



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:09 PM UTC

PDB ID : 9HA4 / pdb_00009ha4
EMDB ID : EMD-51976
Title : Pooled 50S subunit C-CP_(L22)- precursor states supplemented with Api137
Authors : Lauer, S.; Nikolay, R.; Spahn, C.M.T.
Deposited on : 2024-11-01
Resolution : 4.26 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

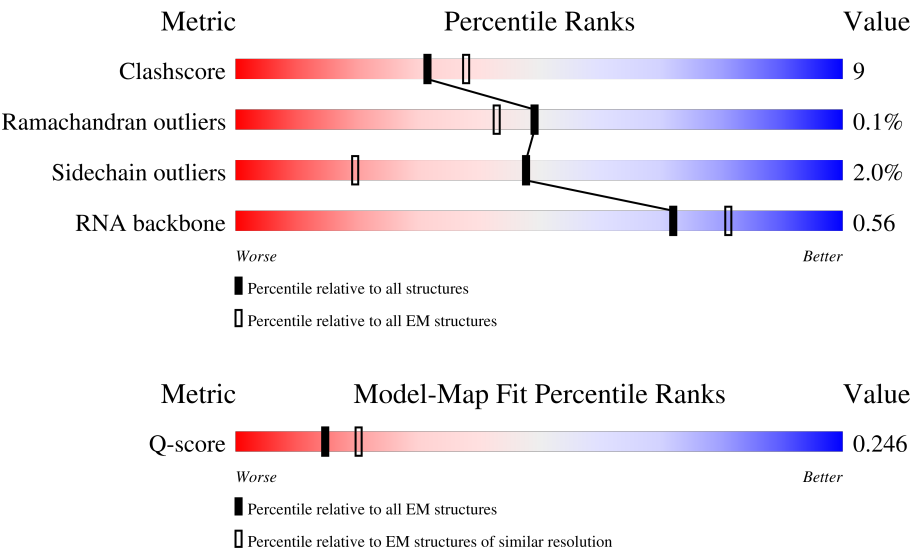
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.26 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4601 (3.76 - 4.76)

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	2	46	
2	B	120	
3	D	209	

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Mol	Chain	Length	Quality of chain
4	F	177	
5	J	142	
6	K	122	
7	N	120	
8	O	116	
9	P	114	
10	Q	117	
11	R	103	
12	T	93	
13	U	102	
14	V	94	
15	W	75	
16	Y	63	
17	Z	58	
18	y	17	
19	A	2903	
20	E	201	
21	L	143	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 60234 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	40	Total	C	N	O	S	0	0
			322	193	79	49	1		

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

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	118	Total	C	N	O	S	0	0
			887	560	156	169	2		

- Molecule 4 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 7 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	111	Total	C	N	O	S	0	0
			882	548	174	156	4		

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 9 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 10 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 11 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	102	Total	C	N	O		0	0
			780	492	146	142			

- Molecule 14 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 15 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	69	Total	C	N	O	S	0	0
			522	328	103	90	1		

- Molecule 16 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	61	Total	C	N	O	S	0	0
			499	308	97	92	2		

- Molecule 17 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 18 is a protein called Apidaecins type 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	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

- Molecule 19 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	A	1977	Total	C	N	O	P	0	0
			42496	18957	7879	13683	1977		

- Molecule 20 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	E	168	Total	C	N	O	S	0	0
			1307	824	231	247	5		

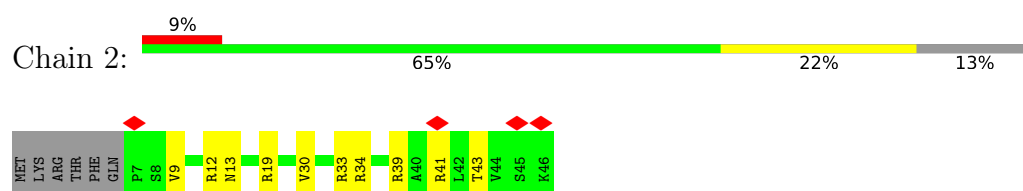
- Molecule 21 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	L	118	Total	C	N	O	0	0
			850	530	163	157		

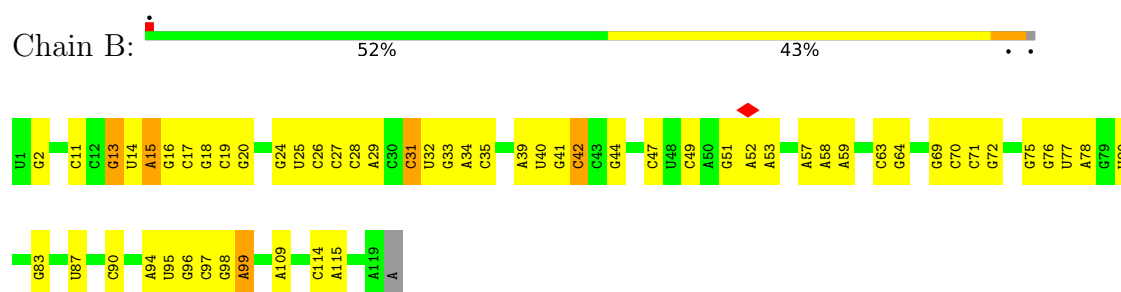
3 Residue-property plots

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.

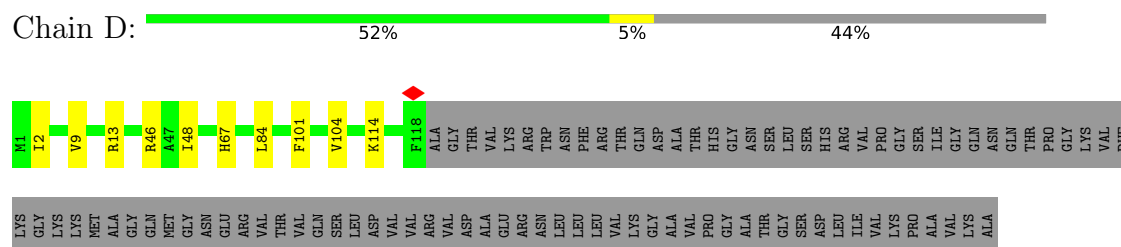
- Molecule 1: Large ribosomal subunit protein bL34



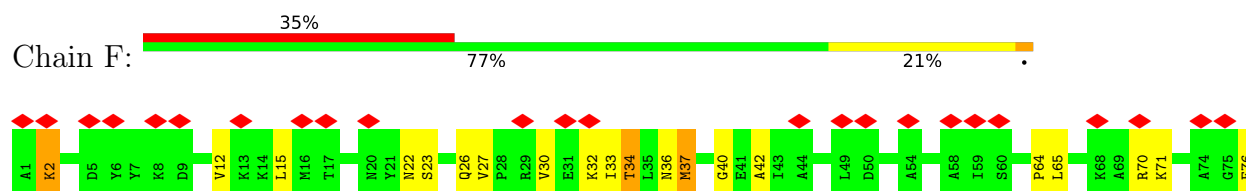
- Molecule 2: 5S ribosomal RNA

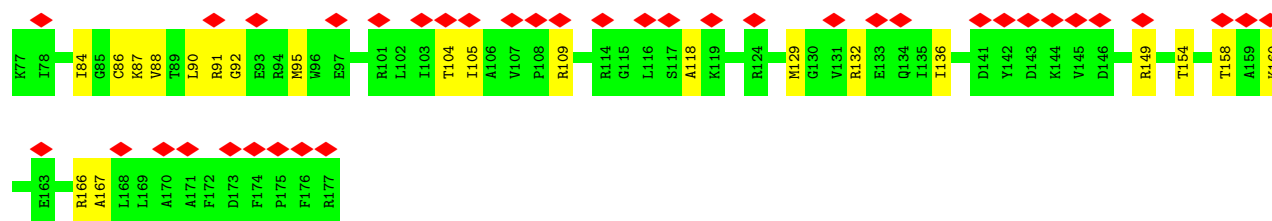


- Molecule 3: 50S ribosomal protein L3

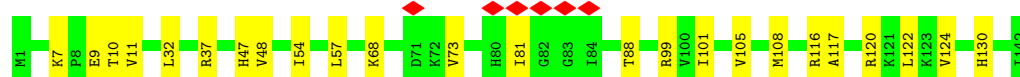
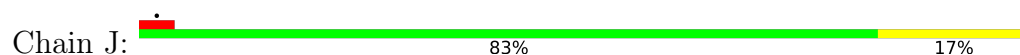


- Molecule 4: Large ribosomal subunit protein uL5

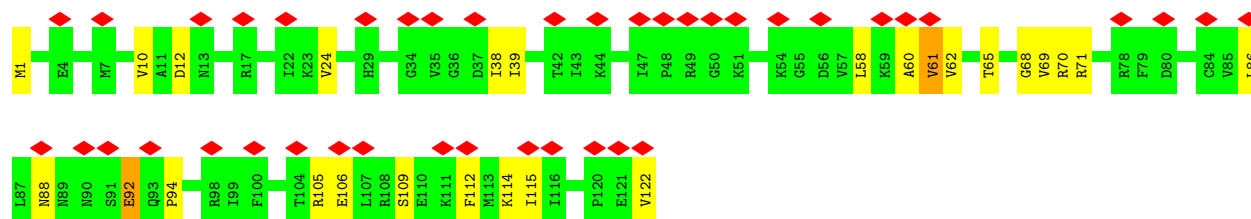
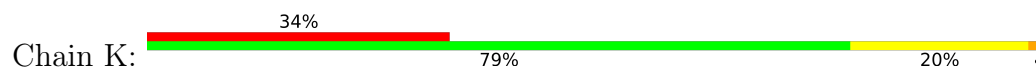




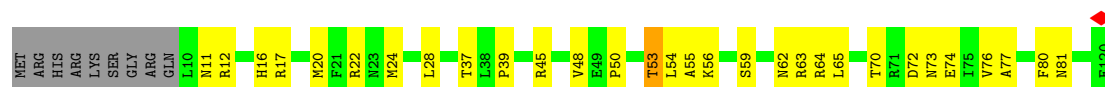
- Molecule 5: Large ribosomal subunit protein uL13



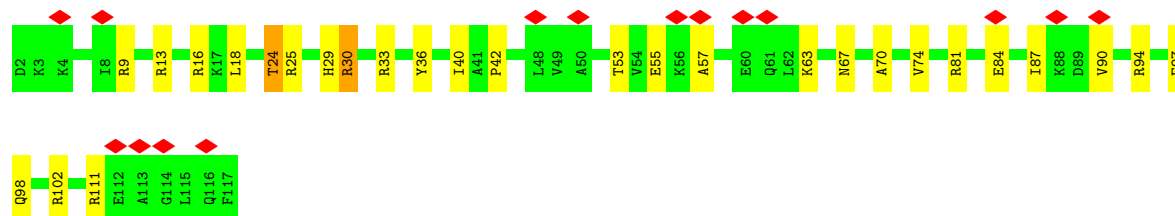
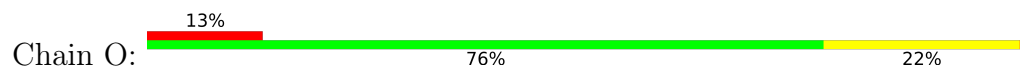
- Molecule 6: Large ribosomal subunit protein uL14



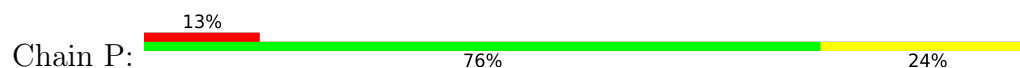
- Molecule 7: Large ribosomal subunit protein bL17

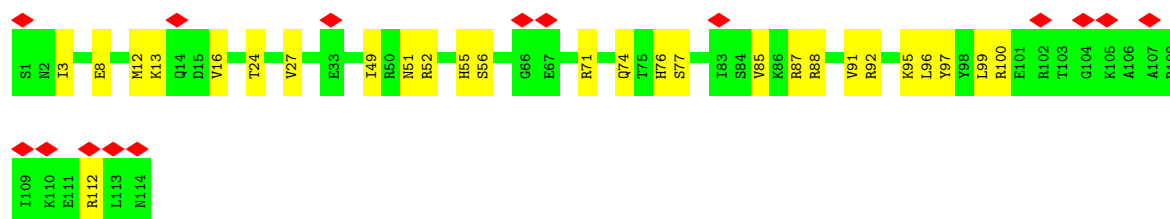


- Molecule 8: Large ribosomal subunit protein uL18

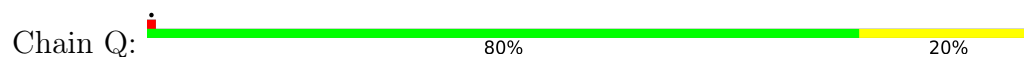


- Molecule 9: Large ribosomal subunit protein bL19

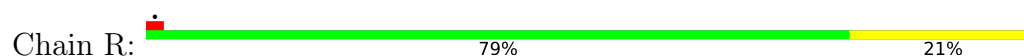




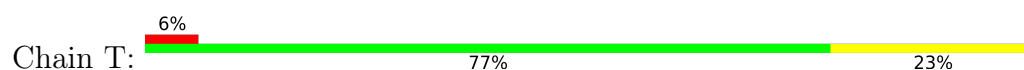
- Molecule 10: Large ribosomal subunit protein bL20



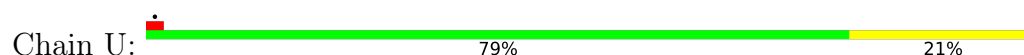
- Molecule 11: Large ribosomal subunit protein bL21



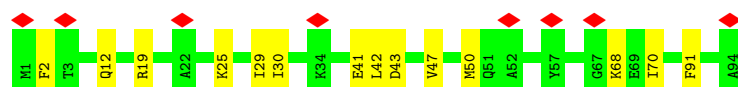
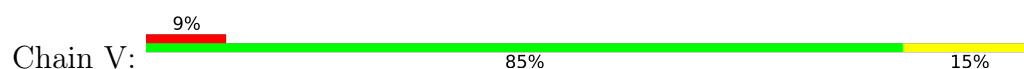
- Molecule 12: Large ribosomal subunit protein uL23



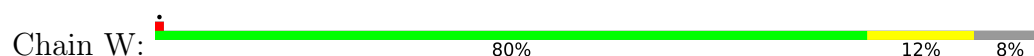
- Molecule 13: Large ribosomal subunit protein uL24

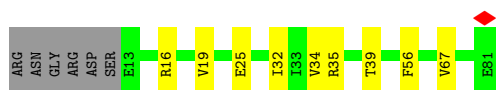


- Molecule 14: Large ribosomal subunit protein bL25



- Molecule 15: Large ribosomal subunit protein bL27





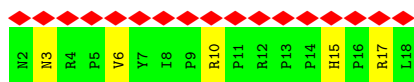
- Molecule 16: Large ribosomal subunit protein uL29



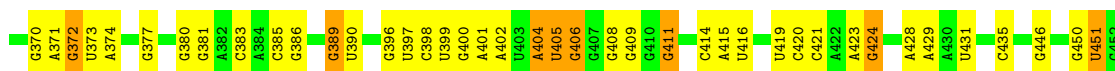
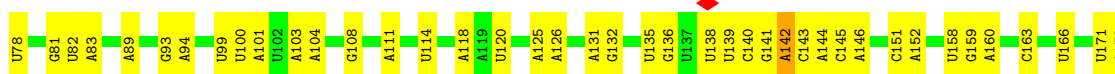
- Molecule 17: Large ribosomal subunit protein uL30



- Molecule 18: Apidaecins type 22

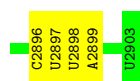


- Molecule 19: 23S ribosomal RNA



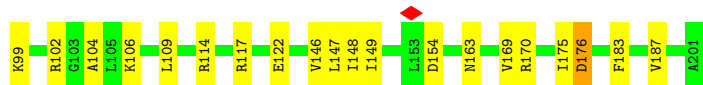
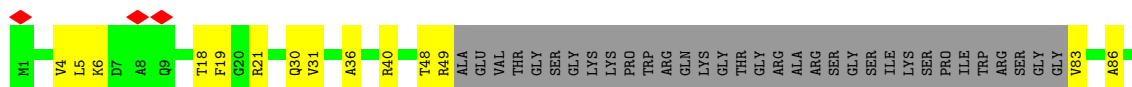
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A1603	G1510	G1417	G1332	A1246	G1171	A	C	U967	C	C923	U	C	G	A616	A538
C1604	G1514	G1418	G1333	A1247	C1172	C	C	C968	C	A825	G	G	G	G622	C540
C1605	G1514	A1419	G1334	G1248	U1173	U	C	G969	A	U828	C	C	C	A627	A541
C1606	A1515	G1421	A1336	A1253	U1174	G	G	G971	C	U829	C	U	A	G542	C542
C1607	C1518	G1422	G1337	A1254	A1175	U	C	G974	U	A828	G	G	A	G643	G543
A1608	G1519	G1423	G1338	U1255	U1176	C	C	A975	C	A830	G	G	G	U546	U546
A1609	U1520	G1424	G1339	G1256	G1177	G	A	G976	A	G831	U	A	G	G629	A547
A1610	G1521	G1425	U1340	C1257	C1178	A	G	G977	C	U832	G	U	G	G630	G548
A1616	G1522	A1426	G1341	A1262	U1179	U	C	A981	C	A833	G	A	C	A631	G549
G1619	U1523	G1427	A1342	U1263	U1180	C	A	A982	A	G834	C	A	A	A633	C550
G1620	G1524	C1428	G1343	A1264	U1181	U	G	G983	C	U839	U	U	G	C634	G551
U1629	A1528	G1432	U1344	A1265	U1182	G	G	A984	C	G840	G	G	G	A637	U552
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G1631	U1534	G1434	G1346	A1268	U1188	C	A	A988	G	U842	G	A	G	U639	U554
A1633	A1535	G1435	C1350	G1271	A1189	U	U	G989	U	G843	C	G	G	G555	G555
A1634	C1536	U1438	G1355	A1272	G1190	C	U	C995	G	A844	C	C	C	A556	G559
A1637	G1537	A1439	G1356	G1277	G1200	G	G	G996	C	U845	U	U	G	C560	C560
C1638	U1538	G1452	C1357	C1278	U1201	U	C	G997	C	U847	G	A	A	G561	G561
C1646	G1539	A1453	G1358	G1279	A1203	U	U	C998	C	C848	G	A	A	U562	U562
U1647	G1540	U1458	A1365	U1282	A1204	A	A	A1000	A	U850	G	C	C	A563	A563
U1648	G1543	C1461	U1371	U1287	G1205	A	G	C1005	C	U852	G	A	A	G564	G564
G1550	C1550	U1467	G1372	A1288	G1211	C	C	C1006	C	G856	U	U	U	U653	U567
A1551	G1555	A1468	G1373	G1289	U1212	U	C	C1007	C	G857	A	A	C	A654	A572
G1555	G1560	A1469	U1378	G1291	A1213	U	G	A1008	G	G858	A	G	U	A655	U573
A1566	A1566	G1471	G1380	G1292	A1214	C	C	A1009	G	G859	G	G	G	G656	G656
G1567	G1567	C1472	G1381	C1295	U1217	C	C	A1010	C	U860	C	C	C	U657	U576
A1568	A1568	U1474	G1382	G1296	G1218	U	U	U1011	C	A863	C	A	A	U658	G579
A1569	A1569	G1475	A1383	G1297	U1219	U	U	C1012	C	G864	A	G	G	C660	U580
A1570	A1570	U1481	C1386	C1298	G1222	U	U	C1013	U	C865	U	C	C	A582	C581
A1571	A1571	G1482	A1387	G1299	U1223	U	U	A1014	C	A866	C	C	C	G583	G583
A1572	A1572	G1483	G1388	G1300	G1224	U	U	A1020	A	U	A	A	C	A586	A586
A1573	A1573	U1484	U1392	A1301	U1225	U	U	G1022	C	G796	C	C	C	C587	U588
C1574	C1574	U1485	A1393	G1311	A1226	A	A	G1023	A	U	A	A	C	G672	U596
C1575	C1575	U1486	U1394	U1312	G1227	U	U	G1024	C	U	C	C	C	C673	G597
U1576	U1576	C1487	U1395	U1313	G1228	G	G	G1025	A	G	A	A	C	G674	U598
C1577	C1577	C1488	A1396	C1314	C1229	A	A	A1027	G	U	U	U	U	A675	A599
A1581	A1581	U1489	C1398	C1315	U1230	C	C	A1028	C	C	C	C	C	G600	G600
C1582	C1582	G1490	U1401	G1317	U1231	A	A	G1031	C	A	A	A	A	C680	C680
A1583	A1583	G1491	U1402	G1320	G1232	G	G	A	U	G	G	G	G	G681	G681
U1584	U1584	G1492	U1406	A1321	U1233	U	U	C	U	G	A	A	U	A602	A602
C1585	C1585	C1493	G1407	G1322	G1234	A	A	U	U	G	G	G	G	A603	A603
A1586	A1586	A1496	U1408	A1323	U1235	A	A	C	C	C	C	C	C	G684	G684
G1587	G1587	U1497	G1409	G1324	G1236	U	U	U	U	G	G	G	G	A	A
G1588	G1588	C1498	G1412	U1325	A1237	A	A	C	C	U	U	U	U	U	U
A1597	A1597	G1501	A1413	A1328	G1238	U	U	G	G	G	G	G	G	U	U
A1598	A1598	A1502	C1414	U1329	U1240	A	A	A	A	C	C	C	C	U	U
					G1243	A	A	A	A	A	A	A	A	C	C

U2804	C2805	A2809	A2810	G2811	G2815	G2816	G2817	G2818	G2819	A2820	A2821	G2822	A2823	G2824	G2825	A2837	G2838	G2839	G2840	C2841	U2845	G2846	U2847	G2848	U2849	A2850	A2851	G2852	G2853	G2854	G2857	G2858	G2859	A2860	G2867	A2868	A2873	G2874	G2875	G2876	C2880	U2881	A2882	A2883	A2886	A2887	G2888	G2889	G2890
U2696	G2697	U2698	C2699	A2700	G2708	G2709	A2710	A2711	G2714	G2718	G2719	U2720	A2726	A2727	U2728	G2729	G2732	A2733	A2736	G2737	A2738	U2739	A2740	G2744	C2745	U2746	G2747	A2748	A2749	A2750	G2751	G2752	G2753	A2758	C2762	G2763	A2764	A2765	A2766	A2778	U2779	G2780	U2783	U2784	C2785	C2788	C2789	C2788	
A	G	U	U	C	G	U	C	C	U	A2614	G2623	G2624	G2625	G2626	G2627	G2628	U2629	G2630	U2636	U2637	G2638	A2639	G2643	G2644	G2645	G2646	U2647	U2656	G2661	A2662	A2665	G2666	C2667	G2668	G2673	G2674	A2675	C2676	G2677	U2680	C2681	A2682	G2683	U2687	G2688	U2689	U2690		
A	G	G	G	U	U	U	U	U	U	U	C	G	C	C	C	A	U	A	U	A	G	C	U	A	C	A	A	G	U	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		
C2422	U2423	C2424	A2425	A2426	C2427	G2428	G2429	A2430	U2431	A2434	A2435	G	G	U	U	U	A	C	U	G	G	C	A	U	A	C	A	A	G	U	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
A2335	A2336	G2345	A2346	C2347	C2350	G2351	A2352	G2357	A2358	C2359	G2360	G2361	G2362	G2363	G2364	G2365	C2368	A2369	G2370	G2371	C2374	G2375	A2376	G2379	G2380	G2383	U2384	C2385	A2386	C2395	G2396	G2397	U2398	G2399	G2400	U2401	U2402	A2406	A2407	U2408	G2409	G2410	A2411	A2412	G2413	G2414	G2415	A2418	U2419
U	U	G	A	C	U	G	G	G	U	C	C2259	C2263	C2264	U2265	A2266	A2267	A2268	G2271	G2279	G2280	A2281	G2282	C2283	G2286	A2287	U2291	U2292	G2293	G2294	A2297	A2298	G2303	G2304	U2305	C2306	G2307	A2311	U2312	C2313	A2314	A2327	G2331	C2332	A2333	U2334				
C	C	C	G	U	C	A	C	U	U	A	C	U	U	A	A	G	C	U	C	U	C	A	G	C	U	U	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
G1750	U1751	C1752	G1753	G1756	A1757	U	U	C	C	A	C	A	C	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
A	U	G	G	U	C	C	U	U	C	C	U	U	C	C	A	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	
G1707	C1708	U1709	G1710	A1713	U1714	G1715	U1716	A1717	U1725	C1726	C1727	C1728	U1729	C1730	G1731	C1732	G1733	G1734	A1735	U1736	G1737	G1738	A1739	G1740	A1746	U1747	A1748	A1749																					



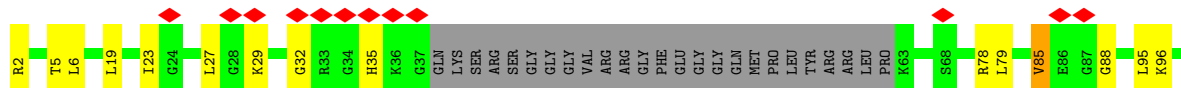
- Molecule 20: Large ribosomal subunit protein uL4

Chain E: 67% 16% 16%



- Molecule 21: Large ribosomal subunit protein uL15

Chain L: 9% 63% 17% 1%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31417	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	0.406	Depositor
Minimum map value	-0.124	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.068	Depositor
Map size (Å)	399.6, 399.6, 399.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.332, 1.332, 1.332	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	0.09	0/324	0.23	0/424
2	B	0.07	0/2850	0.17	0/4444
3	D	0.08	0/898	0.20	0/1207
4	F	0.09	0/1435	0.25	0/1926
5	J	0.07	0/1152	0.18	0/1551
6	K	0.09	0/948	0.25	0/1268
7	N	0.10	0/894	0.29	0/1198
8	O	0.08	0/902	0.23	0/1209
9	P	0.07	0/929	0.21	0/1242
10	Q	0.08	0/960	0.19	0/1278
11	R	0.08	0/829	0.22	0/1107
12	T	0.10	0/745	0.30	0/994
13	U	0.09	0/788	0.26	0/1051
14	V	0.07	0/766	0.20	0/1025
15	W	0.07	0/529	0.19	0/699
16	Y	0.10	0/500	0.30	0/665
17	Z	0.07	0/453	0.19	0/605
18	y	0.15	0/155	0.38	0/212
19	A	0.07	0/47606	0.17	0/74262
20	E	0.08	0/1319	0.21	0/1775
21	L	0.09	0/854	0.35	0/1137
All	All	0.07	0/65836	0.19	0/99279

There are no bond length outliers.

There are no bond angle outliers.

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	322	0	357	7	0
2	B	2549	0	1291	44	0
3	D	887	0	912	7	0
4	F	1411	0	1447	29	0
5	J	1129	0	1162	14	0
6	K	939	0	1012	16	0
7	N	882	0	913	19	0
8	O	892	0	923	24	0
9	P	917	0	965	18	0
10	Q	947	0	1022	21	0
11	R	816	0	839	12	0
12	T	739	0	807	16	0
13	U	780	0	834	16	0
14	V	753	0	780	9	0
15	W	522	0	543	6	0
16	Y	499	0	535	13	0
17	Z	449	0	491	9	0
18	y	148	0	152	4	0
19	A	42496	0	21375	595	0
20	E	1307	0	1365	24	0
21	L	850	0	916	19	0
All	All	60234	0	38641	833	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (833) 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)
19:A:377:G:H1	19:A:397:U:H3	1.14	0.96
19:A:2747:G:H21	19:A:2758:A:H62	1.15	0.90
19:A:1323:C:O2	19:A:1331:G:N2	2.12	0.81
19:A:1282:U:H3	19:A:1286:A:H62	1.25	0.81
19:A:1350:C:N3	19:A:1381:G:N1	2.29	0.80
19:A:2747:G:N2	19:A:2758:A:H62	1.80	0.78
2:B:32:U:H2'	2:B:33:G:C8	2.19	0.77
18:y:10:ARG:HE	19:A:507:A:H2'	1.49	0.77
2:B:78:A:H62	2:B:98:G:H21	1.34	0.76
19:A:539:G:H1	19:A:554:U:H3	1.35	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:N:22:ARG:HG3	7:N:70:THR:HA	1.69	0.74
19:A:2287:A:N6	19:A:2346:A:N7	2.36	0.74
19:A:1323:C:N3	19:A:1331:G:N1	2.36	0.73
2:B:94:A:H5''	14:V:19:ARG:HH21	1.52	0.73
19:A:1423:G:H2'	19:A:1424:G:C8	2.23	0.72
19:A:177:G:OP2	19:A:177:G:N2	2.21	0.72
19:A:320:A:N3	20:E:163:ASN:ND2	2.37	0.72
19:A:1433:A:H61	19:A:1560:G:H1	1.38	0.72
2:B:57:A:N7	2:B:59:A:N6	2.38	0.71
19:A:2345:G:O6	19:A:2371:G:O6	2.09	0.71
9:P:96:LEU:HB3	9:P:99:LEU:HD23	1.74	0.70
19:A:475:C:O2	19:A:479:A:N6	2.22	0.70
19:A:1528:A:N6	19:A:1543:G:O2'	2.25	0.70
19:A:605:G:OP1	20:E:99:LYS:NZ	2.25	0.70
19:A:463:G:N2	19:A:466:A:OP2	2.25	0.69
19:A:212:G:H2'	19:A:213:A:C8	2.28	0.69
19:A:213:A:H2'	19:A:214:G:C8	2.27	0.69
2:B:77:U:O2	2:B:99:A:N7	2.26	0.69
19:A:987:C:O2'	19:A:1000:A:N3	2.25	0.69
2:B:78:A:H62	2:B:98:G:N2	1.91	0.68
19:A:308:G:N2	19:A:477:A:N7	2.41	0.68
19:A:99:U:H5''	19:A:100:U:H5'	1.76	0.68
19:A:659:G:N3	20:E:30:GLN:NE2	2.42	0.67
19:A:966:G:H4'	19:A:2271:G:H22	1.59	0.67
19:A:1329:U:OP2	19:A:1330:C:N4	2.25	0.67
4:F:132:ARG:NH2	19:A:2304:G:O2'	2.28	0.67
19:A:968:C:H2'	19:A:969:G:H8	1.59	0.67
19:A:404:A:N6	19:A:421:C:O2'	2.27	0.66
19:A:2397:G:H1	19:A:2419:U:H3	1.41	0.66
7:N:64:ARG:NH1	19:A:2851:A:O2'	2.29	0.66
8:O:30:ARG:HD2	8:O:102:ARG:HB2	1.76	0.65
19:A:2739:U:O2	19:A:2764:A:N7	2.29	0.65
19:A:453:A:N3	19:A:457:A:O2'	2.29	0.65
19:A:1315:C:O2'	19:A:1392:A:N3	2.28	0.65
9:P:24:THR:HB	9:P:87:ARG:HB3	1.77	0.65
19:A:1597:A:H5''	19:A:1598:A:H5'	1.78	0.65
19:A:302:C:H2'	19:A:303:G:H8	1.62	0.65
20:E:4:VAL:HG22	20:E:6:LYS:H	1.62	0.65
10:Q:54:ARG:HD3	19:A:1155:A:H5''	1.79	0.65
8:O:94:ARG:NH1	8:O:97:PHE:O	2.30	0.65
14:V:30:ILE:HG22	14:V:91:PHE:HB2	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:2853:C:N4	19:A:2854:G:O6	2.30	0.64
19:A:669:G:N2	19:A:672:C:OP1	2.30	0.64
19:A:1168:G:O6	19:A:1181:U:O2	2.15	0.64
10:Q:83:LYS:NZ	19:A:1152:C:OP1	2.28	0.64
19:A:373:U:H2'	19:A:374:A:H8	1.62	0.64
19:A:523:C:H2'	19:A:524:G:C8	2.33	0.64
12:T:61:LEU:HB3	19:A:1341:G:H5'	1.79	0.64
19:A:78:U:H3	19:A:108:G:H1	1.45	0.64
19:A:2740:A:OP2	19:A:2763:G:N1	2.30	0.64
19:A:1007:C:OP2	19:A:1008:A:O2'	2.14	0.64
4:F:37:MET:HB2	4:F:149:ARG:HH22	1.63	0.64
19:A:1350:C:O2	19:A:1381:G:N2	2.19	0.64
7:N:12:ARG:O	7:N:17:ARG:NH1	2.31	0.63
19:A:566:U:O2'	19:A:808:G:OP1	2.16	0.63
19:A:1265:A:N6	19:A:2014:A:OP2	2.31	0.63
7:N:63:ARG:HH21	7:N:76:VAL:HG12	1.64	0.63
16:Y:52:ARG:NH1	19:A:77:G:OP1	2.31	0.63
19:A:194:G:N1	19:A:202:U:N3	2.46	0.63
19:A:489:G:N2	19:A:1320:C:OP1	2.30	0.63
2:B:52:A:N7	8:O:33:ARG:NH2	2.47	0.63
12:T:37:ASP:O	12:T:81:LYS:NZ	2.32	0.63
10:Q:51:GLN:OE1	19:A:559:G:N2	2.32	0.63
21:L:79:LEU:HD13	21:L:116:VAL:HB	1.81	0.63
19:A:26:G:N2	19:A:514:A:N7	2.47	0.62
19:A:2352:A:N6	19:A:2365:G:O2'	2.32	0.62
9:P:13:LYS:HE2	9:P:76:HIS:HA	1.80	0.62
19:A:1395:A:H2'	19:A:1398:C:H41	1.63	0.62
2:B:14:U:OP2	2:B:70:C:O2'	2.17	0.62
19:A:834:G:H1'	19:A:2358:A:H1'	1.81	0.62
19:A:2645:G:OP2	19:A:2645:G:N2	2.29	0.62
19:A:521:U:H2'	19:A:522:A:H8	1.65	0.62
4:F:70:ARG:HG2	4:F:71:LYS:HG3	1.82	0.62
19:A:2747:G:H21	19:A:2758:A:N6	1.93	0.62
19:A:239:C:HO2'	19:A:622:G:HO2'	1.45	0.62
19:A:1433:A:N6	19:A:1560:G:H1	1.98	0.62
8:O:13:ARG:NH1	19:A:2335:A:OP1	2.33	0.62
19:A:1378:A:O2'	19:A:1380:G:OP2	2.17	0.62
19:A:808:G:H2'	19:A:809:G:H8	1.64	0.61
4:F:23:SER:HB3	4:F:26:GLN:HB2	1.82	0.61
19:A:175:G:H2'	19:A:176:A:C8	2.35	0.61
15:W:16:ARG:NH2	19:A:2357:G:OP1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:2857:G:N2	19:A:2860:A:OP2	2.30	0.61
19:A:523:C:H2'	19:A:524:G:H8	1.64	0.61
2:B:51:G:O2'	2:B:52:A:O4'	2.15	0.61
13:U:3:LYS:O	13:U:93:ARG:NH1	2.34	0.61
17:Z:46:MET:HE1	19:A:851:C:H4'	1.82	0.61
19:A:567:U:OP1	21:L:35:HIS:ND1	2.33	0.61
19:A:2875:C:H2'	19:A:2876:G:C8	2.36	0.60
19:A:923:G:H2'	19:A:924:G:H8	1.65	0.60
19:A:1350:C:N4	19:A:1381:G:O6	2.33	0.60
2:B:78:A:N6	2:B:98:G:H21	1.98	0.60
19:A:311:A:N6	19:A:329:G:OP1	2.34	0.60
19:A:2898:U:H2'	19:A:2899:A:C8	2.37	0.60
3:D:46:ARG:HB3	3:D:84:LEU:HD12	1.83	0.60
8:O:111:ARG:NH2	19:A:2376:A:N3	2.49	0.60
19:A:1229:C:H2'	19:A:1230:A:C8	2.37	0.60
19:A:224:U:O4	19:A:232:G:N2	2.34	0.60
19:A:2815:C:H2'	19:A:2816:G:H8	1.67	0.60
13:U:6:ARG:NH1	13:U:25:LYS:O	2.33	0.60
13:U:81:ARG:NH2	19:A:300:A:O5'	2.35	0.60
19:A:31:C:O2'	19:A:1238:G:OP1	2.19	0.60
19:A:1222:U:H3	19:A:1227:G:H1	1.49	0.60
19:A:1358:G:N1	19:A:1372:U:OP2	2.34	0.60
20:E:21:ARG:O	20:E:114:ARG:NH1	2.33	0.60
19:A:808:G:H2'	19:A:809:G:C8	2.36	0.60
19:A:1028:A:OP2	19:A:1126:A:N6	2.35	0.60
19:A:1282:U:O4	19:A:1286:A:N7	2.35	0.60
19:A:1709:U:H2'	19:A:1710:G:H8	1.66	0.60
7:N:37:THR:HG22	7:N:39:PRO:HD2	1.83	0.59
8:O:87:ILE:HB	8:O:90:VAL:HG13	1.84	0.59
10:Q:48:ASP:HA	10:Q:51:GLN:HB2	1.84	0.59
17:Z:55:LYS:NZ	17:Z:57:GLU:OE2	2.35	0.59
19:A:197:A:N6	19:A:2431:U:C2	2.70	0.59
19:A:601:C:O2'	20:E:99:LYS:NZ	2.36	0.59
19:A:2399:G:H2'	19:A:2400:G:C8	2.36	0.59
19:A:860:U:O2	19:A:917:A:N7	2.36	0.59
19:A:2345:G:H5'	19:A:2347:C:H5''	1.82	0.59
1:2:19:ARG:NH1	19:A:125:A:OP2	2.35	0.59
4:F:40:GLY:HA2	4:F:84:ILE:HD11	1.84	0.59
19:A:81:G:O2'	19:A:295:G:O2'	2.20	0.59
19:A:974:G:O2'	19:A:989:G:N2	2.36	0.59
19:A:482:A:O2'	19:A:497:A:N1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:1386:C:H2'	19:A:1387:A:H8	1.68	0.58
19:A:2875:C:H2'	19:A:2876:G:H8	1.68	0.58
10:Q:57:ARG:NH1	19:A:1154:G:OP2	2.37	0.58
19:A:65:U:O2'	19:A:456:C:N3	2.32	0.58
19:A:1223:G:N2	19:A:1226:A:OP2	2.36	0.58
19:A:83:A:O2'	19:A:103:A:N6	2.36	0.58
5:J:32:LEU:HD22	5:J:54:ILE:HG21	1.86	0.58
2:B:32:U:H2'	2:B:33:G:H8	1.65	0.58
19:A:541:A:N6	19:A:553:G:O6	2.36	0.58
19:A:573:U:O4	19:A:2029:G:O2'	2.21	0.58
19:A:956:G:N2	19:A:960:A:OP2	2.37	0.58
19:A:948:C:O2	19:A:984:A:O2'	2.20	0.57
19:A:2385:C:H2'	19:A:2386:A:H8	1.69	0.57
19:A:26:G:H1'	19:A:515:A:H61	1.68	0.57
19:A:1206:G:O6	19:A:1240:U:O2	2.23	0.57
16:Y:57:LEU:HD23	16:Y:60:LYS:HD3	1.86	0.57
19:A:524:G:O2'	19:A:556:A:OP1	2.22	0.57
19:A:1229:C:H2'	19:A:1230:A:H8	1.67	0.57
19:A:1137:G:H2'	19:A:1138:G:C8	2.39	0.57
10:Q:53:LYS:HG2	19:A:995:C:H5''	1.87	0.57
5:J:68:LYS:NZ	19:A:1140:C:OP2	2.36	0.57
19:A:48:G:N2	19:A:177:G:OP1	2.32	0.57
19:A:143:C:H2'	19:A:144:A:H8	1.70	0.57
19:A:1288:G:OP2	19:A:1288:G:N2	2.37	0.57
4:F:15:LEU:HD22	4:F:167:ALA:HB1	1.86	0.57
19:A:302:C:H2'	19:A:303:G:C8	2.40	0.57
19:A:2748:A:N7	19:A:2753:A:N6	2.53	0.57
4:F:129:MET:SD	19:A:2303:G:O2'	2.61	0.57
12:T:19:LYS:NZ	19:A:1340:U:OP1	2.38	0.57
18:y:15:HIS:O	18:y:17:ARG:NH1	2.38	0.57
19:A:2307:G:N2	19:A:2311:A:OP2	2.38	0.57
20:E:148:ILE:HB	20:E:169:VAL:HG22	1.87	0.57
1:2:12:ARG:NH2	1:2:43:THR:O	2.38	0.56
19:A:2279:G:H2'	19:A:2280:G:H8	1.69	0.56
19:A:2385:C:H2'	19:A:2386:A:C8	2.40	0.56
19:A:2643:G:H2'	19:A:2644:G:C8	2.39	0.56
2:B:75:G:H1'	14:V:29:ILE:HD13	1.88	0.56
20:E:176:ASP:N	20:E:176:ASP:OD1	2.34	0.56
6:K:58:LEU:HD11	6:K:86:LEU:HB3	1.87	0.56
19:A:2291:U:O2'	19:A:2374:C:O2	2.21	0.56
8:O:9:ARG:HE	19:A:2334:U:H5'	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:52:ARG:HH21	19:A:2720:U:H5''	1.71	0.56
19:A:2728:U:O2'	19:A:2729:G:H8	1.89	0.56
10:Q:52:ARG:HH21	19:A:535:G:H4'	1.70	0.56
19:A:970:U:H2'	19:A:971:G:C8	2.40	0.56
19:A:951:C:N4	19:A:952:G:O6	2.39	0.55
19:A:1359:A:OP2	19:A:1371:G:N2	2.39	0.55
20:E:5:LEU:HD23	20:E:122:GLU:HG3	1.88	0.55
19:A:658:U:H2'	19:A:659:G:H8	1.70	0.55
19:A:931:U:O2	19:A:1167:C:O2'	2.24	0.55
19:A:1013:C:H2'	19:A:1014:A:H8	1.71	0.55
19:A:1629:U:O4	19:A:1630:A:N6	2.39	0.55
19:A:981:A:O2'	19:A:2036:C:O2'	2.24	0.55
19:A:1418:G:N2	19:A:1581:G:O6	2.40	0.55
19:A:1709:U:H2'	19:A:1710:G:C8	2.41	0.55
19:A:2047:C:O2'	19:A:2823:A:N1	2.37	0.55
4:F:64:PRO:HB3	4:F:88:VAL:HG22	1.89	0.55
19:A:324:A:N6	19:A:338:G:O2'	2.40	0.55
13:U:24:VAL:HG12	13:U:35:VAL:HG22	1.89	0.55
16:Y:24:GLU:HG2	16:Y:28:LEU:HD23	1.89	0.55
19:A:145:C:H2'	19:A:146:A:H8	1.70	0.55
19:A:627:A:H3'	21:L:78:ARG:HH12	1.72	0.55
19:A:645:C:N4	19:A:2368:C:O2'	2.31	0.55
19:A:946:C:H2'	19:A:947:A:C8	2.42	0.55
2:B:39:A:O2'	2:B:40:U:O4'	2.20	0.55
19:A:45:G:H5''	19:A:46:G:H5'	1.89	0.55
19:A:629:G:N2	19:A:639:U:O2'	2.30	0.55
19:A:1386:C:H2'	19:A:1387:A:C8	2.41	0.55
19:A:1475:G:O2'	19:A:1514:G:O6	2.23	0.55
4:F:32:LYS:HD3	4:F:91:ARG:HH21	1.70	0.55
19:A:1432:G:H2'	19:A:1433:A:C8	2.42	0.55
4:F:36:ASN:OD1	4:F:37:MET:N	2.40	0.55
19:A:2023:C:H2'	19:A:2024:G:H8	1.72	0.55
19:A:2818:U:H2'	19:A:2819:G:C8	2.42	0.55
19:A:1227:G:H2'	19:A:1228:G:H8	1.72	0.54
4:F:70:ARG:H	19:A:2312:U:H5''	1.72	0.54
19:A:411:G:OP2	19:A:2406:A:O2'	2.23	0.54
19:A:1736:U:O4	19:A:1737:G:N2	2.41	0.54
9:P:52:ARG:HG2	19:A:2845:U:H4'	1.89	0.54
19:A:1125:G:OP2	19:A:1126:A:O2'	2.23	0.54
19:A:1438:U:H2'	19:A:1439:A:H8	1.72	0.54
8:O:98:GLN:NE2	19:A:2294:G:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:1152:C:H2'	19:A:1153:C:H6	1.73	0.54
2:B:28:C:H2'	2:B:29:A:C8	2.43	0.54
19:A:358:U:O4	19:A:359:G:O6	2.26	0.54
19:A:1472:C:N4	19:A:1473:G:O6	2.40	0.54
19:A:2374:C:N4	19:A:2375:G:O6	2.40	0.54
19:A:2676:C:H2'	19:A:2677:G:C8	2.43	0.54
13:U:88:ASP:OD1	13:U:89:GLY:N	2.40	0.54
13:U:93:ARG:HB2	13:U:102:ILE:HD12	1.89	0.54
19:A:665:U:H2'	19:A:666:A:H8	1.73	0.54
19:A:194:G:C6	19:A:202:U:N3	2.75	0.54
19:A:370:G:O2'	19:A:424:G:OP1	2.26	0.54
19:A:801:G:N1	20:E:48:THR:OG1	2.41	0.54
19:A:2680:U:O2	19:A:2682:A:N6	2.40	0.54
19:A:532:A:OP1	19:A:561:G:N2	2.39	0.54
11:R:14:VAL:HG21	11:R:98:ILE:HD13	1.89	0.53
16:Y:3:ALA:O	16:Y:7:ARG:HG2	2.08	0.53
19:A:250:G:O2'	19:A:251:A:O4'	2.21	0.53
7:N:28:LEU:HD23	7:N:48:VAL:HG21	1.90	0.53
9:P:52:ARG:NH2	19:A:2720:U:OP1	2.41	0.53
19:A:135:U:H2'	19:A:136:G:C8	2.43	0.53
19:A:216:A:N7	19:A:431:U:O2	2.40	0.53
19:A:1483:G:H1	19:A:1506:U:H3	1.55	0.53
2:B:114:C:H2'	2:B:115:A:H8	1.73	0.53
19:A:1335:C:H2'	19:A:1336:A:H8	1.73	0.53
19:A:1752:C:H2'	19:A:1753:G:C8	2.43	0.53
20:E:170:ARG:NH1	20:E:176:ASP:OD1	2.42	0.53
19:A:194:G:N1	19:A:202:U:C2	2.77	0.53
19:A:296:U:H2'	19:A:297:G:H8	1.74	0.53
19:A:1243:C:O2'	21:L:6:LEU:O	2.26	0.53
19:A:2357:G:N2	19:A:2360:G:OP2	2.38	0.53
10:Q:47:ARG:NH2	19:A:560:C:O2	2.41	0.53
13:U:38:ILE:HG13	13:U:39:ASN:H	1.73	0.53
16:Y:1:MET:HA	16:Y:4:LYS:HE3	1.91	0.53
19:A:194:G:C2	19:A:202:U:C2	2.96	0.53
19:A:1550:C:H2'	19:A:1551:A:H8	1.74	0.53
11:R:32:THR:HG22	11:R:62:GLU:HG3	1.91	0.53
15:W:39:THR:OG1	19:A:2331:G:O2'	2.19	0.53
19:A:145:C:H2'	19:A:146:A:C8	2.44	0.53
19:A:307:G:H21	19:A:330:A:H61	1.57	0.53
19:A:665:U:H2'	19:A:666:A:C8	2.44	0.53
19:A:2292:U:H2'	19:A:2293:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:P:88:ARG:HB3	9:P:112:ARG:HD3	1.91	0.53
19:A:929:U:O2'	19:A:930:G:OP1	2.21	0.53
6:K:1:MET:SD	6:K:1:MET:N	2.81	0.52
19:A:194:G:C2	19:A:202:U:O2	2.62	0.52
5:J:108:MET:HE3	5:J:108:MET:O	2.09	0.52
19:A:196:A:H61	19:A:831:G:H4'	1.75	0.52
19:A:523:C:H1'	19:A:554:U:H1'	1.90	0.52
19:A:1264:A:N6	19:A:2014:A:OP2	2.41	0.52
2:B:29:A:O2'	2:B:58:A:N6	2.40	0.52
8:O:18:LEU:HD22	8:O:25:ARG:HD3	1.91	0.52
19:A:36:G:N3	19:A:450:G:O2'	2.41	0.52
19:A:2898:U:H2'	19:A:2899:A:H8	1.73	0.52
16:Y:55:THR:OG1	19:A:72:U:O2	2.24	0.52
19:A:930:G:H2'	19:A:933:A:H8	1.74	0.52
19:A:2265:U:OP2	19:A:2266:A:O2'	2.23	0.52
19:A:2656:U:O2	19:A:2665:A:N7	2.43	0.52
21:L:95:LEU:HD22	21:L:100:ILE:HD12	1.92	0.52
2:B:83:G:O6	2:B:94:A:N6	2.43	0.52
19:A:160:A:N7	19:A:166:U:O4	2.42	0.52
12:T:44:LYS:NZ	12:T:55:VAL:O	2.43	0.52
14:V:2:PHE:HE2	14:V:50:MET:HE3	1.74	0.52
19:A:408:G:H2'	19:A:409:G:H8	1.75	0.52
19:A:2816:G:N3	19:A:2883:A:O2'	2.40	0.52
7:N:54:LEU:HD11	7:N:65:LEU:HD23	1.92	0.52
19:A:968:C:H2'	19:A:969:G:C8	2.43	0.52
19:A:1123:C:H2'	19:A:1124:G:H8	1.74	0.52
4:F:84:ILE:HG21	19:A:2312:U:H4'	1.91	0.52
12:T:38:ALA:HB1	12:T:43:ILE:HD11	1.92	0.52
19:A:1387:A:H2'	19:A:1388:G:C8	2.45	0.52
2:B:13:G:N2	2:B:69:G:O2'	2.44	0.51
2:B:28:C:H2'	2:B:29:A:H8	1.75	0.51
4:F:12:VAL:HG13	4:F:27:VAL:HG11	1.92	0.51
12:T:24:MET:HE2	12:T:30:ILE:HD12	1.92	0.51
19:A:513:A:H2'	19:A:514:A:C8	2.45	0.51
19:A:1574:C:H2'	19:A:1575:C:C6	2.46	0.51
14:V:68:LYS:HE3	14:V:70:ILE:HD11	1.93	0.51
4:F:76:PHE:CG	19:A:2311:A:H5''	2.45	0.51
10:Q:23:TYR:H	10:Q:28:SER:HB3	1.75	0.51
19:A:372:G:N2	19:A:401:A:OP2	2.38	0.51
19:A:1428:C:N4	19:A:1570:A:OP2	2.44	0.51
19:A:93:G:H2'	19:A:94:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:T:1:MET:SD	19:A:142:A:O2'	2.65	0.51
19:A:1417:C:OP1	19:A:1587:G:N2	2.41	0.51
19:A:2292:U:H2'	19:A:2293:G:C8	2.45	0.51
19:A:2848:G:H1'	19:A:2868:A:H61	1.75	0.51
6:K:71:ARG:NE	6:K:106:GLU:OE2	2.44	0.51
8:O:111:ARG:HH12	19:A:2376:A:H1'	1.74	0.51
19:A:184:C:N4	19:A:185:G:O6	2.43	0.51
19:A:296:U:H2'	19:A:297:G:C8	2.46	0.51
19:A:373:U:H2'	19:A:374:A:C8	2.44	0.51
19:A:514:A:N3	19:A:581:C:O2'	2.43	0.51
19:A:581:C:H2'	19:A:582:A:H8	1.75	0.51
19:A:1245:G:H2'	19:A:1246:A:C8	2.46	0.51
19:A:1291:C:H2'	19:A:1292:G:H8	1.74	0.51
19:A:1335:C:H2'	19:A:1336:A:C8	2.46	0.51
19:A:538:A:H62	19:A:555:G:H21	1.59	0.51
19:A:1539:U:H2'	19:A:1540:G:H8	1.76	0.51
19:A:2822:G:HO2'	19:A:2825:G:H1	1.59	0.51
19:A:521:U:H2'	19:A:522:A:C8	2.46	0.51
19:A:1751:U:H2'	19:A:1752:C:C6	2.46	0.51
21:L:132:ARG:HG3	21:L:142:ILE:HD12	1.92	0.51
4:F:158:THR:O	4:F:160:LYS:NZ	2.41	0.50
8:O:24:THR:HB	8:O:42:PRO:HD3	1.93	0.50
11:R:79:ARG:HH21	19:A:572:A:H5'	1.76	0.50
15:W:32:ILE:HA	15:W:56:PHE:HA	1.93	0.50
19:A:848:C:O2'	19:A:849:A:OP1	2.29	0.50
19:A:1140:C:O2	19:A:1143:A:O2'	2.28	0.50
19:A:2699:C:H2'	19:A:2700:A:C8	2.47	0.50
1:2:9:VAL:O	1:2:13:ASN:ND2	2.35	0.50
19:A:171:U:H2'	19:A:172:A:C8	2.46	0.50
19:A:380:G:H2'	19:A:381:G:C8	2.46	0.50
19:A:2291:U:O2	19:A:2374:C:O2'	2.29	0.50
21:L:141:LYS:NZ	21:L:143:GLU:OE1	2.43	0.50
17:Z:23:LEU:HD22	17:Z:28:LEU:HD12	1.93	0.50
19:A:1190:G:OP1	21:L:32:GLY:N	2.42	0.50
19:A:1346:G:N1	19:A:1601:G:O6	2.45	0.50
21:L:27:LEU:HD23	21:L:27:LEU:H	1.76	0.50
16:Y:58:ASN:ND2	19:A:111:A:O2'	2.43	0.50
19:A:1733:G:H2'	19:A:1734:G:H8	1.77	0.50
19:A:2818:U:H4'	19:A:2837:A:H4'	1.94	0.50
8:O:29:HIS:HB3	8:O:36:TYR:HB2	1.94	0.50
19:A:462:C:N4	19:A:463:G:O6	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:823:C:H2'	19:A:824:U:C6	2.47	0.50
19:A:1137:G:H2'	19:A:1138:G:H8	1.77	0.50
7:N:74:GLU:OE2	19:A:1453:A:N6	2.45	0.50
13:U:27:VAL:HG12	13:U:33:VAL:HG22	1.92	0.50
19:A:1217:U:O2	19:A:1232:G:O6	2.30	0.50
19:A:1287:A:H2'	19:A:1288:G:C2	2.46	0.50
19:A:2395:C:H2'	19:A:2396:G:H8	1.75	0.50
4:F:36:ASN:ND2	4:F:87:LYS:HB3	2.27	0.50
10:Q:57:ARG:O	10:Q:61:ILE:HG12	2.12	0.50
19:A:60:G:O6	19:A:89:A:N6	2.45	0.50
19:A:1539:U:H2'	19:A:1540:G:C8	2.47	0.50
12:T:2:ILE:HA	12:T:3:ARG:C	2.36	0.49
19:A:660:C:H2'	19:A:661:A:H8	1.75	0.49
19:A:1387:A:H2'	19:A:1388:G:H8	1.77	0.49
19:A:1469:A:OP2	19:A:1522:A:N6	2.42	0.49
19:A:2746:U:C4	19:A:2747:G:H1'	2.48	0.49
11:R:6:GLN:HB3	11:R:11:GLN:HB3	1.93	0.49
7:N:24:MET:SD	19:A:1277:G:O2'	2.70	0.49
12:T:19:LYS:NZ	19:A:1394:U:O2	2.45	0.49
19:A:946:C:H2'	19:A:947:A:H8	1.75	0.49
19:A:1487:U:H2'	19:A:1488:C:C6	2.47	0.49
19:A:2026:U:H2'	19:A:2027:G:H8	1.77	0.49
19:A:2280:G:H2'	19:A:2281:A:H8	1.78	0.49
5:J:117:ALA:HA	5:J:120:ARG:HE	1.77	0.49
6:K:94:PRO:HG2	6:K:114:LYS:HD3	1.94	0.49
19:A:59:U:H3	19:A:68:G:H1	1.59	0.49
19:A:1135:C:N4	19:A:1138:G:OP2	2.46	0.49
7:N:72:ASP:OD1	7:N:73:ASN:N	2.45	0.49
19:A:402:A:N3	19:A:406:G:O2'	2.43	0.49
19:A:1311:G:N2	19:A:1603:A:H62	2.11	0.49
1:2:34:ARG:NH2	1:2:41:ARG:O	2.46	0.49
19:A:408:G:H1	19:A:419:U:H3	1.59	0.49
19:A:1426:G:O2'	19:A:1572:A:N6	2.46	0.49
19:A:1566:A:O2'	19:A:1568:G:N2	2.46	0.49
19:A:2676:C:H2'	19:A:2677:G:H8	1.77	0.49
13:U:25:LYS:HE3	13:U:36:GLU:HB3	1.94	0.49
18:y:3:ASN:ND2	19:A:61:C:O2'	2.46	0.49
19:A:239:C:H1'	19:A:621:A:H2	1.77	0.49
9:P:92:ARG:NH2	19:A:2849:U:OP2	2.45	0.49
10:Q:83:LYS:NZ	19:A:998:C:OP1	2.45	0.49
19:A:627:A:N6	19:A:637:A:O4'	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:2667:C:H2'	19:A:2668:G:H8	1.77	0.49
19:A:2818:U:H2'	19:A:2819:G:H8	1.77	0.49
2:B:51:G:OP1	8:O:63:LYS:NZ	2.38	0.48
19:A:1518:C:H2'	19:A:1519:G:C8	2.48	0.48
6:K:112:PHE:HB3	6:K:115:ILE:HD11	1.94	0.48
7:N:77:ALA:O	7:N:81:ASN:ND2	2.46	0.48
19:A:318:C:H2'	19:A:319:G:H8	1.78	0.48
19:A:628:G:H2'	19:A:629:G:C8	2.48	0.48
19:A:1492:G:N1	19:A:1496:A:N7	2.61	0.48
19:A:2710:C:H2'	19:A:2711:A:C8	2.48	0.48
19:A:2822:G:O2'	19:A:2825:G:N1	2.46	0.48
19:A:1218:G:N1	19:A:1232:G:N7	2.62	0.48
19:A:177:G:H5''	19:A:178:G:C8	2.48	0.48
19:A:673:C:OP1	20:E:49:ARG:NH1	2.46	0.48
19:A:825:A:H1'	19:A:2358:A:N7	2.28	0.48
19:A:1243:C:H2'	19:A:1244:A:C8	2.48	0.48
19:A:1424:G:H2'	19:A:1425:G:C8	2.48	0.48
2:B:63:C:H2'	2:B:64:G:H8	1.77	0.48
10:Q:10:ARG:NH2	19:A:29:U:O2'	2.42	0.48
10:Q:90:ASP:HB3	10:Q:93:ILE:HG12	1.94	0.48
19:A:2279:G:H2'	19:A:2280:G:C8	2.48	0.48
19:A:2847:U:H2'	19:A:2848:G:O4'	2.13	0.48
20:E:99:LYS:HG2	20:E:102:ARG:HH21	1.78	0.48
21:L:96:LYS:NZ	21:L:105:ILE:O	2.46	0.48
2:B:44:G:N3	2:B:47:C:N4	2.50	0.48
6:K:58:LEU:HD21	6:K:86:LEU:HD23	1.94	0.48
6:K:70:ARG:HH22	19:A:2683:C:H2'	1.78	0.48
11:R:84:ARG:HH22	21:L:23:ILE:HD13	1.77	0.48
9:P:51:ASN:HA	9:P:56:SER:HA	1.94	0.48
19:A:151:C:H2'	19:A:152:A:C8	2.49	0.48
19:A:1313:U:H4'	19:A:1332:G:H4'	1.95	0.48
13:U:35:VAL:HB	13:U:38:ILE:HD11	1.96	0.48
19:A:1316:U:H2'	19:A:1317:G:H8	1.79	0.48
19:A:2026:U:H2'	19:A:2027:G:C8	2.48	0.48
2:B:98:G:O2'	19:A:917:A:O2'	2.32	0.48
6:K:65:THR:HG23	6:K:68:GLY:H	1.79	0.48
19:A:1165:A:H2'	19:A:1166:G:H8	1.78	0.48
19:A:2824:C:OP2	19:A:2825:G:N2	2.47	0.48
2:B:31:C:H2'	2:B:32:U:C5	2.49	0.47
2:B:63:C:H2'	2:B:64:G:C8	2.49	0.47
12:T:11:LEU:O	16:Y:29:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:V:42:LEU:HB3	14:V:47:VAL:HG21	1.95	0.47
19:A:516:C:O2'	19:A:1262:A:OP1	2.32	0.47
19:A:1401:G:O2'	19:A:1522:A:OP2	2.32	0.47
19:A:2719:G:H4'	19:A:2846:G:H4'	1.96	0.47
20:E:146:VAL:HG21	20:E:187:VAL:HG23	1.96	0.47
2:B:11:C:H2'	2:B:15:A:H62	1.79	0.47
20:E:18:THR:HG23	20:E:106:LYS:HG2	1.96	0.47
19:A:389:G:C6	19:A:2413:G:H4'	2.49	0.47
19:A:824:U:H2'	19:A:825:A:C8	2.49	0.47
1:2:43:THR:H	19:A:126:A:H61	1.61	0.47
19:A:177:G:H5''	19:A:178:G:N7	2.29	0.47
19:A:2047:C:H2'	19:A:2048:G:H8	1.79	0.47
19:A:2784:U:H2'	19:A:2785:C:H6	1.80	0.47
2:B:80:U:O2'	19:A:918:A:N3	2.47	0.47
19:A:1434:A:H2'	19:A:1435:G:C8	2.50	0.47
19:A:1550:C:H2'	19:A:1551:A:C8	2.49	0.47
19:A:2425:A:H4'	19:A:2426:A:O5'	2.14	0.47
19:A:2643:G:C6	19:A:2644:G:O6	2.67	0.47
19:A:2848:G:H1'	19:A:2868:A:N6	2.30	0.47
15:W:25:GLU:HG2	19:A:923:G:H1'	1.95	0.47
19:A:131:A:H2'	19:A:132:G:H8	1.80	0.47
19:A:408:G:H2'	19:A:409:G:C8	2.49	0.47
19:A:1619:G:H2'	19:A:1620:G:C8	2.49	0.47
19:A:2687:U:H2'	19:A:2688:G:O4'	2.15	0.47
20:E:149:ILE:HG21	20:E:175:ILE:HD11	1.95	0.47
17:Z:11:SER:HA	17:Z:31:ILE:HD11	1.96	0.47
19:A:43:G:H2'	19:A:44:A:O4'	2.15	0.47
19:A:849:A:H2'	19:A:850:U:H6	1.78	0.47
19:A:1161:C:H2'	19:A:1162:G:C8	2.49	0.47
19:A:1178:C:H2'	19:A:1179:G:C8	2.49	0.47
19:A:1265:A:H61	19:A:2013:A:H3'	1.80	0.47
19:A:1402:U:O2'	19:A:1521:G:O2'	2.30	0.47
19:A:1427:A:N6	19:A:1571:A:OP2	2.41	0.47
19:A:2345:G:H4'	19:A:2346:A:H3'	1.96	0.47
12:T:68:LYS:HG3	12:T:77:ARG:HE	1.80	0.47
10:Q:49:ARG:O	10:Q:53:LYS:NZ	2.46	0.47
19:A:660:C:H2'	19:A:661:A:C8	2.50	0.47
19:A:1434:A:H2'	19:A:1435:G:H8	1.80	0.47
19:A:929:U:H2'	19:A:930:G:C8	2.50	0.46
20:E:154:ASP:OD1	20:E:154:ASP:N	2.46	0.46
21:L:96:LYS:HB3	21:L:103:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:2:LYS:H	4:F:2:LYS:HD3	1.80	0.46
8:O:25:ARG:O	8:O:40:ILE:N	2.48	0.46
13:U:38:ILE:HG13	13:U:39:ASN:N	2.31	0.46
17:Z:8:GLN:HB2	17:Z:28:LEU:HD13	1.97	0.46
19:A:1414:C:H2'	19:A:1415:U:O4'	2.15	0.46
19:A:1492:G:H1	19:A:1498:C:H42	1.64	0.46
19:A:2039:U:H2'	19:A:2040:G:C8	2.50	0.46
19:A:2636:C:H2'	19:A:2637:U:H6	1.79	0.46
19:A:2710:C:H2'	19:A:2711:A:H8	1.80	0.46
19:A:1402:U:O2'	19:A:1470:A:N1	2.48	0.46
19:A:1637:A:H2'	19:A:1638:C:C6	2.50	0.46
2:B:24:G:N3	2:B:27:C:N4	2.63	0.46
8:O:94:ARG:HE	19:A:2376:A:H61	1.64	0.46
19:A:1207:C:H2'	19:A:1208:C:C6	2.51	0.46
6:K:24:VAL:HA	6:K:39:ILE:HG22	1.98	0.46
6:K:39:ILE:O	6:K:60:ALA:N	2.49	0.46
9:P:97:TYR:HB3	9:P:100:ARG:HH12	1.79	0.46
19:A:970:U:H2'	19:A:971:G:H8	1.79	0.46
9:P:49:ILE:O	9:P:95:LYS:NZ	2.39	0.46
19:A:2422:C:O2'	19:A:2424:C:OP1	2.33	0.46
20:E:19:PHE:HE1	20:E:109:LEU:HD13	1.80	0.46
21:L:78:ARG:HG3	21:L:113:ALA:HB3	1.98	0.46
21:L:85:VAL:HB	21:L:88:GLY:HA2	1.97	0.46
3:D:13:ARG:HH21	9:P:55:HIS:HA	1.79	0.46
2:B:70:C:H2'	2:B:71:C:H6	1.80	0.46
19:A:307:G:H21	19:A:330:A:N6	2.14	0.46
19:A:511:U:H4'	19:A:1235:G:H4'	1.98	0.46
19:A:596:U:H2'	19:A:597:G:H8	1.79	0.46
19:A:999:U:H2'	19:A:1000:A:H8	1.81	0.46
19:A:2428:G:H4'	19:A:2429:G:C5	2.51	0.46
14:V:25:LYS:HG2	14:V:43:ASP:HA	1.98	0.46
19:A:1630:A:H2'	19:A:1631:G:O4'	2.16	0.46
19:A:2788:C:O2'	19:A:2809:A:N3	2.40	0.46
12:T:82:LYS:NZ	19:A:1340:U:OP2	2.43	0.45
19:A:499:U:H2'	19:A:500:G:O4'	2.16	0.45
19:A:1024:G:HO2'	19:A:1144:A:HO2'	1.60	0.45
2:B:97:C:O2	19:A:918:A:H4'	2.17	0.45
6:K:105:ARG:HH21	6:K:122:VAL:HA	1.81	0.45
17:Z:16:LEU:O	17:Z:20:LYS:HG2	2.16	0.45
19:A:580:U:H2'	19:A:581:C:C6	2.50	0.45
19:A:832:U:H2'	19:A:833:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:E:83:VAL:HB	20:E:86:ALA:HB2	1.98	0.45
9:P:91:VAL:HG21	9:P:96:LEU:HD11	1.98	0.45
11:R:49:ILE:HG22	11:R:54:VAL:HG13	1.98	0.45
17:Z:47:ILE:O	17:Z:51:SER:HB3	2.17	0.45
19:A:143:C:H2'	19:A:144:A:C8	2.50	0.45
19:A:158:U:H2'	19:A:159:G:O4'	2.16	0.45
19:A:2708:G:H2'	19:A:2709:G:H8	1.80	0.45
13:U:7:ASP:HA	13:U:24:VAL:HG23	1.98	0.45
16:Y:49:ASP:HA	16:Y:52:ARG:HD2	1.98	0.45
19:A:171:U:H2'	19:A:172:A:H8	1.81	0.45
19:A:173:A:H2'	19:A:174:U:C6	2.51	0.45
19:A:370:G:P	19:A:423:A:H62	2.39	0.45
19:A:64:A:H2'	19:A:65:U:H6	1.80	0.45
19:A:305:C:H2'	19:A:306:U:C6	2.52	0.45
19:A:345:A:N3	19:A:347:A:N6	2.64	0.45
19:A:404:A:H4'	19:A:405:U:O5'	2.17	0.45
19:A:500:G:N1	19:A:503:A:OP2	2.34	0.45
19:A:537:G:N2	19:A:555:G:O2'	2.38	0.45
19:A:848:C:H2'	19:A:849:A:H8	1.82	0.45
19:A:1239:G:H2'	19:A:1240:U:O4'	2.17	0.45
19:A:2280:G:H2'	19:A:2281:A:C8	2.51	0.45
2:B:95:U:H2'	2:B:96:G:H8	1.82	0.45
3:D:114:LYS:NZ	19:A:2681:C:OP1	2.37	0.45
18:y:17:ARG:HG3	19:A:1320:C:H4'	1.98	0.45
19:A:1:G:H2'	19:A:2:G:H8	1.81	0.45
19:A:2698:U:H2'	19:A:2699:C:C6	2.52	0.45
19:A:2718:G:O2'	19:A:2847:U:OP1	2.35	0.45
19:A:2788:C:H2'	19:A:2789:C:C6	2.51	0.45
4:F:37:MET:SD	4:F:86:CYS:N	2.85	0.45
11:R:29:THR:HA	11:R:63:VAL:HB	1.99	0.45
16:Y:43:LEU:HD12	19:A:61:C:H5''	1.98	0.45
19:A:817:C:H2'	19:A:818:G:O4'	2.16	0.45
19:A:923:G:H2'	19:A:924:G:C8	2.48	0.45
19:A:1321:A:N6	19:A:1334:G:O4'	2.50	0.45
19:A:1345:C:H2'	19:A:1346:G:C8	2.52	0.45
4:F:118:ALA:O	4:F:166:ARG:NE	2.44	0.45
19:A:864:G:H21	19:A:866:A:N6	2.15	0.45
19:A:1357:C:H2'	19:A:1358:G:O4'	2.17	0.45
11:R:4:VAL:HB	11:R:39:LEU:HB2	1.97	0.45
19:A:672:C:H2'	19:A:673:C:C6	2.52	0.45
19:A:823:C:H2'	19:A:824:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:996:A:H2'	19:A:997:G:C8	2.51	0.45
19:A:1161:C:H2'	19:A:1162:G:H8	1.81	0.45
2:B:24:G:H21	2:B:26:C:H42	1.64	0.45
4:F:36:ASN:ND2	19:A:2313:C:H4'	2.32	0.45
19:A:366:C:H2'	19:A:367:G:C8	2.52	0.45
19:A:598:U:H2'	19:A:599:A:C8	2.52	0.45
19:A:680:C:N4	19:A:681:G:O6	2.49	0.45
19:A:796:C:H2'	19:A:797:G:C8	2.52	0.45
19:A:1415:U:H1'	19:A:1588:G:N2	2.32	0.45
19:A:1421:G:H2'	19:A:1422:G:C8	2.52	0.45
9:P:74:GLN:HB2	9:P:77:SER:HB2	1.99	0.44
19:A:224:U:H2'	19:A:225:C:O4'	2.16	0.44
19:A:655:A:H1'	19:A:656:G:C8	2.52	0.44
19:A:1415:U:O2'	19:A:1416:G:H5'	2.16	0.44
19:A:2362:C:H2'	19:A:2363:G:H8	1.82	0.44
19:A:2626:C:H2'	19:A:2627:G:C8	2.52	0.44
19:A:2821:A:H2'	19:A:2822:G:C8	2.52	0.44
19:A:2838:G:H2'	19:A:2839:G:H8	1.82	0.44
19:A:2896:C:H2'	19:A:2897:U:C6	2.52	0.44
2:B:29:A:N3	2:B:57:A:N6	2.64	0.44
5:J:116:ARG:O	5:J:120:ARG:HG3	2.18	0.44
19:A:67:U:H2'	19:A:68:G:H8	1.82	0.44
19:A:965:C:N4	19:A:966:G:O6	2.51	0.44
19:A:1355:G:H2'	19:A:1356:G:H8	1.82	0.44
19:A:2313:C:H2'	19:A:2314:A:C8	2.52	0.44
19:A:1278:C:H2'	19:A:1279:G:H8	1.81	0.44
10:Q:90:ASP:OD1	10:Q:91:ARG:N	2.51	0.44
13:U:95:PHE:O	13:U:99:SER:HA	2.18	0.44
19:A:82:U:H3	19:A:104:A:H61	1.65	0.44
19:A:428:A:N3	19:A:428:A:H2'	2.33	0.44
19:A:451:U:C4	19:A:453:A:C8	3.06	0.44
19:A:1005:C:H2'	19:A:1006:C:C6	2.52	0.44
19:A:1200:C:H2'	19:A:1201:U:C6	2.53	0.44
19:A:2364:C:H2'	19:A:2365:G:O4'	2.17	0.44
19:A:2674:G:H2'	19:A:2675:A:H8	1.83	0.44
2:B:49:C:OP1	8:O:102:ARG:NE	2.51	0.44
5:J:101:ILE:HG21	5:J:124:VAL:HG21	2.00	0.44
6:K:109:SER:HB2	6:K:112:PHE:HD1	1.81	0.44
19:A:849:A:H2'	19:A:850:U:C6	2.52	0.44
19:A:2762:C:H3'	19:A:2763:G:H8	1.82	0.44
16:Y:50:VAL:HA	16:Y:53:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:30:G:O2'	19:A:1214:A:N3	2.39	0.44
19:A:1272:A:O5'	19:A:1646:C:N4	2.50	0.44
19:A:1498:C:H1'	19:A:1576:U:O2	2.17	0.44
1:2:30:VAL:HG22	1:2:33:ARG:HH22	1.83	0.44
9:P:8:GLU:O	9:P:12:MET:HG2	2.18	0.44
10:Q:71:ASN:HD22	10:Q:109:VAL:HG21	1.83	0.44
19:A:253:C:H2'	19:A:254:G:O4'	2.17	0.44
19:A:1336:A:H2'	19:A:1337:G:C8	2.52	0.44
19:A:2291:U:H1'	19:A:2374:C:H1'	2.00	0.44
20:E:147:LEU:HB2	20:E:183:PHE:CG	2.53	0.44
19:A:2736:A:H2'	19:A:2737:G:C8	2.53	0.44
20:E:117:ARG:NH2	20:E:183:PHE:O	2.48	0.44
2:B:70:C:H2'	2:B:71:C:C6	2.53	0.43
5:J:73:VAL:HA	5:J:88:THR:HA	1.99	0.43
19:A:553:G:H2'	19:A:554:U:H6	1.83	0.43
3:D:2:ILE:HG21	3:D:48:ILE:HD11	1.99	0.43
7:N:53:THR:HA	7:N:56:LYS:HG2	2.00	0.43
10:Q:23:TYR:O	10:Q:27:ARG:HB2	2.16	0.43
19:A:810:U:H5''	19:A:811:U:H5'	2.00	0.43
19:A:1234:U:H2'	19:A:1235:G:O4'	2.18	0.43
19:A:2636:C:H2'	19:A:2637:U:C6	2.53	0.43
19:A:2840:C:H2'	19:A:2841:C:H6	1.83	0.43
2:B:33:G:H2'	2:B:34:A:O4'	2.18	0.43
3:D:101:PHE:HD1	3:D:104:VAL:HG21	1.83	0.43
19:A:18:U:H2'	19:A:19:A:C8	2.52	0.43
19:A:397:U:H2'	19:A:398:C:C6	2.52	0.43
19:A:813:U:H2'	19:A:814:C:H6	1.82	0.43
19:A:1339:G:N2	19:A:1603:A:H1'	2.34	0.43
19:A:32:C:H2'	19:A:33:C:C6	2.53	0.43
19:A:258:G:H2'	19:A:259:G:H8	1.83	0.43
19:A:840:C:H2'	19:A:841:G:C8	2.53	0.43
19:A:1277:G:H2'	19:A:1278:C:H6	1.84	0.43
4:F:104:THR:HG22	4:F:105:ILE:HG23	2.00	0.43
5:J:105:VAL:HG11	5:J:122:LEU:HD22	2.00	0.43
19:A:242:G:N2	19:A:255:A:OP2	2.51	0.43
19:A:1223:G:H21	19:A:1225:G:H8	1.66	0.43
10:Q:26:ALA:HA	10:Q:29:ARG:HG2	2.01	0.43
19:A:1416:G:N2	19:A:1582:C:H42	2.17	0.43
19:A:1753:G:N2	19:A:1756:G:OP2	2.51	0.43
19:A:2413:G:C2	19:A:2414:G:C8	3.06	0.43
2:B:71:C:H2'	2:B:72:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:67:HIS:ND1	19:A:2785:C:O2'	2.48	0.43
19:A:225:C:N3	19:A:231:A:N6	2.64	0.43
19:A:839:U:H2'	19:A:840:C:C6	2.53	0.43
19:A:1278:C:H2'	19:A:1279:G:C8	2.53	0.43
19:A:1328:A:O2'	19:A:1329:U:H2'	2.18	0.43
19:A:1487:U:H2'	19:A:1488:C:H6	1.83	0.43
2:B:76:G:OP2	14:V:12:GLN:NE2	2.46	0.43
8:O:55:GLU:HG3	8:O:57:ALA:H	1.84	0.43
11:R:85:LYS:NZ	19:A:1187:G:OP1	2.39	0.43
19:A:131:A:H2'	19:A:132:G:C8	2.54	0.43
19:A:526:A:O2'	19:A:2043:C:O2	2.35	0.43
19:A:2410:G:H2'	19:A:2411:A:O4'	2.19	0.43
2:B:95:U:H2'	2:B:96:G:C8	2.54	0.43
8:O:94:ARG:HE	19:A:2376:A:N6	2.16	0.43
19:A:1413:A:H2'	19:A:1414:C:C6	2.53	0.43
17:Z:42:ALA:O	17:Z:46:MET:HG2	2.18	0.43
19:A:197:A:N3	19:A:197:A:H2'	2.34	0.43
19:A:551:G:H2'	19:A:552:U:C6	2.54	0.43
19:A:554:U:H2'	19:A:555:G:O4'	2.18	0.43
19:A:929:U:H2'	19:A:930:G:H8	1.83	0.43
19:A:243:U:H2'	19:A:244:A:C8	2.53	0.42
19:A:851:C:H2'	19:A:852:U:C6	2.54	0.42
19:A:924:G:H2'	19:A:925:A:H8	1.84	0.42
6:K:71:ARG:HH12	9:P:71:ARG:NH1	2.17	0.42
15:W:16:ARG:HB3	15:W:35:ARG:NH2	2.34	0.42
16:Y:45:GLN:O	16:Y:47:ARG:N	2.52	0.42
19:A:929:U:HO2'	19:A:930:G:P	2.41	0.42
19:A:1604:C:O2'	19:A:1610:A:N1	2.47	0.42
19:A:4:U:H2'	19:A:5:A:C8	2.54	0.42
19:A:481:G:N1	19:A:507:A:H1'	2.34	0.42
19:A:915:C:H3'	19:A:916:G:H8	1.84	0.42
19:A:1481:U:O2	19:A:1510:G:O6	2.36	0.42
19:A:2647:U:O2	19:A:2673:G:O6	2.37	0.42
19:A:2696:U:H2'	19:A:2697:G:H8	1.84	0.42
7:N:50:PRO:HA	7:N:53:THR:HG22	2.01	0.42
8:O:67:ASN:OD1	8:O:70:ALA:N	2.45	0.42
15:W:19:VAL:HG13	15:W:34:VAL:HB	2.01	0.42
19:A:523:C:H5''	19:A:540:C:O2'	2.19	0.42
19:A:976:G:H2'	19:A:977:G:H8	1.85	0.42
19:A:1139:G:H2'	19:A:1140:C:C6	2.54	0.42
19:A:1734:G:H2'	19:A:1735:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:2840:C:H2'	19:A:2841:C:C6	2.54	0.42
2:B:42:C:H5	4:F:65:LEU:HD13	1.84	0.42
7:N:12:ARG:HE	7:N:16:HIS:CE1	2.38	0.42
12:T:66:LYS:NZ	19:A:1339:G:O6	2.41	0.42
19:A:194:G:H2'	19:A:195:A:C8	2.54	0.42
19:A:987:C:H2'	19:A:988:A:O4'	2.20	0.42
19:A:1716:U:H2'	19:A:1717:A:H8	1.84	0.42
2:B:17:C:H2'	2:B:18:G:H8	1.83	0.42
5:J:9:GLU:HG2	5:J:10:THR:HG23	2.01	0.42
13:U:46:LYS:NZ	19:A:483:A:OP1	2.52	0.42
19:A:5:A:H2'	19:A:6:A:C8	2.55	0.42
19:A:579:G:H4'	19:A:2018:G:H5''	2.02	0.42
19:A:633:A:H3'	19:A:634:C:H6	1.85	0.42
19:A:281:C:H2'	19:A:282:A:C8	2.55	0.42
19:A:2888:C:H2'	19:A:2889:C:C6	2.53	0.42
1:2:39:ARG:NH2	19:A:468:G:N7	2.62	0.42
4:F:33:ILE:HB	4:F:90:LEU:HB2	2.02	0.42
4:F:92:GLY:O	4:F:95:MET:HG2	2.19	0.42
4:F:105:ILE:O	4:F:109:ARG:HG2	2.20	0.42
5:J:57:LEU:HD11	5:J:130:HIS:HD2	1.84	0.42
8:O:24:THR:HG23	8:O:90:VAL:HG12	2.00	0.42
19:A:185:G:H2'	19:A:186:G:C8	2.55	0.42
19:A:197:A:C6	19:A:2431:U:N3	2.88	0.42
19:A:1295:C:H2'	19:A:1296:G:H8	1.84	0.42
19:A:2039:U:H2'	19:A:2040:G:H8	1.85	0.42
20:E:31:VAL:HG21	20:E:104:ALA:HB2	2.01	0.42
21:L:110:VAL:HG21	21:L:122:VAL:HG11	2.01	0.42
3:D:9:VAL:HG21	9:P:3:ILE:HD11	2.02	0.42
19:A:272:A:H2'	19:A:273:G:C8	2.54	0.42
19:A:415:A:H2'	19:A:416:U:C6	2.55	0.42
19:A:565:C:H42	19:A:576:U:H3	1.66	0.42
19:A:842:U:H2'	19:A:843:G:C8	2.55	0.42
19:A:924:G:H2'	19:A:925:A:C8	2.54	0.42
19:A:1298:C:H2'	19:A:1299:G:O4'	2.19	0.42
19:A:1737:G:H2'	19:A:1738:G:C4	2.55	0.42
19:A:2297:A:H2'	19:A:2298:A:H8	1.83	0.42
12:T:88:LYS:HE3	12:T:88:LYS:HB3	1.86	0.42
19:A:1149:G:H2'	19:A:1150:C:C6	2.55	0.42
19:A:1277:G:H2'	19:A:1278:C:C6	2.55	0.42
19:A:1406:U:H2'	19:A:1407:G:C8	2.55	0.42
19:A:1416:G:H22	19:A:1582:C:H42	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:1520:U:H2'	19:A:1521:G:O4'	2.20	0.42
19:A:1576:U:H2'	19:A:1577:C:C6	2.55	0.42
19:A:2674:G:H2'	19:A:2675:A:C8	2.55	0.42
21:L:127:VAL:HG21	21:L:142:ILE:HD13	2.01	0.42
6:K:88:ASN:H	6:K:92:GLU:HA	1.86	0.41
7:N:45:ARG:HA	7:N:48:VAL:HG12	2.01	0.41
12:T:55:VAL:HG13	12:T:85:VAL:HG13	2.02	0.41
19:A:320:A:H4'	19:A:322:A:N7	2.34	0.41
19:A:911:A:O4'	19:A:2263:C:O2'	2.37	0.41
9:P:51:ASN:O	19:A:2845:U:H5''	2.20	0.41
10:Q:13:HIS:ND1	19:A:582:A:OP1	2.47	0.41
16:Y:21:LEU:HD12	16:Y:25:GLN:HG3	2.02	0.41
20:E:36:ALA:O	20:E:40:ARG:HG3	2.21	0.41
4:F:42:ALA:HB3	4:F:84:ILE:HD12	2.01	0.41
19:A:69:C:H2'	19:A:70:G:C8	2.55	0.41
19:A:475:C:N3	19:A:479:A:N7	2.67	0.41
19:A:2817:U:O2'	19:A:2837:A:H1'	2.20	0.41
20:E:21:ARG:HH11	20:E:106:LYS:HE3	1.84	0.41
5:J:99:ARG:HD2	5:J:99:ARG:HA	1.95	0.41
10:Q:32:ARG:NH1	19:A:580:U:OP1	2.54	0.41
11:R:80:ARG:HH21	19:A:572:A:H4'	1.84	0.41
12:T:44:LYS:HG3	12:T:55:VAL:HB	2.02	0.41
19:A:152:A:N6	19:A:175:G:O6	2.54	0.41
19:A:244:A:H2'	19:A:245:G:O4'	2.21	0.41
19:A:414:C:H2'	19:A:415:A:C8	2.54	0.41
19:A:587:C:C4	21:L:19:LEU:HD11	2.55	0.41
19:A:1291:C:H2'	19:A:1292:G:C8	2.54	0.41
19:A:1710:G:H4'	19:A:2858:C:N3	2.35	0.41
7:N:55:ALA:HA	7:N:80:PHE:CE2	2.56	0.41
19:A:181:A:H2'	19:A:182:A:C8	2.55	0.41
19:A:188:G:O2'	19:A:1365:A:N6	2.53	0.41
19:A:304:U:H2'	19:A:305:C:C6	2.56	0.41
19:A:397:U:H2'	19:A:398:C:H6	1.85	0.41
19:A:819:A:N6	19:A:1189:A:H1'	2.36	0.41
19:A:1316:U:H2'	19:A:1317:G:C8	2.56	0.41
19:A:2661:G:H2'	19:A:2662:A:H8	1.86	0.41
19:A:2804:U:H2'	19:A:2805:C:C6	2.56	0.41
13:U:6:ARG:HG3	13:U:7:ASP:H	1.85	0.41
19:A:582:A:H2'	19:A:583:G:C8	2.56	0.41
19:A:843:G:H2'	19:A:844:A:C8	2.56	0.41
19:A:2623:G:H2'	19:A:2624:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:2888:C:H2'	19:A:2889:C:H6	1.85	0.41
10:Q:23:TYR:HB2	10:Q:28:SER:HB3	2.02	0.41
11:R:1:MET:HE3	11:R:101:ILE:HB	2.03	0.41
19:A:49:A:N1	19:A:177:G:N2	2.68	0.41
19:A:246:C:H2'	19:A:247:G:O4'	2.21	0.41
19:A:664:G:O2'	19:A:940:G:OP1	2.27	0.41
19:A:1010:A:N3	19:A:1153:C:H1'	2.35	0.41
19:A:1582:C:O2'	19:A:1585:C:N3	2.50	0.41
19:A:1748:C:H2'	19:A:1749:A:H8	1.86	0.41
21:L:29:LYS:HE3	21:L:35:HIS:HE1	1.85	0.41
5:J:37:ARG:NH1	19:A:1007:C:H5''	2.35	0.41
6:K:38:ILE:HD13	6:K:61:VAL:HB	2.01	0.41
19:A:538:A:H62	19:A:555:G:N2	2.18	0.41
19:A:1123:C:H2'	19:A:1124:G:C8	2.54	0.41
19:A:1202:G:H2'	19:A:1203:U:O4'	2.20	0.41
19:A:1207:C:H2'	19:A:1208:C:H6	1.85	0.41
19:A:2736:A:H2'	19:A:2737:G:H8	1.86	0.41
2:B:19:C:H2'	2:B:20:G:H8	1.86	0.41
4:F:109:ARG:NH1	4:F:136:ILE:O	2.53	0.41
7:N:11:ASN:OD1	7:N:11:ASN:N	2.54	0.41
7:N:20:MET:SD	7:N:24:MET:HE3	2.61	0.41
7:N:59:SER:OG	7:N:62:ASN:OD1	2.32	0.41
8:O:9:ARG:HD2	8:O:9:ARG:HA	1.86	0.41
8:O:53:THR:HG22	8:O:74:VAL:HG21	2.03	0.41
14:V:25:LYS:HD2	14:V:41:GLU:OE2	2.21	0.41
19:A:56:A:H2'	19:A:57:C:C6	2.56	0.41
19:A:323:C:O2'	19:A:1205:A:N6	2.54	0.41
19:A:467:G:H4'	19:A:796:C:O2'	2.21	0.41
19:A:833:A:H2'	19:A:834:G:O4'	2.20	0.41
19:A:1268:A:H62	19:A:2012:G:H21	1.68	0.41
19:A:1336:A:H2'	19:A:1337:G:H8	1.86	0.41
19:A:1550:C:H5'	19:A:1740:G:H22	1.86	0.41
19:A:2379:G:H2'	19:A:2380:C:C6	2.56	0.41
19:A:2688:G:N1	19:A:2720:U:OP2	2.40	0.41
19:A:2881:U:H2'	19:A:2882:A:C8	2.56	0.41
21:L:2:ARG:O	21:L:5:THR:OG1	2.38	0.41
2:B:77:U:C2	2:B:99:A:N7	2.89	0.41
8:O:24:THR:N	8:O:42:PRO:HG3	2.36	0.41
19:A:243:U:H2'	19:A:244:A:H8	1.86	0.41
19:A:399:U:H2'	19:A:400:G:O4'	2.21	0.41
19:A:851:C:H2'	19:A:852:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:1024:G:N2	19:A:1144:A:O4'	2.50	0.41
19:A:1501:G:H2'	19:A:1502:A:C8	2.56	0.41
19:A:2350:C:H2'	19:A:2351:G:O4'	2.21	0.41
11:R:2:TYR:HB2	11:R:13:ARG:HD3	2.03	0.40
19:A:282:A:N1	19:A:359:G:C6	2.89	0.40
19:A:419:U:H2'	19:A:420:C:C6	2.56	0.40
19:A:450:G:N1	19:A:454:A:OP2	2.54	0.40
19:A:611:C:H2'	19:A:612:G:O4'	2.20	0.40
19:A:1378:A:C4	19:A:1380:G:C8	3.09	0.40
19:A:2811:G:N2	19:A:2890:G:H1'	2.36	0.40
19:A:2848:G:O2'	19:A:2867:G:N2	2.54	0.40
4:F:22:ASN:OD1	4:F:23:SER:N	2.54	0.40
13:U:85:ARG:HH22	13:U:99:SER:HB3	1.87	0.40
19:A:267:C:H2'	19:A:268:C:C6	2.56	0.40
19:A:307:G:N1	19:A:309:A:O5'	2.54	0.40
19:A:373:U:H1'	19:A:423:A:C2	2.57	0.40
19:A:383:C:H5''	19:A:385:C:OP2	2.21	0.40
19:A:581:C:H2'	19:A:582:A:C8	2.53	0.40
19:A:1484:U:H2'	19:A:1485:U:C6	2.57	0.40
19:A:2399:G:O6	19:A:2418:A:N6	2.54	0.40
19:A:2783:U:H2'	19:A:2784:U:C6	2.56	0.40
5:J:47:HIS:ND1	5:J:48:VAL:HG13	2.36	0.40
17:Z:11:SER:OG	19:A:989:G:OP2	2.28	0.40
19:A:16:C:H2'	19:A:17:G:H8	1.86	0.40
19:A:258:G:H2'	19:A:259:G:C8	2.56	0.40
19:A:540:C:N4	19:A:541:A:H62	2.20	0.40
19:A:839:U:H3	19:A:939:G:H1	1.70	0.40
19:A:917:A:H3'	19:A:2268:A:H61	1.87	0.40
19:A:2414:G:C2	19:A:2415:G:C8	3.09	0.40
4:F:34:THR:OG1	4:F:154:THR:HB	2.22	0.40
19:A:4:U:H2'	19:A:5:A:H8	1.85	0.40
19:A:542:C:H2'	19:A:543:G:C8	2.56	0.40
19:A:553:G:H2'	19:A:554:U:C6	2.57	0.40
19:A:1604:C:H2'	19:A:1605:C:C6	2.56	0.40
2:B:57:A:H2'	2:B:58:A:H8	1.87	0.40
5:J:7:LYS:O	5:J:11:VAL:HG23	2.21	0.40
6:K:10:VAL:HG12	6:K:12:ASP:H	1.85	0.40
8:O:81:ARG:HA	8:O:84:GLU:HG2	2.04	0.40
19:A:100:U:O2	19:A:101:A:N6	2.55	0.40
19:A:190:A:H2	19:A:799:G:H21	1.68	0.40
19:A:1412:U:H2'	19:A:1413:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:A:1713:A:N6	19:A:1746:A:N1	2.69	0.40
19:A:2407:A:H2'	19:A:2408:U:C6	2.56	0.40
19:A:2643:G:C6	19:A:2644:G:C6	3.10	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	38/46 (83%)	35 (92%)	3 (8%)	0	100	100
3	D	116/209 (56%)	112 (97%)	4 (3%)	0	100	100
4	F	175/177 (99%)	164 (94%)	11 (6%)	0	100	100
5	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
6	K	120/122 (98%)	109 (91%)	11 (9%)	0	100	100
7	N	109/120 (91%)	104 (95%)	5 (5%)	0	100	100
8	O	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
9	P	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
10	Q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
11	R	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
12	T	91/93 (98%)	83 (91%)	8 (9%)	0	100	100
13	U	100/102 (98%)	88 (88%)	12 (12%)	0	100	100
14	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
15	W	67/75 (89%)	67 (100%)	0	0	100	100
16	Y	59/63 (94%)	53 (90%)	5 (8%)	1 (2%)	7	35
17	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
18	y	15/17 (88%)	12 (80%)	3 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	E	164/201 (82%)	159 (97%)	5 (3%)	0	100	100
21	L	114/143 (80%)	104 (91%)	10 (9%)	0	100	100
All	All	1898/2112 (90%)	1800 (95%)	97 (5%)	1 (0%)	49	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	Y	46	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	32/38 (84%)	32 (100%)	0	100	100
3	D	92/164 (56%)	92 (100%)	0	100	100
4	F	148/148 (100%)	144 (97%)	4 (3%)	39	60
5	J	116/116 (100%)	115 (99%)	1 (1%)	70	76
6	K	103/103 (100%)	99 (96%)	4 (4%)	28	50
7	N	92/100 (92%)	91 (99%)	1 (1%)	65	73
8	O	86/86 (100%)	83 (96%)	3 (4%)	32	53
9	P	99/99 (100%)	96 (97%)	3 (3%)	36	57
10	Q	89/89 (100%)	89 (100%)	0	100	100
11	R	84/84 (100%)	82 (98%)	2 (2%)	43	63
12	T	80/80 (100%)	79 (99%)	1 (1%)	61	71
13	U	83/83 (100%)	82 (99%)	1 (1%)	63	73
14	V	78/78 (100%)	78 (100%)	0	100	100
15	W	51/57 (90%)	50 (98%)	1 (2%)	48	66
16	Y	55/55 (100%)	54 (98%)	1 (2%)	51	66
17	Z	48/48 (100%)	45 (94%)	3 (6%)	16	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	y	17/17 (100%)	16 (94%)	1 (6%)	18	41
20	E	141/165 (86%)	140 (99%)	1 (1%)	76	78
21	L	83/102 (81%)	79 (95%)	4 (5%)	23	45
All	All	1577/1712 (92%)	1546 (98%)	31 (2%)	48	66

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	2	LYS
4	F	30	VAL
4	F	34	THR
4	F	37	MET
5	J	81	ILE
6	K	61	VAL
6	K	62	VAL
6	K	69	VAL
6	K	92	GLU
7	N	53	THR
8	O	16	ARG
8	O	24	THR
8	O	30	ARG
9	P	16	VAL
9	P	27	VAL
9	P	85	VAL
11	R	25	LEU
11	R	47	VAL
12	T	16	VAL
13	U	98	ASN
15	W	67	VAL
16	Y	30	MET
17	Z	24	LEU
17	Z	50	VAL
17	Z	56	VAL
18	y	6	VAL
20	E	176	ASP
21	L	85	VAL
21	L	110	VAL
21	L	116	VAL
21	L	136	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18)

such sidechains are listed below:

Mol	Chain	Res	Type
1	2	29	GLN
4	F	62	GLN
5	J	76	HIS
5	J	128	ASN
5	J	130	HIS
6	K	93	GLN
7	N	107	ASN
9	P	55	HIS
10	Q	71	ASN
11	R	91	GLN
12	T	59	ASN
13	U	44	HIS
13	U	73	ASN
13	U	98	ASN
14	V	75	GLN
16	Y	41	HIS
18	y	3	ASN
20	E	115	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	A	1969/2903 (67%)	285 (14%)	7 (0%)
2	B	118/120 (98%)	14 (11%)	0
All	All	2087/3023 (69%)	299 (14%)	7 (0%)

All (299) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	G
2	B	13	G
2	B	15	A
2	B	16	G
2	B	25	U
2	B	31	C
2	B	35	C
2	B	41	G
2	B	42	C
2	B	53	A
2	B	87	U
2	B	90	C

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Mol	Chain	Res	Type
2	B	99	A
2	B	109	A
19	A	12	U
19	A	14	A
19	A	27	G
19	A	34	U
19	A	46	G
19	A	51	G
19	A	63	A
19	A	71	A
19	A	74	A
19	A	75	G
19	A	114	U
19	A	118	A
19	A	120	U
19	A	138	U
19	A	139	U
19	A	140	C
19	A	141	G
19	A	142	A
19	A	163	C
19	A	181	A
19	A	190	A
19	A	204	A
19	A	216	A
19	A	221	A
19	A	222	A
19	A	232	G
19	A	248	G
19	A	255	A
19	A	266	G
19	A	271	G
19	A	272	A
19	A	276	U
19	A	278	A
19	A	285	G
19	A	302	C
19	A	307	G
19	A	311	A
19	A	329	G
19	A	330	A
19	A	359	G

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Mol	Chain	Res	Type
19	A	361	G
19	A	371	A
19	A	372	G
19	A	386	G
19	A	389	G
19	A	390	U
19	A	396	G
19	A	405	U
19	A	406	G
19	A	411	G
19	A	424	G
19	A	429	A
19	A	435	C
19	A	446	G
19	A	451	U
19	A	456	C
19	A	465	G
19	A	467	G
19	A	480	A
19	A	481	G
19	A	491	G
19	A	504	A
19	A	505	A
19	A	509	C
19	A	531	C
19	A	532	A
19	A	533	G
19	A	541	A
19	A	543	G
19	A	546	U
19	A	547	A
19	A	548	G
19	A	550	C
19	A	563	A
19	A	573	U
19	A	586	A
19	A	588	U
19	A	603	A
19	A	613	A
19	A	614	A
19	A	615	U
19	A	616	A

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Mol	Chain	Res	Type
19	A	621	A
19	A	627	A
19	A	631	A
19	A	637	A
19	A	646	U
19	A	647	G
19	A	649	G
19	A	654	A
19	A	664	G
19	A	669	G
19	A	675	A
19	A	684	G
19	A	801	G
19	A	811	U
19	A	812	C
19	A	819	A
19	A	828	U
19	A	829	A
19	A	830	A
19	A	832	U
19	A	845	A
19	A	846	U
19	A	847	U
19	A	849	A
19	A	856	G
19	A	858	G
19	A	859	G
19	A	863	A
19	A	864	G
19	A	865	C
19	A	866	A
19	A	911	A
19	A	912	C
19	A	914	G
19	A	930	G
19	A	941	A
19	A	945	A
19	A	957	C
19	A	959	A
19	A	974	G
19	A	983	A
19	A	995	C

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Mol	Chain	Res	Type
19	A	996	A
19	A	1005	C
19	A	1009	A
19	A	1012	U
19	A	1013	C
19	A	1020	A
19	A	1022	G
19	A	1026	G
19	A	1131	G
19	A	1132	U
19	A	1133	A
19	A	1135	C
19	A	1136	G
19	A	1138	G
19	A	1142	A
19	A	1157	G
19	A	1168	G
19	A	1171	G
19	A	1172	C
19	A	1173	U
19	A	1174	U
19	A	1176	U
19	A	1177	G
19	A	1186	G
19	A	1211	C
19	A	1212	G
19	A	1225	G
19	A	1236	G
19	A	1238	G
19	A	1247	A
19	A	1248	G
19	A	1253	A
19	A	1256	G
19	A	1266	G
19	A	1271	G
19	A	1272	A
19	A	1300	G
19	A	1301	A
19	A	1312	U
19	A	1314	C
19	A	1325	U
19	A	1329	U

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Mol	Chain	Res	Type
19	A	1332	G
19	A	1343	G
19	A	1345	C
19	A	1365	A
19	A	1374	G
19	A	1378	A
19	A	1379	U
19	A	1383	A
19	A	1395	A
19	A	1416	G
19	A	1417	C
19	A	1418	G
19	A	1419	A
19	A	1420	A
19	A	1421	G
19	A	1452	G
19	A	1458	U
19	A	1461	C
19	A	1467	U
19	A	1482	G
19	A	1490	A
19	A	1491	G
19	A	1493	C
19	A	1496	A
19	A	1497	U
19	A	1515	A
19	A	1523	U
19	A	1524	G
19	A	1535	A
19	A	1536	C
19	A	1537	G
19	A	1555	G
19	A	1569	A
19	A	1576	U
19	A	1583	A
19	A	1584	U
19	A	1585	C
19	A	1587	G
19	A	1603	A
19	A	1607	C
19	A	1608	A
19	A	1616	A

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Mol	Chain	Res	Type
19	A	1633	G
19	A	1634	A
19	A	1646	C
19	A	1647	U
19	A	1648	U
19	A	1715	G
19	A	1729	U
19	A	1730	C
19	A	1732	C
19	A	1733	G
19	A	1737	G
19	A	1738	G
19	A	2013	A
19	A	2021	C
19	A	2023	C
19	A	2030	A
19	A	2031	A
19	A	2043	C
19	A	2052	A
19	A	2283	C
19	A	2286	G
19	A	2287	A
19	A	2297	A
19	A	2305	U
19	A	2311	A
19	A	2327	A
19	A	2333	A
19	A	2335	A
19	A	2336	A
19	A	2347	C
19	A	2350	C
19	A	2361	G
19	A	2370	G
19	A	2371	G
19	A	2383	G
19	A	2385	C
19	A	2402	U
19	A	2406	A
19	A	2422	C
19	A	2424	C
19	A	2425	A
19	A	2426	A

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Mol	Chain	Res	Type
19	A	2428	G
19	A	2429	G
19	A	2430	A
19	A	2434	A
19	A	2629	U
19	A	2630	G
19	A	2639	A
19	A	2646	C
19	A	2665	A
19	A	2682	A
19	A	2689	U
19	A	2690	U
19	A	2714	G
19	A	2726	A
19	A	2729	G
19	A	2732	G
19	A	2733	A
19	A	2739	U
19	A	2744	G
19	A	2745	C
19	A	2746	U
19	A	2747	G
19	A	2748	A
19	A	2750	A
19	A	2751	G
19	A	2765	A
19	A	2766	A
19	A	2778	A
19	A	2780	G
19	A	2820	A
19	A	2850	A
19	A	2867	G
19	A	2873	A
19	A	2880	C
19	A	2886	A

All (7) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
19	A	271	G
19	A	404	A
19	A	828	U

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Mol	Chain	Res	Type
19	A	848	C
19	A	929	U
19	A	1328	A
19	A	2425	A

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.

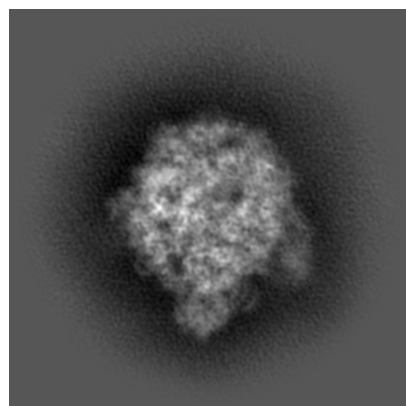
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51976. These allow visual inspection of the internal detail of the map and identification of artifacts.

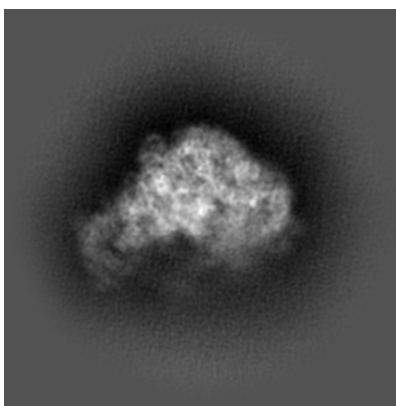
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

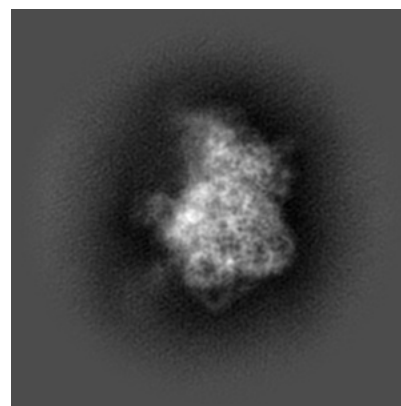
6.1.1 Primary map



X

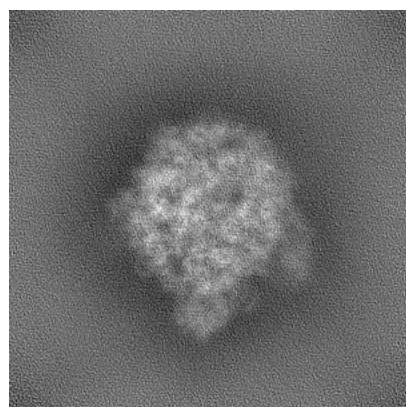


Y

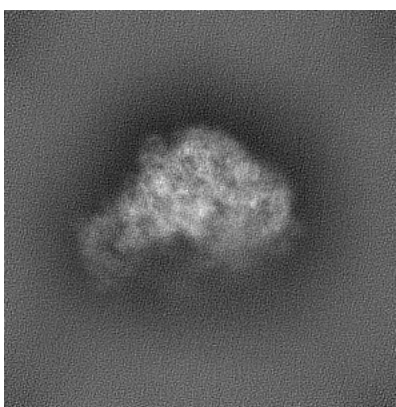


Z

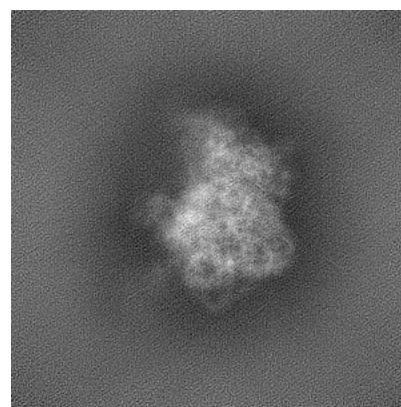
6.1.2 Raw map



X



Y

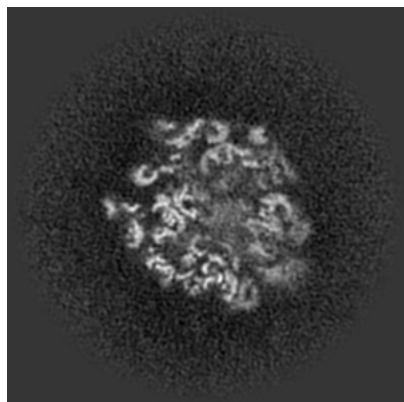


Z

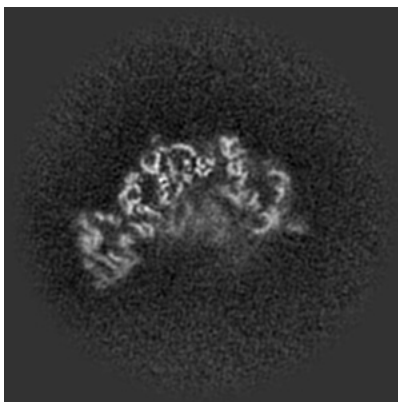
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

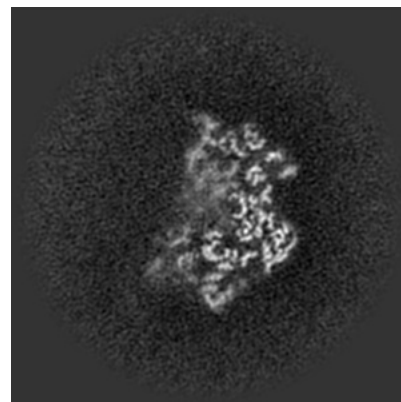
6.2.1 Primary map



X Index: 150

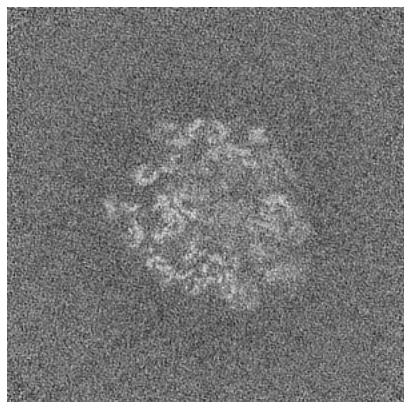


Y Index: 150

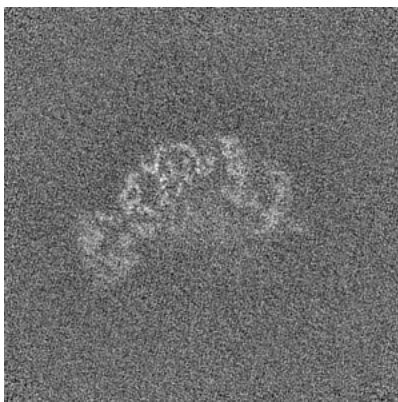


Z Index: 150

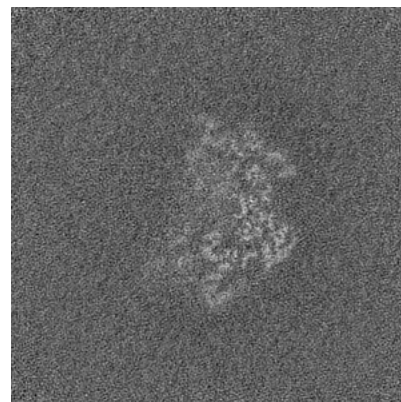
6.2.2 Raw map



X Index: 150



Y Index: 150

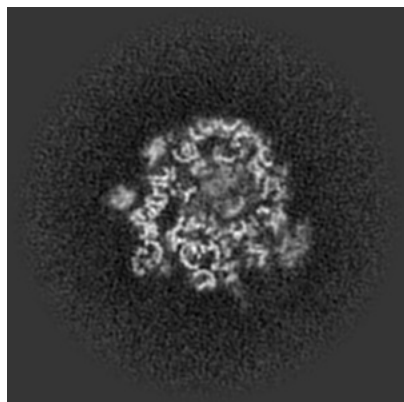


Z Index: 150

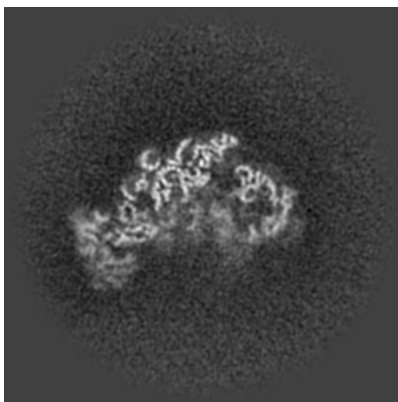
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

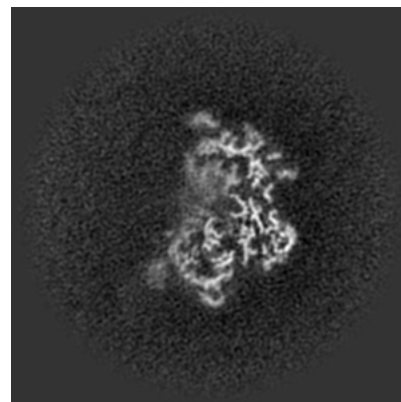
6.3.1 Primary map



X Index: 163

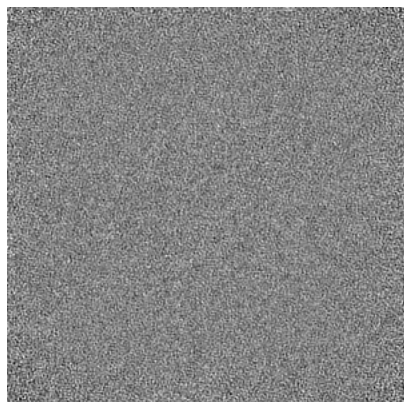


Y Index: 143

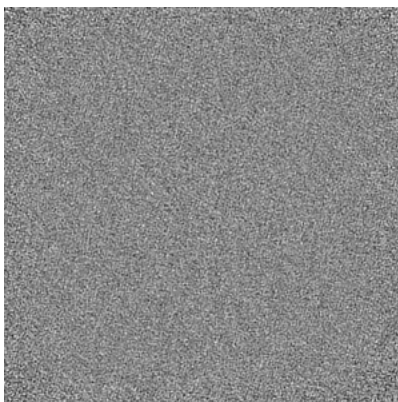


Z Index: 147

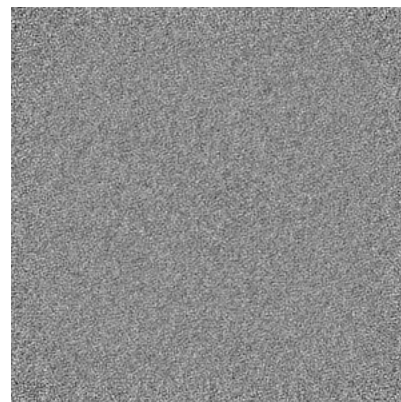
6.3.2 Raw map



X Index: 0



Y Index: 0

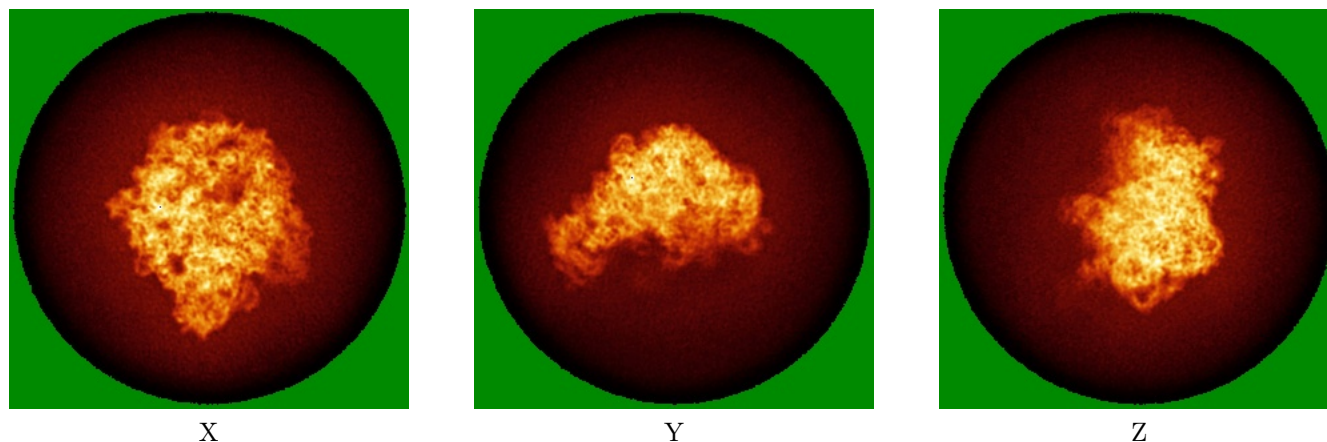


Z Index: 0

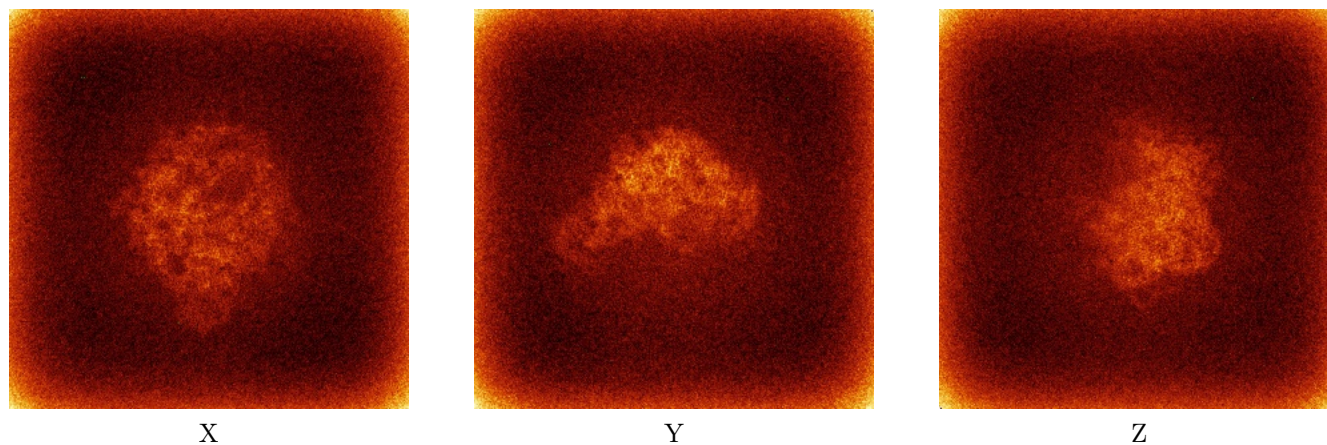
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

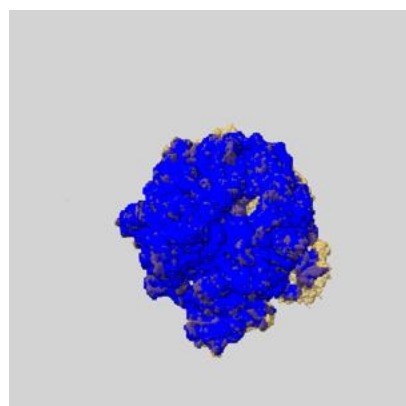
6.6 Mask visualisation [i](#)

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

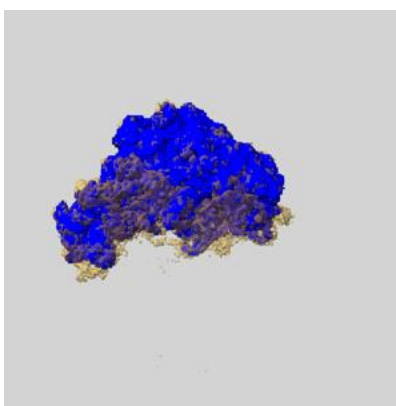
A mask typically either:

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

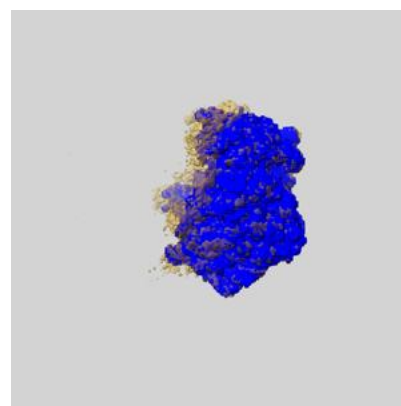
6.6.1 emd_51976_msk_1.map [i](#)



X



Y

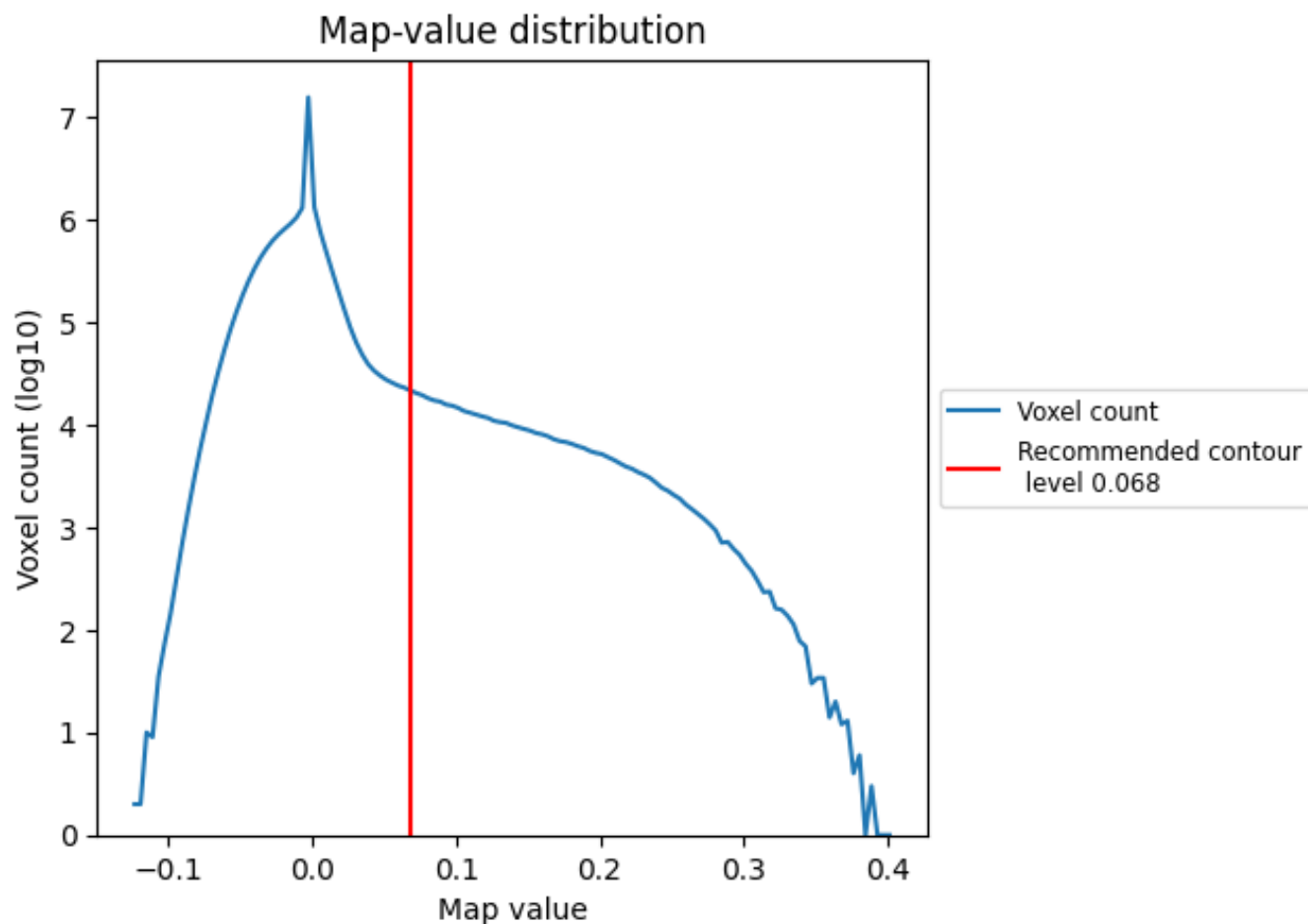


Z

7 Map analysis [i](#)

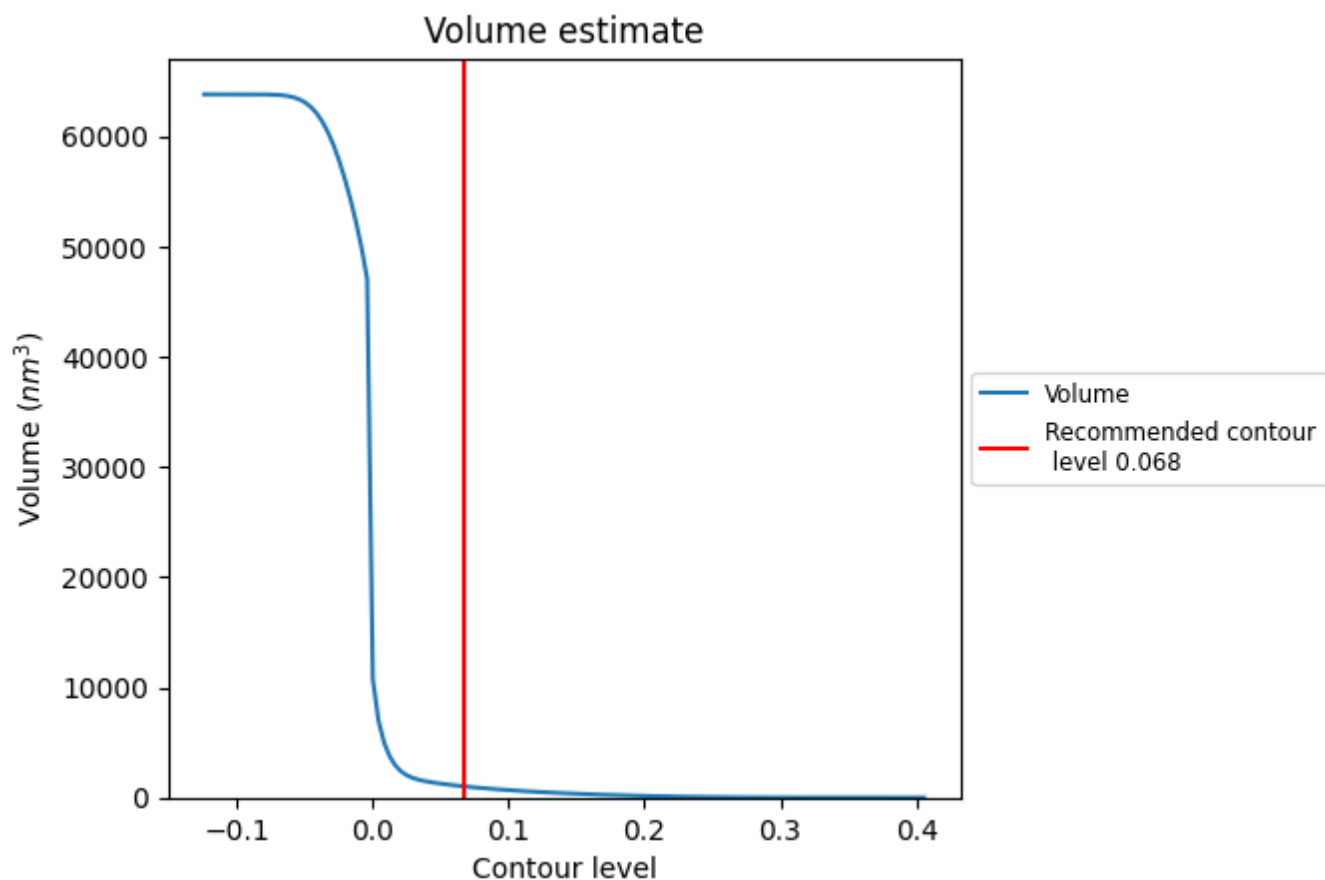
This section contains the results of statistical analysis of the map.

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.

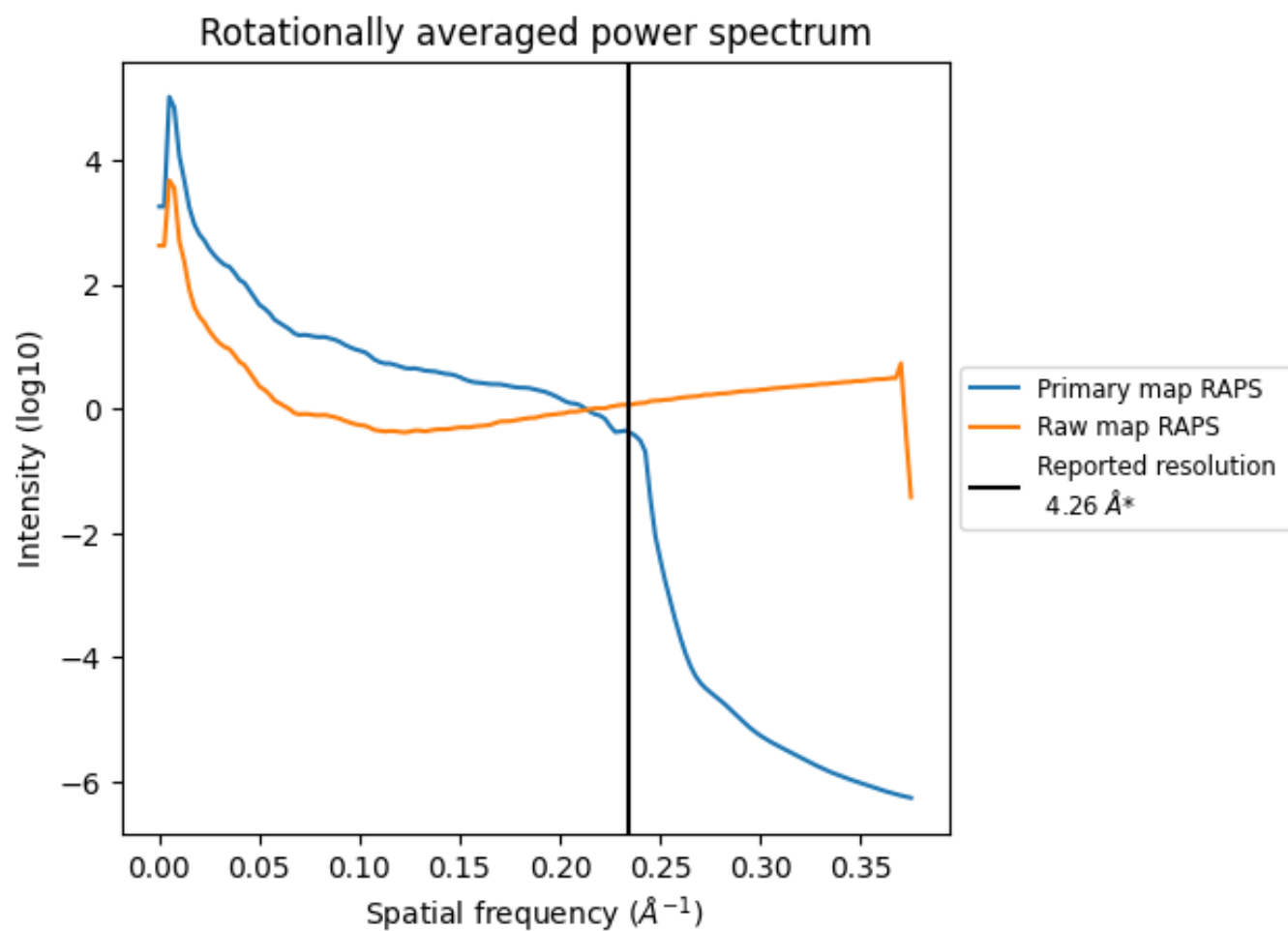
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1007 nm³; this corresponds to an approximate mass of 909 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 [i](#)

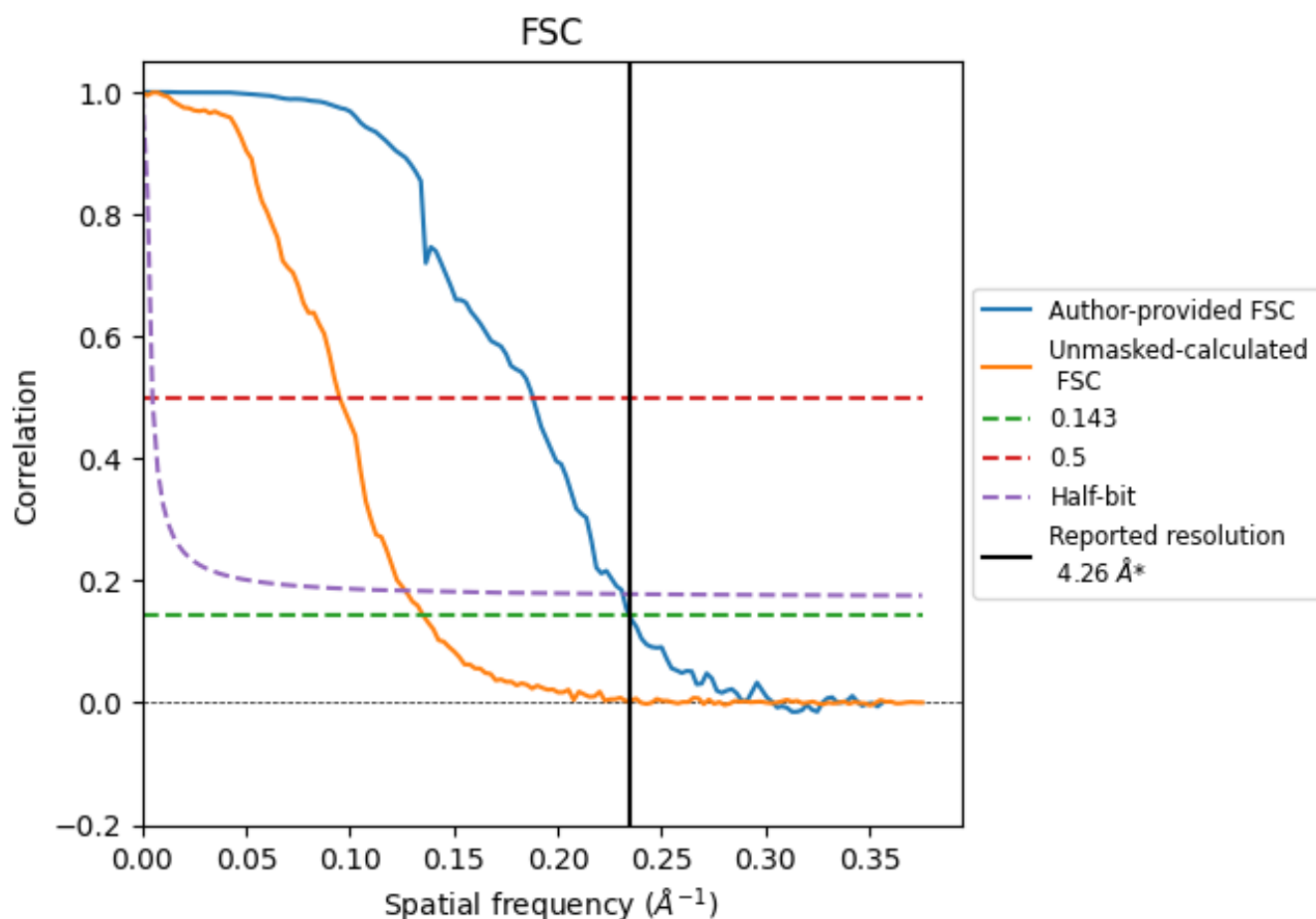


*Reported resolution corresponds to spatial frequency of 0.235 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.235 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.26	-	-
Author-provided FSC curve	4.26	5.32	4.33
Unmasked-calculated*	7.39	10.54	7.89

*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 7.39 differs from the reported value 4.26 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51976 and PDB model 9HA4. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

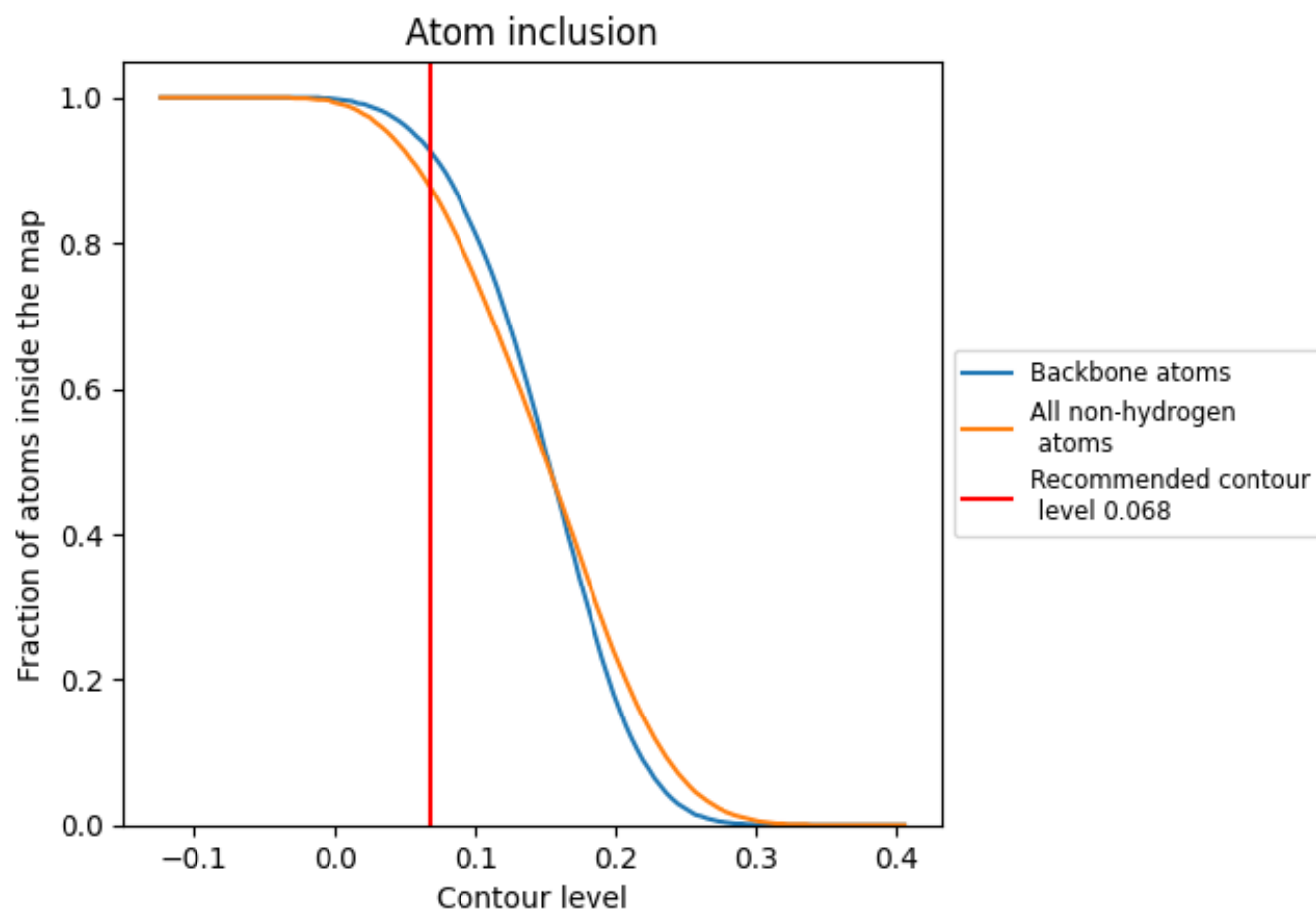


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 88% 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 (0.068) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.2460
2	 0.7220	 0.2150
A	 0.9270	 0.2560
B	 0.9340	 0.2180
D	 0.8350	 0.2810
E	 0.7720	 0.2660
F	 0.5400	 0.0790
J	 0.7870	 0.2590
K	 0.5420	 0.1750
L	 0.7090	 0.2160
N	 0.8170	 0.2360
O	 0.7030	 0.1250
P	 0.6590	 0.2030
Q	 0.8280	 0.2630
R	 0.7750	 0.2850
T	 0.7400	 0.2720
U	 0.8160	 0.2890
V	 0.7290	 0.1860
W	 0.8040	 0.2740
Y	 0.7700	 0.2040
Z	 0.8350	 0.2950
y	 0.0220	 0.0420

