



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 09:46 PM UTC

PDB ID : 9ZTL / pdb_00009ztl
EMDB ID : EMD-74757
Title : Single Particle Cryo EM Analysis of a Ribosome Nascent Globin Complex
Authors : Masse, M.M.; Millan, N.; Morgan, C.; Cavagnero, S.
Deposited on : 2025-12-23
Resolution : 2.91 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

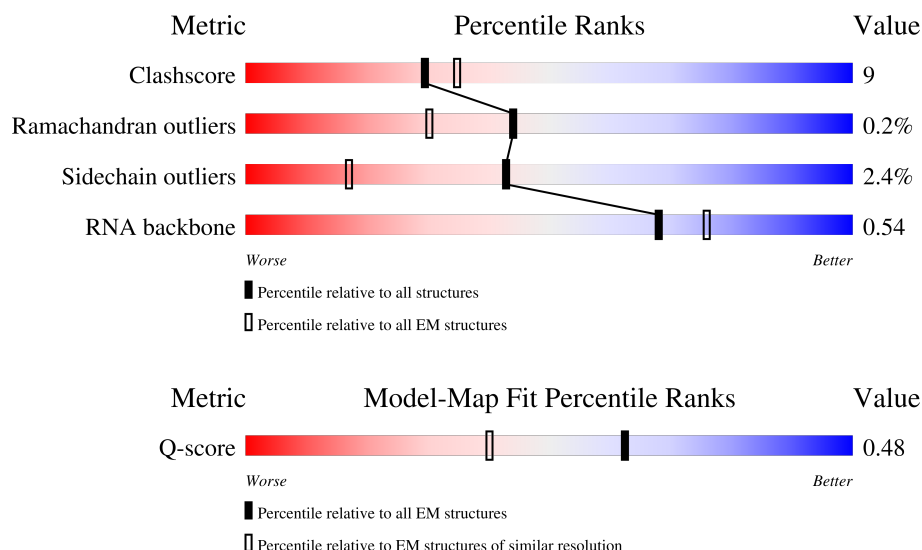
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.91 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	12972 (2.41 - 3.41)

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	55	 65% 27% 7%
2	1	46	 63% 33% .
3	2	65	 77% 20% .

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	5	75	
7	A	1542	
8	B	241	
9	C	233	
10	D	206	
11	E	167	
12	F	135	
13	G	179	
14	H	130	
15	I	130	
16	J	103	
17	K	129	
18	L	124	
19	M	118	
20	N	101	
21	O	89	
22	P	82	
23	Q	84	
24	R	75	
25	S	92	
26	T	87	
27	U	71	
28	X	6	



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Mol	Chain	Length	Quality of chain
29	Y	34	
30	a	2753	
31	b	120	
32	c	273	
33	d	209	
34	e	201	
35	f	179	
36	g	177	
37	h	149	
38	i	142	
39	j	123	
40	k	144	
41	l	136	
42	m	127	
43	n	117	
44	o	115	
45	p	118	
46	q	103	
47	r	110	
48	s	100	
49	t	104	
50	u	94	
51	v	85	
52	w	78	
53	x	63	

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Mol	Chain	Length	Quality of chain
54	y	59	 81% 17% •
55	z	57	 65% 33% •

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 139790 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 L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	75	Total	C	N	O	P	0	0
			1586	710	270	531	75		

- Molecule 7 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 9 is a protein called 30S ribosomal protein S3.

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

- Molecule 10 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	195	Total	C	N	O	S	0	0
			1563	977	300	283	3		

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 14 is a protein called 30S ribosomal protein S8.

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

- Molecule 15 is a protein called 30S ribosomal protein S9.

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

- Molecule 16 is a protein called 30S ribosomal protein S10.

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

- Molecule 17 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 18 is a protein called 30S ribosomal protein S12.

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

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 20 is a protein called 30S ribosomal protein S14.

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

- Molecule 21 is a protein called 30S ribosomal protein S15.

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

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	54	Total	C	N	O		
			446	283	85	78	0	0

- Molecule 25 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 26 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 28 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	6	Total	C	N	O	P	0	0
			131	58	25	42	6		

- Molecule 29 is a protein called apoMyoglobin nascent polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	34	Total	C	N	O		0	0
			170	102	34	34			

- Molecule 30 is a RNA chain called 23s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2753	Total	C	N	O	P	0	0
			59129	26383	10897	19096	2753		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 34 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

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

- Molecule 37 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 38 is a protein called 50S ribosomal protein L13.

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

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 41 is a protein called 50S ribosomal protein L16.

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

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 43 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	116	Total	C	N	O	S	0	0
			892	552	178	162			

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 46 is a protein called 50S ribosomal protein L21.

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

- Molecule 47 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	97	Total	C	N	O	S	0	0
			768	486	143	137	2		

- Molecule 49 is a protein called 50S ribosomal protein L24.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	v	78	Total	C	N	O	S	0
			586	362	116	107	1	0

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

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

- Molecule 54 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 55 is a protein called 50S ribosomal protein L32.

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

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0

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 L33

Chain 0: 



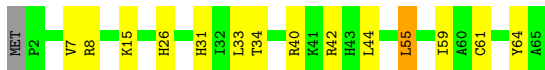
- Molecule 2: 50S ribosomal protein L34

Chain 1: 



- Molecule 3: 50S ribosomal protein L35

Chain 2: 



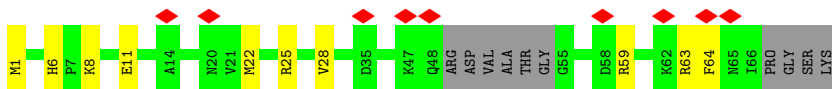
- Molecule 4: 50S ribosomal protein L36

Chain 3: 



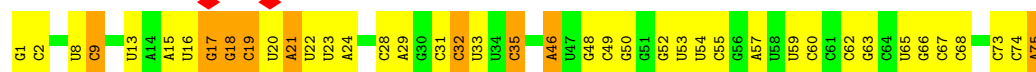
- Molecule 5: 50S ribosomal protein L31

Chain 4: 



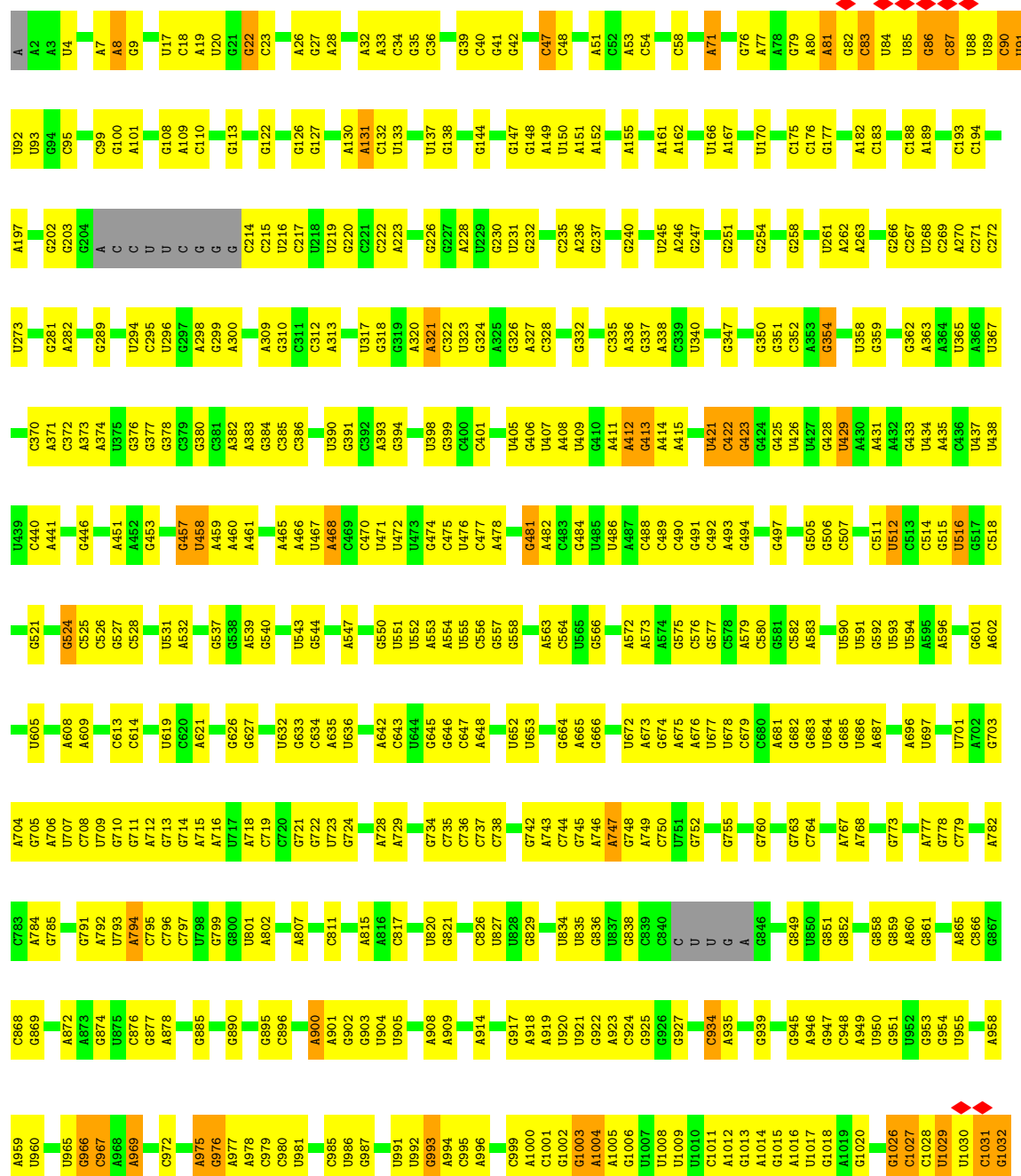
- Molecule 6: P-site tRNA

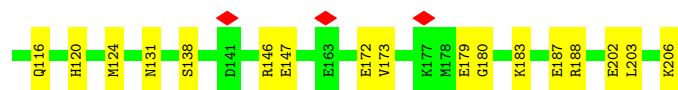
Chain 5: 



• Molecule 7: 16S rRNA

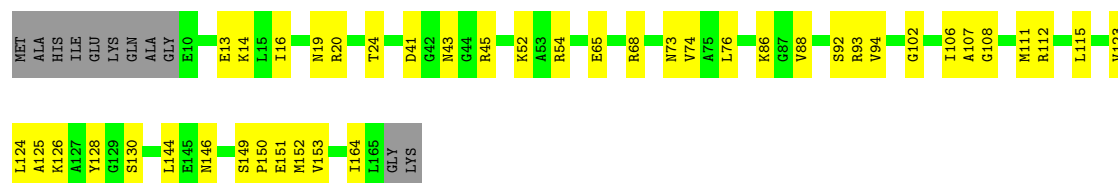
Chain A: 





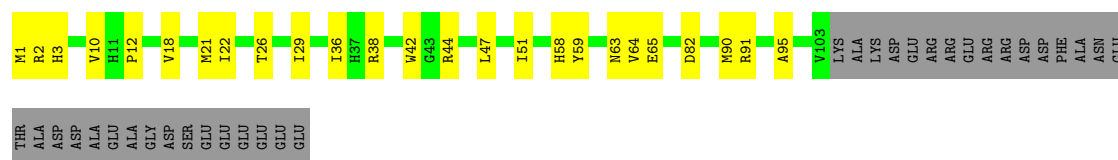
- Molecule 11: 30S ribosomal protein S5

Chain E: 68% 25% 7%



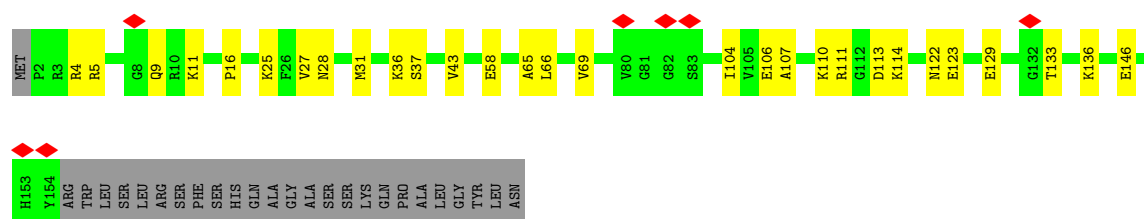
- Molecule 12: 30S ribosomal protein S6

Chain F: 58% 19% 24%



- Molecule 13: 30S ribosomal protein S7

Chain G: 69% 16% 15%



- Molecule 14: 30S ribosomal protein S8

Chain H: 81% 18% ..



- Molecule 15: 30S ribosomal protein S9

Chain I: 71% 27% .

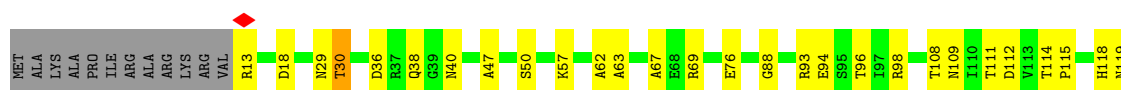




- Molecule 16: 30S ribosomal protein S10



- Molecule 17: 30S ribosomal protein S11



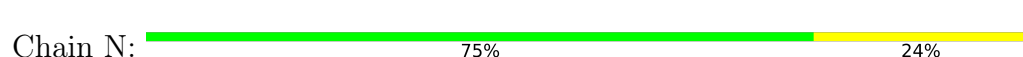
- Molecule 18: 30S ribosomal protein S12



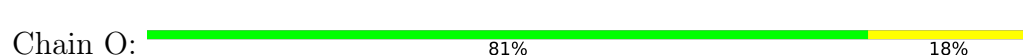
- Molecule 19: 30S ribosomal protein S13



- Molecule 20: 30S ribosomal protein S14

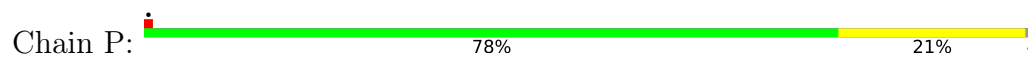


- Molecule 21: 30S ribosomal protein S15

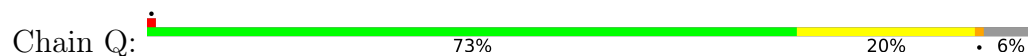




- Molecule 22: 30S ribosomal protein S16



- Molecule 23: 30S ribosomal protein S17



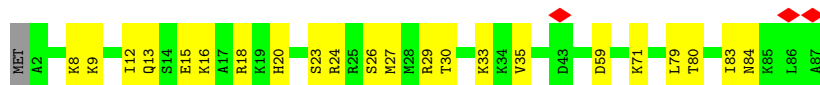
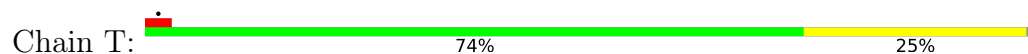
- Molecule 24: 30S ribosomal protein S18



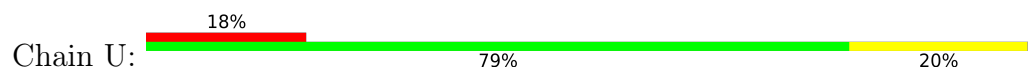
- Molecule 25: 30S ribosomal protein S19



- Molecule 26: 30S ribosomal protein S20



- Molecule 27: 30S ribosomal protein S21



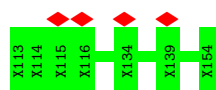
- Molecule 28: mRNA

Chain X:  50% 50%



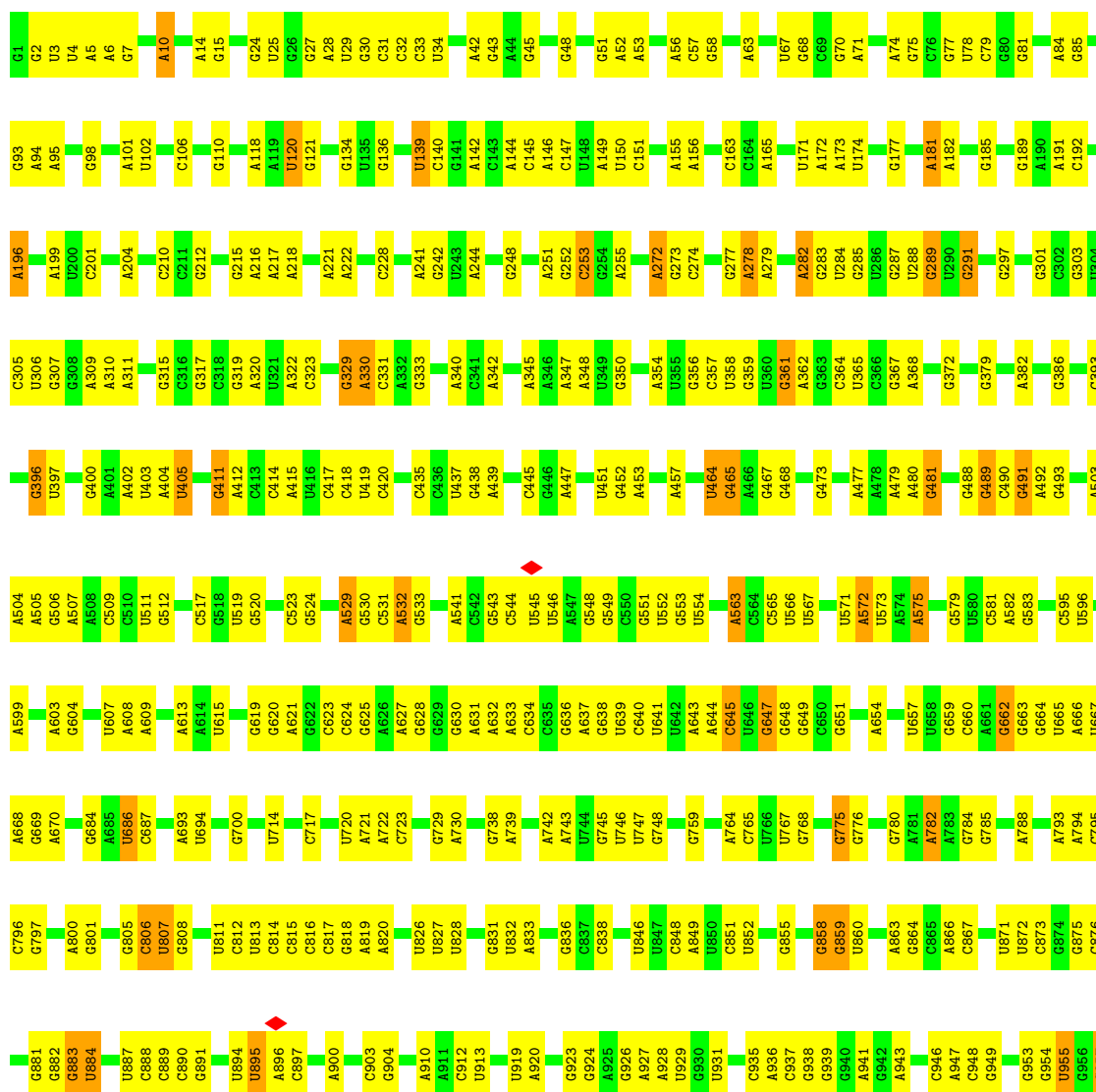
- Molecule 29: apoMyoglobin nascent polypeptide

Chain Y:  12% 100%

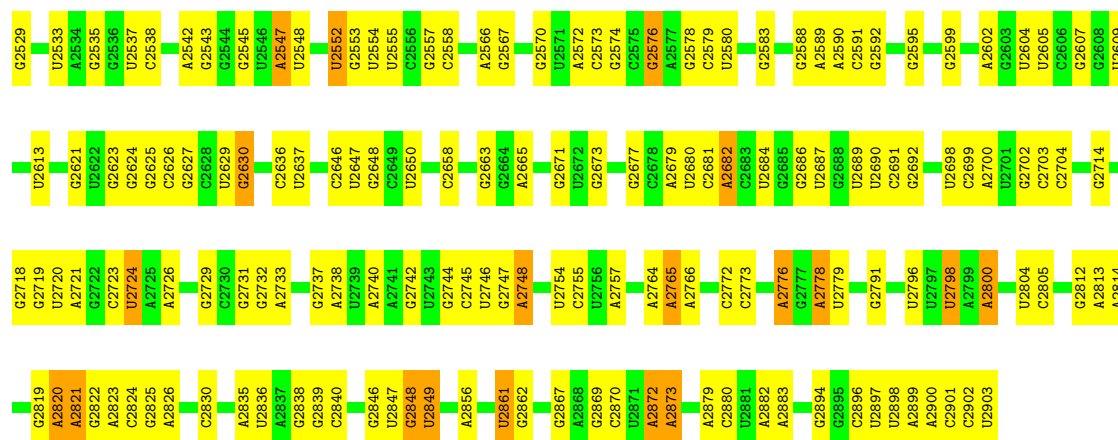


- Molecule 30: 23s rRNA

Chain a:  57% 39% 5%



G2437	G2360	U2249	A2062	G1972	C1881	A1791	G1899	A1608	G1529	A1419	U1316	C1221	G1047	U958
U2438	G2361	G2250	C2063	G1975	A1889	U1796	G1703	A1609	G1530	A1420	G1317	U1222	A1047	A959
A2439	C2362	G2251	C2064	G1976	G1797	U1797	G1704	A1618	G1531	G1421	G1324	U1223	G1110	A960
C2440	G2365	C2258	C2065	G1983	G1896	U1798	G1705	A1619	A1532	G1422	G1325	U1224	A1111	C961
C2441	G2369	C2259	C2066	G1984	G1897	U1799	G1706	G1620	A1533	G1423	U1326	U1225	G1112	C962
C2443	G2370	C2260	U2068	A1987	U1898	C1800	G1707	G1621	G1534	G1424	A1327	U1226	U1113	U963
G2444	C2371	C2261	G2069	G1988	A1899	A1801	G1708	G1623	A1535	G1425	A1328	G1227	C1114	C964
			A2070		G1904	A1802	U1709	U1624	A1536	A1426		G1228		
			A2071	U1991	G1905	A1803	U1710	U1625	G1537	A1427			G1120	G969
			C2072	G1992	G1906	C1804	A1713	U1629	G1538	G1428		U1234	G1124	U970
			C2073	U1993	G1907	A1805	G1715	A1630	U1539	G1429		U1235		G971
					G1908	A1806	U1716	A1632	G1540	G1430		G1239	G1128	A972
			A2082	C1996	G1910	A1808	U1717	A1633	A1545	G1432				G974
			G2093	C1997	U1911	A1809	G1724	G1633	G1546	A1433		A1247	U1132	G977
			G2094	A1998	A1912	A1810	G1725	A1634	G1547	A1434		G1248	A1133	G978
			C2096	G2002	A1913	G1813	U1729	A1637	G1548	G1435			C1135	
			A2097	G2003	C1914	G1814	C1730	A1641	A1549	U1437			G1140	A983
			U2098	C2008	U1915	G1815	G1733	G1642	C1550	U1438				G989
			A2191	A2009	A1916	U1818	G1734	G1643	G1551				U1141	A990
			G2290	G2010	U1917	U1819	A1735	G1644		U1442			A1142	
			G2193	G2011	A1918	A1819	U1736	G1645	A1566	U1443			A1143	
				G2012	U1919		G1737	C1646		G1444			A1144	G993
			G2196	A2013	G1921	G1823	G1738	U1647	A1569				C1145	C995
			U2197	C2013	G1922	G1824		U1648	A1570	G1447		A1262		A996
			A2198	U2016	C1924	U1825	G1739	G1649	A1571	G1448		U1263	C1153	
			A2199	U2017	U1925	G1826	C1741	G1650	A1572	G1449		G1264	G1154	
				G2018	G1929	U1827	U1742	G1651	G1573	G1452		U1265	A1155	
			U2203	G2019	G1930	G1828	A1750	G1652	C1574			G1266	A1156	A1000
			G2204	A2020	A1937	A1829	U1745	A1654	G1575	U1460				A1001
			C2307	C2021	C1938	G1830	U1747	A1655	U1576	G1461		U1267	C1164	C1005
			G2308	U2022	C1939	G1831	G1748	G1656	C1577	G1462		U1268	A1165	C1006
			A2211	C2023	G1935	U1832	A1759	G1657	U1578	G1463		G1270	C1007	
					A1936	G1833	G1760	G1658	A1580	G1464		U1271	A1008	
					C1941	G1834	U1761	G1659	G1465	U1466		U1272	A1009	
			G2029	A2030	A1937	G1835	G1766		C1582			U1273	G1179	U1012
			C2030	A2031	U1939	C1837	A1757	G1663	U1583	G1473			U1180	
			G2032	A2032	U1940	G1838	U1758	A1664	U1584			C1278	U1183	C1013
			A2033	C2033	C1941	G1839	G1767	A1665	G1585			G1279	A1014	
					C1942	G1840	G1768	G1666	C1586	G1482		U1280	U1184	
			U2039	U2040	G1945	U1841	G1769	G1667	A1586	G1483		G1281	G1185	A1021
			G2041	A2042	G1948	C1842	U1765	A1668	G1587	U1484		U1282	G1186	G1022
			C2043	C2044	G1948	C1844	G1766	A1669	G1588	U1485			U1187	U1023
			U2045	C2045	U1955	G1845	G1767	C1670	U1589			G1288	U1188	
			C2046	A2046	G1959	A1847	G1770	U1671	A1590	C1493				G1026
			G2047	C2047	G1959	G1853	A1773	G1674	A1591	G1494		G1296	C1196	A1027
			G2048	G2048	C1962	A1854	U1779	G1675	C1592	G1499		G1297	G1197	A1028
			U2049	G2049	U1963	G1858	U1780	G1684	A1596	U1396		C1298	U1198	A1029
			C2052	A2052	G1964	A1858	U1781	C1686	A1597	U1397		G1299	U1199	
			U2053	C2053	C1965	G1870	G1782	G1691	U1598	G1500			C1200	U1033
			C2055	A2055	A1966	A1870	A1784	C1692	A1509	U1509		A1301	A1204	
			G2056	G2056	G1967	A1871	A1785	C1694	G1510	G1516		C1306	G1036	G1037
					G1968	A1872	G1788	C1695	G1519	G1407		A1307	G1208	G1038
					A1969	G1873	A1789	C1697	U1520			C1307	U1209	A1039
			A2060	G2061	U1971	U1890	C1790	A1698	G1605	G1524		G1310	G1212	A1040
									C1606			U1313	G1041	G1042



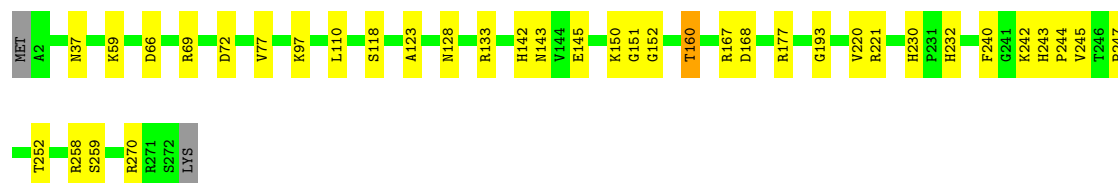
• Molecule 31: 5S rRNA

Chain b: 63% 33% ..



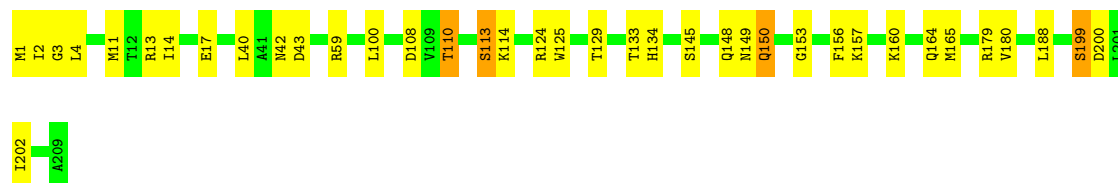
• Molecule 32: 50S ribosomal protein L2

Chain c: 86% 13% .



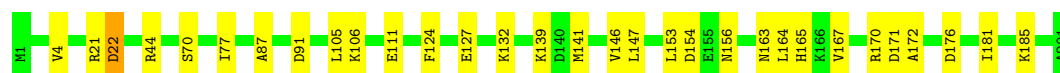
• Molecule 33: 50S ribosomal protein L3

Chain d: 82% 16% .

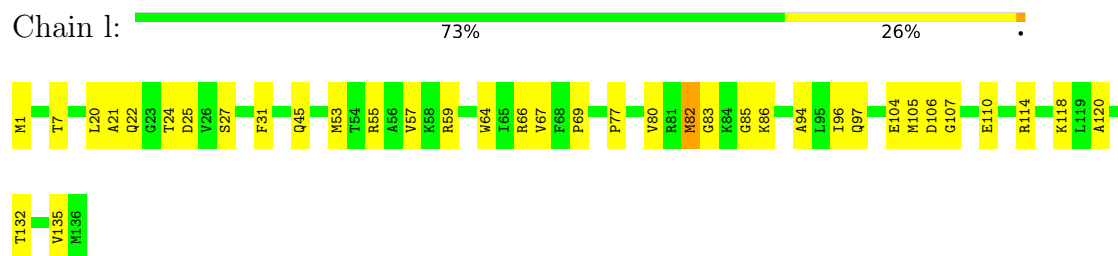


• Molecule 34: Large ribosomal subunit protein uL4

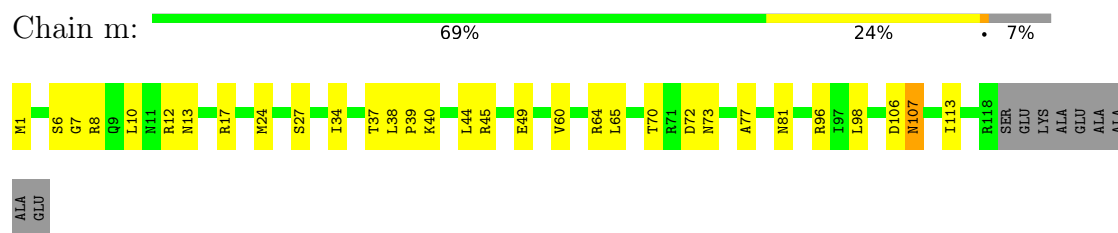
Chain e: 85% 15%



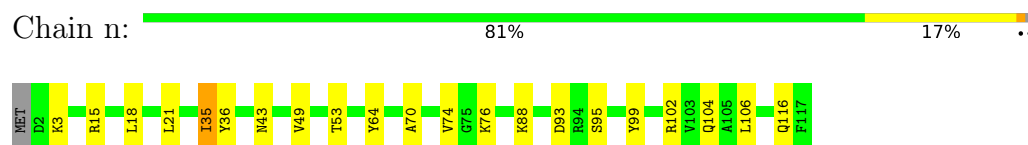
- Molecule 41: 50S ribosomal protein L16



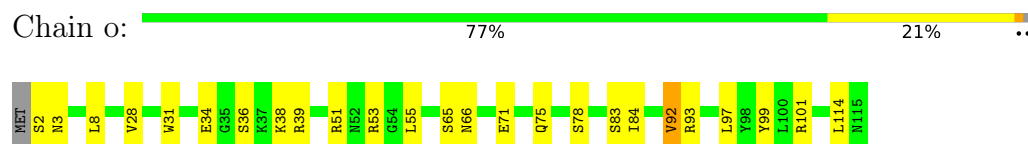
- Molecule 42: 50S ribosomal protein L17



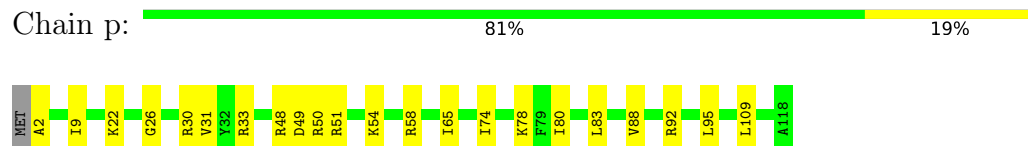
- Molecule 43: 50S ribosomal protein L18



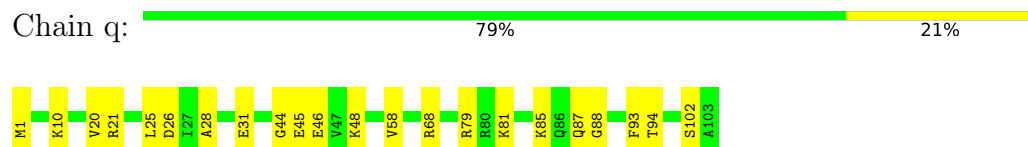
- Molecule 44: 50S ribosomal protein L19




- Molecule 45: 50S ribosomal protein L20



- Molecule 46: 50S ribosomal protein L21




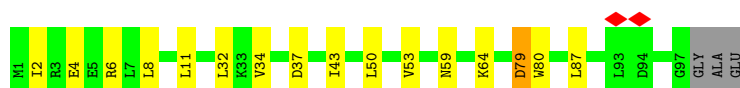
- Molecule 47: Large ribosomal subunit protein uL22

Chain r:  82% 17%



- Molecule 48: 50S ribosomal protein L23

Chain s:  81% 15%




- Molecule 49: 50S ribosomal protein L24

Chain t:  80% 18%



- Molecule 50: 50S ribosomal protein L25

Chain u:  76% 24%



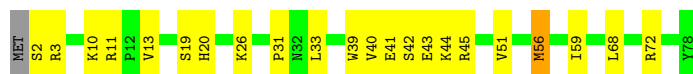
- Molecule 51: 50S ribosomal protein L27

Chain v:  74% 16% 8%




- Molecule 52: 50S ribosomal protein L28

Chain w:  71% 27%

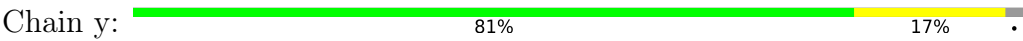


- Molecule 53: 50S ribosomal protein L29

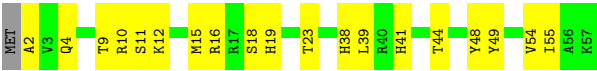
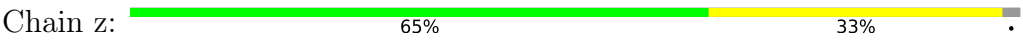
Chain x:  81% 16%



- Molecule 54: Large ribosomal subunit protein uL30



• Molecule 55: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	213770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.310	Depositor
Minimum map value	-1.552	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.087	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	484.864, 484.864, 484.864	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.947, 0.947, 0.947	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, 6MZ, 4OC, UR3, 5MC, H2U, 2MG, 5MU, OMC, OMG, G7M, MA6, OMU, 2MA, PSU, ZN, MEQ

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	0.43	0/424	0.51	0/565
2	1	0.53	0/380	0.71	0/498
3	2	0.51	0/513	0.60	0/676
4	3	0.49	0/303	0.50	0/397
5	4	0.15	0/488	0.38	0/649
6	5	0.22	0/1697	0.31	0/2638
7	A	0.32	0/36236	0.34	2/56520 (0.0%)
8	B	0.24	0/1784	0.43	0/2403
9	C	0.26	0/1651	0.40	0/2225
10	D	0.22	0/1584	0.34	0/2118
11	E	0.34	0/1165	0.47	0/1568
12	F	0.30	0/858	0.48	0/1160
13	G	0.19	0/1219	0.40	0/1635
14	H	0.32	0/989	0.43	0/1326
15	I	0.22	0/1034	0.34	0/1375
16	J	0.24	0/796	0.38	0/1077
17	K	0.35	0/893	0.48	0/1205
18	L	0.29	0/969	0.41	0/1300
19	M	0.21	0/900	0.36	0/1204
20	N	0.27	0/817	0.36	0/1088
21	O	0.27	0/722	0.41	0/964
22	P	0.28	0/653	0.40	0/877
23	Q	0.26	0/650	0.39	0/871
24	R	0.29	0/453	0.42	0/609
25	S	0.20	0/685	0.37	0/922
26	T	0.26	0/676	0.38	0/895
27	U	0.19	0/597	0.26	0/792
28	X	0.32	0/146	0.29	0/226
30	a	0.49	0/65674	0.42	5/102451 (0.0%)
31	b	0.39	0/2850	0.33	0/4444
32	c	0.49	0/2121	0.55	0/2852

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.50	0/1576	0.54	0/2119
34	e	0.47	1/1571 (0.1%)	0.50	0/2113
35	f	0.27	0/1434	0.46	0/1926
36	g	0.34	0/1343	0.46	0/1816
37	h	0.38	0/306	0.56	0/413
38	i	0.50	0/1152	0.47	0/1551
39	j	0.49	0/955	0.50	0/1279
40	k	0.47	0/1062	0.48	0/1413
41	l	0.48	0/1093	0.50	0/1460
42	m	0.51	0/958	0.60	0/1281
43	n	0.36	0/902	0.53	0/1209
44	o	0.49	0/929	0.58	0/1242
45	p	0.56	0/960	0.59	0/1278
46	q	0.45	0/829	0.56	0/1107
47	r	0.46	0/864	0.59	0/1156
48	s	0.46	0/775	0.61	0/1036
49	t	0.43	0/787	0.58	0/1051
50	u	0.44	0/766	0.56	0/1025
51	v	0.48	0/593	0.48	0/785
52	w	0.45	0/635	0.54	0/848
53	x	0.36	0/496	0.49	0/660
54	y	0.48	0/453	0.60	0/605
55	z	0.47	0/450	0.56	0/599
All	All	0.42	1/150816 (0.0%)	0.42	7/225502 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	e	87	ALA	C-N	-6.22	1.22	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1915	U	P-O3'-C3'	-7.88	108.38	120.20
30	a	2251	OMG	P-O3'-C3'	-7.84	108.44	120.20
30	a	1914	C	P-O3'-C3'	-6.71	110.14	120.20
7	A	1207	2MG	P-O3'-C3'	-6.54	110.39	120.20
30	a	1835	2MG	P-O3'-C3'	-6.17	110.94	120.20

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	417	0	451	9	0
2	1	377	0	418	13	0
3	2	504	0	572	11	0
4	3	302	0	340	9	0
5	4	480	0	478	9	0
6	5	1586	0	813	33	0
7	A	32612	0	16432	550	0
8	B	1753	0	1780	38	0
9	C	1624	0	1696	30	0
10	D	1563	0	1618	33	0
11	E	1152	0	1196	28	0
12	F	839	0	833	18	0
13	G	1203	0	1254	28	0
14	H	979	0	1031	18	0
15	I	1022	0	1070	26	0
16	J	786	0	828	23	0
17	K	877	0	887	25	0
18	L	955	0	1016	18	0
19	M	891	0	952	24	0
20	N	805	0	844	22	0
21	O	714	0	734	11	0
22	P	643	0	661	15	0
23	Q	641	0	682	13	0
24	R	446	0	472	16	0
25	S	668	0	693	11	0
26	T	670	0	719	13	0
27	U	589	0	629	11	0
28	X	131	0	66	2	0
29	Y	170	0	47	0	0
30	a	59129	0	29767	796	0
31	b	2549	0	1291	30	0
32	c	2082	0	2154	27	0
33	d	1566	0	1618	28	0
34	e	1552	0	1619	21	0
35	f	1410	0	1444	43	0
36	g	1323	0	1371	20	0
37	h	303	0	327	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	i	1129	0	1162	16	0
39	j	946	0	1023	18	0
40	k	1053	0	1129	22	0
41	l	1074	0	1157	23	0
42	m	945	0	989	20	0
43	n	892	0	923	17	0
44	o	917	0	962	19	0
45	p	947	0	1019	18	0
46	q	816	0	839	15	0
47	r	857	0	922	13	0
48	s	768	0	832	11	0
49	t	779	0	831	13	0
50	u	753	0	780	16	0
51	v	586	0	596	9	0
52	w	625	0	652	14	0
53	x	495	0	526	10	0
54	y	449	0	488	9	0
55	z	444	0	458	13	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
All	All	139790	0	94091	2118	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 9.

The worst 5 of 2118 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)
7:A:409:U:H3	7:A:433:G:H1	1.04	0.98
7:A:1009:U:H3	7:A:1020:G:H1	1.16	0.93
30:a:1047:G:HO2'	30:a:1110:G:H1	0.98	0.92
17:K:98:ARG:HH21	27:U:16:LEU:HD23	1.33	0.92
30:a:1962:5MC:H4'	30:a:1963:U:OP1	1.71	0.87

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	49/55 (89%)	47 (96%)	2 (4%)	0	100	100
2	1	44/46 (96%)	40 (91%)	3 (7%)	1 (2%)	5	18
3	2	62/65 (95%)	51 (82%)	11 (18%)	0	100	100
4	3	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
5	4	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
8	B	222/241 (92%)	210 (95%)	12 (5%)	0	100	100
9	C	204/233 (88%)	200 (98%)	4 (2%)	0	100	100
10	D	191/206 (93%)	189 (99%)	2 (1%)	0	100	100
11	E	154/167 (92%)	152 (99%)	2 (1%)	0	100	100
12	F	101/135 (75%)	100 (99%)	1 (1%)	0	100	100
13	G	151/179 (84%)	144 (95%)	7 (5%)	0	100	100
14	H	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
15	I	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
16	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	37
17	K	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
18	L	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
19	M	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
20	N	98/101 (97%)	98 (100%)	0	0	100	100
21	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
22	P	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
23	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
24	R	52/75 (69%)	50 (96%)	1 (2%)	1 (2%)	6	22
25	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
26	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
27	U	68/71 (96%)	68 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	c	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
33	d	206/209 (99%)	189 (92%)	16 (8%)	1 (0%)	24	53
34	e	199/201 (99%)	183 (92%)	16 (8%)	0	100	100
35	f	175/179 (98%)	164 (94%)	11 (6%)	0	100	100
36	g	174/177 (98%)	162 (93%)	11 (6%)	1 (1%)	21	50
37	h	39/149 (26%)	31 (80%)	8 (20%)	0	100	100
38	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
39	j	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
40	k	142/144 (99%)	132 (93%)	9 (6%)	1 (1%)	18	46
41	l	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
42	m	116/127 (91%)	108 (93%)	7 (6%)	1 (1%)	14	40
43	n	114/117 (97%)	103 (90%)	10 (9%)	1 (1%)	14	40
44	o	112/115 (97%)	98 (88%)	14 (12%)	0	100	100
45	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
46	q	101/103 (98%)	88 (87%)	12 (12%)	1 (1%)	12	37
47	r	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
48	s	95/100 (95%)	86 (90%)	9 (10%)	0	100	100
49	t	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
50	u	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
51	v	76/85 (89%)	74 (97%)	2 (3%)	0	100	100
52	w	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
53	x	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
54	y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
55	z	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
All	All	5465/5913 (92%)	5163 (94%)	293 (5%)	9 (0%)	44	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	45	SER
40	k	29	LYS
16	J	57	VAL
33	d	149	ASN
46	q	45	GLU

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	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	35 (92%)	3 (8%)	11	33
3	2	51/52 (98%)	49 (96%)	2 (4%)	28	61
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	55 (100%)	0	100	100
8	B	186/199 (94%)	184 (99%)	2 (1%)	65	86
9	C	170/190 (90%)	164 (96%)	6 (4%)	32	64
10	D	163/173 (94%)	160 (98%)	3 (2%)	51	79
11	E	119/126 (94%)	116 (98%)	3 (2%)	42	73
12	F	90/116 (78%)	90 (100%)	0	100	100
13	G	126/147 (86%)	126 (100%)	0	100	100
14	H	104/105 (99%)	103 (99%)	1 (1%)	68	87
15	I	105/107 (98%)	105 (100%)	0	100	100
16	J	86/90 (96%)	84 (98%)	2 (2%)	44	74
17	K	90/99 (91%)	88 (98%)	2 (2%)	45	75
18	L	103/104 (99%)	97 (94%)	6 (6%)	18	47
19	M	93/96 (97%)	92 (99%)	1 (1%)	65	86
20	N	83/84 (99%)	83 (100%)	0	100	100
21	O	76/77 (99%)	75 (99%)	1 (1%)	61	84
22	P	65/65 (100%)	65 (100%)	0	100	100
23	Q	73/78 (94%)	71 (97%)	2 (3%)	39	71
24	R	47/65 (72%)	47 (100%)	0	100	100
25	S	72/79 (91%)	70 (97%)	2 (3%)	38	70
26	T	65/66 (98%)	63 (97%)	2 (3%)	35	67
27	U	60/61 (98%)	59 (98%)	1 (2%)	53	80
32	c	216/218 (99%)	211 (98%)	5 (2%)	44	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	d	163/163 (100%)	157 (96%)	6 (4%)	30	63
34	e	165/165 (100%)	161 (98%)	4 (2%)	43	73
35	f	148/150 (99%)	144 (97%)	4 (3%)	39	71
36	g	137/138 (99%)	135 (98%)	2 (2%)	57	82
37	h	32/114 (28%)	30 (94%)	2 (6%)	16	43
38	i	116/116 (100%)	116 (100%)	0	100	100
39	j	104/104 (100%)	100 (96%)	4 (4%)	29	62
40	k	103/103 (100%)	100 (97%)	3 (3%)	37	69
41	l	109/109 (100%)	103 (94%)	6 (6%)	19	49
42	m	98/103 (95%)	96 (98%)	2 (2%)	48	77
43	n	86/87 (99%)	83 (96%)	3 (4%)	32	64
44	o	99/100 (99%)	96 (97%)	3 (3%)	36	68
45	p	89/90 (99%)	88 (99%)	1 (1%)	65	86
46	q	84/84 (100%)	83 (99%)	1 (1%)	63	85
47	r	93/93 (100%)	89 (96%)	4 (4%)	26	58
48	s	83/84 (99%)	81 (98%)	2 (2%)	43	73
49	t	83/85 (98%)	80 (96%)	3 (4%)	31	63
50	u	78/78 (100%)	75 (96%)	3 (4%)	29	62
51	v	58/63 (92%)	55 (95%)	3 (5%)	21	50
52	w	67/68 (98%)	61 (91%)	6 (9%)	9	27
53	x	54/55 (98%)	54 (100%)	0	100	100
54	y	48/49 (98%)	46 (96%)	2 (4%)	26	59
55	z	47/48 (98%)	44 (94%)	3 (6%)	16	43
All	All	4560/4829 (94%)	4449 (98%)	111 (2%)	43	73

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	f	165	GLU
55	z	39	LEU
41	l	27	SER
55	z	23	THR
51	v	71	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
49	t	53	ASN
49	t	99	ASN
54	y	34	HIS
32	c	232	HIS
26	T	78	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	X	5/6 (83%)	0	0
30	a	2749/2753 (99%)	347 (12%)	0
31	b	118/120 (98%)	10 (8%)	0
6	5	74/75 (98%)	14 (18%)	1 (1%)
7	A	1516/1542 (98%)	177 (11%)	3 (0%)
All	All	4462/4496 (99%)	548 (12%)	4 (0%)

5 of 548 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	5	9	C
6	5	13	U
6	5	16	U
6	5	17	G
6	5	18	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	5	17	G
7	A	90	C
7	A	1026	G
7	A	1035	A

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

38 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
7	MA6	A	1519	7	23,26,27	1.53	5 (21%)	33,38,41	2.55	15 (45%)
30	5MU	a	1939	30	19,22,23	0.33	0	27,32,35	0.34	0
30	6MZ	a	2030	30	22,25,26	3.88	10 (45%)	29,36,39	2.76	14 (48%)
30	PSU	a	2504	30	18,21,22	1.11	3 (16%)	21,30,33	1.96	4 (19%)
30	PSU	a	746	30	18,21,22	1.05	3 (16%)	21,30,33	1.81	5 (23%)
30	OMG	a	2251	30,6	23,26,27	0.38	0	32,38,41	0.83	2 (6%)
30	OMU	a	2552	30	19,22,23	3.00	8 (42%)	25,31,34	1.91	5 (20%)
6	PSU	5	54	6	18,21,22	1.09	2 (11%)	21,30,33	1.93	5 (23%)
33	MEQ	d	150	33	8,9,10	0.96	0	5,10,12	1.05	1 (20%)
7	2MG	A	1207	7	23,26,27	0.35	0	33,38,41	0.42	0
7	UR3	A	1498	7	19,22,23	2.60	5 (26%)	26,32,35	1.64	4 (15%)
30	5MC	a	1962	30	19,22,23	0.94	1 (5%)	26,32,35	0.67	0
30	PSU	a	1911	30	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)
30	PSU	a	2457	30	18,21,22	1.02	3 (16%)	21,30,33	1.83	4 (19%)
30	OMC	a	2498	30	19,22,23	0.39	0	25,31,34	0.75	0
7	2MG	A	1516	7	23,26,27	0.34	0	33,38,41	0.46	0
30	5MU	a	747	30	19,22,23	0.28	0	27,32,35	0.49	0
30	2MG	a	1835	30	23,26,27	0.35	0	33,38,41	0.59	0
30	H2U	a	2449	30	18,21,22	0.73	1 (5%)	19,30,33	0.85	1 (5%)
30	PSU	a	2580	30	18,21,22	1.13	3 (16%)	21,30,33	2.11	5 (23%)
6	4OC	5	32	6	20,23,24	3.40	8 (40%)	25,32,35	0.97	1 (4%)
30	2MG	a	2445	30	23,26,27	0.34	0	33,38,41	0.64	1 (3%)
30	G7M	a	2069	30	23,26,27	2.98	9 (39%)	34,39,42	2.20	10 (29%)
30	1MG	a	745	30	23,26,27	2.86	8 (34%)	33,39,42	1.74	6 (18%)
7	2MG	A	966	7	23,26,27	0.35	0	33,38,41	0.48	0
30	PSU	a	2604	30	18,21,22	1.08	3 (16%)	21,30,33	2.03	5 (23%)
7	4OC	A	1402	7	20,23,24	3.33	8 (40%)	25,32,35	0.86	1 (4%)
7	5MC	A	1407	7	19,22,23	0.93	1 (5%)	26,32,35	0.59	0
7	5MC	A	967	7	19,22,23	0.86	1 (5%)	26,32,35	0.53	0
30	PSU	a	2605	30	18,21,22	1.10	2 (11%)	21,30,33	2.14	5 (23%)
6	5MU	5	53	6	19,22,23	0.24	0	27,32,35	0.39	0
7	PSU	A	516	7	18,21,22	1.06	3 (16%)	21,30,33	1.86	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	2MA	a	2503	30	22,25,26	0.83	1 (4%)	32,37,40	1.19	3 (9%)
30	PSU	a	955	30	18,21,22	1.07	3 (16%)	21,30,33	1.87	4 (19%)
7	MA6	A	1518	7	23,26,27	1.52	4 (17%)	33,38,41	2.65	14 (42%)
30	6MZ	a	1618	30	22,25,26	2.40	6 (27%)	29,36,39	2.58	12 (41%)
7	G7M	A	527	7	23,26,27	2.91	9 (39%)	34,39,42	2.26	10 (29%)
30	PSU	a	1917	30	18,21,22	1.04	2 (11%)	21,30,33	1.89	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
7	MA6	A	1519	7	-	6/11/29/30	0/3/3/3
30	5MU	a	1939	30	-	1/7/25/26	0/2/2/2
30	6MZ	a	2030	30	-	3/9/27/28	0/3/3/3
30	PSU	a	2504	30	-	0/7/25/26	0/2/2/2
30	PSU	a	746	30	-	0/7/25/26	0/2/2/2
30	OMG	a	2251	30,6	-	2/9/27/28	0/3/3/3
30	OMU	a	2552	30	-	1/9/27/28	0/2/2/2
6	PSU	5	54	6	-	2/7/25/26	0/2/2/2
33	MEQ	d	150	33	-	4/8/9/11	-
7	2MG	A	1207	7	-	0/9/27/28	0/3/3/3
7	UR3	A	1498	7	-	0/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	4/7/25/26	0/2/2/2
30	PSU	a	1911	30	-	4/7/25/26	0/2/2/2
30	PSU	a	2457	30	-	2/7/25/26	0/2/2/2
30	OMC	a	2498	30	-	5/9/27/28	0/2/2/2
7	2MG	A	1516	7	-	0/9/27/28	0/3/3/3
30	5MU	a	747	30	-	0/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	1/9/27/28	0/3/3/3
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	PSU	a	2580	30	-	0/7/25/26	0/2/2/2
6	4OC	5	32	6	-	0/9/29/30	0/2/2/2
30	2MG	a	2445	30	-	2/9/27/28	0/3/3/3
30	G7M	a	2069	30	-	1/7/25/26	0/3/3/3
30	1MG	a	745	30	-	0/7/25/26	0/3/3/3
7	2MG	A	966	7	-	0/9/27/28	0/3/3/3
30	PSU	a	2604	30	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	4OC	A	1402	7	-	2/9/29/30	0/2/2/2
7	5MC	A	1407	7	-	0/7/25/26	0/2/2/2
7	5MC	A	967	7	-	2/7/25/26	0/2/2/2
30	PSU	a	2605	30	-	1/7/25/26	0/2/2/2
6	5MU	5	53	6	-	0/7/25/26	0/2/2/2
7	PSU	A	516	7	-	0/7/25/26	0/2/2/2
30	2MA	a	2503	30	-	3/7/25/26	0/3/3/3
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
7	MA6	A	1518	7	-	2/11/29/30	0/3/3/3
30	6MZ	a	1618	30	-	2/9/27/28	0/3/3/3
7	G7M	A	527	7	-	0/7/25/26	0/3/3/3
30	PSU	a	1917	30	-	1/7/25/26	0/2/2/2

The worst 5 of 114 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2030	6MZ	C6-N6	9.71	1.45	1.34
30	a	2030	6MZ	C3'-C4'	-8.93	1.30	1.53
30	a	1618	6MZ	C6-N6	8.77	1.44	1.34
30	a	2069	G7M	C5-N7	-8.47	1.29	1.39
30	a	745	1MG	C2-N3	7.92	1.46	1.33

The worst 5 of 150 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1618	6MZ	C5-C4-N3	-6.03	118.41	126.72
30	a	2552	OMU	C4-N3-C2	-5.90	119.28	126.61
7	A	1518	MA6	C5-C4-N3	-5.82	118.71	126.72
30	a	745	1MG	C5-C4-N3	-5.81	119.14	128.39
7	A	1518	MA6	N1-C6-N6	5.72	123.82	116.86

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	967	5MC	O4'-C4'-C5'-O5'
7	A	1518	MA6	C5-C6-N6-C9
7	A	1519	MA6	C5-C6-N6-C9
7	A	1519	MA6	C5-C6-N6-C10
7	A	1519	MA6	N1-C6-N6-C9

There are no ring outliers.

15 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	a	2030	6MZ	1	0
30	a	2552	OMU	1	0
33	d	150	MEQ	1	0
30	a	1962	5MC	1	0
30	a	2457	PSU	1	0
30	a	2498	OMC	1	0
30	a	2449	H2U	1	0
6	5	32	4OC	2	0
7	A	966	2MG	1	0
7	A	1407	5MC	2	0
6	5	53	5MU	1	0
7	A	516	PSU	1	0
30	a	955	PSU	1	0
7	A	1518	MA6	3	0
30	a	1917	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	a	3
29	Y	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	118:UNK	C	124:UNK	N	22.94
1	a	1052:C	O3'	1107:G	P	17.39
1	a	2098:U	O3'	2191:A	P	16.58
1	a	1172:C	O3'	1177:G	P	15.99
1	Y	127:UNK	C	131:UNK	N	10.74

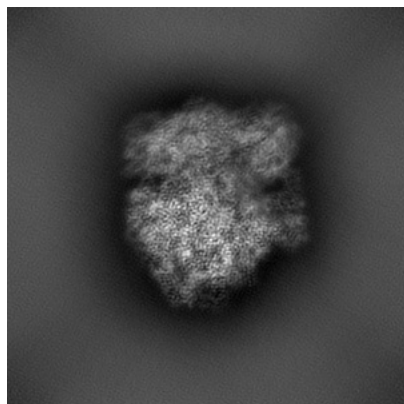
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74757. These allow visual inspection of the internal detail of the map and identification of artifacts.

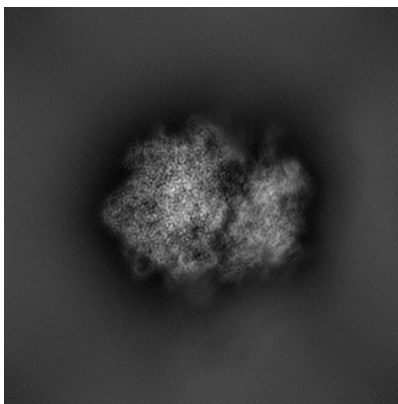
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

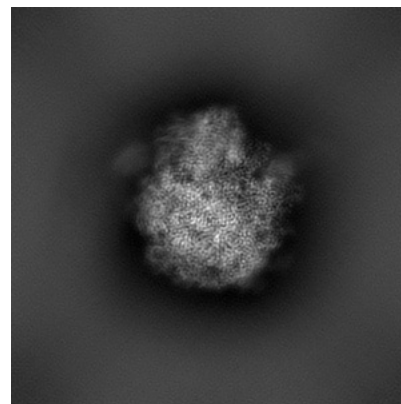
6.1.1 Primary map



X

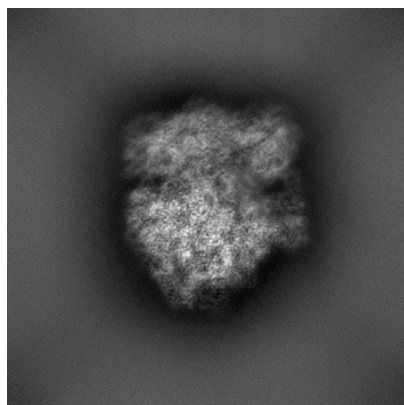


Y

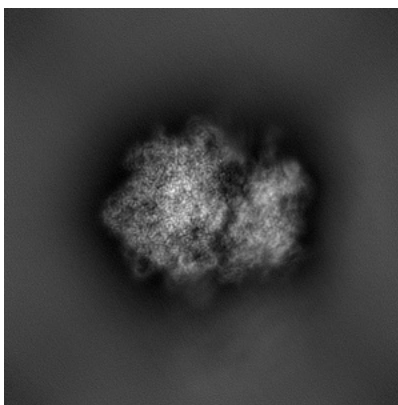


Z

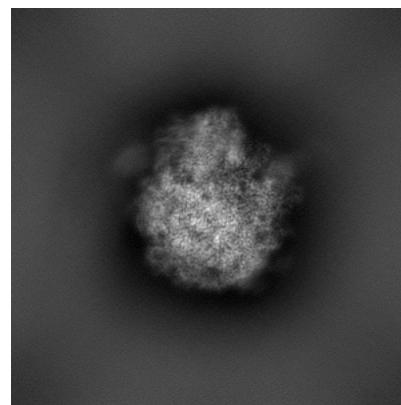
6.1.2 Raw map



X



Y

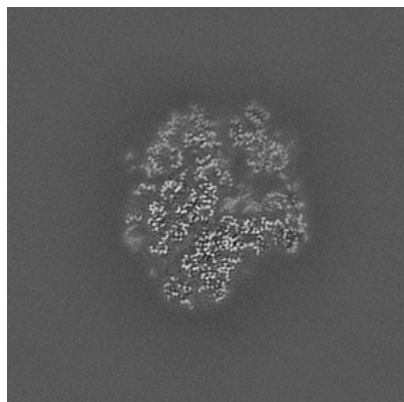


Z

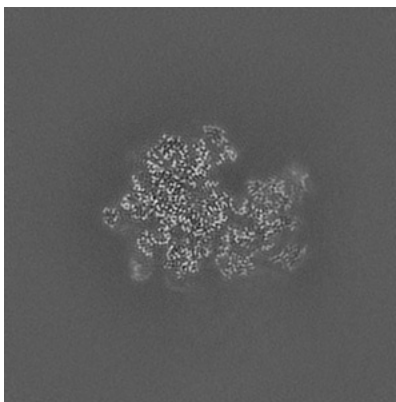
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

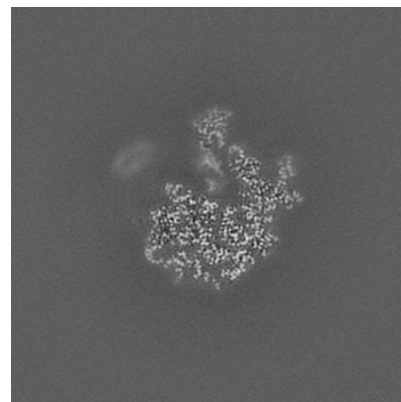
6.2.1 Primary map



X Index: 256

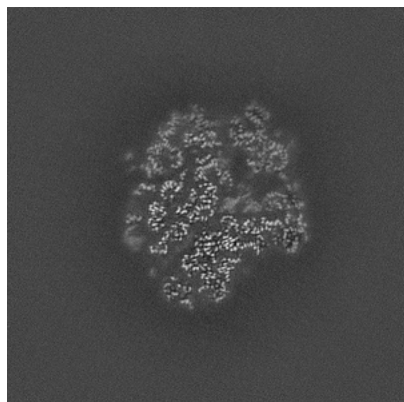


Y Index: 256

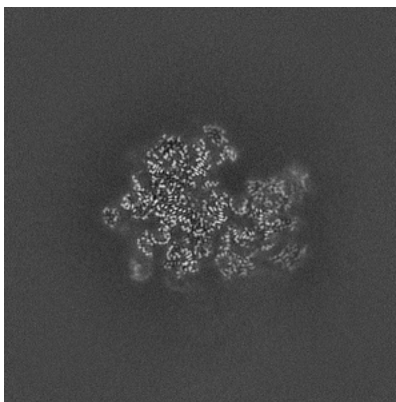


Z Index: 256

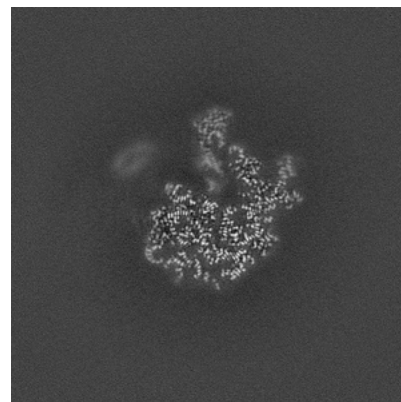
6.2.2 Raw map



X Index: 256



Y Index: 256

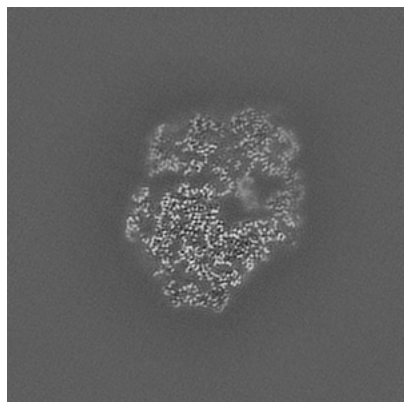


Z Index: 256

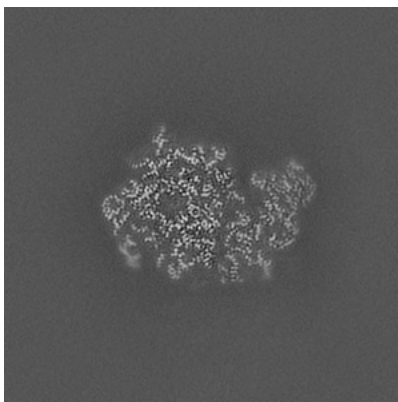
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

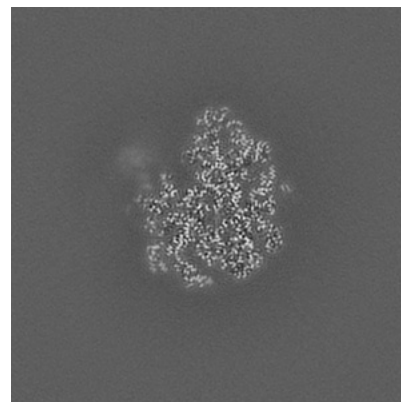
6.3.1 Primary map



X Index: 243

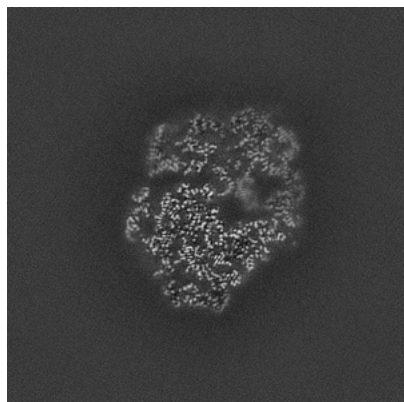


Y Index: 235

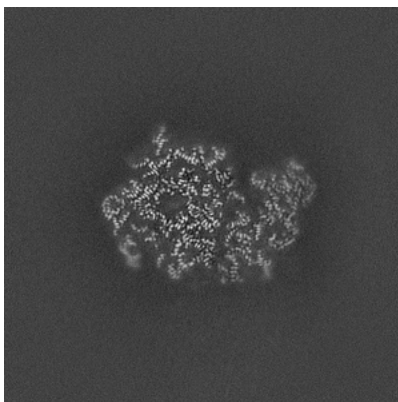


Z Index: 230

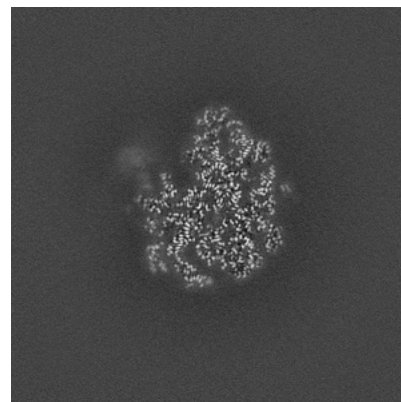
6.3.2 Raw map



X Index: 243



Y Index: 235

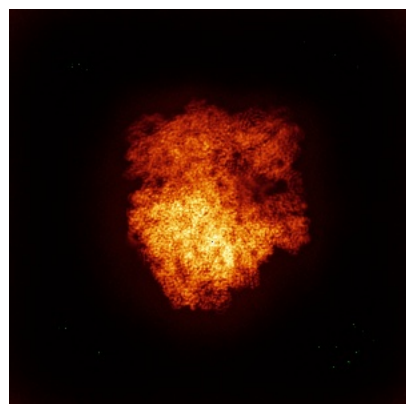


Z Index: 230

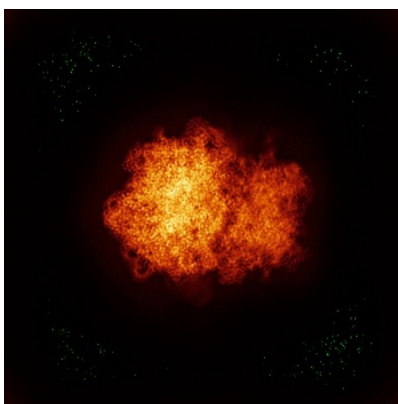
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

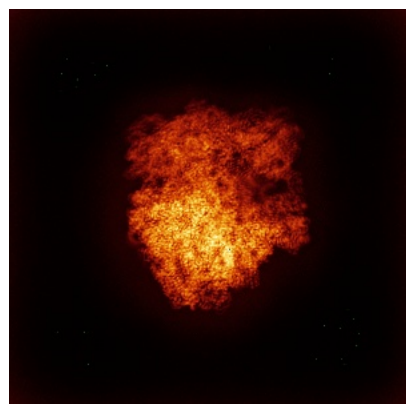


Y

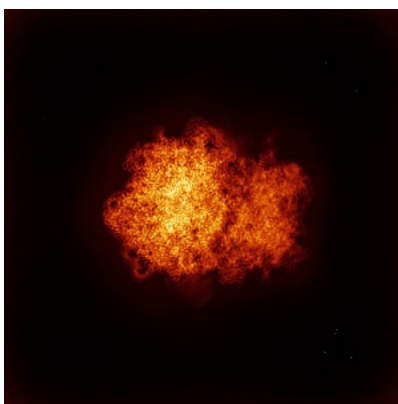


Z

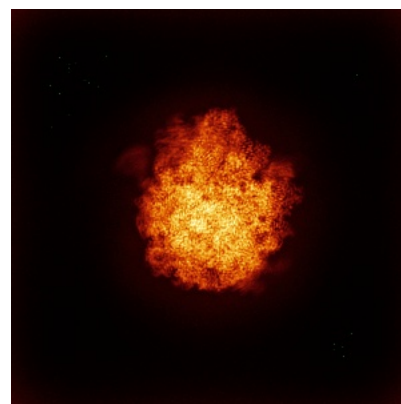
6.4.2 Raw map



X



Y

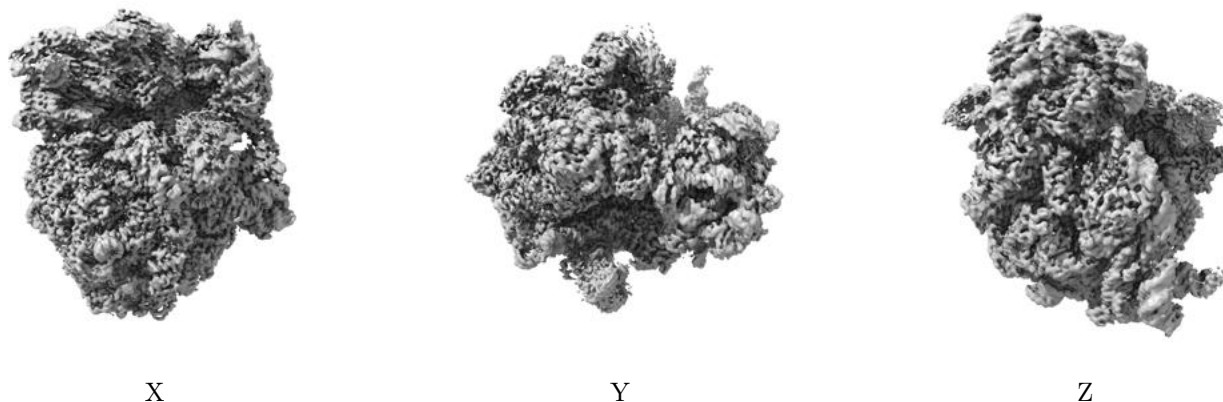


Z

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.

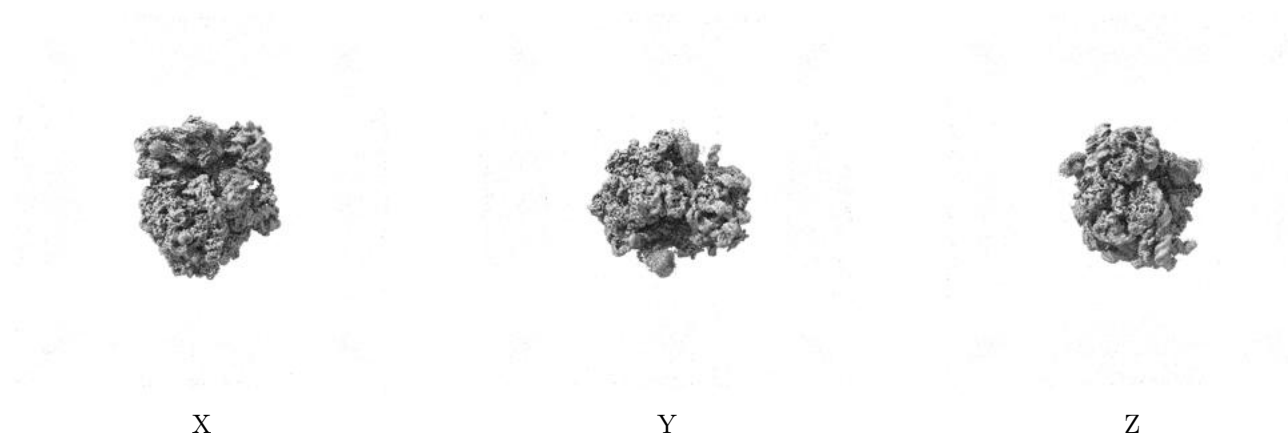
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

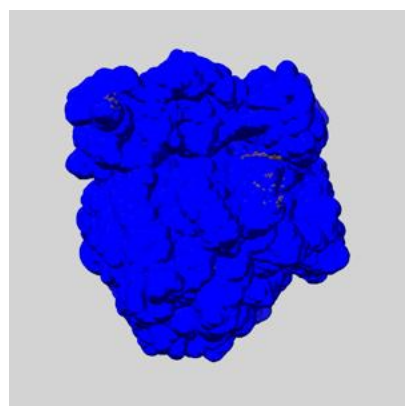
6.6 Mask visualisation [i](#)

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

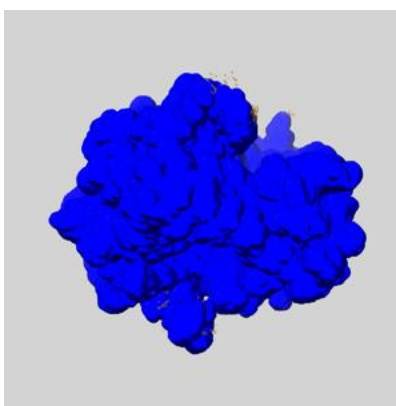
A mask typically either:

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

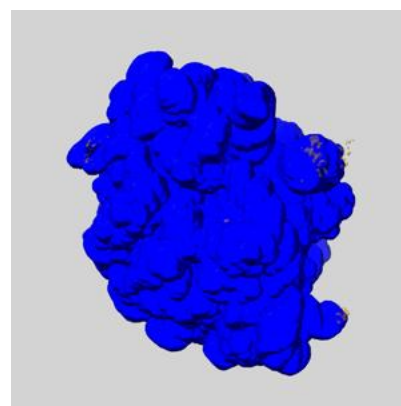
6.6.1 emd_74757_msk_1.map [i](#)



X



Y

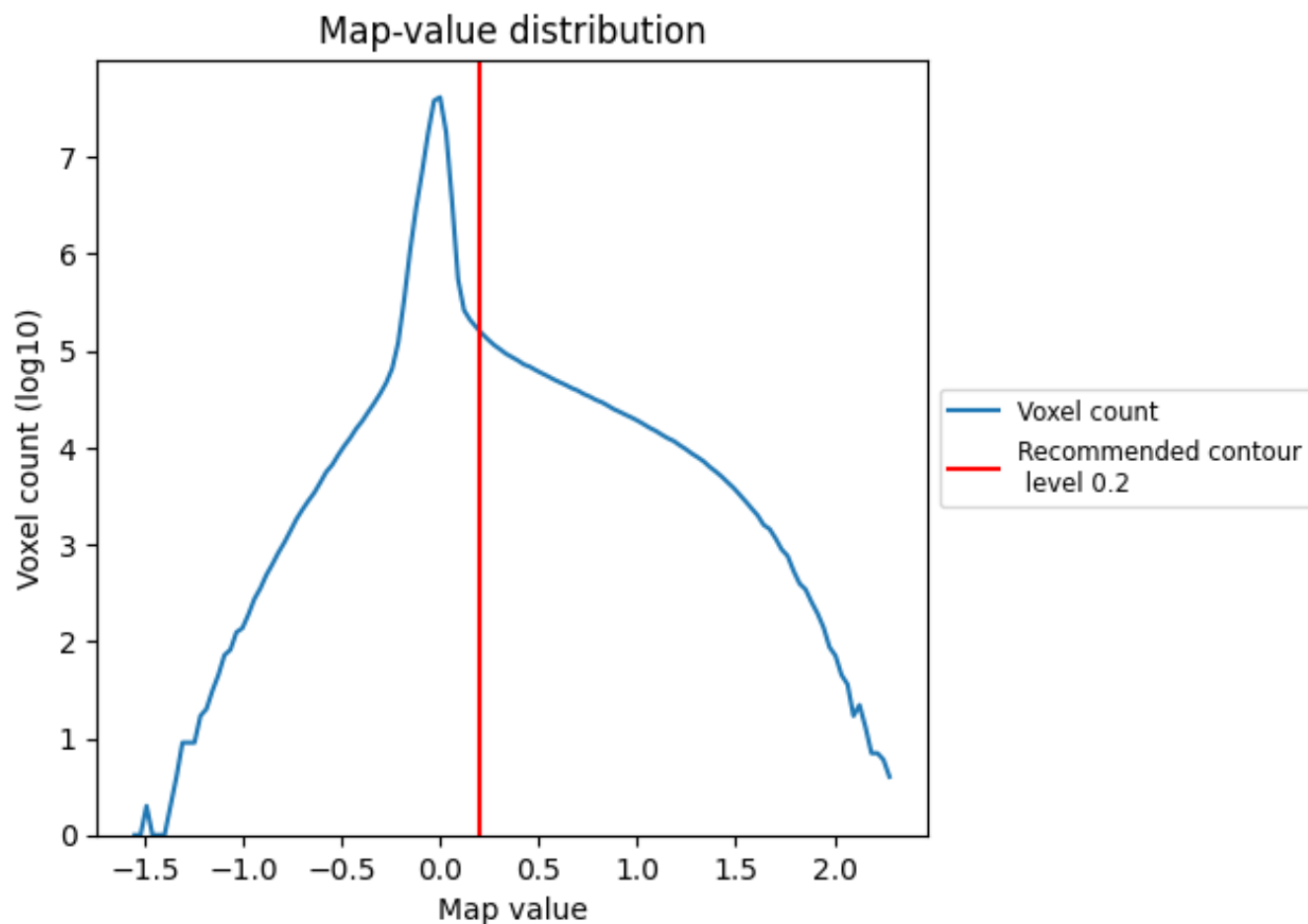


Z

7 Map analysis [i](#)

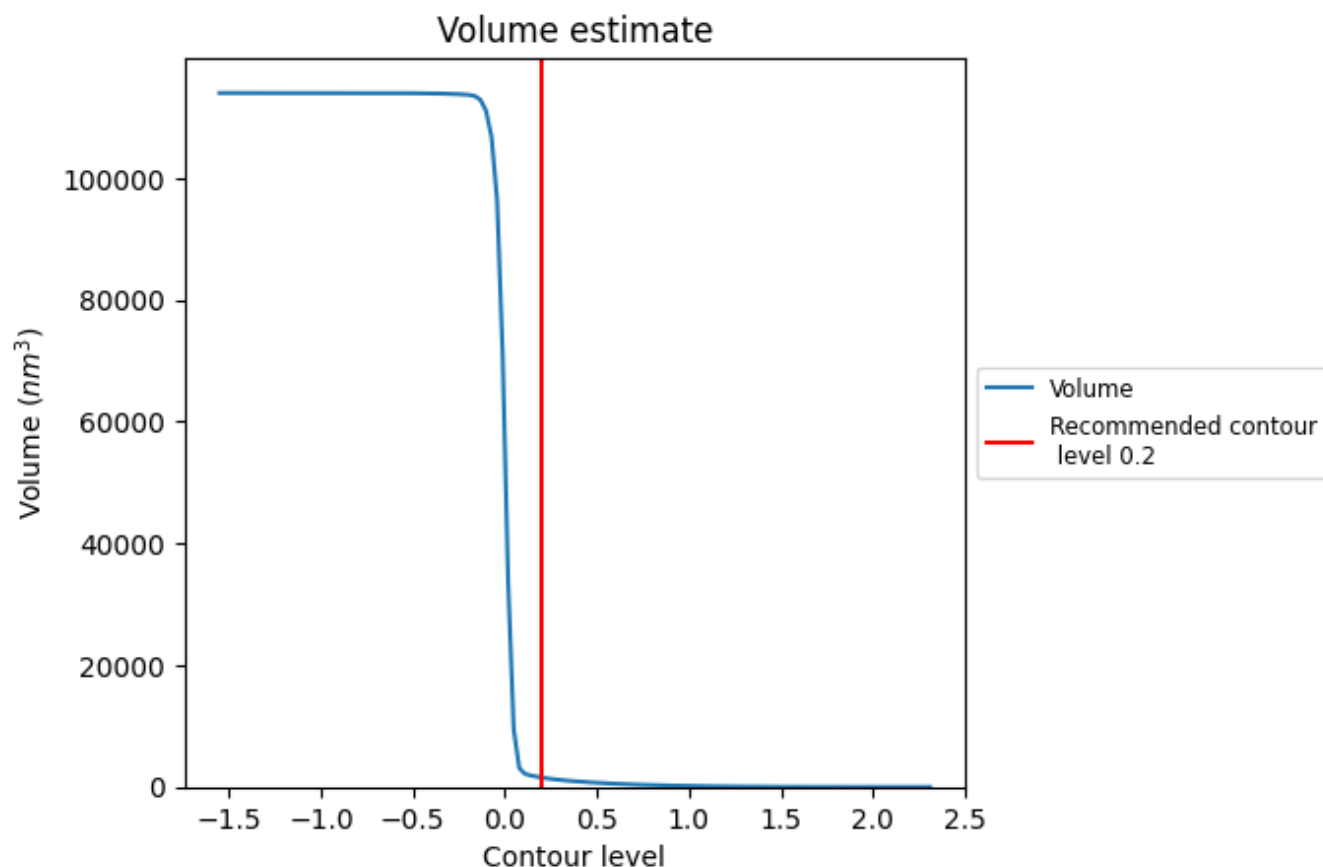
This section contains the results of statistical analysis of the map.

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.

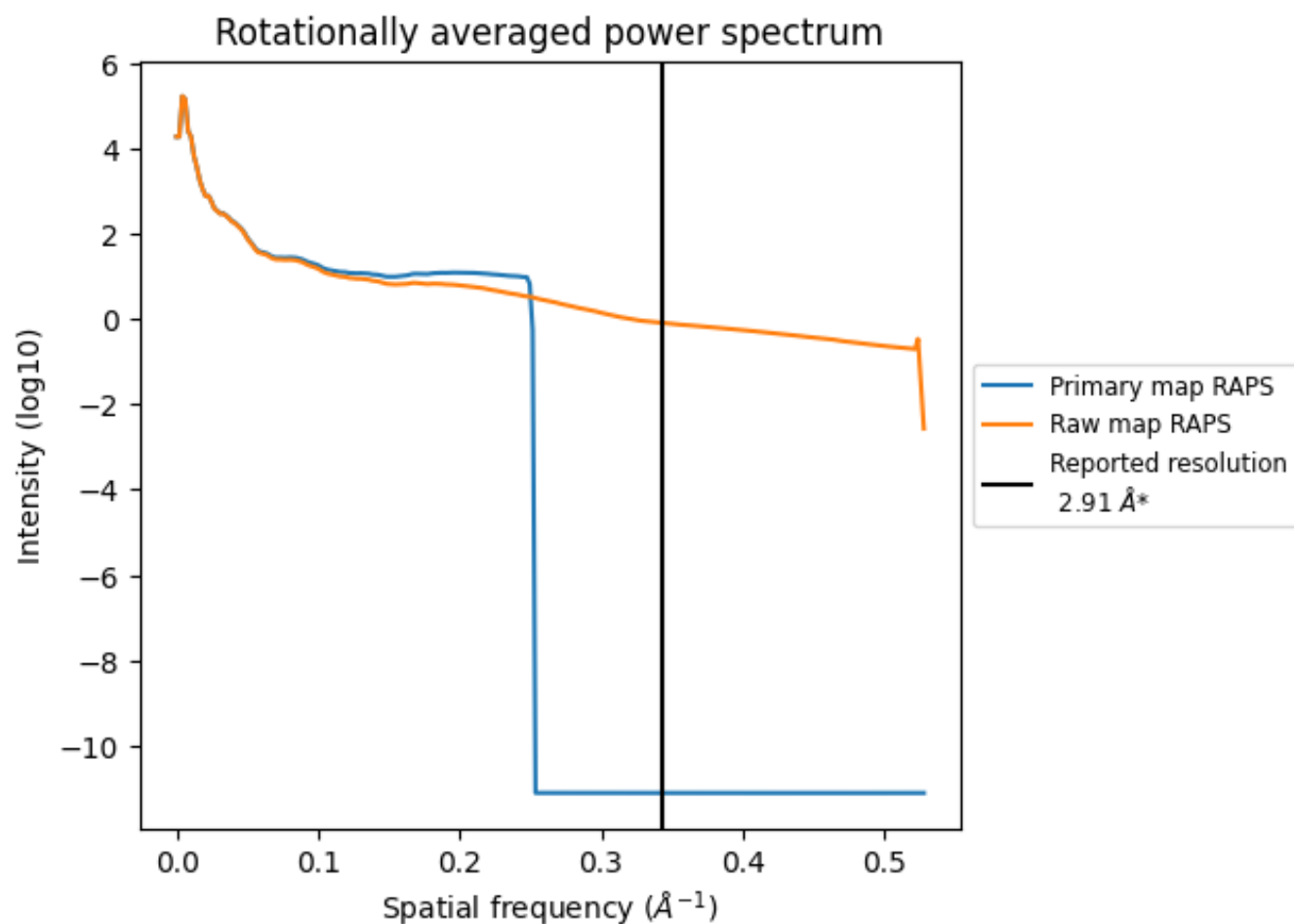
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1534 nm³; this corresponds to an approximate mass of 1385 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 ⓘ

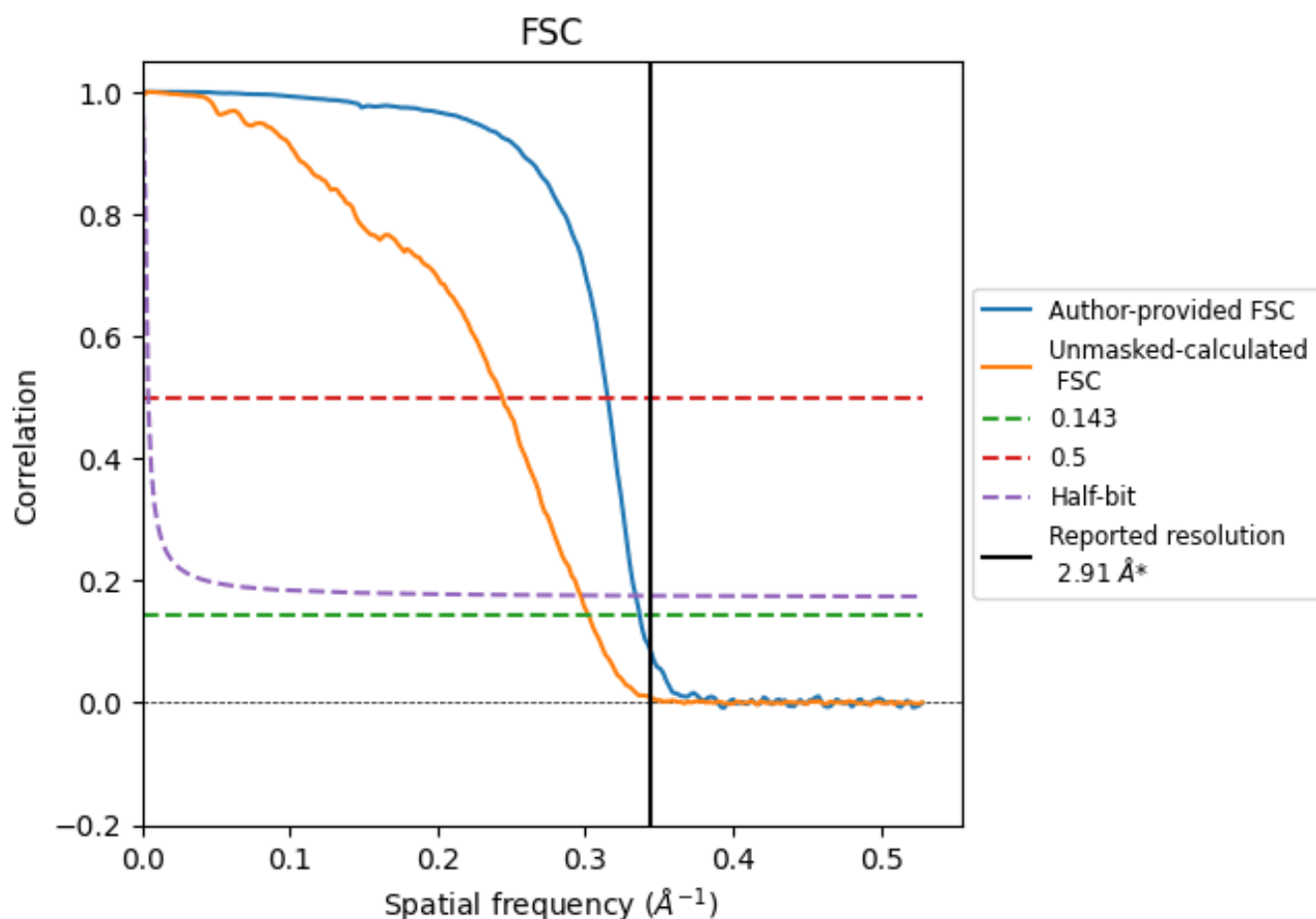


*Reported resolution corresponds to spatial frequency of 0.344 Å⁻¹

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 0.344 \AA^{-1}

8.2 Resolution estimates [i](#)

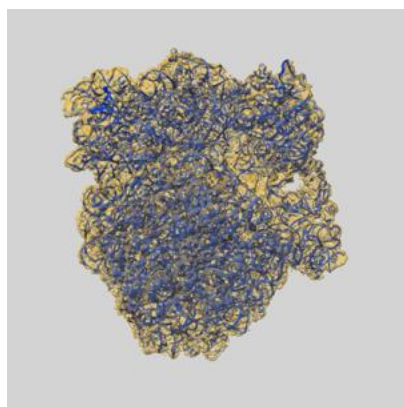
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	2.97	3.17	2.99
Unmasked-calculated*	3.31	4.10	3.37

*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 3.31 differs from the reported value 2.91 by more than 10 %

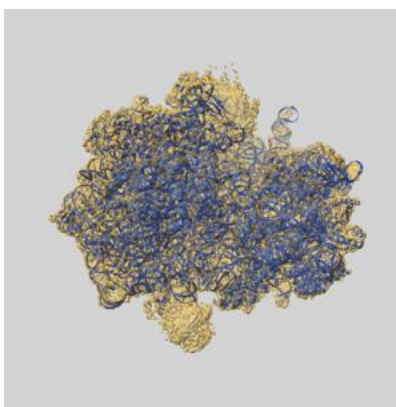
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74757 and PDB model 9ZTL. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

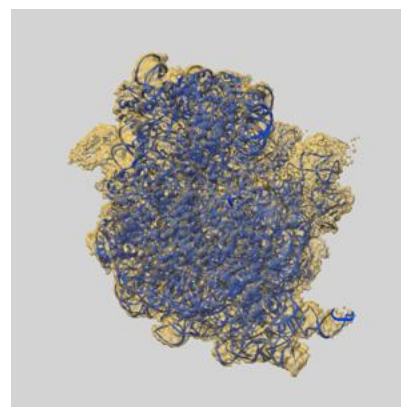
9.1 Map-model overlay [i](#)



X



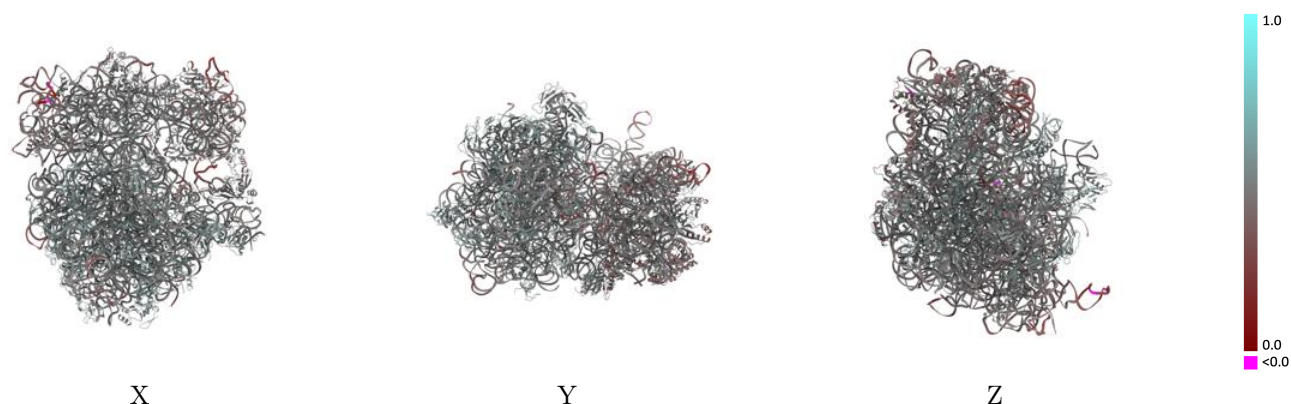
Y



Z

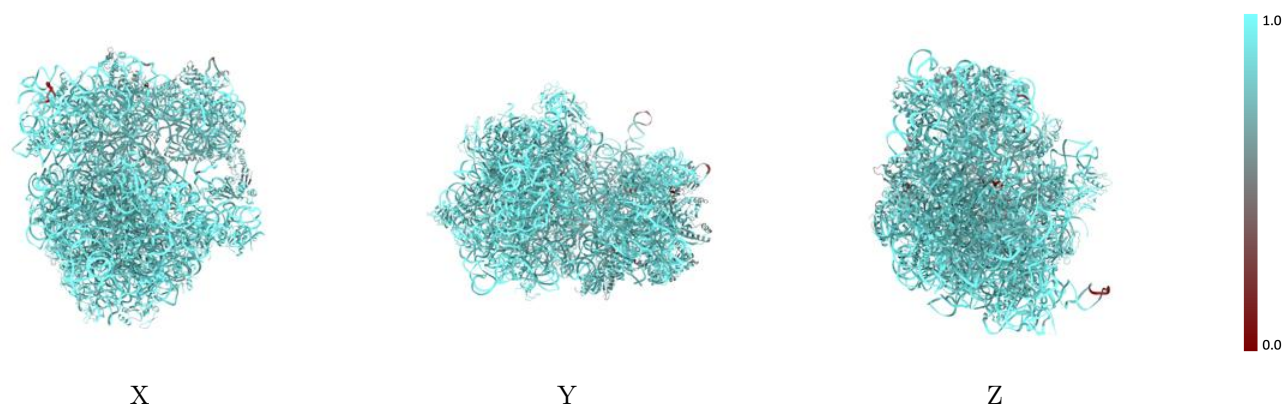
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



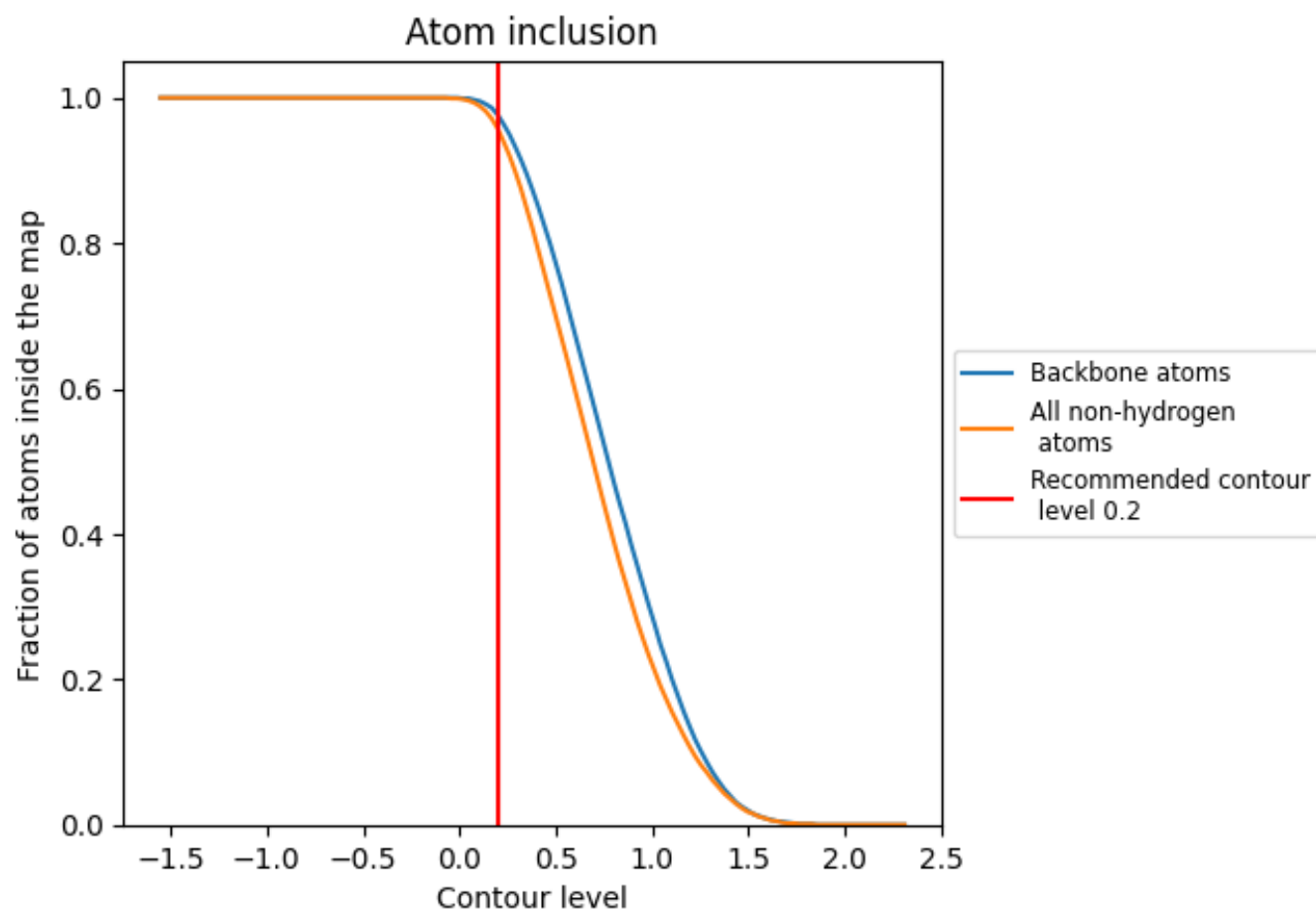
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4800
0	 0.9580	 0.5380
1	 0.9580	 0.5410
2	 0.9880	 0.5490
3	 0.9760	 0.5520
4	 0.6480	 0.4350
5	 0.9530	 0.4080
A	 0.9730	 0.4500
B	 0.7920	 0.4670
C	 0.8560	 0.4940
D	 0.7590	 0.4660
E	 0.9260	 0.5060
F	 0.8800	 0.4860
G	 0.7900	 0.4240
H	 0.9240	 0.5120
I	 0.8730	 0.4540
J	 0.7910	 0.4410
K	 0.8780	 0.4970
L	 0.9160	 0.5070
M	 0.8630	 0.4660
N	 0.9100	 0.4780
O	 0.9490	 0.4920
P	 0.9030	 0.5090
Q	 0.8960	 0.4920
R	 0.9370	 0.5050
S	 0.8470	 0.4570
T	 0.8840	 0.4660
U	 0.6830	 0.4290
X	 0.9160	 0.4320
Y	 0.7530	 0.4470
a	 0.9820	 0.4800
b	 0.9920	 0.4680
c	 0.9640	 0.5410
d	 0.9710	 0.5430
e	 0.9430	 0.5330



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Chain	Atom inclusion	Q-score
f	 0.8940	 0.4700
g	 0.9310	 0.5070
h	 0.9100	 0.5050
i	 0.9660	 0.5400
j	 0.9400	 0.5430
k	 0.9610	 0.5370
l	 0.9660	 0.5380
m	 0.9670	 0.5410
n	 0.9620	 0.5200
o	 0.9380	 0.5470
p	 0.9730	 0.5350
q	 0.9620	 0.5510
r	 0.9450	 0.5430
s	 0.9330	 0.5270
t	 0.9320	 0.5210
u	 0.9550	 0.5370
v	 0.9770	 0.5520
w	 0.9680	 0.5340
x	 0.9320	 0.5130
y	 0.9520	 0.5410
z	 0.9770	 0.5440