



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2025 – 04:19 pm GMT

PDB ID : 9H4N / pdb_00009h4n
EMDB ID : EMD-51865
Title : RPL13 (eL13)-mutant 80S ribosome from mouse
Authors : Orgebin, E.; Astier, A.; Rinaldi, D.; Baud'huin, M.; Plisson-Chastang, C.
Deposited on : 2024-10-21
Resolution : 2.46 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

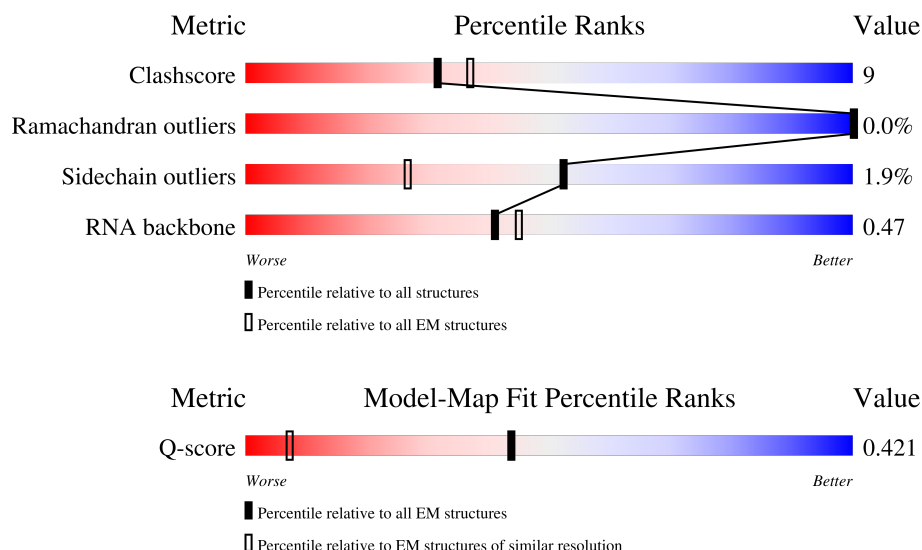
EMDB validation analysis : 0.0.1.dev129
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

1 Overall quality at a glance

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

The reported resolution of this entry is 2.46 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	6014 (1.96 - 2.96)

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	222	<div> <div>5%</div> <div>81%</div> <div>18%</div> </div>
2	B1	232	<div> <div>23%</div> <div>79%</div> <div>16%</div> <div>••</div> </div>
3	C1	190	<div> <div>•</div> <div>88%</div> <div>12%</div> <div>•</div> </div>



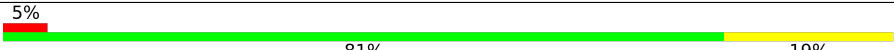
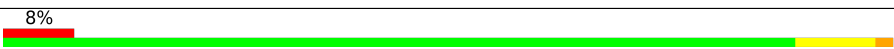

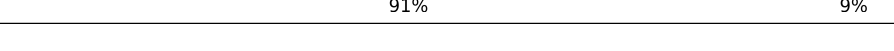
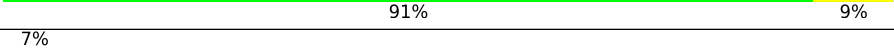
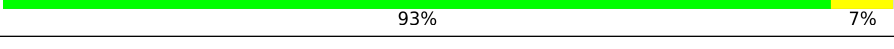




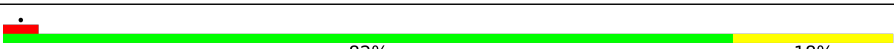

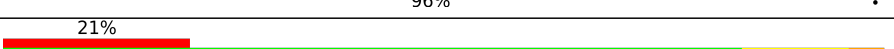
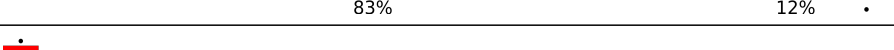









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Mol	Chain	Length	Quality of chain
4	D1	213	
5	E1	174	
6	F1	203	
7	G1	139	
8	H1	203	
9	A2	3609	
10	B2	120	
11	C2	156	
12	D2	251	
13	E2	402	
14	F2	359	
15	G2	293	
16	H2	221	
17	I2	201	
18	J2	153	
19	K2	186	
20	L2	164	
21	M2	175	
22	N2	159	
23	O2	101	
24	P2	129	
25	Q2	62	
26	R2	118	
27	S2	134	
28	T2	135	

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Mol	Chain	Length	Quality of chain
29	U2	147	
30	V2	117	
31	W2	94	
32	X2	107	
33	Y2	128	
34	Z2	109	
35	a2	114	
36	b2	120	
37	c2	102	
38	d2	86	
39	e2	69	
40	f2	50	
41	g2	52	
42	h2	24	
43	i2	103	
44	j2	89	
45	k2	125	
46	m2	1724	
47	n2	75	
48	p2	214	
49	q2	226	
50	r2	262	
51	w2	153	
52	z2	110	
53	o2	214	

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Mol	Chain	Length	Quality of chain
54	s2	142	<div>89%</div> <div>82%17%..</div>
55	v2	58	<div>91%</div> <div>78%21%.</div>
56	x2	130	<div>85%</div> <div>66%33%.</div>
57	y2	144	<div>83%</div> <div>70%30%</div>
58	A3	144	<div>91%</div> <div>83%17%</div>
59	B3	141	<div>86%</div> <div>73%27%</div>
60	C3	16	<div>69%</div> <div>75%25%</div>
61	D3	83	<div>72%</div> <div>86%14%</div>
62	E3	141	<div>78%</div> <div>70%28%.</div>
63	G3	7	<div>100%</div> <div>86%14%</div>
64	H3	54	<div>57%</div> <div>69%31%</div>
65	I3	169	<div>98%</div> <div>85%15%</div>
66	J3	222	<div>54%</div> <div>76%23%.</div>
67	K3	187	<div>96%</div> <div>84%16%</div>
68	L3	185	<div>87%</div> <div>78%22%</div>
69	N3	150	<div>74%</div> <div>79%21%</div>
70	P3	129	<div>38%</div> <div>73%27%</div>
71	Q3	129	<div>98%</div> <div>83%16%.</div>
72	S3	83	<div>77%</div> <div>72%28%</div>
73	T3	41	<div>93%</div> <div>95%5%</div>
74	Bx	10	<div>60%</div> <div>30%60%10%</div>
75	F3	97	<div>32%</div> <div>26%63%10%.</div>
76	O3	133	<div>71%</div> <div>57%39%..</div>

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 204064 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 protein called Large ribosomal subunit protein eL8.

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

- Molecule 3 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 4 is a protein called Large ribosomal subunit protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D1	208	Total	C	N	O	S	0	0
			1690	1073	327	278	12		

- Molecule 5 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 6 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F1	199	Total	C	N	O	S	0	0
			1606	1003	333	266	4		

- Molecule 7 is a protein called 60S ribosomal protein L14.

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

- Molecule 8 is a protein called 60S ribosomal protein L15.

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

- Molecule 9 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A2	3609	Total	C	N	O	P	0	0
			77352	34465	14112	25167	3608		

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B2	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- 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
			3314	1480	585	1094	155		

- Molecule 12 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 16 is a protein called 60S ribosomal protein L6.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

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

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

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

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L2	164	Total	C	N	O	S	0	0
			1367	849	295	214	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL36.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 42 is a protein called Small ribosomal subunit protein eS32.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL28.

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

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m2	1724	Total	C	N	O	P	0	0
			36794	16425	6605	12041	1723		

- Molecule 47 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n2	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 48 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p2	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q2	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 50 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w2	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 52 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z2	110	Total	C	N	O	S	0	0
			874	548	161	162	3		

- Molecule 53 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	s2	142	Total	C	N	O	S	0	0
			1117	690	224	196	7		

- Molecule 55 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	v2	58	Total	C	N	O	S	0	0
			487	317	89	76	5		

- Molecule 56 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x2	130	Total	C	N	O	S	0	0
			1073	681	205	180	7		

- Molecule 57 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y2	144	Total	C	N	O	S	0	0
			1143	726	216	198	3		

- Molecule 58 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A3	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 59 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 60 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	C3	16	Total	C	N	O	0	0
			122	75	21	26		

- Molecule 61 is a protein called Small ribosomal subunit protein eS21.

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

- Molecule 62 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	E3	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 63 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	G3	7	Total	C	N	O	S	0	0
			49	28	9	11	1		

- Molecule 64 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 65 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	I3	169	Total	C	N	O	S	0	0
			1320	831	235	248	6		

- Molecule 66 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	J3	222	Total	C	N	O	S	0	0
			1725	1116	298	302	9		

- Molecule 67 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	K3	187	Total	C	N	O	S	0	0
			1519	949	311	252	7		

- Molecule 68 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	L3	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 69 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 70 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 71 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Q3	129	Total	C	N	O	S	0	0
			1049	662	206	176	5		

- Molecule 72 is a protein called Small ribosomal subunit protein eS27-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	S3	83	Total	C	N	O	S	0	0
			652	409	121	115	7		

- Molecule 73 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	T3	41	Total	C	N	O	S	0	0
			327	197	74	55	1		

- Molecule 74 is a RNA chain called Messenger RNA.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	F3	97	Total	C	N	O	S	0	0
			774	481	160	128	5		

- Molecule 76 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	O3	133	Total	C	N	O	S	0	0
			993	606	196	185	6		

- Molecule 77 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
77	d2	1	Total 1	Zn 1	0
77	g2	1	Total 1	Zn 1	0
77	i2	1	Total 1	Zn 1	0
77	j2	1	Total 1	Zn 1	0
77	H3	1	Total 1	Zn 1	0
77	F3	1	Total 1	Zn 1	0

- Molecule 78 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
78	H3	1	Total 1	Mg 1	0

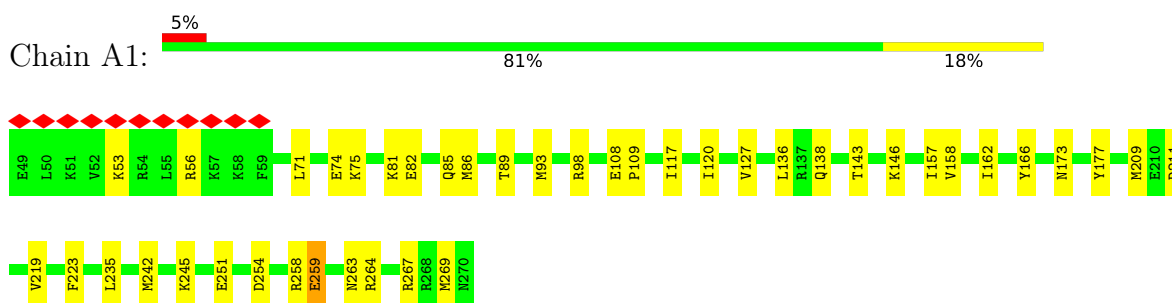
- Molecule 79 is water.

Mol	Chain	Residues	Atoms		AltConf
79	B1	1	Total 1	O 1	0
79	A2	1	Total 1	O 1	0
79	m2	2	Total 2	O 2	0

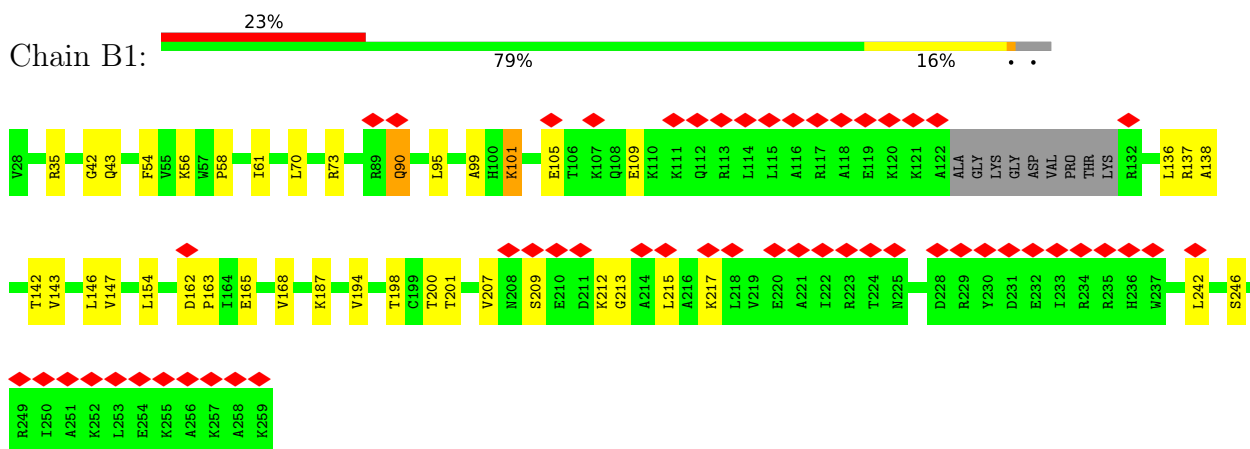
3 Residue-property plots [i](#)

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

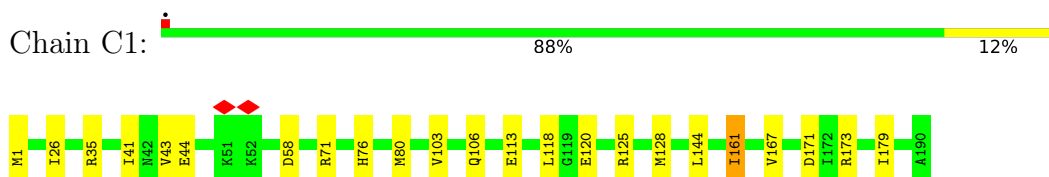
- Molecule 1: Large ribosomal subunit protein uL30



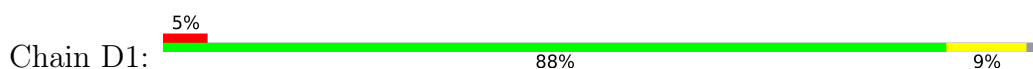
- Molecule 2: Large ribosomal subunit protein eL8



- Molecule 3: Large ribosomal subunit protein uL6

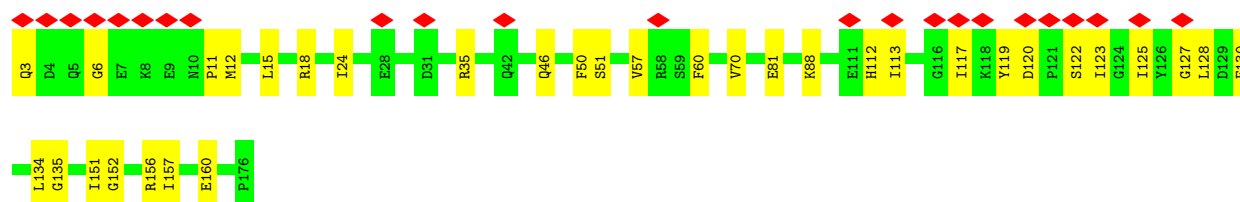
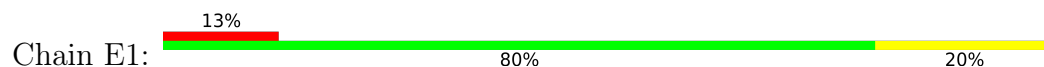


- Molecule 4: Large ribosomal subunit protein uL16-like

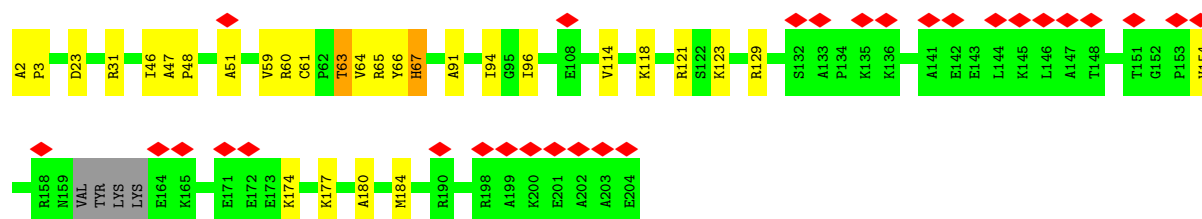
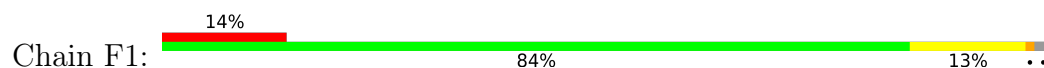




- Molecule 5: Large ribosomal subunit protein uL5



- Molecule 6: Large ribosomal subunit protein eL13



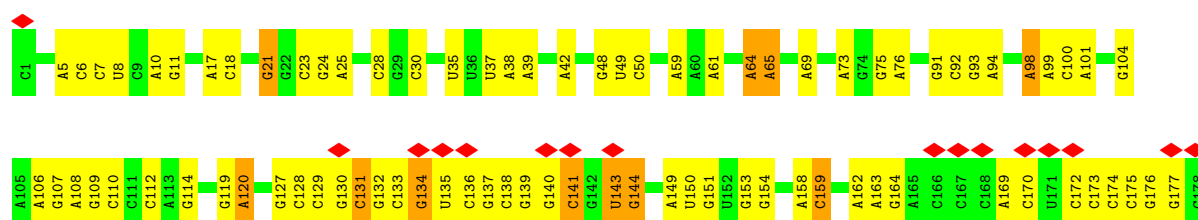
- Molecule 7: 60S ribosomal protein L14



- Molecule 8: 60S ribosomal protein L15

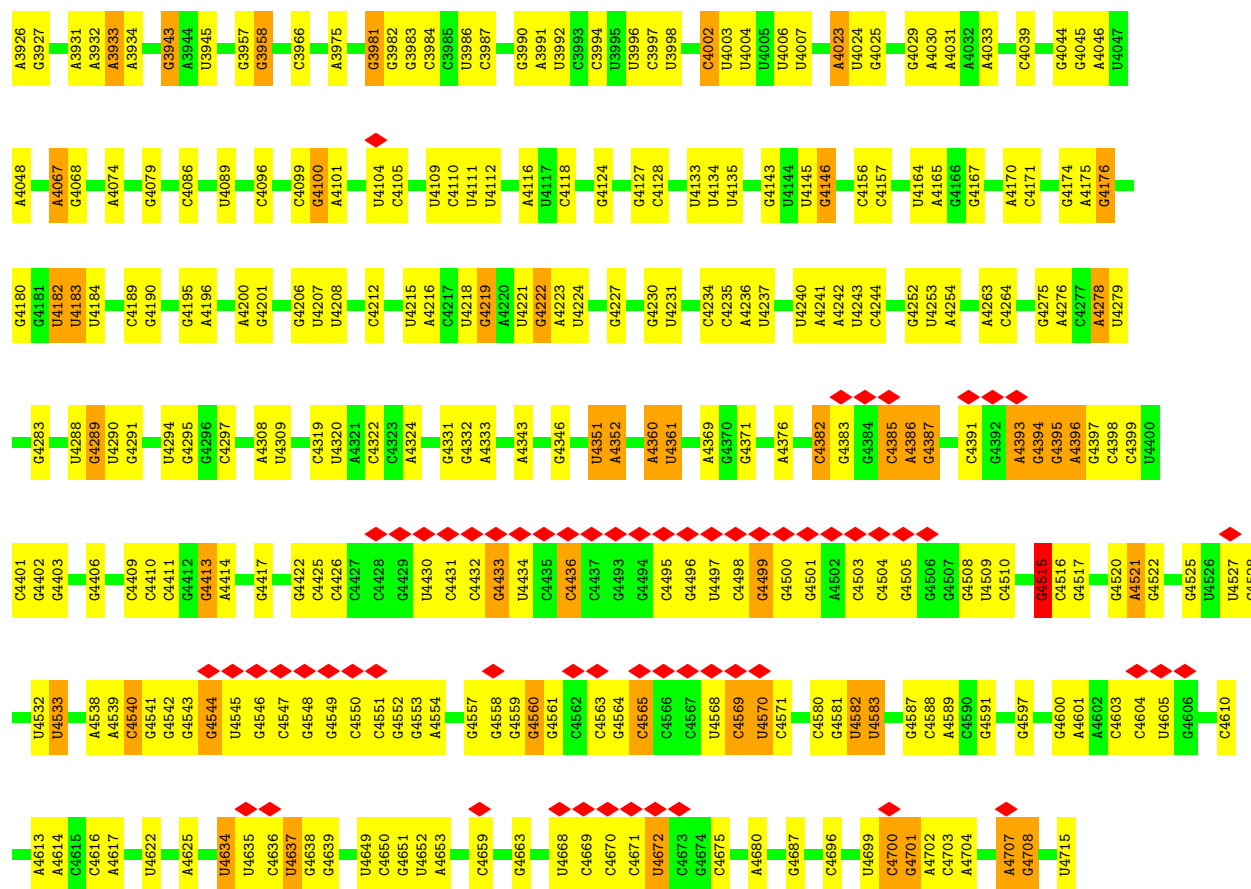


- Molecule 9: 28S ribosomal RNA

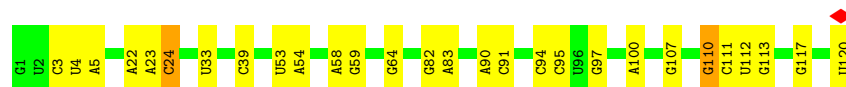
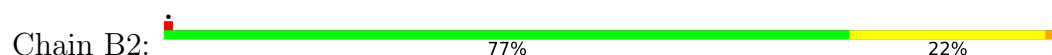




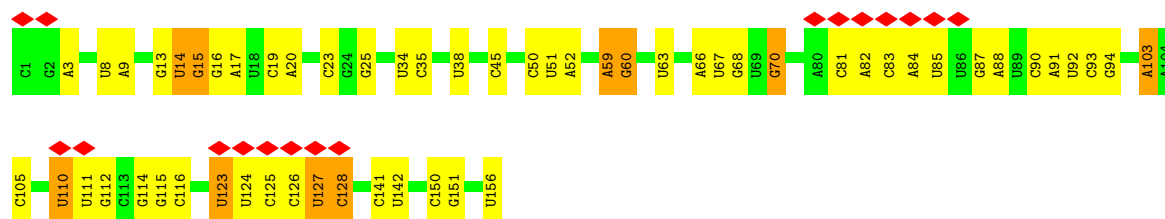
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G3609	A3610	G3611	G3612	U3613	G3614	U3615	A3616	G3617	A3618	A3619	U3620	A3621	A3622	G3623	U3624	G3625	G3626	G3627	A3628	G3629	G3630	G3631	C3632	C3633	G3634	G3635	G3636	G3637	U3638	U3671	C3672	U3673	C3674	C3675	C3676	C3691	G3692	G3693	U3694	G3695	A3696	A3697	A3698	U3699	A3700	A3701	C3702	A3703	C3704	U3705	A3706	C3707	U3708	C3709	U3710	C3711	A3712	U3713	C3714	G3715	U3716	U3717	U3718	U3719
A3518	A3523	G3524	A3527	A3528	G3529	G3530	A3533	G3534	G3535	G3536	G3537	U3548	C3549	A3550	G3553	G3556	A3557	A3562	G3563	A3564	G3565	G3566	G3567	U3568	U3571	G3572	A3573	G3574	C3575	U3576	U3577	G3578	A3579	C3580	U3586	C3593	G3594	G3595	A3597	A3598	A3599	G3600	A3601	G3602	A3603	C3604	A3605	U3606	G3607	A3608														
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G1909	G1910	G1911	A1912	G1913	C1914	G2004	U2005	C2006	G2007	G2008	G2009	A2012	C2013	G2014	C2015	G2016	G2017	A2018	G2019	C2020	C2021	U2022	G2025	A2030	G2031	U2036	C2044	G2052	A2055	G2056	G2061	C2068	G2077	G2081	G2088	G2094	A2102	G2103	C2106	G2113	U2114	A2115																						



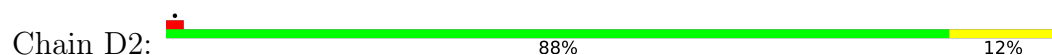
• Molecule 10: 5S ribosomal RNA

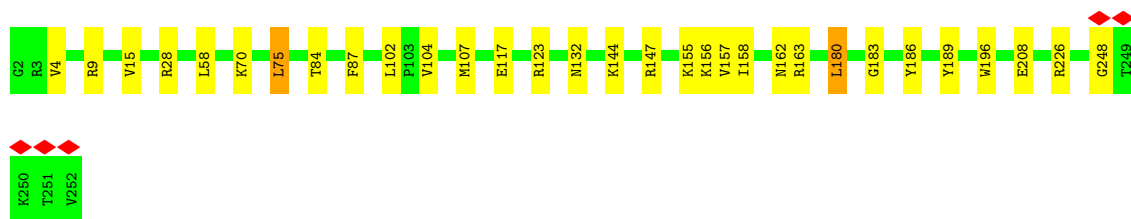


• Molecule 11: 5.8S ribosomal RNA

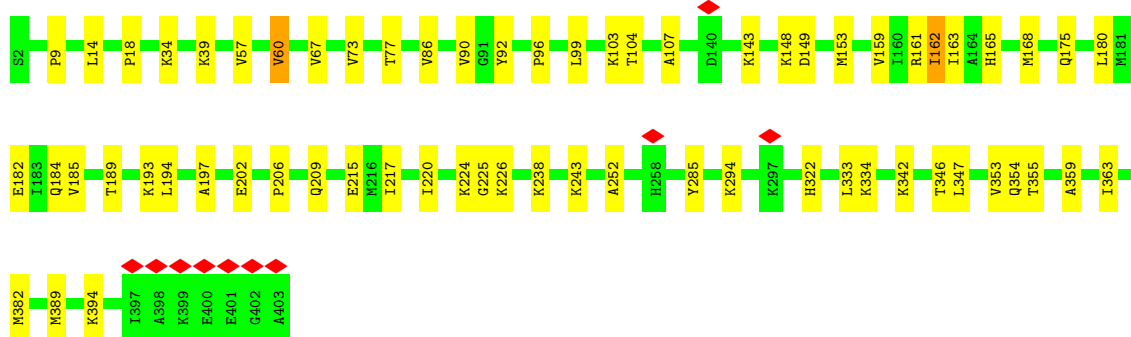
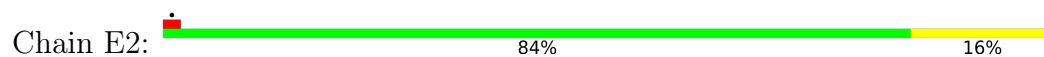


• Molecule 12: Large ribosomal subunit protein uL2

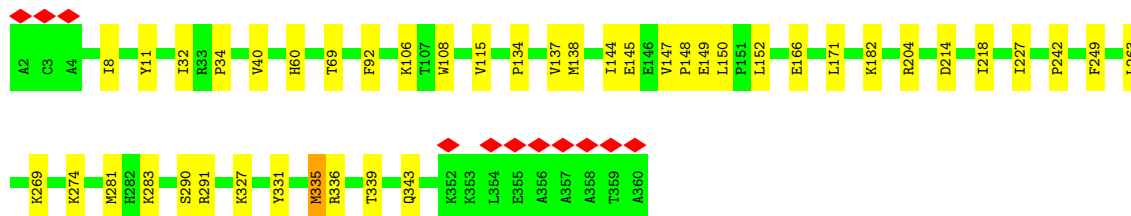
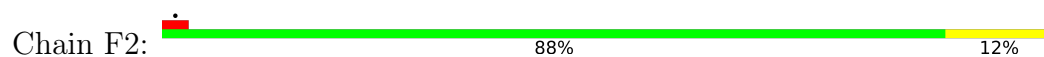




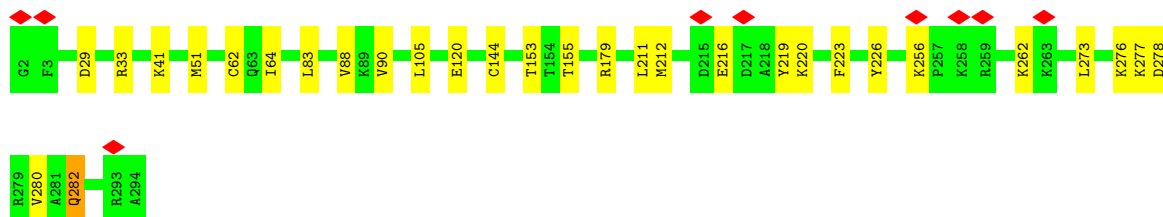
- Molecule 13: Large ribosomal subunit protein uL3



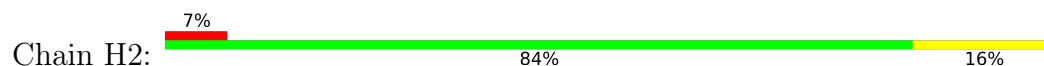
- Molecule 14: Large ribosomal subunit protein uL4

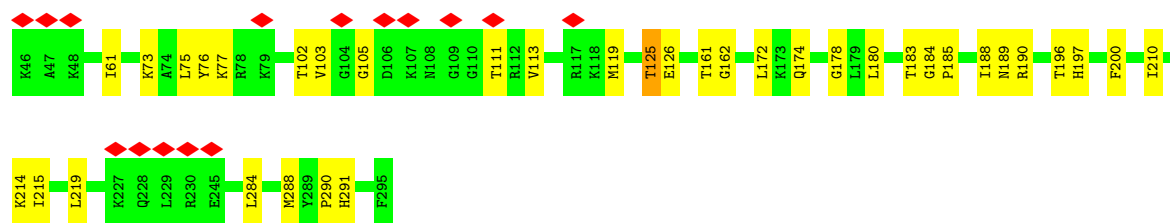


- Molecule 15: Large ribosomal subunit protein uL18

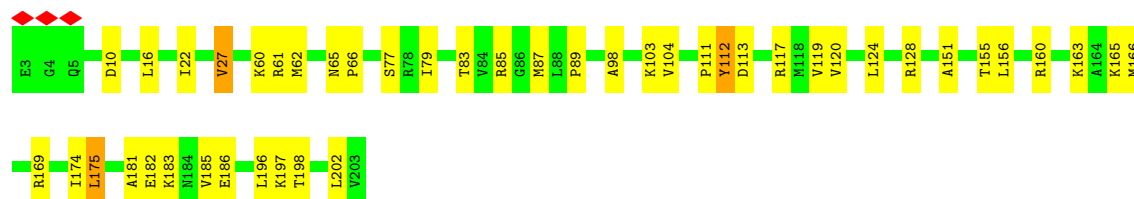
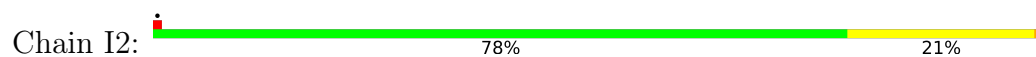


- Molecule 16: 60S ribosomal protein L6

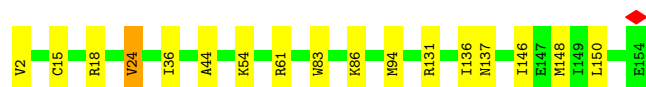




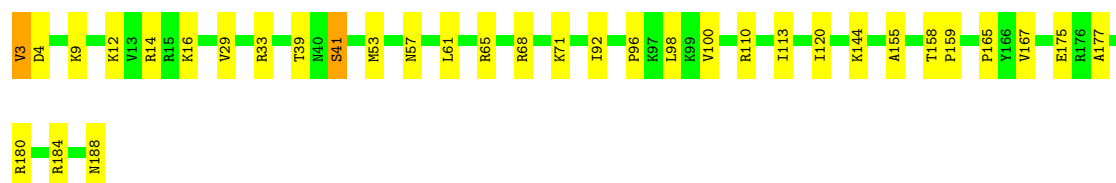
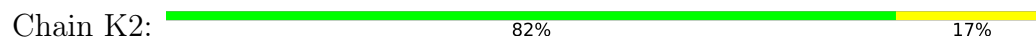
- Molecule 17: Large ribosomal subunit protein uL13



- Molecule 18: 60S ribosomal protein L17



- Molecule 19: Large ribosomal subunit protein eL18



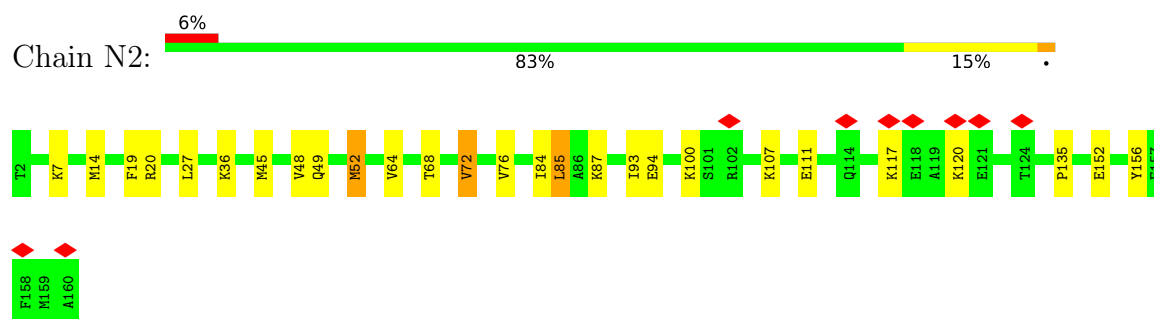
- Molecule 20: Large ribosomal subunit protein eL19



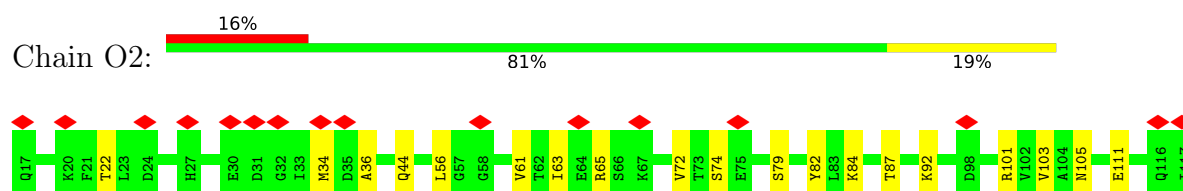
- Molecule 21: Large ribosomal subunit protein eL20



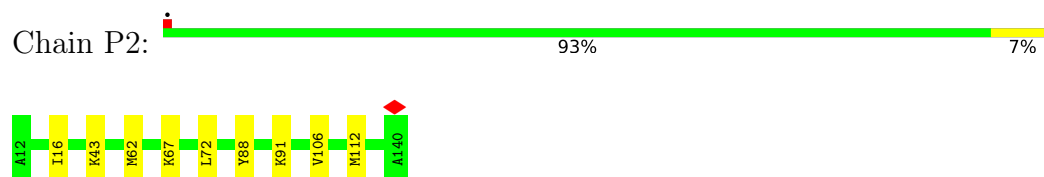
- Molecule 22: Large ribosomal subunit protein eL21



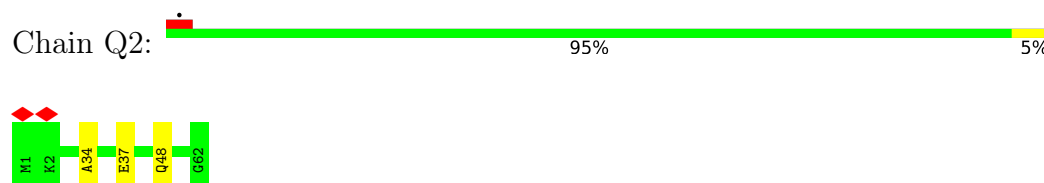
- Molecule 23: Large ribosomal subunit protein eL22



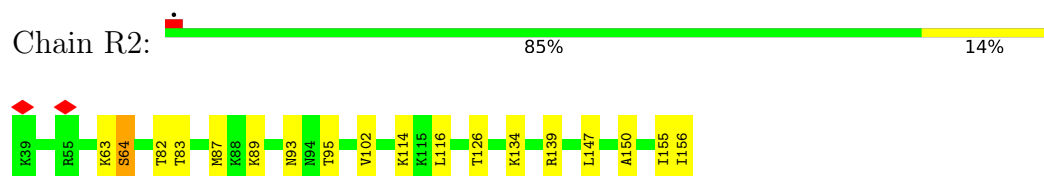
- Molecule 24: 60S ribosomal protein L23



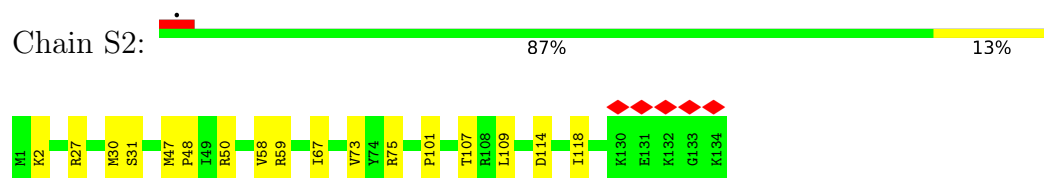
- Molecule 25: Large ribosomal subunit protein eL24



- Molecule 26: 60S ribosomal protein L23a



- Molecule 27: Large ribosomal subunit protein uL24



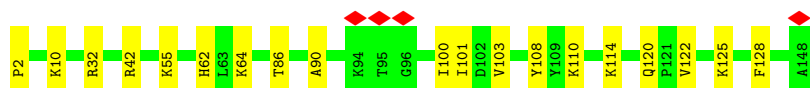
- Molecule 28: Large ribosomal subunit protein eL27

Chain T2:  86% 13%




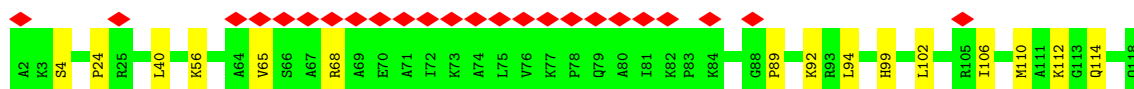
- Molecule 29: 60S ribosomal protein L27a

Chain U2:  87% 13%




- Molecule 30: Large ribosomal subunit protein eL29

Chain V2:  21% 87% 13%




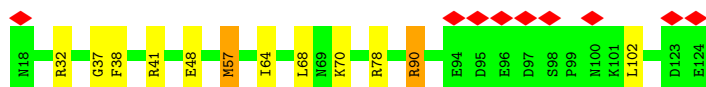
- Molecule 31: Large ribosomal subunit protein eL30

Chain W2:  5% 81% 19%



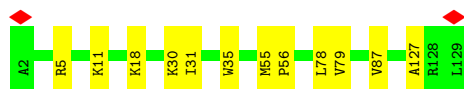
- Molecule 32: Large ribosomal subunit protein eL31

Chain X2:  8% 89% 9%



- Molecule 33: Large ribosomal subunit protein eL32

Chain Y2:  91% 9%

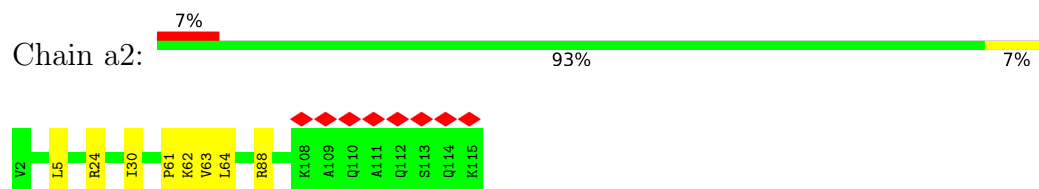


- Molecule 34: 60S ribosomal protein L35a

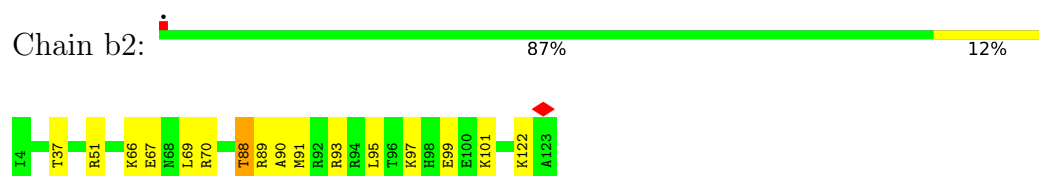
Chain Z2:  91% 9%



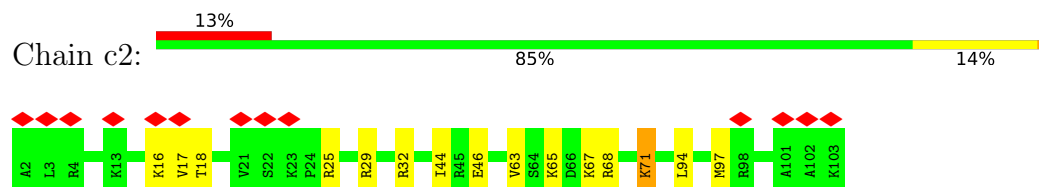
- Molecule 35: 60S ribosomal protein L34



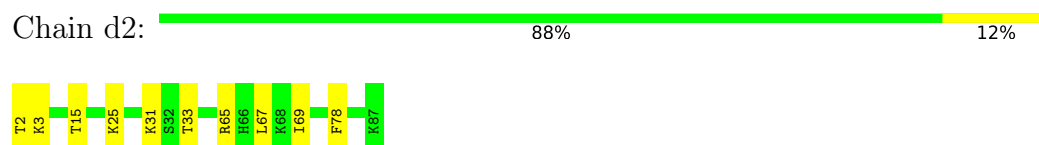
- Molecule 36: Large ribosomal subunit protein uL29



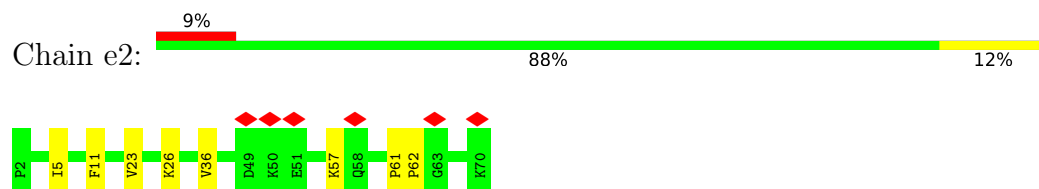
- Molecule 37: Large ribosomal subunit protein eL36



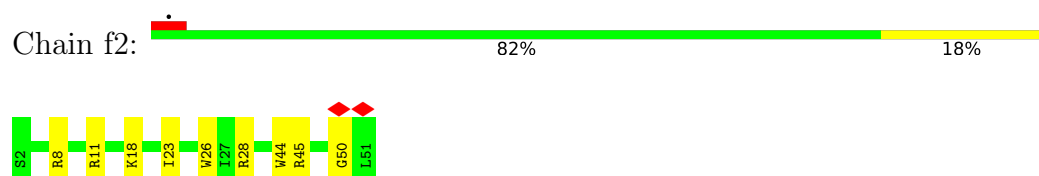
- Molecule 38: Large ribosomal subunit protein eL37



- Molecule 39: 60S ribosomal protein L38

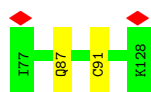


- Molecule 40: Large ribosomal subunit protein eL39

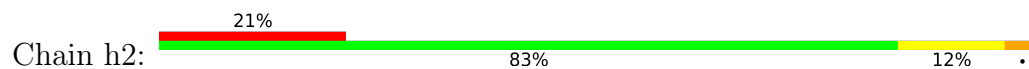


- Molecule 41: Large ribosomal subunit protein eL40

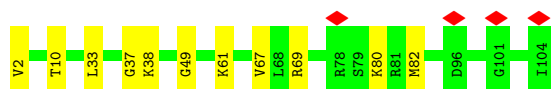




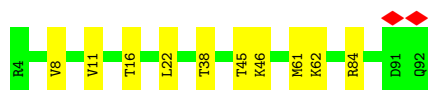
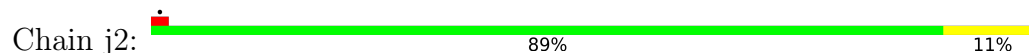
- Molecule 42: Small ribosomal subunit protein eS32



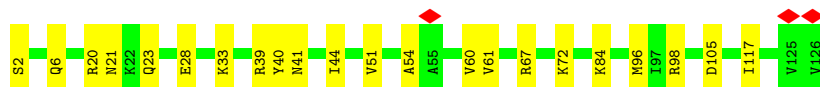
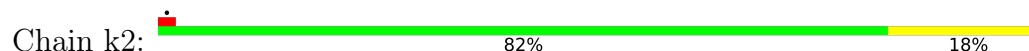
- Molecule 43: Large ribosomal subunit protein eL42



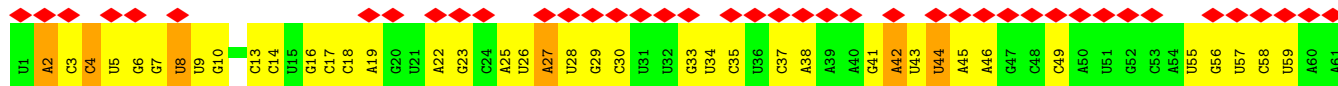
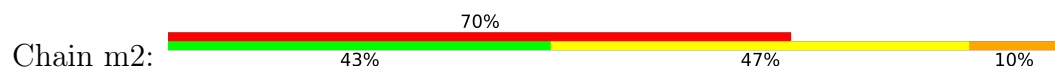
- Molecule 44: Large ribosomal subunit protein eL43



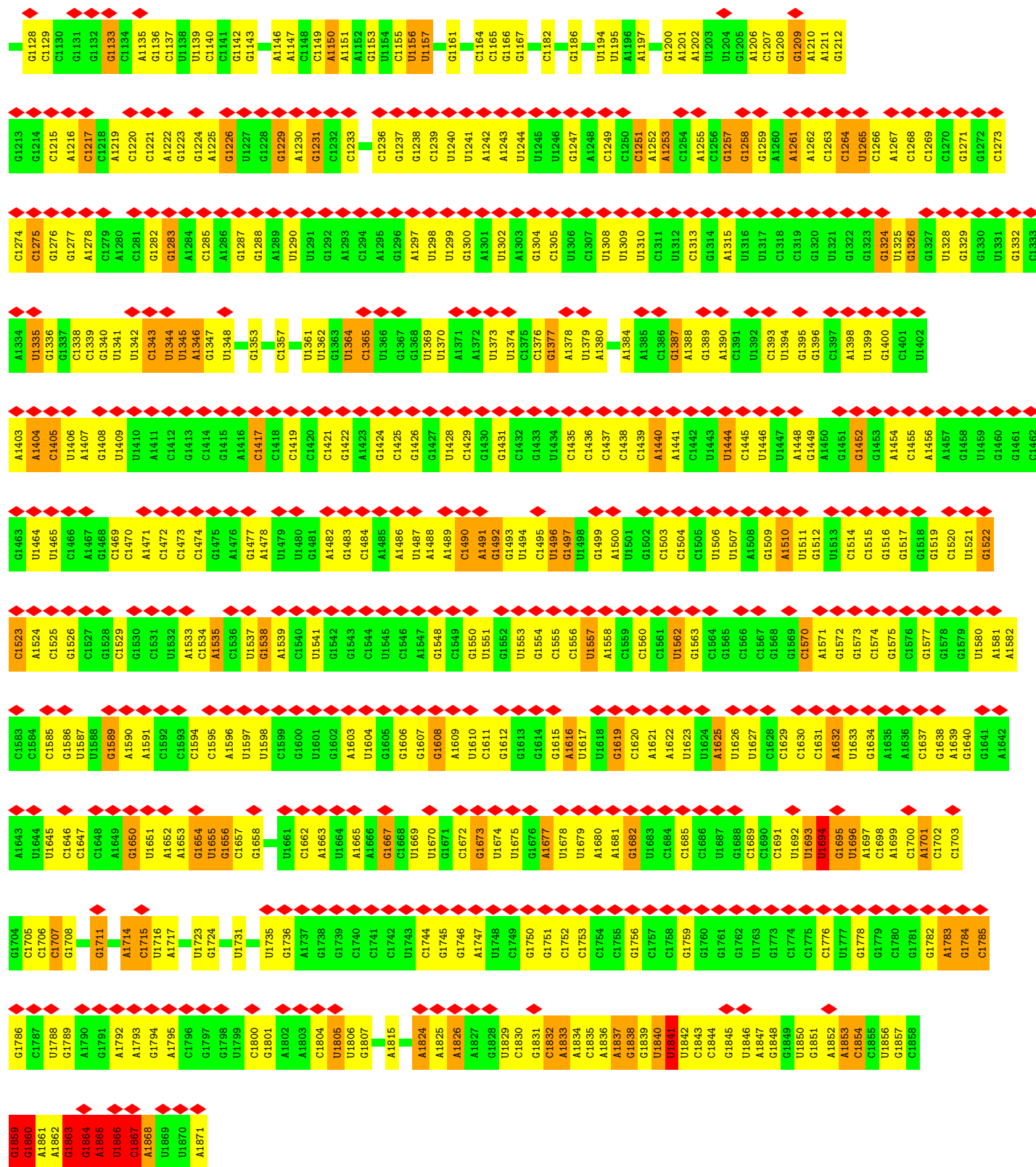
- Molecule 45: Large ribosomal subunit protein eL28



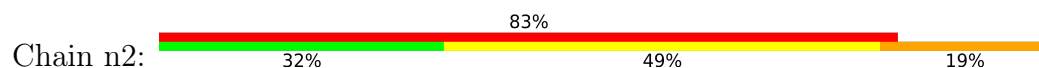
- Molecule 46: 18S ribosomal RNA

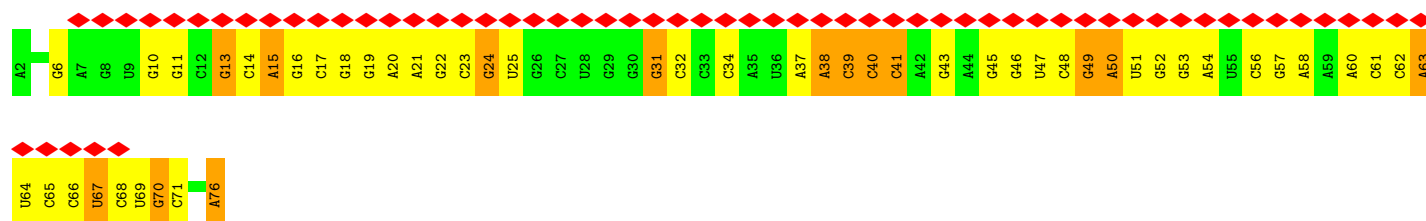


A1062	A992	G931	A871	G809	U880	G619	U559	C499	G439	U374	G314	C194
U1063	G993	C932	A872	A810	A681	C620	G560	C500	G440	G375	A315	C195
A1064	G995	G934	U873	A811	G682	A621	G561	G501	A441	G376	U316	C196
C1065	C996	G935	A874	A812	U684	C623	A562	A502	G442	U377	G317	C197
C1066	G1001	G936	G875	A813	G685	C624	A563	C503	C443	A378	G318	U198
G1067	G937	G937	G876	A814	G686	G625	A564	C504	C444	G379	C319	U199
U1068	G938	C938	A877	A815	A687	C626	G565	C505	U445	U380	C320	C200
C1069	U1004	C939	C878	U816	U688	G627	A566	G506	U446	C381	C321	C201
U1070	U1005	A940	C879	U817	C689	G628	G567	G507	A447	G382	G322	C202
U1071	U1006	U941	G880	A818	U690	U629	U568	G508	G448	C383	G323	G203
A1072	G1007	U942	C881	G819	U691	A630	C569	G509	A449	C384	C324	G204
C1008	C1008	C943	G882	A820	G692	A631	C570	A510	A450	G385	C325	G205
C1009	U1074	G944	G883	G821	G693	U632	A571	A511	U386	C326	G326	G206
A1010	A1010	U945	U884	U822	G694	U633	C572	G512	G387	C327	G327	G207
A1011	A1011	A946	U885	G823	A695	U634	U573	U513	C388	G328	G328	G208
C1077	G1012	U947	U886	G824	G696	C635	U574	A514	C389	G329	G329	G209
G1078	A1013	U948	C886	U824	C697	C635	U575	G515	U390	G330	U330	G210
U1079	G949	G949	U887	U825	C697	A636	A576	U516	A391	G331	G331	A211
C1080	G1016	C950	A888	C926	G698	G637	A577	G517	C392	G332	G332	U212
C1081	U1017	G951	U889	G829	G699	C638	A578	A518	C393	G333	G333	G213
U1018	U1018	C952	U890	A829	G700	U639	U579	C519	A394	G334	G334	C214
U1019	U1019	G953	U891	G830	C732	C640	C580	G520	U395	G335	G335	G215
U1020	G954	C954	U892	C831	G733	C641	C581	A521	G397	G336	G336	U216
C1021	C1021	C955	G893	A832	C735	A642	U582	A522	U398	G337	G337	G217
A1022	U1023	U956	G894	G833	C736	U644	U583	A523	C399	G338	G338	C218
U1023	U1023	A957	U895	G834	C737	A645	U584	A524	A401	G339	G339	A219
U1024	U1024	G958	G896	C835	C738	G646	U585	A525	C402	G340	G340	U220
A1025	A1025	C959	G897	C836	C739	G646	A586	U526	C402	G341	A341	U221
A1026	U1027	G960	U898	C837	G739	C647	C587	U527	U408	G342	G342	U222
U1027	C1028	G961	U899	G838	C740	G648	C588	A528	G409	G343	G343	A223
A1028	A1028	U962	U900	A839	C741	U649	G589	C529	G409	G344	G344	U224
G1081	A1032	G963	U901	C841	U749	A650	A589	A530	C411	G345	C345	C225
A1032	A1032	A964	C902	C942	C750	A652	G591	A531	G412	G346	U346	A226
U1036	A1036	A965	G903	G943	C751	U653	A592	U532	G413	G347	U347	G227
U1037	A1037	U967	G904	C944	C752	U654	U593	A533	G414	G348	G348	A228
G1038	G1038	G968	A905	C945	C753	A655	C594	A534	G415	G349	G349	U289
C1039	C1039	U968	A906	U946	G754	A656	C595	A535	A416	G350	G350	C290
U1040	U1040	C969	C907	U946	C755	G657	C595	A535	A417	G351	A351	G291
C1041	C1041	U970	U908	G847	C755	U658	A596	G536	U417	G352	C352	U292
G1042	G1042	U971	U908	C847	C755	U659	U597	G537	U418	G353	G353	G293
U1043	U1043	G972	G909	U789	C756	U660	U598	A538	C419	G354	U354	A294
A1044	A1044	C973	A910	A849	C757	G661	U598	C539	G422	G355	C355	C295
G1045	G1045	A974	G911	U850	C758	G662	G599	C539	G423	G356	C356	U296
U1046	U1046	C975	G912	A851	C759	U663	G600	U540	G424	G357	G357	C297
C1047	C1047	G976	G912	G791	C792	C664	A601	C541	U424	U425	C358	C297
G1050	G1050	C977	C913	C793	C793	C665	G602	U542	U425	U425	C359	U298
U1051	U1051	G977	G914	C794	C794	U668	G603	U483	C426	U425	C360	A299
A1052	A1052	G978	A915	G795	C795	U669	G604	U543	G427	C426	C360	G300
G1053	G1053	C979	C855	A796	C796	A670	C605	U544	A428	G427	U361	A301
A1054	A1054	C981	A856	A797	A797	A672	C606	C545	U429	G427	A362	A301
U1055	U1055	A982	G917	C857	C798	A673	A607	C546	U430	U429	U363	U302
C1118	C1118	A982	A918	U857	C798	A673	A607	C546	U430	U429	U363	U302
G1119	G1119	U919	U858	C958	C799	A674	A607	C546	U430	U429	U363	U302
C1120	C1120	G984	U920	U859	C800	G675	G608	C548	C431	U430	A365	A303
A1121	A1121	A985	A921	A861	U801	C676	U609	C549	C432	U430	C367	A304
U1122	U1122	A922	A922	G861	U801	C677	C610	C550	G433	U430	U368	C305
C1123	C1123	G923	G923	G862	U802	C678	U611	C551	G434	U430	U369	C306
G1124	G1124	A924	A924	A863	U803	C679	U612	C552	G435	U430	U370	U307
		G925	G925	A864	A804	C679	G612	C552	G436	U430	U370	C308
		G926	G926	A867	C905	C679	G613	C552	G437	U430	U370	C308
		G927	G927	A867	C906	C679	U614	C553	G438	U430	U370	C309
		A928	A928	U868	U806	C679	G615	C554	G439	U430	U370	C309
		C929	C929	G869	U807	C679	G616	C555	G440	U430	U370	C309
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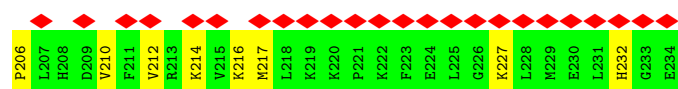
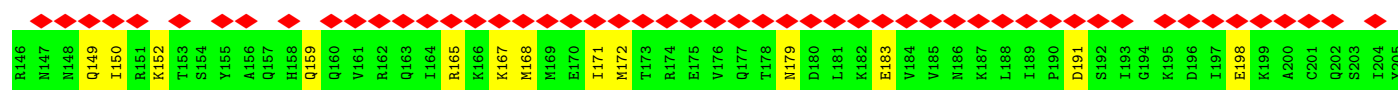
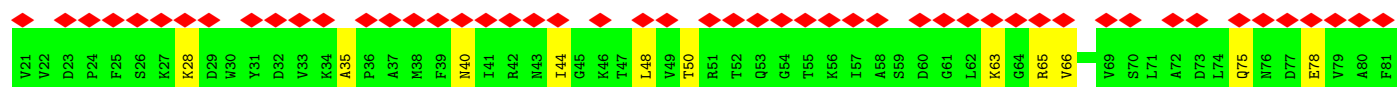
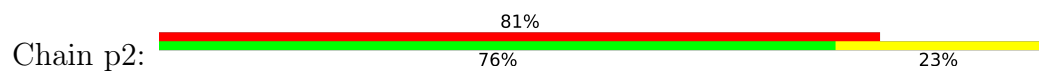


• Molecule 47: Transfer RNA

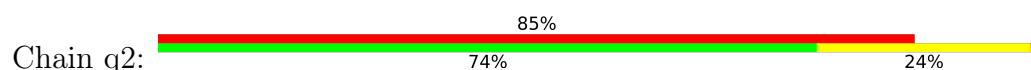




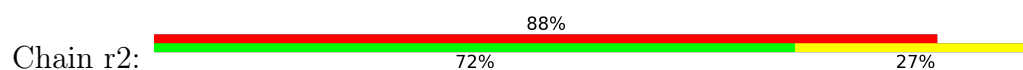
• Molecule 48: Small ribosomal subunit protein eS1

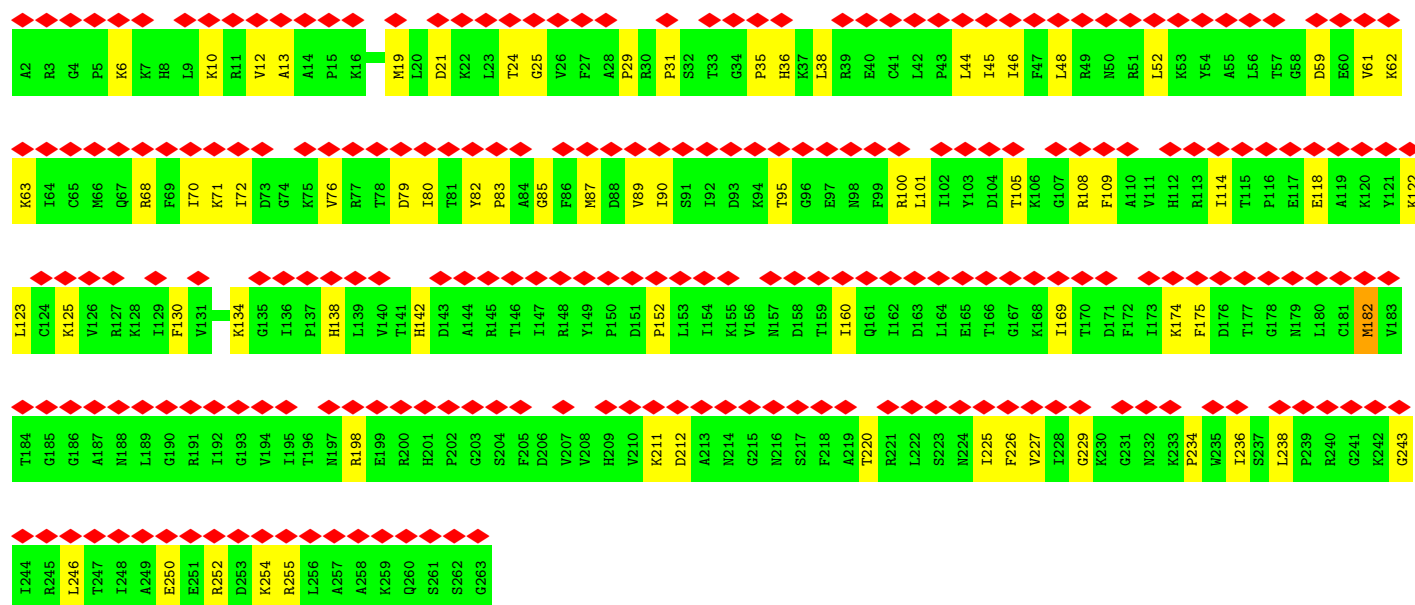


• Molecule 49: Small ribosomal subunit protein uS3

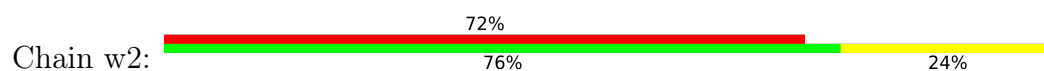


• Molecule 50: Small ribosomal subunit protein eS4

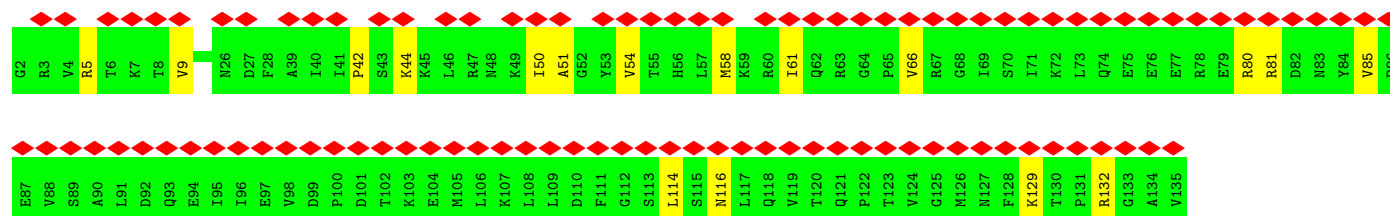
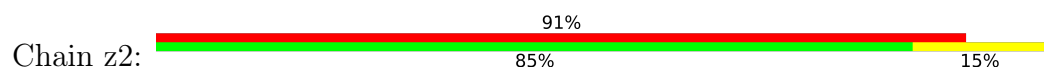




• Molecule 51: Small ribosomal subunit protein uS17

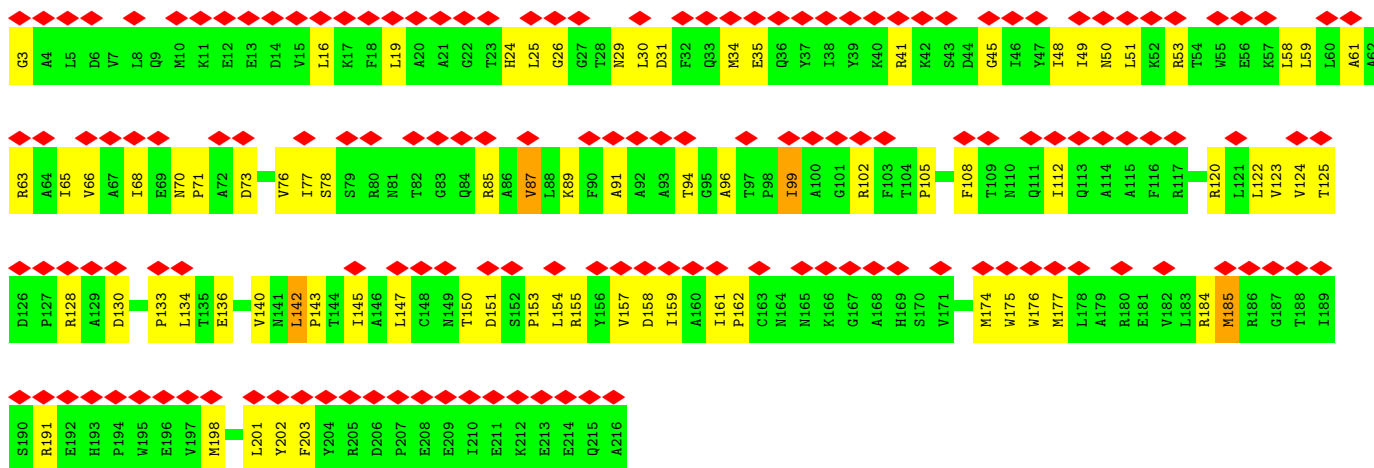


• Molecule 52: 40S ribosomal protein S17

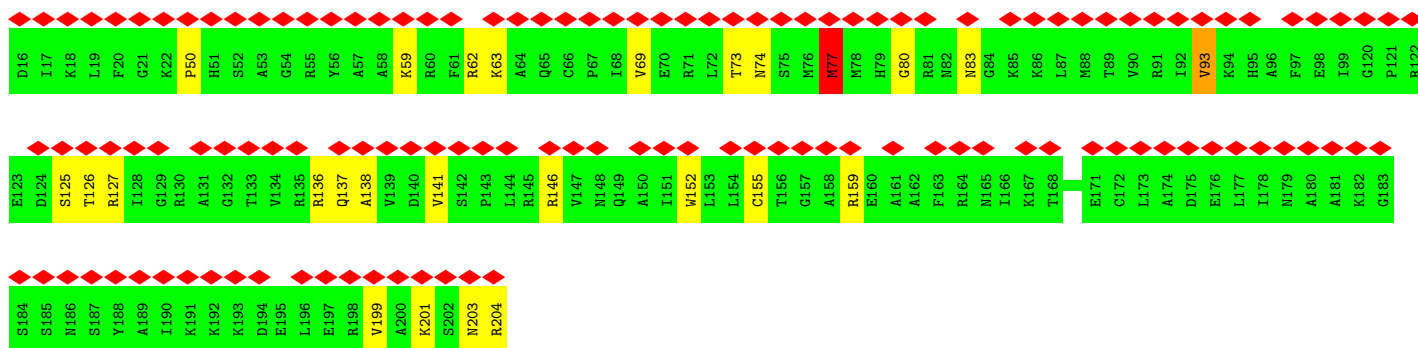
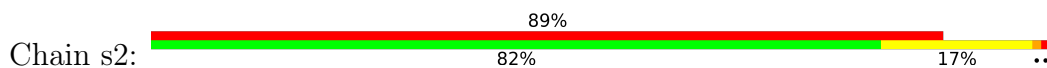


• Molecule 53: Small ribosomal subunit protein uS2

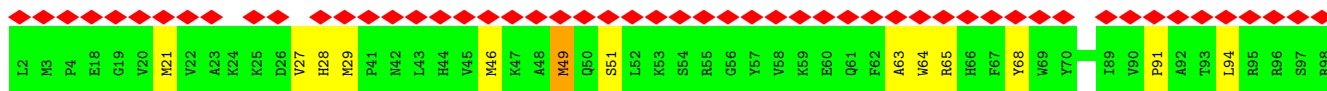
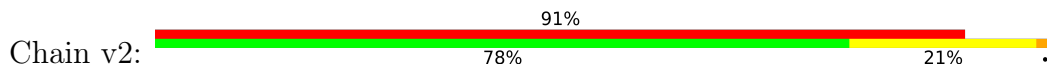




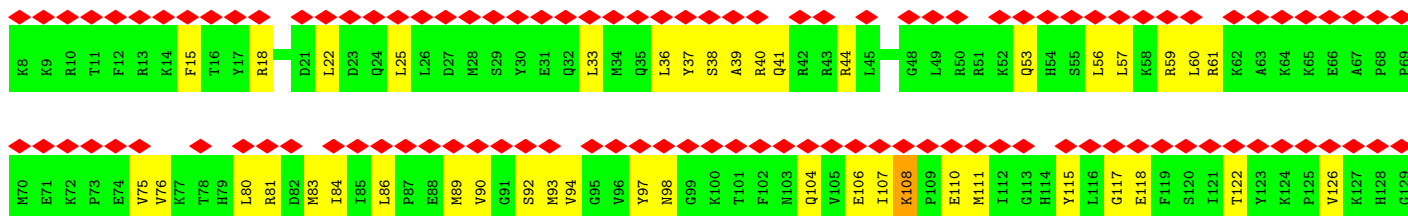
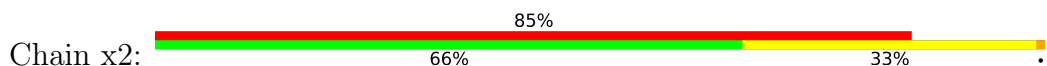
• Molecule 54: 40S ribosomal protein S5



• Molecule 55: 40S ribosomal protein S10

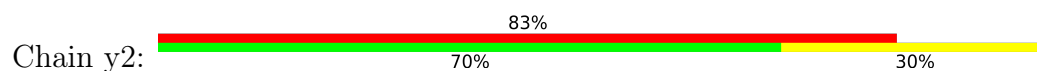


• Molecule 56: Small ribosomal subunit protein uS19

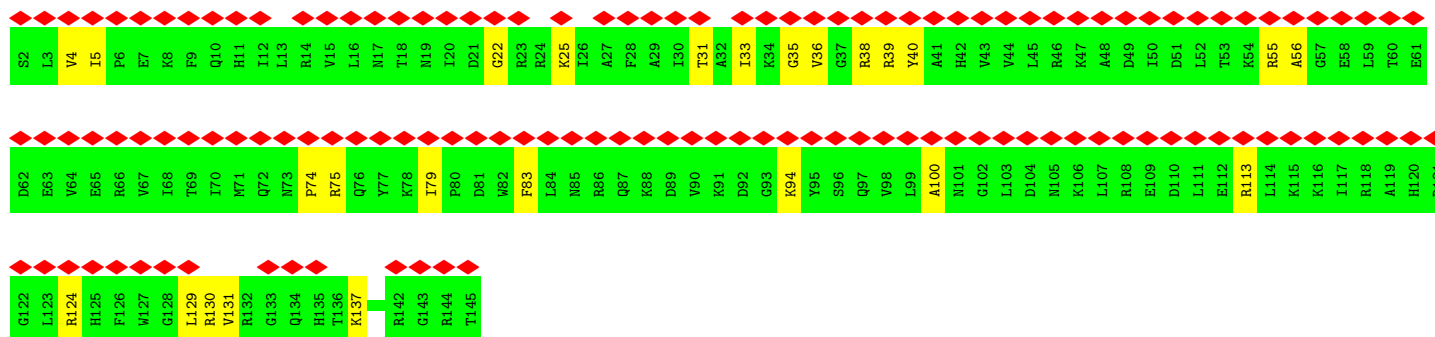
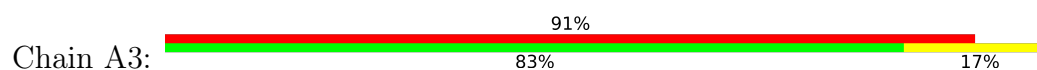




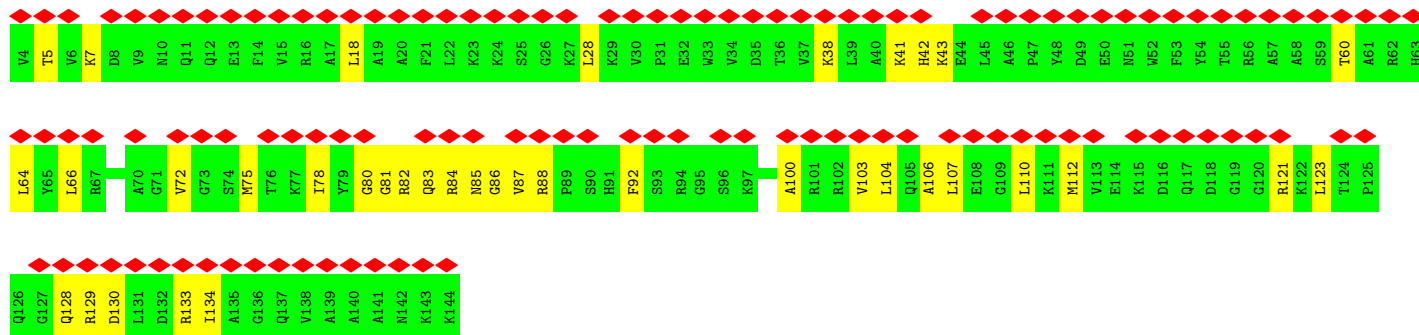
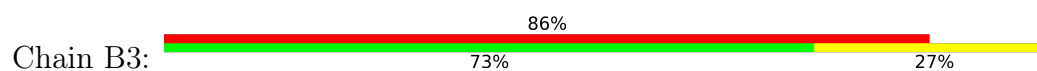
• Molecule 57: Small ribosomal subunit protein uS9



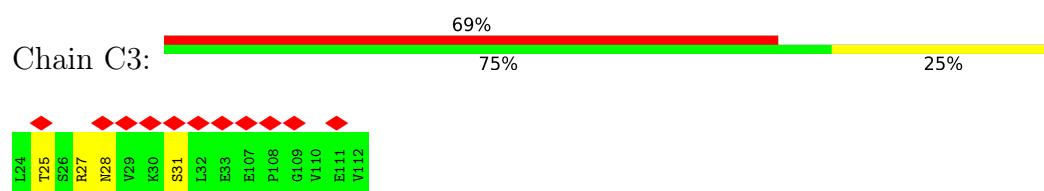
• Molecule 58: Small ribosomal subunit protein uS13



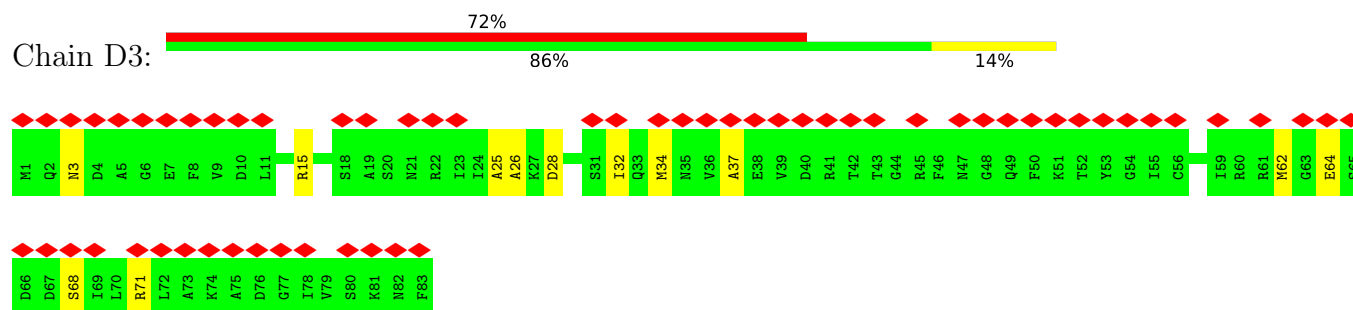
• Molecule 59: Small ribosomal subunit protein eS19



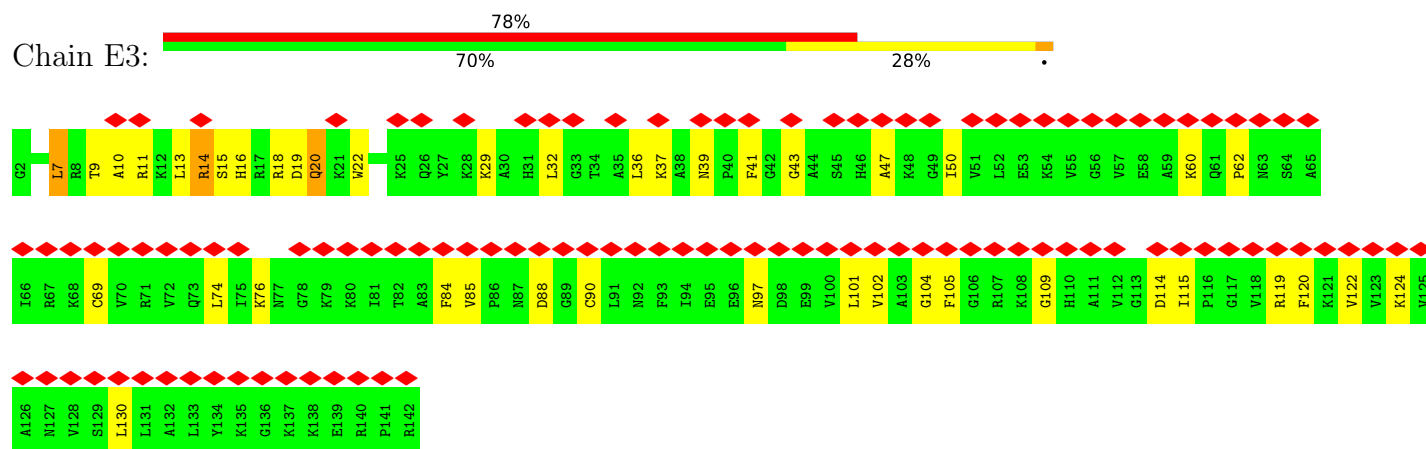
• Molecule 60: 40S ribosomal protein S20



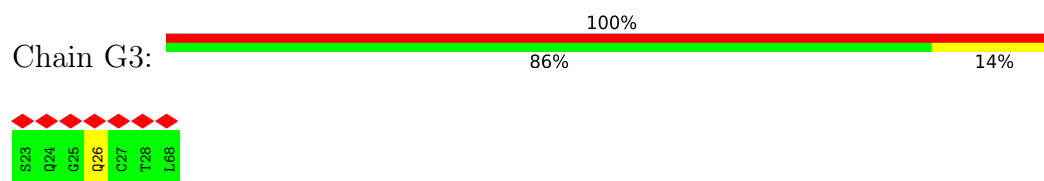
- Molecule 61: Small ribosomal subunit protein eS21



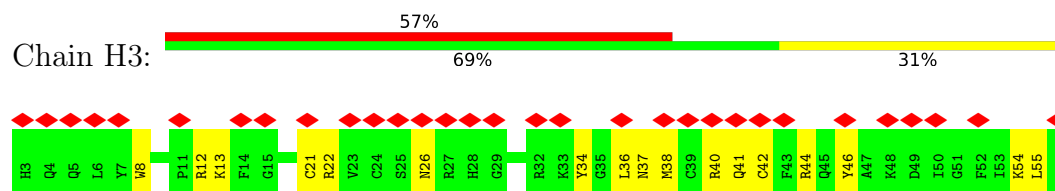
- Molecule 62: Small ribosomal subunit protein uS12



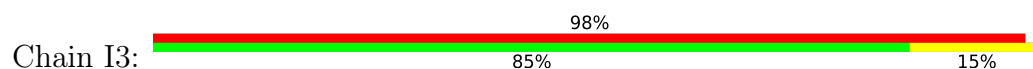
- Molecule 63: 40S ribosomal protein S28

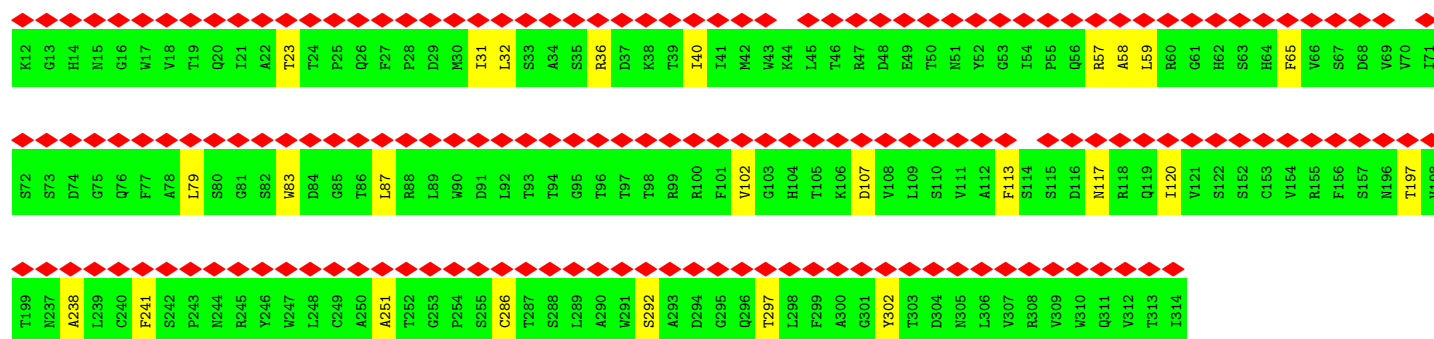


- Molecule 64: Small ribosomal subunit protein uS14

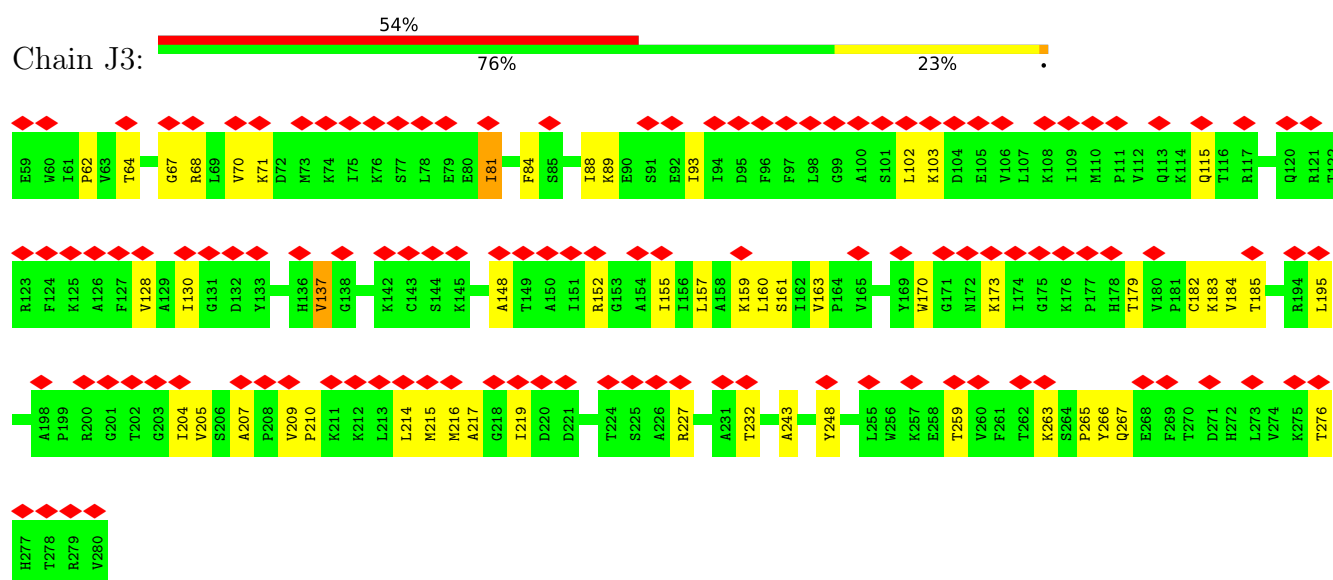


- Molecule 65: Receptor of activated protein C kinase 1

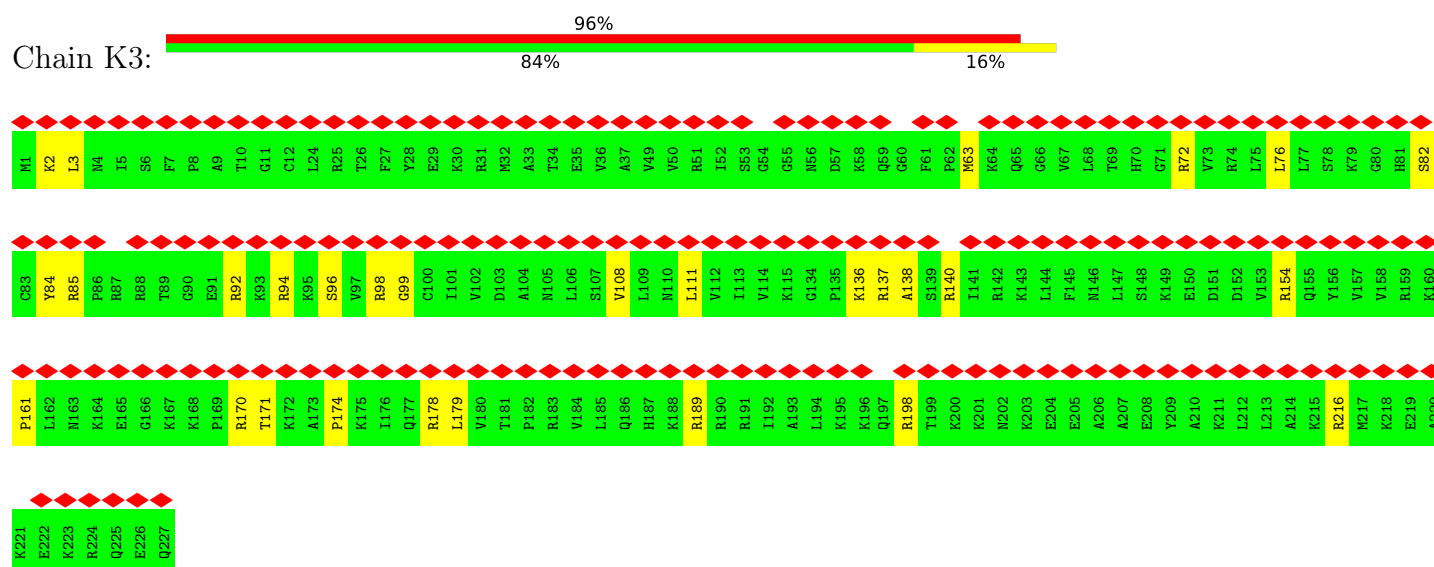




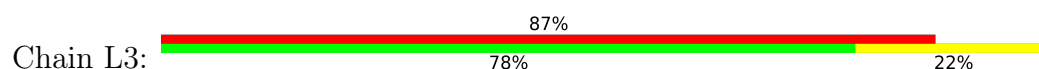
• Molecule 66: Small ribosomal subunit protein uS5

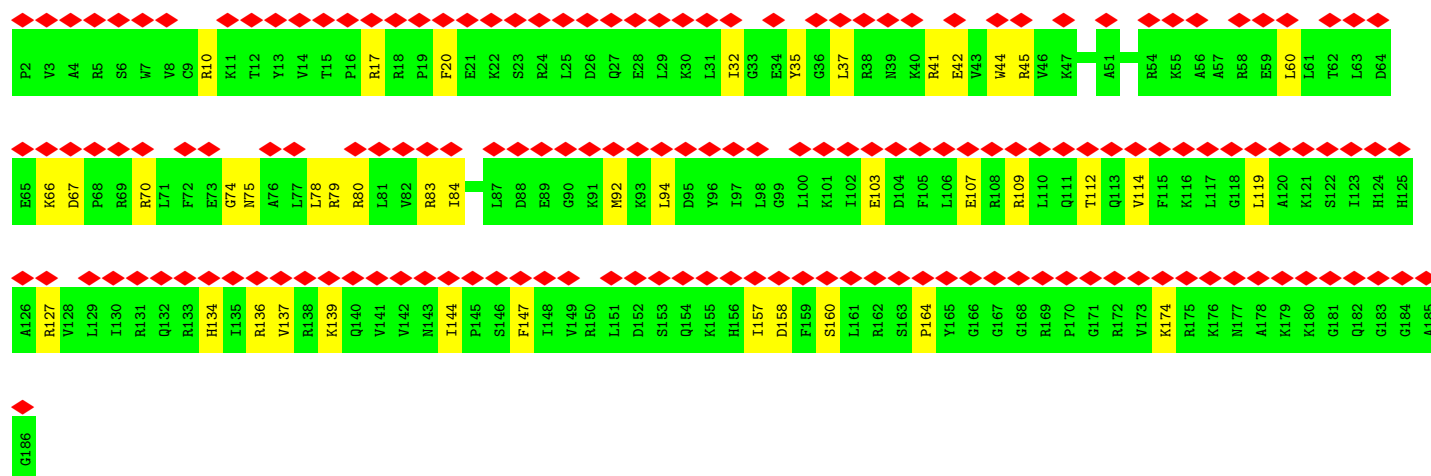


• Molecule 67: 40S ribosomal protein S6

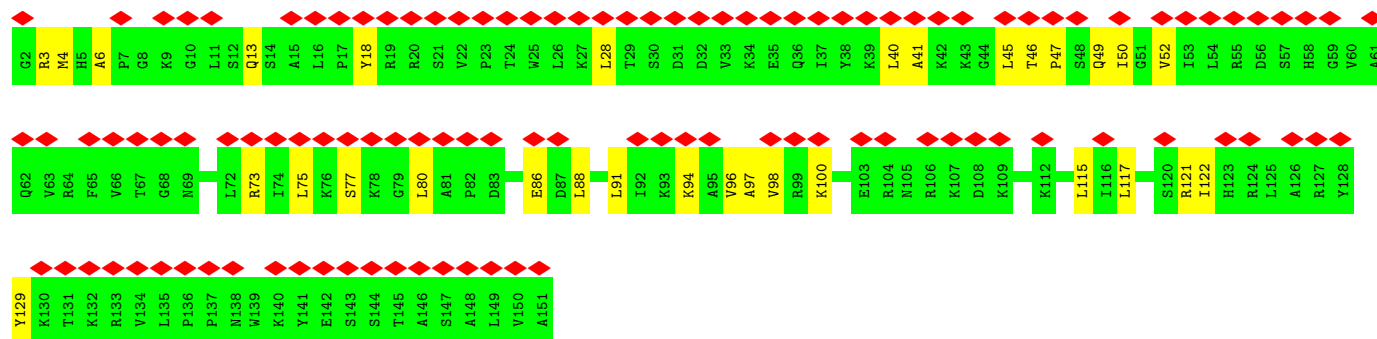
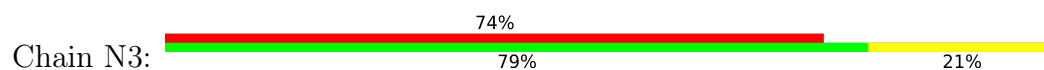


• Molecule 68: Small ribosomal subunit protein uS4

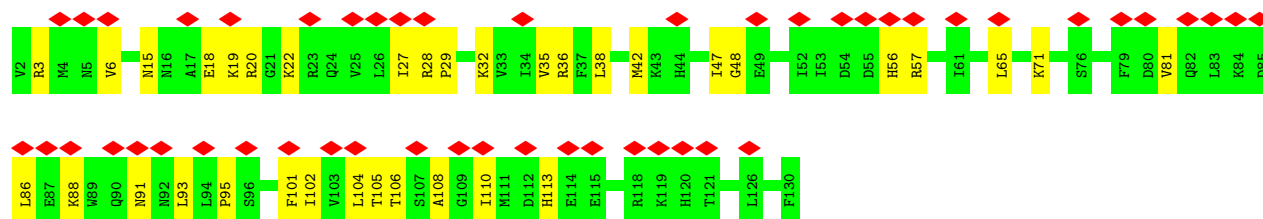
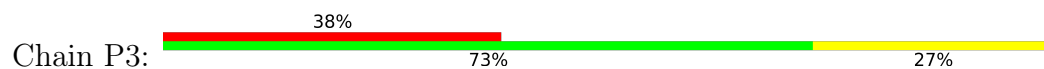




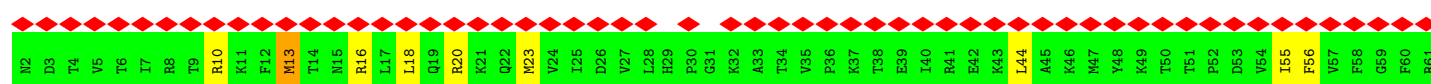
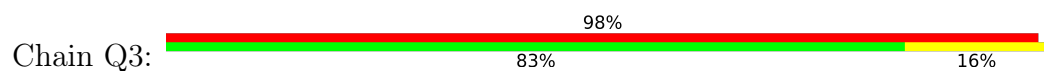
- Molecule 69: Small ribosomal subunit protein uS15



- Molecule 70: Small ribosomal subunit protein uS8

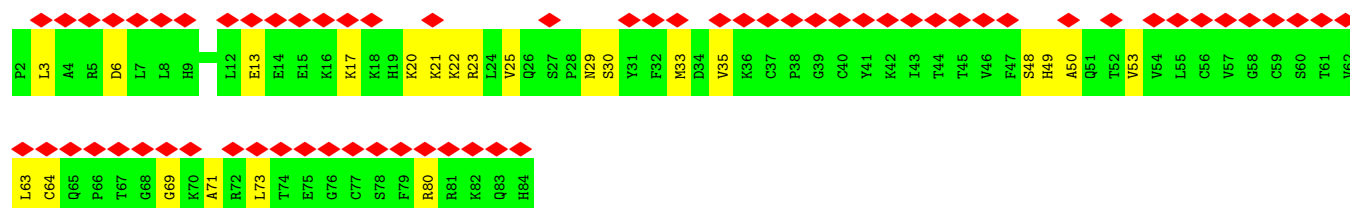
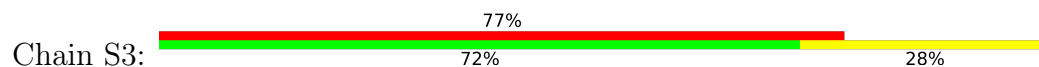


- Molecule 71: Small ribosomal subunit protein eS24





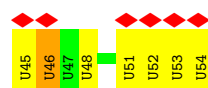
- Molecule 72: Small ribosomal subunit protein eS27-like



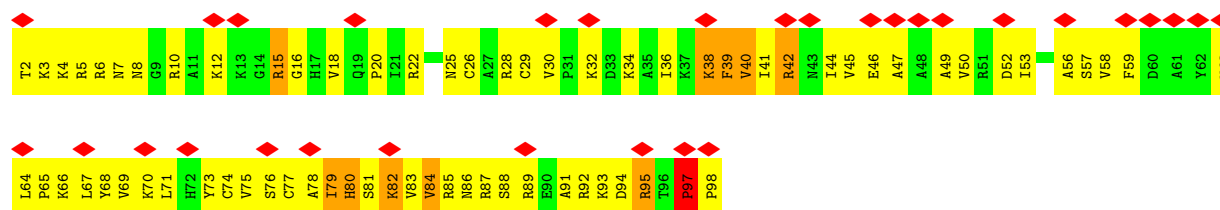
- Molecule 73: 40S ribosomal protein S30



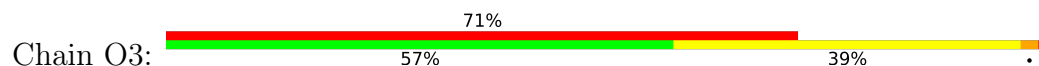
- Molecule 74: Messenger RNA

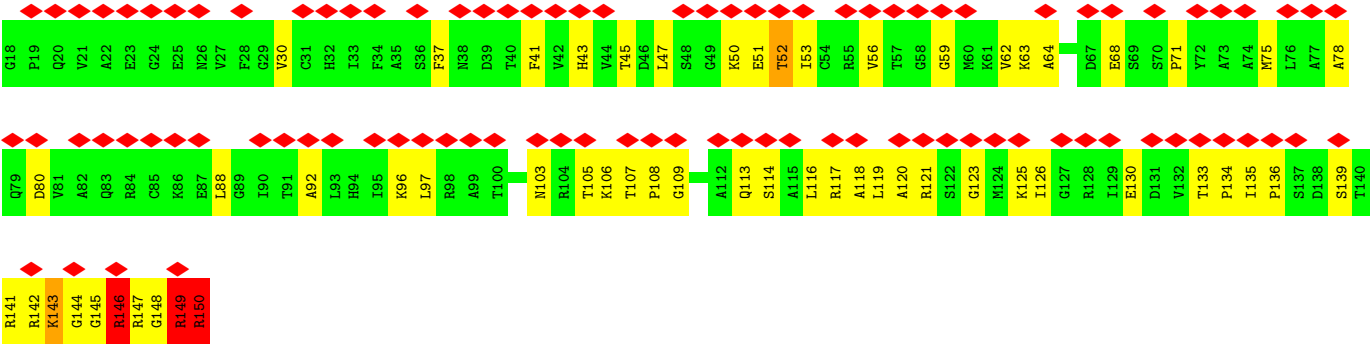


- Molecule 75: Small ribosomal subunit protein eS26



- Molecule 76: Small ribosomal subunit protein uS11





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	235429	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.596	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.068	Depositor
Recommended contour level	0.12	Depositor
Map size (\AA)	322.56, 322.56, 322.56	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.84, 0.84, 0.84	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, OMC, 2MG, 1MA, OMG, MG, ZN

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	0.20	0/1888	0.34	0/2516
2	B1	0.17	0/1847	0.32	0/2486
3	C1	0.22	0/1537	0.35	0/2065
4	D1	0.18	0/1728	0.30	0/2306
5	E1	0.18	0/1420	0.37	0/1899
6	F1	0.17	0/1635	0.35	0/2188
7	G1	0.19	0/1165	0.31	0/1558
8	H1	0.22	0/1746	0.34	0/2338
9	A2	0.21	0/85940	0.31	4/134022 (0.0%)
10	B2	0.21	0/2858	0.27	0/4455
11	C2	0.20	0/3701	0.28	0/5766
12	D2	0.21	0/1959	0.35	0/2627
13	E2	0.21	0/3305	0.39	0/4422
14	F2	0.20	0/2921	0.34	0/3921
15	G2	0.17	0/2435	0.31	0/3260
16	H2	0.18	0/1822	0.34	0/2443
17	I2	0.22	0/1670	0.41	2/2232 (0.1%)
18	J2	0.19	0/1268	0.36	0/1700
19	K2	0.21	0/1535	0.35	0/2048
20	L2	0.17	0/1383	0.28	0/1830
21	M2	0.21	0/1490	0.36	0/2000
22	N2	0.19	0/1327	0.33	0/1771
23	O2	0.13	0/839	0.28	0/1126
24	P2	0.22	0/983	0.37	0/1319
25	Q2	0.17	0/532	0.33	0/708
26	R2	0.17	0/984	0.33	0/1323
27	S2	0.18	0/1132	0.29	0/1504
28	T2	0.19	0/1130	0.31	0/1507
29	U2	0.20	0/1193	0.34	0/1593
30	V2	0.16	0/963	0.30	0/1275
31	W2	0.18	0/742	0.36	0/996
32	X2	0.18	0/903	0.32	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y2	0.20	0/1071	0.31	0/1429
34	Z2	0.20	0/895	0.36	0/1198
35	a2	0.18	0/916	0.34	0/1221
36	b2	0.16	0/1009	0.29	0/1332
37	c2	0.14	0/843	0.30	0/1115
38	d2	0.20	0/720	0.33	0/952
39	e2	0.17	0/574	0.30	0/760
40	f2	0.19	0/454	0.31	0/599
41	g2	0.18	0/435	0.32	0/575
42	h2	0.17	0/231	0.31	0/294
43	i2	0.18	0/855	0.31	0/1128
44	j2	0.20	0/704	0.31	0/935
45	k2	0.20	0/1016	0.36	0/1363
46	m2	0.57	8/41116 (0.0%)	0.38	27/64082 (0.0%)
47	n2	0.12	0/1795	0.29	0/2798
48	p2	0.13	0/1765	0.36	0/2362
49	q2	0.18	0/1784	0.41	2/2402 (0.1%)
50	r2	0.12	0/2118	0.31	0/2849
51	w2	0.14	0/1268	0.34	0/1696
52	z2	0.13	0/883	0.34	0/1184
53	o2	0.12	0/1731	0.33	0/2352
54	s2	0.10	0/1129	0.29	0/1503
55	v2	0.10	0/500	0.28	0/667
56	x2	0.13	0/1094	0.35	0/1460
57	y2	0.13	0/1161	0.34	0/1553
58	A3	0.11	0/1208	0.29	0/1618
59	B3	0.10	0/1122	0.29	0/1503
60	C3	0.08	0/121	0.22	0/161
61	D3	0.12	0/645	0.25	0/863
62	E3	0.12	0/1116	0.34	0/1490
63	G3	0.08	0/47	0.15	0/60
64	H3	0.15	0/466	0.40	0/618
65	I3	0.09	0/1349	0.27	0/1834
66	J3	0.14	0/1762	0.37	0/2382
67	K3	0.09	0/1534	0.24	0/2033
68	L3	0.11	0/1550	0.26	0/2069
69	N3	0.11	0/1232	0.29	0/1656
70	P3	0.15	0/1051	0.36	0/1406
71	Q3	0.09	0/1066	0.25	0/1415
72	S3	0.15	0/665	0.37	0/890
73	T3	0.08	0/328	0.24	0/426
74	Bx	0.10	0/219	0.28	0/336
75	F3	0.69	0/786	1.09	2/1053 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	O3	0.31	0/1006	0.55	0/1350
All	All	0.31	8/219321 (0.0%)	0.34	37/323392 (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
46	m2	0	2
75	F3	0	1
76	O3	0	4
All	All	0	7

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	m2	1865	A	N1-C2	50.41	2.35	1.34
46	m2	1865	A	C6-N1	49.54	2.34	1.35
46	m2	1865	A	C5-C6	45.89	2.32	1.41
46	m2	1865	A	C2-N3	41.70	2.17	1.33
46	m2	1865	A	N3-C4	38.49	2.11	1.34

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	m2	1693	U	P-O3'-C3'	-29.28	76.29	120.20
46	m2	1859	G	O3'-P-O5'	20.91	135.36	104.00
46	m2	1865	A	C5-C6-N6	-14.13	81.30	123.70
46	m2	1859	G	OP1-P-O3'	-13.10	68.71	108.00
46	m2	1867	C	C1'-O4'-C4'	-11.62	98.08	109.70

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
75	F3	97	PRO	Peptide
76	O3	146	ARG	Sidechain
76	O3	147	ARG	Sidechain
46	m2	1864	G	Sidechain
46	m2	1865	A	Sidechain

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	29	0
2	B1	1812	0	1947	28	0
3	C1	1519	0	1603	13	0
4	D1	1690	0	1745	10	0
5	E1	1397	0	1425	22	0
6	F1	1606	0	1705	17	0
7	G1	1143	0	1219	12	0
8	H1	1701	0	1749	25	0
9	A2	77352	0	39086	714	0
10	B2	2558	0	1296	17	0
11	C2	3314	0	1683	24	0
12	D2	1921	0	2022	22	0
13	E2	3238	0	3380	46	0
14	F2	2867	0	3040	30	0
15	G2	2389	0	2420	19	0
16	H2	1789	0	1932	25	0
17	I2	1640	0	1792	38	0
18	J2	1242	0	1274	11	0
19	K2	1511	0	1636	20	0
20	L2	1367	0	1506	14	0
21	M2	1450	0	1488	12	0
22	N2	1299	0	1368	18	0
23	O2	825	0	850	11	0
24	P2	969	0	1031	4	0
25	Q2	519	0	533	2	0
26	R2	967	0	1040	11	0
27	S2	1115	0	1205	12	0
28	T2	1107	0	1182	11	0
29	U2	1164	0	1213	13	0
30	V2	945	0	1037	9	0
31	W2	732	0	769	11	0
32	X2	888	0	930	7	0
33	Y2	1053	0	1147	7	0
34	Z2	876	0	912	9	0
35	a2	906	0	997	5	0
36	b2	1001	0	1138	11	0
37	c2	832	0	917	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	d2	705	0	737	10	0
39	e2	568	0	635	5	0
40	f2	444	0	483	7	0
41	g2	429	0	465	1	0
42	h2	230	0	276	5	0
43	i2	842	0	912	8	0
44	j2	694	0	738	8	0
45	k2	1001	0	1066	12	0
46	m2	36794	0	18585	961	0
47	n2	1604	0	816	20	0
48	p2	1738	0	1809	41	0
49	q2	1756	0	1851	43	0
50	r2	2076	0	2177	52	0
51	w2	1247	0	1323	34	0
52	z2	874	0	913	16	0
53	o2	1694	0	1696	57	0
54	s2	1117	0	1167	22	0
55	v2	487	0	495	9	0
56	x2	1073	0	1128	44	0
57	y2	1143	0	1213	37	0
58	A3	1190	0	1249	17	0
59	B3	1104	0	1139	29	0
60	C3	122	0	124	3	0
61	D3	638	0	635	8	0
62	E3	1098	0	1167	33	0
63	G3	49	0	45	1	0
64	H3	455	0	445	15	0
65	I3	1320	0	1277	15	0
66	J3	1725	0	1815	39	0
67	K3	1519	0	1664	21	0
68	L3	1525	0	1640	31	0
69	N3	1208	0	1294	23	0
70	P3	1034	0	1080	31	0
71	Q3	1049	0	1122	15	0
72	S3	652	0	676	16	0
73	T3	327	0	361	1	0
74	Bx	200	0	101	1	0
75	F3	774	0	817	544	0
76	O3	993	0	1011	290	0
77	F3	1	0	0	0	0
77	H3	1	0	0	0	0
77	d2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
77	g2	1	0	0	0	0
77	i2	1	0	0	0	0
77	j2	1	0	0	0	0
78	H3	1	0	0	0	0
79	A2	1	0	0	0	0
79	B1	1	0	0	0	0
79	m2	2	0	0	0	0
All	All	204064	0	148352	2999	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 9.

The worst 5 of 2999 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)
75:F3:59:PHE:CZ	76:O3:126:ILE:HB	1.24	1.61
75:F3:53:ILE:HD12	76:O3:117:ARG:CD	1.27	1.61
46:m2:1211:A:P	75:F3:82:LYS:HD2	1.42	1.59
75:F3:45:VAL:HG21	76:O3:117:ARG:CD	1.29	1.58
46:m2:1210:A:C4'	75:F3:79:ILE:HG22	1.32	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	221/222 (100%)	217 (98%)	4 (2%)	0	100	100
2	B1	220/232 (95%)	217 (99%)	3 (1%)	0	100	100
3	C1	188/190 (99%)	187 (100%)	1 (0%)	0	100	100
4	D1	204/213 (96%)	199 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E1	172/174 (99%)	164 (95%)	8 (5%)	0	100	100
6	F1	195/203 (96%)	187 (96%)	8 (4%)	0	100	100
7	G1	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
8	H1	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
12	D2	249/251 (99%)	238 (96%)	11 (4%)	0	100	100
13	E2	400/402 (100%)	394 (98%)	6 (2%)	0	100	100
14	F2	357/359 (99%)	350 (98%)	7 (2%)	0	100	100
15	G2	291/293 (99%)	288 (99%)	3 (1%)	0	100	100
16	H2	215/221 (97%)	211 (98%)	4 (2%)	0	100	100
17	I2	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
18	J2	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
19	K2	184/186 (99%)	179 (97%)	5 (3%)	0	100	100
20	L2	162/164 (99%)	161 (99%)	1 (1%)	0	100	100
21	M2	173/175 (99%)	167 (96%)	6 (4%)	0	100	100
22	N2	157/159 (99%)	156 (99%)	1 (1%)	0	100	100
23	O2	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
24	P2	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
25	Q2	60/62 (97%)	60 (100%)	0	0	100	100
26	R2	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
27	S2	132/134 (98%)	131 (99%)	1 (1%)	0	100	100
28	T2	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
29	U2	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
30	V2	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
31	W2	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
32	X2	105/107 (98%)	105 (100%)	0	0	100	100
33	Y2	126/128 (98%)	125 (99%)	1 (1%)	0	100	100
34	Z2	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
35	a2	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
36	b2	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
37	c2	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
38	d2	84/86 (98%)	84 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	e2	67/69 (97%)	67 (100%)	0	0	100	100
40	f2	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
41	g2	50/52 (96%)	50 (100%)	0	0	100	100
42	h2	22/24 (92%)	22 (100%)	0	0	100	100
43	i2	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
44	j2	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
45	k2	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
48	p2	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
49	q2	224/226 (99%)	220 (98%)	4 (2%)	0	100	100
50	r2	260/262 (99%)	252 (97%)	8 (3%)	0	100	100
51	w2	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
52	z2	104/110 (94%)	103 (99%)	1 (1%)	0	100	100
53	o2	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
54	s2	136/142 (96%)	128 (94%)	7 (5%)	1 (1%)	19	24
55	v2	50/58 (86%)	49 (98%)	1 (2%)	0	100	100
56	x2	128/130 (98%)	125 (98%)	3 (2%)	0	100	100
57	y2	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
58	A3	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
59	B3	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
60	C3	12/16 (75%)	12 (100%)	0	0	100	100
61	D3	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
62	E3	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
63	G3	4/7 (57%)	4 (100%)	0	0	100	100
64	H3	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
65	I3	159/169 (94%)	150 (94%)	9 (6%)	0	100	100
66	J3	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
67	K3	179/187 (96%)	176 (98%)	3 (2%)	0	100	100
68	L3	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
69	N3	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
70	P3	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
71	Q3	127/129 (98%)	124 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	S3	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	T3	37/41 (90%)	37 (100%)	0	0	100	100
75	F3	95/97 (98%)	87 (92%)	7 (7%)	1 (1%)	12	13
76	O3	131/133 (98%)	120 (92%)	9 (7%)	2 (2%)	8	8
All	All	10020/10219 (98%)	9778 (98%)	238 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
75	F3	97	PRO
54	s2	77	MET
76	O3	146	ARG
76	O3	143	LYS

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	194/193 (100%)	192 (99%)	2 (1%)	73	83
2	B1	193/198 (98%)	191 (99%)	2 (1%)	73	83
3	C1	169/169 (100%)	166 (98%)	3 (2%)	54	68
4	D1	177/179 (99%)	173 (98%)	4 (2%)	45	61
5	E1	147/147 (100%)	145 (99%)	2 (1%)	62	76
6	F1	166/170 (98%)	158 (95%)	8 (5%)	21	31
7	G1	118/118 (100%)	116 (98%)	2 (2%)	56	70
8	H1	171/171 (100%)	169 (99%)	2 (1%)	67	79
12	D2	193/193 (100%)	188 (97%)	5 (3%)	41	57
13	E2	347/347 (100%)	341 (98%)	6 (2%)	56	70
14	F2	301/301 (100%)	298 (99%)	3 (1%)	73	83
15	G2	246/246 (100%)	241 (98%)	5 (2%)	50	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	H2	198/198 (100%)	196 (99%)	2 (1%)	73	83
17	I2	172/172 (100%)	168 (98%)	4 (2%)	45	61
18	J2	134/134 (100%)	132 (98%)	2 (2%)	60	74
19	K2	164/164 (100%)	159 (97%)	5 (3%)	36	51
20	L2	145/145 (100%)	141 (97%)	4 (3%)	38	54
21	M2	155/155 (100%)	152 (98%)	3 (2%)	52	67
22	N2	139/139 (100%)	132 (95%)	7 (5%)	20	29
23	O2	91/91 (100%)	89 (98%)	2 (2%)	47	62
24	P2	100/100 (100%)	98 (98%)	2 (2%)	50	65
25	Q2	54/54 (100%)	54 (100%)	0	100	100
26	R2	106/106 (100%)	101 (95%)	5 (5%)	22	32
27	S2	124/124 (100%)	123 (99%)	1 (1%)	79	88
28	T2	117/117 (100%)	116 (99%)	1 (1%)	75	86
29	U2	120/120 (100%)	119 (99%)	1 (1%)	79	88
30	V2	98/98 (100%)	96 (98%)	2 (2%)	50	65
31	W2	79/79 (100%)	79 (100%)	0	100	100
32	X2	98/98 (100%)	96 (98%)	2 (2%)	50	65
33	Y2	114/114 (100%)	110 (96%)	4 (4%)	31	45
34	Z2	88/88 (100%)	88 (100%)	0	100	100
35	a2	98/98 (100%)	97 (99%)	1 (1%)	73	83
36	b2	108/108 (100%)	105 (97%)	3 (3%)	38	54
37	c2	86/86 (100%)	82 (95%)	4 (5%)	22	32
38	d2	73/73 (100%)	73 (100%)	0	100	100
39	e2	64/64 (100%)	64 (100%)	0	100	100
40	f2	47/47 (100%)	45 (96%)	2 (4%)	25	37
41	g2	48/48 (100%)	48 (100%)	0	100	100
42	h2	23/23 (100%)	22 (96%)	1 (4%)	25	37
43	i2	91/91 (100%)	89 (98%)	2 (2%)	47	62
44	j2	73/73 (100%)	73 (100%)	0	100	100
45	k2	109/109 (100%)	104 (95%)	5 (5%)	23	33
48	p2	195/195 (100%)	192 (98%)	3 (2%)	60	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	q2	189/189 (100%)	186 (98%)	3 (2%)	58	72
50	r2	224/224 (100%)	222 (99%)	2 (1%)	75	86
51	w2	137/137 (100%)	136 (99%)	1 (1%)	81	89
52	z2	98/98 (100%)	98 (100%)	0	100	100
53	o2	179/179 (100%)	174 (97%)	5 (3%)	38	54
54	s2	116/116 (100%)	114 (98%)	2 (2%)	56	70
55	v2	52/52 (100%)	50 (96%)	2 (4%)	28	41
56	x2	116/116 (100%)	115 (99%)	1 (1%)	75	86
57	y2	119/119 (100%)	119 (100%)	0	100	100
58	A3	125/125 (100%)	125 (100%)	0	100	100
59	B3	112/112 (100%)	112 (100%)	0	100	100
60	C3	15/15 (100%)	15 (100%)	0	100	100
61	D3	67/67 (100%)	66 (98%)	1 (2%)	60	74
62	E3	113/113 (100%)	108 (96%)	5 (4%)	24	36
63	G3	6/6 (100%)	6 (100%)	0	100	100
64	H3	48/48 (100%)	48 (100%)	0	100	100
65	I3	146/146 (100%)	143 (98%)	3 (2%)	48	64
66	J3	188/188 (100%)	184 (98%)	4 (2%)	48	64
67	K3	164/164 (100%)	163 (99%)	1 (1%)	84	91
68	L3	161/161 (100%)	160 (99%)	1 (1%)	84	91
69	N3	130/130 (100%)	130 (100%)	0	100	100
70	P3	112/112 (100%)	110 (98%)	2 (2%)	54	68
71	Q3	111/111 (100%)	108 (97%)	3 (3%)	40	55
72	S3	75/75 (100%)	73 (97%)	2 (3%)	40	55
73	T3	33/33 (100%)	32 (97%)	1 (3%)	36	51
75	F3	84/84 (100%)	72 (86%)	12 (14%)	2	2
76	O3	103/103 (100%)	99 (96%)	4 (4%)	27	41
All	All	8756/8766 (100%)	8589 (98%)	167 (2%)	52	67

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	r2	182	MET

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Mol	Chain	Res	Type
70	P3	19	LYS
53	o2	99	ILE
62	E3	14	ARG
73	T3	26	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
56	x2	98	ASN
75	F3	8	ASN
57	y2	142	GLN
65	I3	64	HIS
75	F3	80	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B2	119/120 (99%)	9 (7%)	0
11	C2	155/156 (99%)	34 (21%)	1 (0%)
46	m2	1717/1724 (99%)	453 (26%)	0
47	n2	74/75 (98%)	37 (50%)	0
74	Bx	9/10 (90%)	6 (66%)	0
9	A2	3588/3609 (99%)	734 (20%)	15 (0%)
All	All	5662/5694 (99%)	1273 (22%)	16 (0%)

5 of 1273 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A2	17	A
9	A2	21	G
9	A2	25	A
9	A2	30	C
9	A2	39	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A2	4582	U
9	A2	4351	U
9	A2	2541	C

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Continued from previous page...

Mol	Chain	Res	Type
9	A2	4183	U
9	A2	2463	U

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

24 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$
9	OMG	A2	3448	9	18,26,27	1.20	2 (11%)	19,38,41	0.77	1 (5%)
9	OMC	A2	2177	9	19,22,23	0.58	0	26,31,34	0.58	0
9	2MG	A2	4517	9	18,25,27	1.18	2 (11%)	19,37,41	0.82	1 (5%)
9	OMG	A2	4515	9	18,25,27	1.23	2 (11%)	19,37,41	0.81	1 (5%)
9	OMG	A2	2179	9	18,26,27	1.17	2 (11%)	19,38,41	0.85	1 (5%)
9	5MC	A2	4099	9	18,22,23	0.74	0	26,32,35	0.66	0
9	OMC	A2	4188	9	18,21,23	0.60	0	26,30,34	0.59	0
9	OMC	A2	2120	9	19,22,23	0.59	0	26,31,34	0.61	0
9	OMC	A2	3525	9	19,22,23	0.61	0	26,31,34	0.56	0
9	OMC	A2	2616	9	19,22,23	0.58	0	26,31,34	0.75	1 (3%)
9	OMC	A2	3357	9	19,22,23	0.61	0	26,31,34	0.60	0
9	5MC	A2	3438	9	18,22,23	0.63	0	26,32,35	0.63	0
9	OMG	A2	4289	9	18,25,27	1.16	2 (11%)	19,37,41	0.85	1 (5%)
9	2MG	A2	1330	9	18,26,27	1.19	2 (11%)	16,38,41	1.01	1 (6%)
9	OMG	A2	4275	9	18,25,27	1.20	2 (11%)	19,37,41	0.87	2 (10%)
9	OMG	A2	2119	9	18,26,27	1.19	2 (11%)	19,38,41	0.86	1 (5%)
9	OMG	A2	1335	9	18,26,27	1.21	3 (16%)	19,38,41	0.91	1 (5%)
9	OMG	A2	1438	9	18,26,27	1.22	2 (11%)	19,38,41	0.90	1 (5%)
9	OMC	A2	3543	9	19,22,23	0.61	0	26,31,34	0.67	0
9	1MA	A2	4067	9	16,25,26	0.91	2 (12%)	18,37,40	1.04	2 (11%)
46	OMG	m2	685	46	18,26,27	1.13	2 (11%)	19,38,41	0.87	1 (5%)
9	OMG	A2	3848	9	18,26,27	1.19	2 (11%)	19,38,41	0.86	1 (5%)
9	OMC	A2	2559	9	19,22,23	0.59	0	26,31,34	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	OMG	A2	4146	9	18,25,27	1.17	2 (11%)	19,37,41	0.81	1 (5%)

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
9	OMG	A2	3448	9	-	0/5/27/28	0/3/3/3
9	OMC	A2	2177	9	-	2/9/27/28	0/2/2/2
9	2MG	A2	4517	9	-	0/3/25/28	0/3/3/3
9	OMG	A2	4515	9	-	3/3/25/28	0/3/3/3
9	OMG	A2	2179	9	-	0/5/27/28	0/3/3/3
9	5MC	A2	4099	9	-	4/7/25/26	0/2/2/2
9	OMC	A2	4188	9	-	0/7/25/28	0/2/2/2
9	OMC	A2	2120	9	-	0/9/27/28	0/2/2/2
9	OMC	A2	3525	9	-	0/9/27/28	0/2/2/2
9	OMC	A2	2616	9	-	0/9/27/28	0/2/2/2
9	OMC	A2	3357	9	-	4/9/27/28	0/2/2/2
9	5MC	A2	3438	9	-	0/7/25/26	0/2/2/2
9	OMG	A2	4289	9	-	2/3/25/28	0/3/3/3
9	2MG	A2	1330	9	-	0/5/27/28	0/3/3/3
9	OMG	A2	4275	9	-	0/3/25/28	0/3/3/3
9	OMG	A2	2119	9	-	1/5/27/28	0/3/3/3
9	OMG	A2	1335	9	-	0/5/27/28	0/3/3/3
9	OMG	A2	1438	9	-	1/5/27/28	0/3/3/3
9	OMC	A2	3543	9	-	1/9/27/28	0/2/2/2
9	1MA	A2	4067	9	-	2/3/25/26	0/3/3/3
46	OMG	m2	685	46	-	2/5/27/28	0/3/3/3
9	OMG	A2	3848	9	-	1/5/27/28	0/3/3/3
9	OMC	A2	2559	9	-	0/9/27/28	0/2/2/2
9	OMG	A2	4146	9	-	0/3/25/28	0/3/3/3

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A2	1438	OMG	C8-N7	-3.18	1.29	1.35
9	A2	1330	2MG	C8-N7	-3.16	1.29	1.35
9	A2	4517	2MG	C8-N7	-3.13	1.29	1.35
9	A2	4515	OMG	C8-N7	-3.13	1.29	1.35
9	A2	3448	OMG	C8-N7	-3.09	1.29	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A2	2119	OMG	O6-C6-C5	2.48	129.22	124.37
9	A2	4275	OMG	O6-C6-C5	2.46	129.18	124.37
9	A2	4146	OMG	O6-C6-C5	2.45	129.17	124.37
9	A2	2179	OMG	O6-C6-C5	2.41	129.08	124.37
9	A2	3848	OMG	O6-C6-C5	2.40	129.05	124.37

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A2	2177	OMC	C1'-C2'-O2'-CM2
9	A2	3357	OMC	C2'-C1'-N1-C6
9	A2	3848	OMG	C1'-C2'-O2'-CM2
9	A2	4289	OMG	O4'-C4'-C5'-O5'
9	A2	4289	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A2	4515	OMG	1	0
9	A2	2179	OMG	1	0
9	A2	4099	5MC	3	0
9	A2	2119	OMG	1	0
9	A2	4067	1MA	2	0
46	m2	685	OMG	1	0
9	A2	3848	OMG	1	0
9	A2	4146	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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
9	A2	20
46	m2	7
65	I3	4
67	K3	3
55	v2	3
16	H2	2
54	s2	2
52	z2	2
60	C3	1
63	G3	1
73	T3	1

The worst 5 of 46 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H2	80:TYR	C	96:LEU	N	37.56
1	K3	115:LYS	C	134:GLY	N	27.50
1	A2	1512:U	O3'	1521:A	P	24.43
1	K3	12:CYS	C	24:LEU	N	21.59
1	s2	99:ILE	C	120:GLY	N	21.17

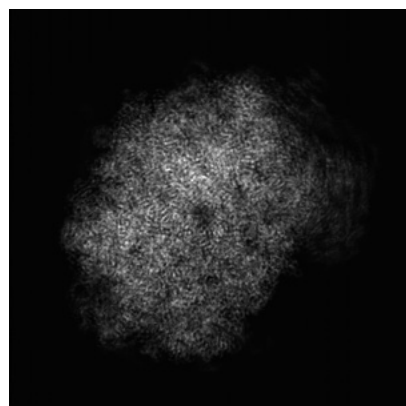
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51865. These allow visual inspection of the internal detail of the map and identification of artifacts.

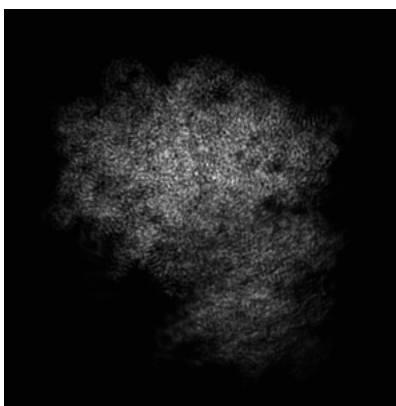
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

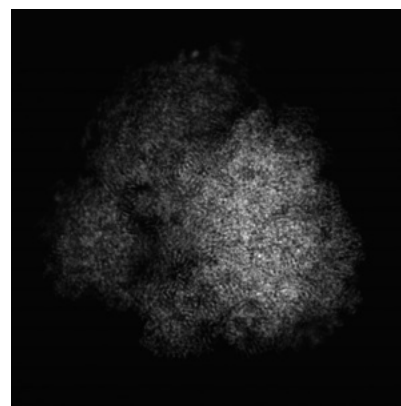
6.1.1 Primary map



X

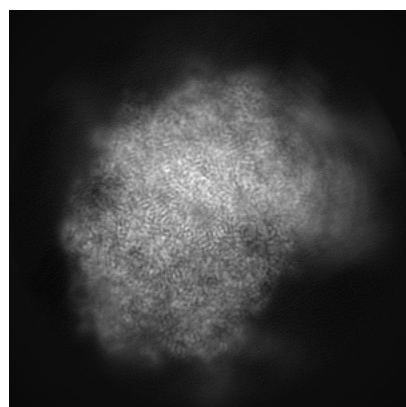


Y

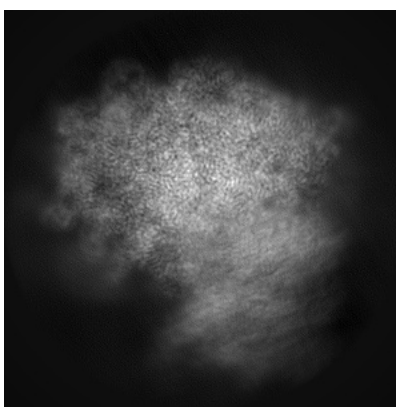


Z

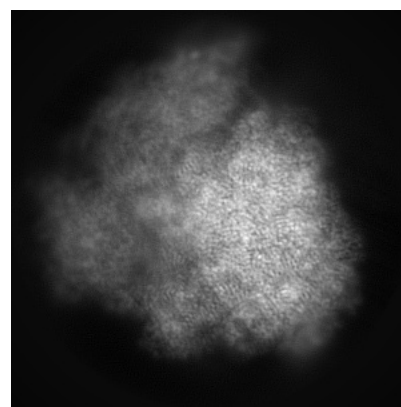
6.1.2 Raw map



X



Y

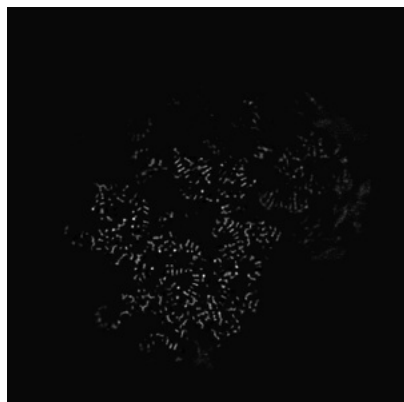


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192

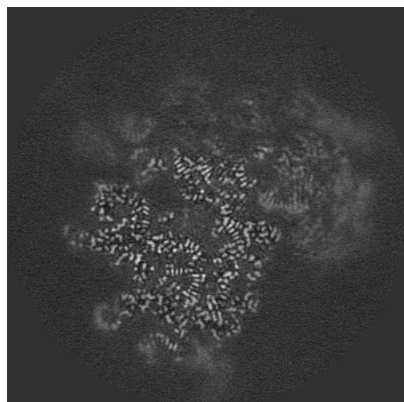


Y Index: 192

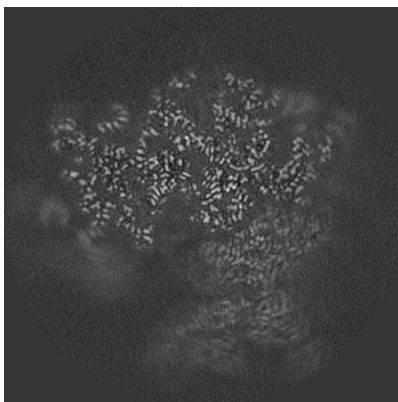


Z Index: 192

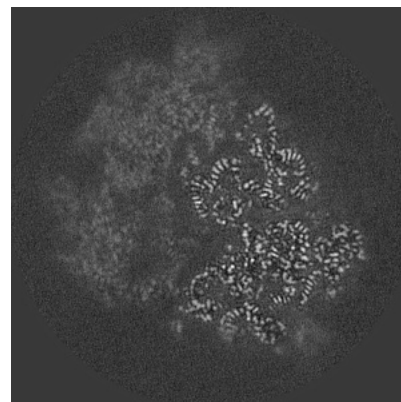
6.2.2 Raw map



X Index: 192



Y Index: 192



Z Index: 192

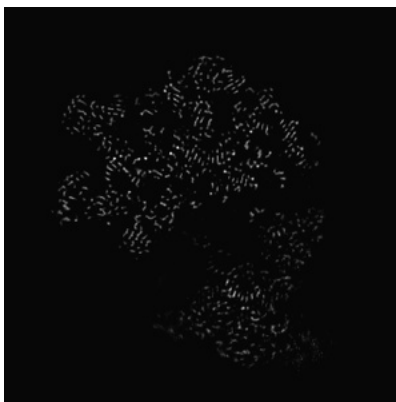
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 221

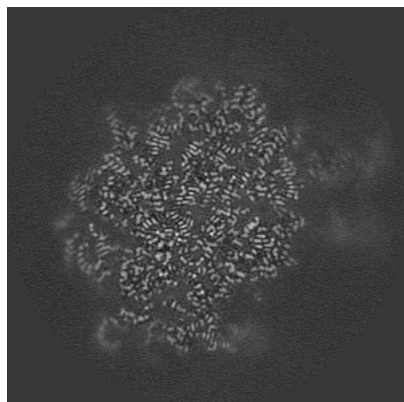


Y Index: 157

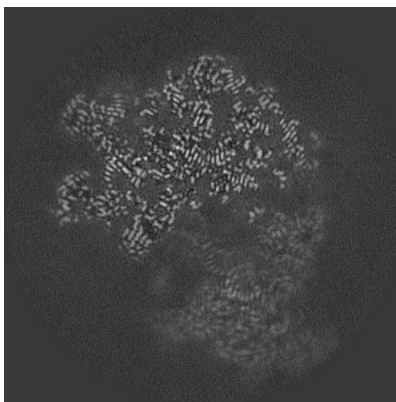


Z Index: 169

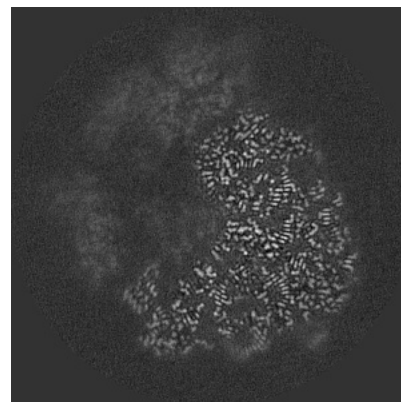
6.3.2 Raw map



X Index: 221



Y Index: 157

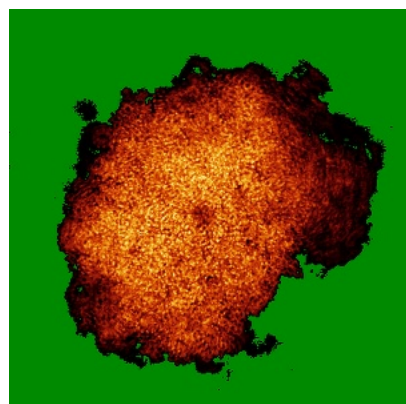


Z Index: 173

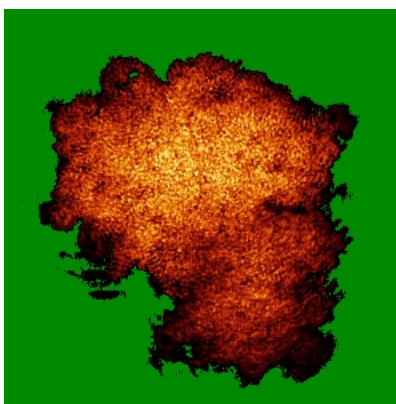
The images above show the largest variance slices of the map in three orthogonal directions.

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

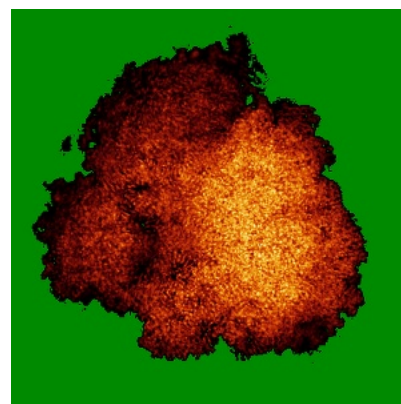
6.4.1 Primary map



X

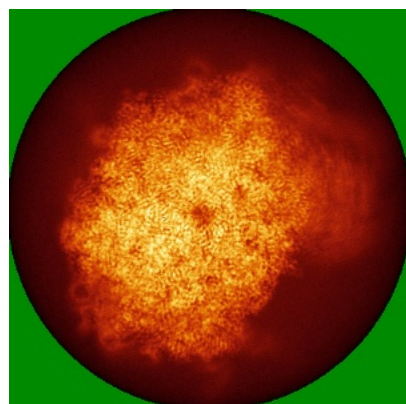


Y

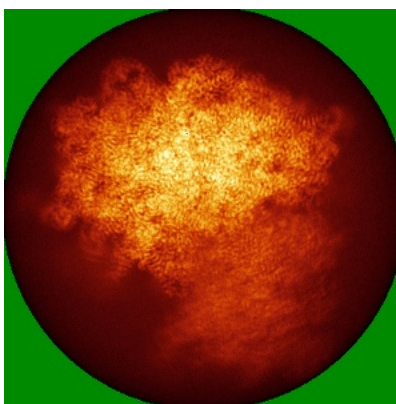


Z

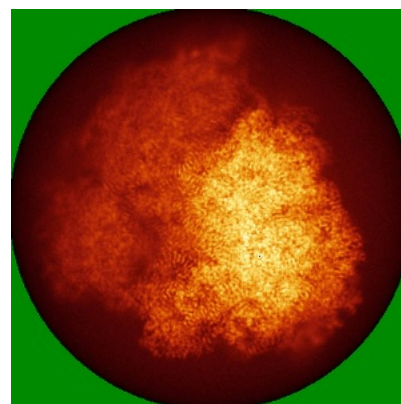
6.4.2 Raw map



X



Y

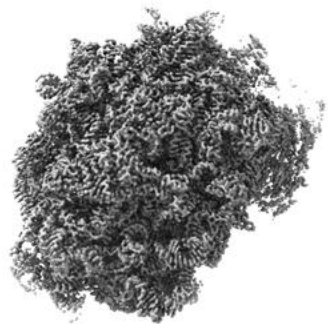


Z

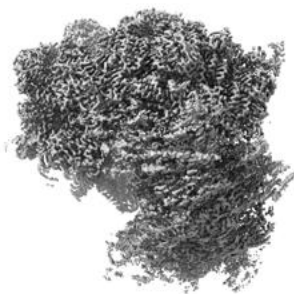
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

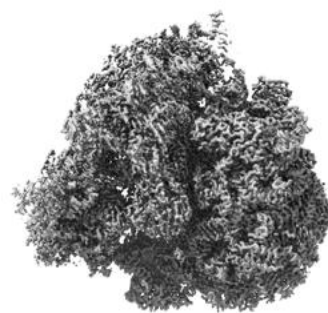
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. 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



X



Y



Z

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.

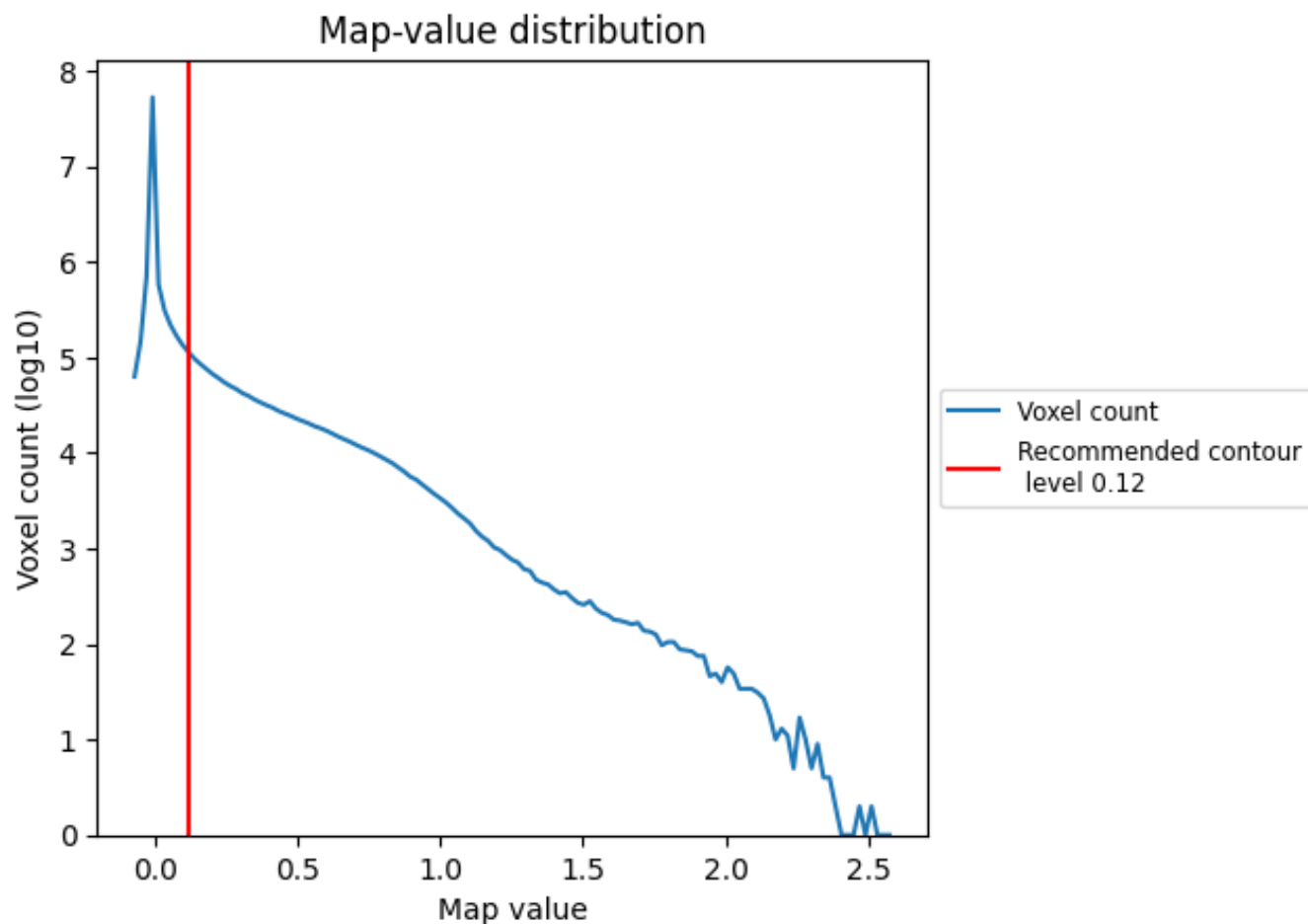
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

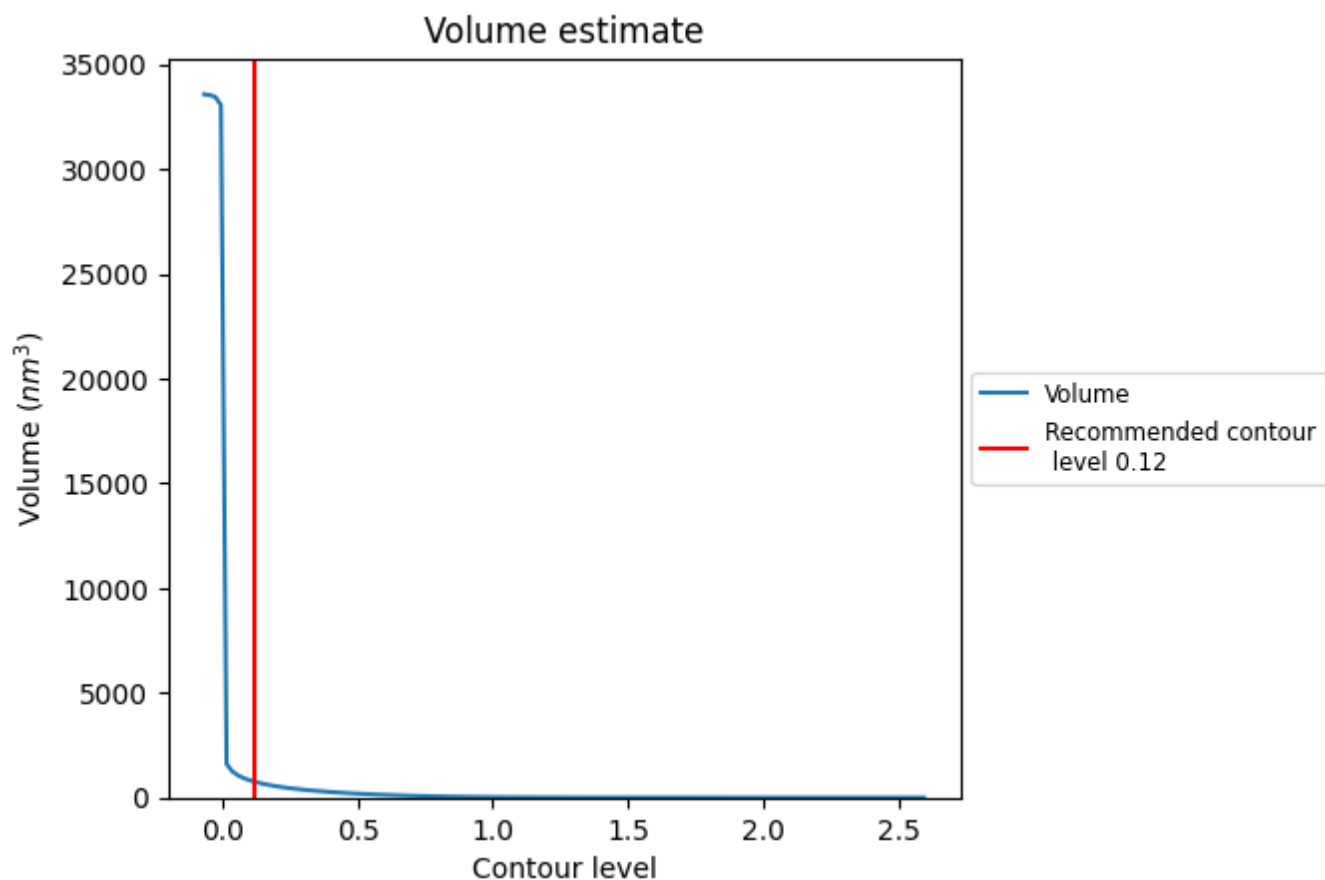
This section contains the results of statistical analysis of the map.

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.

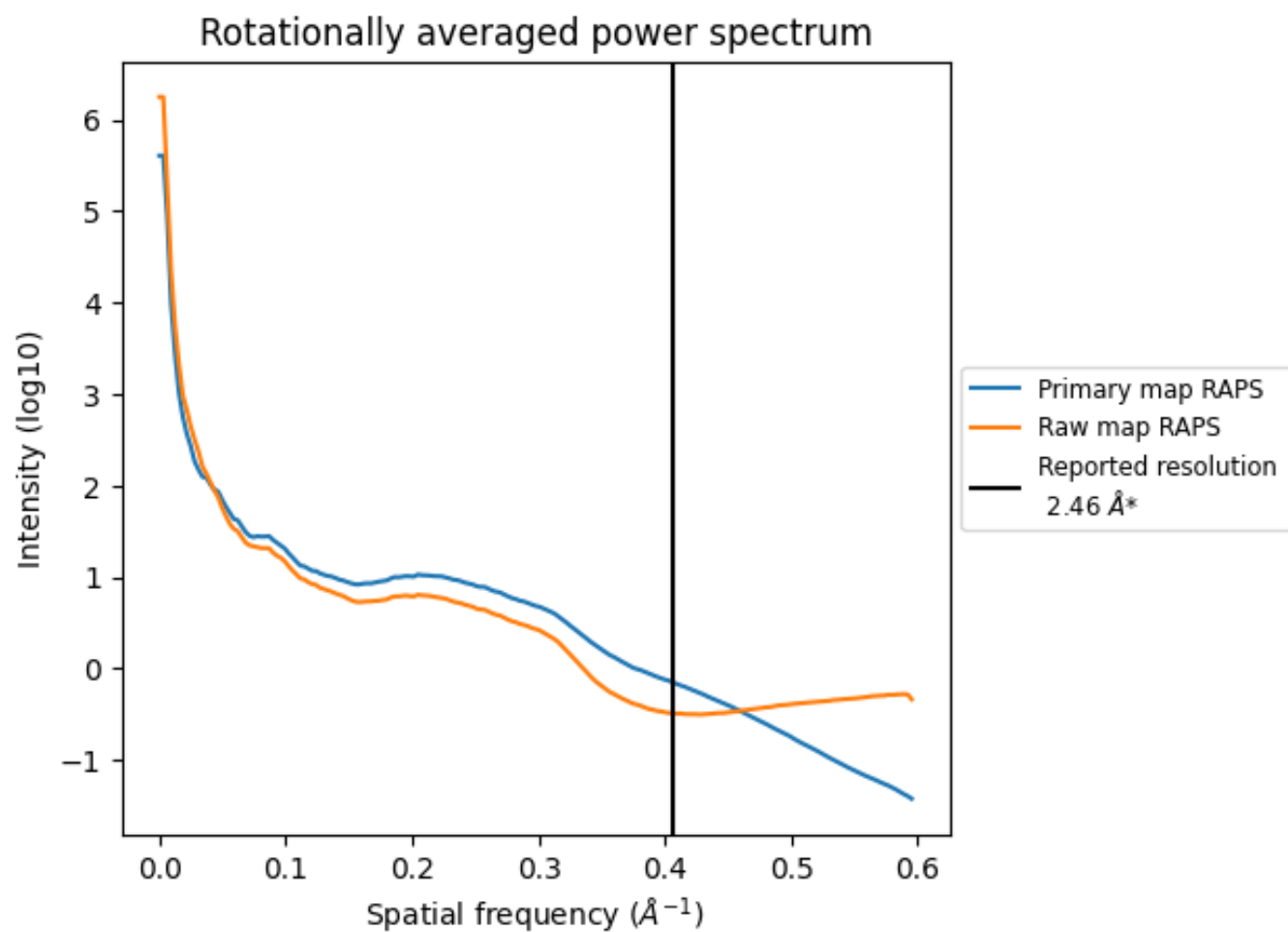
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 747 nm³; this corresponds to an approximate mass of 674 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 ⓘ

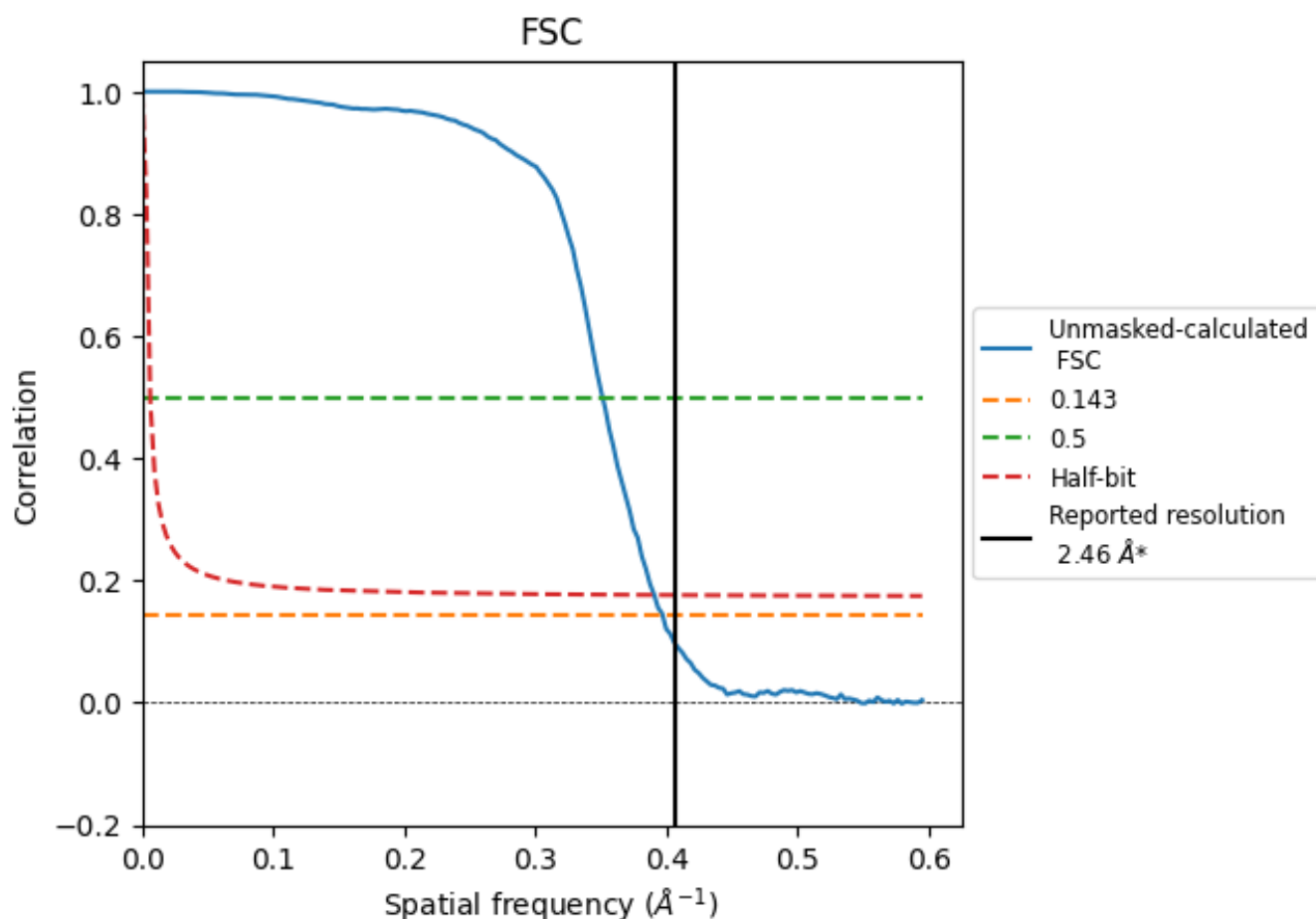


*Reported resolution corresponds to spatial frequency of 0.407 \AA^{-1}

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 0.407 Å⁻¹

8.2 Resolution estimates [i](#)

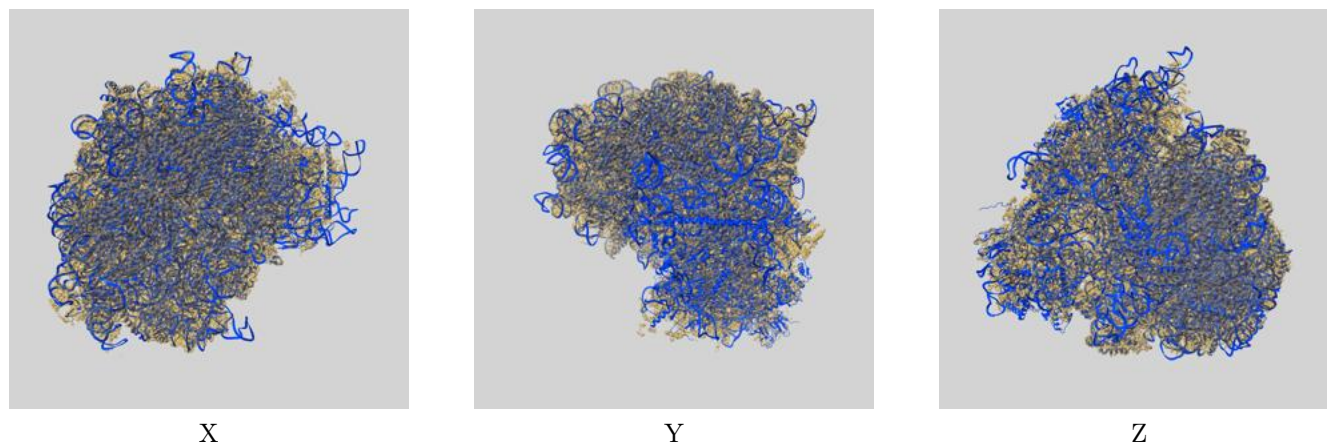
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.46	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.52	2.85	2.56

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

9 Map-model fit [i](#)

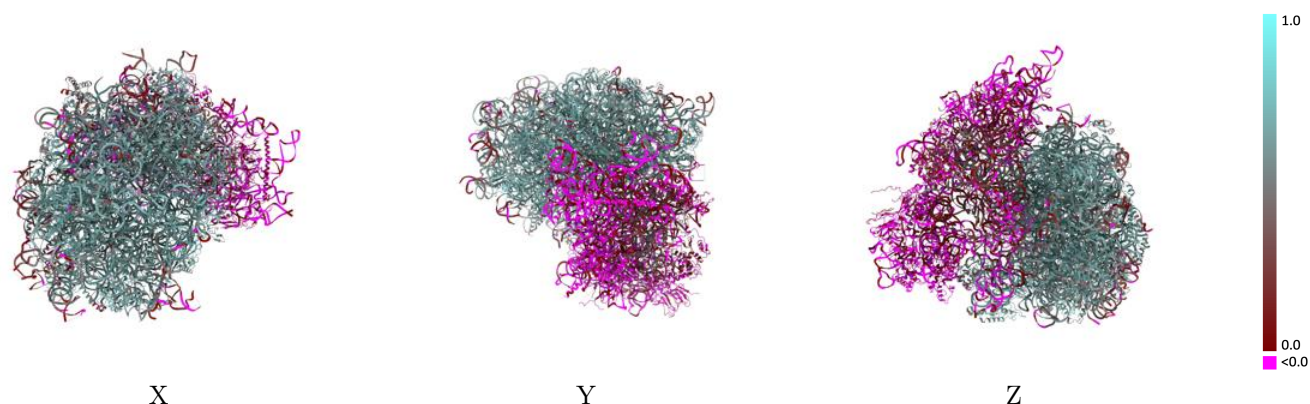
This section contains information regarding the fit between EMDB map EMD-51865 and PDB model 9H4N. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



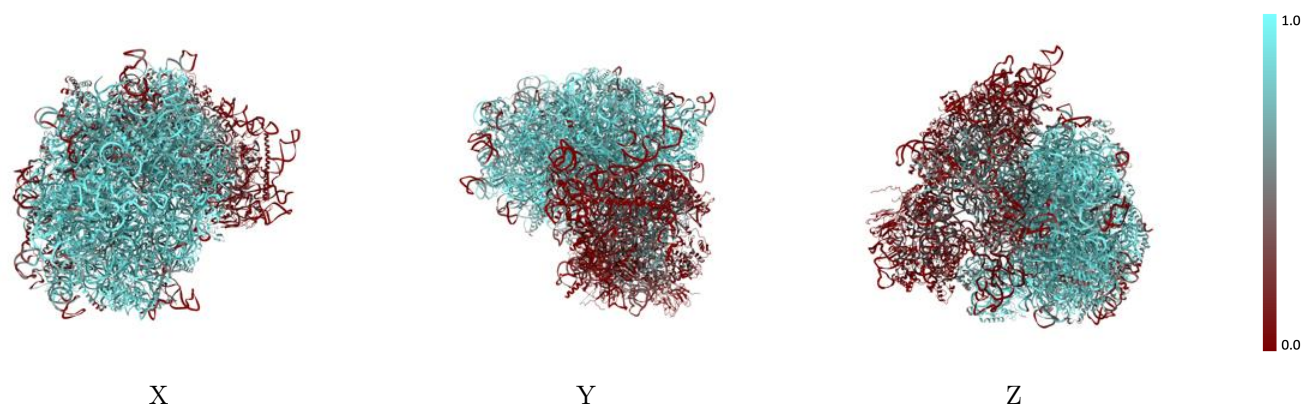
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



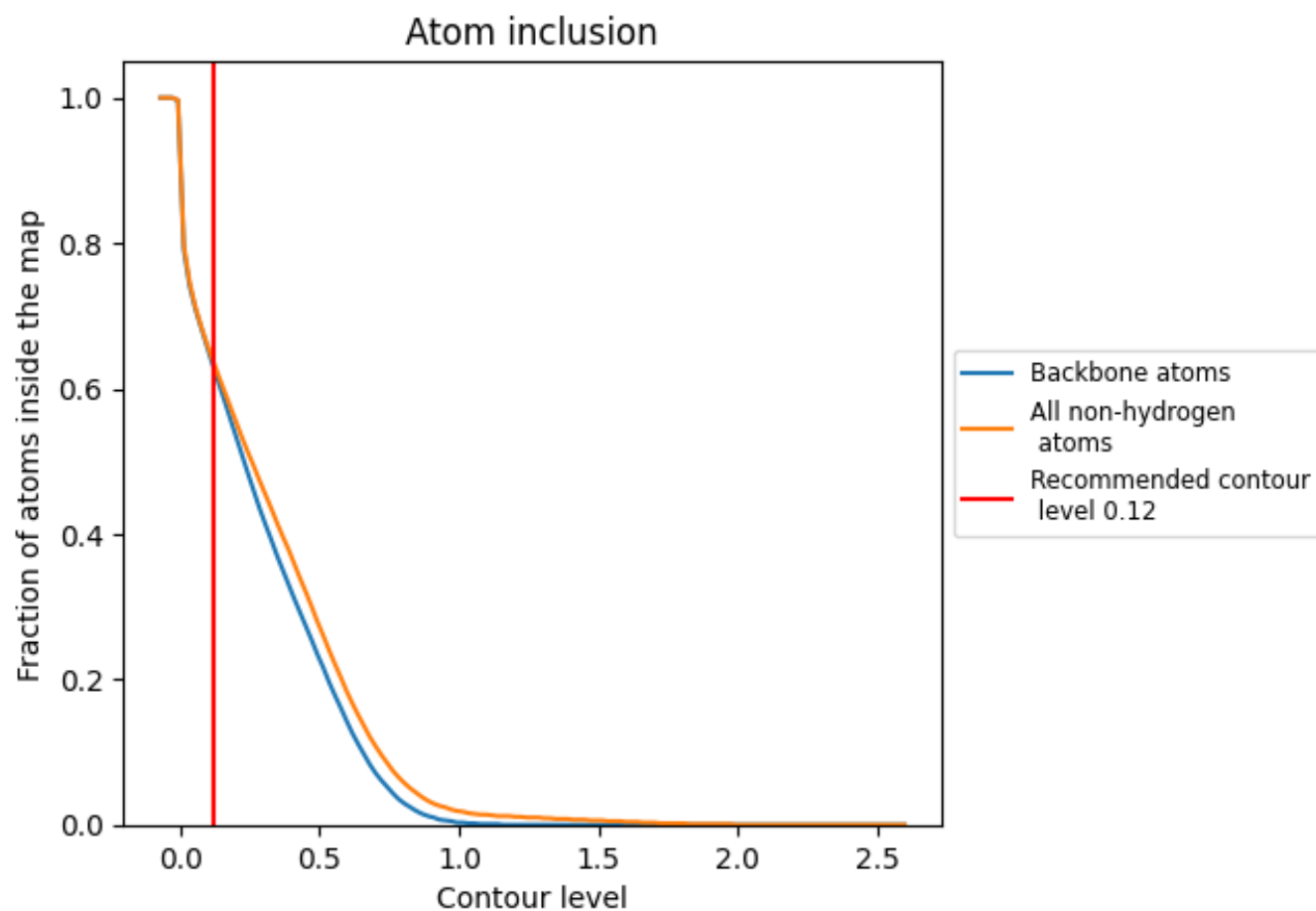
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 63% of all backbone atoms, 64% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6370	 0.4210
A1	 0.8780	 0.6480
A2	 0.8230	 0.5620
A3	 0.0980	 -0.0310
B1	 0.6580	 0.5310
B2	 0.9630	 0.6510
B3	 0.1550	 0.0040
Bx	 0.3550	 0.1930
C1	 0.8900	 0.6590
C2	 0.8640	 0.5850
C3	 0.2330	 0.0580
D1	 0.8530	 0.6320
D2	 0.9010	 0.6520
D3	 0.2640	 0.1990
E1	 0.6870	 0.5030
E2	 0.8830	 0.6550
E3	 0.2180	 0.0790
F1	 0.7500	 0.5910
F2	 0.8920	 0.6520
F3	 0.5330	 0.2940
G1	 0.8840	 0.6630
G2	 0.8430	 0.6260
G3	 0.1630	 -0.0560
H1	 0.9290	 0.6680
H2	 0.8210	 0.6080
H3	 0.3580	 0.0790
I2	 0.9040	 0.6670
I3	 0.0530	 0.0050
J2	 0.8980	 0.6610
J3	 0.3870	 0.2060
K2	 0.9140	 0.6660
K3	 0.0600	 -0.0190
L2	 0.8370	 0.6110
L3	 0.1580	 0.0150
M2	 0.9330	 0.6830



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Chain	Atom inclusion	Q-score
N2	 0.8240	 0.6190
N3	 0.2530	 0.1400
O2	 0.6280	 0.5120
O3	 0.3030	 0.0940
P2	 0.8960	 0.6580
P3	 0.4910	 0.3150
Q2	 0.8740	 0.6520
Q3	 0.0250	 -0.0410
R2	 0.8210	 0.6200
S2	 0.8330	 0.6280
S3	 0.2230	 0.0810
T2	 0.8570	 0.6270
T3	 0.1020	 0.0030
U2	 0.9010	 0.6510
V2	 0.6830	 0.5380
W2	 0.8660	 0.6000
X2	 0.8410	 0.6310
Y2	 0.8950	 0.6630
Z2	 0.9290	 0.6900
a2	 0.8320	 0.6170
b2	 0.8250	 0.6200
c2	 0.7170	 0.5810
d2	 0.8930	 0.6490
e2	 0.6890	 0.5370
f2	 0.8510	 0.6300
g2	 0.8820	 0.6570
h2	 0.5930	 0.4520
i2	 0.8570	 0.6310
j2	 0.8730	 0.6350
k2	 0.9210	 0.6620
m2	 0.2920	 0.1060
n2	 0.1530	 0.0830
o2	 0.2610	 0.1070
p2	 0.2070	 0.0520
q2	 0.1650	 0.0090
r2	 0.1640	 0.0410
s2	 0.1320	 -0.0210
v2	 0.1060	 0.0020
w2	 0.2810	 0.1030
x2	 0.1640	 -0.0010
y2	 0.1750	 0.0120
z2	 0.1090	 0.0130