



Full wwPDB EM Validation Report ⓘ

Nov 6, 2022 – 07:23 PM EST

PDB ID : 6O8X
EMDB ID : EMD-0657
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class02
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.68 Å (reported)
Based on initial models : 4YBB, 5LI0

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

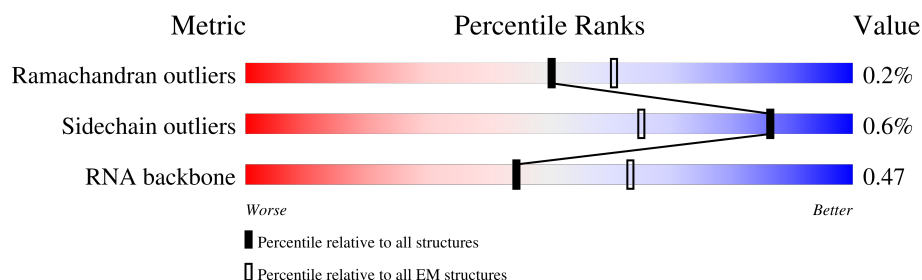
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.68 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.



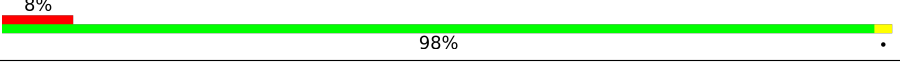
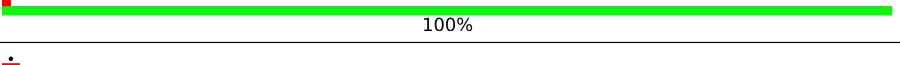
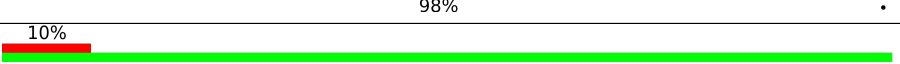
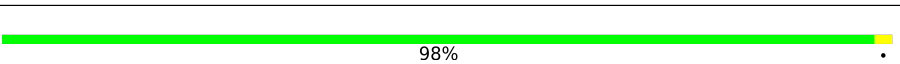
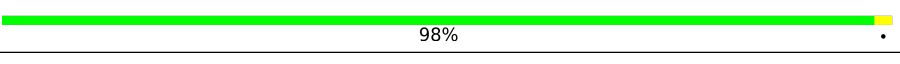
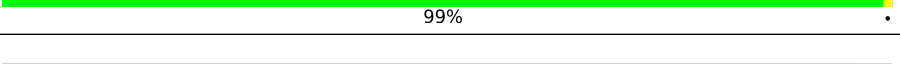
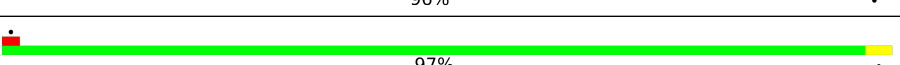
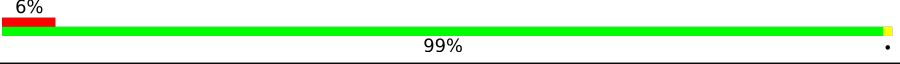
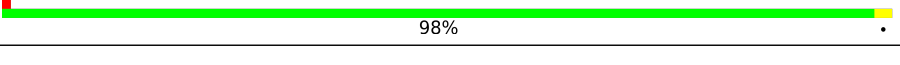

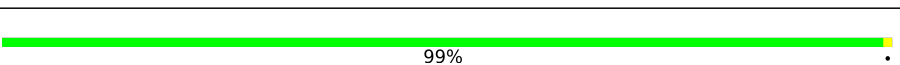
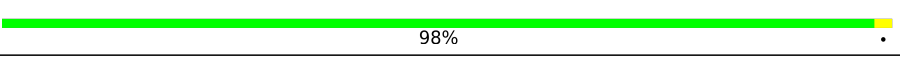
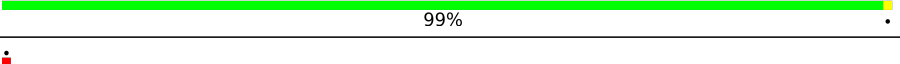
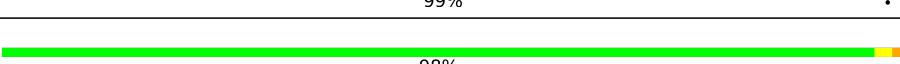
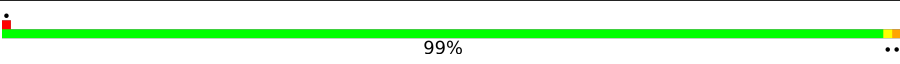
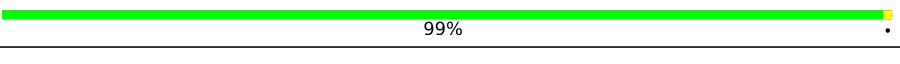
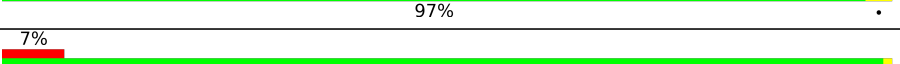
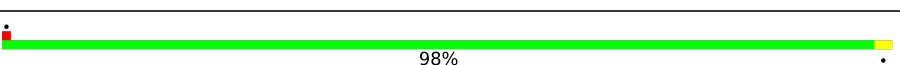
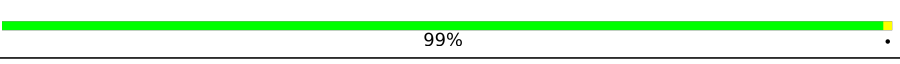
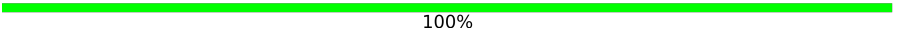



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	a	1528	
2	c	204	
3	d	201	
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	

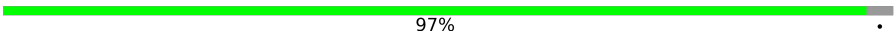

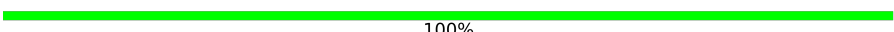
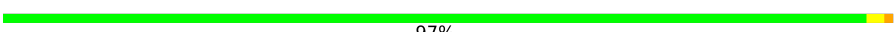
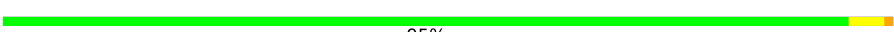








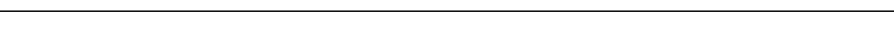
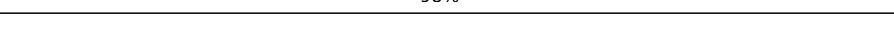
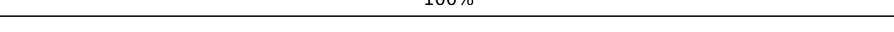
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Mol	Chain	Length	Quality of chain
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	A	2903	
21	B	116	
22	C	275	
23	D	207	
24	E	206	
25	F	177	
26	G	176	
27	K	145	
28	L	122	
29	M	146	
30	N	141	
31	O	123	
32	P	117	
33	Q	114	

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Mol	Chain	Length	Quality of chain
34	R	118	 97%
35	S	102	 99%
36	T	112	 100%
37	U	89	 97%
38	V	101	 95%
39	W	94	 67%
40	X	76	 98%
41	Y	54	 94% 6%
42	Z	61	 100%
43	0	58	 98%
44	1	60	 5%
45	2	56	 100%
46	3	49	 100%
47	4	44	 98%
48	5	64	 100%
49	6	38	 100%

2 Entry composition [i](#)

There are 50 unique types of molecules in this entry. The entry contains 138230 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	a	1528	Total	C	N	O	P	0	0
			32746	14609	5979	10630	1528		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	204	Total	C	N	O	S	0	0
			1610	1012	303	292	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1620	1016	303	297	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	97	Total	C	N	O	S	0	0
			795	501	137	154	3		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	154	Total	C	N	O	S	0	0
			1229	765	236	222	6		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	128	Total	C	N	O	S	0	0
			990	615	197	177	1		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	99	Total	C	N	O	S	0	0
			800	504	147	147	2		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			863	533	165	161	4		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	136	Total	C	N	O	S	0	0
			1065	661	214	188	2		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	112	Total	C	N	O	S	0	0
			884	540	180	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	88	Total	C	N	O	S	0	0
			741	455	152	133	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	89	Total	C	N	O	S	0	0
			708	448	131	127	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	83	Total	C	N	O	S	0	0
			681	427	127	124	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	66	Total	C	N	O	S	0	0
			537	343	99	94	1		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	78	Total	C	N	O	S	0	0
			634	410	113	109	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	81	Total	C	N	O	S	0	0
			610	372	119	117	2		

- Molecule 20 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A	2898	Total	C	N	O	P	0	0
			62196	27761	11436	20101	2898		

- Molecule 21 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B	116	Total	C	N	O	P	0	0
			2478	1105	444	813	116		

- Molecule 22 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	C	275	Total	C	N	O	S	0	0
			2114	1310	416	381	7		

- Molecule 23 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	207	Total	C	N	O	S	0	0
			1578	993	292	289	4		

- Molecule 24 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E	206	Total	C	N	O	S	0	0
			1572	984	289	297	2		

- Molecule 25 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F	177	Total	C	N	O	S	0	0
			1391	886	239	260	6		

- Molecule 26 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	G	176	Total	C	N	O	S	0	0
			1344	841	244	255	4		

- Molecule 27 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	145	Total	C	N	O	S	0	0
			1129	713	205	207	4		

- Molecule 28 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	122	Total	C	N	O	S	0	0
			922	574	176	170	2		

- Molecule 29 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	M	146	Total	C	N	O	S	0	0
			1094	676	212	205	1		

- Molecule 30 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	141	Total	C	N	O	S	0	0
			1117	709	216	185	7		

- Molecule 31 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O	123	Total	C	N	O	S	0	0
			978	603	189	183	3		

- Molecule 32 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	117	Total	C	N	O	S	0	0
			898	555	175	167	1		

- Molecule 33 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	114	Total	C	N	O	0	0
			924	582	185	157		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	R	115	Total	C	N	O	S	0	0
			913	580	172	157	4		

- Molecule 35 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	S	102	Total	C	N	O	S	0	0
			783	500	138	143	2		

- Molecule 36 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	T	112	Total	C	N	O	S	0	0
			849	532	156	159	2		

- Molecule 37 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	89	Total	C	N	O	S	0	0
			719	457	127	132	3		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 39 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	W	94	Total	C	N	O	S	0	0
			757	478	135	140	4		

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	X	76	Total	C	N	O	0	0
			572	351	109	112		

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Y	54	Total	C	N	O	S	0	0
			424	265	86	71	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	51	ALA	THR	conflict	UNP A0A1B4XRZ8

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	61	Total	C	N	O	S	0	0
			504	314	94	95	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	0	58	Total	C	N	O	S	0	0
			435	271	81	82	1		

- Molecule 44 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	60	Total	C	N	O	S	0	0
			475	301	75	97	2		

- Molecule 45 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	56	Total	C	N	O	S	0	0
			429	262	88	73	6		

- Molecule 46 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 47 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	4	44	Total	C	N	O	S	0	0
			373	226	91	54	2		

- Molecule 48 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 49 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

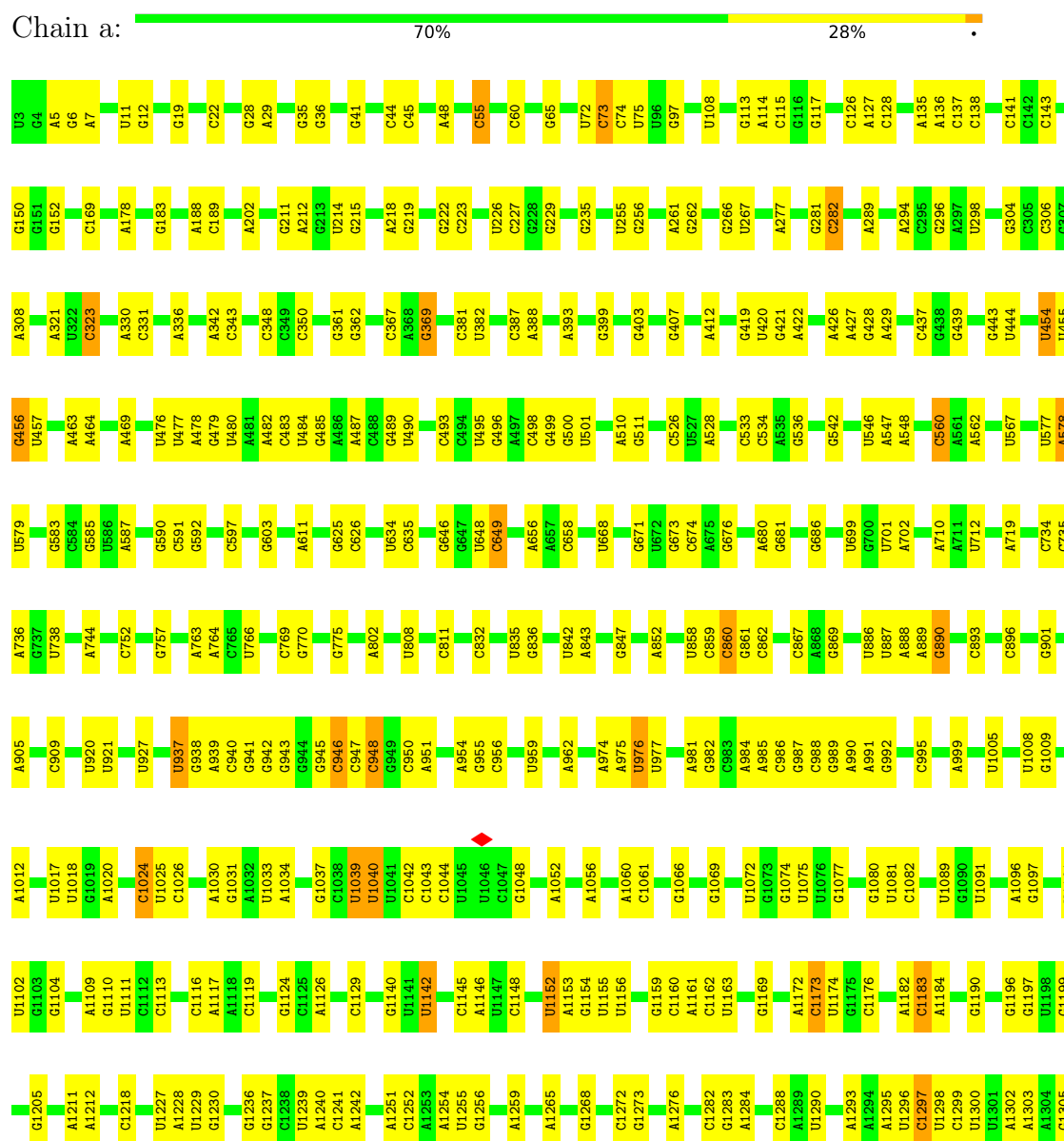
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

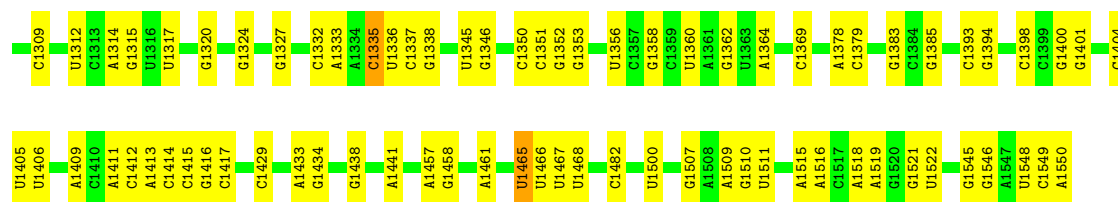
Mol	Chain	Residues	Atoms		AltConf
50	n	1	Total	Zn	0
			1	1	
50	2	1	Total	Zn	0
			1	1	
50	3	1	Total	Zn	0
			1	1	
50	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

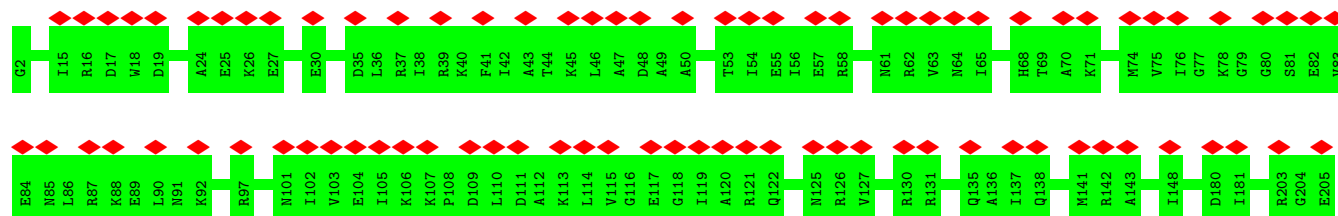
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

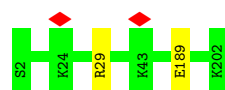




- Molecule 2: 30S ribosomal protein S3



- Molecule 3: 30S ribosomal protein S4



- Molecule 4: 30S ribosomal protein S5



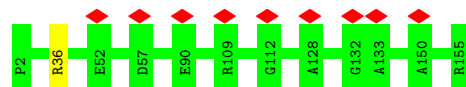
There are no outlier residues recorded for this chain.

- Molecule 5: 30S ribosomal protein S6



There are no outlier residues recorded for this chain.

- Molecule 6: 30S ribosomal protein S7



- Molecule 7: 30S ribosomal protein S8





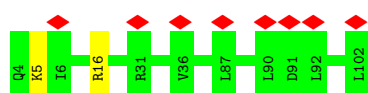
- Molecule 8: 30S ribosomal protein S9

Chain i: 99%



- Molecule 9: 30S ribosomal protein S10

Chain j: 8% 98%



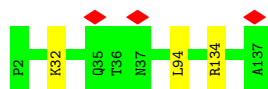
- Molecule 10: 30S ribosomal protein S11

Chain k: 100%



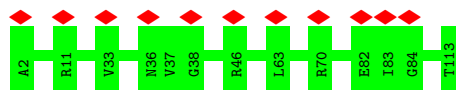
- Molecule 11: 30S ribosomal protein S12

Chain l: 98%



- Molecule 12: 30S ribosomal protein S13

Chain m: 10% 100%




- Molecule 13: 30S ribosomal protein S14 type Z

Chain n: 98%



- Molecule 14: 30S ribosomal protein S15

Chain o:  98% .



- Molecule 15: 30S ribosomal protein S16

Chain p:  99% .



- Molecule 16: 30S ribosomal protein S17

Chain q:  96% .



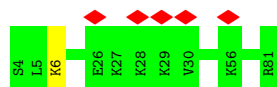
- Molecule 17: 30S ribosomal protein S18

Chain r:  97% .



- Molecule 18: 30S ribosomal protein S19

Chain s:  6% 99% .



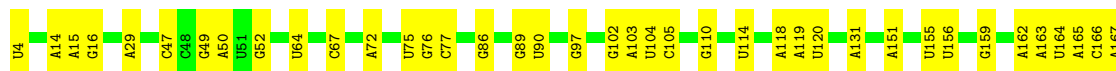
- Molecule 19: 30S ribosomal protein S20

Chain t:  98% .

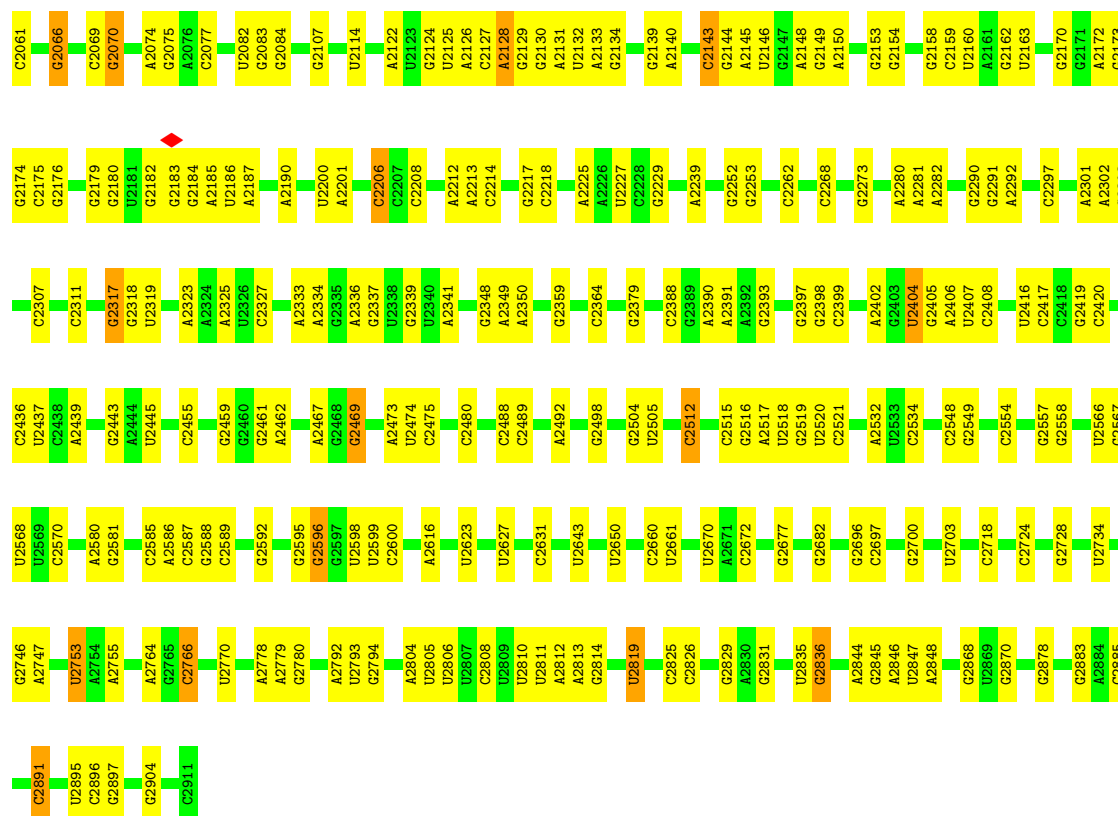


- Molecule 20: 23S rRNA

Chain A:  70% 27% .



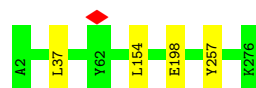
A	G1777	A1615	C1511	A1421	U1292	G1152	A1088	A964	U885	G741	G610	U989	U168
C	G1778	C1623	A1516	C1422	G1293	C1156	C1089	U965	U886	A755	A611	G300	A169
U	A1782	G1428	G1519	G1428	C1294	C1157	C1092	U966	G887	A756	A612	U301	A179
A	G1783	A1629	G1520	A1431	G1302	G1162	U1093	U975	A888	A758	C621	C309	G181
A1931	G1784	A1630	A1521	U1432	G1303	G1163	U1094	G978	A889	A759	G622	G310	U182
A1933	A1787	A1632	U1525	U1433	U1304	A1167	G1095	G978	A890	C759	A623	A311	A163
U1940	G1790	A1633	U1526	C1434	G1308	A1168	G1096	A985	A891	G766	A624	A312	G184
A1942	U1795	C1635	A1530	C1435	A1309	A1169	U1100	G986	U892	G769	G625	A313	A185
G1943	U1796	U1638	G1531	C1436	A1310	A1170	U1101	G986	U893	A770	G626	A318	A189
G1944	A1798	U1639	A1532	U1444	A1311	A1171	G1102	G992	G896	A494	A627	A189	A199
A1952	A1805	C1641	A1536	U1445	G1317	C1174	G1103	A997	G897	A496	G498	C321	U322
U1957	U1805	C1642	U1539	U1446	A1320	C1175	U1104	U997	G900	U786	U499	U322	A199
U1958	C1814	U1645	U1540	U1447	A1321	G1176	U1105	U998	U901	U787	A506	G323	A202
A1959	A1815	A1646	A1545	U1448	A1322	G1177	U1106	A999	A904	G788	A507	U324	A207
U1969	A1816	C1647	U1548	A1451	U1336	C1180	G1108	G1001	G905	A792	G508	A326	G218
U1970	A1817	G1648	C1548	G1452	A1337	U1181	A1109	G1006	C906	A801	G509	G327	A219
C1976	G1821	G1649	U1551	U1453	U1338	A1183	A1110	A1013	A907	A804	G513	G332	A224
G1977	U1822	A1651	A1552	U1454	U1339	A1184	C1112	A1014	G914	G805	G655	G339	A225
C1978	A1823	A1652	A1553	G1455	C1350	A1185	G1113	A1015	A919	G806	G656	G344	A229
C1979	U1827	A1653	A1559	G1456	A1357	C1186	C1115	G1016	G922	G808	A660	G344	A230
A1980	G1828	U1677	G1560	G1457	A1358	A1187	C1116	G1024	G923	G815	G661	C352	A231
C1981	A1829	U1678	C1459	G1458	U1362	A1188	C1117	G1025	C924	G816	C527	U232	U232
A1984	A1830	A1679	A1566	A1461	U1363	A1189	C1118	G1026	C925	C816	C528	C355	U233
A1985	G1831	G1680	C1567	A1462	U1364	A1190	C1119	G1027	C926	G817	C529	A367	C234
G1986	U1832	C1691	G1568	G1463	U1365	C1210	A1120	A1036	A927	A822	G673	U237	G235
U1989	A1833	C1692	G1569	G1464	C1366	C1211	U1121	G1046	G933	A823	A676	A383	A236
C1990	U1834	C1693	G1570	G1465	U1367	A1212	C1122	G1047	G934	U824	C548	G386	A244
A1996	U1841	G1717	A1576	C1470	U1368	U1213	U1123	A1048	U935	U825	C549	C381	G245
G2006	G1842	A1718	A1577	G1471	U1369	G1214	A1124	A1049	U936	U826	G561	C396	U246
U2007	A1843	A1719	A1578	U1475	G1379	G1215	A1125	A1050	A937	U827	C566	C396	G251
C2020	A1862	U1723	U1579	C1479	U1388	U1216	A1126	A1051	C938	A828	C567	A399	A254
A2034	G1872	C1726	G1584	G1488	G1394	C1238	C1131	A1052	C939	G832	C568	G400	G255
G2035	U1878	G1737	A1585	C1489	G1395	G1239	C1132	U1053	C940	A840	C569	A404	C256
U2036	G1881	G1738	G1586	G1490	G1396	G1240	C1133	A1061	A942	G845	A708	G404	A268
A2037	C1882	A1741	A1589	C1493	G1397	A1257	U1134	G1062	U943	C846	G709	G410	G269
C2039	G1886	U1756	C1600	C1494	A1401	U1258	A1135	A1065	A946	G847	A710	A411	C270
A2044	A1896	U1757	G1601	U1496	G1404	U1259	C1136	A1066	U949	G848	C711	G412	C271
G2045	C1907	C1758	C1602	U1497	G1405	A1274	C1137	A1067	A950	G849	A711	U413	C272
A2047	G1907	G1767	G1603	A1500	U1408	A1275	C1138	G1068	A951	U851	A716	A421	A278
U2048	A1913	A1769	C1604	A1501	G1409	C1276	C1139	A1069	U952	U852	U721	A424	C284
G2049	G1917	G1770	A1606	G1503	A1414	C1277	C1140	A1070	A953	G853	U722	A425	U285
C2050	U1925	U1774	C1607	G1504	U1415	A1284	U1145	U1081	C956	U854	U726	G426	U286
A2056	C2057	A1775	A1612	C1505	A1418	G1285	C1146	U1082	U960	U857	C727	G600	C287
C2057	A	A1776	G1614	C1510	A1420	A1290	U1147	C1085	C962	C873	C730	C602	C288



• Molecule 21: 5S rRNA



• Molecule 22: 50S ribosomal protein L2



• Molecule 23: 50S ribosomal protein L3



• Molecule 24: 50S ribosomal protein L4





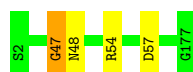
- Molecule 25: 50S ribosomal protein L5

Chain F: 99%



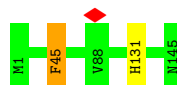
- Molecule 26: 50S ribosomal protein L6

Chain G: 98%



- Molecule 27: 50S ribosomal protein L13

Chain K: 99%



- Molecule 28: 50S ribosomal protein L14

Chain L: 99%



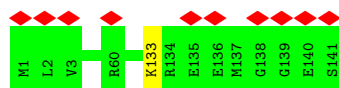
- Molecule 29: 50S ribosomal protein L15

Chain M: 97%



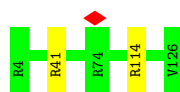
- Molecule 30: 50S ribosomal protein L16

Chain N: 7% 99%



- Molecule 31: 50S ribosomal protein L17

Chain O: 98%



- Molecule 32: 50S ribosomal protein L18

Chain P: 99%



- Molecule 33: 50S ribosomal protein L19

Chain Q: 100%

There are no outlier residues recorded for this chain.

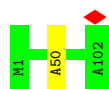
- Molecule 34: 50S ribosomal protein L20

Chain R: 97%



- Molecule 35: 50S ribosomal protein L21

Chain S: 99%



- Molecule 36: 50S ribosomal protein L22

Chain T: 100%

There are no outlier residues recorded for this chain.

- Molecule 37: 50S ribosomal protein L23

Chain U: 97%

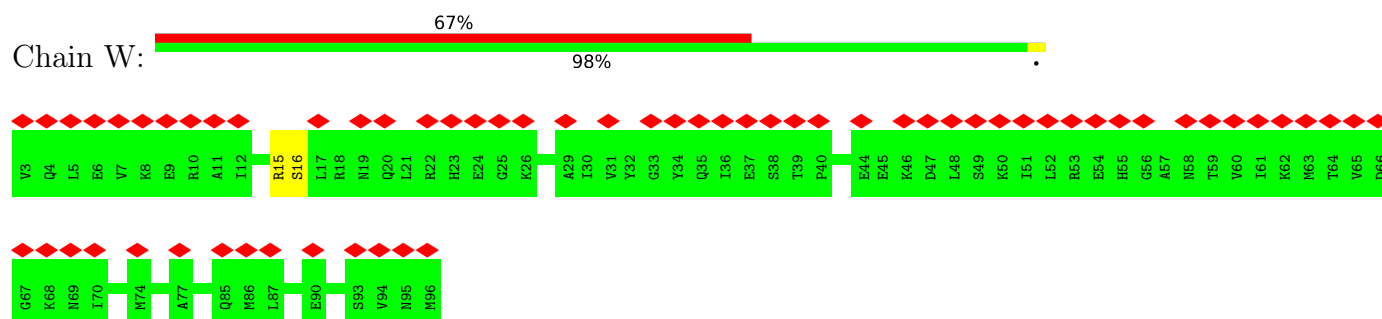


- Molecule 38: 50S ribosomal protein L24

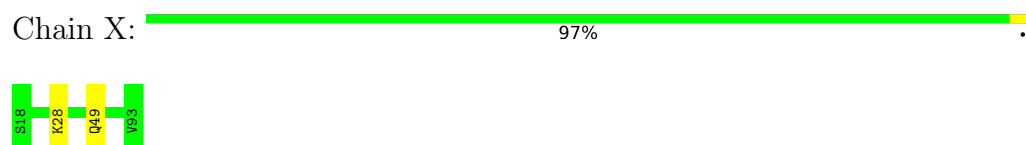
Chain V: 95%



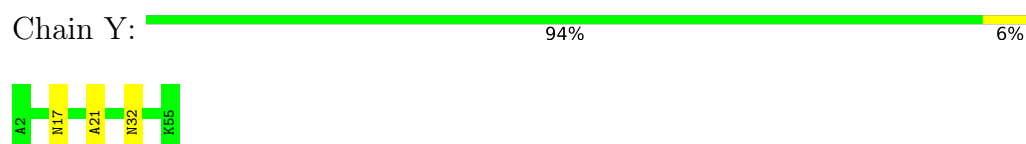
- Molecule 39: 50S ribosomal protein L25



- Molecule 40: 50S ribosomal protein L27



- Molecule 41: 50S ribosomal protein L28

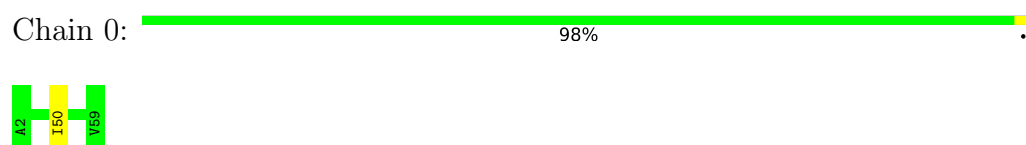


- Molecule 42: 50S ribosomal protein L29

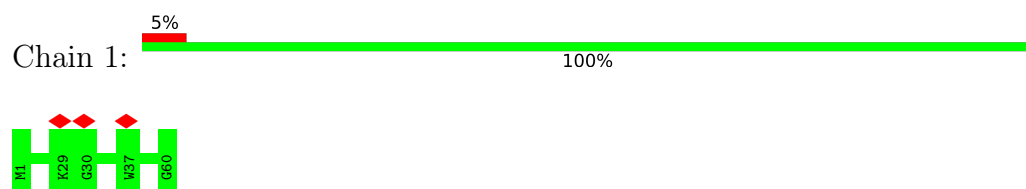


There are no outlier residues recorded for this chain.

- Molecule 43: 50S ribosomal protein L30



- Molecule 44: 50S ribosomal protein L31 type B



- Molecule 45: 50S ribosomal protein L32



There are no outlier residues recorded for this chain.

- Molecule 46: 50S ribosomal protein L33

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 50S ribosomal protein L34

Chain 4:  98%



- Molecule 48: 50S ribosomal protein L35

Chain 5:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L36

Chain 6:  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, C1	Depositor
Number of particles used	32689	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.890	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.238	Depositor
Map size (Å)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.097, 1.097, 1.097	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.66	1/36657 (0.0%)	1.14	181/57173 (0.3%)
2	c	0.28	0/1635	0.57	0/2197
3	d	0.35	0/1650	0.57	0/2217
4	e	0.32	0/1217	0.60	0/1641
5	f	0.36	0/807	0.55	0/1087
6	g	0.30	0/1249	0.55	0/1682
7	h	0.38	0/1054	0.58	0/1417
8	i	0.28	0/1003	0.56	0/1343
9	j	0.28	0/812	0.60	0/1093
10	k	0.34	0/878	0.59	0/1185
11	l	0.33	0/1082	0.65	1/1453 (0.1%)
12	m	0.28	0/890	0.54	0/1195
13	n	0.30	0/504	0.54	0/669
14	o	0.38	0/751	0.58	0/1001
15	p	0.40	0/720	0.61	0/966
16	q	0.38	0/689	0.62	0/920
17	r	0.35	0/544	0.63	0/728
18	s	0.31	0/650	0.55	0/872
19	t	0.33	0/612	0.52	0/818
20	A	0.88	4/69661 (0.0%)	1.20	425/108645 (0.4%)
21	B	0.76	1/2769 (0.0%)	1.22	20/4310 (0.5%)
22	C	0.48	0/2147	0.69	1/2885 (0.0%)
23	D	0.51	0/1598	0.72	0/2145
24	E	0.45	0/1594	0.62	0/2155
25	F	0.35	0/1408	0.57	0/1890
26	G	0.39	0/1362	0.67	1/1833 (0.1%)
27	K	0.49	0/1148	0.71	0/1549
28	L	0.49	0/929	0.68	1/1247 (0.1%)
29	M	0.42	0/1103	0.70	0/1470
30	N	0.46	0/1140	0.69	0/1518
31	O	0.45	0/985	0.76	2/1318 (0.2%)
32	P	0.46	0/907	0.61	0/1214

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Q	0.50	0/938	0.67	0/1262
34	R	0.50	0/923	0.62	0/1227
35	S	0.45	0/794	0.65	0/1064
36	T	0.45	0/858	0.64	0/1157
37	U	0.44	0/724	0.70	0/966
38	V	0.39	0/772	0.71	1/1035 (0.1%)
39	W	0.28	0/766	0.61	0/1030
40	X	0.53	0/578	0.67	0/773
41	Y	0.32	0/430	0.55	0/573
42	Z	0.40	0/505	0.58	0/672
43	0	0.42	0/437	0.66	1/589 (0.2%)
44	1	0.37	0/487	0.64	0/662
45	2	0.47	0/436	0.62	0/578
46	3	0.35	0/423	0.55	0/563
47	4	0.42	0/374	0.68	0/485
48	5	0.42	0/528	0.63	0/689
49	6	0.47	0/309	0.60	0/409
All	All	0.72	6/150437 (0.0%)	1.07	634/225570 (0.3%)

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
3	d	0	2
7	h	0	1
16	q	0	1
19	t	0	1
22	C	0	2
23	D	0	2
24	E	0	1
25	F	0	1
26	G	0	2
27	K	0	2
29	M	0	2
30	N	0	1
32	P	0	1
35	S	0	1
37	U	0	2
38	V	0	2
39	W	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	X	0	2
41	Y	0	1
47	4	0	1
All	All	0	29

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	B	1	U	OP3-P	-10.68	1.48	1.61
20	A	897	G	N9-C4	-5.90	1.33	1.38
20	A	1418	A	N9-C4	-5.32	1.34	1.37
20	A	1805	A	N9-C4	-5.29	1.34	1.37
1	a	939	A	N9-C4	-5.24	1.34	1.37
20	A	1414	A	N9-C4	-5.00	1.34	1.37

All (634) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1335	C	N1-C2-O2	13.14	126.78	118.90
20	A	1130	U	N1-C2-O2	12.36	131.45	122.80
20	A	1130	U	C2-N1-C1'	12.03	132.14	117.70
1	a	1335	C	C2-N1-C1'	11.30	131.22	118.80
20	A	897	G	N3-C4-N9	-11.05	119.37	126.00
20	A	1551	U	N1-C2-O2	10.59	130.22	122.80
20	A	1551	U	C2-N1-C1'	10.52	130.33	117.70
1	a	73	C	N1-C2-O2	10.50	125.20	118.90
20	A	1130	U	N3-C2-O2	-10.45	114.89	122.20
1	a	946	C	C2-N1-C1'	10.31	130.15	118.80
1	a	1335	C	N3-C2-O2	-10.26	114.72	121.90
20	A	1349	U	N3-C2-O2	-10.24	115.03	122.20
1	a	1548	U	N1-C2-O2	10.08	129.86	122.80
20	A	1453	U	C5-C6-N1	9.41	127.41	122.70
20	A	1551	U	N3-C2-O2	-9.36	115.65	122.20
1	a	1465	U	C2-N1-C1'	9.30	128.86	117.70
21	B	68	C	C2-N1-C1'	9.29	129.02	118.80
1	a	1465	U	N1-C2-O2	9.28	129.30	122.80
1	a	141	C	N1-C2-O2	9.08	124.35	118.90
1	a	1548	U	N3-C2-O2	-8.94	115.94	122.20
21	B	68	C	N1-C2-O2	8.91	124.25	118.90
1	a	1548	U	C2-N1-C1'	8.90	128.38	117.70
21	B	73	U	C2-N1-C1'	8.89	128.37	117.70
20	A	1349	U	C2-N1-C1'	8.76	128.21	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1349	U	N1-C2-O2	8.71	128.90	122.80
20	A	2488	C	N1-C2-O2	8.60	124.06	118.90
1	a	1465	U	N3-C2-O2	-8.58	116.20	122.20
20	A	586	A	N1-C6-N6	-8.56	113.47	118.60
1	a	1398	C	N1-C2-O2	8.53	124.02	118.90
20	A	897	G	N3-C4-C5	8.52	132.86	128.60
20	A	1130	U	C6-N1-C1'	-8.50	109.30	121.20
20	A	730	C	C6-N1-C2	-8.47	116.91	120.30
20	A	549	C	N1-C2-O2	8.43	123.96	118.90
20	A	2206	C	C2-N1-C1'	8.40	128.04	118.80
21	B	73	U	N1-C2-O2	8.39	128.67	122.80
21	B	73	U	N3-C2-O2	-8.37	116.34	122.20
20	A	849	G	N1-C6-O6	-8.35	114.89	119.90
20	A	1453	U	C2-N1-C1'	8.31	127.67	117.70
20	A	1907	C	N1-C2-O2	8.29	123.87	118.90
20	A	943	U	C2-N1-C1'	8.28	127.64	117.70
1	a	73	C	N3-C2-O2	-8.21	116.16	121.90
20	A	1907	C	N3-C2-O2	-8.16	116.19	121.90
20	A	164	U	N1-C2-N3	8.12	119.77	114.90
20	A	602	C	C6-N1-C2	-8.04	117.08	120.30
20	A	1148	U	C2-N1-C1'	8.03	127.33	117.70
1	a	1039	U	N1-C2-O2	8.02	128.41	122.80
1	a	1335	C	C6-N1-C2	-8.00	117.10	120.30
20	A	938	C	C6-N1-C2	-7.97	117.11	120.30
20	A	1104	C	N1-C2-O2	7.96	123.67	118.90
1	a	73	C	C2-N1-C1'	7.93	127.53	118.80
20	A	938	C	C5-C6-N1	7.92	124.96	121.00
1	a	946	C	C6-N1-C1'	-7.87	111.35	120.80
20	A	2697	C	N1-C2-O2	7.86	123.62	118.90
20	A	2163	U	C5-C6-N1	7.78	126.59	122.70
1	a	141	C	C6-N1-C2	-7.77	117.19	120.30
20	A	2825	C	N3-C2-O2	-7.74	116.48	121.90
20	A	1452	G	N3-C4-N9	7.71	130.63	126.00
20	A	1758	C	C2-N1-C1'	7.68	127.25	118.80
1	a	579	U	C2-N1-C1'	7.64	126.86	117.70
1	a	1335	C	C6-N1-C1'	-7.64	111.64	120.80
20	A	897	G	N3-C2-N2	-7.63	114.56	119.90
1	a	1113	C	N3-C2-O2	-7.63	116.56	121.90
20	A	1434	C	C2-N1-C1'	7.57	127.12	118.80
1	a	141	C	N3-C2-O2	-7.54	116.62	121.90
20	A	897	G	C4-N9-C1'	-7.51	116.74	126.50
1	a	976	U	C2-N1-C1'	7.50	126.70	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	897	G	C8-N9-C1'	7.50	136.75	127.00
20	A	1093	U	N1-C2-O2	7.48	128.04	122.80
20	A	1452	G	C4-N9-C1'	7.48	136.22	126.50
20	A	2753	U	N1-C2-O2	7.46	128.02	122.80
1	a	1039	U	C2-N1-C1'	7.46	126.65	117.70
20	A	2077	C	N1-C2-O2	7.43	123.36	118.90
21	B	96	G	C4-N9-C1'	7.43	136.15	126.50
20	A	2825	C	N1-C2-O2	7.36	123.31	118.90
20	A	2826	C	C2-N1-C1'	7.34	126.87	118.80
1	a	579	U	N1-C2-O2	7.32	127.92	122.80
20	A	939	C	O4'-C1'-N1	7.29	114.03	108.20
20	A	849	G	C5-C6-O6	7.29	132.97	128.60
20	A	1453	U	N1-C2-O2	7.28	127.90	122.80
20	A	1304	U	C2-N1-C1'	7.25	126.40	117.70
1	a	1398	C	C2-N1-C1'	7.24	126.77	118.80
1	a	976	U	N1-C2-O2	7.20	127.84	122.80
20	A	2208	C	C2-N1-C1'	7.20	126.72	118.80
20	A	901	U	N3-C2-O2	-7.18	117.17	122.20
21	B	89	C	N3-C2-O2	-7.17	116.88	121.90
1	a	141	C	C2-N1-C1'	7.17	126.69	118.80
21	B	68	C	C6-N1-C1'	-7.16	112.21	120.80
20	A	901	U	N1-C2-O2	7.15	127.81	122.80
20	A	1551	U	C6-N1-C1'	-7.12	111.24	121.20
20	A	2794	G	C4-N9-C1'	7.11	135.74	126.50
20	A	1452	G	N3-C4-C5	-7.08	125.06	128.60
20	A	644	U	N1-C2-O2	7.08	127.75	122.80
20	A	644	U	N3-C2-O2	-7.07	117.25	122.20
1	a	940	C	C5-C6-N1	7.06	124.53	121.00
20	A	992	G	N3-C4-N9	7.06	130.24	126.00
1	a	579	U	N3-C2-O2	-7.06	117.26	122.20
20	A	1045	C	N1-C2-O2	7.03	123.12	118.90
1	a	734	C	C6-N1-C2	-7.03	117.49	120.30
20	A	1104	C	N3-C2-O2	-7.01	116.99	121.90
20	A	602	C	N3-C2-O2	-6.96	117.03	121.90
20	A	1502	G	C4-N9-C1'	6.95	135.54	126.50
1	a	454	U	N1-C2-O2	6.94	127.66	122.80
20	A	1647	C	C6-N1-C2	-6.93	117.53	120.30
20	A	1604	A	P-O3'-C3'	6.93	128.01	119.70
1	a	1152	U	C2-N1-C1'	6.92	126.00	117.70
1	a	1039	U	N3-C2-O2	-6.90	117.37	122.20
20	A	1024	G	N3-C4-C5	-6.89	125.16	128.60
20	A	2670	U	C2-N1-C1'	6.88	125.95	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	941	G	C8-N9-C4	-6.88	103.65	106.40
1	a	1335	C	C5-C6-N1	6.87	124.44	121.00
21	B	68	C	N3-C2-O2	-6.87	117.09	121.90
1	a	927	U	N3-C2-O2	-6.86	117.40	122.20
20	A	1970	U	N3-C2-O2	-6.85	117.40	122.20
20	A	1102	G	C6-C5-N7	-6.85	126.29	130.40
20	A	1584	G	P-O3'-C3'	6.85	127.92	119.70
1	a	454	U	N3-C2-O2	-6.82	117.42	122.20
20	A	1758	C	C6-N1-C2	-6.81	117.58	120.30
1	a	941	G	N7-C8-N9	6.80	116.50	113.10
20	A	549	C	N3-C2-O2	-6.80	117.14	121.90
20	A	2488	C	N3-C2-O2	-6.80	117.14	121.90
20	A	1024	G	N3-C4-N9	6.80	130.08	126.00
20	A	943	U	N1-C2-O2	6.80	127.56	122.80
1	a	115	C	N1-C2-O2	6.79	122.98	118.90
20	A	2262	C	C2-N1-C1'	6.78	126.25	118.80
20	A	1304	U	N1-C2-O2	6.77	127.54	122.80
20	A	963	C	C6-N1-C2	-6.77	117.59	120.30
20	A	602	C	C2-N1-C1'	6.76	126.23	118.80
20	A	1970	U	N1-C2-O2	6.75	127.52	122.80
1	a	323	C	N1-C2-O2	6.72	122.93	118.90
20	A	901	U	C2-N1-C1'	6.72	125.76	117.70
1	a	419	G	N3-C4-C5	-6.72	125.24	128.60
1	a	927	U	N1-C2-O2	6.71	127.50	122.80
20	A	2753	U	N3-C2-O2	-6.70	117.51	122.20
1	a	1398	C	N3-C2-O2	-6.69	117.22	121.90
20	A	2724	C	N3-C2-O2	-6.68	117.22	121.90
20	A	1511	C	N3-C2-O2	-6.67	117.23	121.90
1	a	141	C	C5-C6-N1	6.66	124.33	121.00
20	A	527	C	N1-C2-O2	6.66	122.89	118.90
20	A	2035	G	N3-C4-N9	6.65	129.99	126.00
20	A	1045	C	C2-N1-C1'	6.62	126.08	118.80
20	A	602	C	N1-C2-O2	6.62	122.87	118.90
20	A	164	U	N3-C2-O2	-6.61	117.58	122.20
20	A	1024	G	C4-N9-C1'	6.60	135.08	126.50
20	A	939	C	N3-C2-O2	-6.59	117.29	121.90
20	A	1607	C	N1-C2-O2	6.59	122.85	118.90
20	A	2206	C	C6-N1-C2	-6.58	117.67	120.30
1	a	1024	C	N3-C2-O2	-6.58	117.29	121.90
20	A	1790	G	N3-C4-N9	6.57	129.94	126.00
20	A	963	C	N3-C2-O2	-6.55	117.32	121.90
1	a	1548	U	C6-N1-C1'	-6.54	112.04	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1502	G	P-O3'-C3'	6.54	127.55	119.70
20	A	649	C	C5-C6-N1	6.54	124.27	121.00
1	a	940	C	N1-C2-O2	6.54	122.82	118.90
20	A	2044	A	N7-C8-N9	6.53	117.06	113.80
20	A	2408	C	N1-C2-O2	6.53	122.82	118.90
20	A	1210	C	N1-C2-O2	6.52	122.81	118.90
1	a	1152	U	N1-C2-O2	6.50	127.35	122.80
20	A	2554	C	N1-C2-O2	6.50	122.80	118.90
20	A	1452	G	C8-N9-C1'	-6.50	118.56	127.00
20	A	1790	G	C4-N9-C1'	6.50	134.94	126.50
20	A	2554	C	N3-C2-O2	-6.49	117.36	121.90
20	A	2819	U	N3-C2-O2	-6.48	117.66	122.20
20	A	906	C	N1-C2-O2	6.47	122.78	118.90
1	a	115	C	N3-C2-O2	-6.46	117.38	121.90
20	A	1216	G	C5-C6-O6	6.46	132.47	128.60
1	a	734	C	N3-C2-O2	-6.45	117.38	121.90
20	A	561	G	C6-C5-N7	-6.45	126.53	130.40
20	A	848	G	N1-C6-O6	-6.45	116.03	119.90
21	B	96	G	C8-N9-C1'	-6.44	118.63	127.00
20	A	413	U	N3-C2-O2	-6.43	117.70	122.20
20	A	2127	C	C2-N1-C1'	6.43	125.87	118.80
20	A	1210	C	C2-N1-C1'	6.42	125.86	118.80
20	A	1102	G	N3-C4-N9	6.41	129.85	126.00
20	A	992	G	C4-N9-C1'	6.40	134.82	126.50
1	a	712	U	N1-C2-O2	6.39	127.27	122.80
1	a	734	C	C2-N1-C1'	6.39	125.83	118.80
20	A	2020	C	C6-N1-C2	-6.38	117.75	120.30
1	a	1358	G	N7-C8-N9	6.37	116.28	113.10
20	A	549	C	C2-N1-C1'	6.37	125.80	118.80
20	A	1768	C	C6-N1-C2	-6.36	117.76	120.30
20	A	2214	C	C5-C6-N1	6.36	124.18	121.00
1	a	959	U	N3-C2-O2	-6.35	117.76	122.20
20	A	2794	G	C8-N9-C1'	-6.34	118.75	127.00
1	a	22	C	N3-C2-O2	-6.32	117.47	121.90
20	A	1723	U	N3-C2-O2	-6.32	117.78	122.20
1	a	995	C	C2-N1-C1'	6.31	125.74	118.80
20	A	960	U	N3-C2-O2	-6.31	117.78	122.20
20	A	2317	G	P-O3'-C3'	6.31	127.27	119.70
38	V	71	ILE	C-N-CA	6.30	137.46	121.70
1	a	946	C	N1-C2-O2	6.30	122.68	118.90
1	a	1218	C	C5-C6-N1	6.29	124.14	121.00
1	a	995	C	C6-N1-C2	-6.28	117.79	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	164	U	C2-N3-C4	-6.28	123.23	127.00
1	a	143	C	C2-N1-C1'	6.27	125.69	118.80
20	A	906	C	C2-N1-C1'	6.26	125.68	118.80
1	a	456	G	N3-C4-N9	6.25	129.75	126.00
20	A	1093	U	N3-C2-O2	-6.25	117.83	122.20
20	A	1047	C	C6-N1-C2	-6.24	117.80	120.30
20	A	2044	A	C8-N9-C4	-6.24	103.31	105.80
1	a	927	U	C2-N1-C1'	6.23	125.17	117.70
20	A	2007	U	N3-C2-O2	-6.22	117.85	122.20
1	a	1482	C	N3-C2-O2	-6.21	117.56	121.90
20	A	1304	U	N3-C2-O2	-6.20	117.86	122.20
1	a	1482	C	N1-C2-O2	6.20	122.62	118.90
1	a	477	U	N3-C2-O2	-6.20	117.86	122.20
20	A	1502	G	C8-N9-C1'	-6.20	118.94	127.00
20	A	2128	A	C4-N9-C1'	6.19	137.45	126.30
20	A	1648	C	C6-N1-C2	-6.19	117.82	120.30
20	A	287	G	N3-C4-N9	6.19	129.71	126.00
20	A	287	G	N3-C4-C5	-6.18	125.51	128.60
20	A	396	C	C2-N1-C1'	6.18	125.60	118.80
1	a	976	U	N3-C2-O2	-6.18	117.88	122.20
20	A	1210	C	C6-N1-C2	-6.16	117.83	120.30
20	A	1148	U	N1-C2-O2	6.16	127.11	122.80
1	a	1152	U	N3-C2-O2	-6.16	117.89	122.20
20	A	287	G	C4-N9-C1'	6.15	134.49	126.50
20	A	943	U	N3-C2-O2	-6.14	117.90	122.20
20	A	2697	C	N3-C2-O2	-6.14	117.60	121.90
20	A	2724	C	N1-C2-O2	6.14	122.58	118.90
1	a	635	C	N1-C2-O2	6.13	122.58	118.90
20	A	1805	A	N7-C8-N9	6.13	116.87	113.80
20	A	931	C	C2-N1-C1'	6.12	125.53	118.80
20	A	992	G	C8-N9-C1'	-6.12	119.05	127.00
1	a	940	C	C2-N1-C1'	6.11	125.52	118.80
1	a	22	C	N1-C2-O2	6.09	122.56	118.90
20	A	2819	U	N1-C2-O2	6.09	127.06	122.80
1	a	108	U	N3-C2-O2	-6.09	117.94	122.20
1	a	1040	U	C2-N1-C1'	6.09	125.01	117.70
1	a	1173	C	C2-N1-C1'	6.08	125.49	118.80
1	a	995	C	N1-C2-O2	6.08	122.55	118.90
20	A	1502	G	N3-C4-N9	6.07	129.64	126.00
20	A	1197	G	N3-C4-N9	6.07	129.64	126.00
20	A	1827	U	N3-C2-O2	-6.07	117.95	122.20
1	a	893	C	N1-C2-O2	6.05	122.53	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1317	G	C4-N9-C1'	6.05	134.37	126.50
20	A	1758	C	N1-C2-O2	6.05	122.53	118.90
20	A	77	C	C5-C6-N1	6.04	124.02	121.00
20	A	67	C	N1-C2-O2	6.04	122.53	118.90
1	a	1345	U	N1-C2-O2	6.04	127.03	122.80
1	a	567	U	N3-C2-O2	-6.04	117.97	122.20
20	A	272	C	C2-N1-C1'	6.04	125.44	118.80
20	A	509	G	O4'-C1'-N9	6.03	113.02	108.20
20	A	1459	C	N1-C2-O2	6.02	122.51	118.90
1	a	1465	U	C6-N1-C1'	-6.02	112.77	121.20
1	a	456	G	C4-N9-C1'	6.01	134.32	126.50
21	B	36	C	N1-C2-O2	6.01	122.51	118.90
20	A	897	G	C6-C5-N7	6.01	134.01	130.40
20	A	2512	C	C6-N1-C2	-6.01	117.89	120.30
1	a	73	C	C6-N1-C2	-6.01	117.90	120.30
20	A	1695	C	N1-C2-O2	6.00	122.50	118.90
1	a	699	U	N3-C2-O2	-5.99	118.00	122.20
20	A	1695	C	C6-N1-C2	-5.99	117.90	120.30
1	a	560	C	C2-N1-C1'	5.97	125.37	118.80
1	a	55	C	C2-N1-C1'	5.97	125.36	118.80
20	A	1504	G	O4'-C1'-N9	5.97	112.97	108.20
1	a	1297	C	C6-N1-C2	-5.96	117.91	120.30
20	A	325	U	N1-C2-O2	5.96	126.97	122.80
20	A	1981	C	C2-N1-C1'	5.96	125.35	118.80
20	A	1399	C	C2-N1-C1'	5.96	125.35	118.80
20	A	1479	C	C6-N1-C2	-5.95	117.92	120.30
20	A	1502	G	N3-C4-C5	-5.94	125.63	128.60
20	A	114	U	N3-C2-O2	-5.93	118.05	122.20
20	A	730	C	C2-N1-C1'	5.93	125.33	118.80
26	G	54	ARG	NE-CZ-NH1	-5.93	117.33	120.30
1	a	214	U	N3-C2-O2	-5.93	118.05	122.20
20	A	1551	U	C5-C6-N1	5.93	125.67	122.70
20	A	561	G	N3-C4-N9	5.92	129.55	126.00
20	A	1362	U	N1-C2-O2	5.92	126.95	122.80
1	a	946	C	C5-C6-N1	5.92	123.96	121.00
20	A	1350	C	C2-N1-C1'	5.92	125.31	118.80
20	A	897	G	N9-C4-C5	5.92	107.77	105.40
20	A	2007	U	N1-C2-O2	5.91	126.94	122.80
20	A	325	U	N3-C2-O2	-5.91	118.07	122.20
20	A	1146	A	P-O3'-C3'	5.91	126.79	119.70
20	A	2303	G	C8-N9-C4	-5.90	104.04	106.40
1	a	578	A	C4-N9-C1'	5.90	136.91	126.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	B	96	G	N3-C4-N9	5.89	129.54	126.00
20	A	2206	C	C5-C6-N1	5.89	123.94	121.00
21	B	73	U	C5-C6-N1	5.88	125.64	122.70
1	a	625	G	C4-N9-C1'	5.87	134.14	126.50
20	A	256	C	C6-N1-C2	-5.87	117.95	120.30
20	A	1157	C	C2-N1-C1'	5.87	125.25	118.80
20	A	309	C	N1-C2-O2	5.87	122.42	118.90
31	O	41	ARG	CA-CB-CG	5.86	126.29	113.40
20	A	413	U	N1-C2-O2	5.86	126.90	122.80
1	a	1024	C	N1-C2-O2	5.85	122.41	118.90
20	A	992	G	C6-C5-N7	-5.85	126.89	130.40
20	A	527	C	N3-C2-O2	-5.83	117.82	121.90
20	A	1790	G	C8-N9-C1'	-5.83	119.42	127.00
1	a	1218	C	C6-N1-C2	-5.83	117.97	120.30
20	A	2480	C	C6-N1-C2	-5.83	117.97	120.30
20	A	1293	G	N3-C4-N9	5.83	129.50	126.00
20	A	2670	U	N3-C2-O2	-5.82	118.12	122.20
1	a	995	C	C5-C6-N1	5.82	123.91	121.00
1	a	673	G	N7-C8-N9	5.82	116.01	113.10
20	A	2262	C	C6-N1-C2	-5.82	117.97	120.30
20	A	2143	C	N1-C2-O2	5.82	122.39	118.90
20	A	2214	C	C6-N1-C2	-5.81	117.97	120.30
1	a	712	U	N3-C2-O2	-5.81	118.13	122.20
1	a	658	C	C6-N1-C2	-5.81	117.98	120.30
20	A	2206	C	N1-C2-O2	5.81	122.38	118.90
20	A	114	U	C2-N1-C1'	5.81	124.67	117.70
20	A	769	G	N3-C4-N9	-5.80	122.52	126.00
20	A	424	A	C2-N3-C4	5.78	113.49	110.60
1	a	626	C	N1-C2-O2	5.77	122.36	118.90
20	A	943	U	C6-N1-C1'	-5.77	113.12	121.20
20	A	104	U	N1-C2-O2	5.76	126.83	122.80
20	A	1362	U	N3-C2-O2	-5.76	118.17	122.20
20	A	1647	C	N3-C2-O2	-5.75	117.87	121.90
1	a	419	G	C2-N3-C4	5.74	114.77	111.90
20	A	939	C	N1-C2-O2	5.74	122.34	118.90
20	A	2794	G	N3-C4-N9	5.74	129.44	126.00
20	A	1723	U	N1-C2-O2	5.74	126.82	122.80
20	A	1081	U	N1-C2-O2	5.73	126.81	122.80
20	A	1130	U	C5-C6-N1	5.73	125.57	122.70
20	A	286	U	C2-N1-C1'	5.73	124.58	117.70
20	A	1047	C	C2-N1-C1'	5.73	125.10	118.80
20	A	309	C	C6-N1-C2	-5.73	118.01	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1293	G	C4-N9-C1'	5.73	133.94	126.50
20	A	2057	C	C2-N1-C1'	5.72	125.10	118.80
21	B	87	U	C5-C6-N1	5.72	125.56	122.70
1	a	1299	C	C5-C6-N1	5.72	123.86	121.00
20	A	549	C	C6-N1-C2	-5.72	118.01	120.30
20	A	621	C	C5-C6-N1	5.71	123.85	121.00
20	A	1045	C	N3-C2-O2	-5.71	117.90	121.90
20	A	2585	C	C6-N1-C2	-5.71	118.02	120.30
1	a	1288	C	C5-C6-N1	5.70	123.85	121.00
20	A	936	U	N1-C2-O2	5.70	126.79	122.80
20	A	1197	G	C4-N9-C1'	5.69	133.90	126.50
1	a	734	C	N1-C2-O2	5.69	122.31	118.90
1	a	752	C	C6-N1-C2	-5.69	118.02	120.30
20	A	2826	C	N1-C2-O2	5.69	122.31	118.90
21	B	85	U	C5-C6-N1	5.68	125.54	122.70
20	A	936	U	N3-C2-O2	-5.68	118.22	122.20
20	A	730	C	C5-C6-N1	5.68	123.84	121.00
1	a	456	G	C8-N9-C1'	-5.67	119.64	127.00
20	A	769	G	N3-C4-C5	5.66	131.43	128.60
20	A	1530	A	P-O3'-C3'	5.66	126.49	119.70
20	A	2050	C	N1-C2-O2	5.66	122.30	118.90
1	a	752	C	C5-C6-N1	5.66	123.83	121.00
1	a	890	G	N3-C4-N9	5.65	129.39	126.00
1	a	454	U	C5-C6-N1	5.65	125.53	122.70
20	A	2061	C	C6-N1-C2	-5.65	118.04	120.30
1	a	298	U	N3-C2-O2	-5.65	118.25	122.20
20	A	1758	C	N3-C2-O2	-5.64	117.95	121.90
1	a	649	C	N3-C2-O2	-5.64	117.95	121.90
20	A	1718	C	N1-C2-O2	5.64	122.28	118.90
20	A	1408	U	N3-C2-O2	-5.64	118.25	122.20
20	A	2262	C	C5-C6-N1	5.64	123.82	121.00
1	a	940	C	C6-N1-C2	-5.63	118.05	120.30
20	A	1605	C	P-O3'-C3'	5.63	126.46	119.70
1	a	323	C	N3-C2-O2	-5.63	117.96	121.90
20	A	2044	A	C4-N9-C1'	5.62	136.43	126.30
20	A	2127	C	C6-N1-C2	-5.62	118.05	120.30
20	A	1505	C	C6-N1-C2	-5.62	118.05	120.30
20	A	2766	C	N1-C2-O2	5.62	122.27	118.90
20	A	1448	U	C2-N1-C1'	5.61	124.44	117.70
20	A	2311	C	N3-C2-O2	-5.61	117.97	121.90
20	A	895	U	N3-C2-O2	-5.61	118.27	122.20
20	A	2044	A	O4'-C1'-N9	5.61	112.69	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	992	G	N3-C4-C5	-5.61	125.80	128.60
20	A	1317	G	N3-C4-N9	5.61	129.36	126.00
20	A	2229	G	N3-C4-N9	5.61	129.36	126.00
1	a	959	U	N1-C2-O2	5.60	126.72	122.80
20	A	1638	C	C2-N1-C1'	5.60	124.96	118.80
1	a	369	G	C4-N9-C1'	5.60	133.78	126.50
1	a	55	C	N1-C2-O2	5.59	122.26	118.90
20	A	413	U	C2-N1-C1'	5.59	124.41	117.70
20	A	1197	G	C6-C5-N7	-5.59	127.04	130.40
20	A	1293	G	C8-N9-C1'	-5.59	119.73	127.00
21	B	35	C	C6-N1-C2	-5.59	118.06	120.30
20	A	67	C	N3-C2-O2	-5.59	117.99	121.90
20	A	730	C	N3-C2-O2	-5.59	117.99	121.90
20	A	801	A	C5-N7-C8	-5.59	101.11	103.90
20	A	1024	G	C8-N9-C1'	-5.58	119.74	127.00
1	a	769	C	C2-N1-C1'	5.58	124.94	118.80
20	A	2206	C	C6-N1-C1'	-5.58	114.10	120.80
20	A	1695	C	C2-N1-C1'	5.58	124.94	118.80
20	A	2039	C	C2-N1-C1'	5.58	124.94	118.80
20	A	1453	U	C6-N1-C1'	-5.57	113.40	121.20
20	A	2307	C	C5-C6-N1	5.57	123.78	121.00
20	A	1434	C	C5-C6-N1	5.57	123.78	121.00
1	a	55	C	C6-N1-C2	-5.56	118.08	120.30
1	a	1091	U	N3-C2-O2	-5.56	118.31	122.20
20	A	2885	C	N3-C2-O2	-5.55	118.01	121.90
1	a	1338	G	O5'-P-OP1	-5.55	100.70	105.70
20	A	2127	C	N3-C2-O2	-5.55	118.02	121.90
20	A	2408	C	N3-C2-O2	-5.55	118.02	121.90
20	A	730	C	N1-C2-O2	5.55	122.23	118.90
20	A	1211	C	C6-N1-C2	-5.54	118.08	120.30
1	a	1297	C	C5-C6-N1	5.54	123.77	121.00
20	A	2589	C	C6-N1-C2	-5.54	118.08	120.30
20	A	2891	C	N3-C2-O2	-5.54	118.02	121.90
1	a	55	C	C5-C6-N1	5.54	123.77	121.00
20	A	352	C	N1-C2-O2	5.53	122.22	118.90
20	A	167	A	N1-C6-N6	5.53	121.92	118.60
20	A	1024	G	C2-N3-C4	5.53	114.67	111.90
20	A	848	G	C5-C6-O6	5.52	131.91	128.60
20	A	1081	U	N3-C2-O2	-5.52	118.34	122.20
20	A	1156	C	C2-N1-C1'	5.51	124.86	118.80
20	A	1349	U	C6-N1-C1'	-5.51	113.48	121.20
1	a	1398	C	C6-N1-C2	-5.51	118.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1092	C	C6-N1-C2	-5.51	118.10	120.30
21	B	73	U	C6-N1-C1'	-5.50	113.50	121.20
1	a	766	U	N3-C2-O2	-5.50	118.35	122.20
20	A	1590	A	N1-C6-N6	-5.49	115.30	118.60
20	A	104	U	N3-C2-O2	-5.49	118.36	122.20
1	a	1026	C	C6-N1-C2	-5.49	118.10	120.30
20	A	655	G	C8-N9-C4	5.49	108.59	106.40
20	A	960	U	C6-N1-C2	-5.48	117.71	121.00
20	A	2290	G	N3-C4-C5	-5.48	125.86	128.60
20	A	2512	C	C2-N1-C1'	5.48	124.83	118.80
20	A	975	U	N3-C2-O2	-5.47	118.37	122.20
1	a	1163	U	N3-C2-O2	-5.47	118.37	122.20
1	a	1465	U	C5-C6-N1	5.47	125.44	122.70
1	a	597	C	N1-C2-O2	5.47	122.18	118.90
1	a	1401	G	C8-N9-C4	-5.46	104.22	106.40
20	A	2070	G	C4-N9-C1'	5.46	133.60	126.50
20	A	2311	C	C6-N1-C2	-5.46	118.12	120.30
20	A	1790	G	C6-C5-N7	-5.46	127.13	130.40
20	A	1069	A	N7-C8-N9	5.46	116.53	113.80
20	A	499	U	N3-C2-O2	-5.45	118.39	122.20
20	A	1211	C	C5-C4-N4	5.45	124.01	120.20
20	A	272	C	N1-C2-O2	5.45	122.17	118.90
20	A	2826	C	C6-N1-C2	-5.45	118.12	120.30
1	a	1183	C	C2-N1-C1'	5.44	124.79	118.80
1	a	214	U	N1-C2-O2	5.44	126.61	122.80
20	A	4	U	C2-N1-C1'	5.44	124.22	117.70
20	A	823	A	C4-N9-C1'	5.43	136.08	126.30
20	A	1996	U	N3-C2-O2	-5.43	118.40	122.20
1	a	419	G	N3-C4-N9	5.43	129.26	126.00
20	A	1102	G	C4-N9-C1'	5.43	133.55	126.50
1	a	1142	U	N3-C2-O2	-5.42	118.41	122.20
20	A	1148	U	C6-N1-C1'	-5.42	113.61	121.20
21	B	96	G	N3-C4-C5	-5.42	125.89	128.60
1	a	626	C	N3-C2-O2	-5.42	118.11	121.90
20	A	2670	U	N1-C2-O2	5.42	126.59	122.80
20	A	1434	C	C6-N1-C1'	-5.41	114.30	120.80
20	A	2208	C	N1-C2-O2	5.40	122.14	118.90
1	a	649	C	N1-C2-O2	5.39	122.14	118.90
20	A	2474	U	N1-C2-O2	5.39	126.58	122.80
20	A	1574	C	C2-N1-C1'	5.39	124.73	118.80
20	A	1197	G	C4-C5-N7	5.39	112.95	110.80
1	a	921	U	N3-C2-O2	-5.38	118.43	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	2895	U	N3-C2-O2	-5.38	118.43	122.20
20	A	246	U	N3-C2-O2	-5.38	118.43	122.20
20	A	2700	G	N3-C4-C5	-5.38	125.91	128.60
20	A	2077	C	N3-C2-O2	-5.38	118.14	121.90
20	A	602	C	C5-C6-N1	5.37	123.69	121.00
20	A	2672	C	N1-C2-O2	5.37	122.12	118.90
20	A	2896	C	C6-N1-C2	-5.37	118.15	120.30
1	a	282	C	C2-N1-C1'	5.36	124.70	118.80
20	A	2388	C	N3-C2-O2	-5.36	118.15	121.90
20	A	1317	G	C8-N9-C1'	-5.36	120.04	127.00
20	A	956	C	N1-C2-O2	5.35	122.11	118.90
20	A	1317	G	N3-C4-C5	-5.35	125.92	128.60
1	a	948	C	C2-N1-C1'	5.35	124.68	118.80
20	A	975	U	N1-C2-O2	5.34	126.54	122.80
20	A	2836	G	C6-C5-N7	-5.34	127.19	130.40
1	a	348	C	N1-C2-O2	5.34	122.11	118.90
1	a	920	U	N3-C2-O2	-5.34	118.46	122.20
20	A	2127	C	N1-C2-O2	5.34	122.11	118.90
20	A	1128	A	C4-N9-C1'	5.34	135.91	126.30
20	A	2469	G	C4-N9-C1'	5.33	133.44	126.50
1	a	941	G	C5-N7-C8	-5.33	101.64	104.30
20	A	1501	A	C4-N9-C1'	5.33	135.89	126.30
20	A	1479	C	C2-N1-C1'	5.32	124.66	118.80
1	a	635	C	N3-C2-O2	-5.32	118.18	121.90
20	A	2035	G	N3-C4-C5	-5.32	125.94	128.60
20	A	114	U	N1-C2-O2	5.32	126.52	122.80
1	a	959	U	C2-N1-C1'	5.31	124.07	117.70
20	A	780	C	C6-N1-C2	-5.31	118.18	120.30
20	A	1408	U	N1-C2-O2	5.31	126.52	122.80
20	A	2057	C	C6-N1-C2	-5.30	118.18	120.30
20	A	1128	A	N7-C8-N9	5.30	116.45	113.80
20	A	2520	U	N3-C2-O2	-5.30	118.49	122.20
20	A	234	C	N3-C4-C5	5.30	124.02	121.90
1	a	560	C	N1-C2-O2	5.29	122.08	118.90
20	A	716	A	O4'-C1'-N9	5.29	112.43	108.20
1	a	1290	U	C5-C6-N1	5.29	125.35	122.70
1	a	1142	U	N1-C2-O2	5.29	126.50	122.80
20	A	2596	G	C8-N9-C4	-5.29	104.29	106.40
20	A	105	C	C2-N1-C1'	5.28	124.61	118.80
1	a	348	C	C2-N1-C1'	5.28	124.60	118.80
20	A	286	U	C5-C6-N1	5.27	125.34	122.70
20	A	2070	G	C8-N9-C1'	-5.27	120.15	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1024	C	C6-N1-C2	-5.26	118.19	120.30
21	B	24	U	N3-C2-O2	-5.26	118.52	122.20
20	A	287	G	C8-N9-C1'	-5.26	120.16	127.00
20	A	963	C	P-O3'-C3'	5.26	126.01	119.70
20	A	1878	U	C2-N1-C1'	5.26	124.01	117.70
20	A	2311	C	N1-C2-O2	5.26	122.06	118.90
1	a	73	C	C5-C6-N1	5.26	123.63	121.00
1	a	578	A	C8-N9-C1'	-5.25	118.24	127.70
1	a	1369	C	C5-C6-N1	5.25	123.63	121.00
20	A	1238	C	C6-N1-C2	-5.25	118.20	120.30
20	A	2488	C	C2-N1-C1'	5.25	124.58	118.80
1	a	1039	U	C6-N1-C1'	-5.25	113.85	121.20
1	a	1162	C	C6-N1-C2	-5.25	118.20	120.30
20	A	566	C	N1-C2-O2	5.25	122.05	118.90
20	A	1148	U	N3-C2-O2	-5.25	118.53	122.20
20	A	1193	C	C2-N1-C1'	5.25	124.57	118.80
20	A	1210	C	N3-C2-O2	-5.25	118.22	121.90
1	a	73	C	C6-N1-C1'	-5.24	114.52	120.80
20	A	823	A	C2-N3-C4	5.24	113.22	110.60
1	a	143	C	N1-C2-O2	5.23	122.04	118.90
20	A	2404	U	N1-C2-O2	5.23	126.46	122.80
1	a	946	C	C6-N1-C2	-5.23	118.21	120.30
1	a	1173	C	N1-C2-O2	5.23	122.04	118.90
1	a	937	U	N3-C2-O2	-5.23	118.54	122.20
20	A	1434	C	N1-C2-O2	5.22	122.03	118.90
20	A	1128	A	N3-C4-N9	5.22	131.57	127.40
20	A	1092	C	N1-C2-O2	5.21	122.03	118.90
20	A	931	C	N1-C2-O2	5.21	122.03	118.90
11	l	94	LEU	CA-CB-CG	5.21	127.28	115.30
20	A	2070	G	N3-C4-N9	5.21	129.12	126.00
1	a	1345	U	C2-N1-C1'	5.21	123.95	117.70
20	A	721	U	N3-C2-O2	-5.21	118.56	122.20
20	A	722	G	C8-N9-C1'	-5.21	120.23	127.00
20	A	2128	A	C8-N9-C1'	-5.20	118.34	127.70
1	a	350	C	C6-N1-C2	-5.20	118.22	120.30
20	A	1304	U	C5-C6-N1	5.20	125.30	122.70
20	A	1907	C	C2-N1-C1'	5.20	124.52	118.80
1	a	1077	G	N3-C4-N9	5.20	129.12	126.00
20	A	1096	G	N3-C4-C5	-5.20	126.00	128.60
20	A	561	G	C4-N9-C1'	5.19	133.25	126.50
20	A	1882	C	C2-N1-C1'	5.19	124.51	118.80
20	A	561	G	N9-C4-C5	-5.19	103.32	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1293	G	C6-C5-N7	-5.19	127.28	130.40
1	a	1162	C	C5-C6-N1	5.19	123.59	121.00
20	A	1585	U	N3-C2-O2	-5.19	118.57	122.20
20	A	2020	C	C2-N1-C1'	5.19	124.51	118.80
20	A	2520	U	N1-C2-O2	5.19	126.43	122.80
20	A	2175	C	C6-N1-C2	-5.18	118.23	120.30
21	B	73	U	C6-N1-C2	-5.18	117.89	121.00
20	A	1641	C	N1-C2-O2	5.18	122.01	118.90
20	A	1726	C	C5-C6-N1	5.18	123.59	121.00
20	A	591	U	N3-C2-O2	-5.18	118.58	122.20
20	A	1459	C	N3-C2-O2	-5.17	118.28	121.90
20	A	2469	G	N3-C4-C5	-5.17	126.01	128.60
1	a	909	C	N1-C2-O2	5.17	122.00	118.90
20	A	2290	G	C8-N9-C4	-5.17	104.33	106.40
20	A	237	U	N3-C2-O2	-5.17	118.58	122.20
1	a	579	U	C6-N1-C1'	-5.16	113.97	121.20
20	A	1505	C	N3-C2-O2	-5.16	118.29	121.90
20	A	1379	G	C4-N9-C1'	5.16	133.20	126.50
20	A	1831	G	C4-N9-C1'	5.16	133.20	126.50
20	A	873	C	C6-N1-C2	-5.15	118.24	120.30
20	A	1501	A	C2-N3-C4	5.15	113.17	110.60
20	A	355	C	C5-C6-N1	5.15	123.57	121.00
20	A	47	C	C6-N1-C2	-5.15	118.24	120.30
1	a	128	C	C2-N1-C1'	5.15	124.46	118.80
1	a	941	G	C4-C5-N7	5.14	112.86	110.80
20	A	2515	C	C6-N1-C2	-5.14	118.24	120.30
31	O	41	ARG	CB-CG-CD	-5.14	98.23	111.60
20	A	2885	C	N1-C2-O2	5.14	121.98	118.90
20	A	2404	U	N3-C2-O2	-5.14	118.60	122.20
1	a	1299	C	N1-C2-O2	5.13	121.98	118.90
20	A	1096	G	N3-C4-N9	5.13	129.08	126.00
20	A	2825	C	C6-N1-C2	-5.13	118.25	120.30
1	a	1299	C	C6-N1-C2	-5.13	118.25	120.30
20	A	758	A	O4'-C1'-N9	5.13	112.30	108.20
20	A	2084	G	C4-N9-C1'	5.12	133.16	126.50
20	A	960	U	N1-C2-O2	5.12	126.39	122.80
20	A	1695	C	N3-C2-O2	-5.12	118.31	121.90
20	A	2480	C	C2-N1-C1'	5.12	124.44	118.80
20	A	105	C	C6-N1-C2	-5.12	118.25	120.30
1	a	267	U	C2-N1-C1'	5.12	123.84	117.70
1	a	1183	C	N1-C2-O2	5.11	121.97	118.90
20	A	476	C	N3-C2-O2	-5.11	118.33	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	1178	G	C8-N9-C4	-5.11	104.36	106.40
1	a	860	C	C5-C6-N1	5.10	123.55	121.00
20	A	657	C	C6-N1-C2	-5.10	118.26	120.30
20	A	1146	A	OP1-P-O3'	5.10	116.43	105.20
20	A	2474	U	N3-C2-O2	-5.10	118.63	122.20
22	C	37	LEU	CA-CB-CG	5.10	127.03	115.30
20	A	823	A	C8-N9-C4	-5.10	103.76	105.80
1	a	108	U	N1-C2-O2	5.10	126.37	122.80
20	A	621	C	C2-N1-C1'	5.10	124.41	118.80
1	a	1398	C	C5-C6-N1	5.09	123.55	121.00
20	A	1790	G	N3-C4-C5	-5.09	126.05	128.60
20	A	2208	C	C6-N1-C1'	-5.09	114.69	120.80
20	A	2268	C	N1-C2-O2	5.09	121.95	118.90
20	A	892	U	N3-C2-O2	-5.08	118.64	122.20
20	A	1350	C	C5-C6-N1	5.08	123.54	121.00
1	a	976	U	C6-N1-C1'	-5.08	114.08	121.20
20	A	591	U	N1-C2-O2	5.08	126.36	122.80
20	A	2734	U	N3-C2-O2	-5.08	118.64	122.20
20	A	1137	U	N1-C2-O2	5.08	126.35	122.80
20	A	2718	C	N1-C2-O2	5.08	121.94	118.90
1	a	138	C	C2-N1-C1'	5.07	124.38	118.80
20	A	2291	G	N9-C4-C5	5.07	107.43	105.40
1	a	178	A	C8-N9-C4	-5.07	103.77	105.80
1	a	1345	U	N3-C2-O2	-5.07	118.65	122.20
20	A	1641	C	C6-N1-C2	-5.07	118.27	120.30
1	a	1429	C	C2-N1-C1'	5.06	124.37	118.80
1	a	369	G	C8-N9-C1'	-5.06	120.42	127.00
1	a	1252	C	N1-C2-O2	5.06	121.93	118.90
28	L	64	ARG	CA-CB-CG	5.06	124.52	113.40
20	A	1148	U	C5-C6-N1	5.05	125.23	122.70
43	O	50	ILE	CG1-CB-CG2	-5.05	100.28	111.40
20	A	769	G	C2-N3-C4	-5.05	109.37	111.90
20	A	1197	G	C8-N9-C1'	-5.05	120.43	127.00
1	a	498	C	N1-C2-O2	5.05	121.93	118.90
20	A	1147	G	P-O3'-C3'	5.05	125.76	119.70
20	A	1399	C	C6-N1-C2	-5.05	118.28	120.30
1	a	811	C	C2-N1-C1'	5.05	124.36	118.80
20	A	561	G	C8-N9-C1'	-5.05	120.44	127.00
20	A	1459	C	C2-N1-C1'	5.04	124.35	118.80
20	A	1719	A	C8-N9-C4	-5.04	103.78	105.80
20	A	1605	C	OP2-P-O3'	5.04	116.28	105.20
20	A	2404	U	C2-N1-C1'	5.04	123.75	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	A	2467	A	C5-N7-C8	-5.04	101.38	103.90
20	A	638	C	C2-N1-C1'	5.04	124.34	118.80
20	A	396	C	N1-C2-O2	5.03	121.92	118.90
20	A	2631	C	N1-C2-O2	5.03	121.92	118.90
20	A	960	U	P-O3'-C3'	5.03	125.74	119.70
20	A	1585	U	P-O3'-C3'	5.03	125.73	119.70
20	A	1723	U	C2-N1-C1'	5.03	123.73	117.70
20	A	721	U	N1-C2-O2	5.03	126.32	122.80
20	A	2891	C	N1-C2-O2	5.02	121.91	118.90
20	A	2020	C	C5-C6-N1	5.02	123.51	121.00
20	A	2035	G	C4-N9-C1'	5.02	133.03	126.50
1	a	1297	C	C2-N1-C1'	5.02	124.32	118.80
20	A	956	C	N3-C2-O2	-5.01	118.39	121.90
20	A	1379	G	C8-N9-C1'	-5.01	120.48	127.00
20	A	2066	G	C6-C5-N7	-5.01	127.39	130.40
20	A	2794	G	C6-C5-N7	-5.01	127.39	130.40
20	A	1137	U	C2-N1-C1'	5.01	123.71	117.70
1	a	597	C	N3-C2-O2	-5.01	118.39	121.90
20	A	2672	C	N3-C2-O2	-5.01	118.39	121.90
20	A	561	G	C4-C5-N7	5.00	112.80	110.80
20	A	1785	C	C6-N1-C2	-5.00	118.30	120.30
20	A	1907	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
47	4	3	ARG	Peptide
22	C	154	LEU	Peptide
22	C	198	GLU	Peptide
23	D	53	TYR	Peptide
23	D	89	GLY	Peptide
24	E	13	GLN	Peptide
25	F	121	ALA	Peptide
26	G	47	GLY	Peptide
26	G	57	ASP	Peptide
27	K	131	HIS	Peptide
27	K	45	PHE	Peptide
29	M	30	THR	Peptide
29	M	85	PHE	Peptide
30	N	133	LYS	Peptide
32	P	30	ARG	Peptide

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Mol	Chain	Res	Type	Group
35	S	50	ALA	Peptide
37	U	50	VAL	Peptide
37	U	84	GLU	Peptide
38	V	72	ASP	Peptide
38	V	87	ASP	Peptide
39	W	15	ARG	Peptide
40	X	28	LYS	Peptide
40	X	49	GLN	Peptide
41	Y	21	ALA	Peptide
3	d	189	GLU	Peptide
3	d	29	ARG	Peptide
7	h	22	HIS	Peptide
16	q	73	THR	Peptide
19	t	66	ILE	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	c	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
3	d	199/201 (99%)	175 (88%)	24 (12%)	0	100	100
4	e	161/163 (99%)	146 (91%)	15 (9%)	0	100	100
5	f	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
6	g	152/154 (99%)	138 (91%)	14 (9%)	0	100	100
7	h	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
8	i	126/128 (98%)	107 (85%)	19 (15%)	0	100	100
9	j	97/99 (98%)	85 (88%)	12 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	k	115/117 (98%)	93 (81%)	22 (19%)	0	100	100
11	l	134/136 (98%)	107 (80%)	27 (20%)	0	100	100
12	m	110/112 (98%)	90 (82%)	20 (18%)	0	100	100
13	n	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
14	o	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
15	p	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
16	q	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
17	r	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
18	s	76/78 (97%)	69 (91%)	7 (9%)	0	100	100
19	t	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
22	C	271/275 (98%)	228 (84%)	43 (16%)	0	100	100
23	D	205/207 (99%)	177 (86%)	27 (13%)	1 (0%)	29	66
24	E	204/206 (99%)	170 (83%)	34 (17%)	0	100	100
25	F	174/177 (98%)	153 (88%)	21 (12%)	0	100	100
26	G	172/176 (98%)	147 (86%)	23 (13%)	2 (1%)	13	49
27	K	141/145 (97%)	123 (87%)	18 (13%)	0	100	100
28	L	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
29	M	144/146 (99%)	109 (76%)	33 (23%)	2 (1%)	11	45
30	N	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
31	O	119/123 (97%)	94 (79%)	25 (21%)	0	100	100
32	P	115/117 (98%)	98 (85%)	17 (15%)	0	100	100
33	Q	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
34	R	110/118 (93%)	104 (94%)	6 (6%)	0	100	100
35	S	98/102 (96%)	88 (90%)	10 (10%)	0	100	100
36	T	110/112 (98%)	94 (86%)	16 (14%)	0	100	100
37	U	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	6	36
38	V	99/101 (98%)	75 (76%)	21 (21%)	3 (3%)	4	32
39	W	92/94 (98%)	71 (77%)	20 (22%)	1 (1%)	14	50
40	X	74/76 (97%)	62 (84%)	12 (16%)	0	100	100
41	Y	52/54 (96%)	41 (79%)	11 (21%)	0	100	100
42	Z	59/61 (97%)	54 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	0	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
44	1	58/60 (97%)	39 (67%)	19 (33%)	0	100	100
45	2	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
46	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
47	4	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
48	5	62/64 (97%)	53 (86%)	9 (14%)	0	100	100
49	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5102/5212 (98%)	4375 (86%)	716 (14%)	11 (0%)	50	78

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	G	48	ASN
26	G	47	GLY
29	M	95	VAL
38	V	73	PRO
39	W	16	SER
23	D	90	GLU
37	U	52	ASN
29	M	16	ARG
38	V	72	ASP
37	U	50	VAL
38	V	88	GLY

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	c	162/162 (100%)	162 (100%)	0	100	100
3	d	175/175 (100%)	175 (100%)	0	100	100
4	e	126/126 (100%)	126 (100%)	0	100	100
5	f	86/86 (100%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	g	131/131 (100%)	130 (99%)	1 (1%)	81	89
7	h	112/112 (100%)	112 (100%)	0	100	100
8	i	101/101 (100%)	100 (99%)	1 (1%)	76	86
9	j	90/90 (100%)	88 (98%)	2 (2%)	52	72
10	k	91/91 (100%)	91 (100%)	0	100	100
11	l	118/118 (100%)	116 (98%)	2 (2%)	60	79
12	m	95/95 (100%)	95 (100%)	0	100	100
13	n	51/51 (100%)	50 (98%)	1 (2%)	55	74
14	o	78/78 (100%)	76 (97%)	2 (3%)	46	69
15	p	79/79 (100%)	78 (99%)	1 (1%)	69	83
16	q	76/76 (100%)	74 (97%)	2 (3%)	46	69
17	r	57/57 (100%)	55 (96%)	2 (4%)	36	63
18	s	68/68 (100%)	67 (98%)	1 (2%)	65	81
19	t	62/62 (100%)	61 (98%)	1 (2%)	62	79
22	C	225/225 (100%)	224 (100%)	1 (0%)	91	95
23	D	169/170 (99%)	167 (99%)	2 (1%)	71	84
24	E	172/172 (100%)	170 (99%)	2 (1%)	71	84
25	F	153/154 (99%)	153 (100%)	0	100	100
26	G	146/146 (100%)	146 (100%)	0	100	100
27	K	122/122 (100%)	121 (99%)	1 (1%)	81	89
28	L	98/98 (100%)	98 (100%)	0	100	100
29	M	111/112 (99%)	111 (100%)	0	100	100
30	N	111/112 (99%)	111 (100%)	0	100	100
31	O	104/105 (99%)	103 (99%)	1 (1%)	76	86
32	P	91/91 (100%)	91 (100%)	0	100	100
33	Q	97/97 (100%)	97 (100%)	0	100	100
34	R	88/94 (94%)	88 (100%)	0	100	100
35	S	83/83 (100%)	83 (100%)	0	100	100
36	T	95/95 (100%)	95 (100%)	0	100	100
37	U	80/80 (100%)	80 (100%)	0	100	100
38	V	85/85 (100%)	85 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	W	84/85 (99%)	84 (100%)	0	100	100
40	X	61/61 (100%)	61 (100%)	0	100	100
41	Y	46/47 (98%)	44 (96%)	2 (4%)	29	58
42	Z	55/55 (100%)	55 (100%)	0	100	100
43	0	49/49 (100%)	49 (100%)	0	100	100
44	1	54/55 (98%)	54 (100%)	0	100	100
45	2	46/46 (100%)	46 (100%)	0	100	100
46	3	49/49 (100%)	49 (100%)	0	100	100
47	4	38/39 (97%)	38 (100%)	0	100	100
48	5	51/51 (100%)	51 (100%)	0	100	100
49	6	35/35 (100%)	35 (100%)	0	100	100
All	All	4356/4371 (100%)	4331 (99%)	25 (1%)	86	93

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	g	36	ARG
8	i	14	ASN
9	j	5	LYS
9	j	16	ARG
11	l	32	LYS
11	l	134	ARG
13	n	26	ARG
14	o	54	ARG
14	o	89	ARG
15	p	90	LYS
16	q	5	ARG
16	q	6	ASN
17	r	13	LYS
17	r	65	ARG
18	s	6	LYS
19	t	49	LEU
22	C	257	TYR
23	D	119	PHE
23	D	168	ARG
24	E	74	ARG
24	E	169	ASN
27	K	45	PHE

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Mol	Chain	Res	Type
31	O	114	ARG
41	Y	17	ASN
41	Y	32	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
2	c	85	ASN
3	d	97	ASN
3	d	200	ASN
4	e	8	HIS
6	g	28	ASN
6	g	45	ASN
6	g	68	ASN
6	g	148	ASN
7	h	99	ASN
8	i	14	ASN
8	i	66	ASN
9	j	97	ASN
10	k	101	GLN
11	l	90	HIS
13	n	10	ASN
14	o	9	ASN
16	q	6	ASN
16	q	50	HIS
17	r	56	GLN
19	t	67	HIS
19	t	69	ASN
22	C	128	ASN
22	C	177	ASN
22	C	232	HIS
23	D	37	GLN
24	E	14	ASN
24	E	75	GLN
24	E	169	ASN
25	F	2	ASN
25	F	37	ASN
26	G	44	ASN
30	N	123	HIS
32	P	20	ASN
32	P	101	HIS
34	R	38	GLN

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Mol	Chain	Res	Type
34	R	81	HIS
35	S	81	HIS
36	T	65	ASN
41	Y	17	ASN
41	Y	23	ASN
41	Y	32	ASN
41	Y	34	GLN
43	0	52	HIS
45	2	32	ASN
45	2	40	HIS
45	2	48	HIS
46	3	4	ASN
46	3	26	ASN
47	4	8	ASN
48	5	4	GLN
48	5	7	HIS
48	5	31	HIS
48	5	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1528 (99%)	392 (25%)	0
20	A	2890/2903 (99%)	708 (24%)	24 (0%)
21	B	113/116 (97%)	30 (26%)	1 (0%)
All	All	4529/4547 (99%)	1130 (24%)	25 (0%)

All (1130) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A
1	a	6	G
1	a	7	A
1	a	11	U
1	a	12	G
1	a	19	G
1	a	28	G
1	a	29	A
1	a	35	G
1	a	36	G
1	a	41	G

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Mol	Chain	Res	Type
1	a	44	C
1	a	45	C
1	a	48	A
1	a	55	C
1	a	60	C
1	a	65	G
1	a	72	U
1	a	73	C
1	a	74	C
1	a	75	U
1	a	97	G
1	a	113	G
1	a	114	A
1	a	117	G
1	a	126	C
1	a	127	A
1	a	135	A
1	a	136	A
1	a	137	C
1	a	150	G
1	a	152	G
1	a	169	C
1	a	183	G
1	a	188	A
1	a	189	C
1	a	202	A
1	a	211	G
1	a	212	A
1	a	215	G
1	a	218	A
1	a	219	G
1	a	222	G
1	a	223	C
1	a	226	U
1	a	227	C
1	a	229	G
1	a	235	G
1	a	255	U
1	a	256	G
1	a	261	A
1	a	262	G
1	a	266	G

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Mol	Chain	Res	Type
1	a	277	A
1	a	281	G
1	a	282	C
1	a	289	A
1	a	294	A
1	a	296	G
1	a	304	G
1	a	306	C
1	a	308	A
1	a	321	A
1	a	323	C
1	a	330	A
1	a	331	C
1	a	336	A
1	a	342	A
1	a	343	C
1	a	361	G
1	a	362	G
1	a	367	C
1	a	369	G
1	a	381	C
1	a	382	U
1	a	387	C
1	a	388	A
1	a	393	A
1	a	399	G
1	a	403	G
1	a	407	G
1	a	412	A
1	a	420	U
1	a	421	G
1	a	422	A
1	a	426	A
1	a	427	A
1	a	428	G
1	a	429	A
1	a	437	C
1	a	439	G
1	a	443	G
1	a	444	U
1	a	454	U
1	a	455	U

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Mol	Chain	Res	Type
1	a	456	G
1	a	457	U
1	a	463	A
1	a	464	A
1	a	469	A
1	a	476	U
1	a	478	A
1	a	479	G
1	a	480	U
1	a	482	A
1	a	483	C
1	a	484	U
1	a	485	G
1	a	487	A
1	a	489	G
1	a	490	U
1	a	493	C
1	a	495	U
1	a	496	G
1	a	499	G
1	a	500	G
1	a	501	U
1	a	510	A
1	a	511	G
1	a	526	C
1	a	528	A
1	a	533	C
1	a	534	C
1	a	536	G
1	a	542	G
1	a	546	U
1	a	547	A
1	a	548	A
1	a	560	C
1	a	562	A
1	a	577	U
1	a	578	A
1	a	583	G
1	a	585	G
1	a	587	A
1	a	590	G
1	a	591	C

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Mol	Chain	Res	Type
1	a	592	G
1	a	603	G
1	a	611	A
1	a	634	U
1	a	646	G
1	a	648	U
1	a	649	C
1	a	656	A
1	a	668	U
1	a	671	G
1	a	674	C
1	a	676	G
1	a	680	A
1	a	681	G
1	a	686	G
1	a	701	U
1	a	702	A
1	a	710	A
1	a	719	A
1	a	735	C
1	a	736	A
1	a	738	U
1	a	744	A
1	a	757	G
1	a	763	A
1	a	764	A
1	a	770	G
1	a	775	G
1	a	802	A
1	a	808	U
1	a	832	C
1	a	835	U
1	a	836	G
1	a	842	U
1	a	843	A
1	a	847	G
1	a	852	A
1	a	858	U
1	a	859	C
1	a	860	C
1	a	861	G
1	a	862	C

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Mol	Chain	Res	Type
1	a	867	C
1	a	869	G
1	a	886	U
1	a	887	U
1	a	888	A
1	a	889	A
1	a	890	G
1	a	896	C
1	a	901	G
1	a	905	A
1	a	937	U
1	a	938	G
1	a	942	G
1	a	943	G
1	a	945	G
1	a	946	C
1	a	947	C
1	a	948	C
1	a	950	C
1	a	951	A
1	a	954	A
1	a	955	G
1	a	956	C
1	a	962	A
1	a	974	A
1	a	975	A
1	a	976	U
1	a	977	U
1	a	981	A
1	a	982	G
1	a	984	A
1	a	985	A
1	a	986	C
1	a	987	G
1	a	988	C
1	a	989	G
1	a	990	A
1	a	991	A
1	a	992	G
1	a	999	A
1	a	1005	U
1	a	1008	U

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Mol	Chain	Res	Type
1	a	1009	G
1	a	1012	A
1	a	1017	U
1	a	1018	U
1	a	1020	A
1	a	1024	C
1	a	1025	U
1	a	1030	A
1	a	1031	G
1	a	1033	U
1	a	1034	A
1	a	1037	G
1	a	1039	U
1	a	1040	U
1	a	1042	C
1	a	1043	C
1	a	1044	C
1	a	1048	G
1	a	1052	A
1	a	1056	A
1	a	1060	A
1	a	1061	C
1	a	1066	G
1	a	1069	G
1	a	1072	U
1	a	1074	G
1	a	1075	U
1	a	1080	G
1	a	1081	U
1	a	1082	C
1	a	1089	U
1	a	1096	A
1	a	1097	G
1	a	1101	U
1	a	1102	U
1	a	1104	G
1	a	1109	A
1	a	1110	G
1	a	1111	U
1	a	1116	C
1	a	1117	A
1	a	1119	C

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Mol	Chain	Res	Type
1	a	1124	G
1	a	1126	A
1	a	1129	C
1	a	1140	G
1	a	1142	U
1	a	1145	C
1	a	1146	A
1	a	1148	C
1	a	1152	U
1	a	1153	A
1	a	1154	G
1	a	1155	U
1	a	1156	U
1	a	1159	G
1	a	1160	C
1	a	1161	A
1	a	1169	G
1	a	1172	A
1	a	1173	C
1	a	1174	U
1	a	1176	C
1	a	1182	A
1	a	1183	C
1	a	1184	A
1	a	1190	G
1	a	1196	G
1	a	1197	G
1	a	1199	G
1	a	1205	G
1	a	1211	A
1	a	1212	A
1	a	1227	U
1	a	1228	A
1	a	1229	U
1	a	1230	G
1	a	1236	G
1	a	1237	G
1	a	1239	U
1	a	1240	A
1	a	1241	C
1	a	1242	A
1	a	1251	A

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Mol	Chain	Res	Type
1	a	1254	A
1	a	1255	U
1	a	1256	G
1	a	1259	A
1	a	1265	A
1	a	1268	G
1	a	1272	C
1	a	1273	G
1	a	1276	A
1	a	1282	C
1	a	1283	G
1	a	1284	A
1	a	1293	A
1	a	1295	A
1	a	1296	U
1	a	1297	C
1	a	1298	U
1	a	1300	U
1	a	1302	A
1	a	1303	A
1	a	1305	G
1	a	1309	C
1	a	1312	U
1	a	1314	A
1	a	1315	G
1	a	1317	U
1	a	1320	G
1	a	1324	G
1	a	1327	G
1	a	1332	C
1	a	1333	A
1	a	1335	C
1	a	1336	U
1	a	1337	C
1	a	1346	G
1	a	1350	C
1	a	1351	C
1	a	1352	G
1	a	1353	G
1	a	1356	U
1	a	1360	U
1	a	1362	G

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Mol	Chain	Res	Type
1	a	1364	A
1	a	1378	A
1	a	1379	C
1	a	1383	G
1	a	1385	G
1	a	1393	C
1	a	1394	G
1	a	1400	G
1	a	1404	C
1	a	1405	U
1	a	1406	U
1	a	1409	A
1	a	1411	A
1	a	1412	C
1	a	1413	A
1	a	1414	C
1	a	1415	C
1	a	1416	G
1	a	1417	C
1	a	1433	A
1	a	1434	G
1	a	1438	G
1	a	1441	A
1	a	1457	A
1	a	1458	G
1	a	1461	A
1	a	1465	U
1	a	1466	U
1	a	1467	U
1	a	1468	U
1	a	1500	U
1	a	1507	G
1	a	1509	A
1	a	1510	G
1	a	1511	U
1	a	1515	A
1	a	1516	A
1	a	1518	A
1	a	1519	A
1	a	1521	G
1	a	1522	U
1	a	1545	G

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Mol	Chain	Res	Type
1	a	1546	G
1	a	1549	C
1	a	1550	A
20	A	14	A
20	A	15	A
20	A	16	G
20	A	29	A
20	A	49	G
20	A	50	A
20	A	52	G
20	A	64	U
20	A	72	A
20	A	75	U
20	A	76	G
20	A	86	G
20	A	89	G
20	A	90	U
20	A	97	G
20	A	102	G
20	A	103	A
20	A	110	G
20	A	118	A
20	A	119	A
20	A	120	U
20	A	131	A
20	A	151	A
20	A	155	U
20	A	156	U
20	A	159	G
20	A	162	A
20	A	163	A
20	A	165	A
20	A	166	C
20	A	169	A
20	A	180	G
20	A	182	U
20	A	184	G
20	A	185	A
20	A	189	A
20	A	199	A
20	A	202	A
20	A	207	A

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Mol	Chain	Res	Type
20	A	218	G
20	A	219	A
20	A	224	A
20	A	225	A
20	A	229	A
20	A	231	A
20	A	232	U
20	A	233	U
20	A	235	G
20	A	236	A
20	A	244	A
20	A	251	G
20	A	254	A
20	A	255	G
20	A	268	A
20	A	270	C
20	A	278	A
20	A	284	C
20	A	285	U
20	A	286	U
20	A	288	C
20	A	298	U
20	A	300	G
20	A	302	A
20	A	312	U
20	A	313	A
20	A	318	A
20	A	321	C
20	A	322	U
20	A	324	U
20	A	327	G
20	A	332	G
20	A	339	G
20	A	344	G
20	A	367	A
20	A	383	A
20	A	386	G
20	A	391	C
20	A	396	C
20	A	399	A
20	A	400	G
20	A	404	G

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Mol	Chain	Res	Type
20	A	410	G
20	A	411	A
20	A	412	G
20	A	421	A
20	A	424	A
20	A	426	G
20	A	427	A
20	A	445	C
20	A	446	G
20	A	451	G
20	A	452	A
20	A	487	A
20	A	488	U
20	A	494	A
20	A	495	C
20	A	496	C
20	A	497	A
20	A	506	A
20	A	507	G
20	A	513	G
20	A	517	A
20	A	518	A
20	A	521	G
20	A	543	U
20	A	544	A
20	A	547	U
20	A	548	C
20	A	549	C
20	A	561	G
20	A	566	C
20	A	569	C
20	A	570	A
20	A	571	A
20	A	572	G
20	A	580	U
20	A	585	A
20	A	586	A
20	A	587	U
20	A	588	G
20	A	599	U
20	A	600	G
20	A	610	G

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Mol	Chain	Res	Type
20	A	612	A
20	A	613	U
20	A	623	A
20	A	624	G
20	A	640	A
20	A	651	A
20	A	652	A
20	A	653	G
20	A	654	A
20	A	655	G
20	A	660	A
20	A	661	G
20	A	670	A
20	A	673	G
20	A	676	A
20	A	677	G
20	A	682	A
20	A	684	U
20	A	693	U
20	A	694	G
20	A	696	G
20	A	708	A
20	A	710	A
20	A	711	C
20	A	722	G
20	A	726	U
20	A	727	C
20	A	741	G
20	A	756	A
20	A	758	A
20	A	759	C
20	A	766	G
20	A	769	G
20	A	770	A
20	A	786	U
20	A	787	U
20	A	788	G
20	A	792	A
20	A	804	A
20	A	805	G
20	A	808	G
20	A	815	G

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Mol	Chain	Res	Type
20	A	816	C
20	A	817	G
20	A	822	A
20	A	823	A
20	A	824	U
20	A	825	U
20	A	828	A
20	A	832	G
20	A	833	A
20	A	840	A
20	A	845	G
20	A	846	C
20	A	849	G
20	A	851	U
20	A	852	C
20	A	859	A
20	A	861	A
20	A	867	U
20	A	885	U
20	A	886	U
20	A	888	A
20	A	891	A
20	A	897	G
20	A	900	G
20	A	901	U
20	A	904	A
20	A	905	G
20	A	906	C
20	A	907	A
20	A	914	G
20	A	919	A
20	A	922	G
20	A	923	G
20	A	925	C
20	A	926	C
20	A	927	A
20	A	928	U
20	A	932	G
20	A	934	G
20	A	935	U
20	A	939	C
20	A	942	A

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Mol	Chain	Res	Type
20	A	943	U
20	A	946	A
20	A	949	U
20	A	950	A
20	A	951	A
20	A	953	C
20	A	960	U
20	A	961	G
20	A	964	A
20	A	966	U
20	A	978	G
20	A	985	A
20	A	986	G
20	A	993	A
20	A	997	A
20	A	999	A
20	A	1001	G
20	A	1006	G
20	A	1013	A
20	A	1014	A
20	A	1015	A
20	A	1016	G
20	A	1029	G
20	A	1036	A
20	A	1042	G
20	A	1047	C
20	A	1048	A
20	A	1049	A
20	A	1051	A
20	A	1052	U
20	A	1053	A
20	A	1061	A
20	A	1062	G
20	A	1065	G
20	A	1066	A
20	A	1073	U
20	A	1085	C
20	A	1086	A
20	A	1087	G
20	A	1089	C
20	A	1094	A
20	A	1095	G

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Mol	Chain	Res	Type
20	A	1096	G
20	A	1097	A
20	A	1100	U
20	A	1101	U
20	A	1103	G
20	A	1104	C
20	A	1105	U
20	A	1107	A
20	A	1108	G
20	A	1109	A
20	A	1110	A
20	A	1111	G
20	A	1112	C
20	A	1113	A
20	A	1115	C
20	A	1116	C
20	A	1117	A
20	A	1118	C
20	A	1119	C
20	A	1120	A
20	A	1122	U
20	A	1124	A
20	A	1125	A
20	A	1128	A
20	A	1129	G
20	A	1131	G
20	A	1132	C
20	A	1133	G
20	A	1134	U
20	A	1135	A
20	A	1137	U
20	A	1138	A
20	A	1139	G
20	A	1140	C
20	A	1141	U
20	A	1142	C
20	A	1143	A
20	A	1144	C
20	A	1145	U
20	A	1146	A
20	A	1147	G
20	A	1148	U

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Mol	Chain	Res	Type
20	A	1151	A
20	A	1152	G
20	A	1156	C
20	A	1162	G
20	A	1167	A
20	A	1168	A
20	A	1171	G
20	A	1172	U
20	A	1174	C
20	A	1175	C
20	A	1179	G
20	A	1181	U
20	A	1182	A
20	A	1183	A
20	A	1188	A
20	A	1196	A
20	A	1210	C
20	A	1213	U
20	A	1215	A
20	A	1216	G
20	A	1217	G
20	A	1218	U
20	A	1219	G
20	A	1249	G
20	A	1257	A
20	A	1258	U
20	A	1272	G
20	A	1273	G
20	A	1274	A
20	A	1275	G
20	A	1277	G
20	A	1284	A
20	A	1285	G
20	A	1290	A
20	A	1292	U
20	A	1293	G
20	A	1294	C
20	A	1302	A
20	A	1308	G
20	A	1309	A
20	A	1310	A
20	A	1311	A

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Mol	Chain	Res	Type
20	A	1320	A
20	A	1323	A
20	A	1336	U
20	A	1337	A
20	A	1338	U
20	A	1349	U
20	A	1350	C
20	A	1357	A
20	A	1365	U
20	A	1366	C
20	A	1375	G
20	A	1376	U
20	A	1377	U
20	A	1388	U
20	A	1394	G
20	A	1396	G
20	A	1397	G
20	A	1400	G
20	A	1401	A
20	A	1404	G
20	A	1414	A
20	A	1415	U
20	A	1420	A
20	A	1421	A
20	A	1422	C
20	A	1428	G
20	A	1431	A
20	A	1432	U
20	A	1436	U
20	A	1443	G
20	A	1445	U
20	A	1448	U
20	A	1449	U
20	A	1450	U
20	A	1451	U
20	A	1452	G
20	A	1453	U
20	A	1455	U
20	A	1457	A
20	A	1461	A
20	A	1462	U
20	A	1463	G

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Mol	Chain	Res	Type
20	A	1469	A
20	A	1470	C
20	A	1471	G
20	A	1475	U
20	A	1488	G
20	A	1489	C
20	A	1492	G
20	A	1494	G
20	A	1495	A
20	A	1496	U
20	A	1497	U
20	A	1500	A
20	A	1501	A
20	A	1502	G
20	A	1503	U
20	A	1504	G
20	A	1505	C
20	A	1509	U
20	A	1510	C
20	A	1516	A
20	A	1519	G
20	A	1521	G
20	A	1525	U
20	A	1531	G
20	A	1532	A
20	A	1536	A
20	A	1539	U
20	A	1545	A
20	A	1548	C
20	A	1551	U
20	A	1552	A
20	A	1559	A
20	A	1560	G
20	A	1566	A
20	A	1568	G
20	A	1573	G
20	A	1576	A
20	A	1577	A
20	A	1579	U
20	A	1584	G
20	A	1585	U
20	A	1586	A

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Mol	Chain	Res	Type
20	A	1588	C
20	A	1589	G
20	A	1590	A
20	A	1600	C
20	A	1601	G
20	A	1602	U
20	A	1604	A
20	A	1605	C
20	A	1606	A
20	A	1612	A
20	A	1613	A
20	A	1615	A
20	A	1623	C
20	A	1629	A
20	A	1630	G
20	A	1631	A
20	A	1632	A
20	A	1633	A
20	A	1634	A
20	A	1635	C
20	A	1640	G
20	A	1645	U
20	A	1646	A
20	A	1650	U
20	A	1651	A
20	A	1653	A
20	A	1677	U
20	A	1689	A
20	A	1690	G
20	A	1691	C
20	A	1717	G
20	A	1737	C
20	A	1738	G
20	A	1741	A
20	A	1756	U
20	A	1757	U
20	A	1767	G
20	A	1770	G
20	A	1774	A
20	A	1776	A
20	A	1777	G
20	A	1778	G

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Mol	Chain	Res	Type
20	A	1782	A
20	A	1787	A
20	A	1790	G
20	A	1795	U
20	A	1798	A
20	A	1814	C
20	A	1815	A
20	A	1817	A
20	A	1821	G
20	A	1822	U
20	A	1823	A
20	A	1829	A
20	A	1830	A
20	A	1833	A
20	A	1834	U
20	A	1841	U
20	A	1842	G
20	A	1843	A
20	A	1862	A
20	A	1872	G
20	A	1881	G
20	A	1882	C
20	A	1886	G
20	A	1896	A
20	A	1913	A
20	A	1917	G
20	A	1933	A
20	A	1940	U
20	A	1941	A
20	A	1943	G
20	A	1944	G
20	A	1952	A
20	A	1957	U
20	A	1958	U
20	A	1969	U
20	A	1970	U
20	A	1976	C
20	A	1978	G
20	A	1979	C
20	A	1981	C
20	A	1984	A
20	A	1985	A

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Mol	Chain	Res	Type
20	A	1986	G
20	A	1989	G
20	A	1996	U
20	A	2006	G
20	A	2007	U
20	A	2034	A
20	A	2037	A
20	A	2039	C
20	A	2044	A
20	A	2045	A
20	A	2046	G
20	A	2047	A
20	A	2048	U
20	A	2056	A
20	A	2057	C
20	A	2066	G
20	A	2069	C
20	A	2070	G
20	A	2074	A
20	A	2075	G
20	A	2082	U
20	A	2083	G
20	A	2107	G
20	A	2114	U
20	A	2122	A
20	A	2124	G
20	A	2125	U
20	A	2126	A
20	A	2128	A
20	A	2129	G
20	A	2130	G
20	A	2131	A
20	A	2132	U
20	A	2133	A
20	A	2134	G
20	A	2139	G
20	A	2140	A
20	A	2143	C
20	A	2144	G
20	A	2145	A
20	A	2146	U
20	A	2148	A

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Mol	Chain	Res	Type
20	A	2149	G
20	A	2150	A
20	A	2153	G
20	A	2154	G
20	A	2158	G
20	A	2159	C
20	A	2160	U
20	A	2162	G
20	A	2170	G
20	A	2172	A
20	A	2173	G
20	A	2174	G
20	A	2176	G
20	A	2179	G
20	A	2180	G
20	A	2182	G
20	A	2183	G
20	A	2184	G
20	A	2185	A
20	A	2186	U
20	A	2187	A
20	A	2190	A
20	A	2200	U
20	A	2201	A
20	A	2206	C
20	A	2212	A
20	A	2213	A
20	A	2217	G
20	A	2218	C
20	A	2225	A
20	A	2227	U
20	A	2239	A
20	A	2252	G
20	A	2253	G
20	A	2273	G
20	A	2280	A
20	A	2282	A
20	A	2292	A
20	A	2297	C
20	A	2301	A
20	A	2302	A
20	A	2318	G

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Mol	Chain	Res	Type
20	A	2319	U
20	A	2323	A
20	A	2325	A
20	A	2327	C
20	A	2333	A
20	A	2334	A
20	A	2336	A
20	A	2337	G
20	A	2339	G
20	A	2341	A
20	A	2348	G
20	A	2349	A
20	A	2350	A
20	A	2359	G
20	A	2364	C
20	A	2379	G
20	A	2390	A
20	A	2391	A
20	A	2393	G
20	A	2397	G
20	A	2398	G
20	A	2399	C
20	A	2402	A
20	A	2404	U
20	A	2405	G
20	A	2406	A
20	A	2407	U
20	A	2416	U
20	A	2417	C
20	A	2419	G
20	A	2420	C
20	A	2436	C
20	A	2437	U
20	A	2439	A
20	A	2443	G
20	A	2445	U
20	A	2455	C
20	A	2459	G
20	A	2461	G
20	A	2462	A
20	A	2469	G
20	A	2473	A

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Mol	Chain	Res	Type
20	A	2489	C
20	A	2492	A
20	A	2498	G
20	A	2504	G
20	A	2505	U
20	A	2512	C
20	A	2516	G
20	A	2517	A
20	A	2518	U
20	A	2519	G
20	A	2521	C
20	A	2532	A
20	A	2534	C
20	A	2548	C
20	A	2549	G
20	A	2557	G
20	A	2558	G
20	A	2566	U
20	A	2567	G
20	A	2568	U
20	A	2570	C
20	A	2580	A
20	A	2581	G
20	A	2586	A
20	A	2587	C
20	A	2588	G
20	A	2592	G
20	A	2595	G
20	A	2596	G
20	A	2598	U
20	A	2599	U
20	A	2600	C
20	A	2616	A
20	A	2623	U
20	A	2627	U
20	A	2643	U
20	A	2650	U
20	A	2660	C
20	A	2661	U
20	A	2677	G
20	A	2682	G
20	A	2696	G

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Mol	Chain	Res	Type
20	A	2703	U
20	A	2728	G
20	A	2746	G
20	A	2747	A
20	A	2753	U
20	A	2755	A
20	A	2764	A
20	A	2766	C
20	A	2770	U
20	A	2778	A
20	A	2779	A
20	A	2780	G
20	A	2792	A
20	A	2793	U
20	A	2804	A
20	A	2805	U
20	A	2806	U
20	A	2808	C
20	A	2810	U
20	A	2812	A
20	A	2813	A
20	A	2814	G
20	A	2819	U
20	A	2829	G
20	A	2831	G
20	A	2835	U
20	A	2836	G
20	A	2844	A
20	A	2845	G
20	A	2846	A
20	A	2847	U
20	A	2848	A
20	A	2868	G
20	A	2870	G
20	A	2878	G
20	A	2883	G
20	A	2891	C
20	A	2897	G
20	A	2904	G
21	B	8	G
21	B	10	G
21	B	11	A

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Mol	Chain	Res	Type
21	B	13	A
21	B	22	G
21	B	23	A
21	B	29	C
21	B	31	G
21	B	36	C
21	B	40	C
21	B	42	G
21	B	43	A
21	B	50	A
21	B	54	U
21	B	55	A
21	B	70	G
21	B	71	A
21	B	73	U
21	B	74	G
21	B	82	G
21	B	85	U
21	B	86	U
21	B	87	U
21	B	88	C
21	B	94	G
21	B	97	A
21	B	99	A
21	B	102	A
21	B	107	G
21	B	115	G

All (25) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	155	U
20	A	179	A
20	A	311	A
20	A	654	A
20	A	693	U
20	A	755	A
20	A	890	A
20	A	960	U
20	A	963	C
20	A	1100	U
20	A	1138	A

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Mol	Chain	Res	Type
20	A	1142	C
20	A	1146	A
20	A	1147	G
20	A	1502	G
20	A	1530	A
20	A	1584	G
20	A	1585	U
20	A	1604	A
20	A	1605	C
20	A	2281	A
20	A	2317	G
20	A	2475	C
20	A	2811	U
21	B	101	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	A	2
1	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	928:U	O3'	931:C	P	12.58
1	a	75:U	O3'	96:U	P	12.00
1	A	1579:U	O3'	1583:A	P	10.23

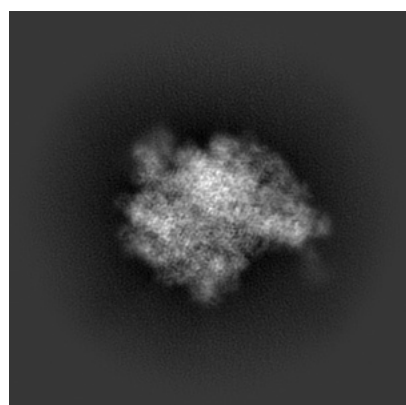
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0657. These allow visual inspection of the internal detail of the map and identification of artifacts.

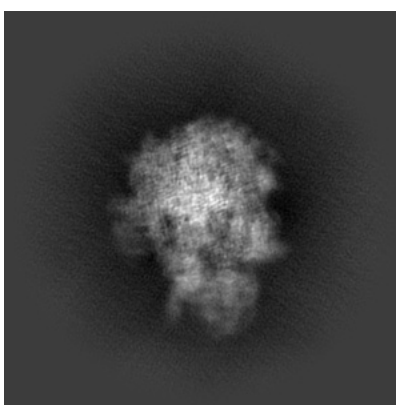
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

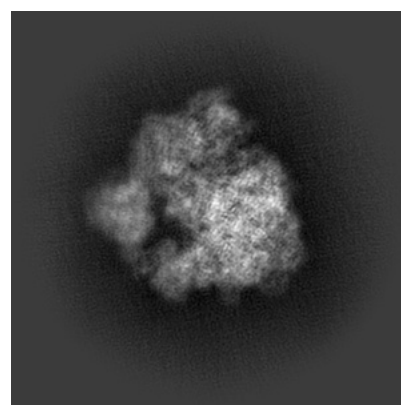
6.1.1 Primary map



X



Y

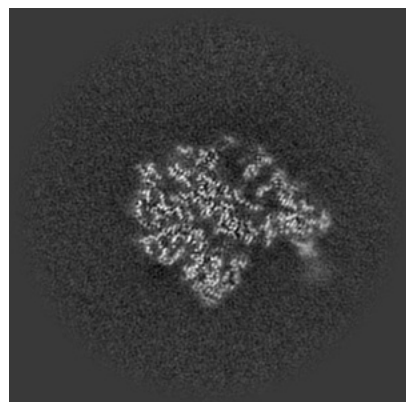


Z

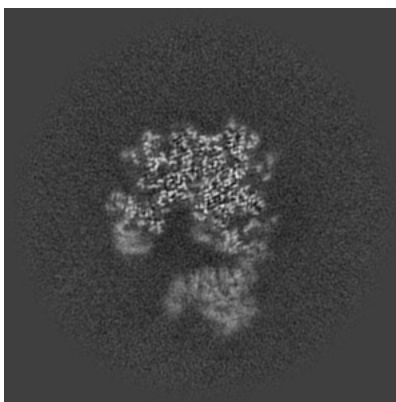
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

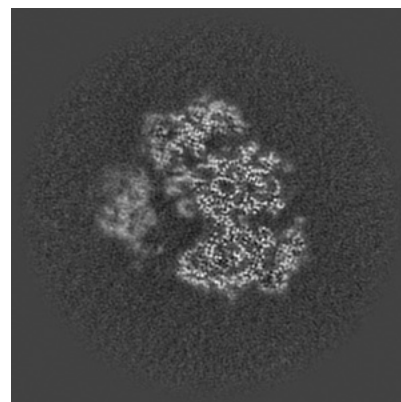
6.2.1 Primary map



X Index: 220



Y Index: 220

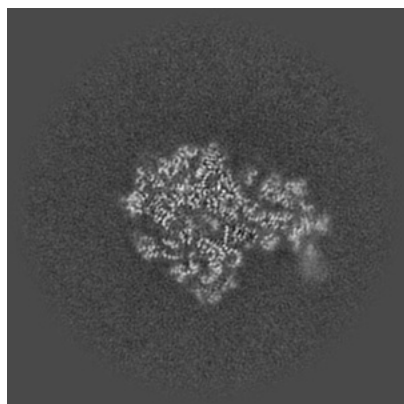


Z Index: 220

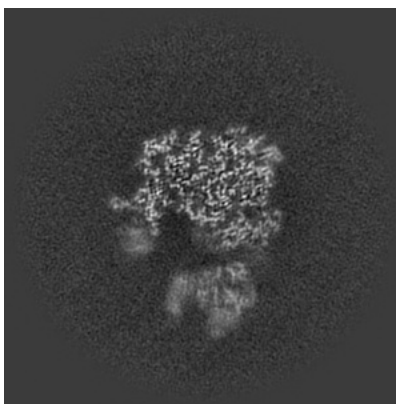
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

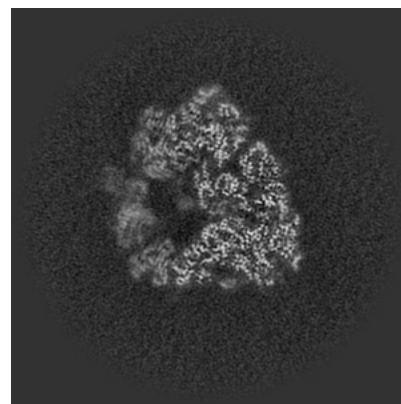
6.3.1 Primary map



X Index: 228



Y Index: 231



Z Index: 209

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 0.238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

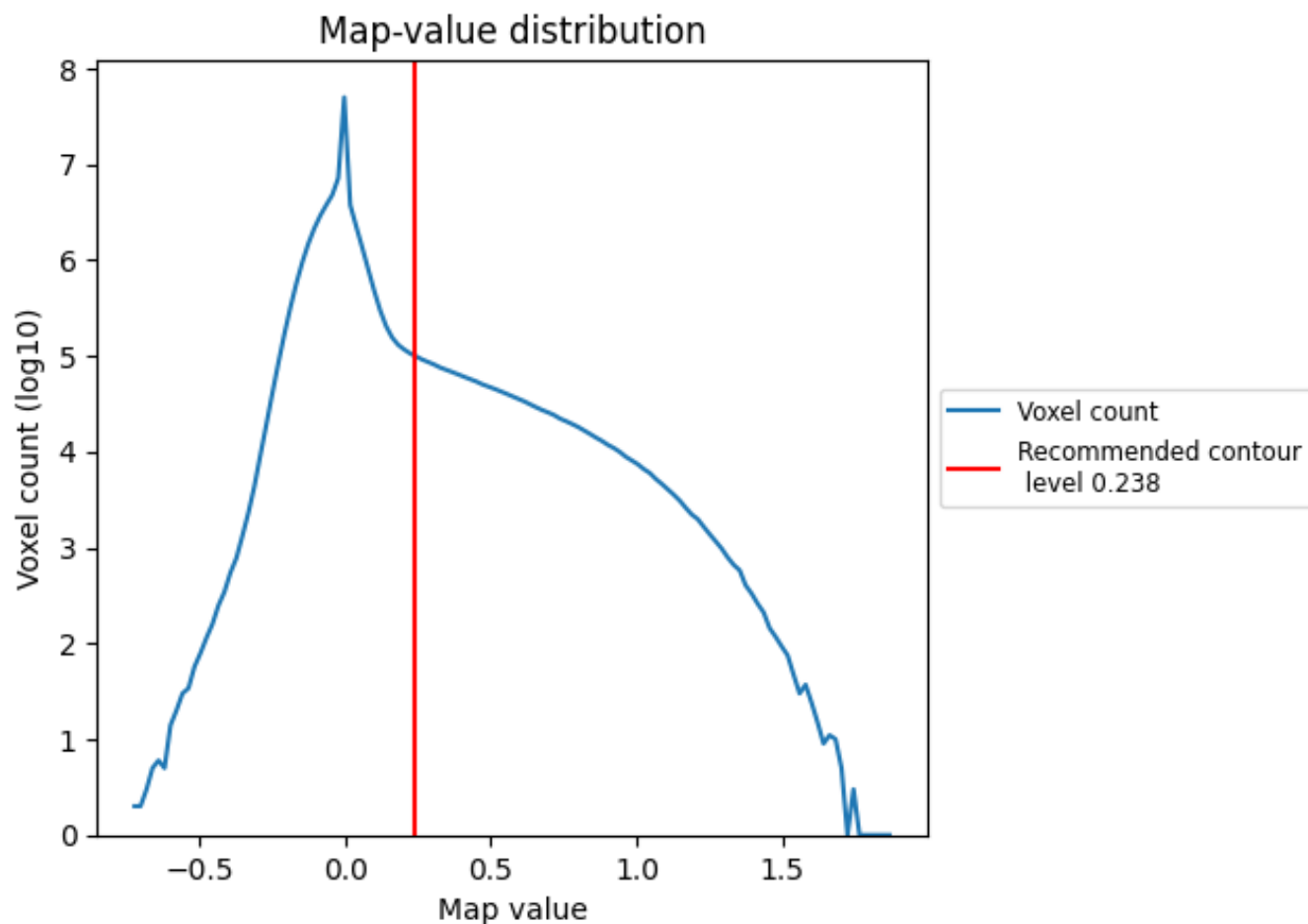
6.5 Mask visualisation

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

7 Map analysis [i](#)

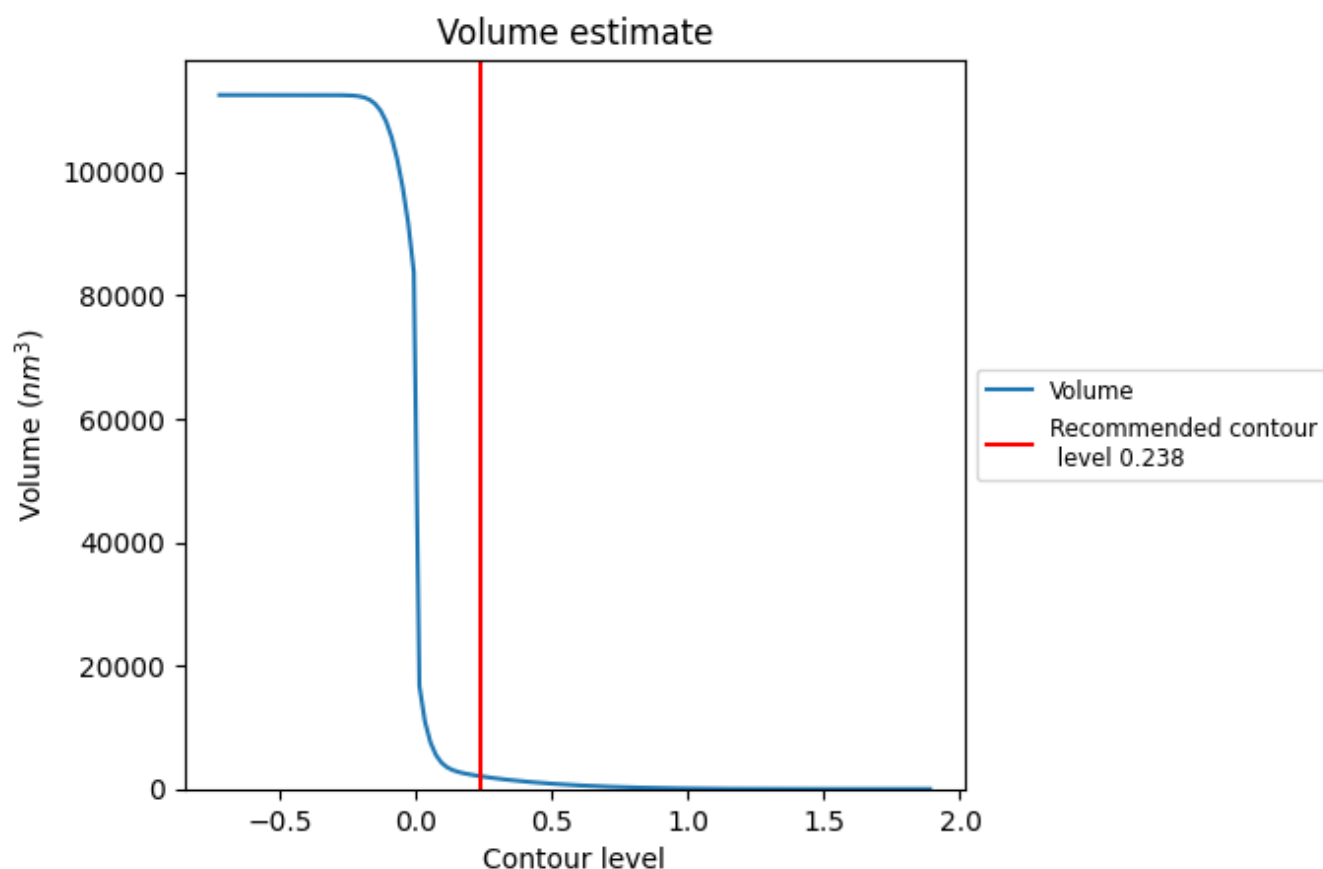
This section contains the results of statistical analysis of the map.

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.

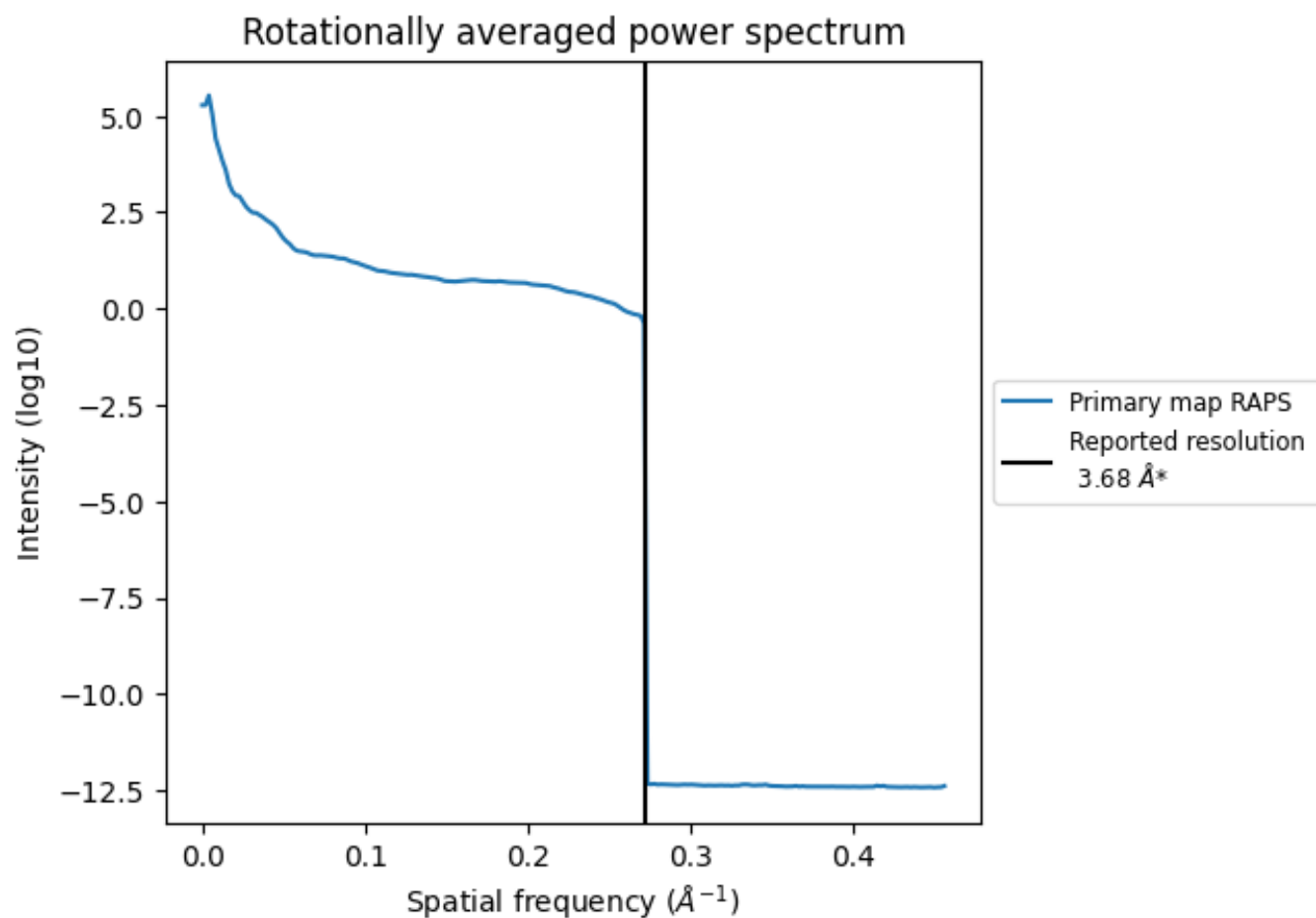
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2048 nm^3 ; this corresponds to an approximate mass of 1850 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 0.272 Å⁻¹

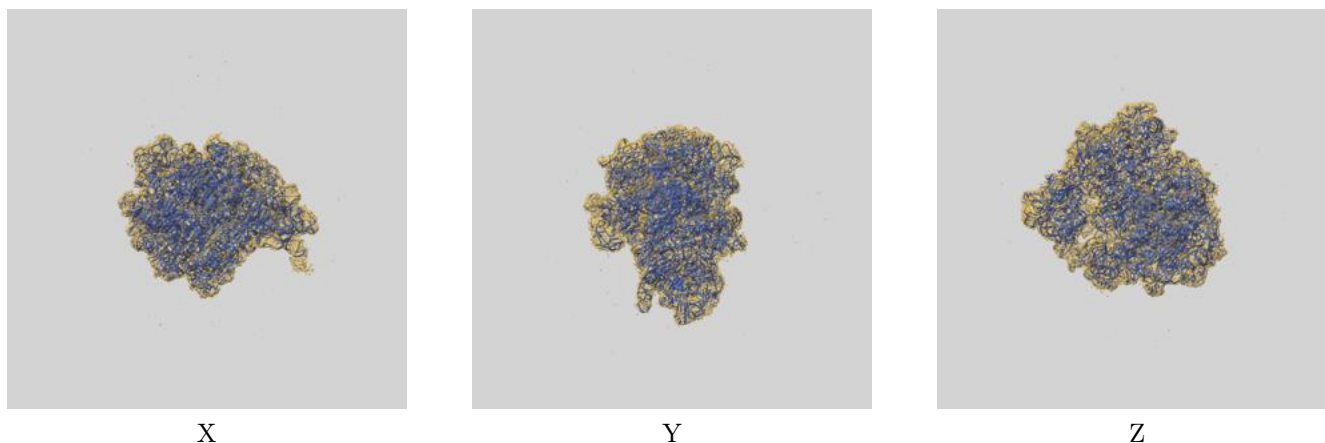
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

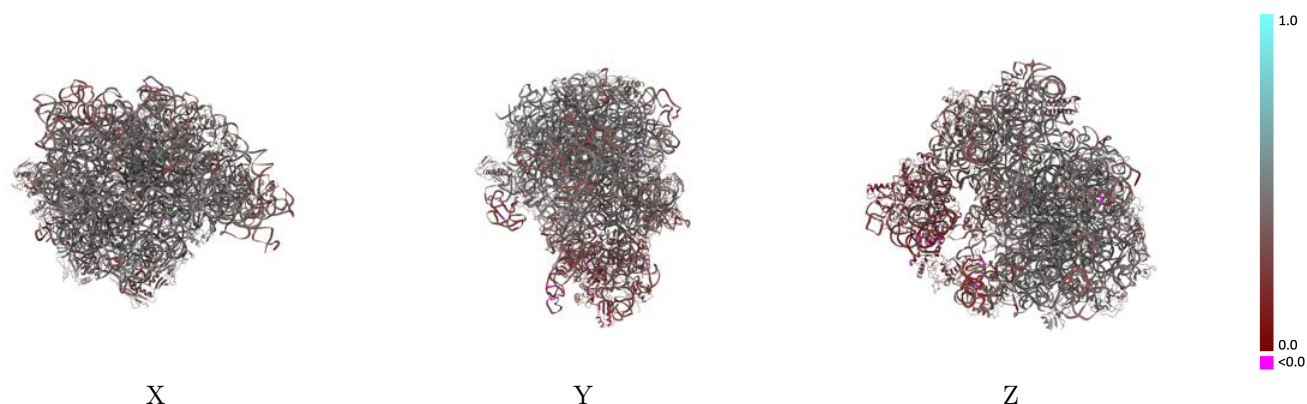
This section contains information regarding the fit between EMDB map EMD-0657 and PDB model 6O8X. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



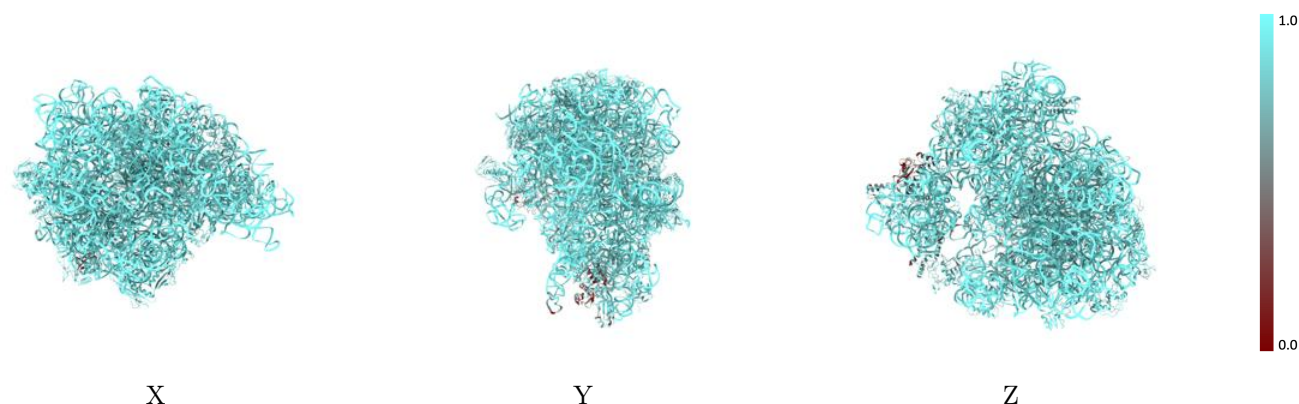
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



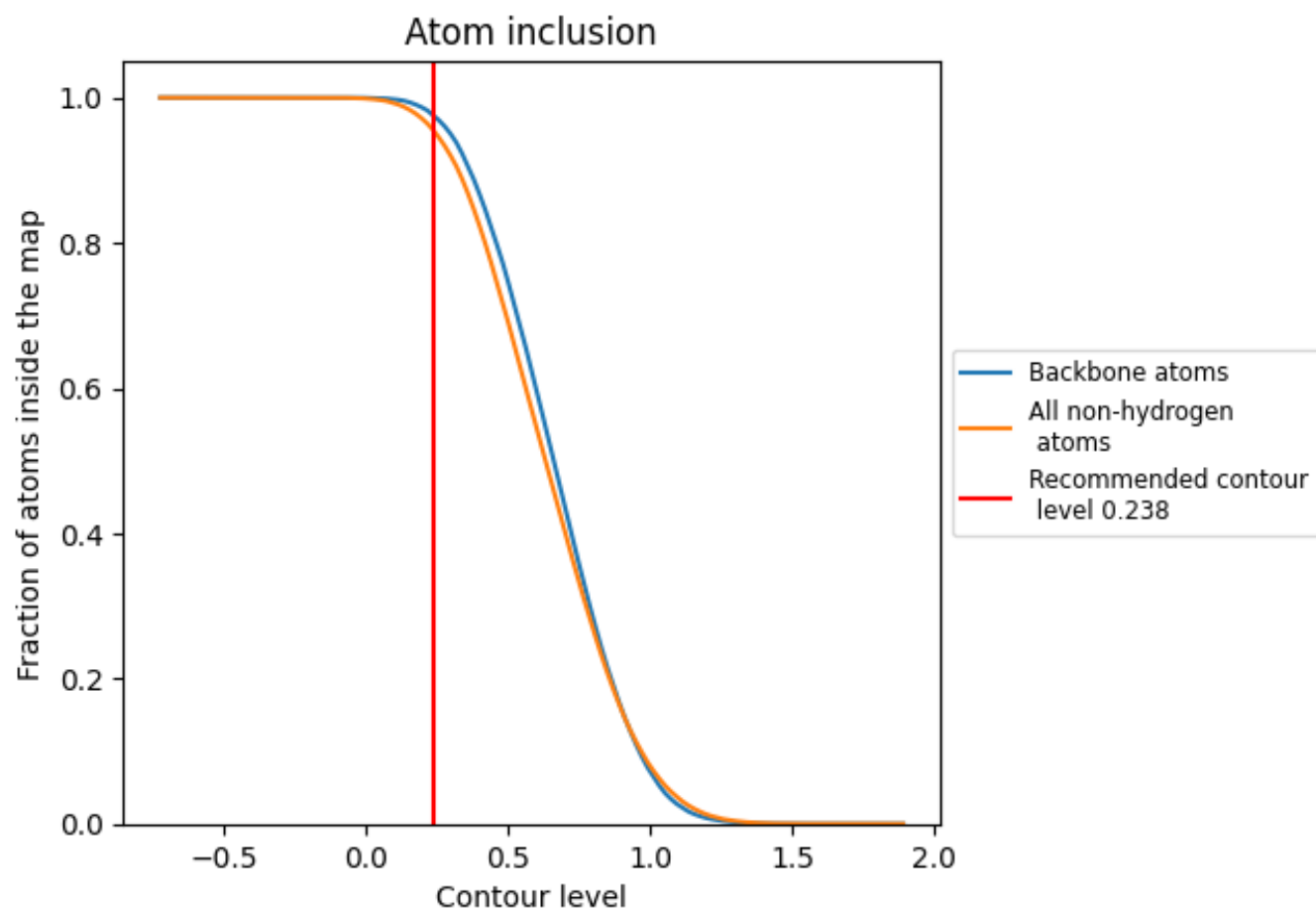
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.238).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9546	 0.4020
0	 0.9091	 0.4630
1	 0.8827	 0.2890
2	 0.9571	 0.4650
3	 0.8762	 0.4560
4	 0.9229	 0.4470
5	 0.9135	 0.4770
6	 0.9559	 0.4600
A	 0.9898	 0.4290
B	 0.9956	 0.4020
C	 0.9261	 0.4520
D	 0.9297	 0.4690
E	 0.9220	 0.4370
F	 0.8602	 0.3250
G	 0.8871	 0.3780
K	 0.9303	 0.4550
L	 0.9041	 0.4720
M	 0.9317	 0.4460
N	 0.8181	 0.4070
O	 0.9183	 0.4350
P	 0.8923	 0.3700
Q	 0.9153	 0.4560
R	 0.9018	 0.4120
S	 0.9239	 0.4500
T	 0.9232	 0.4500
U	 0.9148	 0.4240
V	 0.8647	 0.3960
W	 0.3154	 0.2990
X	 0.9459	 0.4660
Y	 0.8908	 0.4570
Z	 0.9045	 0.3750
a	 0.9879	 0.3700
c	 0.5307	 0.2820
d	 0.8957	 0.3340
e	 0.8848	 0.3640



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Chain	Atom inclusion	Q-score
f	 0.8814	 0.3990
g	 0.8562	 0.2080
h	 0.9154	 0.4090
i	 0.8956	 0.2830
j	 0.8100	 0.2520
k	 0.9092	 0.3700
l	 0.8566	 0.3950
m	 0.7680	 0.2210
n	 0.8926	 0.2790
o	 0.8822	 0.4010
p	 0.9291	 0.3930
q	 0.8763	 0.4040
r	 0.8942	 0.3900
s	 0.8484	 0.2450
t	 0.8865	 0.3680