



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 05:49 pm BST

PDB ID : 9QZP / pdb_00009qzp
EMDB ID : EMD-53473
Title : Mouse Ribosome Classical Pre translocation state
Authors : Santo, P.E.; Astier, A.; Plisson-Chastang, C.
Deposited on : 2025-04-23
Resolution : 3.43 Å(reported)
Based on initial model : 7LS1

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 : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

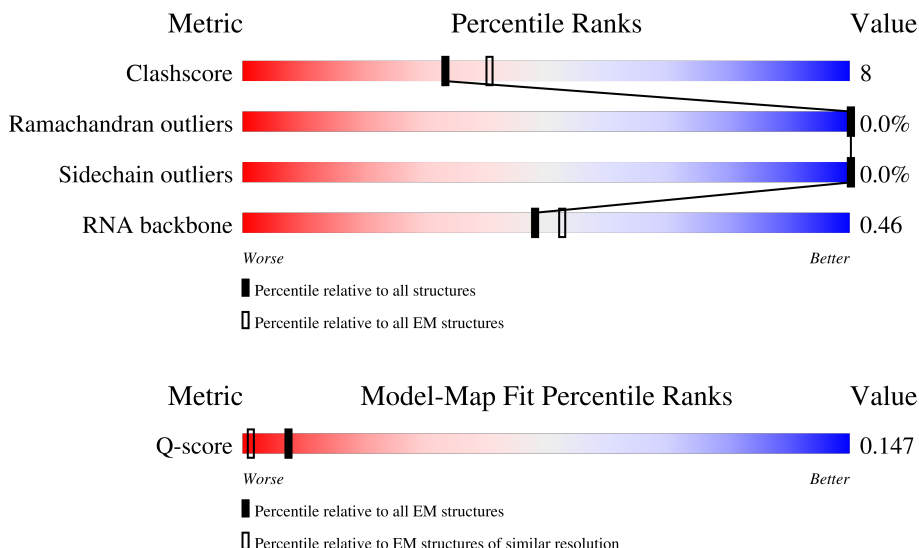
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.43 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	13927 (2.93 - 3.93)

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	A1	270	55% 63% 19% 18%
2	A2	3615	65% 56% 37% 7%
3	A3	152	91% 60% 32% 8%

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Mol	Chain	Length	Quality of chain
4	B1	266	
5	B2	121	
6	B3	145	
7	Bv	76	
7	Bz	76	
7	n2	76	
8	Bx	10	
9	By	22	
10	C1	192	
11	C2	156	
12	C3	119	
13	D1	214	
14	D2	257	
15	D3	83	
16	E1	178	
17	E2	403	
18	E3	143	
19	F1	211	
20	F2	419	
21	F3	115	
22	G1	217	
23	G2	297	
24	G3	69	
25	H1	204	
26	H2	296	

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Mol	Chain	Length	Quality of chain
27	H3	56	
28	I2	203	
29	I3	317	
30	J2	184	
31	J3	293	
32	K2	188	
33	K3	249	
34	L1	217	
35	L2	196	
36	L3	194	
37	M2	176	
38	M3	132	
39	N2	160	
40	N3	151	
41	O2	128	
42	O3	151	
43	P2	140	
44	P3	130	
45	Q2	157	
46	Q3	133	
47	R2	156	
48	R3	125	
49	S2	145	
50	S3	84	
51	T2	136	

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Mol	Chain	Length	Quality of chain
52	T3	133	
53	U2	148	
54	U3	156	
55	V2	160	
56	W2	115	
57	X2	125	
58	Y2	135	
59	Z2	110	
60	a2	117	
61	b2	123	
62	c2	105	
63	d2	97	
64	e2	70	
65	f2	51	
66	g2	128	
67	h2	25	
68	i2	106	
69	j2	92	
70	k2	137	
71	o2	295	
72	p2	264	
73	q2	243	
74	r2	263	
75	s2	204	
76	t2	194	

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Mol	Chain	Length	Quality of chain
77	u2	208	97% 76% 23%
78	v2	165	58% 39% 18% 42%
79	w2	158	91% 79% 16% 5%
80	x2	145	90% 58% 33% 9%
81	y2	146	96% 80% 17%
82	z2	135	50% 38% 13% 49%
83	m2	1635	86% 43% 47% 9%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 214961 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 Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	222	Total	C	N	O	S	1	0
			1851	1190	356	297	8		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	3615	Total	C	N	O	P	0	0
			77547	34568	14148	25217	3614		

- Molecule 3 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A3	140	Total	C	N	O	S	0	0
			1151	725	228	197	1		

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B1	223	Total	C	N	O	S	1	0
			1812	1156	351	301	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B2	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 6 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B3	141	Total	C	N	O	S	0	0
			1104	691	215	196	2		

- Molecule 7 is a RNA chain called transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bv	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
7	Bz	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		
7	n2	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 8 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bx	10	Total	C	N	O	P	0	0
			200	90	20	80	10		

- Molecule 9 is a protein called Nascent protein chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	By	22	Total	C	N	O	0	0
			110	66	22	22		

- Molecule 10 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C1	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

- Molecule 11 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C2	156	Total	C	N	O	P	0	0
			3315	1481	585	1094	155		

- Molecule 12 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C3	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D1	204	Total	C	N	O	S	0	0
			1656	1052	319	272	13		

- Molecule 14 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D2	251	Total	C	N	O	S	0	0
			1921	1204	393	318	6		

- Molecule 15 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D3	83	Total	C	N	O	S	0	0
			638	392	119	122	5		

- Molecule 16 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E1	174	Total	C	N	O	S	0	0
			1397	880	260	251	6		

- Molecule 17 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E2	402	Total	C	N	O	S	0	0
			3238	2060	609	555	14		

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E3	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 19 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F1	203	Total	C	N	O	S	0	0
			1643	1029	339	271	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	F2	359	Total	C	N	O	S	0	0
			2867	1803	573	476	15		

- Molecule 21 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	F3	98	Total	C	N	O	S	1	0
			789	491	164	129	5		

- Molecule 22 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	G1	139	Total	C	N	O	S	0	0
			1143	732	221	183	7		

- Molecule 23 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	G2	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

- Molecule 24 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	G3	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 25 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	H1	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 26 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	H2	221	Total	C	N	O	S	0	0
			1789	1145	342	298	4		

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H3	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 28 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	I2	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 29 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	I3	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 30 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	J2	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 31 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J3	219	Total	C	N	O	S	0	0
			1700	1101	292	298	9		

- Molecule 32 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K2	186	Total	C	N	O	S	0	0
			1511	946	313	248	4		

- Molecule 33 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K3	227	Total	C	N	O	S	0	0
			1840	1149	367	317	7		

- Molecule 34 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L1	161	Total	C	N	O	S	0	0
			1300	833	230	231	6		

- Molecule 35 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L2	179	Total	C	N	O	S	0	0
			1499	927	326	237	9		

- Molecule 36 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L3	184	Total	C	N	O	S	0	0
			1518	964	305	247	2		

- Molecule 37 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M2	175	Total	C	N	O	S	0	0
			1450	924	283	233	10		

- Molecule 38 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M3	122	Total	C	N	O	S	0	0
			952	599	168	177	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M3	69	LEU	CYS	variant	UNP P63323

- Molecule 39 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N2	159	Total	C	N	O	S	0	0
			1299	824	252	217	6		

- Molecule 40 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	N3	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 41 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	O2	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 42 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	O3	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	P2	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 44 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	P3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 45 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Q2	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 46 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Q3	122	Total	C	N	O	S	0	0
			1002	635	196	166	5		

- Molecule 47 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	R2	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 48 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R3	72	Total	C	N	O	S	0	0
			570	366	104	99	1		

- Molecule 49 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 50 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S3	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 51 is a protein called Large ribosomal subunit protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	T2	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 52 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T3	55	Total	C	N	O	S	0	0
			438	271	95	71	1		

- Molecule 53 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	U2	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 54 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	U3	52	Total	C	N	O	S	0	0
			415	260	74	74	7		

- Molecule 55 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	V2	117	Total	C	N	O	S	0	0
			945	596	198	146	5		

- Molecule 56 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	W2	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 57 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	X2	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 58 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Y2	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 59 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z2	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 60 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	a2	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

- Molecule 61 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	b2	120	Total	C	N	O	S	0	0
			1001	634	201	165	1		

- Molecule 62 is a protein called Large ribosomal subunit protein eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	c2	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 63 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	d2	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 64 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	e2	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 65 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	f2	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 66 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	g2	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 67 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	h2	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 68 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	i2	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 69 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	j2	89	Total	C	N	O	S	0	0
			694	436	133	118	7		

- Molecule 70 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	k2	125	Total	C	N	O	S	0	0
			1001	621	207	168	5		

- Molecule 71 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	o2	214	Total	C	N	O	S	0	0
			1694	1077	297	312	8		

- Molecule 72 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	p2	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 73 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	q2	220	Total	C	N	O	S	0	0
			1711	1092	308	304	7		

- Molecule 74 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	r2	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 75 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	s2	183	Total	C	N	O	S	0	0
			1457	912	275	263	7		

- Molecule 76 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	t2	183	Total	C	N	O		0	0
			1278	822	243	213			

- Molecule 77 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	u2	206	Total	C	N	O	S	0	0
			1633	1025	322	281	5		

- Molecule 78 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	v2	95	Total	C	N	O	S	0	0
			800	522	142	131	5		

- Molecule 79 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	w2	150	Total	C	N	O	S	0	0
			1220	776	228	210	6		

- Molecule 80 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	x2	132	Total	C	N	O	S	0	0
			1081	688	203	183	7		

- Molecule 81 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	y2	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 82 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	z2	69	Total	C	N	O	S	0	0
			560	354	113	91	2		

- Molecule 83 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	m2	1635	Total	C	N	O	P	0	0
			34939	15614	6270	11420	1635		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
84	A2	82	Total	Mg	0
			82	82	
84	Bv	2	Total	Mg	0
			2	2	
84	H1	1	Total	Mg	0
			1	1	
84	J2	1	Total	Mg	0
			1	1	
84	P2	1	Total	Mg	0
			1	1	
84	d2	1	Total	Mg	0
			1	1	
84	m2	30	Total	Mg	0
			30	30	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
85	F3	1	Total	Zn	0
			1	1	
85	H3	1	Total	Zn	0
			1	1	
85	d2	1	Total	Zn	0
			1	1	
85	g2	1	Total	Zn	0
			1	1	
85	i2	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
85	j2	1	Total	Zn	0
			1	1	

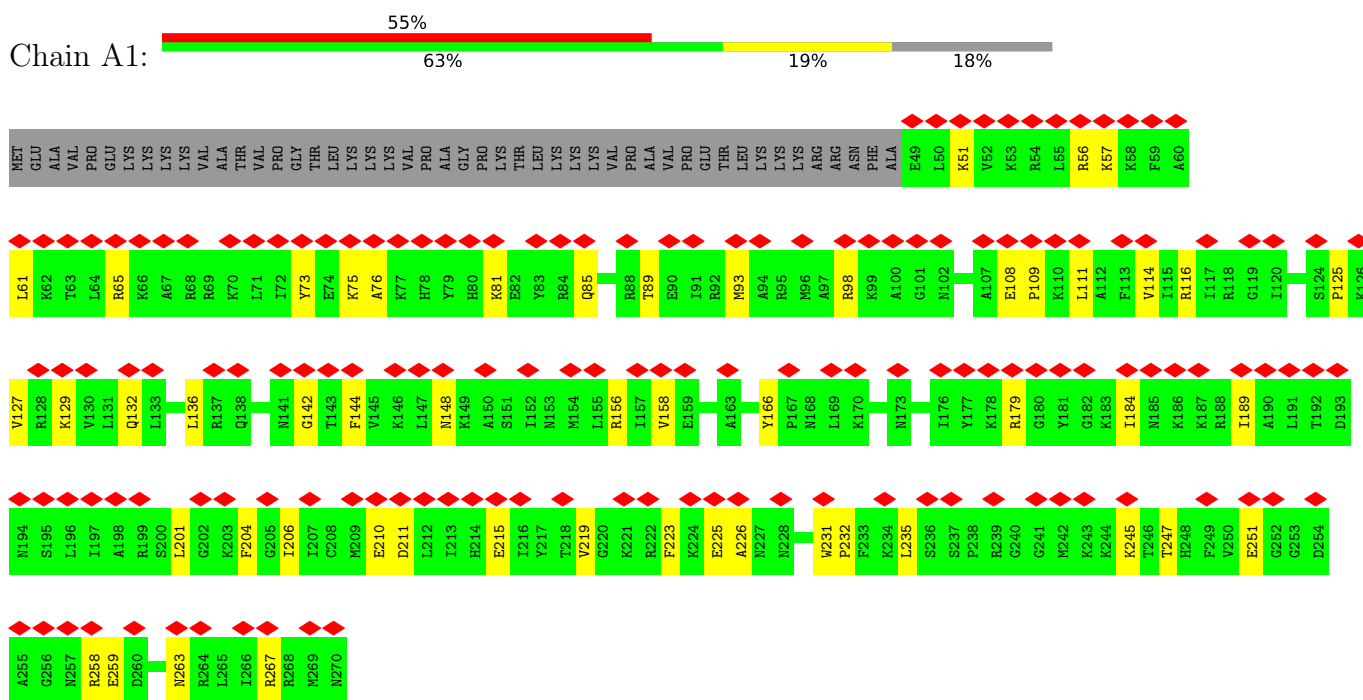
- Molecule 86 is water.

Mol	Chain	Residues	Atoms		AltConf
86	B1	1	Total	O	0
			1	1	

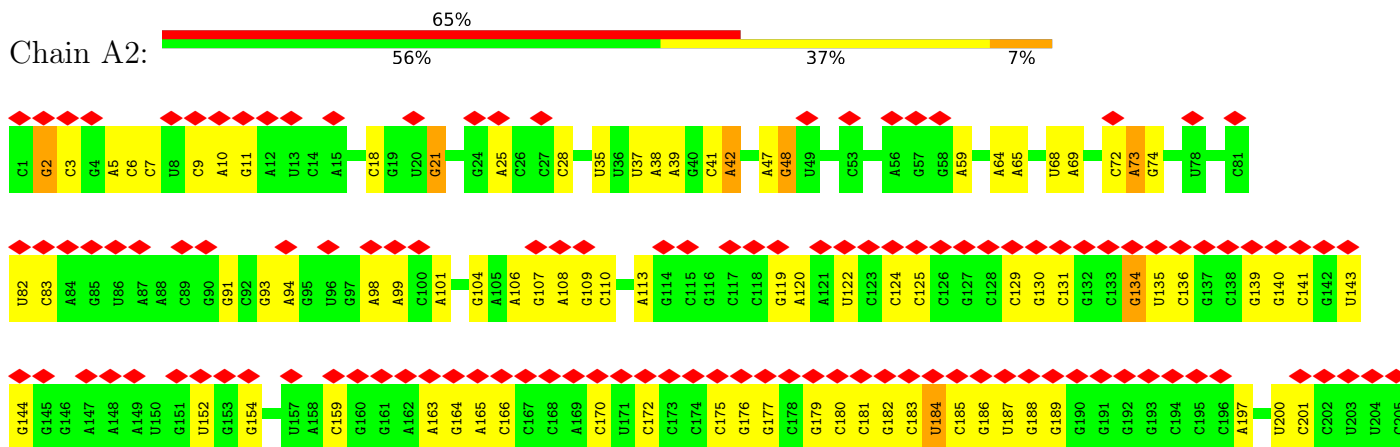
3 Residue-property plots

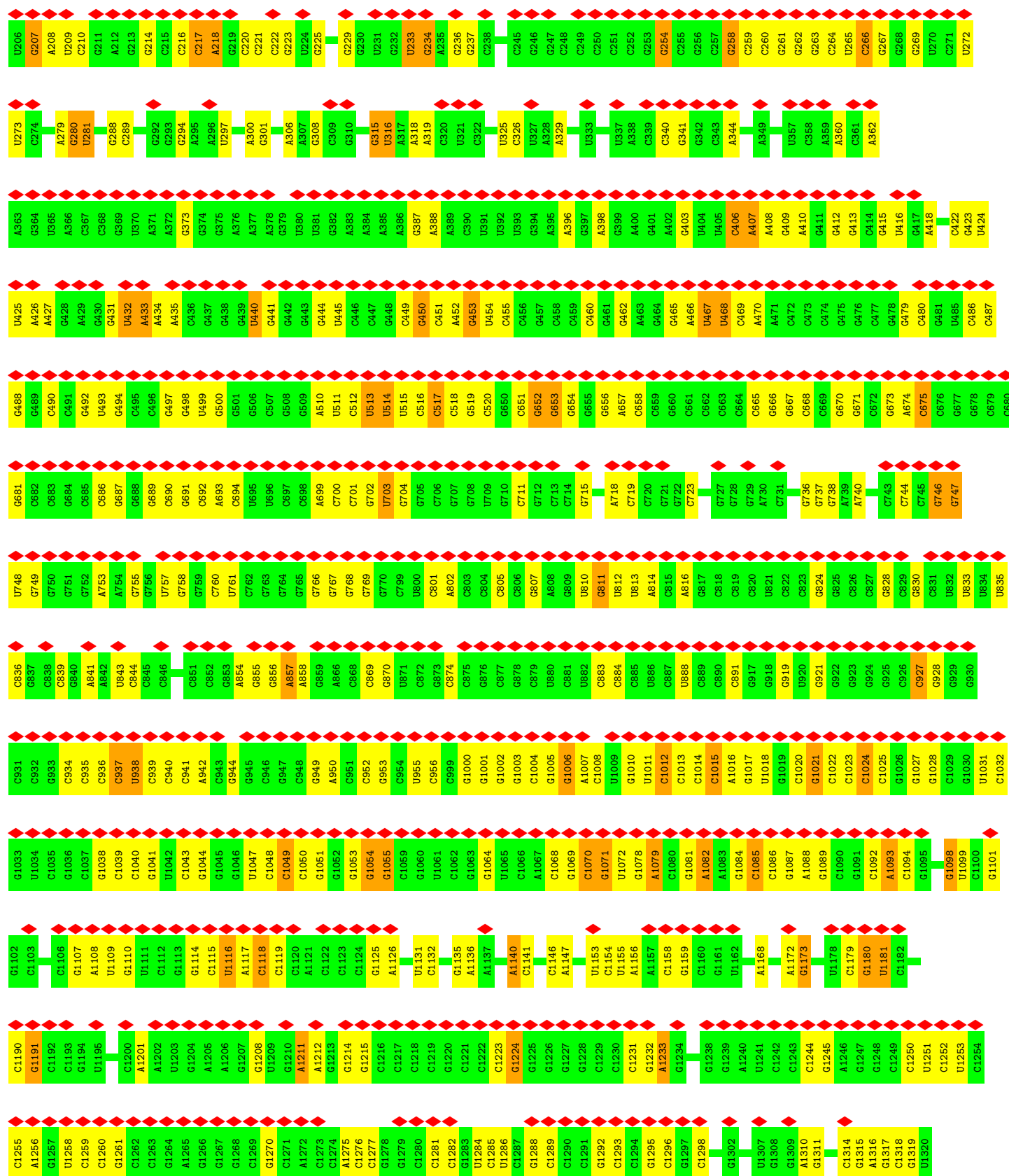
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Large ribosomal subunit protein uL30



- Molecule 2: 28S ribosomal RNA

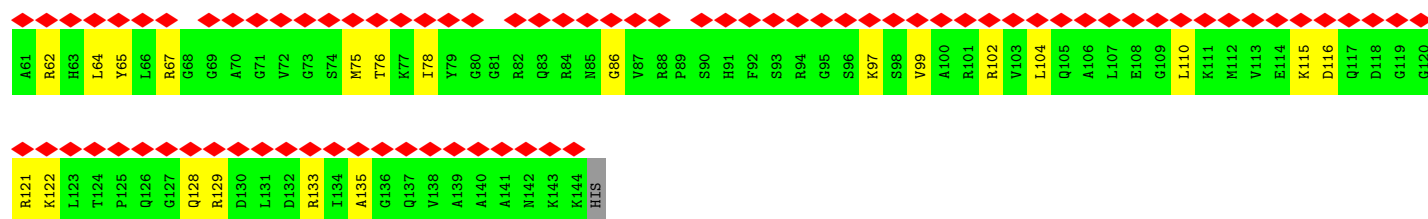




U2279	U2280	C2281	A2282	C2283	A2284	U2285	C2286	C2287	C2288	C2289	A2291	A2292	U2293	C2294	C2295	U2296	C2297	A2298	C2299	U2300	C2301	C2302	C2303	C2304	C2305	A2306	C2307	A2308	U2309	C2310	C2311	C2312	C2313	U2314	C2315	C2316	C2317	C2318	C2319	A2320	C2321	C2322	C2323	C2324	U2325	C2326	C2327	A2328	U2329	U2330	C2331	C2332	C2333	U2334	C2335	A2336	A2337	C2338
G2216	U2217	G2218	C2219	C2220	C2221	U2222	U2223	C2224	C2225	C2226	A2227	A2228	G2229	U2230	G2231	A2232	C2233	C2234	C2235	C2236	C2237	C2238	A2239	U2240	C2241	G2242	C2243	C2244	U2245	C2246	C2247	C2248	U2249	U2250	G2251	C2252	C2253	C2254	U2255	C2256	C2257	C2258	C2259	C2260	G2261	C2264	A2267	A2268	C2269	G2270	C2273	U2274	C2275	C2276	G2277	G2278		
C2147	C2148	G2149	A2150	A2151	G2152	C2153	G2154	G2155	A2156	G2157	A2158	A2159	G2160	G2161	G2162	U2163	U2164	C2165	C2166	A2167	U2168	G2169	U2170	G2171	A2172	A2173	C2174	A2175	G2176	C2177	A2178	G2179	U2180	U2181	G2182	C2185	U2191	C2192	A2193	G2194	C2195	C2196	U2199	C2200	C2201	U2202	G2203	A2204	G2205	A2208	C2212	C2213	G2214	A2215				
C2081	G2085	G2086	A2087	G2088	C2089	C2090	G2091	C2092	C2093	G2094	C2095	A2096	G2097	G2098	U2099	G2100	C2101	A2102	G2103	C2106	U2107	U2111	G2112	A2115	G2116	U2117	A2118	G2119	C2120	A2123	U2124	A2125	U2126	U2127	C2128	A2129	A2130	A2131	C2132	C2133	C2134	G2135	A2136	C2137	C2138	U2139	U2140	U2141	G2142	A2143	A2144	G2145	G2146					
G2004	U2005	C2006	G2007	G2008	G2009	C2010	C2011	C2012	C2013	G2014	C2015	G2016	G2017	A2018	C2019	C2020	C2021	U2022	A2023	C2024	G2025	C2026	C2027	G2030	A2031	C2032	C2033	A2034	A2037	C2044	C2047	U2048	C2049	C2050	G2051	G2052	A2055	C2056	C2057	C2058	U2059	U2060	G2061	A2062	C2065	C2066	U2067	A2068	C2069	G2070	G2071	G2077						
G1848	A1849	U1850	C1853	G1854	C1855	U1856	G1857	G1858	A1859	G1862	U1863	C1864	G1865	G1866	G1867	C1868	C1869	C1870	A1871	U1872	A1873	C1874	G1878	G1881	U1882	C1883	G1884	C1885	C1886	G1887	G1891	U1892	C1893	G1894	G1895	A1896	A1897	C1898	G1899	G1900	A1901	A1902	C1903	G1904	G1905	G1906	A1907	G1908	G1909	G1910	G1911	A1912	G1913	C1914				
C1728	U1729	U1732	C1733	A1734	G1735	A1736	C1737	C1738	C1739	G1742	A1743	A1744	A1745	U1749	G1750	G1753	U1756	G1757	A1758	U1759	A1760	U1761	A1762	G1763	A1764	C1765	A1766	G1767	C1768	A1769	G1770	G1771	A1772	C1821	U1822	G1823	C1824	C1825	G1826	A1827	A1828	U1829	C1830	A1831	A1832	G1836	C1837	G1841	U1846	G1847								
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A1595	A1596	A1597	U1598	G1599	G1600	G1601	U1602	A1603	A1604	G1605	A1606	A1607	G1608	C1611	G1612	G1613	C1614	G1617	C1618	U1619	G1620	G1621	C1622	G1623	U1624	G1625	G1626	A1627	G1628	C1629	G1630	G1631	G1632	G1633	C1634	G1635	U1636	G1637	G1638	A1639	A1640	U1641	G1642	C1643	G1644	A1645	G1646	U1647	U1648	G1649	C1650	U1651	A1652	G1653	U1654	G1655	G1656	
U1528	U1529	U1530	A1531	U1532	C1533	G1534	G1535	U1536	U1537	A1538	G1539	A1540	G1541	C1542	G1543	A1544	A1545	U1546	G1547	A1548	U1549	A1551	U1552	A1553	G1554	G1555	U1556	C1557	U1558	U1559	G1560	G1561	G1562	G1563	C1564	A1572	U1573	C1574	C1575	C1576	A1577	U1578	C1579	C1580	U1581	A1582	U1583	U1584	C1585	U1586	C1587	A1588	U1589	A1590	C1591	U1592	U1593	U1594
A1447	C1448	U1449	A1450	A1451	U1452	C1453	G1454	A1455	A1456	C1457	U1458	A1459	G1467	C1468	U1469	U1470	U1473	C1474	C1475	C1476	A1482	G1483	U1486	C1487	C1488	C1489	U1490	C1491	A1492	G1493	U1496	A1497	G1498	C1499	U1500	G1501	G1502	C1503	G1504	C1505	U1506	C1507	U1508	C1509	G1510	U1511	C1512	A1521	C1522	G1523	C1524	A1525	G1526	U1527				
G1384	U1385	G1386	G1387	A1388	G1389	G1390	U1391	C1392	C1393	G1394	U1395	A1396	G1397	C1398	G1399	G1400	U1401	C1402	U1404	G1405	A1406	C1407	A1408	U1409	A1413	A1414	U1415	C1416	G1417	U1418	U1419	U1422	C1423	C1424	G1425	A1426	C1427	C1428	U1429	G1430	G1431	G1432	U1433	A1434	U1435	A1436	G1437	U1438	G1439	G1440	C1441	U1442	A1443	A1444	A1445	G1446		
A1321	C1322	G1323	C1324	U1325	U1326	G1329	G1330	A1331	C1332	C1333	C1334	A1337	A1338	U1341	G1342	G1343	U1344	G1345	A1346	A1347	C1348	U1349	A1350	U1351	G1352	C1353	U1354	U1355	G1356	G1357	U1358	C1359	A1360	G1361	G1362	G1363	C1364	G1365	A1366	A1367	G1368	C1369	C1370	A1371	G1372	A1373	G1374	G1375	A1376	A1377	A1378	C1379	U1380	C1381	U1382	G1383		







• Molecule 7: transfer RNA



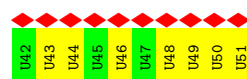
• Molecule 7: transfer RNA



• Molecule 7: transfer RNA



• Molecule 8: messenger RNA

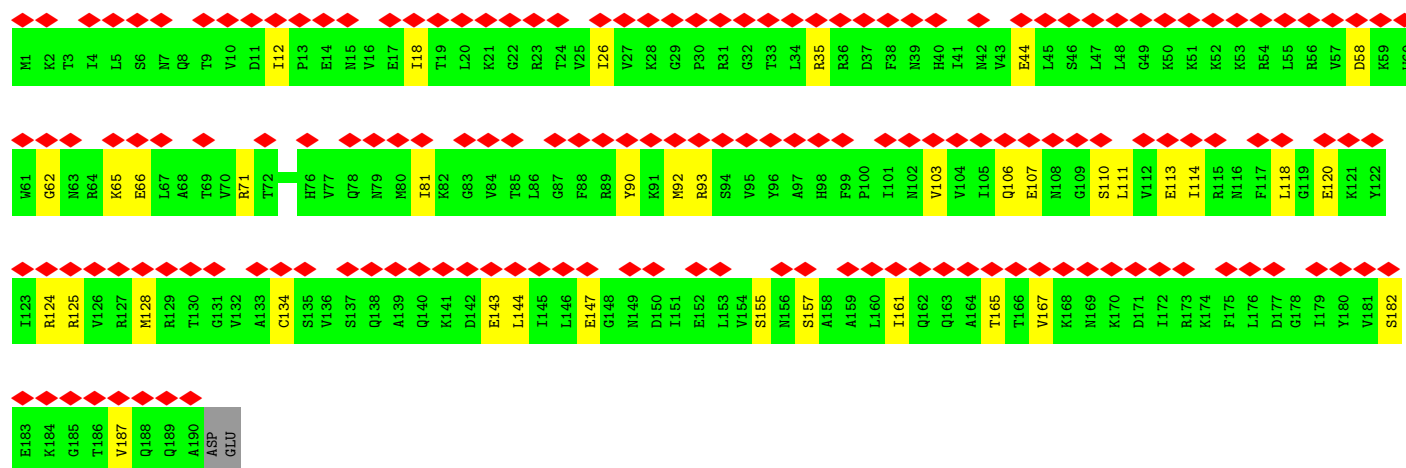
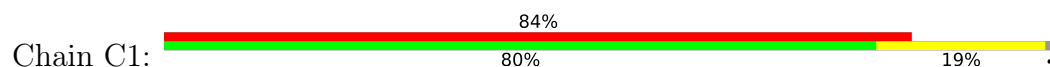


• Molecule 9: Nascent protein chain

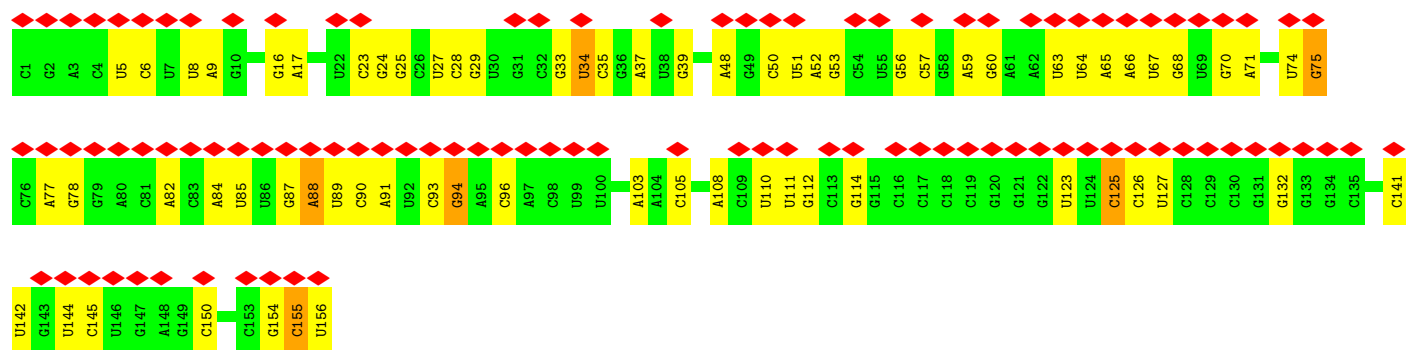




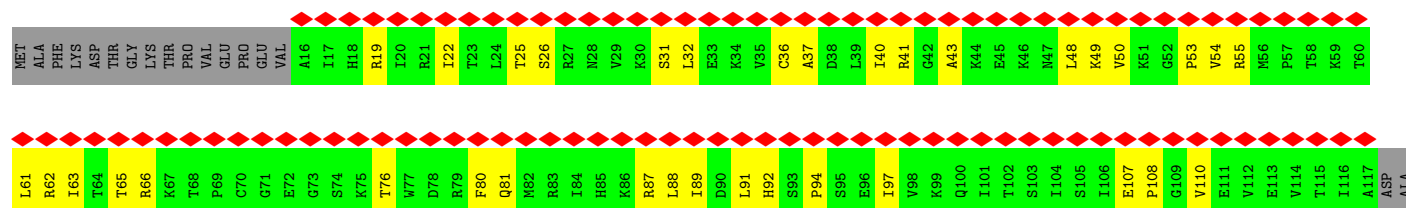
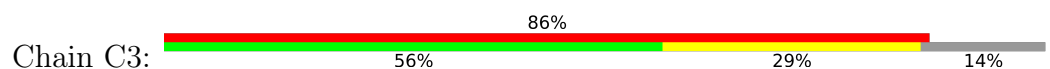
• Molecule 10: Large ribosomal subunit protein uL6



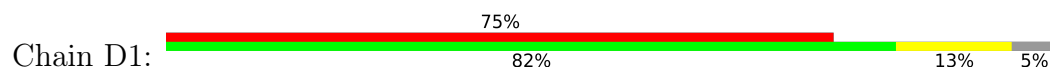
• Molecule 11: 5.8S ribosomal RNA

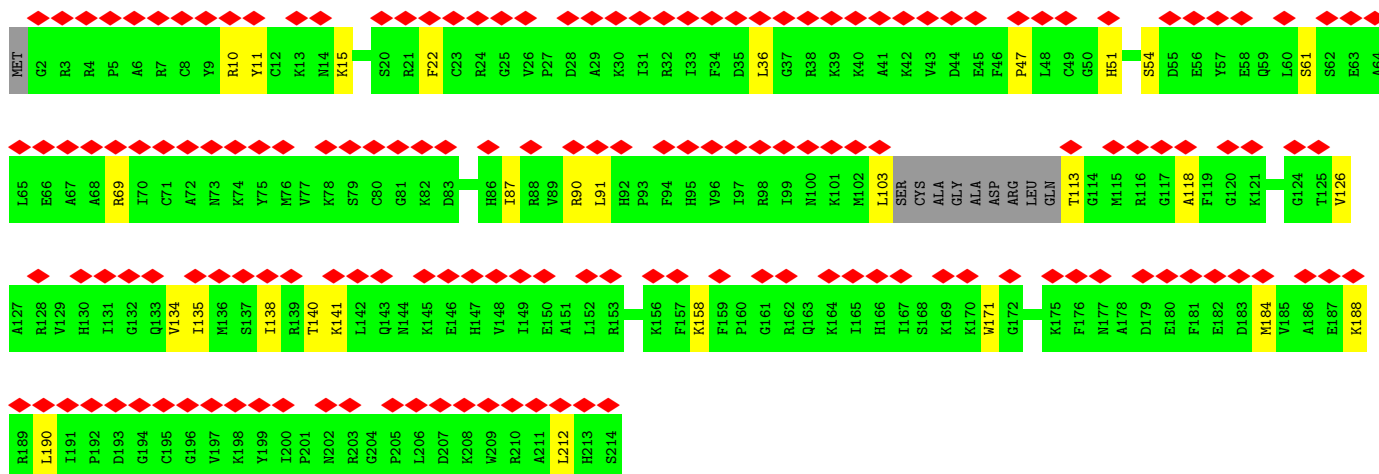


• Molecule 12: Small ribosomal subunit protein uS10

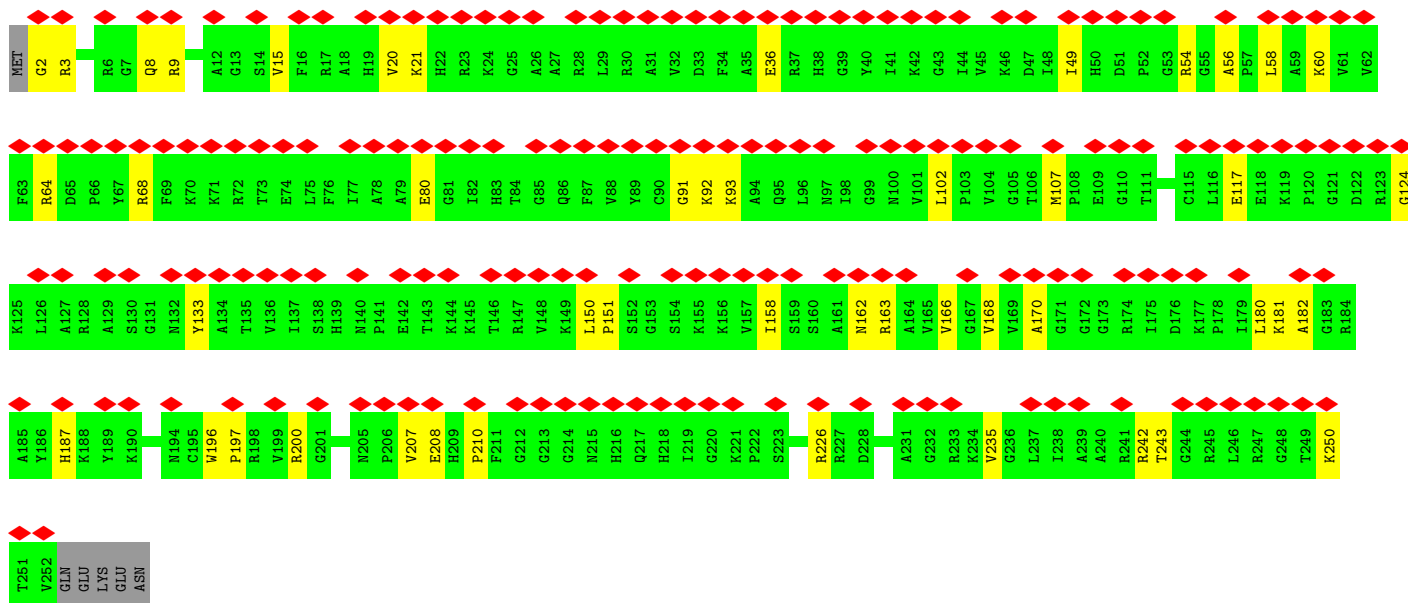
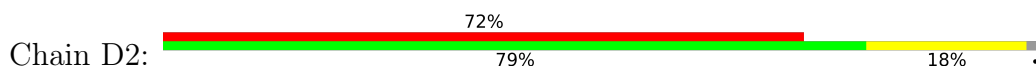


• Molecule 13: Large ribosomal subunit protein uL16

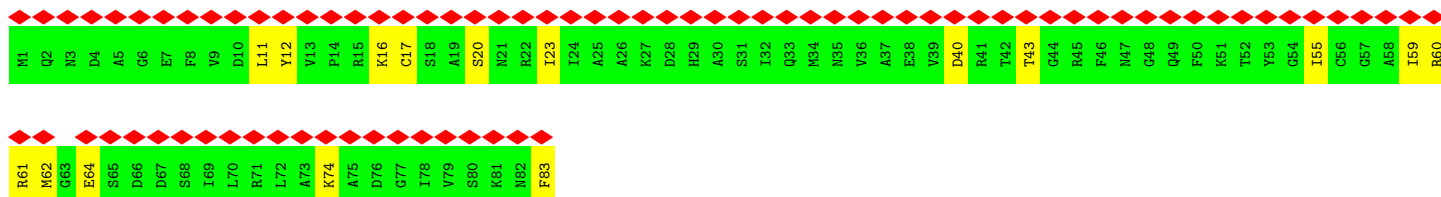
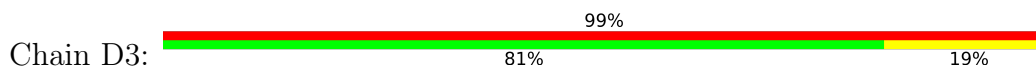




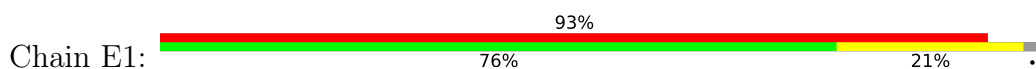
- Molecule 14: Large ribosomal subunit protein uL2



- Molecule 15: Small ribosomal subunit protein eS21

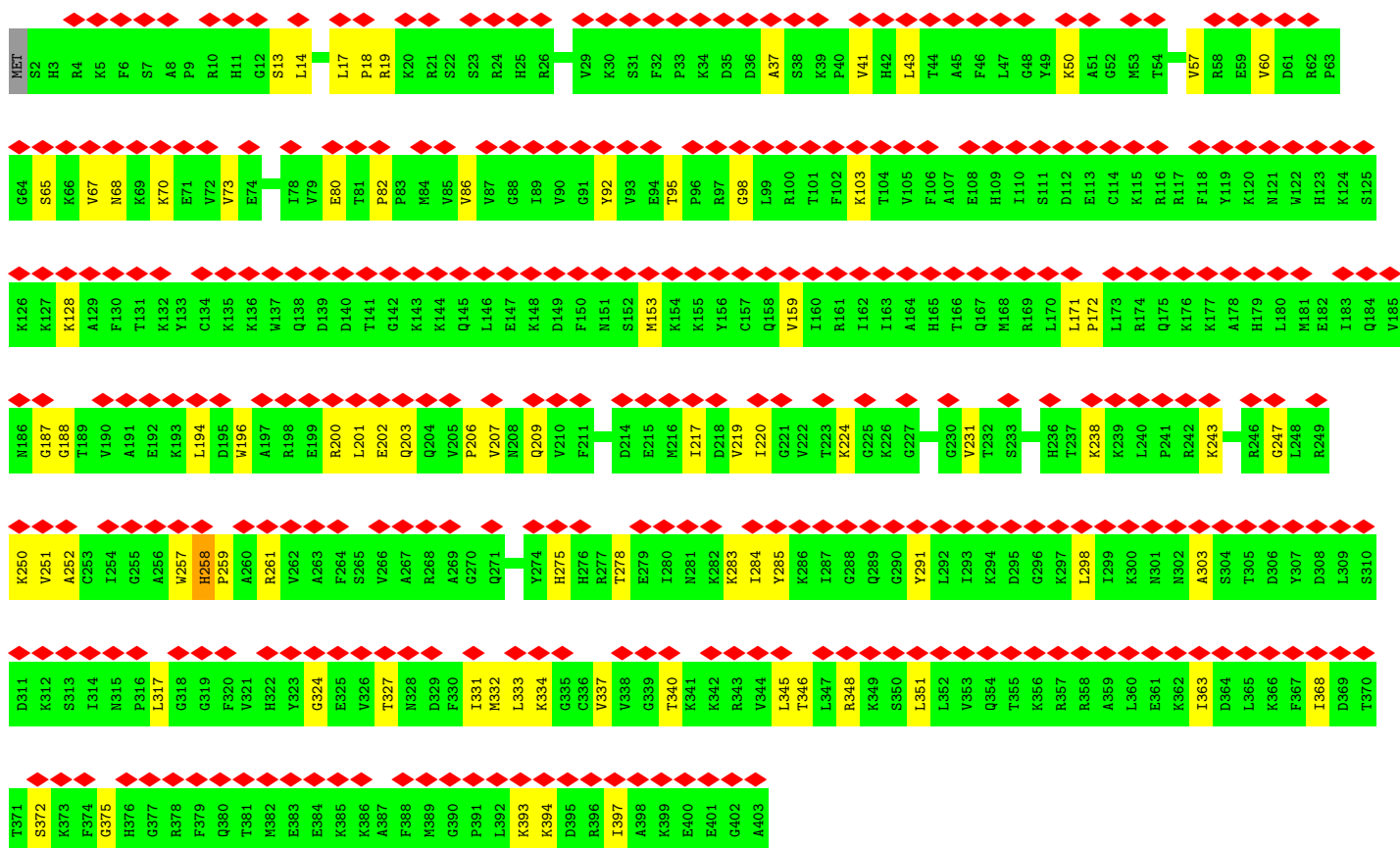
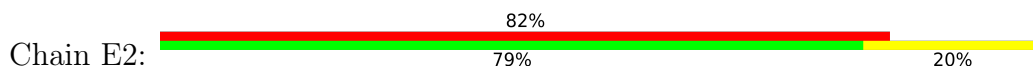


- Molecule 16: Large ribosomal subunit protein uL5

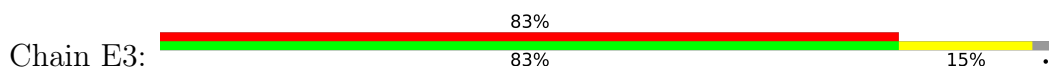


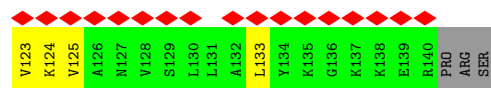


• Molecule 17: Large ribosomal subunit protein uL3

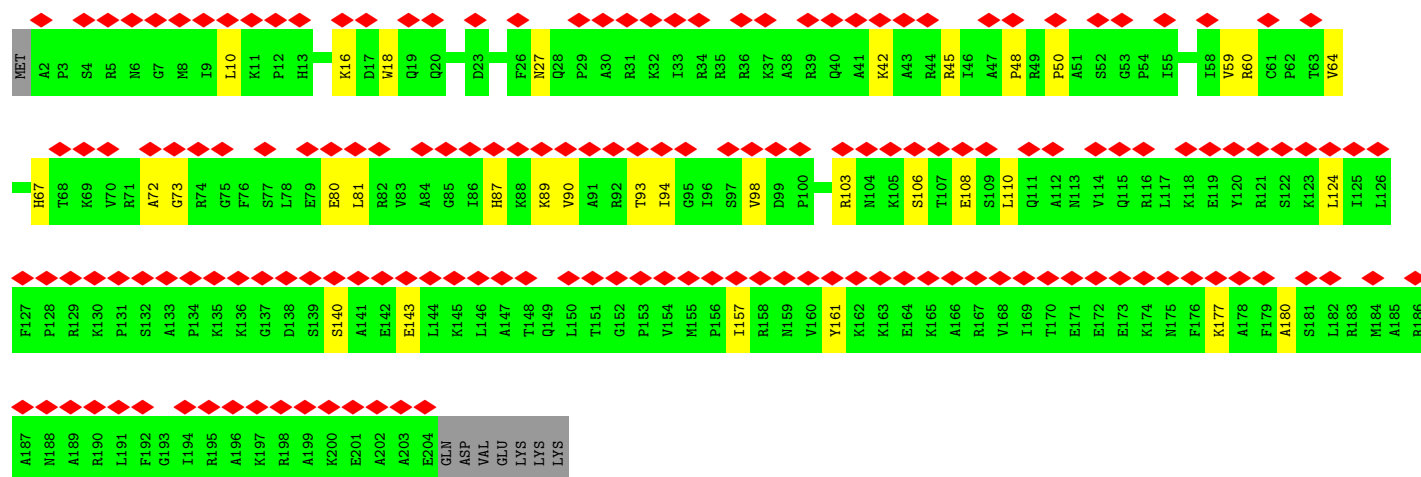
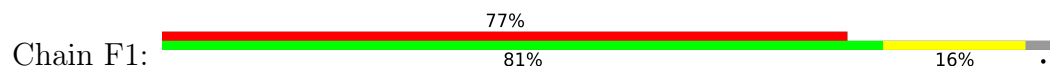


• Molecule 18: Small ribosomal subunit protein uS12

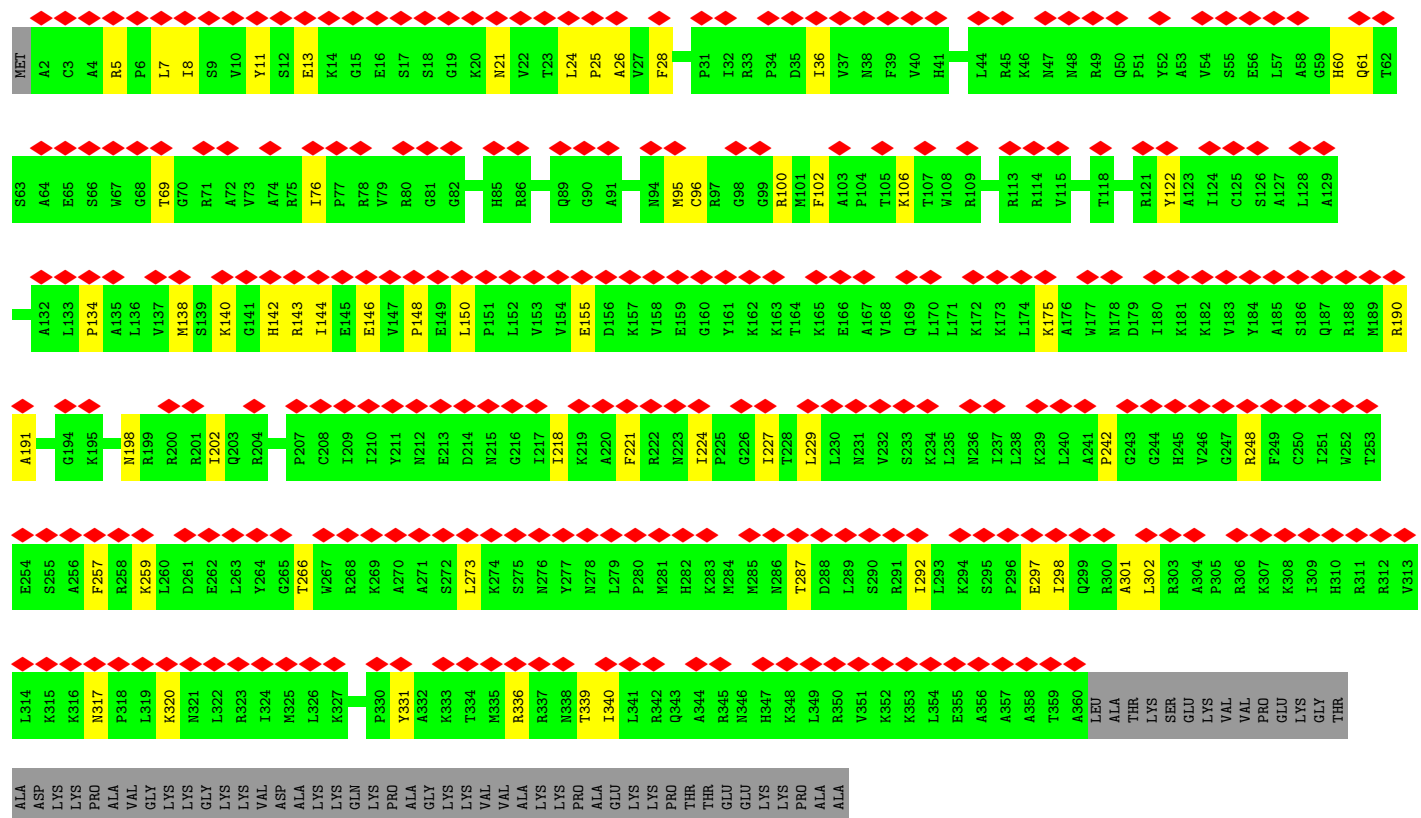
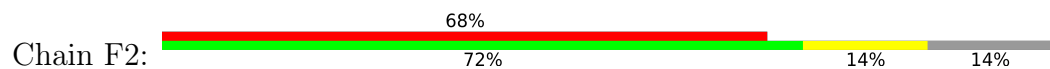




• Molecule 19: Large ribosomal subunit protein eL13

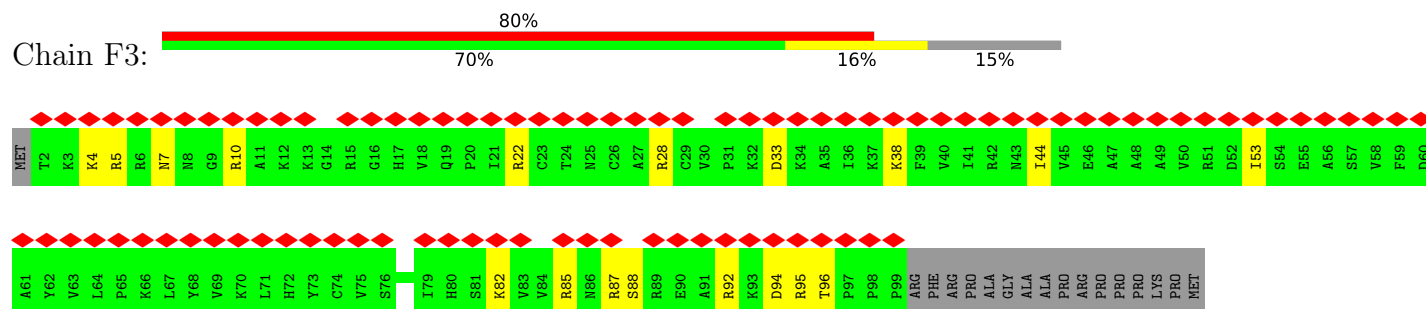


• Molecule 20: Large ribosomal subunit protein uL4



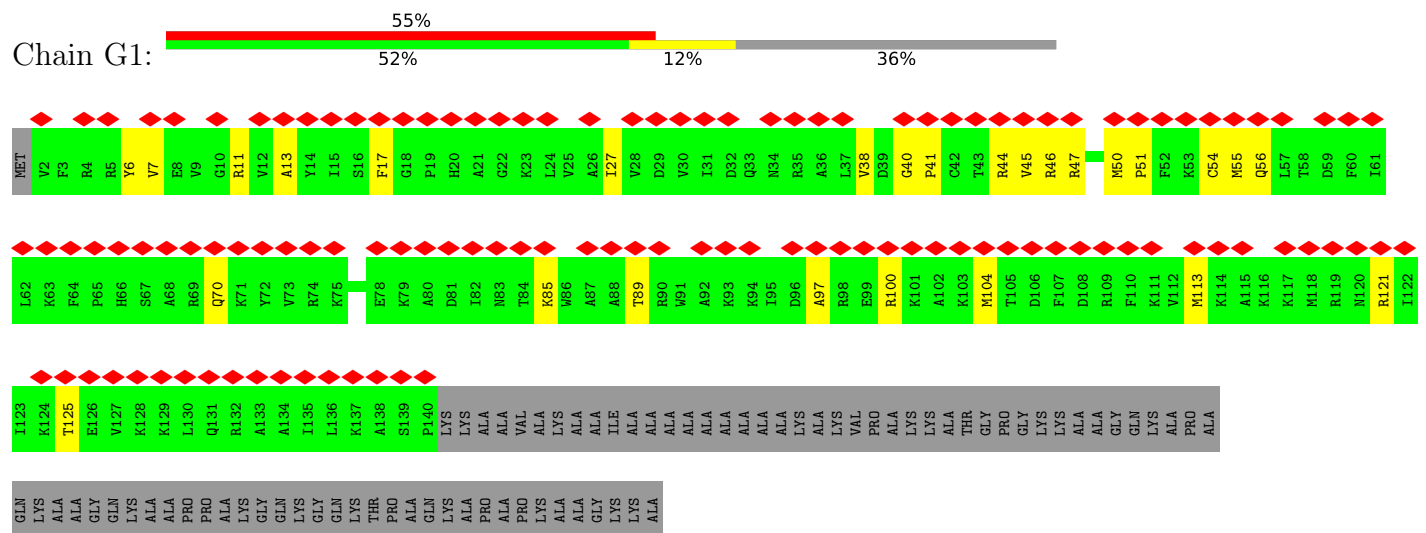
- Molecule 21: Small ribosomal subunit protein eS26

Chain F3:



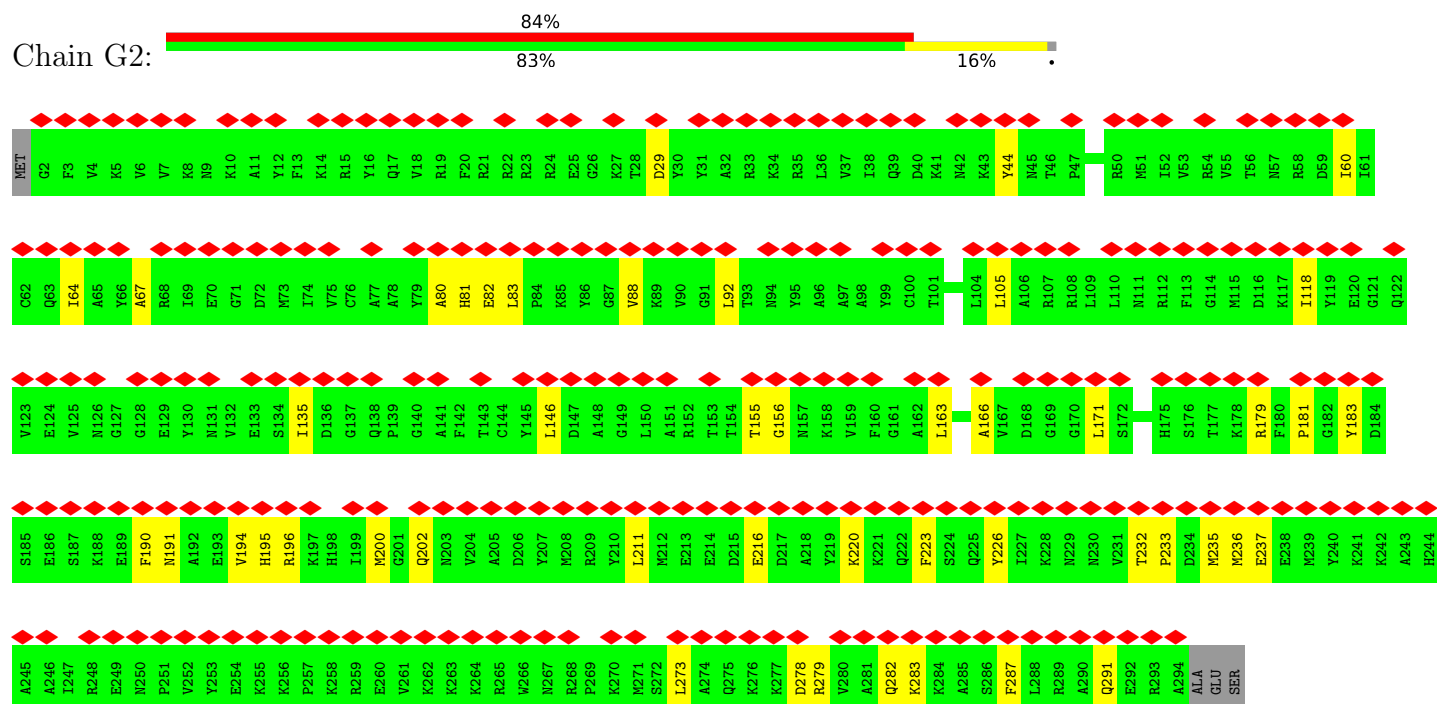
- Molecule 22: Large ribosomal subunit protein eL14

Chain G1:

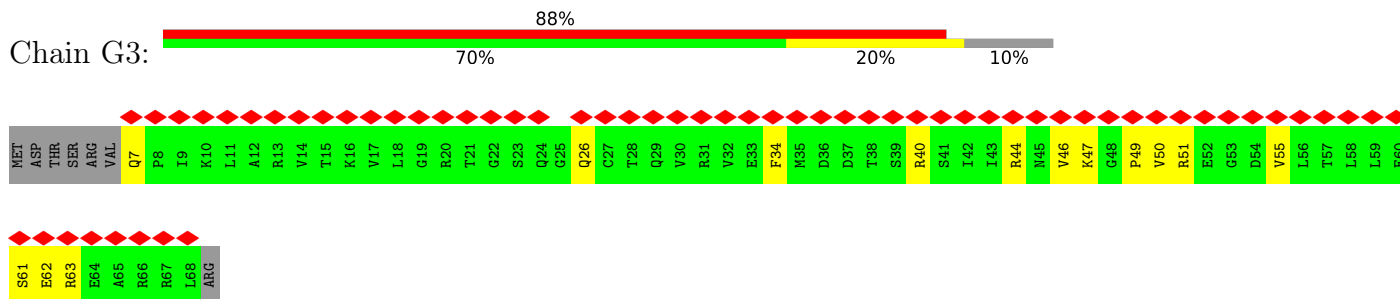


- Molecule 23: Large ribosomal subunit protein uL18

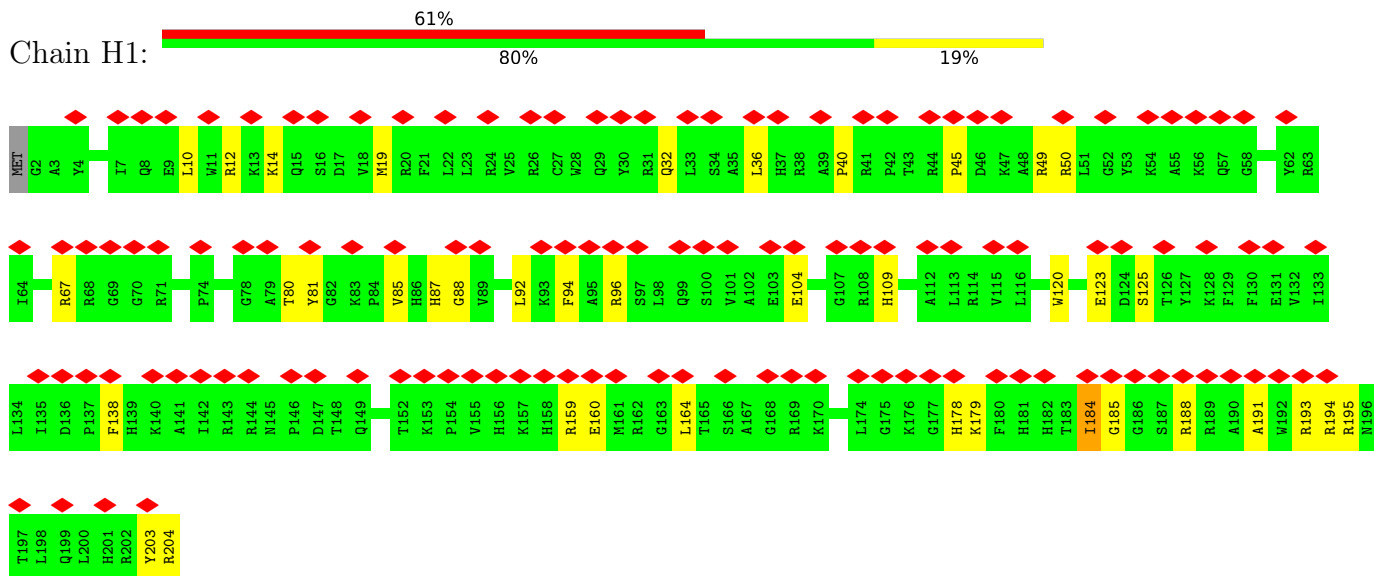
Chain G2:



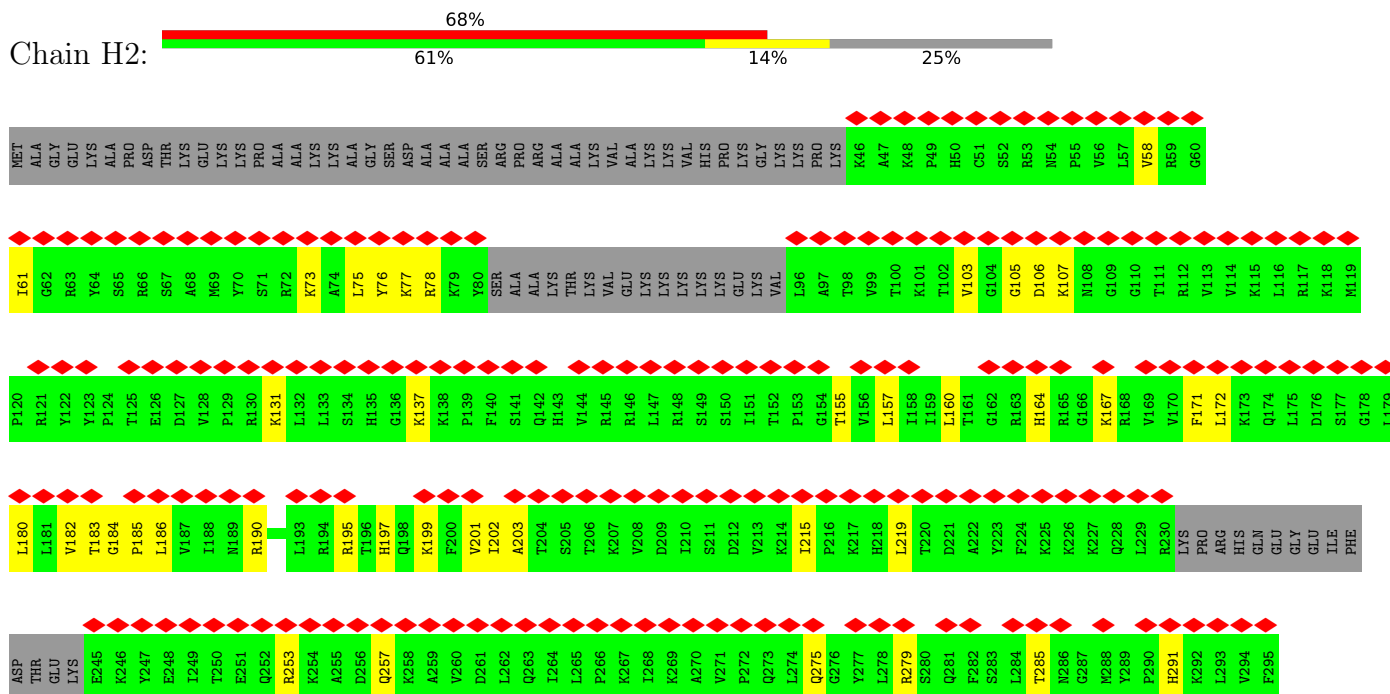
- Chain G3:



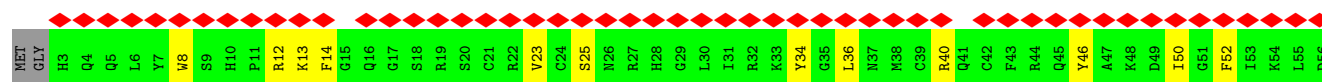
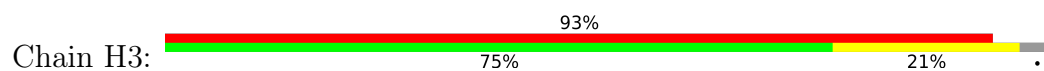
- Chain H1:



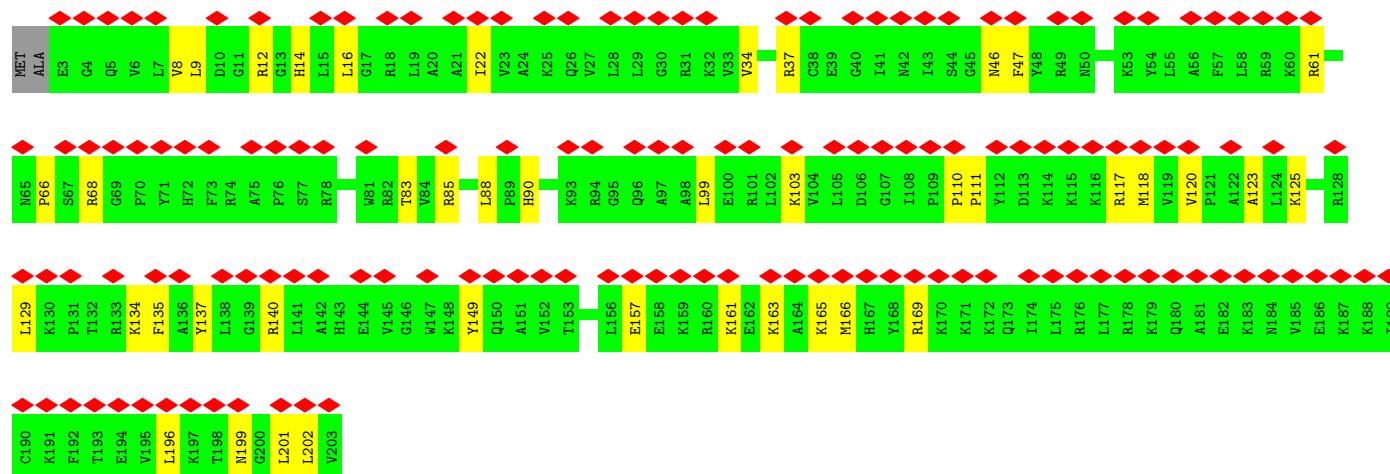
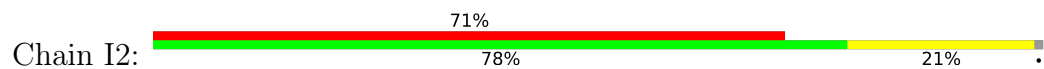
- Chain H2:



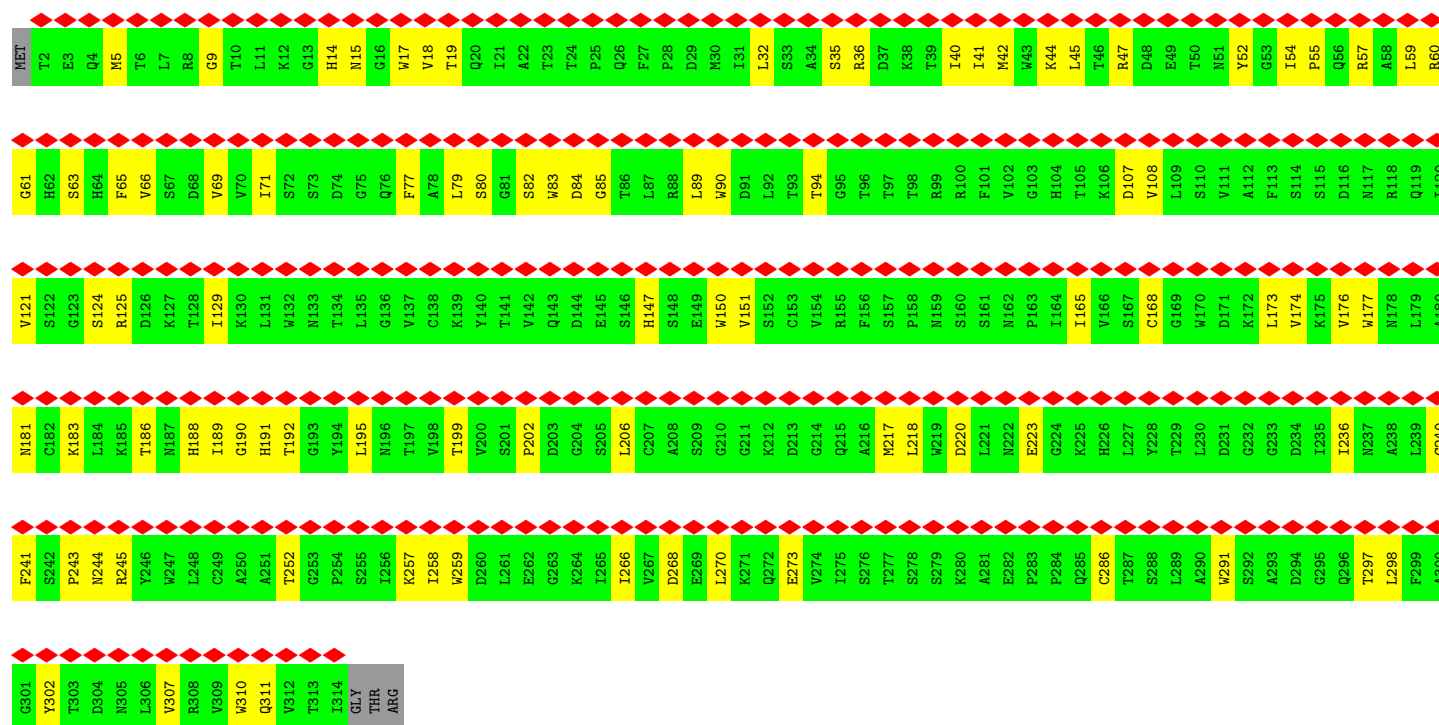
- Molecule 27: Small ribosomal subunit protein uS14



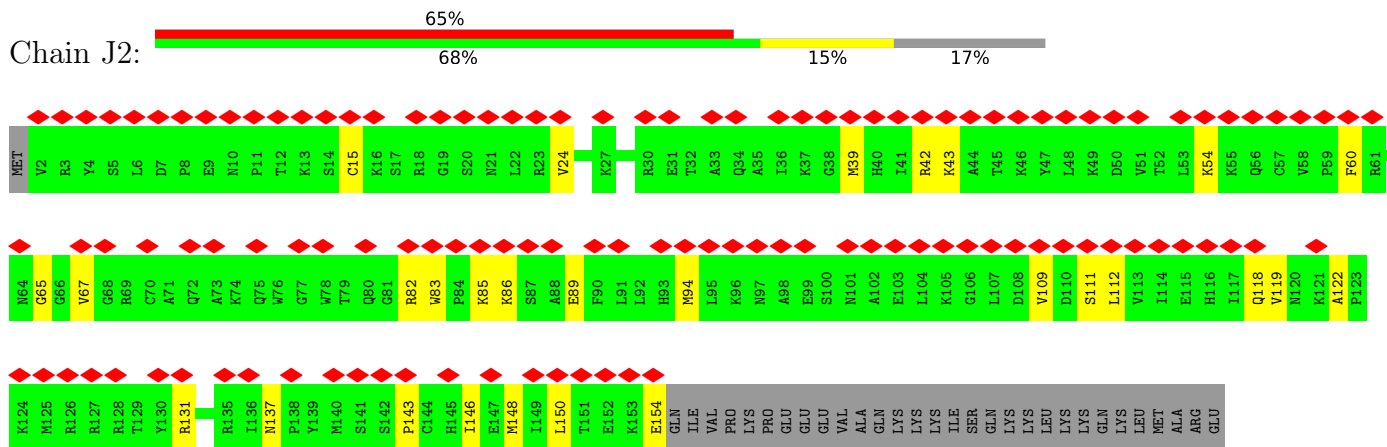
- Molecule 28: Large ribosomal subunit protein uL13



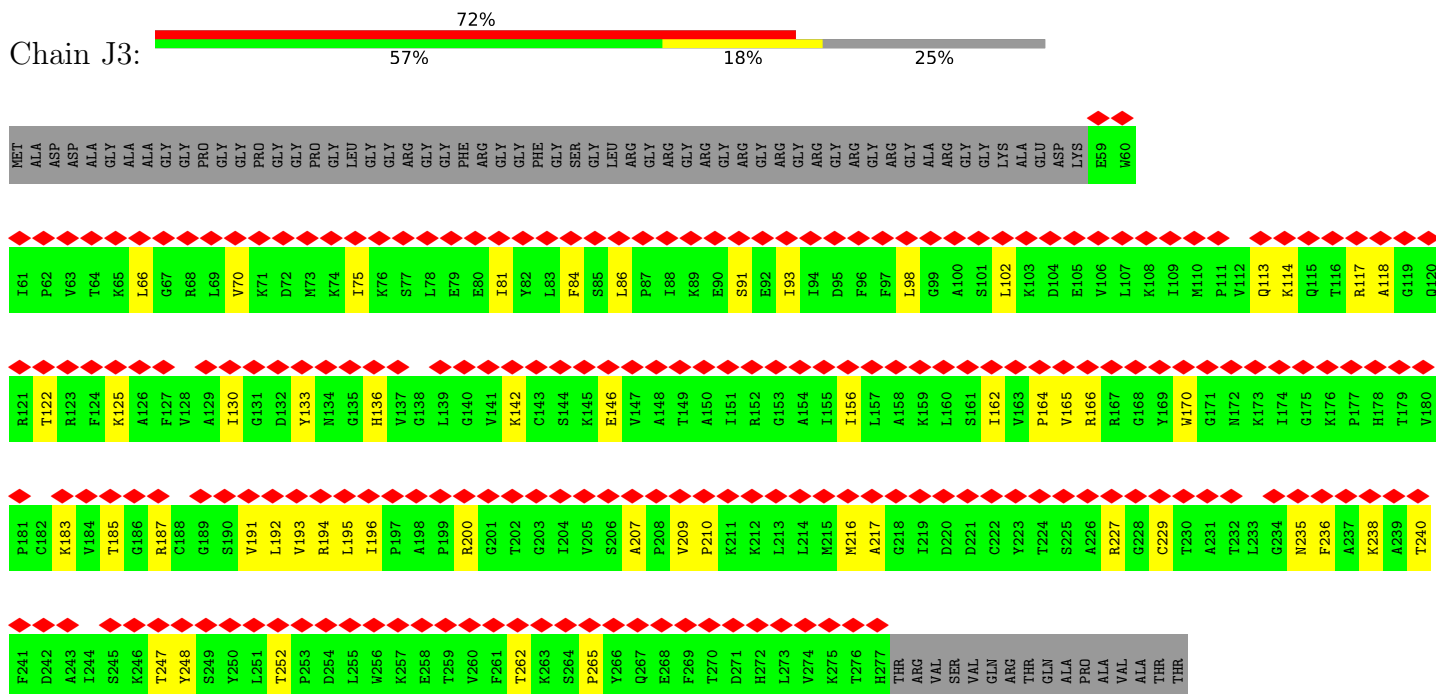
- Molecule 29: Small ribosomal subunit protein RACK1



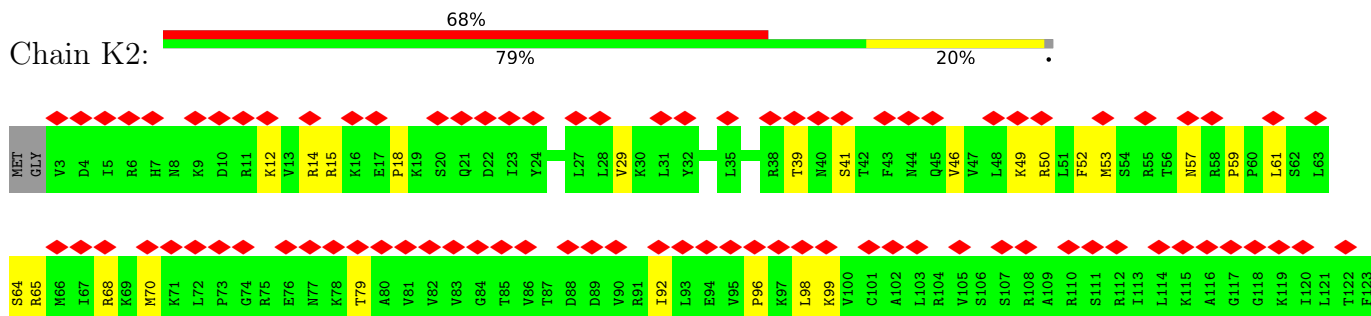
Chain J2:

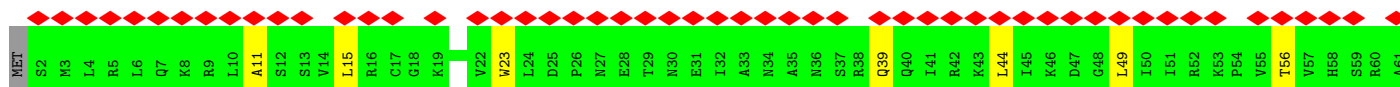


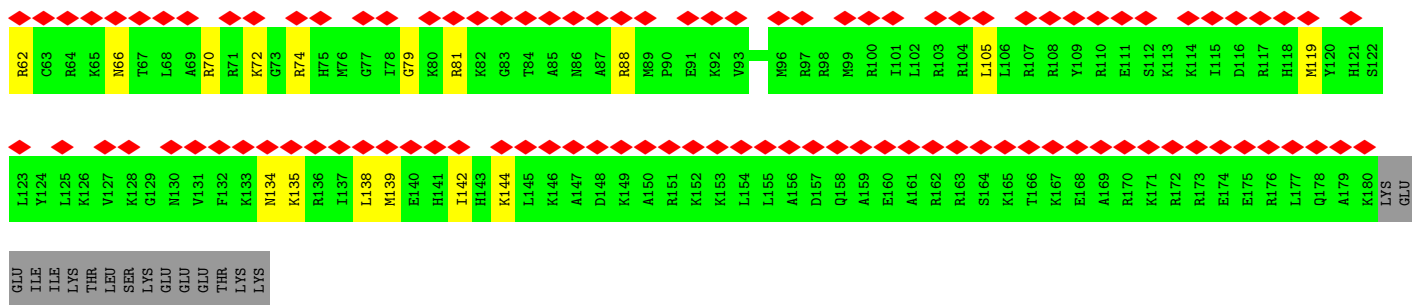
Chain J3:



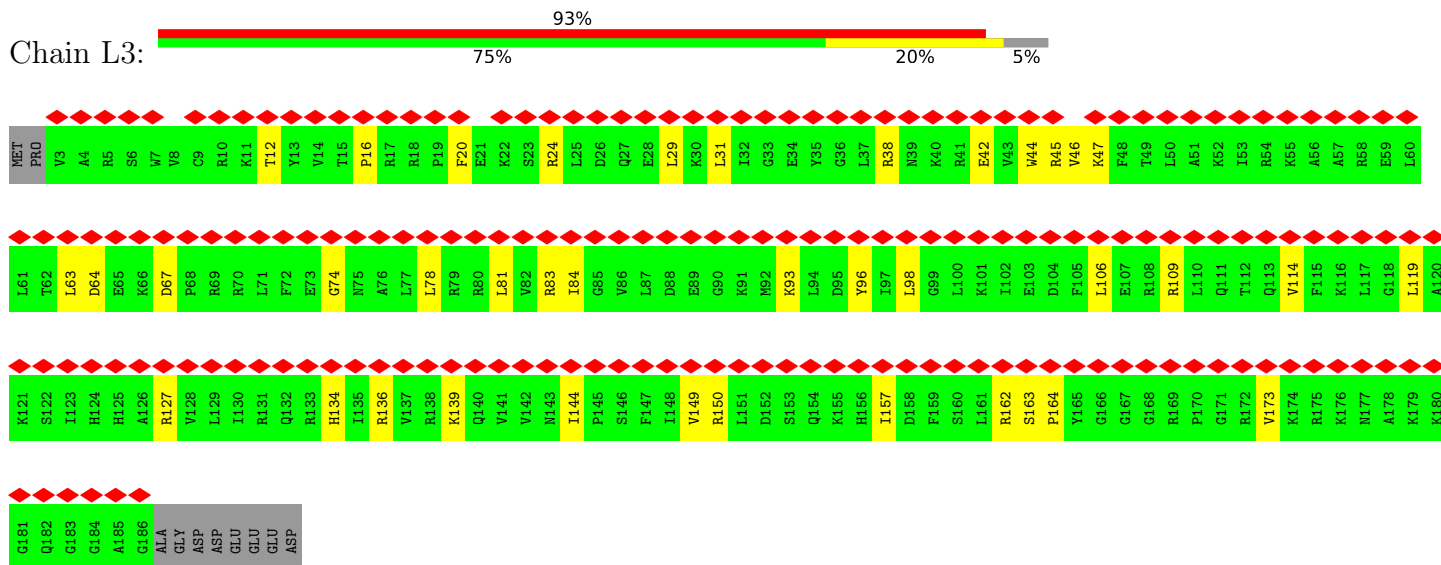
Chain K2:



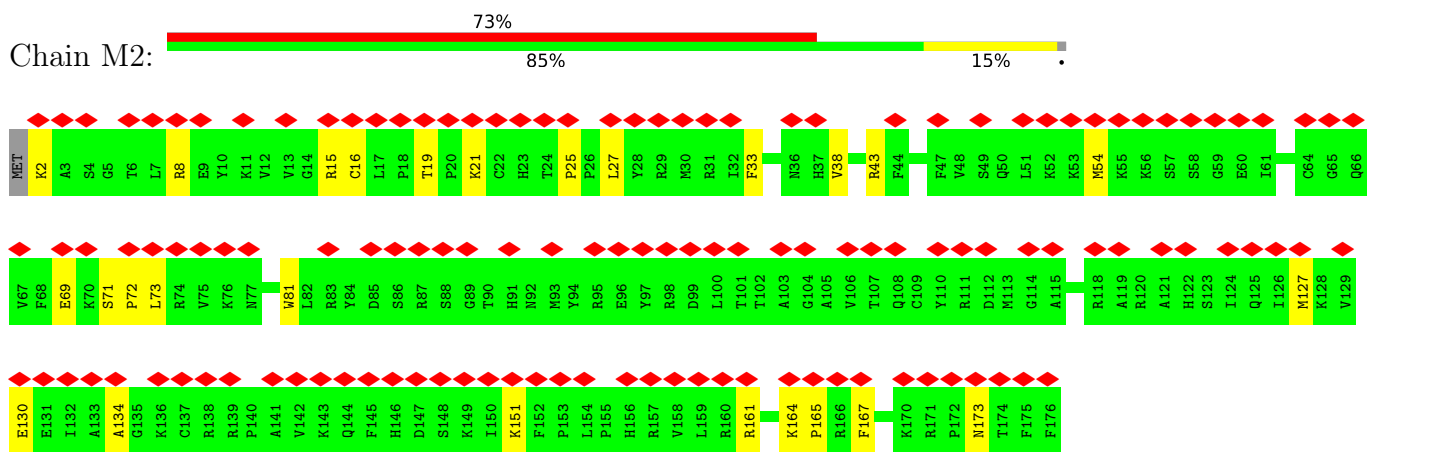




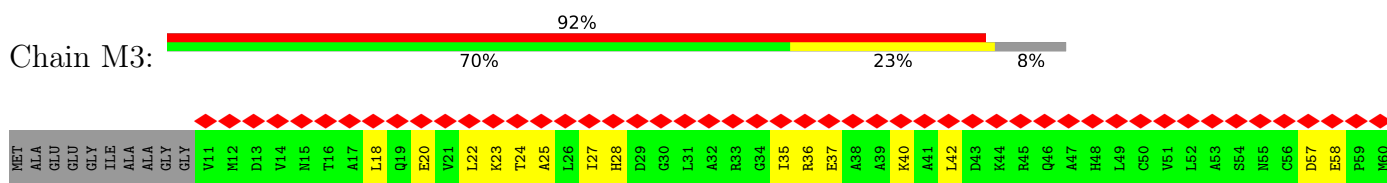
• Molecule 36: Small ribosomal subunit protein uS4

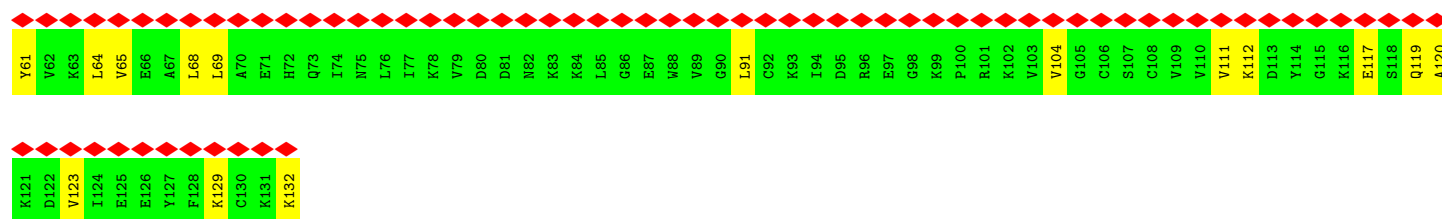


• Molecule 37: Large ribosomal subunit protein eL20



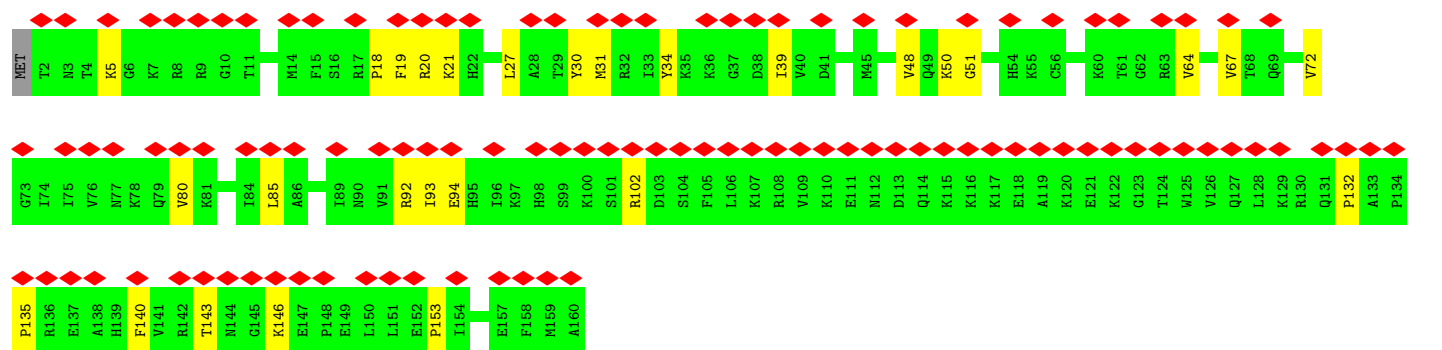
• Molecule 38: Small ribosomal subunit protein eS12





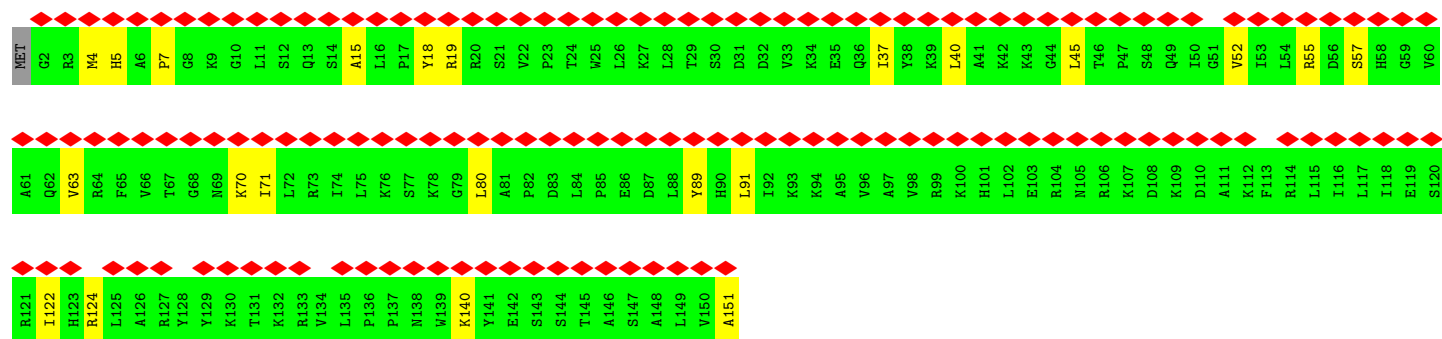
• Molecule 39: Large ribosomal subunit protein eL21

Chain N2:



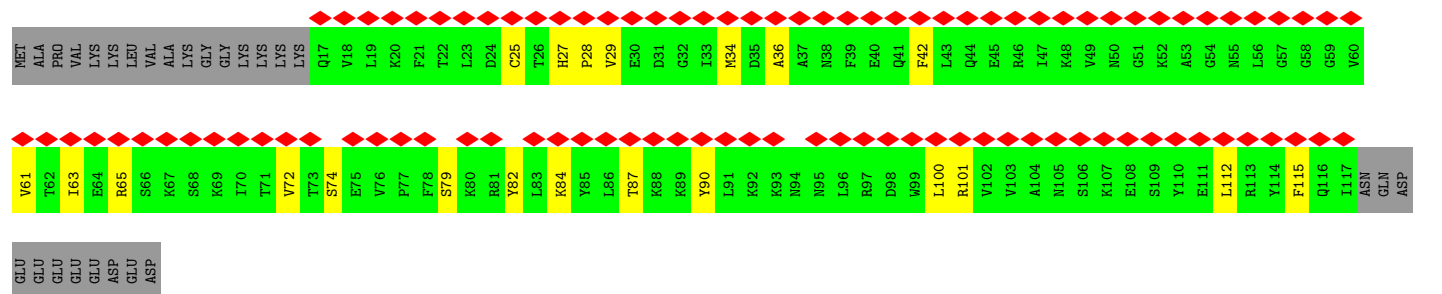
• Molecule 40: Small ribosomal subunit protein uS15

Chain N3:



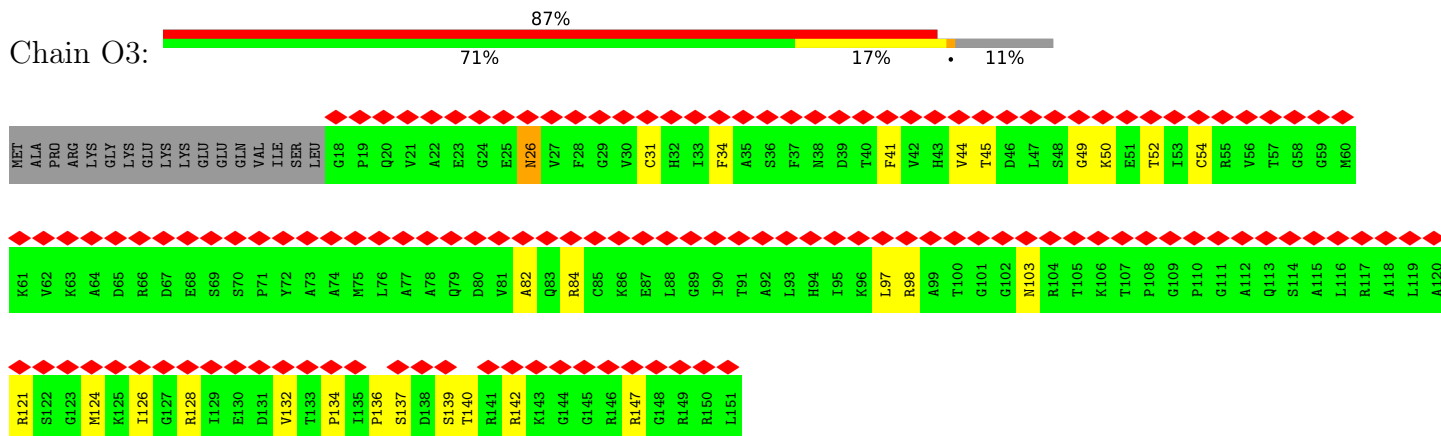
• Molecule 41: Large ribosomal subunit protein eL22

Chain O2:



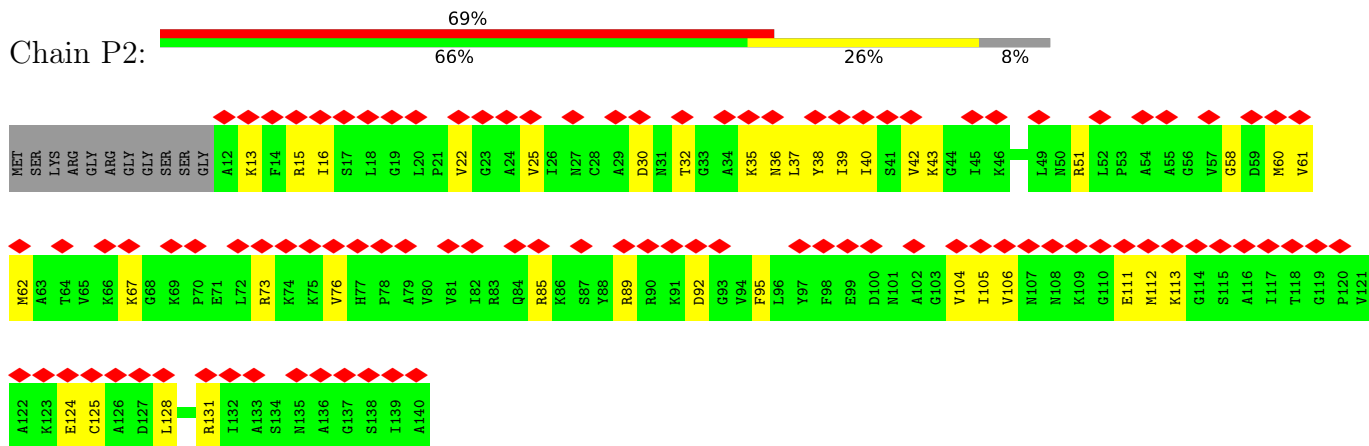
- Molecule 42: Small ribosomal subunit protein uS11

Chain O3:



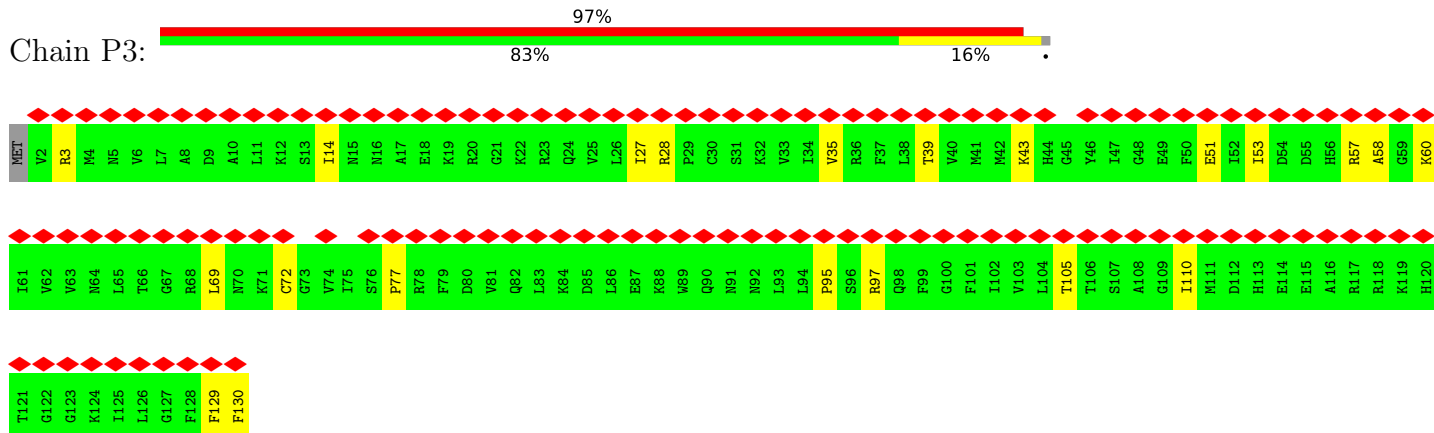
- Molecule 43: Large ribosomal subunit protein uL14

Chain P2:



- Molecule 44: Small ribosomal subunit protein uS8

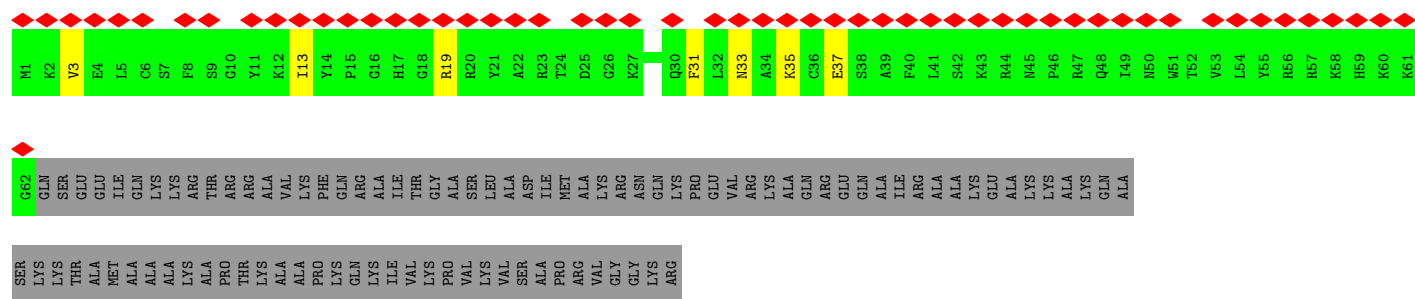
Chain P3:



- Molecule 45: Large ribosomal subunit protein eL24

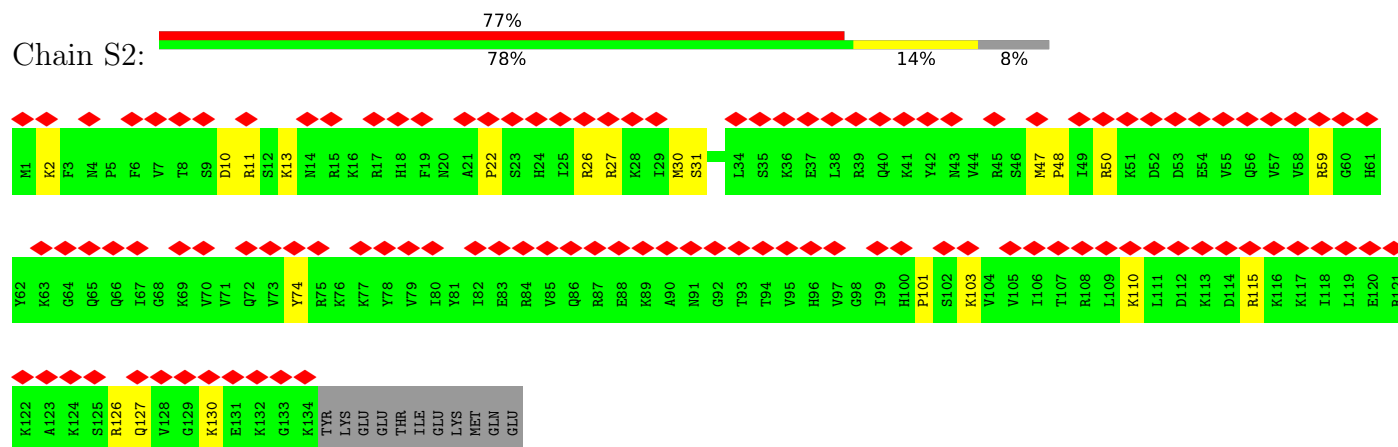
Chain Q2:



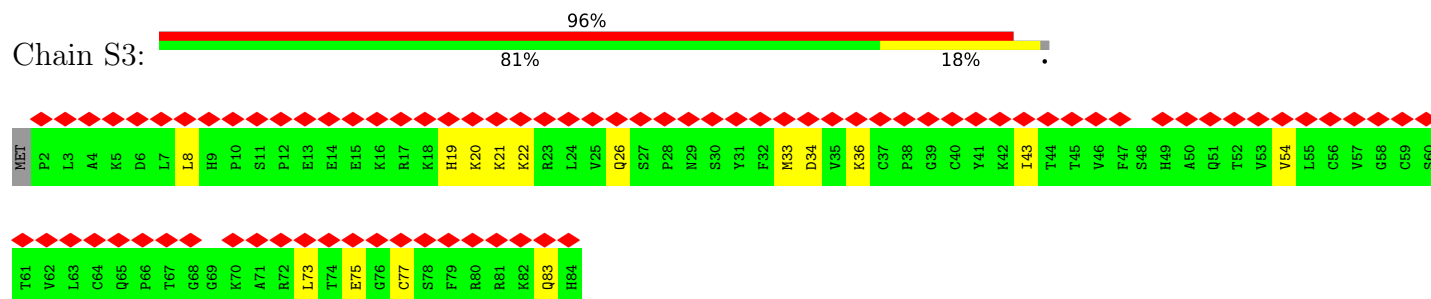


ALA
GLY
GLU
ASP
ALA

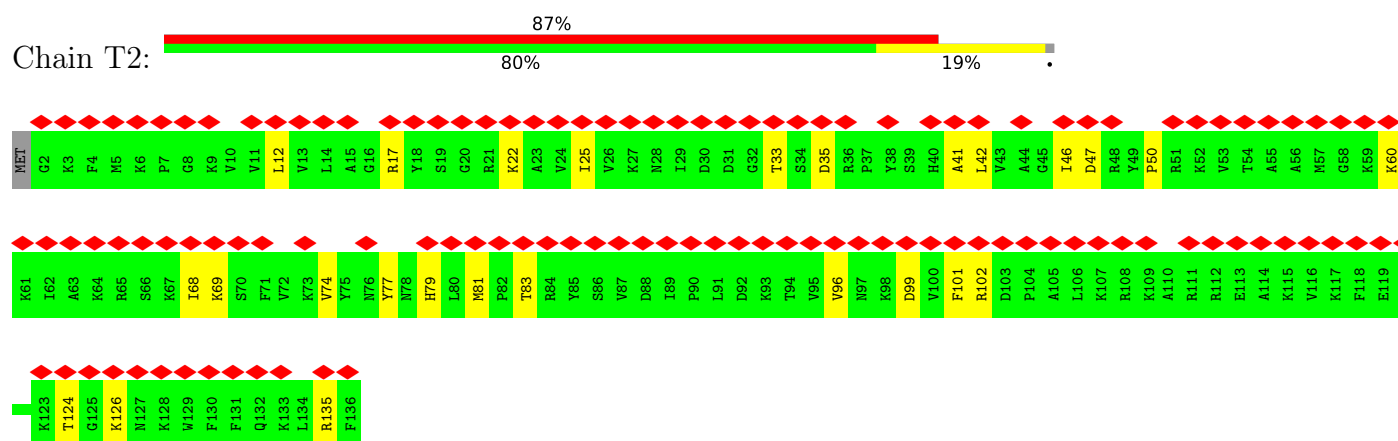
• Molecule 49: Large ribosomal subunit protein uL24



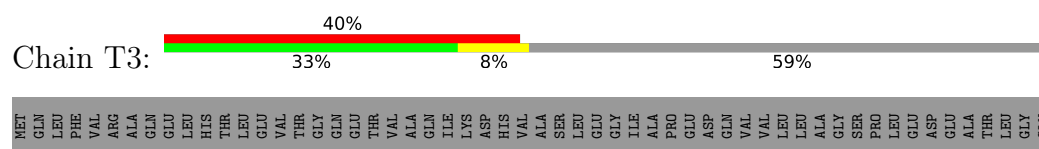
• Molecule 50: Small ribosomal subunit protein eS27

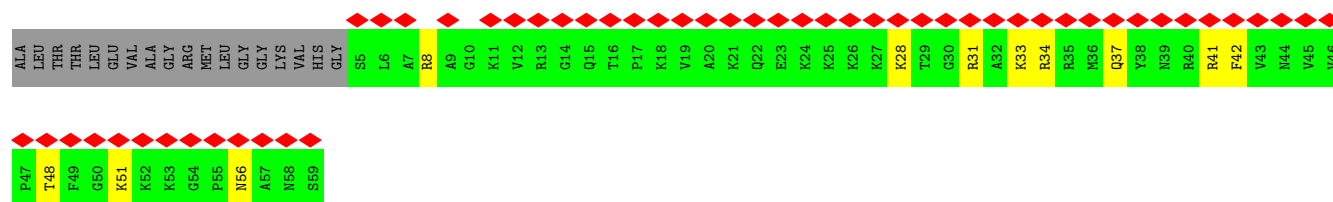


• Molecule 51: Large ribosomal subunit protein eL27

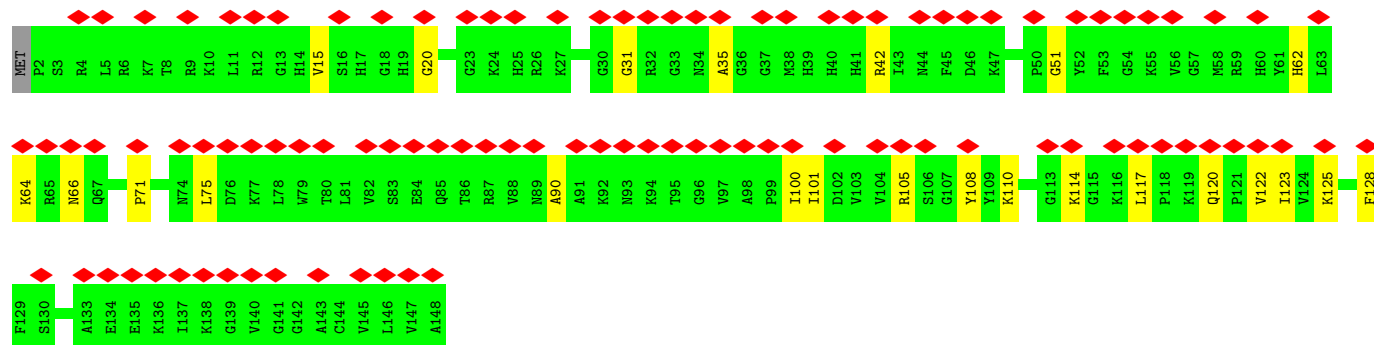
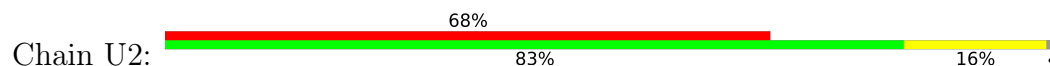


• Molecule 52: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

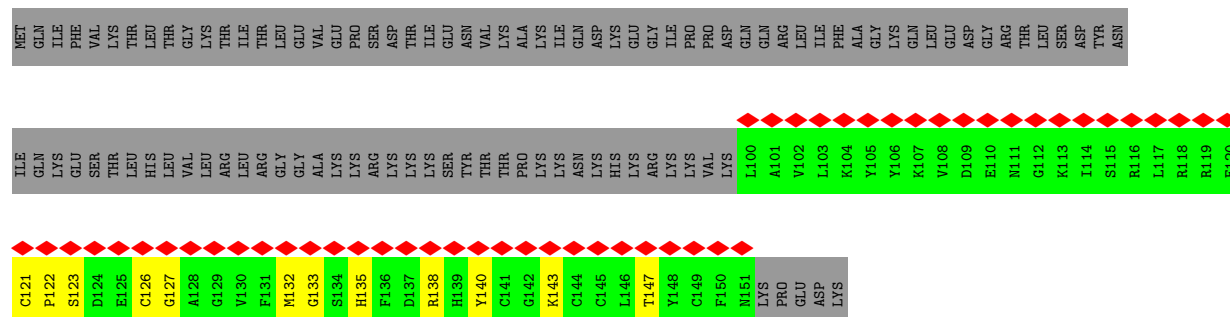




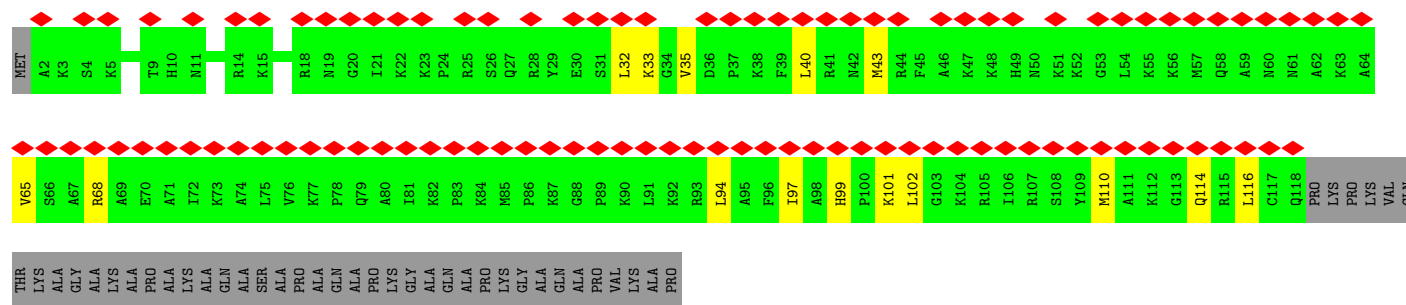
- Molecule 53: Large ribosomal subunit protein uL15



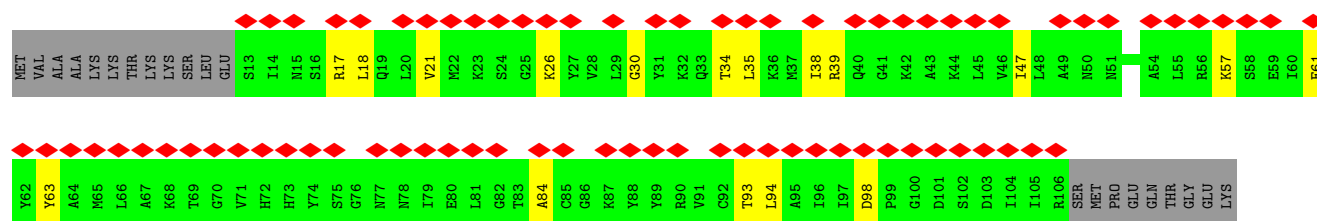
- Molecule 54: Ubiquitin-ribosomal protein eS31 fusion protein



- Molecule 55: Large ribosomal subunit protein eL29



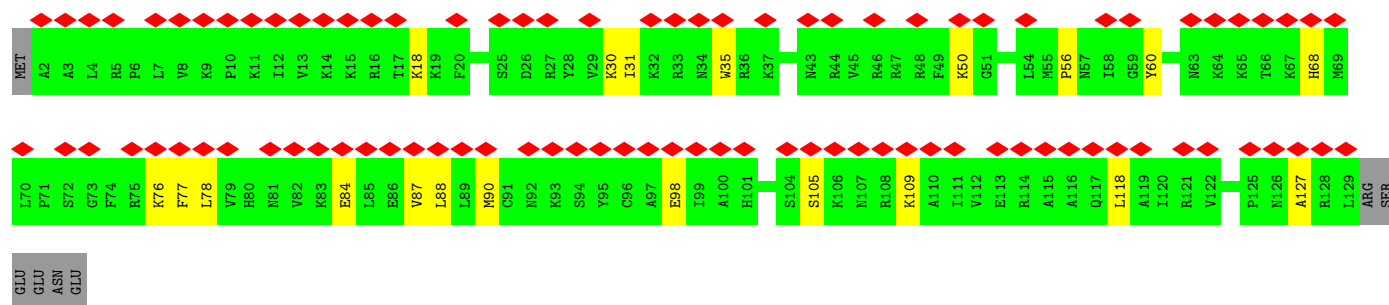
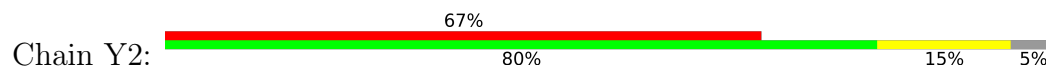
- Molecule 56: Large ribosomal subunit protein eL30



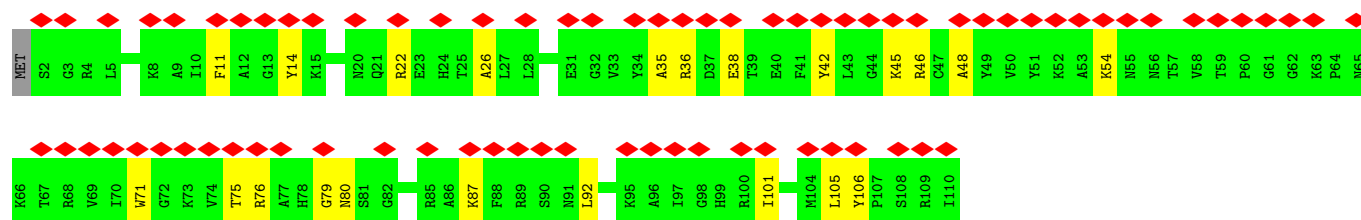
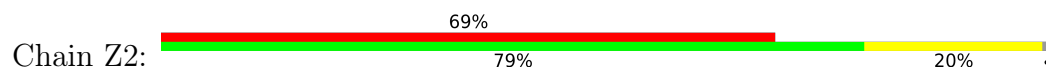
- Molecule 57: Large ribosomal subunit protein eL31



- Molecule 58: Large ribosomal subunit protein eL32

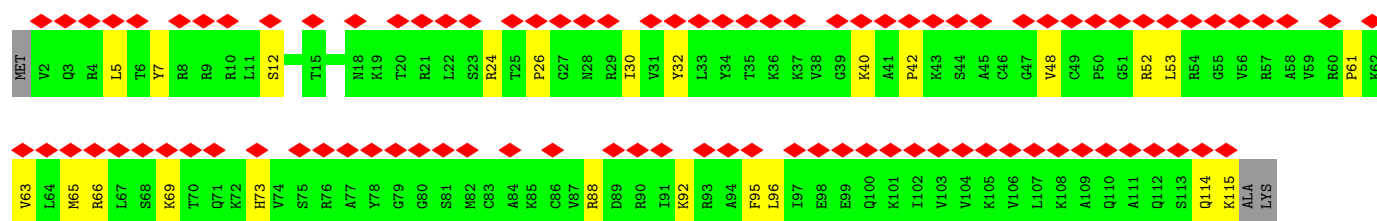


- Molecule 59: Large ribosomal subunit protein eL33



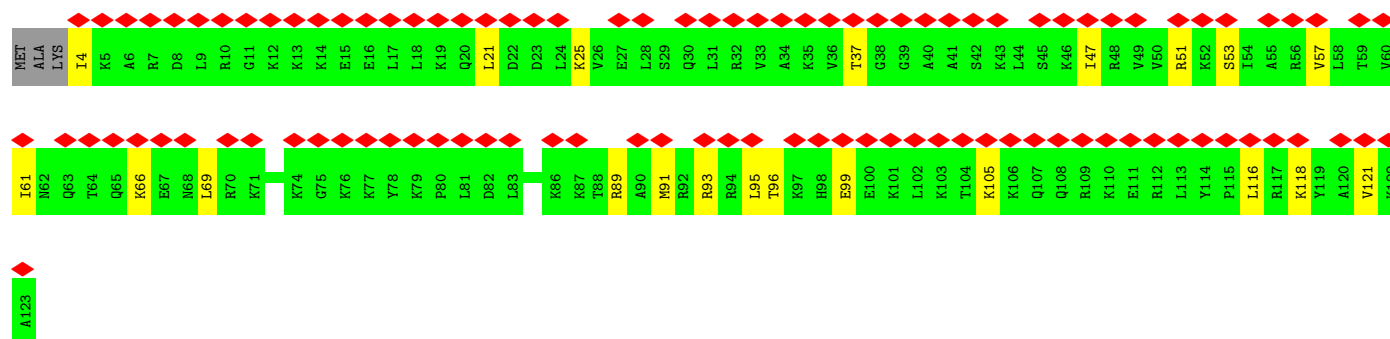
- Molecule 60: Large ribosomal subunit protein eL34

Chain a2: 



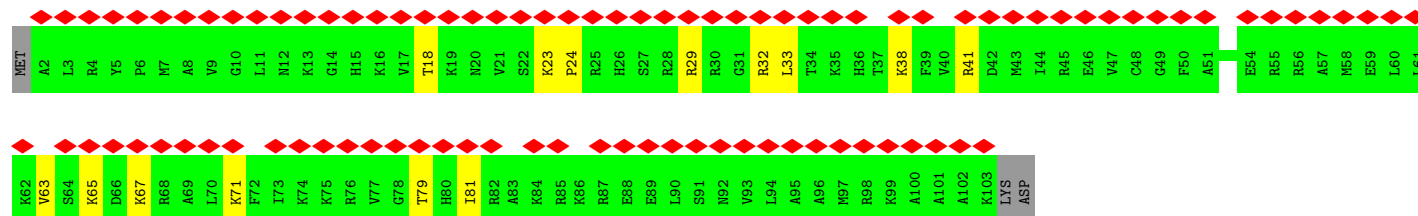
- Molecule 61: Large ribosomal subunit protein uL29

Chain b2: 



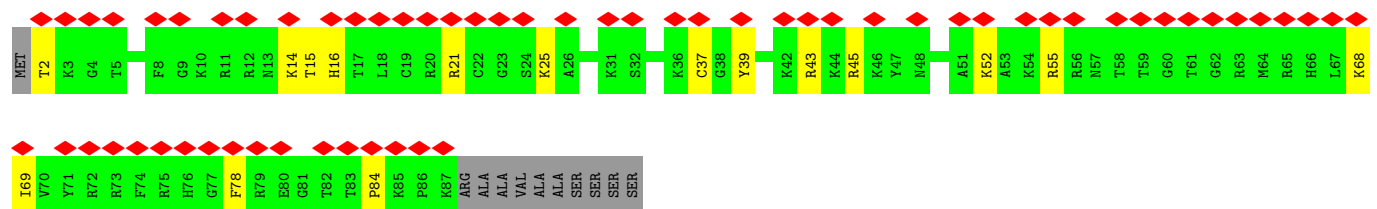
- Molecule 62: Large ribosomal subunit protein eL36

Chain c2: 



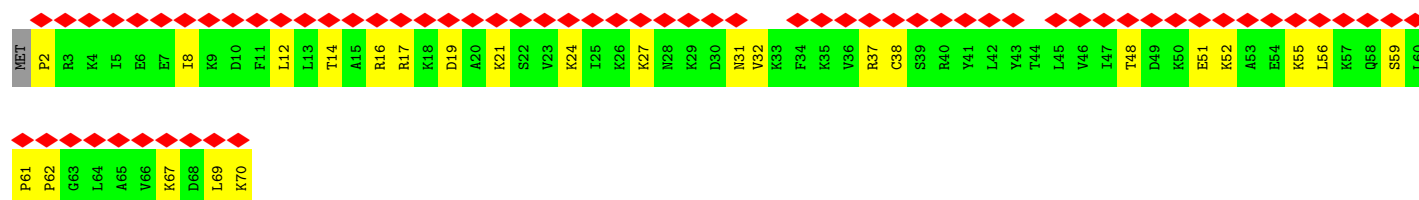
- Molecule 63: Large ribosomal subunit protein eL37

Chain d2: 

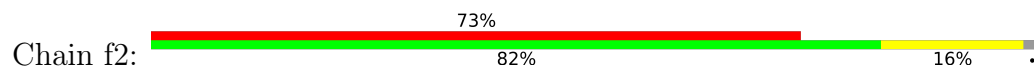


- Molecule 64: Large ribosomal subunit protein eL38

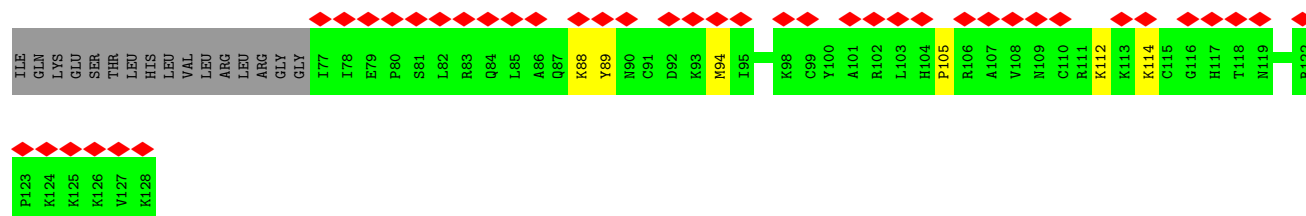
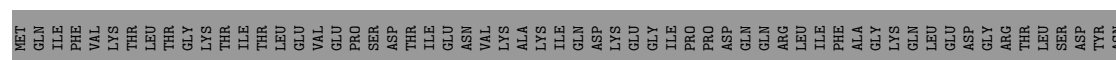
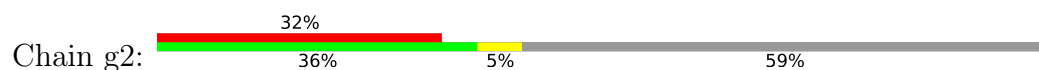
Chain e2: 



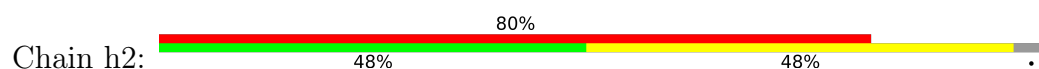
- Molecule 65: Large ribosomal subunit protein eL39



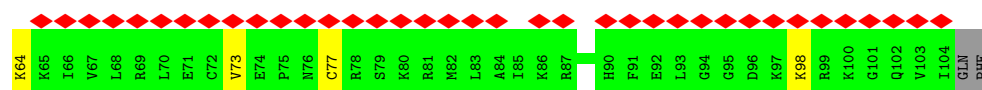
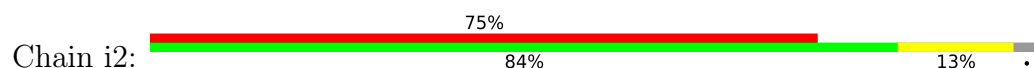
- Molecule 66: Ubiquitin-ribosomal protein eL40 fusion protein



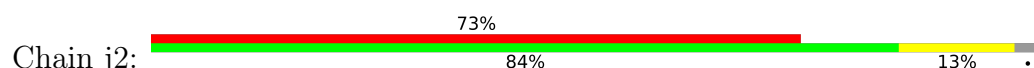
- Molecule 67: 60S ribosomal protein L41

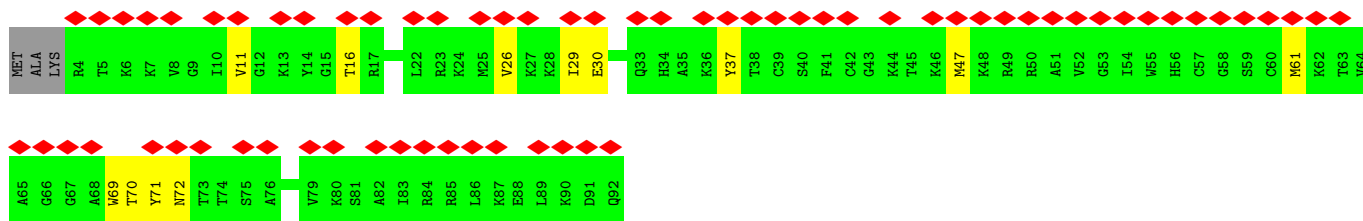


- Molecule 68: Large ribosomal subunit protein eL42

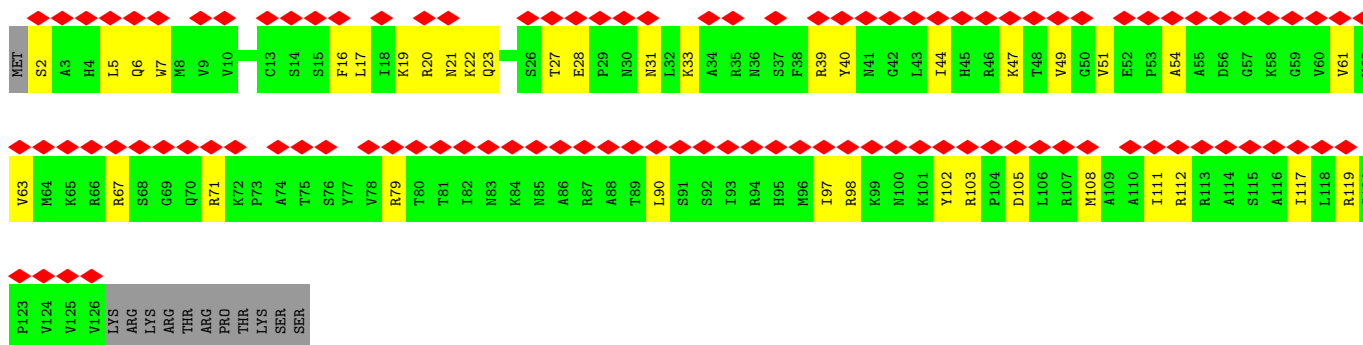
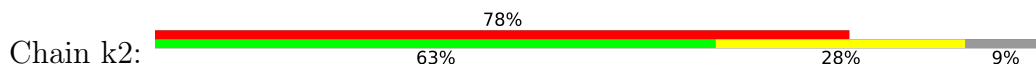


- Molecule 69: Large ribosomal subunit protein eL43

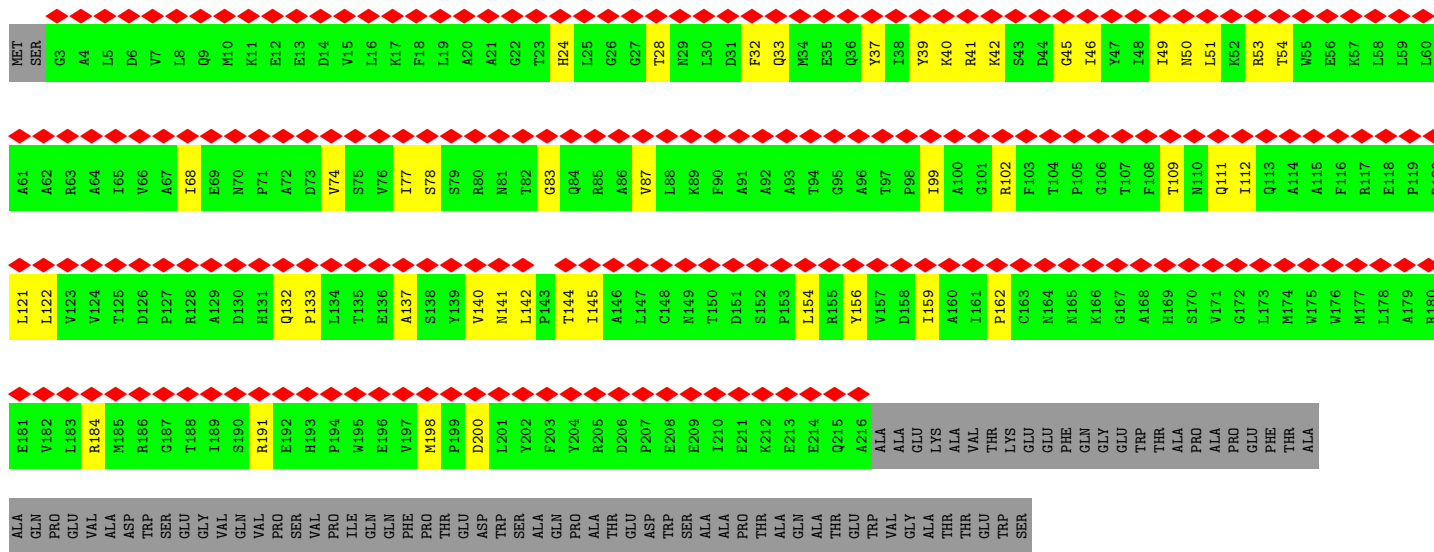
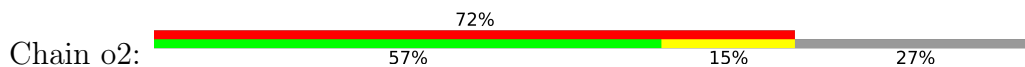




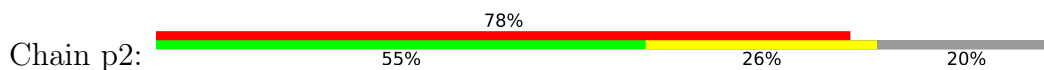
• Molecule 70: Large ribosomal subunit protein eL28

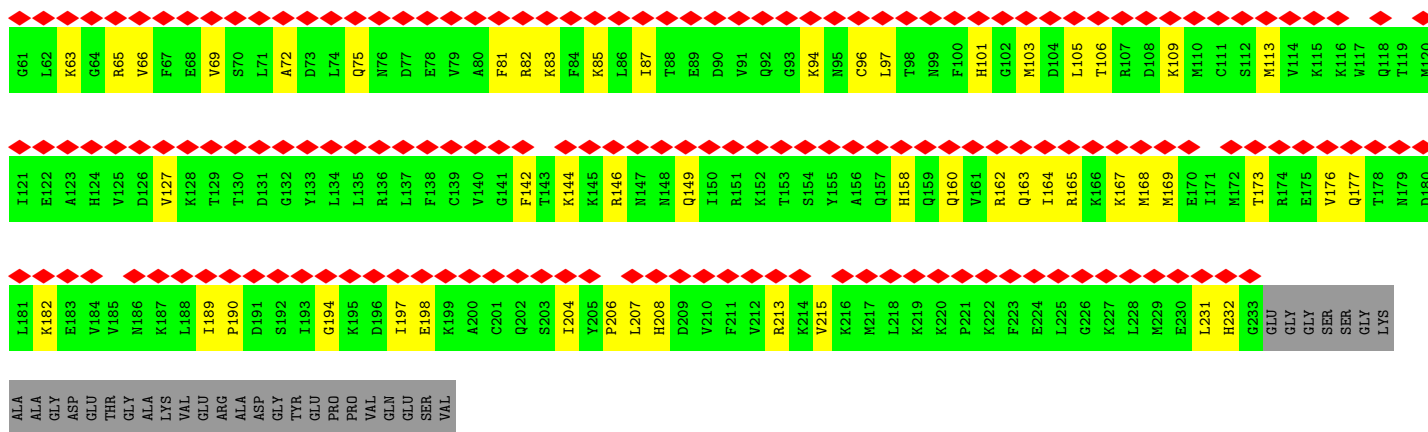


• Molecule 71: Small ribosomal subunit protein uS2



• Molecule 72: 40S ribosomal protein S3a

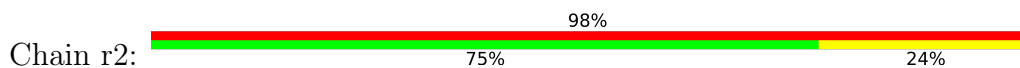


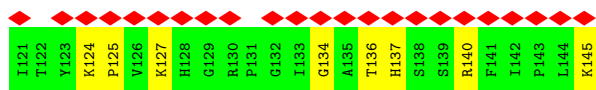


• Molecule 73: Small ribosomal subunit protein uS3

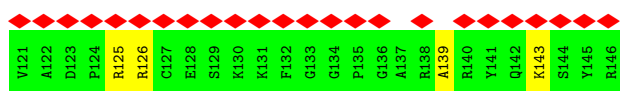
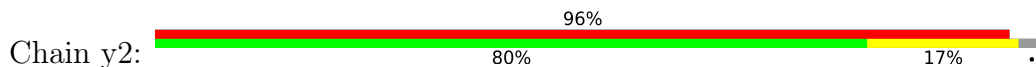


• Molecule 74: Small ribosomal subunit protein eS4

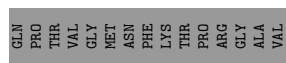
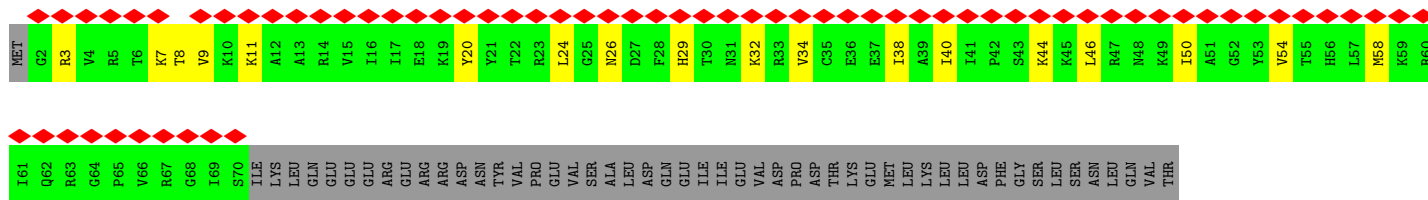
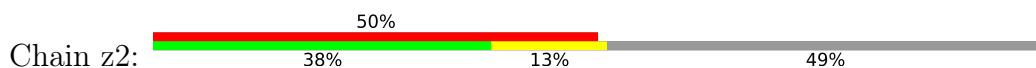




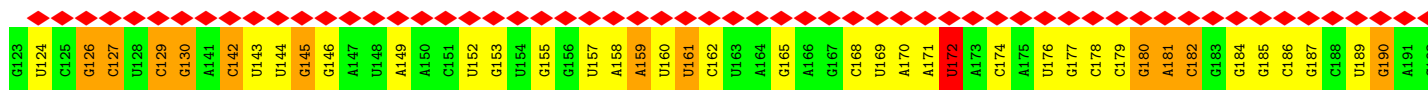
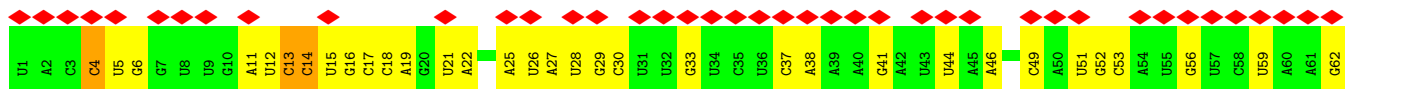
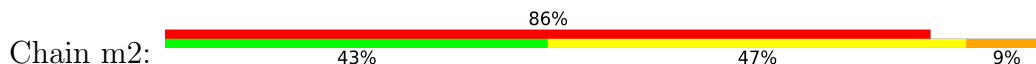
- Molecule 81: Small ribosomal subunit protein uS9



- Molecule 82: Small ribosomal subunit protein eS17



- Molecule 83: 18S ribosomal RNA



C1182	A1121	A992	G931	A871	A811	C640	U579	A502	G442	G382	G314
A1183	U1122	G993	C932	A872	A812	C641	C580	C503	C443	C383	A315
A1184	G1123	A994	C933	U873	A813	A642	C581	C504	C444	C384	U316
A1185	A1124	G997	G934	A874	A814	A643	U582	C505	G445	G385	C317
G1186	C1125	A998	G935	G875	A815	U644	U583	G506	G446	U386	G318
U1188	C1126	A999	G936	G876	U816	A645	U584	G507	A447	G387	C319
U1189	C1127	A1000	G937	A877	U817	U646	A585	G508	G448	U388	A320
U1190	G1128	G1001	G938	G878	A818	C647	A586	G509	A449	C389	C321
A1191	C1129	U1004	C939	G879	U819	U648	A587	A510	A450	U390	G322
A1192	U1130	U1005	A940	G880	A820	A650	C587	G511	A451	A391	C323
C1193	G1131	U1006	U942	C881	G821	U651	A589	G512	C452	C392	C324
U1194	C1132	G1007	U943	G882	U822	A652	G590	U513	G453	C393	G331
U1195	A1133	C1008	C943	G883	U823	U653	G591	A514	A454	A394	G332
A1196	C1134	C1009	G944	U884	U824	U654	A592	G515	C455	U395	C333
A1197	A1135	C1009	U945	U885	U825	A655	U593	U516	U456	U396	G334
G1200	G1136	A1010	A946	C886	C826	A656	C594	A518	C458	G397	G335
A1201	C1137	U1011	U947	U887	A827	U657	C595	C519	C459	U398	C336
A1202	U1138	A1012	U948	A888	A828	C658	A596	G520	A460	G399	G337
U1203	C1139	A1013	C949	U889	A829	U659	U597	A521	C461	A400	A338
U1204	C1140	A1015	C950	U890	G830	U660	U598	A522	A462	C401	C339
G1205	C1141	U1015	G951	U891	C831	C661	G599	A523	U463	C402	G340
A1206	G1142	U1083	C952	U892	A832	U662	G600	A524	C464	A403	A341
C1207	A1143	C953	C953	G893	G833	C664	A601	A525	C465	C404	C342
A1208	U1144	G954	G954	U894	G834	C665	G602	U526	A466	G406	C343
G1209	C1145	C955	C955	U895	C835	U668	G603	A527	A467	G407	C344
A1210	C1146	U956	U956	C896	C836	U669	G604	C528	G468	U408	A345
A1211	U1147	A957	A957	G897	C837	A670	C605	C529	G469	G409	U346
G1212	C1148	G958	G958	U898	G838	A671	A607	A530	A471	A410	U347
G1213	A1151	A959	A959	U899	A839	A672	G608	A531	G472	C411	C348
C1214	C1149	C960	C960	U900	G840	A673	U609	U532	G473	G412	G349
C1215	U1152	A1025	G961	U901	C841	A674	C610	A533	C474	G413	A350
A1216	G1153	A1026	U962	C902	G842	C676	U611	C534	A475	G414	A351
C1217	U1154	U1027	G963	C903	G843	U677	G612	A535	G476	G415	C352
G1218	C1155	C1028	A964	G904	C844	C678	G613	G536	A477	A416	G353
A1219	U1156	A1030	A965	A905	C845	C679	U614	U554	U478	A417	U354
C1220	C1157	G1031	A966	A906	U846	U680	G615	A555	G479	U418	C355
C1221	U1158	A1032	U967	C907	G847	A681	C616	A556	G480	C419	U356
A1222	G1159	A1033	U968	U908	G848	C682	C617	A557	C481	A420	G357
G1223	C1160	C1034	C969	G909	A849	U683	A618	U558	G482	G421	C358
C1224	G1161	U1035	U970	A910	U850	U684	G619	U559	C483	G422	G359
A1225	U1162	A1036	U971	G911	A851	C685	G622	G560	G484	C423	A362
C1226	C1163	U1037	G972	G912	C852	C686	C623	G561	C485	U424	U363
U1227	A1164	A1038	G973	C913	C853	A687	C624	A562	A486	U425	C364
G1228	G1165	C1039	A974	C914	G854	U688	G625	A563	C487	U426	A365
C1229	U1166	U1040	C975	A915	C855	C689	C626	U564	A488	G427	A366
A1230	C1167	C1041	C976	U916	A856	U690	G627	U565	U489	G428	C367
G1231	G1168	G1042	U977	G917	G857	U801	G628	G566	U490	U429	U368
C1232	U1169	U1043	C979	A918	C858	U802	U829	A567	C492	U430	U369
C1233	C1170	G1044	G980	U919	U859	U803	A830	U568	C493	C431	U370
U1234	A1171	G1045	C981	U920	A860	A804	A631	C569	C494	C432	C371
G1235	U1172	G1046	A982	U921	A861	C905	U832	C570	A495	G433	G372
C1236	C1173	U1047	A983	A921	G862	U806	C633	A571	C496	A434	A373
G1237	U1174	U1048	G984	G923	A863	U807	C634	U573	U497	G435	U374
C1238	A1175	U1048	A985	G924	A864	U808	C635	C572	C498	A436	G375
G1239	G1176	G1053	C986	G925	U865	G809	A836	U574	G437	G438	G376
U1240	C1177	A1054	G987	G926	U866	G809	G637	U575	C439	U377	A378
C1241	U1178	C1055	G988	G927	A867	A810	C638	A576	G440	G440	G379
A1242	G1179	G1056	G989	G928	U868	G870	U639	A577	A441	A441	U380
	U1180		C990	A928	G869						C381
	G1181		G991	G930	G870						

G1816	A1243	A1303	G1363	A1423	G1483	G1543	A1603	A1663	U1723	G1816
A1817	U1244	G1304	U1364	G1424	C1484	C1544	U1604	U1664	G1724	A1817
G1818	U1245	C1305	C1365	C1425	A1485	U1545	G1605	A1665	G1725	G1818
G1819	U1246	U1306	U1366	G1426	A1486	C1546	G1606	A1666	A1726	G1819
A1820	G1247	C1307	G1367	U1427	U1487	A1547	G1607	C1667	U1727	A1820
A1821	A1248	U1308	G1368	U1428	A1488	G1548	G1608	C1668	G1728	A1821
G1822	C1249	U1309	U1369	C1429	A1489	C1549	A1609	U1669	G1729	G1822
U1823	B8N1250	U1310	U1370	G1430	C1490	G1550	U1610	U1670	U1730	U1823
A1824	C1251	C1311	A1371	G1431	A1491	U1551	C1611	G1671	G1731	A1824
A1825	A1252	U1312	A1372	C1432	G1492	C1552	G1612	C1672	U1732	A1825
A1826	A1253	C1313	U1373	G1433	G1493	U1553	G1613	G1673	A1733	A1826
A1827	G1254	G1314	U1374	U1434	U1494	G1554	G1614	G1674	G1734	A1827
A1828	A1255	G1315	C1375	C1435	C1495	C1555	G1615	G1675	U1735	A1828
U1829	G1256	A1316	C1376	C1436	U1496	C1556	A1616	G1676	G1736	U1829
C1830	G1257	U1317	G1377	C1437	G1497	U1557	U1617	A1677	A1737	C1830
U1831	G1258	C1318	U1378	C1438	U1498	A1558	U1618	U1678	G1738	U1831
U1832	G1259	C1319	U1379	C1439	G1499	C1559	G1619	U1679	A1739	U1832
A1833	A1260	C1320	A1380	A1440	A1500	C1560	C1620	A1680	A1833	A1833
	A1261	U1321	A1381	A1441	U1501	C1561	A1621	A1681	C1741	
	A1262	G1322	C1382	C1442	G1502	U1562	A1622	G1682	G1742	
	C1263	G1323	G1383	U1443	C1503	G1563	U1623	U1683	U1743	
	C1264	G1324	A1384	U1444	C1504	C1564	C1624	C1684	C1744	
	U1265	U1325	A1385	C1445	C1505	G1565	A1625	C1685	G1745	
	C1266	G1326	C1386	U1446	U1506	C1566	U1626	C1686	G1746	
	A1267	G1327	G1387	U1447	U1507	C1567	U1627	U1687	A1747	
	C1268	U1328	A1388	U1448	A1508	G1568	C1628	G1688	U1748	
	G1269	G1329	G1389	G1449	G1509	G1569	C1629	C1689	G1749	
	C1270	G1330	A1390	A1450	U1510	C1570	C1630	C1690	G1750	
	G1271	U1331	C1391	A1451	A1511	A1571	C1631	C1691	G1751	
	G1272	G1332	U1392	G1452	U1512	G1572	A1632	U1692	C1752	
	C1273	C1333	C1393	G1453	U1513	G1573	U1633	U1693	C1753	
	C1274	A1334	U1394	A1454	C1514	C1574	G1634	G1694	G1754	
	C1275	U1335	G1395	C1455	C1515	G1575	A1635	U1695	C1755	
	G1276	G1336	G1396	A1456	G1516	C1576	A1636	A1696	U1756	
	G1277	G1337	C1397	A1457	U1517	G1577	C1637	C1697	G1757	
	A1278	C1338	A1398	G1458	G1518	G1578	G1638	A1698	A1790	
	C1279	C1339	U1399	U1459	G1519	G1579	A1639	C1700	G1791	
	A1280	G1340	G1400	G1460	C1520	U1580	G1640	A1701	A1792	
	C1281	U1341	G1401	G1461	U1521	A1581	G1641	C1702	A1793	
	G1282	U1342	U1402	C1462	G1522	A1582	A1642	G1703	G1794	
	G1283	C1343	A1403	G1463	C1523	C1583	A1643	G1704	A1795	
	A1284	U1344	A1404	U1464	A1524	C1584	U1644	C1705	G1796	
	C1285	U1345	C1405	U1465	C1525	C1585	U1645	G1706	C1796	
	G1286	A1346	U1406	U1466	G1526	G1586	C1646	C1707	G1797	
	G1287	G1347	A1407	A1467	C1527	U1587	C1647	U1708	G1798	
	G1288	U1348	G1408	G1468	U1528	U1588	C1648	U1709	U1799	
	A1289	U1349	U1409	G1469	C1529	G1589	A1649	C1710	C1800	
	U1290	G1350	U1410	C1470	U1530	A1590	G1650	G1711	G1801	
	U1291	G1351	A1411	A1471	C1531	A1591	U1651	U1712	A1802	
	G1292	U1352	C1412	G1472	U1532	A1592	A1652	A1713	A1803	
	A1293	G1353	G1413	C1473	A1533	C1593	G1653	C1714	C1804	
	C1294	G1354	G1414	G1474	C1534	C1594	G1654	U1715	U1805	
	A1295	A1355	G1415	G1475	A1535	C1595	U1655	A1716	U1806	
	G1296	G1356	A1416	G1476	U1536	C1596	G1656	A1717	G1807	
	U1297	C1357	A1417	G1477	U1537	A1596	C1657	C1718	A1808	
	U1298	G1358	C1418	U1478	G1538	U1597	G1658	G1719	C1809	
	U1299	U1360	C1419	U1479	A1539	U1598	G1659	A1811	U1810	
	G1300	U1361	U1420	U1480	C1540	C1599	G1660	A1721	U1812	
	A1301	U1362	C1421	G1481	U1541	U1601	U1661	U1722	C1813	
	U1302				G1542	G1602	C1662			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9545	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	100000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.172	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.037	Depositor
Map size (Å)	333.3, 333.3, 333.3	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, 5MC, UR3, 4AC, OMC, OMG, B8T, MG, PSU, 2MG, ZN, A2M, 1MA, B8N

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	A1	0.25	0/1888	0.40	0/2516
2	A2	0.23	1/84889 (0.0%)	0.32	0/132400
3	A3	0.15	0/1169	0.41	0/1568
4	B1	0.19	0/1847	0.37	0/2486
5	B2	0.20	0/2836	0.28	0/4421
6	B3	0.13	0/1122	0.33	0/1503
7	Bv	0.23	0/1813	0.39	0/2823
7	Bz	0.23	0/1813	0.41	0/2823
7	n2	0.14	0/1813	0.34	0/2823
8	Bx	0.41	0/219	0.53	0/336
10	C1	0.21	0/1537	0.39	0/2065
11	C2	0.22	0/3675	0.31	0/5725
12	C3	0.13	0/818	0.32	0/1099
13	D1	0.22	0/1694	0.38	0/2261
14	D2	0.25	0/1959	0.44	0/2627
15	D3	0.11	0/645	0.32	0/863
16	E1	0.20	0/1420	0.42	0/1899
17	E2	0.24	0/3305	0.45	0/4422
18	E3	0.13	0/1097	0.39	0/1464
19	F1	0.22	0/1674	0.41	0/2241
20	F2	0.24	0/2921	0.41	0/3921
21	F3	0.14	0/805	0.37	0/1079
22	G1	0.19	0/1165	0.37	0/1558
23	G2	0.20	0/2435	0.38	0/3260
24	G3	0.13	0/490	0.37	0/656
25	H1	0.27	0/1746	0.42	1/2338 (0.0%)
26	H2	0.19	0/1822	0.37	0/2443
27	H3	0.18	0/466	0.43	0/618
28	I2	0.25	0/1670	0.43	0/2232
29	I3	0.12	0/2493	0.36	0/3394
30	J2	0.24	0/1268	0.43	0/1700
31	J3	0.13	0/1737	0.35	0/2348

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	K2	0.23	0/1535	0.40	0/2048
33	K3	0.11	0/1863	0.32	0/2481
34	L1	0.13	0/1318	0.39	0/1767
35	L2	0.22	0/1515	0.36	0/2002
36	L3	0.10	0/1542	0.29	0/2058
37	M2	0.24	0/1490	0.41	0/2000
38	M3	0.10	0/962	0.27	0/1289
39	N2	0.22	0/1327	0.37	0/1771
40	N3	0.11	0/1232	0.31	0/1656
41	O2	0.17	0/839	0.38	0/1126
42	O3	0.12	0/1015	0.32	0/1361
43	P2	0.23	0/983	0.43	0/1319
44	P3	0.12	0/1051	0.31	0/1406
45	Q2	0.22	0/532	0.40	0/708
46	Q3	0.13	0/1019	0.36	0/1354
47	R2	0.21	0/984	0.39	0/1323
48	R3	0.13	0/576	0.35	0/774
49	S2	0.21	0/1132	0.41	0/1504
50	S3	0.14	0/665	0.40	0/891
51	T2	0.20	0/1130	0.39	0/1507
52	T3	0.12	0/443	0.35	0/582
53	U2	0.26	0/1193	0.39	0/1593
54	U3	0.12	0/424	0.32	0/566
55	V2	0.21	0/963	0.38	0/1275
56	W2	0.17	0/742	0.38	0/996
57	X2	0.21	0/903	0.38	0/1216
58	Y2	0.27	0/1071	0.40	0/1429
59	Z2	0.24	0/895	0.39	0/1198
60	a2	0.23	0/916	0.42	0/1221
61	b2	0.20	0/1009	0.39	0/1332
62	c2	0.19	0/843	0.37	0/1115
63	d2	0.26	0/720	0.46	0/952
64	e2	0.19	0/574	0.38	0/760
65	f2	0.24	0/454	0.36	0/599
66	g2	0.24	0/435	0.43	0/575
67	h2	0.15	0/231	0.37	0/294
68	i2	0.23	0/855	0.46	0/1128
69	j2	0.23	0/704	0.42	0/935
70	k2	0.23	0/1016	0.41	0/1363
71	o2	0.11	0/1731	0.28	0/2352
72	p2	0.15	0/1749	0.41	0/2340
73	q2	0.13	0/1739	0.34	0/2342
74	r2	0.14	0/2118	0.37	0/2849

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	s2	0.13	0/1477	0.33	0/1983
76	t2	0.13	0/1299	0.36	0/1767
77	u2	0.12	0/1662	0.36	0/2228
78	v2	0.14	0/824	0.33	0/1112
79	w2	0.13	0/1241	0.38	0/1662
80	x2	0.13	0/1103	0.35	0/1475
81	y2	0.15	0/1146	0.35	0/1534
82	z2	0.12	0/567	0.34	0/756
83	m2	0.42	3/38273 (0.0%)	0.34	12/59642 (0.0%)
All	All	0.26	4/228281 (0.0%)	0.35	13/335428 (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
17	E2	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	m2	1350	G	O3'-P	-75.31	0.48	1.61
2	A2	3441	A2M	O3'-P	5.15	1.61	1.56
83	m2	486	A2M	O3'-P	5.05	1.61	1.56
83	m2	670	A2M	O3'-P	5.03	1.61	1.56

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	m2	1350	G	P-O3'-C3'	21.54	152.50	120.20
83	m2	1350	G	OP2-P-O3'	-17.10	56.70	108.00
83	m2	1350	G	O3'-P-O5'	9.97	118.95	104.00
83	m2	1358	G	O3'-P-O5'	-8.61	91.09	104.00
83	m2	1357	C	C1'-C2'-O2'	-7.40	97.31	108.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	E2	258	HIS	Peptide

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	A1	1851	0	1988	38	0
2	A2	77547	0	39261	880	0
3	A3	1151	0	1202	48	0
4	B1	1812	0	1947	33	0
5	B2	2538	0	1286	13	0
6	B3	1104	0	1139	29	0
7	Bv	1623	0	820	23	0
7	Bz	1623	0	821	31	0
7	n2	1623	0	821	34	0
8	Bx	200	0	101	5	0
9	By	110	0	31	1	0
10	C1	1519	0	1603	24	0
11	C2	3315	0	1685	34	0
12	C3	808	0	878	26	0
13	D1	1656	0	1706	18	0
14	D2	1921	0	2022	38	0
15	D3	638	0	635	13	0
16	E1	1397	0	1425	36	0
17	E2	3238	0	3380	58	0
18	E3	1080	0	1147	16	0
19	F1	1643	0	1750	29	0
20	F2	2867	0	3040	49	0
21	F3	789	0	841	21	0
22	G1	1143	0	1219	22	0
23	G2	2389	0	2420	32	0
24	G3	488	0	514	18	0
25	H1	1701	0	1749	29	0
26	H2	1789	0	1932	27	0
27	H3	455	0	445	17	0
28	I2	1640	0	1792	24	0
29	I3	2436	0	2393	62	0
30	J2	1242	0	1274	22	0
31	J3	1700	0	1786	44	0
32	K2	1511	0	1636	33	0
33	K3	1840	0	1989	38	0
34	L1	1300	0	1375	26	0
35	L2	1499	0	1651	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	L3	1518	0	1632	26	0
37	M2	1450	0	1488	19	0
38	M3	952	0	993	19	0
39	N2	1299	0	1368	20	0
40	N3	1208	0	1294	17	0
41	O2	825	0	850	11	0
42	O3	1002	0	1023	30	0
43	P2	969	0	1031	23	0
44	P3	1034	0	1080	20	0
45	Q2	519	0	533	4	0
46	Q3	1002	0	1075	16	0
47	R2	967	0	1040	17	0
48	R3	570	0	626	16	0
49	S2	1115	0	1205	18	0
50	S3	651	0	672	13	0
51	T2	1107	0	1182	22	0
52	T3	438	0	484	10	0
53	U2	1164	0	1213	17	0
54	U3	415	0	393	9	0
55	V2	945	0	1037	11	0
56	W2	732	0	769	10	0
57	X2	888	0	930	12	0
58	Y2	1053	0	1147	15	0
59	Z2	876	0	912	15	0
60	a2	906	0	997	20	0
61	b2	1001	0	1138	17	0
62	c2	832	0	917	9	0
63	d2	705	0	737	14	0
64	e2	568	0	635	17	0
65	f2	444	0	483	8	0
66	g2	429	0	465	3	0
67	h2	230	0	276	25	0
68	i2	842	0	912	13	0
69	j2	694	0	738	10	0
70	k2	1001	0	1066	28	0
71	o2	1694	0	1696	45	0
72	p2	1722	0	1794	47	0
73	q2	1711	0	1804	48	0
74	r2	2076	0	2177	52	0
75	s2	1457	0	1508	45	0
76	t2	1278	0	1207	26	0
77	u2	1633	0	1664	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
78	v2	800	0	818	25	0
79	w2	1220	0	1289	18	0
80	x2	1081	0	1134	42	0
81	y2	1128	0	1195	19	0
82	z2	560	0	614	13	0
83	m2	34939	0	17651	711	0
84	A2	82	0	0	0	0
84	Bv	2	0	0	0	0
84	H1	1	0	0	0	0
84	J2	1	0	0	0	0
84	P2	1	0	0	0	0
84	d2	1	0	0	0	0
84	m2	30	0	0	0	0
85	F3	1	0	0	0	0
85	H3	1	0	0	0	0
85	d2	1	0	0	0	0
85	g2	1	0	0	0	0
85	i2	1	0	0	0	0
85	j2	1	0	0	0	0
86	B1	1	0	0	0	0
All	All	214961	0	158596	3072	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 8.

The worst 5 of 3072 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)
83:m2:1350:G:H2'	83:m2:1351:G:C5'	1.31	1.59
83:m2:1351:G:C2	83:m2:1383:G:N2	1.76	1.51
83:m2:1350:G:C2'	83:m2:1351:G:H5''	1.29	1.38
2:A2:1376:A:N6	83:m2:1030:A:N1	1.70	1.35
83:m2:1351:G:N1	83:m2:1383:G:C2	1.97	1.32

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A1	221/270 (82%)	215 (97%)	6 (3%)	0	100	100
3	A3	138/152 (91%)	126 (91%)	12 (9%)	0	100	100
4	B1	220/266 (83%)	212 (96%)	8 (4%)	0	100	100
6	B3	139/145 (96%)	135 (97%)	4 (3%)	0	100	100
10	C1	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
12	C3	100/119 (84%)	98 (98%)	2 (2%)	0	100	100
13	D1	200/214 (94%)	193 (96%)	7 (4%)	0	100	100
14	D2	249/257 (97%)	233 (94%)	16 (6%)	0	100	100
15	D3	81/83 (98%)	81 (100%)	0	0	100	100
16	E1	172/178 (97%)	160 (93%)	12 (7%)	0	100	100
17	E2	400/403 (99%)	382 (96%)	18 (4%)	0	100	100
18	E3	137/143 (96%)	133 (97%)	4 (3%)	0	100	100
19	F1	201/211 (95%)	193 (96%)	8 (4%)	0	100	100
20	F2	357/419 (85%)	345 (97%)	12 (3%)	0	100	100
21	F3	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
22	G1	137/217 (63%)	133 (97%)	4 (3%)	0	100	100
23	G2	291/297 (98%)	288 (99%)	3 (1%)	0	100	100
24	G3	60/69 (87%)	57 (95%)	3 (5%)	0	100	100
25	H1	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
26	H2	215/296 (73%)	207 (96%)	8 (4%)	0	100	100
27	H3	52/56 (93%)	45 (86%)	7 (14%)	0	100	100
28	I2	199/203 (98%)	194 (98%)	5 (2%)	0	100	100
29	I3	311/317 (98%)	295 (95%)	16 (5%)	0	100	100
30	J2	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
31	J3	217/293 (74%)	211 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	K2	184/188 (98%)	176 (96%)	8 (4%)	0	100	100
33	K3	225/249 (90%)	222 (99%)	3 (1%)	0	100	100
34	L1	155/217 (71%)	146 (94%)	9 (6%)	0	100	100
35	L2	177/196 (90%)	176 (99%)	1 (1%)	0	100	100
36	L3	182/194 (94%)	177 (97%)	5 (3%)	0	100	100
37	M2	173/176 (98%)	162 (94%)	11 (6%)	0	100	100
38	M3	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
39	N2	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
40	N3	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
41	O2	99/128 (77%)	95 (96%)	4 (4%)	0	100	100
42	O3	132/151 (87%)	128 (97%)	4 (3%)	0	100	100
43	P2	127/140 (91%)	121 (95%)	5 (4%)	1 (1%)	16	47
44	P3	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
45	Q2	60/157 (38%)	57 (95%)	3 (5%)	0	100	100
46	Q3	120/133 (90%)	116 (97%)	4 (3%)	0	100	100
47	R2	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
48	R3	70/125 (56%)	69 (99%)	1 (1%)	0	100	100
49	S2	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
50	S3	81/84 (96%)	76 (94%)	4 (5%)	1 (1%)	10	38
51	T2	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
52	T3	53/133 (40%)	52 (98%)	1 (2%)	0	100	100
53	U2	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
54	U3	50/156 (32%)	45 (90%)	5 (10%)	0	100	100
55	V2	115/160 (72%)	112 (97%)	3 (3%)	0	100	100
56	W2	92/115 (80%)	89 (97%)	3 (3%)	0	100	100
57	X2	105/125 (84%)	101 (96%)	4 (4%)	0	100	100
58	Y2	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
59	Z2	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
60	a2	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
61	b2	118/123 (96%)	117 (99%)	1 (1%)	0	100	100
62	c2	100/105 (95%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	d2	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
64	e2	67/70 (96%)	67 (100%)	0	0	100	100
65	f2	48/51 (94%)	48 (100%)	0	0	100	100
66	g2	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
67	h2	22/25 (88%)	22 (100%)	0	0	100	100
68	i2	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
69	j2	87/92 (95%)	81 (93%)	6 (7%)	0	100	100
70	k2	123/137 (90%)	118 (96%)	5 (4%)	0	100	100
71	o2	212/295 (72%)	205 (97%)	7 (3%)	0	100	100
72	p2	210/264 (80%)	188 (90%)	22 (10%)	0	100	100
73	q2	218/243 (90%)	209 (96%)	9 (4%)	0	100	100
74	r2	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
75	s2	179/204 (88%)	175 (98%)	4 (2%)	0	100	100
76	t2	179/194 (92%)	166 (93%)	13 (7%)	0	100	100
77	u2	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
78	v2	93/165 (56%)	92 (99%)	1 (1%)	0	100	100
79	w2	148/158 (94%)	137 (93%)	10 (7%)	1 (1%)	18	50
80	x2	130/145 (90%)	127 (98%)	3 (2%)	0	100	100
81	y2	140/146 (96%)	132 (94%)	8 (6%)	0	100	100
82	z2	67/135 (50%)	65 (97%)	2 (3%)	0	100	100
All	All	11197/13004 (86%)	10770 (96%)	424 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	P2	92	ASP
50	S3	75	GLU
79	w2	25	LEU

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	A1	194/234 (83%)	194 (100%)	0	100	100
3	A3	121/132 (92%)	121 (100%)	0	100	100
4	B1	193/223 (86%)	193 (100%)	0	100	100
6	B3	112/115 (97%)	112 (100%)	0	100	100
10	C1	169/171 (99%)	169 (100%)	0	100	100
12	C3	93/107 (87%)	93 (100%)	0	100	100
13	D1	174/181 (96%)	174 (100%)	0	100	100
14	D2	193/199 (97%)	193 (100%)	0	100	100
15	D3	67/67 (100%)	67 (100%)	0	100	100
16	E1	147/149 (99%)	147 (100%)	0	100	100
17	E2	347/348 (100%)	347 (100%)	0	100	100
18	E3	111/115 (96%)	111 (100%)	0	100	100
19	F1	170/178 (96%)	170 (100%)	0	100	100
20	F2	301/348 (86%)	301 (100%)	0	100	100
21	F3	86/98 (88%)	86 (100%)	0	100	100
22	G1	118/157 (75%)	118 (100%)	0	100	100
23	G2	246/249 (99%)	246 (100%)	0	100	100
24	G3	55/62 (89%)	55 (100%)	0	100	100
25	H1	171/172 (99%)	171 (100%)	0	100	100
26	H2	198/256 (77%)	198 (100%)	0	100	100
27	H3	48/49 (98%)	48 (100%)	0	100	100
28	I2	172/173 (99%)	172 (100%)	0	100	100
29	I3	272/275 (99%)	272 (100%)	0	100	100
30	J2	134/163 (82%)	134 (100%)	0	100	100
31	J3	185/224 (83%)	185 (100%)	0	100	100
32	K2	164/165 (99%)	164 (100%)	0	100	100
33	K3	198/218 (91%)	198 (100%)	0	100	100
34	L1	147/197 (75%)	147 (100%)	0	100	100
35	L2	158/175 (90%)	158 (100%)	0	100	100
36	L3	160/168 (95%)	160 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	M2	155/156 (99%)	155 (100%)	0	100	100
38	M3	104/108 (96%)	104 (100%)	0	100	100
39	N2	139/140 (99%)	139 (100%)	0	100	100
40	N3	130/131 (99%)	130 (100%)	0	100	100
41	O2	91/114 (80%)	91 (100%)	0	100	100
42	O3	104/119 (87%)	103 (99%)	1 (1%)	68	75
43	P2	100/107 (94%)	100 (100%)	0	100	100
44	P3	112/113 (99%)	112 (100%)	0	100	100
45	Q2	54/126 (43%)	54 (100%)	0	100	100
46	Q3	107/115 (93%)	107 (100%)	0	100	100
47	R2	106/133 (80%)	106 (100%)	0	100	100
48	R3	63/103 (61%)	63 (100%)	0	100	100
49	S2	124/135 (92%)	124 (100%)	0	100	100
50	S3	75/76 (99%)	75 (100%)	0	100	100
51	T2	117/118 (99%)	117 (100%)	0	100	100
52	T3	45/106 (42%)	45 (100%)	0	100	100
53	U2	120/121 (99%)	120 (100%)	0	100	100
54	U3	45/140 (32%)	45 (100%)	0	100	100
55	V2	98/124 (79%)	98 (100%)	0	100	100
56	W2	79/97 (81%)	79 (100%)	0	100	100
57	X2	98/110 (89%)	98 (100%)	0	100	100
58	Y2	114/121 (94%)	114 (100%)	0	100	100
59	Z2	88/89 (99%)	88 (100%)	0	100	100
60	a2	98/100 (98%)	98 (100%)	0	100	100
61	b2	108/110 (98%)	108 (100%)	0	100	100
62	c2	86/89 (97%)	86 (100%)	0	100	100
63	d2	73/80 (91%)	73 (100%)	0	100	100
64	e2	64/65 (98%)	64 (100%)	0	100	100
65	f2	47/48 (98%)	47 (100%)	0	100	100
66	g2	48/116 (41%)	48 (100%)	0	100	100
67	h2	23/24 (96%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	i2	91/94 (97%)	91 (100%)	0	100	100
69	j2	73/75 (97%)	73 (100%)	0	100	100
70	k2	109/121 (90%)	109 (100%)	0	100	100
71	o2	179/242 (74%)	179 (100%)	0	100	100
72	p2	193/229 (84%)	192 (100%)	1 (0%)	81	81
73	q2	184/202 (91%)	184 (100%)	0	100	100
74	r2	224/225 (100%)	224 (100%)	0	100	100
75	s2	156/170 (92%)	156 (100%)	0	100	100
76	t2	110/174 (63%)	110 (100%)	0	100	100
77	u2	165/180 (92%)	165 (100%)	0	100	100
78	v2	86/136 (63%)	86 (100%)	0	100	100
79	w2	134/142 (94%)	134 (100%)	0	100	100
80	x2	118/130 (91%)	118 (100%)	0	100	100
81	y2	117/121 (97%)	117 (100%)	0	100	100
82	z2	60/121 (50%)	60 (100%)	0	100	100
All	All	9718/11064 (88%)	9716 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	O3	26	ASN
72	p2	75	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
52	T3	58	ASN
62	c2	15	HIS
54	U3	135	HIS
58	Y2	80	HIS
68	i2	25	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	C2	155/156 (99%)	31 (20%)	1 (0%)
2	A2	3593/3615 (99%)	764 (21%)	11 (0%)
5	B2	118/121 (97%)	9 (7%)	0
7	Bv	75/76 (98%)	20 (26%)	0
7	Bz	75/76 (98%)	23 (30%)	0
7	n2	75/76 (98%)	33 (44%)	0
8	Bx	9/10 (90%)	4 (44%)	0
83	m2	1627/1635 (99%)	400 (24%)	0
All	All	5727/5765 (99%)	1284 (22%)	12 (0%)

5 of 1284 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A2	2	G
2	A2	5	A
2	A2	21	G
2	A2	25	A
2	A2	39	A

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A2	3253	G
2	A2	4277	C
11	C2	59	A
2	A2	4351	U
2	A2	2259	C

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

108 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	$\# Z > 2$
83	A2M	m2	99	84,83	22,25,26	0.07	0	31,36,39	0.21	0
2	PSU	A2	4183	2	18,21,22	0.52	0	22,30,33	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	A2	3400	2	23,26,27	0.31	0	33,38,41	0.44	0
83	PSU	m2	1245	83	18,21,22	0.54	0	22,30,33	0.56	0
2	A2M	A2	3486	2	22,25,26	0.09	0	31,36,39	0.42	0
2	OMG	A2	3448	2	23,26,27	0.34	0	33,38,41	0.34	0
2	PSU	A2	4152	2	18,21,22	0.53	0	22,30,33	0.65	0
2	OMC	A2	2579	2	19,22,23	0.29	0	26,31,34	0.39	0
2	PSU	A2	4280	2	18,21,22	0.54	0	22,30,33	0.56	0
2	5MC	A2	3438	2,84	18,22,23	0.30	0	26,32,35	0.40	0
83	OMU	m2	121	83	19,22,23	0.30	0	26,31,34	0.46	0
2	OMC	A2	1683	2,84	19,22,23	0.32	0	26,31,34	0.54	0
2	OMC	A2	3357	2	19,22,23	0.25	0	26,31,34	0.42	0
83	A2M	m2	27	83	22,25,26	0.12	0	31,36,39	0.32	0
83	OMG	m2	511	84,83	23,26,27	0.29	0	33,38,41	0.40	0
2	A2M	A2	4223	2	22,25,26	0.11	0	31,36,39	0.26	0
2	OMG	A2	4044	2,84	23,26,27	0.39	0	33,38,41	0.39	0
2	OMC	A2	3543	2	19,22,23	0.33	0	26,31,34	0.45	0
2	OMU	A2	3581	2	19,22,23	0.33	0	26,31,34	0.46	0
2	A2M	A2	3441	2	22,25,26	0.10	0	31,36,39	0.36	0
83	A2M	m2	1680	83	22,25,26	0.08	0	31,36,39	0.16	0
83	OMC	m2	174	83	19,22,23	0.34	0	26,31,34	0.56	0
2	OMG	A2	1438	2	23,26,27	0.27	0	33,38,41	0.40	0
83	OMC	m2	519	83	19,22,23	0.28	0	26,31,34	0.46	0
2	A2M	A2	1337	2	22,25,26	0.12	0	31,36,39	0.28	0
2	OMG	A2	3880	2	23,26,27	0.33	0	33,38,41	0.51	0
2	OMU	A2	3958	2	19,22,23	0.35	0	26,31,34	0.46	0
2	OMG	A2	4289	2	23,26,27	0.36	0	33,38,41	0.38	0
2	OMC	A2	3525	2	19,22,23	0.33	0	26,31,34	0.39	0
2	5MC	A2	4099	2	18,22,23	0.36	0	26,32,35	0.56	0
83	OMG	m2	438	83	23,26,27	0.28	0	33,38,41	0.44	0
2	PSU	A2	3385	2	18,21,22	0.55	0	22,30,33	0.57	0
83	OMU	m2	430	83	19,22,23	0.25	0	26,31,34	0.44	0
2	A2M	A2	3380	2	22,25,26	0.12	0	31,36,39	0.44	0
2	OMG	A2	4151	2	23,26,27	0.37	0	33,38,41	0.53	0
2	OMC	A2	1154	2	19,22,23	0.33	0	26,31,34	0.46	0
2	OMC	A2	2120	2	19,22,23	0.32	0	26,31,34	0.48	0
2	OMC	A2	2106	2	19,22,23	0.32	0	26,31,34	0.38	0
83	B8N	m2	1250	83	24,29,30	0.58	0	29,42,45	0.63	0
83	OMG	m2	603	83	23,26,27	0.27	0	33,38,41	0.33	0
2	OMG	A2	3848	2,7	23,26,27	0.35	0	33,38,41	0.34	0
2	PSU	A2	3945	2	18,21,22	0.52	0	22,30,33	0.59	0
2	PSU	A2	4288	2	18,21,22	0.51	0	22,30,33	0.62	0
83	OMG	m2	646	83	23,26,27	0.27	0	33,38,41	0.35	0
83	PSU	m2	1083	83	18,21,22	0.59	1 (5%)	22,30,33	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMC	A2	2177	2,84	19,22,23	0.32	0	26,31,34	0.44	0
2	2MG	A2	1330	2	23,26,27	0.31	0	32,38,41	0.35	0
2	PSU	A2	2263	2	18,21,22	0.53	0	22,30,33	0.59	0
2	PSU	A2	4102	2,84	18,21,22	0.53	0	22,30,33	0.41	0
83	A2M	m2	1033	83	22,25,26	0.07	0	31,36,39	0.19	0
83	OMU	m2	172	83	19,22,23	0.26	0	26,31,34	0.64	1 (3%)
2	OMG	A2	4022	2	23,26,27	0.31	0	33,38,41	0.39	0
2	A2M	A2	3374	2	22,25,26	0.11	0	31,36,39	0.29	0
83	PSU	m2	614	83	18,21,22	0.50	0	22,30,33	0.62	1 (4%)
2	PSU	A2	3371	2	18,21,22	0.56	0	22,30,33	0.63	1 (4%)
83	A2M	m2	670	84,83	22,25,26	0.09	0	31,36,39	0.34	0
2	OMG	A2	1130	2	23,26,27	0.42	0	33,38,41	0.55	0
2	A2M	A2	398	2	22,25,26	0.10	0	31,36,39	0.29	0
83	PSU	m2	824	83	18,21,22	0.60	1 (5%)	22,30,33	0.67	1 (4%)
2	A2M	A2	2156	2	22,25,26	0.10	0	31,36,39	0.22	0
2	A2M	A2	1673	2	22,25,26	0.11	0	31,36,39	0.50	0
83	OMU	m2	116	83	19,22,23	0.26	0	26,31,34	0.39	0
2	A2M	A2	4175	2,84	22,25,26	0.11	0	31,36,39	0.38	0
2	A2M	A2	1137	2	22,25,26	0.09	0	31,36,39	0.23	0
83	A2M	m2	514	83	22,25,26	0.09	0	31,36,39	0.38	0
2	OMG	A2	2179	2	23,26,27	0.31	0	33,38,41	0.32	0
83	OMG	m2	685	83	23,26,27	0.27	0	33,38,41	0.49	0
2	OMG	A2	3555	2,84	23,26,27	0.39	0	33,38,41	0.54	0
2	A2M	A2	4270	2	22,25,26	0.11	0	31,36,39	0.31	0
2	OMC	A2	3464	2	19,22,23	0.32	0	26,31,34	0.38	0
83	OMG	m2	1330	83	23,26,27	0.31	0	33,38,41	0.34	0
2	OMC	A2	2616	2	19,22,23	0.31	0	26,31,34	0.37	0
2	A2M	A2	2118	2,84	22,25,26	0.10	0	31,36,39	0.28	0
2	OMC	A2	4188	2	19,22,23	0.34	0	26,31,34	0.50	0
83	A2M	m2	486	83	22,25,26	0.08	0	31,36,39	0.21	0
83	OMG	m2	869	83	23,26,27	0.27	0	33,38,41	0.34	0
11	OMG	C2	75	11	23,26,27	0.31	0	33,38,41	0.37	0
2	OMU	A2	2592	2	19,22,23	0.33	0	26,31,34	0.63	0
2	OMU	A2	4150	2	19,22,23	0.31	0	26,31,34	0.47	0
2	OMG	A2	4275	2	23,26,27	0.39	0	33,38,41	0.56	0
2	OMC	A2	2559	2	19,22,23	0.32	0	26,31,34	0.43	0
83	4AC	m2	1844	83	21,24,25	0.31	0	29,34,37	0.30	0
2	OMU	A2	3474	2	19,22,23	0.36	0	26,31,34	0.39	0
83	OMC	m2	1705	83	19,22,23	0.27	0	26,31,34	0.36	0
2	OMC	A2	3497	2	19,22,23	0.33	0	26,31,34	0.42	0
83	UR3	m2	1832	83	19,22,23	0.28	0	26,32,35	0.43	0
2	PSU	A2	4055	2	18,21,22	0.54	0	22,30,33	0.63	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
83	B8T	m2	1339	83	19,22,23	0.38	0	26,31,34	0.36	0
2	A2M	A2	3481	2	22,25,26	0.09	0	31,36,39	0.48	0
2	OMC	A2	4108	2	19,22,23	0.33	0	26,31,34	0.34	0
2	PSU	A2	4094	2	18,21,22	0.59	1 (5%)	22,30,33	0.64	1 (4%)
2	1MA	A2	4067	2	21,25,26	0.33	0	31,37,40	0.47	0
2	PSU	A2	1395	2	18,21,22	0.58	0	22,30,33	0.57	0
2	A2M	A2	2542	2	22,25,26	0.09	0	31,36,39	0.35	0
2	PSU	A2	1490	2	18,21,22	0.91	1 (5%)	22,30,33	0.60	0
83	A2M	m2	578	83	22,25,26	0.08	0	31,36,39	0.27	0
2	A2M	A2	1347	2,84	22,25,26	0.11	0	31,36,39	0.56	1 (3%)
2	A2M	A2	1140	2,84	22,25,26	0.09	0	31,36,39	0.19	0
2	PSU	A2	3420	2	18,21,22	0.54	0	22,30,33	0.37	0
2	OMU	A2	4272	2	19,22,23	0.39	0	26,31,34	0.67	0
2	OMG	A2	1335	2	23,26,27	0.35	0	33,38,41	0.45	0
2	OMG	A2	4146	2	23,26,27	0.34	0	33,38,41	0.43	0
2	A2M	A2	2570	2	22,25,26	0.10	0	31,36,39	0.20	0
2	PSU	A2	1496	2	18,21,22	0.53	0	22,30,33	0.57	0
83	OMC	m2	355	83	19,22,23	0.28	0	26,31,34	0.41	0
2	OMG	A2	2119	2,84	23,26,27	0.33	0	33,38,41	0.43	0
83	PSU	m2	825	83	18,21,22	0.49	0	22,30,33	0.54	0
2	OMG	A2	3283	2	23,26,27	0.34	0	33,38,41	0.48	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
83	A2M	m2	99	84,83	-	1/9/27/28	0/3/3/3
2	PSU	A2	4183	2	-	2/7/25/26	0/2/2/2
2	OMG	A2	3400	2	-	0/9/27/28	0/3/3/3
83	PSU	m2	1245	83	-	1/7/25/26	0/2/2/2
2	A2M	A2	3486	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	3448	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	4152	2	-	1/7/25/26	0/2/2/2
2	OMC	A2	2579	2	-	1/9/27/28	0/2/2/2
2	PSU	A2	4280	2	-	0/7/25/26	0/2/2/2
2	5MC	A2	3438	2,84	-	0/7/25/26	0/2/2/2
83	OMU	m2	121	83	-	0/9/27/28	0/2/2/2
2	OMC	A2	1683	2,84	-	0/9/27/28	0/2/2/2
2	OMC	A2	3357	2	-	4/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	A2M	m2	27	83	-	2/9/27/28	0/3/3/3
83	OMG	m2	511	84,83	-	0/9/27/28	0/3/3/3
2	A2M	A2	4223	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	4044	2,84	-	0/9/27/28	0/3/3/3
2	OMC	A2	3543	2	-	0/9/27/28	0/2/2/2
2	OMU	A2	3581	2	-	0/9/27/28	0/2/2/2
2	A2M	A2	3441	2	-	4/9/27/28	0/3/3/3
83	A2M	m2	1680	83	-	1/9/27/28	0/3/3/3
83	OMC	m2	174	83	-	2/9/27/28	0/2/2/2
2	OMG	A2	1438	2	-	2/9/27/28	0/3/3/3
83	OMC	m2	519	83	-	2/9/27/28	0/2/2/2
2	A2M	A2	1337	2	-	1/9/27/28	0/3/3/3
2	OMG	A2	3880	2	-	0/9/27/28	0/3/3/3
2	OMU	A2	3958	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	4289	2	-	3/9/27/28	0/3/3/3
2	OMC	A2	3525	2	-	1/9/27/28	0/2/2/2
2	5MC	A2	4099	2	-	4/7/25/26	0/2/2/2
83	OMG	m2	438	83	-	0/9/27/28	0/3/3/3
2	PSU	A2	3385	2	-	0/7/25/26	0/2/2/2
83	OMU	m2	430	83	-	4/9/27/28	0/2/2/2
2	A2M	A2	3380	2	-	1/9/27/28	0/3/3/3
2	OMG	A2	4151	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	1154	2	-	1/9/27/28	0/2/2/2
2	OMC	A2	2120	2	-	0/9/27/28	0/2/2/2
2	OMC	A2	2106	2	-	2/9/27/28	0/2/2/2
83	B8N	m2	1250	83	-	3/16/34/35	0/2/2/2
83	OMG	m2	603	83	-	1/9/27/28	0/3/3/3
2	OMG	A2	3848	2,7	-	1/9/27/28	0/3/3/3
2	PSU	A2	3945	2	-	0/7/25/26	0/2/2/2
2	PSU	A2	4288	2	-	3/7/25/26	0/2/2/2
83	OMG	m2	646	83	-	1/9/27/28	0/3/3/3
83	PSU	m2	1083	83	-	1/7/25/26	0/2/2/2
2	OMC	A2	2177	2,84	-	1/9/27/28	0/2/2/2
2	2MG	A2	1330	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	2263	2	-	0/7/25/26	0/2/2/2
2	PSU	A2	4102	2,84	-	3/7/25/26	0/2/2/2
83	A2M	m2	1033	83	-	1/9/27/28	0/3/3/3
83	OMU	m2	172	83	-	3/9/27/28	0/2/2/2
2	OMG	A2	4022	2	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	A2	3374	2	-	0/9/27/28	0/3/3/3
83	PSU	m2	614	83	-	0/7/25/26	0/2/2/2
2	PSU	A2	3371	2	-	0/7/25/26	0/2/2/2
83	A2M	m2	670	84,83	-	2/9/27/28	0/3/3/3
2	OMG	A2	1130	2	-	0/9/27/28	0/3/3/3
2	A2M	A2	398	2	-	0/9/27/28	0/3/3/3
83	PSU	m2	824	83	-	0/7/25/26	0/2/2/2
2	A2M	A2	2156	2	-	1/9/27/28	0/3/3/3
2	A2M	A2	1673	2	-	0/9/27/28	0/3/3/3
83	OMU	m2	116	83	-	1/9/27/28	0/2/2/2
2	A2M	A2	4175	2,84	-	1/9/27/28	0/3/3/3
2	A2M	A2	1137	2	-	0/9/27/28	0/3/3/3
83	A2M	m2	514	83	-	0/9/27/28	0/3/3/3
2	OMG	A2	2179	2	-	1/9/27/28	0/3/3/3
83	OMG	m2	685	83	-	0/9/27/28	0/3/3/3
2	OMG	A2	3555	2,84	-	0/9/27/28	0/3/3/3
2	A2M	A2	4270	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	3464	2	-	0/9/27/28	0/2/2/2
83	OMG	m2	1330	83	-	2/9/27/28	0/3/3/3
2	OMC	A2	2616	2	-	0/9/27/28	0/2/2/2
2	A2M	A2	2118	2,84	-	1/9/27/28	0/3/3/3
2	OMC	A2	4188	2	-	0/9/27/28	0/2/2/2
83	A2M	m2	486	83	-	0/9/27/28	0/3/3/3
83	OMG	m2	869	83	-	1/9/27/28	0/3/3/3
11	OMG	C2	75	11	-	3/9/27/28	0/3/3/3
2	OMU	A2	2592	2	-	0/9/27/28	0/2/2/2
2	OMU	A2	4150	2	-	0/9/27/28	0/2/2/2
2	OMG	A2	4275	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	2559	2	-	0/9/27/28	0/2/2/2
83	4AC	m2	1844	83	-	0/11/29/30	0/2/2/2
2	OMU	A2	3474	2	-	2/9/27/28	0/2/2/2
83	OMC	m2	1705	83	-	1/9/27/28	0/2/2/2
2	OMC	A2	3497	2	-	0/9/27/28	0/2/2/2
83	UR3	m2	1832	83	-	2/7/25/26	0/2/2/2
2	PSU	A2	4055	2	-	0/7/25/26	0/2/2/2
83	B8T	m2	1339	83	-	0/7/27/28	0/2/2/2
2	A2M	A2	3481	2	-	0/9/27/28	0/3/3/3
2	OMC	A2	4108	2	-	0/9/27/28	0/2/2/2
2	PSU	A2	4094	2	-	0/7/25/26	0/2/2/2
2	1MA	A2	4067	2	-	2/7/25/26	0/3/3/3
2	PSU	A2	1395	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	A2	2542	2	-	3/9/27/28	0/3/3/3
2	PSU	A2	1490	2	-	0/7/25/26	0/2/2/2
83	A2M	m2	578	83	-	1/9/27/28	0/3/3/3
2	A2M	A2	1347	2,84	-	3/9/27/28	0/3/3/3
2	A2M	A2	1140	2,84	-	3/9/27/28	0/3/3/3
2	PSU	A2	3420	2	-	2/7/25/26	0/2/2/2
2	OMU	A2	4272	2	-	3/9/27/28	0/2/2/2
2	OMG	A2	1335	2	-	0/9/27/28	0/3/3/3
2	OMG	A2	4146	2	-	1/9/27/28	0/3/3/3
2	A2M	A2	2570	2	-	0/9/27/28	0/3/3/3
2	PSU	A2	1496	2	-	0/7/25/26	0/2/2/2
83	OMC	m2	355	83	-	1/9/27/28	0/2/2/2
2	OMG	A2	2119	2,84	-	1/9/27/28	0/3/3/3
83	PSU	m2	825	83	-	0/7/25/26	0/2/2/2
2	OMG	A2	3283	2	-	0/9/27/28	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A2	1490	PSU	O4'-C1'	-3.40	1.39	1.43
83	m2	824	PSU	O4'-C1'	-2.17	1.40	1.43
83	m2	1083	PSU	O4'-C1'	-2.15	1.40	1.43
2	A2	4094	PSU	O4'-C1'	-2.03	1.41	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	m2	172	OMU	O2'-C2'-C1'	2.48	113.92	109.08
83	m2	614	PSU	O4'-C1'-C2'	2.21	108.26	105.14
2	A2	1347	A2M	C3'-C2'-C1'	-2.20	98.75	102.89
2	A2	3371	PSU	O4'-C1'-C2'	2.10	108.10	105.14
2	A2	4094	PSU	O4'-C1'-C2'	2.10	108.10	105.14

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	C2	75	OMG	C1'-C2'-O2'-CM2
2	A2	1140	A2M	O4'-C4'-C5'-O5'
2	A2	1140	A2M	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	A2	1154	OMC	C1'-C2'-O2'-CM2
2	A2	1347	A2M	C4'-C5'-O5'-P

There are no ring outliers.

58 monomers are involved in 86 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	m2	27	A2M	2	0
83	m2	511	OMG	4	0
2	A2	4044	OMG	2	0
2	A2	3581	OMU	1	0
2	A2	3441	A2M	1	0
83	m2	1680	A2M	2	0
83	m2	174	OMC	1	0
2	A2	1438	OMG	1	0
83	m2	519	OMC	1	0
2	A2	1337	A2M	1	0
2	A2	3880	OMG	1	0
2	A2	3958	OMU	3	0
2	A2	4289	OMG	2	0
2	A2	3525	OMC	1	0
2	A2	4099	5MC	2	0
2	A2	3385	PSU	1	0
2	A2	3380	A2M	1	0
2	A2	1154	OMC	3	0
2	A2	2106	OMC	2	0
83	m2	1250	B8N	2	0
83	m2	603	OMG	3	0
2	A2	3848	OMG	1	0
2	A2	1330	2MG	1	0
83	m2	1033	A2M	2	0
83	m2	172	OMU	1	0
2	A2	4022	OMG	1	0
2	A2	3374	A2M	1	0
2	A2	398	A2M	1	0
2	A2	1673	A2M	1	0
83	m2	116	OMU	3	0
83	m2	514	A2M	1	0
2	A2	2179	OMG	1	0
83	m2	685	OMG	1	0
2	A2	3555	OMG	1	0
2	A2	4270	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	m2	1330	OMG	1	0
2	A2	2616	OMC	1	0
2	A2	2118	A2M	2	0
2	A2	4188	OMC	2	0
83	m2	486	A2M	2	0
83	m2	869	OMG	1	0
11	C2	75	OMG	1	0
2	A2	2559	OMC	1	0
83	m2	1844	4AC	4	0
2	A2	3474	OMU	1	0
83	m2	1705	OMC	2	0
83	m2	1339	B8T	1	0
2	A2	4094	PSU	1	0
2	A2	4067	1MA	1	0
2	A2	1490	PSU	1	0
83	m2	578	A2M	1	0
2	A2	1347	A2M	2	0
2	A2	1140	A2M	1	0
2	A2	4272	OMU	3	0
2	A2	4146	OMG	1	0
2	A2	1496	PSU	1	0
83	m2	355	OMC	2	0
2	A2	2119	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 124 ligands modelled in this entry, 124 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	A2	21
83	m2	9

The worst 5 of 30 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m2	130:G	O3'	141:A	P	24.99
1	A2	1512:U	O3'	1521:A	P	24.63
1	A2	2658:G	O3'	3240:C	P	19.23
1	m2	690:U	O3'	801:U	P	17.52
1	A2	891:C	O3'	917:G	P	17.46

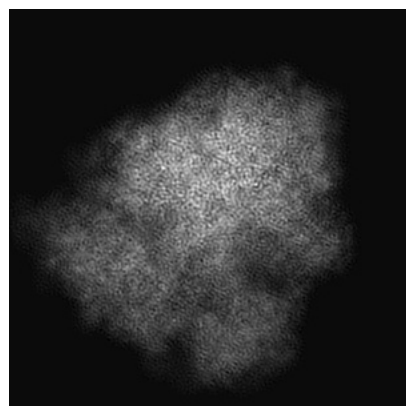
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53473. These allow visual inspection of the internal detail of the map and identification of artifacts.

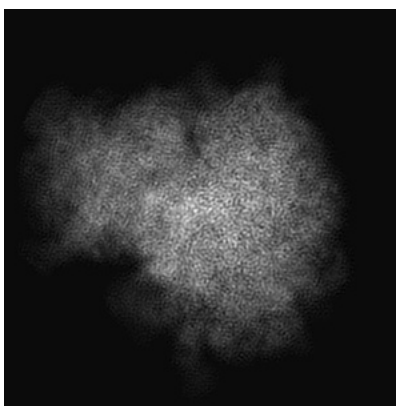
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

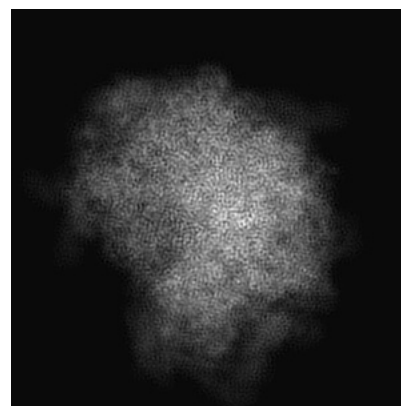
6.1.1 Primary map



X

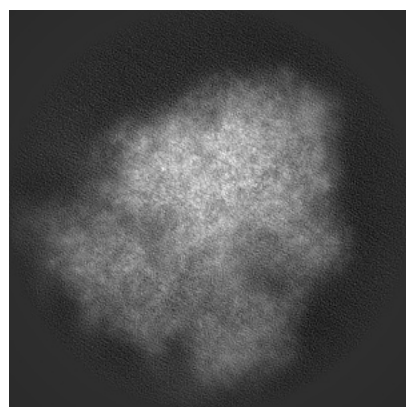


Y

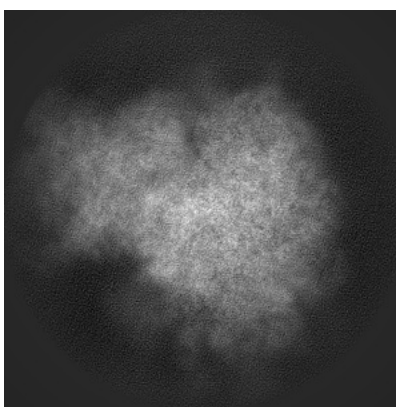


Z

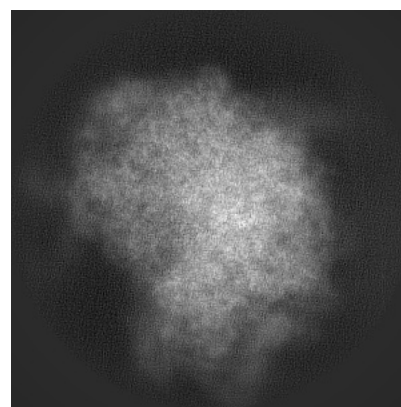
6.1.2 Raw map



X



Y

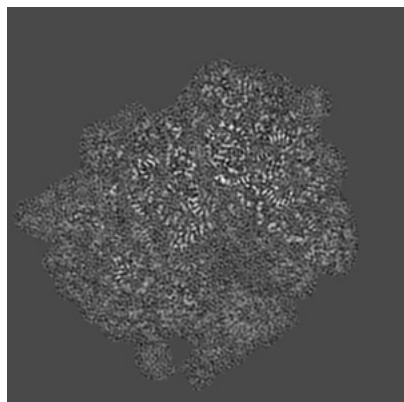


Z

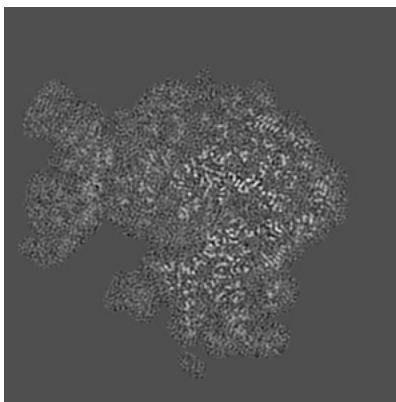
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

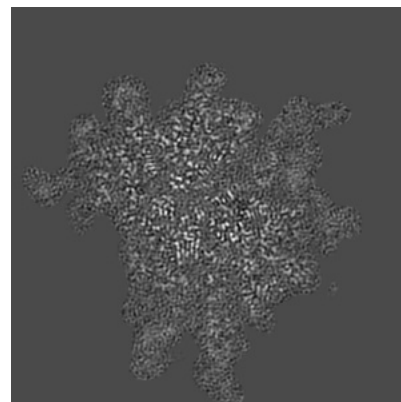
6.2.1 Primary map



X Index: 165

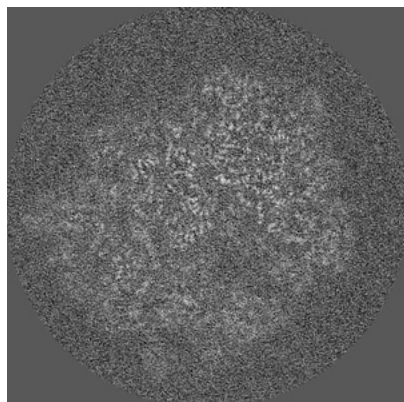


Y Index: 165

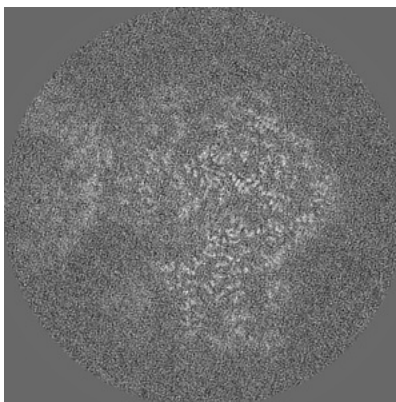


Z Index: 165

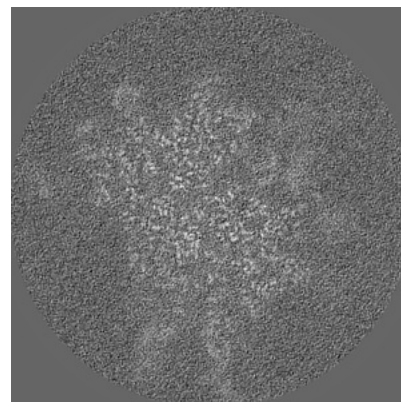
6.2.2 Raw map



X Index: 165



Y Index: 165

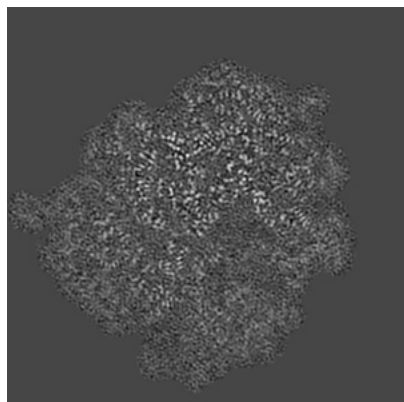


Z Index: 165

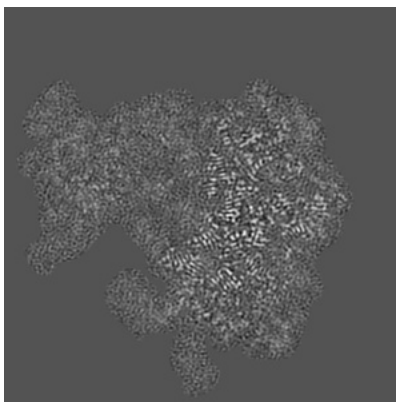
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

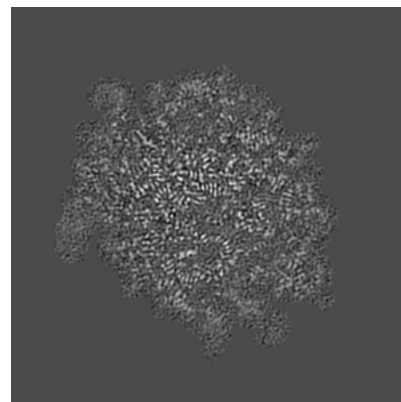
6.3.1 Primary map



X Index: 173

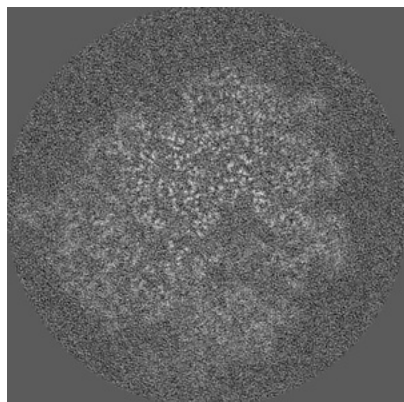


Y Index: 181

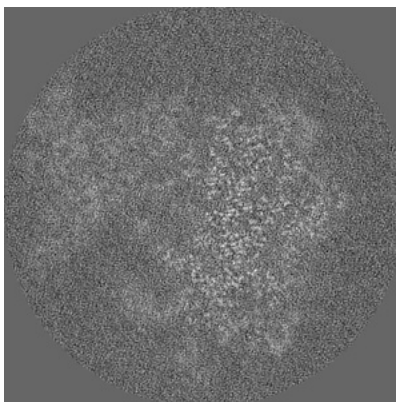


Z Index: 185

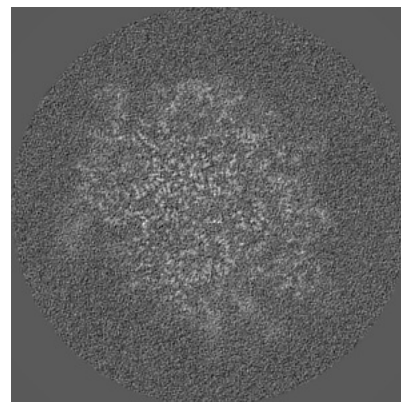
6.3.2 Raw map



X Index: 173



Y Index: 180

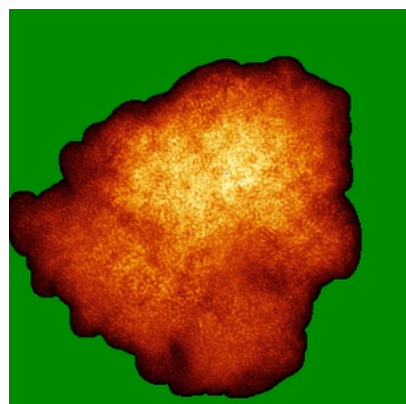


Z Index: 184

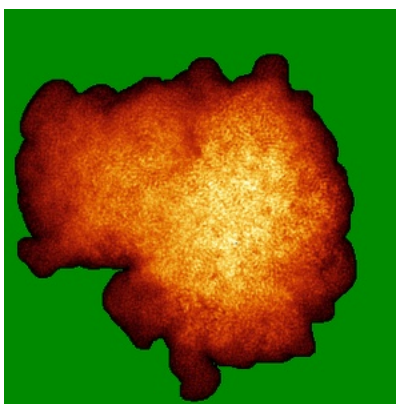
The images above show the largest variance slices of the map in three orthogonal directions.

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

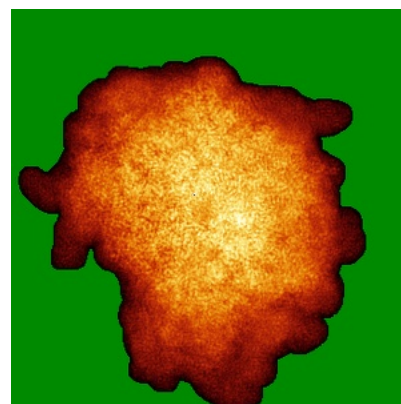
6.4.1 Primary map



X

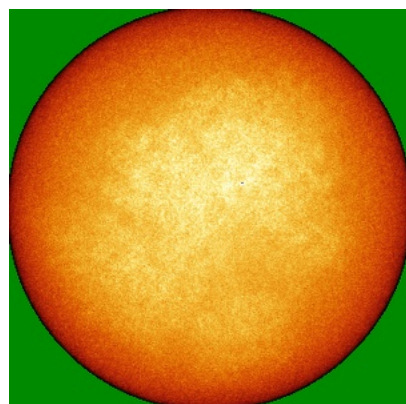


Y

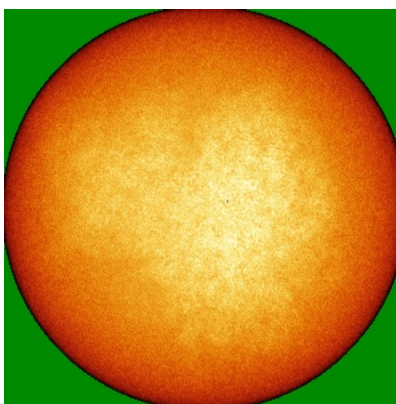


Z

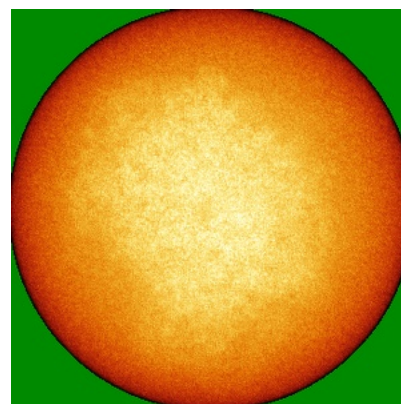
6.4.2 Raw map



X



Y

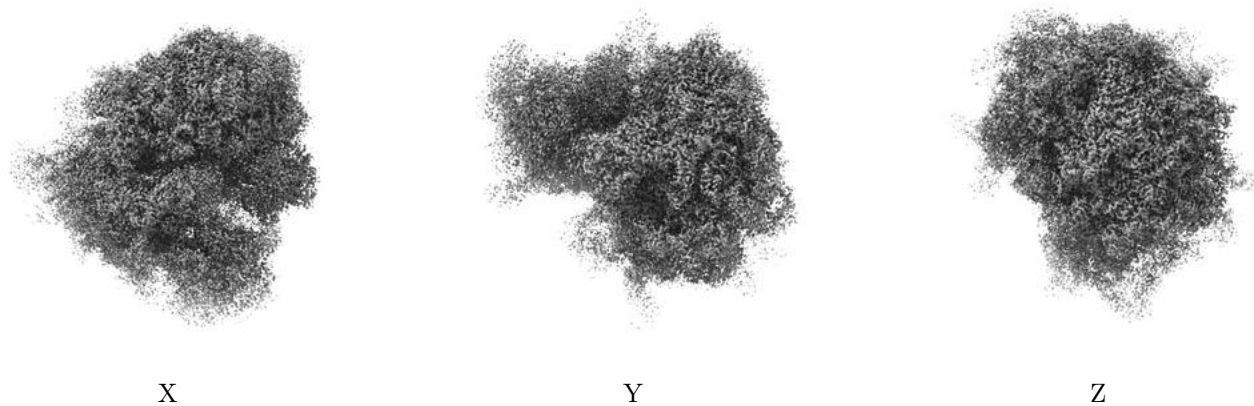


Z

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.

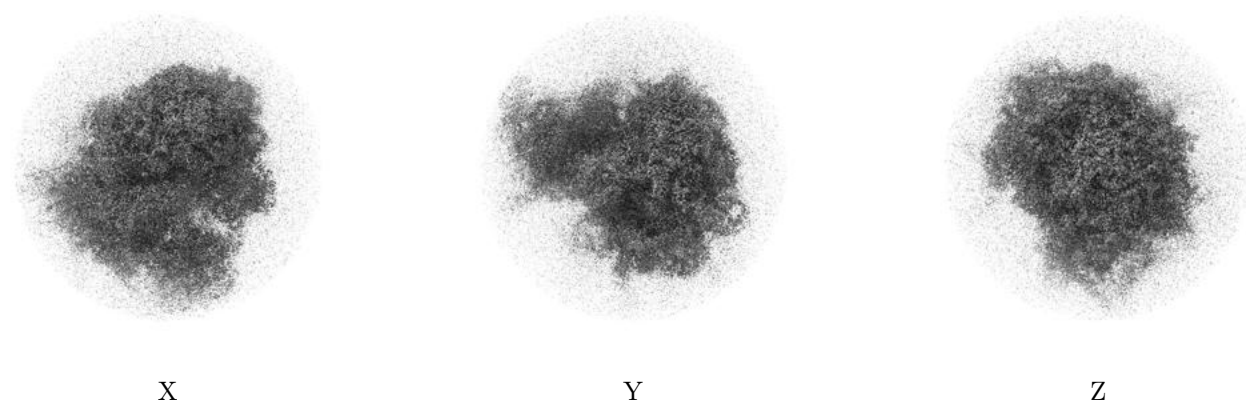
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.037. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

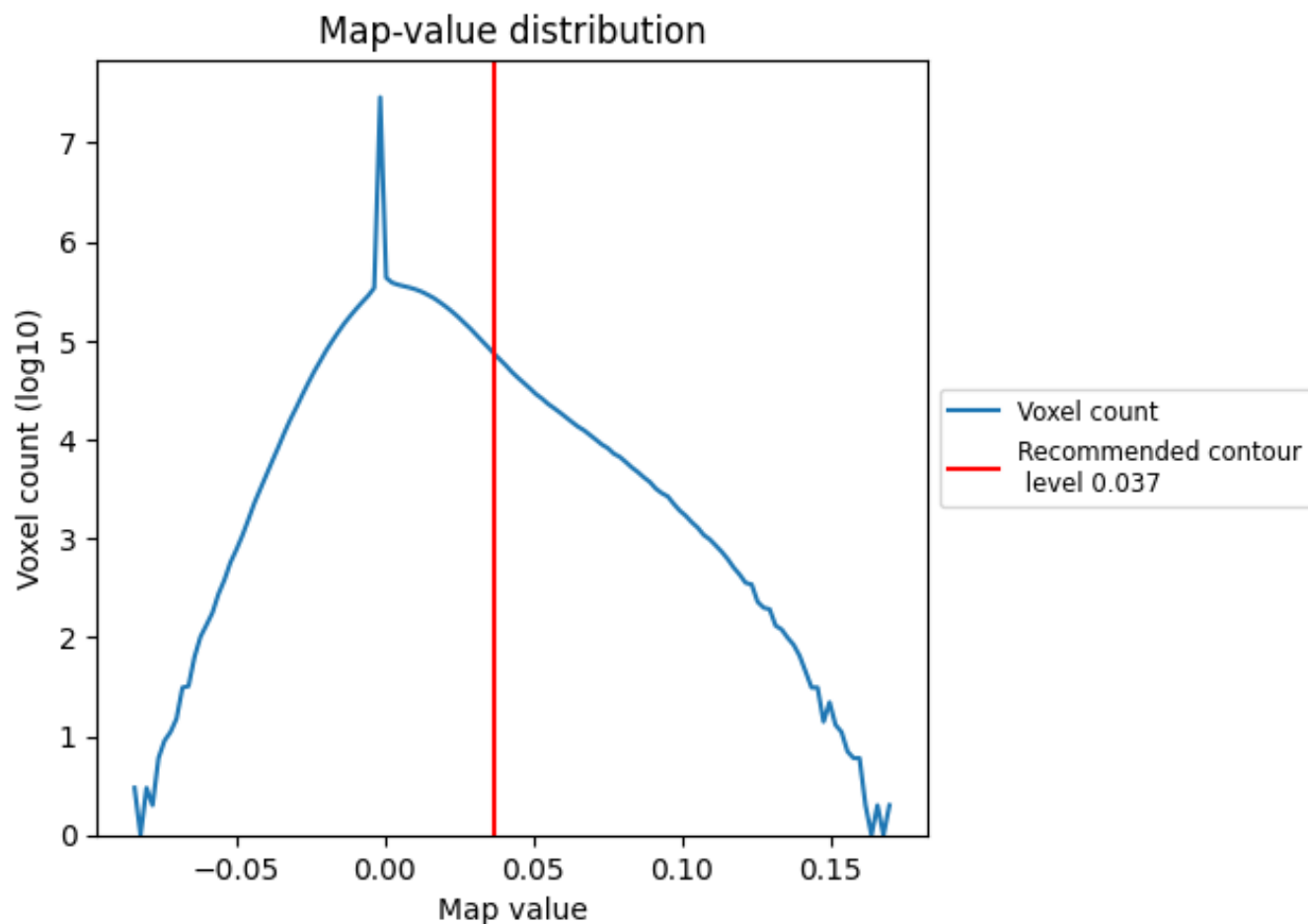
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

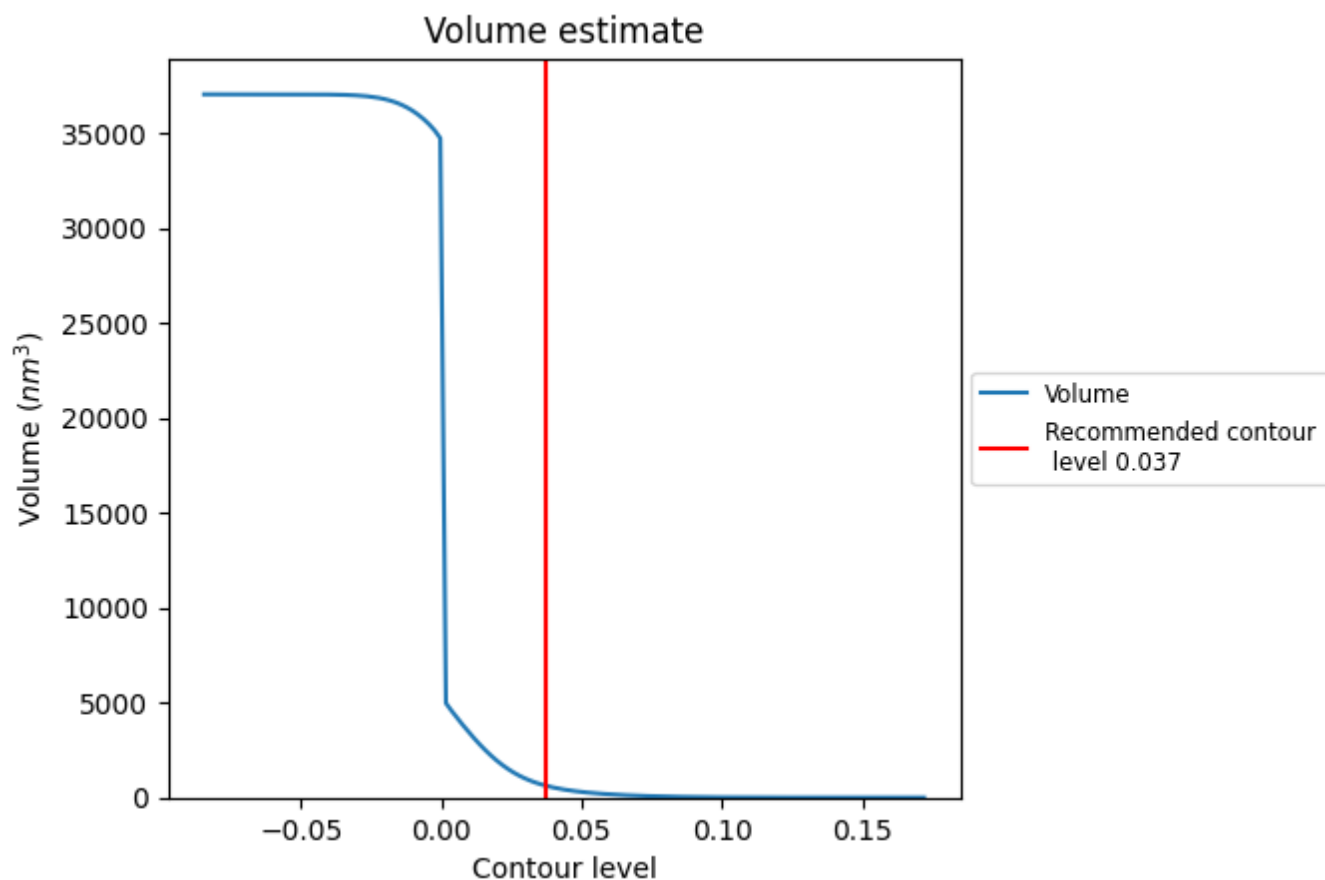
This section contains the results of statistical analysis of the map.

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.

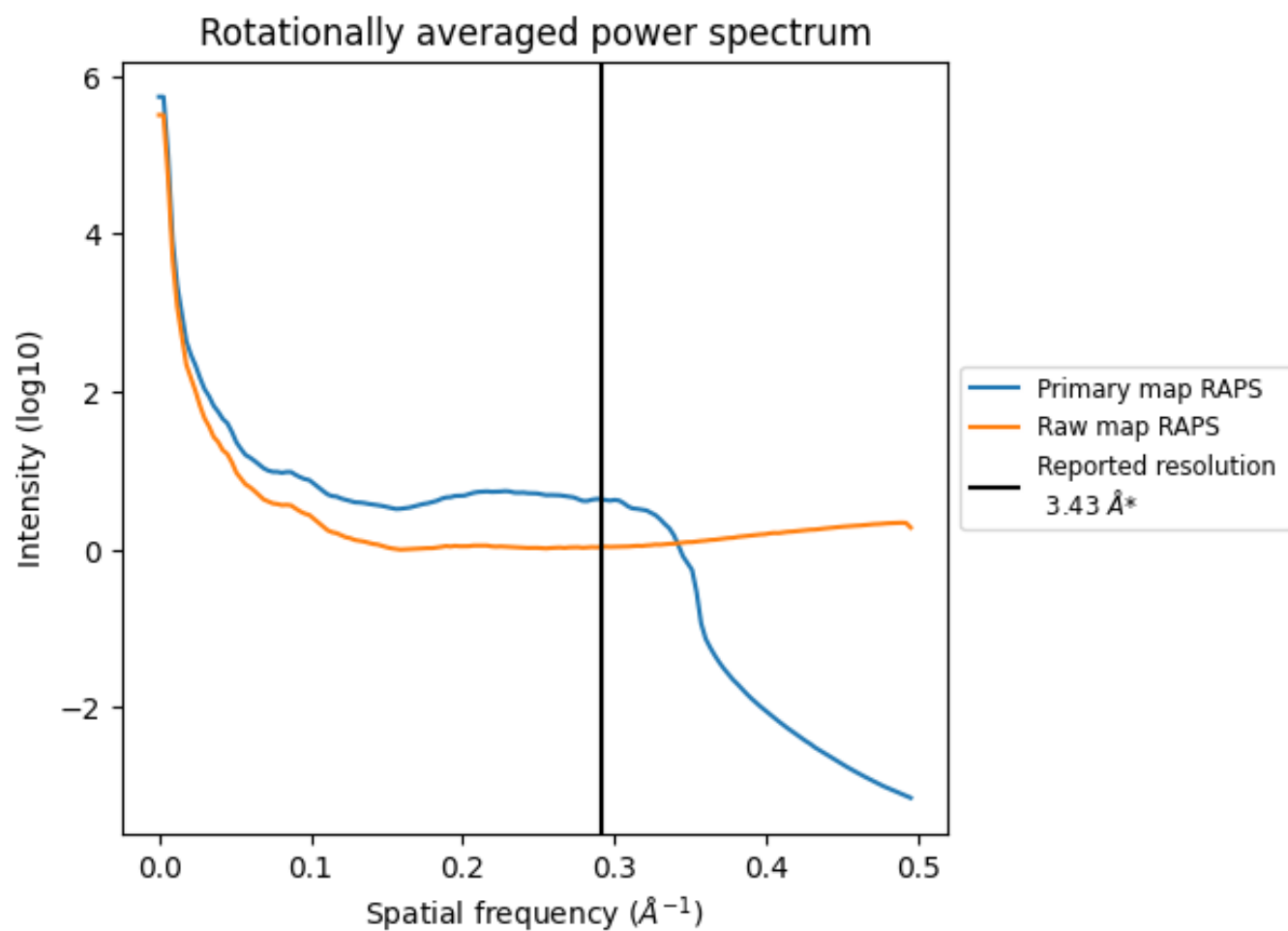
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 639 nm³; this corresponds to an approximate mass of 577 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 ⓘ

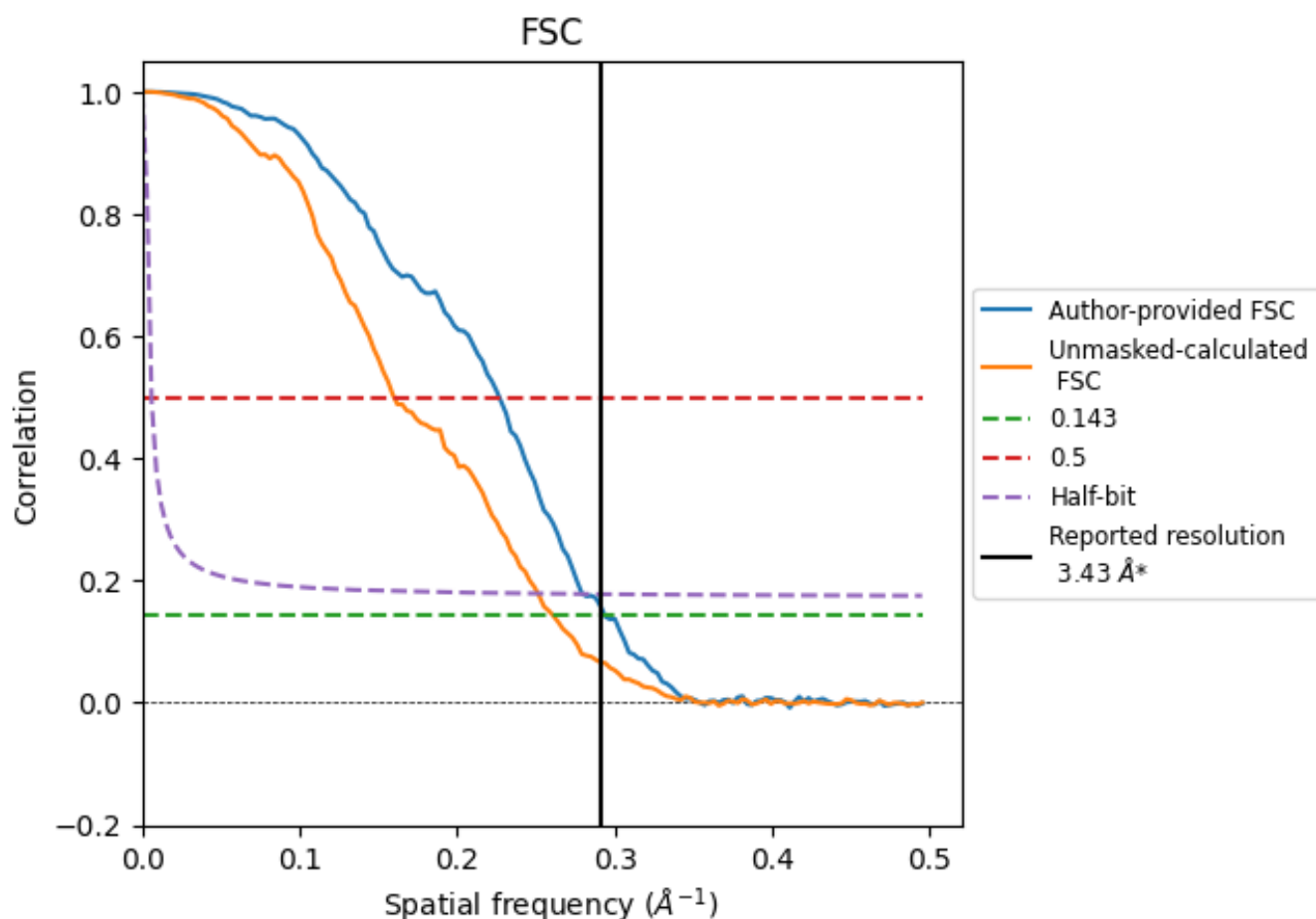


*Reported resolution corresponds to spatial frequency of 0.292 $\text{\AA}^{-1}$

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 $0.292 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

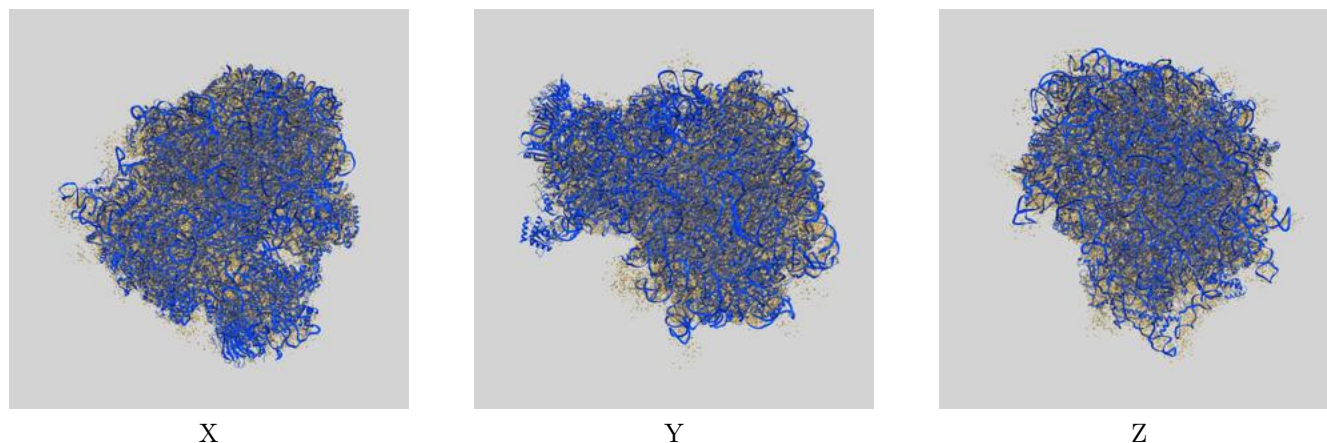
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.43	-	-
Author-provided FSC curve	3.41	4.41	3.57
Unmasked-calculated*	3.84	6.26	3.98

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.84 differs from the reported value 3.43 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53473 and PDB model 9QZP. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



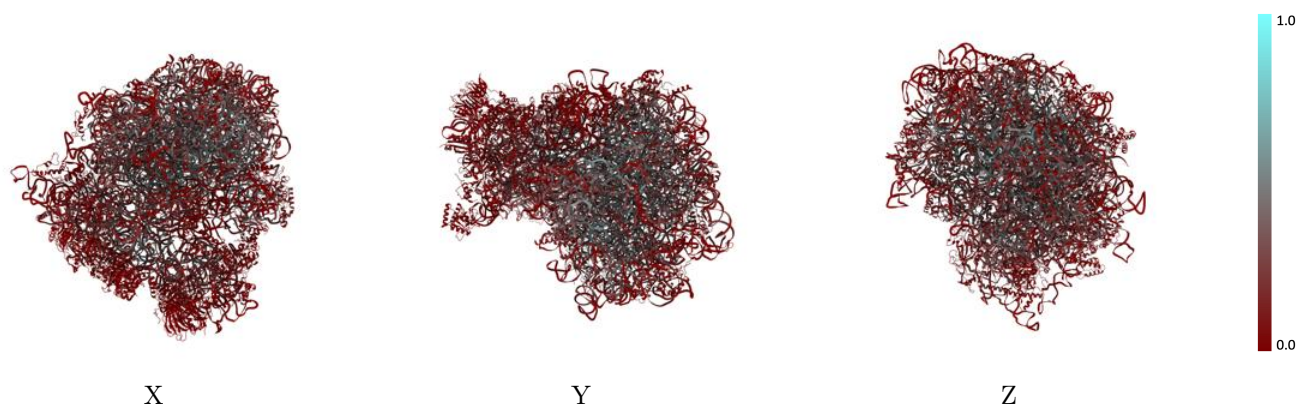
The images above show the 3D surface view of the map at the recommended contour level 0.037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



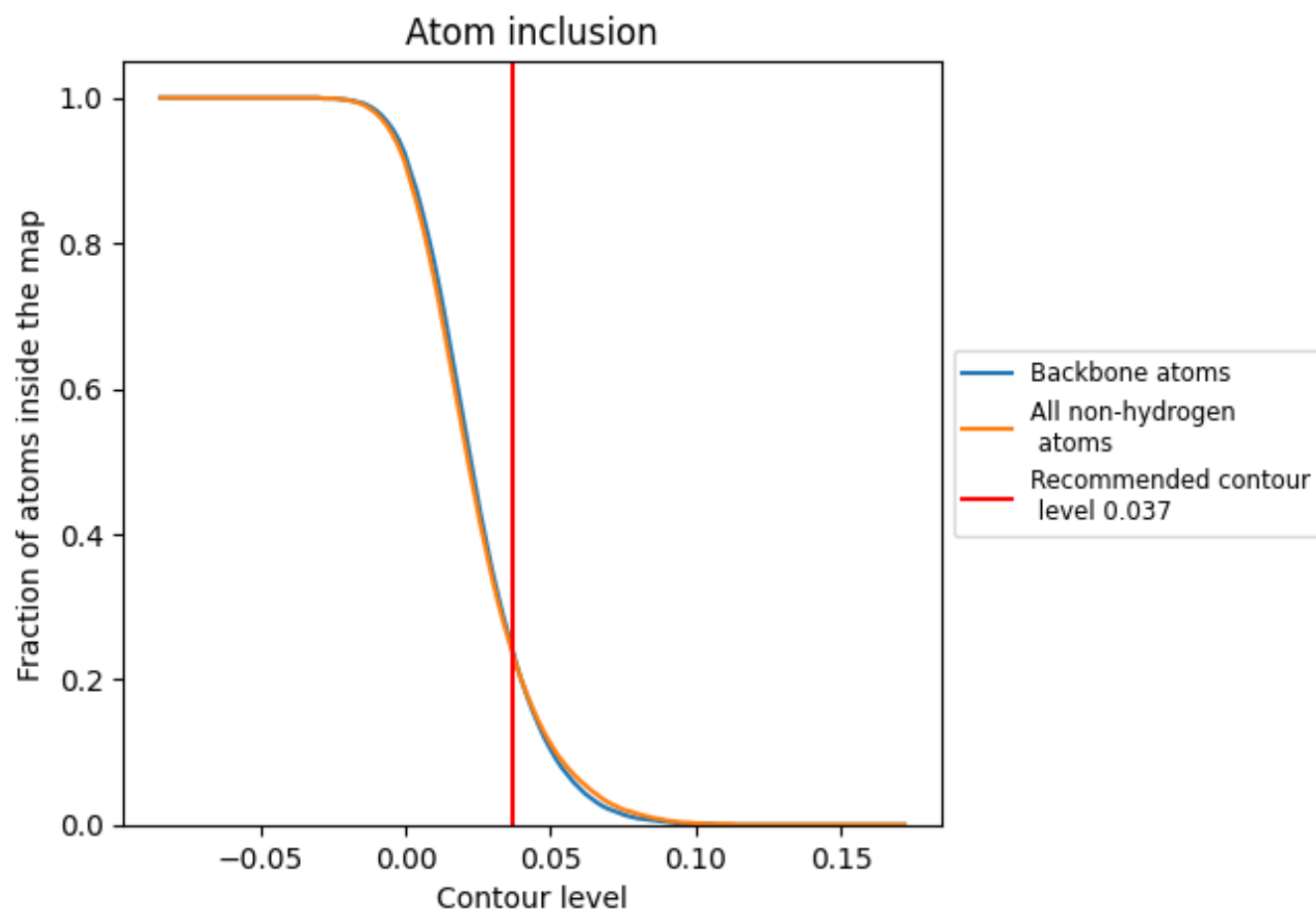
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.037).

9.4 Atom inclusion [i](#)



At the recommended contour level, 24% of all backbone atoms, 24% 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 (0.037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2350	0.1470
A1	0.3230	0.1960
A2	0.3130	0.1510
A3	0.0660	0.1040
B1	0.1860	0.1490
B2	0.4370	0.3050
B3	0.0890	0.1280
Bv	0.0710	0.0640
Bx	0.1400	0.0730
By	0.0450	0.0530
Bz	0.0420	0.0610
C1	0.2260	0.2210
C2	0.3270	0.1570
C3	0.0470	0.0990
D1	0.2650	0.2210
D2	0.2960	0.1690
D3	0.0420	0.0790
E1	0.1430	0.1800
E2	0.2410	0.1500
E3	0.2030	0.1720
F1	0.2360	0.1680
F2	0.2640	0.1720
F3	0.1650	0.1570
G1	0.2250	0.1890
G2	0.2120	0.2410
G3	0.0620	0.1030
H1	0.3710	0.1970
H2	0.1430	0.1250
H3	0.0850	0.1010
I2	0.2800	0.1790
I3	0.0140	0.0420
J2	0.2600	0.1320
J3	0.0930	0.0780
K2	0.3100	0.2250
K3	0.0720	0.0920



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Chain	Atom inclusion	Q-score
L1	0.0050	0.0160
L2	0.2070	0.0900
L3	0.0620	0.0500
M2	0.2930	0.2410
M3	0.0040	0.0240
N2	0.3030	0.2370
N3	0.1190	0.1440
O2	0.1000	0.0940
O3	0.0830	0.1500
P2	0.2640	0.1460
P3	0.1100	0.1030
Q2	0.2020	0.0720
Q3	0.0540	0.0820
R2	0.2030	0.1180
R3	0.0490	0.1140
S2	0.2220	0.1350
S3	0.0550	0.0920
T2	0.2140	0.1970
T3	0.0690	0.1070
U2	0.3270	0.2070
U3	0.0070	0.0230
V2	0.1920	0.1670
W2	0.2490	0.2470
X2	0.2610	0.1740
Y2	0.3140	0.2150
Z2	0.2910	0.1880
a2	0.2640	0.1600
b2	0.2070	0.1220
c2	0.2140	0.1870
d2	0.3040	0.1260
e2	0.1150	0.1340
f2	0.3030	0.1180
g2	0.2690	0.1930
h2	0.2440	0.1220
i2	0.2880	0.2260
j2	0.2430	0.1410
k2	0.2190	0.1470
m2	0.2370	0.1580
n2	0.0220	0.0420
o2	0.0430	0.0870
p2	0.0920	0.1540
q2	0.0520	0.1040

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Chain	Atom inclusion	Q-score
r2	 0.0660	 0.0390
s2	 0.0680	 0.1190
t2	 0.0250	 0.0500
u2	 0.0970	 0.0450
v2	 0.0180	 0.1010
w2	 0.1120	 0.0770
x2	 0.0620	 0.1350
y2	 0.0720	 0.1290
z2	 0.0480	 0.1180