



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 05:17 AM UTC

PDB ID : 6OGF / pdb_00006ogf
EMDB ID : EMD-20056
Title : 70S termination complex with RF2 bound to the UGA codon. Partially rotated ribosome with RF2 bound (Structure III).
Authors : Svidritskiy, E.; Demo, G.; Loveland, A.B.; Xu, C.; Korostelev, A.A.
Deposited on : 2019-04-02
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

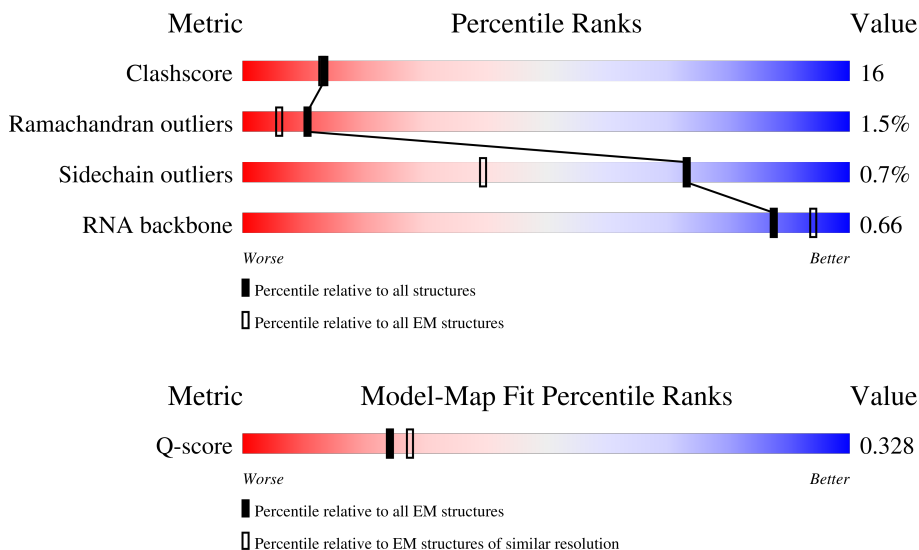
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	b	273	55% (green), 43% (yellow), .. (grey)
2	c	209	60% (green), 39% (yellow), . (grey)
3	d	201	49% (green), 48% (yellow), . (grey)

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Mol	Chain	Length	Quality of chain
4	e	179	42% 55% ..
5	f	177	54% 44% ..
6	g	149	56% 46% 50% 5%
7	j	142	62% 37% .
8	k	123	63% 36% .
9	l	144	70% 26% ..
10	m	136	53% 44% .
11	n	127	54% 39% . 6%
12	o	117	55% 43% ...
13	p	115	52% 43% ..
14	q	118	57% 41% ..
15	r	103	50% 47% .
16	s	110	55% 45%
17	t	100	55% 36% . 7%
18	u	104	52% 43% ..
19	v	94	59% 39% .
20	w	85	60% 28% 12%
21	x	78	51% 46% ..
22	y	63	71% 29%
23	z	59	68% 29% ..
24	B	57	54% 44% .
25	C	55	56% 35% 9%
26	D	46	61% 35% .
27	E	65	57% 38% ..
28	F	38	39% 61%


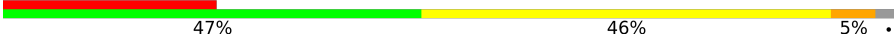
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Mol	Chain	Length	Quality of chain
29	G	241	47% 42% 7%
30	H	233	46% 40% 12%
31	I	206	52% 44%
32	J	167	49% 41% 6%
33	K	131	24% 47% 5% 23%
34	L	156	47% 47% 2% 4%
35	M	130	49% 47% 2% 4%
36	N	130	34% 62% 2% 4%
37	O	103	9% 41% 50% 5% 5%
38	P	129	36% 50% 2% 10%
39	Q	124	44% 50% 5% 2%
40	R	118	43% 51% 2% 4%
41	S	101	42% 53% 2% 3%
42	T	89	46% 48% 2% 4%
43	U	82	44% 55% 2% 1%
44	V	84	50% 44% 2% 5%
45	W	75	49% 36% 2% 13%
46	X	92	41% 43% 2% 14%
47	Y	87	51% 43% 5% 2%
48	Z	71	34% 46% 11% 8%
49	a	234	36% 32% 22% 43%
50	3	1539	55% 41% 2% 2%
51	1	2903	5% 54% 40% 6%
52	2	120	52% 43% 5%
53	5	77	12% 61% 32% 5%

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Mol	Chain	Length	Quality of chain
54	4	27	 <p>41% 26% 7% 26%</p>
55	8	371	 <p>24% 47% 46% 5%</p>

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 147733 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	b	271	2082	1288	423	364	7	0	0

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	c	209	1565	979	288	294	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	d	201	1552	974	283	290	5	0	0

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	e	177	1410	899	249	256	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	f	176	1323	832	243	246	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	g	149	1111	699	197	214	1	0	0

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	j	142	1129	714	212	199	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	k	122	938	587	180	165	6	0	0

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	l	143	1045	649	206	189	1	0	0

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	m	136	1074	686	205	177	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	n	120	960	593	196	166	5	0	0

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	o	116	892	552	178	162	0	0

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	p	114	917	574	179	163	1	0	0

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	u	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 19 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 31 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 32 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 33 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 34 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 35 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	M	129	979	616	173	184	6	0	0

- Molecule 36 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	N	127	1022	634	206	179	3	0	0

- Molecule 37 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	O	98	786	493	150	142	1	0	0

- Molecule 38 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	P	116	869	535	173	158	3	0	0

- Molecule 39 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Q	123	955	590	196	165	4	0	0

- Molecule 40 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	R	114	883	546	178	156	3	0	0

- Molecule 41 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	S	100	805	499	164	139	3	0	0

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 43 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 44 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 45 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 46 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 47 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 49 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	a	134	1026	645	186	193	2	0	0

- Molecule 50 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	3	1539	33012	14725	6052	10697	1538	0	0

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	1	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
52	2	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	expression tag	GB 1370526515

- Molecule 53 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	5	73	1556	694	281	509	72	0	0

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	4	20	437	197	91	130	19	0	0

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	8	361	2860	1758	503	589	10	0	0

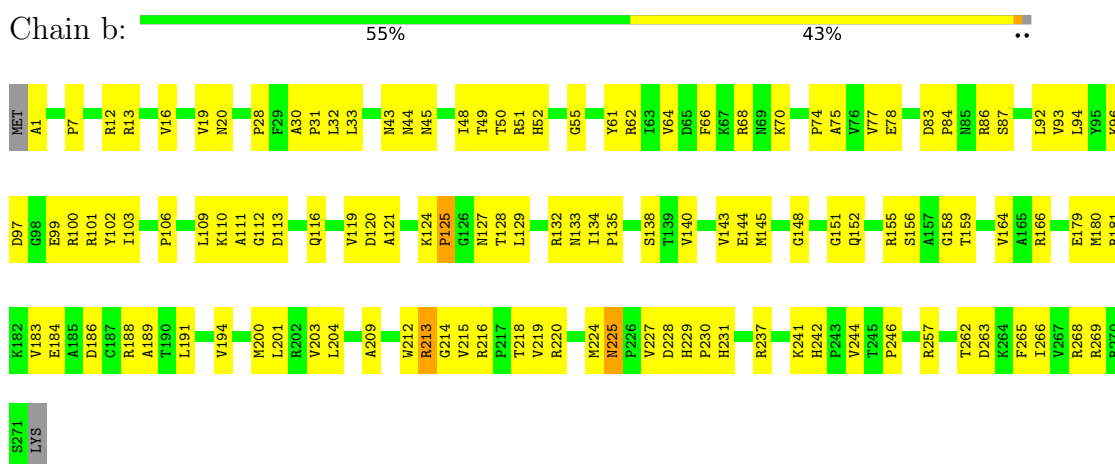
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	-5	MET	-	initiating methionine	UNP A0A2S5ZJX2
8	-4	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-3	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-2	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-1	HIS	-	expression tag	UNP A0A2S5ZJX2
8	0	HIS	-	expression tag	UNP A0A2S5ZJX2
8	1	HIS	-	expression tag	UNP A0A2S5ZJX2

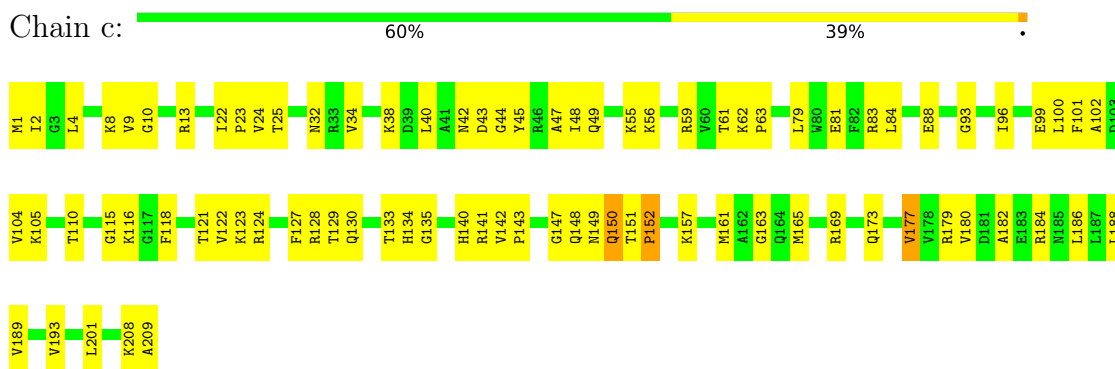
3 Residue-property plots [i](#)

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.

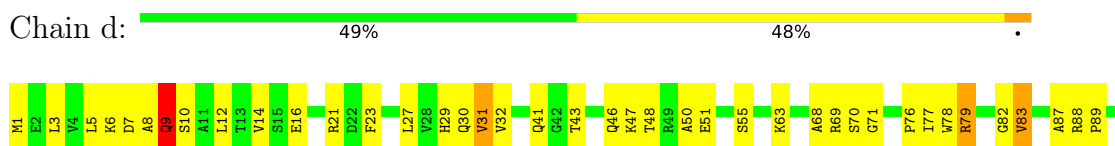
- Molecule 1: 50S ribosomal protein L2

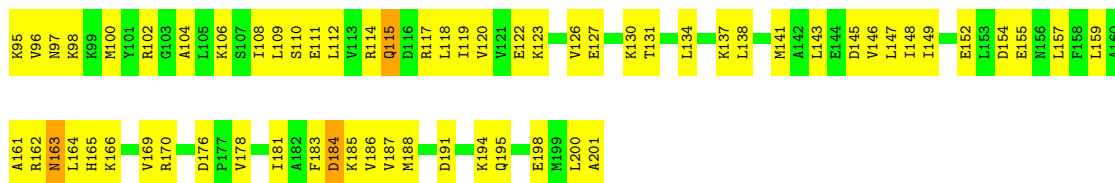


- Molecule 2: 50S ribosomal protein L3

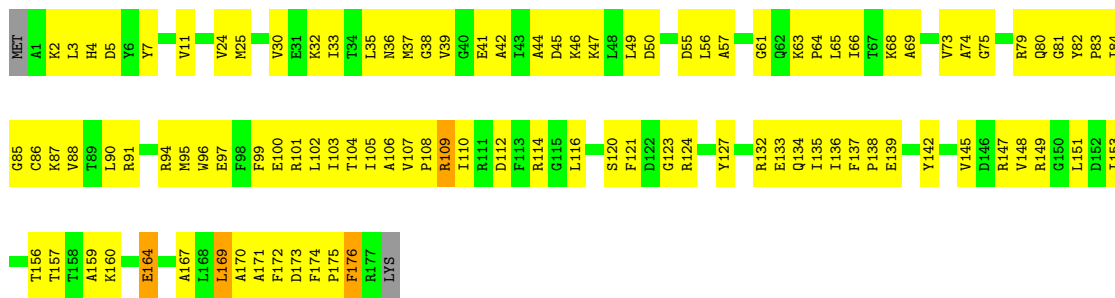


- Molecule 3: 50S ribosomal protein L4

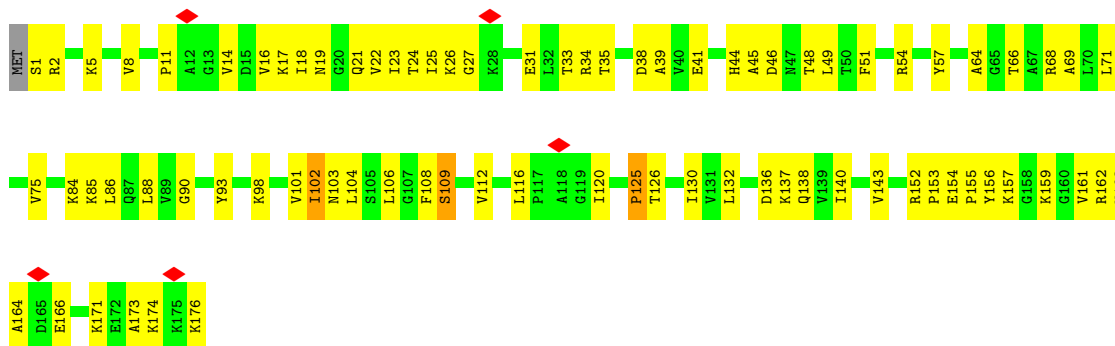




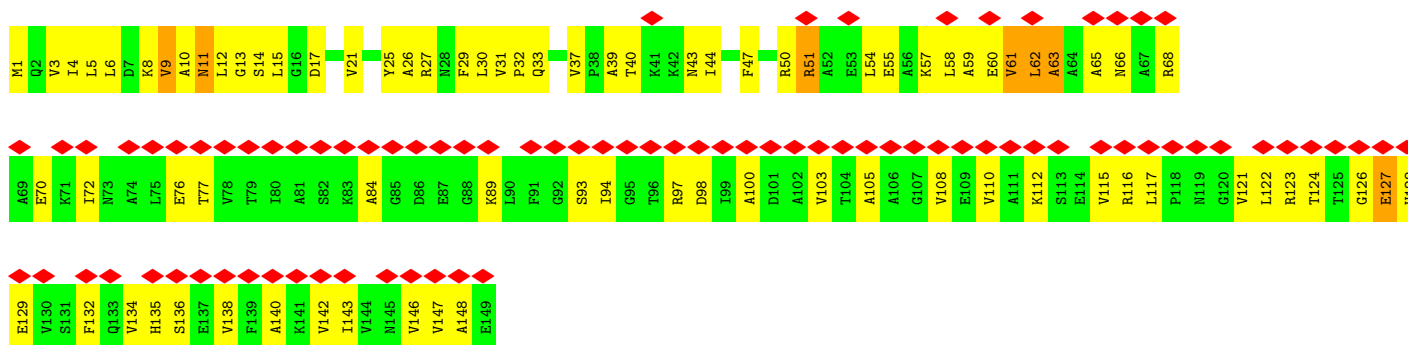
• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9



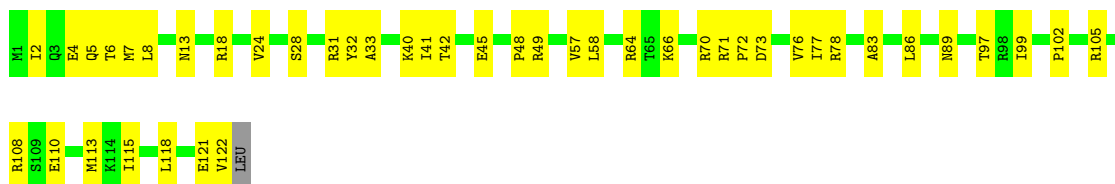
• Molecule 7: 50S ribosomal protein L13

Chain j:  62% 37%



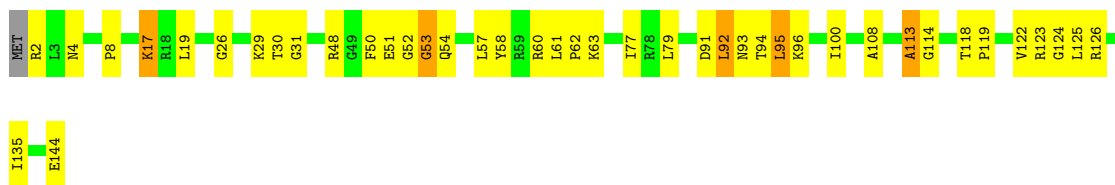
- Molecule 8: 50S ribosomal protein L14

Chain k:  63% 36%



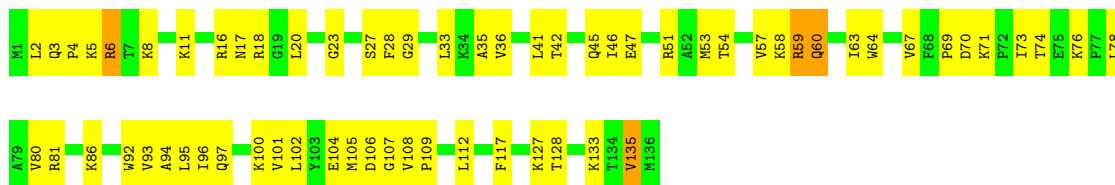
- Molecule 9: 50S ribosomal protein L15

Chain l:  70% 26%



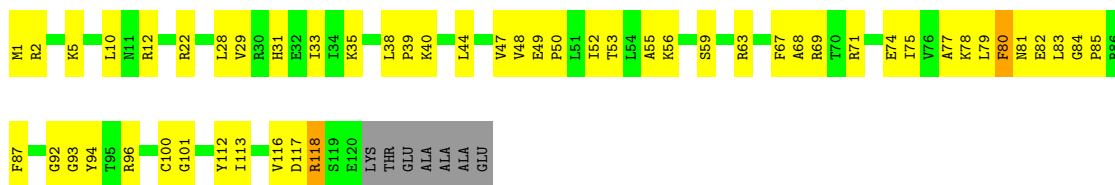
- Molecule 10: 50S ribosomal protein L16

Chain m:  53% 44%



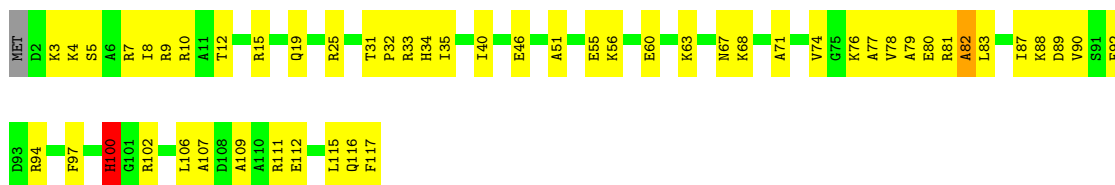
- Molecule 11: 50S ribosomal protein L17

Chain n:  54% 39% 6%



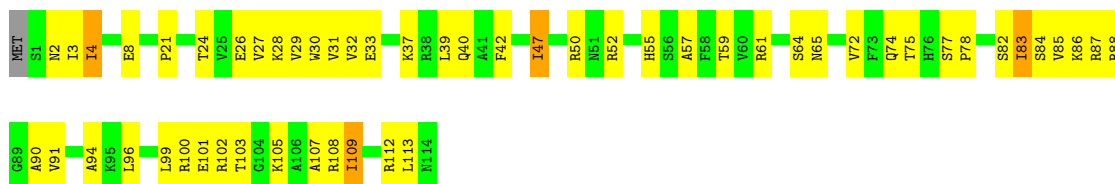
- Molecule 12: 50S ribosomal protein L18

Chain o:  55% 43%



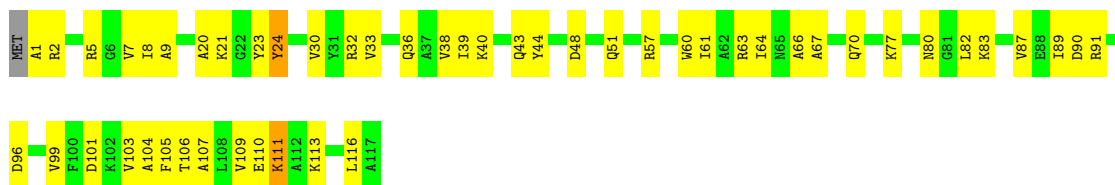
● Molecule 13: 50S ribosomal protein L19

Chain p:  52% 43%



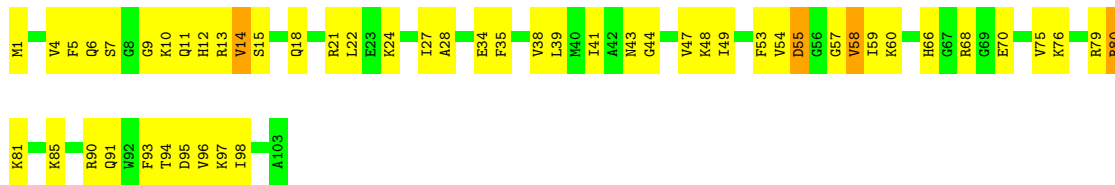
● Molecule 14: 50S ribosomal protein L20

Chain q:  57% 41%



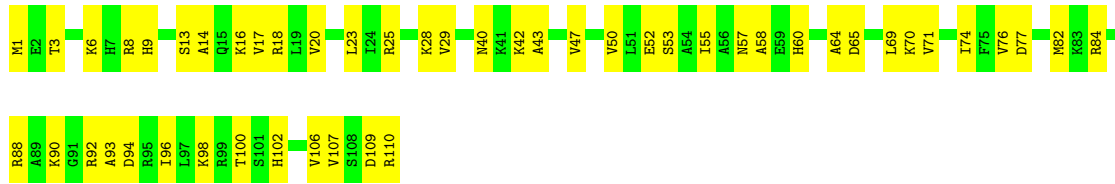
● Molecule 15: 50S ribosomal protein L21

Chain r:  50% 47%



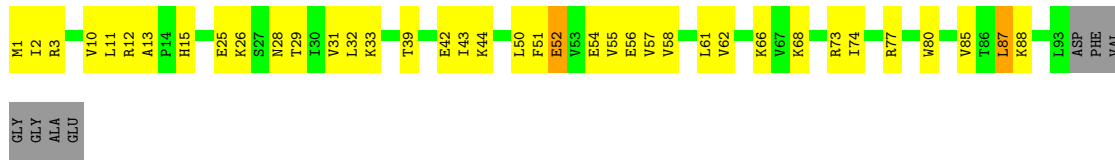
● Molecule 16: 50S ribosomal protein L22

Chain s:  55% 45%



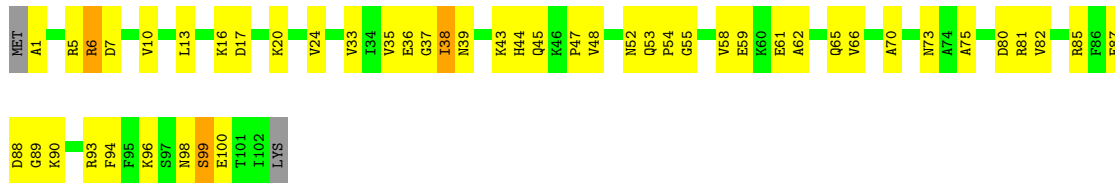
● Molecule 17: 50S ribosomal protein L23

Chain t:  55% 36% 7%



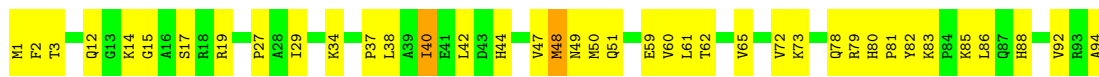
• Molecule 18: 50S ribosomal protein L24

Chain u:  52% 43% 5%



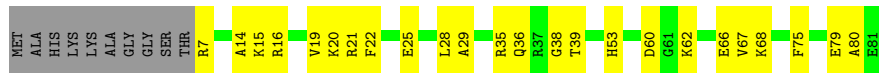
• Molecule 19: 50S ribosomal protein L25

Chain v:  59% 39% 2%



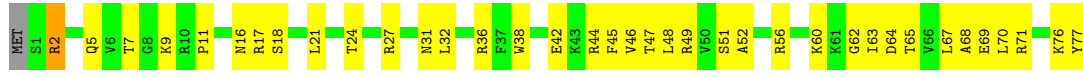
• Molecule 20: 50S ribosomal protein L27

Chain w:  60% 28% 12%



• Molecule 21: 50S ribosomal protein L28

Chain x:  51% 46% 3%



• Molecule 22: 50S ribosomal protein L29

Chain y:  71% 29%



• Molecule 23: 50S ribosomal protein L30

Chain z:  68% 29% 3%



• Molecule 24: 50S ribosomal protein L32



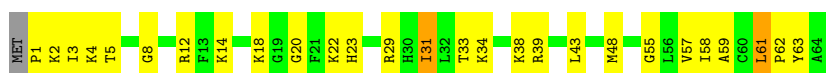
• Molecule 25: 50S ribosomal protein L33



• Molecule 26: 50S ribosomal protein L34



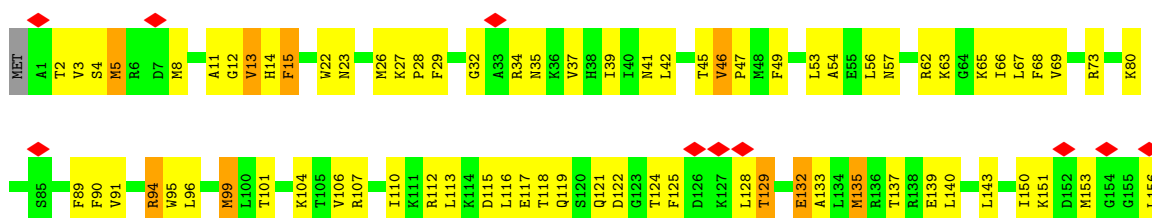
• Molecule 27: 50S ribosomal protein L35



• Molecule 28: 50S ribosomal protein L36

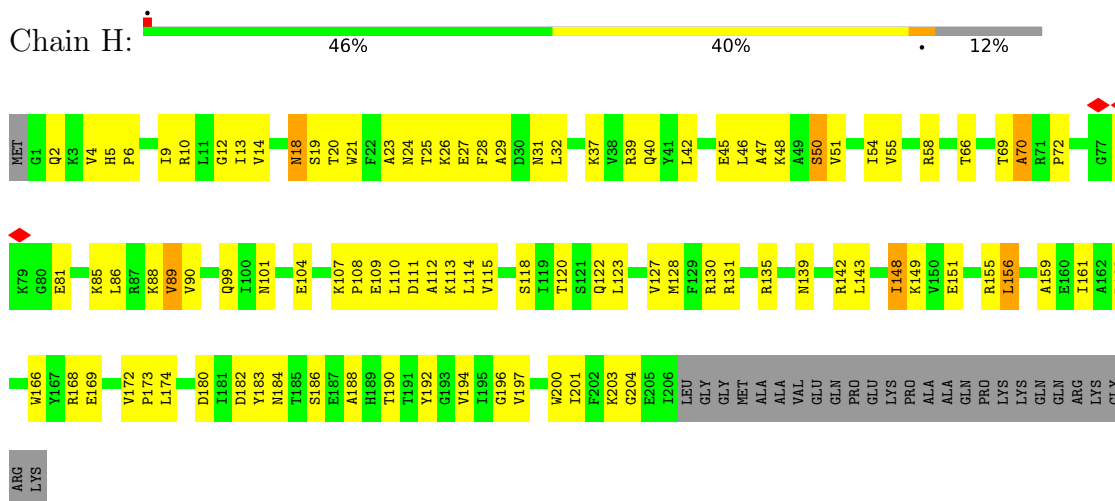


• Molecule 29: 30S ribosomal protein S2

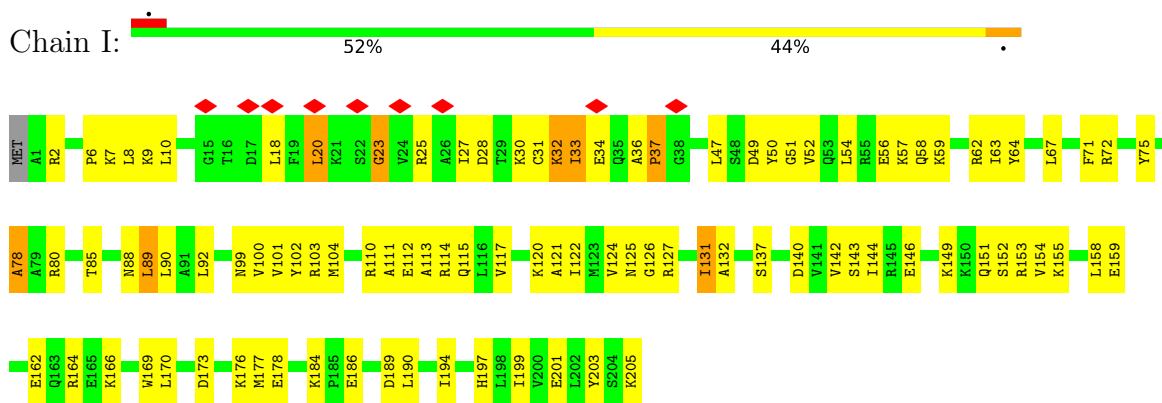




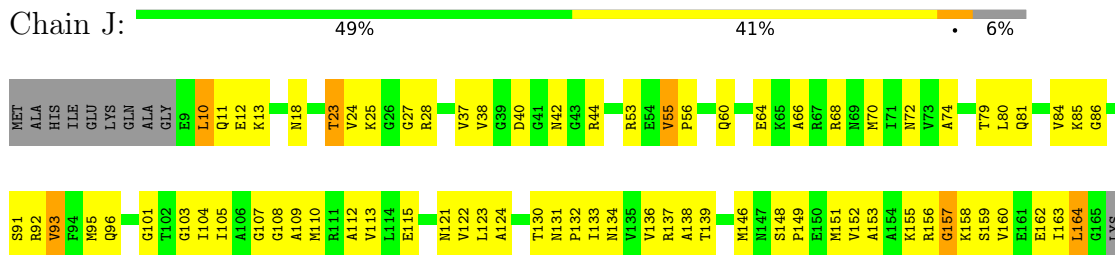
- Molecule 30: 30S ribosomal protein S3



- Molecule 31: 30S ribosomal protein S4

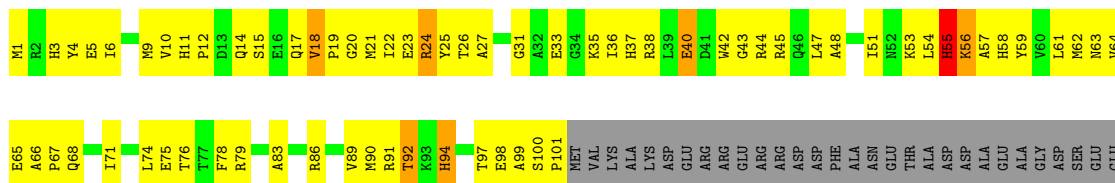


- Molecule 32: 30S ribosomal protein S5

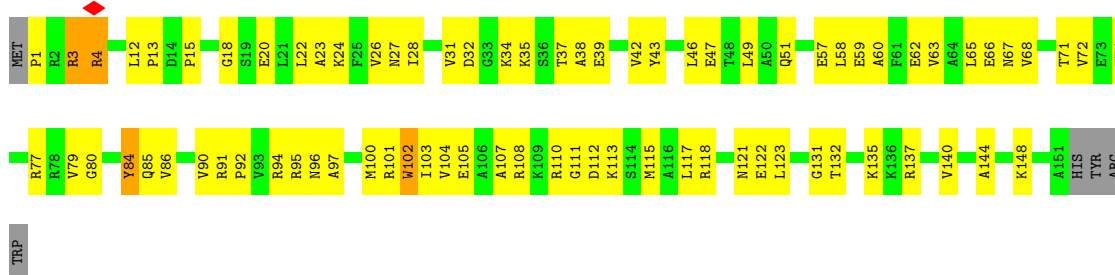


- Molecule 33: 30S ribosomal protein S6

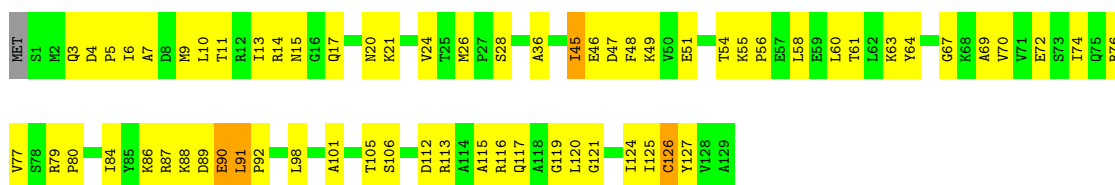




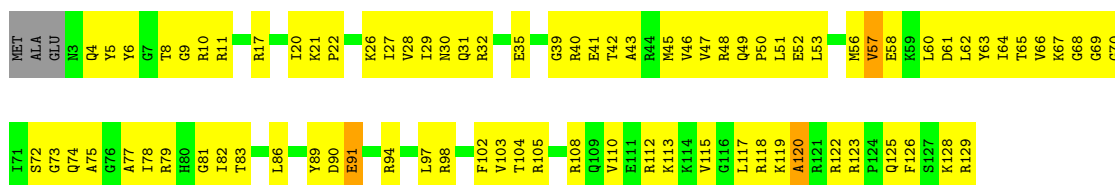
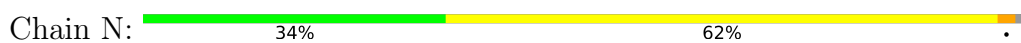
• Molecule 34: 30S ribosomal protein S7



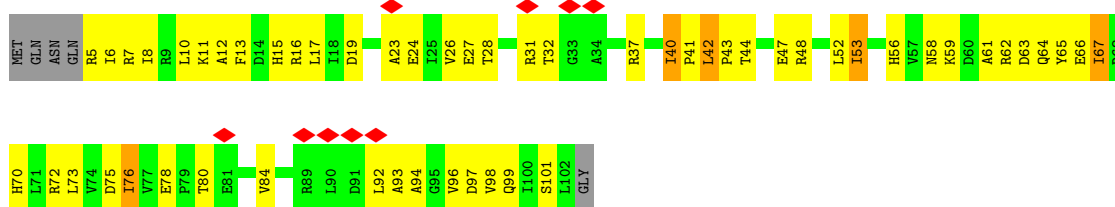
• Molecule 35: 30S ribosomal protein S8

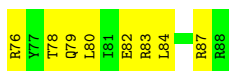


• Molecule 36: 30S ribosomal protein S9

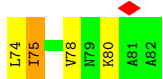
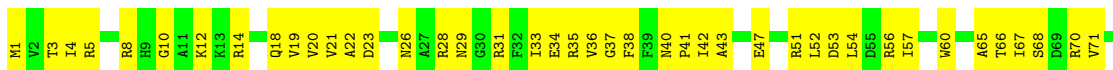


• Molecule 37: 30S ribosomal protein S10

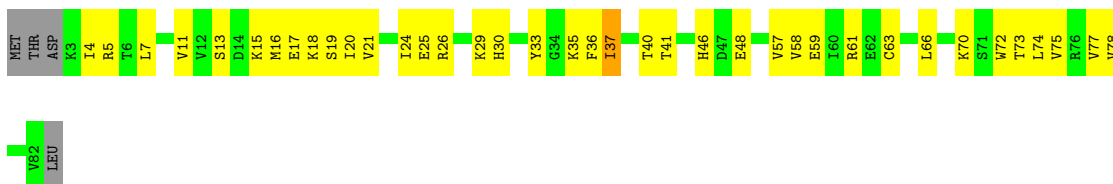




- Molecule 43: 30S ribosomal protein S16



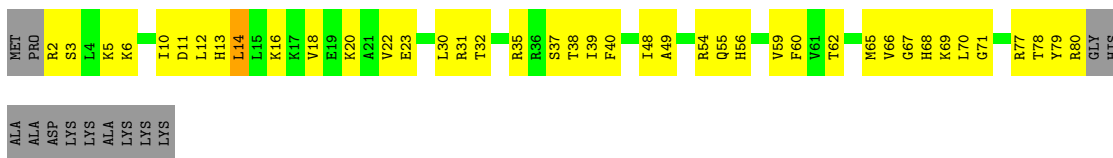
- Molecule 44: 30S ribosomal protein S17



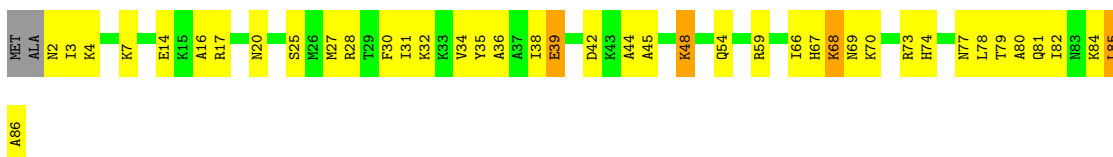
- Molecule 45: 30S ribosomal protein S18



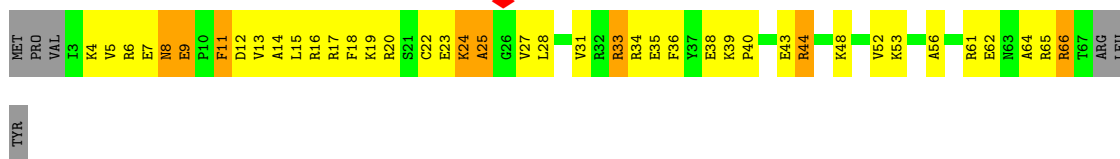
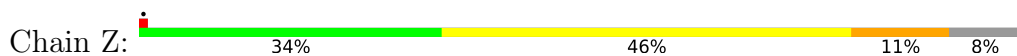
- Molecule 46: 30S ribosomal protein S19



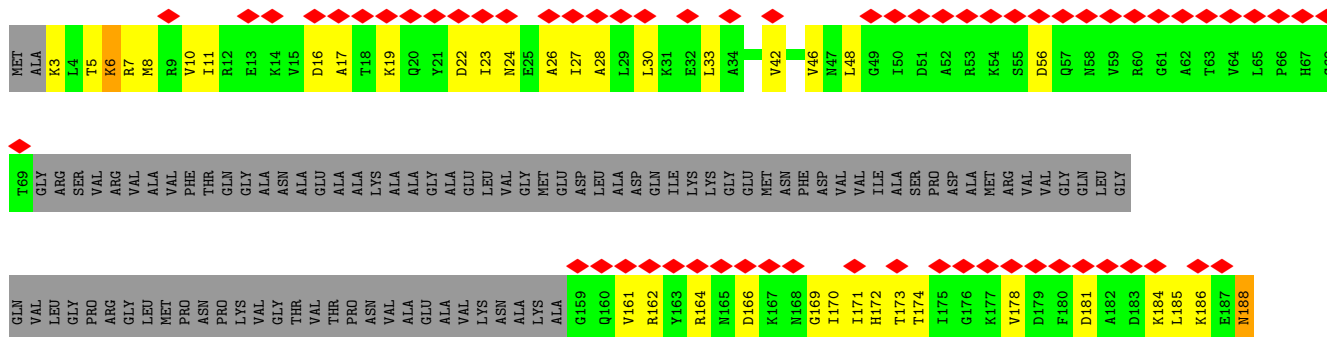
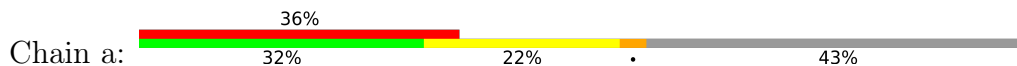
- Molecule 47: 30S ribosomal protein S20



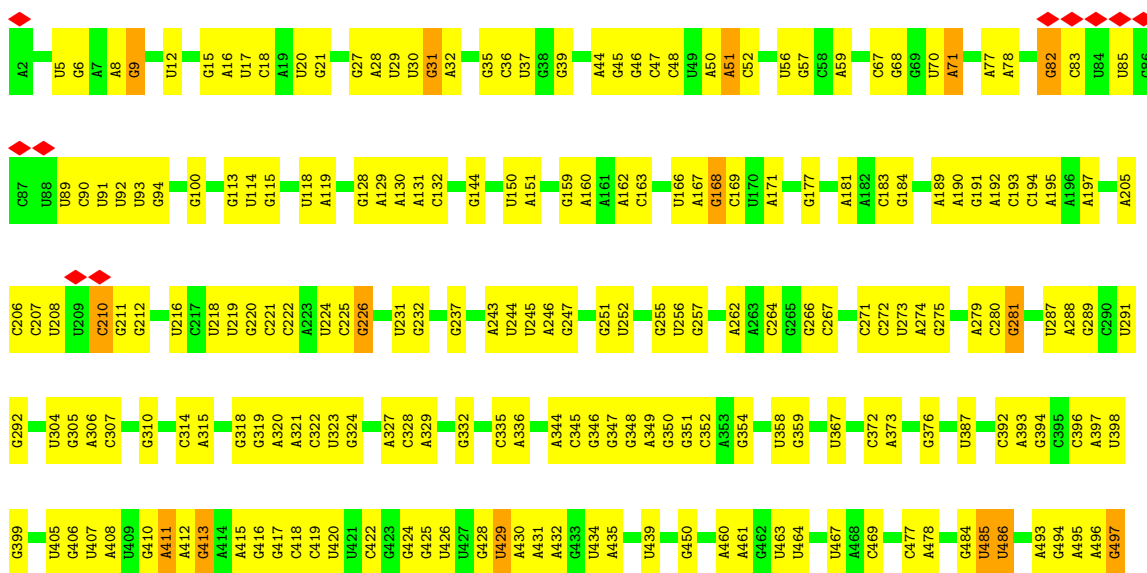
• Molecule 48: 30S ribosomal protein S21

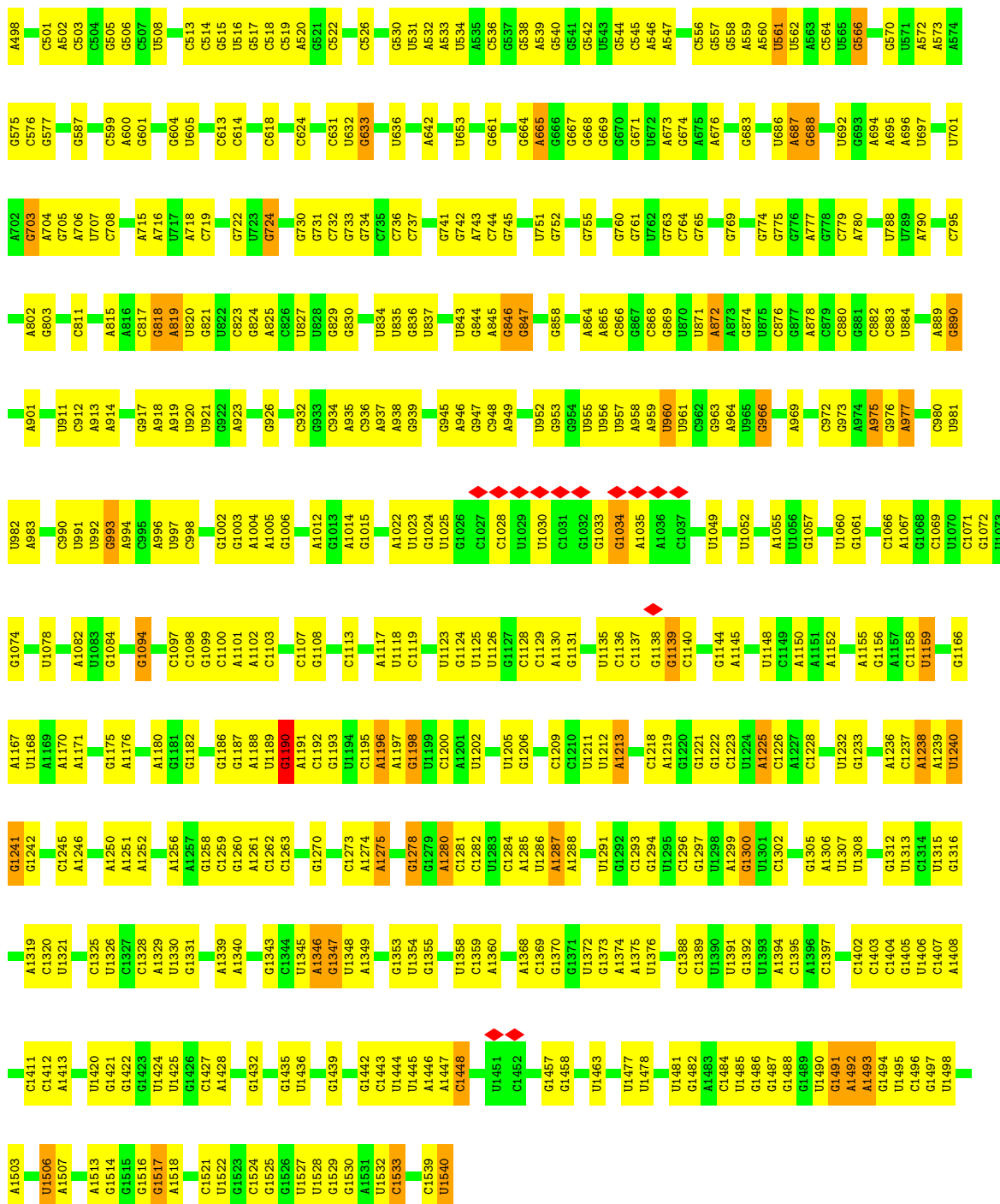


• Molecule 49: 50S ribosomal protein L1

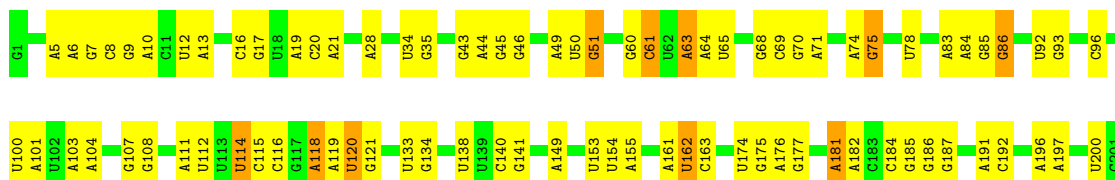


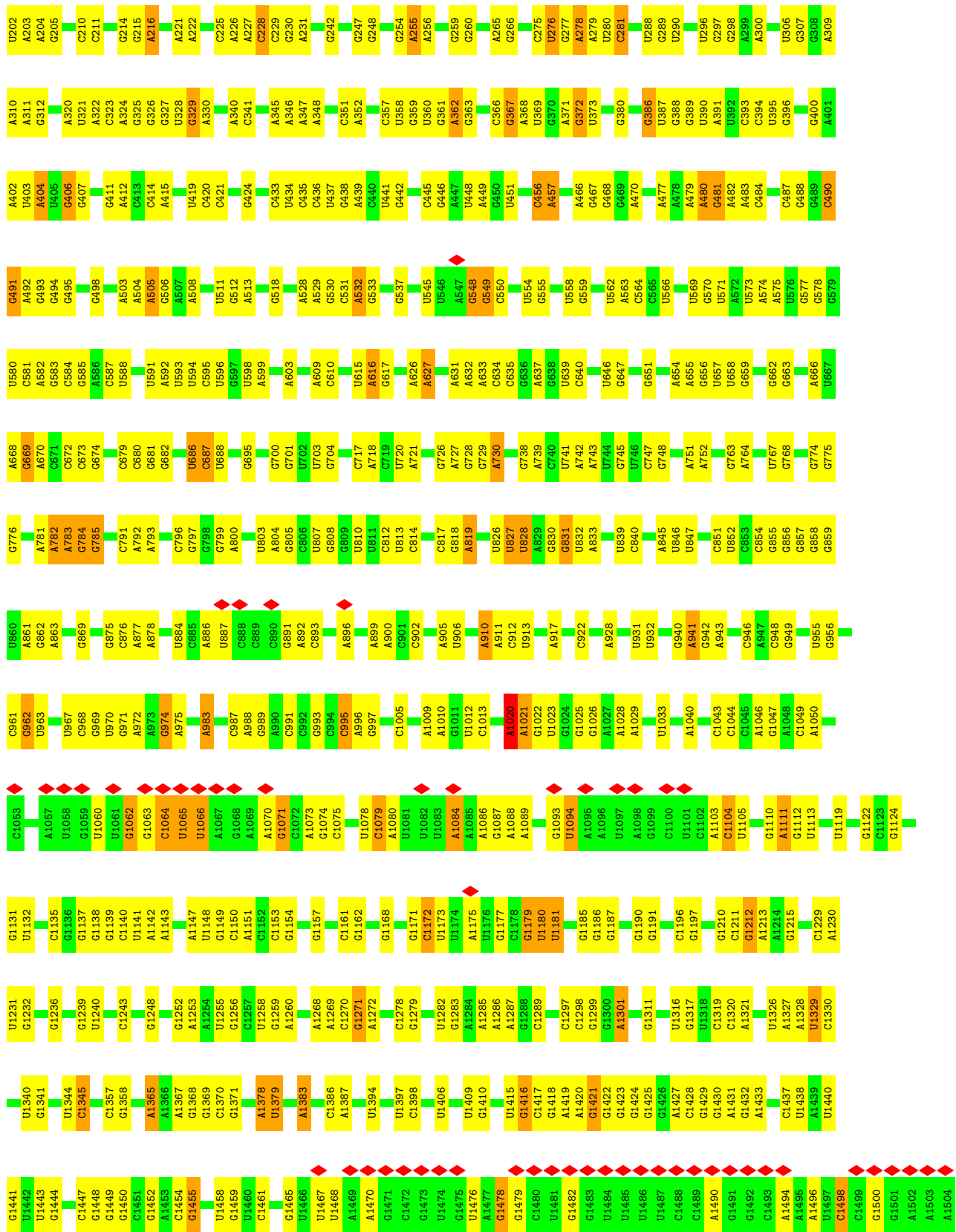
• Molecule 50: 16S ribosomal RNA



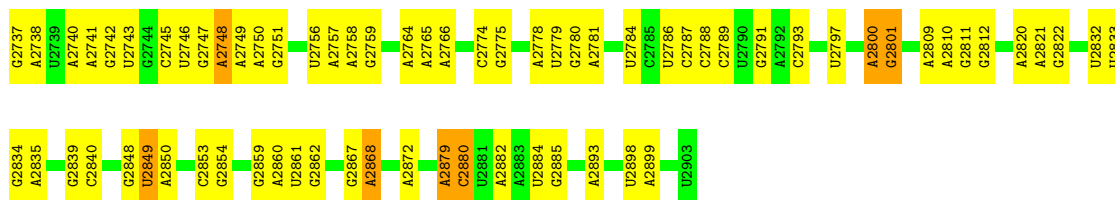


• Molecule 51: 23S ribosomal RNA

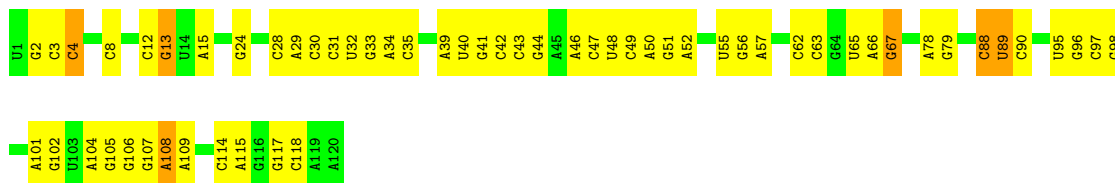




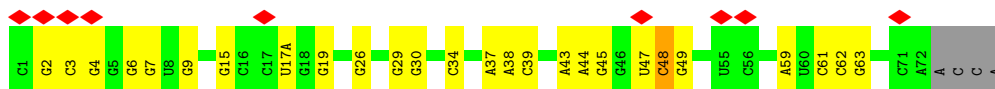
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A1572	U1578	A1579	A1581	U1584	C1586	A1587	C1595	A1596	A1597	A1598	U1599	C1600	G1601	U1602	A1603	C1607	A1608	A1609	C1611	A1614	C1615	A1616	C1639	A1640	G1645	C1646	U1647	U1648	G1649	A1650	G1651	A1655	A1664	A1665	A1666	G1667	A1669	C1670	U1671	G1674	U1680	G1681	G1682	U1683	G1684	C1685	C1686	A1689	A1690	A1691	C1691	G1695	C1696	A1697	A1700	A1701	G1702	G1703	U1704	A1705	C1706	U1709	A1713	U1714	A1715	U1716	A1717	G1718	G1719	G1721	A1722	G1723	G1724	C1728	U1729	C1730	U1731	G1732	G1733	G1738	A1739	G1740	U1742	G1743	A1744	A1745	G1746	U1751	C1752	A1755	U1756	A1757	U1758	C1764
U1765	C1771	A1772	A1773	U1775	G1776	A1786	A1789	U1796	G1797	U1798	C1799	A1800	A1801	A1802	A1803	G1807	A1808	A1809	A1810	G1811	U1812	G1813	C1816	G1817	U1818	A1819	A1820	A1821	C1822	U1825	U1826	U1827	G1828	A1829	C1837	G1846	A1847	A1848	G1849	G1850	A1851	A1852	A1853	A1854	U1855	U1856	G1857	U1858	U1859	U1943	U1944																																											
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U1951	A1952	U1953	U1954	U1955	U1956	C1962	U1963	C1967	A1970	U1971	G1972	G1973	U1978	A1979	G1980	G1984	C1985	U1991	G1992	U1993	C1996	A1997	C1998	C1999	G2010	U2011	A2012	A2019	U2022	C2023	A2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	A2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041																																														
A2042	C2043	C2044	C2045	G2049	C2050	A2051	A2052	C2055	G2056	A2060	C2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	C2069	A2070	A2071	G2072	C2073	U2074	C2078	U2079	A2080	U2081	A2082	G2083	U2086	G2087	G2093	A2094	A2095	C2096	C2104	U2105	U2106	G2107	U2111	G2112	U2113	A2114	U2118	A2119	U2122	G2123	G2124																																													
G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	G2159	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2171	U2172	A2173	C2174	C2175	A2176	C2177	G2178	C2179	U2180	A2183	A2184	U2185	U2189																																							
G2190	G2193	U2194	U2195	U2196	U2197	A2198	G2204	A2205	C2208	G2209	U2213	C2214	C2215	G2216	U2220	G2221	G2224	A2225	C2226	G2230	G2234	G2235	U2236	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	G2250	G2251	G2252	G2253	C2254	G2255	U2256	G2256	U2257	C2258	U2259	U2262	C2263	A2266																																													
A2267	A2268	G2271	U2272	G2277	A2278	C2283	A2284	C2285	G2286	A2287	A2288	U2291	A2292	G2293	G2294	C2295	U2296	A2297	U2298	U2299	C2300	G2304	U2305	C2306	G2307	A2308	A2309	C2310	A2311	U2312	C2313	A2314	G2315	G2316	A2317	G2318	U2321	A2322	G2323	U2324	G2325	C2326	A2327	A2328	U2329	G2330	U2334	A2335	A2336	C2337	C2338	C2339																																										
A2340	U2343	U2344	A2345	A2346	C2350	G2351	C2354	C2355	G2356	G2357	A2358	C2359	G2360	G2361	C2362	G2363	C2364	U2365	A2366	G2367	C2368	A2369	C2374	G2375	A2376	A2377	C2380	A2381	G2382	U2383	U2384	C2385	G2389	U2390	G2391	A2392	U2393	U2402	C2403	U2404	A2411	U2419	C2420	G2421	C2424	A2425	A2426	C2427	G2428																																													
G2429	A2430	U2431	A2432	A2433	A2434	C2440	U2441	C2442	A2443	C2444	G2445	A2448	A2451	C2452	G2455	C2456	U2457	G2458	C2466	A2469	A2470	A2471	C2472	C2475	A2476	U2477	A2478	U2479	C2480	G2481	A2482	C2483	G2484	G2485	U2491	G2494	C2498	G2502	A2503	U2504	G2505	U2506	G2507	G2508	C2512	A2513	U2514																																															
C2515	A2518	U2519	C2520	C2527	U2528	G2529	A2530	A2531	U2532	G2533	A2534	A2542	G2543	G2544	A2547	U2554	U2555	C2556	G2557	U2563	A2564	A2565	U2566	A2567	A2572	C2573	G2574	G2578	C2579	U2580	G2581	G2582	G2583	U2584	U2585	A2590	C2591	G2592	G2599	A2600	C2601	A2602	G2603	U2604	U2605	U2609	A2613																																															
U2614	U2615	C2616	U2617	G2618	C2619	U2629	G2630	C2636	U2637	G2638	G2642	C2646	U2647	C2655	U2656	A2657	C2658	G2659	A2665	C2666	C2667	A2682	C2683	U2689	U2690	U2698	C2699	C2704	A2705	G2709	C2710	A2711	G2714	C2715	C2716	C2717	U2720	U2724	A2725	C2730	G2731	A2732	A2733																																																			



• Molecule 52: 5S ribosomal RNA



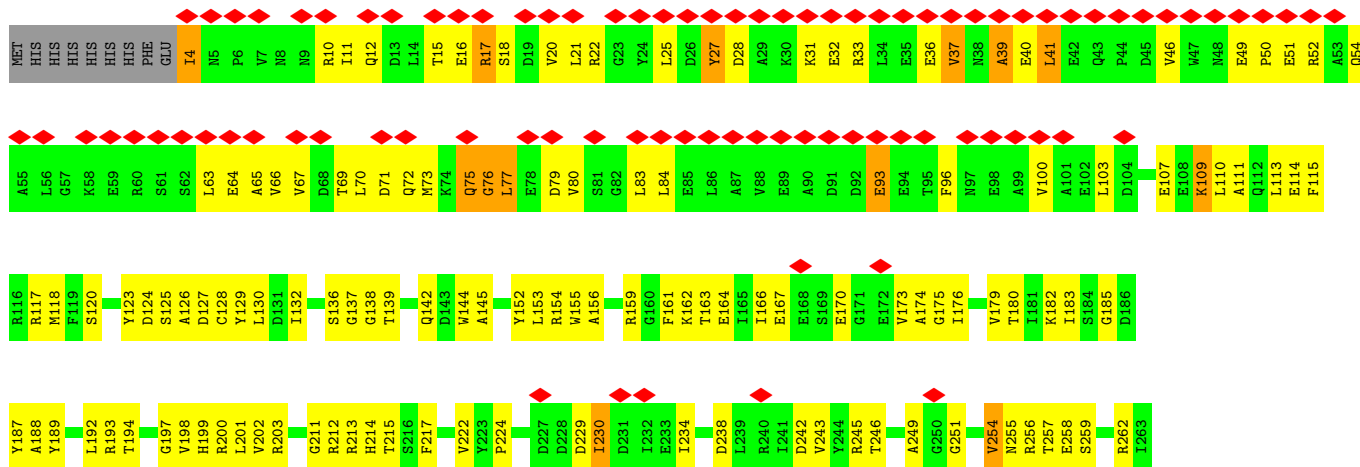
• Molecule 53: tRNA^{fMet}

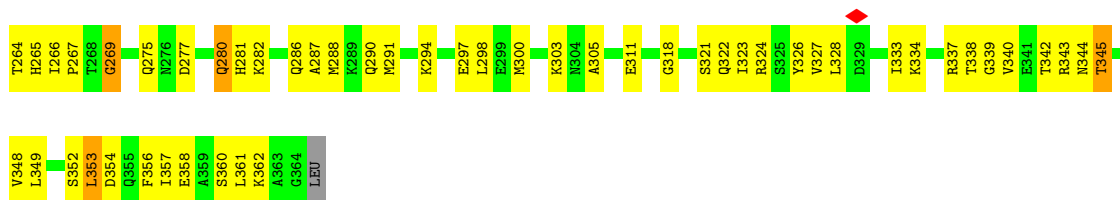


• Molecule 54: mRNA



• Molecule 55: Peptide chain release factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28549	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 ($e^-/\text{\AA}^2$)	29.4	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	7.540	Depositor
Minimum map value	-2.221	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.481	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	416.208, 416.208, 416.208	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	b	0.29	0/2121	0.84	5/2852 (0.2%)
2	c	0.30	0/1586	0.85	3/2134 (0.1%)
3	d	0.29	0/1571	0.86	7/2113 (0.3%)
4	e	0.31	0/1434	0.95	8/1926 (0.4%)
5	f	0.31	0/1343	0.86	1/1816 (0.1%)
6	g	0.33	0/1122	1.00	6/1515 (0.4%)
7	j	0.30	0/1152	0.89	3/1551 (0.2%)
8	k	0.27	0/947	0.89	1/1268 (0.1%)
9	l	0.30	0/1054	0.92	5/1403 (0.4%)
10	m	0.31	0/1093	0.86	3/1460 (0.2%)
11	n	0.29	0/973	0.88	3/1301 (0.2%)
12	o	0.30	0/902	0.85	1/1209 (0.1%)
13	p	0.30	0/929	0.86	1/1242 (0.1%)
14	q	0.29	0/960	0.90	3/1278 (0.2%)
15	r	0.30	0/829	0.88	4/1107 (0.4%)
16	s	0.31	0/864	0.86	2/1156 (0.2%)
17	t	0.28	0/744	0.80	0/994
18	u	0.29	0/787	0.83	1/1051 (0.1%)
19	v	0.31	0/766	0.84	3/1025 (0.3%)
20	w	0.29	0/582	0.83	1/769 (0.1%)
21	x	0.30	0/635	0.86	1/848 (0.1%)
22	y	0.28	0/510	0.92	0/677
23	z	0.29	0/453	0.82	0/605
24	B	0.28	0/450	0.80	0/599
25	C	0.31	0/416	0.71	0/554
26	D	0.30	0/380	0.93	2/498 (0.4%)
27	E	0.29	0/513	0.86	2/676 (0.3%)
28	F	0.33	0/303	0.92	2/397 (0.5%)
29	G	0.32	0/1787	0.96	8/2408 (0.3%)
30	H	0.32	0/1651	0.86	5/2225 (0.2%)
31	I	0.29	0/1665	0.96	7/2227 (0.3%)
32	J	0.33	0/1169	0.97	5/1573 (0.3%)
33	K	0.31	0/843	0.97	5/1140 (0.4%)
34	L	0.29	0/1195	0.97	5/1602 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.30	0/989	0.94	6/1326 (0.5%)
36	N	0.31	0/1034	0.96	3/1375 (0.2%)
37	O	0.32	0/796	0.92	3/1077 (0.3%)
38	P	0.33	0/885	1.07	10/1195 (0.8%)
39	Q	0.31	0/969	1.06	6/1300 (0.5%)
40	R	0.30	0/892	0.97	5/1193 (0.4%)
41	S	0.29	0/817	1.00	3/1088 (0.3%)
42	T	0.30	0/722	1.01	4/964 (0.4%)
43	U	0.32	0/659	0.87	1/884 (0.1%)
44	V	0.30	0/657	0.82	1/881 (0.1%)
45	W	0.31	0/544	0.95	3/731 (0.4%)
46	X	0.33	0/652	0.86	0/877
47	Y	0.29	0/671	0.95	3/888 (0.3%)
48	Z	0.34	0/550	1.10	6/728 (0.8%)
49	a	0.33	0/1033	1.00	11/1387 (0.8%)
50	3	0.41	0/36963	0.46	1/57662 (0.0%)
51	1	0.40	0/69796	0.47	1/108888 (0.0%)
52	2	0.42	0/2872	0.46	0/4479
53	5	0.42	0/1738	0.46	0/2709
54	4	0.39	0/493	0.49	0/769
55	8	0.30	0/2900	1.00	25/3908 (0.6%)
All	All	0.38	0/160361	0.62	195/239508 (0.1%)

There are no bond length outliers.

The worst 5 of 195 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	P	99	LEU	N-CA-C	-9.30	102.07	113.41
39	Q	109	ARG	N-CA-C	-8.90	95.25	109.59
42	T	43	ALA	N-CA-C	-8.80	101.61	111.82
10	m	60	GLN	N-CA-C	8.69	121.53	110.24
48	Z	17	ARG	N-CA-C	-8.67	100.10	113.02

There are no chirality outliers.

There are no planarity outliers.

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	b	2082	0	2157	106	0
2	c	1565	0	1616	85	0
3	d	1552	0	1619	91	0
4	e	1410	0	1447	101	0
5	f	1323	0	1374	83	0
6	g	1111	0	1148	86	0
7	j	1129	0	1162	52	0
8	k	938	0	1012	39	0
9	l	1045	0	1117	52	0
10	m	1074	0	1157	62	0
11	n	960	0	1000	36	0
12	o	892	0	923	52	0
13	p	917	0	965	61	0
14	q	947	0	1022	49	0
15	r	816	0	839	54	0
16	s	857	0	922	39	0
17	t	738	0	807	37	0
18	u	779	0	834	38	0
19	v	753	0	780	33	0
20	w	575	0	592	19	0
21	x	625	0	655	29	0
22	y	509	0	543	19	0
23	z	449	0	491	14	0
24	B	444	0	461	23	0
25	C	409	0	440	23	0
26	D	377	0	418	17	0
27	E	504	0	574	28	0
28	F	302	0	343	18	0
29	G	1756	0	1787	102	0
30	H	1624	0	1699	96	0
31	I	1643	0	1710	102	0
32	J	1156	0	1199	80	0
33	K	824	0	815	77	0
34	L	1181	0	1240	79	0
35	M	979	0	1034	58	0
36	N	1022	0	1070	86	0
37	O	786	0	828	59	0
38	P	869	0	878	71	0
39	Q	955	0	1019	75	0
40	R	883	0	944	66	0
41	S	805	0	847	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	T	714	0	737	34	0
43	U	649	0	666	48	0
44	V	648	0	691	35	0
45	W	535	0	552	25	0
46	X	637	0	665	54	0
47	Y	665	0	714	39	0
48	Z	544	0	579	47	0
49	a	1026	0	1092	60	0
50	3	33012	0	16618	617	0
51	1	62317	0	31346	1008	0
52	2	2568	0	1303	66	0
53	5	1556	0	793	20	0
54	4	437	0	219	12	0
55	8	2860	0	2758	168	0
All	All	147733	0	100221	3994	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 16.

The worst 5 of 3994 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:J:55:VAL:HG23	32:J:56:PRO:HD3	1.24	1.13
51:1:2800:A:H3'	51:1:2801:G:H5'	1.36	1.06
34:L:111:GLY:HA2	34:L:118:ARG:HD3	1.33	1.04
51:1:1645:G:H5''	51:1:1646:C:H5'	1.35	1.03
51:1:2747:G:H2'	51:1:2748:A:H5''	1.41	1.01

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	b	269/273 (98%)	223 (83%)	44 (16%)	2 (1%)	18	53
2	c	207/209 (99%)	183 (88%)	22 (11%)	2 (1%)	12	45
3	d	199/201 (99%)	162 (81%)	34 (17%)	3 (2%)	8	37
4	e	175/179 (98%)	132 (75%)	40 (23%)	3 (2%)	7	35
5	f	174/177 (98%)	152 (87%)	21 (12%)	1 (1%)	21	55
6	g	147/149 (99%)	121 (82%)	22 (15%)	4 (3%)	4	28
7	j	140/142 (99%)	130 (93%)	9 (6%)	1 (1%)	18	53
8	k	120/123 (98%)	106 (88%)	12 (10%)	2 (2%)	7	35
9	l	141/144 (98%)	118 (84%)	22 (16%)	1 (1%)	18	53
10	m	134/136 (98%)	110 (82%)	19 (14%)	5 (4%)	2	22
11	n	118/127 (93%)	105 (89%)	10 (8%)	3 (2%)	4	29
12	o	114/117 (97%)	108 (95%)	5 (4%)	1 (1%)	14	47
13	p	112/115 (97%)	97 (87%)	13 (12%)	2 (2%)	6	34
14	q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
15	r	101/103 (98%)	80 (79%)	18 (18%)	3 (3%)	3	26
16	s	108/110 (98%)	99 (92%)	6 (6%)	3 (3%)	4	27
17	t	91/100 (91%)	80 (88%)	10 (11%)	1 (1%)	11	43
18	u	100/104 (96%)	80 (80%)	18 (18%)	2 (2%)	6	32
19	v	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
20	w	73/85 (86%)	61 (84%)	11 (15%)	1 (1%)	9	38
21	x	75/78 (96%)	70 (93%)	4 (5%)	1 (1%)	9	40
22	y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
23	z	56/59 (95%)	51 (91%)	4 (7%)	1 (2%)	6	34
24	B	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
25	C	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
26	D	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2	19
27	E	62/65 (95%)	55 (89%)	6 (10%)	1 (2%)	7	36
28	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	27
29	G	223/241 (92%)	189 (85%)	29 (13%)	5 (2%)	5	31
30	H	204/233 (88%)	178 (87%)	25 (12%)	1 (0%)	24	59
31	I	203/206 (98%)	169 (83%)	28 (14%)	6 (3%)	3	26
32	J	155/167 (93%)	136 (88%)	16 (10%)	3 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	K	99/131 (76%)	81 (82%)	13 (13%)	5 (5%)	1	17
34	L	149/156 (96%)	131 (88%)	18 (12%)	0	100	100
35	M	127/130 (98%)	110 (87%)	15 (12%)	2 (2%)	7	36
36	N	125/130 (96%)	104 (83%)	17 (14%)	4 (3%)	3	25
37	O	96/103 (93%)	77 (80%)	17 (18%)	2 (2%)	5	31
38	P	114/129 (88%)	93 (82%)	21 (18%)	0	100	100
39	Q	121/124 (98%)	100 (83%)	18 (15%)	3 (2%)	4	29
40	R	112/118 (95%)	101 (90%)	10 (9%)	1 (1%)	14	47
41	S	98/101 (97%)	83 (85%)	14 (14%)	1 (1%)	12	45
42	T	86/89 (97%)	75 (87%)	9 (10%)	2 (2%)	5	30
43	U	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
44	V	78/84 (93%)	67 (86%)	10 (13%)	1 (1%)	9	40
45	W	63/75 (84%)	56 (89%)	7 (11%)	0	100	100
46	X	77/92 (84%)	66 (86%)	10 (13%)	1 (1%)	9	40
47	Y	83/87 (95%)	75 (90%)	7 (8%)	1 (1%)	10	41
48	Z	63/71 (89%)	42 (67%)	16 (25%)	5 (8%)	1	11
49	a	130/234 (56%)	117 (90%)	13 (10%)	0	100	100
55	8	359/371 (97%)	313 (87%)	42 (12%)	4 (1%)	11	43
All	All	6011/6421 (94%)	5172 (86%)	746 (12%)	93 (2%)	11	37

5 of 93 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	9	GLN
3	d	83	VAL
6	g	9	VAL
6	g	11	ASN
15	r	55	ASP

5.3.2 Protein sidechains [i](#)

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	b	216/218 (99%)	215 (100%)	1 (0%)	81	82
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	163 (99%)	2 (1%)	63	72
4	e	148/150 (99%)	147 (99%)	1 (1%)	76	78
5	f	137/138 (99%)	136 (99%)	1 (1%)	76	78
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	75
7	j	116/116 (100%)	116 (100%)	0	100	100
8	k	103/104 (99%)	103 (100%)	0	100	100
9	l	102/103 (99%)	101 (99%)	1 (1%)	68	75
10	m	109/109 (100%)	109 (100%)	0	100	100
11	n	100/104 (96%)	100 (100%)	0	100	100
12	o	86/87 (99%)	85 (99%)	1 (1%)	63	72
13	p	99/100 (99%)	94 (95%)	5 (5%)	21	46
14	q	89/90 (99%)	89 (100%)	0	100	100
15	r	84/84 (100%)	84 (100%)	0	100	100
16	s	93/93 (100%)	93 (100%)	0	100	100
17	t	80/84 (95%)	79 (99%)	1 (1%)	61	71
18	u	83/85 (98%)	83 (100%)	0	100	100
19	v	78/78 (100%)	78 (100%)	0	100	100
20	w	57/63 (90%)	57 (100%)	0	100	100
21	x	67/68 (98%)	67 (100%)	0	100	100
22	y	55/55 (100%)	55 (100%)	0	100	100
23	z	48/49 (98%)	48 (100%)	0	100	100
24	B	47/48 (98%)	47 (100%)	0	100	100
25	C	45/49 (92%)	45 (100%)	0	100	100
26	D	38/38 (100%)	38 (100%)	0	100	100
27	E	51/52 (98%)	51 (100%)	0	100	100
28	F	34/34 (100%)	34 (100%)	0	100	100
29	G	186/199 (94%)	186 (100%)	0	100	100
30	H	170/190 (90%)	170 (100%)	0	100	100
31	I	172/173 (99%)	169 (98%)	3 (2%)	53	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	J	119/126 (94%)	117 (98%)	2 (2%)	53	68
33	K	88/112 (79%)	86 (98%)	2 (2%)	44	63
34	L	124/129 (96%)	123 (99%)	1 (1%)	73	77
35	M	104/105 (99%)	103 (99%)	1 (1%)	68	75
36	N	105/107 (98%)	105 (100%)	0	100	100
37	O	86/90 (96%)	84 (98%)	2 (2%)	44	63
38	P	89/99 (90%)	88 (99%)	1 (1%)	65	74
39	Q	103/104 (99%)	103 (100%)	0	100	100
40	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
41	S	83/84 (99%)	82 (99%)	1 (1%)	63	72
42	T	76/77 (99%)	76 (100%)	0	100	100
43	U	65/65 (100%)	65 (100%)	0	100	100
44	V	74/78 (95%)	73 (99%)	1 (1%)	59	71
45	W	56/65 (86%)	56 (100%)	0	100	100
46	X	70/79 (89%)	69 (99%)	1 (1%)	59	71
47	Y	65/66 (98%)	65 (100%)	0	100	100
48	Z	55/61 (90%)	55 (100%)	0	100	100
49	a	110/181 (61%)	108 (98%)	2 (2%)	51	67
55	8	307/317 (97%)	304 (99%)	3 (1%)	68	75
All	All	5007/5245 (96%)	4972 (99%)	35 (1%)	73	78

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	V	37	ILE
46	X	14	LEU
55	8	4	ILE
13	p	113	LEU
13	p	109	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
42	T	27	GLN

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Mol	Chain	Res	Type
45	W	30	ASN
55	8	38	ASN
16	s	9	HIS
16	s	7	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	134 (8%)	2 (0%)
51	1	2902/2903 (99%)	377 (12%)	4 (0%)
52	2	119/120 (99%)	9 (7%)	1 (0%)
53	5	72/77 (93%)	7 (9%)	0
54	4	19/27 (70%)	4 (21%)	0
All	All	4650/4666 (99%)	531 (11%)	7 (0%)

5 of 531 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	31	G
50	3	32	A
50	3	39	G
50	3	48	C

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	1020	A
51	1	1738	G
52	2	88	C
51	1	2326	C
51	1	490	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

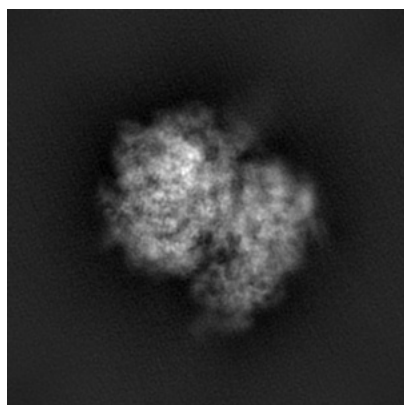
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20056. These allow visual inspection of the internal detail of the map and identification of artifacts.

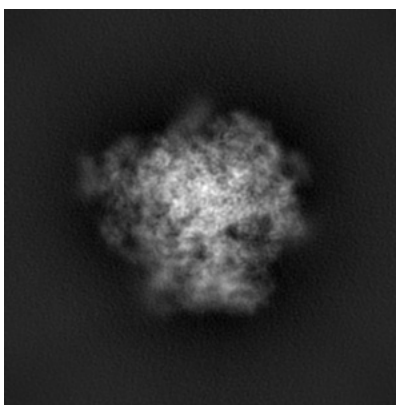
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

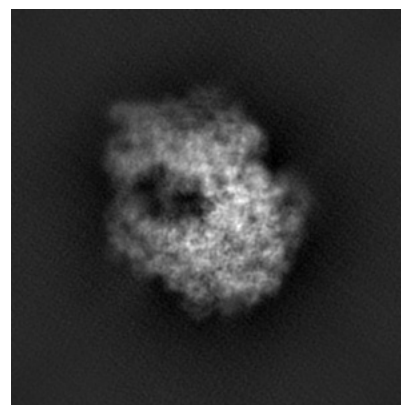
6.1.1 Primary map



X



Y

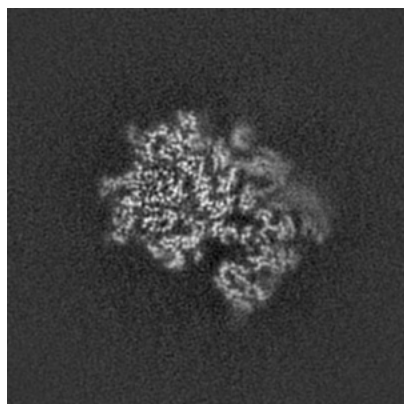


Z

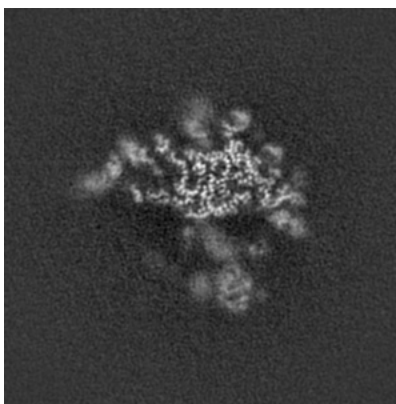
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

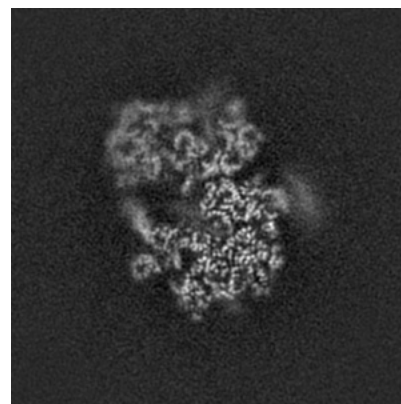
6.2.1 Primary map



X Index: 156



Y Index: 156

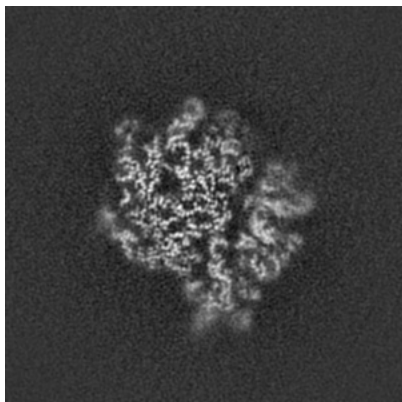


Z Index: 156

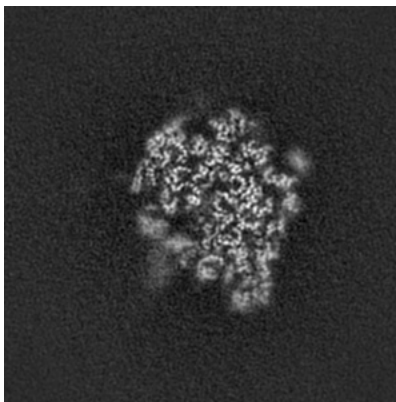
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

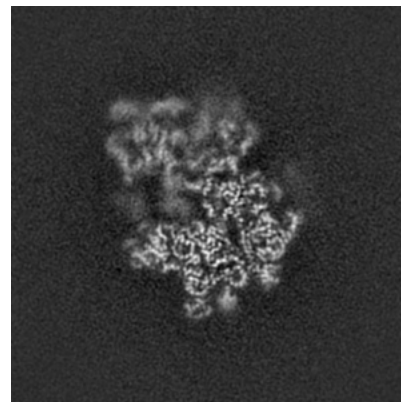
6.3.1 Primary map



X Index: 178



Y Index: 138

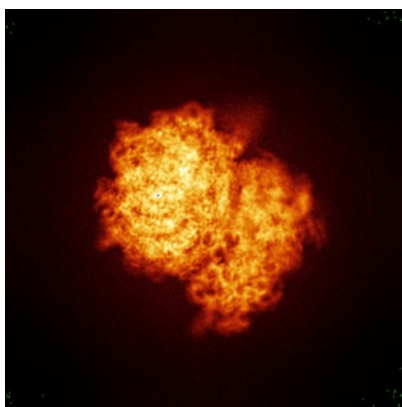


Z Index: 165

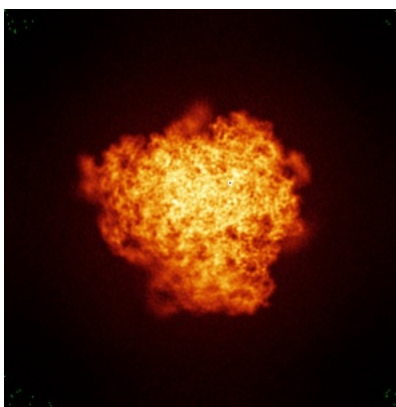
The images above show the largest variance slices of the map in three orthogonal directions.

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

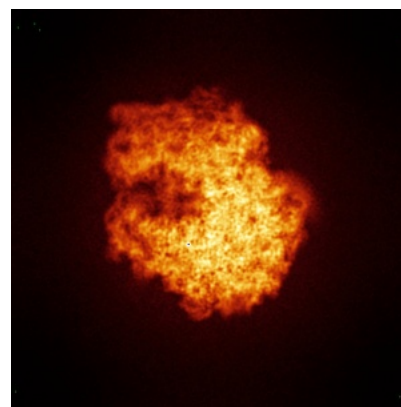
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

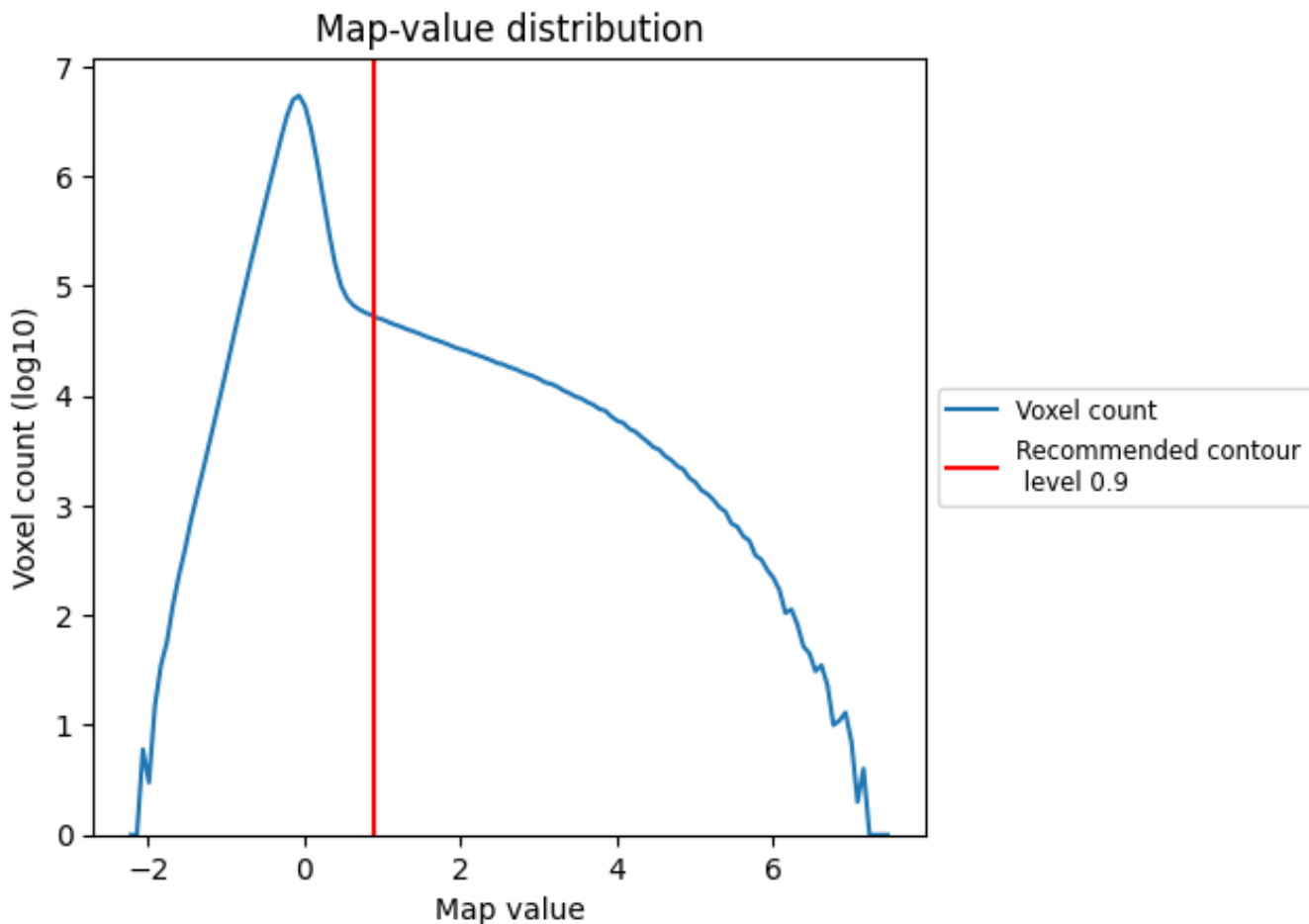
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

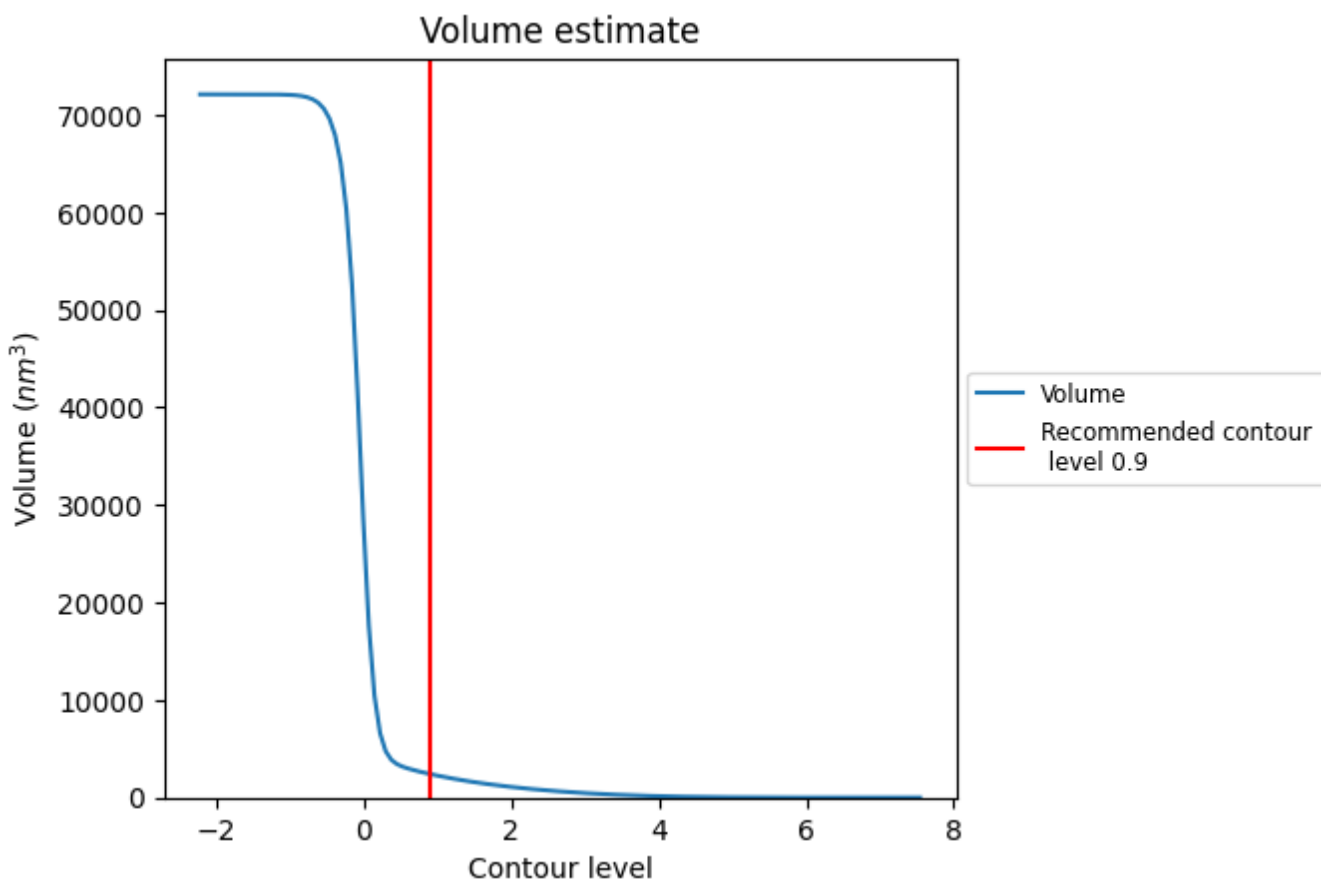
This section contains the results of statistical analysis of the map.

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.

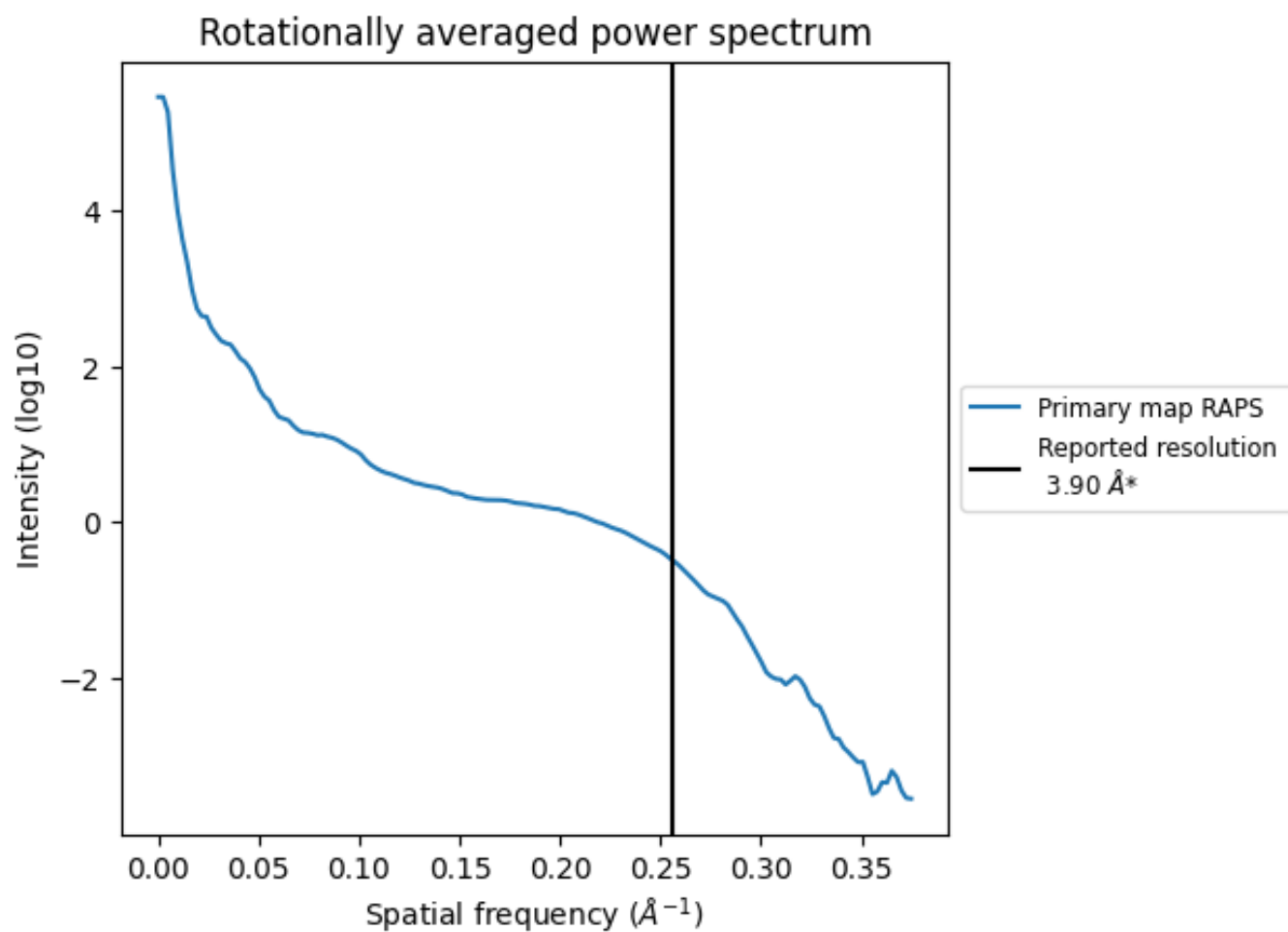
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2406 nm³; this corresponds to an approximate mass of 2174 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

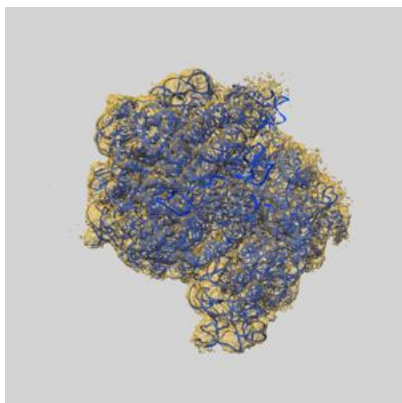
8 Fourier-Shell correlation

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

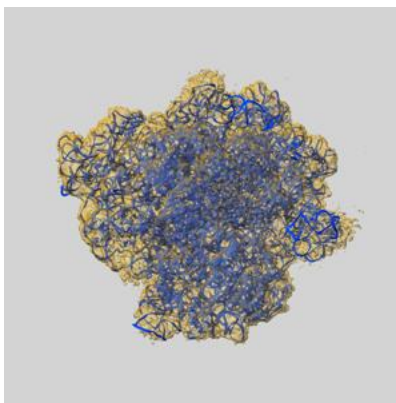
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20056 and PDB model 6OGF. Per-residue inclusion information can be found in section 3 on page 15.

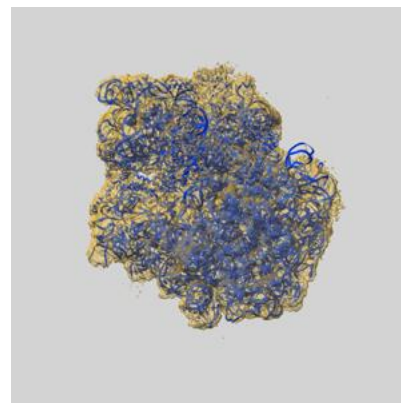
9.1 Map-model overlay [i](#)



X



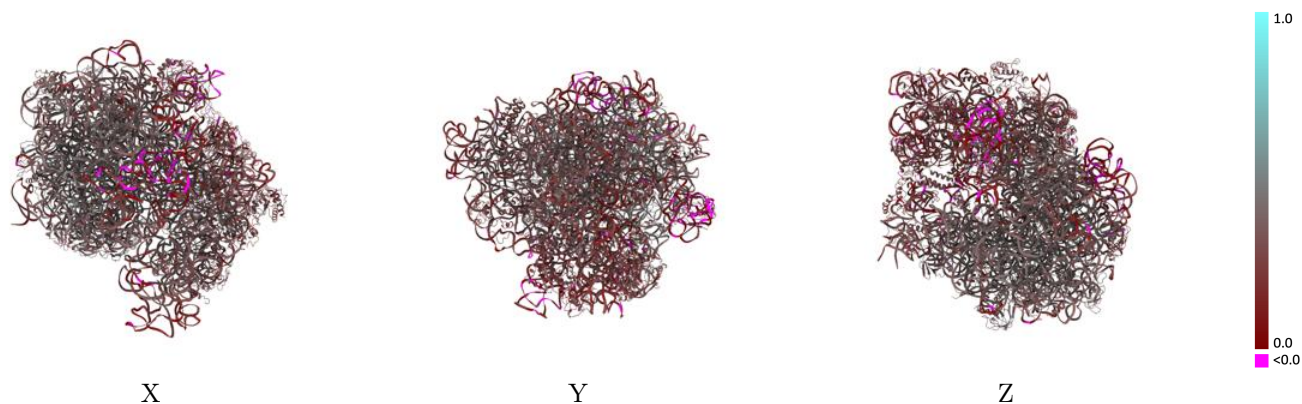
Y



Z

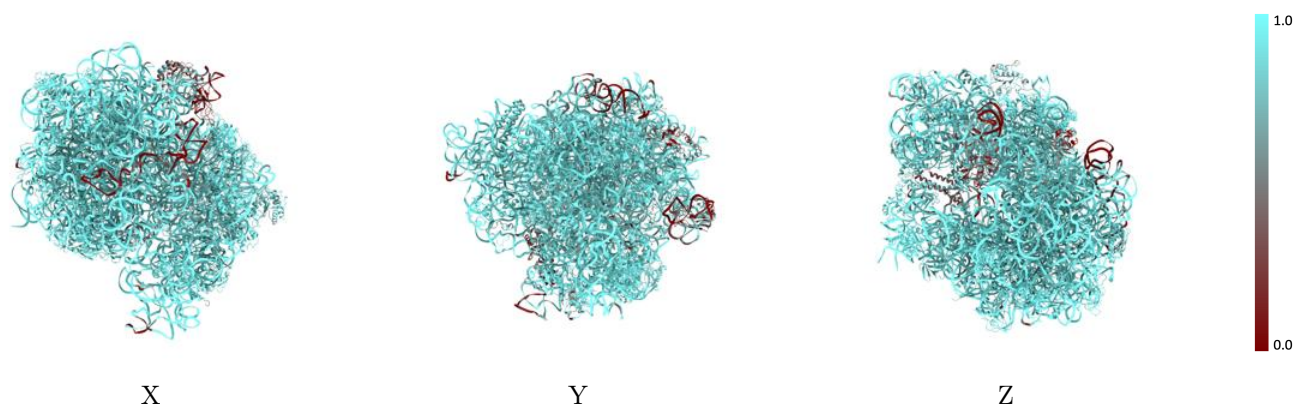
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



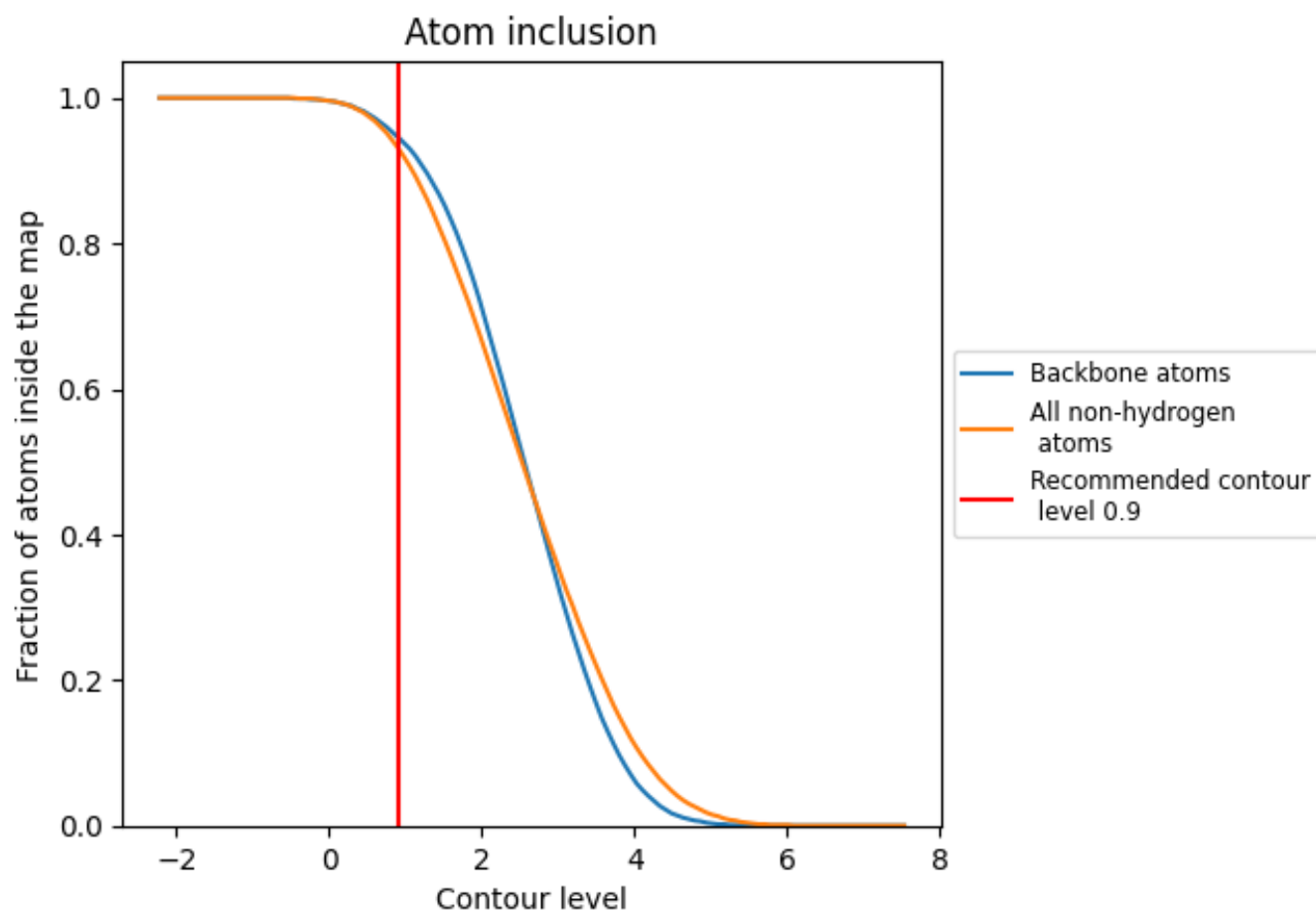
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.9).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9320	 0.3280
1	 0.9400	 0.3440
2	 0.9900	 0.3090
3	 0.9700	 0.2980
4	 0.9450	 0.2110
5	 0.7960	 0.1450
8	 0.6570	 0.2920
B	 0.9600	 0.4020
C	 0.9000	 0.3730
D	 0.9520	 0.4110
E	 0.9430	 0.4160
F	 0.9420	 0.3390
G	 0.8050	 0.2850
H	 0.9090	 0.2980
I	 0.8850	 0.2800
J	 0.9480	 0.3420
K	 0.9800	 0.2690
L	 0.9300	 0.2380
M	 0.9620	 0.3250
N	 0.9560	 0.2660
O	 0.8310	 0.2570
P	 0.9750	 0.2750
Q	 0.9340	 0.3640
R	 0.9340	 0.2510
S	 0.9410	 0.2740
T	 0.9740	 0.2750
U	 0.9440	 0.3720
V	 0.9530	 0.3550
W	 0.9510	 0.2860
X	 0.9490	 0.2570
Y	 0.9460	 0.3160
Z	 0.8670	 0.2450
a	 0.3680	 0.2010
b	 0.9570	 0.4090
c	 0.9680	 0.4190



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Chain	Atom inclusion	Q-score
d	 0.9470	 0.3850
e	 0.9460	 0.2600
f	 0.9040	 0.3010
g	 0.3860	 0.2880
j	 0.9660	 0.4090
k	 0.9420	 0.4210
l	 0.9630	 0.4090
m	 0.9590	 0.4010
n	 0.9710	 0.4170
o	 0.9680	 0.3410
p	 0.9550	 0.4000
q	 0.9590	 0.3940
r	 0.9590	 0.4140
s	 0.9350	 0.4190
t	 0.9430	 0.3960
u	 0.9570	 0.3800
v	 0.9590	 0.3710
w	 0.9520	 0.4140
x	 0.9550	 0.3860
y	 0.9210	 0.3230
z	 0.9340	 0.4070