



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:20 PM UTC

PDB ID : 9F9S / pdb_00009f9s
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:

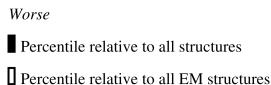
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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ELECTRON MICROSCOPY

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Metric	Percentile Rank	Value
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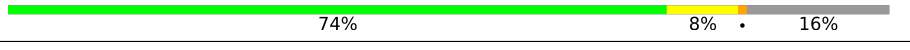
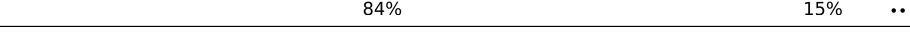
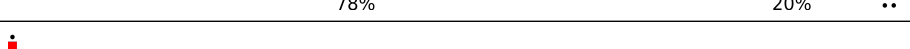
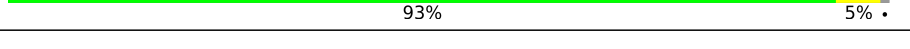
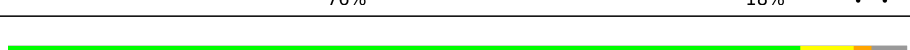
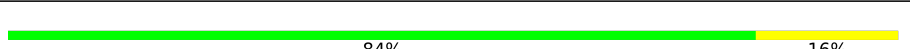
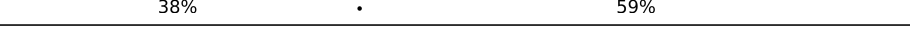
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Mol	Chain	Length	Quality of chain
4	CP	76	
5	L1	3396	
6	L2	158	
6	M2	158	
7	L3	121	
7	M3	121	
8	LA	176	
9	LB	244	
9	MB	244	
10	LC	256	
10	MC	256	
11	LD	191	
11	MD	191	
12	LE	221	
12	ME	221	
13	LF	174	
13	MF	174	
14	LG	199	
14	MG	199	
15	LH	138	
15	MH	138	
16	LI	204	
16	MI	204	
17	LJ	199	
17	MJ	199	

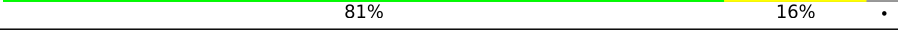
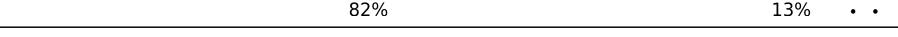
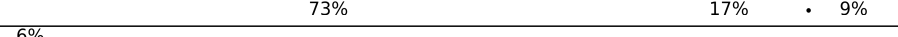
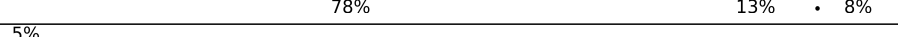
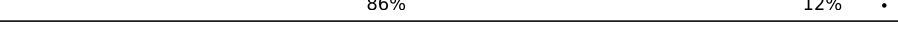
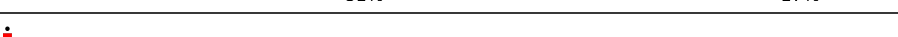
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Mol	Chain	Length	Quality of chain
18	LK	184	
18	MK	184	
19	LL	186	
19	ML	186	
20	LM	189	
20	MM	189	
21	LN	172	
21	MN	172	
22	LO	160	
22	MO	160	
23	La	137	
23	Ma	137	
24	Lb	92	
24	Mb	92	
25	Lc	106	
25	Mc	106	
26	Ld	25	
26	Md	25	
27	Le	128	
27	Me	128	
28	Lf	51	
28	Mf	51	
29	Lg	78	
29	Mg	78	
30	Lh	88	

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Mol	Chain	Length	Quality of chain
30	Mh	88	 84%11%5%
31	Li	100	 5%85%13%..
31	Mi	100	 85%14%. .
32	Lj	120	 86%13%. .
32	Mj	120	 92%8%. .
33	Lk	121	 77%10%. 12%
33	Mk	121	 5%78%12%10%
34	Ll	107	 82%17%. .
34	Ml	107	 89%9%..
35	Lm	130	 82%16%. .
35	Mm	130	 88%8%..
36	Ln	113	 6%81%16%. .
36	Mn	113	 82%13%. . .
37	Lo	105	 73%17%. 9%
37	Mo	105	 6%78%13%. 8%
38	Lp	59	 5%85%12%..
38	Mp	59	 86%12%. .
39	Lq	149	 77%19%..
39	Mq	149	 79%19%..
40	Lr	136	 79%18%..
40	Mr	136	 85%14%. .
41	Ls	127	 81%17%..
41	Ms	127	 83%16%. .
42	Lt	142	 70%13%. 15%
42	Mt	142	 77%7%15%

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Mol	Chain	Length	Quality of chain
43	Lu	155	
43	Mu	155	
44	Lv	121	
44	Mv	121	
45	Lw	254	
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	

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Mol	Chain	Length	Quality of chain
56	RG	319	
56	SG	319	
57	Ra	252	
57	Sa	252	
58	Rb	255	
58	Sb	255	
59	Rc	254	
59	Sc	254	
60	Rd	240	
60	Sd	240	
61	Re	261	
61	Se	261	
62	Rf	225	
62	Sf	225	
63	Rg	236	
63	Sg	236	
64	Rh	190	
64	Sh	190	
65	Ri	200	
65	Si	200	
66	Rj	197	
66	Sj	197	
67	Rk	105	
67	Sk	105	
68	Rl	156	

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Mol	Chain	Length	Quality of chain
68	Sl	156	
69	Rm	143	
69	Sm	143	
70	Rn	151	
70	Sn	151	
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	

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Mol	Chain	Length	Quality of chain
82	Rz	108	
82	Sz	108	
83	RC	67	
84	Ro	138	
85	Rr	136	
86	MA	176	
87	M1	3396	
88	DQ	77	
89	MQ	312	
90	MP	165	
91	DP	76	

2 Entry composition

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	C	N	O	P	0	0
			3353	1500	586	1109	158		

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

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

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

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

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

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

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

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

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

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

- 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	C	N	O	S	0	0
			436	272	97	65	2		
28	Mf	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	C	N	O	0	0
			796	516	131	149		
44	Mv	97	Total	C	N	O	0	0
			770	499	126	145		

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

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

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

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

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

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

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

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

- 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	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

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

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

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

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

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

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

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

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

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

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

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

- 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	0	0
			1476	916	295	263		
65	Ri	188	Total	C	N	O	0	0
			1489	925	298	264		

- 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	C	N	O	0	0
			558	357	103	98		

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

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

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

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

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

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

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

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

- 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	C	N	O	P	0	0
			68285	30524	12313	22258	3190		

- Molecule 88 is a RNA chain called tRNA.

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

- 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 (CCD ID: 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 2	Mg 2	0

- Molecule 93 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

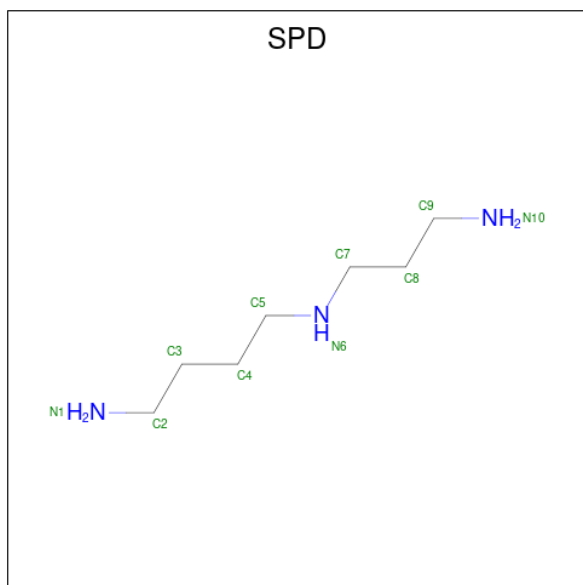
Mol	Chain	Residues	Atoms		AltConf
94	M1	11	Total 11	K 11	0
94	Mw	1	Total 1	K 1	0
94	ME	1	Total 1	K 1	0

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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 (CCD ID: SPD) (formula: $C_7H_{19}N_3$).

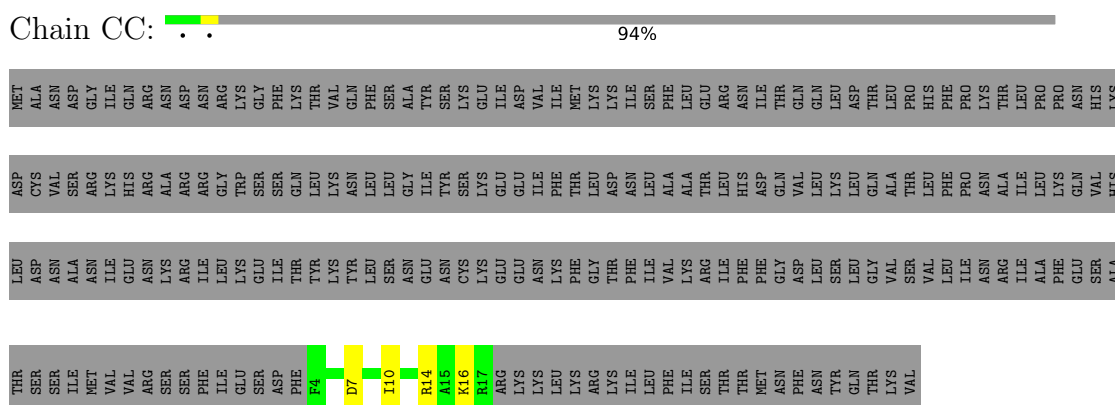


Mol	Chain	Residues	Atoms	AltConf
95	M1	1	Total C N 10 7 3	0
95	M1	1	Total C N 10 7 3	0
95	M1	1	Total C N 10 7 3	0

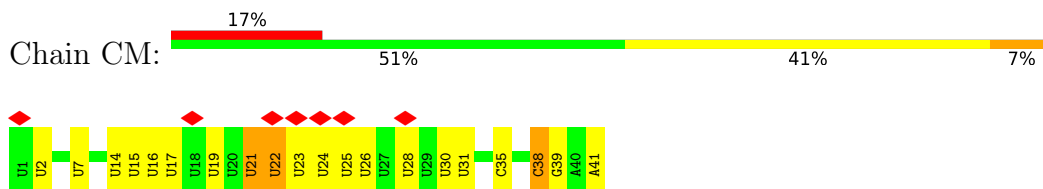
3 Residue-property plots

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.

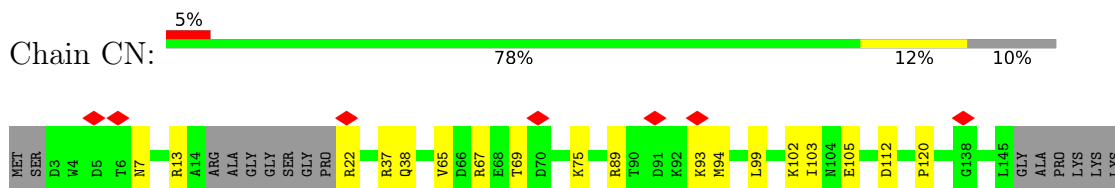
- Molecule 1: Uncharacterized protein YEL057C



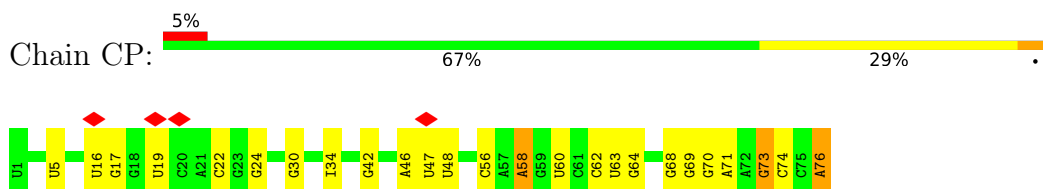
- Molecule 2: mRNA



- Molecule 3: Multiprotein-bridging factor 1

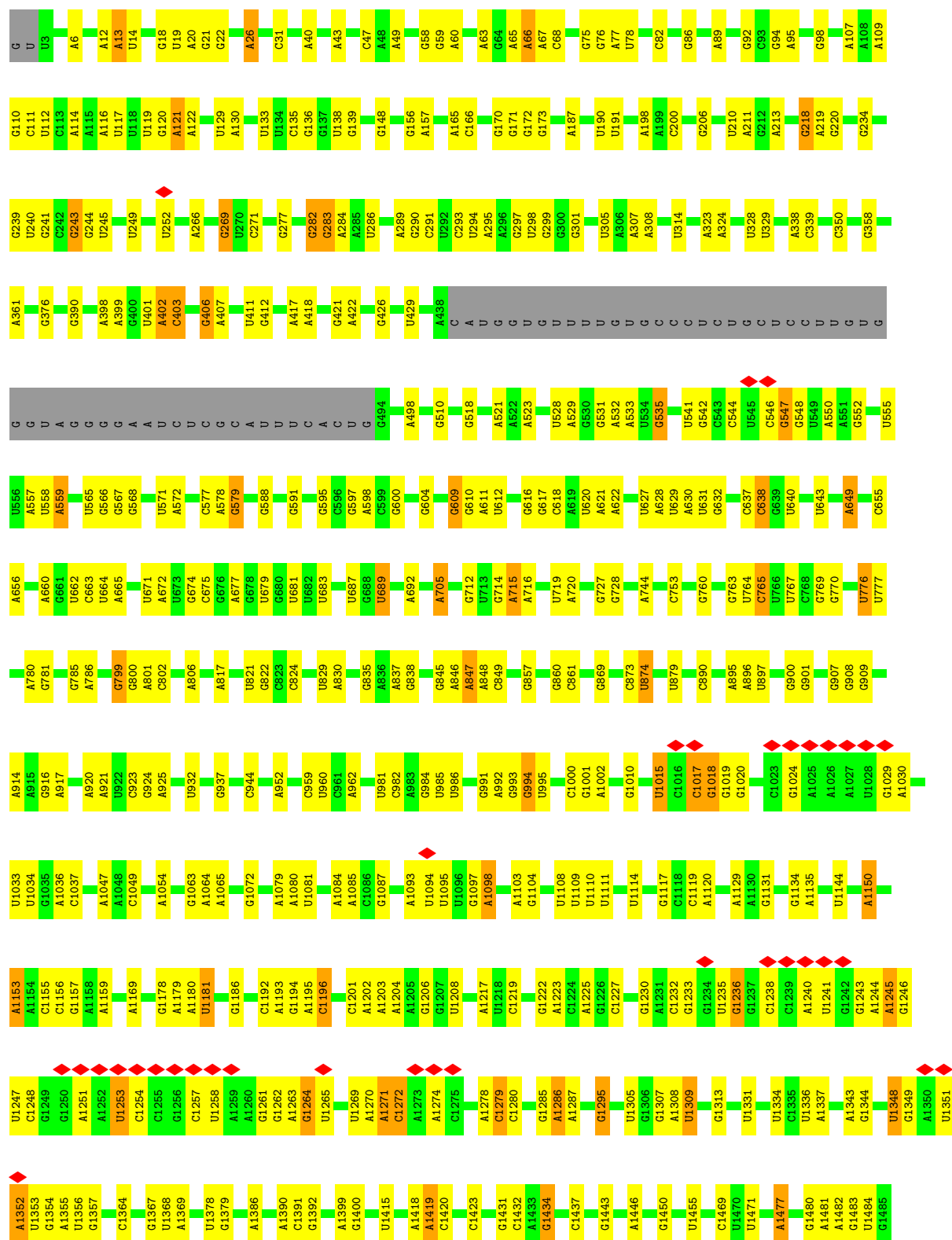


- Molecule 4: tRNA P-site, stalled

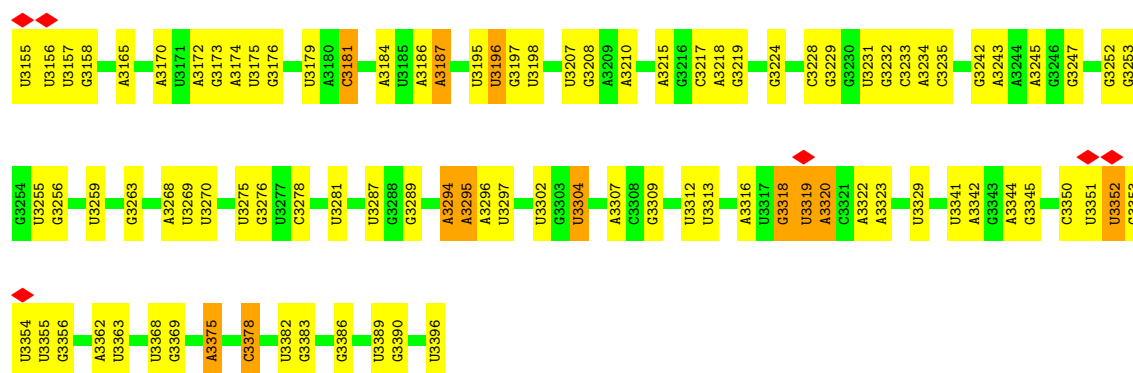


- Molecule 5: *Saccharomyces cerevisiae* S288C 25S ribosomal RNA (RDN25-1)

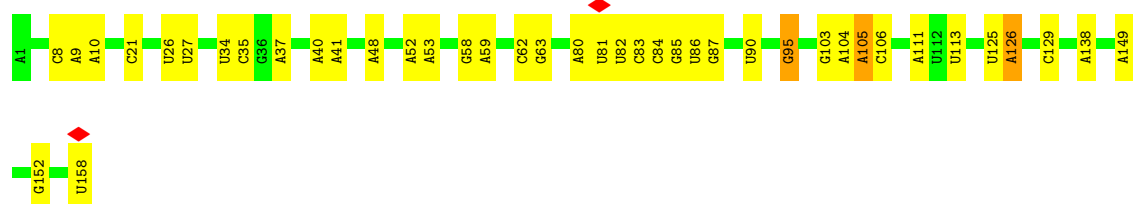
Chain L1:



G2997	C2852	G2728	A2695	U	C2338	A2188	U	C	A1858	G1748	U1607	G1486
A3012	U2855	U2729	C2600	C	A	C2192	U	U	G1863	A1749	C1608	G1487
A3016	C2867	C2741	G2606	U	A	U2193	A	A	A2093	A1750	A1619	G1488
A3017	U2868	A2747	G2607	U	G	G2194	C2094	C	C1866	G1751	A1621	G1492
G3022	G2871	A2748	U2611	U	G	G2201	C2101	U	A1867	A1757	U1622	G1493
G3031	A2872	U2752	U2612	U	U	U2205	U2102	C	U1871	A1760	C1497	C1498
U3038	U2875	G2753	U2613	U	G	A2207	C2108	C	U1877	C1761	A1498	C1499
U3037	C2876	G2761	G2614	A	G	A2208	U2109	U	A1879	C1762	U1629	
C3039	U2882	U2767	A2626	A	A	U2209	G2110	G	A1880	U1763	G1634	C1508
G3044	C2883	U2768	U2629	A	A	G2210	U2112	U	A1881	U1764	C1639	G1513
G3045	U2884	U2769	C2630	G	U	G2211	A2113	C	A1884	U1765	A1642	U1522
A3049	A2887	C2772	U2631	U	A	A2213	G2115	U	U1885	G1766	A1643	U1522
U3050	U2890	C2773	A2637	A	G	A2214	A2120	A	A1886	U1770	G1644	G1536
U3056	A2642	G2777	U2642	U	U	U2225	G2121	C	A1893	G1775	U1645	C1551
C3067	C2894	G2778	U2651	U	G	U2226	G2122	U	A1899	G1778	G1650	G1552
U3068	G2898	C2788	U2652	C	G	A2228	A2126	G	U1900	C1779	A1656	U1553
G3069	A2900	U2792	C2653	U	C	A2229	U2129	C	G1906	G1780	C1657	U1554
A3070	U2901	G2793	A2656	U	U	A2232	G2130	A	C1907	G1786	G1658	C1556
G3075	G2794	U2795	U2662	U	U	A2233	A2131	U	G1914	A1787	U1659	A1557
U3078	A2911	U2796	G2663	C	G	A2244	U2137	C	U1920	C1793	G1660	G1560
C3084	U2923	A2799	C2666	U	C	G2249	U2140	U	U1925	A1797	G1662	C1562
G3085	A2933	G2800	U2672	C	C	G2250	U2141	A	A1798	A1798	G1666	C1563
A3086	U2934	A2801	G2549	C	C	A2402	A2142	G	A1799	A1799	A1667	A1566
G3092	A2936	U2803	U2550	U	C	G2403	A2143	U	A1800	A1800	G1668	U1567
C3093	G2937	A2803	C2552	G	G	A2404	A2144	C	C1805	G1677	U1568	U1569
A3094	U2938	C2809	G2555	U	U	U2411	A2147	U	A1806	U1682	U1683	U1570
G3101	A2940	C2810	U2559	A	A	G2412	A2152	G	A1814	A1683	U1684	A1571
U3104	A2941	C2812	C2560	A	A	G2413	U2153	C	U1815	U1688	U1689	U1572
U3121	C2942	G2813	A2561	U	U	A2419	U2154	A	A1816	U1696	A1575	G1576
A3122	G2947	U2814	C2568	C	C	C2420	U2155	G	U1820	A1697	A1580	C1581
A3129	C2948	G2815	U2569	A	A	U2423	G2160	C	U1821	U1716	C1582	A1583
A3130	U2960	U2816	U2570	C	C	A2424	G2169	G	U1834	U1717	A1587	A1588
U3131	G2961	C2817	U2571	U	U	U2433	U2170	C	A1835	G1718	U1721	A1589
A3139	A2969	A2818	C2572	A	A	G2434	G2171	C	C1836	U1722	A1723	G1590
G3140	C2970	U2819	G2573	C	C	U2435	U2176	U	U1837	U1724	C1725	A1593
A3141	A2971	G2820	G2574	U	U	G2436	U2177	A	G1838	U1736	C1596	C1597
A3142	G2971	C2821	U2575	U	U	A	G2180	C	U1839	U1740	A1605	U1606
C3143	U2983	U2822	G2576	U	U	A	G2181	A	U1841	A1741		
U3151	G2984	G2823	U2584	U	A	G	G2185	C	A1842			
C3154	U2990	C2824	G2585	A	G	U2318	U2186	A	C1846			
	A2991	A2845	G2586	U	U	U2334	G2185	C	C1849			
	U2992	U2719	U2586	G	A	G2335		A	A1850			
	U2996	U2724	C2594	U	U			A				



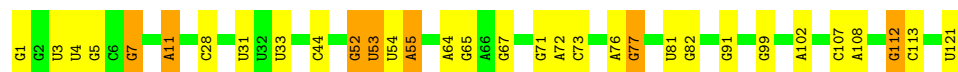
- Molecule 6: *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA



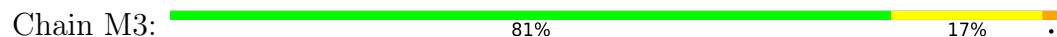
- Molecule 6: *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA



- Molecule 7: *Saccharomyces cerevisiae* S288C 5S ribosomal RNA



- Molecule 7: *Saccharomyces cerevisiae* S288C 5S ribosomal RNA



- Molecule 8: 60S ribosomal protein L6-B

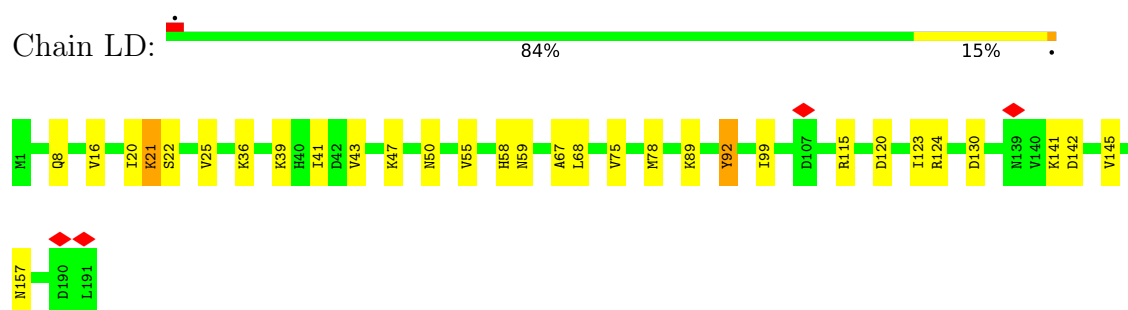
- Molecule 9: 60S ribosomal protein L7-A

- Molecule 9: 60S ribosomal protein L7-A

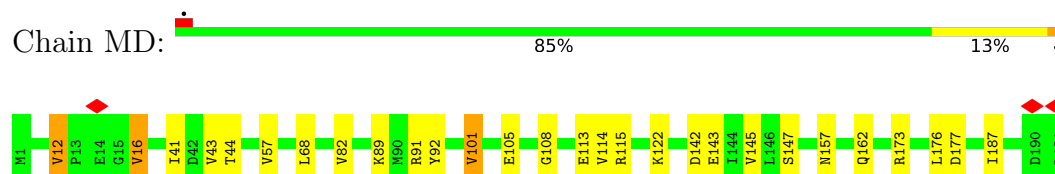
- Molecule 10: 60S ribosomal protein L8-A

- Molecule 10: 60S ribosomal protein L8-A

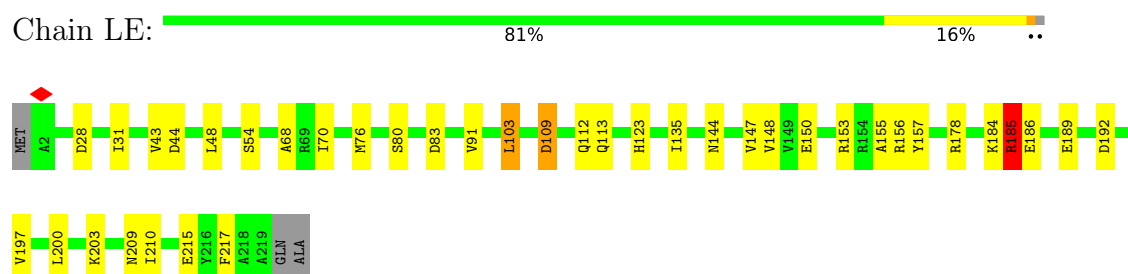
- Molecule 11: 60S ribosomal protein L9-A



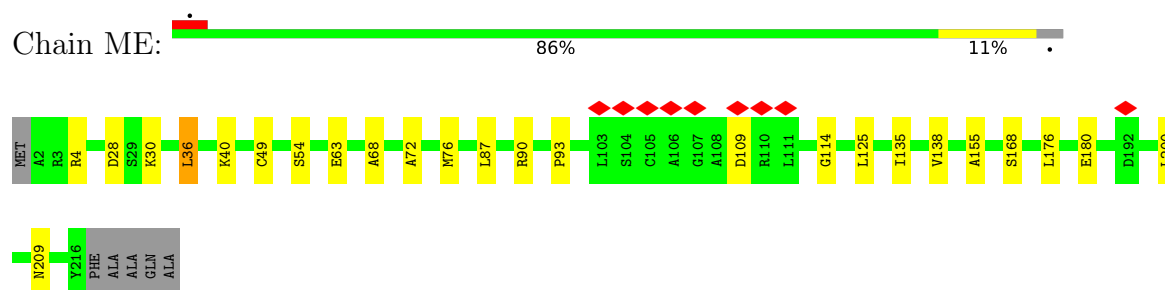
- Molecule 11: 60S ribosomal protein L9-A



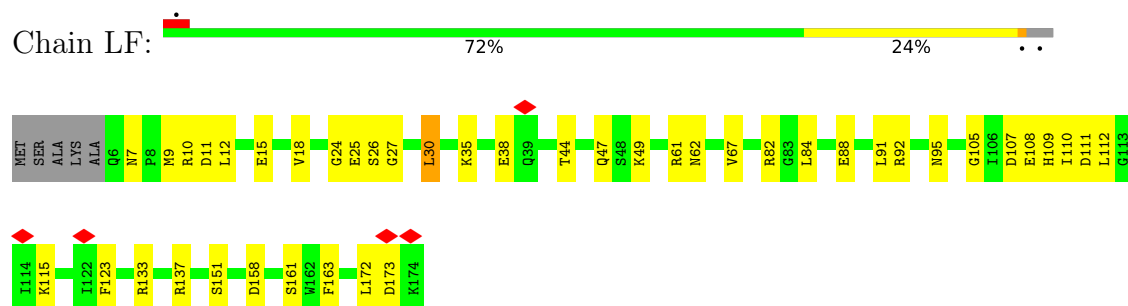
- Molecule 12: 60S ribosomal protein L10



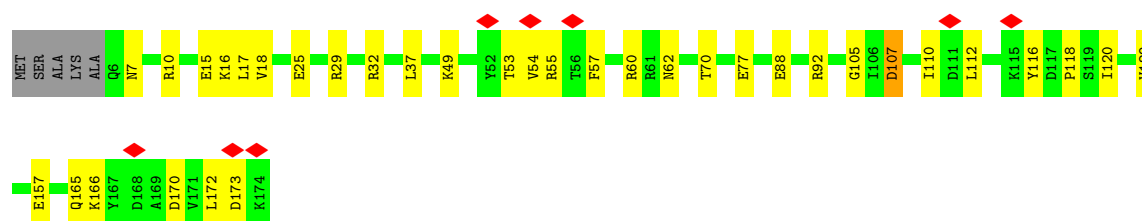
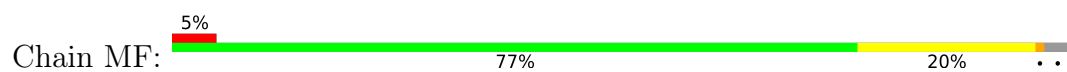
- Molecule 12: 60S ribosomal protein L10



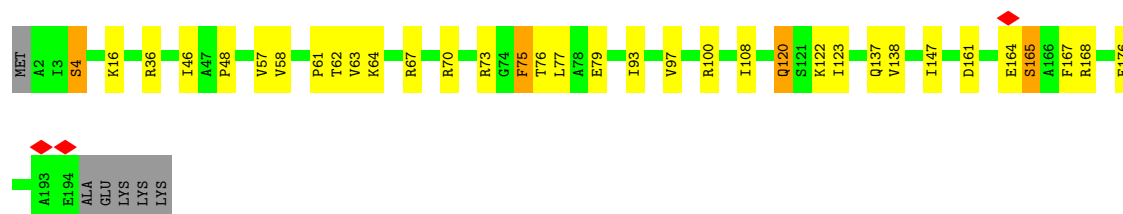
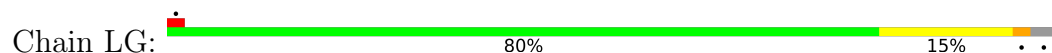
- Molecule 13: 60S ribosomal protein L11-A



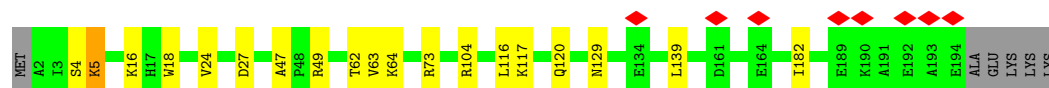
- Molecule 13: 60S ribosomal protein L11-A



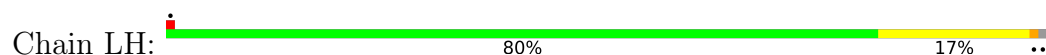
- Molecule 14: 60S ribosomal protein L13-A



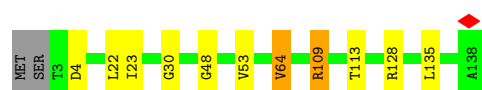
- Molecule 14: 60S ribosomal protein L13-A



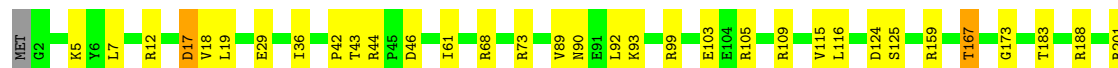
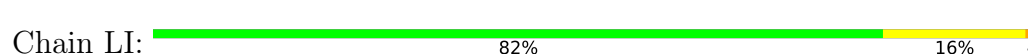
- Molecule 15: 60S ribosomal protein L14-A



- Molecule 15: 60S ribosomal protein L14-A



- Molecule 16: 60S ribosomal protein L15-A





- Molecule 16: 60S ribosomal protein L15-A

Chain MI: 87% 12%



- Molecule 17: 60S ribosomal protein L16-A

Chain LJ: 84% 14% ..



- Molecule 17: 60S ribosomal protein L16-A

Chain MJ: 87% 12% ..



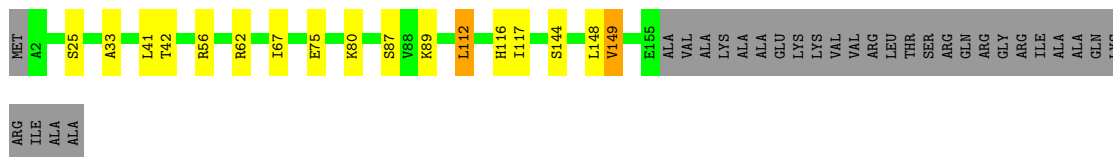
- Molecule 18: 60S ribosomal protein L17-A

Chain LK: 90% 9% ..



- Molecule 18: 60S ribosomal protein L17-A

Chain MK: 74% 8% 16%



- Molecule 19: 60S ribosomal protein L18-A

Chain LL: 84% 15% ..



- Molecule 19: 60S ribosomal protein L18-A

Chain ML:  89% 11% .



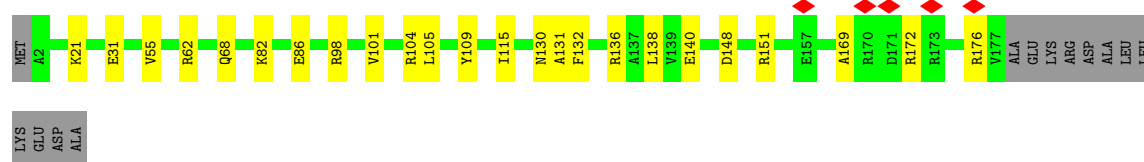
- Molecule 20: 60S ribosomal protein L19-A

Chain LM:  7% 89% 9% ..



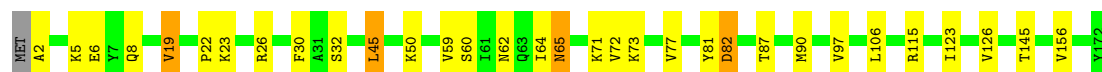
- Molecule 20: 60S ribosomal protein L19-A

Chain MM:  80% 13% 7%



- Molecule 21: 60S ribosomal protein L20-A

Chain LN:  81% 16% ..



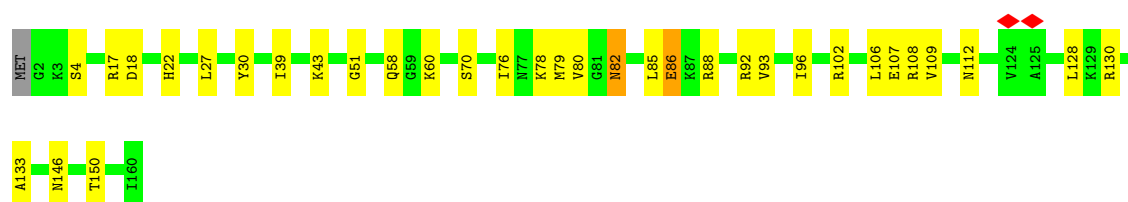
- Molecule 21: 60S ribosomal protein L20-A

Chain MN:  90% 9% .



- Molecule 22: 60S ribosomal protein L21-A

Chain LO:  78% 20% ..



- Molecule 22: 60S ribosomal protein L21-A

Chain MO:  88% 12%



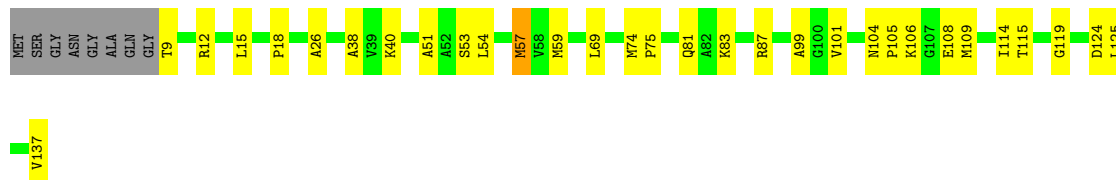
- Molecule 23: 60S ribosomal protein L23-A

Chain La:  88% 12%



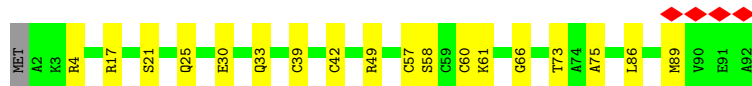
- Molecule 23: 60S ribosomal protein L23-A

Chain Ma:  72% 22% 6%

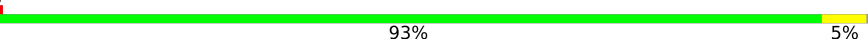


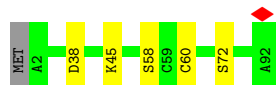
- Molecule 24: 60S ribosomal protein L43-A

Chain Lb:  79% 20%



- Molecule 24: 60S ribosomal protein L43-A

Chain Mb:  93% 5%



- Molecule 25: 60S ribosomal protein L42-A

Chain Lc:  76% 18%

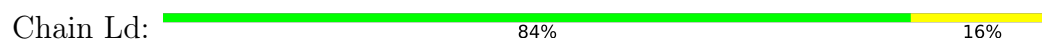


- Molecule 25: 60S ribosomal protein L42-A

Chain Mc:  89% 6%



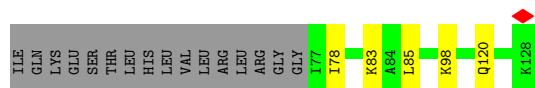
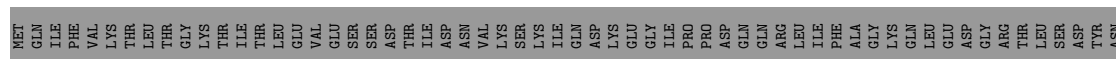
- Molecule 26: 60S ribosomal protein L41-A



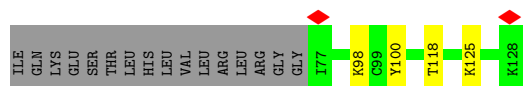
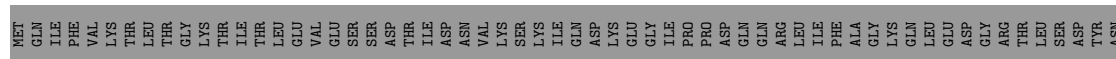
- Molecule 26: 60S ribosomal protein L41-A



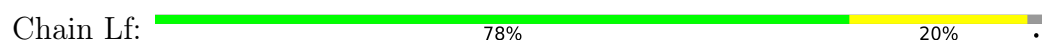
- Molecule 27: Ubiquitin-60S ribosomal protein L40



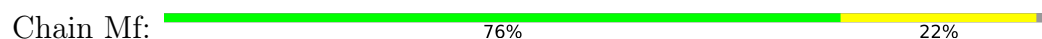
- Molecule 27: Ubiquitin-60S ribosomal protein L40



- Molecule 28: 60S ribosomal protein L39

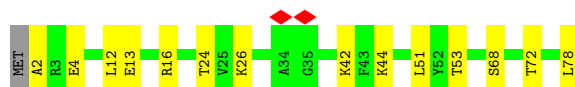
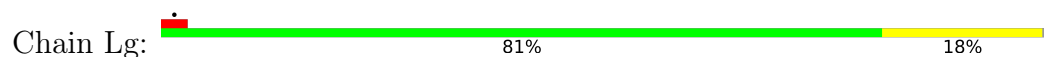


- Molecule 28: 60S ribosomal protein L39

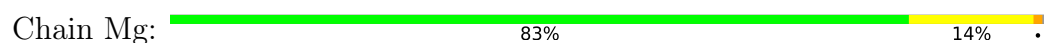




- Molecule 29: 60S ribosomal protein L38



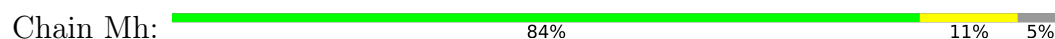
- Molecule 29: 60S ribosomal protein L38



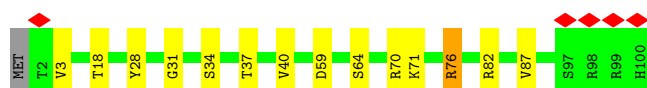
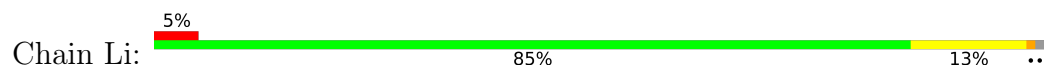
- Molecule 30: 60S ribosomal protein L37-A



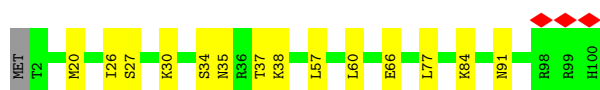
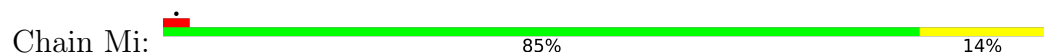
- Molecule 30: 60S ribosomal protein L37-A



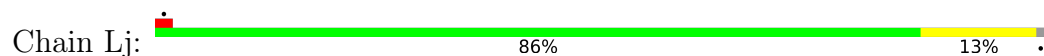
- Molecule 31: 60S ribosomal protein L36-A



- Molecule 31: 60S ribosomal protein L36-A

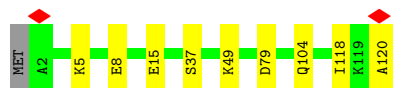


- Molecule 32: 60S ribosomal protein L35-A

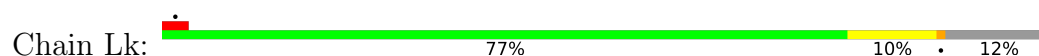




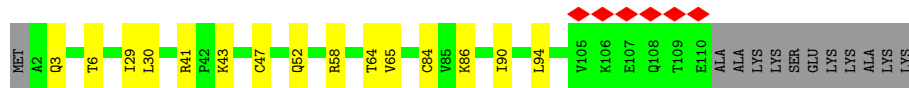
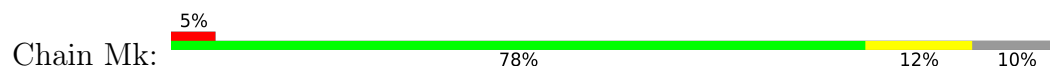
- Molecule 32: 60S ribosomal protein L35-A



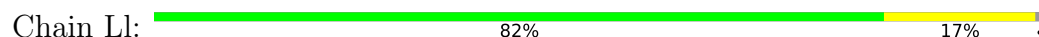
- Molecule 33: 60S ribosomal protein L34-A



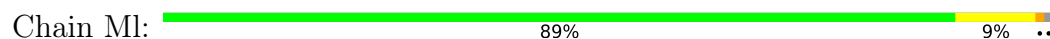
- Molecule 33: 60S ribosomal protein L34-A



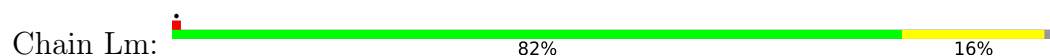
- Molecule 34: 60S ribosomal protein L33-A



- Molecule 34: 60S ribosomal protein L33-A



- Molecule 35: 60S ribosomal protein L32



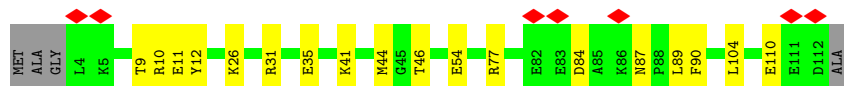
- Molecule 35: 60S ribosomal protein L32

Chain Mm:  88% 8% ..



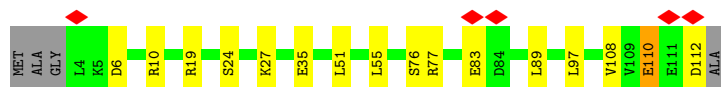
- Molecule 36: 60S ribosomal protein L31-A

Chain Ln:  6% 81% 16% .



- Molecule 36: 60S ribosomal protein L31-A

Chain Mn:  82% 13% ..



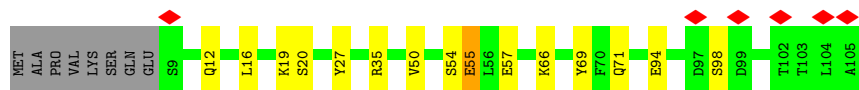
- Molecule 37: 60S ribosomal protein L30

Chain Lo:  73% 17% . 9%



- Molecule 37: 60S ribosomal protein L30

Chain Mo:  6% 78% 13% . 8%



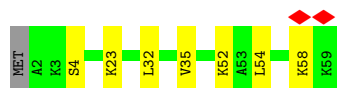
- Molecule 38: 60S ribosomal protein L29

Chain Lp:  5% 85% 12% ..

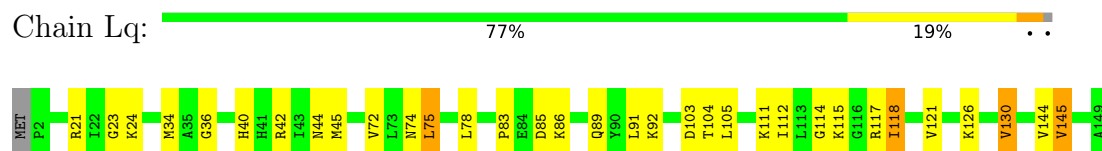


- Molecule 38: 60S ribosomal protein L29

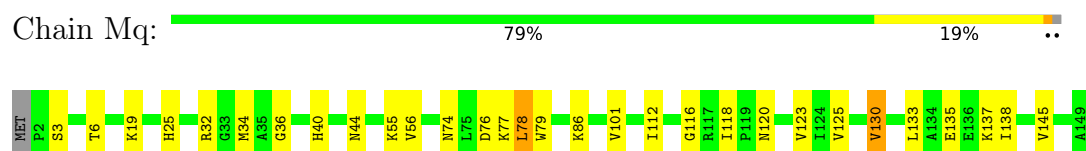
Chain Mp:  86% 12% .



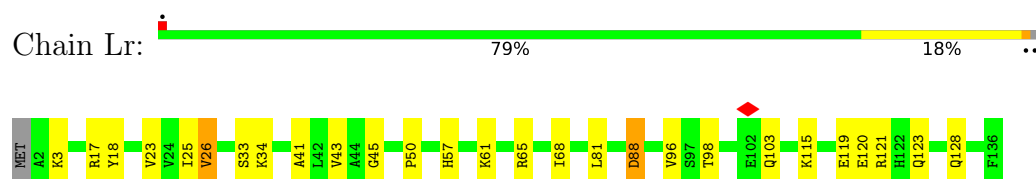
- Molecule 39: 60S ribosomal protein L28



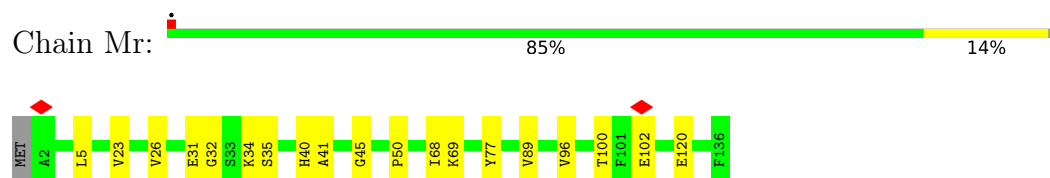
- Molecule 39: 60S ribosomal protein L28



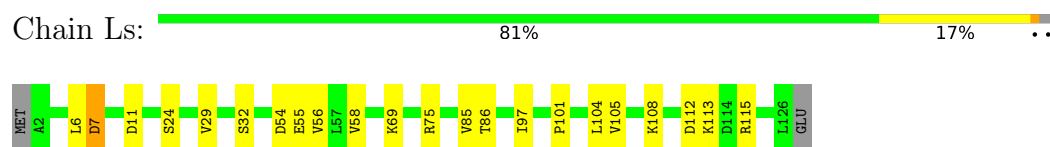
- Molecule 40: 60S ribosomal protein L27-A



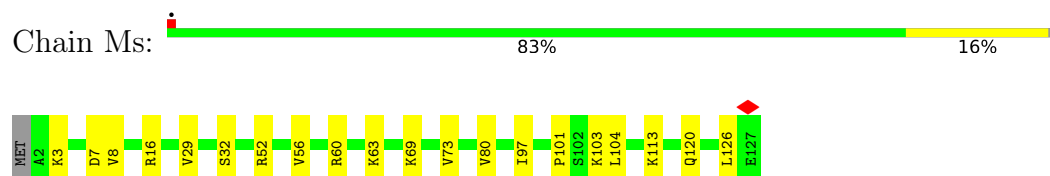
- Molecule 40: 60S ribosomal protein L27-A



- Molecule 41: 60S ribosomal protein L26-A



- Molecule 41: 60S ribosomal protein L26-A

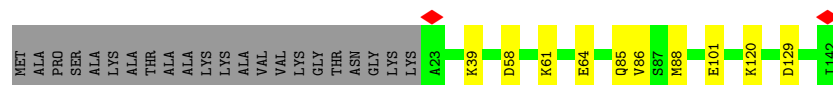
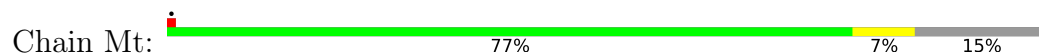


- Molecule 42: 60S ribosomal protein L25

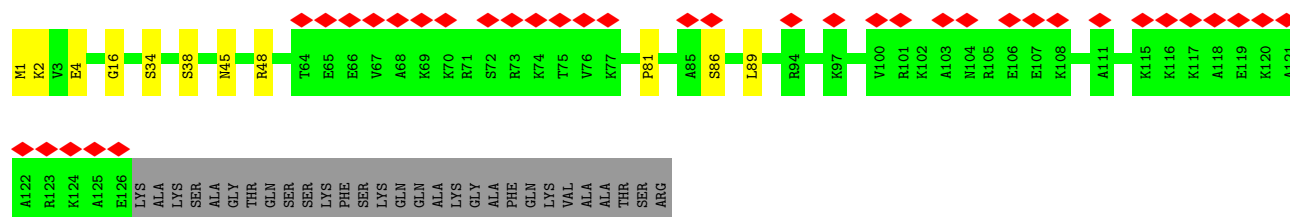
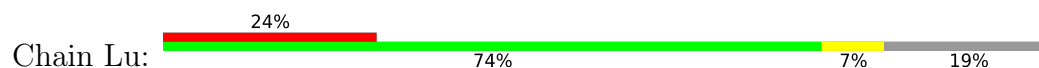




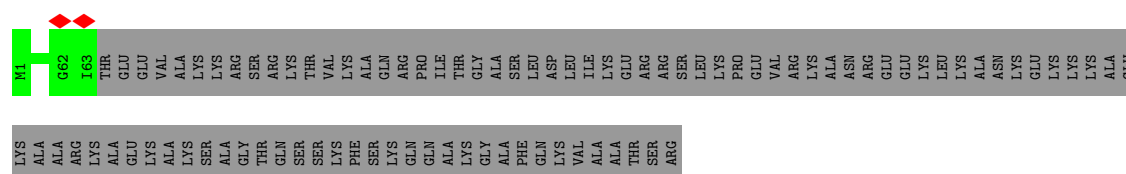
- Molecule 42: 60S ribosomal protein L25



- Molecule 43: 60S ribosomal protein L24-A



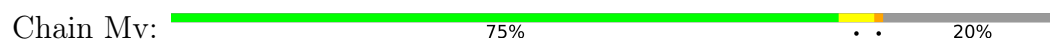
- Molecule 43: 60S ribosomal protein L24-A



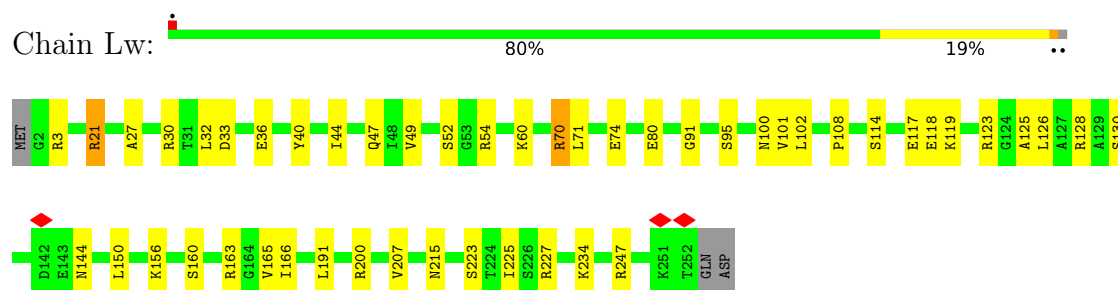
- Molecule 44: 60S ribosomal protein L22-A



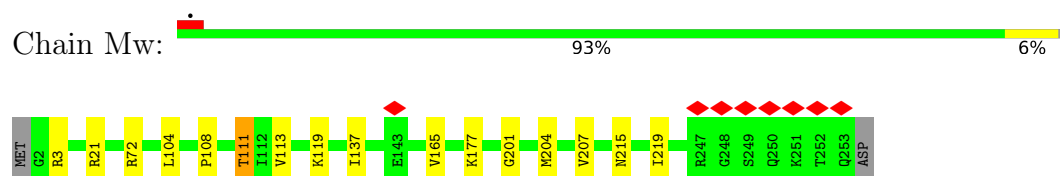
- Molecule 44: 60S ribosomal protein L22-A



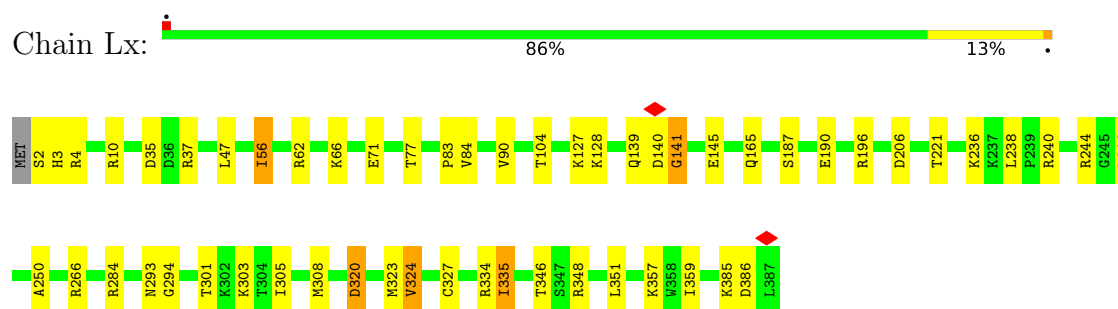
- Molecule 45: 60S ribosomal protein L2-A



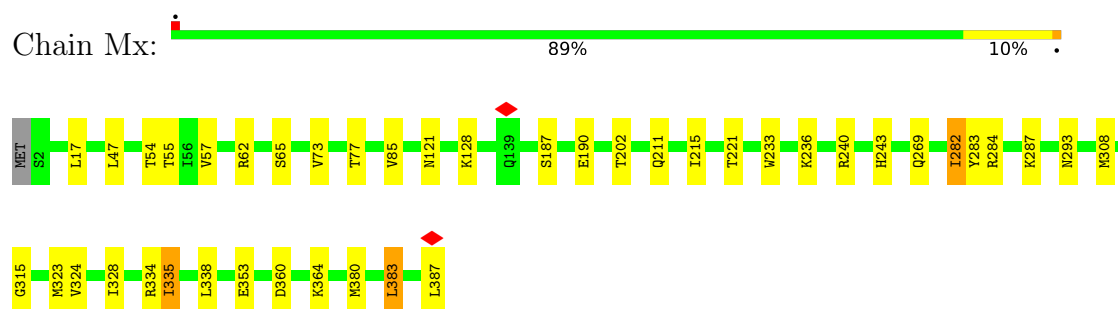
- Molecule 45: 60S ribosomal protein L2-A



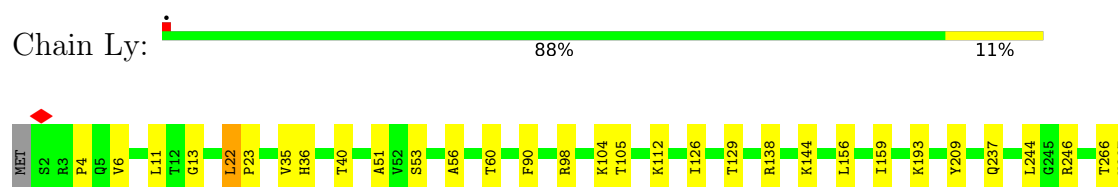
- Molecule 46: 60S ribosomal protein L3

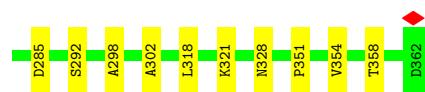


- Molecule 46: 60S ribosomal protein L3



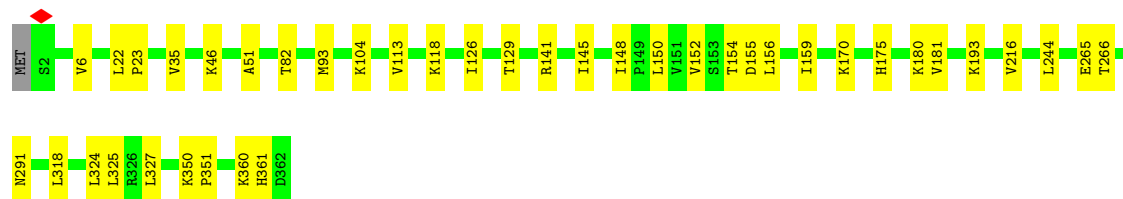
- Molecule 47: 60S ribosomal protein L4-A





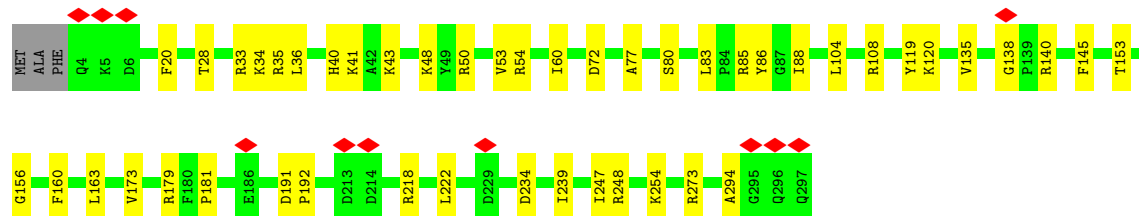
- Molecule 47: 60S ribosomal protein L4-A

Chain My: 89% 11%



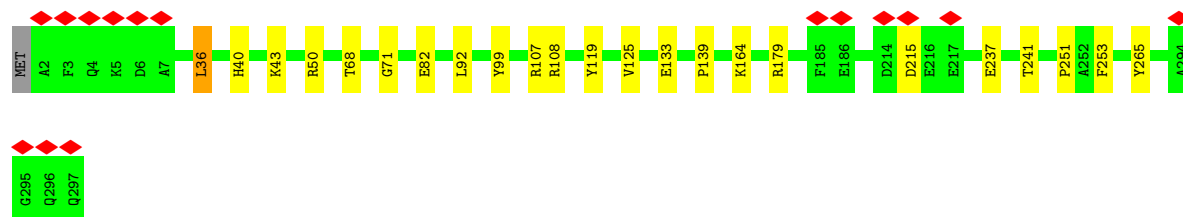
- Molecule 48: 60S ribosomal protein L5

Chain Lz: 83% 16%



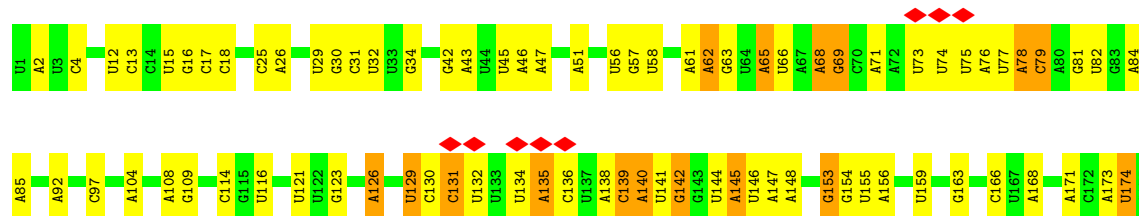
- Molecule 48: 60S ribosomal protein L5

Chain Mz: 5% 92% 7%



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

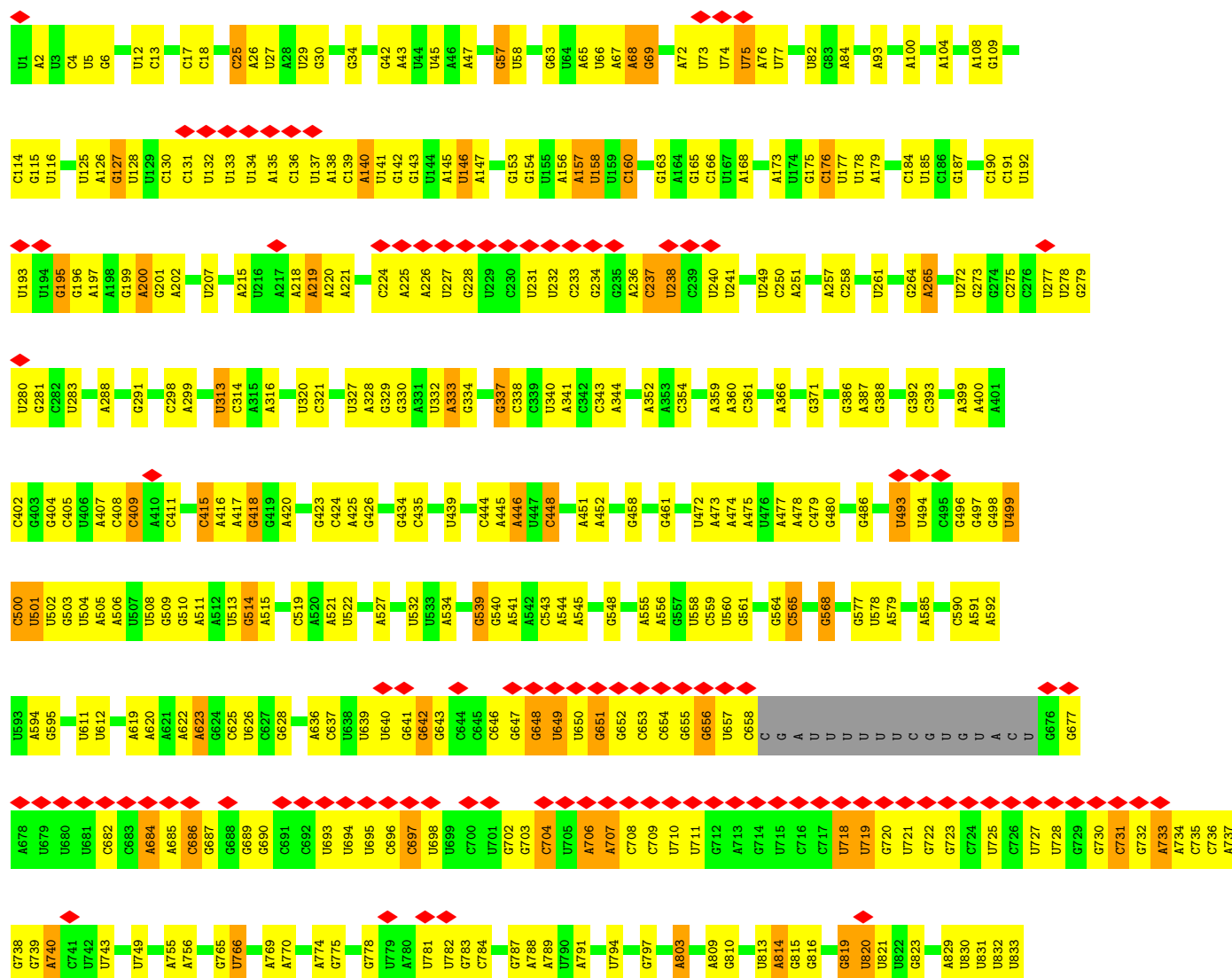
Chain S1: 5% 56% 36% 6%

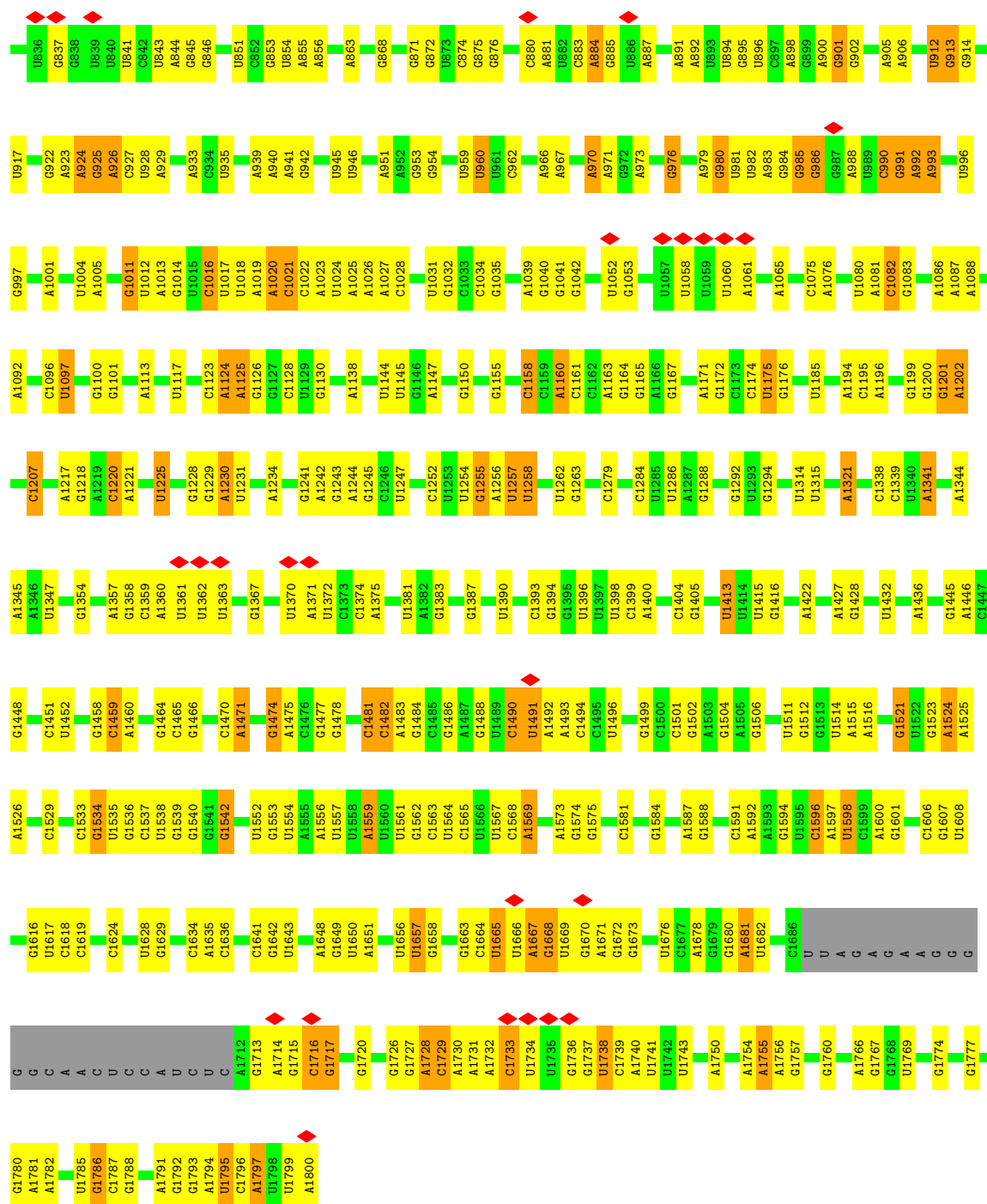






• Molecule 49: *Saccharomyces cerevisiae* S288C 18S ribosomal RNA (RDN18-1)



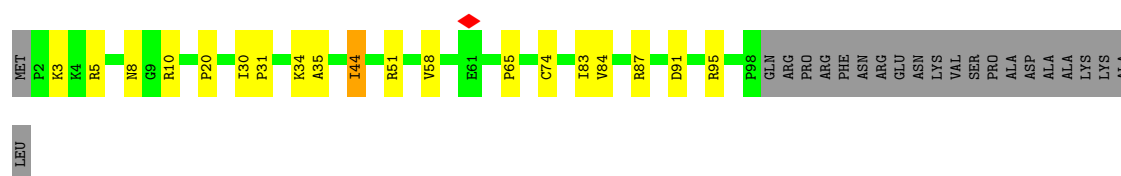


- Molecule 50: Small ribosomal subunit protein eS26A

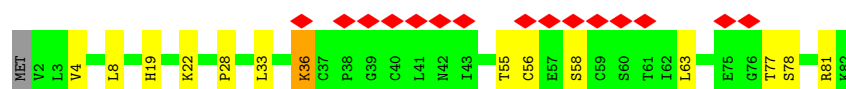
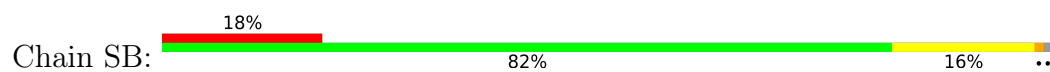
Chain SA: 66% 13% 18%



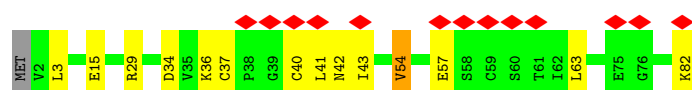
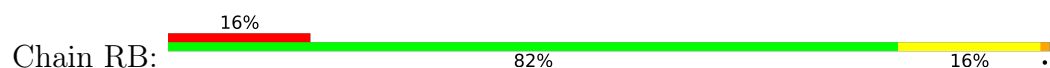
- Molecule 50: Small ribosomal subunit protein eS26A



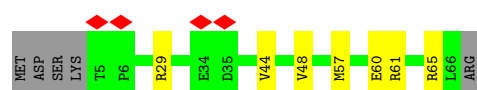
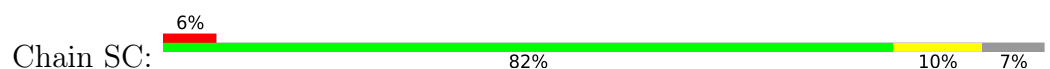
- Molecule 51: 40S ribosomal protein S27-A



- Molecule 51: 40S ribosomal protein S27-A



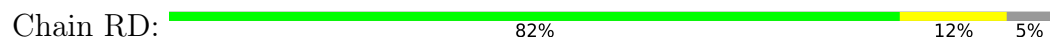
- Molecule 52: Small ribosomal subunit protein eS28B



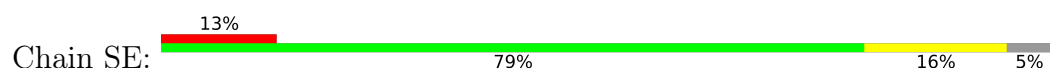
- Molecule 53: Small ribosomal subunit protein uS14A

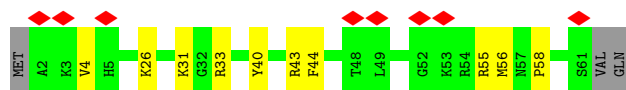


- Molecule 53: Small ribosomal subunit protein uS14A

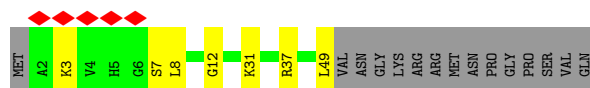


- Molecule 54: 40S ribosomal protein S30-A

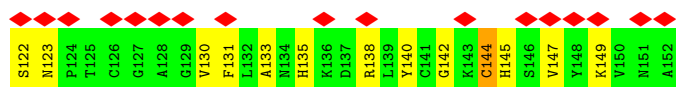
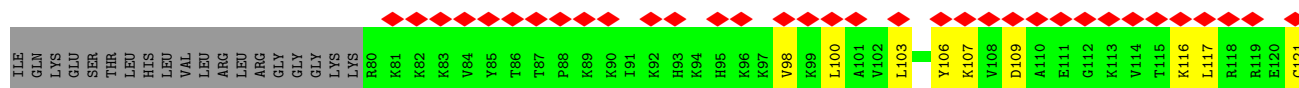
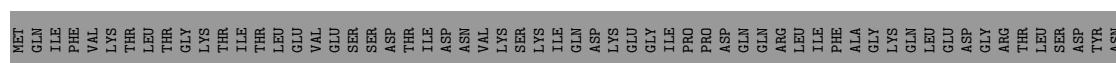
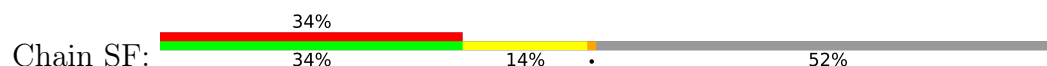




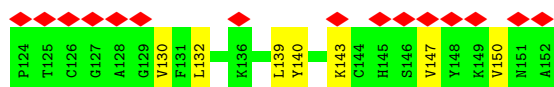
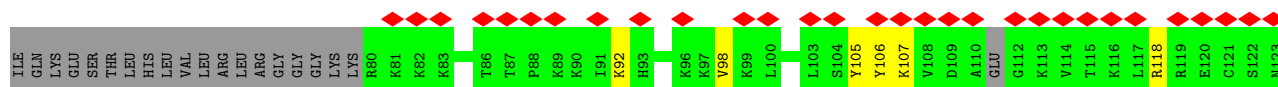
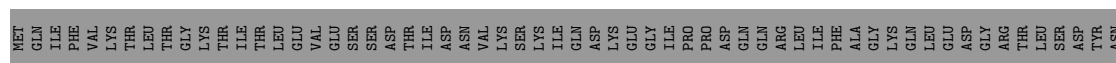
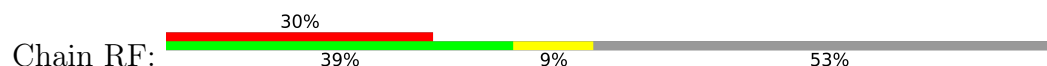
- Molecule 54: 40S ribosomal protein S30-A



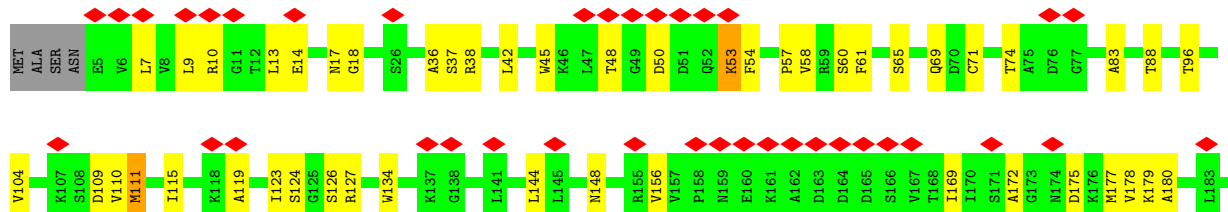
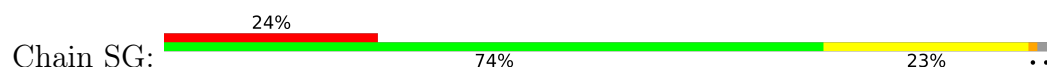
- Molecule 55: Ubiquitin

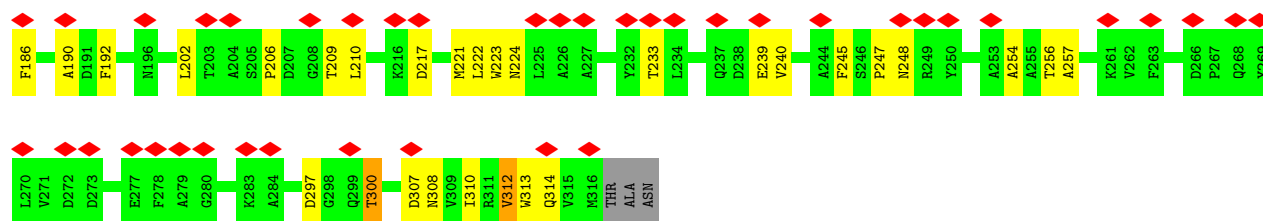


- Molecule 55: Ubiquitin



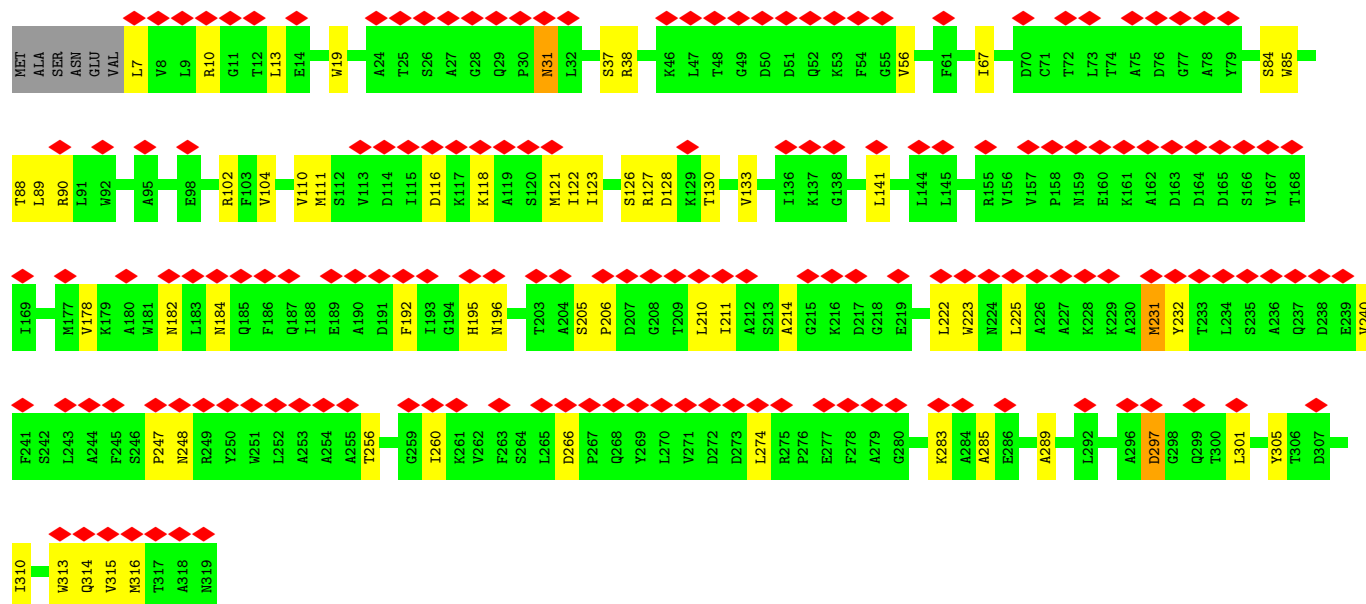
- Molecule 56: Guanine nucleotide-binding protein subunit beta-like protein





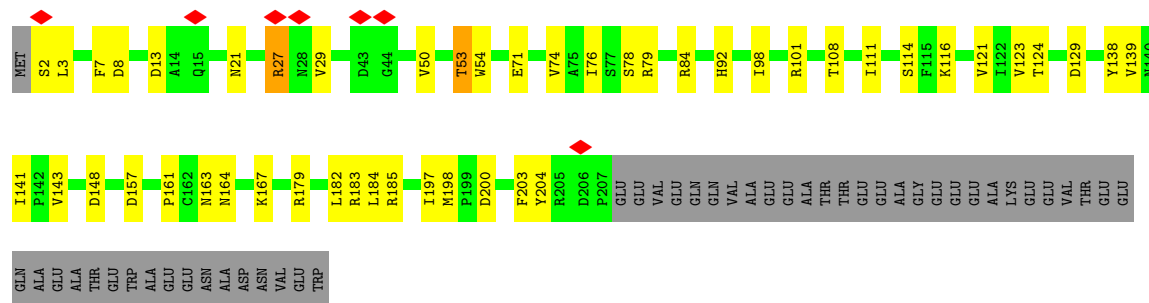
• Molecule 56: Guanine nucleotide-binding protein subunit beta-like protein

Chain RG: 51% 78% 19% ..



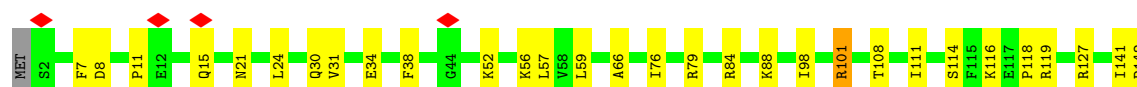
• Molecule 57: 40S ribosomal protein S0-A

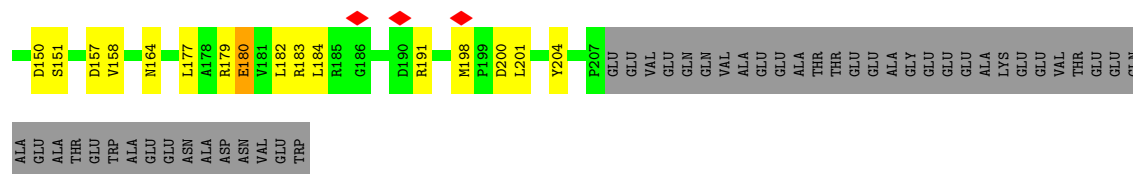
Chain Sa: 63% 18% 18%



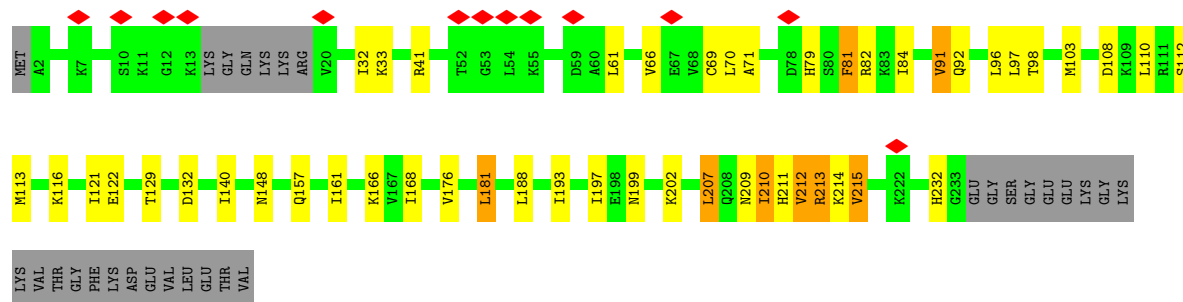
• Molecule 57: 40S ribosomal protein S0-A

Chain Ra: 63% 17% 18%

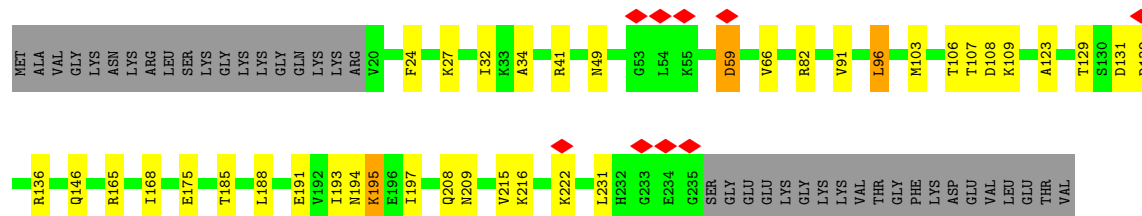




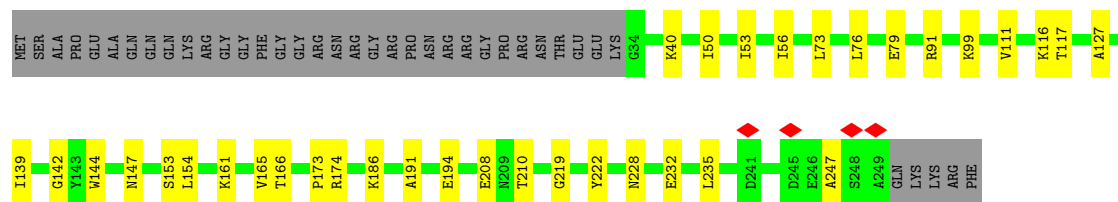
- Molecule 58: 40S ribosomal protein S1-A



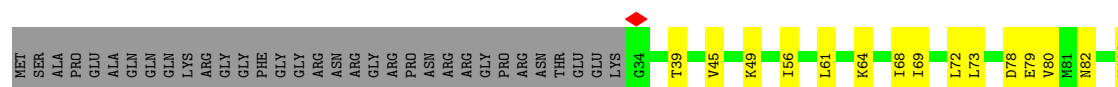
- Molecule 58: 40S ribosomal protein S1-A

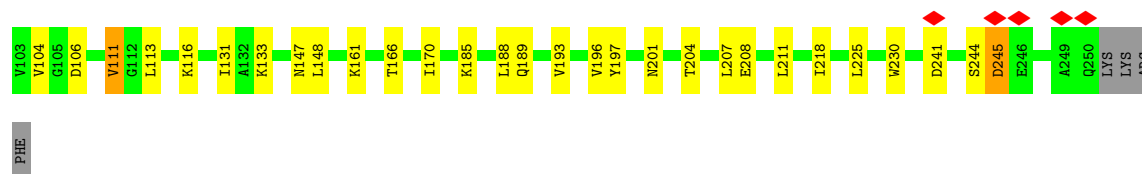


- Molecule 59: 40S ribosomal protein S2

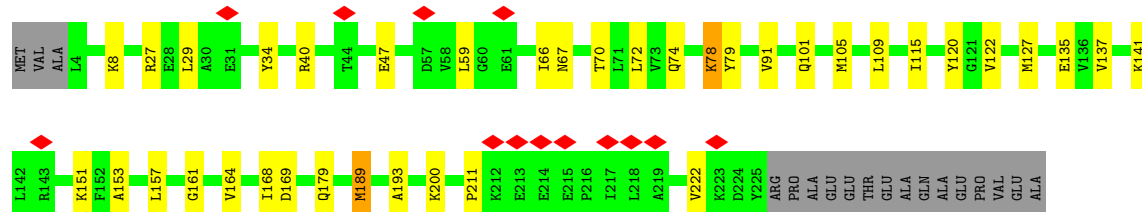
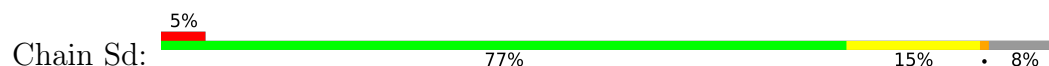


- Molecule 59: 40S ribosomal protein S2

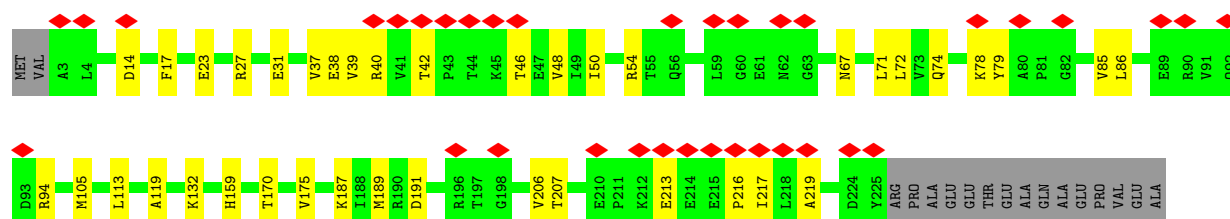
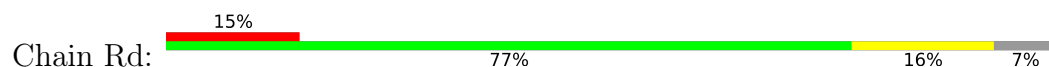




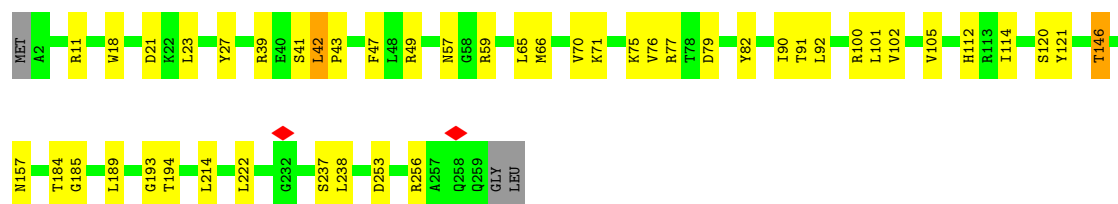
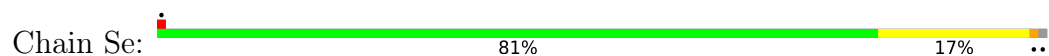
- Molecule 60: Small ribosomal subunit protein uS3



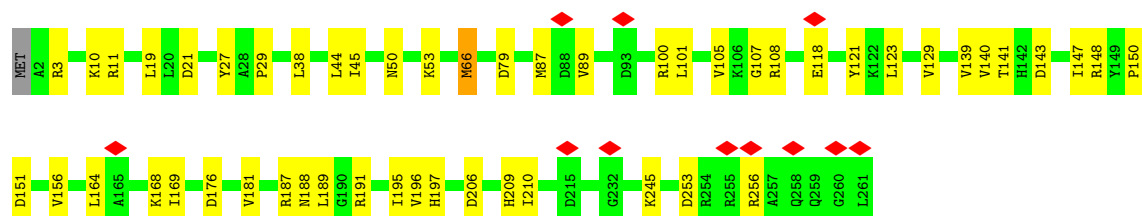
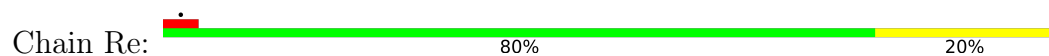
- Molecule 60: Small ribosomal subunit protein uS3



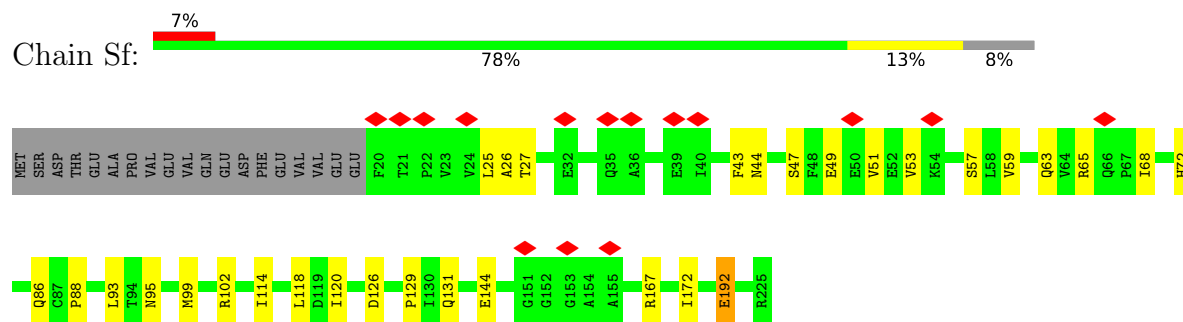
- Molecule 61: 40S ribosomal protein S4-A



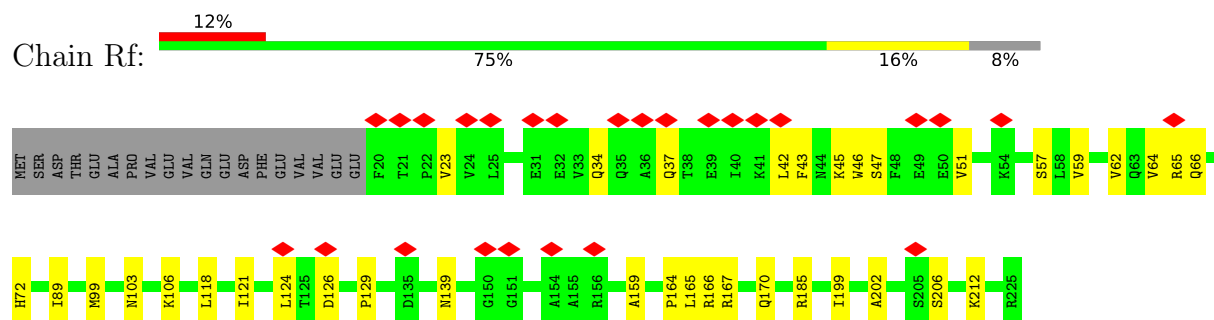
- Molecule 61: 40S ribosomal protein S4-A



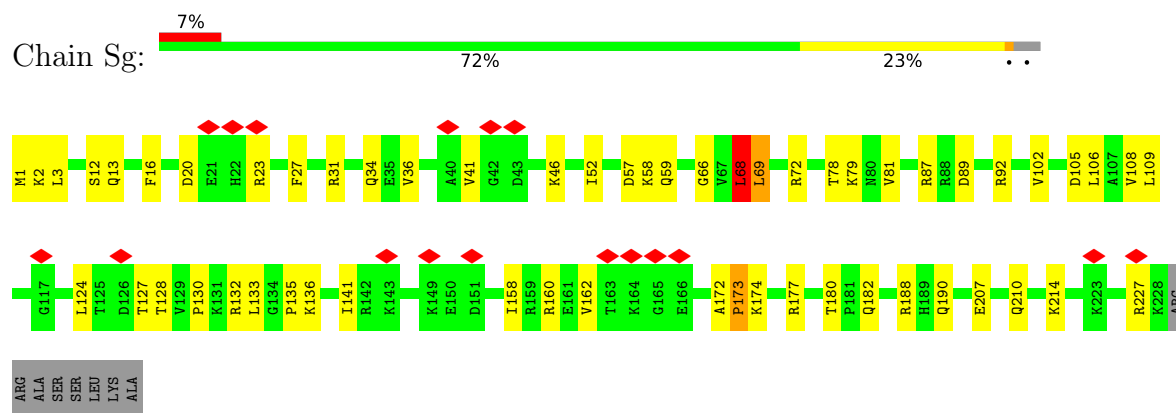
• Molecule 62: 40S ribosomal protein S5



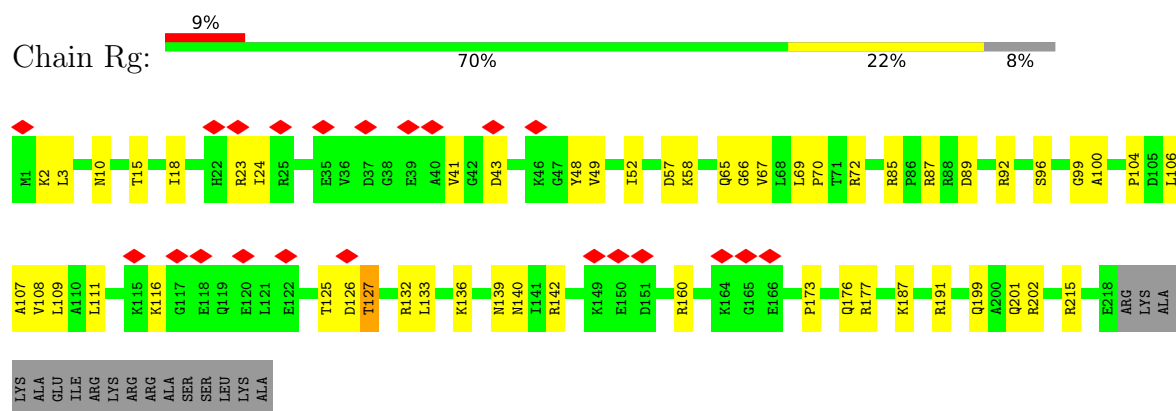
• Molecule 62: 40S ribosomal protein S5



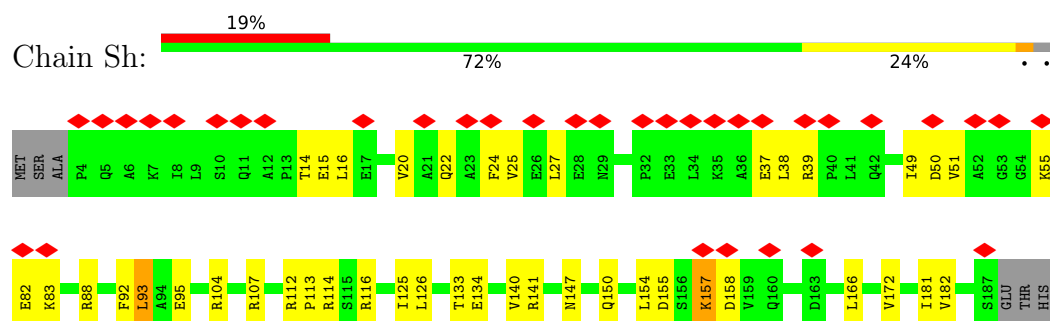
• Molecule 63: 40S ribosomal protein S6-A



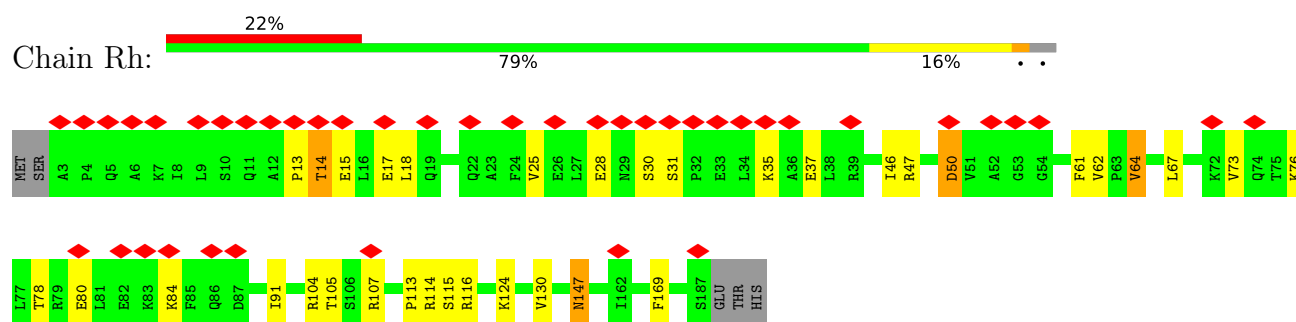
• Molecule 63: 40S ribosomal protein S6-A



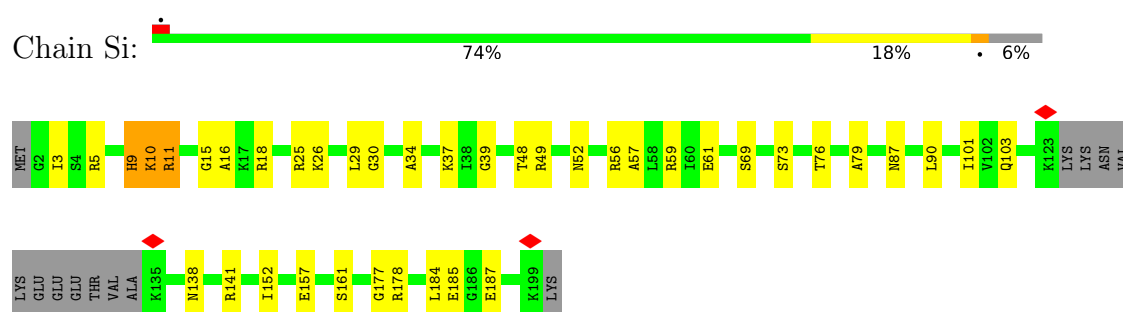
- Molecule 64: 40S ribosomal protein S7-A



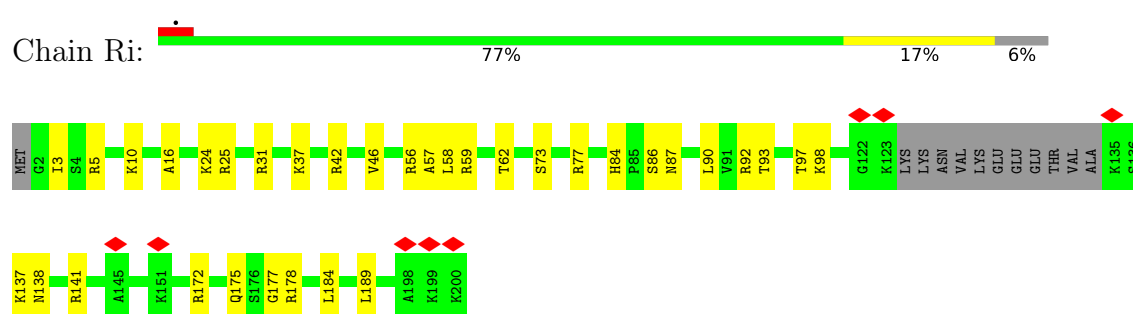
- Molecule 64: 40S ribosomal protein S7-A



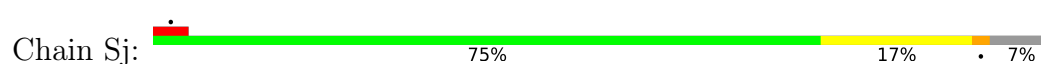
- Molecule 65: 40S ribosomal protein S8-A

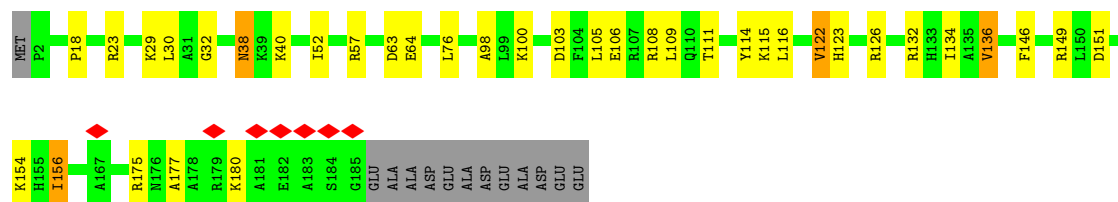


- Molecule 65: 40S ribosomal protein S8-A

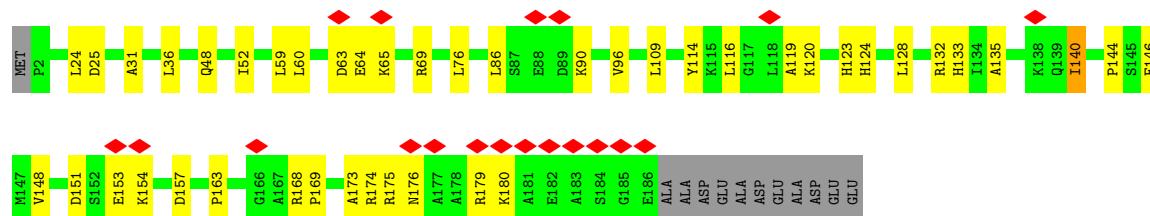
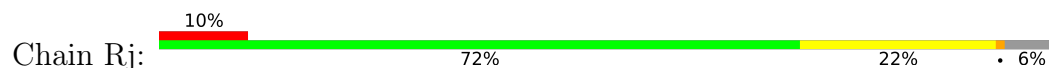


- Molecule 66: 40S ribosomal protein S9-A





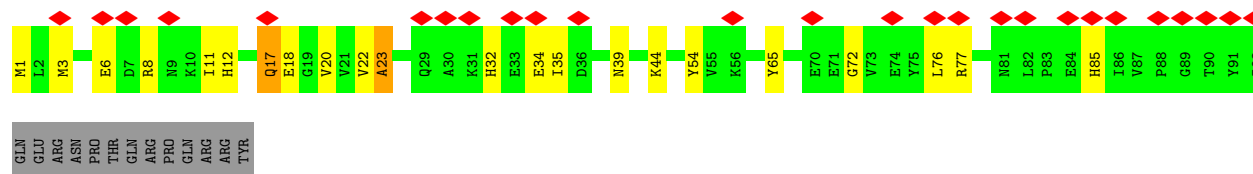
- Molecule 66: 40S ribosomal protein S9-A



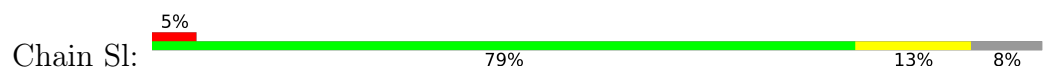
- Molecule 67: 40S ribosomal protein S10-A



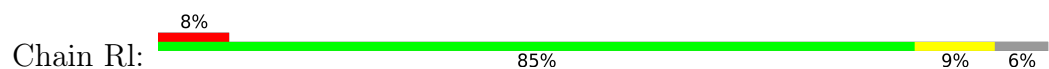
- Molecule 67: 40S ribosomal protein S10-A



- Molecule 68: 40S ribosomal protein S11-A



- Molecule 68: 40S ribosomal protein S11-A

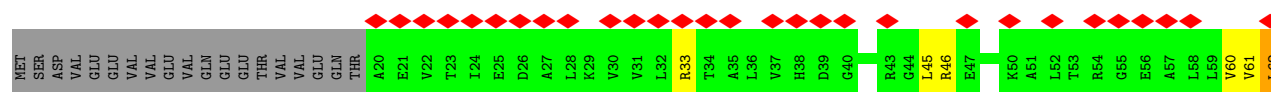
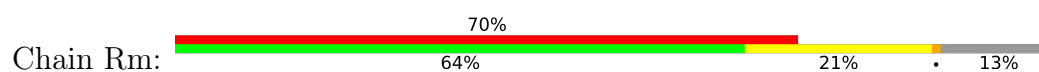




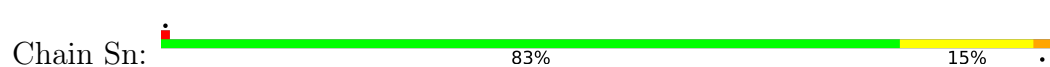
- Molecule 69: 40S ribosomal protein S12



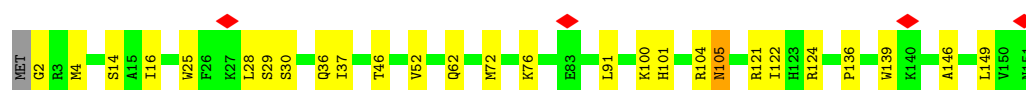
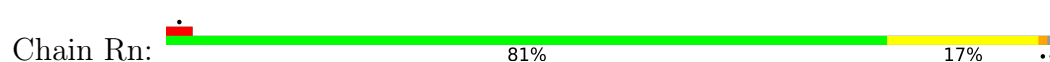
- Molecule 69: 40S ribosomal protein S12



- Molecule 70: 40S ribosomal protein S13

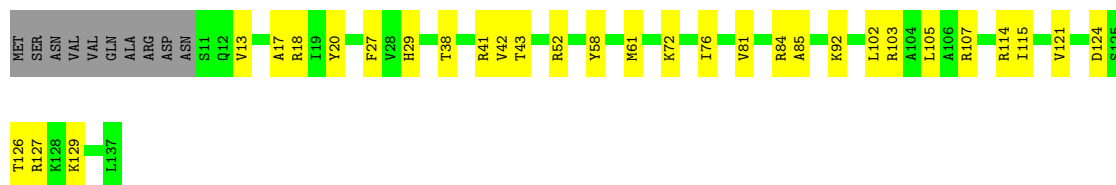


- Molecule 70: 40S ribosomal protein S13



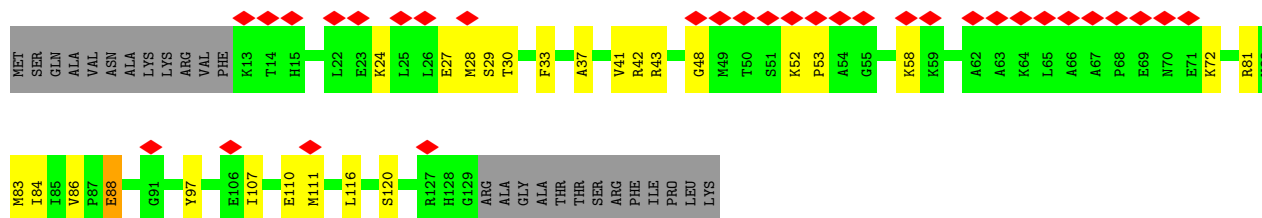
- Molecule 71: 40S ribosomal protein S14-A

Chain So: 



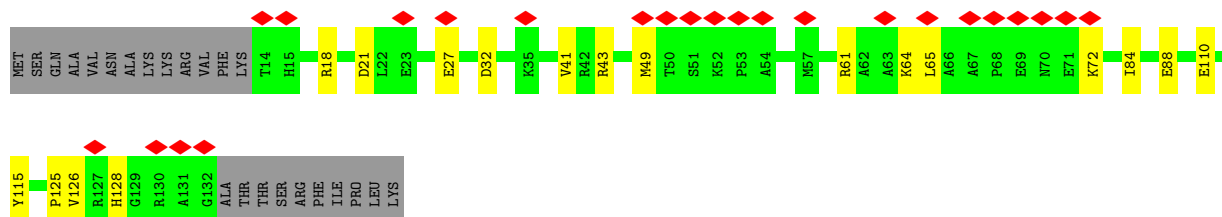
- Molecule 72: 40S ribosomal protein S15

Chain Sp: 



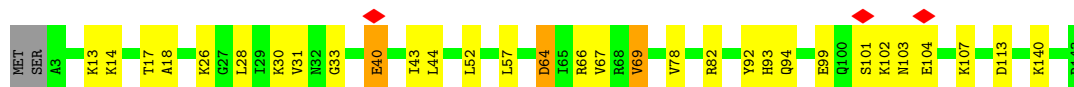
- Molecule 72: 40S ribosomal protein S15

Chain Rp: 



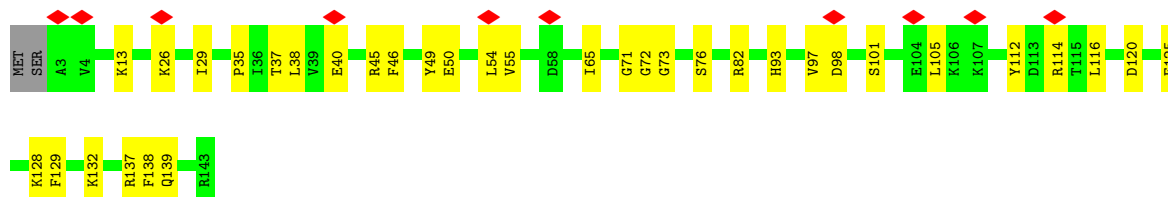
- Molecule 73: 40S ribosomal protein S16-A

Chain Sq: 

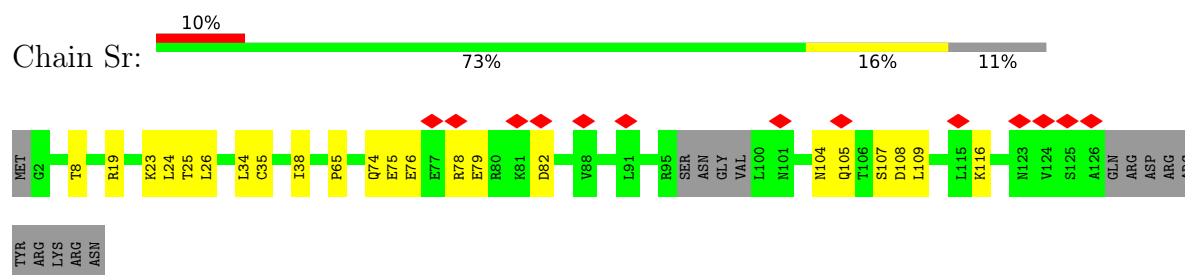


- Molecule 73: 40S ribosomal protein S16-A

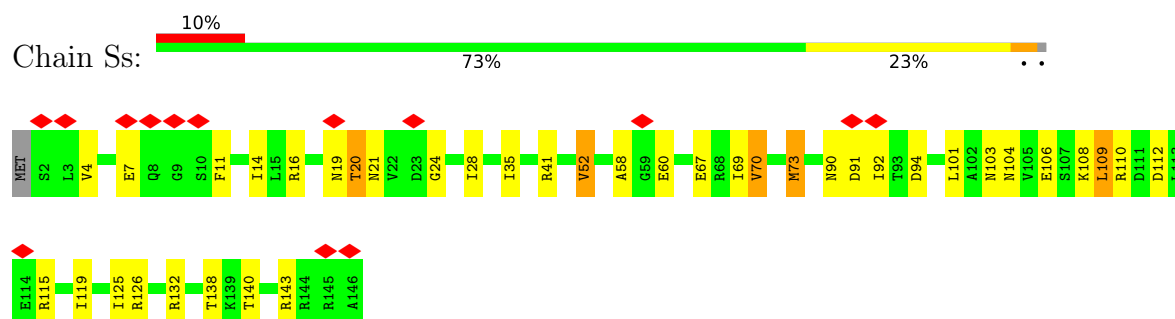
Chain Rq: 



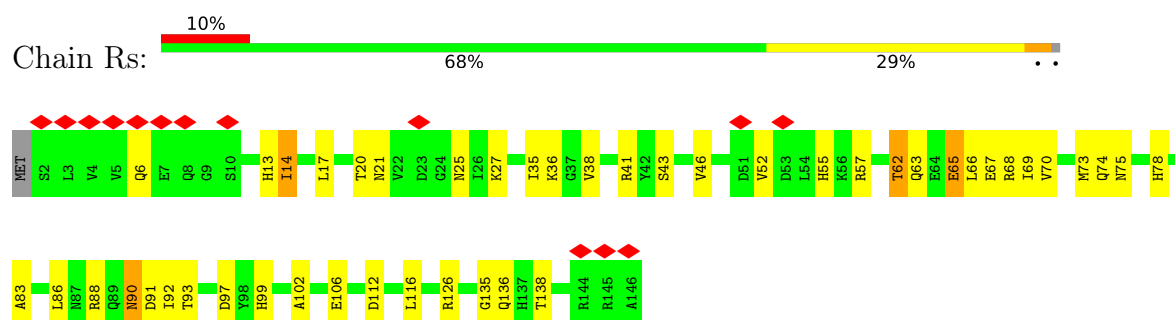
- Molecule 74: 40S ribosomal protein S17-B



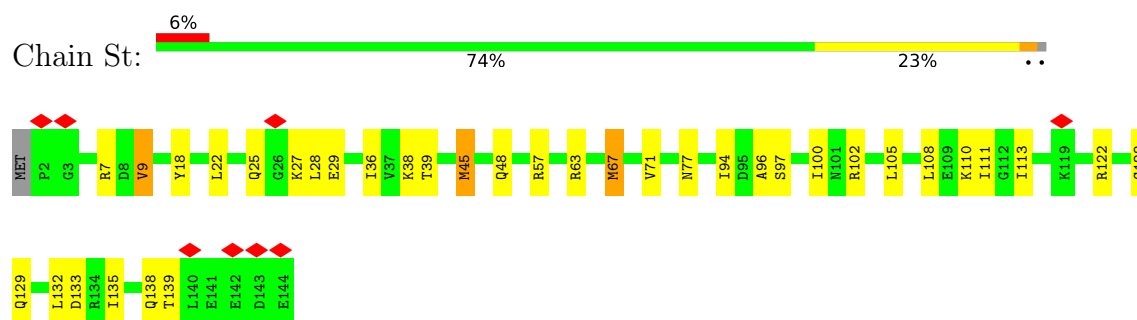
- Molecule 75: 40S ribosomal protein S18-A



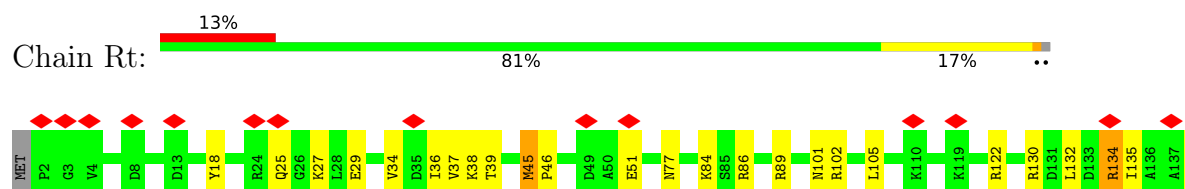
- Molecule 75: 40S ribosomal protein S18-A

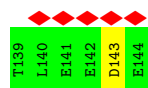


- Molecule 76: 40S ribosomal protein S19-A

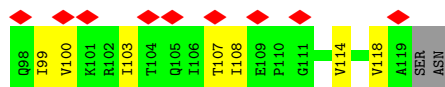


- Molecule 76: 40S ribosomal protein S19-A

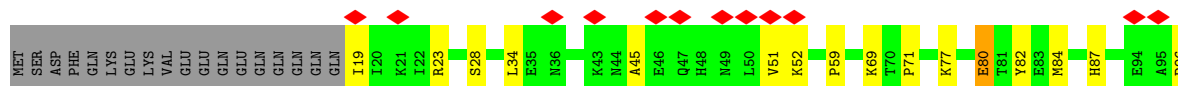




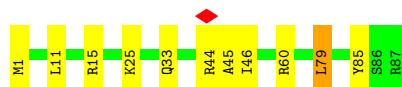
- Molecule 77: Small ribosomal subunit protein uS10



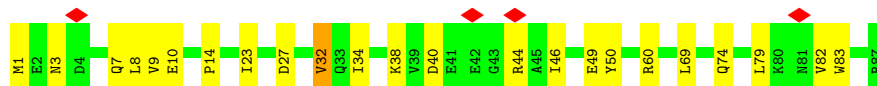
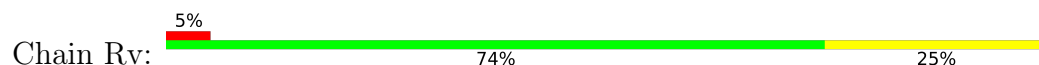
- Molecule 77: Small ribosomal subunit protein uS10



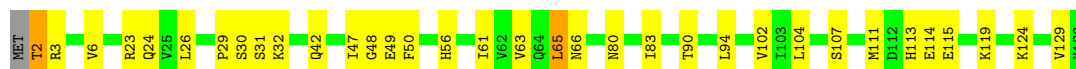
- Molecule 78: Small ribosomal subunit protein eS21A



- Molecule 78: Small ribosomal subunit protein eS21A



- Molecule 79: 40S ribosomal protein S22-A



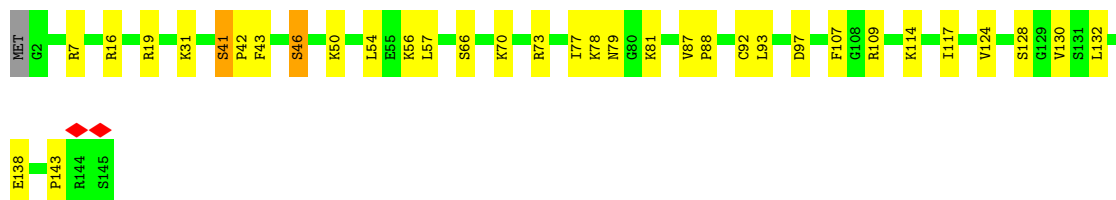
- Molecule 79: 40S ribosomal protein S22-A

Chain Rw:  86% 13% .



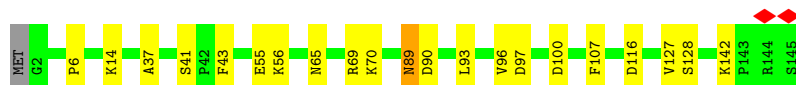
- Molecule 80: 40S ribosomal protein S23-A

Chain Sx:  76% 22% ..



- Molecule 80: 40S ribosomal protein S23-A

Chain Rx:  85% 14% ..



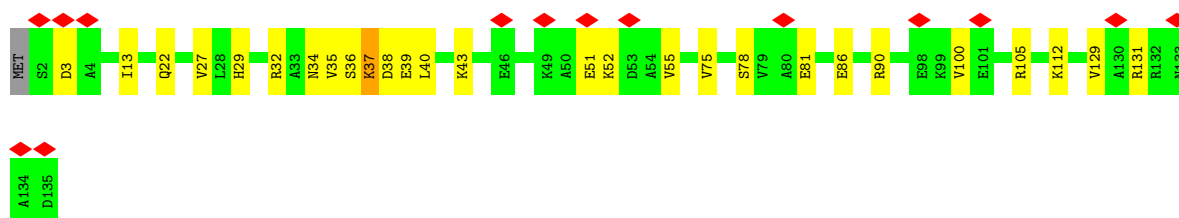
- Molecule 81: 40S ribosomal protein S24-A

Chain Sy:  84% 13% ..



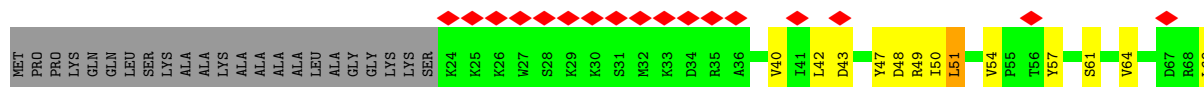
- Molecule 81: 40S ribosomal protein S24-A

Chain Ry:  10% 79% 19% ..



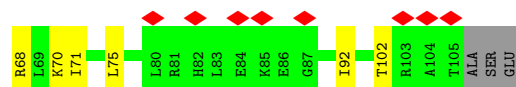
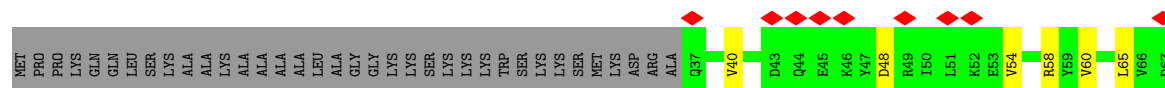
- Molecule 82: 40S ribosomal protein S25-A

Chain Sz:  19% 55% 19% 24%

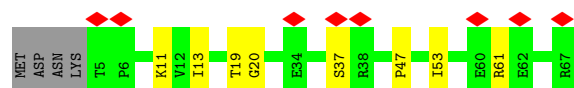
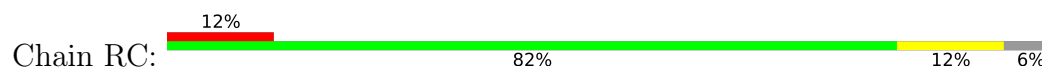




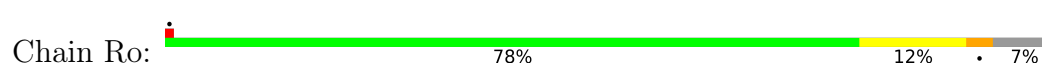
- Molecule 82: 40S ribosomal protein S25-A



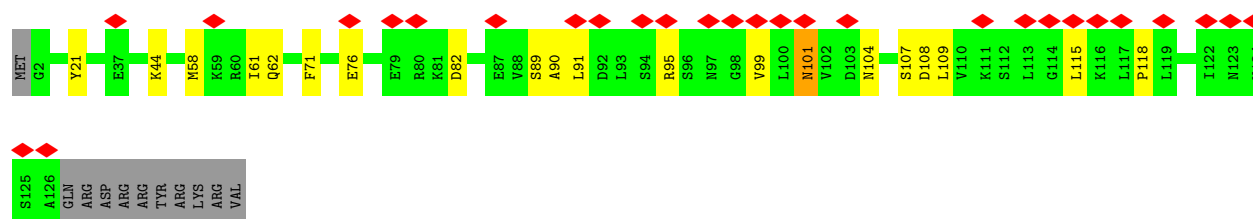
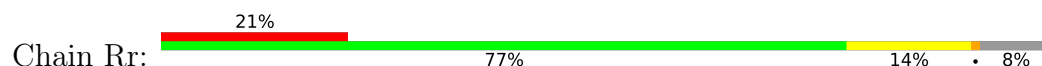
- Molecule 83: 40S ribosomal protein S28-A



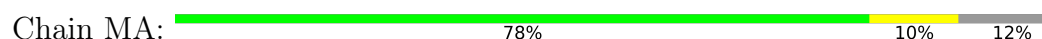
- Molecule 84: 40S ribosomal protein S14-B



- Molecule 85: 40S ribosomal protein S17-A

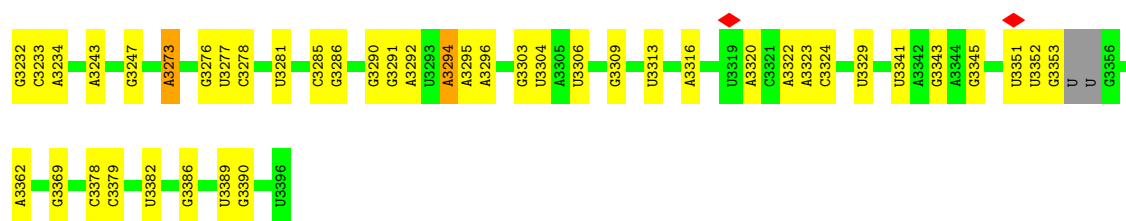


- Molecule 86: 60S ribosomal protein L6-A



GI434	GI435	GI436	GI437	GI446	GI447	GI448	GI449	GI450	GI456	GI469	GI476	GI477	GI481	GI482	GI483	GI484	GI485	GI486	GI487	GI490	GI493	GI496	GI502	GI508	GI525	GI534	GI535	GI536	GI539	GI547	GI553	GI554	GI555	GI556	GI560	GI561	GI562	GI563	GI566	GI567
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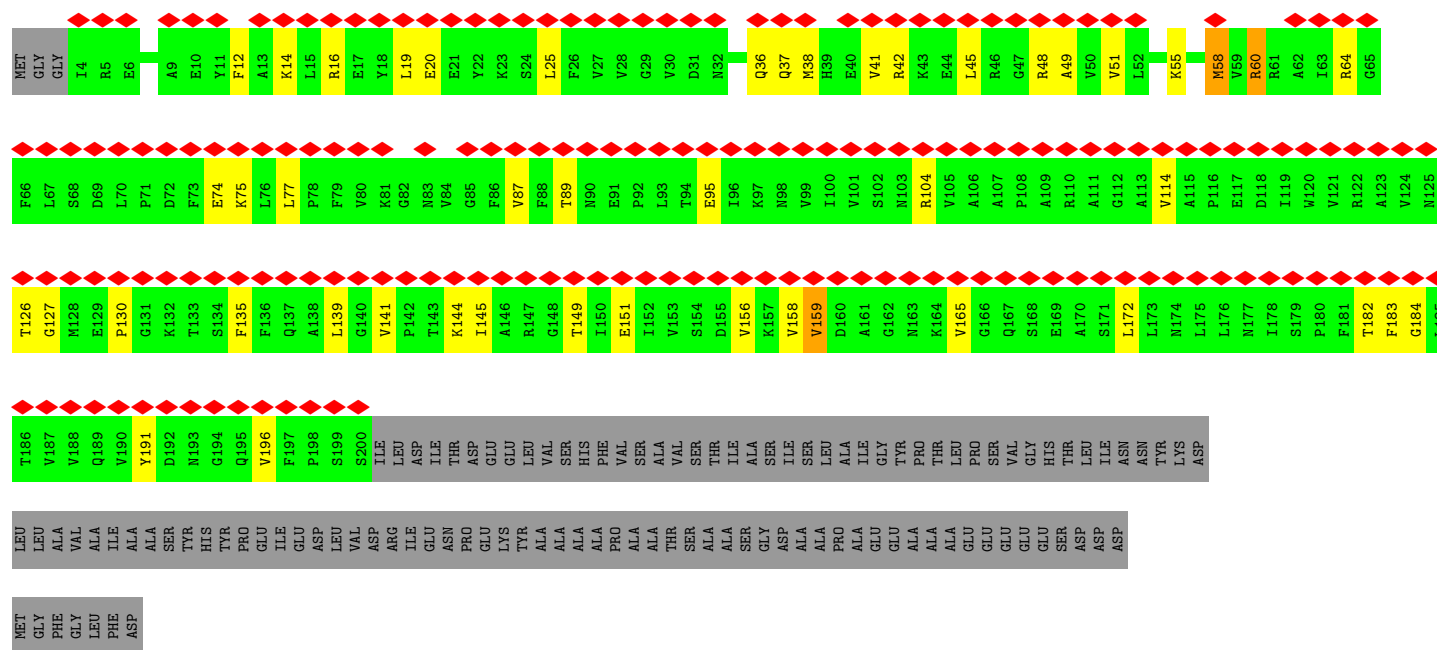
G3080	U2935	G2800	A2674	A	G2454	C2346	C2197	C	U	U	A1816	U1695	U1569
C3092	A2936	A2801	G2677	U	G2457	U2347	A2207	A	G	G	A1696	A1697	U1570
C3096	C2942	A2678	A2679	U	A2458	A2357	A2208	A	A	U	A1697	A1697	A1571
C3097	G2943	A2679	A2679	U	U2459	A2358	U2209	U	C	U	U1705	U1705	U1572
U3121	G2945	A2808	U2683	U	U2460	A2363	A2213	A	U	A	U1705	U1705	G1573
A3122	A2946	A2809	C2684	U	A2461	A2364	A2214	A	C	A	U1716	U1716	C1574
A3130	G2947	A2812	A2685	U	A2462	A2372	G2218	C2094	C	A	U1717	U1717	A1580
U3131	C2948	A2813	A2686	U	U2463	A2373	A2219	G2095	C	A	G1829	G1829	G1576
A3142	G2951	A2814	A2687	U	U2464	A2374	A2220	C2101	C	A	U1718	U1718	A1581
C3143	C2959	A2815	A2688	U	G2465	G2375	A2223	U2102	C	A	G1719	G1719	G1582
U3155	A2960	G2816	A2689	U	G2466	G2376	A2224	U2103	C	A	U1724	U1724	A1583
U3156	G2961	A2817	A2690	U	G2467	G2377	A2225	A2104	C	A	A1842	A1842	A1587
U3157	C2966	U2818	A2691	U	A2468	C2383	U2226	A2107	C	A	G1730	G1730	A1588
U3160	A2967	G2828	A2704	U	G2469	U2388	U2227	G2110	C	A	U1737	U1737	A1589
A3168	G2968	A2829	A2705	U	U2471	U2389	A2229	G2111	C	A	A1741	A1741	A1590
U3169	A2969	A2830	G2714	U	U2472	G2394	A2230	U2112	C	A	U1742	U1742	G1593
A3170	G2970	A2831	G2720	U	G2473	G2395	A2231	A2113	C	A	G1748	G1748	C1596
U3171	C2971	A2832	U2724	U	G2474	A2397	G2253	C2114	C	A	A1750	A1750	A1597
A3172	G2972	U2833	A2727	U	G2475	A2401	U2254	G2122	C	A	G1751	G1751	A1605
A3173	A2973	A2834	A2728	U	G2476	A2402	A2255	U2129	C	A	C1762	C1762	C1615
U3175	G2974	U2835	G2729	U	G2477	A2403	A2256	G2130	C	A	U1763	U1763	U1616
G3176	A3012	A2836	U2736	U	G2478	A2404	G2261	A2131	C	A	G1764	G1764	G1617
U3179	A3013	A2837	A2737	U	A2484	U2411	A2262	U2140	C	A	U1765	U1765	U1629
A3180	G3014	U2838	G2752	U	A2485	G2412	U2267	U2141	C	A	G1766	G1766	U1630
C3181	A3015	A2839	G2753	U	A2486	U2417	U2268	A2142	C	A	U1767	U1767	C1631
G3182	U3023	U2840	G2754	U	A2487	G2418	U2269	A2143	C	A	G1768	G1768	A1632
A3186	A3024	A2841	C2764	U	A2488	A2419	A2270	A2144	C	A	U1769	U1769	G1635
A3187	U3041	U2842	U2767	U	A2489	A2420	G2272	A2145	C	A	G1775	G1775	A1638
G3199	U3042	U2843	U2768	U	A2490	U2421	G2273	C2146	C	A	U1780	U1780	A1642
C3204	A3049	A2844	U2769	U	A2491	G2425	C2278	A2152	C	A	U1785	U1785	A1643
G3205	U3056	U2845	A2772	U	A2492	U2426	A2279	U2153	C	A	G1787	G1787	G1644
U3207	G3059	A2846	G2777	U	A2493	U2427	A2280	A2158	C	A	U1793	U1793	U1645
A3210	U3066	U2847	A2778	U	A2494	U2428	A2281	U2159	C	A	C1657	C1657	G1646
C3211	A3067	A2848	A2779	U	A2495	U2429	A2282	G2160	C	A	U1797	U1797	C1657
U3214	G3068	U2849	A2792	U	A2496	A2435	U2283	G2161	C	A	A1799	A1799	G1661
A3215	U3069	A2850	G2793	U	U2501	A2438	G2304	A2167	C	A	A1800	A1800	G1662
G3216	U3070	U2851	G2794	U	A2502	A2439	G2307	A2168	C	A	C1805	C1805	G1666
C3217	G3071	A2852	U2795	U	A2511	U2440	U2340	G2169	C	A	A1806	A1806	A1667
A3218	U3072	U2853	G2796	U	A2512	A2441	U2341	U2170	C	A	G1807	G1807	G1668
G3219	U3073	A2854	A2671	U	A2513	A2442	U2342	G2171	C	A	G1808	G1808	A1679
U3231	U3074	U2855	G2672	U	A2514	A2443	U2343	U2176	C	A	C1812	C1812	A1683
		A2856	A2673	U	A2515	A2444	U2344	G2185	C	A	A1813	A1813	U1688
		G2673	A2673	C	A2516	A2445	U2345	A2188	C	A	U1814	U1814	
		A2674	A2674		A2517	A2446	U2346	U2193	C	A	U1815	U1815	
		U2675	A2675		A2518	A2447	U2347	G2194	C	A			
		A2676	A2676		A2519	A2448	U2348	U2195	C	A			
		G2677	A2677		A2520	A2449	U2349	G2196	C	A			
		A2678	A2678		A2521	A2450	U2350	U2197	C	A			
		U2679	A2679		A2522	A2451	U2351	U2198	C	A			
		A2680	A2680		A2523	A2452	U2352	G2199	C	A			
		G2681	A2681		A2524	A2453	U2353	U2200	C	A			
		U2682	A2682		A2525	A2454	U2354	U2201	C	A			
		A2683	A2683		A2526	A2455	U2355	U2202	C	A			
		U2684	A2684		A2527	A2456	U2356	U2203	C	A			
		A2685	A2685		A2528	A2457	U2357	U2204	C	A			
		G2686	A2686		A2529	A2458	U2358	U2205	C	A			
		U2687	A2687		A2530	A2459	U2359	U2206	C	A			
		A2688	A2688		A2531	A2460	U2360	U2207	C	A			
		U2689	A2689		A2532	A2461	U2361	U2208	C	A			
		A2690	A2690		A2533	A2462	U2362	U2209	C	A			
		G2691	A2691		A2534	A2463	U2363	U2210	C	A			
		U2692	A2692		A2535	A2464	U2364	U2211	C	A			
		A2693	A2693		A2536	A2465	U2365	U2212	C	A			
		U2694	A2694		A2537	A2466	U2366	U2213	C	A			
		A2695	A2695		A2538	A2467	U2367	U2214	C	A			
		U2696	A2696		A2539	A2468	U2368	U2215	C	A			
		A2697	A2697		A2540	A2469	U2369	U2216	C	A			
		G2698	A2698		A2541	A2470	U2370	U2217	C	A			
		U2699	A2699		A2542	A2471	U2371	U2218	C	A			
		A2700	A2700		A2543	A2472	U2372	U2219	C	A			
		U2701	A2701		A2544	A2473	U2373	U2220	C	A			
		A2702	A2702		A2545	A2474	U2374	U2221	C	A			
		U2703	A2703		A2546	A2475	U2375	U2222	C	A			
		A2704	A2704		A2547	A2476	U2376	U2223	C	A			
		G2705	A2705		A2548	A2477	U2377	U2224	C	A			
		U2706	A2706		A2549	A2478	U2378	U2225	C	A			
		A2707	A2707		A2550	A2479	U2379	U2226	C	A			
		U2708	A2708		A2551	A2480	U2380	U2227	C	A			
		A2709	A2709		A2552	A2481	U2381	U2228	C	A			
		G2710	A2710		A2553	A2482	U2382	U2229	C	A			
		U2711	A2711		A2554	A2483	U2383	U2230	C	A			
		A2712	A2712		A2555	A2484	U2384	U2231	C	A			
		G2713	A2713		A2556	A2485	U2385	U2232	C	A			
		U2714	A2714		A2557	A2486	U2386	U2233	C	A			
		A2715	A2715		A2558	A2487	U2387	U2234	C	A			
		G2716	A2716		A2559	A2488	U2388	U2235	C	A			
		U2717	A2717		A2560	A2489	U2389	U2236	C	A			
		A2718	A2718		A2561	A2490	U2390	U2237	C	A			
		G2719	A2719		A2562	A2491	U2391	U2238	C	A			
		U2720	A2720		A2563	A2492	U2392	U2239	C	A			
		A2721	A2721		A2564	A2493	U2393	U2240	C	A			
		G2722	A2722		A2565	A2494	U2394	U2241	C	A			
		U2723	A2723		A2566	A2495	U2395	U2242	C	A			
		A2724	A2724		A2567	A2496	U2396	U2243	C	A			
		G2725	A2725		A2568	A2497	U2397	U2244	C	A			
		U2726	A2726		A2569	A2498	U2398	U2245	C	A			
		A2727	A2727		A2570	A2499	U2399	U2246	C	A			
		G2728	A2728		A2571	A2500	U2400	U2247	C	A			
		U2729	A2729		A2572	A2501	U2401	U2248	C	A			
		A2730	A2730		A2573	A2502	U2402	U2249	C	A			
		G2731	A2731		A2574	A2503	U2403	U2250	C	A			
		U2732	A2732		A2575	A2504	U2404	U2251	C	A			
		A2733	A2733		A2576	A2505	U2405	U2252	C	A			
		G2734	A2734		A2577	A2506	U2406	U2253	C	A			
		U2735	A2735		A2578	A2507	U2407	U2254	C	A			
		A2736	A2736		A2579	A2508	U2408	U2255	C	A			
		G2737	A2737		A2580	A2509	U2409	U2256	C	A			
		U2738	A2738		A2581	A2510	U2410	U2257	C	A			
		A2739	A2739		A2582	A2511	U2411	U2258	C	A			
		G2740	A2740		A2583	A2512	U2412	U2259	C	A			
		U2741	A2741		A2584	A2513	U2413	U2260	C	A			
		A2742	A2742		A2585	A2514	U2414	U2261	C	A			
		G2743	A2743		A2586	A2515	U2415	U2262	C	A			
		U2744	A2744		A2587	A2516	U2416	U2263	C	A			
		A2745	A2745		A2588	A2517	U2417	U2264	C	A			
		G2746	A2746		A2589	A2518	U2418	U2265	C	A			
		U2747	A2747		A2590	A2519	U2419	U2266	C	A			
		A2748	A2748		A2591	A2520	U2						



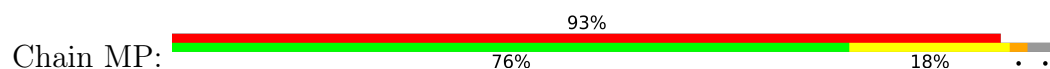
• Molecule 88: tRNA

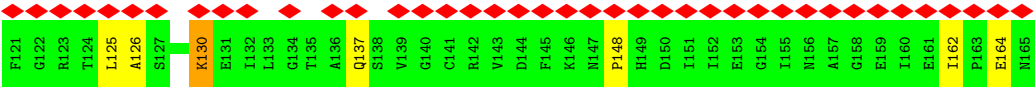


• Molecule 89: 60S acidic ribosomal protein P0

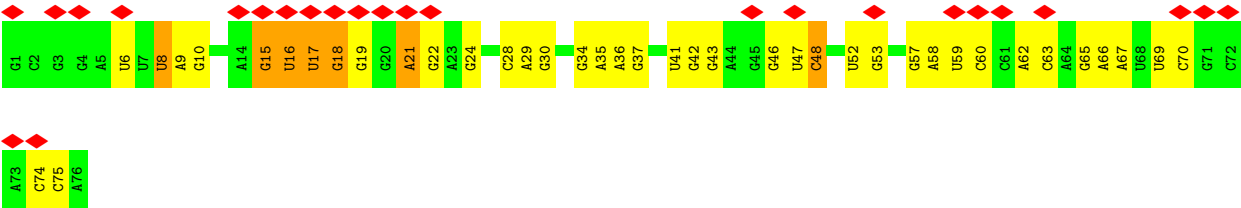


• Molecule 90: 60S ribosomal protein L12-A





• Molecule 91: tRNA



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.24	0/132	0.48	0/175
2	CM	0.21	0/927	0.40	0/1434
3	CN	0.16	0/1053	0.40	0/1414
4	CP	0.36	3/1810 (0.2%)	0.30	0/2817
5	L1	0.35	0/74617	0.38	0/116334
6	L2	0.35	0/3746	0.37	0/5832
6	M2	0.33	0/3746	0.35	0/5832
7	L3	0.29	0/2883	0.31	0/4491
7	M3	0.28	0/2883	0.30	0/4491
8	LA	0.24	0/1327	0.43	0/1791
9	LB	0.32	0/1821	0.45	0/2451
9	MB	0.28	0/1821	0.42	0/2451
10	LC	0.27	0/1836	0.53	0/2481
10	MC	0.25	0/1836	0.48	0/2481
11	LD	0.25	0/1529	0.47	0/2060
11	MD	0.24	0/1539	0.43	0/2073
12	LE	0.28	0/1801	0.50	1/2416 (0.0%)
12	ME	0.25	0/1779	0.40	0/2386
13	LF	0.26	0/1371	0.63	3/1838 (0.2%)
13	MF	0.24	0/1374	0.54	0/1842
14	LG	0.29	0/1568	0.53	0/2106
14	MG	0.28	0/1568	0.50	0/2106
15	LH	0.26	0/1068	0.41	0/1438
15	MH	0.23	0/1068	0.37	0/1438
16	LI	0.32	0/1757	0.42	0/2354
16	MI	0.31	0/1757	0.41	0/2354
17	LJ	0.30	0/1585	0.46	1/2128 (0.0%)
17	MJ	0.27	0/1585	0.45	0/2128
18	LK	0.30	0/1439	0.47	0/1938
18	MK	0.28	0/1245	0.45	0/1676
19	LL	0.30	0/1465	0.48	0/1965
19	ML	0.27	0/1465	0.44	0/1965

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	LM	0.27	0/1532	0.46	0/2043
20	MM	0.25	0/1440	0.49	0/1921
21	LN	0.30	0/1473	0.50	0/1980
21	MN	0.28	0/1481	0.45	0/1990
22	LO	0.30	0/1300	0.49	0/1743
22	MO	0.28	0/1300	0.48	1/1743 (0.1%)
23	La	0.29	0/1018	0.42	0/1369
23	Ma	0.28	0/978	0.46	0/1316
24	Lb	0.29	0/701	0.50	0/934
24	Mb	0.24	0/701	0.43	0/934
25	Lc	0.30	0/836	0.52	0/1104
25	Mc	0.26	0/831	0.49	0/1097
26	Ld	0.29	0/230	0.32	0/296
26	Md	0.28	0/234	0.56	0/300
27	Le	0.32	0/423	0.52	0/562
27	Me	0.24	0/423	0.35	0/562
28	Lf	0.34	0/443	0.43	0/588
28	Mf	0.31	0/443	0.64	0/588
29	Lg	0.23	0/618	0.44	0/826
29	Mg	0.24	0/618	0.48	0/826
30	Lh	0.31	0/685	0.42	0/908
30	Mh	0.33	0/680	0.51	0/901
31	Li	0.26	0/772	0.45	0/1026
31	Mi	0.24	0/778	0.49	0/1034
32	Lj	0.27	0/978	0.42	0/1301
32	Mj	0.26	0/978	0.46	0/1301
33	Lk	0.29	0/846	0.39	0/1130
33	Mk	0.27	0/871	0.40	0/1164
34	Ll	0.33	0/868	0.42	0/1168
34	Ml	0.31	0/868	0.42	0/1168
35	Lm	0.30	0/1038	0.44	0/1390
35	Mm	0.27	0/1041	0.37	0/1394
36	Ln	0.29	0/890	0.45	0/1196
36	Mn	0.28	0/897	0.58	3/1205 (0.2%)
37	Lo	0.27	0/745	0.48	0/1001
37	Mo	0.25	0/750	0.44	0/1008
38	Lp	0.29	0/473	0.65	3/629 (0.5%)
38	Mp	0.25	0/473	0.40	0/629
39	Lq	0.33	0/1204	0.59	0/1612
39	Mq	0.31	0/1204	0.52	0/1612
40	Lr	0.26	0/1118	0.48	0/1497
40	Mr	0.25	0/1118	0.48	0/1497
41	Ls	0.27	0/995	0.46	0/1329

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	Ms	0.26	0/1004	0.45	1/1341 (0.1%)
42	Lt	0.28	0/979	0.48	0/1321
42	Mt	0.29	0/974	0.51	0/1314
43	Lu	0.26	0/850	0.54	0/1152
43	Mu	0.24	0/533	0.43	0/707
44	Lv	0.23	0/812	0.54	0/1099
44	Mv	0.28	0/786	0.64	0/1065
45	Lw	0.32	0/1933	0.49	0/2598
45	Mw	0.29	0/1948	0.42	0/2617
46	Lx	0.31	0/3146	0.51	0/4228
46	Mx	0.27	0/3146	0.45	0/4228
47	Ly	0.31	0/2800	0.47	0/3790
47	My	0.27	0/2800	0.44	0/3790
48	Lz	0.23	0/2400	0.46	0/3239
48	Mz	0.21	0/2425	0.40	0/3271
49	R1	0.23	0/41891	0.37	0/65273
49	S1	0.28	0/42211	0.39	3/65773 (0.0%)
50	RA	0.24	0/782	0.58	0/1047
50	SA	0.30	0/782	0.66	2/1047 (0.2%)
51	RB	0.22	0/620	0.61	0/838
51	SB	0.26	0/620	0.59	1/838 (0.1%)
52	SC	0.26	0/488	0.65	0/656
53	RD	0.17	0/452	0.41	0/600
53	SD	0.24	0/452	0.47	0/600
54	RE	0.31	0/391	0.55	0/520
54	SE	0.23	0/480	0.57	0/639
55	RF	0.21	0/557	0.59	1/749 (0.1%)
55	SF	0.23	0/567	0.67	0/764
56	RG	0.14	0/2456	0.42	0/3343
56	SG	0.20	0/2436	0.56	3/3318 (0.1%)
57	Ra	0.24	0/1623	0.58	0/2222
57	Sa	0.26	0/1644	0.63	1/2249 (0.0%)
58	Rb	0.20	0/1748	0.45	0/2352
58	Sb	0.26	0/1823	0.63	1/2447 (0.0%)
59	Rc	0.22	0/1665	0.44	0/2263
59	Sc	0.29	0/1656	0.57	0/2251
60	Rd	0.21	0/1759	0.51	0/2368
60	Sd	0.21	0/1754	0.47	1/2361 (0.0%)
61	Re	0.19	0/2109	0.47	0/2839
61	Se	0.26	0/2097	0.58	1/2823 (0.0%)
62	Rf	0.20	0/1629	0.52	0/2202
62	Sf	0.23	0/1625	0.53	3/2197 (0.1%)
63	Rg	0.15	0/1779	0.43	1/2379 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
63	Sg	0.20	0/1839	0.48	1/2460 (0.0%)
64	Rh	0.20	0/1511	0.50	0/2036
64	Sh	0.25	0/1498	0.64	2/2019 (0.1%)
65	Ri	0.16	0/1514	0.34	0/2021
65	Si	0.28	0/1501	0.59	0/2006
66	Rj	0.20	0/1519	0.50	1/2035 (0.0%)
66	Sj	0.23	0/1504	0.52	0/2016
67	Rk	0.24	0/757	0.60	0/1022
67	Sk	0.34	0/769	0.93	1/1039 (0.1%)
68	Rl	0.21	0/1194	0.41	0/1610
68	Sl	0.29	0/1185	0.58	0/1598
69	Rm	0.23	0/898	0.70	1/1220 (0.1%)
69	Sm	0.29	0/883	0.90	3/1199 (0.3%)
70	Rn	0.24	0/1215	0.62	1/1638 (0.1%)
70	Sn	0.28	0/1215	0.59	0/1638
71	So	0.28	0/937	0.68	0/1261
72	Rp	0.21	0/959	0.59	1/1288 (0.1%)
72	Sp	0.28	0/936	0.71	1/1259 (0.1%)
73	Rq	0.20	0/1125	0.53	0/1510
73	Sq	0.23	0/1125	0.58	0/1510
74	Sr	0.26	0/957	0.66	1/1283 (0.1%)
75	Rs	0.23	0/1211	0.61	1/1628 (0.1%)
75	Ss	0.27	0/1211	0.65	0/1628
76	Rt	0.22	0/1130	0.59	2/1517 (0.1%)
76	St	0.28	0/1130	0.74	3/1517 (0.2%)
77	Ru	0.24	0/815	0.63	0/1102
77	Su	0.25	0/807	0.64	0/1091
78	Rv	0.24	0/693	0.58	0/935
78	Sv	0.28	0/682	0.60	0/921
79	Rw	0.24	0/1038	0.45	0/1395
79	Sw	0.28	0/1038	0.48	0/1395
80	Rx	0.23	0/1139	0.47	0/1518
80	Sx	0.28	0/1139	0.58	0/1518
81	Ry	0.20	0/1087	0.56	1/1449 (0.1%)
81	Sy	0.22	0/1087	0.54	0/1449
82	Rz	0.26	0/566	0.59	1/761 (0.1%)
82	Sz	0.25	0/661	0.70	0/888
83	RC	0.22	0/499	0.56	0/670
84	Ro	0.29	0/960	0.68	3/1290 (0.2%)
85	Rr	0.22	0/1010	0.57	0/1355
86	MA	0.24	0/1251	0.46	0/1682
87	M1	0.33	1/75384 (0.0%)	0.36	1/117530 (0.0%)
88	DQ	0.17	0/1836	0.29	0/2859

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
89	MQ	0.17	0/1558	0.48	0/2107
90	MP	0.15	0/1210	0.37	0/1627
91	DP	0.14	0/1788	0.28	0/2786
All	All	0.29	4/435297 (0.0%)	0.43	56/639512 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
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)
4	CP	34	I	C5-C6	6.44	1.52	1.39
4	CP	34	I	N3-C4	6.14	1.48	1.35
87	M1	2946	A2M	O3'-P	5.23	1.61	1.56
4	CP	34	I	C2-N3	5.17	1.46	1.35

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	Mn	110	GLU	CA-CB-CG	8.21	130.51	114.10
76	Rt	29	GLU	CA-CB-CG	7.60	129.31	114.10
70	Rn	36	GLN	CA-CB-CG	7.28	128.66	114.10
63	Rg	69	LEU	CA-CB-CG	6.81	140.15	116.30
13	LF	108	GLU	CA-C-N	6.80	134.53	121.54

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](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CC	129	0	120	2	0
2	CM	838	0	421	6	0
3	CN	1046	0	1088	14	0
4	CP	1621	0	821	14	0
5	L1	66660	0	33498	364	0
6	L2	3353	0	1695	14	0
6	M2	3353	0	1695	26	0
7	L3	2579	0	1304	23	0
7	M3	2579	0	1304	9	0
8	LA	1305	0	1372	19	0
9	LB	1784	0	1862	25	0
9	MB	1784	0	1862	9	0
10	LC	1804	0	1877	25	0
10	MC	1804	0	1877	12	0
11	LD	1508	0	1572	21	0
11	MD	1518	0	1587	14	0
12	LE	1764	0	1804	24	0
12	ME	1743	0	1785	14	0
13	LF	1350	0	1381	24	0
13	MF	1353	0	1383	23	0
14	LG	1543	0	1608	22	0
14	MG	1543	0	1608	14	0
15	LH	1053	0	1149	18	0
15	MH	1053	0	1149	7	0
16	LI	1720	0	1779	24	0
16	MI	1720	0	1779	18	0
17	LJ	1555	0	1659	16	0
17	MJ	1555	0	1659	15	0
18	LK	1416	0	1433	9	0
18	MK	1222	0	1231	7	0
19	LL	1441	0	1543	19	0
19	ML	1441	0	1543	13	0
20	LM	1515	0	1606	17	0
20	MM	1423	0	1510	14	0
21	LN	1437	0	1475	21	0
21	MN	1445	0	1487	9	0
22	LO	1276	0	1323	25	0
22	MO	1276	0	1323	9	0
23	La	1003	0	1048	6	0
23	Ma	963	0	1015	17	0
24	Lb	694	0	735	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	Mb	694	0	734	1	0
25	Lc	824	0	888	14	0
25	Mc	819	0	886	5	0
26	Ld	229	0	273	2	0
26	Md	233	0	282	6	0
27	Le	417	0	455	2	0
27	Me	417	0	455	4	0
28	Lf	436	0	475	7	0
28	Mf	436	0	475	8	0
29	Lg	612	0	682	6	0
29	Mg	612	0	682	8	0
30	Lh	670	0	673	6	0
30	Mh	665	0	668	8	0
31	Li	766	0	844	11	0
31	Mi	771	0	849	9	0
32	Lj	969	0	1078	10	0
32	Mj	969	0	1078	6	0
33	Lk	836	0	897	8	0
33	Mk	861	0	918	11	0
34	Ll	850	0	880	12	0
34	Ml	850	0	880	8	0
35	Lm	1017	0	1081	11	0
35	Mm	1020	0	1090	7	0
36	Ln	876	0	912	9	0
36	Mn	883	0	918	8	0
37	Lo	737	0	792	8	0
37	Mo	742	0	797	11	0
38	Lp	462	0	491	3	0
38	Mp	462	0	491	6	0
39	Lq	1173	0	1215	27	0
39	Mq	1173	0	1215	16	0
40	Lr	1092	0	1155	14	0
40	Mr	1092	0	1155	9	0
41	Ls	984	0	1075	10	0
41	Ms	993	0	1081	13	0
42	Lt	964	0	1025	15	0
42	Mt	959	0	1023	5	0
43	Lu	836	0	706	8	0
43	Mu	521	0	551	0	0
44	Lv	796	0	812	10	0
44	Mv	770	0	780	4	0
45	Lw	1899	0	1957	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	Mw	1914	0	1981	8	0
46	Lx	3075	0	3142	35	0
46	Mx	3075	0	3142	25	0
47	Ly	2748	0	2859	27	0
47	My	2748	0	2859	22	0
48	Lz	2351	0	2294	35	0
48	Mz	2375	0	2325	15	0
49	R1	37455	0	18845	350	0
49	S1	37739	0	18987	321	0
50	RA	769	0	818	12	0
50	SA	769	0	818	11	0
51	RB	610	0	631	8	0
51	SB	610	0	633	8	0
52	SC	486	0	522	6	0
53	RD	442	0	432	6	0
53	SD	442	0	428	13	0
54	RE	385	0	431	8	0
54	SE	472	0	521	9	0
55	RF	547	0	542	7	0
55	SF	556	0	546	12	0
56	RG	2403	0	2350	41	0
56	SG	2383	0	2332	52	0
57	Ra	1583	0	1578	33	0
57	Sa	1603	0	1610	33	0
58	Rb	1722	0	1793	25	0
58	Sb	1798	0	1890	27	0
59	Rc	1635	0	1723	28	0
59	Sc	1626	0	1715	21	0
60	Rd	1734	0	1817	25	0
60	Sd	1729	0	1812	23	0
61	Re	2068	0	2154	32	0
61	Se	2056	0	2140	26	0
62	Rf	1609	0	1675	21	0
62	Sf	1605	0	1668	19	0
63	Rg	1755	0	1846	42	0
63	Sg	1815	0	1894	36	0
64	Rh	1486	0	1576	27	0
64	Sh	1473	0	1555	25	0
65	Ri	1489	0	1525	29	0
65	Si	1476	0	1501	27	0
66	Rj	1494	0	1573	31	0
66	Sj	1479	0	1556	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
67	Rk	741	0	691	16	0
67	Sk	752	0	719	17	0
68	Rl	1168	0	1233	7	0
68	Sl	1159	0	1225	11	0
69	Rm	890	0	887	23	0
69	Sm	875	0	878	17	0
70	Rn	1192	0	1255	18	0
70	Sn	1192	0	1255	14	0
71	So	926	0	950	23	0
72	Rp	939	0	968	13	0
72	Sp	916	0	941	17	0
73	Rq	1105	0	1166	20	0
73	Sq	1105	0	1166	18	0
74	Sr	948	0	990	14	0
75	Rs	1192	0	1222	28	0
75	Ss	1192	0	1222	26	0
76	Rt	1112	0	1124	17	0
76	St	1112	0	1124	28	0
77	Ru	805	0	874	14	0
77	Su	797	0	863	16	0
78	Rv	684	0	672	17	0
78	Sv	673	0	662	11	0
79	Rw	1021	0	1060	12	0
79	Sw	1021	0	1060	24	0
80	Rx	1121	0	1196	13	0
80	Sx	1121	0	1196	19	0
81	Ry	1073	0	1132	16	0
81	Sy	1073	0	1132	16	0
82	Rz	558	0	598	7	0
82	Sz	651	0	682	14	0
83	RC	497	0	535	6	0
84	Ro	949	0	985	14	0
85	Rr	1000	0	1063	17	0
86	MA	1230	0	1320	13	0
87	M1	68285	0	34372	359	0
88	DQ	1644	0	837	15	0
89	MQ	1531	0	1571	27	0
90	MP	1196	0	1257	20	0
91	DP	1638	0	836	12	0
92	CP	1	0	0	0	0
92	M1	194	0	0	0	0
92	M2	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	M3	4	0	0	0	0
92	ME	1	0	0	0	0
92	MI	2	0	0	0	0
92	MK	1	0	0	0	0
92	MM	1	0	0	0	0
92	Ma	1	0	0	0	0
92	Mx	1	0	0	0	0
92	S1	84	0	0	0	0
92	Sf	1	0	0	0	0
92	Sx	1	0	0	0	0
93	Lb	1	0	0	0	0
93	Lc	1	0	0	0	0
93	Le	1	0	0	0	0
93	Lh	1	0	0	0	0
93	Lk	1	0	0	0	0
93	Mb	1	0	0	0	0
93	Mc	1	0	0	0	0
93	Me	1	0	0	0	0
93	Mh	1	0	0	0	0
93	Mk	1	0	0	0	0
93	RB	1	0	0	0	0
93	SD	1	0	0	0	0
93	SF	1	0	0	0	0
94	M1	11	0	0	0	0
94	ME	1	0	0	0	0
94	Mc	1	0	0	0	0
94	Mk	1	0	0	0	0
94	Mm	1	0	0	0	0
94	Mw	1	0	0	0	0
95	M1	30	0	57	4	0
All	All	406583	0	300359	3269	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 3269 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L1:1018:G:H1	5:L1:1034:U:H3	1.09	0.95
87:M1:2448:G:H1	87:M1:2499:U:H3	1.15	0.95
49:S1:895:G:H1	49:S1:917:U:H3	1.08	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:R1:142:G:N1	49:R1:173:A:C2	2.36	0.91
49:R1:1588:G:H1	49:R1:1608:U:H3	0.91	0.89

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	12	39
14	MG	191/199 (96%)	173 (91%)	17 (9%)	1 (0%)	24	54
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	MI	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
17	LJ	195/199 (98%)	188 (96%)	5 (3%)	2 (1%)	12	39
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
20	LM	186/189 (98%)	181 (97%)	4 (2%)	1 (0%)	24	54
20	MM	174/189 (92%)	169 (97%)	4 (2%)	1 (1%)	21	51
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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	41
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%)	18	48
39	Mq	146/149 (98%)	133 (91%)	12 (8%)	1 (1%)	18	48
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	44
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%)	24	54
46	Mx	384/387 (99%)	365 (95%)	19 (5%)	0	100	100
47	Ly	359/362 (99%)	331 (92%)	26 (7%)	2 (1%)	21	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	My	359/362 (99%)	340 (95%)	19 (5%)	0	100	100
48	Lz	292/297 (98%)	277 (95%)	14 (5%)	1 (0%)	36	65
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	21
51	RB	79/82 (96%)	69 (87%)	10 (13%)	0	100	100
51	SB	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
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%)	24	54
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	41
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	59
61	Se	256/261 (98%)	230 (90%)	25 (10%)	1 (0%)	30	59
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	41
64	Rh	183/190 (96%)	169 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	11	36
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
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	26
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	44
72	Rp	117/142 (82%)	102 (87%)	14 (12%)	1 (1%)	14	41
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%)	18	48
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	30
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%)	12	39
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%)	18	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	Ry	132/135 (98%)	122 (92%)	9 (7%)	1 (1%)	16	44
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
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%)	44	72

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 ⓘ

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%)	12 (92%)	1 (8%)	12	35
3	CN	112/123 (91%)	111 (99%)	1 (1%)	70	90
8	LA	138/155 (89%)	133 (96%)	5 (4%)	31	65
9	LB	186/205 (91%)	179 (96%)	7 (4%)	29	64
9	MB	186/205 (91%)	184 (99%)	2 (1%)	65	88
10	LC	187/208 (90%)	184 (98%)	3 (2%)	55	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	MC	187/208 (90%)	180 (96%)	7 (4%)	30	64
11	LD	168/171 (98%)	164 (98%)	4 (2%)	43	75
11	MD	171/171 (100%)	164 (96%)	7 (4%)	27	61
12	LE	185/187 (99%)	174 (94%)	11 (6%)	18	48
12	ME	184/187 (98%)	180 (98%)	4 (2%)	45	77
13	LF	146/150 (97%)	137 (94%)	9 (6%)	16	46
13	MF	147/150 (98%)	141 (96%)	6 (4%)	27	61
14	LG	154/159 (97%)	147 (96%)	7 (4%)	24	58
14	MG	154/159 (97%)	152 (99%)	2 (1%)	61	86
15	LH	107/109 (98%)	105 (98%)	2 (2%)	50	79
15	MH	107/109 (98%)	104 (97%)	3 (3%)	38	72
16	LI	175/176 (99%)	169 (97%)	6 (3%)	32	66
16	MI	175/176 (99%)	170 (97%)	5 (3%)	37	71
17	LJ	160/162 (99%)	157 (98%)	3 (2%)	50	79
17	MJ	160/162 (99%)	157 (98%)	3 (2%)	50	79
18	LK	138/146 (94%)	133 (96%)	5 (4%)	31	65
18	MK	125/146 (86%)	118 (94%)	7 (6%)	19	50
19	LL	150/151 (99%)	147 (98%)	3 (2%)	48	78
19	ML	150/151 (99%)	148 (99%)	2 (1%)	61	86
20	LM	152/154 (99%)	149 (98%)	3 (2%)	48	78
20	MM	143/154 (93%)	141 (99%)	2 (1%)	59	85
21	LN	155/156 (99%)	146 (94%)	9 (6%)	18	49
21	MN	156/156 (100%)	151 (97%)	5 (3%)	34	68
22	LO	136/137 (99%)	129 (95%)	7 (5%)	21	53
22	MO	136/137 (99%)	129 (95%)	7 (5%)	21	53
23	La	104/105 (99%)	99 (95%)	5 (5%)	23	55
23	Ma	101/105 (96%)	96 (95%)	5 (5%)	22	53
24	Lb	71/72 (99%)	69 (97%)	2 (3%)	38	72
24	Mb	71/72 (99%)	68 (96%)	3 (4%)	26	60
25	Lc	87/91 (96%)	80 (92%)	7 (8%)	11	34
25	Mc	87/91 (96%)	84 (97%)	3 (3%)	32	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	Ld	22/23 (96%)	20 (91%)	2 (9%)	9	28
26	Md	23/23 (100%)	22 (96%)	1 (4%)	26	60
27	Le	47/116 (40%)	46 (98%)	1 (2%)	47	77
27	Me	47/116 (40%)	47 (100%)	0	100	100
28	Lf	45/46 (98%)	44 (98%)	1 (2%)	45	77
28	Mf	45/46 (98%)	45 (100%)	0	100	100
29	Lg	68/69 (99%)	64 (94%)	4 (6%)	18	48
29	Mg	68/69 (99%)	64 (94%)	4 (6%)	18	48
30	Lh	69/71 (97%)	67 (97%)	2 (3%)	37	71
30	Mh	69/71 (97%)	66 (96%)	3 (4%)	26	60
31	Li	80/82 (98%)	77 (96%)	3 (4%)	29	64
31	Mi	81/82 (99%)	79 (98%)	2 (2%)	42	74
32	Lj	104/105 (99%)	100 (96%)	4 (4%)	29	64
32	Mj	104/105 (99%)	103 (99%)	1 (1%)	68	89
33	Lk	91/103 (88%)	88 (97%)	3 (3%)	33	67
33	Mk	94/103 (91%)	92 (98%)	2 (2%)	47	77
34	Ll	90/91 (99%)	87 (97%)	3 (3%)	33	67
34	Ml	90/91 (99%)	88 (98%)	2 (2%)	45	77
35	Lm	108/111 (97%)	105 (97%)	3 (3%)	38	72
35	Mm	109/111 (98%)	106 (97%)	3 (3%)	38	72
36	Ln	92/97 (95%)	86 (94%)	6 (6%)	15	44
36	Mn	94/97 (97%)	92 (98%)	2 (2%)	47	77
37	Lo	81/88 (92%)	75 (93%)	6 (7%)	13	38
37	Mo	81/88 (92%)	77 (95%)	4 (5%)	22	54
38	Lp	46/47 (98%)	43 (94%)	3 (6%)	15	44
38	Mp	46/47 (98%)	46 (100%)	0	100	100
39	Lq	118/119 (99%)	113 (96%)	5 (4%)	26	60
39	Mq	118/119 (99%)	109 (92%)	9 (8%)	12	36
40	Lr	115/116 (99%)	108 (94%)	7 (6%)	17	46
40	Mr	115/116 (99%)	112 (97%)	3 (3%)	40	73
41	Ls	108/110 (98%)	101 (94%)	7 (6%)	15	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	Ms	109/110 (99%)	108 (99%)	1 (1%)	70	90
42	Lt	104/118 (88%)	101 (97%)	3 (3%)	37	71
42	Mt	104/118 (88%)	101 (97%)	3 (3%)	37	71
43	Lu	56/129 (43%)	56 (100%)	0	100	100
43	Mu	55/129 (43%)	55 (100%)	0	100	100
44	Lv	87/107 (81%)	85 (98%)	2 (2%)	44	76
44	Mv	84/107 (78%)	81 (96%)	3 (4%)	31	65
45	Lw	190/196 (97%)	183 (96%)	7 (4%)	30	64
45	Mw	193/196 (98%)	187 (97%)	6 (3%)	35	69
46	Lx	319/323 (99%)	307 (96%)	12 (4%)	29	64
46	Mx	320/323 (99%)	315 (98%)	5 (2%)	55	83
47	Ly	288/289 (100%)	282 (98%)	6 (2%)	47	77
47	My	288/289 (100%)	280 (97%)	8 (3%)	38	72
48	Lz	241/245 (98%)	238 (99%)	3 (1%)	63	86
48	Mz	244/245 (100%)	241 (99%)	3 (1%)	63	86
50	RA	83/101 (82%)	78 (94%)	5 (6%)	17	47
50	SA	83/101 (82%)	81 (98%)	2 (2%)	43	75
51	RB	70/71 (99%)	68 (97%)	2 (3%)	37	71
51	SB	70/71 (99%)	67 (96%)	3 (4%)	26	60
52	SC	55/60 (92%)	54 (98%)	1 (2%)	51	80
53	RD	47/49 (96%)	46 (98%)	1 (2%)	47	77
53	SD	47/49 (96%)	46 (98%)	1 (2%)	47	77
54	RE	41/54 (76%)	41 (100%)	0	100	100
54	SE	50/54 (93%)	49 (98%)	1 (2%)	48	78
55	RF	55/135 (41%)	52 (94%)	3 (6%)	19	50
55	SF	56/135 (42%)	52 (93%)	4 (7%)	13	40
56	RG	255/262 (97%)	249 (98%)	6 (2%)	43	75
56	SG	250/262 (95%)	247 (99%)	3 (1%)	63	86
57	Ra	165/210 (79%)	161 (98%)	4 (2%)	43	75
57	Sa	170/210 (81%)	166 (98%)	4 (2%)	43	75
58	Rb	192/224 (86%)	186 (97%)	6 (3%)	35	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	Sb	200/224 (89%)	189 (94%)	11 (6%)	19	50
59	Rc	176/205 (86%)	167 (95%)	9 (5%)	21	53
59	Sc	175/205 (85%)	171 (98%)	4 (2%)	44	76
60	Rd	182/195 (93%)	175 (96%)	7 (4%)	29	64
60	Sd	182/195 (93%)	177 (97%)	5 (3%)	39	73
61	Re	221/222 (100%)	216 (98%)	5 (2%)	44	76
61	Se	220/222 (99%)	213 (97%)	7 (3%)	34	68
62	Rf	173/191 (91%)	168 (97%)	5 (3%)	37	71
62	Sf	172/191 (90%)	167 (97%)	5 (3%)	37	71
63	Rg	187/201 (93%)	184 (98%)	3 (2%)	55	83
63	Sg	189/201 (94%)	180 (95%)	9 (5%)	23	55
64	Rh	165/170 (97%)	160 (97%)	5 (3%)	36	70
64	Sh	163/170 (96%)	152 (93%)	11 (7%)	15	43
65	Ri	150/161 (93%)	149 (99%)	1 (1%)	76	92
65	Si	148/161 (92%)	145 (98%)	3 (2%)	48	78
66	Rj	158/166 (95%)	154 (98%)	4 (2%)	42	74
66	Sj	156/166 (94%)	151 (97%)	5 (3%)	34	68
67	Rk	73/98 (74%)	72 (99%)	1 (1%)	59	85
67	Sk	77/98 (79%)	71 (92%)	6 (8%)	11	35
68	Rl	129/137 (94%)	125 (97%)	4 (3%)	35	69
68	Sl	129/137 (94%)	124 (96%)	5 (4%)	28	63
69	Rm	88/119 (74%)	86 (98%)	2 (2%)	44	76
69	Sm	88/119 (74%)	83 (94%)	5 (6%)	18	49
70	Rn	127/128 (99%)	123 (97%)	4 (3%)	35	69
70	Sn	127/128 (99%)	117 (92%)	10 (8%)	11	34
71	So	91/105 (87%)	87 (96%)	4 (4%)	25	59
72	Rp	98/118 (83%)	95 (97%)	3 (3%)	35	69
72	Sp	95/118 (80%)	94 (99%)	1 (1%)	65	88
73	Rq	117/119 (98%)	116 (99%)	1 (1%)	70	90
73	Sq	117/119 (98%)	112 (96%)	5 (4%)	26	60
74	Sr	101/124 (82%)	99 (98%)	2 (2%)	48	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
75	Rs	128/129 (99%)	120 (94%)	8 (6%)	16	45
75	Ss	128/129 (99%)	121 (94%)	7 (6%)	19	50
76	Rt	115/116 (99%)	111 (96%)	4 (4%)	32	66
76	St	115/116 (99%)	110 (96%)	5 (4%)	26	60
77	Ru	94/114 (82%)	92 (98%)	2 (2%)	47	77
77	Su	93/114 (82%)	87 (94%)	6 (6%)	15	44
78	Rv	74/74 (100%)	71 (96%)	3 (4%)	27	61
78	Sv	71/74 (96%)	68 (96%)	3 (4%)	26	60
79	Rw	110/111 (99%)	107 (97%)	3 (3%)	39	73
79	Sw	110/111 (99%)	103 (94%)	7 (6%)	16	44
80	Rx	119/120 (99%)	115 (97%)	4 (3%)	32	66
80	Sx	119/120 (99%)	113 (95%)	6 (5%)	22	53
81	Ry	112/113 (99%)	109 (97%)	3 (3%)	39	73
81	Sy	112/113 (99%)	108 (96%)	4 (4%)	31	65
82	Rz	61/89 (68%)	58 (95%)	3 (5%)	22	54
82	Sz	67/89 (75%)	63 (94%)	4 (6%)	17	47
83	RC	56/60 (93%)	55 (98%)	1 (2%)	51	80
84	Ro	97/105 (92%)	92 (95%)	5 (5%)	21	52
85	Rr	113/124 (91%)	111 (98%)	2 (2%)	51	80
86	MA	133/153 (87%)	131 (98%)	2 (2%)	57	84
89	MQ	167/254 (66%)	162 (97%)	5 (3%)	36	70
90	MP	129/136 (95%)	126 (98%)	3 (2%)	44	76
All	All	18800/20698 (91%)	18181 (97%)	619 (3%)	34	67

5 of 619 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
84	Ro	99	GLN
13	MF	25	GLU
18	MK	42	THR
84	Ro	81	VAL
44	Mv	50	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
66	Rj	139	GLN
40	Mr	78	ASN
70	Rn	58	HIS
90	MP	105	GLN
13	MF	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CM	40/41 (97%)	17 (42%)	1 (2%)
4	CP	73/76 (96%)	10 (13%)	0
49	R1	1755/1800 (97%)	474 (27%)	26 (1%)
49	S1	1768/1800 (98%)	462 (26%)	37 (2%)
5	L1	3111/3396 (91%)	584 (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%)	507 (15%)	14 (0%)
88	DQ	76/77 (98%)	13 (17%)	0
91	DP	75/76 (98%)	26 (34%)	1 (1%)
All	All	10637/11220 (94%)	2167 (20%)	115 (1%)

5 of 2167 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 ⓘ

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	A2M	M1	2220	87	22,25,26	3.56	10 (45%)	30,36,39	3.86	13 (43%)
87	OMG	M1	2793	87	23,26,27	0.64	0	32,38,41	0.51	0
87	OMG	M1	2288	87	23,26,27	0.61	0	32,38,41	0.59	0
87	A2M	M1	1133	92,87	22,25,26	3.56	10 (45%)	30,36,39	3.77	14 (46%)
87	OMU	M1	2921	87	19,22,23	3.00	8 (42%)	25,31,34	1.86	5 (20%)
87	OMC	M1	663	87	19,22,23	0.67	0	25,31,34	0.94	1 (4%)
87	OMC	M1	2948	87	19,22,23	0.66	0	25,31,34	0.95	2 (8%)
87	OMU	M1	898	87	19,22,23	2.92	8 (42%)	25,31,34	1.80	5 (20%)
87	OMU	M1	2729	87	19,22,23	2.91	7 (36%)	25,31,34	1.93	5 (20%)
87	OMG	M1	2791	87	23,26,27	0.55	0	32,38,41	0.54	0
87	OMC	M1	650	92,87	19,22,23	0.73	1 (5%)	25,31,34	0.73	0
87	A2M	M1	876	87	22,25,26	3.52	10 (45%)	30,36,39	3.89	13 (43%)
87	OMG	M1	2619	87	23,26,27	0.57	0	32,38,41	0.50	0
87	OMC	M1	2959	87	19,22,23	0.66	0	25,31,34	0.83	1 (4%)
87	A2M	M1	2281	87	22,25,26	3.47	10 (45%)	30,36,39	3.82	14 (46%)
87	5MC	M1	2278	92,87	19,22,23	0.75	1 (5%)	26,32,35	1.05	2 (7%)
87	OMC	M1	2337	87	19,22,23	0.70	0	25,31,34	0.74	0
87	OMU	M1	2347	87	19,22,23	3.02	7 (36%)	25,31,34	1.90	5 (20%)
87	1MA	M1	2142	92,87	21,25,26	0.71	0	30,37,40	0.92	2 (6%)
87	OMG	M1	2815	87	23,26,27	0.59	0	32,38,41	0.54	0
87	UR3	M1	2634	87	19,22,23	3.04	8 (42%)	26,32,35	1.76	4 (15%)
87	OMG	M1	908	87	23,26,27	0.55	0	32,38,41	0.63	0
87	A2M	M1	2640	87	22,25,26	3.52	10 (45%)	30,36,39	3.84	14 (46%)
87	5MC	M1	2870	94,87	19,22,23	0.84	1 (5%)	26,32,35	0.78	0
87	A2M	M1	2256	87	22,25,26	3.55	10 (45%)	30,36,39	4.09	16 (53%)
87	A2M	M1	649	87	22,25,26	3.46	10 (45%)	30,36,39	3.89	15 (50%)
87	1MA	M1	645	92,87	21,25,26	0.66	0	30,37,40	0.77	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	A2M	M1	807	87	22,25,26	3.55	10 (45%)	30,36,39	4.03	13 (43%)
87	OMG	M1	1450	87	23,26,27	0.59	0	32,38,41	0.50	0
87	OMU	M1	1888	87	19,22,23	2.98	8 (42%)	25,31,34	1.91	5 (20%)
87	OMG	M1	805	87	23,26,27	0.60	0	32,38,41	0.67	1 (3%)
87	A2M	M1	1449	92,87	22,25,26	3.55	10 (45%)	30,36,39	3.86	13 (43%)
87	OMU	M1	2417	87	19,22,23	2.83	7 (36%)	25,31,34	1.90	5 (20%)
87	A2M	M1	2946	92,87	22,25,26	3.46	10 (45%)	30,36,39	3.77	14 (46%)
87	OMG	M1	867	94,87	23,26,27	0.62	0	32,38,41	0.58	0
87	OMU	M1	2724	87	19,22,23	2.93	8 (42%)	25,31,34	1.82	5 (20%)
87	A2M	M1	817	92,87	22,25,26	3.58	10 (45%)	30,36,39	3.89	13 (43%)
91	YYG	DP	37	91	38,42,43	0.67	0	45,62,65	1.31	7 (15%)
87	OMC	M1	1437	92,87	19,22,23	0.69	0	25,31,34	1.03	1 (4%)
87	OMG	M1	2922	91,87	23,26,27	0.57	0	32,38,41	0.46	0
87	OMC	M1	2197	94,87	19,22,23	0.72	1 (5%)	25,31,34	0.67	0
87	A2M	M1	2280	87	22,25,26	3.52	10 (45%)	30,36,39	3.81	13 (43%)
87	OMU	M1	2421	87	19,22,23	2.85	7 (36%)	25,31,34	1.96	5 (20%)

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	A2M	M1	2220	87	-	1/9/27/28	0/3/3/3
87	OMG	M1	2793	87	-	0/9/27/28	0/3/3/3
87	OMG	M1	2288	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	1133	92,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2921	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	663	87	-	0/9/27/28	0/2/2/2
87	OMC	M1	2948	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	898	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	2729	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	2791	87	-	0/9/27/28	0/3/3/3
87	OMC	M1	650	92,87	-	0/9/27/28	0/2/2/2
87	A2M	M1	876	87	-	0/9/27/28	0/3/3/3
87	OMG	M1	2619	87	-	3/9/27/28	0/3/3/3
87	OMC	M1	2959	87	-	0/9/27/28	0/2/2/2
87	A2M	M1	2281	87	-	2/9/27/28	0/3/3/3
87	5MC	M1	2278	92,87	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	OMC	M1	2337	87	-	0/9/27/28	0/2/2/2
87	OMU	M1	2347	87	-	1/9/27/28	0/2/2/2
87	1MA	M1	2142	92,87	-	0/7/25/26	0/3/3/3
87	OMG	M1	2815	87	-	0/9/27/28	0/3/3/3
87	UR3	M1	2634	87	-	0/7/25/26	0/2/2/2
87	OMG	M1	908	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	2640	87	-	0/9/27/28	0/3/3/3
87	5MC	M1	2870	94,87	-	3/7/25/26	0/2/2/2
87	A2M	M1	2256	87	-	2/9/27/28	0/3/3/3
87	A2M	M1	649	87	-	2/9/27/28	0/3/3/3
87	1MA	M1	645	92,87	-	0/7/25/26	0/3/3/3
87	A2M	M1	807	87	-	1/9/27/28	0/3/3/3
87	OMG	M1	1450	87	-	2/9/27/28	0/3/3/3
87	OMU	M1	1888	87	-	0/9/27/28	0/2/2/2
87	OMG	M1	805	87	-	0/9/27/28	0/3/3/3
87	A2M	M1	1449	92,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2417	87	-	1/9/27/28	0/2/2/2
87	A2M	M1	2946	92,87	-	1/9/27/28	0/3/3/3
87	OMG	M1	867	94,87	-	0/9/27/28	0/3/3/3
87	OMU	M1	2724	87	-	1/9/27/28	0/2/2/2
87	A2M	M1	817	92,87	-	2/9/27/28	0/3/3/3
91	YYG	DP	37	91	-	7/24/42/43	0/4/4/4
87	OMC	M1	1437	92,87	-	2/9/27/28	0/2/2/2
87	OMG	M1	2922	91,87	-	3/9/27/28	0/3/3/3
87	OMC	M1	2197	94,87	-	4/9/27/28	0/2/2/2
87	A2M	M1	2280	87	-	2/9/27/28	0/3/3/3
87	OMU	M1	2421	87	-	0/9/27/28	0/2/2/2

The worst 5 of 192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	M1	817	A2M	C2'-C1'	-9.31	1.30	1.53
87	M1	1449	A2M	C2'-C1'	-9.05	1.30	1.53
87	M1	2220	A2M	C2'-C1'	-9.05	1.30	1.53
87	M1	2256	A2M	C2'-C1'	-9.00	1.31	1.53
87	M1	2640	A2M	C2'-C1'	-8.99	1.31	1.53

The worst 5 of 227 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	M1	807	A2M	C1'-N9-C8	-9.94	105.03	127.09
87	M1	2256	A2M	C1'-N9-C8	-9.80	105.33	127.09
87	M1	1449	A2M	C1'-N9-C8	-9.67	105.63	127.09
87	M1	2640	A2M	C1'-N9-C8	-9.52	105.96	127.09
87	M1	876	A2M	C1'-N9-C8	-9.48	106.06	127.09

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.

15 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	M1	2220	A2M	1	0
87	M1	2793	OMG	2	0
87	M1	1133	A2M	1	0
87	M1	663	OMC	2	0
87	M1	2948	OMC	2	0
87	M1	898	OMU	1	0
87	M1	2619	OMG	1	0
87	M1	2281	A2M	1	0
87	M1	2815	OMG	1	0
87	M1	1450	OMG	1	0
87	M1	1449	A2M	2	0
87	M1	2417	OMU	1	0
87	M1	2946	A2M	1	0
87	M1	2724	OMU	1	0
87	M1	1437	OMC	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	3603	-	9,9,9	0.31	0	8,8,8	0.32	0
95	SPD	M1	3604	-	9,9,9	0.28	0	8,8,8	0.40	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	3603	-	-	3/7/7/7	-
95	SPD	M1	3604	-	-	3/7/7/7	-
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	N1-C2-C3-C4
95	M1	3603	SPD	C2-C3-C4-C5
95	M1	3604	SPD	C2-C3-C4-C5
95	M1	3603	SPD	C7-C8-C9-N10

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
95	M1	3603	SPD	3	0
95	M1	3602	SPD	1	0

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.

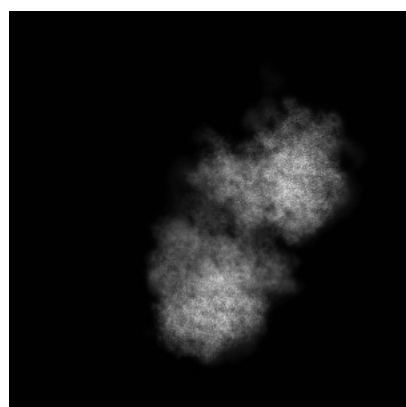
6 Map visualisation [i](#)

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.

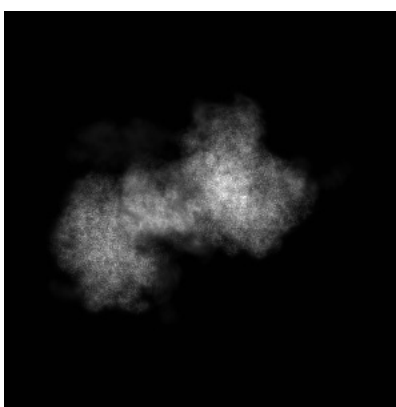
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

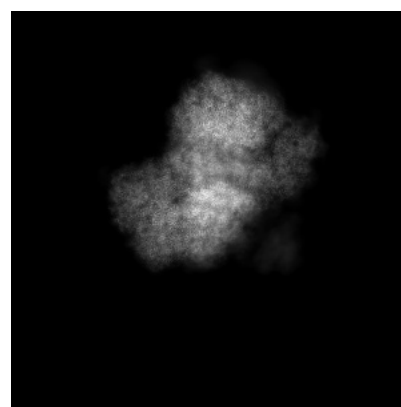
6.1.1 Primary map



X



Y

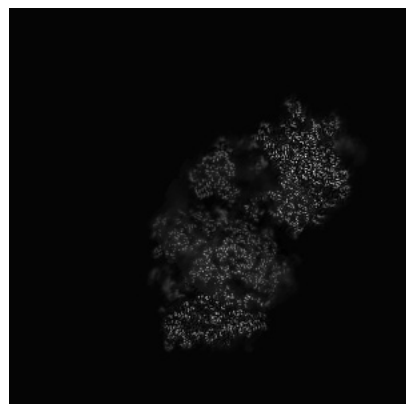


Z

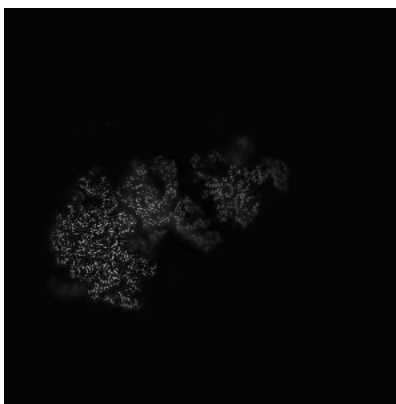
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

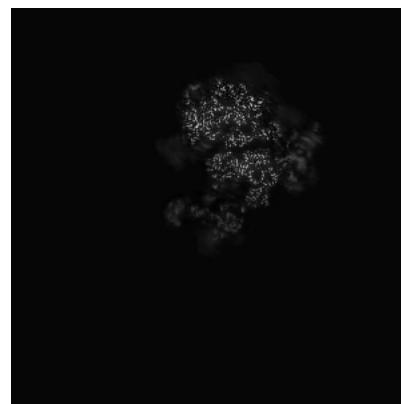
6.2.1 Primary map



X Index: 313



Y Index: 313

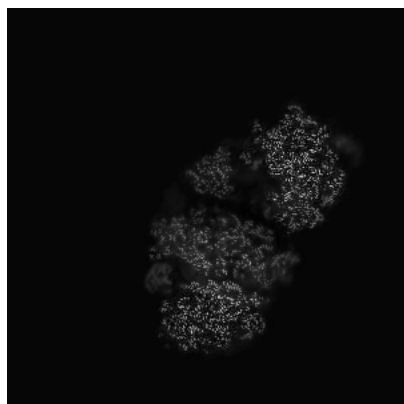


Z Index: 313

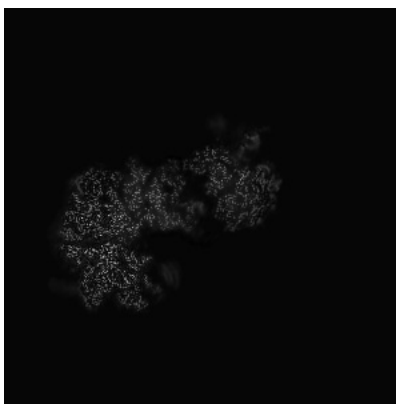
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

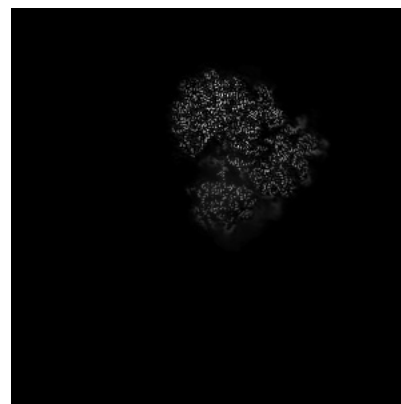
6.3.1 Primary map



X Index: 303



Y Index: 330

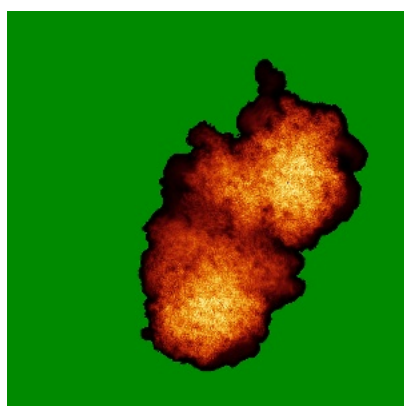


Z Index: 372

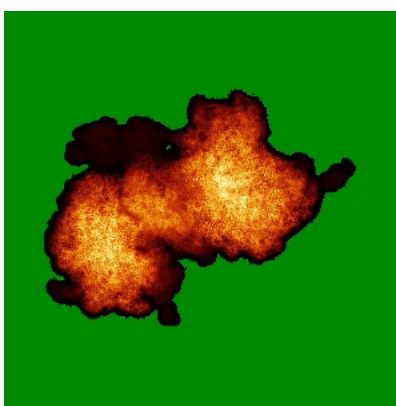
The images above show the largest variance slices of the map in three orthogonal directions.

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

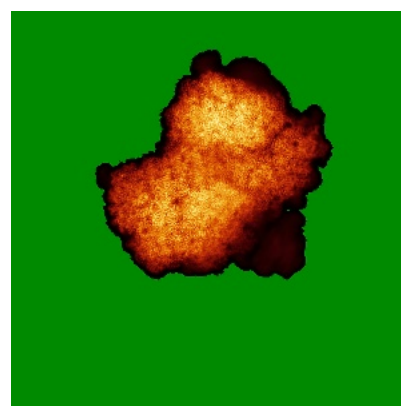
6.4.1 Primary map



X



Y

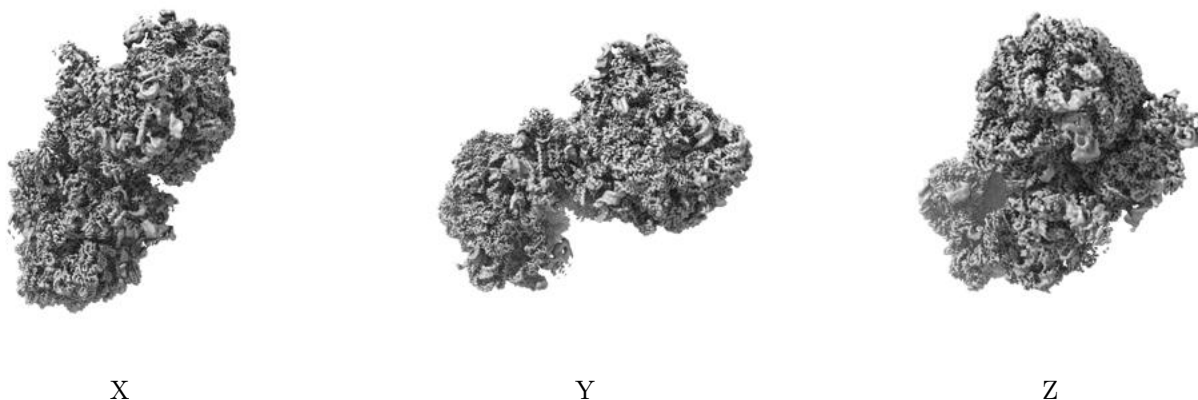


Z

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



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.

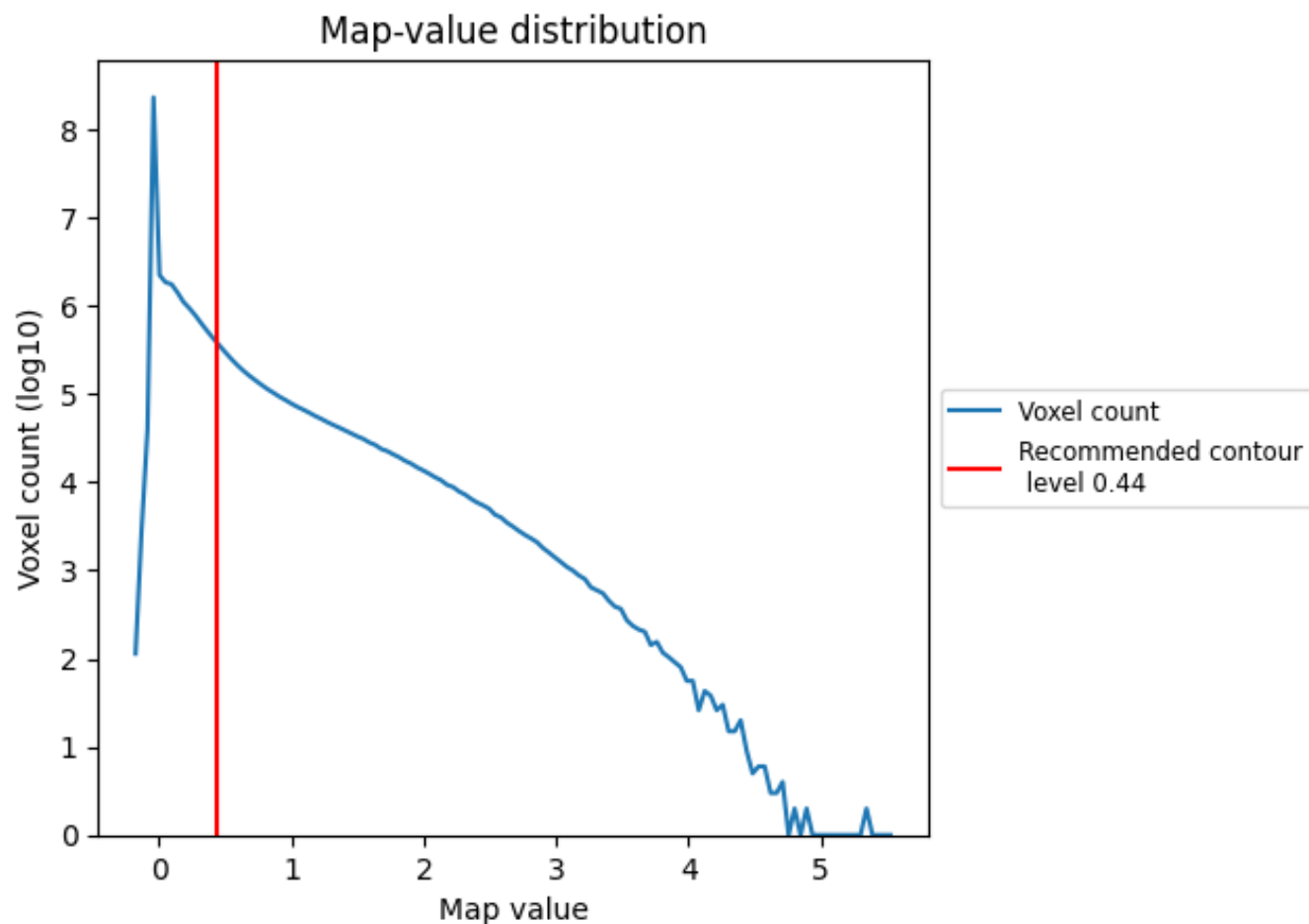
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

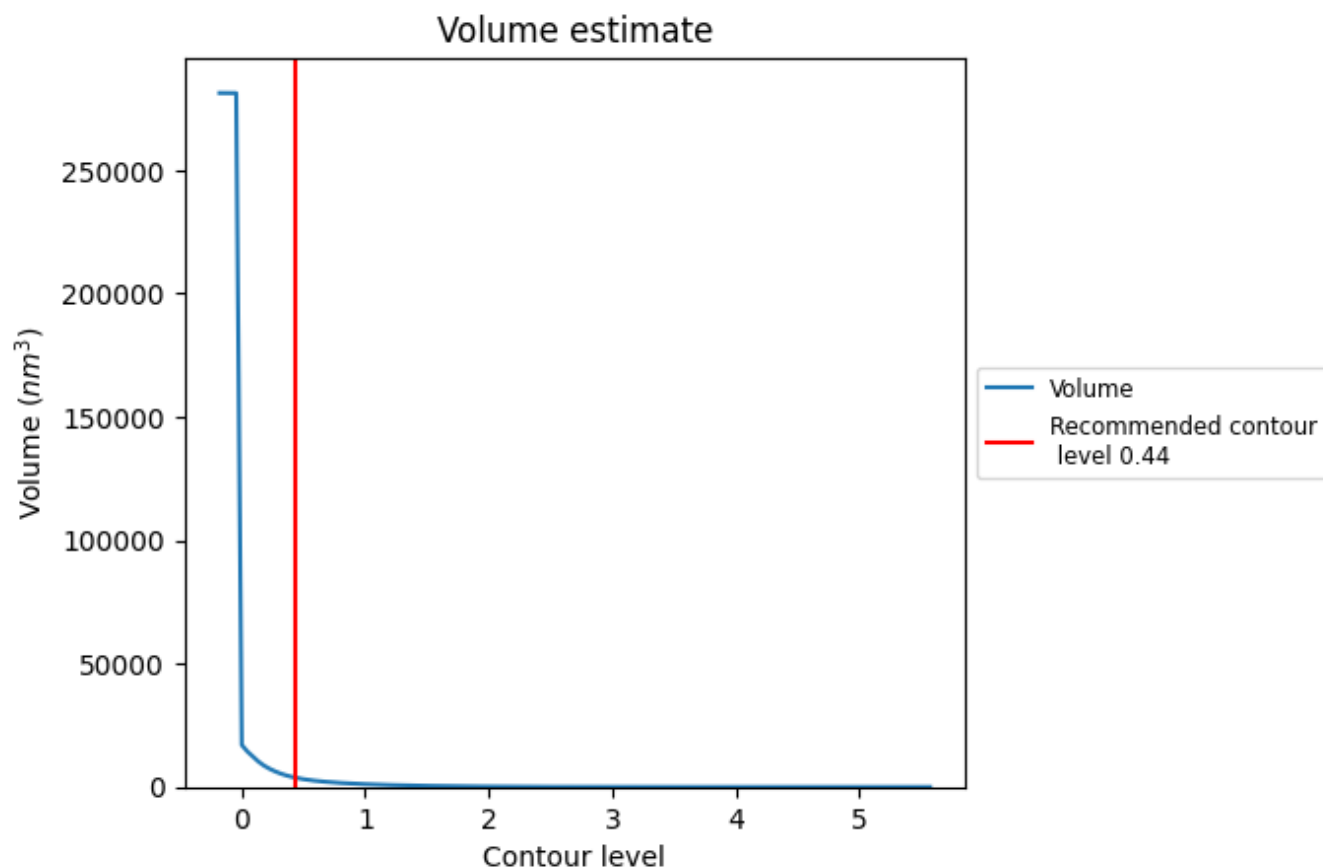
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

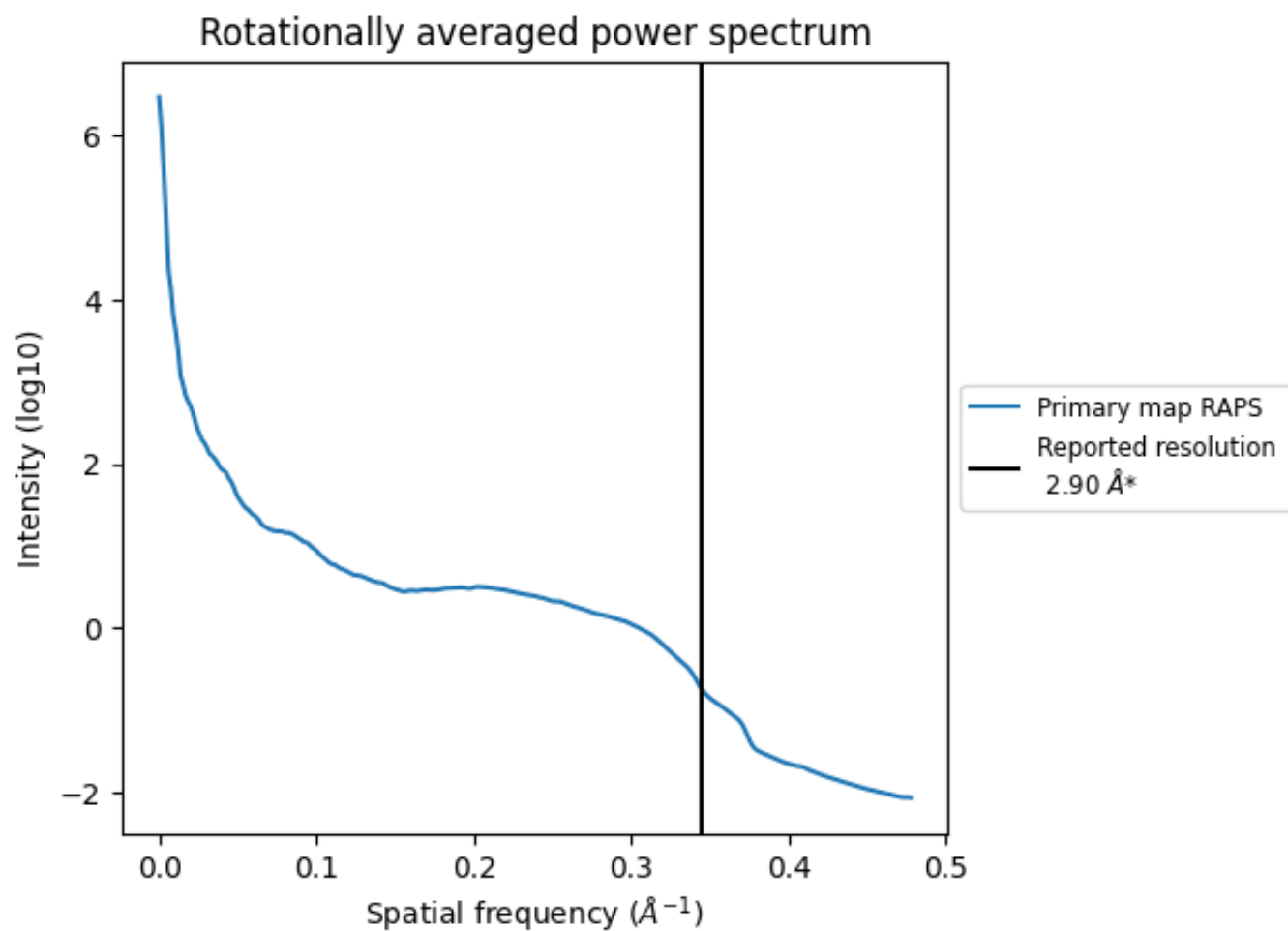
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

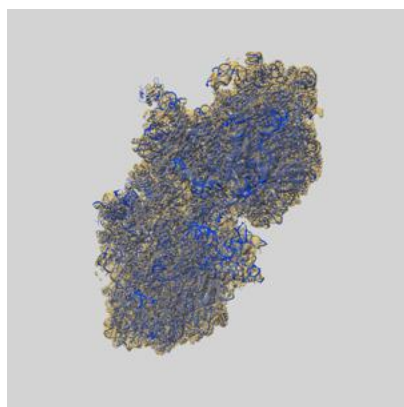
8 Fourier-Shell correlation

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

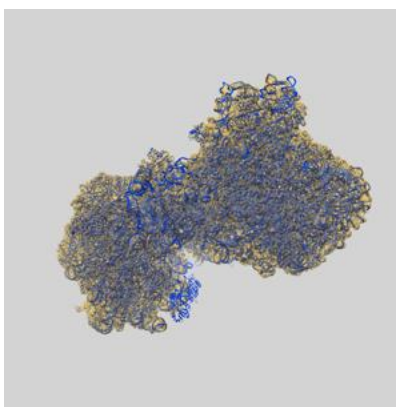
9 Map-model fit [i](#)

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

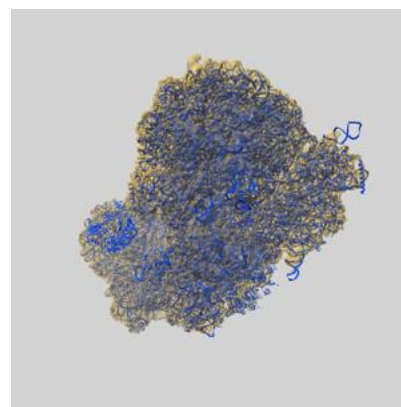
9.1 Map-model overlay [i](#)



X



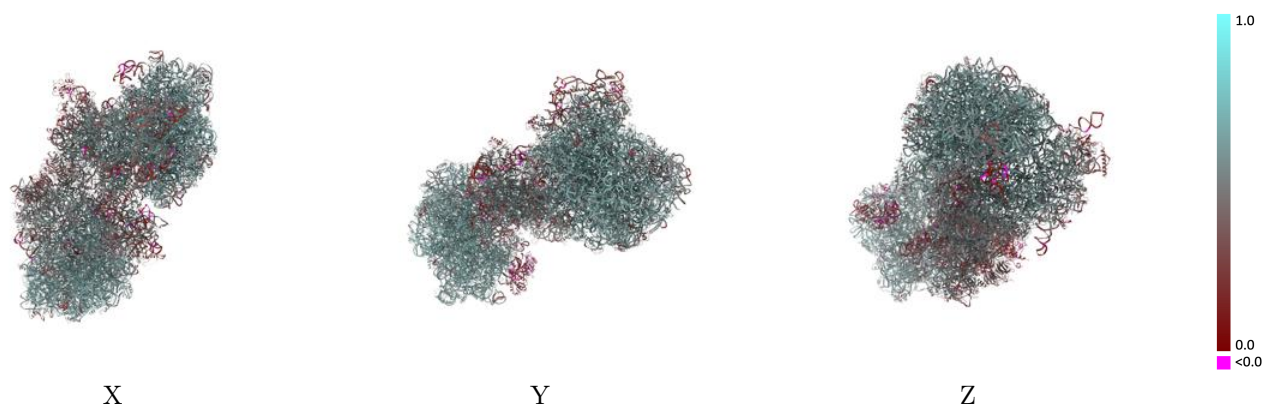
Y



Z

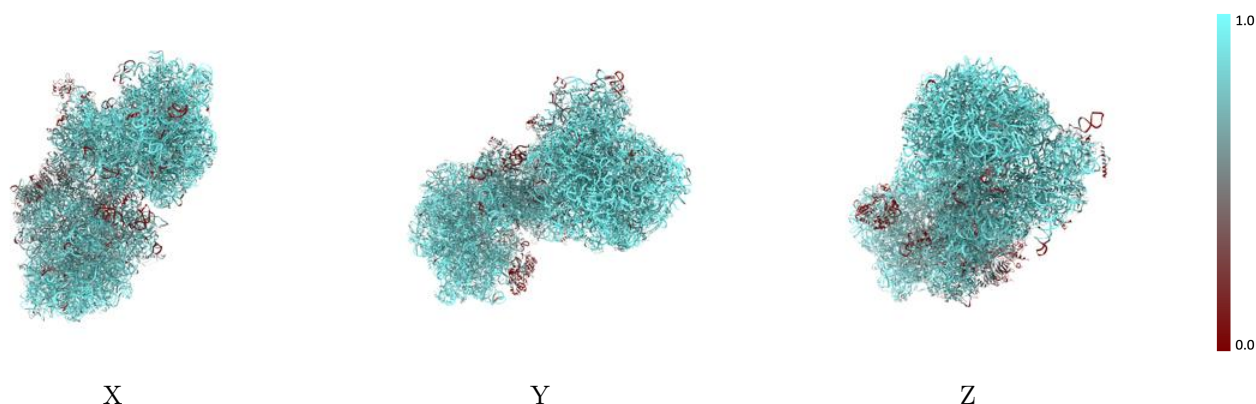
The images above show the 3D surface view of the map at the recommended contour level 0.44 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



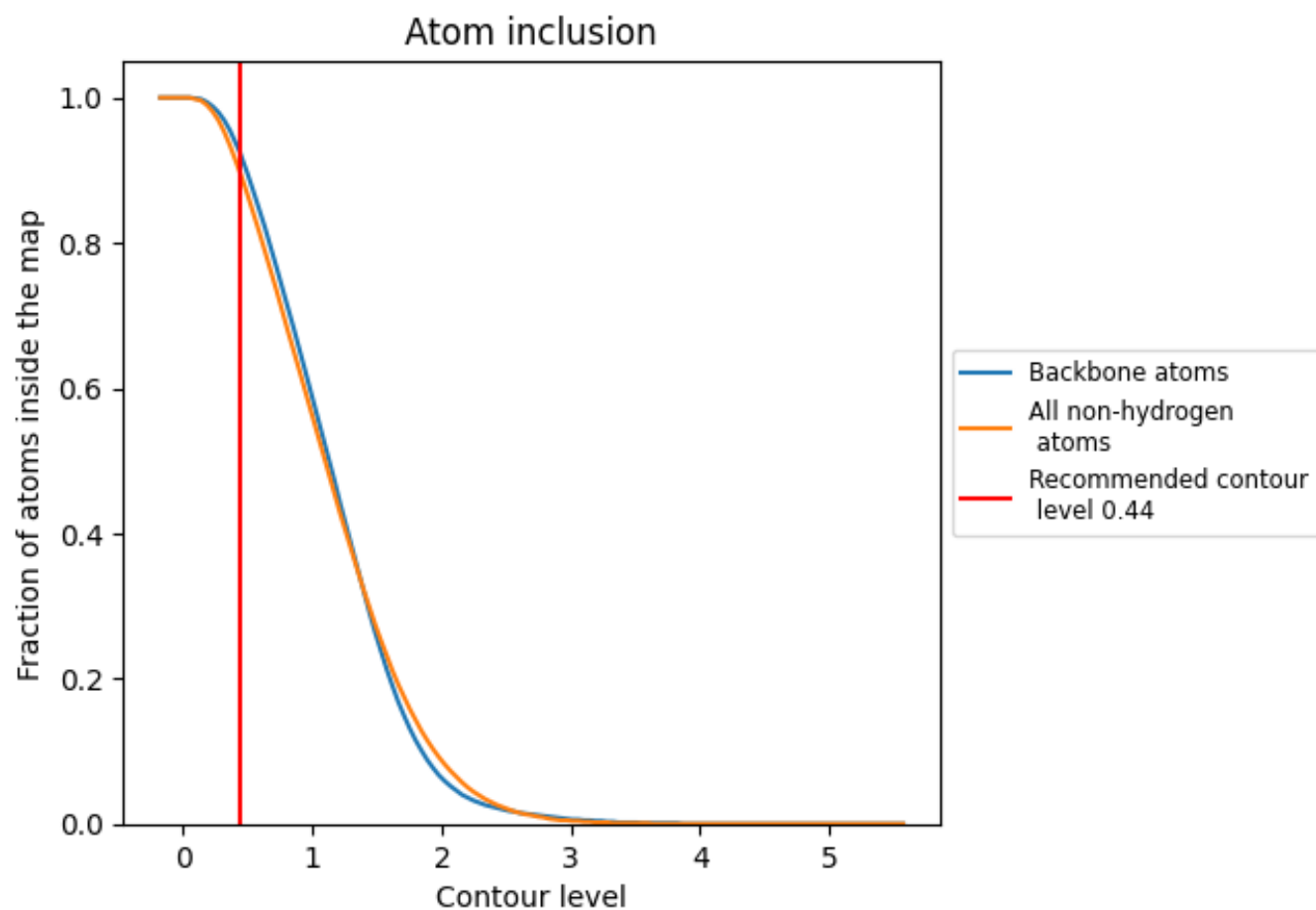
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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