



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 04:05 AM UTC

PDB ID : 8B6C / pdb_00008b6c
EMDB ID : EMD-15863
Title : Cryo-EM structure of ribosome-Sec61 in complex with cyclotriazadisulfonamide derivative CK147
Authors : Pauwels, E.; Shewakramani, N.R.; De Wijngaert, B.; Vermeire, K.; Das, K.
Deposited on : 2022-09-26
Resolution : 2.79 Å (reported)
Based on initial models : 6MTE, 3J7Q

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:

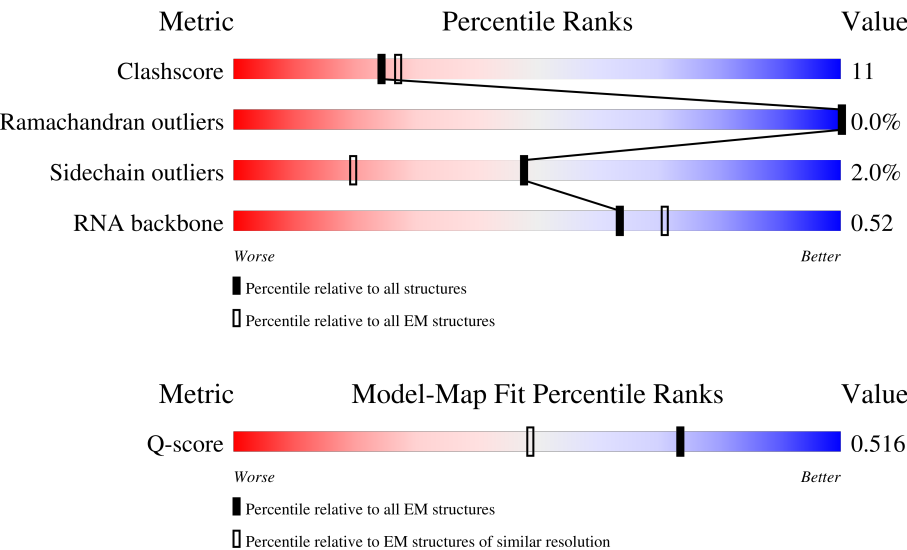
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.79 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	10811 (2.29 - 3.29)

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	T	159	
2	5	4808	
3	F	225	

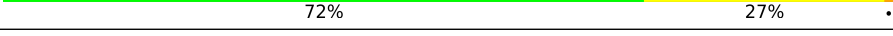
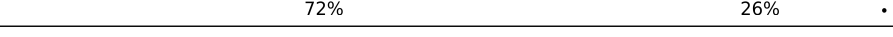
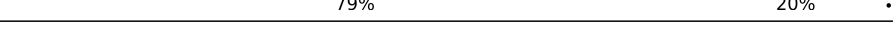
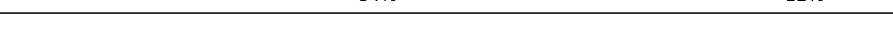
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	293	
5	S	176	
6	b	245	
7	B	394	
8	d	107	
9	8	156	
10	G	319	
11	J	170	
12	c	98	
13	j	86	
14	A	257	
15	I	214	
16	q	68	
17	p	91	
18	V	131	
19	m	52	
20	l	50	
21	P	153	
22	E	291	
23	Q	188	
24	R	196	
25	W	157	
26	O	203	
27	K	476	
28	C	362	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	o	103	
30	r	124	
31	f	109	
32	e	128	
33	Z	135	
34	a	147	
35	g	114	
36	k	70	
37	H	190	
38	L	211	
39	7	120	
40	N	203	
41	i	105	
42	h	122	
43	M	138	
44	Y	134	
45	X	118	
46	U	99	
47	n	25	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 139959 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 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	3619	Total	C	N	O	P	0	0
			77665	34619	14204	25223	3619		

- Molecule 3 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 4 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 5 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 6 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 7 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 8 is a protein called 60S ribosomal protein L31.

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

- Molecule 9 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 11 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 12 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 13 is a protein called Ribosomal protein L37.

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

- Molecule 14 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 15 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 16 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	67	Total	C	N	O	S	0	0
			535	350	93	88	4		

- Molecule 17 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 18 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 19 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 20 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 21 is a protein called 60S ribosomal protein L17.

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

- Molecule 22 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 23 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	134	ARG	CYS	conflict	UNP F6QKI9

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 25 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 27 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	444	Total	C	N	O	S	0	0
			3427	2243	555	607	22		

- Molecule 28 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	C	362	Total	C	N	O	S	0	0
			2884	1813	577	480	14		

- Molecule 29 is a protein called 60S ribosomal protein L36a-like.

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

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 31 is a protein called 60S ribosomal protein L35a.

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

- Molecule 32 is a protein called Ribosomal protein L32.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

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

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 38 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 39 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 40 is a protein called Ribosomal protein L15.

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

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 42 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 43 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 44 is a protein called Ribosomal protein L26.

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

- Molecule 45 is a protein called Ribosomal_L23eN domain-containing protein.

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

- Molecule 46 is a protein called 60S ribosomal protein L22 (Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 47 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	5	161	Total	Mg	0
			161	161	
48	8	5	Total	Mg	0
			5	5	
48	A	1	Total	Mg	0
			1	1	
48	I	1	Total	Mg	0
			1	1	
48	V	1	Total	Mg	0
			1	1	
48	P	1	Total	Mg	0
			1	1	
48	a	1	Total	Mg	0
			1	1	
48	7	7	Total	Mg	0
			7	7	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

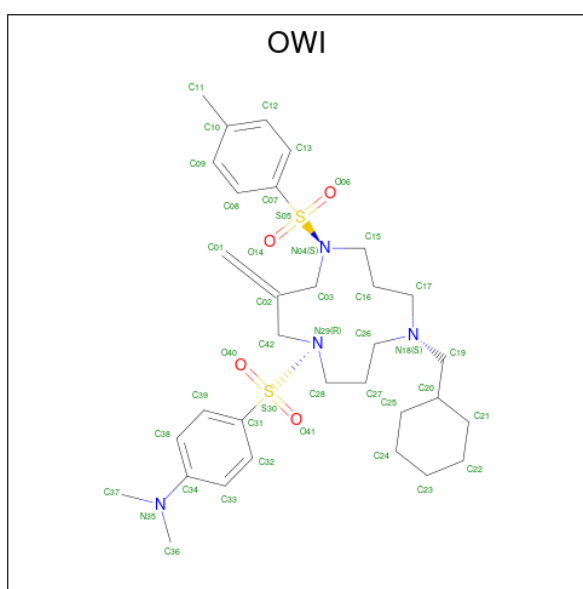
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total	Zn	0
			1	1	
49	p	1	Total	Zn	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
49	m	1	Total	Zn	0
			1	1	
49	o	1	Total	Zn	0
			1	1	
49	g	1	Total	Zn	0
			1	1	

- Molecule 50 is 4-[[9-(cyclohexylmethyl)-3-methyldene-5-(4-methylphenyl)sulfonyl-1,5,9-triazacyclododec-1-yl]sulfonyl]- {N}, {N}-dimethyl-aniline (CCD ID: OWI) (formula: $C_{32}H_{48}N_4O_4S_2$) (labeled as "Ligand of Interest" by depositor).

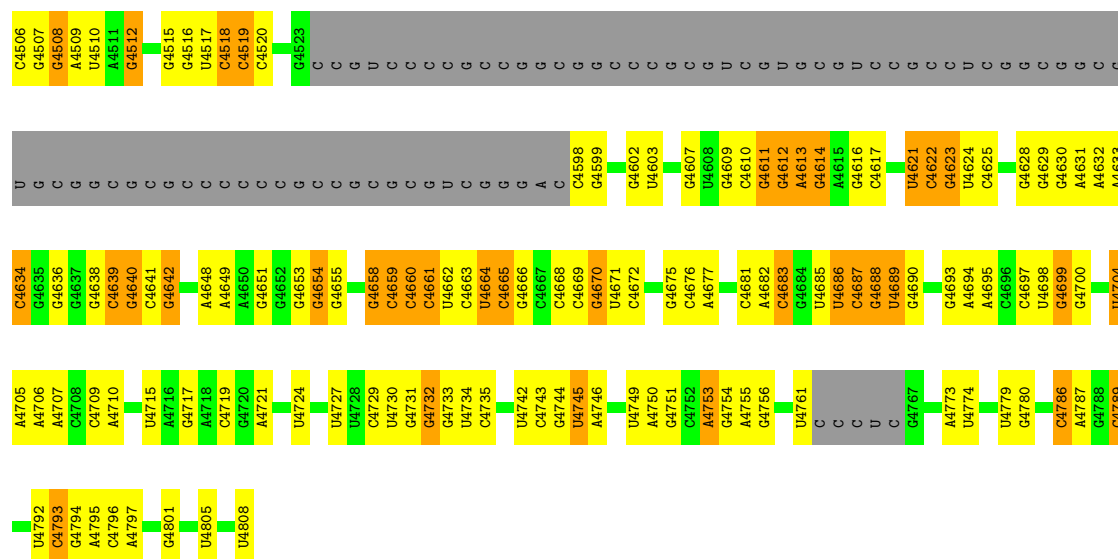


Mol	Chain	Residues	Atoms					AltConf
50	K	1	Total	C	N	O	S	0
			42	32	4	4	2	

G1742	G1743	A1744	G1745	G1746	G1750	G1751	G1752	G1753	G1754	G1755	G1756	G1757	G1758	G1759	G1760	G1658	C1659	G1660	U1665	U1666	U1667	C1670	C1671	G1672	G1673	G1678	C1679	G1680	G1681	G1685	G1686	G1687	G1688	G1689	G1692	U1693	U1694	U1695	U1696	G1697	G1698	G1699	G1700	G1703	A1704	C1705	C1706	C1707	G1708	C1718	C1721	U1722	U1723	G1724	G1725	A1726	A1727	G1728	G1729	G1730	C1731	C1732	G1734	G1735	U1736	G1737	G1738	G1739	G1740	A1741	A1742	G1743	G1744	G1751	G1752	G1753	G1754	G1755	G1756	A1757	C1758																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G1554	A1555	A1556	U1557	G1558	G1559	U1560	G1567	A1568	G1569	G1572	G1579	G1580	C1583	A1586	A1587	G1588	A1589	C1595	C1600	A1601	A1602	G1609	C1610	U1614	U1615	C1616	C1617	C1618	A1624	C1631	U1632	C1633	U1638	A1639	G1640	C1641	G1645	G1646	C1647	C1651	G1652	C	A	A	C	G1657	G1703	A1704	C1705	C1706	C1707	G1708	G1709	U1710	U1711	U1712	A1713	A1714	A1715	G1716	C1717	U1718	A1719	U1720	A1725	A1726	A1727	C1728	U1729	G1736	A1741																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
G1456	G1457	A1458	G1459	C1460	C1464	G1467	U1468	A1469	G1470	G1471	G1472	G1477	A1478	A1479	A1480	G1487	A1488	A1489	C1490	G1500	C1501	A1502	C1506	C1507	A1508	A1509	G1510	A1513	G1514	G1517	C1521	U1522	C1523	G1528	G1529	U1532	U1533	C1534	U1537	U1546	C1551	G1552	C1553	C1554	C1555	C1556	U1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725	C1726	C1727	C1728	C1729	C1730	C1731	C1732	C1733	C1734	C1735	C1736	C1737	C1738	C1739	C1740	C1741	C1742	C1743	C1744	C1745	C1746	C1747	C1748	C1749	C1750	C1751	C1752	C1753	C1754	C1755	C1756	C1757	C1758	C1759	C1760	C1761	C1762	C1763	C1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	C1772	C1773	C1774	C1775	C1776	C1777	C1778	C1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792	C1793	C1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	C1802	C1803	C1804	C1805	C1806	C1807	C1808	C1809	C1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	C1818	C1819	C1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	C1922	C1923	C1924	C1925	C1926	C1927	C1928	C1929	C1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981	C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	C2026	C2027	C2028	C2029	C2030	C2031	C2032	C2033	C2034	C2035	C2036	C2037	C2038	C2039	C2040	C2041	C2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060	C2061	C2062	C2063	C2064	C2065	C2066	C2067	C2068	C2069	C2070	C2071	C2072	C2073	C2074	C2075	C2076	C2077	C2078	C2079	C2080	C2081	C2082	C2083	C2084	C2085	C2086	C2087	C2088	C2089	C2090	C2091	C2092	C2093	C2094	C2095	C2096	C2097	C2098	C2099	C2100	C2101	C2102	C2103	C2104	C2105	C2106	C2107	C2108	C2109	C2110	C2111	C2112	C2113	C2114	C2115	C2116	C2117	C2118	C2119	C2120	C2121	C2122	C2123	C2124	C2125	C2126	C2127	C2128	C2129	C2130	C2131	C2132	C2133	C2134	C2135	C2136	C2137	C2138	C2139	C2140	C2141	C2142	C2143	C2144	C2145	C2146	C2147	C2148	C2149	C2150	C2151	C2152	C2153	C2154	C2155	C2156	C2157	C2158	C2159	C2160	C2161	C2162	C2163	C2164	C2165	C2166	C2167	C2168	C2169	C2170	C2171	C2172	C2173	C2174	C2175	C2176	C2177	C2178	C2179	C2180	C2181	C2182	C2183	C2184	C2185	C2186	C2187	C2188	C2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	C2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208	C2209	C2210	C2211	C2212	C2213	C2214	C2215	C2216	C2217	C2218	C2219	C2220	C2221	C2222	C2223	C2224	C2225	C2226	C2227	C2228	C2229	C2230	C2231	C2232	C2233	C2234	C2235	C2236	C2237	C2238	C2239	C2240	C2241	C2242	C2243	C2244	C2245	C2246	C2247	C2248	C2249	C2250	C2251	C2252	C2253	C2254	C2255	C2256	C2257	C2258	C2259	C2260	C2261	C2262	C2263	C2264	C2265	C2266	C2267	C2268	C2269	C2270	C2271	C2272	C2273	C2274	C2275	C2276	C2277	C2278	C2279	C2280	C2281	C2282	C2283	C2284	C2285	C2286	C2287	C2288	C2289	C2290	C2291	C2292	C2293	C2294	C2295	C2296	C2297	C2298	C2299	C2300	C2301	C2302	C2303	C2304	C2305	C2306	C2307	C2308	C2309	C2310	C2311	C2312	C2313	C2314	C2315	C2316	C2317	C2318	C2319	C2320	C2321	C2322	C2323	C2324	C2325	C2326	C2327	C2328	C2329	C2330	C2331	C2332	C2333	C2334	C2335	C2336	C2337	C2338	C2339	C2340	C2341	C2342	C2343	C2344	C2345	C2346	C2347	C2348	C2349	C2350	C2351	C2352	C2353	C2354	C2355	C2356	C2357	C2358	C2359	C2360	C2361	C2362	C2363	C2364	C2365	C2366	C2367	C2368	C2369	C2370	C2371	C2372	C2373	C2374	C2375	C2376	C2377	C2378	C2379	C2380	C2381	C2382	C2383	C2384	C2385	C2386	C2387	C2388	C2389	C2390	C2391	C2392	C2393	C2394	C2395	C2396	C2397	C2398	C2399	C2400	C2401	C2402	C2403	C2404	C2405	C2406	C2407	C2408	C2409	C2410	C2411	C2412	C2413	C2414	C2415	C2416	C2417	C2418	C2419	C2420	C2421	C2422	C2423	C2424	C2425	C2426	C2427	C2428	C2429	C2430	C2431	C2432	C2433	C2434	C2435	C2436	C2437	C2438	C2439	C2440	C2441	C2442	C2443	C2444	C2445	C2446	C2447	C2448	C2449	C2450	C2451	C2452	C2453	C2454	C2455	C2456	C2457	C2458	C2459	C2460	C2461	C2462	C2463	C2464	C2465	C2466	C2467	C2468	C2469	C2470	C2471	C2472	C2473	C2474	C2475	C2476	C2477	C2478	C2479	C2480	C2481	C2482	C2483	C2484	C2485	C2486	C2487	C2488	C2489	C2490	C2491	C2492	C2493	C2494	C2495	C2496	C2497	C2498	C2499	C2500	C2501	C2502	C2503	C2504	C2505	C2506	C2507	C2508	C2509	C2510	C2511	C2512	C2513	C2514	C2515	C2516	C2517	C2518	C2519	C2520	C2521	C2522	C2523	C2524	C2525	C2526	C2527	C2528	C2529	C2530	C2531	C2532	C2533	C2534	C2535	C2536	C2537	C2538	C2539	C2540	C2541	C2542	C2543	C2544	C2545	C2546	C2547	C2548	C2549	C2550	C2551	C2552	C2553	C2554	C2555	C2556	C2557	C2558	C2559	C2560	C2561	C2562	C2563	C2564	C2565	C2566	C2567	C2568	C2569	C2570	C2571	C2572	C2573	C2574	C2575	C2576	C2577	C2578	C2579	C2580	C2581	C2582	C2583	C2584	C2585	C2586	C2587	C2588	C2589	C2590	C2591	C2592	C2593	C2594	C2595	C2596	C2597	C2598	C2599	C2600	C2601	C2602	C2603	C2604	C2605	C2606	C2607	C2608	C2609	C2610	C2611	C2612	C2613	C2614	C2615	C2616	C2617	C2618	C2619	C2620	C2621	C2622	C2623	C2624	C2625	C2626	C2627	C2628	C2629	C2630	C2631	C2632	C2633	C2634	C2635	C2636	C2637	C2638	C2639	C2640	C2641	C2642	C2643	C2644	C2645	C2646	C2647	C2648	C2649	C2650	C2651	C2652	C2653	C2654	C2655	C2656	C2657	C2658	C2659	C2660	C2661	C2662	C2663	C2664	C2665	C2666	C2667	C2668	C2669	C2670	C2671	C2672	C2673	C2674	C2675	C2676	C2677	C2678	C2679	C2680	C2681	C2682	C2683	C2684	C2685	C2686	C2687	C2688	C2689	C2690	C2691	C2692	C2693	C2694	C2695	C2696	C2697	C2698	C2699	C2700	C2701	C2702	C2703	C2704	C2705	C2706	C2707	C2708	C2709	C2710	C2711	C2712	C2713	C

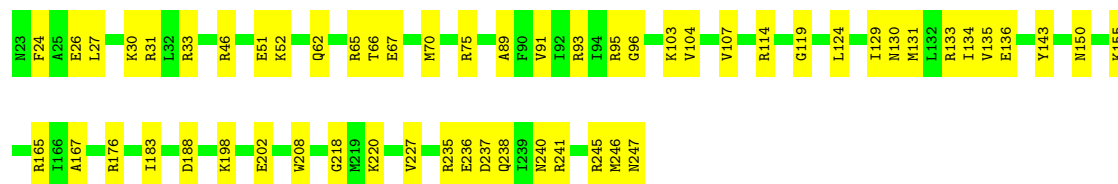


A4418	U4323	U4246	U4141	G4051	C3961	G	G3812	G	G3611	G3508	C3432	G3332	C
U4423	G4324	U4249	A4142	U4052	C3962	C	A3813	U	G3612	G3509	C3433	G3335	C
G4426	U4325	A4249	A4143	A4053	A3965	G	G3814	C	C3619	U3439	U3439	A3336	G
A4427	C4328	C4250	U4144	U4057	A3966	G	G3815	C	G3620	C3440	C3440	C3337	G
A4430	G4332	C4251	U4145	U4058	G3971	G	G3816	C	A3615	C3443	A3443	U3338	U
U4431	A4335	U4252	C4147	A4059	C3975	C	G3817	C	C3625	A3516	A3444	U3339	C
U4432	A4336	A4253	C4148	C4060	U3975	C	G3818	C	A3626	U3517	A3445	A3340	C
A4433	U4337	C4254	U4149	C4064	U3978	G	G3823	G	G3629	U3518	U3446	G3341	G
C4434	U4338	U4255	U4150	U4065	U3979	C	G3824	C	G3630	G3519	A3447	A3342	C
U4435	C4339	A4257	C4151	C4065	A3979	C	A3825	C	G3631	C3520	U3447	A3343	C
G4436	U4340	U4258	A4161	G4068	G3982	G	G3827	U	G3632	C3521	C3448	C	
C4439	C4341	A4259	G4162	A4069	G3882	G	C3828	G	G3633	G3522	A3449	C	
U4440	C4342	A4264	C4163	A4070	G3889	C	C3829	C	A3636	A3523	A3450	C	
G4441	U4346	C4265	U4164	A4071	G3890	C	C	G	G3637	A3451	G3357	G	
U4445	U4347	G4266	U4165	G4072	G3891	G	G	G	G3638	U3453	G3358	G	
A4446	U4347	U4267	C4167	G4074	G3894	C	A	C	A3639	A3454	A3367	G	
U4445	A4348	G4268	A4168	G4075	C3895	C	G	C	A3640	C3455	C3368	C	
A4446	A4357	A4269	G	G4076	A3990	G	G3835	G	C3643	A3456	U3369	G	
A4451	C4358	C4270	C4172	G4077	G3991	C	G3836	C	U3644	U3546	U3373	C	
G4452	U4272	G4271	G4173	C4078	A3997	C	G3837	C	G3647	A3459	A3374	G	
U4455	G4363	G4274	A4186	A4081	A3999	G	U3838	G	A3649	A3460	A3375	G	
C4456	C4364	G4275	C4187	A4082	G4000	C	G3840	U	U3647	U3461	A3378	U	
U4457	U4365	U4276	U4188	A4085	A4001	G	U3841	G	A3648	A3465	A3379	C	
U4366	U4277	U4277	C4189	C4086	A4002	C	G3843	A	A3649	A3466	A3380	C	
G4369	U4278	U4278	U4190	C4087	A4003	A	C3844	A	G3652	U3467	A3383	G	
A4370	C4282	U4088	C4088	C4088	C4004	C	C3911	U	G3653	A3468	A3384	G	
C4371	U4191	U4089	U4191	U4089	C4005	C	G3847	A	G3654	A3469	A3385	C	
A4372	G4283	U4090	U4192	C4091	U4006	C	U3848	C	A3655	C3478	G3386	G	
U4373	C4284	C4091	C4193	C4091	C4007	C	G3849	C	C3656	A3479	U3389	G	
U4374	U4373	C4092	C4194	U4092	C4008	C	G3850	C	U3657	A3480	C3390	C	
C4374	G4287	G4093	A4195	G4093	C4009	A	G3851	C	C3659	G3571	G3391	C	
U4377	A4290	A4094	U4196	U4011	G4010	U	C3852	U	U3662	G3485	A3394	U	
C4378	U4397	C4095	U4197	G4012	C3853	C	C3785	C	C3663	G3486	A3395	C	
A4381	U4198	C4096	U4198	G4013	C3854	C	U3786	C	A3666	G3487	G3396	C	
U4382	A4294	G4101	U4203	A4014	A3855	C	A3855	C	C3667	G3488	G3397	C	
G4383	G4295	C4101	C4204	A4017	C3857	C	G3787	C	C3667	G3488	C3400	U	
U4384	U4300	G4116	U4205	G4018	C3858	C	G3788	C	G3668	G3489	U3400	C	
G4385	U4301	U4117	U4206	A4019	G3931	G	G3769	C	A3681	U3490	A3401	C	
A4386	C4207	C4207	U4118	A4020	A3932	C	A3900	C	G3670	A3491	A3404	G	
U4388	C4306	G4119	G3933	G4021	G3933	A	U3791	C	C3587	A3588	C3405	C	
G4389	A4402	G4119	U3934	U3934	C3792	G	C3792	C	G3671	A3492	G3404	G	
U4389	U4309	G4123	U3935	U3935	G3793	C	G3793	C	A3674	U3493	C3405	C	
A4490	A4310	A4124	G3936	U3936	G3794	C	U3794	C	A3675	A3494	A3414	C	
G4491	C4311	A4125	U3795	U3795	U3795	G	U3795	C	G3676	A3495	C3415	G	
U4492	U4312	A4126	U3796	U3796	U3796	C	U3796	C	G3677	G3496	G3416	C	
C4496	G4313	A4126	G3941	U3797	U3797	C	U3797	C	A3679	C3601	C3417	C	
U4497	C4133	U4038	G3942	U3798	U3798	C	U3798	C	C3602	G3500	G3418	C	
G4498	G4316	U4039	G3943	U3799	U3799	C	C3800	C	U3500	C3501	A3419	G	
U4499	A4317	A4226	C4135	G3942	C3943	C	G3801	C	C3603	G3502	U3420	C	
A4501	U4318	U4227	A4136	G3944	G3944	C	A3801	C	A3681	A3604	G3421	U	
G4502	G4319	U4227	G4137	A3944	A3944	C	C3802	C	U3682	C3503	U3504	C	
U4415	U4320	U4228	G4137	A3949	A3949	C	U3803	C	G3683	G3605	A3424	A	
C4416	U4321	U4239	U4048	A3949	A3949	C	G3804	C	A3684	U3505	A3424	A	
U4505	G4322	G4240	C4049	C3953	C3953	C	C3805	C	G3685	A3506	U3425	G	
			A4050	C	C3806	C	C3806	C	A3687	C3610		A3331	



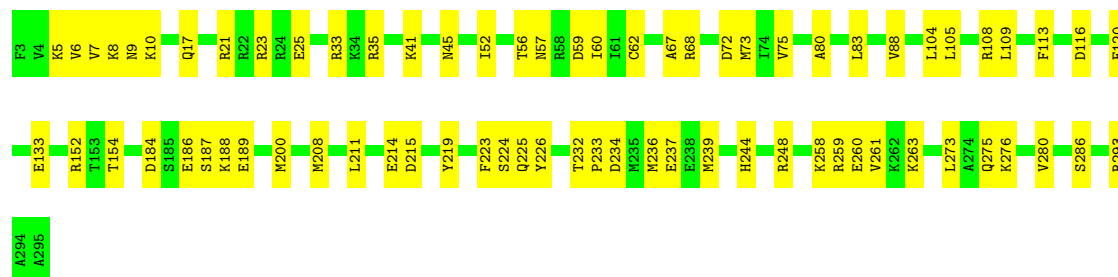
• Molecule 3: 60S ribosomal protein L7

Chain F:  75% 25%



• Molecule 4: Ribosomal_L18_c domain-containing protein

Chain D:  75% 25%

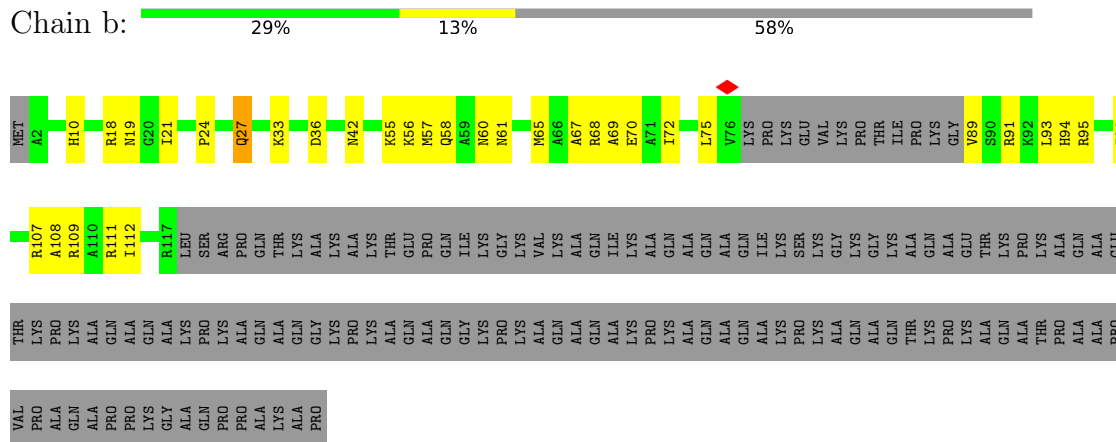


• Molecule 5: 60S ribosomal protein L18a

Chain S:  76% 24%



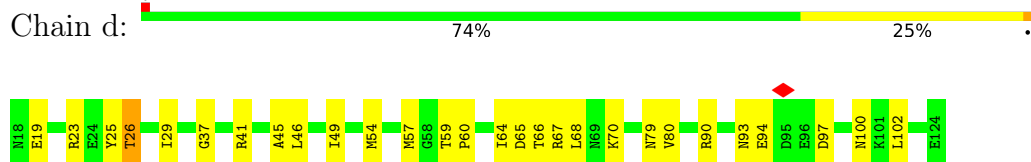
- Molecule 6: 60S ribosomal protein L29



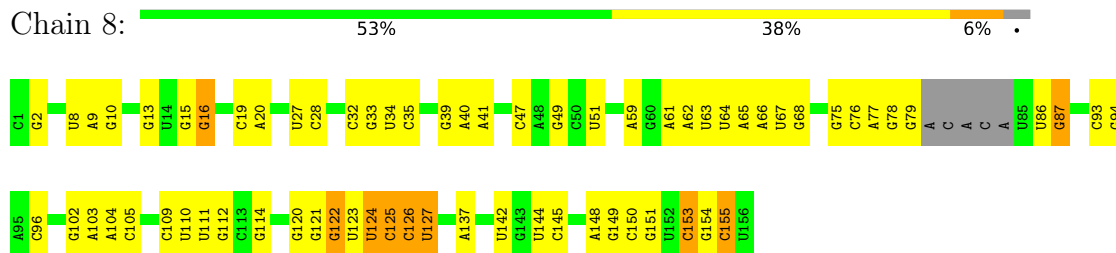
- Molecule 7: Ribosomal protein L3



- Molecule 8: 60S ribosomal protein L31

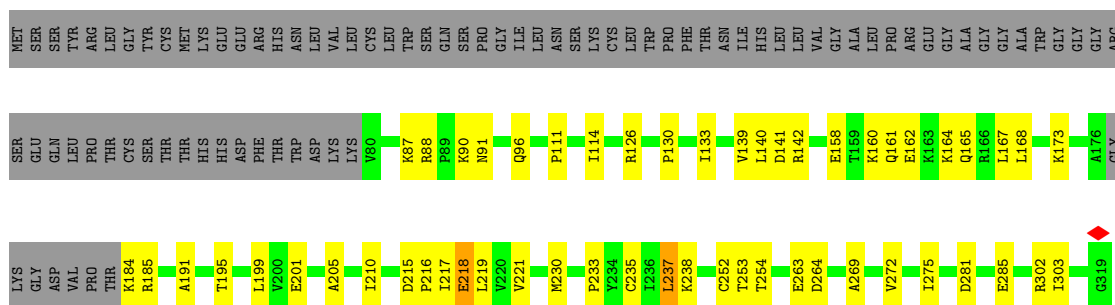


- Molecule 9: 5.8S rRNA

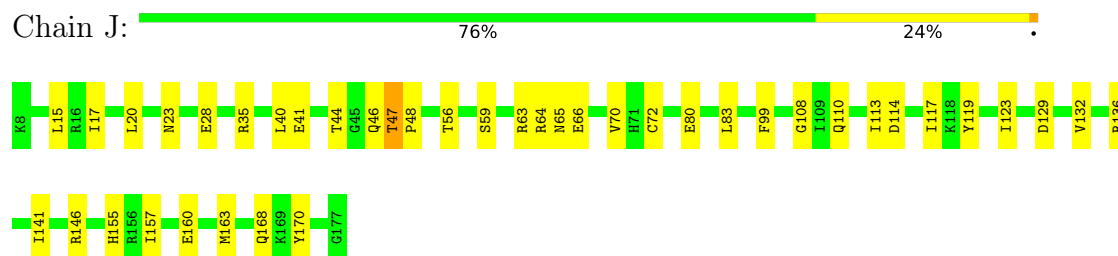


- Molecule 10: 60S ribosomal protein L7a

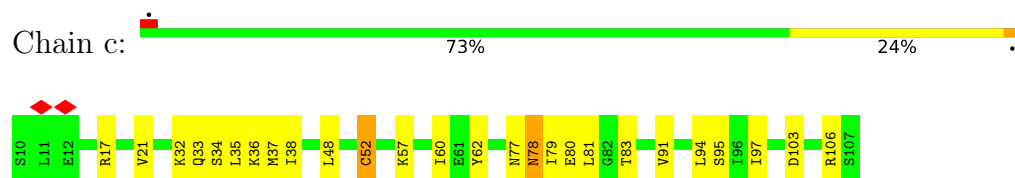




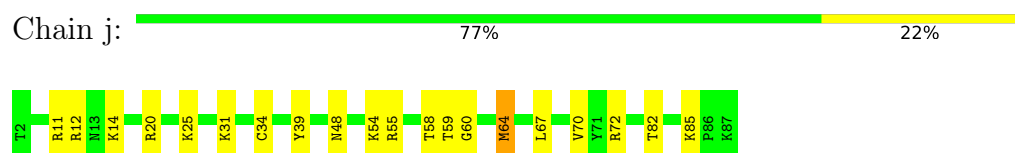
- Molecule 11: 60S ribosomal protein L11



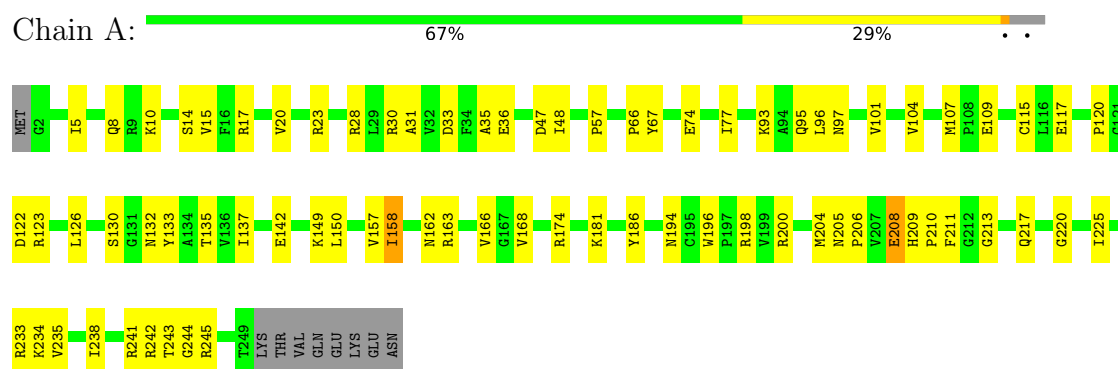
- Molecule 12: 60S ribosomal protein L30



- Molecule 13: Ribosomal protein L37

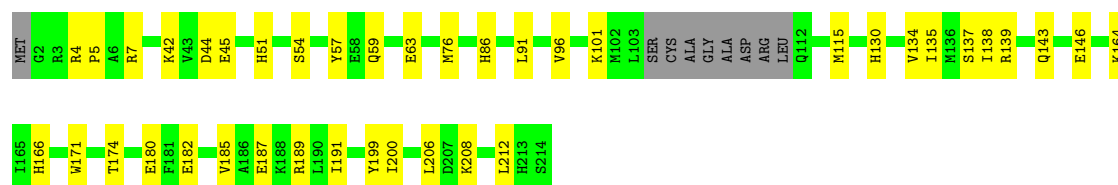


- Molecule 14: Ribosomal protein L8



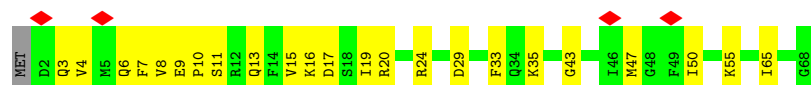
- Molecule 15: Ribosomal protein L10

Chain I:  77% 19%



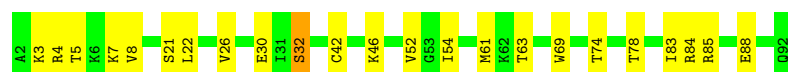
- Molecule 16: Protein transport protein Sec61 subunit gamma

Chain q:  6% 65% 34%



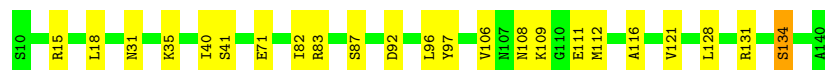
- Molecule 17: 60S ribosomal protein L37a

Chain p:  75% 24%



- Molecule 18: 60S ribosomal protein L23

Chain V:  82% 17%



- Molecule 19: 60S ribosomal protein L40

Chain m:  75% 25%



- Molecule 20: 60S ribosomal protein L39-like

Chain l:  78% 22%

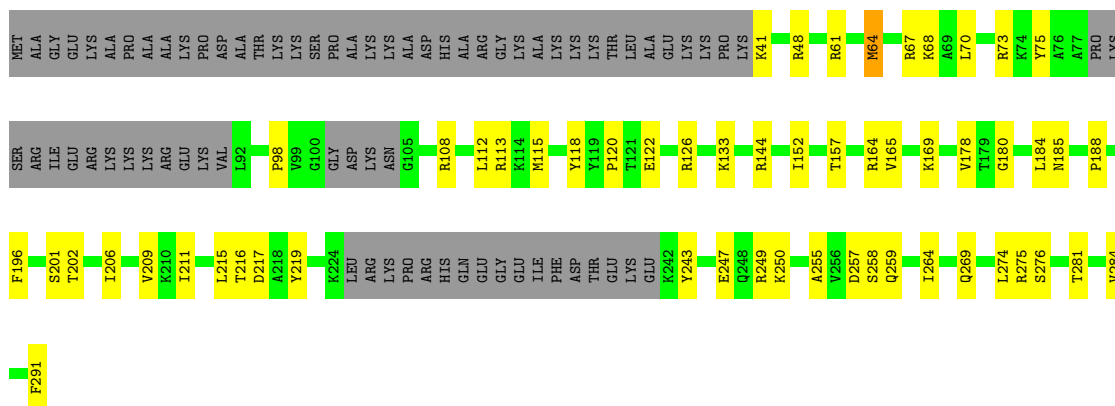


- Molecule 21: 60S ribosomal protein L17

Chain P:  81% 19%

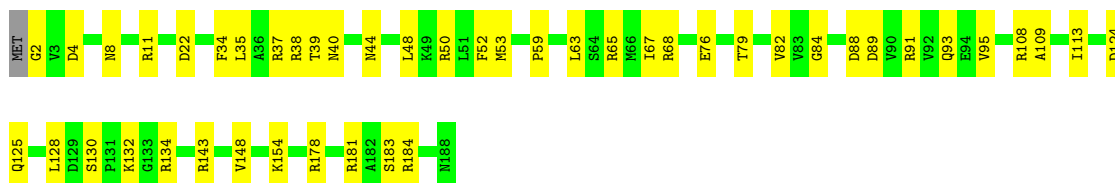
- Molecule 22: 60S ribosomal protein L6

Chain E: 55% 19% 26%

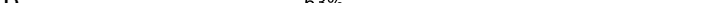


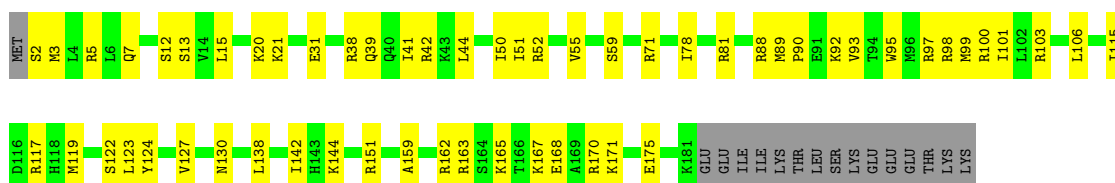
- Molecule 23: eL18

Chain Q: 75% 24%



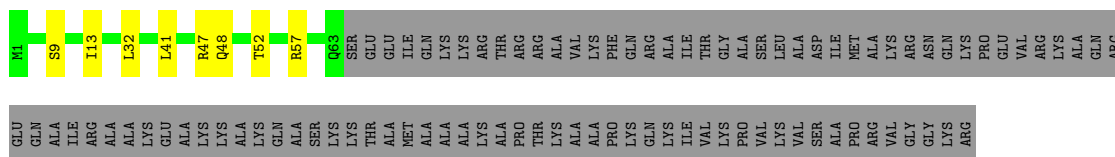
- Molecule 24: 60S ribosomal protein L19

Chain R:  63% 29% 8%



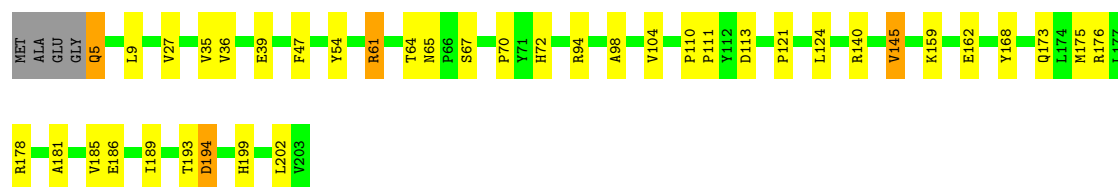
- Molecule 25: Ribosomal protein L24

Chain W:  35% 5% 60%



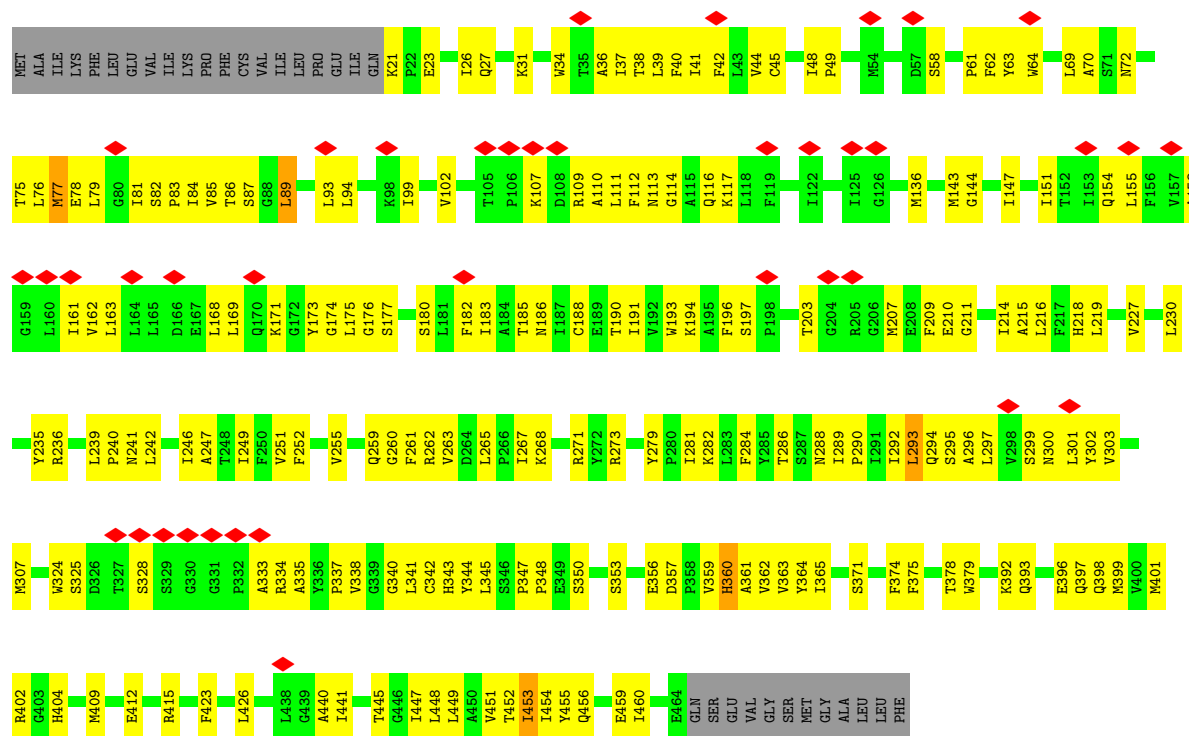
- Molecule 26: 60S ribosomal protein L13a

Chain O:  79% 17% ..



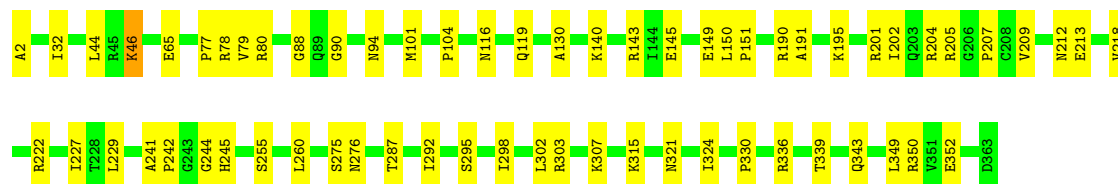
- Molecule 27: Protein transport protein Sec61 subunit alpha isoform 1

Chain K:  8% 52% 40% 7%



- Molecule 28: 60S ribosomal protein L4

Chain C:  83% 17%



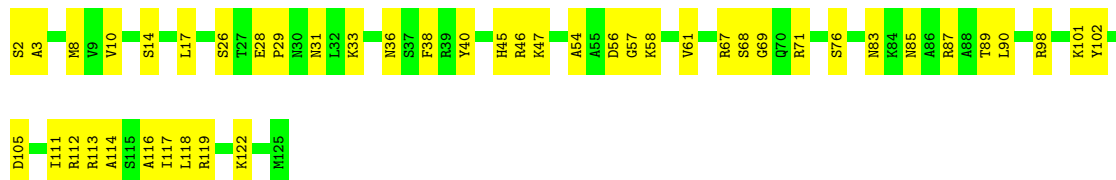
- Molecule 29: 60S ribosomal protein L36a-like

Chain o:  85% 13% .



- Molecule 30: 60S ribosomal protein L28

Chain r: 64% 36%



- Molecule 31: 60S ribosomal protein L35a

Chain f: 75% 25%



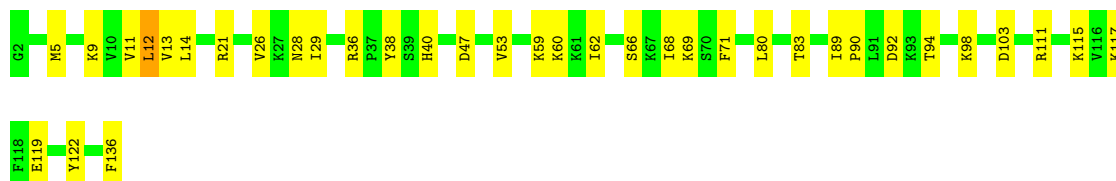
- Molecule 32: Ribosomal protein L32

Chain e: 79% 21%



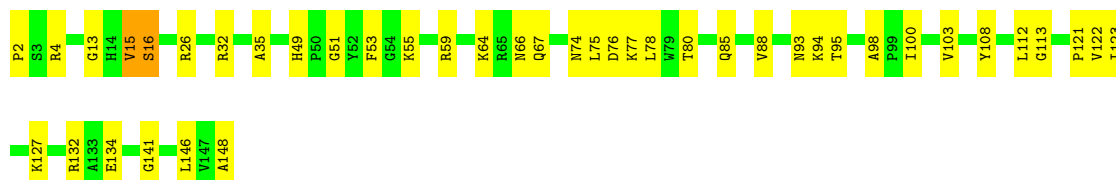
- Molecule 33: 60S ribosomal protein L27

Chain Z: 73% 26%

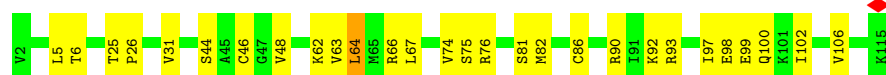
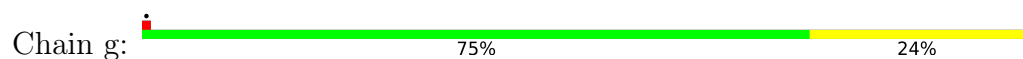


- Molecule 34: 60S ribosomal protein L27a

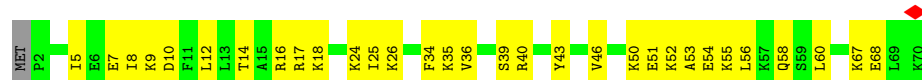
Chain a: 71% 27%



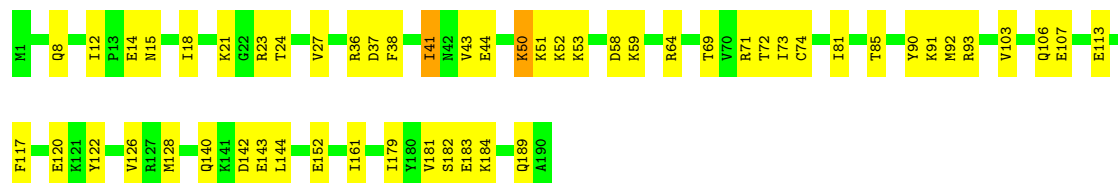
- Molecule 35: 60S ribosomal protein L34



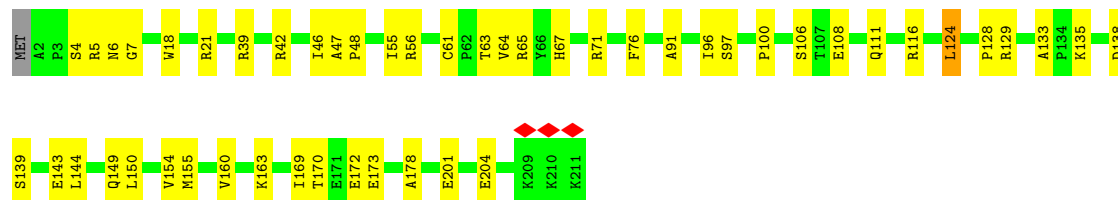
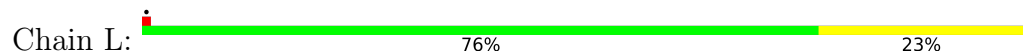
- Molecule 36: 60S ribosomal protein L38



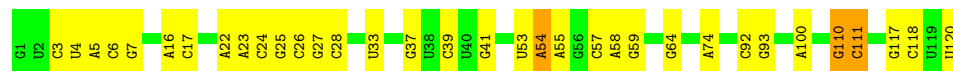
- Molecule 37: 60S ribosomal protein L9



- Molecule 38: 60S ribosomal protein L13



- Molecule 39: 5S rRNA



- Molecule 40: Ribosomal protein L15





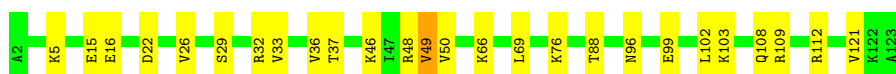
- Molecule 41: 60S ribosomal protein L36

Chain i: 75% 21% ..



- Molecule 42: 60S ribosomal protein L35

Chain h: 79% 20% .



- Molecule 43: 60S ribosomal protein L14

Chain M: 70% 30% .



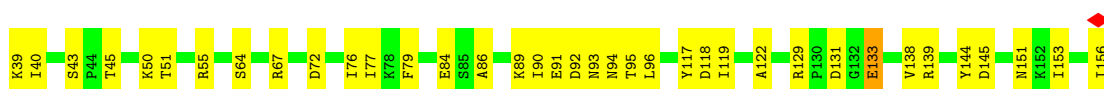
- Molecule 44: Ribosomal protein L26

Chain Y: 63% 35% .



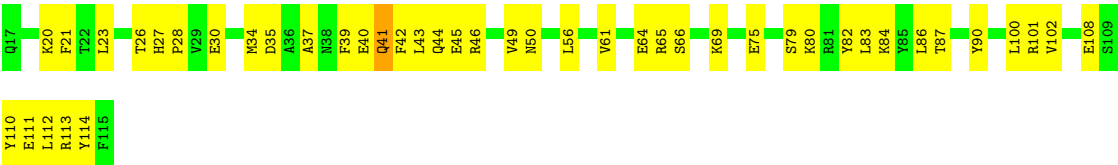
- Molecule 45: Ribosomal_L23eN domain-containing protein

Chain X: 69% 31% .

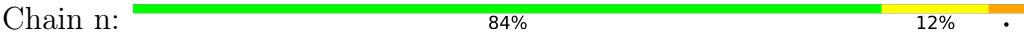


- Molecule 46: 60S ribosomal protein L22 (Fragment)

Chain U: 56% 43% .



- Molecule 47: 60S ribosomal protein L41



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	132229	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.8	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.425	Depositor
Minimum map value	-0.156	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.01581	Depositor
Map size ($\text{\AA}$)	432.96002, 432.96002, 432.96002	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.23, 1.23, 1.23	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: I4U, 1MA, PSU, A2M, MG, E7G, OWI, OMC, 5MC, E6G, P4U, OMG, MLZ, UR3, OMU, B8K, BGH, B8H, 7MG, P7G, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	T	0.24	0/1326	0.45	0/1770
2	5	0.25	4/85271 (0.0%)	0.32	8/132978 (0.0%)
3	F	0.20	0/1911	0.33	0/2549
4	D	0.24	0/2437	0.40	0/3264
5	S	0.23	0/1501	0.42	0/2012
6	b	0.27	0/861	0.53	0/1138
7	B	0.21	0/3240	0.34	0/4339
8	d	0.45	0/903	0.50	0/1216
9	8	0.20	0/3581	0.26	0/5577
10	G	0.32	0/1910	0.48	0/2569
11	J	0.21	0/1385	0.55	0/1852
12	c	0.20	0/771	0.42	0/1034
13	j	0.20	0/720	0.36	0/952
14	A	0.37	0/1936	0.48	0/2596
15	I	0.36	0/1702	0.48	0/2272
16	q	0.23	0/545	0.59	0/728
17	p	0.29	0/718	0.40	0/953
18	V	0.41	0/993	0.41	0/1332
19	m	0.25	0/425	0.49	0/561
20	l	0.19	0/459	0.36	0/608
21	P	0.31	0/1268	0.45	0/1700
22	E	0.22	0/1762	0.36	0/2362
23	Q	0.25	0/1539	0.40	0/2054
24	R	0.22	0/1524	0.41	0/2013
25	W	0.20	0/541	0.37	0/720
26	O	0.25	0/1662	0.41	0/2222
27	K	0.79	0/3502	1.15	4/4749 (0.1%)
28	C	0.36	0/2927	0.45	2/3932 (0.1%)
29	o	0.29	0/855	0.46	0/1128
30	r	0.40	0/1010	0.46	0/1354
31	f	0.21	0/895	0.39	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.20	0/1071	0.35	0/1429
33	Z	0.31	0/1130	0.44	0/1507
34	a	0.20	0/1191	0.69	3/1590 (0.2%)
35	g	0.20	0/916	0.36	0/1220
36	k	0.23	0/575	0.66	2/761 (0.3%)
37	H	0.23	0/1535	0.44	0/2063
38	L	0.30	0/1733	0.44	0/2316
39	7	0.18	0/2858	0.22	0/4455
40	N	0.37	0/1746	0.45	1/2338 (0.0%)
41	i	0.17	0/841	0.34	0/1112
42	h	0.18	0/1021	0.37	0/1348
43	M	0.30	0/1158	0.47	0/1547
44	Y	0.22	0/1132	0.45	0/1504
45	X	0.24	0/984	0.48	0/1323
46	U	0.28	0/823	0.76	1/1104 (0.1%)
47	n	0.14	0/240	0.38	0/305
All	All	0.28	4/149034 (0.0%)	0.40	21/219654 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	732	C	O3'-P	20.59	1.92	1.61
2	5	1390	G	O3'-P	18.62	1.89	1.61
2	5	1392	C	O3'-P	-13.69	1.40	1.61
2	5	731	C	O3'-P	-11.05	1.44	1.61

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	731	C	OP1-P-O3'	-20.55	46.34	108.00
2	5	731	C	O3'-P-O5'	17.98	130.97	104.00
34	a	15	VAL	N-CA-C	-16.58	82.92	109.12
34	a	16	SER	N-CA-CB	15.16	136.11	110.49
2	5	732	C	O3'-P-O5'	8.28	116.42	104.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	1298	0	1366	39	0
2	5	77665	0	39155	1279	0
3	F	1875	0	1995	46	0
4	D	2391	0	2424	53	0
5	S	1462	0	1508	37	0
6	b	848	0	920	35	0
7	B	3172	0	3310	68	0
8	d	888	0	930	18	0
9	8	3208	0	1629	48	0
10	G	1879	0	2027	50	0
11	J	1362	0	1399	29	0
12	c	761	0	794	19	0
13	j	705	0	737	16	0
14	A	1898	0	1993	60	0
15	I	1664	0	1712	29	0
16	q	535	0	565	25	0
17	p	708	0	756	18	0
18	V	979	0	1039	18	0
19	m	430	0	466	11	0
20	l	447	0	480	12	0
21	P	1242	0	1274	19	0
22	E	1729	0	1887	48	0
23	Q	1515	0	1634	40	0
24	R	1508	0	1664	43	0
25	W	528	0	541	4	0
26	O	1630	0	1778	37	0
27	K	3427	0	3530	223	0
28	C	2884	0	3054	48	0
29	o	842	0	912	10	0
30	r	994	0	1051	38	0
31	f	876	0	912	25	0
32	e	1053	0	1147	23	0
33	Z	1107	0	1182	31	0
34	a	1162	0	1209	41	0
35	g	906	0	998	20	0
36	k	569	0	637	31	0
37	H	1516	0	1597	50	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	L	1702	0	1820	44	0
39	7	2558	0	1296	20	0
40	N	1701	0	1749	39	0
41	i	830	0	916	17	0
42	h	1013	0	1147	22	0
43	M	1137	0	1211	34	0
44	Y	1115	0	1205	34	0
45	X	967	0	1040	38	0
46	U	809	0	833	43	0
47	n	239	0	289	3	0
48	5	161	0	0	0	0
48	7	7	0	0	0	0
48	8	5	0	0	0	0
48	A	1	0	0	0	0
48	I	1	0	0	0	0
48	P	1	0	0	0	0
48	V	1	0	0	0	0
48	a	1	0	0	0	0
49	g	1	0	0	0	0
49	j	1	0	0	0	0
49	m	1	0	0	0	0
49	o	1	0	0	0	0
49	p	1	0	0	0	0
50	K	42	0	0	0	0
All	All	139959	0	101718	2553	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 11.

The worst 5 of 2553 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)
27:K:239:LEU:CD1	27:K:240:PRO:HD2	1.67	1.22
26:O:5:GLN:N	26:O:5:GLN:HE21	1.34	1.22
27:K:239:LEU:HD12	27:K:240:PRO:HD2	1.29	1.13
27:K:210:GLU:O	27:K:239:LEU:HD11	1.57	1.04
27:K:21:LYS:HZ2	27:K:168:LEU:HD12	1.23	1.01

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	T	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
3	F	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
4	D	291/293 (99%)	284 (98%)	7 (2%)	0	100	100
5	S	174/176 (99%)	168 (97%)	6 (3%)	0	100	100
6	b	100/245 (41%)	97 (97%)	3 (3%)	0	100	100
7	B	392/394 (100%)	382 (97%)	10 (3%)	0	100	100
8	d	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
10	G	229/319 (72%)	219 (96%)	10 (4%)	0	100	100
11	J	168/170 (99%)	159 (95%)	9 (5%)	0	100	100
12	c	96/98 (98%)	96 (100%)	0	0	100	100
13	j	84/86 (98%)	84 (100%)	0	0	100	100
14	A	246/257 (96%)	229 (93%)	17 (7%)	0	100	100
15	I	201/214 (94%)	193 (96%)	8 (4%)	0	100	100
16	q	65/68 (96%)	65 (100%)	0	0	100	100
17	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
18	V	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
19	m	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
20	l	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
21	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
22	E	208/291 (72%)	198 (95%)	9 (4%)	1 (0%)	24	55
23	Q	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
24	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
25	W	61/157 (39%)	58 (95%)	3 (5%)	0	100	100
26	O	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
27	K	442/476 (93%)	430 (97%)	11 (2%)	1 (0%)	43	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	C	359/362 (99%)	343 (96%)	16 (4%)	0	100	100
29	o	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
30	r	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
31	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
32	e	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
33	Z	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
34	a	145/147 (99%)	138 (95%)	6 (4%)	1 (1%)	18	47
35	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	H	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
38	L	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
40	N	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
41	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
42	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
43	M	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
44	Y	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
45	X	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
46	U	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
47	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	6861/7436 (92%)	6625 (97%)	233 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	a	16	SER
22	E	118	TYR
27	K	110	ALA

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	T	139/139 (100%)	136 (98%)	3 (2%)	45	78
3	F	196/196 (100%)	196 (100%)	0	100	100
4	D	247/247 (100%)	243 (98%)	4 (2%)	55	83
5	S	157/157 (100%)	155 (99%)	2 (1%)	61	86
6	b	84/184 (46%)	82 (98%)	2 (2%)	43	77
7	B	342/342 (100%)	339 (99%)	3 (1%)	70	89
8	d	98/98 (100%)	95 (97%)	3 (3%)	35	70
10	G	200/272 (74%)	196 (98%)	4 (2%)	48	80
11	J	143/143 (100%)	140 (98%)	3 (2%)	47	79
12	c	84/84 (100%)	82 (98%)	2 (2%)	43	77
13	j	73/73 (100%)	72 (99%)	1 (1%)	59	85
14	A	190/199 (96%)	185 (97%)	5 (3%)	40	75
15	I	175/181 (97%)	171 (98%)	4 (2%)	44	78
16	q	58/59 (98%)	58 (100%)	0	100	100
17	p	74/74 (100%)	70 (95%)	4 (5%)	20	51
18	V	101/101 (100%)	97 (96%)	4 (4%)	28	63
19	m	47/47 (100%)	47 (100%)	0	100	100
20	l	47/47 (100%)	47 (100%)	0	100	100
21	P	134/134 (100%)	131 (98%)	3 (2%)	45	78
22	E	190/251 (76%)	188 (99%)	2 (1%)	65	87
23	Q	164/165 (99%)	158 (96%)	6 (4%)	30	65
24	R	159/175 (91%)	155 (98%)	4 (2%)	42	76
25	W	55/126 (44%)	53 (96%)	2 (4%)	31	66
26	O	171/173 (99%)	166 (97%)	5 (3%)	37	73
27	K	370/398 (93%)	359 (97%)	11 (3%)	36	72
28	C	301/301 (100%)	300 (100%)	1 (0%)	86	95
29	o	91/91 (100%)	87 (96%)	4 (4%)	25	59
30	r	108/108 (100%)	107 (99%)	1 (1%)	70	89
31	f	88/88 (100%)	88 (100%)	0	100	100
32	e	114/114 (100%)	114 (100%)	0	100	100
33	Z	117/117 (100%)	114 (97%)	3 (3%)	40	75
34	a	119/119 (100%)	119 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	g	98/98 (100%)	91 (93%)	7 (7%)	13	39
36	k	64/65 (98%)	62 (97%)	2 (3%)	35	70
37	H	169/169 (100%)	167 (99%)	2 (1%)	63	87
38	L	175/176 (99%)	172 (98%)	3 (2%)	53	83
40	N	171/171 (100%)	169 (99%)	2 (1%)	63	87
41	i	86/89 (97%)	81 (94%)	5 (6%)	18	49
42	h	109/109 (100%)	107 (98%)	2 (2%)	51	82
43	M	117/117 (100%)	115 (98%)	2 (2%)	53	83
44	Y	124/124 (100%)	119 (96%)	5 (4%)	28	63
45	X	106/106 (100%)	104 (98%)	2 (2%)	50	81
46	U	89/89 (100%)	89 (100%)	0	100	100
47	n	24/24 (100%)	22 (92%)	2 (8%)	10	32
All	All	5968/6340 (94%)	5848 (98%)	120 (2%)	48	80

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	R	59	SER
43	M	62	LEU
27	K	235	TYR
43	M	44	ARG
47	n	8	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
23	Q	188	ASN
28	C	215	ASN
40	N	156	HIS
27	K	154	GLN
27	K	360	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	5	3602/4808 (74%)	700 (19%)	55 (1%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
39	7	119/120 (99%)	12 (10%)	0
9	8	149/156 (95%)	26 (17%)	1 (0%)
All	All	3870/5084 (76%)	738 (19%)	56 (1%)

5 of 738 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	5	12	A
2	5	13	U
2	5	25	A
2	5	30	C
2	5	39	A

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	5	2028	G
9	8	124	U
2	5	3335	G
2	5	4786	C
2	5	4623	G

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

66 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMC	5	2704	2	19,22,23	2.22	5 (26%)	25,31,34	0.98	2 (8%)
2	PSU	5	4039	2	18,21,22	2.02	5 (27%)	21,30,33	2.06	4 (19%)
2	PSU	5	4149	2	18,21,22	1.60	5 (27%)	21,30,33	2.26	6 (28%)
2	PSU	5	1537	2	18,21,22	2.06	5 (27%)	21,30,33	2.01	4 (19%)
2	A2M	5	398	2	22,25,26	4.01	8 (36%)	30,36,39	2.05	8 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	1MA	5	1266	2	21,25,26	2.02	3 (14%)	30,37,40	1.96	7 (23%)
2	PSU	5	1638	2	18,21,22	2.03	5 (27%)	21,30,33	2.06	4 (19%)
2	PSU	5	3447	2	18,21,22	2.00	5 (27%)	21,30,33	2.00	4 (19%)
2	A2M	5	1489	48,2	22,25,26	4.03	8 (36%)	30,36,39	2.03	9 (30%)
2	A2M	5	4269	48,2	22,25,26	4.00	8 (36%)	30,36,39	2.02	9 (30%)
2	E6G	5	4101	2	24,27,28	1.65	5 (20%)	34,39,42	2.49	13 (38%)
2	UR3	5	4276	2	19,22,23	1.01	1 (5%)	26,32,35	1.82	5 (19%)
2	OMC	5	3601	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
2	OMG	5	1260	2	23,26,27	2.54	5 (21%)	32,38,41	1.96	9 (28%)
2	B8H	5	1799	2	19,22,23	2.06	8 (42%)	21,32,35	2.20	3 (14%)
2	OMG	5	4383	2	23,26,27	2.57	5 (21%)	32,38,41	2.02	10 (31%)
2	OMU	5	4366	2	19,22,23	3.11	7 (36%)	25,31,34	1.94	6 (24%)
2	P4U	5	1292	2	21,24,25	2.42	7 (33%)	28,33,36	1.61	3 (10%)
2	OMG	5	1580	48,2	23,26,27	1.34	4 (17%)	32,38,41	2.00	6 (18%)
2	OMC	5	2208	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
2	OMC	5	4282	2	19,22,23	0.95	1 (5%)	25,31,34	1.08	1 (4%)
2	B8H	5	3494	2	19,22,23	2.03	7 (36%)	21,32,35	2.06	3 (14%)
2	OMG	5	3524	2	23,26,27	2.58	5 (21%)	32,38,41	1.96	9 (28%)
2	P7G	5	3612	2	24,28,29	5.12	6 (25%)	25,41,44	1.13	1 (4%)
2	PSU	5	4382	2	18,21,22	2.02	5 (27%)	21,30,33	2.11	5 (23%)
2	A2M	5	3557	2	22,25,26	4.00	8 (36%)	30,36,39	2.07	8 (26%)
2	5MC	5	4193	2	19,22,23	1.43	3 (15%)	26,32,35	1.38	4 (15%)
2	OMG	5	4369	2	23,26,27	2.56	5 (21%)	32,38,41	1.98	10 (31%)
2	OMG	5	4240	2	23,26,27	2.57	5 (21%)	32,38,41	1.97	8 (25%)
2	PSU	5	3496	2	18,21,22	2.02	6 (33%)	21,30,33	1.92	5 (23%)
2	OMC	5	2647	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	2 (8%)
2	B8K	5	4436	2	24,28,29	5.11	7 (29%)	29,42,45	2.41	7 (24%)
2	OMG	5	2267	2	23,26,27	1.28	4 (17%)	32,38,41	2.10	7 (21%)
2	PSU	5	4374	2	18,21,22	2.04	5 (27%)	21,30,33	2.10	4 (19%)
2	PSU	5	4277	2	18,21,22	1.98	5 (27%)	21,30,33	2.03	4 (19%)
2	OMG	5	2207	2	23,26,27	2.57	5 (21%)	32,38,41	1.94	7 (21%)
2	A2M	5	1270	2	22,25,26	1.49	5 (22%)	30,36,39	2.14	8 (26%)
2	PSU	5	4246	2	18,21,22	2.02	5 (27%)	21,30,33	2.10	5 (23%)
2	B8K	5	3629	2	24,28,29	5.17	7 (29%)	29,42,45	2.36	7 (24%)
2	1MA	5	4161	2	21,25,26	2.01	3 (14%)	30,37,40	1.94	7 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	E7G	5	1736	2	24,27,28	4.30	7 (29%)	28,40,43	2.25	8 (28%)
2	OMC	5	2265	48,2	19,22,23	2.22	5 (26%)	25,31,34	0.97	2 (8%)
2	A2M	5	1479	2	22,25,26	3.97	8 (36%)	30,36,39	2.18	11 (36%)
2	OMG	5	1477	2	23,26,27	2.57	6 (26%)	32,38,41	1.98	10 (31%)
2	7MG	5	1560	2	23,26,27	4.56	6 (26%)	27,39,42	2.23	8 (29%)
2	7MG	5	2365	2	23,26,27	1.41	4 (17%)	27,39,42	2.80	8 (29%)
2	OMC	5	3433	2	19,22,23	2.23	4 (21%)	25,31,34	0.97	2 (8%)
2	A2M	5	3450	2	22,25,26	4.01	8 (36%)	30,36,39	2.02	8 (26%)
2	OMG	5	4116	2	23,26,27	1.29	4 (17%)	32,38,41	2.19	8 (25%)
2	PSU	5	4196	48,2	18,21,22	1.99	6 (33%)	21,30,33	2.06	4 (19%)
28	MLZ	C	333	28	8,9,10	0.46	0	4,9,11	0.65	0
2	A2M	5	3455	2	22,25,26	4.00	8 (36%)	30,36,39	2.04	8 (26%)
2	P7G	5	1848	2	24,28,29	5.05	6 (25%)	25,41,44	1.13	1 (4%)
2	OMU	5	4052	2	19,22,23	3.12	7 (36%)	25,31,34	1.91	6 (24%)
2	BGH	5	3631	2	25,29,30	5.73	12 (48%)	30,43,46	2.44	10 (33%)
2	OMG	5	2616	2	23,26,27	2.57	4 (17%)	32,38,41	1.97	10 (31%)
2	I4U	5	1614	2	20,24,25	2.44	5 (25%)	27,34,37	1.95	2 (7%)
2	PSU	5	4188	2	18,21,22	2.06	6 (33%)	21,30,33	2.11	5 (23%)
19	MLZ	m	72	19	8,9,10	0.49	0	4,9,11	0.53	0
2	A2M	5	1810	48,2	22,25,26	1.48	5 (22%)	30,36,39	2.15	10 (33%)
2	5MC	5	3514	2	19,22,23	2.96	5 (26%)	26,32,35	1.37	3 (11%)
2	B8H	5	4042	2	19,22,23	2.05	8 (42%)	21,32,35	2.20	3 (14%)
2	OMC	5	3619	2	19,22,23	2.23	5 (26%)	25,31,34	0.98	3 (12%)
2	PSU	5	2351	2	18,21,22	2.02	5 (27%)	21,30,33	1.95	4 (19%)
2	PSU	5	1632	2	18,21,22	2.00	5 (27%)	21,30,33	2.11	4 (19%)
2	PSU	5	3461	2	18,21,22	2.05	5 (27%)	21,30,33	1.97	4 (19%)

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
2	OMC	5	2704	2	-	1/9/27/28	0/2/2/2
2	PSU	5	4039	2	-	2/7/25/26	0/2/2/2
2	PSU	5	4149	2	-	2/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	5	1537	2	-	2/7/25/26	0/2/2/2
2	A2M	5	398	2	-	1/9/27/28	0/3/3/3
2	1MA	5	1266	2	-	1/7/25/26	0/3/3/3
2	PSU	5	1638	2	-	0/7/25/26	0/2/2/2
2	PSU	5	3447	2	-	0/7/25/26	0/2/2/2
2	A2M	5	1489	48,2	-	2/9/27/28	0/3/3/3
2	A2M	5	4269	48,2	-	3/9/27/28	0/3/3/3
2	E6G	5	4101	2	-	4/10/28/29	0/3/3/3
2	UR3	5	4276	2	-	0/7/25/26	0/2/2/2
2	OMC	5	3601	2	-	0/9/27/28	0/2/2/2
2	OMG	5	1260	2	-	1/9/27/28	0/3/3/3
2	B8H	5	1799	2	-	0/7/25/26	0/2/2/2
2	OMG	5	4383	2	-	3/9/27/28	0/3/3/3
2	OMU	5	4366	2	-	1/9/27/28	0/2/2/2
2	P4U	5	1292	2	-	4/10/29/30	0/2/2/2
2	OMG	5	1580	48,2	-	0/9/27/28	0/3/3/3
2	OMC	5	2208	2	-	0/9/27/28	0/2/2/2
2	OMC	5	4282	2	-	2/9/27/28	0/2/2/2
2	B8H	5	3494	2	-	2/7/25/26	0/2/2/2
2	OMG	5	3524	2	-	2/9/27/28	0/3/3/3
2	P7G	5	3612	2	-	3/10/40/41	0/3/3/3
2	PSU	5	4382	2	-	3/7/25/26	0/2/2/2
2	A2M	5	3557	2	-	1/9/27/28	0/3/3/3
2	5MC	5	4193	2	-	4/7/25/26	0/2/2/2
2	OMG	5	4369	2	-	1/9/27/28	0/3/3/3
2	OMG	5	4240	2	-	3/9/27/28	0/3/3/3
2	PSU	5	3496	2	-	3/7/25/26	0/2/2/2
2	OMC	5	2647	2	-	1/9/27/28	0/2/2/2
2	B8K	5	4436	2	-	0/11/41/42	0/3/3/3
2	OMG	5	2267	2	-	2/9/27/28	0/3/3/3
2	PSU	5	4374	2	-	0/7/25/26	0/2/2/2
2	PSU	5	4277	2	-	0/7/25/26	0/2/2/2
2	OMG	5	2207	2	-	2/9/27/28	0/3/3/3
2	A2M	5	1270	2	-	3/9/27/28	0/3/3/3
2	PSU	5	4246	2	-	5/7/25/26	0/2/2/2
2	B8K	5	3629	2	-	3/11/41/42	0/3/3/3
2	1MA	5	4161	2	-	1/7/25/26	0/3/3/3
2	E7G	5	1736	2	-	3/9/39/40	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	5	2265	48,2	-	2/9/27/28	0/2/2/2
2	A2M	5	1479	2	-	2/9/27/28	0/3/3/3
2	OMG	5	1477	2	-	0/9/27/28	0/3/3/3
2	7MG	5	1560	2	-	0/7/37/38	0/3/3/3
2	7MG	5	2365	2	-	0/7/37/38	0/3/3/3
2	OMC	5	3433	2	-	4/9/27/28	0/2/2/2
2	A2M	5	3450	2	-	0/9/27/28	0/3/3/3
2	OMG	5	4116	2	-	1/9/27/28	0/3/3/3
2	PSU	5	4196	48,2	-	4/7/25/26	0/2/2/2
28	MLZ	C	333	28	-	0/7/8/10	-
2	A2M	5	3455	2	-	0/9/27/28	0/3/3/3
2	P7G	5	1848	2	-	0/10/40/41	0/3/3/3
2	OMU	5	4052	2	-	3/9/27/28	0/2/2/2
2	BGH	5	3631	2	-	2/13/43/44	0/3/3/3
2	OMG	5	2616	2	-	1/9/27/28	0/3/3/3
2	I4U	5	1614	2	-	1/9/29/30	0/2/2/2
2	PSU	5	4188	2	-	0/7/25/26	0/2/2/2
19	MLZ	m	72	19	-	1/7/8/10	-
2	A2M	5	1810	48,2	-	0/9/27/28	0/3/3/3
2	5MC	5	3514	2	-	0/7/25/26	0/2/2/2
2	B8H	5	4042	2	-	2/7/25/26	0/2/2/2
2	OMC	5	3619	2	-	1/9/27/28	0/2/2/2
2	PSU	5	2351	2	-	0/7/25/26	0/2/2/2
2	PSU	5	1632	2	-	1/7/25/26	0/2/2/2
2	PSU	5	3461	2	-	2/7/25/26	0/2/2/2

The worst 5 of 355 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3629	B8K	C8-N9	-22.47	1.31	1.45
2	5	3631	BGH	C8-N9	-22.39	1.31	1.45
2	5	4436	B8K	C8-N9	-22.15	1.31	1.45
2	5	3612	P7G	C8-N9	-21.39	1.32	1.45
2	5	1848	P7G	C8-N9	-21.09	1.32	1.45

The worst 5 of 372 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	2365	7MG	N9-C4-N3	9.54	139.43	125.46
2	5	1614	I4U	O4-C4-C5	8.34	121.37	115.45

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	4101	E6G	C5-C4-N3	-7.28	119.51	127.18
2	5	4149	PSU	N1-C2-N3	6.94	122.49	115.17
2	5	1799	B8H	N3-C2-N1	6.72	121.71	115.22

There are no chirality outliers.

5 of 98 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	5	1260	OMG	C1'-C2'-O2'-CM2
2	5	1270	A2M	C1'-C2'-O2'-CM'
2	5	1292	P4U	N3-C4-O4-C41
2	5	1292	P4U	O4'-C4'-C5'-O5'
2	5	1537	PSU	C3'-C4'-C5'-O5'

There are no ring outliers.

31 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	5	2704	OMC	2	0
2	5	4149	PSU	1	0
2	5	398	A2M	1	0
2	5	1638	PSU	1	0
2	5	1489	A2M	1	0
2	5	4269	A2M	1	0
2	5	4276	UR3	2	0
2	5	3601	OMC	1	0
2	5	1260	OMG	1	0
2	5	4383	OMG	1	0
2	5	4366	OMU	2	0
2	5	3524	OMG	1	0
2	5	3557	A2M	2	0
2	5	4193	5MC	2	0
2	5	4369	OMG	1	0
2	5	4240	OMG	1	0
2	5	3496	PSU	1	0
2	5	2647	OMC	1	0
2	5	4436	B8K	1	0
2	5	2267	OMG	3	0
2	5	1270	A2M	2	0
2	5	2265	OMC	1	0
2	5	1560	7MG	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	5	2365	7MG	1	0
2	5	3450	A2M	3	0
2	5	4116	OMG	1	0
2	5	3455	A2M	2	0
2	5	4052	OMU	1	0
2	5	2616	OMG	2	0
2	5	1810	A2M	1	0
2	5	1632	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 184 ligands modelled in this entry, 183 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
50	OWI	K	501	-	45,45,45	2.20	12 (26%)	62,64,64	2.87	14 (22%)

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
50	OWI	K	501	-	-	26/52/60/60	0/3/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	K	501	OWI	S05-N04	6.76	1.72	1.63

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	K	501	OWI	S30-N29	6.53	1.72	1.63
50	K	501	OWI	C31-S30	5.60	1.84	1.76
50	K	501	OWI	C07-S05	4.87	1.83	1.76
50	K	501	OWI	C34-N35	3.84	1.46	1.37

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	K	501	OWI	O41-S30-O40	-12.28	100.43	119.59
50	K	501	OWI	O14-S05-O06	-11.97	100.91	119.59
50	K	501	OWI	O41-S30-N29	7.07	113.34	106.69
50	K	501	OWI	O14-S05-N04	6.19	112.52	106.69
50	K	501	OWI	O06-S05-N04	4.63	111.04	106.69

There are no chirality outliers.

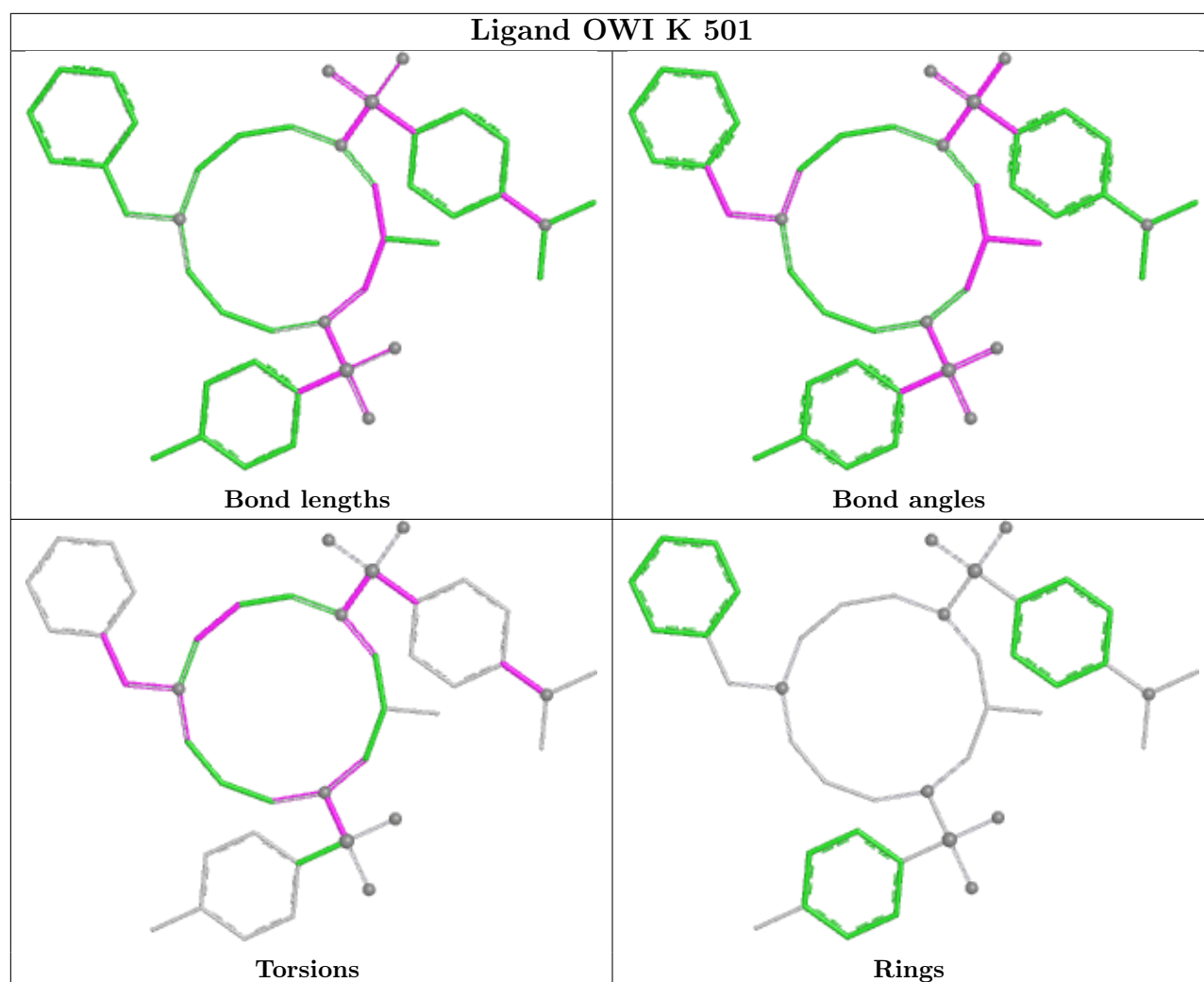
5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	K	501	OWI	C16-C15-N04-S05
50	K	501	OWI	N18-C19-C20-C21
50	K	501	OWI	N18-C19-C20-C25
50	K	501	OWI	C20-C19-N18-C26
50	K	501	OWI	C02-C42-N29-C28

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

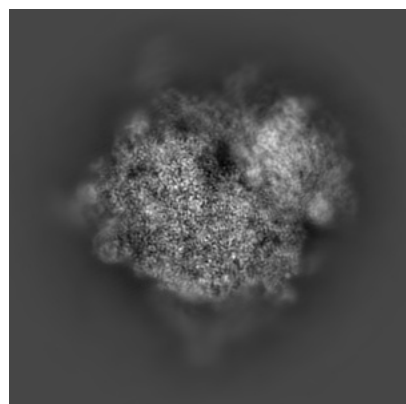
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15863. These allow visual inspection of the internal detail of the map and identification of artifacts.

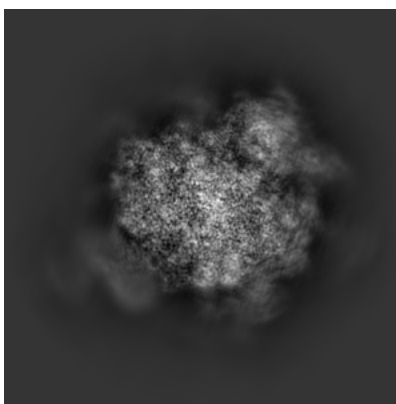
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

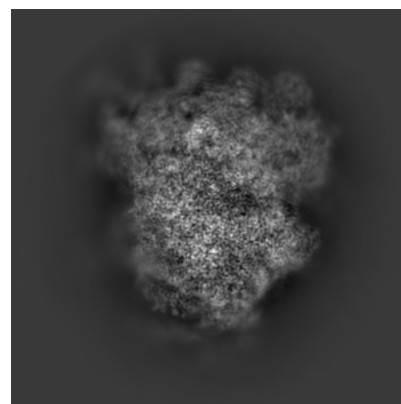
6.1.1 Primary map



X

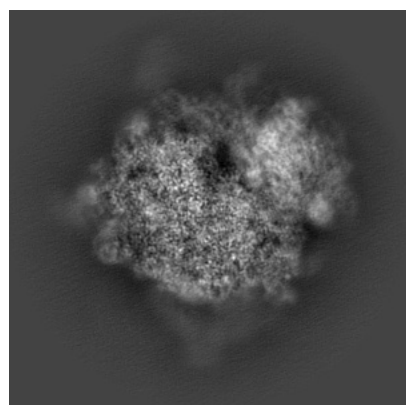


Y

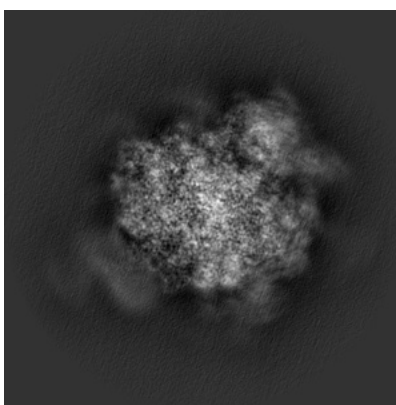


Z

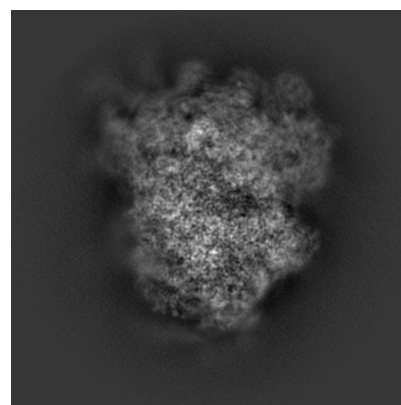
6.1.2 Raw map



X



Y

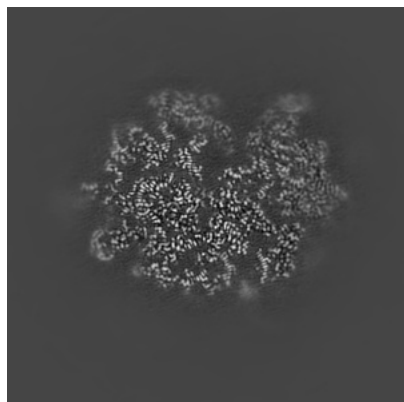


Z

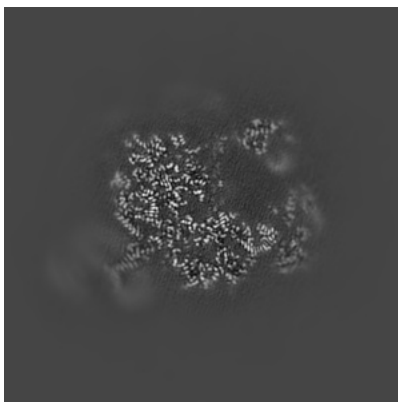
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

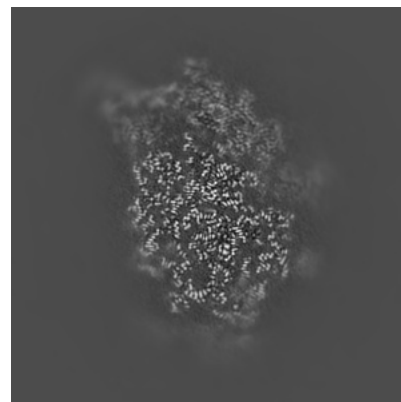
6.2.1 Primary map



X Index: 176

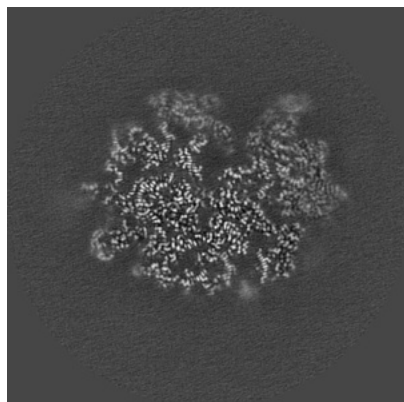


Y Index: 176

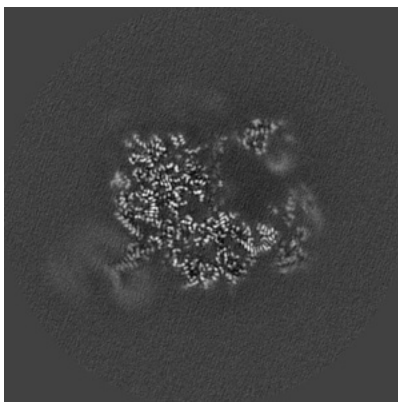


Z Index: 176

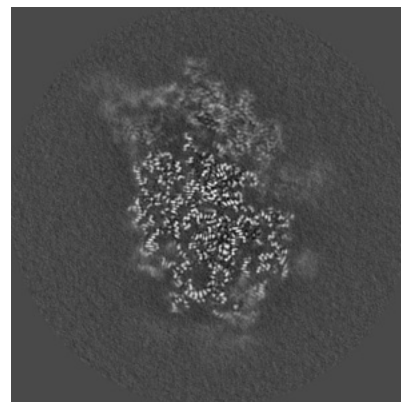
6.2.2 Raw map



X Index: 176



Y Index: 176

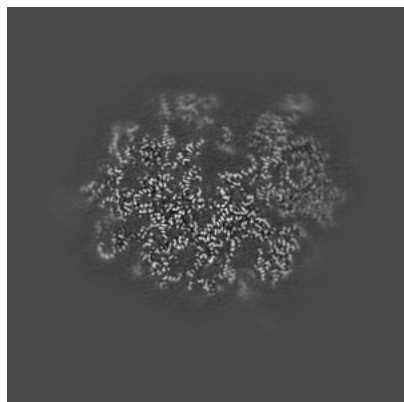


Z Index: 176

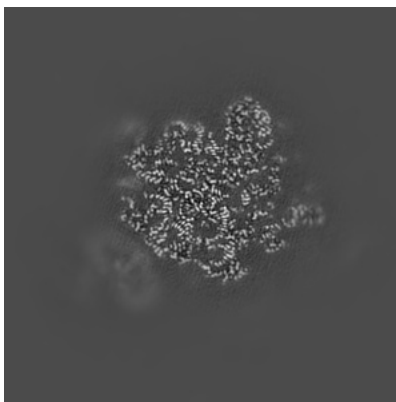
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

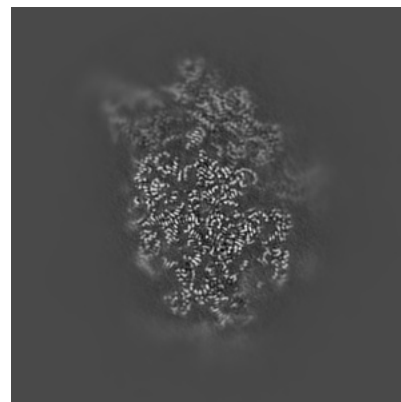
6.3.1 Primary map



X Index: 179

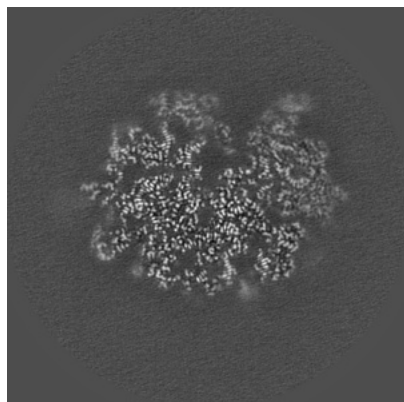


Y Index: 147

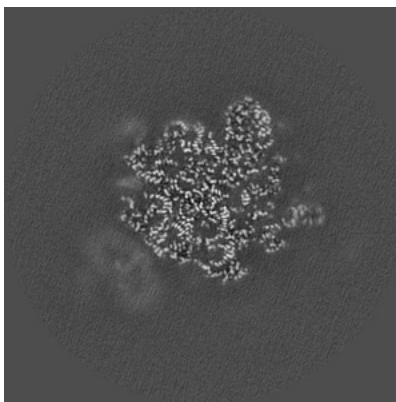


Z Index: 180

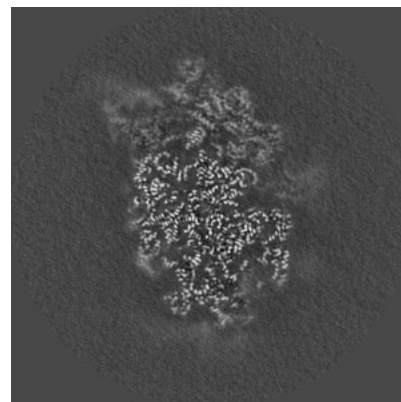
6.3.2 Raw map



X Index: 177



Y Index: 147

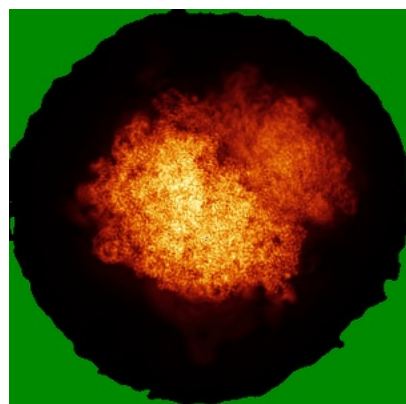


Z Index: 180

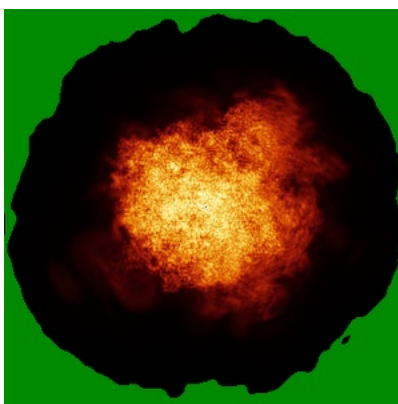
The images above show the largest variance slices of the map in three orthogonal directions.

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

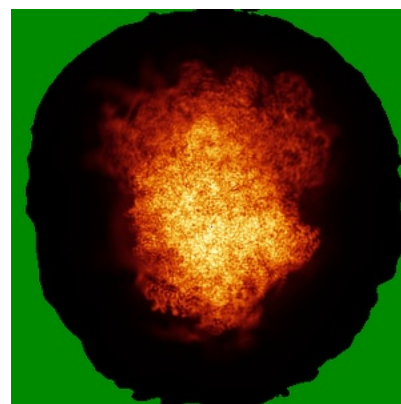
6.4.1 Primary map



X

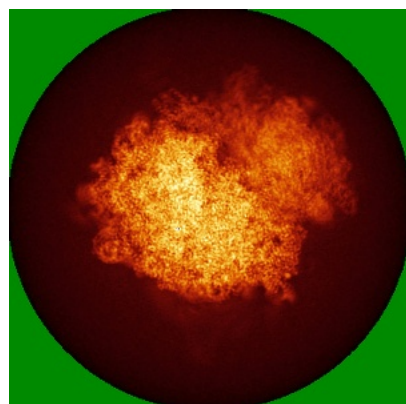


Y

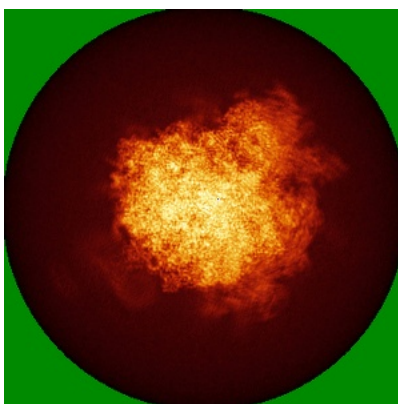


Z

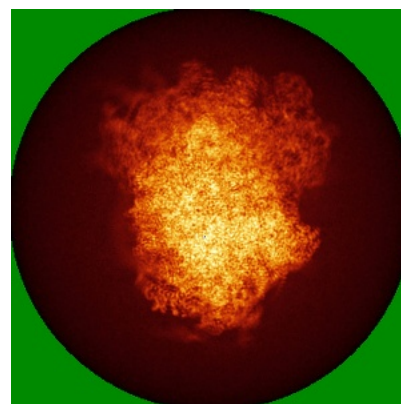
6.4.2 Raw map



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.

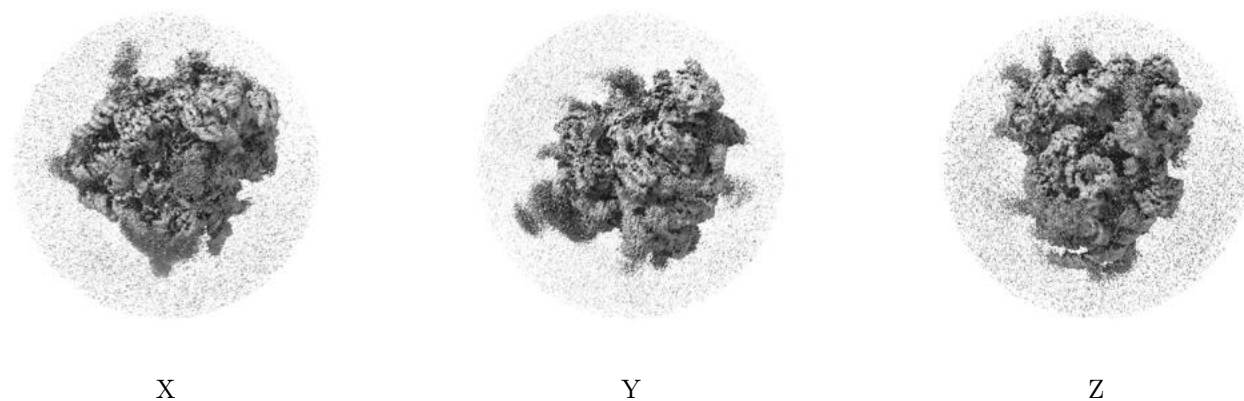
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01581. 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.

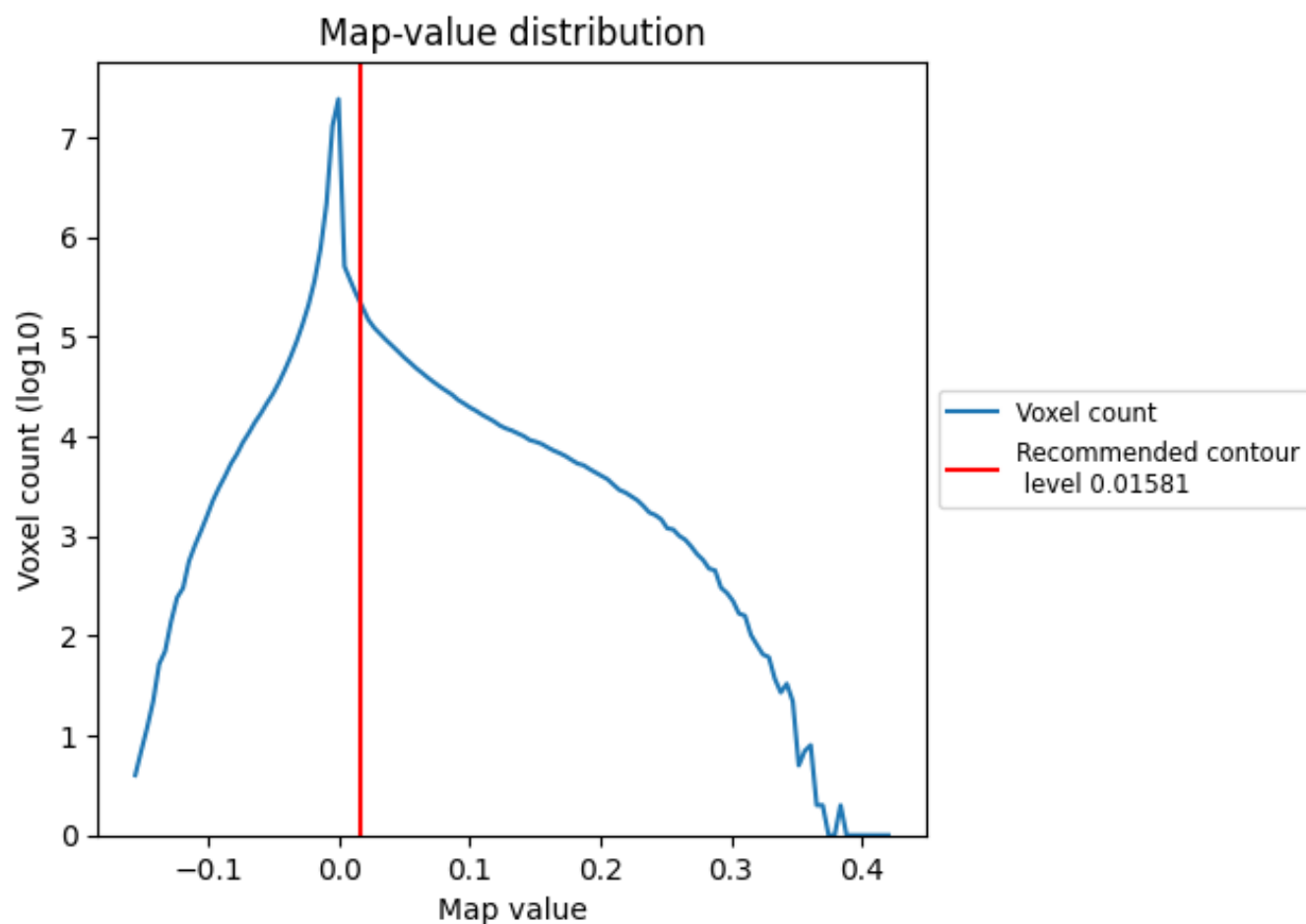
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

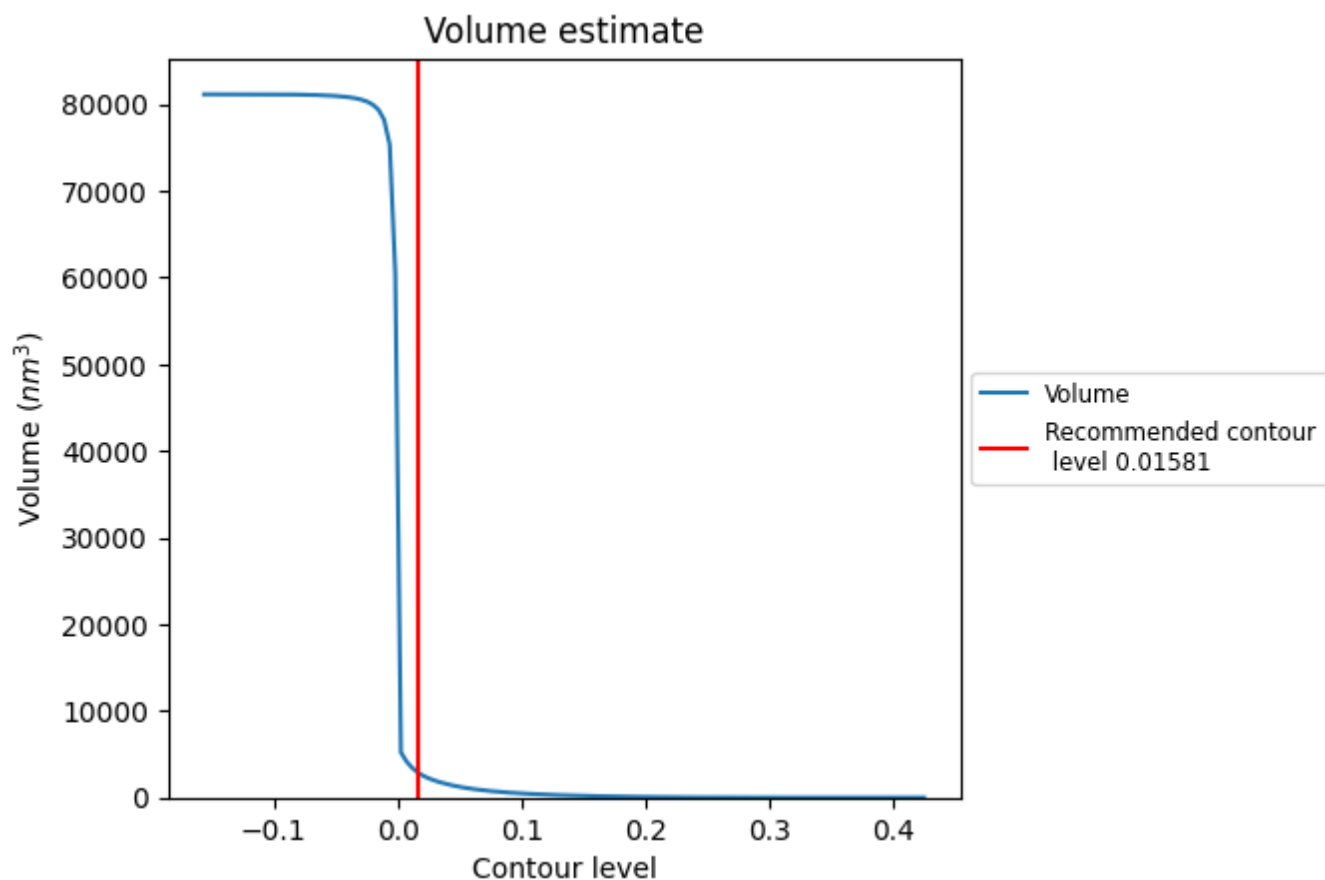
This section contains the results of statistical analysis of the map.

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.

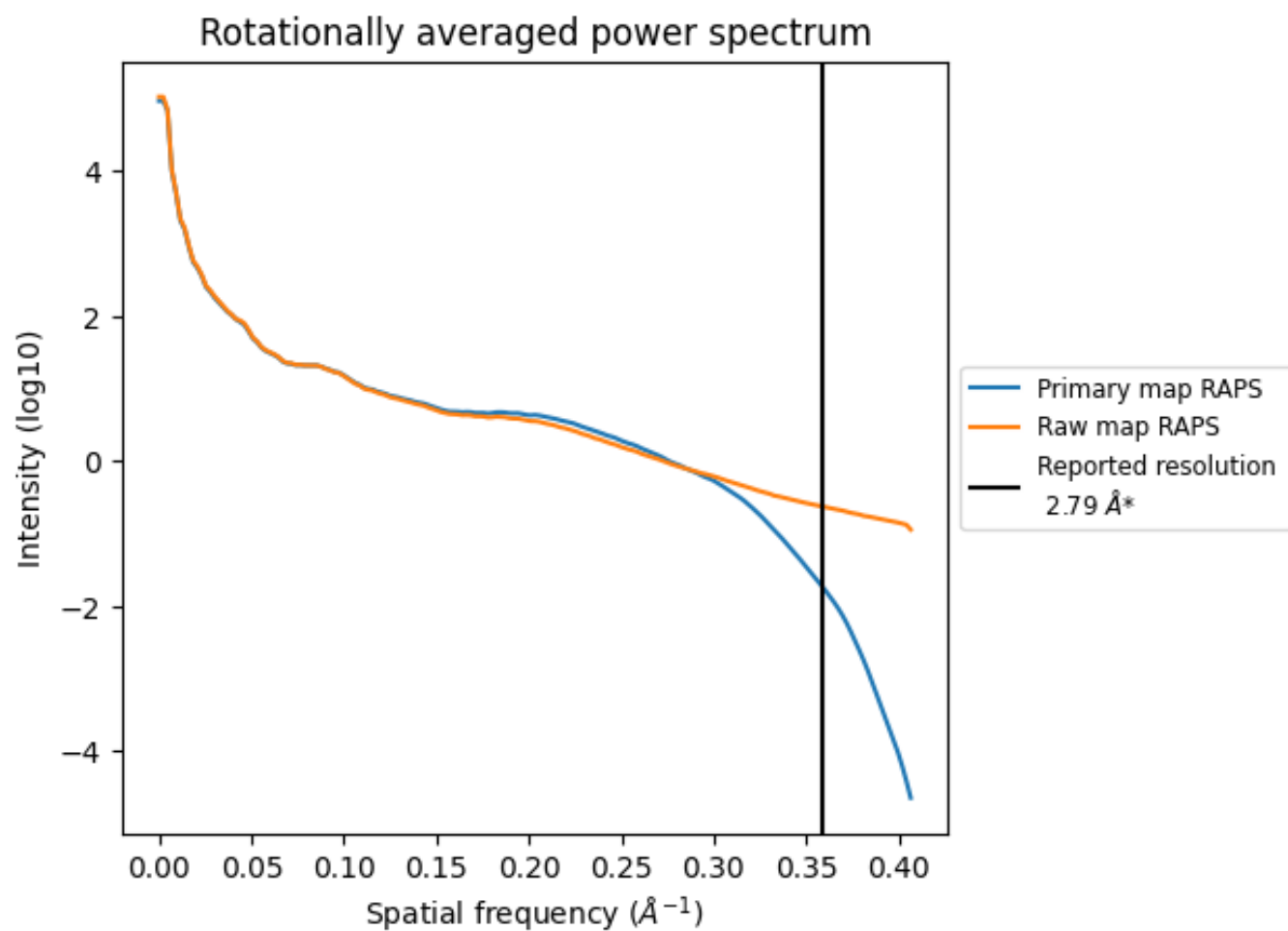
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2951 nm^3 ; this corresponds to an approximate mass of 2665 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 ⓘ

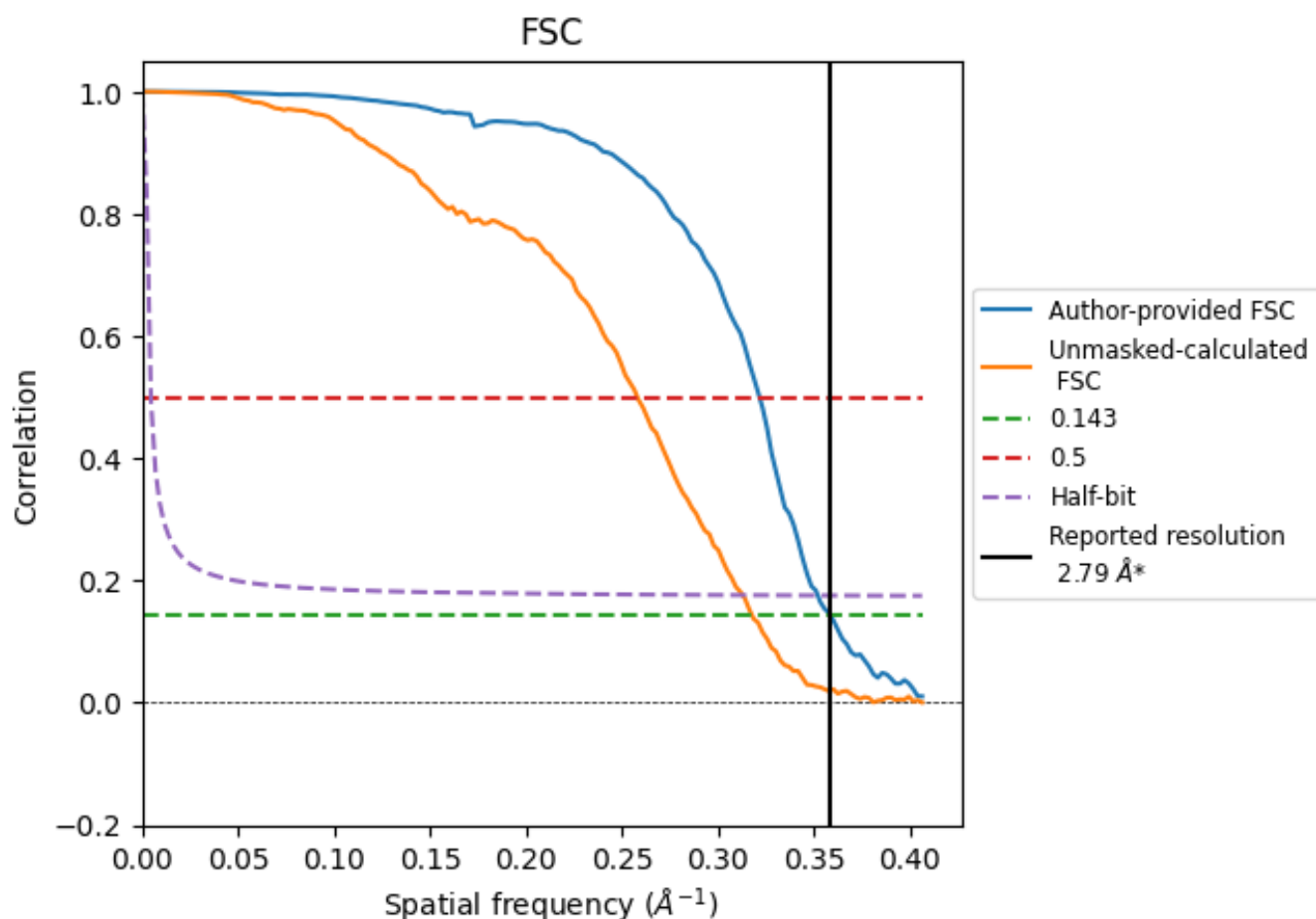


*Reported resolution corresponds to spatial frequency of 0.358 $\text{\AA}^{-1}$

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 0.358 Å⁻¹

8.2 Resolution estimates [i](#)

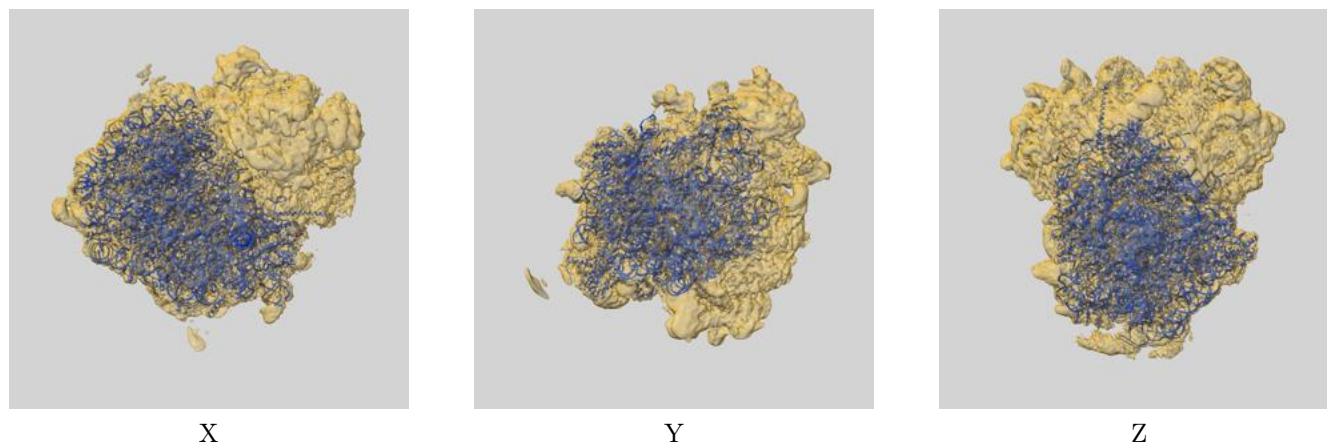
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.79	-	-
Author-provided FSC curve	2.79	3.11	2.84
Unmasked-calculated*	3.15	3.87	3.19

*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 3.15 differs from the reported value 2.79 by more than 10 %

9 Map-model fit [i](#)

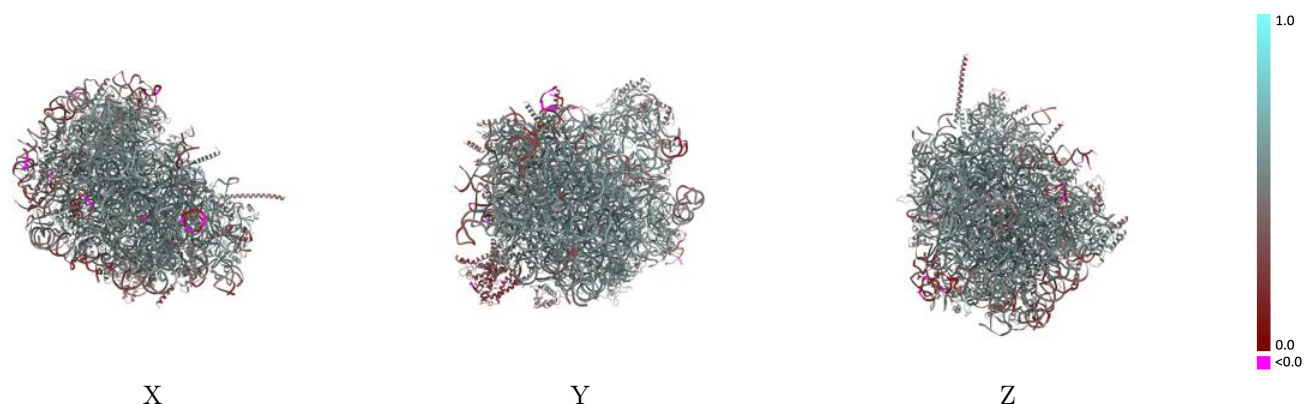
This section contains information regarding the fit between EMDB map EMD-15863 and PDB model 8B6C. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



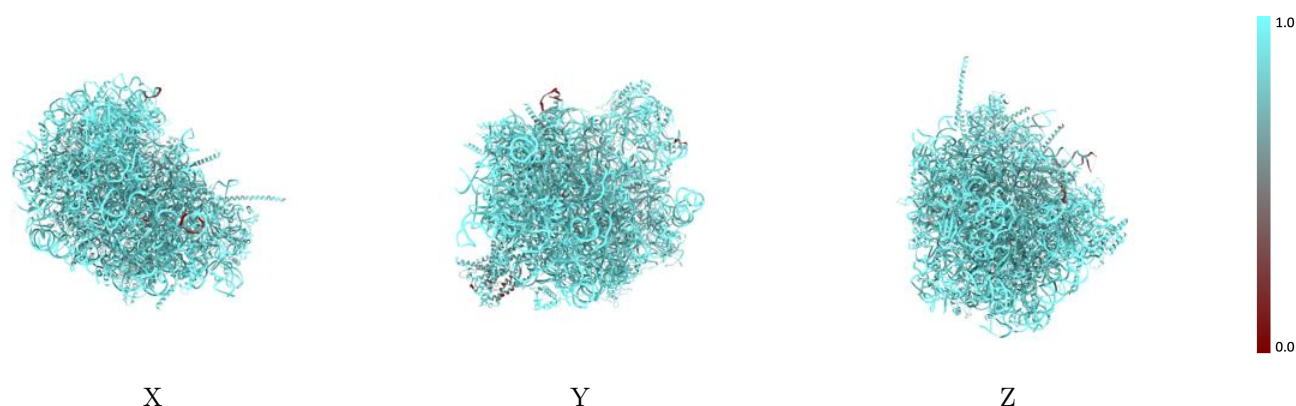
The images above show the 3D surface view of the map at the recommended contour level 0.01581 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



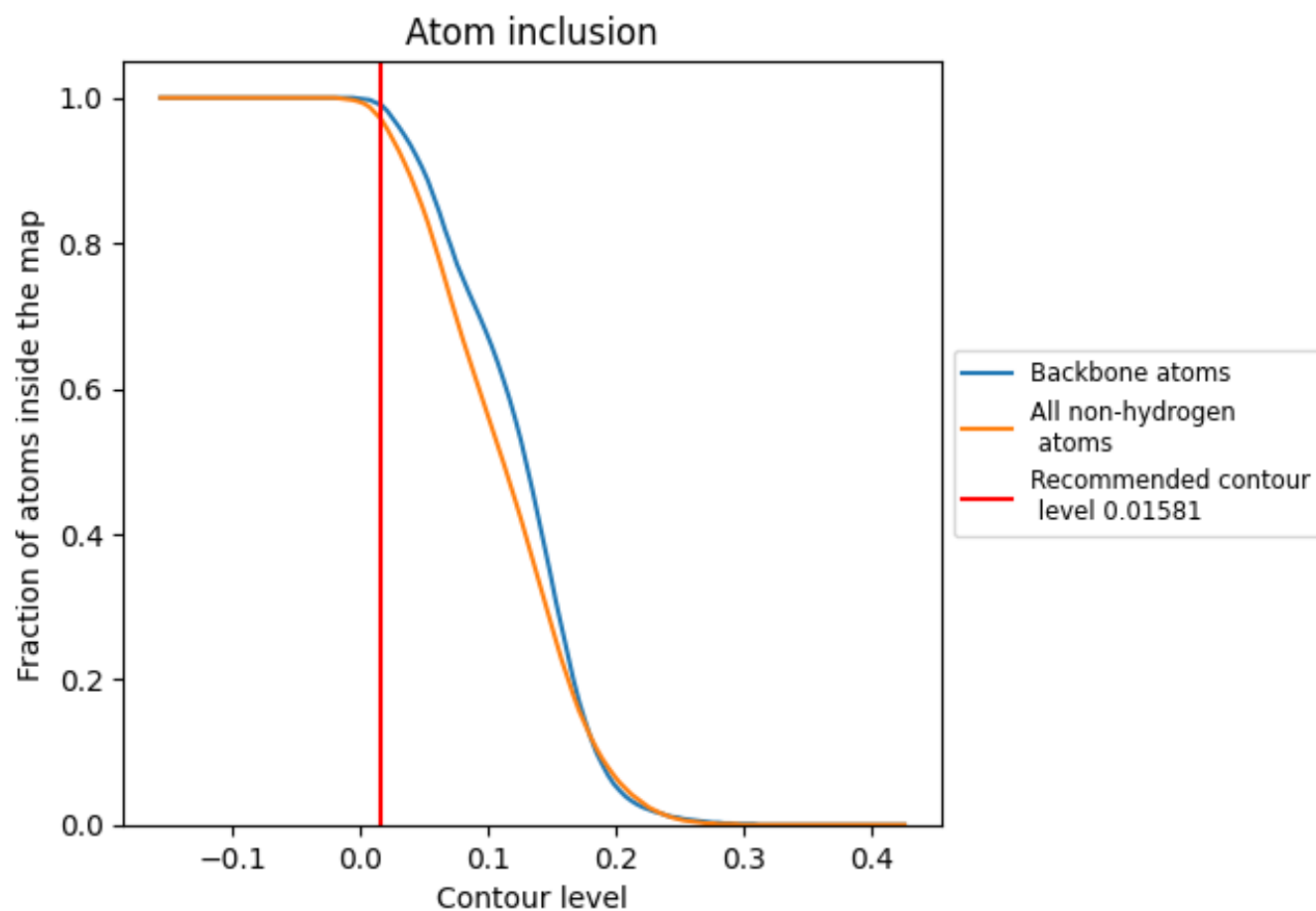
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01581).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.01581) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9710	 0.5160
5	 0.9870	 0.5160
7	 0.9980	 0.5520
8	 0.9950	 0.5410
A	 0.9700	 0.5720
B	 0.9690	 0.5500
C	 0.9660	 0.5490
D	 0.9720	 0.5050
E	 0.9710	 0.5230
F	 0.9590	 0.5510
G	 0.9560	 0.4800
H	 0.9550	 0.5320
I	 0.9590	 0.5400
J	 0.9500	 0.4670
K	 0.7720	 0.2550
L	 0.9370	 0.5110
M	 0.9720	 0.5320
N	 0.9720	 0.5760
O	 0.9750	 0.5530
P	 0.9620	 0.5550
Q	 0.9580	 0.5600
R	 0.9400	 0.4920
S	 0.9720	 0.5580
T	 0.9600	 0.5390
U	 0.9440	 0.4390
V	 0.9560	 0.5610
W	 0.9570	 0.5450
X	 0.9310	 0.5240
Y	 0.9450	 0.5250
Z	 0.9700	 0.5140
a	 0.9750	 0.5680
b	 0.9320	 0.4730
c	 0.9400	 0.4970
d	 0.9510	 0.5230
e	 0.9660	 0.5670



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.9670	 0.5760
g	 0.9450	 0.5440
h	 0.9370	 0.5150
i	 0.9470	 0.4970
j	 0.9780	 0.5790
k	 0.9170	 0.4660
l	 0.9560	 0.5470
m	 0.9520	 0.5540
n	 0.8850	 0.4620
o	 0.9620	 0.5470
p	 0.9420	 0.5400
q	 0.8050	 0.2950
r	 0.9770	 0.5530