



Full wwPDB EM Validation Report ⓘ

Mar 15, 2026 – 08:03 AM UTC

PDB ID : 9H3R / pdb_00009h3r
EMDB ID : EMD-51835
Title : 50S subunit precursor C-CP_YjgA_(L22)-
Authors : Lauer, S.; Nikolay, R.; Spahn, C.M.T.
Deposited on : 2024-10-17
Resolution : 4.12 Å(reported)
Based on initial model : 8RPY

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:

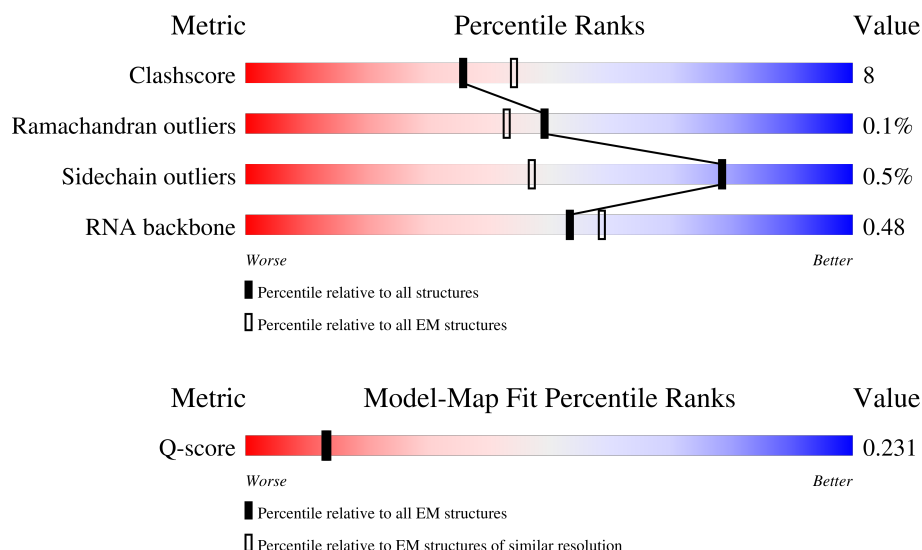
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.12 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.










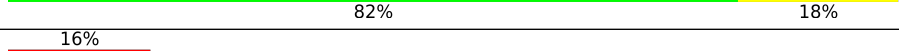
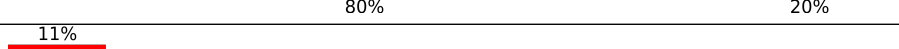
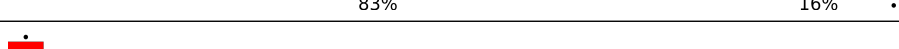
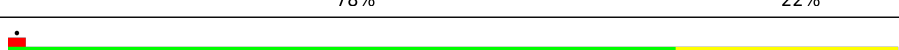

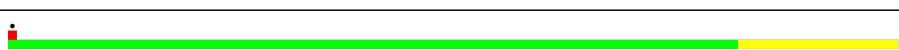

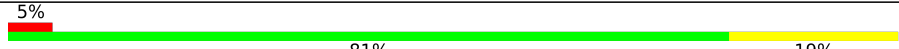





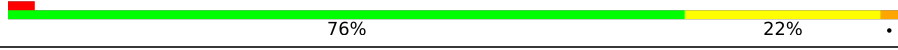

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5662 (3.62 - 4.62)

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	C	183	
2	2	46	
3	4	38	

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Mol	Chain	Length	Quality of chain
4	A	2903	
5	B	120	
6	D	209	
7	E	201	
8	F	177	
9	G	176	
10	H	149	
11	J	142	
12	K	122	
13	L	143	
14	N	120	
15	O	116	
16	P	114	
17	Q	117	
18	R	103	
19	T	93	
20	U	102	
21	V	94	
22	W	75	
23	X	77	
24	Y	63	
25	Z	58	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 77649 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 UPF0307 protein YjgA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	158	Total	C	N	O	S	0	0
			1298	805	253	238	2		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

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

- Molecule 3 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2576	Total	C	N	O	P	0	0
			55316	24673	10186	17881	2576		

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

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 10 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	51	Total	C	N	O	S	0	0
			395	253	72	69	1		

- Molecule 11 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 13 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 16 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 17 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 18 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 21 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 23 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL29.

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

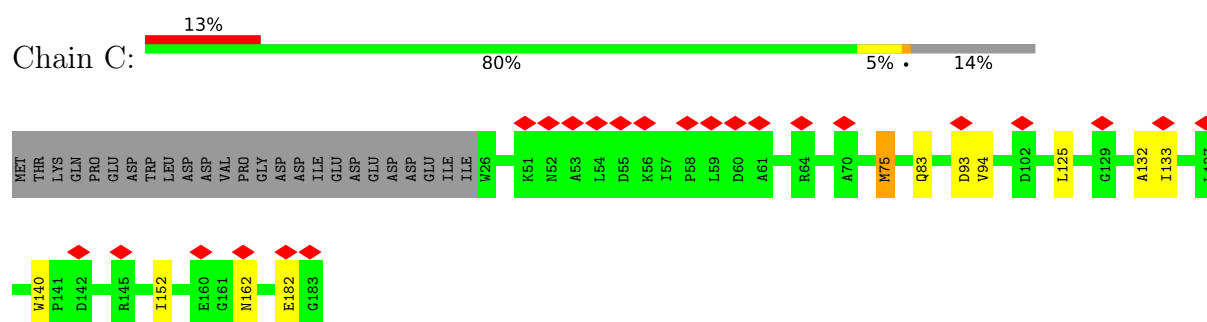
- Molecule 25 is a protein called Large ribosomal subunit protein uL30.

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

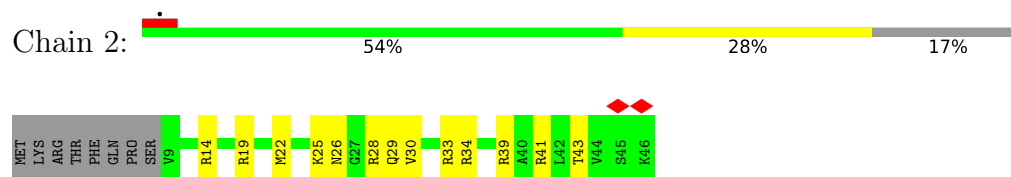
3 Residue-property plots [i](#)

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.

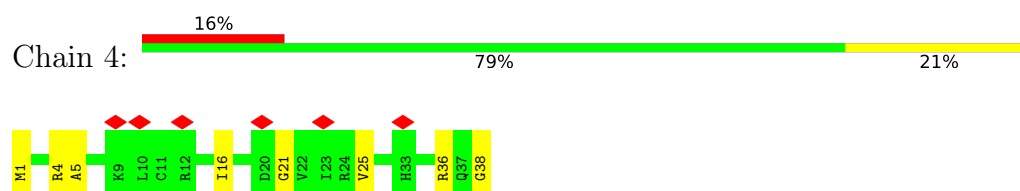
- Molecule 1: UPF0307 protein YjgA



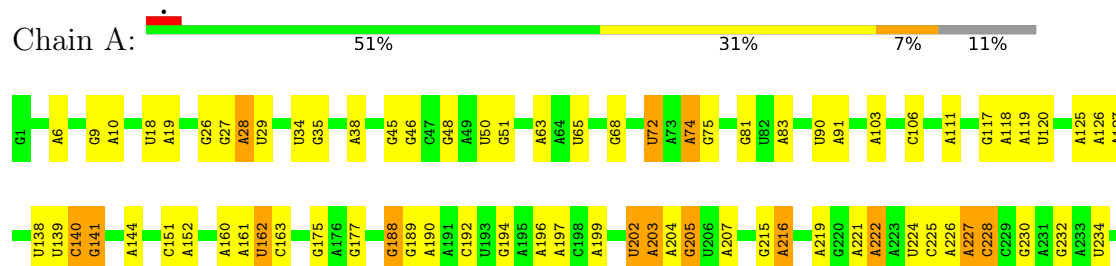
- Molecule 2: Large ribosomal subunit protein bL34

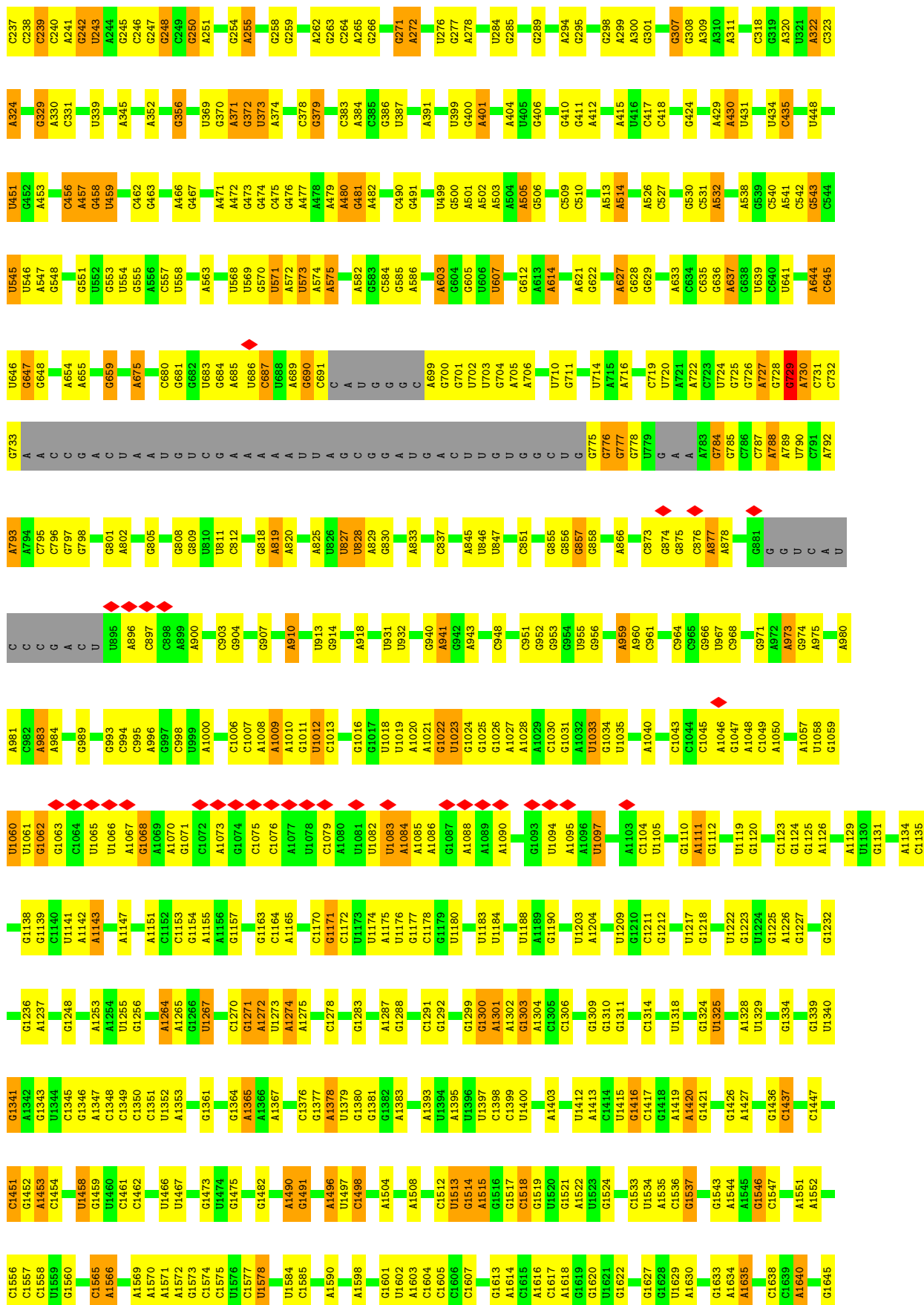


- Molecule 3: Large ribosomal subunit protein bL36A



- Molecule 4: 23S ribosomal RNA

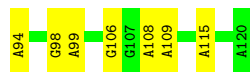
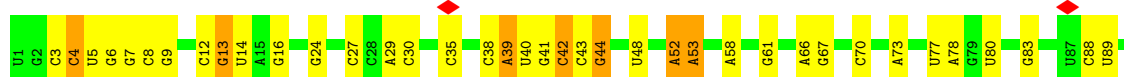




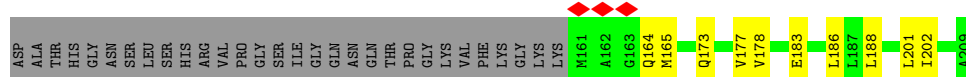
U2728	A2639	G2545	G2454	A2369	G2264	A2170	A2108	A2030	C	U	C	U	U	G1710	C1646
G2729	G2643	U2546	U2457	C2374	U2265	A2171	U2109	A2031	G	A	G	U	U	A1711	U1647
G2730	G2644	A2547	U2457	C2375	A2266	U2172	G2110	G2032	A	A	U	U	A	A1712	U1648
G2731	G2645	U2554	U2457	A2376	A2267	A2173	U2111	U2034	C	A	C	U	U	A1713	G1649
A2732	G2646	G2554	G2472	A2377	A2270	C2175	G2112	G2035	U	C	C	A	A	G1715	A1650
A2733	U2647	G2566	U2473	A2378	G2271	A2176	A2114	C2036	G	C	C	A	A	U1716	G1651
U2743	A2654	G2567	U2474	A2379	U2272	C2177	G2115	U2039	C	C	G	C	C	A1652	G1652
G2744	U2655	G2570	C2475	G2380	A2273	C2178	G2116	C2043	C	G	G	A	A	G1653	A1653
A2748	U2656	C2573	U2477	G2381	A2279	C2179	A2117	C2044	C	C	A	C	C	A1655	G1655
A2749	G2657	G2576	U2478	G2382	G2279	U2180	G2118	U2047	A	C	G	A	A	U1657	U1657
A2750	A2658	A2577	U2479	G2383	G2282	U2181	U2119	C2047	U	U	U	A	A	C1726	C1727
G2751	G2659	A2577	U2492	G2384	G2283	U2182	A2120	C2050	A	A	C	A	G	C1728	G1663
A2752	A2662	G2578	U2493	U2386	A2287	U2189	G2121	A2051	G	A	U	A	C	U1729	A1664
A2753	G2663	G2579	G2494	A2387	A2287	U2198	G2122	A2052	C	C	A	A	C	G1730	A1665
U2754	G2664	U2498	G2495	A2388	U2291	A2198	U2123	G2053	C	U	U	C	A	G1731	G1666
G2755	A2665	G2581	C2496	U2390	U2291	A2199	U2124	A2054	U	A	U	U	C	G1732	G1667
U2756	A2665	G2582	U2497	G2391	A2297	A2199	G2125	C2057	A	A	G	G	U	G1733	A1668
A2757	C2676	U2585	U2498	G2399	U2298	U2182	A2126	A2058	U	U	C	A	A	G1734	A1669
A2764	G2677	U2586	U2499	U2402	U2299	U2189	G2127	A2059	U	U	C	A	A	C1735	C1670
A2765	A2678	G2586	G2494	C2403	U2300	U2198	G2128	A2060	A	A	U	A	A	U1736	U
A2766	U2680	A2587	G2495	U2404	C2301	U2199	G2129	A2061	G	C	C	C	C	G1737	A
A2767	C2681	A2588	C2496	G2405	U2302	U2207	U2131	A2062	U	U	C	A	A	A1744	A
A2768	A2682	A2589	A2497	A2406	G2303	C2208	U2132	C2063	C	C	U	C	A	A1745	A
A2769	G2683	U2593	U2498	G2407	U2304	U2213	U2133	A2064	C	C	U	A	C	A1746	A
U2779	G2684	C2594	G2499	U2408	U2305	C2215	U2134	A2065	C	C	U	A	C	U1747	A
G2780	G2685	G2595	U2500	A2409	U2306	C2216	G2133	A2066	C	C	U	A	C	G1748	U
A2781	G2686	G2596	G2501	G2409	G2307	G2217	G2134	A2067	C	C	U	A	C	A1749	U
G2782	U2687	G2597	G2502	A2418	G2308	G2217	A2135	U2068	U	U	C	A	A	G1750	G
A2783	G2688	C2597	A2503	U2422	A2309	G2221	G2136	C2072	C	A	U	A	A	U1751	C
U2788	U2689	A2598	U2504	G2423	U2312	G2221	U2137	C2073	G	C	G	C	C	C1684	U
G2789	U2690	G2599	U2505	A2424	C2313	A2225	G2138	A2076	C	C	G	C	C	C1685	A
G2791	C2691	A2600	U2506	A2425	A2314	A2226	U2139	A2077	C	C	G	C	C	C1686	A
U2797	G2692	G2601	G2507	G2426	A2317	A2227	G2140	A2078	C	C	G	C	C	G1687	U
A2800	U2696	A2602	G2508	A2427	G2318	G2228	G2141	A2079	A	A	U	C	A	U1688	A
A2801	U2696	U2603	U2513	A2428	U2319	U2229	A2142	A2080	C	C	U	U	C	A	A
G2808	G2702	U2604	A2516	G2429	G2320	U2230	G2143	A2081	C	C	U	U	C	A	A
A2809	C2703	C2606	C2517	A2430	U2321	G2231	G2144	A2082	C	C	U	U	C	A	A
C2704	C2704	U2609	A2518	A2431	U2322	U2232	G2145	A2083	C	C	U	U	C	A	A
A2813	U2707	C2610	U2519	A2434	G2325	G2237	C2146	U2086	C	C	U	U	C	A	A
A2814	A2814	C2611	C2520	A2435	C2326	G2239	A2147	A2090	C	C	U	U	C	A	A
G2815	G2815	U2612	C2521	G2436	A2327	G2240	G2148	A2091	C	C	U	U	C	A	A
G2816	U2817	U2613	G2525	G2437	A2333	A2241	G2152	A2092	C	C	U	U	C	A	A
U2818	U2818	A2614	G2526	U2438	U2334	A2247	C2153	A2093	C	C	U	U	C	A	A
G2819	A2821	U2615	U2528	A2439	A2335	G2250	G2154	A2094	C	C	U	U	C	A	A
A2822	G2822	G2627	A2530	U2441	A2336	G2251	A2155	A2095	C	C	U	U	C	A	A
A2823	A2823	G2627	A2531	G2442	G2345	G2251	G2156	A2096	C	C	U	U	C	A	A
A2826	A2826	U2629	G2532	G2443	G2349	C2254	G2167	C2104	C	C	U	U	C	A	A
A2827	A2827	G2630	G2533	G2444	C2350	G2255	G2168	U2105	C	C	U	U	C	A	A
G2831	A2726	U2637	U2537	G2447	G2357	U2257	G2169	U2106	C	C	U	U	C	A	A
A2727	A2727	G2638	G2544	U2448	U2259	C2258	A2168	G2107	C	C	U	U	C	A	A
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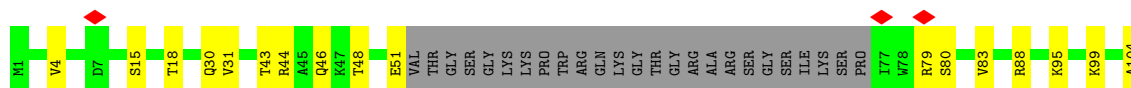
• Molecule 5: 5S ribosomal RNA



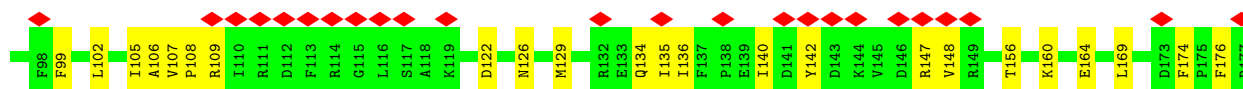
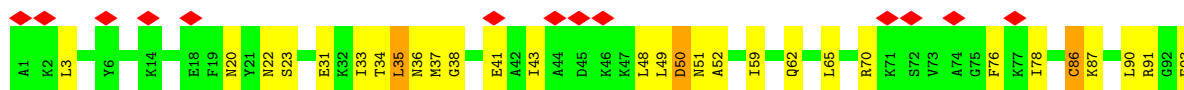
• Molecule 6: 50S ribosomal protein L3



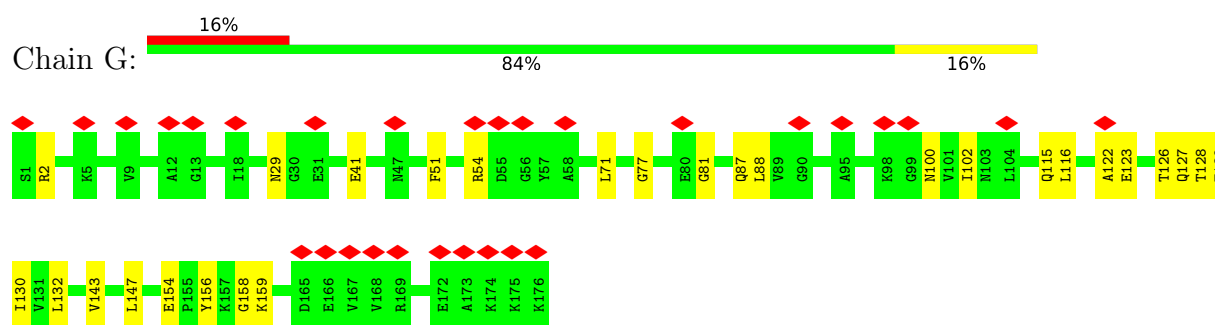
• Molecule 7: Large ribosomal subunit protein uL4



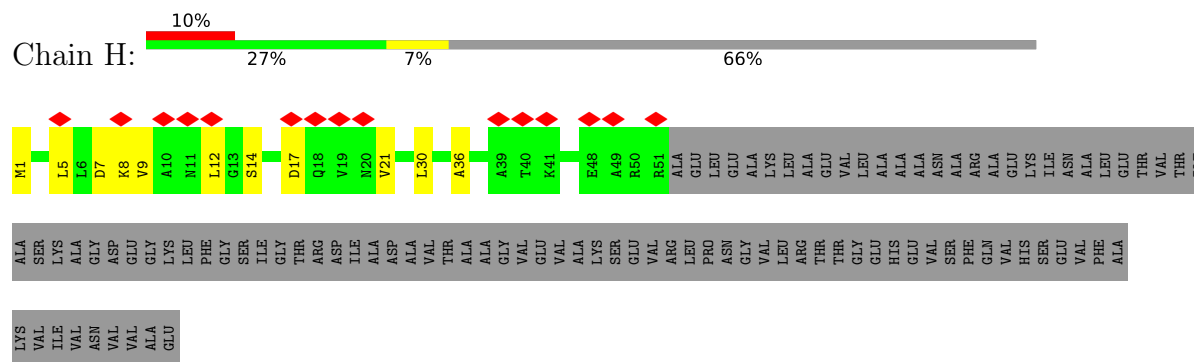
• Molecule 8: Large ribosomal subunit protein uL5



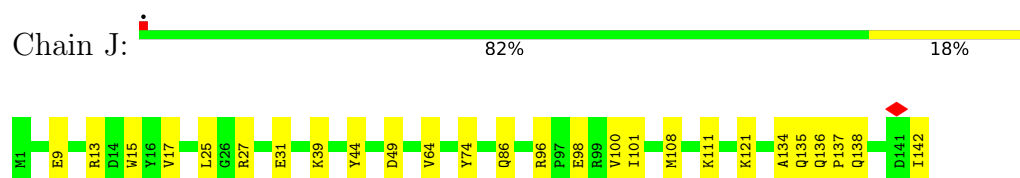
• Molecule 9: Large ribosomal subunit protein uL6



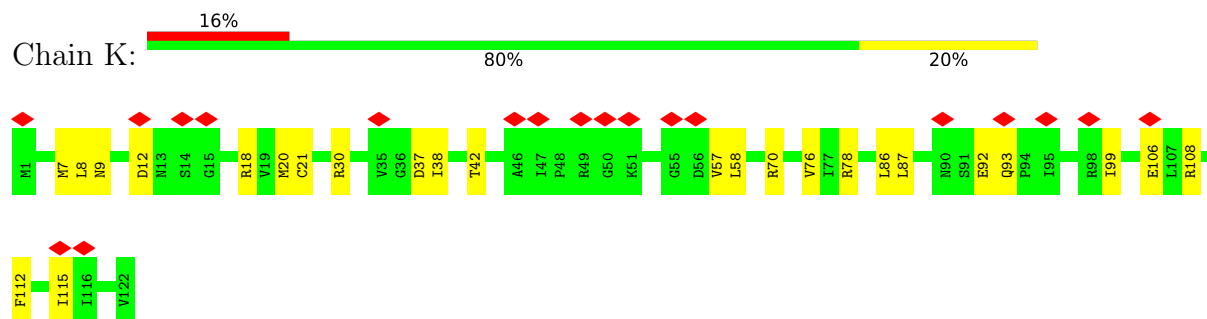
- Molecule 10: Large ribosomal subunit protein bL9



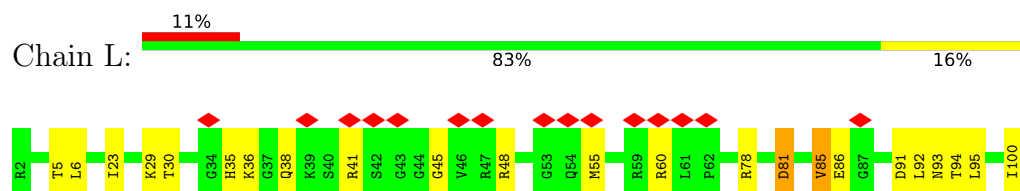
- Molecule 11: Large ribosomal subunit protein uL13




- Molecule 12: Large ribosomal subunit protein uL14



- Molecule 13: Large ribosomal subunit protein uL15




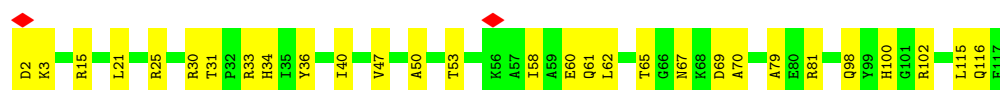
- Molecule 14: Large ribosomal subunit protein bL17

Chain N:  78% 22%




- Molecule 15: Large ribosomal subunit protein uL18

Chain O:  75% 25%




- Molecule 16: Large ribosomal subunit protein bL19

Chain P:  14% 83% 17%




- Molecule 17: Large ribosomal subunit protein bL20

Chain Q:  82% 18%




- Molecule 18: Large ribosomal subunit protein bL21

Chain R:  83% 16%




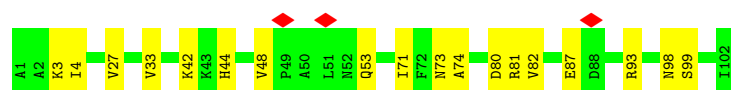
- Molecule 19: Large ribosomal subunit protein uL23

Chain T:  5% 81% 19%

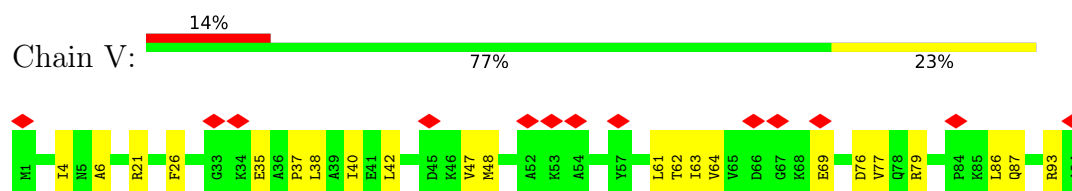


- Molecule 20: Large ribosomal subunit protein uL24

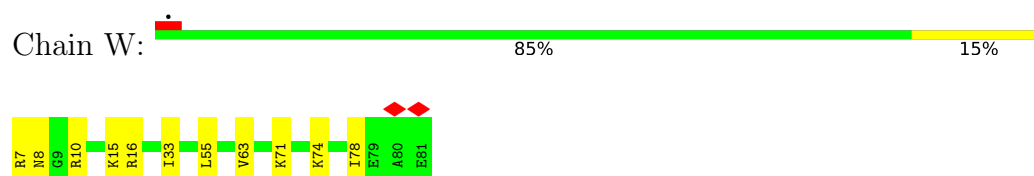
Chain U:  82% 18%



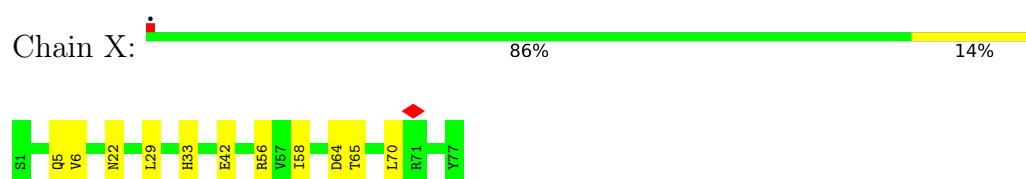
- Molecule 21: Large ribosomal subunit protein bL25



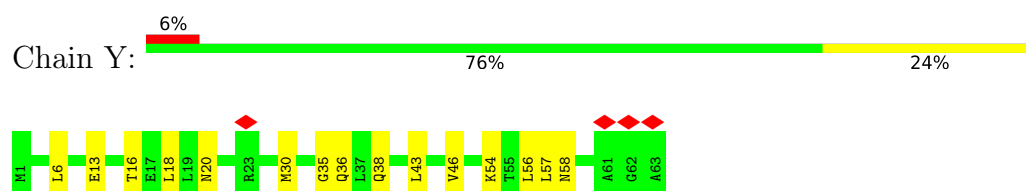
- Molecule 22: Large ribosomal subunit protein bL27



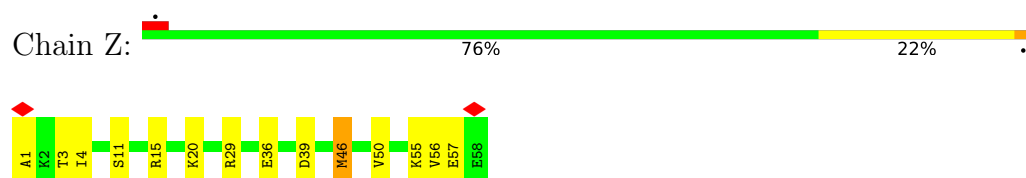
- Molecule 23: Large ribosomal subunit protein bL28



- Molecule 24: Large ribosomal subunit protein uL29



- Molecule 25: Large ribosomal subunit protein uL30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6435	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.582	Depositor
Minimum map value	-0.376	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.337	Depositor
Map size (Å)	424.0, 424.0, 424.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4133333, 1.4133333, 1.4133333	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	C	0.08	0/1311	0.19	0/1753
2	2	0.06	0/310	0.17	0/405
3	4	0.12	0/303	0.18	0/397
4	A	0.13	0/61949	0.23	1/96631 (0.0%)
5	B	0.07	0/2876	0.19	0/4483
6	D	0.08	0/1296	0.21	0/1742
7	E	0.09	0/1382	0.20	0/1860
8	F	0.11	0/1434	0.26	0/1926
9	G	0.09	0/1343	0.21	0/1816
10	H	0.11	0/400	0.24	0/537
11	J	0.09	0/1152	0.19	0/1551
12	K	0.10	0/947	0.25	0/1268
13	L	0.08	0/1054	0.26	0/1403
14	N	0.11	0/973	0.25	0/1301
15	O	0.08	0/902	0.23	0/1209
16	P	0.09	0/929	0.21	0/1242
17	Q	0.09	0/960	0.18	0/1278
18	R	0.11	0/829	0.27	0/1107
19	T	0.10	0/744	0.21	0/994
20	U	0.11	0/787	0.26	0/1051
21	V	0.11	0/766	0.24	0/1025
22	W	0.06	0/582	0.19	0/769
23	X	0.10	0/635	0.20	0/848
24	Y	0.12	0/510	0.30	0/677
25	Z	0.12	0/453	0.23	0/605
All	All	0.12	0/84827	0.23	1/127878 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	729	G	C2'-C3'-O3'	5.67	118.01	109.50

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	C	1298	0	1352	8	0
2	2	309	0	344	9	0
3	4	302	0	343	8	0
4	A	55316	0	27824	604	0
5	B	2572	0	1302	32	0
6	D	1284	0	1339	30	0
7	E	1368	0	1421	31	0
8	F	1410	0	1447	47	0
9	G	1323	0	1374	21	0
10	H	395	0	418	6	0
11	J	1129	0	1162	24	0
12	K	938	0	1012	18	0
13	L	1045	0	1117	22	0
14	N	960	0	1000	22	0
15	O	892	0	923	26	0
16	P	917	0	965	15	0
17	Q	947	0	1022	17	0
18	R	816	0	839	18	0
19	T	738	0	807	17	0
20	U	779	0	834	13	0
21	V	753	0	780	19	0
22	W	575	0	592	11	0
23	X	625	0	655	8	0
24	Y	509	0	543	8	0
25	Z	449	0	491	13	0
All	All	77649	0	49906	941	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 8.

All (941) 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)
4:A:775:G:OP2	4:A:778:G:O4'	1.54	1.25
4:A:775:G:O5'	4:A:777:G:N3	1.96	0.98
4:A:775:G:OP2	4:A:777:G:O2'	1.82	0.97
4:A:2123:G:C2	4:A:2176:A:N6	2.34	0.95
4:A:2676:C:O2	4:A:2732:G:N2	2.00	0.95
4:A:271:G:O2'	4:A:272:A:OP2	1.87	0.94
4:A:689:A:H3'	4:A:690:G:H5''	1.51	0.92
4:A:250:G:O2'	4:A:251:A:O4'	1.87	0.90
4:A:960:A:N3	4:A:2457:U:O2'	2.04	0.90
4:A:1172:C:O2	4:A:1177:G:N2	2.05	0.90
4:A:2377:A:O2'	4:A:2378:A:O4'	1.90	0.90
4:A:2898:U:O2'	11:J:134:ALA:O	1.89	0.89
4:A:2528:U:O4	4:A:2535:G:O6	1.88	0.89
4:A:1378:A:O2'	4:A:1380:G:N7	2.03	0.89
4:A:1007:C:OP2	4:A:1008:A:O2'	1.90	0.88
4:A:1650:A:O2'	4:A:1651:G:O4'	1.92	0.88
4:A:1324:G:O2'	4:A:1328:A:N6	2.07	0.88
4:A:161:A:O2'	4:A:2207:C:O2	1.91	0.87
4:A:1513:U:O2'	4:A:1514:G:O4'	1.93	0.86
4:A:675:A:N3	4:A:2443:C:O2'	2.09	0.86
4:A:700:G:H2'	4:A:701:G:C8	2.11	0.86
4:A:207:A:O2'	4:A:798:G:O2'	1.93	0.85
4:A:1462:C:O2'	4:A:2702:G:O2'	1.94	0.85
4:A:605:G:OP1	7:E:99:LYS:NZ	2.10	0.85
16:P:64:SER:OG	16:P:67:GLU:O	1.94	0.84
4:A:724:U:H4'	4:A:1566:A:H5'	1.60	0.84
4:A:1171:G:N2	4:A:1178:C:O2	2.11	0.83
4:A:2577:A:OP2	4:A:2610:C:O2'	1.96	0.83
4:A:1125:G:OP2	4:A:1126:A:O2'	1.96	0.83
4:A:2299:U:O4	4:A:2318:G:N2	2.11	0.83
4:A:2167:U:O2	4:A:2169:A:N7	2.10	0.83
4:A:1341:G:OP1	4:A:1602:U:O2'	1.97	0.83
6:D:33:ARG:NH2	6:D:53:GLY:O	2.12	0.83
4:A:612:G:N2	4:A:614:A:O2'	2.12	0.82
4:A:989:G:OP2	25:Z:11:SER:OG	1.97	0.82
4:A:48:G:N2	4:A:177:G:OP1	2.13	0.82
5:B:43:C:O2	8:F:91:ARG:NH1	2.12	0.82
7:E:46:GLN:O	7:E:88:ARG:NH2	2.13	0.81
4:A:1534:U:O2'	4:A:1537:G:O6	1.97	0.81
12:K:30:ARG:NH1	12:K:37:ASP:OD2	2.14	0.81
13:L:55:MET:O	13:L:60:ARG:NH1	2.13	0.81
4:A:126:A:O2'	4:A:127:A:O4'	1.97	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1515:A:O2'	4:A:1556:C:O2	1.98	0.80
4:A:627:A:OP1	13:L:78:ARG:NH1	2.15	0.80
4:A:83:A:O2'	4:A:103:A:N6	2.15	0.80
4:A:2333:A:OP2	22:W:71:LYS:NZ	2.14	0.79
4:A:320:A:N3	7:E:163:ASN:ND2	2.31	0.79
9:G:29:ASN:ND2	9:G:77:GLY:O	2.15	0.79
4:A:2659:G:N2	4:A:2662:A:OP2	2.16	0.79
4:A:784:G:O2'	4:A:790:U:O2'	2.00	0.79
4:A:2457:U:O2	4:A:2495:G:O6	2.00	0.79
4:A:820:A:OP2	4:A:973:A:N6	2.16	0.79
4:A:966:G:O4'	4:A:2267:A:N6	2.16	0.79
4:A:2258:C:O2'	4:A:2427:C:OP2	1.99	0.79
4:A:1513:U:O2'	4:A:1514:G:O5'	2.00	0.79
4:A:2479:U:OP1	4:A:2537:U:O2'	2.00	0.79
5:B:38:C:O2	5:B:44:G:N2	2.16	0.78
4:A:951:C:N4	4:A:952:G:O6	2.17	0.78
19:T:6:ARG:O	19:T:10:VAL:HG13	1.84	0.78
4:A:2291:U:O2'	4:A:2374:C:O2	2.02	0.78
4:A:2776:A:O2'	4:A:2782:G:N7	2.15	0.78
4:A:1648:U:O2'	4:A:1650:A:OP1	2.01	0.77
4:A:300:A:O2'	4:A:318:C:O2	2.01	0.77
4:A:910:A:O2'	4:A:2264:C:O2'	2.00	0.77
4:A:2788:C:O2'	4:A:2809:A:N3	2.17	0.77
6:D:16:THR:OG1	6:D:18:ASP:OD1	2.01	0.77
4:A:2092:U:O4	4:A:2227:A:N6	2.17	0.77
4:A:1009:A:O2'	4:A:1010:A:O4'	2.00	0.77
4:A:983:A:N6	4:A:2030:A:OP1	2.18	0.77
4:A:973:A:OP2	18:R:81:LYS:NZ	2.18	0.76
4:A:2110:G:N2	4:A:2180:U:O4	2.18	0.76
4:A:234:U:O4	4:A:263:G:N2	2.19	0.76
4:A:1019:U:OP1	4:A:1035:U:O2'	2.04	0.76
4:A:1217:U:O2	4:A:1232:G:O6	2.04	0.76
5:B:52:A:O2'	5:B:53:A:O5'	2.03	0.75
19:T:91:GLN:N	19:T:91:GLN:OE1	2.19	0.75
4:A:1009:A:O4'	17:Q:58:GLN:NE2	2.20	0.75
3:4:21:GLY:O	4:A:1123:C:O2'	2.05	0.74
4:A:2115:G:N2	4:A:2118:U:OP2	2.20	0.74
4:A:18:U:O4	4:A:19:A:N6	2.20	0.74
4:A:2692:G:N3	4:A:2847:U:O2'	2.21	0.74
21:V:6:ALA:HB2	21:V:63:ILE:HD11	1.69	0.74
5:B:38:C:N3	5:B:44:G:N1	2.36	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2849:U:O4'	4:A:2867:G:N2	2.21	0.74
10:H:14:SER:OG	10:H:17:ASP:OD2	2.05	0.74
9:G:88:LEU:O	9:G:128:THR:OG1	2.05	0.73
4:A:918:A:N3	5:B:80:U:O2'	2.21	0.73
8:F:51:ASN:OD1	8:F:52:ALA:N	2.21	0.73
4:A:2111:U:O4'	4:A:2118:U:O2'	2.06	0.73
4:A:775:G:O5'	4:A:777:G:H1'	1.89	0.73
4:A:993:G:OP2	17:Q:50:ARG:NH2	2.22	0.73
12:K:9:ASN:OD1	12:K:18:ARG:NH1	2.21	0.73
2:2:14:ARG:NH1	4:A:125:A:OP1	2.22	0.72
4:A:475:C:O2	4:A:479:A:N6	2.22	0.72
4:A:2679:A:N6	4:A:2729:G:O6	2.22	0.72
14:N:77:ALA:O	14:N:81:ASN:ND2	2.21	0.72
4:A:111:A:O2'	24:Y:58:ASN:OD1	2.06	0.72
4:A:1171:G:N1	4:A:1178:C:N3	2.38	0.72
4:A:1225:G:O2'	4:A:1226:A:O4'	2.05	0.72
4:A:2265:U:OP2	4:A:2266:A:O2'	2.05	0.72
4:A:2066:C:N4	4:A:2067:G:O6	2.22	0.72
4:A:2077:A:N3	4:A:2434:A:O2'	2.20	0.72
4:A:2017:U:O2'	4:A:2019:A:OP2	2.02	0.72
4:A:629:G:N3	4:A:639:U:O2'	2.23	0.71
4:A:680:C:N4	4:A:681:G:O6	2.23	0.71
4:A:1131:G:O6	4:A:2024:G:O2'	2.06	0.71
4:A:2682:A:N1	4:A:2728:U:O2'	2.23	0.71
4:A:216:A:N7	4:A:431:U:O2	2.23	0.71
4:A:541:A:N6	4:A:553:G:O6	2.24	0.71
4:A:2819:G:O3'	14:N:4:ARG:NH1	2.24	0.71
4:A:2528:U:OP2	4:A:2530:A:N6	2.23	0.71
4:A:1139:G:OP1	11:J:74:TYR:OH	2.07	0.70
4:A:1466:U:HO2'	4:A:1546:G:HO2'	1.35	0.70
4:A:2692:G:N2	4:A:2847:U:O3'	2.24	0.70
13:L:29:LYS:O	13:L:30:THR:OG1	2.08	0.70
4:A:775:G:OP2	4:A:777:G:C2'	2.39	0.70
4:A:1222:U:O2	4:A:1227:G:O6	2.08	0.70
4:A:1361:G:O2'	4:A:2215:C:O2'	1.99	0.70
4:A:1288:G:OP2	4:A:1288:G:N2	2.25	0.70
8:F:62:GLN:OE1	8:F:62:GLN:N	2.24	0.69
4:A:284:U:O2	4:A:356:G:O6	2.10	0.69
4:A:378:C:N4	4:A:379:G:O6	2.24	0.69
9:G:41:GLU:OE2	9:G:54:ARG:NH1	2.25	0.69
12:K:106:GLU:OE1	12:K:106:GLU:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:46:MET:O	25:Z:50:VAL:HG22	1.91	0.69
4:A:1466:U:O2'	4:A:1546:G:O2'	2.05	0.69
4:A:81:G:O2'	4:A:295:G:O2'	2.10	0.69
4:A:998:C:OP2	17:Q:57:ARG:NH2	2.26	0.69
4:A:237:C:N4	4:A:238:C:N4	2.40	0.69
4:A:941:A:O2'	4:A:1190:G:O3'	2.10	0.69
8:F:59:ILE:HG12	8:F:140:ILE:HD11	1.74	0.69
4:A:730:A:H2'	4:A:731:C:C6	2.27	0.69
4:A:2039:U:OP1	11:J:111:LYS:NZ	2.16	0.69
4:A:2687:U:O2	4:A:2722:G:O6	2.11	0.69
2:2:19:ARG:NH1	4:A:125:A:OP2	2.26	0.69
4:A:584:C:N4	4:A:585:G:O6	2.26	0.68
4:A:2816:G:N3	4:A:2883:A:O2'	2.26	0.68
4:A:570:G:OP1	18:R:80:ARG:NH2	2.25	0.68
4:A:453:A:N3	4:A:457:A:O2'	2.26	0.68
4:A:1604:C:C4	4:A:1605:C:N4	2.62	0.68
4:A:2043:C:OP1	4:A:2777:G:O2'	2.07	0.68
4:A:633:A:O2'	4:A:2404:U:OP1	2.12	0.68
21:V:35:GLU:OE2	21:V:93:ARG:NH1	2.27	0.68
4:A:585:G:O2'	4:A:586:A:O4'	2.11	0.68
5:B:77:U:O2	5:B:99:A:N7	2.27	0.68
4:A:18:U:O2'	4:A:554:U:OP1	2.10	0.68
4:A:2061:G:O2'	4:A:2063:C:OP2	2.11	0.67
4:A:457:A:N7	4:A:472:A:N6	2.42	0.67
12:K:93:GLN:N	12:K:93:GLN:OE1	2.27	0.67
4:A:1416:G:O2'	4:A:1417:C:O5'	2.11	0.67
4:A:2849:U:O2'	4:A:2866:U:O2	2.09	0.67
9:G:100:ASN:ND2	9:G:115:GLN:OE1	2.26	0.67
4:A:243:U:N3	4:A:255:A:C8	2.62	0.67
4:A:227:A:O2'	4:A:228:C:O5'	2.08	0.67
4:A:571:U:OP1	18:R:80:ARG:NE	2.27	0.67
4:A:2161:C:O2'	4:A:2173:A:O4'	2.09	0.67
4:A:383:C:N3	4:A:391:A:N6	2.42	0.67
4:A:1352:U:O2'	4:A:1570:A:N3	2.28	0.67
4:A:1687:G:H2'	4:A:1701:A:H61	1.60	0.67
4:A:1287:A:O2'	4:A:1288:G:O4'	2.12	0.67
4:A:2676:C:C2	4:A:2732:G:N2	2.61	0.67
4:A:1018:U:O2'	4:A:1120:G:N2	2.28	0.67
15:O:60:GLU:OE1	15:O:60:GLU:N	2.27	0.67
4:A:2424:C:O2	4:A:2429:G:O2'	2.09	0.66
4:A:2588:G:O6	4:A:2589:A:N6	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:93:ILE:HG21	18:R:4:VAL:HG11	1.78	0.66
4:A:2629:U:O2'	4:A:2630:G:O5'	2.14	0.66
4:A:1613:G:O2'	4:A:2008:C:N4	2.29	0.66
7:E:176:ASP:OD1	7:E:179:SER:OG	2.12	0.66
4:A:777:G:H2'	4:A:778:G:H8	1.61	0.66
4:A:1022:G:N2	4:A:1023:U:O4	2.27	0.66
18:R:49:ILE:HG22	18:R:54:VAL:HG12	1.78	0.66
4:A:1016:G:O6	4:A:1147:A:N6	2.29	0.66
4:A:1447:C:O2'	4:A:1544:A:N3	2.26	0.65
11:J:15:TRP:O	11:J:138:GLN:NE2	2.29	0.65
4:A:462:C:N4	4:A:463:G:O6	2.29	0.65
12:K:70:ARG:HD2	12:K:76:VAL:HG12	1.79	0.65
4:A:777:G:H2'	4:A:778:G:C8	2.32	0.65
4:A:1062:G:O2'	4:A:1063:G:O4'	2.15	0.65
25:Z:3:THR:HG23	25:Z:36:GLU:CD	2.21	0.65
4:A:700:G:H2'	4:A:701:G:H8	1.61	0.65
4:A:1172:C:N3	4:A:1177:G:N1	2.40	0.65
4:A:1604:C:N4	4:A:1605:C:N4	2.45	0.65
4:A:1209:U:O2'	4:A:1237:A:N1	2.30	0.64
4:A:1721:G:H21	4:A:1739:A:H62	1.45	0.64
4:A:117:G:OP2	4:A:119:A:O2'	2.07	0.64
4:A:873:C:N4	4:A:874:G:O6	2.31	0.64
1:C:83:GLN:OE1	4:A:2422:C:O2'	2.13	0.64
4:A:192:C:O2'	4:A:802:A:N3	2.30	0.64
8:F:22:ASN:OD1	8:F:23:SER:N	2.31	0.64
4:A:65:U:O2'	4:A:456:C:O2	2.12	0.64
4:A:1126:A:OP1	4:A:2487:G:O2'	2.15	0.64
19:T:12:ARG:NH2	19:T:34:VAL:O	2.30	0.64
4:A:188:G:O2'	4:A:1365:A:N6	2.31	0.64
4:A:627:A:N6	4:A:637:A:O5'	2.28	0.64
4:A:1992:G:N3	4:A:1994:C:N4	2.45	0.64
7:E:48:THR:OG1	7:E:51:GLU:OE1	2.16	0.64
4:A:2854:G:N1	4:A:2864:G:O6	2.31	0.64
11:J:31:GLU:CG	11:J:142:ILE:HD12	2.28	0.64
5:B:5:U:OP1	5:B:61:G:O2'	2.07	0.63
5:B:40:U:N3	5:B:44:G:OP2	2.30	0.63
4:A:298:G:O2'	4:A:322:A:N1	2.31	0.63
9:G:128:THR:HG23	9:G:129:GLU:OE1	1.98	0.63
5:B:14:U:OP2	5:B:70:C:O2'	2.16	0.63
4:A:2270:A:O2'	22:W:16:ARG:NH1	2.32	0.63
4:A:702:U:H2'	4:A:703:U:C6	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1272:A:O2'	4:A:1274:A:OP1	2.17	0.63
4:A:1353:A:N7	4:A:1377:G:N2	2.46	0.63
4:A:2123:G:C2	4:A:2176:A:C6	2.86	0.63
4:A:2731:G:O2'	4:A:2732:G:O5'	2.16	0.63
6:D:26:VAL:HG12	6:D:186:LEU:HD12	1.79	0.63
4:A:775:G:OP2	4:A:778:G:C1'	2.46	0.63
4:A:1218:G:N1	4:A:1232:G:N7	2.47	0.63
8:F:31:GLU:OE2	8:F:156:THR:OG1	2.08	0.63
11:J:13:ARG:NH2	11:J:49:ASP:O	2.32	0.63
4:A:959:A:O2'	4:A:960:A:O4'	2.13	0.62
4:A:1364:G:N2	4:A:1367:A:OP2	2.28	0.62
4:A:2457:U:O2	4:A:2495:G:C6	2.52	0.62
4:A:2508:G:O6	4:A:2580:U:O2	2.16	0.62
21:V:64:VAL:HG22	21:V:69:GLU:OE1	1.98	0.62
4:A:1030:C:N4	4:A:1031:G:O6	2.31	0.62
4:A:2821:A:OP2	6:D:115:GLY:N	2.31	0.62
6:D:99:GLU:N	6:D:99:GLU:OE1	2.31	0.62
7:E:140:ASP:OD1	7:E:141:MET:N	2.32	0.62
8:F:41:GLU:OE2	8:F:147:ARG:NH2	2.31	0.62
4:A:943:A:OP1	13:L:35:HIS:ND1	2.33	0.62
4:A:1006:C:O3'	11:J:39:LYS:NZ	2.31	0.62
6:D:183:GLU:OE1	6:D:183:GLU:N	2.33	0.62
12:K:108:ARG:NH2	16:P:32:VAL:O	2.32	0.62
21:V:62:THR:OG1	21:V:69:GLU:OE2	2.12	0.62
4:A:227:A:HO2'	4:A:228:C:P	2.22	0.62
4:A:1271:G:N1	4:A:1325:U:OP1	2.32	0.62
4:A:1614:A:N6	4:A:2010:G:O5'	2.31	0.62
15:O:69:ASP:OD1	15:O:70:ALA:N	2.33	0.62
15:O:116:GLN:N	15:O:116:GLN:OE1	2.32	0.62
5:B:48:U:OP1	15:O:30:ARG:NH2	2.33	0.61
25:Z:15:ARG:O	25:Z:20:LYS:NZ	2.33	0.61
21:V:21:ARG:NH2	21:V:87:GLN:O	2.34	0.61
25:Z:55:LYS:NZ	25:Z:57:GLU:OE2	2.32	0.61
4:A:2261:C:OP1	22:W:15:LYS:NZ	2.21	0.61
15:O:21:LEU:HD23	15:O:21:LEU:O	2.01	0.61
6:D:88:GLU:N	6:D:88:GLU:OE1	2.34	0.61
4:A:543:G:O6	4:A:551:G:N1	2.33	0.61
12:K:7:MET:C	12:K:8:LEU:HD12	2.26	0.60
4:A:1565:C:O2'	4:A:1566:A:O5'	2.19	0.60
11:J:31:GLU:HG3	11:J:142:ILE:HD12	1.82	0.60
4:A:725:G:H2'	4:A:726:G:H5'	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2123:G:N2	4:A:2176:A:N6	2.49	0.60
16:P:33:GLU:N	16:P:33:GLU:OE1	2.34	0.60
4:A:1700:A:H3'	4:A:1701:A:H8	1.67	0.60
6:D:3:GLY:C	6:D:4:LEU:HD12	2.27	0.60
12:K:58:LEU:HD11	12:K:86:LEU:HD12	1.84	0.60
4:A:237:C:N4	4:A:238:C:H41	2.00	0.60
4:A:582:A:OP1	17:Q:10:ARG:NH1	2.35	0.60
4:A:948:C:O2	4:A:984:A:O2'	2.19	0.60
4:A:2581:G:N2	4:A:2608:G:OP1	2.35	0.60
7:E:31:VAL:HG21	7:E:104:ALA:HB2	1.84	0.60
7:E:31:VAL:HG21	7:E:104:ALA:CB	2.32	0.60
12:K:12:ASP:HB3	12:K:99:ILE:HG22	1.84	0.60
4:A:829:A:N7	4:A:2247:A:O2'	2.34	0.59
4:A:2312:U:O2	8:F:36:ASN:ND2	2.35	0.59
4:A:2314:A:OP1	8:F:87:LYS:NZ	2.29	0.59
4:A:2623:G:OP1	4:A:2826:A:O2'	2.18	0.59
2:2:22:MET:O	2:2:28:ARG:NH2	2.34	0.59
4:A:245:G:O2'	4:A:384:A:N1	2.33	0.59
4:A:526:A:O2'	4:A:2043:C:O2	2.21	0.59
4:A:399:U:OP2	23:X:56:ARG:NH1	2.34	0.59
4:A:2345:G:O2'	4:A:2381:A:N3	2.29	0.59
4:A:2638:G:O2'	4:A:2778:A:N6	2.34	0.59
4:A:2676:C:N3	4:A:2732:G:N1	2.50	0.59
4:A:729:G:H1'	4:A:730:A:O4'	2.03	0.59
4:A:222:A:N6	4:A:232:G:O2'	2.34	0.59
4:A:1666:G:O2'	4:A:1667:G:N3	2.28	0.59
4:A:1667:G:O2'	4:A:1668:A:OP2	2.17	0.59
15:O:30:ARG:NH2	15:O:98:GLN:OE1	2.36	0.59
17:Q:88:GLU:O	18:R:11:GLN:NE2	2.34	0.59
20:U:48:VAL:O	20:U:53:GLN:NE2	2.35	0.59
4:A:1264:A:N6	4:A:2014:A:OP2	2.36	0.59
4:A:1270:C:O2	4:A:1325:U:O2'	2.09	0.59
17:Q:80:ASN:OD1	17:Q:84:LYS:NZ	2.34	0.59
4:A:627:A:O4'	4:A:637:A:N6	2.36	0.59
4:A:1701:A:H3'	4:A:1702:G:H8	1.68	0.59
11:J:49:ASP:OD1	11:J:121:LYS:NZ	2.29	0.59
13:L:93:ASN:OD1	13:L:94:THR:N	2.35	0.59
4:A:1223:G:N2	4:A:1226:A:OP2	2.34	0.59
5:B:39:A:O2'	5:B:40:U:O4'	2.20	0.59
9:G:122:ALA:HB1	9:G:130:ILE:HD11	1.86	0.58
6:D:26:VAL:CG1	6:D:186:LEU:HD12	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:728:G:H2'	4:A:729:G:C4	2.38	0.58
11:J:100:VAL:HG13	11:J:101:ILE:HD12	1.85	0.58
23:X:29:LEU:HD23	23:X:29:LEU:H	1.68	0.58
4:A:1094:U:N3	4:A:1097:U:OP2	2.36	0.58
14:N:19:ALA:O	14:N:23:ASN:ND2	2.36	0.58
4:A:301:G:OP2	20:U:81:ARG:NH2	2.36	0.58
1:C:140:TRP:NE1	1:C:182:GLU:OE1	2.37	0.58
4:A:2058:A:N6	4:A:2610:C:O4'	2.36	0.58
9:G:154:GLU:OE1	9:G:156:TYR:N	2.37	0.57
4:A:2474:U:O4	4:A:2529:G:N2	2.37	0.57
23:X:6:VAL:HG21	23:X:58:ILE:HD11	1.86	0.57
4:A:1732:C:O2'	4:A:1733:G:OP1	2.18	0.57
4:A:2375:G:N2	4:A:2378:A:OP2	2.37	0.57
4:A:1033:U:C2	4:A:2750:A:N6	2.73	0.57
25:Z:1:ALA:N	25:Z:39:ASP:O	2.38	0.57
4:A:2093:G:O2'	4:A:2198:A:N1	2.33	0.57
4:A:1413:A:N1	4:A:1590:A:N6	2.53	0.57
4:A:2637:U:O4	4:A:2776:A:N7	2.38	0.57
4:A:2314:A:H5'	8:F:34:THR:HG21	1.87	0.57
4:A:1278:C:H5''	14:N:34:ILE:HD11	1.87	0.57
4:A:1068:G:N2	4:A:1095:A:O2'	2.38	0.56
4:A:2457:U:C2	4:A:2495:G:O6	2.58	0.56
4:A:72:U:OP1	24:Y:54:LYS:NZ	2.29	0.56
4:A:1458:U:OP2	4:A:1459:G:N2	2.37	0.56
4:A:2587:A:OP2	4:A:2608:G:N2	2.39	0.56
15:O:31:THR:O	15:O:102:ARG:NH2	2.38	0.56
4:A:1000:A:OP2	4:A:1154:G:N1	2.37	0.56
4:A:1048:A:O2'	4:A:1112:G:N2	2.38	0.56
6:D:34:VAL:HA	6:D:50:VAL:HG12	1.88	0.56
8:F:160:LYS:N	8:F:164:GLU:OE2	2.36	0.56
12:K:58:LEU:HD12	12:K:87:LEU:O	2.05	0.56
12:K:37:ASP:OD1	12:K:38:ILE:N	2.39	0.56
4:A:644:A:O2'	4:A:645:C:O5'	2.17	0.56
4:A:819:A:HO2'	4:A:837:C:HO2'	1.50	0.56
4:A:1351:C:O2'	4:A:1571:A:O2'	2.00	0.56
15:O:31:THR:OG1	15:O:33:ARG:O	2.23	0.56
4:A:1024:G:OP2	4:A:1025:G:O2'	2.14	0.56
4:A:2076:U:OP2	4:A:2238:G:N2	2.38	0.56
4:A:2298:A:OP1	8:F:70:ARG:NH1	2.35	0.56
4:A:2627:G:O2'	4:A:2628:C:O4'	2.20	0.56
4:A:2831:G:N2	4:A:2884:U:OP2	2.29	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2090:A:N6	4:A:2230:G:O6	2.38	0.56
18:R:38:VAL:O	18:R:54:VAL:HG13	2.05	0.56
4:A:784:G:N2	4:A:793:A:OP2	2.37	0.56
21:V:26:PHE:CZ	21:V:47:VAL:HG11	2.41	0.56
4:A:262:A:N3	4:A:430:A:O2'	2.38	0.56
4:A:271:G:O2'	4:A:272:A:P	2.64	0.56
21:V:48:MET:HE1	21:V:86:LEU:HD12	1.87	0.56
4:A:586:A:N1	4:A:809:G:O2'	2.31	0.55
4:A:796:C:N4	4:A:797:G:O6	2.39	0.55
7:E:176:ASP:OD1	7:E:176:ASP:N	2.39	0.55
15:O:61:GLN:C	15:O:62:LEU:HD22	2.31	0.55
4:A:189:G:O6	4:A:205:G:O2'	2.11	0.55
4:A:374:A:N6	4:A:400:G:O2'	2.39	0.55
9:G:51:PHE:CE2	9:G:71:LEU:HD22	2.41	0.55
4:A:775:G:P	4:A:777:G:N3	2.80	0.55
4:A:68:G:N2	4:A:74:A:O5'	2.39	0.55
4:A:1604:C:N4	4:A:1605:C:H41	2.04	0.55
4:A:2684:U:O2'	12:K:78:ARG:NH2	2.35	0.55
11:J:135:GLN:N	11:J:135:GLN:OE1	2.40	0.55
4:A:647:G:N2	4:A:2350:C:O2'	2.40	0.55
4:A:1426:G:O2'	4:A:1572:A:N6	2.39	0.55
4:A:243:U:C2	4:A:255:A:N7	2.75	0.55
4:A:2637:U:H3	4:A:2776:A:H62	1.55	0.55
8:F:140:ILE:HG22	8:F:142:TYR:H	1.72	0.55
20:U:87:GLU:OE1	20:U:87:GLU:N	2.40	0.55
2:2:39:ARG:NH2	4:A:467:G:O6	2.40	0.55
4:A:2303:G:O6	4:A:2314:A:N6	2.40	0.55
4:A:776:G:H4'	4:A:777:G:C8	2.42	0.54
4:A:2576:G:O2'	4:A:2611:C:OP2	2.21	0.54
25:Z:3:THR:HG23	25:Z:36:GLU:OE2	2.07	0.54
4:A:1033:U:N3	4:A:2750:A:C6	2.76	0.54
6:D:24:VAL:HG12	6:D:178:VAL:HG21	1.90	0.54
16:P:30:TRP:NE1	16:P:81:ASP:OD2	2.40	0.54
19:T:4:GLU:HG3	24:Y:18:LEU:HD11	1.89	0.54
13:L:23:ILE:HD12	18:R:82:HIS:NE2	2.20	0.54
13:L:23:ILE:HG23	18:R:82:HIS:CE1	2.42	0.54
20:U:71:ILE:HD12	20:U:82:VAL:HG21	1.88	0.54
4:A:448:U:O4'	7:E:79:ARG:NE	2.41	0.54
4:A:140:C:OP2	4:A:141:G:N2	2.41	0.54
4:A:476:G:N1	4:A:479:A:OP2	2.39	0.54
11:J:17:VAL:HG23	11:J:137:PRO:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:29:VAL:HG11	14:N:75:ILE:HG23	1.90	0.54
4:A:216:A:N7	4:A:431:U:C2	2.76	0.54
4:A:271:G:HO2'	4:A:272:A:P	2.25	0.54
4:A:910:A:C2'	4:A:2264:C:HO2'	2.19	0.54
4:A:1572:A:C2	4:A:1573:G:C8	2.95	0.54
4:A:2595:G:O2'	4:A:2598:A:OP1	2.25	0.54
21:V:4:ILE:O	21:V:63:ILE:HD12	2.08	0.54
4:A:2123:G:N2	4:A:2176:A:C6	2.75	0.54
4:A:2472:G:N2	4:A:2479:U:O4	2.40	0.54
14:N:116:VAL:HG23	14:N:116:VAL:O	2.08	0.54
4:A:2094:A:O4'	4:A:2198:A:N6	2.39	0.54
4:A:953:G:O2'	4:A:2266:A:OP2	2.16	0.54
4:A:1300:G:O2'	4:A:1635:A:OP1	2.23	0.54
4:A:2375:G:O2'	4:A:2377:A:N6	2.41	0.54
16:P:54:LEU:HD23	16:P:54:LEU:O	2.07	0.54
15:O:67:ASN:ND2	15:O:69:ASP:OD1	2.42	0.53
4:A:2499:C:O2'	4:A:2500:U:O4'	2.22	0.53
25:Z:46:MET:HA	25:Z:46:MET:HE2	1.89	0.53
7:E:171:ASP:OD1	7:E:172:ALA:N	2.39	0.53
19:T:69:ARG:NH1	19:T:71:GLY:O	2.40	0.53
25:Z:4:ILE:HD11	25:Z:56:VAL:CG2	2.38	0.53
6:D:21:SER:C	6:D:22:ILE:HD12	2.33	0.53
4:A:1656:C:O2'	4:A:1657:U:O5'	2.22	0.53
4:A:1726:C:H2'	4:A:1727:C:O4'	2.08	0.53
22:W:7:ARG:NH1	22:W:8:ASN:OD1	2.42	0.53
4:A:482:A:N6	4:A:506:G:O2'	2.42	0.53
4:A:568:U:O4	18:R:80:ARG:NH1	2.38	0.53
21:V:48:MET:N	21:V:48:MET:HE2	2.24	0.53
5:B:38:C:O4'	15:O:100:HIS:NE2	2.42	0.53
3:4:4:ARG:NH2	4:A:2477:U:O2	2.42	0.52
4:A:714:U:O2'	4:A:716:A:N7	2.38	0.52
4:A:2167:U:N3	4:A:2169:A:OP2	2.42	0.52
4:A:2167:U:C2	4:A:2169:A:N7	2.78	0.52
20:U:80:ASP:OD1	20:U:81:ARG:N	2.41	0.52
4:A:1139:G:O2'	4:A:1143:A:N1	2.43	0.52
4:A:1730:C:O2'	4:A:1731:G:P	2.67	0.52
4:A:2808:G:O3'	4:A:2890:G:N1	2.42	0.52
8:F:50:ASP:OD1	8:F:51:ASN:N	2.42	0.52
7:E:155:GLU:OE1	7:E:155:GLU:N	2.39	0.52
13:L:38:GLN:NE2	13:L:45:GLY:O	2.42	0.52
20:U:3:LYS:O	20:U:93:ARG:NH1	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:538:A:O2'	11:J:9:GLU:OE1	2.28	0.52
4:A:1341:G:OP1	4:A:1397:U:N3	2.42	0.52
4:A:1350:C:H2'	4:A:1351:C:O4'	2.10	0.52
4:A:2349:G:O6	4:A:2369:A:N6	2.43	0.52
5:B:52:A:O2'	5:B:53:A:P	2.68	0.52
4:A:289:G:O6	4:A:352:A:N6	2.43	0.52
4:A:1318:U:O2	4:A:1334:G:O6	2.27	0.52
4:A:2730:C:H2'	4:A:2731:G:C8	2.44	0.52
19:T:7:LEU:O	19:T:10:VAL:HG22	2.09	0.52
15:O:61:GLN:O	15:O:62:LEU:HD22	2.09	0.52
7:E:79:ARG:O	7:E:80:SER:OG	2.23	0.52
4:A:481:G:OP2	20:U:44:HIS:N	2.42	0.51
4:A:644:A:HO2'	4:A:645:C:P	2.32	0.51
4:A:1048:A:N6	4:A:1110:G:O2'	2.43	0.51
7:E:51:GLU:OE1	7:E:51:GLU:N	2.43	0.51
4:A:1521:G:OP2	4:A:1522:A:O2'	2.26	0.51
4:A:2497:A:N3	4:A:2498:C:N4	2.57	0.51
16:P:14:GLN:OE1	16:P:14:GLN:N	2.44	0.51
4:A:827:U:OP2	4:A:828:U:N3	2.43	0.51
4:A:1668:A:H62	4:A:1704:C:H4'	1.74	0.51
21:V:76:ASP:OD1	21:V:77:VAL:N	2.44	0.51
4:A:373:U:O4	4:A:401:A:N7	2.43	0.51
4:A:1730:C:O2'	4:A:1731:G:OP2	2.24	0.51
4:A:240:C:OP2	4:A:241:A:O2'	2.26	0.51
5:B:38:C:N4	5:B:44:G:O6	2.41	0.51
13:L:95:LEU:HD11	13:L:100:ILE:HD11	1.93	0.51
14:N:69:ARG:O	14:N:70:THR:OG1	2.22	0.51
24:Y:35:GLY:O	24:Y:38:GLN:NE2	2.44	0.51
4:A:1203:U:OP2	4:A:1204:A:O2'	2.15	0.51
4:A:2854:G:H2'	4:A:2855:C:C6	2.46	0.51
7:E:4:VAL:HG23	7:E:4:VAL:O	2.11	0.51
14:N:34:ILE:HG23	14:N:113:ILE:CG2	2.40	0.51
15:O:58:ILE:O	15:O:62:LEU:HD23	2.11	0.51
4:A:237:C:C4	4:A:238:C:N4	2.79	0.50
4:A:1008:A:N3	4:A:1009:A:N6	2.55	0.50
4:A:2047:C:O2'	4:A:2823:A:N1	2.43	0.50
4:A:2260:C:O2	4:A:2388:A:O2'	2.27	0.50
13:L:23:ILE:HD12	18:R:82:HIS:CE1	2.46	0.50
15:O:50:ALA:O	15:O:81:ARG:NH1	2.45	0.50
23:X:5:GLN:O	23:X:70:LEU:HD11	2.11	0.50
4:A:1155:A:O3'	17:Q:54:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:99:ILE:HG21	12:K:115:ILE:HD11	1.92	0.50
6:D:165:MET:HA	6:D:165:MET:HE2	1.93	0.50
4:A:38:A:N3	7:E:43:THR:OG1	2.44	0.50
4:A:641:U:O4	4:A:648:G:N1	2.44	0.50
4:A:1647:U:O2'	4:A:1648:U:OP1	2.16	0.50
4:A:2134:A:N7	4:A:2157:G:O2'	2.44	0.50
15:O:2:ASP:OD1	15:O:3:LYS:N	2.44	0.50
18:R:21:ARG:O	18:R:22:LEU:HD12	2.11	0.50
4:A:513:A:C2'	4:A:514:A:O5'	2.59	0.50
4:A:554:U:H2'	4:A:555:G:O4'	2.11	0.50
4:A:2678:C:N4	4:A:2679:A:H62	2.09	0.50
1:C:75:MET:HE3	1:C:75:MET:HA	1.93	0.50
4:A:106:C:O2	4:A:294:A:O2'	2.26	0.50
4:A:1687:G:H2'	4:A:1701:A:N6	2.26	0.50
16:P:91:VAL:HG11	16:P:96:LEU:HD21	1.94	0.50
4:A:138:U:O4	19:T:3:ARG:NH1	2.45	0.50
4:A:2306:C:N4	8:F:38:GLY:O	2.43	0.50
12:K:42:THR:HG22	12:K:57:VAL:HG22	1.92	0.50
4:A:307:G:N1	4:A:309:A:O5'	2.45	0.50
4:A:1141:U:H4'	4:A:1142:A:O4'	2.12	0.50
4:A:1703:G:H2'	4:A:1704:C:O4'	2.12	0.50
10:H:7:ASP:OD1	10:H:8:LYS:N	2.40	0.50
10:H:30:LEU:HD13	10:H:36:ALA:HB3	1.94	0.50
4:A:463:G:N2	4:A:466:A:OP2	2.37	0.50
4:A:542:C:H2'	4:A:543:G:C8	2.46	0.50
4:A:687:C:H42	4:A:787:C:H4'	1.77	0.50
9:G:123:GLU:O	9:G:130:ILE:HD12	2.12	0.50
4:A:1084:A:O2'	4:A:1105:U:O3'	2.25	0.49
4:A:161:A:H3'	4:A:162:U:H5''	1.93	0.49
4:A:311:A:N6	4:A:329:G:OP1	2.46	0.49
4:A:1138:G:H21	11:J:108:MET:HE1	1.77	0.49
21:V:42:LEU:N	21:V:42:LEU:HD23	2.28	0.49
4:A:2091:C:H5	4:A:2092:U:HO2'	1.59	0.49
14:N:79:LEU:HD23	14:N:83:LEU:HD12	1.94	0.49
17:Q:13:HIS:O	17:Q:17:LEU:HD23	2.13	0.49
4:A:2443:C:N4	4:A:2444:G:O6	2.45	0.49
21:V:6:ALA:HB1	21:V:40:ILE:HG23	1.93	0.49
4:A:1543:G:O2'	4:A:1544:A:N7	2.43	0.49
4:A:2751:G:O4'	9:G:2:ARG:NH1	2.46	0.49
13:L:85:VAL:HG12	13:L:86:GLU:OE1	2.13	0.49
4:A:308:G:N2	4:A:477:A:N7	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:532:A:N1	4:A:2035:G:N2	2.61	0.49
4:A:724:U:H4'	4:A:1566:A:C5'	2.37	0.49
11:J:100:VAL:HG13	11:J:101:ILE:CD1	2.42	0.49
19:T:37:ASP:O	19:T:81:LYS:NZ	2.43	0.49
5:B:42:C:H5	8:F:65:LEU:HD13	1.76	0.49
8:F:33:ILE:O	8:F:90:LEU:HD23	2.13	0.49
14:N:28:LEU:HD13	14:N:34:ILE:HG22	1.94	0.49
14:N:90:ARG:NE	14:N:116:VAL:HG21	2.28	0.49
15:O:34:HIS:CE1	15:O:65:THR:HG21	2.47	0.49
17:Q:85:ALA:O	17:Q:86:SER:OG	2.24	0.49
1:C:125:LEU:HD22	1:C:152:ILE:HD11	1.93	0.49
4:A:202:U:H4'	4:A:203:A:OP1	2.13	0.49
4:A:966:G:H4'	4:A:2271:G:H22	1.77	0.49
4:A:1346:G:C2	4:A:1601:G:C6	3.01	0.49
4:A:1416:G:O2'	4:A:1417:C:O4'	2.28	0.49
4:A:1573:G:C5	4:A:1574:C:C5	3.00	0.49
4:A:242:G:H1'	4:A:243:U:OP2	2.13	0.48
4:A:324:A:N6	4:A:339:U:O4'	2.45	0.48
4:A:575:A:O4'	4:A:2499:C:O2'	2.30	0.48
4:A:1346:G:N1	4:A:1601:G:O6	2.46	0.48
15:O:53:THR:HB	15:O:65:THR:HG22	1.95	0.48
3:4:1:MET:SD	3:4:36:ARG:NH1	2.86	0.48
4:A:573:U:O4	4:A:2029:G:O2'	2.27	0.48
4:A:858:G:OP1	22:W:74:LYS:NZ	2.45	0.48
4:A:1033:U:C4	4:A:2750:A:N1	2.81	0.48
4:A:1291:C:N4	4:A:1292:G:O6	2.46	0.48
4:A:1601:G:H2'	4:A:1602:U:O4'	2.13	0.48
4:A:2748:A:N7	4:A:2754:U:O4	2.46	0.48
4:A:309:A:N3	4:A:329:G:O2'	2.41	0.48
4:A:1618:A:H2'	4:A:1650:A:OP2	2.14	0.48
13:L:91:ASP:OD1	13:L:92:LEU:N	2.40	0.48
14:N:57:THR:HG23	14:N:62:ASN:ND2	2.28	0.48
1:C:162:ASN:O	1:C:162:ASN:ND2	2.47	0.48
4:A:644:A:O2'	4:A:645:C:O4'	2.30	0.48
6:D:28:GLU:HA	6:D:186:LEU:HD13	1.96	0.48
4:A:1613:G:H21	4:A:1649:G:H21	1.61	0.48
21:V:79:ARG:HG3	21:V:86:LEU:HD23	1.96	0.48
4:A:2643:G:H2'	4:A:2644:G:C8	2.48	0.48
6:D:105:LYS:HA	6:D:177:VAL:HG12	1.95	0.48
6:D:108:ASP:OD2	6:D:173:GLN:NE2	2.47	0.48
4:A:242:G:H4'	4:A:243:U:O5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2576:G:OP1	4:A:2576:G:N2	2.46	0.48
4:A:2707:U:O2	14:N:71:ARG:NH1	2.45	0.48
4:A:161:A:O2'	4:A:2217:G:N2	2.47	0.48
4:A:729:G:C8	4:A:730:A:C8	3.02	0.48
4:A:1299:G:H22	4:A:1640:A:H5'	1.79	0.48
4:A:2202:U:O2	4:A:2221:G:O6	2.32	0.48
21:V:26:PHE:HZ	21:V:47:VAL:HG11	1.76	0.48
4:A:90:U:OP2	4:A:91:A:O2'	2.23	0.48
4:A:808:G:O6	13:L:41:ARG:NH1	2.47	0.48
4:A:1043:C:O2	4:A:1048:A:O2'	2.32	0.48
4:A:1267:U:H3	4:A:2013:A:H62	1.60	0.48
6:D:5:VAL:HG22	6:D:202:ILE:HD12	1.96	0.48
6:D:34:VAL:HG22	6:D:50:VAL:HG12	1.95	0.48
4:A:480:A:O2'	20:U:42:LYS:O	2.32	0.47
7:E:46:GLN:N	7:E:46:GLN:OE1	2.46	0.47
7:E:147:LEU:HD12	7:E:168:ASP:O	2.14	0.47
24:Y:16:THR:O	24:Y:20:ASN:ND2	2.41	0.47
4:A:1183:U:OP1	25:Z:29:ARG:NH2	2.47	0.47
4:A:1993:U:O2'	4:A:1994:C:O4'	2.30	0.47
4:A:2314:A:N3	8:F:126:ASN:ND2	2.61	0.47
4:A:2676:C:O2	4:A:2732:G:C2	2.65	0.47
4:A:728:G:C4	4:A:729:G:N7	2.82	0.47
4:A:1153:C:OP1	17:Q:91:ARG:NH1	2.41	0.47
8:F:3:LEU:HD13	8:F:99:PHE:CD2	2.49	0.47
13:L:81:ASP:OD1	13:L:81:ASP:N	2.47	0.47
4:A:994:C:OP1	17:Q:52:ARG:NH2	2.47	0.47
19:T:34:VAL:HG22	19:T:35:ALA:H	1.80	0.47
4:A:243:U:O2	4:A:255:A:N7	2.48	0.47
4:A:705:A:H2'	4:A:706:A:H5'	1.96	0.47
4:A:775:G:P	4:A:777:G:O2'	2.73	0.47
4:A:1218:G:OP2	17:Q:14:LYS:NZ	2.47	0.47
4:A:1490:A:H3'	4:A:1491:G:H5'	1.97	0.47
4:A:728:G:H2'	4:A:729:G:C5	2.49	0.47
4:A:828:U:O2'	4:A:829:A:O4'	2.32	0.47
4:A:1380:G:H2'	4:A:1381:G:C8	2.49	0.47
3:4:5:ALA:C	4:A:1124:G:H21	2.22	0.47
4:A:197:A:N6	4:A:2431:U:O4'	2.41	0.47
4:A:219:A:N3	4:A:234:U:O2'	2.48	0.47
4:A:903:C:N4	4:A:904:G:O6	2.48	0.47
4:A:2129:C:C2	4:A:2159:G:N2	2.82	0.47
4:A:2639:A:O3'	11:J:96:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2702:G:C2	4:A:2703:C:C5	3.03	0.47
11:J:31:GLU:HG2	11:J:142:ILE:HD12	1.94	0.47
4:A:370:G:O2'	4:A:424:G:OP1	2.30	0.47
4:A:571:U:N3	4:A:575:A:N7	2.63	0.47
7:E:15:SER:HB3	7:E:18:THR:HG22	1.97	0.47
7:E:161:ALA:CB	7:E:169:VAL:HG23	2.45	0.47
8:F:140:ILE:N	8:F:140:ILE:HD12	2.29	0.47
8:F:148:VAL:HG12	8:F:148:VAL:O	2.15	0.47
19:T:18:GLU:OE1	19:T:18:GLU:N	2.41	0.47
20:U:73:ASN:O	20:U:74:ALA:HB3	2.14	0.47
4:A:417:C:H2'	4:A:418:C:C6	2.50	0.47
4:A:1346:G:N2	4:A:1347:A:H1'	2.30	0.47
4:A:2855:C:H2'	4:A:2856:A:C8	2.50	0.47
18:R:59:ILE:HD12	18:R:101:ILE:HG12	1.97	0.47
4:A:68:G:N2	4:A:74:A:O4'	2.48	0.46
4:A:1267:U:O4	4:A:2013:A:N7	2.48	0.46
5:B:7:G:H21	15:O:47:VAL:HG21	1.80	0.46
5:B:27:C:O3'	15:O:36:TYR:OH	2.33	0.46
8:F:48:LEU:HD12	8:F:49:LEU:N	2.30	0.46
15:O:79:ALA:HB1	15:O:115:LEU:HD23	1.97	0.46
4:A:1184:U:OP1	25:Z:29:ARG:NE	2.46	0.46
4:A:2229:U:O2	23:X:33:HIS:NE2	2.47	0.46
5:B:6:G:C6	5:B:115:A:C6	3.03	0.46
14:N:103:ARG:NE	14:N:110:MET:SD	2.85	0.46
17:Q:55:GLN:O	17:Q:59:LEU:HD23	2.16	0.46
4:A:1060:U:O2'	4:A:1071:G:OP1	2.33	0.46
4:A:1062:G:N1	4:A:1071:G:OP2	2.48	0.46
4:A:1123:C:N4	4:A:1124:G:O6	2.48	0.46
4:A:2743:U:OP2	4:A:2755:C:N4	2.45	0.46
4:A:2881:U:O2'	14:N:95:THR:O	2.34	0.46
25:Z:4:ILE:HD11	25:Z:56:VAL:HG21	1.98	0.46
2:2:26:ASN:O	2:2:30:VAL:HG23	2.16	0.46
4:A:6:A:N3	11:J:135:GLN:NE2	2.64	0.46
4:A:866:A:N6	4:A:913:U:O4'	2.48	0.46
4:A:1171:G:O6	4:A:1178:C:N4	2.49	0.46
18:R:23:GLU:O	18:R:25:LEU:HD22	2.16	0.46
4:A:1012:U:O2	11:J:27:ARG:NH1	2.49	0.46
12:K:112:PHE:HB3	12:K:115:ILE:HG22	1.97	0.46
4:A:775:G:OP2	4:A:777:G:H2'	2.15	0.46
6:D:17:GLU:OE1	6:D:17:GLU:N	2.42	0.46
9:G:51:PHE:HE2	9:G:71:LEU:HD22	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:67:GLU:N	16:P:67:GLU:OE1	2.49	0.46
4:A:1684:G:H1'	4:A:1685:C:C6	2.51	0.46
6:D:24:VAL:HG23	6:D:24:VAL:O	2.15	0.46
15:O:98:GLN:OE1	15:O:98:GLN:N	2.45	0.46
21:V:48:MET:HE1	21:V:86:LEU:CD1	2.46	0.46
4:A:1084:A:N6	4:A:1085:A:N1	2.64	0.46
4:A:1350:C:H2'	4:A:1351:C:C6	2.51	0.46
4:A:1736:U:H2'	4:A:1737:G:C2	2.50	0.46
4:A:1274:A:H2'	4:A:1646:C:H42	1.80	0.46
8:F:37:MET:SD	8:F:86:CYS:N	2.89	0.46
4:A:238:C:H2'	4:A:239:C:O4'	2.16	0.45
4:A:685:A:H61	4:A:778:G:H1'	1.81	0.45
4:A:729:G:O2'	4:A:730:A:OP2	2.32	0.45
4:A:1517:G:O2'	4:A:1518:C:O5'	2.33	0.45
5:B:6:G:O6	5:B:115:A:N6	2.48	0.45
8:F:20:ASN:ND2	8:F:20:ASN:O	2.50	0.45
17:Q:88:GLU:N	17:Q:88:GLU:OE1	2.49	0.45
9:G:102:ILE:HD11	9:G:116:LEU:HG	1.97	0.45
19:T:4:GLU:OE1	19:T:4:GLU:N	2.42	0.45
4:A:471:A:OP1	7:E:79:ARG:NH1	2.45	0.45
4:A:1027:A:N6	4:A:1126:A:O4'	2.49	0.45
4:A:1398:C:C2	4:A:1399:C:C5	3.04	0.45
4:A:2123:G:N3	4:A:2176:A:C6	2.85	0.45
5:B:3:C:C2'	5:B:4:C:OP1	2.64	0.45
8:F:169:LEU:HD11	8:F:174:PHE:CD2	2.51	0.45
16:P:16:VAL:HG21	16:P:75:THR:CG2	2.46	0.45
18:R:74:ILE:N	18:R:74:ILE:HD12	2.31	0.45
4:A:194:G:N2	4:A:251:A:N3	2.64	0.45
4:A:540:C:N4	4:A:541:A:H62	2.14	0.45
4:A:2508:G:O6	4:A:2580:U:C2	2.69	0.45
5:B:83:G:O6	5:B:94:A:N6	2.48	0.45
4:A:1309:G:O6	4:A:1310:G:O6	2.34	0.45
4:A:2106:U:N3	4:A:2107:G:N7	2.65	0.45
10:H:5:LEU:HD21	10:H:9:VAL:HG23	1.98	0.45
15:O:67:ASN:OD1	15:O:67:ASN:N	2.49	0.45
18:R:1:MET:HE3	18:R:2:TYR:N	2.32	0.45
4:A:710:U:H2'	4:A:711:G:H8	1.81	0.45
19:T:89:GLU:OE1	19:T:89:GLU:N	2.43	0.45
23:X:64:ASP:OD1	23:X:65:THR:N	2.49	0.45
1:C:133:ILE:HD11	1:C:152:ILE:HD12	1.98	0.45
4:A:1301:A:O2'	4:A:1303:G:N7	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2657:A:H62	4:A:2664:G:H21	1.64	0.45
4:A:2688:G:N1	4:A:2720:U:OP2	2.45	0.45
4:A:500:G:O2'	4:A:505:A:N6	2.50	0.45
8:F:93:GLU:OE1	8:F:93:GLU:N	2.44	0.45
8:F:140:ILE:HD12	8:F:140:ILE:H	1.80	0.45
8:F:169:LEU:HD23	8:F:176:PHE:CZ	2.51	0.45
24:Y:6:LEU:HD13	24:Y:56:LEU:HD22	1.99	0.45
2:2:34:ARG:NH2	2:2:41:ARG:O	2.46	0.45
3:4:16:ILE:CD1	3:4:25:VAL:HG22	2.46	0.45
10:H:12:LEU:N	10:H:12:LEU:HD23	2.31	0.45
4:A:204:A:O2'	4:A:205:G:OP2	2.28	0.45
4:A:225:C:H2'	4:A:226:A:O4'	2.17	0.45
4:A:964:C:O2'	4:A:2273:A:N3	2.39	0.45
4:A:1700:A:H3'	4:A:1701:A:C8	2.51	0.45
4:A:2072:C:H2'	4:A:2073:C:C1'	2.47	0.45
4:A:2679:A:H2'	4:A:2680:U:C6	2.52	0.45
6:D:164:GLN:O	6:D:165:MET:HE2	2.16	0.45
4:A:1339:G:N1	4:A:1340:U:O4	2.49	0.44
4:A:1708:C:N4	4:A:2696:U:OP1	2.42	0.44
4:A:2399:G:O6	4:A:2418:A:N6	2.50	0.44
4:A:636:G:C8	13:L:128:THR:HG21	2.52	0.44
4:A:1049:C:H2'	4:A:1050:A:O4'	2.17	0.44
4:A:1650:A:O2'	4:A:1651:G:O5'	2.35	0.44
9:G:102:ILE:N	9:G:102:ILE:HD12	2.33	0.44
1:C:93:ASP:OD1	1:C:94:VAL:N	2.51	0.44
4:A:1653:G:O2'	4:A:1654:A:N7	2.49	0.44
5:B:78:A:H62	5:B:98:G:H21	1.66	0.44
8:F:134:GLN:O	8:F:140:ILE:HD13	2.17	0.44
4:A:194:G:N2	4:A:251:A:C4	2.85	0.44
4:A:557:C:H2'	4:A:558:U:O4'	2.17	0.44
22:W:33:ILE:HD12	22:W:33:ILE:N	2.32	0.44
1:C:125:LEU:HD23	1:C:132:ALA:HB3	1.99	0.44
4:A:369:U:O2'	4:A:370:G:N7	2.48	0.44
4:A:701:G:H2'	4:A:702:U:C6	2.53	0.44
4:A:1303:G:O6	4:A:1304:A:N6	2.50	0.44
4:A:2544:G:H2'	4:A:2545:G:C8	2.53	0.44
4:A:2657:A:O2'	9:G:159:LYS:NZ	2.51	0.44
5:B:9:G:OP1	15:O:25:ARG:NH1	2.50	0.44
16:P:3:ILE:O	16:P:7:LEU:HD23	2.17	0.44
4:A:203:A:OP2	4:A:204:A:O2'	2.36	0.44
4:A:299:A:O2'	4:A:300:A:O4'	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2306:C:H42	8:F:38:GLY:C	2.25	0.44
7:E:149:ILE:HD11	7:E:172:ALA:HA	2.00	0.44
7:E:153:LEU:C	7:E:153:LEU:HD23	2.42	0.44
14:N:106:ASP:N	14:N:106:ASP:OD1	2.51	0.44
21:V:26:PHE:CE1	21:V:42:LEU:HD21	2.52	0.44
4:A:636:G:N7	13:L:128:THR:HG21	2.33	0.44
4:A:955:U:N3	4:A:956:G:N7	2.66	0.44
4:A:1726:C:H2'	4:A:1727:C:C1'	2.48	0.44
10:H:1:MET:N	10:H:21:VAL:O	2.46	0.44
14:N:72:ASP:O	14:N:76:VAL:HG23	2.16	0.44
4:A:1638:C:OP1	4:A:2710:C:O2'	2.36	0.44
4:A:1707:G:H22	4:A:1751:U:H2'	1.83	0.44
5:B:73:A:N3	5:B:73:A:H2'	2.33	0.44
7:E:154:ASP:OD1	7:E:154:ASP:N	2.44	0.44
11:J:25:LEU:CD2	11:J:64:VAL:HG12	2.48	0.44
18:R:86:GLN:N	18:R:86:GLN:OE1	2.50	0.44
4:A:151:C:N4	4:A:152:A:N6	2.66	0.43
4:A:1129:A:O2'	4:A:2570:G:N2	2.51	0.43
8:F:35:LEU:HD12	8:F:35:LEU:N	2.33	0.43
4:A:2898:U:O2'	11:J:136:GLN:NE2	2.45	0.43
8:F:76:PHE:O	8:F:78:ILE:HG23	2.18	0.43
16:P:3:ILE:N	16:P:3:ILE:HD12	2.33	0.43
19:T:39:THR:HG23	19:T:42:GLU:H	1.83	0.43
23:X:42:GLU:OE1	23:X:42:GLU:N	2.51	0.43
4:A:818:G:N1	4:A:1188:U:OP2	2.44	0.43
4:A:877:A:O2'	4:A:900:A:N6	2.51	0.43
4:A:2436:G:H2'	4:A:2437:G:C8	2.53	0.43
4:A:2688:G:N2	4:A:2720:U:OP2	2.51	0.43
7:E:148:ILE:HB	7:E:169:VAL:HG22	2.00	0.43
9:G:126:THR:OG1	9:G:127:GLN:N	2.49	0.43
4:A:1720:U:H2'	4:A:1721:G:O4'	2.18	0.43
4:A:1726:C:H2'	4:A:1727:C:C6	2.54	0.43
4:A:2628:C:O2'	4:A:2782:G:OP1	2.29	0.43
6:D:68:PHE:CZ	6:D:79:LEU:HD21	2.53	0.43
2:2:43:THR:OG1	4:A:126:A:N6	2.52	0.43
4:A:258:G:H2'	4:A:259:G:C8	2.53	0.43
4:A:1451:C:H4'	4:A:1452:G:O4'	2.19	0.43
4:A:1496:A:H3'	4:A:1498:C:H41	1.82	0.43
4:A:1736:U:O2'	4:A:1737:G:N3	2.51	0.43
7:E:140:ASP:OD1	7:E:140:ASP:C	2.62	0.43
20:U:98:ASN:O	20:U:98:ASN:CG	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:61:LEU:HD12	21:V:61:LEU:H	1.84	0.43
4:A:1574:C:C2	4:A:1575:C:C5	3.06	0.43
11:J:44:TYR:O	17:Q:63:ARG:NE	2.50	0.43
4:A:710:U:H2'	4:A:711:G:C8	2.54	0.43
4:A:967:U:H2'	4:A:968:C:C6	2.54	0.43
4:A:2486:C:O2	4:A:2487:G:C8	2.72	0.43
5:B:8:C:O2'	15:O:40:ILE:HG21	2.19	0.43
5:B:29:A:H2'	5:B:30:C:C6	2.54	0.43
8:F:102:LEU:HD12	8:F:106:ALA:CB	2.48	0.43
9:G:143:VAL:O	9:G:147:LEU:HD23	2.19	0.43
4:A:9:G:O2'	4:A:2800:A:N6	2.52	0.43
4:A:701:G:O6	4:A:730:A:N6	2.51	0.43
4:A:1083:U:N3	4:A:1086:A:OP2	2.52	0.43
4:A:1736:U:O2'	4:A:1737:G:O4'	2.34	0.43
12:K:92:GLU:O	12:K:93:GLN:C	2.62	0.43
4:A:28:A:H2'	4:A:29:U:O4'	2.19	0.43
4:A:238:C:H2'	4:A:239:C:C1'	2.49	0.43
4:A:474:G:H3'	4:A:475:C:H5'	2.01	0.43
4:A:545:U:C4	4:A:548:G:O6	2.72	0.43
4:A:1577:C:H2'	4:A:1578:U:C1'	2.49	0.43
12:K:87:LEU:HD22	12:K:92:GLU:HA	2.00	0.43
16:P:112:ARG:C	16:P:113:LEU:HD23	2.43	0.43
4:A:144:A:H4'	19:T:2:ILE:HD11	2.01	0.42
4:A:2385:C:H2'	4:A:2386:A:C8	2.53	0.42
6:D:98:VAL:HG22	6:D:98:VAL:O	2.18	0.42
8:F:37:MET:HE3	8:F:52:ALA:HB1	2.01	0.42
8:F:129:MET:SD	8:F:129:MET:N	2.92	0.42
9:G:87:GLN:OE1	9:G:87:GLN:N	2.52	0.42
4:A:689:A:H3'	4:A:690:G:C5'	2.37	0.42
4:A:2875:C:H2'	4:A:2876:G:C8	2.54	0.42
8:F:51:ASN:OD1	8:F:51:ASN:C	2.62	0.42
4:A:691:C:O5'	4:A:699:A:H5''	2.19	0.42
4:A:1617:C:O2	4:A:1648:U:O2'	2.37	0.42
4:A:2082:A:N7	4:A:2239:G:N1	2.67	0.42
4:A:2302:U:O2'	8:F:122:ASP:O	2.27	0.42
6:D:85:ALA:N	6:D:88:GLU:OE2	2.51	0.42
9:G:154:GLU:O	9:G:158:GLY:N	2.50	0.42
20:U:4:ILE:HD12	20:U:27:VAL:HG11	2.00	0.42
4:A:1311:G:H21	4:A:1603:A:H62	1.68	0.42
4:A:1347:A:C5	4:A:1348:C:C6	3.07	0.42
14:N:34:ILE:HG23	14:N:113:ILE:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1664:A:H2'	4:A:1664:A:N3	2.33	0.42
6:D:22:ILE:HD12	6:D:22:ILE:N	2.34	0.42
7:E:149:ILE:HD13	7:E:188:MET:HE2	2.01	0.42
9:G:88:LEU:N	9:G:88:LEU:HD12	2.35	0.42
4:A:160:A:N3	4:A:2208:C:O2'	2.51	0.42
4:A:248:G:C5	4:A:250:G:N2	2.88	0.42
4:A:1551:A:H2'	4:A:1552:A:O4'	2.19	0.42
4:A:1557:C:OP2	4:A:1558:C:O2'	2.24	0.42
4:A:2318:G:H4'	4:A:2319:G:OP1	2.20	0.42
4:A:2520:C:H2'	4:A:2521:C:O4'	2.19	0.42
4:A:2703:C:H2'	4:A:2704:C:C6	2.54	0.42
9:G:132:LEU:H	9:G:132:LEU:HD23	1.85	0.42
14:N:57:THR:HG23	14:N:62:ASN:HD22	1.84	0.42
22:W:55:LEU:N	22:W:55:LEU:HD12	2.34	0.42
4:A:635:C:O2'	4:A:639:U:OP1	2.38	0.42
4:A:1513:U:HO2'	4:A:1514:G:C5'	2.22	0.42
4:A:2375:G:H21	4:A:2377:A:H8	1.68	0.42
19:T:10:VAL:O	19:T:35:ALA:N	2.52	0.42
4:A:2695:U:O2	4:A:2714:G:O6	2.38	0.42
5:B:42:C:C5	8:F:65:LEU:HD13	2.55	0.42
24:Y:43:LEU:HA	24:Y:46:VAL:HG22	2.02	0.42
4:A:527:C:N4	4:A:2777:G:O2'	2.49	0.42
4:A:956:G:O2'	4:A:959:A:N6	2.52	0.42
4:A:1264:A:OP2	4:A:1265:A:O2'	2.26	0.42
4:A:1629:U:O4	4:A:1630:A:N6	2.53	0.42
4:A:1715:G:N2	4:A:1744:A:OP2	2.42	0.42
4:A:2080:A:C6	4:A:2241:A:N6	2.88	0.42
4:A:2862:G:H2'	4:A:2863:C:O4'	2.20	0.42
6:D:188:LEU:HD12	6:D:188:LEU:N	2.35	0.42
4:A:659:G:N3	7:E:30:GLN:NE2	2.67	0.42
4:A:705:A:N6	4:A:727:A:C4	2.88	0.42
4:A:1352:U:C2	4:A:1378:A:N6	2.88	0.42
4:A:2255:G:C6	4:A:2256:G:C5	3.07	0.42
5:B:3:C:H3'	5:B:4:C:H5''	2.01	0.42
5:B:8:C:OP1	15:O:15:ARG:NH1	2.44	0.42
6:D:27:ILE:HD12	6:D:201:LEU:HB2	2.01	0.42
4:A:415:A:N6	4:A:2409:G:O6	2.53	0.41
4:A:1163:G:C2	4:A:1164:C:C5	3.07	0.41
4:A:239:C:O2'	4:A:622:G:O2'	2.38	0.41
4:A:251:A:OP1	13:L:48:ARG:NH2	2.49	0.41
4:A:451:U:O2	4:A:453:A:N6	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:940:G:H2'	4:A:941:A:O4'	2.20	0.41
4:A:1170:C:N4	4:A:1171:G:O6	2.53	0.41
4:A:1415:U:O2'	4:A:1416:G:H4'	2.20	0.41
9:G:77:GLY:O	9:G:81:GLY:N	2.53	0.41
21:V:6:ALA:HB1	21:V:40:ILE:CG2	2.49	0.41
4:A:371:A:O3'	4:A:372:G:H4'	2.20	0.41
4:A:434:U:O2	4:A:435:C:N4	2.46	0.41
4:A:955:U:O4	4:A:956:G:O6	2.38	0.41
4:A:1309:G:C6	4:A:1310:G:O6	2.74	0.41
4:A:1399:C:C2	4:A:1400:U:C5	3.08	0.41
4:A:1473:G:N1	4:A:1519:G:C6	2.89	0.41
4:A:2033:A:HO2'	4:A:2035:G:P	2.43	0.41
4:A:2050:C:H2'	4:A:2051:A:O4'	2.20	0.41
4:A:2487:G:C2	4:A:2488:G:C5	3.09	0.41
6:D:5:VAL:HG22	6:D:202:ILE:CD1	2.50	0.41
12:K:20:MET:SD	12:K:21:CYS:N	2.92	0.41
22:W:63:VAL:HA	22:W:78:ILE:HD13	2.03	0.41
4:A:391:A:O2'	4:A:410:G:OP1	2.33	0.41
4:A:703:U:C5	4:A:704:G:C5	3.09	0.41
4:A:1111:A:H2'	4:A:1112:G:O4'	2.20	0.41
4:A:1348:C:C2	4:A:1349:C:C6	3.09	0.41
4:A:1497:U:OP2	4:A:1498:C:N4	2.48	0.41
4:A:2312:U:OP1	8:F:70:ARG:N	2.43	0.41
8:F:105:ILE:O	8:F:109:ARG:NH1	2.47	0.41
13:L:92:LEU:O	13:L:92:LEU:HD23	2.20	0.41
3:4:16:ILE:HD12	3:4:25:VAL:HG22	2.02	0.41
4:A:851:C:C4'	25:Z:46:MET:HE3	2.51	0.41
4:A:2531:A:C2	4:A:2532:G:N7	2.88	0.41
4:A:2655:G:N2	4:A:2665:A:OP2	2.54	0.41
4:A:569:U:H1'	4:A:971:G:N2	2.35	0.41
4:A:705:A:H2'	4:A:706:A:C5'	2.51	0.41
4:A:793:A:H2'	4:A:793:A:N3	2.36	0.41
4:A:1301:A:H2'	4:A:1301:A:N3	2.35	0.41
4:A:1665:A:C2	4:A:1666:G:N7	2.89	0.41
4:A:2756:U:H4'	4:A:2757:A:OP1	2.19	0.41
4:A:2871:U:O2'	4:A:2872:A:N7	2.50	0.41
7:E:105:LEU:HD23	7:E:200:LEU:HD21	2.02	0.41
16:P:47:ILE:HD11	16:P:59:THR:HG21	2.02	0.41
16:P:54:LEU:HD23	16:P:54:LEU:C	2.45	0.41
4:A:1271:G:N2	4:A:1325:U:OP2	2.53	0.41
4:A:1649:G:N2	4:A:2008:C:N3	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2300:C:C2	4:A:2317:A:N6	2.89	0.41
8:F:37:MET:SD	8:F:37:MET:O	2.79	0.41
8:F:48:LEU:HD12	8:F:48:LEU:C	2.46	0.41
20:U:98:ASN:O	20:U:99:SER:C	2.63	0.41
22:W:63:VAL:HG22	22:W:78:ILE:CD1	2.51	0.41
2:2:30:VAL:HG22	2:2:33:ARG:NH2	2.35	0.41
4:A:475:C:N3	4:A:479:A:N7	2.68	0.41
4:A:1413:A:C6	4:A:1590:A:N6	2.89	0.41
4:A:2043:C:C2	4:A:2044:C:C5	3.08	0.41
4:A:2144:G:O2'	4:A:2146:C:O4'	2.24	0.41
4:A:2627:G:N2	4:A:2777:G:N3	2.68	0.41
4:A:2717:C:O2'	16:P:93:LYS:NZ	2.34	0.41
8:F:107:VAL:N	8:F:108:PRO:CD	2.84	0.41
19:T:37:ASP:OD1	19:T:37:ASP:N	2.53	0.41
2:2:25:LYS:NZ	2:2:29:GLN:OE1	2.19	0.41
3:4:38:GLY:O	4:A:1031:G:N2	2.53	0.41
4:A:499:U:O4	4:A:503:A:N7	2.54	0.41
4:A:499:U:H2'	4:A:500:G:O4'	2.21	0.41
4:A:513:A:O2'	4:A:514:A:O5'	2.39	0.41
4:A:689:A:C3'	4:A:690:G:H5''	2.35	0.41
4:A:1419:A:O2'	4:A:1420:A:H5'	2.20	0.41
4:A:2011:U:H2'	4:A:2012:G:O3'	2.21	0.41
4:A:2279:G:OP2	22:W:7:ARG:NH2	2.54	0.41
4:A:2531:A:H2'	4:A:2531:A:N3	2.36	0.41
5:B:39:A:H2'	5:B:40:U:C6	2.56	0.41
11:J:98:GLU:OE1	11:J:98:GLU:N	2.48	0.41
13:L:5:THR:O	13:L:5:THR:HG22	2.20	0.41
14:N:45:ARG:HG2	14:N:113:ILE:HD11	2.03	0.41
14:N:103:ARG:NH2	14:N:110:MET:SD	2.91	0.41
15:O:40:ILE:CD1	15:O:47:VAL:HG22	2.51	0.41
20:U:27:VAL:HG12	20:U:33:VAL:HG12	2.02	0.41
4:A:603:A:N6	4:A:655:A:O4'	2.54	0.41
5:B:14:U:O4'	5:B:106:G:N2	2.52	0.41
8:F:169:LEU:HD11	8:F:174:PHE:CE2	2.56	0.41
13:L:93:ASN:O	13:L:94:THR:OG1	2.33	0.41
4:A:417:C:H2'	4:A:418:C:O4'	2.21	0.40
4:A:788:A:N6	4:A:795:C:O4'	2.48	0.40
4:A:981:A:HO2'	4:A:2036:C:HO2'	1.57	0.40
4:A:1453:A:N6	14:N:73:ASN:OD1	2.54	0.40
4:A:2282:G:N2	4:A:2390:U:O2	2.41	0.40
5:B:13:G:N2	5:B:16:G:N3	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:135:ILE:HD12	8:F:142:TYR:CD2	2.56	0.40
13:L:116:VAL:O	13:L:116:VAL:HG13	2.19	0.40
19:T:6:ARG:NH2	19:T:37:ASP:OD2	2.55	0.40
4:A:202:U:O3'	4:A:203:A:O4'	2.39	0.40
4:A:246:C:H2'	4:A:247:G:O4'	2.20	0.40
4:A:543:G:O6	4:A:551:G:C6	2.74	0.40
4:A:775:G:P	4:A:778:G:O4'	2.71	0.40
4:A:808:G:OP2	13:L:36:LYS:NZ	2.54	0.40
4:A:1436:G:H3'	4:A:1437:C:H5''	2.03	0.40
4:A:2079:U:O2'	23:X:22:ASN:OD1	2.34	0.40
4:A:2682:A:C6	6:D:11:MET:HE1	2.57	0.40
4:A:2702:G:N3	4:A:2702:G:H2'	2.36	0.40
11:J:86:GLN:OE1	11:J:86:GLN:N	2.50	0.40
17:Q:68:ALA:HB1	17:Q:73:ILE:HG23	2.03	0.40
21:V:37:PRO:C	21:V:38:LEU:HD22	2.46	0.40
4:A:699:A:N3	4:A:699:A:H2'	2.36	0.40
4:A:719:C:H2'	4:A:720:U:O4'	2.20	0.40
4:A:1164:C:C2	4:A:1165:A:C8	3.09	0.40
4:A:1627:G:C2	4:A:1640:A:C8	3.10	0.40
4:A:2279:G:N7	22:W:10:ARG:NH2	2.69	0.40
4:A:2375:G:N1	4:A:2379:G:O6	2.55	0.40
4:A:2813:A:C2	4:A:2814:A:C8	3.10	0.40
8:F:43:ILE:HD12	8:F:43:ILE:N	2.35	0.40
4:A:458:G:O2'	4:A:459:U:P	2.80	0.40
4:A:501:A:H2'	4:A:502:A:O4'	2.22	0.40
4:A:607:U:OP1	7:E:95:LYS:NZ	2.49	0.40
4:A:825:A:C6	4:A:833:A:N6	2.89	0.40
4:A:856:G:H3'	4:A:857:G:C8	2.57	0.40
4:A:1412:U:O4	4:A:1413:A:N6	2.55	0.40
6:D:12:THR:OG1	6:D:13:ARG:N	2.54	0.40
8:F:109:ARG:NH2	8:F:136:ILE:O	2.53	0.40
24:Y:13:GLU:HG3	24:Y:57:LEU:HD21	2.03	0.40
3:4:5:ALA:O	4:A:1124:G:N2	2.54	0.40
4:A:545:U:O4	4:A:548:G:O6	2.40	0.40
4:A:1248:G:OP1	7:E:44:ARG:NH1	2.55	0.40
4:A:2254:C:C2	4:A:2255:G:C8	3.10	0.40
4:A:2499:C:H2'	4:A:2500:U:C6	2.56	0.40
18:R:1:MET:HE3	18:R:1:MET:HA	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	C	156/183 (85%)	152 (97%)	4 (3%)	0	100	100
2	2	36/46 (78%)	36 (100%)	0	0	100	100
3	4	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
6	D	169/209 (81%)	165 (98%)	4 (2%)	0	100	100
7	E	172/201 (86%)	167 (97%)	4 (2%)	1 (1%)	21	58
8	F	175/177 (99%)	168 (96%)	7 (4%)	0	100	100
9	G	174/176 (99%)	169 (97%)	5 (3%)	0	100	100
10	H	49/149 (33%)	46 (94%)	3 (6%)	0	100	100
11	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
12	K	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
13	L	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
14	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
15	O	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
16	P	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	101/103 (98%)	95 (94%)	5 (5%)	1 (1%)	12	46
19	T	91/93 (98%)	85 (93%)	6 (7%)	0	100	100
20	U	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
21	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
22	W	73/75 (97%)	72 (99%)	1 (1%)	0	100	100
23	X	75/77 (97%)	75 (100%)	0	0	100	100
24	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
25	Z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
All	All	2476/2718 (91%)	2385 (96%)	89 (4%)	2 (0%)	49	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	R	54	VAL
7	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	C	137/161 (85%)	136 (99%)	1 (1%)	76	79
2	2	30/38 (79%)	30 (100%)	0	100	100
3	4	34/34 (100%)	34 (100%)	0	100	100
6	D	134/164 (82%)	134 (100%)	0	100	100
7	E	146/165 (88%)	146 (100%)	0	100	100
8	F	148/148 (100%)	145 (98%)	3 (2%)	48	66
9	G	137/137 (100%)	137 (100%)	0	100	100
10	H	41/114 (36%)	41 (100%)	0	100	100
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	103/103 (100%)	103 (100%)	0	100	100
13	L	102/102 (100%)	99 (97%)	3 (3%)	37	58
14	N	100/100 (100%)	100 (100%)	0	100	100
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	99/99 (100%)	99 (100%)	0	100	100
17	Q	89/89 (100%)	89 (100%)	0	100	100
18	R	84/84 (100%)	83 (99%)	1 (1%)	63	73
19	T	80/80 (100%)	80 (100%)	0	100	100
20	U	83/83 (100%)	83 (100%)	0	100	100
21	V	78/78 (100%)	78 (100%)	0	100	100
22	W	57/57 (100%)	57 (100%)	0	100	100
23	X	67/67 (100%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	Y	55/55 (100%)	53 (96%)	2 (4%)	31	53
25	Z	48/48 (100%)	47 (98%)	1 (2%)	47	65
All	All	2054/2208 (93%)	2043 (100%)	11 (0%)	78	82

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	75	MET
8	F	35	LEU
8	F	50	ASP
8	F	86	CYS
13	L	6	LEU
13	L	81	ASP
13	L	85	VAL
18	R	25	LEU
24	Y	30	MET
24	Y	36	GLN
25	Z	46	MET

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

Mol	Chain	Res	Type
6	D	36	GLN
7	E	30	GLN
7	E	163	ASN
9	G	44	HIS
13	L	38	GLN
13	L	104	GLN
14	N	81	ASN
15	O	29	HIS
15	O	38	GLN
17	Q	55	GLN
17	Q	65	ASN
18	R	82	HIS
22	W	53	HIS
25	Z	19	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	2568/2903 (88%)	541 (21%)	17 (0%)
5	B	119/120 (99%)	17 (14%)	2 (1%)
All	All	2687/3023 (88%)	558 (20%)	19 (0%)

All (558) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	10	A
4	A	26	G
4	A	27	G
4	A	28	A
4	A	34	U
4	A	35	G
4	A	45	G
4	A	46	G
4	A	50	U
4	A	51	G
4	A	63	A
4	A	72	U
4	A	74	A
4	A	75	G
4	A	118	A
4	A	120	U
4	A	139	U
4	A	140	C
4	A	141	G
4	A	162	U
4	A	163	C
4	A	175	G
4	A	188	G
4	A	190	A
4	A	196	A
4	A	199	A
4	A	203	A
4	A	205	G
4	A	215	G
4	A	216	A
4	A	221	A
4	A	222	A
4	A	224	U
4	A	228	C
4	A	230	G
4	A	239	C

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Mol	Chain	Res	Type
4	A	243	U
4	A	248	G
4	A	250	G
4	A	254	G
4	A	255	A
4	A	264	C
4	A	265	A
4	A	266	G
4	A	271	G
4	A	272	A
4	A	276	U
4	A	277	G
4	A	278	A
4	A	285	G
4	A	307	G
4	A	322	A
4	A	323	C
4	A	324	A
4	A	329	G
4	A	330	A
4	A	331	C
4	A	345	A
4	A	356	G
4	A	371	A
4	A	372	G
4	A	373	U
4	A	379	G
4	A	386	G
4	A	387	U
4	A	401	A
4	A	404	A
4	A	406	G
4	A	411	G
4	A	412	A
4	A	430	A
4	A	435	C
4	A	451	U
4	A	456	C
4	A	457	A
4	A	458	G
4	A	459	U
4	A	473	G

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Mol	Chain	Res	Type
4	A	480	A
4	A	481	G
4	A	490	C
4	A	491	G
4	A	505	A
4	A	509	C
4	A	510	C
4	A	514	A
4	A	530	G
4	A	531	C
4	A	532	A
4	A	543	G
4	A	545	U
4	A	546	U
4	A	547	A
4	A	563	A
4	A	571	U
4	A	572	A
4	A	573	U
4	A	574	A
4	A	575	A
4	A	603	A
4	A	607	U
4	A	614	A
4	A	621	A
4	A	627	A
4	A	628	G
4	A	637	A
4	A	645	C
4	A	646	U
4	A	647	G
4	A	654	A
4	A	659	G
4	A	675	A
4	A	683	U
4	A	684	G
4	A	686	U
4	A	687	C
4	A	690	G
4	A	722	A
4	A	727	A
4	A	729	G

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Mol	Chain	Res	Type
4	A	730	A
4	A	732	C
4	A	733	G
4	A	776	G
4	A	777	G
4	A	784	G
4	A	785	G
4	A	788	A
4	A	789	A
4	A	792	A
4	A	793	A
4	A	801	G
4	A	805	G
4	A	811	U
4	A	812	C
4	A	819	A
4	A	827	U
4	A	828	U
4	A	830	G
4	A	845	A
4	A	846	U
4	A	847	U
4	A	855	G
4	A	857	G
4	A	875	G
4	A	876	C
4	A	877	A
4	A	878	A
4	A	896	A
4	A	897	C
4	A	907	G
4	A	910	A
4	A	914	G
4	A	931	U
4	A	932	U
4	A	941	A
4	A	959	A
4	A	961	C
4	A	973	A
4	A	974	G
4	A	975	A
4	A	980	A

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Mol	Chain	Res	Type
4	A	983	A
4	A	995	C
4	A	996	A
4	A	1009	A
4	A	1011	G
4	A	1012	U
4	A	1013	C
4	A	1020	A
4	A	1021	A
4	A	1022	G
4	A	1023	U
4	A	1026	G
4	A	1028	A
4	A	1033	U
4	A	1034	G
4	A	1040	A
4	A	1045	C
4	A	1046	A
4	A	1047	G
4	A	1057	A
4	A	1058	U
4	A	1059	G
4	A	1060	U
4	A	1061	U
4	A	1062	G
4	A	1065	U
4	A	1066	U
4	A	1067	A
4	A	1068	G
4	A	1070	A
4	A	1073	A
4	A	1075	C
4	A	1076	C
4	A	1079	C
4	A	1082	U
4	A	1083	U
4	A	1084	A
4	A	1088	A
4	A	1090	A
4	A	1097	U
4	A	1104	C
4	A	1111	A

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Mol	Chain	Res	Type
4	A	1119	U
4	A	1134	A
4	A	1135	C
4	A	1143	A
4	A	1151	A
4	A	1157	G
4	A	1171	G
4	A	1174	U
4	A	1175	A
4	A	1176	U
4	A	1180	U
4	A	1211	C
4	A	1212	G
4	A	1236	G
4	A	1253	A
4	A	1255	U
4	A	1256	G
4	A	1264	A
4	A	1267	U
4	A	1271	G
4	A	1272	A
4	A	1273	U
4	A	1274	A
4	A	1275	A
4	A	1283	G
4	A	1300	G
4	A	1301	A
4	A	1302	A
4	A	1303	G
4	A	1306	C
4	A	1314	C
4	A	1325	U
4	A	1329	U
4	A	1341	G
4	A	1343	G
4	A	1345	C
4	A	1365	A
4	A	1376	C
4	A	1378	A
4	A	1379	U
4	A	1383	A
4	A	1393	A

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Mol	Chain	Res	Type
4	A	1395	A
4	A	1403	A
4	A	1416	G
4	A	1420	A
4	A	1421	G
4	A	1427	A
4	A	1437	C
4	A	1451	C
4	A	1453	A
4	A	1454	C
4	A	1458	U
4	A	1461	C
4	A	1467	U
4	A	1475	G
4	A	1482	G
4	A	1490	A
4	A	1491	G
4	A	1496	A
4	A	1498	C
4	A	1504	A
4	A	1508	A
4	A	1512	C
4	A	1513	U
4	A	1514	G
4	A	1515	A
4	A	1518	C
4	A	1524	G
4	A	1533	C
4	A	1535	A
4	A	1536	C
4	A	1537	G
4	A	1546	G
4	A	1547	C
4	A	1560	G
4	A	1565	C
4	A	1566	A
4	A	1569	A
4	A	1578	U
4	A	1584	U
4	A	1585	C
4	A	1598	A
4	A	1607	C

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Mol	Chain	Res	Type
4	A	1616	A
4	A	1620	G
4	A	1622	G
4	A	1633	G
4	A	1634	A
4	A	1635	A
4	A	1640	A
4	A	1645	G
4	A	1646	C
4	A	1647	U
4	A	1648	U
4	A	1649	G
4	A	1650	A
4	A	1651	G
4	A	1653	G
4	A	1657	U
4	A	1663	G
4	A	1666	G
4	A	1667	G
4	A	1668	A
4	A	1669	A
4	A	1670	C
4	A	1685	C
4	A	1686	C
4	A	1687	G
4	A	1688	U
4	A	1701	A
4	A	1702	G
4	A	1703	G
4	A	1704	C
4	A	1705	A
4	A	1706	C
4	A	1707	G
4	A	1708	C
4	A	1709	U
4	A	1711	A
4	A	1713	A
4	A	1716	U
4	A	1721	G
4	A	1729	U
4	A	1730	C
4	A	1731	G

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Mol	Chain	Res	Type
4	A	1732	C
4	A	1733	G
4	A	1735	A
4	A	1738	G
4	A	1744	A
4	A	1746	A
4	A	1747	U
4	A	1748	C
4	A	1749	A
4	A	1993	U
4	A	1994	C
4	A	1995	U
4	A	1997	C
4	A	2008	C
4	A	2009	A
4	A	2010	G
4	A	2011	U
4	A	2012	G
4	A	2015	A
4	A	2021	C
4	A	2022	U
4	A	2030	A
4	A	2031	A
4	A	2032	G
4	A	2043	C
4	A	2052	A
4	A	2053	G
4	A	2055	C
4	A	2056	G
4	A	2059	A
4	A	2060	A
4	A	2061	G
4	A	2062	A
4	A	2068	U
4	A	2069	G
4	A	2086	U
4	A	2090	A
4	A	2093	G
4	A	2096	C
4	A	2104	C
4	A	2108	A
4	A	2111	U

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Mol	Chain	Res	Type
4	A	2112	G
4	A	2113	U
4	A	2115	G
4	A	2116	G
4	A	2118	U
4	A	2119	A
4	A	2125	G
4	A	2127	G
4	A	2131	U
4	A	2132	U
4	A	2133	G
4	A	2140	G
4	A	2143	C
4	A	2162	G
4	A	2164	C
4	A	2165	C
4	A	2168	G
4	A	2172	U
4	A	2173	A
4	A	2175	C
4	A	2176	A
4	A	2178	C
4	A	2182	U
4	A	2189	U
4	A	2198	A
4	A	2199	A
4	A	2204	G
4	A	2213	U
4	A	2225	A
4	A	2226	C
4	A	2237	G
4	A	2238	G
4	A	2239	G
4	A	2250	G
4	A	2251	G
4	A	2265	U
4	A	2279	G
4	A	2283	C
4	A	2287	A
4	A	2297	A
4	A	2305	U
4	A	2308	G

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Mol	Chain	Res	Type
4	A	2309	A
4	A	2319	G
4	A	2321	U
4	A	2325	G
4	A	2327	A
4	A	2333	A
4	A	2335	A
4	A	2336	A
4	A	2350	C
4	A	2357	G
4	A	2383	G
4	A	2385	C
4	A	2389	G
4	A	2391	G
4	A	2402	U
4	A	2406	A
4	A	2407	A
4	A	2409	G
4	A	2422	C
4	A	2424	C
4	A	2425	A
4	A	2428	G
4	A	2429	G
4	A	2430	A
4	A	2434	A
4	A	2435	A
4	A	2439	A
4	A	2441	U
4	A	2447	G
4	A	2448	A
4	A	2449	U
4	A	2454	G
4	A	2457	U
4	A	2476	A
4	A	2478	A
4	A	2487	G
4	A	2490	G
4	A	2494	G
4	A	2497	A
4	A	2498	C
4	A	2499	C
4	A	2501	C

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Mol	Chain	Res	Type
4	A	2502	G
4	A	2503	A
4	A	2504	U
4	A	2505	G
4	A	2506	U
4	A	2508	G
4	A	2513	A
4	A	2516	A
4	A	2517	C
4	A	2518	A
4	A	2520	C
4	A	2525	G
4	A	2529	G
4	A	2535	G
4	A	2545	G
4	A	2547	A
4	A	2554	U
4	A	2566	A
4	A	2567	G
4	A	2573	C
4	A	2577	A
4	A	2578	G
4	A	2581	G
4	A	2582	G
4	A	2585	U
4	A	2596	U
4	A	2597	G
4	A	2598	A
4	A	2599	G
4	A	2600	A
4	A	2602	A
4	A	2603	G
4	A	2605	U
4	A	2606	C
4	A	2609	U
4	A	2610	C
4	A	2611	C
4	A	2612	C
4	A	2613	U
4	A	2614	A
4	A	2615	U
4	A	2630	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	A	2646	C
4	A	2647	U
4	A	2654	A
4	A	2655	G
4	A	2656	U
4	A	2665	A
4	A	2681	C
4	A	2682	A
4	A	2685	G
4	A	2689	U
4	A	2690	U
4	A	2714	G
4	A	2718	G
4	A	2726	A
4	A	2732	G
4	A	2733	A
4	A	2744	G
4	A	2748	A
4	A	2753	A
4	A	2757	A
4	A	2764	A
4	A	2765	A
4	A	2766	A
4	A	2778	A
4	A	2779	U
4	A	2780	G
4	A	2791	G
4	A	2800	A
4	A	2808	G
4	A	2809	A
4	A	2818	U
4	A	2820	A
4	A	2833	U
4	A	2835	A
4	A	2848	G
4	A	2860	A
4	A	2867	G
4	A	2879	A
4	A	2880	C
4	A	2883	A
4	A	2884	U
4	A	2891	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	A	2894	G
5	B	4	C
5	B	12	C
5	B	13	G
5	B	24	G
5	B	35	C
5	B	39	A
5	B	41	G
5	B	42	C
5	B	44	G
5	B	53	A
5	B	58	A
5	B	66	A
5	B	67	G
5	B	88	C
5	B	89	U
5	B	108	A
5	B	109	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	202	U
4	A	227	A
4	A	242	G
4	A	271	G
4	A	429	A
4	A	458	G
4	A	644	A
4	A	729	G
4	A	732	C
4	A	776	G
4	A	1020	A
4	A	1022	G
4	A	1730	C
4	A	2318	G
4	A	2599	G
4	A	2629	U
4	A	2655	G
5	B	52	A
5	B	66	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.

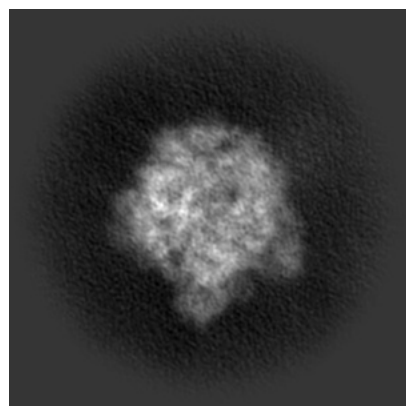
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51835. These allow visual inspection of the internal detail of the map and identification of artifacts.

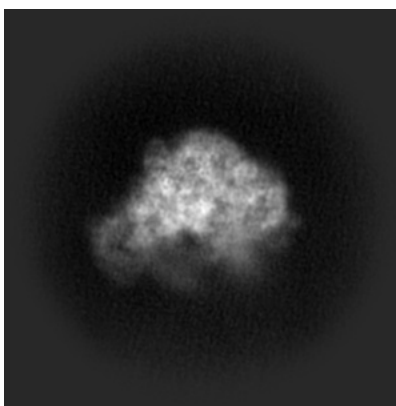
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

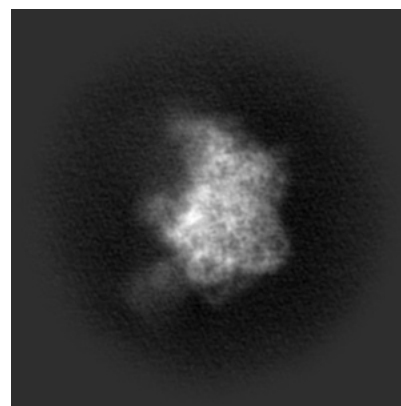
6.1.1 Primary map



X

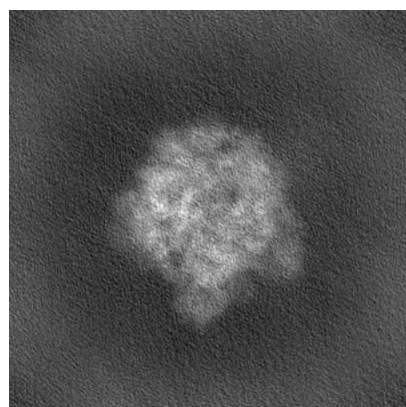


Y

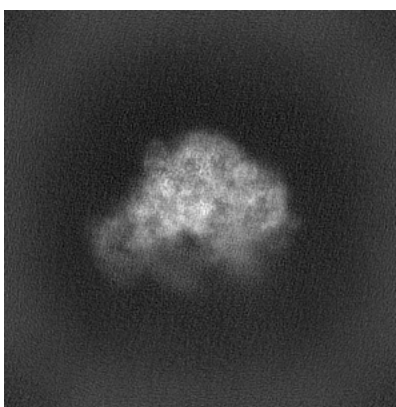


Z

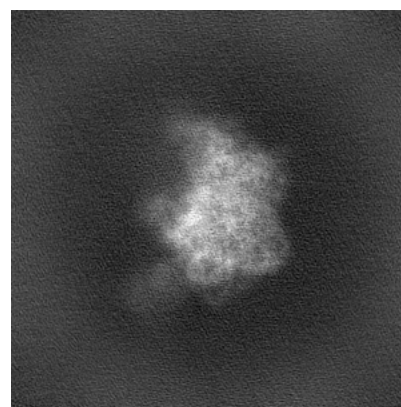
6.1.2 Raw map



X



Y

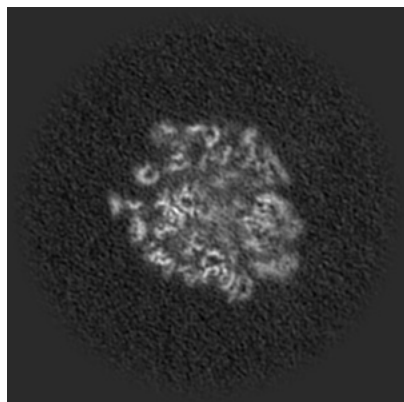


Z

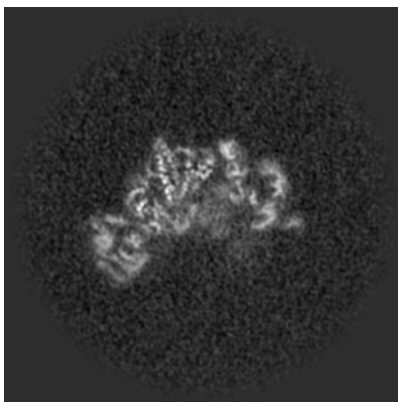
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

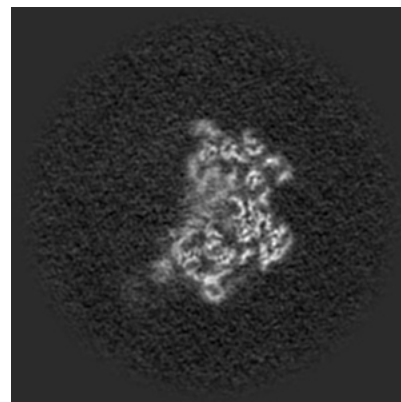
6.2.1 Primary map



X Index: 150

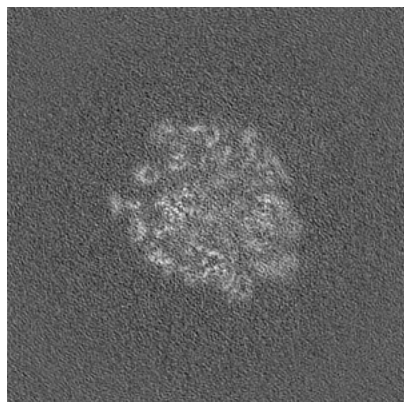


Y Index: 150

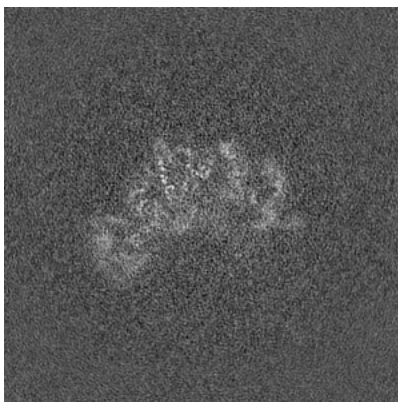


Z Index: 150

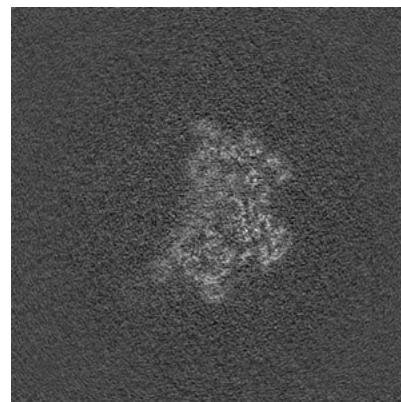
6.2.2 Raw map



X Index: 150



Y Index: 150

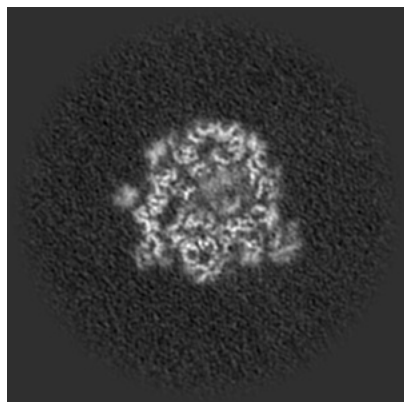


Z Index: 150

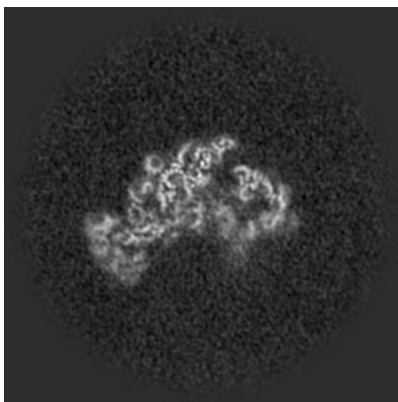
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

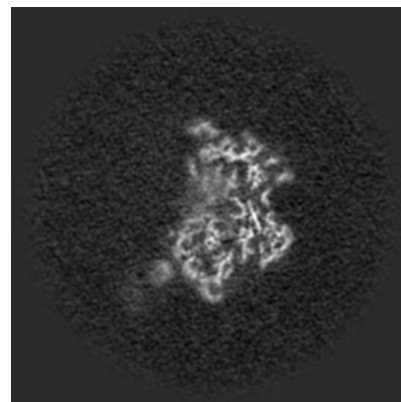
6.3.1 Primary map



X Index: 163

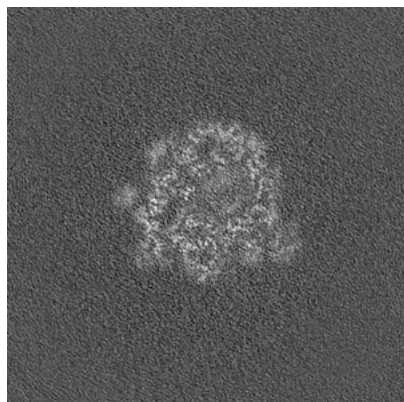


Y Index: 142

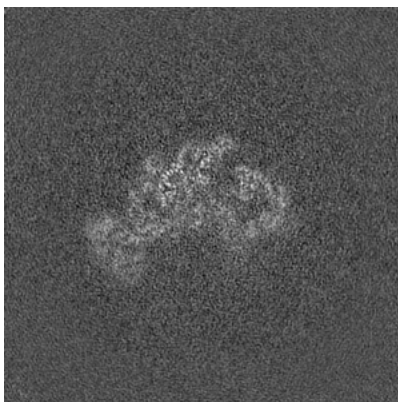


Z Index: 148

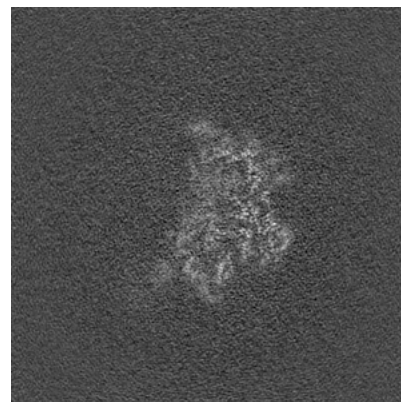
6.3.2 Raw map



X Index: 163



Y Index: 142

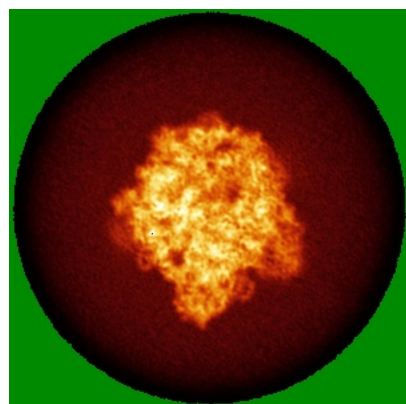


Z Index: 147

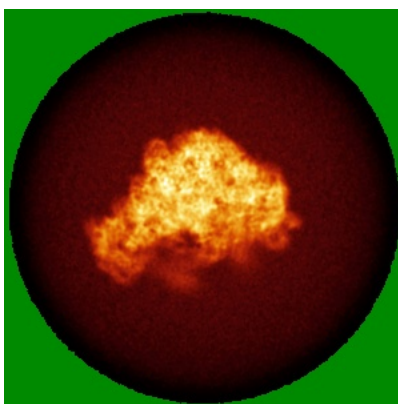
The images above show the largest variance slices of the map in three orthogonal directions.

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

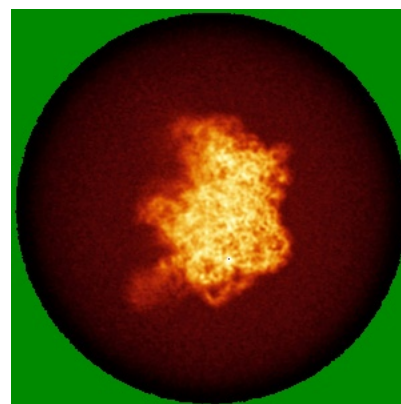
6.4.1 Primary map



X

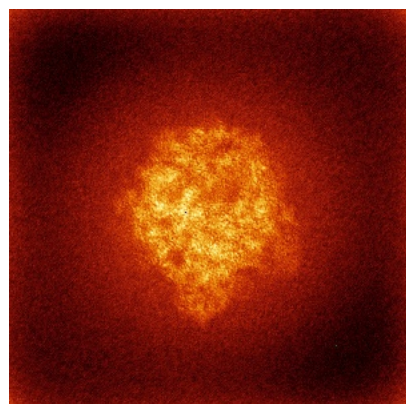


Y

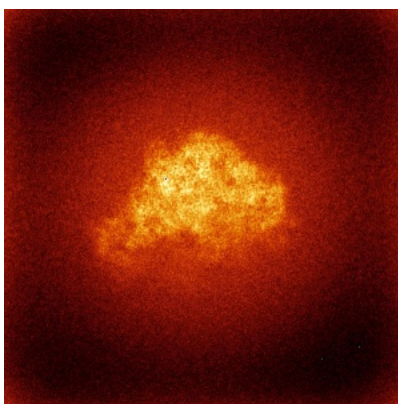


Z

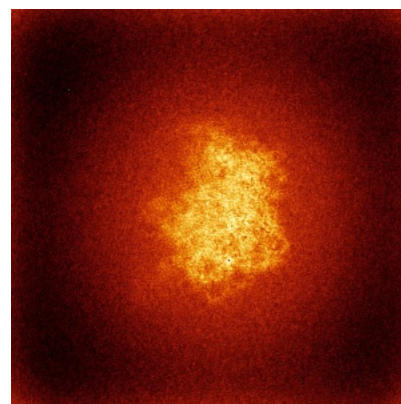
6.4.2 Raw map



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



X



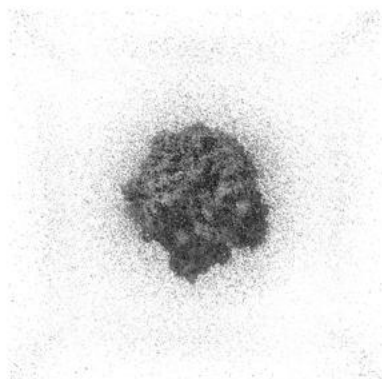
Y



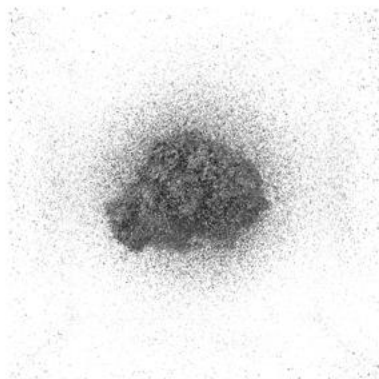
Z

The images above show the 3D surface view of the map at the recommended contour level 0.337. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

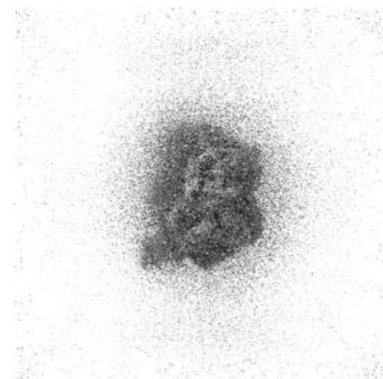
6.5.2 Raw map



X



Y



Z

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.

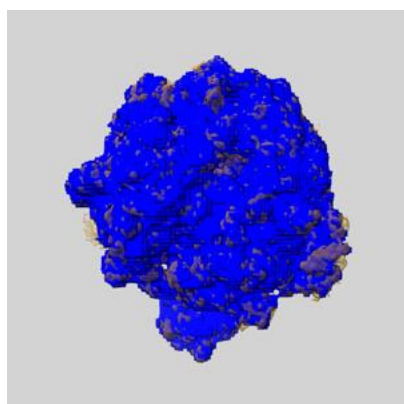
6.6 Mask visualisation [i](#)

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

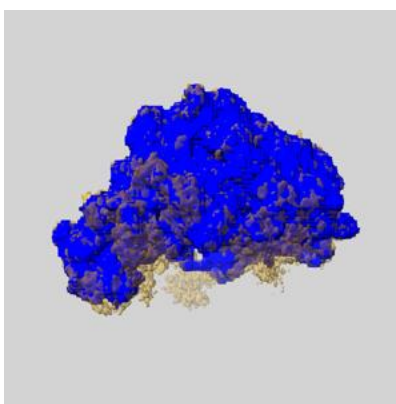
A mask typically either:

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

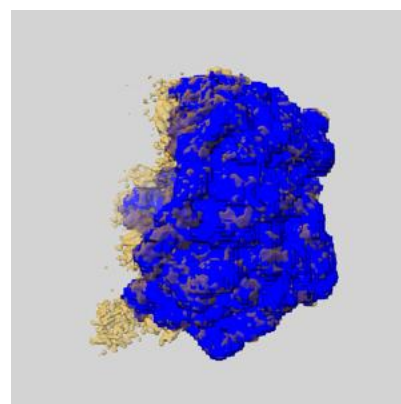
6.6.1 emd_51835_msk_1.map [i](#)



X



Y

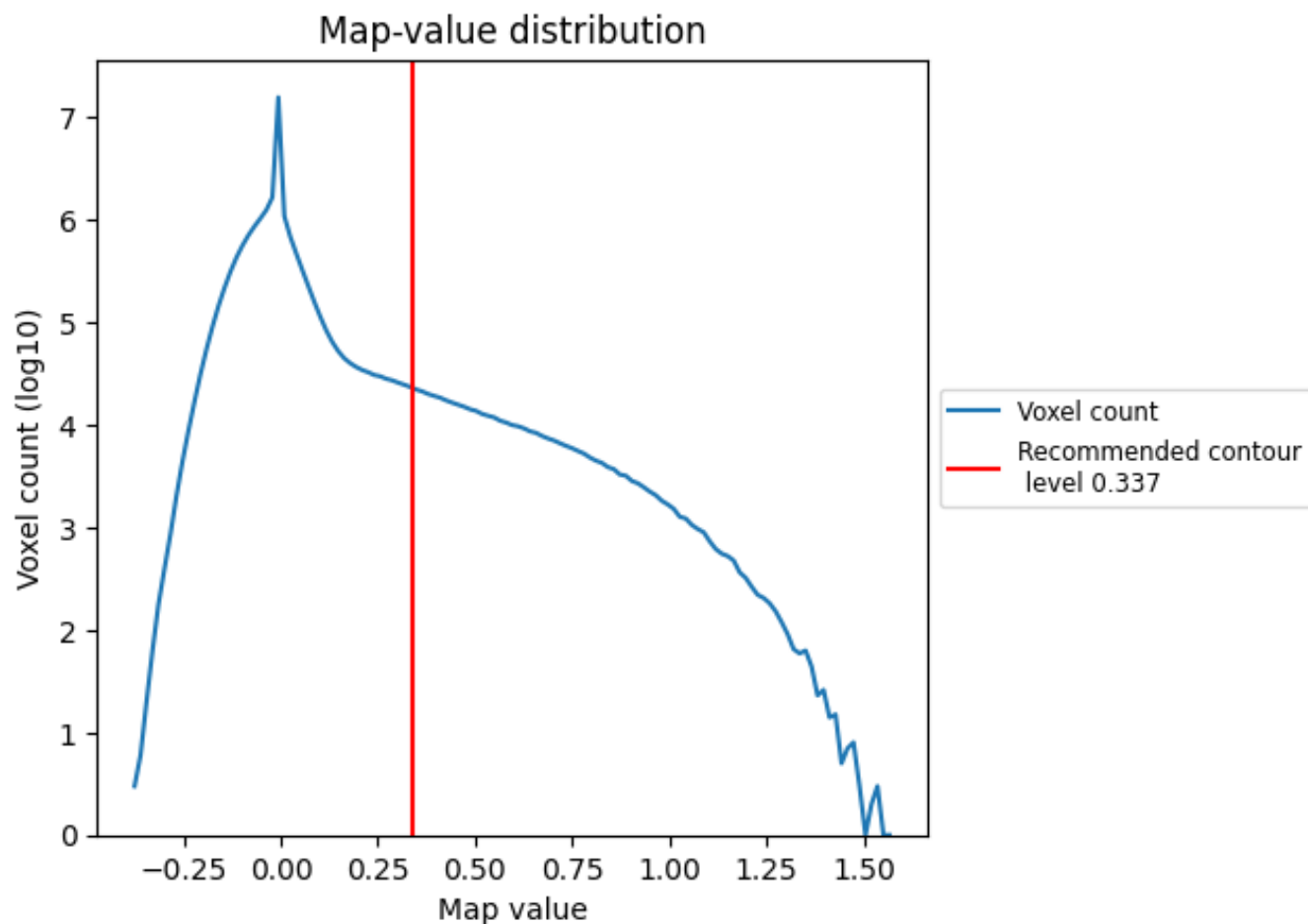


Z

7 Map analysis [i](#)

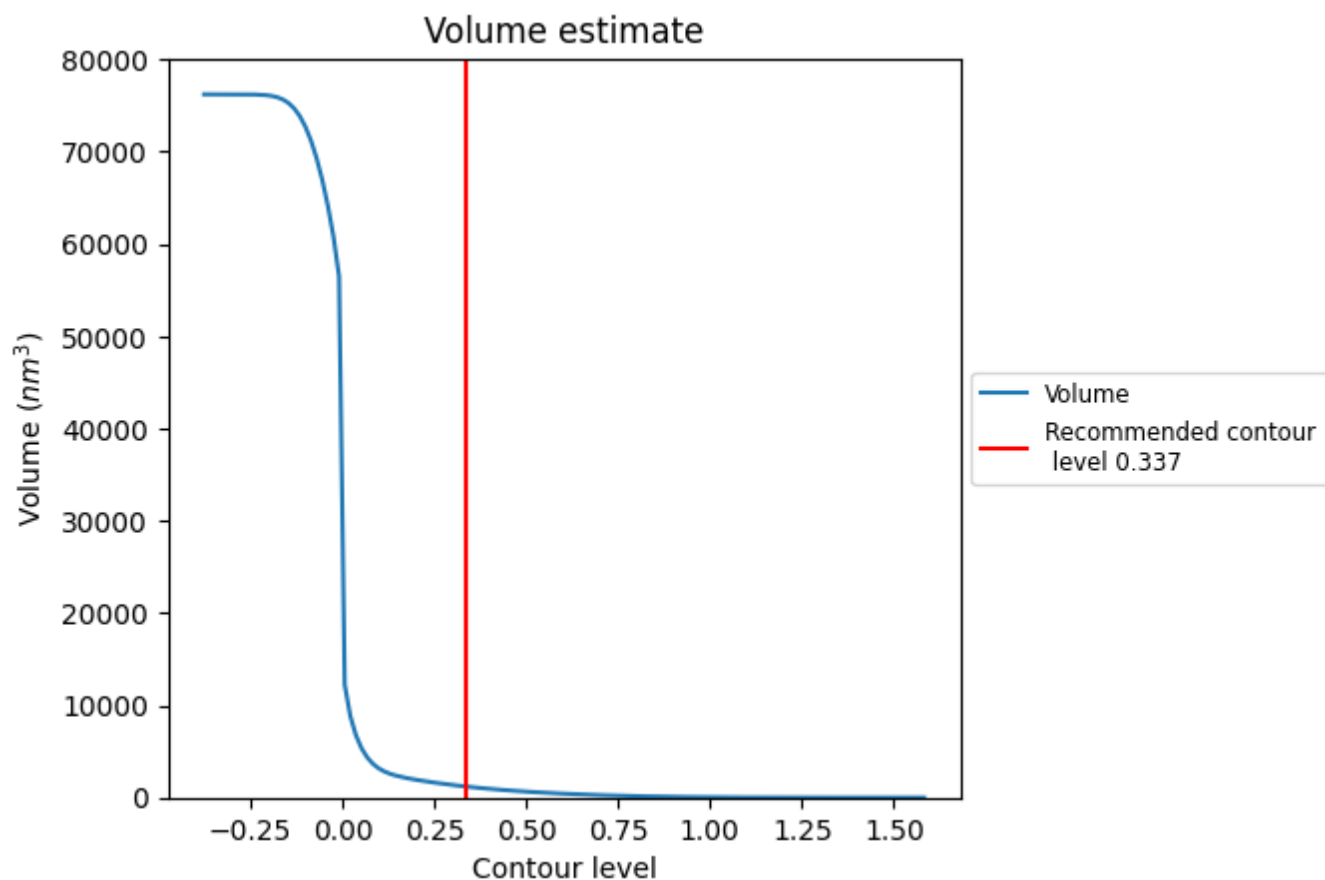
This section contains the results of statistical analysis of the map.

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.

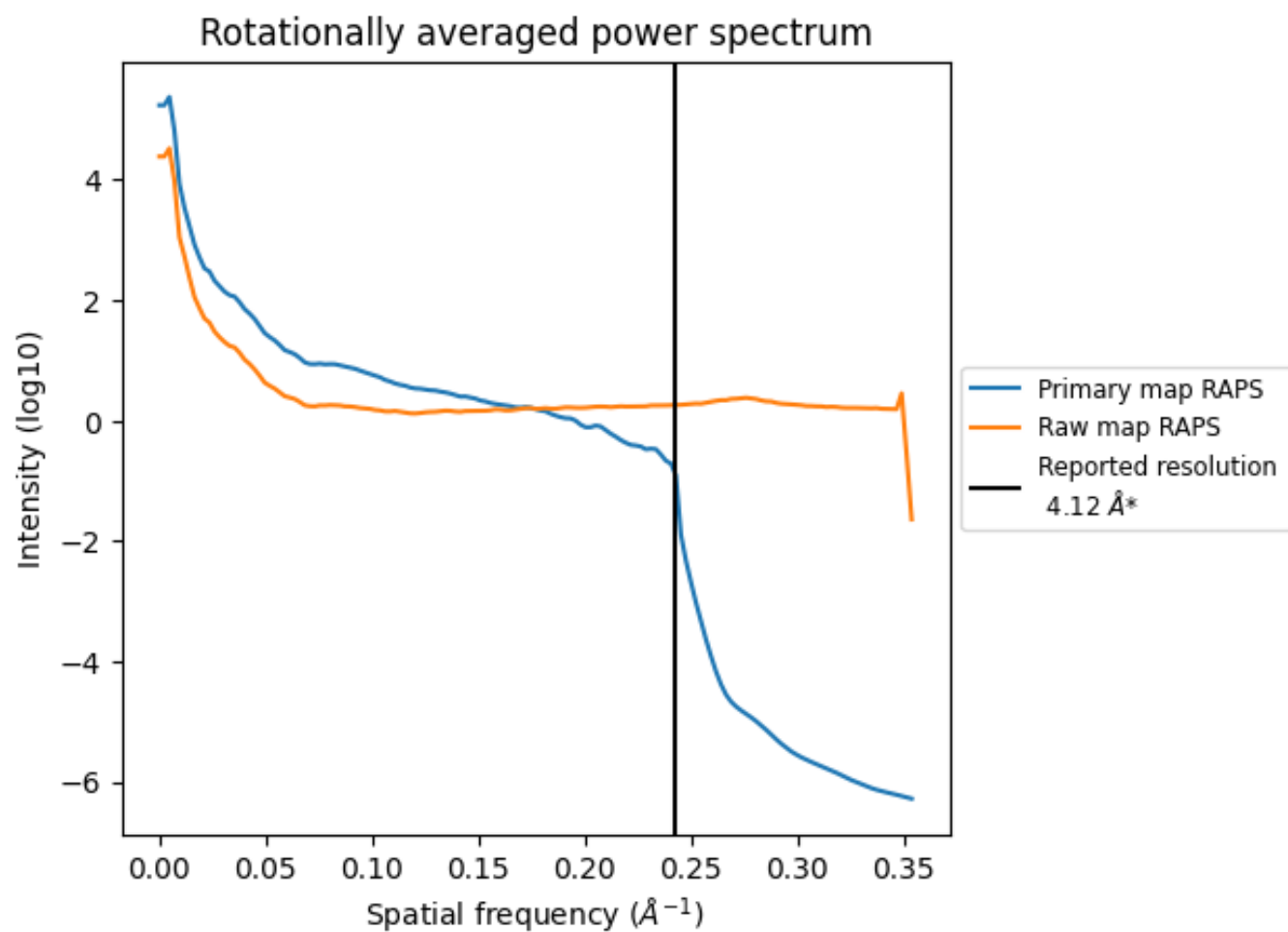
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm³; this corresponds to an approximate mass of 1077 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 ⓘ

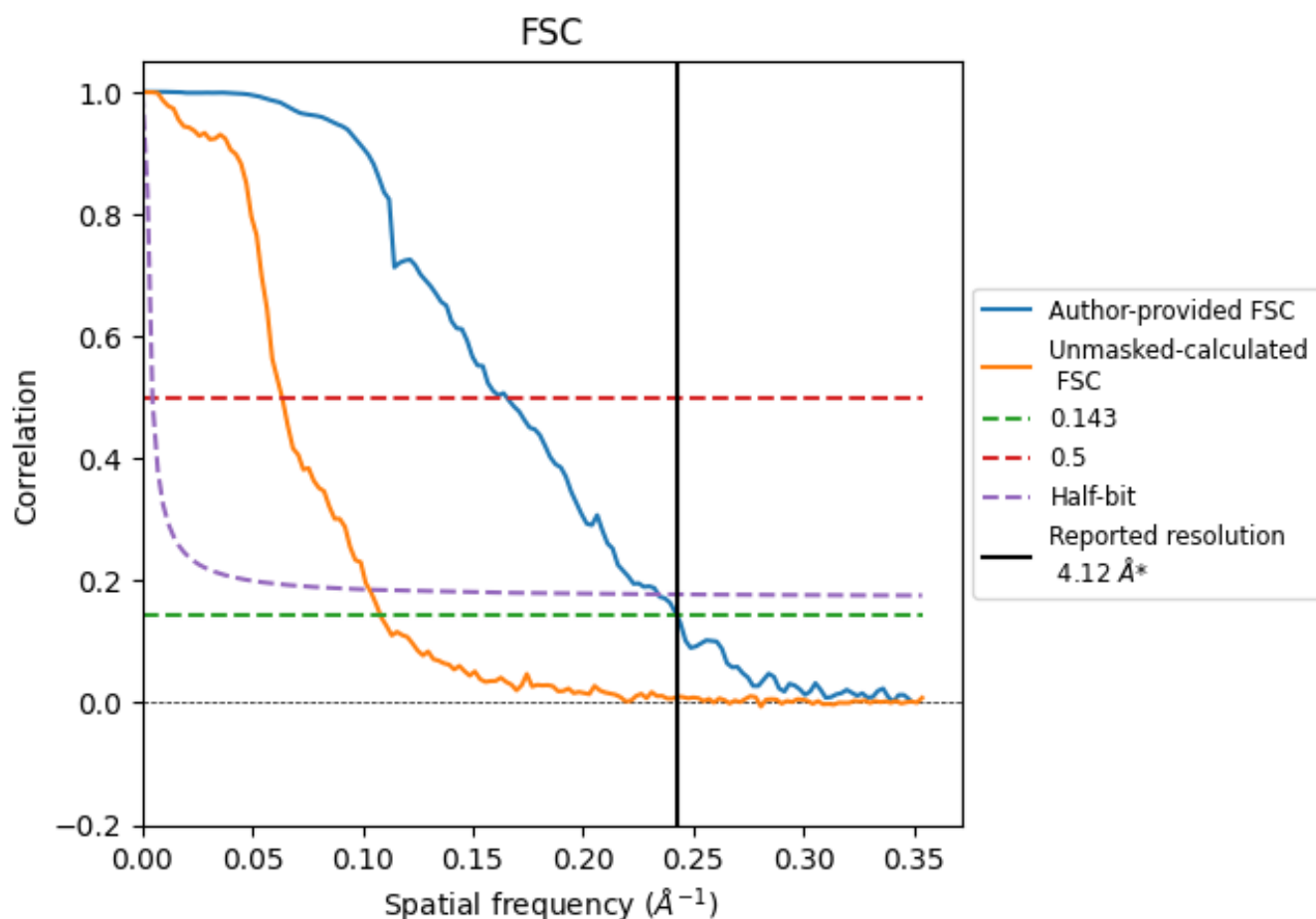


*Reported resolution corresponds to spatial frequency of 0.243 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.243 \AA^{-1}

8.2 Resolution estimates [i](#)

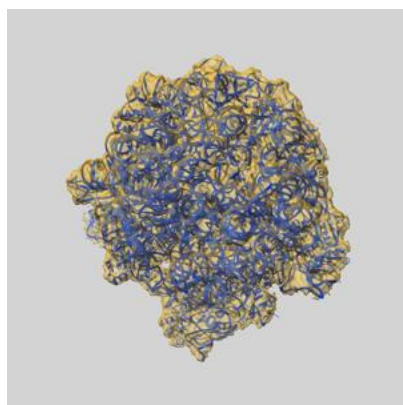
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.12	-	-
Author-provided FSC curve	4.12	6.05	4.27
Unmasked-calculated*	9.25	15.77	9.70

*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 9.25 differs from the reported value 4.12 by more than 10 %

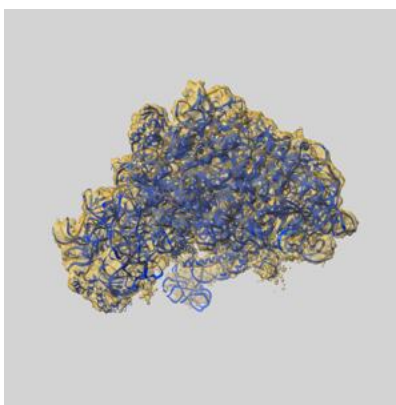
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51835 and PDB model 9H3R. Per-residue inclusion information can be found in section [3](#) on page [8](#).

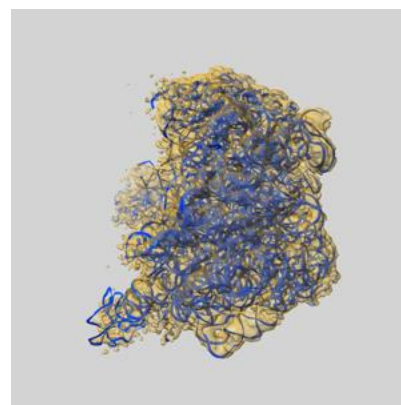
9.1 Map-model overlay [i](#)



X



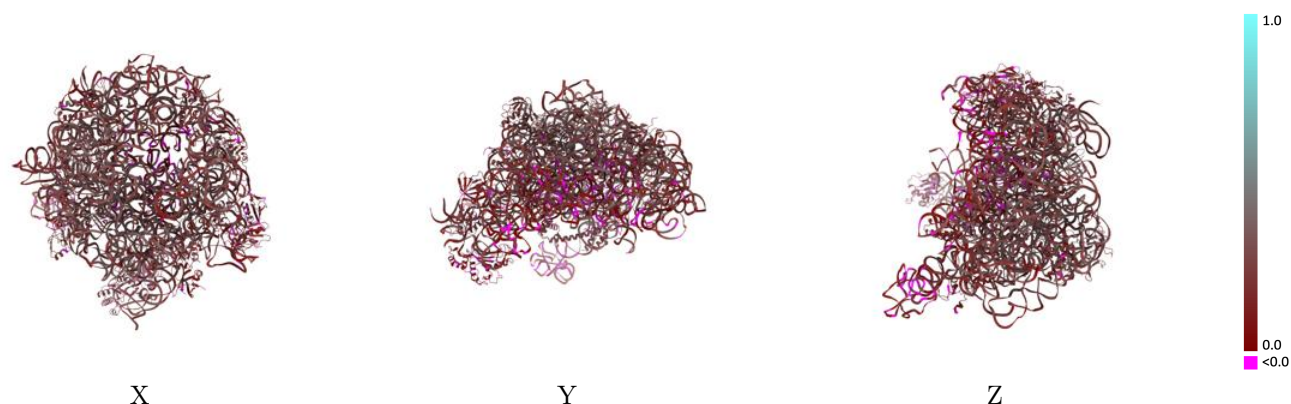
Y



Z

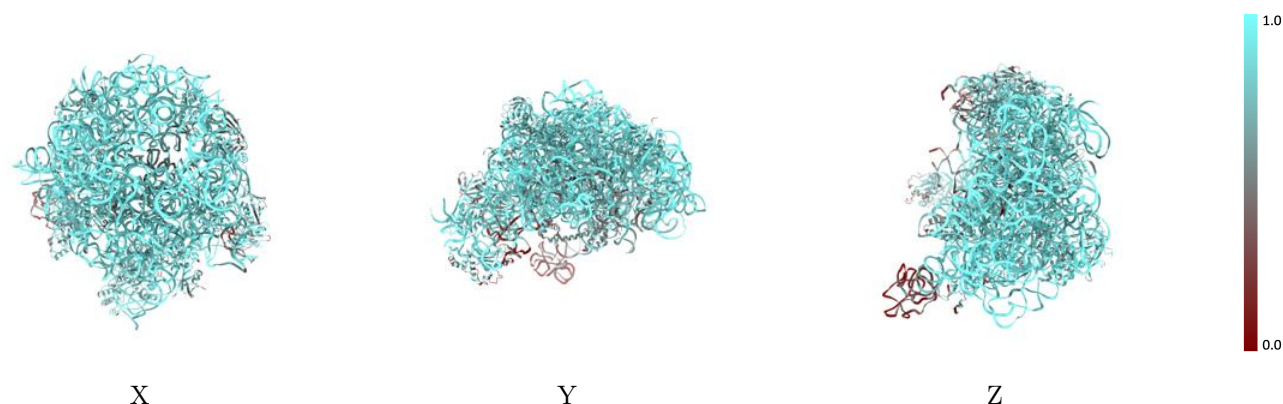
The images above show the 3D surface view of the map at the recommended contour level 0.337 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



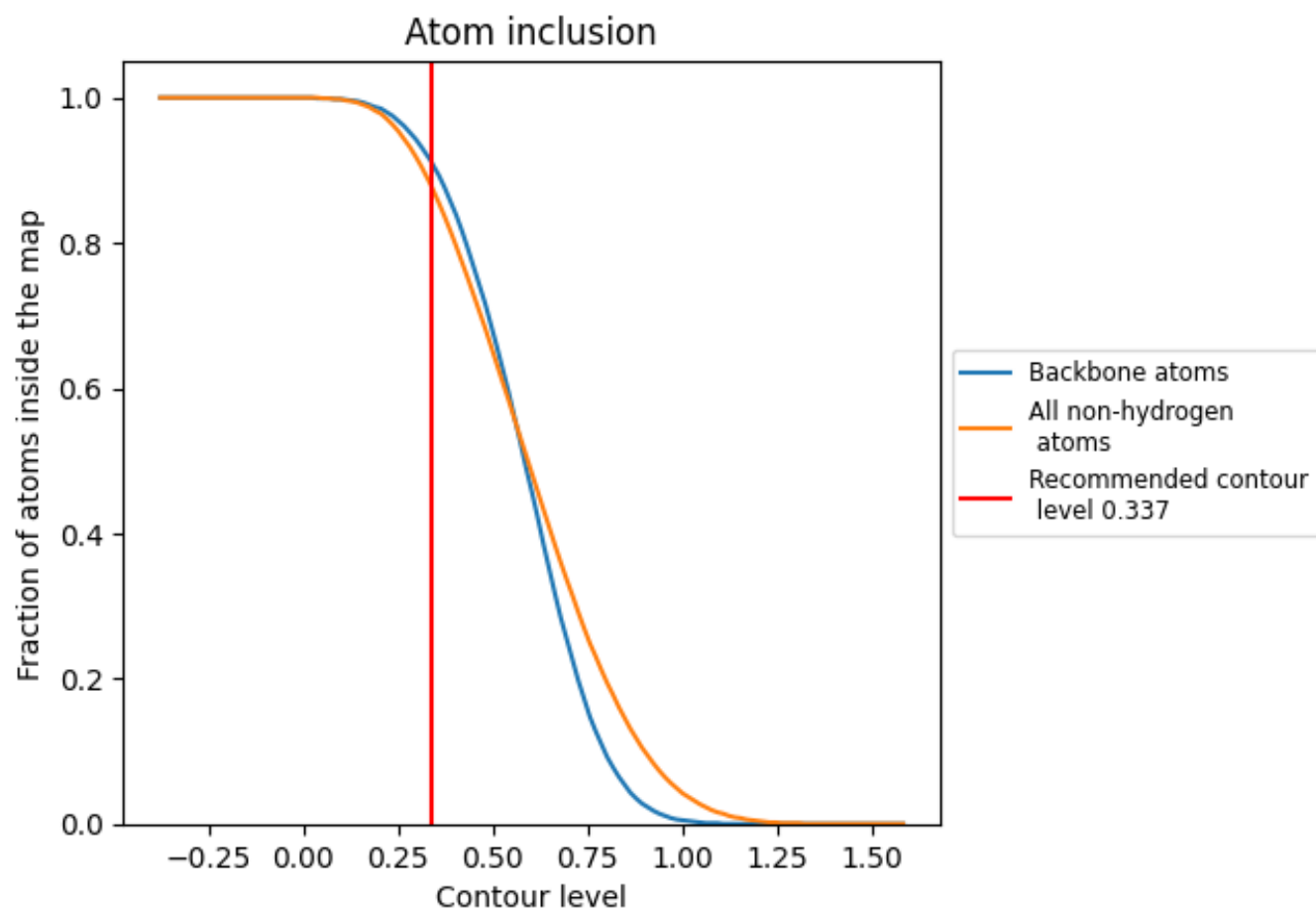
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.337).





















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% 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 (0.337) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.2310
2	 0.8580	 0.2480
4	 0.7190	 0.1200
A	 0.9120	 0.2370
B	 0.9570	 0.2280
C	 0.6580	 0.2010
D	 0.8100	 0.2350
E	 0.8150	 0.2510
F	 0.6760	 0.1020
G	 0.7030	 0.1600
H	 0.6160	 0.1150
J	 0.8720	 0.2850
K	 0.6540	 0.1930
L	 0.7220	 0.1950
N	 0.8410	 0.2180
O	 0.8600	 0.1800
P	 0.6980	 0.1950
Q	 0.8890	 0.2820
R	 0.8460	 0.2800
T	 0.8310	 0.2720
U	 0.8310	 0.2760
V	 0.7100	 0.1720
W	 0.8410	 0.2680
X	 0.8420	 0.2380
Y	 0.8050	 0.2330
Z	 0.8560	 0.2580

