



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:02 PM UTC

PDB ID : 7ST6 / pdb_00007st6
EMDB ID : EMD-25420
Title : Pre translocation, non-rotated 70S ribosome (Structure I)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-12
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

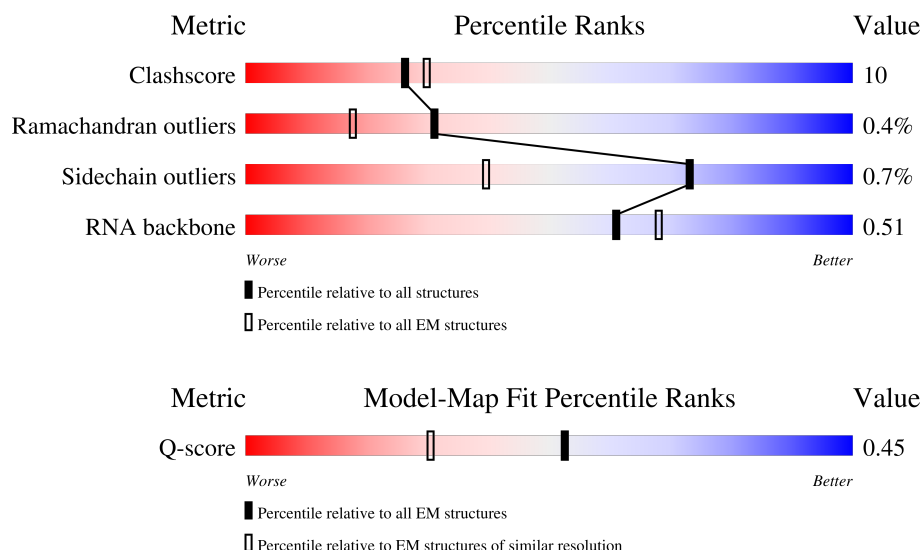
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.



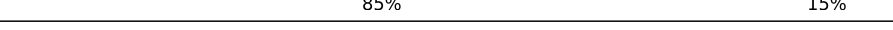
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	3	1539	
2	1	2903	
3	2	120	

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Mol	Chain	Length	Quality of chain
4	5	77	
5	6	77	
5	7	77	
6	b	271	
7	c	209	
8	d	201	
9	e	177	
10	f	176	
11	g	149	
12	i	142	
13	j	142	
14	k	122	
15	l	143	
16	m	136	
17	n	120	
18	o	116	
19	p	114	
20	q	117	
21	r	103	
22	s	110	
23	t	93	
24	u	102	
25	v	94	
26	w	75	
27	x	77	

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Mol	Chain	Length	Quality of chain
28	y	63	
29	z	58	
30	A	66	
31	B	56	
32	C	50	
33	D	46	
34	E	64	
35	F	38	
36	4	35	
37	G	225	
38	H	206	
39	I	205	
40	J	157	
41	K	100	
42	L	151	
43	M	129	
44	N	127	
45	O	98	
46	P	116	
47	Q	123	
48	R	114	
49	S	100	
50	T	88	
51	U	82	
52	V	80	

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Mol	Chain	Length	Quality of chain
53	W	65	 78%22%
54	X	79	 85%15%
55	Y	85	 78%22%
56	Z	65	 69%28%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 147982 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 4 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 5 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
5	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	52	Total	C	N	O	S	0	0
			400	256	73	70	1		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4	18	Total	C	N	O	P	0	0
			390	176	80	117	17		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

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

- Molecule 46 is a protein called 30S ribosomal protein S11.

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

- Molecule 47 is a protein called 30S ribosomal protein S12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

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

- Molecule 49 is a protein called 30S ribosomal protein S14.

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

- Molecule 50 is a protein called 30S ribosomal protein S15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

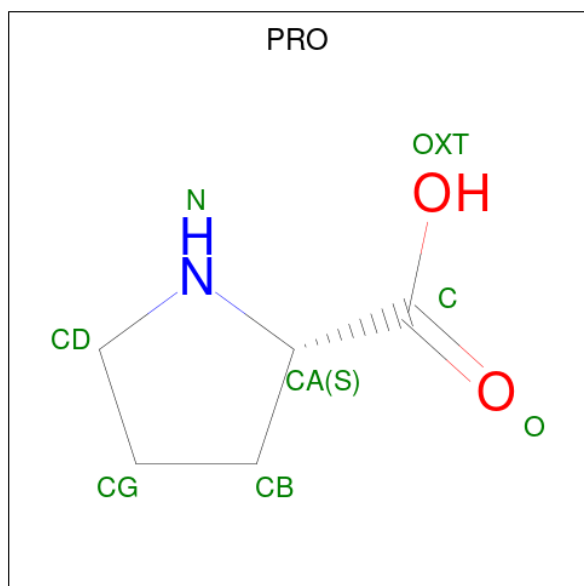
- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 57 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).

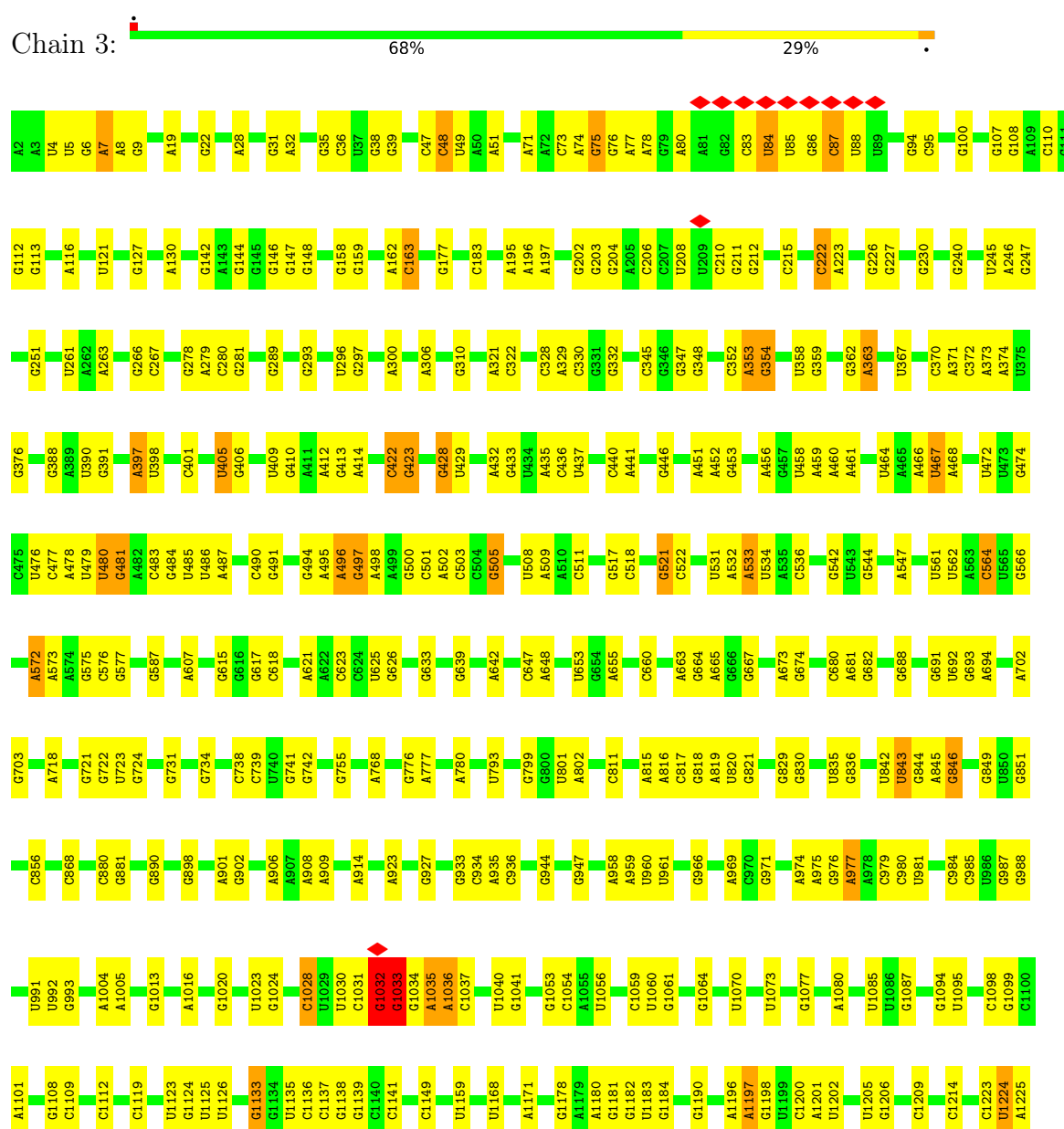


Mol	Chain	Residues	Atoms				AltConf
57	5	1	Total	C	N	O	0
			7	5	1	1	

3 Residue-property plots

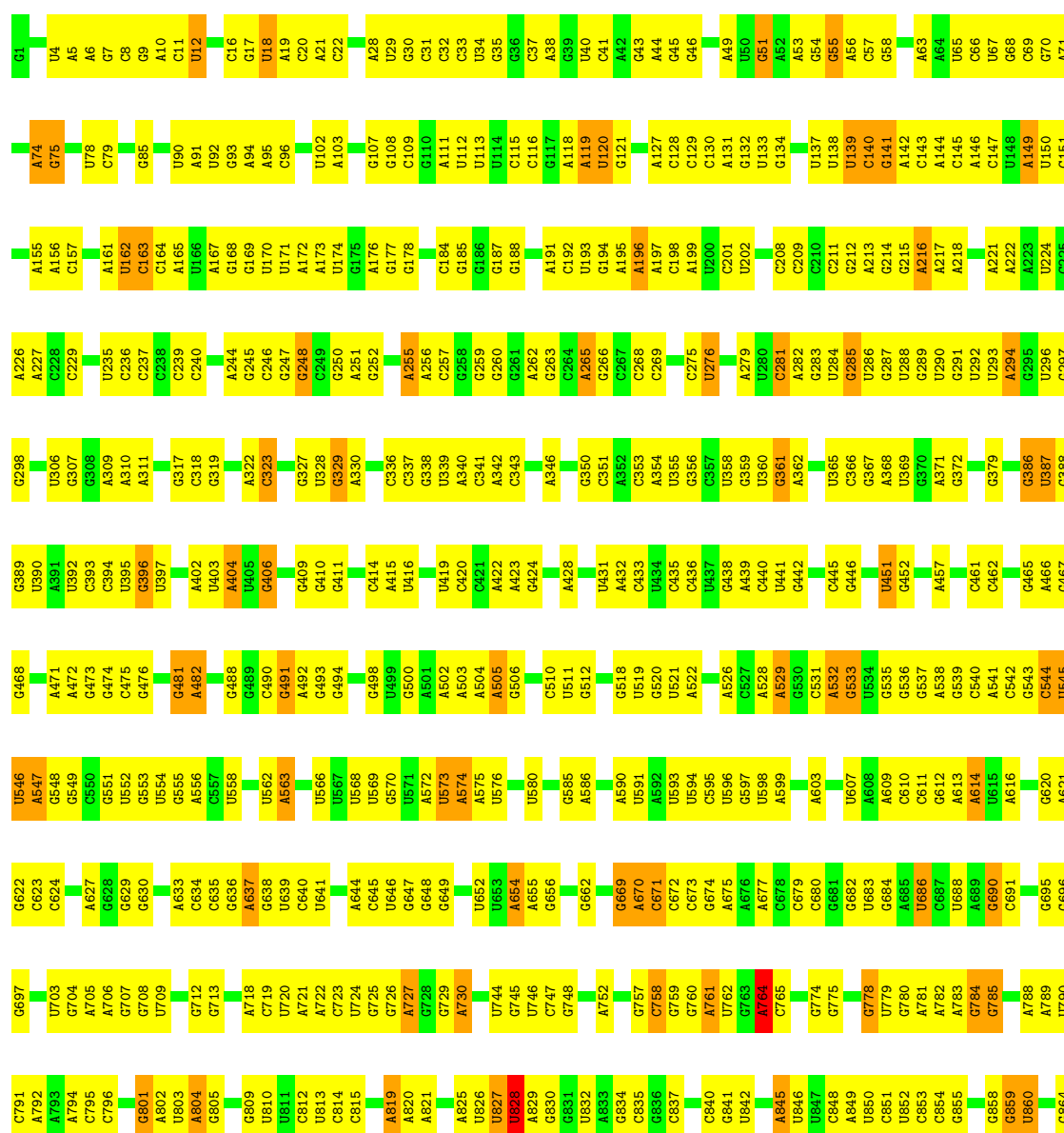
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

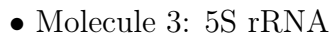




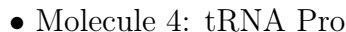
• Molecule 2: 23S rRNA



G1879	C1800	G1733	U1554	U1486	U1316	G1239	C1161	G1091	G0938	C0865
U1955	A1801	G1734	G1585	U1487	G1317	U1240	G1162	C1092	G939	U870
U1956	A1802	A1735	U1588	C1488	U1318	A1246	G1163	C1093	G940	U871
U1963	G1807	U1736	U1589	U1489	C1319	A1247	U1164	U1094	G941	U872
G1964	A1808	G1737	G1590	A1490	C1320	A1247	A1165	A1095	G942	C873
C1965	A1809	U1738	C1561	U1411	A1321	G1260	G1166	A1096	C946	
A1966	A1809	A1739	U1582	U1412	A1322	U1260	C1170	U1097	C947	C876
G1967	A1810	G1740	U1583	A1413	C1323	G1261	G1171	A1098	A972	A877
G1968	G1811	G1741	C1585	C1414	U1324	G1262	C1172	G1099	U955	A878
A1969	U1812	U1742	U1586	U1415	U1325	A1284	U1173	C1100	A956	G879
A1890	G1813	G1743	G1587	U1416	U1326	U1285	U1174	U1101	C957	
	C1815	A1744	G1588	C1417	A1327	U1286	A1175	C1102	U958	C885
C1893	G1816	A1745	A1589	U1418	C1328	G1266	U1176	A1103	A959	A886
C1894	G1817	A1746	A1590	A1419	U1329	C1267	U1177	C1104	A960	A887
	U1818	U1747	A1591	A1420	C1330	U1268	C1178	U1105	C961	C888
A1901	A1819	C1748	U1571	G1425	G1333	G1266	U1179	G1107	C968	C890
C1902	U1820	U1749	A1572	G1426	U1334	U1267	G1180	U1108	C969	C891
	A1821	G1750	G1573	A1427	C1335	U1267	U1181	C1109	U970	A892
C1905	C1822	U1751	C1574	G1428	A1336	C1270	G1182	G1110	U971	A893
G1906	G1823	C1752	C1575	A1429	U1337	A1271	U1183	A1111	A972	U894
G1983	U1824	G1753	U1578	G1430	G1338	G1272	G1184	G1112	A973	U895
G1984	G1825	A1754	A1579	A1431	U1339	A1273	G1185	U1113	A974	A896
C1985	G1826	G1755	U1580	G1432	G1343	U1274	G1186	C1114	C975	C887
C1986	U1827	A1756	G1581	A1433	U1344	A1275	G1187	A1064	A975	C888
	G1828	U1758	C1582	A1434	C1345	A1275	U1188	G1065	A979	A899
G1989	A1829	A1759	A1583	G1435	U1346	C1278	G1193	A1067	A980	U1058
C1990	C1832	U1760	U1584	A1436	C1347	G1279	A1194	G1068	A981	A900
C1991	G1833	G1761	G1585	G1437	C1348	U1280	G1195	U1069	U982	C901
G1992	C1834	U1762	U1586	U1438	C1349	G1281	C1196	U1061	A983	C902
A1916	U1834	C1764	U1589	A1439	U1352	U1282	G1197	G1062	A984	C903
U1917	U1765	U1765	A1590	U1440	A1353	U1283	C1198	G1063	A985	G904
A1918	G1766	G1767	A1591	G1441	C1354	A1284	U1199	G1064	C986	A905
A1919	U1846	U1767	C1592	U1442	A1355	A1285	G1200	U1065	U907	U906
C1920	A1847	C1768	U1593	U1443	C1356	A1286		U1066	C908	C908
G1921	U1848	U1769	U1594	G1444	A1367	A1287	A1204	A1067	A909	A910
G1922	G1845	U1770	C1595	G1445	G1368	C1288	A1205	G1068	C994	A911
U1923	U1846	U1771	A1596	U1446	U1377	C1289		A1069	A996	
C1924	G1846	G1772	A1597	C1451	A1378	G1292	U1209	A1070	C1005	C915
	U1847	U1773	A1598	U1447	U1379	C1293	G1210	G1071		G914
A1927	A1853	C1774	U1599	A1452	G1380	U1294	G1212	C1072		
A1928	U1854	U1775	C1600	A1453	A1381	C1295	A1213	A1073		
G1929	U1855	G1776	G1601	A1454	G1382	G1296		G1074	A1009	A918
U1930	U1856	U1777	U1602	C1455	A1383	C1297	U1219	C1075	A1010	U919
A1931	A1858	U1778	A1603	C1456	C1386	C1298	G1220	C1076	G1011	G923
	U1859	U1779	C1604	C1457	U1387	G1299	G1221	U1077	C1013	G924
G1935	G1863	A1780	C1605	C1458	A1388	G1300	G1222	C1078	A1014	A925
A1936	U1864	U1781	U1606	C1459	G1389	A1301	A1223	C1079	U1015	G926
A1937	U1865	A1782	C1607	U1460	U1390	A1302	A1224	U1080		A927
A1938	A1866	U1783	A1608	U1461	U1391	C1306		U1081	U1019	A928
U1939	G1867	C1788	A1614	C1462	U1394	C1307	G1225	U1082	A1020	U929
	C1868	U1789	C1615	C1463	U1400	G1309	G1226	A1083	A1021	
C1942	U1869	C1790	A1616	U1464	G1401	G1310	G1227	U1084	U1023	U932
U1943	A1870	U1791	C1625	G1465	U1402	G1311	A1228	A1085	G1024	A933
U1944	C1871	C1792	A1626	U1466	U1403	C1314	G1229	A1086	G1025	U934
G1945	U1872	U1793	A1627	U1467	U1404	C1315	G1230	G1087	G1026	A935
	A1873	C1794	A1628	U1468	U1405	G1316	G1231	A1088	U1027	A936
U1948	G1874	U1795	A1629	U1469	U1406	C1317	G1232	A1089		C937
	G1875	C1796	A1630	U1470	U1407	C1318	G1233	A1090		
G2036	U1876	U1797	A1631	U1471	U1408	C1319	A1237			
A2037	G1877	G1798	A1632	U1472	U1409	C1320				
G2038	U1878	U1799	A1633	U1473	U1410	C1321				



78% 19% .

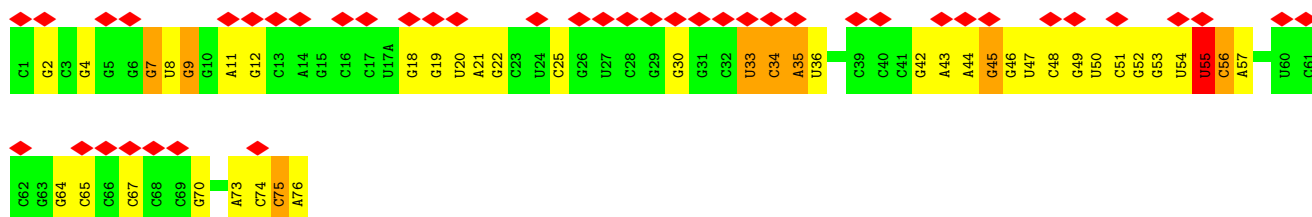


Chain 5:  58% 31% 8% .



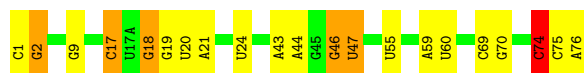
• Molecule 5: tRNA fMet

Chain 7:  45% 56% 43% 10% .



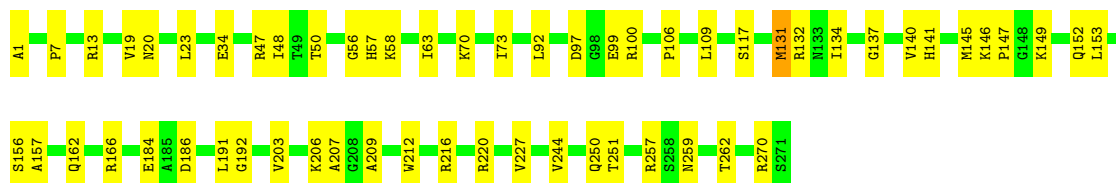
• Molecule 5: tRNA fMet

Chain 6:  73% 19% 6% .



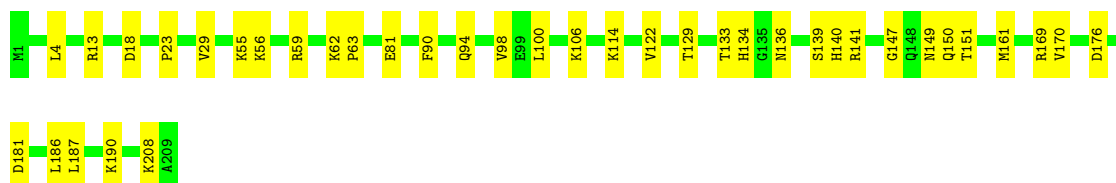
• Molecule 6: 50S ribosomal protein L2

Chain b:  79% 21%



• Molecule 7: 50S ribosomal protein L3

Chain c:  82% 18%



• Molecule 8: 50S ribosomal protein L4

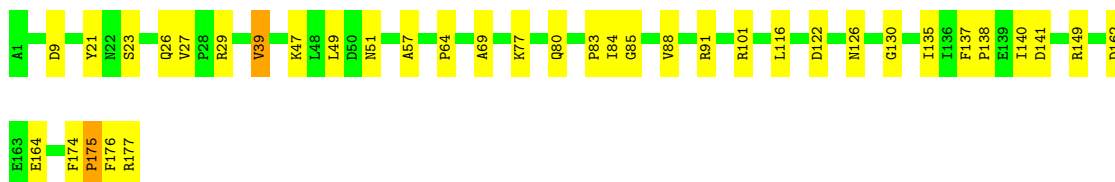
Chain d:  80% 20%





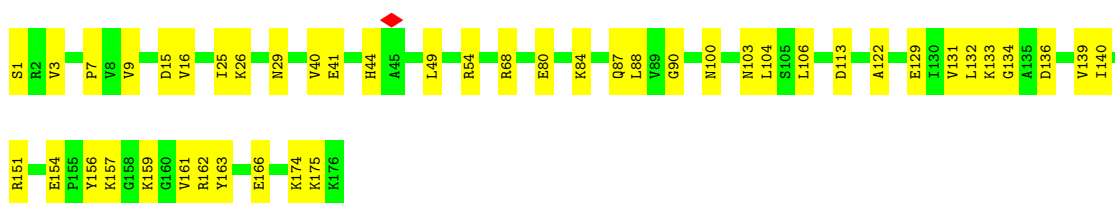
• Molecule 9: 50S ribosomal protein L5

Chain e: 79% 20%



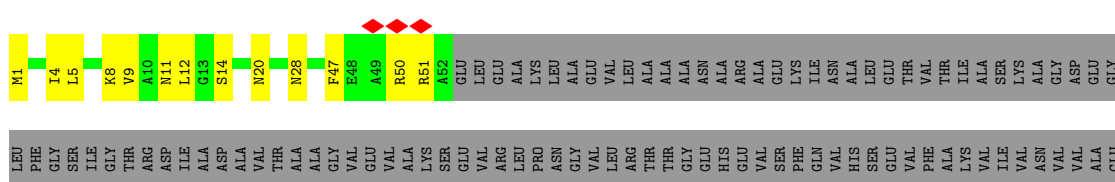
• Molecule 10: 50S ribosomal protein L6

Chain f: 74% 26%



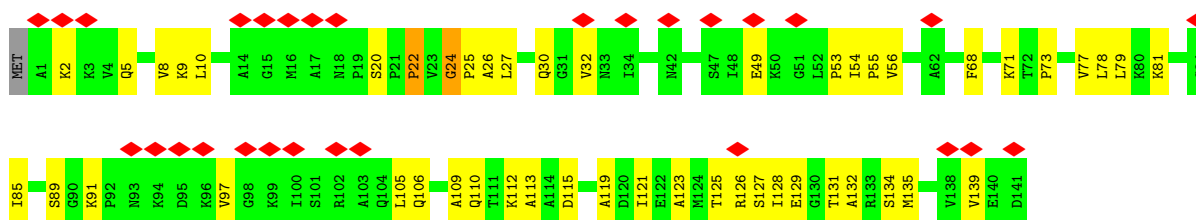
• Molecule 11: 50S ribosomal protein L9

Chain g: 26% 9% 65%



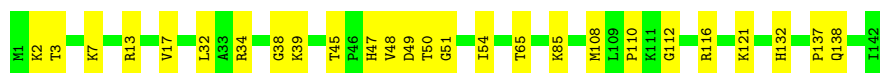
• Molecule 12: 50S ribosomal protein L11

Chain i: 20% 65% 33%

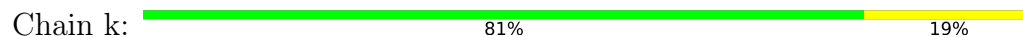


• Molecule 13: 50S ribosomal protein L13

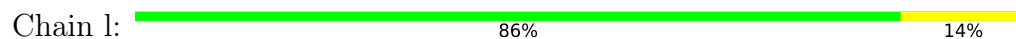
Chain j: 82% 18%



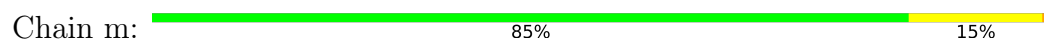
- Molecule 14: 50S ribosomal protein L14



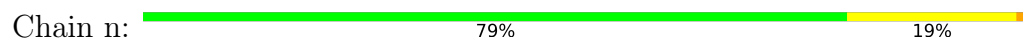
- Molecule 15: 50S ribosomal protein L15



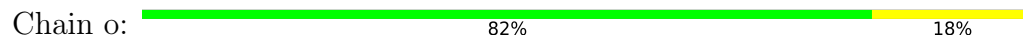
- Molecule 16: 50S ribosomal protein L16



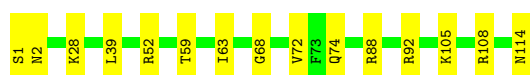
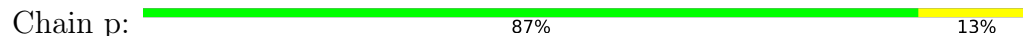
- Molecule 17: 50S ribosomal protein L17



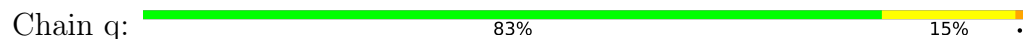
- Molecule 18: 50S ribosomal protein L18



- Molecule 19: 50S ribosomal protein L19



- Molecule 20: 50S ribosomal protein L20

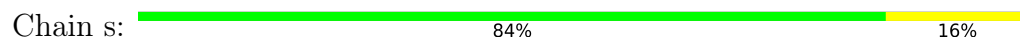




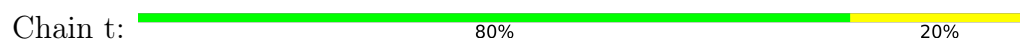
- Molecule 21: 50S ribosomal protein L21



- Molecule 22: 50S ribosomal protein L22



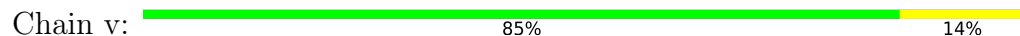
- Molecule 23: 50S ribosomal protein L23



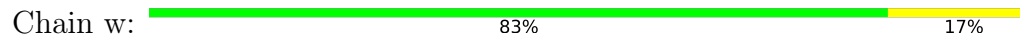
- Molecule 24: 50S ribosomal protein L24



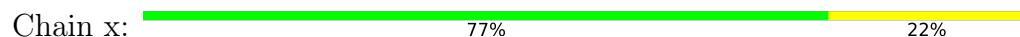
- Molecule 25: 50S ribosomal protein L25



- Molecule 26: 50S ribosomal protein L27

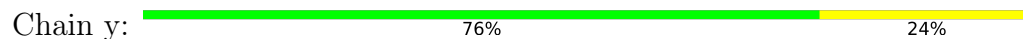


- Molecule 27: 50S ribosomal protein L28

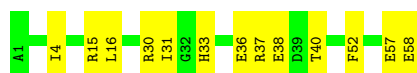
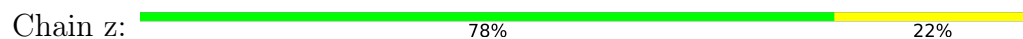




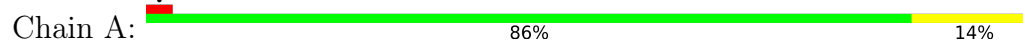
- Molecule 28: 50S ribosomal protein L29



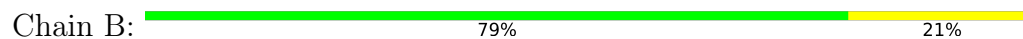
- Molecule 29: 50S ribosomal protein L30



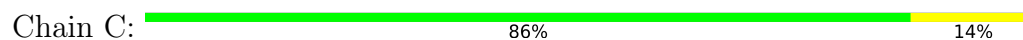
- Molecule 30: 50S ribosomal protein L31



- Molecule 31: 50S ribosomal protein L32



- Molecule 32: 50S ribosomal protein L33



- Molecule 33: 50S ribosomal protein L34



- Molecule 34: 50S ribosomal protein L35



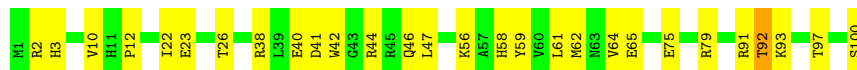
- Molecule 40: 30S ribosomal protein S5

Chain J:  83% 17%



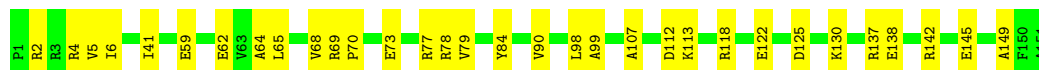
- Molecule 41: 30S ribosomal protein S6

Chain K:  72% 27%



- Molecule 42: 30S ribosomal protein S7

Chain L:  79% 21%



- Molecule 43: 30S ribosomal protein S8

Chain M:  88% 12%



- Molecule 44: 30S ribosomal protein S9

Chain N:  70% 29%



- Molecule 45: 30S ribosomal protein S10

Chain O:  83% 15%



- Molecule 46: 30S ribosomal protein S11

Chain P:  72% 28%



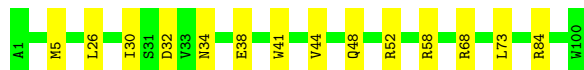
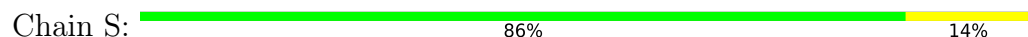
- Molecule 47: 30S ribosomal protein S12



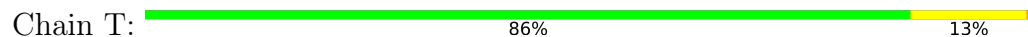
- Molecule 48: 30S ribosomal protein S13



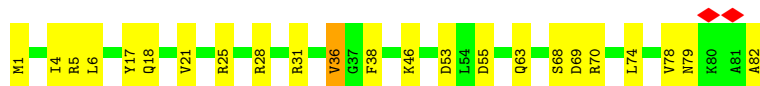
- Molecule 49: 30S ribosomal protein S14



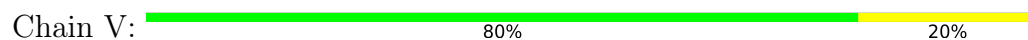
- Molecule 50: 30S ribosomal protein S15



- Molecule 51: 30S ribosomal protein S16



- Molecule 52: 30S ribosomal protein S17



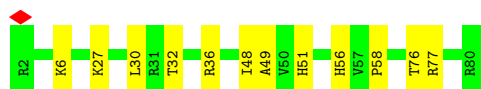
- Molecule 53: 30S ribosomal protein S18

Chain W:  78% 22%



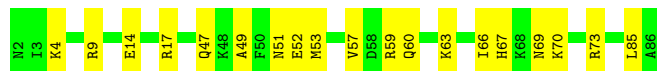
- Molecule 54: 30S ribosomal protein S19

Chain X:  85% 15%



- Molecule 55: 30S ribosomal protein S20

Chain Y:  78% 22%



- Molecule 56: 30S ribosomal protein S21

Chain Z:  69% 28% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37252	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 ($e^-/\text{\AA}^2$)	40.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	14.154	Depositor
Minimum map value	-4.209	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.866	Depositor
Recommended contour level	1.35	Depositor
Map size (Å)	381.8, 381.8, 381.8	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	3	0.40	0/36963	0.40	4/57662 (0.0%)
2	1	0.50	2/69796 (0.0%)	0.62	34/108888 (0.0%)
3	2	0.38	0/2872	0.41	0/4479
4	5	0.38	0/1840	0.60	5/2868 (0.2%)
5	6	0.37	0/1832	0.82	4/2855 (0.1%)
5	7	0.40	0/1832	0.60	3/2855 (0.1%)
6	b	0.47	0/2122	0.64	0/2852
7	c	0.42	0/1586	0.59	2/2134 (0.1%)
8	d	0.37	0/1571	0.62	0/2113
9	e	0.35	0/1435	0.64	4/1926 (0.2%)
10	f	0.28	0/1343	0.54	0/1816
11	g	0.32	0/405	0.75	0/544
12	i	0.31	0/1046	0.77	3/1410 (0.2%)
13	j	0.41	0/1152	0.55	1/1551 (0.1%)
14	k	0.44	0/948	0.66	0/1268
15	l	0.40	0/1054	0.63	0/1403
16	m	0.45	0/1093	0.72	4/1460 (0.3%)
17	n	0.40	0/974	0.70	1/1301 (0.1%)
18	o	0.31	0/902	0.51	0/1209
19	p	0.41	0/929	0.61	0/1242
20	q	0.45	0/960	0.71	3/1278 (0.2%)
21	r	0.38	0/829	0.63	0/1107
22	s	0.39	0/864	0.55	0/1156
23	t	0.33	0/745	0.52	0/994
24	u	0.31	0/788	0.75	0/1051
25	v	0.34	0/766	0.51	0/1025
26	w	0.40	0/582	0.52	0/769
27	x	0.43	0/635	0.63	1/848 (0.1%)
28	y	0.29	0/510	0.64	0/677
29	z	0.41	0/453	0.53	0/605
30	A	0.26	0/532	0.54	0/709
31	B	0.40	0/450	0.60	0/599
32	C	0.27	0/417	0.52	0/554
33	D	0.47	0/380	0.76	2/498 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	E	0.44	0/513	0.58	0/676
35	F	0.42	0/303	0.71	0/397
36	4	0.54	0/439	0.62	0/684
37	G	0.29	0/1736	0.63	2/2338 (0.1%)
38	H	0.34	0/1652	0.55	0/2225
39	I	0.29	0/1665	0.69	0/2227
40	J	0.38	0/1170	0.68	2/1573 (0.1%)
41	K	0.33	0/836	0.75	0/1128
42	L	0.30	0/1196	0.67	3/1602 (0.2%)
43	M	0.34	0/989	0.52	0/1326
44	N	0.31	0/1034	0.72	0/1375
45	O	0.29	0/797	0.69	2/1077 (0.2%)
46	P	0.37	0/886	0.71	1/1195 (0.1%)
47	Q	0.37	0/969	0.87	4/1300 (0.3%)
48	R	0.33	0/893	0.73	2/1193 (0.2%)
49	S	0.32	0/817	0.61	0/1088
50	T	0.36	0/722	0.55	0/964
51	U	0.29	0/659	0.71	2/884 (0.2%)
52	V	0.33	0/658	0.68	0/881
53	W	0.37	0/545	0.68	0/731
54	X	0.27	0/653	0.55	0/877
55	Y	0.28	0/671	0.52	0/888
56	Z	0.34	0/551	0.99	2/728 (0.3%)
All	All	0.44	2/160960 (0.0%)	0.58	91/241063 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	3	1	0
2	1	0	40
4	5	2	0
5	7	1	0
6	b	0	1
8	d	0	1
9	e	0	1
16	m	0	1
17	n	0	1
20	q	0	2
21	r	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	u	0	1
34	E	0	1
35	F	0	1
37	G	0	1
39	I	0	1
41	K	0	1
44	N	0	1
46	P	0	1
47	Q	0	2
50	T	0	1
52	V	0	1
53	W	0	2
56	Z	0	2
All	All	4	65

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	2587	A	O3'-P	8.26	1.73	1.61
2	1	2059	A	O3'-P	-5.30	1.53	1.61

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	6	74	C	OP2-P-O3'	20.86	170.57	108.00
5	6	74	C	P-O3'-C3'	-19.93	90.30	120.20
5	6	74	C	O3'-P-O5'	-18.56	76.16	104.00
5	6	74	C	OP1-P-O3'	-14.65	64.06	108.00
5	7	55	U	C2'-C3'-O3'	11.04	130.25	113.70

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	3	1032	G	C3'
4	5	75	C	C3'
4	5	76	A	C3'
5	7	55	U	C3'

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	18	U	Sidechain

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Mol	Chain	Res	Type	Group
2	1	562	U	Sidechain
2	1	576	U	Sidechain
2	1	683	U	Sidechain
2	1	690	G	Sidechain

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	3	33012	0	16618	204	0
2	1	62317	0	31346	1551	0
3	2	2568	0	1303	12	0
4	5	1647	0	831	34	0
5	6	1640	0	837	12	0
5	7	1640	0	837	33	0
6	b	2083	0	2157	49	0
7	c	1565	0	1616	32	0
8	d	1552	0	1619	28	0
9	e	1411	0	1447	23	0
10	f	1323	0	1374	31	0
11	g	400	0	423	7	0
12	i	1032	0	1088	42	0
13	j	1129	0	1162	22	0
14	k	939	0	1012	18	0
15	l	1045	0	1117	16	0
16	m	1074	0	1157	13	0
17	n	961	0	1000	19	0
18	o	892	0	923	15	0
19	p	917	0	965	16	0
20	q	947	0	1022	15	0
21	r	816	0	839	17	0
22	s	857	0	922	12	0
23	t	739	0	807	11	0
24	u	780	0	834	16	0
25	v	753	0	780	9	0
26	w	575	0	592	9	0
27	x	625	0	655	11	0
28	y	509	0	543	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	z	449	0	491	8	0
30	A	523	0	524	7	0
31	B	444	0	461	9	0
32	C	410	0	440	5	0
33	D	377	0	418	12	0
34	E	504	0	574	4	0
35	F	302	0	343	5	0
36	4	390	0	198	5	0
37	G	1705	0	1732	31	0
38	H	1625	0	1699	25	0
39	I	1643	0	1710	37	0
40	J	1157	0	1199	15	0
41	K	818	0	808	17	0
42	L	1182	0	1240	19	0
43	M	979	0	1034	10	0
44	N	1022	0	1070	25	0
45	O	787	0	828	11	0
46	P	870	0	878	20	0
47	Q	955	0	1019	32	0
48	R	884	0	944	19	0
49	S	805	0	847	11	0
50	T	714	0	737	10	0
51	U	649	0	666	18	0
52	V	649	0	691	9	0
53	W	536	0	552	8	0
54	X	638	0	665	9	0
55	Y	665	0	714	13	0
56	Z	545	0	579	14	0
57	5	7	0	7	0	0
All	All	147982	0	98894	2415	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 10.

The worst 5 of 2415 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)
2:1:2720:U:H5''	19:p:52:ARG:HH21	0.95	1.10
2:1:275:C:H2'	2:1:276:U:H4'	1.37	1.04
2:1:1082:U:H3'	2:1:1083:U:H5''	1.41	1.02
2:1:2713:U:H3'	2:1:2714:G:H5'	1.41	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1672:A:C2	2:1:2582:G:H5'	1.95	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	b	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
7	c	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
8	d	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
9	e	175/177 (99%)	158 (90%)	15 (9%)	2 (1%)	11	43
10	f	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
11	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	28
12	i	139/142 (98%)	116 (84%)	23 (16%)	0	100	100
13	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
14	k	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
15	l	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
16	m	134/136 (98%)	126 (94%)	5 (4%)	3 (2%)	5	26
17	n	118/120 (98%)	101 (86%)	16 (14%)	1 (1%)	16	50
18	o	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
19	p	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
20	q	115/117 (98%)	104 (90%)	8 (7%)	3 (3%)	4	23
21	r	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	s	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
23	t	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
24	u	100/102 (98%)	83 (83%)	17 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
26	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
27	x	75/77 (97%)	72 (96%)	2 (3%)	1 (1%)	9	38
28	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
29	z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
30	A	64/66 (97%)	59 (92%)	5 (8%)	0	100	100
31	B	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	2	15
32	C	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
33	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	E	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7	34
35	F	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
37	G	216/225 (96%)	189 (88%)	27 (12%)	0	100	100
38	H	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
39	I	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
40	J	155/157 (99%)	138 (89%)	17 (11%)	0	100	100
41	K	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	45
42	L	149/151 (99%)	130 (87%)	19 (13%)	0	100	100
43	M	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
44	N	125/127 (98%)	102 (82%)	23 (18%)	0	100	100
45	O	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	12	45
46	P	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	6	31
47	Q	121/123 (98%)	90 (74%)	30 (25%)	1 (1%)	16	50
48	R	112/114 (98%)	99 (88%)	12 (11%)	1 (1%)	14	48
49	S	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
50	T	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
51	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
52	V	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
53	W	63/65 (97%)	53 (84%)	9 (14%)	1 (2%)	7	34
54	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
55	Y	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
56	Z	63/65 (97%)	43 (68%)	18 (29%)	2 (3%)	3	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5620/5825 (96%)	5002 (89%)	595 (11%)	23 (0%)	31	65

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	e	175	PRO
17	n	11	ASN
27	x	25	LYS
9	e	176	PHE
16	m	70	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	
6	b	216/216 (100%)	215 (100%)	1 (0%)	81	89
7	c	164/164 (100%)	164 (100%)	0	100	100
8	d	165/165 (100%)	163 (99%)	2 (1%)	63	82
9	e	148/148 (100%)	147 (99%)	1 (1%)	76	86
10	f	137/137 (100%)	135 (98%)	2 (2%)	57	80
11	g	41/114 (36%)	38 (93%)	3 (7%)	13	42
12	i	109/110 (99%)	108 (99%)	1 (1%)	70	85
13	j	116/116 (100%)	116 (100%)	0	100	100
14	k	103/103 (100%)	103 (100%)	0	100	100
15	l	102/102 (100%)	101 (99%)	1 (1%)	68	84
16	m	109/109 (100%)	109 (100%)	0	100	100
17	n	100/100 (100%)	100 (100%)	0	100	100
18	o	86/86 (100%)	86 (100%)	0	100	100
19	p	99/99 (100%)	99 (100%)	0	100	100
20	q	89/89 (100%)	89 (100%)	0	100	100
21	r	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	s	93/93 (100%)	93 (100%)	0	100	100
23	t	80/80 (100%)	80 (100%)	0	100	100
24	u	83/83 (100%)	82 (99%)	1 (1%)	63	82
25	v	78/78 (100%)	77 (99%)	1 (1%)	61	81
26	w	57/57 (100%)	57 (100%)	0	100	100
27	x	67/67 (100%)	67 (100%)	0	100	100
28	y	55/55 (100%)	55 (100%)	0	100	100
29	z	48/48 (100%)	46 (96%)	2 (4%)	26	61
30	A	59/59 (100%)	58 (98%)	1 (2%)	53	78
31	B	47/47 (100%)	47 (100%)	0	100	100
32	C	45/45 (100%)	44 (98%)	1 (2%)	45	74
33	D	38/38 (100%)	37 (97%)	1 (3%)	40	72
34	E	51/51 (100%)	51 (100%)	0	100	100
35	F	34/34 (100%)	34 (100%)	0	100	100
37	G	180/186 (97%)	179 (99%)	1 (1%)	78	88
38	H	170/170 (100%)	167 (98%)	3 (2%)	51	77
39	I	172/172 (100%)	171 (99%)	1 (1%)	78	88
40	J	119/119 (100%)	117 (98%)	2 (2%)	53	78
41	K	87/87 (100%)	87 (100%)	0	100	100
42	L	124/124 (100%)	124 (100%)	0	100	100
43	M	104/104 (100%)	103 (99%)	1 (1%)	68	84
44	N	105/105 (100%)	103 (98%)	2 (2%)	50	76
45	O	86/86 (100%)	86 (100%)	0	100	100
46	P	89/89 (100%)	89 (100%)	0	100	100
47	Q	103/103 (100%)	102 (99%)	1 (1%)	68	84
48	R	92/92 (100%)	91 (99%)	1 (1%)	65	83
49	S	83/83 (100%)	83 (100%)	0	100	100
50	T	76/76 (100%)	76 (100%)	0	100	100
51	U	65/65 (100%)	64 (98%)	1 (2%)	57	80
52	V	74/74 (100%)	74 (100%)	0	100	100
53	W	56/56 (100%)	55 (98%)	1 (2%)	51	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	X	70/70 (100%)	70 (100%)	0	100	100
55	Y	65/65 (100%)	64 (98%)	1 (2%)	57	80
56	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	4678/4758 (98%)	4645 (99%)	33 (1%)	73	86

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	Q	15	VAL
48	R	64	VAL
55	Y	85	LEU
25	v	72	VAL
24	u	35	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
34	E	30	HIS
40	J	121	ASN
37	G	108	GLN
38	H	99	GLN
43	M	3	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	248 (16%)	3 (0%)
2	1	2902/2903 (99%)	377 (12%)	12 (0%)
3	2	119/120 (99%)	16 (13%)	2 (1%)
36	4	17/35 (48%)	3 (17%)	1 (5%)
4	5	76/77 (98%)	20 (26%)	3 (3%)
5	6	76/77 (98%)	11 (14%)	0
5	7	76/77 (98%)	23 (30%)	2 (2%)
All	All	4804/4828 (99%)	698 (14%)	23 (0%)

5 of 698 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U

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Mol	Chain	Res	Type
1	3	5	U
1	3	6	G
1	3	7	A
1	3	9	G

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	2481	G
4	5	3	G
3	2	66	A
4	5	41	A
2	1	859	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	PRO	5	101	4	6,7,8	4.57	4 (66%)	7,8,10	1.50	1 (14%)

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
57	PRO	5	101	4	-	0/0/9/11	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	5	101	PRO	CA-N	7.75	1.62	1.48
57	5	101	PRO	CD-N	-5.57	1.29	1.49
57	5	101	PRO	O-C	5.00	1.39	1.20
57	5	101	PRO	CB-CA	-2.59	1.32	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	5	101	PRO	O-C-CA	-2.97	117.13	124.77

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 [i](#)

There are no chain breaks in this entry.

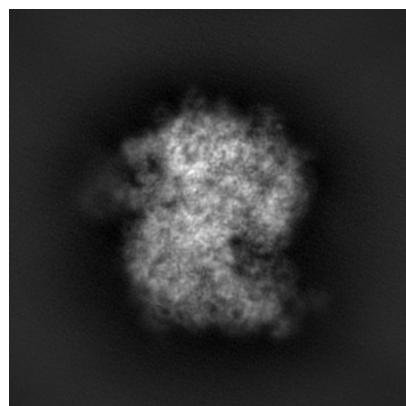
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25420. These allow visual inspection of the internal detail of the map and identification of artifacts.

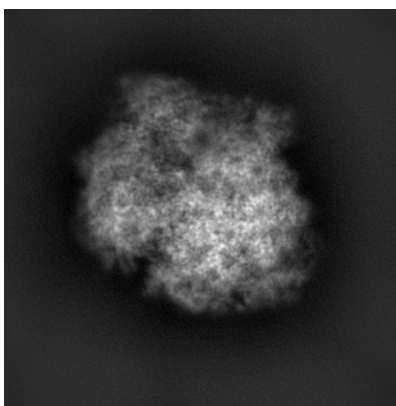
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

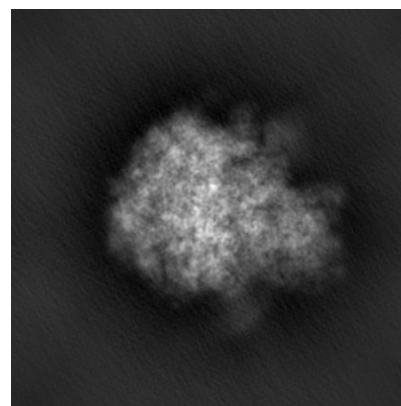
6.1.1 Primary map



X

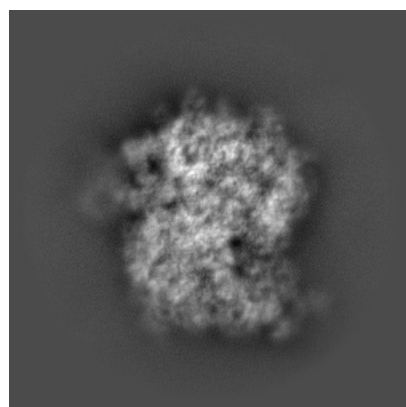


Y

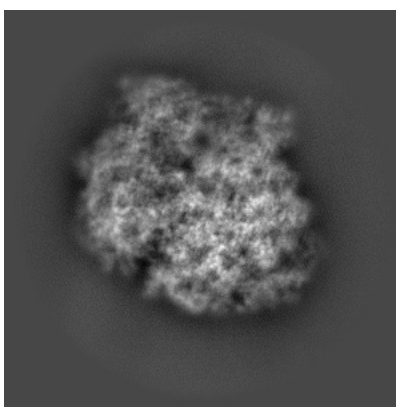


Z

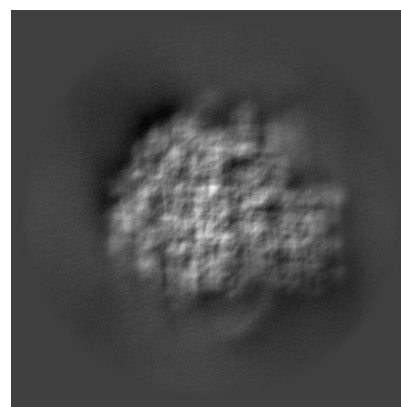
6.1.2 Raw map



X



Y

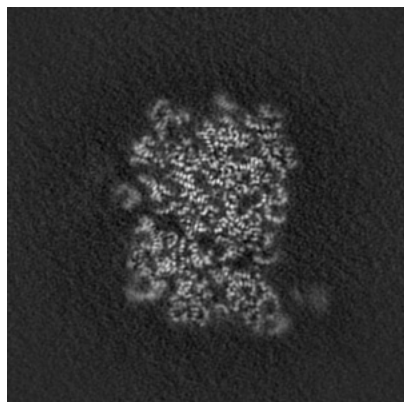


Z

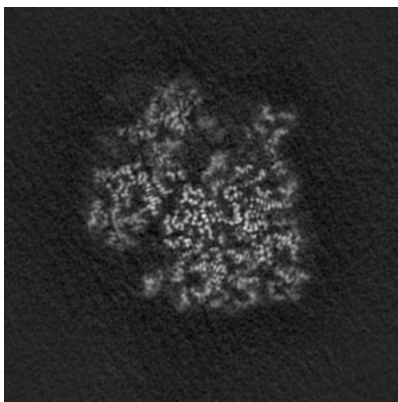
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

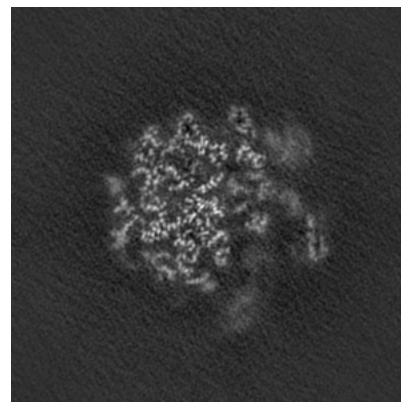
6.2.1 Primary map



X Index: 230

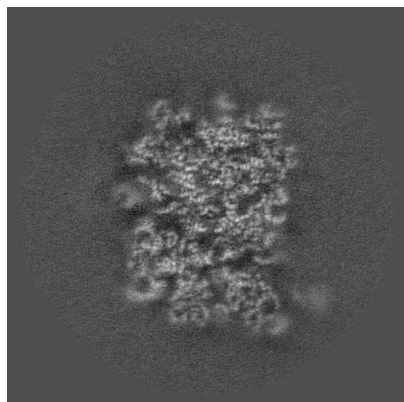


Y Index: 230

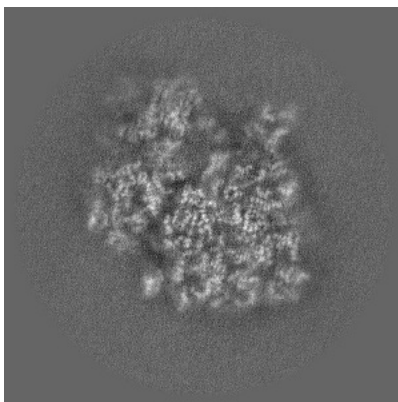


Z Index: 230

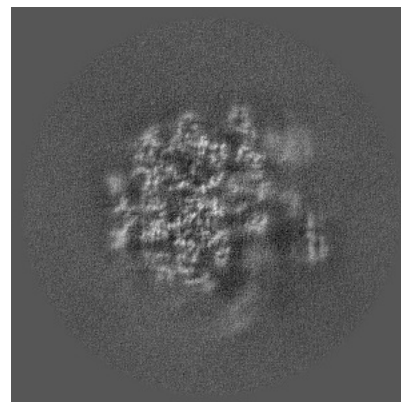
6.2.2 Raw map



X Index: 230



Y Index: 230

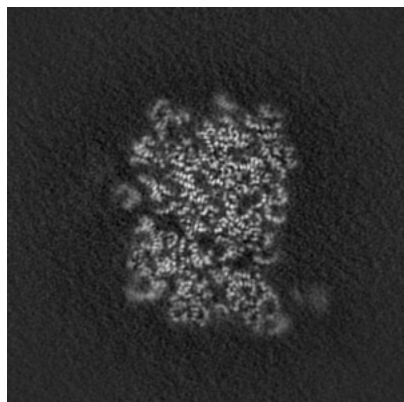


Z Index: 230

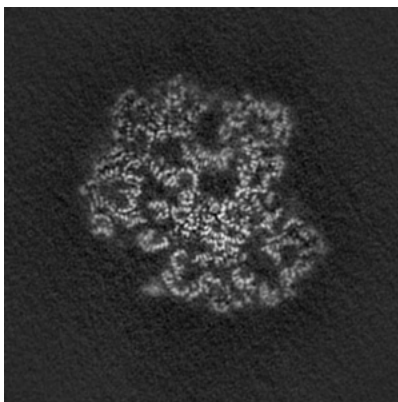
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

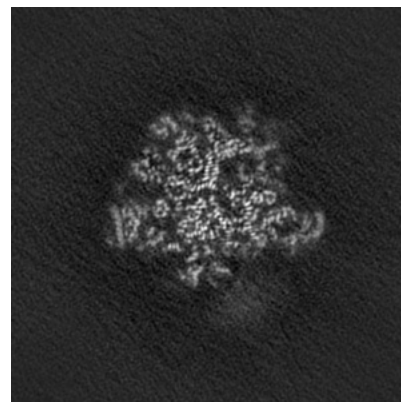
6.3.1 Primary map



X Index: 230

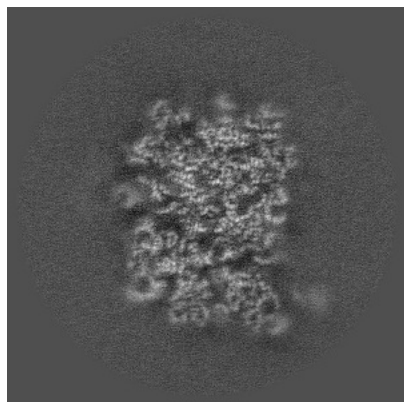


Y Index: 213

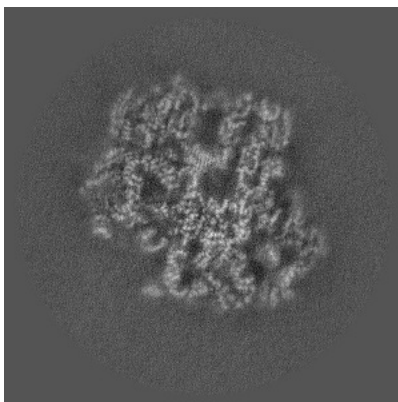


Z Index: 279

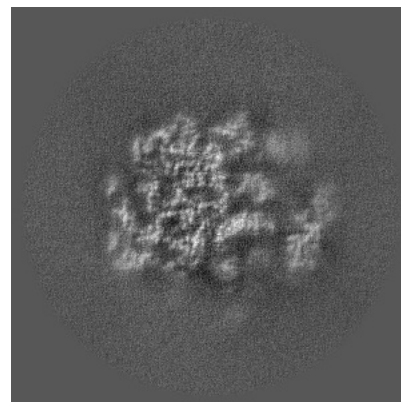
6.3.2 Raw map



X Index: 230



Y Index: 210

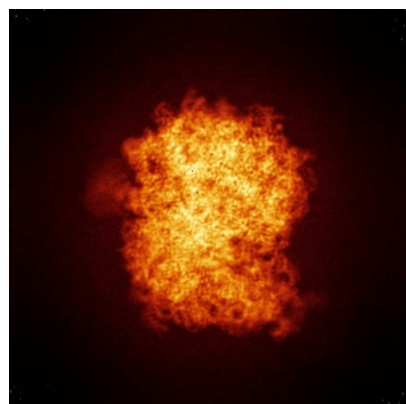


Z Index: 220

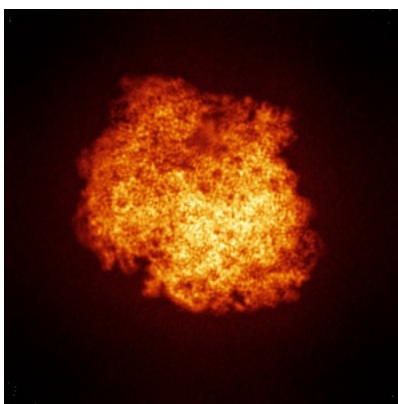
The images above show the largest variance slices of the map in three orthogonal directions.

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

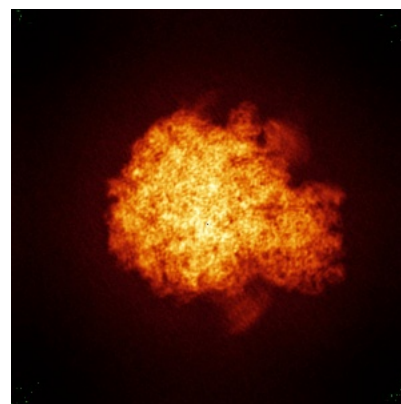
6.4.1 Primary map



X

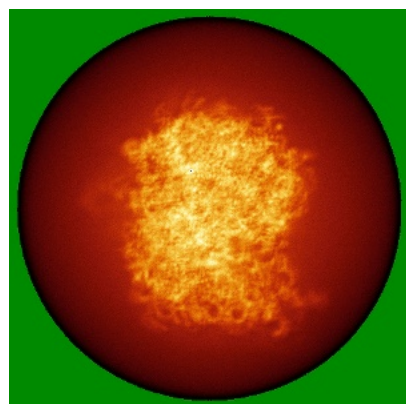


Y

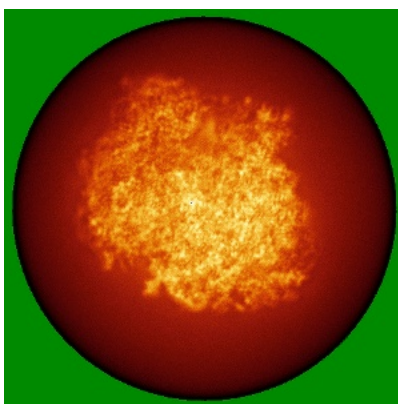


Z

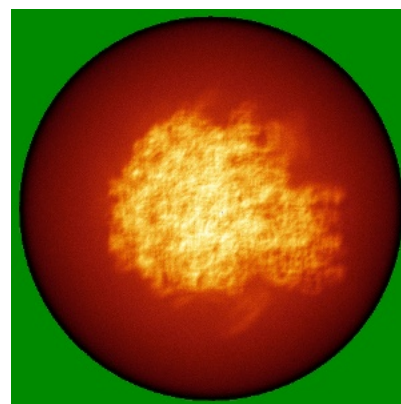
6.4.2 Raw map



X



Y

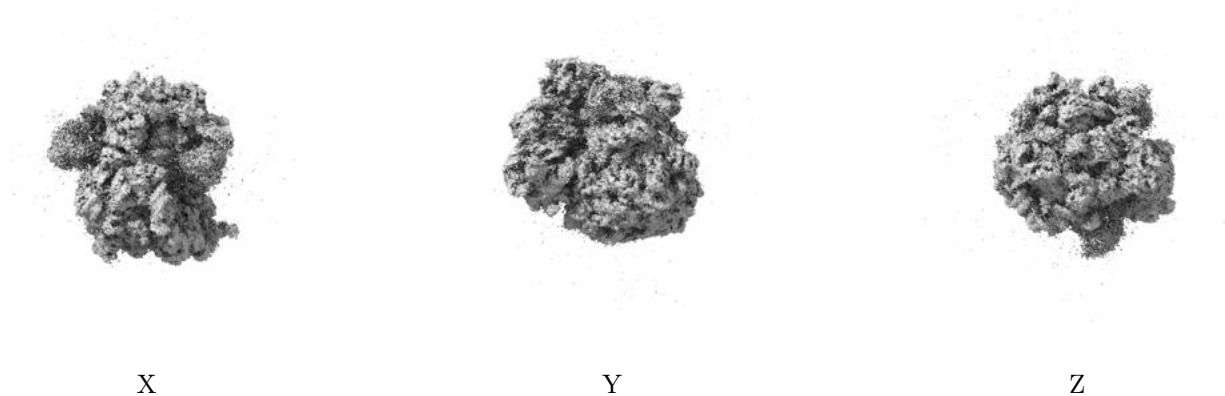


Z

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.

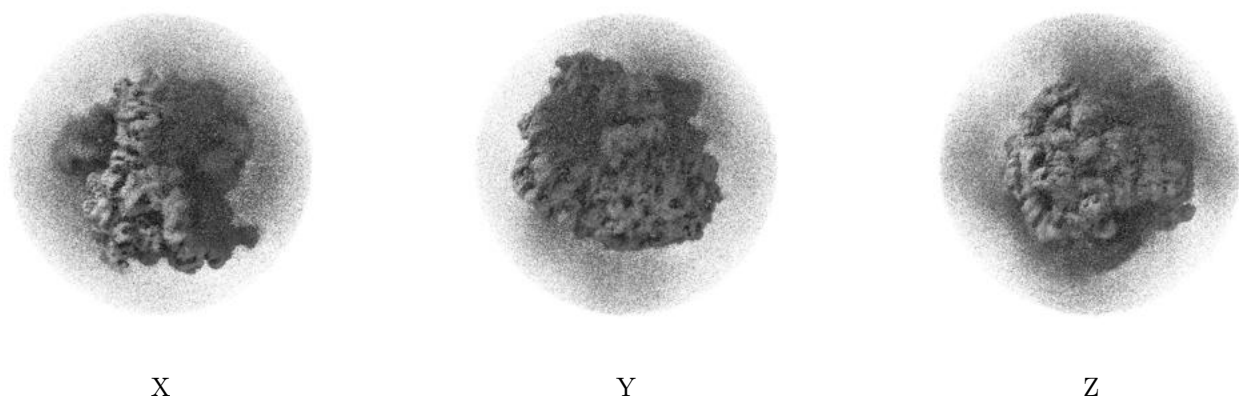
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

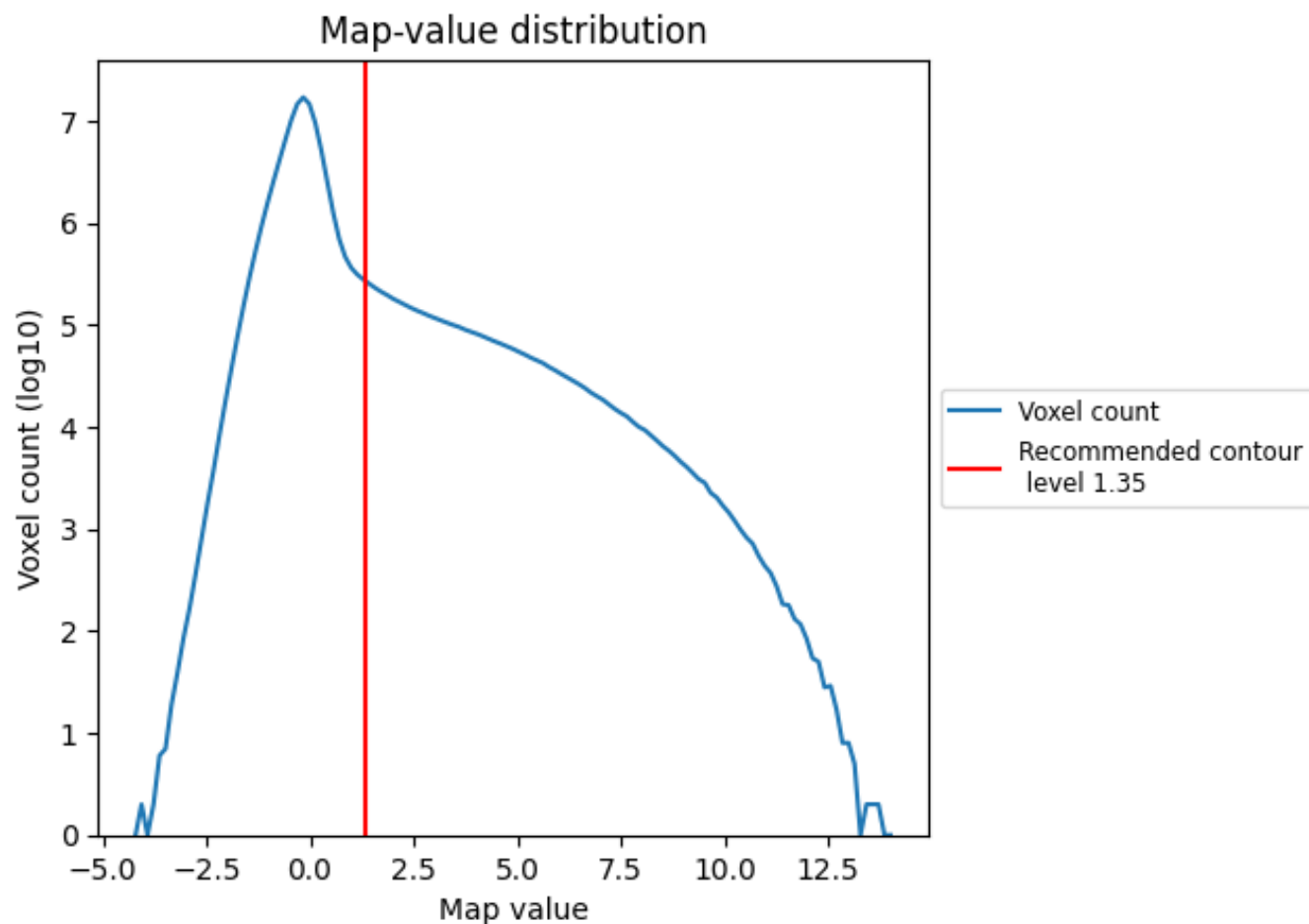
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

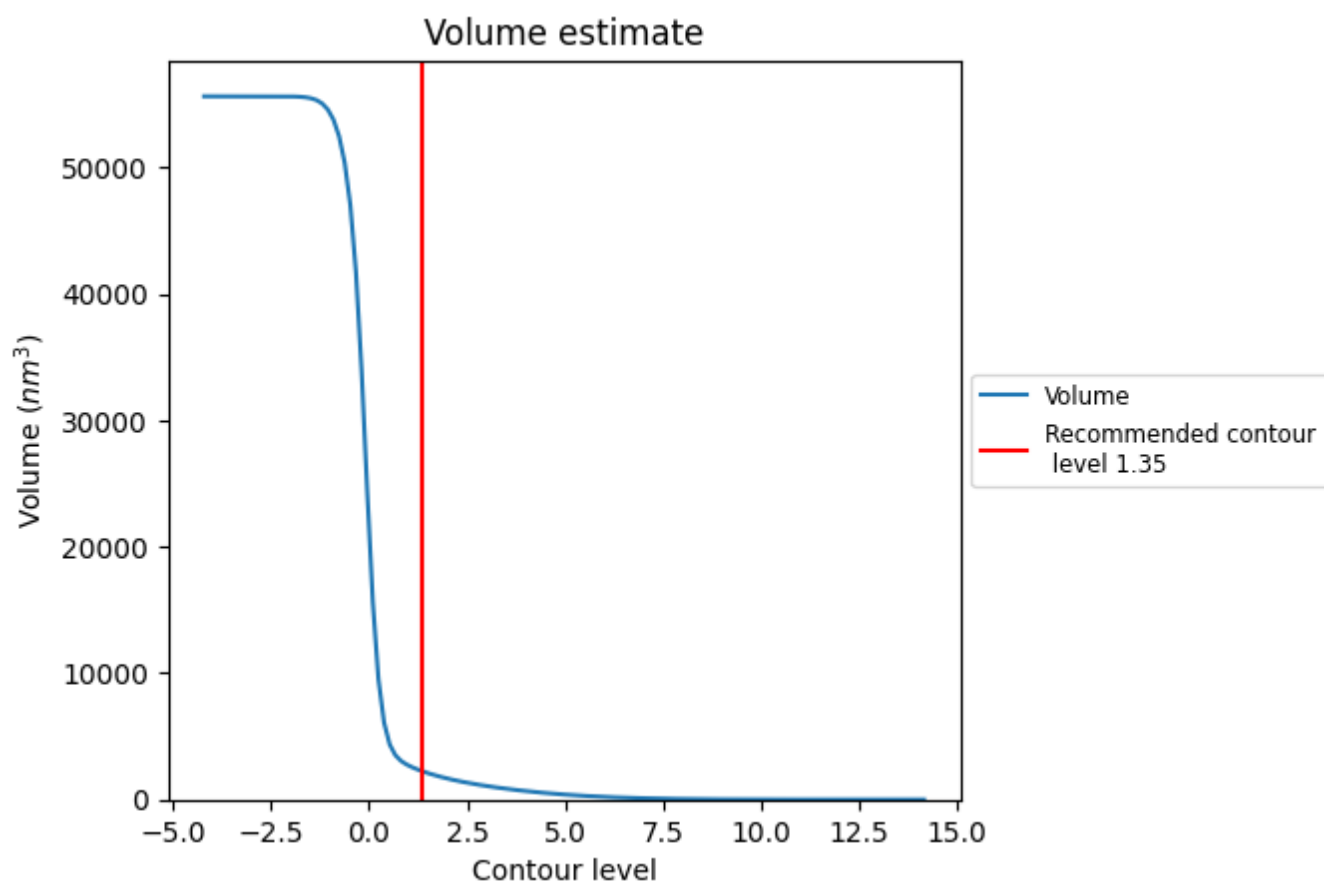
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

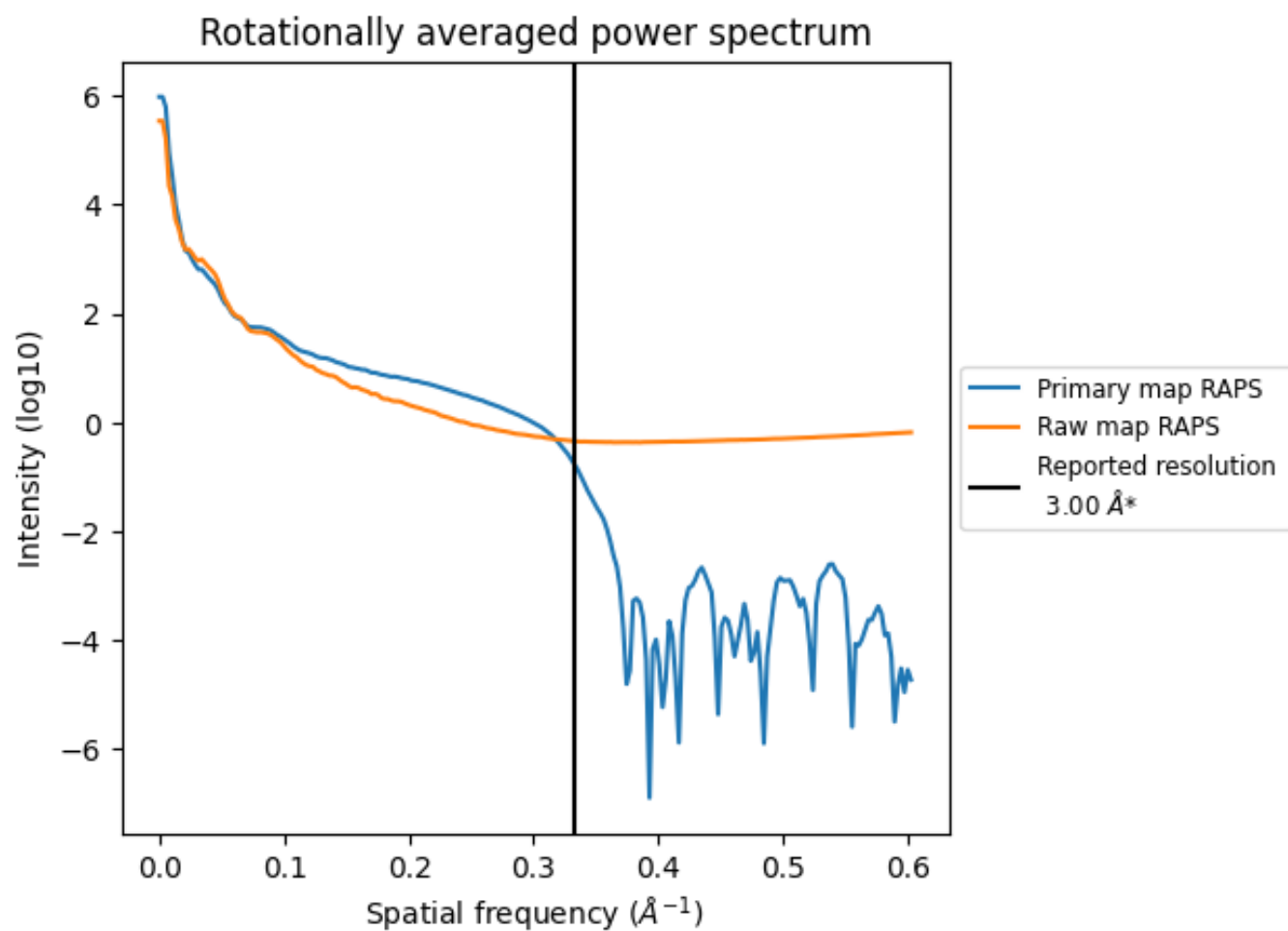
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2252 nm³; this corresponds to an approximate mass of 2034 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 ⓘ

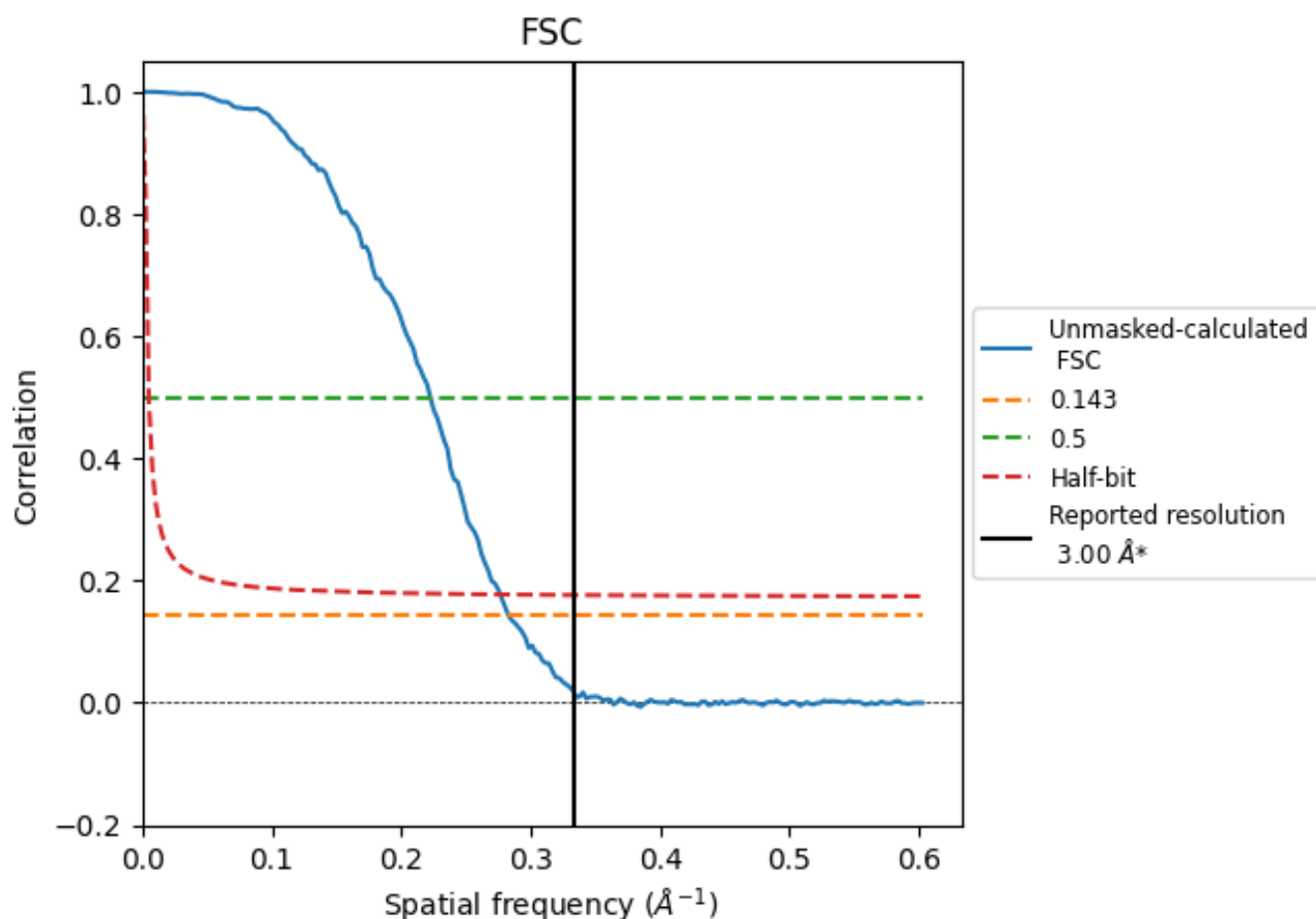


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

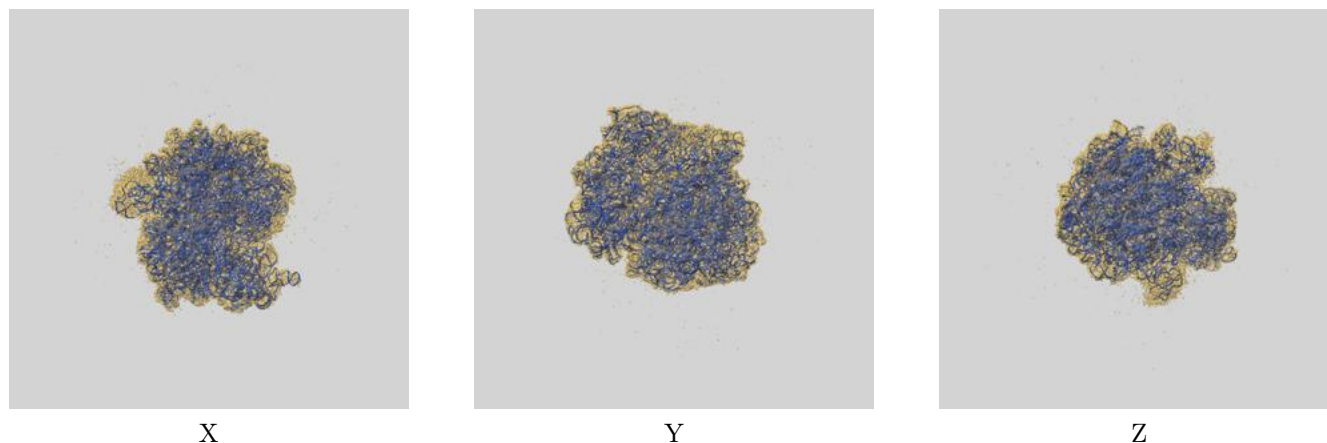
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.54	4.49	3.62

*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 3.54 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

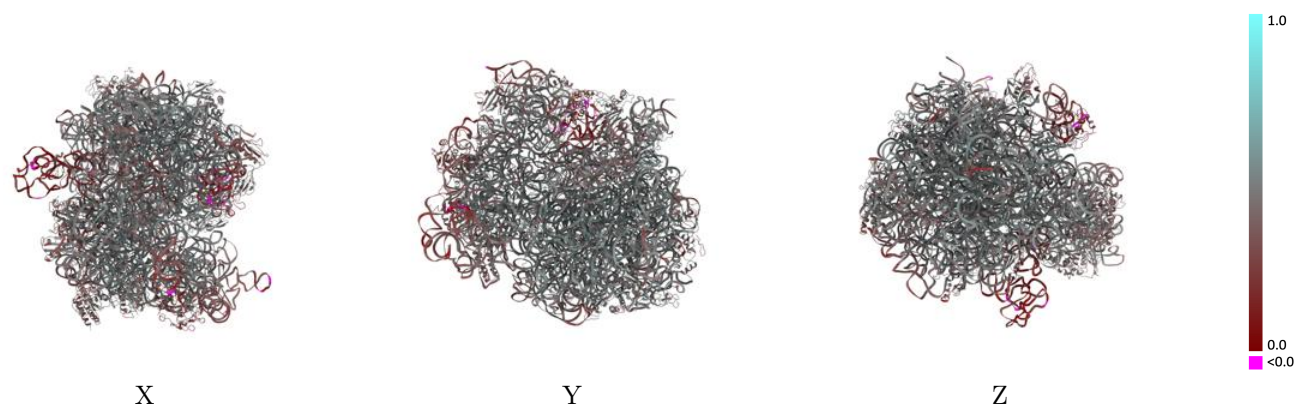
This section contains information regarding the fit between EMDB map EMD-25420 and PDB model 7ST6. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



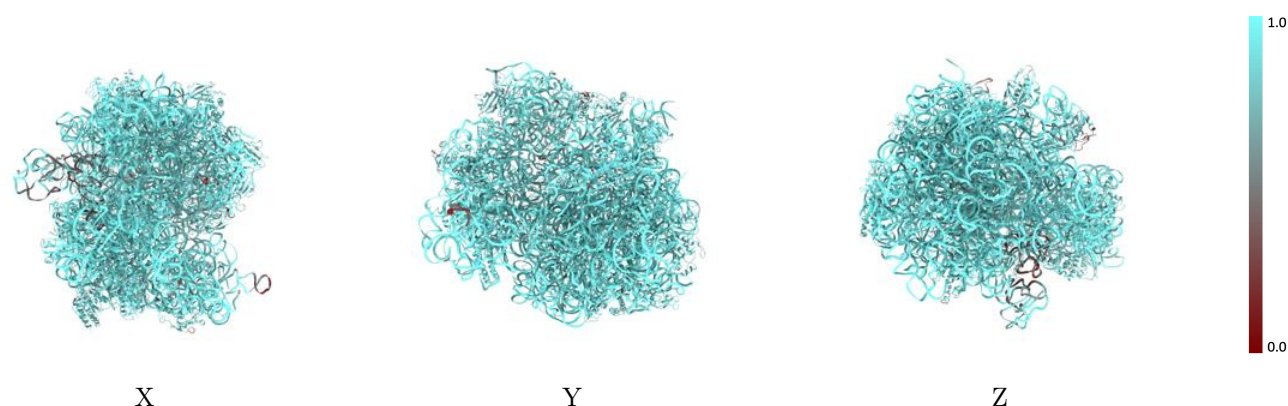
The images above show the 3D surface view of the map at the recommended contour level 1.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



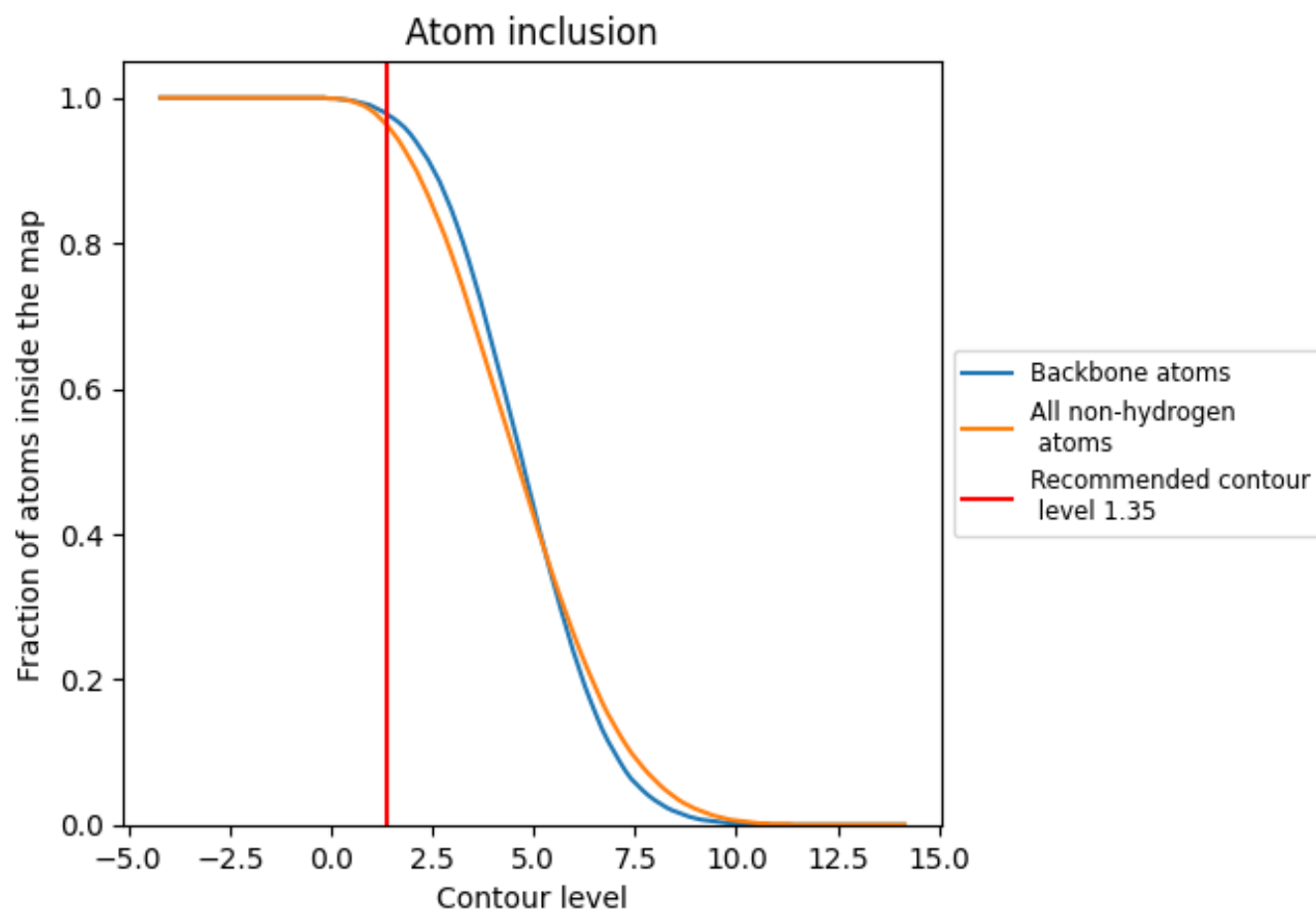
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.35).

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

Chain	Atom inclusion	Q-score
All	 0.9640	 0.4500
1	 0.9870	 0.4610
2	 0.9950	 0.4690
3	 0.9860	 0.4510
4	 0.9510	 0.3680
5	 0.9900	 0.4360
6	 0.9970	 0.4620
7	 0.3890	 0.2140
A	 0.9040	 0.3850
B	 0.9790	 0.4930
C	 0.9500	 0.4560
D	 0.9780	 0.4940
E	 0.9780	 0.5100
F	 0.9490	 0.4910
G	 0.8810	 0.3980
H	 0.8840	 0.4570
I	 0.8650	 0.3460
J	 0.9490	 0.4680
K	 0.9550	 0.4000
L	 0.9130	 0.3990
M	 0.9500	 0.4620
N	 0.9110	 0.4140
O	 0.8160	 0.4130
P	 0.9630	 0.4590
Q	 0.9260	 0.4210
R	 0.9390	 0.4240
S	 0.9300	 0.4350
T	 0.9830	 0.4460
U	 0.9030	 0.4020
V	 0.9750	 0.4120
W	 0.9710	 0.4410
X	 0.9240	 0.4300
Y	 0.9180	 0.3950
Z	 0.8710	 0.3280
b	 0.9790	 0.5090



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Chain	Atom inclusion	Q-score
c	 0.9750	 0.4970
d	 0.9340	 0.4470
e	 0.9510	 0.4240
f	 0.9180	 0.4110
g	 0.8320	 0.3760
i	 0.7020	 0.1810
j	 0.9710	 0.4920
k	 0.9650	 0.5000
l	 0.9690	 0.4910
m	 0.9760	 0.5060
n	 0.9720	 0.4800
o	 0.9640	 0.4540
p	 0.9540	 0.4980
q	 0.9650	 0.4870
r	 0.9330	 0.4780
s	 0.9680	 0.4690
t	 0.9590	 0.4510
u	 0.9350	 0.4380
v	 0.9430	 0.4720
w	 0.9930	 0.5200
x	 0.9750	 0.4840
y	 0.9030	 0.3840
z	 0.9540	 0.4810