



## wwPDB EM Validation Summary Report ⓘ

Apr 2, 2025 – 02:19 am BST

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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

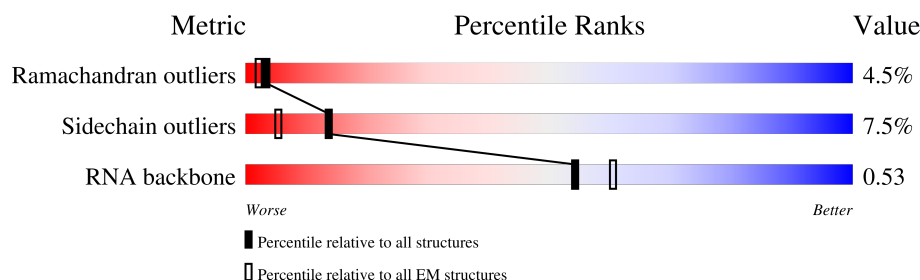
EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

# 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A3	194	<div> <div>81%</div> <div> <div>46%</div> <div>27%</div> <div>8%</div> <div>19%</div> </div> </div>
2	A4	121	<div> <div>98%</div> <div> <div>44%</div> <div>49%</div> <div>6%</div> </div> </div>
3	AA	257	<div> <div>98%</div> <div> <div>92%</div> <div>6%</div> </div> </div>
4	AB	403	<div> <div>98%</div> <div> <div>90%</div> <div>7%</div> </div> </div>
5	AC	427	<div> <div>85%</div> <div> <div>76%</div> <div>8%</div> <div>15%</div> </div> </div>
6	AD	297	<div> <div>99%</div> <div> <div>91%</div> <div>8%</div> </div> </div>
7	AE	288	<div> <div>67%</div> <div> <div>46%</div> <div>18%</div> <div>33%</div> </div> </div>
8	AF	248	<div> <div>94%</div> <div> <div>88%</div> <div>6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
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	
33	Ae	135	

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Mol	Chain	Length	Quality of chain
34	Af	110	<div>99%</div> <div>90% 6% ...</div>
35	Ag	117	<div>97%</div> <div>91% 6% .</div>
36	Ah	123	<div>99%</div> <div>83% 16% .</div>
37	Ai	105	<div>92%</div> <div>85% 8% 8%</div>
38	Aj	97	<div>87%</div> <div>72% 12% . 13%</div>
39	Ak	70	<div>99%</div> <div>66% 24% 9% .</div>
40	Al	51	<div>98%</div> <div>92% 6% .</div>
41	Am	128	<div>39%</div> <div>38% . 61%</div>
42	An	25	<div>100%</div> <div>96% .</div>
43	Ao	106	<div>99%</div> <div>88% 11% .</div>
44	Ap	92	<div>99%</div> <div>93% 5% .</div>
45	Aq	165	<div>84%</div> <div>41% 30% 11% . 16%</div>
46	At	137	<div>89%</div> <div>74% 15% 11%</div>
47	Au	217	<div>100%</div> <div>87% 10% ..</div>
48	A2	5029	<div>72%</div> <div>42% 26% . 28%</div>
49	B1	1869	<div>91%</div> <div>54% 34% . 9%</div>
50	BA	295	<div>73%</div> <div>66% 6% . 27%</div>
51	BB	264	<div>80%</div> <div>68% 12% 20%</div>
52	BC	293	<div>76%</div> <div>69% 7% 24%</div>
53	BD	243	<div>91%</div> <div>84% 6% 9%</div>
54	BE	263	<div>98%</div> <div>90% 6% ..</div>
55	BF	204	<div>93%</div> <div>85% 7% 7%</div>
56	BG	249	<div>93%</div> <div>80% 14% 7%</div>
57	BH	194	<div>94%</div> <div>90% 5% 6%</div>
58	BI	208	<div>100%</div> <div>93% 7%</div>

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Mol	Chain	Length	Quality of chain
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	
83	Bv	76	

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Mol	Chain	Length	Quality of chain
83	Bw	76	<div><div></div><div>100%</div><div>51%49%</div></div>
84	Bx	28	<div><div></div><div>100%</div><div>18%82%</div></div>
85	By	24	<div><div></div><div>100%</div><div>100%</div></div>

## 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...*

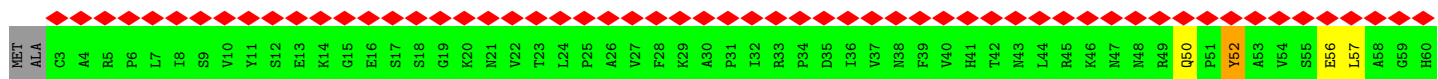
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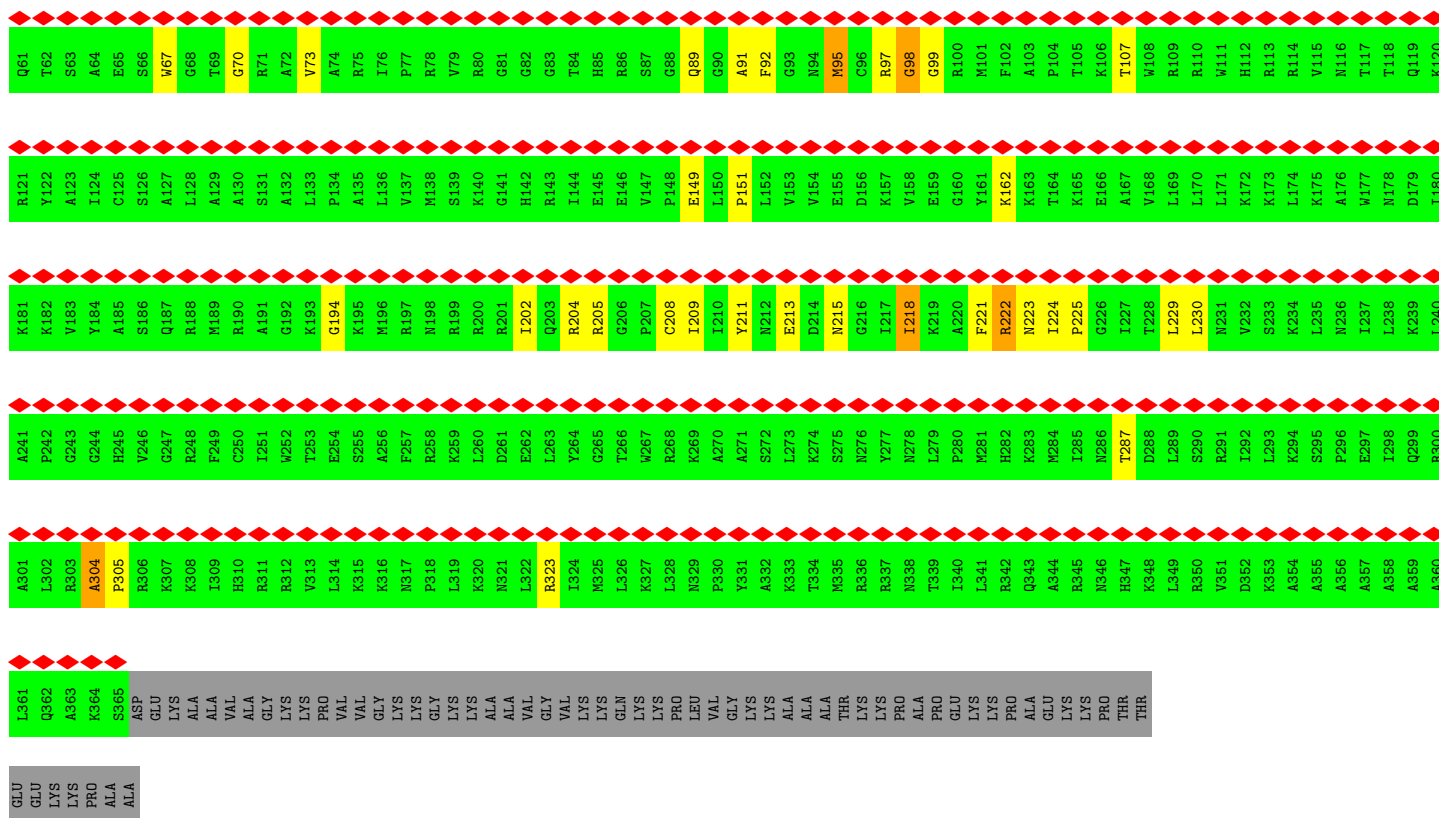
Mol	Chain	Residues	Atoms		AltConf
86	BD	1	Total 1	Mg 1	0
86	BX	1	Total 1	Mg 1	0
86	Bv	2	Total 2	Mg 2	0
86	Bx	1	Total 1	Mg 1	0

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

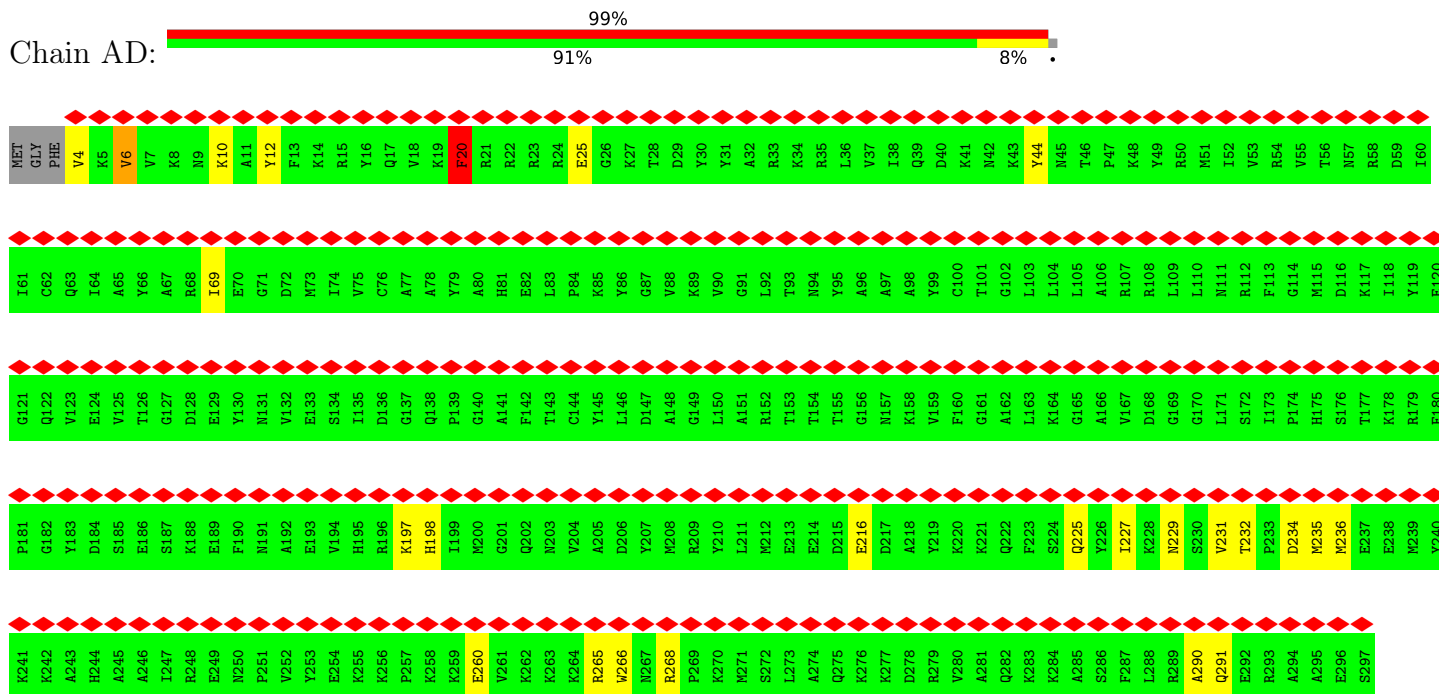
Mol	Chain	Residues	Atoms		AltConf
87	Aj	1	Total 1	Zn 1	0
87	Ao	1	Total 1	Zn 1	0
87	Ap	1	Total 1	Zn 1	0
87	Ba	1	Total 1	Zn 1	0
87	Bd	1	Total 1	Zn 1	0



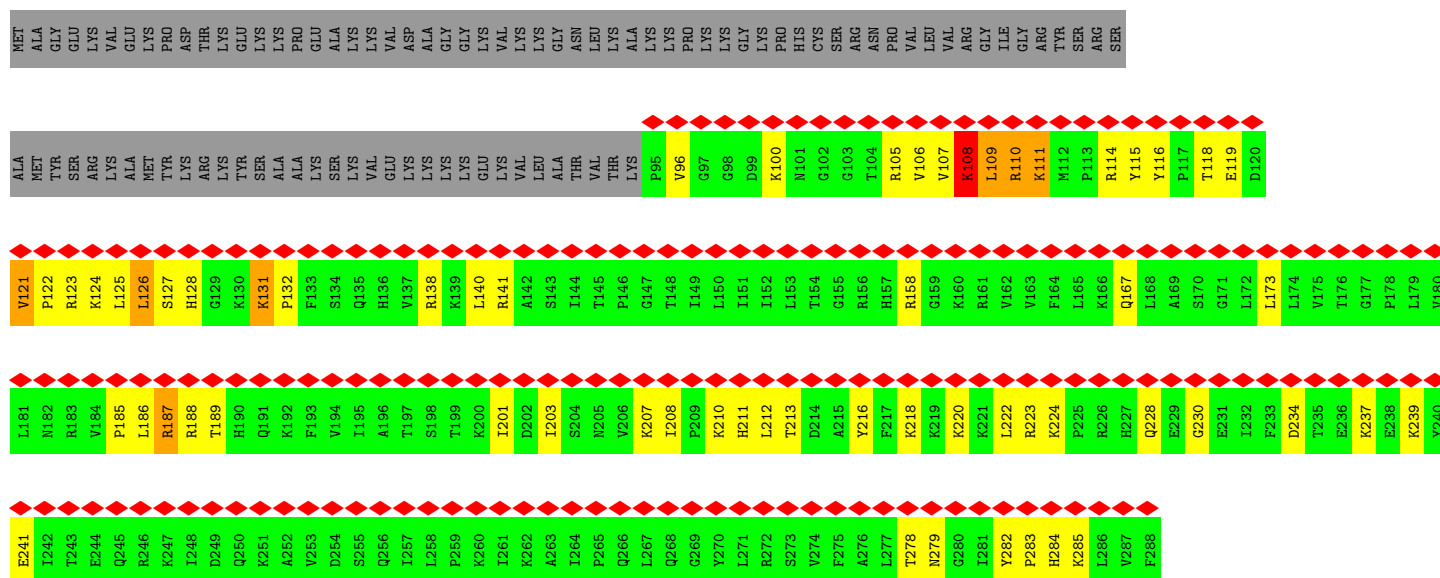




• Molecule 6: 60S ribosomal protein L5

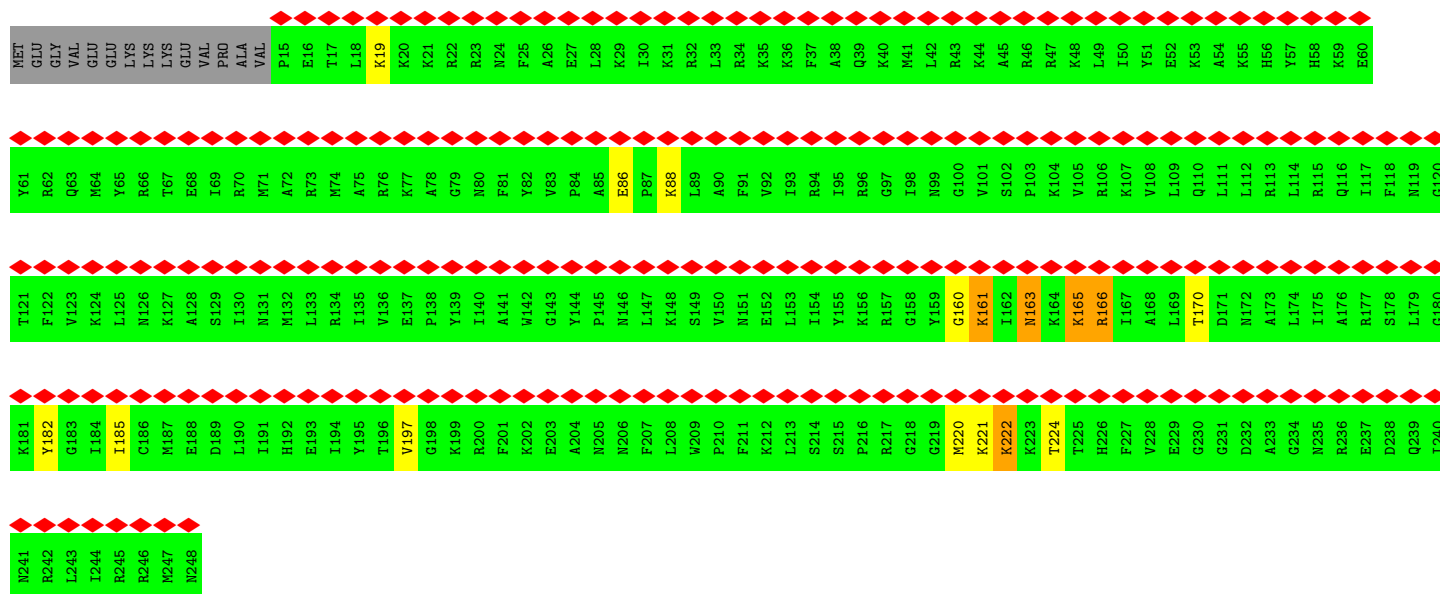


• Molecule 7: 60S ribosomal protein L6



• Molecule 8: 60S ribosomal protein L7

Chain AF:

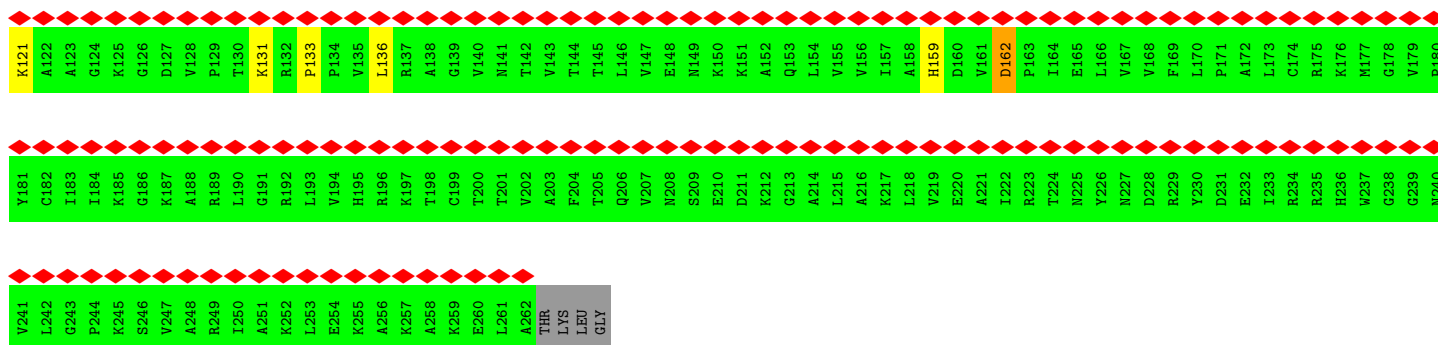


• Molecule 9: 60S ribosomal protein L7a

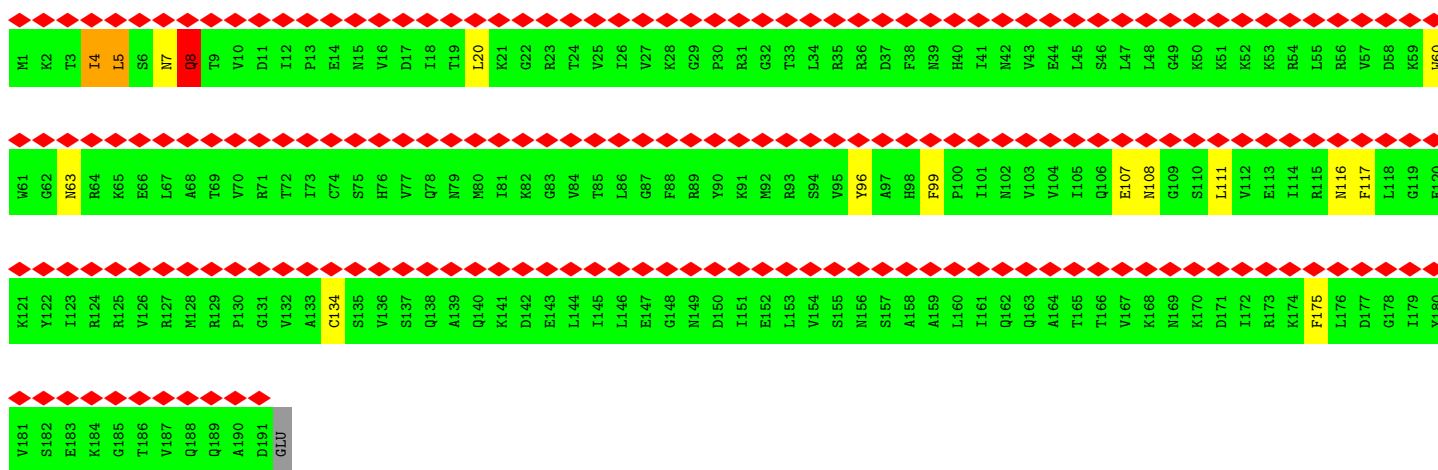
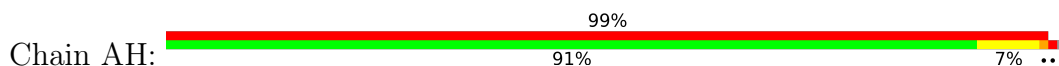
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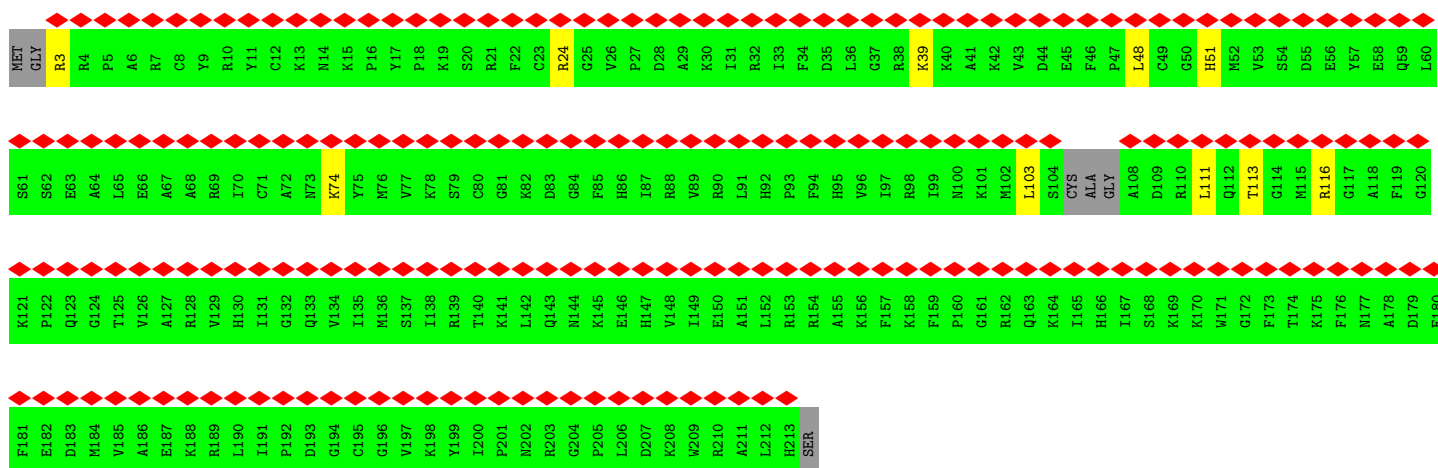
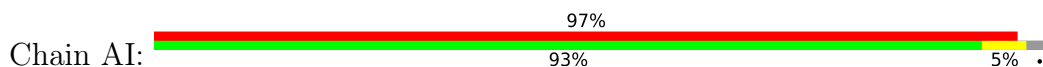




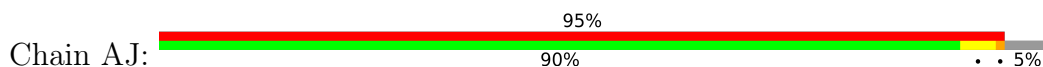
- Molecule 10: 60S ribosomal protein L9

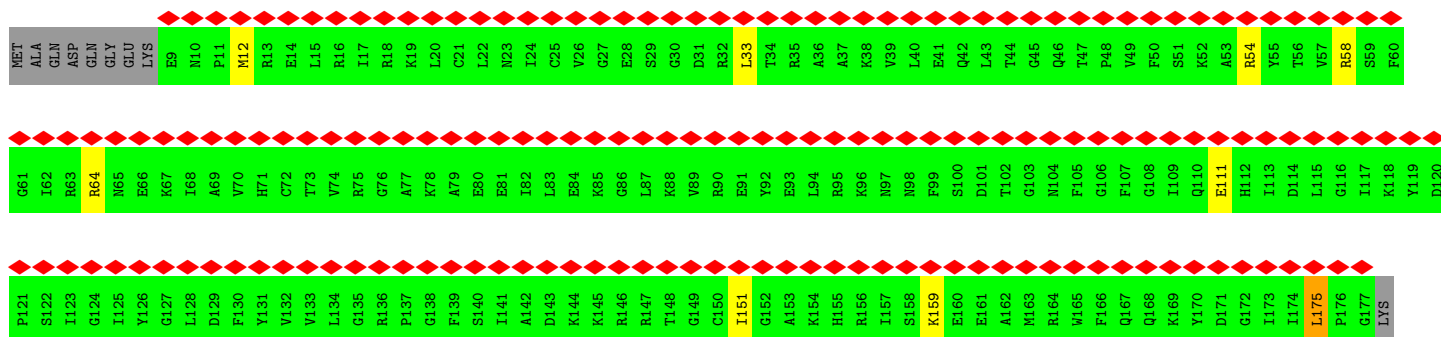


- Molecule 11: 60S ribosomal protein L10

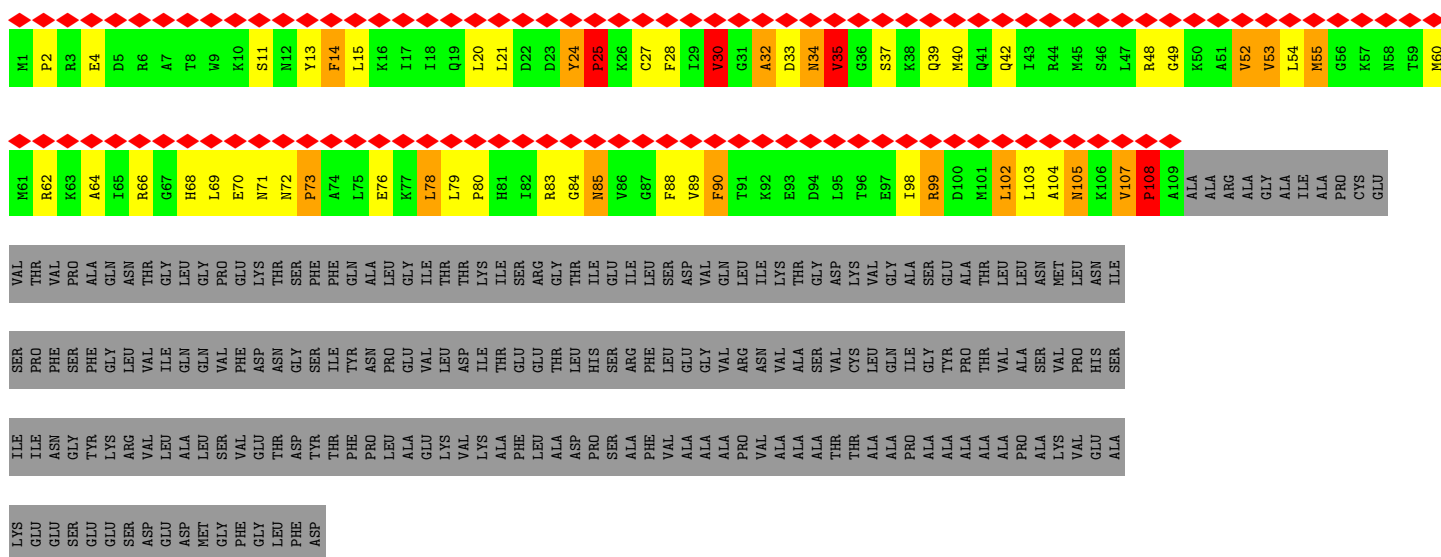


- Molecule 12: 60S ribosomal protein L11

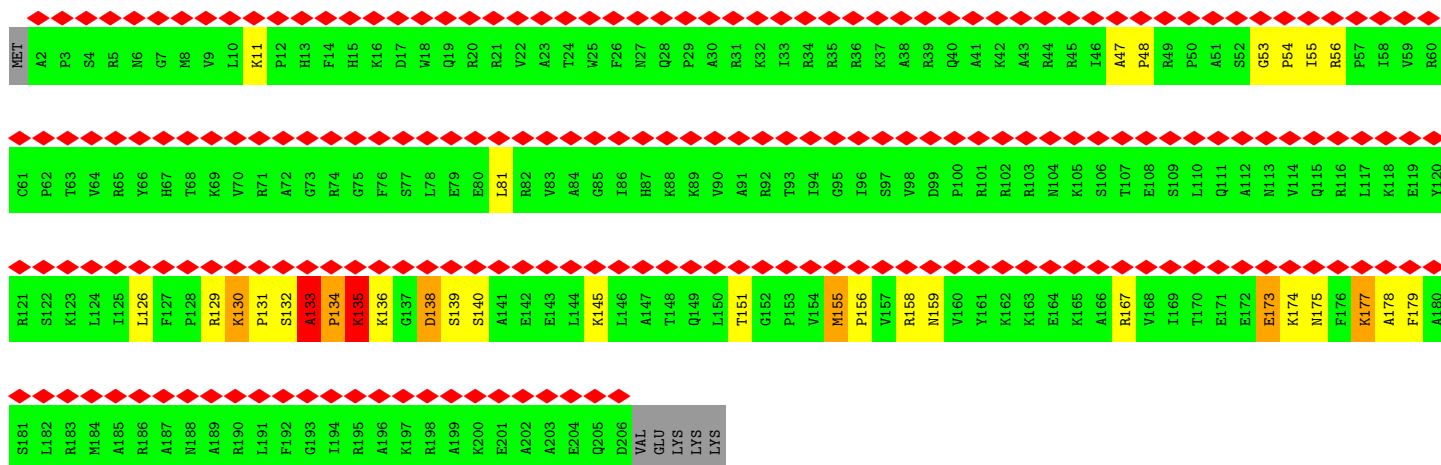
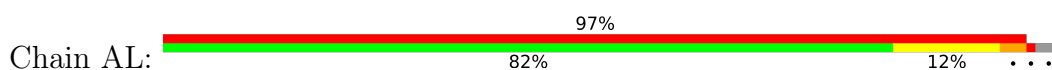




• Molecule 13: 60S acidic ribosomal protein P0



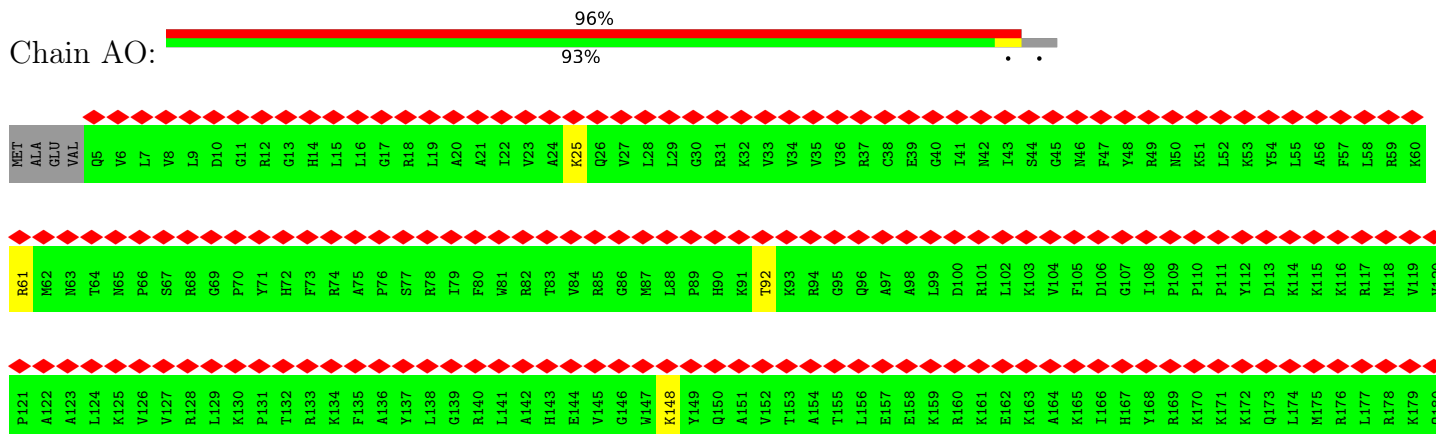
• Molecule 14: 60S ribosomal protein L13

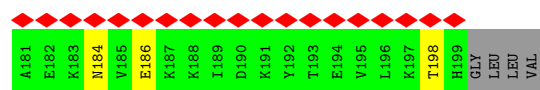


• Molecule 15: 60S ribosomal protein L14

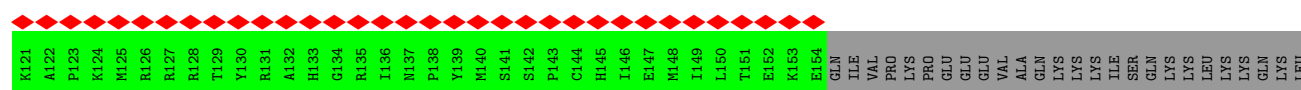
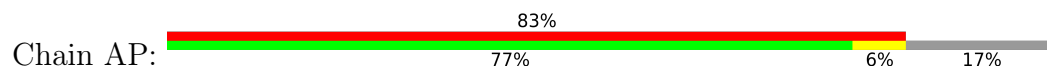
- Molecule 16: 60S ribosomal protein L15

- Molecule 17: 60S ribosomal protein L13a

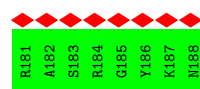
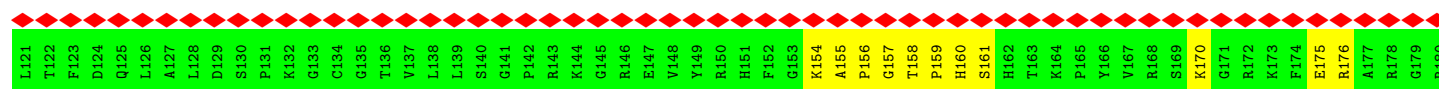
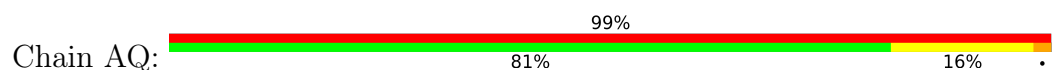




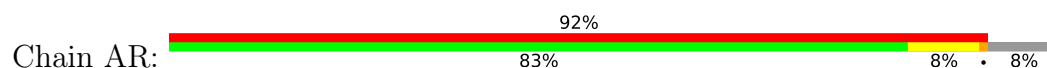
• Molecule 18: 60S ribosomal protein L17

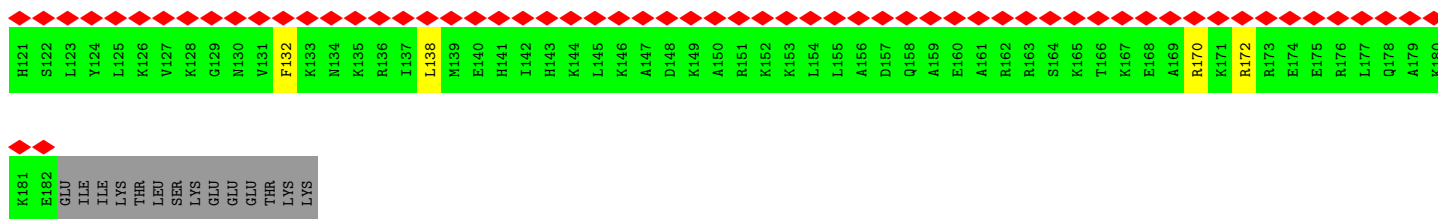


• Molecule 19: 60S ribosomal protein L18



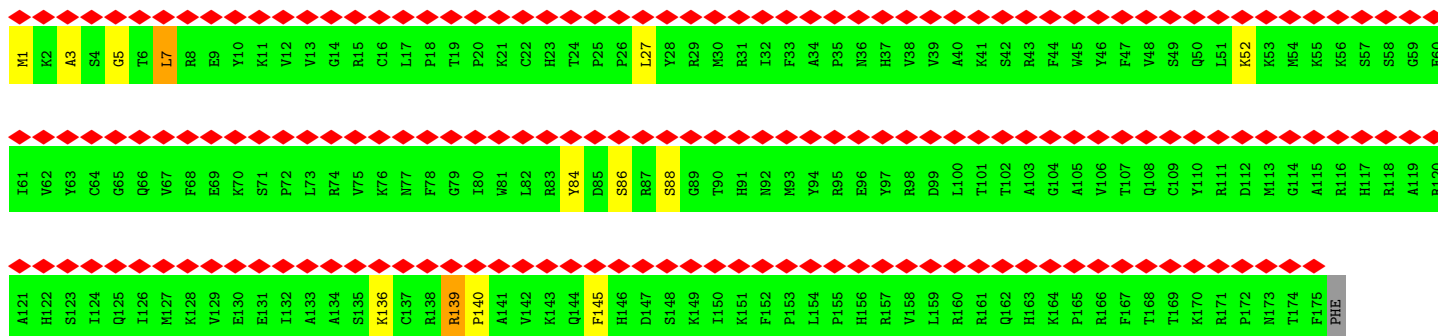
• Molecule 20: 60S ribosomal protein L19





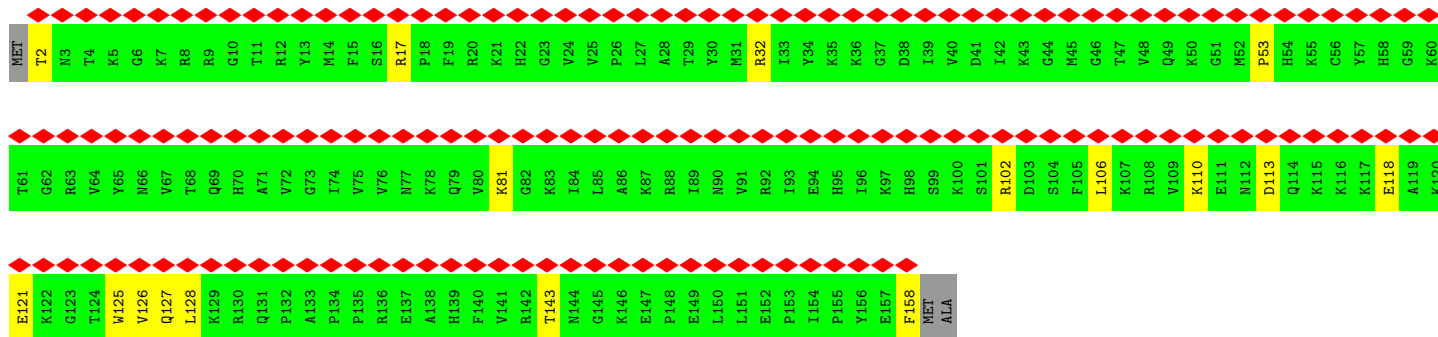
• Molecule 21: 60S ribosomal protein L18a

Chain AS: 99% 92% 6% ..



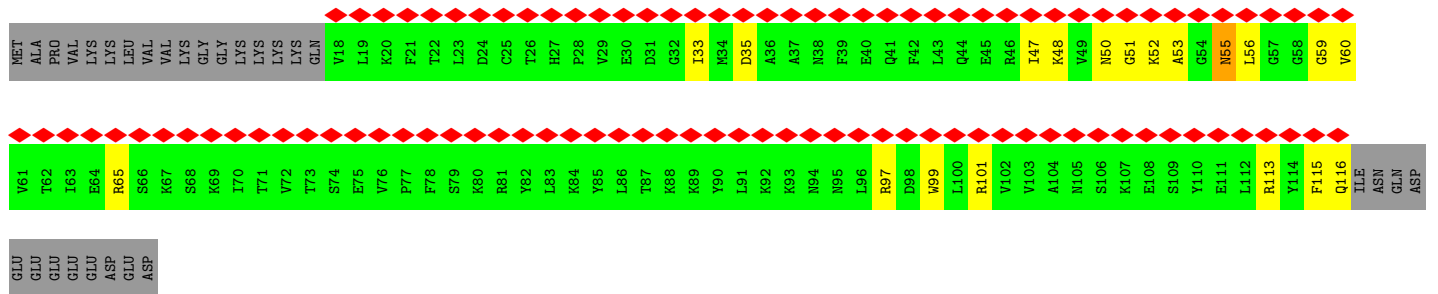
• Molecule 22: 60S ribosomal protein L21

Chain AT: 98% 88% 11% .



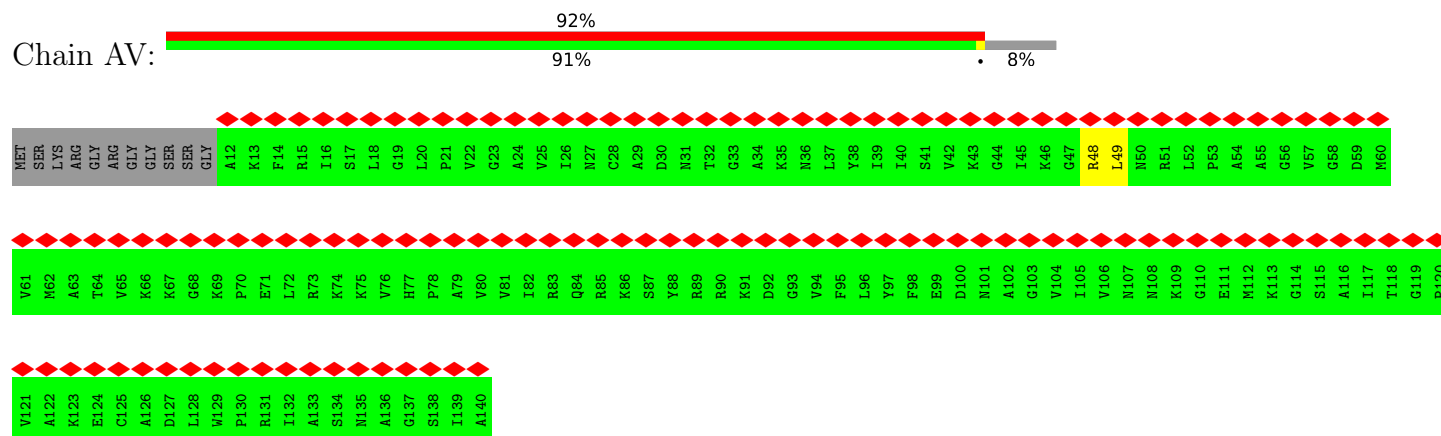
• Molecule 23: 60S ribosomal protein L22

Chain AU: 77% 62% 14% . 23%



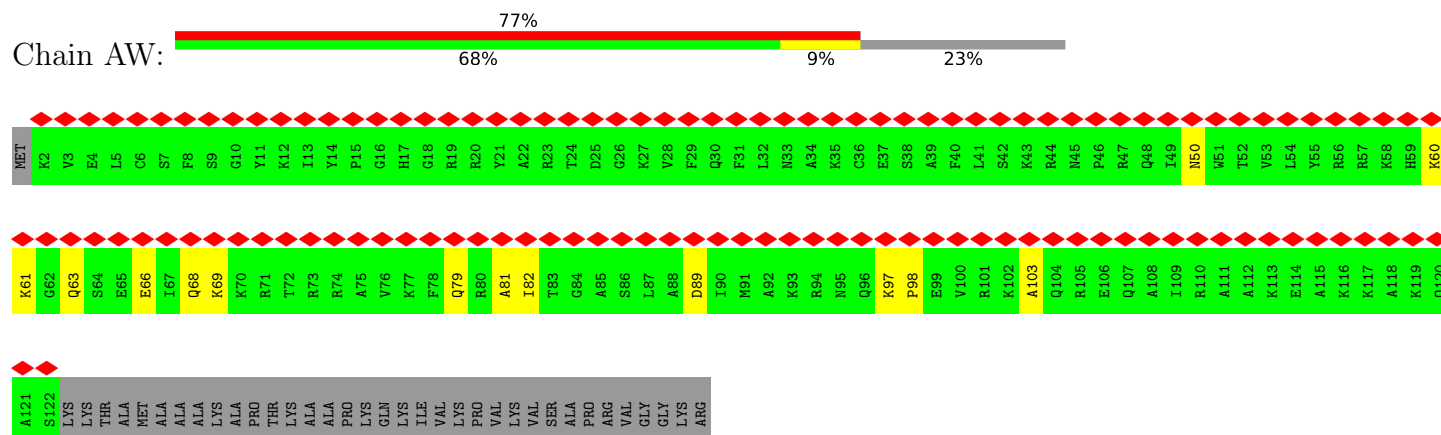
- Molecule 24: 60S ribosomal protein L23

Chain AV:



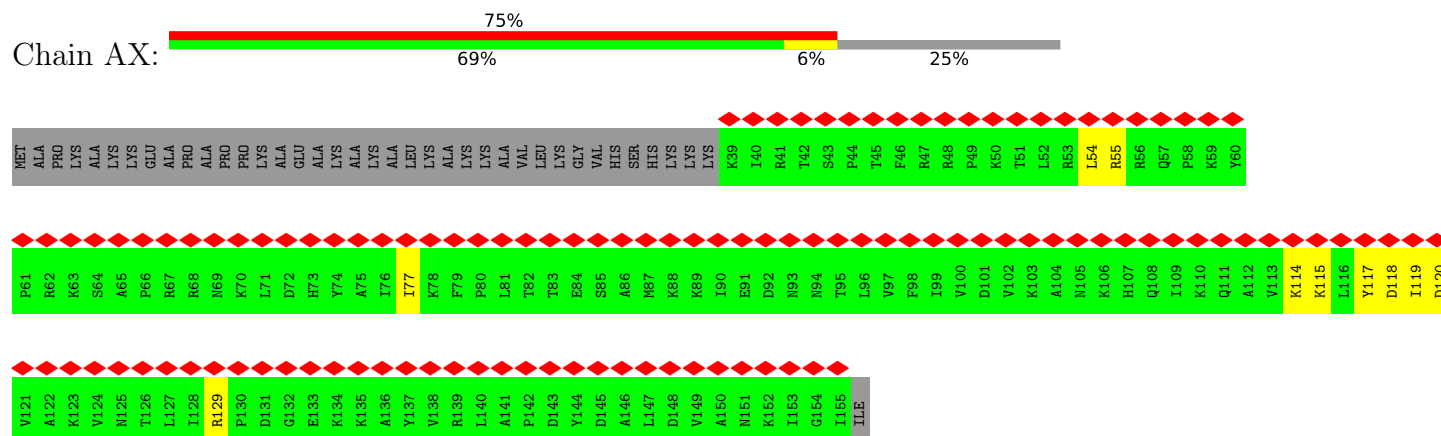
- Molecule 25: 60S ribosomal protein L24

Chain AW:



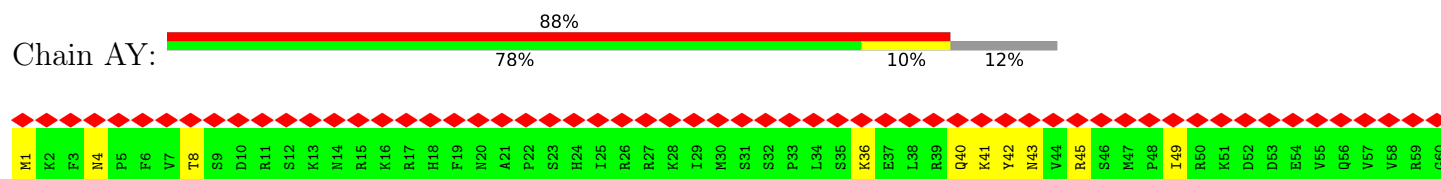
- Molecule 26: 60S ribosomal protein L23a

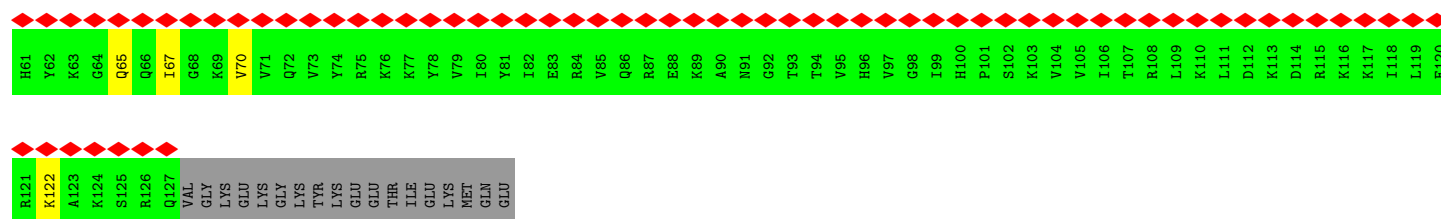
Chain AX:



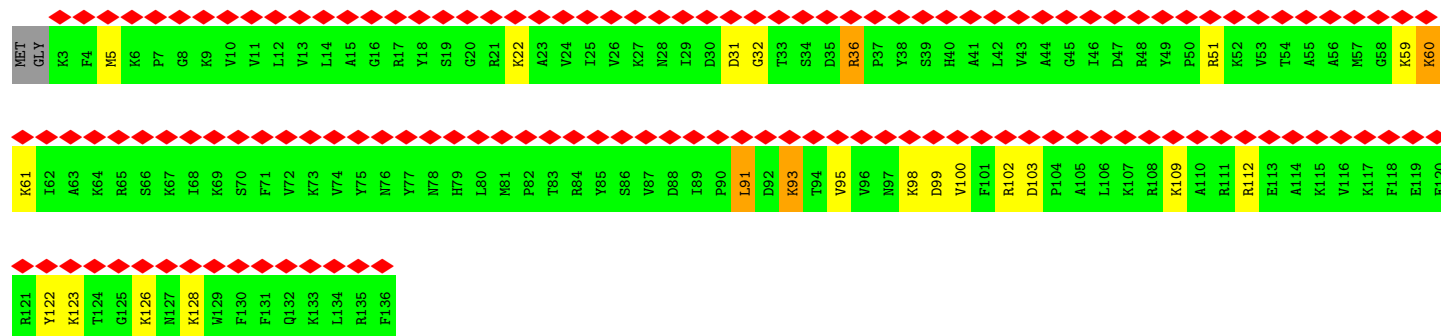
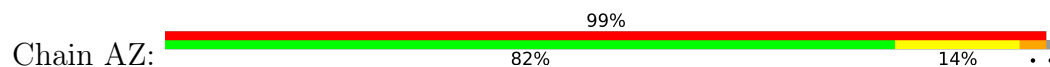
- Molecule 27: 60S ribosomal protein L26

Chain AY:

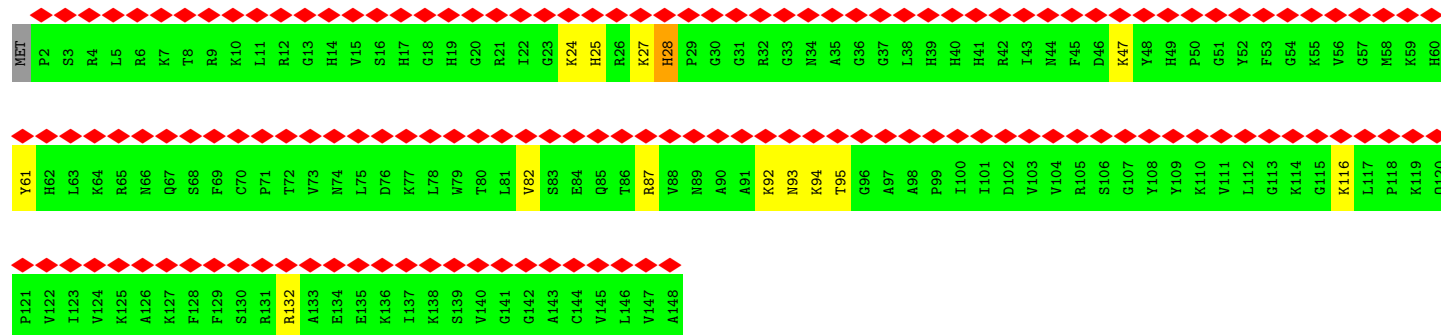
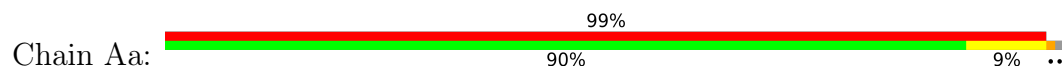




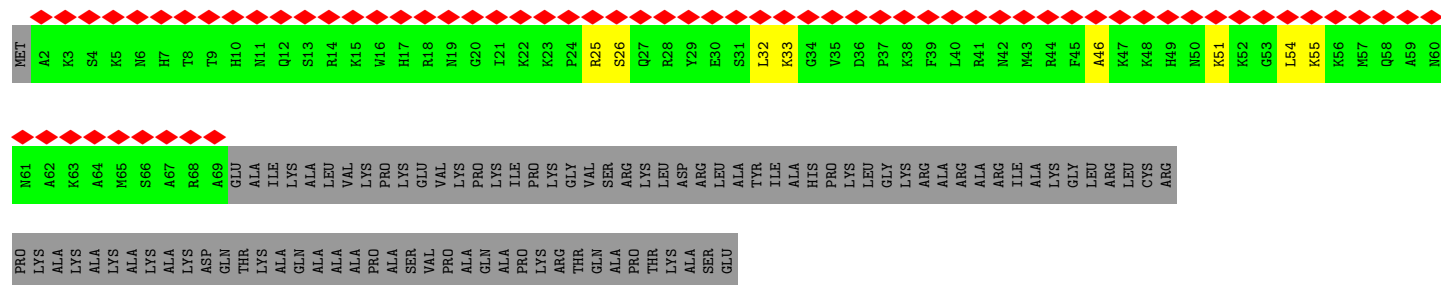
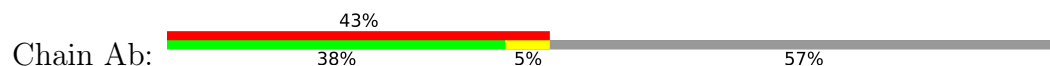
• Molecule 28: 60S ribosomal protein L27



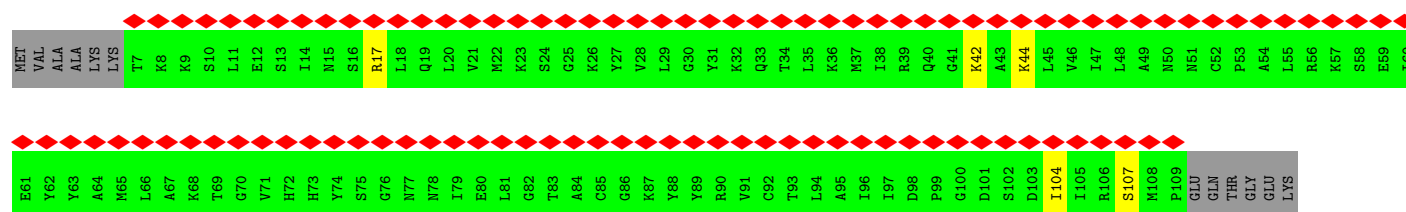
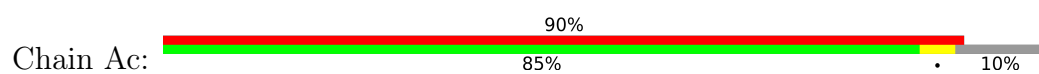
• Molecule 29: 60S ribosomal protein L27a



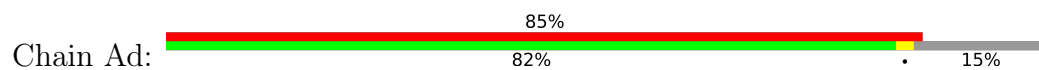
• Molecule 30: 60S ribosomal protein L29



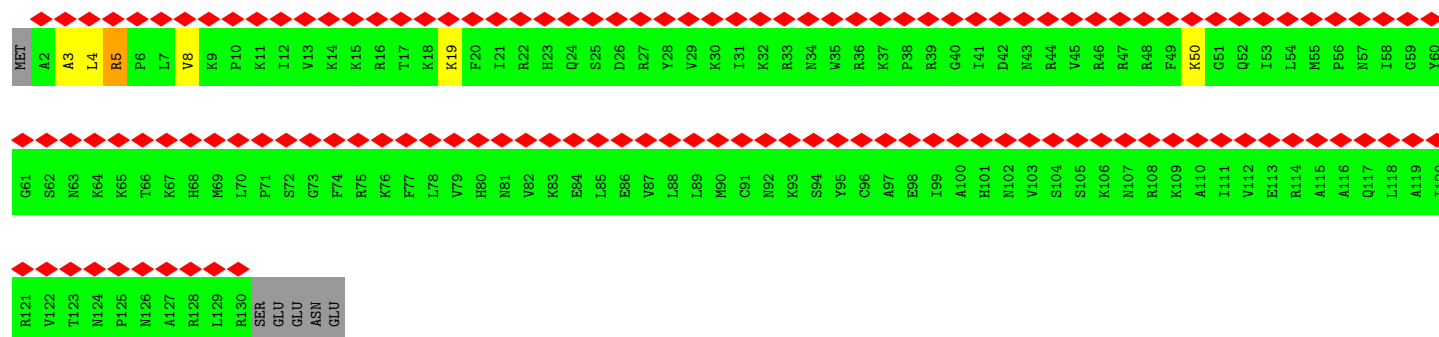
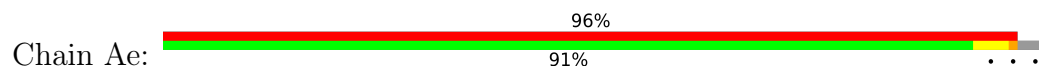
• Molecule 31: 60S ribosomal protein L30



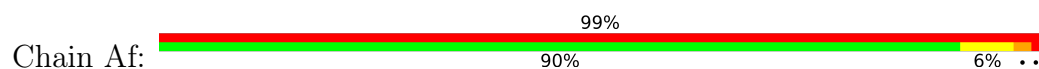
• Molecule 32: 60S ribosomal protein L31



• Molecule 33: 60S ribosomal protein L32

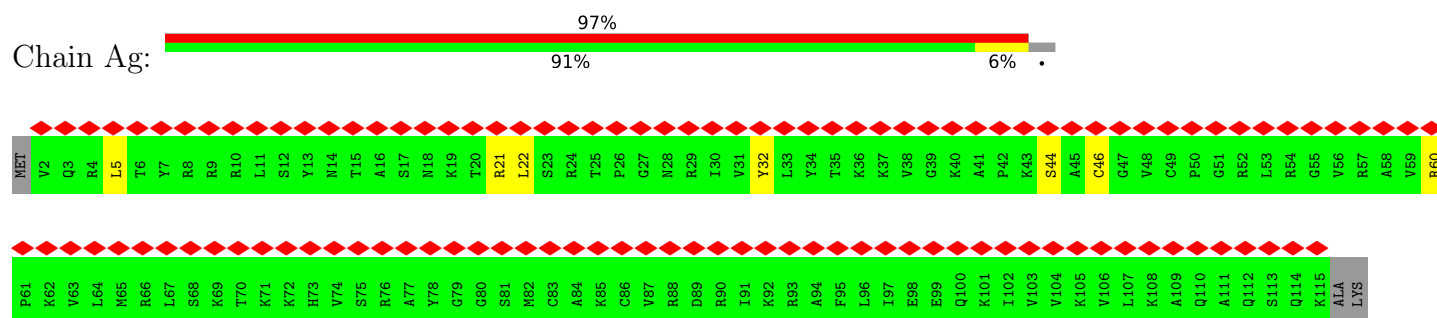


• Molecule 34: 60S ribosomal protein L35a

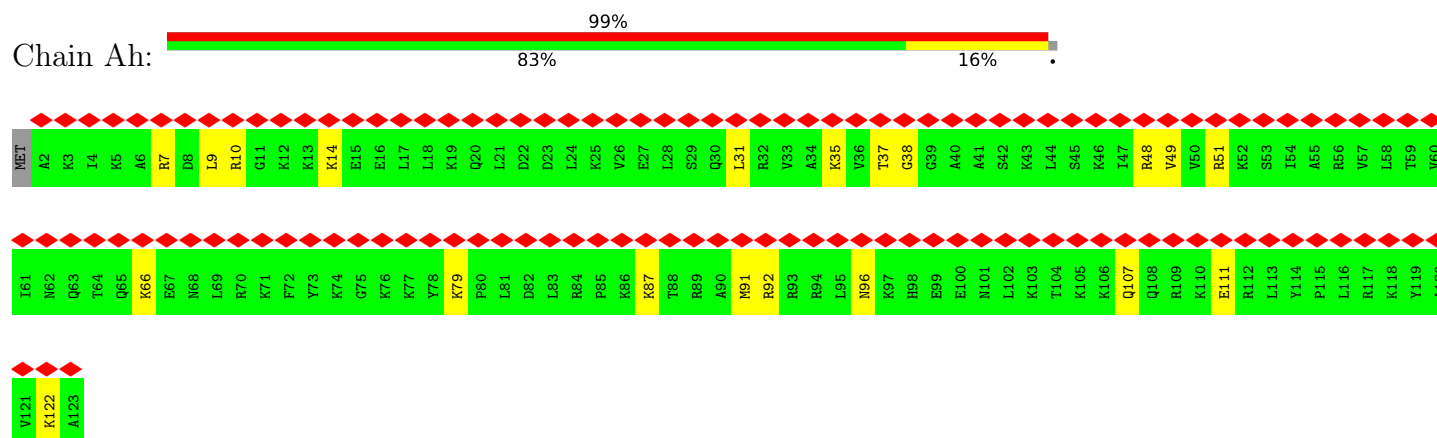


• Molecule 35: 60S ribosomal protein L34

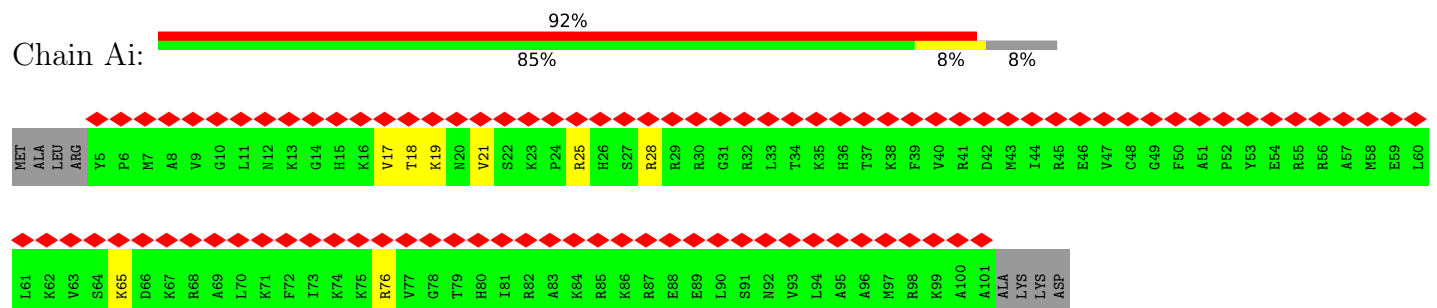




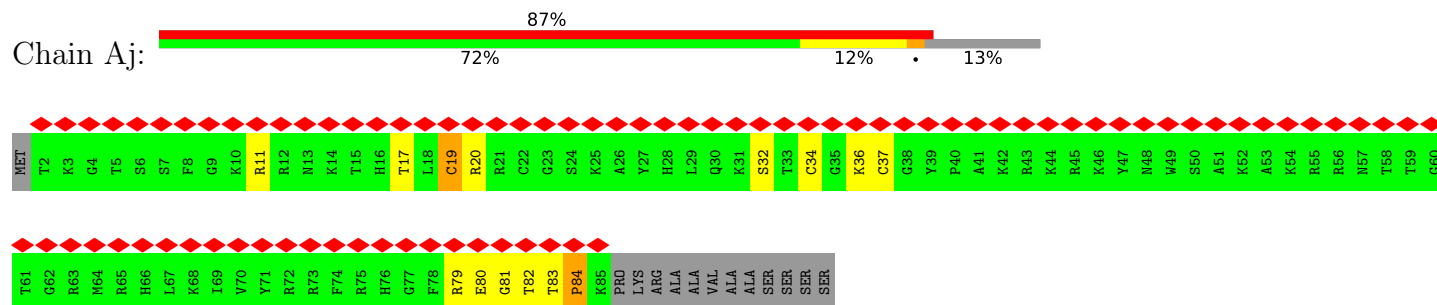
- Molecule 36: 60S ribosomal protein L35



- Molecule 37: 60S ribosomal protein L36



- Molecule 38: 60S ribosomal protein L37

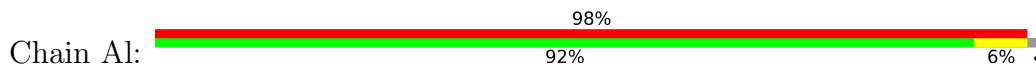


- Molecule 39: 60S ribosomal protein L38

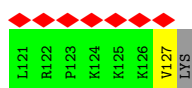
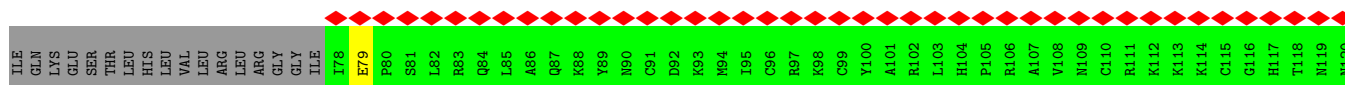




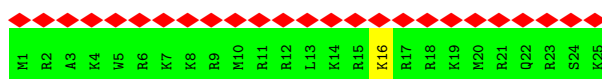
- Molecule 40: 60S ribosomal protein L39



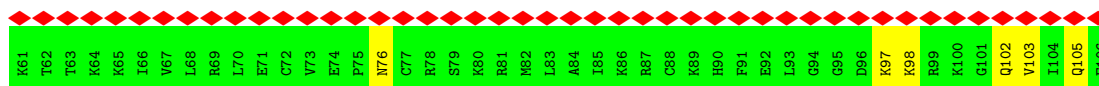
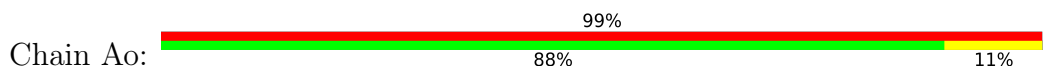
- Molecule 41: Ubiquitin-60S ribosomal protein L40



- Molecule 42: 60S ribosomal protein L41



- Molecule 43: 60S ribosomal protein L36a

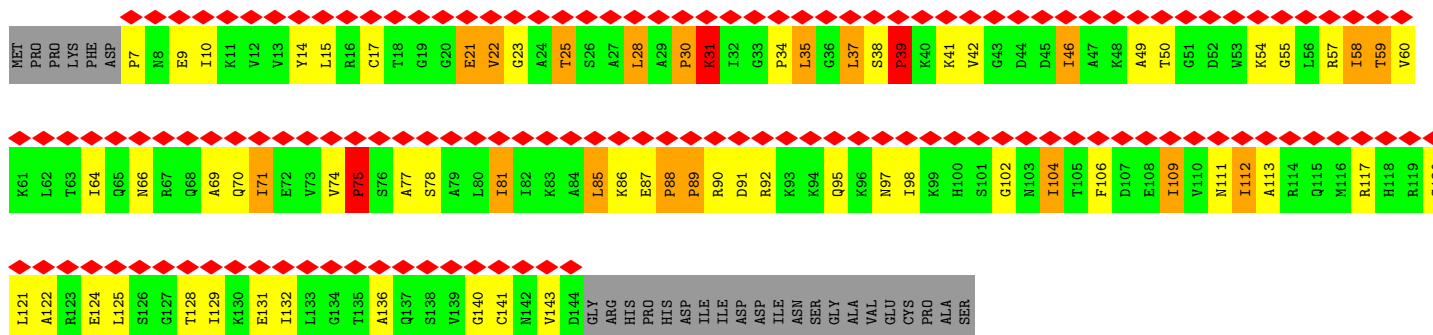
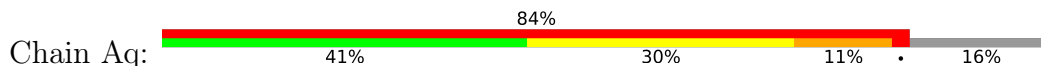


- Molecule 44: 60S ribosomal protein L37a

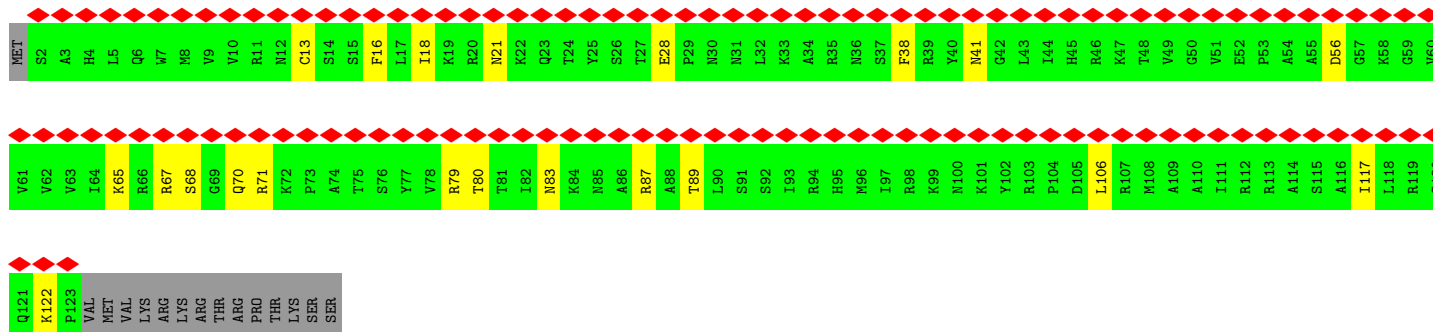
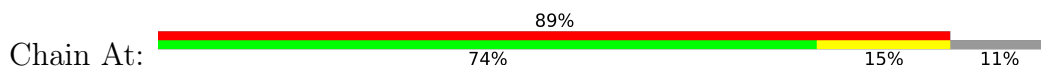




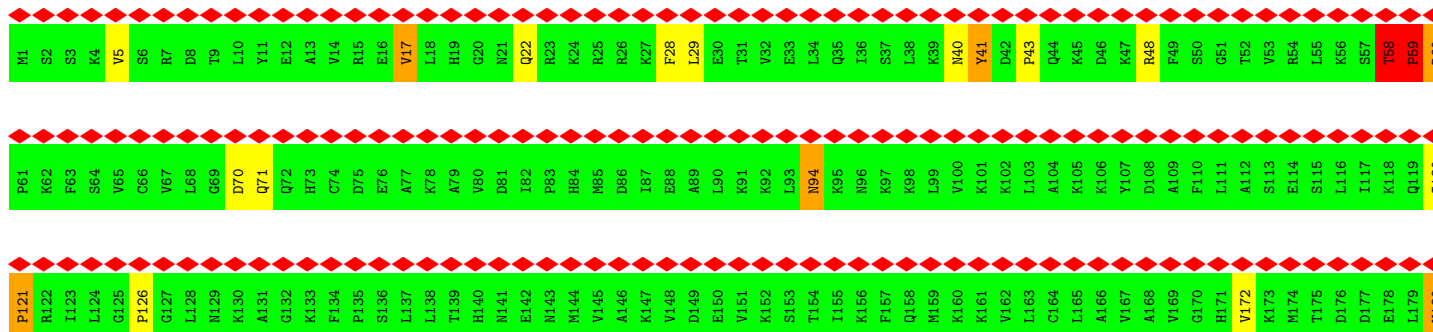
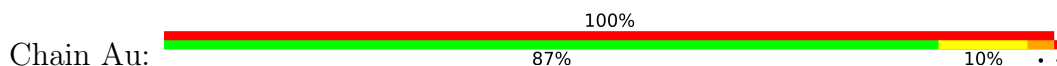
• Molecule 45: 60S ribosomal protein L12

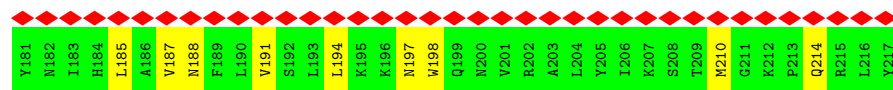


• Molecule 46: 60S ribosomal protein L28

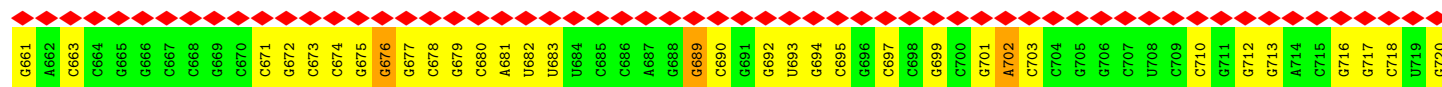
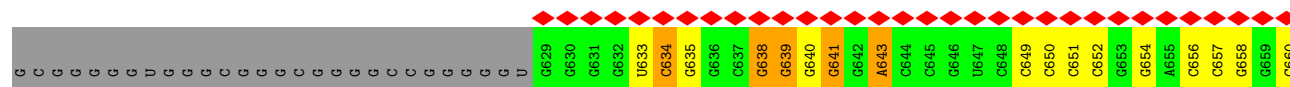
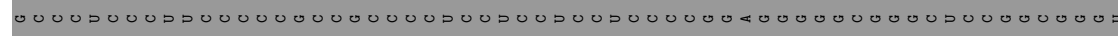
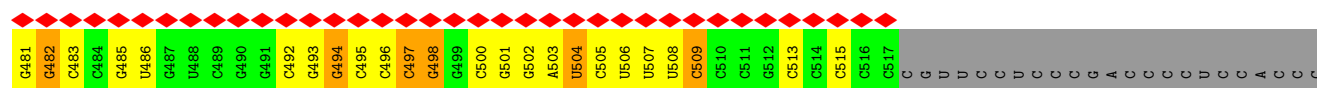
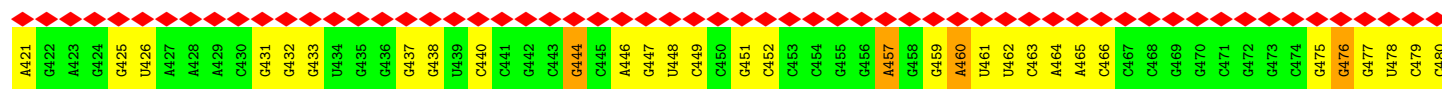
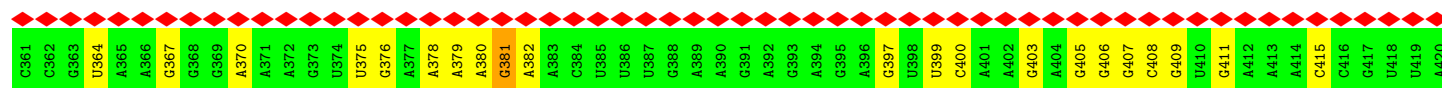
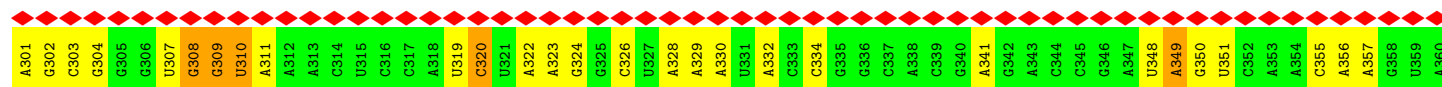
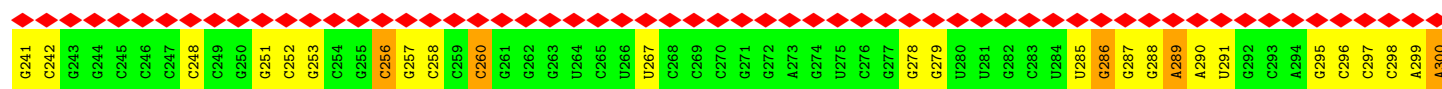
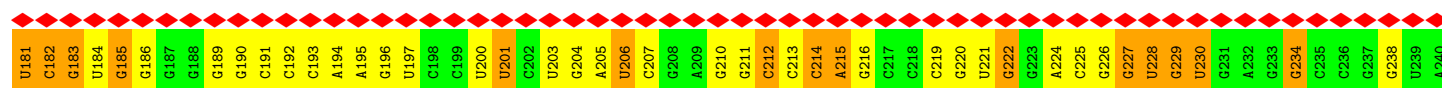
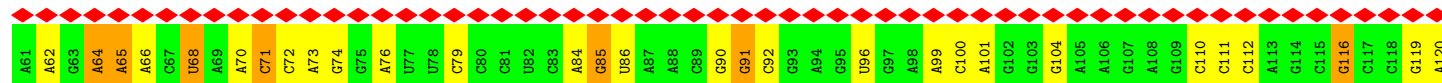
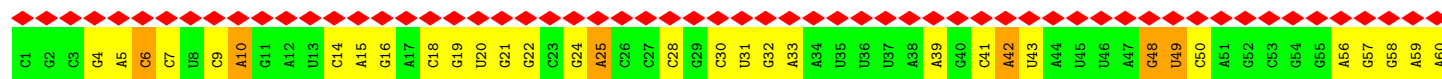
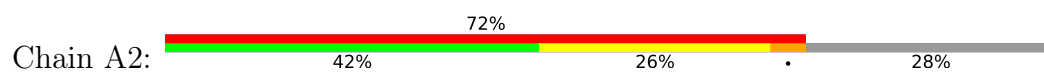


• Molecule 47: 60S ribosomal protein L10a





## • Molecule 48: 28S ribosomal RNA





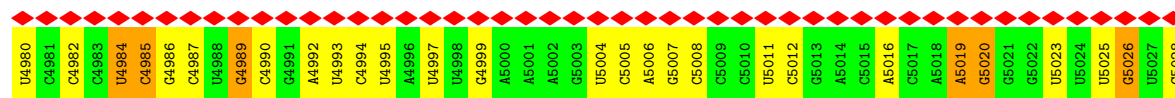


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**PDB**  
PROTEIN DATA BANK

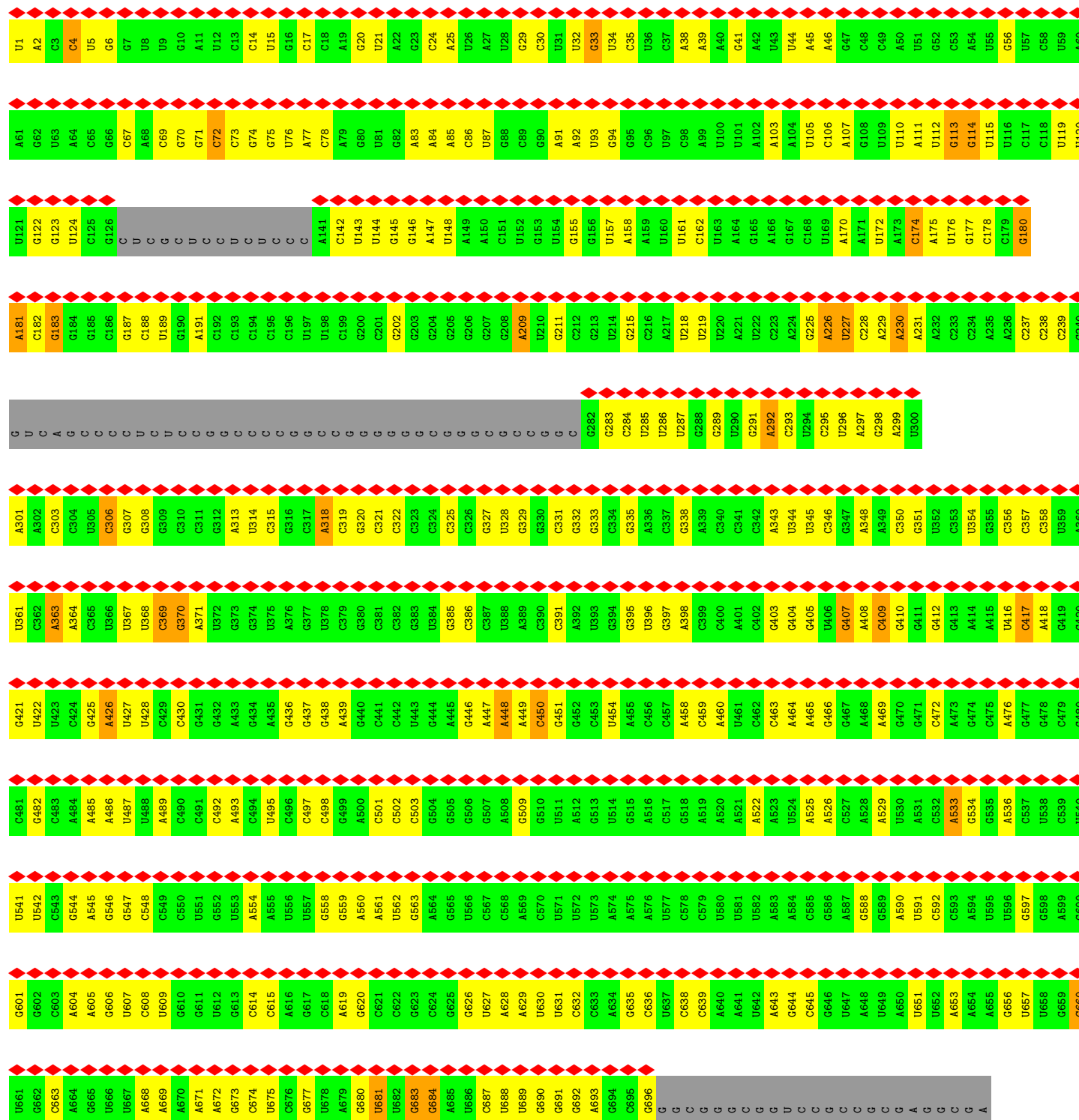
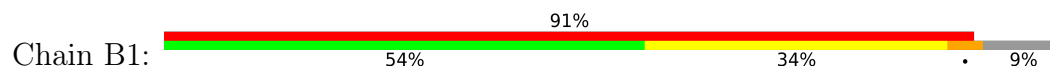




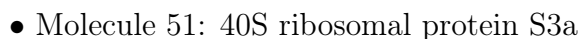
WORLDWIDE  
**PDB**  
PROTEIN DATA BANK



● Molecule 49: 18S ribosomal RNA



U1441	U1442	C1443	U1444	U1445	A1446	G1447	A1448	U1449	G1450	G1451	A1452	C1453	A1454	A1455	G1456	U1457	G1458	G1459	C1460	G1461	U1462	U1463	C1464	A1465	G1466	C1467	U1468	A1469	C1470	C1471	C1472	G1473	A1474	G1475	A1476	U1477	U1478	G1479	A1480	G1481	C1482	A1483	A1484	U1485	A1486	A1487	C1488	A1489	G1490	G1491	U1492	C1493	U1494	G1495	U1496	U1497	A1498	U1499	G1500
G1381	A1382	A1383	C1384	G1385	A1386	G1387	A1388	C1389	U1390	C1391	U1392	G1393	G1394	C1395	A1396	U1397	G1398	C1399	U1400	A1401	A1402	C1403	U1404	A1405	G1406	U1407	U1408	U1409	C1410	G1411	C1412	G1413	A1414	C1415	C1416	C1417	C1418	C1419	G1420	A1421	G1422	C1423	A1424	G1425	U1426	C	C	C	C	U	C	C	C	A1438	A1439	C1440			
G1321	G1322	U1323	G1324	U1325	G1326	G1327	G1328	U1329	G1330	C1331	A1332	U1333	G1334	G1335	C1336	C1337	G1338	U1339	U1340	C1341	U1342	U1343	A1344	G1345	U1346	U1347	G1348	G1349	U1350	G1351	C1352	A1353	G1354	C1355	G1356	A1357	U1358	U1359	U1360	G1361	U1362	C1363	U1364	G1365	G1366	U1367	U1368	C1369	A1370	U1371	U1372	C1373	C1374	G1375	A1376	U1377	A1378	A1379	C1380
C1261	C1262	U1263	C1264	G1265	C1266	C1267	C1268	U1269	G1270	C1271	C1272	C1273	G1274	C1275	A1276	C1277	A1278	C1279	G1280	U1281	A1282	C1283	A1284	G1285	G1286	A1287	U1288	U1289	G1290	A1291	C1292	C1293	G1294	A1295	U1296	U1297	G1298	A1299	U1300	A1301	G1302	C1303	U1304	C1305	U1306	U1307	U1308	C1309	U1310	C1311	G1312	A1313	U1314	U1315	C1316	C1317	U1318	U1319	G1320
G1141	G1142	A1143	A1144	A1145	C1146	C1147	A1148	A1149	A1150	G1151	U1152	C1153	U1154	U1155	U1156	G1157	G1158	G1159	U1160	U1161	C1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	A1170	G1171	U1172	A1173	U1174	G1175	G1176	U1177	U1178	G1179	C1180	A1181	A1182	A1183	G1184	C1185	U1186	G1187	A1188	A1189	A1190	C1191	U1192	U1193	A1194	A1195	A1196	G1197	G1198	A1199	A1200
U1081	A1082	A1083	A1084	C1085	G1086	A1087	U1088	G1089	C1090	C1091	G1092	A1093	C1094	C1095	G1096	G1097	C1098	G1099	A1100	U1101	G1102	C1103	G1104	G1105	C1106	G1107	G1108	C1109	G1110	U1111	U1112	C1113	U1114	U1115	C1116	C1117	C1118	A1119	U1120	G1121	A1122	C1123	G1124	C1125	G1126	C1127	C1128	G1129	U1130	G1131	C1132	A1133	G1134	C1135	U1136	U1137	C1138	C1139	G1140
U1021	U1022	A1023	A1024	U1025	C1026	A1027	A1028	G1029	A1030	A1031	C1032	G1033	A1034	A1035	A1036	G1037	U1038	C1039	G1040	G1041	A1042	G1043	G1044	U1045	U1046	C1047	G1048	A1049	A1050	G1051	A1052	C1053	G1054	A1055	U1056	C1057	A1058	G1059	A1060	U1061	A1062	C1063	G1064	G1065	U1066	C1067	G1068	U1069	A1070	G1071	U1072	U1073	C1074	C1075	G1076	A1077	C1078	C1079	A1080
G961	A962	A963	A964	U965	U966	C967	U968	U969	G970	G971	A972	C973	C974	G975	G976	C977	G978	C979	A980	A981	G982	A983	C984	G985	G986	A987	G988	C989	A990	G991	A992	G993	C994	G995	A996	A997	A998	G999	C1000	A1001	U1002	U1003	U1004	G1005	C1006	C1007	A1008	A1009	G1010	A1011	A1012	U1013	G1014	U1015	U1016	U1017	U1018	C1019	U960
G901	G902	A903	A904	C905	U906	G907	A908	G909	G910	C911	C912	A913	U914	G915	A916	U917	U918	A919	A920	G921	A922	G923	G924	G925	A926	C927	G928	C929	A930	C931	G932	G933	G934	G935	G936	C937	A938	U939	U940	C941	G942	U943	A944	U945	U946	G947	U948	U949	G950	C951	G952	U953	U954	A955	G956	A957	G958	G959	C960
G841	C842	C843	U844	G845	G846	A847	U848	U849	C850	C851	G852	A853	A854	G855	G856	U857	A858	G859	A860	A861	A862	U863	A864	A865	U866	G867	G868	A869	A870	U871	A872	G873	U874	A875	C876	C877	G878	C879	G880	G881	U882	U883	A884	A885	A886	U887	U888	U889	U890	G891	U892	U893	G894	G895	U896	U897	U898	U899	C900
C	C	C	A	C	C	C	C	C	U	C	C	A795	G796	C797	G798	U799	U800	U801	A802	C803	U804	U805	U806	G807	U808	A809	A810	A811	A812	A813	U814	U815	U816	G817	A818	G819	U820	G821	U822	U823	C824	A825	A826	A827	G828	C829	A830	G831	G832	C833	C834	G835	G836	A837	G838	C839	C840		
G	C	C	A	C	C	C	C	C	U	C	C	G737	C738	C739	C740	C741	U742	U743	G744	C745	C746	U747	C748	U749	C750	G751	G	C	C	C	C	C	C	U	C	C	A	U	U	G	C	U	U	U	A	G	C	C	U	U	A	G	U	U	U	U			



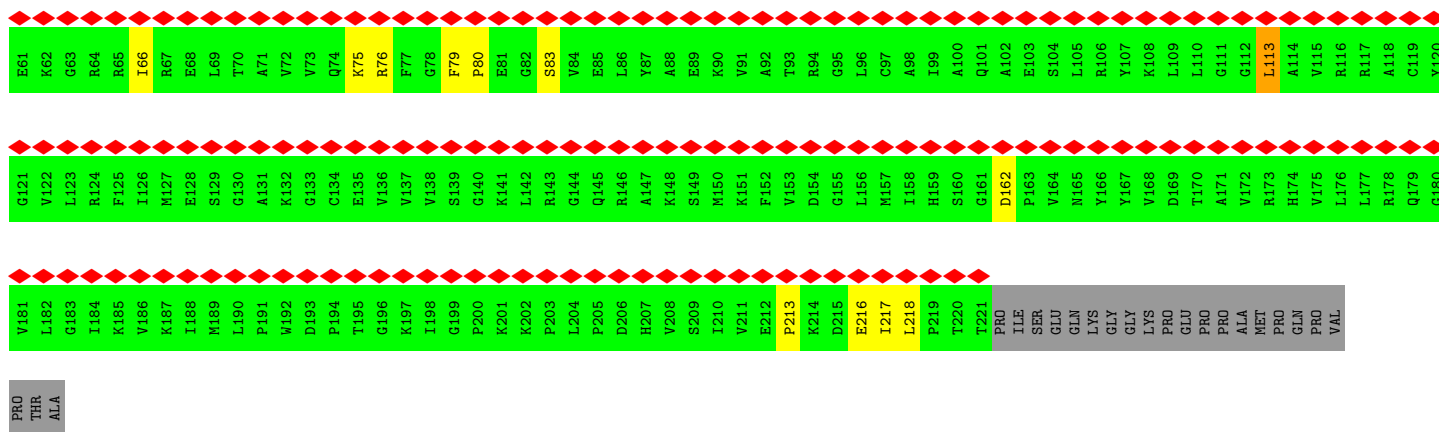
Chain BB:

- Molecule 52: 40S ribosomal protein S2

Chain BC:

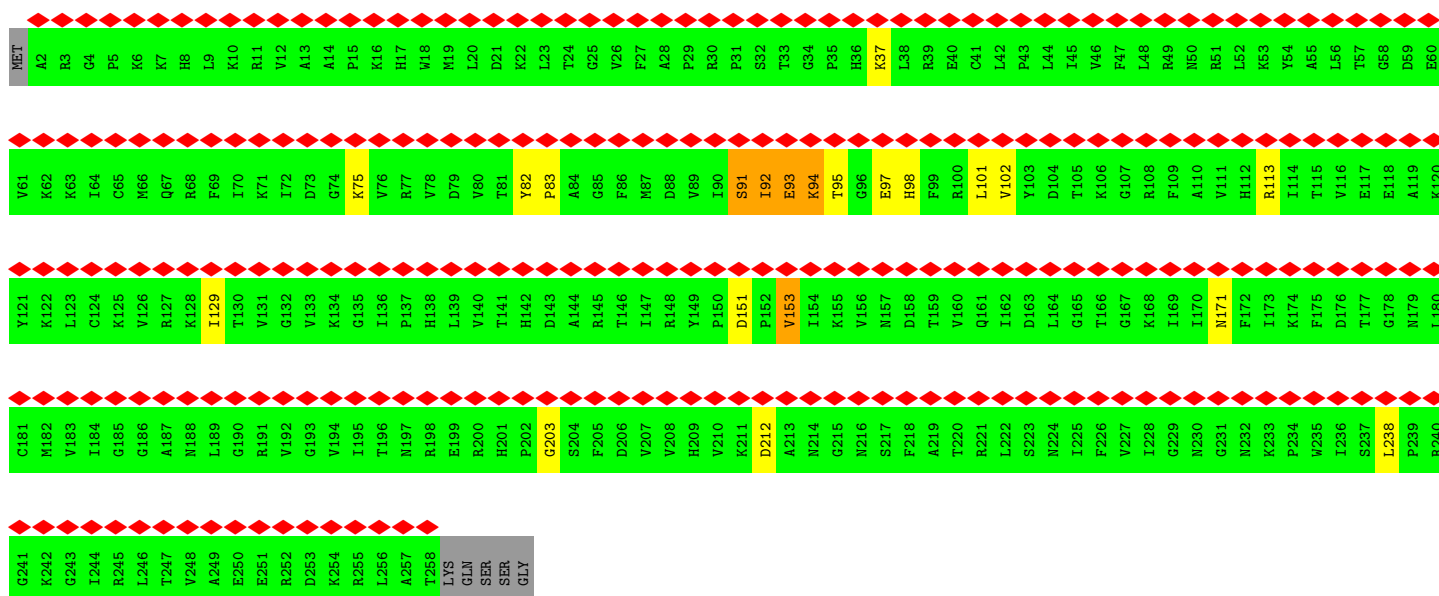
- Molecule 53: 40S ribosomal protein S3

Chain BD:



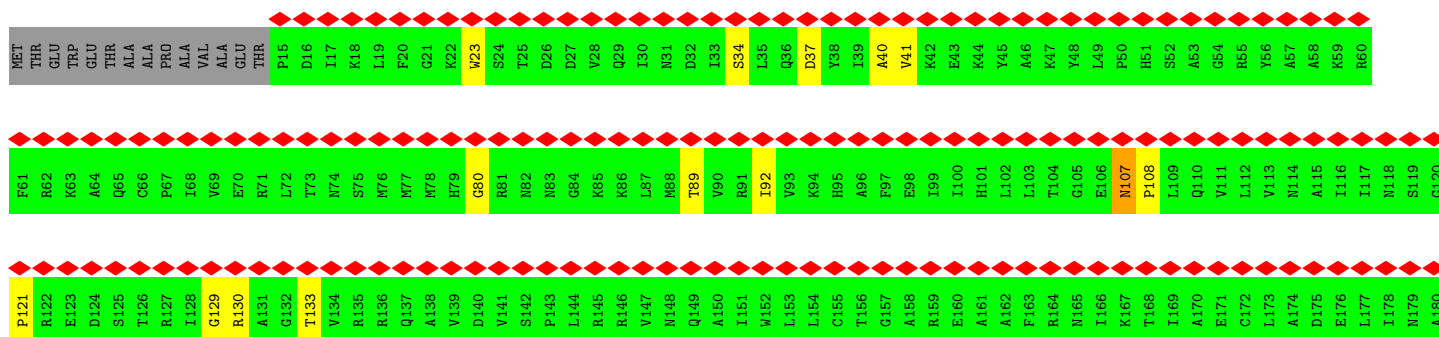
• Molecule 54: 40S ribosomal protein S4, Y isoform 1

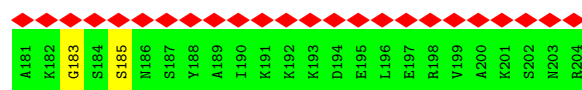
Chain BE:



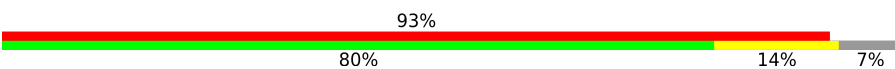
• Molecule 55: 40S ribosomal protein S5

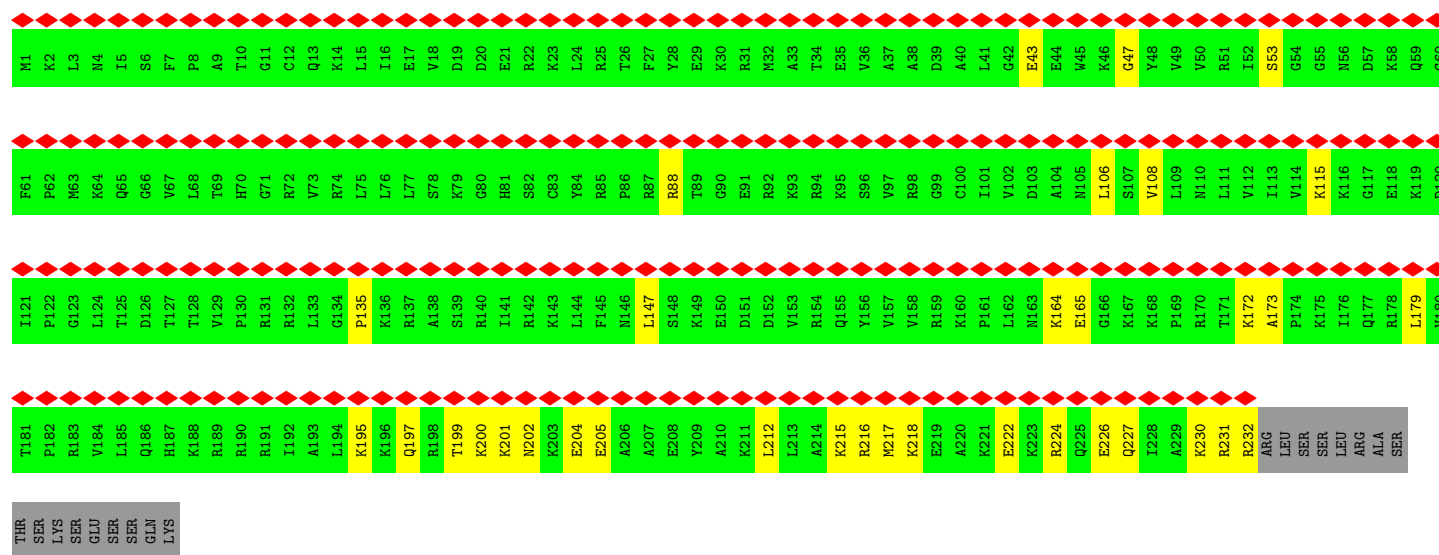
Chain BF:



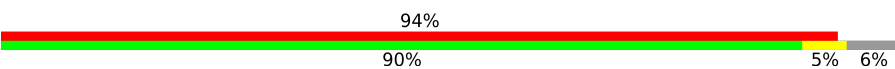


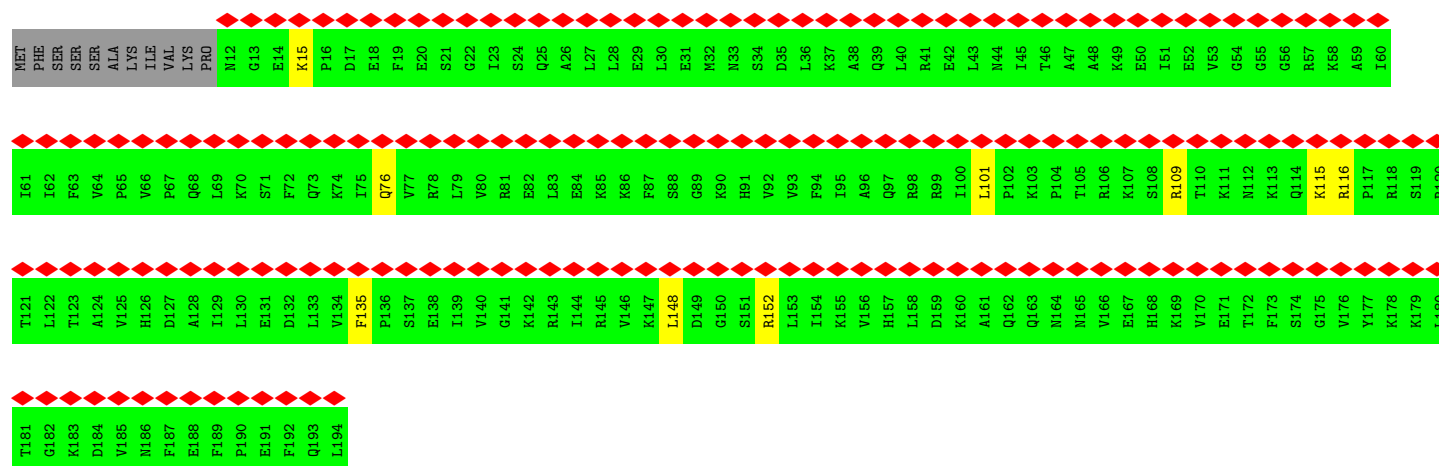
• Molecule 56: 40S ribosomal protein S6

Chain BG: 



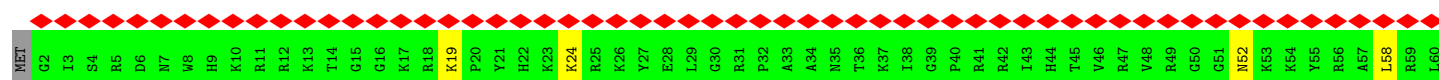
• Molecule 57: 40S ribosomal protein S7

Chain BH: 



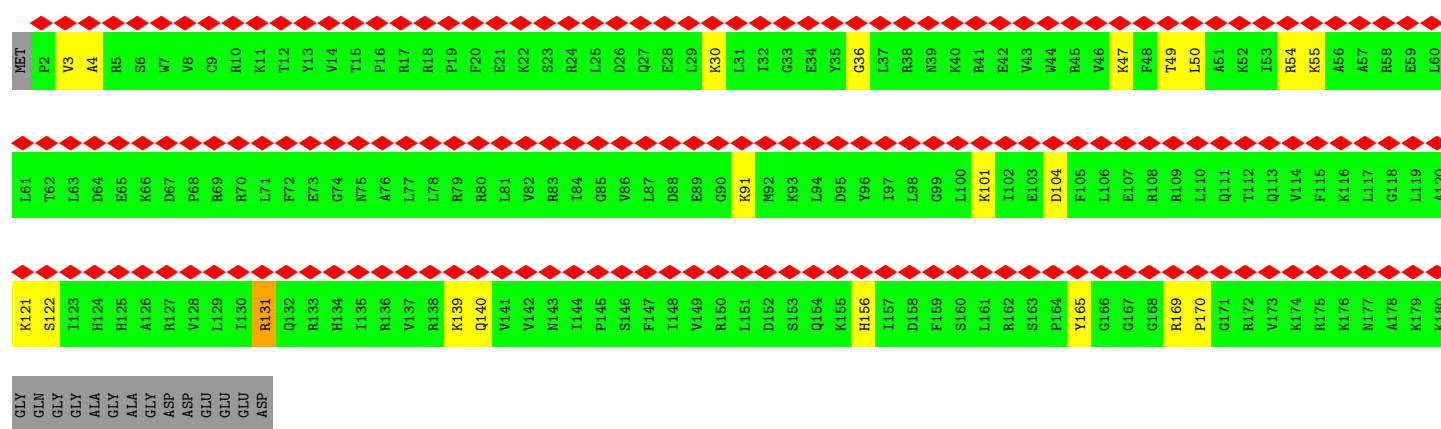
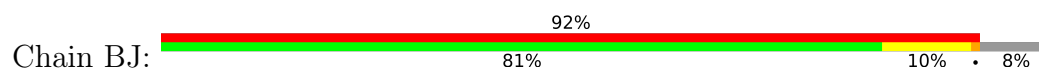
• Molecule 58: 40S ribosomal protein S8

Chain BI: 

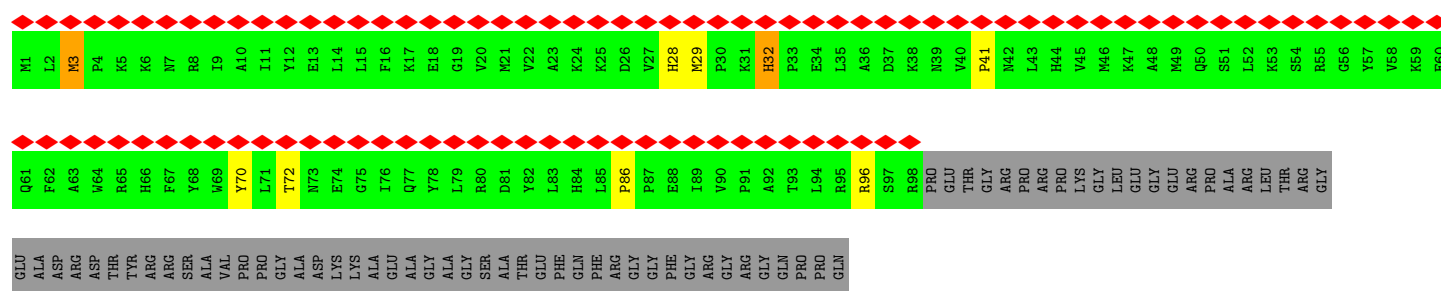




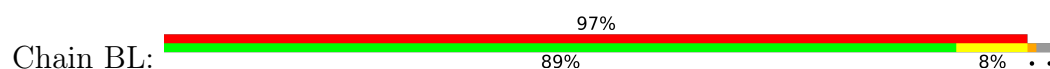
• Molecule 59: 40S ribosomal protein S9



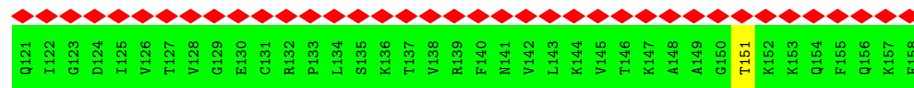
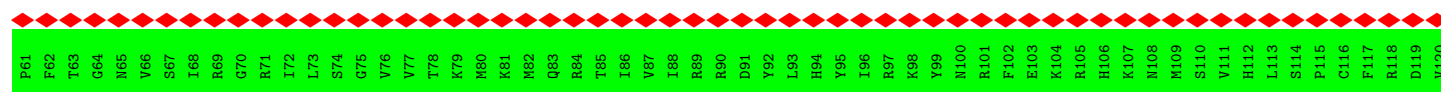
• Molecule 60: 40S ribosomal protein S10



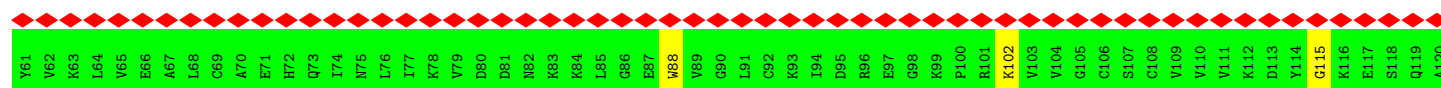
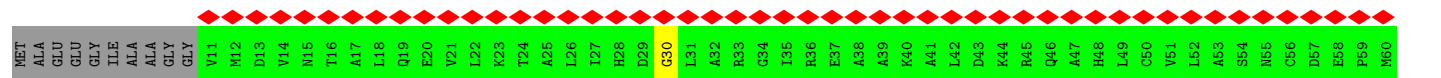
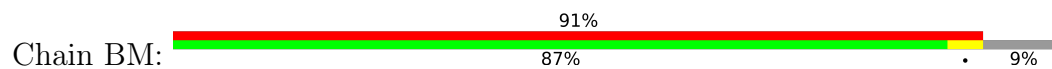
• Molecule 61: 40S ribosomal protein S11



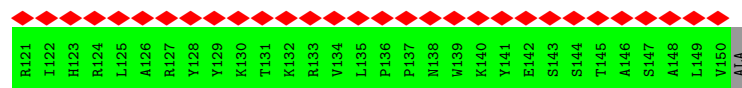
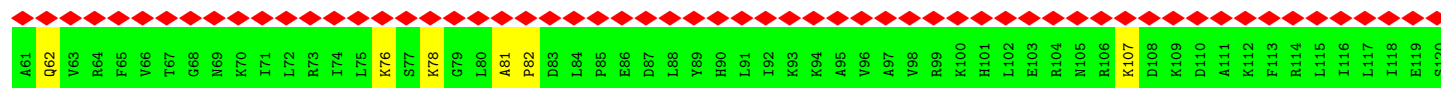
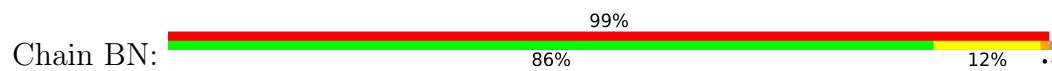




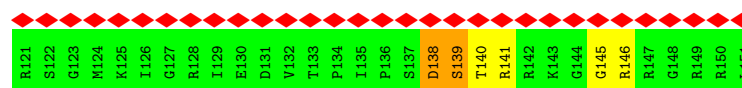
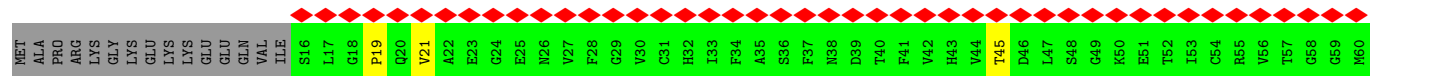
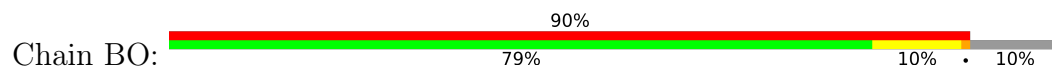
• Molecule 62: 40S ribosomal protein S12



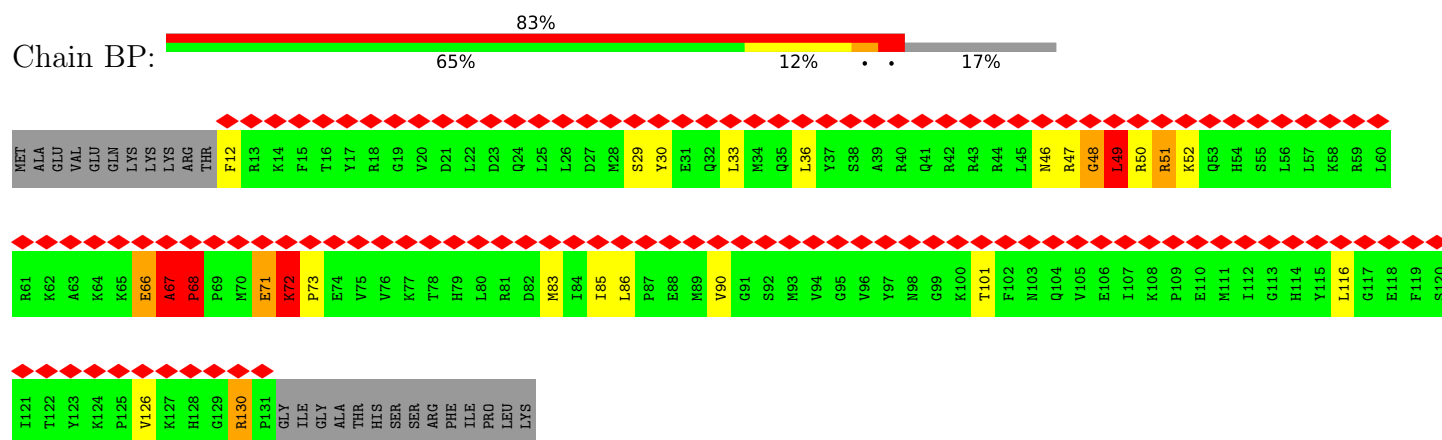
• Molecule 63: 40S ribosomal protein S13



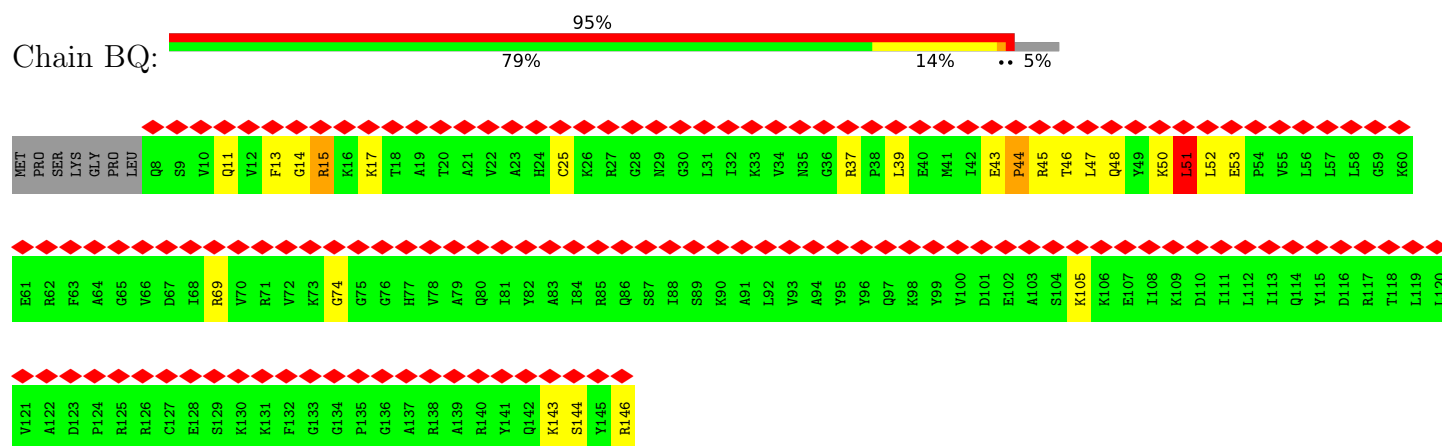
• Molecule 64: 40S ribosomal protein S14



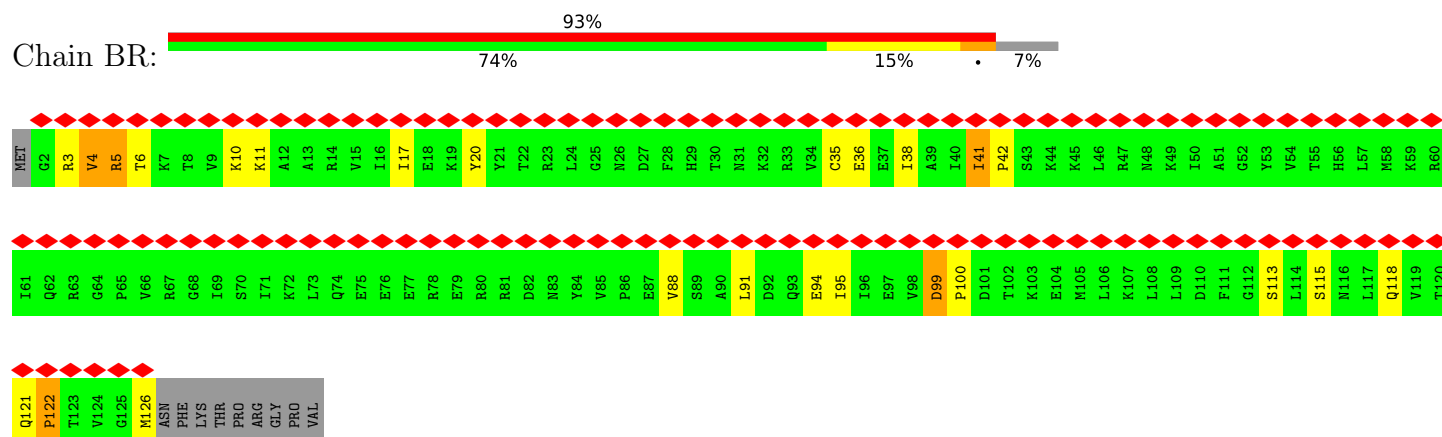
- Molecule 65: 40S ribosomal protein S15



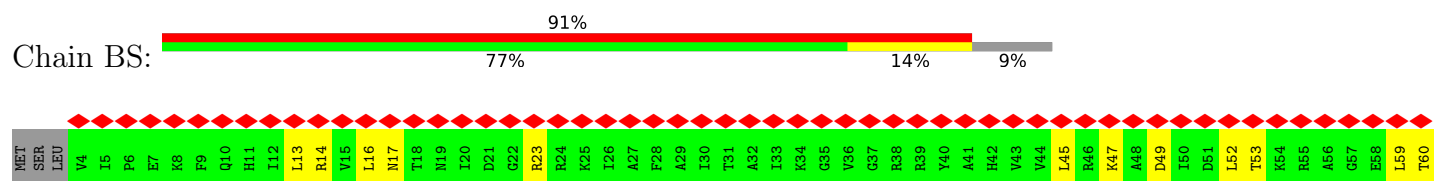
- Molecule 66: 40S ribosomal protein S16

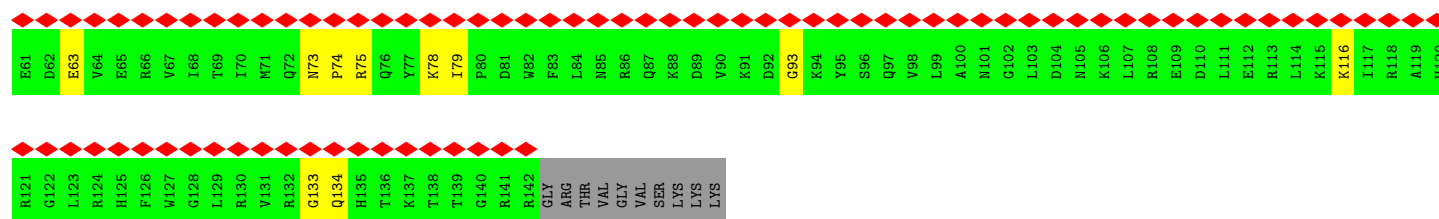


- Molecule 67: 40S ribosomal protein S17-like

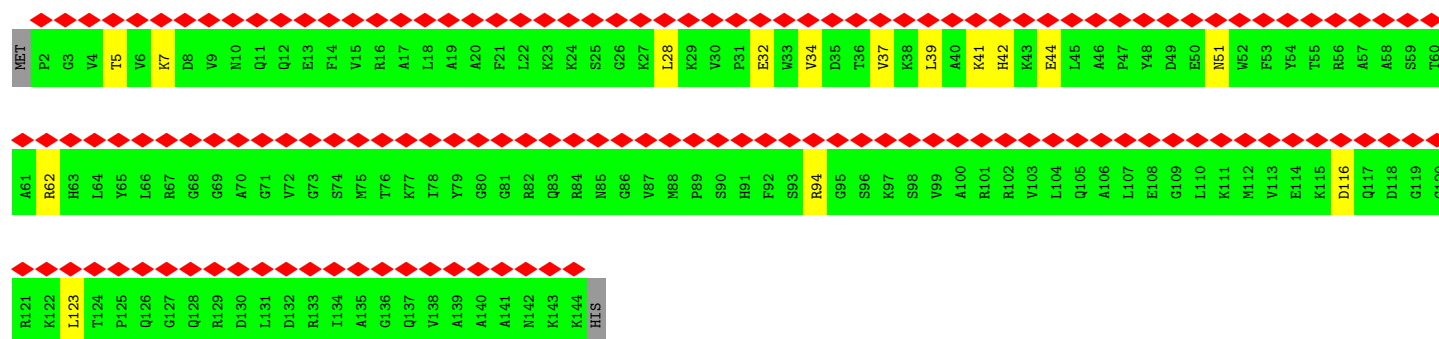
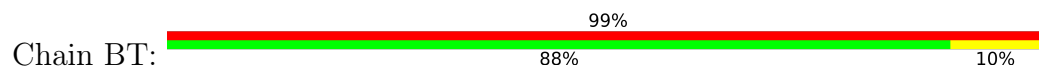


- Molecule 68: 40S ribosomal protein S18

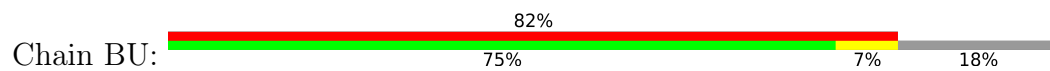




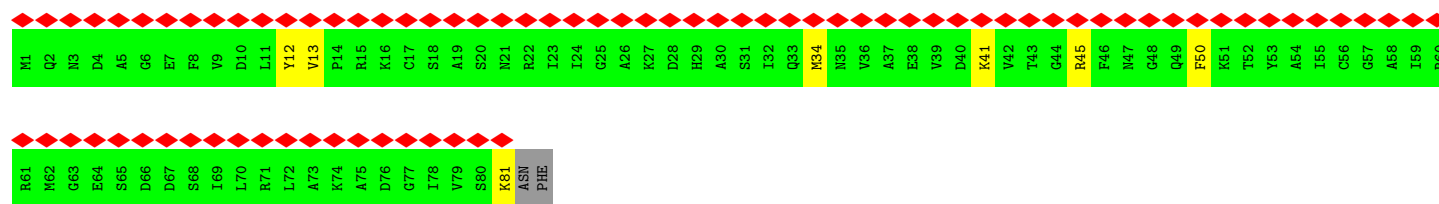
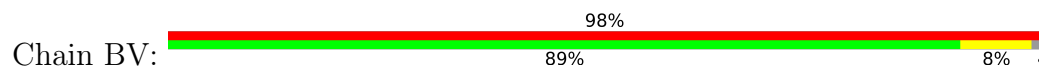
• Molecule 69: 40S ribosomal protein S19



• Molecule 70: 40S ribosomal protein S20

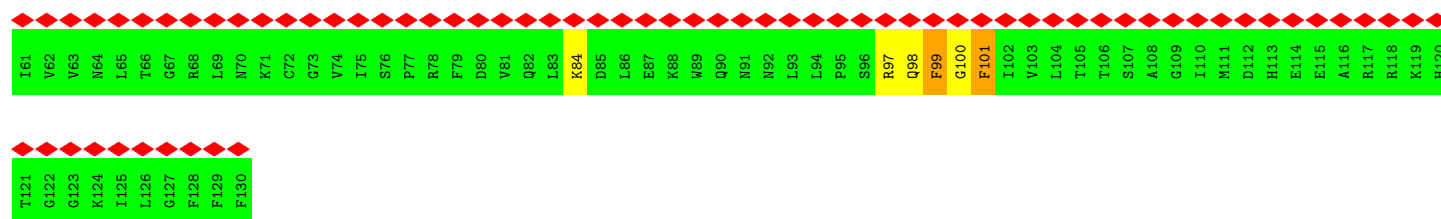


• Molecule 71: 40S ribosomal protein S21

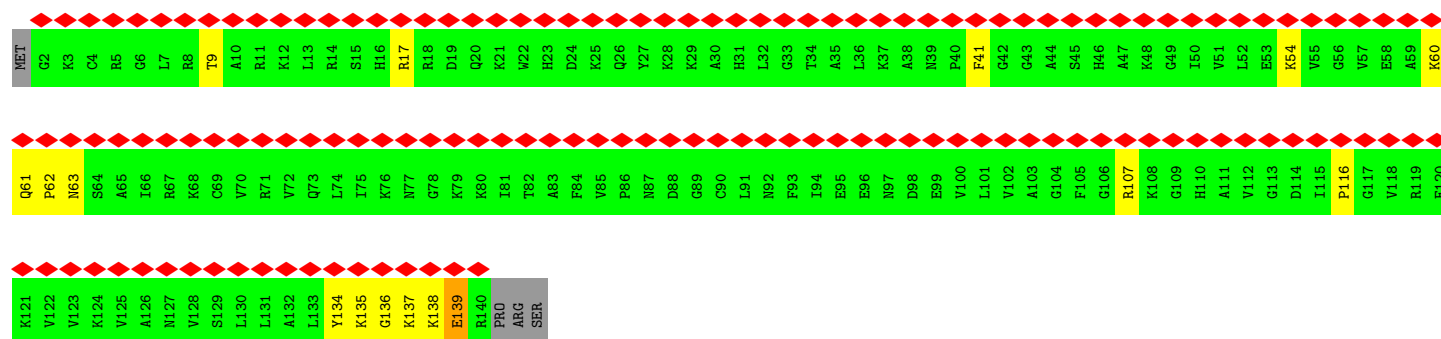
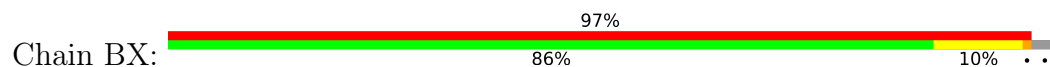


• Molecule 72: 40S ribosomal protein S15a

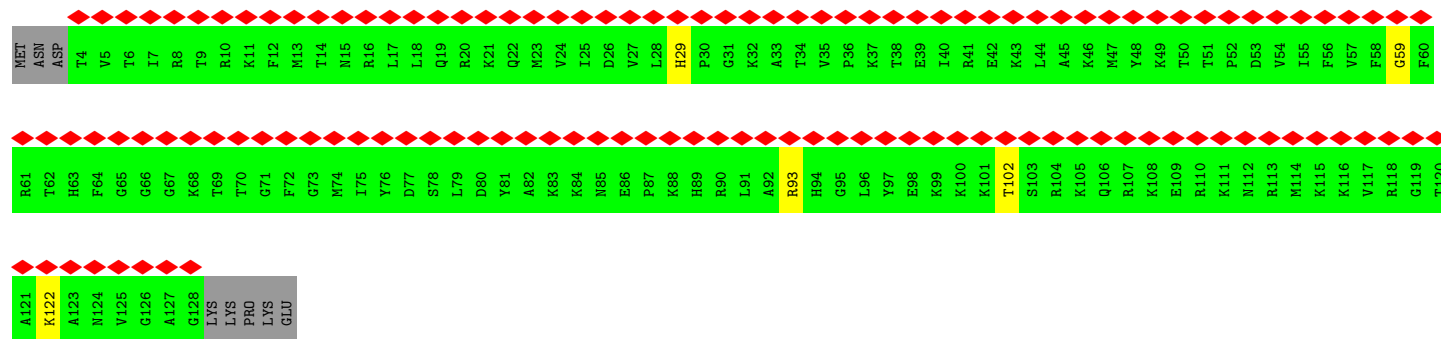
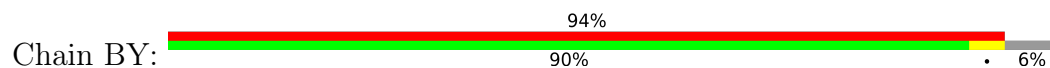




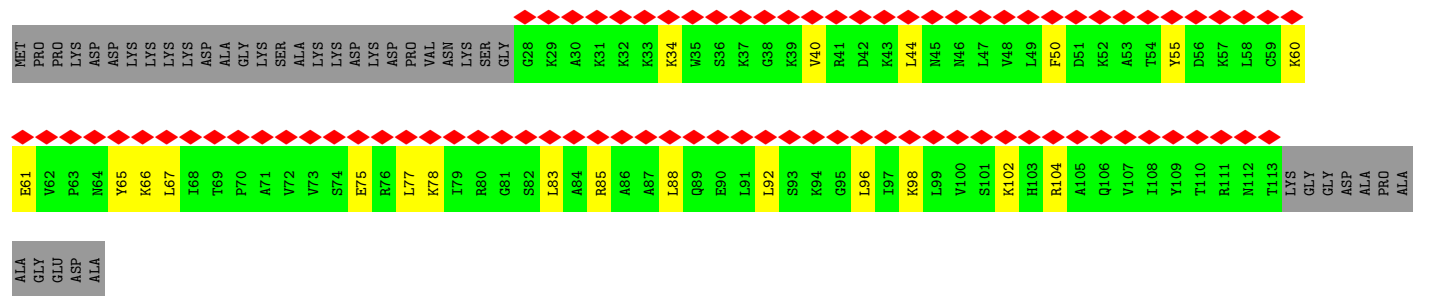
• Molecule 73: 40S ribosomal protein S23



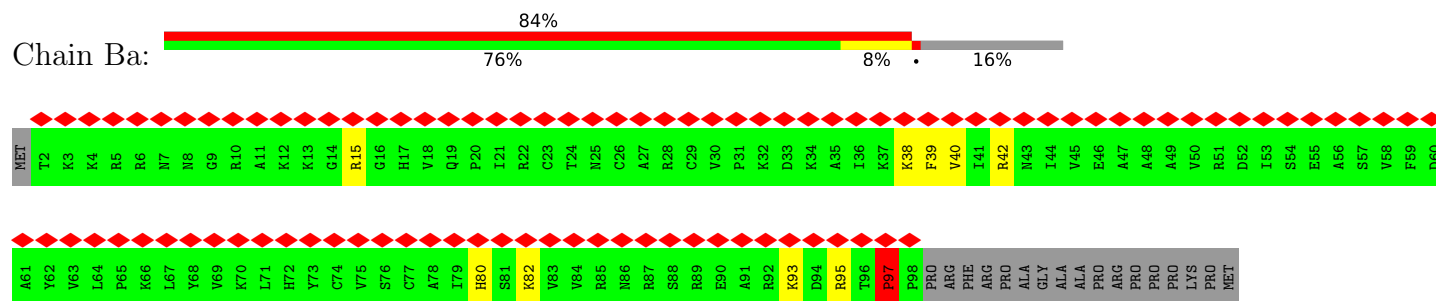
• Molecule 74: 40S ribosomal protein S24



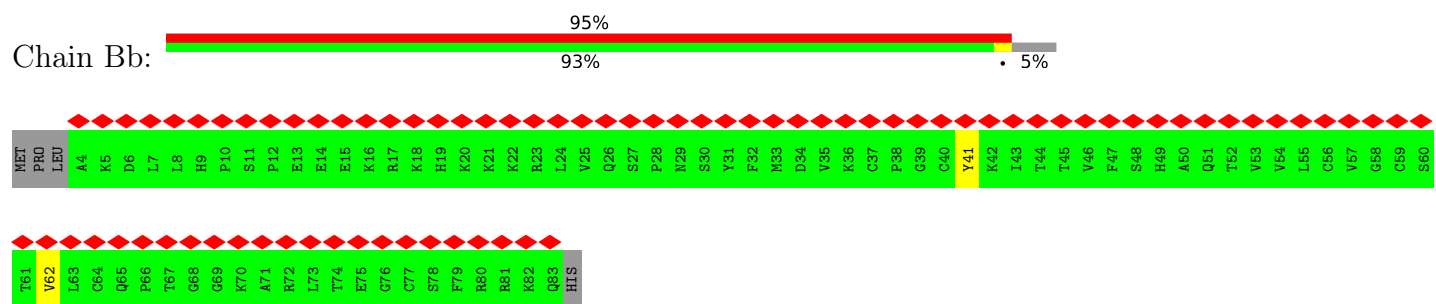
• Molecule 75: 40S ribosomal protein S25



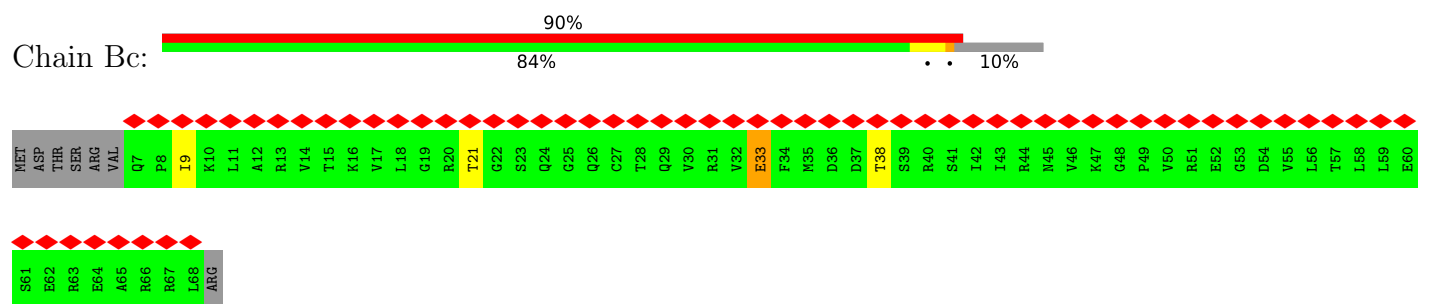
## • Molecule 76: 40S ribosomal protein S26



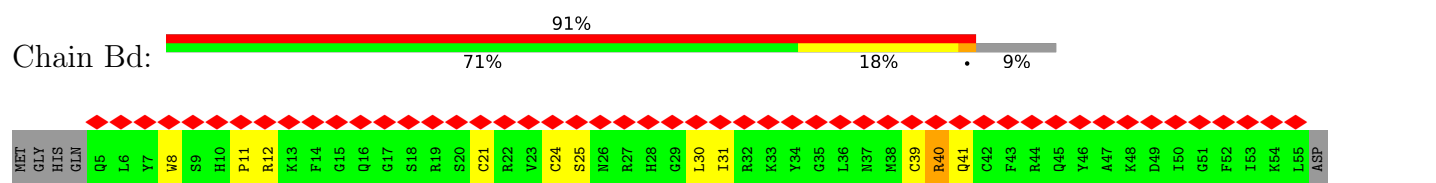
## • Molecule 77: 40S ribosomal protein S27



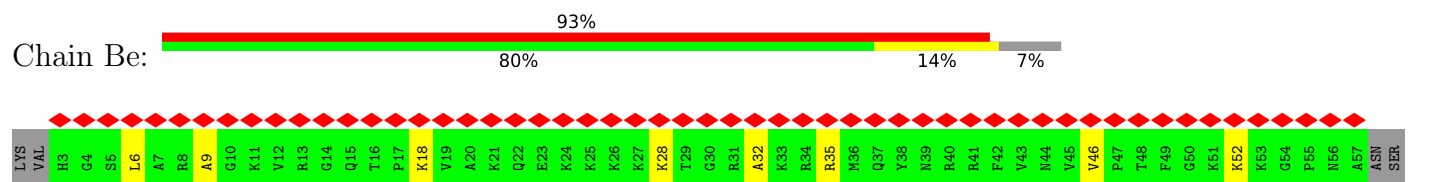
## • Molecule 78: 40S ribosomal protein S28



## • Molecule 79: 40S ribosomal protein S29

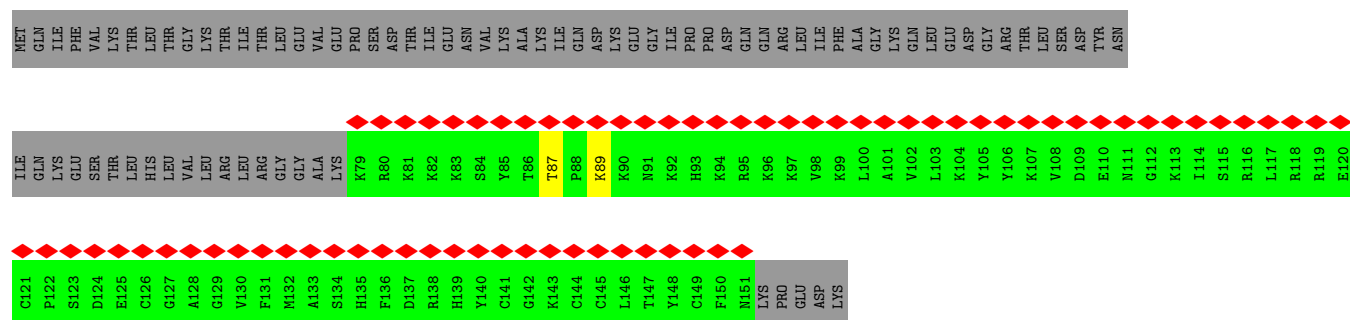


## • Molecule 80: 40S ribosomal protein S30

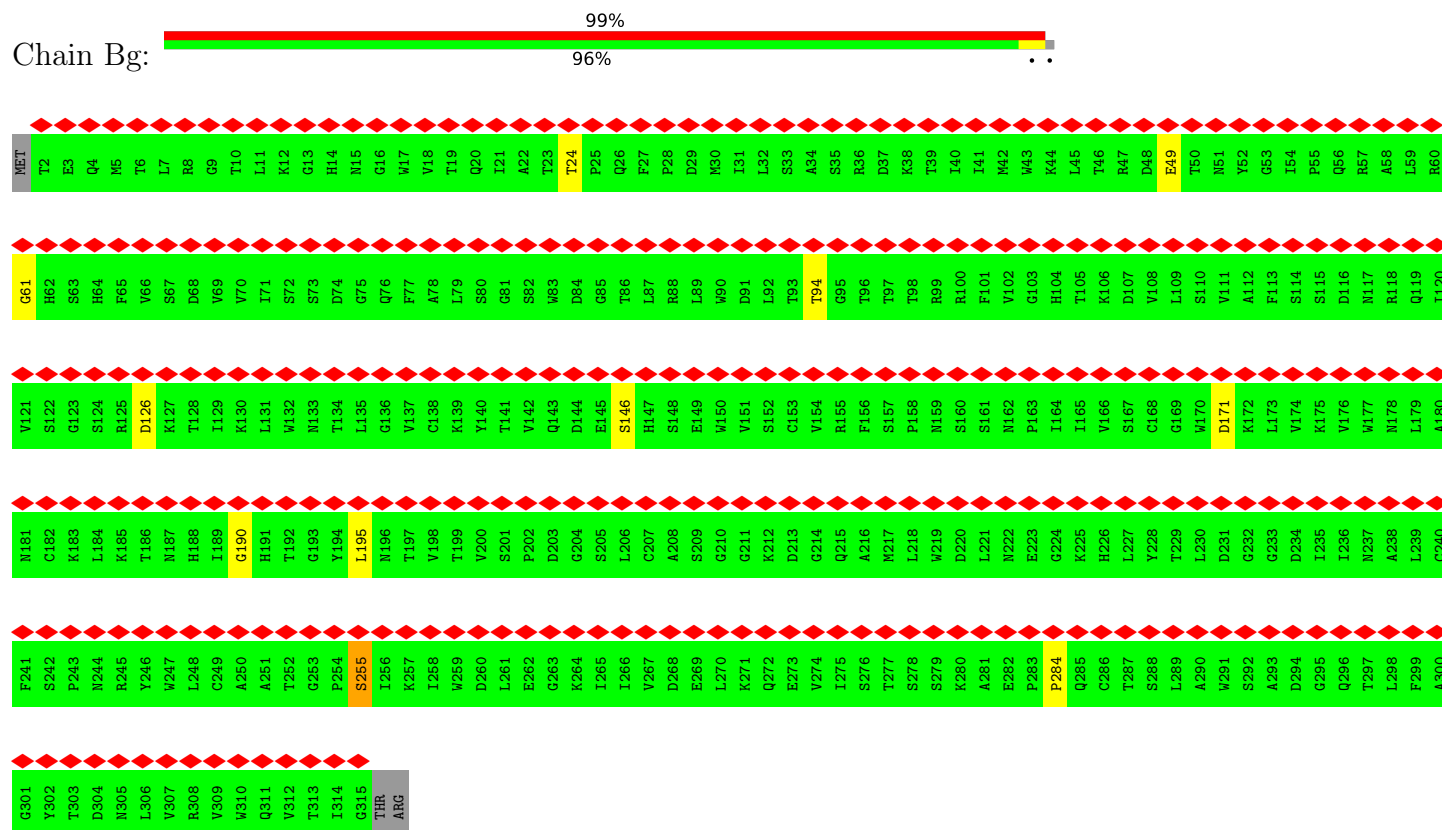


## • Molecule 81: Ubiquitin-40S ribosomal protein S27a

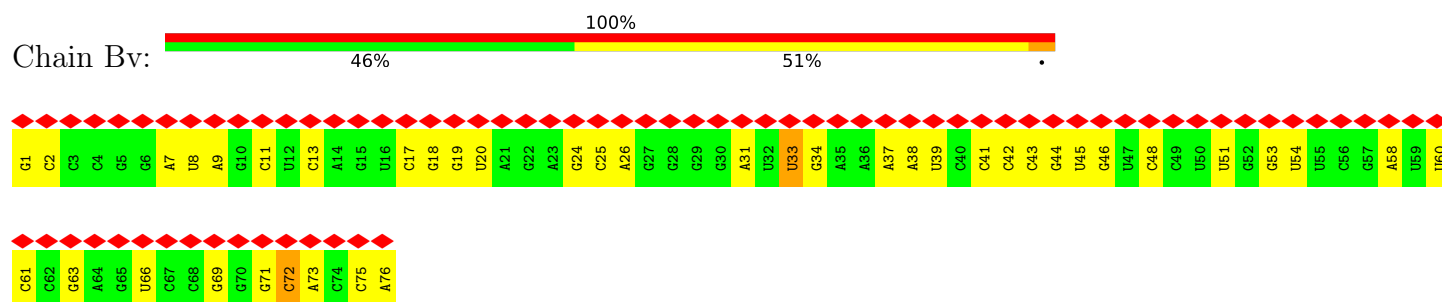




• Molecule 82: Guanine nucleotide-binding protein subunit beta-2-like 1

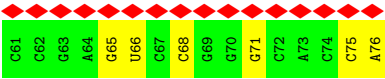
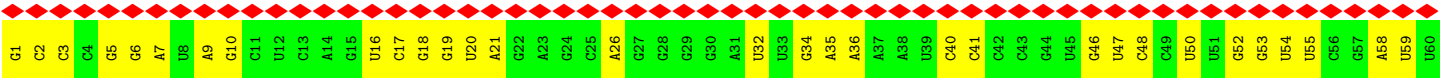


• Molecule 83: tRNA

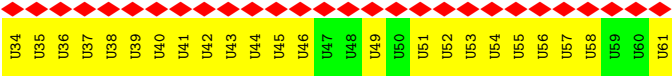


• Molecule 83: tRNA

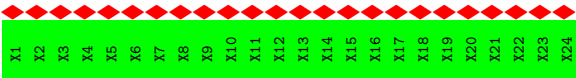




• Molecule 84: mRNA



• 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	1.12	40/3726 (1.1%)	1.17	52/5804 (0.9%)
2	A4	1.10	32/2839 (1.1%)	1.13	40/4425 (0.9%)
3	AA	0.44	0/1968	0.65	1/2639 (0.0%)
4	AB	0.39	0/3246	0.64	0/4345
5	AC	0.41	1/2942 (0.0%)	0.62	3/3951 (0.1%)
6	AD	0.42	0/2437	0.65	2/3262 (0.1%)
7	AE	0.50	0/1603	0.80	4/2153 (0.2%)
8	AF	0.37	0/1986	0.57	0/2644
9	AG	0.38	0/1913	0.57	0/2576
10	AH	0.38	0/1545	0.54	1/2077 (0.0%)
11	AI	0.41	0/1730	0.61	1/2311 (0.0%)
12	AJ	0.39	0/1376	0.59	0/1841
13	AK	0.85	3/886 (0.3%)	1.53	23/1188 (1.9%)
14	AL	0.48	3/1688 (0.2%)	0.73	5/2260 (0.2%)
15	AM	0.39	0/1161	0.64	0/1554
16	AN	0.39	0/1746	0.57	0/2338
17	AO	0.37	0/1638	0.60	0/2191
18	AP	0.42	0/1268	0.70	0/1701
19	AQ	0.47	2/1537 (0.1%)	0.63	3/2052 (0.1%)
20	AR	0.38	0/1533	0.63	1/2025 (0.0%)
21	AS	0.38	1/1488 (0.1%)	0.60	1/1997 (0.1%)
22	AT	0.38	0/1312	0.60	0/1753
23	AU	0.35	0/822	0.58	0/1103
24	AV	0.37	0/983	0.55	0/1319
25	AW	0.42	1/1004 (0.1%)	0.74	3/1332 (0.2%)
26	AX	0.34	0/975	0.51	0/1312
27	AY	0.35	0/1081	0.56	0/1439
28	AZ	0.42	0/1126	0.69	2/1502 (0.1%)
29	Aa	0.50	0/1191	0.70	1/1591 (0.1%)
30	Ab	0.36	0/569	0.58	0/750
31	Ac	0.38	0/812	0.60	0/1089
32	Ad	0.38	0/894	0.58	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Ae	0.42	0/1082	0.58	1/1443 (0.1%)
34	Af	0.47	0/895	0.73	2/1198 (0.2%)
35	Ag	0.39	0/916	0.58	0/1220
36	Ah	0.37	0/1023	0.63	1/1351 (0.1%)
37	Ai	0.35	0/805	0.58	0/1065
38	Aj	0.47	1/703 (0.1%)	0.92	3/929 (0.3%)
39	Ak	0.51	0/575	0.74	0/761
40	Al	0.37	0/454	0.54	0/599
41	Am	0.42	0/417	0.59	0/553
42	An	0.36	0/241	0.60	0/305
43	Ao	0.39	0/877	0.66	0/1156
44	Ap	0.39	0/718	0.60	0/953
45	Aq	0.89	3/1058 (0.3%)	1.93	34/1424 (2.4%)
46	At	0.41	0/995	0.69	0/1334
47	Au	0.73	1/1772 (0.1%)	1.28	17/2375 (0.7%)
48	A2	0.98	666/86613 (0.8%)	1.13	1094/135108 (0.8%)
49	B1	0.96	275/40767 (0.7%)	1.13	515/63536 (0.8%)
50	BA	0.52	1/1741 (0.1%)	0.72	5/2366 (0.2%)
51	BB	0.42	0/1749	0.62	0/2340
52	BC	0.37	0/1761	0.58	0/2379
53	BD	0.44	1/1736 (0.1%)	0.63	1/2338 (0.0%)
54	BE	0.41	1/2072 (0.0%)	0.59	1/2793 (0.0%)
55	BF	0.40	1/1524 (0.1%)	0.62	1/2048 (0.0%)
56	BG	0.41	0/1907	0.62	1/2538 (0.0%)
57	BH	0.43	0/1501	0.64	1/2009 (0.0%)
58	BI	0.41	0/1725	0.59	0/2298
59	BJ	0.36	0/1520	0.55	1/2030 (0.0%)
60	BK	0.43	0/851	0.68	0/1147
61	BL	0.44	1/1281 (0.1%)	0.65	2/1710 (0.1%)
62	BM	0.39	0/941	0.63	0/1264
63	BN	0.40	1/1226 (0.1%)	0.57	1/1649 (0.1%)
64	BO	0.43	0/1029	0.64	0/1380
65	BP	0.50	1/1019 (0.1%)	0.74	3/1361 (0.2%)
66	BQ	0.38	0/1126	0.58	2/1506 (0.1%)
67	BR	0.49	3/1023 (0.3%)	0.68	3/1373 (0.2%)
68	BS	0.42	1/1172 (0.1%)	0.63	1/1570 (0.1%)
69	BT	0.36	0/1131	0.60	0/1515
70	BU	0.45	0/778	0.65	1/1045 (0.1%)
71	BV	0.41	0/623	0.60	1/833 (0.1%)
72	BW	0.37	0/1051	0.55	0/1406
73	BX	0.44	1/1097 (0.1%)	0.61	1/1464 (0.1%)
74	BY	0.40	0/1032	0.64	0/1371
75	BZ	0.43	0/696	0.62	0/929

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Ba	0.49	0/786	0.75	2/1053 (0.2%)
77	Bb	0.42	0/637	0.59	0/854
78	Bc	0.40	0/490	0.66	0/656
79	Bd	0.54	0/437	0.89	3/580 (0.5%)
80	Be	0.37	0/443	0.60	0/583
81	Bf	0.44	0/613	0.62	0/811
82	Bg	0.40	0/2497	0.60	0/3399
83	Bv	0.58	4/1813 (0.2%)	0.84	5/2823 (0.2%)
83	Bw	0.43	2/1813 (0.1%)	0.90	4/2823 (0.1%)
84	Bx	0.60	2/616 (0.3%)	1.20	11/948 (1.2%)
All	All	0.80	1049/234393 (0.4%)	0.98	1861/344230 (0.5%)

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 1049 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	A2	3612	U	O3'-P	-21.32	1.35	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	B1	842	C	O3'-P	20.18	1.85	1.61
48	A2	2689	C	O3'-P	-19.59	1.37	1.61
49	B1	558	G	O3'-P	19.39	1.84	1.61
49	B1	497	C	O3'-P	18.59	1.83	1.61

The worst 5 of 1861 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	Aq	75	PRO	CA-N-CD	-36.28	60.70	111.50
48	A2	1225	G	O5'-P-OP1	-28.99	75.91	110.70
48	A2	131	C	C4'-C3'-O3'	28.78	170.56	113.00
49	B1	558	G	P-O3'-C3'	-28.42	85.60	119.70
48	A2	137	G	C4'-C3'-O3'	26.49	165.98	113.00

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 [i](#)

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

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AA	250/257 (97%)	237 (95%)	7 (3%)	6 (2%)	5	30
4	AB	392/403 (97%)	370 (94%)	10 (3%)	12 (3%)	3	26
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	28
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	21
9	AG	232/266 (87%)	217 (94%)	10 (4%)	5 (2%)	5	31
10	AH	189/192 (98%)	175 (93%)	8 (4%)	6 (3%)	3	25
11	AI	204/214 (95%)	192 (94%)	7 (3%)	5 (2%)	4	29
12	AJ	167/178 (94%)	154 (92%)	7 (4%)	6 (4%)	3	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%)	3	22
16	AN	201/204 (98%)	193 (96%)	6 (3%)	2 (1%)	13	46
17	AO	193/203 (95%)	187 (97%)	3 (2%)	3 (2%)	8	38
18	AP	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
19	AQ	185/188 (98%)	163 (88%)	10 (5%)	12 (6%)	1	12
20	AR	179/196 (91%)	171 (96%)	4 (2%)	4 (2%)	5	31
21	AS	173/176 (98%)	156 (90%)	11 (6%)	6 (4%)	3	24
22	AT	155/160 (97%)	144 (93%)	6 (4%)	5 (3%)	3	25
23	AU	97/128 (76%)	81 (84%)	7 (7%)	9 (9%)	0	7
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	25
28	AZ	132/136 (97%)	118 (89%)	6 (4%)	8 (6%)	1	13
29	Aa	145/148 (98%)	135 (93%)	6 (4%)	4 (3%)	4	27
30	Ab	66/159 (42%)	57 (86%)	5 (8%)	4 (6%)	1	13
31	Ac	101/115 (88%)	97 (96%)	2 (2%)	2 (2%)	6	33
32	Ad	104/125 (83%)	99 (95%)	3 (3%)	2 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	Ae	127/135 (94%)	116 (91%)	6 (5%)	5 (4%)	2	21
34	Af	107/110 (97%)	93 (87%)	5 (5%)	9 (8%)	0	8
35	Ag	112/117 (96%)	107 (96%)	3 (3%)	2 (2%)	7	35
36	Ah	120/123 (98%)	112 (93%)	2 (2%)	6 (5%)	1	16
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	3
40	Al	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Am	48/128 (38%)	44 (92%)	3 (6%)	1 (2%)	5	32
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	103/106 (97%)	94 (91%)	5 (5%)	4 (4%)	2	21
44	Ap	89/92 (97%)	84 (94%)	3 (3%)	2 (2%)	5	31
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	29
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	34
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	20
53	BD	218/243 (90%)	201 (92%)	10 (5%)	7 (3%)	3	25
54	BE	255/263 (97%)	230 (90%)	14 (6%)	11 (4%)	2	19
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	24
57	BH	181/194 (93%)	169 (93%)	8 (4%)	4 (2%)	5	31
58	BI	205/208 (99%)	175 (85%)	20 (10%)	10 (5%)	2	16
59	BJ	177/194 (91%)	137 (77%)	28 (16%)	12 (7%)	1	11
60	BK	96/165 (58%)	84 (88%)	7 (7%)	5 (5%)	1	15
61	BL	151/158 (96%)	133 (88%)	11 (7%)	7 (5%)	2	18
62	BM	118/132 (89%)	113 (96%)	1 (1%)	4 (3%)	3	24
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	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	BQ	137/146 (94%)	120 (88%)	10 (7%)	7 (5%)	1	16
67	BR	123/135 (91%)	106 (86%)	9 (7%)	8 (6%)	1	12
68	BS	137/152 (90%)	125 (91%)	7 (5%)	5 (4%)	3	22
69	BT	141/145 (97%)	131 (93%)	6 (4%)	4 (3%)	4	27
70	BU	95/119 (80%)	91 (96%)	2 (2%)	2 (2%)	5	32
71	BV	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
72	BW	127/130 (98%)	120 (94%)	3 (2%)	4 (3%)	3	26
73	BX	137/143 (96%)	124 (90%)	8 (6%)	5 (4%)	3	22
74	BY	123/133 (92%)	116 (94%)	6 (5%)	1 (1%)	16	51
75	BZ	84/125 (67%)	80 (95%)	1 (1%)	3 (4%)	3	22
76	Ba	95/115 (83%)	87 (92%)	7 (7%)	1 (1%)	12	45
77	Bb	78/84 (93%)	72 (92%)	4 (5%)	2 (3%)	4	28
78	Bc	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	25
79	Bd	49/56 (88%)	42 (86%)	4 (8%)	3 (6%)	1	13
80	Be	53/59 (90%)	49 (92%)	2 (4%)	2 (4%)	2	21
81	Bf	71/156 (46%)	63 (89%)	7 (10%)	1 (1%)	9	40
82	Bg	312/317 (98%)	292 (94%)	12 (4%)	8 (3%)	4	28
All	All	11580/13387 (86%)	10401 (90%)	657 (6%)	522 (4%)	3	18

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%)	185 (95%)	9 (5%)	23	52
4	AB	343/349 (98%)	323 (94%)	20 (6%)	17	44
5	AC	302/348 (87%)	278 (92%)	24 (8%)	10	34
6	AD	248/250 (99%)	229 (92%)	19 (8%)	10	34
7	AE	174/252 (69%)	127 (73%)	47 (27%)	0	2
8	AF	203/215 (94%)	193 (95%)	10 (5%)	21	50
9	AG	199/223 (89%)	192 (96%)	7 (4%)	31	59
10	AH	170/171 (99%)	160 (94%)	10 (6%)	16	44
11	AI	178/181 (98%)	174 (98%)	4 (2%)	47	70
12	AJ	142/149 (95%)	138 (97%)	4 (3%)	38	65
13	AK	95/258 (37%)	70 (74%)	25 (26%)	0	3
14	AL	171/177 (97%)	156 (91%)	15 (9%)	8	31
15	AM	118/161 (73%)	104 (88%)	14 (12%)	4	21
16	AN	171/172 (99%)	163 (95%)	8 (5%)	22	51
17	AO	168/174 (97%)	164 (98%)	4 (2%)	44	68
18	AP	134/163 (82%)	123 (92%)	11 (8%)	9	33
19	AQ	164/165 (99%)	144 (88%)	20 (12%)	4	20
20	AR	160/175 (91%)	145 (91%)	15 (9%)	7	29
21	AS	156/157 (99%)	149 (96%)	7 (4%)	23	53
22	AT	138/140 (99%)	126 (91%)	12 (9%)	8	31
23	AU	89/115 (77%)	78 (88%)	11 (12%)	4	20
24	AV	100/107 (94%)	98 (98%)	2 (2%)	50	72
25	AW	100/126 (79%)	94 (94%)	6 (6%)	16	43
26	AX	105/133 (79%)	95 (90%)	10 (10%)	7	28
27	AY	119/135 (88%)	109 (92%)	10 (8%)	9	32
28	AZ	117/118 (99%)	100 (86%)	17 (14%)	2	15
29	Aa	120/121 (99%)	110 (92%)	10 (8%)	9	32
30	Ab	58/126 (46%)	54 (93%)	4 (7%)	13	39
31	Ac	88/97 (91%)	85 (97%)	3 (3%)	32	60
32	Ad	97/110 (88%)	96 (99%)	1 (1%)	73	84
33	Ae	115/121 (95%)	114 (99%)	1 (1%)	75	86
34	Af	88/89 (99%)	85 (97%)	3 (3%)	32	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	Ag	98/100 (98%)	93 (95%)	5 (5%)	20	48
36	Ah	109/110 (99%)	96 (88%)	13 (12%)	4	21
37	Ai	83/89 (93%)	80 (96%)	3 (4%)	30	59
38	Aj	71/80 (89%)	65 (92%)	6 (8%)	8	32
39	Ak	64/65 (98%)	46 (72%)	18 (28%)	0	2
40	Al	47/48 (98%)	44 (94%)	3 (6%)	14	41
41	Am	46/116 (40%)	45 (98%)	1 (2%)	47	70
42	An	24/24 (100%)	23 (96%)	1 (4%)	25	54
43	Ao	93/94 (99%)	85 (91%)	8 (9%)	8	32
44	Ap	74/75 (99%)	71 (96%)	3 (4%)	26	55
45	Aq	114/137 (83%)	90 (79%)	24 (21%)	1	5
46	At	106/121 (88%)	88 (83%)	18 (17%)	1	10
47	Au	196/196 (100%)	180 (92%)	16 (8%)	9	33
50	BA	180/243 (74%)	165 (92%)	15 (8%)	9	32
51	BB	193/231 (84%)	177 (92%)	16 (8%)	9	32
52	BC	188/225 (84%)	177 (94%)	11 (6%)	16	44
53	BD	183/202 (91%)	175 (96%)	8 (4%)	24	53
54	BE	220/225 (98%)	213 (97%)	7 (3%)	34	62
55	BF	160/170 (94%)	155 (97%)	5 (3%)	35	63
56	BG	202/218 (93%)	177 (88%)	25 (12%)	4	20
57	BH	164/174 (94%)	160 (98%)	4 (2%)	44	68
58	BI	179/180 (99%)	175 (98%)	4 (2%)	47	70
59	BJ	160/168 (95%)	151 (94%)	9 (6%)	17	45
60	BK	89/136 (65%)	83 (93%)	6 (7%)	13	40
61	BL	138/142 (97%)	134 (97%)	4 (3%)	37	64
62	BM	102/108 (94%)	101 (99%)	1 (1%)	73	84
63	BN	130/131 (99%)	122 (94%)	8 (6%)	15	42
64	BO	106/119 (89%)	99 (93%)	7 (7%)	14	41
65	BP	109/130 (84%)	93 (85%)	16 (15%)	2	15
66	BQ	115/121 (95%)	102 (89%)	13 (11%)	4	22
67	BR	113/122 (93%)	97 (86%)	16 (14%)	2	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	BS	121/132 (92%)	106 (88%)	15 (12%)	4	20
69	BT	113/115 (98%)	102 (90%)	11 (10%)	6	27
70	BU	90/107 (84%)	85 (94%)	5 (6%)	17	45
71	BV	65/67 (97%)	59 (91%)	6 (9%)	7	29
72	BW	112/113 (99%)	108 (96%)	4 (4%)	30	59
73	BX	111/115 (96%)	101 (91%)	10 (9%)	8	30
74	BY	107/115 (93%)	103 (96%)	4 (4%)	29	58
75	BZ	75/103 (73%)	57 (76%)	18 (24%)	0	3
76	Ba	84/98 (86%)	75 (89%)	9 (11%)	5	24
77	Bb	72/76 (95%)	72 (100%)	0	100	100
78	Bc	55/62 (89%)	52 (94%)	3 (6%)	18	46
79	Bd	45/49 (92%)	40 (89%)	5 (11%)	5	23
80	Be	44/48 (92%)	38 (86%)	6 (14%)	3	17
81	Bf	66/140 (47%)	65 (98%)	1 (2%)	60	77
82	Bg	272/275 (99%)	268 (98%)	4 (2%)	60	77
All	All	10112/11392 (89%)	9354 (92%)	758 (8%)	14	35

5 of 758 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	At	89	THR
58	BI	19	LYS
47	Au	185	LEU
46	At	87	ARG
52	BC	166	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 196 such sidechains are listed below:

Mol	Chain	Res	Type
46	At	70	GLN
57	BH	114	GLN
47	Au	143	ASN
52	BC	235	ASN
61	BL	13	GLN

### 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%)	695 (19%)	48 (1%)
49	B1	1701/1869 (91%)	290 (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%)	1126 (19%)	72 (1%)

5 of 1126 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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

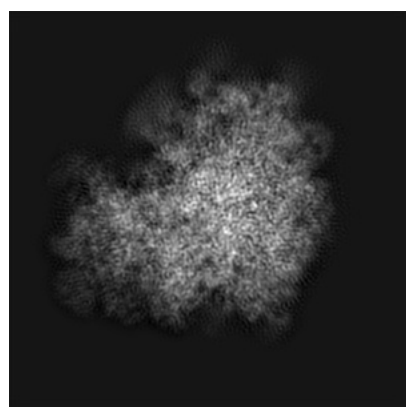
## 6 Map visualisation [i](#)

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.

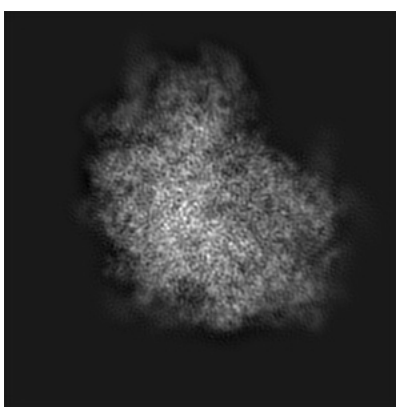
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

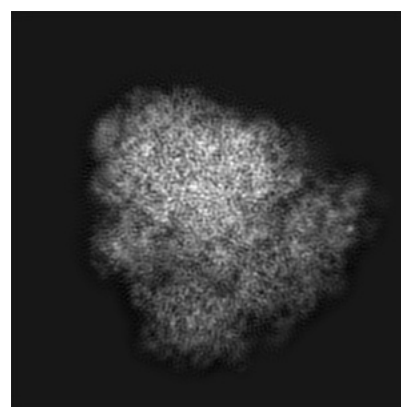
#### 6.1.1 Primary map



X



Y

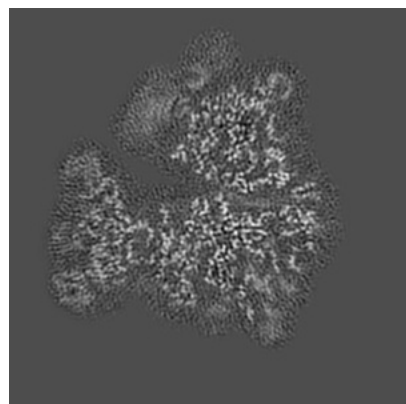


Z

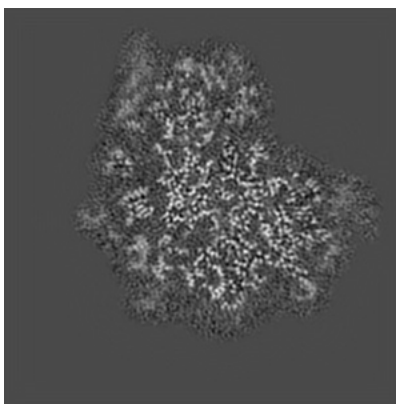
The images above show the map projected in three orthogonal directions.

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

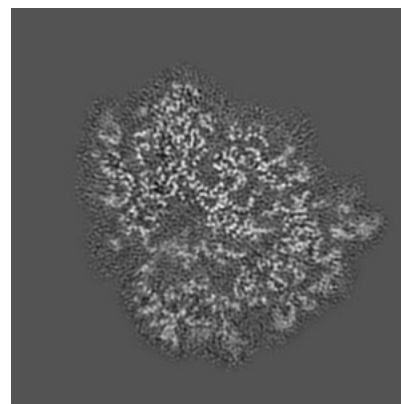
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

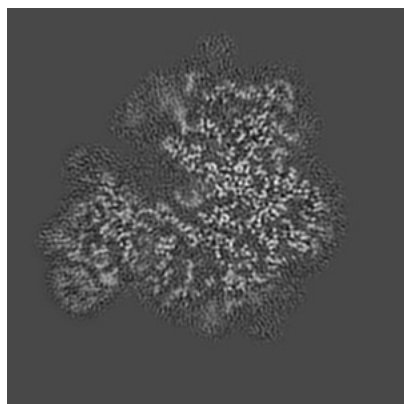


Z Index: 200

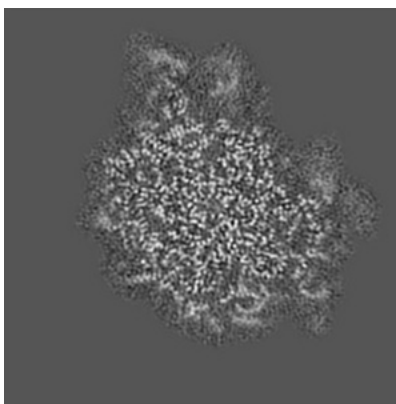
The images above show central slices of the map in three orthogonal directions.

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

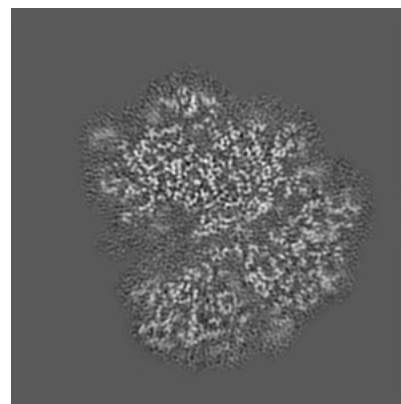
### 6.3.1 Primary map



X Index: 186



Y Index: 220

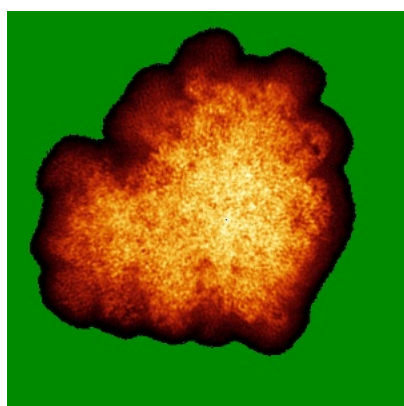


Z Index: 184

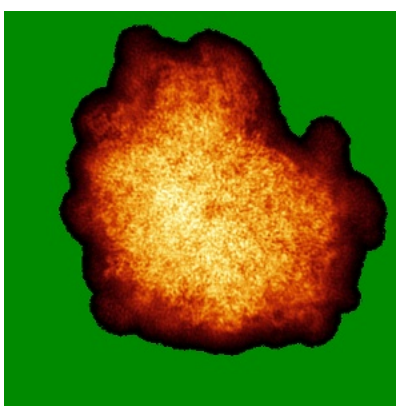
The images above show the largest variance slices of the map in three orthogonal directions.

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

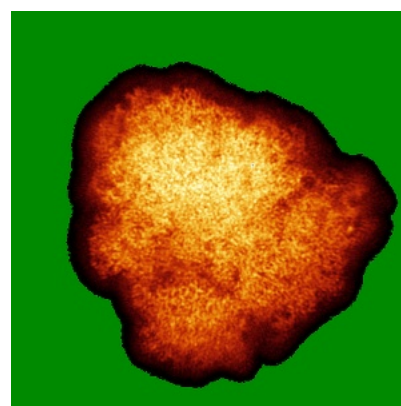
### 6.4.1 Primary map



X



Y

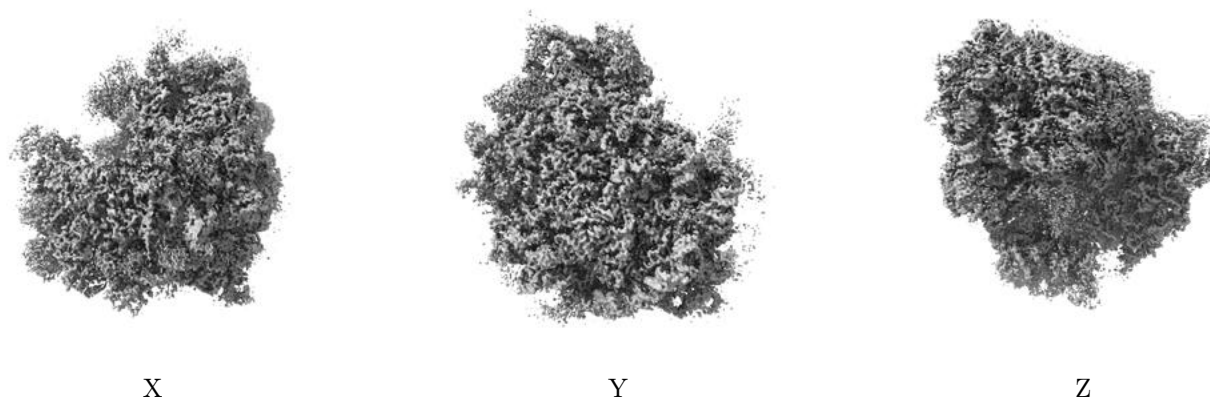


Z

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.

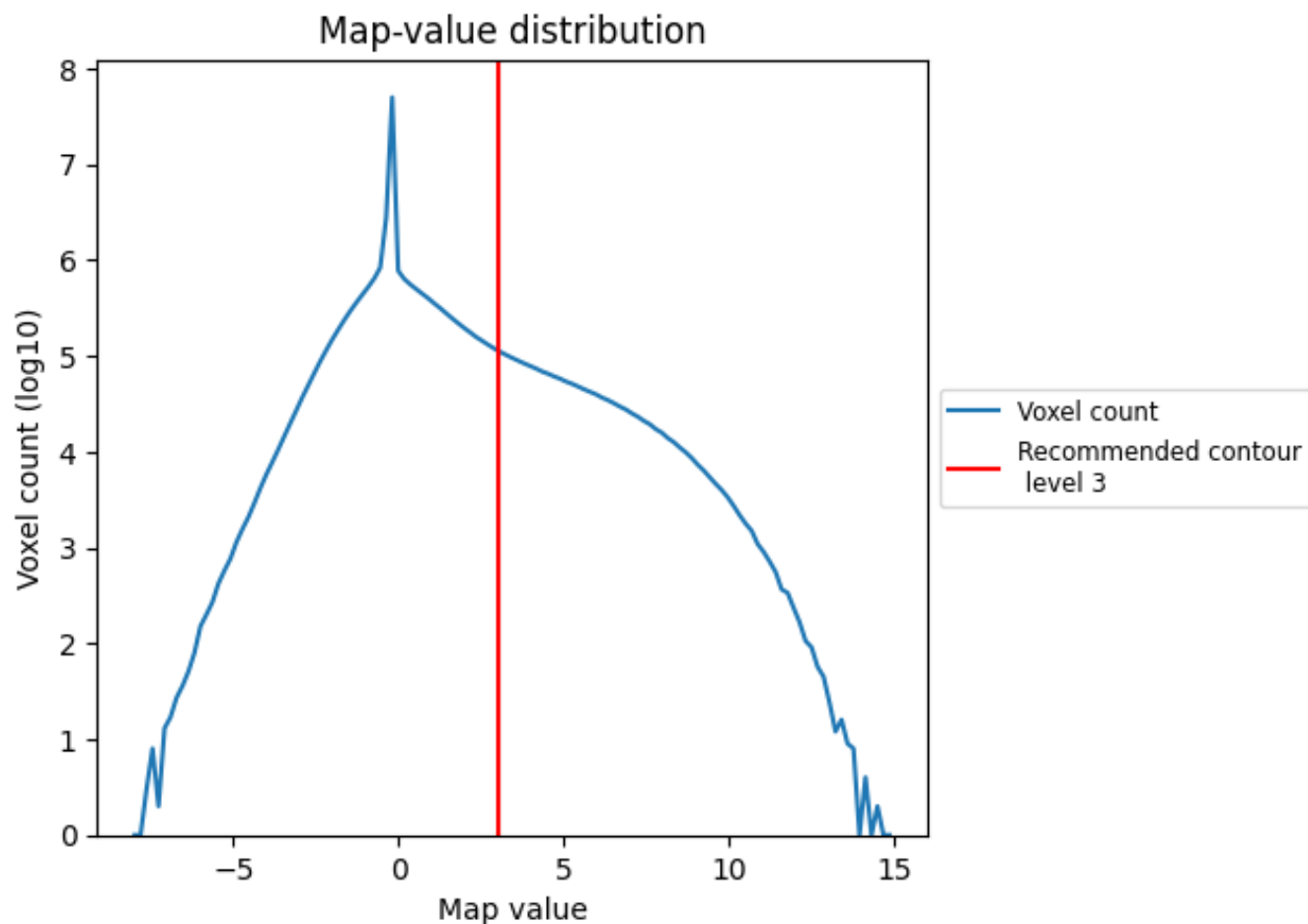
## 6.6 Mask visualisation [i](#)

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.

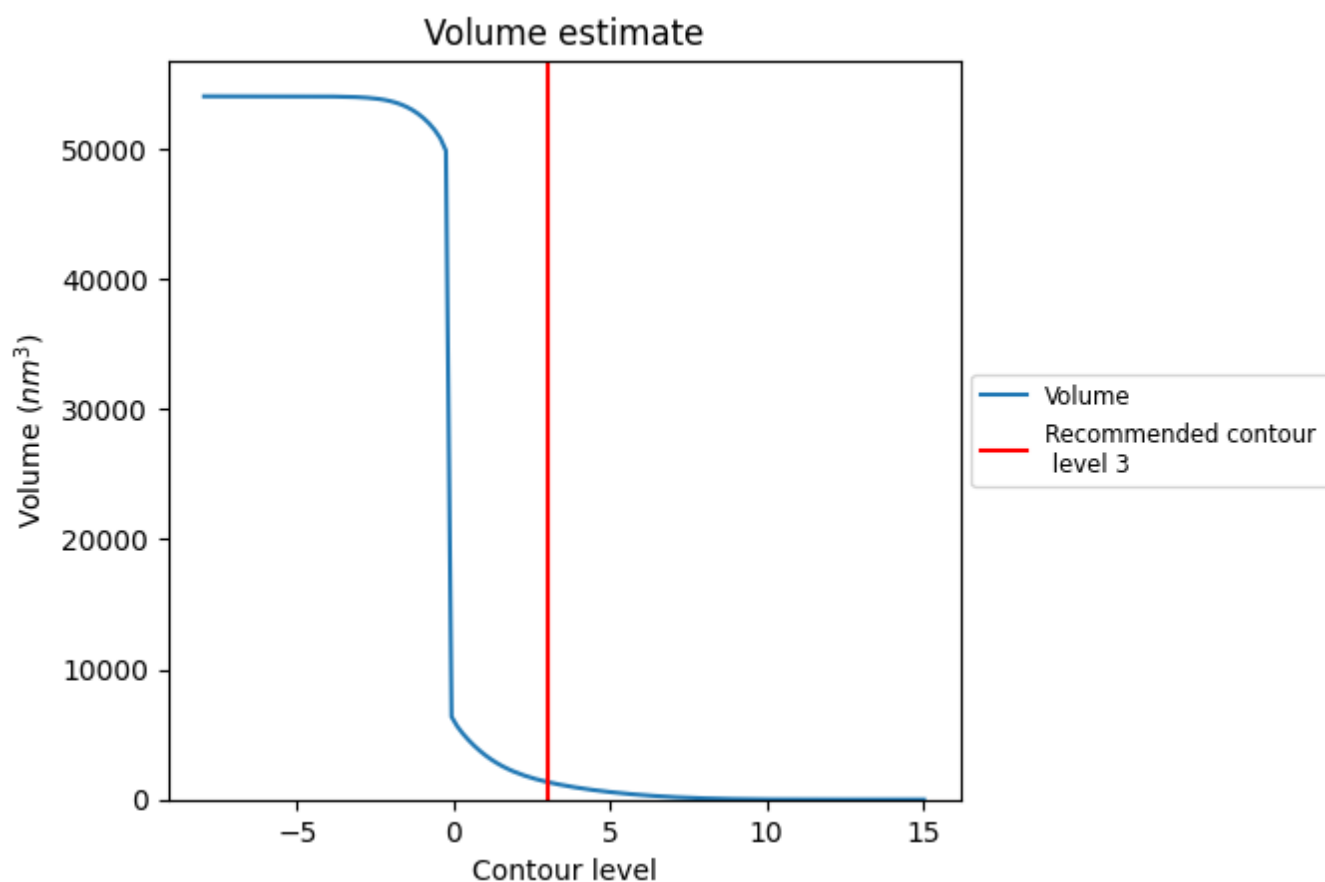
### 7.1 Map-value distribution [i](#)



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.



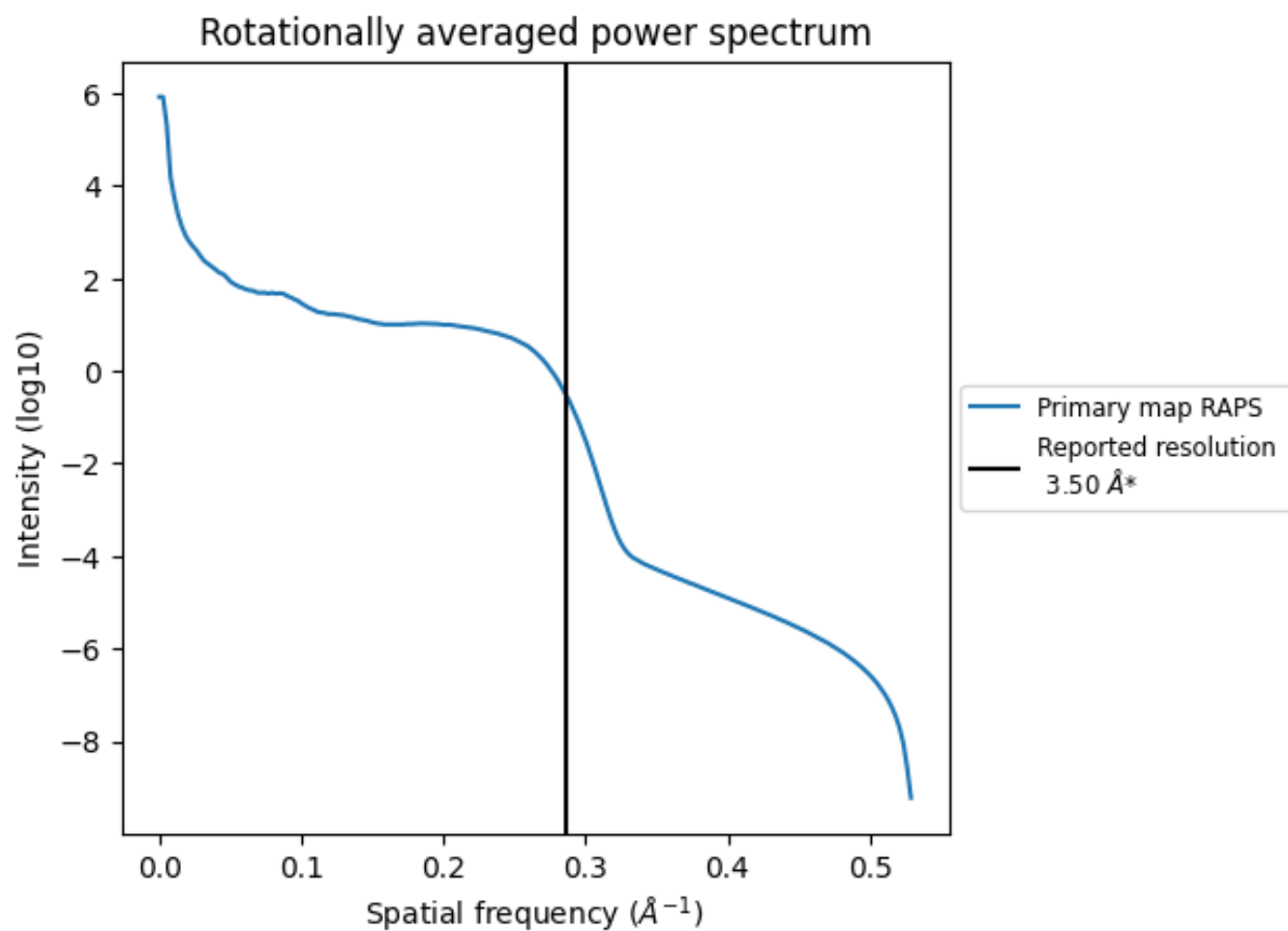
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1346 nm<sup>3</sup>; 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<sup>-1</sup>

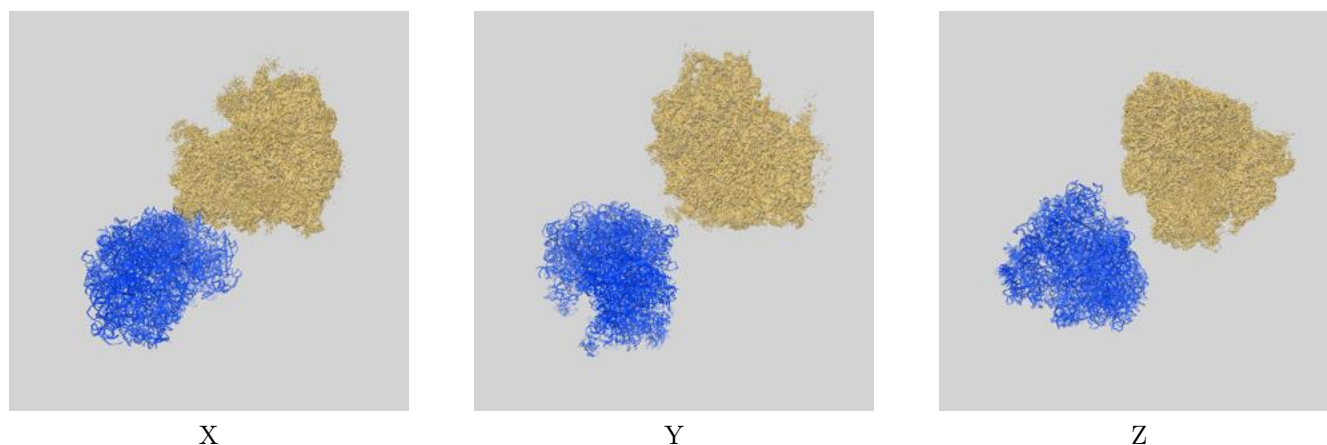
## 8 Fourier-Shell correlation

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

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

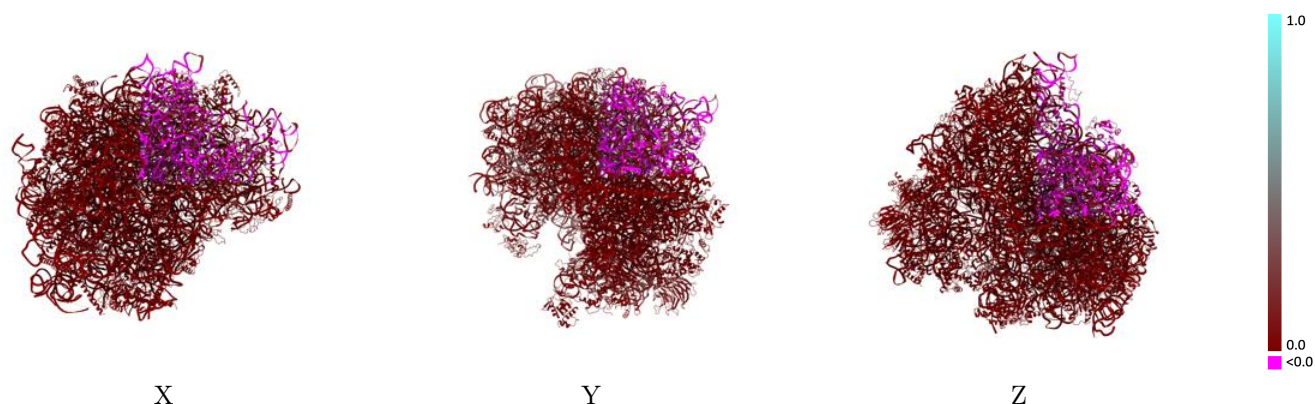
This section contains information regarding the fit between EMDB map EMD-2875 and PDB model 5AJ0. Per-residue inclusion information can be found in section [3](#) on page [21](#).

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



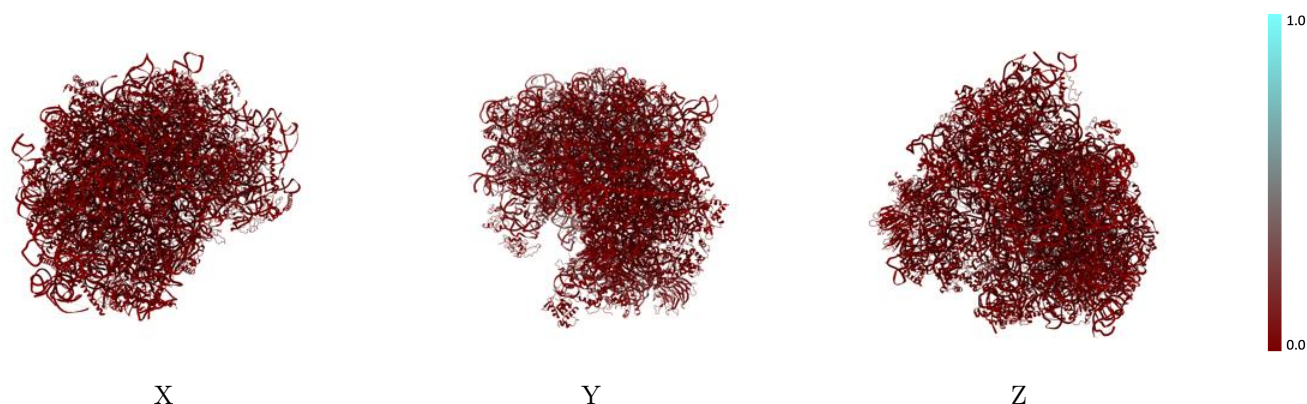
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



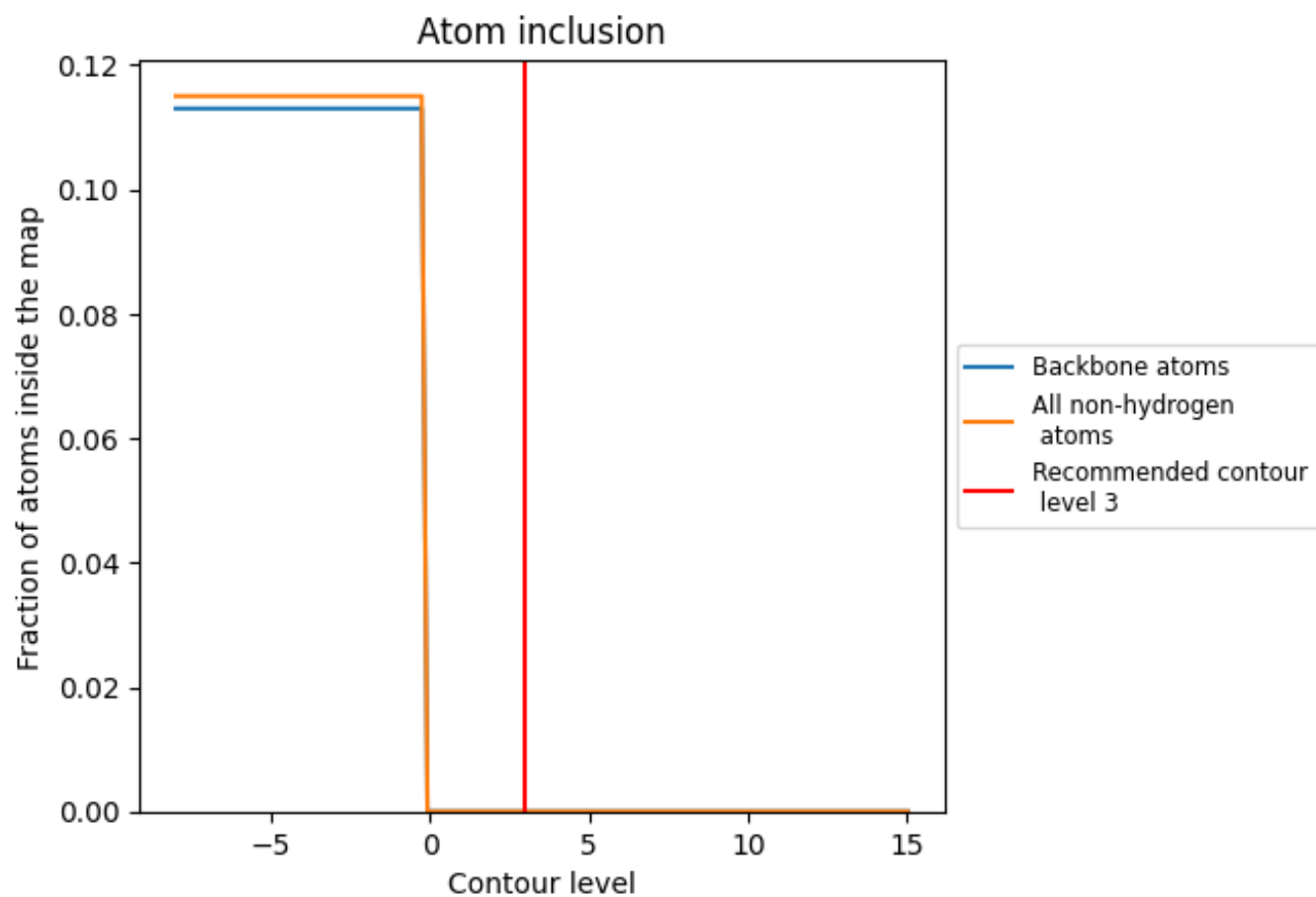
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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