



Full wwPDB EM Validation Report ⓘ

Nov 6, 2022 – 09:29 AM EST

PDB ID : 6DZI
EMDB ID : EMD-8932
Title : Cryo-EM Structure of Mycobacterium smegmatis 70S C(minus) ribosome 70S-MPY complex
Authors : Sharma, M.R.; Li, Y.; Korripella, R.; Yang, Y.; Kaushal, P.S.; Lin, Q.; Wade, J.T.; Gray, A.G.; Derbyshire, K.M.; Agrawal, R.K.; Ojha, A.
Deposited on : 2018-07-05
Resolution : 3.46 Å(reported)

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

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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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

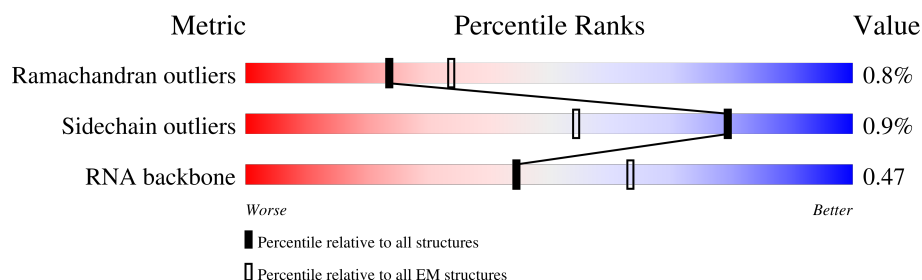
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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.



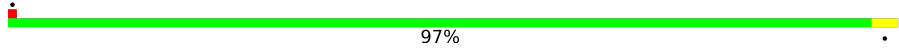
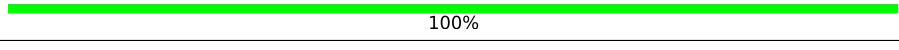
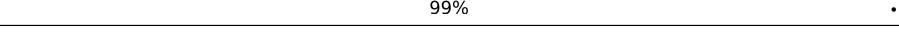
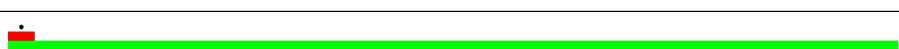
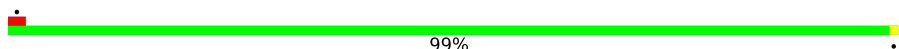
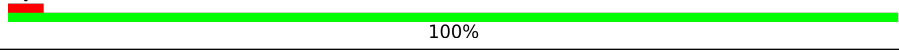
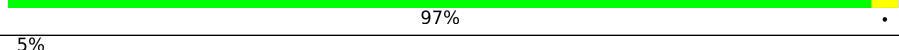
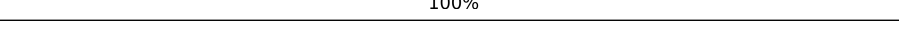


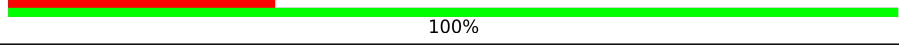
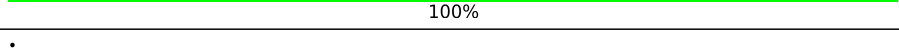

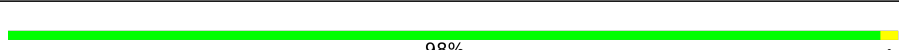
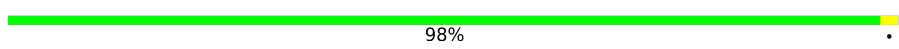
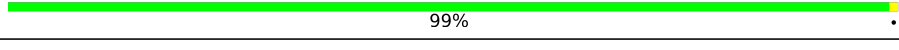
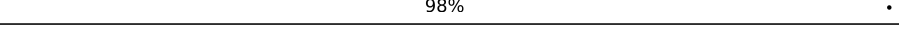

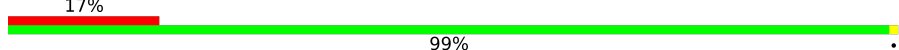
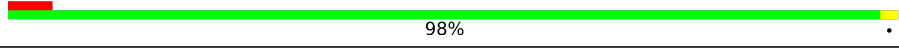
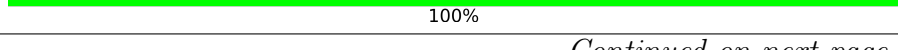



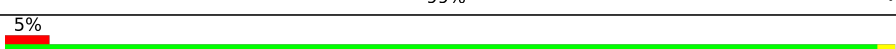
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	h	1511	
2	j	32	
3	k	208	
4	l	200	
5	m	180	
6	n	96	
7	p	155	
8	q	131	


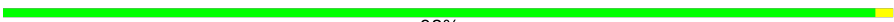









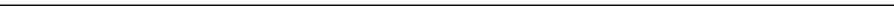


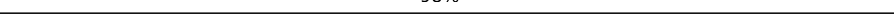
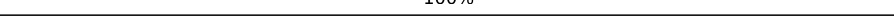
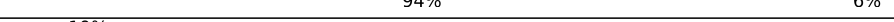

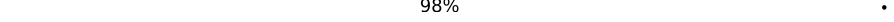
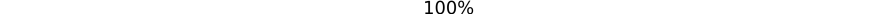
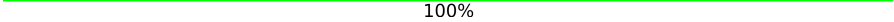


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Mol	Chain	Length	Quality of chain
9	4	126	 97%
10	s	99	 100%
11	t	115	 99%
12	u	122	 98%
13	v	116	 100%
14	x	88	 99%
15	z	113	 100%
16	5	94	 97%
17	6	82	 100%
18	7	85	 95%
19	8	228	 83%
20	r	84	 100%
21	Y	103	 100%
22	9	100	 100%
23	A	3119	 69%
24	B	118	 79%
25	C	275	 98%
26	D	214	 98%
27	E	209	 99%
28	F	182	 98%
29	G	176	 99%
30	H	151	 99%
31	I	126	 99%
32	J	133	 98%
33	K	146	 100%

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Mol	Chain	Length	Quality of chain
34	L	122	 100%
35	M	145	 98% .
36	N	136	 99% ..
37	O	118	 100%
38	P	126	 98% .
39	Q	113	 96% . .
40	R	124	 100%
41	S	100	 99% .
42	T	114	 97% .
43	U	97	 100%
44	V	105	 91% . 8%
45	W	192	 99% .
46	X	79	 97% .
47	Z	64	 98% .
48	a	59	 100%
49	b	54	 94% 6%
50	c	53	 19% 79% 19% .
51	d	46	 98% .
52	e	63	 100%
53	f	37	 100%
54	g	82	 82% 10% 9%
55	y	77	 83% 14% .
56	3	23	 100%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 150868 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	h	1511	Total	C	N	O	P	0	0
			32439	14448	5930	10550	1511		

- Molecule 2 is a protein called CONSERVED PROTEIN DOMAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	k	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	l	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	m	180	Total	C	N	O	S	0	0
			1296	812	245	235	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	n	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	p	155	Total	C	N	O	S	0	0
			1232	768	241	221	2		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	4	126	Total	C	N	O	0	0
			994	630	194	170		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	s	99	Total	C	N	O	S	0	0
			788	495	146	144	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	t	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	u	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	v	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	x	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	z	113	Total	C	N	O	0	0
			891	570	162	159		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	5	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 17 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	6	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	7	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 19 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	8	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 20 is a protein called 30S ribosomal protein S18 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r	84	Total	C	N	O	S	0	0
			659	408	131	116	4		

- Molecule 21 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Y	103	Total	C	N	O	S	0	0
			861	529	175	155	2		

- Molecule 22 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	9	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 23 is a RNA chain called 23 S rRNA (3119-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	3119	Total	C	N	O	P	0	0
			66981	29854	12313	21695	3119		

- Molecule 24 is a RNA chain called 5S RNA (118-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	151	Total	C	N	O	S	0	0
			1119	695	209	214	1		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	100	Total	C	N	O		0	0
			754	478	137	139			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 48 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 50 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	c	53	Total	C	N	O	S	0	0
			456	281	97	78			

- Molecule 51 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 52 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	e	63	Total	C	N	O	S	0	0
			502	302	115	85			

- Molecule 53 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	g	75	Total	C	N	O	S	0	0
			593	379	103	110	1		

- Molecule 55 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	77	Total	C	N	O	S	0	0
			617	377	132	106	2		

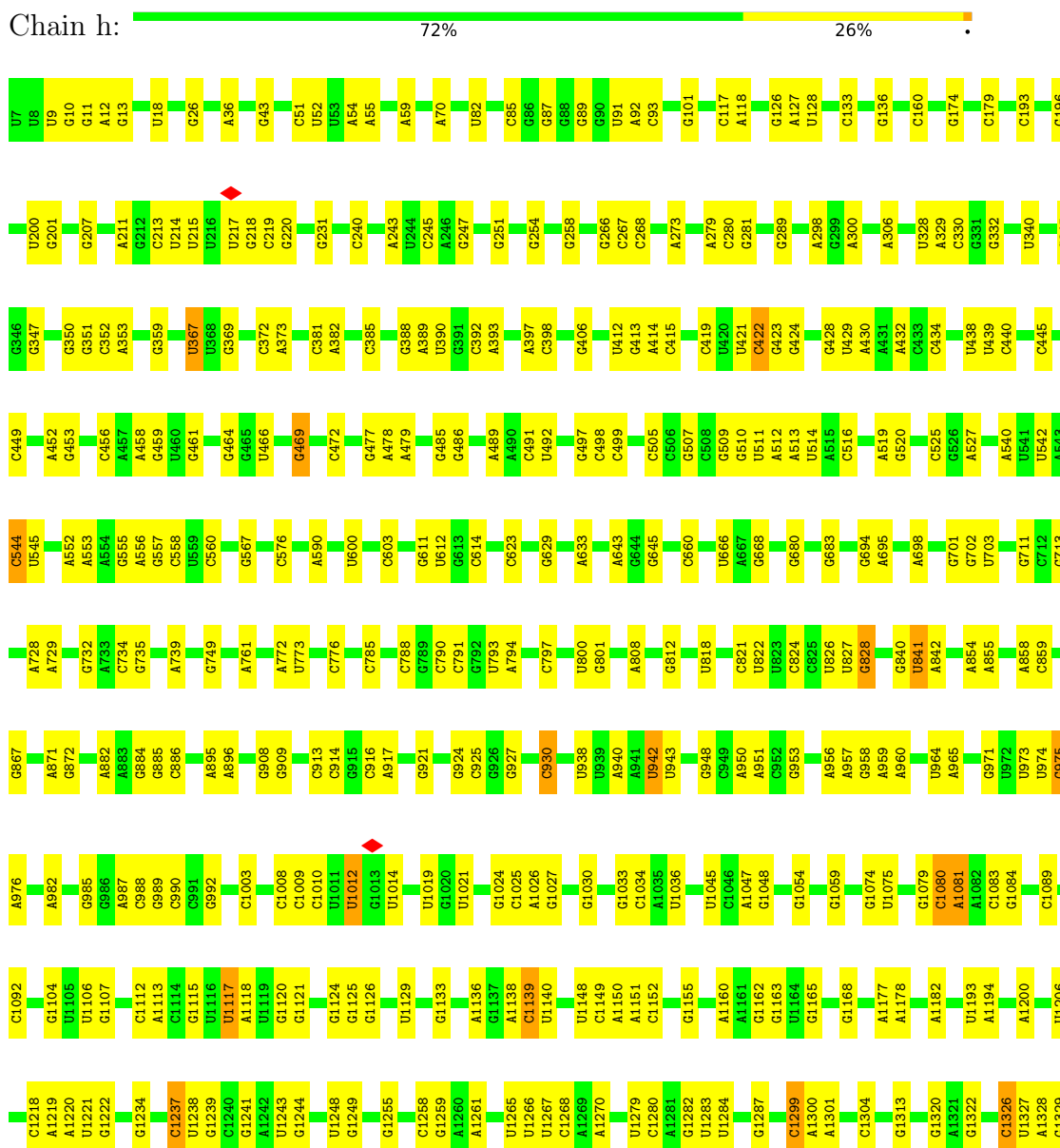
- Molecule 56 is a protein called Uncharacterized protein.

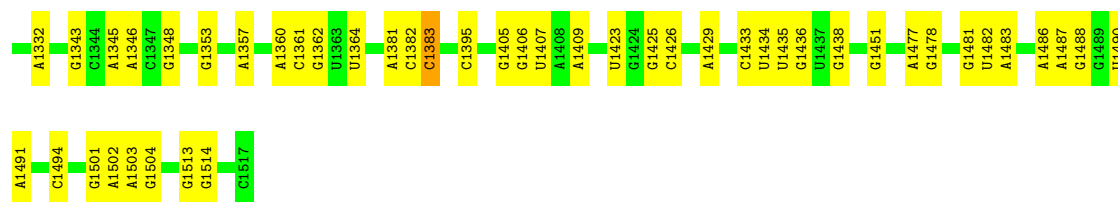
Mol	Chain	Residues	Atoms				AltConf	Trace
56	3	23	Total	C	N	O	0	0
			189	111	50	28		

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

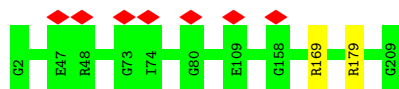




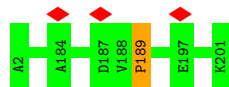
• Molecule 2: CONSERVED PROTEIN DOMAIN



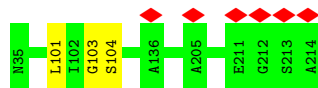
• Molecule 3: 30S ribosomal protein S3



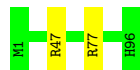
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

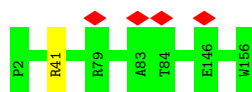


• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7





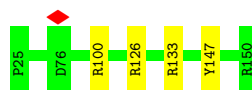
- Molecule 8: 30S ribosomal protein S8

Chain q: 98%



- Molecule 9: 30S ribosomal protein S9

Chain 4: 97%



- Molecule 10: 30S ribosomal protein S10

Chain s: 100%

There are no outlier residues recorded for this chain.

- Molecule 11: 30S ribosomal protein S11

Chain t: 99%



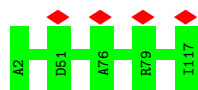
- Molecule 12: 30S ribosomal protein S12

Chain u: 98%



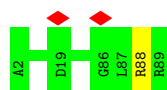
- Molecule 13: 30S ribosomal protein S13

Chain v: 100%

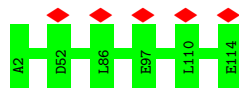


- Molecule 14: 30S ribosomal protein S15

Chain x: 99%



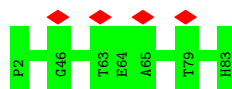
- Molecule 15: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S17



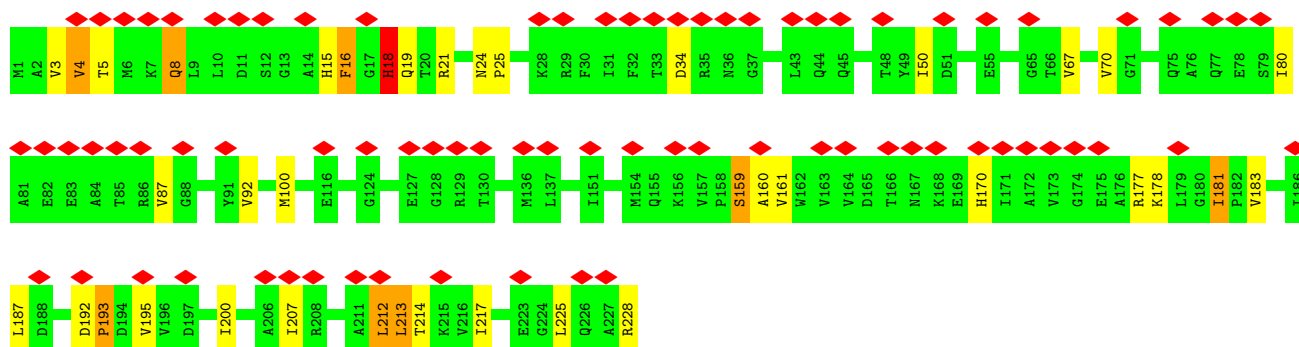
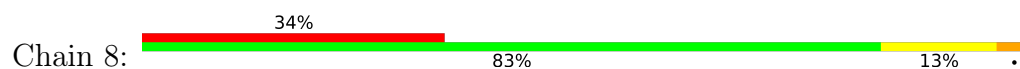
- Molecule 17: 30S ribosomal protein S19



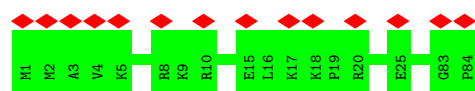
- Molecule 18: 30S ribosomal protein S20



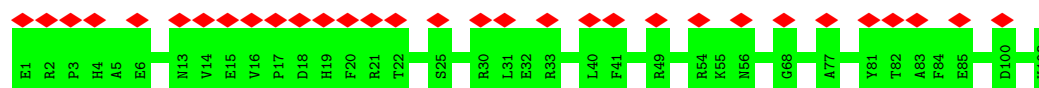
- Molecule 19: 30S ribosomal protein S2



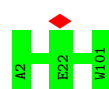
- Molecule 20: 30S ribosomal protein S18 1



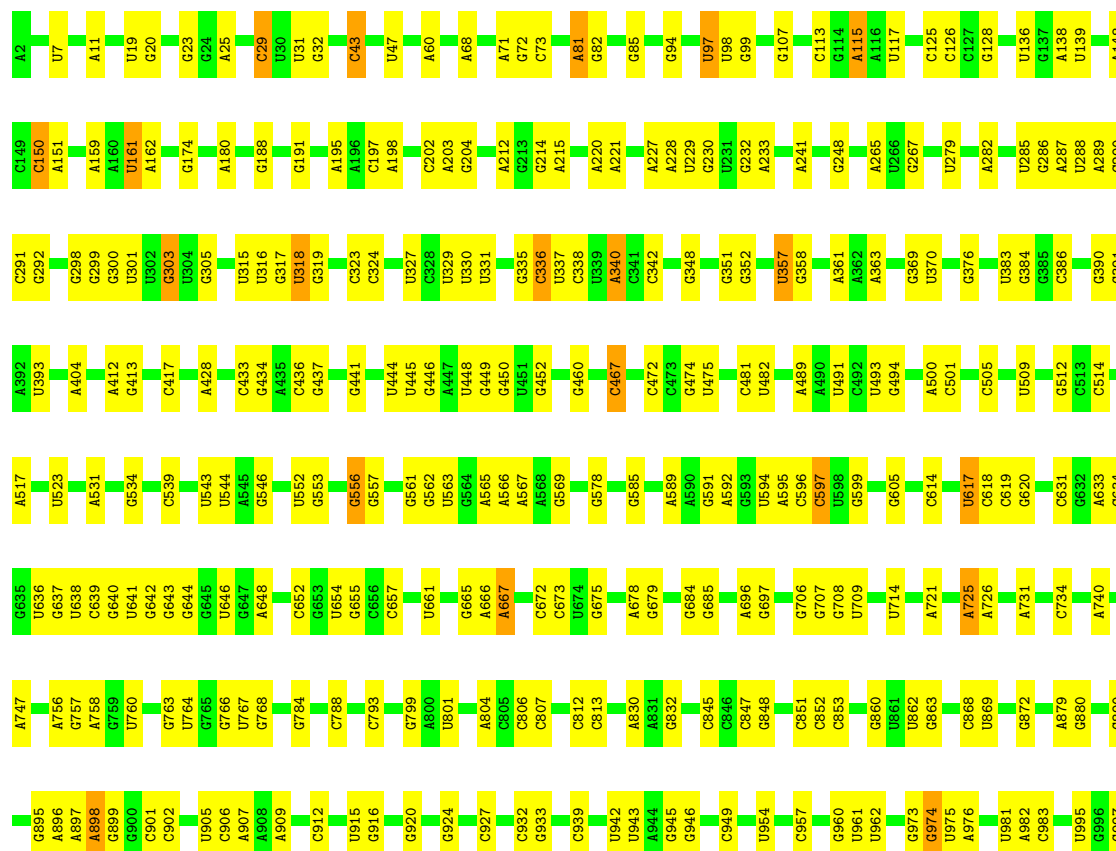
- Molecule 21: Ribosome hibernation promoting factor



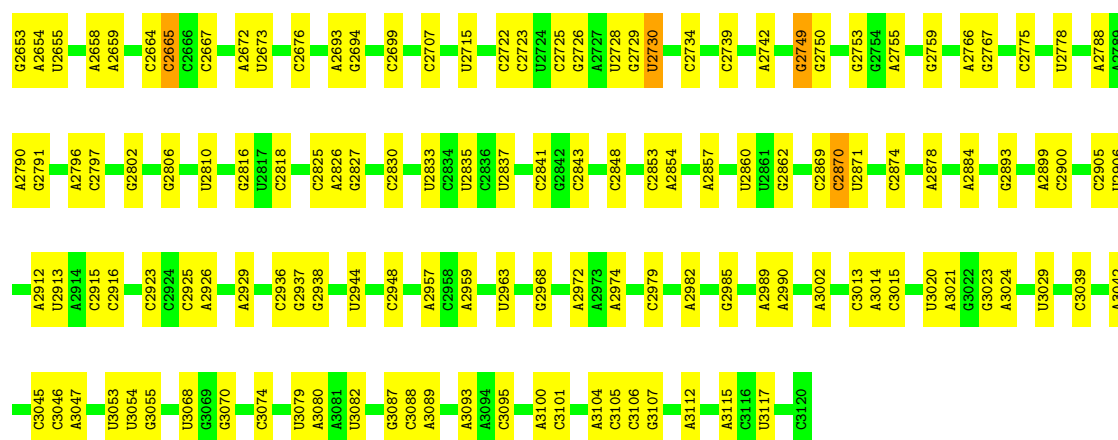
- Molecule 22: 30S ribosomal protein S14



- Molecule 23: 23 S rRNA (3119-MER)



A2492	G2367	C2274	U2167	A2026	G1891	G1754	G1625	C1558	G1462	G1343	A1216	A1119	C1001
G2503	C2368	A2275	U2168	A2027	G1892	A1755	G1626	A1559	G1463	A1344	U1219	G1120	C1002
C2507	U2373	G2276	G2169	U2033	C1893	U1756	A1627	U1560	C1465	G1345	U1219	G1121	C1003
C2509	G2375	G2280	G2178	A2036	A1894	U1757	A1628	C1561	C1466	A1352	U1223	G1122	C1004
A2510	G2380	U2374	U2180	U2036	C1901	G1760	U1630	C1562	C1472	A1353	G1224	G1123	C1005
A2511	G2385	G2284	C2181	C2043	C1902	U1767	G1632	A1564	G1473	G1359	U1226	C1124	G1006
C2519	A2380	G2285	A2184	A2046	C1909	C1775	G1637	A1565	A1480	A1362	G1230	G1130	G1007
U2520	C2381	C2286	C2185	C2047	C1912	A1778	G1639	A1566	C1481	U1234	U1234	G1131	A1011
C2521	U2382	C2287	C2191	G2048	A1916	U1787	A1648	C1567	G1492	U1235	U1235	G1140	U1013
G2528	C2383	C2288	C2191	C2049	G1917	G1788	G1649	C1568	A1499	G1238	G1238	U1141	G1014
A2529	U2384	C2289	C2191	C2050	G1918	A1790	G1650	A1569	A1500	G1239	G1240	G1142	A1015
C2530	C2385	G2290	C2191	U2061	G1921	A1791	G1658	A1570	C1501	A1144	A1144	C1022	C1022
G2531	G2386	U2387	A2194	U2062	A1925	G1793	G1674	C1571	G1507	U1151	U1151	U1151	A1025
U2532	U2387	U2195	G1917	U2063	A1931	C1801	G1674	C1572	A1508	U1152	U1152	U1152	A1026
C2533	U2388	C2294	G1918	C2064	U1946	G1802	A1679	C1573	U1509	U1153	U1153	U1153	C1027
A2534	U2389	C2295	G1918	A2065	U1947	A1803	A1680	C1574	A1510	A1164	A1164	U1157	U1028
U2535	G2390	C2296	C2198	C2066	U1948	A1813	U1681	C1575	A1511	G1165	G1165	U1157	C1029
A2536	G2391	U2390	G2199	U2066	C1949	C1813	G1688	C1576	U1512	U1244	U1244	U1157	C1030
G2549	A2392	U2315	C2203	U2086	A1931	C1801	G1674	C1577	C1513	U1245	U1245	U1157	U1034
C2556	A2393	G2316	U2215	C2087	U1946	G1802	A1679	C1578	A1518	U1246	U1246	U1157	G1035
A2559	U2394	U2316	G2216	C2088	U1947	A1803	A1680	C1579	A1522	A1261	A1261	C1171	C1046
G2560	C2395	U2317	U2217	C2089	U1948	A1813	U1681	C1580	U1523	U1262	U1262	G1173	C1047
U2561	U2396	C2318	U2218	U2090	C1949	C1822	U1688	C1581	G1524	U1267	U1267	U1178	A1048
C2566	G2397	U2319	U2219	U2091	G1950	A1822	G1696	C1582	U1525	U1267	U1267	U1179	G1049
U2567	U2401	C2320	U2220	C2093	U1968	C1823	G1703	C1583	U1526	U1270	U1270	U1179	A1058
C2568	C2402	U2321	A2221	G2094	U1968	C1824	U1713	C1584	G1527	G1271	G1271	G1180	U1184
U2569	U2403	C2322	C2223	G2096	C1971	C1825	A1710	C1585	U1528	G1272	G1272	U1184	A1062
C2571	C2407	C2224	C2224	C2096	A1972	C1826	G1711	C1586	G1529	G1273	G1273	U1184	A1063
U2574	G2408	C2230	C2230	A2106	C1973	C1830	G1712	C1587	U1530	G1276	G1276	U1185	G1063
U2585	U2411	C2233	G2233	U2112	A1975	A1834	U1716	C1588	U1531	C1277	C1277	U1186	U1075
G2596	G2412	C2234	C2234	A2124	U1979	C1835	U1717	C1589	C1534	C1290	C1290	A1187	A1076
A2601	C2419	C2235	C2235	U2139	G1960	C1835	U1717	C1590	C1535	A1415	A1415	G1188	A1077
U2605	U2420	C2241	U2241	A2141	U1981	C1843	G1720	C1591	C1536	G1291	G1291	G1189	G1078
G2606	A2421	C2242	C2242	U2141	A1990	A1852	G1724	C1592	U1537	U1292	U1292	A1191	C1081
C2607	U2434	C2243	C2243	A2136	C1991	C1856	G1724	C1593	U1538	U1294	U1294	G1192	C1082
G2608	U2435	C2244	C2244	A2137	U1992	C1857	G1727	C1594	A1539	C1298	C1298	U1200	G1083
A2609	U2437	C2245	C2245	C2138	C1998	U1857	U1728	C1595	U1540	G1302	G1302	A1201	U1084
C2610	U2449	C2246	C2246	C2139	C2003	U1864	A1729	C1596	U1544	U1303	U1303	A1202	G1085
U2626	C2450	C2247	C2247	A2141	A2004	C1866	A1731	C1597	C1545	C1311	C1311	A1203	C1089
G2639	G2462	C2248	C2248	U2141	C2005	C1866	A1731	C1598	C1546	G1302	G1302	G1205	G1090
U2643	U2463	C2249	C2249	U2141	C2005	C1866	A1731	C1599	U1547	U1303	U1303	G1207	A1091
U2647	U2468	C2250	C2250	A2152	A2008	G1871	G1736	C1600	G1550	U1320	U1320	U1208	G1092
C2648	A2490	C2251	C2251	G2153	C2016	A1872	A1737	G1601	U1551	U1326	U1326	A1101	A1101
A2649	U2491	C2252	C2252	U2155	C2017	A1874	G1738	G1602	A1552	G1332	G1332	G1102	C1103
		C2253	C2253	U2155	C2018	C1878	G1746	G1603	U1553	U1339	U1339	C1104	C1104
		C2254	C2254	U2155	C2018	C1878	G1746	G1604	U1554			U1212	G1102
		C2255	C2255	U2155	C2018	C1878	G1746	G1605	A1555			A1213	C1103
		C2256	C2256	U2155	C2018	C1878	G1746	G1606	A1556			A1214	C1104
		C2257	C2257	U2155	C2018	C1878	G1746	G1607	C1557			U1215	G1114
		C2258	C2258	U2155	C2018	C1878	G1746	G1608					
		C2259	C2259	U2155	C2018	C1878	G1746	G1609					
		C2260	C2260	U2155	C2018	C1878	G1746	G1610					
		C2261	C2261	U2155	C2018	C1878	G1746	G1611					
		C2262	C2262	U2155	C2018	C1878	G1746	G1612					
		C2263	C2263	U2155	C2018	C1878	G1746	G1613					
		C2264	C2264	U2155	C2018	C1878	G1746	G1614					
		C2265	C2265	U2155	C2018	C1878	G1746	G1615					
		C2266	C2266	U2155	C2018	C1878	G1746	G1616					
		C2267	C2267	U2155	C2018	C1878	G1746	G1617					
		C2268	C2268	U2155	C2018	C1878	G1746	G1618					
		C2269	C2269	U2155	C2018	C1878	G1746	G1619					
		C2270	C2270	U2155	C2018	C1878	G1746	G1620					
		C2271	C2271	U2155	C2018	C1878	G1746	G1621					
		C2272	C2272	U2155	C2018	C1878	G1746	G1622					
		C2273	C2273	U2155	C2018	C1878	G1746	G1623					
		C2274	C2274	U2155	C2018	C1878	G1746	G1624					



• Molecule 24: 5S RNA (118-MER)

Chain B: 79% 20% .



• Molecule 25: 50S ribosomal protein L2

Chain C: 98% .



• Molecule 26: 50S ribosomal protein L3

Chain D: 98% .



• Molecule 27: 50S ribosomal protein L4

Chain E: 99% .



• Molecule 28: 50S ribosomal protein L5

Chain F: 98% .



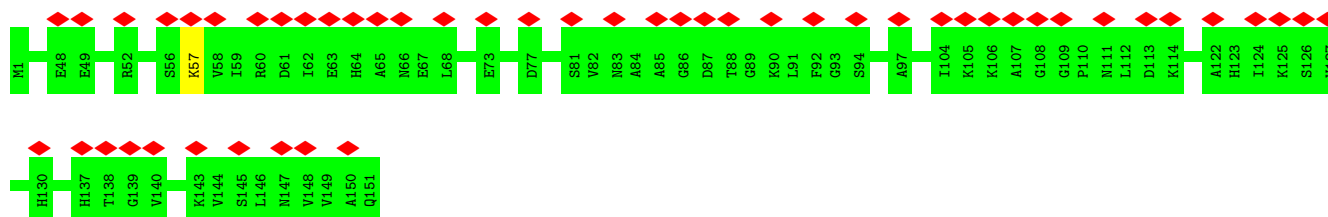
• Molecule 29: 50S ribosomal protein L6

Chain G:  99%



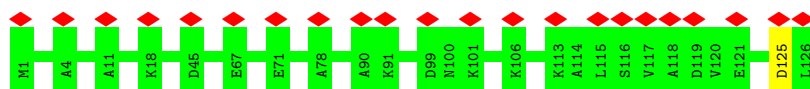
- Molecule 30: 50S ribosomal protein L9

Chain H:  99%



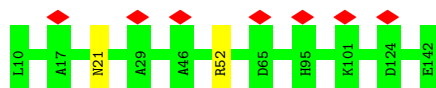
- Molecule 31: 50S ribosomal protein L10

Chain I:  99%



- Molecule 32: 50S ribosomal protein L11

Chain J:  98%



- Molecule 33: 50S ribosomal protein L13

Chain K:  100%

There are no outlier residues recorded for this chain.

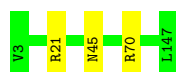
- Molecule 34: 50S ribosomal protein L14

Chain L:  100%

There are no outlier residues recorded for this chain.

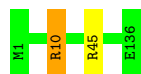
- Molecule 35: 50S ribosomal protein L15

Chain M:  98%



- Molecule 36: 50S ribosomal protein L16

Chain N:  99% ..



- Molecule 37: 50S ribosomal protein L17

Chain O:  100%

There are no outlier residues recorded for this chain.

- Molecule 38: 50S ribosomal protein L18

Chain P:  98% .



- Molecule 39: 50S ribosomal protein L19

Chain Q:  96% ..



- Molecule 40: 50S ribosomal protein L20

Chain R:  100%

There are no outlier residues recorded for this chain.

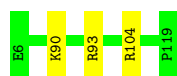
- Molecule 41: 50S ribosomal protein L21

Chain S:  99% .



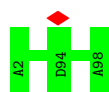
- Molecule 42: 50S ribosomal protein L22

Chain T:  97% .

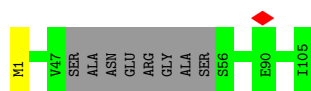
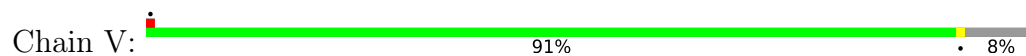


- Molecule 43: 50S ribosomal protein L23

Chain U:  100%



- Molecule 44: 50S ribosomal protein L24



- Molecule 45: 50S ribosomal protein L25



- Molecule 46: 50S ribosomal protein L27



- Molecule 47: 50S ribosomal protein L29



- Molecule 48: 50S ribosomal protein L30

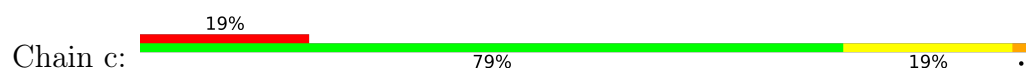


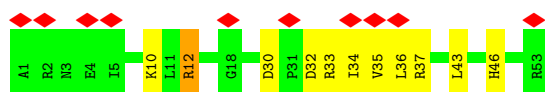
There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L32



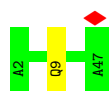
- Molecule 50: 50S ribosomal protein L33 2





- Molecule 51: 50S ribosomal protein L34

Chain d: 98%



- Molecule 52: 50S ribosomal protein L35

Chain e: 100%

There are no outlier residues recorded for this chain.

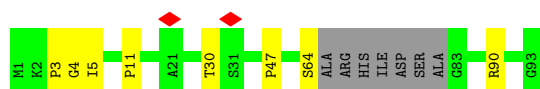
- Molecule 53: 50S ribosomal protein L36

Chain f: 100%

There are no outlier residues recorded for this chain.

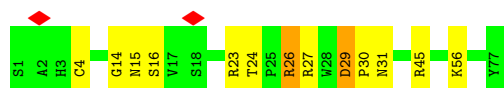
- Molecule 54: 50S ribosomal protein L31

Chain g: 82% 10% 9%



- Molecule 55: 50S ribosomal protein L28

Chain y: 83% 14%



- Molecule 56: Uncharacterized protein

Chain 3: 100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	66840	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 ($e^-/\text{\AA}^2$)	67.10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.313	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	485.78003, 485.78003, 485.78003	wwPDB
Map dimensions	454, 454, 454	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	h	0.75	0/36309	1.06	78/56657 (0.1%)
2	j	0.54	0/280	0.87	0/359
3	k	0.37	0/1684	0.62	0/2261
4	l	0.38	0/1672	0.65	0/2251
5	m	0.42	0/1312	0.63	0/1772
6	n	0.44	0/782	0.61	0/1059
7	p	0.35	0/1252	0.67	0/1690
8	q	0.44	0/1025	0.65	1/1385 (0.1%)
9	4	0.34	0/1012	0.66	0/1362
10	s	0.35	0/802	0.62	0/1086
11	t	0.42	0/873	0.65	0/1180
12	u	0.47	0/969	0.79	2/1294 (0.2%)
13	v	0.35	0/942	0.72	0/1260
14	x	0.47	0/729	0.73	0/977
15	z	0.41	0/908	0.65	0/1226
16	5	0.42	0/759	0.69	0/1016
17	6	0.37	0/680	0.62	0/915
18	7	0.44	0/663	0.65	0/882
19	8	0.46	0/1822	1.21	28/2457 (1.1%)
20	r	0.41	0/665	0.72	0/889
21	Y	0.36	0/875	0.67	0/1169
22	9	0.36	0/830	0.65	0/1106
23	A	1.26	88/75001 (0.1%)	1.23	313/117027 (0.3%)
24	B	0.99	0/2821	1.12	5/4396 (0.1%)
25	C	0.76	1/2153 (0.0%)	0.77	4/2895 (0.1%)
26	D	0.80	0/1609	0.79	1/2165 (0.0%)
27	E	0.66	0/1592	0.67	1/2153 (0.0%)
28	F	0.49	0/1467	0.67	0/1973
29	G	0.53	0/1369	0.70	1/1848 (0.1%)
30	H	0.42	0/1129	0.75	0/1524
31	I	0.34	0/925	0.58	0/1246
32	J	0.34	0/1006	0.62	0/1364
33	K	0.71	0/1157	0.65	0/1567
34	L	0.80	0/946	0.74	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.70	0/1091	0.76	1/1457 (0.1%)
36	N	0.70	0/1118	0.75	2/1506 (0.1%)
37	O	0.75	0/945	0.73	0/1267
38	P	0.60	0/966	0.74	1/1298 (0.1%)
39	Q	0.80	1/921 (0.1%)	0.73	1/1236 (0.1%)
40	R	0.86	0/1000	0.75	0/1341
41	S	0.69	0/764	0.63	0/1030
42	T	0.76	0/887	0.76	0/1204
43	U	0.68	0/766	0.64	0/1030
44	V	0.55	0/738	0.63	0/987
45	W	0.52	0/1443	0.64	0/1970
46	X	0.80	0/595	0.73	0/798
47	Z	0.60	0/534	0.74	1/713 (0.1%)
48	a	0.70	0/477	0.69	0/640
49	b	0.67	0/427	0.79	1/572 (0.2%)
50	c	0.50	0/463	0.88	1/621 (0.2%)
51	d	0.84	0/380	0.99	2/500 (0.4%)
52	e	0.69	0/507	0.75	0/672
53	f	0.85	0/303	0.71	0/401
54	g	0.42	0/613	0.76	2/835 (0.2%)
55	y	0.53	0/629	0.82	1/843 (0.1%)
56	3	0.72	0/191	0.79	0/247
All	All	0.98	90/163778 (0.1%)	1.07	447/244847 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	l	0	1
19	8	0	10
26	D	0	1
32	J	0	1
45	W	0	1
All	All	0	14

All (90) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	Q	50	GLN	CA-CB	-8.43	1.35	1.53
23	A	1081	C	N1-C6	-6.45	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2841	C	N1-C6	-6.26	1.33	1.37
23	A	901	C	N1-C6	-6.19	1.33	1.37
23	A	202	C	N1-C6	-6.10	1.33	1.37
23	A	2008	A	N9-C4	-6.04	1.34	1.37
23	A	1376	C	N1-C6	-6.04	1.33	1.37
23	A	1822	C	N1-C6	-6.03	1.33	1.37
23	A	1125	C	N1-C6	-5.97	1.33	1.37
23	A	2223	C	N1-C6	-5.96	1.33	1.37
23	A	2905	C	N1-C6	-5.88	1.33	1.37
23	A	902	C	N1-C6	-5.84	1.33	1.37
23	A	1888	C	C4-C5	-5.80	1.38	1.43
23	A	2915	C	C4-C5	-5.78	1.38	1.43
23	A	1027	C	N1-C6	-5.77	1.33	1.37
23	A	847	C	C4-C5	-5.76	1.38	1.43
23	A	678	A	N7-C5	-5.76	1.35	1.39
23	A	2005	C	C4-C5	-5.72	1.38	1.43
23	A	2667	C	N1-C6	-5.70	1.33	1.37
23	A	197	C	C4-C5	-5.69	1.38	1.43
23	A	2233	G	N9-C8	-5.68	1.33	1.37
23	A	2923	C	N1-C6	-5.68	1.33	1.37
23	A	2830	C	N1-C6	-5.68	1.33	1.37
23	A	799	G	N9-C4	-5.65	1.33	1.38
23	A	793	C	C4-C5	-5.65	1.38	1.43
23	A	2248	C	C4-C5	-5.64	1.38	1.43
23	A	2916	C	N1-C6	-5.62	1.33	1.37
23	A	813	C	N1-C6	-5.60	1.33	1.37
23	A	1413	C	C4-C5	-5.58	1.38	1.43
23	A	848	G	C6-N1	-5.56	1.35	1.39
23	A	2224	C	N1-C6	-5.54	1.33	1.37
23	A	906	C	C4-C5	-5.51	1.38	1.43
23	A	2766	A	C6-N6	-5.50	1.29	1.33
23	A	949	C	N1-C6	-5.47	1.33	1.37
23	A	1866	C	N1-C6	-5.46	1.33	1.37
23	A	678	A	N9-C8	-5.43	1.33	1.37
23	A	675	G	N9-C8	-5.41	1.34	1.37
23	A	1856	C	C4-C5	-5.40	1.38	1.43
23	A	2870	C	C4-C5	-5.40	1.38	1.43
23	A	725	A	N9-C4	-5.38	1.34	1.37
23	A	852	C	C4-C5	-5.38	1.38	1.43
23	A	1874	C	C4-C5	-5.38	1.38	1.43
23	A	2235	C	C4-C5	-5.37	1.38	1.43
23	A	2218	C	C4-C5	-5.30	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2274	C	C4-C5	-5.27	1.38	1.43
23	A	939	C	C4-C5	-5.26	1.38	1.43
23	A	2043	C	N1-C6	-5.23	1.34	1.37
23	A	2220	C	N1-C6	-5.22	1.34	1.37
23	A	1311	C	C4-C5	-5.22	1.38	1.43
23	A	847	C	N1-C6	-5.21	1.34	1.37
23	A	1441	C	C4-C5	-5.21	1.38	1.43
23	A	2049	C	N1-C6	-5.20	1.34	1.37
23	A	788	C	N1-C6	-5.20	1.34	1.37
23	A	1277	C	C4-C5	-5.20	1.38	1.43
23	A	2230	C	C4-C5	-5.18	1.38	1.43
23	A	879	A	C6-N6	-5.18	1.29	1.33
23	A	924	G	N9-C8	-5.18	1.34	1.37
23	A	1466	C	N1-C6	-5.18	1.34	1.37
23	A	2948	C	N1-C6	-5.17	1.34	1.37
25	C	34	VAL	C-N	-5.16	1.22	1.34
23	A	807	C	C4-C5	-5.16	1.38	1.43
23	A	2295	C	N1-C6	-5.16	1.34	1.37
23	A	2260	C	C4-C5	-5.15	1.38	1.43
23	A	2274	C	N3-C4	-5.14	1.30	1.33
23	A	2218	C	N1-C6	-5.14	1.34	1.37
23	A	2234	G	N9-C8	-5.13	1.34	1.37
23	A	678	A	C5-C6	-5.12	1.36	1.41
23	A	932	C	C4-C5	-5.11	1.38	1.43
23	A	939	C	N1-C6	-5.10	1.34	1.37
23	A	2739	C	N1-C6	-5.10	1.34	1.37
23	A	2915	C	N1-C6	-5.09	1.34	1.37
23	A	1445	C	N1-C6	-5.09	1.34	1.37
23	A	1124	C	N1-C6	-5.09	1.34	1.37
23	A	2289	C	C4-C5	-5.08	1.38	1.43
23	A	1272	C	N1-C6	-5.08	1.34	1.37
23	A	1413	C	N1-C6	-5.07	1.34	1.37
23	A	657	C	N1-C6	-5.07	1.34	1.37
23	A	1104	C	N1-C6	-5.07	1.34	1.37
23	A	672	C	C4-C5	-5.07	1.38	1.43
23	A	1124	C	C4-C5	-5.07	1.38	1.43
23	A	806	C	N1-C6	-5.06	1.34	1.37
23	A	2848	C	C4-C5	-5.05	1.39	1.43
23	A	2004	A	N7-C5	-5.04	1.36	1.39
23	A	2253	A	N9-C4	-5.03	1.34	1.37
23	A	1429	C	C4-C5	-5.02	1.39	1.43
23	A	2830	C	C4-C5	-5.02	1.39	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	807	C	N1-C6	-5.02	1.34	1.37
23	A	1856	C	N1-C6	-5.01	1.34	1.37
23	A	2004	A	C5-C6	-5.01	1.36	1.41
23	A	2816	G	N9-C8	-5.01	1.34	1.37

All (447) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	213	LEU	CA-CB-CG	14.81	149.37	115.30
1	h	1081	A	O4'-C1'-N9	11.00	117.00	108.20
23	A	2509	C	O4'-C1'-N1	10.71	116.77	108.20
23	A	1012	C	C2-N1-C1'	10.54	130.39	118.80
23	A	2245	C	C2-N1-C1'	10.28	130.10	118.80
19	8	213	LEU	CB-CG-CD2	9.79	127.64	111.00
23	A	1012	C	N1-C2-O2	9.62	124.67	118.90
23	A	2245	C	N1-C2-O2	9.13	124.38	118.90
19	8	187	LEU	C-N-CA	9.07	144.38	121.70
23	A	2025	C	C6-N1-C2	-9.04	116.68	120.30
23	A	2274	C	N1-C2-O2	8.99	124.30	118.90
23	A	2025	C	N3-C2-O2	-8.61	115.88	121.90
23	A	2025	C	N1-C2-O2	8.20	123.82	118.90
19	8	18	HIS	C-N-CA	7.96	141.60	121.70
23	A	2245	C	C6-N1-C1'	-7.88	111.34	120.80
23	A	1441	C	C5-C4-N4	-7.85	114.70	120.20
24	B	87	U	N3-C2-O2	-7.75	116.78	122.20
1	h	85	C	N1-C2-O2	7.72	123.53	118.90
23	A	2468	U	N3-C4-O4	7.66	124.76	119.40
23	A	197	C	C6-N1-C2	-7.65	117.24	120.30
23	A	2491	A	N1-C6-N6	-7.63	114.02	118.60
23	A	1012	C	N3-C2-O2	-7.61	116.57	121.90
23	A	848	G	N1-C2-N2	-7.58	109.38	116.20
23	A	2511	A	O4'-C1'-N9	7.57	114.25	108.20
23	A	1012	C	C6-N1-C1'	-7.53	111.77	120.80
23	A	1421	C	C5-C4-N4	-7.52	114.94	120.20
23	A	336	C	N3-C2-O2	-7.52	116.64	121.90
23	A	2521	C	C6-N1-C2	-7.47	117.31	120.30
23	A	2248	C	N1-C2-O2	7.43	123.36	118.90
1	h	841	U	C5'-C4'-O4'	7.41	117.99	109.10
23	A	1888	C	C5-C4-N4	-7.39	115.02	120.20
23	A	3045	C	C5-C4-N4	-7.38	115.03	120.20
23	A	1747	C	N3-C2-O2	-7.36	116.75	121.90
1	h	544	C	C6-N1-C2	-7.33	117.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	8	212	LEU	CA-CB-CG	7.32	132.13	115.30
23	A	962	U	C2-N1-C1'	7.31	126.47	117.70
1	h	85	C	C2-N1-C1'	7.30	126.83	118.80
23	A	2944	U	C5-C4-O4	-7.29	121.53	125.90
19	8	92	VAL	CG1-CB-CG2	7.25	122.51	110.90
23	A	1992	U	C5-C4-O4	-7.24	121.56	125.90
23	A	2245	C	N3-C2-O2	-7.23	116.84	121.90
23	A	597	C	C5-C4-N4	-7.21	115.15	120.20
23	A	2185	C	C5-C4-N4	-7.19	115.16	120.20
1	h	1139	C	C2-N1-C1'	7.19	126.71	118.80
23	A	318	U	C2-N1-C1'	7.18	126.31	117.70
23	A	1429	C	C6-N1-C2	-7.14	117.44	120.30
23	A	318	U	N1-C2-O2	7.14	127.80	122.80
1	h	415	C	N1-C2-O2	7.13	123.18	118.90
23	A	2730	U	C2-N1-C1'	7.09	126.21	117.70
23	A	932	C	C5-C4-N4	-7.08	115.24	120.20
23	A	2509	C	C6-N1-C2	-7.08	117.47	120.30
23	A	1277	C	C5-C4-N4	-7.06	115.26	120.20
23	A	726	A	C5-C6-N6	-7.05	118.06	123.70
23	A	652	C	C5-C4-N4	-7.03	115.28	120.20
19	8	183	VAL	CG1-CB-CG2	7.01	122.12	110.90
23	A	2944	U	N3-C4-O4	7.01	124.31	119.40
23	A	2900	C	N1-C2-O2	6.97	123.08	118.90
23	A	336	C	N1-C2-O2	6.94	123.06	118.90
1	h	560	C	C5-C4-N4	-6.94	115.34	120.20
19	8	178	LYS	C-N-CA	6.93	139.03	121.70
1	h	1326	C	N3-C2-O2	-6.88	117.09	121.90
19	8	3	VAL	CG1-CB-CG2	6.83	121.82	110.90
23	A	2766	A	C5-C6-N6	-6.82	118.24	123.70
1	h	415	C	N3-C2-O2	-6.82	117.13	121.90
1	h	1383	C	C2-N1-C1'	6.82	126.30	118.80
19	8	50	ILE	CG1-CB-CG2	6.82	126.39	111.40
23	A	879	A	C5-C6-N1	6.81	121.10	117.70
1	h	1299	C	C2-N1-C1'	6.80	126.28	118.80
1	h	1383	C	N1-C2-O2	6.77	122.96	118.90
23	A	673	C	N1-C2-O2	6.77	122.96	118.90
23	A	2519	C	C5-C4-N4	-6.77	115.46	120.20
23	A	1513	C	C5-C4-N4	-6.73	115.49	120.20
23	A	197	C	C5-C6-N1	6.71	124.36	121.00
23	A	318	U	N3-C2-O2	-6.69	117.52	122.20
23	A	557	G	C2-N3-C4	-6.69	108.56	111.90
1	h	1012	U	C2-N1-C1'	6.68	125.72	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	h	1299	C	N1-C2-O2	6.67	122.90	118.90
23	A	2905	C	C5-C4-N4	-6.65	115.54	120.20
23	A	2468	U	C5-C4-O4	-6.63	121.92	125.90
23	A	1843	C	C5-C4-N4	-6.60	115.58	120.20
19	8	195	VAL	CG1-CB-CG2	6.60	121.46	110.90
19	8	80	ILE	CG1-CB-CG2	6.58	125.88	111.40
19	8	181	ILE	CG1-CB-CG2	6.58	125.88	111.40
39	Q	93	ARG	C-N-CA	6.58	138.14	121.70
23	A	2825	C	C5-C4-N4	-6.57	115.60	120.20
23	A	1030	C	C5-C4-N4	-6.57	115.60	120.20
23	A	2870	C	C5-C4-N4	-6.56	115.61	120.20
23	A	1893	C	C5-C4-N4	-6.53	115.63	120.20
23	A	3046	C	C2-N1-C1'	6.52	125.97	118.80
1	h	842	A	C5'-C4'-O4'	6.50	116.90	109.10
23	A	939	C	C5-C4-N4	-6.47	115.67	120.20
23	A	1272	C	N1-C2-O2	6.47	122.78	118.90
23	A	2223	C	C5-C4-N4	-6.46	115.68	120.20
1	h	734	C	C2-N1-C1'	6.45	125.90	118.80
23	A	2676	C	C5-C4-N4	-6.44	115.69	120.20
23	A	597	C	N3-C4-N4	6.43	122.50	118.00
23	A	1562	C	C6-N1-C2	-6.42	117.73	120.30
38	P	24	ARG	NE-CZ-NH1	6.42	123.51	120.30
23	A	2287	C	C5-C4-N4	-6.40	115.72	120.20
23	A	2288	C	C5-C4-N4	-6.40	115.72	120.20
23	A	1473	G	C2-N3-C4	-6.38	108.71	111.90
23	A	197	C	N1-C2-O2	6.37	122.72	118.90
24	B	87	U	N1-C2-O2	6.37	127.26	122.80
1	h	1299	C	C6-N1-C2	-6.36	117.76	120.30
23	A	2830	C	C5-C4-N4	-6.36	115.75	120.20
23	A	804	A	C5-C6-N1	6.34	120.87	117.70
1	h	1012	U	N1-C2-O2	6.34	127.24	122.80
1	h	1299	C	N3-C2-O2	-6.34	117.47	121.90
23	A	1429	C	C2-N1-C1'	6.33	125.76	118.80
19	8	217	ILE	CG1-CB-CG2	6.33	125.31	111.40
23	A	481	C	N1-C2-O2	6.32	122.69	118.90
1	h	85	C	N3-C2-O2	-6.31	117.48	121.90
1	h	415	C	C6-N1-C2	-6.30	117.78	120.30
19	8	200	ILE	CG1-CB-CG2	6.30	125.26	111.40
23	A	1012	C	C6-N1-C2	-6.30	117.78	120.30
23	A	2915	C	C5-C4-N4	-6.28	115.81	120.20
25	C	221	VAL	C-N-CA	6.28	137.39	121.70
23	A	197	C	N3-C4-N4	6.25	122.38	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1458	G	C4-N9-C1'	6.25	134.63	126.50
1	h	791	C	C5-C4-N4	-6.23	115.84	120.20
23	A	2775	C	N1-C2-O2	6.22	122.63	118.90
1	h	1080	C	C2'-C3'-O3'	6.18	123.59	113.70
23	A	1298	C	N1-C2-O2	6.17	122.61	118.90
54	g	4	GLY	N-CA-C	-6.17	97.68	113.10
23	A	1311	C	C5-C4-N4	-6.16	115.89	120.20
23	A	1874	C	C5-C4-N4	-6.13	115.91	120.20
23	A	29	C	N1-C2-O2	6.11	122.57	118.90
1	h	1081	A	N9-C1'-C2'	6.11	121.94	114.00
1	h	544	C	N1-C2-O2	6.10	122.56	118.90
23	A	1458	G	C8-N9-C1'	-6.10	119.08	127.00
19	8	67	VAL	CG1-CB-CG2	6.09	120.65	110.90
19	8	70	VAL	CG1-CB-CG2	6.09	120.64	110.90
19	8	4	VAL	CG1-CB-CG2	6.07	120.62	110.90
23	A	1992	U	N3-C4-O4	6.07	123.65	119.40
23	A	1428	U	C2-N1-C1'	6.07	124.98	117.70
23	A	853	C	N1-C2-O2	6.06	122.54	118.90
23	A	2870	C	N3-C4-N4	6.06	122.24	118.00
23	A	804	A	C5-C6-N6	-6.05	118.86	123.70
1	h	1012	U	N3-C2-O2	-6.03	117.98	122.20
19	8	187	LEU	CB-CG-CD2	6.02	121.24	111.00
23	A	793	C	N1-C2-O2	6.02	122.51	118.90
23	A	799	G	C2-N3-C4	-6.01	108.89	111.90
23	A	599	G	O4'-C1'-N9	5.99	112.99	108.20
1	h	544	C	C2-N1-C1'	5.98	125.38	118.80
23	A	1234	U	C6-N1-C2	-5.98	117.41	121.00
23	A	848	G	C4-N9-C1'	5.97	134.26	126.50
23	A	2003	A	C5'-C4'-O4'	5.97	116.27	109.10
23	A	1747	C	N1-C2-O2	5.97	122.48	118.90
1	h	1406	G	C4-N9-C1'	5.97	134.26	126.50
23	A	933	G	N1-C2-N2	-5.96	110.83	116.20
1	h	328	U	N1-C2-O2	5.96	126.97	122.80
23	A	1856	C	C5-C4-N4	-5.96	116.03	120.20
23	A	2725	C	N1-C2-O2	5.96	122.48	118.90
23	A	2005	C	C5-C4-N4	-5.96	116.03	120.20
23	A	3074	C	C5-C4-N4	-5.96	116.03	120.20
1	h	1083	C	C5'-C4'-O4'	5.95	116.25	109.10
19	8	100	MET	C-N-CA	5.95	136.57	121.70
23	A	2869	C	C2-N1-C1'	5.95	125.34	118.80
23	A	2870	C	C5-C6-N1	5.95	123.97	121.00
24	B	87	U	C6-N1-C2	-5.95	117.43	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	2004	A	N1-C6-N6	5.94	122.17	118.60
23	A	2556	C	N1-C2-O2	5.94	122.46	118.90
23	A	1492	G	C2-N3-C4	-5.93	108.94	111.90
23	A	2023	C	N1-C2-O2	5.92	122.45	118.90
23	A	2262	C	N1-C2-O2	5.91	122.45	118.90
23	A	556	G	C6-C5-N7	-5.91	126.86	130.40
23	A	1122	C	N1-C2-O2	5.90	122.44	118.90
23	A	1788	G	C8-N9-C1'	5.89	134.65	127.00
1	h	614	C	N3-C2-O2	-5.88	117.78	121.90
23	A	1384	G	C6-C5-N7	-5.88	126.87	130.40
23	A	1843	C	N3-C4-N4	5.88	122.11	118.00
23	A	2235	C	C5-C4-N4	-5.87	116.09	120.20
23	A	2925	C	N1-C2-O2	5.85	122.41	118.90
1	h	544	C	N3-C2-O2	-5.85	117.80	121.90
23	A	848	G	C6-C5-N7	-5.85	126.89	130.40
23	A	174	G	C5-C6-O6	-5.84	125.09	128.60
23	A	848	G	N3-C2-N2	5.83	123.98	119.90
1	h	1482	U	P-O3'-C3'	5.83	126.69	119.70
51	d	9	GLN	N-CA-C	-5.82	95.29	111.00
23	A	390	G	N1-C2-N2	-5.81	110.97	116.20
23	A	1124	C	C5-C4-N4	-5.80	116.14	120.20
1	h	895	A	P-O3'-C3'	5.80	126.66	119.70
1	h	1395	C	C5-C4-N4	-5.80	116.14	120.20
23	A	799	G	N3-C4-C5	5.80	131.50	128.60
1	h	942	U	C2-N1-C1'	5.80	124.66	117.70
23	A	556	G	C4-C5-N7	5.80	113.12	110.80
23	A	2749	G	N3-C4-N9	-5.79	122.53	126.00
23	A	2047	C	N3-C4-N4	5.79	122.05	118.00
23	A	2734	C	C5-C4-N4	-5.79	116.15	120.20
23	A	812	C	C5-C4-N4	-5.78	116.15	120.20
23	A	2874	C	C5-C4-N4	-5.78	116.16	120.20
23	A	851	C	N1-C2-O2	5.76	122.35	118.90
23	A	1234	U	N3-C2-O2	-5.75	118.17	122.20
23	A	1571	C	N1-C2-O2	-5.75	115.45	118.90
23	A	912	C	N1-C2-O2	5.75	122.35	118.90
23	A	1298	C	C2-N1-C1'	5.74	125.11	118.80
19	8	159	SER	C-N-CA	5.74	136.04	121.70
23	A	2749	G	N3-C4-C5	5.72	131.46	128.60
1	h	614	C	N1-C2-O2	5.71	122.33	118.90
23	A	1788	G	C4-N9-C1'	-5.71	119.08	126.50
23	A	2047	C	C5-C4-N4	-5.70	116.21	120.20
23	A	197	C	C2-N1-C1'	5.69	125.06	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	h	328	U	N3-C2-O2	-5.68	118.22	122.20
23	A	1092	G	O4'-C1'-N9	5.67	112.74	108.20
23	A	2818	C	N1-C2-O2	5.67	122.30	118.90
23	A	2841	C	C5-C4-N4	-5.67	116.23	120.20
23	A	2004	A	C5-C6-N6	-5.67	119.16	123.70
23	A	848	G	C2-N3-C4	-5.67	109.06	111.90
23	A	386	C	C5-C4-N4	-5.66	116.24	120.20
23	A	1260	C	C2-N1-C1'	5.66	125.03	118.80
23	A	2181	C	C5-C4-N4	-5.66	116.24	120.20
23	A	2274	C	N3-C2-O2	-5.66	117.94	121.90
23	A	2723	C	C5-C4-N4	-5.65	116.24	120.20
1	h	1406	G	C8-N9-C1'	-5.65	119.65	127.00
23	A	1409	C	N3-C4-N4	5.63	121.94	118.00
23	A	1302	G	N1-C6-O6	5.62	123.27	119.90
23	A	1089	C	N1-C2-O2	5.61	122.26	118.90
23	A	472	C	C6-N1-C2	-5.60	118.06	120.30
23	A	2508	C	N1-C2-O2	5.60	122.26	118.90
23	A	2766	A	C5-C6-N1	5.59	120.50	117.70
1	h	749	G	N1-C2-N2	-5.59	111.17	116.20
23	A	1968	U	C5-C4-O4	-5.58	122.55	125.90
23	A	1830	C	C5-C4-N4	-5.57	116.30	120.20
1	h	422	C	P-O3'-C3'	5.57	126.38	119.70
23	A	932	C	N1-C2-O2	5.57	122.24	118.90
23	A	2626	U	C2-N1-C1'	5.57	124.38	117.70
23	A	2725	C	N3-C2-O2	-5.56	118.01	121.90
23	A	2218	C	C5-C4-N4	-5.56	116.31	120.20
23	A	1119	A	N1-C6-N6	-5.54	115.27	118.60
23	A	2230	C	C5-C4-N4	-5.54	116.32	120.20
23	A	852	C	C5-C4-N4	-5.53	116.33	120.20
23	A	657	C	C5-C4-N4	-5.53	116.33	120.20
25	C	213	ARG	NE-CZ-NH1	5.53	123.06	120.30
23	A	848	G	C8-N9-C1'	-5.52	119.82	127.00
23	A	1472	C	N1-C2-O2	5.52	122.21	118.90
23	A	1486	G	C2-N3-C4	-5.52	109.14	111.90
23	A	2198	C	C5-C4-N4	-5.52	116.34	120.20
1	h	623	C	N3-C2-O2	-5.52	118.04	121.90
23	A	898	A	C4-N9-C1'	5.52	136.23	126.30
1	h	439	U	C6-N1-C2	-5.50	117.70	121.00
23	A	726	A	N1-C6-N6	5.50	121.90	118.60
1	h	1494	C	N1-C2-O2	5.50	122.20	118.90
23	A	336	C	C6-N1-C2	-5.49	118.10	120.30
1	h	749	G	N3-C2-N2	5.48	123.74	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1120	G	C4-C5-N7	5.47	112.99	110.80
23	A	1273	G	C2-N3-C4	-5.47	109.16	111.90
1	h	1243	U	N3-C2-O2	-5.46	118.38	122.20
1	h	925	C	N1-C2-O2	5.46	122.18	118.90
23	A	2419	C	C6-N1-C2	-5.46	118.11	120.30
23	A	2004	A	C4-C5-N7	5.46	113.43	110.70
23	A	3046	C	N3-C2-O2	-5.46	118.08	121.90
1	h	885	G	C4-N9-C1'	5.45	133.59	126.50
1	h	942	U	N3-C2-O2	-5.45	118.38	122.20
23	A	472	C	C2-N1-C1'	5.45	124.79	118.80
23	A	2004	A	N9-C4-C5	-5.45	103.62	105.80
23	A	2124	A	N1-C6-N6	5.45	121.87	118.60
23	A	2610	C	N1-C2-O2	5.45	122.17	118.90
23	A	2848	C	C5-C4-N4	-5.44	116.39	120.20
1	h	1383	C	N3-C2-O2	-5.44	118.09	121.90
23	A	1384	G	N7-C8-N9	5.44	115.82	113.10
23	A	2005	C	N3-C4-N4	5.44	121.81	118.00
1	h	1152	C	C6-N1-C2	-5.44	118.12	120.30
1	h	1395	C	N3-C4-N4	5.43	121.80	118.00
23	A	1104	C	N1-C2-O2	5.43	122.16	118.90
23	A	501	C	C5-C4-N4	-5.43	116.40	120.20
23	A	2290	C	N1-C2-O2	5.42	122.16	118.90
23	A	546	G	O4'-C1'-N9	5.42	112.54	108.20
23	A	467	C	C5-C4-N4	-5.42	116.41	120.20
23	A	2260	C	N3-C4-N4	5.42	121.79	118.00
23	A	2249	G	N7-C8-N9	5.42	115.81	113.10
23	A	3045	C	N3-C4-N4	5.42	121.79	118.00
23	A	2605	C	C5-C4-N4	-5.41	116.41	120.20
23	A	2185	C	N3-C4-N4	5.41	121.79	118.00
23	A	974	G	P-O3'-C3'	5.41	126.19	119.70
23	A	1311	C	N3-C4-N4	5.41	121.79	118.00
23	A	2184	A	N9-C4-C5	-5.41	103.64	105.80
29	G	65	LEU	CA-CB-CG	5.41	127.74	115.30
1	h	558	C	C5-C4-N4	-5.41	116.42	120.20
23	A	191	G	C4-N9-C1'	5.41	133.53	126.50
1	h	791	C	N3-C4-N4	5.40	121.78	118.00
19	8	8	GLN	CA-CB-CG	5.40	125.29	113.40
23	A	1123	C	C6-N1-C2	-5.40	118.14	120.30
23	A	2296	C	N1-C2-O2	5.40	122.14	118.90
1	h	1237	C	N3-C2-O2	-5.40	118.12	121.90
1	h	1117	U	P-O3'-C3'	5.40	126.18	119.70
55	y	29	ASP	C-N-CD	5.40	139.73	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	726	A	C4-C5-N7	5.39	113.40	110.70
23	A	860	G	N1-C2-N2	-5.39	111.35	116.20
23	A	1303	U	C5-C4-O4	-5.39	122.66	125.90
23	A	1413	C	C2-N1-C1'	5.39	124.73	118.80
19	8	207	ILE	CG1-CB-CG2	5.39	123.25	111.40
23	A	726	A	N9-C4-C5	-5.39	103.64	105.80
23	A	2419	C	C2-N1-C1'	5.39	124.73	118.80
1	h	828	G	C6-C5-N7	-5.38	127.17	130.40
25	C	222	ARG	NE-CZ-NH1	5.38	122.99	120.30
23	A	851	C	C5-C4-N4	-5.38	116.43	120.20
23	A	1901	C	C5-C4-N4	-5.38	116.43	120.20
23	A	2203	C	N1-C2-O2	5.38	122.13	118.90
23	A	1035	G	C2-N3-C4	-5.37	109.22	111.90
1	h	415	C	C2-N1-C1'	5.36	124.70	118.80
23	A	2249	G	C6-C5-N7	-5.36	127.19	130.40
47	Z	51	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	h	942	U	N1-C2-O2	5.35	126.54	122.80
1	h	975	G	C8-N9-C1'	-5.34	120.05	127.00
23	A	2016	G	C2-N3-C4	-5.34	109.23	111.90
23	A	1561	C	C6-N1-C2	-5.34	118.17	120.30
23	A	1902	C	C5-C4-N4	-5.33	116.47	120.20
23	A	1823	C	N1-C2-O2	5.33	122.10	118.90
1	h	85	C	C6-N1-C1'	-5.33	114.41	120.80
23	A	799	G	N3-C4-N9	-5.33	122.80	126.00
23	A	2521	C	C2-N1-C1'	5.33	124.66	118.80
23	A	2339	G	O4'-C1'-N9	-5.32	103.94	108.20
23	A	2561	G	N1-C6-O6	5.32	123.09	119.90
23	A	896	A	C5'-C4'-O4'	5.32	115.48	109.10
23	A	1012	C	C5-C6-N1	5.32	123.66	121.00
23	A	534	G	C2-N3-C4	-5.31	109.24	111.90
23	A	1436	C	C6-N1-C2	-5.31	118.17	120.30
12	u	7	LEU	CB-CG-CD2	5.31	120.02	111.00
23	A	1027	C	N1-C2-O2	5.31	122.08	118.90
23	A	1638	C	C5-C4-N4	-5.30	116.49	120.20
51	d	9	GLN	C-N-CD	5.29	139.52	128.40
23	A	43	C	C5-C4-N4	-5.29	116.50	120.20
23	A	1030	C	N3-C4-N4	5.29	121.70	118.00
23	A	1509	U	O4'-C1'-N1	-5.29	103.97	108.20
1	h	788	C	N3-C2-O2	-5.28	118.20	121.90
23	A	1413	C	N1-C2-O2	5.28	122.07	118.90
23	A	2230	C	C6-N1-C2	-5.27	118.19	120.30
19	8	228	ARG	N-CA-C	5.27	125.23	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1298	C	N3-C2-O2	-5.26	118.22	121.90
23	A	1775	C	N1-C2-O2	5.26	122.05	118.90
23	A	2169	G	C5-C6-O6	-5.25	125.45	128.60
19	8	87	VAL	CG1-CB-CG2	5.25	119.29	110.90
23	A	617	U	C2-N1-C1'	5.24	123.98	117.70
23	A	2398	C	N1-C2-O2	-5.24	115.76	118.90
23	A	2510	A	N1-C6-N6	5.24	121.74	118.60
23	A	390	G	N3-C2-N2	5.23	123.56	119.90
23	A	2818	C	C5-C4-N4	-5.23	116.54	120.20
23	A	667	A	C5-C6-N1	5.22	120.31	117.70
23	A	1378	U	C5-C4-O4	-5.22	122.77	125.90
23	A	1788	G	N3-C4-N9	-5.22	122.87	126.00
23	A	81	A	C5'-C4'-O4'	5.22	115.36	109.10
23	A	1409	C	C6-N1-C2	-5.22	118.21	120.30
23	A	939	C	N3-C4-N4	5.21	121.65	118.00
23	A	436	C	N3-C2-O2	-5.21	118.25	121.90
23	A	2730	U	N3-C2-O2	-5.20	118.56	122.20
23	A	2248	C	C2-N1-C1'	5.20	124.52	118.80
23	A	1022	C	N1-C2-O2	5.20	122.02	118.90
23	A	1276	G	C4-N9-C1'	5.20	133.26	126.50
23	A	2841	C	N3-C4-N4	5.20	121.64	118.00
23	A	631	C	N1-C2-O2	5.20	122.02	118.90
23	A	1082	C	C5-C4-N4	-5.20	116.56	120.20
23	A	2900	C	N3-C2-O2	-5.20	118.26	121.90
1	h	886	C	C5-C4-N4	-5.19	116.56	120.20
1	h	419	C	N1-C2-O2	-5.19	115.79	118.90
23	A	1874	C	N3-C4-N4	5.19	121.63	118.00
23	A	202	C	C5-C4-N4	-5.19	116.57	120.20
1	h	1326	C	N1-C2-O2	5.18	122.01	118.90
23	A	617	U	N1-C2-O2	5.18	126.43	122.80
23	A	1251	A	O4'-C1'-N9	5.18	112.35	108.20
23	A	2249	G	C4-C5-N7	5.18	112.87	110.80
23	A	2005	C	C5'-C4'-O4'	5.18	115.32	109.10
23	A	2260	C	C5-C6-N1	5.18	123.59	121.00
23	A	2574	C	C5-C4-N4	-5.18	116.57	120.20
23	A	1458	G	C6-C5-N7	-5.18	127.29	130.40
23	A	1570	C	C6-N1-C2	-5.18	118.23	120.30
36	N	45	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	h	975	G	C4-N9-C1'	5.17	133.22	126.50
23	A	974	G	C8-N9-C4	-5.17	104.33	106.40
23	A	357	U	P-O3'-C3'	5.17	125.90	119.70
23	A	2843	C	C5-C4-N4	-5.17	116.58	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	1022	C	N3-C2-O2	-5.16	118.29	121.90
1	h	385	C	N1-C2-O2	5.16	122.00	118.90
19	8	214	THR	OG1-CB-CG2	5.16	121.86	110.00
23	A	97	U	P-O3'-C3'	5.16	125.89	119.70
23	A	2775	C	C2-N1-C1'	5.16	124.47	118.80
23	A	734	C	C5-C4-N4	-5.16	116.59	120.20
23	A	1393	C	C5-C4-N4	-5.16	116.59	120.20
23	A	652	C	N3-C4-N4	5.15	121.61	118.00
26	D	160	VAL	N-CA-CB	-5.15	100.16	111.50
23	A	2899	A	C5-C6-N6	-5.14	119.58	123.70
23	A	902	C	N1-C2-O2	5.14	121.98	118.90
23	A	73	C	C5-C4-N4	-5.13	116.61	120.20
23	A	962	U	C6-N1-C1'	-5.13	114.02	121.20
23	A	1752	C	C5-C4-N4	-5.13	116.61	120.20
23	A	1171	C	C5-C4-N4	-5.13	116.61	120.20
24	B	85	C	C5-C4-N4	-5.13	116.61	120.20
24	B	87	U	C5-C6-N1	5.12	125.26	122.70
23	A	1793	G	C6-C5-N7	-5.12	127.33	130.40
1	h	1139	C	C6-N1-C1'	-5.11	114.66	120.80
23	A	853	C	C2-N1-C1'	5.11	124.42	118.80
23	A	2665	C	C5-C4-N4	-5.11	116.62	120.20
1	h	975	G	C5-C6-O6	-5.11	125.53	128.60
19	8	225	LEU	CB-CG-CD2	5.10	119.68	111.00
50	c	30	ASP	C-N-CD	5.10	139.12	128.40
23	A	174	G	N1-C6-O6	5.10	122.96	119.90
23	A	2230	C	C5-C6-N1	5.10	123.55	121.00
1	h	367	U	C5-C6-N1	5.10	125.25	122.70
23	A	174	G	C4-C5-N7	5.10	112.84	110.80
19	8	170	HIS	C-N-CA	5.09	134.44	121.70
49	b	3	VAL	C-N-CD	5.09	139.10	128.40
1	h	885	G	C8-N9-C1'	-5.09	120.38	127.00
23	A	115	A	C8-N9-C4	-5.09	103.77	105.80
23	A	869	U	C5-C4-O4	-5.08	122.85	125.90
23	A	2561	G	C5-C6-O6	-5.08	125.55	128.60
23	A	1091	A	C5-C6-N1	5.08	120.24	117.70
54	g	90	ARG	N-CA-C	-5.08	97.28	111.00
23	A	161	U	N1-C2-O2	5.08	126.36	122.80
23	A	340	A	N9-C4-C5	-5.08	103.77	105.80
23	A	872	G	N3-C4-C5	5.08	131.14	128.60
1	h	623	C	N1-C2-O2	5.07	121.94	118.90
23	A	139	U	C2-N1-C1'	5.07	123.78	117.70
23	A	946	G	N1-C2-N2	-5.07	111.64	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	113	C	N1-C2-O2	5.07	121.94	118.90
27	E	101	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	h	273	A	C4-C5-N7	5.05	113.23	110.70
1	h	1117	U	OP1-P-O3'	5.05	116.32	105.20
23	A	1638	C	N3-C4-N4	5.05	121.54	118.00
23	A	357	U	OP2-P-O3'	5.05	116.31	105.20
23	A	501	C	N3-C4-N4	5.05	121.53	118.00
23	A	2626	U	N1-C2-O2	5.05	126.33	122.80
1	h	1383	C	C6-N1-C1'	-5.05	114.74	120.80
23	A	957	C	N1-C2-O2	5.05	121.93	118.90
23	A	1894	A	C5-N7-C8	-5.04	101.38	103.90
23	A	1971	C	C5-C4-N4	-5.04	116.67	120.20
23	A	1384	G	C4-N9-C1'	5.04	133.05	126.50
12	u	9	ARG	NE-CZ-NH1	5.04	122.82	120.30
23	A	2610	C	C2-N1-C1'	5.03	124.34	118.80
36	N	10	ARG	NE-CZ-NH1	5.03	122.81	120.30
23	A	1410	C	C6-N1-C2	-5.03	118.29	120.30
23	A	2249	G	C5-N7-C8	-5.03	101.79	104.30
35	M	21	ARG	NE-CZ-NH1	5.03	122.81	120.30
23	A	150	C	C5-C4-N4	-5.02	116.68	120.20
1	h	930	C	N1-C2-O2	5.02	121.91	118.90
23	A	2003	A	C5'-C4'-C3'	5.02	124.03	116.00
23	A	191	G	C8-N9-C1'	-5.01	120.48	127.00
23	A	197	C	C5-C4-N4	-5.01	116.69	120.20
23	A	1473	G	N1-C2-N2	-5.01	111.69	116.20
23	A	303	G	N3-C2-N2	-5.01	116.39	119.90
23	A	709	U	N1-C2-O2	5.01	126.31	122.80
23	A	1234	U	C2-N1-C1'	5.01	123.71	117.70
25	C	218	ARG	NE-CZ-NH2	-5.01	117.80	120.30
8	q	42	ARG	NE-CZ-NH1	5.01	122.80	120.30
23	A	895	G	C2-N3-C4	-5.01	109.40	111.90
1	h	469	G	N3-C4-N9	5.00	129.00	126.00
23	A	898	A	N7-C8-N9	5.00	116.30	113.80
23	A	726	A	C5-N7-C8	-5.00	101.40	103.90
23	A	1102	G	N7-C8-N9	5.00	115.60	113.10

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	8	159	SER	Peptide
19	8	160	ALA	Peptide

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Mol	Chain	Res	Type	Group
19	8	181	ILE	Peptide
19	8	192	ASP	Peptide
19	8	193	PRO	Peptide
19	8	24	ASN	Peptide
19	8	34	ASP	Peptide
19	8	4	VAL	Peptide
19	8	5	THR	Peptide
19	8	8	GLN	Peptide
26	D	147	ARG	Peptide
32	J	21	ASN	Peptide
45	W	153	ALA	Peptide
4	l	189	PRO	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	j	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
3	k	206/208 (99%)	182 (88%)	24 (12%)	0	100	100
4	l	198/200 (99%)	178 (90%)	19 (10%)	1 (0%)	29	66
5	m	178/180 (99%)	154 (86%)	22 (12%)	2 (1%)	14	50
6	n	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
7	p	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
8	q	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
9	4	124/126 (98%)	111 (90%)	12 (10%)	1 (1%)	19	57
10	s	97/99 (98%)	89 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	t	113/115 (98%)	100 (88%)	13 (12%)	0	100	100
12	u	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
13	v	114/116 (98%)	100 (88%)	14 (12%)	0	100	100
14	x	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
15	z	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
16	5	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
17	6	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
18	7	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
19	8	226/228 (99%)	196 (87%)	23 (10%)	7 (3%)	4	29
20	r	82/84 (98%)	75 (92%)	7 (8%)	0	100	100
21	Y	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	9	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
25	C	273/275 (99%)	232 (85%)	41 (15%)	0	100	100
26	D	212/214 (99%)	182 (86%)	28 (13%)	2 (1%)	17	54
27	E	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
28	F	180/182 (99%)	165 (92%)	14 (8%)	1 (1%)	25	62
29	G	174/176 (99%)	157 (90%)	17 (10%)	0	100	100
30	H	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
31	I	124/126 (98%)	117 (94%)	6 (5%)	1 (1%)	19	57
32	J	131/133 (98%)	116 (88%)	15 (12%)	0	100	100
33	K	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
34	L	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
35	M	143/145 (99%)	120 (84%)	21 (15%)	2 (1%)	11	44
36	N	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
37	O	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
38	P	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
39	Q	111/113 (98%)	94 (85%)	15 (14%)	2 (2%)	8	39
40	R	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
41	S	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
42	T	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
43	U	95/97 (98%)	81 (85%)	14 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	V	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
45	W	190/192 (99%)	169 (89%)	20 (10%)	1 (0%)	29	66
46	X	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
47	Z	62/64 (97%)	62 (100%)	0	0	100	100
48	a	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
49	b	52/54 (96%)	47 (90%)	4 (8%)	1 (2%)	8	38
50	c	51/53 (96%)	26 (51%)	15 (29%)	10 (20%)	0	1
51	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
52	e	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
53	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
54	g	71/82 (87%)	50 (70%)	16 (22%)	5 (7%)	1	11
55	y	75/77 (97%)	56 (75%)	8 (11%)	11 (15%)	0	2
56	3	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	6173/6298 (98%)	5524 (90%)	602 (10%)	47 (1%)	24	57

All (47) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	m	103	GLY
19	8	16	PHE
19	8	25	PRO
19	8	161	VAL
26	D	156	THR
28	F	131	GLY
49	b	9	SER
50	c	10	LYS
50	c	12	ARG
50	c	33	ARG
50	c	34	ILE
50	c	36	LEU
54	g	3	PRO
55	y	16	SER
55	y	24	THR
55	y	27	ARG
55	y	31	ASN
9	4	147	TYR
19	8	15	HIS

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Mol	Chain	Res	Type
50	c	32	ASP
50	c	37	ARG
50	c	46	HIS
55	y	23	ARG
55	y	30	PRO
19	8	18	HIS
19	8	193	PRO
31	I	125	ASP
54	g	47	PRO
55	y	14	GLY
55	y	15	ASN
5	m	104	SER
35	M	45	ASN
50	c	43	LEU
54	g	30	THR
26	D	162	LYS
35	M	70	ARG
39	Q	93	ARG
50	c	35	VAL
55	y	4	CYS
55	y	26	ARG
55	y	29	ASP
19	8	21	ARG
39	Q	3	THR
54	g	5	ILE
4	l	189	PRO
45	W	154	GLY
54	g	11	PRO

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	
2	j	30/30 (100%)	30 (100%)	0	100	100
3	k	170/170 (100%)	168 (99%)	2 (1%)	71	87
4	l	175/175 (100%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	m	127/127 (100%)	126 (99%)	1 (1%)	81	92
6	n	85/85 (100%)	83 (98%)	2 (2%)	49	76
7	p	131/131 (100%)	130 (99%)	1 (1%)	81	92
8	q	107/107 (100%)	106 (99%)	1 (1%)	78	91
9	4	102/102 (100%)	99 (97%)	3 (3%)	42	71
10	s	89/89 (100%)	89 (100%)	0	100	100
11	t	89/89 (100%)	88 (99%)	1 (1%)	73	88
12	u	103/103 (100%)	102 (99%)	1 (1%)	76	89
13	v	99/99 (100%)	99 (100%)	0	100	100
14	x	76/76 (100%)	75 (99%)	1 (1%)	69	86
15	z	92/92 (100%)	92 (100%)	0	100	100
16	5	80/80 (100%)	77 (96%)	3 (4%)	33	64
17	6	73/73 (100%)	73 (100%)	0	100	100
18	7	69/69 (100%)	65 (94%)	4 (6%)	20	52
19	8	191/191 (100%)	185 (97%)	6 (3%)	40	70
20	r	70/70 (100%)	70 (100%)	0	100	100
21	Y	91/91 (100%)	91 (100%)	0	100	100
22	9	85/85 (100%)	85 (100%)	0	100	100
25	C	215/215 (100%)	215 (100%)	0	100	100
26	D	160/160 (100%)	159 (99%)	1 (1%)	86	95
27	E	169/169 (100%)	168 (99%)	1 (1%)	86	95
28	F	151/151 (100%)	149 (99%)	2 (1%)	69	86
29	G	148/148 (100%)	148 (100%)	0	100	100
30	H	116/116 (100%)	115 (99%)	1 (1%)	78	91
31	I	89/89 (100%)	89 (100%)	0	100	100
32	J	102/102 (100%)	101 (99%)	1 (1%)	76	89
33	K	119/119 (100%)	119 (100%)	0	100	100
34	L	100/100 (100%)	100 (100%)	0	100	100
35	M	112/112 (100%)	112 (100%)	0	100	100
36	N	114/114 (100%)	113 (99%)	1 (1%)	78	91
37	O	97/97 (100%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	P	93/93 (100%)	92 (99%)	1 (1%)	73	88
39	Q	100/100 (100%)	99 (99%)	1 (1%)	76	89
40	R	97/97 (100%)	97 (100%)	0	100	100
41	S	81/81 (100%)	80 (99%)	1 (1%)	71	87
42	T	90/90 (100%)	87 (97%)	3 (3%)	38	68
43	U	83/83 (100%)	83 (100%)	0	100	100
44	V	81/86 (94%)	80 (99%)	1 (1%)	71	87
45	W	155/155 (100%)	155 (100%)	0	100	100
46	X	58/58 (100%)	56 (97%)	2 (3%)	37	67
47	Z	58/58 (100%)	58 (100%)	0	100	100
48	a	52/52 (100%)	52 (100%)	0	100	100
49	b	43/43 (100%)	42 (98%)	1 (2%)	50	76
50	c	49/49 (100%)	48 (98%)	1 (2%)	55	79
51	d	35/35 (100%)	35 (100%)	0	100	100
52	e	53/53 (100%)	53 (100%)	0	100	100
53	f	35/35 (100%)	35 (100%)	0	100	100
54	g	64/70 (91%)	63 (98%)	1 (2%)	62	83
55	y	64/64 (100%)	61 (95%)	3 (5%)	26	59
56	3	18/18 (100%)	18 (100%)	0	100	100
All	All	5135/5146 (100%)	5087 (99%)	48 (1%)	79	91

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	k	169	ARG
3	k	179	ARG
5	m	101	LEU
6	n	47	ARG
6	n	77	ARG
7	p	41	ARG
8	q	78	ARG
9	4	100	ARG
9	4	126	ARG
9	4	133	ARG
11	t	137	ARG

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Mol	Chain	Res	Type
12	u	83	ARG
14	x	88	ARG
16	5	17	ARG
16	5	54	ARG
16	5	89	ARG
18	7	18	ARG
18	7	20	ARG
18	7	33	ARG
18	7	56	ARG
19	8	16	PHE
19	8	18	HIS
19	8	19	GLN
19	8	177	ARG
19	8	212	LEU
19	8	213	LEU
26	D	201	ARG
27	E	46	ARG
28	F	78	ARG
28	F	95	ARG
30	H	57	LYS
32	J	52	ARG
36	N	10	ARG
38	P	26	ARG
39	Q	38	ARG
41	S	81	LYS
42	T	90	LYS
42	T	93	ARG
42	T	104	ARG
44	V	1	MET
46	X	14	ARG
46	X	85	ARG
49	b	6	ARG
50	c	12	ARG
54	g	64	SER
55	y	26	ARG
55	y	45	ARG
55	y	56	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
10	s	70	HIS

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Mol	Chain	Res	Type
14	x	28	GLN
17	6	29	GLN
21	Y	50	ASN
25	C	53	HIS
25	C	91	ASN
27	E	182	GLN
28	F	31	ASN
30	H	46	GLN
38	P	41	ASN
54	g	58	HIS
55	y	19	HIS
55	y	21	HIS
55	y	33	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	h	1510/1511 (99%)	391 (25%)	0
23	A	3118/3119 (99%)	771 (24%)	32 (1%)
24	B	117/118 (99%)	23 (19%)	1 (0%)
All	All	4745/4748 (99%)	1185 (24%)	33 (0%)

All (1185) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	h	9	U
1	h	10	G
1	h	11	G
1	h	12	A
1	h	13	G
1	h	18	U
1	h	26	G
1	h	36	A
1	h	43	G
1	h	51	C
1	h	52	U
1	h	54	A
1	h	55	A
1	h	59	A
1	h	70	A
1	h	82	U

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Mol	Chain	Res	Type
1	h	87	G
1	h	89	G
1	h	91	U
1	h	92	A
1	h	93	C
1	h	101	G
1	h	117	C
1	h	118	A
1	h	126	G
1	h	127	A
1	h	128	U
1	h	133	C
1	h	136	G
1	h	160	C
1	h	174	G
1	h	179	C
1	h	193	C
1	h	196	G
1	h	200	U
1	h	201	G
1	h	207	G
1	h	211	A
1	h	213	C
1	h	214	U
1	h	215	U
1	h	217	U
1	h	218	G
1	h	219	C
1	h	220	G
1	h	231	G
1	h	240	C
1	h	243	A
1	h	245	C
1	h	247	G
1	h	251	G
1	h	254	G
1	h	258	G
1	h	266	G
1	h	267	C
1	h	268	C
1	h	279	A
1	h	280	C

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Mol	Chain	Res	Type
1	h	281	G
1	h	289	G
1	h	298	A
1	h	300	A
1	h	306	A
1	h	329	A
1	h	330	C
1	h	332	G
1	h	340	U
1	h	345	C
1	h	347	G
1	h	350	G
1	h	351	G
1	h	352	C
1	h	353	A
1	h	359	G
1	h	367	U
1	h	369	G
1	h	372	C
1	h	373	A
1	h	381	C
1	h	382	A
1	h	388	G
1	h	389	A
1	h	390	U
1	h	392	C
1	h	393	A
1	h	397	A
1	h	398	C
1	h	406	G
1	h	412	U
1	h	413	G
1	h	414	A
1	h	421	U
1	h	422	C
1	h	423	G
1	h	424	G
1	h	428	G
1	h	429	U
1	h	430	A
1	h	432	A
1	h	434	C

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Mol	Chain	Res	Type
1	h	438	U
1	h	440	C
1	h	445	C
1	h	449	C
1	h	452	A
1	h	453	G
1	h	456	C
1	h	458	A
1	h	459	G
1	h	461	G
1	h	464	G
1	h	466	U
1	h	469	G
1	h	472	C
1	h	477	G
1	h	478	A
1	h	479	A
1	h	485	G
1	h	486	G
1	h	489	A
1	h	491	C
1	h	492	U
1	h	497	G
1	h	498	C
1	h	499	C
1	h	505	C
1	h	507	G
1	h	509	G
1	h	510	G
1	h	511	U
1	h	512	A
1	h	513	A
1	h	514	U
1	h	516	C
1	h	519	A
1	h	520	G
1	h	525	C
1	h	527	A
1	h	540	A
1	h	542	U
1	h	544	C
1	h	545	U

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Mol	Chain	Res	Type
1	h	552	A
1	h	553	A
1	h	555	G
1	h	556	A
1	h	557	G
1	h	567	G
1	h	576	C
1	h	590	A
1	h	600	U
1	h	603	C
1	h	611	G
1	h	612	U
1	h	629	G
1	h	633	A
1	h	643	A
1	h	645	G
1	h	660	C
1	h	666	U
1	h	668	G
1	h	680	G
1	h	683	G
1	h	694	G
1	h	695	A
1	h	698	A
1	h	701	G
1	h	702	G
1	h	703	U
1	h	711	G
1	h	713	G
1	h	728	A
1	h	729	A
1	h	732	G
1	h	735	G
1	h	739	A
1	h	761	A
1	h	772	A
1	h	773	U
1	h	776	C
1	h	785	C
1	h	790	C
1	h	793	U
1	h	794	A

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Mol	Chain	Res	Type
1	h	797	C
1	h	800	U
1	h	801	G
1	h	808	A
1	h	812	G
1	h	818	U
1	h	821	C
1	h	822	U
1	h	824	C
1	h	826	U
1	h	827	U
1	h	828	G
1	h	840	G
1	h	841	U
1	h	854	A
1	h	855	A
1	h	858	A
1	h	859	C
1	h	867	G
1	h	871	A
1	h	872	G
1	h	882	A
1	h	884	G
1	h	896	A
1	h	908	G
1	h	909	G
1	h	913	C
1	h	914	C
1	h	916	C
1	h	917	A
1	h	921	G
1	h	924	G
1	h	927	G
1	h	930	C
1	h	938	U
1	h	940	A
1	h	942	U
1	h	943	U
1	h	948	G
1	h	950	A
1	h	951	A
1	h	953	G

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Mol	Chain	Res	Type
1	h	956	A
1	h	957	A
1	h	958	G
1	h	959	A
1	h	960	A
1	h	964	U
1	h	965	A
1	h	971	G
1	h	973	U
1	h	974	U
1	h	975	G
1	h	976	A
1	h	982	A
1	h	985	G
1	h	987	A
1	h	988	C
1	h	989	G
1	h	990	C
1	h	992	G
1	h	1003	C
1	h	1008	C
1	h	1009	C
1	h	1010	C
1	h	1012	U
1	h	1014	U
1	h	1019	U
1	h	1021	U
1	h	1024	G
1	h	1025	C
1	h	1026	A
1	h	1027	G
1	h	1030	G
1	h	1033	G
1	h	1034	C
1	h	1036	U
1	h	1045	U
1	h	1047	A
1	h	1048	G
1	h	1054	G
1	h	1059	G
1	h	1074	G
1	h	1075	U

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Mol	Chain	Res	Type
1	h	1079	G
1	h	1080	C
1	h	1081	A
1	h	1084	G
1	h	1089	C
1	h	1092	C
1	h	1104	G
1	h	1106	U
1	h	1107	G
1	h	1112	C
1	h	1113	A
1	h	1115	G
1	h	1117	U
1	h	1118	A
1	h	1120	G
1	h	1121	G
1	h	1124	G
1	h	1125	G
1	h	1126	G
1	h	1129	U
1	h	1133	G
1	h	1136	A
1	h	1138	A
1	h	1139	C
1	h	1140	U
1	h	1148	U
1	h	1149	C
1	h	1150	A
1	h	1151	A
1	h	1155	G
1	h	1160	A
1	h	1162	G
1	h	1163	G
1	h	1165	G
1	h	1168	G
1	h	1177	A
1	h	1178	A
1	h	1182	A
1	h	1193	U
1	h	1194	A
1	h	1200	A
1	h	1206	U

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Mol	Chain	Res	Type
1	h	1218	C
1	h	1219	A
1	h	1220	A
1	h	1221	U
1	h	1222	G
1	h	1234	G
1	h	1237	C
1	h	1238	U
1	h	1239	G
1	h	1241	G
1	h	1244	G
1	h	1248	U
1	h	1249	G
1	h	1255	G
1	h	1258	C
1	h	1259	G
1	h	1261	A
1	h	1265	U
1	h	1266	U
1	h	1267	U
1	h	1268	C
1	h	1270	A
1	h	1279	U
1	h	1280	C
1	h	1282	G
1	h	1283	U
1	h	1284	U
1	h	1287	G
1	h	1299	C
1	h	1300	A
1	h	1301	A
1	h	1304	C
1	h	1313	G
1	h	1320	G
1	h	1322	G
1	h	1326	C
1	h	1327	U
1	h	1328	A
1	h	1329	G
1	h	1332	A
1	h	1343	G
1	h	1345	A

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Mol	Chain	Res	Type
1	h	1346	A
1	h	1348	G
1	h	1353	G
1	h	1357	A
1	h	1360	A
1	h	1361	C
1	h	1362	G
1	h	1364	U
1	h	1381	A
1	h	1382	C
1	h	1383	C
1	h	1405	G
1	h	1407	U
1	h	1409	A
1	h	1423	U
1	h	1425	G
1	h	1426	C
1	h	1429	A
1	h	1433	C
1	h	1434	U
1	h	1435	U
1	h	1436	G
1	h	1438	G
1	h	1451	G
1	h	1477	A
1	h	1478	G
1	h	1481	G
1	h	1483	A
1	h	1486	A
1	h	1487	A
1	h	1488	G
1	h	1490	U
1	h	1491	A
1	h	1501	G
1	h	1502	A
1	h	1503	A
1	h	1504	G
1	h	1513	G
1	h	1514	G
23	A	7	U
23	A	11	A
23	A	19	U

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Mol	Chain	Res	Type
23	A	20	G
23	A	23	G
23	A	25	A
23	A	29	C
23	A	31	U
23	A	32	G
23	A	43	C
23	A	47	U
23	A	60	A
23	A	68	A
23	A	71	A
23	A	72	G
23	A	81	A
23	A	82	G
23	A	85	G
23	A	94	G
23	A	98	U
23	A	99	G
23	A	107	G
23	A	115	A
23	A	117	U
23	A	125	C
23	A	126	C
23	A	128	G
23	A	136	U
23	A	138	A
23	A	148	A
23	A	150	C
23	A	151	A
23	A	159	A
23	A	161	U
23	A	162	A
23	A	180	A
23	A	188	G
23	A	195	A
23	A	198	A
23	A	203	A
23	A	204	G
23	A	212	A
23	A	214	G
23	A	215	A
23	A	220	A

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Mol	Chain	Res	Type
23	A	221	A
23	A	227	A
23	A	229	U
23	A	230	G
23	A	232	G
23	A	233	A
23	A	241	A
23	A	248	G
23	A	265	A
23	A	267	G
23	A	279	U
23	A	282	A
23	A	285	U
23	A	286	G
23	A	287	A
23	A	288	U
23	A	289	A
23	A	290	C
23	A	291	C
23	A	292	G
23	A	298	G
23	A	299	G
23	A	300	G
23	A	301	U
23	A	303	G
23	A	305	G
23	A	315	U
23	A	316	U
23	A	317	G
23	A	318	U
23	A	319	G
23	A	323	C
23	A	324	C
23	A	327	U
23	A	329	U
23	A	330	U
23	A	331	U
23	A	335	G
23	A	336	C
23	A	337	U
23	A	338	C
23	A	340	A

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Mol	Chain	Res	Type
23	A	342	C
23	A	348	G
23	A	351	G
23	A	352	G
23	A	357	U
23	A	358	G
23	A	361	A
23	A	363	A
23	A	369	G
23	A	370	U
23	A	376	G
23	A	383	U
23	A	384	G
23	A	391	G
23	A	393	U
23	A	404	A
23	A	412	A
23	A	413	G
23	A	417	C
23	A	428	A
23	A	433	C
23	A	434	G
23	A	437	G
23	A	441	G
23	A	444	U
23	A	445	U
23	A	446	G
23	A	448	U
23	A	449	G
23	A	450	G
23	A	452	G
23	A	460	G
23	A	467	C
23	A	474	G
23	A	475	U
23	A	482	U
23	A	489	A
23	A	491	U
23	A	493	U
23	A	494	G
23	A	500	A
23	A	505	C

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Mol	Chain	Res	Type
23	A	509	U
23	A	512	G
23	A	514	C
23	A	517	A
23	A	523	U
23	A	531	A
23	A	539	C
23	A	543	U
23	A	544	U
23	A	552	U
23	A	553	G
23	A	556	G
23	A	561	G
23	A	562	G
23	A	563	U
23	A	565	A
23	A	566	A
23	A	567	A
23	A	569	G
23	A	578	G
23	A	585	G
23	A	589	A
23	A	591	G
23	A	592	A
23	A	594	U
23	A	595	A
23	A	596	C
23	A	597	C
23	A	605	G
23	A	614	C
23	A	617	U
23	A	618	C
23	A	619	C
23	A	620	G
23	A	633	A
23	A	634	C
23	A	636	U
23	A	637	G
23	A	638	U
23	A	639	C
23	A	640	G
23	A	642	G

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Mol	Chain	Res	Type
23	A	644	G
23	A	646	U
23	A	648	A
23	A	654	U
23	A	655	G
23	A	661	U
23	A	665	G
23	A	666	A
23	A	667	A
23	A	679	G
23	A	684	G
23	A	685	G
23	A	696	A
23	A	697	G
23	A	706	G
23	A	707	G
23	A	708	G
23	A	714	U
23	A	721	A
23	A	725	A
23	A	731	A
23	A	740	A
23	A	747	A
23	A	756	A
23	A	757	G
23	A	758	A
23	A	760	U
23	A	763	G
23	A	764	U
23	A	766	G
23	A	767	U
23	A	768	G
23	A	784	G
23	A	801	U
23	A	830	A
23	A	832	G
23	A	845	C
23	A	862	U
23	A	863	G
23	A	868	C
23	A	880	G
23	A	890	G

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Mol	Chain	Res	Type
23	A	897	A
23	A	898	A
23	A	899	G
23	A	905	U
23	A	907	A
23	A	909	A
23	A	915	U
23	A	916	G
23	A	920	G
23	A	927	C
23	A	942	U
23	A	943	U
23	A	945	G
23	A	954	U
23	A	960	G
23	A	961	U
23	A	973	G
23	A	974	G
23	A	975	U
23	A	976	A
23	A	981	U
23	A	982	A
23	A	983	C
23	A	995	U
23	A	997	G
23	A	1001	C
23	A	1002	C
23	A	1003	A
23	A	1004	C
23	A	1005	A
23	A	1006	G
23	A	1007	G
23	A	1008	G
23	A	1011	A
23	A	1012	C
23	A	1013	U
23	A	1015	A
23	A	1025	A
23	A	1027	C
23	A	1028	U
23	A	1029	C
23	A	1030	C

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Mol	Chain	Res	Type
23	A	1034	U
23	A	1046	C
23	A	1047	A
23	A	1049	G
23	A	1058	A
23	A	1062	A
23	A	1063	G
23	A	1075	U
23	A	1076	A
23	A	1078	G
23	A	1084	U
23	A	1085	G
23	A	1091	A
23	A	1092	G
23	A	1101	A
23	A	1103	C
23	A	1114	G
23	A	1121	G
23	A	1130	C
23	A	1131	G
23	A	1140	G
23	A	1141	U
23	A	1143	G
23	A	1144	A
23	A	1151	U
23	A	1152	G
23	A	1153	U
23	A	1157	G
23	A	1164	A
23	A	1165	G
23	A	1173	G
23	A	1178	U
23	A	1179	U
23	A	1180	G
23	A	1184	U
23	A	1185	A
23	A	1186	G
23	A	1187	A
23	A	1188	A
23	A	1189	G
23	A	1190	C
23	A	1191	A

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Mol	Chain	Res	Type
23	A	1192	G
23	A	1200	U
23	A	1201	G
23	A	1202	A
23	A	1203	A
23	A	1205	G
23	A	1206	A
23	A	1207	G
23	A	1208	U
23	A	1209	G
23	A	1212	U
23	A	1213	A
23	A	1214	A
23	A	1215	U
23	A	1216	A
23	A	1219	U
23	A	1223	U
23	A	1224	G
23	A	1226	U
23	A	1230	G
23	A	1234	U
23	A	1235	U
23	A	1238	G
23	A	1240	G
23	A	1244	A
23	A	1246	A
23	A	1251	A
23	A	1253	C
23	A	1260	C
23	A	1261	A
23	A	1267	A
23	A	1270	G
23	A	1290	C
23	A	1292	U
23	A	1293	G
23	A	1294	U
23	A	1320	U
23	A	1325	U
23	A	1332	G
23	A	1339	G
23	A	1343	G
23	A	1344	A

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Mol	Chain	Res	Type
23	A	1345	G
23	A	1352	A
23	A	1353	G
23	A	1359	G
23	A	1362	A
23	A	1365	G
23	A	1370	U
23	A	1371	G
23	A	1380	A
23	A	1386	G
23	A	1387	A
23	A	1389	U
23	A	1404	C
23	A	1408	C
23	A	1415	A
23	A	1416	A
23	A	1435	C
23	A	1437	A
23	A	1440	C
23	A	1444	U
23	A	1445	C
23	A	1456	G
23	A	1457	A
23	A	1462	G
23	A	1465	C
23	A	1480	A
23	A	1481	C
23	A	1499	A
23	A	1501	C
23	A	1507	G
23	A	1508	A
23	A	1510	A
23	A	1511	U
23	A	1518	A
23	A	1522	G
23	A	1524	G
23	A	1525	U
23	A	1529	U
23	A	1530	G
23	A	1531	C
23	A	1534	C
23	A	1536	A

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Mol	Chain	Res	Type
23	A	1537	U
23	A	1538	G
23	A	1540	U
23	A	1544	U
23	A	1546	A
23	A	1547	G
23	A	1550	G
23	A	1551	U
23	A	1552	A
23	A	1553	C
23	A	1554	U
23	A	1555	A
23	A	1556	A
23	A	1558	C
23	A	1559	A
23	A	1561	C
23	A	1564	A
23	A	1565	A
23	A	1567	C
23	A	1570	C
23	A	1571	C
23	A	1572	G
23	A	1574	G
23	A	1579	C
23	A	1580	A
23	A	1584	U
23	A	1587	G
23	A	1588	G
23	A	1589	G
23	A	1595	G
23	A	1598	U
23	A	1599	U
23	A	1600	G
23	A	1604	G
23	A	1605	G
23	A	1607	C
23	A	1608	U
23	A	1611	A
23	A	1616	A
23	A	1617	C
23	A	1623	U
23	A	1625	G

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Mol	Chain	Res	Type
23	A	1627	U
23	A	1629	G
23	A	1630	U
23	A	1631	A
23	A	1632	G
23	A	1637	G
23	A	1638	C
23	A	1639	G
23	A	1640	A
23	A	1648	A
23	A	1649	C
23	A	1650	G
23	A	1658	G
23	A	1674	G
23	A	1679	A
23	A	1680	A
23	A	1681	U
23	A	1688	G
23	A	1696	G
23	A	1703	G
23	A	1710	A
23	A	1711	G
23	A	1713	U
23	A	1716	A
23	A	1717	U
23	A	1720	G
23	A	1724	G
23	A	1727	A
23	A	1728	U
23	A	1730	U
23	A	1731	A
23	A	1736	G
23	A	1737	A
23	A	1738	G
23	A	1746	G
23	A	1751	G
23	A	1754	G
23	A	1755	A
23	A	1756	G
23	A	1757	U
23	A	1760	G
23	A	1767	U

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Mol	Chain	Res	Type
23	A	1778	A
23	A	1787	A
23	A	1789	A
23	A	1791	A
23	A	1801	C
23	A	1802	G
23	A	1803	A
23	A	1813	C
23	A	1820	U
23	A	1825	C
23	A	1834	A
23	A	1835	C
23	A	1852	A
23	A	1857	U
23	A	1864	U
23	A	1865	A
23	A	1866	C
23	A	1871	G
23	A	1872	A
23	A	1878	G
23	A	1890	C
23	A	1892	G
23	A	1895	A
23	A	1909	C
23	A	1912	C
23	A	1916	A
23	A	1917	G
23	A	1918	A
23	A	1921	G
23	A	1925	A
23	A	1931	A
23	A	1946	U
23	A	1947	U
23	A	1948	A
23	A	1950	G
23	A	1973	C
23	A	1975	A
23	A	1979	A
23	A	1980	G
23	A	1981	U
23	A	1990	A
23	A	1998	C

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Mol	Chain	Res	Type
23	A	2003	A
23	A	2004	A
23	A	2017	C
23	A	2018	G
23	A	2024	G
23	A	2025	C
23	A	2026	A
23	A	2027	A
23	A	2033	U
23	A	2036	A
23	A	2046	A
23	A	2047	C
23	A	2050	C
23	A	2052	G
23	A	2064	A
23	A	2065	A
23	A	2066	G
23	A	2086	U
23	A	2088	C
23	A	2089	C
23	A	2090	U
23	A	2092	U
23	A	2093	G
23	A	2094	G
23	A	2095	G
23	A	2096	G
23	A	2106	A
23	A	2107	G
23	A	2112	U
23	A	2130	G
23	A	2136	A
23	A	2138	C
23	A	2140	A
23	A	2141	U
23	A	2152	A
23	A	2153	G
23	A	2154	G
23	A	2155	U
23	A	2161	A
23	A	2162	A
23	A	2163	U
23	A	2164	U

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Mol	Chain	Res	Type
23	A	2165	C
23	A	2166	C
23	A	2167	U
23	A	2178	G
23	A	2179	U
23	A	2191	C
23	A	2194	A
23	A	2195	U
23	A	2196	G
23	A	2197	G
23	A	2199	G
23	A	2215	U
23	A	2217	U
23	A	2221	A
23	A	2241	U
23	A	2246	U
23	A	2255	A
23	A	2256	G
23	A	2257	A
23	A	2267	C
23	A	2276	G
23	A	2279	C
23	A	2280	G
23	A	2284	A
23	A	2285	G
23	A	2286	A
23	A	2293	G
23	A	2300	A
23	A	2315	U
23	A	2316	G
23	A	2325	U
23	A	2327	C
23	A	2329	G
23	A	2331	U
23	A	2334	U
23	A	2335	G
23	A	2336	U
23	A	2338	G
23	A	2339	G
23	A	2341	U
23	A	2342	A
23	A	2343	G

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Mol	Chain	Res	Type
23	A	2346	G
23	A	2347	G
23	A	2348	G
23	A	2350	G
23	A	2351	A
23	A	2352	C
23	A	2353	U
23	A	2354	G
23	A	2355	U
23	A	2356	G
23	A	2358	A
23	A	2359	G
23	A	2363	A
23	A	2367	G
23	A	2368	C
23	A	2373	G
23	A	2375	G
23	A	2380	G
23	A	2381	A
23	A	2382	G
23	A	2383	U
23	A	2384	C
23	A	2385	G
23	A	2387	U
23	A	2388	G
23	A	2389	U
23	A	2390	U
23	A	2392	A
23	A	2394	A
23	A	2395	U
23	A	2399	A
23	A	2401	U
23	A	2402	C
23	A	2403	U
23	A	2407	C
23	A	2408	G
23	A	2411	U
23	A	2413	G
23	A	2421	A
23	A	2434	A
23	A	2436	A
23	A	2437	U

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Mol	Chain	Res	Type
23	A	2449	A
23	A	2450	C
23	A	2454	G
23	A	2462	G
23	A	2463	G
23	A	2490	A
23	A	2492	A
23	A	2503	G
23	A	2507	C
23	A	2508	C
23	A	2510	A
23	A	2511	A
23	A	2520	U
23	A	2521	C
23	A	2528	G
23	A	2529	A
23	A	2530	C
23	A	2532	G
23	A	2534	A
23	A	2549	G
23	A	2559	A
23	A	2566	C
23	A	2571	C
23	A	2574	C
23	A	2585	U
23	A	2596	G
23	A	2601	A
23	A	2607	G
23	A	2609	A
23	A	2626	U
23	A	2627	C
23	A	2639	G
23	A	2643	U
23	A	2647	U
23	A	2649	A
23	A	2653	G
23	A	2654	A
23	A	2655	U
23	A	2658	A
23	A	2659	A
23	A	2664	C
23	A	2665	C

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Mol	Chain	Res	Type
23	A	2672	A
23	A	2673	U
23	A	2693	A
23	A	2694	G
23	A	2699	C
23	A	2707	C
23	A	2715	U
23	A	2722	C
23	A	2726	G
23	A	2728	U
23	A	2729	G
23	A	2730	U
23	A	2742	A
23	A	2749	G
23	A	2750	G
23	A	2753	G
23	A	2755	A
23	A	2759	G
23	A	2767	G
23	A	2778	U
23	A	2788	A
23	A	2790	A
23	A	2791	G
23	A	2796	A
23	A	2797	C
23	A	2802	G
23	A	2806	G
23	A	2810	U
23	A	2826	A
23	A	2827	G
23	A	2833	U
23	A	2835	U
23	A	2837	U
23	A	2853	C
23	A	2854	A
23	A	2857	A
23	A	2860	U
23	A	2862	G
23	A	2870	C
23	A	2871	U
23	A	2878	A
23	A	2884	A

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Mol	Chain	Res	Type
23	A	2893	G
23	A	2906	U
23	A	2912	A
23	A	2913	U
23	A	2926	A
23	A	2929	A
23	A	2936	C
23	A	2937	G
23	A	2938	G
23	A	2957	A
23	A	2959	A
23	A	2963	U
23	A	2968	G
23	A	2972	A
23	A	2974	A
23	A	2979	C
23	A	2982	A
23	A	2985	G
23	A	2989	A
23	A	2990	A
23	A	3002	A
23	A	3013	C
23	A	3014	A
23	A	3015	C
23	A	3020	U
23	A	3021	A
23	A	3023	G
23	A	3024	A
23	A	3029	U
23	A	3039	C
23	A	3042	A
23	A	3047	A
23	A	3053	U
23	A	3054	U
23	A	3055	G
23	A	3068	U
23	A	3070	G
23	A	3079	U
23	A	3080	A
23	A	3082	U
23	A	3087	G
23	A	3088	C

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Mol	Chain	Res	Type
23	A	3089	A
23	A	3093	A
23	A	3095	C
23	A	3100	A
23	A	3101	C
23	A	3104	A
23	A	3105	C
23	A	3106	C
23	A	3107	G
23	A	3112	A
23	A	3115	A
23	A	3117	U
24	B	4	A
24	B	5	C
24	B	9	G
24	B	11	U
24	B	12	C
24	B	13	C
24	B	14	A
24	B	26	A
24	B	30	G
24	B	36	U
24	B	37	C
24	B	41	U
24	B	42	C
24	B	43	C
24	B	45	G
24	B	56	C
24	B	67	A
24	B	87	U
24	B	89	C
24	B	90	G
24	B	103	G
24	B	107	A
24	B	114	A

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	81	A
23	A	97	U
23	A	228	A

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Mol	Chain	Res	Type
23	A	316	U
23	A	336	C
23	A	357	U
23	A	445	U
23	A	552	U
23	A	641	U
23	A	643	G
23	A	899	G
23	A	974	G
23	A	1002	C
23	A	1004	C
23	A	1006	G
23	A	1014	G
23	A	1046	C
23	A	1084	U
23	A	1186	G
23	A	1293	G
23	A	1436	C
23	A	1510	A
23	A	2003	A
23	A	2005	C
23	A	2088	C
23	A	2094	G
23	A	2139	U
23	A	2165	C
23	A	2350	G
23	A	2384	C
23	A	2389	U
23	A	2626	U
24	B	10	G

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

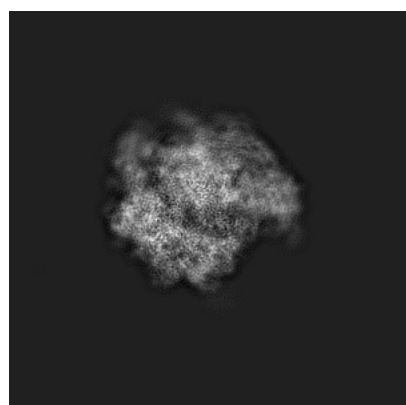
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8932. These allow visual inspection of the internal detail of the map and identification of artifacts.

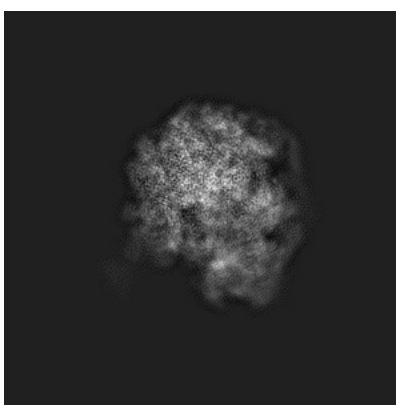
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

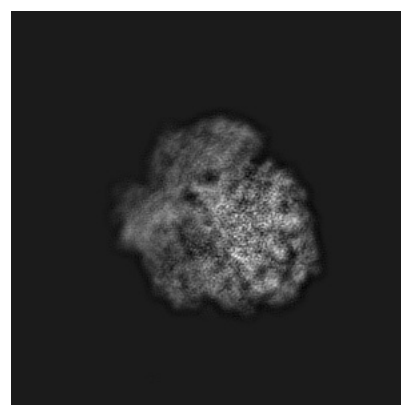
6.1.1 Primary map



X



Y

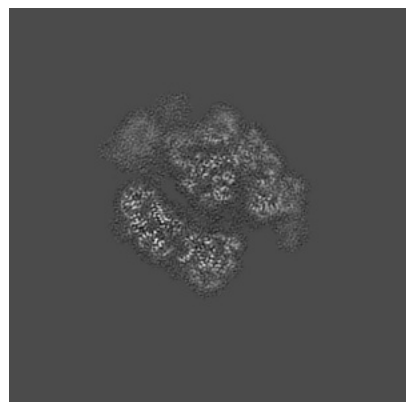


Z

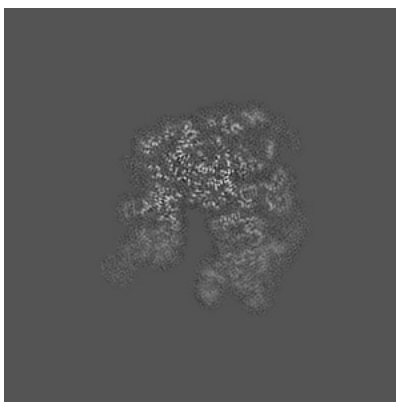
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

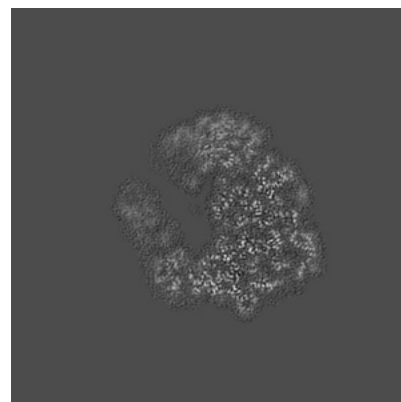
6.2.1 Primary map



X Index: 227



Y Index: 227

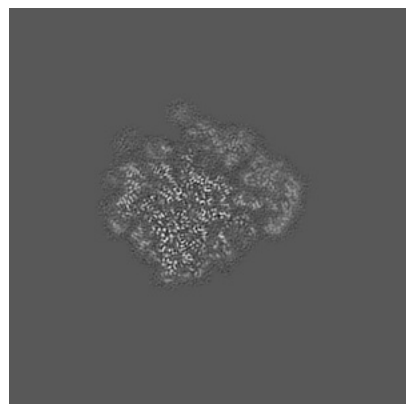


Z Index: 227

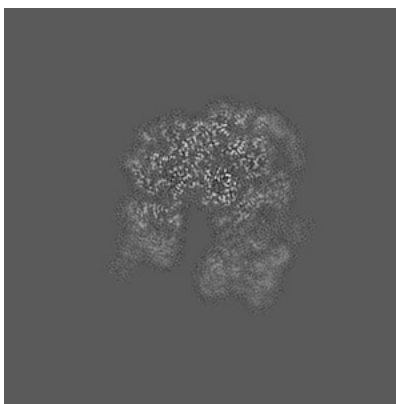
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

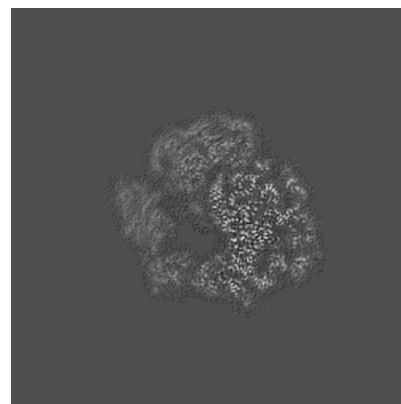
6.3.1 Primary map



X Index: 255



Y Index: 216

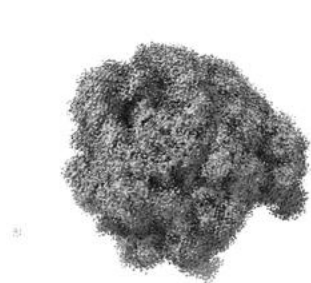


Z Index: 238

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

6.4 Orthogonal surface views [i](#)

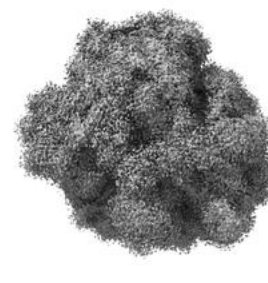
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

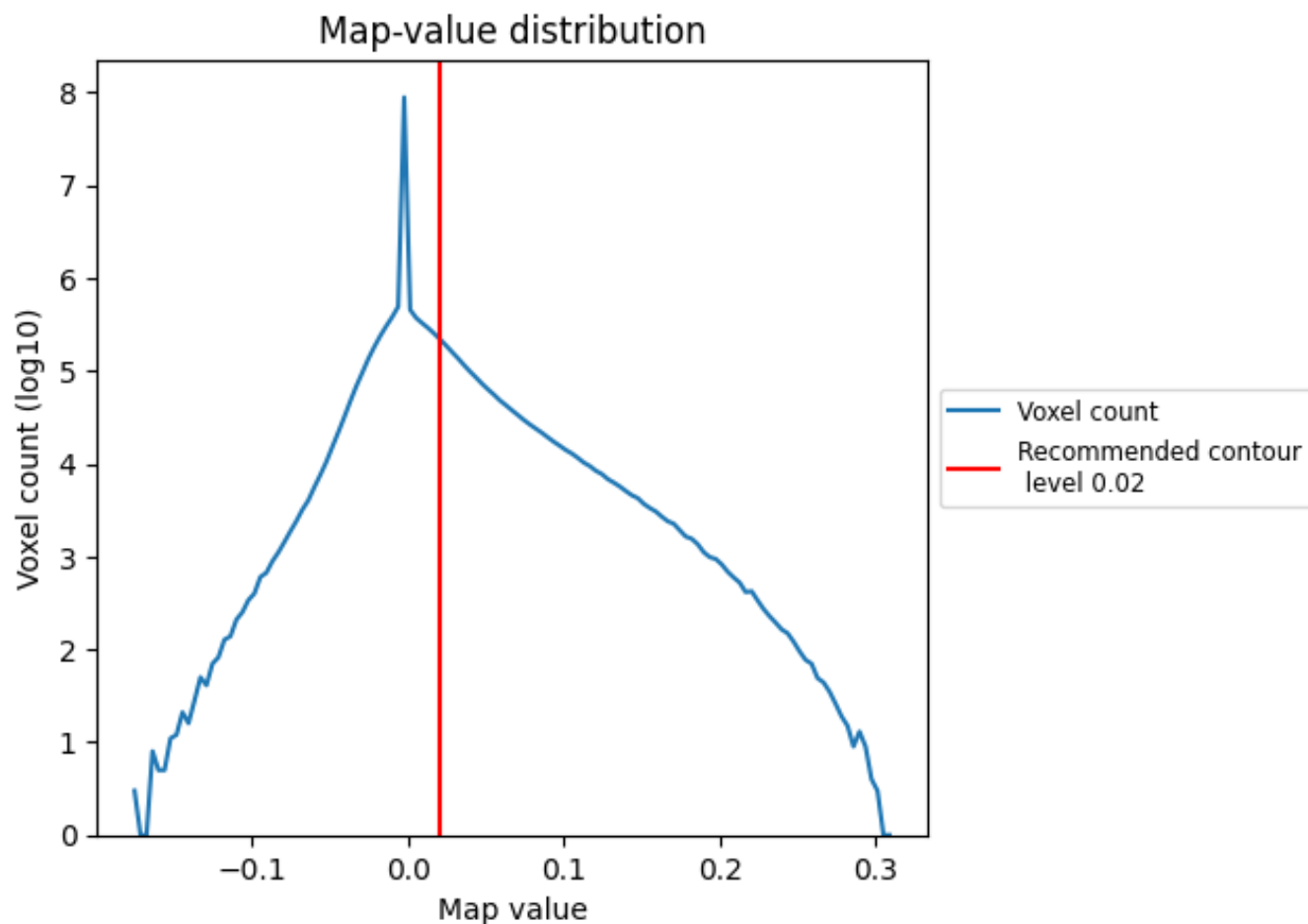
6.5 Mask visualisation

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

7 Map analysis [i](#)

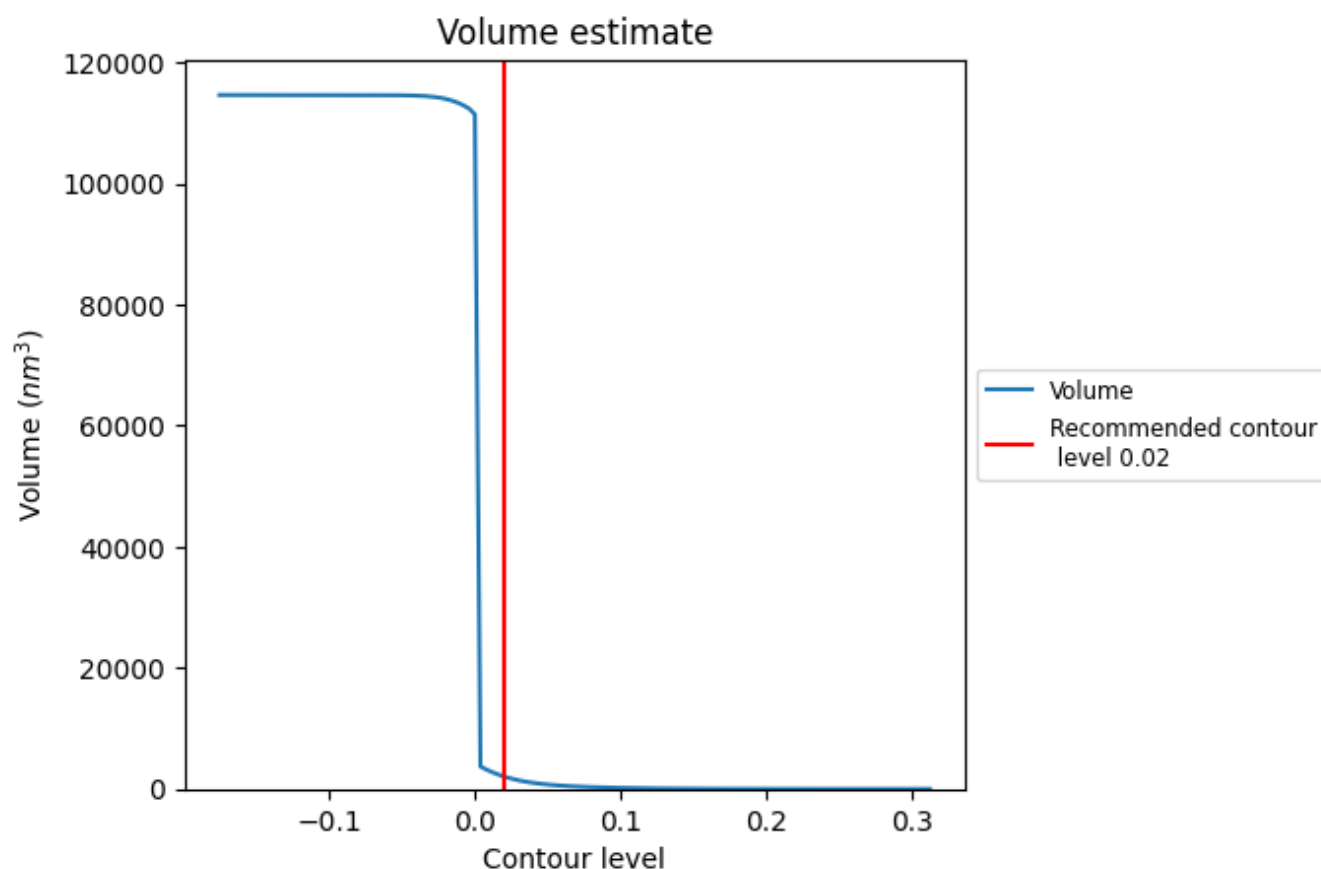
This section contains the results of statistical analysis of the map.

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.

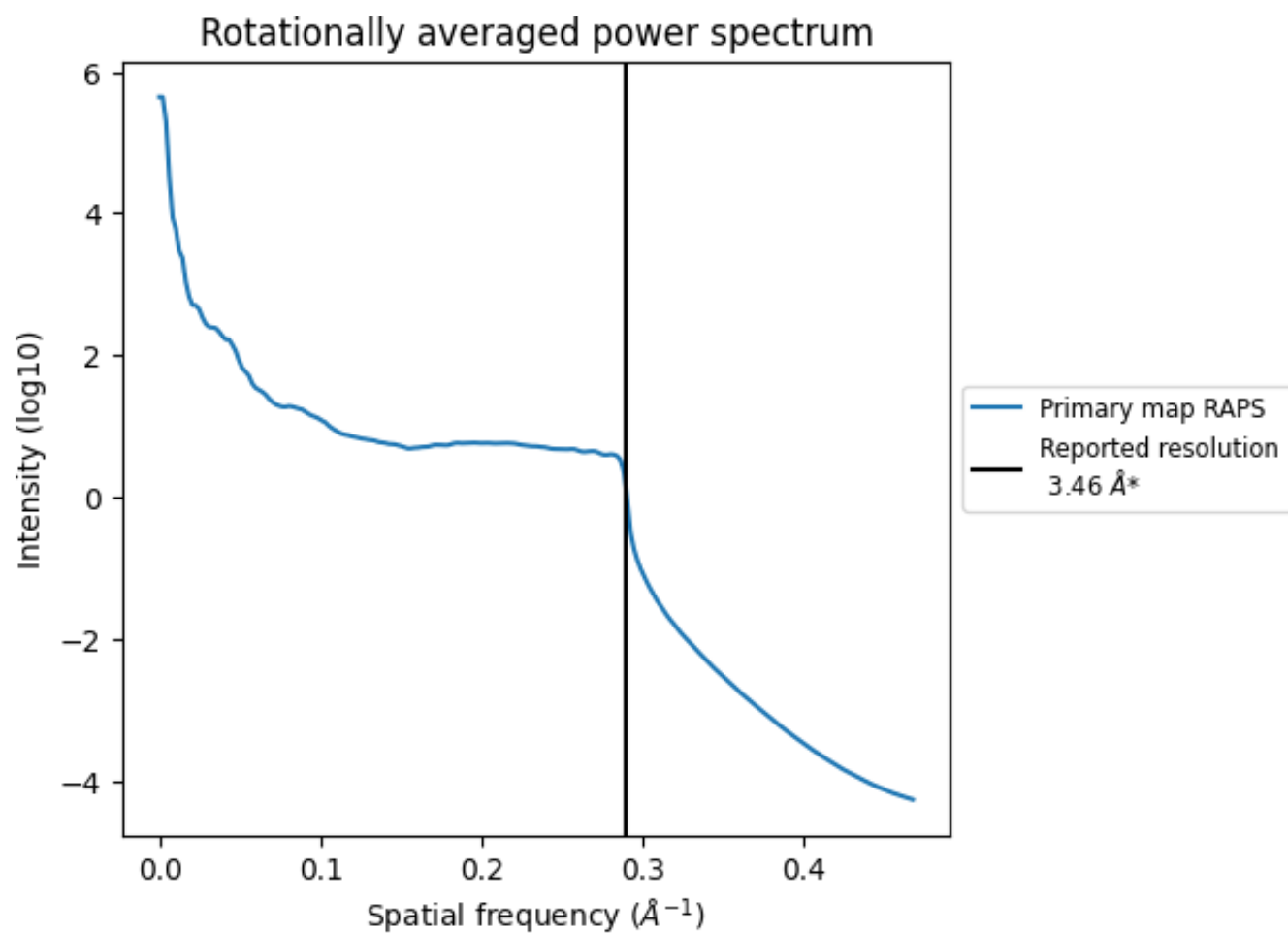
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2059 nm³; this corresponds to an approximate mass of 1860 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 ⓘ

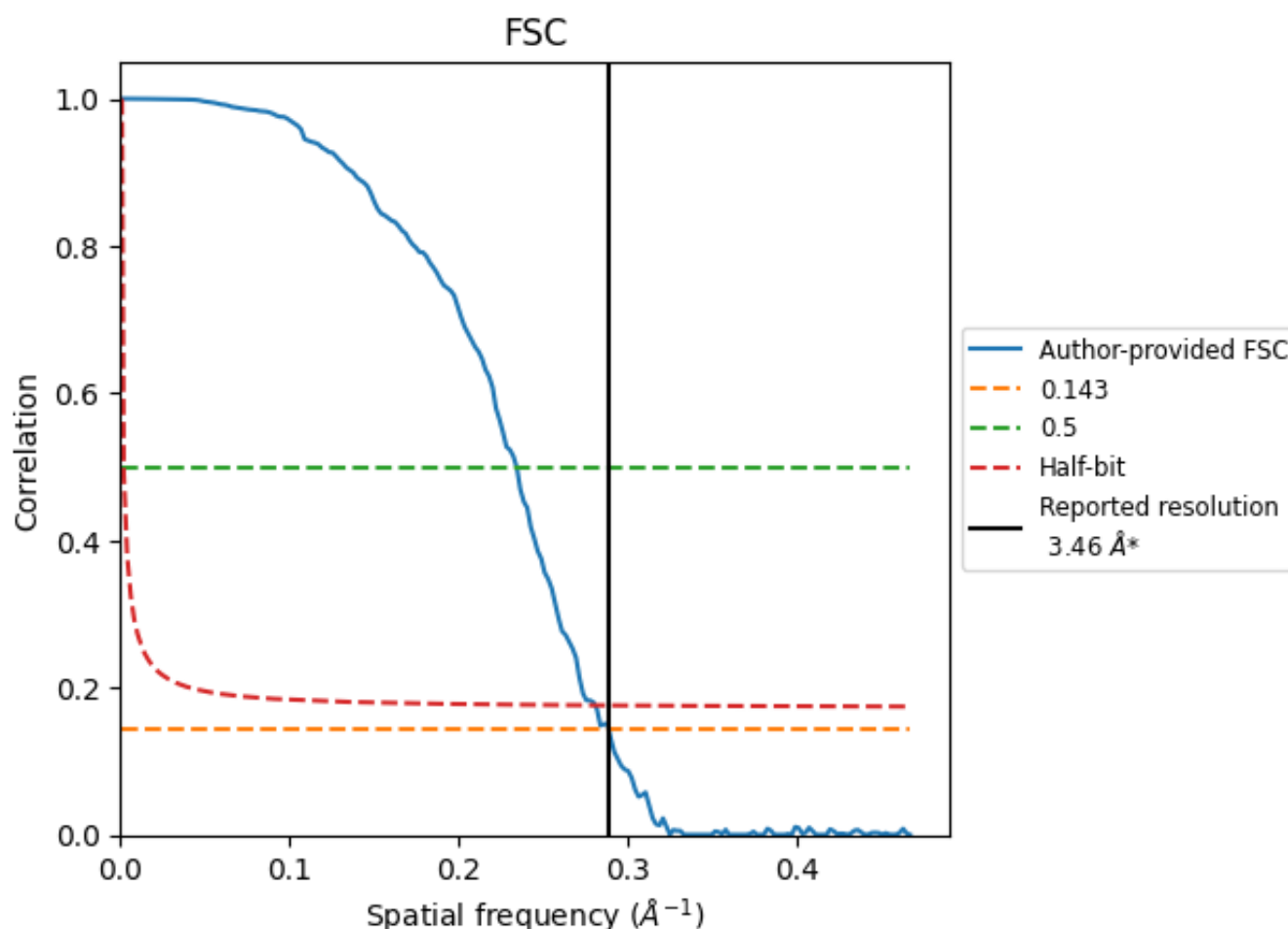


*Reported resolution corresponds to spatial frequency of 0.289 Å⁻¹

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 0.289 Å⁻¹

8.2 Resolution estimates [i](#)

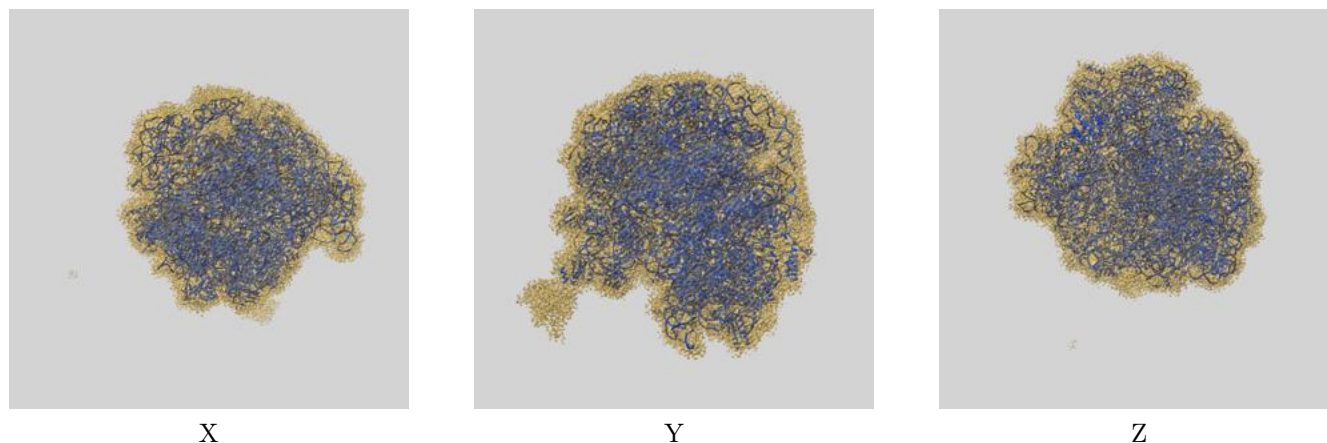
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	3.46	4.27	3.56
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

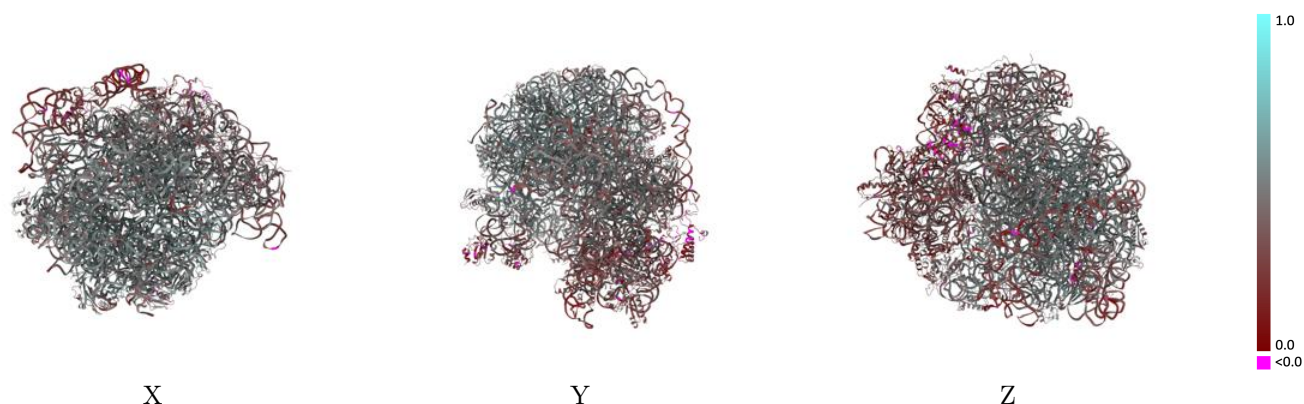
This section contains information regarding the fit between EMDB map EMD-8932 and PDB model 6DZI. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



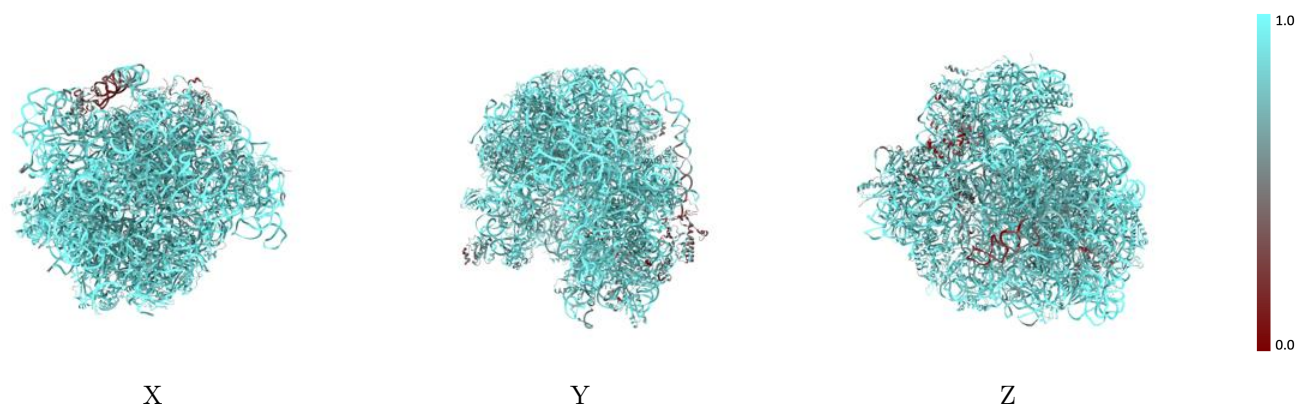
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



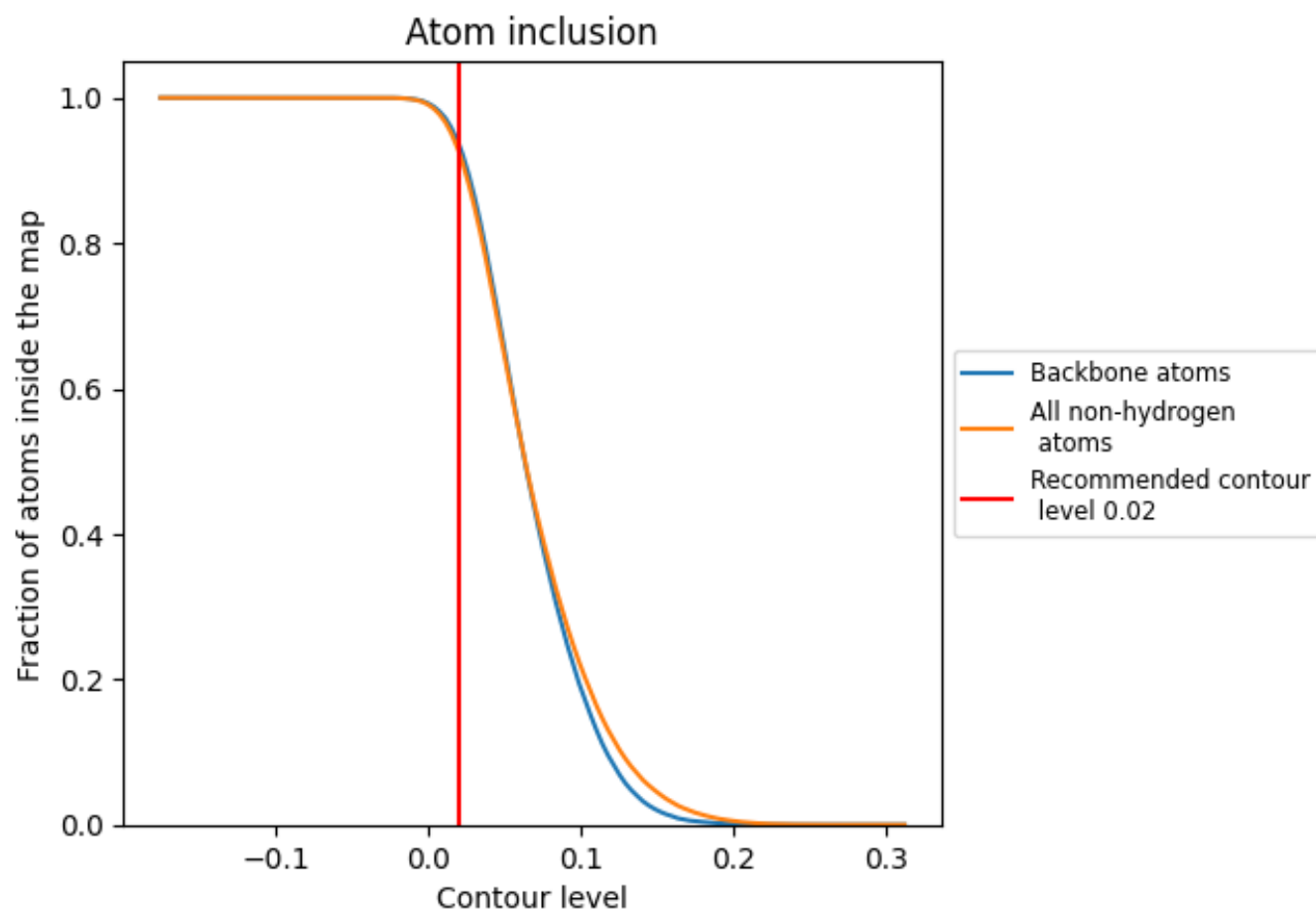
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9277	 0.4380
3	 0.9106	 0.5190
4	 0.8929	 0.3240
5	 0.8733	 0.4370
6	 0.7957	 0.3270
7	 0.8875	 0.3630
8	 0.5225	 0.1690
9	 0.8693	 0.3250
A	 0.9617	 0.4760
B	 0.9826	 0.4620
C	 0.8919	 0.5100
D	 0.9333	 0.5100
E	 0.9213	 0.4830
F	 0.9158	 0.4010
G	 0.9261	 0.4290
H	 0.5669	 0.2940
I	 0.6284	 0.2350
J	 0.7937	 0.2780
K	 0.9377	 0.5090
L	 0.8934	 0.5020
M	 0.9292	 0.4940
N	 0.9112	 0.5050
O	 0.9247	 0.5030
P	 0.9469	 0.4560
Q	 0.8920	 0.4730
R	 0.9123	 0.5060
S	 0.9503	 0.5090
T	 0.9109	 0.4950
U	 0.9108	 0.4620
V	 0.9028	 0.4270
W	 0.8955	 0.4510
X	 0.9329	 0.5160
Y	 0.5182	 0.2720
Z	 0.9333	 0.4440
a	 0.9346	 0.4990



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Chain	Atom inclusion	Q-score
b	 0.9353	 0.4940
c	 0.7622	 0.3500
d	 0.8997	 0.5200
e	 0.9146	 0.5140
f	 0.9373	 0.5230
g	 0.8478	 0.2800
h	 0.9635	 0.4050
j	 0.7824	 0.4360
k	 0.8206	 0.3330
l	 0.8405	 0.3100
m	 0.8562	 0.3790
n	 0.8545	 0.3930
p	 0.8081	 0.3130
q	 0.9253	 0.4160
r	 0.7210	 0.3310
s	 0.8305	 0.3250
t	 0.8556	 0.4150
u	 0.8755	 0.4180
v	 0.8499	 0.3210
x	 0.8846	 0.4130
y	 0.8739	 0.4340
z	 0.8537	 0.3830