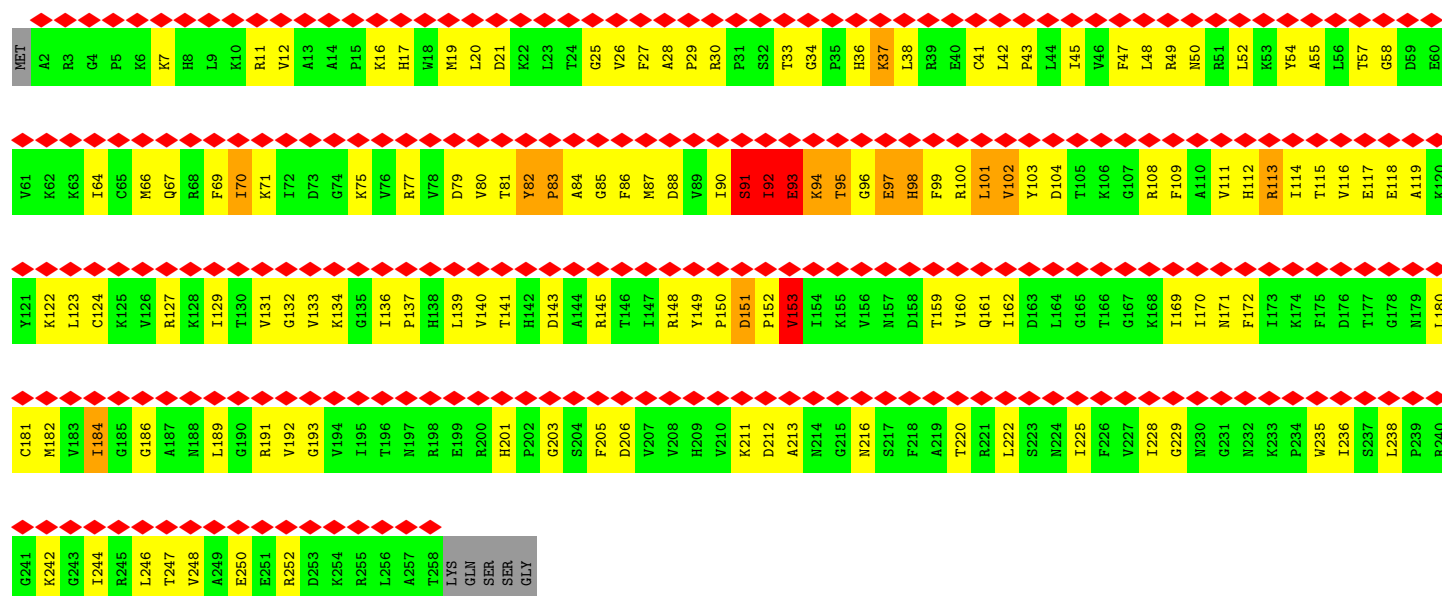


• Molecule 53: 40S ribosomal protein S3





- Molecule 54: 40S ribosomal protein S4, Y isoform 1

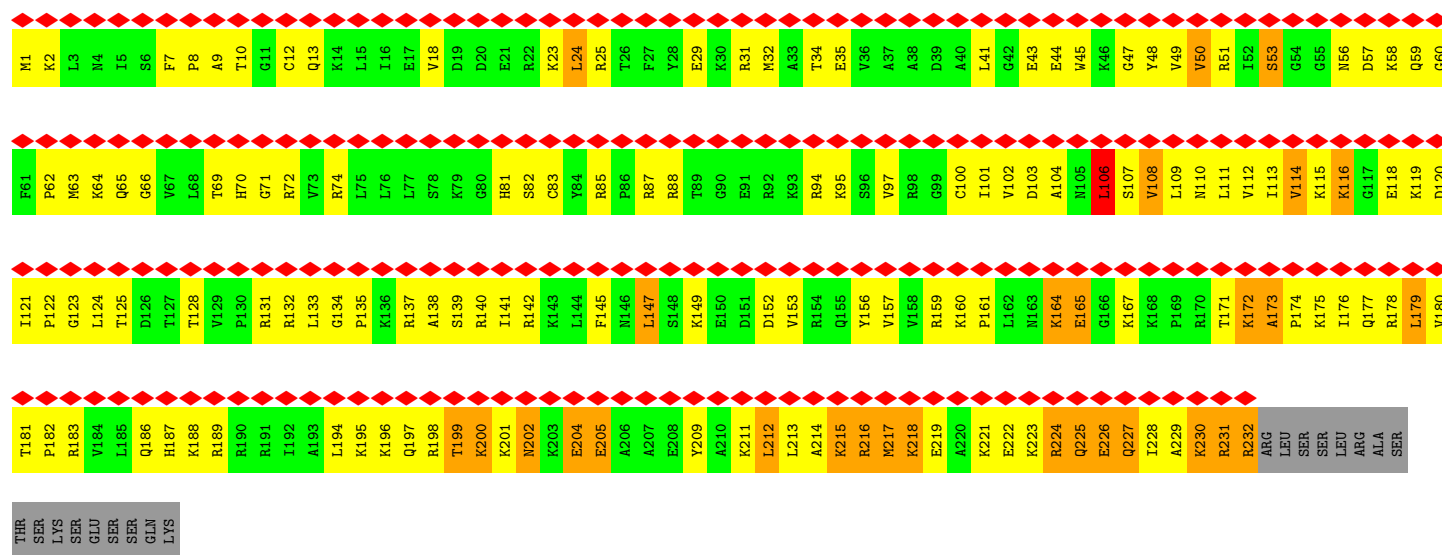


- Molecule 55: 40S ribosomal protein S5

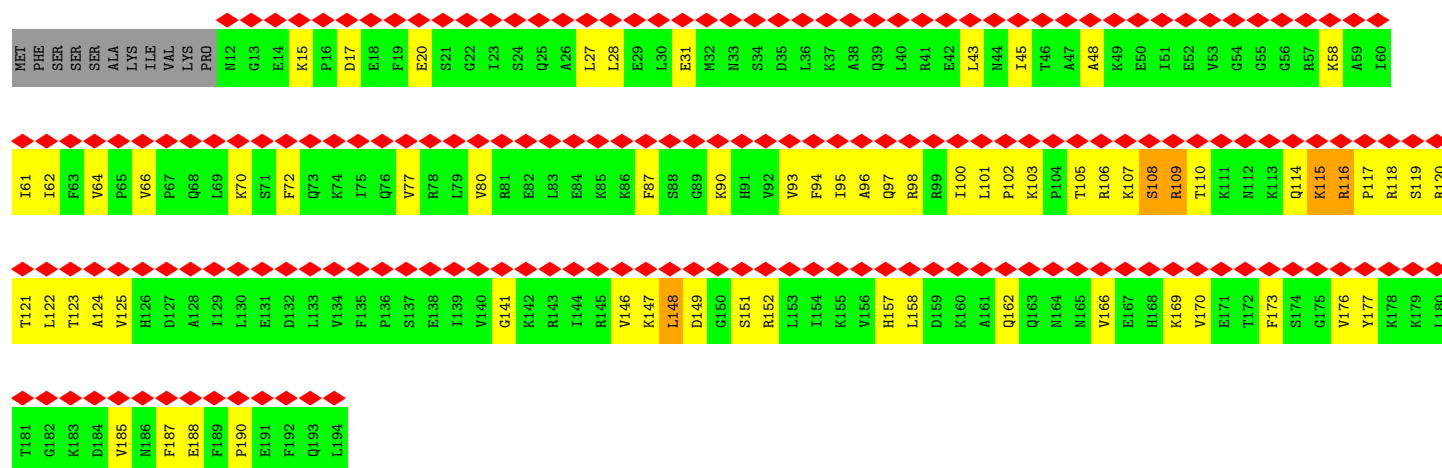




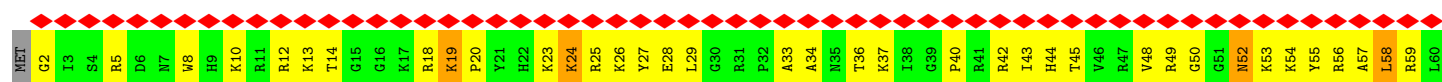
• Molecule 56: 40S ribosomal protein S6

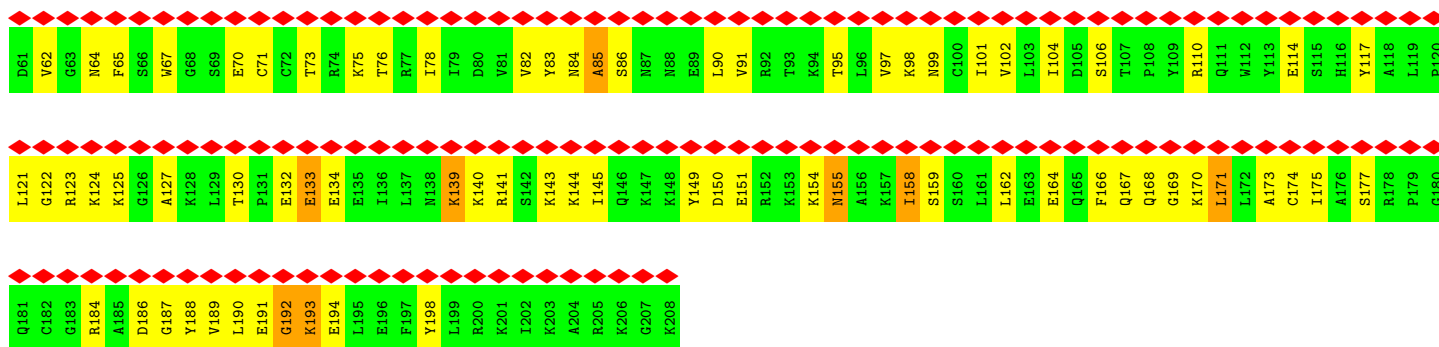


• Molecule 57: 40S ribosomal protein S7

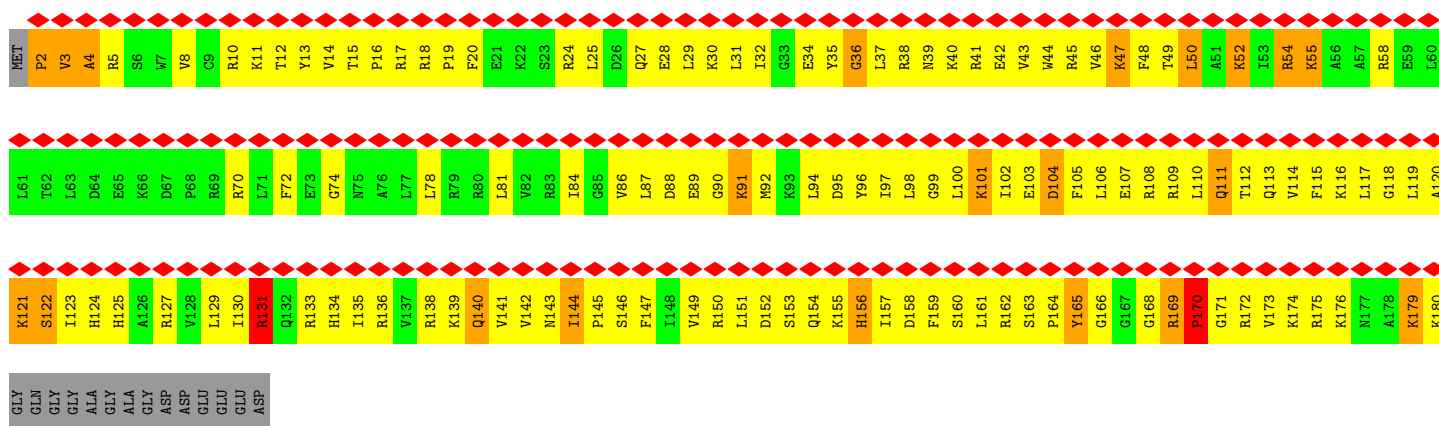


• Molecule 58: 40S ribosomal protein S8

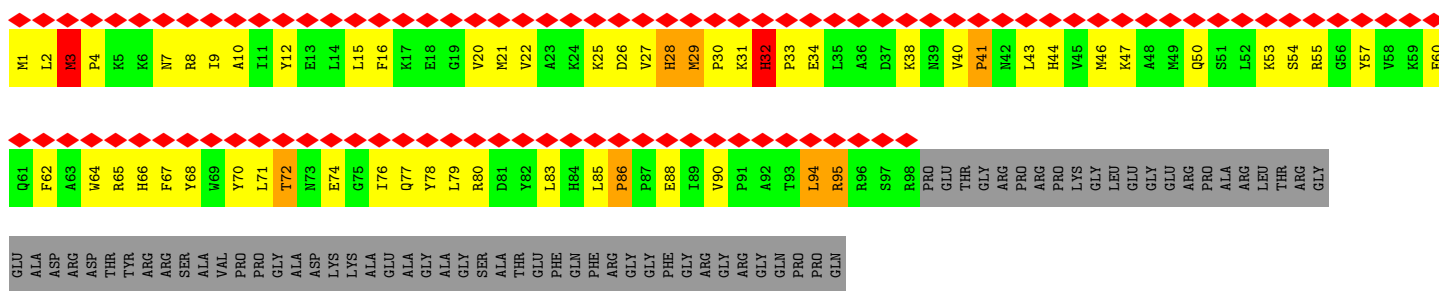
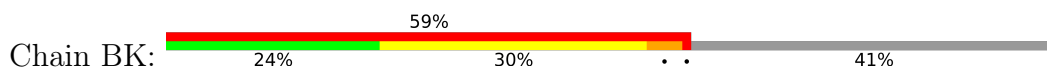




• Molecule 59: 40S ribosomal protein S9

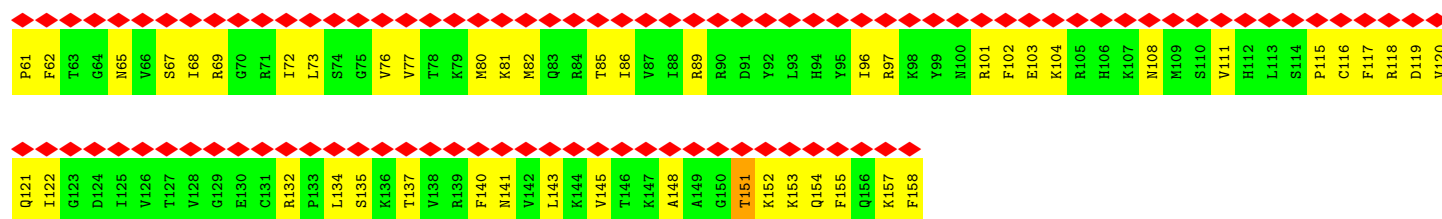


• Molecule 60: 40S ribosomal protein S10



• Molecule 61: 40S ribosomal protein S11

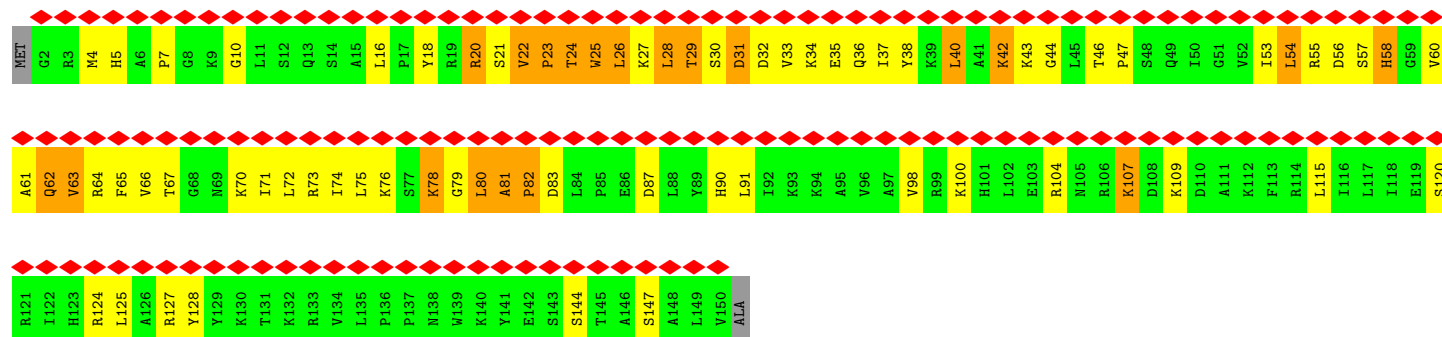




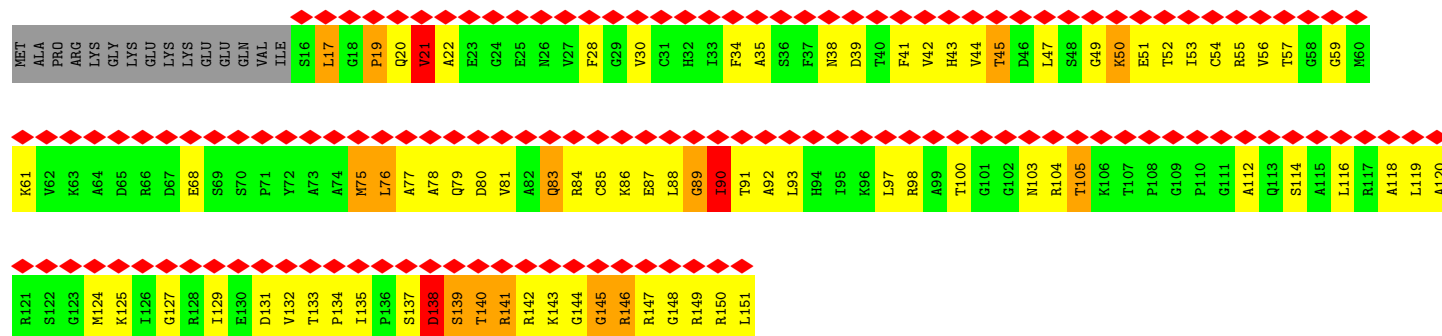
• Molecule 62: 40S ribosomal protein S12



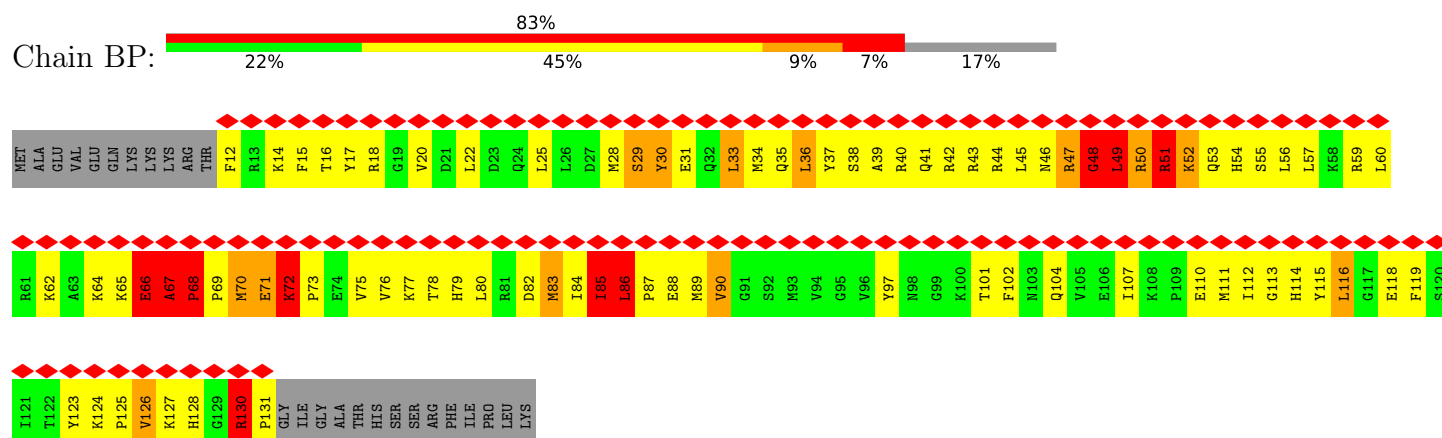
• Molecule 63: 40S ribosomal protein S13



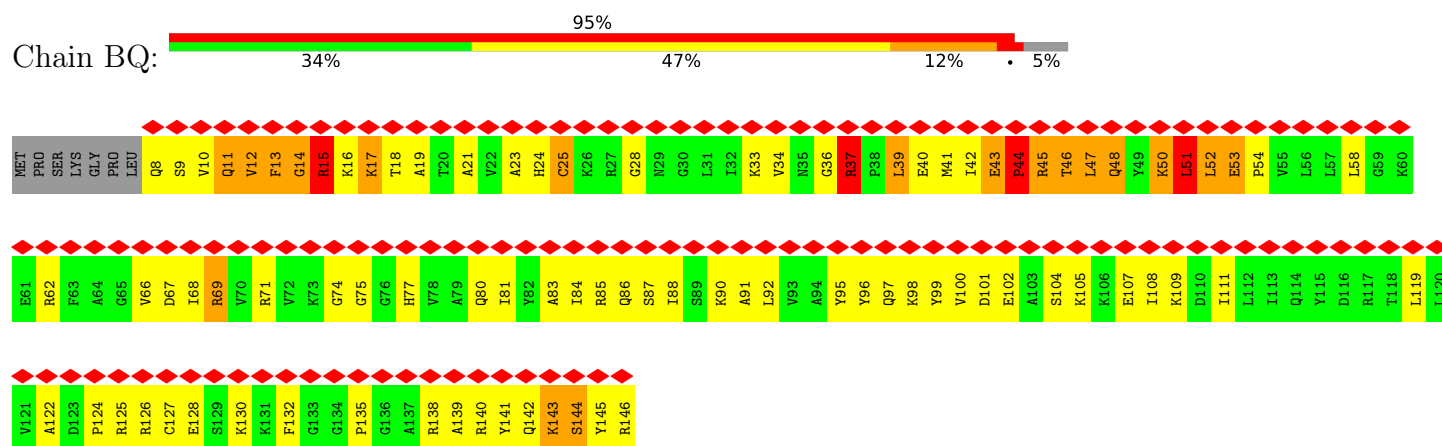
• Molecule 64: 40S ribosomal protein S14



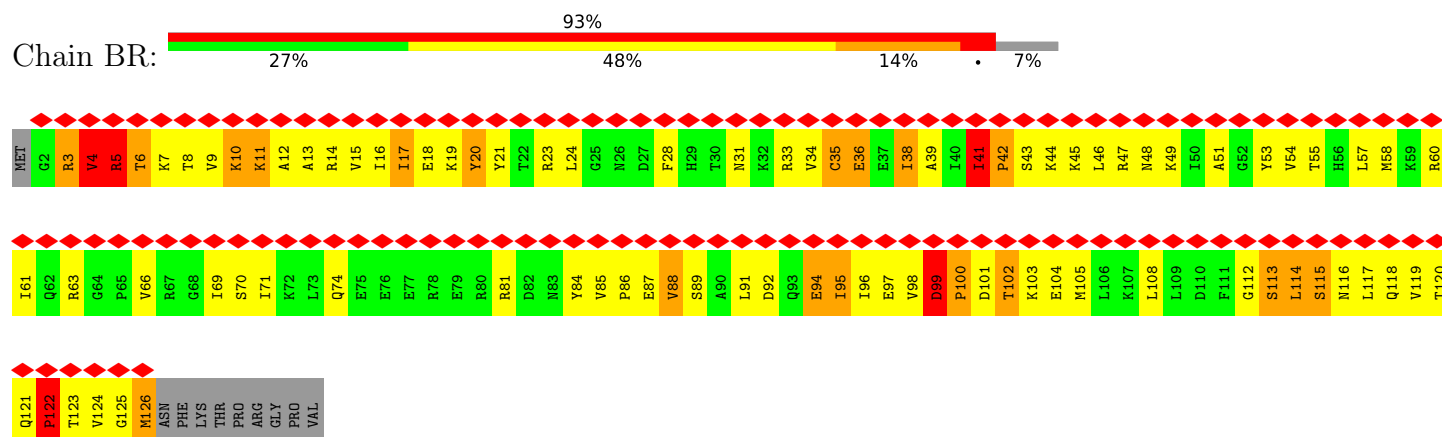
- Molecule 65: 40S ribosomal protein S15



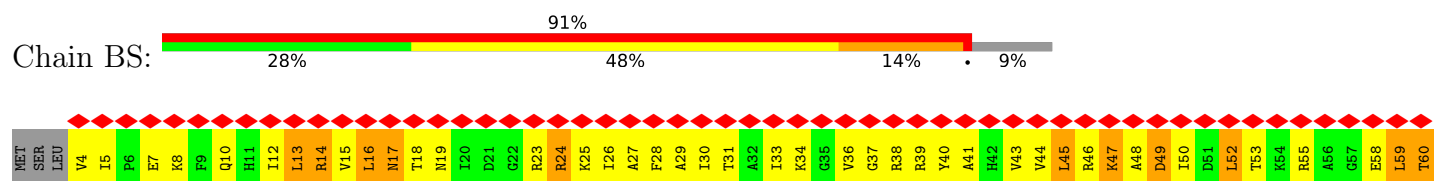
- Molecule 66: 40S ribosomal protein S16

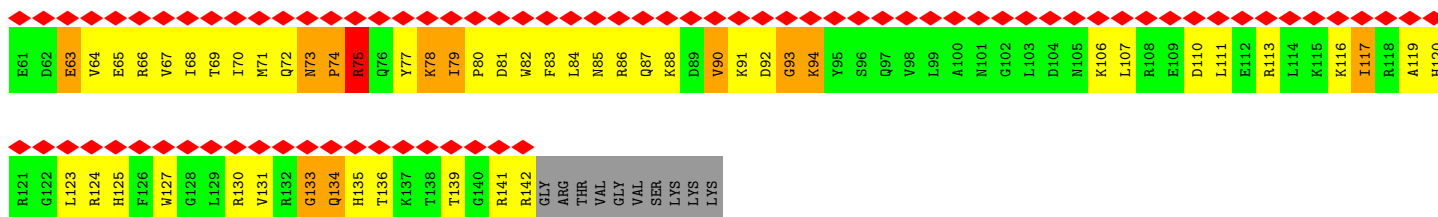


- Molecule 67: 40S ribosomal protein S17-like

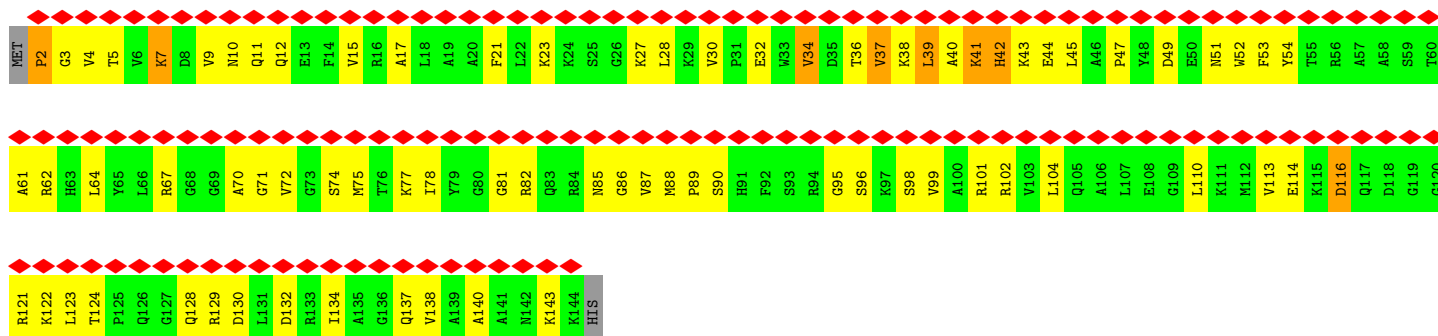


- Molecule 68: 40S ribosomal protein S18

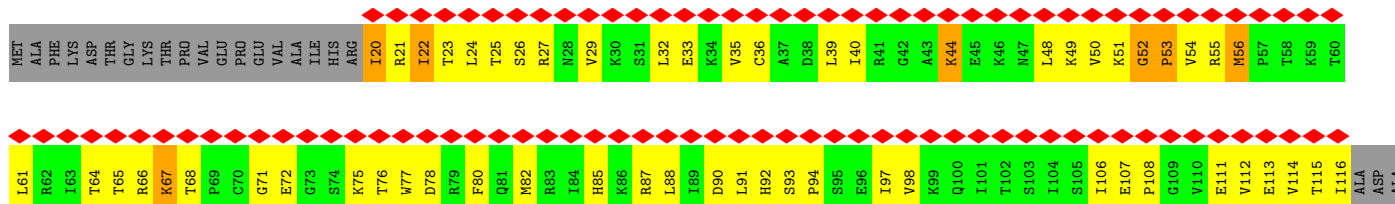
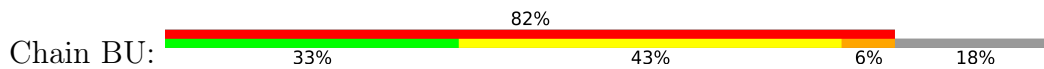




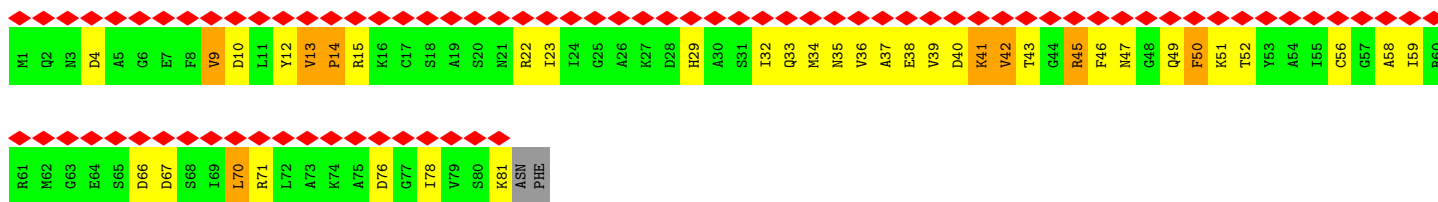
• Molecule 69: 40S ribosomal protein S19



• Molecule 70: 40S ribosomal protein S20

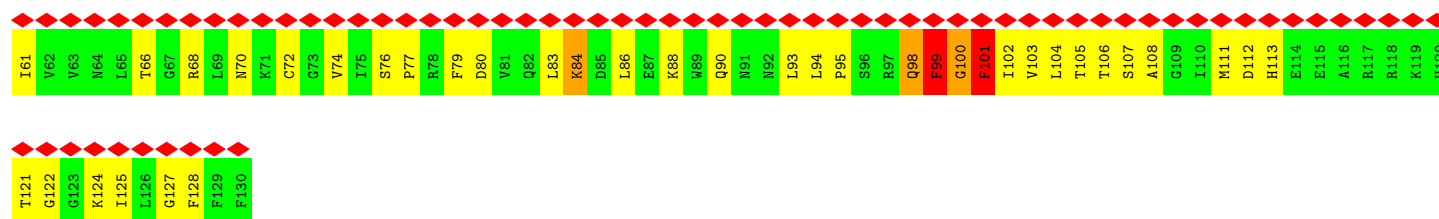


• Molecule 71: 40S ribosomal protein S21



• Molecule 72: 40S ribosomal protein S15a

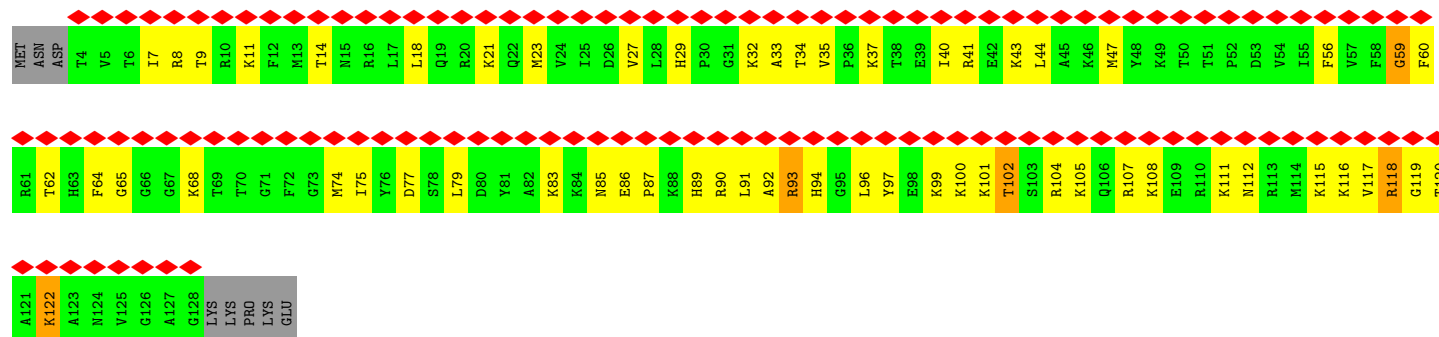




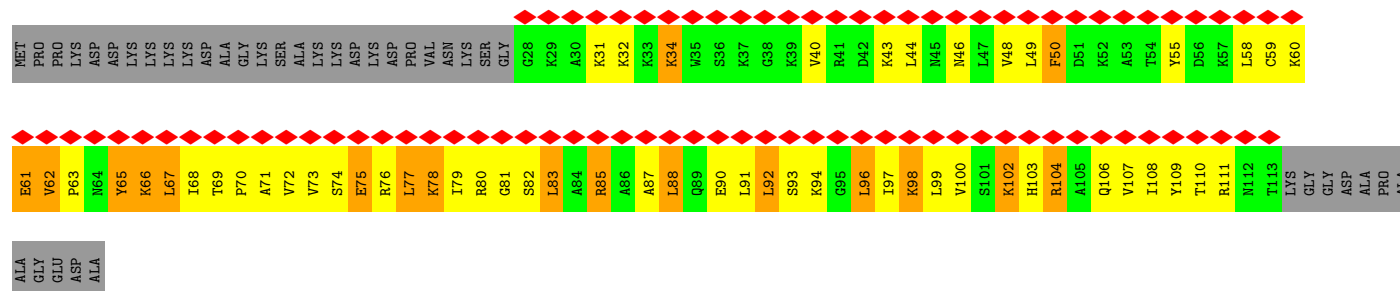
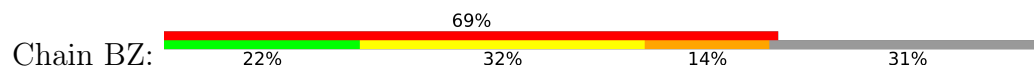
• Molecule 73: 40S ribosomal protein S23



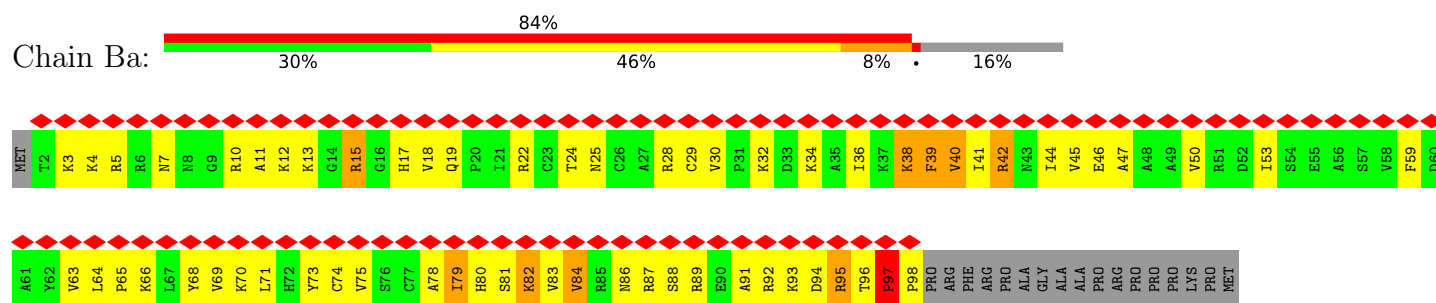
• Molecule 74: 40S ribosomal protein S24



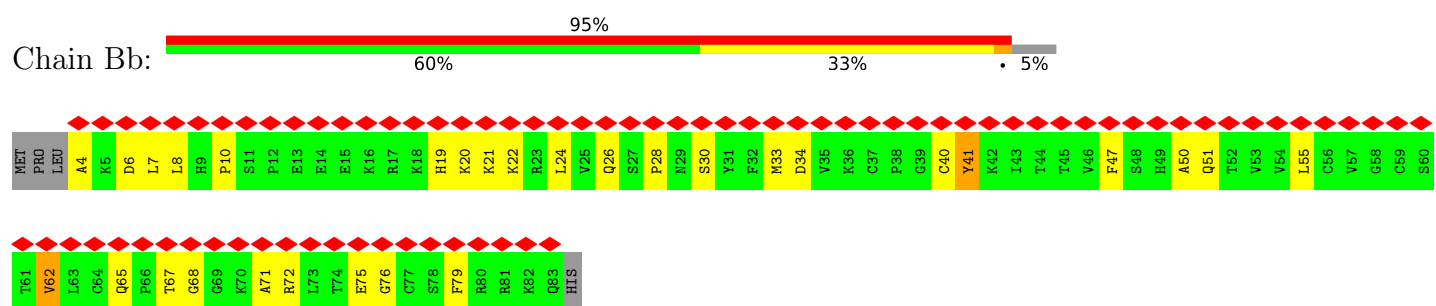
• Molecule 75: 40S ribosomal protein S25



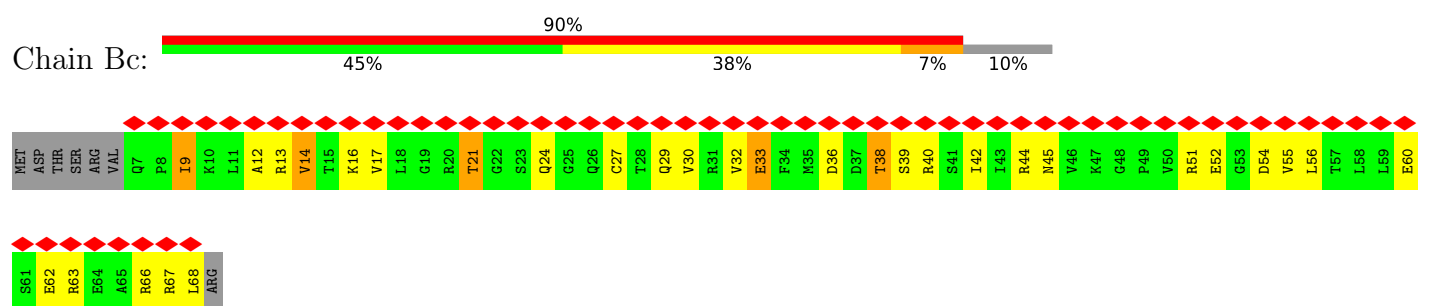
- Molecule 76: 40S ribosomal protein S26



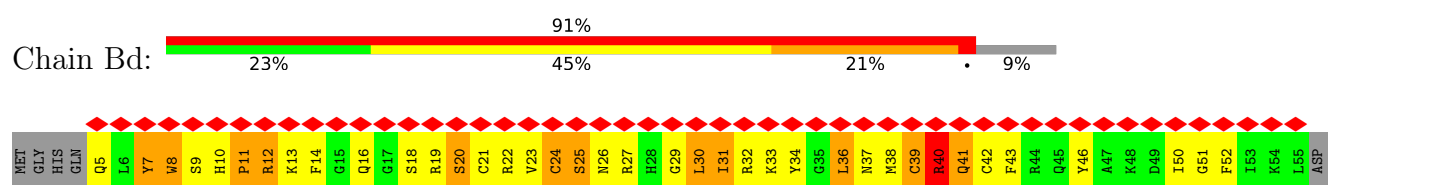
- Molecule 77: 40S ribosomal protein S27



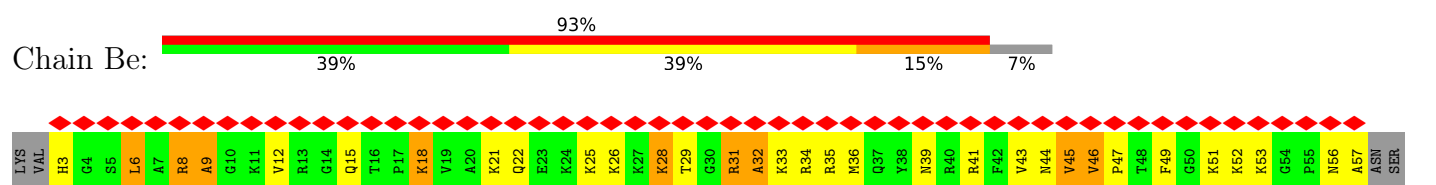
- Molecule 78: 40S ribosomal protein S28



- Molecule 79: 40S ribosomal protein S29

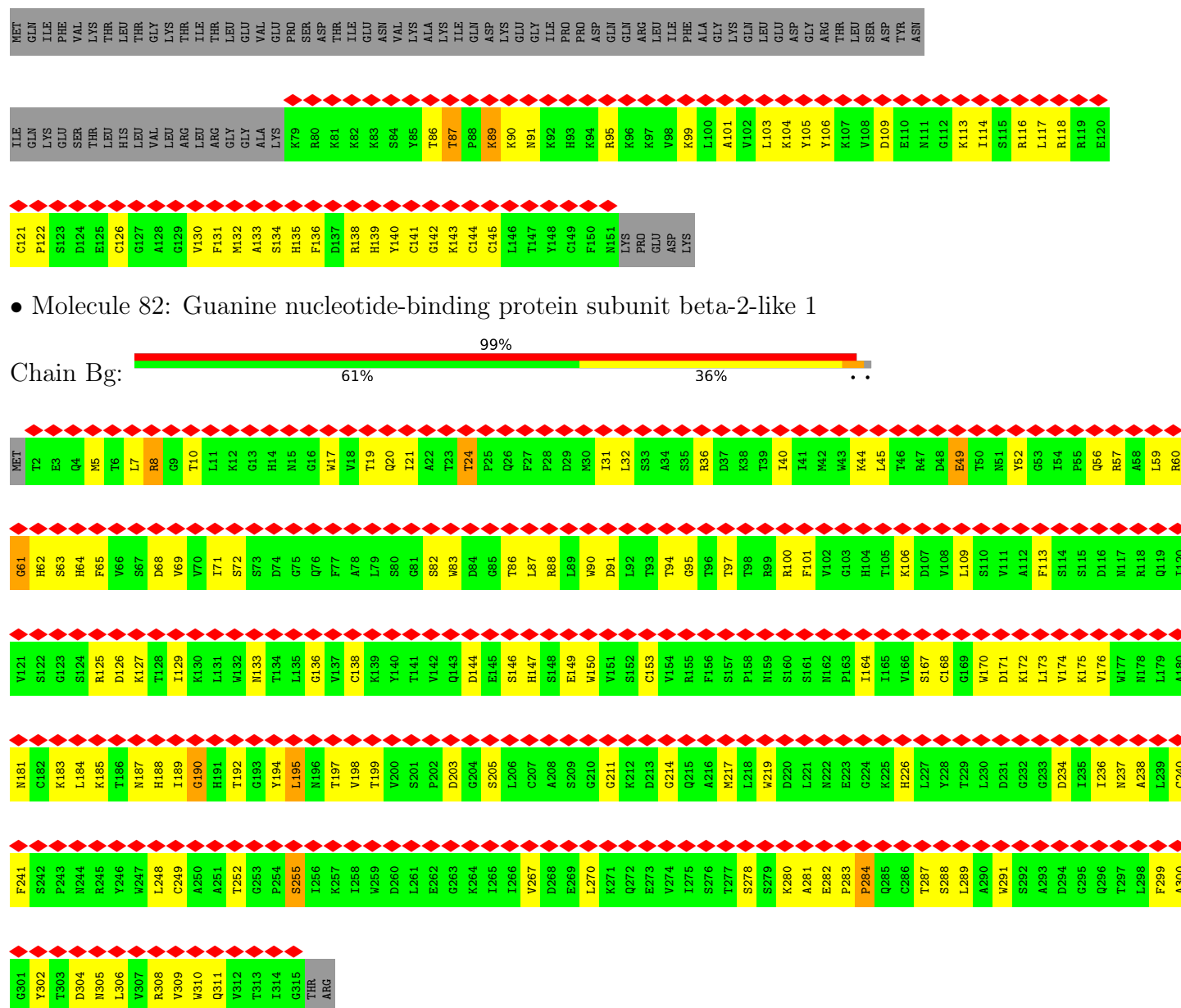


- Molecule 80: 40S ribosomal protein S30



- Molecule 81: Ubiquitin-40S ribosomal protein S27a

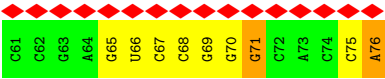
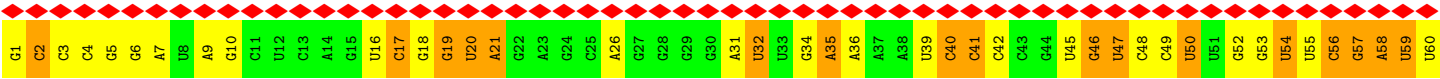




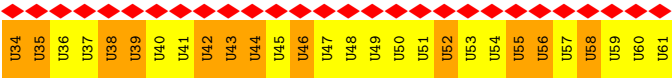
• Molecule 82: Guanine nucleotide-binding protein subunit beta-2-like 1

• Molecule 83: tRNA

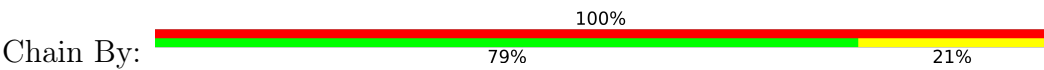
• Molecule 83: tRNA



• Molecule 84: mRNA



• Molecule 85: Nascent protein chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	313321	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20.00	Depositor
Minimum defocus (nm)	2000.00	Depositor
Maximum defocus (nm)	4500.00	Depositor
Magnification	205000	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	15.028	Depositor
Minimum map value	-7.978	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size ($\text{\AA}$)	378.0, 378.0, 378.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.945, 0.945, 0.945	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A3	0.92	32/3726 (0.9%)	1.14	55/5804 (0.9%)
2	A4	0.90	23/2839 (0.8%)	0.97	31/4425 (0.7%)
3	AA	0.69	1/1968 (0.1%)	1.04	7/2639 (0.3%)
4	AB	0.60	0/3246	1.00	3/4345 (0.1%)
5	AC	0.63	4/2942 (0.1%)	1.01	10/3951 (0.3%)
6	AD	0.65	1/2437 (0.0%)	1.06	9/3262 (0.3%)
7	AE	0.73	1/1603 (0.1%)	1.27	16/2153 (0.7%)
8	AF	0.59	0/1986	0.96	4/2644 (0.2%)
9	AG	0.64	0/1913	0.94	3/2576 (0.1%)
10	AH	0.57	2/1545 (0.1%)	0.94	2/2077 (0.1%)
11	AI	0.67	0/1730	1.10	10/2311 (0.4%)
12	AJ	0.62	0/1376	0.97	3/1841 (0.2%)
13	AK	0.90	3/886 (0.3%)	1.74	32/1188 (2.7%)
14	AL	0.71	7/1688 (0.4%)	1.23	14/2260 (0.6%)
15	AM	0.64	0/1161	0.98	2/1554 (0.1%)
16	AN	0.61	0/1746	0.95	5/2338 (0.2%)
17	AO	0.62	0/1638	0.98	2/2191 (0.1%)
18	AP	0.63	0/1268	1.05	3/1701 (0.2%)
19	AQ	0.70	4/1537 (0.3%)	1.06	10/2052 (0.5%)
20	AR	0.59	0/1533	1.01	6/2025 (0.3%)
21	AS	0.59	2/1488 (0.1%)	0.96	2/1997 (0.1%)
22	AT	0.58	0/1312	0.97	3/1753 (0.2%)
23	AU	0.57	0/822	0.90	1/1103 (0.1%)
24	AV	0.58	0/983	0.98	1/1319 (0.1%)
25	AW	0.57	3/1004 (0.3%)	1.02	7/1332 (0.5%)
26	AX	0.56	0/975	0.88	0/1312
27	AY	0.58	0/1081	0.98	4/1439 (0.3%)
28	AZ	0.67	1/1126 (0.1%)	1.13	12/1502 (0.8%)
29	Aa	0.76	3/1191 (0.3%)	1.12	10/1591 (0.6%)
30	Ab	0.57	0/569	0.94	0/750
31	Ac	0.62	0/812	1.01	5/1089 (0.5%)
32	Ad	0.60	0/894	0.98	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ae	0.63	1/1082 (0.1%)	0.92	2/1443 (0.1%)
34	Af	0.69	0/895	1.14	7/1198 (0.6%)
35	Ag	0.57	0/916	0.86	0/1220
36	Ah	0.63	0/1023	1.12	10/1351 (0.7%)
37	Ai	0.60	0/805	0.93	1/1065 (0.1%)
38	Aj	0.66	1/703 (0.1%)	1.23	11/929 (1.2%)
39	Ak	0.71	2/575 (0.3%)	1.12	6/761 (0.8%)
40	Al	0.62	0/454	0.91	0/599
41	Am	0.70	0/417	0.93	0/553
42	An	0.50	0/241	0.85	0/305
43	Ao	0.58	0/877	1.02	3/1156 (0.3%)
44	Ap	0.60	0/718	0.97	3/953 (0.3%)
45	Aq	0.98	3/1058 (0.3%)	2.06	39/1424 (2.7%)
46	At	0.63	0/995	1.12	5/1334 (0.4%)
47	Au	0.85	3/1772 (0.2%)	1.63	20/2375 (0.8%)
48	A2	0.80	509/86613 (0.6%)	1.04	1075/135108 (0.8%)
49	B1	0.78	213/40767 (0.5%)	1.07	543/63536 (0.9%)
50	BA	0.80	6/1741 (0.3%)	1.23	23/2366 (1.0%)
51	BB	0.65	0/1749	1.04	11/2340 (0.5%)
52	BC	0.57	0/1761	0.95	0/2379
53	BD	0.66	1/1736 (0.1%)	1.07	1/2338 (0.0%)
54	BE	0.65	2/2072 (0.1%)	1.00	6/2793 (0.2%)
55	BF	0.62	2/1524 (0.1%)	0.98	5/2048 (0.2%)
56	BG	0.62	0/1907	1.00	9/2538 (0.4%)
57	BH	0.65	0/1501	1.08	4/2009 (0.2%)
58	BI	0.69	0/1725	0.96	2/2298 (0.1%)
59	BJ	0.53	1/1520 (0.1%)	0.92	5/2030 (0.2%)
60	BK	0.71	0/851	1.09	2/1147 (0.2%)
61	BL	0.59	1/1281 (0.1%)	1.01	6/1710 (0.4%)
62	BM	0.65	0/941	1.01	2/1264 (0.2%)
63	BN	0.59	2/1226 (0.2%)	0.91	2/1649 (0.1%)
64	BO	0.66	0/1029	0.99	2/1380 (0.1%)
65	BP	0.68	2/1019 (0.2%)	1.15	9/1361 (0.7%)
66	BQ	0.54	0/1126	0.98	5/1506 (0.3%)
67	BR	0.69	5/1023 (0.5%)	1.11	8/1373 (0.6%)
68	BS	0.66	2/1172 (0.2%)	1.05	5/1570 (0.3%)
69	BT	0.57	0/1131	0.93	1/1515 (0.1%)
70	BU	0.63	1/778 (0.1%)	1.08	4/1045 (0.4%)
71	BV	0.60	2/623 (0.3%)	1.07	3/833 (0.4%)
72	BW	0.60	0/1051	0.93	0/1406
73	BX	0.66	2/1097 (0.2%)	1.03	2/1464 (0.1%)
74	BY	0.63	0/1032	1.02	2/1371 (0.1%)
75	BZ	0.58	0/696	1.04	2/929 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ba	0.69	0/786	1.09	2/1053 (0.2%)
77	Bb	0.66	0/637	0.95	0/854
78	Bc	0.63	0/490	1.12	2/656 (0.3%)
79	Bd	0.76	0/437	1.32	6/580 (1.0%)
80	Be	0.56	0/443	0.99	0/583
81	Bf	0.66	0/613	0.93	0/811
82	Bg	0.65	0/2497	0.98	3/3399 (0.1%)
83	Bv	0.46	2/1813 (0.1%)	0.73	9/2823 (0.3%)
83	Bw	0.34	1/1813 (0.1%)	0.82	7/2823 (0.2%)
84	Bx	0.41	1/616 (0.2%)	1.26	10/948 (1.1%)
All	All	0.74	852/234393 (0.4%)	1.05	2157/344230 (0.6%)

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
4	AB	0	3
5	AC	0	2
7	AE	0	1
8	AF	0	2
10	AH	0	3
13	AK	0	3
14	AL	0	6
39	Ak	0	1
48	A2	2	3
49	B1	1	0
54	BE	0	6
63	BN	0	2
64	BO	0	2
65	BP	0	11
66	BQ	0	6
72	BW	0	3
76	Ba	0	1
79	Bd	0	1
All	All	3	56

The worst 5 of 852 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	A2	3612	U	O3'-P	-17.06	1.35	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	B1	842	C	O3'-P	16.14	1.85	1.61
48	A2	2689	C	O3'-P	-15.67	1.37	1.61
49	B1	558	G	O3'-P	15.52	1.84	1.61
49	B1	497	C	O3'-P	14.87	1.83	1.61

The worst 5 of 2157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	A2	131	C	C4'-C3'-O3'	38.38	170.56	113.00
45	Aq	75	PRO	CA-N-CD	-36.64	60.70	112.00
48	A2	1341	G	C4'-C3'-O3'	35.73	162.99	109.40
48	A2	137	G	C4'-C3'-O3'	35.32	165.98	113.00
49	B1	842	C	O3'-P-O5'	-32.49	55.26	104.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
48	A2	131	C	C3'
48	A2	137	G	C3'
49	B1	1289	U	C4'

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	AB	295	ASP	Peptide
4	AB	296	GLY	Peptide
4	AB	297	LYS	Peptide
5	AC	98	GLY	Peptide
5	AC	99	GLY	Peptide

5.2 Too-close contacts

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	A3	3337	0	1691	214	0
2	A4	2541	0	1284	159	0
3	AA	1930	0	2030	183	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AB	3178	0	3314	340	0
5	AC	2888	0	3064	461	0
6	AD	2392	0	2424	347	0
7	AE	1571	0	1698	459	0
8	AF	1950	0	2093	286	0
9	AG	1880	0	2018	148	0
10	AH	1526	0	1605	141	0
11	AI	1692	0	1744	81	0
12	AJ	1353	0	1386	97	0
13	AK	872	0	916	353	0
14	AL	1657	0	1764	252	0
15	AM	1138	0	1204	158	0
16	AN	1701	0	1748	138	0
17	AO	1606	0	1745	137	0
18	AP	1242	0	1269	90	0
19	AQ	1513	0	1628	205	0
20	AR	1517	0	1665	231	0
21	AS	1449	0	1493	171	0
22	AT	1284	0	1352	163	0
23	AU	808	0	831	82	0
24	AV	969	0	1031	88	0
25	AW	989	0	1041	158	0
26	AX	958	0	1029	93	0
27	AY	1064	0	1145	99	0
28	AZ	1103	0	1179	149	0
29	Aa	1162	0	1213	215	0
30	Ab	559	0	590	79	0
31	Ac	801	0	845	50	0
32	Ad	879	0	924	53	0
33	Ae	1064	0	1160	126	0
34	Af	876	0	912	122	0
35	Ag	906	0	1002	74	0
36	Ah	1015	0	1147	101	0
37	Ai	794	0	870	75	0
38	Aj	689	0	717	116	0
39	Ak	569	0	637	119	0
40	Al	444	0	483	48	0
41	Am	411	0	443	29	0
42	An	240	0	289	25	0
43	Ao	863	0	929	77	0
44	Ap	708	0	756	61	0
45	Aq	1046	0	1116	241	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	At	980	0	1041	197	0
47	Au	1744	0	1859	347	0
48	A2	77427	0	39103	4535	0
49	B1	36456	0	18412	2629	0
50	BA	1704	0	1703	325	0
51	BB	1722	0	1794	294	0
52	BC	1724	0	1808	200	0
53	BD	1709	0	1801	196	0
54	BE	2031	0	2138	311	0
55	BF	1502	0	1557	187	0
56	BG	1884	0	2044	371	0
57	BH	1479	0	1563	130	0
58	BI	1696	0	1785	192	0
59	BJ	1495	0	1615	409	0
60	BK	827	0	854	152	0
61	BL	1258	0	1334	143	0
62	BM	931	0	961	114	0
63	BN	1202	0	1289	178	0
64	BO	1016	0	1039	174	0
65	BP	999	0	1046	254	0
66	BQ	1109	0	1174	264	0
67	BR	1011	0	1063	323	0
68	BS	1154	0	1210	234	0
69	BT	1112	0	1146	164	0
70	BU	769	0	837	131	0
71	BV	617	0	622	80	0
72	BW	1034	0	1080	138	0
73	BX	1080	0	1147	124	0
74	BY	1015	0	1085	163	0
75	BZ	688	0	766	176	0
76	Ba	774	0	821	156	0
77	Bb	625	0	646	43	0
78	Bc	488	0	514	43	0
79	Bd	427	0	426	203	0
80	Be	437	0	483	102	0
81	Bf	601	0	625	104	0
82	Bg	2440	0	2396	110	0
83	Bv	1623	0	820	71	0
83	Bw	1623	0	821	98	0
84	Bx	561	0	281	54	0
85	By	120	0	32	10	0
86	A2	220	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	A3	8	0	0	0	0
86	A4	9	0	0	0	0
86	AA	1	0	0	0	0
86	AB	2	0	0	0	0
86	AN	2	0	0	0	0
86	AY	1	0	0	0	0
86	Aa	3	0	0	0	0
86	Ae	2	0	0	0	0
86	An	1	0	0	0	0
86	B1	72	0	0	2	0
86	BD	1	0	0	0	0
86	BX	1	0	0	0	0
86	Bv	2	0	0	0	0
86	Bx	1	0	0	1	0
87	Aj	1	0	0	0	0
87	Ao	1	0	0	0	0
87	Ap	1	0	0	0	0
87	Ba	1	0	0	0	0
87	Bd	1	0	0	0	0
All	All	218559	0	162165	16253	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 43.

The worst 5 of 16253 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)
6:AD:286:SER:HB3	48:A2:1163:C:C5'	1.21	1.68
64:BO:54:CYS:SG	64:BO:81:VAL:HG22	1.31	1.67
10:AH:5:LEU:HD13	10:AH:60:TRP:CH2	1.32	1.65
75:BZ:79:ILE:HG21	75:BZ:83:LEU:CD1	1.18	1.64
10:AH:5:LEU:HB3	10:AH:60:TRP:CZ3	1.14	1.63

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	250/257 (97%)	237 (95%)	7 (3%)	6 (2%)	4	29
4	AB	392/403 (97%)	370 (94%)	10 (3%)	12 (3%)	3	25
5	AC	361/427 (84%)	333 (92%)	13 (4%)	15 (4%)	2	19
6	AD	292/297 (98%)	270 (92%)	14 (5%)	8 (3%)	4	27
7	AE	192/288 (67%)	161 (84%)	12 (6%)	19 (10%)	0	6
8	AF	232/248 (94%)	213 (92%)	10 (4%)	9 (4%)	2	20
9	AG	232/266 (87%)	217 (94%)	10 (4%)	5 (2%)	5	30
10	AH	189/192 (98%)	175 (93%)	8 (4%)	6 (3%)	3	24
11	AI	204/214 (95%)	192 (94%)	7 (3%)	5 (2%)	4	28
12	AJ	167/178 (94%)	154 (92%)	7 (4%)	6 (4%)	2	22
13	AK	107/317 (34%)	34 (32%)	37 (35%)	36 (34%)	0	0
14	AL	203/211 (96%)	175 (86%)	14 (7%)	14 (7%)	1	10
15	AM	137/215 (64%)	127 (93%)	5 (4%)	5 (4%)	2	22
16	AN	201/204 (98%)	193 (96%)	6 (3%)	2 (1%)	12	44
17	AO	193/203 (95%)	187 (97%)	3 (2%)	3 (2%)	7	36
18	AP	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
19	AQ	185/188 (98%)	163 (88%)	10 (5%)	12 (6%)	1	11
20	AR	179/196 (91%)	171 (96%)	4 (2%)	4 (2%)	5	30
21	AS	173/176 (98%)	156 (90%)	11 (6%)	6 (4%)	3	23
22	AT	155/160 (97%)	144 (93%)	6 (4%)	5 (3%)	3	24
23	AU	97/128 (76%)	81 (84%)	7 (7%)	9 (9%)	0	6
24	AV	127/140 (91%)	125 (98%)	2 (2%)	0	100	100
25	AW	119/157 (76%)	96 (81%)	18 (15%)	5 (4%)	2	19
26	AX	115/156 (74%)	113 (98%)	2 (2%)	0	100	100
27	AY	125/145 (86%)	119 (95%)	2 (2%)	4 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	AZ	132/136 (97%)	118 (89%)	6 (4%)	8 (6%)	1	12
29	Aa	145/148 (98%)	135 (93%)	6 (4%)	4 (3%)	4	26
30	Ab	66/159 (42%)	57 (86%)	5 (8%)	4 (6%)	1	12
31	Ac	101/115 (88%)	97 (96%)	2 (2%)	2 (2%)	6	32
32	Ad	104/125 (83%)	99 (95%)	3 (3%)	2 (2%)	6	33
33	Ae	127/135 (94%)	116 (91%)	6 (5%)	5 (4%)	2	20
34	Af	107/110 (97%)	93 (87%)	5 (5%)	9 (8%)	0	7
35	Ag	112/117 (96%)	107 (96%)	3 (3%)	2 (2%)	6	34
36	Ah	120/123 (98%)	112 (93%)	2 (2%)	6 (5%)	1	15
37	Ai	95/105 (90%)	83 (87%)	7 (7%)	5 (5%)	1	14
38	Aj	82/97 (84%)	69 (84%)	7 (8%)	6 (7%)	1	9
39	Ak	67/70 (96%)	50 (75%)	7 (10%)	10 (15%)	0	2
40	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Am	48/128 (38%)	44 (92%)	3 (6%)	1 (2%)	5	31
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	103/106 (97%)	94 (91%)	5 (5%)	4 (4%)	2	20
44	Ap	89/92 (97%)	84 (94%)	3 (3%)	2 (2%)	5	30
45	Aq	136/165 (82%)	40 (29%)	47 (35%)	49 (36%)	0	0
46	At	120/137 (88%)	107 (89%)	10 (8%)	3 (2%)	4	28
47	Au	215/217 (99%)	185 (86%)	20 (9%)	10 (5%)	2	17
50	BA	213/295 (72%)	197 (92%)	12 (6%)	4 (2%)	6	33
51	BB	210/264 (80%)	180 (86%)	12 (6%)	18 (9%)	0	7
52	BC	220/293 (75%)	204 (93%)	7 (3%)	9 (4%)	2	19
53	BD	218/243 (90%)	201 (92%)	10 (5%)	7 (3%)	3	24
54	BE	255/263 (97%)	230 (90%)	14 (6%)	11 (4%)	2	18
55	BF	188/204 (92%)	163 (87%)	15 (8%)	10 (5%)	1	14
56	BG	230/249 (92%)	211 (92%)	11 (5%)	8 (4%)	3	23
57	BH	181/194 (93%)	169 (93%)	8 (4%)	4 (2%)	5	30
58	BI	205/208 (99%)	175 (85%)	20 (10%)	10 (5%)	1	16
59	BJ	177/194 (91%)	137 (77%)	28 (16%)	12 (7%)	1	10
60	BK	96/165 (58%)	84 (88%)	7 (7%)	5 (5%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	BL	151/158 (96%)	133 (88%)	11 (7%)	7 (5%)	2	17
62	BM	118/132 (89%)	113 (96%)	1 (1%)	4 (3%)	3	23
63	BN	147/151 (97%)	126 (86%)	13 (9%)	8 (5%)	1	14
64	BO	134/151 (89%)	113 (84%)	11 (8%)	10 (8%)	1	9
65	BP	118/145 (81%)	100 (85%)	9 (8%)	9 (8%)	1	8
66	BQ	137/146 (94%)	120 (88%)	10 (7%)	7 (5%)	1	15
67	BR	123/135 (91%)	106 (86%)	9 (7%)	8 (6%)	1	11
68	BS	137/152 (90%)	125 (91%)	7 (5%)	5 (4%)	2	22
69	BT	141/145 (97%)	131 (93%)	6 (4%)	4 (3%)	4	26
70	BU	95/119 (80%)	91 (96%)	2 (2%)	2 (2%)	5	31
71	BV	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
72	BW	127/130 (98%)	120 (94%)	3 (2%)	4 (3%)	3	25
73	BX	137/143 (96%)	124 (90%)	8 (6%)	5 (4%)	2	22
74	BY	123/133 (92%)	116 (94%)	6 (5%)	1 (1%)	16	49
75	BZ	84/125 (67%)	80 (95%)	1 (1%)	3 (4%)	2	22
76	Ba	95/115 (83%)	87 (92%)	7 (7%)	1 (1%)	11	43
77	Bb	78/84 (93%)	72 (92%)	4 (5%)	2 (3%)	4	27
78	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	23
79	Bd	49/56 (88%)	42 (86%)	4 (8%)	3 (6%)	1	12
80	Be	53/59 (90%)	49 (92%)	2 (4%)	2 (4%)	2	20
81	Bf	71/156 (46%)	63 (89%)	7 (10%)	1 (1%)	9	38
82	Bg	312/317 (98%)	292 (94%)	12 (4%)	8 (3%)	4	27
All	All	11580/13387 (86%)	10401 (90%)	657 (6%)	522 (4%)	3	17

5 of 522 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AA	138	SER
3	AA	144	LYS
3	AA	197	PRO
4	AB	189	THR
4	AB	356	LYS

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	
3	AA	194/199 (98%)	182 (94%)	12 (6%)	16	43
4	AB	343/349 (98%)	318 (93%)	25 (7%)	13	38
5	AC	302/348 (87%)	275 (91%)	27 (9%)	9	32
6	AD	248/250 (99%)	227 (92%)	21 (8%)	10	34
7	AE	174/252 (69%)	124 (71%)	50 (29%)	0	2
8	AF	203/215 (94%)	192 (95%)	11 (5%)	20	46
9	AG	199/223 (89%)	190 (96%)	9 (4%)	24	50
10	AH	170/171 (99%)	158 (93%)	12 (7%)	13	38
11	AI	178/181 (98%)	174 (98%)	4 (2%)	45	65
12	AJ	142/149 (95%)	138 (97%)	4 (3%)	38	61
13	AK	95/258 (37%)	68 (72%)	27 (28%)	0	2
14	AL	171/177 (97%)	154 (90%)	17 (10%)	7	29
15	AM	118/161 (73%)	105 (89%)	13 (11%)	6	26
16	AN	171/172 (99%)	166 (97%)	5 (3%)	37	60
17	AO	168/174 (97%)	164 (98%)	4 (2%)	43	64
18	AP	134/163 (82%)	122 (91%)	12 (9%)	9	32
19	AQ	164/165 (99%)	145 (88%)	19 (12%)	5	24
20	AR	160/175 (91%)	146 (91%)	14 (9%)	9	32
21	AS	156/157 (99%)	149 (96%)	7 (4%)	24	50
22	AT	138/140 (99%)	126 (91%)	12 (9%)	9	33
23	AU	89/115 (77%)	79 (89%)	10 (11%)	6	25
24	AV	100/107 (94%)	97 (97%)	3 (3%)	36	60
25	AW	100/126 (79%)	95 (95%)	5 (5%)	22	48
26	AX	105/133 (79%)	94 (90%)	11 (10%)	6	27
27	AY	119/135 (88%)	107 (90%)	12 (10%)	7	28
28	AZ	117/118 (99%)	100 (86%)	17 (14%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	Aa	120/121 (99%)	109 (91%)	11 (9%)	8	32
30	Ab	58/126 (46%)	54 (93%)	4 (7%)	14	39
31	Ac	88/97 (91%)	86 (98%)	2 (2%)	44	64
32	Ad	97/110 (88%)	96 (99%)	1 (1%)	68	75
33	Ae	115/121 (95%)	114 (99%)	1 (1%)	70	76
34	Af	88/89 (99%)	84 (96%)	4 (4%)	24	50
35	Ag	98/100 (98%)	93 (95%)	5 (5%)	21	48
36	Ah	109/110 (99%)	96 (88%)	13 (12%)	5	23
37	Ai	83/89 (93%)	79 (95%)	4 (5%)	23	49
38	Aj	71/80 (89%)	65 (92%)	6 (8%)	10	34
39	Ak	64/65 (98%)	44 (69%)	20 (31%)	0	2
40	Al	47/48 (98%)	43 (92%)	4 (8%)	10	34
41	Am	46/116 (40%)	45 (98%)	1 (2%)	45	65
42	An	24/24 (100%)	23 (96%)	1 (4%)	26	52
43	Ao	93/94 (99%)	82 (88%)	11 (12%)	5	23
44	Ap	74/75 (99%)	70 (95%)	4 (5%)	20	46
45	Aq	114/137 (83%)	87 (76%)	27 (24%)	1	4
46	At	106/121 (88%)	87 (82%)	19 (18%)	2	10
47	Au	196/196 (100%)	179 (91%)	17 (9%)	9	33
50	BA	180/243 (74%)	165 (92%)	15 (8%)	10	34
51	BB	193/231 (84%)	174 (90%)	19 (10%)	7	30
52	BC	188/225 (84%)	179 (95%)	9 (5%)	23	49
53	BD	183/202 (91%)	175 (96%)	8 (4%)	25	51
54	BE	220/225 (98%)	214 (97%)	6 (3%)	39	62
55	BF	160/170 (94%)	154 (96%)	6 (4%)	29	55
56	BG	202/218 (93%)	175 (87%)	27 (13%)	4	20
57	BH	164/174 (94%)	163 (99%)	1 (1%)	78	79
58	BI	179/180 (99%)	174 (97%)	5 (3%)	38	61
59	BJ	160/168 (95%)	151 (94%)	9 (6%)	19	46
60	BK	89/136 (65%)	85 (96%)	4 (4%)	24	50
61	BL	138/142 (97%)	134 (97%)	4 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	BM	102/108 (94%)	100 (98%)	2 (2%)	48	67
63	BN	130/131 (99%)	121 (93%)	9 (7%)	14	39
64	BO	106/119 (89%)	97 (92%)	9 (8%)	10	34
65	BP	109/130 (84%)	92 (84%)	17 (16%)	2	15
66	BQ	115/121 (95%)	103 (90%)	12 (10%)	7	27
67	BR	113/122 (93%)	95 (84%)	18 (16%)	2	14
68	BS	121/132 (92%)	103 (85%)	18 (15%)	3	17
69	BT	113/115 (98%)	104 (92%)	9 (8%)	11	35
70	BU	90/107 (84%)	86 (96%)	4 (4%)	25	51
71	BV	65/67 (97%)	58 (89%)	7 (11%)	6	26
72	BW	112/113 (99%)	109 (97%)	3 (3%)	39	62
73	BX	111/115 (96%)	100 (90%)	11 (10%)	7	29
74	BY	107/115 (93%)	103 (96%)	4 (4%)	30	56
75	BZ	75/103 (73%)	58 (77%)	17 (23%)	1	5
76	Ba	84/98 (86%)	72 (86%)	12 (14%)	3	18
77	Bb	72/76 (95%)	72 (100%)	0	100	100
78	Bc	55/62 (89%)	53 (96%)	2 (4%)	31	57
79	Bd	45/49 (92%)	39 (87%)	6 (13%)	4	20
80	Be	44/48 (92%)	33 (75%)	11 (25%)	0	4
81	Bf	66/140 (47%)	65 (98%)	1 (2%)	57	71
82	Bg	272/275 (99%)	267 (98%)	5 (2%)	51	69
All	All	10112/11392 (89%)	9304 (92%)	808 (8%)	13	35

5 of 808 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	Aq	37	LEU
54	BE	153	VAL
80	Be	46	VAL
45	Aq	109	ILE
45	Aq	35	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 268 such sidechains are listed below:

Mol	Chain	Res	Type
69	BT	42	HIS
72	BW	44	HIS
82	Bg	56	GLN
24	AV	101	ASN
23	AU	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A3	156/194 (80%)	28 (17%)	4 (2%)
2	A4	118/121 (97%)	23 (19%)	1 (0%)
48	A2	3600/5029 (71%)	698 (19%)	48 (1%)
49	B1	1701/1869 (91%)	291 (17%)	19 (1%)
83	Bv	75/76 (98%)	38 (50%)	0
83	Bw	75/76 (98%)	34 (45%)	0
84	Bx	27/28 (96%)	18 (66%)	0
All	All	5752/7393 (77%)	1130 (19%)	72 (1%)

5 of 1130 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A3	2	G
1	A3	12	G
1	A3	16	G
1	A3	35	C
1	A3	59	A

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	B1	283	G
49	B1	1756	C
49	B1	369	C
49	B1	797	C
48	A2	1402	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 331 ligands modelled in this entry, 331 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
49	B1	8
48	A2	5

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	842:C	O3'	843:C	P	1.85
1	B1	558:G	O3'	559:G	P	1.84
1	B1	497:C	O3'	498:C	P	1.83
1	B1	72:C	O3'	73:C	P	1.82
1	B1	1253:A	O3'	1254:C	P	1.82

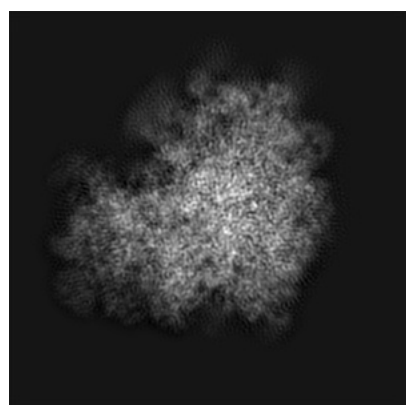
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2875. These allow visual inspection of the internal detail of the map and identification of artifacts.

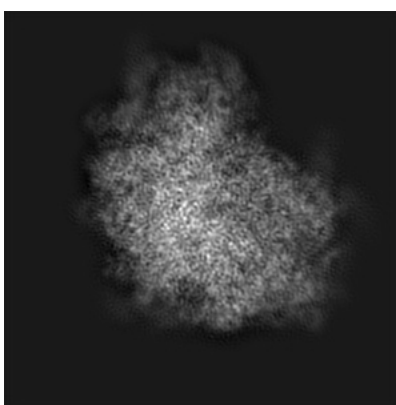
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

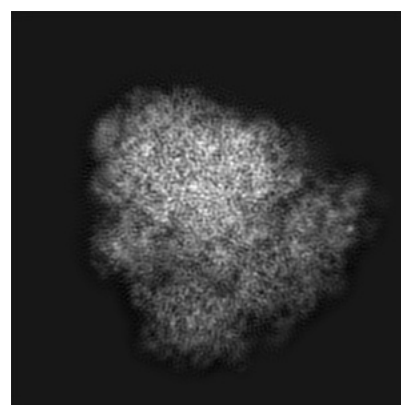
6.1.1 Primary map



X



Y

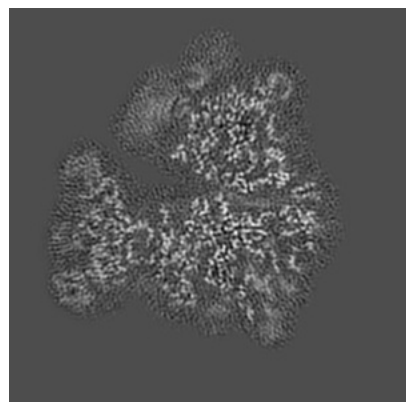


Z

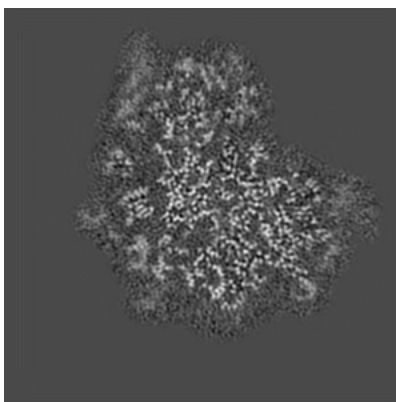
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

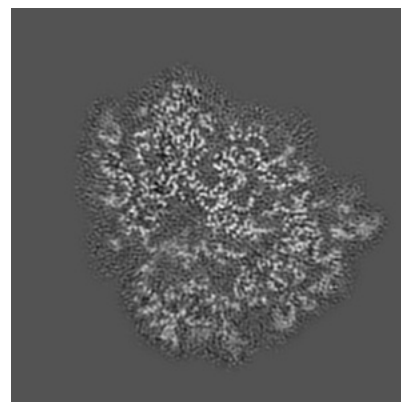
6.2.1 Primary map



X Index: 200



Y Index: 200

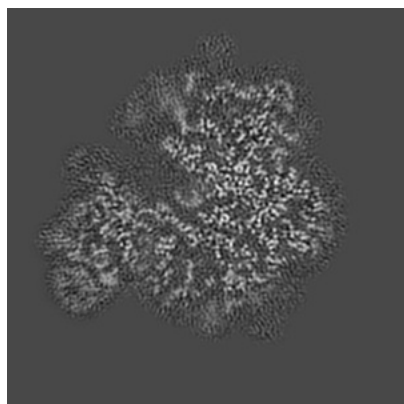


Z Index: 200

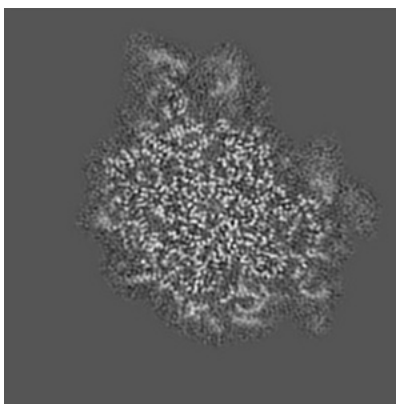
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

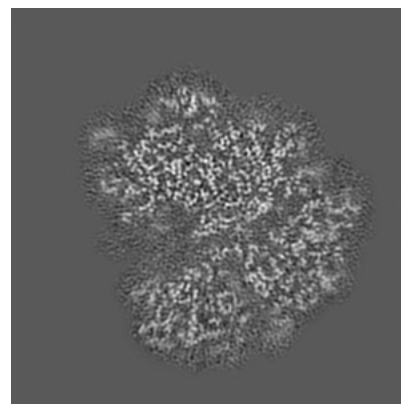
6.3.1 Primary map



X Index: 186



Y Index: 220

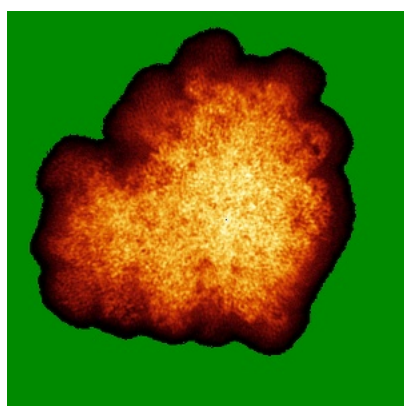


Z Index: 184

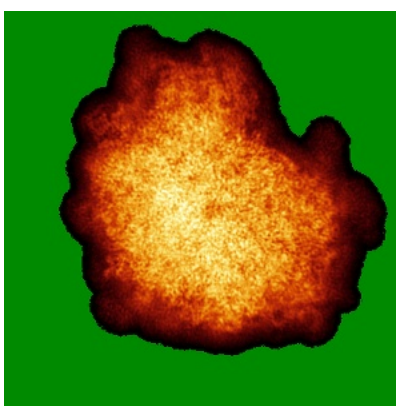
The images above show the largest variance slices of the map in three orthogonal directions.

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

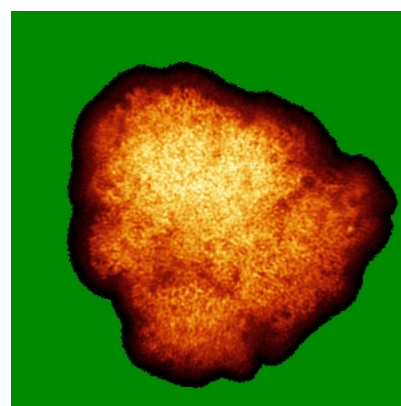
6.4.1 Primary map



X



Y

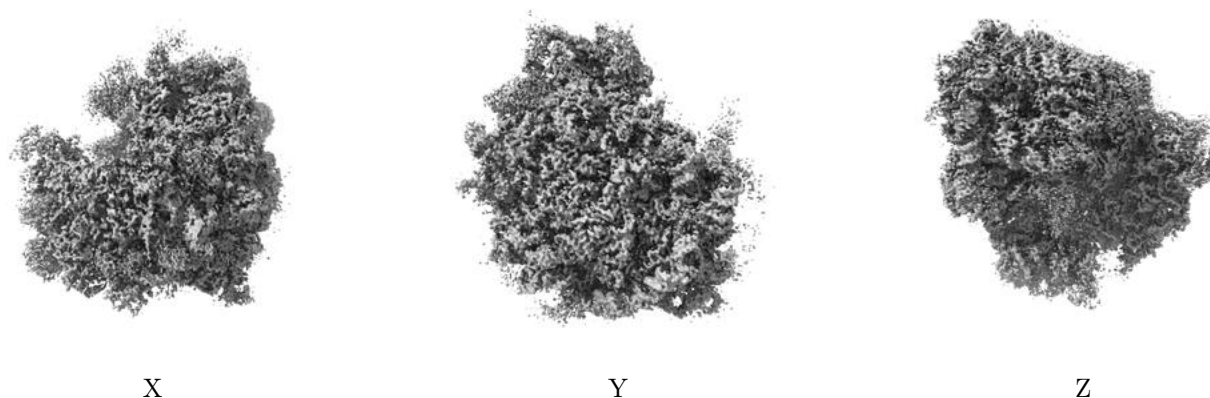


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

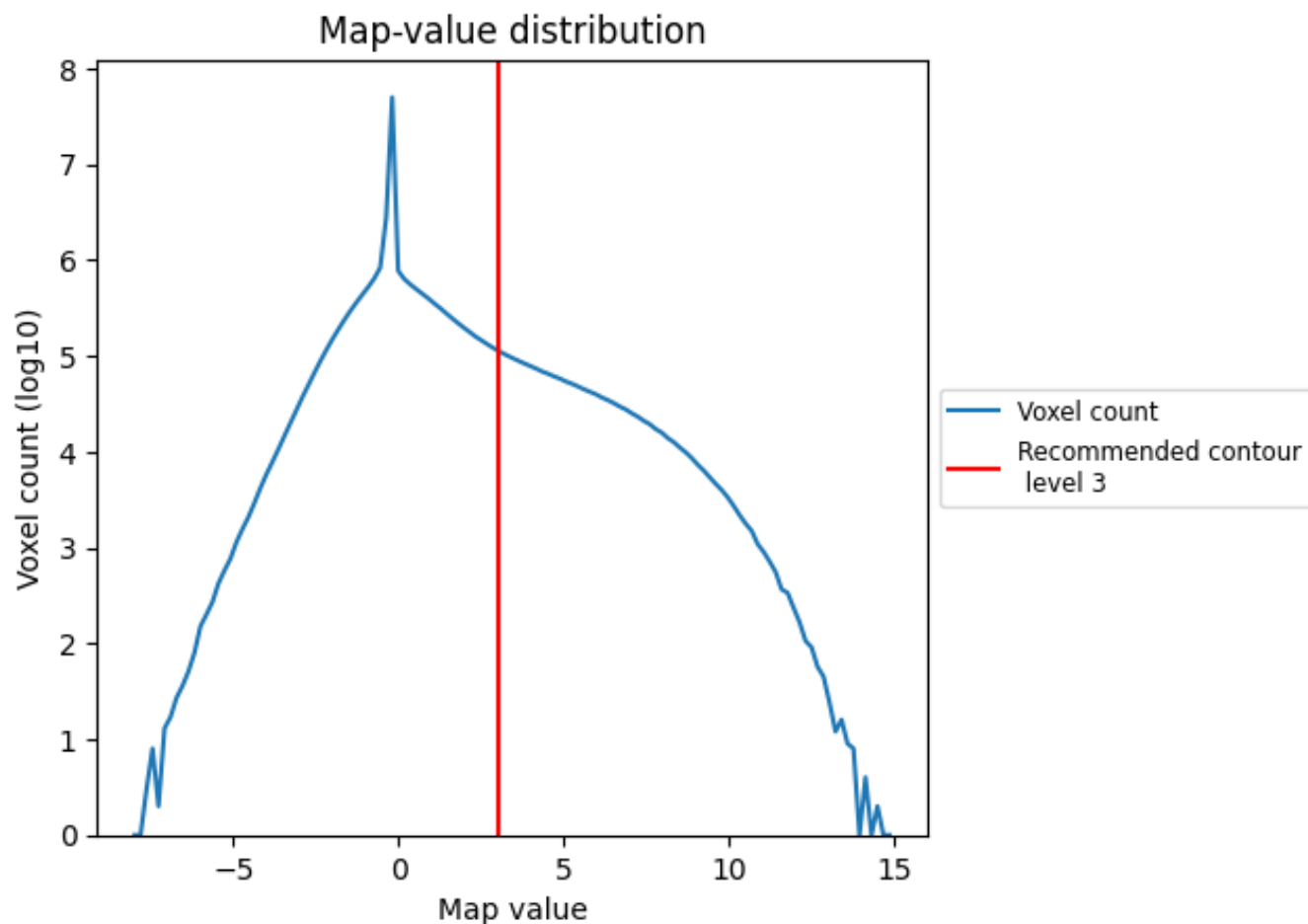
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

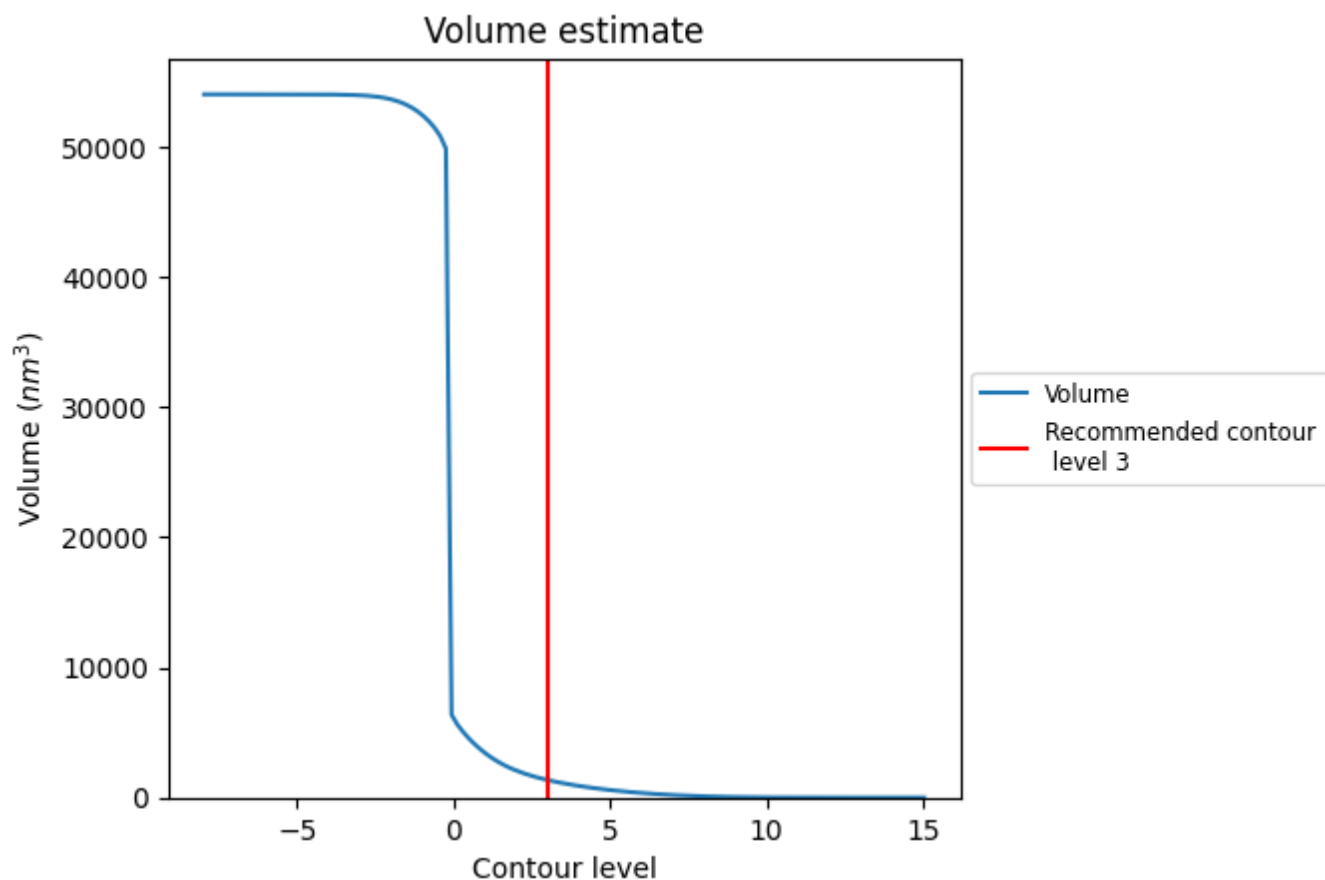
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

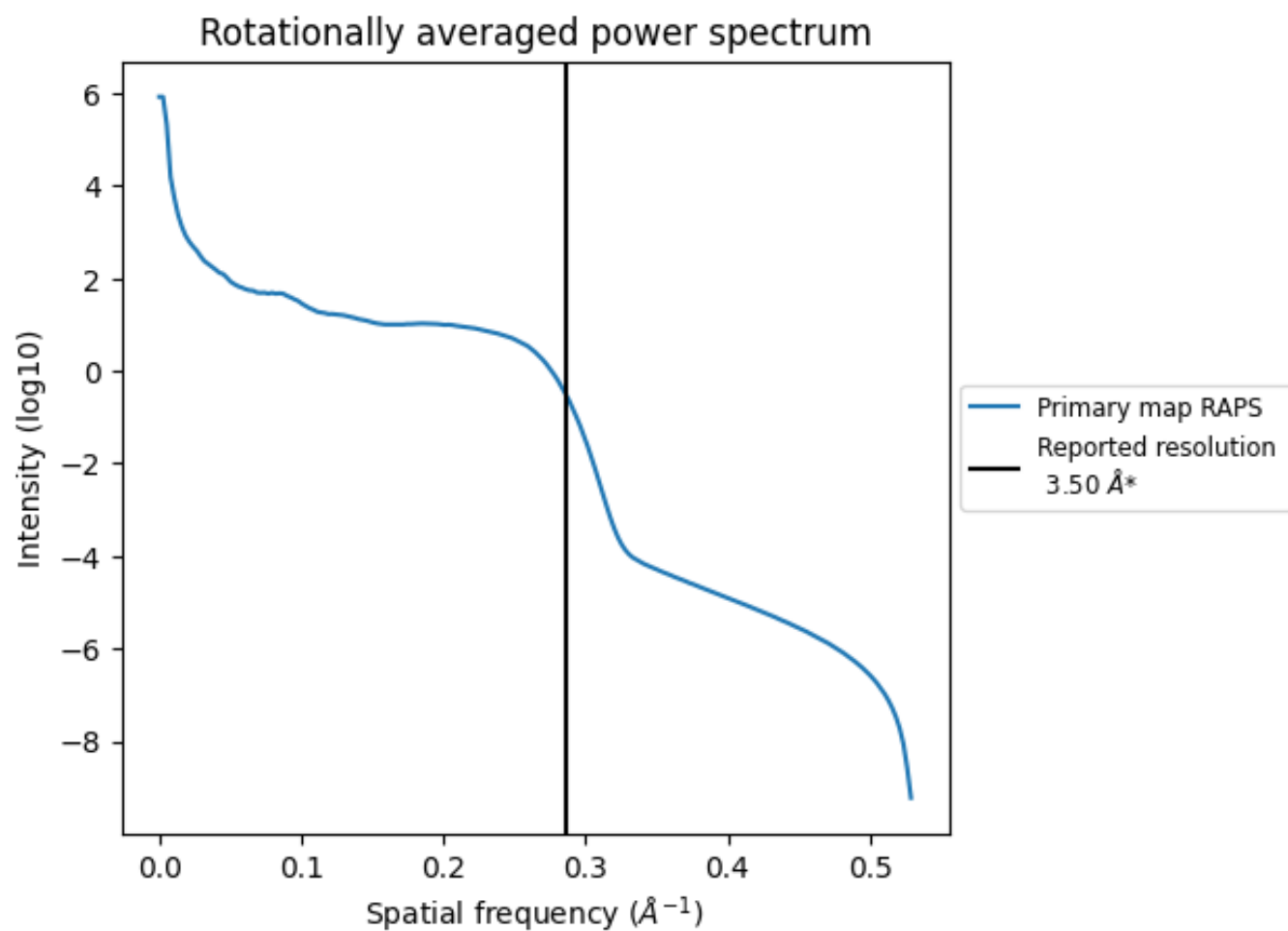
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1346 nm³; this corresponds to an approximate mass of 1216 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 0.286 Å⁻¹

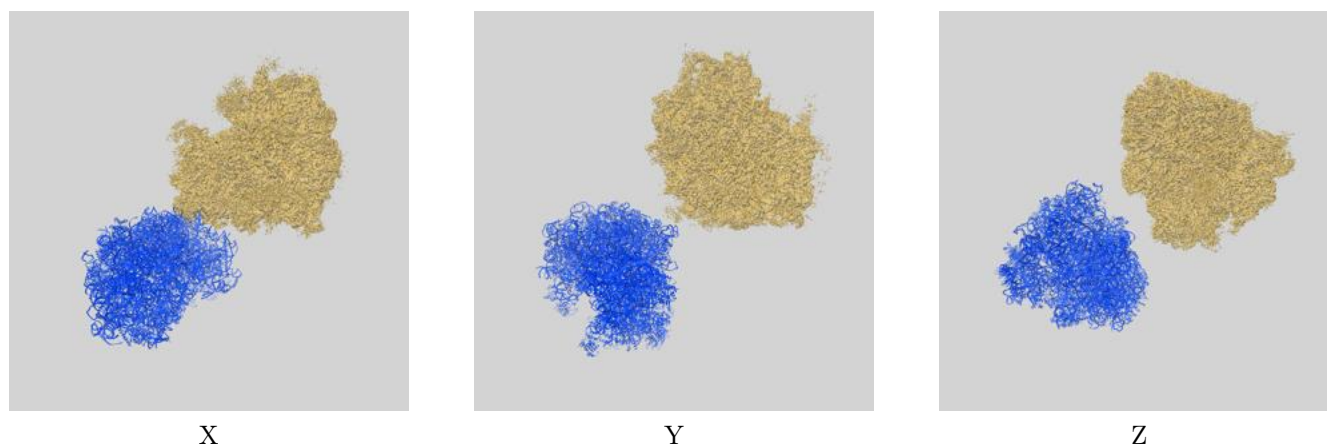
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

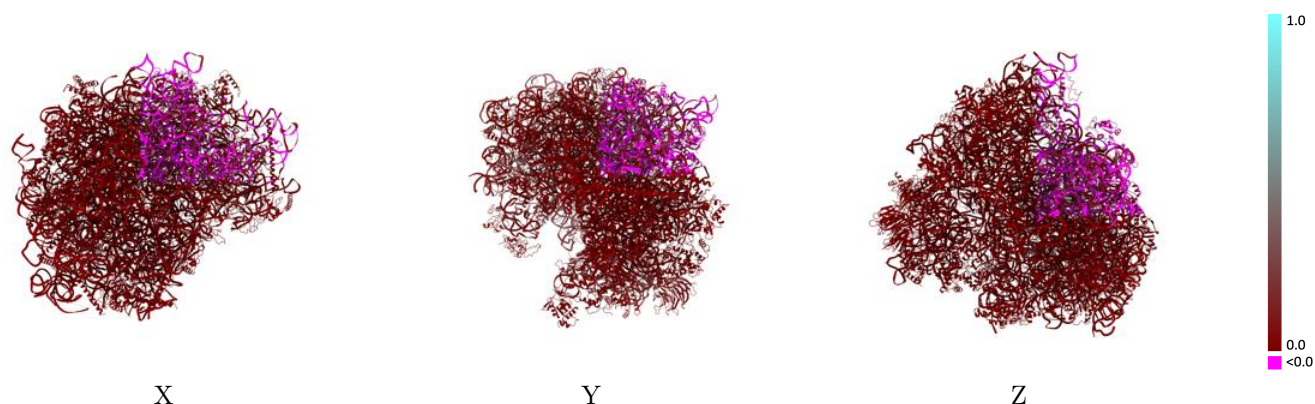
This section contains information regarding the fit between EMDB map EMD-2875 and PDB model 5AJ0. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



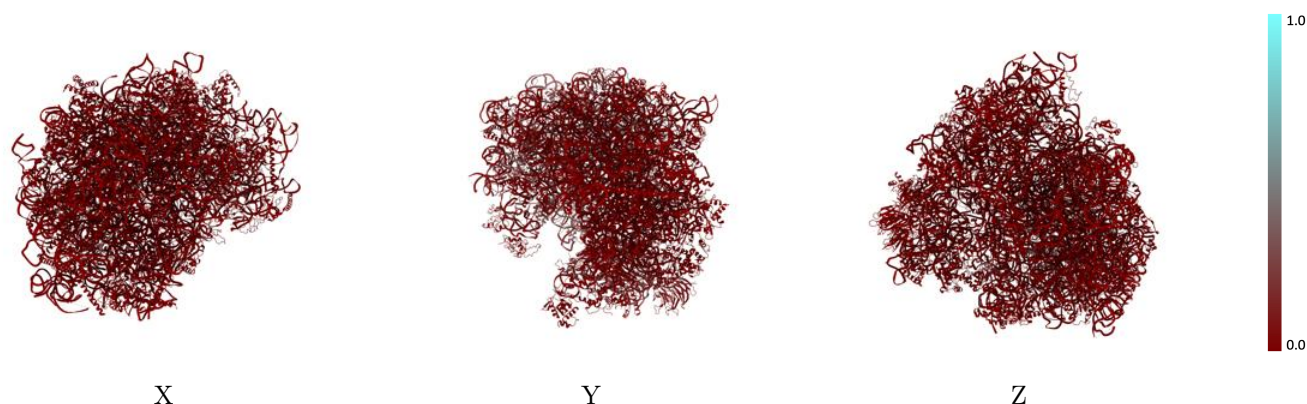
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



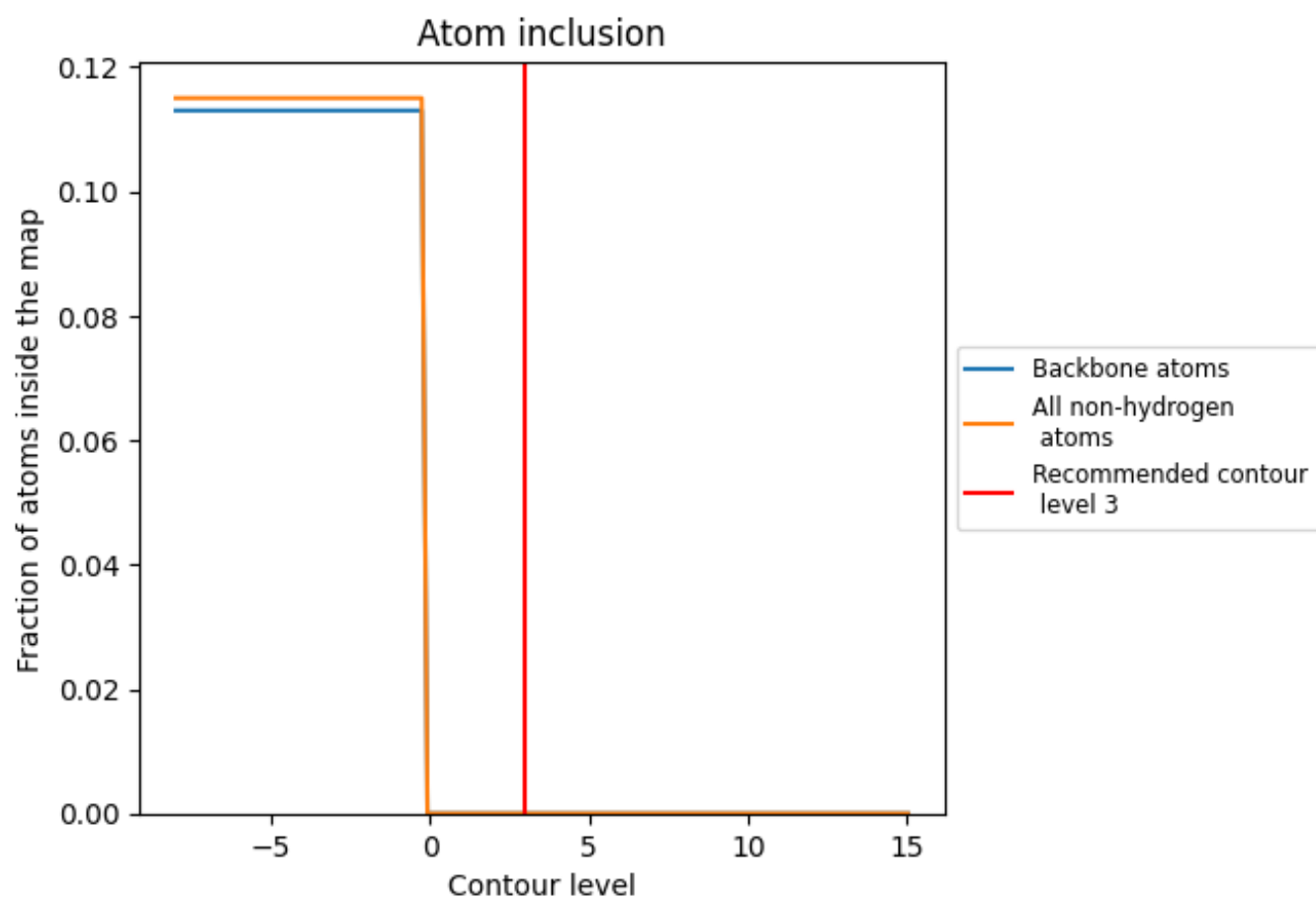
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.0000
A2	0.0000	0.0000
A3	0.0000	0.0030
A4	0.0000	0.0000
AA	0.0000	0.0010
AB	0.0000	0.0000
AC	0.0000	0.0000
AD	0.0000	0.0000
AE	0.0000	0.0000
AF	0.0000	0.0000
AG	0.0000	-0.0010
AH	0.0000	0.0000
AI	0.0000	0.0000
AJ	0.0000	0.0000
AK	0.0000	0.0000
AL	0.0000	0.0000
AM	0.0000	0.0000
AN	0.0000	0.0000
AO	0.0000	0.0000
AP	0.0000	0.0010
AQ	0.0000	0.0000
AR	0.0000	0.0150
AS	0.0000	0.0000
AT	0.0000	0.0000
AU	0.0000	-0.0210
AV	0.0000	0.0000
AW	0.0000	0.0000
AX	0.0000	0.0020
AY	0.0000	0.0000
AZ	0.0000	0.0050
Aa	0.0000	0.0000
Ab	0.0000	0.0000
Ac	0.0000	-0.0080
Ad	0.0000	0.0000
Ae	0.0000	0.0000



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Chain	Atom inclusion	Q-score
Af	0.0000	0.0000
Ag	0.0000	0.0190
Ah	0.0000	0.0000
Ai	0.0000	0.0000
Aj	0.0000	-0.0050
Ak	0.0000	0.0040
Al	0.0000	0.0220
Am	0.0000	0.0000
An	0.0000	0.0000
Ao	0.0000	0.0000
Ap	0.0000	-0.0110
Aq	0.0000	0.0000
At	0.0000	0.0000
Au	0.0000	0.0000
B1	0.0000	0.0000
BA	0.0000	0.0000
BB	0.0000	0.0000
BC	0.0000	0.0000
BD	0.0000	0.0000
BE	0.0000	0.0000
BF	0.0000	0.0000
BG	0.0000	0.0000
BH	0.0000	0.0000
BI	0.0000	0.0150
BJ	0.0000	0.0000
BK	0.0000	0.0000
BL	0.0000	0.0040
BM	0.0000	0.0000
BN	0.0000	0.0010
BO	0.0000	0.0000
BP	0.0000	0.0000
BQ	0.0000	0.0000
BR	0.0000	0.0000
BS	0.0000	0.0000
BT	0.0000	0.0000
BU	0.0000	0.0000
BV	0.0000	0.0000
BW	0.0000	0.0000
BX	0.0000	0.0000
BY	0.0000	0.0000
BZ	0.0000	0.0000
Ba	0.0000	0.0000

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Chain	Atom inclusion	Q-score
Bb	 0.0000	 0.0000
Bc	 0.0000	 0.0000
Bd	 0.0000	 0.0000
Be	 0.0000	 0.0000
Bf	 0.0000	 0.0000
Bg	 0.0000	 0.0000
Bv	 0.0000	 0.0000
Bw	 0.0000	 0.0000
Bx	 0.0000	 0.0000
By	 0.0000	 0.0210