



## Full wwPDB EM Validation Report ⓘ

Feb 22, 2025 – 01:10 PM EST

PDB ID : 9HA7  
EMDB ID : EMD-51979  
Title : Pooled 50S subunit C-CP\_(L22)- H61 precursor states supplemented with Api137  
Authors : Lauer, S.; Nikolay, R.; Spahn, C.M.T.  
Deposited on : 2024-11-01  
Resolution : 4.37 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.4

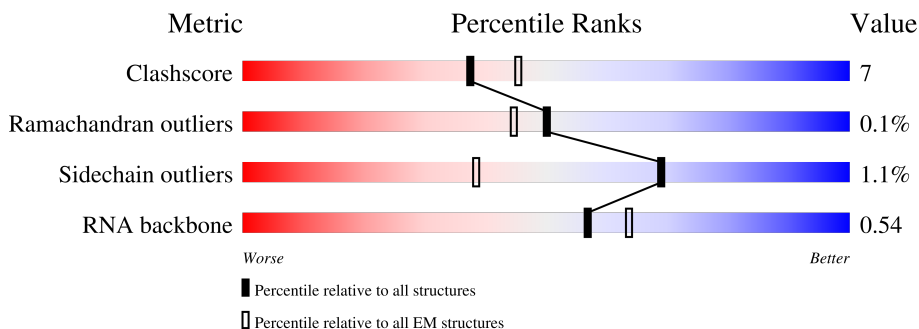
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.37 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.











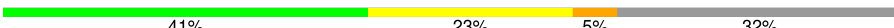



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	2	46	
2	B	120	
3	F	177	
4	J	142	
5	L	143	
6	N	120	
7	O	116	

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Mol	Chain	Length	Quality of chain
8	Q	117	 85% 15%
9	R	103	 77% 22% .
10	T	93	 86% 14%
11	U	102	 82% 17% .
12	V	94	 77% 23%
13	W	75	 81% 19%
14	Y	63	 89% 11%
15	Z	58	 81% 19%
16	A	2903	 41% 23% 5% 32%
17	D	209	 68% 14% 17%
18	E	201	 64% 23% 12%
19	y	17	 59% 94% 6%

## 2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 59416 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	38	Total	C	N	O	S	0	0
			309	185	77	46	1		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

- Molecule 3 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 4 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 6 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	120	Total	C	N	O	S	0	0
			957	592	196	164	5		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 8 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 9 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 11 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 12 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 13 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 16 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	A	1988	Total	C	N	O	P	0	0
			42736	19062	7924	13762	1988		

- Molecule 17 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	173	Total	C	N	O	S	0	0
			1284	805	231	244	4		

- Molecule 18 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	E	176	Total	C	N	O	S	0	0
			1368	862	243	258	5		

- Molecule 19 is a protein called Apidaecins type 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	y	17	Total	C	N	O	0	0
			148	94	33	21		

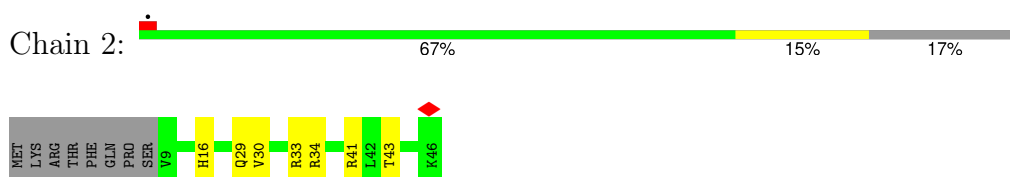
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	10	ARG	GLN	conflict	UNP P35581

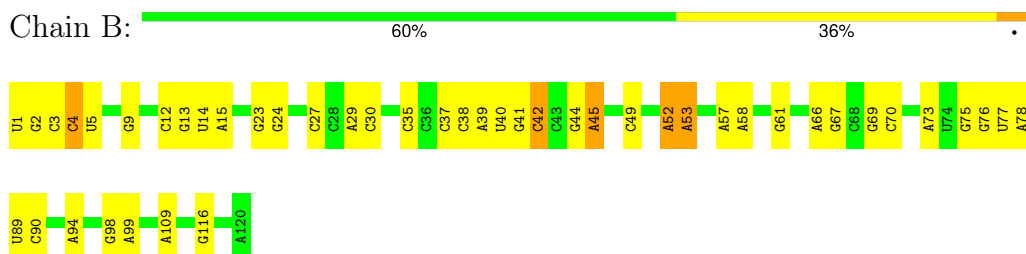
### 3 Residue-property plots [i](#)

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

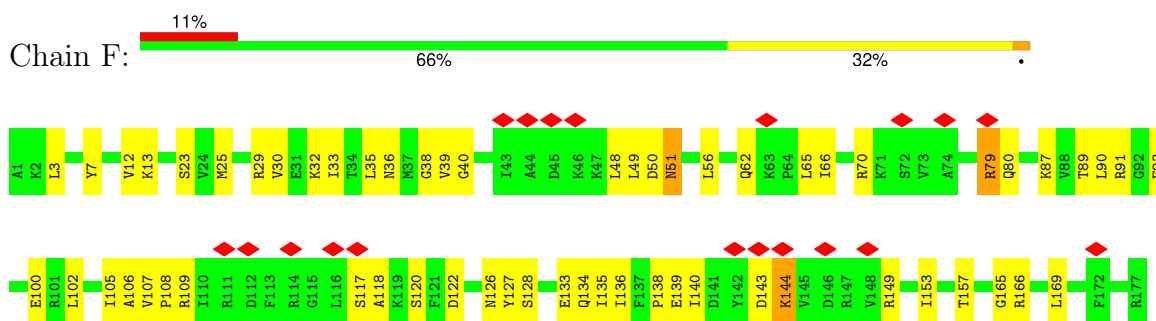
- Molecule 1: Large ribosomal subunit protein bL34



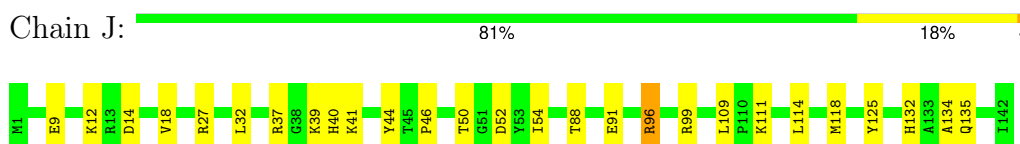
- Molecule 2: 5S ribosomal RNA



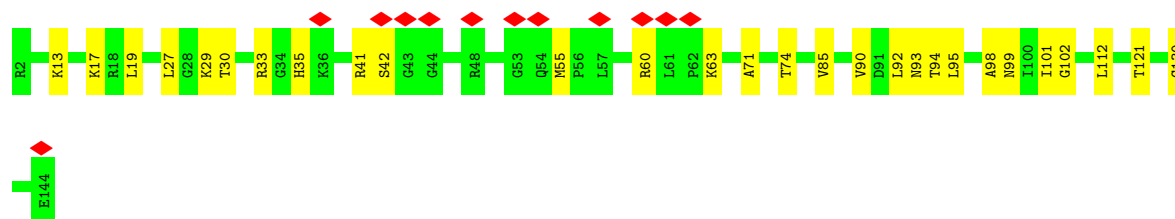
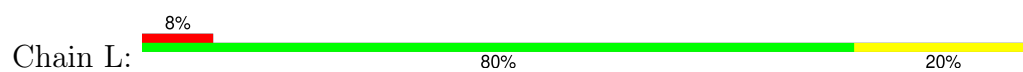
- Molecule 3: Large ribosomal subunit protein uL5



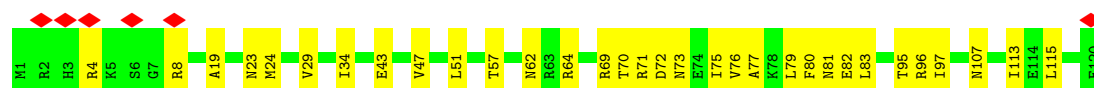
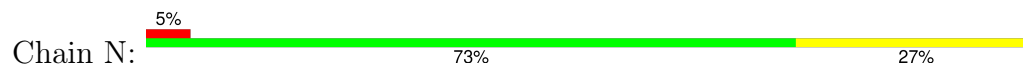
- Molecule 4: Large ribosomal subunit protein uL13



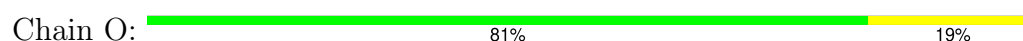
- Molecule 5: Large ribosomal subunit protein uL15



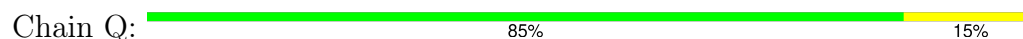
- Molecule 6: Large ribosomal subunit protein bL17



- Molecule 7: Large ribosomal subunit protein uL18



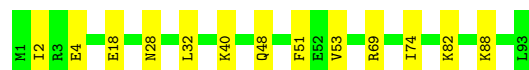
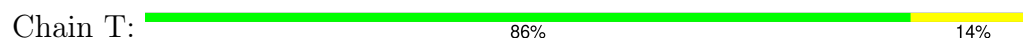
- Molecule 8: Large ribosomal subunit protein bL20



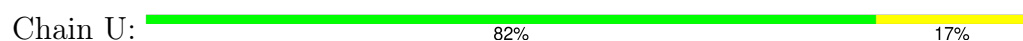
- Molecule 9: Large ribosomal subunit protein bL21



- Molecule 10: Large ribosomal subunit protein uL23

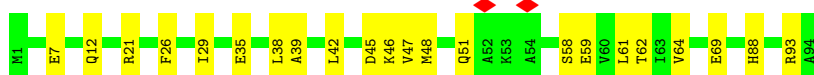
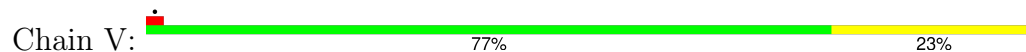


- Molecule 11: Large ribosomal subunit protein uL24

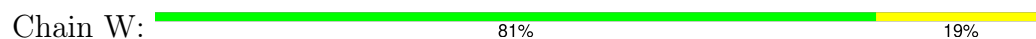




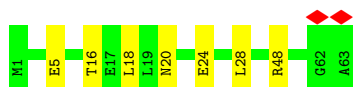
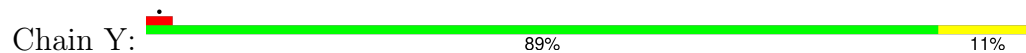
- Molecule 12: Large ribosomal subunit protein bL25



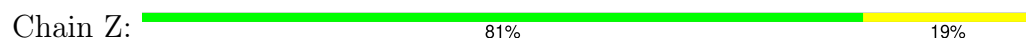
- Molecule 13: Large ribosomal subunit protein bL27



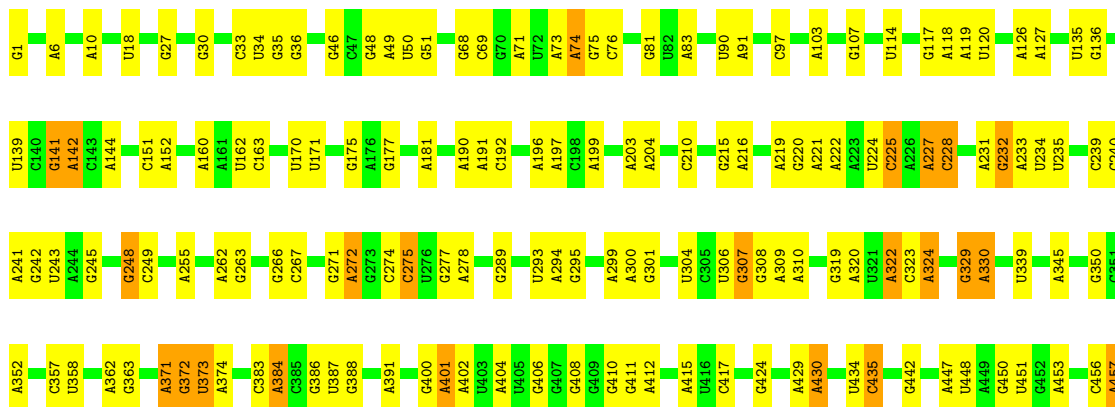
- Molecule 14: Large ribosomal subunit protein uL29



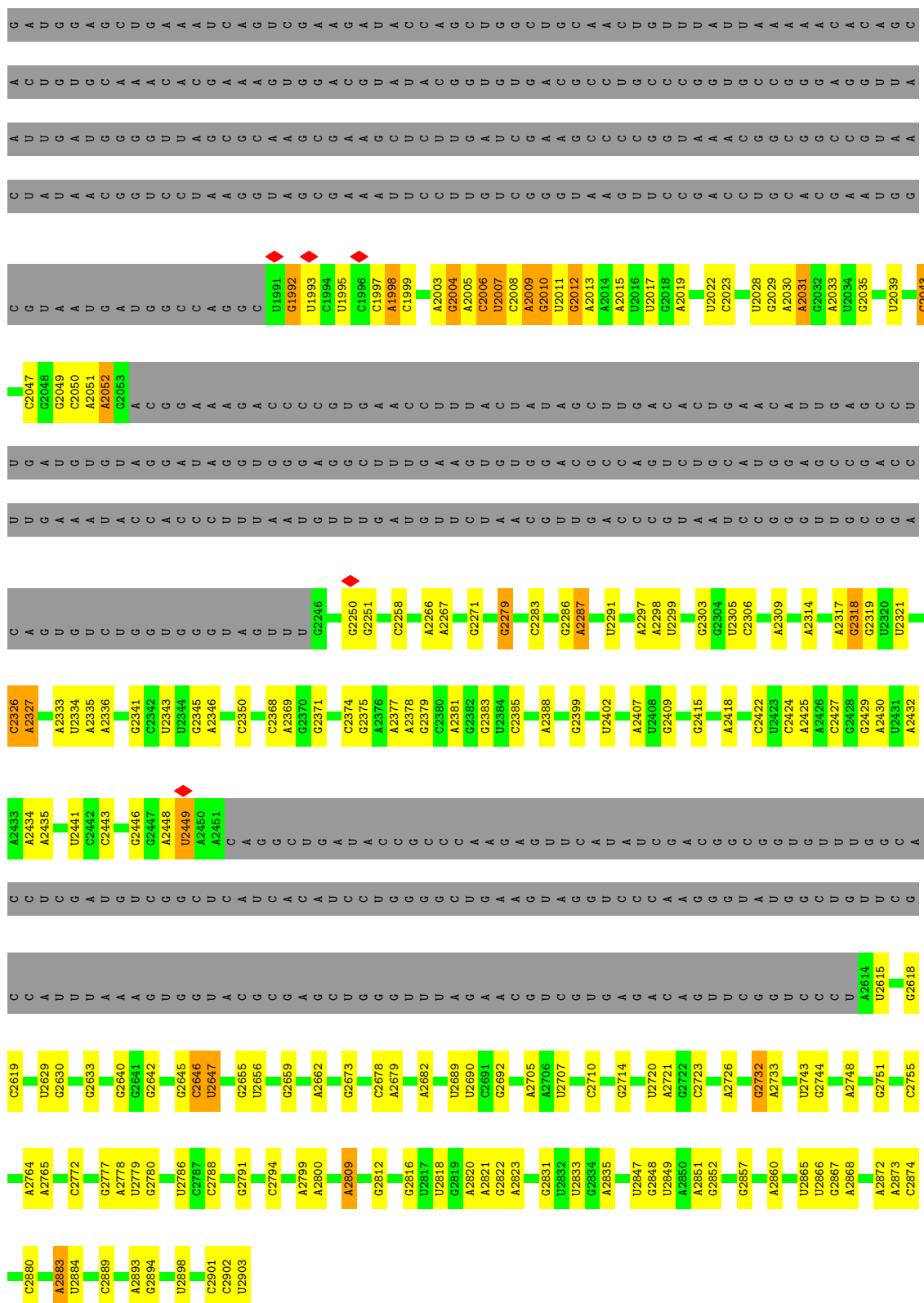
- Molecule 15: Large ribosomal subunit protein uL30



- Molecule 16: 23S ribosomal RNA

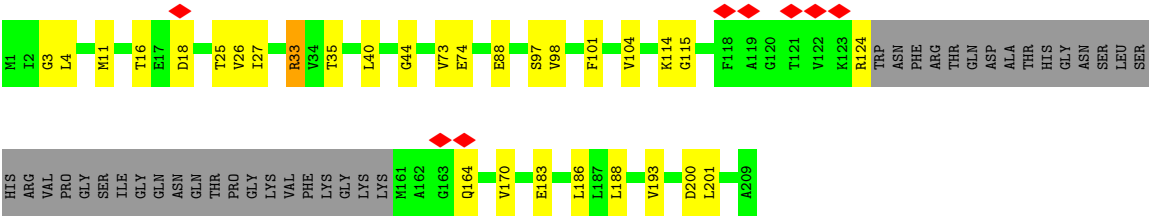


G1603	A1585	A1383	G1210	A975	A1794	A	G669	U568	G458
C1604	C1536	A1384	C1211	G976	G801	A	A670	U569	U459
A	A	A1385	G1212	A981	A802	C	C671	G570	G463
A	A	C1386	C1320	C982	C980	C	C672	U571	G570
A	A	A1387	C1321	A983	G805	G	G673	U572	U464
U	U	G1388	G1225	A984	C906	C	C674	A573	G465
U	U	U1389	U1234	C985	U807	C	A675	U574	A466
G	G	U1390	G1235	C986	U810	U	C678	A575	A471
G	G	A1391	U1236	C987	U811	A	G684	A472	A472
U	U	A1392	A1237	C988	C812	U	A	G474	G474
A	A	A1393	G1244	C989	A819	G	A	C475	C475
C	C	U1394	G1245	C990	A820	U	A	A479	A479
C	C	A1395	A1246	A991	U827	A	U	C587	A480
U	U	U1396	G1250	C992	U830	C	G	U588	G481
A	A	U1397	G1251	C993	A833	A	A	U591	G491
C	C	U1400	A1253	C994	A844	C	C	A592	A499
C	C	G1401	A1254	C995	A845	C	A	G600	G500
C	C	U1402	U1255	A996	U846	C	U	A603	A505
A	A	A1403	U1256	A997	U847	A	G	G604	C509
C	C	C1404	G1257	C998	U848	G	A	G605	C510
C	C	G1407	A1263	C999	U849	C	C	G612	C514
A	A	A1413	A1264	C1000	U850	C	A	A614	A514
C	C	C1414	A1265	A1001	U851	C	U	A621	A526
C	C	G1415	U1266	A1002	U852	C	A	G622	A529
C	C	G1416	A1267	A1003	U853	C	U	A627	G530
C	C	A1419	A1268	C1004	U854	C	U	G628	C531
C	C	A1420	C1269	A1005	U855	C	U	G629	A532
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C	C	U1422	C1271	A1007	U857	C	A	A631	U534
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C	C	C1424	U1273	A1009	U859	C	U	G543	G543
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C	C	G1426	A1275	A1011	U861	C	U	U545	U545
C	C	A1427	A1276	A1012	U862	C	U	G546	G546
C	C	C1428	U1277	A1013	U863	C	U	A547	A547
C	C	G1429	C1278	A1014	U864	C	U	G548	G548
C	C	A1430	U1279	A1015	U865	C	U	G549	G549
C	C	A1431	G1280	A1016	U866	C	U	C550	C550
C	C	A1432	A1281	A1017	U867	C	U	G551	G551
C	C	A1433	C1361	A1018	U868	C	U	U554	U554
C	C	A1434	U1282	A1019	U869	C	U	G555	G555
C	C	G1435	G1362	A1020	U870	C	U	A556	A556
C	C	A1436	A1363	A1021	U871	C	U	C557	C557
C	C	G1437	U1364	A1022	U872	C	U	G561	G561
C	C	A1438	A1365	A1023	U873	C	U	U562	U562
C	C	G1439	A1366	A1024	U874	C	U	A563	A563
C	C	U1440	A1367	A1025	U875	C	U	U567	U567
C	C	G1441	C1370	A1026	U876	C	U	A644	A644
C	C	U1442	U1371	A1027	U877	C	U	C645	C645
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C	C	U1445	C1305	A1030	U880	C	U	A654	A654
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C	C	U1447	A1307	A1032	U882	C	U	G659	G659
C	C	G1448	G1308	A1033	U883	C	U	A668	A668
C	C	U1449	A1309	A1034	U884	C	U	A	A
C	C	G1450	G1310	A1035	U885	C	U	A	A
C	C	C1451	U1311	A1036	U886	C	U	A	A
C	C	A1452	A1312	A1037	U887	C	U	A	A
C	C	G1453	U1313	A1038	U888	C	U	A	A
C	C	U1454	G1314	A1039	U889	C	U	A	A
C	C	A1455	A1315	A1040	U890	C	U	A	A
C	C	C1456	U1316	A1041	U891	C	U	A	A
C	C	U1457	G1317	A1042	U892	C	U	A	A
C	C	G1458	A1318	A1043	U893	C	U	A	A
C	C	U1459	U1319	A1044	U894	C	U	A	A
C	C	A1460	G1320	A1045	U895	C	U	A	A
C	C	C1461	A1321	A1046	U896	C	U	A	A
C	C	U1462	G1322	A1047	U897	C	U	A	A
C	C	A1463	U1323	A1048	U898	C	U	A	A
C	C	U1464	A1324	A1049	U899	C	U	A	A
C	C	U1465	G1325	A1050	U900	C	U	A	A
C	C	A1466	U1326	A1051	U901	C	U	A	A
C	C	U1467	A1327	A1052	U902	C	U	A	A
C	C	U1468	U1328	A1053	U903	C	U	A	A
C	C	A1469	A1329	A1054	U904	C	U	A	A
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C	C	G1471	G1331	A1056	U906	C	U	A	A
C	C	U1472	A1332	A1057	U907	C	U	A	A
C	C	U1473	G1333	A1058	U908	C	U	A	A
C	C	U1474	U1334	A1059	U909	C	U	A	A
C	C	G1475	A1335	A1060	U910	C	U	A	A
C	C	U1476	G1336	A1061	U911	C	U	A	A
C	C	U1477	U1337	A1062	U912	C	U	A	A
C	C	A1478	A1338	A1063	U913	C	U	A	A
C	C	U1479	G1339	A1064	U914	C	U	A	A
C	C	U1480	U1340	A1065	U915	C	U	A	A
C	C	A1481	A1341	A1066	U916	C	U	A	A
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C	C	G1483	U1343	A1068	U918	C	U	A	A
C	C	U1484	A1344	A1069	U919	C	U	A	A
C	C	U1485	G1345	A1070	U920	C	U	A	A
C	C	U1486	U1346	A1071	U921	C	U	A	A
C	C	A1487	A1347	A1072	U922	C	U	A	A
C	C	U1488	G1348	A1073	U923	C	U	A	A
C	C	U1489	U1349	A1074	U924	C	U	A	A
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C	C	U1495	A1355	A1080	U930	C	U	A	A
C	C	U1496	G1356	A1081	U931	C	U	A	A
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C	C	U1498	A1358	A1083	U933	C	U	A	A
C	C	U1499	G1359	A1084	U934	C	U	A	A
C	C	U1500	U1360	A1085	U935	C	U	A	A
C	C	U1501	A1361	A1086	U936	C	U	A	A
C	C	U1502	G1362	A1087	U937	C	U	A	A
C	C	U1503	U1363	A1088	U938	C	U	A	A
C	C	U1504	A1364	A1089	U939	C	U	A	A
C	C	U1505	G1365	A1090	U940	C	U	A	A
C	C	U1506	U1366	A1091	U941	C	U	A	A
C	C	U1507	A1367	A1092	U942	C	U	A	A
C	C	U1508	G1368	A1093	U943	C	U	A	A
C	C	U1509	U1369	A1094	U944	C	U	A	A
C	C	U1510	A1370	A1095	U945	C	U	A	A
C	C	U1511	G1371	A1096	U946	C	U	A	A
C	C	U1512	U1372	A1097	U947	C	U	A	A
C	C	U1513	A1373	A1098	U948	C	U	A	A
C	C	U1514	G1374	A1099	U949	C	U	A	A
C	C	U1515	U1375	A1100	U950	C	U	A	A
C	C	U1516	A1376	A1101	U951	C	U	A	A
C	C	U1517	G1377	A1102	U952	C	U	A	A
C	C	U1518	U1378	A1103	U953	C	U	A	A
C	C	U1519	A1379	A1104	U954	C	U	A	A
C	C	U1520	G1380	A1105	U955	C	U	A	A
C	C	U1521	U1381	A1106	U956	C	U	A	A
C	C	U1522	A1382	A1107	U957	C	U	A	A
C	C	U1523	G1383	A1108	U958	C	U	A	A
C	C	U1524	U1384	A1109	U959	C	U	A	A
C	C	U1525	A1385	A1110	U960	C	U	A	A
C	C	U1526	G1386	A1111	U961	C	U	A	A
C	C	U1527	U1387	A1112	U962	C	U	A	A
C	C	U1528	A1388	A1113	U963	C	U	A	A
C	C	U1529	G1389	A1114	U964	C	U	A	A
C	C	U1530	U1390	A1115	U965	C	U	A	A
C	C	U1531	G1391	A1116	U966	C	U	A	A
C	C	U1532	A1392	A1117	U967	C	U	A	A
C	C	U1533	U1393	A1118	U968	C	U	A	A
C	C	U1534	A1394	A1119	U969	C	U	A	A
C	C	U1535	G1395	A1120	U970	C	U	A	A
C	C	U1536	U1396	A1121	U971	C	U	A	A
C	C	U1537	A1397	A1122	U972	C	U	A	A
C	C	U1538	G1398	A1123	U973	C	U	A	A
C	C	U1539	U1399	A1124	U974	C	U	A	A
C	C	U1540	G1400	A1125	U975	C	U	A	A
C	C	U1541	A1401	A1126	U976	C	U	A	A
C	C	U1542	U1402	A1127	U977	C	U	A	A
C	C	U1543	G1403	A1128	U978	C	U	A	A
C	C	U1544	A1404	A1129	U979	C	U	A	A
C	C	U1545	C1405	A1130	U980	C	U	A	A
C	C	U1546	G1406	A1131	U981	C	U	A	A
C	C	U1547	U1407	A1132	U982	C	U	A	A
C	C	U1548	A1408	A1133	U983	C	U	A	A
C	C	U1549	G1409	A1134	U984	C	U	A	A
C	C	U1550	A1410	A1135	U985	C	U	A	A
C	C	U1551	C1411	A1136	U986	C	U	A	A
C	C	U1552	U1412	A1137	U987	C	U	A	A
C	C	U1553	A1413	A1138	U988	C	U	A	A
C	C	U1554	G1414	A1139	U989	C	U	A	A
C	C	U1555	U1415	A1140	U990	C	U	A	A
C	C	U1556	A1416	A1141	U991	C	U	A	A
C	C	U1557	G1417	A1142	U992	C	U	A	A
C	C	U1558	U1418	A1143	U993	C	U	A	A
C	C	U1559	A1419						

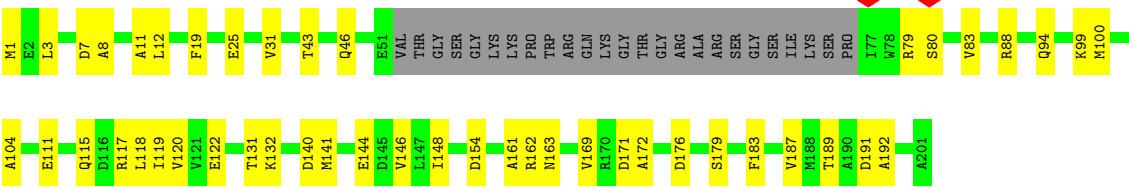


• Molecule 17: 50S ribosomal protein L3

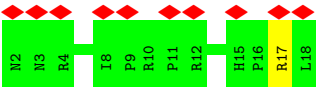
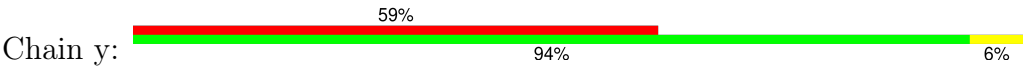
Chain D: 68% 14% 17%



• Molecule 18: Large ribosomal subunit protein uL4



• Molecule 19: Apidaecins type 22



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	28649	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	46.2	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.499	Depositor
Minimum map value	-0.761	Depositor
Average map value	-0.012	Depositor
Map value standard deviation	0.142	Depositor
Recommended contour level	0.255	Depositor
Map size (Å)	399.6, 399.6, 399.6	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.998, 1.998, 1.998	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	2	0.23	0/310	0.65	0/405
2	B	0.24	1/2876 (0.0%)	0.69	0/4483
3	F	0.25	0/1434	0.52	0/1926
4	J	0.24	0/1152	0.49	0/1551
5	L	0.25	0/1054	0.57	0/1403
6	N	0.25	0/970	0.58	0/1297
7	O	0.24	0/902	0.54	0/1209
8	Q	0.24	0/960	0.52	0/1278
9	R	0.25	0/829	0.53	0/1107
10	T	0.24	0/744	0.50	0/994
11	U	0.25	0/787	0.51	0/1051
12	V	0.25	0/766	0.49	0/1025
13	W	0.25	0/582	0.53	0/769
14	Y	0.25	0/510	0.49	0/677
15	Z	0.24	0/453	0.54	0/605
16	A	0.16	1/47875 (0.0%)	0.72	6/74684 (0.0%)
17	D	0.25	0/1296	0.52	0/1742
18	E	0.24	0/1382	0.47	0/1860
19	y	0.48	0/155	0.65	0/212
All	All	0.19	2/65037 (0.0%)	0.68	6/98278 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	A	1	G	OP3-P	-10.70	1.48	1.61
2	B	1	U	OP3-P	-10.57	1.48	1.61

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	A	1541	C	N3-C2-O2	-7.06	116.96	121.90
16	A	1541	C	N1-C2-O2	6.82	122.99	118.90
16	A	1512	C	N3-C2-O2	-5.58	117.99	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	A	363	G	N1-C2-N2	-5.55	111.21	116.20
16	A	1529	G	N3-C4-N9	5.39	129.23	126.00
16	A	1512	C	N1-C2-O2	5.19	122.02	118.90

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	309	0	344	5	0
2	B	2572	0	1302	33	0
3	F	1410	0	1447	46	0
4	J	1129	0	1162	22	0
5	L	1045	0	1117	23	0
6	N	957	0	998	22	0
7	O	892	0	923	17	0
8	Q	947	0	1022	16	0
9	R	816	0	839	16	0
10	T	738	0	807	10	0
11	U	779	0	834	14	0
12	V	753	0	780	17	0
13	W	575	0	592	9	0
14	Y	509	0	543	5	0
15	Z	449	0	491	11	0
16	A	42736	0	21494	377	0
17	D	1284	0	1339	24	0
18	E	1368	0	1421	35	0
19	y	148	0	151	0	0
All	All	59416	0	37606	621	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (621) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:239:C:HO2'	16:A:622:G:HO2'	1.07	0.95
16:A:1007:C:OP2	16:A:1008:A:O2'	1.90	0.88
16:A:1667:G:N2	16:A:1669:A:N6	2.24	0.86
4:J:134:ALA:O	16:A:2898:U:O2'	1.94	0.86
16:A:951:C:N4	16:A:952:G:O6	2.10	0.85
16:A:909:A:O2'	16:A:911:A:OP2	1.95	0.84
16:A:514:A:N3	16:A:581:C:O2'	2.08	0.84
16:A:2865:U:OP2	16:A:2866:U:O2'	1.95	0.84
16:A:542:C:N4	16:A:543:G:O6	2.11	0.83
16:A:1492:G:OP2	16:A:1493:C:O2'	1.96	0.83
16:A:2642:G:N2	16:A:2772:C:O2	2.11	0.83
16:A:1315:C:O2'	16:A:1392:A:N3	2.11	0.82
16:A:1378:A:O2'	16:A:1380:G:N7	2.12	0.82
16:A:83:A:O2'	16:A:103:A:N6	2.11	0.82
16:A:571:U:O2'	16:A:573:U:OP2	1.98	0.82
16:A:126:A:O2'	16:A:127:A:O4'	1.96	0.82
16:A:1287:A:N1	16:A:1648:U:O2'	2.11	0.82
16:A:1414:C:O2'	16:A:1415:U:O4'	1.98	0.81
18:E:46:GLN:O	18:E:88:ARG:NH2	2.13	0.81
2:B:39:A:O2'	2:B:40:U:O4'	1.99	0.81
3:F:109:ARG:NH2	3:F:136:ILE:O	2.14	0.81
16:A:675:A:N3	16:A:2443:C:O2'	2.13	0.81
16:A:177:G:OP2	16:A:177:G:N2	2.13	0.80
16:A:2049:G:N2	16:A:2619:C:O2	2.13	0.80
3:F:38:GLY:O	16:A:2306:C:N4	2.15	0.80
7:O:50:ALA:O	7:O:81:ARG:NH1	2.15	0.80
16:A:1667:G:H21	16:A:1669:A:N6	1.77	0.80
16:A:548:G:O2'	16:A:549:G:O4'	1.98	0.79
16:A:2743:U:OP2	16:A:2755:C:N4	2.15	0.79
2:B:14:U:OP2	2:B:70:C:O2'	2.01	0.79
16:A:1604:C:O2'	16:A:1610:A:N1	2.13	0.79
3:F:87:LYS:NZ	16:A:2314:A:OP1	2.16	0.79
2:B:5:U:OP1	2:B:61:G:O2'	2.00	0.79
16:A:1667:G:N2	16:A:1669:A:H62	1.80	0.78
12:V:58:SER:OG	12:V:59:GLU:OE1	2.01	0.78
16:A:2678:C:OP1	17:D:124:ARG:NH2	2.16	0.78
16:A:463:G:N2	16:A:466:A:OP2	2.16	0.78
3:F:70:ARG:NH1	16:A:2298:A:OP1	2.16	0.78
11:U:3:LYS:O	11:U:93:ARG:NH1	2.16	0.77
5:L:41:ARG:NH2	16:A:807:U:OP2	2.18	0.77
16:A:2050:C:O2	16:A:2618:G:N2	2.16	0.77
16:A:532:A:N1	16:A:2035:G:N2	2.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:966:G:O4'	16:A:2267:A:N6	2.18	0.77
16:A:2326:C:O2'	16:A:2327:A:OP1	2.02	0.77
16:A:234:U:O4	16:A:263:G:N2	2.19	0.76
16:A:2645:G:OP2	16:A:2645:G:N2	2.17	0.76
16:A:2816:G:N3	16:A:2883:A:O2'	2.18	0.76
6:N:77:ALA:O	6:N:81:ASN:ND2	2.18	0.76
16:A:569:U:OP1	16:A:945:A:O2'	2.03	0.76
16:A:629:G:N3	16:A:639:U:O2'	2.19	0.76
16:A:2646:C:OP2	16:A:2732:G:O2'	2.02	0.76
3:F:133:GLU:OE1	3:F:133:GLU:N	2.19	0.76
16:A:1466:U:HO2'	16:A:1546:G:HO2'	1.00	0.76
16:A:227:A:O2'	16:A:228:C:O5'	2.02	0.76
3:F:120:SER:OG	3:F:128:SER:O	2.03	0.76
16:A:2788:C:O2'	16:A:2809:A:N3	2.17	0.75
16:A:117:G:OP2	16:A:119:A:O2'	2.03	0.75
16:A:805:G:N2	16:A:829:A:OP1	2.20	0.75
16:A:2009:A:O2'	16:A:2010:G:O4'	2.01	0.75
15:Z:18:LYS:NZ	16:A:850:U:OP1	2.19	0.74
16:A:2258:C:O2'	16:A:2427:C:OP2	2.05	0.74
2:B:75:G:O2'	12:V:88:HIS:NE2	2.20	0.74
16:A:1322:A:N1	16:A:1333:G:O2'	2.20	0.74
16:A:570:G:O2'	16:A:983:A:N1	2.20	0.74
17:D:16:THR:OG1	17:D:18:ASP:OD1	2.03	0.74
16:A:220:G:O2'	16:A:233:A:O2'	2.05	0.74
1:2:16:HIS:NE2	16:A:464:U:O2	2.21	0.72
16:A:192:C:O2'	16:A:802:A:N3	2.20	0.72
16:A:1359:A:OP2	16:A:1371:G:N2	2.21	0.72
16:A:322:A:OP1	18:E:162:ARG:NE	2.21	0.72
16:A:1024:G:OP2	16:A:1025:G:O2'	2.03	0.71
16:A:239:C:O2'	16:A:622:G:O2'	1.96	0.71
16:A:1588:G:O2'	16:A:1589:U:O4'	2.05	0.71
6:N:95:THR:HB	6:N:113:ILE:HD11	1.72	0.71
16:A:18:U:O2'	16:A:554:U:OP1	2.07	0.71
5:L:55:MET:O	5:L:60:ARG:NH1	2.23	0.70
4:J:88:THR:OG1	4:J:91:GLU:OE1	2.09	0.70
16:A:931:U:O2	16:A:1167:C:O2'	2.09	0.70
16:A:1272:A:N6	16:A:1619:G:OP2	2.24	0.70
16:A:48:G:N2	16:A:177:G:OP1	2.22	0.70
18:E:122:GLU:N	18:E:122:GLU:OE1	2.25	0.70
9:R:80:ARG:NH1	16:A:572:A:OP2	2.25	0.70
3:F:117:SER:O	3:F:127:TYR:OH	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:46:PRO:HD3	8:Q:59:LEU:HD11	1.73	0.69
14:Y:48:ARG:NH1	16:A:76:C:OP1	2.25	0.69
12:V:48:MET:SD	12:V:51:GLN:NE2	2.64	0.69
16:A:550:C:N4	16:A:551:G:O6	2.25	0.69
16:A:2043:C:OP1	16:A:2777:G:O2'	2.07	0.69
5:L:95:LEU:HD23	5:L:101:ILE:HD13	1.75	0.69
15:Z:4:ILE:HD11	15:Z:56:VAL:CG2	2.22	0.69
16:A:464:U:O4	16:A:684:G:O2'	2.11	0.69
16:A:372:G:O2'	16:A:373:U:O5'	2.12	0.68
16:A:961:C:O2	16:A:2031:A:N6	2.26	0.68
16:A:1319:C:O2'	16:A:1320:C:OP1	2.12	0.68
16:A:1125:G:OP2	16:A:1126:A:O2'	2.08	0.68
1:2:29:GLN:NE2	16:A:210:C:OP1	2.26	0.68
12:V:64:VAL:HG22	12:V:69:GLU:OE1	1.93	0.68
12:V:45:ASP:OD1	12:V:46:LYS:N	2.28	0.67
7:O:60:GLU:OE1	7:O:60:GLU:N	2.26	0.67
16:A:612:G:N2	16:A:614:A:O2'	2.27	0.67
16:A:475:C:O2	16:A:479:A:N6	2.27	0.67
16:A:224:U:OP2	16:A:408:G:N2	2.27	0.67
16:A:1341:G:OP1	16:A:1602:U:O2'	2.10	0.67
16:A:1638:C:OP1	16:A:2710:C:O2'	2.13	0.67
3:F:89:THR:OG1	3:F:91:ARG:NH2	2.27	0.67
10:T:48:GLN:NE2	10:T:53:VAL:O	2.27	0.67
10:T:40:LYS:NZ	16:A:1343:G:OP1	2.28	0.67
15:Z:30:ARG:NH2	16:A:1184:U:OP2	2.28	0.67
16:A:248:G:O2'	16:A:2432:A:OP1	2.09	0.66
2:B:9:G:OP2	7:O:15:ARG:NH2	2.28	0.66
16:A:1651:G:O5'	16:A:2006:C:N4	2.29	0.66
16:A:659:G:O3'	18:E:94:GLN:NE2	2.27	0.66
16:A:1415:U:O2	16:A:1587:G:N2	2.28	0.66
2:B:42:C:H5	3:F:65:LEU:HD13	1.61	0.66
16:A:627:A:O4'	16:A:637:A:N6	2.29	0.66
5:L:93:ASN:O	5:L:94:THR:OG1	2.09	0.66
16:A:453:A:N3	16:A:457:A:O2'	2.28	0.66
16:A:227:A:HO2'	16:A:228:C:P	2.19	0.66
2:B:37:C:O2	7:O:100:HIS:NE2	2.28	0.65
7:O:2:ASP:OD1	7:O:3:LYS:N	2.29	0.65
16:A:605:G:OP1	18:E:99:LYS:NZ	2.29	0.65
9:R:23:GLU:OE2	9:R:91:GLN:NE2	2.29	0.65
16:A:631:A:N3	16:A:2415:G:O2'	2.27	0.65
16:A:191:A:O2'	16:A:678:C:O2	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:2751:G:N2	16:A:2751:G:OP1	2.26	0.65
16:A:1390:U:O2	16:A:1395:A:N7	2.30	0.65
3:F:23:SER:OG	3:F:25:MET:SD	2.54	0.64
8:Q:52:ARG:NH2	16:A:994:C:OP1	2.30	0.64
3:F:50:ASP:OD1	3:F:51:ASN:N	2.30	0.64
5:L:13:LYS:NZ	16:A:1245:G:OP1	2.29	0.64
16:A:1209:U:O2'	16:A:1237:A:N1	2.25	0.64
8:Q:88:GLU:N	8:Q:88:GLU:OE1	2.31	0.64
16:A:1650:A:O2'	16:A:1652:A:OP1	2.14	0.64
16:A:2822:G:OP1	17:D:164:GLN:NE2	2.30	0.64
6:N:64:ARG:NH1	16:A:2851:A:O2'	2.31	0.64
6:N:8:ARG:N	6:N:43:GLU:OE2	2.29	0.64
16:A:1024:G:O2'	16:A:1144:A:O2'	2.16	0.64
16:A:1413:A:O2'	16:A:1414:C:O4'	2.14	0.64
4:J:91:GLU:OE1	4:J:91:GLU:N	2.31	0.63
6:N:24:MET:SD	16:A:1277:G:O2'	2.56	0.63
16:A:2291:U:O2'	16:A:2374:C:O2	2.16	0.63
16:A:2659:G:N2	16:A:2662:A:OP2	2.31	0.63
4:J:109:LEU:HD13	4:J:118:MET:HG3	1.81	0.63
11:U:81:ARG:NH2	16:A:301:G:OP2	2.32	0.63
15:Z:4:ILE:HD11	15:Z:56:VAL:HG23	1.81	0.63
16:A:2633:G:N2	16:A:2786:U:O2	2.32	0.62
16:A:1422:G:O2'	16:A:1492:G:N2	2.32	0.62
16:A:569:U:O2'	16:A:971:G:N2	2.31	0.62
11:U:9:GLU:OE1	11:U:9:GLU:N	2.33	0.62
16:A:1270:C:O2	16:A:2010:G:N1	2.32	0.62
18:E:111:GLU:OE2	18:E:115:GLN:NE2	2.32	0.62
5:L:27:LEU:HD23	5:L:27:LEU:H	1.65	0.62
16:A:1651:G:N2	16:A:2006:C:OP2	2.31	0.62
16:A:448:U:O4'	18:E:79:ARG:NE	2.31	0.61
2:B:77:U:OP1	12:V:21:ARG:NH1	2.32	0.61
16:A:844:A:N1	16:A:845:A:N6	2.48	0.61
8:Q:4:LYS:NZ	16:A:30:G:OP2	2.27	0.61
16:A:97:C:O2	16:A:103:A:O2'	2.17	0.61
17:D:26:VAL:CG1	17:D:186:LEU:HD12	2.30	0.61
4:J:39:LYS:NZ	16:A:1007:C:OP1	2.31	0.61
16:A:1026:G:OP2	16:A:1134:A:O2'	2.10	0.61
1:2:34:ARG:NH2	1:2:41:ARG:O	2.34	0.61
16:A:612:G:N2	16:A:614:A:HO2'	1.98	0.61
16:A:2446:G:N2	16:A:2449:U:O2	2.30	0.60
11:U:80:ASP:OD1	11:U:81:ARG:N	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:69:C:O2	16:A:73:A:O2'	2.18	0.60
17:D:33:ARG:HG3	17:D:73:VAL:HG13	1.83	0.60
3:F:35:LEU:HG	3:F:56:LEU:HD11	1.82	0.60
18:E:117:ARG:NH2	18:E:183:PHE:O	2.35	0.60
16:A:372:G:HO2'	16:A:373:U:P	2.24	0.60
2:B:27:C:OP1	7:O:34:HIS:NE2	2.34	0.60
6:N:107:ASN:ND2	16:A:1652:A:OP2	2.34	0.60
9:R:58:VAL:N	9:R:102:SER:OG	2.35	0.60
16:A:68:G:N2	16:A:74:A:O4'	2.35	0.60
16:A:1534:U:O2'	16:A:1535:A:OP1	2.20	0.60
16:A:442:G:N2	18:E:43:THR:O	2.33	0.60
17:D:25:THR:HG21	17:D:193:VAL:HG22	1.83	0.60
16:A:644:A:O2'	16:A:645:C:O5'	2.20	0.59
3:F:133:GLU:HG2	3:F:135:ILE:HG22	1.84	0.59
5:L:63:LYS:NZ	16:A:249:C:O2'	2.24	0.59
8:Q:57:ARG:NH2	16:A:998:C:OP2	2.36	0.59
16:A:2399:G:O6	16:A:2418:A:N6	2.35	0.59
16:A:152:A:N6	16:A:175:G:O6	2.36	0.59
16:A:2341:G:N2	16:A:2374:C:O3'	2.35	0.59
10:T:82:LYS:NZ	16:A:1339:G:OP1	2.36	0.59
3:F:93:GLU:OE1	3:F:93:GLU:N	2.35	0.59
4:J:135:GLN:N	4:J:135:GLN:OE1	2.36	0.59
16:A:1271:G:N2	16:A:1615:C:H42	2.01	0.58
18:E:46:GLN:N	18:E:46:GLN:OE1	2.36	0.58
5:L:33:ARG:NH2	16:A:587:C:O2	2.36	0.58
7:O:116:GLN:N	7:O:116:GLN:OE1	2.36	0.58
5:L:99:ASN:ND2	16:A:621:A:OP2	2.37	0.58
16:A:1651:G:H22	16:A:2006:C:P	2.26	0.58
6:N:96:ARG:O	6:N:113:ILE:HD12	2.04	0.58
3:F:134:GLN:N	3:F:134:GLN:OE1	2.36	0.58
16:A:2375:G:O2'	16:A:2377:A:N6	2.37	0.58
17:D:88:GLU:N	17:D:88:GLU:OE1	2.37	0.58
16:A:1451:C:O2'	16:A:1452:G:O4'	2.17	0.58
10:T:28:ASN:ND2	10:T:88:LYS:O	2.37	0.58
16:A:548:G:O2'	16:A:549:G:O5'	2.21	0.58
16:A:603:A:N6	16:A:655:A:O4'	2.37	0.57
16:A:1589:U:O4	16:A:1590:A:N6	2.37	0.57
16:A:2050:C:N3	16:A:2618:G:N1	2.45	0.57
6:N:82:GLU:HG2	6:N:83:LEU:HD22	1.86	0.57
16:A:224:U:O4	16:A:232:G:N2	2.36	0.57
16:A:324:A:N6	16:A:339:U:O4'	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:10:ARG:NH2	16:A:2279:G:N7	2.52	0.57
16:A:2007:U:O2'	16:A:2009:A:OP2	2.17	0.57
16:A:526:A:O2'	16:A:2043:C:O2	2.22	0.57
18:E:176:ASP:OD1	18:E:179:SER:OG	2.15	0.57
16:A:2049:G:N1	16:A:2619:C:N3	2.44	0.56
5:L:19:LEU:HD23	5:L:27:LEU:HD12	1.87	0.56
16:A:371:A:N6	16:A:402:A:OP2	2.38	0.56
16:A:2326:C:HO2'	16:A:2327:A:P	2.27	0.56
2:B:80:U:O2'	16:A:918:A:N3	2.36	0.56
16:A:2692:G:N3	16:A:2847:U:O2'	2.34	0.56
2:B:75:G:HO2'	12:V:88:HIS:CD2	2.22	0.56
5:L:93:ASN:OD1	5:L:94:THR:N	2.38	0.56
16:A:1271:G:H22	16:A:1615:C:N4	2.04	0.56
16:A:987:C:O2'	16:A:1000:A:N3	2.34	0.56
16:A:2375:G:N2	16:A:2378:A:OP2	2.38	0.56
18:E:171:ASP:OD1	18:E:172:ALA:N	2.39	0.56
1:2:43:THR:OG1	16:A:126:A:N6	2.39	0.56
16:A:864:G:O2'	16:A:914:G:O6	2.23	0.56
3:F:30:VAL:HG22	3:F:157:THR:HG22	1.88	0.55
2:B:38:C:O4'	7:O:100:HIS:NE2	2.39	0.55
16:A:1515:A:O2'	16:A:1556:C:O2	2.23	0.55
17:D:3:GLY:C	17:D:4:LEU:HD12	2.27	0.55
2:B:42:C:C5	3:F:65:LEU:HD13	2.41	0.55
7:O:31:THR:OG1	7:O:33:ARG:O	2.22	0.55
18:E:144:GLU:N	18:E:144:GLU:OE1	2.40	0.55
16:A:673:C:P	16:A:801:G:H21	2.29	0.55
18:E:1:MET:SD	18:E:1:MET:N	2.79	0.55
3:F:62:GLN:OE1	3:F:62:GLN:N	2.40	0.55
16:A:644:A:O2'	16:A:645:C:O4'	2.23	0.54
3:F:134:GLN:NE2	3:F:149:ARG:O	2.40	0.54
2:B:76:G:OP2	12:V:12:GLN:NE2	2.39	0.54
16:A:271:G:O2'	16:A:272:A:OP2	2.22	0.54
16:A:976:G:HO2'	16:A:1155:A:HO2'	1.55	0.54
4:J:37:ARG:NH1	4:J:44:TYR:OH	2.41	0.53
16:A:1432:G:H2'	16:A:1433:A:C8	2.43	0.53
4:J:96:ARG:NH1	16:A:2640:G:OP1	2.42	0.53
16:A:549:G:HO2'	16:A:550:C:P	2.31	0.53
16:A:1414:C:HO2'	16:A:1415:U:C4'	2.20	0.53
8:Q:48:ASP:OD1	8:Q:49:ARG:N	2.42	0.53
16:A:549:G:O2'	16:A:550:C:OP1	2.26	0.53
18:E:189:THR:OG1	18:E:191:ASP:OD1	2.18	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:A:OP2	2:B:69:G:N2	2.37	0.53
5:L:30:THR:HG22	16:A:810:U:O4	2.08	0.53
16:A:659:G:O2'	18:E:94:GLN:NE2	2.42	0.53
16:A:1319:C:HO2'	16:A:1320:C:P	2.30	0.53
8:Q:48:ASP:OD2	16:A:534:U:O2'	2.17	0.53
13:W:14:ALA:O	13:W:16:ARG:NH1	2.39	0.53
16:A:289:G:O6	16:A:352:A:N6	2.42	0.53
13:W:7:ARG:O	13:W:10:ARG:NH1	2.42	0.53
3:F:143:ASP:OD1	3:F:144:LYS:N	2.42	0.52
16:A:308:G:O2'	16:A:329:G:N2	2.43	0.52
16:A:1596:A:H2'	16:A:1597:A:H5'	1.92	0.52
16:A:2857:G:N2	16:A:2860:A:OP2	2.36	0.52
14:Y:16:THR:O	14:Y:20:ASN:ND2	2.41	0.52
16:A:2345:G:O2'	16:A:2381:A:N3	2.38	0.52
16:A:2821:A:OP2	17:D:115:GLY:N	2.40	0.52
16:A:532:A:OP1	16:A:561:G:N2	2.33	0.52
9:R:15:SER:OG	9:R:18:GLN:NE2	2.43	0.52
16:A:1352:U:O2'	16:A:1570:A:N3	2.39	0.52
2:B:52:A:O2'	2:B:53:A:O5'	2.27	0.52
16:A:2017:U:O2'	16:A:2019:A:OP2	2.10	0.52
4:J:114:LEU:HD12	4:J:114:LEU:H	1.75	0.52
4:J:41:LYS:NZ	4:J:52:ASP:OD1	2.25	0.51
11:U:71:ILE:HD12	11:U:82:VAL:HG21	1.91	0.51
16:A:1244:A:N6	16:A:1245:G:O6	2.44	0.51
16:A:1656:C:N4	16:A:1657:U:O4	2.43	0.51
3:F:35:LEU:HD12	3:F:36:ASN:N	2.26	0.51
10:T:32:LEU:HD12	10:T:32:LEU:O	2.10	0.51
16:A:1021:A:N6	16:A:1142:A:H61	2.08	0.51
16:A:1271:G:H22	16:A:1615:C:H42	1.56	0.51
16:A:1358:G:O2'	16:A:1359:A:O5'	2.25	0.51
9:R:49:ILE:HG21	9:R:54:VAL:HG12	1.92	0.51
16:A:373:U:O4	16:A:401:A:N7	2.44	0.51
16:A:584:C:N4	16:A:585:G:O6	2.43	0.51
2:B:75:G:HO2'	12:V:88:HIS:CE1	2.27	0.51
9:R:38:VAL:O	9:R:54:VAL:HG13	2.11	0.51
16:A:274:C:H2'	16:A:275:C:C1'	2.39	0.51
16:A:673:C:OP1	16:A:801:G:N2	2.39	0.51
16:A:1402:U:O2'	16:A:1470:A:N1	2.29	0.51
16:A:2299:U:O4	16:A:2318:G:N2	2.44	0.51
16:A:2317:A:H2'	16:A:2318:G:O4'	2.11	0.51
16:A:2705:A:O2'	16:A:2852:G:OP1	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:40:HIS:O	8:Q:70:GLN:NE2	2.43	0.51
6:N:4:ARG:NH2	16:A:2874:C:OP1	2.43	0.51
4:J:27:ARG:NH1	16:A:1012:U:O2	2.44	0.51
9:R:100:GLY:O	9:R:101:ILE:HD13	2.11	0.51
12:V:29:ILE:HD12	12:V:38:LEU:O	2.11	0.51
7:O:53:THR:HG23	7:O:74:VAL:CG2	2.40	0.51
12:V:26:PHE:HZ	12:V:47:VAL:HG11	1.76	0.51
16:A:1303:G:O6	16:A:1304:A:N6	2.44	0.51
18:E:140:ASP:OD1	18:E:141:MET:N	2.43	0.51
16:A:1329:U:OP2	16:A:1330:C:N4	2.42	0.51
2:B:52:A:O2'	2:B:53:A:P	2.68	0.50
16:A:68:G:N2	16:A:74:A:O5'	2.44	0.50
3:F:120:SER:OG	16:A:2303:G:O2'	2.29	0.50
6:N:73:ASN:OD1	16:A:1454:C:N4	2.43	0.50
17:D:200:ASP:C	17:D:201:LEU:HD12	2.30	0.50
6:N:69:ARG:O	6:N:70:THR:OG1	2.19	0.50
6:N:71:ARG:NH1	16:A:2707:U:O2	2.44	0.50
16:A:1016:G:O6	16:A:1147:A:N6	2.44	0.50
16:A:299:A:N3	16:A:319:G:O2'	2.25	0.50
16:A:1020:A:H4'	16:A:1021:A:O5'	2.12	0.50
10:T:51:PHE:O	10:T:53:VAL:HG13	2.11	0.50
4:J:135:GLN:NE2	16:A:6:A:N3	2.60	0.50
16:A:1205:A:O2'	16:A:1206:G:OP1	2.29	0.50
16:A:1413:A:H2'	16:A:1414:C:C6	2.47	0.50
16:A:1992:G:N1	16:A:1995:U:O4	2.45	0.50
16:A:591:U:O4	16:A:592:A:N6	2.43	0.50
16:A:640:C:N4	16:A:641:U:O4	2.45	0.50
16:A:2723:C:OP1	17:D:114:LYS:NZ	2.28	0.50
18:E:25:GLU:OE1	18:E:25:GLU:N	2.40	0.50
6:N:57:THR:HG23	6:N:62:ASN:ND2	2.27	0.49
12:V:35:GLU:N	12:V:35:GLU:OE1	2.45	0.49
11:U:33:VAL:HG13	11:U:66:VAL:HG22	1.93	0.49
15:Z:57:GLU:N	15:Z:57:GLU:OE1	2.44	0.49
18:E:148:ILE:HB	18:E:169:VAL:HG22	1.93	0.49
16:A:245:G:O2'	16:A:384:A:N1	2.42	0.49
10:T:18:GLU:OE1	10:T:18:GLU:N	2.41	0.49
16:A:434:U:O2	16:A:435:C:N4	2.41	0.49
2:B:49:C:OP2	7:O:30:ARG:NH1	2.46	0.49
3:F:32:LYS:C	3:F:33:ILE:HD12	2.33	0.49
10:T:2:ILE:HD11	16:A:144:A:H4'	1.93	0.49
16:A:554:U:H2'	16:A:555:G:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:231:A:H2'	16:A:232:G:O4'	2.12	0.49
17:D:40:LEU:HD13	17:D:44:GLY:O	2.12	0.49
18:E:3:LEU:HD13	18:E:120:VAL:HG21	1.94	0.49
16:A:307:G:N1	16:A:309:A:O5'	2.46	0.49
16:A:549:G:O2'	16:A:550:C:P	2.70	0.49
16:A:948:C:O2	16:A:984:A:O2'	2.07	0.49
16:A:1512:C:H2'	16:A:1513:U:N1	2.27	0.49
16:A:141:G:N2	16:A:142:A:N3	2.60	0.49
16:A:2647:U:O2	16:A:2673:G:O6	2.31	0.49
2:B:42:C:C5	3:F:65:LEU:HD22	2.48	0.49
16:A:1028:A:OP2	16:A:1126:A:N6	2.44	0.49
3:F:3:LEU:HD22	3:F:100:GLU:HG2	1.93	0.49
9:R:63:VAL:HA	9:R:96:VAL:HG12	1.95	0.49
15:Z:4:ILE:HD12	15:Z:58:GLU:OE2	2.13	0.49
16:A:90:U:OP2	16:A:91:A:O2'	2.27	0.49
5:L:112:LEU:HD22	5:L:130:GLY:HA3	1.94	0.48
11:U:81:ARG:NH2	16:A:300:A:O5'	2.46	0.48
16:A:1170:C:N4	16:A:1171:G:O6	2.47	0.48
2:B:42:C:N3	3:F:89:THR:HG22	2.28	0.48
8:Q:57:ARG:NH1	16:A:997:G:OP2	2.45	0.48
12:V:62:THR:OG1	12:V:69:GLU:OE2	2.19	0.48
16:A:1386:C:H2'	16:A:1387:A:C8	2.47	0.48
2:B:3:C:H3'	2:B:4:C:H5''	1.94	0.48
6:N:97:ILE:CD1	6:N:113:ILE:HD13	2.43	0.48
16:A:1441:G:H2'	16:A:1442:U:C6	2.48	0.48
12:V:7:GLU:N	12:V:7:GLU:OE1	2.47	0.48
16:A:391:A:O2'	16:A:410:G:OP1	2.32	0.48
16:A:1266:G:N2	16:A:2012:G:O2'	2.47	0.48
16:A:1608:A:N7	16:A:1621:U:O2	2.46	0.48
16:A:330:A:N7	16:A:1210:G:O2'	2.42	0.48
2:B:78:A:H62	2:B:98:G:H21	1.61	0.48
16:A:956:G:O2'	16:A:960:A:N6	2.47	0.48
16:A:1448:G:H2'	16:A:1449:G:O4'	2.14	0.48
18:E:161:ALA:CB	18:E:169:VAL:HG23	2.43	0.48
18:E:191:ASP:OD1	18:E:192:ALA:N	2.46	0.48
16:A:1324:G:O2'	16:A:1328:A:N6	2.46	0.48
4:J:125:TYR:HH	4:J:132:HIS:HE2	1.61	0.47
16:A:1266:G:N2	16:A:2012:G:HO2'	2.12	0.47
16:A:1588:G:H2'	16:A:1589:U:C6	2.49	0.47
17:D:33:ARG:NH2	17:D:74:GLU:OE1	2.48	0.47
18:E:7:ASP:OD1	18:E:8:ALA:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:102:LEU:HD12	3:F:106:ALA:CB	2.45	0.47
6:N:19:ALA:O	6:N:23:ASN:ND2	2.42	0.47
16:A:320:A:N7	18:E:132:LYS:NZ	2.59	0.47
16:A:415:A:N6	16:A:2409:G:O6	2.48	0.47
16:A:1434:A:H2'	16:A:1435:G:C8	2.49	0.47
16:A:1449:G:H3'	16:A:1450:G:O4'	2.15	0.47
7:O:43:ASN:OD1	7:O:44:GLY:N	2.47	0.47
15:Z:22:THR:HG22	16:A:850:U:O2'	2.14	0.47
16:A:1435:G:H2'	16:A:1436:G:C8	2.49	0.47
16:A:1466:U:O2'	16:A:1546:G:O2'	1.93	0.47
16:A:1386:C:H2'	16:A:1387:A:H8	1.79	0.47
2:B:39:A:H2'	2:B:40:U:C6	2.49	0.47
8:Q:85:ALA:O	8:Q:86:SER:OG	2.25	0.47
12:V:61:LEU:HD12	12:V:61:LEU:N	2.30	0.47
16:A:36:G:N3	16:A:450:G:O2'	2.48	0.47
16:A:573:U:O4	16:A:2029:G:O2'	2.20	0.47
16:A:107:G:O3'	16:A:293:U:O2'	2.26	0.47
18:E:31:VAL:HG21	18:E:104:ALA:HB2	1.96	0.47
5:L:85:VAL:HG13	5:L:98:ALA:HB2	1.97	0.47
17:D:26:VAL:HG12	17:D:186:LEU:HD12	1.97	0.47
9:R:11:GLN:N	9:R:11:GLN:OE1	2.48	0.47
15:Z:18:LYS:O	15:Z:22:THR:HG23	2.14	0.47
4:J:50:THR:O	4:J:50:THR:HG22	2.15	0.46
5:L:35:HIS:NE2	16:A:567:U:OP1	2.48	0.46
12:V:38:LEU:HD23	12:V:39:ALA:N	2.30	0.46
16:A:357:C:C2	16:A:358:U:C5	3.03	0.46
16:A:2375:G:N1	16:A:2379:G:O6	2.48	0.46
6:N:72:ASP:O	6:N:76:VAL:HG23	2.14	0.46
16:A:203:A:OP2	16:A:204:A:O2'	2.14	0.46
16:A:1510:G:H2'	16:A:1511:G:C8	2.50	0.46
16:A:224:U:H2'	16:A:225:C:O4'	2.15	0.46
16:A:1551:A:H2'	16:A:1552:A:O4'	2.16	0.46
10:T:69:ARG:HG2	10:T:74:ILE:HG22	1.97	0.46
3:F:139:GLU:OE1	3:F:139:GLU:N	2.45	0.46
6:N:34:ILE:HD11	16:A:1278:C:O3'	2.16	0.46
16:A:600:G:H1'	18:E:100:MET:HE3	1.97	0.46
16:A:974:G:OP1	16:A:1187:G:O2'	2.18	0.46
16:A:1524:G:H2'	16:A:1525:A:C8	2.51	0.46
13:W:32:ILE:N	13:W:32:ILE:HD12	2.30	0.46
16:A:451:U:C4	16:A:453:A:C8	3.03	0.46
16:A:1345:C:N4	16:A:1346:G:O6	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:35:LEU:HD13	3:F:153:ILE:HD13	1.97	0.46
13:W:79:GLU:OE1	13:W:79:GLU:N	2.49	0.46
15:Z:4:ILE:HD11	15:Z:56:VAL:HG21	1.95	0.46
16:A:932:U:O2'	16:A:934:U:O4	2.28	0.46
16:A:1000:A:OP2	16:A:1154:G:N1	2.43	0.46
16:A:1263:U:H2'	16:A:1264:A:N9	2.31	0.46
16:A:1360:G:C8	16:A:1361:G:C8	3.04	0.46
16:A:2047:C:O2'	16:A:2823:A:N1	2.46	0.46
9:R:58:VAL:H	9:R:102:SER:HG	1.61	0.46
2:B:116:G:H4'	7:O:54:VAL:HG12	1.97	0.45
15:Z:19:HIS:O	15:Z:23:LEU:HD23	2.15	0.45
16:A:549:G:C2'	16:A:550:C:O5'	2.64	0.45
16:A:1344:U:H3'	16:A:1345:C:H5'	1.98	0.45
5:L:17:LYS:CE	5:L:27:LEU:HD13	2.46	0.45
16:A:1269:A:H2'	16:A:1270:C:O4'	2.16	0.45
17:D:183:GLU:OE1	17:D:183:GLU:N	2.43	0.45
2:B:29:A:O2'	2:B:58:A:N1	2.49	0.45
6:N:79:LEU:HD13	6:N:83:LEU:HB2	1.99	0.45
8:Q:75:TYR:OH	8:Q:91:ARG:NH1	2.48	0.45
13:W:60:ASP:OD1	13:W:61:GLY:N	2.49	0.45
16:A:81:G:O2'	16:A:295:G:O2'	2.33	0.45
17:D:27:ILE:N	17:D:27:ILE:HD12	2.31	0.45
16:A:543:G:O6	16:A:551:G:O6	2.34	0.45
18:E:79:ARG:O	18:E:80:SER:OG	2.32	0.45
16:A:299:A:N6	16:A:322:A:O2'	2.46	0.45
16:A:1413:A:C2'	16:A:1414:C:O4'	2.65	0.45
16:A:219:A:N3	16:A:234:U:O2'	2.50	0.45
3:F:33:ILE:O	3:F:90:LEU:HD23	2.17	0.45
4:J:114:LEU:HD11	16:A:557:C:O2'	2.17	0.45
16:A:500:G:O2'	16:A:505:A:N6	2.50	0.45
16:A:307:G:H22	16:A:309:A:H3'	1.82	0.45
16:A:1351:C:H2'	16:A:1352:U:O4'	2.16	0.45
16:A:1601:G:H2'	16:A:1602:U:O4'	2.17	0.45
16:A:2679:A:H5'	17:D:170:VAL:HG21	1.98	0.45
2:B:2:G:H2'	2:B:3:C:C6	2.52	0.44
2:B:23:G:O2'	2:B:24:G:O4'	2.35	0.44
7:O:106:LEU:HD23	7:O:106:LEU:O	2.17	0.44
16:A:543:G:H2'	16:A:544:C:C6	2.52	0.44
16:A:1309:G:N2	16:A:1611:C:O4'	2.43	0.44
16:A:1484:U:H2'	16:A:1485:U:O4'	2.16	0.44
18:E:146:VAL:HG21	18:E:187:VAL:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:39:VAL:HG11	3:F:149:ARG:HH21	1.82	0.44
3:F:48:LEU:HD12	3:F:49:LEU:N	2.32	0.44
16:A:1542:U:H2'	16:A:1543:G:C8	2.53	0.44
16:A:320:A:H2'	18:E:131:THR:HG21	1.99	0.44
16:A:1443:U:C2	16:A:1444:G:C8	3.05	0.44
13:W:11:ASP:OD1	13:W:12:SER:N	2.51	0.44
16:A:548:G:C2'	16:A:549:G:O4'	2.65	0.44
16:A:820:A:OP2	16:A:973:A:N6	2.42	0.44
16:A:1307:A:H2'	16:A:1308:A:O4'	2.17	0.44
16:A:1342:A:O2'	16:A:1345:C:N4	2.50	0.44
16:A:1349:C:C2	16:A:1350:C:C5	3.05	0.44
16:A:1478:G:H2'	16:A:1479:G:C1'	2.48	0.44
18:E:176:ASP:OD1	18:E:176:ASP:N	2.50	0.44
16:A:49:A:N1	16:A:177:G:N2	2.66	0.44
16:A:374:A:N6	16:A:400:G:O2'	2.51	0.44
16:A:151:C:N4	16:A:152:A:H62	2.16	0.44
16:A:471:A:OP1	18:E:79:ARG:NH1	2.47	0.44
6:N:115:LEU:HD12	6:N:115:LEU:H	1.83	0.44
7:O:31:THR:O	7:O:102:ARG:NH2	2.49	0.44
9:R:40:MET:SD	9:R:41:ILE:N	2.91	0.44
16:A:383:C:N3	16:A:391:A:N6	2.64	0.44
3:F:118:ALA:O	3:F:166:ARG:NH1	2.48	0.44
4:J:32:LEU:HD23	4:J:54:ILE:HD13	2.00	0.44
5:L:90:VAL:N	5:L:121:THR:O	2.46	0.44
8:Q:68:ALA:HB1	8:Q:73:ILE:HG23	1.99	0.44
16:A:262:A:N3	16:A:430:A:O2'	2.41	0.44
16:A:966:G:H4'	16:A:2271:G:H22	1.83	0.44
9:R:74:ILE:N	9:R:74:ILE:HD12	2.31	0.43
16:A:630:G:N2	16:A:633:A:OP2	2.43	0.43
1:2:30:VAL:HG22	1:2:33:ARG:NH2	2.34	0.43
2:B:30:C:H1'	2:B:57:A:H61	1.83	0.43
11:U:27:VAL:HG12	11:U:33:VAL:HG12	2.00	0.43
17:D:188:LEU:HD12	17:D:188:LEU:N	2.33	0.43
2:B:77:U:O2	2:B:99:A:N7	2.51	0.43
16:A:240:C:OP2	16:A:241:A:O2'	2.20	0.43
5:L:42:SER:OG	16:A:672:C:OP2	2.32	0.43
9:R:98:ILE:HG21	9:R:101:ILE:HD11	2.00	0.43
17:D:26:VAL:C	17:D:27:ILE:HD12	2.38	0.43
4:J:9:GLU:OE1	4:J:9:GLU:N	2.46	0.43
16:A:549:G:H2'	16:A:550:C:O4'	2.18	0.43
16:A:1346:G:H2'	16:A:1347:A:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:1348:C:C2	16:A:1349:C:C6	3.07	0.43
16:A:1425:G:H2'	16:A:1426:G:O4'	2.18	0.43
16:A:2321:U:O2	16:A:2321:U:H2'	2.19	0.43
17:D:97:SER:OG	17:D:98:VAL:N	2.52	0.43
18:E:118:LEU:HD23	18:E:119:ILE:N	2.33	0.43
3:F:66:ILE:N	3:F:66:ILE:HD12	2.33	0.43
6:N:29:VAL:HG11	6:N:75:ILE:HG23	2.00	0.43
16:A:235:U:O4	16:A:263:G:N2	2.52	0.43
16:A:1205:A:HO2'	16:A:1206:G:P	2.42	0.43
16:A:1494:A:N3	16:A:1494:A:H2'	2.34	0.43
6:N:47:VAL:O	6:N:51:LEU:HD23	2.19	0.43
8:Q:8:ILE:HD12	8:Q:8:ILE:H	1.84	0.43
16:A:545:U:O4	16:A:548:G:O6	2.36	0.43
16:A:1566:A:H2'	16:A:1566:A:N3	2.34	0.43
16:A:2009:A:C2'	16:A:2010:G:O4'	2.66	0.43
11:U:97:SER:O	11:U:98:ASN:OD1	2.36	0.43
16:A:1414:C:O2'	16:A:1415:U:C4'	2.67	0.43
14:Y:5:GLU:OE1	14:Y:5:GLU:N	2.47	0.43
16:A:33:C:O2	16:A:447:A:N6	2.51	0.43
16:A:2004:G:H2'	16:A:2005:A:O4'	2.18	0.43
17:D:101:PHE:HA	17:D:104:VAL:HG12	2.01	0.43
3:F:39:VAL:HG23	3:F:40:GLY:N	2.34	0.42
4:J:111:LYS:NZ	16:A:2039:U:OP1	2.37	0.42
16:A:465:G:H21	16:A:684:G:H1'	1.84	0.42
18:E:11:ALA:C	18:E:12:LEU:HD22	2.39	0.42
4:J:12:LYS:NZ	4:J:14:ASP:OD1	2.50	0.42
6:N:79:LEU:O	6:N:80:PHE:HB2	2.19	0.42
16:A:544:C:H2'	16:A:545:U:C2	2.53	0.42
16:A:2051:A:N3	16:A:2052:A:N6	2.67	0.42
5:L:29:LYS:O	5:L:30:THR:OG1	2.30	0.42
16:A:1141:U:H4'	16:A:1142:A:O4'	2.20	0.42
16:A:1245:G:H2'	16:A:1246:A:C8	2.55	0.42
16:A:1319:C:O2'	16:A:1320:C:P	2.77	0.42
16:A:1364:G:O2'	16:A:1367:A:N6	2.53	0.42
16:A:1591:A:H2'	16:A:1592:C:O4'	2.18	0.42
5:L:92:LEU:O	5:L:92:LEU:HD23	2.20	0.42
16:A:170:U:C2	16:A:171:U:C5	3.07	0.42
16:A:832:U:O2	16:A:833:A:C8	2.73	0.42
16:A:1576:U:H2'	16:A:1577:C:C6	2.55	0.42
16:A:2287:A:N6	16:A:2346:A:N7	2.68	0.42
3:F:165:GLY:O	3:F:169:LEU:HD13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:2028:U:O4	16:A:2033:A:N7	2.52	0.42
5:L:71:ALA:HA	5:L:74:THR:HG22	2.01	0.42
12:V:35:GLU:OE2	12:V:93:ARG:NH1	2.53	0.42
13:W:66:GLU:N	13:W:66:GLU:OE1	2.52	0.42
14:Y:24:GLU:O	14:Y:28:LEU:HD12	2.20	0.42
16:A:1370:C:H2'	16:A:1371:G:O4'	2.20	0.42
16:A:1430:G:C4	16:A:1431:A:C8	3.08	0.42
16:A:2399:G:C6	16:A:2418:A:C6	3.08	0.42
2:B:73:A:N3	2:B:73:A:H2'	2.35	0.42
9:R:75:VAL:HG22	9:R:86:GLN:OE1	2.19	0.42
11:U:98:ASN:O	11:U:98:ASN:CG	2.58	0.42
16:A:1208:C:H2'	16:A:1209:U:O4'	2.19	0.42
16:A:1357:C:H2'	16:A:1358:G:O4'	2.20	0.42
17:D:33:ARG:CG	17:D:73:VAL:HG13	2.48	0.42
18:E:31:VAL:HG21	18:E:104:ALA:CB	2.48	0.42
16:A:1021:A:H61	16:A:1142:A:H61	1.68	0.42
16:A:1389:G:H2'	16:A:1390:U:O4'	2.20	0.42
16:A:1480:C:H2'	16:A:1481:U:O4'	2.19	0.42
16:A:1998:A:H2'	16:A:1999:C:C6	2.55	0.42
3:F:122:ASP:OD2	3:F:126:ASN:ND2	2.44	0.41
10:T:4:GLU:CD	14:Y:18:LEU:HD13	2.41	0.41
16:A:1504:A:N1	16:A:1505:A:N6	2.67	0.41
16:A:2831:G:N2	16:A:2884:U:OP2	2.53	0.41
8:Q:8:ILE:HD12	8:Q:8:ILE:N	2.35	0.41
3:F:48:LEU:O	3:F:51:ASN:ND2	2.53	0.41
7:O:108:ASP:OD1	7:O:109:ALA:N	2.54	0.41
8:Q:60:TRP:O	8:Q:64:ILE:HG12	2.20	0.41
13:W:64:LYS:N	13:W:77:SER:O	2.48	0.41
16:A:2345:G:O6	16:A:2371:G:O6	2.39	0.41
5:L:17:LYS:HE3	5:L:27:LEU:HD13	2.03	0.41
8:Q:91:ARG:NH1	16:A:1153:C:OP1	2.47	0.41
15:Z:46:MET:O	15:Z:50:VAL:HG22	2.20	0.41
16:A:1327:A:H2'	16:A:1328:A:O4'	2.21	0.41
16:A:1385:A:H1'	16:A:1386:C:C6	2.55	0.41
16:A:1561:C:H2'	16:A:1562:U:O4'	2.20	0.41
16:A:2720:U:C2	16:A:2721:A:C8	3.09	0.41
3:F:107:VAL:N	3:F:108:PRO:CD	2.84	0.41
16:A:1595:C:H2'	16:A:1596:A:O4'	2.20	0.41
16:A:2848:G:O2'	16:A:2868:A:N6	2.46	0.41
9:R:23:GLU:OE1	9:R:24:LYS:N	2.50	0.41
16:A:1346:G:N1	16:A:1601:G:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:1353:A:N7	16:A:1377:G:N2	2.68	0.41
16:A:1414:C:C2'	16:A:1415:U:O4'	2.68	0.41
3:F:12:VAL:HG13	3:F:13:LYS:N	2.36	0.41
3:F:33:ILE:HD12	3:F:33:ILE:N	2.36	0.41
9:R:82:HIS:ND1	9:R:82:HIS:O	2.53	0.41
16:A:967:U:H2'	16:A:968:C:C6	2.56	0.41
16:A:1234:U:H2'	16:A:1235:G:O4'	2.21	0.41
16:A:1593:A:H2'	16:A:1594:U:O4'	2.21	0.41
3:F:65:LEU:HD23	3:F:65:LEU:H	1.86	0.41
11:U:85:ARG:NH2	11:U:101:THR:OG1	2.54	0.41
16:A:306:U:H2'	16:A:307:G:O4'	2.20	0.41
16:A:1358:G:N1	16:A:1372:U:OP2	2.45	0.41
16:A:1451:C:C2'	16:A:1452:G:OP2	2.69	0.41
16:A:1528:A:OP2	16:A:1543:G:N2	2.41	0.41
4:J:18:VAL:CG2	4:J:54:ILE:HD11	2.51	0.41
11:U:35:VAL:HG23	11:U:38:ILE:HB	2.02	0.41
16:A:1425:G:N2	16:A:1574:C:N4	2.69	0.41
16:A:1607:C:O4'	16:A:1621:U:N3	2.53	0.41
16:A:1630:A:H2'	16:A:1631:G:O4'	2.20	0.41
16:A:1665:A:C2'	16:A:1666:G:O5'	2.69	0.41
2:B:83:G:O6	2:B:94:A:N6	2.53	0.41
3:F:79:ARG:NH1	3:F:80:GLN:O	2.54	0.41
16:A:1351:C:H1'	16:A:1572:A:H1'	2.03	0.41
16:A:2368:C:O2	16:A:2369:A:C8	2.74	0.41
3:F:105:ILE:HD12	3:F:138:PRO:HG2	2.03	0.40
7:O:62:LEU:HD22	7:O:62:LEU:N	2.36	0.40
11:U:9:GLU:O	11:U:72:PHE:N	2.46	0.40
11:U:28:LEU:HD22	11:U:28:LEU:N	2.36	0.40
16:A:1354:A:H62	16:A:1377:G:H21	1.68	0.40
17:D:25:THR:HG21	17:D:193:VAL:CG2	2.50	0.40
16:A:1513:U:H2'	16:A:1514:G:O4'	2.22	0.40
16:A:2812:G:N2	16:A:2889:C:C2	2.89	0.40
2:B:45:A:O4'	3:F:91:ARG:NH1	2.55	0.40
18:E:154:ASP:OD1	18:E:154:ASP:N	2.48	0.40
3:F:140:ILE:N	3:F:140:ILE:HD12	2.36	0.40
16:A:635:C:O2'	16:A:639:U:OP1	2.40	0.40
16:A:928:A:H2'	16:A:929:U:C6	2.56	0.40
16:A:1347:A:C5	16:A:1348:C:C6	3.09	0.40
17:D:35:THR:HG22	17:D:73:VAL:HG11	2.04	0.40
5:L:101:ILE:HG13	5:L:102:GLY:N	2.37	0.40
16:A:458:G:C2'	16:A:459:U:OP2	2.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:A:499:U:H2'	16:A:500:G:O4'	2.22	0.40
16:A:1372:U:O4	16:A:1373:A:N6	2.55	0.40
16:A:1394:U:H2'	16:A:1395:A:O4'	2.22	0.40
16:A:1413:A:H2'	16:A:1414:C:O4'	2.22	0.40
16:A:1574:C:H2'	16:A:1575:C:O4'	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	36/46 (78%)	36 (100%)	0	0	100	100
3	F	175/177 (99%)	169 (97%)	6 (3%)	0	100	100
4	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
5	L	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
6	N	118/120 (98%)	107 (91%)	11 (9%)	0	100	100
7	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
8	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
9	R	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	13	48
10	T	91/93 (98%)	86 (94%)	5 (6%)	0	100	100
11	U	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
12	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
13	W	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
14	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
15	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
17	D	169/209 (81%)	163 (96%)	6 (4%)	0	100	100
18	E	172/201 (86%)	168 (98%)	3 (2%)	1 (1%)	22	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	y	15/17 (88%)	11 (73%)	4 (27%)	0	100	100
All	All	1769/1876 (94%)	1692 (96%)	75 (4%)	2 (0%)	50	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	R	54	VAL
18	E	83	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	30/38 (79%)	30 (100%)	0	100	100
3	F	148/148 (100%)	143 (97%)	5 (3%)	32	53
4	J	116/116 (100%)	114 (98%)	2 (2%)	56	73
5	L	102/102 (100%)	102 (100%)	0	100	100
6	N	99/100 (99%)	99 (100%)	0	100	100
7	O	86/86 (100%)	86 (100%)	0	100	100
8	Q	89/89 (100%)	89 (100%)	0	100	100
9	R	84/84 (100%)	83 (99%)	1 (1%)	67	79
10	T	80/80 (100%)	80 (100%)	0	100	100
11	U	83/83 (100%)	82 (99%)	1 (1%)	67	79
12	V	78/78 (100%)	77 (99%)	1 (1%)	65	77
13	W	57/57 (100%)	56 (98%)	1 (2%)	54	71
14	Y	55/55 (100%)	55 (100%)	0	100	100
15	Z	48/48 (100%)	48 (100%)	0	100	100
17	D	134/164 (82%)	132 (98%)	2 (2%)	60	75
18	E	146/165 (88%)	144 (99%)	2 (1%)	62	76
19	y	17/17 (100%)	16 (94%)	1 (6%)	16	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1452/1510 (96%)	1436 (99%)	16 (1%)	69 80

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	7	TYR
3	F	29	ARG
3	F	51	ASN
3	F	79	ARG
3	F	144	LYS
4	J	96	ARG
4	J	99	ARG
9	R	22	LEU
11	U	98	ASN
12	V	42	LEU
13	W	65	PHE
17	D	11	MET
17	D	33	ARG
18	E	19	PHE
18	E	163	ASN
19	y	17	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
4	J	80	HIS
5	L	99	ASN
6	N	107	ASN
8	Q	70	GLN
9	R	18	GLN
18	E	94	GLN
19	y	3	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	A	1981/2903 (68%)	428 (21%)	17 (0%)
2	B	119/120 (99%)	14 (11%)	2 (1%)
All	All	2100/3023 (69%)	442 (21%)	19 (0%)

All (442) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	4	C
2	B	12	C
2	B	13	G
2	B	35	C
2	B	41	G
2	B	42	C
2	B	44	G
2	B	45	A
2	B	53	A
2	B	66	A
2	B	67	G
2	B	89	U
2	B	90	C
2	B	109	A
16	A	10	A
16	A	27	G
16	A	34	U
16	A	35	G
16	A	46	G
16	A	50	U
16	A	51	G
16	A	71	A
16	A	74	A
16	A	75	G
16	A	114	U
16	A	118	A
16	A	120	U
16	A	135	U
16	A	136	G
16	A	139	U
16	A	141	G
16	A	142	A
16	A	160	A
16	A	162	U
16	A	163	C
16	A	181	A
16	A	190	A
16	A	196	A
16	A	197	A
16	A	199	A
16	A	215	G
16	A	216	A

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Mol	Chain	Res	Type
16	A	221	A
16	A	222	A
16	A	225	C
16	A	228	C
16	A	232	G
16	A	242	G
16	A	243	U
16	A	248	G
16	A	255	A
16	A	266	G
16	A	267	C
16	A	272	A
16	A	275	C
16	A	277	G
16	A	278	A
16	A	294	A
16	A	304	U
16	A	307	G
16	A	310	A
16	A	322	A
16	A	323	C
16	A	324	A
16	A	329	G
16	A	330	A
16	A	345	A
16	A	350	G
16	A	362	A
16	A	371	A
16	A	372	G
16	A	373	U
16	A	384	A
16	A	386	G
16	A	387	U
16	A	388	G
16	A	401	A
16	A	404	A
16	A	406	G
16	A	411	G
16	A	412	A
16	A	417	C
16	A	424	G
16	A	429	A

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Mol	Chain	Res	Type
16	A	430	A
16	A	435	C
16	A	456	C
16	A	457	A
16	A	458	G
16	A	459	U
16	A	465	G
16	A	466	A
16	A	473	G
16	A	480	A
16	A	481	G
16	A	491	G
16	A	505	A
16	A	509	C
16	A	510	C
16	A	529	A
16	A	530	G
16	A	531	C
16	A	532	A
16	A	543	G
16	A	544	C
16	A	545	U
16	A	547	A
16	A	549	G
16	A	550	C
16	A	563	A
16	A	568	U
16	A	572	A
16	A	573	U
16	A	575	A
16	A	588	U
16	A	603	A
16	A	614	A
16	A	621	A
16	A	627	A
16	A	637	A
16	A	645	C
16	A	646	U
16	A	647	G
16	A	654	A
16	A	668	A
16	A	669	G

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Mol	Chain	Res	Type
16	A	670	A
16	A	671	C
16	A	675	A
16	A	684	G
16	A	801	G
16	A	805	G
16	A	812	C
16	A	819	A
16	A	827	U
16	A	828	U
16	A	830	G
16	A	845	A
16	A	846	U
16	A	847	U
16	A	856	G
16	A	857	G
16	A	910	A
16	A	914	G
16	A	918	A
16	A	931	U
16	A	932	U
16	A	941	A
16	A	946	C
16	A	952	G
16	A	953	G
16	A	957	C
16	A	959	A
16	A	961	C
16	A	973	A
16	A	974	G
16	A	981	A
16	A	983	A
16	A	985	C
16	A	995	C
16	A	996	A
16	A	1009	A
16	A	1012	U
16	A	1013	C
16	A	1021	A
16	A	1022	G
16	A	1023	U
16	A	1026	G

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Mol	Chain	Res	Type
16	A	1129	A
16	A	1132	U
16	A	1135	C
16	A	1143	A
16	A	1151	A
16	A	1157	G
16	A	1169	A
16	A	1171	G
16	A	1174	U
16	A	1175	A
16	A	1176	U
16	A	1178	C
16	A	1180	U
16	A	1206	G
16	A	1212	G
16	A	1225	G
16	A	1236	G
16	A	1250	G
16	A	1253	A
16	A	1255	U
16	A	1256	G
16	A	1263	U
16	A	1265	A
16	A	1266	G
16	A	1267	U
16	A	1269	A
16	A	1271	G
16	A	1272	A
16	A	1273	U
16	A	1274	A
16	A	1275	A
16	A	1280	G
16	A	1284	A
16	A	1288	G
16	A	1289	C
16	A	1300	G
16	A	1301	A
16	A	1306	C
16	A	1307	A
16	A	1312	U
16	A	1315	C
16	A	1320	C

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Mol	Chain	Res	Type
16	A	1321	A
16	A	1325	U
16	A	1327	A
16	A	1329	U
16	A	1332	G
16	A	1333	G
16	A	1334	G
16	A	1340	U
16	A	1341	G
16	A	1343	G
16	A	1345	C
16	A	1352	U
16	A	1355	G
16	A	1356	G
16	A	1359	A
16	A	1361	G
16	A	1362	C
16	A	1365	A
16	A	1374	G
16	A	1379	U
16	A	1380	G
16	A	1383	A
16	A	1386	C
16	A	1391	U
16	A	1394	U
16	A	1395	A
16	A	1397	U
16	A	1400	U
16	A	1403	A
16	A	1404	C
16	A	1407	G
16	A	1413	A
16	A	1416	G
16	A	1419	A
16	A	1420	A
16	A	1421	G
16	A	1427	A
16	A	1428	C
16	A	1432	G
16	A	1434	A
16	A	1436	G
16	A	1445	G

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Mol	Chain	Res	Type
16	A	1449	G
16	A	1450	G
16	A	1452	G
16	A	1453	A
16	A	1454	C
16	A	1458	U
16	A	1459	G
16	A	1461	C
16	A	1467	U
16	A	1468	U
16	A	1469	A
16	A	1473	G
16	A	1474	U
16	A	1475	G
16	A	1478	G
16	A	1480	C
16	A	1482	G
16	A	1483	G
16	A	1484	U
16	A	1486	U
16	A	1493	C
16	A	1495	A
16	A	1497	U
16	A	1498	C
16	A	1501	G
16	A	1504	A
16	A	1508	A
16	A	1509	A
16	A	1515	A
16	A	1516	G
16	A	1519	G
16	A	1528	A
16	A	1529	G
16	A	1532	A
16	A	1535	A
16	A	1536	C
16	A	1537	G
16	A	1542	U
16	A	1546	G
16	A	1548	A
16	A	1553	A
16	A	1554	U

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Mol	Chain	Res	Type
16	A	1555	G
16	A	1558	C
16	A	1559	U
16	A	1560	G
16	A	1563	U
16	A	1566	A
16	A	1567	G
16	A	1569	A
16	A	1575	C
16	A	1576	U
16	A	1578	U
16	A	1579	A
16	A	1583	A
16	A	1584	U
16	A	1585	C
16	A	1592	C
16	A	1593	A
16	A	1596	A
16	A	1597	A
16	A	1598	A
16	A	1603	A
16	A	1607	C
16	A	1608	A
16	A	1613	G
16	A	1614	A
16	A	1615	C
16	A	1616	A
16	A	1618	A
16	A	1619	G
16	A	1620	G
16	A	1622	G
16	A	1627	G
16	A	1628	G
16	A	1634	A
16	A	1635	A
16	A	1636	U
16	A	1637	A
16	A	1644	C
16	A	1647	U
16	A	1648	U
16	A	1649	G
16	A	1650	A

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Mol	Chain	Res	Type
16	A	1651	G
16	A	1652	A
16	A	1653	G
16	A	1654	A
16	A	1656	C
16	A	1657	U
16	A	1660	G
16	A	1662	U
16	A	1663	G
16	A	1664	A
16	A	1666	G
16	A	1667	G
16	A	1992	G
16	A	1993	U
16	A	1997	C
16	A	1998	A
16	A	2003	A
16	A	2004	G
16	A	2006	C
16	A	2007	U
16	A	2008	C
16	A	2009	A
16	A	2011	U
16	A	2012	G
16	A	2013	A
16	A	2015	A
16	A	2022	U
16	A	2023	C
16	A	2030	A
16	A	2031	A
16	A	2043	C
16	A	2052	A
16	A	2250	G
16	A	2251	G
16	A	2266	A
16	A	2279	G
16	A	2283	C
16	A	2286	G
16	A	2287	A
16	A	2297	A
16	A	2305	U
16	A	2309	A

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Mol	Chain	Res	Type
16	A	2319	G
16	A	2327	A
16	A	2333	A
16	A	2334	U
16	A	2335	A
16	A	2336	A
16	A	2343	U
16	A	2350	C
16	A	2383	G
16	A	2385	C
16	A	2388	A
16	A	2402	U
16	A	2407	A
16	A	2422	C
16	A	2424	C
16	A	2425	A
16	A	2429	G
16	A	2430	A
16	A	2434	A
16	A	2435	A
16	A	2441	U
16	A	2448	A
16	A	2449	U
16	A	2615	U
16	A	2629	U
16	A	2630	G
16	A	2646	C
16	A	2647	U
16	A	2655	G
16	A	2656	U
16	A	2682	A
16	A	2689	U
16	A	2690	U
16	A	2714	G
16	A	2726	A
16	A	2732	G
16	A	2733	A
16	A	2744	G
16	A	2748	A
16	A	2764	A
16	A	2765	A
16	A	2778	A

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Mol	Chain	Res	Type
16	A	2779	U
16	A	2780	G
16	A	2791	G
16	A	2794	C
16	A	2799	A
16	A	2800	A
16	A	2809	A
16	A	2818	U
16	A	2820	A
16	A	2833	U
16	A	2835	A
16	A	2849	U
16	A	2867	G
16	A	2872	A
16	A	2873	A
16	A	2880	C
16	A	2883	A
16	A	2893	A
16	A	2894	G
16	A	2901	C
16	A	2902	C
16	A	2903	U

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	52	A
2	B	66	A
16	A	227	A
16	A	242	G
16	A	372	G
16	A	458	G
16	A	548	G
16	A	549	G
16	A	644	A
16	A	1020	A
16	A	1022	G
16	A	1319	C
16	A	1358	G
16	A	1427	A
16	A	1534	U
16	A	2010	G

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Mol	Chain	Res	Type
16	A	2318	G
16	A	2326	C
16	A	2655	G

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

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

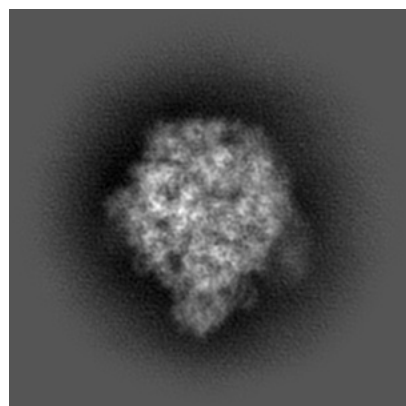
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51979. These allow visual inspection of the internal detail of the map and identification of artifacts.

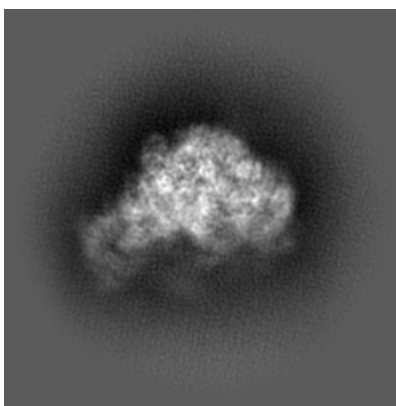
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

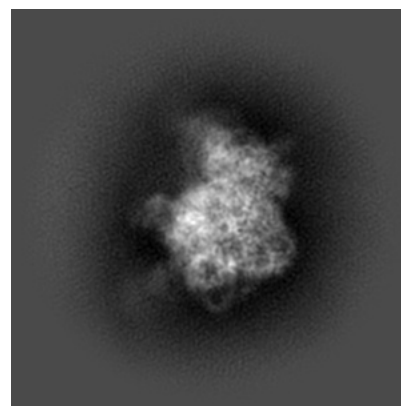
#### 6.1.1 Primary map



X

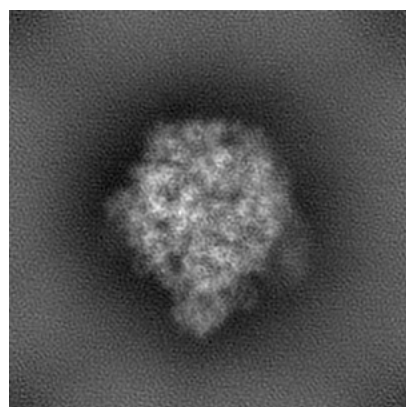


Y

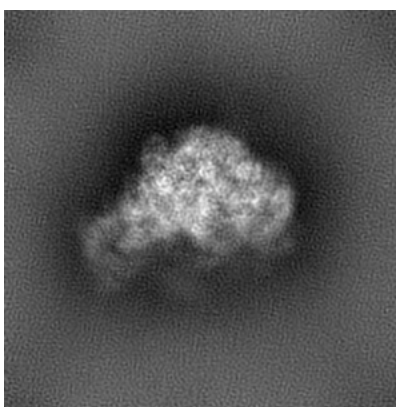


Z

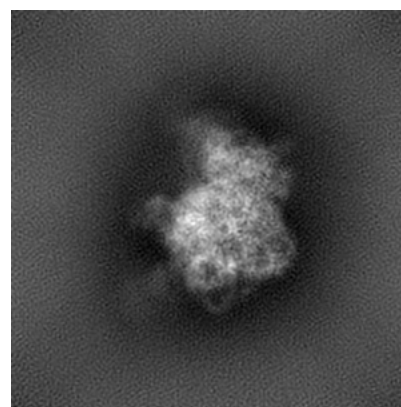
#### 6.1.2 Raw map



X



Y

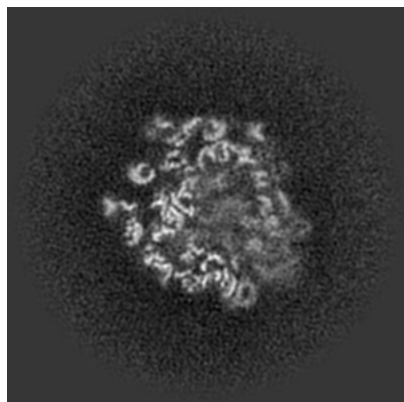


Z

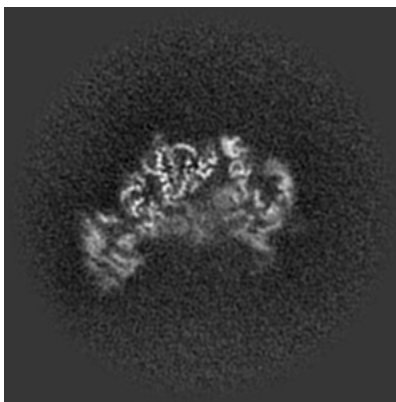
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

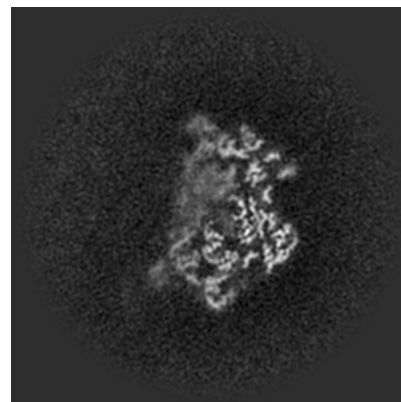
### 6.2.1 Primary map



X Index: 100

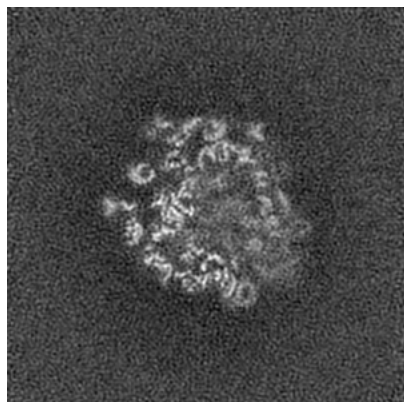


Y Index: 100

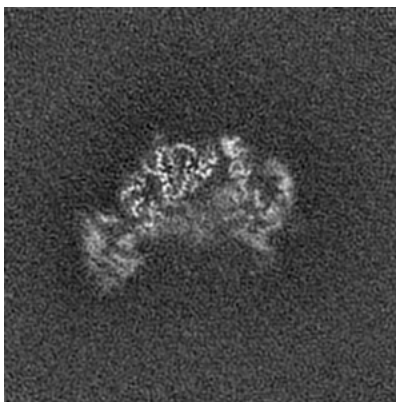


Z Index: 100

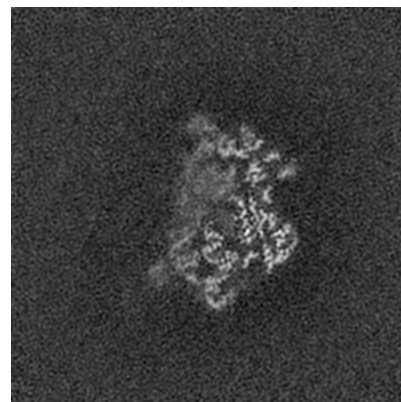
### 6.2.2 Raw map



X Index: 100



Y Index: 100

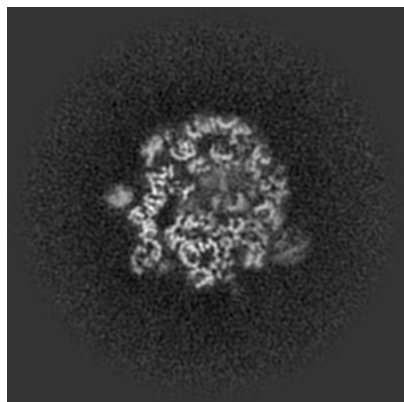


Z Index: 100

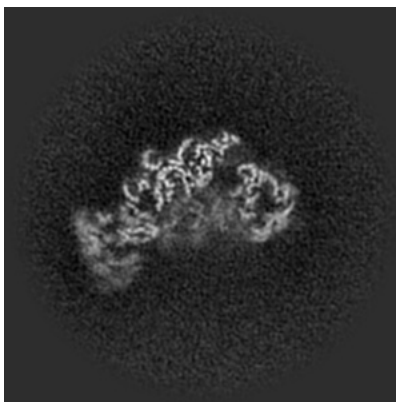
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

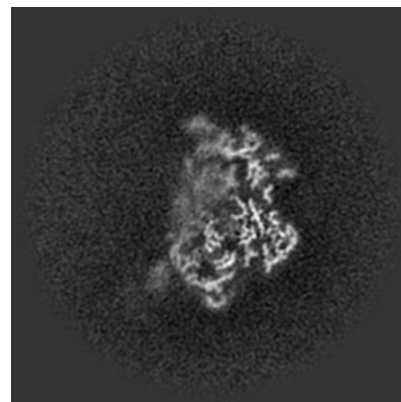
### 6.3.1 Primary map



X Index: 109

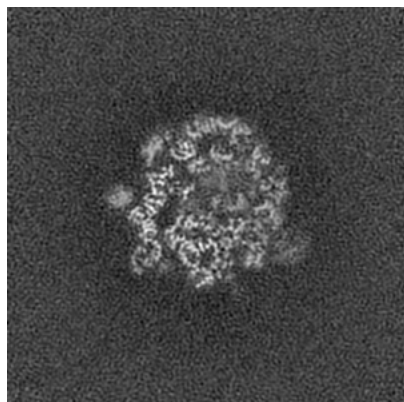


Y Index: 95

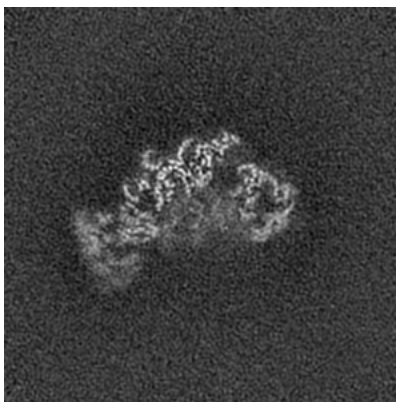


Z Index: 99

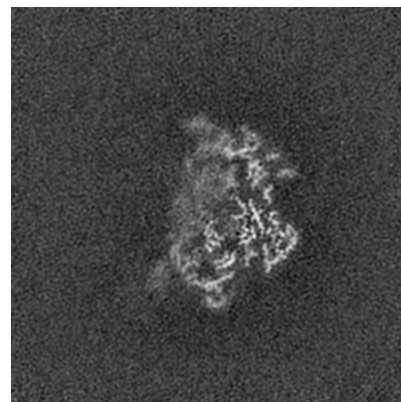
### 6.3.2 Raw map



X Index: 109



Y Index: 95

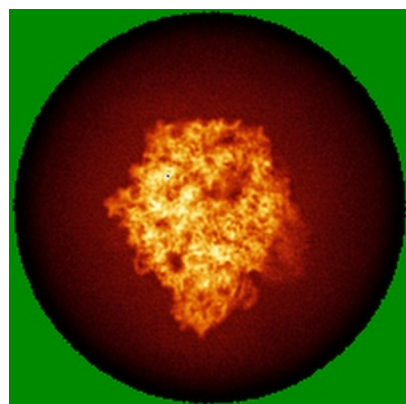


Z Index: 99

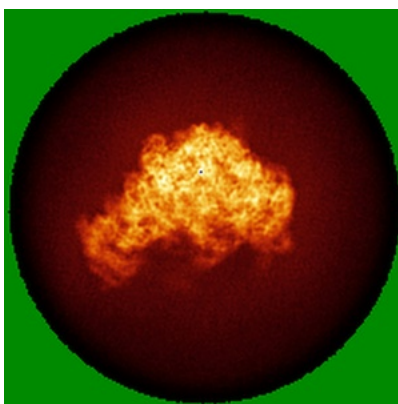
The images above show the largest variance slices of the map in three orthogonal directions.

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

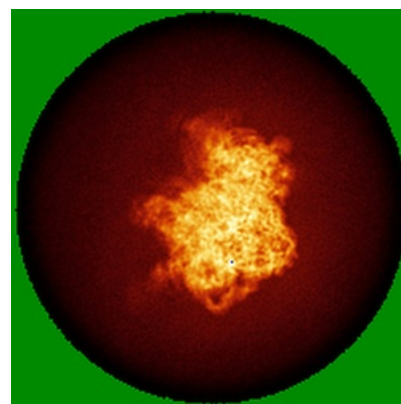
### 6.4.1 Primary map



X

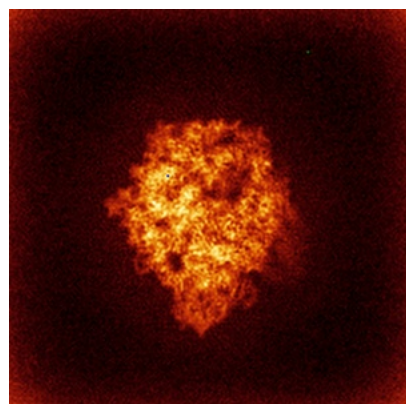


Y

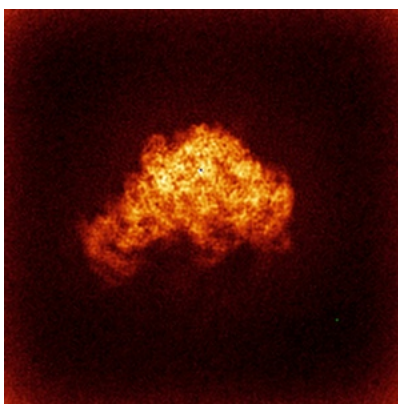


Z

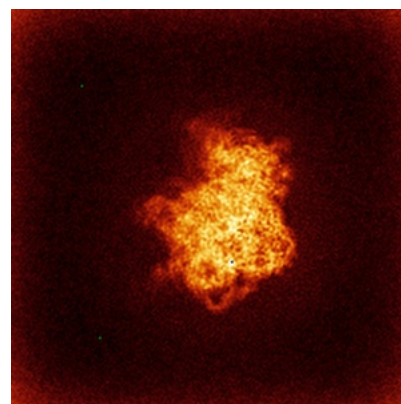
### 6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

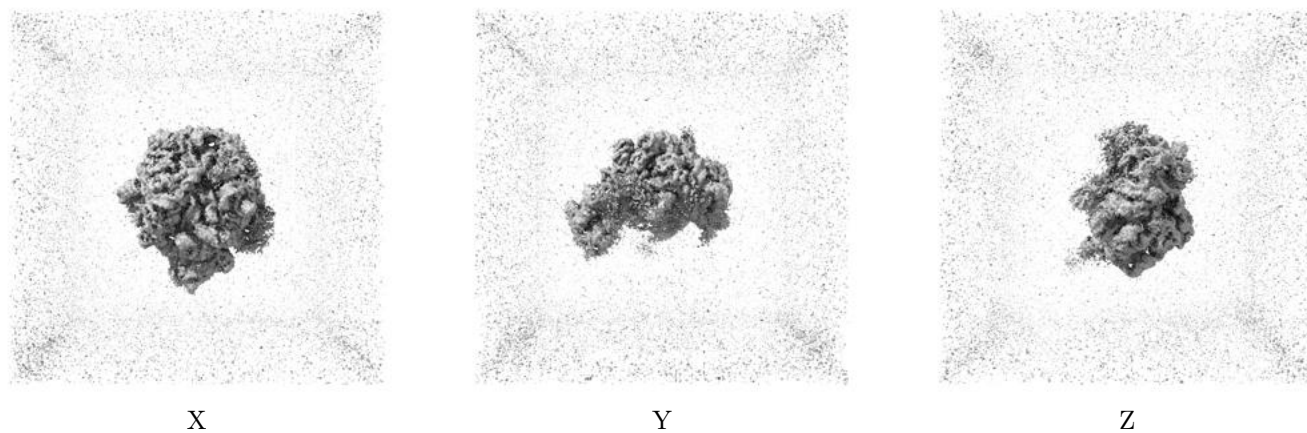
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.255. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

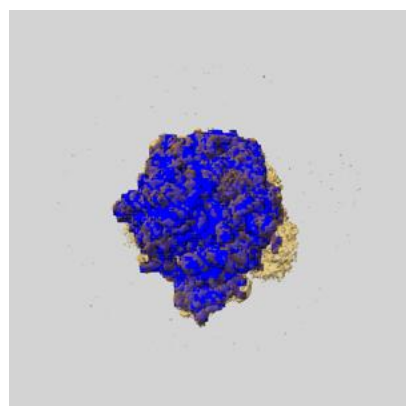
## 6.6 Mask visualisation [i](#)

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

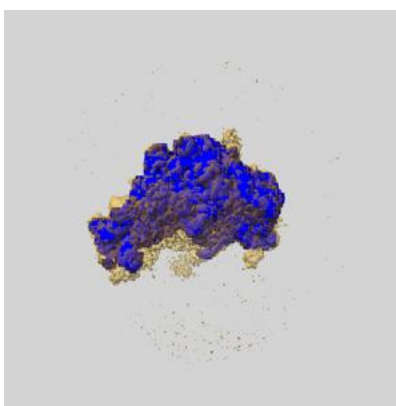
A mask typically either:

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

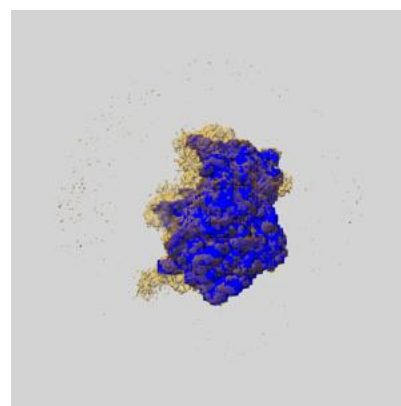
### 6.6.1 emd\_51979\_msk\_1.map [i](#)



X



Y

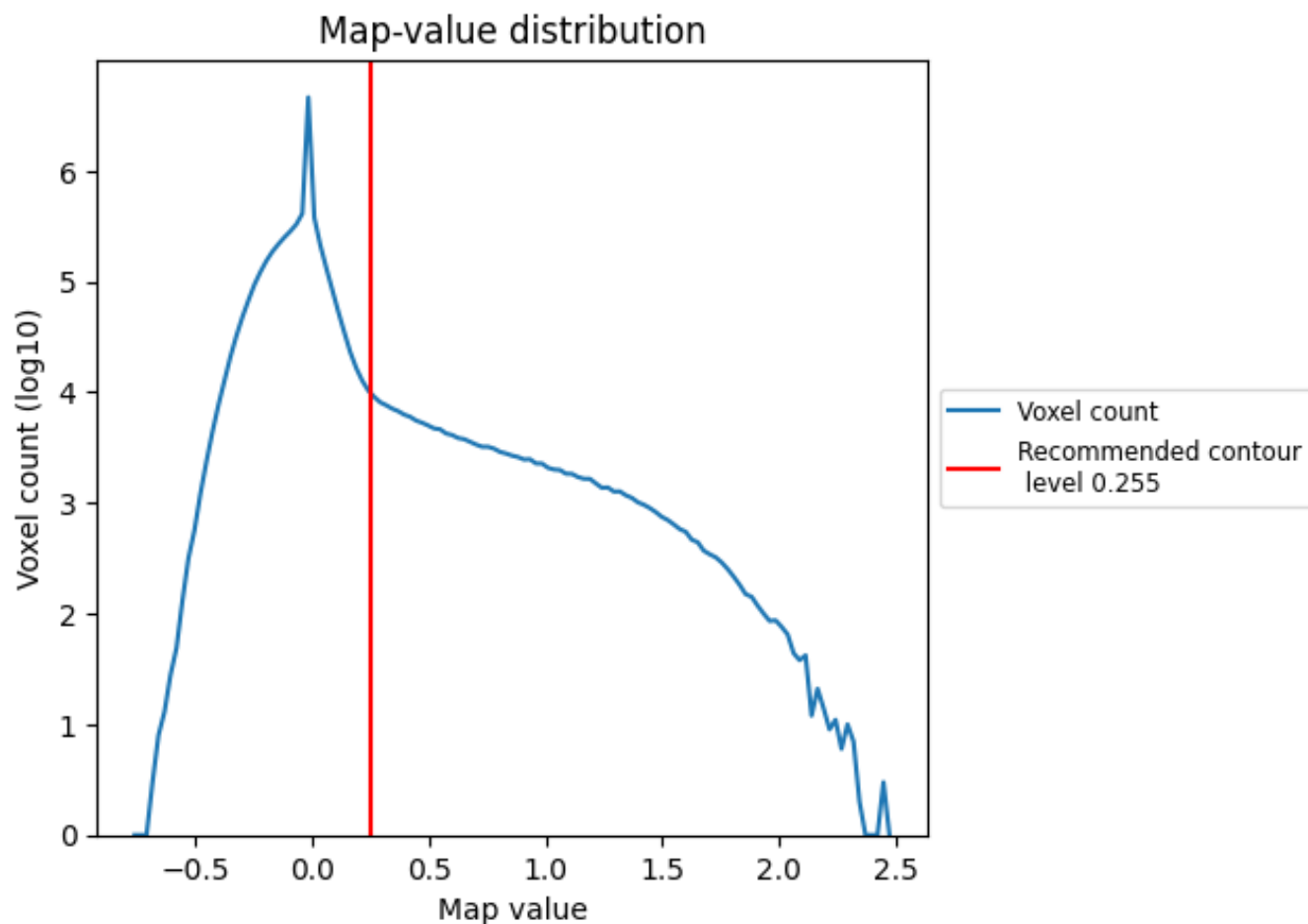


Z

## 7 Map analysis [i](#)

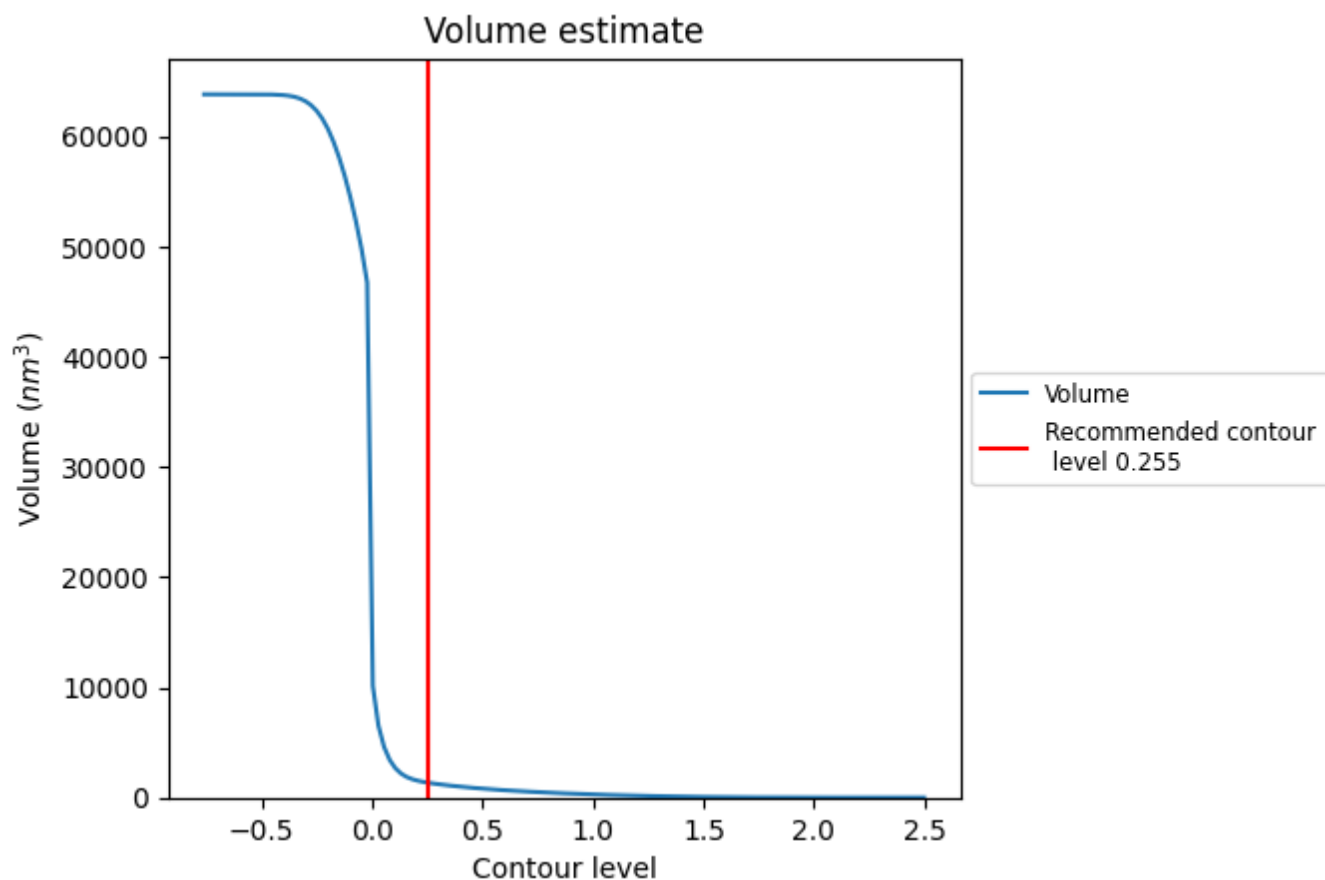
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

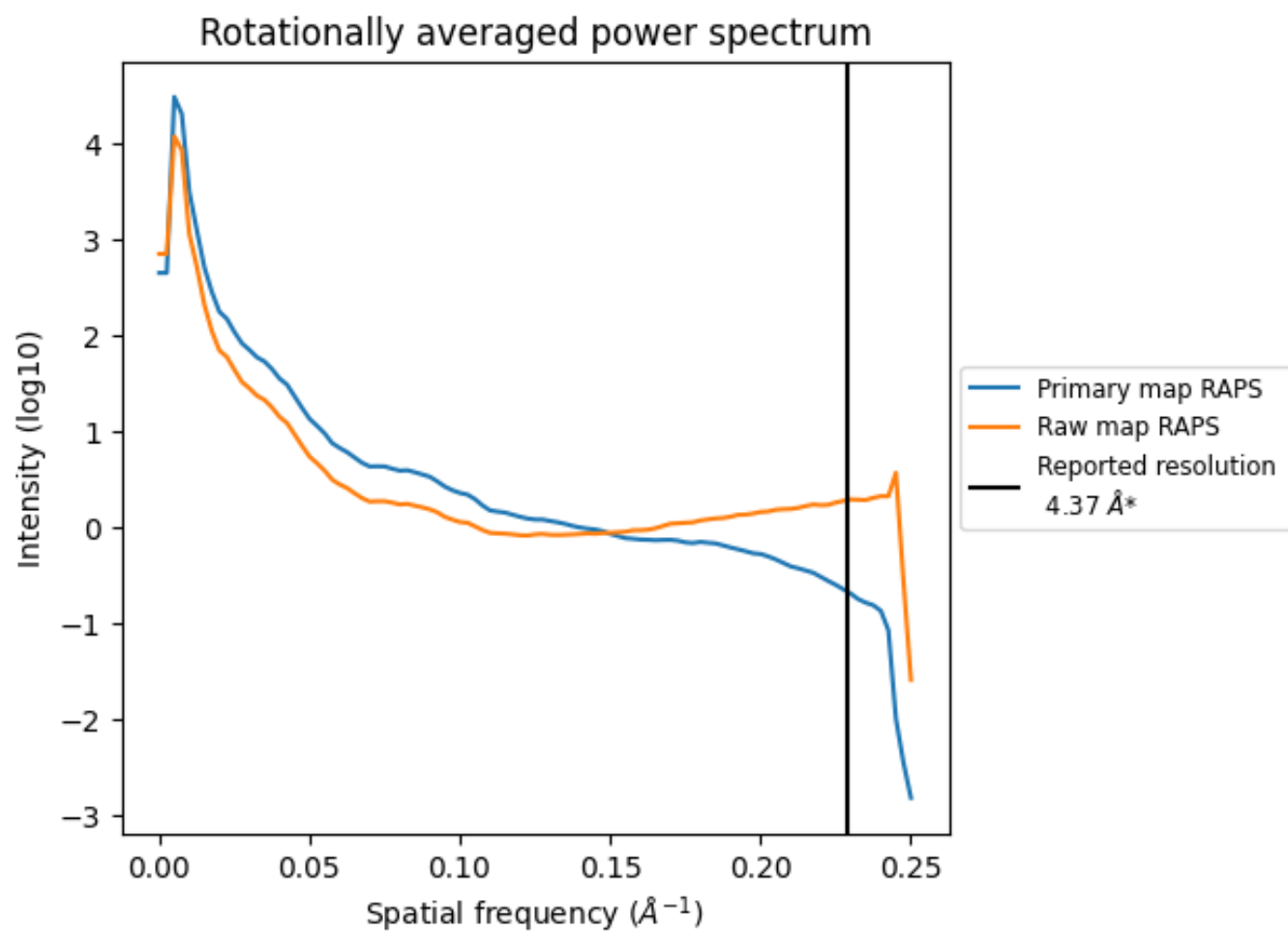
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1342 nm<sup>3</sup>; this corresponds to an approximate mass of 1212 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 ⓘ

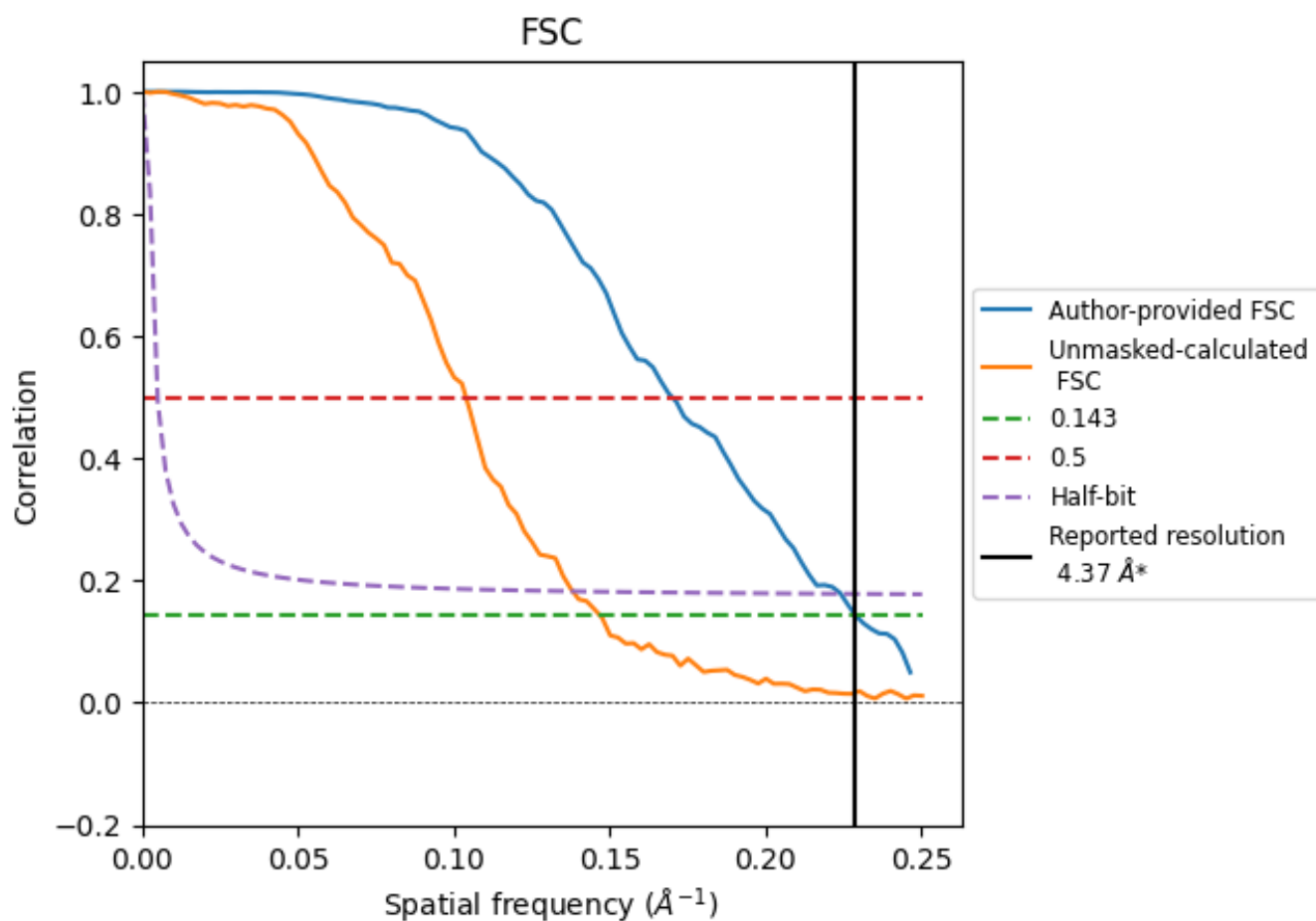


\*Reported resolution corresponds to spatial frequency of 0.229 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.229 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

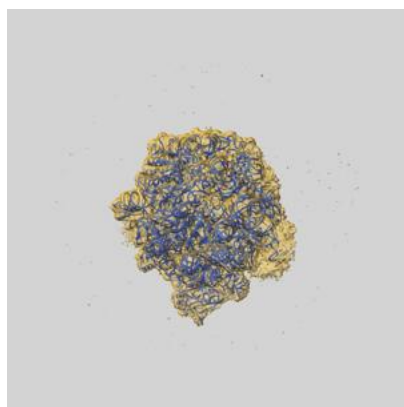
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.37	-	-
Author-provided FSC curve	4.37	5.88	4.46
Unmasked-calculated*	6.81	9.62	7.24

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.81 differs from the reported value 4.37 by more than 10 %

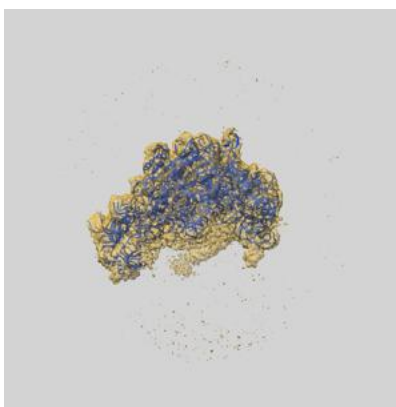
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51979 and PDB model 9HA7. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

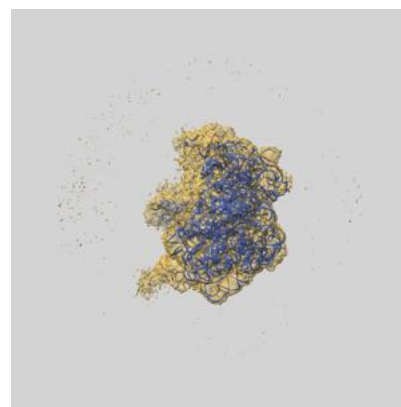
### 9.1 Map-model overlay [i](#)



X



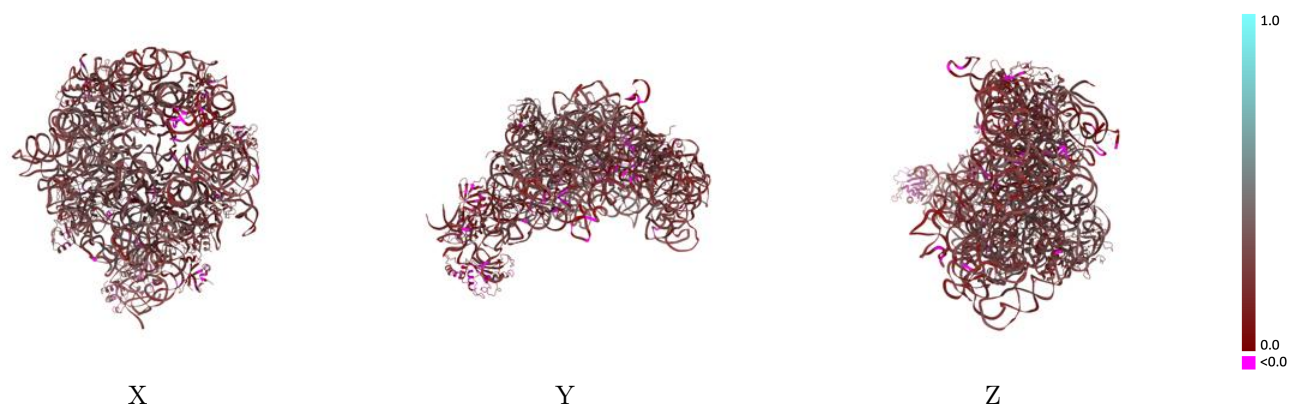
Y



Z

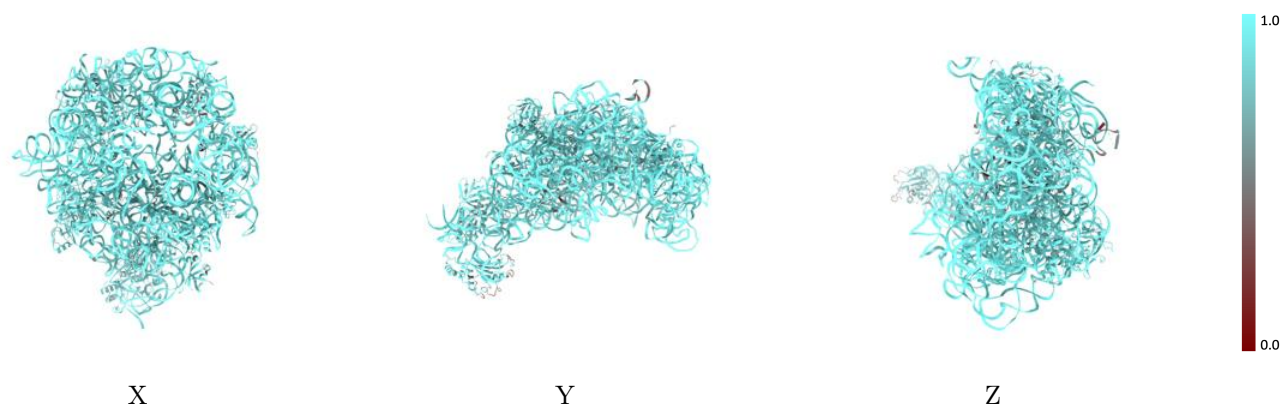
The images above show the 3D surface view of the map at the recommended contour level 0.255 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



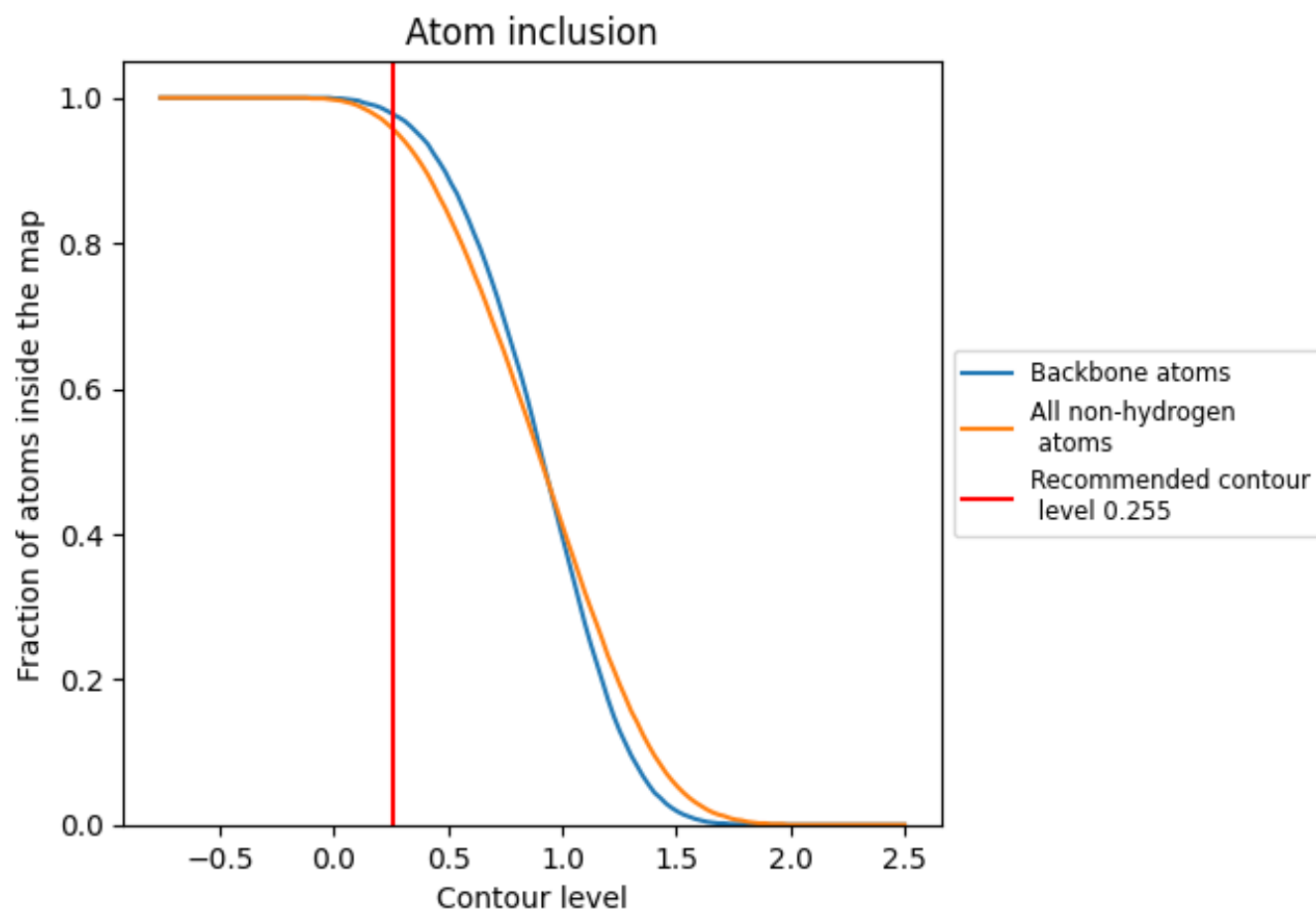
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.255).









































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.255) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.2430
2	 0.9030	 0.2520
A	 0.9810	 0.2550
B	 0.9760	 0.1940
D	 0.8870	 0.1710
E	 0.8960	 0.2690
F	 0.8030	 0.1160
J	 0.9370	 0.2770
L	 0.8130	 0.1800
N	 0.8760	 0.1920
O	 0.9300	 0.1730
Q	 0.9350	 0.2620
R	 0.9250	 0.3000
T	 0.8890	 0.2500
U	 0.9330	 0.2920
V	 0.8560	 0.1370
W	 0.9120	 0.2270
Y	 0.8790	 0.2260
Z	 0.9290	 0.2440
y	 0.4100	 0.0950

