wwPDB EM Validation Summary Report

Dec 8, 2024 – 09:57 am GMT

PDB ID	:	9F9S
EMDB ID	:	EMD-50259
Title	:	Yeast SDD1 Disome with Mbf1
Authors	:	Denk, T.; Beckmann, R.
Deposited on	:	2024-05-08
Resolution	:	2.90 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:

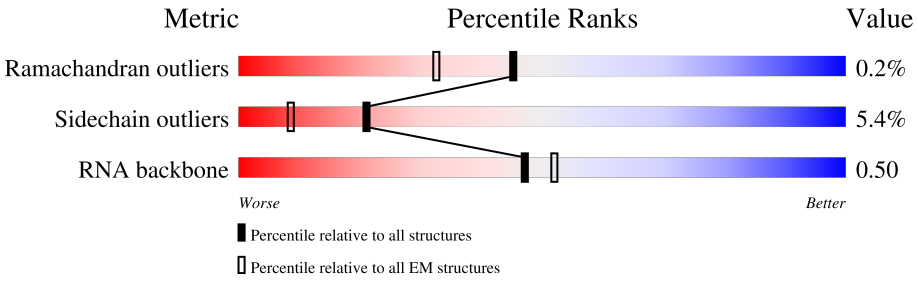
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 2.90 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	CC	233	5% · 94%
2	CM	41	17% 56% 39% 5%
3	CN	151	5% 85% 5% 10%
4	CP	76	5% 86% 13% ·
5	L1	3396	· 73% 18% · 8%
6	L2	158	· 82% 18% ·
6	M2	158	· 84% 16%
7	L3	121	88% 12%

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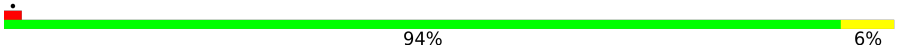
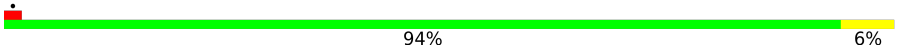
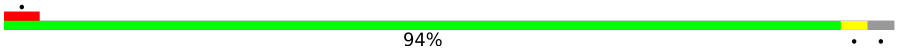
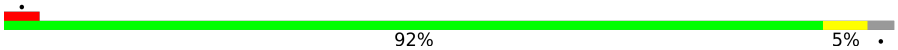
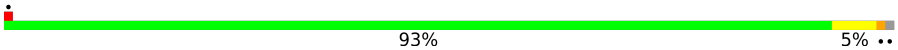
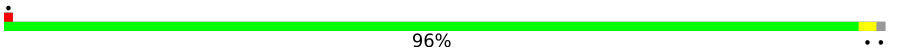
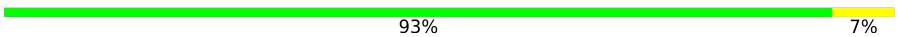
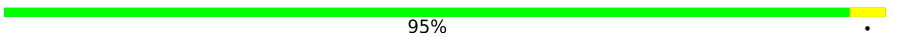
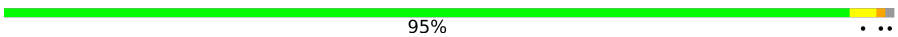
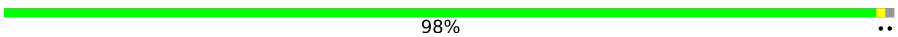
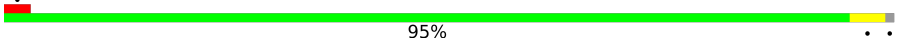
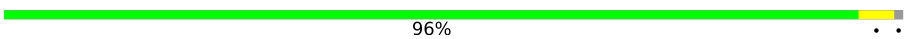
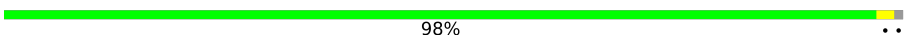
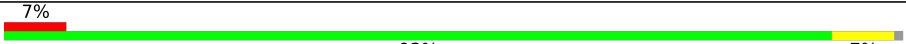
Mol	Chain	Length	Quality of chain
7	M3	121	
8	LA	176	
9	LB	244	
9	MB	244	
10	LC	256	
10	MC	256	
11	LD	191	
11	MD	191	
12	LE	221	
12	ME	221	
13	LF	174	
13	MF	174	
14	LG	199	
14	MG	199	
15	LH	138	
15	MH	138	
16	LI	204	
16	MI	204	
17	LJ	199	
17	MJ	199	
18	LK	184	
18	MK	184	
19	LL	186	
19	ML	186	
20	LM	189	

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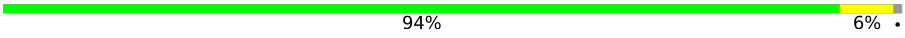
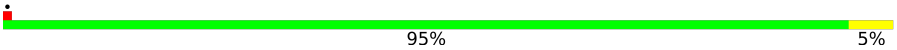
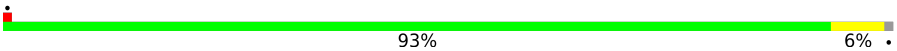
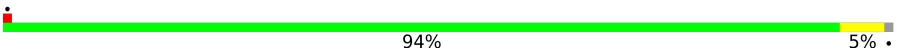
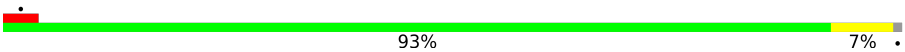
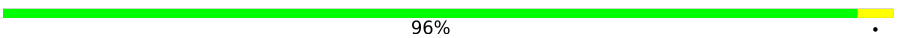
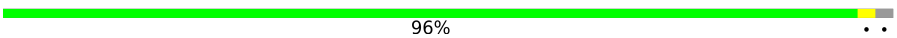
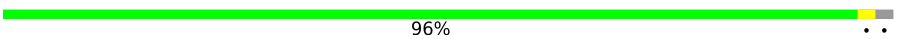
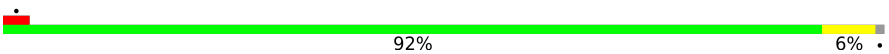
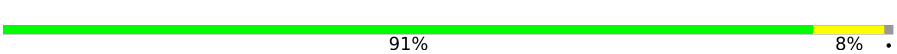
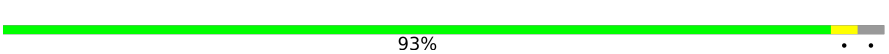
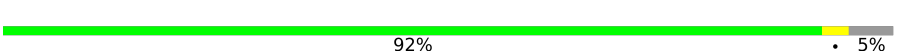
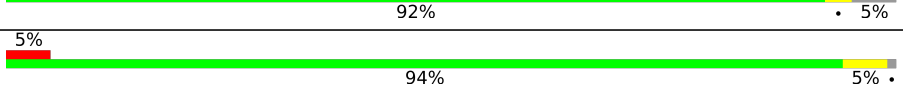
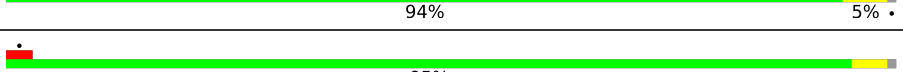
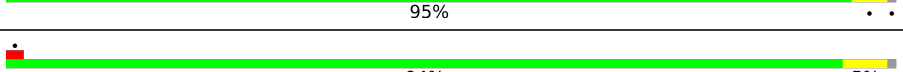
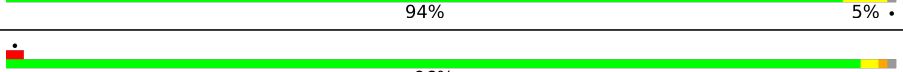
Mol	Chain	Length	Quality of chain
20	MM	189	
21	LN	172	
21	MN	172	
22	LO	160	
22	MO	160	
23	La	137	
23	Ma	137	
24	Lb	92	
24	Mb	92	
25	Lc	106	
25	Mc	106	
26	Ld	25	
26	Md	25	
27	Le	128	
27	Me	128	
28	Lf	51	
28	Mf	51	
29	Lg	78	
29	Mg	78	
30	Lh	88	
30	Mh	88	
31	Li	100	
31	Mi	100	
32	Lj	120	
32	Mj	120	

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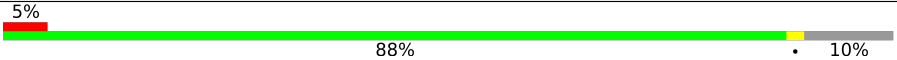
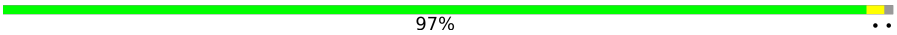
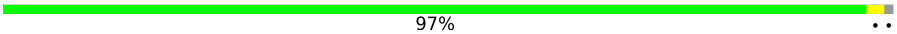
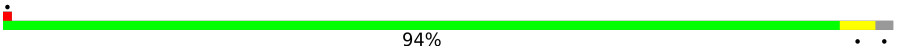
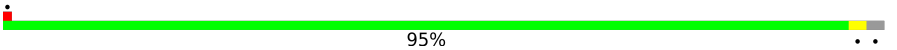
Mol	Chain	Length	Quality of chain
33	Lk	121	
33	Mk	121	
34	Ll	107	
34	Ml	107	
35	Lm	130	
35	Mm	130	
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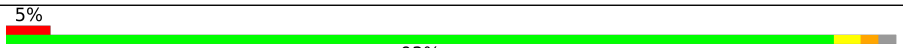
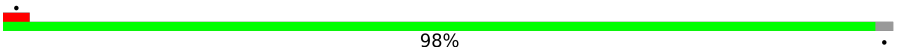
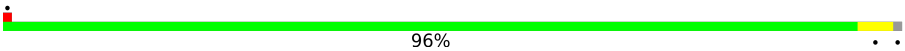
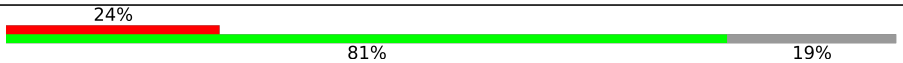
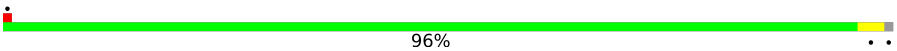
36	Mn	113	
37	Lo	105	
37	Mo	105	
38	Lp	59	
38	Mp	59	
39	Lq	149	
39	Mq	149	
40	Lr	136	
40	Mr	136	
41	Ls	127	
41	Ms	127	
42	Lt	142	
42	Mt	142	
43	Lu	155	
43	Mu	155	
44	Lv	121	
44	Mv	121	
45	Lw	254	

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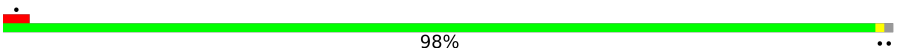
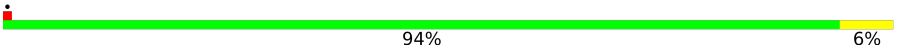
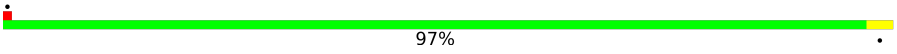
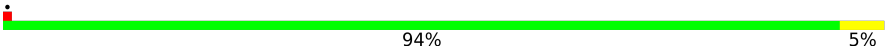
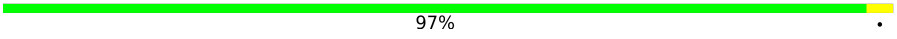
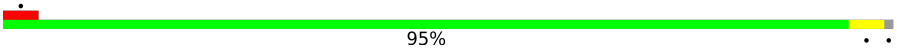
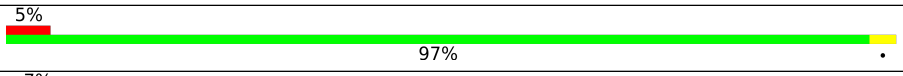
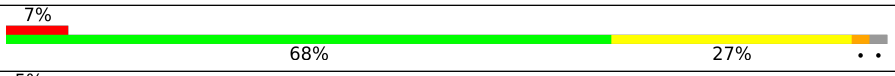
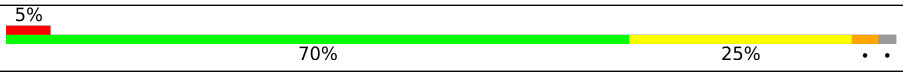
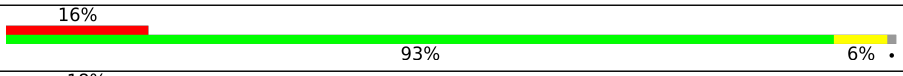
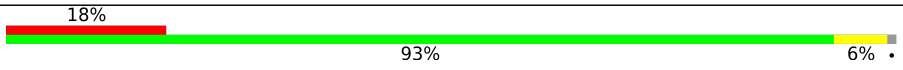
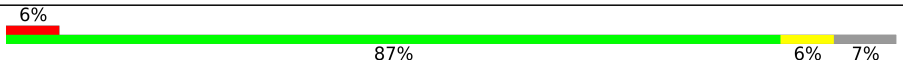
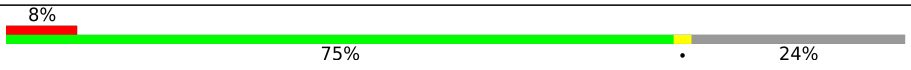
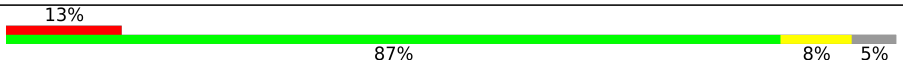
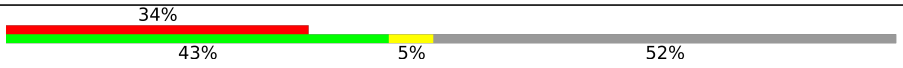
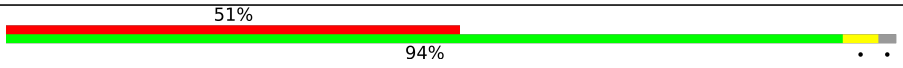
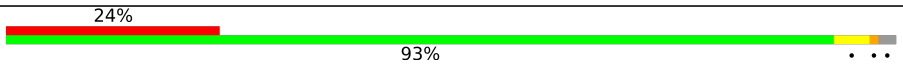
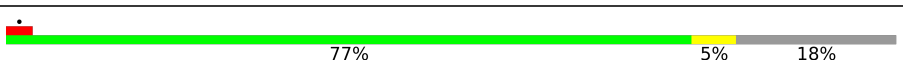
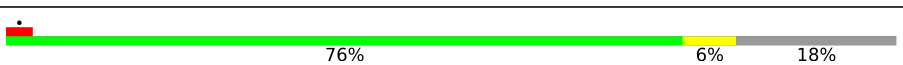
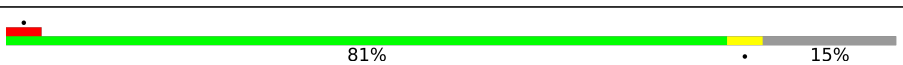
Mol	Chain	Length	Quality of chain
45	Mw	254	
46	Lx	387	
46	Mx	387	
47	Ly	362	
47	My	362	
48	Lz	297	
48	Mz	297	
49	R1	1800	
49	S1	1800	
50	RA	119	
50	SA	119	
51	RB	82	
51	SB	82	
52	SC	67	
53	RD	56	
53	SD	56	
54	RE	63	
54	SE	63	
55	RF	152	
55	SF	152	
56	RG	319	
56	SG	319	
57	Ra	252	
57	Sa	252	
58	Rb	255	

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Mol	Chain	Length	Quality of chain
58	Sb	255	5% 80% 7% 11%
59	Rc	254	84% 15%
59	Sc	254	81% 15%
60	Rd	240	15% 85% 7% 7%
60	Sd	240	5% 87% 5% 8%
61	Re	261	96%
61	Se	261	94% 5%
62	Rf	225	12% 89% 8%
62	Sf	225	7% 88% 8%
63	Rg	236	9% 89% 8%
63	Sg	236	7% 90% 6%
64	Rh	190	22% 92% 5%
64	Sh	190	19% 89% 7%
65	Ri	200	92% 6%
65	Si	200	88% 6%
66	Rj	197	10% 89% 6%
66	Sj	197	87% 7% 7%
67	Rk	105	25% 82% 6% 12%
67	Sk	105	12% 73% 13% 12%
68	Rl	156	8% 88% 6% 6%
68	Sl	156	5% 87% 6% 8%
69	Rm	143	70% 80% 7% 13%
69	Sm	143	66% 73% 10% 15%
70	Rn	151	93% 5%
70	Sn	151	93% 7%

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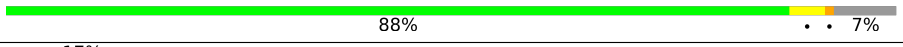
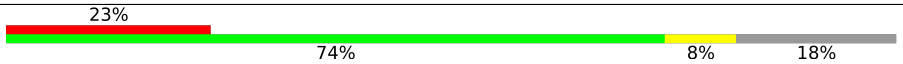
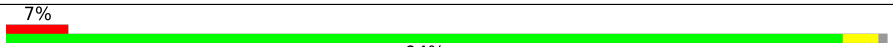
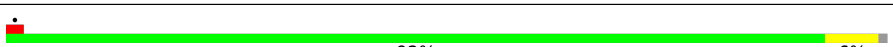
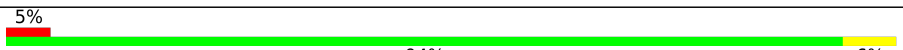
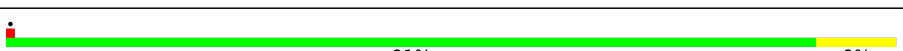
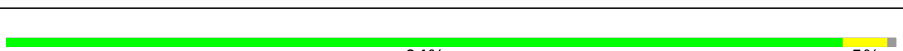
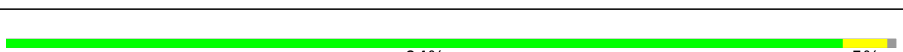
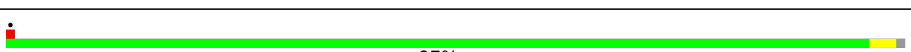
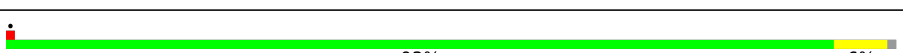
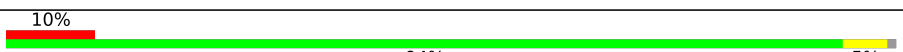
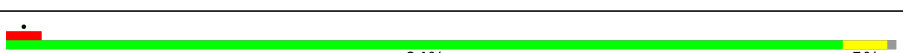
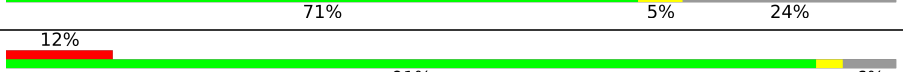
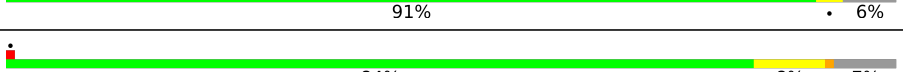
Mol	Chain	Length	Quality of chain
71	So	137	
72	Rp	142	
72	Sp	142	
73	Rq	143	
73	Sq	143	
74	Sr	136	
75	Rs	146	
75	Ss	146	
76	Rt	144	
76	St	144	
77	Ru	121	
77	Su	121	
78	Rv	87	
78	Sv	87	
79	Rw	130	
79	Sw	130	
80	Rx	145	
80	Sx	145	
81	Ry	135	
81	Sy	135	
82	Rz	108	
82	Sz	108	
83	RC	67	
84	Ro	138	
85	Rr	136	

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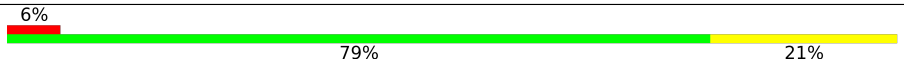
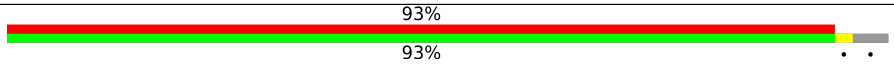
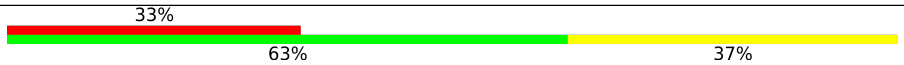
Mol	Chain	Length	Quality of chain
86	MA	176	
87	M1	3396	
88	DQ	77	
89	MQ	312	
90	MP	165	
91	DP	76	

2 Entry composition (i)

There are 95 unique types of molecules in this entry. The entry contains 406583 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 protein called Uncharacterized protein YEL057C.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CC	14	Total	C	N	O	S	0	0
			129	85	21	22	1		

- Molecule 2 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CM	41	Total	C	N	O	P	0	0
			838	377	108	312	41		

- Molecule 3 is a protein called Multiprotein-bridging factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CN	136	Total	C	N	O	S	0	0
			1046	636	210	199	1		

- Molecule 4 is a RNA chain called tRNA P-site, stalled.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CP	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 5 is a RNA chain called Saccharomyces cerevisiae S288C 25S ribosomal RNA (RDN25-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L1	3116	Total	C	N	O	P	0	0
			66660	29774	12025	21745	3116		

- Molecule 6 is a RNA chain called Saccharomyces cerevisiae S288C 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	M2	158	Total 3353	C 1500	N 586	O 1109	P 158	0	0

- Molecule 7 is a RNA chain called Saccharomyces cerevisiae S288C 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L3	121	Total 2579	C 1152	N 461	O 845	P 121	0	0
7	M3	121	Total 2579	C 1152	N 461	O 845	P 121	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	LA	167	Total 1305	C 842	N 234	O 229	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LB	222	Total 1784	C 1151	N 324	O 308	S 1	0	0
9	MB	222	Total 1784	C 1151	N 324	O 308	S 1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	233	Total 1804	C 1151	N 323	O 327	S 3	0	0
10	MC	233	Total 1804	C 1151	N 323	O 327	S 3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	191	Total 1508	C 957	N 274	O 273	S 4	0	0
11	MD	191	Total 1518	C 963	N 274	O 277	S 4	0	0

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		
12	ME	215	Total	C	N	O	S	0	0
			1743	1102	331	303	7		

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		
13	MF	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	LG	193	Total	C	N	O	0	0
			1543	962	315	266		
14	MG	193	Total	C	N	O	0	0
			1543	962	315	266		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		
15	MH	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		
16	MI	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	MJ	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	LK	183	Total	C	N	O	0	0
			1416	879	284	253		
18	MK	154	Total	C	N	O	0	0
			1222	761	237	224		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LL	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		
19	ML	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	LM	188	Total	C	N	O	0	0
			1515	932	323	260		
20	MM	176	Total	C	N	O	0	0
			1423	875	308	240		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LO	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		
22	MO	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	La	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		
23	Ma	129	Total	C	N	O	S	0	0
			963	607	180	169	7		

- Molecule 24 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Lb	91	Total	C	N	O	S	0	0
			694	429	138	121	6		
24	Mb	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 25 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Lc	103	Total	C	N	O	S	0	0
			824	517	167	135	5		
25	Mc	102	Total	C	N	O	S	0	0
			819	514	166	134	5		

- Molecule 26 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ld	25	Total	C	N	O	S	0	0
			229	139	62	27	1		
26	Md	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Le	52	Total	C	N	O	S	0	0
			417	259	86	67	5		
27	Me	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 28 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lf	50	Total 436	C 272	N 97	O 65	S 2	0	0
28	Mf	50	Total 436	C 272	N 97	O 65	S 2	0	0

- Molecule 29 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Lg	77	Total 612	C 391	N 115	O 106	0	0
29	Mg	77	Total 612	C 391	N 115	O 106	0	0

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lh	85	Total 670	C 408	N 146	O 111	S 5	0	0
30	Mh	84	Total 665	C 405	N 145	O 110	S 5	0	0

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Li	99	Total 766	C 478	N 154	O 132	S 2	0	0
31	Mi	99	Total 771	C 481	N 156	O 132	S 2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lj	119	Total 969	C 615	N 186	O 167	S 1	0	0
32	Mj	119	Total 969	C 615	N 186	O 167	S 1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lk	106	Total 836	C 519	N 171	O 142	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
33	Mk	109	Total 861	C 533	N 175	O 149	S 4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ll	106	Total 850	C 540	N 165	O 144	S 1	0	0
34	Ml	106	Total 850	C 540	N 165	O 144	S 1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lm	127	Total 1017	C 644	N 205	O 167	S 1	0	0
35	Mm	127	Total 1020	C 647	N 205	O 167	S 1	0	0

- Molecule 36 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lo	96	Total 737	C 476	N 123	O 137	S 1	0	0
37	Mo	97	Total 742	C 479	N 124	O 138	S 1	0	0

- Molecule 38 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Lp	58	Total 462	C 289	N 100	O 73	0	0
38	Mp	58	Total 462	C 289	N 100	O 73	0	0

- Molecule 39 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lq	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		
39	Mq	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 40 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	Lr	135	Total	C	N	O	0	0
			1092	710	202	180		
40	Mr	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 41 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Ls	125	Total	C	N	O	0	0
			984	620	191	173		
41	Ms	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 42 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lt	121	Total	C	N	O	S	0	0
			964	620	169	173	2		
42	Mt	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 43 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lu	126	Total	C	N	O	S	0	0
			836	525	165	145	1		
43	Mu	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 44 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	Lv	100	Total 796	C 516	N 131	O 149	0	0
44	Mv	97	Total 770	C 499	N 126	O 145	0	0

- Molecule 45 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lw	251	Total 1899	C 1182	N 385	O 331	S 1	0	0
45	Mw	252	Total 1914	C 1191	N 388	O 334	S 1	0	0

- Molecule 46 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lx	386	Total 3075	C 1950	N 584	O 533	S 8	0	0
46	Mx	386	Total 3075	C 1950	N 584	O 533	S 8	0	0

- Molecule 47 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ly	361	Total 2748	C 1729	N 522	O 494	S 3	0	0
47	My	361	Total 2748	C 1729	N 522	O 494	S 3	0	0

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lz	294	Total 2351	C 1484	N 410	O 455	S 2	0	0
48	Mz	296	Total 2375	C 1501	N 414	O 458	S 2	0	0

- Molecule 49 is a RNA chain called Saccharomyces cerevisiae S288C 18S ribosomal RNA (RDN18-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S1	1771	Total 37739	C 16872	N 6683	O 12413	P 1771	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
49	R1	1758	Total 37455	C 16745	N 6624	O 12328	P 1758	0	0

- Molecule 50 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	97	Total 769	C 475	N 160	O 129	S 5	0	0
50	RA	97	Total 769	C 475	N 160	O 129	S 5	0	0

- Molecule 51 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	81	Total 610	C 382	N 110	O 113	S 5	0	0
51	RB	81	Total 610	C 382	N 110	O 113	S 5	0	0

- Molecule 52 is a protein called Small ribosomal subunit protein eS28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	62	Total 486	C 300	N 95	O 90	S 1	0	0

- Molecule 53 is a protein called Small ribosomal subunit protein uS14A.

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

- Molecule 54 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	60	Total 472	C 298	N 97	O 76	S 1	0	0
54	RE	48	Total 385	C 246	N 77	O 62		0	0

- Molecule 55 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	73	Total	C	N	O	S	0	0
			556	352	105	95	4		
55	RF	72	Total	C	N	O	S	0	0
			547	347	104	92	4		

- Molecule 56 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		
56	RG	313	Total	C	N	O	S	0	0
			2403	1521	411	463	8		

- Molecule 57 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 58 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Sb	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		
58	Rb	216	Total	C	N	O	S	0	0
			1722	1091	312	315	4		

- Molecule 59 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Sc	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		
59	Rc	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 60 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Sd	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
60	Rd	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 61 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Se	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		
61	Re	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 62 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Sf	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		
62	Rf	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 63 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Sg	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		
63	Rg	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 64 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	Sh	184	Total	C	N	O	0	0
			1473	946	263	264		
64	Rh	185	Total	C	N	O	0	0
			1486	954	266	266		

- Molecule 65 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Si	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		
65	Ri	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 66 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sj	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		
66	Rj	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 67 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sk	92	Total	C	N	O	S	0	0
			752	487	122	141	2		
67	Rk	92	Total	C	N	O	S	0	0
			741	478	121	140	2		

- Molecule 68 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sl	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		
68	Rl	146	Total	C	N	O	S	0	0
			1168	747	221	197	3		

- Molecule 69 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sm	121	Total	C	N	O	S	0	0
			875	551	153	169	2		
69	Rm	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 70 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sn	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		
70	Rn	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 71 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	So	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 72 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sp	117	Total	C	N	O	S	0	0
			916	583	171	155	7		
72	Rp	119	Total	C	N	O	S	0	0
			939	595	176	161	7		

- Molecule 73 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	Sq	141	Total	C	N	O	0	0
			1105	708	203	194		
73	Rq	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 74 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sr	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 75 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ss	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		
75	Rs	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 76 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	St	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		
76	Rt	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 77 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Su	100	Total	C	N	O	S	0	0
			797	506	144	146	1		
77	Ru	101	Total	C	N	O	S	0	0
			805	512	145	147	1		

- Molecule 78 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sv	87	Total	C	N	O	S	0	0
			673	415	125	131	2		
78	Rv	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 79 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sw	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		
79	Rw	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 80 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sx	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		
80	Rx	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 81 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Sy	134	Total	C	N	O	0	0
			1073	676	208	189		
81	Ry	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 82 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	Sz	82	Total	C	N	O	0	0
			651	416	123	112		

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Mol	Chain	Residues	Atoms				AltConf	Trace
82	Rz	69	Total 558	C 357	N 103	O 98	0	0

- Molecule 83 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	RC	63	Total 497	C 306	N 99	O 91	S 1	0	0

- Molecule 84 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Ro	128	Total 949	C 582	N 188	O 176	S 3	0	0

- Molecule 85 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Rr	125	Total 1000	C 625	N 188	O 185	S 2	0	0

- Molecule 86 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	MA	155	Total 1230	C 795	N 221	O 213	S 1	0	0

- Molecule 87 is a RNA chain called Saccharomyces cerevisiae S288C 18S ribosomal RNA (RDN18-1) with modifications.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	M1	3190	Total 68285	C 30524	N 12313	O 22258	P 3190	0	0

- Molecule 88 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	DQ	77	Total 1644	C 732	N 298	O 537	P 77	0	0

- Molecule 89 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	MQ	197	Total	C	N	O	S	0	0
			1531	980	266	281	4		

- Molecule 90 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	MP	158	Total	C	N	O	S	0	0
			1196	750	216	228	2		

- Molecule 91 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	DP	76	Total	C	N	O	P	0	0
			1638	736	294	533	75		

- Molecule 92 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
92	CP	1	Total	Mg	0
			1	1	
92	S1	84	Total	Mg	0
			84	84	
92	Sf	1	Total	Mg	0
			1	1	
92	Sx	1	Total	Mg	0
			1	1	
92	M1	194	Total	Mg	0
			194	194	
92	MK	1	Total	Mg	0
			1	1	
92	M3	4	Total	Mg	0
			4	4	
92	M2	3	Total	Mg	0
			3	3	
92	MM	1	Total	Mg	0
			1	1	
92	Mx	1	Total	Mg	0
			1	1	
92	Ma	1	Total	Mg	0
			1	1	
92	ME	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
92	MI	2	Total Mg 2 2	0

- Molecule 93 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
93	Lb	1	Total Zn 1 1	0
93	Lc	1	Total Zn 1 1	0
93	Le	1	Total Zn 1 1	0
93	Lh	1	Total Zn 1 1	0
93	Lk	1	Total Zn 1 1	0
93	SD	1	Total Zn 1 1	0
93	SF	1	Total Zn 1 1	0
93	RB	1	Total Zn 1 1	0
93	Mk	1	Total Zn 1 1	0
93	Mh	1	Total Zn 1 1	0
93	Me	1	Total Zn 1 1	0
93	Mc	1	Total Zn 1 1	0
93	Mb	1	Total Zn 1 1	0

- Molecule 94 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
94	M1	11	Total K 11 11	0
94	Mw	1	Total K 1 1	0
94	ME	1	Total K 1 1	0

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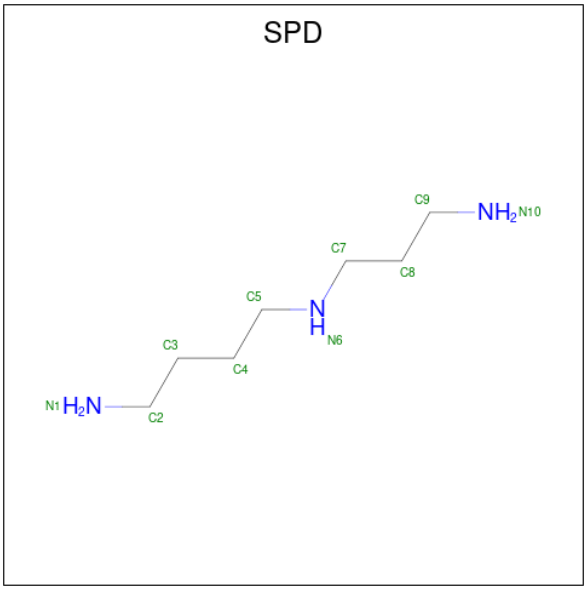
Mol	Chain	Residues	Atoms	AltConf
94	Mm	1	Total K 1 1	0
94	Mk	1	Total K 1 1	0
94	Mc	1	Total K 1 1	0

- Molecule 95 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



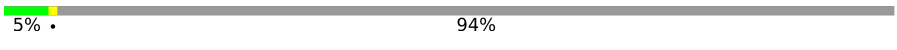
Mol	Chain	Residues	Atoms	AltConf
95	M1	1	Total C N 10 7 3	0
95	M1	1	Total C N 10 7 3	0
95	M1	1	Total C N 10 7 3	0

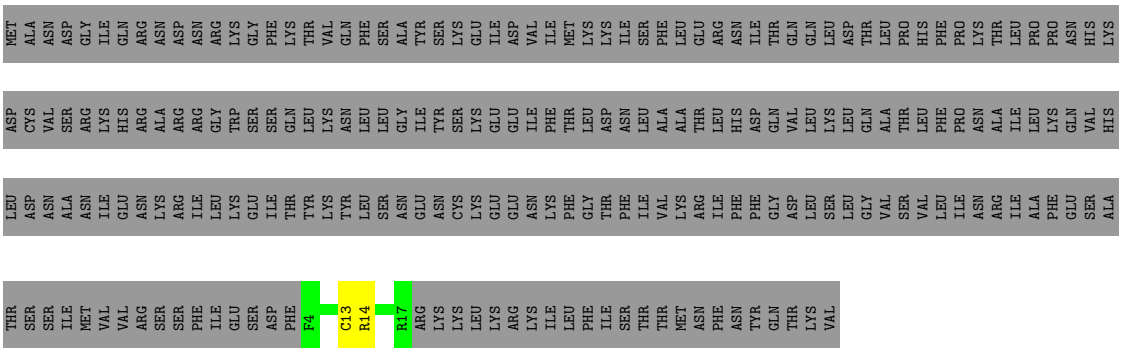
3 Residue-property plots (i)

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: Uncharacterized protein YEL057C

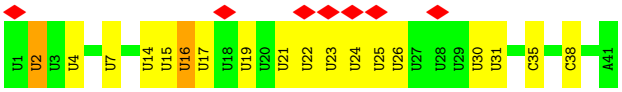
Chain CC:





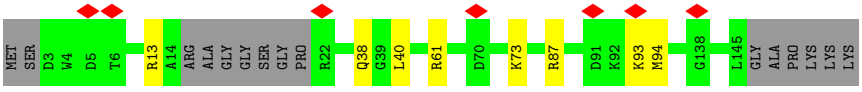
• Molecule 2: mRNA

Chain CM:



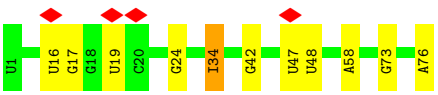
• Molecule 3: Multiprotein-bridging factor 1

Chain CN:



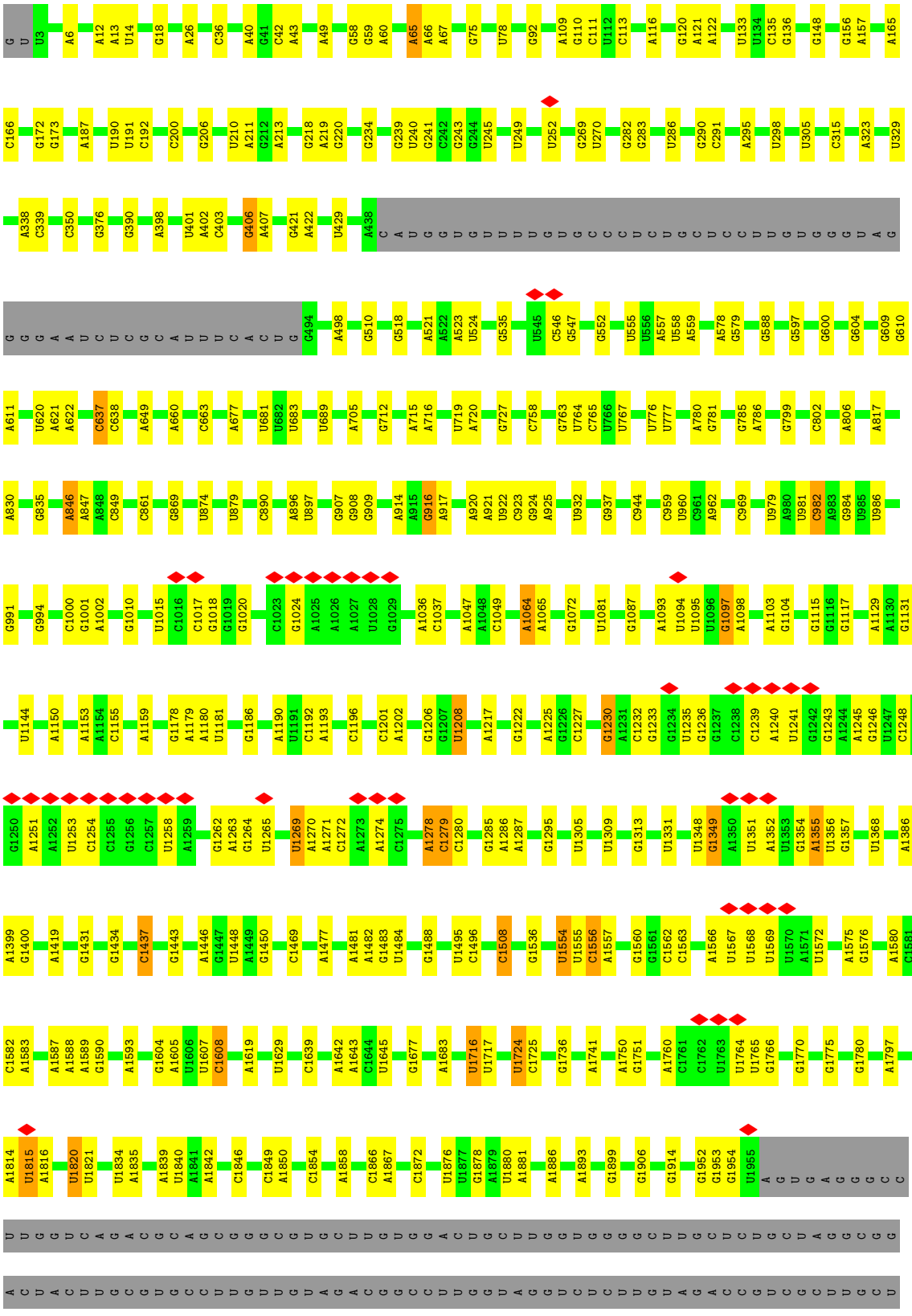
• Molecule 4: tRNA P-site, stalled

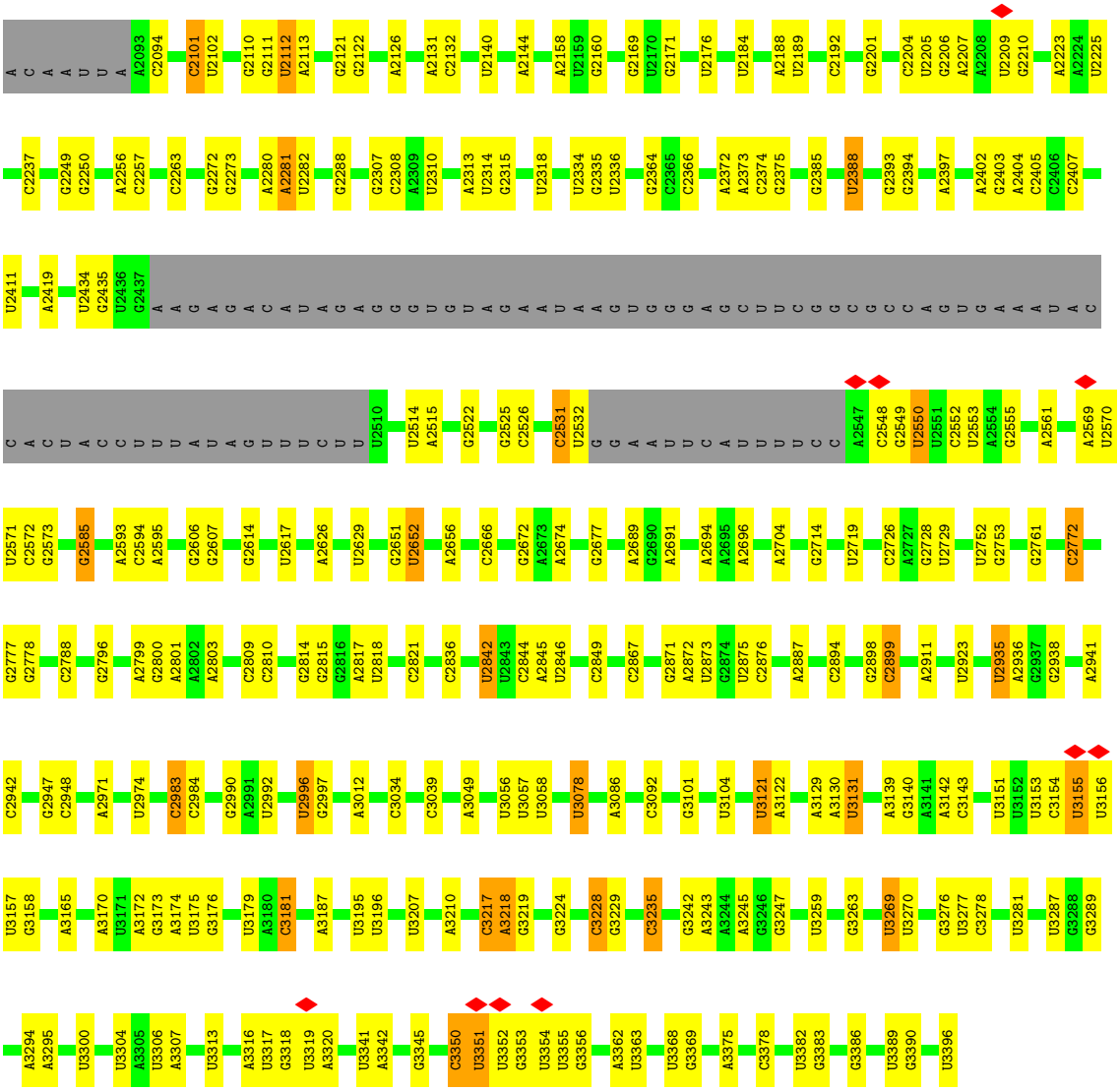
Chain CP:



• Molecule 5: Saccharomyces cerevisiae S288C 25S ribosomal RNA (RDN25-1)

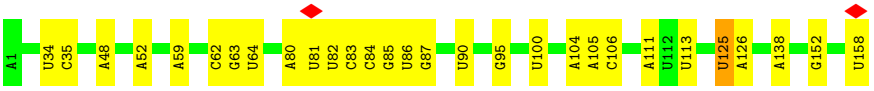
Chain L1:





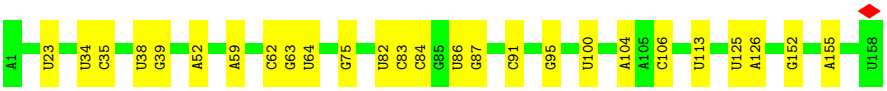
• Molecule 6: Saccharomyces cerevisiae S288C 5.8S ribosomal RNA

Chain L2:



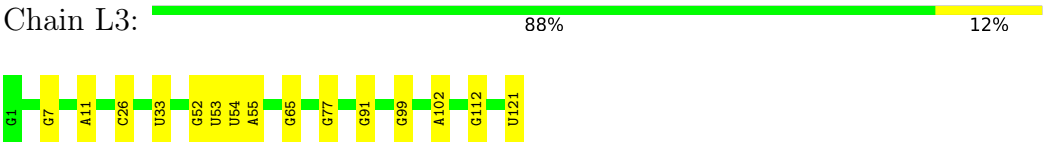
• Molecule 6: Saccharomyces cerevisiae S288C 5.8S ribosomal RNA

Chain M2:



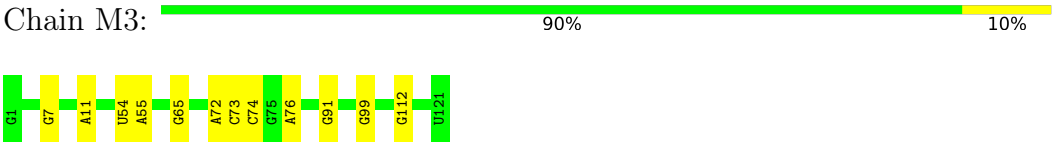
• Molecule 7: Saccharomyces cerevisiae S288C 5S ribosomal RNA

Chain L3:



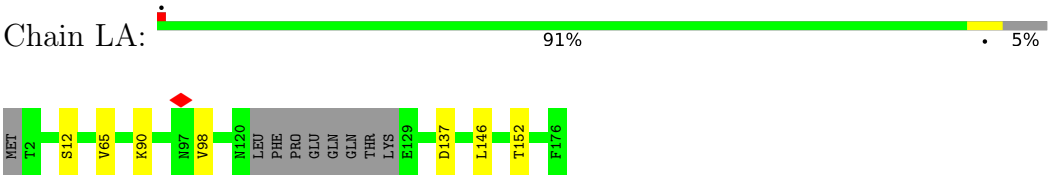
• Molecule 7: Saccharomyces cerevisiae S288C 5S ribosomal RNA

Chain M3:



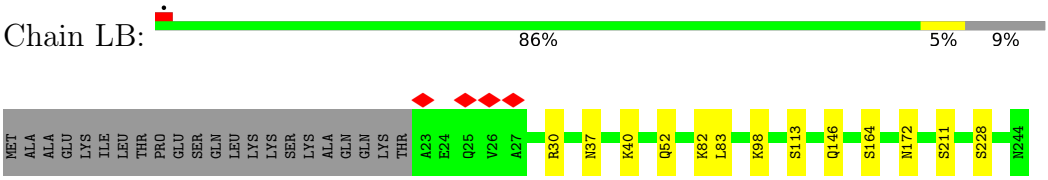
• Molecule 8: 60S ribosomal protein L6-B

Chain LA:



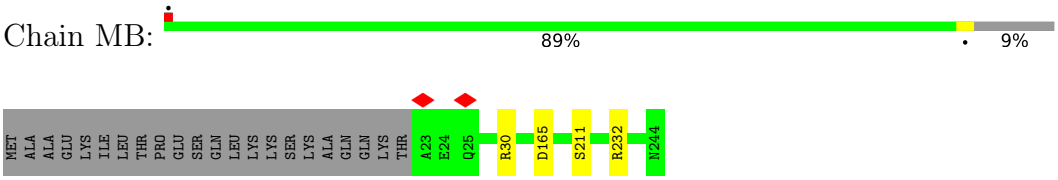
• Molecule 9: 60S ribosomal protein L7-A

Chain LB:



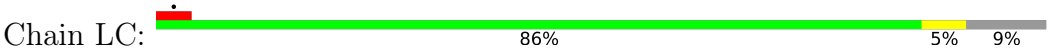
• Molecule 9: 60S ribosomal protein L7-A

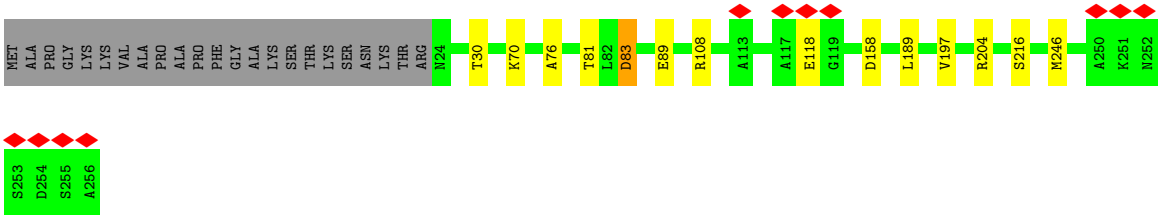
Chain MB:



• Molecule 10: 60S ribosomal protein L8-A

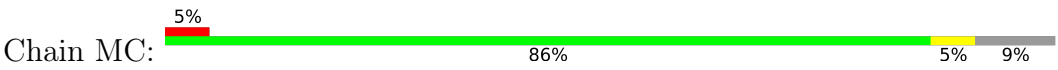
Chain LC:

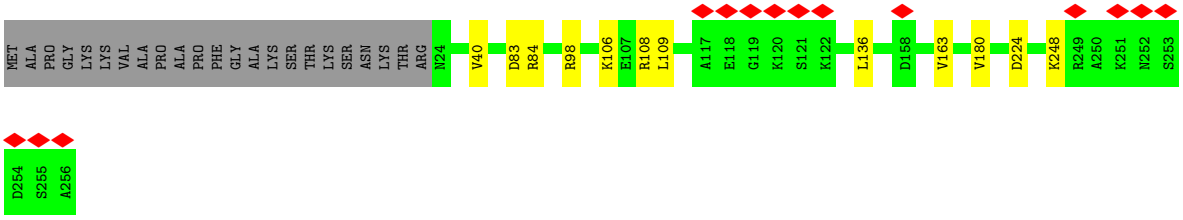




• Molecule 10: 60S ribosomal protein L8-A

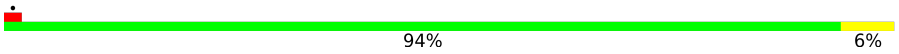
Chain MC:

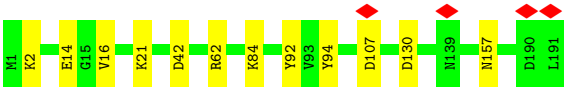




• Molecule 11: 60S ribosomal protein L9-A

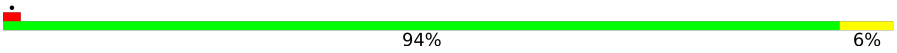
Chain LD:

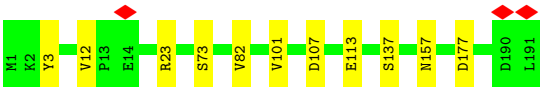




• Molecule 11: 60S ribosomal protein L9-A

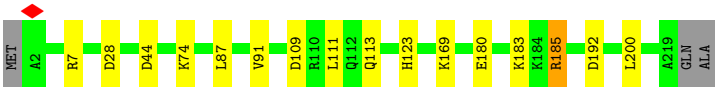
Chain MD:





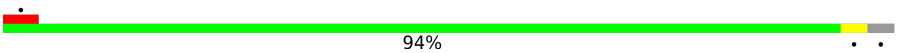
• Molecule 12: 60S ribosomal protein L10

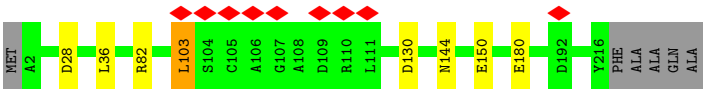
Chain LE:



• Molecule 12: 60S ribosomal protein L10

Chain ME:



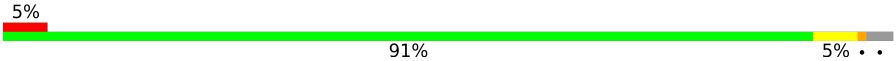


• Molecule 13: 60S ribosomal protein L11-A

Chain LF:

• Molecule 13: 60S ribosomal protein L11-A

Chain MF:

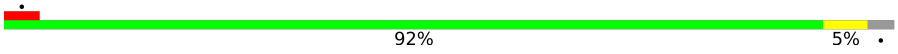


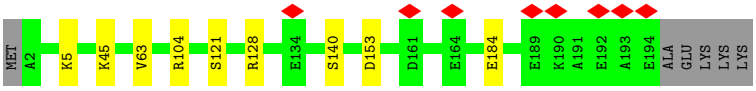
• Molecule 14: 60S ribosomal protein L13-A

Chain LG:

• Molecule 14: 60S ribosomal protein L13-A

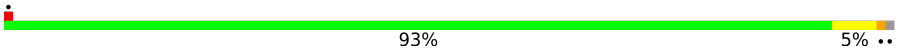
Chain MG:

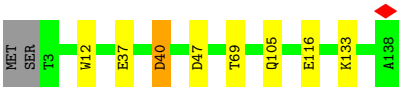




• Molecule 15: 60S ribosomal protein L14-A

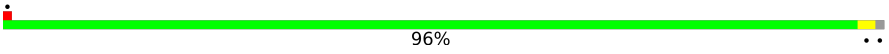
Chain LH:

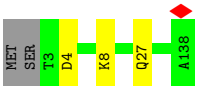




• Molecule 15: 60S ribosomal protein L14-A

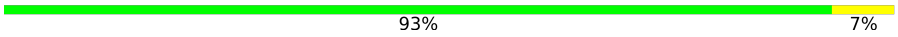
Chain MH:

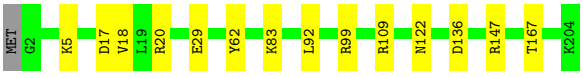




• Molecule 16: 60S ribosomal protein L15-A

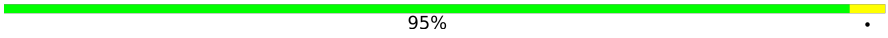
Chain LI:





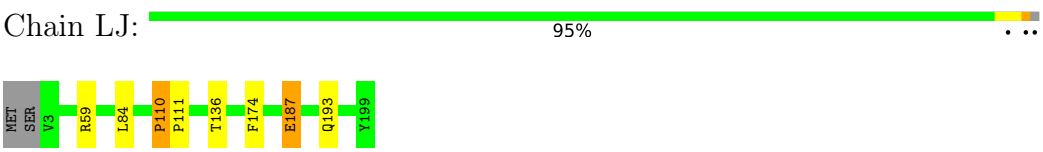
• Molecule 16: 60S ribosomal protein L15-A

Chain MI:



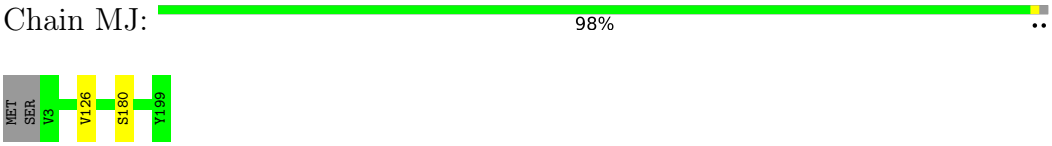
• Molecule 17: 60S ribosomal protein L16-A

Chain LJ:



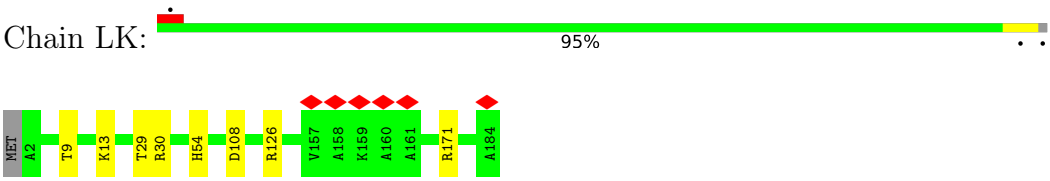
• Molecule 17: 60S ribosomal protein L16-A

Chain MJ:



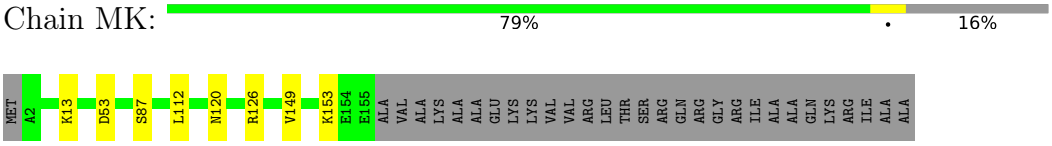
• Molecule 18: 60S ribosomal protein L17-A

Chain LK:



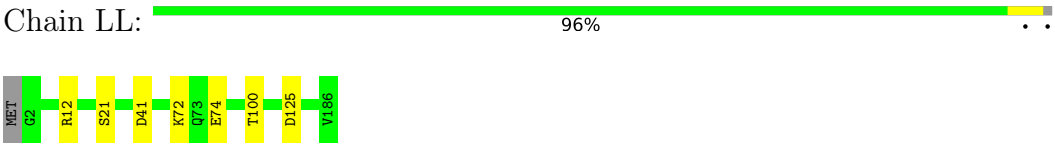
• Molecule 18: 60S ribosomal protein L17-A

Chain MK:



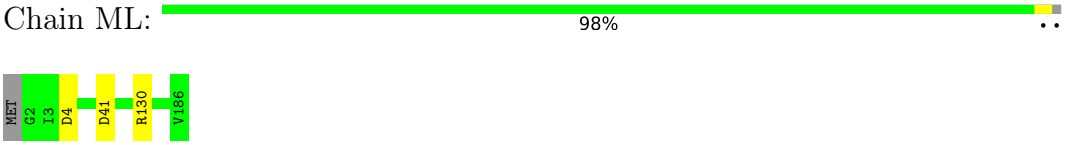
• Molecule 19: 60S ribosomal protein L18-A

Chain LL:



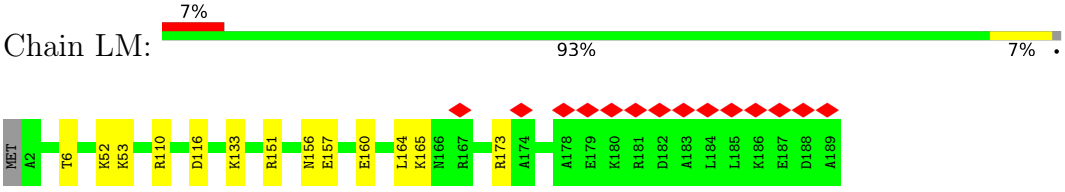
• Molecule 19: 60S ribosomal protein L18-A

Chain ML:



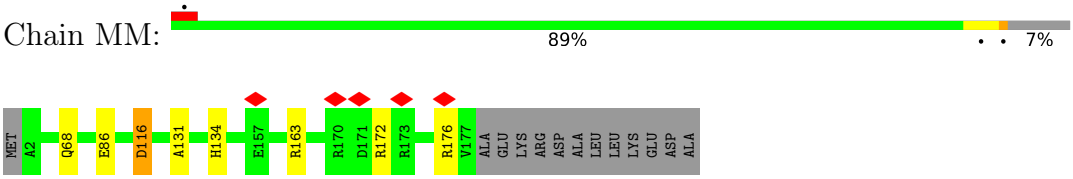
• Molecule 20: 60S ribosomal protein L19-A

Chain LM:



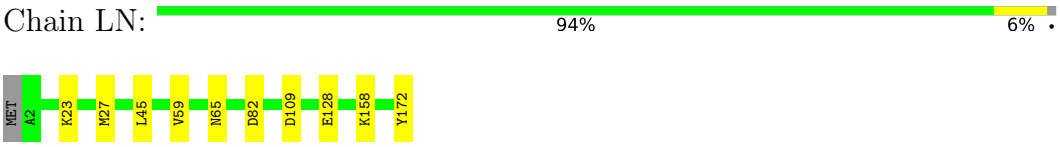
• Molecule 20: 60S ribosomal protein L19-A

Chain MM:



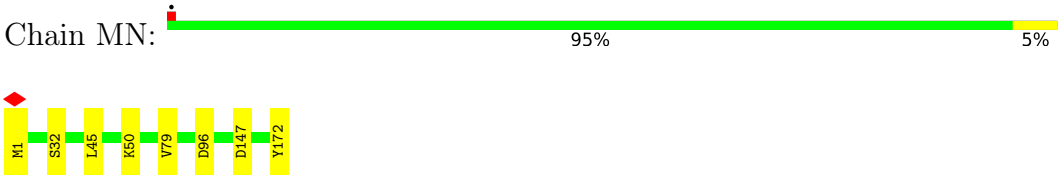
• Molecule 21: 60S ribosomal protein L20-A

Chain LN:



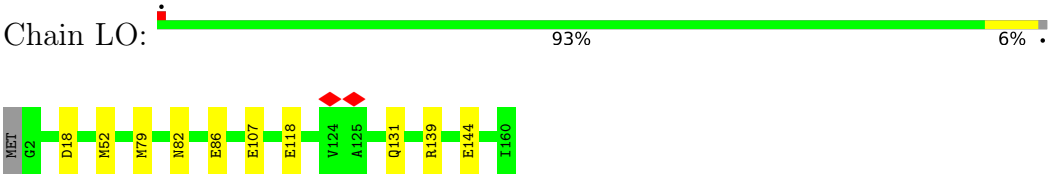
• Molecule 21: 60S ribosomal protein L20-A

Chain MN:



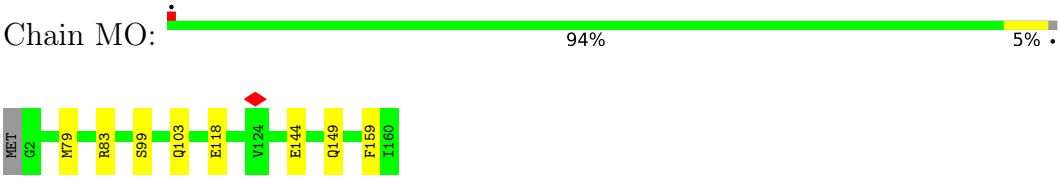
• Molecule 22: 60S ribosomal protein L21-A

Chain LO:



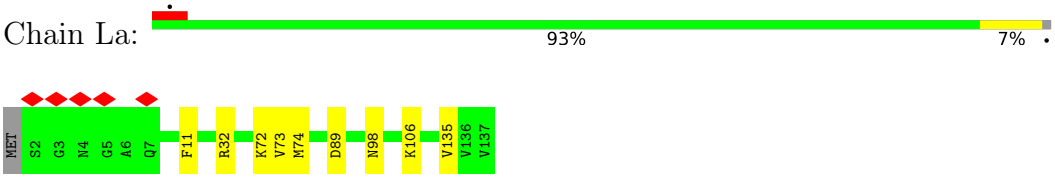
• Molecule 22: 60S ribosomal protein L21-A

Chain MO:



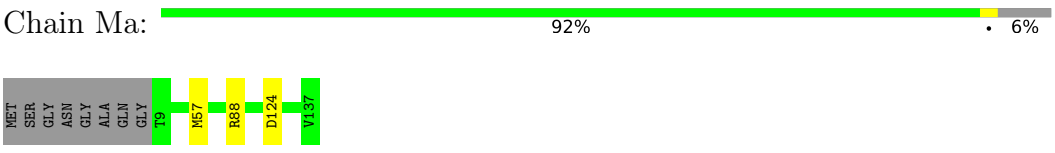
• Molecule 23: 60S ribosomal protein L23-A

Chain La:



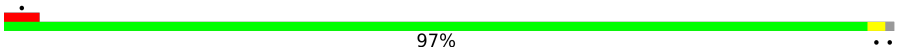
• Molecule 23: 60S ribosomal protein L23-A

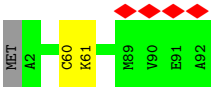
Chain Ma:



• Molecule 24: 60S ribosomal protein L43-A

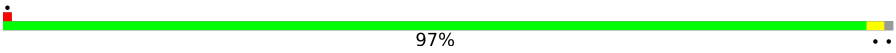
Chain Lb:

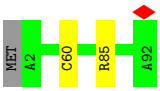




• Molecule 24: 60S ribosomal protein L43-A

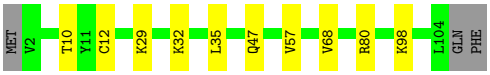
Chain Mb:





• Molecule 25: 60S ribosomal protein L42-A

Chain Lc:

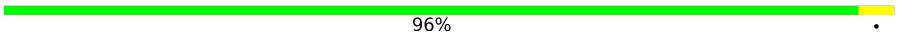


• Molecule 25: 60S ribosomal protein L42-A

Chain Mc:

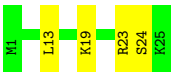
• Molecule 26: 60S ribosomal protein L41-A

Chain Ld:



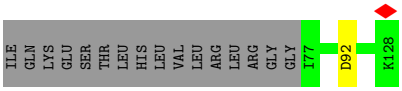
• Molecule 26: 60S ribosomal protein L41-A

Chain Md:



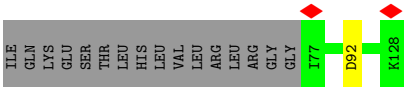
• Molecule 27: Ubiquitin-60S ribosomal protein L40

Chain Le:



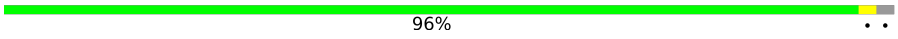
• Molecule 27: Ubiquitin-60S ribosomal protein L40

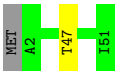
Chain Me:



• Molecule 28: 60S ribosomal protein L39

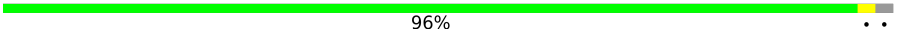
Chain Lf:

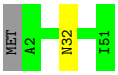




• Molecule 28: 60S ribosomal protein L39

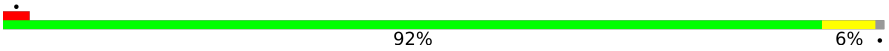
Chain Mf:

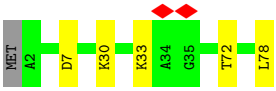




• Molecule 29: 60S ribosomal protein L38

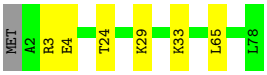
Chain Lg:





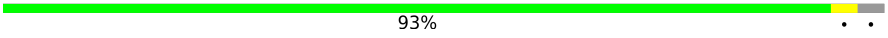
• Molecule 29: 60S ribosomal protein L38

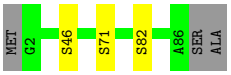
Chain Mg:



• Molecule 30: 60S ribosomal protein L37-A

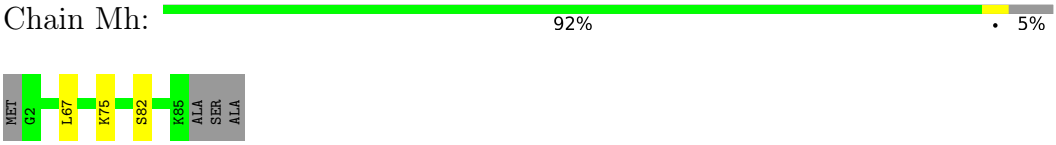
Chain Lh:





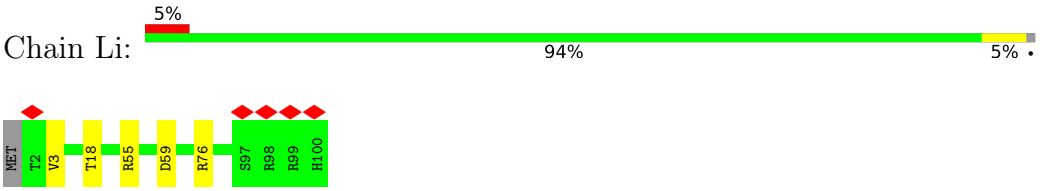
• Molecule 30: 60S ribosomal protein L37-A

Chain Mh:



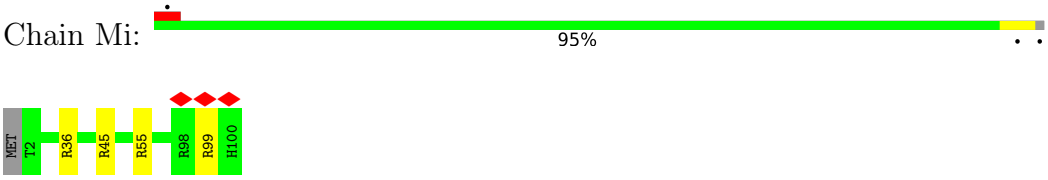
• Molecule 31: 60S ribosomal protein L36-A

Chain Li:



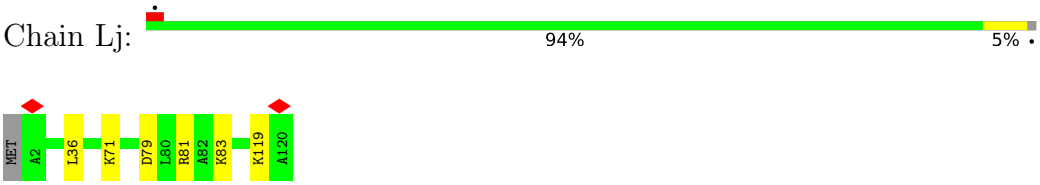
• Molecule 31: 60S ribosomal protein L36-A

Chain Mi:



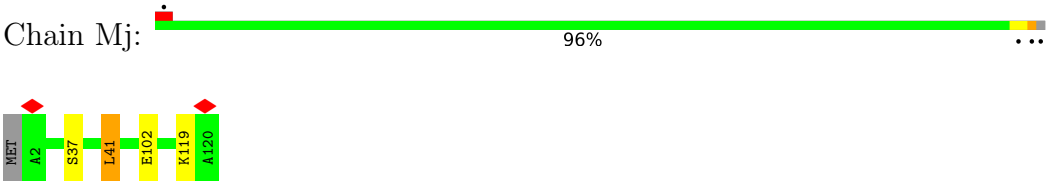
• Molecule 32: 60S ribosomal protein L35-A

Chain Lj:



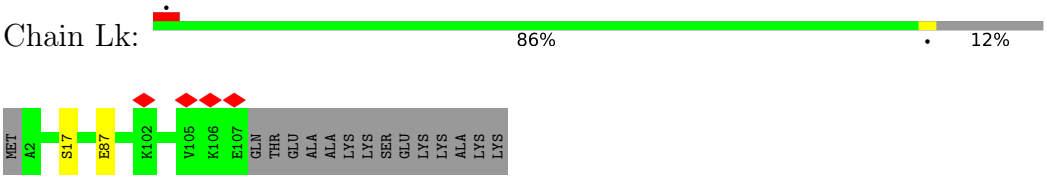
• Molecule 32: 60S ribosomal protein L35-A

Chain Mj:



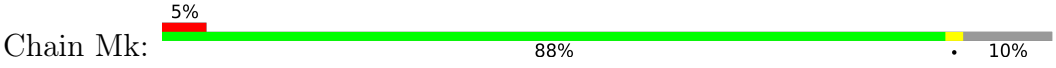
• Molecule 33: 60S ribosomal protein L34-A

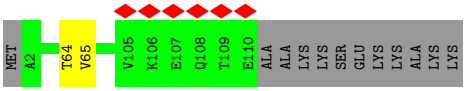
Chain Lk:



• Molecule 33: 60S ribosomal protein L34-A

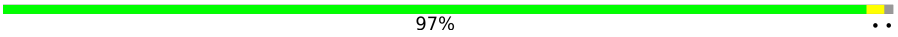
Chain Mk:





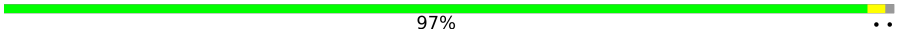
• Molecule 34: 60S ribosomal protein L33-A

Chain Ll:



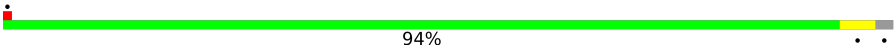
• Molecule 34: 60S ribosomal protein L33-A

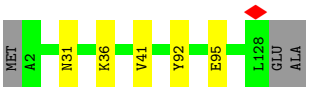
Chain Ml:



• Molecule 35: 60S ribosomal protein L32

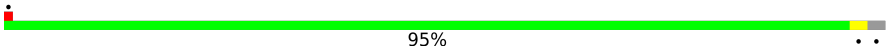
Chain Lm:

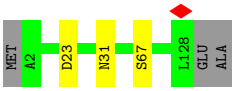




• Molecule 35: 60S ribosomal protein L32

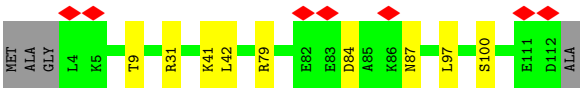
Chain Mm:





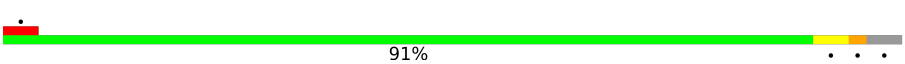
• Molecule 36: 60S ribosomal protein L31-A

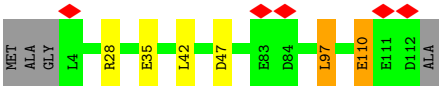
Chain Ln:



• Molecule 36: 60S ribosomal protein L31-A

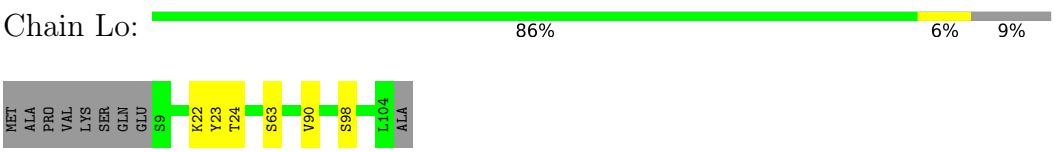
Chain Mn:





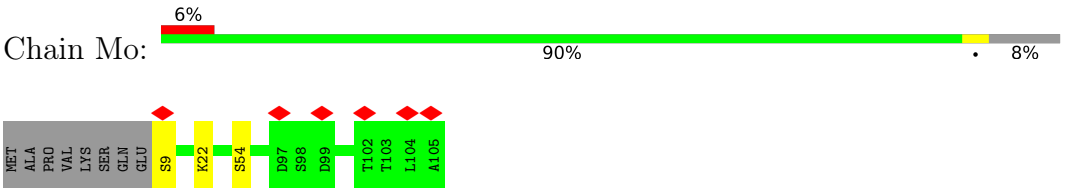
• Molecule 37: 60S ribosomal protein L30

Chain Lo:



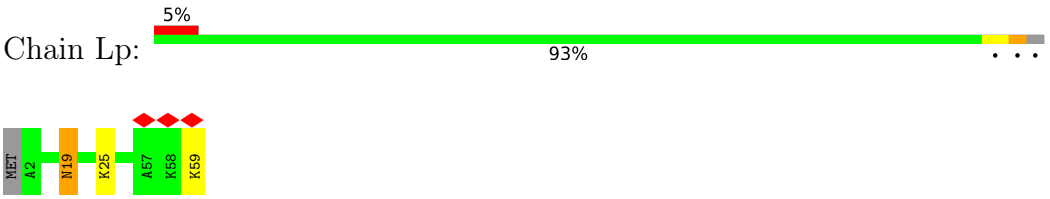
• Molecule 37: 60S ribosomal protein L30

Chain Mo:



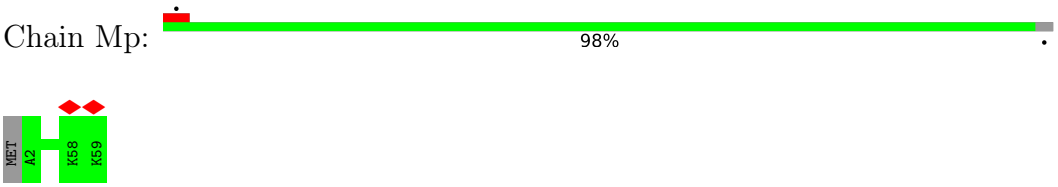
• Molecule 38: 60S ribosomal protein L29

Chain Lp:



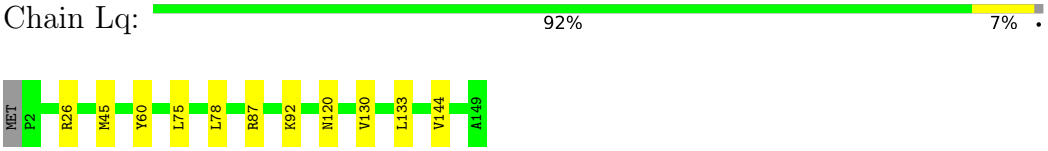
• Molecule 38: 60S ribosomal protein L29

Chain Mp:



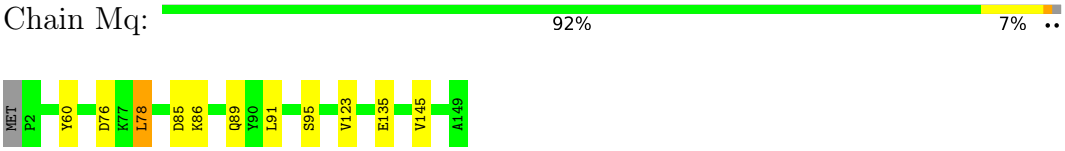
• Molecule 39: 60S ribosomal protein L28

Chain Lq:



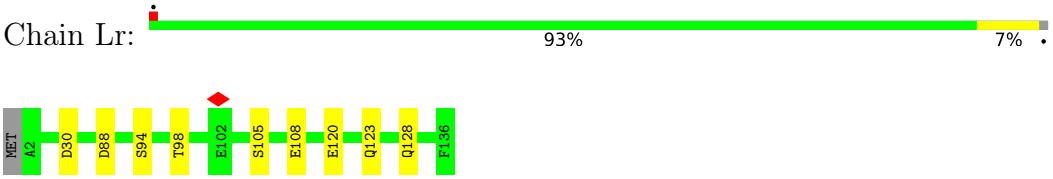
• Molecule 39: 60S ribosomal protein L28

Chain Mq:



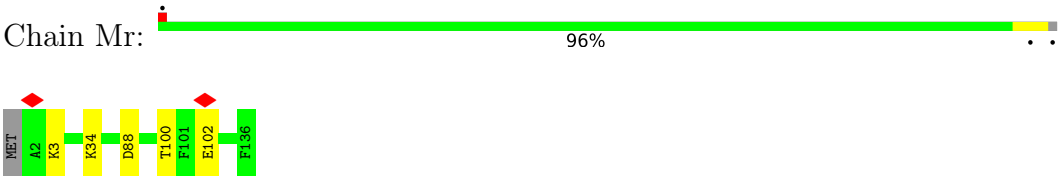
• Molecule 40: 60S ribosomal protein L27-A

Chain Lr:



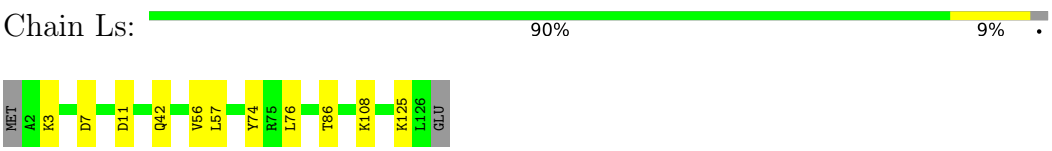
• Molecule 40: 60S ribosomal protein L27-A

Chain Mr:



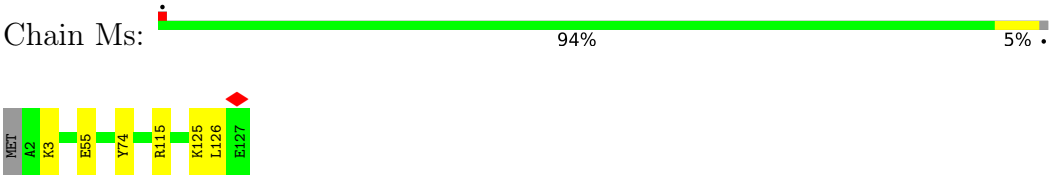
• Molecule 41: 60S ribosomal protein L26-A

Chain Ls:



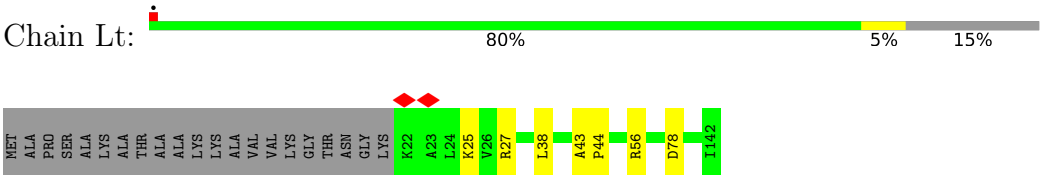
• Molecule 41: 60S ribosomal protein L26-A

Chain Ms:



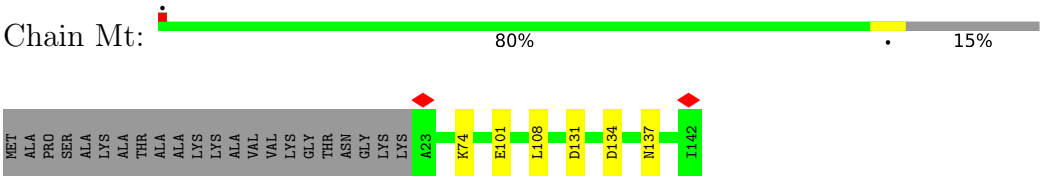
• Molecule 42: 60S ribosomal protein L25

Chain Lt:



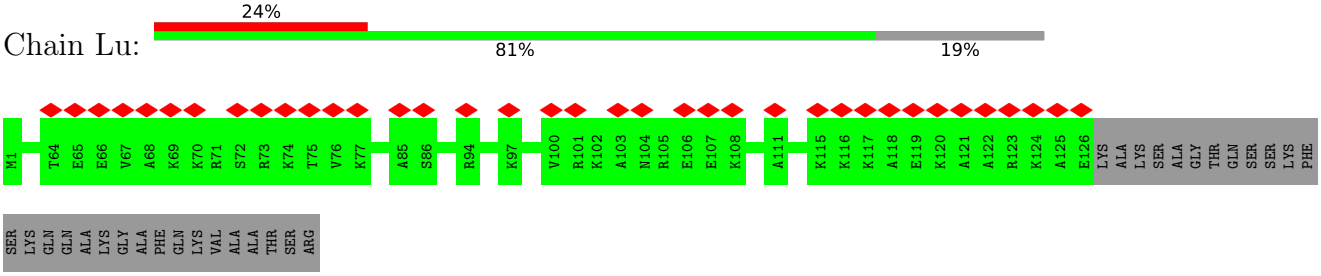
• Molecule 42: 60S ribosomal protein L25

Chain Mt:



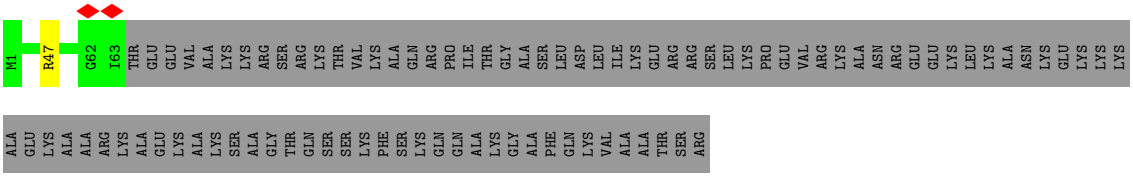
• Molecule 43: 60S ribosomal protein L24-A

Chain Lu:

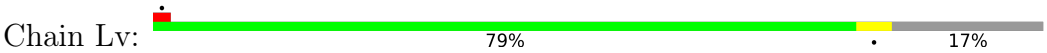


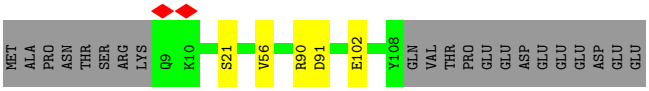
• Molecule 43: 60S ribosomal protein L24-A

Chain Mu:

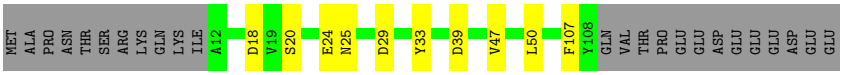


• Molecule 44: 60S ribosomal protein L22-A

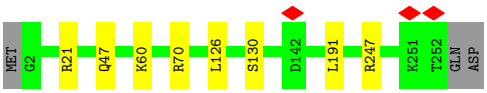




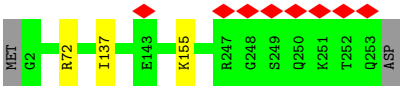
• Molecule 44: 60S ribosomal protein L22-A



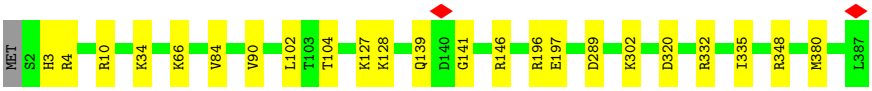
• Molecule 45: 60S ribosomal protein L2-A



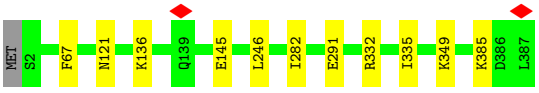
• Molecule 45: 60S ribosomal protein L2-A



• Molecule 46: 60S ribosomal protein L3

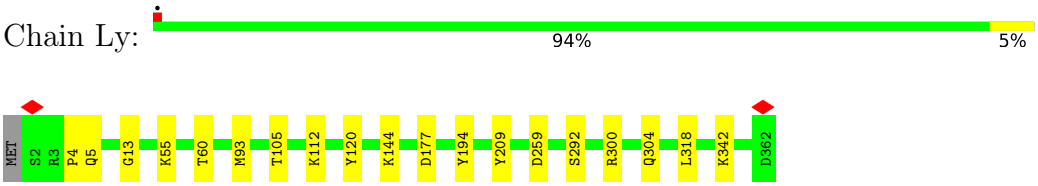


• Molecule 46: 60S ribosomal protein L3



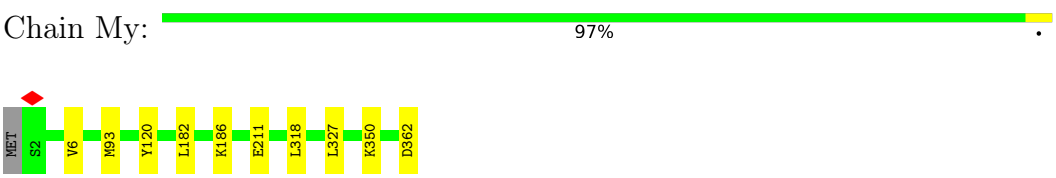
• Molecule 47: 60S ribosomal protein L4-A

Chain Ly:



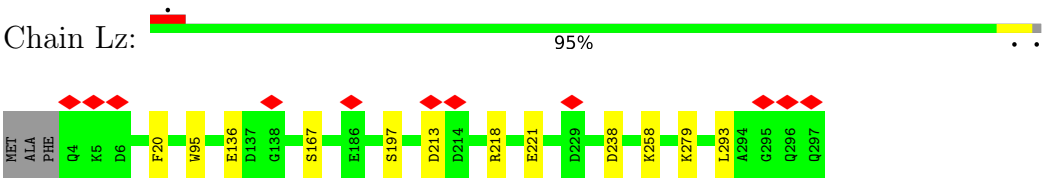
• Molecule 47: 60S ribosomal protein L4-A

Chain My:



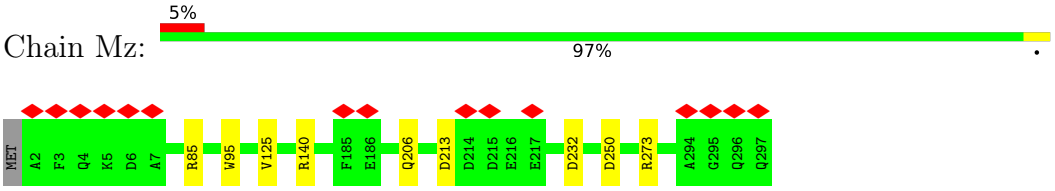
• Molecule 48: 60S ribosomal protein L5

Chain Lz:



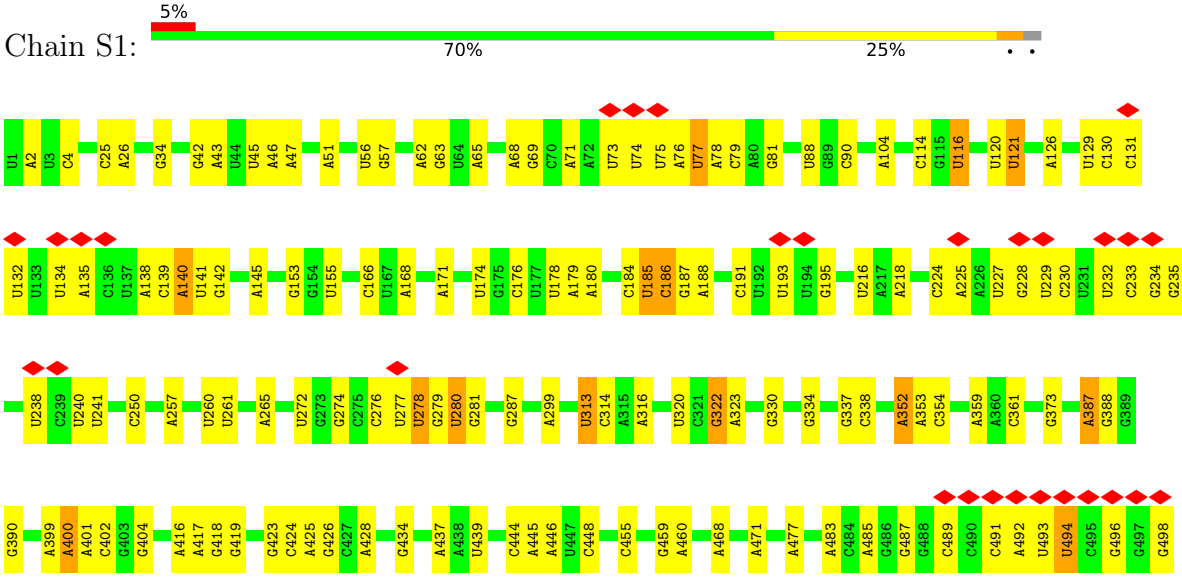
• Molecule 48: 60S ribosomal protein L5

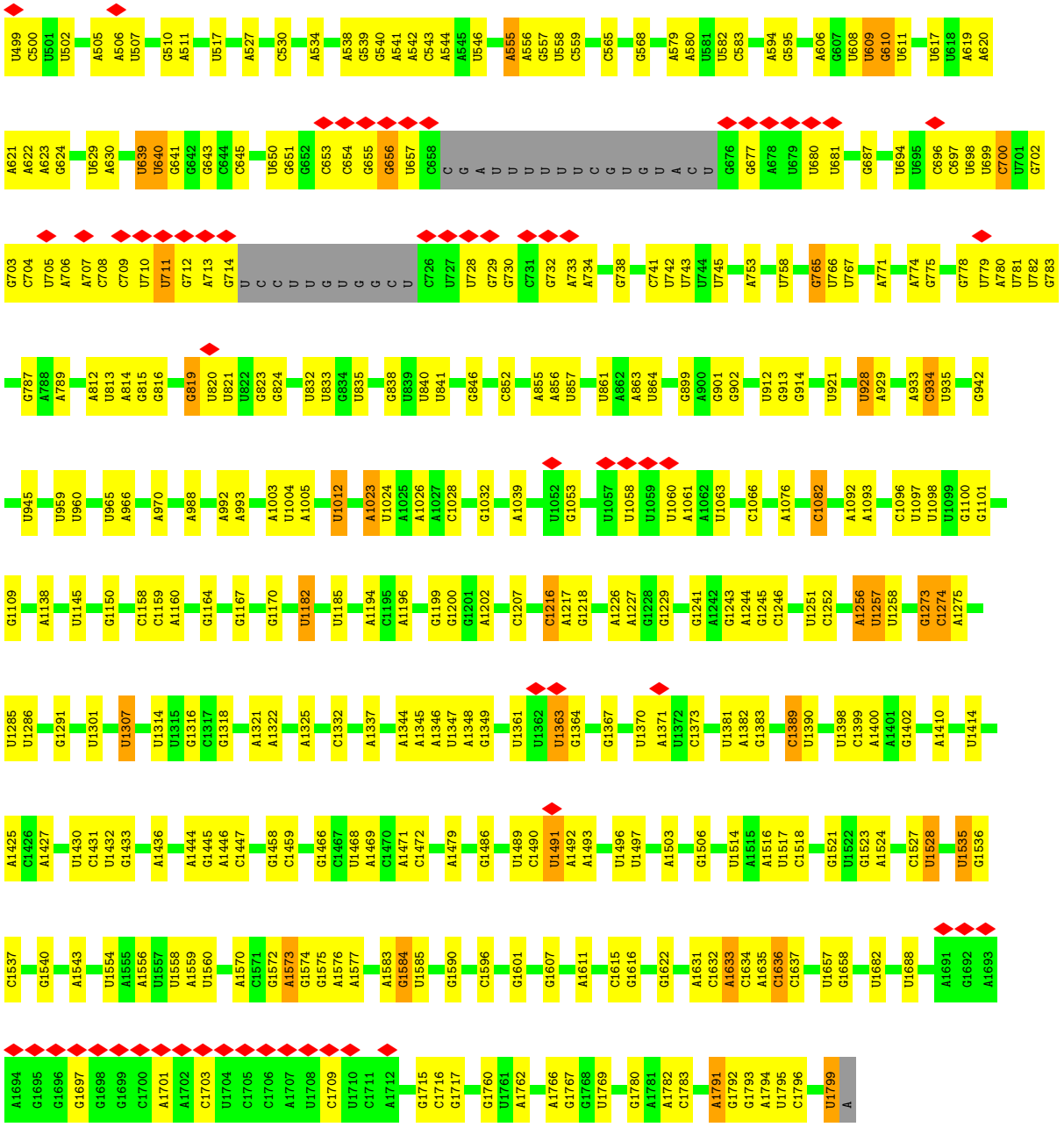
Chain Mz:



• Molecule 49: Saccharomyces cerevisiae S288C 18S ribosomal RNA (RDN18-1)

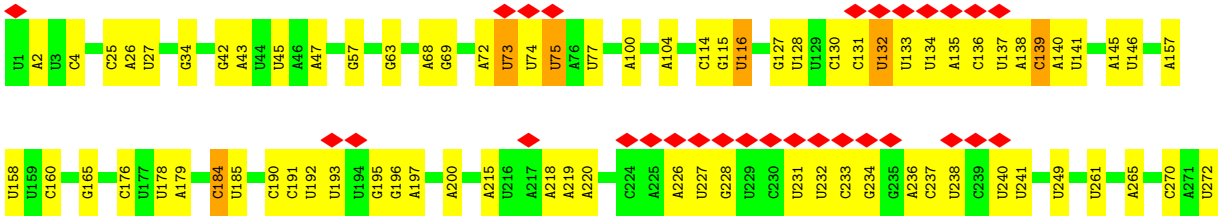
Chain S1:

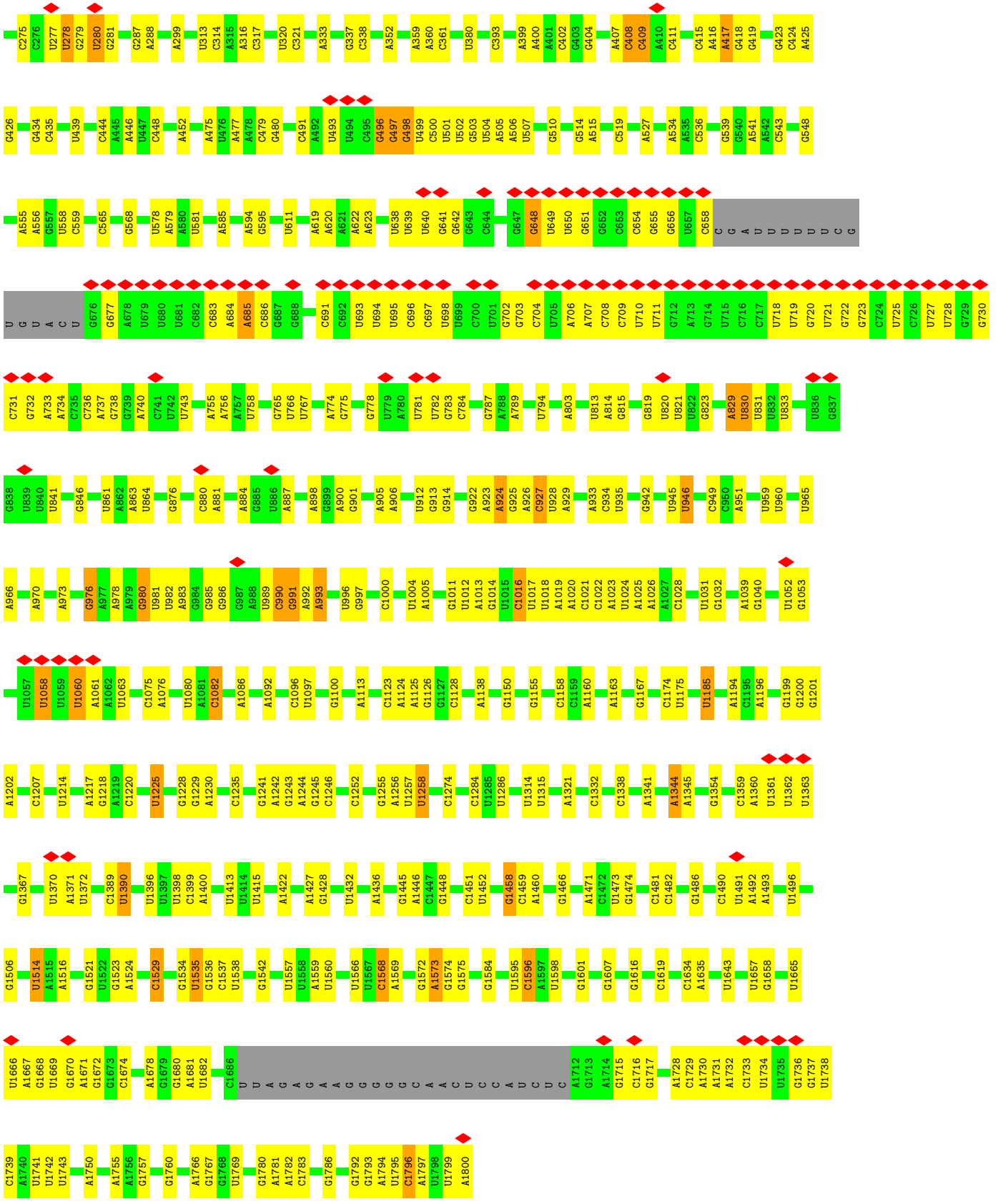




• Molecule 49: Saccharomyces cerevisiae S288C 18S ribosomal RNA (RDN18-1)

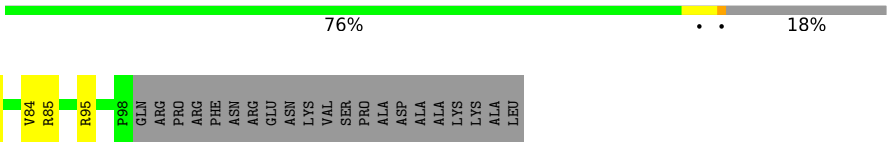
Chain R1:





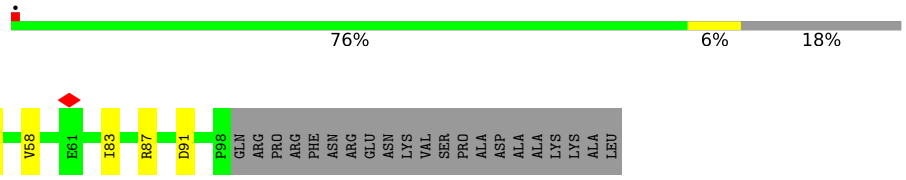
• Molecule 50: Small ribosomal subunit protein eS26A

Chain SA:



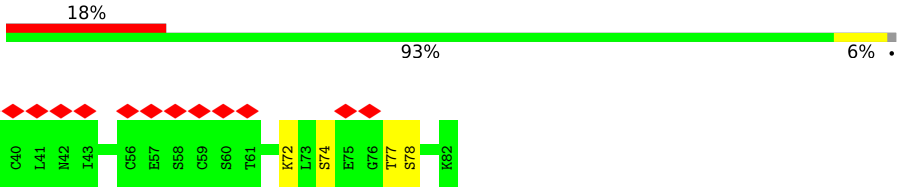
• Molecule 50: Small ribosomal subunit protein eS26A

Chain RA:



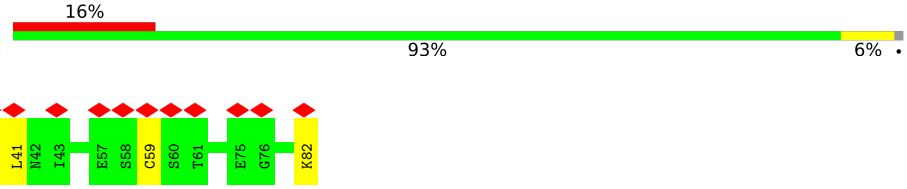
• Molecule 51: 40S ribosomal protein S27-A

Chain SB:



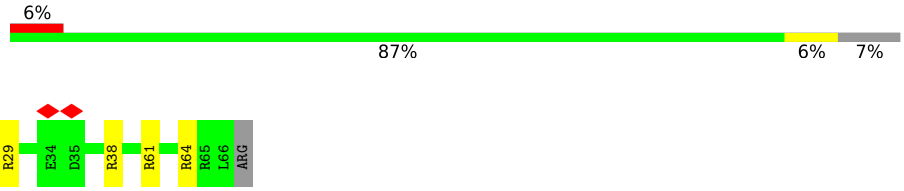
• Molecule 51: 40S ribosomal protein S27-A

Chain RB:



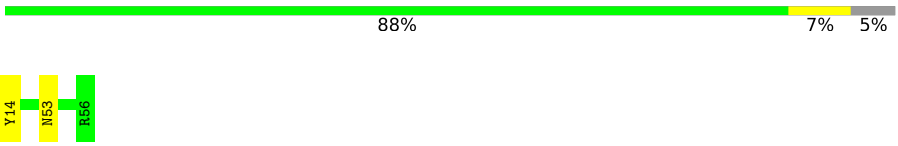
• Molecule 52: Small ribosomal subunit protein eS28B

Chain SC:



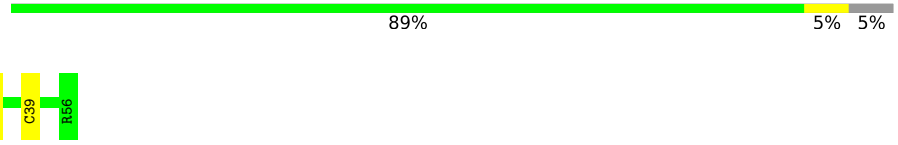
• Molecule 53: Small ribosomal subunit protein uS14A

Chain SD:



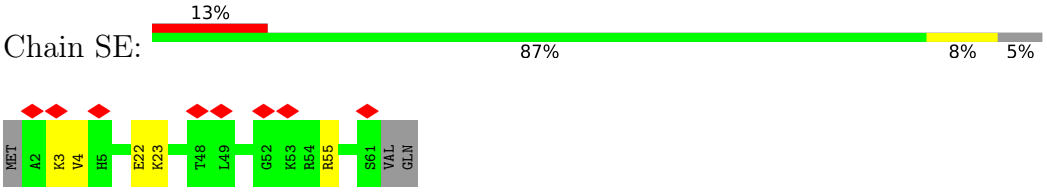
• Molecule 53: Small ribosomal subunit protein uS14A

Chain RD:



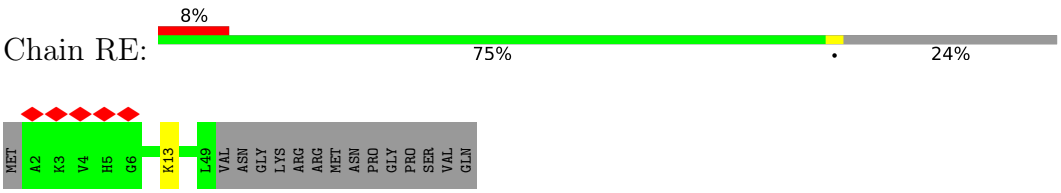
• Molecule 54: 40S ribosomal protein S30-A

Chain SE:



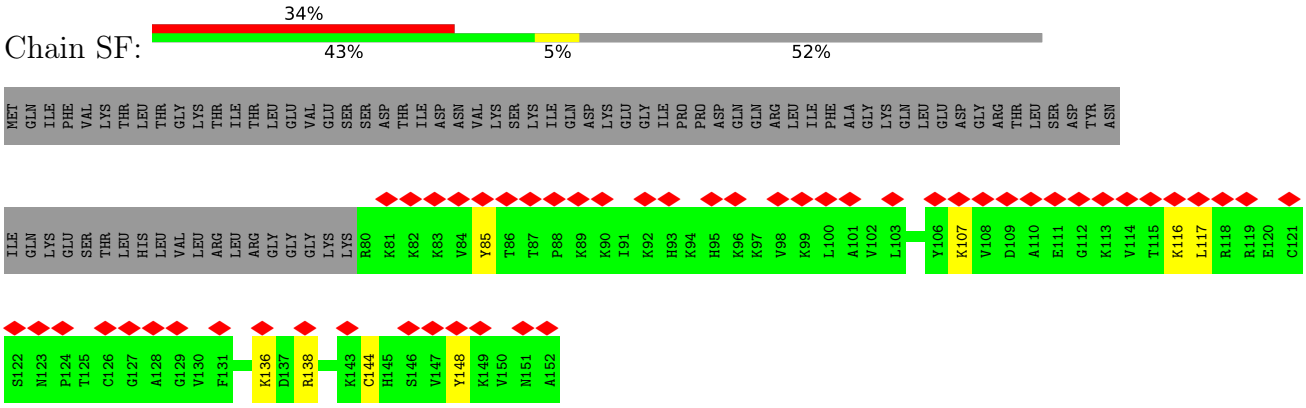
• Molecule 54: 40S ribosomal protein S30-A

Chain RE:



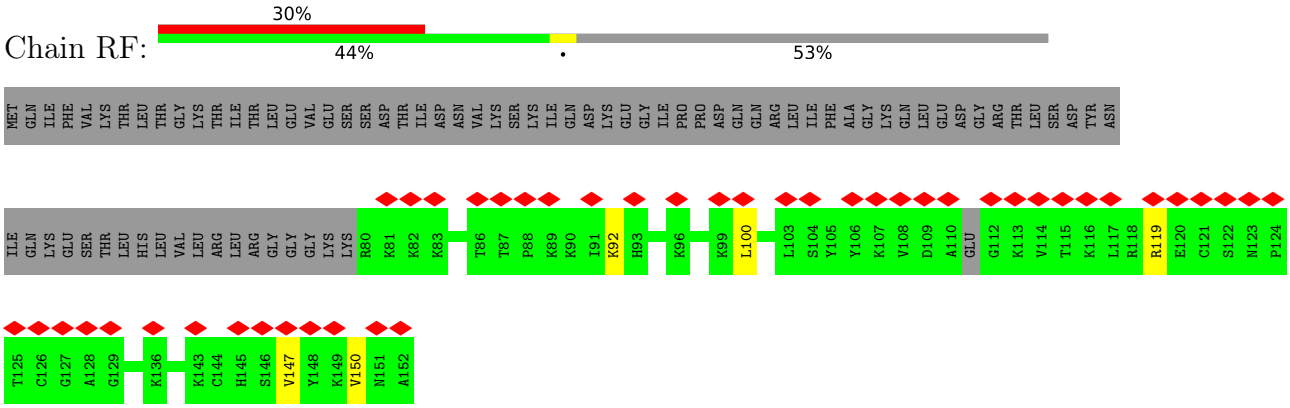
• Molecule 55: Ubiquitin

Chain SF:



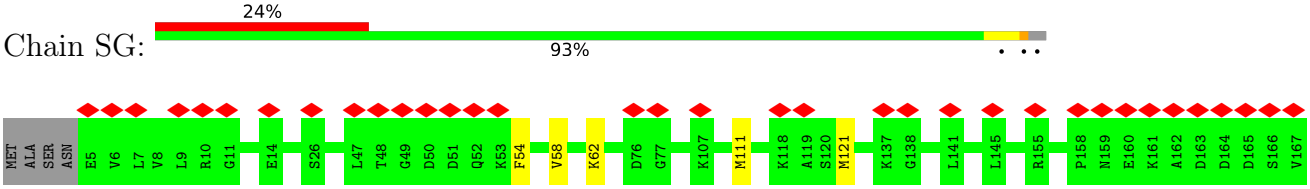
• Molecule 55: Ubiquitin

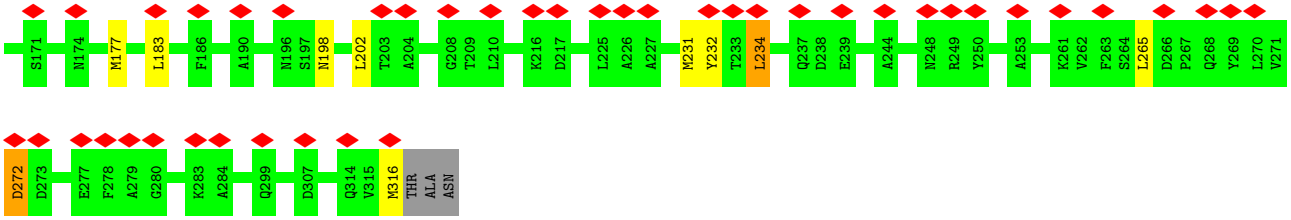
Chain RF:



• Molecule 56: Guanine nucleotide-binding protein subunit beta-like protein

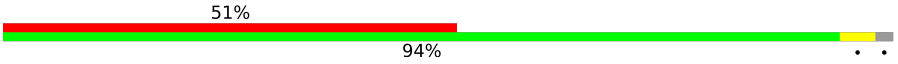
Chain SG:

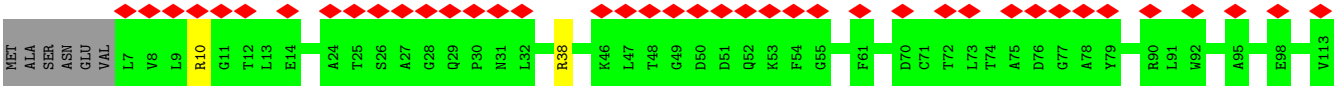


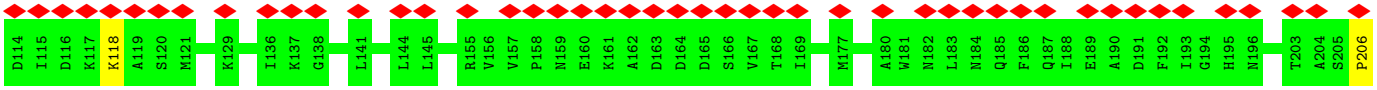


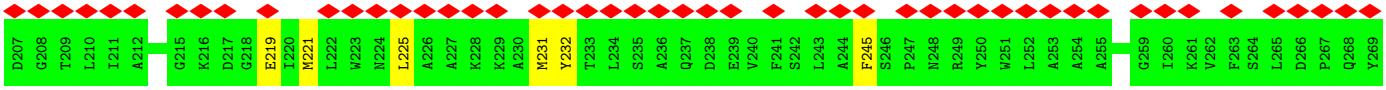
• Molecule 56: Guanine nucleotide-binding protein subunit beta-like protein

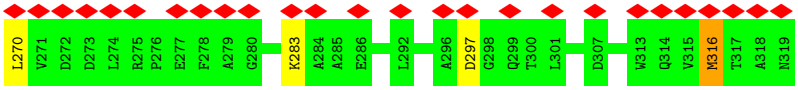
Chain RG:





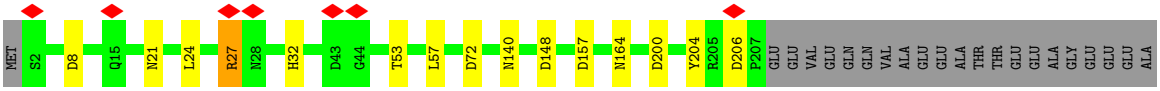






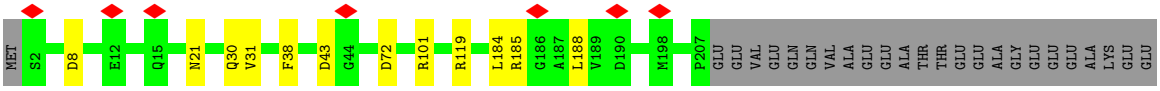
• Molecule 57: 40S ribosomal protein S0-A

Chain Sa:



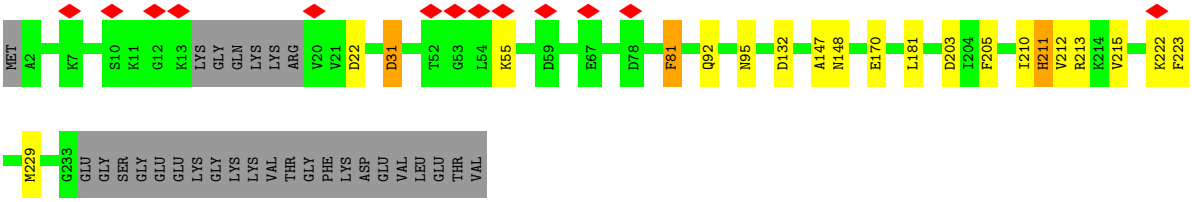
• Molecule 57: 40S ribosomal protein S0-A

Chain Ra:

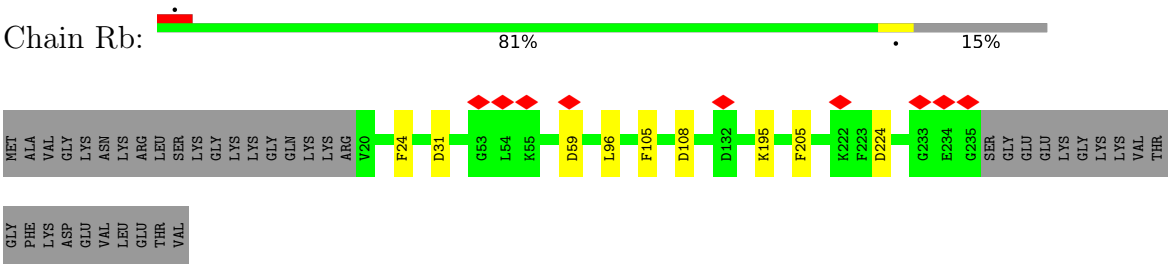


• Molecule 58: 40S ribosomal protein S1-A

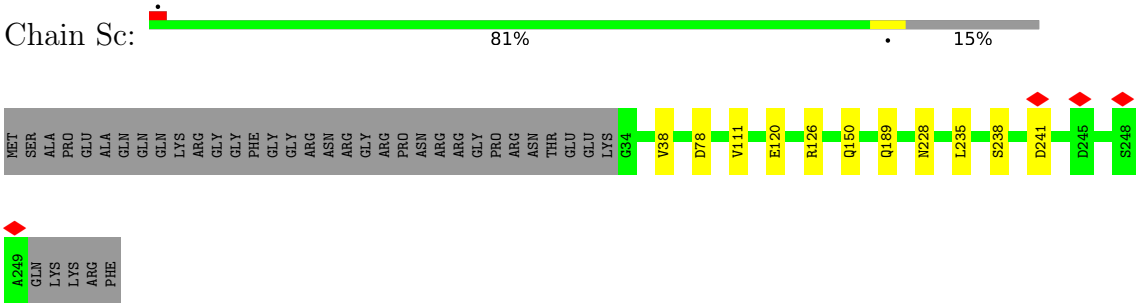
Chain Sb:



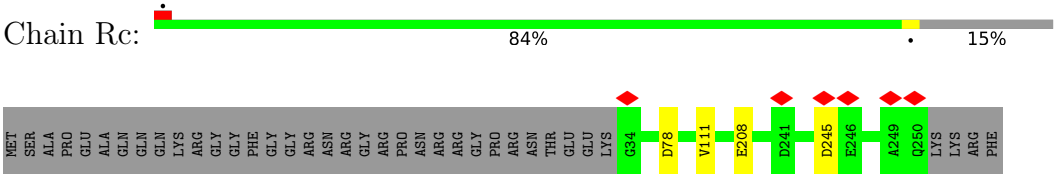
• Molecule 58: 40S ribosomal protein S1-A



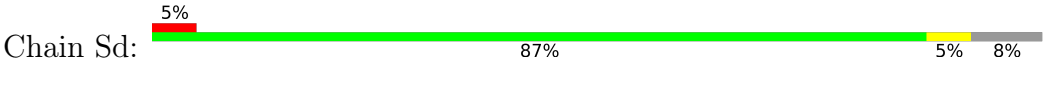
• Molecule 59: 40S ribosomal protein S2

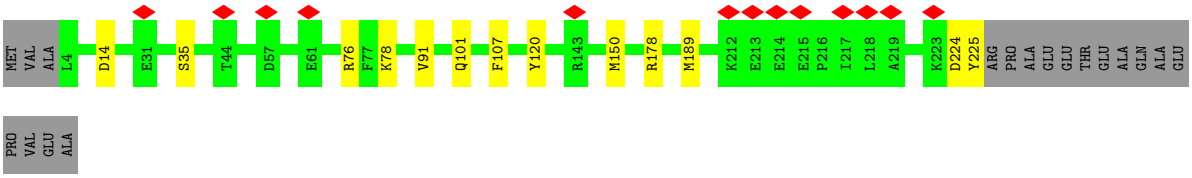


• Molecule 59: 40S ribosomal protein S2

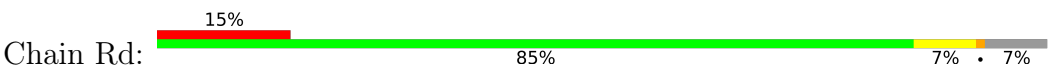


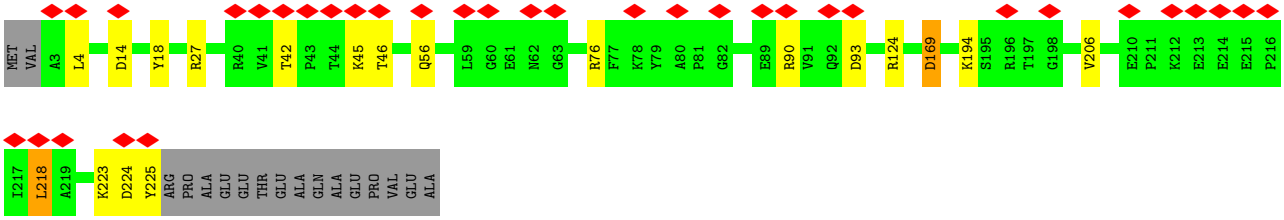
• Molecule 60: Small ribosomal subunit protein uS3



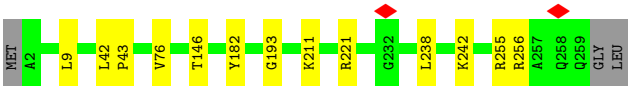


• Molecule 60: Small ribosomal subunit protein uS3

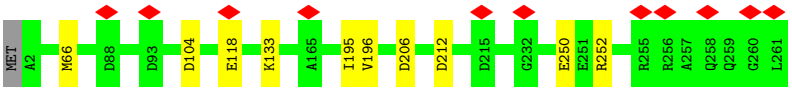




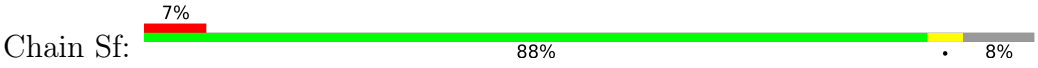
• Molecule 61: 40S ribosomal protein S4-A

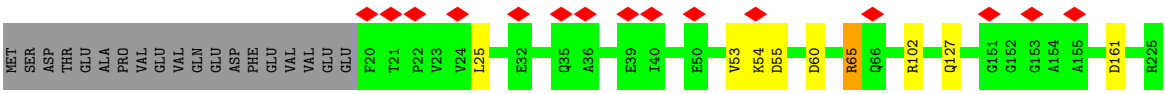


• Molecule 61: 40S ribosomal protein S4-A

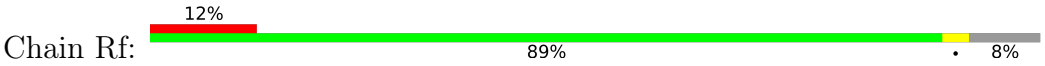


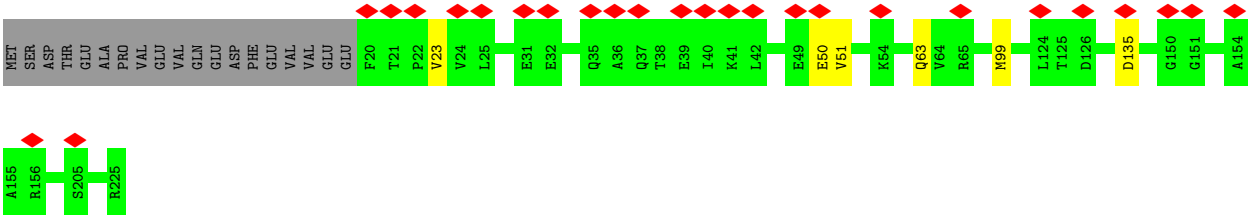
• Molecule 62: 40S ribosomal protein S5



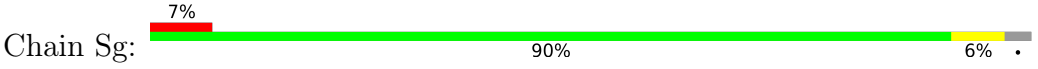


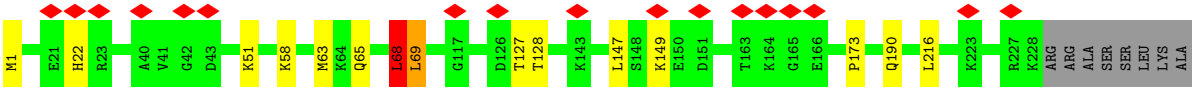
• Molecule 62: 40S ribosomal protein S5





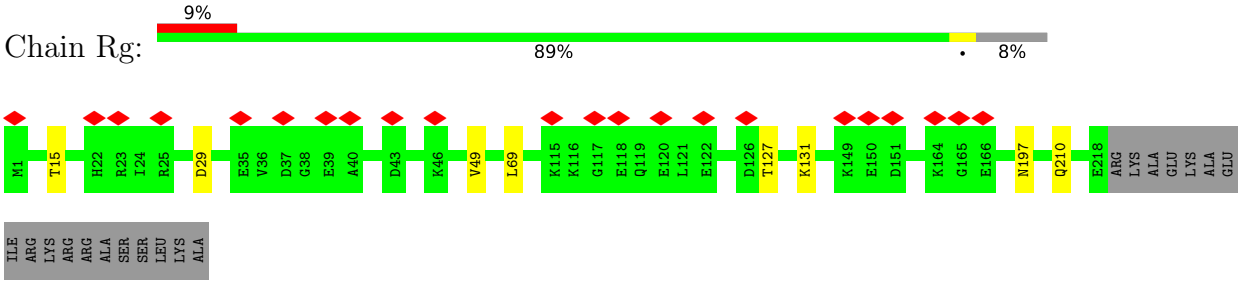
• Molecule 63: 40S ribosomal protein S6-A





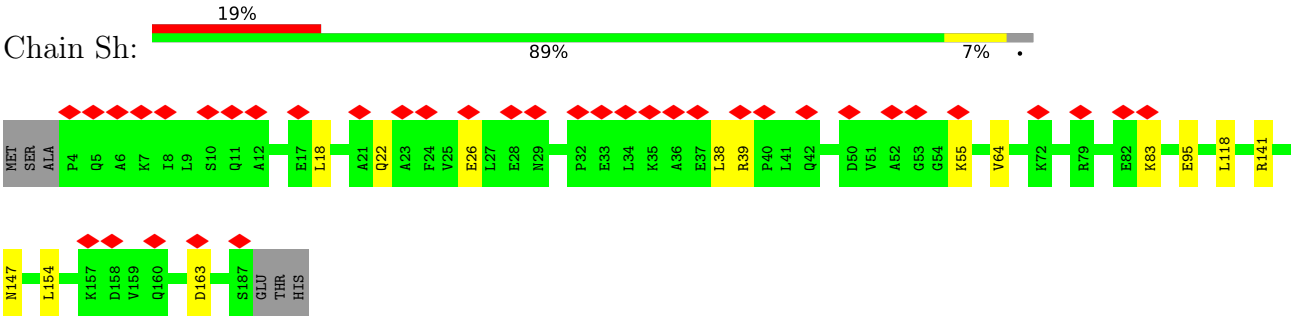
• Molecule 63: 40S ribosomal protein S6-A

Chain Rg:



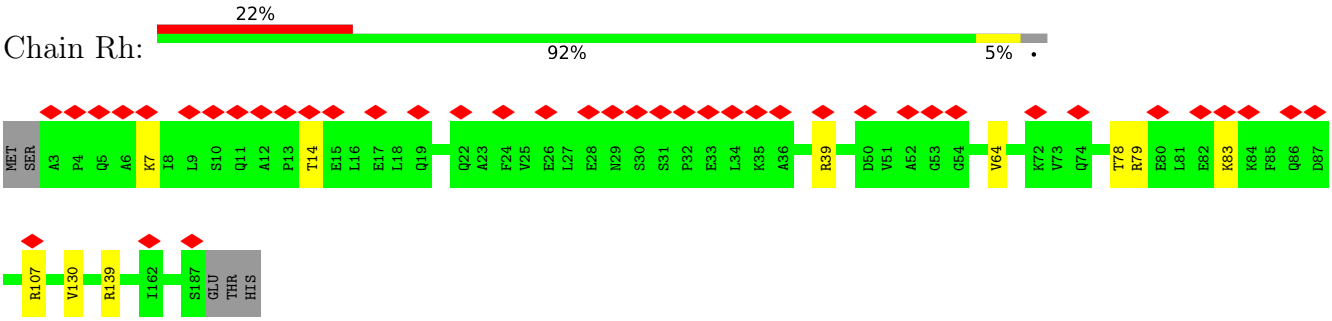
• Molecule 64: 40S ribosomal protein S7-A

Chain Sh:



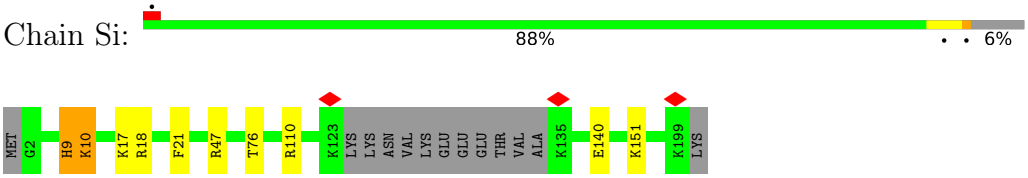
• Molecule 64: 40S ribosomal protein S7-A

Chain Rh:



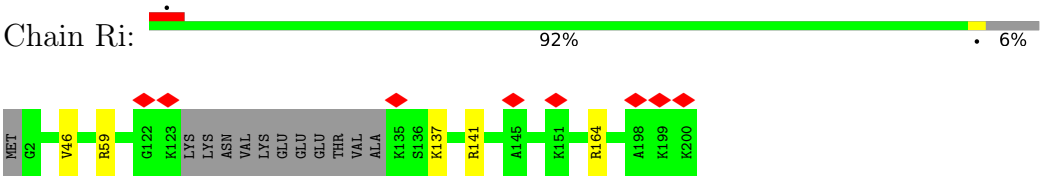
• Molecule 65: 40S ribosomal protein S8-A

Chain Si:



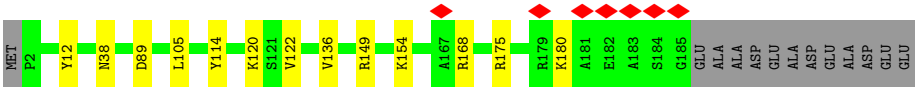
• Molecule 65: 40S ribosomal protein S8-A

Chain Ri:

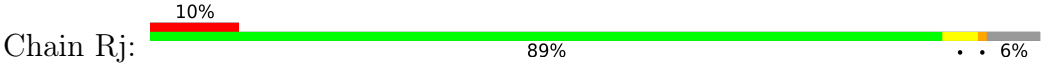


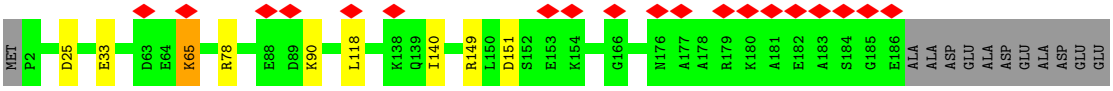
• Molecule 66: 40S ribosomal protein S9-A

Chain Sj:

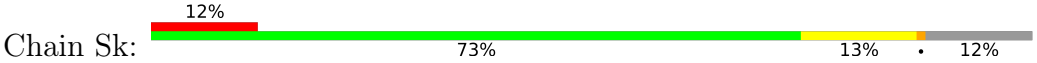


• Molecule 66: 40S ribosomal protein S9-A

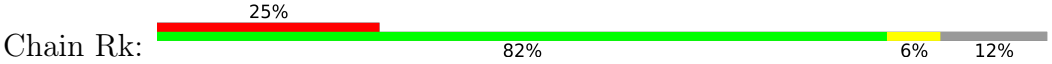


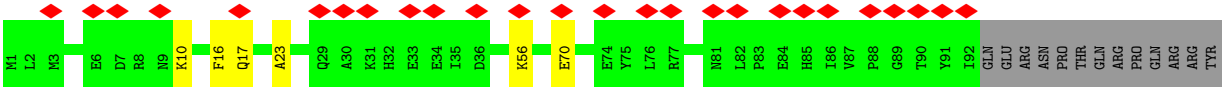


• Molecule 67: 40S ribosomal protein S10-A

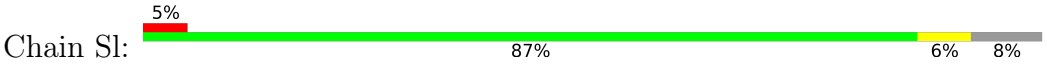


• Molecule 67: 40S ribosomal protein S10-A

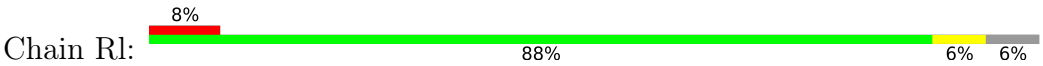


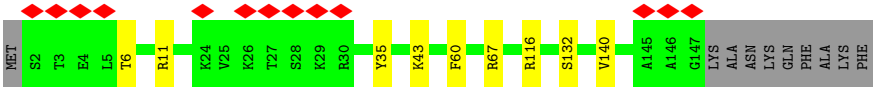


• Molecule 68: 40S ribosomal protein S11-A

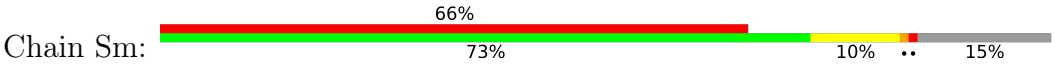


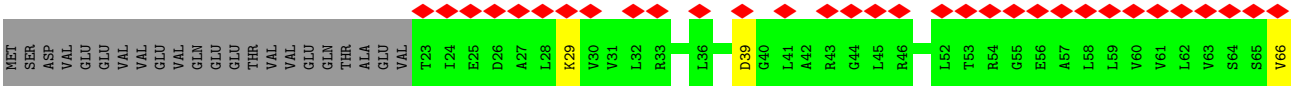
• Molecule 68: 40S ribosomal protein S11-A

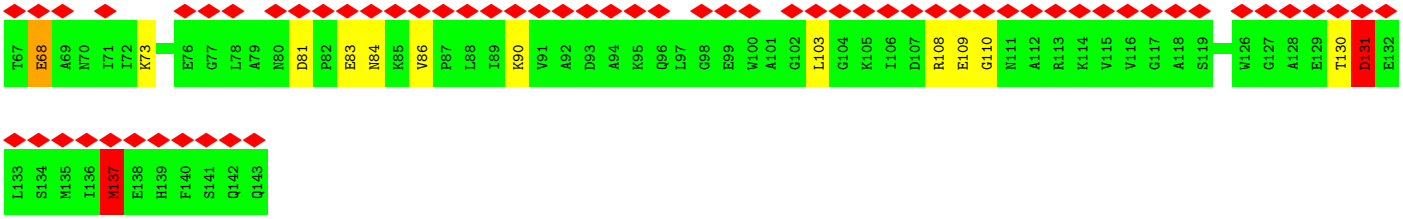




• Molecule 69: 40S ribosomal protein S12

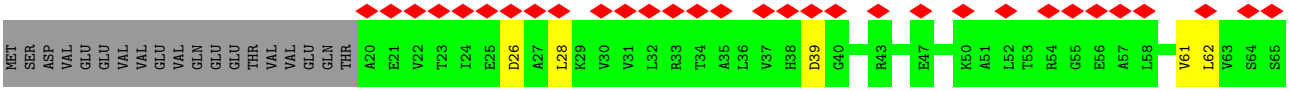


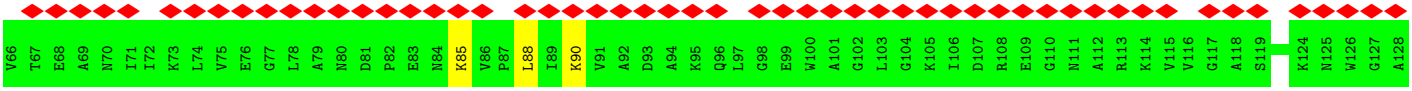


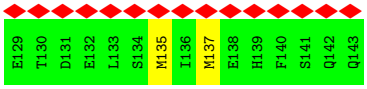


• Molecule 69: 40S ribosomal protein S12

Chain Rm:

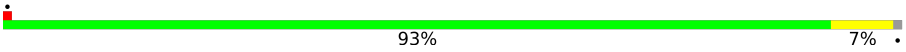






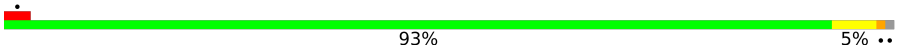
• Molecule 70: 40S ribosomal protein S13

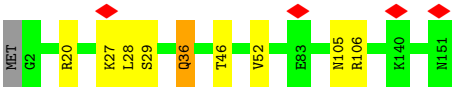
Chain Sn:



• Molecule 70: 40S ribosomal protein S13

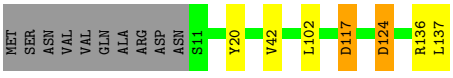
Chain Rn:





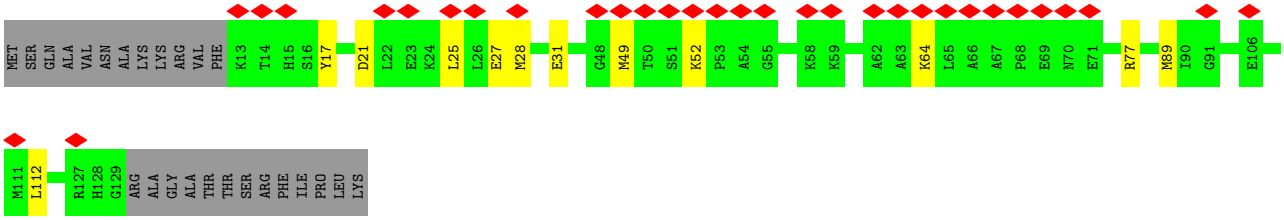
• Molecule 71: 40S ribosomal protein S14-A

Chain So:

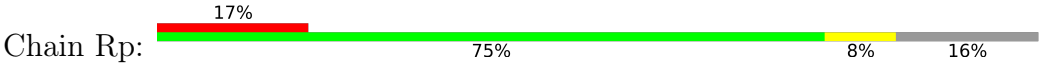


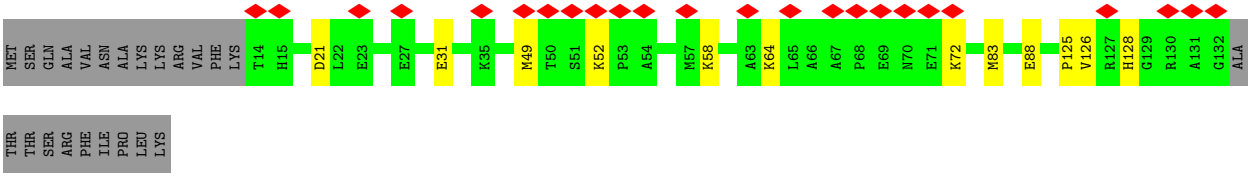
• Molecule 72: 40S ribosomal protein S15

Chain Sp:

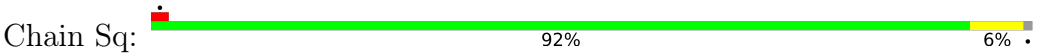


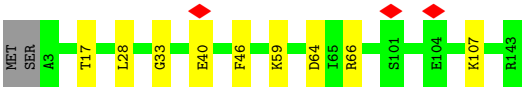
• Molecule 72: 40S ribosomal protein S15



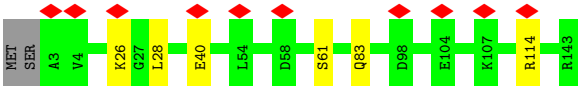


• Molecule 73: 40S ribosomal protein S16-A

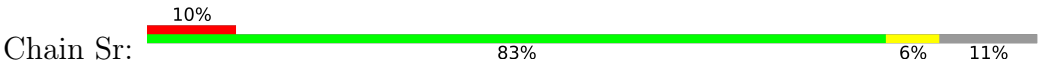


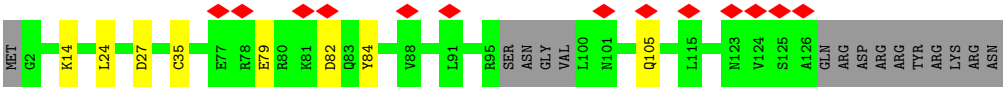


• Molecule 73: 40S ribosomal protein S16-A

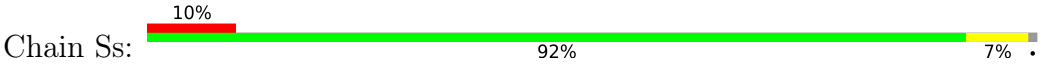


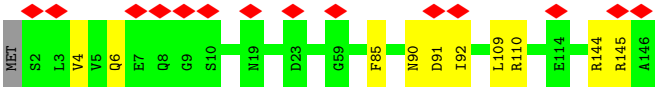
• Molecule 74: 40S ribosomal protein S17-B





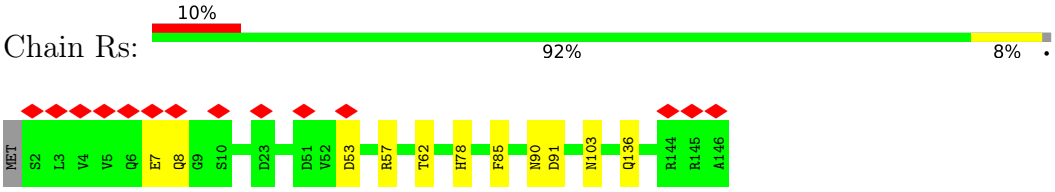
• Molecule 75: 40S ribosomal protein S18-A





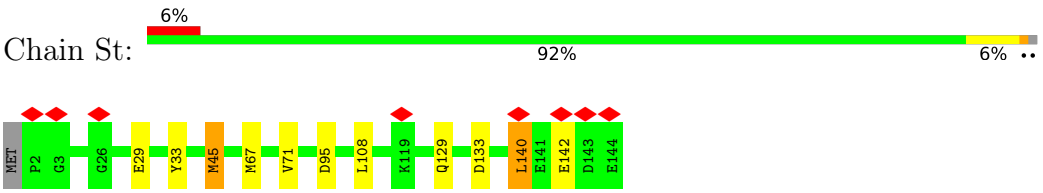
• Molecule 75: 40S ribosomal protein S18-A

Chain Rs:



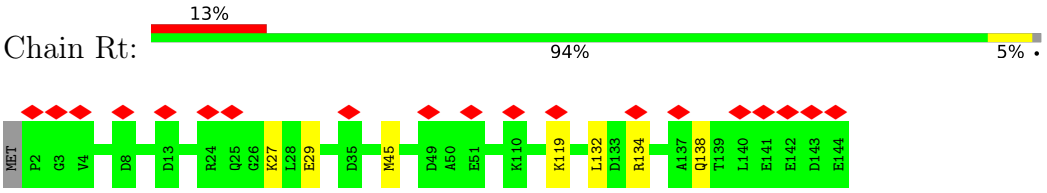
• Molecule 76: 40S ribosomal protein S19-A

Chain St:



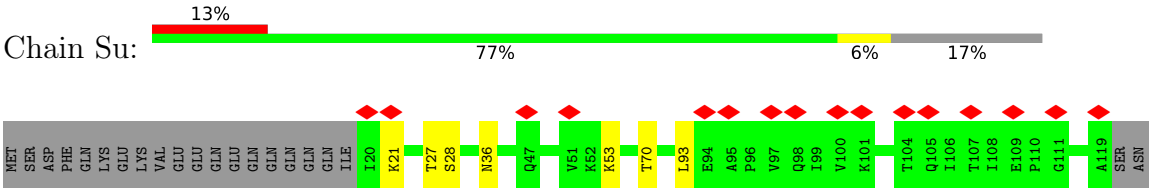
• Molecule 76: 40S ribosomal protein S19-A

Chain Rt:



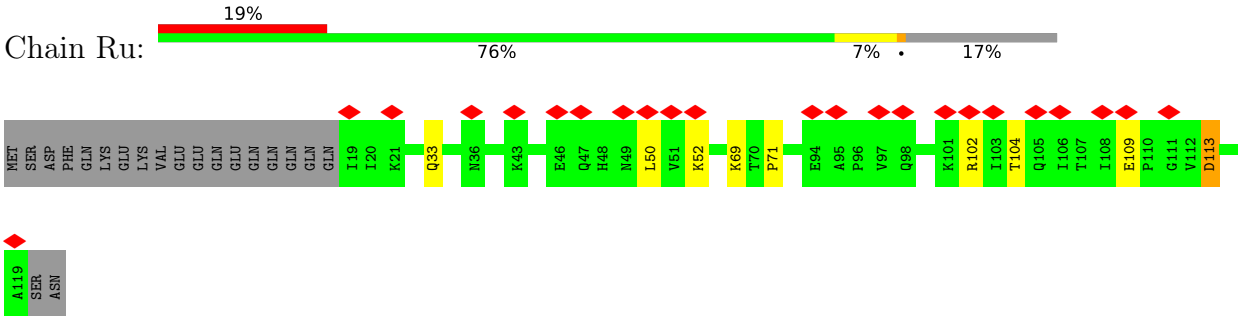
• Molecule 77: Small ribosomal subunit protein uS10

Chain Su:



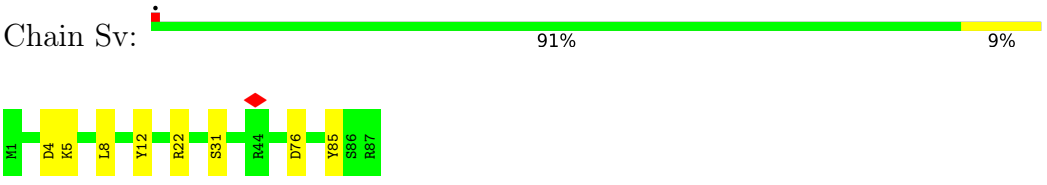
• Molecule 77: Small ribosomal subunit protein uS10

Chain Ru:



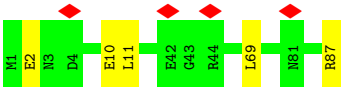
• Molecule 78: Small ribosomal subunit protein eS21A

Chain Sv:



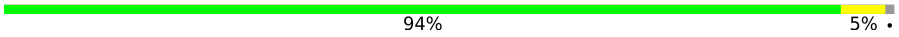
• Molecule 78: Small ribosomal subunit protein eS21A

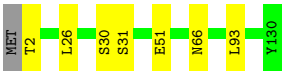
Chain Rv:



• Molecule 79: 40S ribosomal protein S22-A

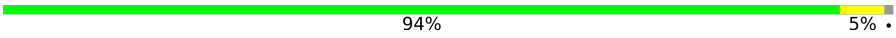
Chain Sw:

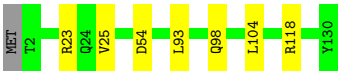




• Molecule 79: 40S ribosomal protein S22-A

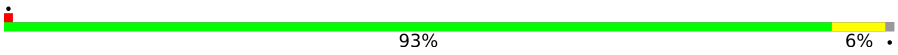
Chain Rw:

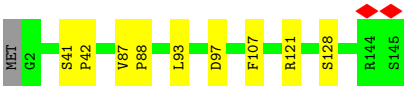




• Molecule 80: 40S ribosomal protein S23-A

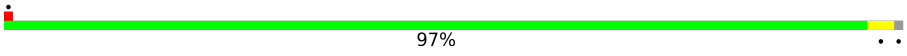
Chain Sx:





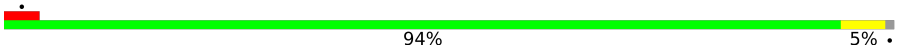
• Molecule 80: 40S ribosomal protein S23-A

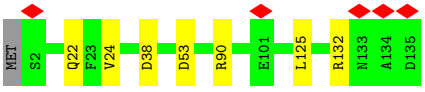
Chain Rx:



• Molecule 81: 40S ribosomal protein S24-A

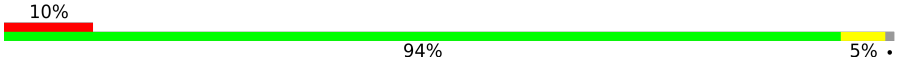
Chain Sy:

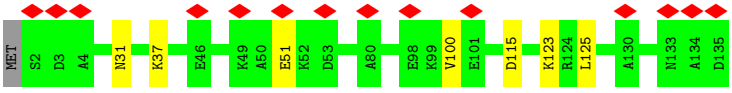




• Molecule 81: 40S ribosomal protein S24-A

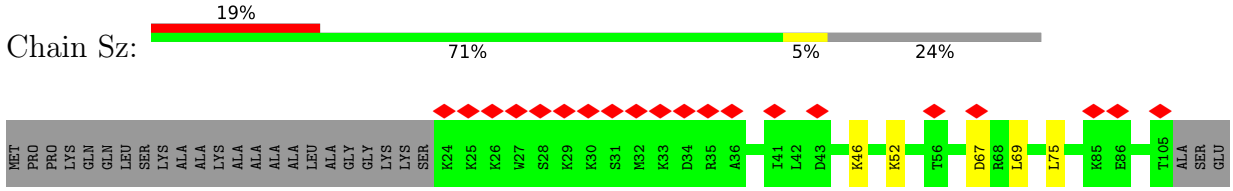
Chain Ry:





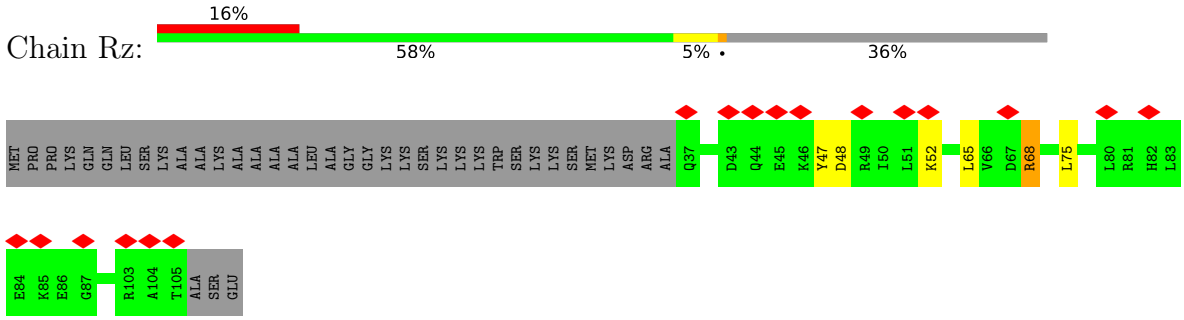
• Molecule 82: 40S ribosomal protein S25-A

Chain Sz:



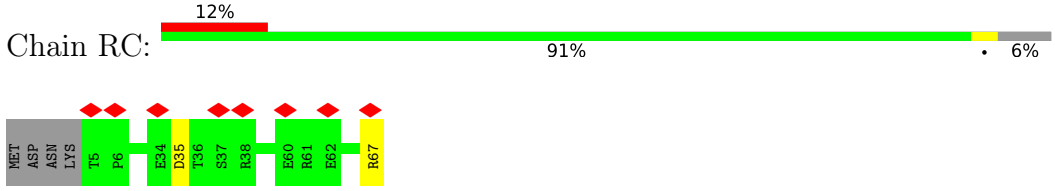
• Molecule 82: 40S ribosomal protein S25-A

Chain Rz:



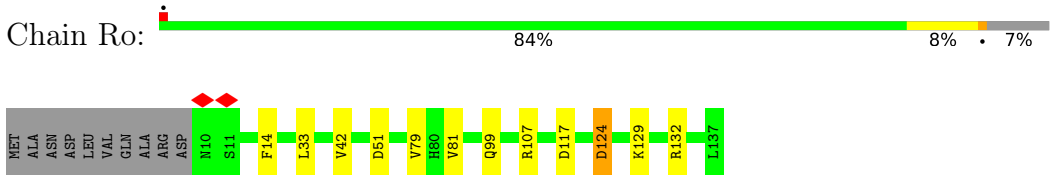
• Molecule 83: 40S ribosomal protein S28-A

Chain RC:



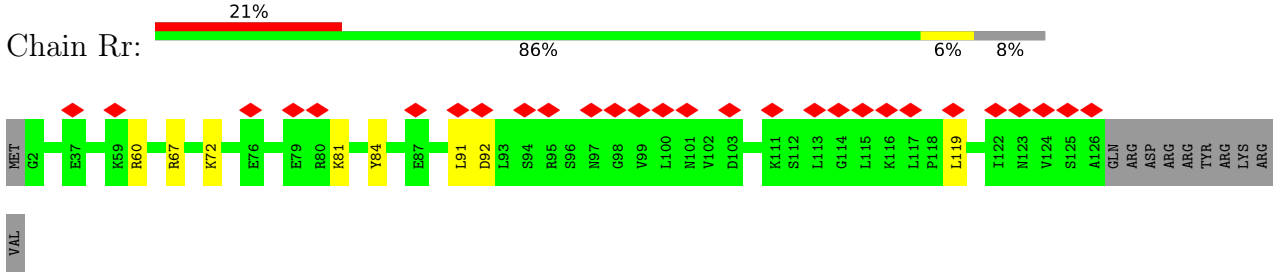
• Molecule 84: 40S ribosomal protein S14-B

Chain Ro:



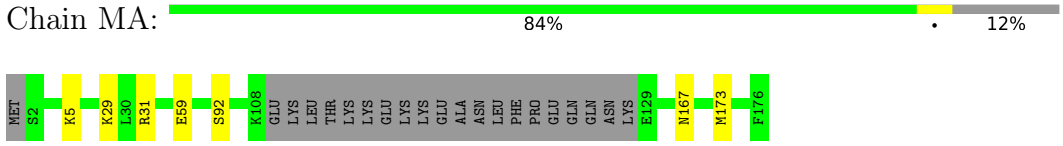
• Molecule 85: 40S ribosomal protein S17-A

Chain Rr:



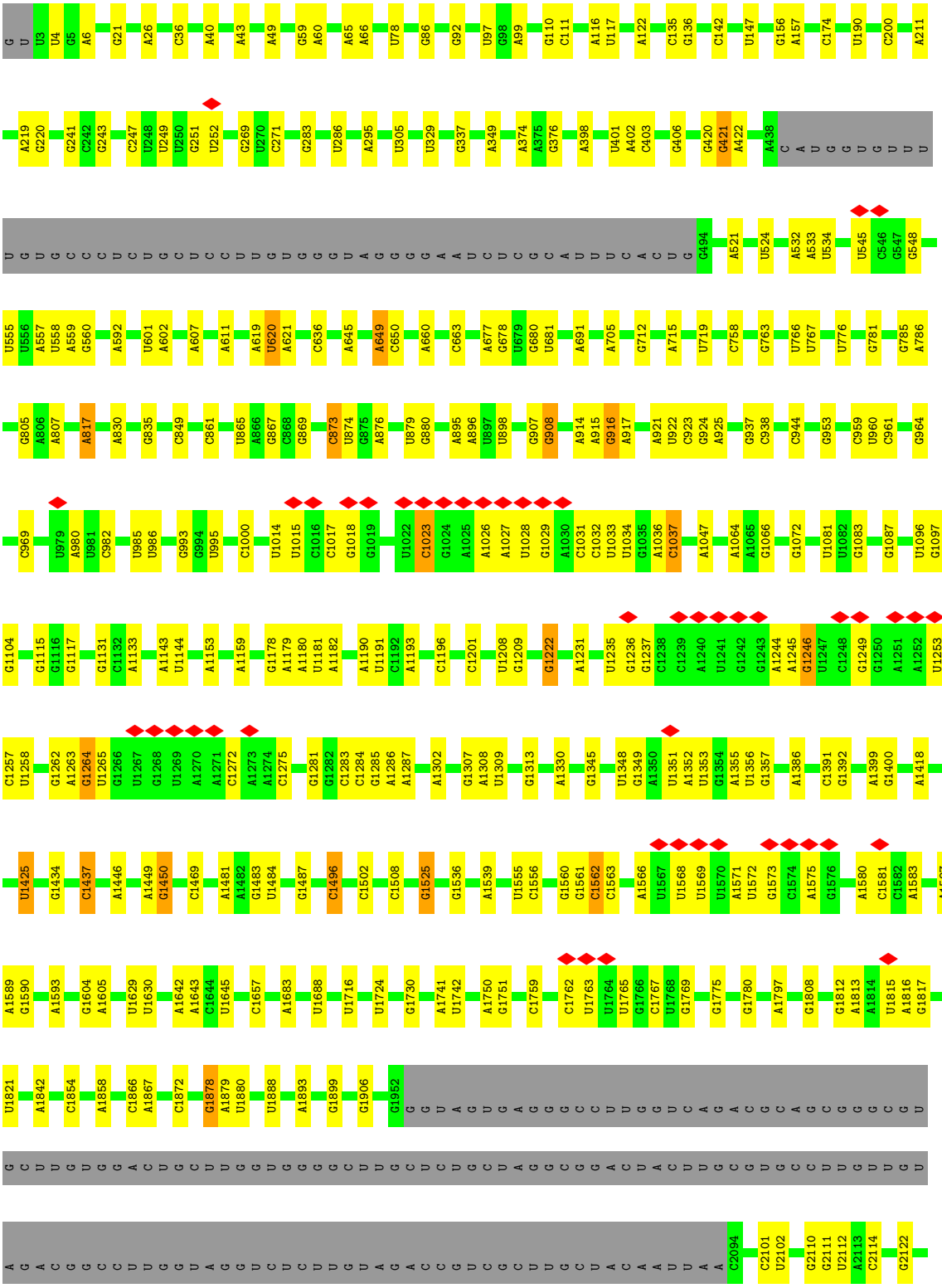
• Molecule 86: 60S ribosomal protein L6-A

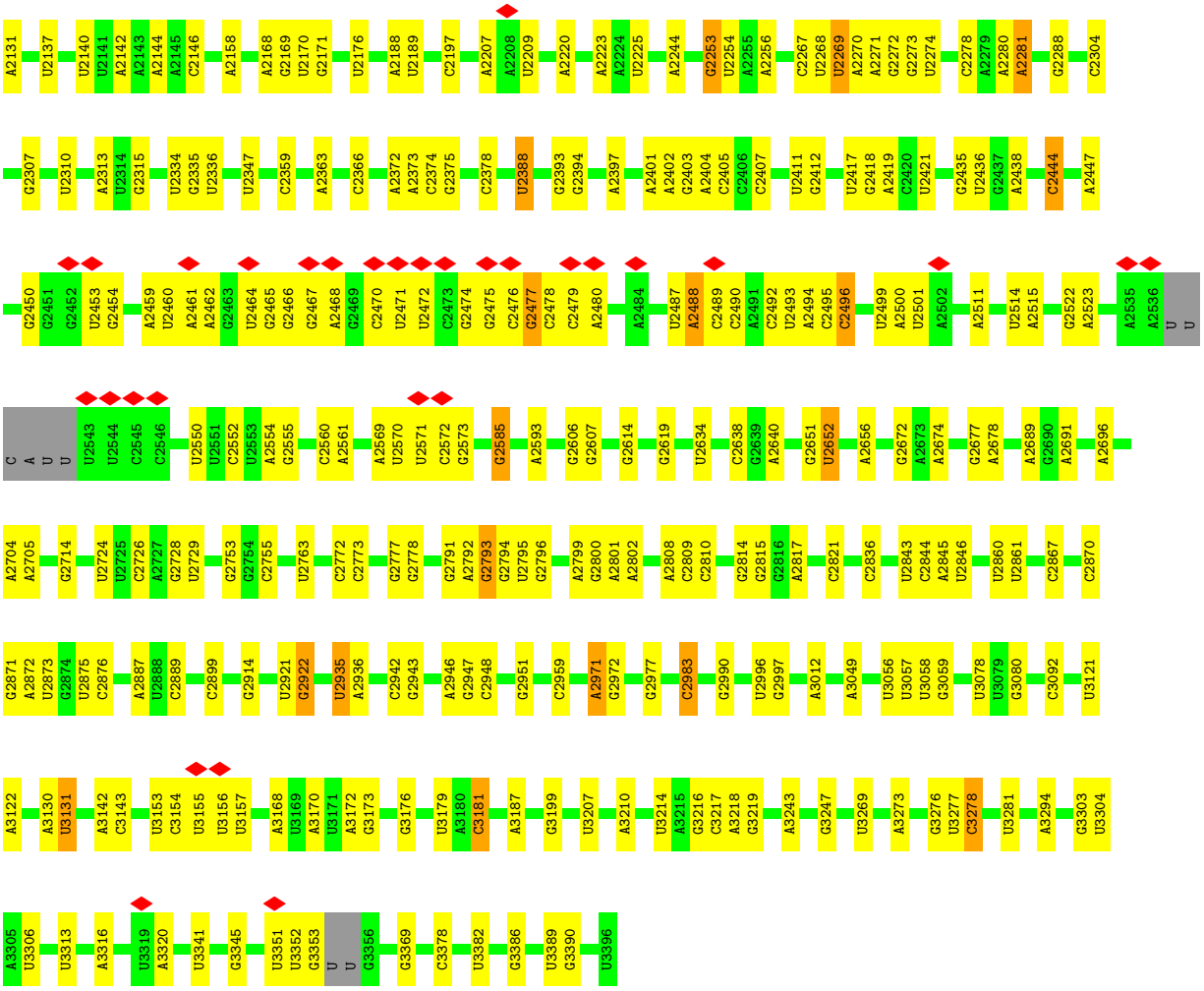
Chain MA:



• Molecule 87: Saccharomyces cerevisiae S288C 18S ribosomal RNA (RDN18-1) with modifications

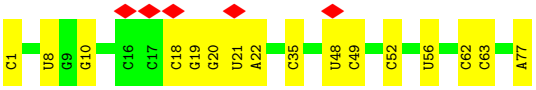
Chain M1:





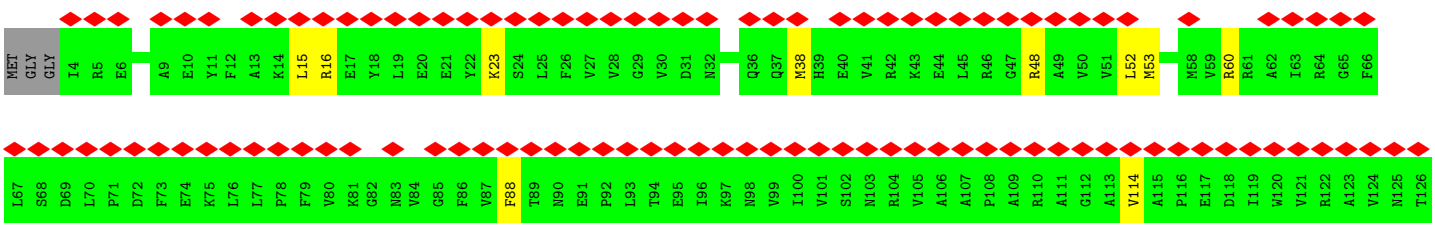
• Molecule 88: tRNA

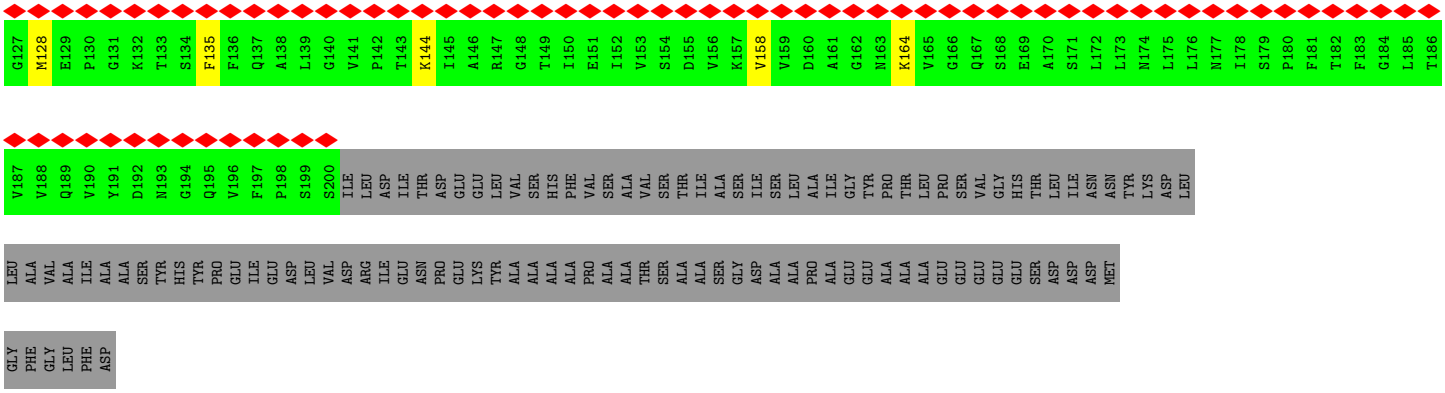
Chain DQ:



• Molecule 89: 60S acidic ribosomal protein P0

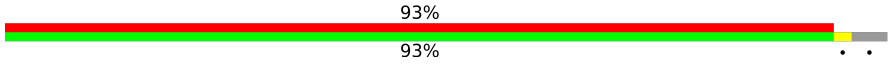
Chain MQ:

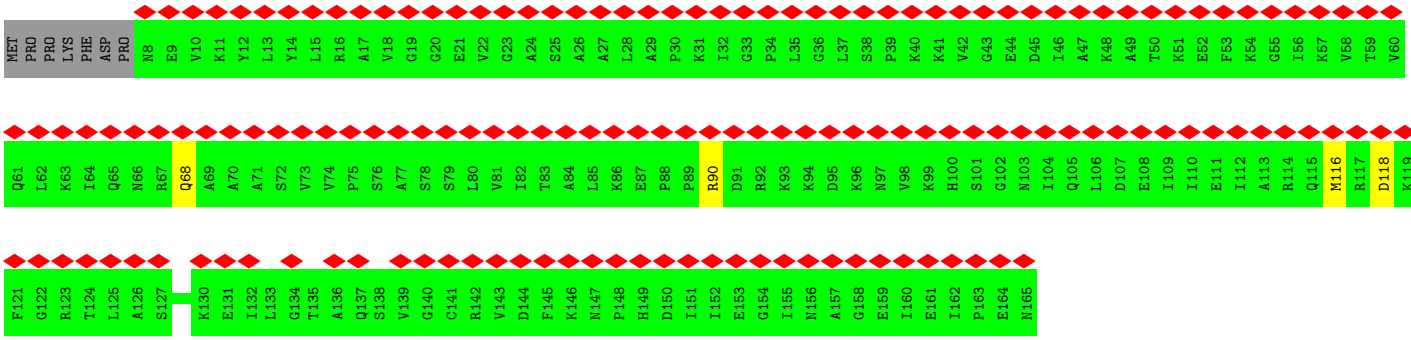




• Molecule 90: 60S ribosomal protein L12-A

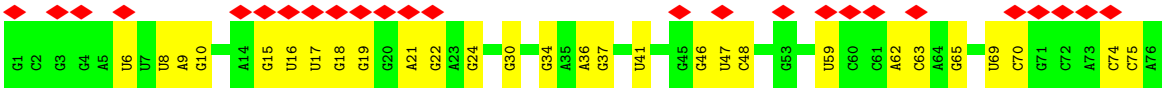
Chain MP:





• Molecule 91: tRNA

Chain DP:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	189911	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	43.6	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.572	Depositor
Minimum map value	-0.178	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.125	Depositor
Recommended contour level	0.44	Depositor
Map size (Å)	655.21497, 655.21497, 655.21497	wwPDB
Map dimensions	627, 627, 627	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: K, 5MC, MG, A2M, OMC, OMU, SPD, 1MA, OMG, ZN, UR3, YYG

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	CC	0.36	0/132	0.69	0/175
2	CM	0.41	0/927	1.14	11/1434 (0.8%)
3	CN	0.26	0/1053	0.59	0/1414
4	CP	0.47	3/1810 (0.2%)	0.86	0/2817
5	L1	0.74	0/74617	0.96	192/116334 (0.2%)
6	L2	0.72	0/3746	0.94	8/5832 (0.1%)
6	M2	0.69	0/3746	0.88	2/5832 (0.0%)
7	L3	0.60	0/2883	0.89	2/4491 (0.0%)
7	M3	0.59	0/2883	0.88	0/4491
8	LA	0.35	0/1327	0.56	0/1791
9	LB	0.39	0/1821	0.56	0/2451
9	MB	0.35	0/1821	0.53	0/2451
10	LC	0.36	0/1836	0.59	1/2481 (0.0%)
10	MC	0.33	0/1836	0.57	2/2481 (0.1%)
11	LD	0.34	0/1529	0.59	0/2060
11	MD	0.33	0/1539	0.56	0/2073
12	LE	0.38	0/1801	0.64	1/2416 (0.0%)
12	ME	0.35	0/1779	0.59	1/2386 (0.0%)
13	LF	0.36	0/1371	0.73	2/1838 (0.1%)
13	MF	0.33	0/1374	0.65	1/1842 (0.1%)
14	LG	0.36	0/1568	0.63	0/2106
14	MG	0.36	0/1568	0.61	0/2106
15	LH	0.33	0/1068	0.60	1/1438 (0.1%)
15	MH	0.33	0/1068	0.54	0/1438
16	LI	0.39	0/1757	0.65	1/2354 (0.0%)
16	MI	0.39	0/1757	0.61	0/2354
17	LJ	0.39	0/1585	0.57	1/2128 (0.0%)
17	MJ	0.36	0/1585	0.55	0/2128
18	LK	0.37	0/1439	0.64	1/1938 (0.1%)
18	MK	0.38	0/1245	0.57	0/1676
19	LL	0.37	0/1465	0.63	1/1965 (0.1%)
19	ML	0.34	0/1465	0.62	1/1965 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
20	LM	0.35	0/1532	0.64	2/2043 (0.1%)
20	MM	0.33	0/1440	0.63	1/1921 (0.1%)
21	LN	0.39	0/1473	0.65	1/1980 (0.1%)
21	MN	0.38	0/1481	0.59	0/1990
22	LO	0.40	0/1300	0.61	0/1743
22	MO	0.36	0/1300	0.59	0/1743
23	La	0.38	0/1018	0.61	0/1369
23	Ma	0.35	0/978	0.60	0/1316
24	Lb	0.37	0/701	0.65	0/934
24	Mb	0.33	0/701	0.61	0/934
25	Lc	0.40	0/836	0.66	0/1104
25	Mc	0.35	0/831	0.60	0/1097
26	Ld	0.34	0/230	0.69	0/296
26	Md	0.34	0/234	0.86	0/300
27	Le	0.35	0/423	0.70	1/562 (0.2%)
27	Me	0.32	0/423	0.55	0/562
28	Lf	0.37	0/443	0.66	0/588
28	Mf	0.35	0/443	0.72	0/588
29	Lg	0.33	0/618	0.71	1/826 (0.1%)
29	Mg	0.33	0/618	0.64	0/826
30	Lh	0.39	0/685	0.62	0/908
30	Mh	0.39	0/680	0.65	0/901
31	Li	0.32	0/772	0.60	0/1026
31	Mi	0.31	0/778	0.61	0/1034
32	Lj	0.35	0/978	0.57	0/1301
32	Mj	0.34	0/978	0.59	1/1301 (0.1%)
33	Lk	0.37	0/846	0.60	0/1130
33	Mk	0.35	0/871	0.59	0/1164
34	Ll	0.42	0/868	0.58	0/1168
34	Ml	0.39	0/868	0.59	0/1168
35	Lm	0.37	0/1038	0.59	0/1390
35	Mm	0.35	0/1041	0.54	0/1394
36	Ln	0.37	0/890	0.63	2/1196 (0.2%)
36	Mn	0.38	0/897	0.73	3/1205 (0.2%)
37	Lo	0.39	0/745	0.56	0/1001
37	Mo	0.35	0/750	0.53	0/1008
38	Lp	0.34	0/473	0.66	1/629 (0.2%)
38	Mp	0.30	0/473	0.52	0/629
39	Lq	0.39	0/1204	0.65	1/1612 (0.1%)
39	Mq	0.37	0/1204	0.61	1/1612 (0.1%)
40	Lr	0.38	0/1118	0.59	0/1497
40	Mr	0.34	0/1118	0.56	0/1497
41	Ls	0.34	0/995	0.60	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
41	Ms	0.35	0/1004	0.64	1/1341 (0.1%)
42	Lt	0.38	0/979	0.64	2/1321 (0.2%)
42	Mt	0.38	0/974	0.66	1/1314 (0.1%)
43	Lu	0.33	0/850	0.60	0/1152
43	Mu	0.34	0/533	0.58	0/707
44	Lv	0.34	0/812	0.64	2/1099 (0.2%)
44	Mv	0.38	0/786	0.82	3/1065 (0.3%)
45	Lw	0.39	0/1933	0.63	0/2598
45	Mw	0.37	0/1948	0.59	0/2617
46	Lx	0.40	0/3146	0.63	0/4228
46	Mx	0.35	0/3146	0.58	0/4228
47	Ly	0.38	0/2800	0.58	0/3790
47	My	0.34	0/2800	0.57	1/3790 (0.0%)
48	Lz	0.33	0/2400	0.61	2/3239 (0.1%)
48	Mz	0.31	0/2425	0.56	1/3271 (0.0%)
49	R1	0.47	0/41891	0.99	183/65273 (0.3%)
49	S1	0.57	0/42211	0.98	151/65773 (0.2%)
50	RA	0.31	0/782	0.73	2/1047 (0.2%)
50	SA	0.34	0/782	0.71	0/1047
51	RB	0.31	0/620	0.68	0/838
51	SB	0.33	0/620	0.68	1/838 (0.1%)
52	SC	0.38	0/488	0.78	0/656
53	RD	0.29	0/452	0.55	0/600
53	SD	0.35	0/452	0.63	0/600
54	RE	0.47	0/391	0.70	0/520
54	SE	0.33	0/480	0.68	0/639
55	RF	0.29	0/557	0.62	0/749
55	SF	0.30	0/567	0.69	0/764
56	RG	0.26	0/2456	0.57	2/3343 (0.1%)
56	SG	0.30	0/2436	0.69	4/3318 (0.1%)
57	Ra	0.33	0/1623	0.65	1/2222 (0.0%)
57	Sa	0.35	0/1644	0.70	3/2249 (0.1%)
58	Rb	0.29	0/1748	0.56	1/2352 (0.0%)
58	Sb	0.34	0/1823	0.73	5/2447 (0.2%)
59	Rc	0.32	0/1665	0.54	0/2263
59	Sc	0.37	0/1656	0.64	1/2251 (0.0%)
60	Rd	0.30	0/1759	0.66	3/2368 (0.1%)
60	Sd	0.30	0/1754	0.59	1/2361 (0.0%)
61	Re	0.30	0/2109	0.58	0/2839
61	Se	0.34	0/2097	0.65	1/2823 (0.0%)
62	Rf	0.29	0/1629	0.63	0/2202
62	Sf	0.30	0/1625	0.66	4/2197 (0.2%)
63	Rg	0.27	0/1779	0.62	1/2379 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
63	Sg	0.29	0/1839	0.64	3/2460 (0.1%)
64	Rh	0.28	0/1511	0.58	0/2036
64	Sh	0.34	0/1498	0.73	1/2019 (0.0%)
65	Ri	0.28	0/1514	0.57	0/2021
65	Si	0.37	0/1501	0.68	0/2006
66	Rj	0.31	0/1519	0.64	2/2035 (0.1%)
66	Sj	0.31	0/1504	0.66	2/2016 (0.1%)
67	Rk	0.36	0/757	0.61	0/1022
67	Sk	0.44	0/769	0.95	5/1039 (0.5%)
68	Rl	0.32	0/1194	0.57	0/1610
68	Sl	0.39	0/1185	0.64	0/1598
69	Rm	0.30	0/898	0.75	2/1220 (0.2%)
69	Sm	0.32	0/883	0.85	4/1199 (0.3%)
70	Rn	0.35	0/1215	0.70	2/1638 (0.1%)
70	Sn	0.38	0/1215	0.68	1/1638 (0.1%)
71	So	0.34	0/937	0.83	4/1261 (0.3%)
72	Rp	0.32	0/959	0.71	1/1288 (0.1%)
72	Sp	0.37	0/936	0.82	1/1259 (0.1%)
73	Rq	0.30	0/1125	0.60	1/1510 (0.1%)
73	Sq	0.34	0/1125	0.63	0/1510
74	Sr	0.38	0/957	0.79	1/1283 (0.1%)
75	Rs	0.32	0/1211	0.71	1/1628 (0.1%)
75	Ss	0.34	0/1211	0.71	0/1628
76	Rt	0.32	0/1130	0.66	2/1517 (0.1%)
76	St	0.37	0/1130	0.79	5/1517 (0.3%)
77	Ru	0.33	0/815	0.72	2/1102 (0.2%)
77	Su	0.33	0/807	0.72	1/1091 (0.1%)
78	Rv	0.35	0/693	0.67	0/935
78	Sv	0.37	0/682	0.73	1/921 (0.1%)
79	Rw	0.33	0/1038	0.64	1/1395 (0.1%)
79	Sw	0.35	0/1038	0.58	0/1395
80	Rx	0.31	0/1139	0.60	0/1518
80	Sx	0.35	0/1139	0.64	0/1518
81	Ry	0.33	0/1087	0.69	3/1449 (0.2%)
81	Sy	0.33	0/1087	0.67	1/1449 (0.1%)
82	Rz	0.35	0/566	0.72	0/761
82	Sz	0.34	0/661	0.80	1/888 (0.1%)
83	RC	0.32	0/499	0.78	1/670 (0.1%)
84	Ro	0.36	0/960	0.82	3/1290 (0.2%)
85	Rr	0.32	0/1010	0.73	2/1355 (0.1%)
86	MA	0.34	0/1251	0.58	0/1682
87	M1	0.69	0/75384	0.94	153/117530 (0.1%)
88	DQ	0.43	1/1836 (0.1%)	0.89	3/2859 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
89	MQ	0.27	0/1558	0.60	2/2107 (0.1%)
90	MP	0.25	0/1210	0.52	0/1627
91	DP	0.29	0/1788	0.95	0/2786
All	All	0.54	4/435297 (0.0%)	0.85	833/639512 (0.1%)

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
9	MB	0	1
10	LC	0	3
11	LD	0	1
13	LF	0	1
14	LG	0	2
15	LH	0	1
16	LI	0	1
17	LJ	0	1
20	LM	0	1
25	Mc	0	1
28	Mf	0	1
32	Lj	0	1
38	Lp	0	1
40	Mr	0	1
42	Lt	0	1
45	Lw	0	1
46	Lx	0	4
47	Ly	0	2
47	My	0	1
50	SA	0	1
55	SF	0	1
57	Ra	0	1
58	Sb	0	2
61	Re	0	1
61	Se	0	1
63	Sg	0	1
64	Rh	0	2
64	Sh	0	1
65	Si	0	1
67	Rk	0	1
69	Sm	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	Sp	0	1
73	Rq	0	1
73	Sq	0	1
75	Rs	0	1
75	Ss	0	1
77	Ru	0	1
80	Sx	0	2
82	Rz	0	1
All	All	0	54

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	DQ	1	C	OP3-P	-10.57	1.48	1.61
4	CP	34	I	C5-C6	6.44	1.52	1.39
4	CP	34	I	N3-C4	6.14	1.48	1.35
4	CP	34	I	C2-N3	5.17	1.46	1.35

The worst 5 of 833 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
87	M1	3278	C	C2-N1-C1'	12.14	132.16	118.80
87	M1	3278	C	N1-C2-O2	11.78	125.97	118.90
49	R1	989	U	N1-C2-O2	11.08	130.56	122.80
63	Rg	69	LEU	CA-CB-CG	10.80	140.15	115.30
49	R1	989	U	N3-C2-O2	-10.47	114.87	122.20

There are no chirality outliers.

5 of 54 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LC	158	ASP	Peptide
10	LC	30	THR	Peptide
10	LC	76	ALA	Peptide
11	LD	21	LYS	Peptide
13	LF	115	LYS	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	
1	CC	12/233 (5%)	11 (92%)	1 (8%)	0	100	100
3	CN	132/151 (87%)	130 (98%)	2 (2%)	0	100	100
8	LA	163/176 (93%)	153 (94%)	10 (6%)	0	100	100
9	LB	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
9	MB	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
10	LC	231/256 (90%)	215 (93%)	16 (7%)	0	100	100
10	MC	231/256 (90%)	221 (96%)	10 (4%)	0	100	100
11	LD	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
11	MD	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
12	LE	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
12	ME	213/221 (96%)	202 (95%)	11 (5%)	0	100	100
13	LF	167/174 (96%)	151 (90%)	16 (10%)	0	100	100
13	MF	167/174 (96%)	153 (92%)	14 (8%)	0	100	100
14	LG	191/199 (96%)	173 (91%)	16 (8%)	2 (1%)	13	40
14	MG	191/199 (96%)	173 (91%)	17 (9%)	1 (0%)	25	56
15	LH	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
15	MH	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
16	LI	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
16	MI	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
17	LJ	195/199 (98%)	188 (96%)	5 (3%)	2 (1%)	13	40
17	MJ	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
18	LK	181/184 (98%)	171 (94%)	10 (6%)	0	100	100
18	MK	152/184 (83%)	149 (98%)	3 (2%)	0	100	100
19	LL	183/186 (98%)	171 (93%)	12 (7%)	0	100	100
19	ML	183/186 (98%)	177 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LM	186/189 (98%)	181 (97%)	4 (2%)	1 (0%)	25	56
20	MM	174/189 (92%)	169 (97%)	4 (2%)	1 (1%)	22	52
21	LN	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
21	MN	170/172 (99%)	159 (94%)	11 (6%)	0	100	100
22	LO	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
22	MO	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
23	La	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
23	Ma	127/137 (93%)	123 (97%)	4 (3%)	0	100	100
24	Lb	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
24	Mb	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
25	Lc	101/106 (95%)	96 (95%)	5 (5%)	0	100	100
25	Mc	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
26	Ld	23/25 (92%)	23 (100%)	0	0	100	100
26	Md	23/25 (92%)	23 (100%)	0	0	100	100
27	Le	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
27	Me	50/128 (39%)	50 (100%)	0	0	100	100
28	Lf	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
28	Mf	48/51 (94%)	41 (85%)	7 (15%)	0	100	100
29	Lg	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
29	Mg	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
30	Lh	83/88 (94%)	80 (96%)	3 (4%)	0	100	100
30	Mh	82/88 (93%)	75 (92%)	7 (8%)	0	100	100
31	Li	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
31	Mi	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
32	Lj	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
32	Mj	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
33	Lk	104/121 (86%)	100 (96%)	4 (4%)	0	100	100
33	Mk	107/121 (88%)	105 (98%)	2 (2%)	0	100	100
34	Ll	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
34	Ml	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
35	Lm	125/130 (96%)	121 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Mm	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
36	Ln	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
36	Mn	107/113 (95%)	98 (92%)	8 (8%)	1 (1%)	14	43
37	Lo	94/105 (90%)	94 (100%)	0	0	100	100
37	Mo	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
38	Lp	56/59 (95%)	46 (82%)	10 (18%)	0	100	100
38	Mp	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
39	Lq	146/149 (98%)	124 (85%)	21 (14%)	1 (1%)	19	49
39	Mq	146/149 (98%)	133 (91%)	12 (8%)	1 (1%)	19	49
40	Lr	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
40	Mr	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
41	Ls	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
41	Ms	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
42	Lt	119/142 (84%)	112 (94%)	6 (5%)	1 (1%)	16	45
42	Mt	118/142 (83%)	112 (95%)	6 (5%)	0	100	100
43	Lu	124/155 (80%)	115 (93%)	9 (7%)	0	100	100
43	Mu	61/155 (39%)	61 (100%)	0	0	100	100
44	Lv	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
44	Mv	95/121 (78%)	86 (90%)	9 (10%)	0	100	100
45	Lw	249/254 (98%)	227 (91%)	22 (9%)	0	100	100
45	Mw	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
46	Lx	384/387 (99%)	356 (93%)	26 (7%)	2 (0%)	25	56
46	Mx	384/387 (99%)	365 (95%)	19 (5%)	0	100	100
47	Ly	359/362 (99%)	331 (92%)	26 (7%)	2 (1%)	22	52
47	My	359/362 (99%)	340 (95%)	19 (5%)	0	100	100
48	Lz	292/297 (98%)	277 (95%)	14 (5%)	1 (0%)	37	66
48	Mz	294/297 (99%)	278 (95%)	16 (5%)	0	100	100
50	RA	95/119 (80%)	82 (86%)	13 (14%)	0	100	100
50	SA	95/119 (80%)	83 (87%)	10 (10%)	2 (2%)	5	22
51	RB	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
51	SB	79/82 (96%)	67 (85%)	12 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	SC	60/67 (90%)	58 (97%)	2 (3%)	0	100	100
53	RD	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
53	SD	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
54	RE	46/63 (73%)	45 (98%)	1 (2%)	0	100	100
54	SE	58/63 (92%)	52 (90%)	6 (10%)	0	100	100
55	RF	68/152 (45%)	53 (78%)	15 (22%)	0	100	100
55	SF	71/152 (47%)	50 (70%)	21 (30%)	0	100	100
56	RG	311/319 (98%)	297 (96%)	14 (4%)	0	100	100
56	SG	310/319 (97%)	282 (91%)	28 (9%)	0	100	100
57	Ra	204/252 (81%)	173 (85%)	30 (15%)	1 (0%)	25	56
57	Sa	204/252 (81%)	181 (89%)	23 (11%)	0	100	100
58	Rb	214/255 (84%)	201 (94%)	13 (6%)	0	100	100
58	Sb	222/255 (87%)	194 (87%)	26 (12%)	2 (1%)	14	43
59	Rc	215/254 (85%)	208 (97%)	7 (3%)	0	100	100
59	Sc	214/254 (84%)	203 (95%)	11 (5%)	0	100	100
60	Rd	221/240 (92%)	207 (94%)	14 (6%)	0	100	100
60	Sd	220/240 (92%)	211 (96%)	9 (4%)	0	100	100
61	Re	258/261 (99%)	239 (93%)	18 (7%)	1 (0%)	30	60
61	Se	256/261 (98%)	230 (90%)	25 (10%)	1 (0%)	30	60
62	Rf	204/225 (91%)	186 (91%)	18 (9%)	0	100	100
62	Sf	204/225 (91%)	190 (93%)	14 (7%)	0	100	100
63	Rg	216/236 (92%)	204 (94%)	12 (6%)	0	100	100
63	Sg	226/236 (96%)	210 (93%)	14 (6%)	2 (1%)	14	43
64	Rh	183/190 (96%)	169 (92%)	14 (8%)	0	100	100
64	Sh	182/190 (96%)	169 (93%)	13 (7%)	0	100	100
65	Ri	184/200 (92%)	178 (97%)	6 (3%)	0	100	100
65	Si	183/200 (92%)	162 (88%)	19 (10%)	2 (1%)	12	37
66	Rj	183/197 (93%)	166 (91%)	17 (9%)	0	100	100
66	Sj	182/197 (92%)	164 (90%)	18 (10%)	0	100	100
67	Rk	90/105 (86%)	73 (81%)	17 (19%)	0	100	100
67	Sk	90/105 (86%)	79 (88%)	11 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Rl	144/156 (92%)	135 (94%)	9 (6%)	0	100	100
68	Sl	142/156 (91%)	129 (91%)	13 (9%)	0	100	100
69	Rm	122/143 (85%)	101 (83%)	21 (17%)	0	100	100
69	Sm	119/143 (83%)	90 (76%)	27 (23%)	2 (2%)	7	27
70	Rn	148/151 (98%)	137 (93%)	11 (7%)	0	100	100
70	Sn	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
71	So	125/137 (91%)	108 (86%)	16 (13%)	1 (1%)	16	45
72	Rp	117/142 (82%)	102 (87%)	14 (12%)	1 (1%)	14	43
72	Sp	115/142 (81%)	103 (90%)	12 (10%)	0	100	100
73	Rq	139/143 (97%)	129 (93%)	10 (7%)	0	100	100
73	Sq	139/143 (97%)	126 (91%)	12 (9%)	1 (1%)	19	49
74	Sr	117/136 (86%)	111 (95%)	6 (5%)	0	100	100
75	Rs	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
75	Ss	143/146 (98%)	128 (90%)	13 (9%)	2 (1%)	9	31
76	Rt	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
76	St	141/144 (98%)	126 (89%)	15 (11%)	0	100	100
77	Ru	99/121 (82%)	90 (91%)	8 (8%)	1 (1%)	13	40
77	Su	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
78	Rv	85/87 (98%)	79 (93%)	6 (7%)	0	100	100
78	Sv	85/87 (98%)	73 (86%)	12 (14%)	0	100	100
79	Rw	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
79	Sw	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
80	Rx	142/145 (98%)	133 (94%)	9 (6%)	0	100	100
80	Sx	142/145 (98%)	123 (87%)	18 (13%)	1 (1%)	19	49
81	Ry	132/135 (98%)	122 (92%)	9 (7%)	1 (1%)	16	45
81	Sy	132/135 (98%)	123 (93%)	9 (7%)	0	100	100
82	Rz	67/108 (62%)	63 (94%)	4 (6%)	0	100	100
82	Sz	80/108 (74%)	69 (86%)	11 (14%)	0	100	100
83	RC	61/67 (91%)	58 (95%)	3 (5%)	0	100	100
84	Ro	126/138 (91%)	106 (84%)	20 (16%)	0	100	100
85	Rr	123/136 (90%)	116 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
86	MA	151/176 (86%)	140 (93%)	11 (7%)	0	100 100
89	MQ	195/312 (62%)	189 (97%)	6 (3%)	0	100 100
90	MP	156/165 (94%)	146 (94%)	10 (6%)	0	100 100
All	All	22304/24622 (91%)	20726 (93%)	1541 (7%)	37 (0%)	45 73

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	LJ	111	PRO
50	SA	84	VAL
65	Si	10	LYS
14	MG	63	VAL
14	LG	63	VAL

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
1	CC	13/215 (6%)	11 (85%)	2 (15%)	2 7
3	CN	112/123 (91%)	104 (93%)	8 (7%)	12 36
8	LA	138/155 (89%)	131 (95%)	7 (5%)	20 51
9	LB	186/205 (91%)	173 (93%)	13 (7%)	12 36
9	MB	186/205 (91%)	183 (98%)	3 (2%)	58 84
10	LC	187/208 (90%)	176 (94%)	11 (6%)	16 45
10	MC	187/208 (90%)	177 (95%)	10 (5%)	19 49
11	LD	168/171 (98%)	157 (94%)	11 (6%)	14 40
11	MD	171/171 (100%)	160 (94%)	11 (6%)	14 41
12	LE	185/187 (99%)	169 (91%)	16 (9%)	8 27
12	ME	184/187 (98%)	176 (96%)	8 (4%)	25 57
13	LF	146/150 (97%)	137 (94%)	9 (6%)	15 43
13	MF	147/150 (98%)	137 (93%)	10 (7%)	13 38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	LG	154/159 (97%)	144 (94%)	10 (6%)	14 40
14	MG	154/159 (97%)	146 (95%)	8 (5%)	19 50
15	LH	107/109 (98%)	100 (94%)	7 (6%)	14 40
15	MH	107/109 (98%)	104 (97%)	3 (3%)	38 73
16	LI	175/176 (99%)	163 (93%)	12 (7%)	13 37
16	MI	175/176 (99%)	166 (95%)	9 (5%)	20 51
17	LJ	160/162 (99%)	154 (96%)	6 (4%)	28 63
17	MJ	160/162 (99%)	158 (99%)	2 (1%)	65 88
18	LK	138/146 (94%)	131 (95%)	7 (5%)	20 51
18	MK	125/146 (86%)	117 (94%)	8 (6%)	14 41
19	LL	150/151 (99%)	144 (96%)	6 (4%)	27 61
19	ML	150/151 (99%)	148 (99%)	2 (1%)	65 88
20	LM	152/154 (99%)	143 (94%)	9 (6%)	16 45
20	MM	143/154 (93%)	136 (95%)	7 (5%)	21 53
21	LN	155/156 (99%)	146 (94%)	9 (6%)	17 46
21	MN	156/156 (100%)	148 (95%)	8 (5%)	20 51
22	LO	136/137 (99%)	126 (93%)	10 (7%)	11 34
22	MO	136/137 (99%)	128 (94%)	8 (6%)	16 45
23	La	104/105 (99%)	95 (91%)	9 (9%)	8 27
23	Ma	101/105 (96%)	98 (97%)	3 (3%)	36 71
24	Lb	71/72 (99%)	69 (97%)	2 (3%)	38 73
24	Mb	71/72 (99%)	69 (97%)	2 (3%)	38 73
25	Lc	87/91 (96%)	77 (88%)	10 (12%)	4 15
25	Mc	87/91 (96%)	82 (94%)	5 (6%)	17 47
26	Ld	22/23 (96%)	21 (96%)	1 (4%)	23 56
26	Md	23/23 (100%)	19 (83%)	4 (17%)	1 5
27	Le	47/116 (40%)	47 (100%)	0	100 100
27	Me	47/116 (40%)	46 (98%)	1 (2%)	48 78
28	Lf	45/46 (98%)	44 (98%)	1 (2%)	47 78
28	Mf	45/46 (98%)	45 (100%)	0	100 100
29	Lg	68/69 (99%)	64 (94%)	4 (6%)	16 45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
29	Mg	68/69 (99%)	62 (91%)	6 (9%)	8 26
30	Lh	69/71 (97%)	66 (96%)	3 (4%)	25 57
30	Mh	69/71 (97%)	66 (96%)	3 (4%)	25 57
31	Li	80/82 (98%)	75 (94%)	5 (6%)	15 42
31	Mi	81/82 (99%)	77 (95%)	4 (5%)	21 53
32	Lj	104/105 (99%)	99 (95%)	5 (5%)	21 54
32	Mj	104/105 (99%)	100 (96%)	4 (4%)	28 63
33	Lk	91/103 (88%)	89 (98%)	2 (2%)	47 78
33	Mk	94/103 (91%)	92 (98%)	2 (2%)	48 78
34	Ll	90/91 (99%)	88 (98%)	2 (2%)	47 78
34	Ml	90/91 (99%)	88 (98%)	2 (2%)	47 78
35	Lm	108/111 (97%)	103 (95%)	5 (5%)	23 55
35	Mm	109/111 (98%)	106 (97%)	3 (3%)	38 73
36	Ln	92/97 (95%)	85 (92%)	7 (8%)	11 32
36	Mn	94/97 (97%)	90 (96%)	4 (4%)	25 57
37	Lo	81/88 (92%)	75 (93%)	6 (7%)	11 34
37	Mo	81/88 (92%)	78 (96%)	3 (4%)	29 64
38	Lp	46/47 (98%)	44 (96%)	2 (4%)	25 57
38	Mp	46/47 (98%)	46 (100%)	0	100 100
39	Lq	118/119 (99%)	109 (92%)	9 (8%)	11 32
39	Mq	118/119 (99%)	108 (92%)	10 (8%)	8 27
40	Lr	115/116 (99%)	106 (92%)	9 (8%)	10 31
40	Mr	115/116 (99%)	111 (96%)	4 (4%)	31 66
41	Ls	108/110 (98%)	97 (90%)	11 (10%)	6 19
41	Ms	109/110 (99%)	104 (95%)	5 (5%)	23 55
42	Lt	104/118 (88%)	101 (97%)	3 (3%)	37 72
42	Mt	104/118 (88%)	99 (95%)	5 (5%)	21 54
43	Lu	56/129 (43%)	56 (100%)	0	100 100
43	Mu	55/129 (43%)	54 (98%)	1 (2%)	54 82
44	Lv	87/107 (81%)	84 (97%)	3 (3%)	32 67
44	Mv	84/107 (78%)	77 (92%)	7 (8%)	9 28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
45	Lw	190/196 (97%)	183 (96%)	7 (4%)	29 64
45	Mw	193/196 (98%)	190 (98%)	3 (2%)	58 84
46	Lx	319/323 (99%)	302 (95%)	17 (5%)	19 49
46	Mx	320/323 (99%)	309 (97%)	11 (3%)	32 67
47	Ly	288/289 (100%)	273 (95%)	15 (5%)	19 50
47	My	288/289 (100%)	280 (97%)	8 (3%)	38 73
48	Lz	241/245 (98%)	232 (96%)	9 (4%)	29 64
48	Mz	244/245 (100%)	236 (97%)	8 (3%)	33 68
50	RA	83/101 (82%)	77 (93%)	6 (7%)	12 35
50	SA	83/101 (82%)	79 (95%)	4 (5%)	21 54
51	RB	70/71 (99%)	65 (93%)	5 (7%)	12 36
51	SB	70/71 (99%)	66 (94%)	4 (6%)	17 47
52	SC	55/60 (92%)	51 (93%)	4 (7%)	11 34
53	RD	47/49 (96%)	44 (94%)	3 (6%)	14 41
53	SD	47/49 (96%)	43 (92%)	4 (8%)	8 27
54	RE	41/54 (76%)	40 (98%)	1 (2%)	44 76
54	SE	50/54 (93%)	45 (90%)	5 (10%)	6 20
55	RF	55/135 (41%)	50 (91%)	5 (9%)	7 25
55	SF	56/135 (42%)	49 (88%)	7 (12%)	3 12
56	RG	255/262 (97%)	242 (95%)	13 (5%)	20 51
56	SG	250/262 (95%)	237 (95%)	13 (5%)	19 50
57	Ra	165/210 (79%)	156 (94%)	9 (6%)	18 48
57	Sa	170/210 (81%)	157 (92%)	13 (8%)	11 32
58	Rb	192/224 (86%)	184 (96%)	8 (4%)	25 59
58	Sb	200/224 (89%)	185 (92%)	15 (8%)	11 33
59	Rc	176/205 (86%)	172 (98%)	4 (2%)	45 77
59	Sc	175/205 (85%)	165 (94%)	10 (6%)	17 47
60	Rd	182/195 (93%)	164 (90%)	18 (10%)	6 21
60	Sd	182/195 (93%)	170 (93%)	12 (7%)	14 39
61	Re	221/222 (100%)	213 (96%)	8 (4%)	30 65
61	Se	220/222 (99%)	210 (96%)	10 (4%)	23 56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	Rf	173/191 (91%)	167 (96%)	6 (4%)	31	66
62	Sf	172/191 (90%)	166 (96%)	6 (4%)	31	66
63	Rg	187/201 (93%)	180 (96%)	7 (4%)	29	64
63	Sg	189/201 (94%)	177 (94%)	12 (6%)	15	42
64	Rh	165/170 (97%)	157 (95%)	8 (5%)	21	54
64	Sh	163/170 (96%)	151 (93%)	12 (7%)	11	34
65	Ri	150/161 (93%)	145 (97%)	5 (3%)	33	68
65	Si	148/161 (92%)	139 (94%)	9 (6%)	15	43
66	Rj	158/166 (95%)	150 (95%)	8 (5%)	20	51
66	Sj	156/166 (94%)	145 (93%)	11 (7%)	12	36
67	Rk	73/98 (74%)	68 (93%)	5 (7%)	13	38
67	Sk	77/98 (79%)	65 (84%)	12 (16%)	2	7
68	Rl	129/137 (94%)	120 (93%)	9 (7%)	12	36
68	Sl	129/137 (94%)	120 (93%)	9 (7%)	12	36
69	Rm	88/119 (74%)	80 (91%)	8 (9%)	7	25
69	Sm	88/119 (74%)	78 (89%)	10 (11%)	4	15
70	Rn	127/128 (99%)	119 (94%)	8 (6%)	15	42
70	Sn	127/128 (99%)	118 (93%)	9 (7%)	12	36
71	So	91/105 (87%)	86 (94%)	5 (6%)	18	48
72	Rp	98/118 (83%)	88 (90%)	10 (10%)	6	19
72	Sp	95/118 (80%)	85 (90%)	10 (10%)	5	18
73	Rq	117/119 (98%)	113 (97%)	4 (3%)	32	67
73	Sq	117/119 (98%)	110 (94%)	7 (6%)	16	44
74	Sr	101/124 (82%)	94 (93%)	7 (7%)	13	37
75	Rs	128/129 (99%)	119 (93%)	9 (7%)	12	36
75	Ss	128/129 (99%)	121 (94%)	7 (6%)	18	48
76	Rt	115/116 (99%)	110 (96%)	5 (4%)	25	57
76	St	115/116 (99%)	107 (93%)	8 (7%)	12	36
77	Ru	94/114 (82%)	88 (94%)	6 (6%)	14	41
77	Su	93/114 (82%)	87 (94%)	6 (6%)	14	40
78	Rv	74/74 (100%)	69 (93%)	5 (7%)	13	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
78	Sv	71/74 (96%)	64 (90%)	7 (10%)	6 21
79	Rw	110/111 (99%)	104 (94%)	6 (6%)	18 48
79	Sw	110/111 (99%)	103 (94%)	7 (6%)	14 41
80	Rx	119/120 (99%)	115 (97%)	4 (3%)	32 67
80	Sx	119/120 (99%)	113 (95%)	6 (5%)	20 52
81	Ry	112/113 (99%)	109 (97%)	3 (3%)	40 73
81	Sy	112/113 (99%)	106 (95%)	6 (5%)	18 49
82	Rz	61/89 (68%)	55 (90%)	6 (10%)	6 21
82	Sz	67/89 (75%)	63 (94%)	4 (6%)	16 44
83	RC	56/60 (93%)	55 (98%)	1 (2%)	54 82
84	Ro	97/105 (92%)	87 (90%)	10 (10%)	6 19
85	Rr	113/124 (91%)	107 (95%)	6 (5%)	19 49
86	MA	133/153 (87%)	126 (95%)	7 (5%)	19 49
89	MQ	167/254 (66%)	154 (92%)	13 (8%)	10 31
90	MP	129/136 (95%)	125 (97%)	4 (3%)	35 70
All	All	18800/20698 (91%)	17781 (95%)	1019 (5%)	21 49

5 of 1019 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	Sl	11	ARG
48	Mz	232	ASP
75	Rs	57	ARG
47	My	362	ASP
13	MF	11	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
69	Sm	139	HIS
70	Rn	58	HIS
74	Sr	105	GLN
28	Mf	33	ASN
62	Rf	37	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CM	40/41 (97%)	17 (42%)	1 (2%)
4	CP	75/76 (98%)	11 (14%)	0
49	R1	1755/1800 (97%)	474 (27%)	26 (1%)
49	S1	1768/1800 (98%)	461 (26%)	37 (2%)
5	L1	3111/3396 (91%)	583 (18%)	33 (1%)
6	L2	157/158 (99%)	26 (16%)	1 (0%)
6	M2	157/158 (99%)	24 (15%)	0
7	L3	120/121 (99%)	13 (10%)	1 (0%)
7	M3	120/121 (99%)	11 (9%)	1 (0%)
87	M1	3185/3396 (93%)	505 (15%)	14 (0%)
88	DQ	76/77 (98%)	13 (17%)	0
91	DP	75/76 (98%)	26 (34%)	1 (1%)
All	All	10639/11220 (94%)	2164 (20%)	115 (1%)

5 of 2164 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CM	2	U
2	CM	7	U
2	CM	14	U
2	CM	15	U
2	CM	16	U

5 of 115 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S1	928	U
87	M1	2792	A
49	S1	1636	C
87	M1	2500	A
87	M1	601	U

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

43 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
87	UR3	M1	2634	87	19,22,23	2.99	8 (42%)	26,32,35	1.42	3 (11%)
87	A2M	M1	2640	87	18,25,26	4.21	8 (44%)	18,36,39	4.26	4 (22%)
87	OMU	M1	2921	87	19,22,23	2.95	8 (42%)	26,31,34	1.75	4 (15%)
87	OMG	M1	867	94,87	18,26,27	1.29	2 (11%)	19,38,41	0.93	1 (5%)
87	OMU	M1	2421	87	19,22,23	2.81	7 (36%)	26,31,34	1.85	5 (19%)
87	OMC	M1	2337	87	19,22,23	0.72	0	26,31,34	0.73	0
87	OMG	M1	1450	87	18,26,27	1.26	3 (16%)	19,38,41	0.88	1 (5%)
87	OMU	M1	2729	87	19,22,23	2.87	7 (36%)	26,31,34	1.81	5 (19%)
87	OMG	M1	2793	87	18,26,27	1.36	3 (16%)	19,38,41	0.86	1 (5%)
87	OMG	M1	908	87	18,26,27	1.26	2 (11%)	19,38,41	0.89	1 (5%)
87	OMG	M1	2922	91,87	18,26,27	1.25	3 (16%)	19,38,41	0.83	1 (5%)
87	OMU	M1	1888	87	19,22,23	2.94	8 (42%)	26,31,34	1.80	5 (19%)
87	OMG	M1	2791	87	18,26,27	1.24	2 (11%)	19,38,41	0.81	1 (5%)
87	5MC	M1	2870	94,87	18,22,23	0.85	1 (5%)	26,32,35	0.78	0
87	OMC	M1	663	87	19,22,23	0.69	0	26,31,34	0.93	1 (3%)
87	OMU	M1	898	87	19,22,23	2.88	8 (42%)	26,31,34	1.70	5 (19%)
87	OMC	M1	650	92,87	19,22,23	0.73	1 (5%)	26,31,34	0.73	0
87	OMG	M1	2288	87	18,26,27	1.32	3 (16%)	19,38,41	0.77	1 (5%)
87	A2M	M1	2281	87	18,25,26	4.00	7 (38%)	18,36,39	4.09	4 (22%)
87	OMC	M1	1437	92,87	19,22,23	0.71	0	26,31,34	0.99	1 (3%)
87	A2M	M1	1133	92,87	18,25,26	4.25	7 (38%)	18,36,39	4.05	4 (22%)
87	OMU	M1	2347	87	19,22,23	2.97	7 (36%)	26,31,34	1.78	5 (19%)
87	A2M	M1	817	92,87	18,25,26	4.16	8 (44%)	18,36,39	4.33	4 (22%)
87	OMG	M1	2619	87	18,26,27	1.25	3 (16%)	19,38,41	0.86	1 (5%)
87	A2M	M1	807	87	18,25,26	4.16	7 (38%)	18,36,39	4.33	4 (22%)
87	A2M	M1	2220	87	18,25,26	4.25	7 (38%)	18,36,39	4.26	4 (22%)
87	5MC	M1	2278	92,87	18,22,23	0.75	1 (5%)	26,32,35	1.05	2 (7%)
87	OMG	M1	2815	87	18,26,27	1.25	3 (16%)	19,38,41	0.95	1 (5%)
87	A2M	M1	1449	92,87	18,25,26	4.25	8 (44%)	18,36,39	4.35	4 (22%)
87	A2M	M1	2256	87	18,25,26	4.16	7 (38%)	18,36,39	4.36	7 (38%)
87	A2M	M1	2946	92,87	18,25,26	4.19	8 (44%)	18,36,39	4.26	5 (27%)
87	1MA	M1	2142	92,87	16,25,26	1.12	2 (12%)	18,37,40	1.12	1 (5%)
87	A2M	M1	649	87	18,25,26	4.10	7 (38%)	18,36,39	4.39	5 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
87	A2M	M1	2280	87	18,25,26	4.27	8 (44%)	18,36,39	4.24	4 (22%)
87	OMC	M1	2197	94,87	19,22,23	0.71	1 (5%)	26,31,34	0.67	0
91	YYG	DP	37	91	31,42,43	1.20	4 (12%)	33,62,65	1.90	3 (9%)
87	A2M	M1	876	87	18,25,26	4.23	8 (44%)	18,36,39	4.41	4 (22%)
87	OMU	M1	2417	87	19,22,23	2.79	7 (36%)	26,31,34	1.79	5 (19%)
87	OMU	M1	2724	87	19,22,23	2.88	8 (42%)	26,31,34	1.71	5 (19%)
87	OMC	M1	2948	87	19,22,23	0.68	0	26,31,34	0.93	2 (7%)
87	1MA	M1	645	92,87	16,25,26	1.07	2 (12%)	18,37,40	1.06	1 (5%)
87	OMG	M1	805	87	18,26,27	1.27	3 (16%)	19,38,41	0.93	1 (5%)
87	OMC	M1	2959	87	19,22,23	0.68	0	26,31,34	0.82	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	UR3	M1	2634	87	-	0/7/25/26	0/2/2/2
87	A2M	M1	2640	87	-	0/5/27/28	0/3/3/3
87	OMU	M1	2921	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	867	94,87	-	0/5/27/28	0/3/3/3
87	OMU	M1	2421	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	2337	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	1450	87	-	2/5/27/28	0/3/3/3
87	OMU	M1	2729	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	2793	87	-	0/5/27/28	0/3/3/3
87	OMG	M1	908	87	-	0/5/27/28	0/3/3/3
87	OMG	M1	2922	91,87	-	4/5/27/28	0/3/3/3
87	OMU	M1	1888	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	2791	87	-	0/5/27/28	0/3/3/3
87	5MC	M1	2870	94,87	-	4/7/25/26	0/2/2/2
87	OMC	M1	663	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	898	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	650	92,87	-	0/9/27/28	0/2/2/2
87	OMG	M1	2288	87	-	0/5/27/28	0/3/3/3
87	A2M	M1	2281	87	-	2/5/27/28	0/3/3/3
87	OMC	M1	1437	92,87	-	2/9/27/28	0/2/2/2
87	A2M	M1	1133	92,87	-	0/5/27/28	0/3/3/3
87	OMU	M1	2347	87	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	A2M	M1	817	92,87	-	2/5/27/28	0/3/3/3
87	OMG	M1	2619	87	-	3/5/27/28	0/3/3/3
87	A2M	M1	807	87	-	0/5/27/28	0/3/3/3
87	A2M	M1	2220	87	-	1/5/27/28	0/3/3/3
87	5MC	M1	2278	92,87	-	2/7/25/26	0/2/2/2
87	OMG	M1	2815	87	-	0/5/27/28	0/3/3/3
87	A2M	M1	1449	92,87	-	0/5/27/28	0/3/3/3
87	A2M	M1	2256	87	-	2/5/27/28	0/3/3/3
87	A2M	M1	2946	92,87	-	1/5/27/28	0/3/3/3
87	1MA	M1	2142	92,87	-	0/3/25/26	0/3/3/3
87	A2M	M1	649	87	-	2/5/27/28	0/3/3/3
87	A2M	M1	2280	87	-	2/5/27/28	0/3/3/3
87	OMC	M1	2197	94,87	-	4/9/27/28	0/2/2/2
91	YYG	DP	37	91	-	6/20/42/43	0/3/4/4
87	A2M	M1	876	87	-	0/5/27/28	0/3/3/3
87	OMU	M1	2417	87	-	1/9/27/28	0/2/2/2
87	OMU	M1	2724	87	-	1/9/27/28	0/2/2/2
87	OMC	M1	2948	87	-	0/9/27/28	0/2/2/2
87	1MA	M1	645	92,87	-	0/3/25/26	0/3/3/3
87	OMG	M1	805	87	-	0/5/27/28	0/3/3/3
87	OMC	M1	2959	87	-	0/9/27/28	0/2/2/2

The worst 5 of 197 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	2280	A2M	O4'-C1'	15.14	1.62	1.41
87	M1	2220	A2M	O4'-C1'	15.11	1.62	1.41
87	M1	1449	A2M	O4'-C1'	15.06	1.62	1.41
87	M1	1133	A2M	O4'-C1'	15.03	1.62	1.41
87	M1	876	A2M	O4'-C1'	15.01	1.62	1.41

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
87	M1	649	A2M	C5-C6-N6	12.00	138.59	120.35
87	M1	817	A2M	C5-C6-N6	11.99	138.57	120.35
87	M1	876	A2M	C5-C6-N6	11.91	138.45	120.35
87	M1	807	A2M	C5-C6-N6	11.60	137.98	120.35
87	M1	1449	A2M	C5-C6-N6	11.48	137.80	120.35

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
87	M1	1437	OMC	C1'-C2'-O2'-CM2
87	M1	1450	OMG	O4'-C4'-C5'-O5'
87	M1	2220	A2M	C1'-C2'-O2'-CM'
87	M1	2256	A2M	C1'-C2'-O2'-CM'
87	M1	2417	OMU	C1'-C2'-O2'-CM2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 327 ligands modelled in this entry, 324 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
95	SPD	M1	3604	-	9,9,9	0.28	0	8,8,8	0.41	0
95	SPD	M1	3603	-	9,9,9	0.31	0	8,8,8	0.32	0
95	SPD	M1	3602	-	9,9,9	0.28	0	8,8,8	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
95	SPD	M1	3604	-	-	3/7/7/7	-
95	SPD	M1	3603	-	-	3/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
95	SPD	M1	3602	-	-	1/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
95	M1	3604	SPD	C8-C7-N6-C5
95	M1	3603	SPD	C7-C8-C9-N10
95	M1	3603	SPD	N1-C2-C3-C4
95	M1	3603	SPD	C2-C3-C4-C5
95	M1	3604	SPD	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

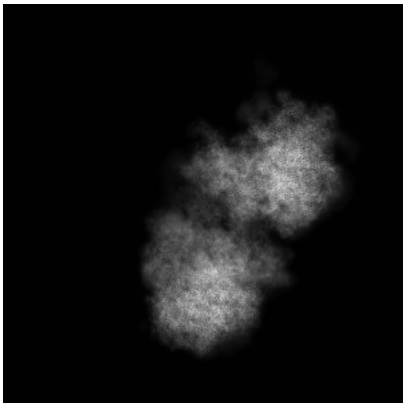
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-50259. These allow visual inspection of the internal detail of the map and identification of artifacts.

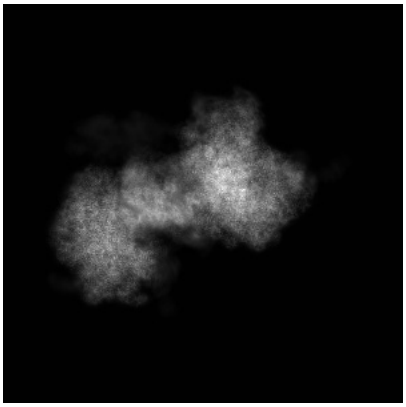
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

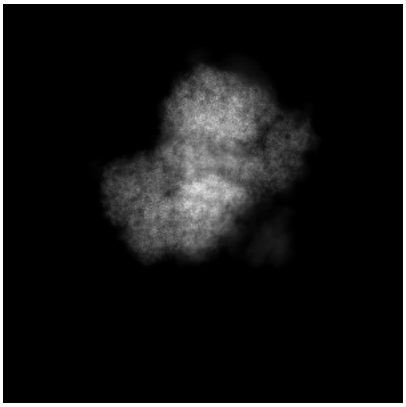
6.1.1 Primary map



X



Y

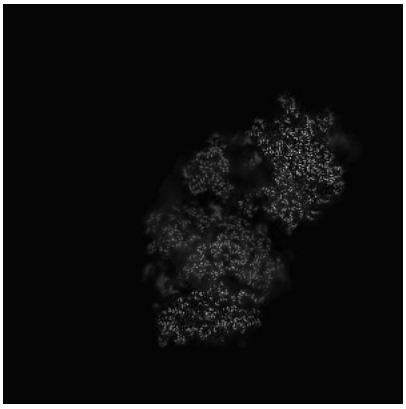


Z

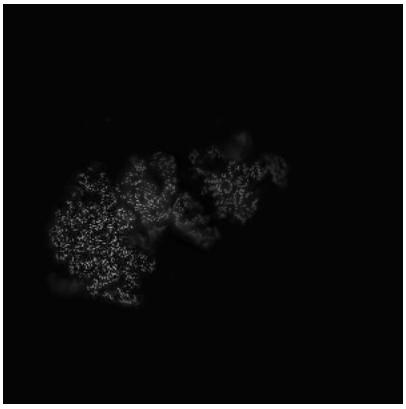
The images above show the map projected in three orthogonal directions.

6.2 Central slices

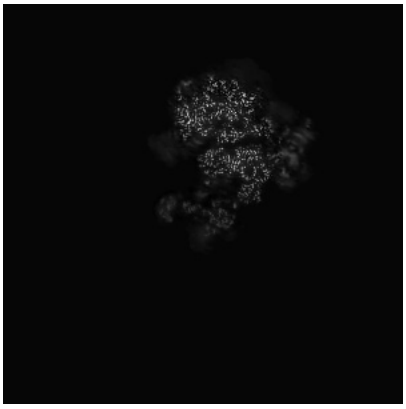
6.2.1 Primary map



X Index: 313



Y Index: 313

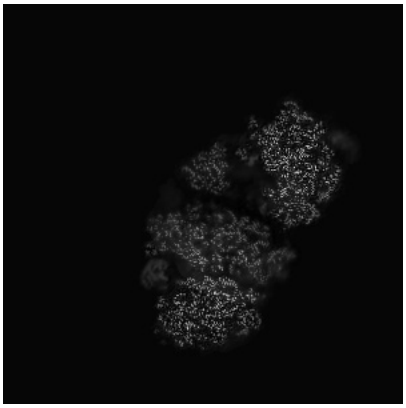


Z Index: 313

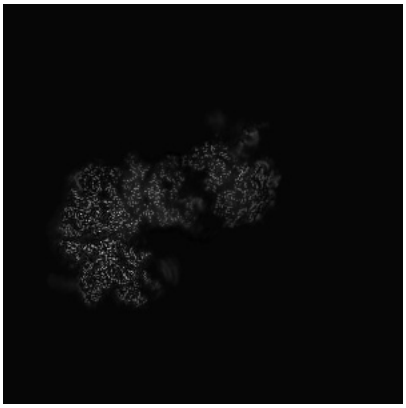
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

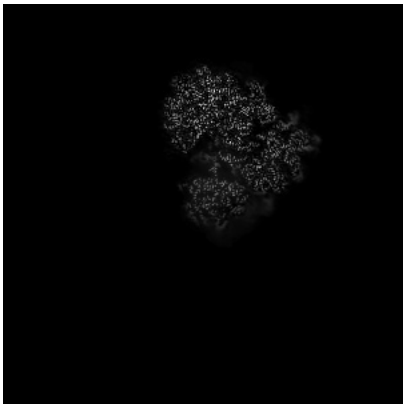
6.3.1 Primary map



X Index: 303



Y Index: 330

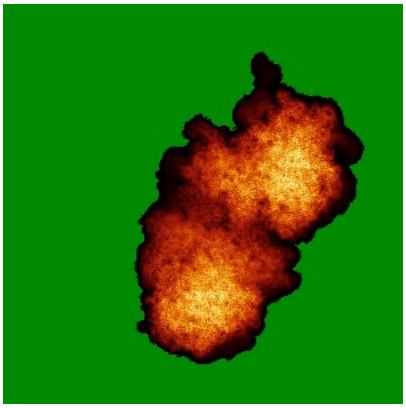


Z Index: 372

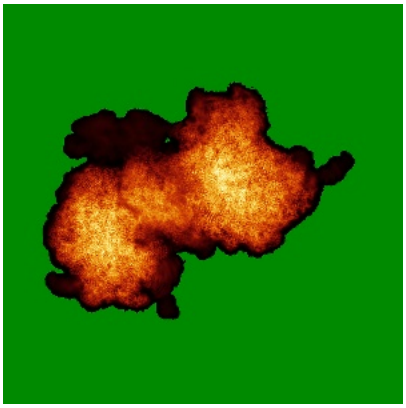
The images above show the largest variance slices of the map in three orthogonal directions.

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

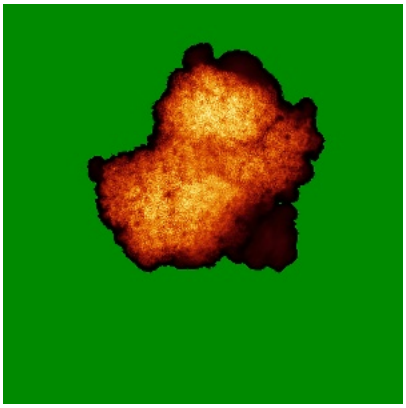
6.4.1 Primary map



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 0.44. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

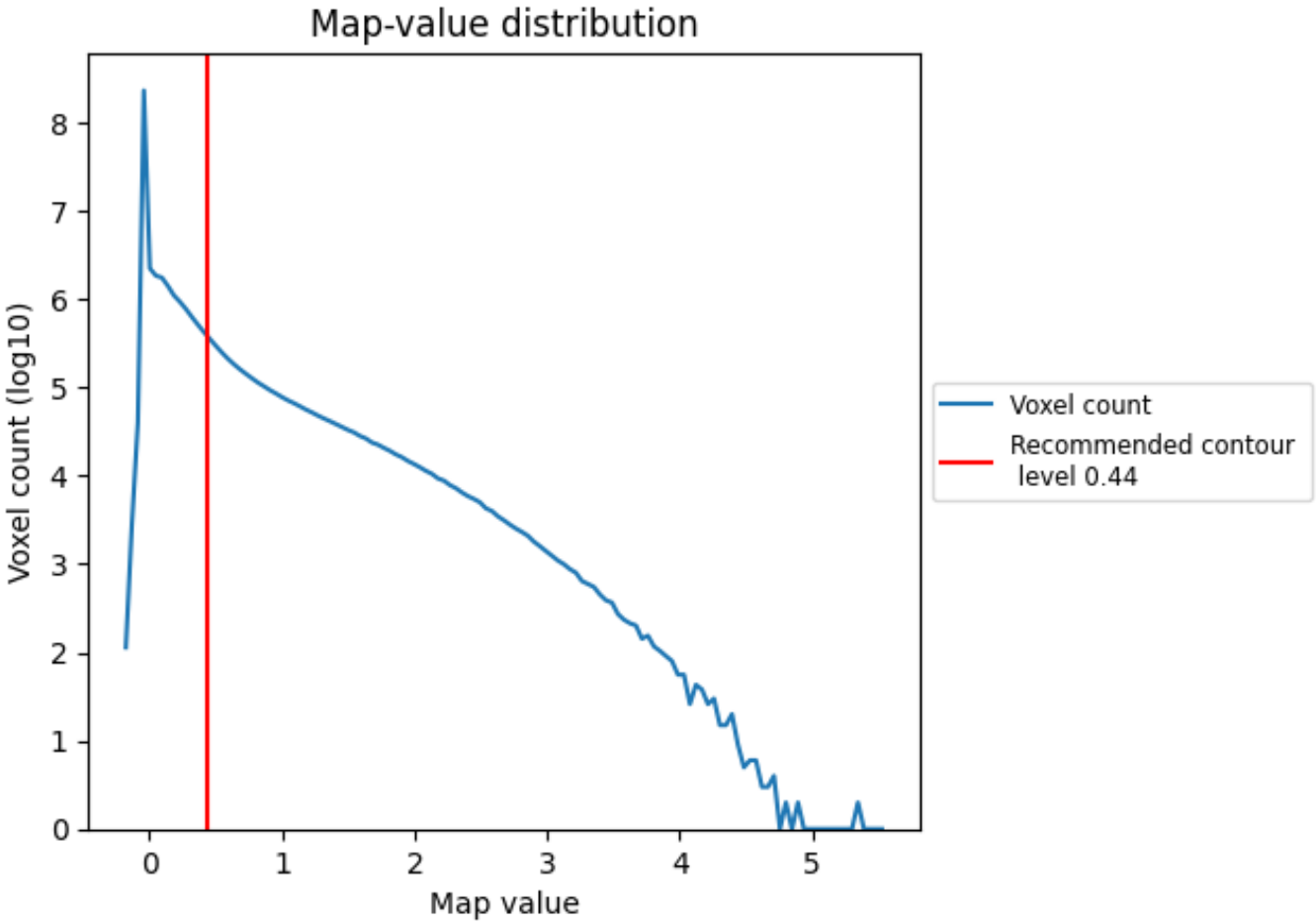
6.6 Mask visualisation (i)

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

7 Map analysis

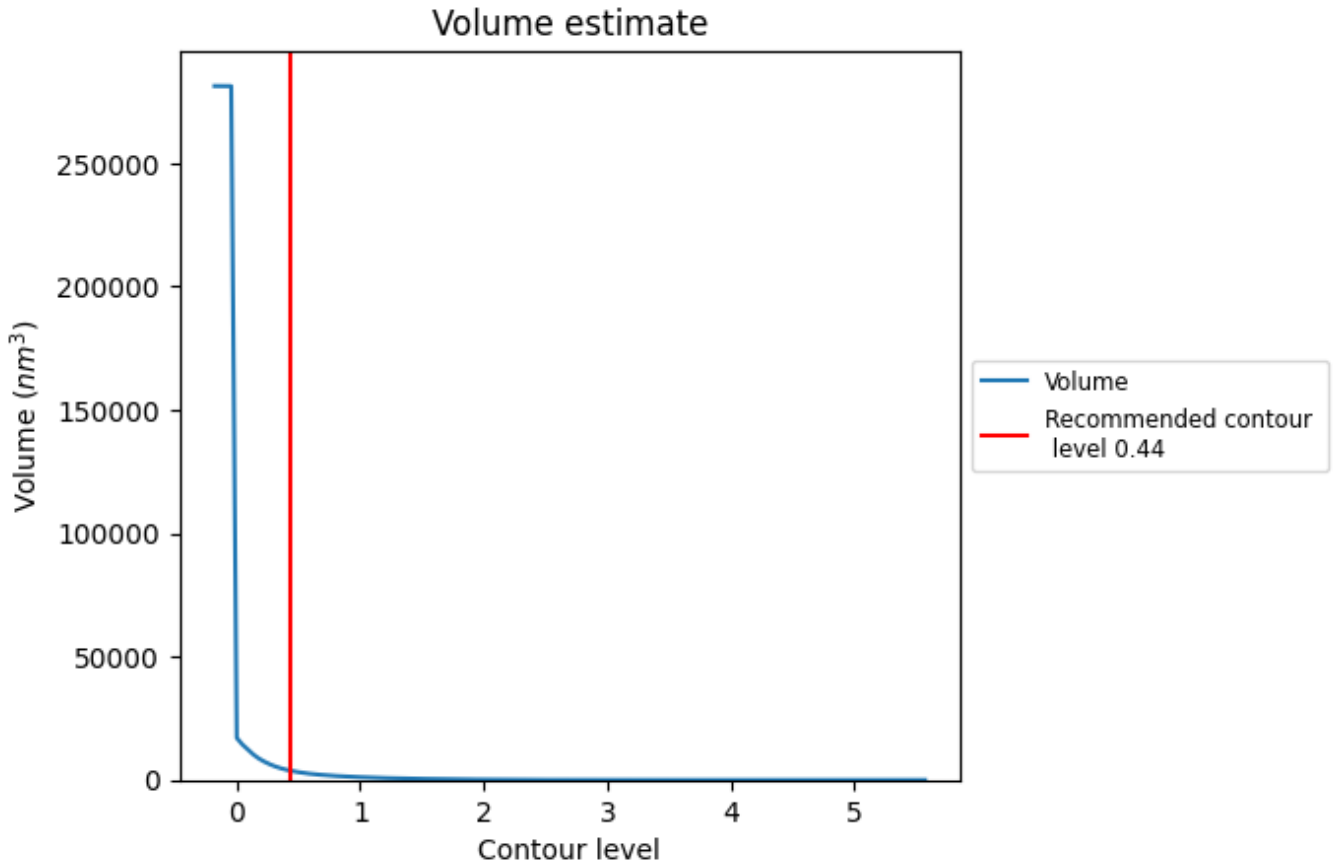
This section contains the results of statistical analysis of the map.

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.

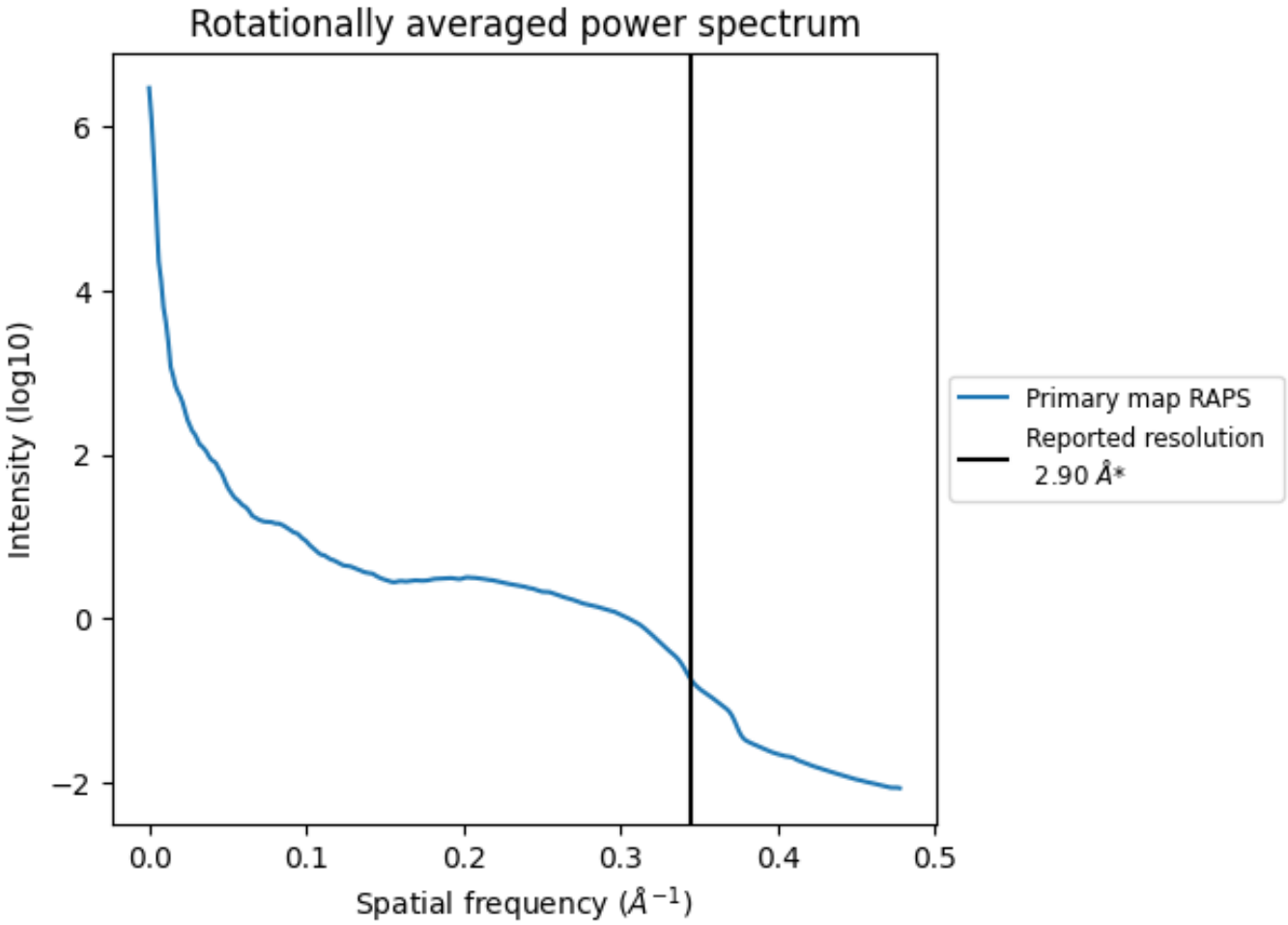
7.2 Volume estimate



The volume at the recommended contour level is 3730 nm^3; this corresponds to an approximate mass of 3369 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 0.345 Å^{-1}

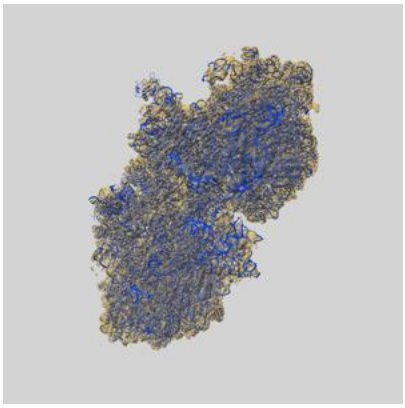
8 Fourier-Shell correlation (i)

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

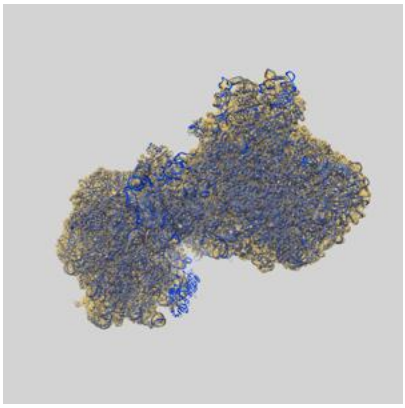
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-50259 and PDB model 9F9S. Per-residue inclusion information can be found in section 3 on page 29.

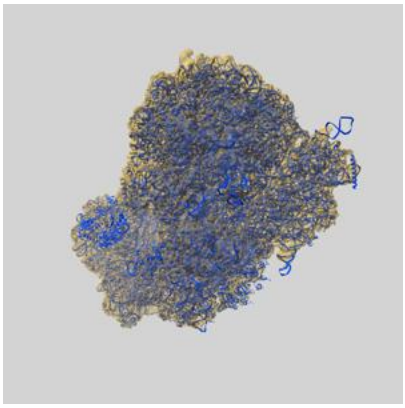
9.1 Map-model overlay



X



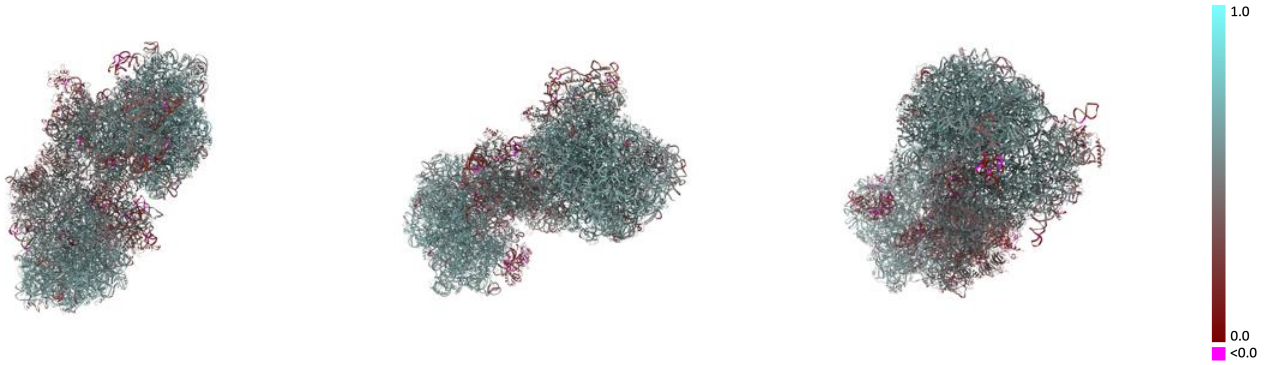
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.44 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.

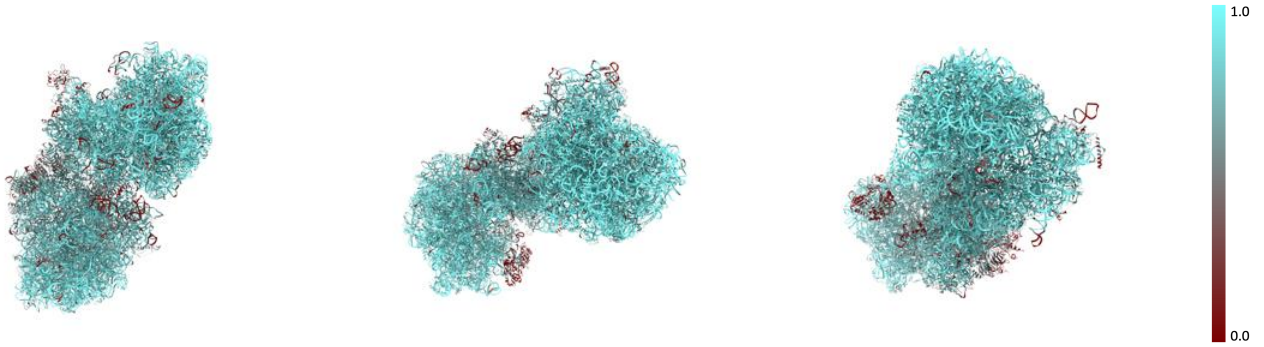
9.2 Q-score mapped to coordinate model (i)



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.

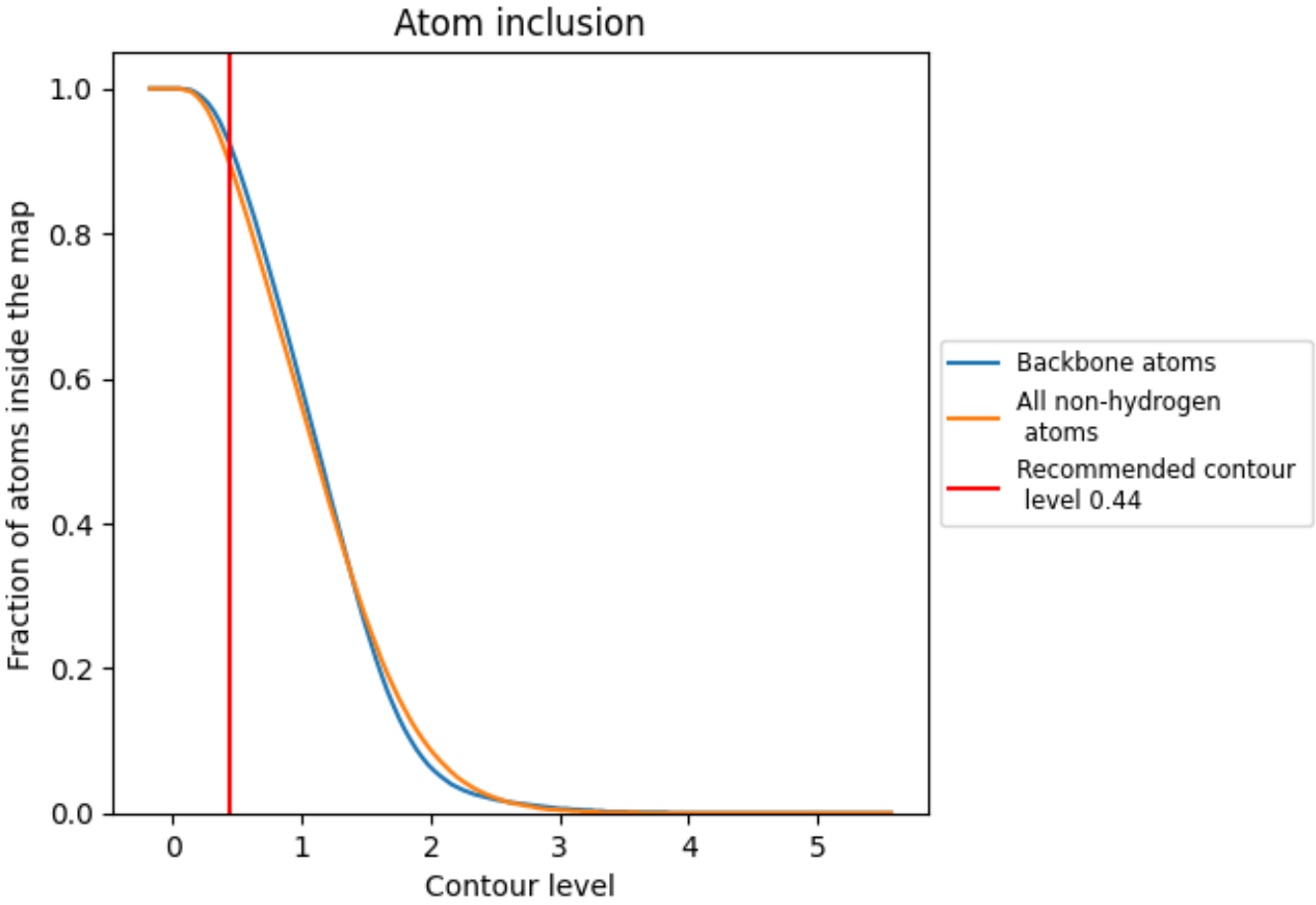
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.44).

9.4 Atom inclusion (i)



At the recommended contour level, 92% 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 (0.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.5400
CC	0.9590	0.5410
CM	0.7410	0.4200
CN	0.7350	0.4190
CP	0.9150	0.4080
DP	0.5840	0.3000
DQ	0.8320	0.3620
L1	0.9700	0.5780
L2	0.9780	0.6010
L3	0.9930	0.5740
LA	0.9190	0.5220
LB	0.9590	0.5860
LC	0.8560	0.5130
LD	0.9140	0.5420
LE	0.9100	0.5550
LF	0.8290	0.4730
LG	0.9210	0.5680
LH	0.9520	0.5560
LI	0.9930	0.6230
LJ	0.9680	0.5970
LK	0.9560	0.6060
LL	0.9770	0.5990
LM	0.8660	0.5520
LN	0.9530	0.5840
LO	0.9420	0.5750
La	0.9350	0.5950
Lb	0.9300	0.5960
Lc	0.9380	0.5810
Ld	0.9860	0.6140
Le	0.9280	0.5680
Lf	0.9810	0.6260
Lg	0.8830	0.5210
Lh	0.9940	0.6260
Li	0.8990	0.5420
Lj	0.9410	0.5710

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Chain	Atom inclusion	Q-score
Lk	0.9240	0.5810
Ll	0.9900	0.6200
Lm	0.9760	0.6100
Ln	0.9020	0.5650
Lo	0.8850	0.5570
Lp	0.9270	0.5400
Lq	0.9510	0.5940
Lr	0.9120	0.5500
Ls	0.9630	0.5870
Lt	0.9460	0.5670
Lu	0.7240	0.4730
Lv	0.8720	0.4970
Lw	0.9720	0.6150
Lx	0.9540	0.5890
Ly	0.9610	0.5870
Lz	0.8620	0.5020
M1	0.9580	0.5960
M2	0.9840	0.6280
M3	0.9940	0.6080
MA	0.9220	0.5750
MB	0.9640	0.6240
MC	0.8440	0.5670
MD	0.9230	0.5830
ME	0.9090	0.6030
MF	0.8270	0.5030
MG	0.9240	0.6000
MH	0.9540	0.5930
MI	0.9850	0.6600
MJ	0.9700	0.6290
MK	0.9760	0.6510
ML	0.9800	0.6360
MM	0.9040	0.5790
MN	0.9590	0.6190
MO	0.9550	0.6160
MP	0.0240	0.0980
MQ	0.1020	0.1700
Ma	0.9680	0.6250
Mb	0.9580	0.6300
Mc	0.9380	0.6180
Md	0.9430	0.5880
Me	0.9430	0.6070
Mf	0.9830	0.6400

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Chain	Atom inclusion	Q-score
Mg	0.8660	0.5590
Mh	0.9980	0.6600
Mi	0.8950	0.5720
Mj	0.9420	0.5970
Mk	0.9050	0.6200
Ml	0.9850	0.6610
Mm	0.9710	0.6390
Mn	0.9110	0.5900
Mo	0.8510	0.5690
Mp	0.9430	0.5890
Mq	0.9690	0.6370
Mr	0.8870	0.5780
Ms	0.9710	0.6160
Mt	0.9530	0.6130
Mu	0.9430	0.6150
Mv	0.8810	0.5320
Mw	0.9590	0.6420
Mx	0.9650	0.6250
My	0.9650	0.6260
Mz	0.8580	0.5390
R1	0.8920	0.4830
RA	0.9260	0.5700
RB	0.7380	0.5050
RC	0.7070	0.4550
RD	0.9290	0.5460
RE	0.7990	0.4710
RF	0.3350	0.2440
RG	0.4030	0.3360
Ra	0.8030	0.4990
Rb	0.7870	0.5340
Rc	0.8760	0.5540
Rd	0.6730	0.4540
Re	0.7810	0.4810
Rf	0.6890	0.4390
Rg	0.7280	0.4120
Rh	0.6050	0.4160
Ri	0.8280	0.4570
Rj	0.7860	0.4660
Rk	0.6120	0.4190
Rl	0.8300	0.5010
Rm	0.1910	0.2300
Rn	0.8680	0.5280

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Chain	Atom inclusion	Q-score
Ro	0.8890	0.5600
Rp	0.6740	0.4390
Rq	0.7220	0.4430
Rr	0.6490	0.4220
Rs	0.7280	0.4570
Rt	0.7110	0.4360
Ru	0.6100	0.3840
Rv	0.8010	0.5210
Rw	0.9490	0.5810
Rx	0.9250	0.5650
Ry	0.7210	0.4250
Rz	0.5680	0.4300
S1	0.9150	0.5010
SA	0.9650	0.5730
SB	0.7570	0.4950
SC	0.8310	0.4860
SD	0.9240	0.5240
SE	0.7700	0.4520
SF	0.2870	0.2220
SG	0.5650	0.3430
Sa	0.8150	0.4860
Sb	0.7960	0.5110
Sc	0.9140	0.5480
Sd	0.7660	0.4560
Se	0.8940	0.5200
Sf	0.7810	0.4550
Sg	0.7910	0.4380
Sh	0.6500	0.4400
Si	0.9180	0.5520
Sj	0.8660	0.4920
Sk	0.6640	0.3720
Sl	0.9010	0.5640
Sm	0.2030	0.1860
Sn	0.8820	0.5440
So	0.9340	0.5440
Sp	0.6250	0.3830
Sq	0.8180	0.4670
Sr	0.7540	0.4590
Ss	0.7620	0.4140
St	0.7800	0.4090
Su	0.7060	0.4080
Sv	0.8320	0.5090

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Chain	Atom inclusion	Q-score
Sw	0.9560	0.5730
Sx	0.9320	0.5700
Sy	0.8290	0.4550
Sz	0.5950	0.3370