



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:56 AM UTC

PDB ID : 6T83 / pdb_00006t83
EMDB ID : EMD-10398
Title : Structure of yeast disome (di-ribosome) stalled on poly(A) tract.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-24
Resolution : 4.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

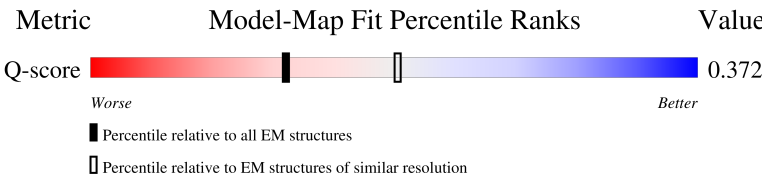
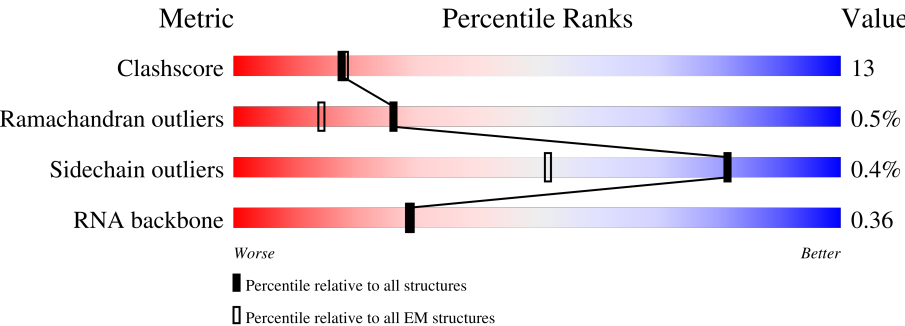
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	2b	1800	
1	a	1800	
2	Ab	252	

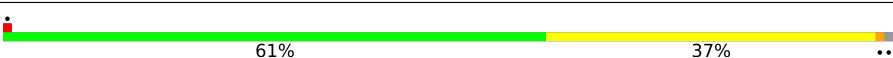
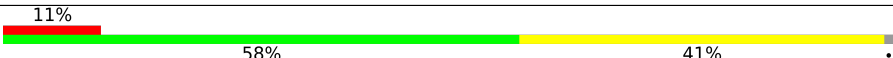
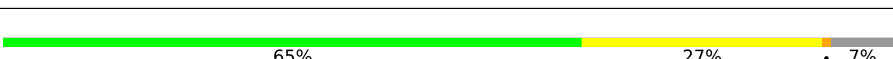
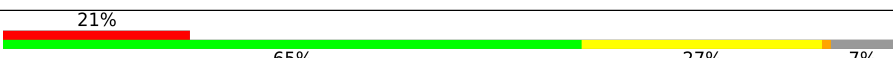
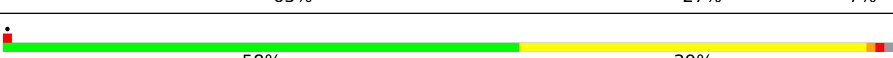
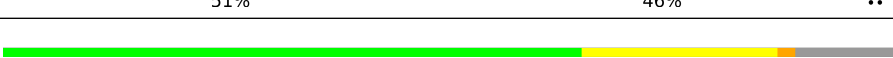
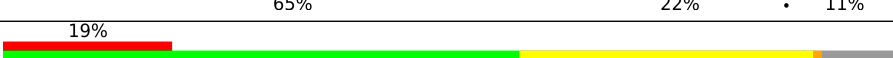
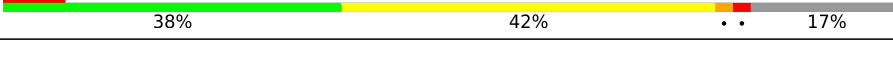
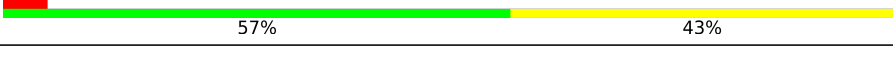
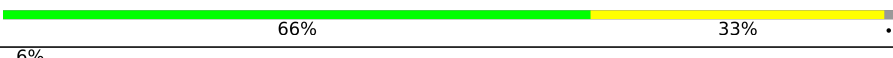
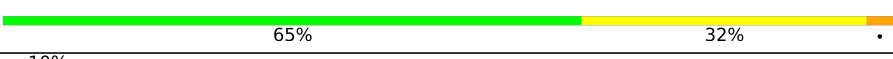
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Mol	Chain	Length	Quality of chain
2	b	252	
3	Ba	255	
3	c	255	
4	Pb	142	
4	q	142	
5	Cb	254	
5	d	254	
6	Db	240	
6	e	240	
7	Eb	261	
7	f	261	
8	Fb	225	
8	g	225	
9	Gb	236	
9	h	236	
10	Hb	190	
10	i	190	
11	Ib	200	
11	j	200	
12	Jb	197	
12	k	197	
13	Kb	105	
13	l	105	
14	Lb	156	
14	m	156	

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Mol	Chain	Length	Quality of chain
15	Mb	143	
15	n	143	
16	Nb	151	
16	o	151	
17	Ob	137	
17	p	137	
18	Qb	143	
18	r	143	
19	Rb	136	
19	s	136	
20	Sb	146	
20	t	146	
21	Tb	144	
21	u	144	
22	Ub	121	
22	v	121	
23	Vb	87	
23	w	87	
24	Wb	130	
24	x	130	
25	Xb	145	
25	y	145	
26	Yb	135	
26	z	135	
27	0	108	

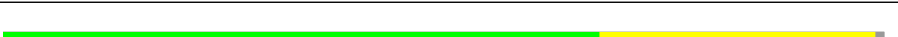
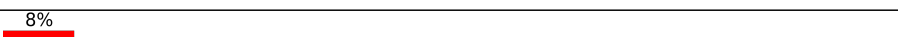
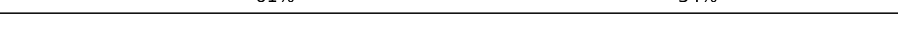
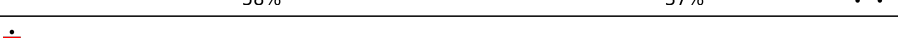
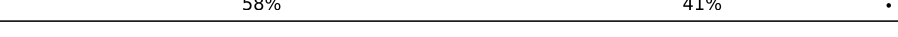
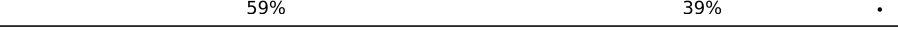
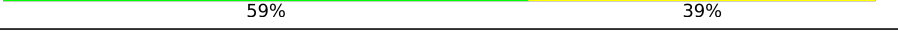
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Mol	Chain	Length	Quality of chain
27	Zb	108	
28	1	119	
28	ab	119	
29	2	82	
29	bb	82	
30	4	56	
30	db	56	
31	5	63	
31	eb	63	
32	6	152	
32	fb	152	
33	7	319	
33	gb	319	
34	3	67	
34	cb	67	
35	4b	121	
35	Bb	121	
36	3b	158	
36	Ca	158	
37	Ay	254	
37	Da	254	
38	By	387	
38	Ea	387	
39	Cy	362	
39	Fa	362	

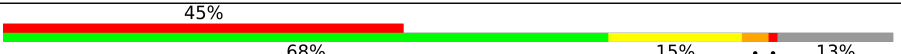
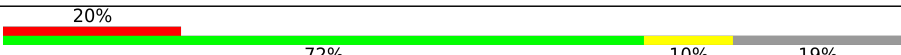
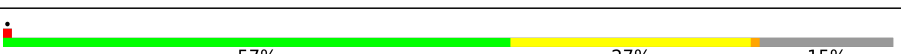
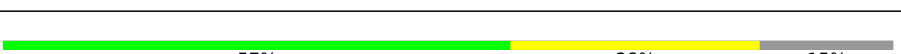
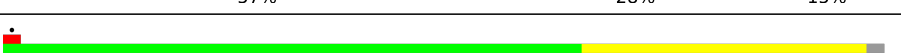
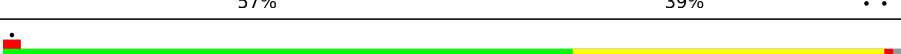
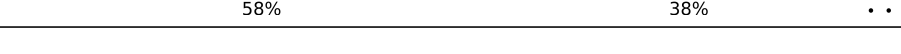
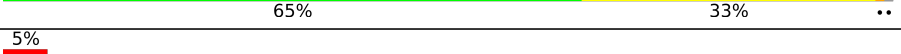
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Mol	Chain	Length	Quality of chain
40	Dy	297	
40	Ga	297	
41	Ey	176	
41	Ha	176	
42	Fy	244	
42	Ia	244	
43	Gy	256	
43	Ja	256	
44	Hy	191	
44	Ka	191	
45	Iy	221	
45	La	221	
46	Jy	174	
46	Ma	174	
47	Ly	199	
47	Na	199	
48	My	138	
48	Oa	138	
49	Ny	204	
49	Pa	204	
50	Oy	199	
50	Qa	199	
51	A	184	
51	Py	184	
52	B	186	

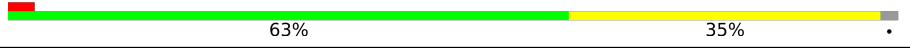
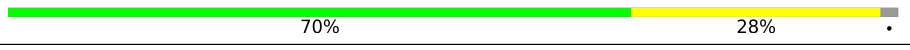
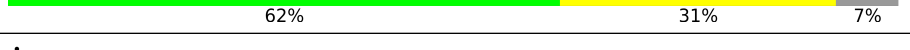
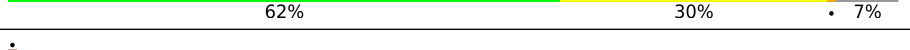
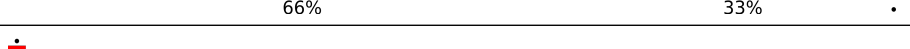
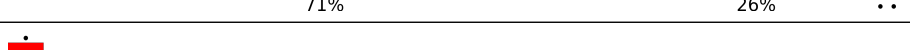
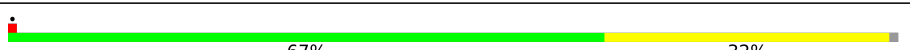
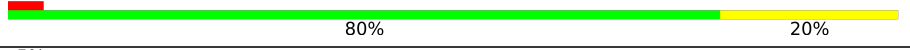
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Mol	Chain	Length	Quality of chain
52	Qy	186	
53	C	189	
53	Ry	189	
54	D	172	
54	Sy	172	
55	E	160	
55	Ty	160	
56	F	121	
56	Uy	121	
57	G	137	
57	Vy	137	
58	H	155	
58	Wy	155	
59	I	142	
59	Xy	142	
60	J	127	
60	Yy	127	
61	K	136	
61	Zy	136	
62	L	149	
62	ay	149	
63	M	59	
63	by	59	
64	N	105	
64	cy	105	

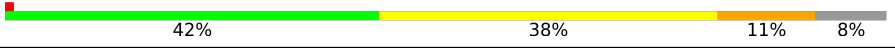
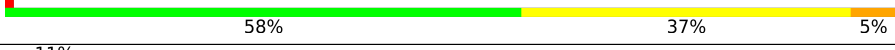
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Mol	Chain	Length	Quality of chain
65	O	113	
65	dy	113	
66	P	130	
66	ey	130	
67	Q	107	
67	fy	107	
68	R	121	
68	gy	121	
69	S	120	
69	hb	120	
70	T	100	
70	ib	100	
71	U	88	
71	jb	88	
72	V	78	
72	kb	78	
73	W	51	
73	lb	51	
74	X	128	
74	mb	128	
75	Y	25	
75	nb	25	
76	Z	106	
76	ob	106	
77	aa	92	

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Mol	Chain	Length	Quality of chain
77	pb	92	
78	1b	3396	
78	Aa	3396	
79	6b	76	
79	8	76	
80	ba	311	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 401820 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2b	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		
1	a	1758	Total	C	N	O	P	0	0
			37455	16745	6624	12328	1758		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		
2	b	206	Total	C	N	O	S	0	0
			1583	1017	281	283	2		

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Ba	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		
3	c	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 4 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Pb	117	Total	C	N	O	S	0	0
			916	583	171	155	7		
4	q	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Cb	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		
5	d	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 6 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Db	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		
6	e	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Eb	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		
7	f	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 8 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Fb	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		
8	g	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 9 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Gb	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		
9	h	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 10 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Hb	184	Total	C	N	O		0	0
			1473	946	263	264			

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Mol	Chain	Residues	Atoms				AltConf	Trace
10	i	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 11 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Ib	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		
11	j	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 12 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Jb	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		
12	k	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 13 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Kb	92	Total	C	N	O	S	0	0
			752	487	122	141	2		
13	l	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 14 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Lb	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		
14	m	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 15 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Mb	121	Total	C	N	O	S	0	0
			875	551	153	169	2		
15	n	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 16 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Nb	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		
16	o	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 17 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ob	127	Total	C	N	O	S	0	0
			926	569	185	169	3		
17	p	128	Total	C	N	O	S	0	0
			949	582	188	176	3		

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Qb	141	Total	C	N	O	0	0
			1105	708	203	194		
18	r	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 19 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Rb	121	Total	C	N	O	S	0	0
			948	596	179	171	2		
19	s	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sb	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		
20	t	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Tb	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		
21	u	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 22 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ub	100	Total	C	N	O	S	0	0
			797	506	144	146	1		
22	v	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Vb	87	Total	C	N	O	S	0	0
			673	415	125	131	2		
23	w	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Wb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		
24	x	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Xb	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		
25	y	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Yb	134	Total	C	N	O	0	0
			1073	676	208	189		

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Mol	Chain	Residues	Atoms				AltConf	Trace
26	z	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Zb	82	Total	C	N	O	0	0
			651	416	123	112		
27	0	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 28 is a protein called 40S ribosomal protein S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	ab	97	Total	C	N	O	S	0	0
			769	475	160	129	5		
28	1	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		
29	2	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 30 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	db	53	Total	C	N	O	S	0	0
			442	274	92	72	4		
30	4	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	eb	60	Total	C	N	O	S	0	0
			472	298	97	76	1		
31	5	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	fb	73	Total	C	N	O	S	0	0
			556	352	105	95	4		
32	6	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	gb	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		
33	7	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 34 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	cb	63	Total	C	N	O	S	0	0
			491	303	96	91	1		
34	3	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 35 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4b	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		
35	Bb	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 36 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	3b	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		
36	Ca	157	Total	C	N	O	P	0	0
			3333	1491	584	1101	157		

- Molecule 37 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ay	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		
37	Da	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 38 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	By	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		
38	Ea	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 39 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cy	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		
39	Fa	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 40 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Dy	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		
40	Ga	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 41 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ey	167	Total	C	N	O	S	0	0
			1303	840	234	228	1		
41	Ha	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 42 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Fy	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ia	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Gy	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		
43	Ja	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Hy	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		
44	Ka	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Iy	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		
45	La	209	Total	C	N	O	S	0	0
			1696	1077	321	293	5		

- Molecule 46 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Jy	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		
46	Ma	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 47 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Ly	193	Total	C	N	O	0	0
			1543	962	315	266		
47	Na	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 48 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	My	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		
48	Oa	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ny	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		
49	Pa	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 50 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Oy	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		
50	Qa	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 51 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Py	183	Total	C	N	O	S	0	0
			1416	879	284	253			
51	A	175	Total	C	N	O	S	0	0
			1378	856	273	249			

- Molecule 52 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Qy	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		
52	B	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 53 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	Ry	188	Total	C	N	O	0	0
			1515	932	323	260		
53	C	183	Total	C	N	O	0	0
			1482	911	320	251		

- Molecule 54 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Sy	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		
54	D	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 55 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ty	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		
55	E	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 56 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	Uy	100	Total	C	N	O	0	0
			796	516	131	149		
56	F	98	Total	C	N	O	0	0
			778	505	127	146		

- Molecule 57 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Vy	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		
57	G	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 58 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Wy	126	Total	C	N	O	S	0	0
			849	532	167	149	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	H	135	Total	C	N	O	S	0	0
			1089	682	219	187	1		

- Molecule 59 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Xy	121	Total	C	N	O	S	0	0
			964	620	169	173	2		
59	I	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Yy	125	Total	C	N	O		0	0
			984	620	191	173			
60	J	124	Total	C	N	O		0	0
			976	614	190	172			

- Molecule 61 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Zy	135	Total	C	N	O		0	0
			1092	710	202	180			
61	K	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 62 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ay	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		
62	L	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 63 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	by	58	Total	C	N	O		0	0
			462	289	100	73			
63	M	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 64 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	cy	96	Total	C	N	O	S	0	0
			737	476	123	137	1		
64	N	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 65 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	dy	109	Total	C	N	O	S	0	0
			876	556	167	152	1		
65	O	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 66 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ey	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		
66	P	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	fy	106	Total	C	N	O	S	0	0
			850	540	165	144	1		
67	Q	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 68 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	gy	112	Total	C	N	O	S	0	0
			880	545	179	152	4		
68	R	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 69 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	hb	119	Total	C	N	O	S	0	0
			969	615	186	167	1		
69	S	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	ib	99	Total	C	N	O	S	0	0
			766	478	154	132	2		
70	T	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	jb	85	Total	C	N	O	S	0	0
			670	408	146	111	5		
71	U	82	Total	C	N	O	S	0	0
			650	396	142	107	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	kb	77	Total	C	N	O	0	0
			612	391	115	106		
72	V	77	Total	C	N	O	0	0
			608	388	114	106		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	lb	50	Total	C	N	O	S	0	0
			436	272	97	65	2		
73	W	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	mb	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	X	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 75 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	nb	25	Total	C	N	O	S	0	0
			229	139	62	27	1		
75	Y	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 76 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ob	103	Total	C	N	O	S	0	0
			824	517	167	135	5		
76	Z	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	pb	91	Total	C	N	O	S	0	0
			694	429	138	121	6		
77	aa	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 78 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	1b	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		
78	Aa	3127	Total	C	N	O	P	0	0
			66891	29878	12066	21820	3127		

- Molecule 79 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	6b	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		
79	8	76	Total	C	N	O	P	0	0
			1616	721	281	538	76		

- Molecule 80 is a protein called 60S acidic ribosomal protein P0.

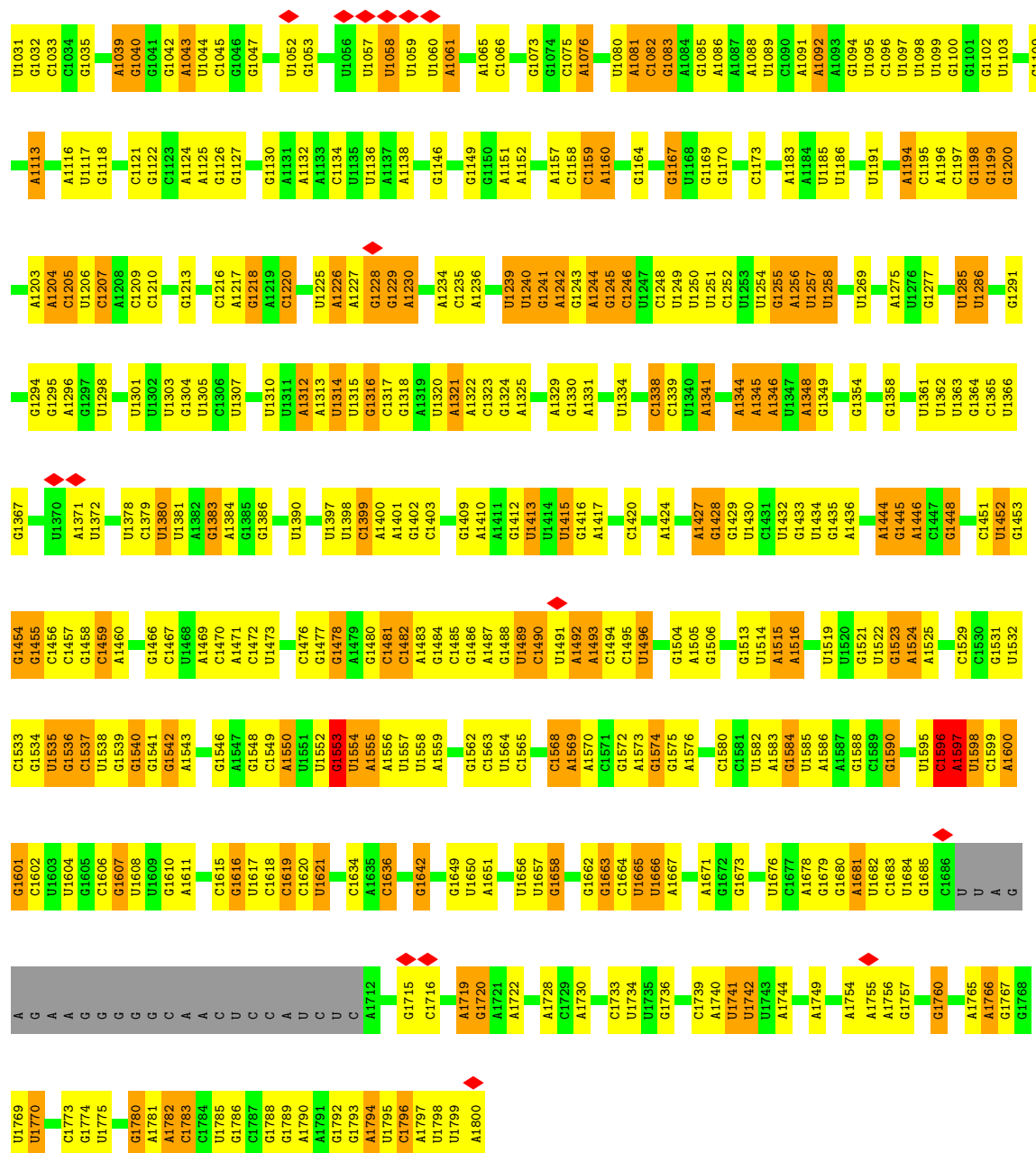
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	ba	138	1052	672	187	190	3	0	0

U1769	U1770	C1773	G1774	U1775	G1778	U1779	A1780	A1781	A1782	C1783	G1786	G1789	A1790	A1791	A1792	A1793	A1794	A1795	A1796	A1797	A1798	A1799	A1800	A1801	A1802	A1803	A1804	A1805	A1806	A1807	A1808	A1809	A1810	A1811	A1812	A1813	A1814																																											
U1884	U1888	A1889	G1890	A1894	G1895	U1896	A1897	A1898	A1899	C1900	G1901	G1902	A1903	A1904	A1905	A1906	A1907	A1908	A1909	A1910	A1911	A1912	A1913	A1914	A1915	A1916	A1917	A1918	A1919	A1920	A1921	A1922	A1923	A1924	A1925	A1926	A1927	A1928	A1929	A1930	A1931	A1932	A1933	A1934	A1935	A1936	A1937	A1938	A1939	A1940	A1941	A1942	A1943	A1944	A1945	A1946	A1947	A1948	A1949	A1950	A1951	A1952	A1953	A1954	A1955	A1956	A1957	A1958	A1959	A1960	A1961	A1962	A1963	A1964	A1965	A1966	A1967	A1968	A1969	A1970
U1519	U1520	U1521	U1522	G1523	A1524	A1525	A1526	A1527	U1528	U1529	G1530	G1531	U1532	C1533	G1534	U1535	G1536	C1537	U1538	G1539	G1540	G1541	G1542	A1543	U1544	A1545	G1546	A1547	G1548	U1552	G1553	U1554	A1555	C1556	U1557	U1558	A1559	U1560	U1561	G1562	C1563	U1564	C1565	A1570	G1571	G1572	A1573	G1574	G1575	A1576	A1577	C1581	U1582	A1583	G1584	U1585																								
A1586	A1587	G1588	A1589	A1590	A1591	A1592	A1593	A1594	A1595	A1596	A1597	A1600	G1601	C1602	G1605	G1606	G1607	U1608	U1609	G1610	A1611	A1612	A1613	A1614	A1615	G1616	U1617	C1618	C1619	G1622	C1632	A1633	C1634	A1635	U1636	C1637	G1638	G1649	U1650	U1651	U1652	A1653	U1654	U1655	U1656	U1657	G1658	U1666	A1671	C1675	U1676	C1677	A1678	G1679	G1680	A1681	A1682	C1683																						
U1684	U1688	A1689	G1690	A1694	G1695	U1696	G1697	A1698	A1699	A1700	C1703	C1706	A1707	U1708	C1709	U1710	C1711	A1712	G1715	C1716	G1717	G1718	A1721	U1724	U1725	G1726	G1727	A1728	G1736	U1742	U1743	A1749	A1750	C1751	A1753	A1756	G1757	U1758	C1759	G1760	C1764	A1765	A1766	G1767	G1768																																			
U1769	U1770	C1773	G1774	U1775	G1778	U1779	A1780	A1781	A1782	C1783	G1786	G1789	A1790	A1791	A1792	A1793	A1794	A1795	A1796	A1797	A1798	A1799	A1800	A1801	A1802	A1803	A1804	A1805	A1806	A1807	A1808	A1809	A1810	A1811	A1812	A1813	A1814																																											

• Molecule 1: 18S rRNA

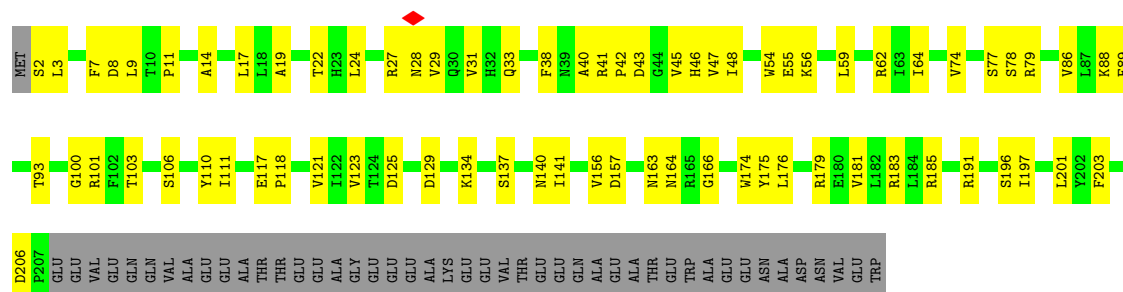
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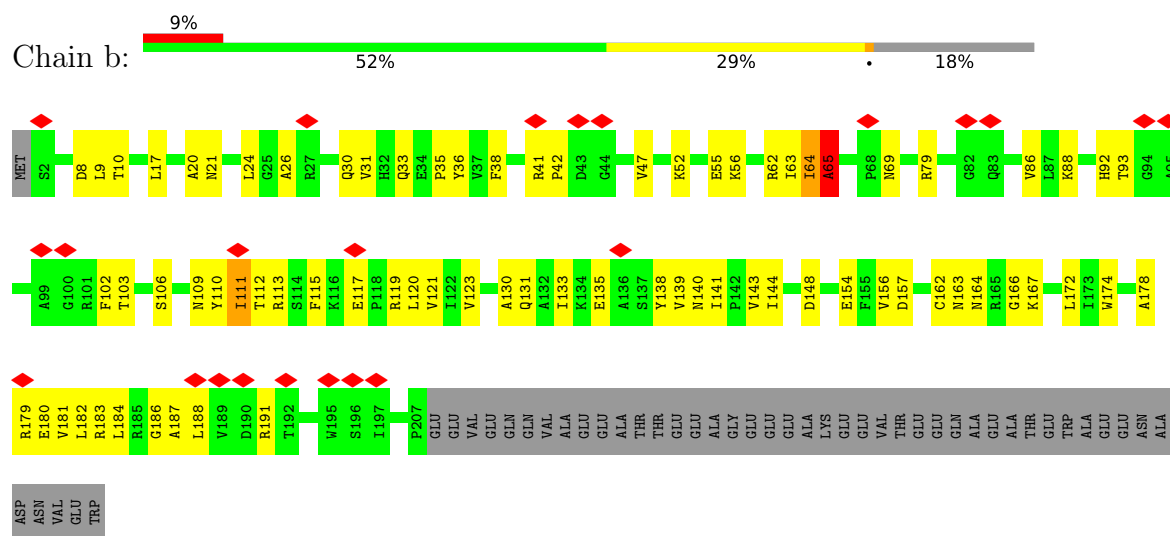


• Molecule 2: 40S ribosomal protein S0-A

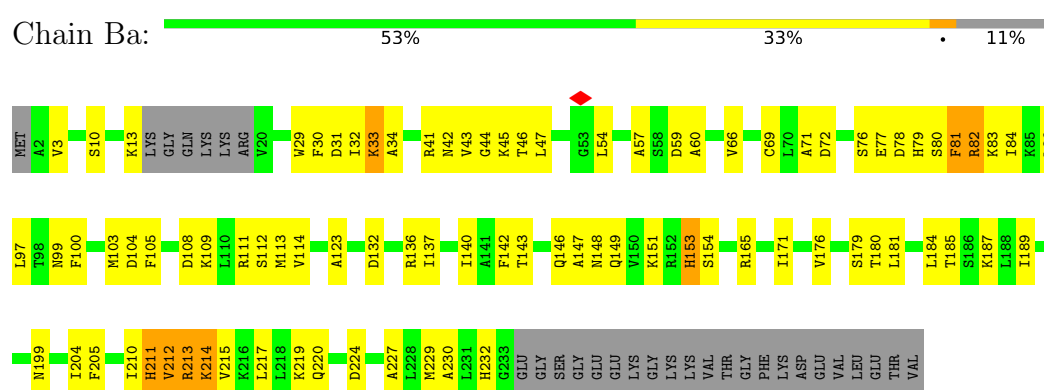
Chain Ab: 53% 29% 18%



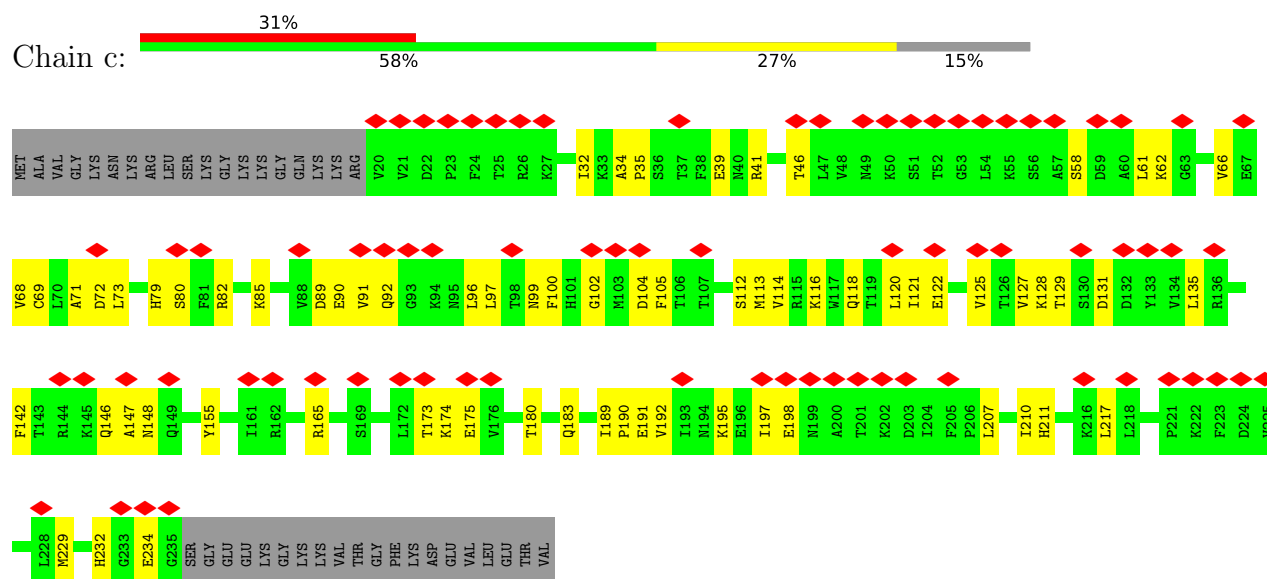
- Molecule 2: 40S ribosomal protein S0-A



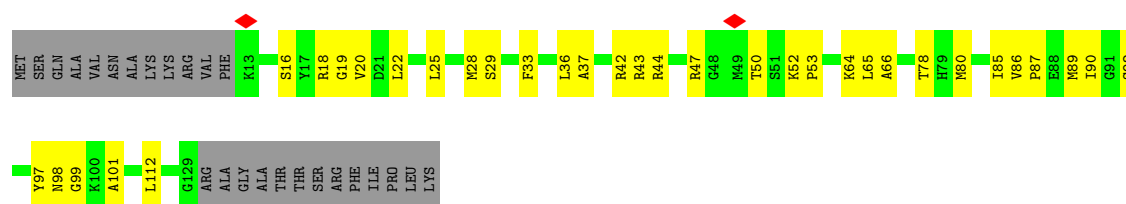
- Molecule 3: 40S ribosomal protein S1-A



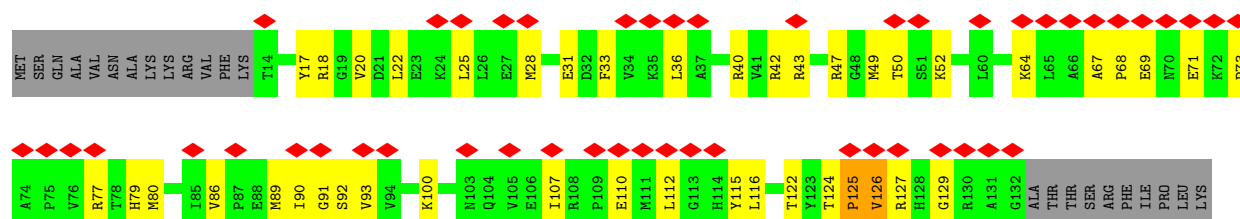
- Molecule 3: 40S ribosomal protein S1-A



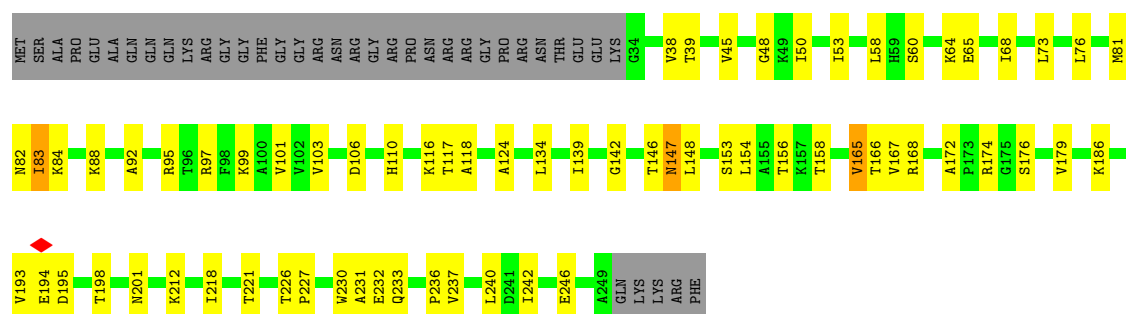
- Molecule 4: 40S ribosomal protein S15



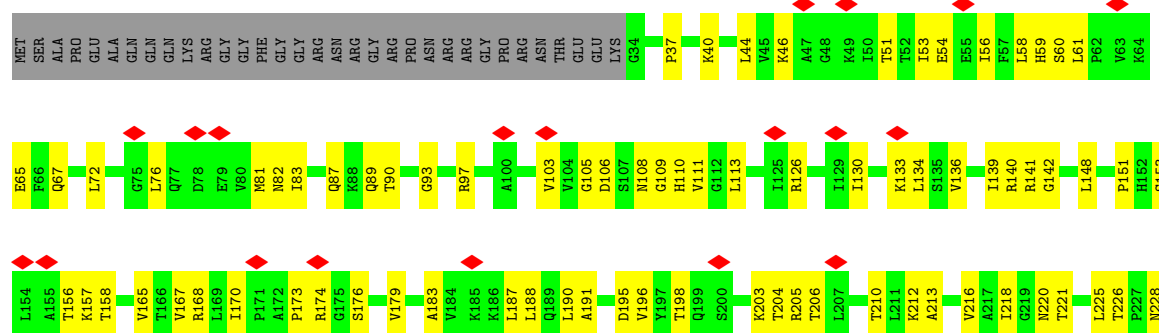
• Molecule 4: 40S ribosomal protein S15



• Molecule 5: 40S ribosomal protein S2



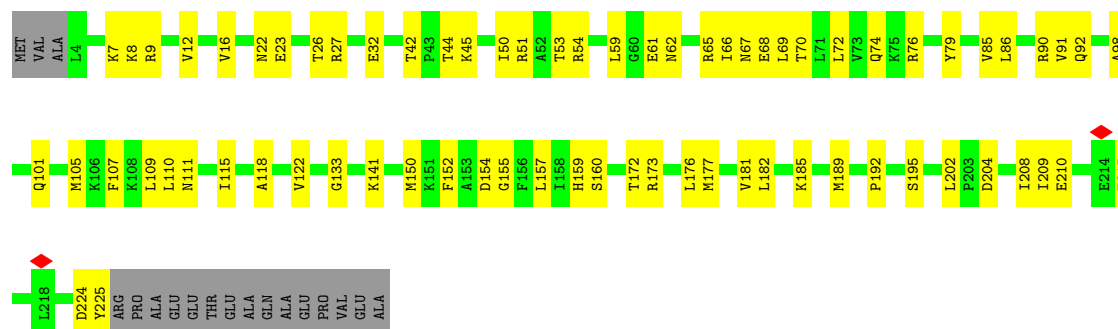
• Molecule 5: 40S ribosomal protein S2





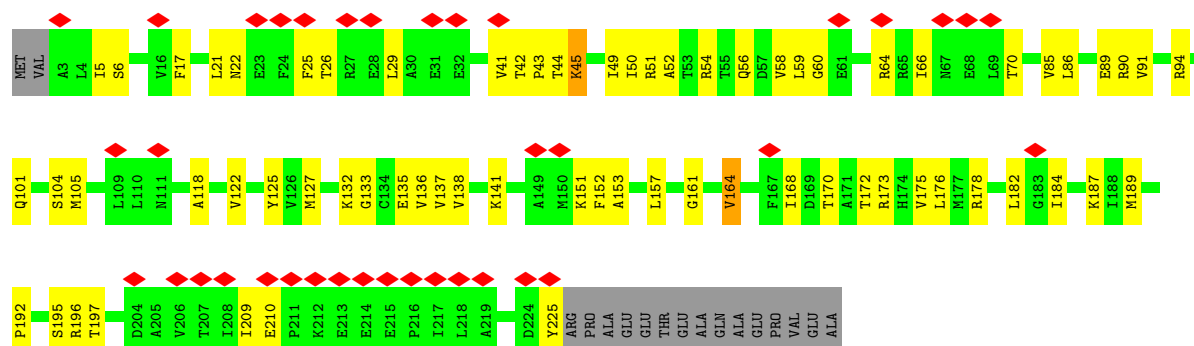
- Molecule 6: 40S ribosomal protein S3

Chain Db: 62% 30% 8%



- Molecule 6: 40S ribosomal protein S3

Chain e: 15% 64% 28% 7%



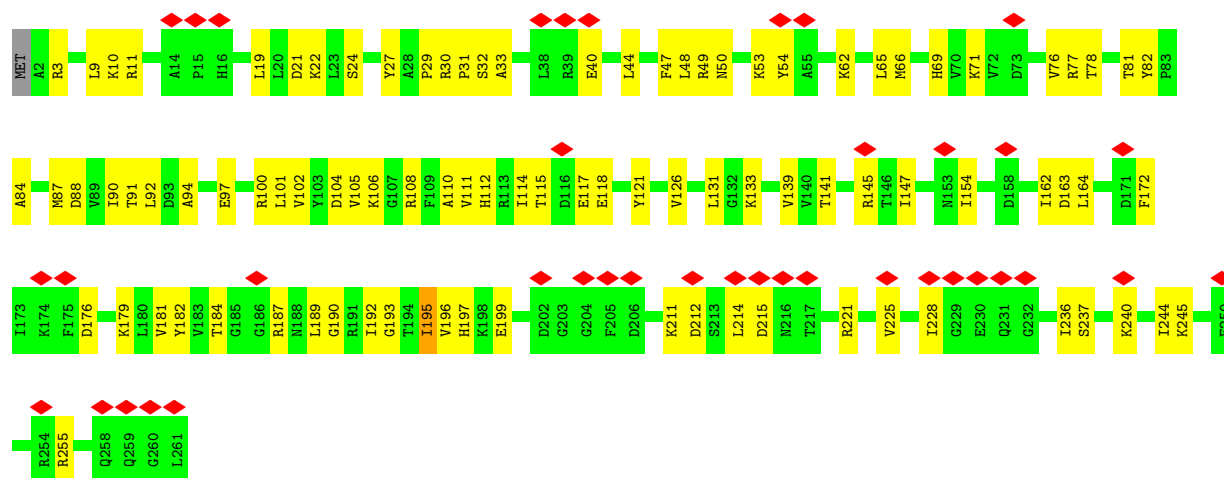
- Molecule 7: 40S ribosomal protein S4-A

Chain Eb: 60% 39% 1%

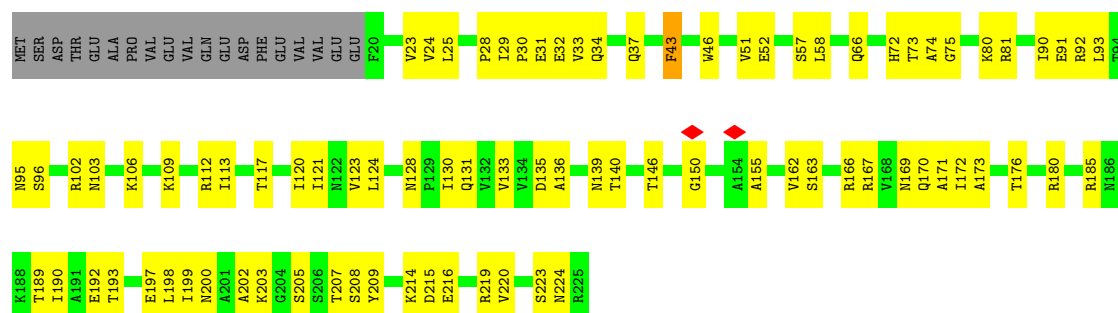


- Molecule 7: 40S ribosomal protein S4-A

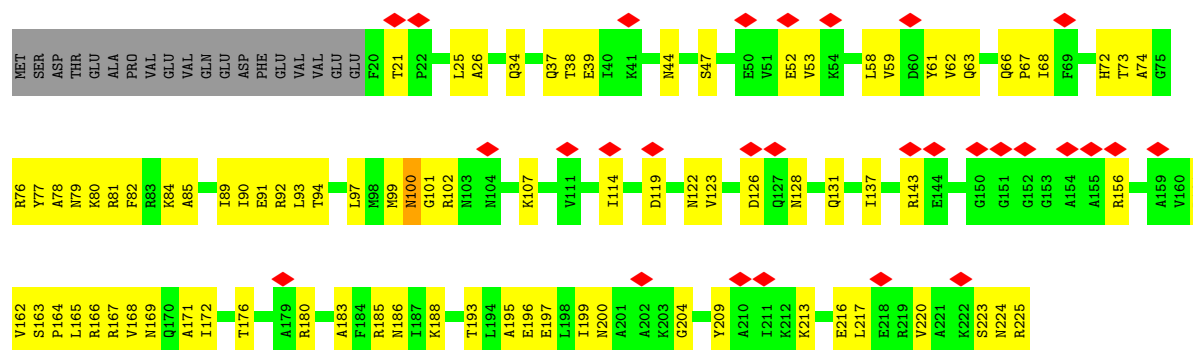
Chain f: 15% 64% 36%



• Molecule 8: Rps5p



• Molecule 8: Rps5p

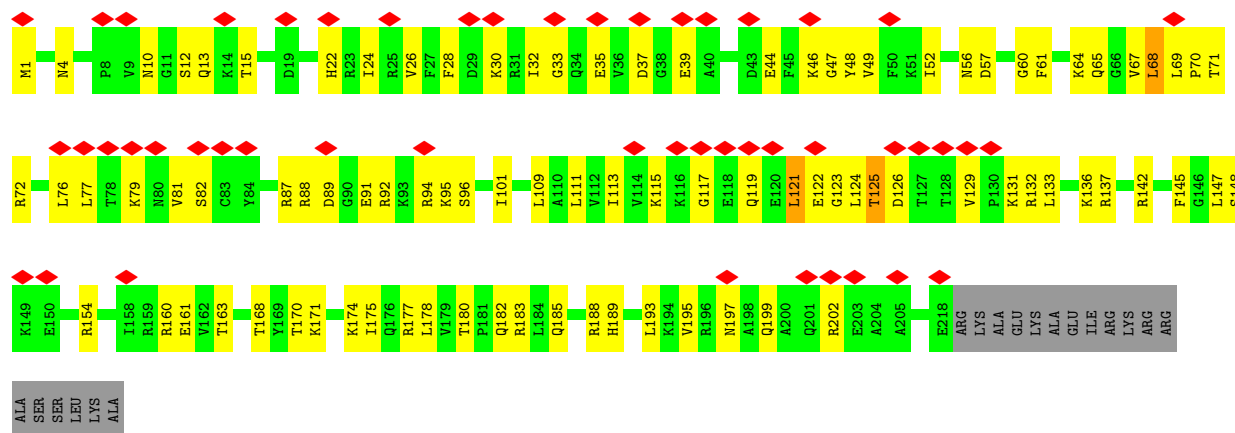


• Molecule 9: 40S ribosomal protein S6-A

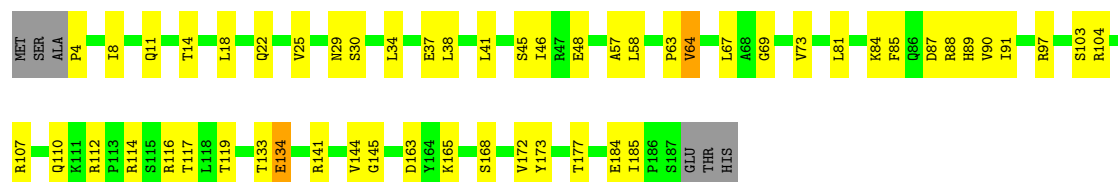




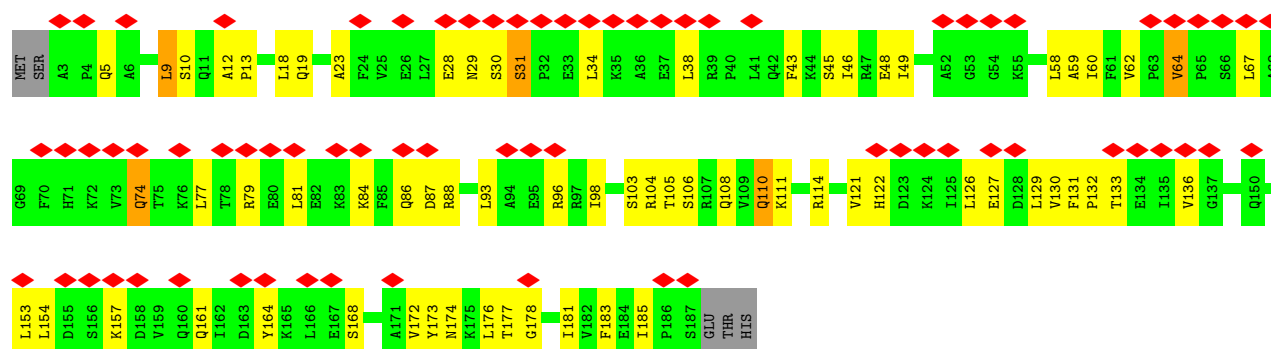
• Molecule 9: 40S ribosomal protein S6-A



• Molecule 10: 40S ribosomal protein S7-A

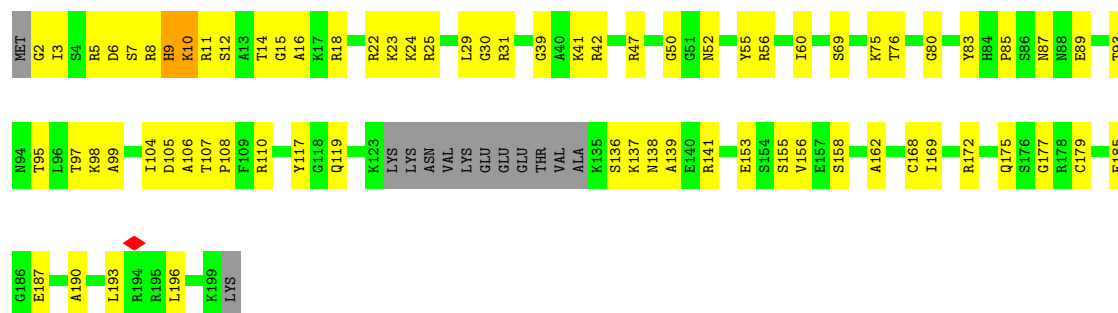


• Molecule 10: 40S ribosomal protein S7-A

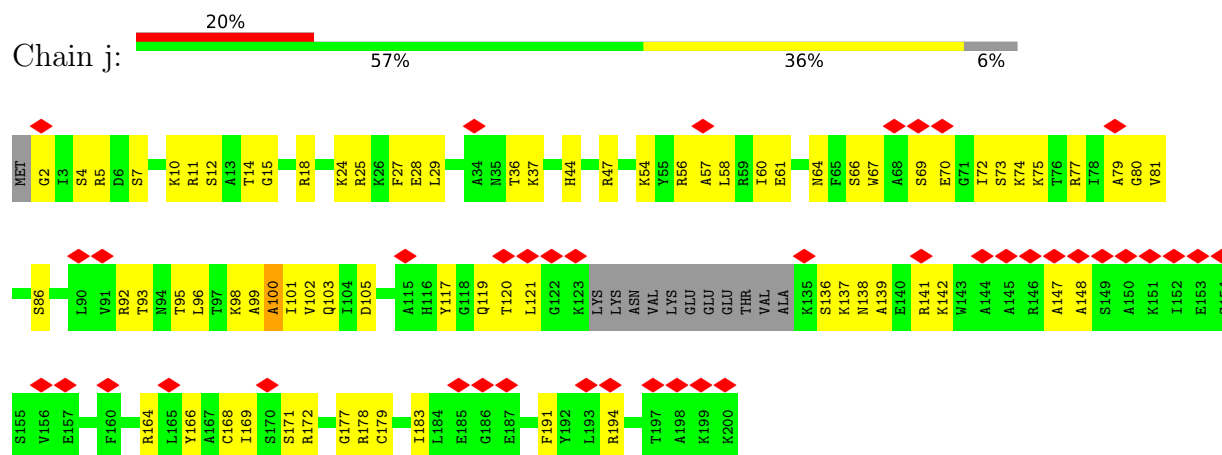


• Molecule 11: 40S ribosomal protein S8-A

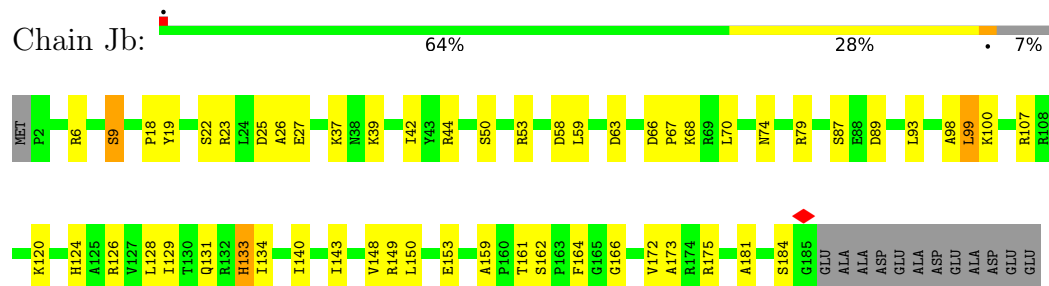




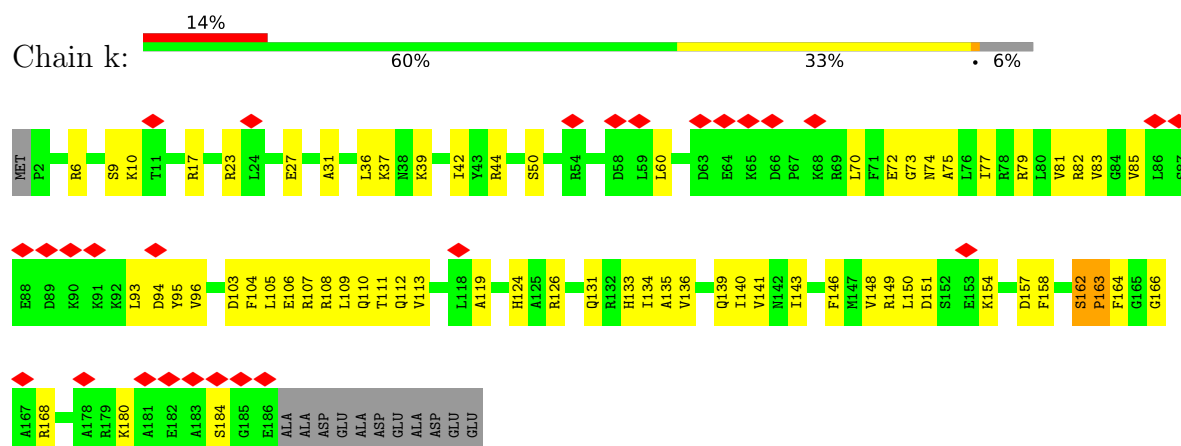
• Molecule 11: 40S ribosomal protein S8-A



• Molecule 12: 40S ribosomal protein S9-A



• Molecule 12: 40S ribosomal protein S9-A



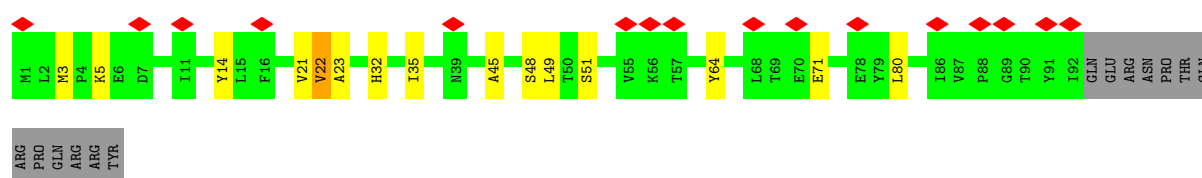
- Molecule 13: 40S ribosomal protein S10-A

Chain Kb: 



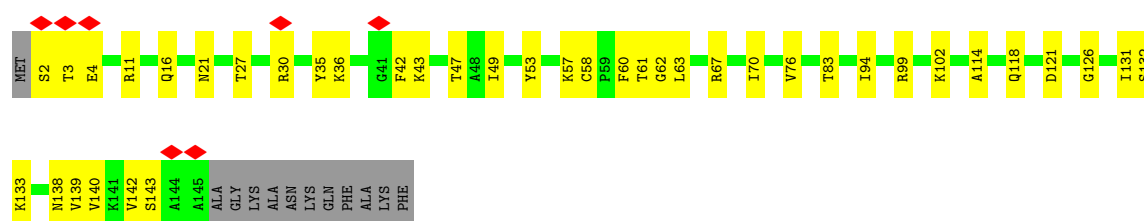
- Molecule 13: 40S ribosomal protein S10-A

Chain l: 



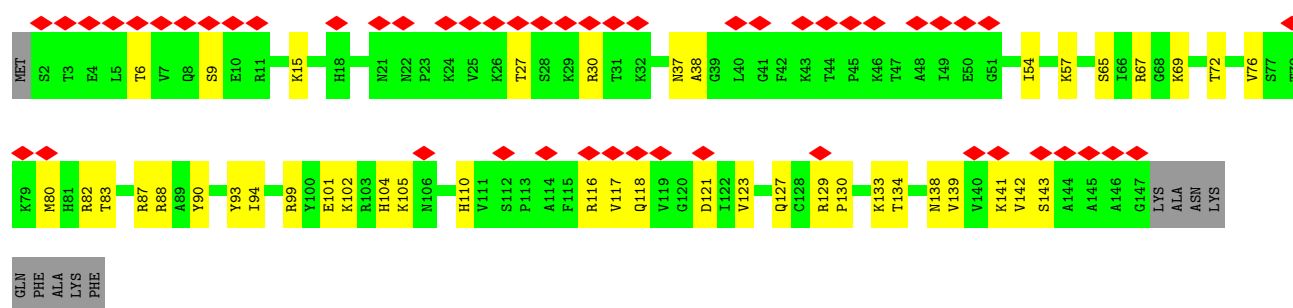
- Molecule 14: 40S ribosomal protein S11-A

Chain Lb: 



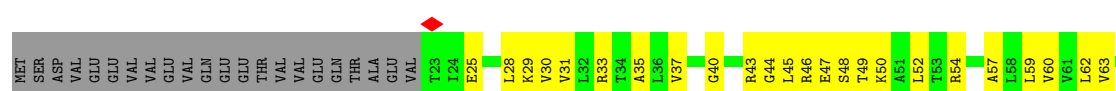
- Molecule 14: 40S ribosomal protein S11-A

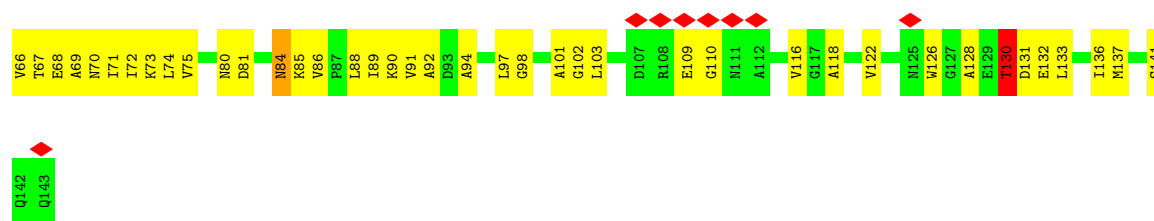
Chain m: 



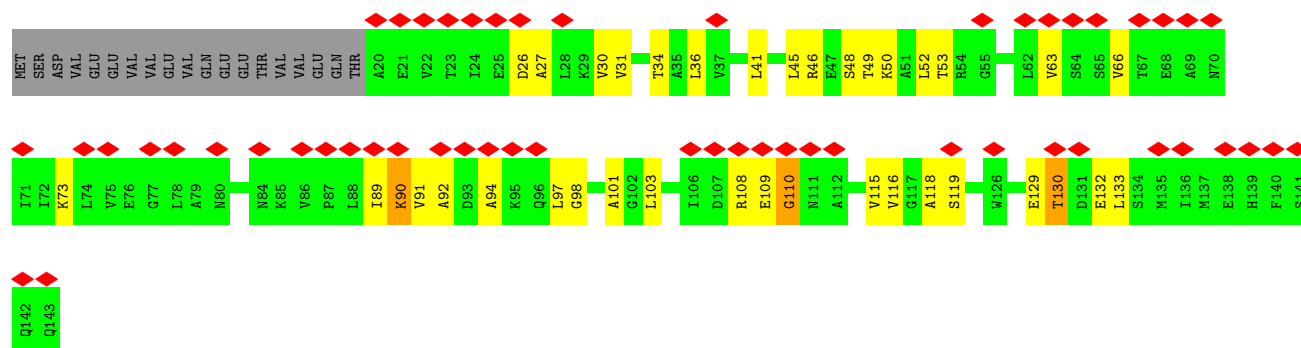
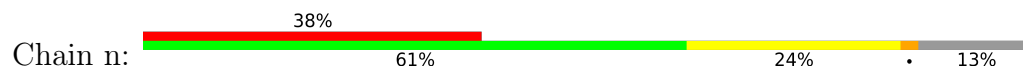
- Molecule 15: 40S ribosomal protein S12

Chain Mb: 

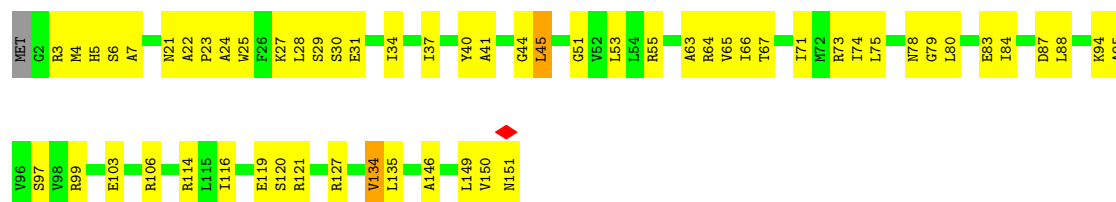




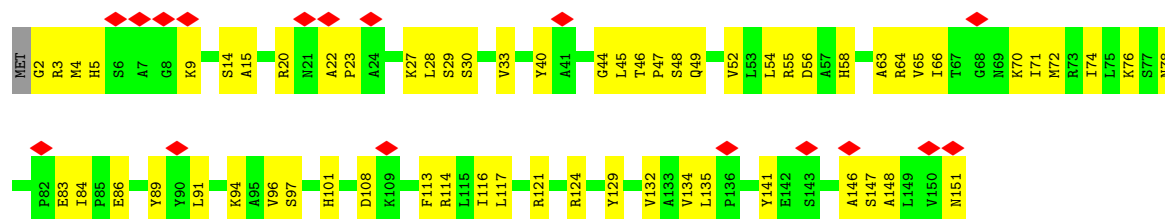
• Molecule 15: 40S ribosomal protein S12



• Molecule 16: 40S ribosomal protein S13

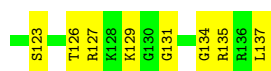


• Molecule 16: 40S ribosomal protein S13

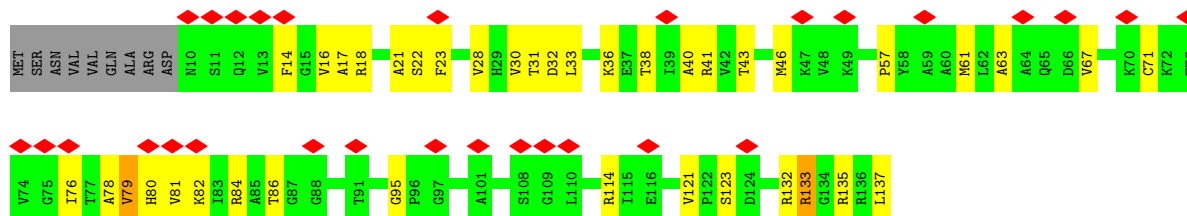


• Molecule 17: 40S ribosomal protein S14-A

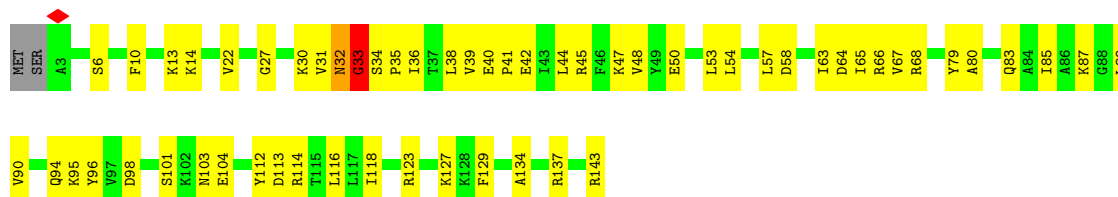




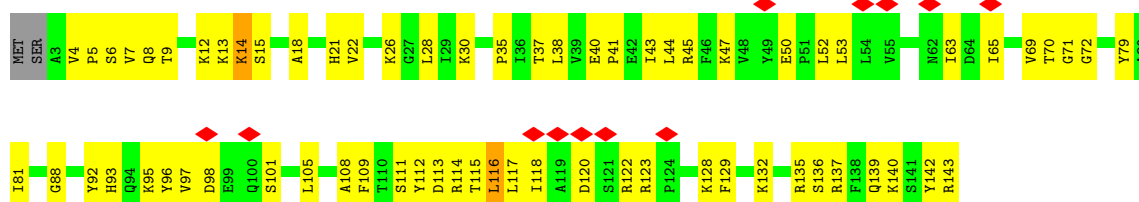
- Molecule 17: 40S ribosomal protein S14-A



- Molecule 18: 40S ribosomal protein S16-A



- Molecule 18: 40S ribosomal protein S16-A

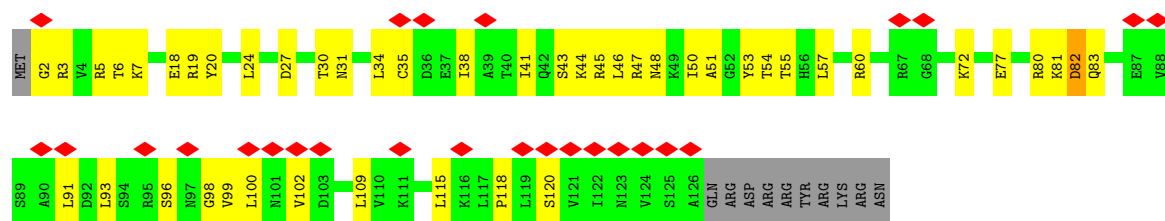


- Molecule 19: 40S ribosomal protein S17-B

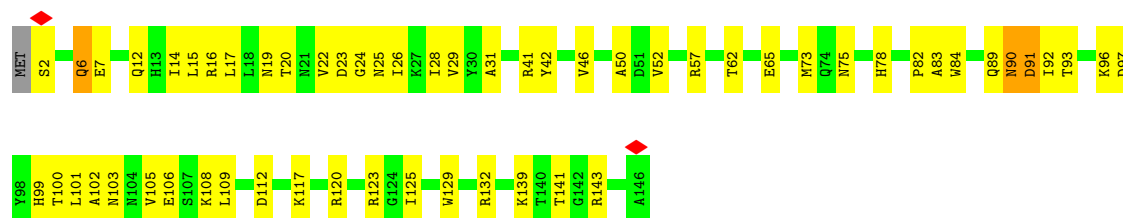


- Molecule 19: 40S ribosomal protein S17-B

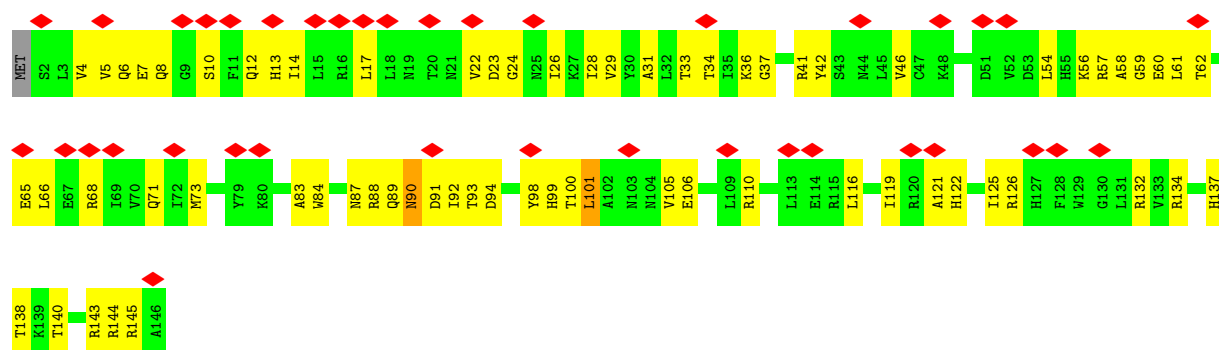




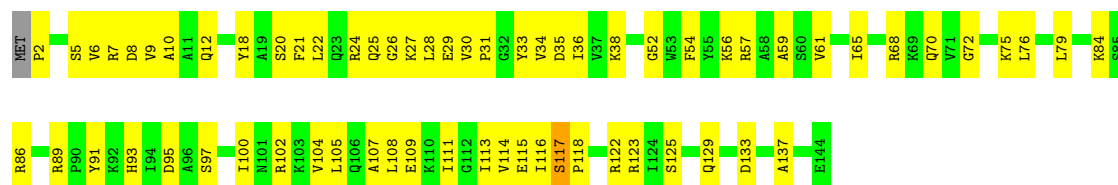
- Molecule 20: 40S ribosomal protein S18-A



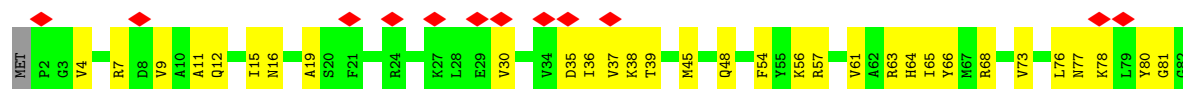
- Molecule 20: 40S ribosomal protein S18-A

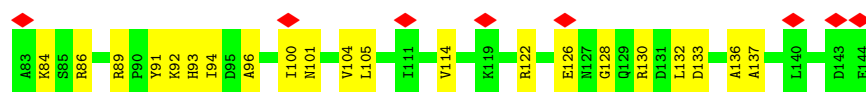


- Molecule 21: 40S ribosomal protein S19-A



- Molecule 21: 40S ribosomal protein S19-A

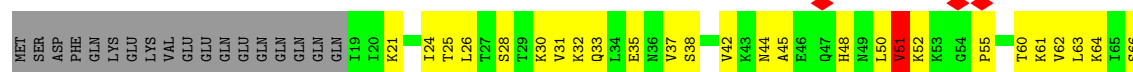




- Molecule 22: 40S ribosomal protein S20



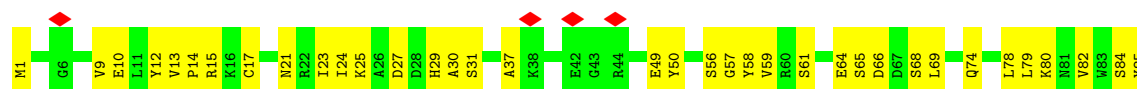
- Molecule 22: 40S ribosomal protein S20



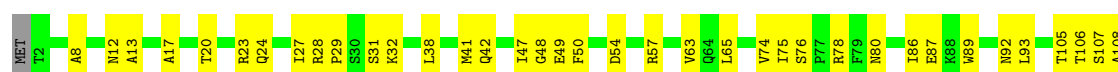
- Molecule 23: 40S ribosomal protein S21-A



- Molecule 23: 40S ribosomal protein S21-A



- Molecule 24: 40S ribosomal protein S22-A





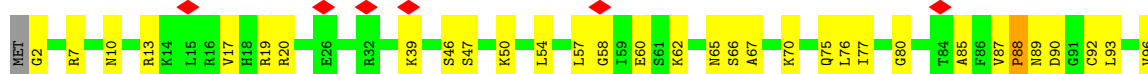
- Molecule 24: 40S ribosomal protein S22-A



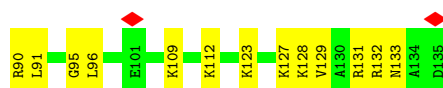
- Molecule 25: 40S ribosomal protein S23-A



- Molecule 25: 40S ribosomal protein S23-A

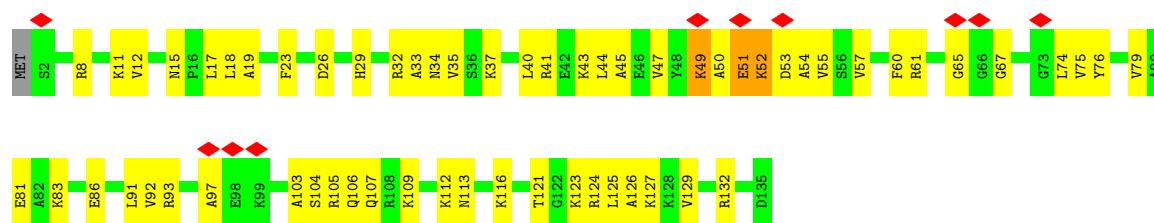


- Molecule 26: 40S ribosomal protein S24-A

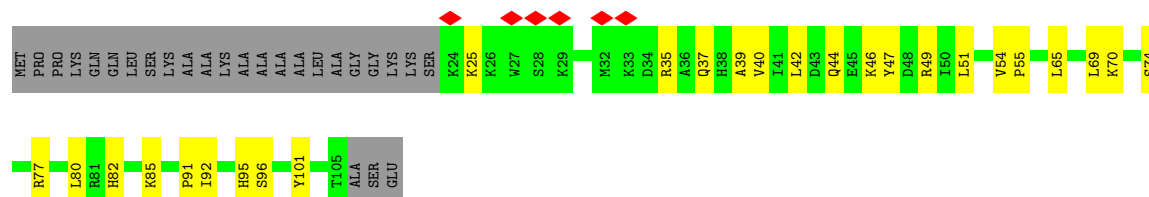


- Molecule 26: 40S ribosomal protein S24-A

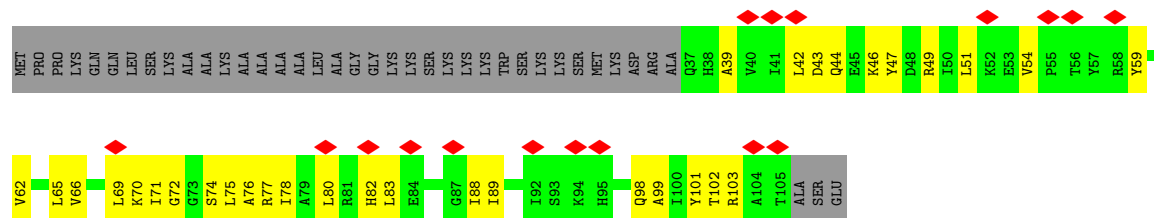




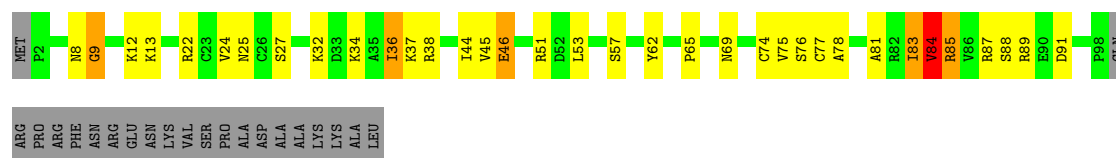
- Molecule 27: 40S ribosomal protein S25-A



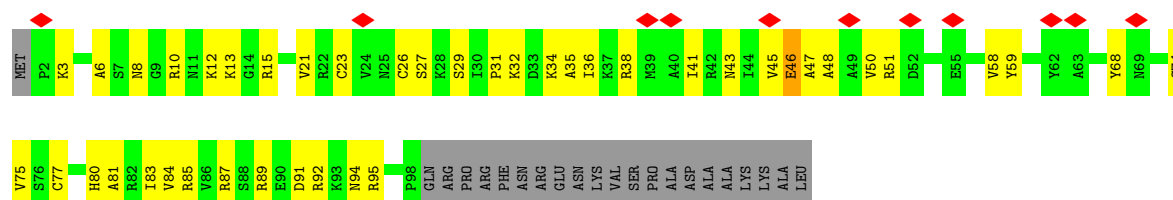
- Molecule 27: 40S ribosomal protein S25-A



- Molecule 28: 40S ribosomal protein S26-A

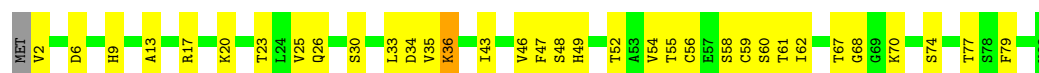


- Molecule 28: 40S ribosomal protein S26-A



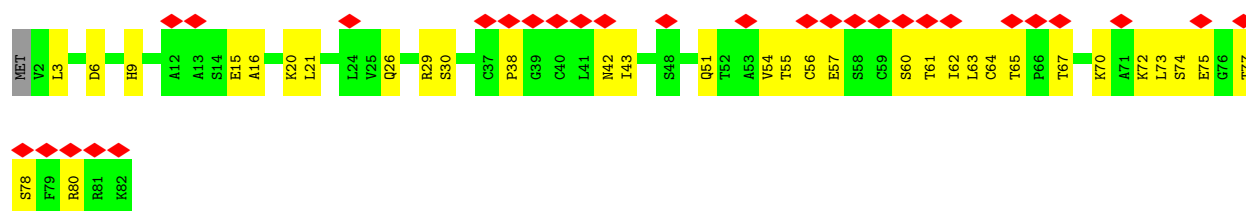
- Molecule 29: 40S ribosomal protein S27-A

Chain bb: 



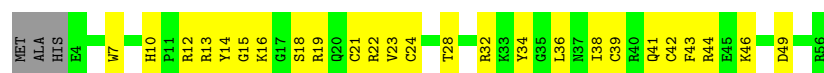
- Molecule 29: 40S ribosomal protein S27-A

Chain 2: 

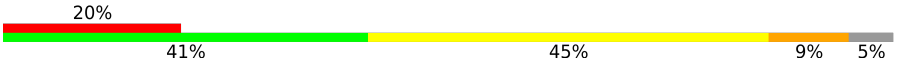


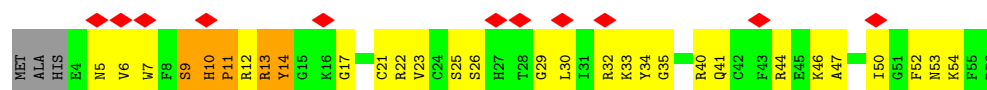
- Molecule 30: 40S ribosomal protein S29-A

Chain db: 



- Molecule 30: 40S ribosomal protein S29-A

Chain 4: 



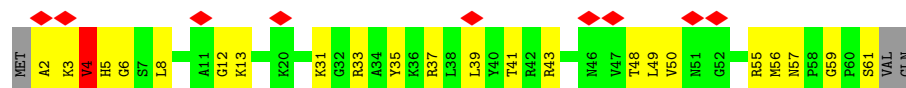
- Molecule 31: 40S ribosomal protein S30-A

Chain eb: 



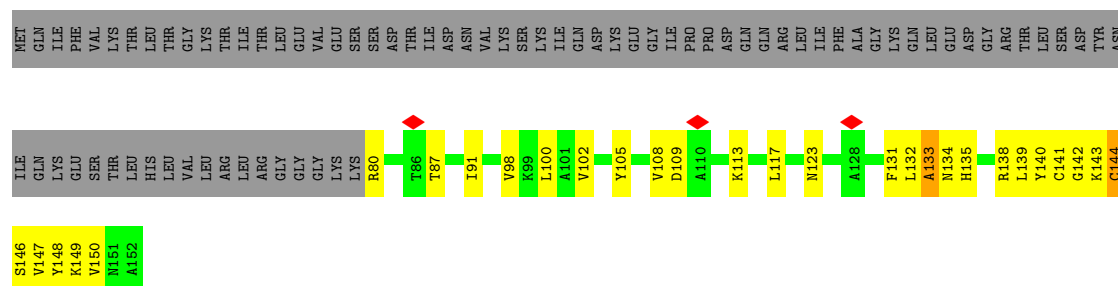
- Molecule 31: 40S ribosomal protein S30-A

Chain 5: 

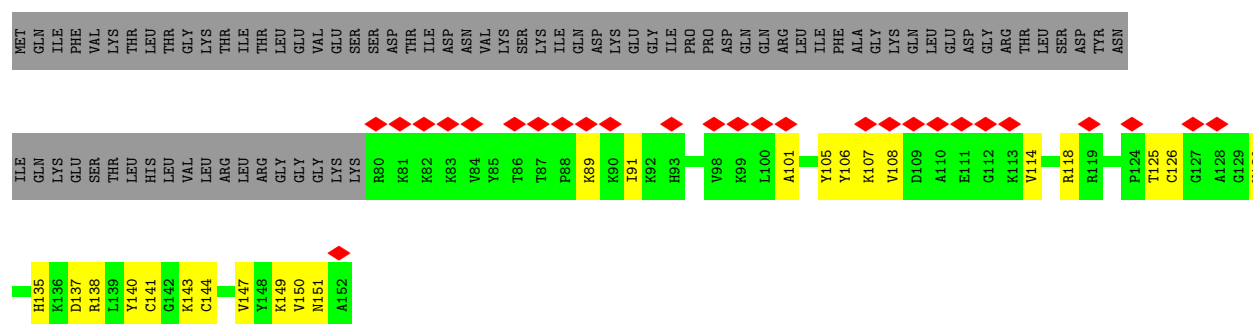
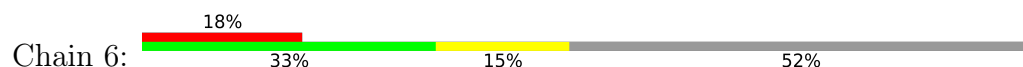


- Molecule 32: Ubiquitin-40S ribosomal protein S31

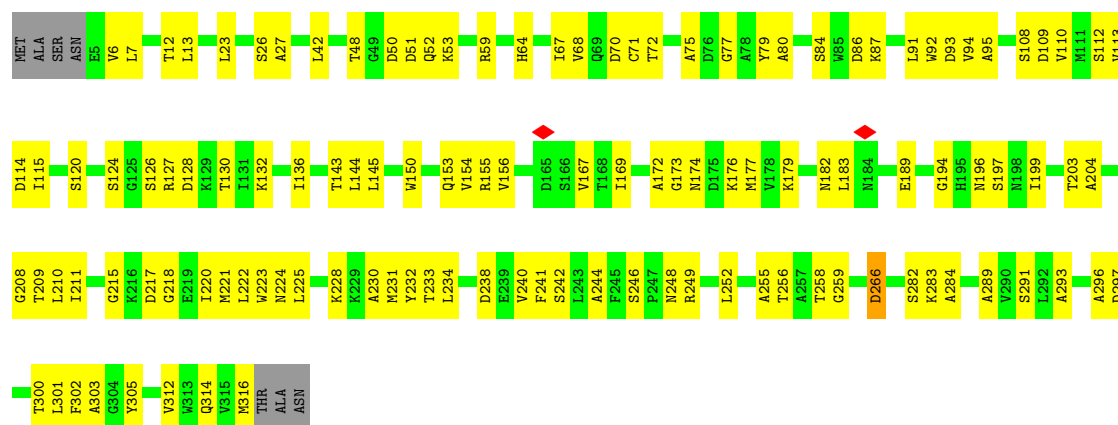
Chain fb: 



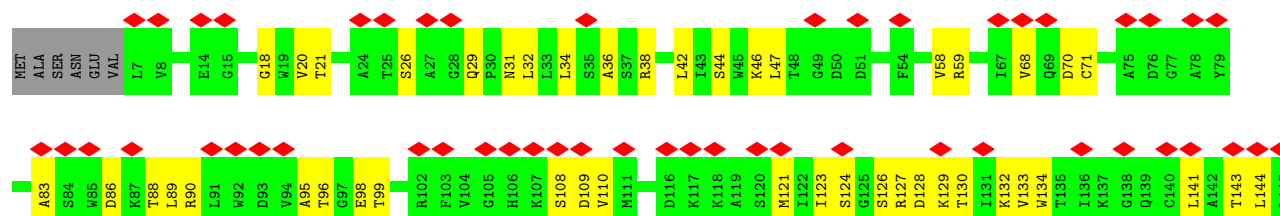
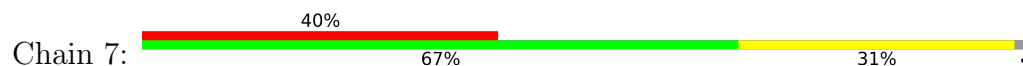
• Molecule 32: Ubiquitin-40S ribosomal protein S31

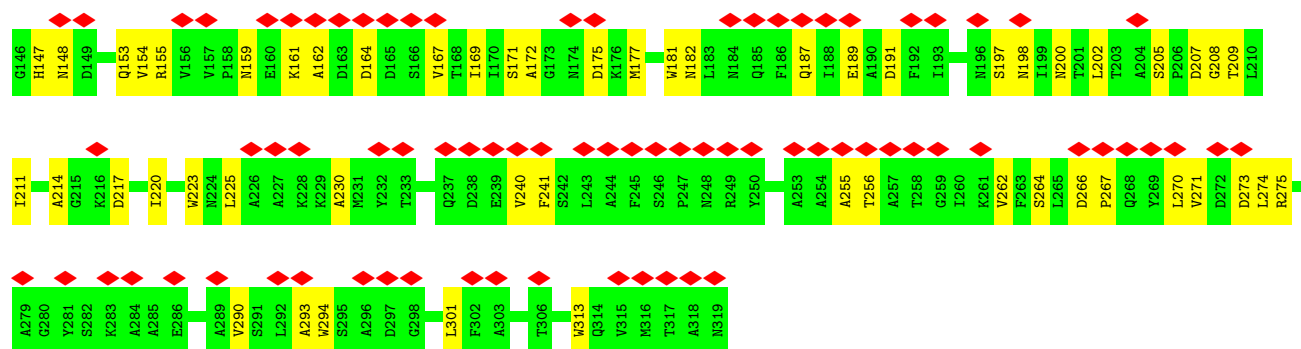


• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

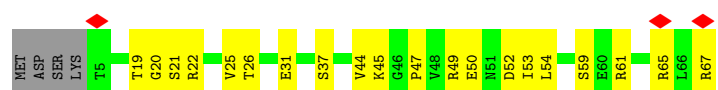


• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

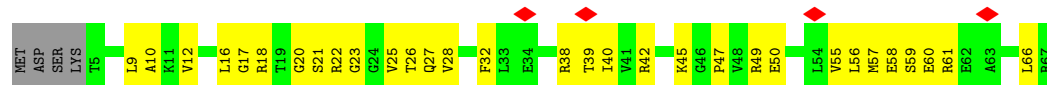




• Molecule 34: 40S ribosomal protein S28-B



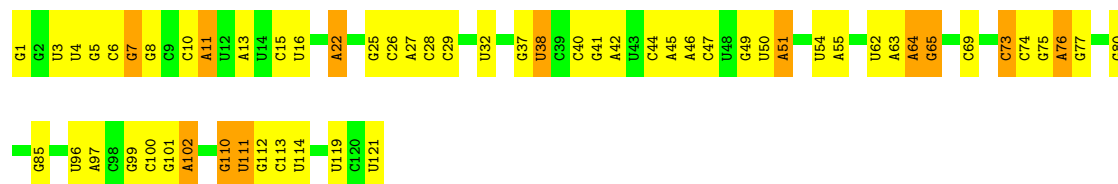
• Molecule 34: 40S ribosomal protein S28-B



• Molecule 35: 5S rRNA

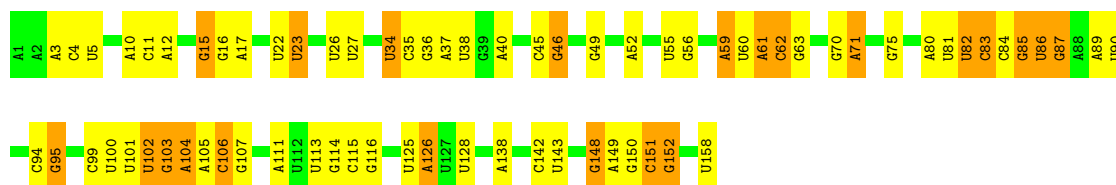


• Molecule 35: 5S rRNA



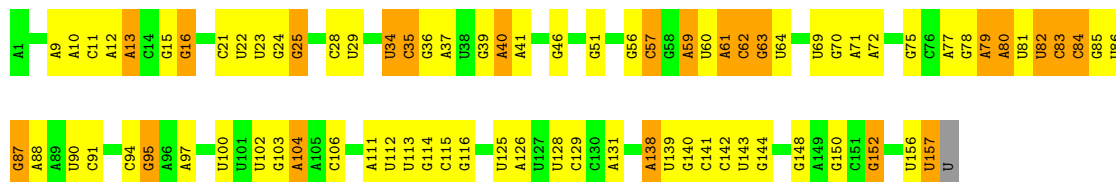
• Molecule 36: 5.8S rRNA





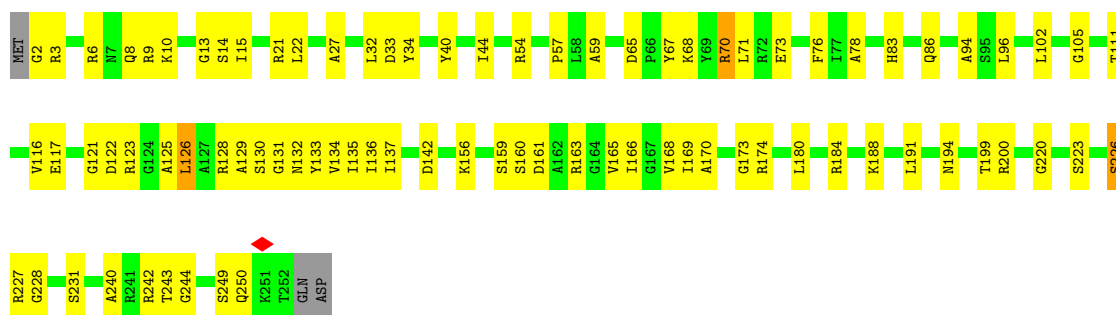
- Molecule 36: 5.8S rRNA

Chain Ca: 48% 37% 14%



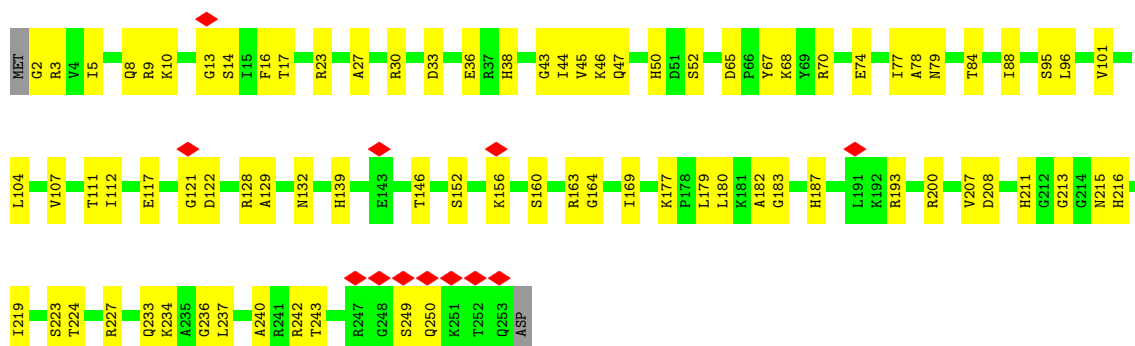
- Molecule 37: 60S ribosomal protein L2-A

Chain Ay: 66% 32%



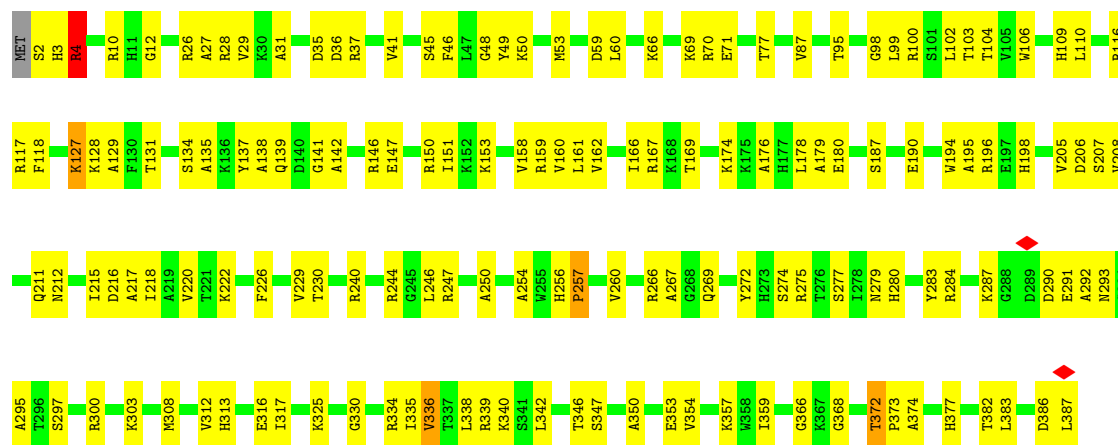
- Molecule 37: 60S ribosomal protein L2-A

Chain Da: 5% 67% 32%

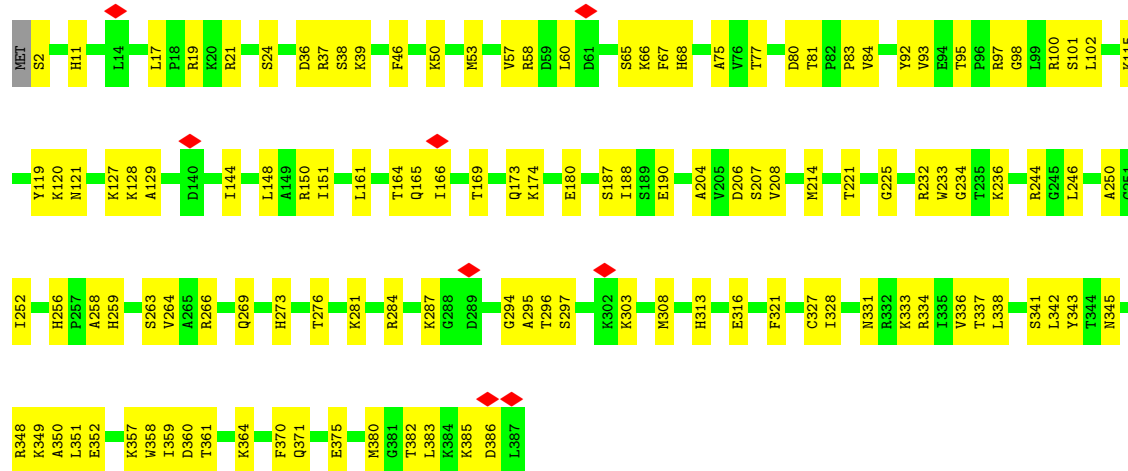


- Molecule 38: 60S ribosomal protein L3

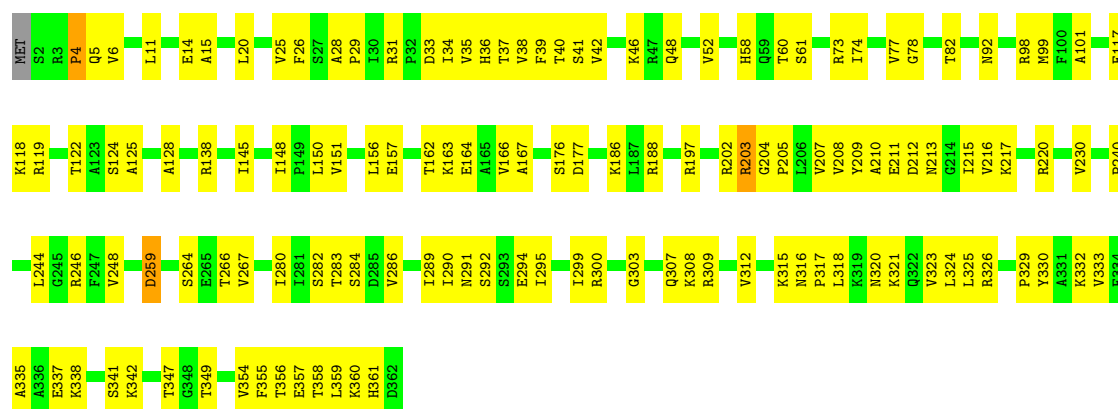
Chain By: 61% 38%



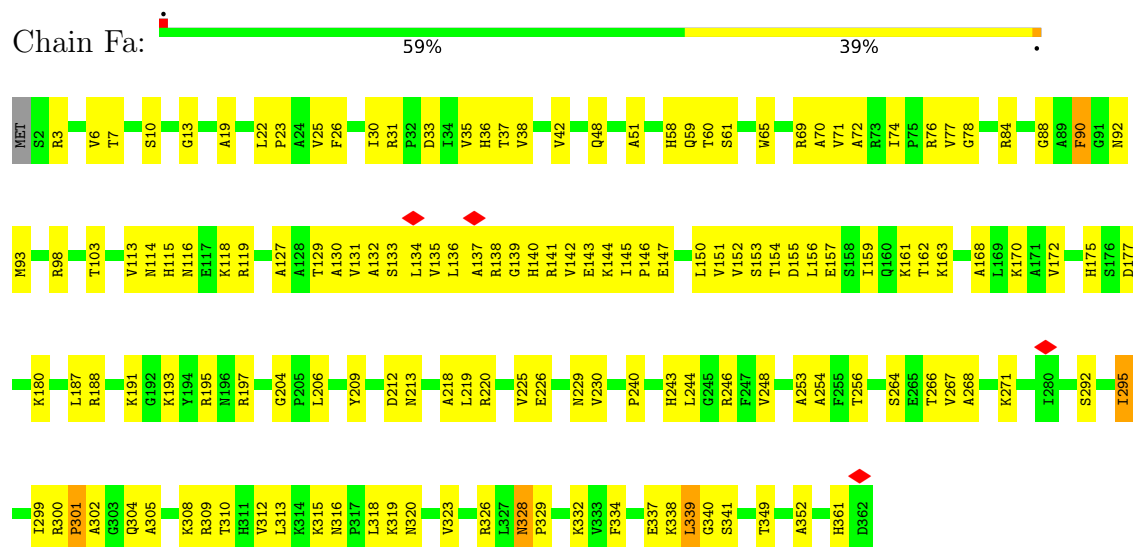
• Molecule 38: 60S ribosomal protein L3



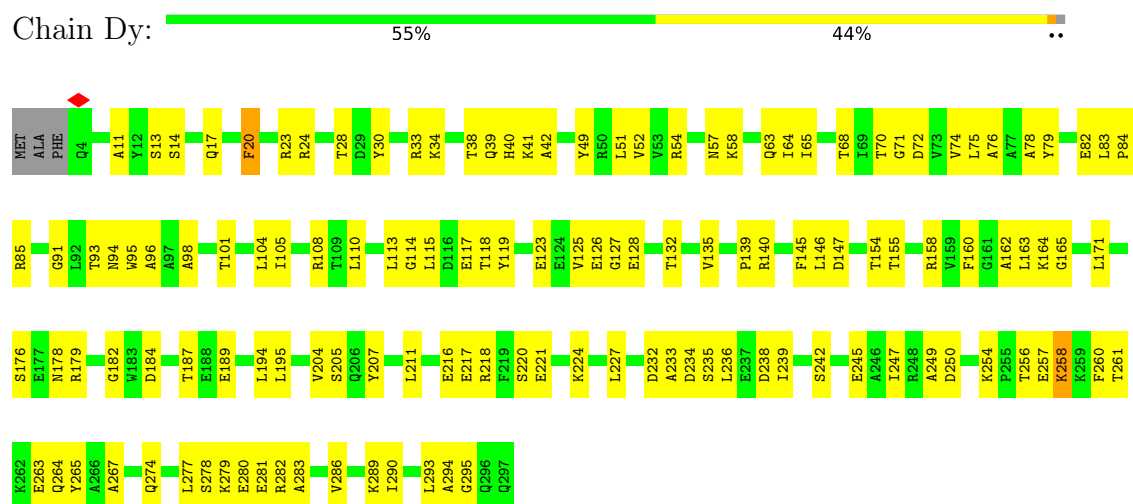
• Molecule 39: 60S ribosomal protein L4-A



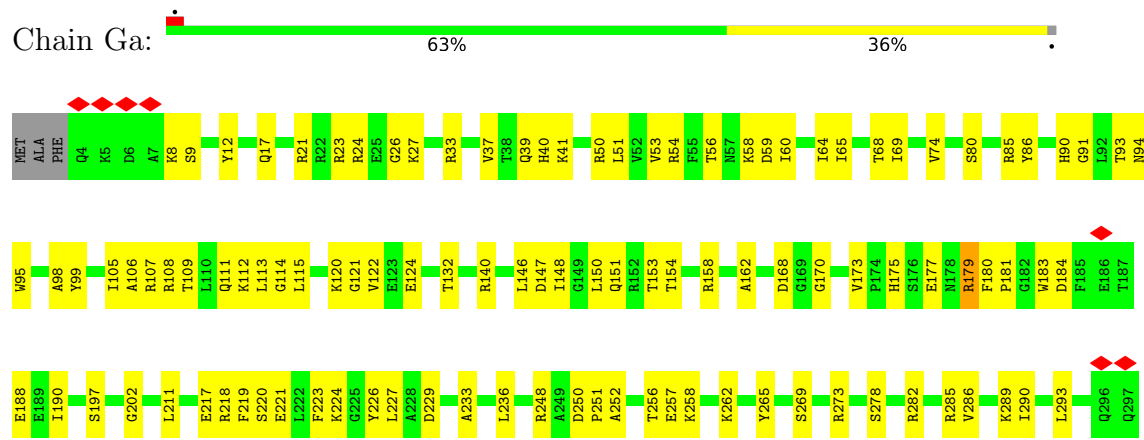
• Molecule 39: 60S ribosomal protein L4-A



• Molecule 40: 60S ribosomal protein L5

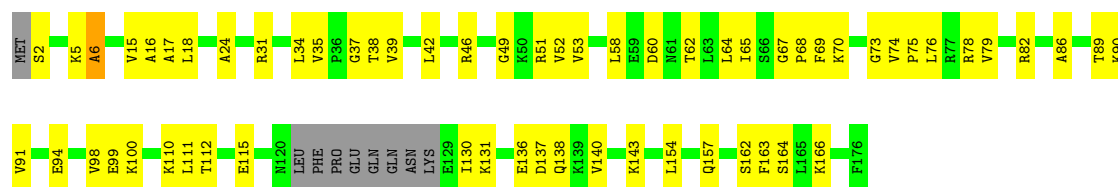


• Molecule 40: 60S ribosomal protein L5



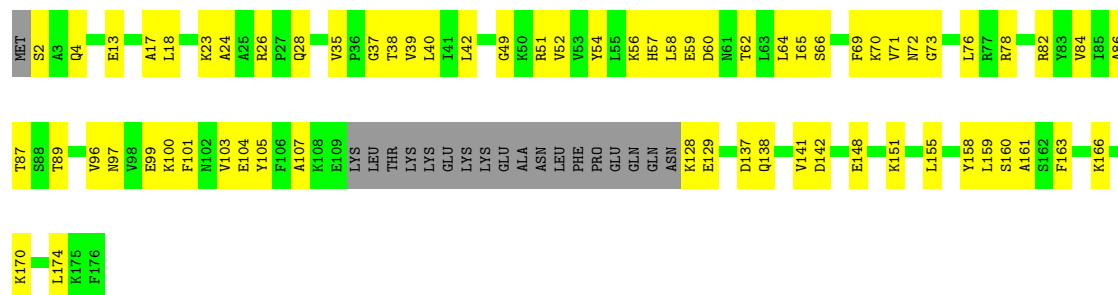
• Molecule 41: 60S ribosomal protein L6-A

Chain Ey:  60% 34% 5%



- Molecule 41: 60S ribosomal protein L6-A

Chain Ha:  52% 38% 11%



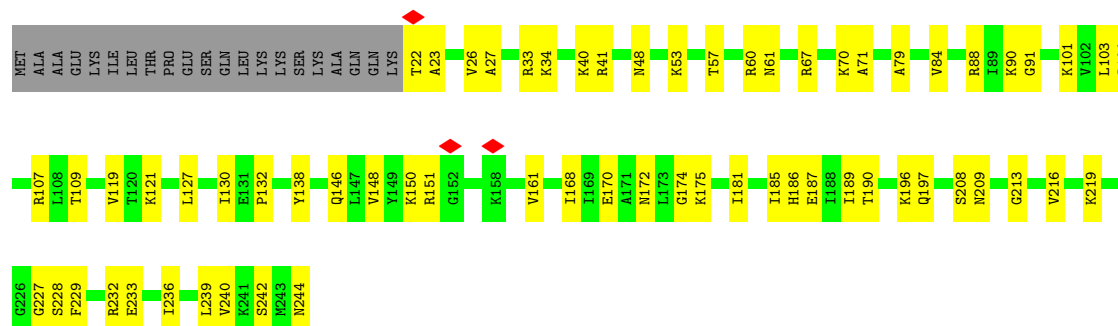
- Molecule 42: 60S ribosomal protein L7-A

Chain Fy:  64% 26% 9%

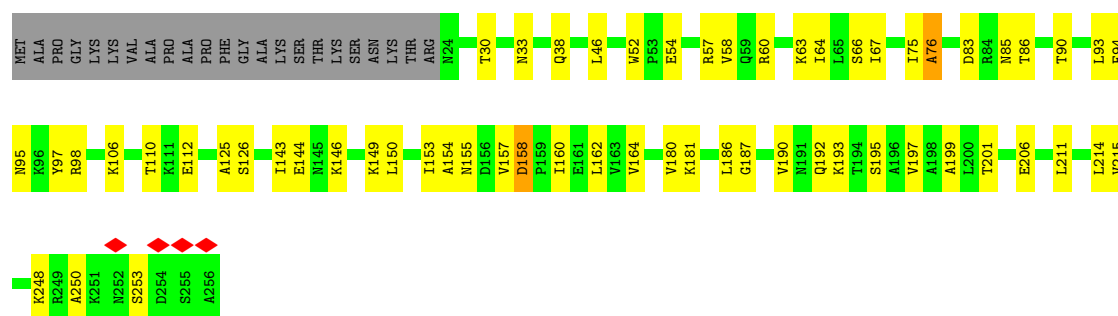


- Molecule 42: 60S ribosomal protein L7-A

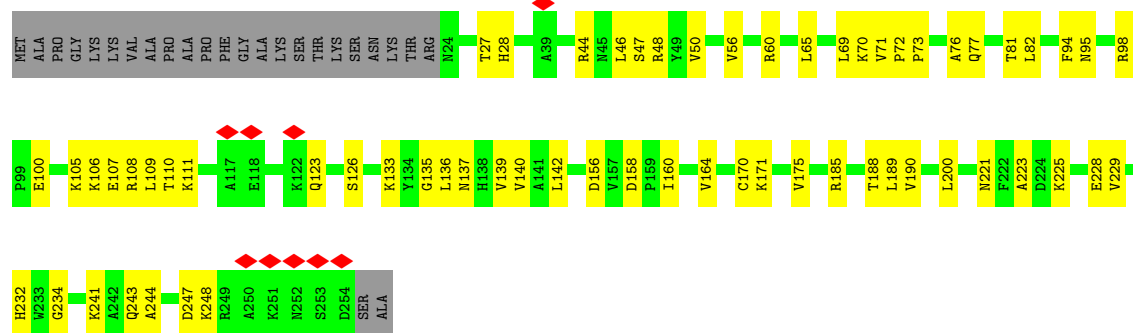
Chain Ia:  64% 27% 9%



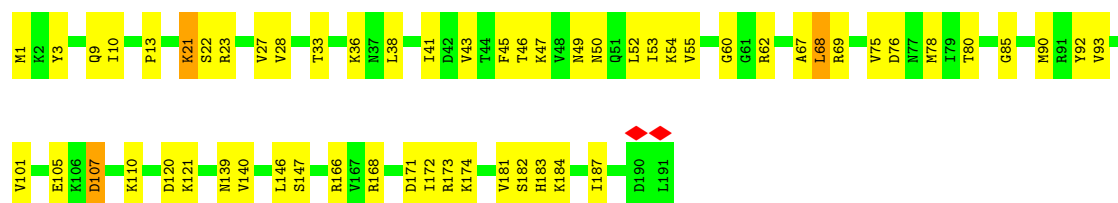
• Molecule 43: 60S ribosomal protein L8-A

Chain Gy:  68% 23% 9%

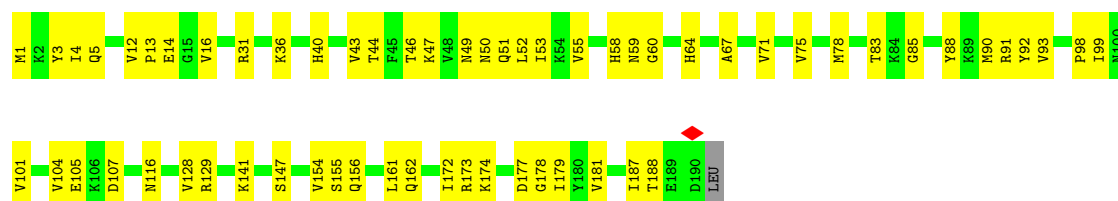
• Molecule 43: 60S ribosomal protein L8-A

Chain Ja:  66% 25% 10%

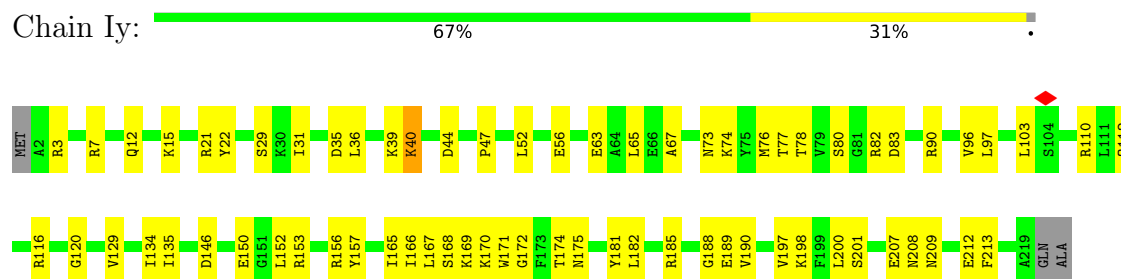
• Molecule 44: 60S ribosomal protein L9-A

Chain Hy:  70% 29% 1%

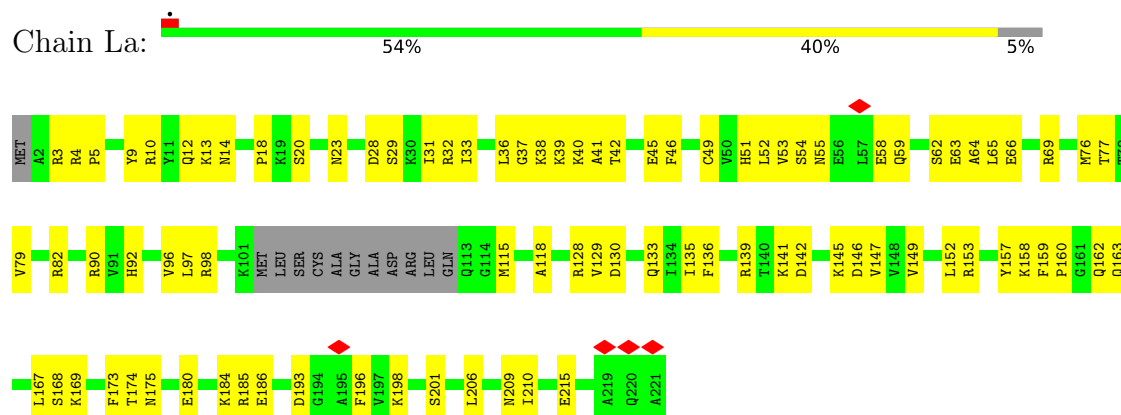
• Molecule 44: 60S ribosomal protein L9-A

Chain Ka:  68% 32% 0%

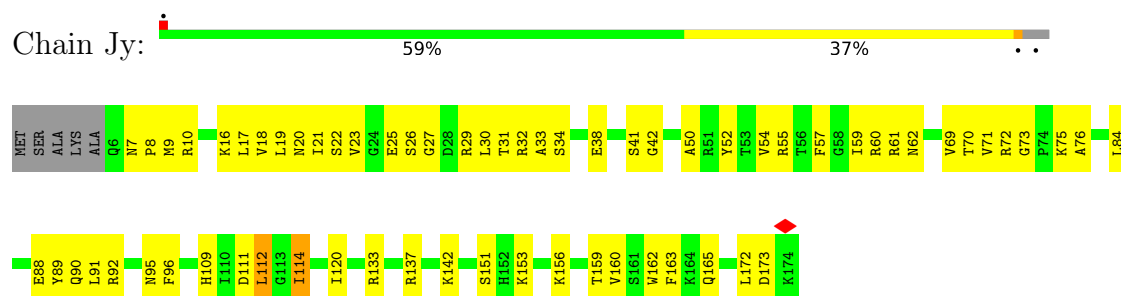
- Molecule 45: 60S ribosomal protein L10



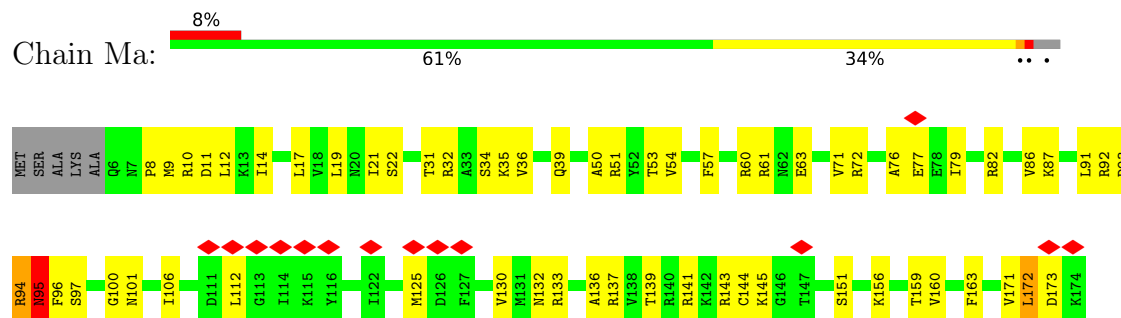
- Molecule 45: 60S ribosomal protein L10



- Molecule 46: 60S ribosomal protein L11-A

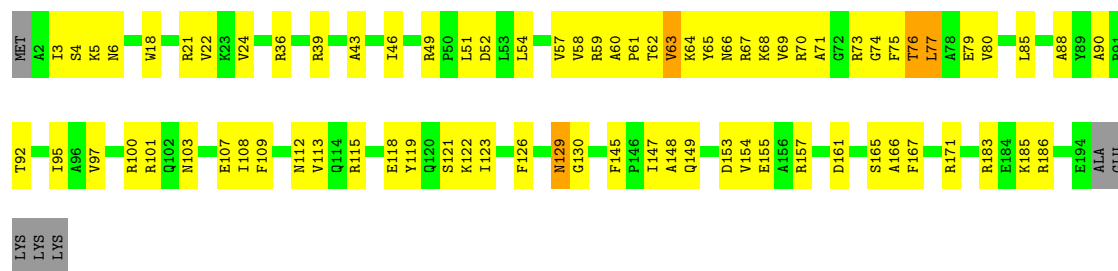


- Molecule 46: 60S ribosomal protein L11-A

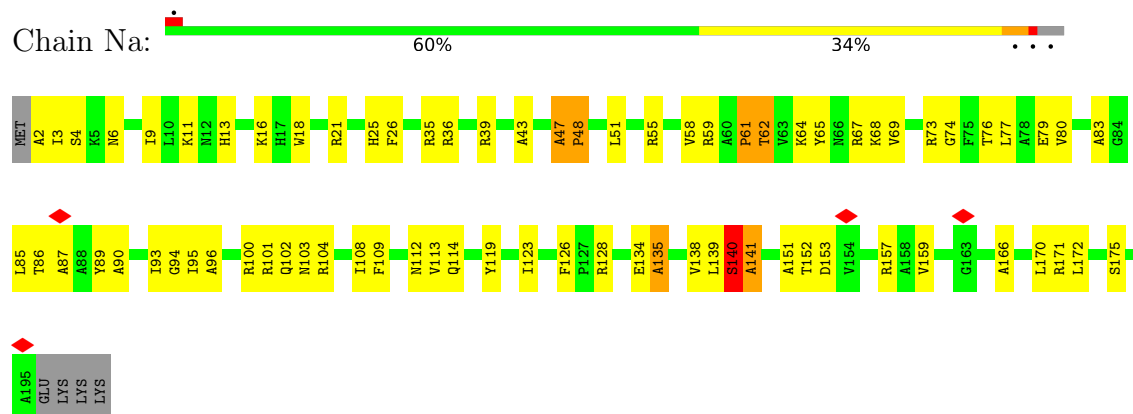


- Molecule 47: 60S ribosomal protein L13-A

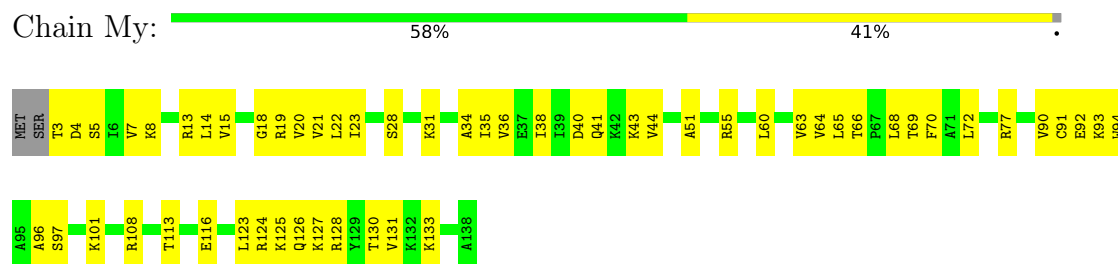




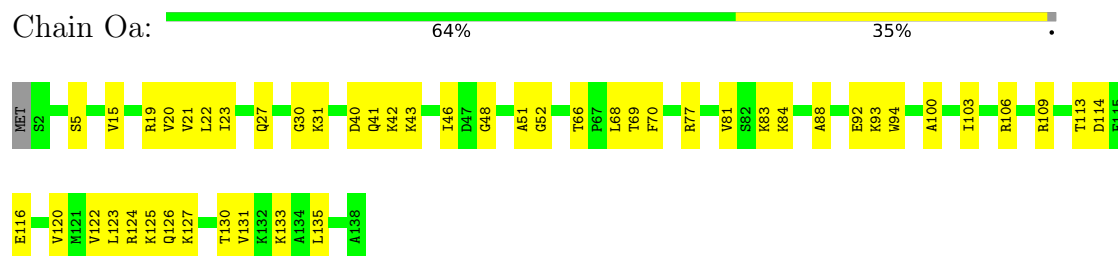
- Molecule 47: 60S ribosomal protein L13-A



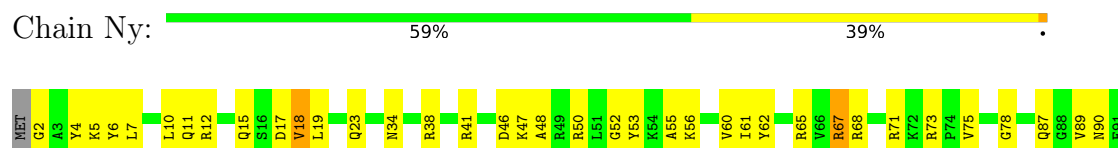
- Molecule 48: 60S ribosomal protein L14-A



- Molecule 48: 60S ribosomal protein L14-A

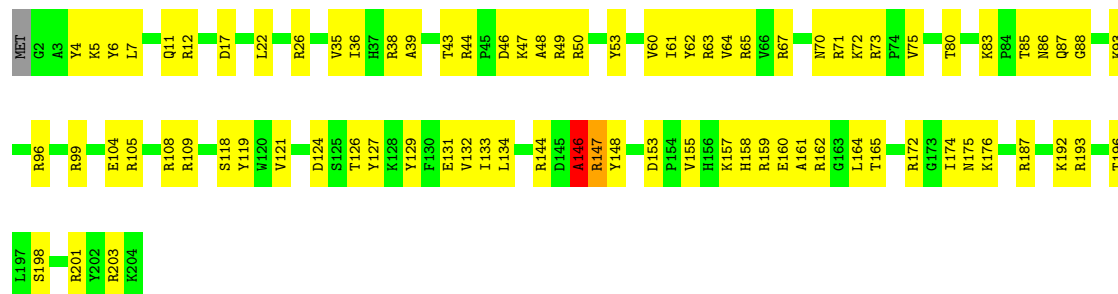


- Molecule 49: 60S ribosomal protein L15-A

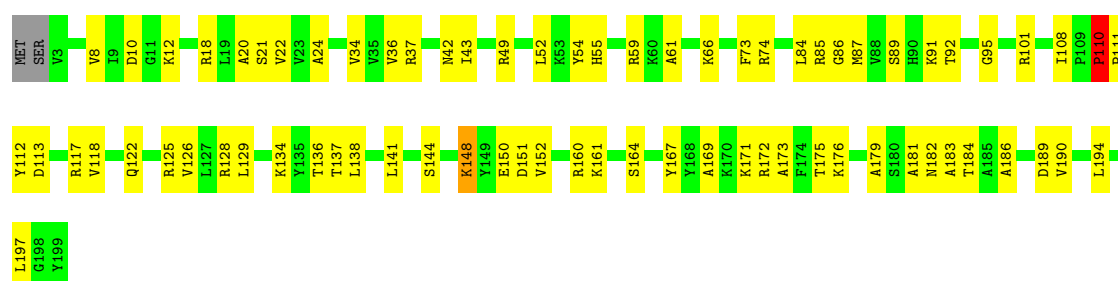




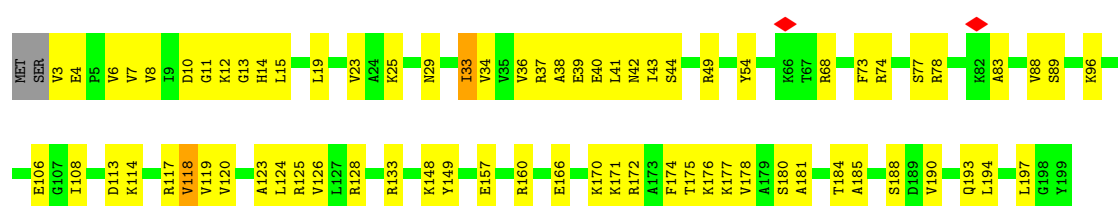
• Molecule 49: 60S ribosomal protein L15-A



• Molecule 50: 60S ribosomal protein L16-A



• Molecule 50: 60S ribosomal protein L16-A



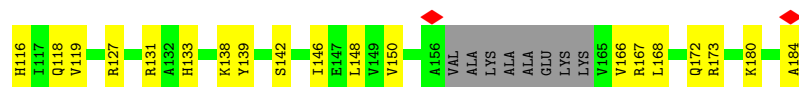
• Molecule 51: 60S ribosomal protein L17-A





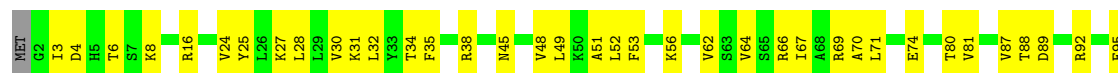
- Molecule 51: 60S ribosomal protein L17-A

Chain A: 66% 29% 5%



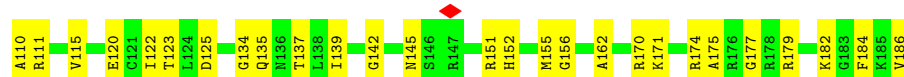
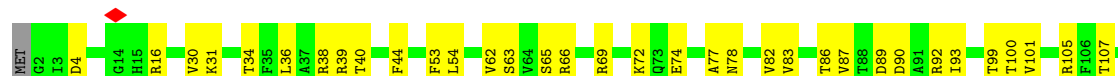
- Molecule 52: 60S ribosomal protein L18-A

Chain Qy: 63% 36%



- Molecule 52: 60S ribosomal protein L18-A

Chain B: 67% 33%



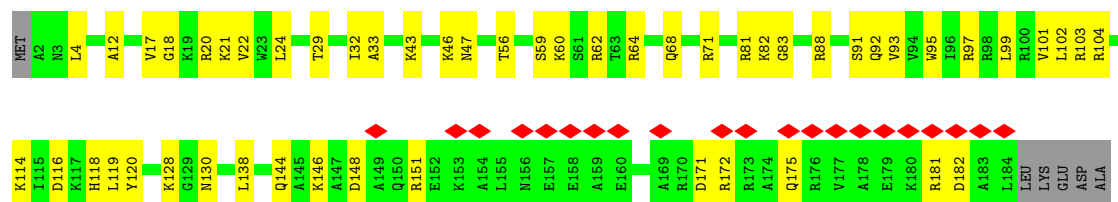
- Molecule 53: 60S ribosomal protein L19-A

Chain Ry: 75% 23%



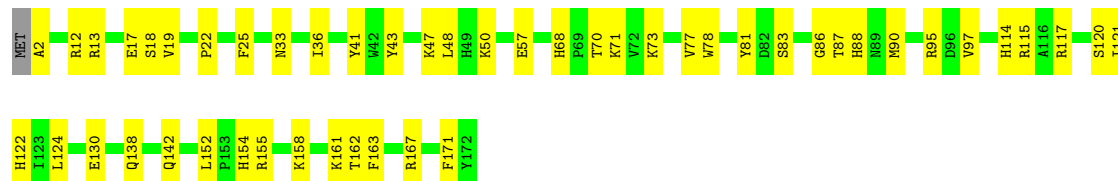
- Molecule 53: 60S ribosomal protein L19-A

Chain C: 11% 69% 28%



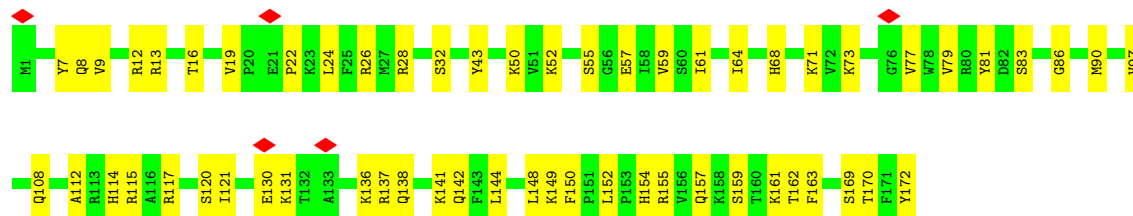
- Molecule 54: 60S ribosomal protein L20-A

Chain Sy: 71% 28%



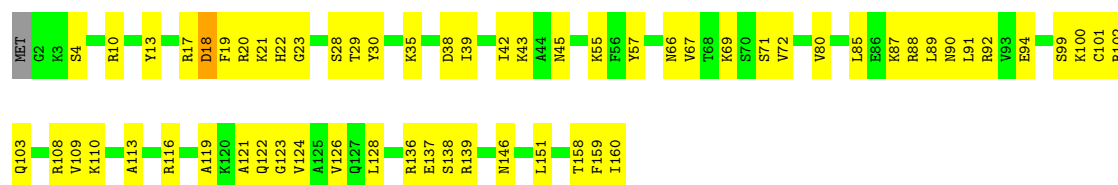
- Molecule 54: 60S ribosomal protein L20-A

Chain D: 66% 34%



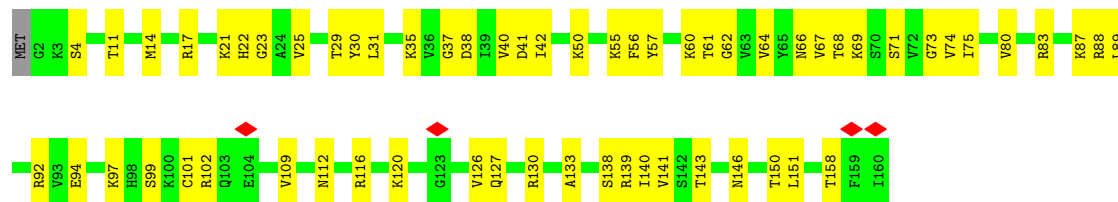
- Molecule 55: 60S ribosomal protein L21-A

Chain Ty: 61% 38%



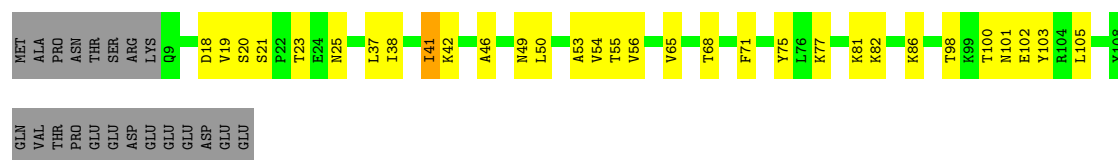
- Molecule 55: 60S ribosomal protein L21-A

Chain E: 61% 38%



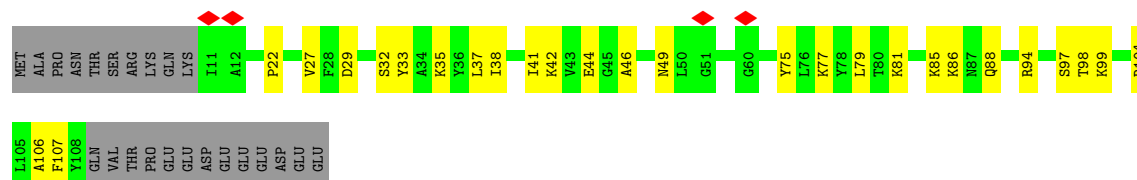
- Molecule 56: 60S ribosomal protein L22-A

Chain Uy:  57% 25% 17%



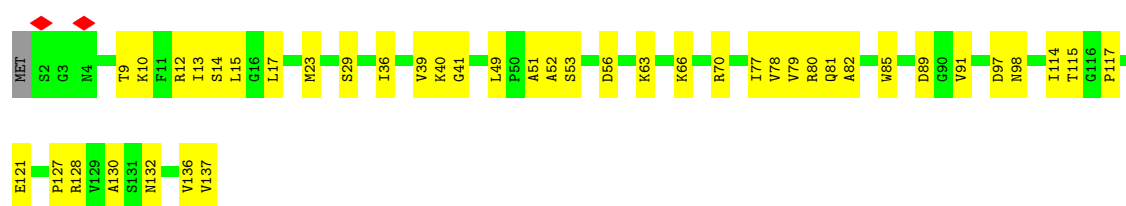
- Molecule 56: 60S ribosomal protein L22-A

Chain F:  59% 22% 19%



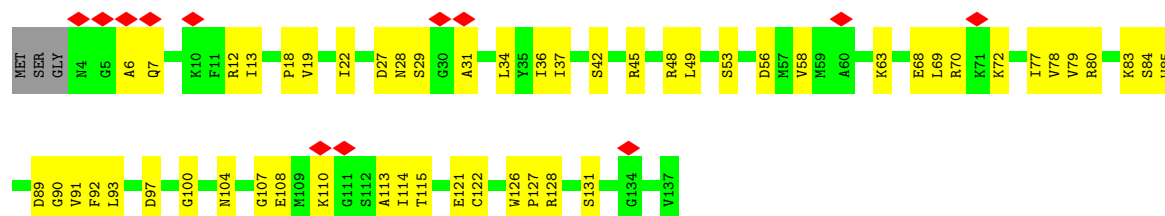
- Molecule 57: 60S ribosomal protein L23-A

Chain Vy:  69% 31%



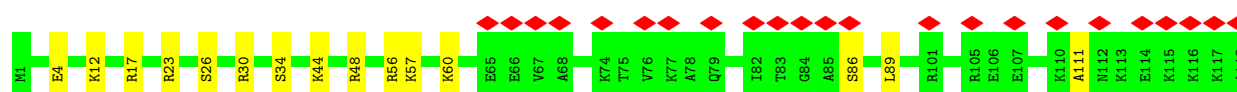
- Molecule 57: 60S ribosomal protein L23-A

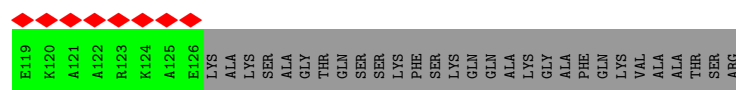
Chain G:  9% 59% 39%



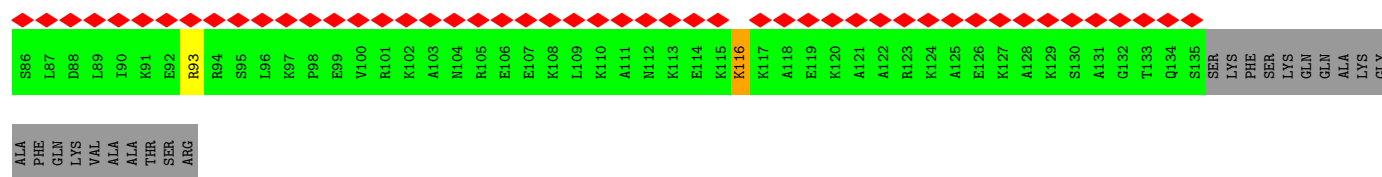
- Molecule 58: 60S ribosomal protein L24-A

Chain Wy:  20% 72% 10% 19%

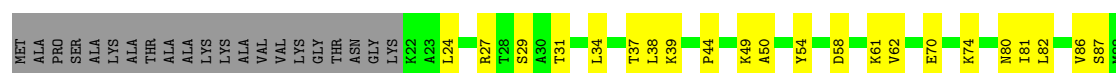




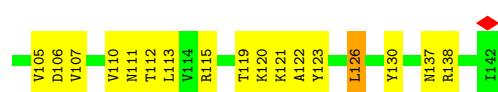
• Molecule 58: 60S ribosomal protein L24-A



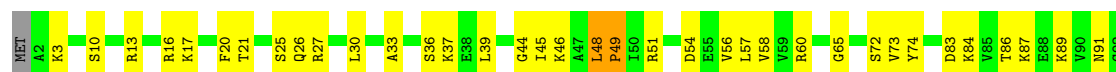
• Molecule 59: 60S ribosomal protein L25



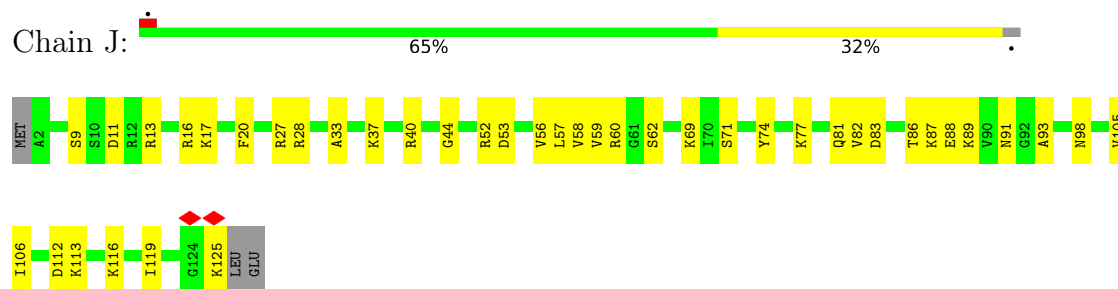
• Molecule 59: 60S ribosomal protein L25



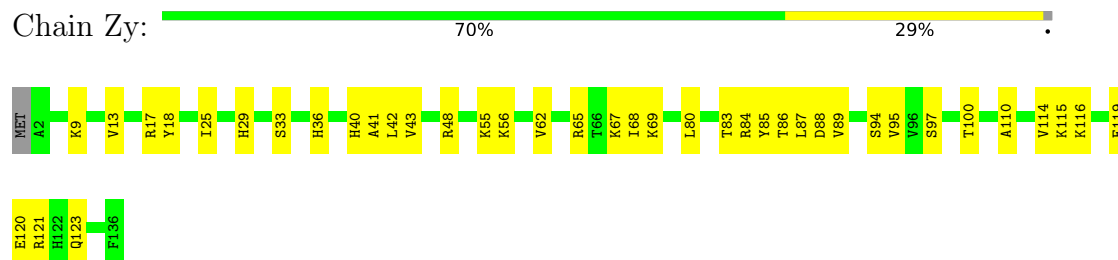
• Molecule 60: 60S ribosomal protein L26-A



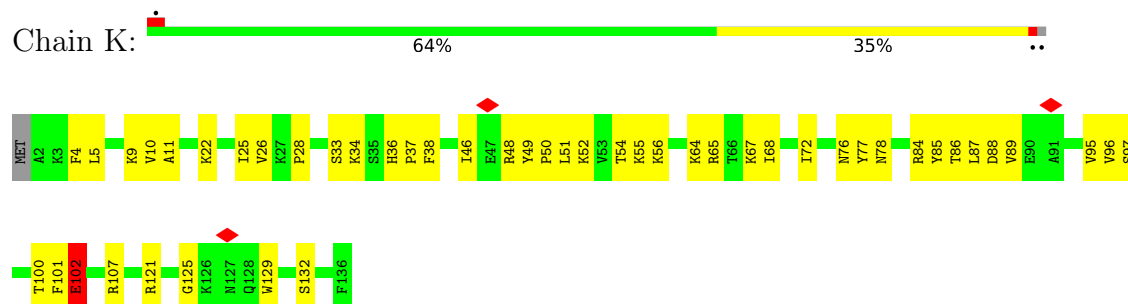
• Molecule 60: 60S ribosomal protein L26-A



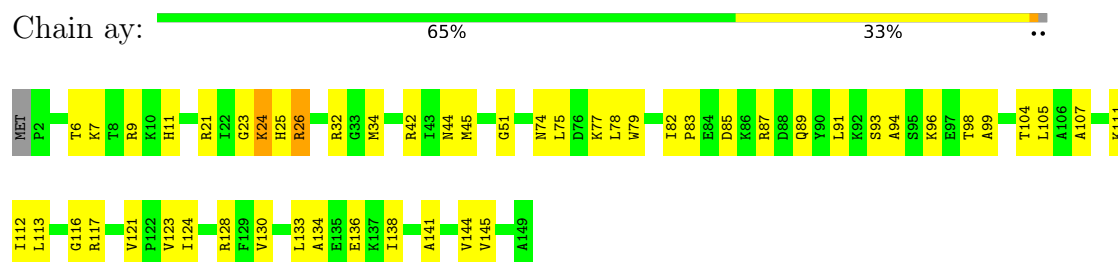
- Molecule 61: 60S ribosomal protein L27-A



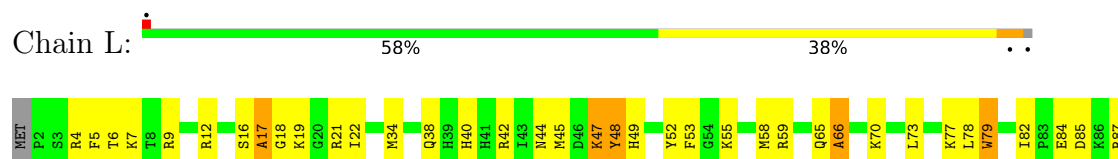
- Molecule 61: 60S ribosomal protein L27-A



- Molecule 62: 60S ribosomal protein L28

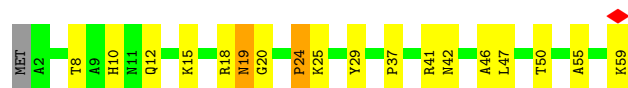


- Molecule 62: 60S ribosomal protein L28

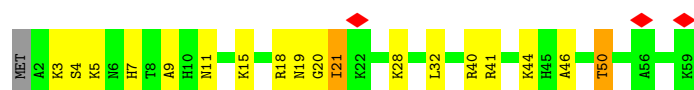




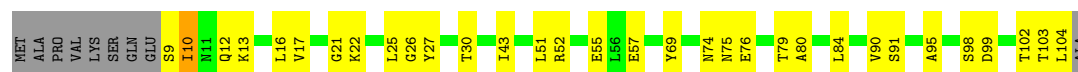
- Molecule 63: 60S ribosomal protein L29



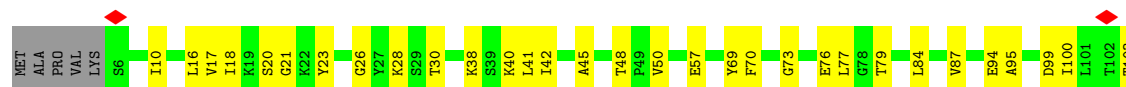
- Molecule 63: 60S ribosomal protein L29



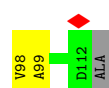
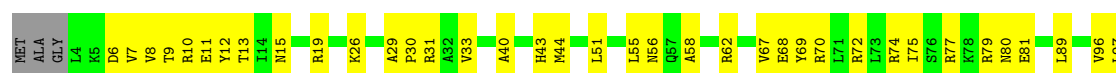
- Molecule 64: 60S ribosomal protein L30



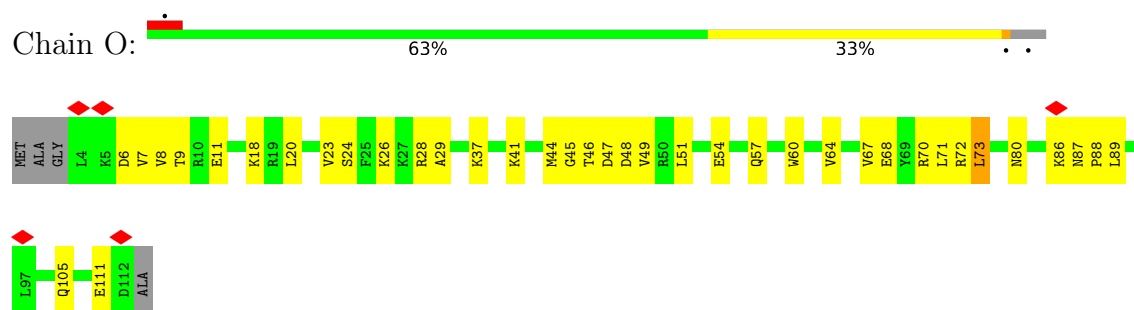
- Molecule 64: 60S ribosomal protein L30



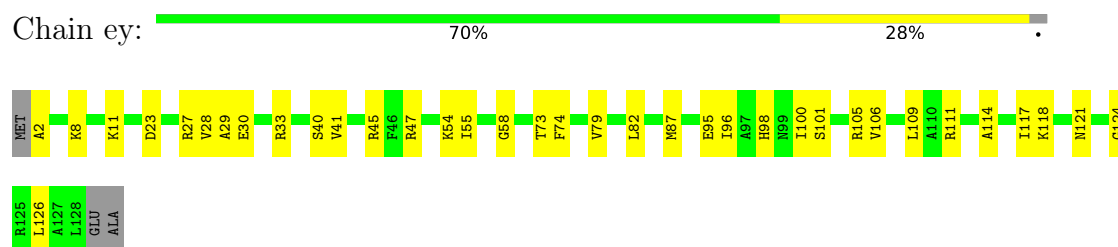
- Molecule 65: 60S ribosomal protein L31-A



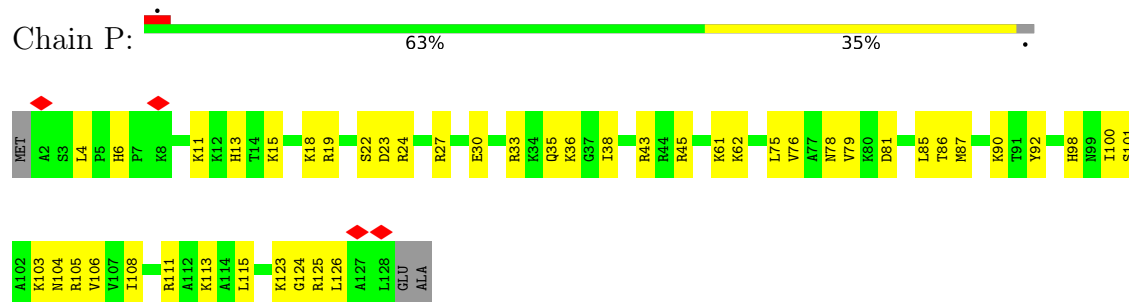
- Molecule 65: 60S ribosomal protein L31-A



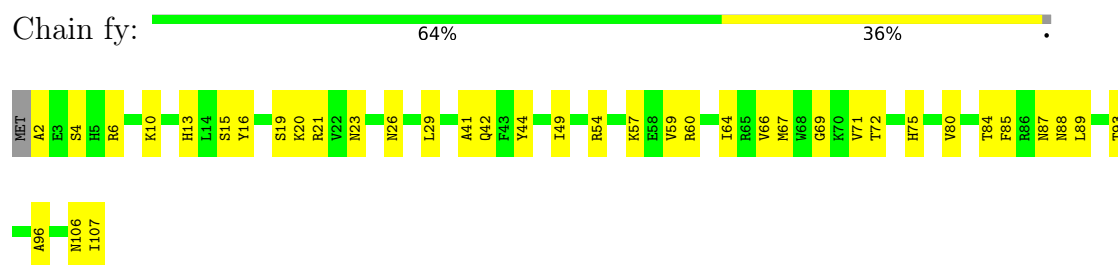
- Molecule 66: 60S ribosomal protein L32



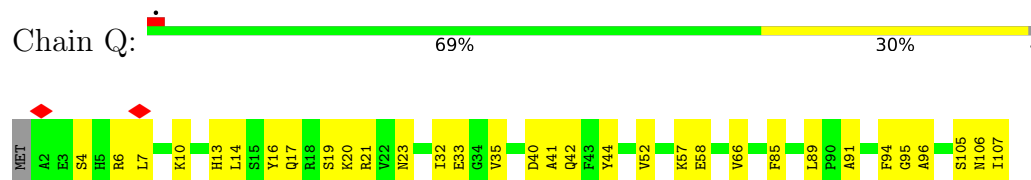
- Molecule 66: 60S ribosomal protein L32



- Molecule 67: 60S ribosomal protein L33-A

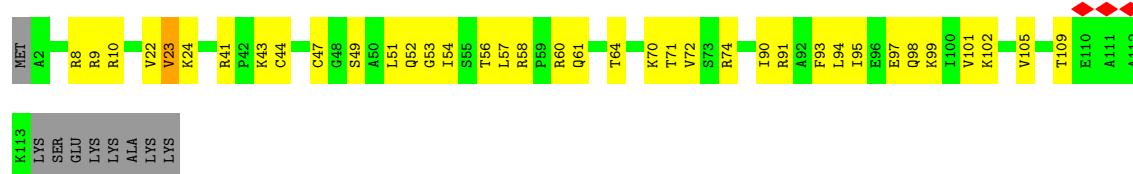


- Molecule 67: 60S ribosomal protein L33-A



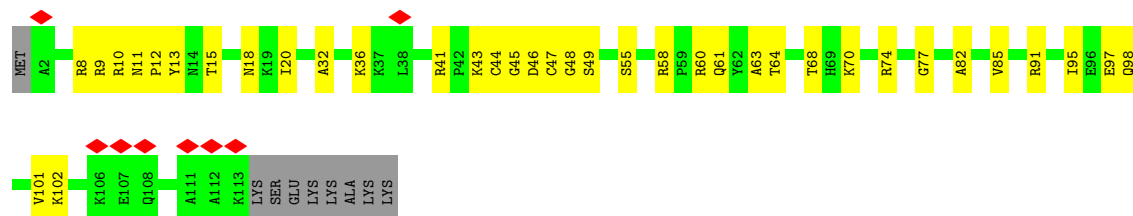
- Molecule 68: 60S ribosomal protein L34-A

Chain gy:  62% 30% 7%



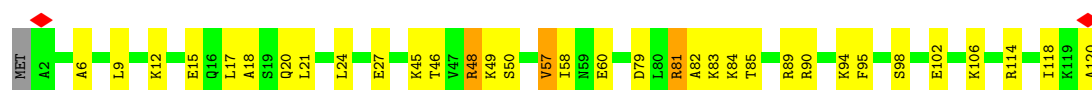
- Molecule 68: 60S ribosomal protein L34-A

Chain R:  7% 62% 31% 7%



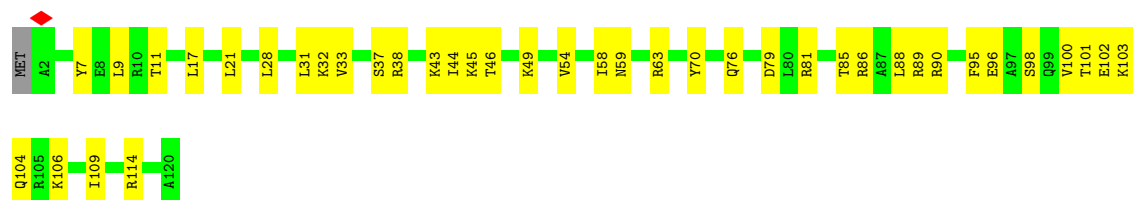
- Molecule 69: 60S ribosomal protein L35-A

Chain hb:  71% 26% 2%



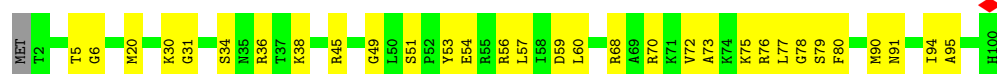
- Molecule 69: 60S ribosomal protein L35-A

Chain S:  66% 33% 1%



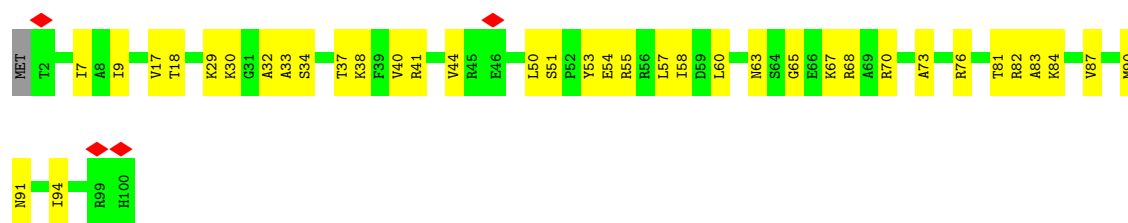
- Molecule 70: 60S ribosomal protein L36-A

Chain ib:  68% 31% 1%

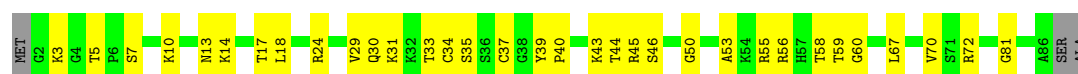


- Molecule 70: 60S ribosomal protein L36-A

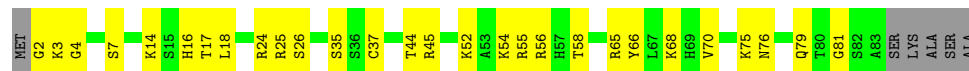
Chain T:  62% 37% 1%



- Molecule 71: 60S ribosomal protein L37-A



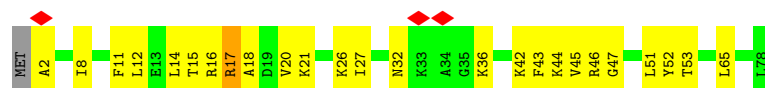
- Molecule 71: 60S ribosomal protein L37-A



- Molecule 72: 60S ribosomal protein L38



- Molecule 72: 60S ribosomal protein L38



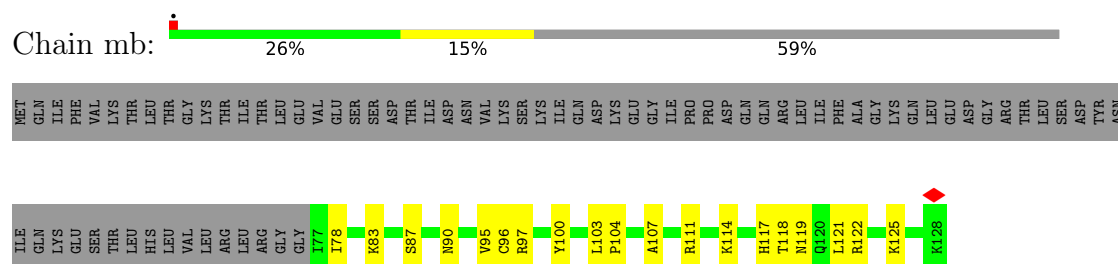
- Molecule 73: 60S ribosomal protein L39



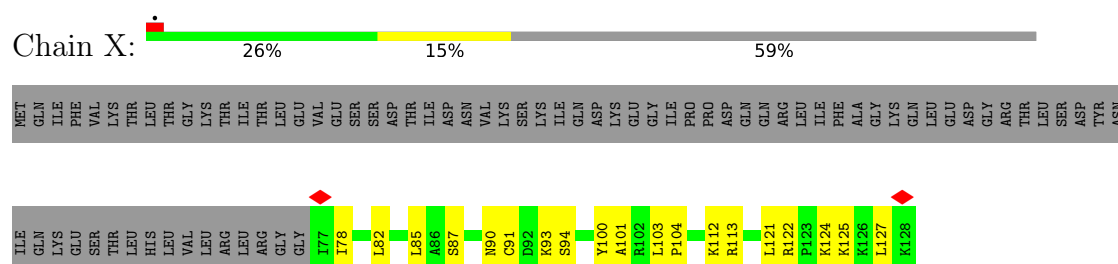
- Molecule 73: 60S ribosomal protein L39



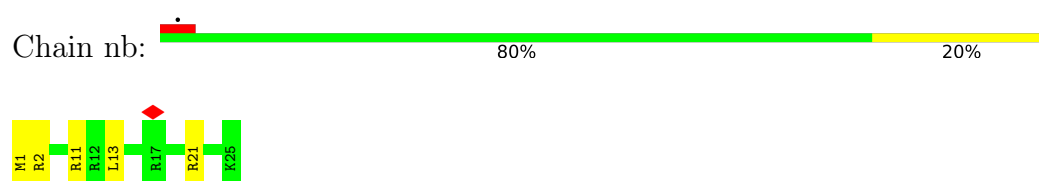
- Molecule 74: Ubiquitin-60S ribosomal protein L40



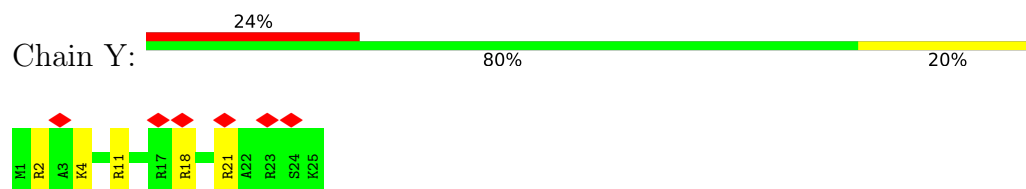
- Molecule 74: Ubiquitin-60S ribosomal protein L40



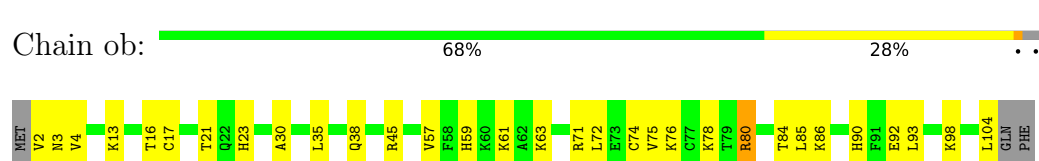
- Molecule 75: 60S ribosomal protein L41-A



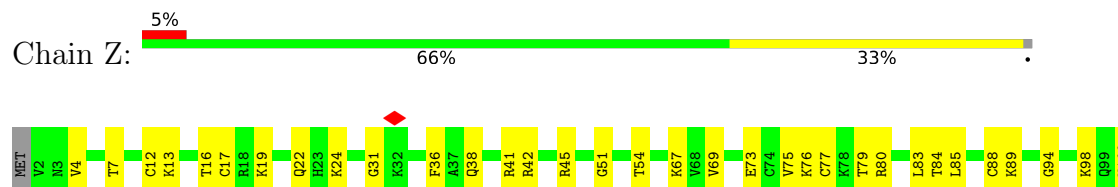
- Molecule 75: 60S ribosomal protein L41-A



- Molecule 76: 60S ribosomal protein L42-A

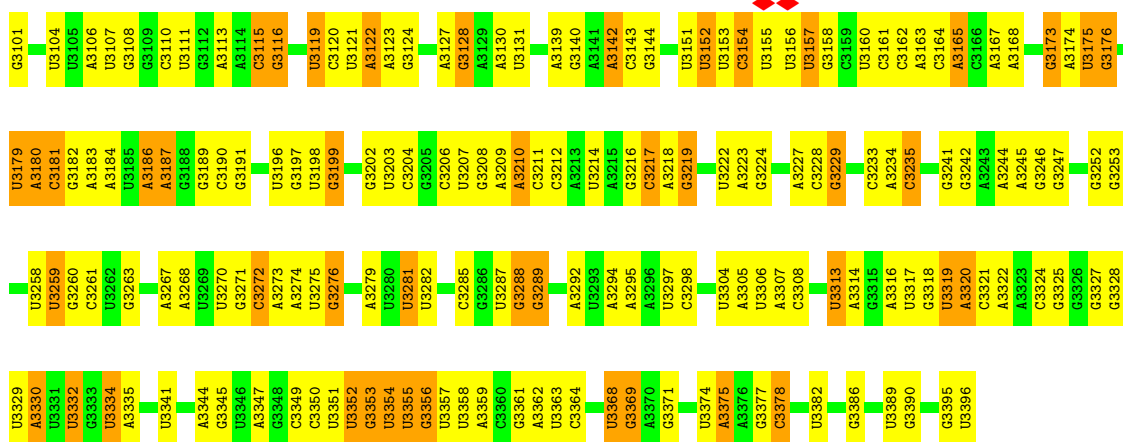


- Molecule 76: 60S ribosomal protein L42-A



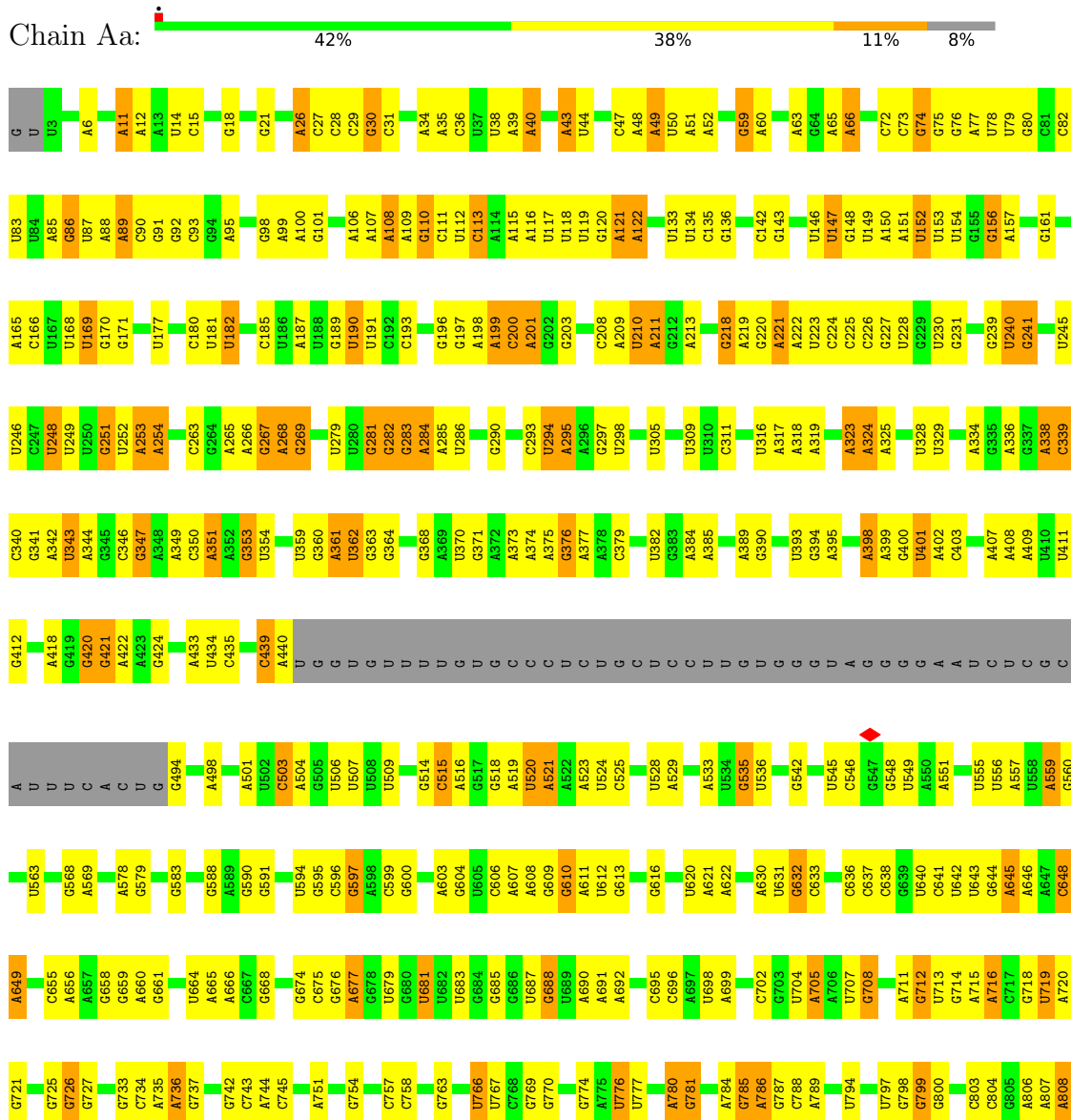
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G1796	U1720	U1630	G1481	U1384	A1294	G1150	U1051	A980	U899	A816	G718
A1797	U1721	A1559	A1482	C1386	G1295	U1151	A1052	U981	U900	U1052	U719
A1798	U1722	A1632	G1483	C1388	G1296	G1152	A1053	C982	G901	C818	A720
A1799	G1633	G1633	U1484	G1389	G1300	A1153	A1057	A984	A904	U821	G721
C1803	U1724	G1634	C1562	G1392	A1301	A1154	G1063	G987	G907	G822	G726
	C1725	G1635	U1564	G1392	A1302	C1155	G1063	U987	G908	G823	
		U1636	G1565	C1393	A1303	C1156	A1064	U988	G908	G824	G733
G1808	A1729	A1637	A1489	A1393	A1304	U1157	A1065	U989	G909	U825	
A1809	G1730	A1566	A1490	A1399	U1305	G1158	A1065	U990	G910	A735	C734
A1810	A1731	C1639	A1491	G1400	G1306	A1159	U1069	G991	G911	A736	A736
G1811	U1732	U1568	G1492	G1400	G1307	A1160	U1070	A992	G912	G737	
G1812		U1568	G1493	G1400	A1308	G1161	U1071	G993	A913	A830	
A1813	G1736	U1569	U1494	G1404	U1309	G1161	G1072	G994	A914	G831	
A1814	U1737	U1570	U1495		G1310	A1165	U1073	U995	A915	G832	G740
U1815	C1738	C1496	C1497	A1407	G1311	U1167	U1074	U996	A916	G833	U741
A1816	U1739	C1497	C1498	G1411	G1312	G1176	G1075		A917	U834	G742
G1817	U1740	C1499	C1499	G1411	G1313	G1177	U1076			G835	C743
U1818	A1741	C1499	G1500	G1416	C1314	G1178	A1079	G999	A921	A836	A744
U1819	U1742	A1575	G1500	G1416	U1315	G1178	A1080	U1008	A922	A837	
U1820		G1576	G1500		C1316	A1179	A1081	A1009	U922	G838	G754
U1821	C1745	G1577	A1503	A1419	A1317	G1179	U1082	A1010	C923	C839	
	U1746	C1578	C1508	G1421	A1317	A1181	G1083	A925	G924	C840	C758
G1824	G1747	C1579	C1508	G1422	C1320	G1182	A1084	A926	A926	G845	U759
G1825	U1748	A1580	C1516		U1324	G1182	G1087	A927	C927	A846	A761
	A1749	C1581	A1515		U1325	A1182	G1087	A928	C928	A847	U762
	U1750	C1582	C1516	U1425	U1325	A1182	G1087	A929	U932	A848	G763
U1828	A1752	A1583	G1517		A1330	A1182	G1087	A930	U933	C849	U764
G1829	G1751	A1587	G1521	A1428	A1330	A1182	G1087	A931	U934	C851	C765
G1830	U1752	A1588	U1522	G1429	A1330	A1182	G1087	A932	U935	U852	U766
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U1834	C1762	G1591	U1525	G1432	G1345	G1186	G1087	A935	G937	U855	G769
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	U1764	U1593	U1526	G1434	U1347	A1190	G1087	A937	U939	G857	A771
U1840	U1765	A1594	U1526	G1437	U1348	A1191	G1087	A938	U939	G857	
A1841	G1766	U1595	A1529		U1349	U1191	G1087	A939	U939	G857	
A1842		C1596	U1530	G1443	A1350	C1192	G1087	A940	U939	G857	G774
C1843	G1770	C1597	C1531	U1444	U1351	A1193	G1087	A941	U939	G857	A775
G1844	C1771	U1601	U1532	G1444	A1352	A1193	G1087	A942	U939	G857	U776
G1845	U1772	A1602	U1533	U1445	U1353	C1196	G1087	A943	U939	G857	U777
C1846	U1772	U1603	U1534	A1446	U1354	C1196	G1087	A944	U939	G857	
A1847	G1775	A1604	A1535		A1355	C1198	G1087	A945	U939	G857	A780
G1848		U1604	A1535	G1450	U1356	C1199	G1087	A946	U939	G857	G781
C1849	U1776	A1605	A1539	C1451	G1357	A1200	G1087	A947	U939	G857	U782
A1850	C1779	U1606	U1540	A1452	C1358	C1201	G1087	A948	U939	G857	A783
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	C1781	C1608	G1542	U1454	C1360	A1204	G1087	A950	U939	G857	G785
A1859	U1782	U1609	G1543	U1455	C1364	A1205	G1087	A951	U939	G857	A786
G1860	U1783	C1609	G1544	U1456	C1364	A1206	G1087	A952	U939	G857	
	U1784		A1545	U1457	C1364	G1206	G1087	A953	U939	G857	
	G1785	A1613	A1546	U1457	C1364	G1207	G1087	A954	U939	G857	
G1863		U1616	U1547	U1459	G1371	G1208	G1087	A955	U939	G857	G792
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A1867	U1791	U1620	C1551	U1467	G1371	G1212	G1087	A959	U939	G857	A806
	C1792	U1716	G1552	U1468	G1371	G1213	G1087	A960	U939	G857	A807
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C1872	G1794	G1718	C1556	U1477	G1371	G1215	G1087	A962	U939	G857	U814

C3025	C3026	C3027	C3028	C3029	C3030	C3031	C3034	C3035	C3036	C3037	C3038	C3039	C3040	C3041	C3042	A3048	C3055	C3056	C3057	C3058	C3059	C3060	C3061	C3066	C3067	C3068	C3069	A3070	C3071	C3072	C3073	C3074	C3075	C3076	C3077	C3078	C3079	C3080	C3083	C3084	C3085	C3086	C3089	C3090	A3091	C3092	C3093	A3094	C3095	C3096	C3099	U3100
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C2776	G2777	G2778	U2781	G2784	A2785	G2786	G2787	G2788	U2789	A2790	G2794	U2795	G2796	A2799	G2800	A2801	A2802	A2803	A2804	G2805	U2806	U2807	A2808	C2809	C2810	A2811	C2812	A2813	C2814	G2815	G2816	A2817	U2818	G2819	C2821	U2822	C2825	G2828	G2834	U2835	C2836	A2837	U2838	G2839	C2840	G2841	U2842	U2843	C2844	A2845	U2846	
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G2377	C2383	A2386	A2387	U2388	C2392	G2393	A2394	A2397	A2402	G2403	A2404	C2405	C2406	C2407	U2411	G2412	A2413	G2418	A2419	C2420	U2421	U2422	U2423	A2424	G2429	U2432	U2433	U2434	G2437	A2438	A2439	A2443	C2444	U2445	U2446	A2447	G2448	A2449	G2450	G2451	G2452	U	U	U	A	A	A					
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U	A	G	U	G	G	A	C	U	U	U	C	G	C	C	A</																																					



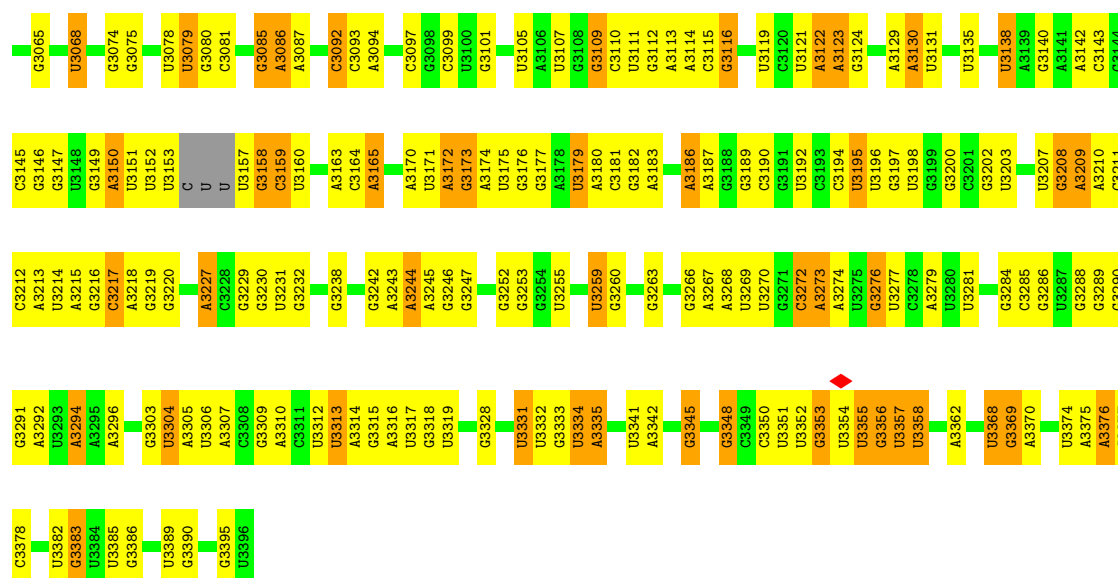
• Molecule 78: 25S rRNA

Chain Aa:









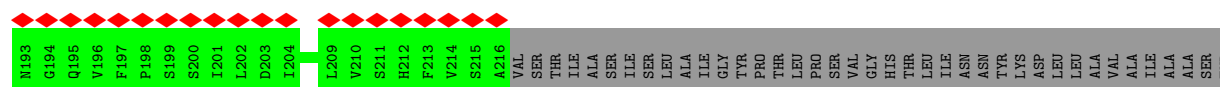
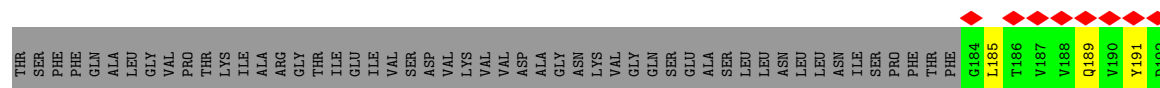
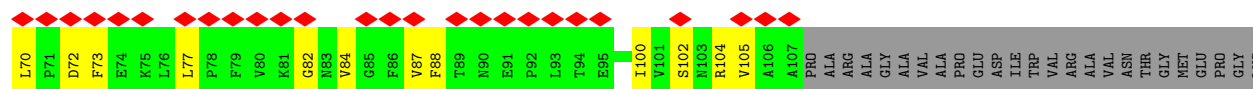
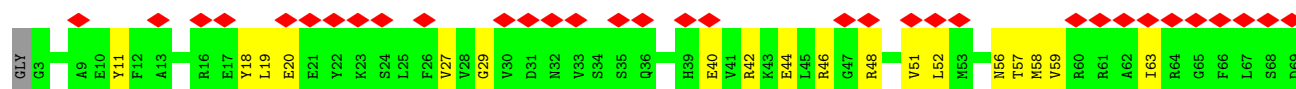
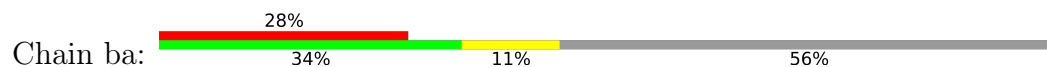
• Molecule 79: tRNA



• Molecule 79: tRNA



• Molecule 80: 60S acidic ribosomal protein P0



HIS	TYR	PRO	GLU	ILE	GLU	ASP	LEU	VAL	ASP	ARG	ILE	GLU	ASN	PRO	GLU	LYS	TYR	ALA	ALA	ALA	ALA	PRO	ALA	ALA	THR	SER	ALA	ALA	SER	GLY	ASP	ALA	ALA	PRO	ALA	GLU	GLU	ALA	ALA	ALA	GLU	GLU	GLU	GLU	SER	ASP	ASP	ASP	MET	GLY	PHE	GLY	GLY	PHE	LEU	PHE	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19459	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.335	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	574.52, 574.52, 574.52	wwPDB
Map dimensions	530, 530, 530	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	2b	0.86	0/42211	0.68	10/65773 (0.0%)
1	a	0.58	12/41891 (0.0%)	0.49	6/65273 (0.0%)
2	Ab	0.80	0/1644	0.68	0/2249
2	b	0.39	0/1623	0.68	2/2222 (0.1%)
3	Ba	0.92	1/1823 (0.1%)	0.80	2/2447 (0.1%)
3	c	0.38	1/1748 (0.1%)	0.62	0/2352
4	Pb	0.71	0/936	0.66	0/1259
4	q	0.31	0/959	0.66	0/1288
5	Cb	1.05	1/1656 (0.1%)	0.78	0/2251
5	d	0.43	0/1665	0.60	0/2263
6	Db	0.78	0/1754	0.66	0/2361
6	e	0.35	0/1759	0.60	0/2368
7	Eb	0.93	0/2097	0.78	1/2823 (0.0%)
7	f	0.38	0/2109	0.62	0/2839
8	Fb	0.82	0/1625	0.69	0/2197
8	g	0.37	0/1629	0.61	1/2202 (0.0%)
9	Gb	0.71	0/1839	0.76	1/2460 (0.0%)
9	h	0.37	0/1779	0.64	0/2379
10	Hb	0.76	0/1498	0.68	0/2019
10	i	0.34	0/1511	0.62	0/2036
11	Ib	1.01	1/1501 (0.1%)	0.82	2/2006 (0.1%)
11	j	0.42	0/1514	0.63	0/2021
12	Jb	0.90	1/1504 (0.1%)	0.79	1/2016 (0.0%)
12	k	0.39	0/1519	0.62	0/2035
13	Kb	0.61	0/769	0.61	0/1039
13	l	0.30	0/757	0.68	2/1022 (0.2%)
14	Lb	1.12	0/1185	0.75	0/1598
14	m	0.40	0/1194	0.58	0/1610
15	Mb	0.45	0/883	0.80	0/1199
15	n	0.30	0/898	0.76	0/1220
16	Nb	1.12	1/1215 (0.1%)	0.80	0/1638
16	o	0.46	0/1215	0.67	1/1638 (0.1%)
17	Ob	1.00	0/937	0.84	0/1261
17	p	0.43	0/960	0.68	0/1290

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	Qb	0.88	0/1125	0.72	0/1510
18	r	0.38	0/1125	0.71	0/1510
19	Rb	0.77	0/957	0.77	1/1283 (0.1%)
19	s	0.37	0/1010	0.60	0/1355
20	Sb	0.68	0/1211	0.72	0/1628
20	t	0.35	0/1211	0.65	1/1628 (0.1%)
21	Tb	0.84	0/1130	0.75	0/1517
21	u	0.40	0/1130	0.59	0/1517
22	Ub	0.80	0/807	0.68	0/1091
22	v	0.39	0/815	0.68	1/1102 (0.1%)
23	Vb	0.89	0/682	0.78	1/921 (0.1%)
23	w	0.43	0/693	0.62	1/935 (0.1%)
24	Wb	1.17	0/1038	0.80	0/1395
24	x	0.49	0/1038	0.62	0/1395
25	Xb	1.08	0/1139	0.78	0/1518
25	y	0.48	0/1139	0.68	0/1518
26	Yb	0.78	0/1087	0.67	0/1449
26	z	0.38	0/1087	0.66	0/1449
27	0	0.32	0/566	0.66	0/761
27	Zb	0.65	0/661	0.70	1/888 (0.1%)
28	1	0.51	0/782	0.81	0/1047
28	ab	1.18	1/782 (0.1%)	0.89	0/1047
29	2	0.35	0/620	0.57	0/838
29	bb	0.84	1/620 (0.2%)	0.75	0/838
30	4	1.95	2/452 (0.4%)	1.83	4/600 (0.7%)
30	db	0.91	0/452	0.73	0/600
31	5	0.35	0/483	0.65	0/643
31	eb	0.77	0/480	0.70	0/639
32	6	0.34	0/567	0.76	0/764
32	fb	0.46	0/567	0.75	0/764
33	7	0.29	0/2456	0.55	0/3343
33	gb	0.59	0/2436	0.68	0/3318
34	3	0.36	0/499	0.60	0/670
34	cb	0.82	0/493	0.71	0/663
35	4b	0.83	0/2883	0.63	0/4491
35	Bb	0.53	0/2883	0.49	0/4491
36	3b	1.02	0/3746	0.73	0/5832
36	Ca	0.61	0/3724	0.58	0/5798
37	Ay	1.28	0/1933	0.87	1/2598 (0.0%)
37	Da	0.73	0/1946	0.74	0/2614
38	By	1.21	1/3146 (0.0%)	0.79	0/4228
38	Ea	0.64	0/3146	0.68	0/4228
39	Cy	1.22	0/2800	0.83	1/3790 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	Fa	0.69	1/2800 (0.0%)	0.74	0/3790
40	Dy	0.83	0/2400	0.67	1/3239 (0.0%)
40	Ga	0.51	1/2408 (0.0%)	0.60	0/3248
41	Ey	0.88	0/1324	0.77	0/1782
41	Ha	0.53	0/1269	0.64	0/1705
42	Fy	1.19	0/1821	0.83	1/2451 (0.0%)
42	Ia	0.68	0/1828	0.69	0/2461
43	Gy	0.97	0/1836	0.78	0/2481
43	Ja	0.54	0/1795	0.66	0/2429
44	Hy	0.89	0/1529	0.69	0/2060
44	Ka	0.55	0/1531	0.64	0/2062
45	Iy	0.95	1/1801 (0.1%)	0.74	0/2416
45	La	0.56	0/1732	0.64	0/2323
46	Jy	0.81	0/1371	0.67	0/1838
46	Ma	0.42	0/1374	0.72	0/1842
47	Ly	1.32	2/1568 (0.1%)	0.83	2/2106 (0.1%)
47	Na	0.62	0/1573	0.77	1/2113 (0.0%)
48	My	0.94	0/1068	0.77	0/1438
48	Oa	0.58	0/1074	0.67	0/1446
49	Ny	1.41	0/1757	0.83	1/2354 (0.0%)
49	Pa	0.77	0/1757	0.78	0/2354
50	Oy	1.27	0/1585	0.77	0/2128
50	Qa	0.71	0/1585	0.68	0/2128
51	A	0.69	0/1400	0.65	0/1882
51	Py	1.28	0/1439	0.85	0/1938
52	B	0.60	0/1465	0.68	0/1965
52	Qy	1.18	0/1465	0.76	0/1965
53	C	0.60	0/1499	0.64	0/1998
53	Ry	1.12	0/1532	0.79	0/2043
54	D	0.64	0/1481	0.62	0/1990
54	Sy	1.10	0/1473	0.75	0/1980
55	E	0.63	0/1300	0.66	0/1743
55	Ty	1.14	0/1300	0.70	0/1743
56	F	0.47	0/794	0.56	0/1076
56	Uy	0.72	0/812	0.66	0/1099
57	G	0.60	0/1008	0.61	0/1356
57	Vy	1.21	0/1018	0.77	0/1369
58	H	2.49	1/1103 (0.1%)	0.89	7/1458 (0.5%)
58	Wy	0.89	0/863	0.65	0/1169
59	I	0.65	0/974	0.68	0/1314
59	Xy	1.09	0/979	0.76	0/1321
60	J	0.59	0/987	0.67	0/1318
60	Yy	1.07	0/995	0.82	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
61	K	0.54	0/1118	0.65	0/1497
61	Zy	0.98	1/1118 (0.1%)	0.69	0/1497
62	L	0.70	0/1204	0.79	3/1612 (0.2%)
62	ay	1.24	0/1204	0.79	0/1612
63	M	0.57	0/473	0.81	0/629
63	by	1.02	0/473	0.73	0/629
64	N	0.62	0/775	0.68	0/1040
64	cy	1.11	0/745	0.77	0/1001
65	O	0.64	0/897	0.65	0/1205
65	dy	1.10	0/890	0.78	0/1196
66	P	0.66	0/1041	0.70	0/1394
66	ey	1.16	0/1038	0.77	0/1390
67	Q	0.73	0/868	0.71	0/1168
67	fy	1.29	0/868	0.78	0/1168
68	R	0.66	0/890	0.75	0/1189
68	gy	1.26	1/890 (0.1%)	0.80	0/1189
69	S	0.56	0/974	0.67	0/1297
69	hb	1.08	0/978	0.75	0/1301
70	T	0.60	0/777	0.73	0/1033
70	ib	0.97	0/772	0.77	0/1026
71	U	0.77	0/665	0.71	0/882
71	jb	1.38	0/685	0.86	0/908
72	V	0.50	0/614	0.65	0/822
72	kb	0.82	0/618	0.68	0/826
73	W	0.75	0/443	0.70	0/588
73	lb	1.39	0/443	0.84	0/588
74	X	0.52	0/423	0.54	0/562
74	mb	0.97	0/423	0.71	0/562
75	Y	0.46	0/234	0.63	0/300
75	nb	0.95	0/230	0.91	0/296
76	Z	0.64	0/860	0.69	0/1136
76	ob	1.02	0/836	0.78	0/1104
77	aa	0.69	0/701	0.69	1/934 (0.1%)
77	pb	1.31	0/701	0.79	0/934
78	lb	1.03	0/76214	0.73	4/118821 (0.0%)
78	Aa	0.61	0/74873	0.57	5/116727 (0.0%)
79	6b	0.69	0/1804	0.62	0/2809
79	8	0.27	0/1804	0.41	0/2809
80	ba	0.30	0/1067	0.59	0/1439
All	All	0.82	31/431658 (0.0%)	0.67	67/634238 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	Ab	0	1
2	b	0	5
3	Ba	0	6
4	Pb	0	1
4	q	0	3
5	Cb	0	3
7	Eb	0	1
7	f	0	1
8	g	0	2
9	h	0	3
10	Hb	0	2
10	i	0	4
11	Ib	0	2
11	j	0	1
12	Jb	0	4
13	l	0	1
14	Lb	0	1
15	Mb	0	4
15	n	0	3
16	o	0	1
17	Ob	0	2
17	p	0	1
18	Qb	0	3
18	r	0	2
20	Sb	0	2
20	t	0	3
21	Tb	0	2
22	Ub	0	1
22	v	0	3
24	Wb	0	2
25	Xb	0	3
26	z	0	2
28	1	0	1
28	ab	0	3
30	4	0	3
31	5	0	2
32	6	0	4
32	fb	0	3
33	gb	0	1
38	By	0	3
39	Fa	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	Fy	0	1
43	Gy	0	3
44	Hy	0	2
45	La	0	1
46	Jy	0	2
46	Ma	0	4
47	Ly	0	1
47	Na	0	5
49	Ny	0	2
49	Pa	0	1
50	Oy	0	2
50	Qa	0	1
52	Qy	0	1
53	Ry	0	1
54	Sy	0	1
55	E	0	1
55	Ty	0	1
57	G	0	1
57	Vy	0	1
58	H	0	4
60	Yy	0	1
61	K	0	1
62	L	0	2
62	ay	0	3
63	M	0	2
63	by	0	3
64	cy	0	1
69	hb	0	1
All	All	0	146

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	H	116	LYS	CG-CD	80.59	3.94	1.52
1	a	1597	A	C6-N1	39.89	2.15	1.35
1	a	1597	A	N1-C2	39.32	2.12	1.34
1	a	1597	A	N3-C4	34.21	2.03	1.34
1	a	1597	A	C2-N3	33.03	1.99	1.33

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	4	13	ARG	CA-C-N	26.43	163.44	122.74
30	4	13	ARG	C-N-CA	26.43	163.44	122.74
1	a	1597	A	N1-C2-N3	-10.10	99.01	129.30
1	a	1553	G	C4'-C3'-O3'	9.17	126.75	113.00
78	1b	846	A	C4-N9-C1'	8.54	151.91	126.30

There are no chirality outliers.

5 of 146 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Ab	42	PRO	Peptide
3	Ba	147	ALA	Peptide
3	Ba	151	LYS	Peptide
3	Ba	44	GLY	Peptide
3	Ba	81	PHE	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2b	37739	0	18910	798	0
1	a	37455	0	18845	855	0
2	Ab	1603	0	1610	49	0
2	b	1583	0	1578	60	0
3	Ba	1798	0	1889	72	0
3	c	1722	0	1793	52	0
4	Pb	916	0	941	26	0
4	q	939	0	968	42	0
5	Cb	1626	0	1715	51	0
5	d	1635	0	1723	68	0
6	Db	1729	0	1812	50	0
6	e	1734	0	1817	50	0
7	Eb	2056	0	2140	79	0
7	f	2068	0	2154	88	0
8	Fb	1605	0	1669	77	0
8	g	1609	0	1675	60	0
9	Gb	1815	0	1894	69	0
9	h	1755	0	1846	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	Hb	1473	0	1555	39	0
10	i	1486	0	1576	50	0
11	Ib	1476	0	1501	61	0
11	j	1489	0	1525	65	0
12	Jb	1479	0	1556	43	0
12	k	1494	0	1573	56	0
13	Kb	752	0	719	20	0
13	l	741	0	691	14	0
14	Lb	1159	0	1225	27	0
14	m	1168	0	1233	34	0
15	Mb	875	0	878	49	0
15	n	890	0	887	27	0
16	Nb	1192	0	1255	45	0
16	o	1192	0	1255	48	0
17	Ob	926	0	950	33	0
17	p	949	0	985	38	0
18	Qb	1105	0	1166	47	0
18	r	1105	0	1166	54	0
19	Rb	948	0	990	34	0
19	s	1000	0	1063	39	0
20	Sb	1192	0	1222	45	0
20	t	1192	0	1222	46	0
21	Tb	1112	0	1124	49	0
21	u	1112	0	1124	45	0
22	Ub	797	0	863	36	0
22	v	805	0	874	46	0
23	Vb	673	0	662	26	0
23	w	684	0	672	30	0
24	Wb	1021	0	1060	34	0
24	x	1021	0	1060	44	0
25	Xb	1121	0	1196	48	0
25	y	1121	0	1196	43	0
26	Yb	1073	0	1132	45	0
26	z	1073	0	1132	64	0
27	0	558	0	598	33	0
27	Zb	651	0	682	23	0
28	1	769	0	816	38	0
28	ab	769	0	818	28	0
29	2	610	0	633	26	0
29	bb	610	0	633	28	0
30	4	442	0	431	71	0
30	db	442	0	430	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	5	475	0	525	21	0
31	eb	472	0	521	18	0
32	6	556	0	549	16	0
32	fb	556	0	547	39	0
33	7	2403	0	2350	62	0
33	gb	2383	0	2332	87	0
34	3	497	0	535	28	0
34	cb	491	0	524	13	0
35	4b	2579	0	1302	54	0
35	Bb	2579	0	1304	62	0
36	3b	3353	0	1682	64	0
36	Ca	3333	0	1685	78	0
37	Ay	1899	0	1957	73	0
37	Da	1912	0	1976	77	0
38	By	3075	0	3142	116	0
38	Ea	3075	0	3142	107	0
39	Cy	2748	0	2859	117	0
39	Fa	2748	0	2859	129	0
40	Dy	2351	0	2294	108	0
40	Ga	2359	0	2311	101	0
41	Ey	1303	0	1376	52	0
41	Ha	1248	0	1339	49	0
42	Fy	1784	0	1862	48	0
42	Ia	1791	0	1869	60	0
43	Gy	1804	0	1877	41	0
43	Ja	1763	0	1819	49	0
44	Hy	1508	0	1572	58	0
44	Ka	1510	0	1576	55	0
45	Iy	1764	0	1804	59	0
45	La	1696	0	1731	68	0
46	Jy	1350	0	1381	51	0
46	Ma	1353	0	1383	51	0
47	Ly	1543	0	1607	58	0
47	Na	1548	0	1613	68	0
48	My	1053	0	1149	53	0
48	Oa	1059	0	1154	52	0
49	Ny	1720	0	1779	75	0
49	Pa	1720	0	1779	80	0
50	Oy	1555	0	1659	61	0
50	Qa	1555	0	1659	69	0
51	A	1378	0	1404	46	0
51	Py	1416	0	1433	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	B	1441	0	1543	47	0
52	Qy	1441	0	1543	55	0
53	C	1482	0	1578	46	0
53	Ry	1515	0	1606	42	0
54	D	1445	0	1487	50	0
54	Sy	1437	0	1475	45	0
55	E	1276	0	1323	57	0
55	Ty	1276	0	1323	56	0
56	F	778	0	791	20	0
56	Uy	796	0	812	26	0
57	G	993	0	1040	38	0
57	Vy	1003	0	1048	37	0
58	H	1089	0	1183	55	0
58	Wy	849	0	727	12	0
59	I	959	0	1023	29	0
59	Xy	964	0	1025	34	0
60	J	976	0	1064	40	0
60	Yy	984	0	1075	43	0
61	K	1092	0	1155	41	0
61	Zy	1092	0	1155	31	0
62	L	1173	0	1215	52	0
62	ay	1173	0	1215	43	0
63	M	462	0	491	17	0
63	by	462	0	491	11	0
64	N	767	0	816	26	0
64	cy	737	0	792	26	0
65	O	883	0	918	30	0
65	dy	876	0	912	29	0
66	P	1020	0	1090	38	0
66	ey	1017	0	1081	27	0
67	Q	850	0	880	27	0
67	fy	850	0	880	37	0
68	R	880	0	945	31	0
68	gy	880	0	945	44	0
69	S	965	0	1067	36	0
69	hb	969	0	1078	22	0
70	T	770	0	846	38	0
70	ib	766	0	844	29	0
71	U	650	0	654	29	0
71	jb	670	0	675	33	0
72	V	608	0	671	22	0
72	kb	612	0	682	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	W	436	0	475	18	0
73	lb	436	0	475	17	0
74	X	417	0	457	20	0
74	mb	417	0	459	18	0
75	Y	233	0	284	6	0
75	nb	229	0	273	5	0
76	Z	847	0	915	29	0
76	ob	824	0	892	27	0
77	aa	694	0	738	26	0
77	pb	694	0	738	28	0
78	1b	68091	0	33899	1154	0
78	Aa	66891	0	33616	1306	0
79	6b	1616	0	814	15	0
79	8	1616	0	816	10	0
80	ba	1052	0	1028	25	0
All	All	401820	0	296572	8919	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 13.

The worst 5 of 8919 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)
1:a:74:U:N3	1:a:74:U:C2	1.69	1.55
1:a:74:U:N3	1:a:74:U:C4	1.68	1.54
1:a:1597:A:C5	1:a:1597:A:C6	1.98	1.51
1:a:1597:A:C5	1:a:1597:A:C4	1.89	1.46
30:4:13:ARG:C	30:4:14:TYR:N	1.73	1.45

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ab	204/252 (81%)	170 (83%)	33 (16%)	1 (0%)	24	60
2	b	204/252 (81%)	165 (81%)	38 (19%)	1 (0%)	24	60
3	Ba	222/255 (87%)	182 (82%)	36 (16%)	4 (2%)	6	34
3	c	214/255 (84%)	192 (90%)	21 (10%)	1 (0%)	24	60
4	Pb	115/142 (81%)	101 (88%)	14 (12%)	0	100	100
4	q	117/142 (82%)	97 (83%)	16 (14%)	4 (3%)	3	24
5	Cb	214/254 (84%)	187 (87%)	26 (12%)	1 (0%)	24	60
5	d	215/254 (85%)	183 (85%)	32 (15%)	0	100	100
6	Db	220/240 (92%)	199 (90%)	21 (10%)	0	100	100
6	e	221/240 (92%)	188 (85%)	32 (14%)	1 (0%)	24	60
7	Eb	256/261 (98%)	211 (82%)	44 (17%)	1 (0%)	30	65
7	f	258/261 (99%)	224 (87%)	33 (13%)	1 (0%)	30	65
8	Fb	204/225 (91%)	176 (86%)	27 (13%)	1 (0%)	24	60
8	g	204/225 (91%)	175 (86%)	28 (14%)	1 (0%)	24	60
9	Gb	226/236 (96%)	194 (86%)	28 (12%)	4 (2%)	6	34
9	h	216/236 (92%)	196 (91%)	19 (9%)	1 (0%)	24	60
10	Hb	182/190 (96%)	156 (86%)	25 (14%)	1 (0%)	24	60
10	i	183/190 (96%)	156 (85%)	25 (14%)	2 (1%)	11	44
11	Ib	183/200 (92%)	159 (87%)	22 (12%)	2 (1%)	11	44
11	j	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
12	Jb	182/197 (92%)	155 (85%)	25 (14%)	2 (1%)	11	44
12	k	183/197 (93%)	162 (88%)	19 (10%)	2 (1%)	11	44
13	Kb	90/105 (86%)	67 (74%)	23 (26%)	0	100	100
13	l	90/105 (86%)	74 (82%)	15 (17%)	1 (1%)	11	44
14	Lb	142/156 (91%)	113 (80%)	29 (20%)	0	100	100
14	m	144/156 (92%)	124 (86%)	20 (14%)	0	100	100
15	Mb	119/143 (83%)	74 (62%)	40 (34%)	5 (4%)	2	21
15	n	122/143 (85%)	79 (65%)	40 (33%)	3 (2%)	4	29
16	Nb	148/151 (98%)	121 (82%)	26 (18%)	1 (1%)	18	54
16	o	148/151 (98%)	128 (86%)	20 (14%)	0	100	100
17	Ob	125/137 (91%)	104 (83%)	21 (17%)	0	100	100
17	p	126/137 (92%)	105 (83%)	21 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	Qb	139/143 (97%)	117 (84%)	21 (15%)	1 (1%)	18	54
18	r	139/143 (97%)	121 (87%)	15 (11%)	3 (2%)	5	31
19	Rb	117/136 (86%)	104 (89%)	11 (9%)	2 (2%)	7	36
19	s	123/136 (90%)	110 (89%)	12 (10%)	1 (1%)	16	52
20	Sb	143/146 (98%)	113 (79%)	26 (18%)	4 (3%)	4	27
20	t	143/146 (98%)	124 (87%)	17 (12%)	2 (1%)	9	39
21	Tb	141/144 (98%)	114 (81%)	25 (18%)	2 (1%)	9	39
21	u	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
22	Ub	98/121 (81%)	86 (88%)	12 (12%)	0	100	100
22	v	99/121 (82%)	87 (88%)	10 (10%)	2 (2%)	6	33
23	Vb	85/87 (98%)	65 (76%)	19 (22%)	1 (1%)	10	42
23	w	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
24	Wb	127/130 (98%)	103 (81%)	24 (19%)	0	100	100
24	x	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
25	Xb	142/145 (98%)	110 (78%)	30 (21%)	2 (1%)	9	39
25	y	142/145 (98%)	123 (87%)	17 (12%)	2 (1%)	9	39
26	Yb	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	16	52
26	z	132/135 (98%)	109 (83%)	21 (16%)	2 (2%)	8	38
27	0	67/108 (62%)	61 (91%)	6 (9%)	0	100	100
27	Zb	80/108 (74%)	63 (79%)	17 (21%)	0	100	100
28	1	95/119 (80%)	71 (75%)	23 (24%)	1 (1%)	11	44
28	ab	95/119 (80%)	64 (67%)	26 (27%)	5 (5%)	1	18
29	2	79/82 (96%)	64 (81%)	15 (19%)	0	100	100
29	bb	79/82 (96%)	63 (80%)	16 (20%)	0	100	100
30	4	51/56 (91%)	38 (74%)	13 (26%)	0	100	100
30	db	51/56 (91%)	42 (82%)	9 (18%)	0	100	100
31	5	58/63 (92%)	43 (74%)	14 (24%)	1 (2%)	7	36
31	eb	58/63 (92%)	45 (78%)	13 (22%)	0	100	100
32	6	71/152 (47%)	41 (58%)	29 (41%)	1 (1%)	9	39
32	fb	71/152 (47%)	43 (61%)	28 (39%)	0	100	100
33	7	311/319 (98%)	281 (90%)	30 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	gb	310/319 (97%)	264 (85%)	45 (14%)	1 (0%)	36	70
34	3	61/67 (91%)	54 (88%)	7 (12%)	0	100	100
34	cb	61/67 (91%)	47 (77%)	14 (23%)	0	100	100
37	Ay	249/254 (98%)	199 (80%)	48 (19%)	2 (1%)	16	52
37	Da	250/254 (98%)	205 (82%)	45 (18%)	0	100	100
38	By	384/387 (99%)	314 (82%)	68 (18%)	2 (0%)	24	60
38	Ea	384/387 (99%)	342 (89%)	42 (11%)	0	100	100
39	Cy	359/362 (99%)	292 (81%)	65 (18%)	2 (1%)	21	57
39	Fa	359/362 (99%)	297 (83%)	58 (16%)	4 (1%)	11	44
40	Dy	292/297 (98%)	251 (86%)	40 (14%)	1 (0%)	36	70
40	Ga	292/297 (98%)	265 (91%)	27 (9%)	0	100	100
41	Ey	163/176 (93%)	138 (85%)	24 (15%)	1 (1%)	21	57
41	Ha	153/176 (87%)	132 (86%)	21 (14%)	0	100	100
42	Fy	220/244 (90%)	178 (81%)	40 (18%)	2 (1%)	14	48
42	Ia	221/244 (91%)	198 (90%)	23 (10%)	0	100	100
43	Gy	231/256 (90%)	196 (85%)	35 (15%)	0	100	100
43	Ja	229/256 (90%)	187 (82%)	42 (18%)	0	100	100
44	Hy	189/191 (99%)	164 (87%)	25 (13%)	0	100	100
44	Ka	188/191 (98%)	176 (94%)	12 (6%)	0	100	100
45	Iy	216/221 (98%)	187 (87%)	29 (13%)	0	100	100
45	La	205/221 (93%)	178 (87%)	27 (13%)	0	100	100
46	Jy	167/174 (96%)	129 (77%)	35 (21%)	3 (2%)	6	34
46	Ma	167/174 (96%)	141 (84%)	24 (14%)	2 (1%)	10	42
47	Ly	191/199 (96%)	148 (78%)	39 (20%)	4 (2%)	5	32
47	Na	192/199 (96%)	149 (78%)	38 (20%)	5 (3%)	4	29
48	My	134/138 (97%)	114 (85%)	20 (15%)	0	100	100
48	Oa	135/138 (98%)	123 (91%)	12 (9%)	0	100	100
49	Ny	201/204 (98%)	160 (80%)	41 (20%)	0	100	100
49	Pa	201/204 (98%)	182 (90%)	17 (8%)	2 (1%)	12	45
50	Oy	195/199 (98%)	161 (83%)	32 (16%)	2 (1%)	12	45
50	Qa	195/199 (98%)	183 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	A	171/184 (93%)	160 (94%)	11 (6%)	0	100	100
51	Py	181/184 (98%)	149 (82%)	32 (18%)	0	100	100
52	B	183/186 (98%)	158 (86%)	25 (14%)	0	100	100
52	Qy	183/186 (98%)	152 (83%)	31 (17%)	0	100	100
53	C	181/189 (96%)	171 (94%)	10 (6%)	0	100	100
53	Ry	186/189 (98%)	168 (90%)	16 (9%)	2 (1%)	11	44
54	D	170/172 (99%)	157 (92%)	13 (8%)	0	100	100
54	Sy	169/172 (98%)	150 (89%)	19 (11%)	0	100	100
55	E	157/160 (98%)	137 (87%)	20 (13%)	0	100	100
55	Ty	157/160 (98%)	132 (84%)	25 (16%)	0	100	100
56	F	96/121 (79%)	91 (95%)	5 (5%)	0	100	100
56	Uy	98/121 (81%)	87 (89%)	11 (11%)	0	100	100
57	G	132/137 (96%)	121 (92%)	11 (8%)	0	100	100
57	Vy	134/137 (98%)	115 (86%)	19 (14%)	0	100	100
58	H	133/155 (86%)	109 (82%)	24 (18%)	0	100	100
58	Wy	124/155 (80%)	97 (78%)	27 (22%)	0	100	100
59	I	118/142 (83%)	102 (86%)	16 (14%)	0	100	100
59	Xy	119/142 (84%)	98 (82%)	20 (17%)	1 (1%)	16	52
60	J	122/127 (96%)	113 (93%)	9 (7%)	0	100	100
60	Yy	123/127 (97%)	101 (82%)	22 (18%)	0	100	100
61	K	133/136 (98%)	115 (86%)	16 (12%)	2 (2%)	8	38
61	Zy	133/136 (98%)	116 (87%)	17 (13%)	0	100	100
62	L	146/149 (98%)	116 (80%)	27 (18%)	3 (2%)	5	32
62	ay	146/149 (98%)	113 (77%)	30 (20%)	3 (2%)	5	32
63	M	56/59 (95%)	43 (77%)	13 (23%)	0	100	100
63	by	56/59 (95%)	39 (70%)	15 (27%)	2 (4%)	2	23
64	N	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
64	cy	94/105 (90%)	86 (92%)	8 (8%)	0	100	100
65	O	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
65	dy	107/113 (95%)	91 (85%)	16 (15%)	0	100	100
66	P	125/130 (96%)	110 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	ey	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
67	Q	104/107 (97%)	90 (86%)	14 (14%)	0	100	100
67	fy	104/107 (97%)	87 (84%)	17 (16%)	0	100	100
68	R	110/121 (91%)	103 (94%)	7 (6%)	0	100	100
68	gy	110/121 (91%)	92 (84%)	18 (16%)	0	100	100
69	S	117/120 (98%)	100 (86%)	17 (14%)	0	100	100
69	hb	117/120 (98%)	102 (87%)	15 (13%)	0	100	100
70	T	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
70	ib	97/100 (97%)	80 (82%)	17 (18%)	0	100	100
71	U	80/88 (91%)	70 (88%)	10 (12%)	0	100	100
71	jb	83/88 (94%)	67 (81%)	16 (19%)	0	100	100
72	V	75/78 (96%)	69 (92%)	5 (7%)	1 (1%)	9	41
72	kb	75/78 (96%)	67 (89%)	8 (11%)	0	100	100
73	W	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
73	lb	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
74	X	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
74	mb	50/128 (39%)	40 (80%)	10 (20%)	0	100	100
75	Y	23/25 (92%)	23 (100%)	0	0	100	100
75	nb	23/25 (92%)	23 (100%)	0	0	100	100
76	Z	103/106 (97%)	91 (88%)	12 (12%)	0	100	100
76	ob	101/106 (95%)	87 (86%)	14 (14%)	0	100	100
77	aa	89/92 (97%)	76 (85%)	13 (15%)	0	100	100
77	pb	89/92 (97%)	71 (80%)	18 (20%)	0	100	100
80	ba	134/311 (43%)	128 (96%)	6 (4%)	0	100	100
All	All	22066/24071 (92%)	18754 (85%)	3191 (14%)	121 (0%)	26	60

5 of 121 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	Jb	99	LEU
28	ab	84	VAL
18	r	116	LEU
19	s	82	ASP
26	z	52	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	
2	Ab	170/210 (81%)	169 (99%)	1 (1%)	78	81
2	b	165/210 (79%)	165 (100%)	0	100	100
3	Ba	200/224 (89%)	198 (99%)	2 (1%)	68	76
3	c	192/224 (86%)	191 (100%)	1 (0%)	81	82
4	Pb	95/118 (80%)	95 (100%)	0	100	100
4	q	98/118 (83%)	98 (100%)	0	100	100
5	Cb	175/205 (85%)	174 (99%)	1 (1%)	78	81
5	d	176/205 (86%)	176 (100%)	0	100	100
6	Db	182/195 (93%)	182 (100%)	0	100	100
6	e	182/195 (93%)	181 (100%)	1 (0%)	81	82
7	Eb	220/222 (99%)	219 (100%)	1 (0%)	81	82
7	f	221/222 (100%)	221 (100%)	0	100	100
8	Fb	172/191 (90%)	172 (100%)	0	100	100
8	g	173/191 (91%)	173 (100%)	0	100	100
9	Gb	189/201 (94%)	187 (99%)	2 (1%)	65	74
9	h	187/201 (93%)	187 (100%)	0	100	100
10	Hb	163/170 (96%)	163 (100%)	0	100	100
10	i	165/170 (97%)	165 (100%)	0	100	100
11	Ib	148/161 (92%)	148 (100%)	0	100	100
11	j	150/161 (93%)	150 (100%)	0	100	100
12	Jb	156/166 (94%)	156 (100%)	0	100	100
12	k	158/166 (95%)	158 (100%)	0	100	100
13	Kb	77/98 (79%)	76 (99%)	1 (1%)	61	72
13	l	73/98 (74%)	73 (100%)	0	100	100
14	Lb	129/137 (94%)	126 (98%)	3 (2%)	44	64
14	m	129/137 (94%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	Mb	88/119 (74%)	88 (100%)	0	100	100
15	n	88/119 (74%)	88 (100%)	0	100	100
16	Nb	127/128 (99%)	125 (98%)	2 (2%)	55	70
16	o	127/128 (99%)	126 (99%)	1 (1%)	73	77
17	Ob	91/105 (87%)	91 (100%)	0	100	100
17	p	97/105 (92%)	96 (99%)	1 (1%)	68	76
18	Qb	117/119 (98%)	117 (100%)	0	100	100
18	r	117/119 (98%)	117 (100%)	0	100	100
19	Rb	101/124 (82%)	101 (100%)	0	100	100
19	s	113/124 (91%)	113 (100%)	0	100	100
20	Sb	128/129 (99%)	128 (100%)	0	100	100
20	t	128/129 (99%)	127 (99%)	1 (1%)	73	77
21	Tb	115/116 (99%)	114 (99%)	1 (1%)	70	76
21	u	115/116 (99%)	115 (100%)	0	100	100
22	Ub	93/114 (82%)	92 (99%)	1 (1%)	65	74
22	v	94/114 (82%)	94 (100%)	0	100	100
23	Vb	71/74 (96%)	71 (100%)	0	100	100
23	w	74/74 (100%)	74 (100%)	0	100	100
24	Wb	110/111 (99%)	109 (99%)	1 (1%)	70	76
24	x	110/111 (99%)	110 (100%)	0	100	100
25	Xb	119/120 (99%)	119 (100%)	0	100	100
25	y	119/120 (99%)	119 (100%)	0	100	100
26	Yb	112/113 (99%)	111 (99%)	1 (1%)	70	76
26	z	112/113 (99%)	112 (100%)	0	100	100
27	0	61/89 (68%)	61 (100%)	0	100	100
27	Zb	67/89 (75%)	67 (100%)	0	100	100
28	1	83/101 (82%)	83 (100%)	0	100	100
28	ab	83/101 (82%)	82 (99%)	1 (1%)	63	73
29	2	70/71 (99%)	70 (100%)	0	100	100
29	bb	70/71 (99%)	70 (100%)	0	100	100
30	4	47/49 (96%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	db	47/49 (96%)	46 (98%)	1 (2%)	47	65
31	5	51/54 (94%)	51 (100%)	0	100	100
31	eb	50/54 (93%)	50 (100%)	0	100	100
32	6	56/135 (42%)	56 (100%)	0	100	100
32	fb	56/135 (42%)	56 (100%)	0	100	100
33	7	255/262 (97%)	255 (100%)	0	100	100
33	gb	250/262 (95%)	249 (100%)	1 (0%)	84	84
34	3	56/60 (93%)	56 (100%)	0	100	100
34	cb	55/60 (92%)	55 (100%)	0	100	100
37	Ay	190/196 (97%)	187 (98%)	3 (2%)	55	70
37	Da	192/196 (98%)	192 (100%)	0	100	100
38	By	319/323 (99%)	314 (98%)	5 (2%)	55	70
38	Ea	318/323 (98%)	318 (100%)	0	100	100
39	Cy	288/289 (100%)	286 (99%)	2 (1%)	76	79
39	Fa	288/289 (100%)	287 (100%)	1 (0%)	86	85
40	Dy	241/245 (98%)	240 (100%)	1 (0%)	84	84
40	Ga	243/245 (99%)	243 (100%)	0	100	100
41	Ey	137/153 (90%)	137 (100%)	0	100	100
41	Ha	135/153 (88%)	135 (100%)	0	100	100
42	Fy	186/205 (91%)	185 (100%)	1 (0%)	81	82
42	Ia	187/205 (91%)	186 (100%)	1 (0%)	81	82
43	Gy	187/208 (90%)	184 (98%)	3 (2%)	55	70
43	Ja	177/208 (85%)	177 (100%)	0	100	100
44	Hy	168/171 (98%)	165 (98%)	3 (2%)	51	68
44	Ka	170/171 (99%)	168 (99%)	2 (1%)	63	73
45	Iy	185/187 (99%)	183 (99%)	2 (1%)	65	74
45	La	177/187 (95%)	177 (100%)	0	100	100
46	Jy	146/150 (97%)	146 (100%)	0	100	100
46	Ma	147/150 (98%)	146 (99%)	1 (1%)	76	79
47	Ly	154/159 (97%)	153 (99%)	1 (1%)	78	81
47	Na	154/159 (97%)	153 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	My	107/109 (98%)	107 (100%)	0	100	100
48	Oa	108/109 (99%)	107 (99%)	1 (1%)	70	76
49	Ny	175/176 (99%)	174 (99%)	1 (1%)	78	81
49	Pa	175/176 (99%)	175 (100%)	0	100	100
50	Oy	160/162 (99%)	160 (100%)	0	100	100
50	Qa	160/162 (99%)	159 (99%)	1 (1%)	78	81
51	A	139/146 (95%)	139 (100%)	0	100	100
51	Py	138/146 (94%)	135 (98%)	3 (2%)	45	65
52	B	150/151 (99%)	150 (100%)	0	100	100
52	Qy	150/151 (99%)	150 (100%)	0	100	100
53	C	149/154 (97%)	149 (100%)	0	100	100
53	Ry	152/154 (99%)	149 (98%)	3 (2%)	48	66
54	D	156/156 (100%)	156 (100%)	0	100	100
54	Sy	155/156 (99%)	155 (100%)	0	100	100
55	E	136/137 (99%)	136 (100%)	0	100	100
55	Ty	136/137 (99%)	136 (100%)	0	100	100
56	F	85/107 (79%)	85 (100%)	0	100	100
56	Uy	87/107 (81%)	86 (99%)	1 (1%)	65	74
57	G	103/105 (98%)	103 (100%)	0	100	100
57	Vy	104/105 (99%)	104 (100%)	0	100	100
58	H	114/129 (88%)	114 (100%)	0	100	100
58	Wy	60/129 (46%)	60 (100%)	0	100	100
59	I	104/118 (88%)	103 (99%)	1 (1%)	68	76
59	Xy	104/118 (88%)	103 (99%)	1 (1%)	68	76
60	J	107/110 (97%)	107 (100%)	0	100	100
60	Yy	108/110 (98%)	107 (99%)	1 (1%)	70	76
61	K	115/116 (99%)	115 (100%)	0	100	100
61	Zy	115/116 (99%)	115 (100%)	0	100	100
62	L	118/119 (99%)	118 (100%)	0	100	100
62	ay	118/119 (99%)	117 (99%)	1 (1%)	73	77
63	M	46/47 (98%)	45 (98%)	1 (2%)	45	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	by	46/47 (98%)	46 (100%)	0	100	100
64	N	84/88 (96%)	84 (100%)	0	100	100
64	cy	81/88 (92%)	80 (99%)	1 (1%)	63	73
65	O	94/97 (97%)	93 (99%)	1 (1%)	65	74
65	dy	92/97 (95%)	92 (100%)	0	100	100
66	P	109/111 (98%)	109 (100%)	0	100	100
66	ey	108/111 (97%)	108 (100%)	0	100	100
67	Q	90/91 (99%)	90 (100%)	0	100	100
67	fy	90/91 (99%)	90 (100%)	0	100	100
68	R	95/103 (92%)	95 (100%)	0	100	100
68	gy	95/103 (92%)	95 (100%)	0	100	100
69	S	103/105 (98%)	103 (100%)	0	100	100
69	hb	104/105 (99%)	100 (96%)	4 (4%)	29	51
70	T	80/82 (98%)	80 (100%)	0	100	100
70	ib	80/82 (98%)	80 (100%)	0	100	100
71	U	67/71 (94%)	67 (100%)	0	100	100
71	jb	69/71 (97%)	69 (100%)	0	100	100
72	V	67/69 (97%)	67 (100%)	0	100	100
72	kb	68/69 (99%)	68 (100%)	0	100	100
73	W	45/46 (98%)	45 (100%)	0	100	100
73	lb	45/46 (98%)	45 (100%)	0	100	100
74	X	47/116 (40%)	47 (100%)	0	100	100
74	mb	47/116 (40%)	47 (100%)	0	100	100
75	Y	23/23 (100%)	23 (100%)	0	100	100
75	nb	22/23 (96%)	22 (100%)	0	100	100
76	Z	90/91 (99%)	90 (100%)	0	100	100
76	ob	87/91 (96%)	86 (99%)	1 (1%)	65	74
77	aa	71/72 (99%)	71 (100%)	0	100	100
77	pb	71/72 (99%)	71 (100%)	0	100	100
80	ba	105/253 (42%)	105 (100%)	0	100	100
All	All	18566/20221 (92%)	18492 (100%)	74 (0%)	81	84

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
76	ob	80	ARG
59	I	126	LEU
6	e	164	VAL
44	Ka	64	HIS
38	By	104	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 273 such sidechains are listed below:

Mol	Chain	Res	Type
51	A	54	HIS
54	D	65	ASN
68	R	52	GLN
52	Qy	136	ASN
51	Py	55	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2b	1768/1800 (98%)	639 (36%)	0
1	a	1755/1800 (97%)	534 (30%)	0
35	4b	120/121 (99%)	20 (16%)	0
35	Bb	120/121 (99%)	17 (14%)	0
36	3b	157/158 (99%)	41 (26%)	0
36	Ca	156/158 (98%)	37 (23%)	0
78	1b	3180/3396 (93%)	881 (27%)	0
78	Aa	3120/3396 (91%)	804 (25%)	0
79	6b	75/76 (98%)	16 (21%)	0
79	8	75/76 (98%)	18 (24%)	0
All	All	10526/11102 (94%)	3007 (28%)	0

5 of 3007 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2b	2	A
1	2b	4	C
1	2b	6	G
1	2b	8	U
1	2b	10	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	4	1
39	Fa	1
16	Nb	1
45	Iy	1
3	Ba	1
47	Ly	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	4	13:ARG	C	14:TYR	N	1.73
1	Fa	19:ALA	C	20:LEU	N	1.20
1	Nb	134:VAL	C	135:LEU	N	1.19
1	Iy	120:GLY	C	121:LYS	N	1.17
1	Ba	33:LYS	C	34:ALA	N	1.11

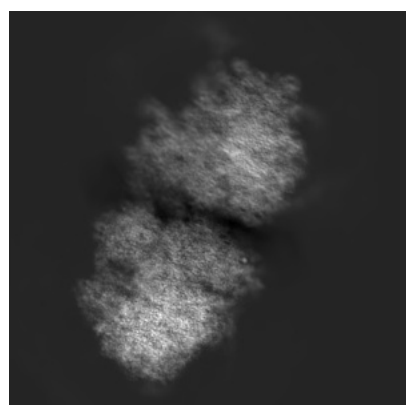
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10398. These allow visual inspection of the internal detail of the map and identification of artifacts.

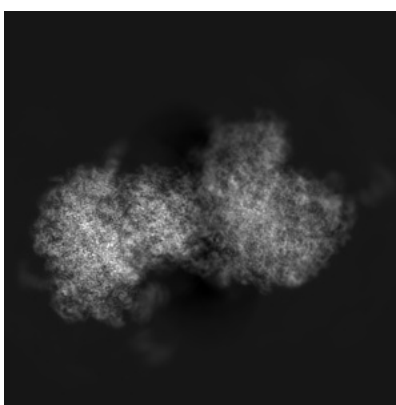
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

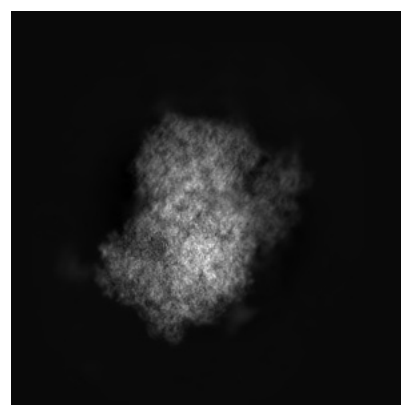
6.1.1 Primary map



X



Y

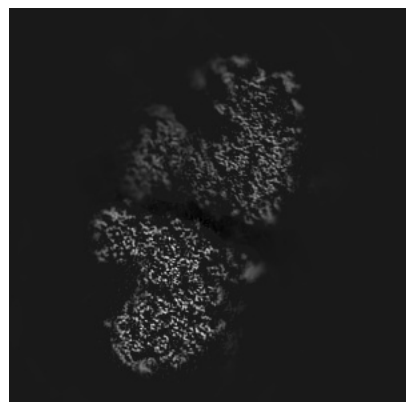


Z

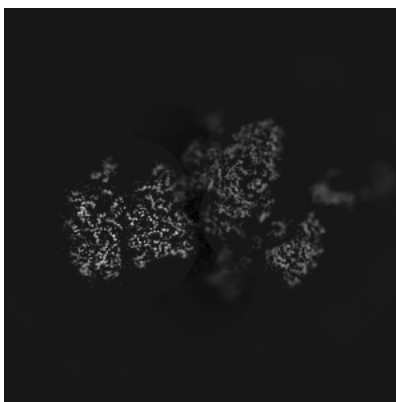
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

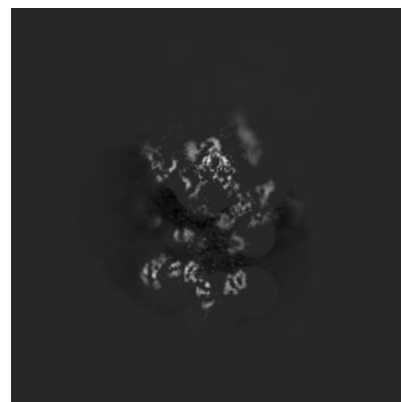
6.2.1 Primary map



X Index: 265



Y Index: 265

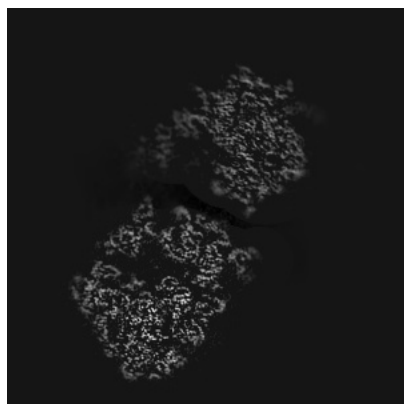


Z Index: 265

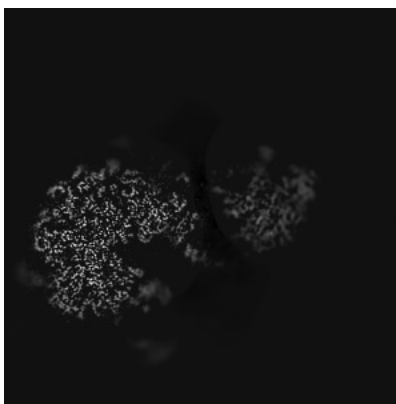
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

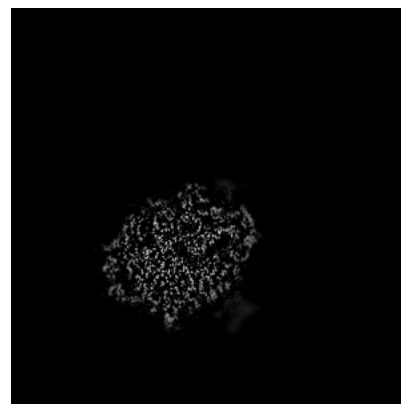
6.3.1 Primary map



X Index: 218



Y Index: 197

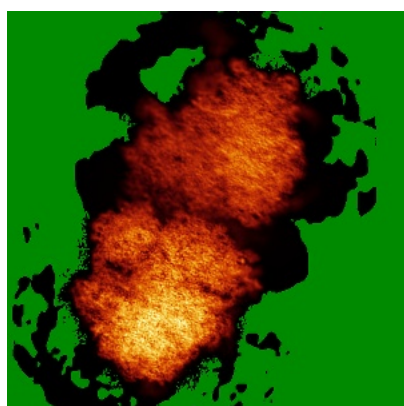


Z Index: 119

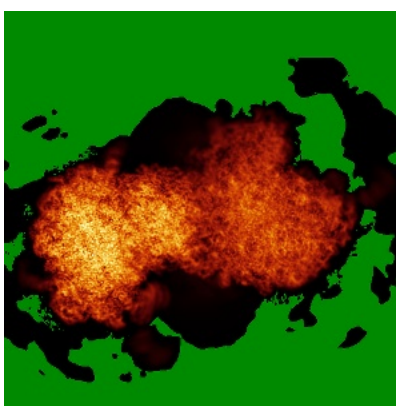
The images above show the largest variance slices of the map in three orthogonal directions.

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

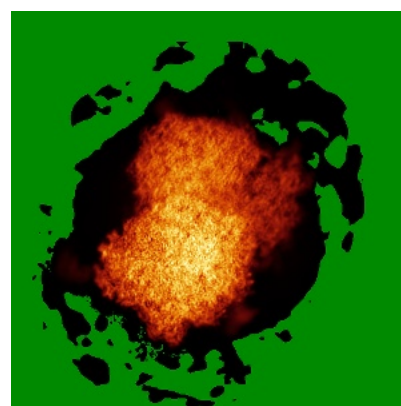
6.4.1 Primary map



X



Y

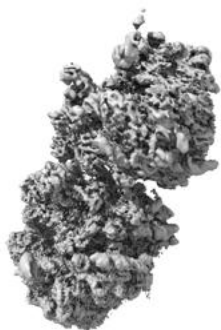


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

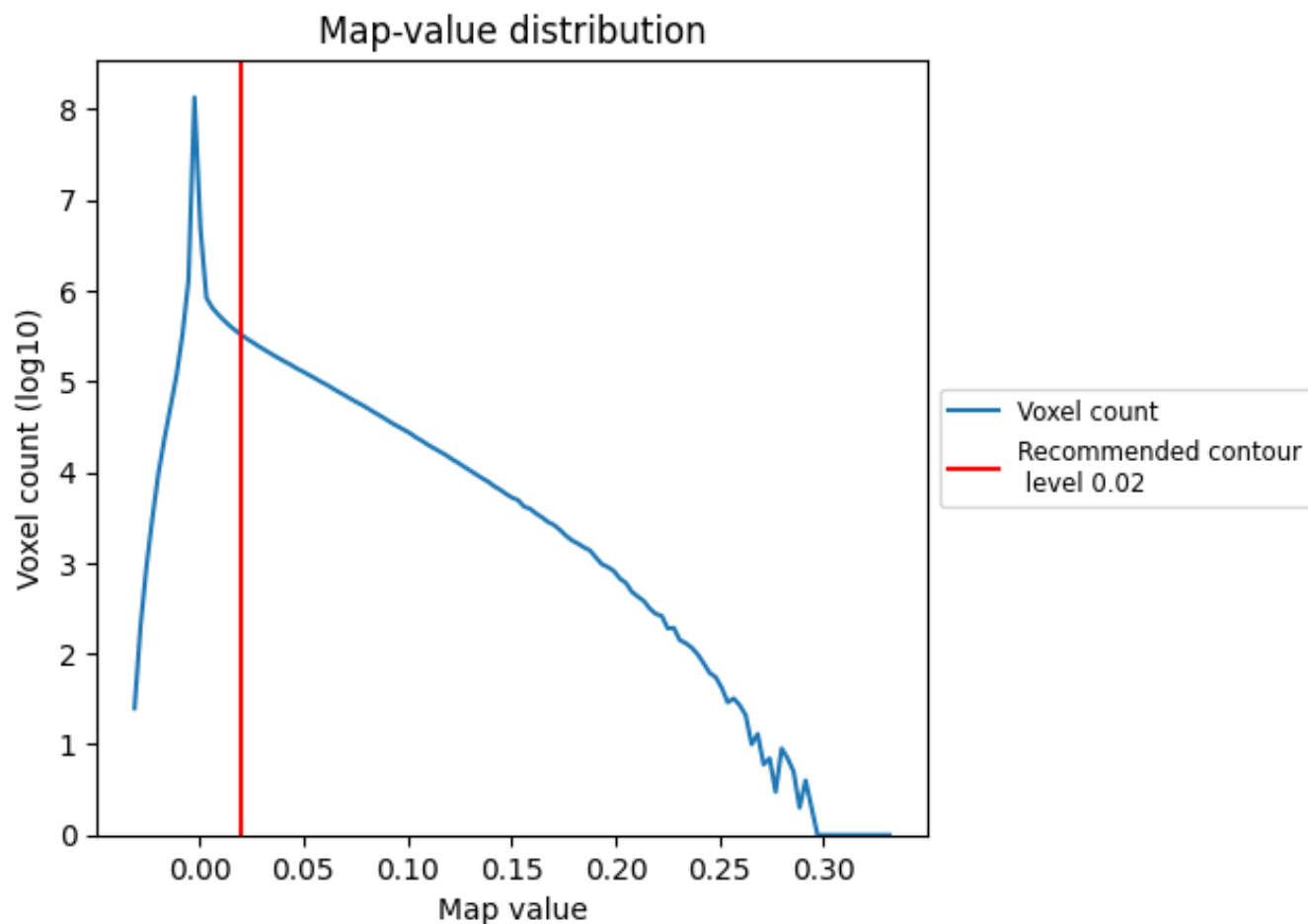
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

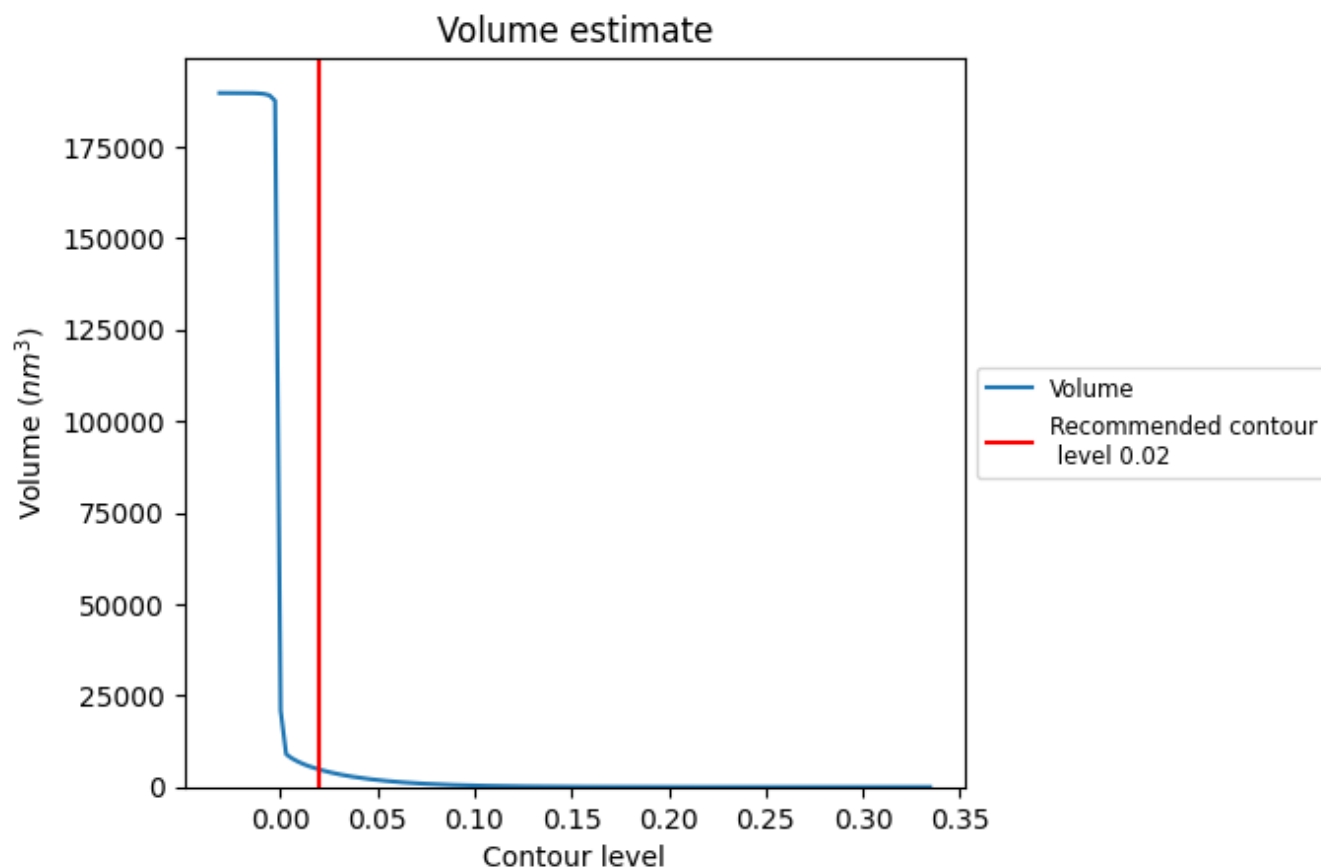
This section contains the results of statistical analysis of the map.

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.

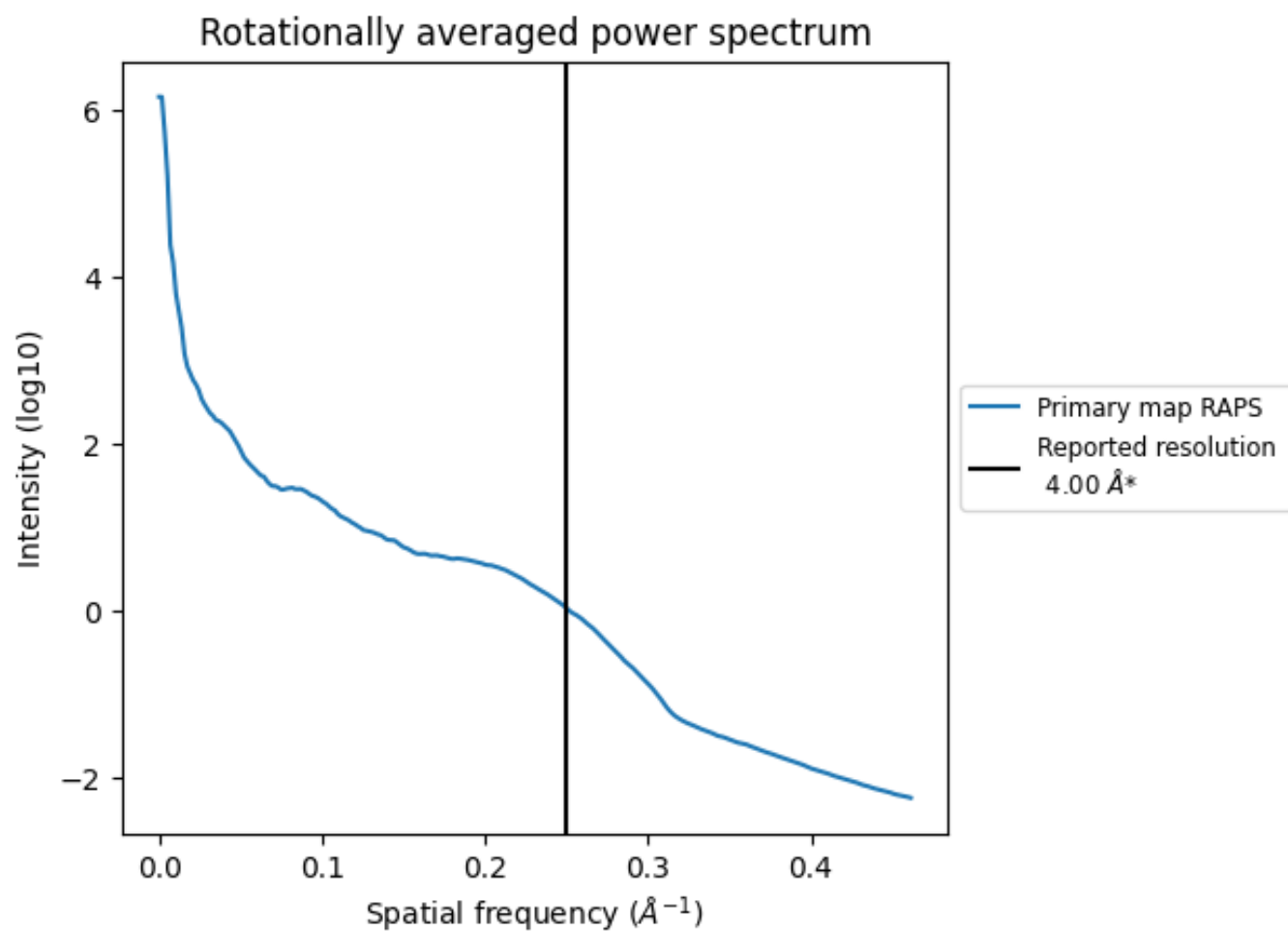
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4789 nm^3 ; this corresponds to an approximate mass of 4326 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 0.250 Å⁻¹

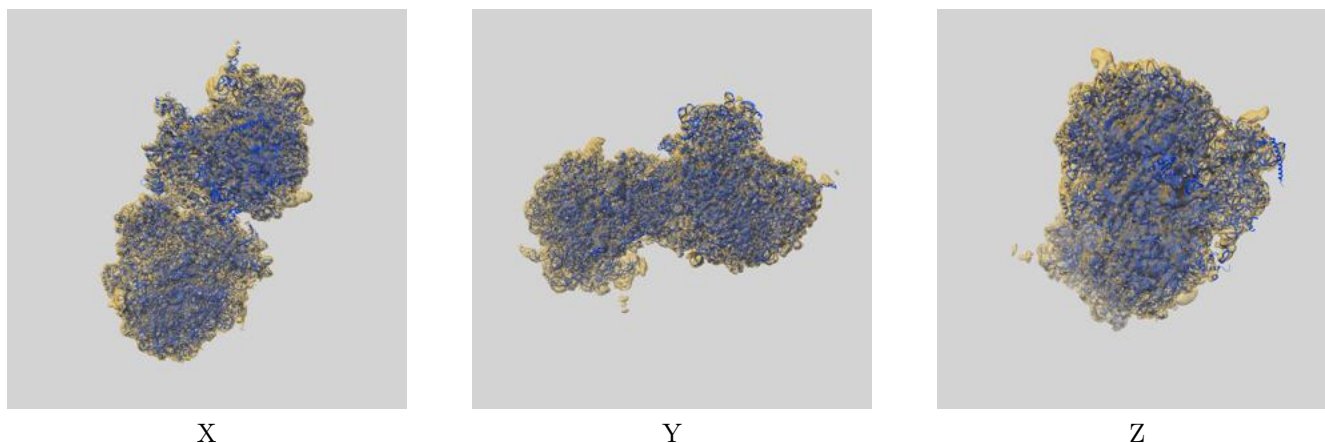
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

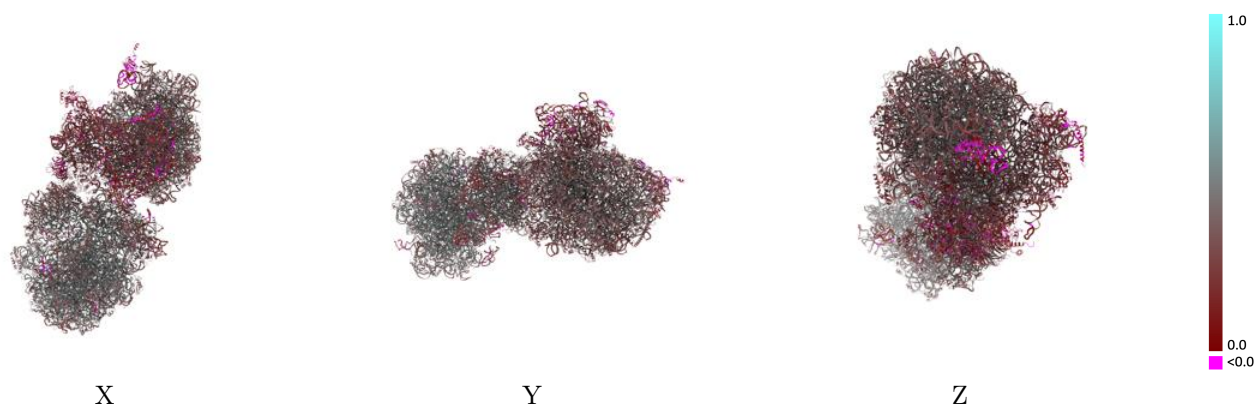
This section contains information regarding the fit between EMDB map EMD-10398 and PDB model 6T83. Per-residue inclusion information can be found in [section 3](#) on [page 26](#).

9.1 Map-model overlay [i](#)



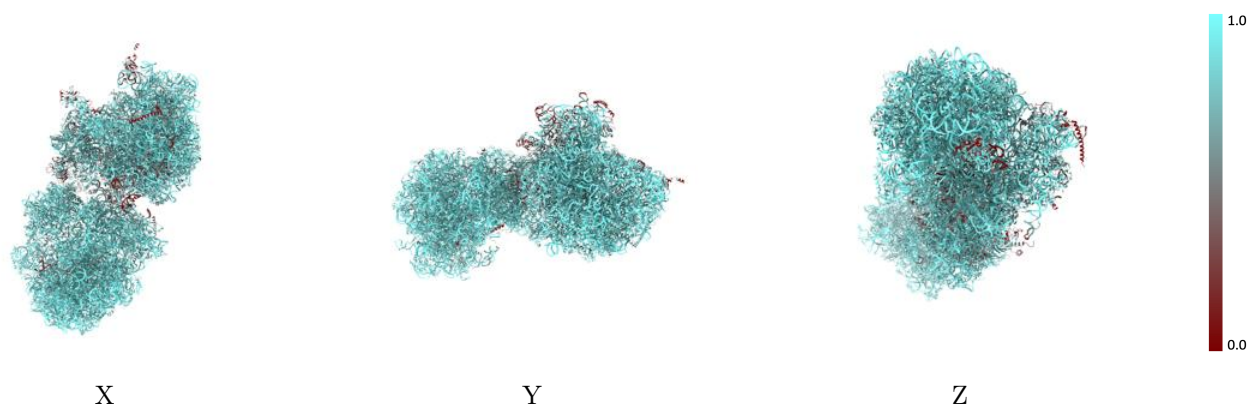
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



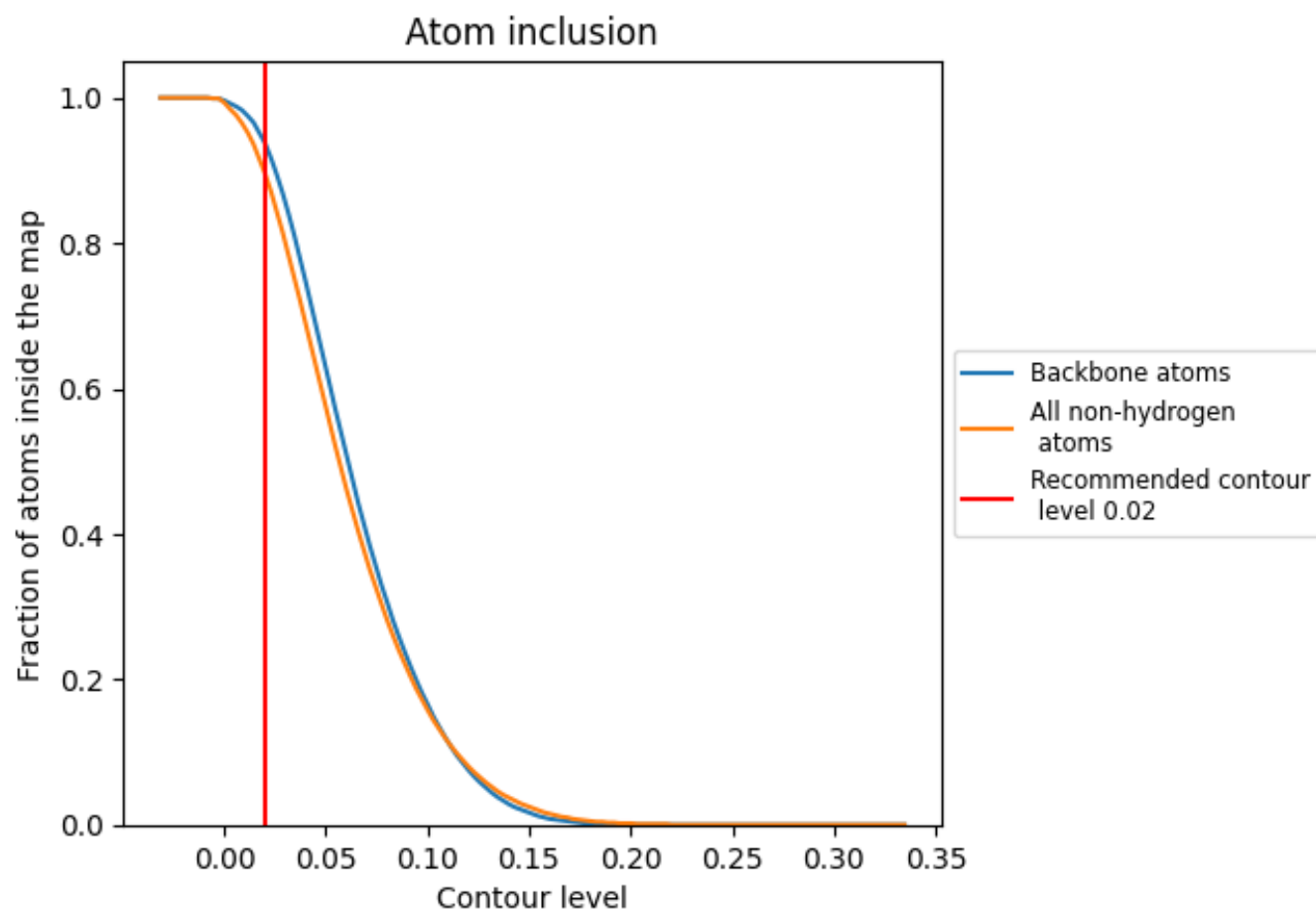
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8970	 0.3720
0	 0.6440	 0.1400
1	 0.7620	 0.3220
1b	 0.9780	 0.4500
2	 0.5360	 0.3050
2b	 0.9570	 0.4070
3	 0.7780	 0.2390
3b	 0.9850	 0.4590
4	 0.6760	 0.0740
4b	 0.9930	 0.4270
5	 0.7300	 0.2160
6	 0.5800	 0.1370
6b	 0.9620	 0.3880
7	 0.4990	 0.1450
8	 0.7390	 0.2520
A	 0.8730	 0.3870
Aa	 0.9550	 0.3780
Ab	 0.8700	 0.3760
Ay	 0.9120	 0.4880
B	 0.8330	 0.3560
Ba	 0.8810	 0.3970
Bb	 0.9910	 0.3470
By	 0.9280	 0.4590
C	 0.7770	 0.3330
Ca	 0.9700	 0.3930
Cb	 0.8730	 0.4230
Cy	 0.9390	 0.4560
D	 0.8220	 0.3600
Da	 0.8270	 0.4040
Db	 0.8290	 0.3710
Dy	 0.9380	 0.3800
E	 0.8390	 0.3740
Ea	 0.8430	 0.3740
Eb	 0.8690	 0.4070
Ey	 0.9300	 0.4030



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Chain	Atom inclusion	Q-score
F	 0.8090	 0.2970
Fa	 0.8790	 0.3720
Fb	 0.8760	 0.3690
Fy	 0.9290	 0.4400
G	 0.7460	 0.3770
Ga	 0.8680	 0.2740
Gb	 0.9010	 0.3480
Gy	 0.9110	 0.4020
H	 0.4150	 0.1670
Ha	 0.8200	 0.3140
Hb	 0.8770	 0.3410
Hy	 0.9040	 0.4150
I	 0.8280	 0.3620
Ia	 0.8410	 0.3530
Ib	 0.9130	 0.4190
Iy	 0.8960	 0.4040
J	 0.8750	 0.3330
Ja	 0.7960	 0.3100
Jb	 0.8590	 0.3780
Jy	 0.9020	 0.3690
K	 0.8110	 0.3160
Ka	 0.8370	 0.3500
Kb	 0.8290	 0.3270
L	 0.8480	 0.3680
La	 0.8410	 0.3130
Lb	 0.8660	 0.4400
Ly	 0.9440	 0.4460
M	 0.8470	 0.3440
Ma	 0.7500	 0.1980
Mb	 0.8160	 0.2290
My	 0.9300	 0.3990
N	 0.7770	 0.3260
Na	 0.8490	 0.3320
Nb	 0.9050	 0.4220
Ny	 0.9430	 0.4980
O	 0.8160	 0.3540
Oa	 0.8940	 0.3290
Ob	 0.8940	 0.4230
Oy	 0.9330	 0.4690
P	 0.8270	 0.3900
Pa	 0.8700	 0.3950
Pb	 0.8640	 0.3410

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Chain	Atom inclusion	Q-score
Py	 0.9430	 0.4660
Q	 0.8600	 0.4110
Qa	 0.8620	 0.3830
Qb	 0.8850	 0.3960
Qy	 0.9410	 0.4590
R	 0.7810	 0.3810
Rb	 0.8870	 0.3670
Ry	 0.8950	 0.4170
S	 0.8410	 0.3330
Sb	 0.8720	 0.3570
Sy	 0.9090	 0.4440
T	 0.7960	 0.3170
Tb	 0.9070	 0.3590
Ty	 0.9210	 0.4590
U	 0.9210	 0.4330
Ub	 0.8650	 0.3570
Uy	 0.9190	 0.3700
V	 0.8170	 0.3060
Vb	 0.8700	 0.4080
Vy	 0.8950	 0.4680
W	 0.8600	 0.4080
Wb	 0.9100	 0.4500
Wy	 0.7540	 0.3600
X	 0.7690	 0.3400
Xb	 0.8850	 0.4440
Xy	 0.9220	 0.4370
Y	 0.5800	 0.2890
Yb	 0.8720	 0.3580
Yy	 0.9400	 0.4290
Z	 0.8140	 0.3380
Zb	 0.8150	 0.3320
Zy	 0.9090	 0.4060
a	 0.9040	 0.2810
aa	 0.8070	 0.3670
ab	 0.9160	 0.4620
ay	 0.9330	 0.4730
b	 0.6870	 0.2350
ba	 0.3520	 0.0150
bb	 0.9130	 0.4110
by	 0.9160	 0.4480
c	 0.4900	 0.2180
cb	 0.8690	 0.3940

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Chain	Atom inclusion	Q-score
cy	 0.9060	 0.4270
d	 0.7390	 0.2710
db	 0.9150	 0.4360
dy	 0.9150	 0.4550
e	 0.6540	 0.2260
eb	 0.8470	 0.3930
ey	 0.9330	 0.4810
f	 0.7050	 0.2360
fb	 0.8620	 0.2360
fy	 0.9390	 0.4950
g	 0.7280	 0.1950
gb	 0.8590	 0.3220
gy	 0.8930	 0.4490
h	 0.6560	 0.2140
hb	 0.9330	 0.4220
i	 0.5170	 0.2290
ib	 0.9190	 0.4090
j	 0.6570	 0.2100
jb	 0.9670	 0.5060
k	 0.7070	 0.2310
kb	 0.9030	 0.3930
l	 0.6370	 0.1880
lb	 0.9250	 0.4850
m	 0.5540	 0.2500
mb	 0.9300	 0.4540
n	 0.4820	 0.1210
nb	 0.8320	 0.4600
o	 0.7130	 0.2980
ob	 0.9020	 0.4400
p	 0.6560	 0.2770
pb	 0.9060	 0.4680
q	 0.4930	 0.1440
r	 0.7550	 0.2030
s	 0.6110	 0.2190
t	 0.6190	 0.1730
u	 0.7560	 0.1740
v	 0.7110	 0.2210
w	 0.7890	 0.2640
x	 0.7630	 0.2980
y	 0.7670	 0.3010
z	 0.7910	 0.1960