



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:31 PM UTC

PDB ID : 6OFX / pdb_00006ofx
EMDB ID : EMD-20048
Title : Non-rotated ribosome (Structure I)
Authors : Svidritskiy, E.; Demo, G.; Loveland, A.B.; Xu, C.; Korostelev, A.A.
Deposited on : 2019-04-01
Resolution : 3.30 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:

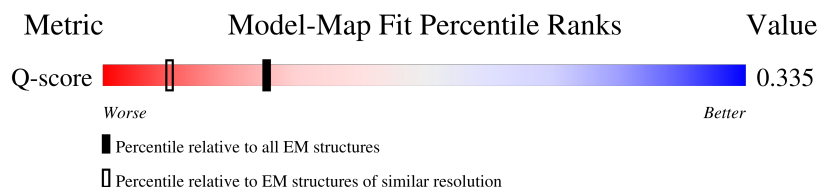
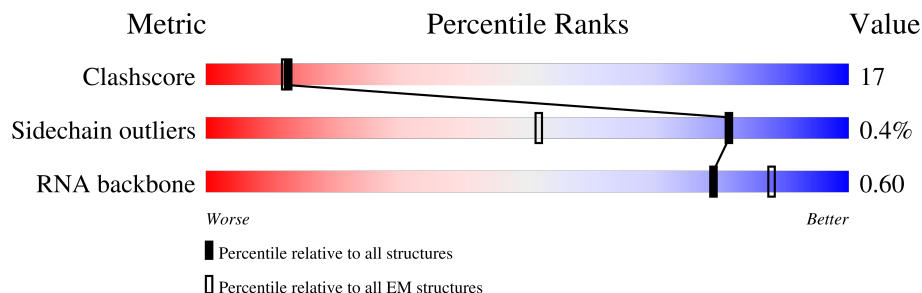
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.30 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.






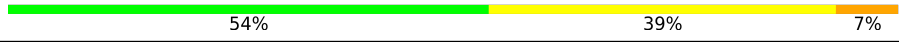
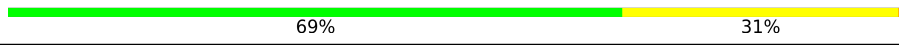








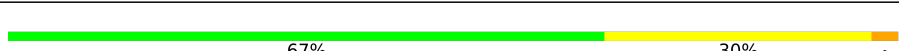
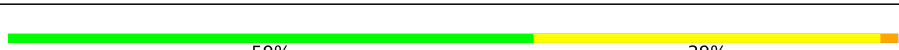

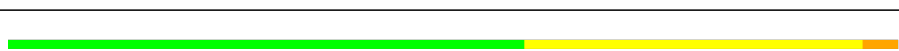




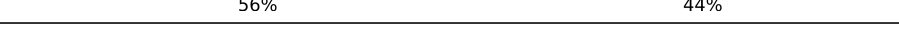
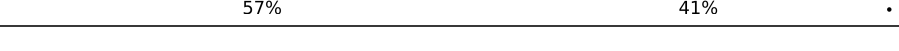


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	271	55% 42% .
2	c	209	67% 32% .
3	d	201	62% 37% .
4	e	177	35% 54% 10% .



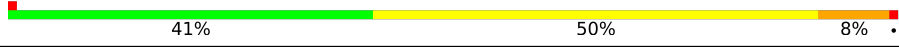
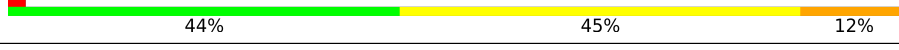



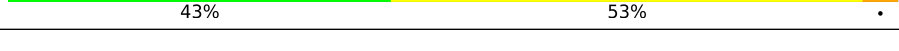
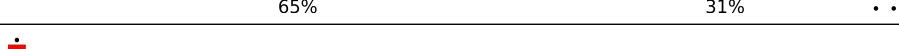
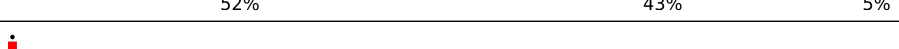

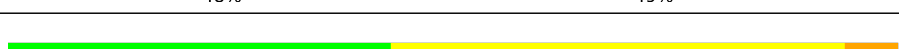
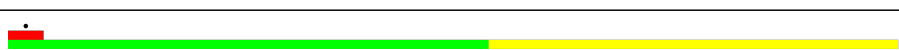

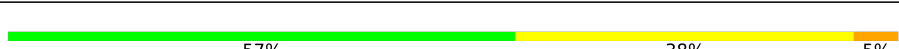
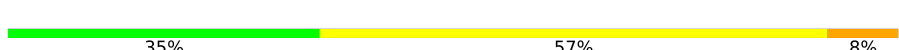




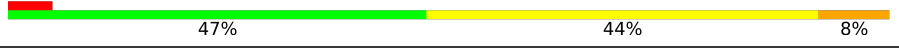

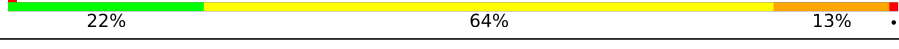
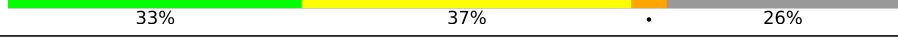

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Mol	Chain	Length	Quality of chain
5	f	176	
6	g	149	
7	j	142	
8	k	122	
9	l	143	
10	m	136	
11	n	120	
12	o	116	
13	p	114	
14	q	117	
15	r	103	
16	s	110	
17	t	93	
18	u	102	
19	v	94	
20	w	75	
21	x	77	
22	y	63	
23	z	58	
24	B	56	
25	C	50	
26	D	46	
27	E	64	
28	F	38	
29	G	225	

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Mol	Chain	Length	Quality of chain
30	H	206	
31	I	205	
32	J	157	
33	K	101	
34	L	151	
35	M	129	
36	N	127	
37	O	98	
38	P	116	
39	Q	123	
40	R	114	
41	S	100	
42	T	88	
43	U	82	
44	V	80	
45	W	65	
46	X	79	
47	Y	85	
48	Z	65	
49	a	223	
50	3	1539	
51	1	2903	
52	2	120	
53	5	77	
54	4	27	

2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 144986 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	2083	1288	423	365	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	1411	899	249	257	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	939	587	180	166	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	961	593	196	167	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
			739	466	139	132	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
			780	492	146	142		

- 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
			410	263	75	72		

- 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
			1757	1111	315	323	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
			1625	1028	305	289	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
			1157	719	218	214	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
			1182	735	227	216	4		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

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

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

- 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
			649	411	121	114	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
			536	339	100	96	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
			638	408	120	108	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
			545	335	117	92	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

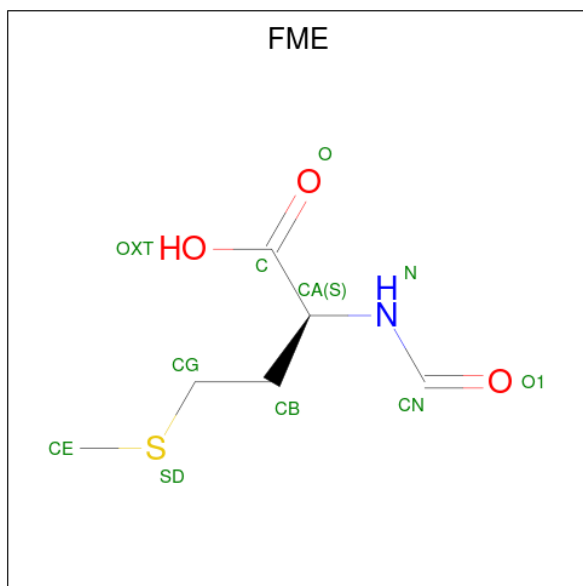
- Molecule 53 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 54 is a RNA chain called mRNA.

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

- Molecule 55 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).

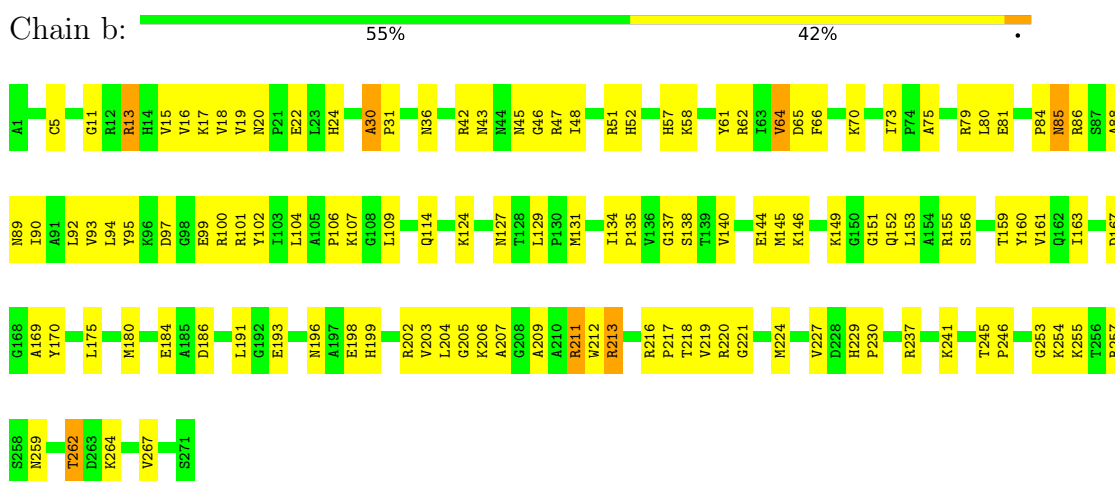


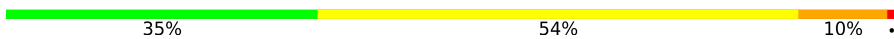
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
55	5	1	10	6	1	2	1	0

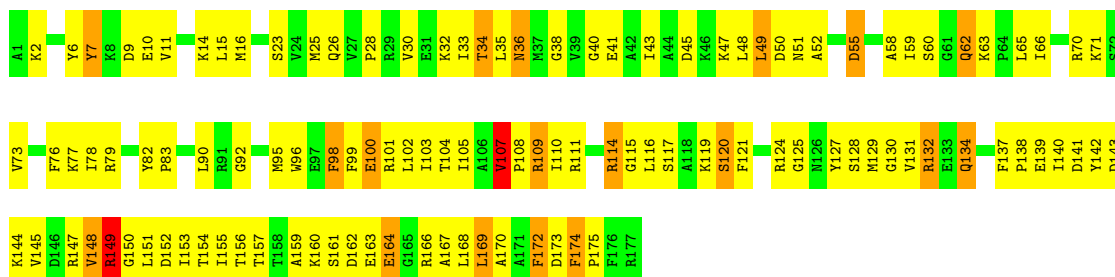
3 Residue-property plots

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

- Molecule 1: 50S ribosomal protein L2

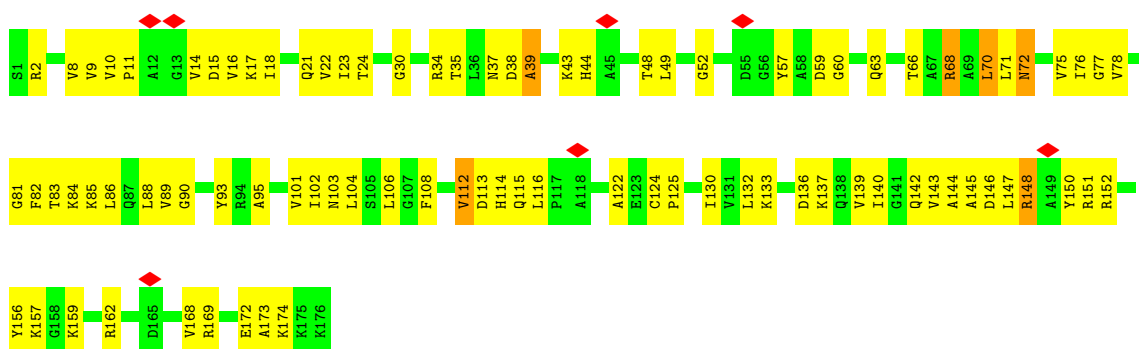


Chain e:  35% 54% 10%



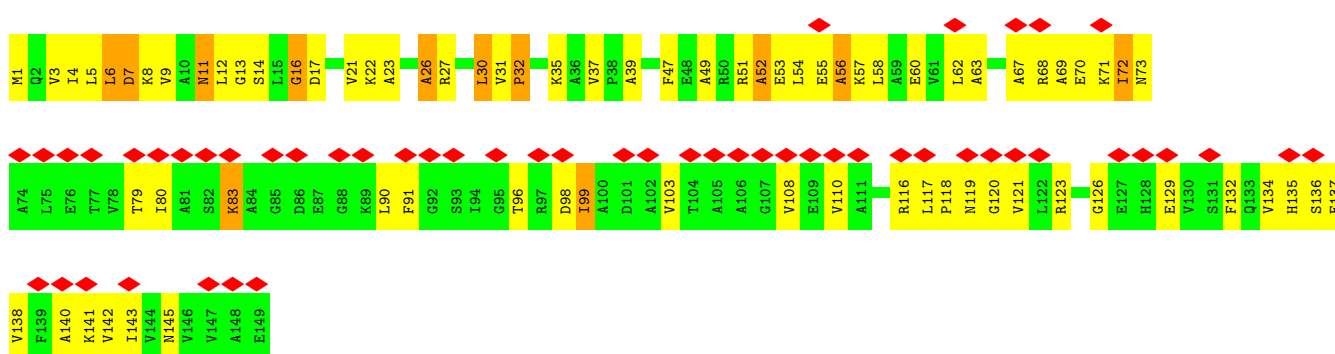
• Molecule 5: 50S ribosomal protein L6

Chain f:  49% 47%



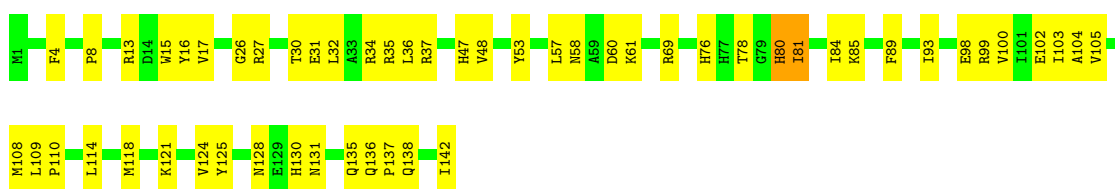
• Molecule 6: 50S ribosomal protein L9

Chain g:  36% 49% 43% 8%



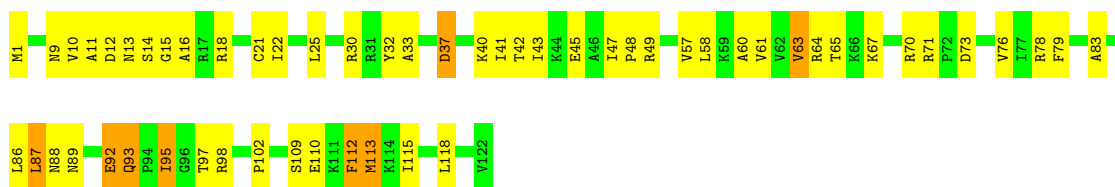
• Molecule 7: 50S ribosomal protein L13

Chain j:  62% 37%



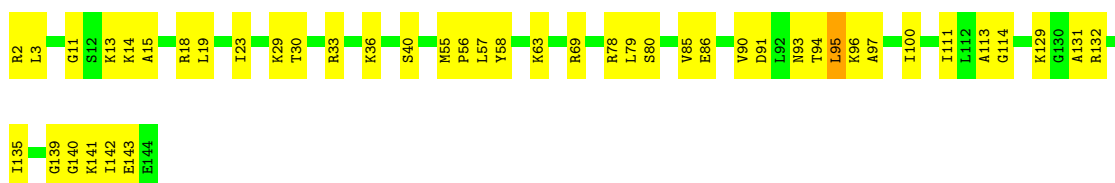
- Molecule 8: 50S ribosomal protein L14

Chain k: 



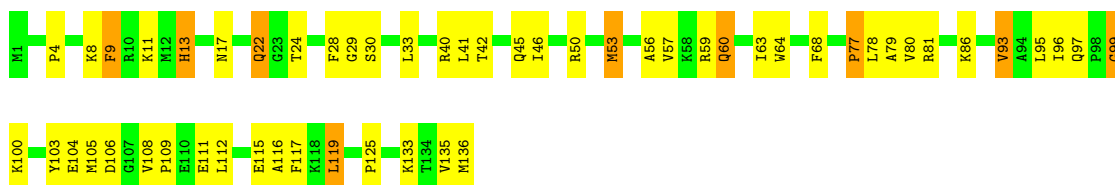
- Molecule 9: 50S ribosomal protein L15

Chain l: 



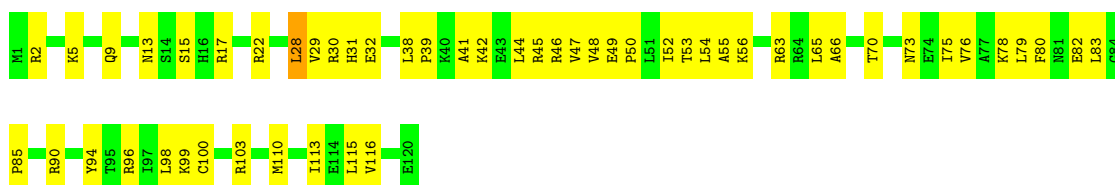
- Molecule 10: 50S ribosomal protein L16

Chain m: 



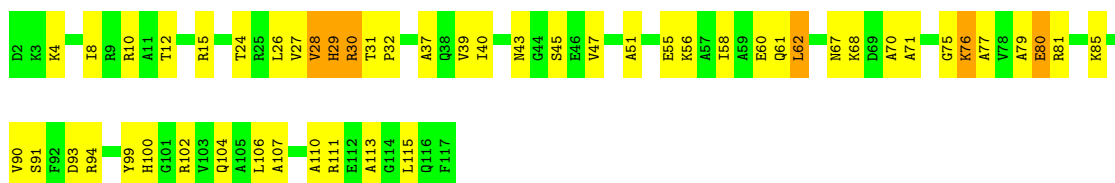
- Molecule 11: 50S ribosomal protein L17

Chain n: 



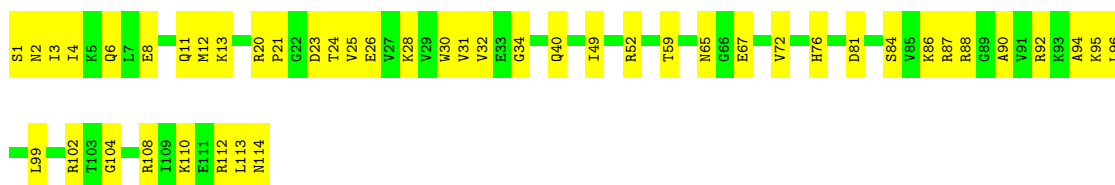
- Molecule 12: 50S ribosomal protein L18

Chain o: 



- Molecule 13: 50S ribosomal protein L19

Chain p:  60% 40%



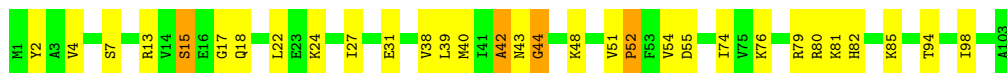
- Molecule 14: 50S ribosomal protein L20

Chain q:  67% 32%



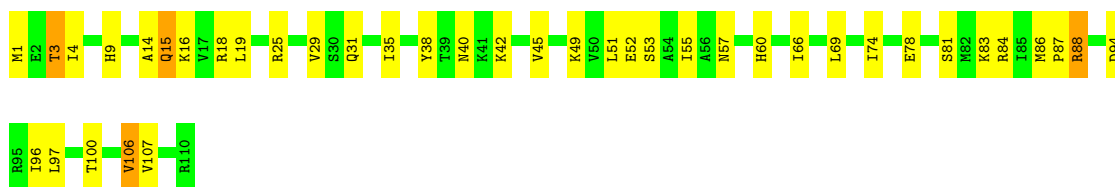
- Molecule 15: 50S ribosomal protein L21

Chain r:  70% 26%



- Molecule 16: 50S ribosomal protein L22

Chain s:  64% 33%



- Molecule 17: 50S ribosomal protein L23

Chain t:  59% 39%

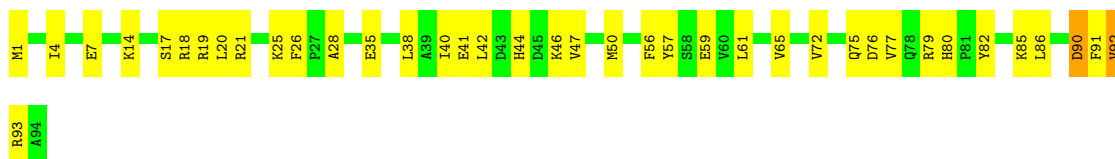


- Molecule 18: 50S ribosomal protein L24

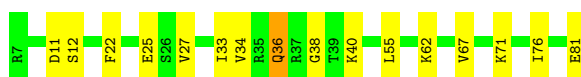
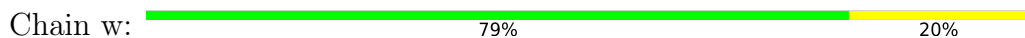
Chain u:  67% 30%



• Molecule 19: 50S ribosomal protein L25



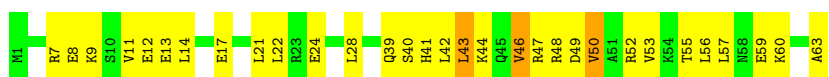
• Molecule 20: 50S ribosomal protein L27



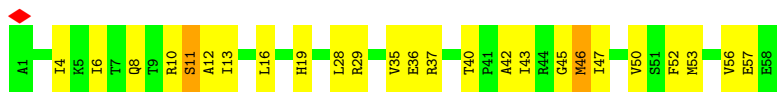
• Molecule 21: 50S ribosomal protein L28



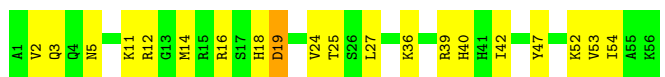
• Molecule 22: 50S ribosomal protein L29



• Molecule 23: 50S ribosomal protein L30



• Molecule 24: 50S ribosomal protein L32



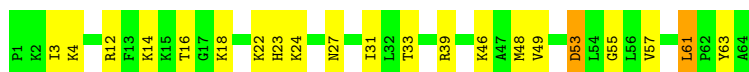
• Molecule 25: 50S ribosomal protein L33



• Molecule 26: 50S ribosomal protein L34



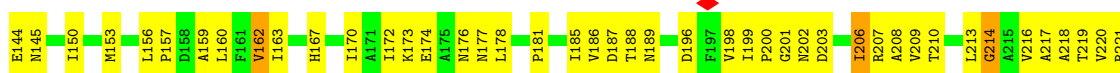
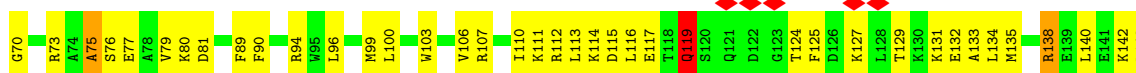
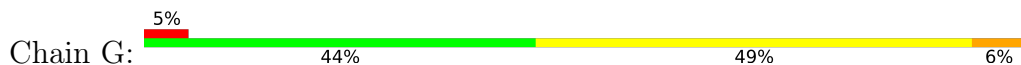
• Molecule 27: 50S ribosomal protein L35



• Molecule 28: 50S ribosomal protein L36

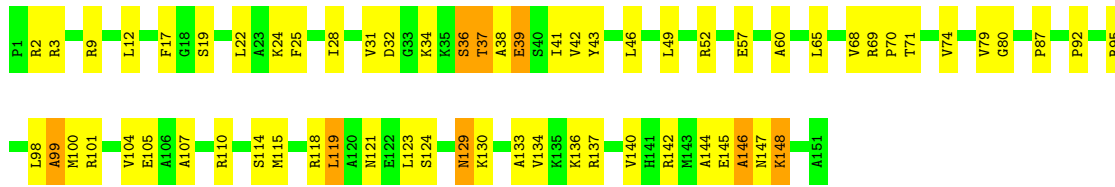


• Molecule 29: 30S ribosomal protein S2

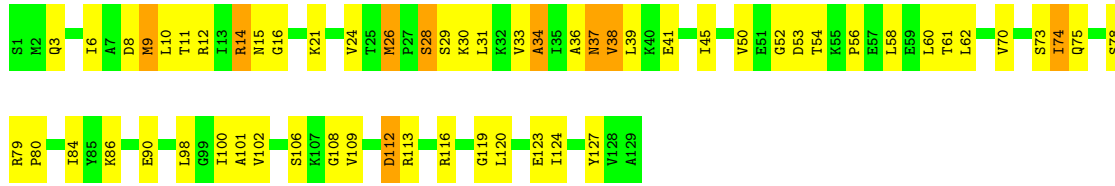


• Molecule 30: 30S ribosomal protein S3

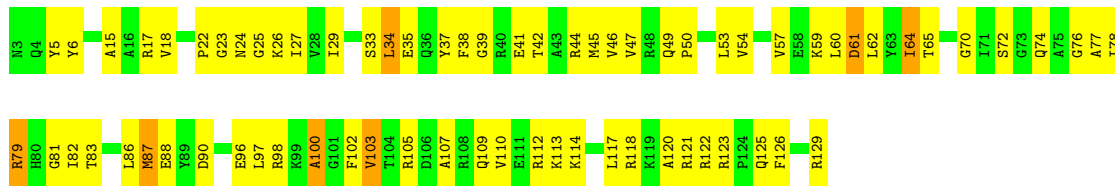




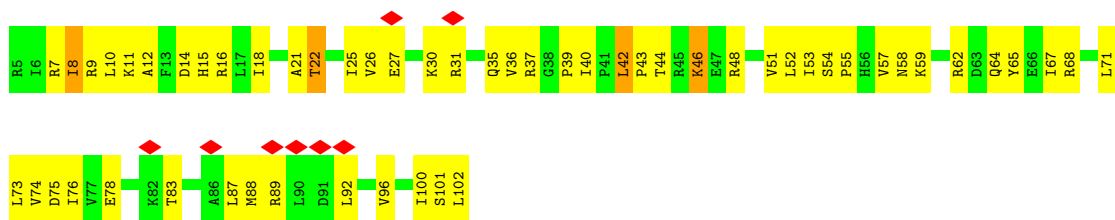
• Molecule 35: 30S ribosomal protein S8



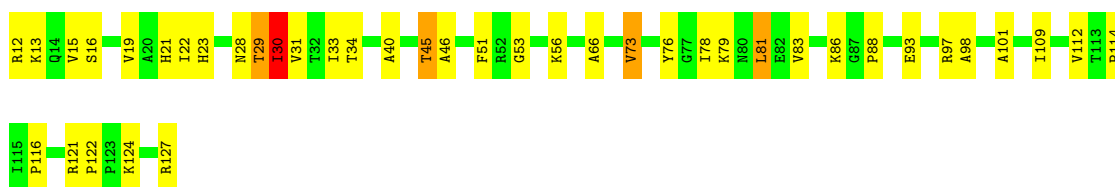
• Molecule 36: 30S ribosomal protein S9



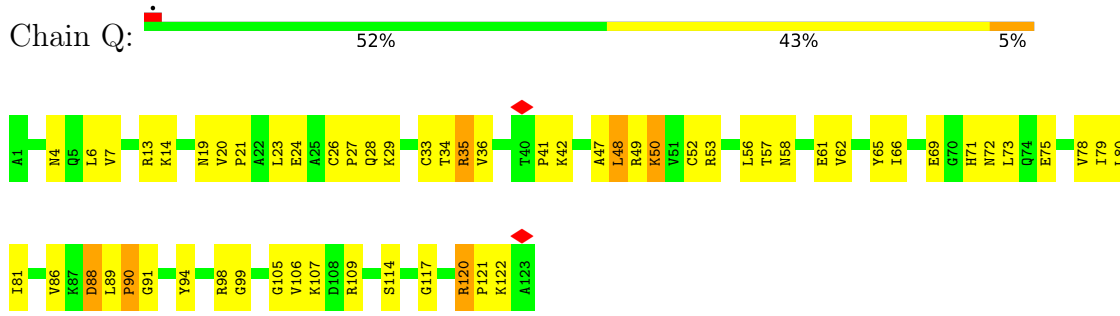
• Molecule 37: 30S ribosomal protein S10



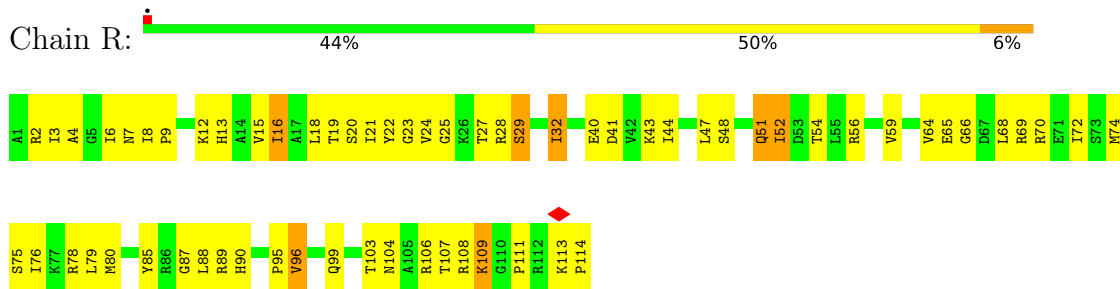
• Molecule 38: 30S ribosomal protein S11



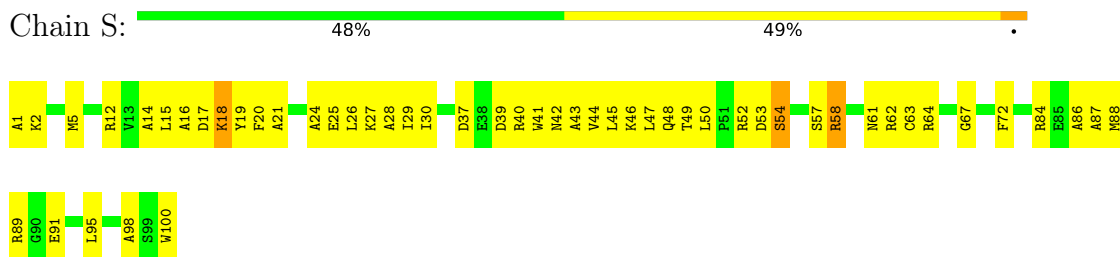
• Molecule 39: 30S ribosomal protein S12



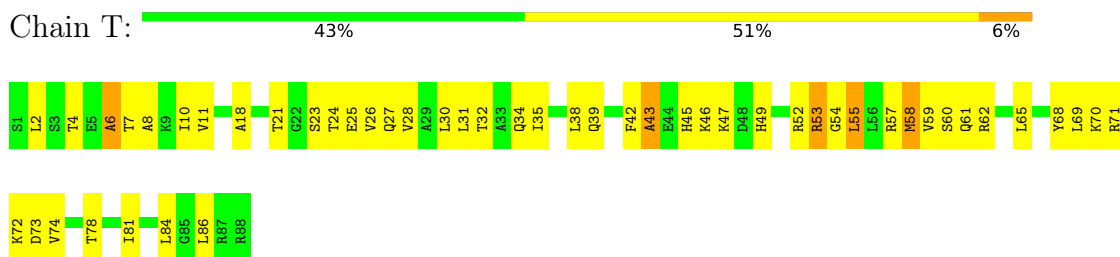
• Molecule 40: 30S ribosomal protein S13



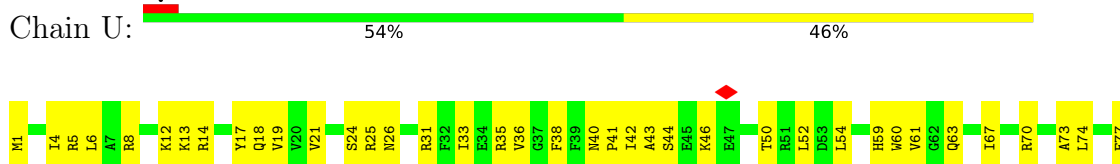
• Molecule 41: 30S ribosomal protein S14



• Molecule 42: 30S ribosomal protein S15



• Molecule 43: 30S ribosomal protein S16





- Molecule 44: 30S ribosomal protein S17

Chain V: 48% 49%



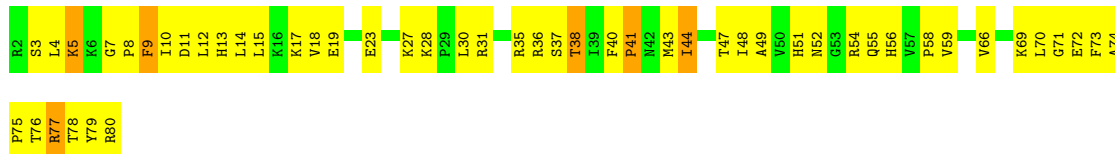
- Molecule 45: 30S ribosomal protein S18

Chain W: 57% 38% 5%



- Molecule 46: 30S ribosomal protein S19

Chain X: 35% 57% 8%



- Molecule 47: 30S ribosomal protein S20

Chain Y: 58% 39%



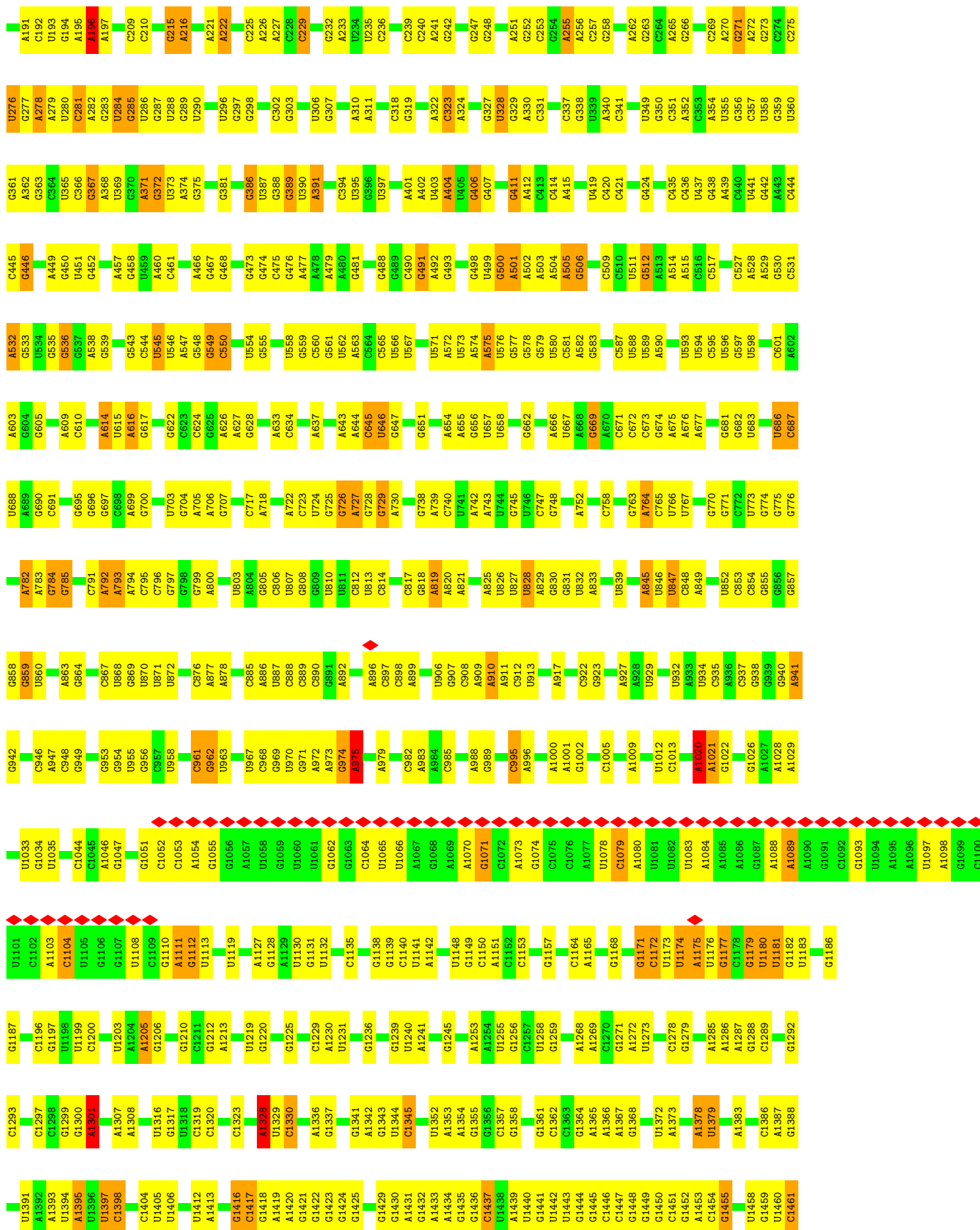
- Molecule 48: 30S ribosomal protein S21

Chain Z: 45% 51% 5%

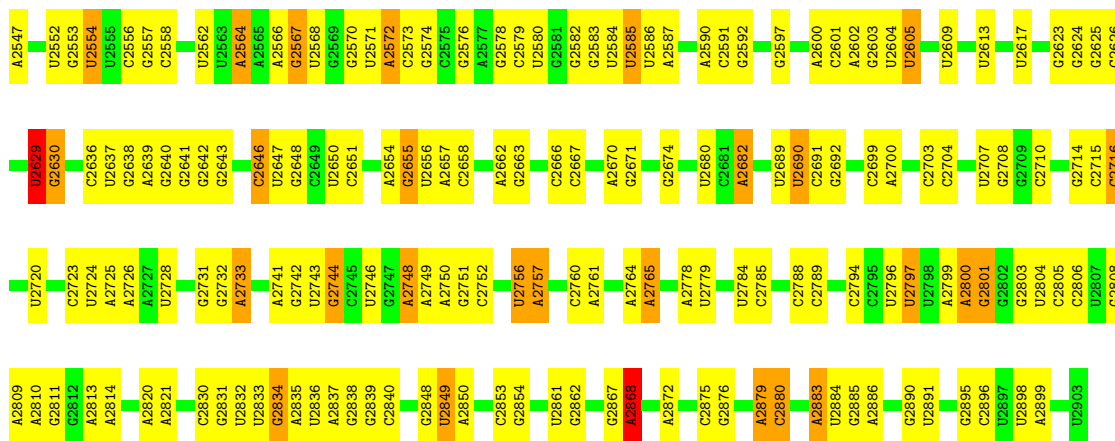


- Molecule 49: 50S ribosomal protein L1

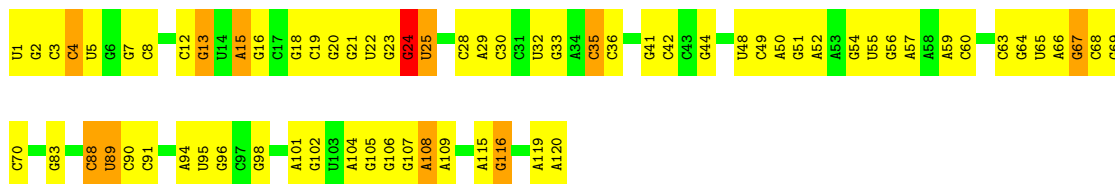
Chain a: 26% 29% 27% 40%



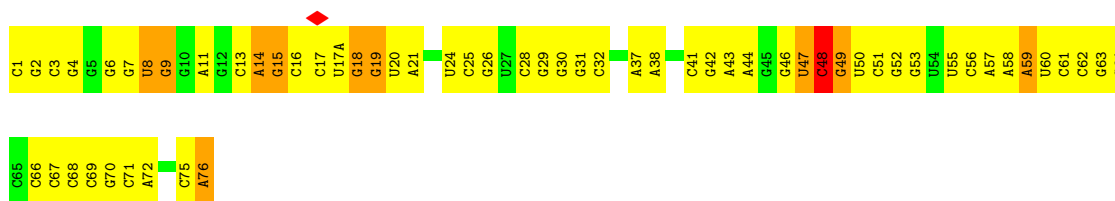
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G1524	A1525	C1526	G1527	A1528	G1529	U1530	C1531	A1532	C1533	U1534	A1535	C1536	G1537	G1538	U1539	G1540	C1541	U1542	A1543	A1544	A1545	C1546	A1547	A1548	A1549	C1550	A1551	U1554	U1555	C1556	C1557	C1558	U1559	G1560	C1561	U1562	U1563	C1564	C1565	A1569	A1570	A1571	A1572	C1577	U1578	A1579	G1580	G1581	A1582	C1585	A1586	G1587	G1588	U1589	A1590		
A1591	U1594	C1595	A1596	A1597	A1598	G1601	U1602	A1603	A1608	A1609	A1610	C1611	G1612	G1613	A1614	G1615	A1630	G1631	A1634	A1635	U1636	A1637	G1642	G1643	C1644	G1645	G1646	U1647	U1648	G1649	A1650	G1651	A1668	A1669	C1670	G1674	A1678	A1679	U1680	G1681	G1682	U1683	G1684	U1688	A1689	A1690	A1698										
G1699	A1700	U1701	G1702	G1703	A1711	U1712	A1713	U1714	G1715	U1716	A1717	G1718	G1719	U1720	A1721	A1722	G1723	G1724	U1725	C1726	C1727	C1728	U1729	C1730	A1731	C1732	G1733	G1734	G1737	G1738	A1739	G1740	C1741	U1742	G1743	A1744	A1745	U1746	U1747	U1751	C1752	G1753	A1754	G1755	G1756	A1757	U1758	A1759	C1760	C1764	U1688	A1689	G1766	C1771	A1772		
A1773	C1774	U1775	G1776	A1784	A1789	C1790	A1791	A1794	G1795	U1796	U1797	U1798	G1799	C1800	A1801	A1802	A1803	C1806	C1807	C1808	A1809	A1810	G1811	C1816	U1817	U1818	A1819	U1820	A1821	C1822	G1823	G1824	U1825	U1826	U1827	G1828	A1829	C1830	C1837	C1838	U1841	U1842	G1843	G1844	G1845	C1846	A1847	A1848	G1849	G1850	U1851	U1852	A1932				
A1853	A1854	U1855	U1856	A1857	U1858	G1860	A1866	G1867	C1868	G1869	C1870	A1871	G1872	A1873	C1874	G1875	A1876	G1878	C1879	U1880	C1891	G1884	A1885	U1886	A1889	G1891	U1898	A1899	A1900	A1901	C1902	G1906	C1909	G1910	U1911	A1912	A1913	U1914	U1915	A1916	U1917	A1918	A1919	G1922	U1923	G1929	G1930	U1931	U1932								
G1933	C1934	G1935	A1936	A1937	U1940	U1943	U1944	G1948	A1952	A1953	G1954	U1955	U1956	A1960	C1961	U1962	U1963	C1967	A1970	U1971	G1972	A1977	A1978	U1979	G1980	A1987	G1988	U1991	C1997	A1998	C1999	C2008	A2009	G2010	U2011	G2012	U2016	A2020	C2021	C2022	C2023	G2026	G2027	U2028													
G2029	A2030	A2031	G2032	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	G2046	C2050	A2051	C2055	G2056	A2060	G2061	A2062	C2065	C2066	G2067	U2068	C2069	A2070	A2071	C2072	C2073	U2074	U2075	A2080	U2081	A2082	C2083	U2085	U2086	G2087	C2091	U2092	G2093	C2096	A2097	U2098	U2099	C2104	U2105	G2106	G2107									
A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	U2118	A2119	U2122	G2123	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	C2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	U2156	G2157	A2158	C2159	C2160	C2161	G2162	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173			
G2174	C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	U2194	U2195	C2196	U2197	A2198	U2203	G2204	C2207	C2208	G2209	A2212	U2213	C2214	C2215	G2216	G2217	U2220	G2221	C2222	G2223	G2224	A2225	C2226	U2227	G2228	U2229	U2233	G2234	G2235	G2236	G2237	G2238	A2239	A2241	G2242	U2245						
G2246	A2247	C2248	U2249	G2250	U2257	C2258	U2259	C2260	C2261	U2262	C2263	C2264	U2265	A2266	A2267	G2269	A2270	U2271	U2272	A2273	A2274	G2275	G2276	A2277	A2278	C2283	G2284	C2285	G2286	A2287	A2288	U2291	U2292	G2293	G2294	C2295	U2296	A2297	A2298	U2299	C2300	C2301	G2302	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	G2314	A2392	
G2315	G2316	G2317	G2318	G2319	U2320	U2321	A2322	U2323	U2324	G2325	G2326	A2327	A2328	U2329	G2330	A2333	U2334	C2339	A2340	U2343	U2344	G2345	G2349	C2350	G2351	A2352	C2353	G2354	G2356	A2366	G2367	G2370	G2371	U2372	G2373	C2374	G2375	A2376	A2377	G2378	G2379	C2380	A2381	G2382	G2383	U2384	C2385	G2389	U2390	G2391	G2392						
U2393	C2394	U2398	G2399	U2400	G2401	A2402	A2403	A2404	G2405	A2406	A2407	U2408	A2418	U2419	C2420	U2423	A2424	A2425	A2426	C2427	G2428	A2429	A2430	U2431	A2432	A2433	A2434	A2435	G2436	G2437	U2438	A2439	C2440	U2441	C2442	G2443	G2444	G2445	G2446	G2447	A2448	C2452	G2455	C2456	U2457	G2458	A2461	U2462	C2466	C2467	A2468	G2469	C2470				
A2471	G2472	C2475	A2476	U2477	A2478	U2479	C2480	G2481	G2485	G2488	U2489	C2490	U2491	G2494	C2498	C2499	G2502	U2504	G2505	C2506	C2507	C2508	U2511	C2512	A2513	U2514	C2515	A2516	C2517	A2518	C2519	C2520	G2526	C2527	U2528	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	C2538	G2543	G2544	G2545	C2546	U2546								



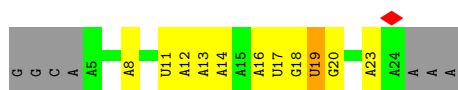
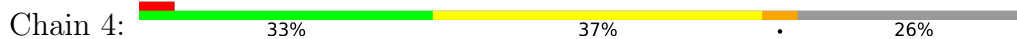
• Molecule 52: 5S ribosomal RNA



• Molecule 53: tRNA^{fMet}



• Molecule 54: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102723	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	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	6.503	Depositor
Minimum map value	-1.639	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.401	Depositor
Recommended contour level	0.7	Depositor
Map size (\AA)	416.208, 416.208, 416.208	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.334, 1.334, 1.334	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	0.80	4/2122 (0.2%)	1.10	12/2852 (0.4%)
2	c	0.81	4/1586 (0.3%)	1.11	11/2134 (0.5%)
3	d	0.82	7/1571 (0.4%)	1.05	6/2113 (0.3%)
4	e	0.98	12/1435 (0.8%)	1.22	19/1926 (1.0%)
5	f	1.00	9/1343 (0.7%)	1.16	14/1816 (0.8%)
6	g	1.25	15/1122 (1.3%)	1.36	20/1515 (1.3%)
7	j	0.78	4/1152 (0.3%)	1.09	3/1551 (0.2%)
8	k	0.84	2/948 (0.2%)	1.27	13/1268 (1.0%)
9	l	0.70	1/1054 (0.1%)	1.12	10/1403 (0.7%)
10	m	0.92	6/1093 (0.5%)	1.10	4/1460 (0.3%)
11	n	0.73	1/974 (0.1%)	1.10	5/1301 (0.4%)
12	o	1.10	8/902 (0.9%)	1.17	8/1209 (0.7%)
13	p	0.64	1/929 (0.1%)	0.93	0/1242
14	q	0.80	1/960 (0.1%)	1.15	2/1278 (0.2%)
15	r	0.70	3/829 (0.4%)	0.96	2/1107 (0.2%)
16	s	0.89	6/864 (0.7%)	1.14	6/1156 (0.5%)
17	t	0.83	2/745 (0.3%)	1.04	2/994 (0.2%)
18	u	0.67	1/788 (0.1%)	0.96	5/1051 (0.5%)
19	v	0.72	2/766 (0.3%)	0.97	4/1025 (0.4%)
20	w	0.60	2/582 (0.3%)	0.91	0/769
21	x	0.90	4/635 (0.6%)	1.09	3/848 (0.4%)
22	y	0.89	1/510 (0.2%)	1.18	6/677 (0.9%)
23	z	0.63	1/453 (0.2%)	0.83	0/605
24	B	0.67	0/450	0.93	3/599 (0.5%)
25	C	0.68	1/417 (0.2%)	0.78	0/554
26	D	0.71	1/380 (0.3%)	1.18	4/498 (0.8%)
27	E	0.85	3/513 (0.6%)	1.06	0/676
28	F	1.09	3/303 (1.0%)	1.32	5/397 (1.3%)
29	G	1.24	27/1788 (1.5%)	1.36	27/2408 (1.1%)
30	H	1.07	17/1652 (1.0%)	1.13	15/2225 (0.7%)
31	I	1.08	13/1665 (0.8%)	1.26	18/2227 (0.8%)
32	J	1.15	9/1170 (0.8%)	1.38	22/1573 (1.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	K	1.26	14/843 (1.7%)	1.32	14/1140 (1.2%)
34	L	1.02	12/1196 (1.0%)	1.24	10/1602 (0.6%)
35	M	1.05	12/989 (1.2%)	1.19	10/1326 (0.8%)
36	N	1.01	7/1034 (0.7%)	1.18	4/1375 (0.3%)
37	O	1.01	4/797 (0.5%)	1.16	7/1077 (0.6%)
38	P	0.85	4/886 (0.5%)	1.12	6/1195 (0.5%)
39	Q	0.82	2/969 (0.2%)	1.20	13/1300 (1.0%)
40	R	1.11	8/893 (0.9%)	1.30	8/1193 (0.7%)
41	S	1.01	4/817 (0.5%)	1.25	14/1088 (1.3%)
42	T	1.09	7/722 (1.0%)	1.26	8/964 (0.8%)
43	U	0.61	0/659	1.00	1/884 (0.1%)
44	V	0.63	2/658 (0.3%)	0.86	0/881
45	W	1.03	2/545 (0.4%)	1.24	5/731 (0.7%)
46	X	0.93	3/653 (0.5%)	1.22	8/877 (0.9%)
47	Y	1.03	6/671 (0.9%)	1.21	1/888 (0.1%)
48	Z	1.13	5/551 (0.9%)	1.38	7/728 (1.0%)
49	a	1.20	12/1034 (1.2%)	1.29	17/1387 (1.2%)
50	3	0.41	0/36963	0.51	3/57662 (0.0%)
51	1	0.40	0/69796	0.53	8/108888 (0.0%)
52	2	0.42	0/2872	0.50	0/4479
53	5	0.42	0/1832	0.54	1/2855 (0.0%)
54	4	0.41	0/493	0.51	0/769
All	All	0.61	275/157574 (0.2%)	0.74	394/235746 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	e	0	1
29	G	0	1
32	J	0	2
50	3	0	10
51	1	0	41
52	2	0	1
All	All	0	56

The worst 5 of 275 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	a	59	VAL	C-O	15.37	1.40	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	I	61	ARG	C-O	14.67	1.41	1.24
12	o	58	ILE	C-O	14.63	1.41	1.23
45	W	12	PHE	C-O	14.14	1.40	1.24
2	c	157	LYS	C-O	13.65	1.41	1.23

The worst 5 of 394 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	G	201	GLY	CA-C-N	-12.84	101.95	120.82
29	G	201	GLY	C-N-CA	-12.84	101.95	120.82
7	j	80	HIS	CA-C-N	-12.52	103.95	120.98
7	j	80	HIS	C-N-CA	-12.52	103.95	120.98
29	G	202	ASN	N-CA-C	12.36	126.30	110.24

There are no chirality outliers.

5 of 56 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	3	297	G	Sidechain
29	G	14	HIS	Mainchain
32	J	86	GLY	Mainchain
32	J	92	ARG	Mainchain
4	e	149	ARG	Mainchain

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	2083	0	2157	120	0
2	c	1565	0	1616	55	0
3	d	1552	0	1619	55	0
4	e	1411	0	1447	122	0
5	f	1323	0	1374	69	0
6	g	1111	0	1148	57	0
7	j	1129	0	1162	55	0
8	k	939	0	1012	54	0
9	l	1045	0	1117	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	m	1074	0	1157	50	0
11	n	961	0	1000	37	0
12	o	892	0	923	42	0
13	p	917	0	965	45	0
14	q	947	0	1022	36	0
15	r	816	0	839	31	0
16	s	857	0	922	27	0
17	t	739	0	807	31	0
18	u	780	0	834	21	0
19	v	753	0	780	33	0
20	w	575	0	592	13	0
21	x	625	0	655	26	0
22	y	509	0	543	24	0
23	z	449	0	491	24	0
24	B	444	0	461	17	0
25	C	410	0	440	14	0
26	D	377	0	418	17	0
27	E	504	0	574	17	0
28	F	302	0	343	24	0
29	G	1757	0	1787	98	0
30	H	1625	0	1699	89	0
31	I	1643	0	1710	110	0
32	J	1157	0	1198	74	0
33	K	824	0	815	42	0
34	L	1182	0	1240	52	0
35	M	979	0	1034	46	0
36	N	1022	0	1070	71	0
37	O	787	0	828	48	0
38	P	870	0	878	31	0
39	Q	955	0	1019	64	0
40	R	884	0	944	65	0
41	S	805	0	847	58	0
42	T	714	0	737	33	0
43	U	649	0	666	47	0
44	V	649	0	691	41	0
45	W	536	0	552	21	0
46	X	638	0	665	52	0
47	Y	665	0	714	31	0
48	Z	545	0	579	34	0
49	a	1027	0	1092	59	0
50	3	33012	0	16618	872	0
51	1	62317	0	31346	1187	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	2	2568	0	1303	65	0
53	5	1640	0	836	56	0
54	4	437	0	219	9	0
55	5	10	0	10	1	0
All	All	144986	0	97515	4022	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 17.

The worst 5 of 4022 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)
51:1:2800:A:H3'	51:1:2801:G:H5'	1.26	1.16
44:V:46:HIS:HB2	44:V:70:LYS:HD3	1.20	1.13
30:H:112:ALA:HB3	30:H:184:ASN:HD22	1.14	1.12
51:1:783:A:H2'	51:1:784:G:H4'	1.12	1.11
51:1:2245:U:H5'	51:1:2246:G:H5''	1.37	1.04

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	216/216 (100%)	215 (100%)	1 (0%)	81	83
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	75
3	d	165/165 (100%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	e	148/148 (100%)	144 (97%)	4 (3%)	39	63
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100
7	j	116/116 (100%)	116 (100%)	0	100	100
8	k	103/103 (100%)	102 (99%)	1 (1%)	68	76
9	l	102/102 (100%)	102 (100%)	0	100	100
10	m	109/109 (100%)	107 (98%)	2 (2%)	51	70
11	n	100/100 (100%)	100 (100%)	0	100	100
12	o	86/86 (100%)	86 (100%)	0	100	100
13	p	99/99 (100%)	99 (100%)	0	100	100
14	q	89/89 (100%)	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	80/80 (100%)	80 (100%)	0	100	100
18	u	83/83 (100%)	83 (100%)	0	100	100
19	v	78/78 (100%)	78 (100%)	0	100	100
20	w	57/57 (100%)	57 (100%)	0	100	100
21	x	67/67 (100%)	67 (100%)	0	100	100
22	y	55/55 (100%)	55 (100%)	0	100	100
23	z	48/48 (100%)	47 (98%)	1 (2%)	47	67
24	B	47/47 (100%)	47 (100%)	0	100	100
25	C	45/45 (100%)	45 (100%)	0	100	100
26	D	38/38 (100%)	38 (100%)	0	100	100
27	E	51/51 (100%)	50 (98%)	1 (2%)	48	68
28	F	34/34 (100%)	34 (100%)	0	100	100
29	G	186/186 (100%)	185 (100%)	1 (0%)	81	83
30	H	170/170 (100%)	170 (100%)	0	100	100
31	I	172/172 (100%)	171 (99%)	1 (1%)	78	81
32	J	119/119 (100%)	119 (100%)	0	100	100
33	K	88/88 (100%)	87 (99%)	1 (1%)	65	76
34	L	124/124 (100%)	124 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	M	104/104 (100%)	102 (98%)	2 (2%)	50	68
36	N	105/105 (100%)	105 (100%)	0	100	100
37	O	86/86 (100%)	86 (100%)	0	100	100
38	P	89/89 (100%)	88 (99%)	1 (1%)	65	76
39	Q	103/103 (100%)	102 (99%)	1 (1%)	68	76
40	R	92/92 (100%)	92 (100%)	0	100	100
41	S	83/83 (100%)	83 (100%)	0	100	100
42	T	76/76 (100%)	76 (100%)	0	100	100
43	U	65/65 (100%)	65 (100%)	0	100	100
44	V	74/74 (100%)	73 (99%)	1 (1%)	59	73
45	W	56/56 (100%)	56 (100%)	0	100	100
46	X	70/70 (100%)	70 (100%)	0	100	100
47	Y	65/65 (100%)	65 (100%)	0	100	100
48	Z	55/55 (100%)	55 (100%)	0	100	100
49	a	110/174 (63%)	110 (100%)	0	100	100
All	All	4700/4764 (99%)	4680 (100%)	20 (0%)	81	84

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	K	89	VAL
38	P	30	ILE
44	V	37	ILE
39	Q	88	ASP
4	e	148	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
36	N	80	HIS
49	a	160	GLN
37	O	64	GLN
43	U	79	ASN
12	o	38	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	182 (11%)	2 (0%)
51	1	2902/2903 (99%)	423 (14%)	13 (0%)
52	2	119/120 (99%)	16 (13%)	1 (0%)
53	5	76/77 (98%)	14 (18%)	0
54	4	19/27 (70%)	5 (26%)	0
All	All	4654/4666 (99%)	640 (13%)	16 (0%)

5 of 640 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	3	A
50	3	9	G
50	3	22	G
50	3	31	G
50	3	32	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	2756	U
51	1	2529	G
51	1	2286	G
51	1	2436	G
51	1	1875	G

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	FME	5	101	-	8,9,10	1.27	1 (12%)	8,9,11	1.28	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	FME	5	101	-	-	1/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	5	101	FME	CA-N	2.88	1.50	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	5	101	FME	CA-N-CN	2.31	126.37	122.82

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	5	101	FME	CB-CA-N-CN

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	5	101	FME	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	J	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	86:GLY	C	87:VAL	N	1.15

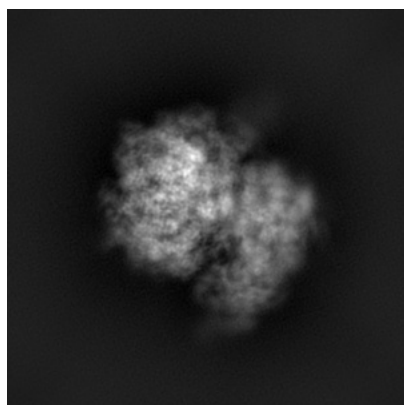
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20048. These allow visual inspection of the internal detail of the map and identification of artifacts.

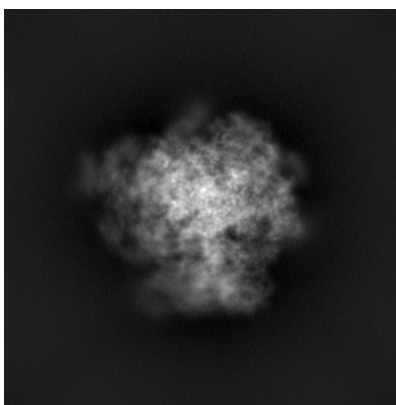
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

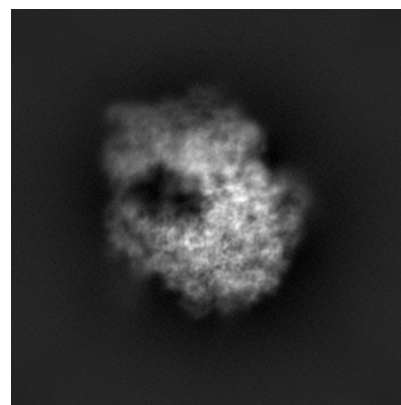
6.1.1 Primary map



X



Y

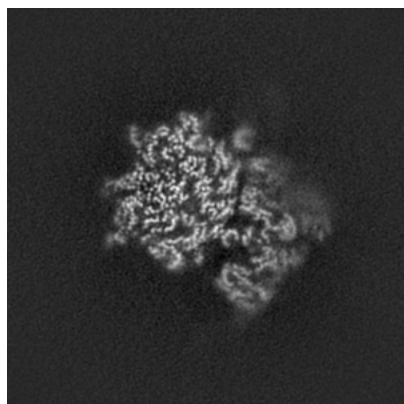


Z

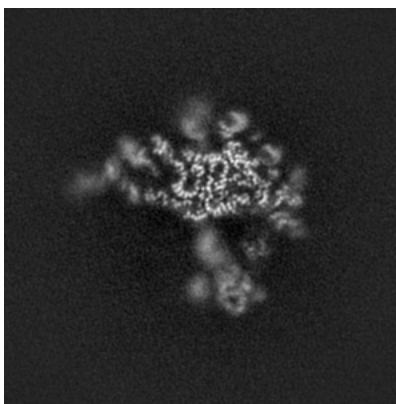
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

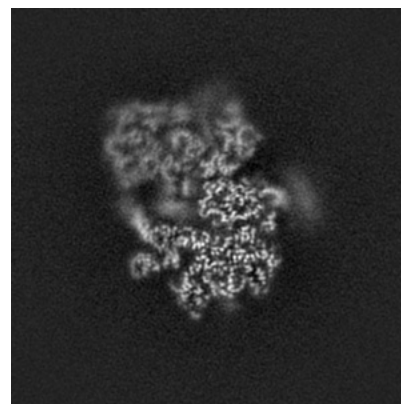
6.2.1 Primary map



X Index: 156



Y Index: 156

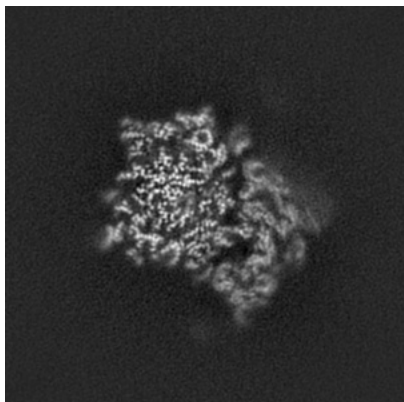


Z Index: 156

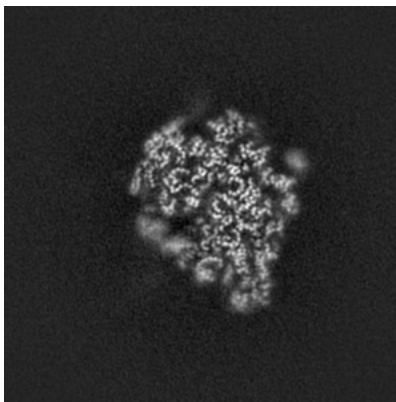
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

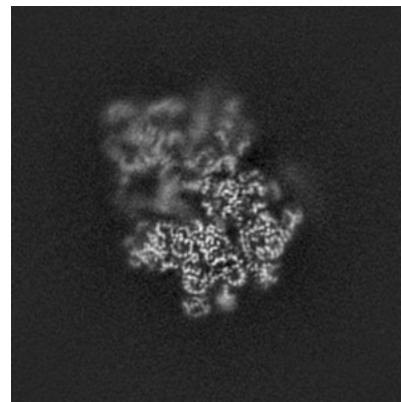
6.3.1 Primary map



X Index: 161



Y Index: 139

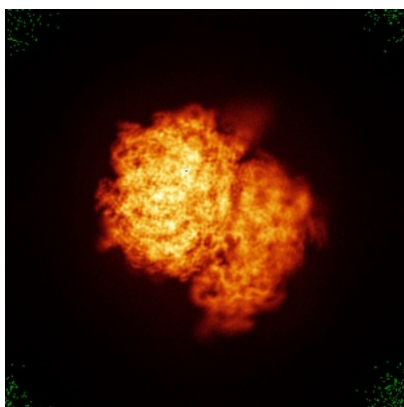


Z Index: 164

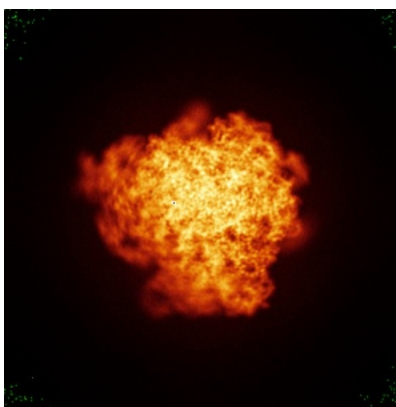
The images above show the largest variance slices of the map in three orthogonal directions.

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

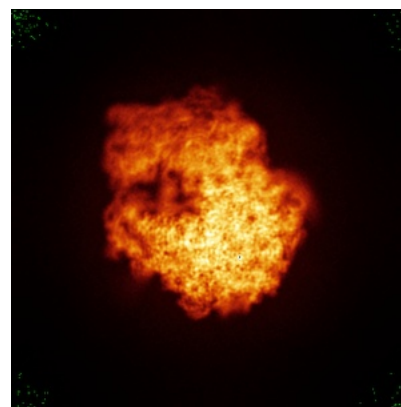
6.4.1 Primary map



X



Y

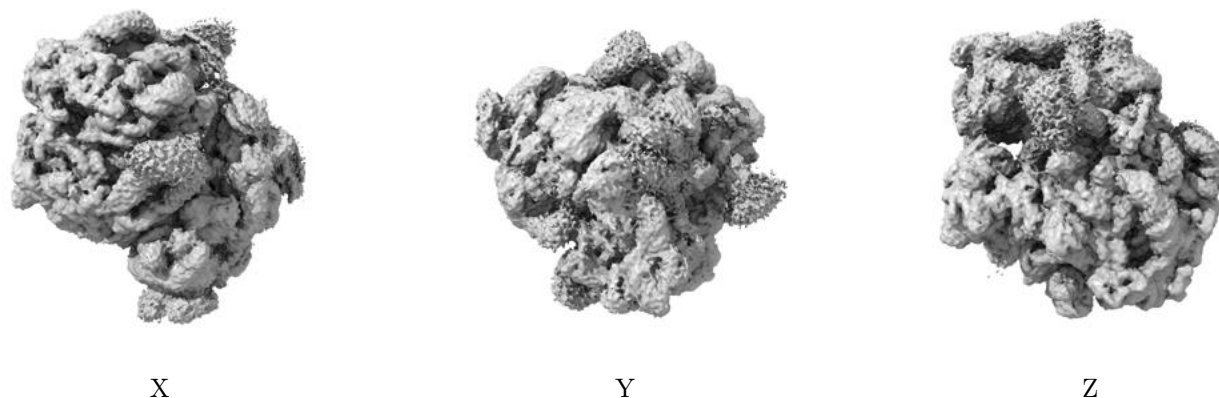


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

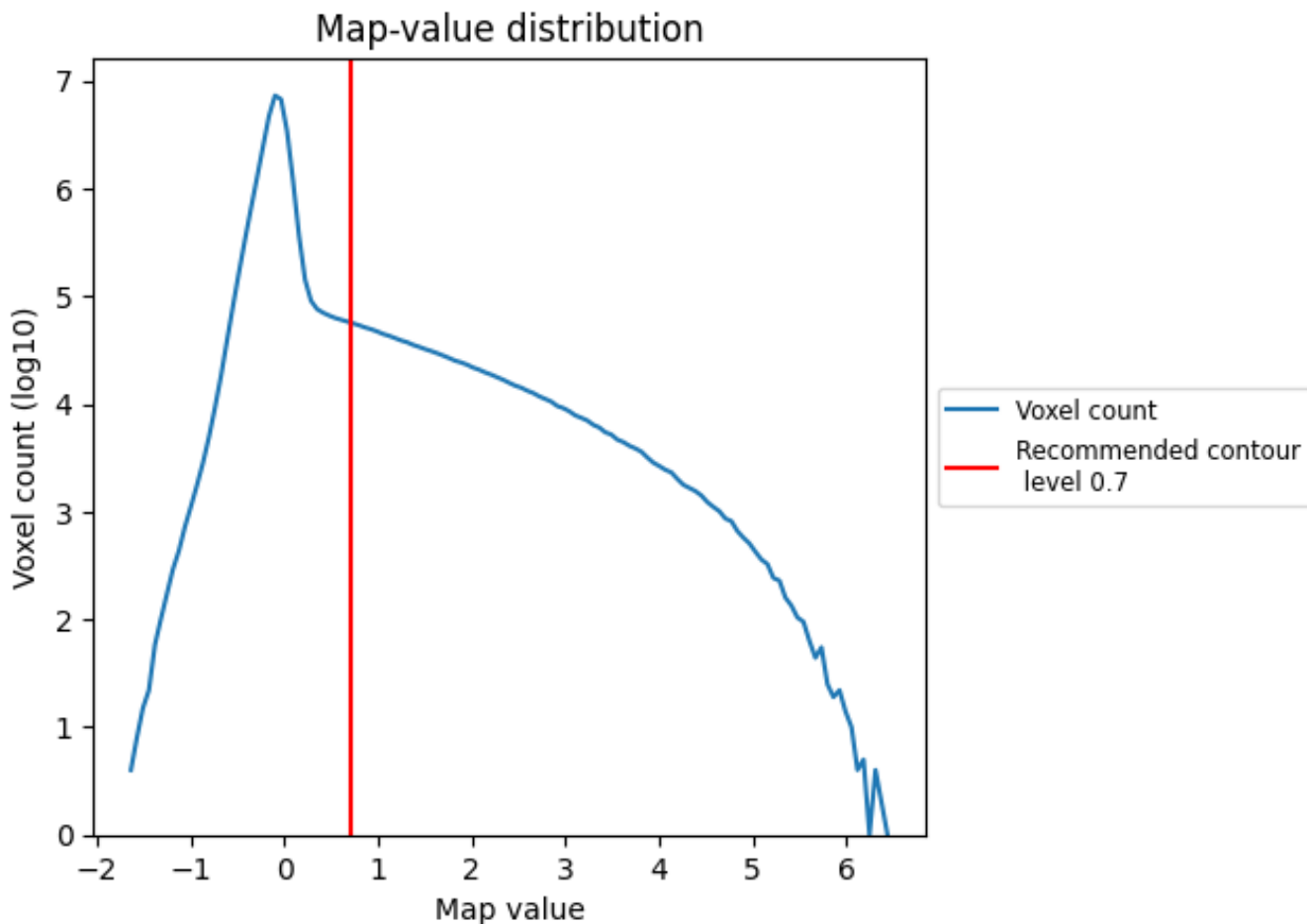
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

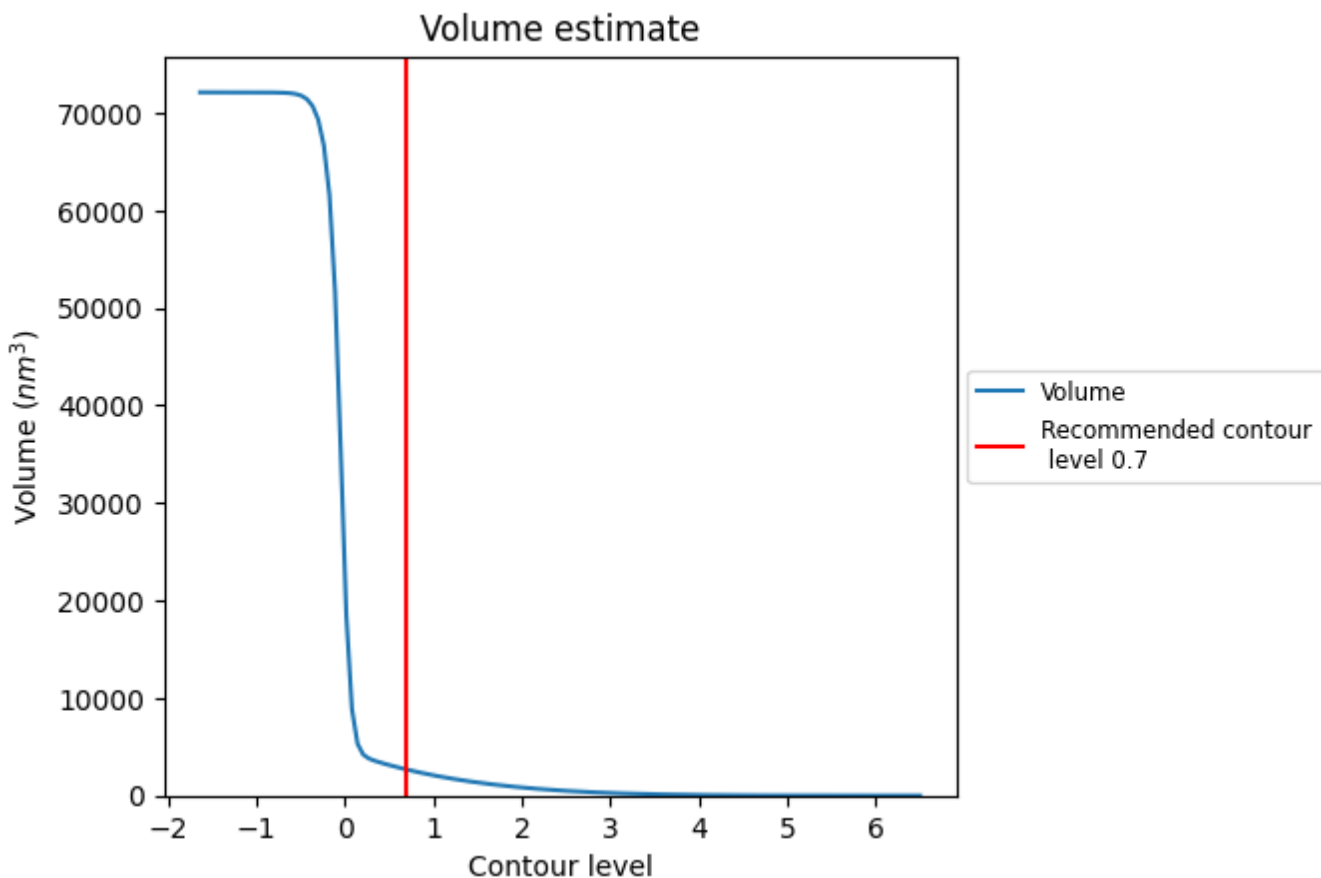
This section contains the results of statistical analysis of the map.

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.

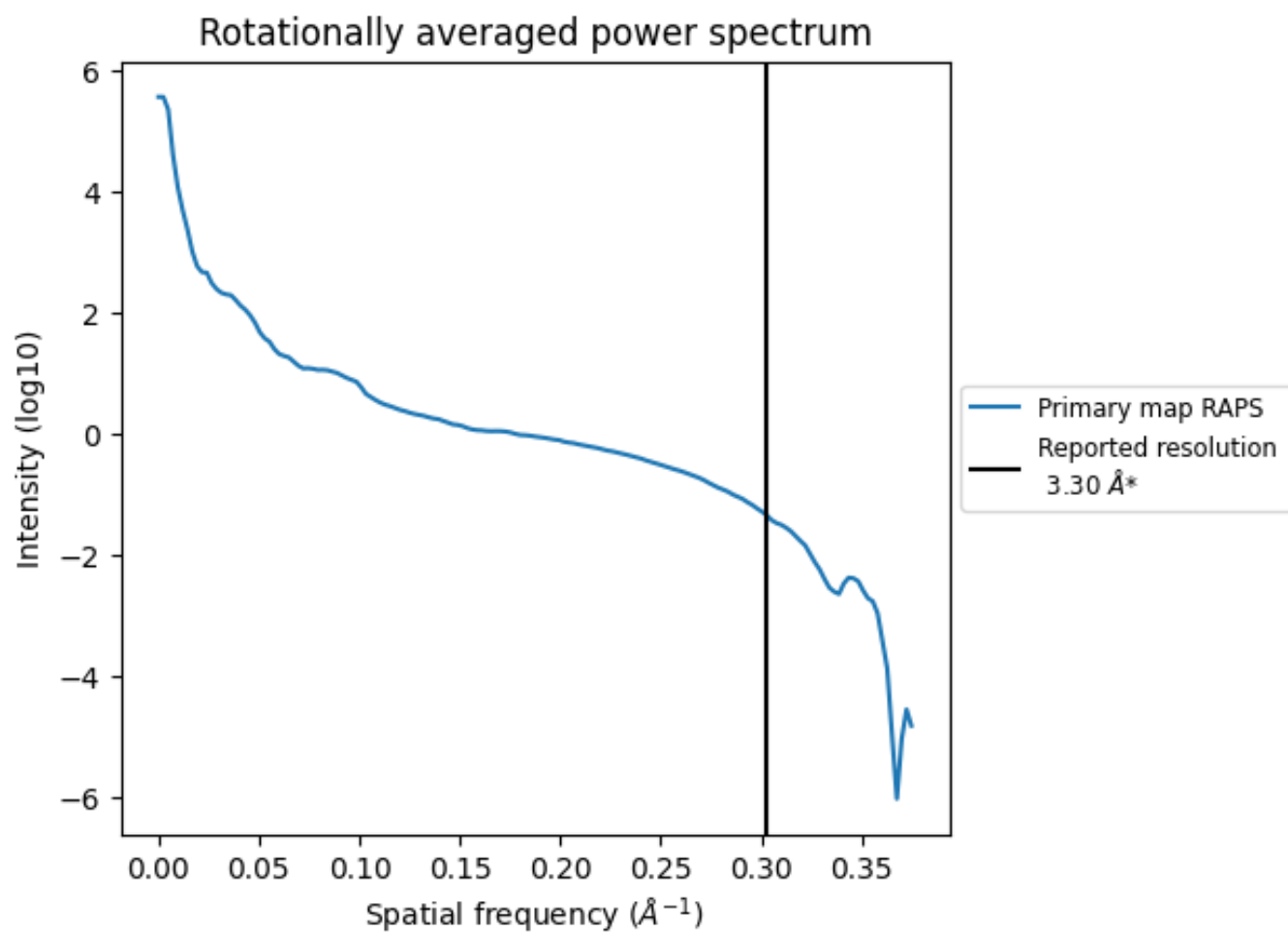
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2665 nm³; this corresponds to an approximate mass of 2407 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 0.303 \AA^{-1}

8 Fourier-Shell correlation

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

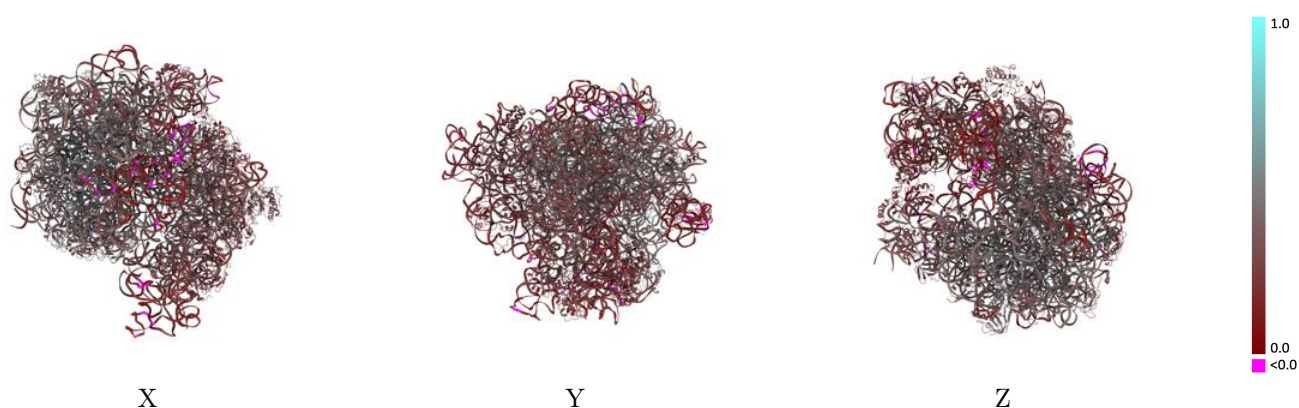
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20048 and PDB model 6OFX. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)

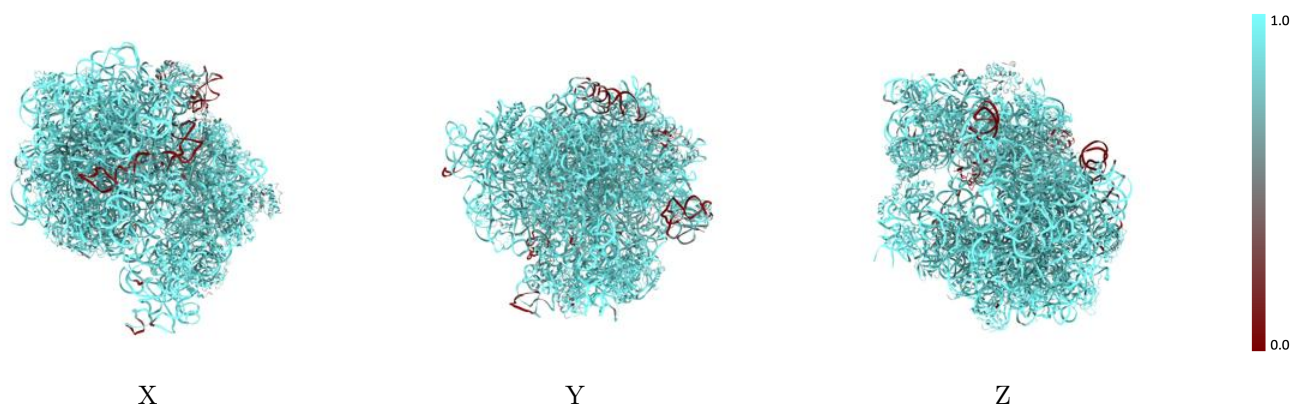
This section was not generated.

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



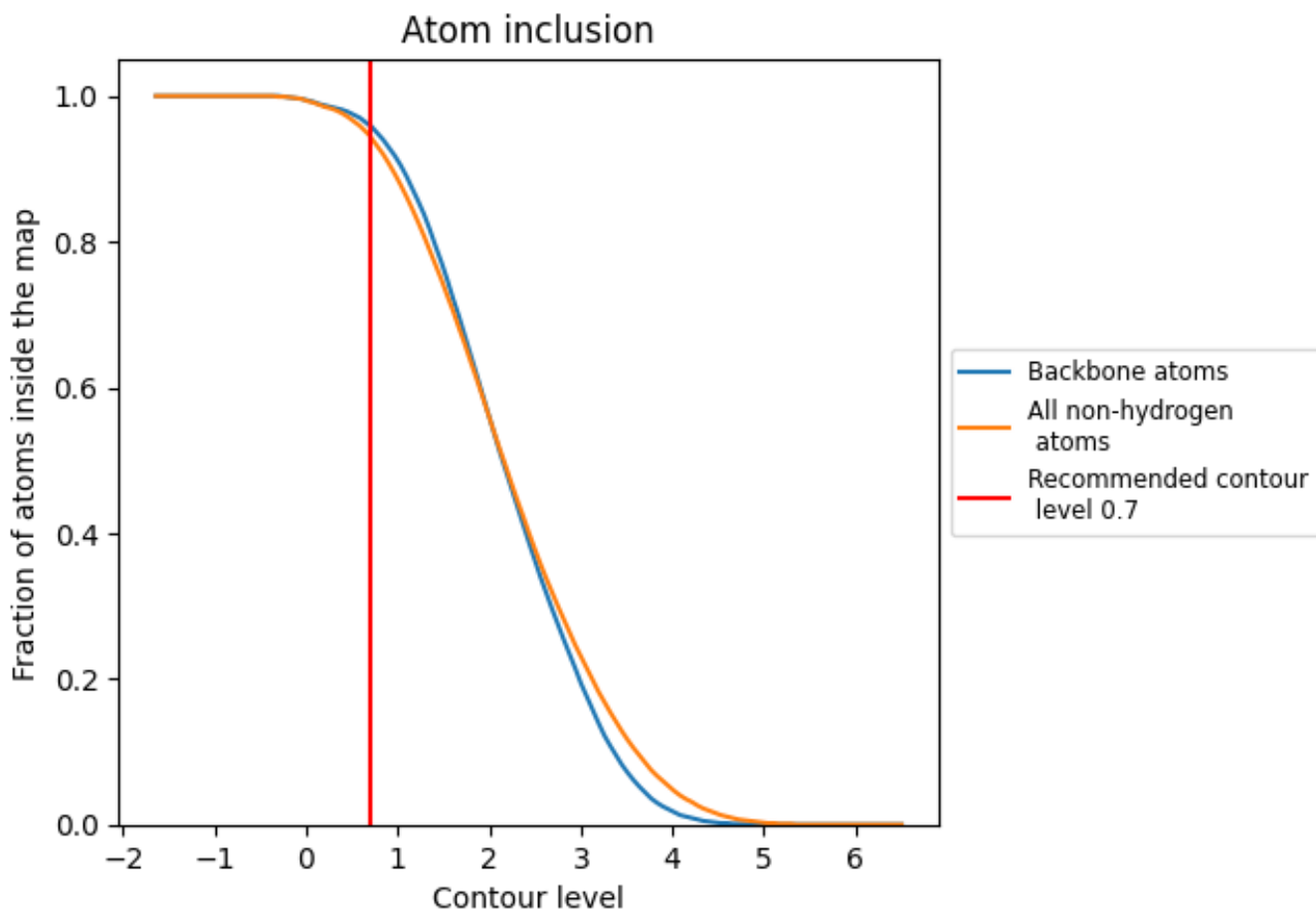
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9450	 0.3350
1	 0.9380	 0.3650
2	 0.9980	 0.3280
3	 0.9750	 0.2890
4	 0.8970	 0.2230
5	 0.9510	 0.1920
B	 0.9700	 0.4130
C	 0.9300	 0.3790
D	 0.9690	 0.4370
E	 0.9650	 0.4330
F	 0.9350	 0.3190
G	 0.8200	 0.2840
H	 0.9110	 0.2960
I	 0.9230	 0.2240
J	 0.9600	 0.3240
K	 0.9360	 0.2930
L	 0.9340	 0.2570
M	 0.9780	 0.3140
N	 0.9770	 0.2350
O	 0.8520	 0.2740
P	 0.9750	 0.3330
Q	 0.9250	 0.2930
R	 0.9370	 0.2130
S	 0.9570	 0.2380
T	 0.9520	 0.2810
U	 0.9510	 0.3060
V	 0.9810	 0.2880
W	 0.9900	 0.3060
X	 0.9790	 0.2080
Y	 0.9630	 0.2760
Z	 0.9360	 0.2700
a	 0.5140	 0.1640
b	 0.9740	 0.4110
c	 0.9830	 0.4350
d	 0.9580	 0.3950



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Chain	Atom inclusion	Q-score
e	 0.9590	 0.2200
f	 0.7980	 0.3080
g	 0.5650	 0.3070
j	 0.9780	 0.4150
k	 0.9720	 0.4170
l	 0.9660	 0.4170
m	 0.9740	 0.4140
n	 0.9780	 0.4270
o	 0.9700	 0.3360
p	 0.9720	 0.4040
q	 0.9710	 0.4200
r	 0.9670	 0.4170
s	 0.9550	 0.4250
t	 0.9700	 0.4020
u	 0.9700	 0.3850
v	 0.9690	 0.3650
w	 0.9680	 0.4410
x	 0.9630	 0.3870
y	 0.9520	 0.3250
z	 0.9470	 0.4070