



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2026 – 07:43 PM EDT

PDB ID : 5UQ8 / pdb_00005uq8
EMDB ID : EMD-8597
Title : 70S ribosome complex with dnaX mRNA stem-loop and E-site tRNA ("out" conformation)
Authors : Zhang, Y.; Hong, S.; Skiniotis, G.; Dunham, C.M.
Deposited on : 2017-02-07
Resolution : 3.20 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:

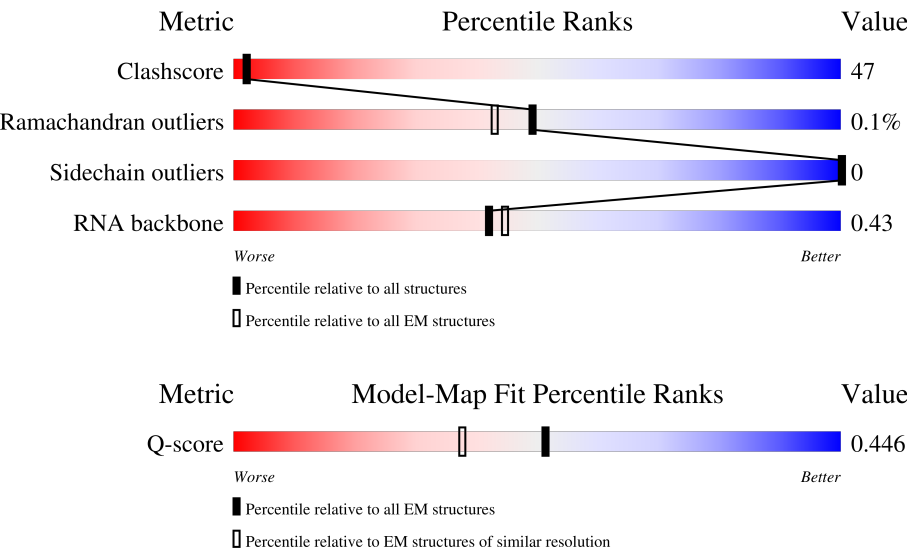
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 3.20 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	15020 (2.70 - 3.70)

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	A	2915	9% 9% 69% 20% .
2	B	120	5% 7% 78% 16%
3	D	275	10% 35% 65%

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Mol	Chain	Length	Quality of chain
4	E	204	
5	F	203	
6	G	181	
7	H	173	
8	I	146	
9	N	140	
10	O	122	
11	P	149	
12	Q	141	
13	R	118	
14	S	110	
15	T	131	
16	U	116	
17	V	101	
18	W	112	
19	X	95	
20	Y	107	
21	Z	187	
22	0	77	
23	1	97	
24	2	70	
25	3	59	
26	4	69	
27	5	59	
28	6	53	

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Mol	Chain	Length	Quality of chain
29	7	48	
30	8	64	
31	9	37	
32	a	1521	
33	b	231	
34	c	206	
35	d	208	
36	e	148	
37	f	100	
38	g	155	
39	h	137	
40	i	126	
41	j	96	
42	k	114	
43	l	122	
44	m	114	
45	n	60	
46	o	88	
47	p	82	
48	q	99	
49	r	68	
50	s	83	
51	t	98	
52	u	23	
53	y	77	

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Mol	Chain	Length	Quality of chain
54	C	226	100% 19%81%
55	z	76	96% 5%58%37%
56	x	55	95% 18%47%35%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 148590 atoms, of which 4 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2867	Total	C	N	O	P	0	0
			61758	27491	11552	19850	2865		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2573	1146	476	832	119		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	275	Total	C	N	O	S	0	0
			2136	1349	423	361	3		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	204	Total	C	N	O	S	0	0
			1559	985	298	270	6		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	203	Total	C	N	O	S	0	1
			1580	1007	297	274	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	181	Total	C	N	O	S	0	0
			1424	912	259	249	4		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	173	Total	C	N	O	S	0	0
			1324	842	247	234	1		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	146	Total	C	N	O	S	0	0
			1076	687	186	202	1		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	140	Total	C	N	O	S	0	0
			1117	719	207	187	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	149	Total	C	N	O	S	0	0
			1135	706	230	196	3		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	118	Total	C	N	O	S	0	0
			968	604	203	160	1		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	S	110	Total	C	N	O		
			870	549	173	148	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	T	131	Total	C	N	O	S	
			1083	675	224	183	1	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	U	116	Total	C	N	O	S	
			959	608	201	149	1	0

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	V	101	Total	C	N	O	S	
			771	495	140	135	1	0

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	W	112	Total	C	N	O	S	
			886	557	174	153	2	0

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	95	Total	C	N	O	S	
			750	488	135	126	1	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Y	107	Total	C	N	O	S	
			810	519	153	132	6	0

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	187	Total	C	N	O	S	0	0
			1459	932	257	268	2		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	77	Total	C	N	O	S	0	0
			608	375	129	103	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	97	Total	C	N	O	S	0	0
			759	478	149	131	1		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	70	Total	C	N	O	S	0	0
			592	368	119	103	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	3	59	Total	C	N	O	0	0
			464	296	90	78		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	69	Total	C	N	O	S	0	0
			536	342	98	91	5		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	59	Total	C	N	O	S	0	0
			455	285	89	76	5		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	53	Total	C	N	O	S	0	0
			449	279	91	75	4		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	48	Total	C	N	O	S	0	0
			418	257	104	55	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	8	64	Total	C	N	O	S	0	0
			517	331	102	82	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1513	Total	C	N	O	P	0	0
			32532	14488	6021	10510	1513		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1542	G	-	insertion	GB 55771382
a	1543	C	-	insertion	GB 55771382
a	1544	U	-	insertion	GB 55771382

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	231	Total	C	N	O	S	0	0
			1825	1167	326	327	5		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	206	Total	C	N	O	S	0	0
			1542	968	300	273	1		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	208	Total	C	N	O	S	0	0
			1668	1047	330	284	7		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	148	Total	C	N	O	S	0	0
			1133	716	214	199	4		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	100	Total	C	N	O	S	0	0
			816	516	146	151	3		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	155	Total	C	N	O	S	0	0
			1229	766	241	216	6		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	137	Total	C	N	O	S	0	0
			1088	689	206	191	2		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	126	Total	C	N	O		0	0
			966	613	186	167			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	j	96	Total	C	N	O	0	0
			710	442	137	131		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	114	Total	C	N	O	S	0	0
			833	519	156	155	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	122	Total	C	N	O	S	0	0
			932	586	185	159	2		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	114	Total	C	N	O	S	0	0
			895	550	186	157	2		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	88	Total	C	N	O	S	0	0
			728	456	144	126	2		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	82	Total	C	N	O	S	0	0
			677	430	133	113	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	68	Total	C	N	O		0	0
			555	355	108	92			

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	83	Total	C	N	O	S	0	0
			645	410	118	115	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	98	Total	C	N	O	S	0	0
			733	451	154	126	2		

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	u	23	Total	C	N	O		
			199	122	48	29	0	0

- Molecule 53 is a RNA chain called P-site tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	77	Total	C	N	O	P	0	0
			1640	732	298	534	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	17B	C	U	conflict	GB 1126835761

- Molecule 54 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	C	225	Total	C	N	O	S	0	0
			1718	1085	315	316	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	MET	deletion	UNP Q5SLP7

- Molecule 55 is a RNA chain called E-site tRNA Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

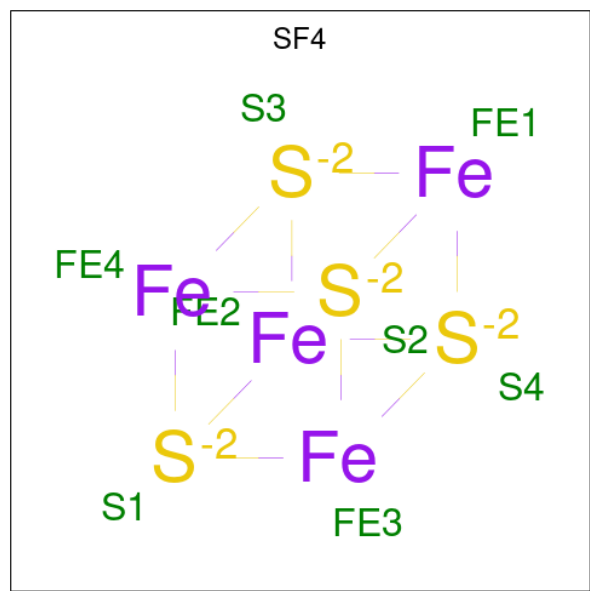
- Molecule 56 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	55	Total	C	H	N	O	P	
			1180	527	4	219	376	54	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Y	1	Total	Zn	0
			1	1	
57	4	1	Total	Zn	0
			1	1	
57	5	1	Total	Zn	0
			1	1	
57	6	1	Total	Zn	0
			1	1	
57	9	1	Total	Zn	0
			1	1	
57	n	1	Total	Zn	0
			1	1	

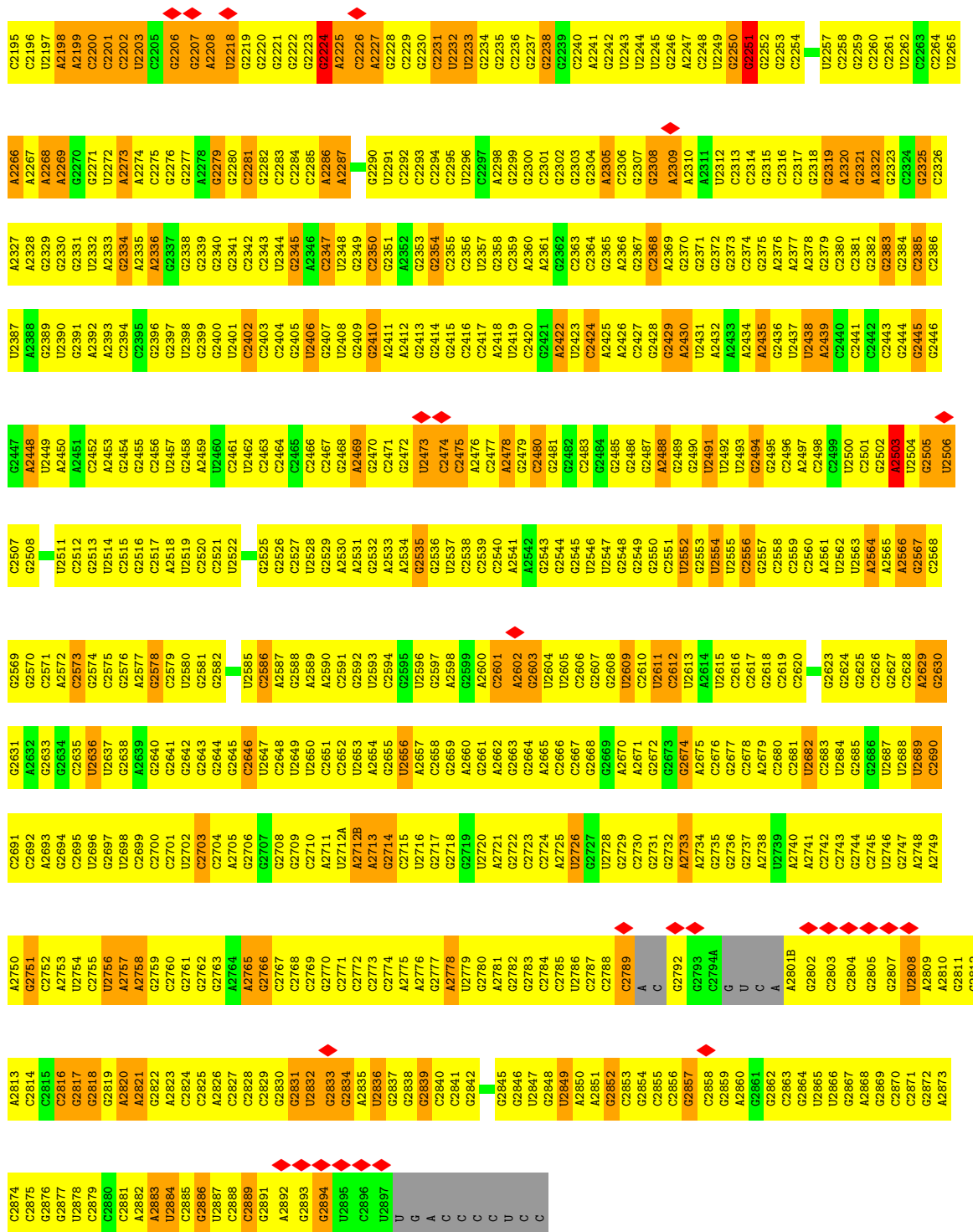
- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).

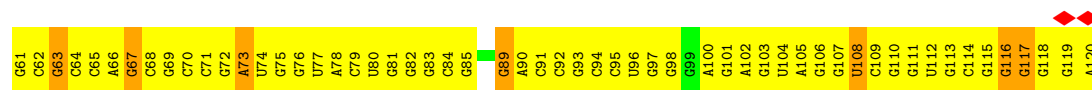


Mol	Chain	Residues	Atoms			AltConf
58	d	1	Total	Fe	S	0
			8	4	4	

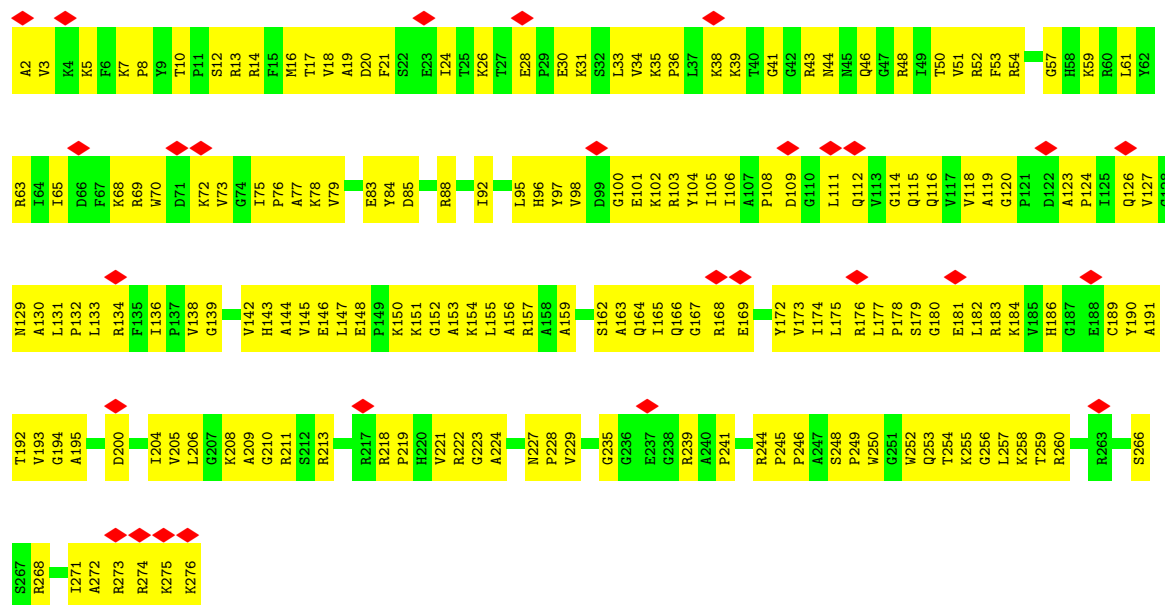
C1298	C1299	G1236	G1237	G1114	A1054	C992	U930	C867	U807	U747	G886	G647	C589	C527
G1299	U1300	G1238	G1239	G1115	G1055	G993	G931	U868	G808	G748	C887	G648	A590	A528
A1301	G1239	G1117	G1118	G1116	G1056	C994	G932	G869	G809	C749	U888	G649	C591	A529
A1241	U1240	C1178	C1119	C1117	A1057	C995	A933	G870	G810	A750	G889	C650	G592	G530
A1242	C1180	C1179	C1119	C1118	G1058	A996	G934	U871	G811	A751	G890	C651	C593	C531
	C1121	C1180	C1120	C1119	G1059	G997	C935	A872	C812	A752	C691	C652A	U594	A532
		C1181	G1122	G1122	U1060	G998	C936	G873	U813	C753	C692	A652B	C595	G533
					U	A1000	G937	G874	C814	C754	C693	A652C	C596	U534
						A1001	G938	C875	C815	C755	C694	A652D	U597	U535
							G939	C876	C816	C756	G695	C652E	C598	A536
							G940	U877	C817	C757	C696	G652F	C599	C537
							A941	A878	G818	C758	C697	G	G600	G538
							G942	C879	A819	C759	C698	C	G539	G539
							U943	G879	A820	C760	A699	C	C601	G539
							G944	C880	A821	C761	A699	C	G602	C540
							A945	G881	U822	C762	G700	C	A603	C541
							G946	C882	G823	C763	G701	C	G604	G542
							G947	G882	A824	C764	G702	C	C543	C543
							G948	G883	C825	C765	G703	A	U606	G545
							C949	C883	C826	C766	G704	C	U607	C
							G950	C884	U827	C767	A705	C	A608	A
							C951	C885	U828	C768	A706	C	A609	A
							G952	C886	A829	C769	G610	C	G707	G549
							A953	A887	G830	C770	C708	C	C611	G551
							G954	C887	G831	C771	C709	C	C612	G552
							C955	C888	G832	C772	G710	C	G613	G553
							U1019	C889	G833	C773	U614A	C	U614A	G554
							A1020	C890	U833	C774	U614B	C	U614B	U555
							C1075	A890	C834	A774	G652M	C	G614C	U555
							G1076	G958	G835	C775	A614D	C	A614D	G557
							U1077	G959	G836	C776	U714	C	G615	U557
							C1078	C993	G837	C777	G715	C	G616	G558
							G1079	C994	C838	C778	A716	C	G617	G559
							C1080	C995	C839	C779	G717	C	G618	G560
							U1081	A896	C840	C780	C619	C	G619	G561
							G1082	C997	G841	A781	G720	C	G620	U562
							C1083	A898	G842	C782	C621	C	G621	G563
							U1084	C999	G843	A783	G721	C	G622	C564
							G1085	A900	C844	C784	G722	C	G623	C565
							C1086	C901	G845	A785	G723	C	G624	U566
							G1087	C902	C846	C786	G725	C	G625	A567
							U1088	C903	U847	C787	G726	C	U626	U568
							G1089	C904	G848	A788	A627	C	G627	U569
							C1090	C905	C850	C789	G728	C	G628	G570
							U1091	C906	U851	C790	G729	C	G629	A571
							G1092	U907	G852	C791	G730	C	G630	C572
							C1093	C908	G853	C792	C731	C	A632	C574
							U1094	C909	G854	C793	C732	C	A633	A575
							A1095	A909	C855	C794	G733	C	C634	U576
							G1096	C910	C856	C795	A734	C	C635	G577
							U1097	C911	C857	C796	C736	C	C636	A578
							C1098	A911	U858	C797	C737	C	A637	G579
							G1099	C912	G859	C798	A676	C	G638	C580
							U1100	C913	U860	C799	A677	C	U639	C581
							C1101	C914	G861	C801	A678	C	C640	G582
							G1102	C915	G862	G802	C679	C	C641	G583
							U1103	A917	G863	C803	A643	C	G642	C584
							C1104	C918	G864	C804	A644	C	A644	G585
							U1105	C919	C865	C805	G681	C	C645	C587
							G1106	C920	A866	C806	G682	C	G646	U588
							U1107	C921			A885	C		
							C1108	U922						
							U1109	C923						
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G2189	G2130	U2074	U1950	C1886	C1751	C1751	C1752	A1609	A1543	G1485	G1422
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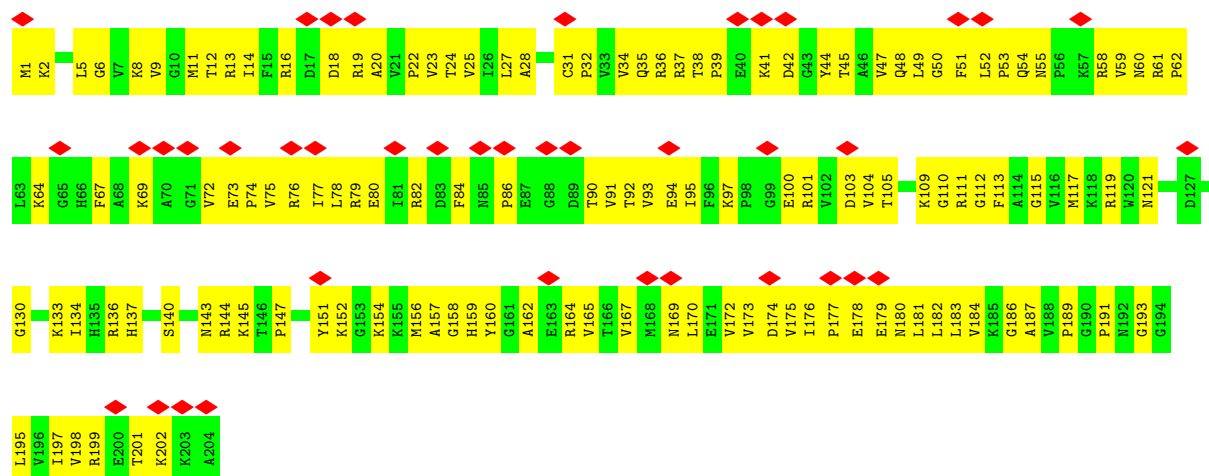




• Molecule 3: 50S ribosomal protein L2

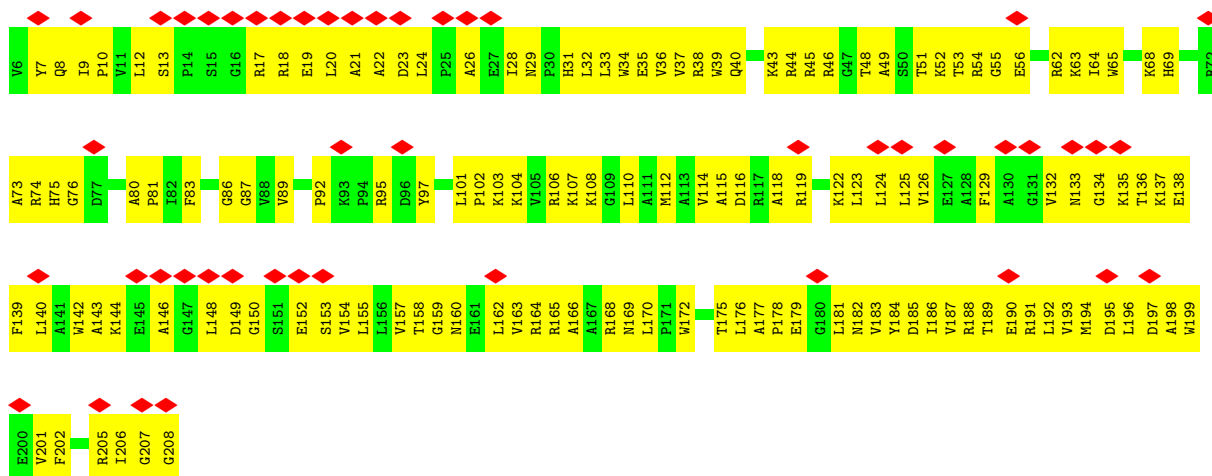


• Molecule 4: 50S ribosomal protein L3

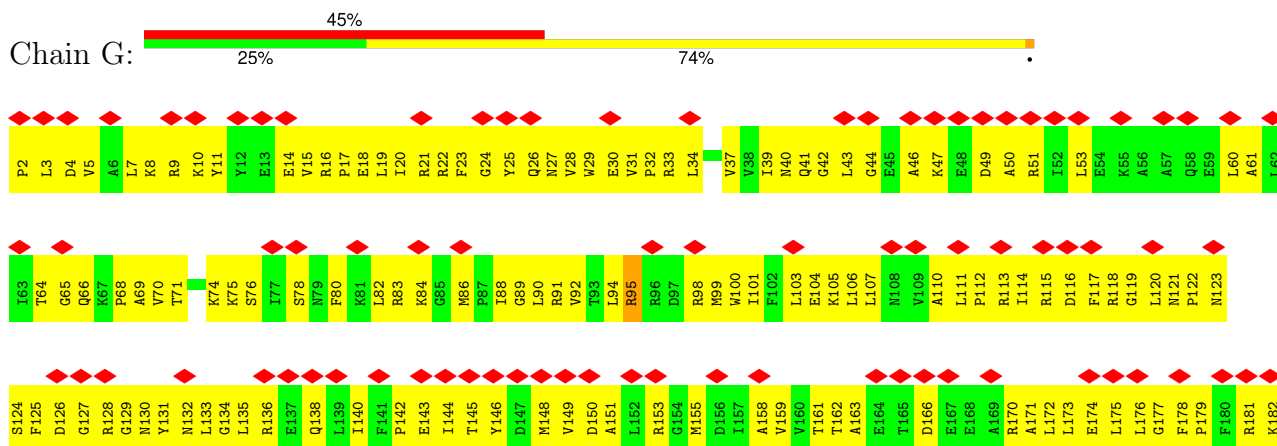


• Molecule 5: 50S ribosomal protein L4

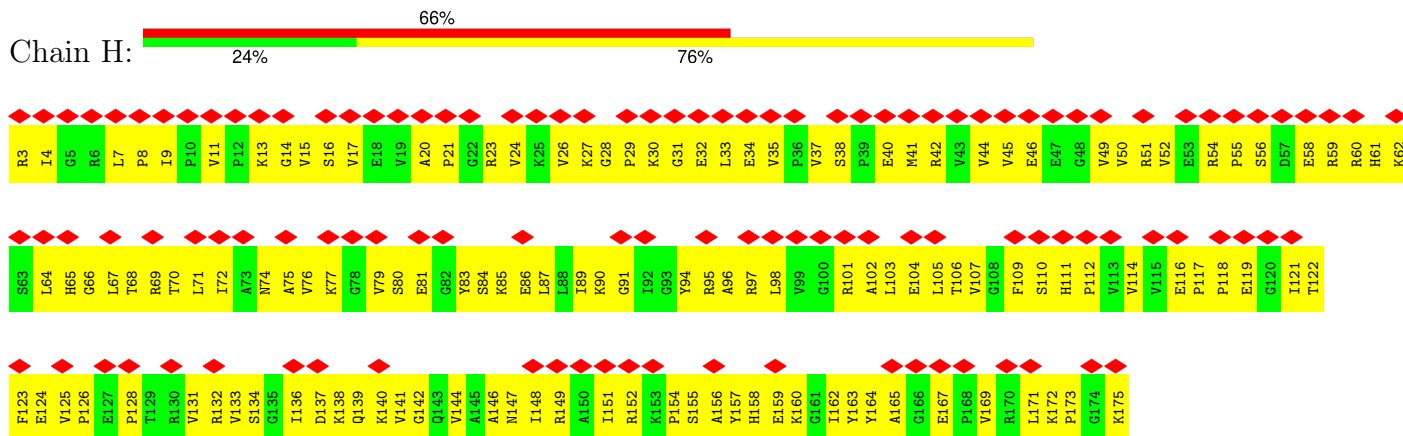




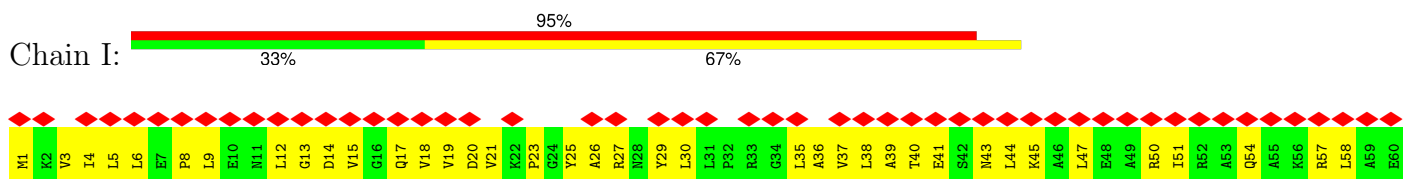
• Molecule 6: 50S ribosomal protein L5

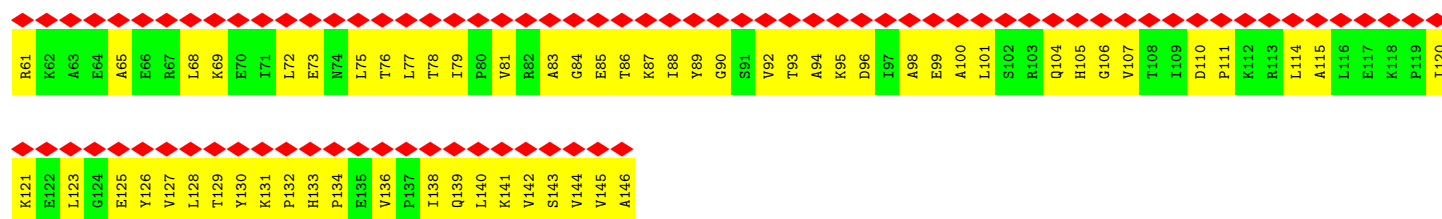


• Molecule 7: 50S ribosomal protein L6

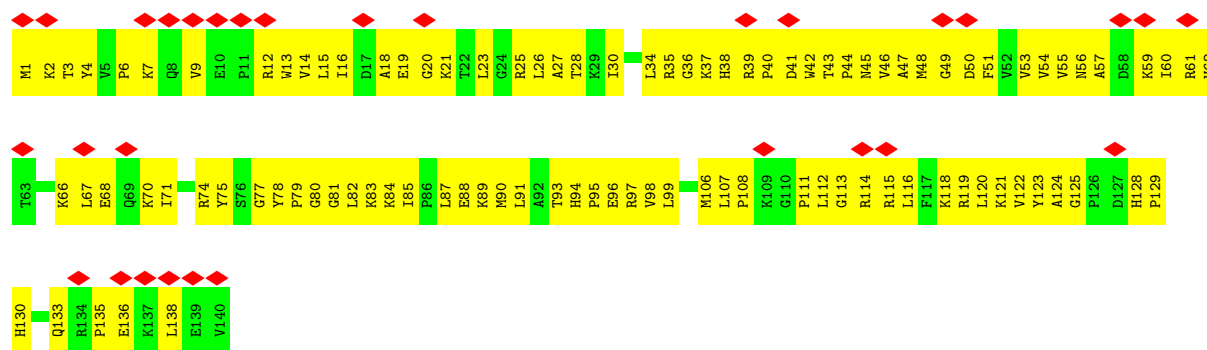


• Molecule 8: 50S ribosomal protein L9

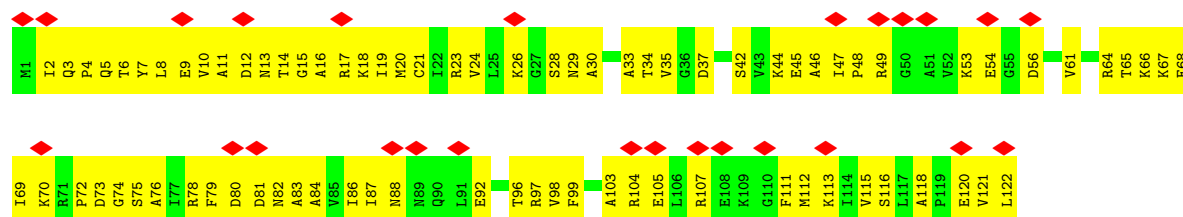




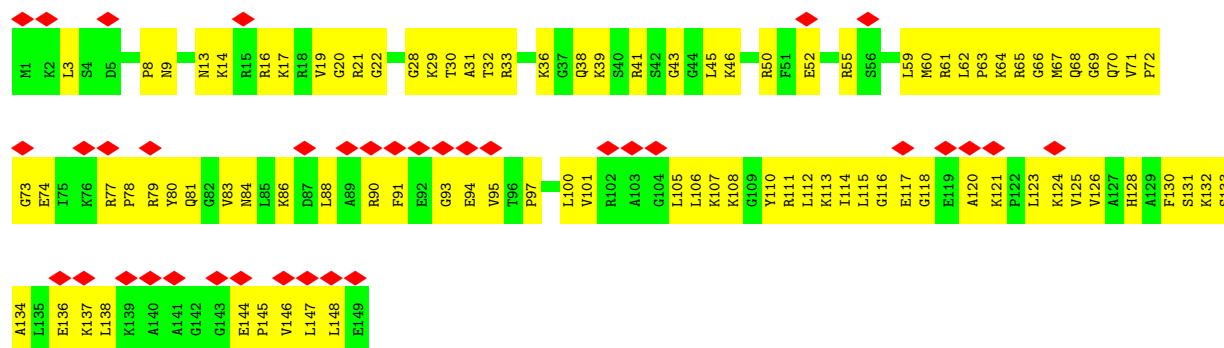
• Molecule 9: 50S ribosomal protein L13



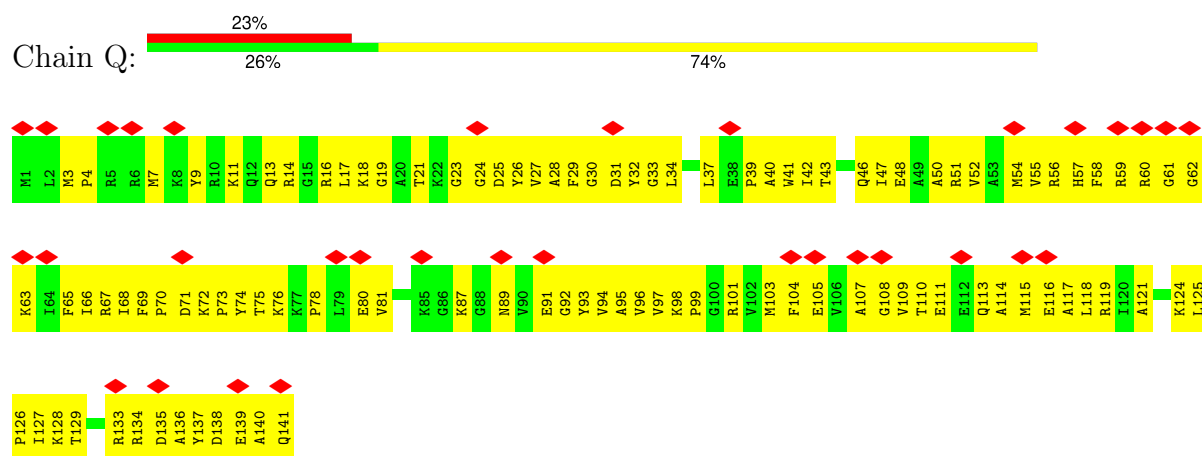
• Molecule 10: 50S ribosomal protein L14



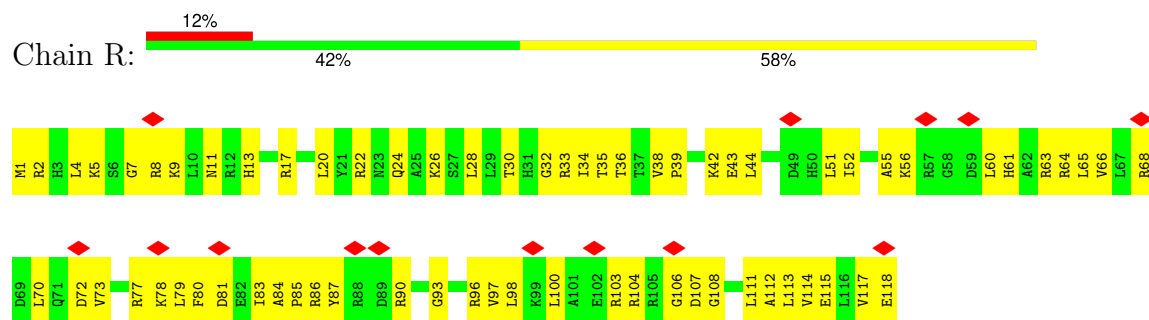
• Molecule 11: 50S ribosomal protein L15



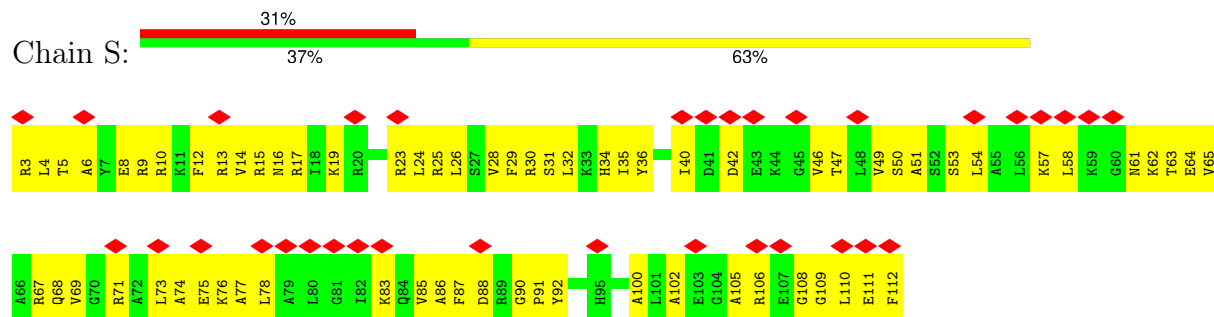
• Molecule 12: 50S ribosomal protein L16



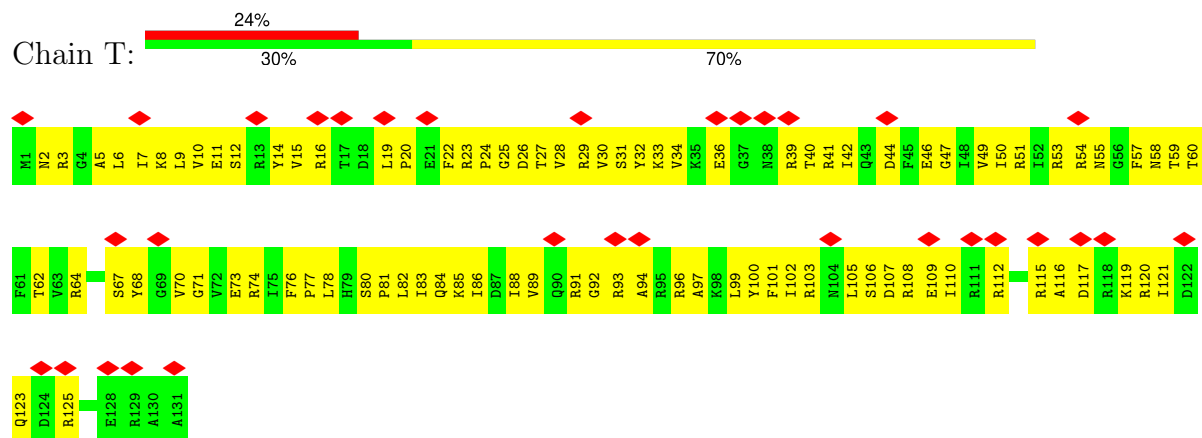
• Molecule 13: 50S ribosomal protein L17



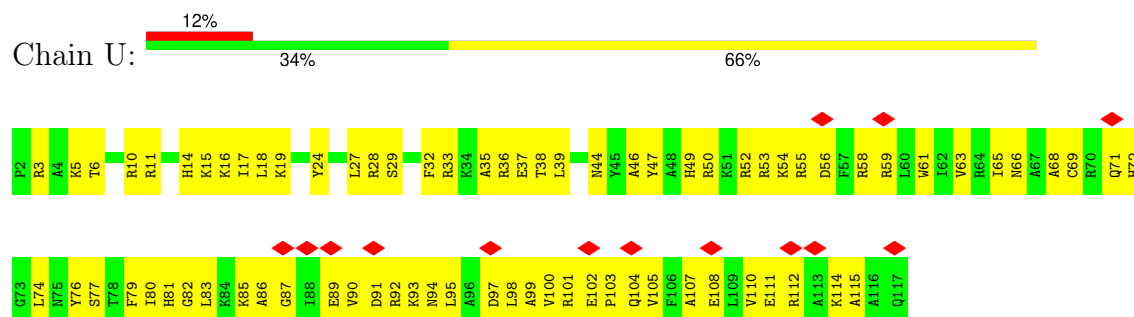
• Molecule 14: 50S ribosomal protein L18



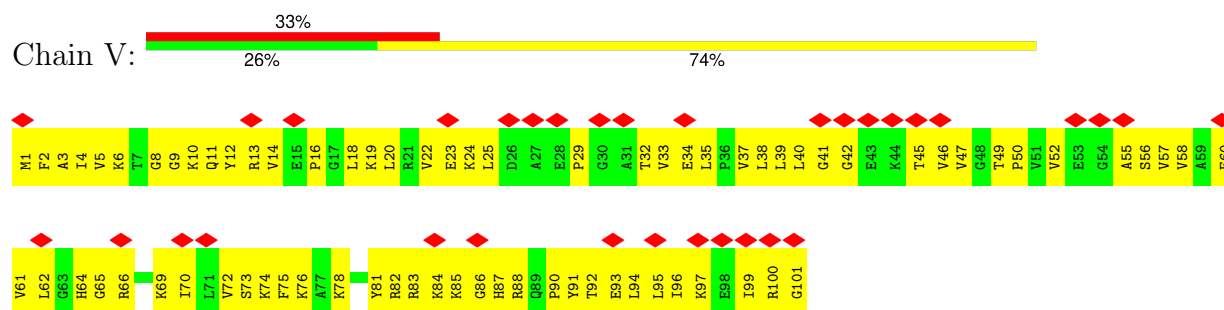
• Molecule 15: 50S ribosomal protein L19



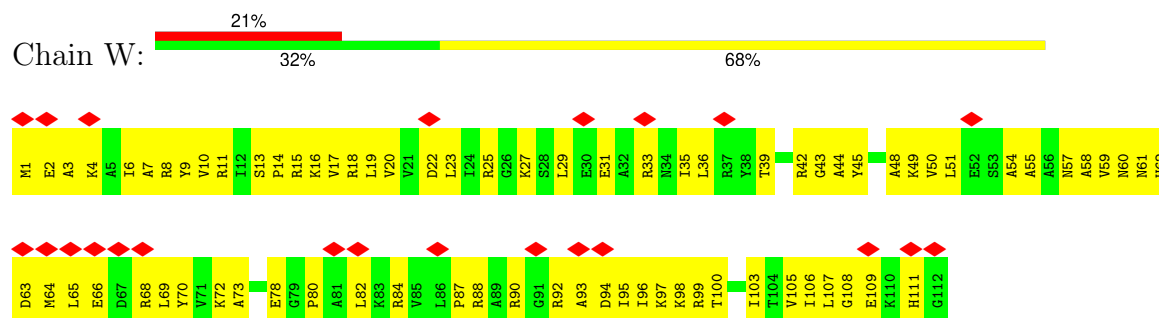
- Molecule 16: 50S ribosomal protein L20



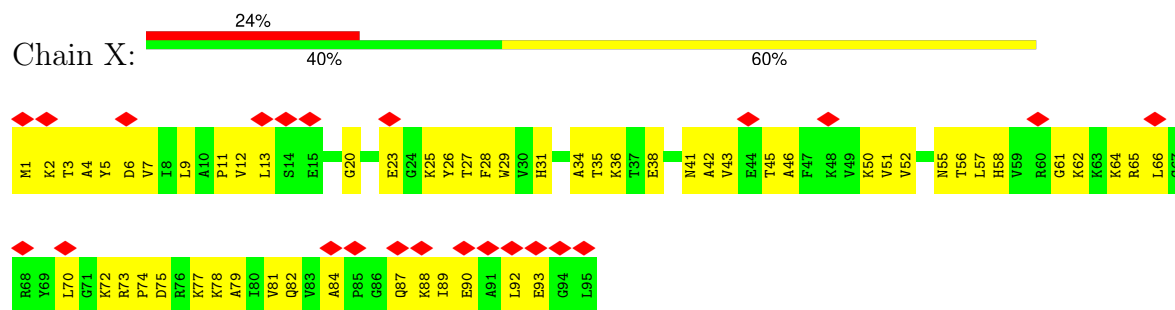
- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22

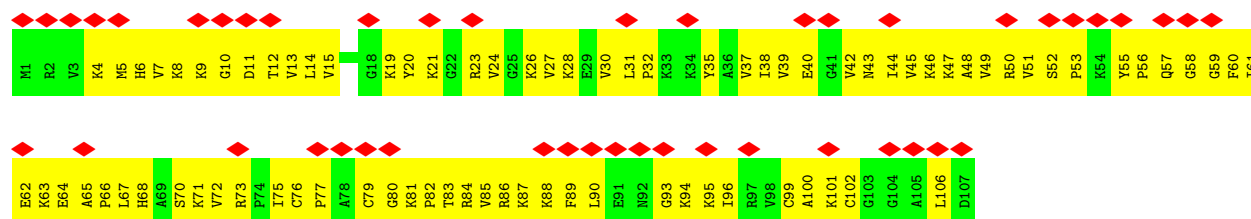


- Molecule 19: 50S ribosomal protein L23

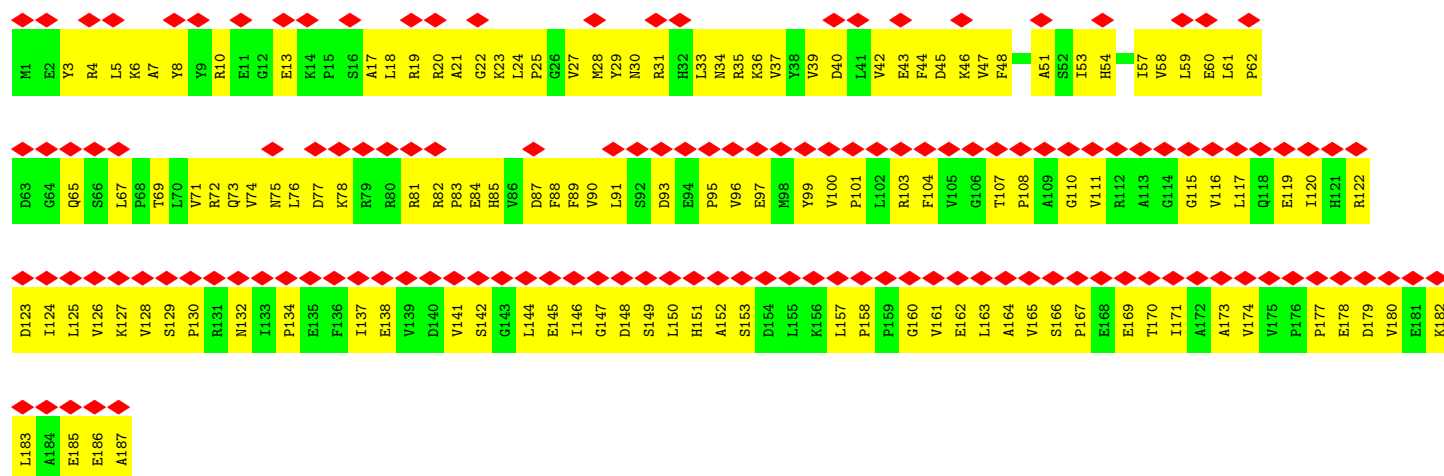


- Molecule 20: 50S ribosomal protein L24

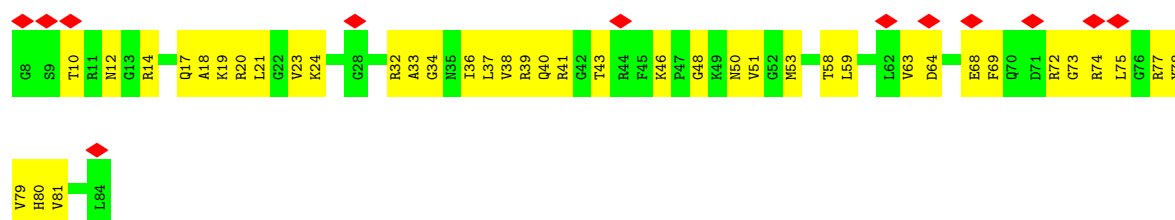




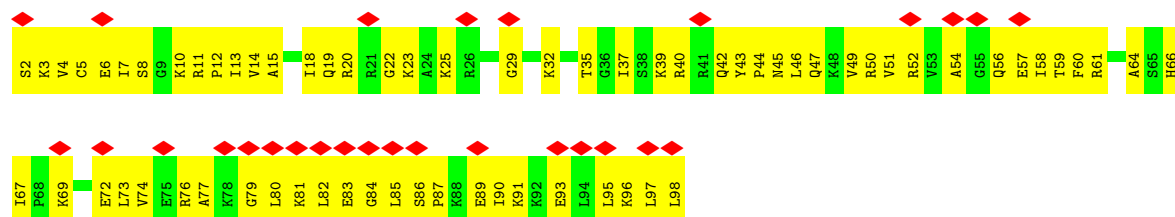
• Molecule 21: 50S ribosomal protein L25



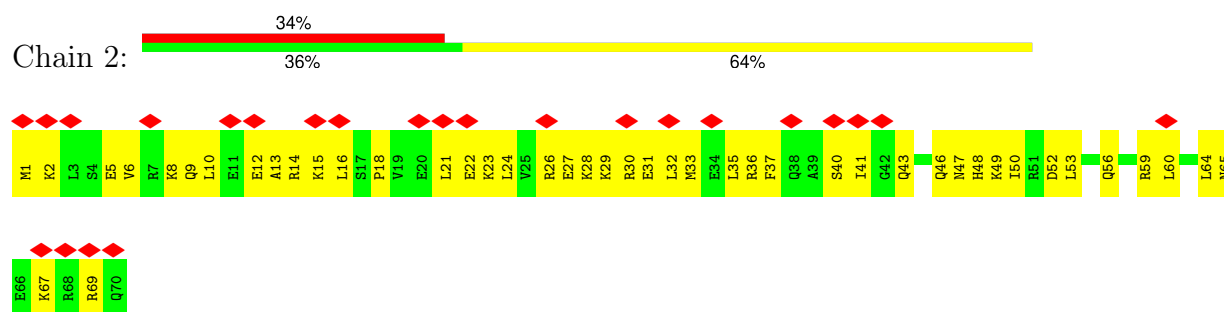
• Molecule 22: 50S ribosomal protein L27



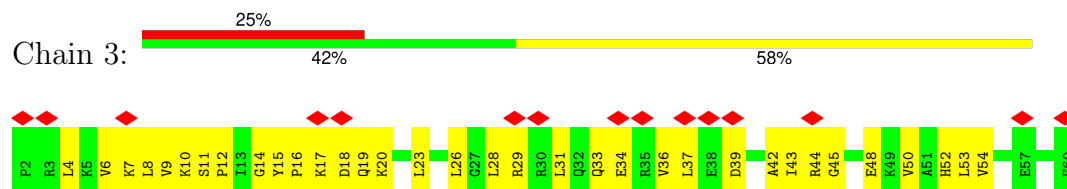
• Molecule 23: 50S ribosomal protein L28



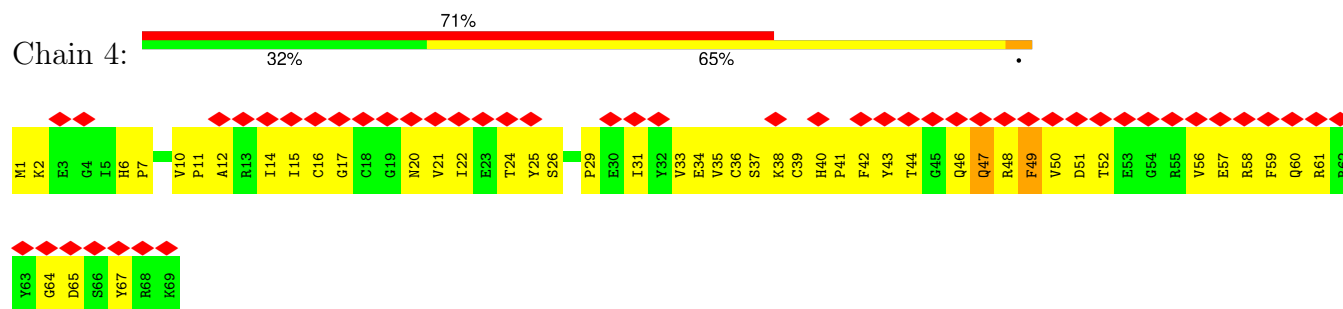
• Molecule 24: 50S ribosomal protein L29



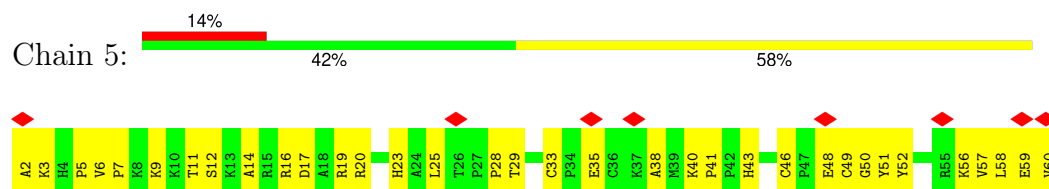
- Molecule 25: 50S ribosomal protein L30



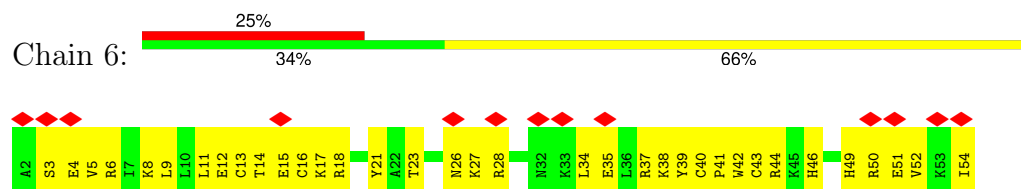
- Molecule 26: 50S ribosomal protein L31



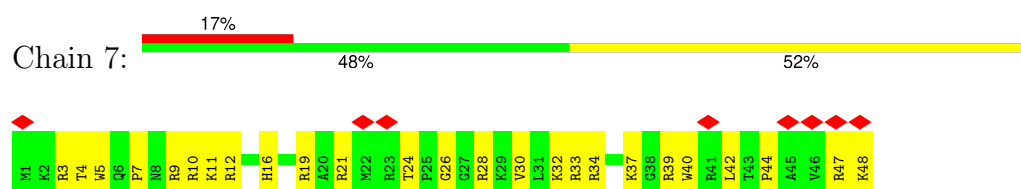
- Molecule 27: 50S ribosomal protein L32



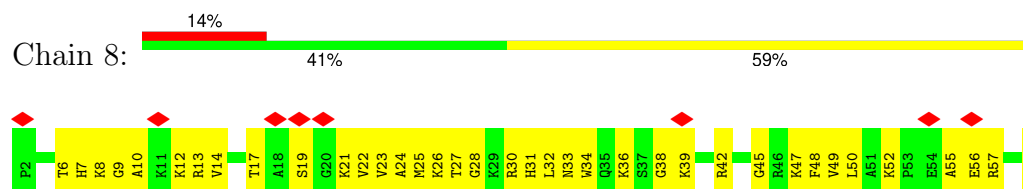
- Molecule 28: 50S ribosomal protein L33



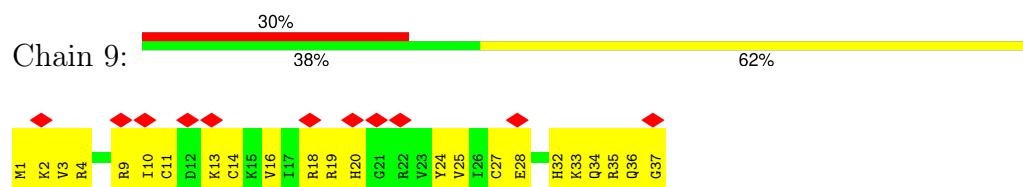
- Molecule 29: 50S ribosomal protein L34



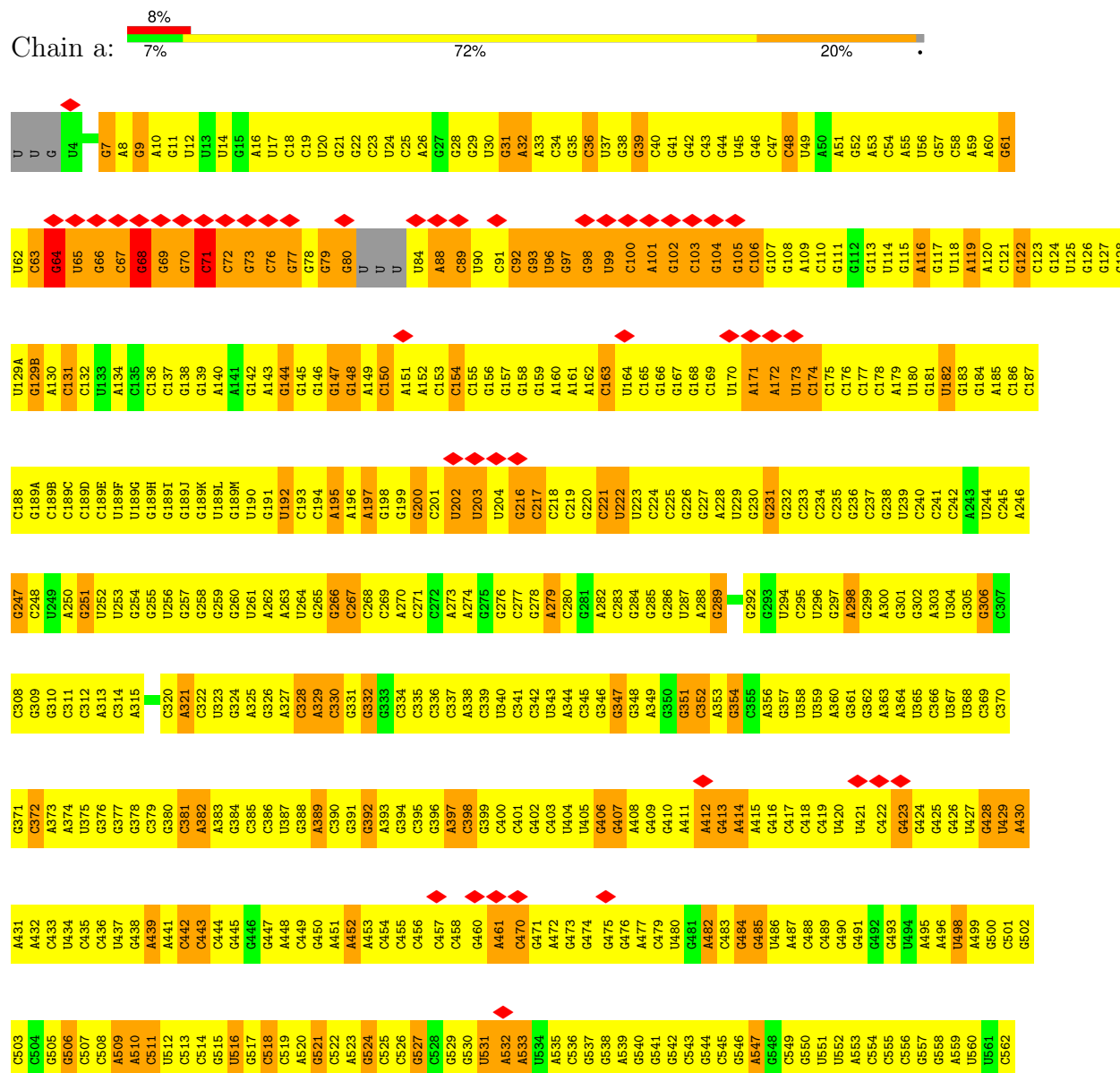
• Molecule 30: 50S ribosomal protein L35



• Molecule 31: 50S ribosomal protein L36



• Molecule 32: 16S rRNA



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G839	C840	G841	G842	U843	G844	G845	A846	G847	C848	G849	U850	A851	U852	G853	C854	U855	U856	U857	A858	A859	U860	U861	G862	C863	G864	A865	G866	U867	G868	A869	C870	G871	C872	A873	A874	A875	G876	C877	G878	C879	A880	A881	U882	A883	U884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	C895	A896	U897	G898																																																																																																																																				
C811	C812	U813	A814	C815	A816	C817	G818	A819	U820	G821	A822	C823	C824	G825	C826	U827	A828	G829	U830	U831	C832	U833	G834	A835	G836	G837	A838	U839	C840	A841	U842	C843	A844	U845	U846	C847	A848	C849	U850	G851	C852	G853	C854	A855	C856	C857	A858	A859	A860	A861	A862	A863	A864	A865	A866	A867	A868	A869	A870	A871	A872	A873	A874	A875	A876	A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938																																																																
C747	C748	C749	G750	C751	G752	A753	C754	G755	C756	A757	G758	A759	C760	G761	C762	A763	G764	C765	A766	G767	A768	C769	G770	A771	C772	G773	A774	C775	G776	A777	C778	G779	A780	C781	G782	A783	C784	G785	A786	C787	A788	G789	A790	C791	A792	U793	A794	C795	G796	C797	G798	G799	U800	A801	C802	A803	C804	U805	A806	C807	A808	C809	A810	C811	A812	C813	A814	C815	A816	C817	A818	C819	A820	C821	A822	C823	A824	C825	A826	C827	A828	C829	A830	C831	A832	C833	A834	C835	A836	C837	A838	C839	A840	C841	A842	C843	A844	C845	A846	C847	A848	C849	A850	C851	A852	C853	A854	C855	A856	C857	A858	C859	A860	C861	A862	C863	A864	C865	A866	C867	A868	C869	A870	C871	A872	C873	A874	C875	A876	C877	A878	C879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938
A563	C564	U565	G566	G567	G570	U571	A572	G573	A574	G575	G576	G577	C578	G579	U580	G581	U582	A583	G584	C585	G586	G589	C590	U591	G592	G593	G594	G595	C596	G597	U598	C599	G600	C601	A602	U603	G604	U605	G606	A607	U608	A609	G610	A611	C612	G613	A614	C615	G616	C617	U618	C619	A620	G621	A622	C623	G624																																																																																																																																						

- Molecule 33: 30S ribosomal protein S2

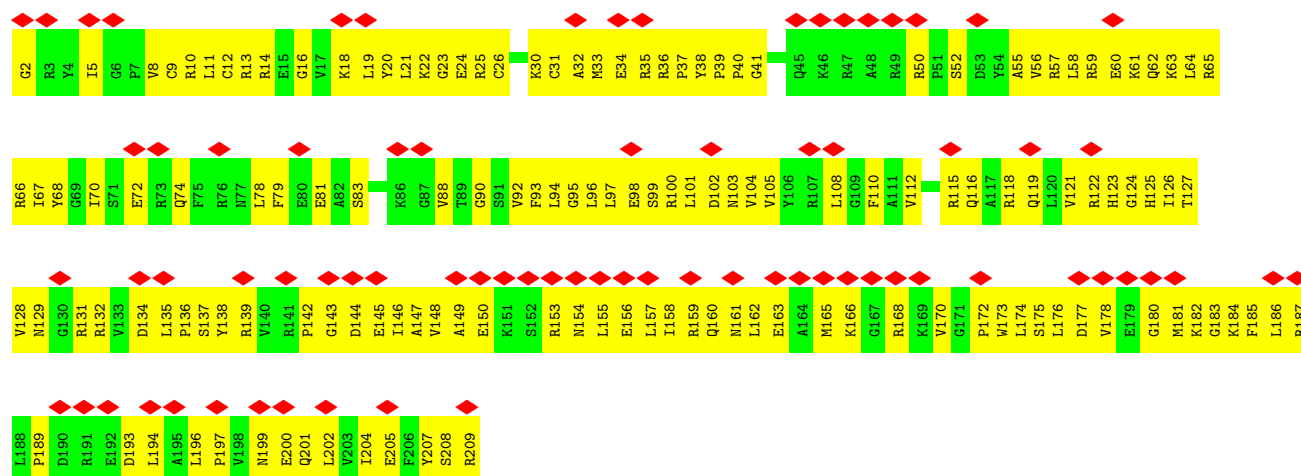


- Molecule 34: 30S ribosomal protein S3

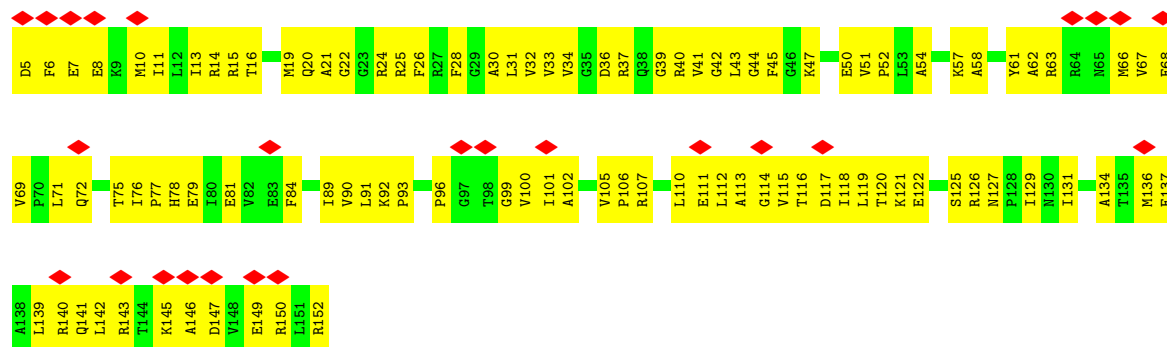


- Molecule 35: 30S ribosomal protein S4

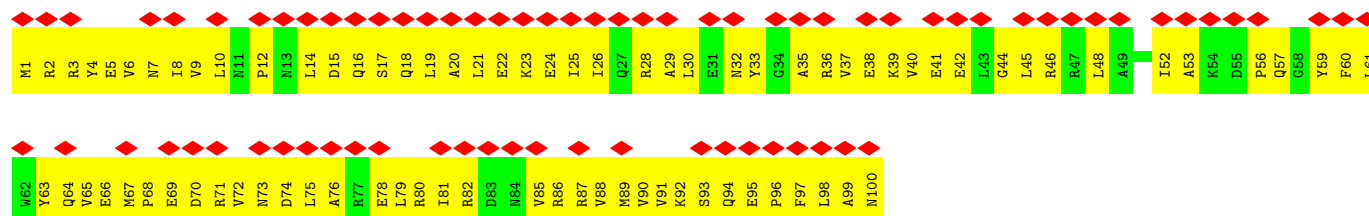
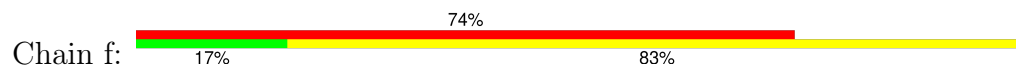




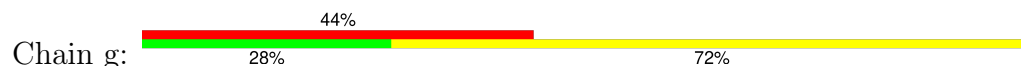
- Molecule 36: 30S ribosomal protein S5

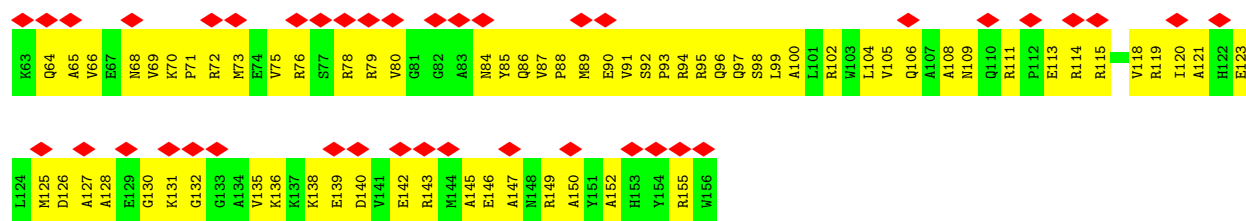


- Molecule 37: 30S ribosomal protein S6

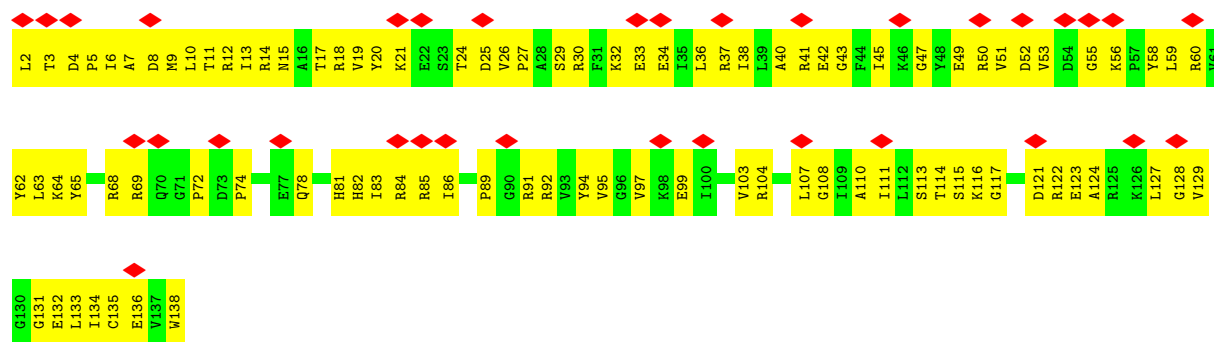
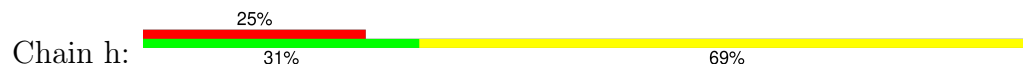


- Molecule 38: 30S ribosomal protein S7

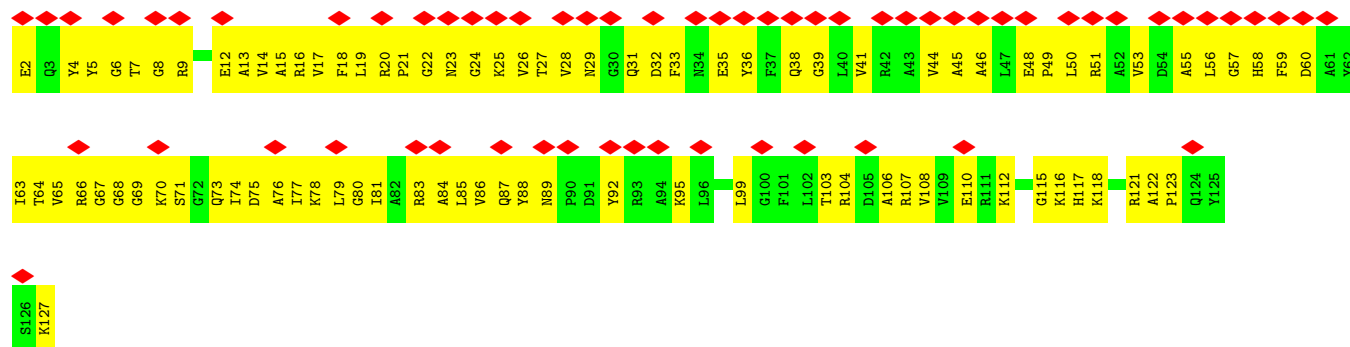




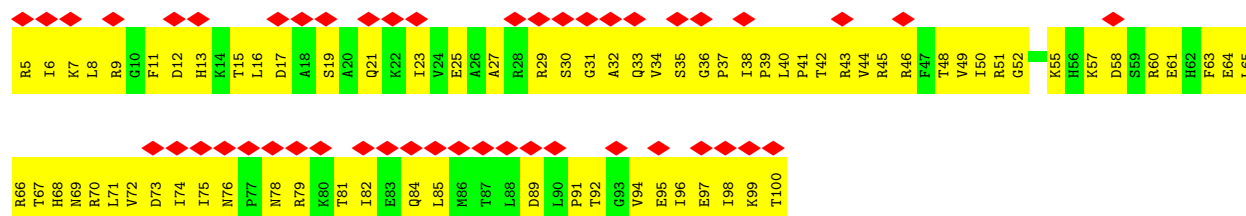
• Molecule 39: 30S ribosomal protein S8



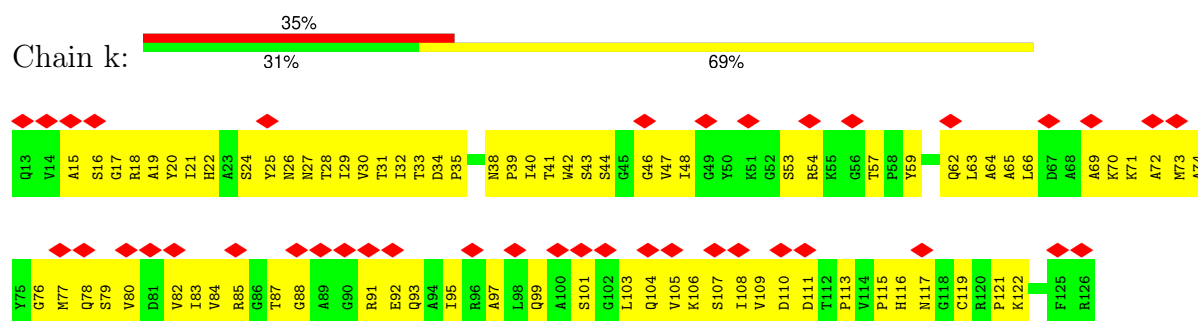
• Molecule 40: 30S ribosomal protein S9



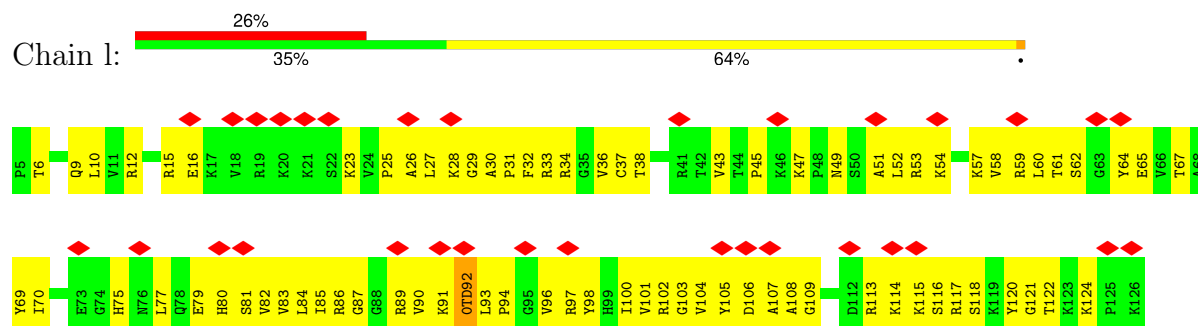
• Molecule 41: 30S ribosomal protein S10



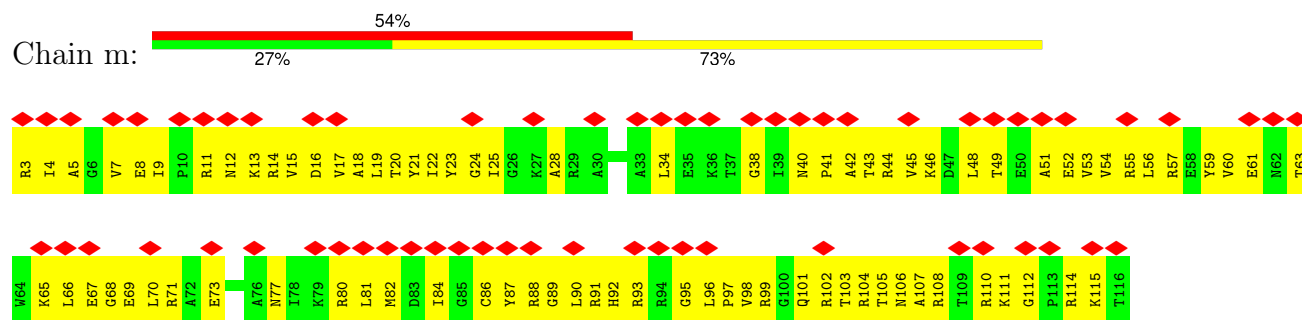
• Molecule 42: 30S ribosomal protein S11



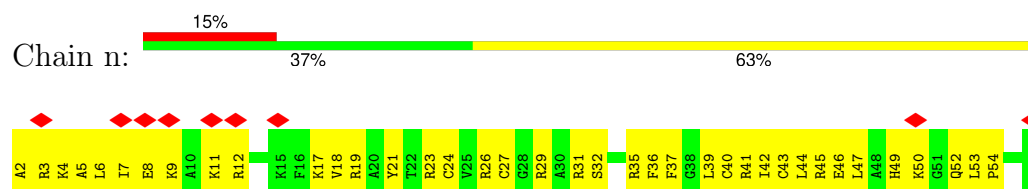
• Molecule 43: 30S ribosomal protein S12



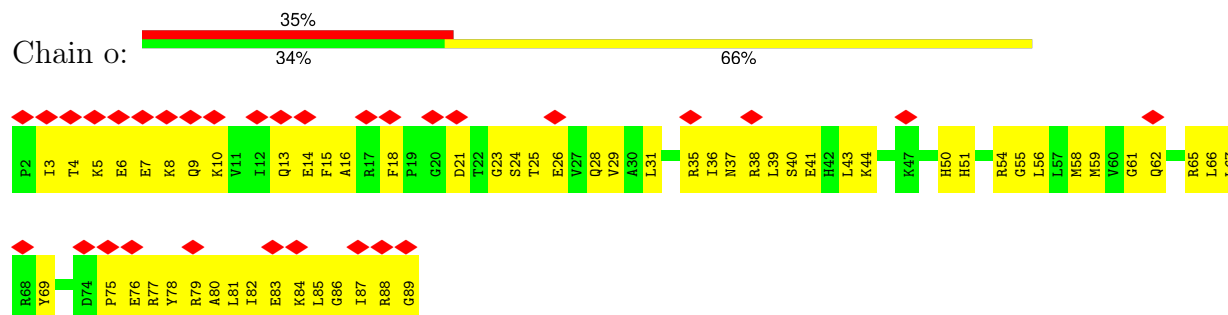
• Molecule 44: 30S ribosomal protein S13



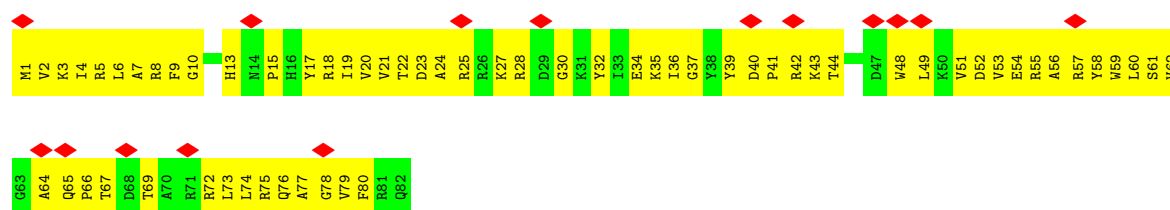
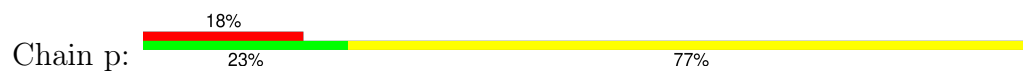
• Molecule 45: 30S ribosomal protein S14 type Z



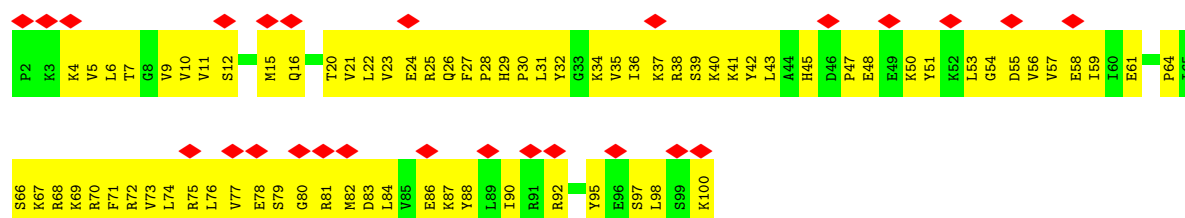
• Molecule 46: 30S ribosomal protein S15



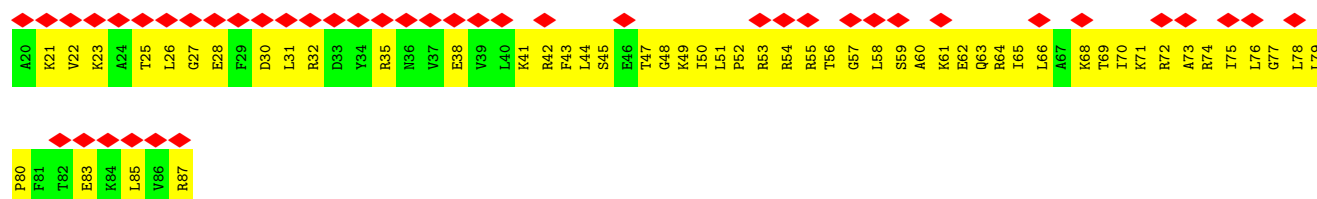
- Molecule 47: 30S ribosomal protein S16



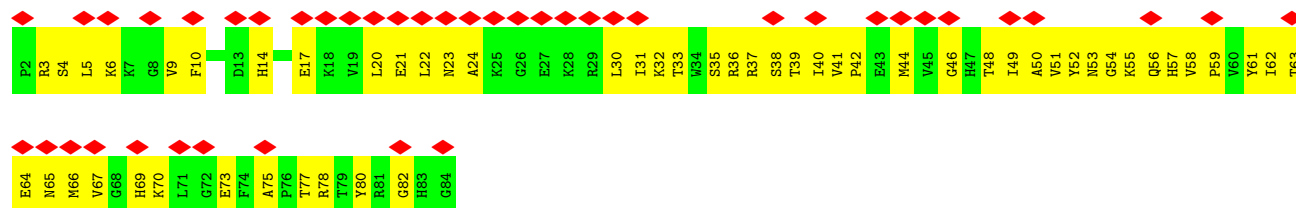
- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18

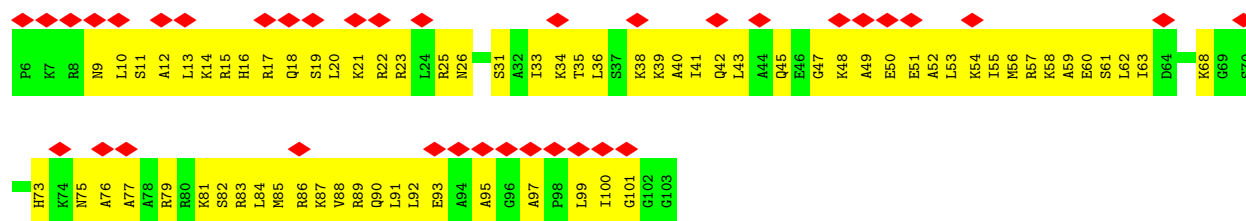


- Molecule 50: 30S ribosomal protein S19

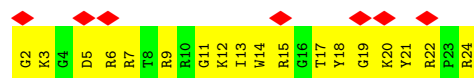


- Molecule 51: 30S ribosomal protein S20

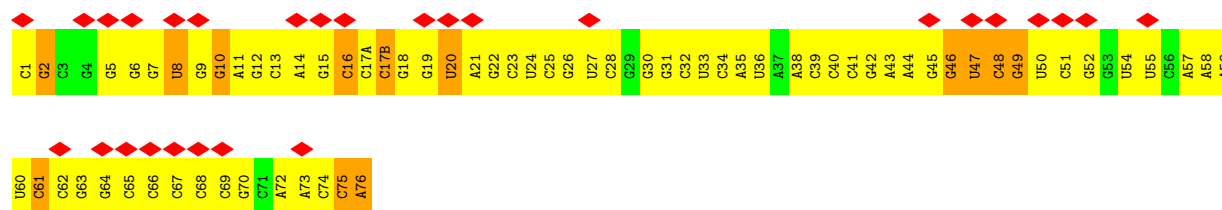




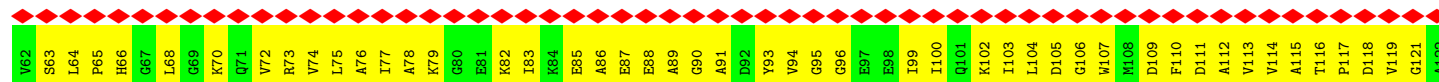
• Molecule 52: 30S ribosomal protein Thx



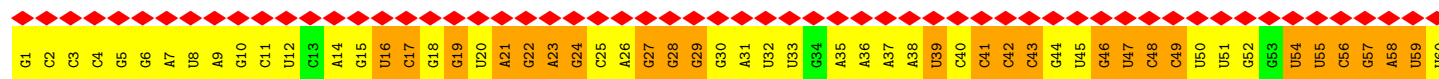
• Molecule 53: P-site tRNA fMet

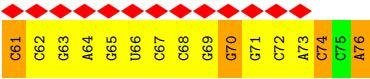


• Molecule 54: 50S ribosomal protein L1

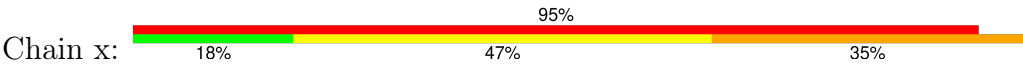


• Molecule 55: E-site tRNA Phe





● Molecule 56: messenger RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36361	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.150	Depositor
Minimum map value	-0.080	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, M2G, 5MC, OMG, 5MU, 2MA, SF4, 4OC, 2MU, UR3, PSU, MA6, 0TD, ZN, 2MG

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	A	0.40	0/68899	0.36	4/107536 (0.0%)
2	B	0.35	0/2878	0.31	0/4490
3	D	0.38	0/2186	0.46	0/2944
4	E	0.37	0/1592	0.50	0/2149
5	F	0.34	0/1615	0.43	0/2188
6	G	0.29	0/1449	0.45	0/1957
7	H	0.27	0/1347	0.44	0/1817
8	I	0.18	0/1091	0.39	0/1490
9	N	0.35	0/1144	0.44	0/1543
10	O	0.37	0/943	0.42	0/1269
11	P	0.34	0/1152	0.46	0/1533
12	Q	0.37	0/1143	0.44	0/1527
13	R	0.35	0/982	0.52	0/1312
14	S	0.31	0/880	0.44	0/1172
15	T	0.36	0/1097	0.49	0/1468
16	U	0.35	0/977	0.45	0/1301
17	V	0.33	0/782	0.46	0/1049
18	W	0.37	0/897	0.45	0/1205
19	X	0.34	0/764	0.41	0/1025
20	Y	0.28	0/823	0.41	0/1100
21	Z	0.25	0/1491	0.44	0/2029
22	0	0.36	0/616	0.48	0/821
23	1	0.35	0/766	0.46	0/1018
24	2	0.32	0/594	0.47	0/785
25	3	0.33	0/469	0.44	0/630
26	4	0.27	0/549	0.62	0/741
27	5	0.33	0/469	0.42	0/635
28	6	0.38	0/456	0.50	0/608
29	7	0.38	0/426	0.51	0/561
30	8	0.35	0/525	0.45	0/691
31	9	0.33	0/310	0.52	0/407
32	a	0.64	7/36109 (0.0%)	0.38	2/56341 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.27	0/1860	0.42	0/2518
34	c	0.32	0/1566	0.40	0/2119
35	d	0.29	0/1698	0.42	0/2277
36	e	0.36	0/1149	0.46	0/1548
37	f	0.27	0/829	0.39	0/1123
38	g	0.29	0/1248	0.40	0/1676
39	h	0.34	0/1108	0.44	0/1494
40	i	0.29	0/985	0.46	1/1329 (0.1%)
41	j	0.29	0/723	0.42	0/984
42	k	0.29	0/848	0.40	0/1149
43	l	0.32	0/937	0.46	0/1260
44	m	0.30	0/905	0.48	0/1217
45	n	0.33	0/501	0.45	0/664
46	o	0.32	0/739	0.43	0/985
47	p	0.33	0/693	0.45	0/935
48	q	0.36	0/836	0.44	0/1117
49	r	0.28	0/560	0.43	0/746
50	s	0.27	0/660	0.40	0/893
51	t	0.31	0/736	0.51	0/976
52	u	0.33	0/203	0.52	0/266
53	y	0.30	0/1832	0.34	0/2855
54	C	0.15	0/1748	0.42	0/2354
55	z	0.21	0/1809	0.33	0/2819
56	x	0.18	0/1315	0.34	0/2046
All	All	0.44	7/160909 (0.0%)	0.39	7/240692 (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
6	G	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	71	C	C2-N3	41.51	2.18	1.35
32	a	71	C	N1-C2	41.29	2.22	1.40
32	a	71	C	N3-C4	40.36	2.14	1.33
32	a	71	C	N1-C6	39.59	2.16	1.37
32	a	71	C	C4-C5	37.79	2.18	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2224	G	OP1-P-O3'	-10.30	77.11	108.00
1	A	2883	A	OP2-P-O3'	-8.84	81.48	108.00
1	A	2883	A	OP1-P-O3'	-8.51	82.47	108.00
1	A	2224	G	OP2-P-O3'	-7.57	85.30	108.00
40	i	44	VAL	N-CA-C	-6.52	107.51	113.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	G	95	ARG	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	61758	0	31153	3990	0
2	B	2573	0	1306	177	0
3	D	2136	0	2218	231	0
4	E	1559	0	1618	181	0
5	F	1580	0	1619	199	0
6	G	1424	0	1441	193	0
7	H	1324	0	1399	206	0
8	I	1076	0	1094	141	0
9	N	1117	0	1184	121	0
10	O	933	0	996	99	0
11	P	1135	0	1212	150	0
12	Q	1122	0	1179	154	0
13	R	968	0	1033	83	0
14	S	870	0	923	93	0
15	T	1083	0	1136	126	0
16	U	959	0	1019	97	0
17	V	771	0	830	102	0
18	W	886	0	940	84	0
19	X	750	0	814	68	0
20	Y	810	0	887	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Z	1459	0	1457	192	0
22	0	608	0	622	52	0
23	1	759	0	837	87	0
24	2	592	0	654	49	0
25	3	464	0	514	45	0
26	4	536	0	514	95	0
27	5	455	0	465	46	0
28	6	449	0	469	43	0
29	7	418	0	467	39	0
30	8	517	0	582	59	0
31	9	307	0	335	24	0
32	a	32532	0	16451	2589	0
33	b	1825	0	1828	234	0
34	c	1542	0	1517	149	0
35	d	1668	0	1707	234	0
36	e	1133	0	1191	142	0
37	f	816	0	808	139	0
38	g	1229	0	1238	125	0
39	h	1088	0	1126	113	0
40	i	966	0	953	121	0
41	j	710	0	661	98	0
42	k	833	0	836	111	0
43	l	932	0	981	123	0
44	m	895	0	920	144	0
45	n	492	0	529	66	0
46	o	728	0	760	71	0
47	p	677	0	686	93	0
48	q	823	0	891	92	0
49	r	555	0	618	83	0
50	s	645	0	635	80	0
51	t	733	0	795	116	0
52	u	199	0	208	22	0
53	y	1640	0	838	122	0
54	C	1718	0	1767	363	0
55	z	1619	0	822	134	0
56	x	1176	4	596	56	0
57	4	1	0	0	0	0
57	5	1	0	0	0	0
57	6	1	0	0	0	0
57	9	1	0	0	0	0
57	Y	1	0	0	0	0
57	n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	d	8	0	0	1	0
All	All	148586	4	100279	11478	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 47.

The worst 5 of 11478 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)
32:a:64:G:C3'	32:a:64:G:O3'	1.65	1.44
32:a:71:C:C5	32:a:71:C:C6	2.09	1.38
32:a:71:C:C5	32:a:71:C:C4	2.18	1.29
7:H:16:SER:O	7:H:26:VAL:HA	1.36	1.22
32:a:71:C:C4	32:a:71:C:N3	2.14	1.14

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	
3	D	273/275 (99%)	245 (90%)	28 (10%)	0	100	100
4	E	202/204 (99%)	188 (93%)	14 (7%)	0	100	100
5	F	201/203 (99%)	193 (96%)	7 (4%)	1 (0%)	24	59
6	G	179/181 (99%)	160 (89%)	19 (11%)	0	100	100
7	H	166/173 (96%)	152 (92%)	14 (8%)	0	100	100
8	I	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
9	N	138/140 (99%)	127 (92%)	11 (8%)	0	100	100
10	O	120/122 (98%)	112 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	P	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
12	Q	139/141 (99%)	128 (92%)	11 (8%)	0	100	100
13	R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
15	T	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
16	U	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
17	V	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
18	W	110/112 (98%)	97 (88%)	13 (12%)	0	100	100
19	X	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
20	Y	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
21	Z	185/187 (99%)	161 (87%)	24 (13%)	0	100	100
22	0	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
23	1	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
24	2	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
25	3	57/59 (97%)	56 (98%)	1 (2%)	0	100	100
26	4	67/69 (97%)	55 (82%)	10 (15%)	2 (3%)	3	23
27	5	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
28	6	51/53 (96%)	46 (90%)	5 (10%)	0	100	100
29	7	46/48 (96%)	46 (100%)	0	0	100	100
30	8	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
31	9	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
33	b	229/231 (99%)	209 (91%)	20 (9%)	0	100	100
34	c	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
35	d	206/208 (99%)	201 (98%)	5 (2%)	0	100	100
36	e	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
37	f	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
38	g	153/155 (99%)	145 (95%)	8 (5%)	0	100	100
39	h	135/137 (98%)	123 (91%)	12 (9%)	0	100	100
40	i	124/126 (98%)	112 (90%)	12 (10%)	0	100	100
41	j	94/96 (98%)	82 (87%)	11 (12%)	1 (1%)	11	43
42	k	112/114 (98%)	107 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	l	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
44	m	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
45	n	58/60 (97%)	57 (98%)	1 (2%)	0	100	100
46	o	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
47	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
48	q	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
49	r	66/68 (97%)	64 (97%)	2 (3%)	0	100	100
50	s	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
51	t	96/98 (98%)	84 (88%)	12 (12%)	0	100	100
52	u	21/23 (91%)	21 (100%)	0	0	100	100
54	C	221/226 (98%)	199 (90%)	22 (10%)	0	100	100
All	All	5919/6028 (98%)	5464 (92%)	451 (8%)	4 (0%)	49	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	4	49	PHE
26	4	47	GLN
41	j	55	LYS
5	F	207	GLY

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	
3	D	215/217 (99%)	215 (100%)	0	100	100
4	E	164/165 (99%)	164 (100%)	0	100	100
5	F	159/161 (99%)	159 (100%)	0	100	100
6	G	142/155 (92%)	142 (100%)	0	100	100
7	H	143/144 (99%)	143 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	I	108/122 (88%)	108 (100%)	0	100	100
9	N	118/119 (99%)	118 (100%)	0	100	100
10	O	100/100 (100%)	100 (100%)	0	100	100
11	P	115/116 (99%)	115 (100%)	0	100	100
12	Q	111/111 (100%)	111 (100%)	0	100	100
13	R	101/101 (100%)	101 (100%)	0	100	100
14	S	85/87 (98%)	85 (100%)	0	100	100
15	T	113/115 (98%)	113 (100%)	0	100	100
16	U	93/93 (100%)	93 (100%)	0	100	100
17	V	80/82 (98%)	80 (100%)	0	100	100
18	W	90/91 (99%)	90 (100%)	0	100	100
19	X	77/77 (100%)	77 (100%)	0	100	100
20	Y	86/88 (98%)	86 (100%)	0	100	100
21	Z	156/164 (95%)	156 (100%)	0	100	100
22	0	61/62 (98%)	61 (100%)	0	100	100
23	1	81/82 (99%)	81 (100%)	0	100	100
24	2	66/66 (100%)	66 (100%)	0	100	100
25	3	50/51 (98%)	50 (100%)	0	100	100
26	4	54/62 (87%)	54 (100%)	0	100	100
27	5	50/51 (98%)	50 (100%)	0	100	100
28	6	50/51 (98%)	50 (100%)	0	100	100
29	7	41/41 (100%)	41 (100%)	0	100	100
30	8	54/54 (100%)	54 (100%)	0	100	100
31	9	34/34 (100%)	34 (100%)	0	100	100
33	b	187/199 (94%)	187 (100%)	0	100	100
34	c	140/160 (88%)	140 (100%)	0	100	100
35	d	172/180 (96%)	172 (100%)	0	100	100
36	e	114/114 (100%)	114 (100%)	0	100	100
37	f	85/90 (94%)	85 (100%)	0	100	100
38	g	119/126 (94%)	119 (100%)	0	100	100
39	h	114/118 (97%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	i	88/97 (91%)	88 (100%)	0	100	100
41	j	68/86 (79%)	68 (100%)	0	100	100
42	k	83/86 (96%)	83 (100%)	0	100	100
43	l	96/102 (94%)	96 (100%)	0	100	100
44	m	87/93 (94%)	87 (100%)	0	100	100
45	n	49/49 (100%)	49 (100%)	0	100	100
46	o	78/79 (99%)	78 (100%)	0	100	100
47	p	68/71 (96%)	68 (100%)	0	100	100
48	q	94/94 (100%)	94 (100%)	0	100	100
49	r	59/59 (100%)	59 (100%)	0	100	100
50	s	67/72 (93%)	67 (100%)	0	100	100
51	t	70/76 (92%)	70 (100%)	0	100	100
52	u	18/18 (100%)	18 (100%)	0	100	100
54	C	177/178 (99%)	177 (100%)	0	100	100
All	All	4830/5009 (96%)	4830 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
47	p	65	GLN
50	s	69	HIS
20	Y	43	ASN
19	X	82	GLN
50	s	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2857/2915 (98%)	634 (22%)	46 (1%)
2	B	119/120 (99%)	23 (19%)	0
32	a	1509/1521 (99%)	331 (21%)	0
53	y	76/77 (98%)	13 (17%)	0
55	z	75/76 (98%)	29 (38%)	0
56	x	54/55 (98%)	24 (44%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4690/4764 (98%)	1054 (22%)	46 (0%)

5 of 1054 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	10	G
1	A	12	U
1	A	14	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1491	G
1	A	2172	U
1	A	1493	C
1	A	2126	A
1	A	2321	G

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
1	5MC	A	1962	1	19,22,23	1.42	3 (15%)	26,32,35	1.25	2 (7%)
32	5MC	a	1400	32	19,22,23	1.44	3 (15%)	26,32,35	1.20	2 (7%)
32	MA6	a	1519	32	23,26,27	1.41	5 (21%)	33,38,41	2.48	14 (42%)
32	7MG	a	527	32	23,26,27	1.35	4 (17%)	27,39,42	2.71	7 (25%)
1	5MC	A	1942	1	19,22,23	1.41	3 (15%)	26,32,35	1.17	2 (7%)
32	4OC	a	1402	32	20,23,24	0.77	1 (5%)	25,32,35	0.93	0
43	0TD	l	92	43	8,9,10	2.21	1 (12%)	6,11,13	1.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	UR3	a	1498	32	19,22,23	0.94	2 (10%)	26,32,35	1.76	3 (11%)
1	2MU	A	2552	1	19,22,24	1.37	4 (21%)	25,31,36	2.22	6 (24%)
1	5MU	A	1939	1	19,22,23	1.37	3 (15%)	27,32,35	2.35	6 (22%)
32	M2G	a	966	32	24,27,28	1.30	5 (20%)	33,40,43	1.87	6 (18%)
32	5MC	a	967	32	19,22,23	1.44	3 (15%)	26,32,35	1.14	2 (7%)
1	PSU	A	1911	1	18,21,22	1.40	3 (16%)	21,30,33	2.19	4 (19%)
1	4OC	A	1920	1	19,22,24	0.81	1 (5%)	25,31,35	0.85	0
32	5MC	a	1407	32	19,22,23	1.47	3 (15%)	26,32,35	1.26	2 (7%)
1	5MU	A	1915	1	19,22,23	1.42	5 (26%)	27,32,35	2.44	9 (33%)
1	PSU	A	1917	1	18,21,22	1.39	3 (16%)	21,30,33	2.11	5 (23%)
1	OMG	A	2251	53,1	23,26,27	1.25	4 (17%)	32,38,41	2.00	6 (18%)
1	2MA	A	2503	1	22,25,26	1.46	5 (22%)	32,37,40	2.26	7 (21%)
32	MA6	a	1518	32	23,26,27	1.41	5 (21%)	33,38,41	2.41	14 (42%)
32	PSU	a	516	32	18,21,22	1.45	5 (27%)	21,30,33	2.19	5 (23%)
32	2MG	a	1207	32	23,26,27	1.27	4 (17%)	33,38,41	2.23	10 (30%)
1	PSU	A	2605	1	18,21,22	1.45	4 (22%)	21,30,33	2.25	4 (19%)
32	5MC	a	1404	32	19,22,23	1.51	3 (15%)	26,32,35	1.25	3 (11%)

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
1	5MC	A	1962	1	-	0/7/25/26	0/2/2/2
32	5MC	a	1400	32	-	2/7/25/26	0/2/2/2
32	MA6	a	1519	32	-	4/11/29/30	0/3/3/3
32	7MG	a	527	32	-	3/7/37/38	0/3/3/3
1	5MC	A	1942	1	-	0/7/25/26	0/2/2/2
32	4OC	a	1402	32	-	0/9/29/30	0/2/2/2
43	0TD	l	92	43	-	4/7/12/14	-
32	UR3	a	1498	32	-	0/7/25/26	0/2/2/2
1	2MU	A	2552	1	-	0/9/27/28	0/2/2/2
1	5MU	A	1939	1	-	0/7/25/26	0/2/2/2
32	M2G	a	966	32	-	0/11/29/30	0/3/3/3
32	5MC	a	967	32	-	0/7/25/26	0/2/2/2
1	PSU	A	1911	1	-	0/7/25/26	0/2/2/2
1	4OC	A	1920	1	-	0/9/27/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	a	1407	32	-	0/7/25/26	0/2/2/2
1	5MU	A	1915	1	-	2/7/25/26	0/2/2/2
1	PSU	A	1917	1	-	0/7/25/26	0/2/2/2
1	OMG	A	2251	53,1	-	2/9/27/28	0/3/3/3
1	2MA	A	2503	1	-	1/7/25/26	0/3/3/3
32	MA6	a	1518	32	-	1/11/29/30	0/3/3/3
32	PSU	a	516	32	-	0/7/25/26	0/2/2/2
32	2MG	a	1207	32	-	0/9/27/28	0/3/3/3
1	PSU	A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	a	1404	32	-	1/7/25/26	0/2/2/2

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	a	1404	5MC	C5-C4	5.05	1.47	1.44
32	a	1407	5MC	C5-C4	5.03	1.47	1.44
43	l	92	0TD	CB-CA	-4.99	1.53	1.54
1	A	1942	5MC	C5-C4	4.86	1.47	1.44
32	a	967	5MC	C5-C4	4.86	1.47	1.44

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	a	527	7MG	N9-C4-N3	9.30	139.09	125.46
1	A	2503	2MA	C5-C4-N3	-8.18	118.57	127.18
32	a	1498	UR3	C4-N3-C2	-7.06	118.90	124.58
1	A	2605	PSU	N1-C2-N3	6.90	122.45	115.17
32	a	516	PSU	N1-C2-N3	6.80	122.34	115.17

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1915	5MU	O4'-C1'-N1-C2
1	A	1915	5MU	O4'-C1'-N1-C6
32	a	527	7MG	C3'-C4'-C5'-O5'
32	a	1519	MA6	O4'-C4'-C5'-O5'
43	l	92	0TD	O-C-CA-CB

There are no ring outliers.

22 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1962	5MC	3	0
32	a	1400	5MC	2	0
32	a	1519	MA6	4	0
1	A	1942	5MC	2	0
32	a	1402	4OC	5	0
43	l	92	0TD	1	0
32	a	1498	UR3	4	0
1	A	2552	2MU	2	0
1	A	1939	5MU	1	0
32	a	966	M2G	4	0
32	a	967	5MC	4	0
1	A	1911	PSU	1	0
1	A	1920	4OC	4	0
32	a	1407	5MC	3	0
1	A	1915	5MU	1	0
1	A	1917	PSU	3	0
1	A	2251	OMG	4	0
1	A	2503	2MA	3	0
32	a	1518	MA6	7	0
32	a	516	PSU	4	0
32	a	1207	2MG	2	0
32	a	1404	5MC	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, 6 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	SF4	d	301	35	0,12,12	-	-	-		

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
58	SF4	d	301	35	-	-	0/6/5/5

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	d	301	SF4	1	0

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
32	a	4
7	H	3
1	A	2

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1000:U	O3'	1001(A):A	P	4.17
1	a	1029:C	O3'	1030(A):C	P	4.08
1	A	2103:C	O3'	2104:G	P	3.60
1	A	2180:U	O3'	2181:G	P	3.49
1	H	3:ARG	C	4:ILE	N	3.23

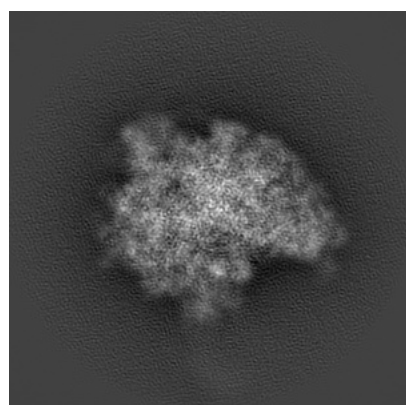
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8597. These allow visual inspection of the internal detail of the map and identification of artifacts.

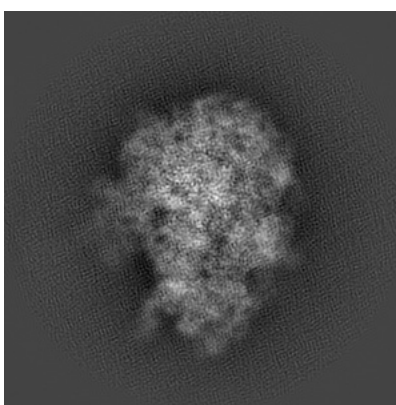
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

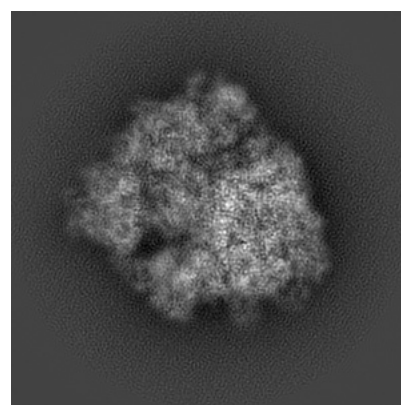
6.1.1 Primary map



X



Y

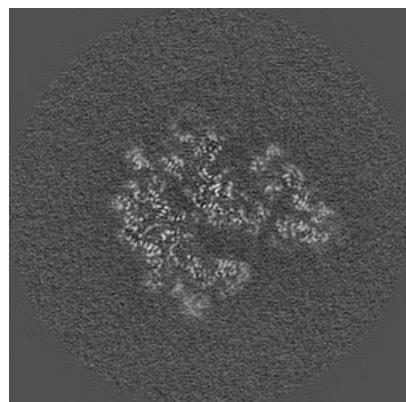


Z

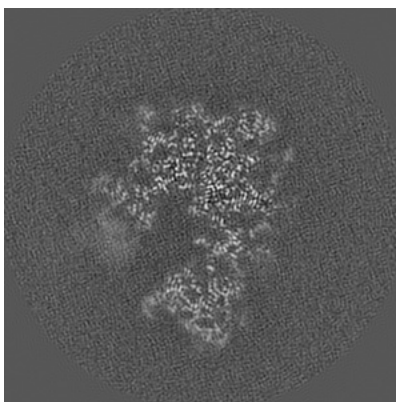
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

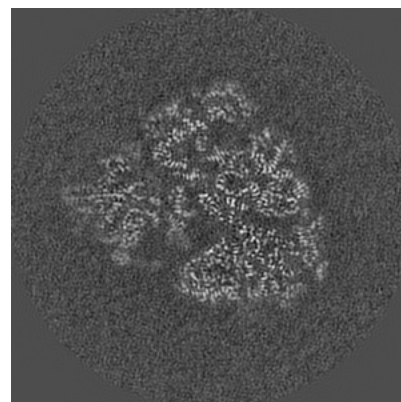
6.2.1 Primary map



X Index: 192



Y Index: 192

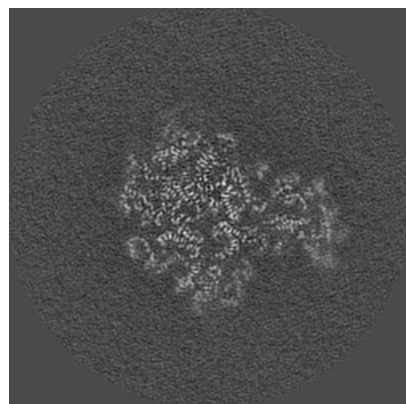


Z Index: 192

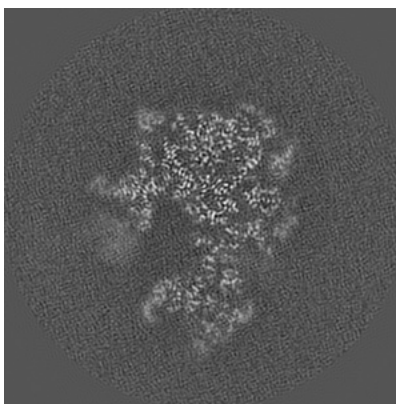
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

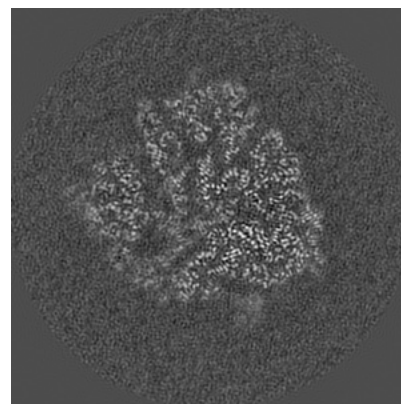
6.3.1 Primary map



X Index: 203



Y Index: 197

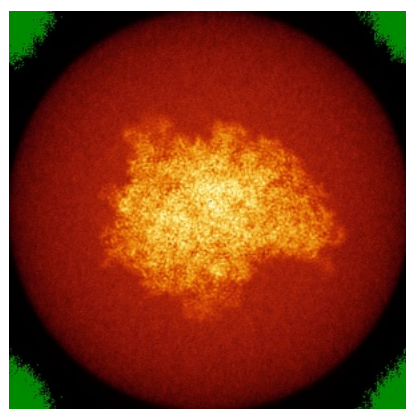


Z Index: 184

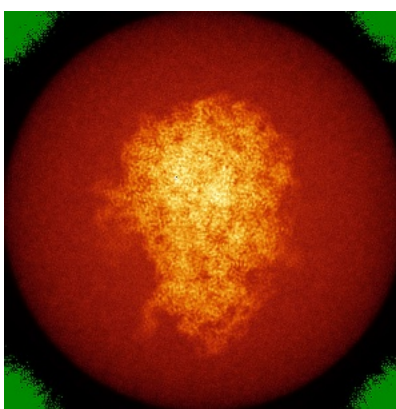
The images above show the largest variance slices of the map in three orthogonal directions.

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

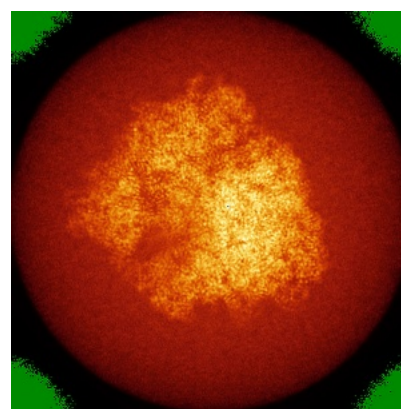
6.4.1 Primary map



X



Y



Z

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

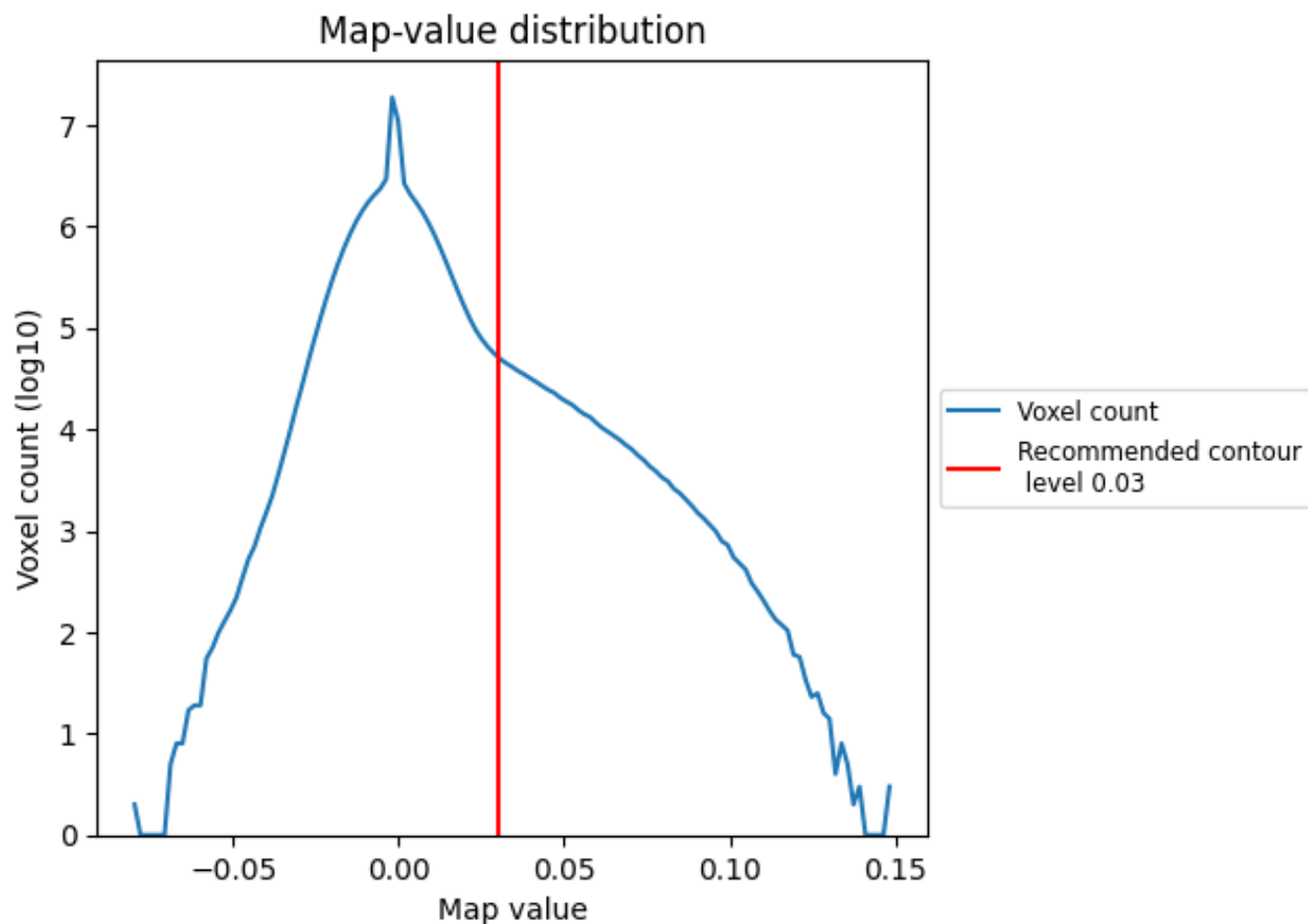
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

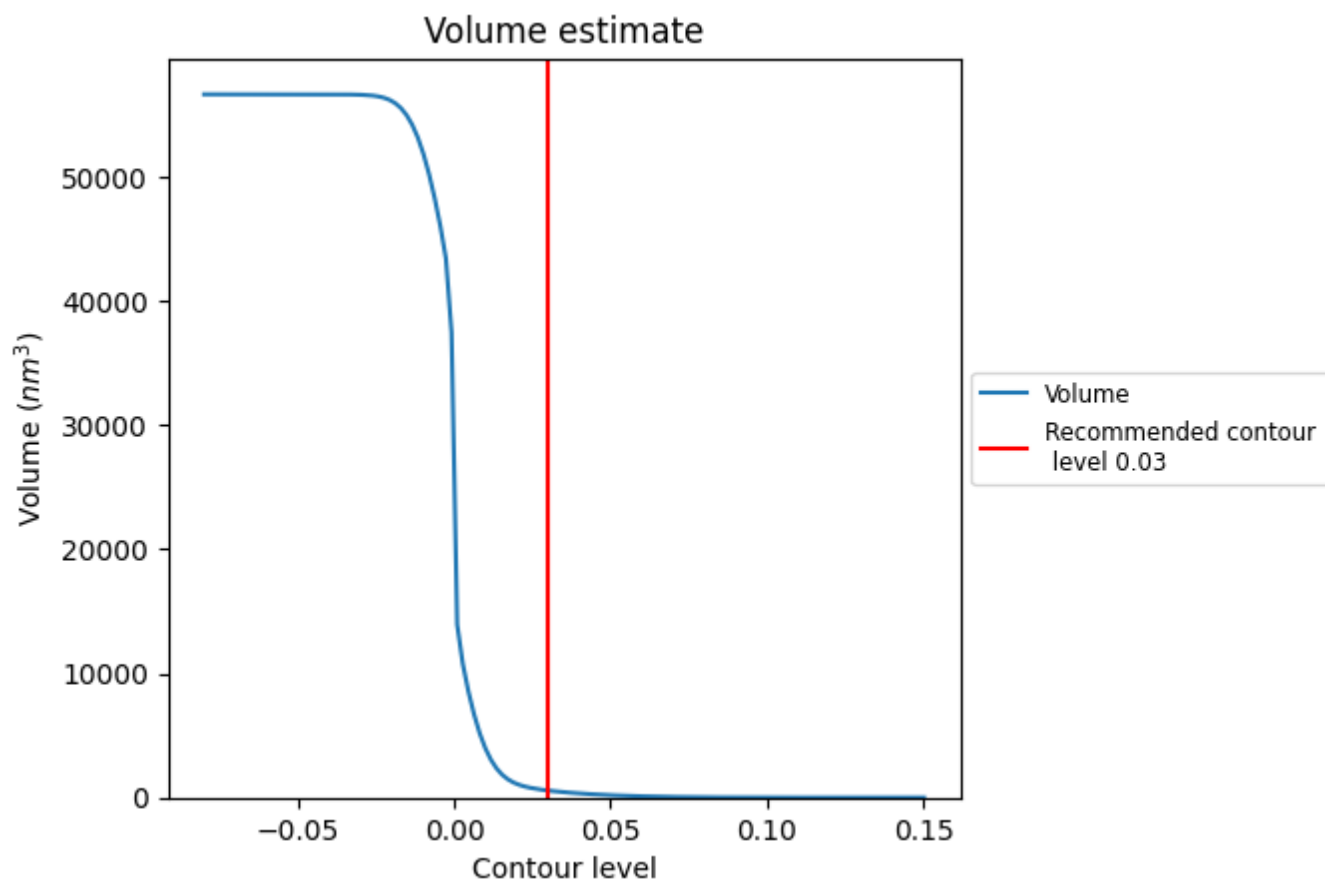
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

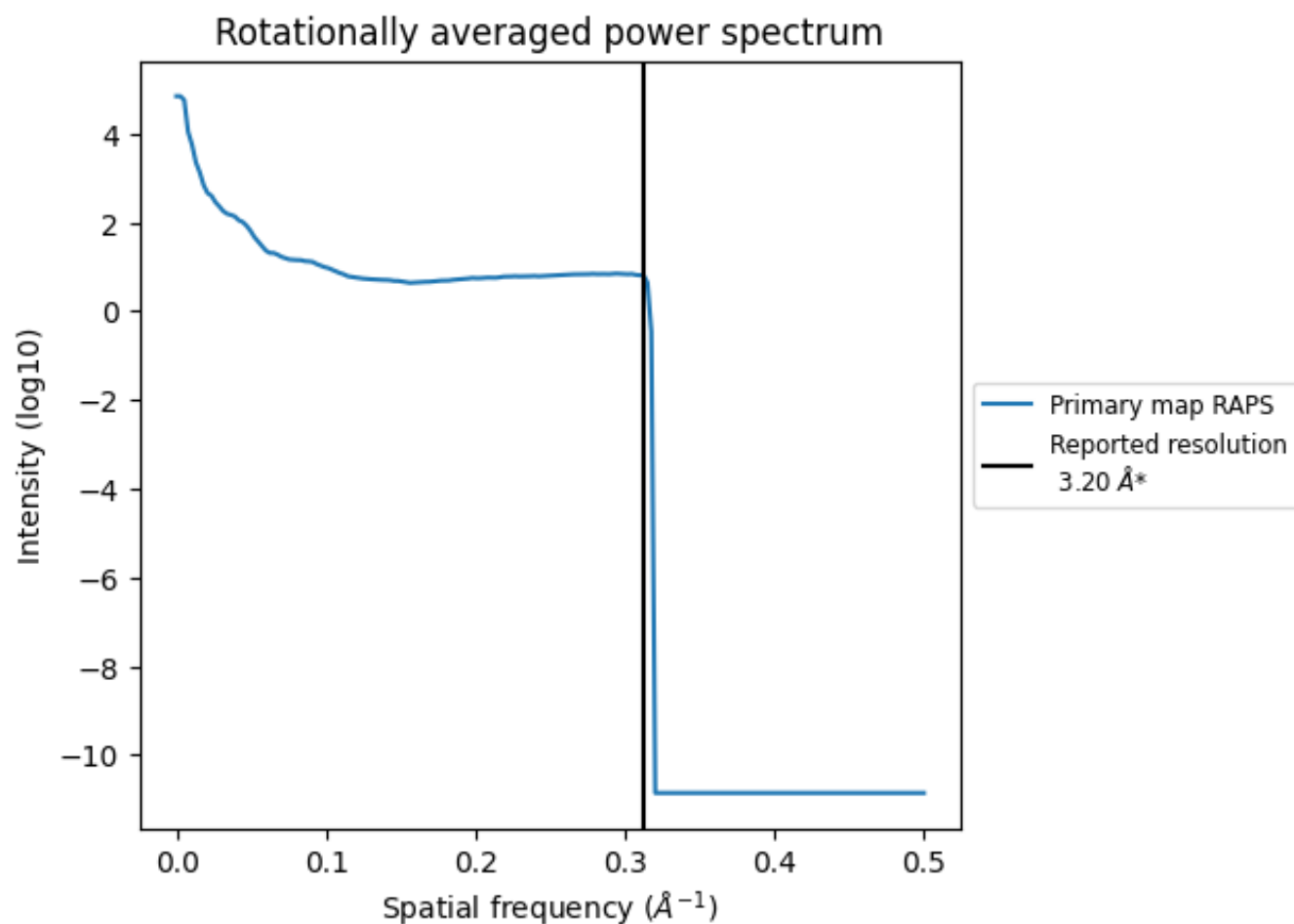
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 568 nm³; this corresponds to an approximate mass of 513 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 0.312 $\text{\AA}^{-1}$

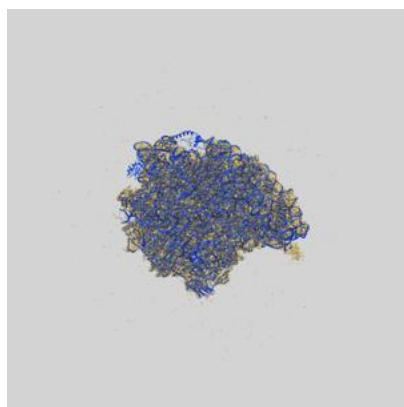
8 Fourier-Shell correlation

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

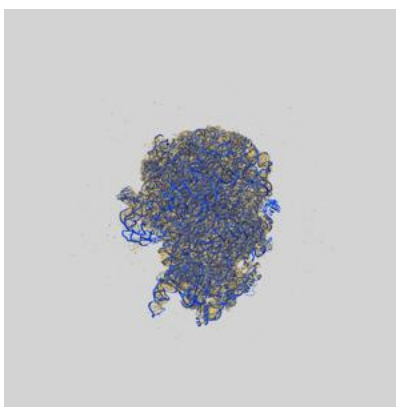
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8597 and PDB model 5UQ8. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

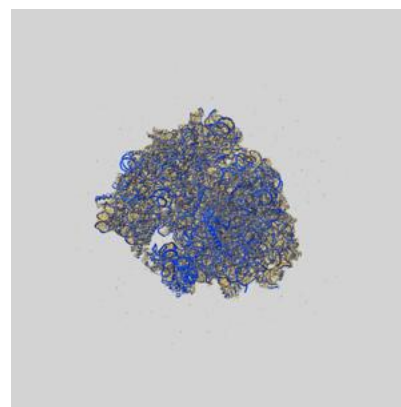
9.1 Map-model overlay [i](#)



X



Y



Z

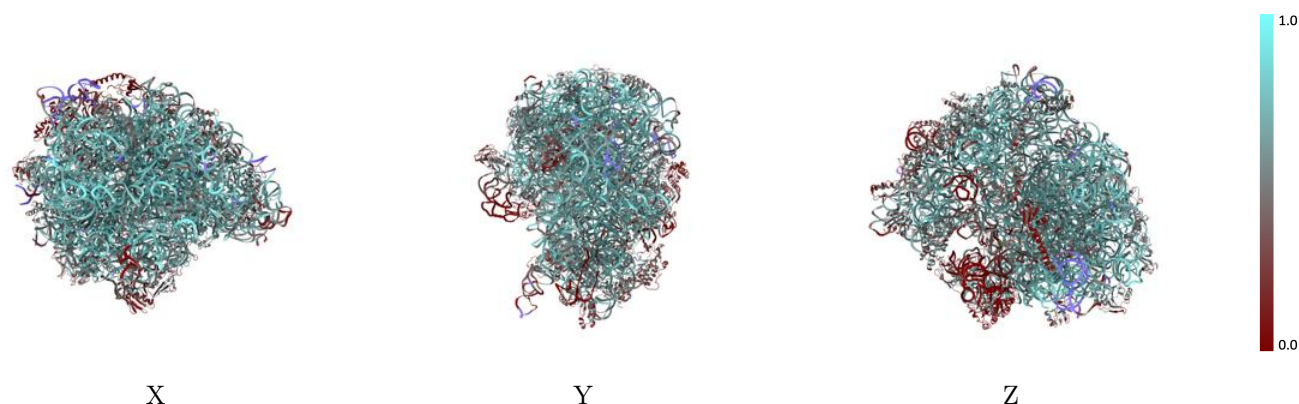
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



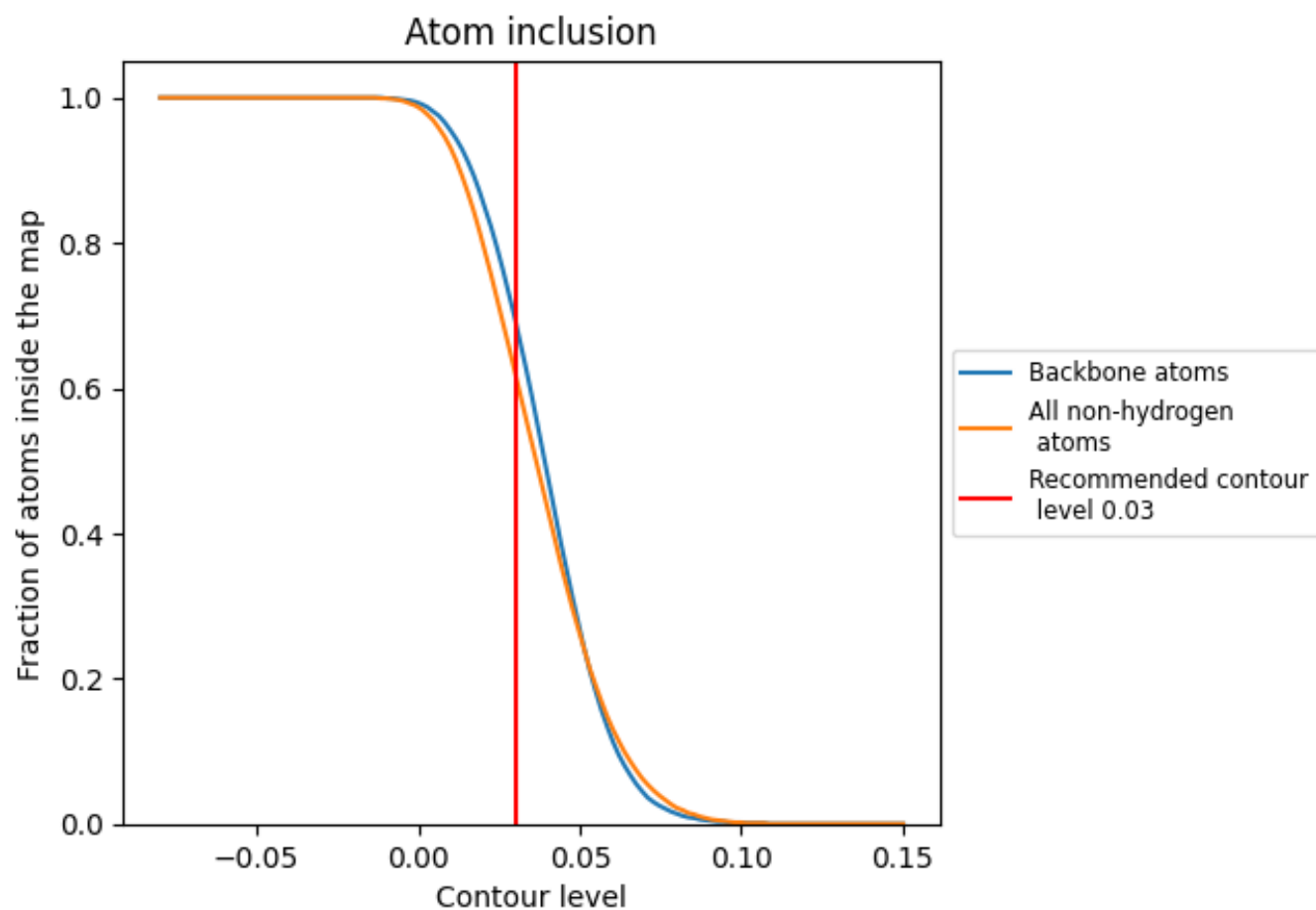
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6210	 0.4460
0	 0.6220	 0.5150
1	 0.4800	 0.4560
2	 0.4580	 0.4020
3	 0.5340	 0.4700
4	 0.2580	 0.2770
5	 0.6240	 0.4980
6	 0.6010	 0.4790
7	 0.6310	 0.5220
8	 0.5980	 0.5070
9	 0.5630	 0.4940
A	 0.7190	 0.4760
B	 0.6900	 0.4450
C	 0.0040	 0.1160
D	 0.6390	 0.5080
E	 0.5950	 0.4920
F	 0.5630	 0.4650
G	 0.4270	 0.3970
H	 0.3290	 0.3420
I	 0.0860	 0.2550
N	 0.5440	 0.4750
O	 0.5470	 0.4920
P	 0.5390	 0.4670
Q	 0.5380	 0.4550
R	 0.6130	 0.4880
S	 0.5100	 0.4270
T	 0.5540	 0.4570
U	 0.6370	 0.4910
V	 0.5000	 0.4490
W	 0.5840	 0.4930
X	 0.5290	 0.4570
Y	 0.4260	 0.4240
Z	 0.2590	 0.3350
a	 0.6970	 0.4530
b	 0.3650	 0.3780



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Chain	Atom inclusion	Q-score
c	 0.4980	 0.4410
d	 0.4770	 0.4090
e	 0.5410	 0.4680
f	 0.3390	 0.3510
g	 0.4250	 0.3840
h	 0.5610	 0.4710
i	 0.4220	 0.3910
j	 0.4030	 0.3890
k	 0.4760	 0.4330
l	 0.5440	 0.4880
m	 0.4260	 0.3980
n	 0.5790	 0.4760
o	 0.4890	 0.4180
p	 0.5700	 0.4630
q	 0.5150	 0.4750
r	 0.3600	 0.3650
s	 0.4030	 0.3860
t	 0.4630	 0.3910
u	 0.4890	 0.4420
x	 0.0590	 0.1030
y	 0.4630	 0.4070
z	 0.0920	 0.1510