wwPDB EM Validation Summary Report

Oct 28, 2024 – 07:45 am GMT

PDB ID	:	6T83
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:

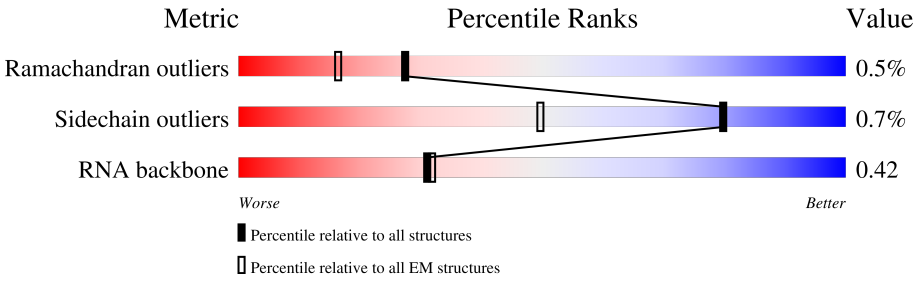
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=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	38% 49% 11%
1	a	1800	65% 31%
2	Ab	252	81% 18%
2	b	252	9% 79% 18%
3	Ba	255	82% 6% 11%
3	c	255	31% 84% 15%
4	Pb	142	82% 18%
4	q	142	35% 80% 16%

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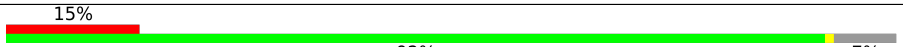
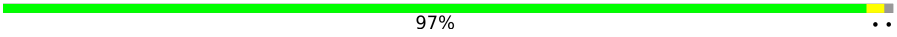
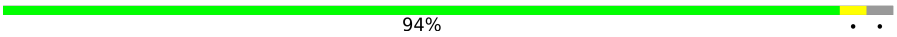
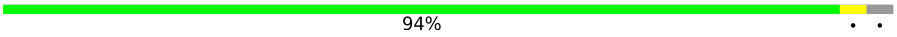
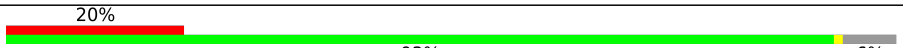
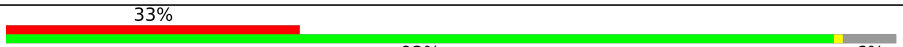
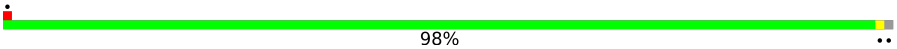
Mol	Chain	Length	Quality of chain
5	Cb	254	
5	d	254	
6	Db	240	
6	e	240	
7	Eb	261	
7	f	261	
8	Fb	225	
8	g	225	
9	Gb	236	
9	h	236	
10	Hb	190	
10	i	190	
11	Ib	200	
11	j	200	
12	Jb	197	
12	k	197	
13	Kb	105	
13	l	105	
14	Lb	156	
14	m	156	
15	Mb	143	
15	n	143	
16	Nb	151	
16	o	151	
17	Ob	137	

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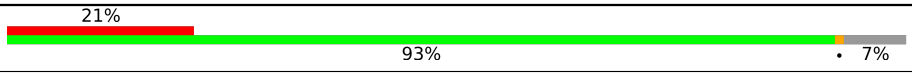
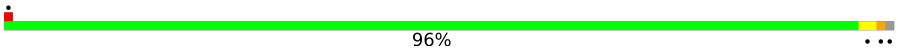
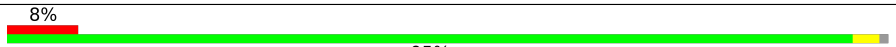
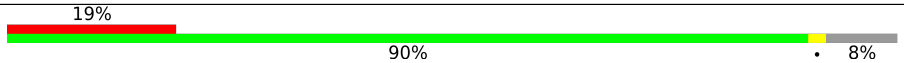
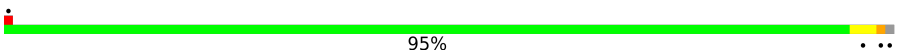
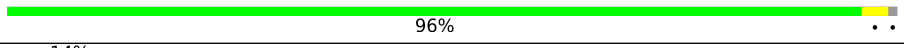
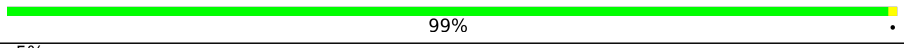
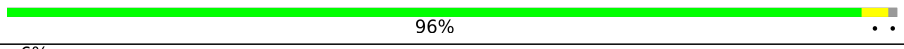
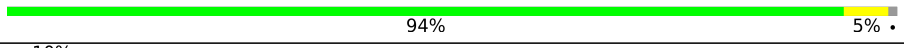
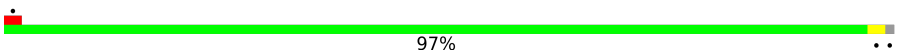
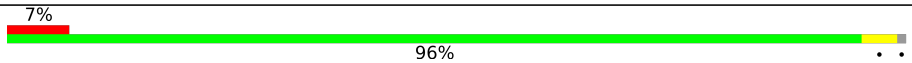
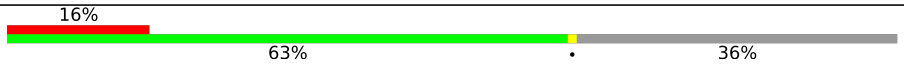
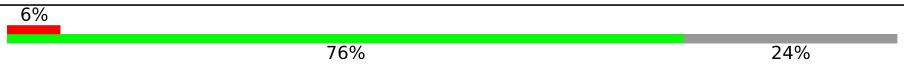
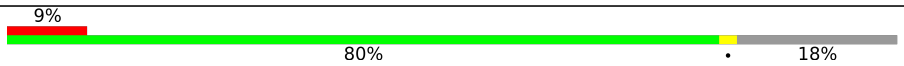
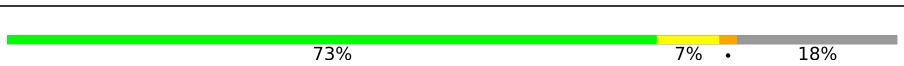
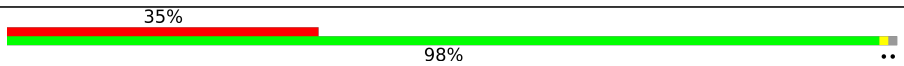
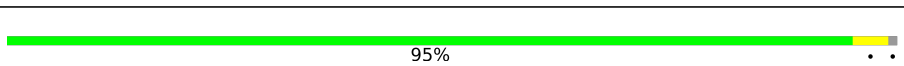
Mol	Chain	Length	Quality of chain
17	p	137	
18	Qb	143	
18	r	143	
19	Rb	136	
19	s	136	
20	Sb	146	
20	t	146	
21	Tb	144	
21	u	144	
22	Ub	121	
22	v	121	
23	Vb	87	
23	w	87	
24	Wb	130	
24	x	130	
25	Xb	145	
25	y	145	
26	Yb	135	
26	z	135	
27	0	108	
27	Zb	108	
28	1	119	
28	ab	119	
29	2	82	
29	bb	82	

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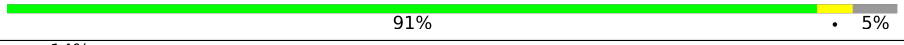
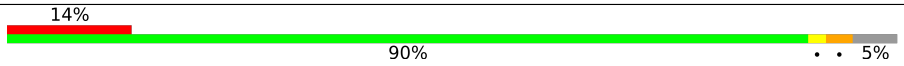
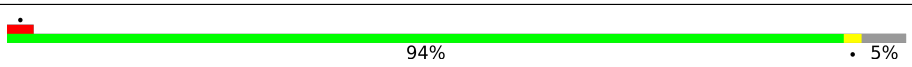
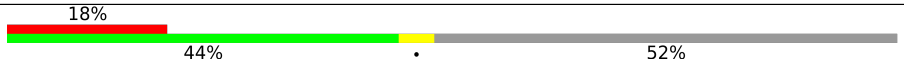
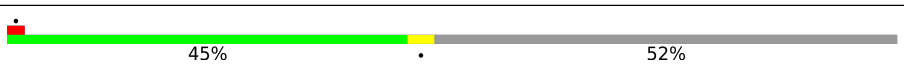
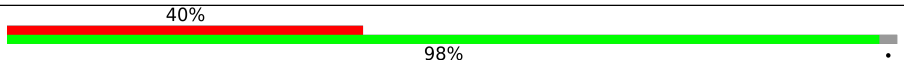
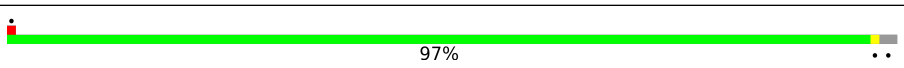
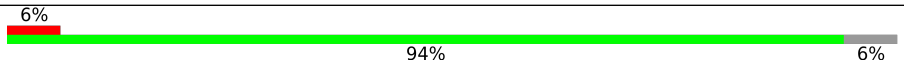
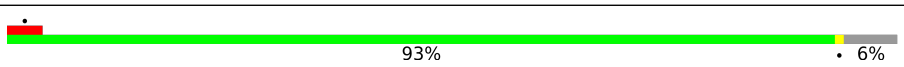
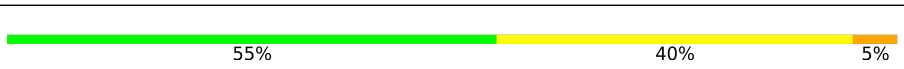
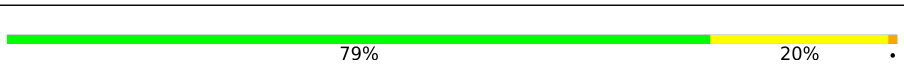
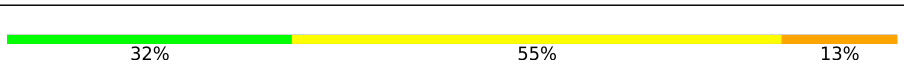
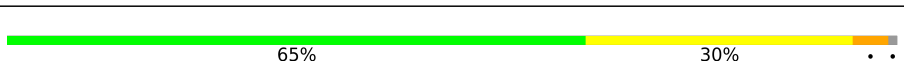
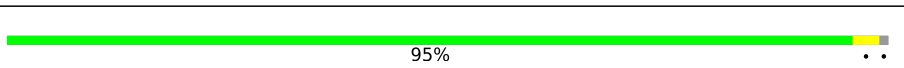
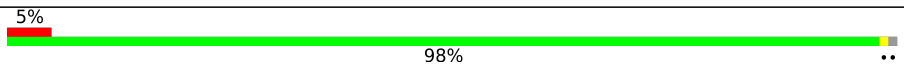
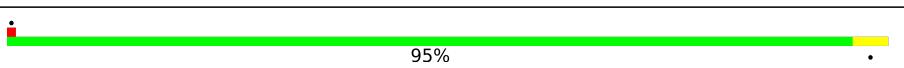
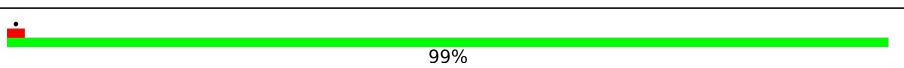
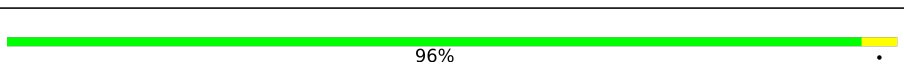
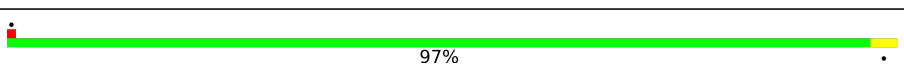
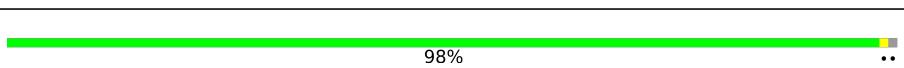
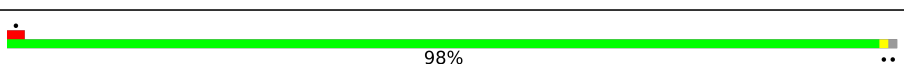
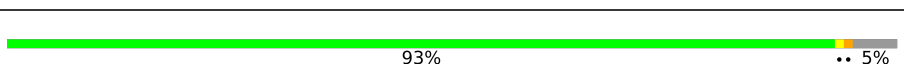
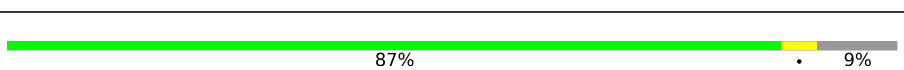
Mol	Chain	Length	Quality of chain
30	4	56	
30	db	56	
31	5	63	
31	eb	63	
32	6	152	
32	fb	152	
33	7	319	
33	gb	319	
34	3	67	
34	cb	67	
35	4b	121	
35	Bb	121	
36	3b	158	
36	Ca	158	
37	Ay	254	
37	Da	254	
38	By	387	
38	Ea	387	
39	Cy	362	
39	Fa	362	
40	Dy	297	
40	Ga	297	
41	Ey	176	
41	Ha	176	
42	Fy	244	

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Mol	Chain	Length	Quality of chain
42	Ia	244	91% 9%
43	Gy	256	88% 9%
43	Ja	256	89% 10%
44	Hy	191	98%
44	Ka	191	98%
45	Iy	221	97%
45	La	221	94% 5%
46	Jy	174	94%
46	Ma	174	8% 94%
47	Ly	199	90% 6%
47	Na	199	94%
48	My	138	99%
48	Oa	138	99%
49	Ny	204	90% 9%
49	Pa	204	98%
50	Oy	199	95%
50	Qa	199	98%
51	A	184	95% 5%
51	Py	184	96%
52	B	186	99%
52	Qy	186	97%
53	C	189	11% 96%
53	Ry	189	96%
54	D	172	100%
54	Sy	172	97%

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Mol	Chain	Length	Quality of chain
55	E	160	96%
55	Ty	160	98%
56	F	121	81% 19%
56	Uy	121	82% 17%
57	G	137	9% 97%
57	Vy	137	95%
58	H	155	45% 82% 5% 13%
58	Wy	155	20% 81% 19%
59	I	142	85% 15%
59	Xy	142	84% 15%
60	J	127	98%
60	Yy	127	98%
61	K	136	98%
61	Zy	136	99%
62	L	149	96%
62	ay	149	93% 6%
63	M	59	5% 93% 5%
63	by	59	92% 5%
64	N	105	95% 5%
64	cy	105	90% 9%
65	O	113	96%
65	dy	113	95%
66	P	130	98%
66	ey	130	95%
67	Q	107	99%

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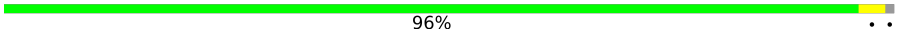
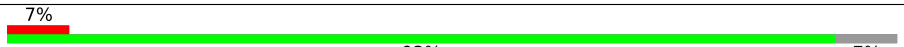
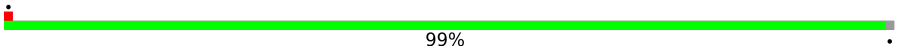
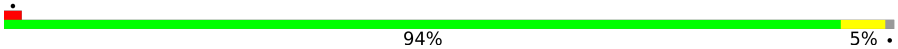
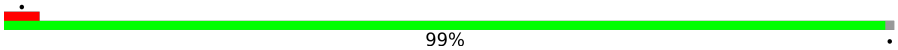
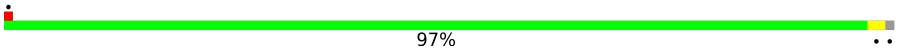
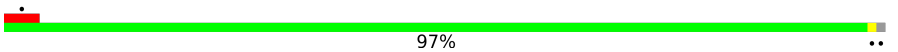
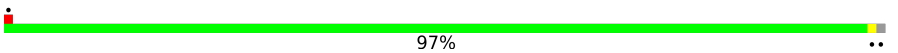
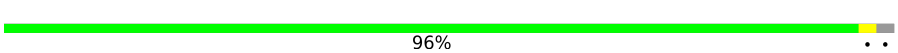
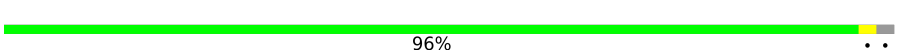
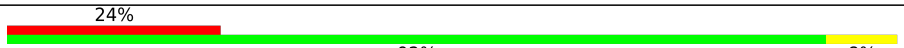
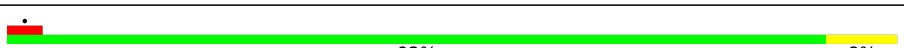
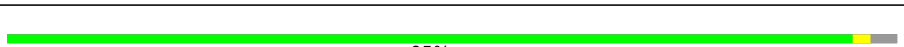
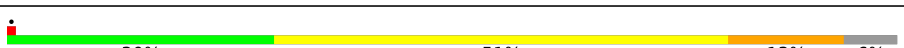
Mol	Chain	Length	Quality of chain
67	fy	107	
68	R	121	
68	gy	121	
69	S	120	
69	hb	120	
70	T	100	
70	ib	100	
71	U	88	
71	jb	88	
72	V	78	
72	kb	78	
73	W	51	
73	lb	51	
74	X	128	
74	mb	128	
75	Y	25	
75	nb	25	
76	Z	106	
76	ob	106	
77	aa	92	
77	pb	92	
78	1b	3396	
78	Aa	3396	
79	6b	76	
79	8	76	

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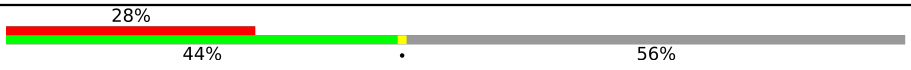
Mol	Chain	Length	Quality of chain
80	ba	311	

2 Entry composition (i)

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 37739	C 16872	N 6683	O 12413	P 1771	0	0
1	a	1758	Total 37455	C 16745	N 6624	O 12328	P 1758	0	0

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

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

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

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

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

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

- 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 1486	C 954	N 266	O 266	0	0

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

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

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

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

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

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

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

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

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

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

- 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 1073	C 676	N 208	O 189	0	0

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

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

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

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

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

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

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

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

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

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

- 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	0	0
			1416	879	284	253		
51	A	175	Total	C	N	O	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 1515	C 932	N 323	O 260	0	0
53	C	183	Total 1482	C 911	N 320	O 251	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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 969	C 615	N 186	O 167	S 1	0	0
69	S	119	Total 965	C 612	N 185	O 167	S 1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 79 is a RNA chain called tRNA.

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

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

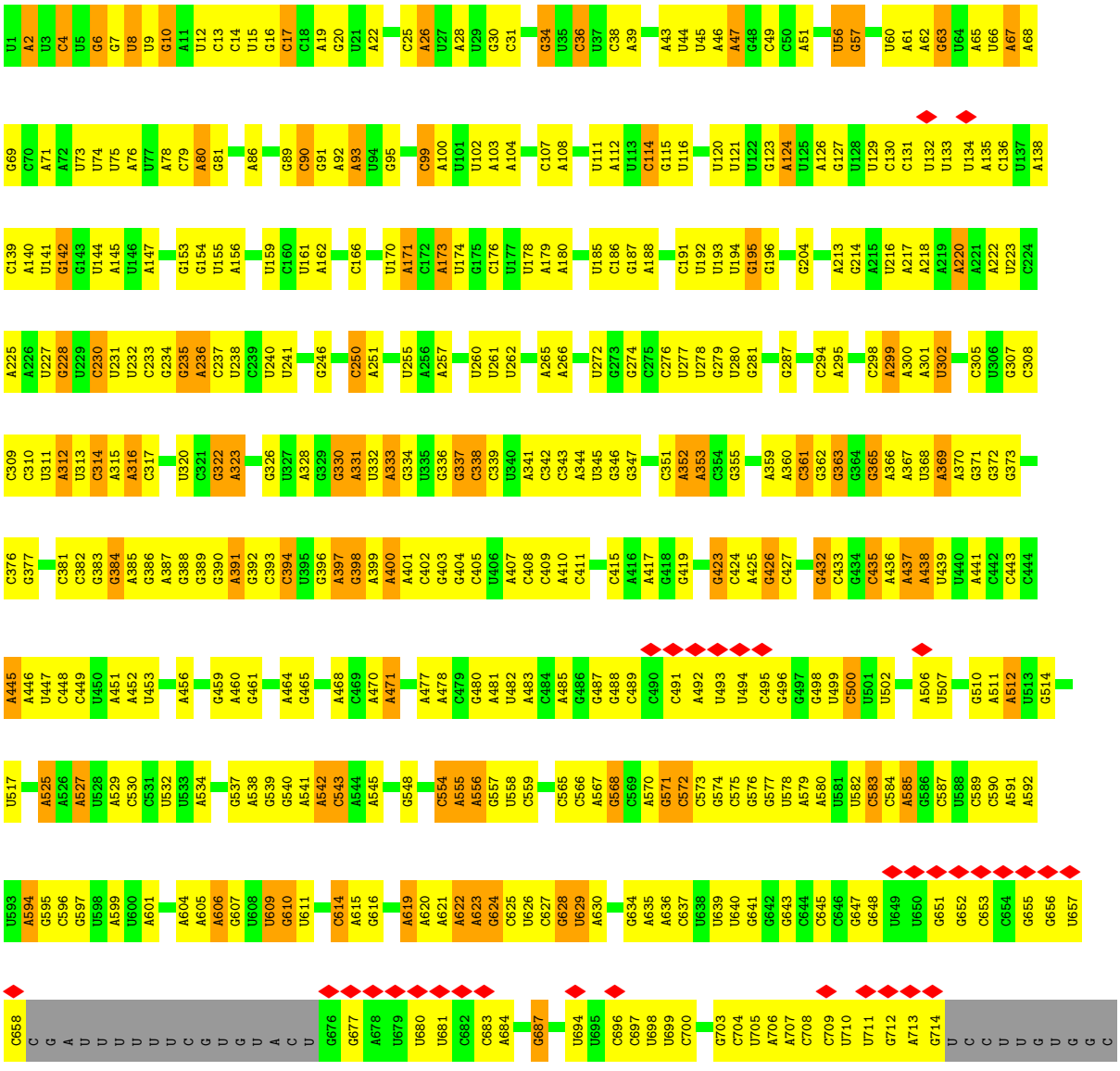
Mol	Chain	Residues	Atoms					AltConf	Trace
80	ba	138	Total	C	N	O	S	0	0
			1052	672	187	190	3		

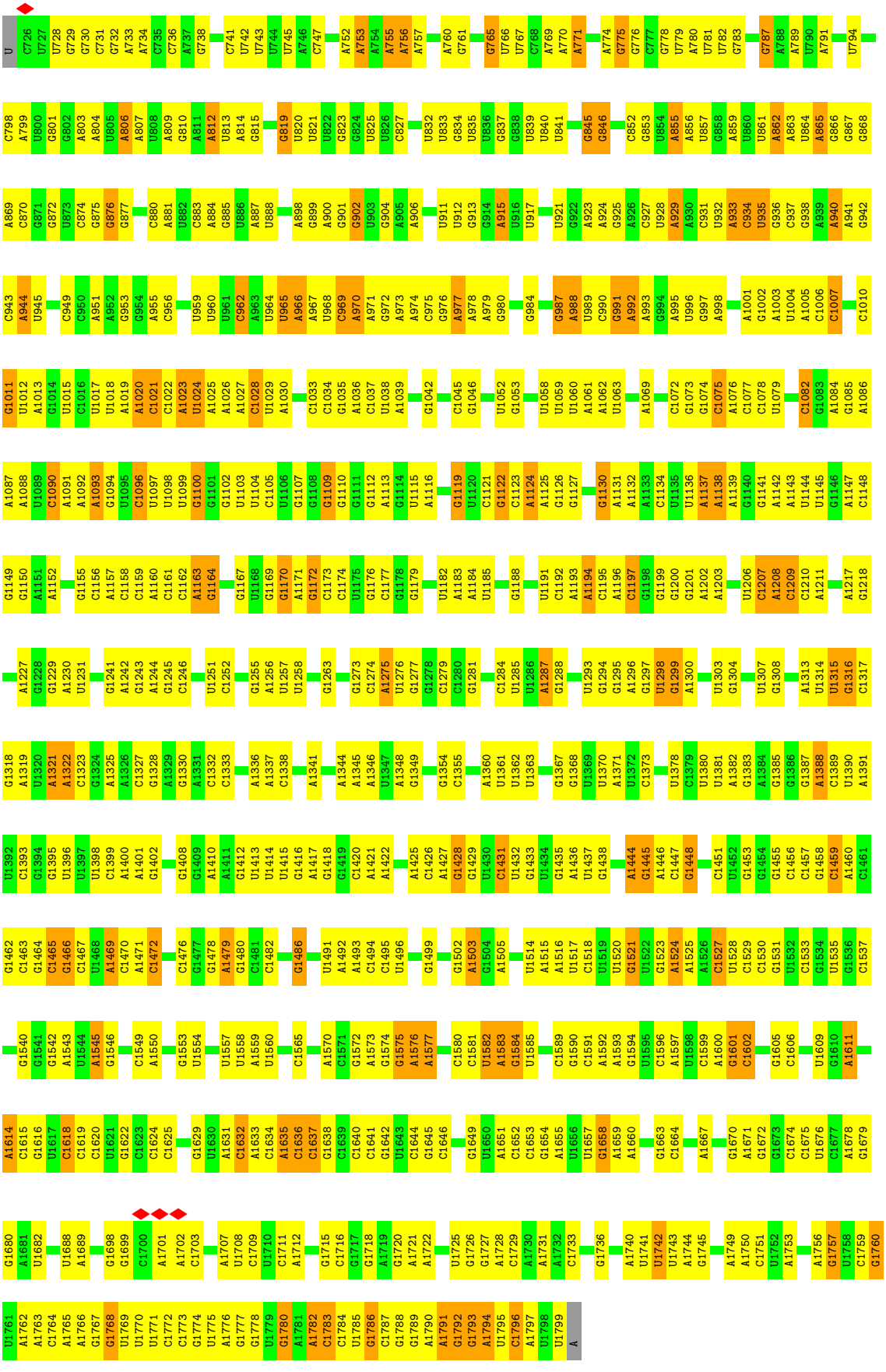
3 Residue-property plots (i)

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

- Molecule 1: 18S rRNA

Chain 2b:

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C798 A799 U800 G801 G802 A803 A804 U805 A806 A807 U808 A809 G810 A811 A812 U813 A814 G815 G819 U820 U821 U822 G823 G824 U825 U826 C827 U832 U833 G834 U835 U836 G837 G838 U839 U840 U841 G845 G846 C852 G853 U854 A855 A856 U857 G858 A859 U860 U861 A862 A863 U864 A865 G866 G867 G868
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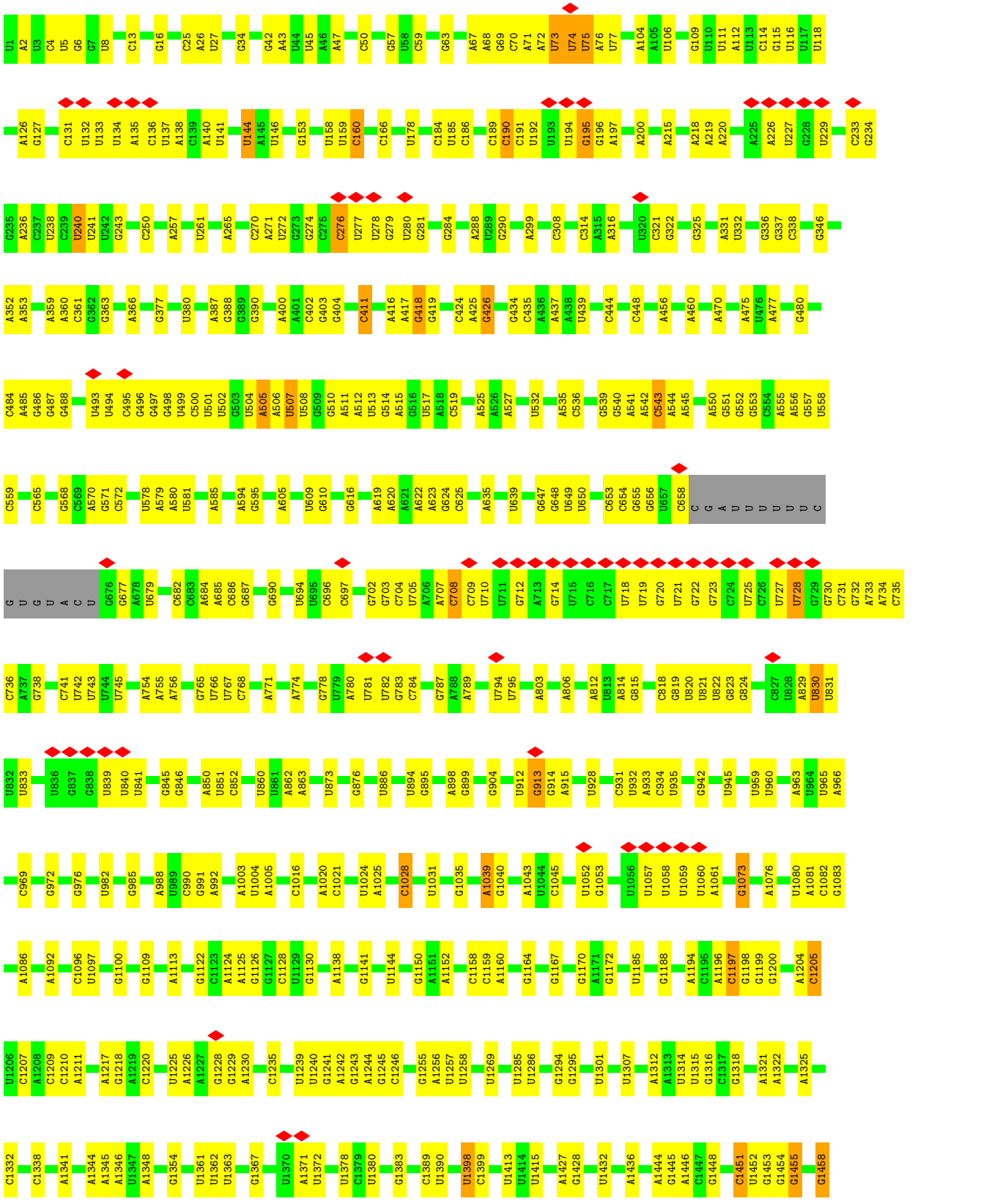
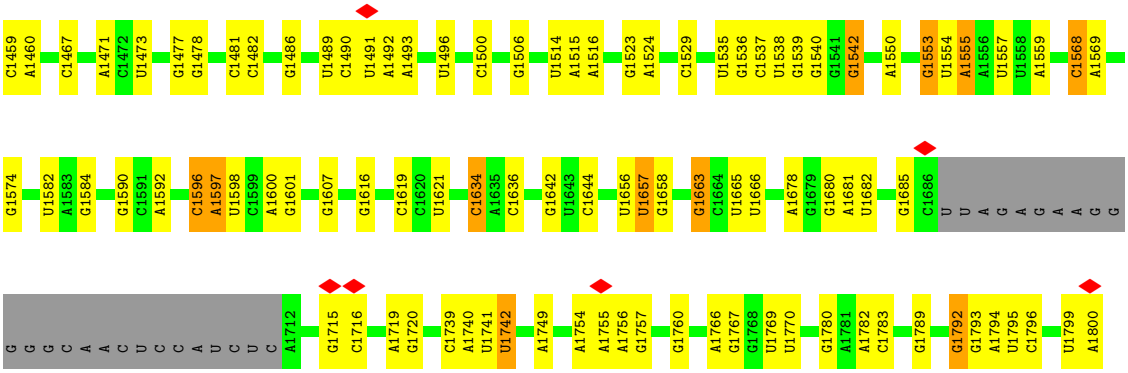
G1011 U1012 A1013 G1014 U1015 C1016 U1017 U1018 A1019 A1020 C1021 C1022 A1023 U1024 A1025 A1026 A1027 C1028 U1029 A1030 C1033 C1034 C1035 A1036 C1037 U1038 A1039 G1042 C1045 G1046 U1052 G1053 U1058 U1059 U1060 A1061 A1062 U1063 A1069 C1072 G1073 G1074 C1075 A1076 C1077 C1078 U1079 C1082 G1083 A1084 G1085 A1086
A1087 A1088 U1089 C1090 A1091 A1092 A1093 G1094 U1095 C1096 U1097 U1098 U1099 G1100 G1101 G1102 U1103 U1104 C1105 U1106 G1107 G1108 G1109 G1110 G1111 G1112 A1113 G1114 U1115 A1116 G1119 U1120 C1121 G1122 C1123 A1124 A1125 G1126 G1127 G1130 A1131 A1132 A1133 C1134 U1135 U1136 A1137 A1138 A1139 G1140 G1141 A1142 A1143 U1144 U1145 G1146 A1147 C1148
G1149 G1150 A1151 A1152 G1155 C1156 A1157 C1158 C1159 A1160 C1161 C1162 A1163 G1164 G1167 U1168 G1169 G1170 A1171 G1172 C1173 C1174 U1175 G1176 C1177 G1178 G1179 U1182 A1183 A1184 U1185 G1188 U1191 C1192 A1193 A1194 C1195 A1196 C1197 G1198 G1199 G1200 G1201 A1202 A1203 U1206 C1207 A1208 C1209 C1210 A1211 A1217 G1218
A1227 G1228 G1229 A1230 U1231 G1241 A1242 G1243 A1244 G1245 C1246 U1251 C1252 G1255 A1256 U1257 U1258 G1263 G1273 C1274 A1275 U1276 G1277 G1278 C1279 C1280 G1281 C1284 U1285 U1286 A1287 G1288 U1293 G1294 G1295 A1296 G1297 U1298 G1299 A1300 U1303 G1304 U1307 G1308 A1313 U1314 U1315 G1316 C1317
G1318 A1319 U1320 A1321 A1322 C1323 G1324 A1325 A1326 C1327 G1328 A1329 G1330 A1331 C1332 C1333 A1336 A1337 C1338 A1341 A1344 A1345 A1346 U1347 A1348 G1349 G1354 C1355 A1360 U1361 U1362 U1363 G1367 G1368 U1369 U1370 A1371 U1372 C1373 U1378 C1379 U1380 U1381 A1382 G1383 A1384 G1385 G1386 G1387 A1388 C1389 U1390 A1391
U1392 C1393 G1394 G1395 U1396 U1397 U1398 C1399 A1400 A1401 G1402 G1408 G1409 A1410 A1411 G1412 U1413 U1414 U1415 G1416 A1417 G1418 G1419 C1420 A1421 A1422 A1425 C1426 A1427 G1428 G1429 U1430 C1431 U1432 G1433 U1434 G1435 A1436 U1437 G1438 A1444 G1445 A1446 C1447 G1448 C1451 U1452 G1453 G1454 G1455 C1456 C1457 G1458 C1459 A1460 C1461
G1462 C1463 G1464 C1465 G1466 C1467 U1468 A1469 C1470 A1471 C1472 C1476 G1477 G1478 A1479 G1480 C1481 C1482 G1486 U1491 A1492 A1493 C1494 C1495 U1496 G1499 G1502 A1503 G1504 A1505 U1514 A1515 A1516 U1517 C1518 U1519 U1520 G1521 U1522 G1523 A1524 A1525 A1526 C1527 U1528 C1529 C1530 G1531 U1532 C1533 G1534 U1535 G1536 C1537
G1540 G1541 G1542 A1543 U1544 A1545 G1546 C1549 A1550 G1553 U1554 U1557 U1558 A1559 U1560 C1565 A1570 C1571 G1572 A1573 G1574 G1575 A1576 A1577 C1580 C1581 U1582 A1583 G1584 U1585 C1589 G1590 C1591 A1592 A1593 G1594 U1595 C1596 A1597 U1598 C1599 A1600 G1601 C1602 G1605 C1606 U1609 G1610 A1611
A1614 C1615 G1616 U1617 C1618 C1619 C1620 U1621 G1622 C1623 C1624 C1625 G1629 U1630 A1631 C1632 A1633 C1634 A1635 C1636 C1637 G1638 C1639 C1640 C1641 G1642 U1643 C1644 G1645 C1646 G1649 U1650 A1651 C1652 C1653 G1654 A1655 U1656 U1657 G1658 A1659 A1660 G1663 C1664 A1667 G1670 A1671 G1672 G1673 C1674 C1675 U1676 C1677 A1678 G1679
G1680 A1681 U1682 U1688 A1689 G1698 G1699 C1700 A1701 A1702 C1703 A1707 U1708 C1709 U1710 C1711 A1712 G1715 C1716 G1717 G1718 A1719 G1720 A1721 A1722 U1725 G1726 G1727 A1728 C1729 A1730 A1731 A1732 C1733 G1736 A1740 U1741 U1742 U1743 A1744 G1745 A1749 A1750 C1751 U1752 A1753 A1756 G1757 U1758 C1759 G1760
U1761 A1762 A1763 C1764 A1765 A1766 G1767 G1768 U1769 U1770 U1771 C1772 C1773 G1774 U1775 A1776 G1777 G1778 U1779 G1780 A1781 A1782 C1783 C1784 U1785 G1786 C1787 G1788 G1789 A1790 A1791 G1792 G1793 A1794 U1795 C1796 A1797 U1798 U1799 A

• Molecule 1: 18S rRNA

Chain a:





• Molecule 2: 40S ribosomal protein S0-A

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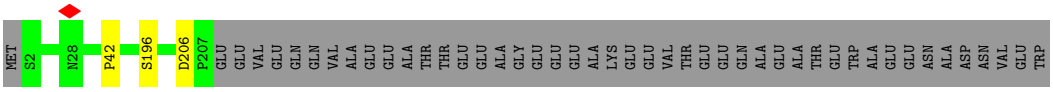

• Molecule 2: 40S ribosomal protein S0-A

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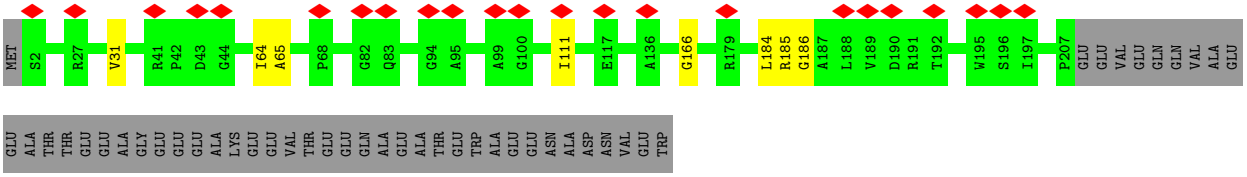
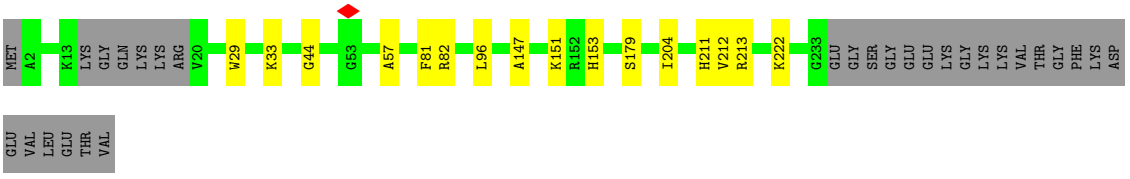


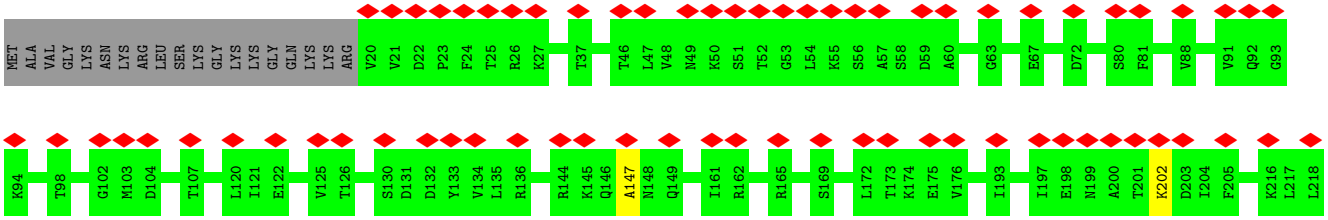
• Molecule 3: 40S ribosomal protein S1-A

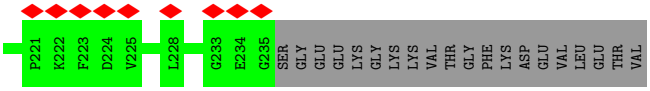
Chain Ba:



• Molecule 3: 40S ribosomal protein S1-A

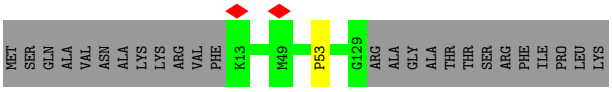
Chain c:





• Molecule 4: 40S ribosomal protein S15

Chain Pb:



• Molecule 4: 40S ribosomal protein S15

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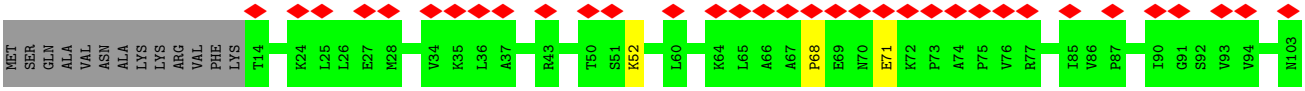
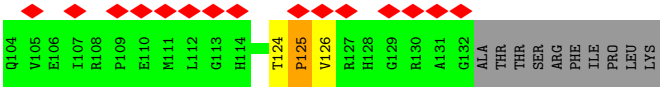
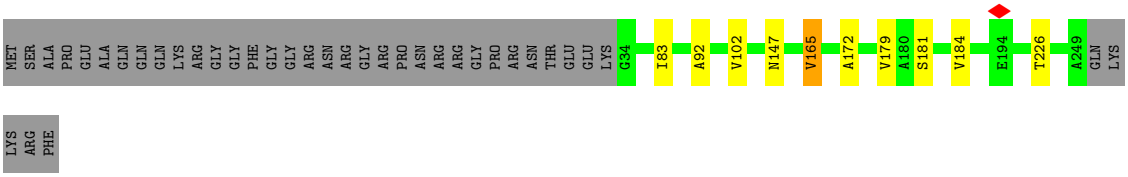




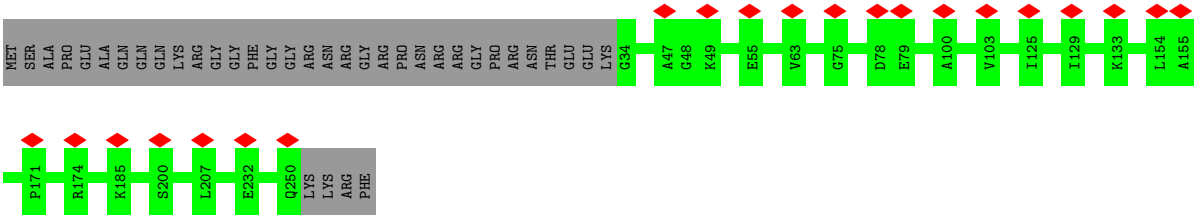
• Molecule 5: 40S ribosomal protein S2

Chain Cb:



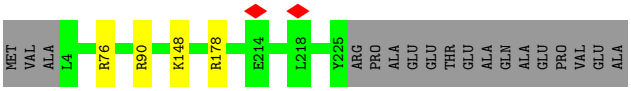
• Molecule 5: 40S ribosomal protein S2

Chain d:



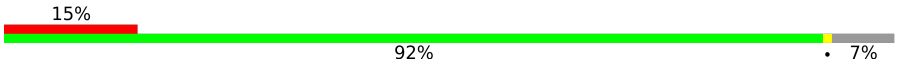
• Molecule 6: 40S ribosomal protein S3

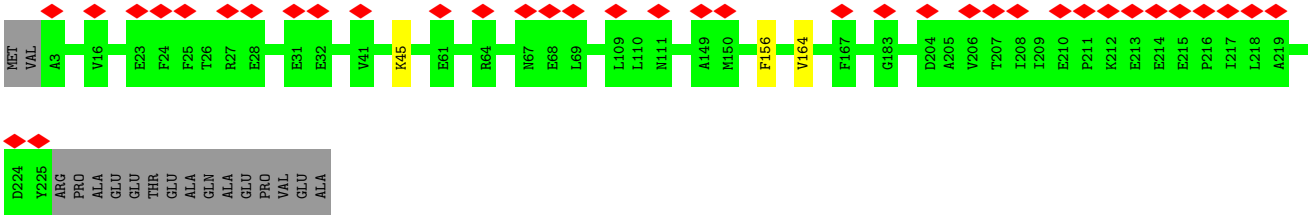
Chain Db:



• Molecule 6: 40S ribosomal protein S3

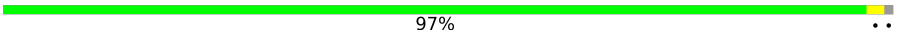
Chain e:

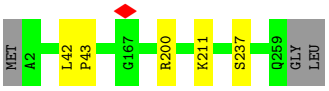




• Molecule 7: 40S ribosomal protein S4-A

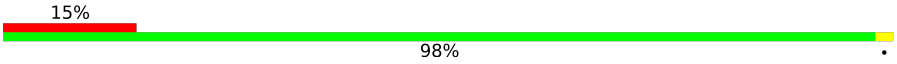
Chain Eb:

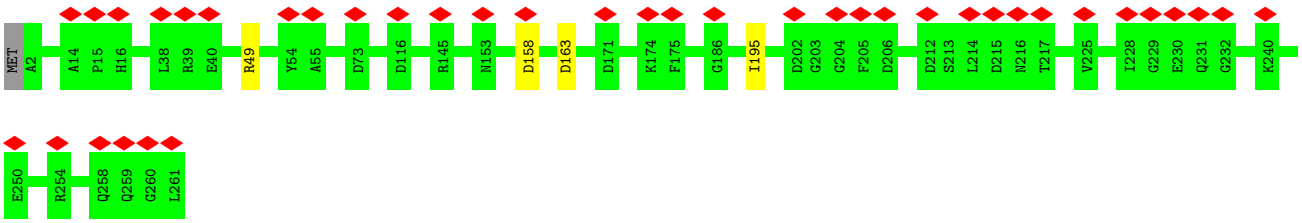




• Molecule 7: 40S ribosomal protein S4-A

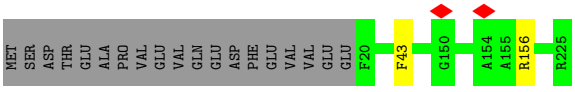
Chain f:





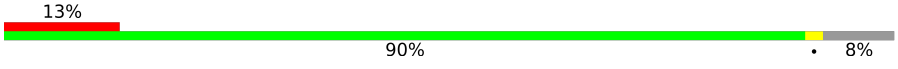
• Molecule 8: Rps5p

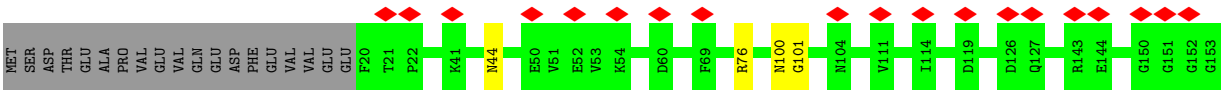
Chain Fb:

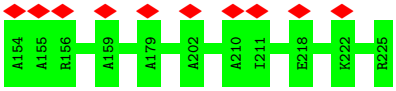


• Molecule 8: Rps5p

Chain g:

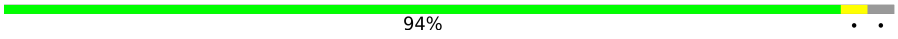


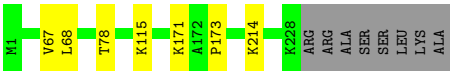




• Molecule 9: 40S ribosomal protein S6-A

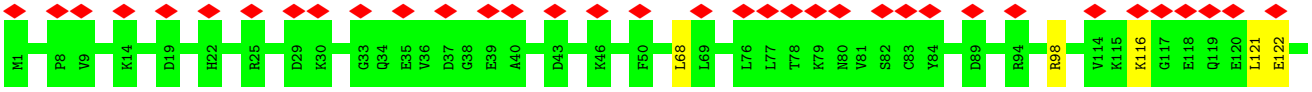
Chain Gb:

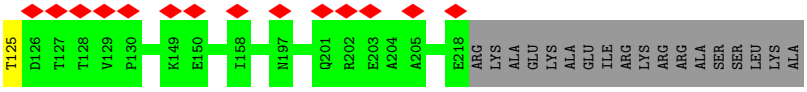




• Molecule 9: 40S ribosomal protein S6-A

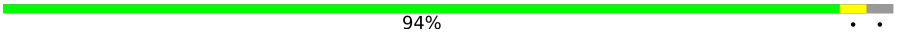
Chain h:

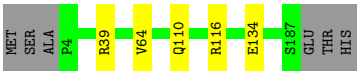




• Molecule 10: 40S ribosomal protein S7-A

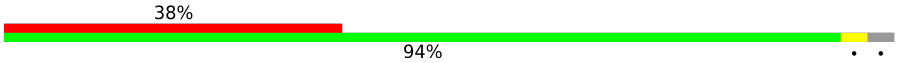
Chain Hb:

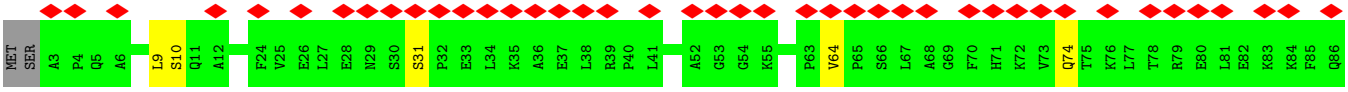


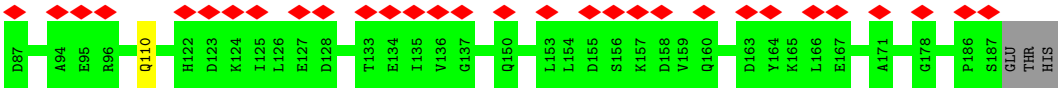


• Molecule 10: 40S ribosomal protein S7-A

Chain i:

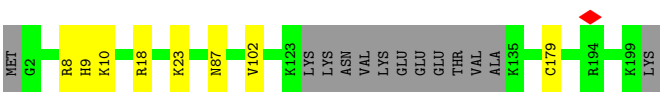






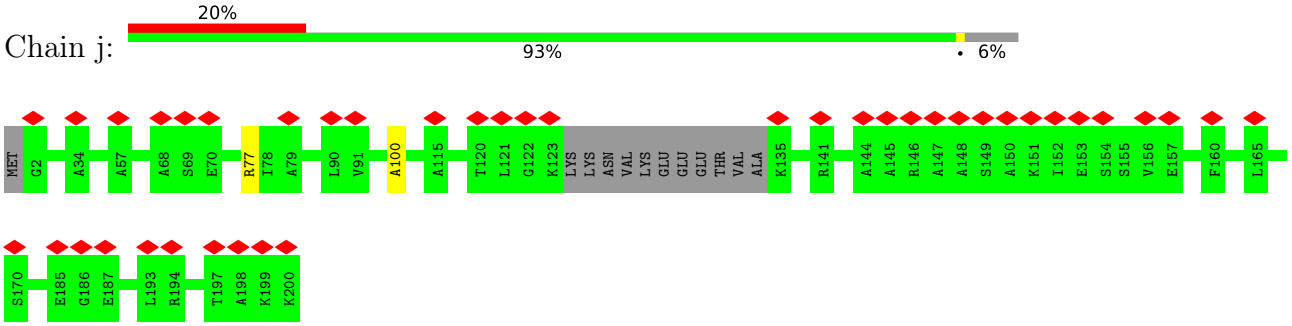
• Molecule 11: 40S ribosomal protein S8-A

Chain Ib:



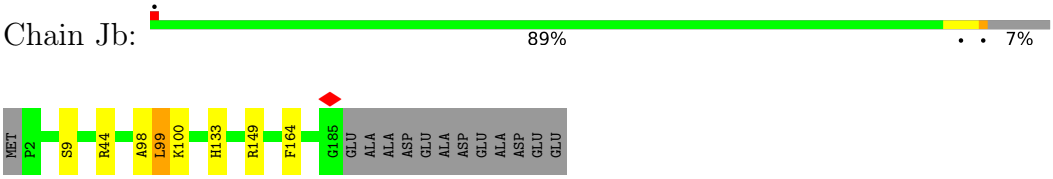
• Molecule 11: 40S ribosomal protein S8-A

Chain j:



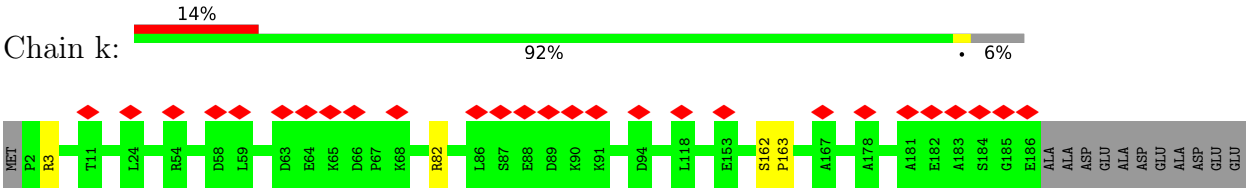
• Molecule 12: 40S ribosomal protein S9-A

Chain Jb:



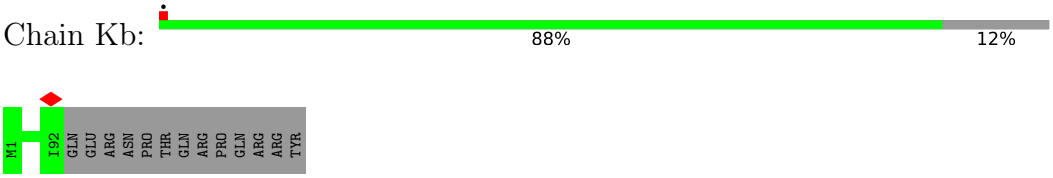
• Molecule 12: 40S ribosomal protein S9-A

Chain k:



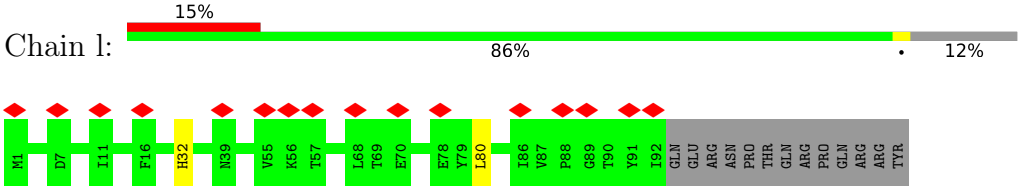
• Molecule 13: 40S ribosomal protein S10-A

Chain Kb:



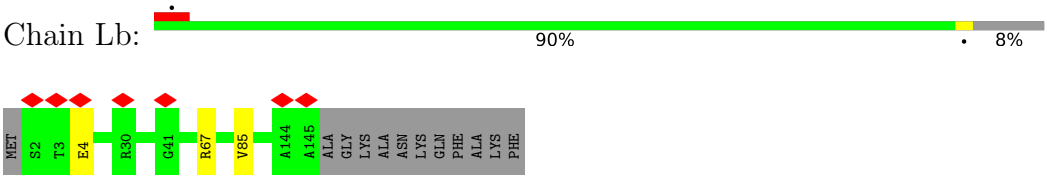
• Molecule 13: 40S ribosomal protein S10-A

Chain l:



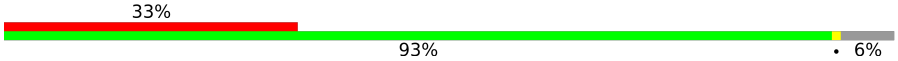
• Molecule 14: 40S ribosomal protein S11-A

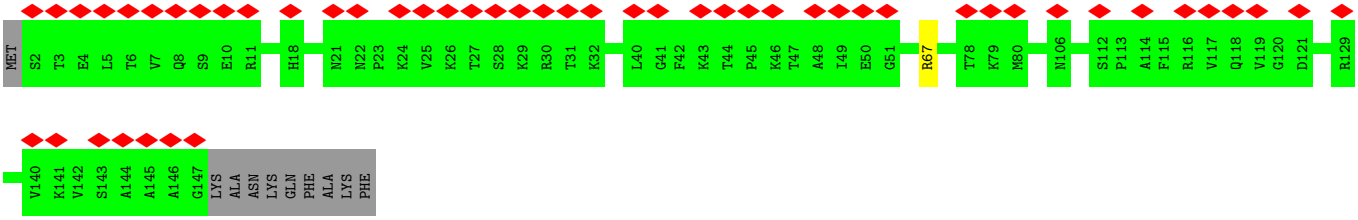
Chain Lb:



• Molecule 14: 40S ribosomal protein S11-A

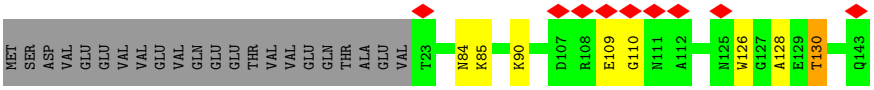
Chain m:





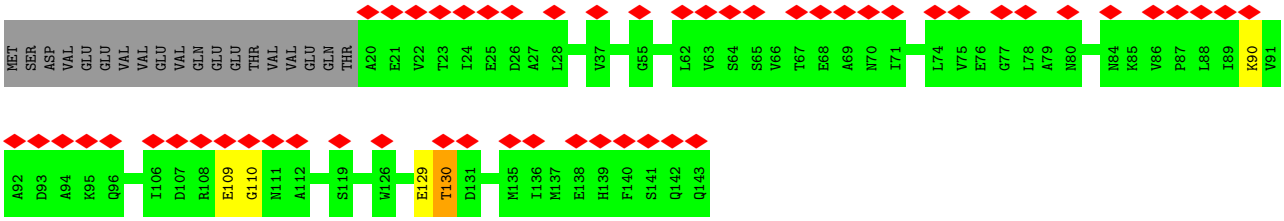
• Molecule 15: 40S ribosomal protein S12

Chain Mb:



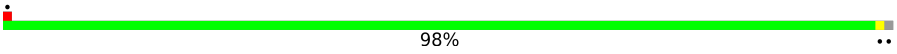
• Molecule 15: 40S ribosomal protein S12

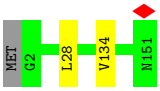
Chain n:



• Molecule 16: 40S ribosomal protein S13

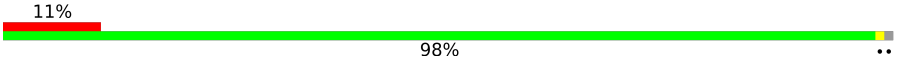
Chain Nb:

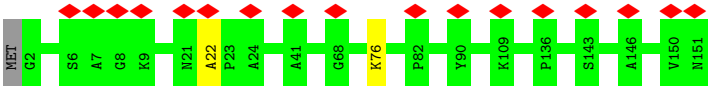




• Molecule 16: 40S ribosomal protein S13

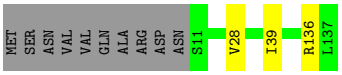
Chain o:





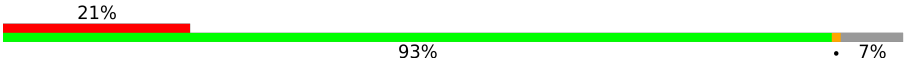
• Molecule 17: 40S ribosomal protein S14-A

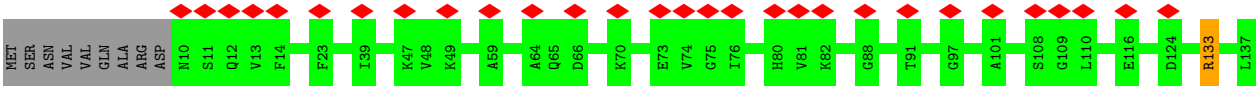
Chain Ob:



• Molecule 17: 40S ribosomal protein S14-A

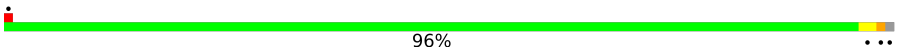
Chain p:

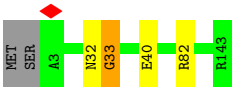




• Molecule 18: 40S ribosomal protein S16-A

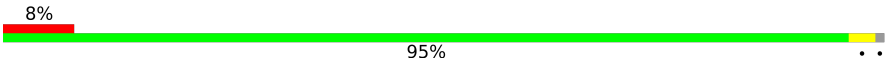
Chain Qb:

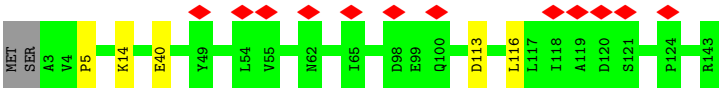




• Molecule 18: 40S ribosomal protein S16-A

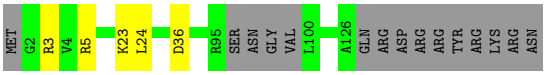
Chain r:





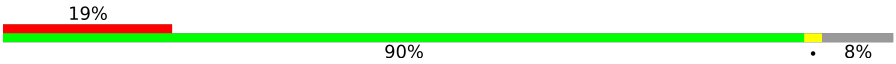
• Molecule 19: 40S ribosomal protein S17-B

Chain Rb:



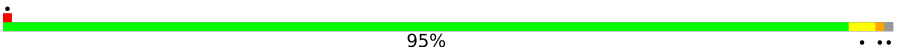
• Molecule 19: 40S ribosomal protein S17-B

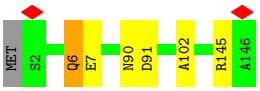
Chain s:



• Molecule 20: 40S ribosomal protein S18-A

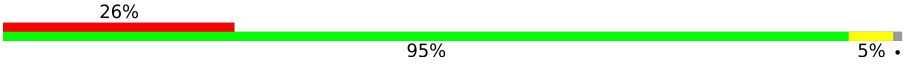
Chain Sb:

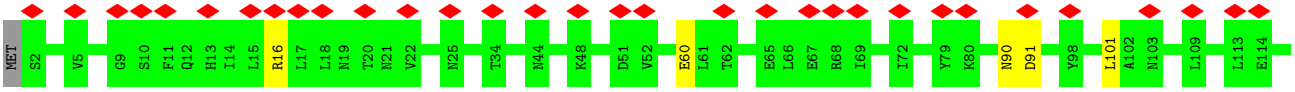


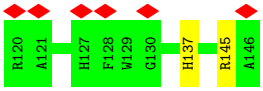


• Molecule 20: 40S ribosomal protein S18-A

Chain t:

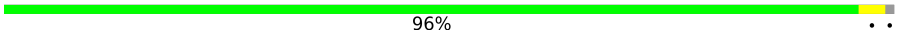






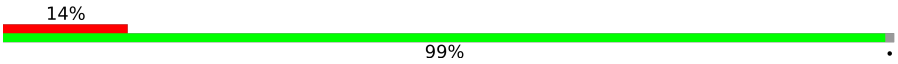
• Molecule 21: 40S ribosomal protein S19-A

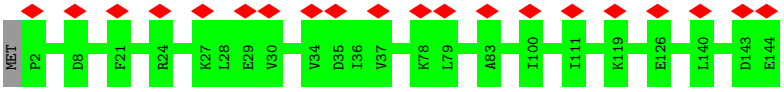
Chain Tb:



• Molecule 21: 40S ribosomal protein S19-A

Chain u:



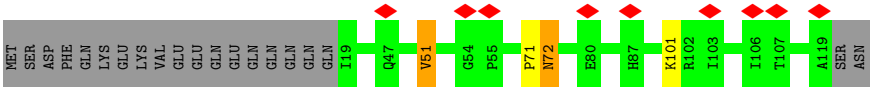


• Molecule 22: 40S ribosomal protein S20

Chain Ub:

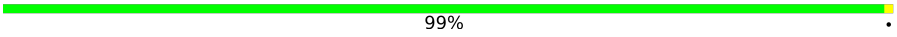
• Molecule 22: 40S ribosomal protein S20

Chain v:



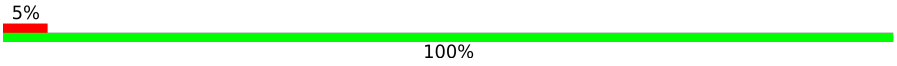
• Molecule 23: 40S ribosomal protein S21-A

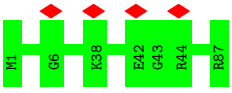
Chain Vb:



• Molecule 23: 40S ribosomal protein S21-A

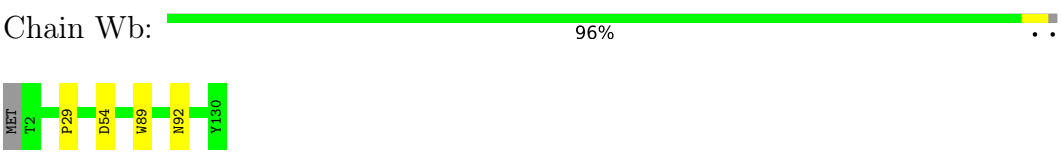
Chain w:





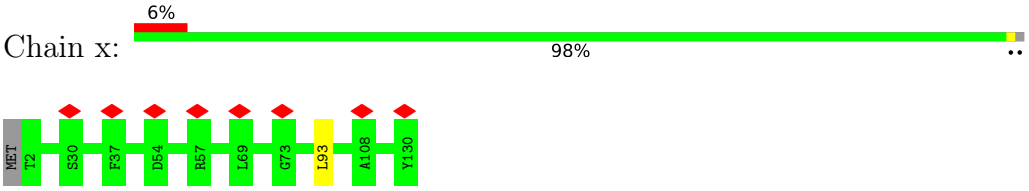
• Molecule 24: 40S ribosomal protein S22-A

Chain Wb:



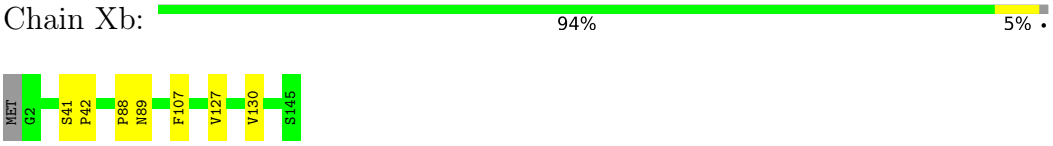
• Molecule 24: 40S ribosomal protein S22-A

Chain x:



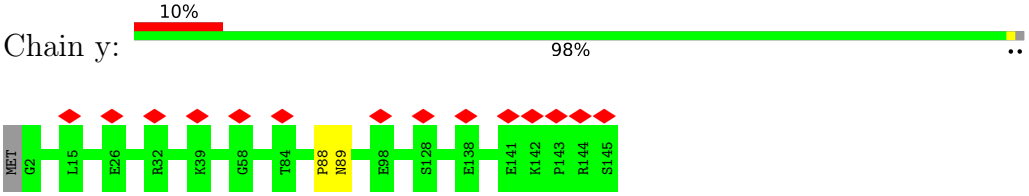
• Molecule 25: 40S ribosomal protein S23-A

Chain Xb:



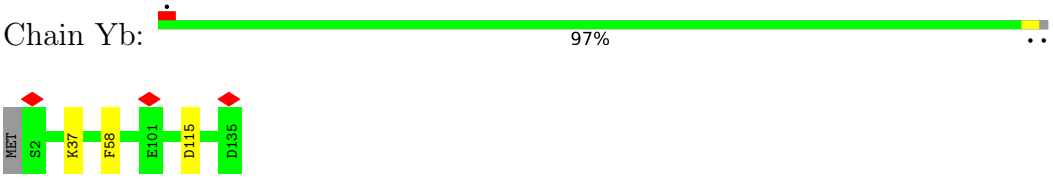
• Molecule 25: 40S ribosomal protein S23-A

Chain y:



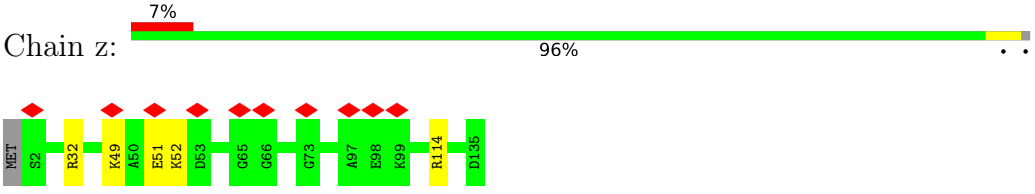
• Molecule 26: 40S ribosomal protein S24-A

Chain Yb:



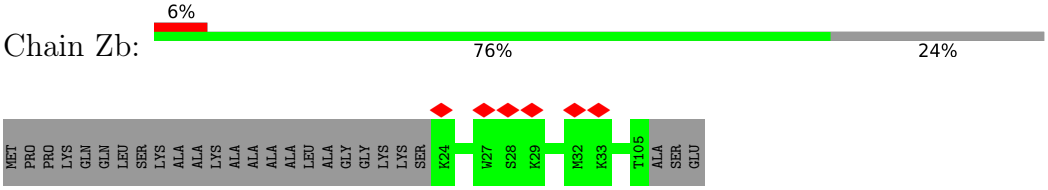
• Molecule 26: 40S ribosomal protein S24-A

Chain z:



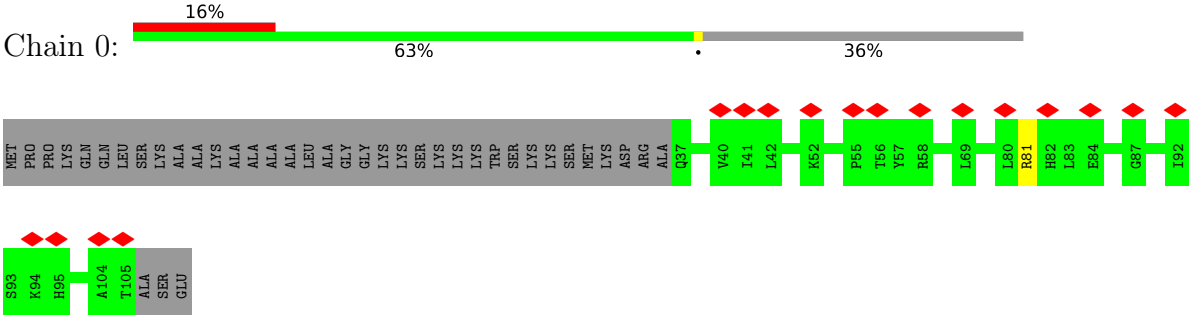
• Molecule 27: 40S ribosomal protein S25-A

Chain Zb:



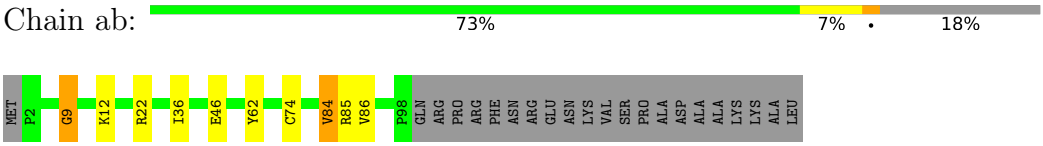
• Molecule 27: 40S ribosomal protein S25-A

Chain 0:



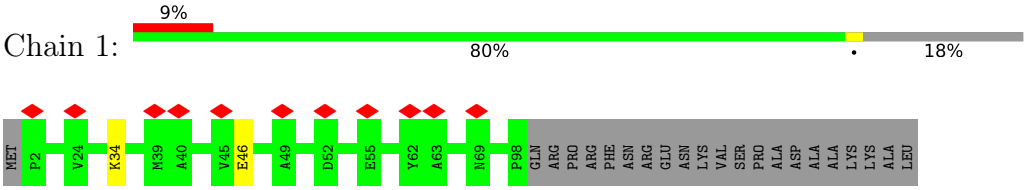
• Molecule 28: 40S ribosomal protein S26-A

Chain ab:



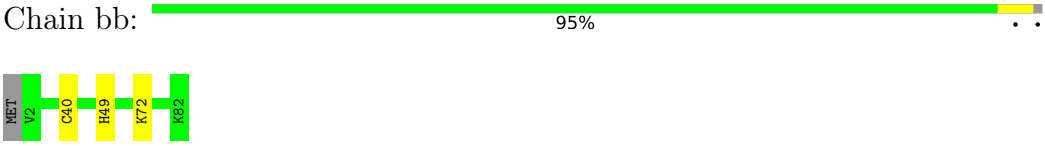
• Molecule 28: 40S ribosomal protein S26-A

Chain 1:



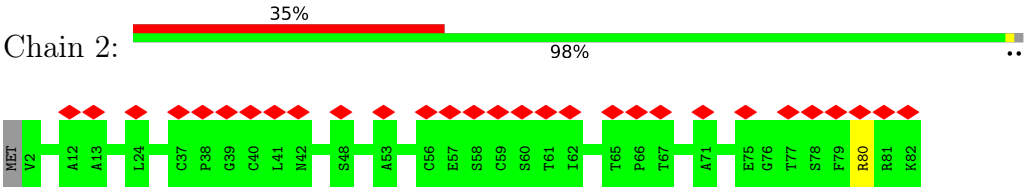
• Molecule 29: 40S ribosomal protein S27-A

Chain bb:



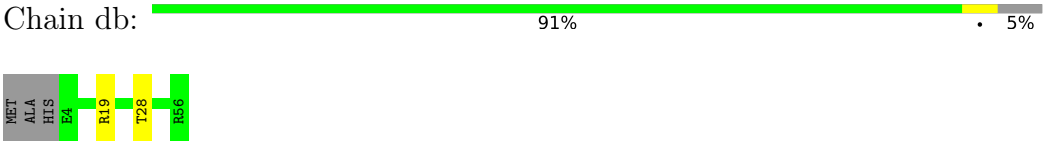
• Molecule 29: 40S ribosomal protein S27-A

Chain 2:



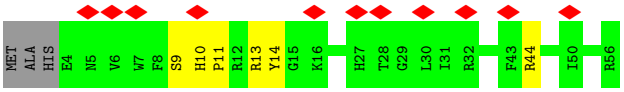
• Molecule 30: 40S ribosomal protein S29-A

Chain db:



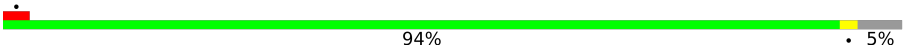
• Molecule 30: 40S ribosomal protein S29-A

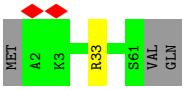
Chain 4:



• Molecule 31: 40S ribosomal protein S30-A

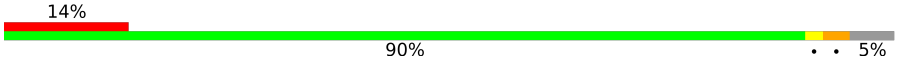
Chain eb:

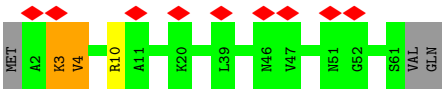




• Molecule 31: 40S ribosomal protein S30-A

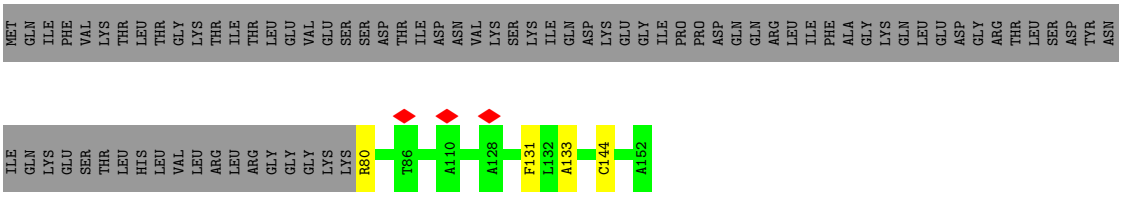
Chain 5:





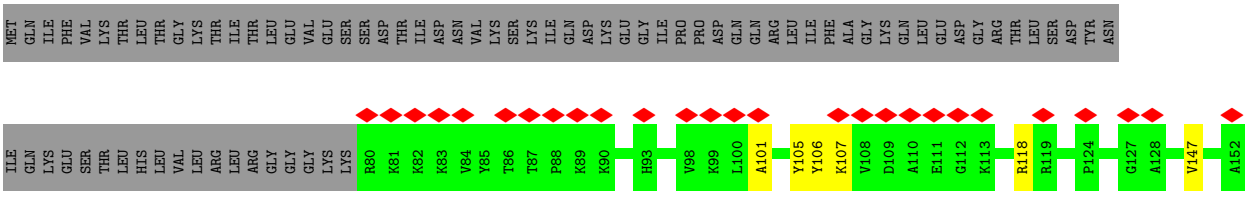
• Molecule 32: Ubiquitin-40S ribosomal protein S31

Chain fb:



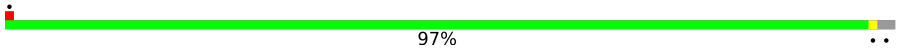
• Molecule 32: Ubiquitin-40S ribosomal protein S31

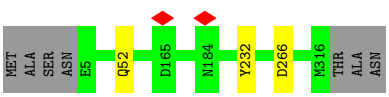
Chain 6:



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

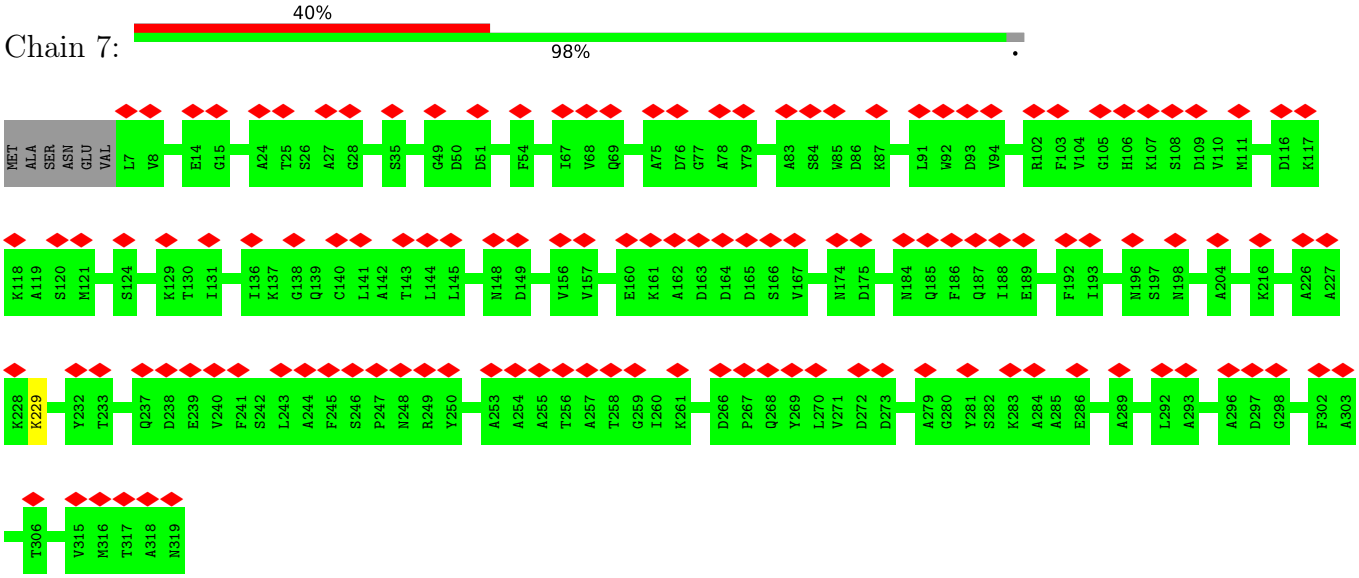
Chain gb:





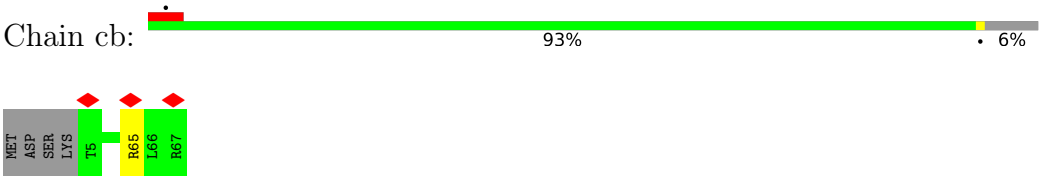
• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

Chain 7:



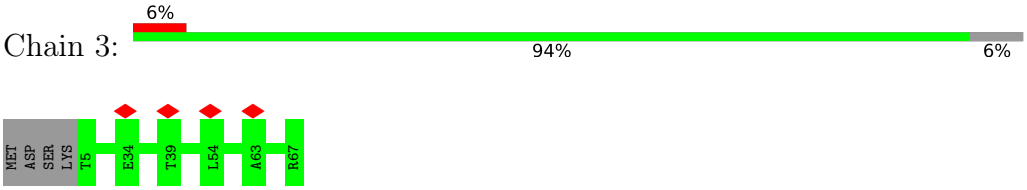
• Molecule 34: 40S ribosomal protein S28-B

Chain cb:



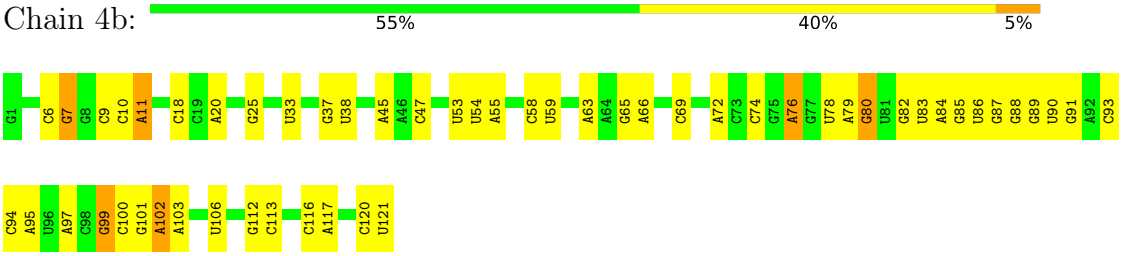
• Molecule 34: 40S ribosomal protein S28-B

Chain 3:



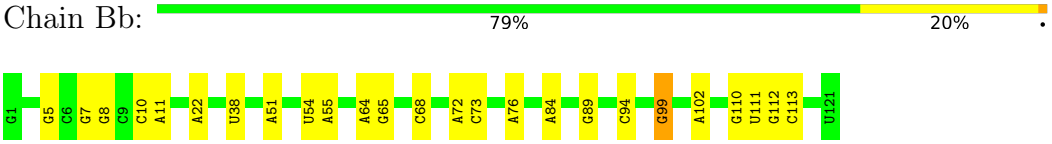
• Molecule 35: 5S rRNA

Chain 4b:



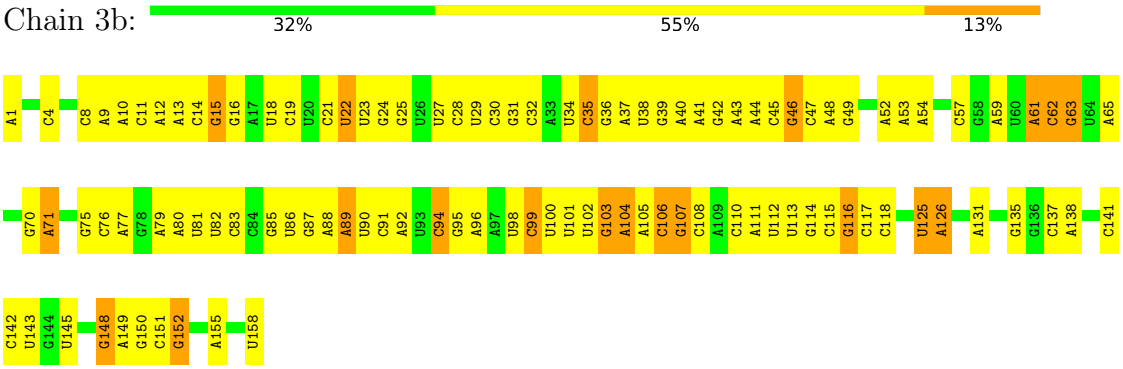
• Molecule 35: 5S rRNA

Chain Bb:



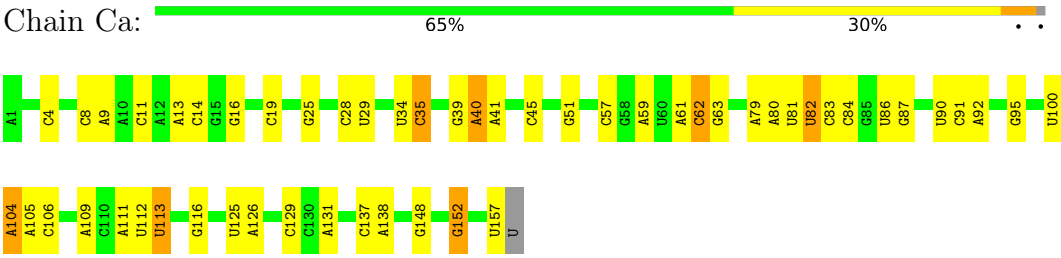
• Molecule 36: 5.8S rRNA

Chain 3b:



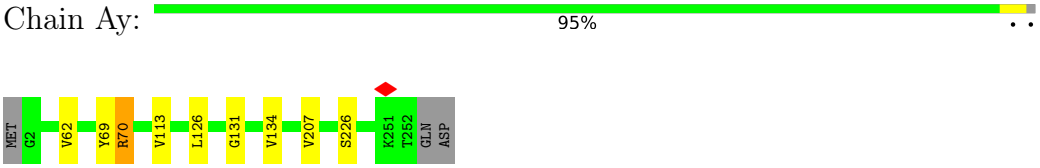
• Molecule 36: 5.8S rRNA

Chain Ca:



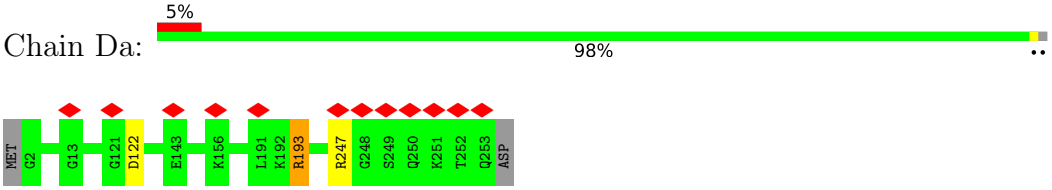
• Molecule 37: 60S ribosomal protein L2-A

Chain Ay:



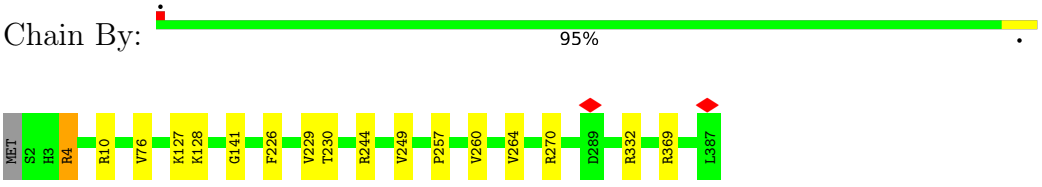
• Molecule 37: 60S ribosomal protein L2-A

Chain Da:



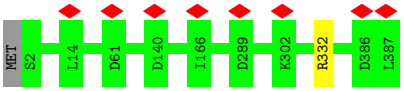
• Molecule 38: 60S ribosomal protein L3

Chain By:



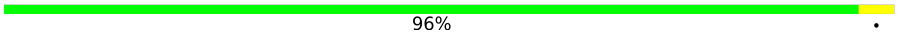
• Molecule 38: 60S ribosomal protein L3

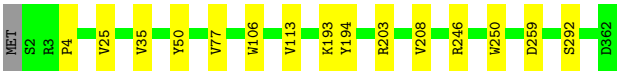
Chain Ea:



• Molecule 39: 60S ribosomal protein L4-A

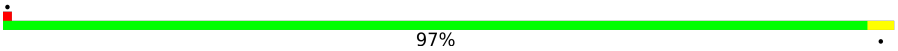
Chain Cy:

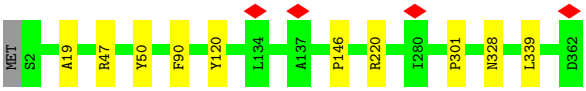




• Molecule 39: 60S ribosomal protein L4-A

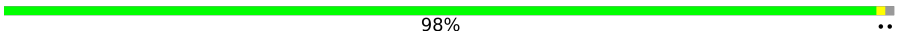
Chain Fa:

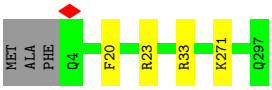




• Molecule 40: 60S ribosomal protein L5

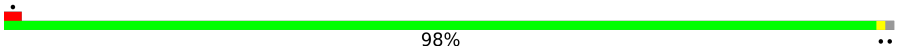
Chain Dy:

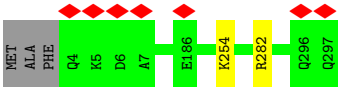




• Molecule 40: 60S ribosomal protein L5

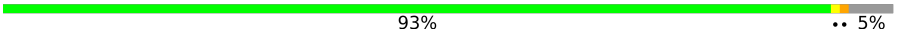
Chain Ga:

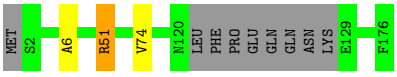




• Molecule 41: 60S ribosomal protein L6-A

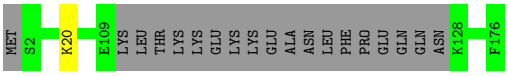
Chain Ey:





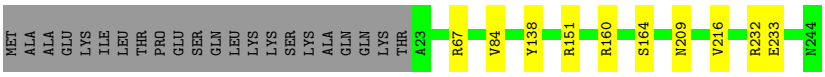
• Molecule 41: 60S ribosomal protein L6-A

Chain Ha:



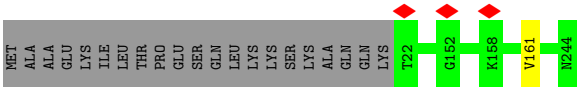
• Molecule 42: 60S ribosomal protein L7-A

Chain Fy:



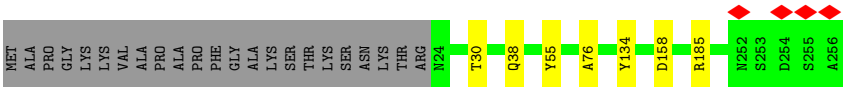
• Molecule 42: 60S ribosomal protein L7-A

Chain Ia:



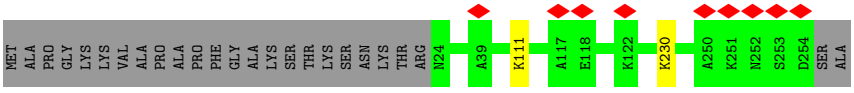
• Molecule 43: 60S ribosomal protein L8-A

Chain Gy:



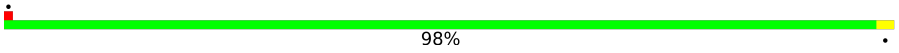
• Molecule 43: 60S ribosomal protein L8-A

Chain Ja:



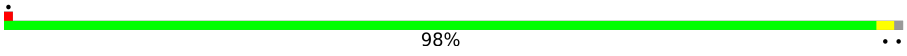
• Molecule 44: 60S ribosomal protein L9-A

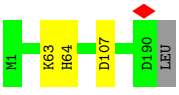
Chain Hy:



• Molecule 44: 60S ribosomal protein L9-A

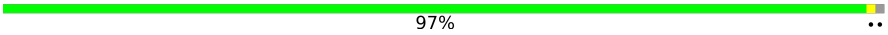
Chain Ka:

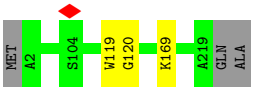




• Molecule 45: 60S ribosomal protein L10

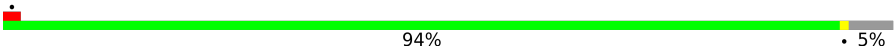
Chain Iy:

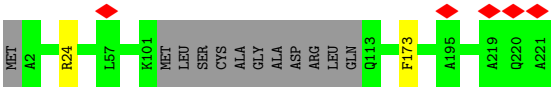




• Molecule 45: 60S ribosomal protein L10

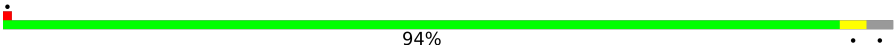
Chain La:

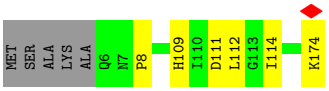




• Molecule 46: 60S ribosomal protein L11-A

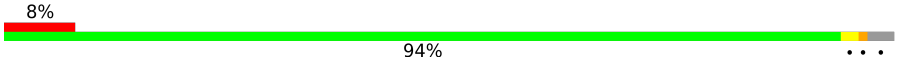
Chain Jy:

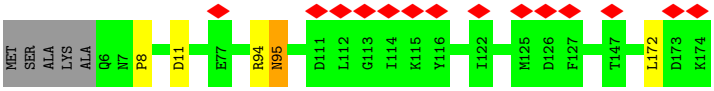




• Molecule 46: 60S ribosomal protein L11-A

Chain Ma:



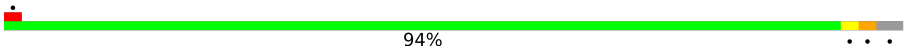


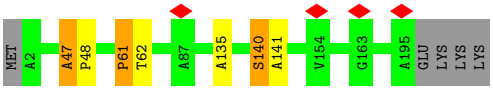
• Molecule 47: 60S ribosomal protein L13-A

Chain Ly:

• Molecule 47: 60S ribosomal protein L13-A

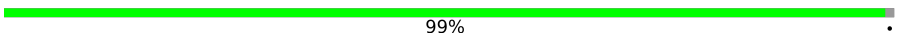
Chain Na:





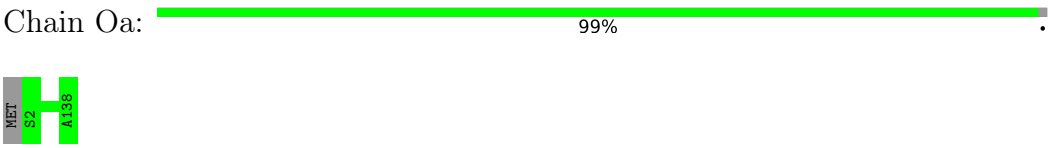
• Molecule 48: 60S ribosomal protein L14-A

Chain My:



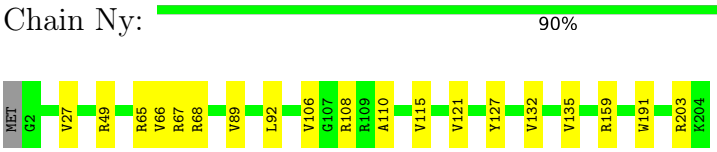
• Molecule 48: 60S ribosomal protein L14-A

Chain Oa:



• Molecule 49: 60S ribosomal protein L15-A

Chain Ny:

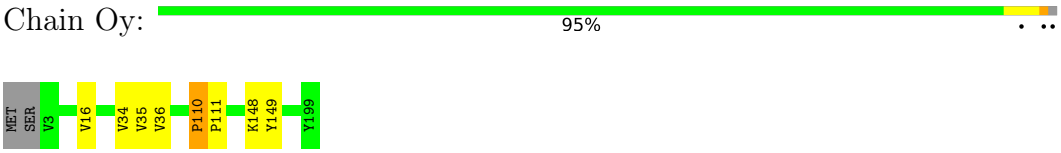


• Molecule 49: 60S ribosomal protein L15-A

Chain Pa:

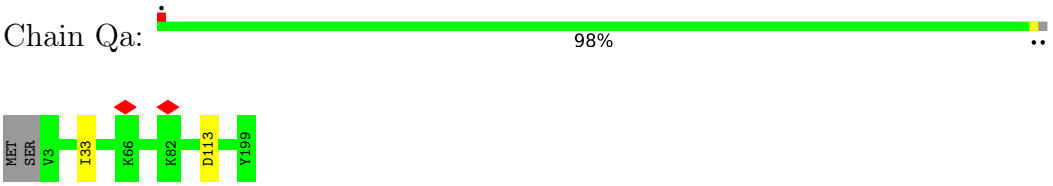
• Molecule 50: 60S ribosomal protein L16-A

Chain Oy:



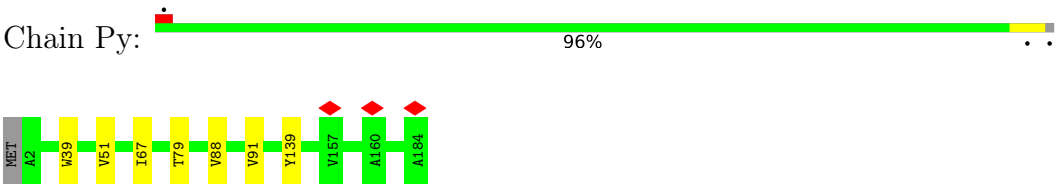
• Molecule 50: 60S ribosomal protein L16-A

Chain Qa:



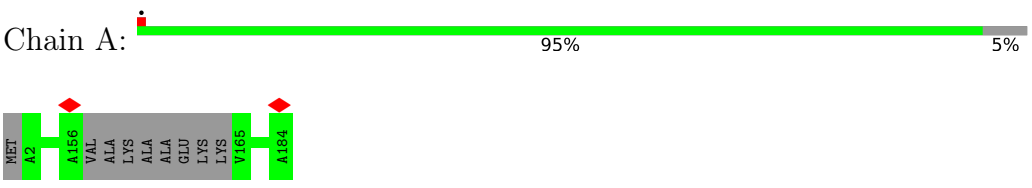
• Molecule 51: 60S ribosomal protein L17-A

Chain Py:



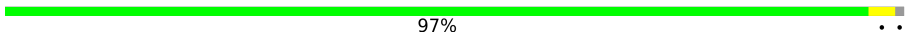
• Molecule 51: 60S ribosomal protein L17-A

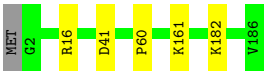
Chain A:



• Molecule 52: 60S ribosomal protein L18-A

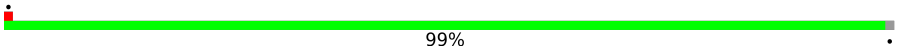
Chain Qy:

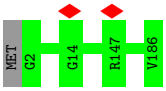




• Molecule 52: 60S ribosomal protein L18-A

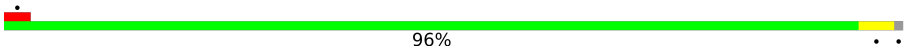
Chain B:





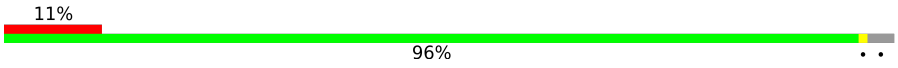
• Molecule 53: 60S ribosomal protein L19-A

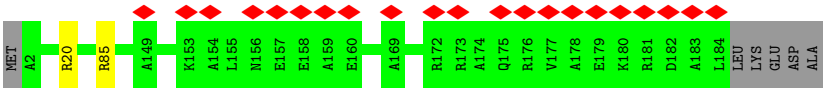
Chain Ry:



• Molecule 53: 60S ribosomal protein L19-A

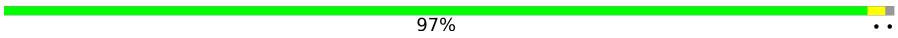
Chain C:

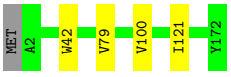




• Molecule 54: 60S ribosomal protein L20-A

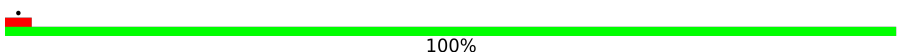
Chain Sy:

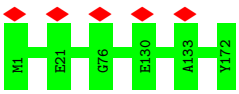




• Molecule 54: 60S ribosomal protein L20-A

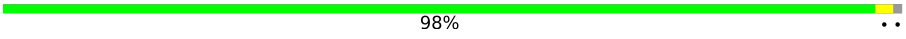
Chain D:





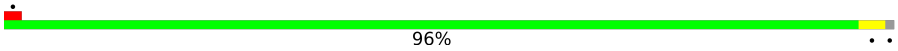
• Molecule 55: 60S ribosomal protein L21-A

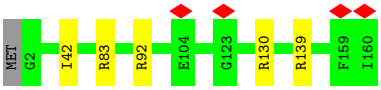
Chain Ty:



• Molecule 55: 60S ribosomal protein L21-A

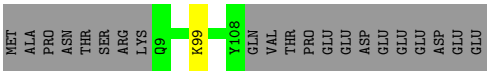
Chain E:





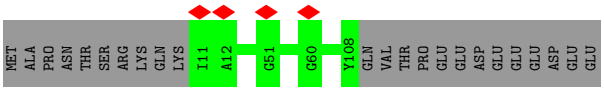
• Molecule 56: 60S ribosomal protein L22-A

Chain Uy:



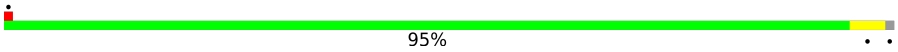
• Molecule 56: 60S ribosomal protein L22-A

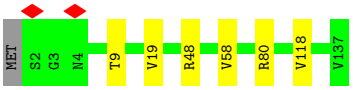
Chain F:



• Molecule 57: 60S ribosomal protein L23-A

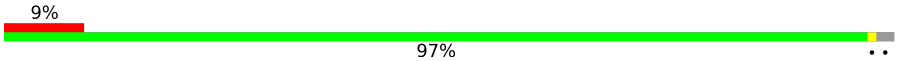
Chain Vy:

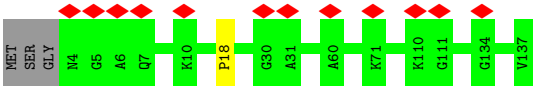




• Molecule 57: 60S ribosomal protein L23-A

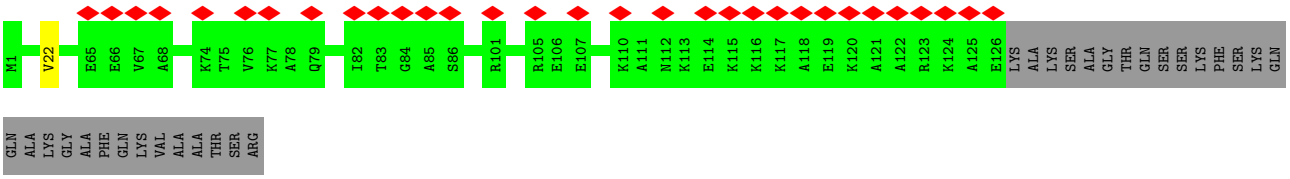
Chain G:





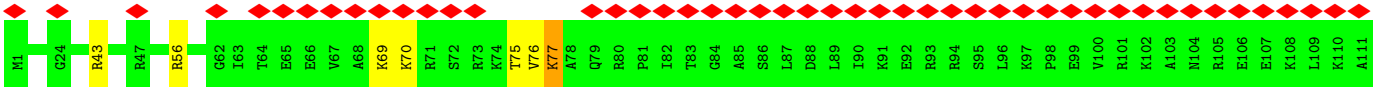
• Molecule 58: 60S ribosomal protein L24-A

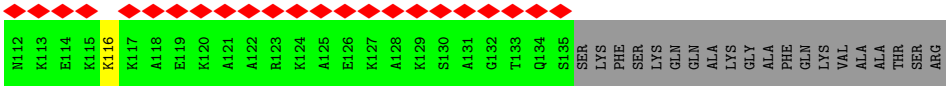
Chain Wy:



• Molecule 58: 60S ribosomal protein L24-A

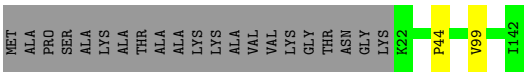
Chain H:





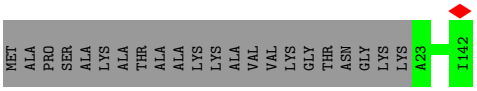
• Molecule 59: 60S ribosomal protein L25

Chain Xy:



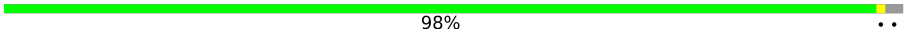
• Molecule 59: 60S ribosomal protein L25

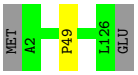
Chain I:



• Molecule 60: 60S ribosomal protein L26-A

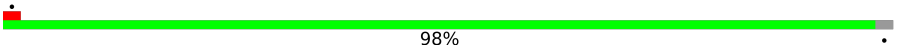
Chain Yy:

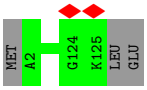




• Molecule 60: 60S ribosomal protein L26-A

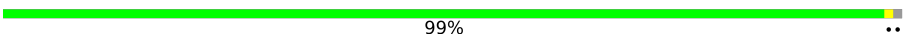
Chain J:





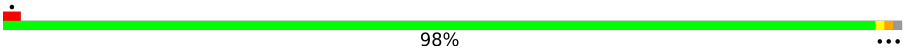
• Molecule 61: 60S ribosomal protein L27-A

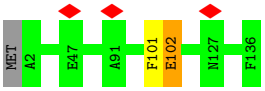
Chain Zy:



• Molecule 61: 60S ribosomal protein L27-A

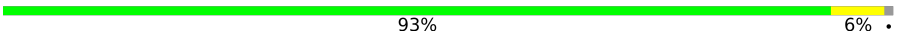
Chain K:

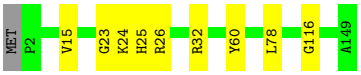




• Molecule 62: 60S ribosomal protein L28

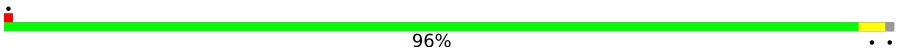
Chain ay:

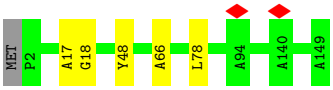




• Molecule 62: 60S ribosomal protein L28

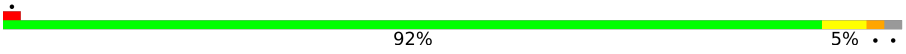
Chain L:

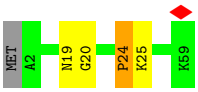




• Molecule 63: 60S ribosomal protein L29

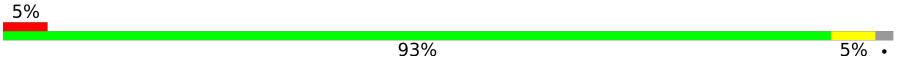
Chain by:

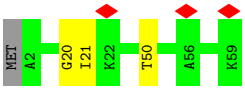




• Molecule 63: 60S ribosomal protein L29

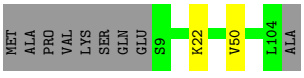
Chain M:





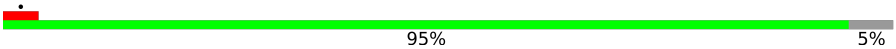
• Molecule 64: 60S ribosomal protein L30

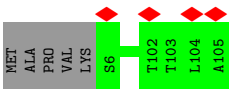
Chain cy:



• Molecule 64: 60S ribosomal protein L30

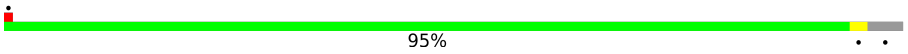
Chain N:

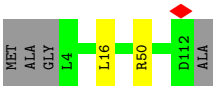




• Molecule 65: 60S ribosomal protein L31-A

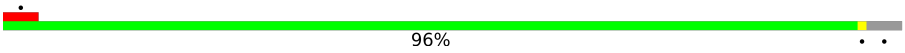
Chain dy:

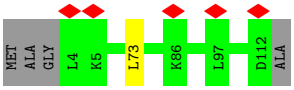




• Molecule 65: 60S ribosomal protein L31-A

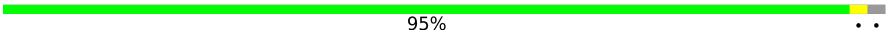
Chain O:

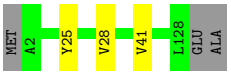




• Molecule 66: 60S ribosomal protein L32

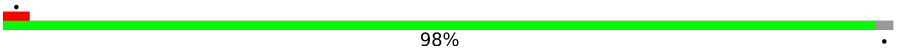
Chain ey:

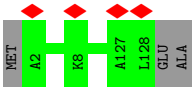




• Molecule 66: 60S ribosomal protein L32

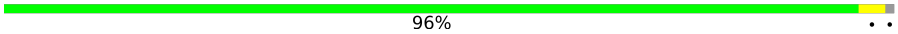
Chain P:

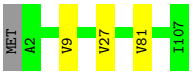




• Molecule 67: 60S ribosomal protein L33-A

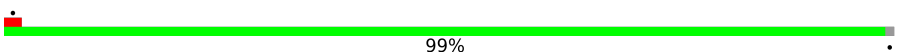
Chain fy:

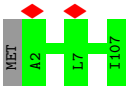




• Molecule 67: 60S ribosomal protein L33-A

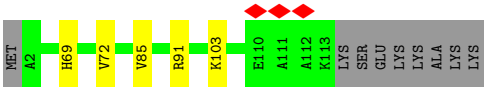
Chain Q:





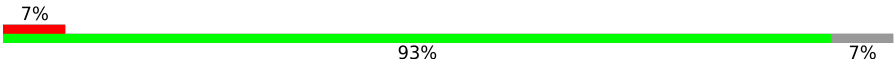
• Molecule 68: 60S ribosomal protein L34-A

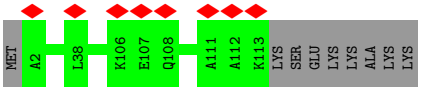
Chain gy:



• Molecule 68: 60S ribosomal protein L34-A

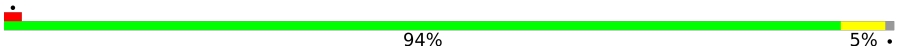
Chain R:

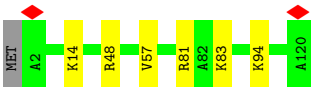




• Molecule 69: 60S ribosomal protein L35-A

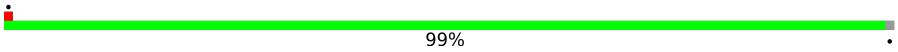
Chain hb:





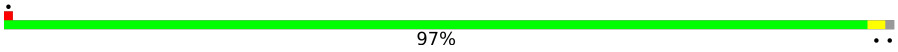
• Molecule 69: 60S ribosomal protein L35-A

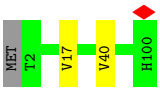
Chain S:



• Molecule 70: 60S ribosomal protein L36-A

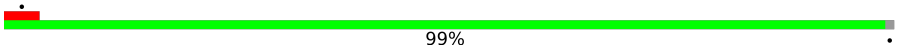
Chain ib:

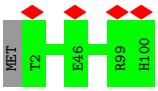




• Molecule 70: 60S ribosomal protein L36-A

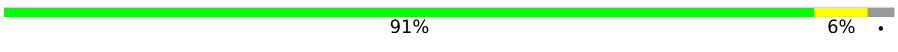
Chain T:

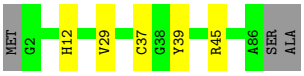




• Molecule 71: 60S ribosomal protein L37-A

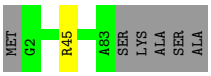
Chain jb:





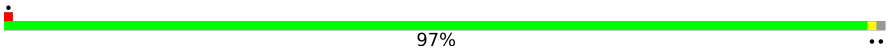
• Molecule 71: 60S ribosomal protein L37-A

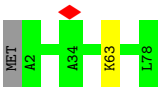
Chain U:



• Molecule 72: 60S ribosomal protein L38

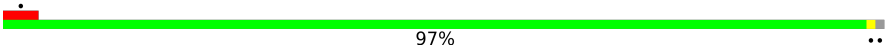
Chain kb:

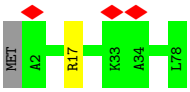




• Molecule 72: 60S ribosomal protein L38

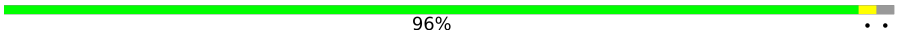
Chain V:

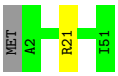




• Molecule 73: 60S ribosomal protein L39

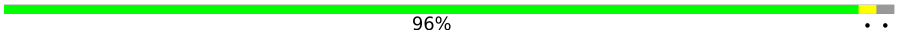
Chain lb:

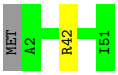




• Molecule 73: 60S ribosomal protein L39

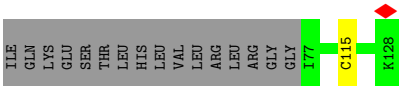
Chain W:





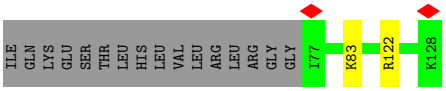
• Molecule 74: Ubiquitin-60S ribosomal protein L40

Chain mb:



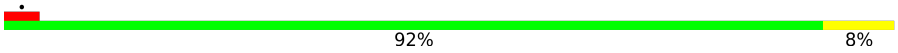
• Molecule 74: Ubiquitin-60S ribosomal protein L40

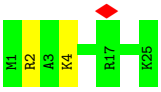
Chain X:



• Molecule 75: 60S ribosomal protein L41-A

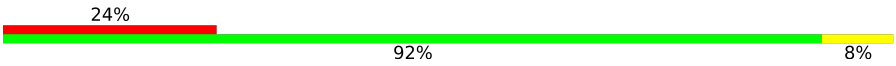
Chain nb:

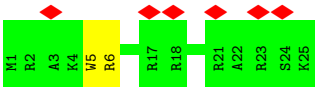




• Molecule 75: 60S ribosomal protein L41-A

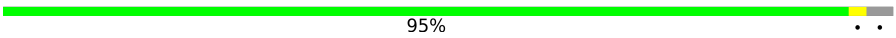
Chain Y:





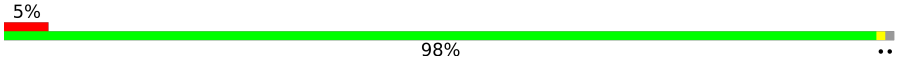
• Molecule 76: 60S ribosomal protein L42-A

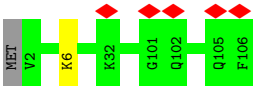
Chain ob:



• Molecule 76: 60S ribosomal protein L42-A

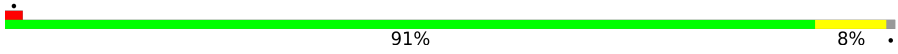
Chain Z:

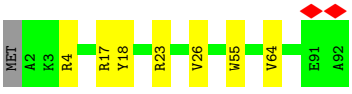




• Molecule 77: 60S ribosomal protein L43-A

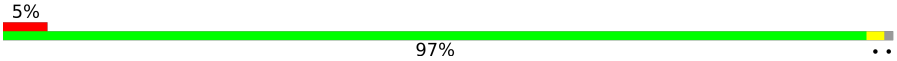
Chain pb:

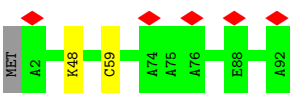




• Molecule 77: 60S ribosomal protein L43-A

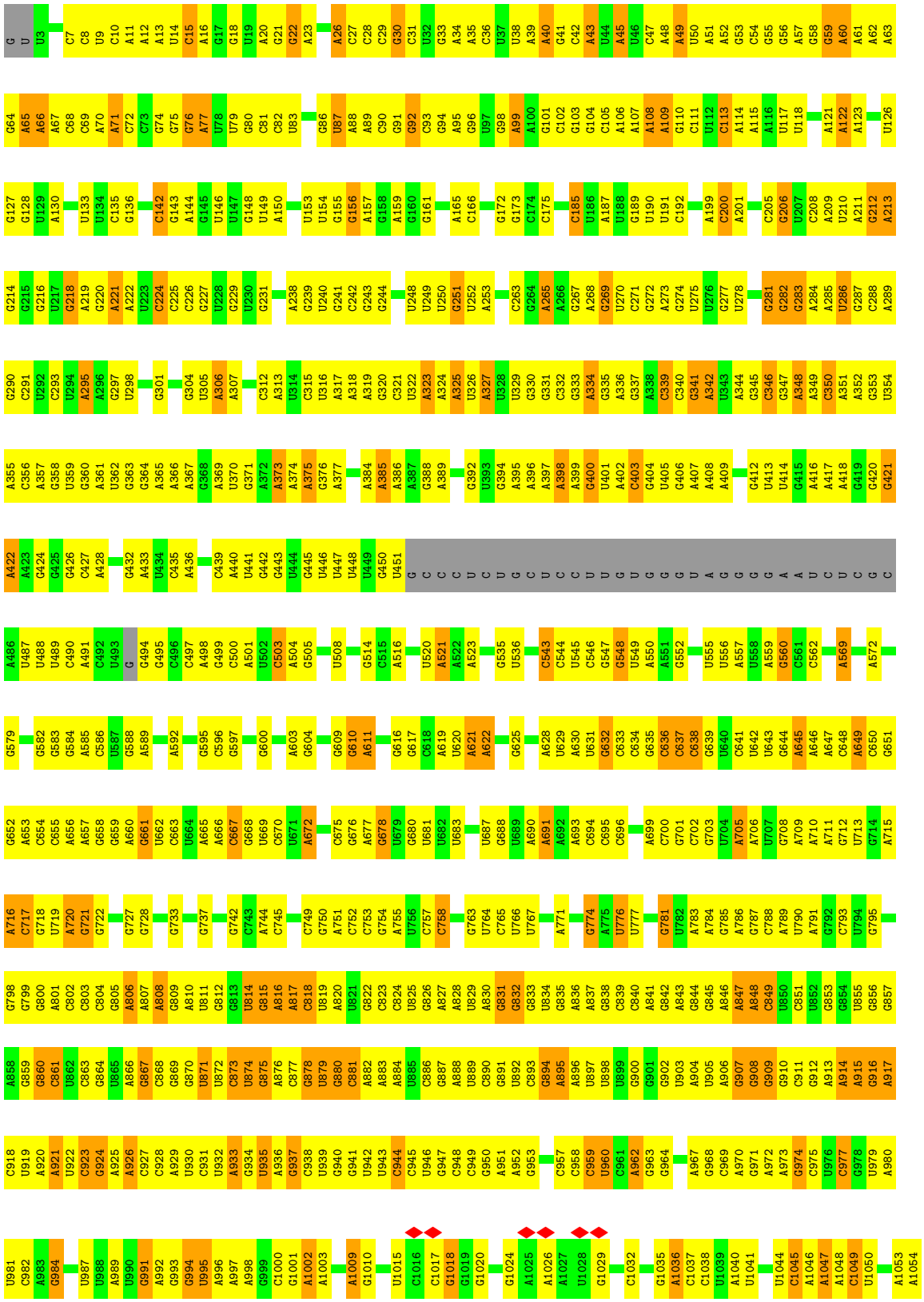
Chain aa:

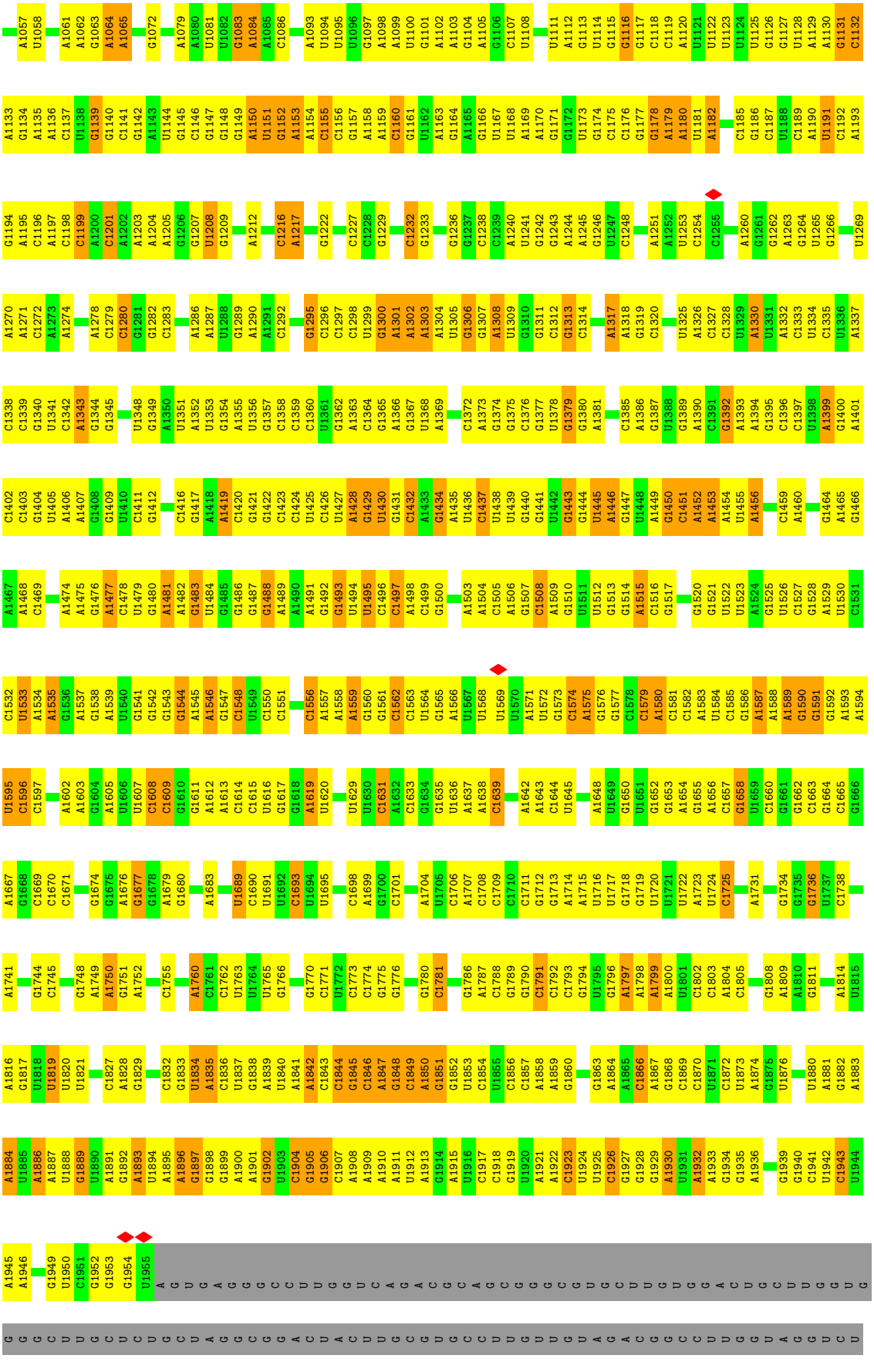


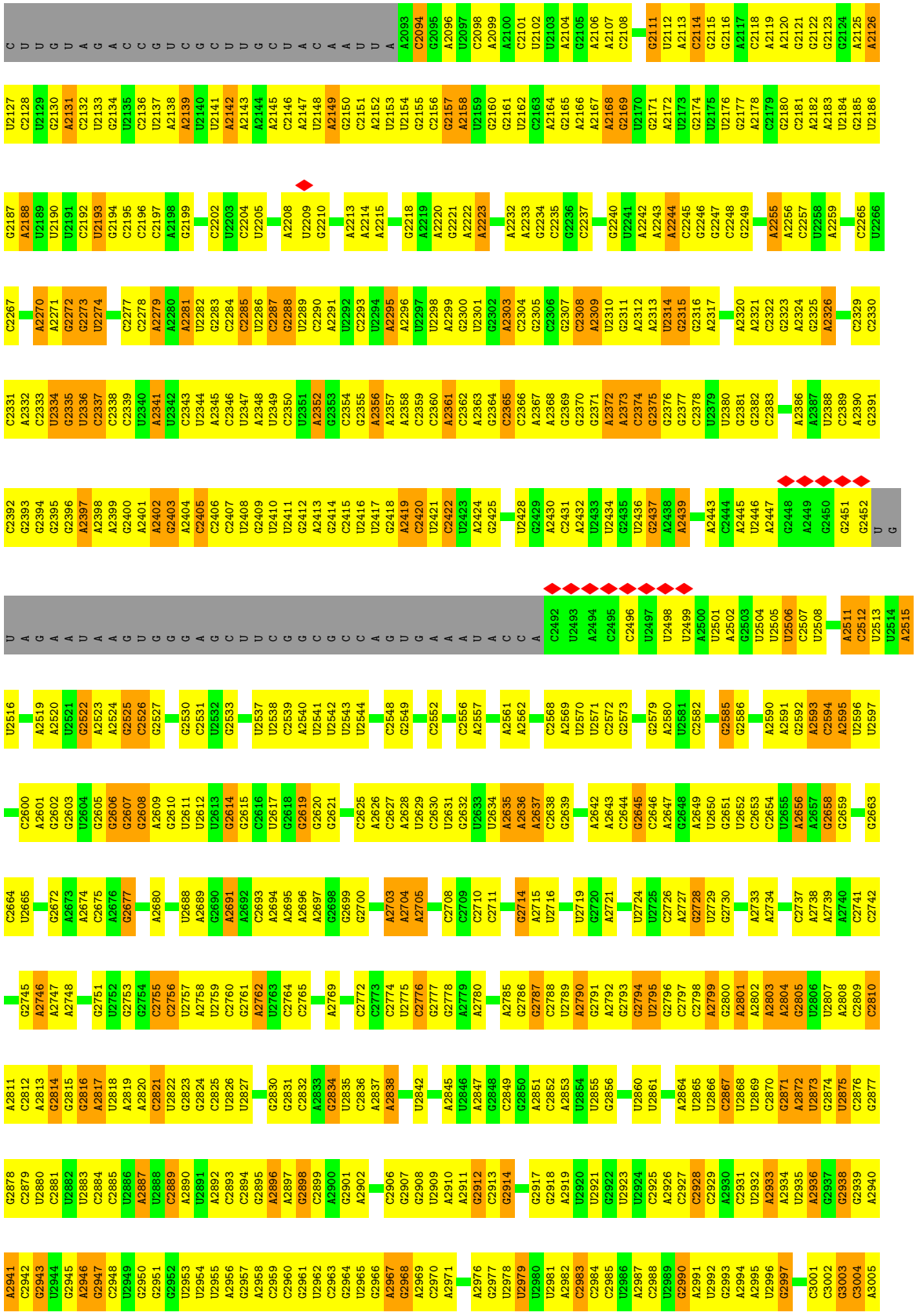


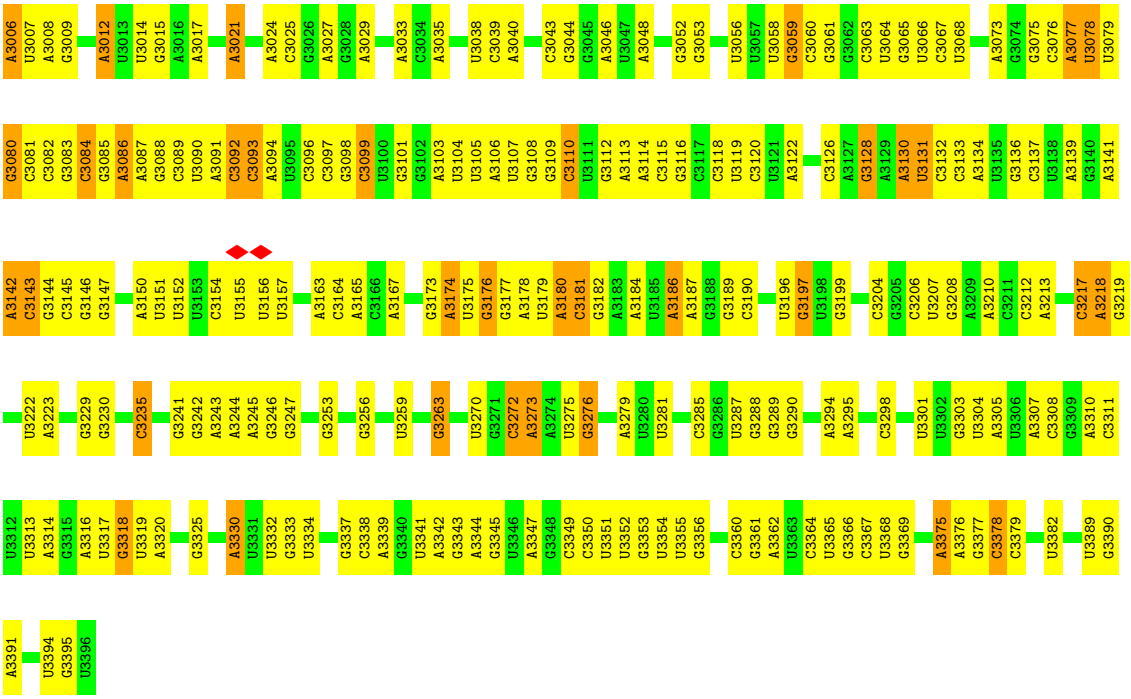
• Molecule 78: 25S rRNA

Chain 1b:



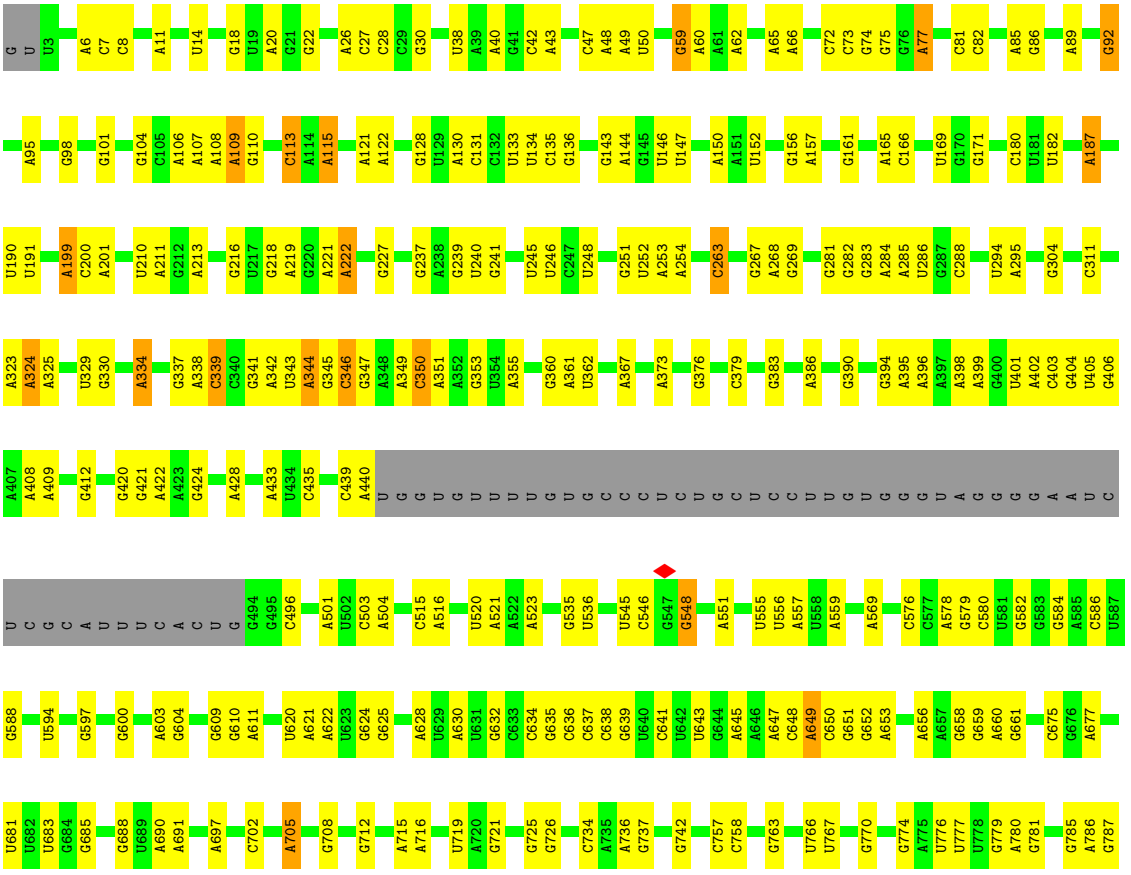


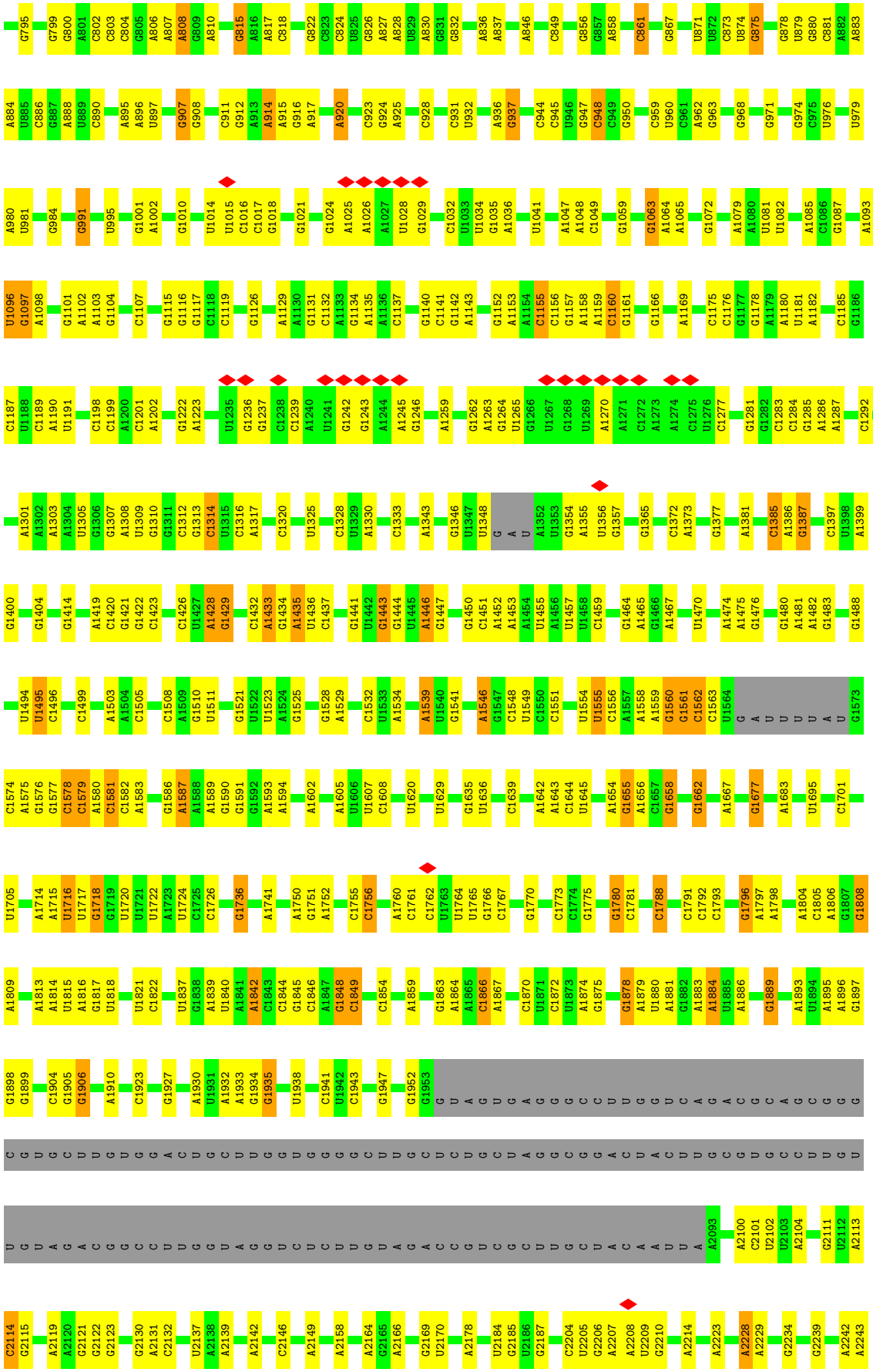


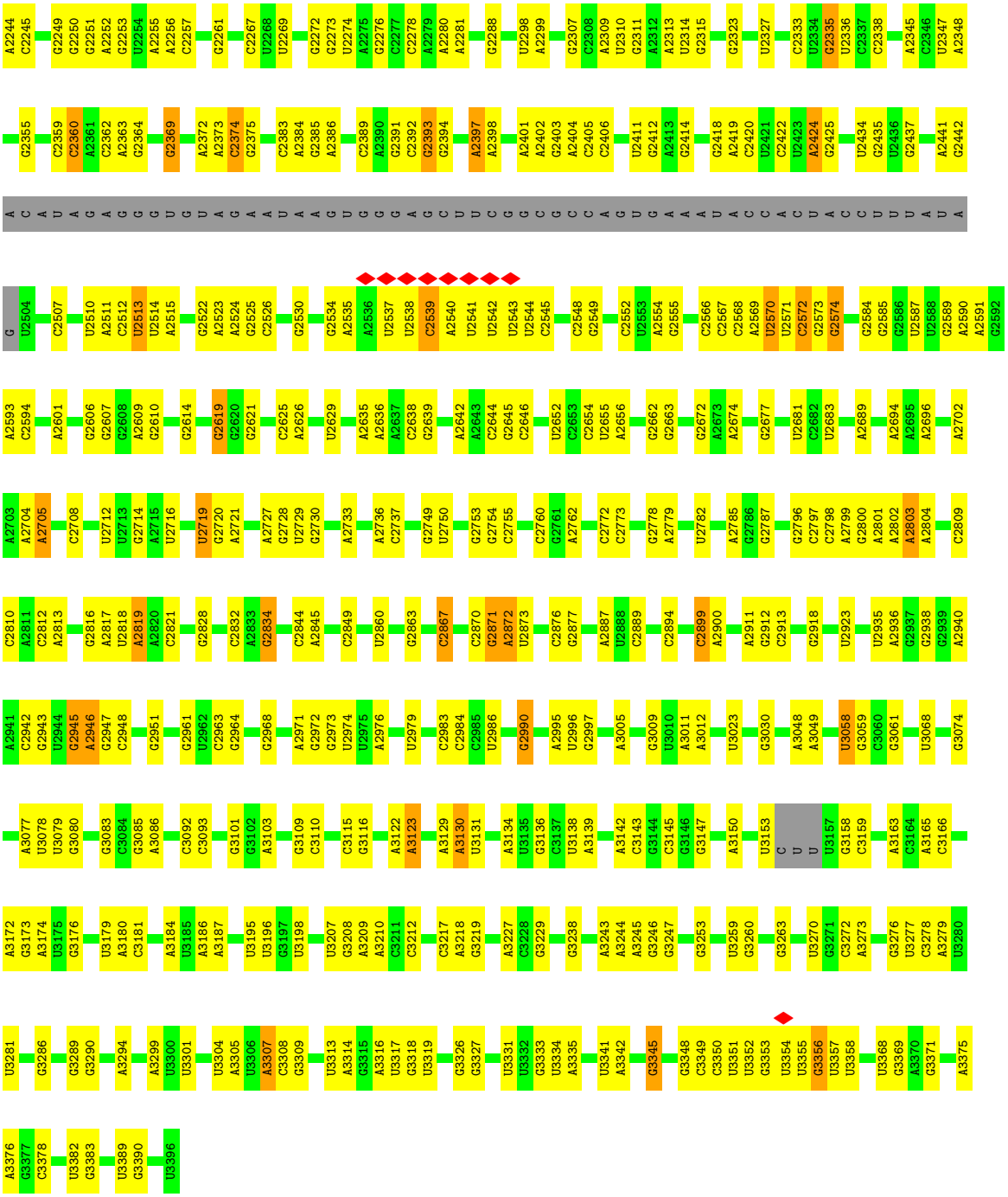


• Molecule 78: 25S rRNA

Chain Aa:

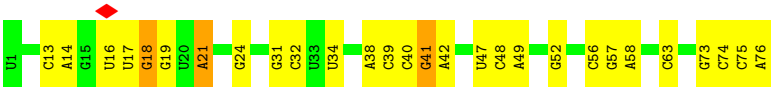






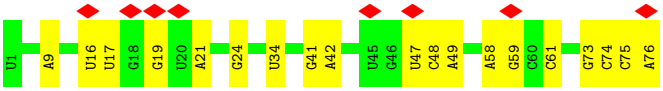
• Molecule 79: tRNA

Chain 6b:



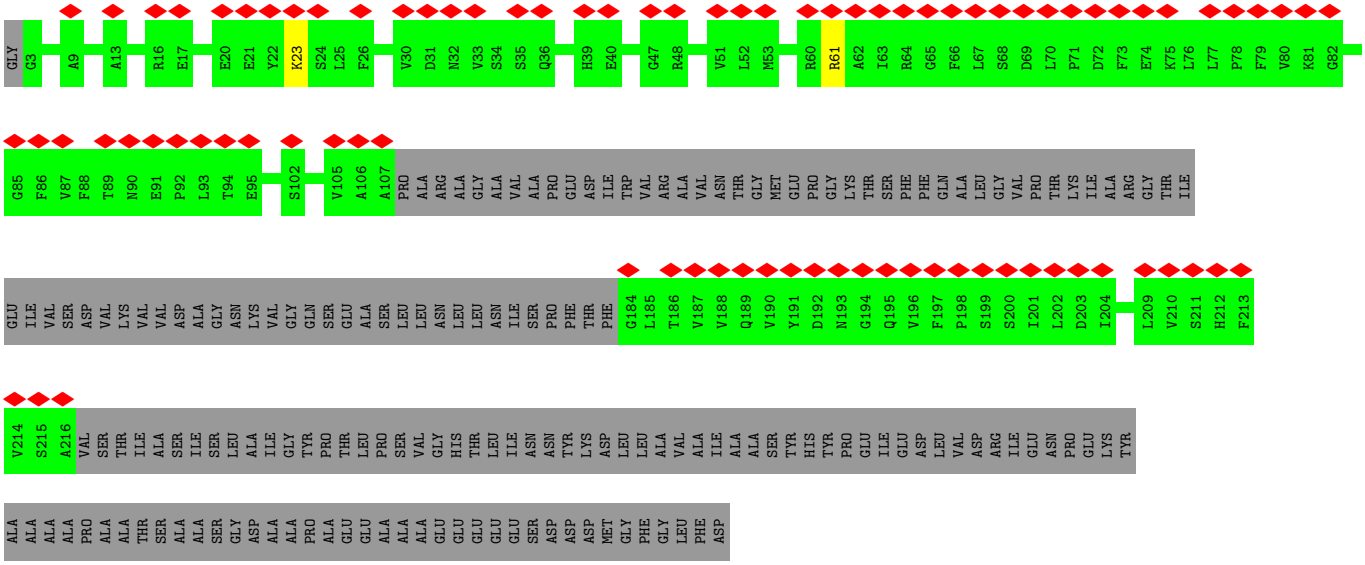
• Molecule 79: tRNA

Chain 8:



• Molecule 80: 60S acidic ribosomal protein P0

Chain ba:



4 Experimental information (i)

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 ($e^-/Å^2$)	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 (i)

5.1 Standard geometry (i)

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	1.84	750/42211 (1.8%)	1.64	1016/65773 (1.5%)
1	a	1.40	19/41891 (0.0%)	1.22	201/65273 (0.3%)
2	Ab	0.75	0/1644	0.66	0/2249
2	b	0.40	0/1623	0.64	1/2222 (0.0%)
3	Ba	0.85	2/1823 (0.1%)	0.76	0/2447
3	c	0.40	0/1748	0.60	0/2352
4	Pb	0.71	0/936	0.64	0/1259
4	q	0.36	0/959	0.63	0/1288
5	Cb	1.04	5/1656 (0.3%)	0.74	0/2251
5	d	0.45	0/1665	0.60	0/2263
6	Db	0.74	0/1754	0.65	0/2361
6	e	0.38	0/1759	0.58	0/2368
7	Eb	0.92	1/2097 (0.0%)	0.72	0/2823
7	f	0.40	0/2109	0.62	0/2839
8	Fb	0.76	0/1625	0.67	0/2197
8	g	0.37	0/1629	0.59	0/2202
9	Gb	0.67	0/1839	0.75	0/2460
9	h	0.39	0/1779	0.64	0/2379
10	Hb	0.76	0/1498	0.67	0/2019
10	i	0.37	0/1511	0.61	0/2036
11	Ib	0.96	2/1501 (0.1%)	0.77	0/2006
11	j	0.43	0/1514	0.63	0/2021
12	Jb	0.86	1/1504 (0.1%)	0.75	1/2016 (0.0%)
12	k	0.40	0/1519	0.60	0/2035
13	Kb	0.66	0/769	0.59	0/1039
13	l	0.38	0/757	0.57	0/1022
14	Lb	1.19	1/1185 (0.1%)	0.74	0/1598
14	m	0.44	0/1194	0.63	0/1610
15	Mb	0.40	0/883	0.70	0/1199
15	n	0.33	0/898	0.64	0/1220
16	Nb	1.08	1/1215 (0.1%)	0.75	0/1638
16	o	0.46	0/1215	0.62	0/1638
17	Ob	0.98	0/937	0.87	0/1261
17	p	0.43	0/960	0.71	1/1290 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	Qb	0.86	0/1125	0.69	0/1510
18	r	0.41	0/1125	0.64	0/1510
19	Rb	0.72	0/957	0.72	2/1283 (0.2%)
19	s	0.37	0/1010	0.60	0/1355
20	Sb	0.63	0/1211	0.68	0/1628
20	t	0.39	0/1211	0.64	0/1628
21	Tb	0.78	0/1130	0.69	0/1517
21	u	0.40	0/1130	0.58	0/1517
22	Ub	0.79	0/807	0.68	0/1091
22	v	0.41	0/815	0.60	0/1102
23	Vb	0.89	0/682	0.72	0/921
23	w	0.47	0/693	0.61	0/935
24	Wb	1.12	1/1038 (0.1%)	0.80	0/1395
24	x	0.49	0/1038	0.65	1/1395 (0.1%)
25	Xb	1.07	1/1139 (0.1%)	0.76	0/1518
25	y	0.49	0/1139	0.64	0/1518
26	Yb	0.77	0/1087	0.69	0/1449
26	z	0.42	0/1087	0.66	0/1449
27	0	0.36	0/566	0.61	0/761
27	Zb	0.60	0/661	0.67	0/888
28	1	0.50	0/782	0.70	0/1047
28	ab	1.16	2/782 (0.3%)	0.89	2/1047 (0.2%)
29	2	0.37	0/620	0.59	0/838
29	bb	0.82	1/620 (0.2%)	0.72	0/838
30	4	1.27	2/452 (0.4%)	1.14	2/600 (0.3%)
30	db	0.94	0/452	0.74	0/600
31	5	0.40	0/483	0.61	0/643
31	eb	0.79	0/480	0.72	1/639 (0.2%)
32	6	0.36	0/567	0.59	0/764
32	fb	0.53	0/567	0.69	0/764
33	7	0.34	0/2456	0.58	0/3343
33	gb	0.59	0/2436	0.66	0/3318
34	3	0.38	0/499	0.67	0/670
34	cb	0.83	0/493	0.77	0/663
35	4b	1.77	33/2883 (1.1%)	1.58	62/4491 (1.4%)
35	Bb	1.11	0/2883	1.26	17/4491 (0.4%)
36	3b	2.14	109/3746 (2.9%)	1.82	142/5832 (2.4%)
36	Ca	1.28	5/3724 (0.1%)	1.38	42/5798 (0.7%)
37	Ay	1.25	7/1933 (0.4%)	0.85	1/2598 (0.0%)
37	Da	0.72	0/1946	0.73	2/2614 (0.1%)
38	By	1.20	5/3146 (0.2%)	0.80	5/4228 (0.1%)
38	Ea	0.63	0/3146	0.68	0/4228
39	Cy	1.24	14/2800 (0.5%)	0.79	1/3790 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	Fa	0.66	1/2800 (0.0%)	0.69	2/3790 (0.1%)
40	Dy	0.82	0/2400	0.69	2/3239 (0.1%)
40	Ga	0.52	0/2408	0.62	0/3248
41	Ey	0.88	1/1324 (0.1%)	0.74	1/1782 (0.1%)
41	Ha	0.57	0/1269	0.62	0/1705
42	Fy	1.19	4/1821 (0.2%)	0.78	2/2451 (0.1%)
42	Ia	0.67	0/1828	0.66	0/2461
43	Gy	0.95	1/1836 (0.1%)	0.74	0/2481
43	Ja	0.53	0/1795	0.58	0/2429
44	Hy	0.90	0/1529	0.71	0/2060
44	Ka	0.58	0/1531	0.62	0/2062
45	Iy	0.97	2/1801 (0.1%)	0.73	0/2416
45	La	0.58	0/1732	0.62	0/2323
46	Jy	0.79	0/1371	0.68	0/1838
46	Ma	0.42	0/1374	0.68	0/1842
47	Ly	1.16	5/1568 (0.3%)	0.79	3/2106 (0.1%)
47	Na	0.60	0/1573	0.71	0/2113
48	My	0.87	0/1068	0.75	0/1438
48	Oa	0.54	0/1074	0.67	0/1446
49	Ny	1.48	13/1757 (0.7%)	0.90	6/2354 (0.3%)
49	Pa	0.80	2/1757 (0.1%)	0.76	0/2354
50	Oy	1.30	6/1585 (0.4%)	0.75	0/2128
50	Qa	0.72	0/1585	0.66	1/2128 (0.0%)
51	A	0.69	0/1400	0.65	0/1882
51	Py	1.26	5/1439 (0.3%)	0.84	0/1938
52	B	0.58	0/1465	0.71	0/1965
52	Qy	1.13	1/1465 (0.1%)	0.77	2/1965 (0.1%)
53	C	0.59	0/1499	0.66	2/1998 (0.1%)
53	Ry	1.06	2/1532 (0.1%)	0.77	1/2043 (0.0%)
54	D	0.66	0/1481	0.66	0/1990
54	Sy	1.14	3/1473 (0.2%)	0.73	0/1980
55	E	0.68	0/1300	0.70	2/1743 (0.1%)
55	Ty	1.16	1/1300 (0.1%)	0.75	1/1743 (0.1%)
56	F	0.51	0/794	0.58	0/1076
56	Uy	0.75	0/812	0.68	0/1099
57	G	0.61	0/1008	0.65	0/1356
57	Vy	1.21	4/1018 (0.4%)	0.83	3/1369 (0.2%)
58	H	2.21	1/1103 (0.1%)	0.76	3/1458 (0.2%)
58	Wy	0.89	1/863 (0.1%)	0.65	0/1169
59	I	0.65	0/974	0.66	0/1314
59	Xy	1.10	1/979 (0.1%)	0.72	0/1321
60	J	0.56	0/987	0.69	0/1318
60	Yy	1.00	0/995	0.81	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
61	K	0.57	0/1118	0.61	0/1497
61	Zy	1.03	0/1118	0.67	0/1497
62	L	0.68	0/1204	0.71	0/1612
62	ay	1.22	2/1204 (0.2%)	0.82	1/1612 (0.1%)
63	M	0.53	0/473	0.73	0/629
63	by	0.96	0/473	0.69	0/629
64	N	0.62	0/775	0.61	0/1040
64	cy	1.10	1/745 (0.1%)	0.74	0/1001
65	O	0.64	0/897	0.66	0/1205
65	dy	1.11	0/890	0.79	1/1196 (0.1%)
66	P	0.65	0/1041	0.65	0/1394
66	ey	1.14	3/1038 (0.3%)	0.74	0/1390
67	Q	0.76	0/868	0.69	0/1168
67	fy	1.36	3/868 (0.3%)	0.80	0/1168
68	R	0.67	0/890	0.72	0/1189
68	gy	1.23	2/890 (0.2%)	0.82	1/1189 (0.1%)
69	S	0.53	0/974	0.65	0/1297
69	hb	1.03	1/978 (0.1%)	0.71	0/1301
70	T	0.54	0/777	0.66	0/1033
70	ib	0.95	2/772 (0.3%)	0.71	0/1026
71	U	0.82	0/665	0.82	2/882 (0.2%)
71	jb	1.39	3/685 (0.4%)	0.89	1/908 (0.1%)
72	V	0.46	0/614	0.65	0/822
72	kb	0.76	0/618	0.66	0/826
73	W	0.73	0/443	0.75	1/588 (0.2%)
73	lb	1.30	0/443	0.82	0/588
74	X	0.52	0/423	0.65	1/562 (0.2%)
74	mb	0.96	1/423 (0.2%)	0.73	0/562
75	Y	0.46	0/234	0.75	0/300
75	nb	0.93	0/230	0.98	2/296 (0.7%)
76	Z	0.63	0/860	0.70	0/1136
76	ob	1.01	0/836	0.79	1/1104 (0.1%)
77	aa	0.75	0/701	0.67	0/934
77	pb	1.38	5/701 (0.7%)	0.83	4/934 (0.4%)
78	1b	2.21	2892/76214 (3.8%)	1.81	2772/118821 (2.3%)
78	Aa	1.29	109/74873 (0.1%)	1.38	699/116727 (0.6%)
79	6b	1.50	9/1804 (0.5%)	1.54	35/2809 (1.2%)
79	8	0.57	0/1804	1.04	1/2809 (0.0%)
80	ba	0.37	0/1067	0.61	0/1439
All	All	1.43	4049/431658 (0.9%)	1.29	5053/634238 (0.8%)

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 4049 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	1597	A	N3-C4	114.04	2.03	1.34
1	a	1597	A	C6-N1	113.96	2.15	1.35
1	a	1597	A	N1-C2	87.38	2.12	1.34
1	a	1597	A	C2-N3	73.39	1.99	1.33
1	a	1597	A	C5-C4	72.97	1.89	1.38

The worst 5 of 5053 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	a	1597	A	N1-C2-N3	-60.58	99.01	129.30
1	a	1597	A	C2-N3-C4	50.02	135.61	110.60
78	1b	846	A	C8-N9-C4	-33.16	92.54	105.80
78	1b	846	A	N7-C8-N9	27.18	127.39	113.80
1	a	1597	A	C4-C5-N7	-23.61	98.89	110.70

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)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	Ab	204/252 (81%)	170 (83%)	33 (16%)	1 (0%)	25 61
2	b	204/252 (81%)	165 (81%)	38 (19%)	1 (0%)	25 61
3	Ba	222/255 (87%)	182 (82%)	36 (16%)	4 (2%)	7 36
3	c	214/255 (84%)	192 (90%)	21 (10%)	1 (0%)	25 61
4	Pb	115/142 (81%)	101 (88%)	14 (12%)	0	100 100
4	q	117/142 (82%)	97 (83%)	16 (14%)	4 (3%)	3 25
5	Cb	214/254 (84%)	187 (87%)	26 (12%)	1 (0%)	25 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	25	61
7	Eb	256/261 (98%)	211 (82%)	44 (17%)	1 (0%)	30	66
7	f	258/261 (99%)	224 (87%)	33 (13%)	1 (0%)	30	66
8	Fb	204/225 (91%)	176 (86%)	27 (13%)	1 (0%)	25	61
8	g	204/225 (91%)	175 (86%)	28 (14%)	1 (0%)	25	61
9	Gb	226/236 (96%)	194 (86%)	28 (12%)	4 (2%)	7	36
9	h	216/236 (92%)	196 (91%)	19 (9%)	1 (0%)	25	61
10	Hb	182/190 (96%)	156 (86%)	25 (14%)	1 (0%)	25	61
10	i	183/190 (96%)	156 (85%)	25 (14%)	2 (1%)	12	45
11	Ib	183/200 (92%)	159 (87%)	22 (12%)	2 (1%)	12	45
11	j	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
12	Jb	182/197 (92%)	155 (85%)	25 (14%)	2 (1%)	12	45
12	k	183/197 (93%)	162 (88%)	19 (10%)	2 (1%)	12	45
13	Kb	90/105 (86%)	67 (74%)	23 (26%)	0	100	100
13	l	90/105 (86%)	74 (82%)	15 (17%)	1 (1%)	12	45
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	22
15	n	122/143 (85%)	79 (65%)	40 (33%)	3 (2%)	4	30
16	Nb	148/151 (98%)	121 (82%)	26 (18%)	1 (1%)	19	55
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
18	Qb	139/143 (97%)	117 (84%)	21 (15%)	1 (1%)	19	55
18	r	139/143 (97%)	121 (87%)	15 (11%)	3 (2%)	5	32
19	Rb	117/136 (86%)	104 (89%)	11 (9%)	2 (2%)	7	37
19	s	123/136 (90%)	110 (89%)	12 (10%)	1 (1%)	16	53
20	Sb	143/146 (98%)	113 (79%)	26 (18%)	4 (3%)	4	28
20	t	143/146 (98%)	124 (87%)	17 (12%)	2 (1%)	9	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
21	Tb	141/144 (98%)	114 (81%)	25 (18%)	2 (1%)	9 40
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 34
23	Vb	85/87 (98%)	65 (76%)	19 (22%)	1 (1%)	11 43
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 40
25	y	142/145 (98%)	123 (87%)	17 (12%)	2 (1%)	9 40
26	Yb	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	16 53
26	z	132/135 (98%)	109 (83%)	21 (16%)	2 (2%)	8 40
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%)	12 45
28	ab	95/119 (80%)	64 (67%)	26 (27%)	5 (5%)	1 19
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 37
31	eb	58/63 (92%)	45 (78%)	13 (22%)	0	100 100
32	6	71/152 (47%)	41 (58%)	29 (41%)	1 (1%)	9 40
32	fb	71/152 (47%)	43 (61%)	28 (39%)	0	100 100
33	7	311/319 (98%)	281 (90%)	30 (10%)	0	100 100
33	gb	310/319 (97%)	264 (85%)	45 (14%)	1 (0%)	37 71
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 53
37	Da	250/254 (98%)	205 (82%)	45 (18%)	0	100 100
38	By	384/387 (99%)	314 (82%)	68 (18%)	2 (0%)	25 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	Ea	384/387 (99%)	342 (89%)	42 (11%)	0	100	100
39	Cy	359/362 (99%)	292 (81%)	65 (18%)	2 (1%)	22	58
39	Fa	359/362 (99%)	297 (83%)	58 (16%)	4 (1%)	12	45
40	Dy	292/297 (98%)	251 (86%)	40 (14%)	1 (0%)	37	71
40	Ga	292/297 (98%)	265 (91%)	27 (9%)	0	100	100
41	Ey	163/176 (93%)	138 (85%)	24 (15%)	1 (1%)	22	58
41	Ha	153/176 (87%)	132 (86%)	21 (14%)	0	100	100
42	Fy	220/244 (90%)	178 (81%)	40 (18%)	2 (1%)	14	49
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%)	7	36
46	Ma	167/174 (96%)	141 (84%)	24 (14%)	2 (1%)	11	43
47	Ly	191/199 (96%)	148 (78%)	39 (20%)	4 (2%)	5	33
47	Na	192/199 (96%)	149 (78%)	38 (20%)	5 (3%)	4	30
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%)	13	47
50	Oy	195/199 (98%)	161 (83%)	32 (16%)	2 (1%)	13	47
50	Qa	195/199 (98%)	183 (94%)	12 (6%)	0	100	100
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%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	53
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	40
61	Zy	133/136 (98%)	116 (87%)	17 (13%)	0	100	100
62	L	146/149 (98%)	116 (80%)	27 (18%)	3 (2%)	5	33
62	ay	146/149 (98%)	113 (77%)	30 (20%)	3 (2%)	5	33
63	M	56/59 (95%)	43 (77%)	13 (23%)	0	100	100
63	by	56/59 (95%)	39 (70%)	15 (27%)	2 (4%)	3	24
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	10	42
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%)	27	61

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 (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	Ab	170/210 (81%)	169 (99%)	1 (1%)	84 88
2	b	165/210 (79%)	164 (99%)	1 (1%)	84 88
3	Ba	200/224 (89%)	196 (98%)	4 (2%)	50 68
3	c	192/224 (86%)	191 (100%)	1 (0%)	86 89
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%)	173 (99%)	2 (1%)	70 80
5	d	176/205 (86%)	176 (100%)	0	100 100
6	Db	182/195 (93%)	178 (98%)	4 (2%)	47 65
6	e	182/195 (93%)	180 (99%)	2 (1%)	70 80
7	Eb	220/222 (99%)	218 (99%)	2 (1%)	75 83
7	f	221/222 (100%)	219 (99%)	2 (1%)	75 83
8	Fb	172/191 (90%)	171 (99%)	1 (1%)	84 88
8	g	173/191 (91%)	172 (99%)	1 (1%)	84 88
9	Gb	189/201 (94%)	186 (98%)	3 (2%)	58 74
9	h	187/201 (93%)	185 (99%)	2 (1%)	70 80
10	Hb	163/170 (96%)	161 (99%)	2 (1%)	67 78
10	i	165/170 (97%)	165 (100%)	0	100 100
11	Ib	148/161 (92%)	146 (99%)	2 (1%)	62 75
11	j	150/161 (93%)	149 (99%)	1 (1%)	81 86
12	Jb	156/166 (94%)	155 (99%)	1 (1%)	84 88
12	k	158/166 (95%)	156 (99%)	2 (1%)	65 77
13	Kb	77/98 (79%)	77 (100%)	0	100 100
13	l	73/98 (74%)	73 (100%)	0	100 100
14	Lb	129/137 (94%)	128 (99%)	1 (1%)	79 84
14	m	129/137 (94%)	128 (99%)	1 (1%)	79 84
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%)	127 (100%)	0	100 100
16	o	127/128 (99%)	126 (99%)	1 (1%)	79 84
17	Ob	91/105 (87%)	90 (99%)	1 (1%)	70 80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	p	97/105 (92%)	97 (100%)	0	100	100
18	Qb	117/119 (98%)	116 (99%)	1 (1%)	75	83
18	r	117/119 (98%)	117 (100%)	0	100	100
19	Rb	101/124 (82%)	100 (99%)	1 (1%)	73	81
19	s	113/124 (91%)	111 (98%)	2 (2%)	54	71
20	Sb	128/129 (99%)	127 (99%)	1 (1%)	79	84
20	t	128/129 (99%)	126 (98%)	2 (2%)	58	74
21	Tb	115/116 (99%)	114 (99%)	1 (1%)	75	83
21	u	115/116 (99%)	115 (100%)	0	100	100
22	Ub	93/114 (82%)	93 (100%)	0	100	100
22	v	94/114 (82%)	93 (99%)	1 (1%)	70	80
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%)	75	83
24	x	110/111 (99%)	110 (100%)	0	100	100
25	Xb	119/120 (99%)	118 (99%)	1 (1%)	79	84
25	y	119/120 (99%)	119 (100%)	0	100	100
26	Yb	112/113 (99%)	110 (98%)	2 (2%)	54	71
26	z	112/113 (99%)	111 (99%)	1 (1%)	75	83
27	0	61/89 (68%)	60 (98%)	1 (2%)	58	74
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%)	67	78
29	2	70/71 (99%)	69 (99%)	1 (1%)	62	75
29	bb	70/71 (99%)	68 (97%)	2 (3%)	37	58
30	4	47/49 (96%)	46 (98%)	1 (2%)	48	66
30	db	47/49 (96%)	45 (96%)	2 (4%)	25	48
31	5	51/54 (94%)	49 (96%)	2 (4%)	27	50
31	eb	50/54 (93%)	50 (100%)	0	100	100
32	6	56/135 (42%)	55 (98%)	1 (2%)	54	71
32	fb	56/135 (42%)	55 (98%)	1 (2%)	54	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
33	7	255/262 (97%)	254 (100%)	1 (0%)	89 91
33	gb	250/262 (95%)	249 (100%)	1 (0%)	89 91
34	3	56/60 (93%)	56 (100%)	0	100 100
34	cb	55/60 (92%)	54 (98%)	1 (2%)	54 71
37	Ay	190/196 (97%)	188 (99%)	2 (1%)	70 80
37	Da	192/196 (98%)	190 (99%)	2 (1%)	73 81
38	By	319/323 (99%)	315 (99%)	4 (1%)	65 77
38	Ea	318/323 (98%)	317 (100%)	1 (0%)	91 92
39	Cy	288/289 (100%)	286 (99%)	2 (1%)	81 86
39	Fa	288/289 (100%)	286 (99%)	2 (1%)	81 86
40	Dy	241/245 (98%)	240 (100%)	1 (0%)	89 91
40	Ga	243/245 (99%)	241 (99%)	2 (1%)	79 84
41	Ey	137/153 (90%)	136 (99%)	1 (1%)	81 86
41	Ha	135/153 (88%)	134 (99%)	1 (1%)	81 86
42	Fy	186/205 (91%)	185 (100%)	1 (0%)	86 89
42	Ia	187/205 (91%)	186 (100%)	1 (0%)	86 89
43	Gy	187/208 (90%)	184 (98%)	3 (2%)	58 74
43	Ja	177/208 (85%)	175 (99%)	2 (1%)	70 80
44	Hy	168/171 (98%)	166 (99%)	2 (1%)	67 78
44	Ka	170/171 (99%)	167 (98%)	3 (2%)	54 71
45	Iy	185/187 (99%)	184 (100%)	1 (0%)	86 89
45	La	177/187 (95%)	176 (99%)	1 (1%)	84 88
46	Jy	146/150 (97%)	145 (99%)	1 (1%)	81 86
46	Ma	147/150 (98%)	147 (100%)	0	100 100
47	Ly	154/159 (97%)	152 (99%)	2 (1%)	65 77
47	Na	154/159 (97%)	154 (100%)	0	100 100
48	My	107/109 (98%)	107 (100%)	0	100 100
48	Oa	108/109 (99%)	108 (100%)	0	100 100
49	Ny	175/176 (99%)	175 (100%)	0	100 100
49	Pa	175/176 (99%)	175 (100%)	0	100 100
50	Oy	160/162 (99%)	160 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
50	Qa	160/162 (99%)	160 (100%)	0	100 100
51	A	139/146 (95%)	139 (100%)	0	100 100
51	Py	138/146 (94%)	136 (99%)	2 (1%)	62 75
52	B	150/151 (99%)	150 (100%)	0	100 100
52	Qy	150/151 (99%)	149 (99%)	1 (1%)	81 86
53	C	149/154 (97%)	148 (99%)	1 (1%)	81 86
53	Ry	152/154 (99%)	151 (99%)	1 (1%)	81 86
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%)	134 (98%)	2 (2%)	60 75
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%)	70 80
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%)	112 (98%)	2 (2%)	54 71
58	Wy	60/129 (46%)	60 (100%)	0	100 100
59	I	104/118 (88%)	104 (100%)	0	100 100
59	Xy	104/118 (88%)	104 (100%)	0	100 100
60	J	107/110 (97%)	107 (100%)	0	100 100
60	Yy	108/110 (98%)	108 (100%)	0	100 100
61	K	115/116 (99%)	115 (100%)	0	100 100
61	Zy	115/116 (99%)	114 (99%)	1 (1%)	75 83
62	L	118/119 (99%)	118 (100%)	0	100 100
62	ay	118/119 (99%)	118 (100%)	0	100 100
63	M	46/47 (98%)	45 (98%)	1 (2%)	47 65
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%)	81 (100%)	0	100 100
65	O	94/97 (97%)	93 (99%)	1 (1%)	70 80
65	dy	92/97 (95%)	91 (99%)	1 (1%)	70 80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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%)	93 (98%)	2 (2%)	48 66
69	S	103/105 (98%)	103 (100%)	0	100 100
69	hb	104/105 (99%)	100 (96%)	4 (4%)	28 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%)	68 (99%)	1 (1%)	62 75
72	V	67/69 (97%)	67 (100%)	0	100 100
72	kb	68/69 (99%)	67 (98%)	1 (2%)	60 75
73	W	45/46 (98%)	45 (100%)	0	100 100
73	lb	45/46 (98%)	44 (98%)	1 (2%)	47 65
74	X	47/116 (40%)	46 (98%)	1 (2%)	48 66
74	mb	47/116 (40%)	47 (100%)	0	100 100
75	Y	23/23 (100%)	21 (91%)	2 (9%)	8 29
75	nb	22/23 (96%)	22 (100%)	0	100 100
76	Z	90/91 (99%)	89 (99%)	1 (1%)	70 80
76	ob	87/91 (96%)	86 (99%)	1 (1%)	70 80
77	aa	71/72 (99%)	69 (97%)	2 (3%)	38 59
77	pb	71/72 (99%)	71 (100%)	0	100 100
80	ba	105/253 (42%)	103 (98%)	2 (2%)	52 70
All	All	18566/20221 (92%)	18432 (99%)	134 (1%)	80 86

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	Ka	63	LYS
53	C	85	ARG
77	aa	48	LYS

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Mol	Chain	Res	Type
40	Dy	271	LYS
39	Cy	259	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 239 such sidechains are listed below:

Mol	Chain	Res	Type
68	gy	108	GLN
65	O	57	GLN
20	t	44	ASN
63	M	19	ASN
76	Z	105	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2b	1768/1800 (98%)	638 (36%)	0
1	a	1755/1800 (97%)	533 (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%)	879 (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%)	3003 (28%)	0

5 of 3003 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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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

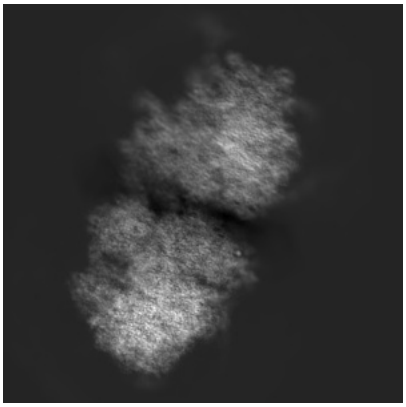
6 Map visualisation

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.

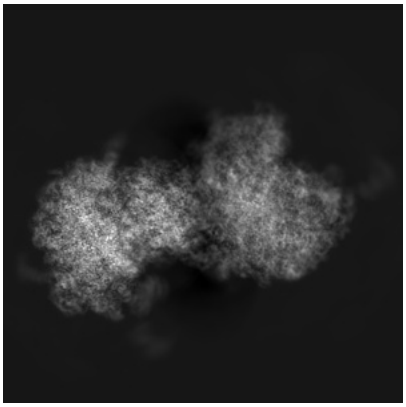
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

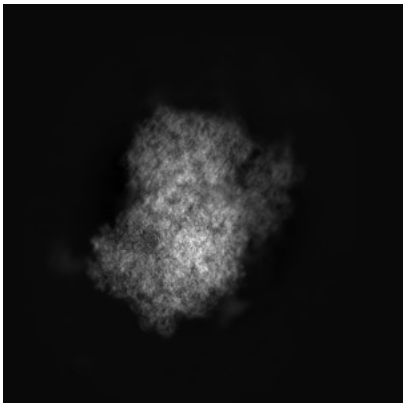
6.1.1 Primary map



X



Y

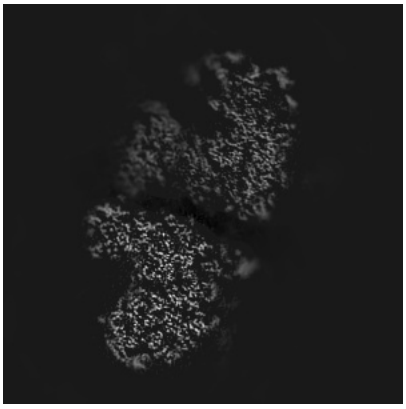


Z

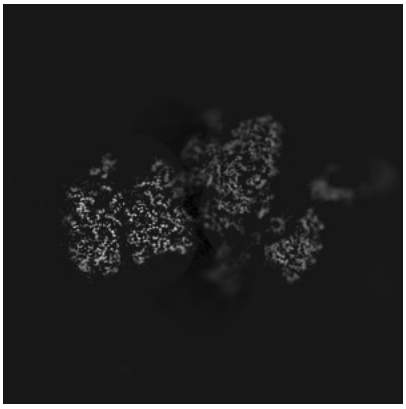
The images above show the map projected in three orthogonal directions.

6.2 Central slices

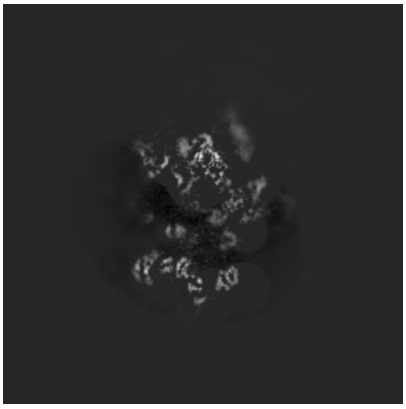
6.2.1 Primary map



X Index: 265



Y Index: 265

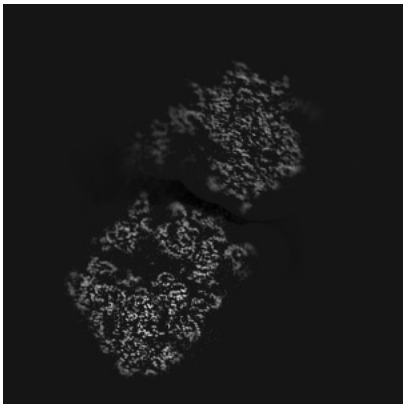


Z Index: 265

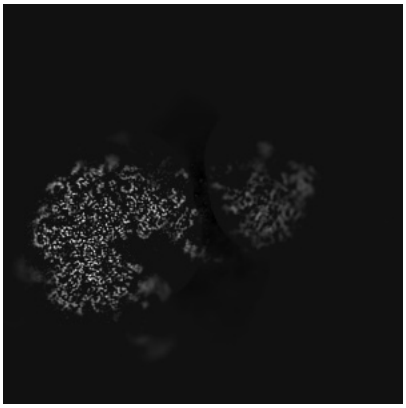
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

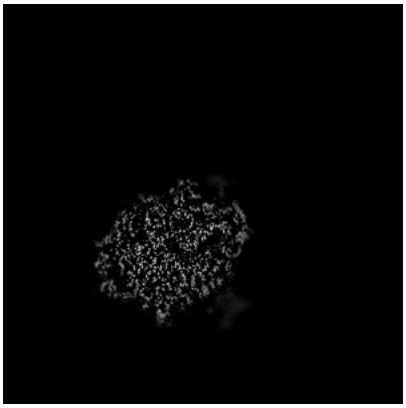
6.3.1 Primary map



X Index: 218



Y Index: 197

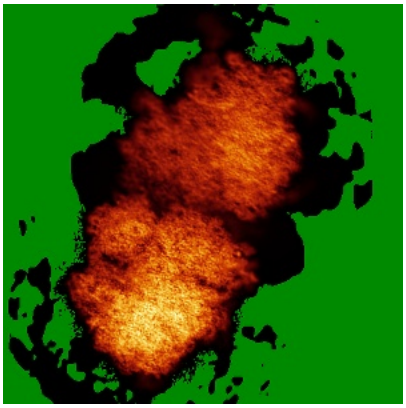


Z Index: 119

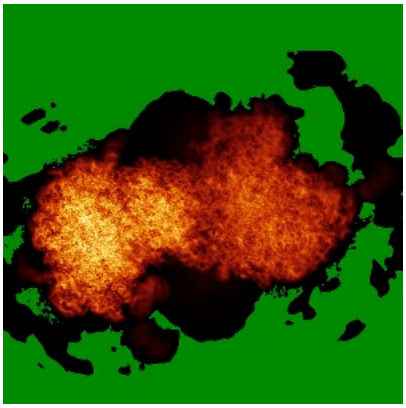
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

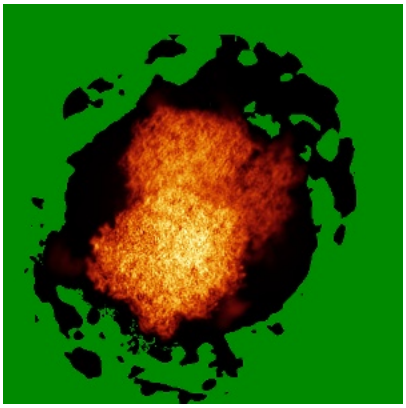
6.4.1 Primary map



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.

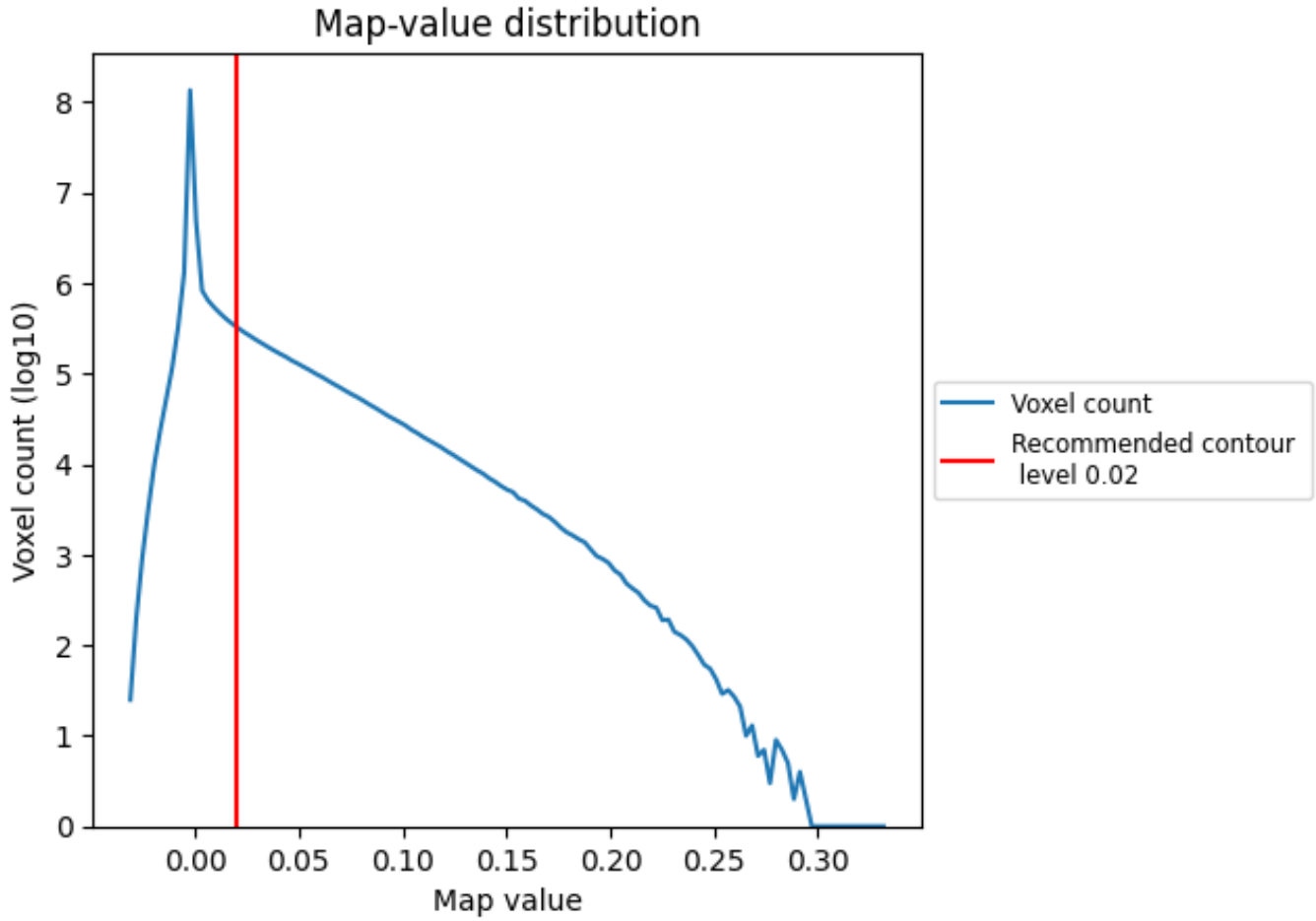
6.6 Mask visualisation (i)

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

7 Map analysis

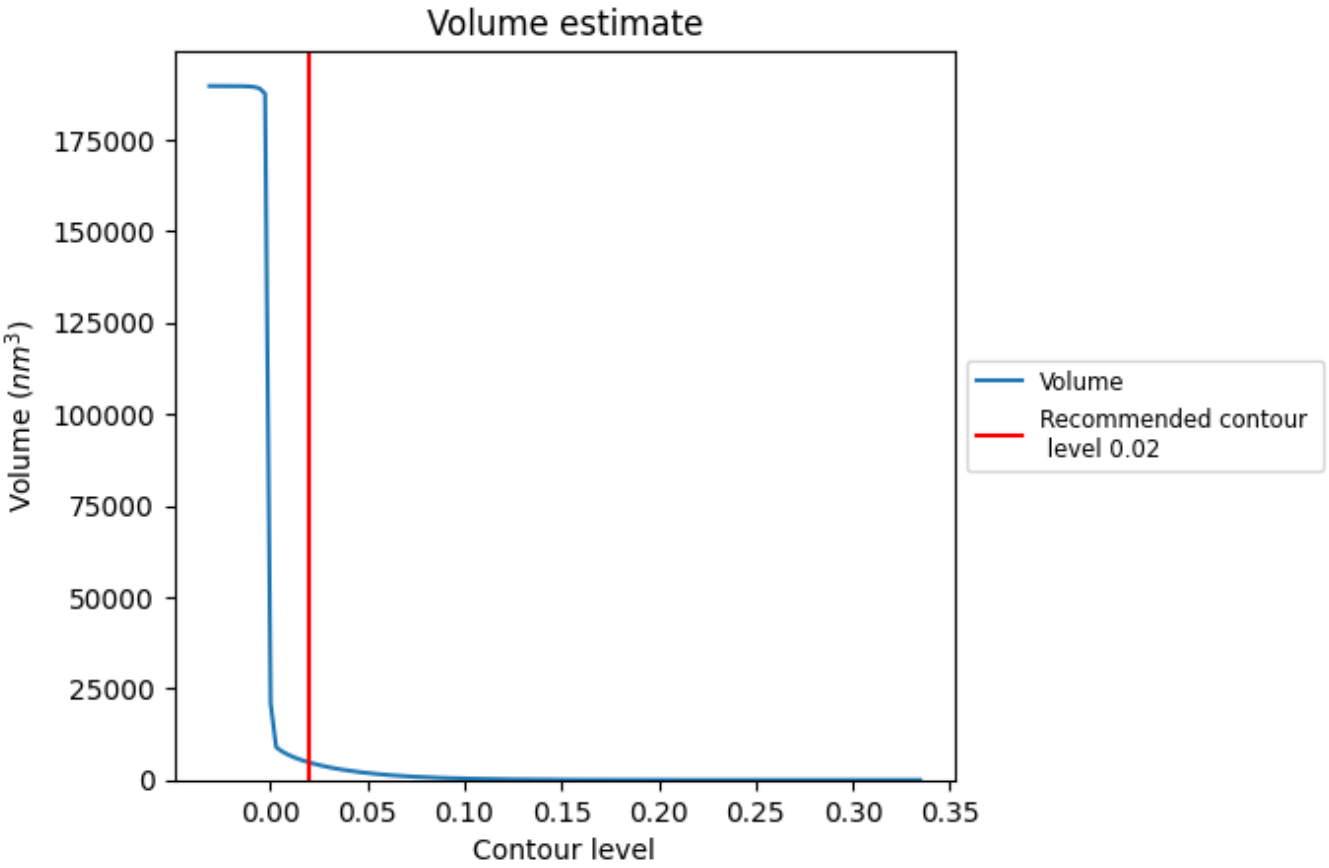
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

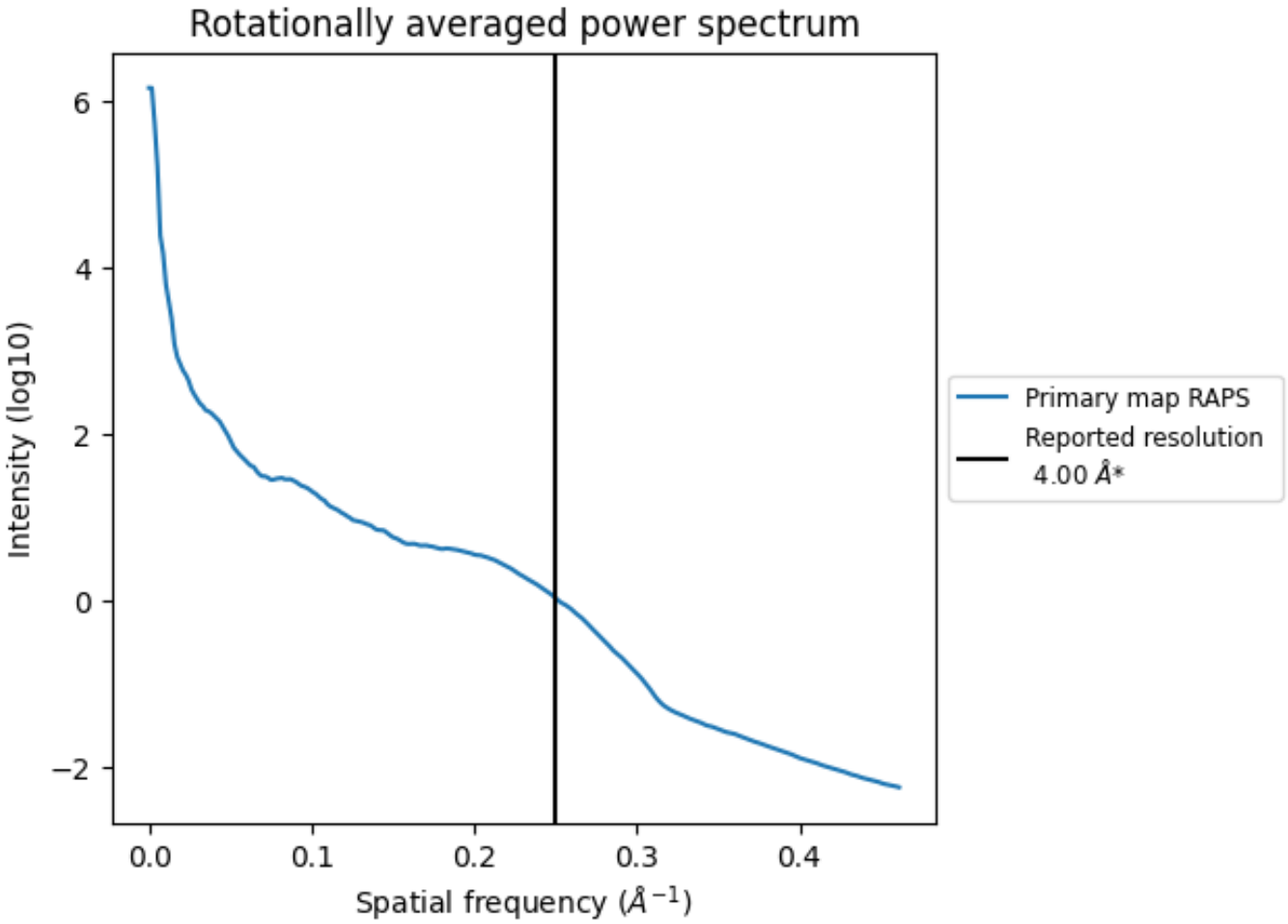
7.2 Volume estimate (i)



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 (i)



*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

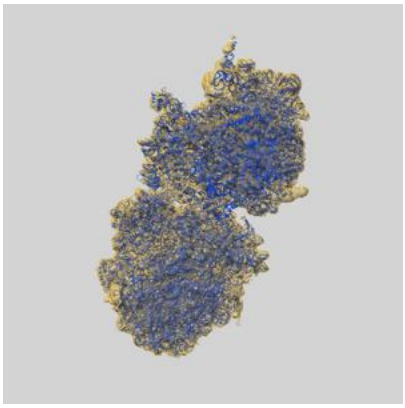
8 Fourier-Shell correlation

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

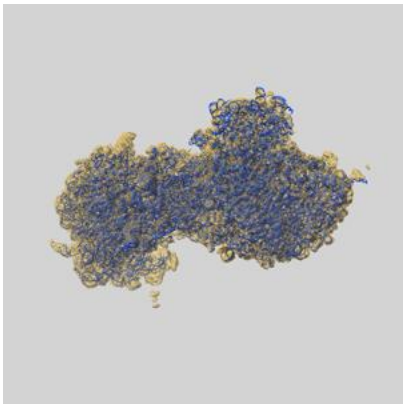
9 Map-model fit

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.

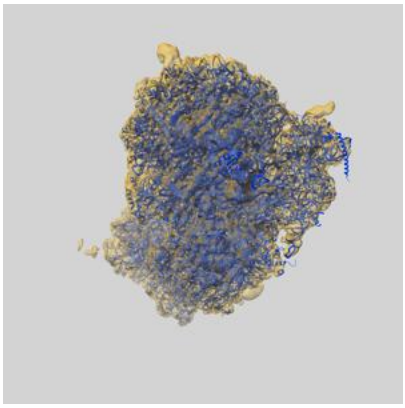
9.1 Map-model overlay



X



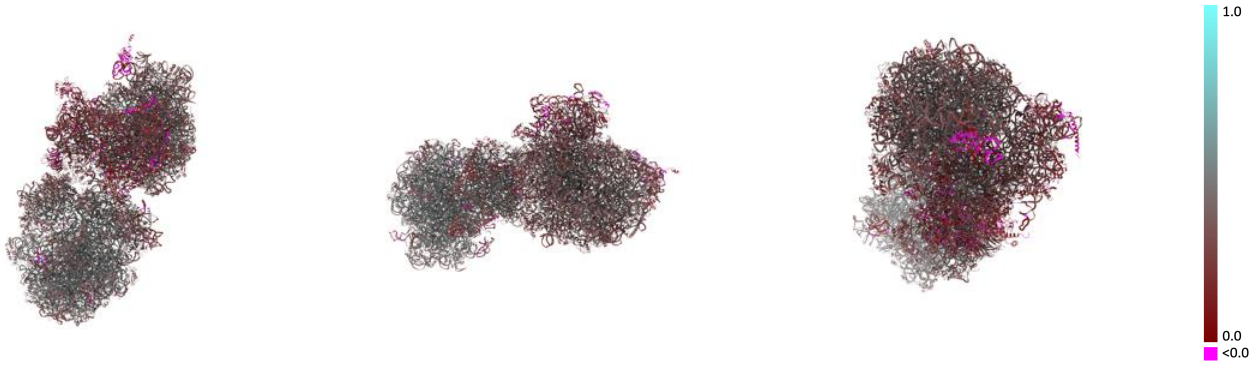
Y



Z

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.

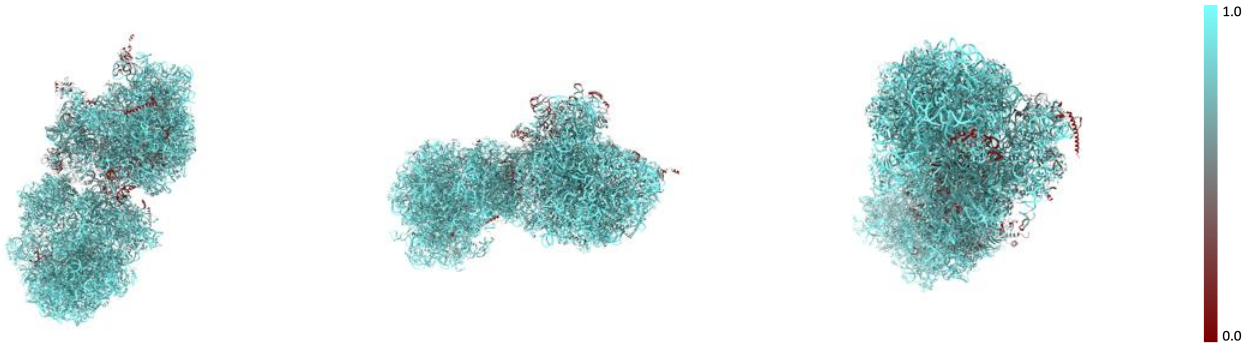
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

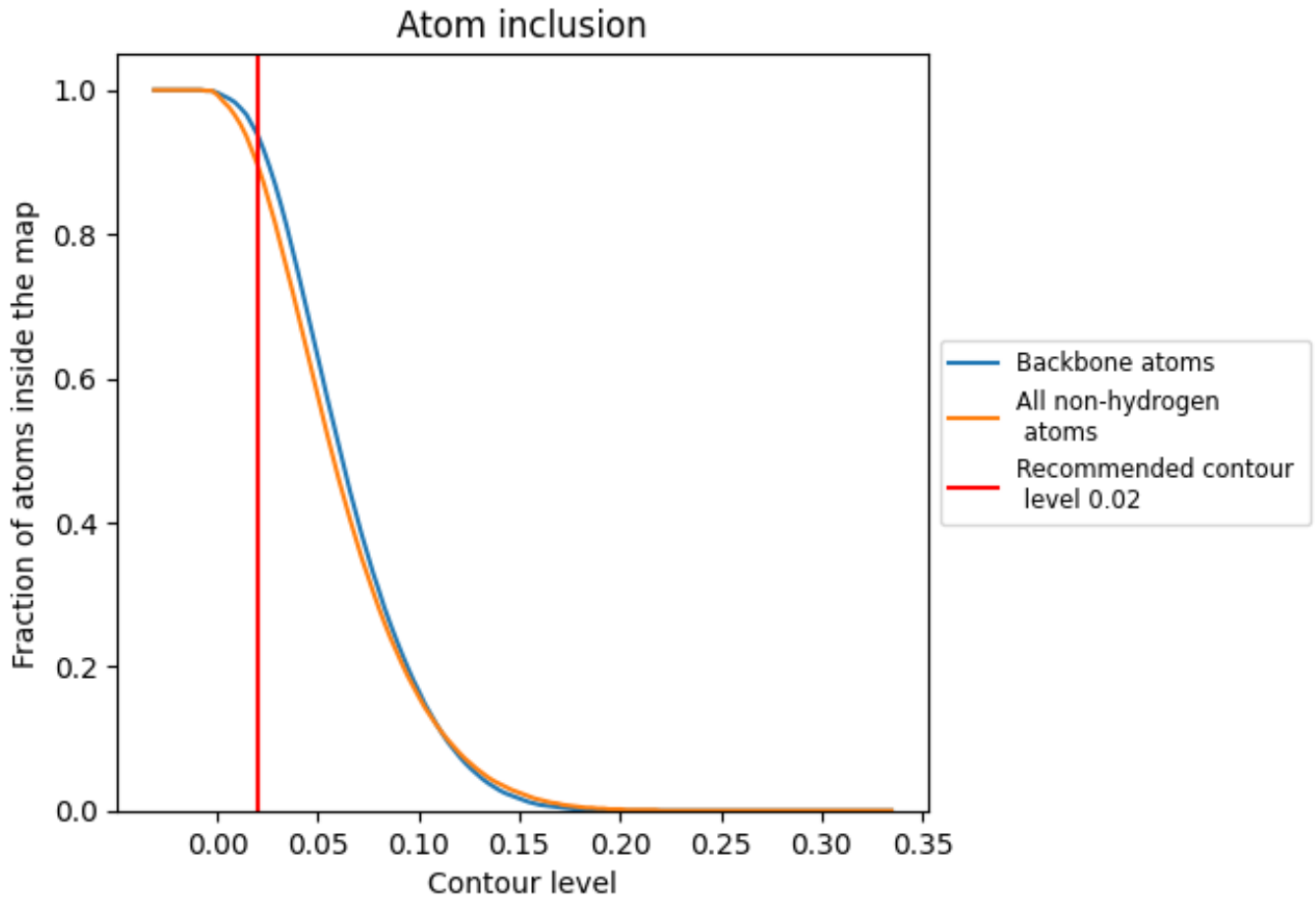
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (i)



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	0.0160
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