



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:56 PM UTC

PDB ID : 7Q0R / pdb_00007q0r
EMDB ID : EMD-13750
Title : Structure of the Candida albicans 80S ribosome in complex with blasticidin s
Authors : Kolosova, O.; Zgadzay, Y.; Stetsenko, A.; Jenner, L.; Guskov, A.; Yusupova, G.; Yusupov, M.
Deposited on : 2021-10-16
Resolution : 2.67 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:

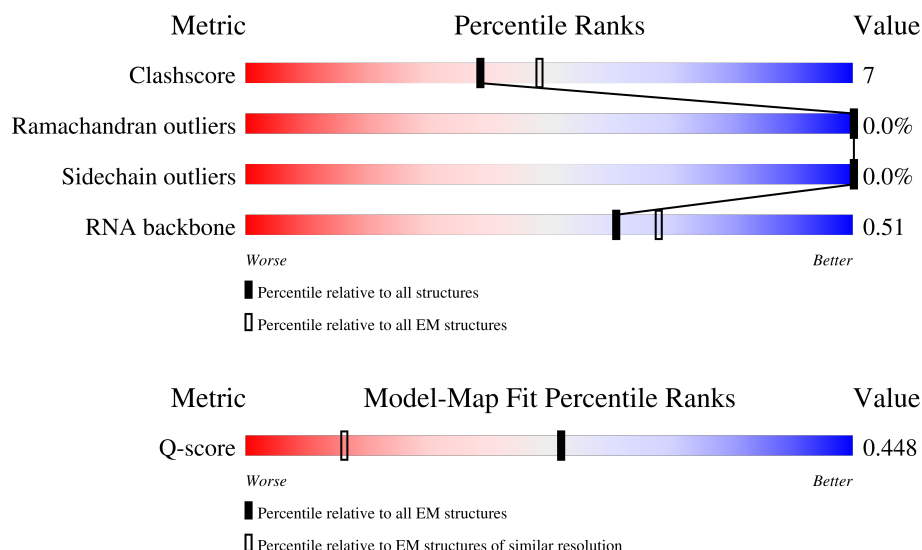
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.67 Å.

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



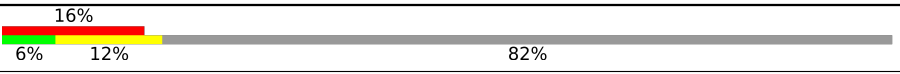
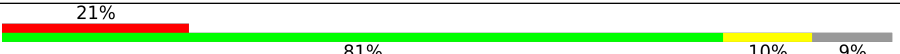
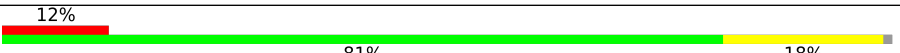
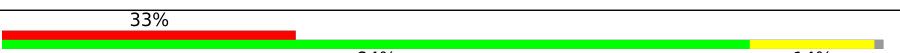
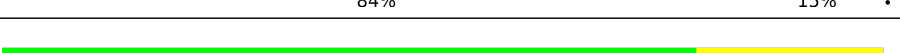
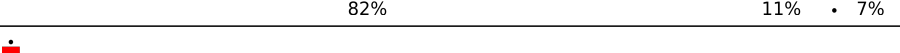
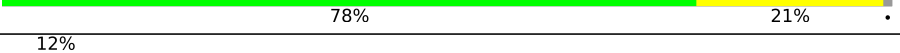
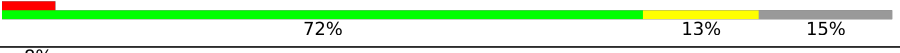
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9182 (2.17 - 3.17)

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

Mol	Chain	Length	Quality of chain
1	1	3359	
2	3	121	
3	4	158	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	10	77	
5	j	254	
6	k	389	
7	l	363	
8	m	298	
9	n	176	
10	o	241	
11	p	262	
12	q	191	
13	r	220	
14	s	174	
15	t	202	
16	u	131	
17	v	204	
18	w	200	
19	x	185	
20	y	186	
21	z	190	
22	0	172	
23	2	160	
24	5	124	
25	6	137	
26	7	155	
27	8	142	
28	9	127	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	AA	136	
30	AB	149	
31	AC	63	
32	AD	106	
33	AE	112	
34	AF	131	
35	AG	107	
36	AH	122	
37	AI	120	
38	AJ	99	
39	AK	90	
40	AL	78	
41	AM	51	
42	AN	52	
43	AO	25	
44	AP	106	
45	AQ	92	
46	i	267	
47	A	1787	
48	B	261	
49	C	256	
50	D	249	
51	E	251	
52	F	262	
53	G	225	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	H	236	
55	I	186	
56	J	206	
57	K	189	
58	L	118	
59	M	155	
60	N	143	
61	O	151	
62	P	132	
63	Q	142	
64	R	142	
65	S	137	
66	T	145	
67	U	145	
68	V	119	
69	W	87	
70	X	130	
71	Y	145	
72	Z	135	
73	a	105	
74	b	119	
75	c	82	
76	d	67	
77	e	56	
78	f	63	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	g	193	36% 20% 16% 64%
80	h	317	98% 74% 24%

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 199598 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3209	Total	C	N	O	P	0	0
			68595	30642	12317	22427	3209		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	121	Total	C	N	O	P	0	0
			2579	1153	463	842	121		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	158	Total	C	N	O	P	0	0
			3353	1500	585	1110	158		

- Molecule 4 is a RNA chain called Mixture of the endogenous E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	10	14	Total	C	N	O	P	0	0
			298	133	54	97	14		

- Molecule 5 is a protein called Ribosomal 60S subunit protein L2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	249	Total	C	N	O	S	1	0
			1894	1185	377	330	2		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	k	386	Total	C	N	O	S	1	0
			3084	1955	584	538	7		

- Molecule 7 is a protein called Ribosomal 60S subunit protein L4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	l	361	Total	C	N	O	S	0	0
			2751	1729	529	490	3		

- Molecule 8 is a protein called Ribosomal 60S subunit protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	m	292	Total	C	N	O	S	0	0
			2394	1526	416	450	2		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	n	155	Total	C	N	O	S	1	0
			1237	794	226	217			

- Molecule 10 is a protein called Ribosomal 60S subunit protein L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	o	234	Total	C	N	O	S	1	0
			1893	1213	348	331	1		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	p	238	Total	C	N	O	S	0	0
			1839	1175	327	334	3		

- Molecule 12 is a protein called Ribosomal 60S subunit protein L9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	q	190	Total	C	N	O	S	0	0
			1519	958	276	281	4		

- Molecule 13 is a protein called Ribosomal 60S subunit protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	r	208	Total	C	N	O	S	0	0
			1689	1069	322	291	7		

- Molecule 14 is a protein called Ribosomal 60S subunit protein L11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	s	172	Total	C	N	O	S	1	0
			1385	864	262	255	4		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	t	200	Total	C	N	O		0	0
			1610	1009	318	283			

- Molecule 16 is a protein called Ribosomal 60S subunit protein L14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	130	Total	C	N	O	S	0	0
			1029	660	193	175	1		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	203	Total	C	N	O	S	0	0
			1713	1075	356	280	2		

- Molecule 18 is a protein called Ribosomal 60S subunit protein L16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	199	Total	C	N	O	S	0	0
			1590	1025	294	269	2		

- Molecule 19 is a protein called Ribosomal 60S subunit protein L17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	172	Total	C	N	O		0	0
			1375	850	279	246			

- Molecule 20 is a protein called Ribosomal 60S subunit protein L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	y	185	Total	C	N	O		3	0
			1478	930	302	246			

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	z	179	Total	C	N	O	S	1	0
			1462	904	311	244	3		

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	171	Total	C	N	O	S	2	0
			1442	933	262	244	3		

- Molecule 23 is a protein called Ribosomal 60S subunit protein L21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	159	Total	C	N	O	S	2	0
			1276	807	244	223	2		

- Molecule 24 is a protein called Ribosomal 60S subunit protein L22B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	5	103	Total	C	N	O		2	0
			848	553	139	156			

- Molecule 25 is a protein called Ribosomal 60S subunit protein L23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	6	131	Total	C	N	O	S	1	0
			986	621	186	171	8		

- Molecule 26 is a protein called Ribosomal 60S subunit protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	7	63	Total	C	N	O	S	0	0
			524	334	103	86	1		

- Molecule 27 is a protein called Ribosomal 60S subunit protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	8	121	Total	C	N	O	S	0	0
			974	622	175	176	1		

- Molecule 28 is a protein called Ribosomal 60S subunit protein L26B.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	9	126	Total	C	N	O		
			989	618	190	181	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AA	135	Total	C	N	O	S		
			1087	705	197	183	2	0	0

- Molecule 30 is a protein called Ribosomal 60S subunit protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AB	148	Total	C	N	O	S		
			1170	741	231	197	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AC	63	Total	C	N	O	S		
			509	317	109	82	1	1	0

- Molecule 32 is a protein called Ribosomal 60S subunit protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AD	96	Total	C	N	O	S		
			729	469	121	137	2	0	0

- Molecule 33 is a protein called Ribosomal 60S subunit protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AE	109	Total	C	N	O	S		
			889	562	167	158	2	0	0

- Molecule 34 is a protein called Ribosomal 60S subunit protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AF	125	Total	C	N	O	S		
			1015	649	197	168	1	1	0

- Molecule 35 is a protein called Ribosomal 60S subunit protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AG	106	Total	C	N	O	S	3	0
			867	558	166	142	1		

- Molecule 36 is a protein called Ribosomal 60S subunit protein L34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AH	112	Total	C	N	O	S	4	0
			913	567	188	154	4		

- Molecule 37 is a protein called Ribosomal 60S subunit protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AI	119	Total	C	N	O	S	1	0
			990	629	195	166			

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	AJ	98	Total	C	N	O	S	1	0
			772	481	158	131	2		

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AK	86	Total	C	N	O	S	0	0
			677	413	148	110	6		

- Molecule 40 is a protein called Ribosomal 60S subunit protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AL	77	Total	C	N	O	S	1	0
			623	398	116	109			

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AM	50	Total	C	N	O	S	1	0
			446	280	100	66			

- Molecule 42 is a protein called Rpl40bp.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AN	52	Total	C	N	O	S	1	0
			427	265	89	67	6		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AO	24	Total	C	N	O	S	0	0
			227	138	61	27	1		

- Molecule 44 is a protein called Ribosomal 60S subunit protein L42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AP	103	Total	C	N	O	S	2	0
			843	533	168	137	5		

- Molecule 45 is a protein called Ribosomal 60S subunit protein L43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AQ	91	Total	C	N	O	S	0	0
			698	430	140	124	4		

- Molecule 46 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	i	113	Total	C	N	O		0	0
			853	512	155	186			

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A	1692	Total	C	N	O	P	0	0
			36083	16130	6412	11849	1692		

- Molecule 48 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B	208	Total	C	N	O	S	0	0
			1627	1041	284	297	5		

- Molecule 49 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C	214	Total	C	N	O	S	0	0
			1724	1094	313	313	4		

- Molecule 50 is a protein called Ribosomal 40S subunit protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	D	216	Total	C	N	O	S	0	0
			1620	1033	287	295	5		

- Molecule 51 is a protein called Ribosomal 40S subunit protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	E	223	Total	C	N	O	S	0	0
			1707	1087	311	305	4		

- Molecule 52 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F	260	Total	C	N	O	S	0	0
			2055	1306	386	358	5		

- Molecule 53 is a protein called Ribosomal 40S subunit protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	G	206	Total	C	N	O	S	0	0
			1614	1008	301	301	4		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	H	226	Total	C	N	O	S	0	0
			1820	1133	351	330	6		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	I	182	Total	C	N	O	0	0
			1466	939	264	263		

- Molecule 56 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	J	203	Total	C	N	O	S	0	0
			1579	973	322	283	1		

- Molecule 57 is a protein called Ribosomal 40S subunit protein S9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	K	178	Total	C	N	O	S	0	0
			1453	918	286	248	1		

- Molecule 58 is a protein called Ribosomal 40S subunit protein S10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	L	93	Total	C	N	O	S	0	0
			783	511	129	142	1		

- Molecule 59 is a protein called Ribosomal 40S subunit protein S11A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	M	141	Total	C	N	O	S	0	0
			1129	722	212	192	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	N	116	Total	C	N	O	S	0	0
			885	550	158	172	5		

- Molecule 61 is a protein called Ribosomal 40S subunit protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O	150	Total	C	N	O	S	0	0
			1187	757	219	210	1		

- Molecule 62 is a protein called Ribosomal 40S subunit protein S14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	P	127	Total	C	N	O	S	0	0
			942	579	186	174	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	119	IAS	ASP	conflict	UNP A0A1D8PDT3

- Molecule 63 is a protein called Ribosomal 40S subunit protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q	118	Total	C	N	O	S	0	0
			935	598	169	162	6		

- Molecule 64 is a protein called Ribosomal 40S subunit protein S16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	R	140	Total	C	N	O	S	0	0
			1091	700	198	192	1		

- Molecule 65 is a protein called Ribosomal 40S subunit protein S17B.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S	125	Total	C	N	O	S	0	0
			1002	631	184	186	1		

- Molecule 66 is a protein called Ribosomal 40S subunit protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	T	142	Total	C	N	O	S	0	0
			1169	733	228	205	3		

- Molecule 67 is a protein called Ribosomal 40S subunit protein S19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	U	141	Total	C	N	O	S	0	0
			1100	689	210	200	1		

- Molecule 68 is a protein called Ribosomal 40S subunit protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	V	100	Total	C	N	O	S	0	0
			790	499	146	143	2		

- Molecule 69 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	W	87	Total	C	N	O	S	0	0
			676	415	126	133	2		

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	X	129	Total	C	N	O	S	0	0
			1032	655	191	183	3		

- Molecule 71 is a protein called Ribosomal 40S subunit protein S23B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Y	143	Total	C	N	O	S	0	0
			1110	701	219	188	2		

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Z	132	Total	C	N	O		0	0
			1072	670	216	186			

- Molecule 73 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	a	72	Total	C	N	O		0	0
			578	369	103	106			

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	b	100	Total	C	N	O	S	0	0
			799	494	169	130	6		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	c	81	Total	C	N	O	S	0	0
			614	383	110	114	7		

- Molecule 76 is a protein called Ribosomal 40S subunit protein S28B.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	d	62	Total	C	N	O	S	0	0
			487	299	98	88	2		

- Molecule 77 is a protein called Ribosomal 40S subunit protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	e	55	Total	C	N	O	S	0	0
			454	281	94	75	4		

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	f	56	Total	C	N	O	S	0	0
			444	278	89	75	2		

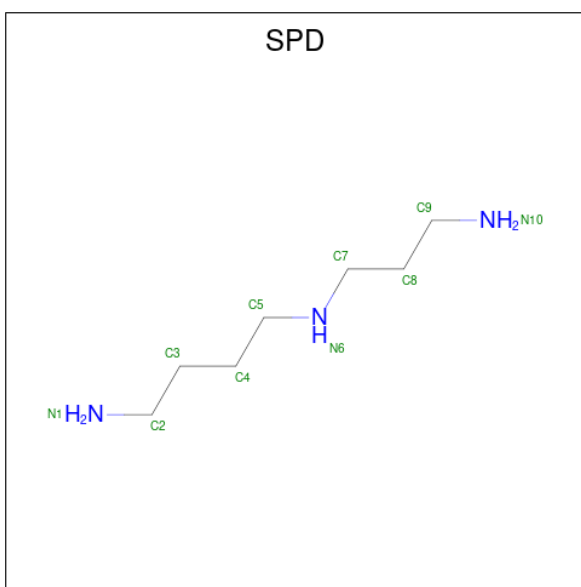
- Molecule 79 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	g	70	Total	C	N	O	S	0	0
			574	362	113	93	6		

- Molecule 80 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

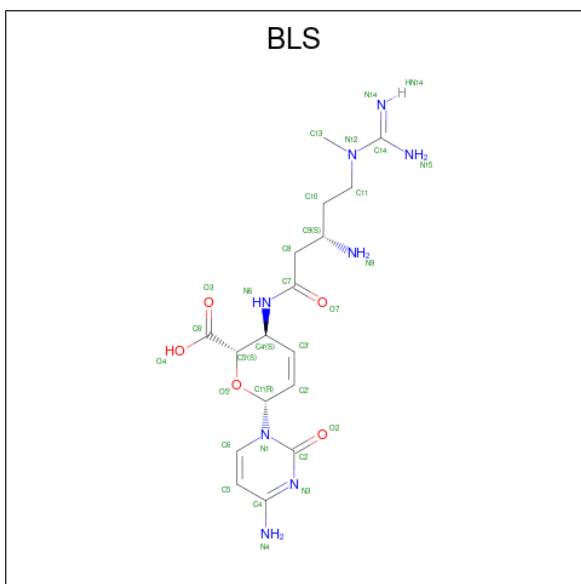
Mol	Chain	Residues	Atoms					AltConf	Trace
80	h	311	Total	C	N	O	S	0	0
			2398	1519	412	462	5		

- Molecule 81 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
81	1	1	Total	C	N	0
			10	7	3	
81	1	1	Total	C	N	0
			10	7	3	

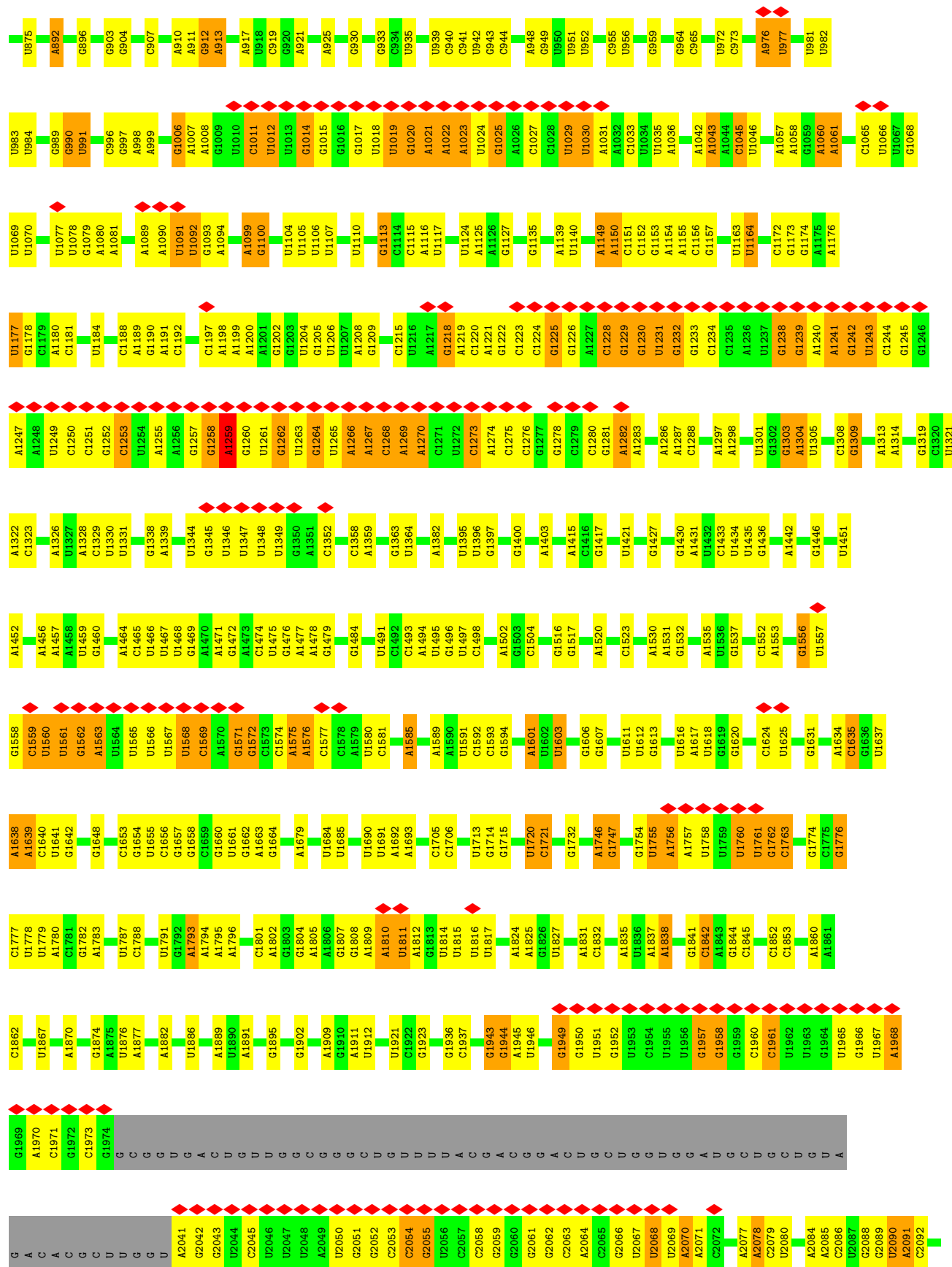
- Molecule 82 is BLASTICIDIN S (CCD ID: BLS) (formula: $C_{17}H_{26}N_8O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
82	1	1	Total	C	N	O	0
			30	17	8	5	

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

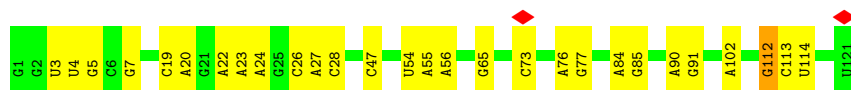
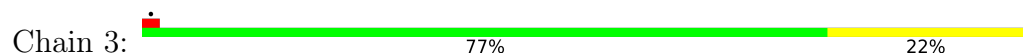
Mol	Chain	Residues	Atoms		AltConf
83	AK	1	Total 1	Zn 1	0
83	AN	1	Total 1	Zn 1	0
83	AP	1	Total 1	Zn 1	0
83	AQ	1	Total 1	Zn 1	0
83	b	1	Total 1	Zn 1	0
83	c	1	Total 1	Zn 1	0
83	e	1	Total 1	Zn 1	0
83	g	1	Total 1	Zn 1	0



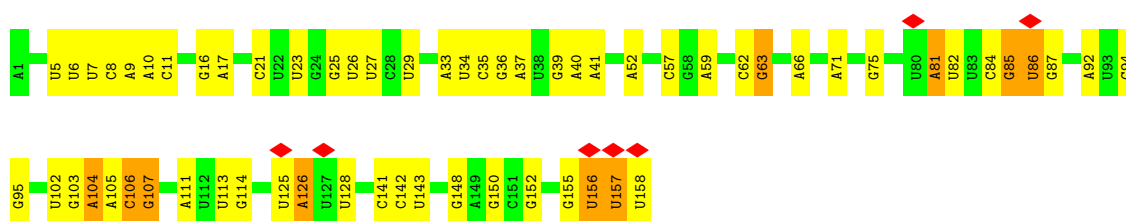




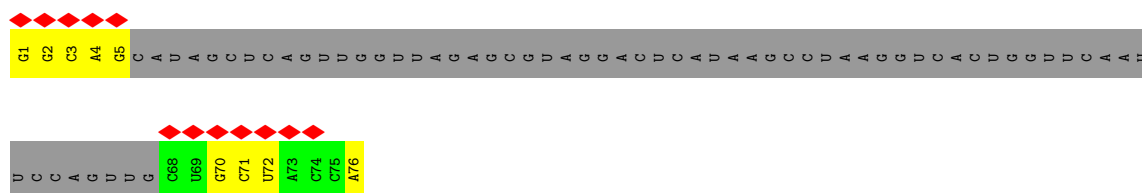
- Molecule 2: 5S ribosomal RNA



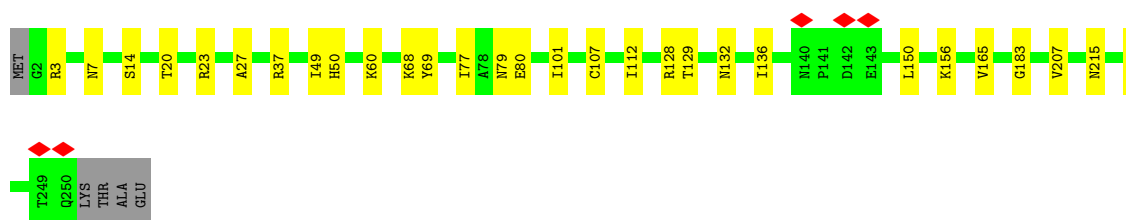
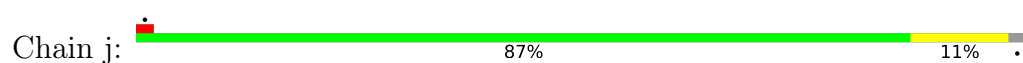
- Molecule 3: 5.8S ribosomal RNA



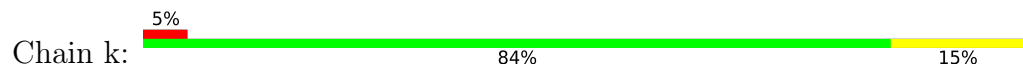
- Molecule 4: Mixture of the endogenous E-tRNA

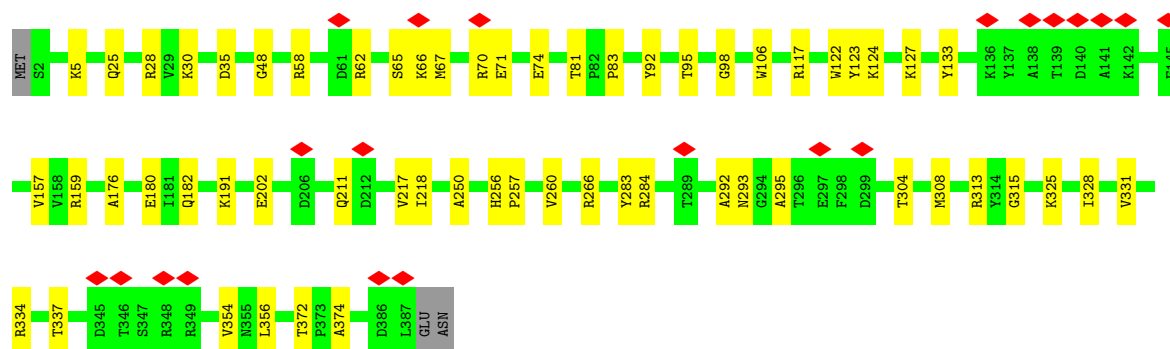


- Molecule 5: Ribosomal 60S subunit protein L2A

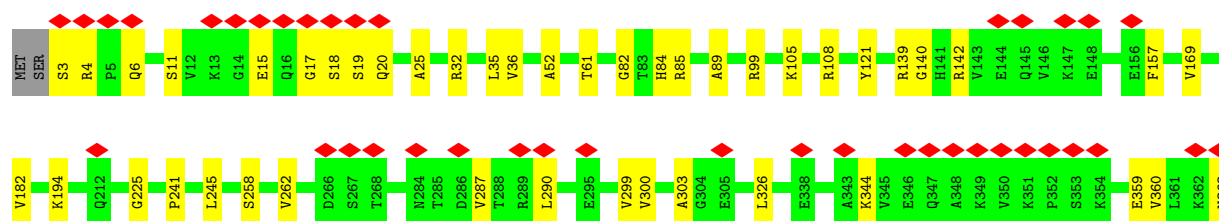
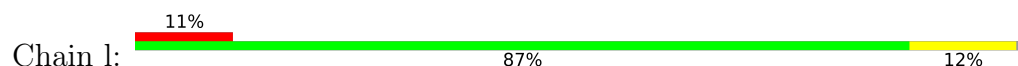


- Molecule 6: 60S ribosomal protein L3

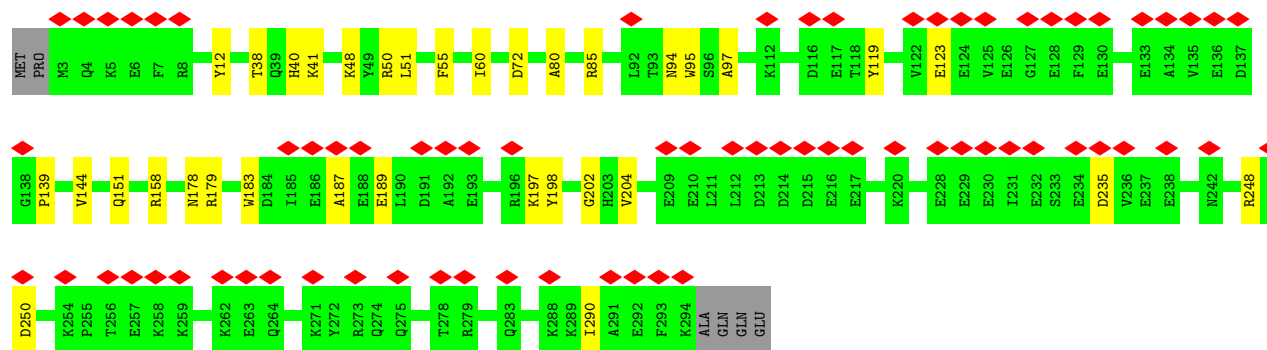
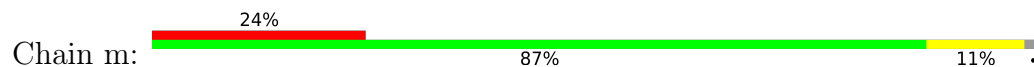




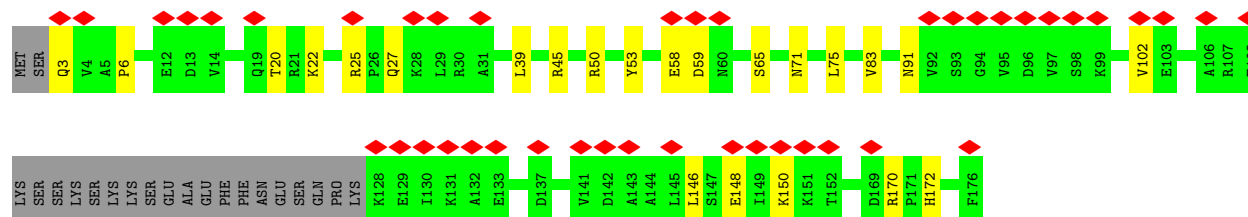
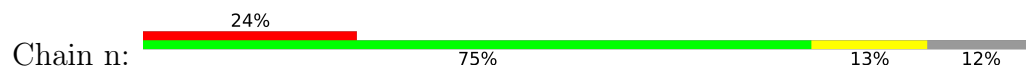
• Molecule 7: Ribosomal 60S subunit protein L4B



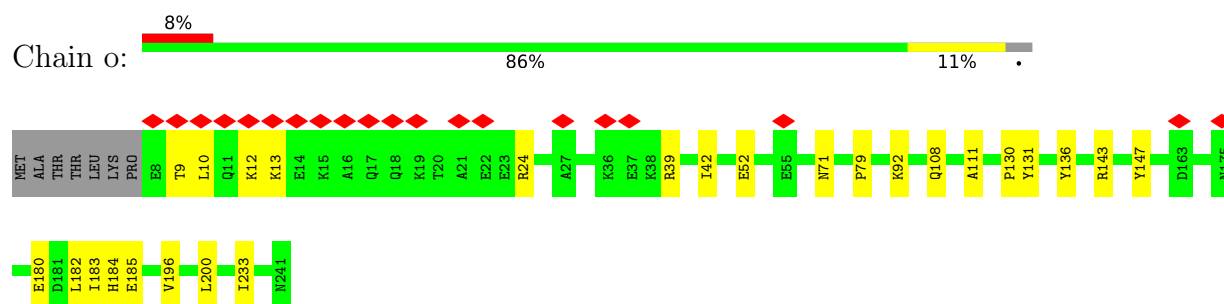
• Molecule 8: Ribosomal 60S subunit protein L5



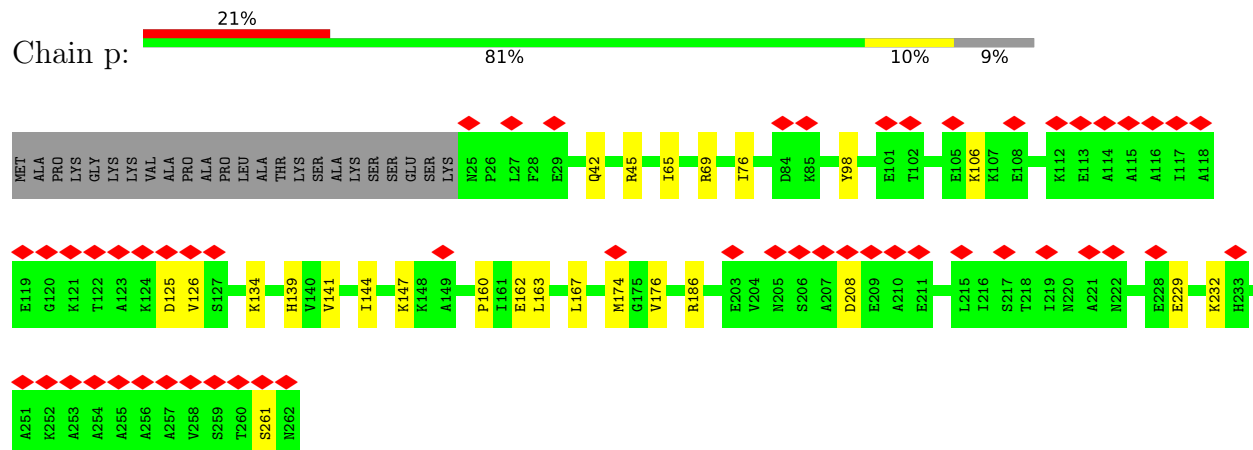
• Molecule 9: 60S ribosomal protein L6



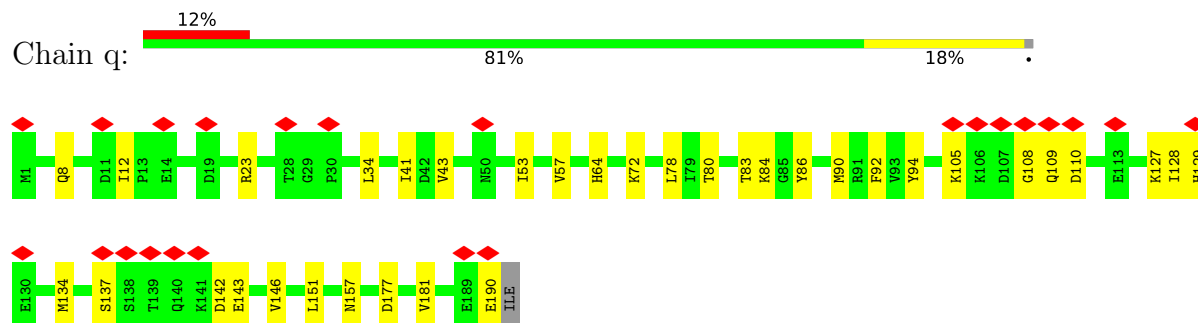
• Molecule 10: Ribosomal 60S subunit protein L7A



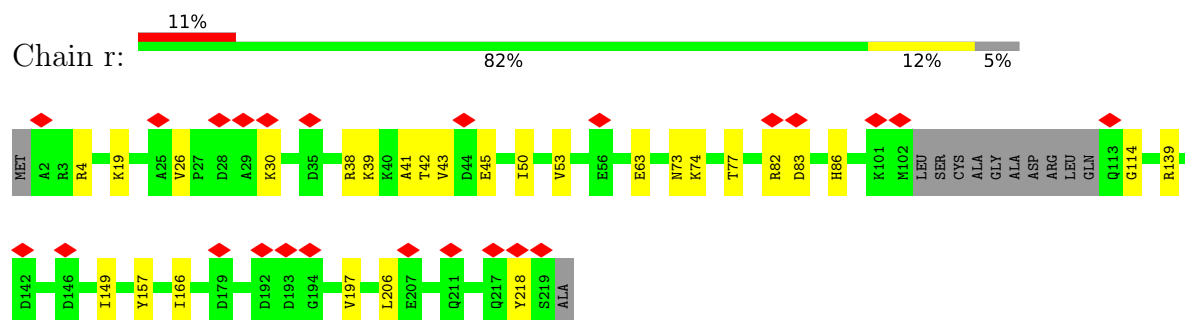
• Molecule 11: 60S ribosomal protein L8



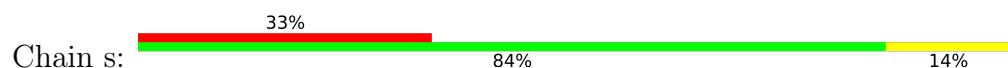
• Molecule 12: Ribosomal 60S subunit protein L9B

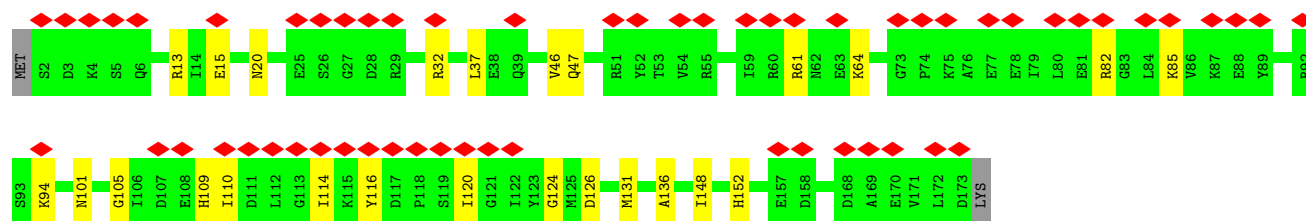


• Molecule 13: Ribosomal 60S subunit protein L10

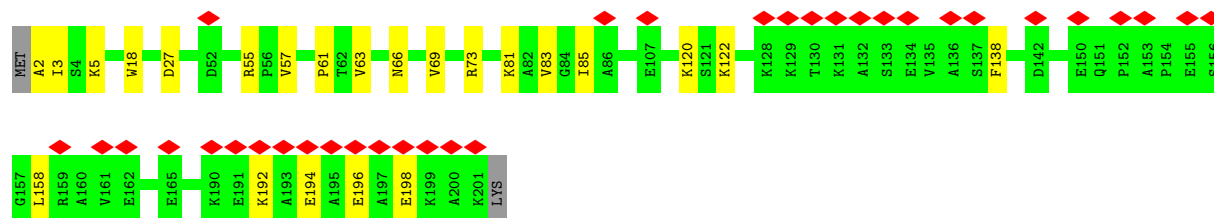
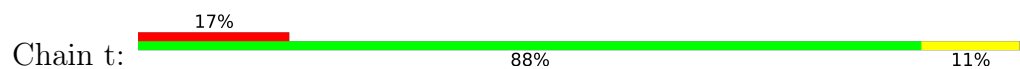


• Molecule 14: Ribosomal 60S subunit protein L11B

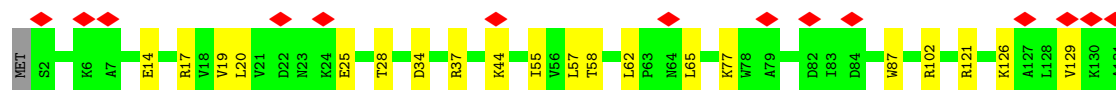
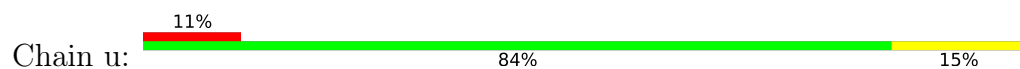




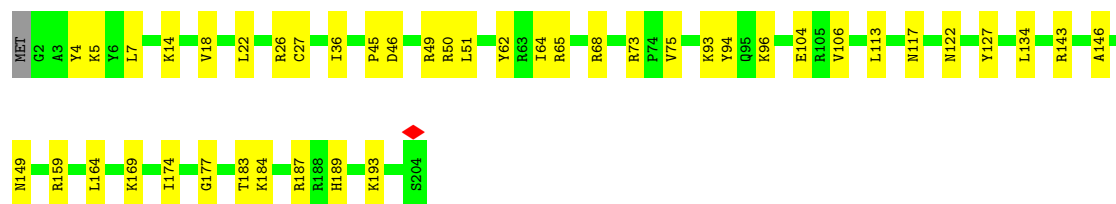
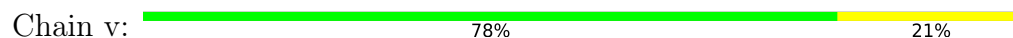
• Molecule 15: 60S ribosomal protein L13



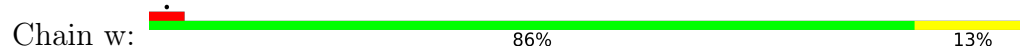
• Molecule 16: Ribosomal 60S subunit protein L14B



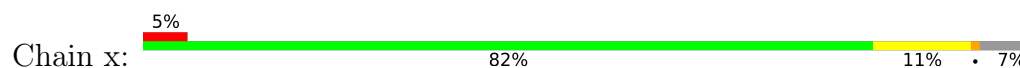
• Molecule 17: Ribosomal protein L15

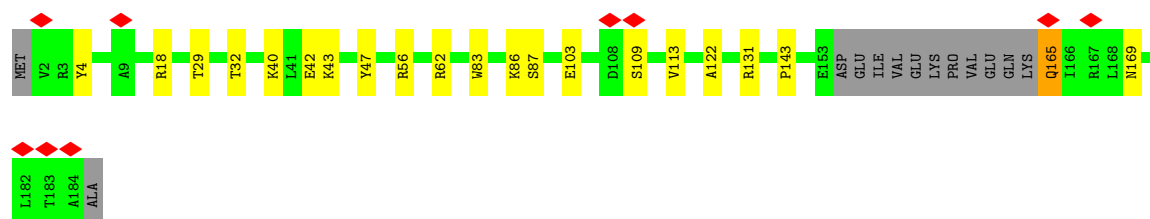


• Molecule 18: Ribosomal 60S subunit protein L16A

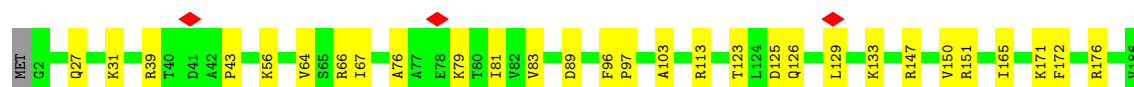
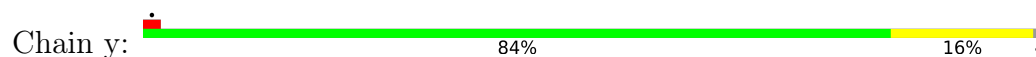


• Molecule 19: Ribosomal 60S subunit protein L17B

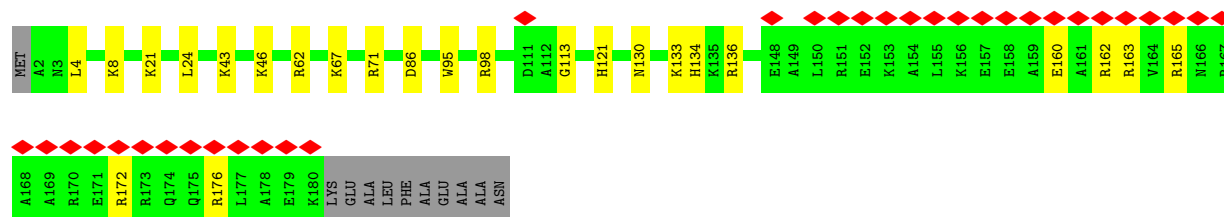
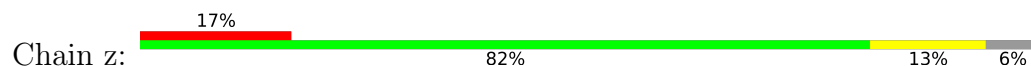




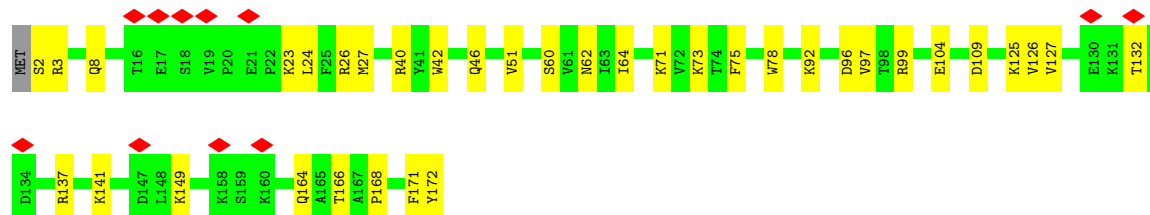
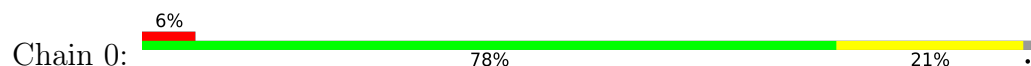
- Molecule 20: Ribosomal 60S subunit protein L18A



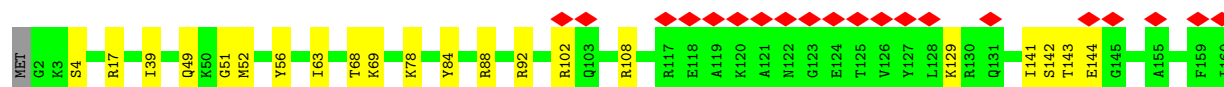
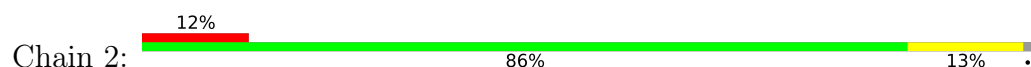
- Molecule 21: Ribosomal protein L19



- Molecule 22: 60S ribosomal protein L20

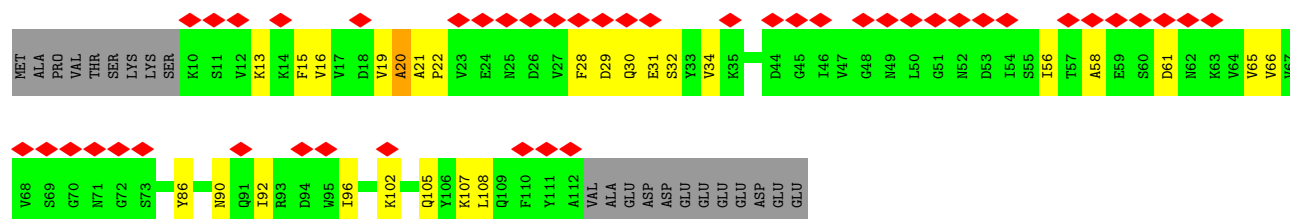


- Molecule 23: Ribosomal 60S subunit protein L21A

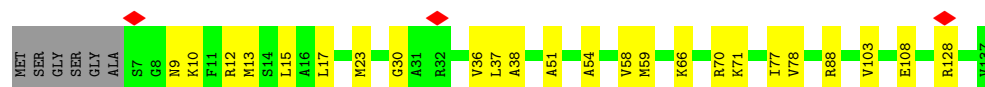
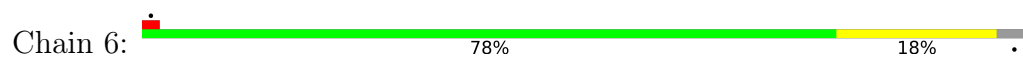


- Molecule 24: Ribosomal 60S subunit protein L22B

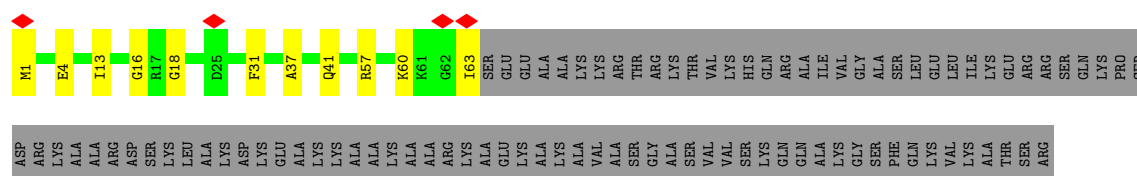
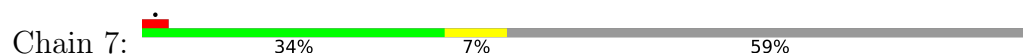




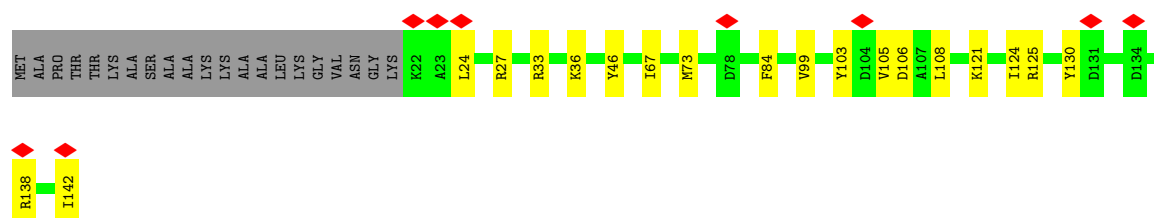
- Molecule 25: Ribosomal 60S subunit protein L23B



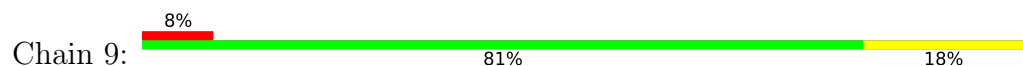
- Molecule 26: Ribosomal 60S subunit protein L24A



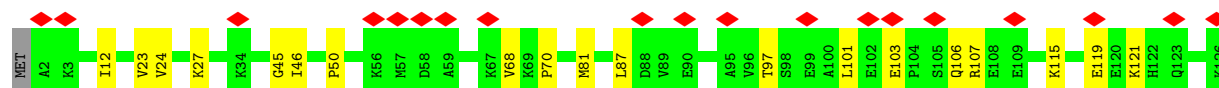
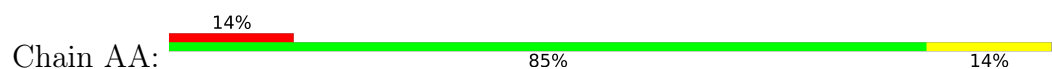
- Molecule 27: Ribosomal 60S subunit protein L25



- Molecule 28: Ribosomal 60S subunit protein L26B



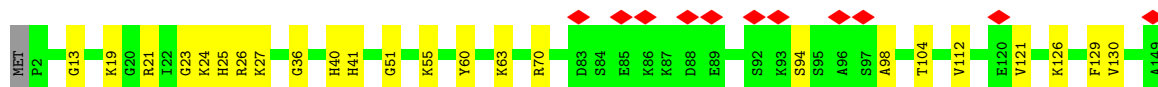
- Molecule 29: 60S ribosomal protein L27





- Molecule 30: Ribosomal 60S subunit protein L28

Chain AB: 7% 83% 16%



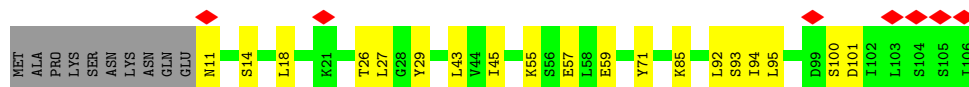
- Molecule 31: 60S ribosomal protein L29

Chain AC: 24% 86% 14%



- Molecule 32: Ribosomal 60S subunit protein L30

Chain AD: 7% 73% 18% 9%



- Molecule 33: Ribosomal 60S subunit protein L31B

Chain AE: 13% 88% 9%



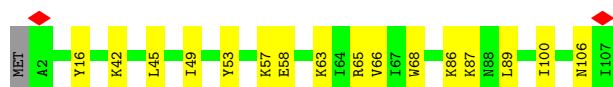
- Molecule 34: Ribosomal 60S subunit protein L32

Chain AF: 5% 79% 16% 5%

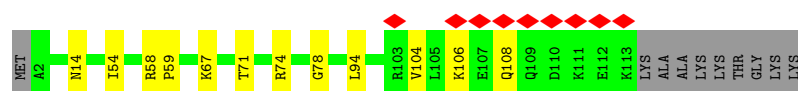
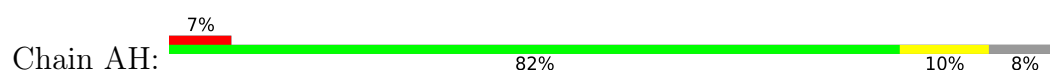


- Molecule 35: Ribosomal 60S subunit protein L33A

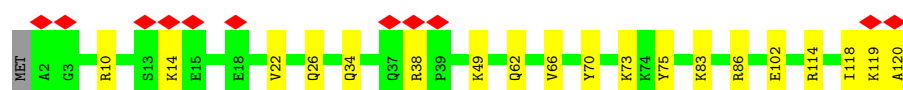
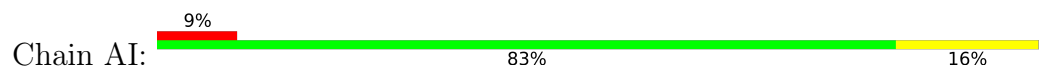
Chain AG: 84% 15%



- Molecule 36: Ribosomal 60S subunit protein L34B



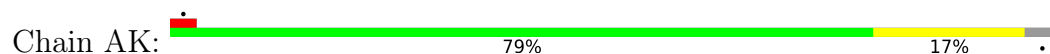
- Molecule 37: Ribosomal 60S subunit protein L35A



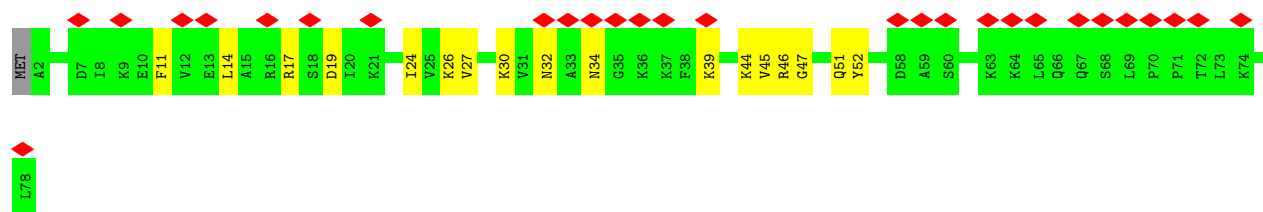
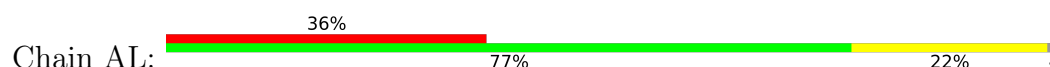
- Molecule 38: 60S ribosomal protein L36



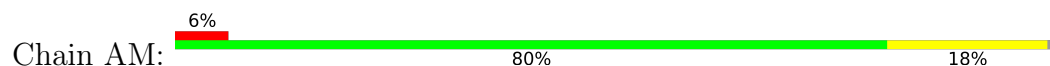
- Molecule 39: Ribosomal protein L37



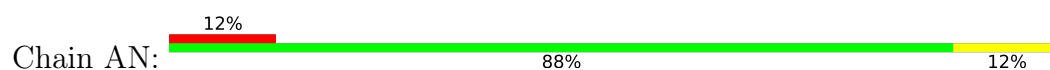
- Molecule 40: Ribosomal 60S subunit protein L38

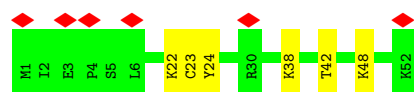


- Molecule 41: 60S ribosomal protein L39

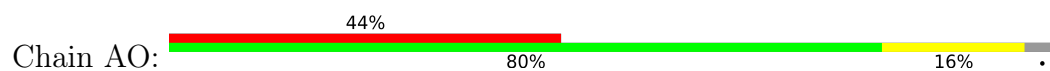


- Molecule 42: Rpl40bp

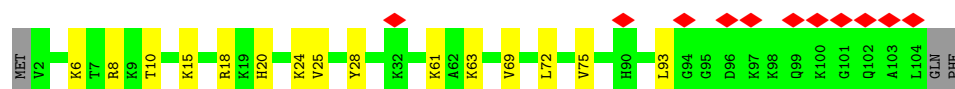
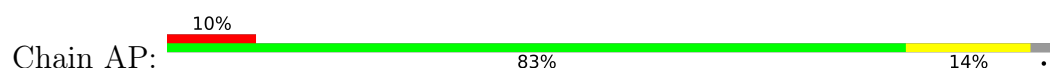




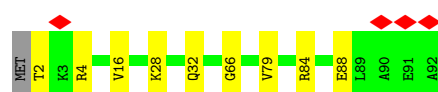
- Molecule 43: 60S ribosomal protein L41



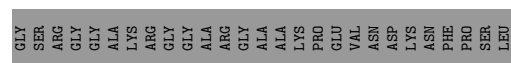
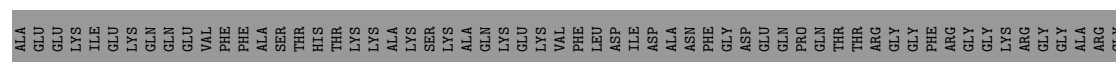
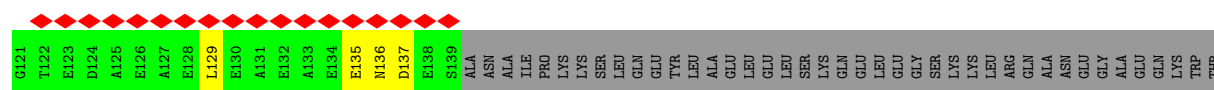
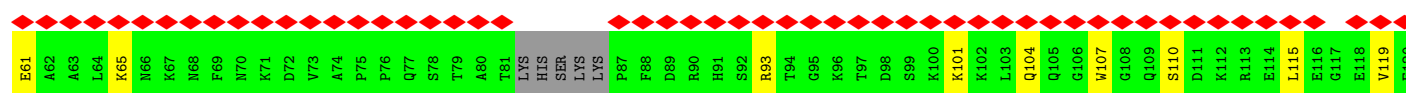
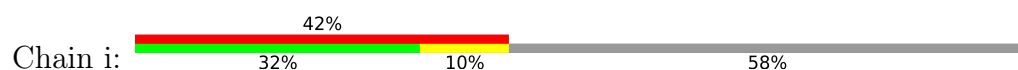
- Molecule 44: Ribosomal 60S subunit protein L42A



- Molecule 45: Ribosomal 60S subunit protein L43A

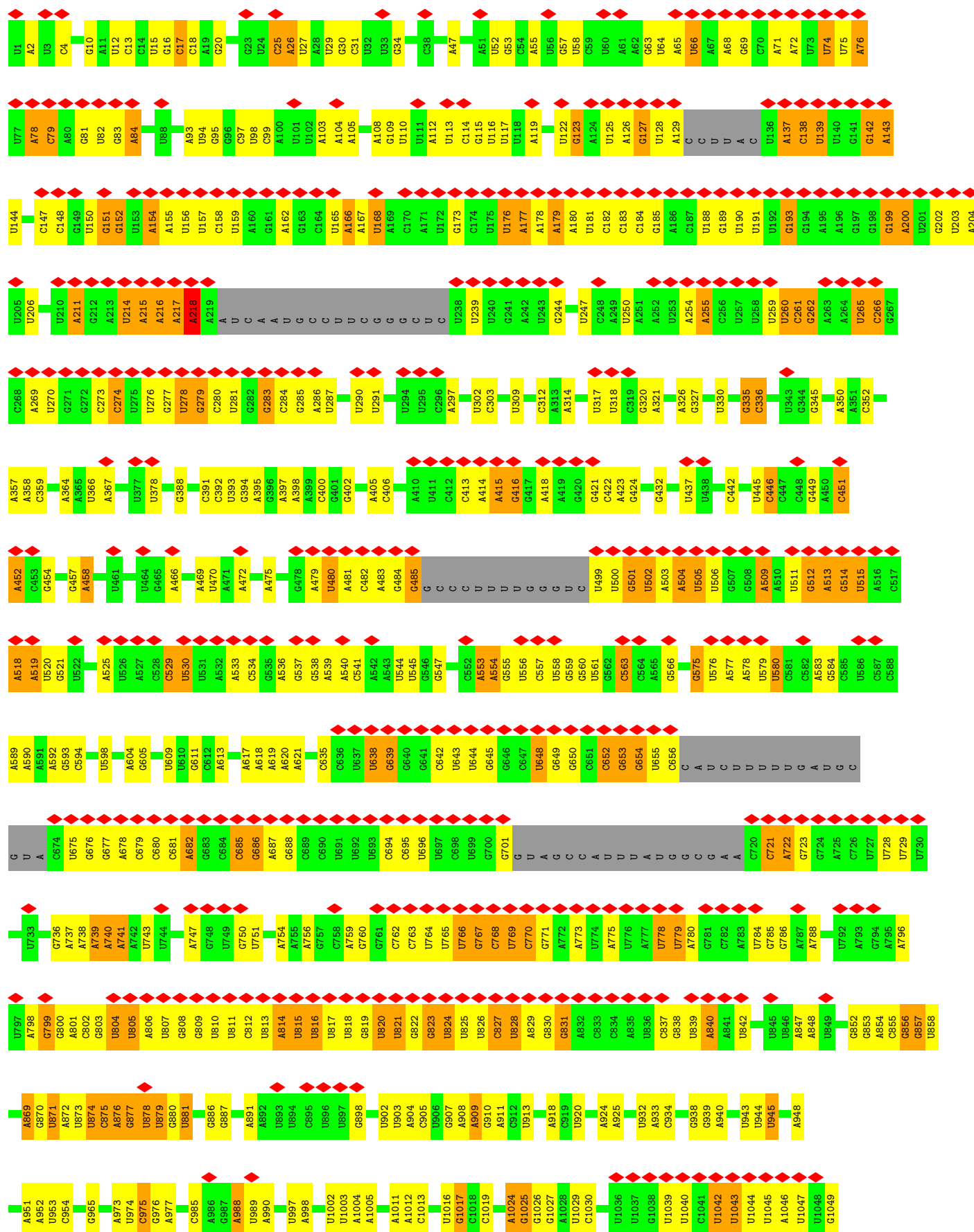


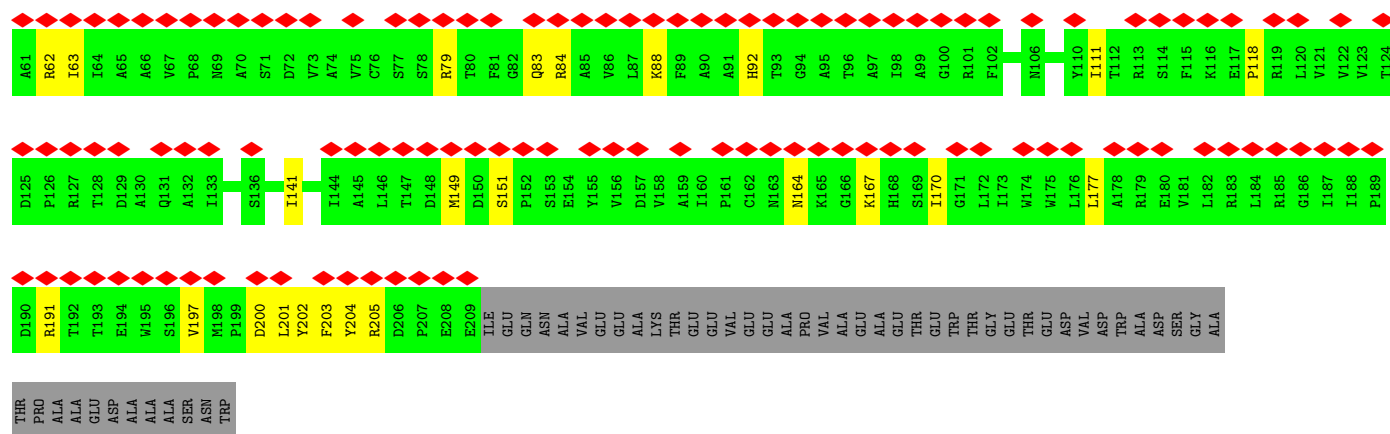
- Molecule 46: HABP4_PAI-RBP1 domain-containing protein



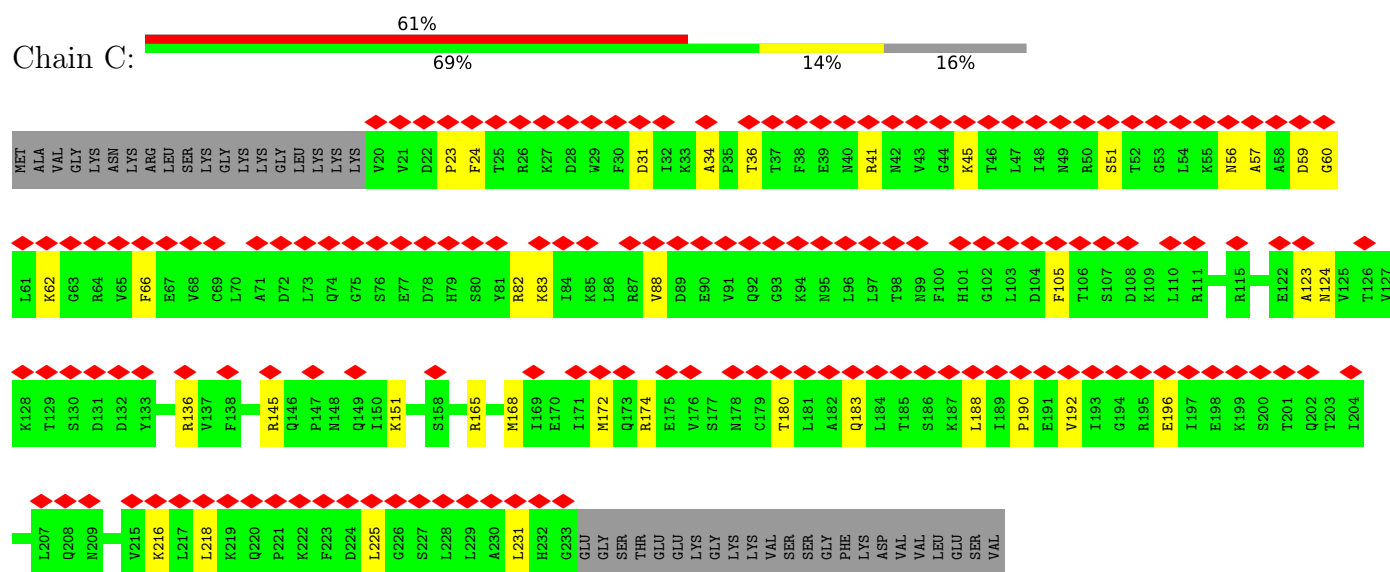
- Molecule 47: 18S ribosomal RNA



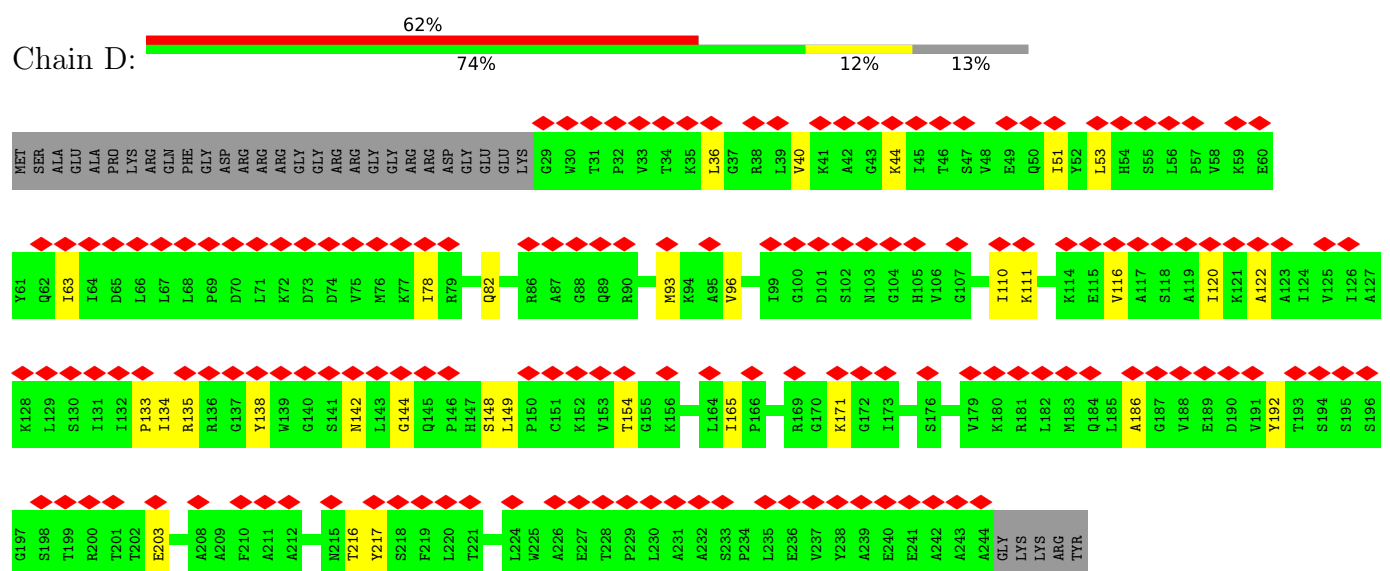




• Molecule 49: 40S ribosomal protein S1

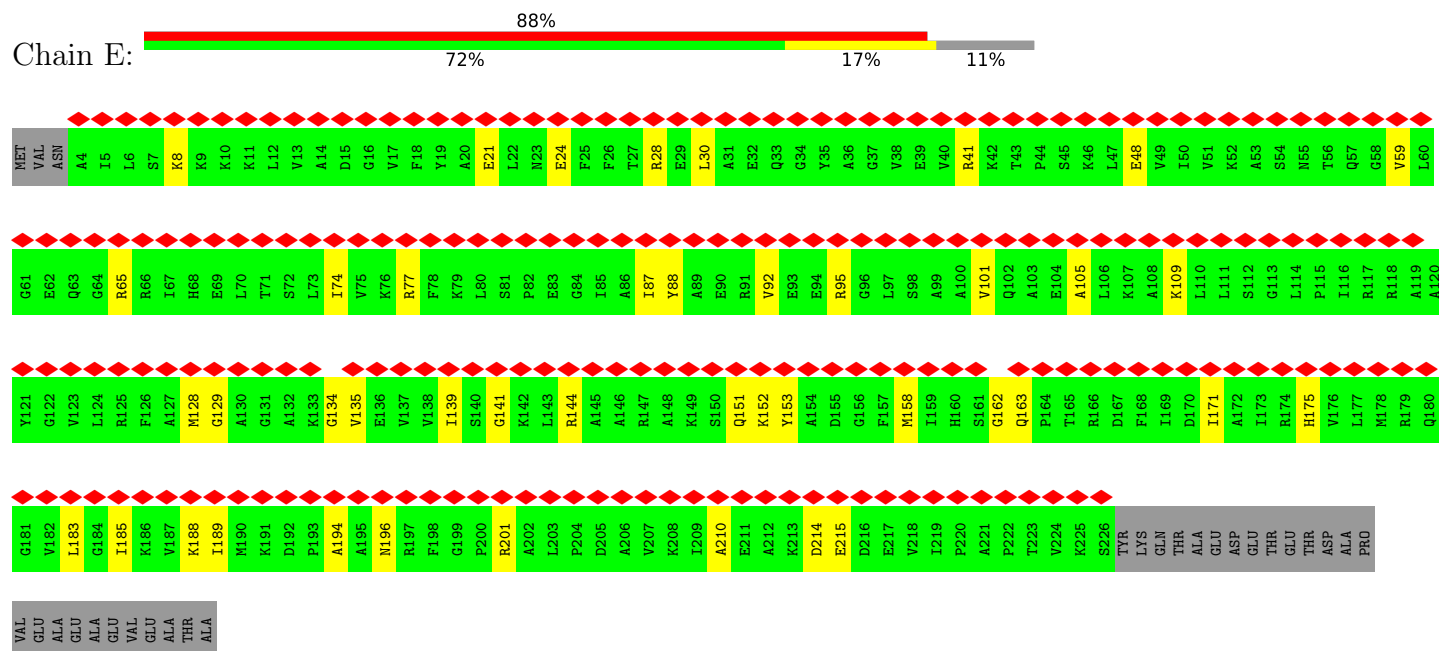


• Molecule 50: Ribosomal 40S subunit protein S2



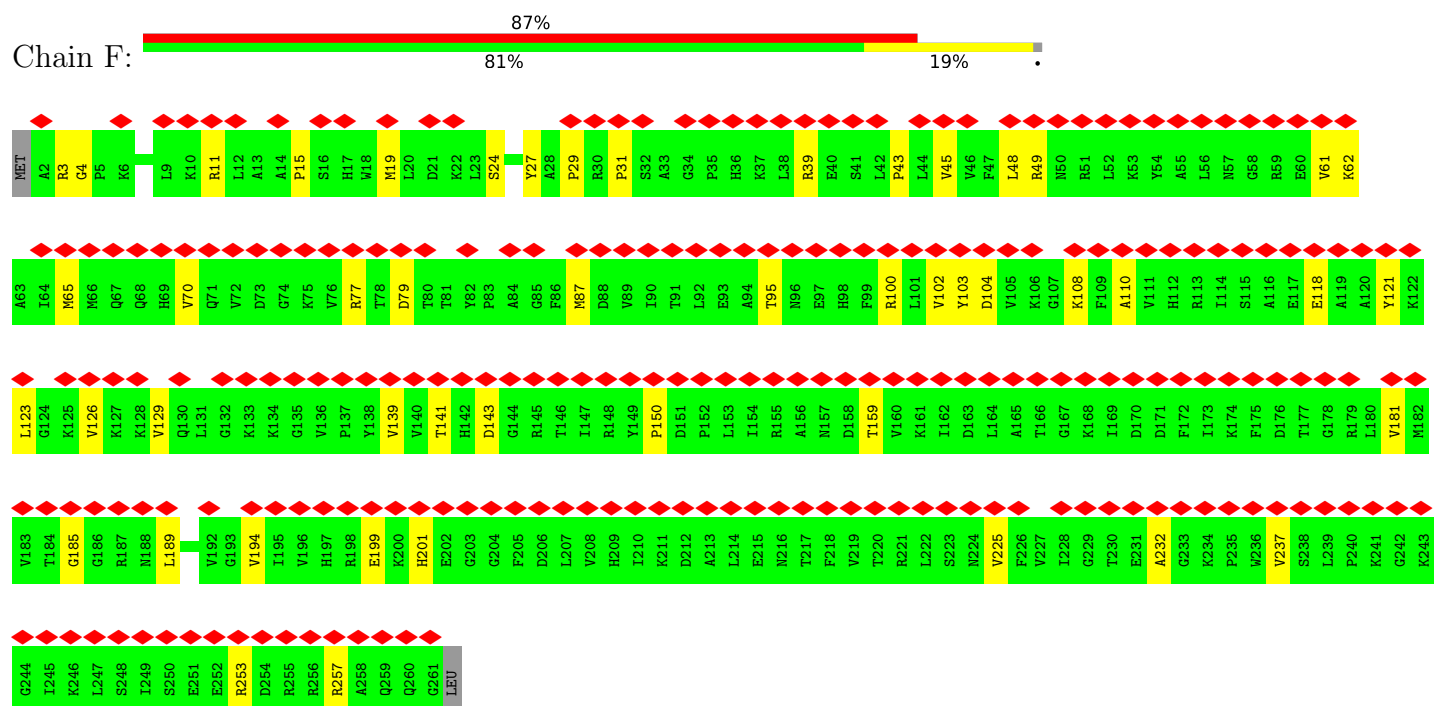
- Molecule 51: Ribosomal 40S subunit protein S3

Chain E:



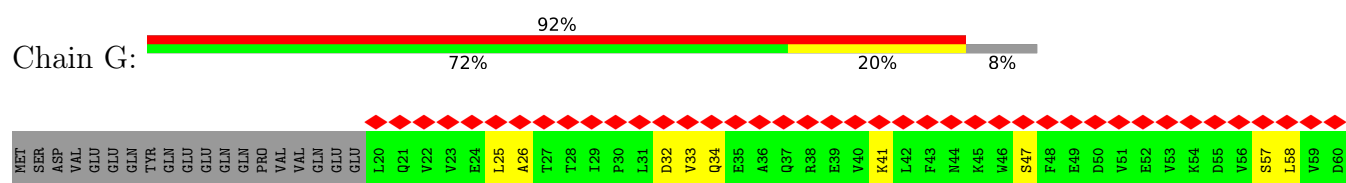
- Molecule 52: 40S ribosomal protein S4

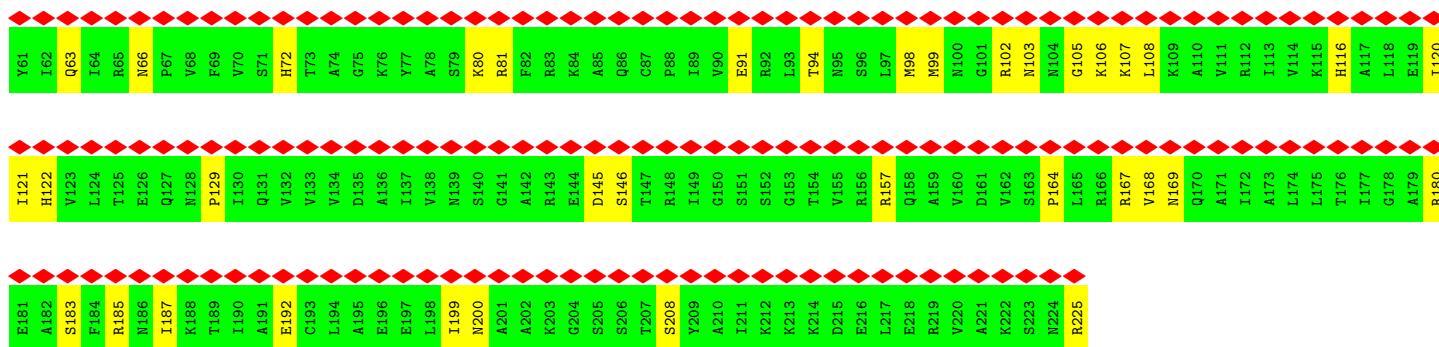
Chain F:



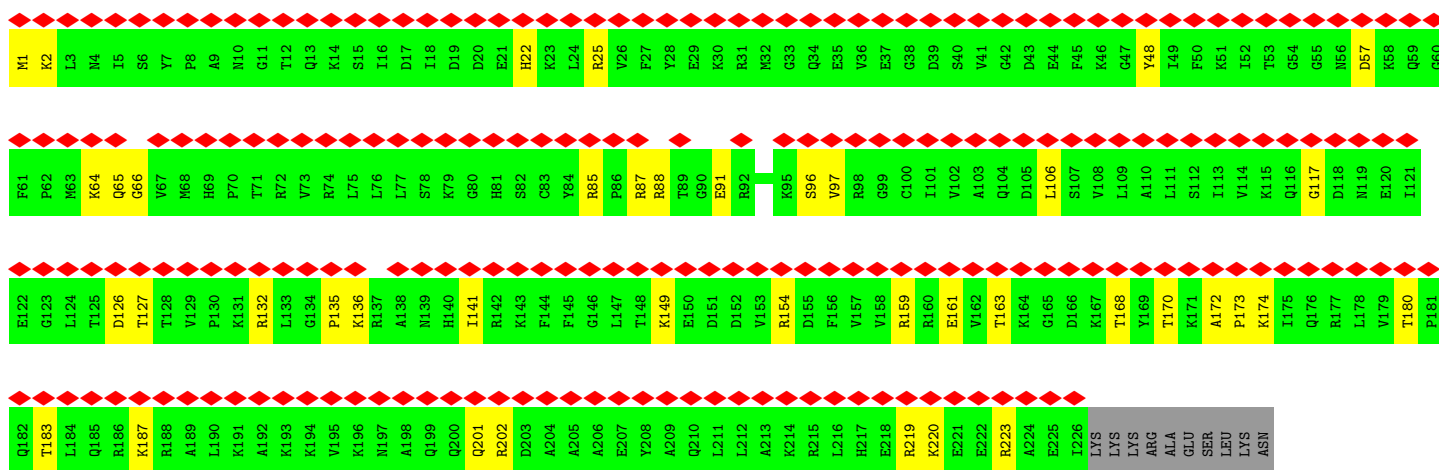
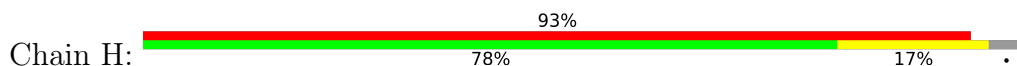
- Molecule 53: Ribosomal 40S subunit protein S5

Chain G:

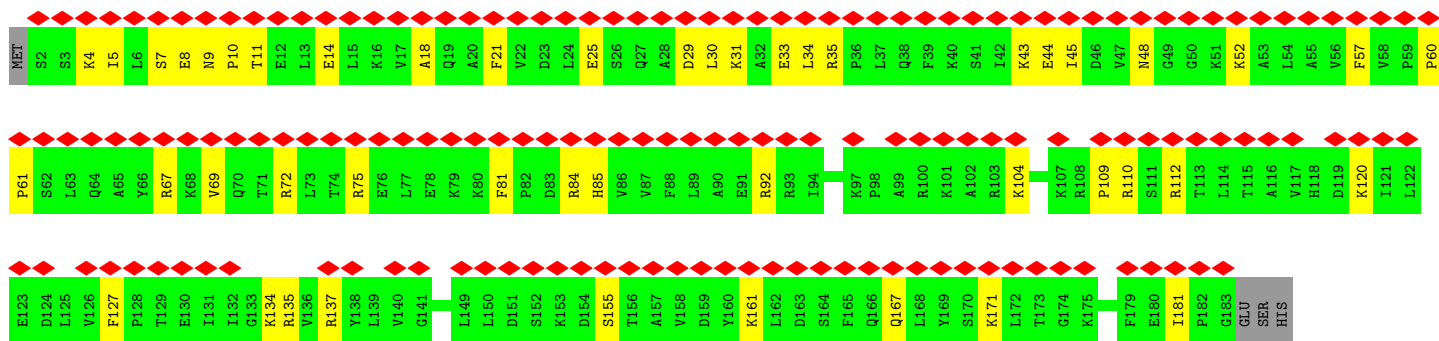
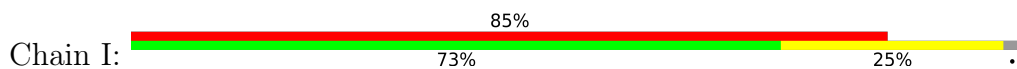




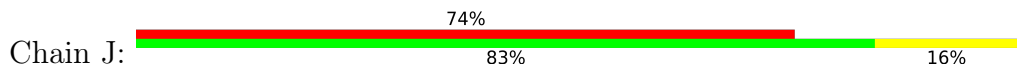
• Molecule 54: 40S ribosomal protein S6

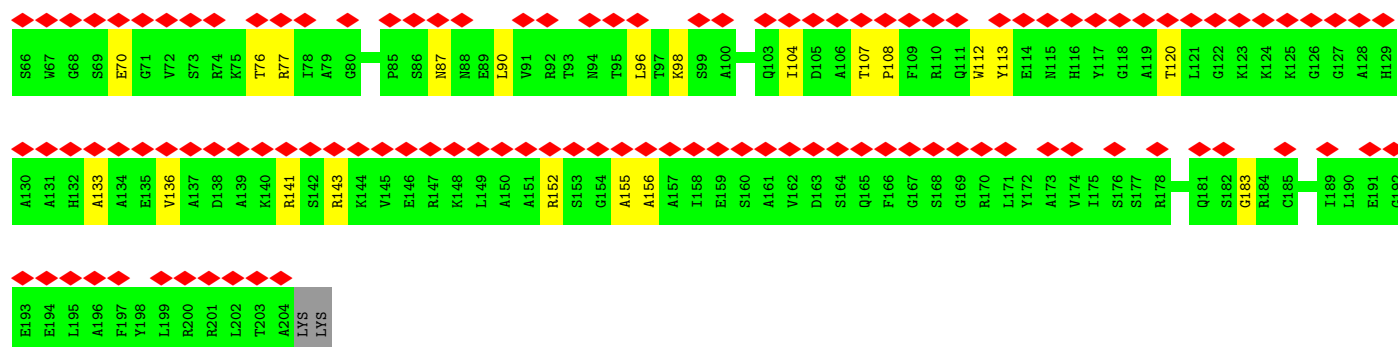


• Molecule 55: 40S ribosomal protein S7

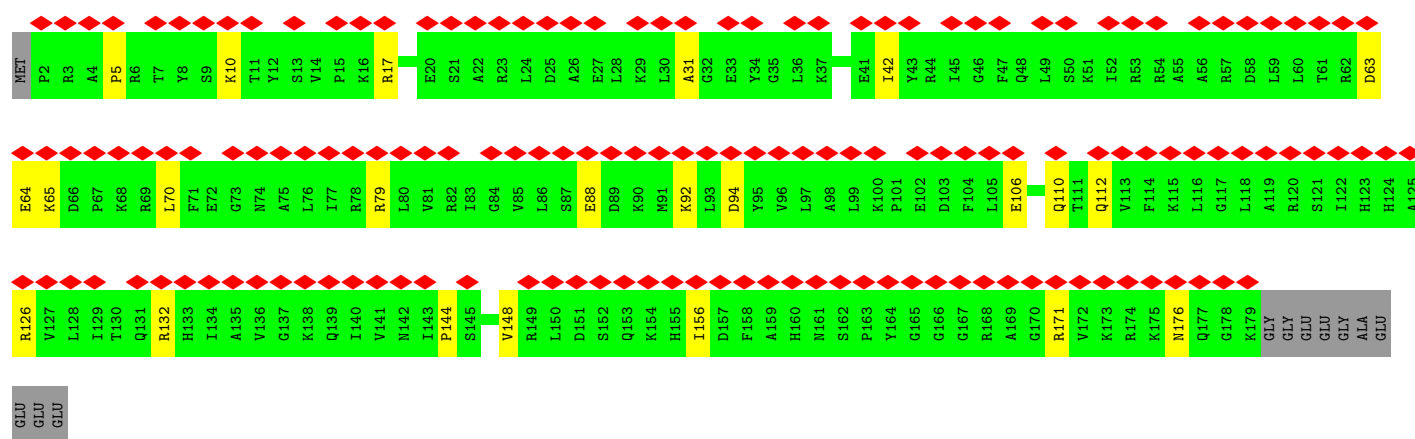
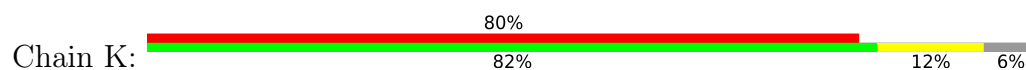


• Molecule 56: 40S ribosomal protein S8

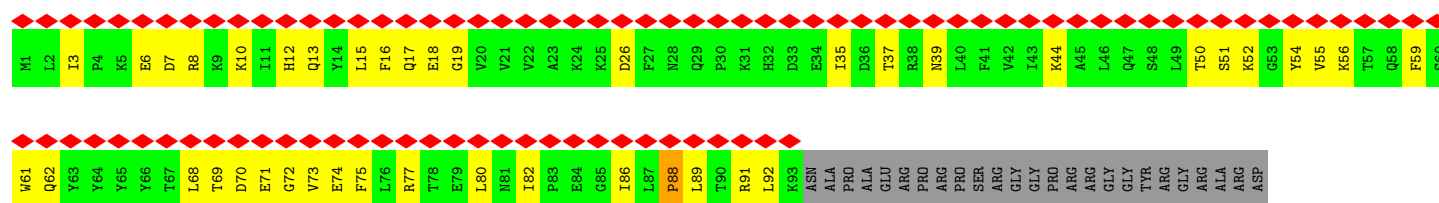
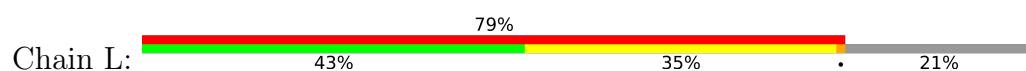




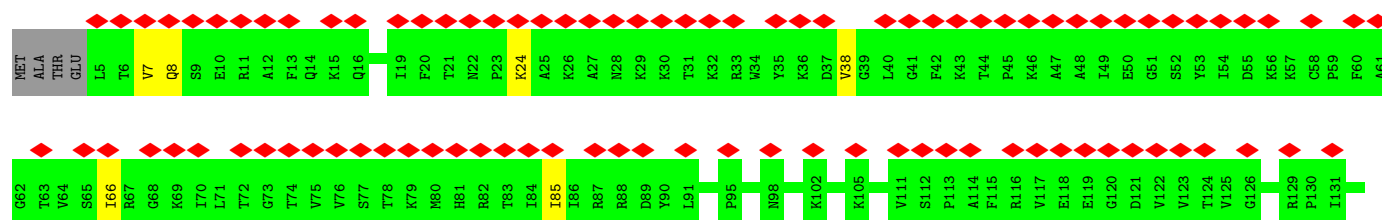
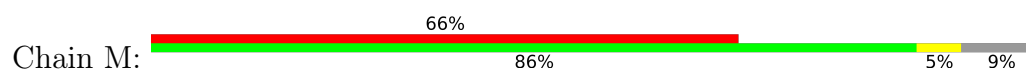
• Molecule 57: Ribosomal 40S subunit protein S9B



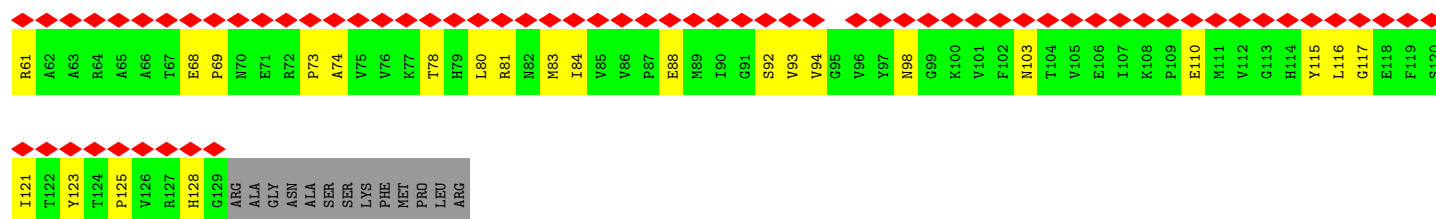
• Molecule 58: Ribosomal 40S subunit protein S10A



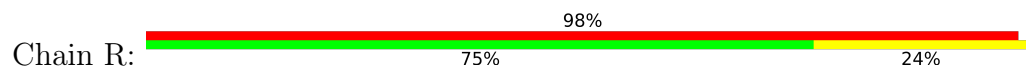
• Molecule 59: Ribosomal 40S subunit protein S11A



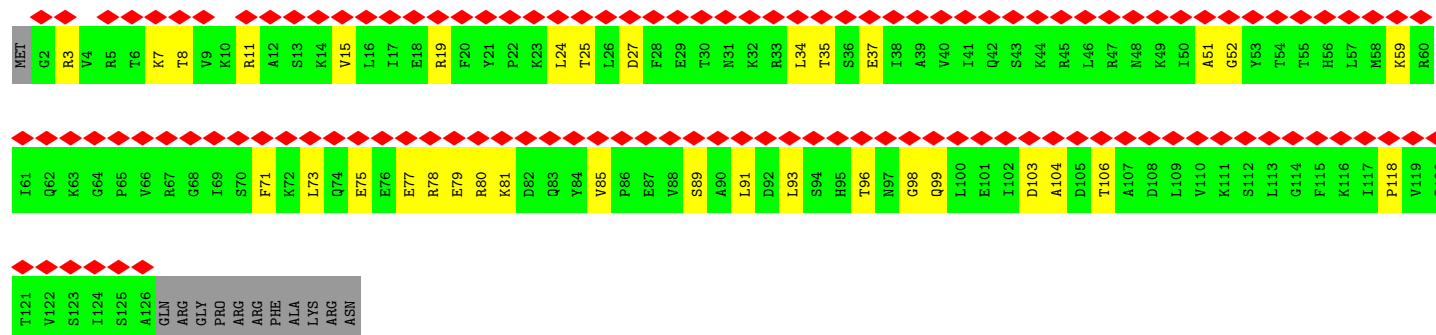
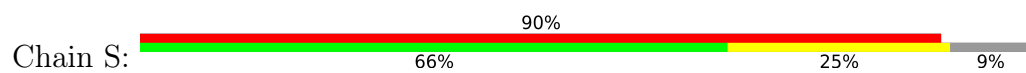




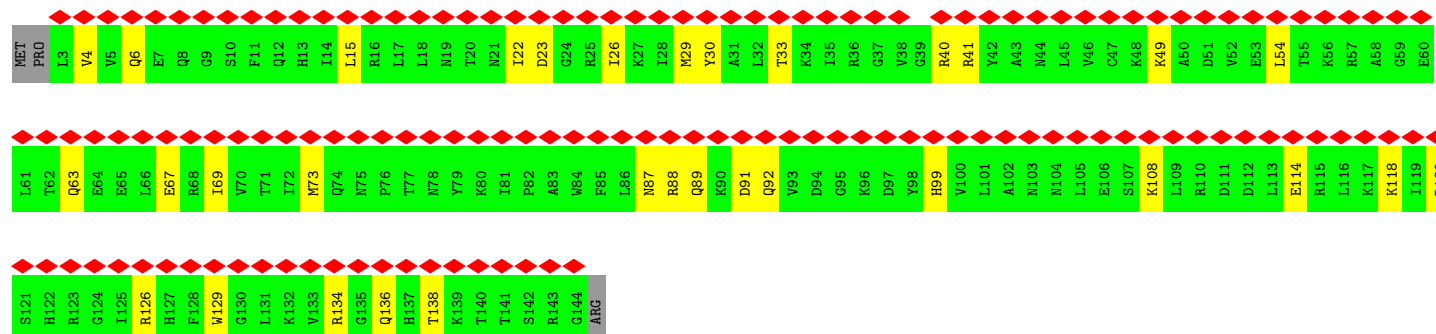
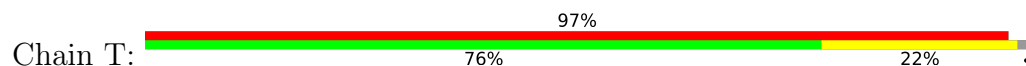
• Molecule 64: Ribosomal 40S subunit protein S16A



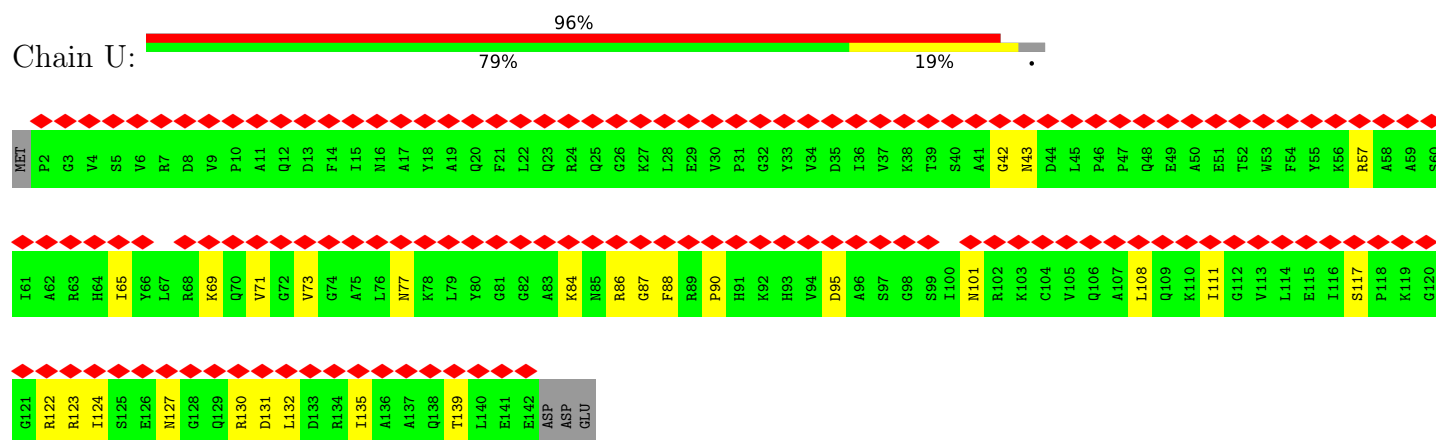
• Molecule 65: Ribosomal 40S subunit protein S17B



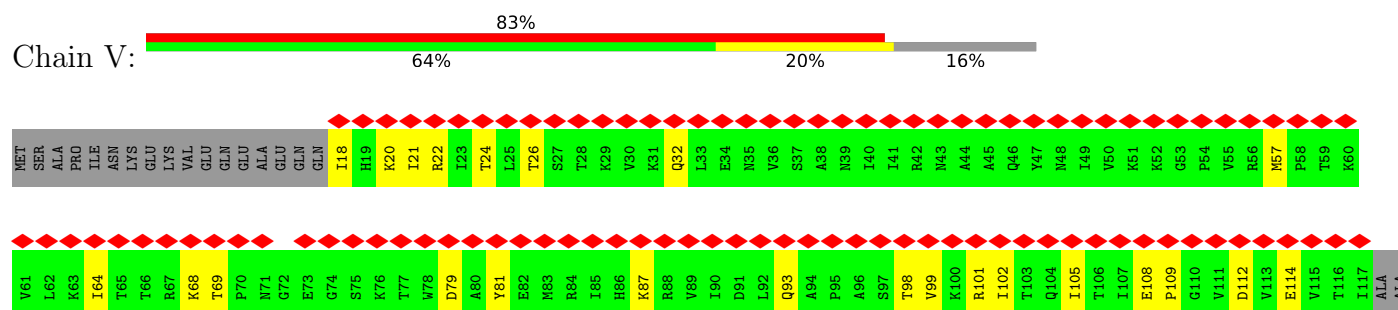
• Molecule 66: Ribosomal 40S subunit protein S18B



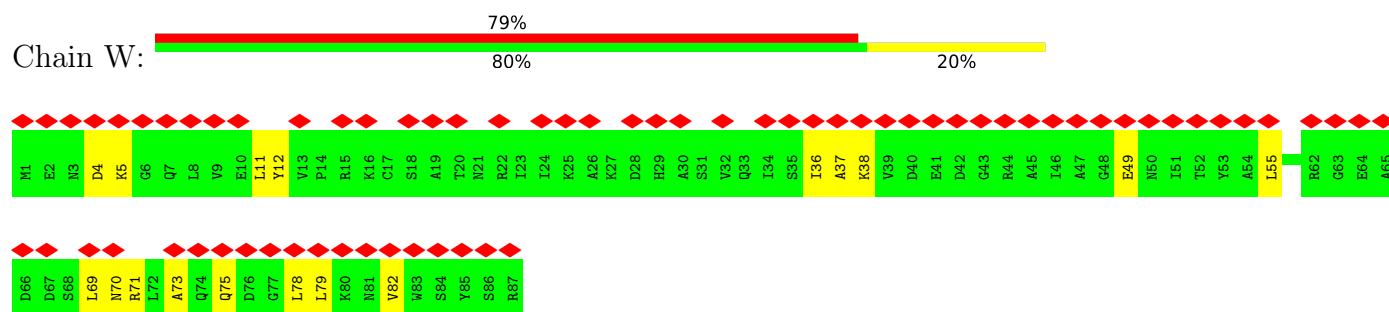
- Molecule 67: Ribosomal 40S subunit protein S19A



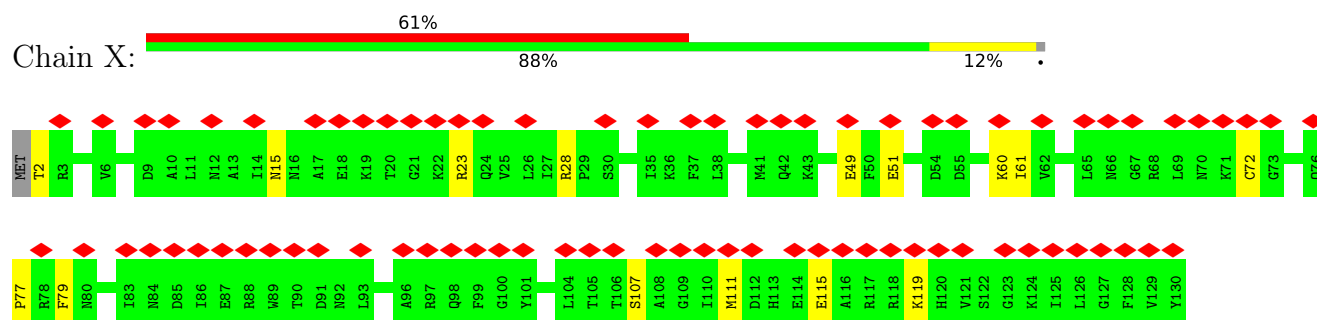
- Molecule 68: Ribosomal 40S subunit protein S20



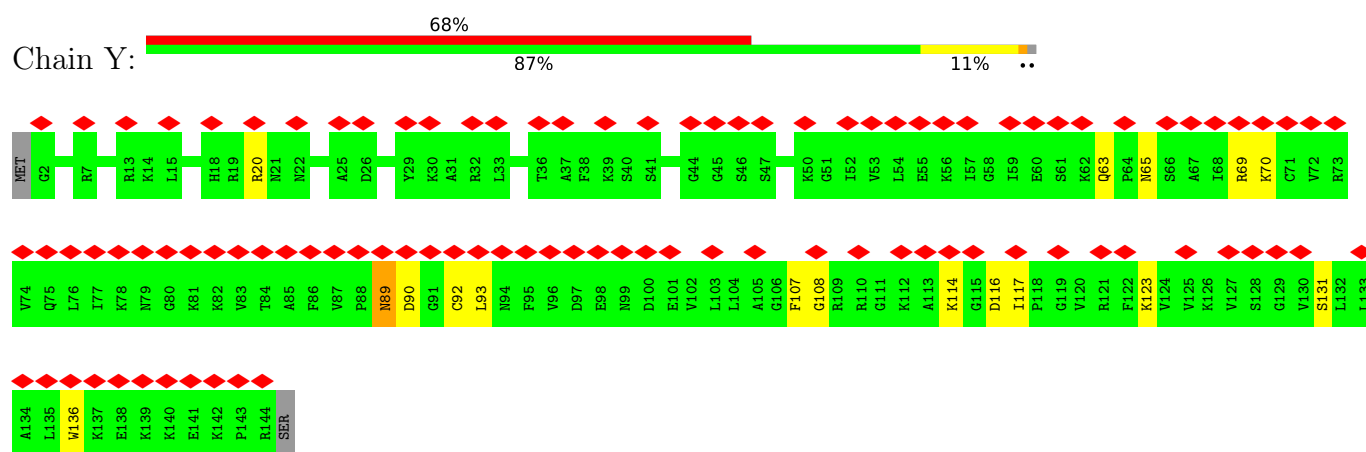
- Molecule 69: 40S ribosomal protein S21



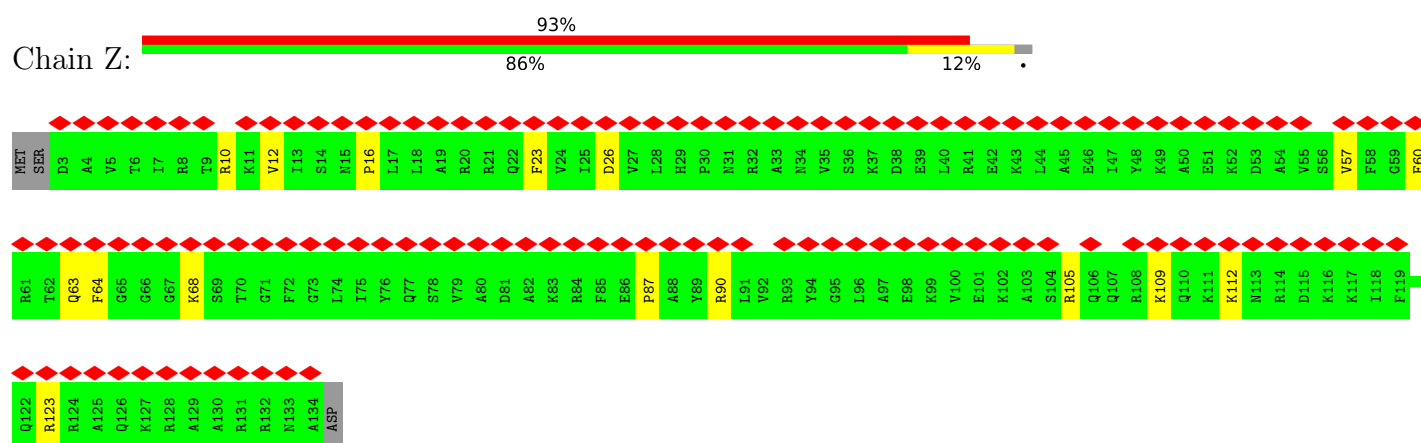
- Molecule 70: 40S ribosomal protein S22-A



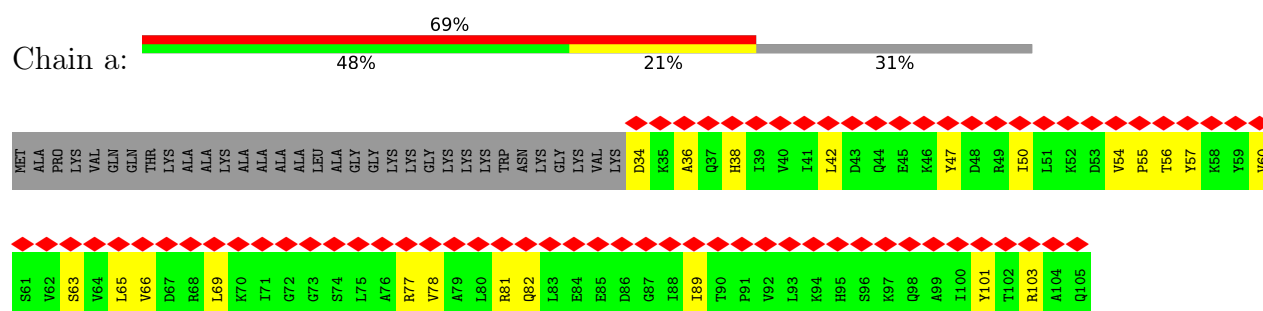
- Molecule 71: Ribosomal 40S subunit protein S23B



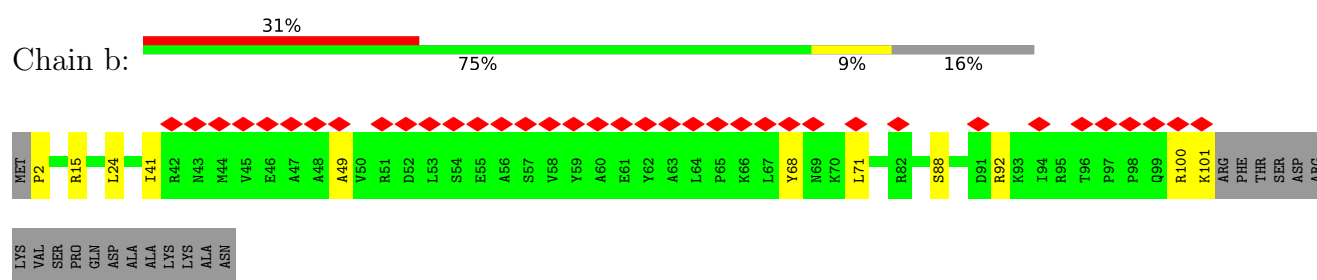
• Molecule 72: 40S ribosomal protein S24



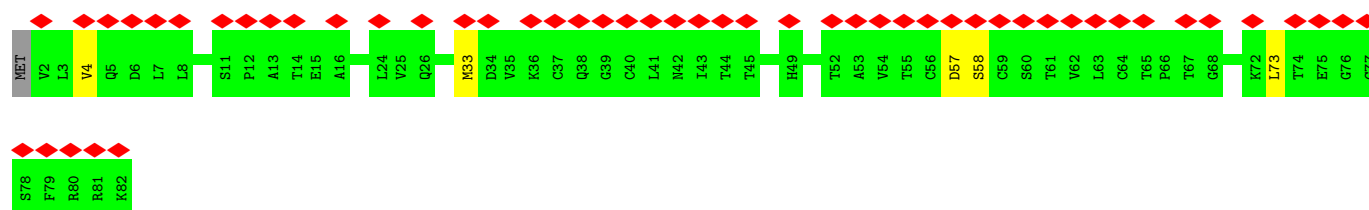
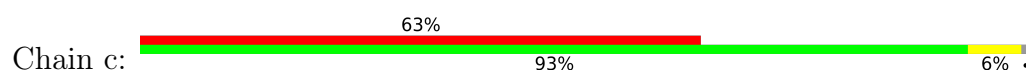
• Molecule 73: 40S ribosomal protein S25



• Molecule 74: 40S ribosomal protein S26



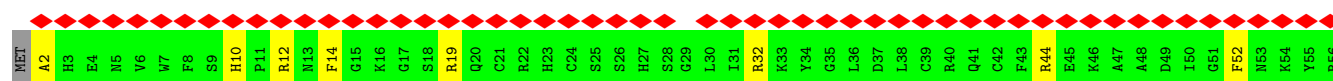
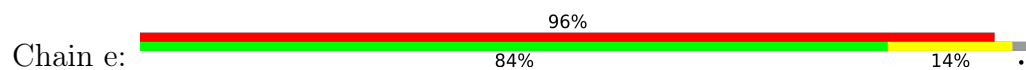
• Molecule 75: 40S ribosomal protein S27



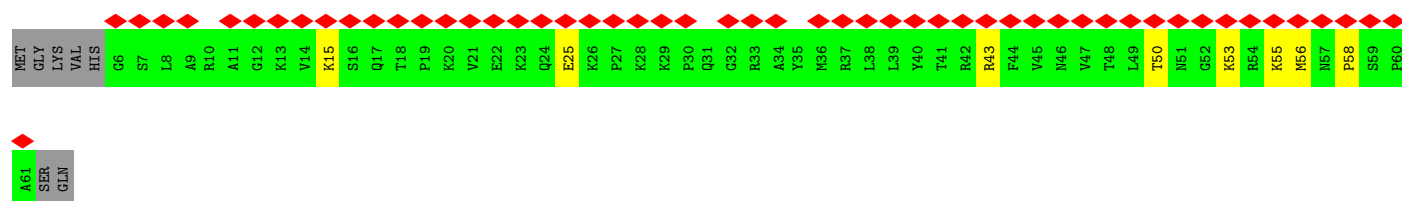
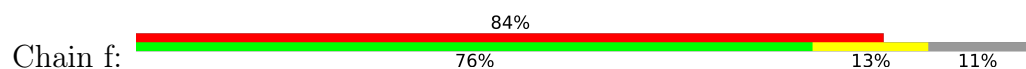
- Molecule 76: Ribosomal 40S subunit protein S28B



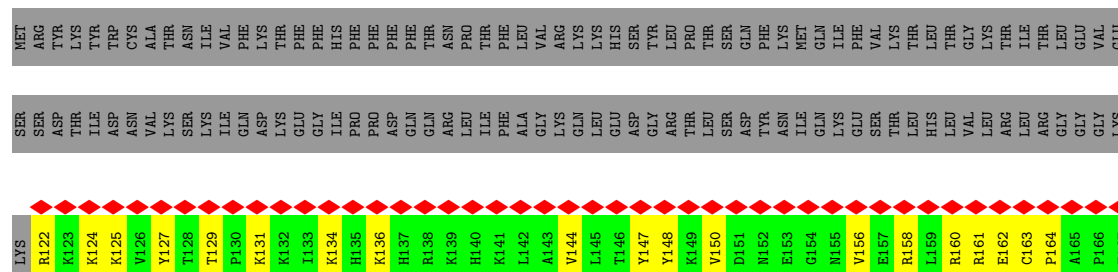
- Molecule 77: Ribosomal 40S subunit protein S29A

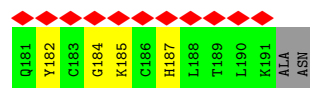


- Molecule 78: 40S ribosomal protein S30

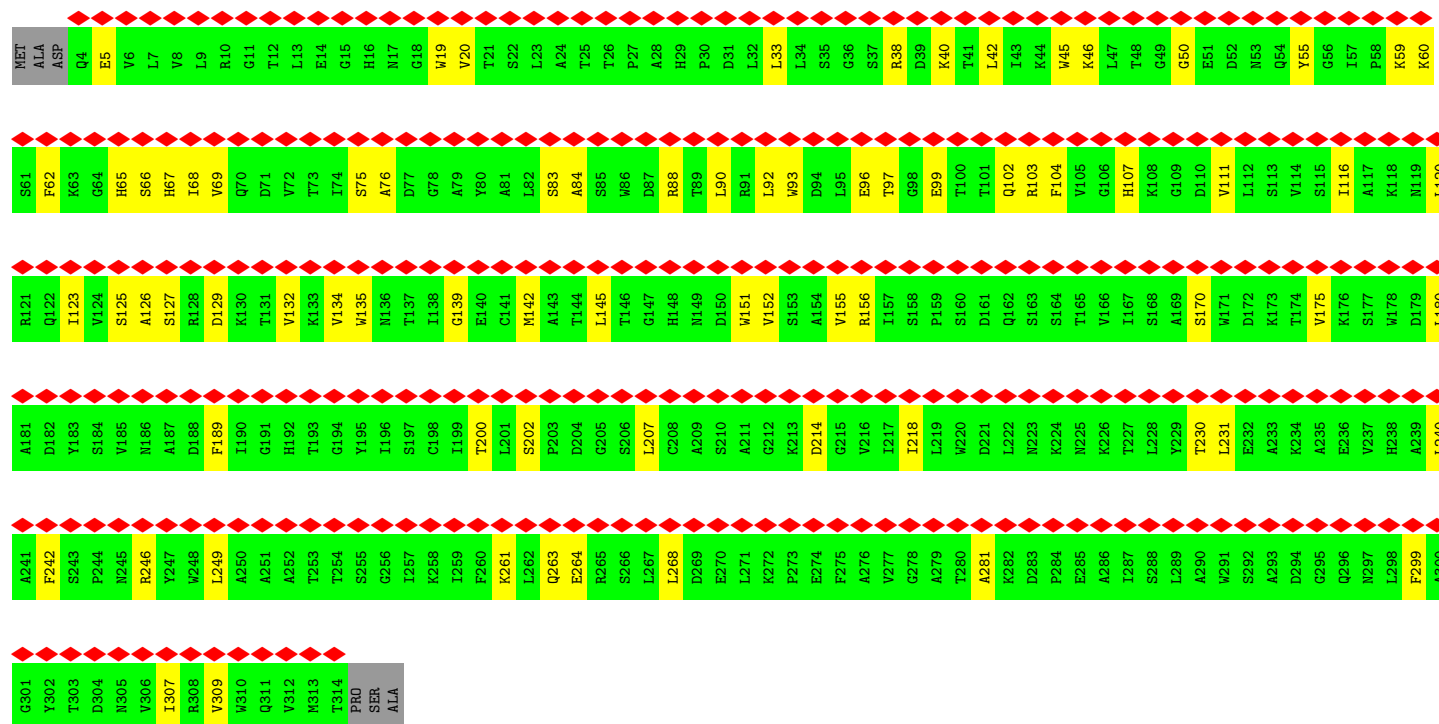
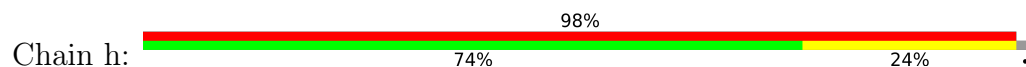


- Molecule 79: Ubiquitin-ribosomal 40S subunit protein S31 fusion protein





- Molecule 80: Guanine nucleotide-binding protein subunit beta-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136638	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	4.211	Depositor
Minimum map value	-1.789	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.141	Depositor
Recommended contour level	0.632	Depositor
Map size (Å)	426.36002, 426.36002, 426.36002	wwPDB
Map dimensions	510, 510, 510	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.836, 0.836, 0.836	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, OMG, BLS, SPD, MLZ, ZN, IAS

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	1	0.23	6/76718 (0.0%)	0.33	3/119600 (0.0%)
2	3	0.18	0/2884	0.25	0/4492
3	4	0.21	0/3746	0.29	0/5832
4	10	0.16	0/331	0.19	0/511
5	j	0.20	0/1931	0.33	0/2592
6	k	0.20	0/3156	0.35	0/4246
7	l	0.17	0/2799	0.35	0/3777
8	m	0.15	0/2447	0.31	0/3294
9	n	0.16	0/1258	0.30	0/1696
10	o	0.18	0/1929	0.36	0/2589
11	p	0.15	0/1869	0.30	0/2519
12	q	0.16	0/1537	0.29	0/2067
13	r	0.16	0/1724	0.29	0/2314
14	s	0.14	0/1404	0.29	0/1880
15	t	0.23	0/1637	0.41	0/2195
16	u	0.17	0/1044	0.33	0/1407
17	v	0.20	0/1753	0.35	0/2347
18	w	0.18	0/1620	0.32	0/2167
19	x	0.18	0/1398	0.33	0/1879
20	y	0.18	0/1511	0.34	0/2022
21	z	0.16	0/1483	0.27	0/1972
22	0	0.19	0/1483	0.32	0/1997
23	2	0.17	0/1305	0.29	0/1749
24	5	0.14	0/871	0.37	0/1175
25	6	0.17	0/994	0.36	0/1339
26	7	0.17	0/536	0.29	0/712
27	8	0.18	0/990	0.32	0/1337
28	9	0.17	0/999	0.35	0/1334
29	AA	0.16	0/1112	0.26	0/1488
30	AB	0.19	0/1199	0.32	0/1607
31	AC	0.15	0/522	0.27	0/692
32	AD	0.16	0/738	0.25	0/994

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	AE	0.17	0/902	0.31	0/1212
34	AF	0.18	0/1039	0.35	0/1390
35	AG	0.20	0/895	0.31	0/1201
36	AH	0.17	0/934	0.34	0/1242
37	AI	0.16	0/1004	0.38	0/1337
38	AJ	0.14	0/780	0.27	0/1033
39	AK	0.22	0/690	0.41	0/916
40	AL	0.18	0/632	0.33	0/842
41	AM	0.17	0/458	0.27	0/609
42	AN	0.15	0/436	0.31	0/577
43	AO	0.10	0/228	0.32	0/293
44	AP	0.16	0/840	0.29	0/1108
45	AQ	0.18	0/705	0.33	0/940
46	i	0.12	0/864	0.35	0/1156
47	A	0.20	1/40362 (0.0%)	0.32	0/62888
48	B	0.16	0/1666	0.29	0/2273
49	C	0.15	0/1750	0.27	0/2354
50	D	0.17	0/1648	0.28	0/2237
51	E	0.14	0/1731	0.32	0/2324
52	F	0.17	0/2096	0.30	0/2822
53	G	0.14	0/1631	0.32	0/2199
54	H	0.14	0/1845	0.27	0/2464
55	I	0.16	0/1490	0.31	0/2004
56	J	0.16	0/1606	0.28	0/2150
57	K	0.16	0/1478	0.25	0/1978
58	L	0.17	0/801	0.52	0/1081
59	M	0.18	0/1154	0.28	0/1553
60	N	0.14	0/892	0.49	0/1203
61	O	0.15	0/1210	0.26	0/1631
62	P	0.15	0/944	0.28	0/1265
63	Q	0.15	0/954	0.41	0/1282
64	R	0.15	0/1109	0.35	0/1486
65	S	0.13	0/1014	0.32	0/1361
66	T	0.12	0/1186	0.28	0/1590
67	U	0.15	0/1120	0.33	0/1508
68	V	0.14	0/800	0.29	0/1082
69	W	0.17	0/683	0.37	0/918
70	X	0.19	0/1049	0.27	0/1412
71	Y	0.22	0/1128	0.38	0/1505
72	Z	0.16	0/1086	0.24	0/1447
73	a	0.14	0/585	0.30	0/789
74	b	0.16	0/811	0.30	0/1085
75	c	0.17	0/624	0.30	0/843

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	d	0.15	0/489	0.39	0/654
77	e	0.14	0/466	0.31	0/620
78	f	0.15	0/451	0.31	0/601
79	g	0.13	0/585	0.41	0/778
80	h	0.14	0/2451	0.33	0/3337
All	All	0.20	7/214230 (0.0%)	0.32	3/314402 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	A	218	A	O3'-P	-11.02	1.44	1.61
1	1	1259	A	O3'-P	-8.18	1.48	1.61
1	1	482	U	C1'-N1	6.32	1.57	1.48
1	1	477	U	C1'-N1	6.31	1.57	1.48
1	1	483	U	C1'-N1	6.12	1.57	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1259	A	P-O3'-C3'	18.97	148.66	120.20
1	1	1259	A	OP2-P-O3'	7.61	130.84	108.00
1	1	1259	A	OP1-P-O3'	-6.80	87.60	108.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	1	68595	0	34479	820	0
2	3	2579	0	1304	16	0
3	4	3353	0	1694	47	0
4	10	298	0	154	5	0
5	j	1894	0	1975	25	0
6	k	3084	0	3173	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	l	2751	0	2879	38	0
8	m	2394	0	2362	25	0
9	n	1237	0	1316	17	0
10	o	1893	0	1990	16	0
11	p	1839	0	1957	18	0
12	q	1519	0	1588	18	0
13	r	1689	0	1731	20	0
14	s	1385	0	1418	19	0
15	t	1610	0	1686	20	0
16	u	1029	0	1116	16	0
17	v	1713	0	1764	32	0
18	w	1590	0	1705	18	0
19	x	1375	0	1403	18	0
20	y	1478	0	1590	26	0
21	z	1462	0	1570	29	0
22	0	1442	0	1500	31	0
23	2	1276	0	1333	16	0
24	5	848	0	864	19	0
25	6	986	0	1040	16	0
26	7	524	0	545	7	0
27	8	974	0	1032	25	0
28	9	989	0	1064	15	0
29	AA	1087	0	1154	12	0
30	AB	1170	0	1203	20	0
31	AC	509	0	545	10	0
32	AD	729	0	775	12	0
33	AE	889	0	936	8	0
34	AF	1015	0	1095	14	0
35	AG	867	0	932	13	0
36	AH	913	0	1002	9	0
37	AI	990	0	1094	16	0
38	AJ	772	0	863	9	0
39	AK	677	0	697	12	0
40	AL	623	0	688	11	0
41	AM	446	0	488	9	0
42	AN	427	0	473	4	0
43	AO	227	0	272	5	0
44	AP	843	0	914	9	0
45	AQ	698	0	734	10	0
46	i	853	0	830	23	0
47	A	36083	0	18151	598	0
48	B	1627	0	1644	32	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	C	1724	0	1805	24	0
50	D	1620	0	1715	20	0
51	E	1707	0	1807	35	0
52	F	2055	0	2137	32	0
53	G	1614	0	1688	37	0
54	H	1820	0	1896	34	0
55	I	1466	0	1561	35	0
56	J	1579	0	1602	23	0
57	K	1453	0	1532	16	0
58	L	783	0	799	33	0
59	M	1129	0	1183	6	0
60	N	885	0	915	33	0
61	O	1187	0	1249	12	0
62	P	942	0	980	16	0
63	Q	935	0	970	31	0
64	R	1091	0	1155	26	0
65	S	1002	0	1058	32	0
66	T	1169	0	1216	24	0
67	U	1100	0	1114	19	0
68	V	790	0	855	19	0
69	W	676	0	677	14	0
70	X	1032	0	1066	13	0
71	Y	1110	0	1182	13	0
72	Z	1072	0	1123	13	0
73	a	578	0	613	18	0
74	b	799	0	860	8	0
75	c	614	0	627	3	0
76	d	487	0	523	20	0
77	e	454	0	431	9	0
78	f	444	0	483	7	0
79	g	574	0	606	29	0
80	h	2398	0	2374	55	0
81	1	20	0	38	1	0
82	1	30	0	24	4	0
83	AK	1	0	0	0	0
83	AN	1	0	0	0	0
83	AP	1	0	0	0	0
83	AQ	1	0	0	0	0
83	b	1	0	0	0	0
83	c	1	0	0	0	0
83	e	1	0	0	0	0
83	g	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	199598	0	148586	2492	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 7.

The worst 5 of 2492 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)
78:f:50:THR:OG1	78:f:53:LYS:HB2	1.28	1.33
1:1:1575:A:H2'	27:8:33:ARG:NH1	1.81	0.95
1:1:1575:A:H2'	27:8:33:ARG:HH12	1.31	0.93
4:10:1:G:H1	4:10:72:U:H3	1.10	0.92
36:AH:58:ARG:HD3	36:AH:59:PRO:HD2	1.50	0.92

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	
5	j	248/254 (98%)	240 (97%)	8 (3%)	0	100	100
6	k	385/389 (99%)	373 (97%)	12 (3%)	0	100	100
7	l	359/363 (99%)	349 (97%)	10 (3%)	0	100	100
8	m	290/298 (97%)	279 (96%)	11 (4%)	0	100	100
9	n	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
10	o	233/241 (97%)	226 (97%)	7 (3%)	0	100	100
11	p	236/262 (90%)	231 (98%)	5 (2%)	0	100	100
12	q	188/191 (98%)	183 (97%)	5 (3%)	0	100	100
13	r	204/220 (93%)	201 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	s	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
15	t	198/202 (98%)	195 (98%)	3 (2%)	0	100	100
16	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
17	v	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
18	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
19	x	168/185 (91%)	165 (98%)	3 (2%)	0	100	100
20	y	186/186 (100%)	182 (98%)	4 (2%)	0	100	100
21	z	178/190 (94%)	175 (98%)	3 (2%)	0	100	100
22	0	171/172 (99%)	170 (99%)	1 (1%)	0	100	100
23	2	159/160 (99%)	157 (99%)	2 (1%)	0	100	100
24	5	103/124 (83%)	97 (94%)	5 (5%)	1 (1%)	12	28
25	6	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
26	7	61/155 (39%)	61 (100%)	0	0	100	100
27	8	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
28	9	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
29	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
30	AB	146/149 (98%)	138 (94%)	8 (6%)	0	100	100
31	AC	62/63 (98%)	61 (98%)	1 (2%)	0	100	100
32	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
33	AE	107/112 (96%)	106 (99%)	1 (1%)	0	100	100
34	AF	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
35	AG	107/107 (100%)	104 (97%)	3 (3%)	0	100	100
36	AH	114/122 (93%)	112 (98%)	2 (2%)	0	100	100
37	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
38	AJ	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
39	AK	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
40	AL	76/78 (97%)	73 (96%)	3 (4%)	0	100	100
41	AM	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
42	AN	51/52 (98%)	51 (100%)	0	0	100	100
43	AO	22/25 (88%)	22 (100%)	0	0	100	100
44	AP	101/106 (95%)	100 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
46	i	109/267 (41%)	102 (94%)	7 (6%)	0	100	100
48	B	206/261 (79%)	201 (98%)	5 (2%)	0	100	100
49	C	212/256 (83%)	207 (98%)	5 (2%)	0	100	100
50	D	214/249 (86%)	209 (98%)	5 (2%)	0	100	100
51	E	221/251 (88%)	214 (97%)	7 (3%)	0	100	100
52	F	258/262 (98%)	254 (98%)	4 (2%)	0	100	100
53	G	204/225 (91%)	197 (97%)	7 (3%)	0	100	100
54	H	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
55	I	180/186 (97%)	174 (97%)	6 (3%)	0	100	100
56	J	201/206 (98%)	200 (100%)	1 (0%)	0	100	100
57	K	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
58	L	91/118 (77%)	84 (92%)	6 (7%)	1 (1%)	11	26
59	M	139/155 (90%)	136 (98%)	3 (2%)	0	100	100
60	N	114/143 (80%)	96 (84%)	18 (16%)	0	100	100
61	O	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
62	P	123/132 (93%)	119 (97%)	4 (3%)	0	100	100
63	Q	116/142 (82%)	107 (92%)	9 (8%)	0	100	100
64	R	138/142 (97%)	134 (97%)	4 (3%)	0	100	100
65	S	123/137 (90%)	120 (98%)	3 (2%)	0	100	100
66	T	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
67	U	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
68	V	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
69	W	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
70	X	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
71	Y	141/145 (97%)	139 (99%)	0	2 (1%)	9	21
72	Z	130/135 (96%)	130 (100%)	0	0	100	100
73	a	70/105 (67%)	69 (99%)	1 (1%)	0	100	100
74	b	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
75	c	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
76	d	60/67 (90%)	55 (92%)	5 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
77	e	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
78	f	54/63 (86%)	52 (96%)	2 (4%)	0	100	100
79	g	68/193 (35%)	61 (90%)	7 (10%)	0	100	100
80	h	309/317 (98%)	291 (94%)	18 (6%)	0	100	100
All	All	11010/12138 (91%)	10714 (97%)	292 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	L	88	PRO
24	5	20	ALA
71	Y	90	ASP
71	Y	89	ASN

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	
5	j	191/194 (98%)	191 (100%)	0	100	100
6	k	326/328 (99%)	326 (100%)	0	100	100
7	l	290/292 (99%)	290 (100%)	0	100	100
8	m	247/252 (98%)	247 (100%)	0	100	100
9	n	135/154 (88%)	135 (100%)	0	100	100
10	o	199/204 (98%)	199 (100%)	0	100	100
11	p	198/216 (92%)	198 (100%)	0	100	100
12	q	169/170 (99%)	169 (100%)	0	100	100
13	r	178/186 (96%)	178 (100%)	0	100	100
14	s	148/149 (99%)	148 (100%)	0	100	100
15	t	166/168 (99%)	165 (99%)	1 (1%)	78	90
16	u	108/109 (99%)	108 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	v	177/178 (99%)	177 (100%)	0	100	100
18	w	166/167 (99%)	166 (100%)	0	100	100
19	x	142/154 (92%)	141 (99%)	1 (1%)	76	89
20	y	156/154 (101%)	156 (100%)	0	100	100
21	z	147/153 (96%)	147 (100%)	0	100	100
22	0	158/157 (101%)	158 (100%)	0	100	100
23	2	135/134 (101%)	135 (100%)	0	100	100
24	5	95/112 (85%)	93 (98%)	2 (2%)	47	73
25	6	101/103 (98%)	101 (100%)	0	100	100
26	7	57/127 (45%)	57 (100%)	0	100	100
27	8	108/121 (89%)	108 (100%)	0	100	100
28	9	111/112 (99%)	111 (100%)	0	100	100
29	AA	117/118 (99%)	117 (100%)	0	100	100
30	AB	120/121 (99%)	120 (100%)	0	100	100
31	AC	50/49 (102%)	50 (100%)	0	100	100
32	AD	81/90 (90%)	81 (100%)	0	100	100
33	AE	98/100 (98%)	98 (100%)	0	100	100
34	AF	111/115 (96%)	111 (100%)	0	100	100
35	AG	94/92 (102%)	94 (100%)	0	100	100
36	AH	99/102 (97%)	99 (100%)	0	100	100
37	AI	106/106 (100%)	106 (100%)	0	100	100
38	AJ	79/79 (100%)	79 (100%)	0	100	100
39	AK	70/73 (96%)	70 (100%)	0	100	100
40	AL	69/69 (100%)	69 (100%)	0	100	100
41	AM	47/47 (100%)	47 (100%)	0	100	100
42	AN	48/47 (102%)	48 (100%)	0	100	100
43	AO	23/24 (96%)	23 (100%)	0	100	100
44	AP	88/89 (99%)	88 (100%)	0	100	100
45	AQ	72/73 (99%)	72 (100%)	0	100	100
46	i	92/212 (43%)	92 (100%)	0	100	100
48	B	176/215 (82%)	176 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	C	194/229 (85%)	194 (100%)	0	100	100
50	D	174/198 (88%)	174 (100%)	0	100	100
51	E	174/196 (89%)	174 (100%)	0	100	100
52	F	218/220 (99%)	218 (100%)	0	100	100
53	G	178/197 (90%)	178 (100%)	0	100	100
54	H	195/204 (96%)	195 (100%)	0	100	100
55	I	163/167 (98%)	163 (100%)	0	100	100
56	J	157/160 (98%)	157 (100%)	0	100	100
57	K	153/160 (96%)	153 (100%)	0	100	100
58	L	87/104 (84%)	87 (100%)	0	100	100
59	M	122/134 (91%)	122 (100%)	0	100	100
60	N	98/123 (80%)	98 (100%)	0	100	100
61	O	129/130 (99%)	129 (100%)	0	100	100
62	P	96/101 (95%)	96 (100%)	0	100	100
63	Q	102/121 (84%)	102 (100%)	0	100	100
64	R	114/116 (98%)	114 (100%)	0	100	100
65	S	112/122 (92%)	112 (100%)	0	100	100
66	T	126/129 (98%)	126 (100%)	0	100	100
67	U	113/117 (97%)	113 (100%)	0	100	100
68	V	90/105 (86%)	90 (100%)	0	100	100
69	W	71/71 (100%)	71 (100%)	0	100	100
70	X	112/113 (99%)	112 (100%)	0	100	100
71	Y	116/118 (98%)	116 (100%)	0	100	100
72	Z	109/112 (97%)	109 (100%)	0	100	100
73	a	64/85 (75%)	64 (100%)	0	100	100
74	b	86/102 (84%)	86 (100%)	0	100	100
75	c	72/73 (99%)	72 (100%)	0	100	100
76	d	54/58 (93%)	54 (100%)	0	100	100
77	e	47/48 (98%)	47 (100%)	0	100	100
78	f	48/54 (89%)	48 (100%)	0	100	100
79	g	62/175 (35%)	62 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	h	259/263 (98%)	259 (100%)	0	100	100
All	All	9443/10220 (92%)	9439 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	t	5	LYS
19	x	165	GLN
24	5	31[A]	GLU
24	5	31[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
59	M	92	HIS
61	O	62	GLN
66	T	92	GLN
22	0	13	ASN
21	z	134	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3205/3359 (95%)	561 (17%)	36 (1%)
2	3	120/121 (99%)	9 (7%)	0
3	4	157/158 (99%)	24 (15%)	3 (1%)
4	10	12/77 (15%)	2 (16%)	0
47	A	1685/1787 (94%)	390 (23%)	47 (2%)
All	All	5179/5502 (94%)	986 (19%)	86 (1%)

5 of 986 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	24	U
1	1	25	A
1	1	29	G
1	1	39	A
1	1	42	A

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	A	553	A
47	A	1335	U
47	A	638	U
47	A	820	U
47	A	1396	A

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

6 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	$\# Z > 2$
25	MLZ	6	110	25	8,9,10	0.73	0	4,9,11	0.90	0
44	MLZ	AP	55	44	8,9,10	0.68	0	4,9,11	0.81	0
1	OMG	1	2765	1	23,26,27	2.35	9 (39%)	32,38,41	1.86	9 (28%)
1	OMC	1	2808	1	19,22,23	2.97	8 (42%)	25,31,34	1.21	3 (12%)
44	MLZ	AP	40	44	8,9,10	0.72	0	4,9,11	0.94	0
62	IAS	P	119	62	6,7,8	1.05	0	3,8,10	1.66	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
25	MLZ	6	110	25	-	3/7/8/10	-
44	MLZ	AP	55	44	-	3/7/8/10	-
1	OMG	1	2765	1	-	0/9/27/28	0/3/3/3
1	OMC	1	2808	1	-	3/9/27/28	0/2/2/2
44	MLZ	AP	40	44	-	0/7/8/10	-
62	IAS	P	119	62	-	1/7/7/8	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2808	OMC	C2-N3	6.33	1.48	1.36
1	1	2765	OMG	C4-N3	6.29	1.48	1.34
1	1	2808	OMC	C6-C5	5.80	1.48	1.35
1	1	2765	OMG	C2-N3	5.34	1.46	1.33
1	1	2808	OMC	C2-N1	4.86	1.50	1.40

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2765	OMG	C5-C4-N3	-4.68	120.94	128.39
1	1	2765	OMG	C2-N3-C4	4.58	120.19	112.30
1	1	2765	OMG	N9-C8-N7	-3.24	107.39	113.40
1	1	2808	OMC	O2-C2-N3	-3.17	117.34	122.33
1	1	2765	OMG	C2-N1-C6	-2.89	119.87	125.11

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	2808	OMC	O4'-C1'-N1-C2
1	1	2808	OMC	O4'-C1'-N1-C6
25	6	110	MLZ	N-CA-CB-CG
25	6	110	MLZ	C-CA-CB-CG
25	6	110	MLZ	CD-CE-NZ-CM

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2808	OMC	3	0
62	P	119	IAS	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 8 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	$\# Z > 2$
81	SPD	1	3401	-	9,9,9	0.31	0	8,8,8	0.83	0
82	BLS	1	3403	-	30,31,31	0.67	1 (3%)	30,43,43	0.74	1 (3%)
81	SPD	1	3402	-	9,9,9	0.16	0	8,8,8	0.20	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
81	SPD	1	3401	-	-	1/7/7/7	-
82	BLS	1	3403	-	-	6/25/38/38	0/2/2/2
81	SPD	1	3402	-	-	4/7/7/7	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	1	3403	BLS	O4-C6'	-3.05	1.20	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	1	3403	BLS	N15-C14-N12	2.08	120.92	118.64

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

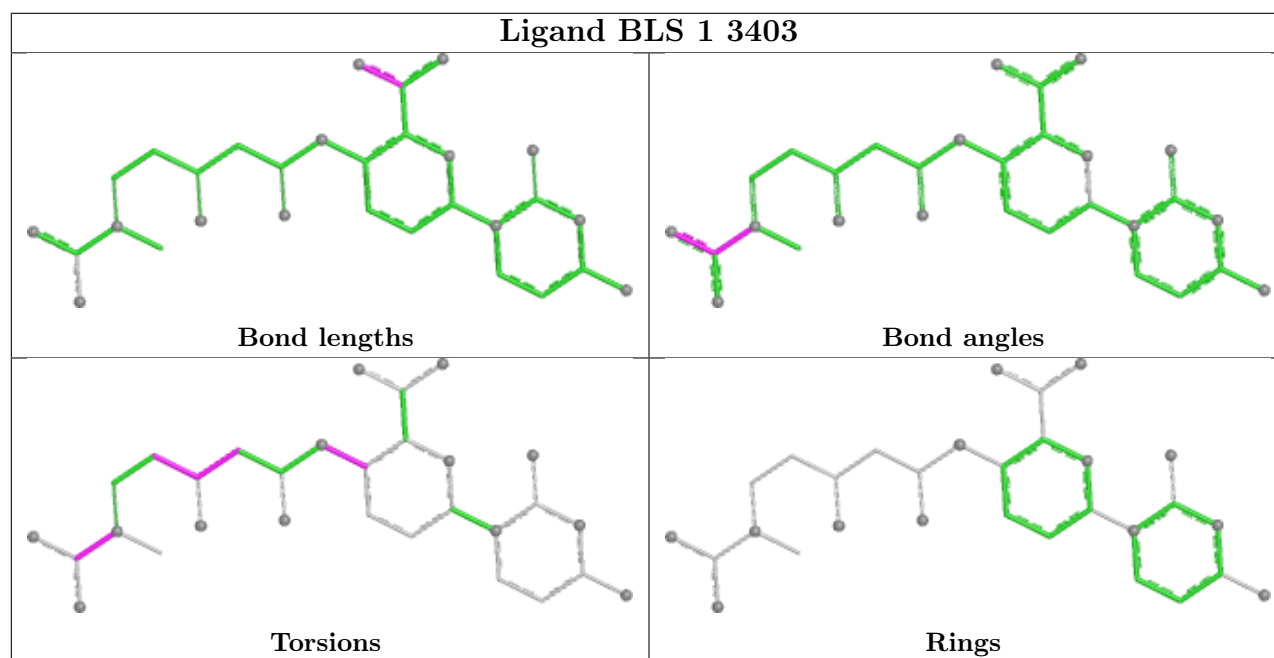
Mol	Chain	Res	Type	Atoms
82	1	3403	BLS	C7-C8-C9-N9
82	1	3403	BLS	C11-C10-C9-C8
82	1	3403	BLS	C11-C10-C9-N9
81	1	3402	SPD	C4-C5-N6-C7
81	1	3402	SPD	C7-C8-C9-N10

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	1	3401	SPD	1	0
82	1	3403	BLS	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

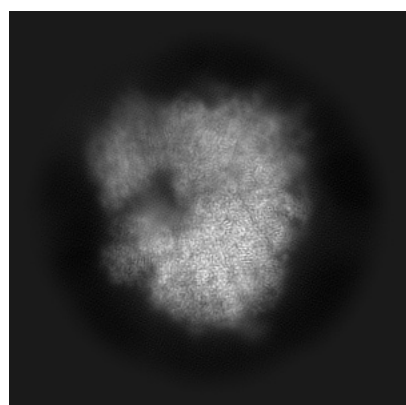
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13750. These allow visual inspection of the internal detail of the map and identification of artifacts.

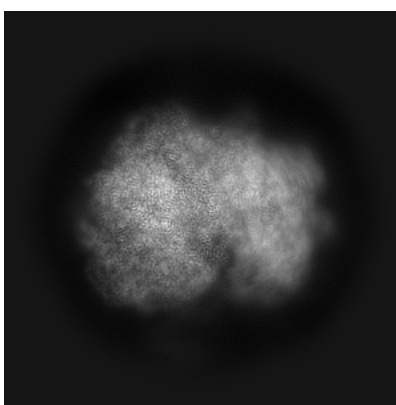
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

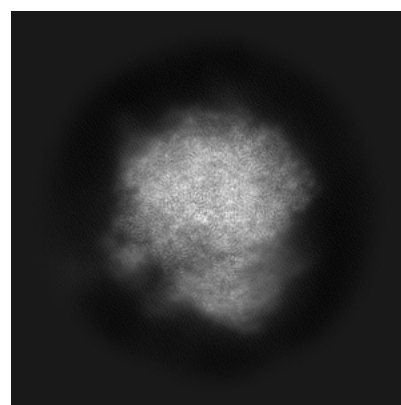
6.1.1 Primary map



X



Y

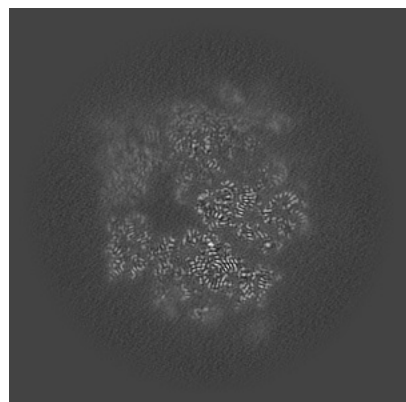


Z

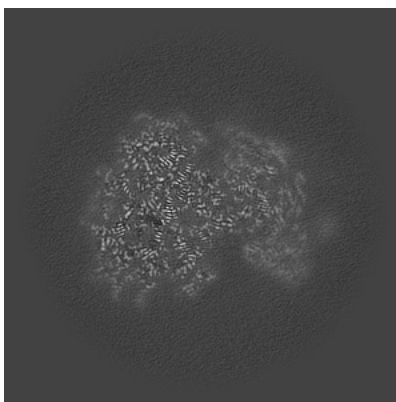
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

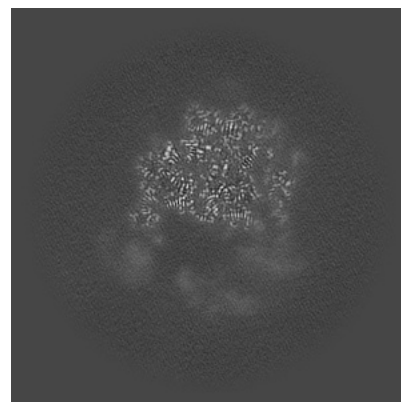
6.2.1 Primary map



X Index: 255



Y Index: 255

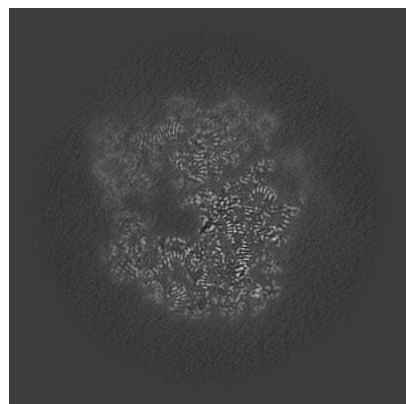


Z Index: 255

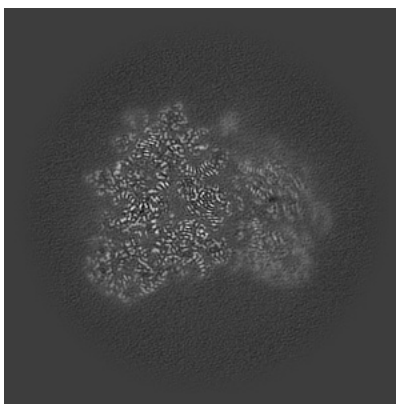
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

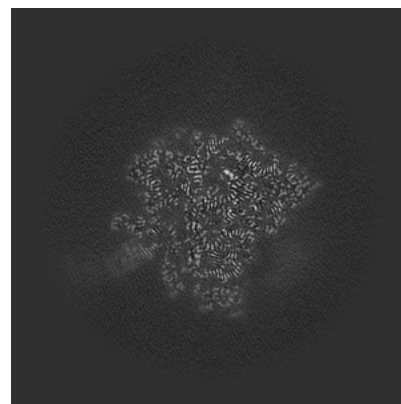
6.3.1 Primary map



X Index: 275



Y Index: 273

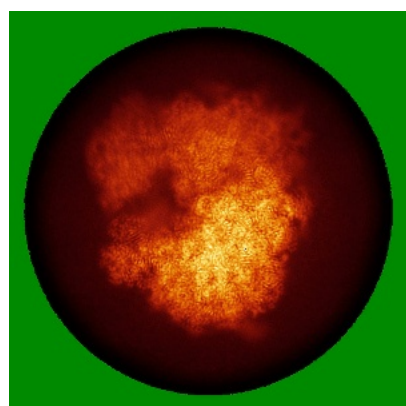


Z Index: 206

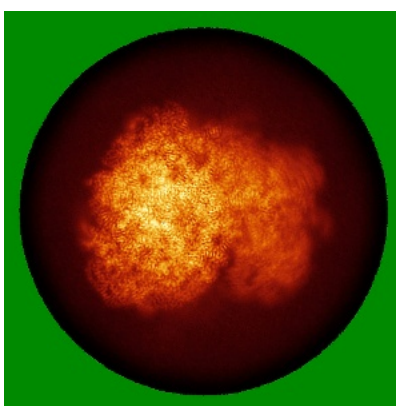
The images above show the largest variance slices of the map in three orthogonal directions.

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

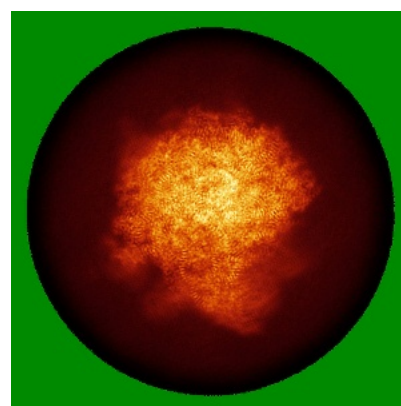
6.4.1 Primary map



X



Y

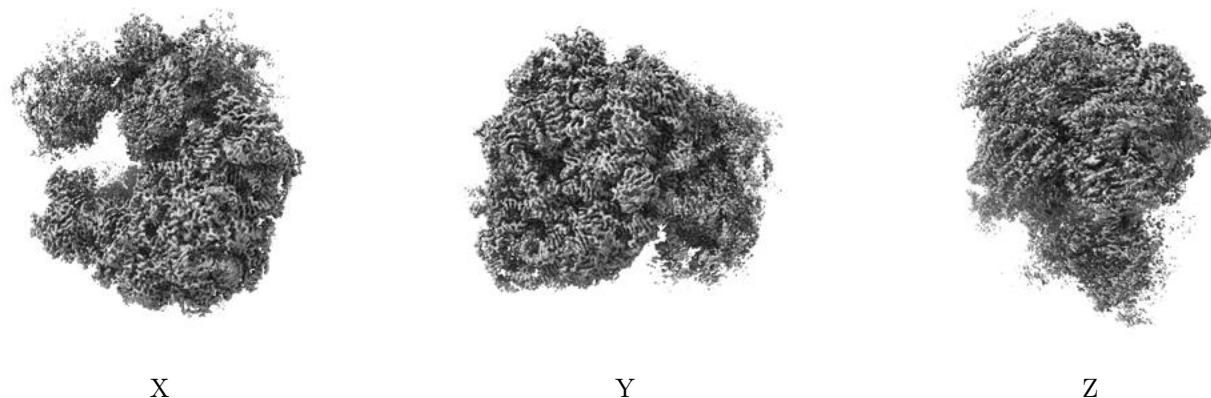


Z

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

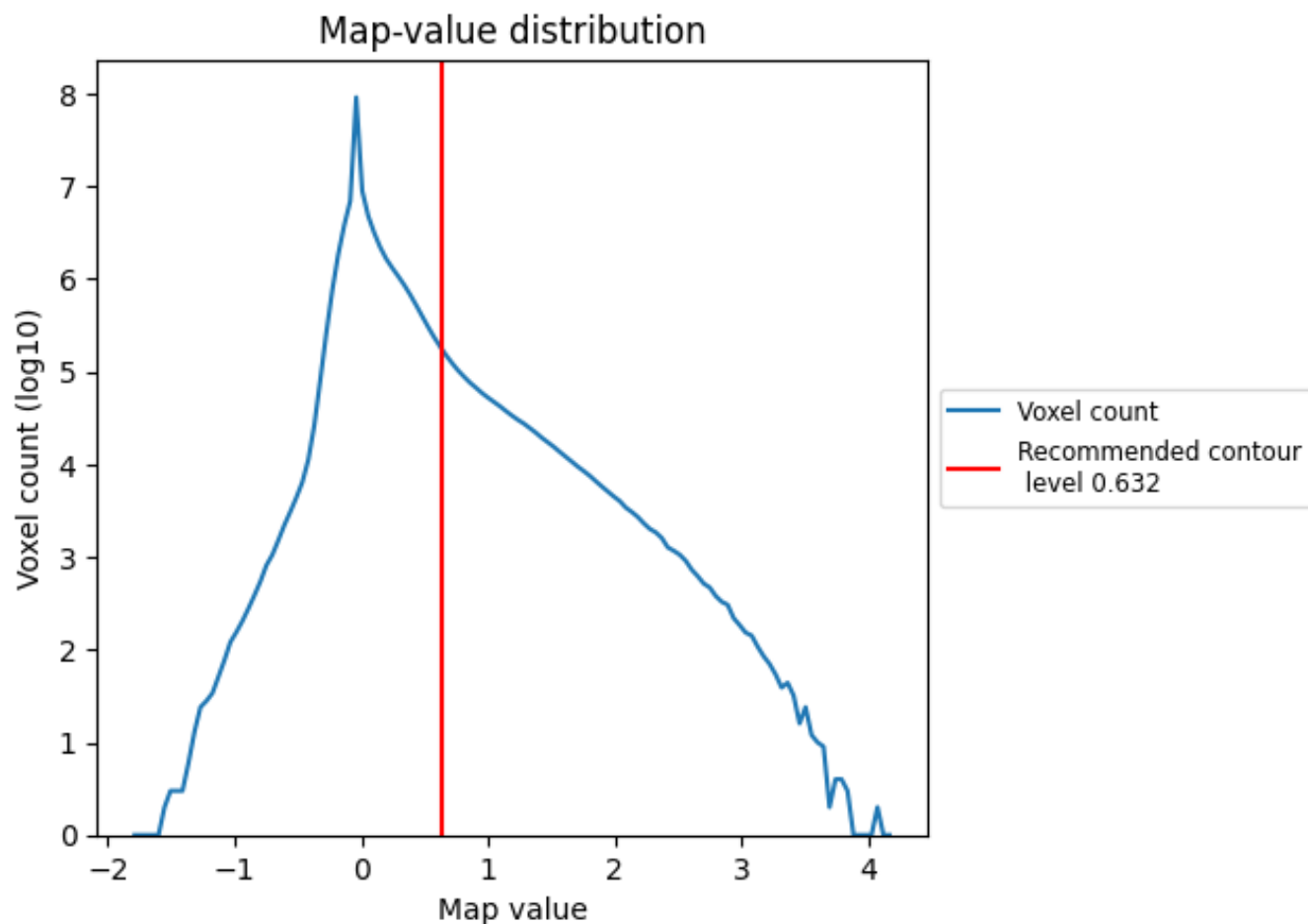
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

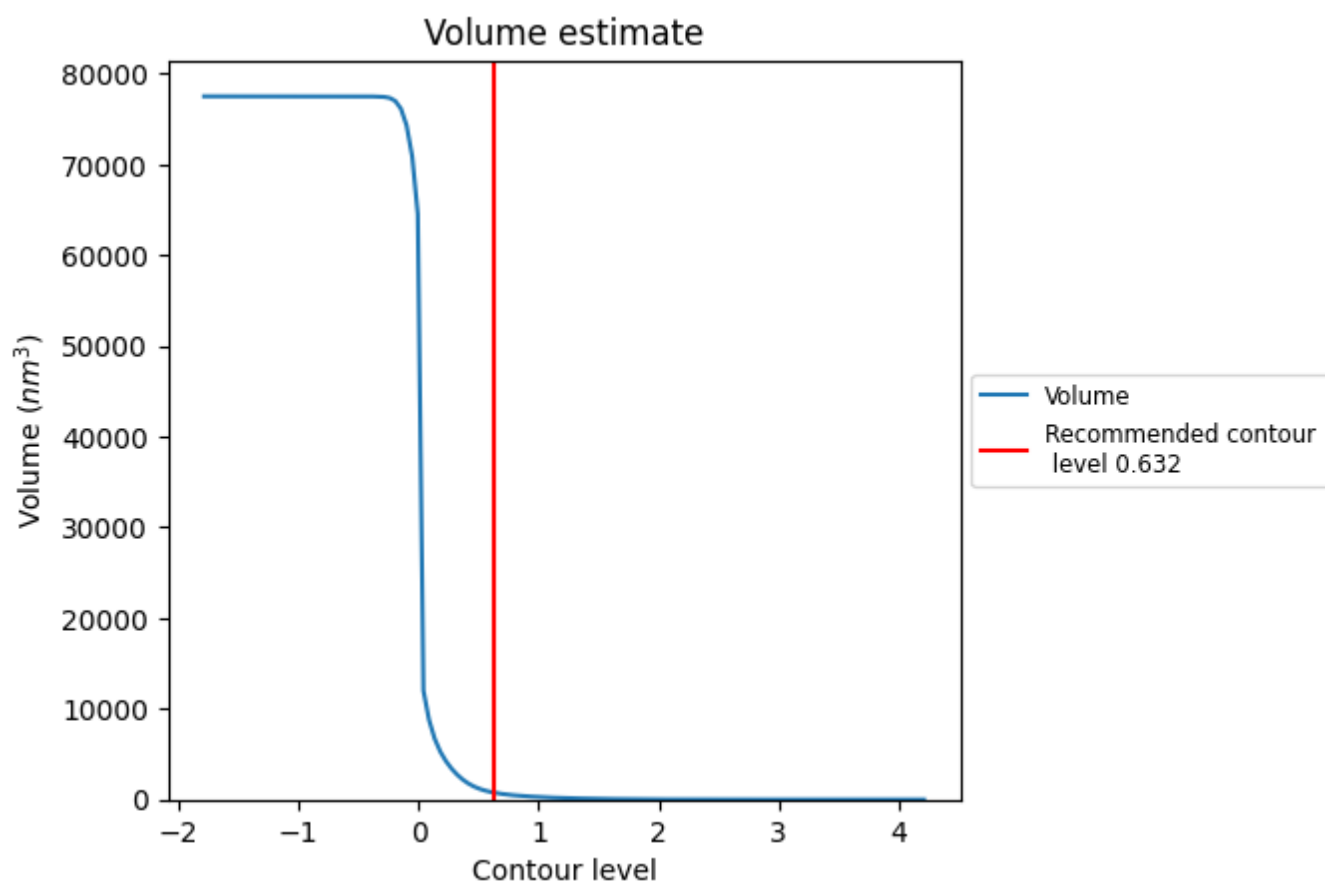
This section contains the results of statistical analysis of the map.

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.

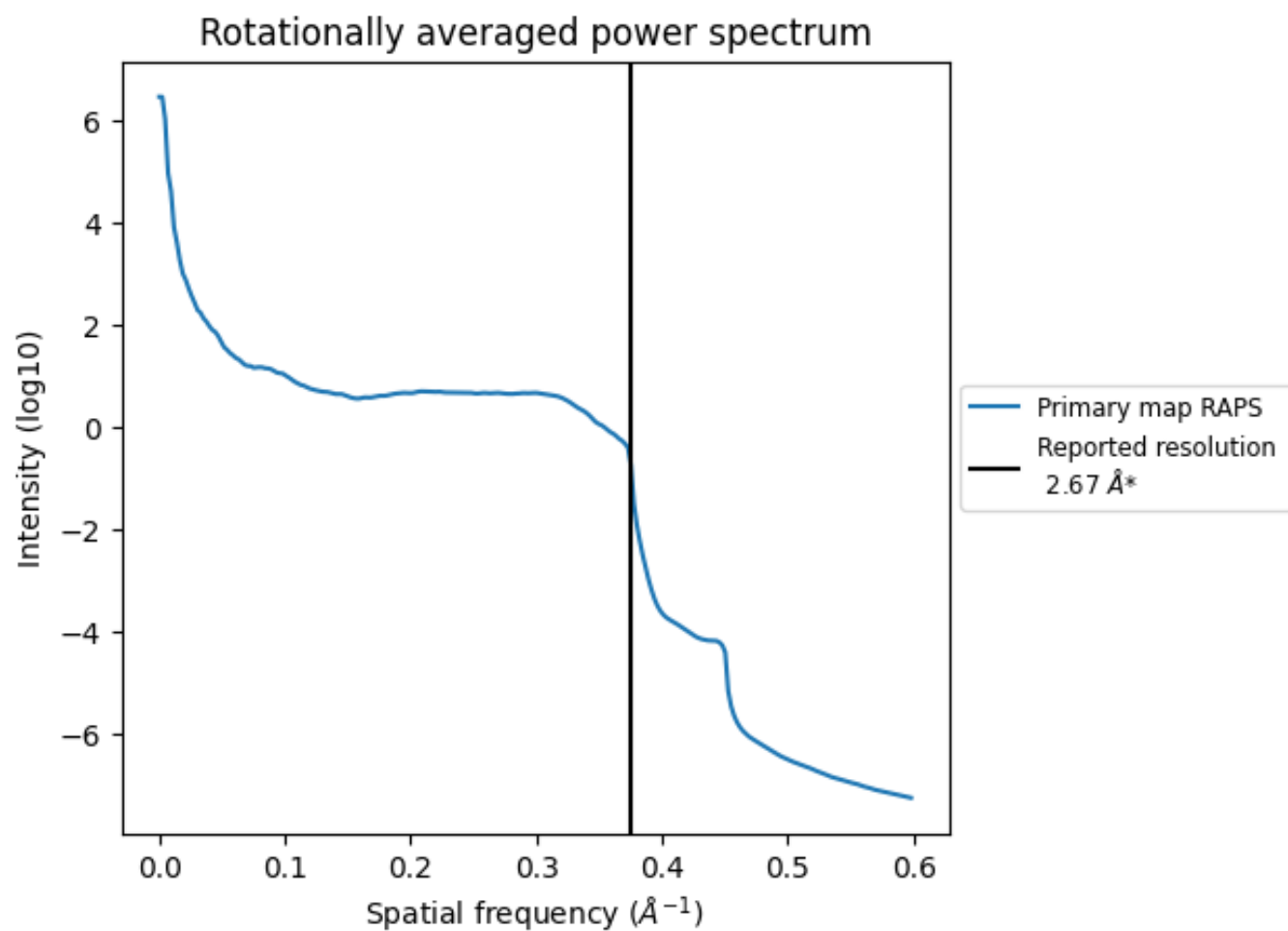
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 755 nm^3 ; this corresponds to an approximate mass of 682 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 ⓘ

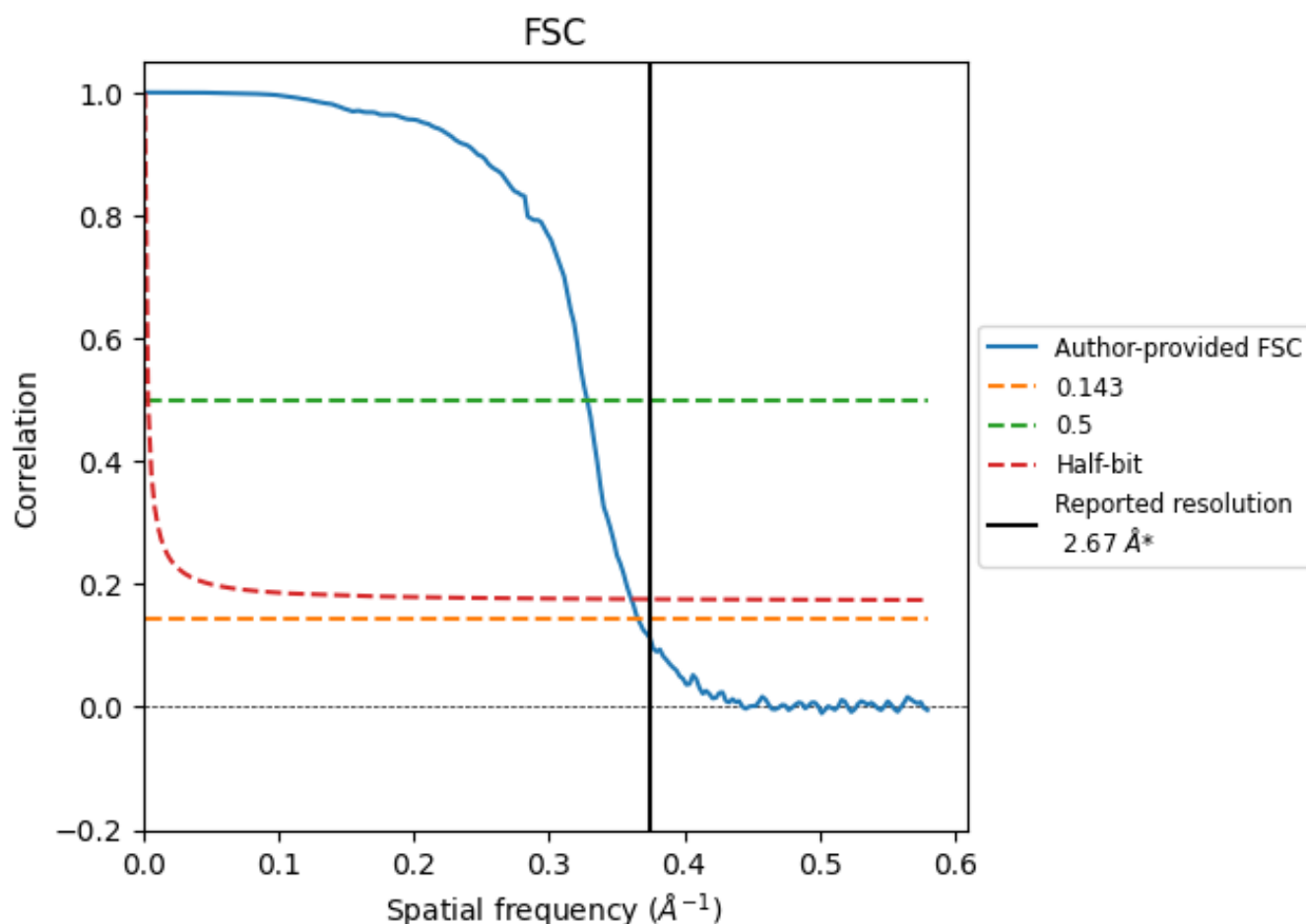


*Reported resolution corresponds to spatial frequency of 0.375 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.375 Å⁻¹

8.2 Resolution estimates [i](#)

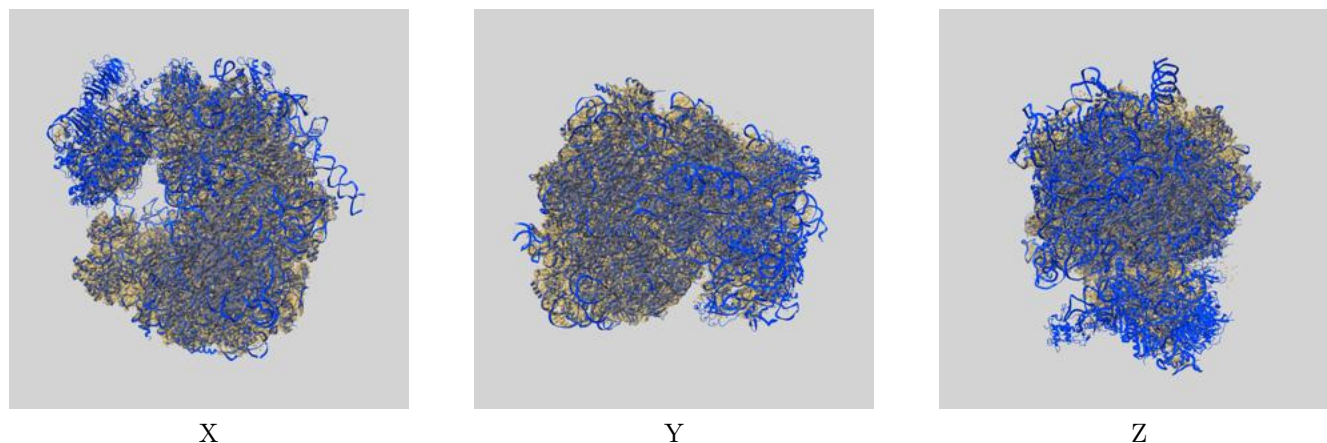
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.73	3.05	2.77
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

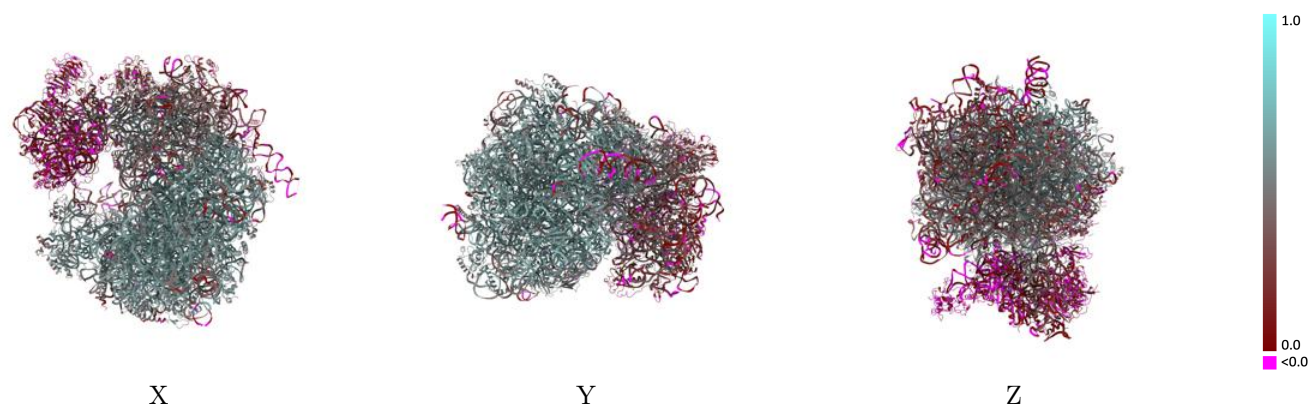
This section contains information regarding the fit between EMDB map EMD-13750 and PDB model 7Q0R. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



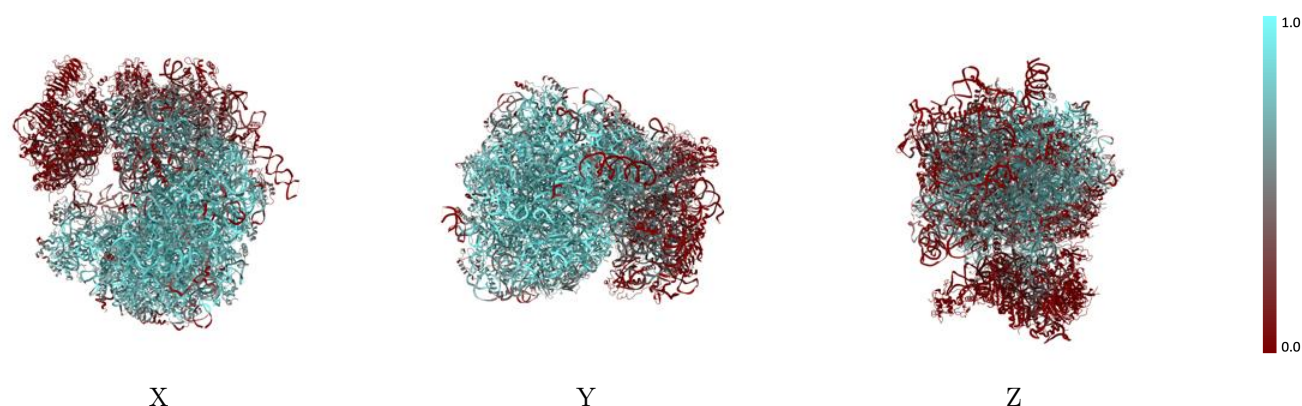
The images above show the 3D surface view of the map at the recommended contour level 0.632 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



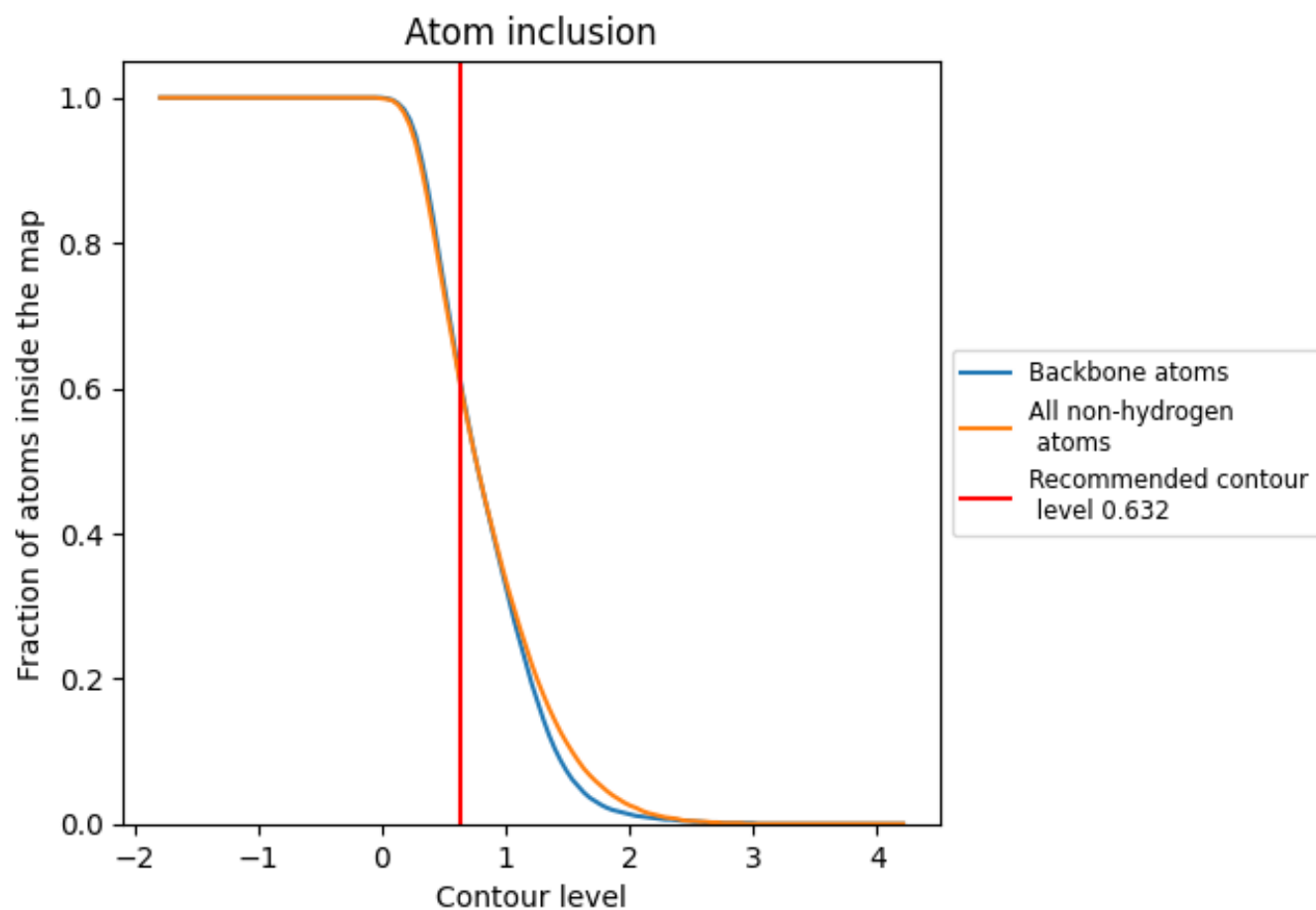
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.632).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 61% 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 (0.632) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6070	 0.4480
0	 0.7570	 0.5820
1	 0.8420	 0.5610
10	 0.1510	 0.3800
2	 0.7160	 0.5530
3	 0.8870	 0.5850
4	 0.8960	 0.5870
5	 0.4880	 0.4490
6	 0.8000	 0.5860
7	 0.7860	 0.5770
8	 0.7700	 0.5570
9	 0.7130	 0.5390
A	 0.4340	 0.3120
AA	 0.6810	 0.5490
AB	 0.8210	 0.5870
AC	 0.6600	 0.4950
AD	 0.7630	 0.5510
AE	 0.7380	 0.5690
AF	 0.8120	 0.5880
AG	 0.8410	 0.6140
AH	 0.7780	 0.5770
AI	 0.7010	 0.5330
AJ	 0.6610	 0.5210
AK	 0.8710	 0.6140
AL	 0.5370	 0.4940
AM	 0.8250	 0.5790
AN	 0.7290	 0.5550
AO	 0.4710	 0.4930
AP	 0.7290	 0.5580
AQ	 0.7910	 0.5900
B	 0.2010	 0.2870
C	 0.2720	 0.3510
D	 0.3010	 0.3480
E	 0.0380	 0.0780
F	 0.1660	 0.2630



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
G	 0.0200	 0.0750
H	 0.0840	 0.2160
I	 0.1390	 0.2810
J	 0.2460	 0.2830
K	 0.1800	 0.2800
L	 0.0140	 0.0080
M	 0.2600	 0.2820
N	 0.0000	 0.0070
O	 0.4660	 0.4060
P	 0.3250	 0.4100
Q	 0.0150	 0.0630
R	 0.0560	 0.1740
S	 0.0610	 0.2160
T	 0.0270	 0.0660
U	 0.0320	 0.1240
V	 0.0310	 0.0930
W	 0.2130	 0.2830
X	 0.3760	 0.3920
Y	 0.3060	 0.3210
Z	 0.0810	 0.2390
a	 0.0020	 0.0420
b	 0.5050	 0.4280
c	 0.3020	 0.3370
d	 0.0360	 0.0750
e	 0.0460	 0.0700
f	 0.1190	 0.2180
g	 0.0020	 -0.0260
h	 0.0040	 0.1120
i	 0.0180	 0.1440
j	 0.8600	 0.6180
k	 0.8140	 0.5980
l	 0.7330	 0.5600
m	 0.6070	 0.4940
n	 0.5880	 0.5210
o	 0.7410	 0.5630
p	 0.6210	 0.5120
q	 0.6400	 0.5200
r	 0.7090	 0.5550
s	 0.5180	 0.4670
t	 0.6960	 0.5340
u	 0.6670	 0.5380
v	 0.8860	 0.6160

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
w	 0.7850	 0.5880
x	 0.8440	 0.5870
y	 0.8000	 0.5790
z	 0.7020	 0.5340