



Full wwPDB EM Validation Report ⓘ

Oct 6, 2024 – 08:47 pm BST

PDB ID : 6YS3
EMDB ID : EMD-10891
Title : Cryo-EM structure of the 50S ribosomal subunit at 2.58 Angstroms with modeled GBC SecM peptide
Authors : Schulte, L.; Reitz, J.; Kudlinzki, D.; Hodirnau, V.V.; Frangakis, A.; Schwalbe, H.
Deposited on : 2020-04-20
Resolution : 2.58 Å (reported)
Based on initial model : 3JBU

This is a Full wwPDB EM Validation 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

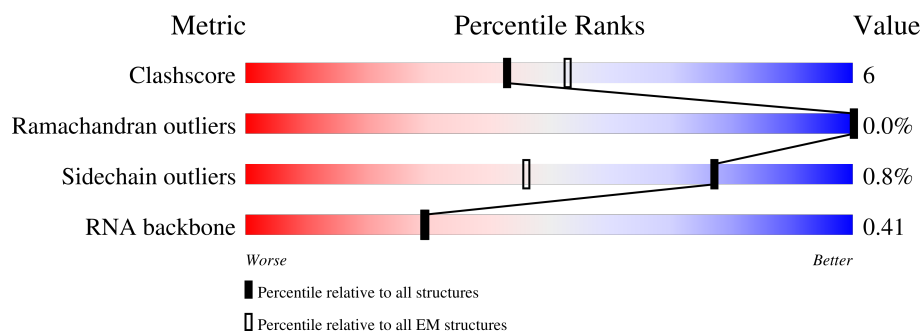
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.58 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.



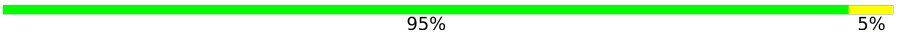


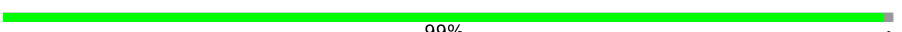
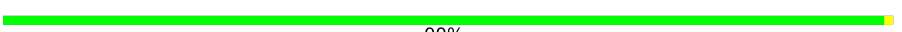
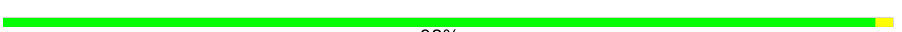






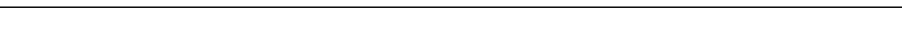

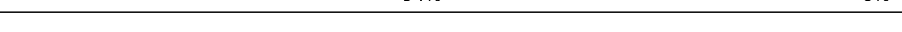
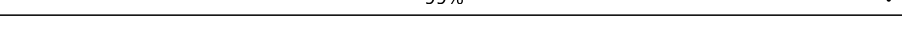
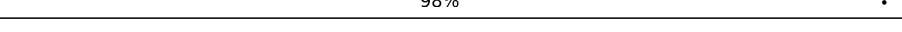
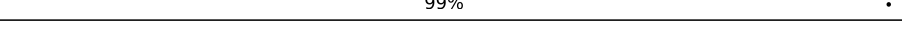
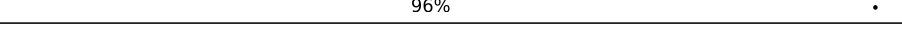
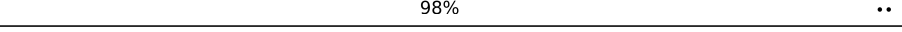

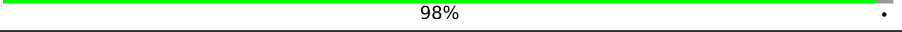

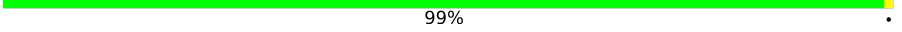

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	78	92% 6% .
2	1	63	83% 14% .
3	2	59	93% . .
4	3	57	84% 12% .
5	4	55	84% 7% 9%
6	6	46	96% .
7	7	65	92% . . .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	8	38	 95% 5%
9	a	120	 70% 27% . .
10	b	2906	 67% 29% . .
11	c	273	 99% .
12	d	209	 99% .
13	e	201	 98% .
14	f	179	 98% ..
15	g	177	 98% ..
16	h	149	 26% . 74%
17	j	142	 100%
18	k	123	 98% ..
19	l	144	 99% .
20	m	136	 99% .
21	n	127	 94% . 6%
22	o	117	 99% .
23	p	115	 98% .
24	q	118	 99% .
25	r	103	 96% .
26	s	110	 98% ..
27	t	100	 92% . 7%
28	u	104	 98% .
29	v	75	 8% 48% 44% 8%
30	w	94	 99% .
31	y	85	 86% . 13%
32	z	61	 43% 15% 43%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90553 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 L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2528	1126	464	821	117		

- Molecule 10 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	2888	Total	C	N	O	P	0	0
			62008	27660	11413	20047	2888		

- Molecule 11 is a protein called 50S ribosomal protein L2.

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

- Molecule 12 is a protein called 50S ribosomal protein L3.

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

- Molecule 13 is a protein called 50S ribosomal protein L4.

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

- Molecule 14 is a protein called 50S ribosomal protein L5.

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

- Molecule 15 is a protein called 50S ribosomal protein L6.

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

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	l	143	Total	C	N	O	S	0	0
			1042	648	206	186	2		

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	113	Total	C	N	O	S	0	0
			908	570	177	160	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	r	99	Total	C	N	O	S	0	0
			791	500	149	140	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	s	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a RNA chain called glycine-tRNA glyT.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	v	75	Total	C	N	O	P	0	0
			1583	707	270	531	75		

- Molecule 30 is a protein called 50S ribosomal protein L25.

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

- Molecule 31 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	74	Total	C	N	O	S	0	0
			559	348	112	98	1		

- Molecule 32 is a protein called Gamma-crystallin B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	35	Total	C	N	O	S	0	0
			275	172	48	51	4		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	-12	MET	-	initiating methionine	UNP P02526
z	-11	GLY	-	expression tag	UNP P02526
z	-10	HIS	-	expression tag	UNP P02526
z	-9	HIS	-	expression tag	UNP P02526
z	-8	HIS	-	expression tag	UNP P02526
z	-7	HIS	-	expression tag	UNP P02526
z	-6	HIS	-	expression tag	UNP P02526
z	-5	HIS	-	expression tag	UNP P02526
z	-4	HIS	-	expression tag	UNP P02526
z	-3	HIS	-	expression tag	UNP P02526
z	-2	HIS	-	expression tag	UNP P02526
z	-1	HIS	-	expression tag	UNP P02526

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
z	150	PHE	ASN	conflict	UNP P02526
z	152	THR	ILE	conflict	UNP P02526
z	153	PRO	ARG	conflict	UNP P02526
z	155	TRP	-	expression tag	UNP P02526
z	156	ILE	-	expression tag	UNP P02526
z	157	SER	-	expression tag	UNP P02526
z	158	GLN	-	expression tag	UNP P02526
z	159	ALA	-	expression tag	UNP P02526
z	160	GLN	-	expression tag	UNP P02526
z	161	GLY	-	expression tag	UNP P02526
z	162	ILE	-	expression tag	UNP P02526
z	163	ARG	-	expression tag	UNP P02526
z	164	ALA	-	expression tag	UNP P02526
z	165	GLY	-	expression tag	UNP P02526

3 Residue-property plots [i](#)


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

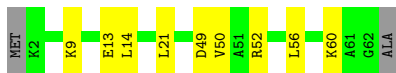
- Molecule 1: 50S ribosomal protein L28

Chain 0:  92% 6% .



- Molecule 2: 50S ribosomal protein L29

Chain 1:  83% 14% .




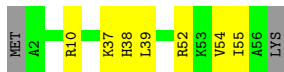
- Molecule 3: 50S ribosomal protein L30

Chain 2:  93% . .




- Molecule 4: 50S ribosomal protein L32

Chain 3:  84% 12% .



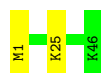
- Molecule 5: 50S ribosomal protein L33

Chain 4:  84% 7% 9%



- Molecule 6: 50S ribosomal protein L34

Chain 6:  96%



- Molecule 7: 50S ribosomal protein L35

Chain 7:  92%



- Molecule 8: 50S ribosomal protein L36

Chain 8:  95%



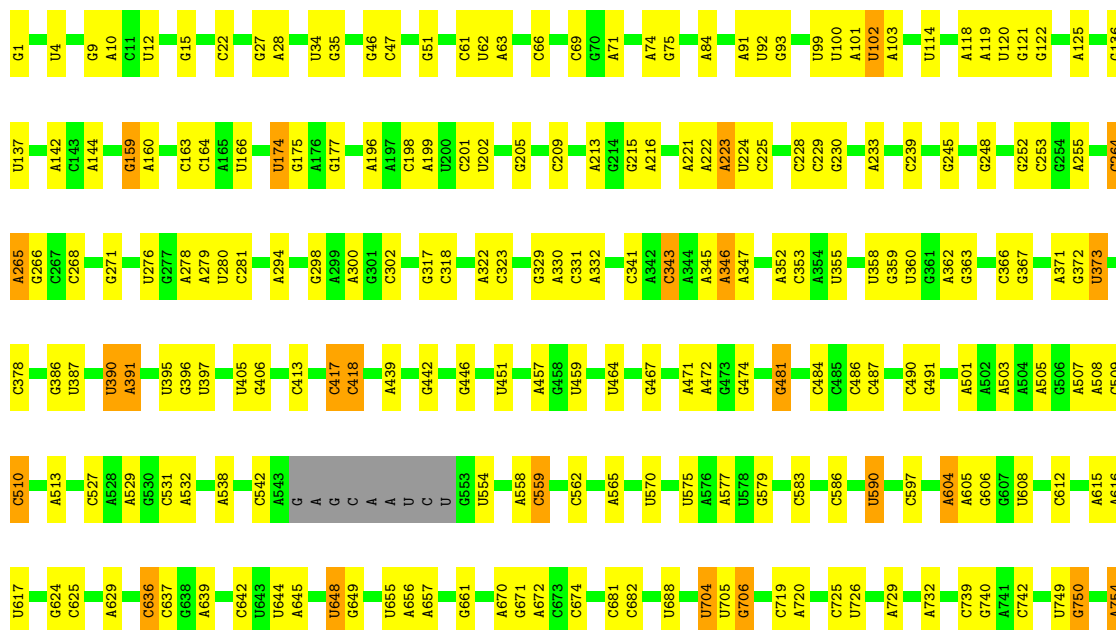
- Molecule 9: 5S rRNA

Chain a:  70%

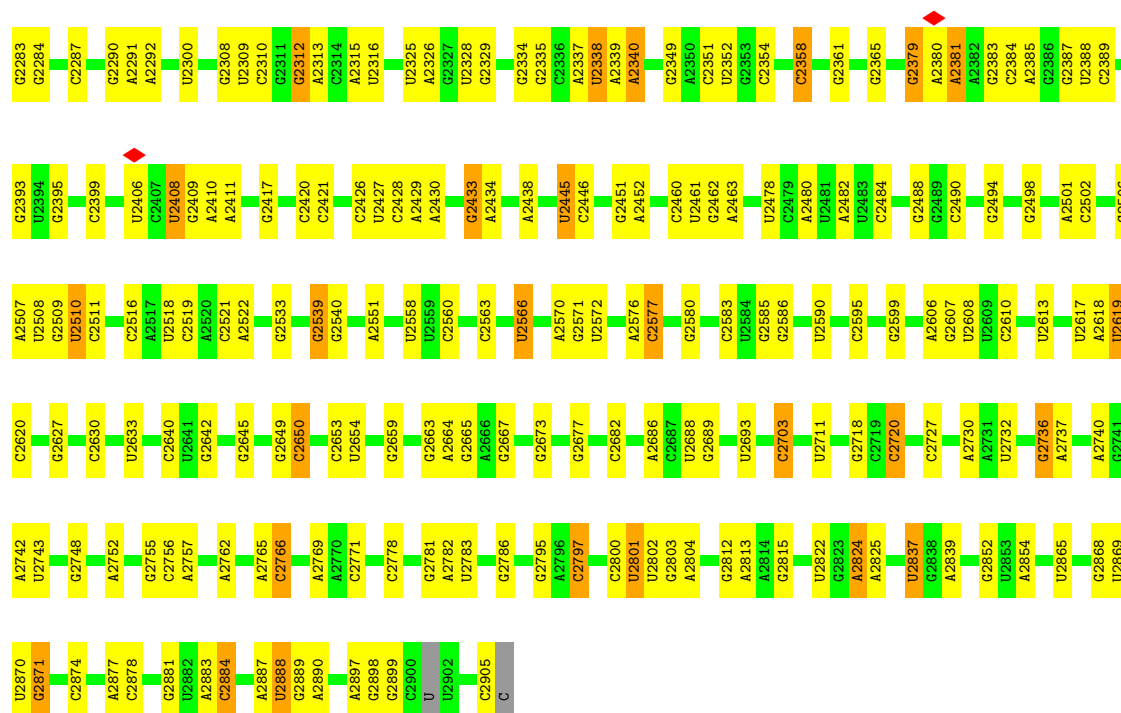


- Molecule 10: 23S rRNA

Chain b:  67%

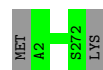


C2168	C2169	U2170	U2171	C2172	A2173	A2174	U2175	C2176	C2177	C2178	C2179	A2180	C2181	C2182	C2183	U2184	U2185	U2186	U2189	U2190	U2191	U2192	U2196	A2202	A2203	U2207	C2208	C2215	A2216	U2217	C2218	C2219	U2224	A2229	U2233	C2236	G2242	G2243	U2244	U2247	G2254	C2265	A2272	G2275																																																																																																																																																																																																																																																																																														
G2104	A2105	G2106	C2107	C2108	U2109	U2110	G2111	A2112	U2113	G2114	U2115	G2116	G2119	G2120	A2121	U2122	A2123	G2124	G2125	U2126	G2127	G2128	G2129	A2130	G2131	G2132	C2133	U2134	U2136	U2138	U2139	G2140	U2141	G2142	U2143	A2146	C2149	C2150	A2151	G2152	U2153	C2154	U2155	G2156	C2157	A2158	U2159	G2160	A2161	G2163	C2164	G2165	G2166	G2167																																																																																																																																																																																																																																																																																				
C1989	U1995	G1996	G1997	C1998	C2001	A2002	C2003	C2004	C2010	U2011	C2012	A2024	C2027	A2034	A2035	G2036	A2037	U2038	G2039	C2040	A2046	C2047	C2048	G2053	C2059	G2060	A2064	G2065	A2066	C2067	C2068	C2069	C2070	G2071	G2072	G2073	C2077	A2081	A2084	C2093	C2097	U2102	U2103																																																																																																																																																																																																																																																																																															
C1883	U1886	U1887	G1888	G1889	G1892	C1896	C1897	C1898	C1899	G1910	G1911	C1912	C1913	G1914	A1917	C1918	A1922	A1923	C1924	C1928	C1929	A1931	A1932	G1933	U1934	U1935	A1941	A1942	U1943	U1944	U1947	U1959	U1960	G1968	C1971	A1974	U1975	G1976	G1977	C1978	C1979	A1985	U1986																																																																																																																																																																																																																																																																																															
U1760	A1764	G1765	C1766	U1771	A1775	U1777	G1778	U1781	A1782	U1783	U1784	A1785	A1786	A1787	A1788	A1793	C1797	C1802	A1803	A1810	G1813	C1818	U1829	G1830	A1831	C1832	C1835	C1839	G1844	G1851	G1859	G1864	C1870	G1871	U1872	A1873	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
C1611	A1612	C1613	U1614	C1615	U1616	C1617	U1618	C1619	U1620	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																																																																																																																																																																																						
A1511	C1512	C1513	C1514	U1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	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																																																																																																																																																																																																																																							
A1397	U1398	U1399	C1400	C1401	U1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510																																																																																																																																																																																																																									
A1289	G1290	C1291	C1292	C1293	U1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510																																																																																																													
G1188	G1189	U1190	G1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1																																																																																					



• Molecule 11: 50S ribosomal protein L2

Chain c: 99%



• Molecule 12: 50S ribosomal protein L3

Chain d: 99%



• Molecule 13: 50S ribosomal protein L4

Chain e: 98%



• Molecule 14: 50S ribosomal protein L5

Chain f: 98%



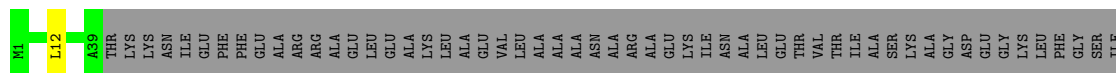
- Molecule 15: 50S ribosomal protein L6

Chain g:  98%



- Molecule 16: 50S ribosomal protein L9

Chain h:  26%



- Molecule 17: 50S ribosomal protein L13

Chain j:  100%

There are no outlier residues recorded for this chain.

- Molecule 18: 50S ribosomal protein L14

Chain k:  98%



- Molecule 19: 50S ribosomal protein L15

Chain l:  99%



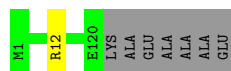
- Molecule 20: 50S ribosomal protein L16

Chain m:  99%



- Molecule 21: 50S ribosomal protein L17

Chain n:  94%



- Molecule 22: 50S ribosomal protein L18

Chain o:  99% .



- Molecule 23: 50S ribosomal protein L19

Chain p:  98% .



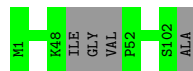
- Molecule 24: 50S ribosomal protein L20

Chain q:  99% .



- Molecule 25: 50S ribosomal protein L21

Chain r:  96% .



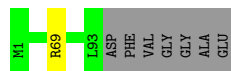
- Molecule 26: 50S ribosomal protein L22

Chain s:  98% ..



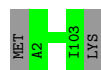
- Molecule 27: 50S ribosomal protein L23

Chain t:  92% . 7%

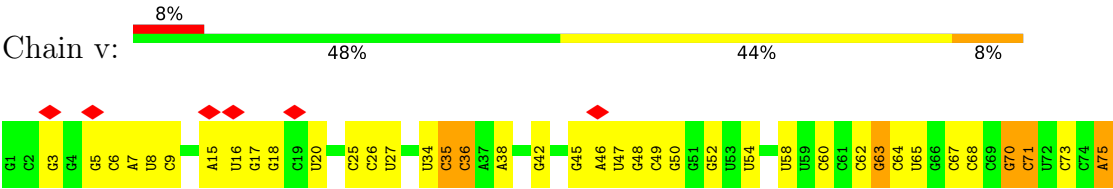


- Molecule 28: 50S ribosomal protein L24

Chain u:  98% .



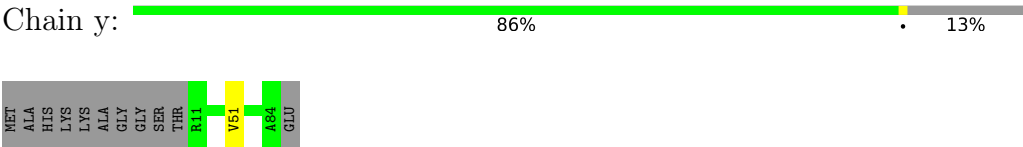
- Molecule 29: glycine-tRNA glyT



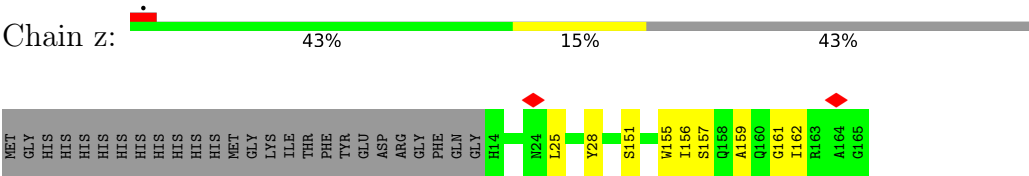
- Molecule 30: 50S ribosomal protein L25



- Molecule 31: 50S ribosomal protein L27



- Molecule 32: Gamma-crystallin B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	196254	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.109	Depositor
Minimum map value	-0.034	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00741	Depositor
Map size (Å)	503.99997, 503.99997, 503.99997	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.57	0/635	0.58	0/848
2	1	0.45	0/496	0.55	0/660
3	2	0.53	0/443	0.62	0/593
4	3	0.69	0/440	0.62	0/588
5	4	0.47	0/416	0.62	0/554
6	6	0.69	0/380	0.56	0/498
7	7	0.61	0/513	0.57	0/676
8	8	0.67	0/303	0.68	0/397
9	a	0.97	0/2824	1.07	3/4402 (0.1%)
10	b	1.42	1/69446 (0.0%)	1.22	537/108330 (0.5%)
11	c	0.66	0/2121	0.64	0/2852
12	d	0.65	0/1586	0.62	0/2134
13	e	0.59	0/1571	0.68	1/2113 (0.0%)
14	f	0.40	0/1434	0.63	0/1926
15	g	0.43	0/1343	0.74	2/1816 (0.1%)
16	h	0.44	0/290	0.74	0/392
17	j	0.63	0/1152	0.58	0/1551
18	k	0.62	0/947	0.64	0/1268
19	l	0.61	0/1051	0.65	0/1400
20	m	0.63	0/1093	0.58	0/1460
21	n	0.63	0/973	0.65	0/1301
22	o	0.44	0/902	0.62	0/1209
23	p	0.58	0/920	0.57	0/1231
24	q	0.76	0/960	0.63	0/1278
25	r	0.64	0/803	0.61	0/1070
26	s	0.60	0/852	0.58	0/1142
27	t	0.54	0/744	0.60	0/994
28	u	0.50	0/787	0.65	0/1051
29	v	0.64	0/1764	1.29	17/2744 (0.6%)
30	w	0.50	0/766	0.61	1/1025 (0.1%)
31	y	0.63	0/566	0.61	0/750
32	z	0.35	0/284	1.39	9/386 (2.3%)
All	All	1.24	1/98805 (0.0%)	1.11	570/148639 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	b	1	G	OP3-P	-10.15	1.49	1.61

All (570) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	g	45	HIS	N-CA-C	-12.39	77.55	111.00
32	z	159	ALA	N-CA-C	-11.50	79.94	111.00
10	b	2888	U	N3-C2-O2	-10.24	115.03	122.20
10	b	2027	C	N1-C2-O2	10.23	125.04	118.90
10	b	819	C	C6-N1-C2	-10.12	116.25	120.30
10	b	1315	U	N1-C2-O2	9.98	129.78	122.80
10	b	2462	G	O4'-C1'-N9	9.88	116.11	108.20
10	b	878	C	N1-C2-O2	9.76	124.76	118.90
10	b	849	U	N3-C2-O2	-9.70	115.41	122.20
10	b	2462	G	N7-C8-N9	9.68	117.94	113.10
10	b	1315	U	C2-N1-C1'	9.64	129.26	117.70
10	b	976	G	N7-C8-N9	9.63	117.91	113.10
32	z	156	ILE	N-CA-C	9.61	136.93	111.00
10	b	1315	U	N3-C2-O2	-9.52	115.53	122.20
10	b	2059	C	C6-N1-C2	-9.41	116.54	120.30
10	b	265	A	O4'-C1'-N9	9.39	115.71	108.20
10	b	2577	C	N1-C2-O2	9.31	124.49	118.90
10	b	2462	G	C8-N9-C4	-9.25	102.70	106.40
10	b	2577	C	C2-N1-C1'	9.08	128.78	118.80
32	z	28	TYR	N-CA-C	-8.98	86.76	111.00
10	b	2650	C	C6-N1-C2	-8.96	116.72	120.30
10	b	960	U	N1-C2-O2	8.91	129.03	122.80
10	b	2164	C	C5-C6-N1	8.87	125.44	121.00
29	v	36	C	N1-C2-O2	8.76	124.16	118.90
10	b	1781	U	C5-C6-N1	-8.75	118.33	122.70
10	b	2358	C	N1-C2-O2	8.59	124.06	118.90
10	b	849	U	N1-C2-O2	8.58	128.81	122.80
10	b	1818	C	N1-C2-O2	8.58	124.05	118.90
10	b	2164	C	C6-N1-C2	-8.52	116.89	120.30
10	b	2462	G	C5-N7-C8	-8.45	100.08	104.30
10	b	1776	C	C6-N1-C2	-8.39	116.94	120.30
10	b	1514	C	N1-C2-O2	8.36	123.92	118.90
10	b	2159	U	N1-C2-O2	8.32	128.63	122.80
10	b	976	G	C5-N7-C8	-8.30	100.15	104.30
10	b	878	C	C2-N1-C1'	8.30	127.92	118.80
10	b	2069	C	C6-N1-C2	-8.26	117.00	120.30
29	v	73	C	N1-C2-O2	8.24	123.84	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	g	46	ALA	N-CA-C	-8.23	88.78	111.00
10	b	976	G	C8-N9-C4	-8.13	103.15	106.40
29	v	58	U	N1-C2-O2	8.12	128.48	122.80
10	b	1641	C	N1-C2-O2	8.01	123.70	118.90
10	b	2650	C	C5-C6-N1	8.01	125.00	121.00
10	b	960	U	N3-C2-O2	-7.93	116.65	122.20
10	b	2510	U	N3-C2-O2	-7.92	116.65	122.20
10	b	830	U	N3-C2-O2	-7.89	116.68	122.20
10	b	830	U	C2-N1-C1'	7.89	127.17	117.70
10	b	830	U	N1-C2-O2	7.81	128.27	122.80
10	b	2358	C	N3-C2-O2	-7.79	116.44	121.90
10	b	1947	U	N3-C2-O2	-7.78	116.76	122.20
10	b	1587	C	N1-C2-O2	7.62	123.47	118.90
10	b	2159	U	N3-C2-O2	-7.60	116.88	122.20
10	b	201	C	C6-N1-C2	-7.59	117.26	120.30
10	b	2837	U	N1-C2-O2	7.59	128.11	122.80
10	b	1960	U	N3-C2-O2	-7.59	116.89	122.20
10	b	2027	C	N3-C2-O2	-7.57	116.60	121.90
10	b	2837	U	N3-C2-O2	-7.57	116.90	122.20
10	b	1456	C	N1-C2-O2	7.55	123.43	118.90
10	b	2290	G	C4-C5-N7	7.52	113.81	110.80
10	b	1456	C	O4'-C1'-N1	7.52	114.22	108.20
10	b	2510	U	N1-C2-O2	7.52	128.06	122.80
10	b	2379	G	C4-N9-C1'	7.52	136.27	126.50
10	b	2254	G	N3-C4-C5	7.50	132.35	128.60
10	b	1456	C	N3-C2-O2	-7.49	116.65	121.90
10	b	976	G	C4-C5-N7	7.49	113.80	110.80
10	b	2446	C	C6-N1-C2	-7.44	117.32	120.30
10	b	2379	G	N3-C4-C5	-7.44	124.88	128.60
10	b	1008	C	C6-N1-C2	-7.42	117.33	120.30
10	b	2577	C	N3-C2-O2	-7.42	116.71	121.90
32	z	155	TRP	N-CA-C	-7.42	90.98	111.00
10	b	874	U	C5-C6-N1	7.41	126.41	122.70
10	b	750	G	O4'-C1'-N9	7.41	114.12	108.20
10	b	390	U	N3-C2-O2	-7.39	117.03	122.20
29	v	35	C	N3-C2-O2	-7.39	116.73	121.90
10	b	912	A	O4'-C1'-N9	7.38	114.10	108.20
10	b	1641	C	N3-C2-O2	-7.35	116.75	121.90
10	b	984	C	N3-C2-O2	-7.31	116.78	121.90
10	b	625	C	C6-N1-C2	-7.29	117.38	120.30
10	b	2338	U	C2-N1-C1'	7.27	126.43	117.70
10	b	2837	U	C2-N1-C1'	7.26	126.41	117.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	v	36	C	N3-C2-O2	-7.26	116.82	121.90
10	b	2608	U	N3-C2-O2	-7.25	117.12	122.20
10	b	1316	C	C6-N1-C2	-7.25	117.40	120.30
10	b	1209	C	N1-C2-O2	7.23	123.24	118.90
10	b	346	A	N7-C8-N9	7.22	117.41	113.80
10	b	2254	G	C2-N3-C4	-7.19	108.31	111.90
10	b	2379	G	N3-C4-N9	7.15	130.29	126.00
10	b	1106	C	C6-N1-C2	-7.14	117.44	120.30
10	b	264	C	N1-C2-O2	7.14	123.18	118.90
10	b	1291	C	N1-C2-O2	7.14	123.18	118.90
29	v	35	C	N1-C2-O2	7.13	123.18	118.90
10	b	1316	C	C5-C6-N1	7.11	124.56	121.00
10	b	47	C	C6-N1-C2	-7.11	117.46	120.30
10	b	2888	U	N1-C2-O2	7.10	127.77	122.80
10	b	481	G	O4'-C1'-N9	7.10	113.88	108.20
10	b	917	C	N1-C2-O2	7.08	123.15	118.90
10	b	2608	U	N1-C2-O2	7.07	127.75	122.80
10	b	890	C	C6-N1-C2	-7.07	117.47	120.30
10	b	268	C	N1-C2-O2	7.06	123.14	118.90
10	b	1202	C	C6-N1-C2	-7.03	117.49	120.30
10	b	1094	C	C5-C6-N1	7.02	124.51	121.00
10	b	1646	C	N1-C2-O2	7.02	123.11	118.90
10	b	2059	C	C5-C6-N1	7.01	124.50	121.00
10	b	1461	G	N3-C4-C5	6.98	132.09	128.60
10	b	1119	C	C6-N1-C2	-6.98	117.51	120.30
10	b	1892	G	O4'-C1'-N9	6.98	113.78	108.20
10	b	2040	C	N1-C2-O2	6.97	123.08	118.90
10	b	343	C	N1-C2-O2	6.97	123.08	118.90
10	b	2871	G	C4-C5-N7	6.94	113.58	110.80
10	b	878	C	N3-C2-O2	-6.93	117.05	121.90
10	b	99	U	C2-N1-C1'	6.92	126.00	117.70
10	b	102	U	N1-C2-O2	6.92	127.64	122.80
13	e	124	PHE	N-CA-C	-6.92	92.33	111.00
10	b	1269	U	N3-C2-O2	-6.91	117.36	122.20
10	b	1730	C	C5-C6-N1	6.91	124.45	121.00
10	b	2563	C	N1-C2-O2	6.88	123.03	118.90
10	b	1514	C	N3-C2-O2	-6.85	117.11	121.90
10	b	1007	C	N1-C2-O2	6.81	122.99	118.90
10	b	373	U	N3-C2-O2	-6.81	117.43	122.20
10	b	239	C	N1-C2-O2	6.80	122.98	118.90
29	v	58	U	C2-N1-C1'	6.80	125.86	117.70
10	b	268	C	N3-C2-O2	-6.79	117.15	121.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2610	C	C6-N1-C2	-6.78	117.59	120.30
10	b	417	C	O4'-C1'-N1	6.75	113.60	108.20
10	b	1646	C	N3-C2-O2	-6.73	117.19	121.90
29	v	58	U	N3-C2-O2	-6.73	117.49	122.20
10	b	1315	U	C6-N1-C1'	-6.71	111.80	121.20
10	b	559	C	C6-N1-C2	-6.70	117.62	120.30
10	b	209	C	C6-N1-C2	-6.70	117.62	120.30
10	b	2340	A	C5-N7-C8	-6.69	100.56	103.90
10	b	2640	C	N1-C2-O2	6.69	122.91	118.90
10	b	2583	C	C6-N1-C2	-6.67	117.63	120.30
10	b	1316	C	N1-C2-O2	6.67	122.90	118.90
10	b	2871	G	C4-N9-C1'	6.66	135.16	126.50
10	b	253	C	N1-C2-O2	6.66	122.89	118.90
10	b	2703	C	C6-N1-C2	-6.65	117.64	120.30
29	v	73	C	N3-C2-O2	-6.62	117.27	121.90
10	b	976	G	C4-N9-C1'	6.62	135.10	126.50
10	b	2727	C	C6-N1-C2	-6.61	117.66	120.30
29	v	73	C	C2-N1-C1'	6.61	126.07	118.80
10	b	1321	C	C6-N1-C2	-6.59	117.66	120.30
10	b	767	C	N1-C2-O2	6.58	122.85	118.90
10	b	264	C	N3-C2-O2	-6.58	117.29	121.90
10	b	562	C	C6-N1-C2	-6.58	117.67	120.30
10	b	2254	G	C4-C5-N7	6.58	113.43	110.80
10	b	2325	U	C2-N1-C1'	6.57	125.58	117.70
10	b	625	C	C5-C6-N1	6.56	124.28	121.00
10	b	637	C	C6-N1-C2	-6.56	117.68	120.30
10	b	1316	C	C2-N1-C1'	6.54	126.00	118.80
10	b	2510	U	C2-N1-C1'	6.51	125.52	117.70
10	b	2069	C	C5-C6-N1	6.50	124.25	121.00
10	b	2290	G	C5-N7-C8	-6.47	101.06	104.30
10	b	1384	G	O4'-C1'-N9	6.47	113.38	108.20
10	b	1577	C	N1-C2-O2	6.46	122.78	118.90
10	b	1732	C	N1-C2-O2	6.46	122.77	118.90
10	b	1456	C	C2-N1-C1'	6.45	125.90	118.80
10	b	1934	G	P-O3'-C3'	6.43	127.42	119.70
10	b	1301	G	C2'-C3'-O3'	6.43	123.99	113.70
10	b	2408	U	N1-C2-O2	6.43	127.30	122.80
10	b	559	C	C5-C6-N1	6.43	124.21	121.00
10	b	604	A	N7-C8-N9	6.43	117.01	113.80
10	b	2507	A	C2-N3-C4	6.41	113.81	110.60
10	b	2577	C	C6-N1-C1'	-6.41	113.11	120.80
10	b	2801	U	C5-C6-N1	6.41	125.90	122.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2610	C	C5-C6-N1	6.41	124.20	121.00
10	b	1014	U	N3-C4-O4	-6.41	114.92	119.40
10	b	2150	C	C6-N1-C2	-6.38	117.75	120.30
10	b	1106	C	N1-C2-O2	6.38	122.73	118.90
10	b	102	U	N3-C2-O2	-6.38	117.74	122.20
10	b	891	C	N1-C2-O2	6.38	122.72	118.90
10	b	2743	U	N1-C2-O2	6.38	127.26	122.80
10	b	341	C	C6-N1-C2	-6.37	117.75	120.30
10	b	2871	G	C6-C5-N7	-6.36	126.58	130.40
10	b	22	C	C6-N1-C2	-6.36	117.76	120.30
10	b	1365	C	C6-N1-C2	-6.35	117.76	120.30
10	b	2379	G	C2-N3-C4	6.35	115.08	111.90
10	b	346	A	C8-N9-C4	-6.34	103.26	105.80
10	b	1978	C	N1-C2-O2	6.33	122.70	118.90
10	b	2254	G	C5-N7-C8	-6.32	101.14	104.30
10	b	323	C	C2-N1-C1'	6.32	125.75	118.80
10	b	2182	C	C2-N1-C1'	6.32	125.75	118.80
10	b	69	C	N1-C2-O2	6.31	122.68	118.90
10	b	2040	C	N3-C2-O2	-6.30	117.49	121.90
10	b	767	C	N3-C2-O2	-6.30	117.49	121.90
10	b	830	U	C6-N1-C1'	-6.30	112.38	121.20
10	b	343	C	C6-N1-C2	-6.29	117.78	120.30
10	b	586	C	C6-N1-C2	-6.28	117.79	120.30
10	b	343	C	N3-C2-O2	-6.28	117.50	121.90
10	b	1001	U	N3-C2-O2	-6.28	117.81	122.20
10	b	2340	A	N7-C8-N9	6.28	116.94	113.80
10	b	198	C	C5-C6-N1	6.27	124.14	121.00
10	b	849	U	C2-N1-C1'	6.25	125.20	117.70
10	b	1935	U	N1-C2-O2	6.25	127.17	122.80
10	b	341	C	C5-C6-N1	6.24	124.12	121.00
10	b	706	G	O4'-C1'-N9	6.24	113.19	108.20
10	b	1321	C	N1-C2-O2	6.24	122.64	118.90
10	b	921	U	N1-C2-O2	6.23	127.16	122.80
10	b	2358	C	C6-N1-C2	-6.23	117.81	120.30
10	b	1453	C	C2-N1-C1'	6.22	125.65	118.80
10	b	1609	C	C2-N1-C1'	6.22	125.64	118.80
10	b	2379	G	C8-N9-C1'	-6.22	118.92	127.00
10	b	2159	U	C2-N1-C1'	6.21	125.16	117.70
10	b	1347	C	C6-N1-C2	-6.20	117.82	120.30
10	b	2824	A	OP1-P-O3'	6.20	118.84	105.20
10	b	2047	C	C5-C6-N1	6.19	124.10	121.00
10	b	878	C	C6-N1-C1'	-6.19	113.38	120.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	739	C	C6-N1-C2	-6.18	117.83	120.30
10	b	1829	U	N1-C2-O2	6.18	127.13	122.80
10	b	2736	G	O4'-C1'-N9	6.18	113.14	108.20
10	b	1818	C	N3-C2-O2	-6.18	117.57	121.90
10	b	2736	G	C4-C5-N7	6.18	113.27	110.80
10	b	2874	C	C6-N1-C2	-6.17	117.83	120.30
10	b	1776	C	C5-C6-N1	6.17	124.08	121.00
10	b	99	U	N3-C2-O2	-6.16	117.89	122.20
32	z	151	SER	CB-CA-C	-6.14	98.43	110.10
10	b	2888	U	C2-N1-C1'	6.14	125.07	117.70
10	b	1462	U	N3-C2-O2	-6.13	117.91	122.20
10	b	2519	C	C6-N1-C2	-6.13	117.85	120.30
10	b	542	C	N1-C2-O2	6.11	122.56	118.90
10	b	1094	C	C6-N1-C2	-6.08	117.87	120.30
10	b	2577	C	C5-C6-N1	6.07	124.03	121.00
10	b	390	U	P-O3'-C3'	6.06	126.98	119.70
10	b	1701	G	C4-C5-N7	6.06	113.22	110.80
10	b	1321	C	C2-N1-C1'	6.05	125.46	118.80
10	b	1365	C	C5-C6-N1	6.05	124.03	121.00
10	b	1732	C	C2-N1-C1'	6.03	125.44	118.80
10	b	159	G	P-O3'-C3'	6.03	126.93	119.70
10	b	1797	C	C6-N1-C2	-6.03	117.89	120.30
29	v	36	C	C2-N1-C1'	6.02	125.43	118.80
10	b	742	C	N1-C2-O2	6.02	122.51	118.90
10	b	976	G	C6-C5-N7	-6.02	126.79	130.40
10	b	2640	C	C2-N1-C1'	6.02	125.42	118.80
10	b	510	C	N1-C2-O2	6.00	122.50	118.90
10	b	2381	A	O5'-P-OP2	-6.00	100.30	105.70
10	b	1898	C	N1-C2-O2	5.98	122.49	118.90
10	b	2151	A	C2-N3-C4	5.97	113.58	110.60
10	b	890	C	C5-C6-N1	5.96	123.98	121.00
10	b	1646	C	C6-N1-C2	-5.96	117.92	120.30
10	b	1960	U	N1-C2-O2	5.96	126.97	122.80
10	b	174	U	N3-C2-O2	-5.96	118.03	122.20
10	b	984	C	C2-N1-C1'	5.96	125.35	118.80
10	b	1832	C	C6-N1-C2	-5.95	117.92	120.30
10	b	1007	C	C6-N1-C2	-5.94	117.92	120.30
10	b	917	C	N3-C2-O2	-5.94	117.74	121.90
10	b	1453	C	C4-C5-C6	5.94	120.37	117.40
32	z	151	SER	N-CA-C	5.94	127.03	111.00
10	b	490	C	N1-C2-O2	5.94	122.46	118.90
10	b	1296	U	N3-C2-O2	-5.93	118.05	122.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	1155	C	C6-N1-C2	-5.93	117.93	120.30
10	b	2766	C	C6-N1-C2	-5.93	117.93	120.30
10	b	1001	U	N1-C2-O2	5.92	126.94	122.80
10	b	2048	C	C6-N1-C2	-5.92	117.93	120.30
10	b	705	U	P-O3'-C3'	5.91	126.79	119.70
10	b	2630	C	C6-N1-C2	-5.90	117.94	120.30
10	b	917	C	C2-N1-C1'	5.90	125.29	118.80
10	b	1870	C	N1-C2-O2	5.89	122.44	118.90
10	b	1400	C	N1-C2-O2	5.89	122.44	118.90
10	b	1106	C	C5-C6-N1	5.89	123.94	121.00
10	b	1730	C	C6-N1-C2	-5.89	117.94	120.30
10	b	268	C	C6-N1-C2	-5.89	117.94	120.30
10	b	1706	C	P-O3'-C3'	5.89	126.76	119.70
10	b	1912	C	N1-C2-O2	5.88	122.43	118.90
10	b	604	A	C5-N7-C8	-5.88	100.96	103.90
10	b	967	C	N1-C2-O2	5.88	122.42	118.90
10	b	2502	C	N1-C2-O2	5.87	122.42	118.90
10	b	2743	U	N3-C2-O2	-5.87	118.09	122.20
10	b	2516	C	C6-N1-C2	-5.87	117.95	120.30
10	b	1008	C	C5-C6-N1	5.86	123.93	121.00
9	a	66	A	P-O3'-C3'	5.86	126.73	119.70
10	b	681	C	N1-C2-O2	5.86	122.42	118.90
10	b	948	C	C6-N1-C2	-5.84	117.96	120.30
10	b	816	C	N1-C2-O2	5.84	122.40	118.90
10	b	1781	U	C4-C5-C6	5.84	123.20	119.70
10	b	228	C	P-O3'-C3'	5.83	126.70	119.70
10	b	681	C	N3-C2-O2	-5.83	117.82	121.90
10	b	554	U	N3-C2-O2	-5.82	118.12	122.20
10	b	1384	G	C4-C5-N7	5.82	113.13	110.80
10	b	209	C	C5-C6-N1	5.82	123.91	121.00
10	b	346	A	C5-N7-C8	-5.81	101.00	103.90
10	b	1892	G	N7-C8-N9	5.80	116.00	113.10
10	b	413	C	C6-N1-C2	-5.80	117.98	120.30
10	b	1677	C	N3-C2-O2	-5.79	117.84	121.90
10	b	542	C	N3-C2-O2	-5.79	117.85	121.90
10	b	1883	C	C6-N1-C2	-5.79	117.98	120.30
10	b	2010	C	N3-C2-O2	-5.79	117.85	121.90
10	b	1321	C	N3-C2-O2	-5.79	117.85	121.90
10	b	2736	G	C5-N7-C8	-5.78	101.41	104.30
10	b	917	C	C6-N1-C2	-5.77	117.99	120.30
10	b	2408	U	N3-C2-O2	-5.77	118.16	122.20
10	b	1453	C	N3-C2-O2	-5.77	117.86	121.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	1236	U	N1-C2-O2	5.76	126.84	122.80
10	b	1014	U	C5-C4-O4	5.75	129.35	125.90
10	b	1646	C	C2-N1-C1'	5.75	125.13	118.80
10	b	2619	U	C5-C6-N1	5.75	125.58	122.70
10	b	1788	A	O4'-C1'-N9	5.75	112.80	108.20
10	b	2871	G	N7-C8-N9	5.75	115.97	113.10
10	b	2004	C	N1-C2-O2	5.75	122.35	118.90
10	b	960	U	C5-C6-N1	5.74	125.57	122.70
10	b	1829	U	N3-C2-O2	-5.74	118.18	122.20
10	b	2563	C	N3-C2-O2	-5.74	117.88	121.90
10	b	2566	U	N3-C2-O2	-5.74	118.18	122.20
10	b	1269	U	N1-C2-O2	5.74	126.82	122.80
29	v	71	C	N1-C2-O2	5.73	122.34	118.90
29	v	75	A	OP1-P-OP2	-5.73	111.00	119.60
10	b	2507	A	N1-C2-N3	-5.73	126.44	129.30
10	b	1007	C	N3-C2-O2	-5.72	117.89	121.90
10	b	2001	C	N1-C2-O2	5.72	122.33	118.90
10	b	1154	C	C6-N1-C2	-5.71	118.02	120.30
10	b	967	C	N3-C2-O2	-5.71	117.91	121.90
29	v	63	G	C4-N9-C1'	5.70	133.91	126.50
10	b	786	G	C5-N7-C8	-5.69	101.45	104.30
10	b	837	C	N1-C2-O2	5.69	122.32	118.90
10	b	1236	U	N3-C2-O2	-5.69	118.22	122.20
9	a	117	G	C8-N9-C1'	5.68	134.39	127.00
10	b	1996	G	O4'-C1'-N9	-5.68	103.66	108.20
10	b	1236	U	C2-N1-C1'	5.68	124.52	117.70
10	b	2110	U	P-O3'-C3'	5.67	126.51	119.70
10	b	2460	C	N3-C2-O2	-5.67	117.93	121.90
10	b	413	C	C5-C6-N1	5.67	123.84	121.00
10	b	373	U	O5'-P-OP2	-5.67	100.60	105.70
10	b	2328	U	OP2-P-O3'	5.67	117.67	105.20
10	b	1454	G	C4-C5-N7	5.66	113.07	110.80
10	b	1978	C	N3-C2-O2	-5.66	117.94	121.90
10	b	1461	G	C6-N1-C2	5.66	128.50	125.10
10	b	69	C	N3-C2-O2	-5.66	117.94	121.90
10	b	2046	A	N1-C6-N6	5.66	121.99	118.60
10	b	913	A	N7-C8-N9	5.65	116.63	113.80
10	b	1119	C	N1-C2-O2	5.65	122.29	118.90
10	b	1892	G	C4-N9-C1'	5.65	133.84	126.50
10	b	1587	C	C5-C6-N1	5.64	123.82	121.00
10	b	2340	A	C4-C5-N7	5.64	113.52	110.70
10	b	2720	C	N1-C2-O2	5.64	122.28	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2801	U	C2-N1-C1'	5.62	124.45	117.70
10	b	99	U	N1-C2-O2	5.62	126.73	122.80
10	b	921	U	N3-C2-O2	-5.61	118.27	122.20
10	b	953	C	N1-C2-O2	5.60	122.26	118.90
10	b	1514	C	C2-N1-C1'	5.60	124.96	118.80
10	b	164	C	N1-C2-O2	5.60	122.26	118.90
10	b	1577	C	N3-C2-O2	-5.59	117.98	121.90
10	b	1354	U	N3-C2-O2	-5.58	118.29	122.20
10	b	786	G	C4-C5-N7	5.58	113.03	110.80
10	b	205	G	O4'-C1'-N9	5.58	112.66	108.20
10	b	510	C	N3-C2-O2	-5.57	118.00	121.90
10	b	1759	A	O4'-C1'-N9	5.57	112.65	108.20
10	b	1384	G	C5-N7-C8	-5.56	101.52	104.30
9	a	15	A	O4'-C1'-N9	5.56	112.65	108.20
10	b	1587	C	N3-C2-O2	-5.56	118.01	121.90
10	b	1209	C	N3-C2-O2	-5.56	118.01	121.90
32	z	161	GLY	N-CA-C	5.56	126.99	113.10
10	b	2109	U	N1-C2-O2	5.55	126.68	122.80
29	v	73	C	C6-N1-C2	-5.54	118.08	120.30
10	b	1461	G	N3-C4-N9	-5.54	122.68	126.00
10	b	1293	C	C6-N1-C2	-5.53	118.09	120.30
10	b	2577	C	C6-N1-C2	-5.53	118.09	120.30
10	b	2884	C	N1-C2-O2	5.53	122.22	118.90
10	b	1345	G	C4-N9-C1'	5.53	133.69	126.50
10	b	253	C	N3-C2-O2	-5.52	118.04	121.90
10	b	114	U	C2-N1-C1'	5.51	124.31	117.70
10	b	542	C	C6-N1-C2	-5.51	118.10	120.30
10	b	1308	C	N1-C2-O2	5.51	122.20	118.90
10	b	984	C	C6-N1-C2	-5.50	118.10	120.30
10	b	2445	U	N1-C2-O2	5.50	126.65	122.80
10	b	2460	C	N1-C2-O2	5.50	122.20	118.90
10	b	2771	C	N1-C2-O2	5.50	122.20	118.90
10	b	2012	C	C6-N1-C2	-5.50	118.10	120.30
10	b	2047	C	C6-N1-C2	-5.49	118.10	120.30
10	b	2338	U	N1-C2-O2	5.49	126.64	122.80
10	b	1455	A	N7-C8-N9	5.49	116.55	113.80
32	z	162	ILE	N-CA-C	5.49	125.82	111.00
10	b	2642	G	O4'-C1'-N9	5.48	112.59	108.20
10	b	2778	C	C6-N1-C2	-5.48	118.11	120.30
10	b	1499	U	N3-C2-O2	-5.48	118.36	122.20
10	b	1771	U	N1-C2-O2	5.48	126.63	122.80
10	b	66	C	N1-C2-O2	5.46	122.17	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	v	63	G	C8-N9-C1'	-5.46	119.91	127.00
10	b	198	C	C6-N1-C2	-5.45	118.12	120.30
10	b	1354	U	N1-C2-O2	5.45	126.62	122.80
10	b	2185	U	P-O3'-C3'	5.45	126.25	119.70
10	b	1944	U	N3-C2-O2	-5.45	118.38	122.20
32	z	159	ALA	CB-CA-C	5.45	118.28	110.10
10	b	636	C	C6-N1-C2	-5.45	118.12	120.30
10	b	2399	C	C6-N1-C2	-5.45	118.12	120.30
10	b	1935	U	N3-C2-O2	-5.45	118.39	122.20
10	b	2420	C	C5-C6-N1	5.44	123.72	121.00
10	b	1781	U	C2-N3-C4	-5.44	123.74	127.00
10	b	612	C	C5-C6-N1	5.44	123.72	121.00
10	b	1064	G	N3-C4-N9	5.44	129.26	126.00
10	b	674	C	C6-N1-C2	-5.43	118.13	120.30
10	b	1672	C	N1-C2-O2	5.43	122.16	118.90
10	b	1381	U	N1-C2-O2	5.42	126.60	122.80
10	b	1587	C	C2-N1-C1'	5.42	124.77	118.80
10	b	953	C	N3-C2-O2	-5.42	118.11	121.90
10	b	1701	G	C5-N7-C8	-5.42	101.59	104.30
10	b	2338	U	C6-N1-C1'	-5.41	113.62	121.20
10	b	2868	G	P-O3'-C3'	5.41	126.20	119.70
10	b	2871	G	C5-N7-C8	-5.41	101.59	104.30
10	b	1102	C	C5-C6-N1	5.41	123.70	121.00
10	b	2871	G	C8-N9-C1'	-5.41	119.97	127.00
10	b	1308	C	N3-C2-O2	-5.41	118.12	121.90
10	b	268	C	C2-N1-C1'	5.40	124.74	118.80
10	b	486	C	N1-C2-O2	5.40	122.14	118.90
10	b	1566	C	C5-C6-N1	5.40	123.70	121.00
10	b	166	U	C5-C6-N1	5.40	125.40	122.70
10	b	1007	C	C5-C6-N1	5.40	123.70	121.00
10	b	1609	C	N1-C2-O2	5.40	122.14	118.90
10	b	2511	C	N1-C2-O2	5.39	122.14	118.90
10	b	1989	C	N1-C2-O2	5.39	122.14	118.90
10	b	1064	G	C4-N9-C1'	5.38	133.50	126.50
10	b	1202	C	C5-C6-N1	5.38	123.69	121.00
10	b	819	C	C5-C6-N1	5.38	123.69	121.00
10	b	1832	C	C5-C6-N1	5.38	123.69	121.00
10	b	1912	C	N3-C2-O2	-5.38	118.14	121.90
10	b	2290	G	C6-C5-N7	-5.38	127.17	130.40
10	b	2216	A	N7-C8-N9	5.37	116.48	113.80
10	b	2462	G	C4-N9-C1'	5.37	133.48	126.50
10	b	682	C	C6-N1-C2	-5.37	118.15	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2328	U	P-O3'-C3'	5.37	126.14	119.70
10	b	1771	U	N3-C2-O2	-5.36	118.45	122.20
10	b	778	G	C6-C5-N7	-5.36	127.18	130.40
10	b	360	U	N1-C2-O2	5.36	126.55	122.80
10	b	814	C	C5-C6-N1	5.36	123.68	121.00
10	b	1998	C	N1-C2-O2	5.36	122.11	118.90
10	b	1000	C	C6-N1-C2	-5.35	118.16	120.30
10	b	114	U	C5-C6-N1	5.34	125.37	122.70
10	b	1320	U	C5-C6-N1	5.34	125.37	122.70
10	b	27	G	P-O3'-C3'	5.34	126.11	119.70
10	b	1381	U	N3-C2-O2	-5.34	118.47	122.20
10	b	510	C	C6-N1-C2	-5.32	118.17	120.30
10	b	2358	C	C2-N1-C1'	5.32	124.65	118.80
10	b	2003	C	C5-C6-N1	5.32	123.66	121.00
10	b	1602	C	C6-N1-C2	-5.32	118.17	120.30
10	b	2077	C	C6-N1-C2	-5.31	118.18	120.30
10	b	1320	U	N1-C2-O2	5.31	126.52	122.80
10	b	2539	G	P-O3'-C3'	5.30	126.06	119.70
10	b	2682	C	N1-C2-O2	5.30	122.08	118.90
10	b	2736	G	C5-C6-N1	5.29	114.15	111.50
10	b	213	A	C8-N9-C4	5.29	107.92	105.80
10	b	2107	C	C6-N1-C2	-5.29	118.19	120.30
10	b	1892	G	C6-C5-N7	-5.29	127.23	130.40
10	b	2244	U	N1-C2-O2	5.29	126.50	122.80
10	b	2595	C	C6-N1-C2	-5.29	118.19	120.30
10	b	2236	C	C6-N1-C2	-5.28	118.19	120.30
10	b	562	C	C5-C6-N1	5.27	123.64	121.00
10	b	2312	G	C8-N9-C4	-5.27	104.29	106.40
10	b	590	U	C2-N1-C1'	5.27	124.02	117.70
10	b	1528	C	C6-N1-C2	-5.27	118.19	120.30
10	b	1898	C	N3-C2-O2	-5.27	118.21	121.90
10	b	648	U	C6-N1-C2	-5.26	117.84	121.00
10	b	2446	C	C5-C6-N1	5.26	123.63	121.00
10	b	2109	U	N3-C2-O2	-5.26	118.52	122.20
10	b	1810	A	C5-C6-N6	-5.26	119.49	123.70
10	b	202	U	N3-C2-O2	-5.26	118.52	122.20
10	b	2338	U	N3-C2-O2	-5.25	118.52	122.20
10	b	1032	C	C6-N1-C2	-5.25	118.20	120.30
29	v	70	G	C4-N9-C1'	5.25	133.32	126.50
10	b	1119	C	N3-C2-O2	-5.25	118.23	121.90
10	b	1892	G	C5-N7-C8	-5.25	101.68	104.30
10	b	2265	C	N1-C2-O2	5.25	122.05	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	2462	G	C4-C5-N7	5.25	112.90	110.80
10	b	484	C	C5-C6-N1	5.24	123.62	121.00
10	b	1297	C	N1-C2-O2	5.24	122.05	118.90
10	b	174	U	N1-C2-O2	5.24	126.47	122.80
10	b	373	U	N1-C2-O2	5.24	126.47	122.80
30	w	66	ASP	CB-CG-OD2	5.24	123.01	118.30
10	b	2408	U	C2-N1-C1'	5.23	123.98	117.70
10	b	1597	C	P-O3'-C3'	5.23	125.97	119.70
10	b	1396	U	C5-C6-N1	5.22	125.31	122.70
10	b	61	C	N1-C2-O2	5.22	122.03	118.90
10	b	2433	G	OP2-P-O3'	5.22	116.68	105.20
10	b	1291	C	N3-C2-O2	-5.22	118.25	121.90
10	b	1928	C	C6-N1-C2	-5.21	118.21	120.30
10	b	2797	C	N1-C2-O2	5.21	122.03	118.90
10	b	2649	G	N3-C4-C5	5.21	131.21	128.60
10	b	786	G	N7-C8-N9	5.21	115.70	113.10
10	b	1280	C	N1-C2-O2	5.21	122.03	118.90
10	b	1345	G	C8-N9-C1'	-5.21	120.23	127.00
10	b	1166	C	C6-N1-C2	-5.21	118.22	120.30
10	b	1119	C	C5-C6-N1	5.20	123.60	121.00
10	b	1453	C	C6-N1-C1'	-5.20	114.56	120.80
10	b	2047	C	N1-C2-O2	5.20	122.02	118.90
10	b	2727	C	C5-C6-N1	5.20	123.60	121.00
10	b	1540	G	P-O3'-C3'	5.20	125.94	119.70
10	b	750	G	N1-C6-O6	-5.19	116.79	119.90
10	b	754	A	C5-N7-C8	-5.19	101.31	103.90
10	b	1416	C	C5-C6-N1	5.19	123.59	121.00
10	b	2619	U	C2-N1-C1'	5.18	123.92	117.70
10	b	1892	G	C8-N9-C4	-5.18	104.33	106.40
10	b	2224	U	N3-C2-O2	-5.18	118.57	122.20
10	b	2428	C	N1-C2-O2	5.18	122.01	118.90
10	b	2580	G	C4-N9-C1'	5.17	133.22	126.50
10	b	590	U	C5-C6-N1	5.17	125.28	122.70
10	b	645	A	O4'-C1'-N9	5.17	112.33	108.20
10	b	1297	C	N3-C2-O2	-5.17	118.28	121.90
10	b	2620	C	C6-N1-C2	-5.17	118.23	120.30
10	b	1587	C	C6-N1-C2	-5.17	118.23	120.30
10	b	583	C	N3-C2-O2	-5.16	118.28	121.90
10	b	1672	C	N3-C2-O2	-5.16	118.29	121.90
10	b	2254	G	C6-N1-C2	5.16	128.20	125.10
10	b	102	U	C5-C6-N1	5.16	125.28	122.70
10	b	276	U	C5-C6-N1	5.16	125.28	122.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	9	G	P-O3'-C3'	5.15	125.89	119.70
10	b	704	U	N1-C2-O2	5.15	126.41	122.80
10	b	1671	A	C8-N9-C4	-5.15	103.74	105.80
10	b	898	A	C4-N9-C1'	5.15	135.57	126.30
10	b	2801	U	N1-C2-O2	5.15	126.40	122.80
10	b	2254	G	N3-C4-N9	-5.14	122.91	126.00
10	b	2884	C	N3-C2-O2	-5.14	118.30	121.90
10	b	967	C	C6-N1-C2	-5.14	118.24	120.30
10	b	1558	C	N3-C2-O2	-5.14	118.30	121.90
10	b	1078	C	C6-N1-C2	-5.14	118.25	120.30
10	b	814	C	C6-N1-C2	-5.13	118.25	120.30
10	b	2484	C	N3-C2-O2	-5.13	118.31	121.90
10	b	2511	C	N3-C2-O2	-5.13	118.31	121.90
10	b	786	G	C8-N9-C4	-5.13	104.35	106.40
10	b	1929	C	C6-N1-C2	-5.12	118.25	120.30
10	b	2888	U	C5-C4-O4	5.12	128.97	125.90
10	b	2093	C	N3-C2-O2	-5.12	118.32	121.90
10	b	239	C	N3-C2-O2	-5.12	118.32	121.90
10	b	2518	U	C6-N1-C2	-5.12	117.93	121.00
10	b	1896	C	C5-C6-N1	5.12	123.56	121.00
10	b	481	G	C4-N9-C1'	-5.11	119.86	126.50
10	b	69	C	C6-N1-C2	-5.11	118.26	120.30
10	b	459	U	N3-C2-O2	-5.11	118.63	122.20
10	b	2510	U	C6-N1-C2	-5.10	117.94	121.00
10	b	1308	C	C6-N1-C2	-5.09	118.26	120.30
10	b	1455	A	C5-N7-C8	-5.09	101.36	103.90
10	b	378	C	C6-N1-C2	-5.09	118.26	120.30
10	b	2143	U	N1-C2-O2	5.09	126.36	122.80
10	b	1563	C	C5-C6-N1	5.09	123.54	121.00
10	b	2182	C	N1-C2-O2	5.09	121.95	118.90
10	b	1968	G	O4'-C1'-N9	-5.08	104.14	108.20
10	b	1280	C	N3-C2-O2	-5.07	118.35	121.90
10	b	597	C	C6-N1-C2	-5.06	118.27	120.30
10	b	2878	C	N1-C2-O2	5.06	121.94	118.90
10	b	418	C	C6-N1-C2	-5.06	118.28	120.30
10	b	2736	G	N7-C8-N9	5.06	115.63	113.10
10	b	1106	C	N3-C2-O2	-5.05	118.36	121.90
10	b	726	U	C2-N1-C1'	5.05	123.76	117.70
10	b	390	U	N1-C2-O2	5.05	126.33	122.80
10	b	1672	C	C6-N1-C2	-5.05	118.28	120.30
10	b	1998	C	N3-C2-O2	-5.04	118.37	121.90
10	b	2420	C	C6-N1-C2	-5.04	118.28	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b	397	U	C5-C6-N1	5.04	125.22	122.70
10	b	1439	C	N1-C2-O2	5.04	121.93	118.90
10	b	2001	C	N3-C2-O2	-5.04	118.37	121.90
10	b	1242	U	C2-N1-C1'	5.04	123.75	117.70
10	b	604	A	C8-N9-C4	-5.04	103.78	105.80
10	b	2566	U	N1-C2-O2	5.04	126.33	122.80
10	b	391	A	N7-C8-N9	5.04	116.32	113.80
10	b	1074	C	N1-C2-O2	5.04	121.92	118.90
10	b	2421	C	C6-N1-C2	-5.04	118.29	120.30
10	b	323	C	C6-N1-C1'	-5.03	114.76	120.80
10	b	1764	A	P-O3'-C3'	5.03	125.74	119.70
10	b	976	G	O4'-C1'-N9	5.02	112.22	108.20
10	b	1321	C	C5-C6-N1	5.02	123.51	121.00
10	b	223	A	O4'-C1'-N9	5.02	112.22	108.20
10	b	1047	C	N3-C4-C5	5.02	123.91	121.90
10	b	1359	C	N1-C2-O2	5.02	121.91	118.90
10	b	705	U	C2'-C3'-O3'	5.02	121.73	113.70
10	b	1544	U	N1-C2-O2	5.02	126.31	122.80
10	b	225	C	N1-C2-O2	5.02	121.91	118.90
10	b	1613	C	N1-C2-O2	5.02	121.91	118.90
10	b	1381	U	C2-N1-C1'	5.02	123.72	117.70
10	b	939	C	C6-N1-C2	-5.01	118.29	120.30
10	b	1693	C	C6-N1-C2	-5.01	118.30	120.30
10	b	963	C	O5'-P-OP2	-5.01	101.19	105.70
10	b	1839	C	C6-N1-C2	-5.01	118.30	120.30
10	b	343	C	C5-C6-N1	5.01	123.50	121.00
10	b	1718	U	N1-C2-O2	5.01	126.31	122.80
10	b	1439	C	C2-N1-C1'	5.00	124.31	118.80
10	b	2308	G	O4'-C1'-N9	5.00	112.20	108.20

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	0	625	0	652	2	0
2	1	495	0	526	6	0
3	2	439	0	482	1	0
4	3	434	0	445	4	0
5	4	409	0	440	2	0
6	6	377	0	418	2	0
7	7	504	0	572	5	0
8	8	302	0	341	1	0
9	a	2528	0	1283	0	0
10	b	62008	0	31185	0	0
11	c	2082	0	2154	0	0
12	d	1565	0	1616	0	0
13	e	1552	0	1619	0	0
14	f	1410	0	1444	0	0
15	g	1323	0	1371	0	0
16	h	287	0	307	0	0
17	j	1129	0	1162	0	0
18	k	938	0	1012	0	0
19	l	1042	0	1121	0	0
20	m	1074	0	1157	0	0
21	n	960	0	1000	0	0
22	o	892	0	923	0	0
23	p	908	0	956	0	0
24	q	947	0	1019	0	0
25	r	791	0	811	0	0
26	s	845	0	908	0	0
27	t	738	0	807	0	0
28	u	779	0	831	0	0
29	v	1583	0	807	0	0
30	w	753	0	780	0	0
31	y	559	0	575	0	0
32	z	275	0	247	0	0
All	All	90553	0	58971	23	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 6.

All (23) 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)
3:2:12:SER:HB3	3:2:32:ILE:HD11	1.88	0.56
2:1:14:LEU:HD11	2:1:56:LEU:HD23	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:9:LYS:HE3	2:1:13:GLU:HG2	1.90	0.52
6:6:1:MET:SD	6:6:1:MET:N	2.74	0.51
2:1:49:ASP:OD1	2:1:52:ARG:NH2	2.43	0.51
4:3:54:VAL:HG23	4:3:55:ILE:HG12	1.92	0.50
2:1:21:LEU:HB3	2:1:50:VAL:HG12	1.94	0.50
5:4:37:LYS:HG2	5:4:48:ILE:HG13	1.93	0.49
4:3:52:ARG:HH11	4:3:54:VAL:HA	1.80	0.46
7:7:32:ILE:HG22	7:7:32:ILE:O	2.16	0.46
6:6:25:LYS:HB3	6:6:25:LYS:HE3	1.82	0.45
4:3:38:HIS:ND1	4:3:39:LEU:O	2.37	0.45
2:1:14:LEU:HD21	2:1:56:LEU:HG	1.98	0.45
8:8:4:ARG:O	8:8:38:GLY:N	2.49	0.45
7:7:31:HIS:H	7:7:31:HIS:CD2	2.36	0.44
1:0:3:ARG:CD	1:0:30:LEU:HD23	2.48	0.44
4:3:37:LYS:HB2	4:3:37:LYS:HE3	1.84	0.42
7:7:30:ARG:HD2	7:7:30:ARG:HA	1.75	0.42
1:0:72:ARG:HG3	1:0:78:TYR:HE2	1.83	0.42
2:1:60:LYS:HB3	2:1:60:LYS:HE2	1.84	0.42
5:4:9:ILE:HA	5:4:53:LYS:HB2	2.02	0.41
7:7:31:HIS:H	7:7:31:HIS:HD2	1.69	0.41
7:7:8:ARG:HD2	7:7:8:ARG:HA	1.90	0.40

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	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	53 (90%)	6 (10%)	0	100	100
3	2	55/59 (93%)	51 (93%)	4 (7%)	0	100	100
4	3	53/57 (93%)	51 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
6	6	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
7	7	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
11	c	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
12	d	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
13	e	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
14	f	175/179 (98%)	155 (89%)	20 (11%)	0	100	100
15	g	174/177 (98%)	160 (92%)	13 (8%)	1 (1%)	22	41
16	h	37/149 (25%)	33 (89%)	4 (11%)	0	100	100
17	j	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
18	k	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
19	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
20	m	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
21	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
22	o	114/117 (97%)	104 (91%)	10 (9%)	0	100	100
23	p	111/115 (96%)	106 (96%)	5 (4%)	0	100	100
24	q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
25	r	95/103 (92%)	85 (90%)	10 (10%)	0	100	100
26	s	107/110 (97%)	103 (96%)	4 (4%)	0	100	100
27	t	91/100 (91%)	84 (92%)	7 (8%)	0	100	100
28	u	100/104 (96%)	80 (80%)	20 (20%)	0	100	100
30	w	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
31	y	72/85 (85%)	67 (93%)	5 (7%)	0	100	100
32	z	33/61 (54%)	25 (76%)	8 (24%)	0	100	100
All	All	3076/3328 (92%)	2855 (93%)	220 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	g	47	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	67/68 (98%)	66 (98%)	1 (2%)	60	80
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	47/49 (96%)	47 (100%)	0	100	100
4	3	46/48 (96%)	45 (98%)	1 (2%)	47	70
5	4	45/49 (92%)	45 (100%)	0	100	100
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	49 (96%)	2 (4%)	27	51
8	8	34/34 (100%)	34 (100%)	0	100	100
11	c	216/218 (99%)	216 (100%)	0	100	100
12	d	164/164 (100%)	162 (99%)	2 (1%)	67	84
13	e	165/165 (100%)	162 (98%)	3 (2%)	54	75
14	f	148/150 (99%)	146 (99%)	2 (1%)	62	81
15	g	137/138 (99%)	137 (100%)	0	100	100
16	h	30/114 (26%)	29 (97%)	1 (3%)	33	57
17	j	116/116 (100%)	116 (100%)	0	100	100
18	k	103/104 (99%)	102 (99%)	1 (1%)	73	87
19	l	102/103 (99%)	102 (100%)	0	100	100
20	m	109/109 (100%)	108 (99%)	1 (1%)	75	89
21	n	100/103 (97%)	99 (99%)	1 (1%)	73	87
22	o	86/87 (99%)	86 (100%)	0	100	100
23	p	98/100 (98%)	98 (100%)	0	100	100
24	q	89/90 (99%)	89 (100%)	0	100	100
25	r	82/84 (98%)	82 (100%)	0	100	100
26	s	92/93 (99%)	91 (99%)	1 (1%)	70	86
27	t	80/84 (95%)	79 (99%)	1 (1%)	65	83
28	u	83/85 (98%)	83 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	w	78/78 (100%)	78 (100%)	0	100	100
31	y	55/63 (87%)	54 (98%)	1 (2%)	54	75
32	z	31/53 (58%)	29 (94%)	2 (6%)	14	29
All	All	2546/2694 (94%)	2526 (99%)	20 (1%)	77	91

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	28	ARG
4	3	10	ARG
7	7	30	ARG
7	7	31	HIS
12	d	121	THR
12	d	184	ARG
13	e	134	LEU
13	e	137	LYS
13	e	138	LEU
14	f	115	ARG
14	f	169	LEU
16	h	12	LEU
18	k	49	ARG
20	m	75	GLU
21	n	12	ARG
26	s	29	VAL
27	t	69	ARG
31	y	51	VAL
32	z	25	LEU
32	z	157	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
5	4	26	ASN
14	f	27	GLN
14	f	135	GLN
15	g	73	ASN
32	z	24	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	b	2882/2906 (99%)	765 (26%)	0
29	v	74/75 (98%)	37 (50%)	0
9	a	116/120 (96%)	33 (28%)	0
All	All	3072/3101 (99%)	835 (27%)	0

All (835) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	4	C
9	a	5	U
9	a	7	G
9	a	9	G
9	a	13	G
9	a	24	G
9	a	25	U
9	a	26	C
9	a	29	A
9	a	30	C
9	a	35	C
9	a	39	A
9	a	42	C
9	a	43	C
9	a	44	G
9	a	52	A
9	a	53	A
9	a	56	G
9	a	66	A
9	a	67	G
9	a	87	U
9	a	88	C
9	a	89	U
9	a	90	C
9	a	91	C
9	a	93	C
9	a	99	A
9	a	109	A
9	a	112	G
9	a	113	C
9	a	114	C
9	a	117	G
9	a	118	C
10	b	4	U
10	b	10	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	12	U
10	b	15	G
10	b	28	A
10	b	34	U
10	b	35	G
10	b	46	G
10	b	51	G
10	b	62	U
10	b	63	A
10	b	71	A
10	b	74	A
10	b	75	G
10	b	84	A
10	b	91	A
10	b	92	U
10	b	93	G
10	b	100	U
10	b	101	A
10	b	102	U
10	b	103	A
10	b	118	A
10	b	119	A
10	b	120	U
10	b	121	G
10	b	122	G
10	b	125	A
10	b	136	G
10	b	137	U
10	b	142	A
10	b	144	A
10	b	159	G
10	b	160	A
10	b	163	C
10	b	174	U
10	b	175	G
10	b	177	G
10	b	196	A
10	b	199	A
10	b	215	G
10	b	216	A
10	b	221	A
10	b	222	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	223	A
10	b	224	U
10	b	229	C
10	b	230	G
10	b	233	A
10	b	245	G
10	b	248	G
10	b	252	G
10	b	255	A
10	b	264	C
10	b	265	A
10	b	266	G
10	b	271	G
10	b	278	A
10	b	279	A
10	b	280	U
10	b	281	C
10	b	294	A
10	b	298	G
10	b	300	A
10	b	302	C
10	b	317	G
10	b	318	C
10	b	322	A
10	b	329	G
10	b	330	A
10	b	331	C
10	b	332	A
10	b	343	C
10	b	345	A
10	b	346	A
10	b	347	A
10	b	352	A
10	b	353	C
10	b	355	U
10	b	358	U
10	b	359	G
10	b	362	A
10	b	363	G
10	b	366	C
10	b	367	G
10	b	371	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	372	G
10	b	373	U
10	b	386	G
10	b	387	U
10	b	390	U
10	b	391	A
10	b	395	U
10	b	396	G
10	b	405	U
10	b	406	G
10	b	417	C
10	b	418	C
10	b	439	A
10	b	442	G
10	b	446	G
10	b	451	U
10	b	457	A
10	b	464	U
10	b	467	G
10	b	471	A
10	b	472	A
10	b	474	G
10	b	481	G
10	b	487	C
10	b	491	G
10	b	501	A
10	b	503	A
10	b	505	A
10	b	507	A
10	b	508	A
10	b	509	C
10	b	510	C
10	b	513	A
10	b	527	C
10	b	529	A
10	b	531	C
10	b	532	A
10	b	538	A
10	b	558	A
10	b	559	C
10	b	565	A
10	b	570	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	575	U
10	b	577	A
10	b	579	G
10	b	590	U
10	b	604	A
10	b	605	A
10	b	606	G
10	b	608	U
10	b	615	A
10	b	616	A
10	b	617	U
10	b	624	G
10	b	629	A
10	b	636	C
10	b	639	A
10	b	642	C
10	b	644	U
10	b	648	U
10	b	649	G
10	b	655	U
10	b	656	A
10	b	657	A
10	b	661	G
10	b	670	A
10	b	671	G
10	b	672	A
10	b	688	U
10	b	704	U
10	b	706	G
10	b	719	C
10	b	720	A
10	b	725	C
10	b	729	A
10	b	732	A
10	b	740	G
10	b	749	U
10	b	750	G
10	b	754	A
10	b	759	G
10	b	764	U
10	b	766	A
10	b	767	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	777	G
10	b	778	G
10	b	784	A
10	b	786	G
10	b	787	G
10	b	791	A
10	b	793	C
10	b	807	G
10	b	808	C
10	b	811	G
10	b	813	U
10	b	814	C
10	b	821	A
10	b	829	U
10	b	832	G
10	b	848	U
10	b	849	U
10	b	858	G
10	b	860	G
10	b	861	G
10	b	868	A
10	b	871	G
10	b	874	U
10	b	875	C
10	b	878	C
10	b	879	A
10	b	880	A
10	b	882	G
10	b	883	G
10	b	884	G
10	b	885	G
10	b	886	U
10	b	889	U
10	b	890	C
10	b	896	U
10	b	897	U
10	b	898	A
10	b	899	C
10	b	902	A
10	b	909	G
10	b	912	A
10	b	913	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	914	C
10	b	921	U
10	b	933	U
10	b	943	A
10	b	947	A
10	b	948	C
10	b	963	C
10	b	975	A
10	b	976	G
10	b	985	A
10	b	991	G
10	b	992	A
10	b	998	A
10	b	1005	G
10	b	1007	C
10	b	1012	A
10	b	1014	U
10	b	1015	C
10	b	1021	U
10	b	1024	G
10	b	1028	G
10	b	1035	U
10	b	1037	U
10	b	1040	G
10	b	1049	G
10	b	1055	C
10	b	1056	A
10	b	1058	G
10	b	1059	A
10	b	1060	U
10	b	1061	G
10	b	1062	U
10	b	1063	U
10	b	1064	G
10	b	1066	C
10	b	1068	U
10	b	1069	A
10	b	1070	G
10	b	1071	A
10	b	1072	A
10	b	1073	G
10	b	1075	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1076	G
10	b	1077	C
10	b	1078	C
10	b	1079	A
10	b	1080	U
10	b	1081	C
10	b	1082	A
10	b	1083	U
10	b	1086	A
10	b	1087	A
10	b	1088	A
10	b	1089	G
10	b	1090	A
10	b	1091	A
10	b	1092	A
10	b	1097	A
10	b	1099	U
10	b	1100	A
10	b	1101	G
10	b	1102	C
10	b	1103	U
10	b	1104	C
10	b	1106	C
10	b	1107	U
10	b	1108	G
10	b	1111	C
10	b	1113	A
10	b	1114	G
10	b	1119	C
10	b	1121	U
10	b	1132	U
10	b	1134	U
10	b	1135	A
10	b	1136	A
10	b	1137	C
10	b	1138	G
10	b	1144	A
10	b	1170	G
10	b	1171	A
10	b	1172	C
10	b	1173	G
10	b	1174	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1175	U
10	b	1177	A
10	b	1178	U
10	b	1179	G
10	b	1187	G
10	b	1189	G
10	b	1190	U
10	b	1197	G
10	b	1206	A
10	b	1207	A
10	b	1208	G
10	b	1209	C
10	b	1212	G
10	b	1214	G
10	b	1226	U
10	b	1229	G
10	b	1234	G
10	b	1238	G
10	b	1239	A
10	b	1240	G
10	b	1242	U
10	b	1243	A
10	b	1244	U
10	b	1246	A
10	b	1249	A
10	b	1251	U
10	b	1252	G
10	b	1255	A
10	b	1257	U
10	b	1258	G
10	b	1268	G
10	b	1273	G
10	b	1274	A
10	b	1275	U
10	b	1277	A
10	b	1278	A
10	b	1281	G
10	b	1286	A
10	b	1289	A
10	b	1291	C
10	b	1302	G
10	b	1303	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1304	A
10	b	1313	G
10	b	1321	C
10	b	1323	A
10	b	1328	U
10	b	1331	U
10	b	1336	G
10	b	1342	U
10	b	1346	U
10	b	1354	U
10	b	1361	A
10	b	1367	A
10	b	1370	G
10	b	1380	A
10	b	1381	U
10	b	1382	G
10	b	1385	A
10	b	1388	C
10	b	1397	A
10	b	1398	U
10	b	1402	U
10	b	1412	G
10	b	1413	U
10	b	1417	U
10	b	1418	G
10	b	1421	A
10	b	1422	A
10	b	1423	G
10	b	1429	A
10	b	1430	C
10	b	1444	U
10	b	1453	C
10	b	1454	G
10	b	1455	A
10	b	1456	C
10	b	1457	G
10	b	1461	G
10	b	1462	U
10	b	1463	C
10	b	1469	U
10	b	1471	A
10	b	1473	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1477	G
10	b	1478	U
10	b	1479	A
10	b	1480	G
10	b	1484	G
10	b	1495	C
10	b	1497	A
10	b	1498	A
10	b	1499	U
10	b	1500	C
10	b	1505	A
10	b	1507	A
10	b	1510	A
10	b	1511	A
10	b	1525	U
10	b	1526	G
10	b	1531	G
10	b	1534	A
10	b	1535	C
10	b	1538	C
10	b	1539	G
10	b	1540	G
10	b	1541	U
10	b	1542	G
10	b	1544	U
10	b	1545	G
10	b	1549	C
10	b	1554	A
10	b	1556	U
10	b	1558	C
10	b	1561	U
10	b	1567	C
10	b	1568	A
10	b	1570	G
10	b	1571	A
10	b	1580	U
10	b	1583	G
10	b	1585	A
10	b	1586	U
10	b	1587	C
10	b	1598	A
10	b	1601	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1609	C
10	b	1610	A
10	b	1612	A
10	b	1620	A
10	b	1621	G
10	b	1649	U
10	b	1650	U
10	b	1651	G
10	b	1662	G
10	b	1670	A
10	b	1676	G
10	b	1677	C
10	b	1680	A
10	b	1697	G
10	b	1705	G
10	b	1707	A
10	b	1708	C
10	b	1709	G
10	b	1717	G
10	b	1720	G
10	b	1723	G
10	b	1724	A
10	b	1732	C
10	b	1733	G
10	b	1735	G
10	b	1736	G
10	b	1740	G
10	b	1750	C
10	b	1758	G
10	b	1759	A
10	b	1760	U
10	b	1765	G
10	b	1766	C
10	b	1775	A
10	b	1778	G
10	b	1783	U
10	b	1784	U
10	b	1786	A
10	b	1788	A
10	b	1793	A
10	b	1802	C
10	b	1803	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	1810	A
10	b	1813	G
10	b	1818	C
10	b	1831	A
10	b	1835	C
10	b	1844	G
10	b	1851	G
10	b	1859	G
10	b	1864	G
10	b	1870	C
10	b	1886	U
10	b	1888	G
10	b	1899	C
10	b	1910	G
10	b	1911	G
10	b	1912	C
10	b	1914	G
10	b	1917	A
10	b	1918	C
10	b	1922	A
10	b	1924	C
10	b	1931	A
10	b	1933	G
10	b	1934	G
10	b	1935	U
10	b	1941	A
10	b	1942	A
10	b	1944	U
10	b	1959	U
10	b	1971	C
10	b	1974	A
10	b	1975	U
10	b	1976	G
10	b	1978	C
10	b	1979	G
10	b	1985	A
10	b	1986	U
10	b	1995	U
10	b	1996	G
10	b	1997	U
10	b	2001	C
10	b	2024	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2027	C
10	b	2034	A
10	b	2035	A
10	b	2036	G
10	b	2037	A
10	b	2039	G
10	b	2040	C
10	b	2047	C
10	b	2053	G
10	b	2059	C
10	b	2060	G
10	b	2064	A
10	b	2065	G
10	b	2066	A
10	b	2067	C
10	b	2071	G
10	b	2073	G
10	b	2081	A
10	b	2084	A
10	b	2097	G
10	b	2102	U
10	b	2103	U
10	b	2105	A
10	b	2109	U
10	b	2111	G
10	b	2112	A
10	b	2113	U
10	b	2115	U
10	b	2116	G
10	b	2119	G
10	b	2120	G
10	b	2121	A
10	b	2122	U
10	b	2124	G
10	b	2125	G
10	b	2126	U
10	b	2127	G
10	b	2128	G
10	b	2129	G
10	b	2131	G
10	b	2132	G
10	b	2134	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2136	U
10	b	2139	A
10	b	2140	G
10	b	2142	G
10	b	2146	A
10	b	2149	C
10	b	2150	C
10	b	2151	A
10	b	2152	G
10	b	2153	U
10	b	2155	U
10	b	2156	G
10	b	2159	U
10	b	2160	G
10	b	2162	A
10	b	2163	G
10	b	2164	C
10	b	2166	G
10	b	2167	G
10	b	2168	C
10	b	2169	C
10	b	2170	U
10	b	2172	G
10	b	2173	A
10	b	2174	A
10	b	2176	U
10	b	2177	A
10	b	2179	C
10	b	2180	A
10	b	2181	C
10	b	2183	C
10	b	2185	U
10	b	2186	U
10	b	2189	U
10	b	2191	U
10	b	2192	U
10	b	2196	U
10	b	2202	A
10	b	2203	A
10	b	2207	U
10	b	2208	G
10	b	2215	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2216	A
10	b	2217	U
10	b	2218	C
10	b	2229	A
10	b	2233	U
10	b	2242	G
10	b	2243	G
10	b	2247	U
10	b	2272	A
10	b	2275	G
10	b	2283	G
10	b	2284	G
10	b	2287	C
10	b	2291	A
10	b	2292	A
10	b	2300	U
10	b	2309	U
10	b	2310	C
10	b	2312	G
10	b	2313	A
10	b	2315	A
10	b	2316	U
10	b	2326	A
10	b	2329	G
10	b	2334	G
10	b	2335	G
10	b	2337	A
10	b	2338	U
10	b	2339	A
10	b	2340	A
10	b	2349	G
10	b	2351	C
10	b	2352	U
10	b	2354	C
10	b	2358	C
10	b	2361	G
10	b	2365	G
10	b	2379	G
10	b	2380	A
10	b	2381	A
10	b	2383	G
10	b	2384	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2385	A
10	b	2387	G
10	b	2388	U
10	b	2389	C
10	b	2393	G
10	b	2395	G
10	b	2406	U
10	b	2408	U
10	b	2409	G
10	b	2410	A
10	b	2411	A
10	b	2417	G
10	b	2426	C
10	b	2427	U
10	b	2429	A
10	b	2430	A
10	b	2433	G
10	b	2434	A
10	b	2438	A
10	b	2445	U
10	b	2451	G
10	b	2452	A
10	b	2461	U
10	b	2463	A
10	b	2478	U
10	b	2480	A
10	b	2482	A
10	b	2488	G
10	b	2490	C
10	b	2494	G
10	b	2498	G
10	b	2501	A
10	b	2506	G
10	b	2508	U
10	b	2509	G
10	b	2510	U
10	b	2521	C
10	b	2522	A
10	b	2533	G
10	b	2539	G
10	b	2540	G
10	b	2551	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2558	U
10	b	2560	C
10	b	2566	U
10	b	2570	A
10	b	2571	G
10	b	2572	U
10	b	2576	A
10	b	2577	C
10	b	2585	G
10	b	2586	G
10	b	2590	U
10	b	2599	G
10	b	2606	A
10	b	2607	G
10	b	2613	U
10	b	2617	U
10	b	2618	A
10	b	2619	U
10	b	2627	G
10	b	2633	U
10	b	2645	G
10	b	2650	C
10	b	2653	C
10	b	2654	U
10	b	2659	G
10	b	2663	G
10	b	2664	A
10	b	2665	G
10	b	2667	G
10	b	2673	G
10	b	2677	G
10	b	2686	A
10	b	2688	U
10	b	2689	G
10	b	2693	U
10	b	2703	C
10	b	2711	U
10	b	2718	G
10	b	2720	C
10	b	2730	A
10	b	2732	U
10	b	2736	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2737	A
10	b	2740	A
10	b	2742	A
10	b	2748	G
10	b	2752	A
10	b	2755	G
10	b	2756	C
10	b	2757	A
10	b	2762	A
10	b	2765	A
10	b	2766	C
10	b	2769	A
10	b	2781	G
10	b	2782	A
10	b	2783	U
10	b	2786	G
10	b	2795	G
10	b	2797	C
10	b	2800	C
10	b	2801	U
10	b	2802	U
10	b	2803	G
10	b	2804	A
10	b	2812	G
10	b	2813	A
10	b	2815	G
10	b	2822	U
10	b	2824	A
10	b	2825	A
10	b	2837	U
10	b	2839	A
10	b	2852	G
10	b	2854	A
10	b	2865	U
10	b	2869	U
10	b	2870	U
10	b	2871	G
10	b	2877	A
10	b	2881	G
10	b	2883	A
10	b	2884	C
10	b	2887	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	b	2888	U
10	b	2889	G
10	b	2890	A
10	b	2897	A
10	b	2898	G
10	b	2899	G
10	b	2905	C
29	v	3	G
29	v	5	G
29	v	6	C
29	v	7	A
29	v	8	U
29	v	9	C
29	v	15	A
29	v	16	U
29	v	17	G
29	v	18	G
29	v	20	U
29	v	25	C
29	v	26	C
29	v	27	U
29	v	34	U
29	v	35	C
29	v	36	C
29	v	38	A
29	v	42	G
29	v	45	G
29	v	46	A
29	v	47	U
29	v	48	G
29	v	49	C
29	v	50	G
29	v	52	G
29	v	54	U
29	v	60	C
29	v	62	C
29	v	63	G
29	v	64	C
29	v	65	U
29	v	67	C
29	v	68	C
29	v	70	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	v	71	C
29	v	75	A

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

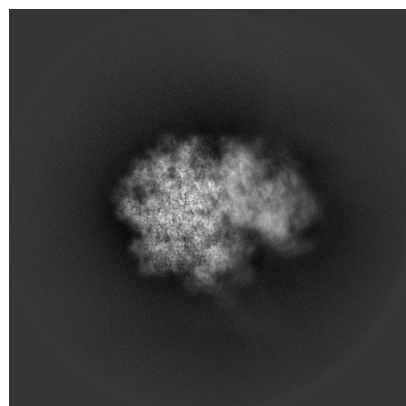
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10891. These allow visual inspection of the internal detail of the map and identification of artifacts.

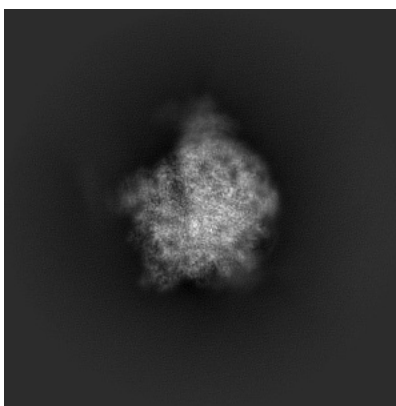
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

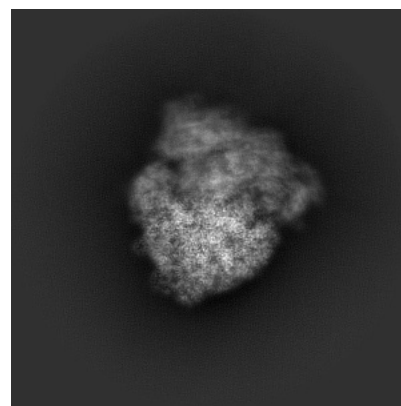
6.1.1 Primary map



X

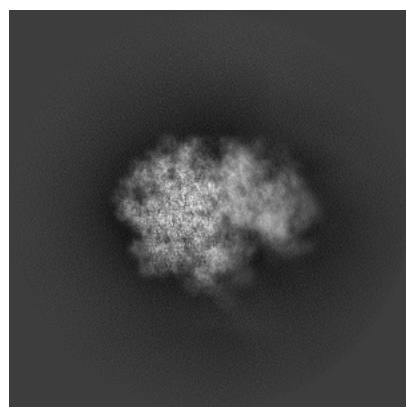


Y

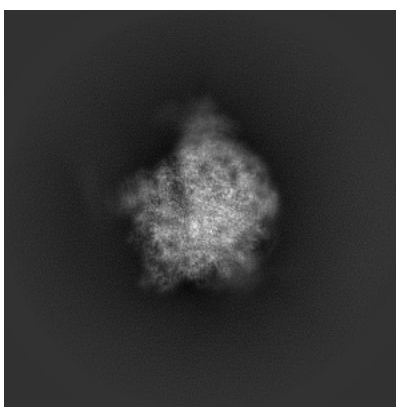


Z

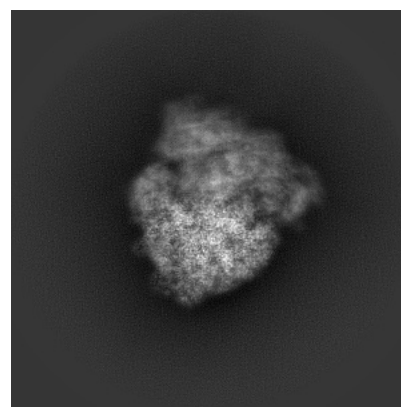
6.1.2 Raw map



X



Y

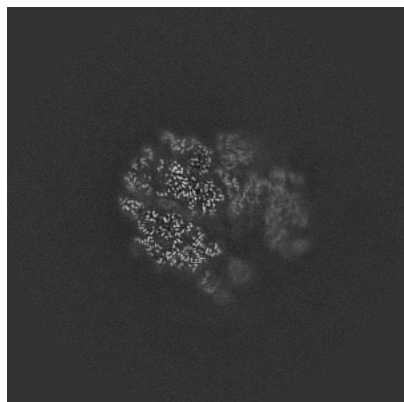


Z

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

6.2 Central slices [i](#)

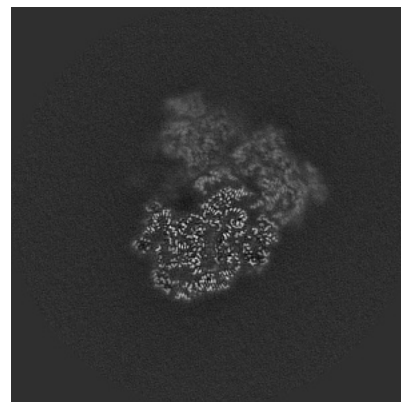
6.2.1 Primary map



X Index: 240

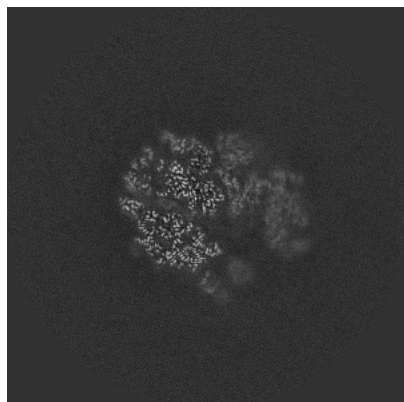


Y Index: 240



Z Index: 240

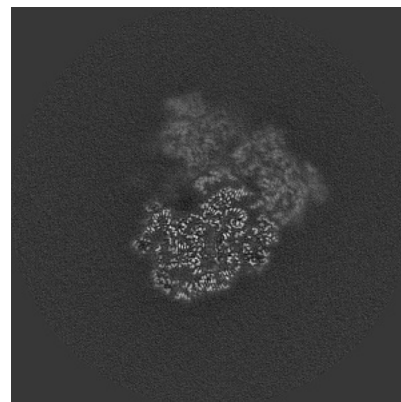
6.2.2 Raw map



X Index: 240



Y Index: 240

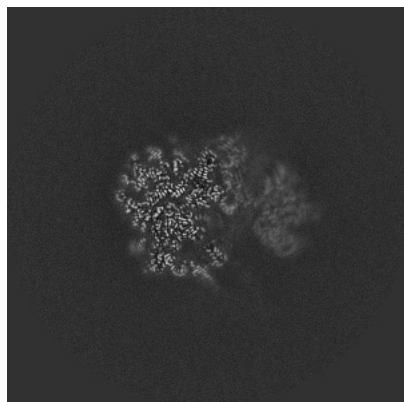


Z Index: 240

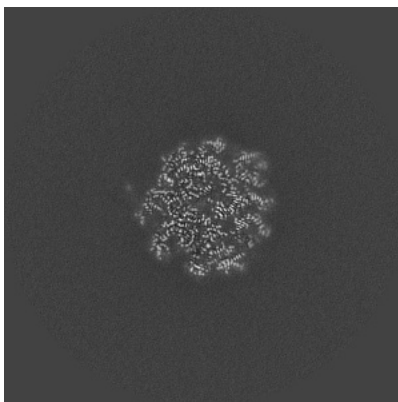
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

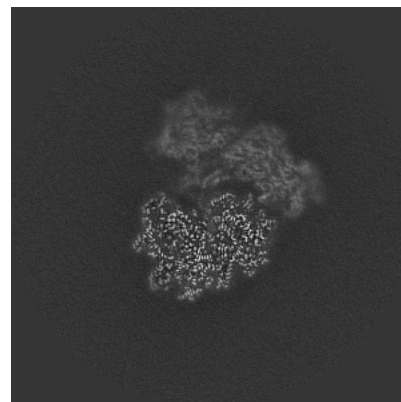
6.3.1 Primary map



X Index: 230

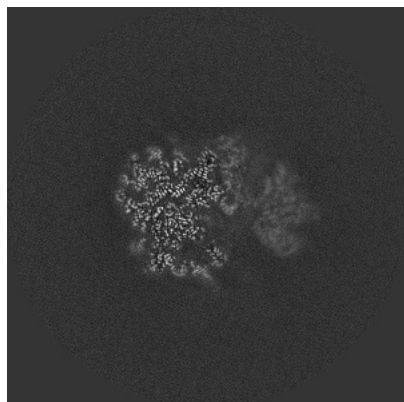


Y Index: 208

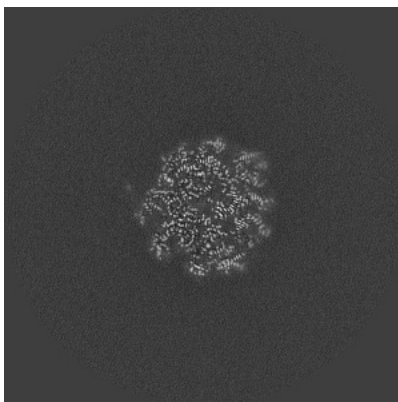


Z Index: 231

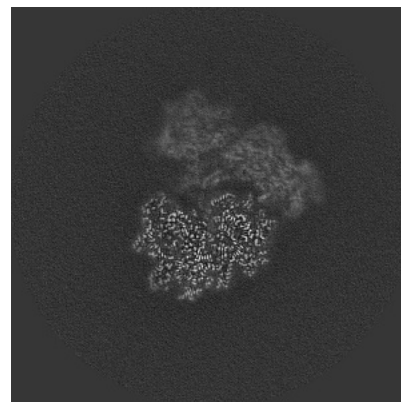
6.3.2 Raw map



X Index: 230



Y Index: 208

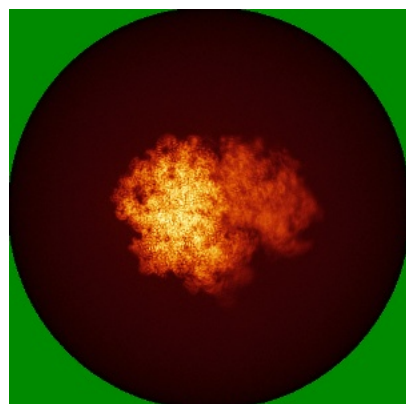


Z Index: 231

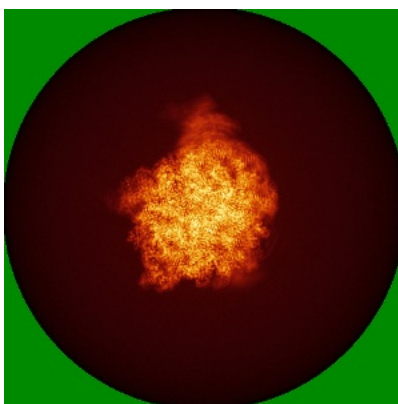
The images above show the largest variance slices of the map in three orthogonal directions.

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

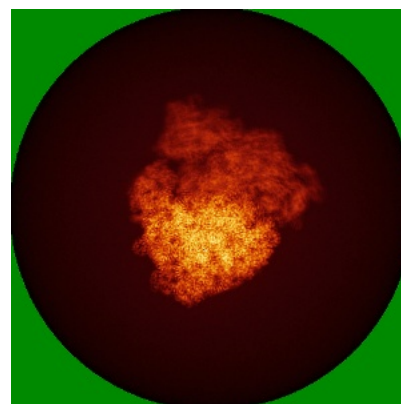
6.4.1 Primary map



X

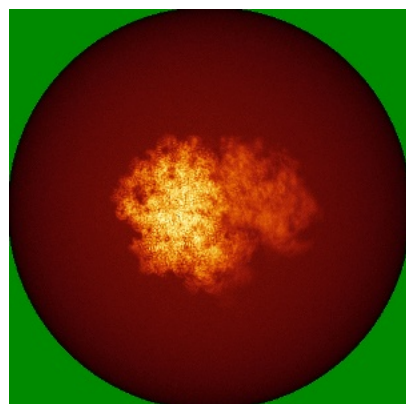


Y

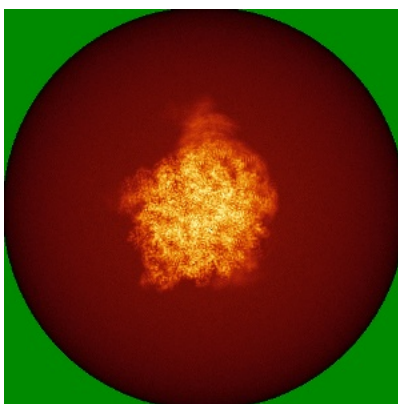


Z

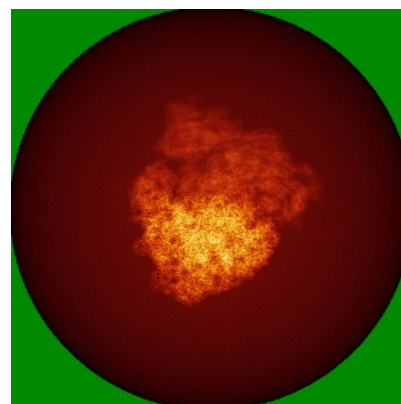
6.4.2 Raw map



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



X



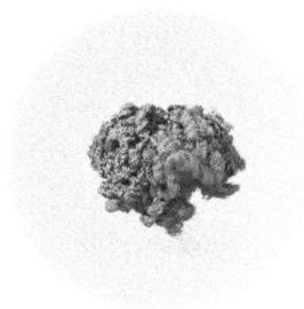
Y



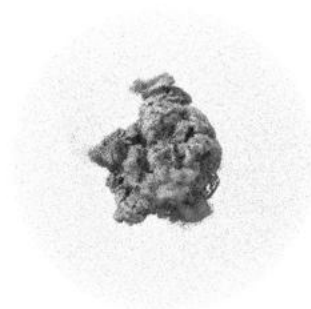
Z

The images above show the 3D surface view of the map at the recommended contour level 0.00741. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

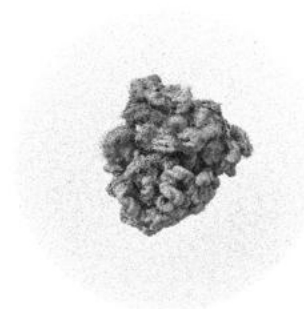
6.5.2 Raw map



X



Y



Z

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

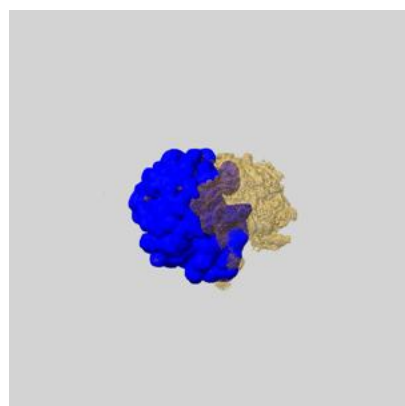
6.6 Mask visualisation [i](#)

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

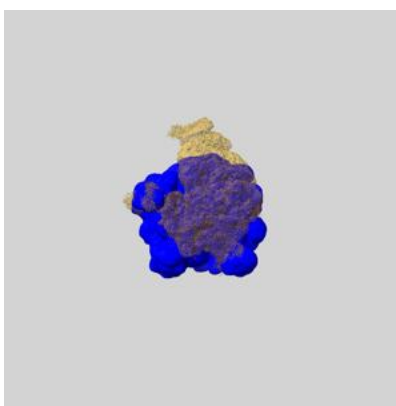
A mask typically either:

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

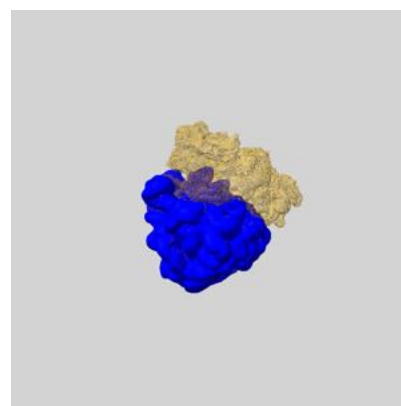
6.6.1 emd_10891_msk_1.map [i](#)



X



Y

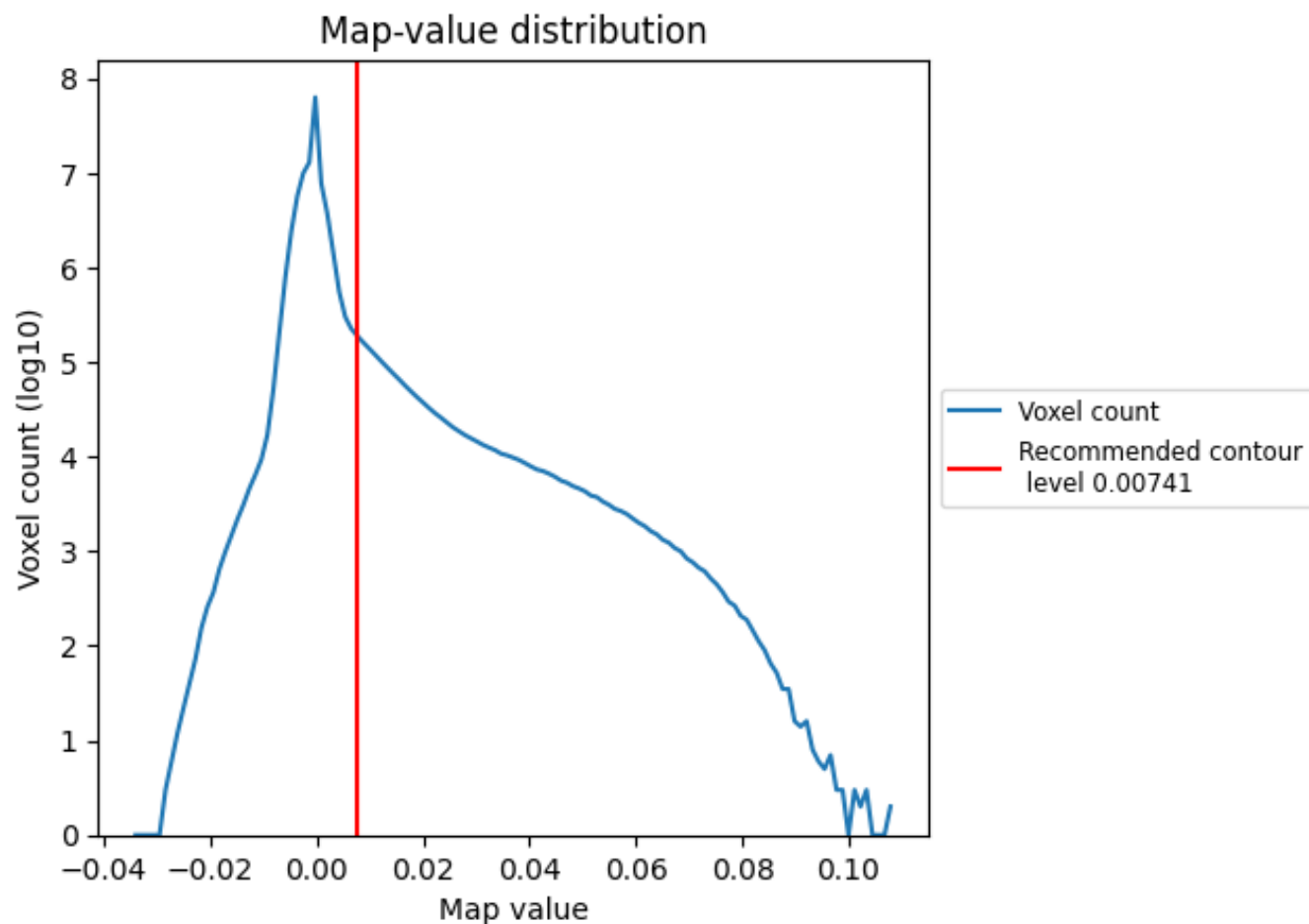


Z

7 Map analysis [i](#)

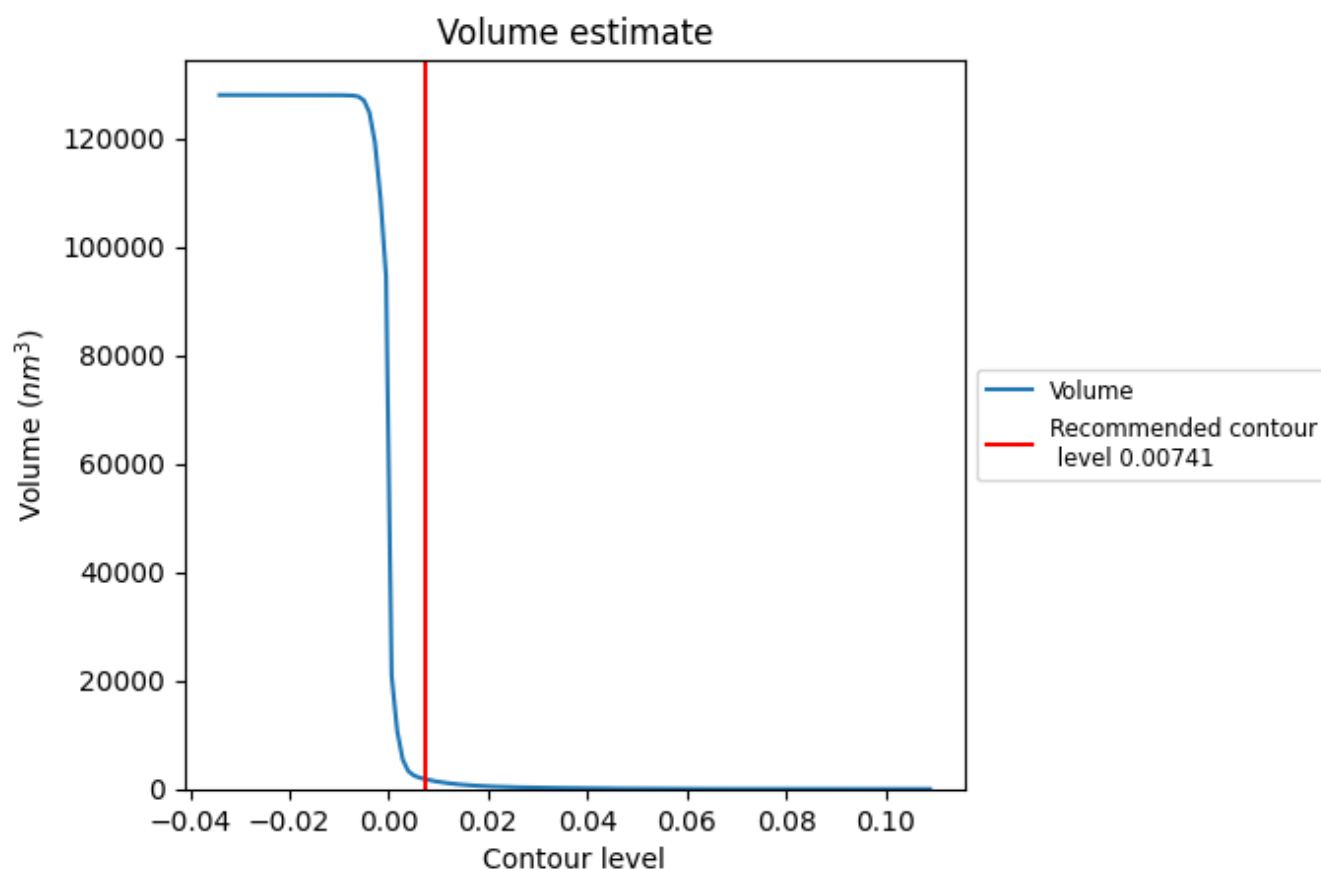
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

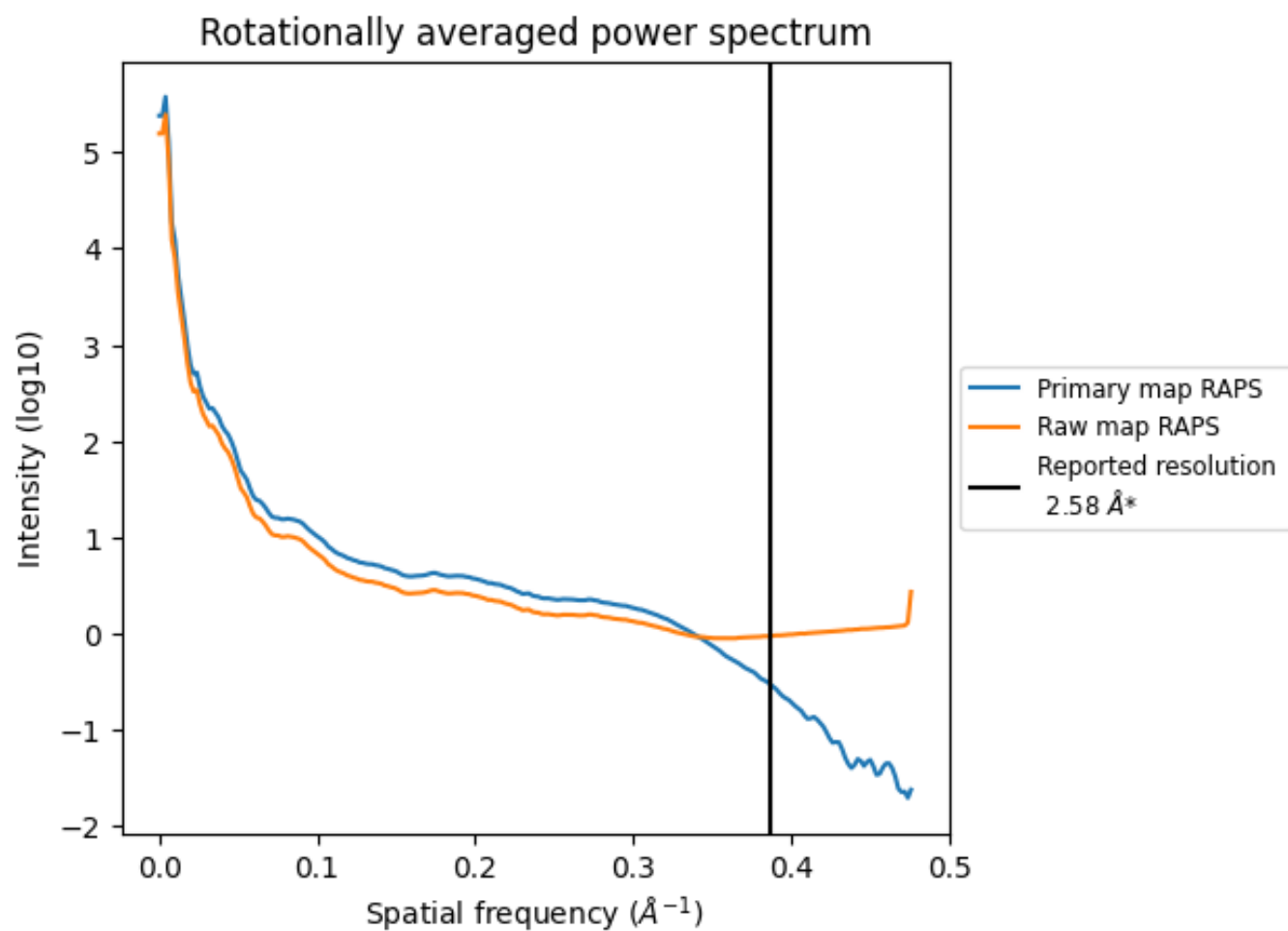
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1796 nm^3 ; this corresponds to an approximate mass of 1623 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 ⓘ

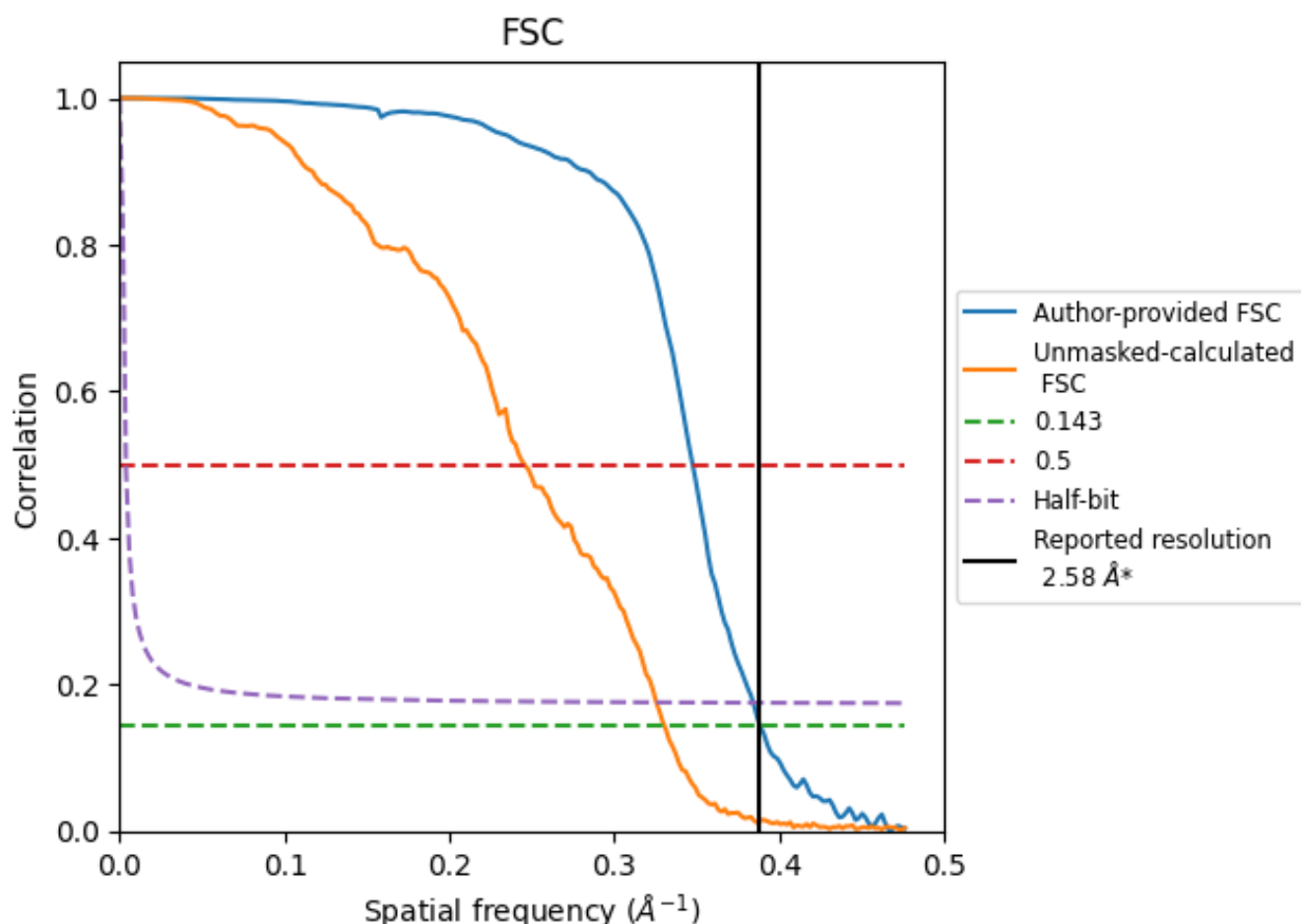


*Reported resolution corresponds to spatial frequency of 0.388 Å⁻¹

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 0.388 Å⁻¹

8.2 Resolution estimates [i](#)

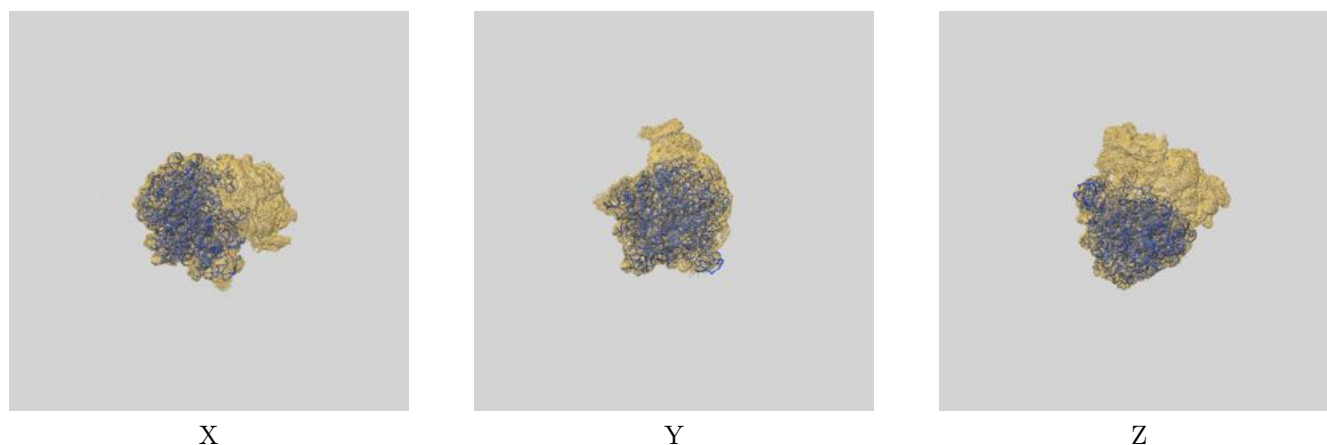
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.58	-	-
Author-provided FSC curve	2.57	2.88	2.60
Unmasked-calculated*	3.03	4.07	3.07

*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 3.03 differs from the reported value 2.58 by more than 10 %

9 Map-model fit [i](#)

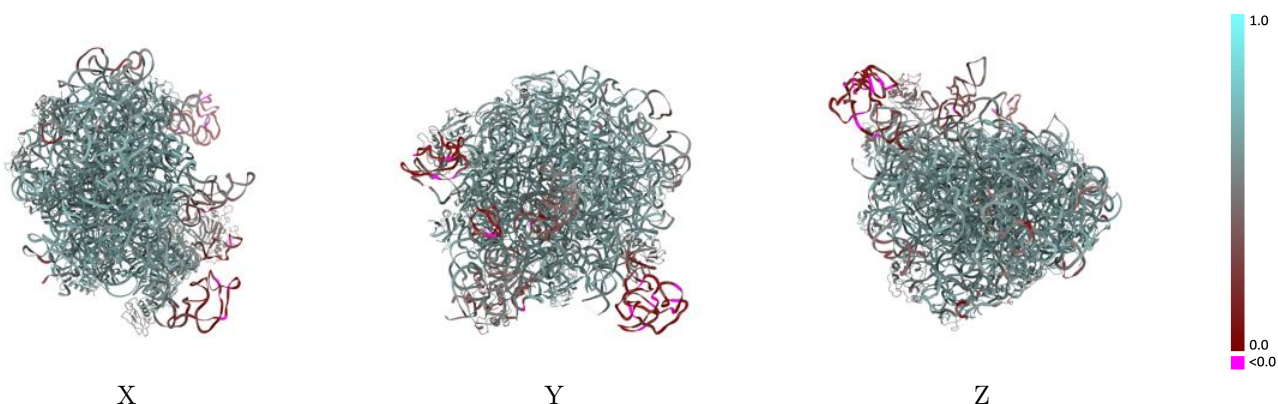
This section contains information regarding the fit between EMDB map EMD-10891 and PDB model 6YS3. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



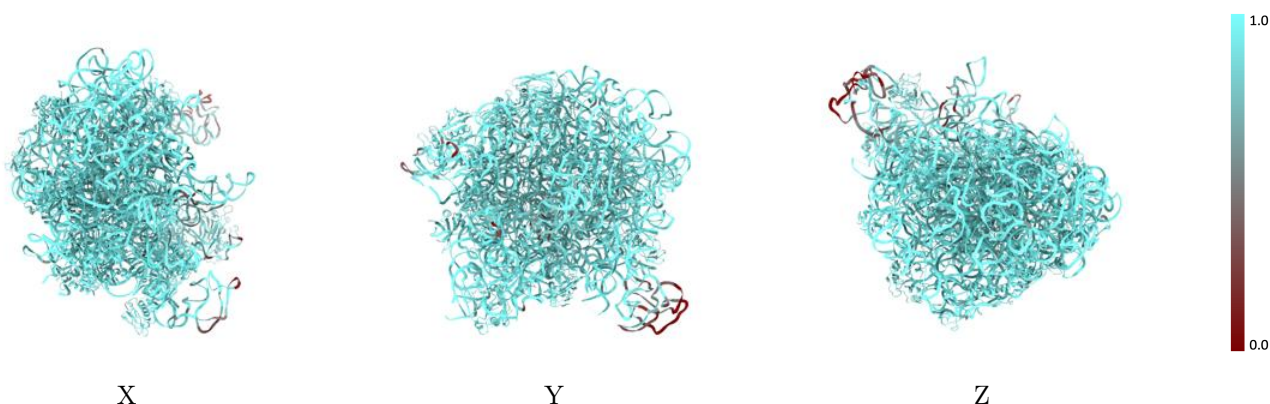
The images above show the 3D surface view of the map at the recommended contour level 0.00741 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



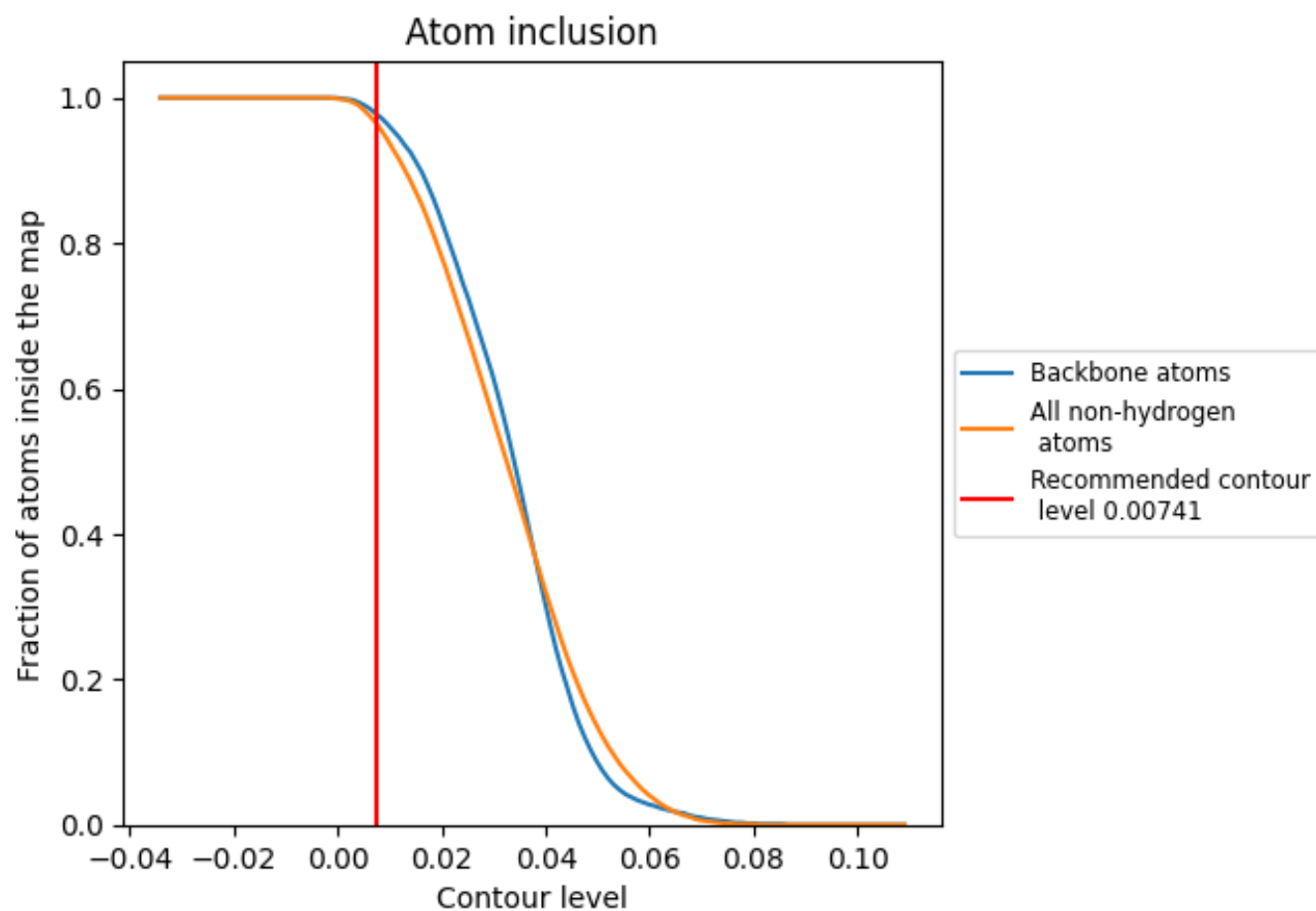
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00741).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.00741) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9650	 0.5680
0	 0.9680	 0.5890
1	 0.9250	 0.5280
2	 0.9630	 0.5880
3	 0.9830	 0.6010
4	 0.9280	 0.5590
6	 0.9800	 0.6240
7	 0.9800	 0.6330
8	 0.9690	 0.5930
a	 0.9870	 0.5370
b	 0.9750	 0.5750
c	 0.9720	 0.6040
d	 0.9630	 0.6020
e	 0.9400	 0.5640
f	 0.8810	 0.3830
g	 0.9220	 0.4980
h	 0.8870	 0.4860
j	 0.9660	 0.6040
k	 0.9560	 0.5900
l	 0.9610	 0.5910
m	 0.9660	 0.6000
n	 0.9860	 0.6090
o	 0.9470	 0.4960
p	 0.9410	 0.5770
q	 0.9770	 0.6140
r	 0.9560	 0.5860
s	 0.9610	 0.6020
t	 0.9430	 0.5570
u	 0.9450	 0.5310
v	 0.7420	 0.3480
w	 0.9420	 0.5670
y	 0.9730	 0.6070
z	 0.7430	 0.3460

