



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:56 AM UTC

PDB ID : 7PIO / pdb_00007pio
EMDB ID : EMD-13445
Title : 70S ribosome with P-site tRNA in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.50 Å (reported)
Based on initial models : 7OOC, 4V7C, 7OOD

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:

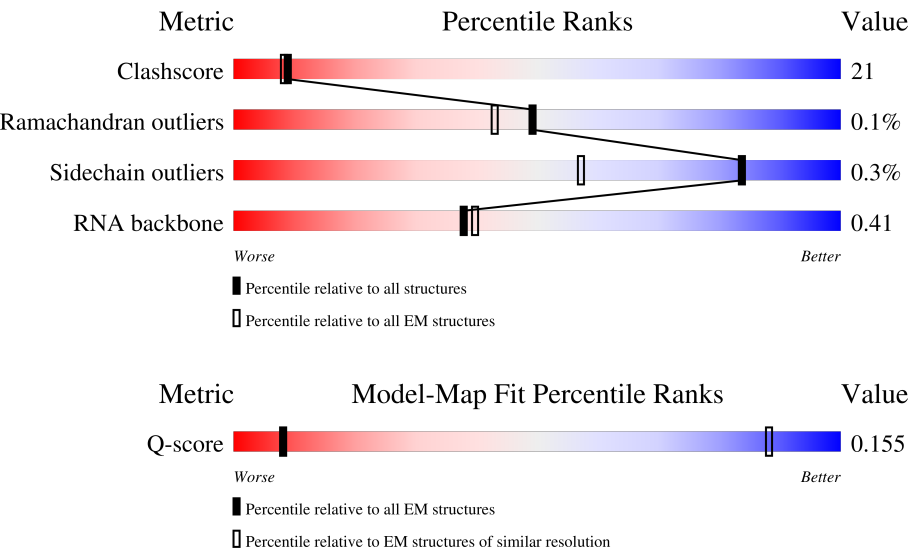
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.50 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	234 (9.00 - 10.00)

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	0	48	8% 46% 52% .
2	1	59	24% 51% 49%
3	2	37	19% 62% 38%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	7	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144502 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	145	Total	C	N	O	S	0
			1160	746	204	207	3	0

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	126	Total	C	N	O	S	0
			960	612	167	178	3	0

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	128	Total	C	N	O	S	0
			959	616	160	177	6	0

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	i	144	Total	C	N	O	S	0
			1164	737	213	209	5	0

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	j	122	Total	C	N	O	S	0
			944	595	178	167	4	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

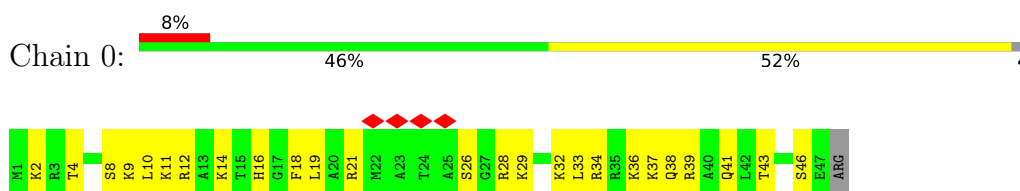
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

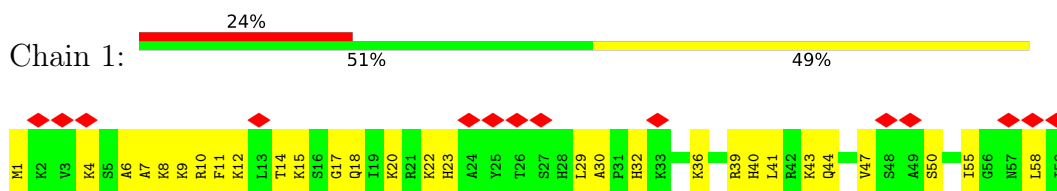
3 Residue-property plots [i](#)

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.

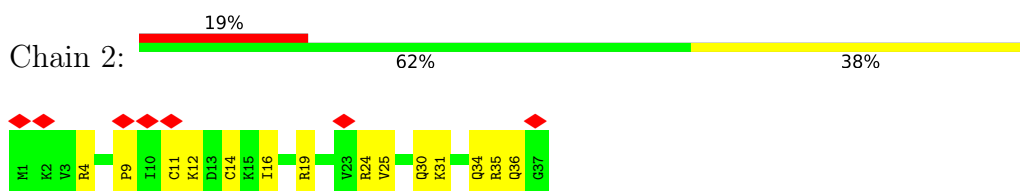
- Molecule 1: 50S ribosomal protein L34



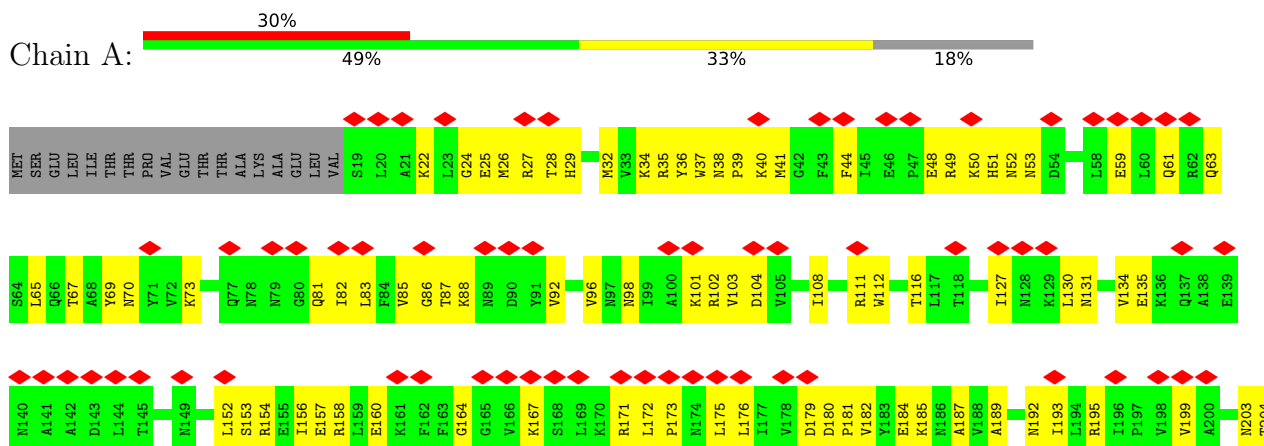
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

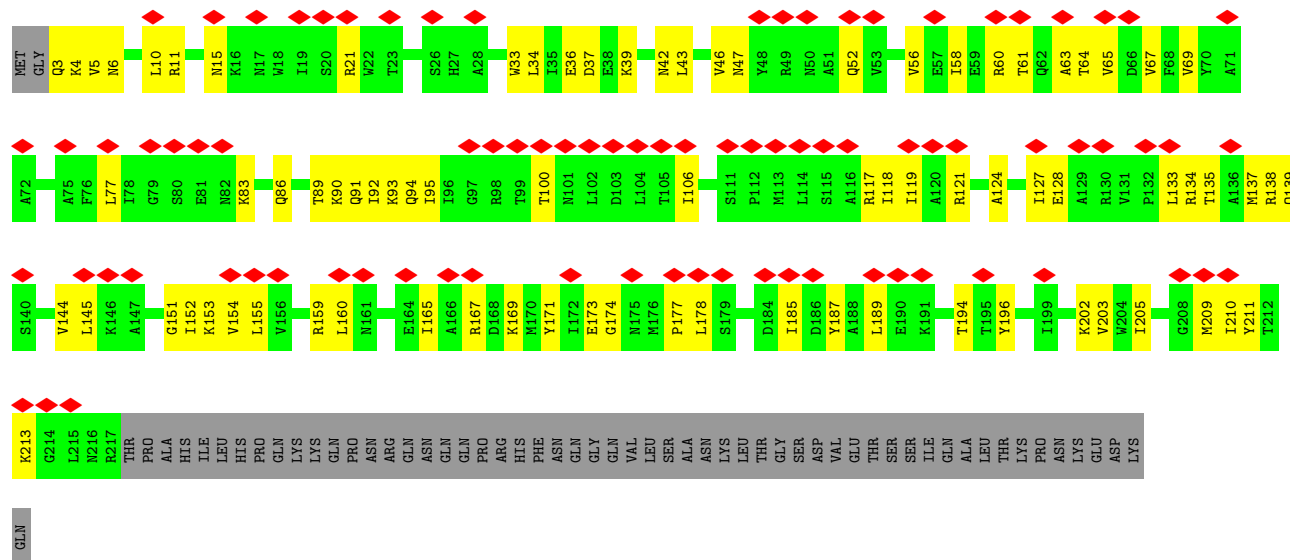


- Molecule 4: 30S ribosomal protein S2

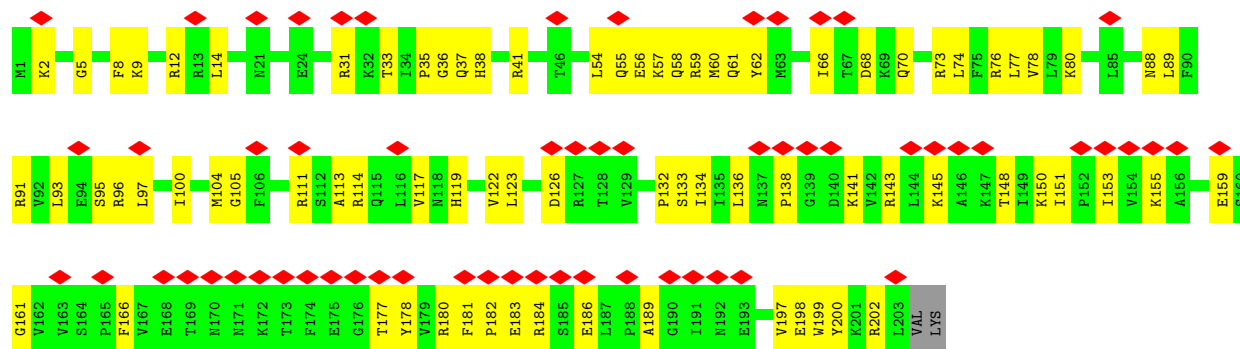




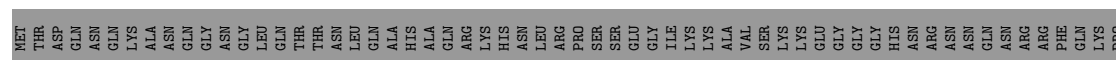
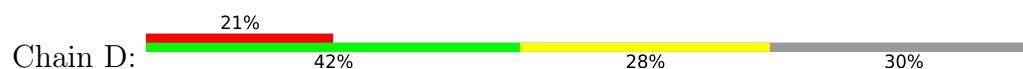
• Molecule 5: 30S ribosomal protein S3

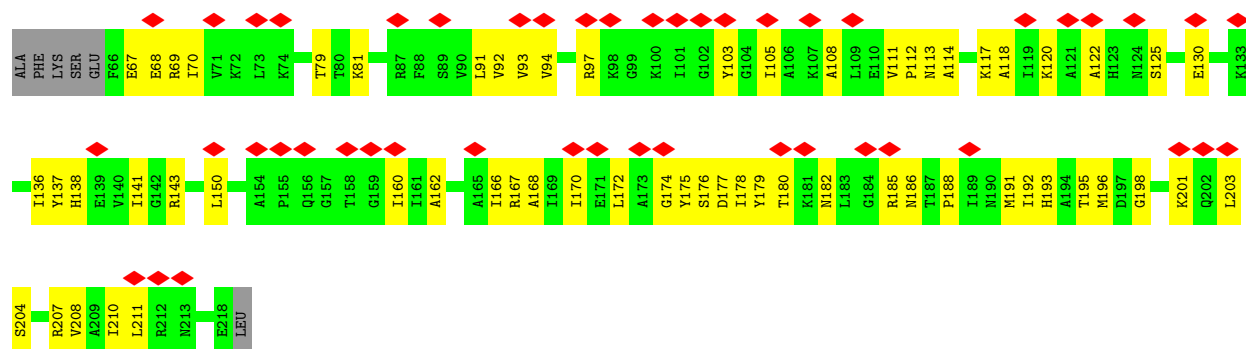


• Molecule 6: 30S ribosomal protein S4

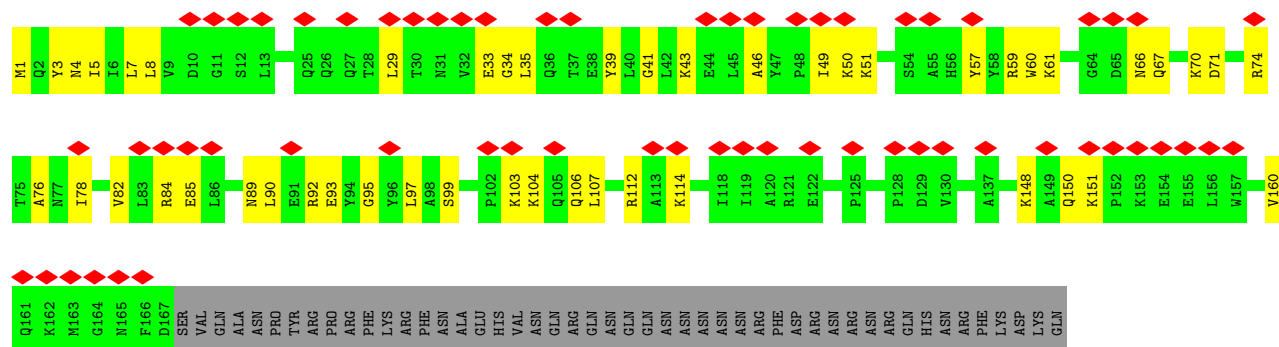


• Molecule 7: 30S ribosomal protein S5

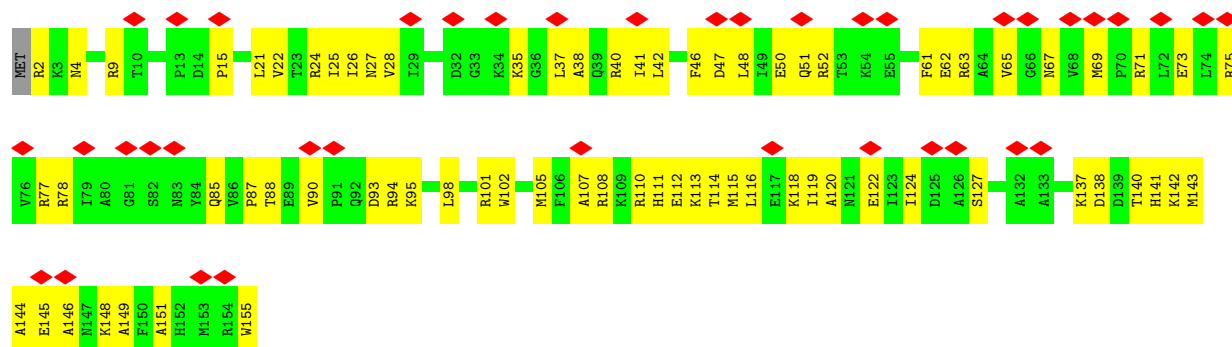




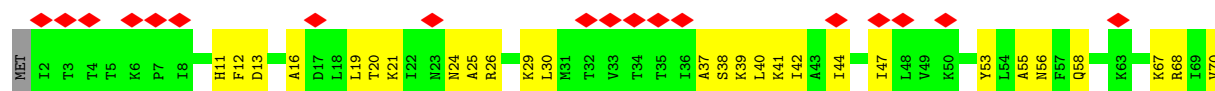
• Molecule 8: 30S ribosomal protein S6

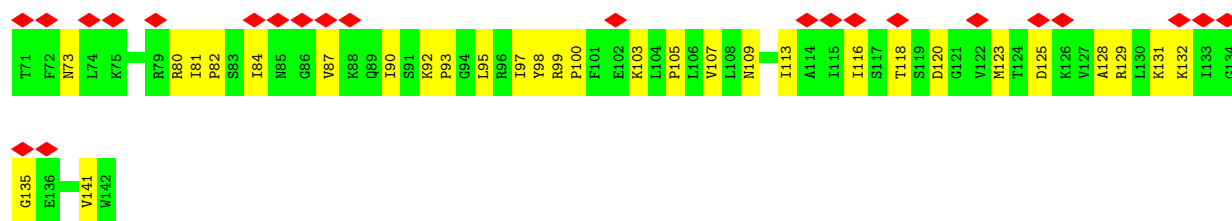


• Molecule 9: 30S ribosomal protein S7

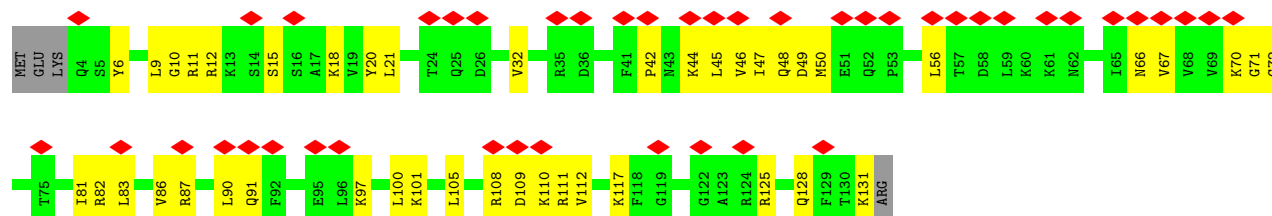


• Molecule 10: 30S ribosomal protein S8

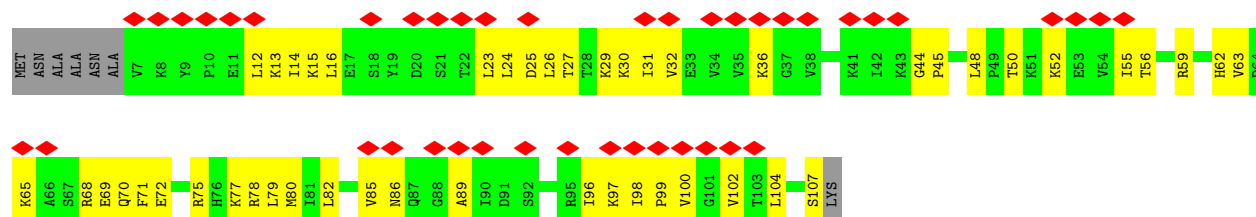
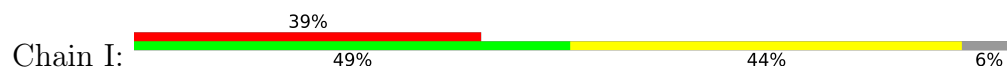




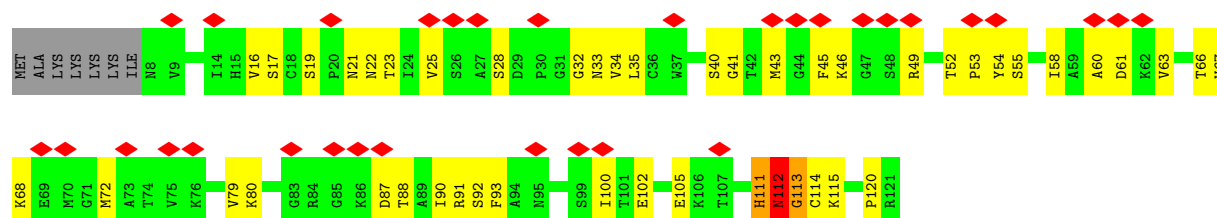
- Molecule 11: 30S ribosomal protein S9



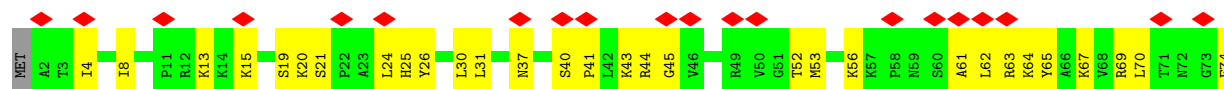
- Molecule 12: 30S ribosomal protein S10

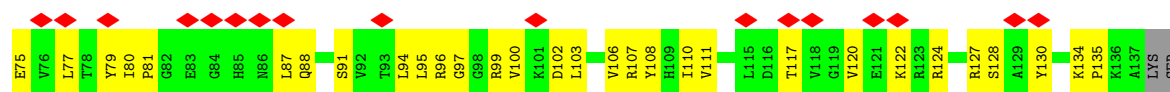


- Molecule 13: 30S ribosomal protein S11

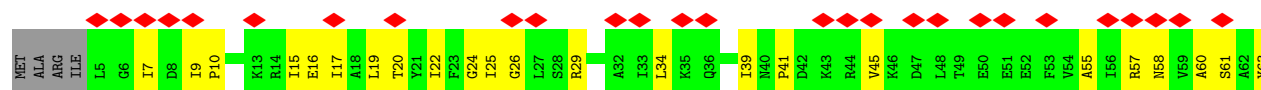


- Molecule 14: 30S ribosomal protein S12

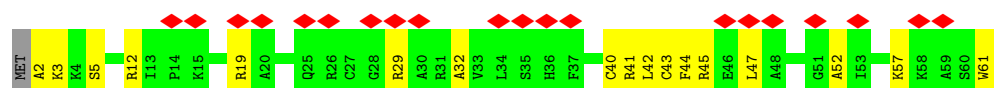




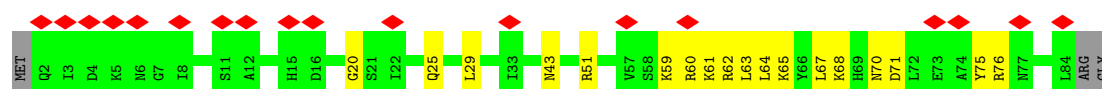
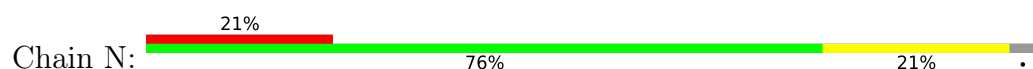
- Molecule 15: 30S ribosomal protein S13



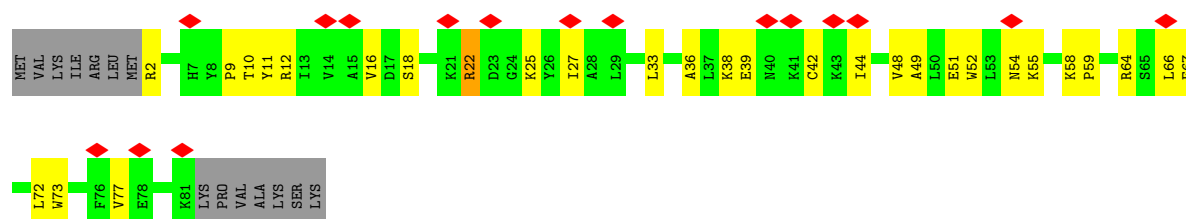
- Molecule 16: 30S ribosomal protein S14 type Z



- Molecule 17: 30S ribosomal protein S15



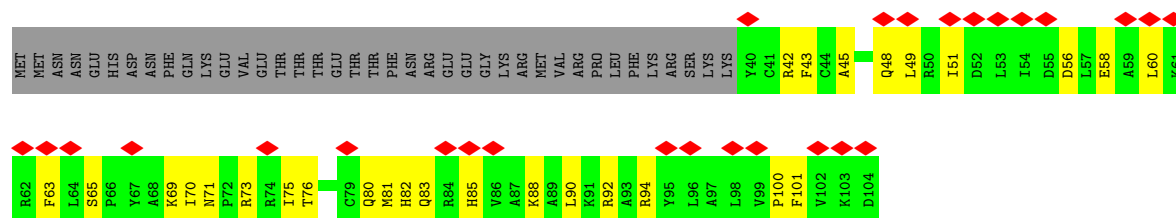
- Molecule 18: 30S ribosomal protein S16



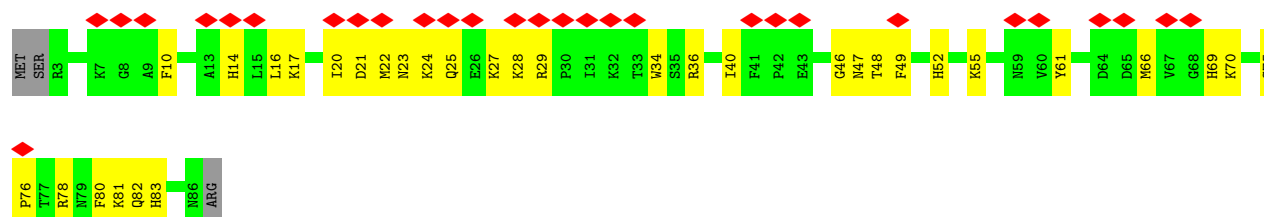
- Molecule 19: 30S ribosomal protein S17



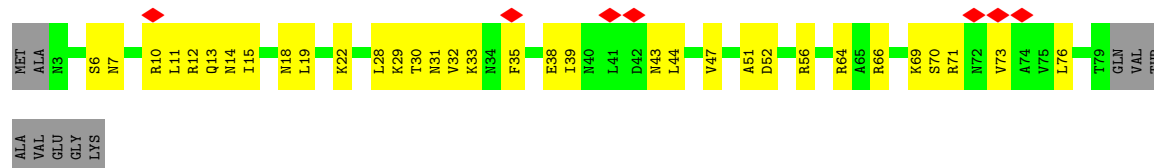
- Molecule 20: 30S ribosomal protein S18



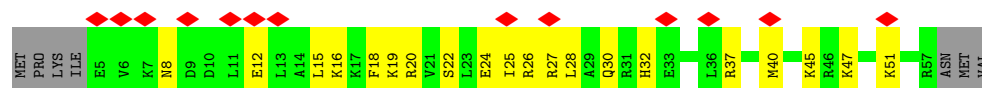
- Molecule 21: 30S ribosomal protein S19



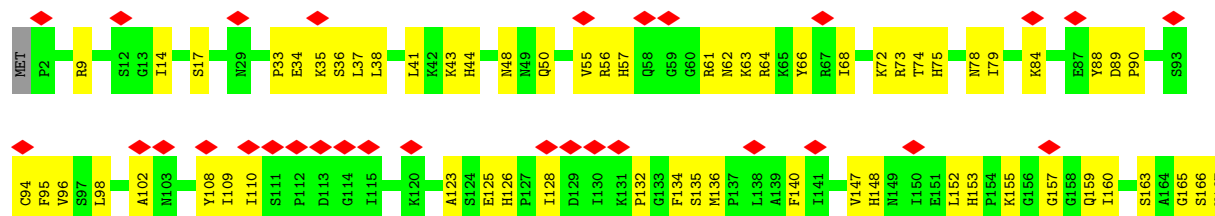
- Molecule 22: 30S ribosomal protein S20

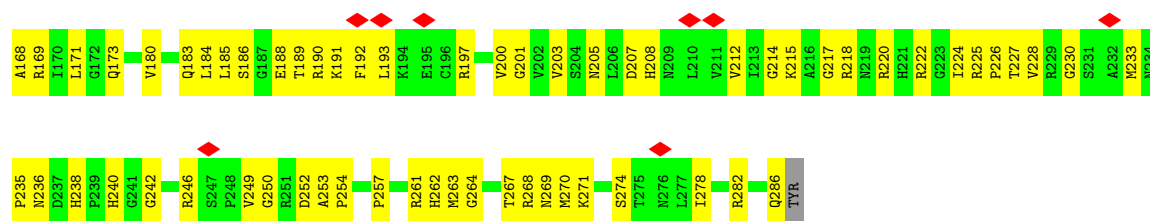


- Molecule 23: 30S ribosomal protein S21

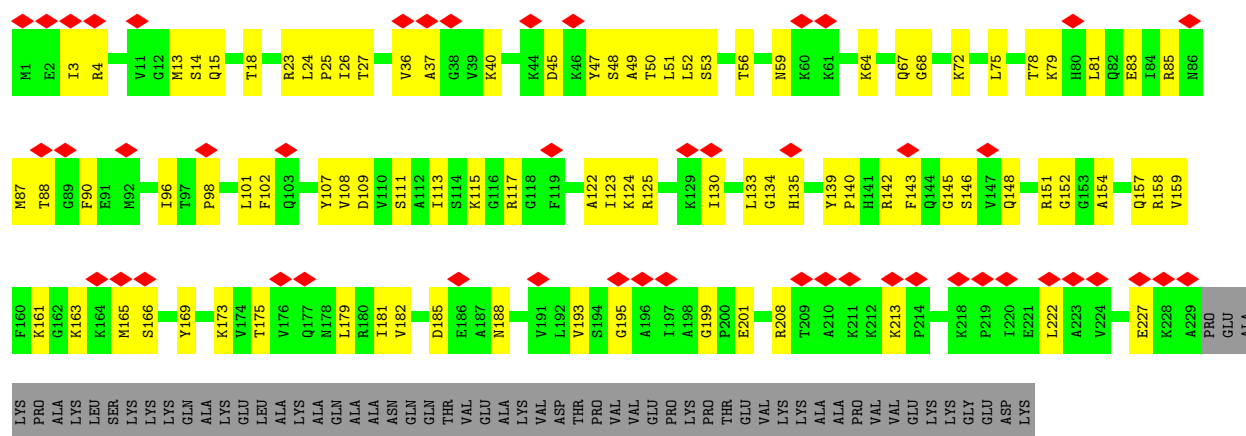


- Molecule 24: 50S ribosomal protein L2

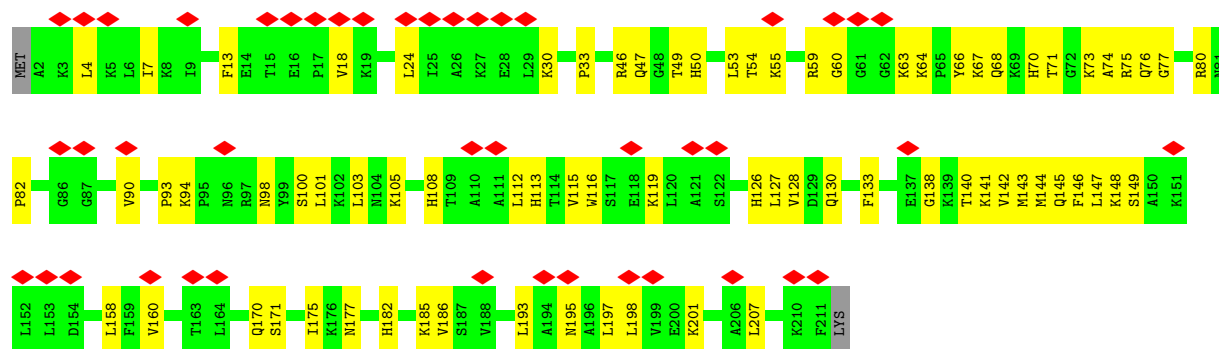




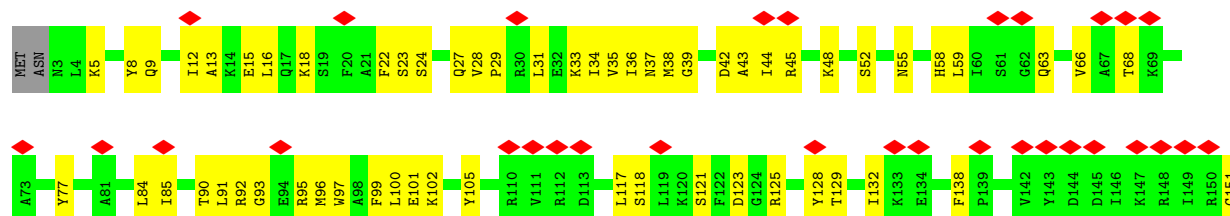
• Molecule 25: 50S ribosomal protein L3

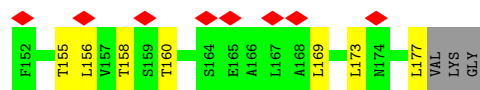


• Molecule 26: 50S ribosomal protein L4

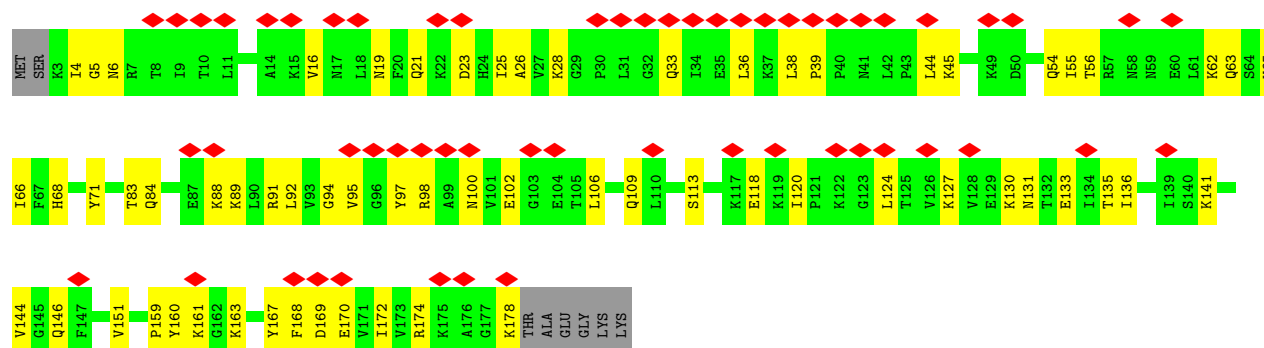


• Molecule 27: 50S ribosomal protein L5

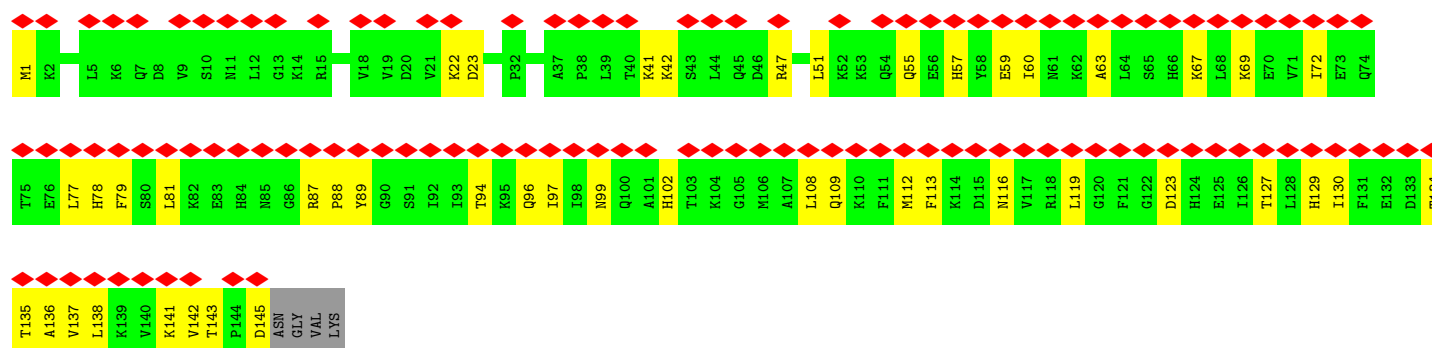
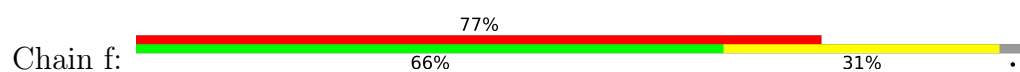




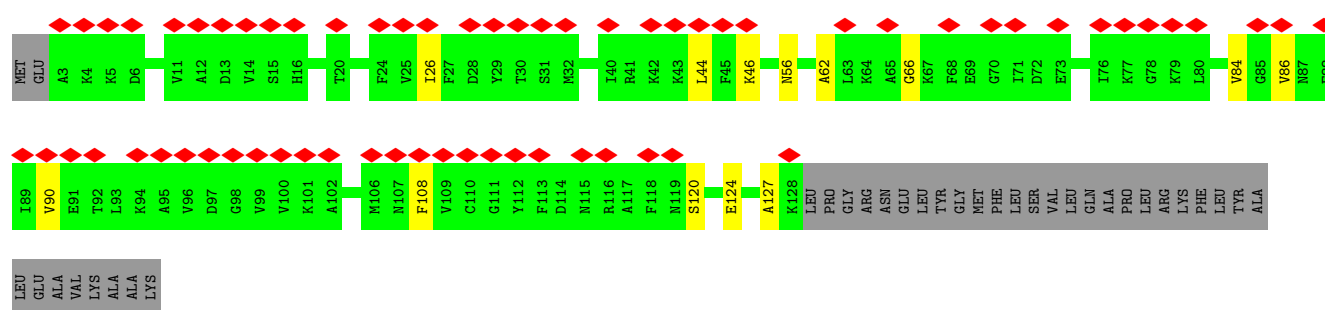
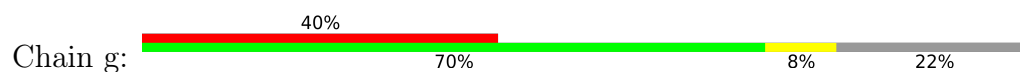
• Molecule 28: 50S ribosomal protein L6



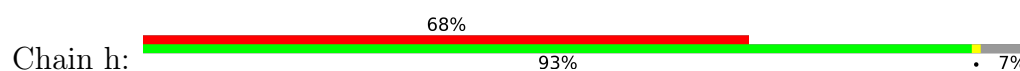
• Molecule 29: 50S ribosomal protein L9

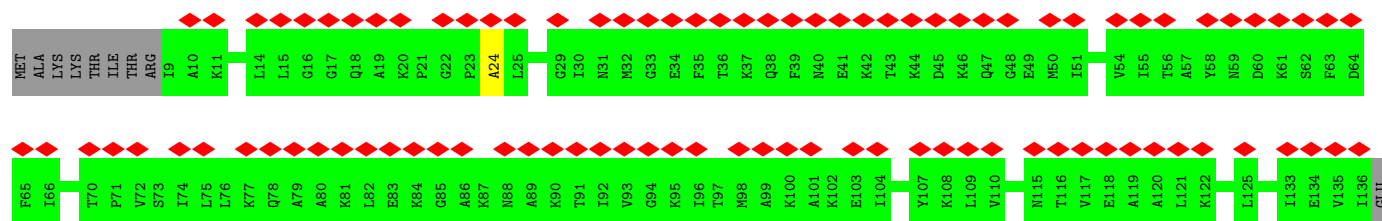


• Molecule 30: 50S ribosomal protein L10

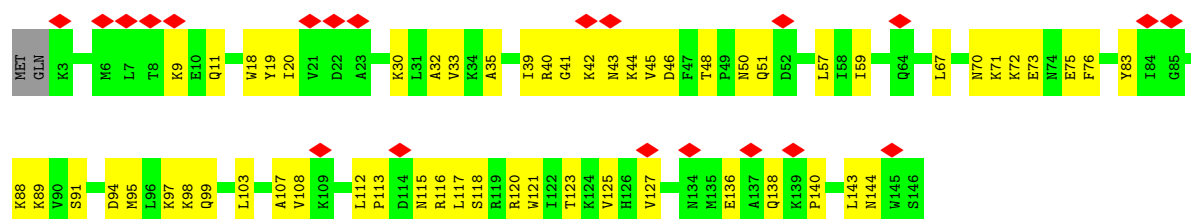


• Molecule 31: 50S ribosomal protein L11

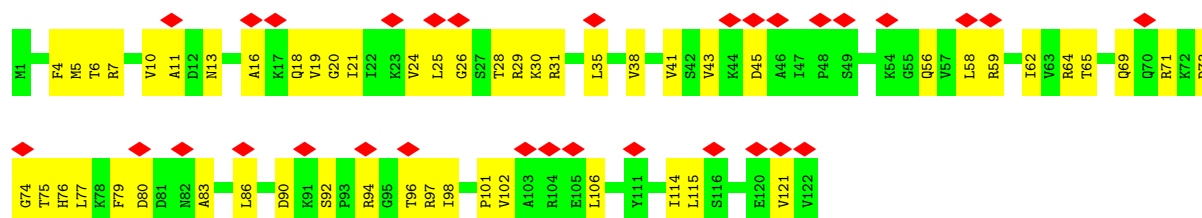




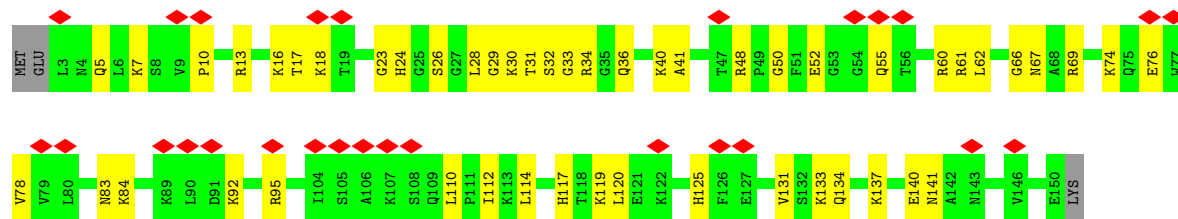
• Molecule 32: 50S ribosomal protein L13



• Molecule 33: 50S ribosomal protein L14

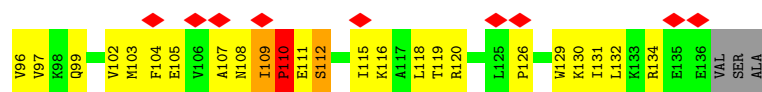


• Molecule 34: 50S ribosomal protein L15



• Molecule 35: 50S ribosomal protein L16

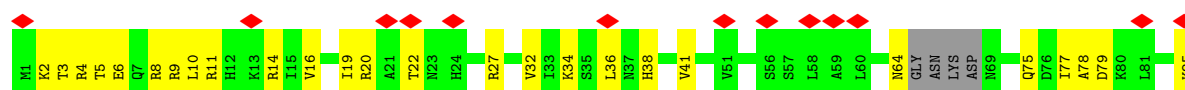




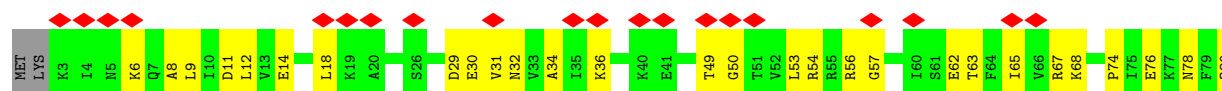
• Molecule 36: 50S ribosomal protein L17



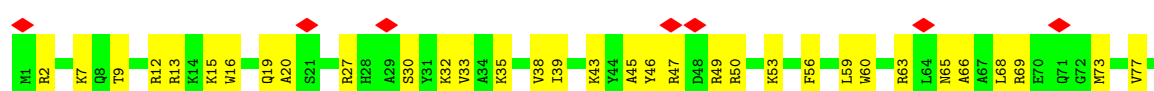
• Molecule 37: 50S ribosomal protein L18



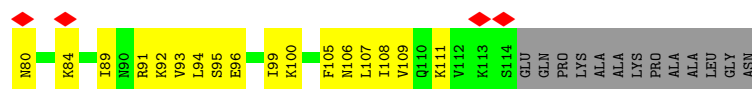
• Molecule 38: 50S ribosomal protein L19

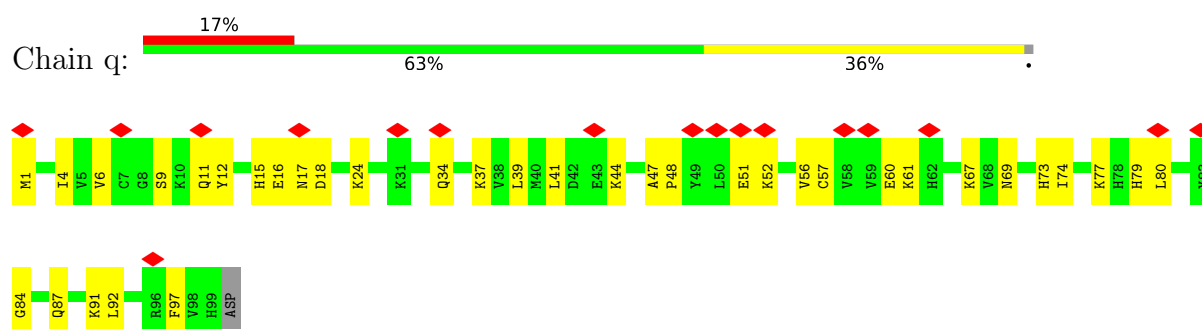


• Molecule 39: 50S ribosomal protein L20

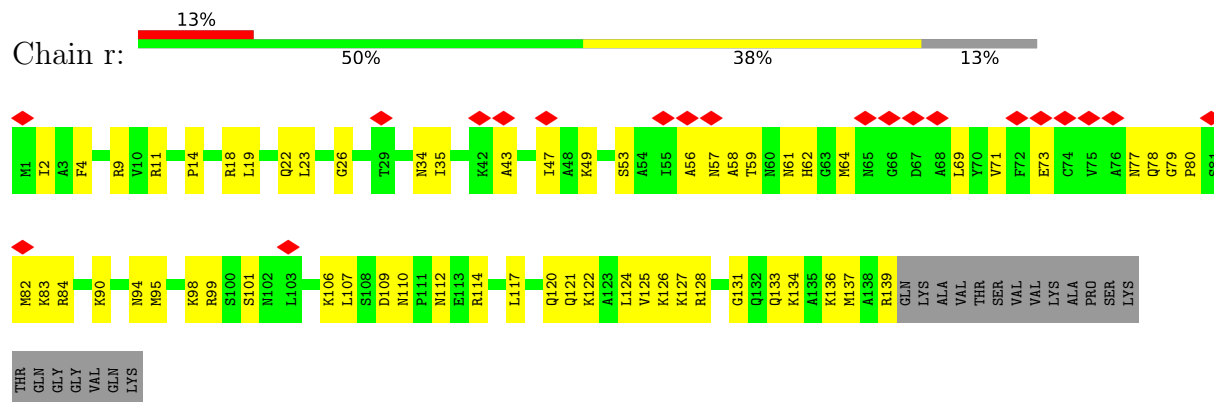


• Molecule 40: 50S ribosomal protein L21

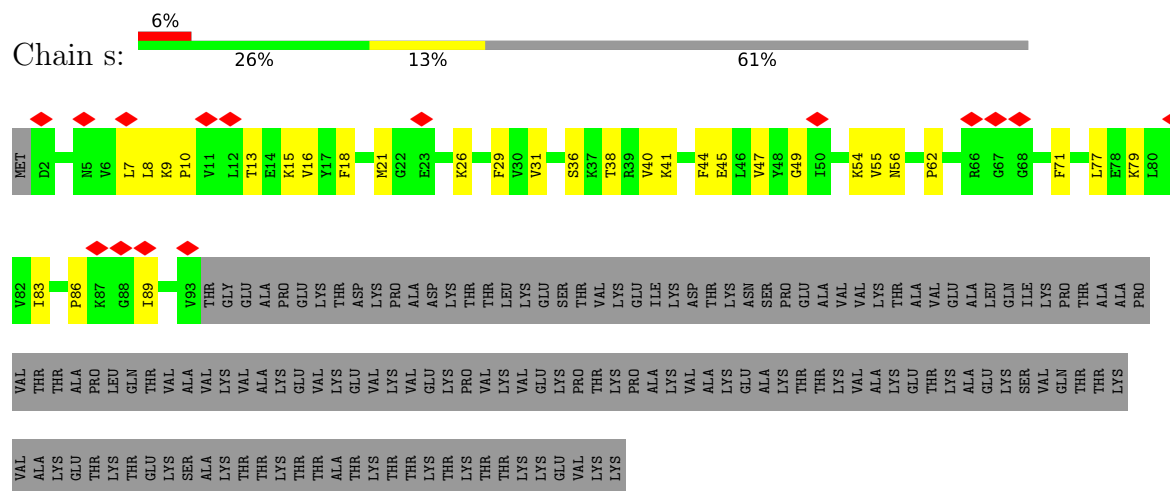




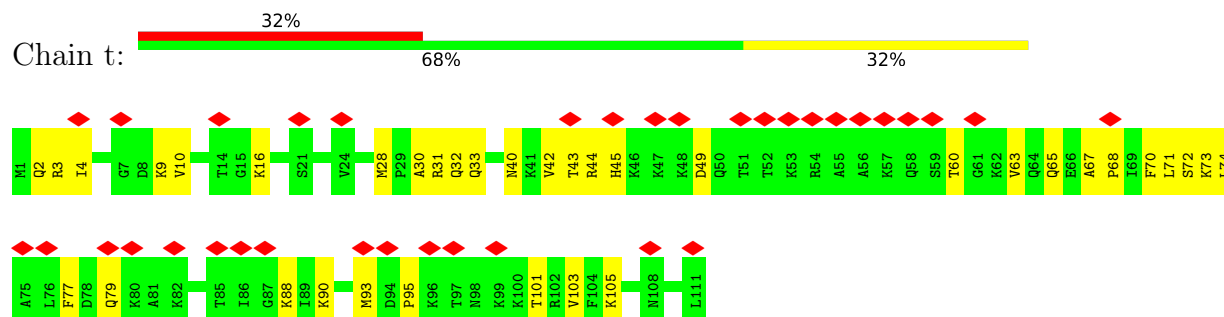
• Molecule 41: 50S ribosomal protein L22



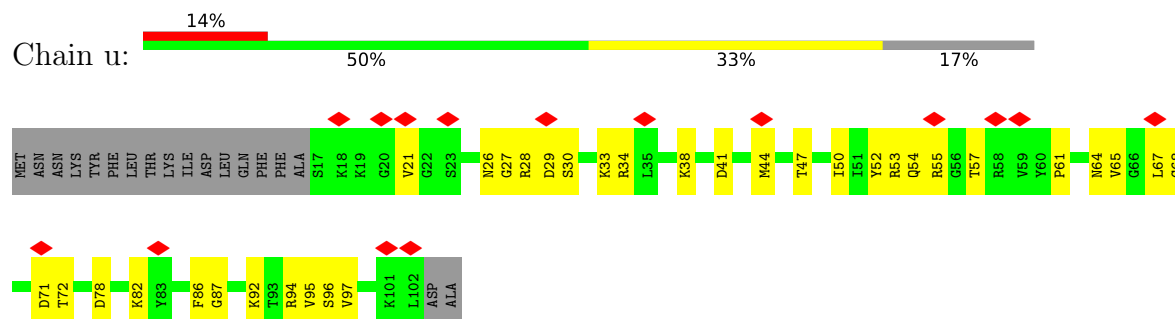
• Molecule 42: 50S ribosomal protein L23



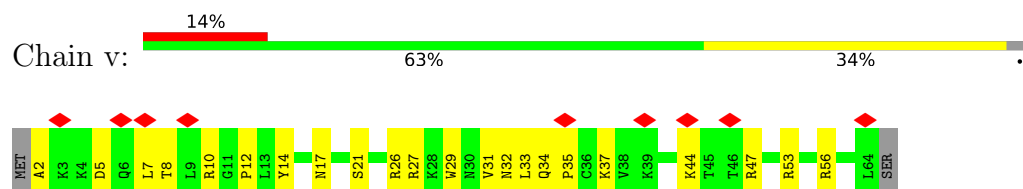
• Molecule 43: 50S ribosomal protein L24



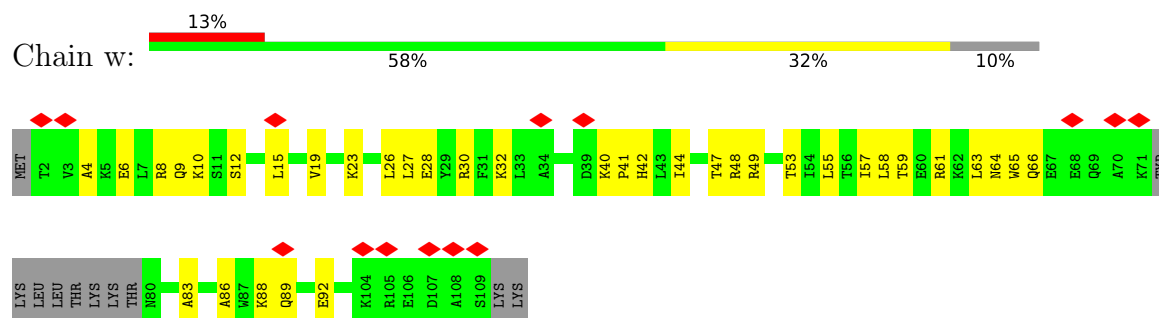
- Molecule 44: 50S ribosomal protein L27



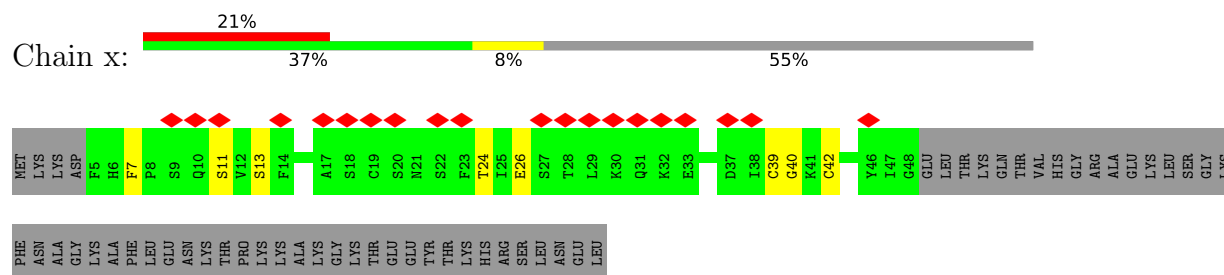
- Molecule 45: 50S ribosomal protein L28



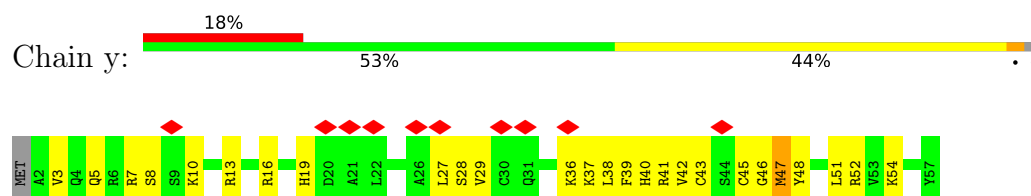
- Molecule 46: 50S ribosomal protein L29



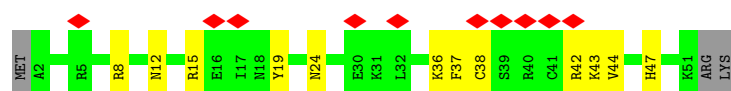
- Molecule 47: 50S ribosomal protein L31



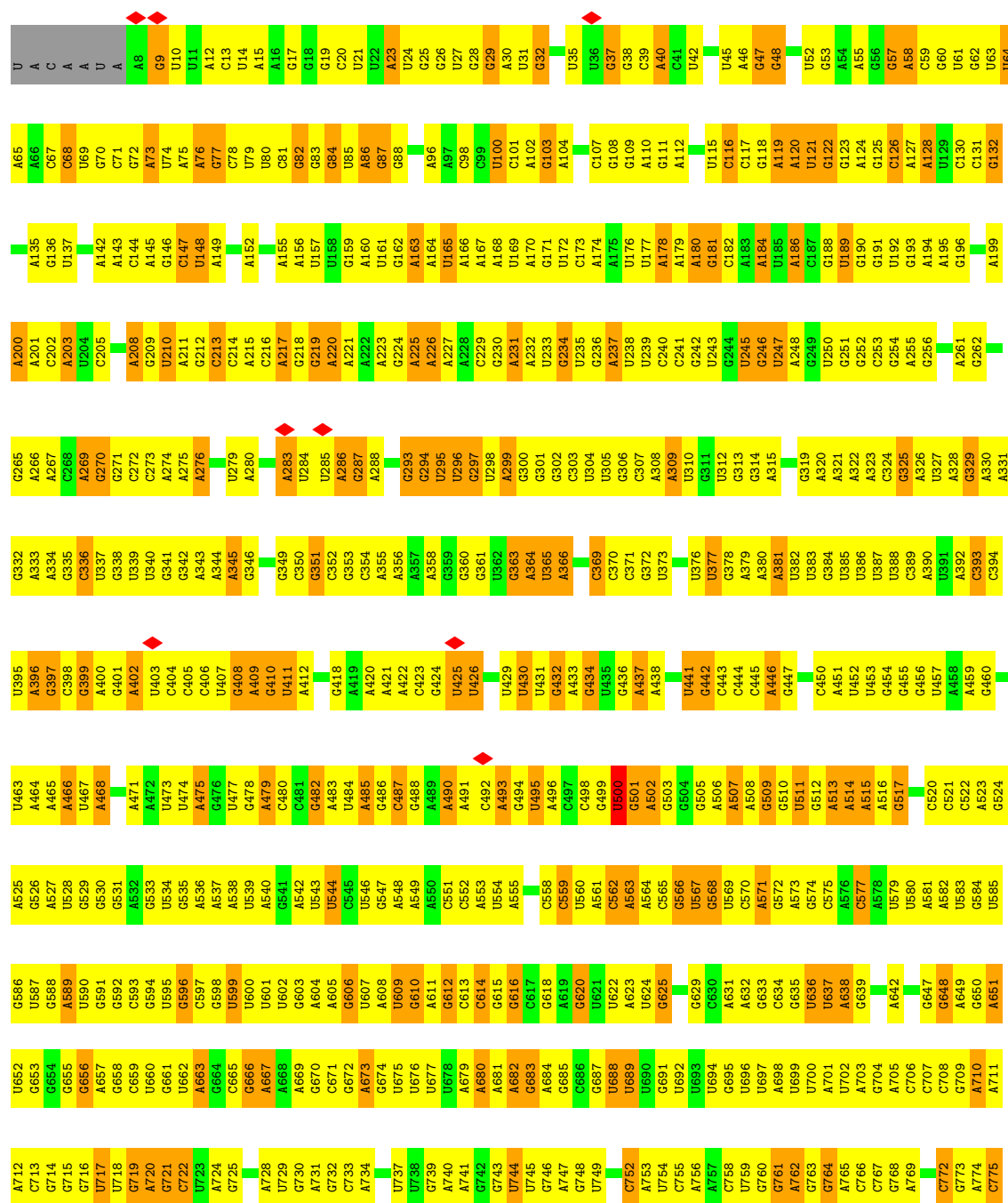
- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33 1

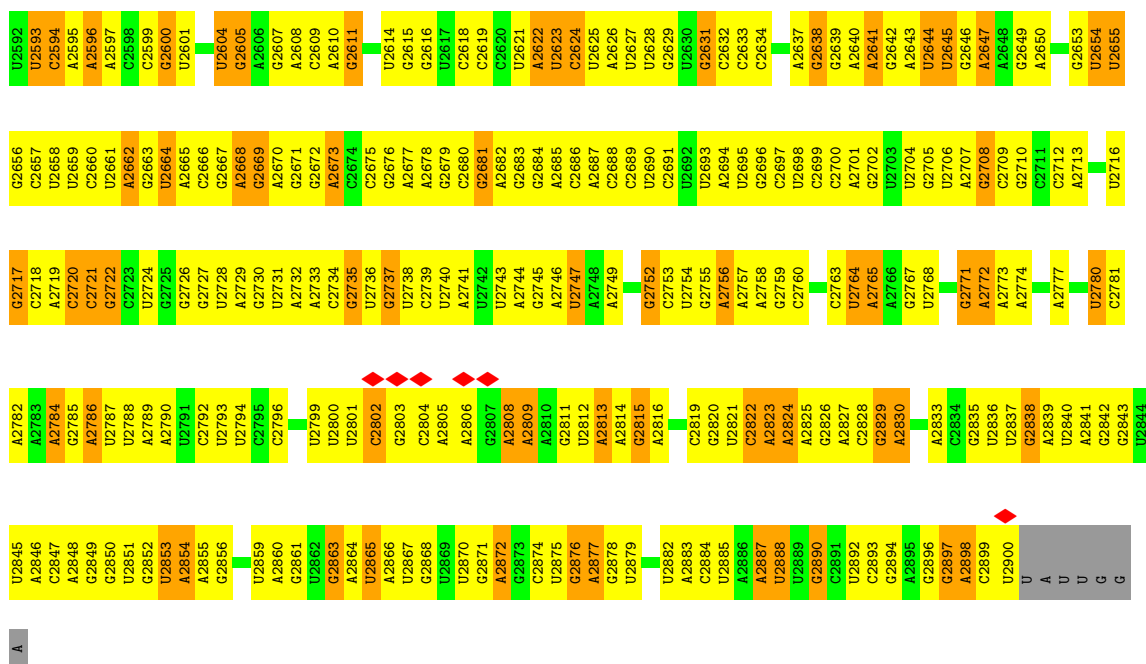


Chain 3: 21% 57% 21%

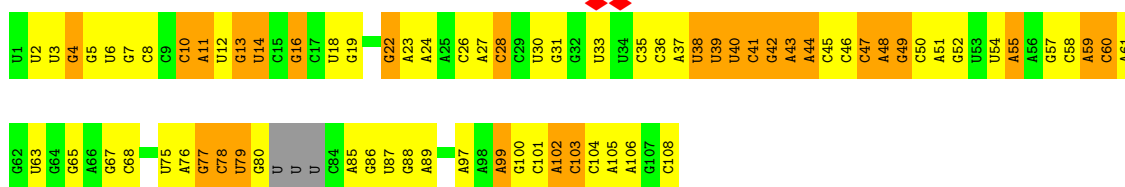
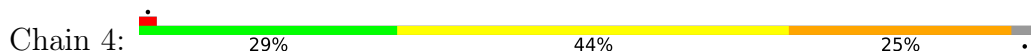


A1637	C1638	C1639	G1640	A1641	G1642	A1643	A1644	G1645	G1646	A1647	A1648	C1649	A1650	C1651	A1652	C1653	G1654	A1655	A1656	G1657	C1658	C1659	A1660	A1661	G1662	G1663	A1666	G1667	A1668	A1669	U1670	C1671	C1672	U1673	A1674	A1675	G1676	U1679	A1680	G1681	C1682	G1685	U1686	A1688	A1689	C1690	U1691	A1692	U1693	A1694	G1695	C1696	C1697	A1698	A1699			
A1573	G1574	A1577	A1578	G1579	G1580	U1581	G1582	G1583	G1584	A1585	U1586	U1587	A1588	A1589	U1590	U1593	G1594	U1595	U1596	U1597	U1598	U1599	A1600	A1601	G1602	A1603	A1604	A1605	A1606	G1607	C1608	U1609	U1610	C1611	U1612	A1613	G1614	G1615	U1618	A1619	A1620	U1621	C1622	U1623	A1624	U1627	G1628	U1629	A1630	A1631	C1632	C1633	A1634	G1635	A1636			
U1509	C1444	U1445	U1446	A1447	G1448	G1449	G1450	A1451	G1452	U1453	U1454	A1455	U1456	A1457	U1458	U1459	G1460	A1461	A1462	G1463	U1464	U1465	U1466	U1467	C1470	A1471	C1472	U1473	C1474	C1475	C1476	U1477	U1478	U1479	U1480	U1481	U1482	G1483	G1484	A1485	U1486	U1487	G1490	G1491	G1492	U1493	U1494	A1495	A1496	U1501	A1502	A1503	G1504	G1505	U1506	G1507	A1508	
C1518	A1519	A1520	A1521	U1522	C1523	U1526	U1527	G1528	U1529	G1530	C1531	A1532	U1533	A1534	A1535	C1536	A1537	U1538	U1539	G1540	A1541	G1542	U1543	G1544	U1545	U1546	U1547	A1548	U1549	G1550	U1551	C1552	G1553	A1554	C1555	U1556	A1559	U1560	U1561	U1562	U1563	U1564	U1565	U1566	U1567	U1568	U1569	U1570	G1571	U1572								
C1444	U1445	U1446	A1447	G1448	G1449	G1450	A1451	G1452	U1453	U1454	A1455	U1456	A1457	U1458	U1459	G1460	A1461	A1462	G1463	U1464	U1465	U1466	U1467	C1470	A1471	C1472	U1473	C1474	C1475	C1476	U1477	U1478	U1479	U1480	U1481	U1482	G1483	G1484	A1485	U1486	U1487	G1490	G1491	G1492	U1493	U1494	A1495	A1496	U1501	A1502	A1503	G1504	G1505	U1506	G1507	A1508		
U1509	C1518	A1519	A1520	A1521	U1522	C1523	U1526	U1527	G1528	U1529	G1530	C1531	A1532	U1533	A1534	A1535	C1536	A1537	U1538	U1539	G1540	A1541	G1542	U1543	G1544	U1545	U1546	U1547	A1548	U1549	G1550	U1551	C1552	G1553	A1554	C1555	U1556	A1559	U1560	U1561	U1562	U1563	U1564	U1565	U1566	U1567	U1568	U1569	U1570	G1571	U1572							
A1573	G1574	A1577	A1578	G1579	G1580	U1581	G1582	G1583	G1584	A1585	U1586	U1587	A1588	A1589	U1590	U1593	G1594	U1595	U1596	U1597	U1598	U1599	A1600	A1601	G1602	A1603	A1604	A1605	A1606	G1607	C1608	U1609	U1610	C1611	U1612	A1613	G1614	G1615	U1618	A1619	A1620	U1621	C1622	U1623	A1624	U1627	G1628	U1629	A1630	A1631	C1632	C1633	A1634	G1635	A1636			
G840	C841	U842	G843	U844	G845	U846	C847	U848	G849	G850	U851	C852	G853	A854	U855	A856	U857	G858	C859	G860	U861	U862	U863	A864	A865	G866	U867	G868	U869	A870	G871	C872	G873	U874	G875	A876	G877	U878	C879	U880	U881	U882	A883	A884	U885	G889	U890	G891	G892	A893	G894	G895	U896	U897	A898	A899	G900	C901
U902	A903	C904	U905	G906	U907	A908	U909	G910	U911	C912	U913	G914	A915	U916	G917	A918	C919	U920	C921	C922	A	C	U	A	G928	U932	A933	U934	U935	G936	U939	A940	C941	A942	A943	U944	U945	A946	U947	A948	C949	U950	C951	U952	G953	A954	U955	U956	G957	U961	A1032	A1033	A1034	U1035	A1036	A1037		
G975	C976	A977	U978	C980	A981	U982	A983	U984	A985	U986	U987	G988	U989	A990	G991	G992	U993	U994	A995	A996	C997	C998	U999	U1000	C1001	A1002	G1005	U1006	C1007	A1008	U1009	G1010	A1011	G1012	G1013	G1014	G1015	A1016	G1017	G1018	A1019	G1020	C1021	G1025	A1026	U1027	C1028	A1029	A1032	A1033	A1034	U1035	A1036	A1037				
G1038	C1041	U1042	U1043	C1044	A1045	U1046	A1047	U1048	U1049	A1052	C1053	U1054	A1055	U1056	G1057	A1061	A1062	A1063	A1064	G1065	G1066	A1067	U1068	U1069	C1070	U1071	C1072	A1073	U1074	C1075	U1076	U1079	A1080	U1081	A1082	U1083	G1084	U1085	U1086	A1087	A1088	A1089	G1090	U1091	A1092	U1093	G1094	U1095	U1096	U1097	U1101	A1102	G1103	A1104				
A1105	C1107	U1108	C1109	C1110	C1111	A1112	U1113	C1114	G1115	U1116	U1117	U1118	A1119	U1120	A1121	G1122	A1123	G1124	U1125	G1126	C1127	G1128	U1129	A1130	C1131	C1132	A1133	C1137	A1138	C1139	U1140	U1141	G1142	A1146	G1147	U1148	G1149	U1150	U1151	U1154	G1155	C1158	U1159	G1160	A1161	A1162	U1165	G1166	U1167	A1168	A1169	C1170	G1171					
G1172	U1173	C1174	U1175	U1176	U1177	A1178	C1179	A1183	U1184	U1185	A1186	C1187	U1188	U1189	A1190	U1191	U1192	U1193	U1194	A1195	U1196	G1197	G1198	A1199	U1200	A1201	A1202	G1203	A1208	U1209	A1210	U1211	C1212	U1213	U1214	G1215	U1216	G1217	G1218	U1219	U1220	G1221	A1222	C1223	G1224	C1227	G1228	U1229	U1230	G1231	U1232	A1233	U1234	G1235	U1236	G1237		
A1238	G1239	U1242	A1243	A1244	U1245	U1246	C1247	A1248	U1249	A1250	G1251	C1252	U1253	U1254	G1255	A1256	G1257	G1258	A1259	U1260	U1261	G1262	G1263	U1264	G1265	A1266	U1267	U1268	U1273	A1274	A1277	U1278	G1280	A1281	G1282	A1283	A1284	U1285	U1286	G1289	G1290	C1291	U1292	U1293	G1294	A1295	G1296	U1297	A1298	A1299	C1300	G1301	C1302					
G1306	G1307	A1308	G1309	U1310	G1311	A1314	A1315	U1316	C1317	U1318	U1319	C1320	C1321	A1322	A1323	A1324	C1325	G1326	G1327	A1328	U1329	U1330	G1331	A1332	A1335	U1336	G1337	U1338	U1339	U1340	U1341	C1342	U1343	U1344	G1345	G1346	A1347	A1350	G1353	U1354	C1355	G1356	U1357	C1358	C1359	U1360	U1361	C1362	C1363	A1364	G1365	G1366	G1367	U1368	U1369			
A1370	G1371	U1372	C1379	U1380	A1381	A1382	G1383	C1384	U1385	G1386	A1387	U1391	G1392	A1393	A1394	A1395	A1396	G1397	U1398	U1399	G1402	G1405	A1406	U1407	G1408	G1409	C1414	A1415	G1416	U1417	U1418	U1419	A1420	A1421	U1422	A1423	U1424	U1425	C1426	C1427	U1428	G1429	U1430	A1431	A1435	C1436	A1437	U1438	G1439	U1440	A1441	A1443						
C1444	U1445	U1446	A1447	G1448	G1449	G1450	A1451	G1452	U1453	U1454	A1455	U1456	A1457	U1458	U1459	G1460	A1461	A1462	G1463	U1464	U1465	U1466	U1467	C1470	A1471	C1472	U1473	C1474	C1475	C1476	U1477	U1478	U1479	U1480	U1481	U1482	G1483	G1484	A1485	U1486	U1487	G1490	G1491	G1492	U1493	U1494	A1495	A1496	U1501	A1502	A1503	G1504	G1505	U1506	G1507	A1508		
U1509	C1518	A1519	A1520	A1521	U1522	C1523	U1526	U1527	G1528	U1529	G1530	C1531	A1532	U1533	A1534	A1535	C1536	A1537	U1538	U1539	G1540	A1541	G1542	U1543	G1544	U1545	U1546	U1547	A1548	U1549	G1550	U1551	C1552	G1553	A1554	C1555	U1556	A1559	U1560	U1561	U1562	U1563	U1564	U1565	U1566	U1567	U1568	U1569	U1570	G1571	U1572							
A1573	G1574	A1577	A1578	G1579	G1580	U1581	G1582	G1583	G1584	A1585	U1586	U1587	A1588	A1589	U1590	U1593	G1594	U1595	U1596	U1597	U1598	U1599	A1600	A1601	G1602	A1603	A1604	A1605	A1606	G1607	C1608	U1609	U1610	C1611	U1612	A1613	G1614	G1615	U1618	A1619	A1620	U1621	C1622	U1623	A1624	U1627	G1628	U1629	A1630	A1631	C1632	C1633	A1634	G1635	A1636			

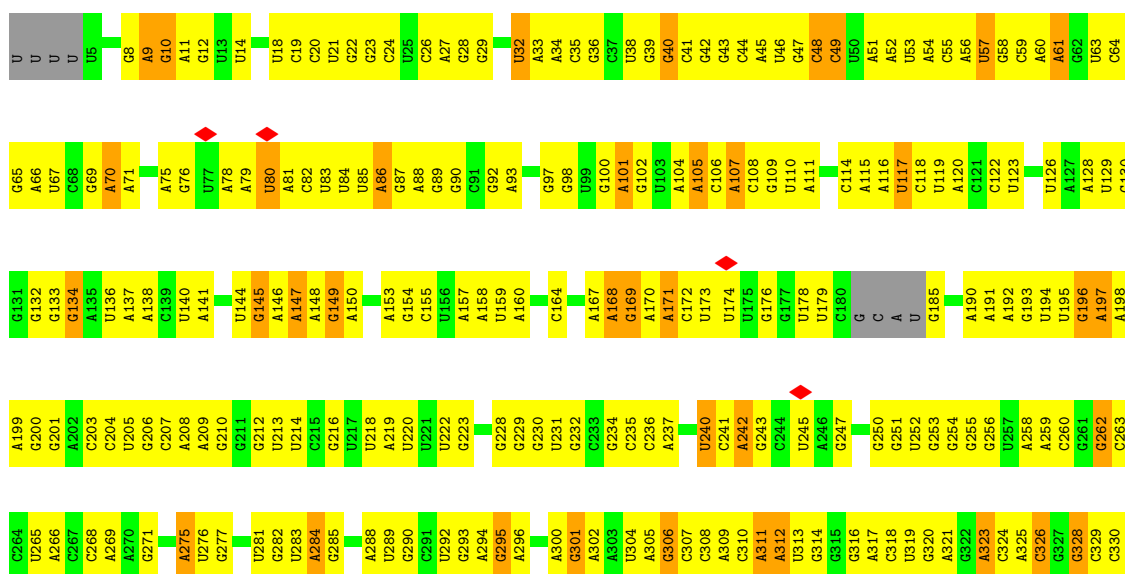
A2526	U2527	C2528	C2529	C2530	C2531	C2532	A2533	C2534	C2535	C2536	C2537	C2538	A2539	C2540	C2541	C2542	C2543	C2544	U2545	C2548	A2549	C2550	C2551	C2552	C2553	U2554	C2555	C2556	C2557	C2558	C2559	U2560	C2561	U2562	C2567	C2568	A2569	U2570	C2571	A2572	C2573	A2574	C2575	A2576	A2580	C2581	C2582	C2583	C2584	A2585	C2586	C2587	C2588	C2589	C2590	C2591							
U2398	C2399	A2400	U2401	C2402	C2403	C2404	C2405	U2406	C2407	C2408	C2409	C2410	C2411	A2412	C2413	U2414	A2415	U2416	C2419	A2420	U2421	G2422	G2423	C2424	C2425	A2426	U2427	C2430	U2431	C2432	A2433	A2434	C2435	G2436	C2437	A2438	U2439	A2440	A2441	A2442	A2443	G2444	A2447	U2448	C2449	C2450	C2451	C2452	C2453	C2454	C2455	C2456	C2457	U2458	C2459	C2460							
G2461	G2462	C2463	C2464	U2465	U2466	C2467	U2468	A2469	C2470	C2471	C2472	C2473	C2474	C2475	A2476	A2479	C2480	C2483	A2484	U2485	A2486	U2487	C2488	C2489	A2490	C2491	C2492	C2493	C2494	A2495	U2499	U2500	U2501	C2502	C2503	C2504	U2505	C2506	C2507	U2508	A2509	C2510	A2511	U2512	C2513	C2516	A2517	C2518	U2519	C2520	A2521	U2522	C2523	C2524	C2525	U2526	C2527						
A2335	A2336	C2337	C2338	C2339	U2340	C2341	U2342	A2343	A2344	C2345	C2346	C2347	U2348	C2349	C2350	U2351	C2352	C2353	A2354	C2355	U2356	C2357	C2358	C2359	C2363	A2364	U2365	C2366	C2367	A2368	C2369	C2370	U2371	C2372	C2373	A2374	C2375	C2376	C2377	C2378	C2379	U2380	C2381	A2382	C2383	A2386	U2387	C2388	A2389	C2390	C2391	C2392	C2393	A2394	U2395	C2396	C2397						
A2274	A2275	A2276	A2277	C2278	C2279	U2280	A2281	C2284	C2285	C2286	C2287	C2288	C2289	C2290	U2291	C2292	C2293	A2294	C2295	A2296	C2297	C2298	U2299	A2300	C2301	C2302	U2303	C2304	C2305	A2306	C2307	U2308	C2309	C2310	C2311	C2312	U2313	C2314	C2315	C2316	A2317	A2318	A2319	U2320	C2321	C2322	U2323	A2324	U2325	C2326	C2327	A2328	C2329	C2330	C2331	U2332	U2333	U2334					
G2211	U2212	A2213	A2214	C2215	U2216	C2217	U2218	U2219	A2220	U2221	C2222	C2223	A2224	G2225	U2228	C2229	A2230	C2231	G2232	A2233	C2234	A2235	C2236	U2237	G2238	U2239	U2240	A2241	C2242	G2243	G2246	C2247	C2248	A2249	C2250	U2251	U2252	U2253	C2254	A2255	G2258	C2259	G2260	C2261	C2262	C2263	C2264	U2265	C2266	C2267	C2268	C2269	U2270	C2271	C2272	U2273							
C2147	U2148	U2149	C2150	C2151	C2152	U2153	A2154	C2155	G2156	C2157	C2158	U2159	U2160	G2161	U2162	U2163	G2164	A2165	C2166	C2167	C2168	G2169	A2170	C2171	A2172	C2173	C2174	U2175	C2176	A2179	U2180	A2181	C2182	C2186	C2187	U2188	U2189	C2190	C2191	U2192	U2193	C2194	U2195	C2196	U2197	C2198	C2199	U2200	C2201	U2202	U2203	C2204	U2205	A2206	U2207								
U2087	U2088	A2089	C2090	C2091	C2092	C2093	A2094	C2095	U2096	A2097	U2098	U2099	C2100	A2101	U2102	C2103	A2104	C2105	G2106	A2107	C2108	A2109	U2110	U2111	A2112	U2113	C2114	A2115	U2116	C2117	U2118	A2119	C2120	A2121	C2122	U2123	A2124	U2125	A2126	C2127	U2128	U2129	A2130	C2131	C2132	A2133	C2134	C2135	C2136	A2137	U2138	C2139	C2140	A2141	U2142	C2143	C2144	A2145	A2146				
G1829	G1830	G1831	G1832	G1833	U1834	G1835	A1836	C1837	G1838	C1839	C1840	C1841	C1842	C1843	C1844	U1845	C1846	C1847	U1848	C1849	C1850	U1851	A1852	C1853	A1854	C1855	C1856	G1857	U1858	C1859	A1860	C1861	A1862	C1863	C1866	G1867	A1868	C1869	U1870	U1871	U1872	A1873	C1874	C1875	U1876	A1877	A1878	C1879	C1880	C1881	C1882	C1885	C1886	U1887	U1888	U1889	U1890	A1891					
G1700	G1701	A1702	C1703	C1704	C1705	C1706	A1707	C1708	C1709	A1710	C1711	U1712	U1713	U1714	A1715	A1716	G1717	C1718	U1719	U1720	C1721	U1722	A1723	A1724	C1725	U1726	U1727	A1729	C1730	G1731	A1732	C1733	C1734	C1735	A1736	C1737	U1738	A1739	C1740	C1741	A1742	U1743	C1747	U1748	A1749	A1750	A1751	C1752	C1753	U1754	A1755	A1756	C1757	C1758	C1759	G1760	C1761	A1762	C1763	U1764	C1765	A1766	U1767
A1892	C1895	A1896	C1897	C1898	C1899	A1903	G1904	U1905	C1906	A1907	A1908	G1911	C1912	G1913	G1914	C1915	C1916	C1917	A1918	U1919	A1920	C1921	U1922	C1923	A1924	A1925	U1930	C1931	C1932	U1933	A1934	C1935	C1936	U1937	U1938	A1939	C1940	C1941	C1942	A1945	U1946	U1947	C1948	C1949	U1950	A1951	C1952	U1953	C1954	C1955	C1956	U1957	U1958	U1959	A1959								
G1960	A1961	U1962	U1963	C1970	G1971	C1972	C1973	U1974	C1975	A1976	A1977	U1978	C1979	G1980	C1981	C1982	C1986	C1987	A1988	U1989	C1990	A1991	C1992	U1993	U1994	C1995	A1996	C1997	U1998	C1999	U2000	C2001	C2002	C2003	C2004	C2005	C2006	A2007	C2008	U2009	A2010	C2011	A2012	C2013	U2014	C2015	C2016	C2017	U2018	C2019	C2020	A2021	C2022	U2023	C2024	C2025	U2026						
G2027	C2028	U2029	A2030	C2031	C2032	C2033	C2034	U2035	C2036	A2037	A2038	C2039	A2040	C2041	A2042	C2043	C2044	C2045	C2046	U2047	U2048	A2049	C2050	C2051	C2052	C2053	C2054	A2055	C2056	C2057	C2058	C2059	C2060	A2061	C2062	C2063	C2064	A2065	C2066	A2067	C2068	A2069	C2070	C2071	C2072	C2073	C2074	U2075	C2076	A2077	A2078	C2079	C2080	U2081	C2082	U2083	A2084	C2085	U2086				



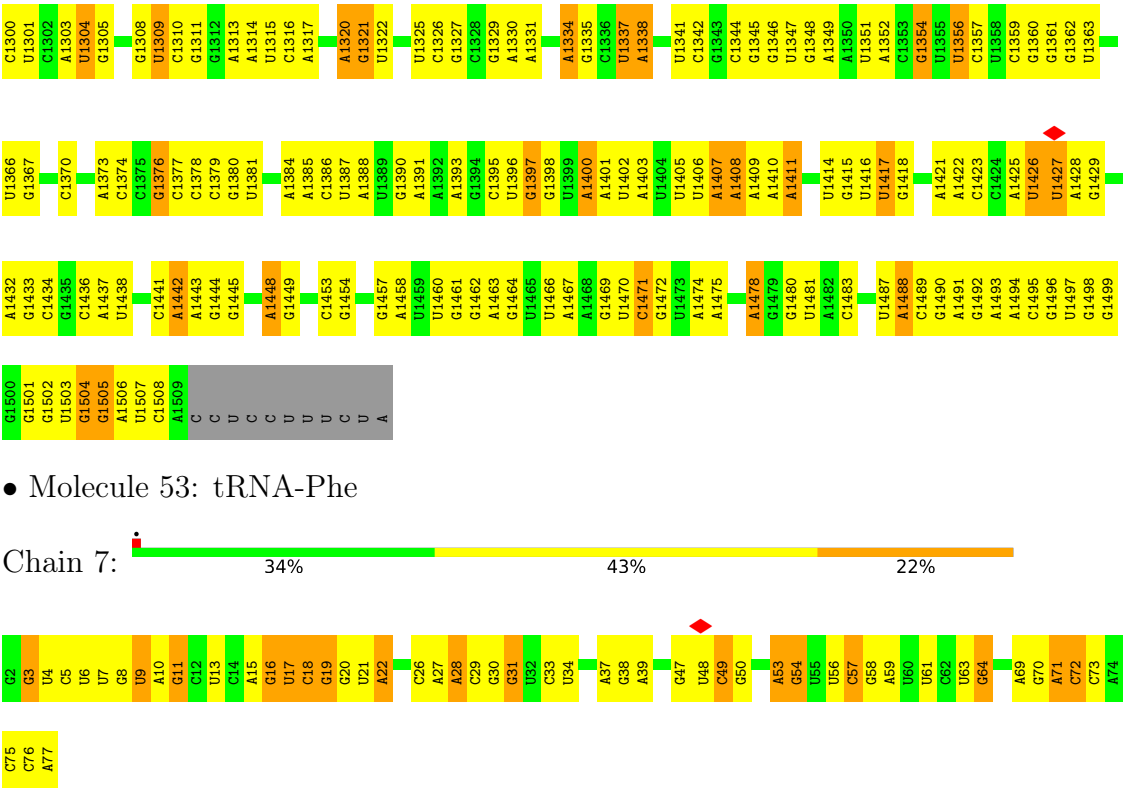
• Molecule 51: 5S ribosomal RNA



• Molecule 52: 16S ribosomal RNA



A1236	G1237	U1173	C1174	U1175	U1176	U1177	C1178	A1179	U1180	C1181	C1182	A1183	C1184	U1185	U1186	U1187	A1188	U1189	G1190	U1191	C1192	U1193	A1194	G1195	C1196	A1262	A1263	G1197	U1265	U1198	U1138	U1266	G1267	C1201	A1202	U1141	U1269	U1270	C1271	A1204	C1205	A1273	G1274	U1275	U1276	C1277	G1278	A1211	C1212	U1150	A1151	A1213	A1214	U1215	U1216	G1217	C1218	U1222	A1159	C1286	G1287	C1288	U1289	A1163	A1226	C1227	U1227	A1229	G1230	U1294	U1295	C1232	G1233	C1234	A1171	U1298
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583	U647	C584	G585	G586	A457	C522																
C459	A460	G586	A650	G651	A652	G653	U654	G655	A591	A592	U466	A531	U532	A535	U536	C597	G662	A664	U666	U669	G670	G671	A672	A673	U674	U675	U676	C677	C616	A551	U552	C553	C554	G555	G556	C567	A507	U569	A509	U510	A446	U511	U512	G513	A448	U514	G515	C516	C517	A518	U464	A645	C580	G583																						



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1457	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.466	Depositor
Minimum map value	-0.600	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0	0.24	0/383	0.60	0/504
2	1	0.20	0/484	0.52	0/637
3	2	0.11	0/306	0.43	0/401
4	A	0.17	0/1954	0.50	0/2642
5	B	0.17	0/1721	0.53	0/2323
6	C	0.15	0/1691	0.41	0/2267
7	D	0.17	0/1188	0.50	0/1593
8	E	0.14	0/1384	0.42	0/1867
9	F	0.21	0/1266	0.64	0/1700
10	G	0.20	0/1126	0.51	0/1517
11	H	0.16	0/1044	0.46	0/1395
12	I	0.17	0/820	0.51	0/1103
13	J	0.27	0/844	0.66	2/1136 (0.2%)
14	K	0.28	0/1094	0.58	0/1468
15	L	0.18	0/962	0.51	0/1289
16	M	0.16	0/483	0.47	0/643
17	N	0.13	0/679	0.38	0/907
18	O	0.17	0/659	0.54	2/885 (0.2%)
19	P	0.13	0/684	0.39	0/913
20	Q	0.16	0/545	0.48	0/730
21	R	0.16	0/698	0.49	0/936
22	S	0.12	0/631	0.36	0/838
23	T	0.17	0/475	0.44	0/621
24	a	0.15	0/2267	0.44	0/3044
25	b	0.16	0/1795	0.46	0/2412
26	c	0.16	0/1671	0.45	0/2246
27	d	0.18	0/1409	0.52	0/1894
28	e	0.17	0/1420	0.51	2/1912 (0.1%)
29	f	0.15	0/1183	0.48	0/1587
30	g	0.41	0/969	0.67	0/1295
31	h	0.15	0/968	0.44	0/1298
32	i	0.16	0/1186	0.43	0/1592
33	j	0.15	0/953	0.46	0/1275
34	k	0.13	0/1170	0.40	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.27	0/1104	0.58	2/1481 (0.1%)
36	m	0.14	0/973	0.47	0/1309
37	n	0.17	0/897	0.49	2/1198 (0.2%)
38	o	0.17	0/948	0.44	0/1262
39	p	0.15	0/961	0.45	0/1278
40	q	0.15	0/828	0.44	0/1111
41	r	0.15	0/1077	0.42	0/1441
42	s	0.13	0/732	0.38	0/988
43	t	0.18	0/879	0.43	0/1165
44	u	0.16	0/665	0.50	0/884
45	v	0.18	0/519	0.51	0/695
46	w	0.15	0/826	0.43	0/1104
47	x	0.17	0/353	0.48	0/474
48	y	0.32	0/457	0.59	0/601
49	z	0.15	0/412	0.44	0/547
50	3	0.10	0/69073	0.25	1/107710 (0.0%)
51	4	0.10	0/2505	0.29	0/3902
52	5	0.09	0/35768	0.24	0/55764
53	7	0.10	0/1808	0.27	0/2817
All	All	0.13	0/156897	0.33	11/234160 (0.0%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	l	110	PRO	N-CA-C	6.79	126.47	112.47
13	J	111	HIS	N-CA-C	-6.40	105.42	112.72
28	e	168	PHE	CA-C-N	6.18	133.35	121.54
28	e	168	PHE	C-N-CA	6.18	133.35	121.54
13	J	112	ASN	CB-CA-C	6.06	122.48	110.42

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	0	380	0	429	24	0
2	1	477	0	530	24	0
3	2	304	0	350	11	0
4	A	1921	0	1973	77	0
5	B	1698	0	1768	62	0
6	C	1660	0	1719	71	0
7	D	1173	0	1267	51	0
8	E	1362	0	1377	40	0
9	F	1246	0	1308	60	0
10	G	1110	0	1226	54	0
11	H	1028	0	1094	41	0
12	I	809	0	894	45	0
13	J	829	0	855	47	0
14	K	1076	0	1170	62	0
15	L	951	0	1014	47	0
16	M	474	0	509	19	0
17	N	673	0	730	17	0
18	O	646	0	677	26	0
19	P	675	0	728	15	0
20	Q	535	0	562	29	0
21	R	682	0	691	30	0
22	S	629	0	681	29	0
23	T	471	0	522	18	0
24	a	2225	0	2301	123	0
25	b	1762	0	1808	78	0
26	c	1644	0	1731	64	0
27	d	1388	0	1469	63	0
28	e	1396	0	1481	48	0
29	f	1160	0	1172	30	0
30	g	960	0	1014	4	0
31	h	959	0	1039	1	0
32	i	1164	0	1192	50	0
33	j	944	0	1019	42	0
34	k	1153	0	1256	51	0
35	l	1079	0	1134	55	0
36	m	958	0	1011	44	0
37	n	889	0	952	36	0
38	o	938	0	1008	40	0
39	p	947	0	1028	46	0
40	q	811	0	858	28	0
41	r	1068	0	1150	50	0
42	s	720	0	803	23	0
43	t	872	0	972	34	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	u	657	0	695	37	0
45	v	513	0	560	23	0
46	w	818	0	870	30	0
47	x	344	0	333	5	0
48	y	452	0	472	25	0
49	z	408	0	440	11	0
50	3	61664	0	30954	2138	0
51	4	2239	0	1137	63	0
52	5	31943	0	16058	1111	0
53	7	1618	0	821	37	0
All	All	144502	0	98812	4704	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 21.

The worst 5 of 4704 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)
50:3:900:G:N2	50:3:903:A:H61	1.43	1.17
50:3:341:G:N2	50:3:364:A:H61	1.43	1.16
50:3:341:G:H21	50:3:364:A:N6	1.46	1.12
50:3:900:G:H21	50:3:903:A:N6	1.51	1.08
50:3:29:G:H1	50:3:547:G:HO2'	1.07	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	0	45/48 (94%)	42 (93%)	3 (7%)	0	100	100
2	1	57/59 (97%)	49 (86%)	8 (14%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	A	238/294 (81%)	209 (88%)	29 (12%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	193 (96%)	8 (4%)	0	100	100
7	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
8	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
9	F	152/155 (98%)	138 (91%)	14 (9%)	0	100	100
10	G	139/142 (98%)	128 (92%)	11 (8%)	0	100	100
11	H	126/132 (96%)	120 (95%)	6 (5%)	0	100	100
12	I	99/108 (92%)	91 (92%)	8 (8%)	0	100	100
13	J	112/121 (93%)	106 (95%)	5 (4%)	1 (1%)	14	51
14	K	134/139 (96%)	116 (87%)	18 (13%)	0	100	100
15	L	116/124 (94%)	107 (92%)	9 (8%)	0	100	100
16	M	58/61 (95%)	58 (100%)	0	0	100	100
17	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	56 (89%)	7 (11%)	0	100	100
21	R	82/87 (94%)	70 (85%)	12 (15%)	0	100	100
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	48 (94%)	3 (6%)	0	100	100
24	a	283/287 (99%)	263 (93%)	20 (7%)	0	100	100
25	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100
26	c	208/212 (98%)	192 (92%)	16 (8%)	0	100	100
27	d	173/180 (96%)	158 (91%)	15 (9%)	0	100	100
28	e	174/184 (95%)	159 (91%)	14 (8%)	1 (1%)	21	59
29	f	143/149 (96%)	128 (90%)	15 (10%)	0	100	100
30	g	124/161 (77%)	111 (90%)	13 (10%)	0	100	100
31	h	126/137 (92%)	107 (85%)	19 (15%)	0	100	100
32	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
33	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	k	146/151 (97%)	136 (93%)	10 (7%)	0	100	100
35	l	134/139 (96%)	125 (93%)	6 (4%)	3 (2%)	5	29
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
38	o	113/119 (95%)	109 (96%)	4 (4%)	0	100	100
39	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100
42	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
43	t	109/111 (98%)	103 (94%)	6 (6%)	0	100	100
44	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
45	v	61/65 (94%)	57 (93%)	4 (7%)	0	100	100
46	w	96/111 (86%)	87 (91%)	9 (9%)	0	100	100
47	x	42/97 (43%)	36 (86%)	6 (14%)	0	100	100
48	y	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5820/6670 (87%)	5390 (93%)	425 (7%)	5 (0%)	49	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	l	109	ILE
35	l	112	SER
28	e	169	ASP
35	l	110	PRO
13	J	113	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	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	121 (98%)	2 (2%)	55	70
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	90 (99%)	1 (1%)	65	76
14	K	117/120 (98%)	114 (97%)	3 (3%)	40	62
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	101/129 (78%)	95 (94%)	6 (6%)	18	39
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5078 (100%)	15 (0%)	84	86

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	44	LEU
48	y	51	LEU
30	g	46	LYS
48	y	52	ARG
30	g	90	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
37	n	99	HIS
39	p	36	GLN
41	r	120	GLN
19	P	36	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	P	25	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	849 (29%)	38 (1%)
51	4	103/108 (95%)	39 (37%)	5 (4%)
52	5	1490/1520 (98%)	385 (25%)	2 (0%)
53	7	75/76 (98%)	24 (32%)	1 (1%)
All	All	4543/4611 (98%)	1297 (28%)	46 (1%)

5 of 1297 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	12	A
50	3	13	C
50	3	14	U
50	3	15	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2220	A
50	3	2808	A
50	3	2504	C
50	3	2668	A
50	3	2897	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

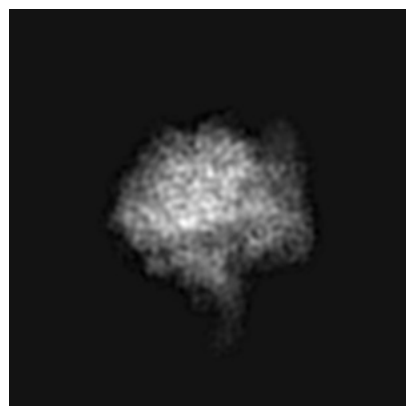
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13445. These allow visual inspection of the internal detail of the map and identification of artifacts.

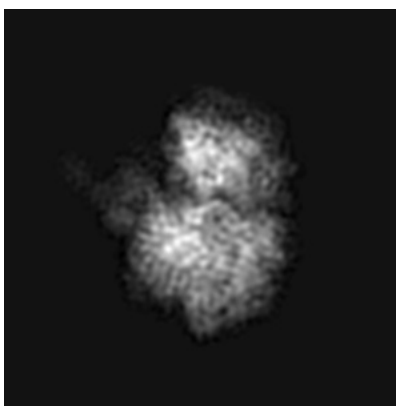
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

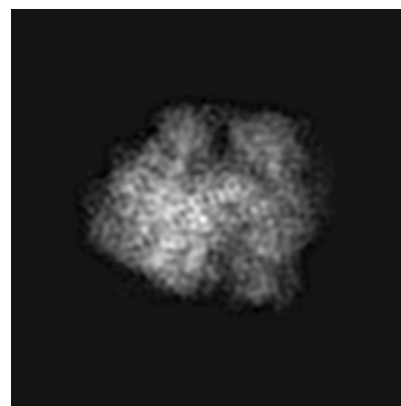
6.1.1 Primary map



X

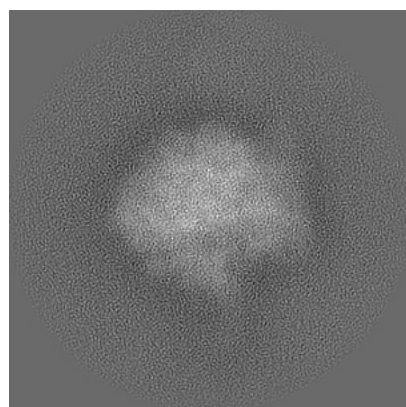


Y

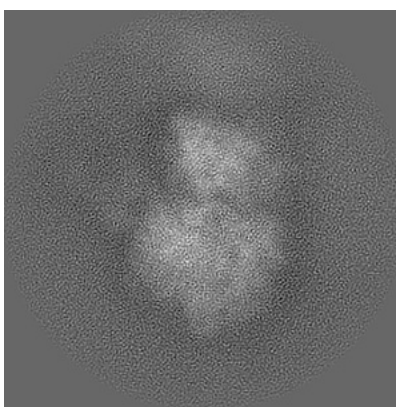


Z

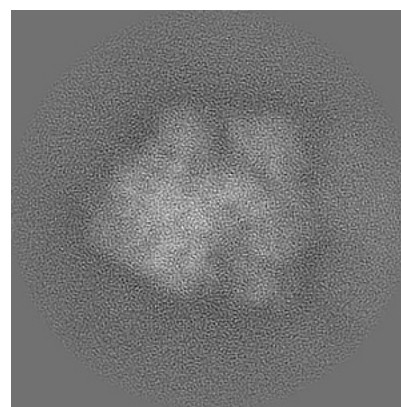
6.1.2 Raw map



X



Y

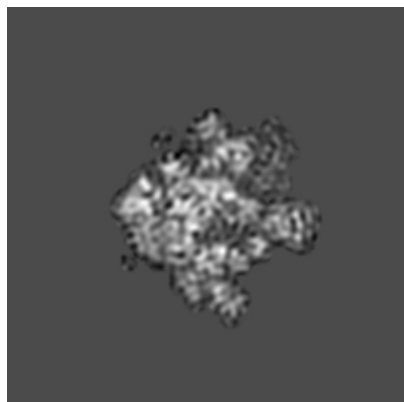


Z

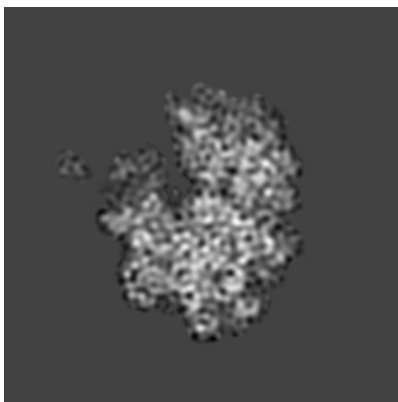
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

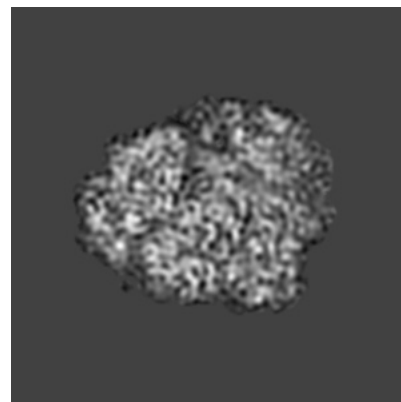
6.2.1 Primary map



X Index: 128

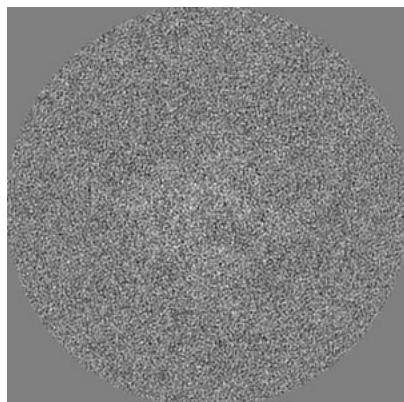


Y Index: 128

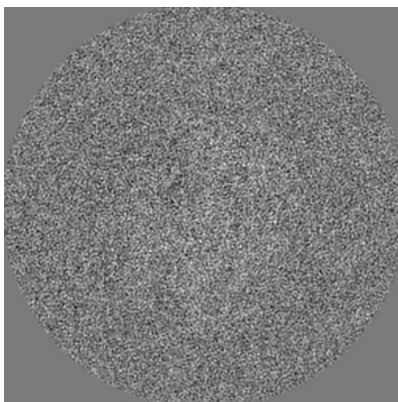


Z Index: 128

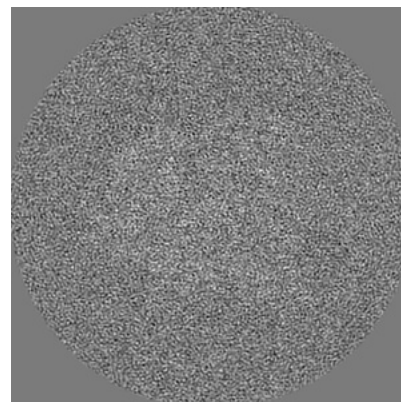
6.2.2 Raw map



X Index: 128



Y Index: 128

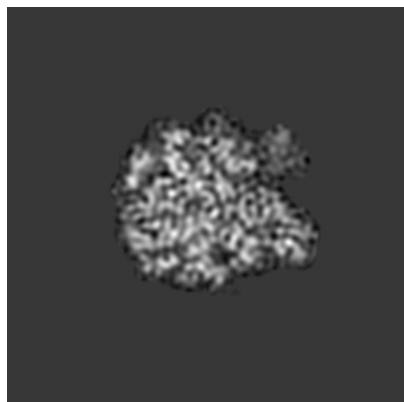


Z Index: 128

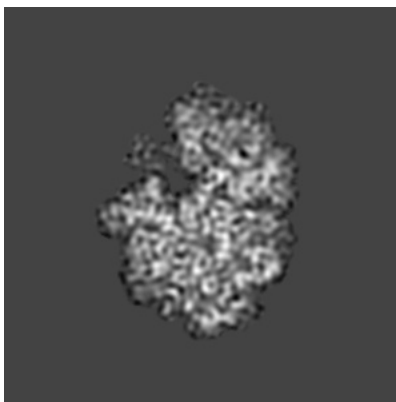
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

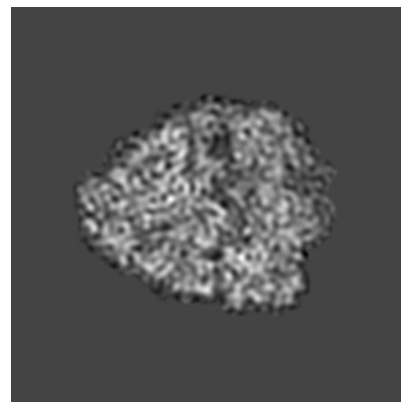
6.3.1 Primary map



X Index: 103

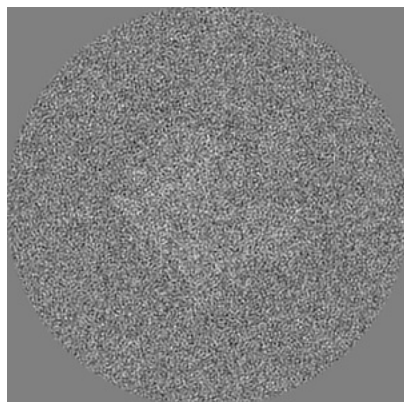


Y Index: 121

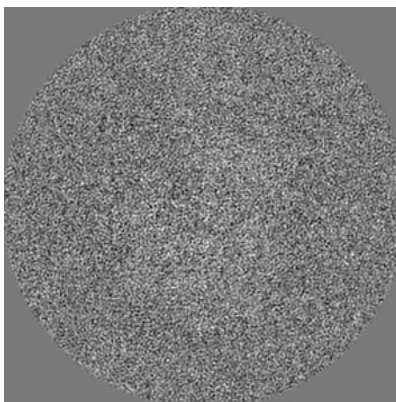


Z Index: 124

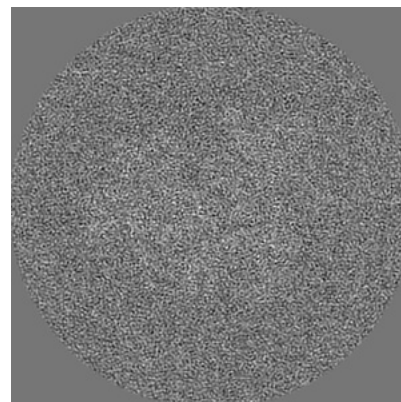
6.3.2 Raw map



X Index: 118



Y Index: 126

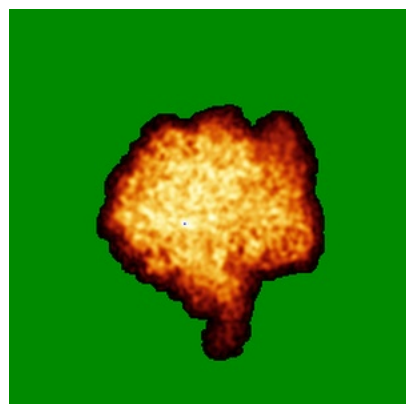


Z Index: 132

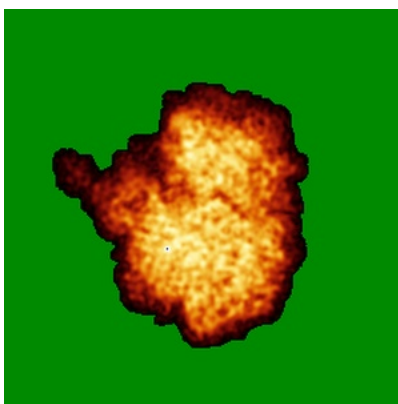
The images above show the largest variance slices of the map in three orthogonal directions.

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

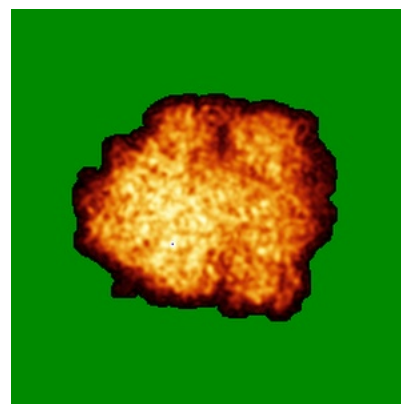
6.4.1 Primary map



X

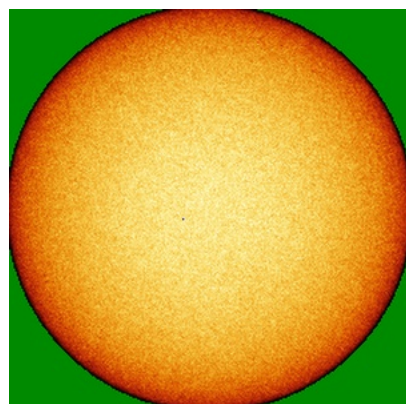


Y

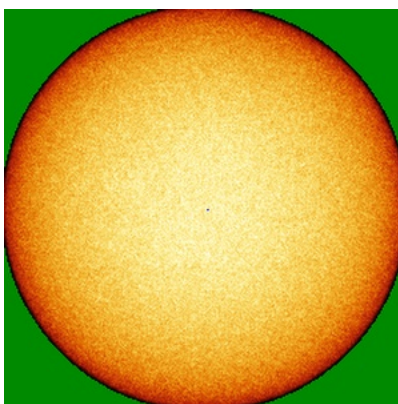


Z

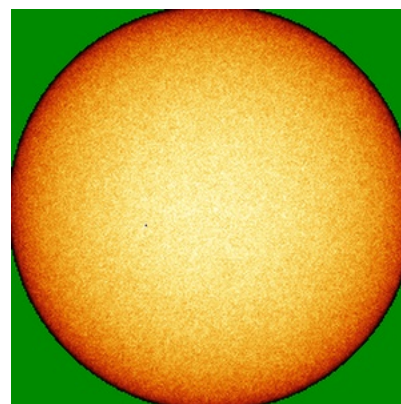
6.4.2 Raw map



X



Y



Z

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

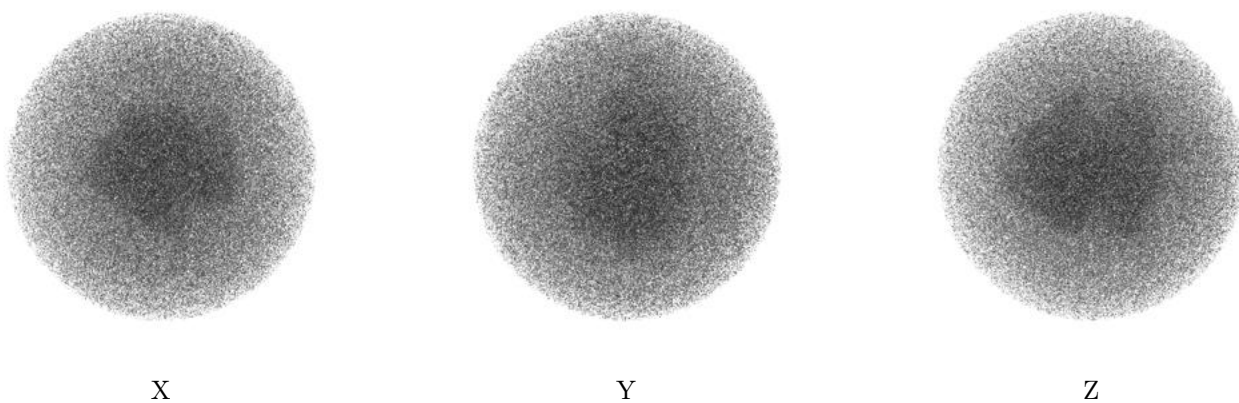
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

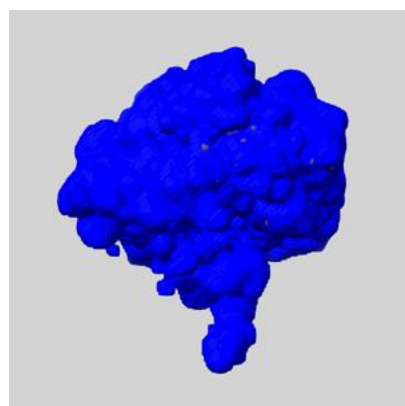
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

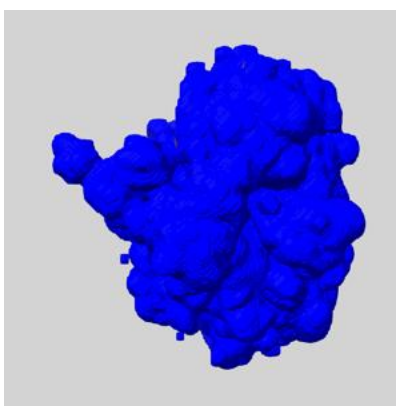
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

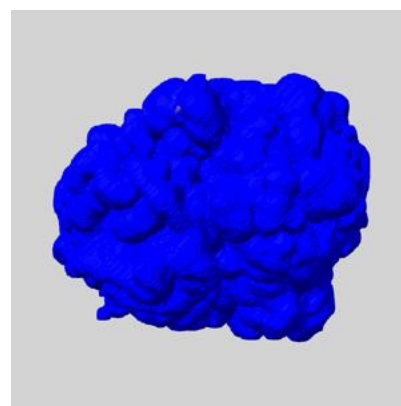
6.6.1 emd_13445_msk_1.map [i](#)



X



Y

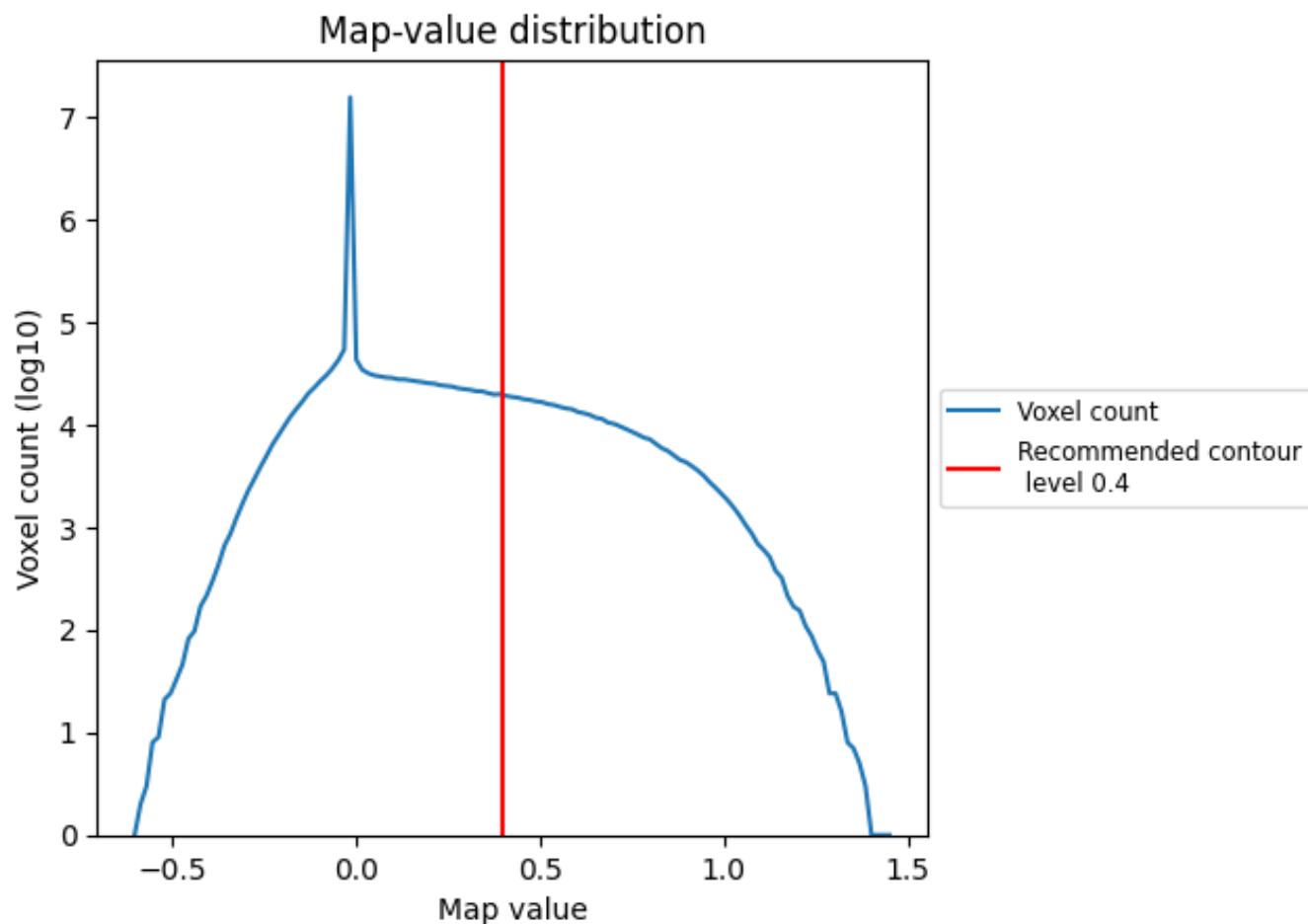


Z

7 Map analysis [i](#)

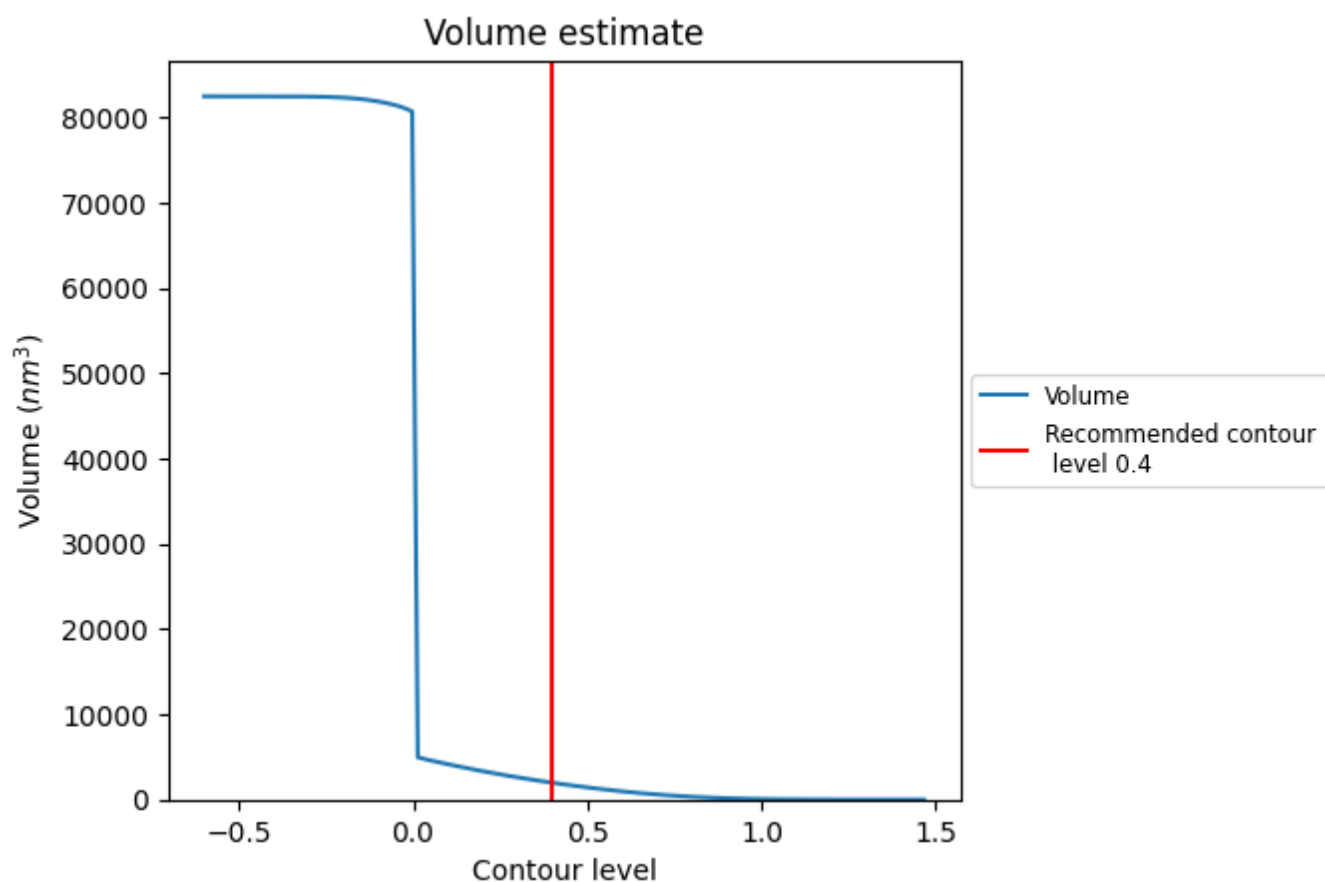
This section contains the results of statistical analysis of the map.

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.

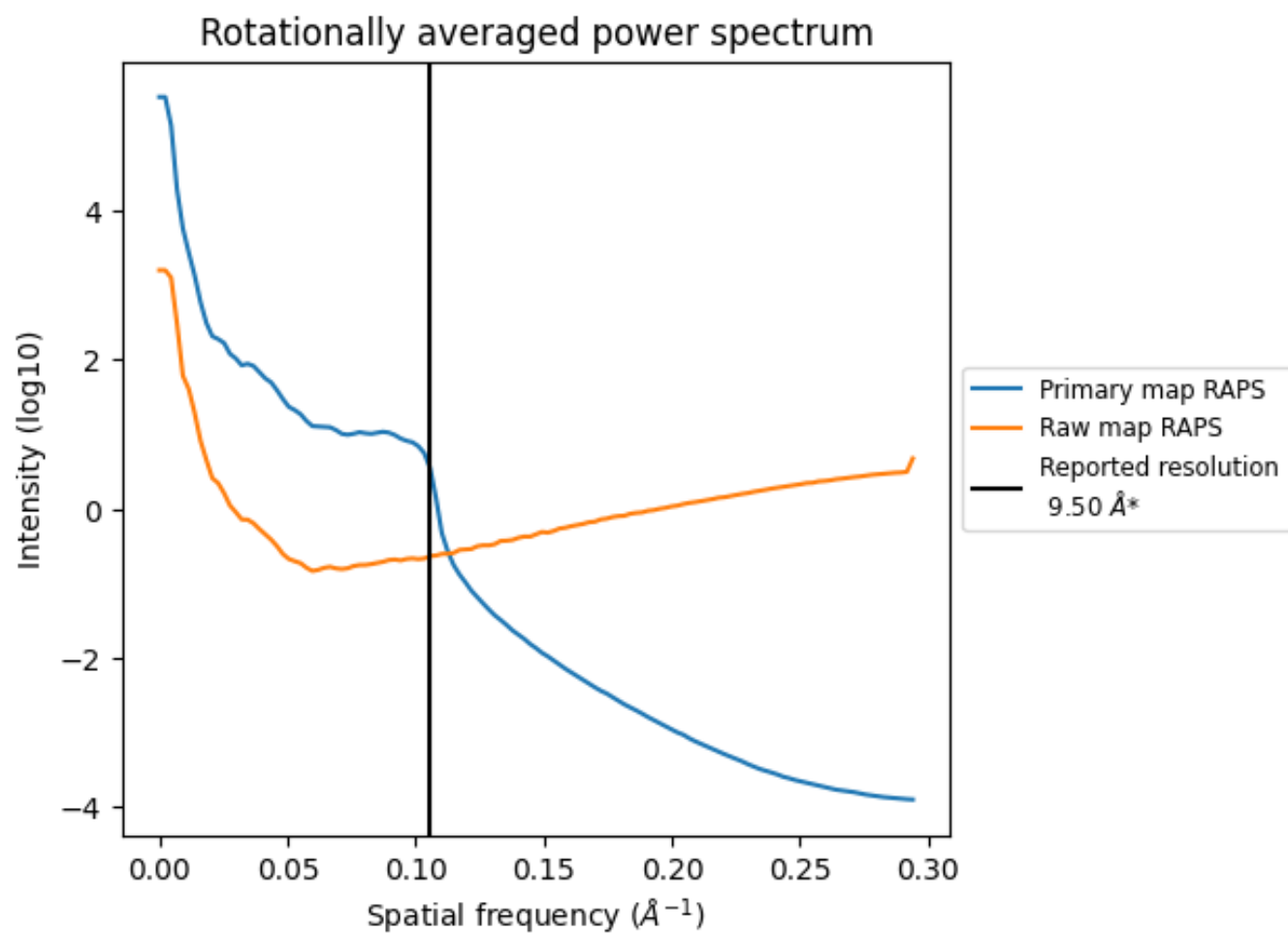
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1971 nm³; this corresponds to an approximate mass of 1780 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 ⓘ

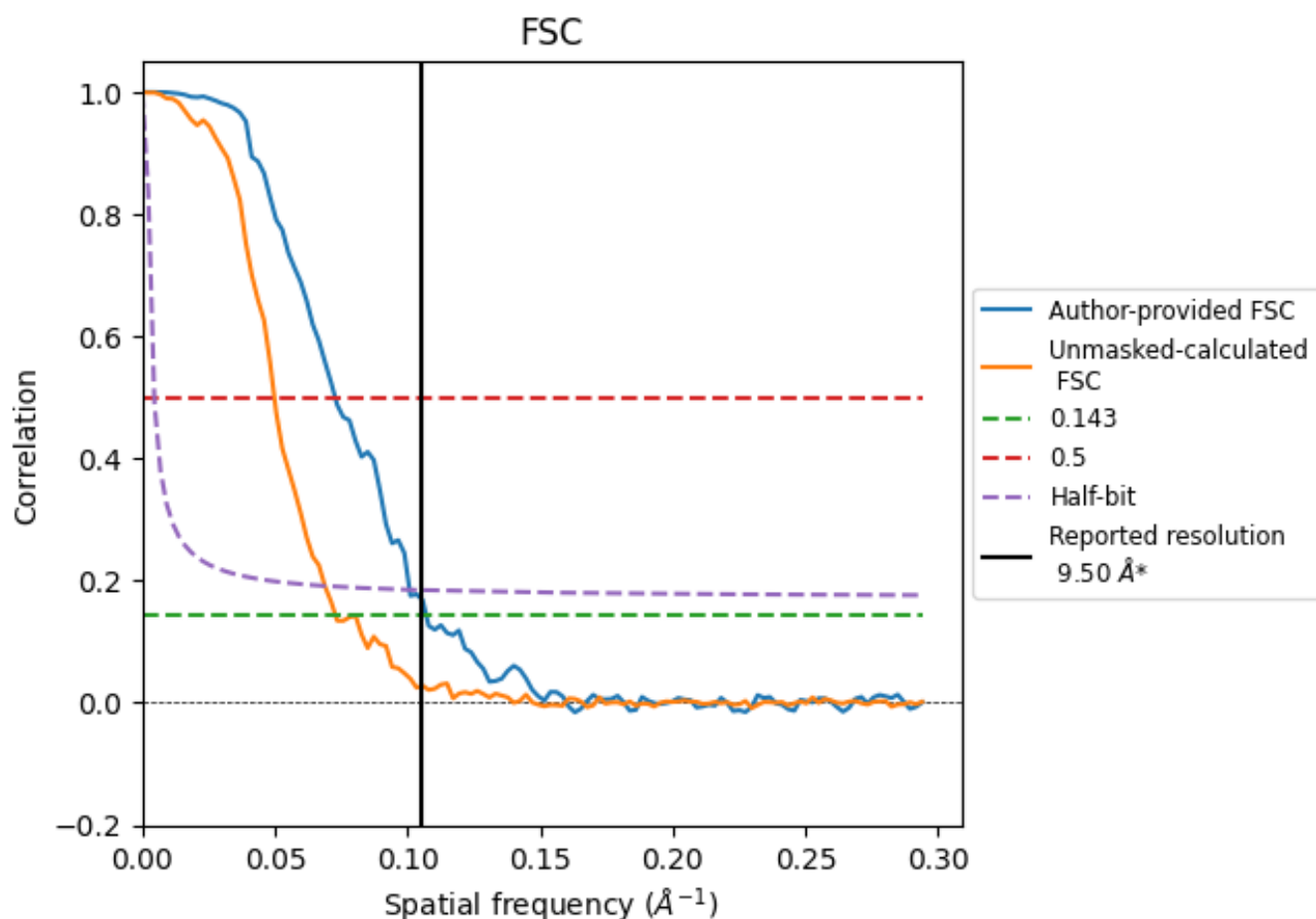


*Reported resolution corresponds to spatial frequency of 0.105 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.105 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

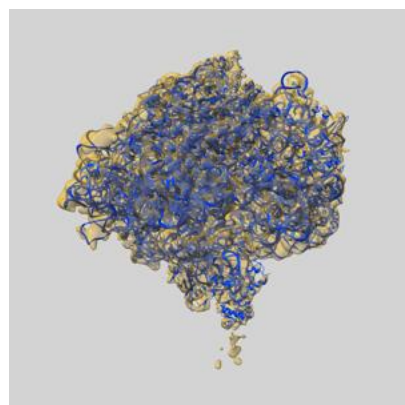
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.50	-	-
Author-provided FSC curve	9.35	13.76	9.92
Unmasked-calculated*	13.72	20.08	14.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.72 differs from the reported value 9.5 by more than 10 %

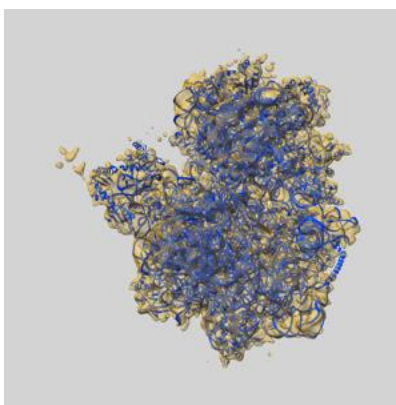
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13445 and PDB model 7PIO. Per-residue inclusion information can be found in section [3](#) on page [13](#).

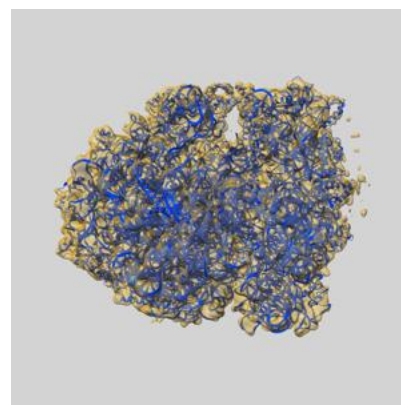
9.1 Map-model overlay [i](#)



X



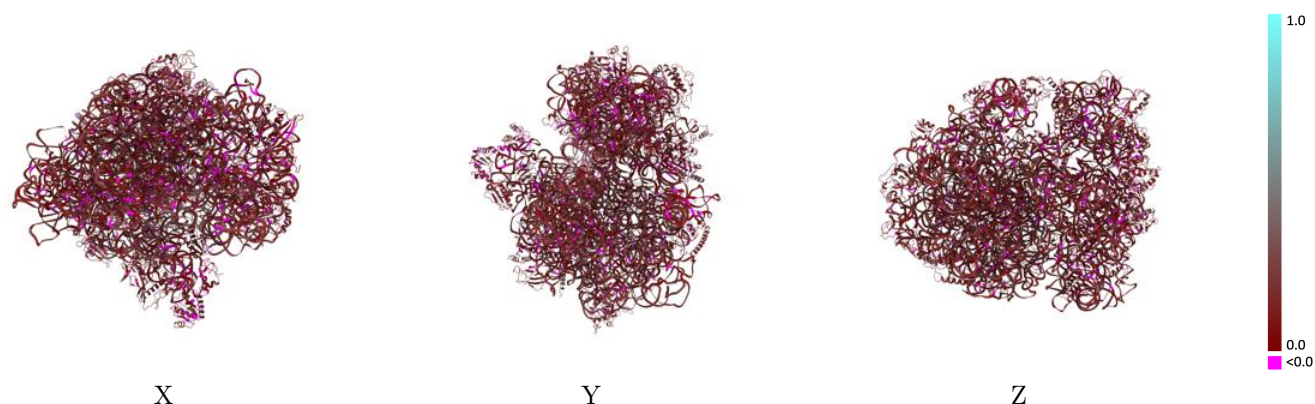
Y



Z

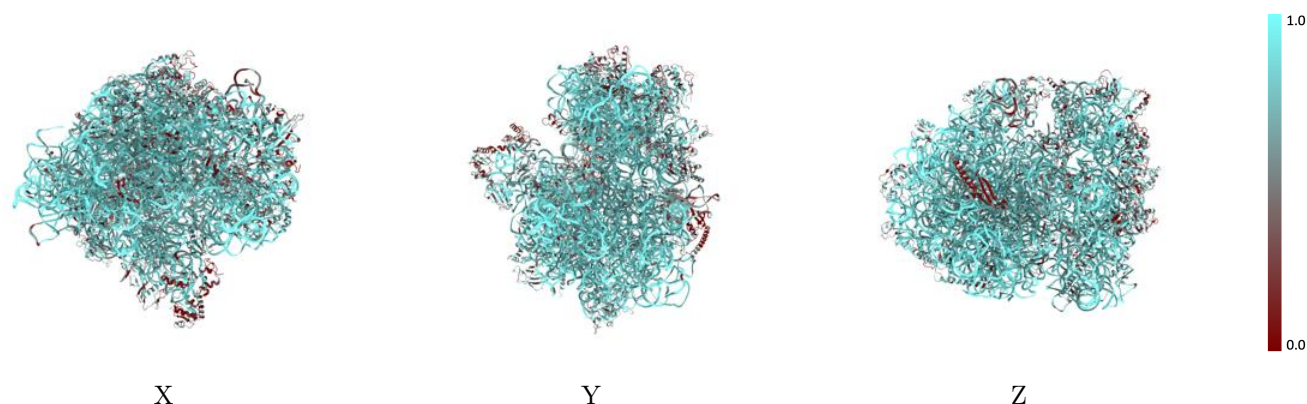
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



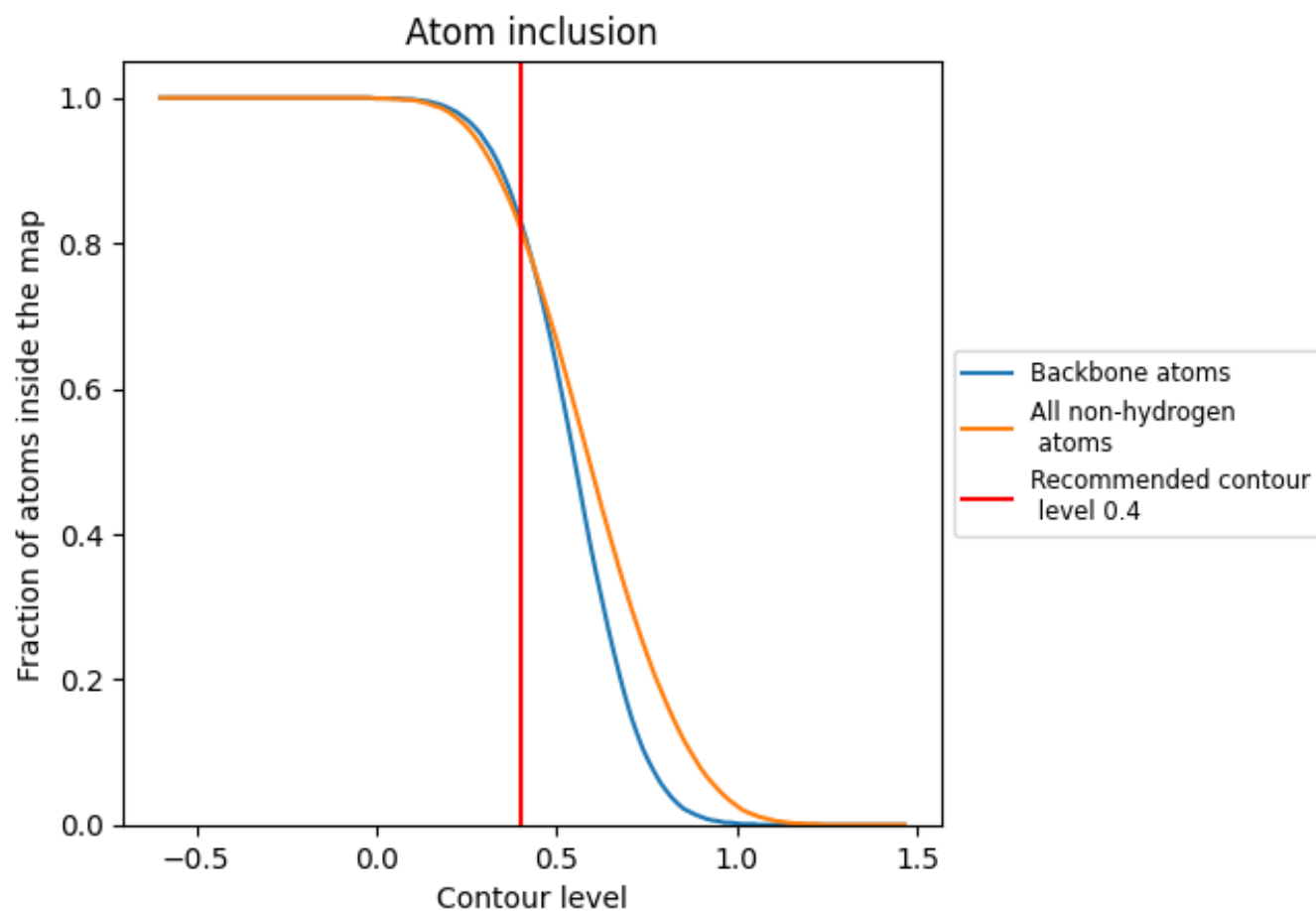
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion ⓘ



At the recommended contour level, 83% of all backbone atoms, 82% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8210	 0.1550
0	 0.8110	 0.1480
1	 0.6460	 0.1130
2	 0.7130	 0.0970
3	 0.9270	 0.1650
4	 0.9400	 0.1820
5	 0.9180	 0.1580
7	 0.8690	 0.1760
A	 0.5250	 0.1680
B	 0.5240	 0.1400
C	 0.5790	 0.1290
D	 0.5810	 0.1360
E	 0.5080	 0.1630
F	 0.5840	 0.1510
G	 0.5950	 0.1360
H	 0.5540	 0.1010
I	 0.5110	 0.1320
J	 0.6080	 0.1210
K	 0.6270	 0.1240
L	 0.5730	 0.1380
M	 0.5800	 0.1120
N	 0.6570	 0.1710
O	 0.6710	 0.1300
P	 0.6150	 0.1090
Q	 0.5370	 0.1180
R	 0.5600	 0.0880
S	 0.7380	 0.1530
T	 0.6270	 0.1720
a	 0.7150	 0.1300
b	 0.6730	 0.1190
c	 0.6720	 0.1530
d	 0.6350	 0.1390
e	 0.5590	 0.1500
f	 0.1940	 0.1330
g	 0.3970	 0.1230



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.2460	 0.0890
i	 0.6920	 0.1400
j	 0.5840	 0.1360
k	 0.6880	 0.1340
l	 0.7170	 0.1360
m	 0.6960	 0.1250
n	 0.6590	 0.1500
o	 0.6100	 0.1440
p	 0.7430	 0.1310
q	 0.6610	 0.1490
r	 0.6940	 0.1440
s	 0.7040	 0.1670
t	 0.5730	 0.1510
u	 0.6770	 0.1060
v	 0.6710	 0.1310
w	 0.6890	 0.1830
x	 0.4930	 0.1750
y	 0.6940	 0.1110
z	 0.6930	 0.1410