



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 07:43 PM UTC

PDB ID : 5NJT / pdb_00005njt
EMDB ID : EMD-3656
Title : Structure of the Bacillus subtilis hibernating 100S ribosome reveals the basis for 70S dimerization.
Authors : Beckert, B.; Abdelshahid, M.; Schaefer, H.; Steinchen, W.; Arenz, S.; Berninghausen, O.; Beckmann, R.; Bange, G.; Turgay, K.; Wilson, D.N.
Deposited on : 2017-03-29
Resolution : 3.80 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

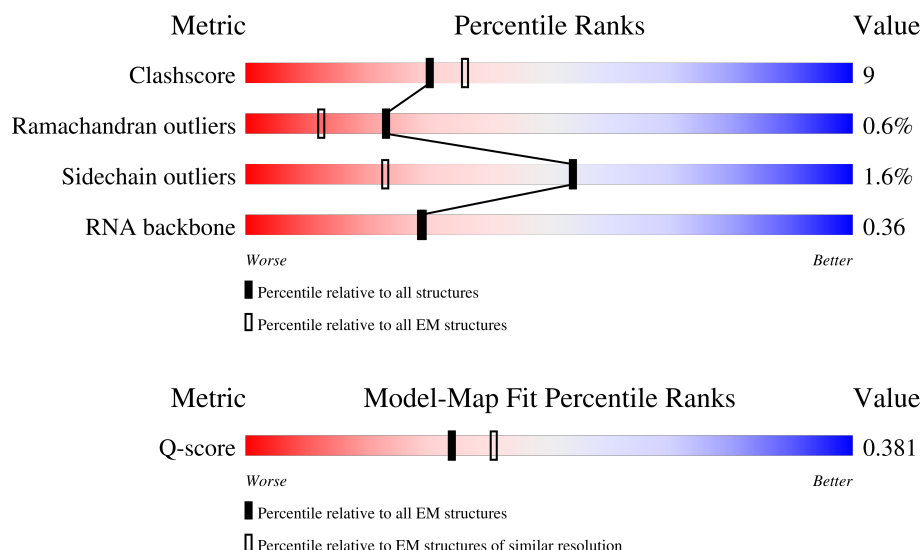
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1544	
2	B	224	
3	C	210	

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Mol	Chain	Length	Quality of chain
4	D	199	
5	E	165	
6	F	95	
7	G	153	
8	H	131	
9	I	130	
10	J	102	
11	K	118	
12	L	137	
13	M	111	
14	N	60	
15	O	88	
16	P	89	
17	Q	86	
18	R	71	
19	S	80	
20	T	86	
21	U	2923	
22	V	112	
23	W	275	
24	X	207	
25	Y	205	
26	Z	178	
27	a	175	
28	b	123	

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Mol	Chain	Length	Quality of chain
29	c	142	
30	d	122	
31	e	146	
32	f	138	
33	g	119	
34	h	120	
35	i	114	
36	j	117	
37	k	101	
38	l	109	
39	m	93	
40	n	100	
41	o	82	
42	p	54	
43	q	48	
44	r	44	
45	s	64	
46	t	36	
47	u	58	
48	v	65	
49	w	58	
50	y	64	
51	x	104	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 133097 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	224	Total	C	N	O	0	0
			896	448	224	224		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	210	Total	C	N	O	0	0
			840	420	210	210		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	199	Total	C	N	O	0	0
			797	398	199	200		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	165	Total	C	N	O	0	0
			661	330	165	166		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	95	Total	C	N	O	0	0
			381	190	95	96		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	153	Total	C	N	O	0	0
			613	306	153	154		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	131	Total	C	N	O	0	0
			525	262	131	132		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	130	Total	C	N	O	0	0
			521	260	130	131		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	102	Total	C	N	O	0	0
			409	204	102	103		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	118	Total	C	N	O	0	0
			472	236	118	118		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	137	Total	C	N	O	0	0
			549	274	137	138		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	111	Total	C	N	O	0	0
			444	222	111	111		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	80	Total	C	N	O	0	0
			320	160	80	80		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 21 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	1558	C	G	conflict	GB 467326

- Molecule 22 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 23 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 24 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 25 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 26 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 27 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 28 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 29 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 30 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 31 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 32 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 33 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 34 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 35 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	114	Total	C	N	O	S	0	0
			936	595	184	157			

- Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	101	Total	C	N	O	S	0	0
			786	501	139	146			

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	o	82	Total	C	N	O		
			630	390	123	117	0	0

- Molecule 42 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	54	Total	C	N	O	S		
			426	262	86	71	7	0	0

- Molecule 43 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	48	Total	C	N	O	S		
			401	244	80	73	4	0	0

- Molecule 44 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	44	Total	C	N	O	S		
			367	222	89	54	2	0	0

- Molecule 45 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	64	Total	C	N	O	S		
			512	321	107	82	2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	36	Total	C	N	O	S		
			288	181	59	44	4	0	0

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	58	Total	C	N	O	S		
			444	275	92	75	2	0	0

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	64	Total	C	N	O	S	0	0
			503	314	92	92	5		

- Molecule 51 is a protein called Ribosome hibernation promotion factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	104	Total	C	N	O	S	0	0
			866	537	159	167	3		

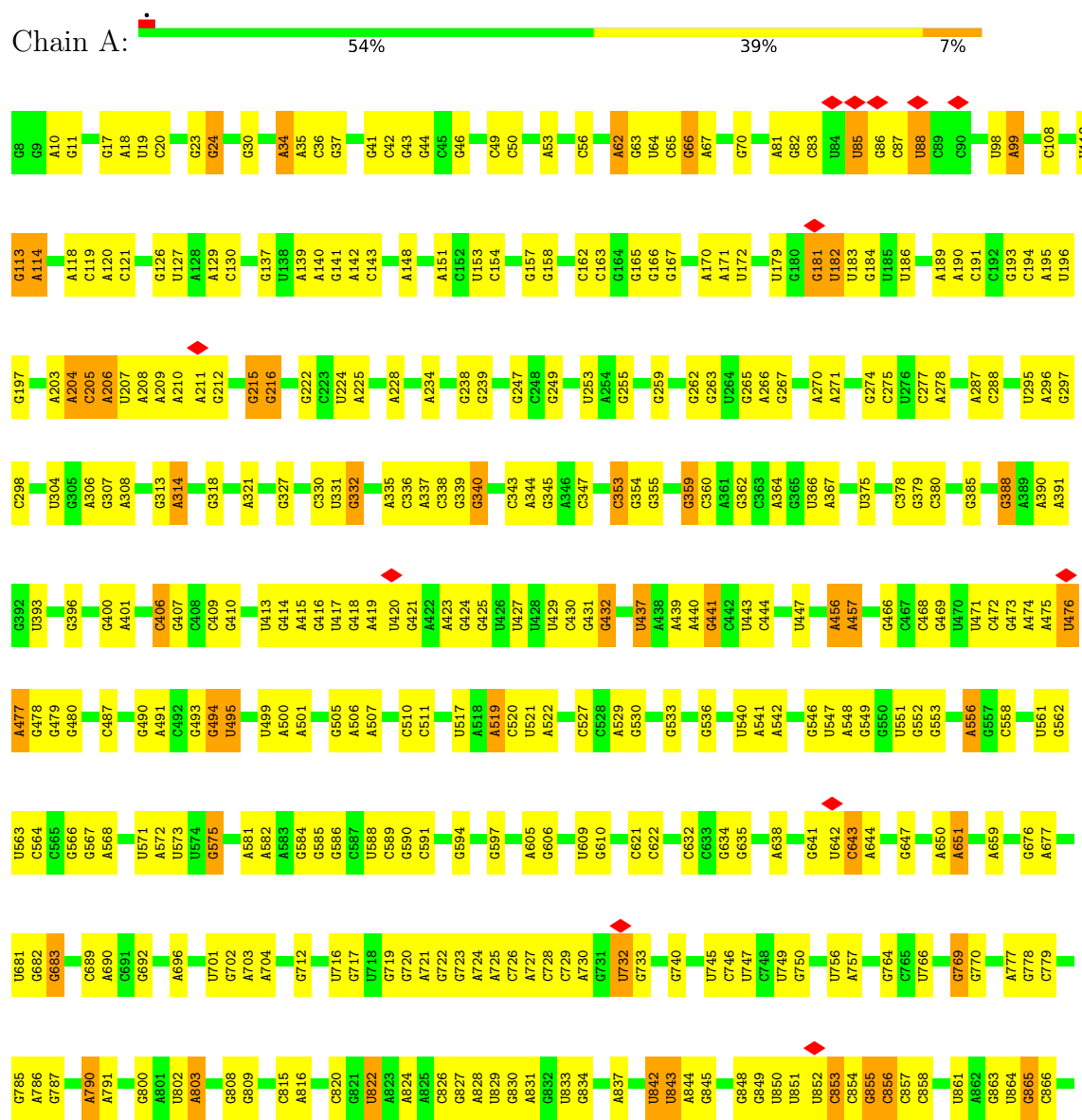
There is a discrepancy between the modelled and reference sequences:

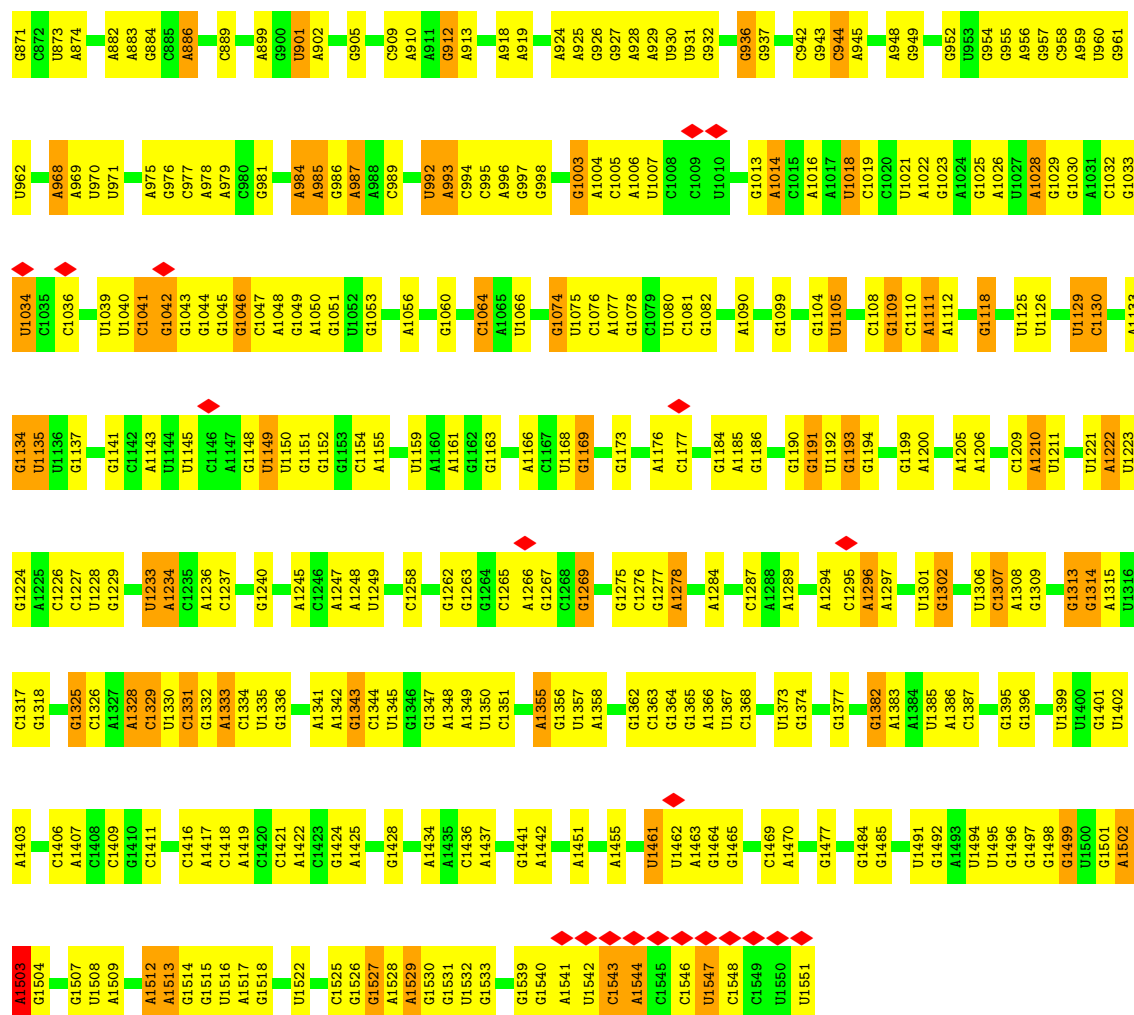
Chain	Residue	Modelled	Actual	Comment	Reference
x	103	GLU	GLY	conflict	UNP P28368

3 Residue-property plots

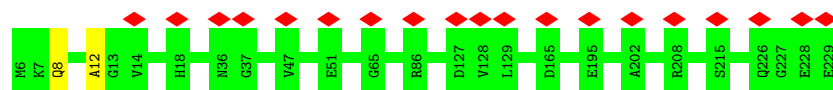
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

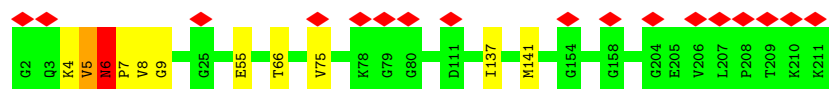




- Molecule 2: 30S ribosomal protein S2

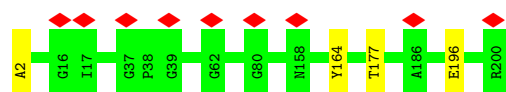


- Molecule 3: 30S ribosomal protein S3



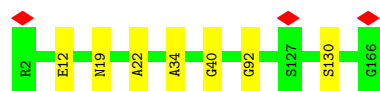
- Molecule 4: 30S ribosomal protein S4





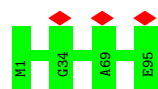
- Molecule 5: 30S ribosomal protein S5

Chain E: 96%



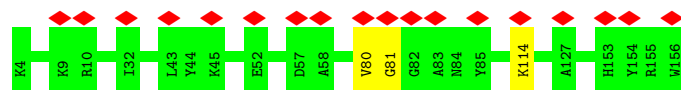
- Molecule 6: 30S ribosomal protein S6

Chain F: 100%



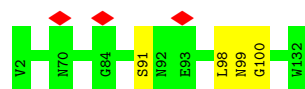
- Molecule 7: 30S ribosomal protein S7

Chain G: 12% 98%



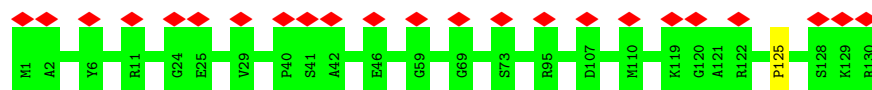
- Molecule 8: 30S ribosomal protein S8

Chain H: 97%



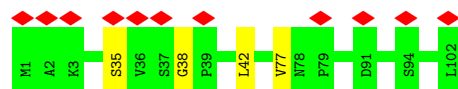
- Molecule 9: 30S ribosomal protein S9

Chain I: 18% 99%

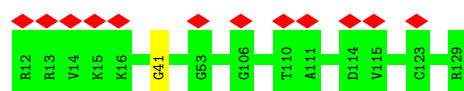


- Molecule 10: 30S ribosomal protein S10

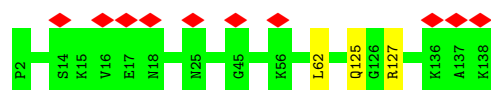
Chain J: 11% 96%



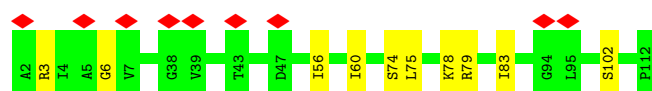
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

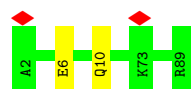


- Molecule 14: 30S ribosomal protein S14

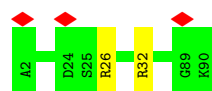


There are no outlier residues recorded for this chain.

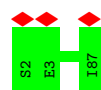
- Molecule 15: 30S ribosomal protein S15



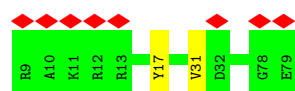
- Molecule 16: 30S ribosomal protein S16



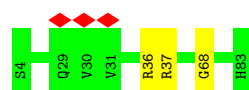
- Molecule 17: 30S ribosomal protein S17



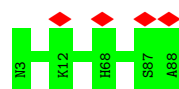
- Molecule 18: 30S ribosomal protein S18



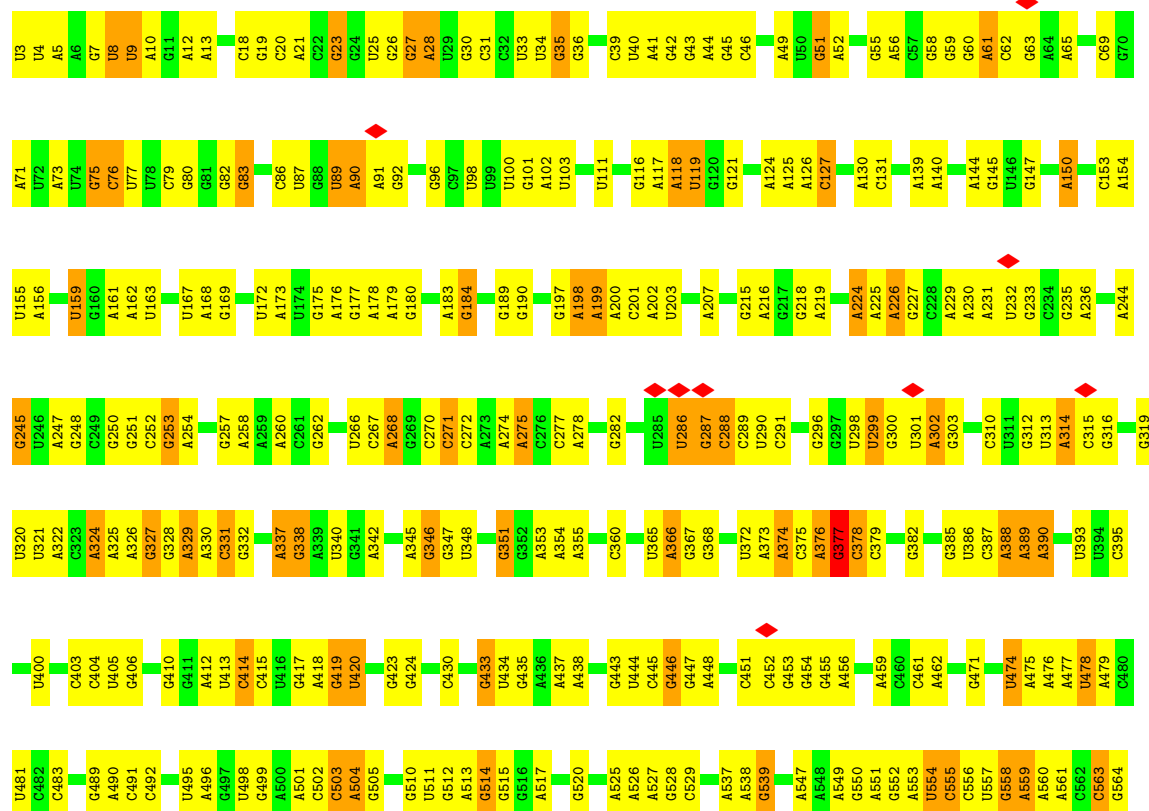
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20

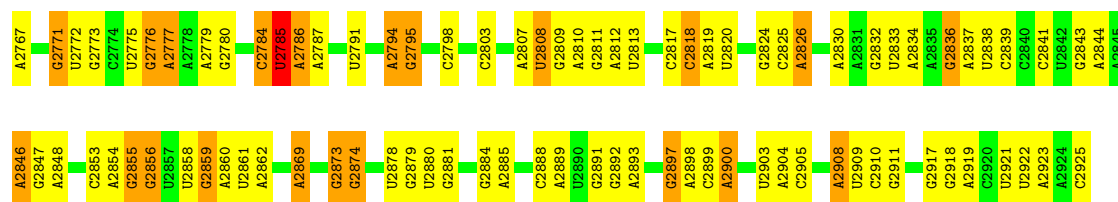


- Molecule 21: 23S ribosomal RNA

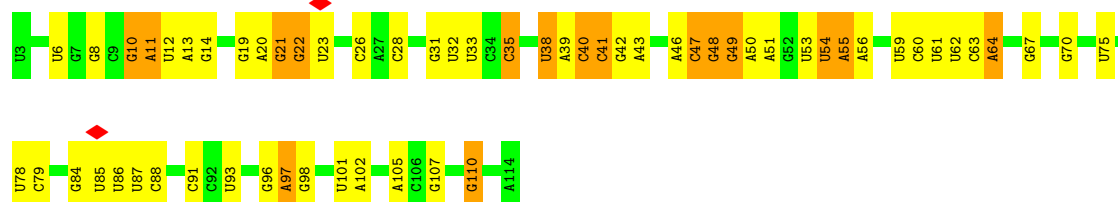




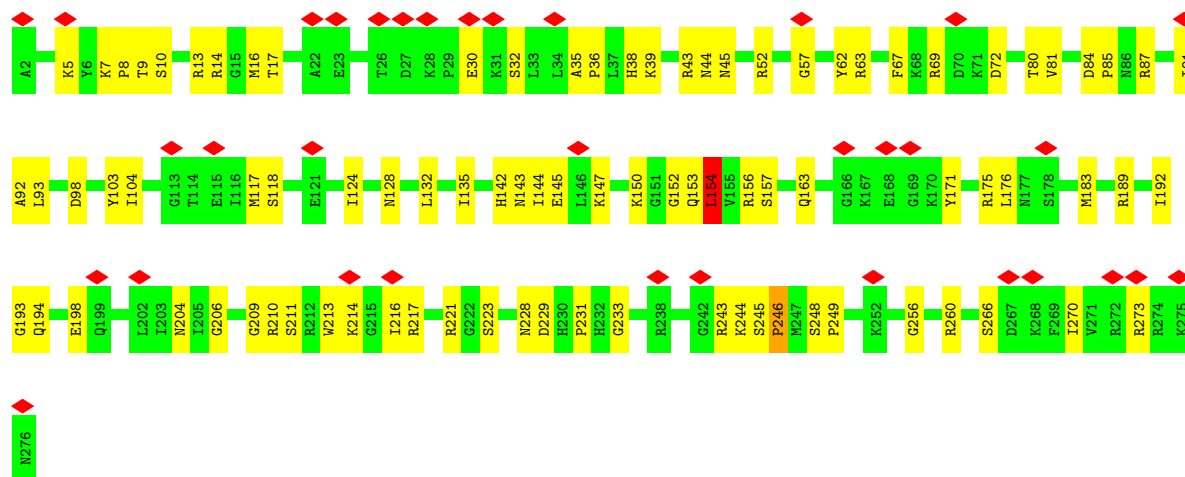
G1635	A1709	U1790	U1880	G1964	A2047	G2130	A2191	U2265	G2347	G2426	C2504	G2578	C2680
A1636	G1712	A1791	U1881	A1965	U2048	U2131	G2194	G2266	A2351	U2427	A2505	U2583	A2683
G1637	G1713	A1792	A1882	A1966	A2049	A2132	G2195	G2267	G2352	G2428	C2509	U2584	A2684
A1638	A1714	G1793	A1883	A1967	G2050	C2133	G2196	G2268	U2353	G2429	G2510	U2585	A2685
G1639	G1715	G1794	A1884	U1968	U2051	C2134	U2197	U2272	G2354	U2430	A2511	U2586	A2686
G1640	U1716	G1799	A1885	U1969	A2052	C2135	G2198	U2273	U2355	U2431	C2512	U2587	G2687
U1641			G1886	C1970	C2053	C2136	G2199	U2274	A2356	C2432	G2513	A2593	G2688
			G1887	C1971	C2054	U2137	G2200	U2275	A2357	C2433	G2514	A2594	
			A1888	U1972	U2055	U2138	G2201	A2276	A2358	G2434	G2515	G2595	A2691
C1645	G1719	A1802	U1893	U1973	G2056	U2139	U2202	U2277		U2435	G2516	G2596	G2692
U1646	U1722	C1803	U1894	U1974	U2057	U2140	U2203	U2278		U2436	G2517	G2597	G2693
U1647	A1723	U1808	A1895	A1981	G2058	U2141	U2204	U2279		U2437	G2518	G2598	A2694
	U1724	U1809	G1886	A1982	A2059	C2142	U2205	G2280		G2438	G2519	G2599	
G1651	U1725	G1810	G1887	G1983	A2060	A2143	U2206	G2281		G2439	U2520	G2611	
C1652	A1727	U1812	G1888	U1984	G2061	C2144	U2207	G2282		U2440	U2521	U2614	
A1653		U1813	U1889	A1989	A2062	U2145	U2208	G2283			U2522		G2703
U1654	U1733	A1814	A1900	A1989	U2063	G2146	U2209	G2284		C2451	G2523		
A1655	U1734	U1815	A1901	C1992	G2064	U2147	U2210	C2290		U2452	G2524		
C1656	A1735	A1820	G1902	G1993	C2065	A2148	U2211	A2295		C2453			A2708
C1657	U1738	U1823	A1905	C1994	A2066	C2149	U2212	A2296		A2454			C2709
G1658	G1739	C1824	G1910	C1995	C2072	G2150	U2213	A2297		A2455			C2710
C1660	U1740	U1825	G1911	A1995		U2151	U2214	A2298		A2456			G2711
A1661	G1741	U1826	G1912	A1996		A2152	U2215	A2299		G2457			C2712
C1662	G1742	C1826	G1913	A1997		C2082	U2216	G2300		U2458			G2713
G1664	U1743	U1827	A1913	A1998		A2083	U2217	U2301		A2459			C2714
	G1744	U1828	A1914	C1999		G2084	U2218	A2302		A2460			G2715
A1667	A1745	C1829	A1915	C1999		G2085	U2219	A2303		U2461			U2716
		U1830	A1916	A2006		U2153	U2220	G2304		A2462			U2717
G1673	U1751	C1834	A1917	A2007		G2154	U2221	U2305		A2463			U2718
G1674	G1752	U1835	A1918	A2008		U2155	U2222	U2306		U2464			A2719
		U1836	A1919	A2009		C2098	U2223	A2307		U2465			C2720
A1677	C1755	C1835	G1920	G2009		G2156	U2224	U2308		A2466			C2721
G1678	U1756	U1836	G1921	A2010		C2157	U2225	G2309		C2467			A2722
A1679	G1757	U1837	A1922	U2011		U2158	U2226	C2310		C2468			U2642
U1680	U1758	U1838	A1923	C2012		U2159	U2227	C2311		A2469			U2643
U1681	U1759	C1933	C1933	G2013		U2160	U2228	C2312		C2470			U2644
C1682		A1839	G1932	G2014		G2161	U2229	C2313		C2471			U2645
G1683		U1840	G1933	G2015		C2162	U2230	A2314		C2472			C2649
U1684	G1763		G1934	C2019		U2163	U2231	A2315		G2473			
A1685	U1764		G1935	C2020		A2164	U2232	A2316		U2474			U2730
G1686	G1765		G1936	U2021		C2165	U2233	A2317		G2475			G2731
G1687				G2022		C2166	U2234	U2320		A2476			C2732
				U2023		G2167	U2235	U2321		G2477			C2733
G1690	C1770		A1941	U2024		C2168	U2240	U2322		U2478			G2743
A1691	C1771		A1942	U2025		U2169	U2241	U2323		A2479			G2744
C1693	A1774		C1943	A2026		C2170	U2242	U2324					U2745
G1694	G1775		U1944	A2027		G2171	U2243	U2325		A2480			
A1695	U1776		A1945				U2244	U2326		G2411			A2750
G1696	G1777		U1946				U2245	U2327		U2412			U2751
U1697	U1778		A1947				U2246	U2328		G2413			G2752
G1698	C1779		A1948				U2247	U2329		U2414			A2753
A1699	C1780		C1953				U2248	U2330		U2415			C2754
	G1782		A1956				U2249	U2331		U2416			U2755
U1704	C1783		A1957				U2250	U2332		U2417			U2756
C1705	A1784		G1958				U2251	U2333		G2418			G2757
G1706	U1785		U1959				U2252	U2334		U2419			U2758
U1707	G1786		U1960				U2253	U2335		U2420			C2759
U1708	G1787						U2254	U2336		U2421			G2760
							U2255	U2337		U2422			G2761
							U2256	U2338		U2423			A2762
							U2257	U2339		U2424			
							U2258	U2340		U2425			G2766
							U2259	U2341		U2426			
							U2260	U2342		U2427			
							U2261	U2343		U2428			
							U2262	U2344		U2429			
							U2263	U2345		U2430			
							U2264	U2346		U2431			
							U2265	U2347		U2432			
							U2266	U2348		U2433			
							U2267	U2349		U2434			
							U2268	U2350		U2435			
							U2269	U2351		U2436			
							U2270	U2352		U2437			
							U2271	U2353		U2438			
							U2272	U2354		U2439			
							U2273	U2355		U2440			
							U2274	U2356		U2441			
							U2275	U2357		U2442			
							U2276	U2358		U2443			
							U2277	U2359		U2444			
							U2278	U2360		U2445			
							U2279	U2361		U2446			
							U2280	U2362		U2447			
							U2281	U2363		U2448			
							U2282	U2364		U2449			
							U2283	U2365		U2450			
							U2284	U2366		U2451			
							U2285	U2367		U2452			
							U2286	U2368		U2453			
							U2287	U2369		U2454			
							U2288	U2370		U2455			
							U2289	U2371		U2456			
							U2290	U2372		U2457			
							U2291	U2373		U2458			
							U2292	U2374		U2459			
							U2293	U2375		U2460			
							U2294	U2376		U2461			
							U2295	U2377		U2462			
							U2296	U2378		U2463			
							U2297	U2379		U2464			
							U2298	U2380		U2465			
							U2299	U2381		U2466			
							U2300	U2382		U2467			
							U2301	U2383		U2468			
							U2302	U2384		U2469			
							U2303	U2385		U2470			
							U2304	U2386		U2471			
							U2305	U2387		U2472			
							U2306	U2388		U2473			
							U2307	U2389		U2474			
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							U2309	U2391		U2476			
							U2310	U2392		U2477			
							U2311	U2393		U2478			
							U2312	U2394		U2479			
							U2313	U2395		U2480			
							U2314	U2396		U2481			
							U2315	U2397		U2482			
							U2316	U2398		U2483			
							U2317	U2399		U2484			
							U2318	U2400		U2485			
							U2319	U2401		U2486			
							U2320	U2402		U2487			
							U2321	U2403		U2488			
							U2322	U2404		U2489			
							U2323	U2405		U2490			
							U2324	U2406		U2491			
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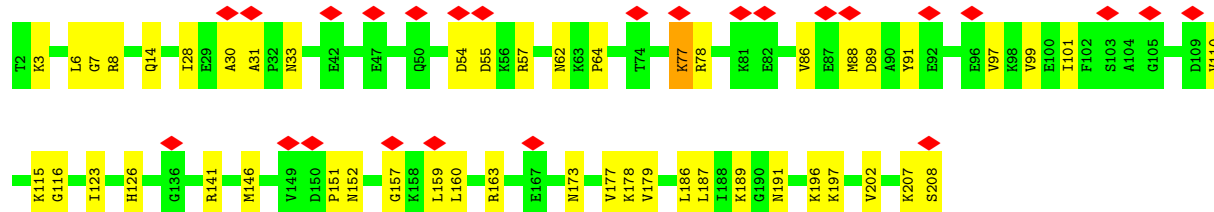
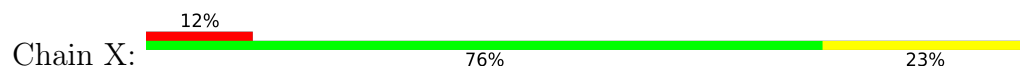
• Molecule 22: 5S ribosomal RNA



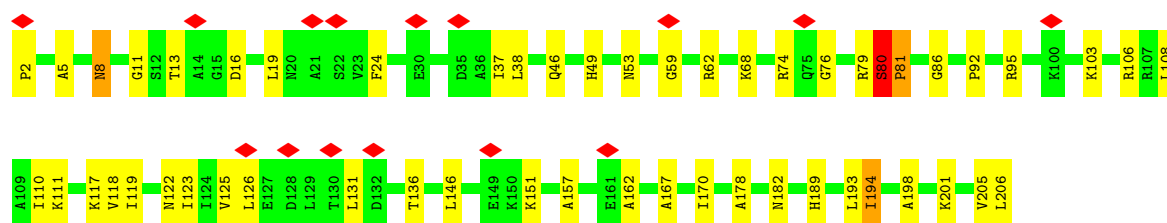
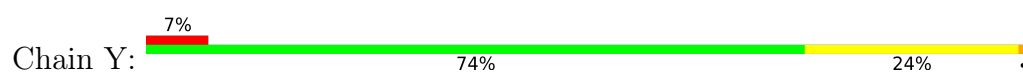
• Molecule 23: 50S ribosomal protein L2



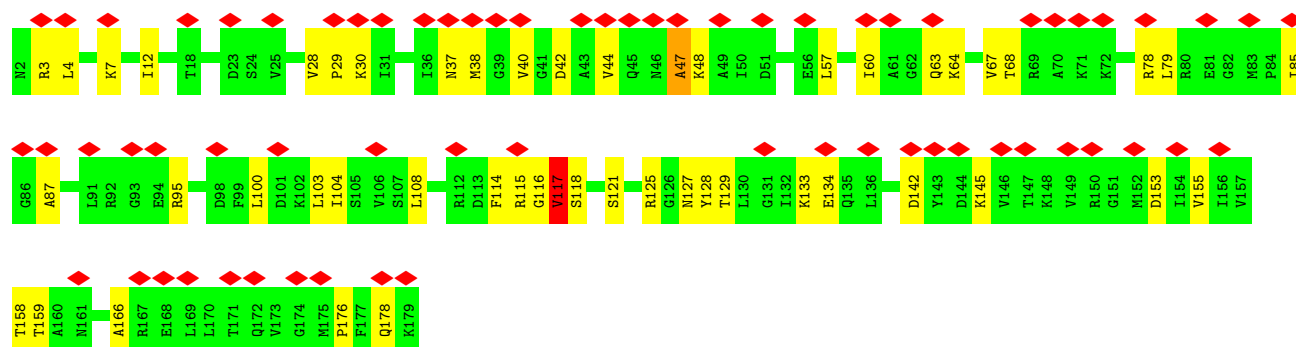
• Molecule 24: 50S ribosomal protein L3



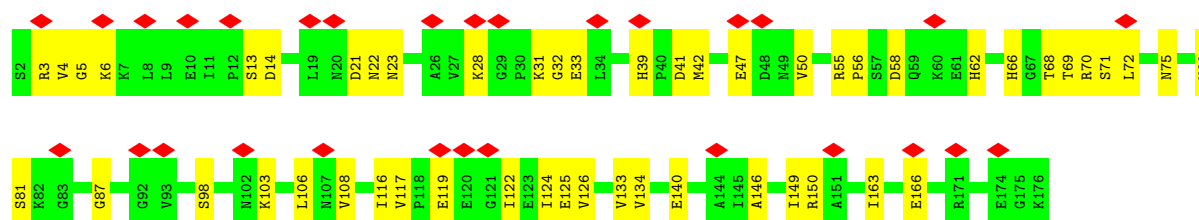
• Molecule 25: 50S ribosomal protein L4



• Molecule 26: 50S ribosomal protein L5



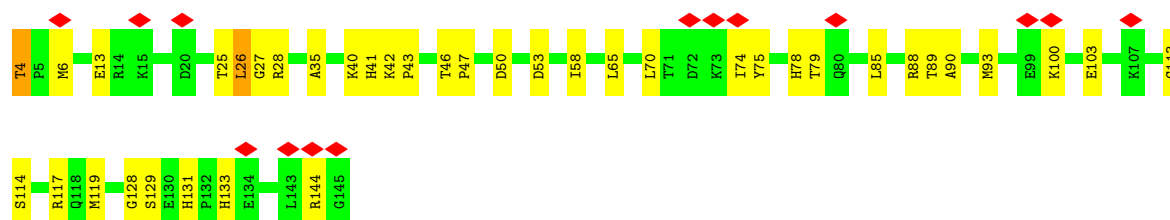
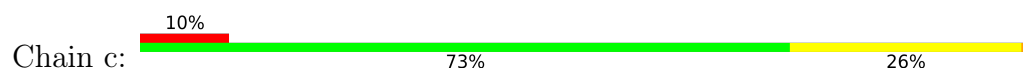
• Molecule 27: 50S ribosomal protein L6



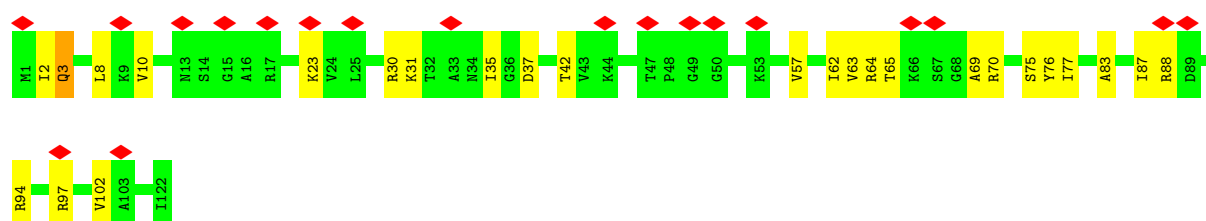
• Molecule 28: 50S ribosomal protein L10



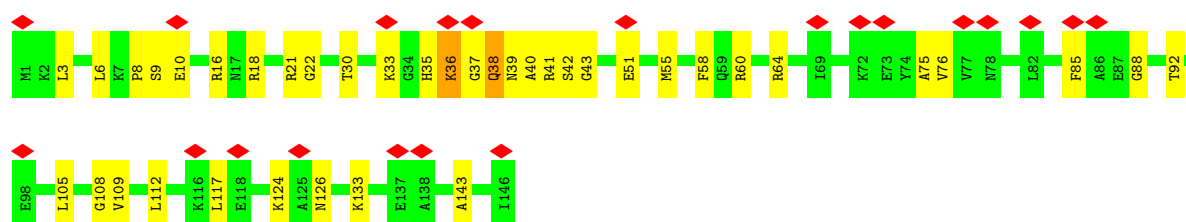
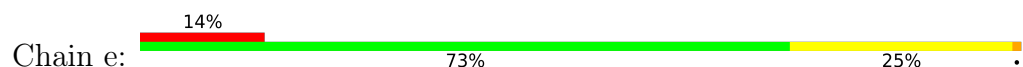
- Molecule 29: 50S ribosomal protein L13



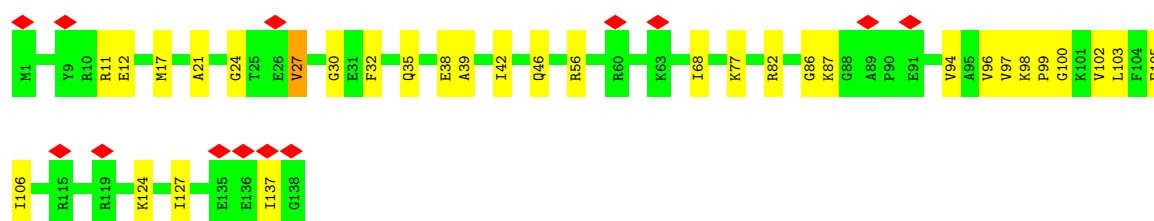
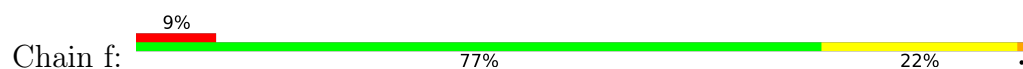
- Molecule 30: 50S ribosomal protein L14



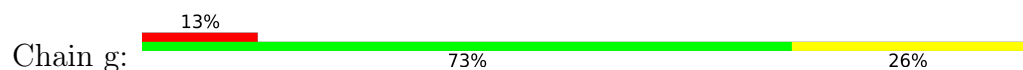
- Molecule 31: 50S ribosomal protein L15

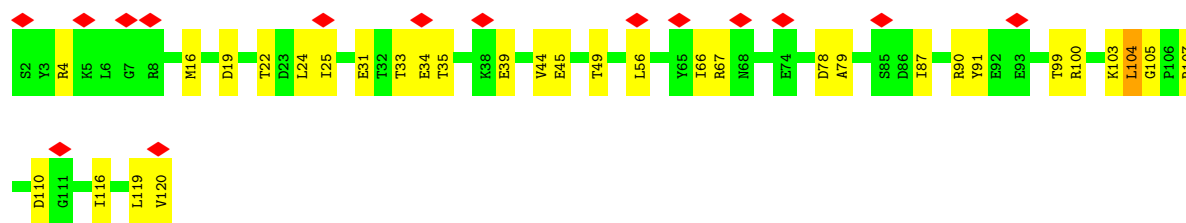


- Molecule 32: 50S ribosomal protein L16

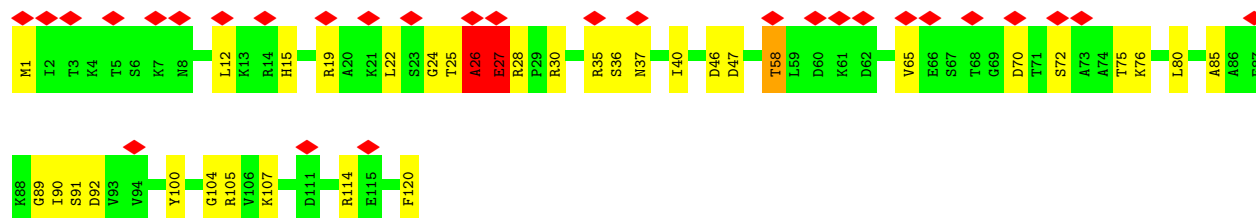


- Molecule 33: 50S ribosomal protein L17

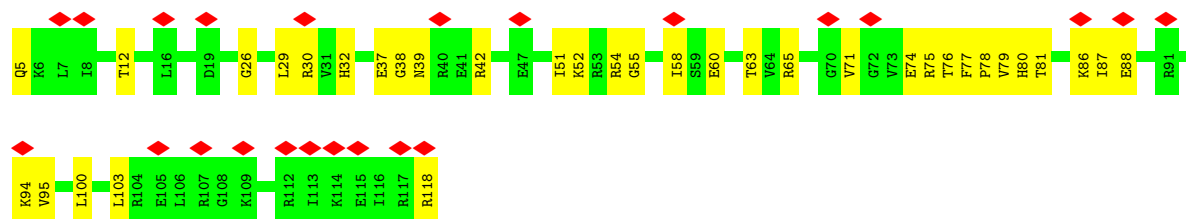




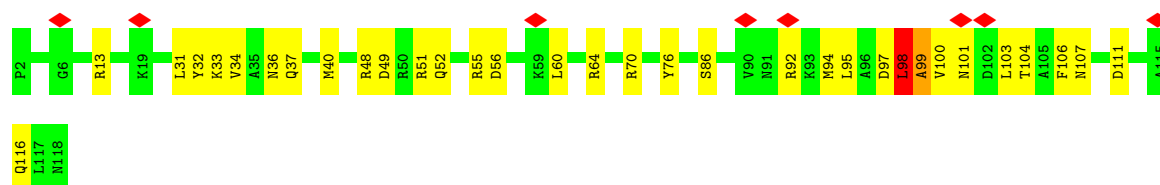
• Molecule 34: 50S ribosomal protein L18



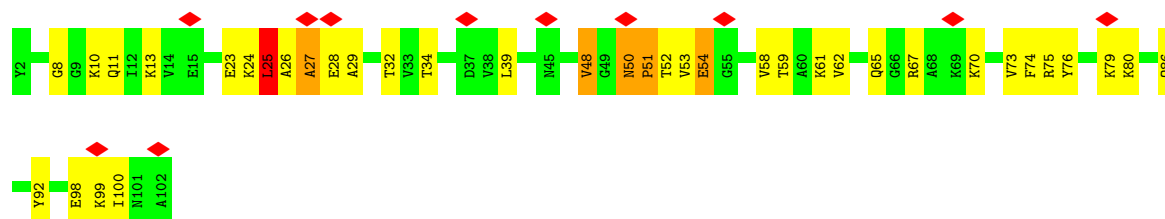
• Molecule 35: 50S ribosomal protein L19



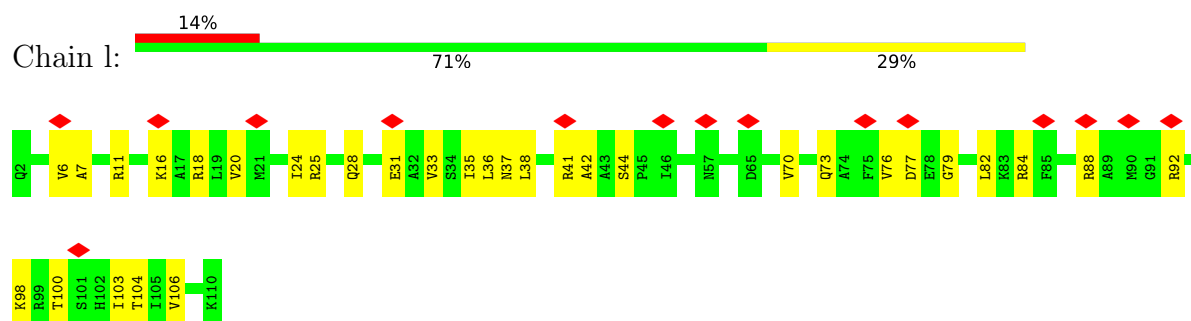
• Molecule 36: 50S ribosomal protein L20



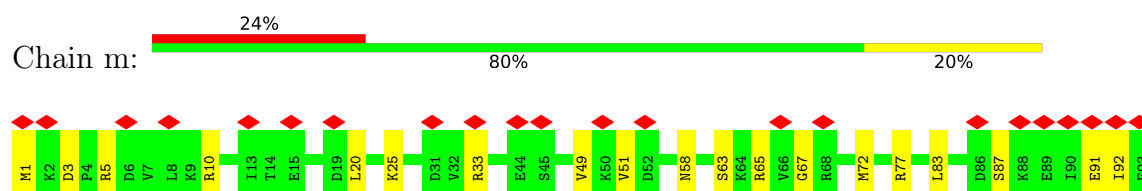
• Molecule 37: 50S ribosomal protein L21



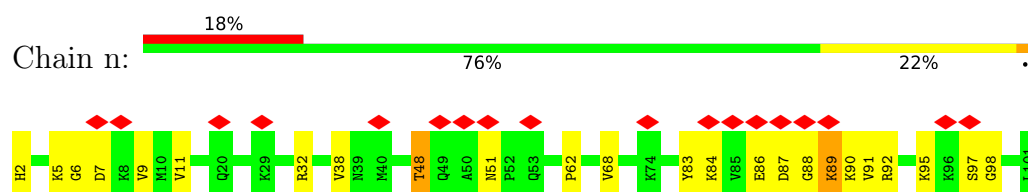
- Molecule 38: 50S ribosomal protein L22



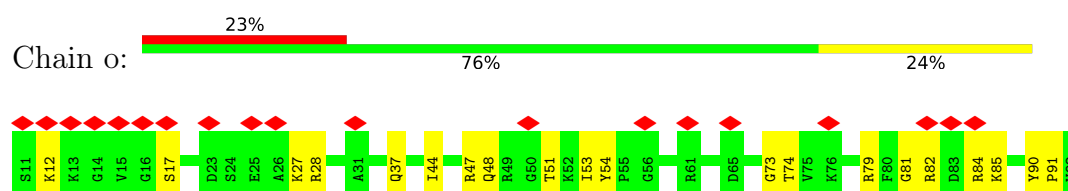
- Molecule 39: 50S ribosomal protein L23



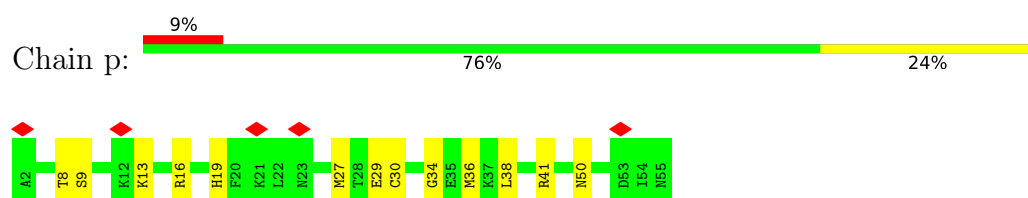
- Molecule 40: 50S ribosomal protein L24



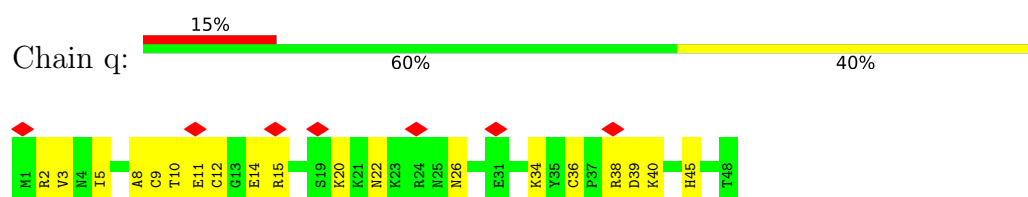
- Molecule 41: 50S ribosomal protein L27



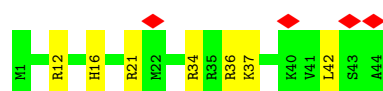
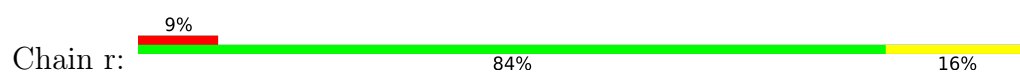
- Molecule 42: 50S ribosomal protein L32



- Molecule 43: 50S ribosomal protein L33 1



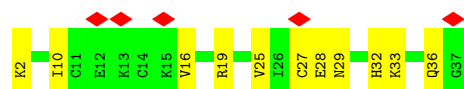
- Molecule 44: 50S ribosomal protein L34



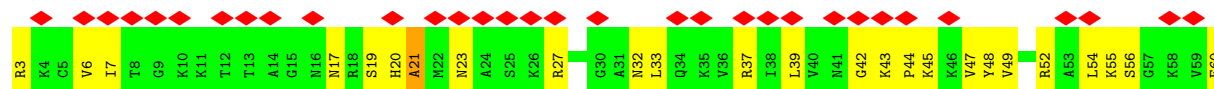
- Molecule 45: 50S ribosomal protein L35



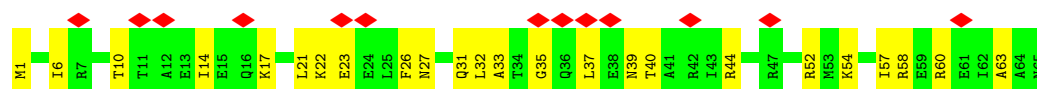
- Molecule 46: 50S ribosomal protein L36



- Molecule 47: 50S ribosomal protein L28



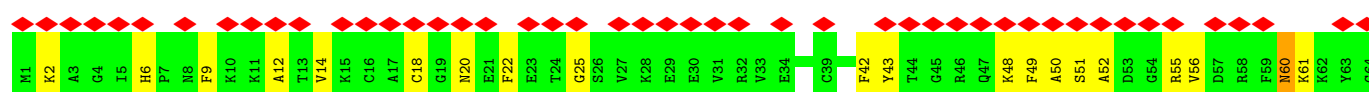
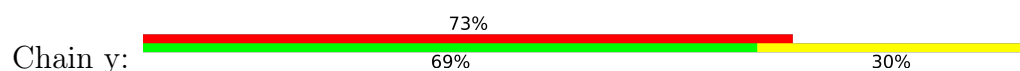
- Molecule 48: 50S ribosomal protein L29



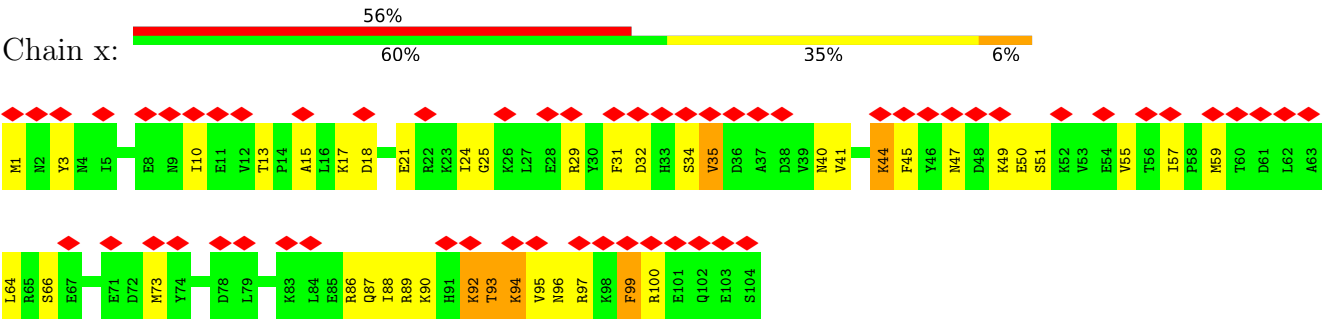
- Molecule 49: 50S ribosomal protein L30



- Molecule 50: 50S ribosomal protein L31



● Molecule 51: Ribosome hibernation promotion factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24546	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	55.100	Depositor
Minimum map value	-33.631	Depositor
Average map value	0.128	Depositor
Map value standard deviation	2.386	Depositor
Recommended contour level	11	Depositor
Map size (Å)	487.8, 487.8, 487.8	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	A	0.39	0/37074	0.50	5/57834 (0.0%)
2	B	0.23	0/895	0.52	0/1117
3	C	0.84	5/839 (0.6%)	1.10	8/1047 (0.8%)
4	D	0.21	0/796	0.48	0/992
5	E	0.24	0/660	0.50	0/822
6	F	0.26	0/380	0.50	0/472
7	G	0.18	0/612	0.39	0/762
8	H	0.22	0/524	0.47	0/652
9	I	0.22	0/520	0.65	0/647
10	J	0.22	0/408	0.52	0/507
11	K	0.21	0/471	0.46	0/587
12	L	0.24	0/548	0.61	0/682
13	M	0.22	0/443	0.64	0/552
14	N	0.24	0/240	0.55	0/297
15	O	0.19	0/352	0.47	0/437
16	P	0.24	0/356	0.56	0/442
17	Q	0.21	0/344	0.48	0/427
18	R	0.24	0/284	0.76	1/352 (0.3%)
19	S	0.24	0/319	0.62	0/397
20	T	0.22	0/344	0.39	0/427
21	U	0.44	0/70307	0.57	8/109687 (0.0%)
22	V	0.36	0/2678	0.54	0/4174
23	W	0.47	0/2148	0.72	2/2881 (0.1%)
24	X	0.43	0/1597	0.74	0/2140
25	Y	0.43	0/1580	0.76	2/2132 (0.1%)
26	Z	0.33	0/1423	0.83	3/1910 (0.2%)
27	a	0.34	0/1360	0.63	0/1832
28	b	0.32	0/963	0.82	3/1298 (0.2%)
29	c	0.47	0/1146	0.77	2/1542 (0.1%)
30	d	0.44	0/927	0.77	0/1245
31	e	0.42	0/1093	0.82	2/1457 (0.1%)
32	f	0.43	0/1120	0.71	2/1496 (0.1%)
33	g	0.46	0/960	0.71	0/1284
34	h	0.34	0/921	0.86	4/1236 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.42	0/949	0.71	0/1269
36	j	0.49	0/952	0.74	0/1266
37	k	0.45	0/797	0.87	2/1070 (0.2%)
38	l	0.44	0/851	0.81	0/1146
39	m	0.40	0/759	0.72	0/1011
40	n	0.40	0/764	0.87	2/1022 (0.2%)
41	o	0.46	0/638	0.69	0/847
42	p	0.52	0/433	0.81	0/574
43	q	0.36	0/406	0.68	0/540
44	r	0.49	0/370	0.77	0/483
45	s	0.47	0/519	0.79	2/680 (0.3%)
46	t	0.39	0/291	0.65	0/383
47	u	0.42	0/448	1.02	5/596 (0.8%)
48	v	0.34	0/531	0.67	0/707
49	w	0.46	0/457	0.68	0/613
50	y	0.36	0/513	0.75	0/683
51	x	0.41	0/878	0.93	3/1178 (0.3%)
All	All	0.42	5/145188 (0.0%)	0.59	56/217834 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
29	c	0	1
40	n	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	5	VAL	C-O	-13.56	1.07	1.24
3	C	6	ASN	CA-C	10.90	1.66	1.52
3	C	6	ASN	N-CA	10.36	1.60	1.46
3	C	5	VAL	N-CA	9.47	1.58	1.46
3	C	6	ASN	C-O	6.62	1.32	1.24

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6	ASN	CA-C-N	-16.93	98.68	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6	ASN	C-N-CA	-16.93	98.68	119.84
3	C	5	VAL	N-CA-C	14.49	139.48	109.34
37	k	50	ASN	C-N-CD	-11.29	78.72	125.00
34	h	27	GLU	N-CA-C	-10.80	99.08	112.47
31	e	117	LEU	CA-C-N	9.85	139.43	121.70
31	e	117	LEU	C-N-CA	9.85	139.43	121.70
3	C	6	ASN	CA-C-O	8.25	131.47	120.16
40	n	48	THR	CA-C-N	8.06	136.20	121.70
40	n	48	THR	C-N-CA	8.06	136.20	121.70
47	u	21	ALA	N-CA-C	-7.86	100.68	111.28
3	C	6	ASN	N-CA-C	7.37	126.10	109.81
47	u	45	LYS	CA-C-N	6.57	133.52	121.70
47	u	45	LYS	C-N-CA	6.57	133.52	121.70
3	C	5	VAL	CA-C-O	-6.52	112.63	120.78
29	c	26	LEU	CA-C-N	6.51	133.41	121.70
29	c	26	LEU	C-N-CA	6.51	133.41	121.70
32	f	137	ILE	CA-C-N	6.42	133.25	121.70
32	f	137	ILE	C-N-CA	6.42	133.25	121.70
51	x	99	PHE	N-CA-C	-6.23	104.84	112.88
3	C	5	VAL	O-C-N	-6.13	114.90	122.57
26	Z	47	ALA	CA-C-N	6.06	132.61	121.70
26	Z	47	ALA	C-N-CA	6.06	132.61	121.70
21	U	1245	G	O4'-C1'-N9	6.03	117.24	108.20
47	u	23	ASN	CA-C-N	5.96	132.42	121.70
47	u	23	ASN	C-N-CA	5.96	132.42	121.70
3	C	75	VAL	N-CA-C	-5.86	107.79	113.53
18	R	31	VAL	N-CA-C	-5.82	107.62	113.20
34	h	65	VAL	CA-C-N	5.80	132.15	121.70
34	h	65	VAL	C-N-CA	5.80	132.15	121.70
45	s	20	GLY	CA-C-N	5.72	132.00	121.70
45	s	20	GLY	C-N-CA	5.72	132.00	121.70
25	Y	8	ASN	CA-C-N	5.70	132.43	121.54
25	Y	8	ASN	C-N-CA	5.70	132.43	121.54
28	b	108	ILE	CA-C-N	5.57	129.01	120.82
28	b	108	ILE	C-N-CA	5.57	129.01	120.82
26	Z	117	VAL	N-CA-C	5.55	120.88	109.34
21	U	2785	U	P-O3'-C3'	5.52	128.48	120.20
1	A	1111	A	P-O3'-C3'	5.51	128.47	120.20
21	U	377	G	C2'-C3'-O3'	5.46	117.70	109.50
37	k	50	ASN	N-CA-C	-5.44	100.26	112.23
1	A	1210	A	P-O3'-C3'	5.39	128.28	120.20
21	U	785	C	C2'-C3'-O3'	5.25	121.57	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	214	LYS	CA-C-N	5.20	131.05	121.70
23	W	214	LYS	C-N-CA	5.20	131.05	121.70
21	U	2376	C	O4'-C1'-N1	5.18	115.97	108.20
21	U	2785	U	C2'-C3'-O3'	5.16	117.23	109.50
28	b	93	ALA	N-CA-C	-5.16	108.01	114.56
34	h	26	ALA	N-CA-C	-5.07	100.00	110.80
1	A	1330	U	N1-C1'-C2'	5.06	119.59	112.00
21	U	1245	G	P-O3'-C3'	5.06	127.79	120.20
1	A	1461	U	P-O3'-C3'	5.04	127.76	120.20
1	A	1503	A	P-O3'-C3'	5.04	127.76	120.20
51	x	47	ASN	CA-C-N	5.04	131.16	121.54
51	x	47	ASN	C-N-CA	5.04	131.16	121.54
21	U	271	C	C2'-C3'-O3'	5.02	121.23	113.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	c	4	THR	Peptide
40	n	95	LYS	Peptide

5.2 Too-close contacts [i](#)

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	A	33115	0	16675	337	0
2	B	896	0	244	1	0
3	C	840	0	241	7	0
4	D	797	0	224	3	0
5	E	661	0	197	4	0
6	F	381	0	104	0	0
7	G	613	0	164	3	0
8	H	525	0	146	1	0
9	I	521	0	155	0	0
10	J	409	0	104	3	0
11	K	472	0	135	1	0
12	L	549	0	157	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	444	0	129	7	0
14	N	241	0	62	0	0
15	O	353	0	94	1	0
16	P	357	0	95	2	0
17	Q	345	0	90	0	0
18	R	285	0	76	0	0
19	S	320	0	89	8	0
20	T	345	0	89	0	0
21	U	62767	0	31584	779	0
22	V	2395	0	1212	27	0
23	W	2111	0	2200	77	0
24	X	1575	0	1642	36	0
25	Y	1561	0	1647	47	0
26	Z	1404	0	1467	45	0
27	a	1342	0	1388	34	0
28	b	955	0	990	22	0
29	c	1123	0	1162	33	0
30	d	920	0	977	36	0
31	e	1081	0	1132	32	0
32	f	1097	0	1165	21	0
33	g	953	0	983	19	0
34	h	912	0	947	22	0
35	i	936	0	1008	57	0
36	j	940	0	1005	57	0
37	k	786	0	826	37	0
38	l	842	0	899	24	0
39	m	752	0	802	14	0
40	n	754	0	809	15	0
41	o	630	0	644	16	0
42	p	426	0	445	14	0
43	q	401	0	413	18	0
44	r	367	0	410	8	0
45	s	512	0	564	20	0
46	t	288	0	330	8	0
47	u	444	0	487	19	0
48	v	530	0	568	17	0
49	w	455	0	491	14	0
50	y	503	0	494	29	0
51	x	866	0	863	49	0
All	All	133097	0	78824	1780	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 (1780) 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)
36:j:95:LEU:HA	36:j:98:LEU:CD2	1.22	1.57
36:j:95:LEU:CA	36:j:98:LEU:HD21	1.38	1.48
36:j:94:MET:O	36:j:98:LEU:CD2	1.71	1.39
26:Z:3:ARG:NH1	50:y:22:PHE:HB3	1.33	1.36
21:U:28:A:N6	21:U:558:G:C2	1.94	1.34
26:Z:3:ARG:HH12	50:y:22:PHE:CB	1.41	1.33
30:d:3:GLN:HG3	30:d:31:LYS:O	1.17	1.32
35:i:60:GLU:CB	35:i:79:VAL:HG21	1.61	1.29
36:j:95:LEU:HA	36:j:98:LEU:CG	1.64	1.27
51:x:97:ARG:HD3	51:x:99:PHE:CE2	1.72	1.22
3:C:6:ASN:O	3:C:7:PRO:C	1.66	1.19
51:x:97:ARG:CD	51:x:99:PHE:HE2	1.56	1.18
30:d:3:GLN:NE2	30:d:31:LYS:HB3	1.57	1.18
40:n:88:GLY:O	40:n:91:VAL:HG23	1.43	1.17
30:d:3:GLN:CG	30:d:31:LYS:O	1.92	1.16
36:j:97:ASP:O	36:j:100:VAL:HG23	1.44	1.15
37:k:26:ALA:O	37:k:65:GLN:NE2	1.81	1.13
51:x:97:ARG:HD3	51:x:99:PHE:HE2	0.98	1.13
30:d:3:GLN:HE21	30:d:31:LYS:CB	1.60	1.13
36:j:95:LEU:CA	36:j:98:LEU:CD2	2.09	1.12
1:A:473:G:N2	1:A:477:A:H2	1.46	1.11
21:U:760:G:N2	21:U:765:A:H2	1.48	1.11
19:S:68:GLY:HA3	50:y:61:LYS:HE2	1.11	1.10
36:j:94:MET:O	36:j:98:LEU:HD23	0.92	1.08
19:S:68:GLY:CA	50:y:61:LYS:HE2	1.85	1.07
21:U:1888:A:N6	21:U:1912:G:H21	1.53	1.07
51:x:93:THR:CG2	51:x:94:LYS:H	1.67	1.06
35:i:78:PRO:HB2	35:i:81:THR:HG22	1.36	1.04
1:A:388:G:H21	1:A:391:A:N6	1.55	1.04
51:x:31:PHE:HE1	51:x:92:LYS:NZ	1.55	1.04
1:A:1269:G:N2	1:A:1284:A:H62	1.55	1.04
37:k:50:ASN:O	37:k:51:PRO:O	1.73	1.04
35:i:60:GLU:HB3	35:i:79:VAL:HG21	1.08	1.03
51:x:93:THR:HG23	51:x:94:LYS:N	1.65	1.03
35:i:75:ARG:NE	35:i:77:PHE:CZ	2.25	1.02
3:C:6:ASN:O	3:C:8:VAL:N	1.91	1.02
35:i:78:PRO:HG2	35:i:81:THR:HG21	1.40	1.02
1:A:471:U:H3	1:A:479:G:H1	1.02	1.02
1:A:473:G:N2	1:A:477:A:C2	2.23	1.01
21:U:275:A:H62	21:U:296:G:N2	1.57	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d:3:GLN:HE21	30:d:31:LYS:CG	1.73	1.00
21:U:2137:U:H3	21:U:2210:G:H1	1.05	1.00
1:A:1358:A:H62	1:A:1382:G:N2	1.59	1.00
25:Y:80:SER:OG	25:Y:81:PRO:HD2	1.62	1.00
21:U:1886:G:N2	21:U:1914:A:H62	1.60	0.99
35:i:78:PRO:HB2	35:i:81:THR:CG2	1.92	0.99
23:W:144:ILE:O	23:W:154:LEU:HB2	1.63	0.98
36:j:94:MET:C	36:j:98:LEU:CD2	2.36	0.98
21:U:351:G:H21	21:U:374:A:N6	1.61	0.98
21:U:2381:A:N7	21:U:2394:G:N2	2.10	0.98
51:x:93:THR:HG23	51:x:94:LYS:H	0.85	0.98
1:A:791:A:H62	1:A:809:G:N2	1.60	0.98
1:A:1269:G:H21	1:A:1284:A:N6	1.62	0.98
36:j:94:MET:C	36:j:98:LEU:HD23	1.89	0.97
1:A:1313:G:N2	1:A:1342:A:H62	1.62	0.97
21:U:1888:A:H62	21:U:1912:G:N2	1.61	0.96
1:A:437:U:H3	1:A:439:A:H62	1.13	0.96
1:A:388:G:N2	1:A:391:A:N7	2.13	0.96
19:S:68:GLY:HA3	50:y:61:LYS:CE	1.97	0.95
51:x:31:PHE:CE1	51:x:92:LYS:NZ	2.31	0.95
37:k:24:LYS:O	37:k:25:LEU:O	1.85	0.95
21:U:1888:A:N7	21:U:1912:G:N2	2.15	0.94
21:U:159:U:H3	21:U:169:G:H1	1.14	0.94
21:U:19:G:H1	21:U:567:U:H3	1.10	0.94
51:x:93:THR:O	51:x:96:ASN:N	2.01	0.93
37:k:26:ALA:C	37:k:65:GLN:HE22	1.76	0.93
26:Z:95:ARG:NH2	50:y:9:PHE:CE2	2.36	0.93
21:U:2873:G:H21	21:U:2893:A:H62	1.17	0.93
21:U:1735:A:H62	21:U:1742:G:H21	1.02	0.92
1:A:1313:G:H21	1:A:1342:A:H62	0.96	0.92
22:V:79:C:H42	22:V:93:U:H3	1.13	0.92
21:U:9:U:H3	21:U:2658:A:H62	1.00	0.92
21:U:9:U:H3	21:U:2658:A:N6	1.68	0.92
21:U:1886:G:H21	21:U:1914:A:H62	0.92	0.91
1:A:960:U:H3	1:A:1240:G:H1	1.16	0.91
1:A:791:A:H62	1:A:809:G:H21	0.92	0.90
21:U:1513:U:H3	21:U:1572:G:H1	0.95	0.90
21:U:1496:G:H1	21:U:1507:U:H3	0.98	0.89
28:b:111:GLY:O	28:b:113:ILE:N	2.05	0.89
35:i:60:GLU:CB	35:i:79:VAL:CG2	2.50	0.89
21:U:883:G:H1	21:U:989:U:H3	1.16	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1087:U:H3	21:U:1160:G:H1	1.21	0.89
1:A:1358:A:H62	1:A:1382:G:H21	0.94	0.88
21:U:1491:A:N6	21:U:1512:G:H1	1.71	0.88
1:A:1358:A:N6	1:A:1382:G:H21	1.70	0.88
35:i:60:GLU:C	35:i:79:VAL:HG23	1.98	0.88
21:U:1735:A:H62	21:U:1742:G:N2	1.70	0.88
30:d:3:GLN:HG3	30:d:31:LYS:C	1.98	0.88
36:j:95:LEU:N	36:j:98:LEU:HD21	1.89	0.88
1:A:388:G:H21	1:A:391:A:H62	1.17	0.88
23:W:144:ILE:HB	23:W:154:LEU:HD12	1.56	0.88
21:U:1759:U:H3	21:U:1774:A:H62	0.91	0.87
26:Z:116:GLY:O	26:Z:117:VAL:HG12	1.73	0.87
21:U:2665:U:H3	21:U:2811:G:H1	1.19	0.87
1:A:791:A:N6	1:A:809:G:H21	1.71	0.87
22:V:70:G:H21	22:V:102:A:H62	1.22	0.87
21:U:760:G:N2	21:U:765:A:C2	2.31	0.87
23:W:154:LEU:CD1	23:W:176:LEU:HD21	2.05	0.87
21:U:275:A:H62	21:U:296:G:H21	1.18	0.86
51:x:31:PHE:HE1	51:x:92:LYS:HZ3	0.87	0.86
25:Y:80:SER:CB	25:Y:81:PRO:HD2	2.06	0.86
1:A:1313:G:H21	1:A:1342:A:N6	1.73	0.86
40:n:88:GLY:O	40:n:91:VAL:CG2	2.24	0.86
21:U:1735:A:N6	21:U:1742:G:H21	1.73	0.86
36:j:95:LEU:HA	36:j:98:LEU:HD21	0.88	0.85
1:A:331:U:H3	1:A:335:A:H62	1.17	0.85
36:j:95:LEU:CB	36:j:98:LEU:HD21	2.07	0.85
51:x:93:THR:O	51:x:95:VAL:N	2.09	0.85
35:i:78:PRO:CG	35:i:81:THR:HG21	2.05	0.85
21:U:1886:G:H21	21:U:1914:A:N6	1.75	0.84
21:U:351:G:H21	21:U:374:A:H62	1.24	0.84
21:U:28:A:C6	21:U:558:G:C2	2.65	0.84
21:U:904:A:H61	21:U:967:G:H1	1.21	0.84
19:S:68:GLY:CA	50:y:61:LYS:CE	2.54	0.83
36:j:95:LEU:HA	36:j:98:LEU:HG	1.60	0.83
21:U:1238:G:N1	21:U:1289:U:O2	2.13	0.82
29:c:43:PRO:HB2	36:j:100:VAL:HG11	1.59	0.82
34:h:26:ALA:O	34:h:28:ARG:HG3	1.79	0.82
21:U:1393:A:H62	21:U:1416:G:H21	1.23	0.82
25:Y:80:SER:CB	25:Y:81:PRO:CD	2.58	0.82
35:i:75:ARG:NH2	35:i:77:PHE:CE1	2.46	0.81
1:A:437:U:H3	1:A:439:A:N6	1.79	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:k:24:LYS:O	37:k:25:LEU:C	2.23	0.81
35:i:60:GLU:HB2	35:i:79:VAL:HG21	1.59	0.81
21:U:275:A:N6	21:U:296:G:H21	1.78	0.81
21:U:1888:A:H62	21:U:1912:G:H21	0.84	0.81
21:U:1497:G:H1	21:U:1505:U:H3	1.28	0.81
22:V:6:U:H3	22:V:110:G:H1	1.29	0.81
51:x:97:ARG:CD	51:x:99:PHE:CE2	2.47	0.81
23:W:154:LEU:HD13	23:W:176:LEU:HD21	1.61	0.81
30:d:3:GLN:NE2	30:d:31:LYS:HD3	1.96	0.80
30:d:3:GLN:HE22	30:d:31:LYS:HD3	1.45	0.80
21:U:673:A:H62	31:e:112:LEU:HB3	1.47	0.80
21:U:1799:G:H22	21:U:2011:U:H3	1.29	0.80
21:U:2873:G:N2	21:U:2893:A:H62	1.78	0.80
30:d:3:GLN:NE2	30:d:31:LYS:CG	2.45	0.80
21:U:904:A:N6	21:U:967:G:H1	1.78	0.80
28:b:111:GLY:C	28:b:113:ILE:H	1.90	0.79
25:Y:80:SER:OG	25:Y:81:PRO:CD	2.30	0.79
35:i:78:PRO:CB	35:i:81:THR:CG2	2.61	0.79
21:U:2900:A:HO2'	35:i:5:GLN:N	1.81	0.79
3:C:6:ASN:O	3:C:9:GLY:N	2.16	0.79
31:e:37:GLY:O	31:e:39:ASN:N	2.16	0.78
35:i:78:PRO:HG2	35:i:81:THR:CG2	2.12	0.78
21:U:2128:U:H3	21:U:2219:G:H1	0.85	0.78
35:i:60:GLU:C	35:i:79:VAL:CG2	2.56	0.78
51:x:92:LYS:HZ2	51:x:92:LYS:HB3	1.47	0.78
21:U:28:A:N6	21:U:558:G:N3	2.32	0.78
21:U:1111:U:O2	21:U:1119:A:C6	2.37	0.78
26:Z:116:GLY:O	26:Z:117:VAL:CG1	2.31	0.77
36:j:95:LEU:O	36:j:98:LEU:HG	1.85	0.77
21:U:199:A:N6	21:U:878:G:H21	1.82	0.76
21:U:1497:G:N1	21:U:1505:U:N3	2.32	0.76
1:A:473:G:H21	1:A:477:A:H2	0.82	0.76
21:U:1289:U:H2'	31:e:18:ARG:HH22	1.50	0.76
1:A:1269:G:H21	1:A:1284:A:H62	0.82	0.75
3:C:137:ILE:O	3:C:141:MET:CA	2.34	0.75
30:d:3:GLN:HE21	30:d:31:LYS:HB3	1.13	0.75
21:U:1465:A:H62	21:U:1626:U:H3	1.33	0.75
1:A:388:G:N2	1:A:391:A:C5	2.53	0.75
23:W:153:GLN:O	23:W:154:LEU:O	2.05	0.75
22:V:38:U:H5	50:y:2:LYS:HE3	1.51	0.74
36:j:95:LEU:CA	36:j:98:LEU:CG	2.54	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:75:ARG:NH2	35:i:77:PHE:CZ	2.56	0.74
21:U:1326:A:H62	33:g:110:ASP:HB3	1.53	0.73
21:U:1759:U:H3	21:U:1774:A:N6	1.77	0.73
21:U:28:A:N6	21:U:558:G:N1	2.36	0.73
21:U:1709:A:H61	21:U:2025:C:N4	1.86	0.73
21:U:2543:U:H3	21:U:2599:G:H1	1.34	0.73
21:U:424:G:H1	21:U:444:U:H3	1.37	0.73
30:d:2:ILE:HD11	30:d:65:THR:HG22	1.71	0.73
35:i:78:PRO:CG	35:i:81:THR:CG2	2.67	0.73
21:U:1491:A:N6	21:U:1512:G:N1	2.37	0.73
1:A:331:U:H3	1:A:335:A:N6	1.86	0.72
21:U:1000:G:H1	21:U:1009:U:H3	1.36	0.72
51:x:93:THR:O	51:x:94:LYS:C	2.29	0.72
26:Z:95:ARG:NH2	50:y:9:PHE:CD2	2.56	0.72
26:Z:116:GLY:C	26:Z:117:VAL:CG1	2.62	0.72
1:A:388:G:N2	1:A:391:A:H62	1.87	0.72
31:e:37:GLY:O	31:e:38:GLN:C	2.32	0.72
36:j:98:LEU:C	36:j:100:VAL:H	1.96	0.72
30:d:3:GLN:CD	30:d:31:LYS:HB3	2.13	0.72
51:x:92:LYS:O	51:x:96:ASN:HB2	1.90	0.72
21:U:1347:A:H62	21:U:1651:G:H8	1.38	0.71
21:U:2685:U:C2	21:U:2694:A:N7	2.58	0.71
21:U:1829:C:H42	21:U:1846:G:H22	1.38	0.71
21:U:2873:G:H21	21:U:2893:A:N6	1.87	0.71
25:Y:80:SER:O	25:Y:86:GLY:O	2.08	0.71
35:i:78:PRO:CB	35:i:81:THR:HB	2.19	0.71
49:w:5:GLU:HB2	49:w:57:LYS:HB3	1.73	0.71
21:U:351:G:N2	21:U:374:A:H62	1.89	0.71
30:d:3:GLN:NE2	30:d:31:LYS:CB	2.30	0.71
21:U:1393:A:H62	21:U:1416:G:N2	1.89	0.70
23:W:154:LEU:HD13	23:W:176:LEU:CD2	2.21	0.70
50:y:51:SER:HA	50:y:52:ALA:HB3	1.72	0.70
23:W:144:ILE:CB	23:W:154:LEU:HD12	2.20	0.70
37:k:25:LEU:O	37:k:65:GLN:NE2	2.25	0.70
21:U:1709:A:H61	21:U:2025:C:H42	1.39	0.70
21:U:1847:U:O2'	23:W:154:LEU:O	2.06	0.70
42:p:30:CYS:HB2	42:p:34:GLY:H	1.56	0.69
1:A:1169:G:H1	1:A:1185:A:N6	1.91	0.69
21:U:732:A:H62	21:U:825:G:H21	1.39	0.69
21:U:446:G:OP2	47:u:55:LYS:NZ	2.26	0.69
27:a:116:ILE:HD13	27:a:149:ILE:HG12	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:c:47:PRO:HD3	36:j:60:LEU:HD21	1.75	0.68
21:U:1041:C:N3	29:c:4:THR:N	2.41	0.68
21:U:28:A:C6	21:U:558:G:N3	2.60	0.68
21:U:224:A:N6	21:U:474:U:C2	2.62	0.68
46:t:27:CYS:SG	46:t:28:GLU:N	2.67	0.68
23:W:69:ARG:HH21	23:W:118:SER:HB3	1.59	0.68
30:d:88:ARG:HD3	30:d:94:ARG:HE	1.59	0.68
13:M:56:ILE:O	13:M:60:ILE:CA	2.42	0.68
21:U:28:A:N6	21:U:558:G:N2	2.41	0.68
51:x:25:GLY:O	51:x:29:ARG:HB2	1.94	0.68
21:U:1130:A:H5''	28:b:55:TYR:HA	1.76	0.67
1:A:1169:G:H1	1:A:1185:A:H61	1.42	0.67
26:Z:116:GLY:C	26:Z:117:VAL:HG13	2.20	0.67
21:U:512:G:OP1	44:r:12:ARG:NH2	2.27	0.67
1:A:609:U:H3	1:A:647:G:H1	1.42	0.67
21:U:2333:G:H22	21:U:2341:U:H3	1.43	0.67
51:x:10:ILE:HD12	51:x:44:LYS:HZ1	1.58	0.67
33:g:100:ARG:HE	33:g:120:VAL:HG11	1.59	0.67
21:U:1501:U:O4	21:U:2733:C:N3	2.28	0.67
1:A:1184:G:H2'	1:A:1185:A:H8	1.60	0.66
21:U:929:G:N1	21:U:941:U:N3	2.43	0.66
21:U:1397:G:H21	21:U:1412:A:H62	1.44	0.66
28:b:58:THR:HG21	28:b:83:ALA:HA	1.77	0.66
35:i:75:ARG:CZ	35:i:77:PHE:CZ	2.77	0.66
1:A:388:G:N2	1:A:391:A:N6	2.38	0.66
1:A:471:U:O2	1:A:479:G:N2	2.28	0.66
1:A:347:C:OP2	30:d:97:ARG:NH1	2.28	0.66
51:x:17:LYS:O	51:x:21:GLU:HB2	1.96	0.66
30:d:3:GLN:NE2	30:d:31:LYS:CD	2.58	0.66
21:U:694:G:H2'	21:U:695:G:H8	1.60	0.66
39:m:49:VAL:HG13	39:m:87:SER:HB3	1.77	0.66
21:U:732:A:N6	21:U:825:G:H21	1.94	0.65
1:A:1532:U:H2'	1:A:1533:G:H8	1.61	0.65
1:A:1133:A:H4'	10:J:38:GLY:HA3	1.79	0.65
21:U:52:A:H62	21:U:118:A:H62	1.44	0.65
24:X:6:LEU:H	24:X:33:ASN:HD21	1.43	0.65
1:A:779:C:H1'	1:A:909:C:H42	1.61	0.65
21:U:444:U:H5''	47:u:32:ASN:HB2	1.79	0.65
21:U:2686:A:H62	21:U:2693:G:H21	1.43	0.65
21:U:26:G:H1'	21:U:561:A:H61	1.61	0.65
35:i:60:GLU:O	35:i:79:VAL:HG23	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1111:U:O2	21:U:1119:A:C5	2.49	0.65
21:U:1941:A:H62	21:U:1946:U:H3	1.44	0.65
1:A:984:A:H4'	1:A:985:A:H3'	1.80	0.64
35:i:75:ARG:HE	35:i:77:PHE:HZ	1.37	0.64
21:U:760:G:H21	21:U:765:A:H2	0.75	0.64
21:U:1374:C:OP1	39:m:65:ARG:NH1	2.30	0.64
21:U:2817:C:O2'	21:U:2834:A:N3	2.31	0.64
51:x:97:ARG:HD2	51:x:99:PHE:HE2	1.58	0.64
7:G:80:VAL:O	51:x:100:ARG:HG2	1.98	0.64
21:U:1189:A:N6	29:c:27:GLY:O	2.31	0.64
23:W:43:ARG:NH1	23:W:44:ASN:O	2.31	0.64
28:b:27:ILE:HB	28:b:83:ALA:HB3	1.79	0.64
1:A:561:U:H2'	1:A:562:G:H8	1.63	0.64
21:U:607:G:H1	21:U:622:A:N6	1.96	0.64
21:U:9:U:N3	21:U:2658:A:N6	2.36	0.64
22:V:79:C:N4	22:V:93:U:H3	1.90	0.64
21:U:327:G:N2	21:U:400:U:O2	2.29	0.64
1:A:1335:U:H2'	1:A:1336:G:H8	1.63	0.63
21:U:447:G:O6	47:u:52:ARG:NH1	2.31	0.63
21:U:970:A:O2'	41:o:37:GLN:NE2	2.31	0.63
26:Z:125:ARG:HG3	34:h:1:MET:HE3	1.79	0.63
1:A:1356:G:H22	1:A:1382:G:H2'	1.62	0.63
21:U:830:A:H2'	21:U:831:U:H4'	1.78	0.63
21:U:1403:G:OP1	47:u:3:ARG:NH1	2.31	0.63
34:h:26:ALA:C	34:h:28:ARG:N	2.50	0.63
21:U:268:A:N6	21:U:475:A:N7	2.46	0.63
21:U:2524:G:H5''	32:f:82:ARG:HD3	1.79	0.63
1:A:56:C:OP1	1:A:359:G:N2	2.32	0.63
21:U:2137:U:O2	21:U:2210:G:N2	2.28	0.63
21:U:2314:C:OP2	43:q:2:ARG:NH2	2.32	0.63
21:U:2378:G:OP1	45:s:45:ARG:NH1	2.32	0.63
37:k:98:GLU:HG2	37:k:99:LYS:HG2	1.80	0.63
21:U:1393:A:N6	21:U:1416:G:H21	1.96	0.63
35:i:78:PRO:HB2	35:i:81:THR:CB	2.29	0.62
21:U:199:A:H62	21:U:878:G:H21	1.46	0.62
21:U:659:A:N1	25:Y:46:GLN:NE2	2.47	0.62
26:Z:133:LYS:HG3	26:Z:134:GLU:HG3	1.79	0.62
35:i:60:GLU:OE1	35:i:79:VAL:HG11	1.99	0.62
1:A:1275:G:N2	1:A:1278:A:OP2	2.33	0.62
27:a:42:MET:HG3	27:a:69:THR:HG21	1.80	0.62
21:U:2146:A:N6	21:U:2191:A:OP1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:70:G:N2	22:V:102:A:H62	1.95	0.62
1:A:427:U:H3	1:A:432:G:H1	1.48	0.62
21:U:1653:A:N7	21:U:1656:C:N4	2.47	0.62
21:U:2685:U:N3	21:U:2694:A:C8	2.66	0.62
35:i:75:ARG:HH21	35:i:77:PHE:HE1	1.41	0.62
36:j:94:MET:C	36:j:98:LEU:HD21	2.09	0.62
1:A:683:G:O6	1:A:725:A:N1	2.33	0.62
5:E:92:GLY:HA2	5:E:130:SER:H	1.64	0.62
21:U:353:A:N7	21:U:374:A:N6	2.47	0.62
43:q:36:CYS:SG	43:q:45:HIS:NE2	2.72	0.62
21:U:127:C:OP2	39:m:33:ARG:NH2	2.33	0.61
25:Y:80:SER:HG	25:Y:81:PRO:HD2	1.63	0.61
45:s:54:ASP:OD1	45:s:57:ARG:NH2	2.32	0.61
21:U:1759:U:O4	21:U:1774:A:N7	2.32	0.61
26:Z:40:VAL:HG12	26:Z:42:ASP:H	1.65	0.61
21:U:1880:U:H3	21:U:1920:G:H1	1.48	0.61
25:Y:49:HIS:HD2	25:Y:92:PRO:HB2	1.65	0.61
21:U:673:A:O2'	21:U:674:G:O4'	2.19	0.61
21:U:1238:G:C6	21:U:1289:U:O2	2.54	0.61
25:Y:103:LYS:HA	25:Y:106:ARG:HB2	1.83	0.61
21:U:515:G:OP2	44:r:37:LYS:NZ	2.34	0.61
1:A:960:U:O2	1:A:1240:G:N2	2.34	0.61
21:U:351:G:N2	21:U:374:A:N6	2.42	0.61
21:U:1101:G:N2	21:U:1151:U:O2	2.34	0.61
21:U:1191:C:H2'	21:U:1192:G:H8	1.66	0.61
36:j:98:LEU:C	36:j:100:VAL:N	2.57	0.61
1:A:331:U:O4	1:A:335:A:N7	2.33	0.61
21:U:601:U:H2'	21:U:602:G:H8	1.66	0.61
21:U:2794:A:OP2	21:U:2795:G:N2	2.34	0.61
27:a:41:ASP:HB3	27:a:56:PRO:HG3	1.82	0.61
21:U:515:G:O2'	25:Y:62:ARG:NH2	2.34	0.61
24:X:28:ILE:HB	24:X:186:LEU:HB2	1.82	0.61
25:Y:8:ASN:HB2	25:Y:13:THR:HB	1.83	0.61
26:Z:117:VAL:HA	26:Z:178:GLN:HB2	1.83	0.61
31:e:55:MET:O	31:e:60:ARG:NH1	2.33	0.61
35:i:60:GLU:HB3	35:i:79:VAL:CG2	2.04	0.61
21:U:499:G:N2	21:U:504:A:O2'	2.33	0.60
21:U:2169:G:O6	21:U:2180:U:C4	2.53	0.60
47:u:49:VAL:HG11	47:u:54:LEU:HD22	1.83	0.60
21:U:140:A:N6	21:U:1640:G:O2'	2.35	0.60
21:U:1659:A:N6	38:l:88:ARG:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:194:GLN:NE2	23:W:198:GLU:OE2	2.33	0.60
21:U:268:A:N6	21:U:474:U:O2'	2.34	0.60
21:U:734:C:H42	21:U:834:C:H4'	1.66	0.60
21:U:2315:A:OP2	43:q:22:ASN:ND2	2.35	0.60
1:A:427:U:O2	1:A:432:G:N2	2.29	0.60
21:U:576:G:O2'	21:U:578:A:N7	2.33	0.60
21:U:1148:C:H2'	21:U:1149:A:H8	1.66	0.60
21:U:1820:A:N6	21:U:1857:G:O2'	2.35	0.60
21:U:2194:G:OP2	21:U:2195:G:N2	2.34	0.60
1:A:388:G:N2	1:A:391:A:C6	2.69	0.60
1:A:1005:C:N3	1:A:1056:A:O2'	2.33	0.60
21:U:712:C:H2'	21:U:713:G:H8	1.65	0.60
21:U:828:A:OP1	23:W:217:ARG:NH1	2.34	0.60
28:b:103:HIS:CE1	28:b:107:GLU:O	2.54	0.60
36:j:32:TYR:OH	36:j:36:ASN:ND2	2.34	0.60
21:U:1493:C:O2'	21:U:1592:A:N3	2.33	0.60
30:d:3:GLN:HE21	30:d:31:LYS:HG2	1.62	0.60
51:x:51:SER:OG	51:x:73:MET:SD	2.57	0.60
21:U:879:G:H5'	31:e:38:GLN:HB3	1.82	0.60
43:q:2:ARG:HH21	43:q:22:ASN:HD21	1.49	0.60
21:U:26:G:N1	21:U:559:A:OP2	2.35	0.60
21:U:2197:G:N1	21:U:2199:G:N7	2.48	0.60
21:U:2685:U:O2	21:U:2694:A:N7	2.35	0.60
1:A:473:G:N1	1:A:476:U:OP2	2.34	0.59
21:U:1046:A:O2'	49:w:10:ARG:NH1	2.34	0.59
21:U:1616:G:OP2	23:W:63:ARG:NH1	2.35	0.59
31:e:51:GLU:OE1	45:s:57:ARG:NH1	2.35	0.59
21:U:1347:A:H61	21:U:1653:A:H61	1.49	0.59
21:U:2343:A:H1'	26:Z:155:VAL:HG11	1.85	0.59
24:X:8:ARG:NH1	24:X:197:LYS:O	2.35	0.59
45:s:15:LYS:HB3	45:s:23:LYS:HB2	1.83	0.59
23:W:84:ASP:OD2	23:W:87:ARG:NH1	2.35	0.59
36:j:95:LEU:CA	36:j:98:LEU:HG	2.27	0.59
1:A:777:A:N3	1:A:1522:U:O2'	2.35	0.59
21:U:775:G:H5'	23:W:13:ARG:HH21	1.67	0.59
21:U:1220:G:H2'	21:U:1221:A:H8	1.67	0.59
21:U:2125:U:O4	21:U:2222:C:N3	2.36	0.59
21:U:2760:G:OP1	24:X:173:ASN:ND2	2.35	0.59
23:W:245:SER:O	23:W:246:PRO:C	2.45	0.59
21:U:677:A:OP1	31:e:64:ARG:NH2	2.36	0.59
34:h:26:ALA:H	34:h:28:ARG:H	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2874:G:O2'	21:U:2891:G:N2	2.36	0.59
22:V:54:U:H4'	22:V:55:A:H5'	1.85	0.59
25:Y:80:SER:O	25:Y:86:GLY:C	2.46	0.59
28:b:111:GLY:C	28:b:113:ILE:N	2.54	0.59
36:j:95:LEU:C	36:j:98:LEU:HG	2.27	0.59
1:A:1081:C:H2'	1:A:1082:G:H8	1.68	0.59
21:U:2325:U:H3	21:U:2364:A:H62	1.50	0.59
22:V:41:C:OP1	50:y:6:HIS:NE2	2.22	0.59
37:k:27:ALA:HB1	37:k:62:VAL:HG21	1.85	0.59
1:A:10:A:N6	4:D:196:GLU:O	2.36	0.59
21:U:1706:G:N2	21:U:2717:G:OP1	2.35	0.59
21:U:2685:U:O2	21:U:2694:A:C5	2.56	0.59
35:i:78:PRO:CB	35:i:81:THR:CB	2.80	0.58
33:g:34:GLU:OE2	33:g:103:LYS:NZ	2.33	0.58
36:j:95:LEU:N	36:j:98:LEU:CD2	2.56	0.58
29:c:13:GLU:O	29:c:42:LYS:NZ	2.36	0.58
49:w:17:GLU:HG2	49:w:20:ARG:HD2	1.84	0.58
21:U:1173:A:N7	21:U:2517:A:O2'	2.36	0.58
23:W:81:VAL:HA	23:W:92:ALA:HA	1.85	0.58
25:Y:157:ALA:O	25:Y:201:LYS:NZ	2.35	0.58
1:A:1013:G:N2	1:A:1047:C:N3	2.52	0.58
21:U:277:C:H2'	21:U:278:A:H8	1.68	0.58
21:U:644:G:N2	21:U:650:U:OP1	2.32	0.58
21:U:1181:C:N4	21:U:1184:G:OP2	2.35	0.58
31:e:85:PHE:HB3	31:e:88:GLY:HA3	1.85	0.58
21:U:420:U:H3	21:U:448:A:H62	1.52	0.58
21:U:517:A:OP1	25:Y:79:ARG:NH2	2.33	0.58
21:U:929:G:N2	21:U:941:U:O2	2.36	0.58
21:U:1467:G:O2'	21:U:1540:A:N6	2.37	0.58
31:e:92:THR:HG22	31:e:124:LYS:HB2	1.85	0.58
21:U:505:G:N2	21:U:517:A:OP2	2.35	0.58
34:h:25:THR:HB	34:h:46:ASP:HB2	1.85	0.58
35:i:60:GLU:HB2	35:i:79:VAL:CG2	2.24	0.58
21:U:79:C:O2'	21:U:390:A:N3	2.36	0.58
21:U:827:G:N2	21:U:832:G:N7	2.51	0.58
21:U:2361:C:OP1	41:o:84:ARG:NH1	2.36	0.58
47:u:49:VAL:HG21	47:u:54:LEU:HD13	1.85	0.58
31:e:9:SER:OG	31:e:10:GLU:N	2.37	0.58
21:U:840:A:OP2	21:U:2100:A:O2'	2.21	0.58
23:W:142:HIS:ND1	23:W:193:GLY:O	2.37	0.58
29:c:131:HIS:HD2	29:c:133:HIS:HB2	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:731:G:OP1	44:r:16:HIS:ND1	2.37	0.57
21:U:752:A:OP2	21:U:772:G:N1	2.30	0.57
21:U:2062:A:O2'	21:U:2064:G:OP2	2.21	0.57
21:U:1517:A:H61	21:U:1568:G:H8	1.52	0.57
23:W:144:ILE:CG2	23:W:154:LEU:HD12	2.34	0.57
26:Z:29:PRO:HA	26:Z:159:THR:HB	1.86	0.57
30:d:3:GLN:CG	30:d:31:LYS:HB3	2.34	0.57
48:v:23:GLU:O	48:v:27:ASN:ND2	2.37	0.57
1:A:224:U:HO2'	1:A:473:G:HO2'	1.52	0.57
1:A:418:G:N2	1:A:439:A:N7	2.53	0.57
1:A:457:A:H62	1:A:495:U:H3	1.52	0.57
45:s:15:LYS:HD3	45:s:23:LYS:HD3	1.86	0.57
1:A:1307:C:N4	7:G:114:LYS:O	2.38	0.57
21:U:2518:G:O2'	21:U:2547:A:N6	2.38	0.57
26:Z:68:THR:OG1	26:Z:85:ILE:O	2.23	0.57
37:k:32:THR:HG22	37:k:61:LYS:HG2	1.86	0.57
1:A:871:G:HO2'	1:A:884:G:HO2'	1.51	0.57
21:U:790:A:O2'	21:U:1704:U:OP1	2.22	0.57
21:U:1774:A:H3'	21:U:1775:G:H8	1.70	0.57
29:c:41:HIS:NE2	29:c:53:ASP:OD2	2.36	0.57
32:f:35:GLN:HE21	32:f:100:GLY:HA2	1.68	0.57
33:g:31:GLU:HG2	33:g:116:ILE:HG12	1.85	0.57
36:j:40:MET:HA	37:k:74:PHE:HE2	1.68	0.57
21:U:9:U:C2	21:U:2658:A:N6	2.73	0.57
23:W:63:ARG:HH22	23:W:85:PRO:HD2	1.70	0.57
21:U:525:A:H4'	40:n:32:ARG:HH12	1.70	0.57
21:U:2713:U:OP2	35:i:54:ARG:NH1	2.38	0.57
36:j:52:GLN:HA	36:j:55:ARG:HG2	1.87	0.57
21:U:2859:G:OP1	24:X:57:ARG:NH1	2.38	0.57
37:k:27:ALA:CB	37:k:62:VAL:HG21	2.35	0.57
21:U:753:A:OP1	23:W:7:LYS:NZ	2.37	0.56
21:U:82:G:N1	21:U:102:A:OP2	2.37	0.56
21:U:2844:A:O2'	21:U:2846:A:N7	2.35	0.56
25:Y:8:ASN:HB3	25:Y:11:GLY:H	1.70	0.56
1:A:437:U:N3	1:A:439:A:N6	2.47	0.56
1:A:1356:G:N1	1:A:1383:A:OP2	2.38	0.56
21:U:65:A:O2'	21:U:503:C:N3	2.35	0.56
21:U:118:A:H4'	21:U:119:U:H5'	1.85	0.56
21:U:1888:A:C5	21:U:1912:G:N2	2.73	0.56
21:U:2711:G:O2'	24:X:14:GLN:NE2	2.39	0.56
21:U:2718:U:OP2	21:U:2897:G:N1	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:55:GLY:HA2	35:i:60:GLU:HG2	1.87	0.56
36:j:98:LEU:HD23	36:j:98:LEU:H	1.69	0.56
38:l:28:GLN:HE22	38:l:70:VAL:HG22	1.70	0.56
21:U:20:C:H2'	21:U:21:A:H8	1.69	0.56
21:U:721:G:H5''	25:Y:76:GLY:H	1.71	0.56
21:U:2669:G:OP1	29:c:100:LYS:NZ	2.38	0.56
25:Y:126:LEU:HD13	25:Y:193:LEU:HB3	1.87	0.56
36:j:97:ASP:O	36:j:100:VAL:N	2.38	0.56
50:y:48:LYS:O	50:y:50:ALA:N	2.37	0.56
1:A:1064:C:N4	51:x:50:GLU:OE1	2.36	0.56
21:U:662:U:H2'	21:U:663:G:H8	1.69	0.56
21:U:732:A:H62	21:U:825:G:N2	2.03	0.56
21:U:1306:G:N2	21:U:1307:U:O4	2.36	0.56
23:W:163:GLN:OE1	23:W:175:ARG:NH1	2.38	0.56
34:h:76:LYS:O	34:h:80:LEU:N	2.38	0.56
36:j:95:LEU:HD11	37:k:13:LYS:HB2	1.86	0.56
39:m:63:SER:HA	39:m:72:MET:HA	1.87	0.56
1:A:1141:G:H1	1:A:1152:G:H21	1.54	0.56
21:U:965:A:N3	22:V:78:U:O2'	2.36	0.56
21:U:2143:A:O2'	21:U:2197:G:OP1	2.23	0.56
47:u:20:HIS:O	47:u:21:ALA:HB3	2.05	0.56
21:U:2448:U:OP1	45:s:41:LYS:NZ	2.32	0.56
45:s:57:ARG:HG3	45:s:58:ILE:HG23	1.87	0.56
21:U:1036:A:N3	37:k:75:ARG:NH1	2.53	0.56
51:x:93:THR:C	51:x:95:VAL:N	2.64	0.56
1:A:165:G:H2'	1:A:166:G:H8	1.70	0.56
21:U:28:A:C6	21:U:558:G:N2	2.74	0.56
21:U:2514:G:OP1	32:f:46:GLN:NE2	2.37	0.56
21:U:2703:G:H4'	30:d:30:ARG:HD3	1.88	0.56
22:V:38:U:C5	50:y:2:LYS:HE3	2.37	0.56
51:x:93:THR:CG2	51:x:94:LYS:N	2.38	0.56
21:U:111:U:OP1	48:v:58:ARG:NE	2.37	0.56
21:U:2234:C:H2'	21:U:2235:G:H8	1.70	0.56
21:U:2474:G:OP1	25:Y:74:ARG:NH2	2.39	0.56
21:U:2039:G:OP2	38:l:41:ARG:NH1	2.39	0.55
21:U:2130:G:H1	21:U:2217:U:H3	1.55	0.55
1:A:36:C:H2'	1:A:37:G:H8	1.71	0.55
21:U:2130:G:N2	21:U:2217:U:O2	2.38	0.55
21:U:2562:U:OP1	21:U:2694:A:O2'	2.24	0.55
23:W:144:ILE:HB	23:W:154:LEU:CD1	2.33	0.55
24:X:123:ILE:HD13	24:X:141:ARG:HE	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:112:VAL:O	28:b:112:VAL:HG12	2.07	0.55
1:A:1329:C:N4	19:S:37:ARG:O	2.40	0.55
21:U:199:A:H62	21:U:878:G:N2	2.04	0.55
21:U:704:U:H2'	21:U:705:A:C8	2.40	0.55
21:U:1614:A:OP1	23:W:210:ARG:NH2	2.34	0.55
21:U:2775:U:H1'	27:a:140:GLU:HG2	1.88	0.55
37:k:39:LEU:HD23	37:k:48:VAL:HG21	1.88	0.55
21:U:365:U:H5''	25:Y:136:THR:HG23	1.88	0.55
21:U:1983:G:N1	21:U:2015:G:OP1	2.36	0.55
21:U:2776:G:N1	21:U:2785:U:OP1	2.35	0.55
30:d:42:THR:HG22	30:d:57:VAL:HG22	1.87	0.55
32:f:77:LYS:NZ	32:f:86:GLY:O	2.39	0.55
21:U:1738:U:OP2	21:U:1739:C:N4	2.39	0.55
21:U:2385:C:O3'	41:o:28:ARG:NH2	2.40	0.55
37:k:10:LYS:NZ	37:k:23:GLU:OE2	2.38	0.55
21:U:1271:U:H2'	21:U:1272:G:H8	1.72	0.55
21:U:1503:G:O6	21:U:2731:G:O6	2.24	0.55
21:U:2082:G:H4'	24:X:152:ASN:HD22	1.72	0.55
1:A:722:G:H2'	1:A:723:G:C8	2.42	0.55
21:U:848:G:O6	25:Y:53:ASN:ND2	2.40	0.55
21:U:1173:A:N6	21:U:2517:A:N3	2.54	0.55
21:U:2686:A:H62	21:U:2693:G:N2	2.04	0.55
26:Z:100:LEU:HD23	26:Z:103:LEU:HD12	1.89	0.55
51:x:88:ILE:O	51:x:92:LYS:HG2	2.06	0.55
21:U:1263:G:OP2	37:k:67:ARG:NH1	2.39	0.55
21:U:1713:A:H62	21:U:2020:U:H3	1.54	0.55
21:U:2374:G:O6	21:U:2400:G:N2	2.38	0.55
21:U:2544:C:H2'	21:U:2545:G:H8	1.72	0.55
21:U:2841:C:OP1	42:p:41:ARG:NH2	2.38	0.55
24:X:178:LYS:HB2	24:X:187:LEU:HD12	1.88	0.55
27:a:55:ARG:NH1	27:a:58:ASP:OD1	2.39	0.55
29:c:78:HIS:HD2	29:c:85:LEU:HB3	1.71	0.55
30:d:63:VAL:HG12	30:d:64:ARG:HG3	1.89	0.55
21:U:989:U:OP1	31:e:35:HIS:HB2	2.06	0.55
21:U:1918:A:N3	21:U:2115:U:O2'	2.37	0.55
23:W:145:GLU:HG2	23:W:152:GLY:HA2	1.88	0.55
36:j:99:ALA:O	36:j:106:PHE:HB2	2.07	0.55
21:U:184:G:N3	44:r:36:ARG:NH2	2.54	0.54
21:U:2841:C:O2	21:U:2908:A:O2'	2.24	0.54
21:U:2853:C:H2'	21:U:2854:A:H8	1.72	0.54
25:Y:2:PRO:HB2	25:Y:19:LEU:HD13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:e:105:LEU:HD11	31:e:109:VAL:HB	1.89	0.54
35:i:60:GLU:HB2	35:i:79:VAL:CB	2.36	0.54
1:A:701:U:O2'	1:A:703:A:N7	2.33	0.54
21:U:924:U:N3	21:U:946:G:N1	2.56	0.54
21:U:965:A:OP2	21:U:2297:A:N6	2.40	0.54
21:U:1709:A:N6	21:U:2025:C:H42	2.05	0.54
27:a:28:LYS:HA	27:a:33:GLU:HG2	1.89	0.54
28:b:42:ARG:HA	28:b:45:LEU:HB2	1.89	0.54
38:l:24:ILE:HD11	38:l:36:LEU:HD21	1.89	0.54
1:A:1314:G:N2	1:A:1341:A:OP2	2.40	0.54
21:U:19:G:O6	21:U:567:U:O4	2.26	0.54
21:U:1476:C:H2'	21:U:1477:A:H8	1.72	0.54
1:A:682:G:H2'	1:A:683:G:C8	2.42	0.54
38:l:88:ARG:HB3	38:l:92:ARG:HB2	1.89	0.54
1:A:969:A:HO2'	1:A:994:C:HO2'	1.54	0.54
24:X:31:ALA:HB2	24:X:99:VAL:HG23	1.89	0.54
30:d:3:GLN:CB	30:d:31:LYS:O	2.54	0.54
21:U:275:A:N6	21:U:296:G:N2	2.37	0.54
27:a:31:LYS:NZ	27:a:81:SER:O	2.41	0.54
28:b:26:ILE:HD13	28:b:116:LYS:HE3	1.88	0.54
46:t:2:LYS:N	46:t:33:LYS:O	2.41	0.54
1:A:609:U:H2'	1:A:610:G:H8	1.72	0.54
21:U:724:A:O2'	21:U:2099:G:O2'	2.24	0.54
49:w:7:THR:HG22	49:w:34:THR:HG22	1.89	0.54
1:A:643:C:H2'	1:A:644:A:H8	1.73	0.54
21:U:574:A:OP2	29:c:117:ARG:NH1	2.41	0.54
21:U:2758:G:O3'	24:X:189:LYS:NZ	2.41	0.54
43:q:9:CYS:SG	43:q:10:THR:N	2.80	0.54
51:x:90:LYS:HA	51:x:93:THR:HG22	1.89	0.54
21:U:1067:A:H2'	21:U:1068:G:H4'	1.90	0.54
27:a:3:ARG:HD2	27:a:6:LYS:HD3	1.89	0.54
1:A:1074:G:O2'	1:A:1199:G:N2	2.40	0.54
21:U:1250:G:H5''	21:U:1251:U:H3'	1.89	0.54
1:A:842:U:O2	1:A:863:G:N2	2.37	0.53
21:U:287:G:OP2	21:U:288:C:N4	2.41	0.53
21:U:1087:U:O2	21:U:1160:G:N2	2.31	0.53
21:U:1524:A:H2'	21:U:1525:G:H8	1.73	0.53
21:U:2766:G:H2'	21:U:2767:A:C8	2.43	0.53
21:U:2771:G:O6	21:U:2791:U:C2	2.62	0.53
23:W:152:GLY:O	23:W:156:ARG:NE	2.38	0.53
31:e:75:ALA:HB1	31:e:76:VAL:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1421:C:H2'	1:A:1422:A:C8	2.43	0.53
21:U:880:C:O2'	45:s:57:ARG:NH1	2.41	0.53
26:Z:118:SER:OG	26:Z:128:TYR:OH	2.27	0.53
35:i:37:GLU:OE1	35:i:42:ARG:NH1	2.42	0.53
1:A:1329:C:N4	19:S:36:ARG:O	2.37	0.53
21:U:340:U:H3	21:U:385:G:H1	1.56	0.53
21:U:2129:G:O6	21:U:2218:U:O2	2.27	0.53
27:a:47:GLU:HB2	27:a:50:VAL:HB	1.90	0.53
1:A:556:A:OP2	4:D:2:ALA:N	2.41	0.53
21:U:1046:A:OP2	21:U:1200:G:N1	2.35	0.53
21:U:1246:G:H1'	21:U:1247:G:H5'	1.90	0.53
21:U:2591:U:O2	30:d:23:LYS:NZ	2.42	0.53
21:U:2766:G:H2'	21:U:2767:A:H8	1.73	0.53
32:f:42:ILE:HD12	32:f:97:VAL:HG21	1.89	0.53
34:h:70:ASP:O	34:h:105:ARG:NH1	2.42	0.53
21:U:2721:C:H2'	21:U:2722:A:H8	1.73	0.53
36:j:52:GLN:O	36:j:56:ASP:N	2.40	0.53
21:U:2710:C:OP2	24:X:115:LYS:NZ	2.37	0.53
21:U:987:A:N3	21:U:1231:G:O2'	2.41	0.53
21:U:1304:G:OP1	42:p:16:ARG:NH2	2.41	0.53
21:U:2344:U:O4'	26:Z:127:ASN:ND2	2.39	0.53
26:Z:38:MET:HB2	26:Z:87:ALA:H	1.74	0.53
41:o:73:GLY:HA3	41:o:91:PRO:HA	1.91	0.53
51:x:92:LYS:NZ	51:x:92:LYS:HB3	2.21	0.53
21:U:199:A:N6	21:U:878:G:N2	2.53	0.53
21:U:834:C:OP1	21:U:1809:A:N6	2.42	0.53
21:U:1212:U:H2'	21:U:1213:G:H8	1.73	0.53
21:U:1545:C:H2'	21:U:1546:G:H8	1.74	0.53
21:U:1965:A:N6	21:U:1992:C:O2'	2.42	0.53
21:U:2342:C:O2'	26:Z:37:ASN:ND2	2.39	0.53
24:X:177:VAL:HG12	24:X:178:LYS:HG3	1.90	0.53
49:w:11:SER:OG	49:w:12:VAL:N	2.40	0.53
21:U:121:G:OP1	21:U:150:A:O2'	2.27	0.53
21:U:178:A:O2'	21:U:179:A:N7	2.34	0.53
21:U:254:A:H61	21:U:433:G:H1	1.57	0.53
21:U:1964:G:N2	21:U:1993:G:O5'	2.42	0.53
21:U:2543:U:O4	21:U:2599:G:O6	2.27	0.53
1:A:547:U:OP1	12:L:125:GLN:N	2.40	0.53
1:A:937:G:H1	1:A:1399:U:H3	1.55	0.53
21:U:732:A:N6	21:U:825:G:N2	2.57	0.53
21:U:776:G:OP1	23:W:10:SER:OG	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:57:LEU:HD12	26:Z:60:ILE:HD13	1.90	0.53
26:Z:114:PHE:HE2	50:y:43:TYR:HH	1.55	0.53
1:A:1003:G:O2'	1:A:1004:A:N7	2.42	0.52
21:U:563:C:O2'	38:l:18:ARG:NH2	2.43	0.52
21:U:1425:C:H2'	21:U:1426:A:C8	2.43	0.52
21:U:1659:A:OP1	21:U:1662:C:N4	2.42	0.52
21:U:1863:U:H5''	21:U:1864:G:H5'	1.91	0.52
21:U:2060:A:N3	21:U:2484:G:O2'	2.38	0.52
21:U:2219:G:H2'	21:U:2220:A:C8	2.43	0.52
24:X:55:ASP:HA	24:X:77:LYS:HA	1.90	0.52
26:Z:38:MET:HB3	26:Z:40:VAL:HG23	1.91	0.52
28:b:4:ALA:O	28:b:7:THR:OG1	2.27	0.52
1:A:521:U:H2'	1:A:522:A:H8	1.73	0.52
21:U:1856:U:OP2	23:W:221:ARG:NH2	2.43	0.52
21:U:2169:G:O6	21:U:2180:U:O4	2.28	0.52
21:U:2290:C:H5''	41:o:27:LYS:HZ1	1.73	0.52
27:a:106:LEU:HB3	27:a:108:VAL:HG23	1.90	0.52
33:g:99:THR:HA	33:g:119:LEU:HA	1.92	0.52
21:U:2489:U:H5	21:U:2521:U:H3	1.56	0.52
21:U:2661:A:HO2'	21:U:2836:G:HO2'	1.57	0.52
21:U:2818:C:O2'	21:U:2917:G:N2	2.42	0.52
1:A:1416:C:H2'	1:A:1417:A:H8	1.74	0.52
21:U:372:U:O2	21:U:376:A:N7	2.43	0.52
21:U:1196:C:H2'	21:U:1197:A:H8	1.73	0.52
21:U:1615:A:H3'	23:W:85:PRO:HG3	1.91	0.52
1:A:842:U:H3	1:A:863:G:H1	1.58	0.52
21:U:634:A:OP1	25:Y:95:ARG:NH1	2.43	0.52
21:U:1365:U:O2'	21:U:2039:G:O2'	2.24	0.52
21:U:1365:U:O4	21:U:1692:U:O2'	2.22	0.52
21:U:2561:G:O2'	21:U:2686:A:N1	2.41	0.52
23:W:69:ARG:O	23:W:189:ARG:NH1	2.42	0.52
27:a:103:LYS:HG2	27:a:117:VAL:HG22	1.90	0.52
32:f:12:GLU:O	32:f:87:LYS:NZ	2.39	0.52
1:A:815:C:H2'	1:A:816:A:C8	2.44	0.52
1:A:960:U:O4	1:A:1240:G:O6	2.27	0.52
7:G:81:GLY:HA3	51:x:100:ARG:HD2	1.91	0.52
21:U:254:A:OP1	45:s:7:HIS:NE2	2.37	0.52
21:U:262:G:N3	21:U:667:A:O2'	2.43	0.52
21:U:2300:G:H4'	41:o:28:ARG:HE	1.74	0.52
21:U:2869:A:H1'	35:i:5:GLN:HE21	1.74	0.52
22:V:11:A:N6	22:V:67:G:O2'	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:5:LYS:HG2	23:W:17:THR:HG22	1.90	0.52
30:d:69:ALA:HB3	30:d:77:ILE:HB	1.92	0.52
38:l:28:GLN:H	38:l:31:GLU:HB3	1.74	0.52
1:A:42:C:H2'	1:A:43:G:H8	1.74	0.52
1:A:440:A:H3'	1:A:441:G:H8	1.74	0.52
21:U:337:A:O2'	21:U:338:G:O4'	2.27	0.52
21:U:1242:U:H2'	21:U:1243:A:H8	1.75	0.52
21:U:1516:A:N7	21:U:1517:A:N6	2.57	0.52
21:U:1518:G:O6	21:U:1567:U:O4	2.28	0.52
24:X:99:VAL:HG12	24:X:179:VAL:HG13	1.92	0.52
32:f:35:GLN:HB2	32:f:102:VAL:HG22	1.92	0.52
33:g:22:THR:HA	33:g:25:ILE:HD12	1.92	0.52
35:i:79:VAL:O	35:i:79:VAL:HG12	2.09	0.52
1:A:552:G:H2'	1:A:553:G:H8	1.74	0.52
1:A:723:G:H2'	1:A:724:A:C8	2.45	0.52
2:B:8:GLN:O	2:B:12:ALA:N	2.43	0.52
21:U:1042:A:OP2	36:j:92:ARG:NE	2.33	0.52
21:U:2057:U:H3	21:U:2062:A:H62	1.58	0.52
21:U:2063:U:O2'	21:U:2064:G:O4'	2.28	0.52
21:U:2784:C:OP1	46:t:19:ARG:NH2	2.42	0.52
30:d:2:ILE:HG22	30:d:2:ILE:O	2.08	0.52
48:v:17:LYS:O	48:v:21:LEU:N	2.32	0.52
50:y:12:ALA:H	50:y:25:GLY:HA2	1.75	0.52
19:S:68:GLY:N	50:y:61:LYS:HE2	2.24	0.52
21:U:75:G:OP1	48:v:44:ARG:NH2	2.43	0.52
21:U:583:G:H22	21:U:599:G:H2'	1.75	0.52
21:U:1431:G:N2	21:U:1432:A:N1	2.57	0.52
21:U:2620:C:H2'	21:U:2621:G:H8	1.75	0.52
21:U:2699:G:H2'	21:U:2700:A:H8	1.75	0.52
41:o:53:ILE:HG12	41:o:85:LYS:HB2	1.92	0.52
51:x:13:THR:HG22	51:x:15:ALA:H	1.75	0.52
21:U:1092:A:OP2	28:b:61:ARG:NH1	2.42	0.52
21:U:2133:C:H2'	21:U:2134:A:H8	1.75	0.52
35:i:51:ILE:HG23	35:i:100:LEU:H	1.75	0.52
37:k:8:GLY:HA3	37:k:10:LYS:N	2.25	0.52
50:y:14:VAL:HB	50:y:22:PHE:HB2	1.92	0.52
21:U:2128:U:O4	21:U:2219:G:O6	2.27	0.51
1:A:1126:U:O2	1:A:1193:G:N2	2.42	0.51
29:c:78:HIS:ND1	29:c:79:THR:O	2.43	0.51
33:g:4:ARG:HD2	33:g:39:GLU:HB2	1.92	0.51
47:u:55:LYS:HG2	47:u:55:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:x:34:SER:OG	51:x:59:MET:SD	2.67	0.51
21:U:633:U:OP1	31:e:16:ARG:NH2	2.44	0.51
21:U:1829:C:H42	21:U:1846:G:N2	2.04	0.51
21:U:2478:U:O2'	21:U:2530:C:N4	2.43	0.51
29:c:144:ARG:HH12	36:j:70:ARG:HD3	1.76	0.51
1:A:406:C:H2'	1:A:407:G:H8	1.75	0.51
21:U:80:G:O2'	21:U:337:A:N6	2.43	0.51
21:U:1263:G:O6	37:k:70:LYS:NZ	2.44	0.51
21:U:1363:G:H3'	21:U:1364:C:H4'	1.91	0.51
33:g:33:THR:HG22	33:g:107:ARG:HH12	1.75	0.51
1:A:1525:C:H2'	1:A:1526:G:H8	1.75	0.51
21:U:573:C:N4	21:U:2808:U:OP2	2.44	0.51
21:U:1546:G:N2	23:W:98:ASP:O	2.43	0.51
21:U:2083:A:OP1	21:U:2084:C:O2'	2.27	0.51
31:e:133:LYS:NZ	31:e:143:ALA:O	2.44	0.51
1:A:332:G:N1	1:A:335:A:OP2	2.37	0.51
19:S:68:GLY:N	50:y:61:LYS:CE	2.74	0.51
21:U:1897:C:H3'	21:U:1898:G:H8	1.76	0.51
26:Z:158:THR:HG21	26:Z:166:ALA:HB1	1.92	0.51
1:A:1295:C:H2'	1:A:1296:A:H4'	1.91	0.51
4:D:164:TYR:O	4:D:177:THR:N	2.42	0.51
21:U:1174:A:O2'	21:U:2519:G:OP1	2.24	0.51
21:U:1202:A:O4'	36:j:51:ARG:NH1	2.44	0.51
21:U:1829:C:N4	21:U:1846:G:H22	2.06	0.51
21:U:2320:U:H2'	21:U:2321:U:C6	2.46	0.51
21:U:2476:G:N2	21:U:2479:A:OP2	2.35	0.51
30:d:69:ALA:N	30:d:77:ILE:O	2.39	0.51
21:U:116:G:OP2	21:U:118:A:O2'	2.28	0.51
21:U:999:A:H2'	21:U:1000:G:H8	1.76	0.51
21:U:1464:A:N6	21:U:1626:U:OP2	2.40	0.51
21:U:2922:U:H2'	21:U:2923:A:H8	1.76	0.51
37:k:73:VAL:HB	37:k:86:GLN:HB3	1.91	0.51
21:U:607:G:H21	36:j:37:GLN:HE22	1.59	0.51
21:U:2307:A:OP2	32:f:11:ARG:NH2	2.40	0.51
21:U:664:C:OP2	25:Y:103:LYS:NZ	2.41	0.51
21:U:747:G:O2'	21:U:1677:A:N3	2.40	0.51
27:a:125:GLU:N	27:a:133:VAL:O	2.44	0.51
1:A:62:A:OP1	1:A:339:G:N1	2.38	0.50
1:A:203:A:H2'	1:A:204:A:H8	1.76	0.50
1:A:1356:G:N2	1:A:1357:U:O4	2.38	0.50
21:U:563:C:OP1	42:p:13:LYS:NZ	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1478:G:H2'	21:U:1479:G:C8	2.46	0.50
21:U:1799:G:O2'	21:U:1967:A:OP1	2.27	0.50
1:A:330:C:N3	1:A:340:G:N2	2.59	0.50
21:U:61:A:H1'	48:v:40:THR:HB	1.93	0.50
21:U:86:C:H4'	21:U:103:U:H1'	1.94	0.50
21:U:553:A:N3	21:U:555:C:N4	2.60	0.50
21:U:1065:U:OP1	21:U:1081:U:O2'	2.28	0.50
29:c:113:GLY:O	29:c:117:ARG:NH1	2.45	0.50
39:m:91:GLU:HG3	39:m:92:ILE:H	1.76	0.50
1:A:1313:G:N2	1:A:1342:A:N6	2.45	0.50
21:U:706:C:H2'	21:U:707:G:H8	1.77	0.50
21:U:1034:A:OP1	49:w:11:SER:N	2.38	0.50
21:U:1828:G:N1	21:U:1848:A:OP2	2.43	0.50
21:U:2856:G:OP1	24:X:57:ARG:NH2	2.44	0.50
25:Y:80:SER:HB3	25:Y:81:PRO:HD2	1.89	0.50
30:d:3:GLN:HG3	30:d:31:LYS:HB3	1.93	0.50
40:n:9:VAL:HG13	40:n:68:VAL:HG13	1.92	0.50
1:A:216:G:H21	1:A:475:A:H61	1.60	0.50
1:A:800:G:N1	1:A:1508:U:OP1	2.42	0.50
1:A:1045:G:H2'	1:A:1046:G:C8	2.46	0.50
1:A:1245:A:H4'	1:A:1313:G:H4'	1.94	0.50
21:U:342:A:N1	21:U:366:A:O2'	2.35	0.50
23:W:39:LYS:NZ	23:W:57:GLY:O	2.35	0.50
51:x:40:ASN:C	51:x:41:VAL:HG13	2.37	0.50
1:A:456:A:O2'	1:A:494:G:N2	2.45	0.50
1:A:926:G:H2'	1:A:927:G:H8	1.76	0.50
21:U:250:G:O2'	21:U:253:G:O6	2.30	0.50
21:U:2809:G:N1	29:c:103:GLU:OE1	2.39	0.50
24:X:146:MET:HE1	24:X:160:LEU:HD21	1.92	0.50
25:Y:24:PHE:HB3	25:Y:118:VAL:HG21	1.93	0.50
32:f:17:MET:HE2	32:f:96:VAL:HG13	1.93	0.50
47:u:17:ASN:HD21	47:u:27:ARG:HD2	1.76	0.50
51:x:44:LYS:O	51:x:50:GLU:O	2.30	0.50
1:A:415:A:H2'	1:A:416:G:H8	1.77	0.50
21:U:1053:C:OP1	29:c:40:LYS:NZ	2.42	0.50
21:U:1517:A:H2'	21:U:1518:G:C8	2.46	0.50
21:U:2392:U:OP1	45:s:40:GLN:NE2	2.42	0.50
1:A:409:C:H2'	1:A:410:G:H8	1.75	0.50
1:A:1496:G:H2'	1:A:1497:G:C8	2.47	0.50
21:U:2501:G:N2	21:U:2558:G:O6	2.45	0.50
24:X:54:ASP:OD2	24:X:78:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:n:7:ASP:OD2	40:n:92:ARG:NH1	2.45	0.50
44:r:34:ARG:HG3	44:r:42:LEU:HD12	1.93	0.50
46:t:16:VAL:HG22	46:t:25:VAL:HG22	1.94	0.50
51:x:92:LYS:HZ2	51:x:92:LYS:CB	2.21	0.50
21:U:27:G:O2'	21:U:28:A:N7	2.44	0.50
21:U:340:U:OP1	40:n:90:LYS:HD3	2.12	0.50
21:U:492:C:O2'	21:U:496:A:N3	2.42	0.50
38:l:6:VAL:HG22	38:l:104:THR:HG22	1.94	0.50
21:U:226:A:N6	21:U:454:G:O2'	2.45	0.50
21:U:901:U:H2'	21:U:902:G:H8	1.77	0.50
21:U:1836:G:N2	21:U:1839:A:OP2	2.34	0.50
21:U:2030:A:H2'	21:U:2031:G:H8	1.77	0.50
21:U:2163:A:H2	21:U:2188:G:H1'	1.76	0.50
21:U:2342:C:H2'	21:U:2343:A:H8	1.77	0.50
21:U:2394:G:O6	45:s:43:LYS:NZ	2.42	0.50
29:c:88:ARG:NH1	29:c:93:MET:SD	2.82	0.50
34:h:26:ALA:C	34:h:28:ARG:H	2.18	0.50
37:k:26:ALA:C	37:k:28:GLU:H	2.18	0.50
1:A:1025:G:H2'	1:A:1026:A:H8	1.76	0.49
21:U:557:U:H4'	21:U:1275:G:H4'	1.93	0.49
21:U:2757:U:H2'	21:U:2758:G:H8	1.77	0.49
47:u:33:LEU:HD22	47:u:48:TYR:HB3	1.94	0.49
51:x:86:ARG:O	51:x:90:LYS:HB2	2.12	0.49
1:A:790:A:H3'	1:A:791:A:H8	1.76	0.49
1:A:936:G:O6	51:x:90:LYS:NZ	2.36	0.49
1:A:1543:C:H3'	1:A:1544:A:C8	2.47	0.49
5:E:12:GLU:N	5:E:40:GLY:O	2.45	0.49
21:U:1936:G:O6	21:U:1953:C:N4	2.45	0.49
21:U:2284:G:N2	41:o:17:SER:OG	2.45	0.49
21:U:2544:C:H2'	21:U:2545:G:C8	2.48	0.49
21:U:2688:G:N2	21:U:2691:A:OP2	2.32	0.49
23:W:144:ILE:C	23:W:154:LEU:HB2	2.36	0.49
50:y:56:VAL:HG11	50:y:60:ASN:HD22	1.77	0.49
21:U:514:G:OP2	44:r:34:ARG:NH2	2.36	0.49
21:U:2897:G:O2'	21:U:2898:A:O4'	2.29	0.49
24:X:196:LYS:HG2	24:X:197:LYS:HG3	1.94	0.49
30:d:88:ARG:HE	30:d:94:ARG:HA	1.77	0.49
33:g:19:ASP:OD1	33:g:67:ARG:NE	2.45	0.49
38:l:38:LEU:HD23	42:p:38:LEU:HB3	1.93	0.49
1:A:30:G:O2'	1:A:304:U:OP1	2.28	0.49
1:A:366:U:H2'	1:A:367:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1169:G:O6	1:A:1191:G:O6	2.30	0.49
21:U:726:C:H2'	21:U:727:A:H8	1.78	0.49
21:U:1825:U:H2'	21:U:1826:C:C6	2.47	0.49
21:U:2665:U:O4	21:U:2811:G:O6	2.31	0.49
1:A:692:G:N2	11:K:41:GLY:O	2.46	0.49
1:A:928:A:H2'	1:A:929:A:C8	2.47	0.49
21:U:854:U:OP2	31:e:41:ARG:NH2	2.43	0.49
21:U:1069:U:OP2	21:U:1071:G:O2'	2.27	0.49
21:U:2620:C:H2'	21:U:2621:G:C8	2.47	0.49
23:W:132:LEU:HD23	23:W:135:ILE:HD12	1.94	0.49
35:i:26:GLY:HA3	35:i:95:VAL:HG21	1.93	0.49
38:l:33:VAL:O	38:l:37:ASN:ND2	2.46	0.49
49:w:5:GLU:HA	49:w:36:VAL:HG22	1.93	0.49
1:A:942:C:H2'	1:A:943:G:C8	2.48	0.49
1:A:944:C:H42	1:A:948:A:N6	2.09	0.49
1:A:1013:G:H2'	1:A:1014:A:H4'	1.94	0.49
21:U:1513:U:O4	21:U:1572:G:O6	2.31	0.49
21:U:2512:C:O2	32:f:124:LYS:NZ	2.41	0.49
21:U:2824:G:O2'	21:U:2826:A:N6	2.46	0.49
22:V:35:C:O2	22:V:46:A:O2'	2.30	0.49
27:a:150:ARG:HA	27:a:163:ILE:HB	1.95	0.49
1:A:1503:A:N6	21:U:1942:A:O2'	2.46	0.49
21:U:559:A:N6	21:U:560:A:N1	2.60	0.49
21:U:631:G:OP2	31:e:21:ARG:NH2	2.35	0.49
21:U:1090:U:O2'	21:U:1157:A:N1	2.45	0.49
21:U:1476:C:H2'	21:U:1477:A:C8	2.48	0.49
23:W:211:SER:O	23:W:216:ILE:N	2.44	0.49
23:W:223:SER:HA	23:W:233:GLY:HA2	1.94	0.49
1:A:732:U:H3	1:A:866:C:H5'	1.77	0.49
1:A:803:A:O2'	1:A:1531:G:O2'	2.29	0.49
21:U:726:C:H2'	21:U:727:A:C8	2.48	0.49
21:U:899:C:H5'	49:w:45:GLY:HA3	1.95	0.49
21:U:1284:A:H4'	31:e:8:PRO:HD3	1.94	0.49
22:V:10:G:C2	41:o:79:ARG:HD2	2.47	0.49
25:Y:108:LEU:HA	25:Y:111:LYS:HB2	1.93	0.49
36:j:98:LEU:O	36:j:100:VAL:N	2.46	0.49
1:A:318:G:OP1	16:P:32:ARG:N	2.46	0.49
1:A:343:C:H2'	1:A:344:A:C8	2.48	0.49
1:A:650:A:H4'	1:A:651:A:H5'	1.94	0.49
21:U:403:C:H2'	21:U:404:C:C6	2.48	0.49
21:U:625:C:H2'	21:U:626:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1246:G:O6	21:U:1281:C:N4	2.45	0.49
23:W:209:GLY:O	23:W:213:TRP:N	2.45	0.49
35:i:94:LYS:HG3	35:i:118:ARG:HH21	1.78	0.49
1:A:724:A:H2'	1:A:725:A:C8	2.46	0.49
21:U:1245:G:H2'	21:U:1246:G:H21	1.78	0.49
25:Y:131:LEU:HB2	25:Y:162:ALA:HB1	1.95	0.49
25:Y:157:ALA:HB2	25:Y:198:ALA:HB2	1.95	0.49
45:s:14:PHE:HB3	45:s:22:LEU:HD23	1.93	0.49
1:A:139:A:H2'	1:A:140:A:H8	1.78	0.48
1:A:413:U:H1'	1:A:507:A:H2'	1.94	0.48
1:A:1234:A:OP2	13:M:102:SER:N	2.46	0.48
1:A:1258:C:O2	1:A:1297:A:N6	2.46	0.48
1:A:1325:G:N1	1:A:1328:A:OP2	2.44	0.48
21:U:615:U:O2'	21:U:617:G:OP2	2.28	0.48
38:l:38:LEU:HD22	42:p:27:MET:HE3	1.94	0.48
39:m:49:VAL:HG12	39:m:83:LEU:HD22	1.95	0.48
1:A:23:G:H2'	1:A:24:G:C8	2.48	0.48
1:A:681:U:H2'	1:A:682:G:H8	1.78	0.48
21:U:539:G:O2'	38:l:7:ALA:O	2.26	0.48
21:U:608:C:OP1	37:k:76:TYR:OH	2.27	0.48
21:U:1115:A:O2'	21:U:1143:U:OP1	2.27	0.48
21:U:1334:C:H2'	21:U:1335:A:H8	1.78	0.48
21:U:1465:A:N7	21:U:1626:U:O4	2.46	0.48
21:U:2874:G:N2	21:U:2891:G:O2'	2.46	0.48
23:W:117:MET:N	23:W:128:ASN:OD1	2.45	0.48
35:i:32:HIS:HB2	35:i:86:LYS:H	1.78	0.48
35:i:78:PRO:HG2	35:i:81:THR:CB	2.43	0.48
36:j:97:ASP:O	36:j:99:ALA:N	2.45	0.48
46:t:29:ASN:HB2	46:t:32:HIS:HD2	1.77	0.48
1:A:224:U:H2'	1:A:225:A:C8	2.48	0.48
1:A:779:C:O2'	1:A:909:C:N3	2.41	0.48
1:A:1081:C:H2'	1:A:1082:G:C8	2.48	0.48
1:A:1422:A:H2	1:A:1497:G:H22	1.59	0.48
21:U:1394:G:OP1	23:W:43:ARG:NH2	2.46	0.48
21:U:1618:A:H2'	21:U:1619:A:C8	2.48	0.48
21:U:2275:G:H2'	21:U:2276:A:C8	2.48	0.48
21:U:2361:C:OP1	41:o:54:TYR:OH	2.31	0.48
29:c:70:LEU:HA	29:c:90:ALA:HB3	1.95	0.48
48:v:6:ILE:HG23	48:v:60:ARG:HH21	1.78	0.48
1:A:901:U:H2'	1:A:902:A:H8	1.77	0.48
1:A:944:C:N4	1:A:948:A:H61	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:952:G:H1	1:A:1350:U:H3	1.60	0.48
1:A:1013:G:N2	1:A:1014:A:O2'	2.46	0.48
1:A:1159:U:O2'	10:J:42:LEU:O	2.31	0.48
1:A:1527:G:N3	21:U:1948:A:O2'	2.44	0.48
21:U:1207:C:O2'	37:k:8:GLY:O	2.22	0.48
21:U:1808:U:OP2	21:U:1813:A:N6	2.47	0.48
21:U:2374:G:H5'	21:U:2376:C:H5'	1.95	0.48
27:a:124:ILE:HA	27:a:134:VAL:HA	1.95	0.48
30:d:64:ARG:H	30:d:83:ALA:HB3	1.79	0.48
43:q:9:CYS:SG	43:q:11:GLU:N	2.87	0.48
1:A:70:G:H22	1:A:99:A:H2	1.62	0.48
1:A:499:U:H2'	1:A:500:A:C8	2.49	0.48
1:A:987:A:O2'	1:A:989:C:OP2	2.31	0.48
1:A:1418:C:H2'	1:A:1419:A:C8	2.49	0.48
21:U:717:A:H5''	31:e:43:GLY:HA2	1.95	0.48
21:U:1103:A:O2'	28:b:34:ASN:ND2	2.46	0.48
21:U:1292:G:C2	36:j:33:LYS:HG2	2.48	0.48
21:U:1840:G:N3	23:W:45:ASN:ND2	2.51	0.48
21:U:2275:G:H2'	21:U:2276:A:H8	1.78	0.48
26:Z:115:ARG:O	50:y:42:PHE:CZ	2.66	0.48
27:a:119:GLU:HB2	27:a:122:ILE:HD13	1.95	0.48
31:e:58:PHE:O	45:s:13:ARG:NH1	2.46	0.48
35:i:63:THR:HG22	35:i:76:THR:HG22	1.96	0.48
37:k:59:THR:OG1	37:k:98:GLU:O	2.32	0.48
1:A:344:A:H2'	1:A:345:G:H8	1.78	0.48
1:A:510:C:H1'	1:A:558:C:H1'	1.95	0.48
21:U:247:A:OP2	45:s:8:ARG:NH1	2.46	0.48
21:U:1124:C:O2'	21:U:1134:A:N3	2.42	0.48
23:W:69:ARG:HH11	23:W:104:ILE:HG21	1.77	0.48
32:f:17:MET:HA	32:f:98:LYS:HZ3	1.77	0.48
38:l:11:ARG:HE	38:l:98:LYS:HD2	1.79	0.48
1:A:918:A:H2'	1:A:919:A:C8	2.48	0.48
13:M:75:LEU:O	13:M:79:ARG:CA	2.62	0.48
21:U:970:A:H2'	21:U:971:A:C8	2.49	0.48
21:U:992:G:O6	21:U:1018:G:N2	2.46	0.48
21:U:1074:A:H2'	21:U:1075:A:C8	2.48	0.48
21:U:1212:U:H2'	21:U:1213:G:C8	2.49	0.48
21:U:1582:U:O2'	21:U:1584:U:OP2	2.32	0.48
21:U:1829:C:O2	21:U:1846:G:O6	2.32	0.48
23:W:8:PRO:HB3	23:W:14:ARG:HG2	1.96	0.48
24:X:33:ASN:N	24:X:97:VAL:O	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:b:41:LEU:O	28:b:45:LEU:N	2.46	0.48
46:t:29:ASN:HB2	46:t:32:HIS:CD2	2.49	0.48
47:u:39:LEU:HG	47:u:44:PRO:HG3	1.95	0.48
51:x:45:PHE:HA	51:x:49:LYS:HA	1.96	0.48
1:A:1401:G:O2'	1:A:1512:A:OP1	2.32	0.48
5:E:19:ASN:N	5:E:34:ALA:O	2.47	0.48
21:U:286:U:H3'	21:U:287:G:H8	1.79	0.48
21:U:1681:U:H2'	21:U:1682:C:C6	2.49	0.48
21:U:1944:U:O2'	21:U:1945:A:O4'	2.32	0.48
21:U:2776:G:H21	21:U:2786:A:H62	1.62	0.48
45:s:24:ARG:O	45:s:48:ALA:N	2.46	0.48
1:A:1418:C:H2'	1:A:1419:A:H8	1.77	0.48
21:U:737:C:O3'	23:W:217:ARG:NH2	2.46	0.48
21:U:1316:A:H2'	21:U:1317:G:C8	2.49	0.48
21:U:1316:A:H2'	21:U:1317:G:H8	1.78	0.48
21:U:1384:C:H2'	21:U:1385:G:H8	1.79	0.48
21:U:2197:G:N2	21:U:2199:G:O6	2.43	0.48
26:Z:47:ALA:H	26:Z:48:LYS:HA	1.79	0.48
43:q:36:CYS:HB2	43:q:39:ASP:HB2	1.96	0.48
45:s:17:THR:OG1	45:s:21:LYS:O	2.27	0.48
1:A:1233:U:O2'	1:A:1331:C:OP1	2.30	0.48
21:U:69:C:O2'	21:U:73:A:O2'	2.32	0.48
21:U:720:C:H5'	25:Y:81:PRO:CG	2.43	0.48
21:U:2333:G:O2'	26:Z:153:ASP:OD1	2.29	0.48
27:a:55:ARG:HB3	27:a:66:HIS:CD2	2.49	0.48
32:f:21:ALA:HB2	32:f:98:LYS:HB2	1.96	0.48
32:f:38:GLU:HB2	32:f:127:ILE:HG23	1.95	0.48
42:p:38:LEU:HD11	42:p:41:ARG:HD2	1.95	0.48
1:A:594:G:O2'	1:A:889:C:OP1	2.31	0.47
1:A:958:C:H2'	1:A:959:A:H8	1.79	0.47
1:A:1395:G:H2'	1:A:1396:G:H8	1.78	0.47
21:U:929:G:N1	21:U:941:U:C2	2.82	0.47
21:U:1068:G:N2	21:U:1069:U:O4	2.47	0.47
21:U:1826:C:H5'	23:W:256:GLY:HA2	1.96	0.47
21:U:2296:A:N6	21:U:2301:U:O2	2.42	0.47
21:U:2467:U:O2'	21:U:2469:C:OP1	2.26	0.47
23:W:30:GLU:HG2	23:W:32:SER:H	1.79	0.47
26:Z:3:ARG:HH12	50:y:22:PHE:HB3	0.48	0.47
30:d:2:ILE:HG21	30:d:8:LEU:HD11	1.96	0.47
34:h:19:ARG:NH2	34:h:47:ASP:OD2	2.40	0.47
1:A:205:C:H2'	1:A:206:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:49:G:H2'	22:V:50:A:C8	2.49	0.47
24:X:3:LYS:HG2	24:X:101:ILE:HG21	1.96	0.47
27:a:124:ILE:HG12	27:a:134:VAL:HG22	1.95	0.47
29:c:128:GLY:HA2	29:c:129:SER:HA	1.58	0.47
30:d:63:VAL:HG11	30:d:102:VAL:HG22	1.96	0.47
36:j:104:THR:HB	36:j:107:ASN:HB3	1.96	0.47
37:k:39:LEU:CD2	37:k:48:VAL:HG21	2.44	0.47
38:l:73:GLN:HB2	38:l:106:VAL:HB	1.96	0.47
21:U:20:C:H2'	21:U:21:A:C8	2.48	0.47
21:U:274:A:N3	21:U:415:C:O2'	2.44	0.47
21:U:2276:A:H2'	21:U:2277:C:H6	1.79	0.47
21:U:2315:A:H5''	43:q:26:ASN:HD21	1.79	0.47
21:U:2554:G:O2'	21:U:2771:G:O2'	2.32	0.47
26:Z:3:ARG:NH1	50:y:22:PHE:CD1	2.82	0.47
26:Z:44:VAL:HG12	26:Z:78:ARG:HB2	1.96	0.47
28:b:19:LEU:HD23	28:b:70:ASN:HD21	1.78	0.47
35:i:65:ARG:HG2	35:i:74:GLU:HA	1.96	0.47
39:m:58:ASN:HB3	39:m:77:ARG:HG3	1.96	0.47
21:U:1231:G:OP1	31:e:30:THR:OG1	2.31	0.47
39:m:5:ARG:HH21	48:v:26:PHE:HB3	1.78	0.47
1:A:193:G:N1	1:A:196:U:OP2	2.37	0.47
1:A:499:U:H2'	1:A:500:A:H8	1.79	0.47
21:U:966:U:HO2'	22:V:79:C:HO2'	1.56	0.47
25:Y:167:ALA:HA	25:Y:170:ILE:HD12	1.96	0.47
36:j:97:ASP:C	36:j:99:ALA:N	2.71	0.47
1:A:548:A:H2'	1:A:549:G:C8	2.49	0.47
21:U:346:G:H2'	21:U:347:G:H8	1.79	0.47
21:U:906:G:O2'	21:U:963:G:O6	2.29	0.47
21:U:1545:C:H2'	21:U:1546:G:C8	2.50	0.47
21:U:1919:A:H3'	21:U:1920:G:H8	1.80	0.47
21:U:2472:C:H2'	21:U:2473:G:C8	2.49	0.47
23:W:144:ILE:HB	23:W:154:LEU:CB	2.45	0.47
34:h:104:GLY:H	34:h:107:LYS:H	1.61	0.47
1:A:477:A:H3'	1:A:478:G:H8	1.80	0.47
1:A:643:C:H2'	1:A:644:A:C8	2.50	0.47
1:A:822:U:OP1	1:A:913:A:O2'	2.33	0.47
1:A:937:G:O2'	1:A:1513:A:N6	2.43	0.47
1:A:1078:G:OP1	1:A:1396:G:O2'	2.29	0.47
21:U:198:A:N6	21:U:201:C:OP2	2.47	0.47
21:U:419:G:N2	21:U:448:A:OP2	2.46	0.47
21:U:446:G:N7	47:u:52:ARG:NH2	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:898:U:H2'	21:U:899:C:H6	1.80	0.47
21:U:1306:G:O2'	21:U:2041:G:O6	2.32	0.47
21:U:1493:C:H2'	21:U:1494:G:C8	2.50	0.47
21:U:1835:C:O2	23:W:44:ASN:ND2	2.42	0.47
21:U:1873:U:H2'	21:U:1874:G:C8	2.49	0.47
21:U:2128:U:O2	21:U:2219:G:N2	2.31	0.47
21:U:2624:G:O2'	21:U:2626:G:O6	2.31	0.47
21:U:2624:G:H21	21:U:2626:G:H8	1.63	0.47
21:U:2855:G:OP1	24:X:78:ARG:NH2	2.48	0.47
22:V:6:U:O4	22:V:110:G:O6	2.32	0.47
22:V:101:U:H2'	22:V:102:A:H8	1.79	0.47
24:X:7:GLY:HA3	24:X:30:ALA:HA	1.97	0.47
26:Z:63:GLN:HE21	26:Z:95:ARG:HG2	1.79	0.47
36:j:107:ASN:O	36:j:111:ASP:N	2.42	0.47
1:A:912:G:H2'	1:A:913:A:H8	1.79	0.47
1:A:1108:C:H2'	1:A:1109:G:H8	1.80	0.47
21:U:594:C:OP1	37:k:92:TYR:OH	2.33	0.47
21:U:1316:A:H4'	33:g:16:MET:HE1	1.96	0.47
21:U:1742:G:H4'	21:U:2007:A:H5''	1.97	0.47
21:U:83:G:N2	21:U:102:A:OP2	2.43	0.47
21:U:601:U:H2'	21:U:602:G:C8	2.49	0.47
21:U:1038:C:H2'	21:U:1039:G:C8	2.50	0.47
21:U:1160:G:H2'	21:U:1161:A:H8	1.79	0.47
21:U:2498:A:N6	21:U:2510:G:O2'	2.48	0.47
26:Z:114:PHE:CE2	50:y:43:TYR:OH	2.68	0.47
31:e:37:GLY:C	31:e:39:ASN:N	2.72	0.47
37:k:79:LYS:HB2	37:k:80:LYS:HD2	1.97	0.47
1:A:609:U:OP1	8:H:91:SER:N	2.39	0.47
1:A:1184:G:H2'	1:A:1185:A:C8	2.47	0.47
21:U:314:A:O2'	21:U:316:G:N7	2.48	0.47
21:U:619:A:OP2	21:U:2528:C:O2'	2.29	0.47
21:U:1081:U:O2	21:U:1166:G:O6	2.33	0.47
21:U:1246:G:O6	21:U:1280:G:O6	2.32	0.47
21:U:2353:U:H5''	21:U:2354:G:H5''	1.97	0.47
21:U:2722:A:H2'	21:U:2723:G:H8	1.79	0.47
23:W:270:ILE:HG21	23:W:273:ARG:HB2	1.96	0.47
25:Y:157:ALA:HA	25:Y:178:ALA:HB2	1.97	0.47
47:u:6:VAL:HG13	47:u:7:ILE:HG13	1.96	0.47
1:A:108:C:O2'	16:P:26:ARG:O	2.32	0.46
1:A:968:A:N3	1:A:995:C:O2'	2.41	0.46
21:U:626:G:H2'	21:U:627:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:883:G:O6	21:U:989:U:O4	2.32	0.46
35:i:29:LEU:HD13	35:i:87:ILE:HG23	1.96	0.46
39:m:20:LEU:HB3	39:m:25:LYS:HG3	1.97	0.46
45:s:4:MET:O	45:s:64:ASN:ND2	2.48	0.46
1:A:343:C:H2'	1:A:344:A:H8	1.80	0.46
21:U:277:C:H2'	21:U:278:A:C8	2.49	0.46
21:U:660:G:H2'	21:U:661:A:H8	1.79	0.46
21:U:1512:G:O2'	21:U:1594:G:O2'	2.26	0.46
21:U:2164:A:N6	21:U:2185:G:O2'	2.48	0.46
27:a:146:ALA:HA	27:a:149:ILE:HD12	1.97	0.46
43:q:36:CYS:O	43:q:40:LYS:N	2.46	0.46
46:t:10:ILE:HB	46:t:32:HIS:CE1	2.50	0.46
1:A:851:U:O2	1:A:855:G:O6	2.33	0.46
21:U:789:C:H2'	21:U:790:A:C8	2.50	0.46
21:U:865:G:H21	21:U:1230:A:H62	1.63	0.46
21:U:2120:U:O2	21:U:2257:G:O6	2.34	0.46
21:U:2357:A:H2'	21:U:2358:A:C8	2.51	0.46
21:U:2656:G:O2'	21:U:2810:A:N1	2.39	0.46
21:U:2859:G:H5''	24:X:57:ARG:HH12	1.80	0.46
21:U:2922:U:H2'	21:U:2923:A:C8	2.50	0.46
22:V:75:U:O2	22:V:97:A:N7	2.49	0.46
23:W:124:ILE:HG23	23:W:192:ILE:HD13	1.96	0.46
25:Y:111:LYS:HZ1	25:Y:206:LEU:HB2	1.80	0.46
40:n:2:HIS:O	40:n:92:ARG:NH2	2.48	0.46
1:A:479:G:H2'	1:A:480:G:H8	1.80	0.46
1:A:511:C:OP1	12:L:127:ARG:N	2.45	0.46
1:A:962:U:O2'	1:A:975:A:N1	2.48	0.46
1:A:1125:U:H3	1:A:1194:G:H1	1.63	0.46
1:A:1365:G:H2'	1:A:1366:A:C8	2.50	0.46
1:A:1385:U:H2'	1:A:1386:A:C8	2.50	0.46
13:M:75:LEU:C	13:M:79:ARG:H	2.24	0.46
21:U:601:U:O3'	29:c:114:SER:OG	2.34	0.46
21:U:660:G:H2'	21:U:661:A:C8	2.51	0.46
21:U:858:U:OP2	31:e:22:GLY:N	2.48	0.46
21:U:999:A:H61	21:U:1010:C:H42	1.64	0.46
21:U:1828:G:N2	21:U:1847:U:O2'	2.48	0.46
21:U:2262:A:H2'	21:U:2263:G:C8	2.51	0.46
41:o:74:THR:N	41:o:90:TYR:O	2.47	0.46
47:u:19:SER:OG	47:u:20:HIS:N	2.49	0.46
1:A:745:U:H2'	1:A:746:C:C6	2.50	0.46
1:A:956:A:H2'	1:A:957:G:C8	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1074:G:N2	1:A:1199:G:O2'	2.48	0.46
3:C:6:ASN:C	3:C:8:VAL:N	2.65	0.46
21:U:423:G:H2'	21:U:424:G:H8	1.79	0.46
21:U:626:G:H2'	21:U:627:G:C8	2.51	0.46
21:U:1189:A:N7	29:c:28:ARG:NE	2.64	0.46
22:V:70:G:H21	22:V:102:A:N6	2.03	0.46
23:W:16:MET:HB3	23:W:206:GLY:HA3	1.97	0.46
26:Z:118:SER:HB2	26:Z:121:SER:OG	2.15	0.46
30:d:75:SER:HB3	35:i:77:PHE:CD1	2.51	0.46
1:A:521:U:H2'	1:A:522:A:C8	2.50	0.46
21:U:796:A:H4'	21:U:1311:G:H1'	1.98	0.46
21:U:1497:G:N2	21:U:1505:U:O2	2.48	0.46
22:V:97:A:H3'	22:V:98:G:H8	1.81	0.46
35:i:60:GLU:C	35:i:79:VAL:HG21	2.33	0.46
21:U:189:G:H2'	21:U:190:G:H8	1.80	0.46
21:U:1016:U:OP1	49:w:20:ARG:NH2	2.46	0.46
21:U:2059:A:H5''	21:U:2060:A:H5'	1.98	0.46
24:X:88:MET:HA	24:X:89:ASP:HA	1.53	0.46
30:d:64:ARG:HH12	35:i:71:VAL:HG21	1.79	0.46
34:h:12:LEU:HD13	34:h:15:HIS:HB3	1.97	0.46
37:k:34:THR:HG22	37:k:59:THR:HG22	1.96	0.46
21:U:1291:A:OP1	36:j:13:ARG:NH2	2.43	0.46
21:U:1402:C:O2'	21:U:1838:A:N3	2.40	0.46
1:A:19:U:H2'	1:A:20:C:C6	2.51	0.46
1:A:1262:G:H2'	1:A:1263:G:C8	2.51	0.46
21:U:4:U:H2'	21:U:5:A:H8	1.80	0.46
21:U:476:A:H2'	21:U:477:A:C8	2.50	0.46
21:U:827:G:H21	21:U:830:A:H62	1.63	0.46
21:U:2846:A:OP1	24:X:116:GLY:N	2.48	0.46
36:j:48:ARG:NH1	36:j:49:ASP:OD1	2.49	0.46
40:n:83:TYR:CD1	40:n:90:LYS:HG2	2.51	0.46
21:U:224:A:N6	21:U:474:U:N3	2.60	0.46
21:U:1298:C:H2'	21:U:1299:G:C8	2.51	0.46
21:U:2833:U:H2'	21:U:2834:A:H8	1.80	0.46
33:g:104:LEU:HD13	33:g:105:GLY:H	1.81	0.46
36:j:92:ARG:HB2	37:k:11:GLN:HB2	1.98	0.46
37:k:26:ALA:O	37:k:28:GLU:N	2.48	0.46
37:k:50:ASN:O	37:k:51:PRO:C	2.51	0.46
1:A:208:A:H2'	1:A:209:A:C8	2.50	0.45
1:A:1222:A:O2'	1:A:1224:G:N7	2.48	0.45
21:U:1756:U:H3'	21:U:1757:G:H2'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2065:C:H2'	21:U:2066:A:C8	2.51	0.45
21:U:2659:G:H2'	21:U:2660:G:H8	1.80	0.45
32:f:68:ILE:HD11	32:f:103:LEU:HB3	1.98	0.45
35:i:38:GLY:HA2	35:i:39:ASN:HA	1.65	0.45
1:A:43:G:H2'	1:A:44:G:H8	1.81	0.45
1:A:66:G:H4'	1:A:67:A:H3'	1.98	0.45
1:A:997:G:H2'	1:A:998:G:H8	1.81	0.45
1:A:1491:U:H2'	1:A:1492:G:H8	1.81	0.45
21:U:111:U:H5'	48:v:58:ARG:HG2	1.99	0.45
21:U:647:A:H61	21:U:701:G:H1'	1.80	0.45
21:U:2144:G:H5''	21:U:2195:G:H2'	1.98	0.45
21:U:2880:U:H2'	21:U:2881:G:H8	1.81	0.45
29:c:43:PRO:HB2	36:j:100:VAL:CG1	2.39	0.45
35:i:51:ILE:HD11	35:i:103:LEU:HD11	1.98	0.45
40:n:32:ARG:HG2	40:n:62:PRO:HB2	1.97	0.45
1:A:181:G:H1'	1:A:182:U:H5'	1.98	0.45
1:A:500:A:H2'	1:A:501:A:C8	2.51	0.45
1:A:1048:A:H2'	1:A:1049:G:C8	2.52	0.45
1:A:1048:A:H2'	1:A:1049:G:H8	1.80	0.45
21:U:1014:A:H2'	21:U:1015:G:C8	2.51	0.45
21:U:1056:A:H1'	21:U:1199:C:H1'	1.97	0.45
23:W:67:PHE:HB3	23:W:152:GLY:H	1.81	0.45
47:u:42:GLY:HA2	47:u:43:LYS:HA	1.59	0.45
1:A:36:C:H2'	1:A:37:G:C8	2.51	0.45
1:A:960:U:H2'	1:A:961:G:C8	2.51	0.45
21:U:762:A:H2'	21:U:763:A:C8	2.51	0.45
21:U:816:U:H2'	21:U:817:G:H8	1.81	0.45
21:U:1038:C:H2'	21:U:1039:G:H8	1.81	0.45
21:U:1460:G:O2'	21:U:1631:A:N6	2.49	0.45
21:U:2336:G:OP1	21:U:2336:G:N2	2.37	0.45
28:b:11:VAL:HG13	28:b:66:GLN:HG2	1.98	0.45
30:d:37:ASP:HB2	30:d:62:ILE:HD12	1.98	0.45
34:h:114:ARG:NH2	34:h:120:PHE:O	2.50	0.45
47:u:37:ARG:NH2	47:u:60:GLU:O	2.49	0.45
1:A:689:C:H2'	1:A:690:A:H8	1.80	0.45
21:U:23:G:H21	38:l:77:ASP:CG	2.25	0.45
21:U:139:A:N6	21:U:1640:G:O2'	2.48	0.45
21:U:920:G:H2'	21:U:921:G:H8	1.81	0.45
21:U:995:U:H2'	21:U:996:G:H8	1.80	0.45
21:U:1956:A:H2'	21:U:1957:A:C8	2.52	0.45
21:U:2118:U:H3	21:U:2259:G:H1	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2498:A:O2'	32:f:56:ARG:NE	2.48	0.45
27:a:55:ARG:HB3	27:a:66:HIS:HD2	1.82	0.45
33:g:78:ASP:OD1	33:g:79:ALA:N	2.49	0.45
50:y:55:ARG:HA	50:y:56:VAL:HA	1.54	0.45
51:x:89:ARG:O	51:x:92:LYS:HG3	2.16	0.45
1:A:1509:A:H1'	1:A:1529:A:H2'	1.99	0.45
21:U:510:G:N2	21:U:513:A:OP2	2.47	0.45
21:U:575:A:O2'	21:U:576:G:N3	2.50	0.45
21:U:689:A:N6	21:U:2398:A:O2'	2.50	0.45
21:U:1111:U:C2	21:U:1119:A:C6	3.05	0.45
38:l:82:LEU:HD22	38:l:84:ARG:HH22	1.81	0.45
1:A:85:U:O2	1:A:86:G:N1	2.49	0.45
1:A:955:G:N2	1:A:1343:G:O2'	2.50	0.45
1:A:1032:C:N4	1:A:1033:G:N7	2.65	0.45
21:U:324:A:H2'	21:U:325:A:C8	2.52	0.45
21:U:731:G:N2	21:U:835:A:OP2	2.43	0.45
21:U:1176:U:C2	24:X:151:PRO:HB3	2.52	0.45
21:U:2041:G:OP2	38:l:16:LYS:NZ	2.39	0.45
21:U:2043:A:H2'	21:U:2044:A:C8	2.51	0.45
21:U:2838:U:H2'	21:U:2839:C:H6	1.82	0.45
23:W:171:TYR:HD2	23:W:183:MET:HB3	1.80	0.45
29:c:35:ALA:HB1	29:c:40:LYS:HB2	1.99	0.45
48:v:37:LEU:HD13	48:v:39:ASN:HB2	1.99	0.45
1:A:1025:G:H2'	1:A:1026:A:C8	2.52	0.45
1:A:1424:G:H2'	1:A:1425:A:H8	1.81	0.45
1:A:1436:C:H2'	1:A:1437:A:H8	1.81	0.45
1:A:1528:A:H2'	1:A:1529:A:C8	2.52	0.45
3:C:6:ASN:O	3:C:7:PRO:O	2.24	0.45
21:U:35:G:O2'	21:U:501:A:O4'	2.33	0.45
21:U:319:G:O2'	21:U:326:A:N6	2.50	0.45
21:U:478:U:H2'	21:U:479:A:C8	2.51	0.45
21:U:706:C:H2'	21:U:707:G:C8	2.51	0.45
21:U:732:A:O2'	21:U:820:U:O4	2.27	0.45
21:U:774:A:H2	23:W:9:THR:HG21	1.82	0.45
21:U:1540:A:H2'	21:U:1541:A:C8	2.52	0.45
21:U:1652:C:N4	21:U:1667:A:OP2	2.44	0.45
21:U:2122:G:N3	21:U:2227:A:N6	2.65	0.45
23:W:35:ALA:N	23:W:62:TYR:O	2.45	0.45
27:a:98:SER:HA	27:a:126:VAL:HG11	1.98	0.45
29:c:53:ASP:OD1	29:c:53:ASP:N	2.44	0.45
41:o:54:TYR:HE2	41:o:84:ARG:HH11	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:U:OP1	1:A:393:U:O2'	2.35	0.45
21:U:622:A:C8	21:U:2047:A:H5'	2.52	0.45
21:U:675:C:O2	21:U:685:U:O2'	2.33	0.45
21:U:1475:G:OP2	21:U:1607:C:O2'	2.33	0.45
51:x:44:LYS:HB3	51:x:45:PHE:H	1.60	0.45
1:A:114:A:H61	1:A:321:A:H1'	1.81	0.45
1:A:424:G:H2'	1:A:425:G:H8	1.82	0.45
1:A:552:G:H2'	1:A:553:G:C8	2.52	0.45
1:A:745:U:H2'	1:A:746:C:H6	1.82	0.45
21:U:513:A:P	44:r:34:ARG:HH22	2.40	0.45
21:U:731:G:OP1	44:r:21:ARG:NH2	2.43	0.45
21:U:1014:A:H2'	21:U:1015:G:H8	1.82	0.45
22:V:55:A:H2'	22:V:56:A:H8	1.82	0.45
29:c:50:ASP:HA	29:c:119:MET:HE1	1.98	0.45
35:i:75:ARG:NH2	35:i:77:PHE:HE1	2.03	0.45
1:A:1441:G:O2'	1:A:1477:G:N1	2.49	0.44
21:U:1242:U:H2'	21:U:1243:A:C8	2.52	0.44
21:U:2104:U:O2'	21:U:2626:G:N2	2.45	0.44
21:U:2134:A:H2'	21:U:2135:G:H8	1.82	0.44
23:W:142:HIS:CD2	23:W:143:ASN:HB2	2.52	0.44
29:c:78:HIS:CD2	29:c:85:LEU:HB3	2.49	0.44
31:e:33:LYS:HB3	31:e:40:ALA:HA	1.99	0.44
36:j:97:ASP:O	36:j:98:LEU:C	2.60	0.44
36:j:97:ASP:O	36:j:100:VAL:CG2	2.38	0.44
1:A:262:G:H2'	1:A:263:G:H8	1.83	0.44
1:A:415:A:H2'	1:A:416:G:C8	2.52	0.44
1:A:437:U:C4	1:A:439:A:N6	2.85	0.44
1:A:1262:G:H2'	1:A:1263:G:H8	1.82	0.44
1:A:1495:U:H2'	1:A:1496:G:H8	1.82	0.44
1:A:1525:C:H2'	1:A:1526:G:C8	2.51	0.44
21:U:329:A:H2'	21:U:330:A:H8	1.83	0.44
21:U:1696:G:O5'	33:g:35:THR:OG1	2.32	0.44
24:X:62:ASN:HB3	24:X:64:PRO:HD2	1.99	0.44
25:Y:126:LEU:N	25:Y:194:ILE:O	2.50	0.44
27:a:71:SER:O	27:a:75:ASN:ND2	2.50	0.44
32:f:35:GLN:HA	32:f:102:VAL:HA	1.98	0.44
1:A:215:G:H1	1:A:224:U:H3	1.65	0.44
1:A:634:G:H2'	1:A:635:G:H8	1.81	0.44
1:A:1248:A:N6	1:A:1306:U:O4'	2.49	0.44
1:A:1276:C:N4	1:A:1336:G:O2'	2.49	0.44
21:U:461:C:H2'	21:U:462:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:602:G:H2'	21:U:603:G:H8	1.81	0.44
21:U:776:G:H5'	21:U:777:C:H5''	1.98	0.44
21:U:801:U:H2'	21:U:802:G:C8	2.53	0.44
21:U:826:U:H2'	21:U:827:G:C8	2.52	0.44
21:U:1015:G:N2	21:U:1031:C:OP1	2.38	0.44
21:U:1699:A:H1'	21:U:2848:A:H5'	1.98	0.44
35:i:51:ILE:HG12	35:i:100:LEU:HB2	1.98	0.44
39:m:3:ASP:OD2	48:v:22:LYS:NZ	2.51	0.44
1:A:746:C:H2'	1:A:747:U:C6	2.52	0.44
1:A:918:A:H2'	1:A:919:A:H8	1.82	0.44
21:U:139:A:H61	21:U:1640:G:H1'	1.83	0.44
21:U:266:U:O2'	21:U:476:A:N3	2.48	0.44
21:U:1847:U:H5''	23:W:157:SER:HB3	1.99	0.44
21:U:2721:C:H2'	21:U:2722:A:C8	2.52	0.44
23:W:72:ASP:N	23:W:72:ASP:OD1	2.51	0.44
23:W:245:SER:O	23:W:246:PRO:O	2.35	0.44
32:f:32:PHE:O	32:f:106:ILE:N	2.45	0.44
41:o:81:GLY:HA2	41:o:82:ARG:HA	1.69	0.44
51:x:40:ASN:C	51:x:41:VAL:CG1	2.89	0.44
1:A:277:C:H2'	1:A:278:A:C8	2.53	0.44
1:A:307:G:N2	1:A:575:G:O6	2.40	0.44
1:A:719:G:H2'	1:A:720:G:H8	1.83	0.44
1:A:960:U:H2'	1:A:961:G:H8	1.82	0.44
1:A:1417:A:H2	1:A:1502:A:H62	1.66	0.44
21:U:455:G:H2'	21:U:456:A:H8	1.82	0.44
21:U:792:G:O2'	21:U:797:A:N6	2.50	0.44
21:U:934:U:N3	21:U:938:G:N7	2.65	0.44
21:U:1185:G:H5'	29:c:26:LEU:HD12	1.98	0.44
21:U:1414:G:H2'	21:U:1415:C:H6	1.83	0.44
21:U:2012:C:H4'	21:U:2635:C:H4'	1.99	0.44
21:U:2151:U:H2'	21:U:2152:A:C8	2.53	0.44
51:x:40:ASN:O	51:x:41:VAL:CG1	2.65	0.44
51:x:44:LYS:HD3	51:x:44:LYS:HA	1.35	0.44
51:x:66:SER:HB3	51:x:87:GLN:HE22	1.82	0.44
1:A:366:U:H2'	1:A:367:A:C8	2.52	0.44
1:A:1228:U:H2'	1:A:1229:G:C8	2.53	0.44
1:A:1363:C:H2'	1:A:1364:G:H8	1.83	0.44
13:M:3:ARG:N	13:M:6:GLY:O	2.50	0.44
21:U:1303:U:O3'	42:p:8:THR:OG1	2.35	0.44
21:U:1393:A:H5'	23:W:38:HIS:CE1	2.52	0.44
21:U:1497:G:O6	21:U:1505:U:O4	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1531:G:H2'	21:U:1532:A:C8	2.52	0.44
21:U:2030:A:H2'	21:U:2031:G:C8	2.52	0.44
23:W:80:THR:O	23:W:93:LEU:N	2.47	0.44
26:Z:121:SER:O	26:Z:129:THR:OG1	2.29	0.44
35:i:78:PRO:HB3	35:i:81:THR:HB	1.98	0.44
48:v:54:LYS:HA	48:v:57:ILE:HD12	1.99	0.44
21:U:9:U:H2'	21:U:10:A:H8	1.82	0.44
21:U:636:G:H2'	21:U:637:A:H8	1.82	0.44
21:U:782:A:H1'	21:U:1679:A:H2	1.82	0.44
21:U:1074:A:N3	21:U:2515:G:O2'	2.43	0.44
26:Z:104:ILE:HA	26:Z:108:LEU:HD12	2.00	0.44
27:a:5:GLY:HA2	27:a:70:ARG:HD3	2.00	0.44
27:a:87:GLY:O	27:a:166:GLU:N	2.48	0.44
36:j:86:SER:HB3	36:j:116:GLN:HB2	1.99	0.44
1:A:746:C:H2'	1:A:747:U:H6	1.82	0.44
1:A:1296:A:H2	1:A:1362:G:H1'	1.82	0.44
21:U:247:A:H62	21:U:257:G:H21	1.66	0.44
21:U:861:C:H2'	21:U:862:U:H6	1.83	0.44
21:U:1338:G:N1	21:U:1685:A:OP2	2.35	0.44
21:U:1503:G:O6	21:U:2732:C:N4	2.51	0.44
43:q:2:ARG:HD2	43:q:20:LYS:HB3	2.00	0.44
48:v:1:MET:HB2	48:v:52:ARG:HH11	1.81	0.44
1:A:1469:C:H2'	1:A:1470:A:H8	1.83	0.44
21:U:704:U:H2'	21:U:705:A:H8	1.82	0.44
21:U:1238:G:O6	21:U:1289:U:O2	2.35	0.44
21:U:1264:G:H2'	21:U:1265:A:C8	2.53	0.44
23:W:210:ARG:HA	23:W:213:TRP:HD1	1.83	0.44
24:X:126:HIS:CD2	24:X:159:LEU:HB3	2.52	0.44
40:n:5:LYS:HA	40:n:6:GLY:HA2	1.62	0.44
1:A:1016:A:C6	1:A:1034:U:H1'	2.53	0.43
21:U:1201:A:H5''	36:j:55:ARG:HD3	1.99	0.43
38:l:82:LEU:HB2	38:l:98:LYS:HB2	2.00	0.43
1:A:313:G:H4'	1:A:314:A:H5''	2.00	0.43
1:A:1023:G:N1	1:A:1026:A:OP2	2.44	0.43
21:U:675:C:OP1	21:U:696:C:O2'	2.36	0.43
21:U:1066:A:N1	21:U:1187:U:O2'	2.40	0.43
21:U:1199:C:H5'	36:j:76:TYR:HE2	1.82	0.43
21:U:1733:U:O2'	21:U:1745:A:N7	2.38	0.43
21:U:2142:C:H42	21:U:2197:G:H4'	1.84	0.43
26:Z:114:PHE:HE2	50:y:43:TYR:OH	2.01	0.43
29:c:74:ILE:HG12	29:c:89:THR:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:h:27:GLU:OE1	34:h:27:GLU:HA	2.11	0.43
1:A:621:C:H2'	1:A:622:C:H6	1.82	0.43
1:A:766:U:OP1	1:A:831:A:O2'	2.35	0.43
21:U:633:U:H2'	21:U:634:A:H8	1.83	0.43
21:U:2224:U:H2'	21:U:2225:C:H6	1.82	0.43
21:U:2282:G:O6	41:o:12:LYS:NZ	2.39	0.43
22:V:47:C:H2'	22:V:48:G:C8	2.52	0.43
23:W:231:PRO:HB2	23:W:243:ARG:HH21	1.83	0.43
25:Y:182:ASN:OD1	25:Y:182:ASN:N	2.49	0.43
26:Z:3:ARG:NH1	50:y:22:PHE:CG	2.86	0.43
27:a:22:ASN:HA	27:a:23:ASN:HA	1.77	0.43
34:h:36:SER:OG	34:h:37:ASN:N	2.51	0.43
34:h:40:ILE:N	34:h:58:THR:OG1	2.52	0.43
37:k:26:ALA:C	37:k:28:GLU:N	2.76	0.43
1:A:170:A:H2'	1:A:171:A:C8	2.53	0.43
1:A:855:G:H2'	1:A:856:C:C6	2.54	0.43
1:A:1105:U:OP1	1:A:1118:G:N2	2.37	0.43
1:A:1495:U:H2'	1:A:1496:G:C8	2.53	0.43
21:U:1140:U:O2'	21:U:1143:U:O4	2.36	0.43
21:U:1397:G:N2	21:U:1412:A:H62	2.11	0.43
21:U:1486:G:H1	21:U:1599:U:H3	1.65	0.43
21:U:2462:A:H2	47:u:21:ALA:HB1	1.83	0.43
25:Y:110:ILE:HD11	25:Y:182:ASN:HA	2.01	0.43
25:Y:117:LYS:HG2	25:Y:122:ASN:HB2	2.00	0.43
32:f:39:ALA:HB2	32:f:99:PRO:HD3	2.00	0.43
41:o:44:ILE:HD13	41:o:47:ARG:HE	1.83	0.43
1:A:62:A:N6	1:A:108:C:N4	2.67	0.43
21:U:3:U:N3	21:U:2925:C:O2	2.52	0.43
21:U:1524:A:H2'	21:U:1525:G:C8	2.53	0.43
21:U:2204:U:O4	21:U:2205:A:N6	2.51	0.43
21:U:2325:U:O4	21:U:2364:A:N7	2.52	0.43
25:Y:201:LYS:O	25:Y:205:VAL:N	2.50	0.43
31:e:37:GLY:O	31:e:40:ALA:N	2.38	0.43
34:h:90:ILE:HG23	34:h:91:SER:HB3	1.98	0.43
1:A:112:U:H2'	1:A:113:G:C8	2.53	0.43
1:A:468:C:H2'	1:A:469:G:H8	1.83	0.43
1:A:563:U:H2'	1:A:564:C:H6	1.84	0.43
1:A:1341:A:H3'	1:A:1342:A:H8	1.83	0.43
1:A:1542:U:H2'	1:A:1543:C:H6	1.83	0.43
21:U:51:G:O2'	21:U:118:A:N1	2.48	0.43
21:U:1523:U:H5''	21:U:1524:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2649:C:OP1	24:X:157:GLY:N	2.52	0.43
21:U:2665:U:H2'	21:U:2666:U:C6	2.54	0.43
21:U:2699:G:H2'	21:U:2700:A:C8	2.54	0.43
1:A:995:C:H2'	1:A:996:A:C8	2.54	0.43
1:A:1129:U:H2'	1:A:1130:C:H6	1.84	0.43
21:U:8:U:H2'	21:U:9:U:C6	2.54	0.43
21:U:607:G:H1	21:U:622:A:H61	1.65	0.43
21:U:1533:A:H2'	21:U:1534:A:C8	2.53	0.43
21:U:2653:G:H1'	42:p:19:HIS:CE1	2.54	0.43
33:g:4:ARG:HB2	33:g:39:GLU:HG3	2.00	0.43
37:k:58:VAL:HG22	37:k:100:ILE:HA	1.99	0.43
43:q:2:ARG:NE	43:q:22:ASN:OD1	2.39	0.43
49:w:6:ILE:HG22	49:w:28:LEU:HD21	2.01	0.43
1:A:378:C:H2'	1:A:379:G:H8	1.84	0.43
1:A:406:C:H2'	1:A:407:G:C8	2.53	0.43
1:A:689:C:H2'	1:A:690:A:C8	2.54	0.43
1:A:791:A:OP1	1:A:1531:G:N2	2.44	0.43
21:U:40:U:H2'	21:U:41:A:C8	2.54	0.43
21:U:377:G:H2'	21:U:378:C:H6	1.82	0.43
21:U:638:U:H2'	21:U:639:C:C6	2.54	0.43
21:U:1160:G:H2'	21:U:1161:A:C8	2.53	0.43
21:U:1943:C:H1'	21:U:1944:U:H5'	2.01	0.43
23:W:144:ILE:HG21	23:W:154:LEU:HD12	2.01	0.43
34:h:92:ASP:OD1	34:h:92:ASP:N	2.52	0.43
36:j:31:LEU:HB2	36:j:34:VAL:HG22	2.00	0.43
38:l:7:ALA:HB3	38:l:103:ILE:H	1.84	0.43
38:l:76:VAL:HG22	38:l:103:ILE:HA	2.01	0.43
40:n:48:THR:OG1	40:n:51:ASN:O	2.27	0.43
42:p:27:MET:HE2	42:p:36:MET:HE3	2.01	0.43
43:q:9:CYS:SG	43:q:12:CYS:N	2.83	0.43
1:A:989:C:O2	1:A:1326:C:N4	2.47	0.43
1:A:1355:A:H61	1:A:1383:A:H3'	1.84	0.43
21:U:302:A:H2'	21:U:303:G:C8	2.54	0.43
21:U:690:A:H2'	21:U:692:A:C8	2.53	0.43
21:U:1005:A:H2'	21:U:1006:A:C8	2.54	0.43
21:U:1077:G:H21	46:t:36:GLN:HE22	1.67	0.43
21:U:2777:A:H5'	27:a:4:VAL:HG21	2.00	0.43
21:U:2888:C:H2'	21:U:2889:A:C8	2.54	0.43
29:c:46:THR:OG1	36:j:64:ARG:NH2	2.52	0.43
49:w:15:ARG:HE	49:w:52:HIS:CE1	2.37	0.43
1:A:42:C:H2'	1:A:43:G:C8	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:C:O2'	1:A:298:C:O2	2.36	0.43
1:A:277:C:H2'	1:A:278:A:H8	1.83	0.43
1:A:1301:U:H2'	1:A:1302:G:C8	2.53	0.43
21:U:153:C:H2'	21:U:154:A:H8	1.82	0.43
21:U:172:U:H2'	21:U:173:A:C8	2.54	0.43
21:U:346:G:H2'	21:U:347:G:C8	2.54	0.43
21:U:611:U:O3'	31:e:36:LYS:HE2	2.19	0.43
21:U:673:A:H2	21:U:683:A:C4	2.37	0.43
21:U:968:C:H2'	21:U:969:C:H6	1.82	0.43
21:U:1220:G:H2'	21:U:1221:A:C8	2.50	0.43
21:U:1531:G:H2'	21:U:1532:A:H8	1.83	0.43
21:U:2065:C:H2'	21:U:2066:A:H8	1.83	0.43
21:U:2234:C:H2'	21:U:2235:G:C8	2.52	0.43
26:Z:3:ARG:NH1	50:y:22:PHE:CB	2.25	0.43
27:a:62:HIS:O	27:a:66:HIS:N	2.52	0.43
33:g:45:GLU:O	33:g:49:THR:OG1	2.33	0.43
43:q:9:CYS:HB3	43:q:14:GLU:H	1.84	0.43
1:A:857:C:H2'	1:A:858:C:H6	1.84	0.42
1:A:1021:U:H2'	1:A:1022:A:C8	2.53	0.42
21:U:154:A:H2'	21:U:155:U:C6	2.54	0.42
21:U:167:U:H2'	21:U:168:A:H8	1.83	0.42
21:U:224:A:H62	21:U:474:U:H3	1.62	0.42
21:U:387:C:H2'	21:U:388:A:H8	1.83	0.42
21:U:631:G:H22	31:e:33:LYS:HE3	1.85	0.42
21:U:1189:A:H62	29:c:28:ARG:HD3	1.83	0.42
21:U:1390:C:N3	21:U:1420:G:N1	2.67	0.42
21:U:2203:C:H2'	21:U:2204:U:C6	2.53	0.42
21:U:2278:U:O2'	21:U:2281:G:OP2	2.31	0.42
21:U:2429:G:O3'	43:q:38:ARG:NH1	2.52	0.42
21:U:2623:C:H2'	21:U:2624:G:C8	2.53	0.42
22:V:64:A:H61	22:V:105:A:H2'	1.84	0.42
25:Y:80:SER:HB3	25:Y:81:PRO:CD	2.44	0.42
35:i:78:PRO:HB2	35:i:81:THR:HB	1.95	0.42
36:j:103:LEU:HD12	36:j:104:THR:HA	2.01	0.42
1:A:519:A:O2'	1:A:551:U:O2	2.34	0.42
1:A:749:U:H2'	1:A:750:G:C8	2.54	0.42
1:A:1145:U:N3	1:A:1149:U:O4	2.51	0.42
1:A:1317:C:H2'	1:A:1318:G:H8	1.84	0.42
21:U:34:U:O2	21:U:501:A:O2'	2.37	0.42
21:U:739:C:H2'	21:U:740:A:H8	1.84	0.42
21:U:904:A:N1	21:U:967:G:N2	2.61	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:929:G:O6	21:U:941:U:O4	2.36	0.42
21:U:1919:A:H2	21:U:2264:G:H1'	1.84	0.42
24:X:55:ASP:N	24:X:55:ASP:OD1	2.49	0.42
27:a:13:SER:HA	27:a:14:ASP:HA	1.83	0.42
27:a:21:ASP:HA	27:a:22:ASN:HA	1.86	0.42
1:A:190:A:H2'	1:A:191:C:C6	2.54	0.42
1:A:1313:G:N2	1:A:1341:A:OP2	2.49	0.42
21:U:565:U:H5''	38:l:25:ARG:HH12	1.85	0.42
21:U:767:U:H2'	21:U:768:G:C8	2.53	0.42
21:U:1130:A:N6	28:b:37:GLU:OE2	2.45	0.42
21:U:1270:C:H2'	21:U:1271:U:C6	2.54	0.42
23:W:91:ILE:HG21	23:W:103:TYR:HB3	2.00	0.42
28:b:38:VAL:HG13	28:b:42:ARG:HG3	2.01	0.42
43:q:34:LYS:HB2	43:q:45:HIS:ND1	2.34	0.42
1:A:417:U:O2	1:A:441:G:N2	2.43	0.42
1:A:1226:C:H2'	1:A:1227:C:H6	1.85	0.42
1:A:1416:C:H2'	1:A:1417:A:C8	2.53	0.42
1:A:1491:U:H2'	1:A:1492:G:C8	2.54	0.42
21:U:89:U:H5''	21:U:90:A:H2'	2.00	0.42
21:U:827:G:N1	23:W:229:ASP:OD2	2.53	0.42
21:U:898:U:H2'	21:U:899:C:C6	2.55	0.42
21:U:925:A:N6	21:U:946:G:O2'	2.51	0.42
21:U:1683:C:O2	21:U:2727:U:O2'	2.37	0.42
21:U:1882:A:H2'	21:U:1883:A:C8	2.55	0.42
21:U:2686:A:N6	21:U:2693:G:H21	2.15	0.42
22:V:101:U:H2'	22:V:102:A:C8	2.54	0.42
24:X:110:VAL:HG22	24:X:202:VAL:HA	2.01	0.42
25:Y:194:ILE:HG22	25:Y:198:ALA:HB3	2.00	0.42
26:Z:28:VAL:HG13	26:Z:30:LYS:HE2	2.00	0.42
29:c:6:MET:O	36:j:64:ARG:NH1	2.44	0.42
30:d:70:ARG:HG3	30:d:76:TYR:CE1	2.54	0.42
34:h:35:ARG:HB3	34:h:100:TYR:CE1	2.54	0.42
40:n:89:LYS:HA	40:n:89:LYS:HD3	1.75	0.42
1:A:64:U:H2'	1:A:65:C:C6	2.54	0.42
1:A:353:C:O2	1:A:354:G:N2	2.49	0.42
1:A:409:C:H2'	1:A:410:G:C8	2.53	0.42
1:A:834:G:O6	1:A:886:A:N6	2.52	0.42
1:A:1041:C:H4'	1:A:1042:G:C4	2.55	0.42
21:U:245:G:O2'	21:U:257:G:O6	2.32	0.42
21:U:299:U:H1'	21:U:303:G:H1'	2.01	0.42
21:U:1317:G:H2'	21:U:1318:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:1484:U:H3	21:U:1601:A:H62	1.67	0.42
23:W:244:LYS:HE2	23:W:244:LYS:HB3	1.87	0.42
25:Y:59:GLY:HA3	25:Y:79:ARG:HG3	2.01	0.42
37:k:8:GLY:HA3	37:k:10:LYS:H	1.85	0.42
1:A:833:U:H2'	1:A:834:G:C8	2.54	0.42
1:A:1006:A:H2'	1:A:1007:U:C6	2.55	0.42
21:U:168:A:H3'	21:U:169:G:H8	1.84	0.42
21:U:892:U:H2'	21:U:893:A:C8	2.55	0.42
21:U:968:C:H2'	21:U:969:C:C6	2.54	0.42
21:U:2655:C:H2'	21:U:2656:G:C8	2.55	0.42
21:U:2909:U:O2	42:p:50:ASN:ND2	2.52	0.42
23:W:17:THR:OG1	23:W:204:ASN:N	2.52	0.42
27:a:39:HIS:CE1	27:a:41:ASP:HB2	2.55	0.42
37:k:53:VAL:O	37:k:54:GLU:C	2.62	0.42
50:y:18:CYS:SG	50:y:20:ASN:ND2	2.93	0.42
1:A:417:U:H3	1:A:441:G:H1	1.67	0.42
1:A:1411:C:H41	51:x:86:ARG:CZ	2.33	0.42
21:U:1173:A:H62	21:U:2517:A:H1'	1.85	0.42
21:U:1493:C:H2'	21:U:1494:G:H8	1.83	0.42
21:U:1673:G:H2'	21:U:1674:G:H8	1.84	0.42
23:W:52:ARG:HH12	23:W:249:PRO:HG3	1.84	0.42
24:X:207:LYS:HA	24:X:208:SER:HA	1.88	0.42
33:g:90:ARG:HH21	33:g:91:TYR:HE1	1.67	0.42
45:s:38:GLN:HA	45:s:41:LYS:HB2	2.02	0.42
48:v:14:ILE:HD13	48:v:57:ILE:HG12	2.01	0.42
49:w:10:ARG:HB3	49:w:53:LEU:HD12	2.02	0.42
51:x:1:MET:HB2	51:x:35:VAL:HB	2.02	0.42
1:A:510:C:O2	1:A:558:C:O2'	2.34	0.42
1:A:676:G:H2'	1:A:677:A:H8	1.85	0.42
21:U:1013:U:H2'	21:U:1014:A:C8	2.55	0.42
21:U:1819:C:H3'	21:U:1857:G:H22	1.85	0.42
21:U:2420:G:OP2	45:s:35:ASN:ND2	2.42	0.42
29:c:70:LEU:HA	29:c:70:LEU:HD23	1.90	0.42
33:g:24:LEU:HD12	33:g:44:VAL:HG21	2.00	0.42
51:x:21:GLU:HA	51:x:24:ILE:HG22	2.02	0.42
1:A:17:G:N2	5:E:22:ALA:O	2.42	0.42
1:A:34:A:H2'	1:A:35:A:C8	2.54	0.42
1:A:468:C:H2'	1:A:469:G:C8	2.55	0.42
1:A:589:C:H2'	1:A:590:G:C8	2.55	0.42
1:A:957:G:HO2'	1:A:1315:A:HO2'	1.63	0.42
1:A:1498:G:H2'	1:A:1499:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:275:A:O2'	21:U:414:C:O2'	2.33	0.42
21:U:757:C:H2'	21:U:758:A:C8	2.55	0.42
21:U:1497:G:N1	21:U:1505:U:C2	2.82	0.42
21:U:1639:G:H2'	21:U:1640:G:H8	1.85	0.42
27:a:3:ARG:HB2	27:a:6:LYS:HE2	2.02	0.42
28:b:51:GLU:OE1	28:b:89:VAL:CG2	2.68	0.42
28:b:103:HIS:ND1	28:b:107:GLU:O	2.52	0.42
35:i:52:LYS:HE2	35:i:63:THR:HG23	2.02	0.42
37:k:29:ALA:HB2	37:k:65:GLN:HG3	2.02	0.42
48:v:31:GLN:O	48:v:35:GLY:N	2.40	0.42
1:A:721:A:H2'	1:A:722:G:C8	2.55	0.42
1:A:1018:U:H2'	1:A:1019:C:C6	2.55	0.42
1:A:1227:C:H2'	1:A:1228:U:C6	2.55	0.42
1:A:1385:U:H2'	1:A:1386:A:H8	1.85	0.42
13:M:74:SER:O	13:M:78:LYS:CA	2.68	0.42
21:U:613:U:H5'	21:U:992:G:H1'	2.01	0.42
21:U:705:A:H2'	21:U:706:C:C6	2.55	0.42
21:U:743:U:H2'	21:U:744:C:C6	2.55	0.42
21:U:1008:A:H2'	21:U:1009:U:C6	2.55	0.42
21:U:1503:G:O6	21:U:2731:G:C6	2.73	0.42
21:U:1965:A:H2	21:U:1972:U:H3	1.68	0.42
21:U:2133:C:H2'	21:U:2134:A:C8	2.54	0.42
21:U:2771:G:O6	21:U:2791:U:O2	2.37	0.42
23:W:52:ARG:NH1	23:W:249:PRO:HG3	2.35	0.42
45:s:22:LEU:HD21	45:s:62:LEU:HD11	2.02	0.42
1:A:1134:G:N2	1:A:1135:U:O4	2.29	0.41
21:U:639:C:H2'	21:U:640:U:C6	2.55	0.41
21:U:639:C:H2'	21:U:640:U:H6	1.85	0.41
21:U:1292:G:N2	36:j:33:LYS:HG2	2.35	0.41
21:U:2884:G:H2'	21:U:2885:A:C8	2.55	0.41
25:Y:146:LEU:HD23	25:Y:146:LEU:HA	1.92	0.41
37:k:34:THR:HA	37:k:59:THR:HA	2.02	0.41
40:n:97:SER:HA	40:n:98:GLY:HA2	1.80	0.41
41:o:48:GLN:NE2	41:o:53:ILE:H	2.18	0.41
1:A:976:G:H2'	1:A:977:C:C6	2.55	0.41
10:J:35:SER:O	10:J:77:VAL:N	2.52	0.41
21:U:377:G:H2'	21:U:378:C:C6	2.55	0.41
21:U:789:C:H2'	21:U:790:A:H8	1.85	0.41
21:U:831:U:O4	23:W:228:ASN:ND2	2.45	0.41
21:U:958:A:N1	21:U:2306:G:O2'	2.50	0.41
21:U:2659:G:H2'	21:U:2660:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2717:G:H21	21:U:2750:A:H62	1.67	0.41
23:W:67:PHE:O	23:W:152:GLY:N	2.52	0.41
1:A:179:U:O2	1:A:209:A:N6	2.53	0.41
1:A:265:G:H2'	1:A:266:A:C8	2.55	0.41
1:A:266:A:H2'	1:A:267:G:H8	1.85	0.41
1:A:529:A:OP2	12:L:62:LEU:N	2.47	0.41
1:A:1421:C:H2'	1:A:1422:A:H8	1.84	0.41
21:U:389:A:O2'	21:U:390:A:N7	2.38	0.41
21:U:1414:G:H2'	21:U:1415:C:C6	2.55	0.41
21:U:1829:C:N3	21:U:1846:G:N1	2.63	0.41
21:U:2624:G:N2	21:U:2626:G:H8	2.19	0.41
21:U:2772:U:OP2	21:U:2784:C:N4	2.53	0.41
23:W:30:GLU:HB3	23:W:103:TYR:HE1	1.84	0.41
24:X:86:VAL:HG21	24:X:91:TYR:HE2	1.84	0.41
35:i:12:THR:HB	35:i:58:ILE:HG13	2.01	0.41
1:A:732:U:N3	1:A:865:G:O2'	2.53	0.41
1:A:992:U:H4'	1:A:993:A:H5'	2.03	0.41
1:A:1401:G:H2'	1:A:1402:U:C6	2.55	0.41
15:O:6:GLU:O	15:O:10:GLN:CA	2.68	0.41
21:U:2250:G:H2'	21:U:2251:G:H8	1.84	0.41
33:g:19:ASP:O	33:g:22:THR:OG1	2.28	0.41
33:g:22:THR:HG22	33:g:66:ILE:HG23	2.01	0.41
35:i:79:VAL:HG12	35:i:80:HIS:CD2	2.55	0.41
1:A:295:U:H2'	1:A:296:A:C8	2.55	0.41
1:A:307:G:H2'	1:A:308:A:C8	2.55	0.41
1:A:1265:C:O2'	1:A:1287:C:N4	2.53	0.41
21:U:145:G:O2'	39:m:1:MET:O	2.26	0.41
21:U:837:U:N3	21:U:841:A:O2'	2.53	0.41
21:U:1530:G:H2'	21:U:1531:G:H8	1.85	0.41
23:W:147:LYS:HB2	23:W:150:LYS:HE3	2.01	0.41
26:Z:67:VAL:HA	26:Z:87:ALA:HA	2.02	0.41
27:a:3:ARG:HB2	27:a:6:LYS:HG2	2.01	0.41
31:e:108:GLY:HA2	31:e:126:ASN:HD22	1.85	0.41
1:A:997:G:H2'	1:A:998:G:C8	2.54	0.41
21:U:999:A:H2'	21:U:1000:G:C8	2.54	0.41
21:U:1171:G:H3'	21:U:1172:A:H8	1.85	0.41
21:U:1285:G:H4'	25:Y:38:LEU:HD21	2.02	0.41
21:U:2099:G:H2'	21:U:2100:A:C8	2.56	0.41
21:U:2357:A:H2'	21:U:2358:A:H8	1.86	0.41
21:U:2427:U:O2'	43:q:15:ARG:NH2	2.54	0.41
21:U:2486:U:H3	21:U:2523:G:H1	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2878:U:H2'	21:U:2879:G:C8	2.55	0.41
25:Y:37:ILE:HD13	31:e:6:LEU:HD11	2.02	0.41
47:u:6:VAL:HB	47:u:47:VAL:HG11	2.03	0.41
1:A:927:G:H2'	1:A:928:A:C8	2.55	0.41
3:C:55:GLU:O	3:C:66:THR:N	2.54	0.41
21:U:153:C:H2'	21:U:154:A:C8	2.56	0.41
21:U:1326:A:H61	21:U:1694:G:H1'	1.85	0.41
21:U:1338:G:O2'	21:U:1340:A:N6	2.54	0.41
21:U:2134:A:H2'	21:U:2135:G:C8	2.56	0.41
35:i:77:PHE:HA	35:i:78:PRO:HD3	1.90	0.41
48:v:10:THR:HA	48:v:14:ILE:HD12	2.02	0.41
51:x:97:ARG:HD2	51:x:99:PHE:CE2	2.43	0.41
1:A:344:A:H2'	1:A:345:G:C8	2.55	0.41
1:A:1277:G:H2'	1:A:1278:A:C4	2.55	0.41
1:A:1347:G:H2'	1:A:1348:A:C8	2.56	0.41
21:U:796:A:H61	21:U:800:G:H21	1.69	0.41
21:U:894:A:H62	21:U:979:U:H3	1.69	0.41
21:U:1007:G:H22	21:U:2059:A:P	2.44	0.41
21:U:1716:U:N3	21:U:1719:G:OP2	2.51	0.41
21:U:2224:U:H2'	21:U:2225:C:C6	2.56	0.41
31:e:75:ALA:HA	31:e:76:VAL:HA	1.76	0.41
39:m:10:ARG:HB2	48:v:33:ALA:HB2	2.03	0.41
40:n:11:VAL:HG21	40:n:38:VAL:HG11	2.03	0.41
43:q:3:VAL:HG12	43:q:5:ILE:HG13	2.03	0.41
43:q:8:ALA:HA	43:q:15:ARG:HA	2.02	0.41
49:w:39:ASP:OD2	49:w:44:ARG:NH2	2.54	0.41
1:A:769:G:H3'	1:A:770:G:H8	1.86	0.41
1:A:853:C:H3'	1:A:854:C:H6	1.86	0.41
1:A:1028:A:H2'	1:A:1029:G:C8	2.55	0.41
1:A:1546:C:H2'	1:A:1547:U:C6	2.56	0.41
21:U:144:A:H2'	21:U:145:G:H8	1.86	0.41
21:U:331:C:H2'	21:U:332:G:C8	2.56	0.41
21:U:768:G:H2'	21:U:769:A:H8	1.86	0.41
21:U:840:A:N6	21:U:2101:G:O3'	2.54	0.41
21:U:899:C:O2'	21:U:900:U:O4'	2.37	0.41
21:U:954:U:OP1	32:f:24:GLY:N	2.53	0.41
21:U:1114:G:H1	21:U:1141:A:H2'	1.86	0.41
21:U:1417:A:O2'	21:U:1419:G:OP2	2.39	0.41
21:U:1719:G:H21	21:U:1722:A:H61	1.68	0.41
21:U:1741:G:N2	21:U:2006:A:O2'	2.50	0.41
21:U:1941:A:N7	21:U:1946:U:O4	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:2521:U:H2'	21:U:2522:U:C6	2.56	0.41
21:U:2861:U:H2'	21:U:2862:A:C8	2.56	0.41
26:Z:142:ASP:HB2	26:Z:145:LYS:HB2	2.03	0.41
35:i:75:ARG:NE	35:i:77:PHE:HZ	2.03	0.41
40:n:83:TYR:O	40:n:84:LYS:CB	2.69	0.41
49:w:6:ILE:HD13	49:w:26:LEU:HD13	2.02	0.41
1:A:566:G:H2'	1:A:567:G:C8	2.55	0.41
1:A:716:U:H2'	1:A:717:G:H8	1.86	0.41
1:A:1050:A:H2'	1:A:1051:G:C8	2.56	0.41
1:A:1333:A:H2'	1:A:1334:C:C6	2.56	0.41
1:A:1364:G:H2'	1:A:1365:G:H8	1.86	0.41
1:A:1364:G:H2'	1:A:1365:G:C8	2.56	0.41
21:U:76:C:H2'	21:U:77:U:H6	1.86	0.41
21:U:478:U:H2'	21:U:479:A:H8	1.86	0.41
21:U:860:U:H2'	21:U:861:C:H6	1.86	0.41
21:U:1042:A:H5'	36:j:92:ARG:NH2	2.35	0.41
21:U:1299:G:H2'	21:U:1300:G:C8	2.55	0.41
21:U:2786:A:N1	27:a:68:THR:HG21	2.36	0.41
22:V:40:C:H4'	26:Z:64:LYS:HB3	2.03	0.41
23:W:69:ARG:NH1	23:W:104:ILE:HG21	2.36	0.41
25:Y:5:ALA:HA	25:Y:16:ASP:HA	2.03	0.41
25:Y:151:LYS:HB3	25:Y:189:HIS:ND1	2.36	0.41
27:a:32:GLY:H	27:a:80:VAL:HG13	1.85	0.41
29:c:25:THR:OG1	29:c:26:LEU:N	2.54	0.41
30:d:2:ILE:HD11	30:d:65:THR:CG2	2.48	0.41
32:f:27:VAL:HB	32:f:102:VAL:HG11	2.02	0.41
36:j:98:LEU:O	36:j:101:ASN:N	2.52	0.41
47:u:54:LEU:HD12	47:u:54:LEU:HA	1.92	0.41
1:A:82:G:N2	1:A:88:U:O2	2.54	0.40
1:A:121:C:O2	1:A:247:G:N2	2.54	0.40
1:A:954:G:N1	1:A:1347:G:OP2	2.53	0.40
1:A:1436:C:O2	1:A:1484:G:N2	2.54	0.40
21:U:444:U:H2'	21:U:445:C:C6	2.57	0.40
21:U:1327:U:O2'	21:U:1366:C:N4	2.54	0.40
21:U:1426:A:H2'	21:U:1427:G:H8	1.86	0.40
21:U:1682:C:H2'	21:U:1683:C:C6	2.56	0.40
21:U:2335:U:H5''	21:U:2336:G:H2'	2.03	0.40
21:U:2344:U:H2'	21:U:2345:U:C6	2.55	0.40
21:U:2414:C:H2'	21:U:2415:U:C6	2.55	0.40
29:c:75:TYR:HB2	29:c:88:ARG:HG3	2.01	0.40
39:m:65:ARG:NH2	39:m:67:GLY:O	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:v:60:ARG:HA	48:v:63:ALA:HB3	2.02	0.40
51:x:18:ASP:HA	51:x:21:GLU:HB3	2.03	0.40
1:A:857:C:H2'	1:A:858:C:C6	2.56	0.40
21:U:719:C:H5	31:e:42:SER:HB3	1.86	0.40
21:U:2013:U:H2'	21:U:2014:G:H8	1.86	0.40
21:U:2019:C:H2'	21:U:2020:U:C6	2.55	0.40
28:b:23:LYS:HG3	28:b:92:PRO:HG3	2.02	0.40
32:f:30:GLY:N	32:f:105:GLU:OE1	2.47	0.40
34:h:24:GLY:HA2	34:h:30:ARG:HD3	2.03	0.40
42:p:30:CYS:HB2	42:p:34:GLY:N	2.32	0.40
1:A:203:A:H2'	1:A:204:A:C8	2.56	0.40
1:A:270:A:H2'	1:A:271:A:H8	1.86	0.40
1:A:833:U:H2'	1:A:834:G:H8	1.85	0.40
1:A:843:U:H2'	1:A:844:A:H8	1.86	0.40
1:A:1080:U:H2'	1:A:1081:C:C6	2.56	0.40
21:U:796:A:N6	21:U:800:G:H21	2.19	0.40
21:U:888:A:H2'	21:U:889:A:C8	2.57	0.40
21:U:1036:A:O2'	37:k:75:ARG:NH2	2.48	0.40
21:U:2089:A:H3'	25:Y:68:LYS:HE2	2.02	0.40
21:U:2290:C:O3'	21:U:2416:U:O2'	2.32	0.40
21:U:2372:U:O2'	21:U:2402:A:O2'	2.34	0.40
21:U:2853:C:H2'	21:U:2854:A:C8	2.55	0.40
22:V:21:G:H2'	22:V:22:G:C5	2.57	0.40
22:V:48:G:O2'	22:V:49:G:O4'	2.39	0.40
26:Z:4:LEU:HD12	26:Z:7:LYS:HD3	2.03	0.40
26:Z:78:ARG:HA	26:Z:79:LEU:HA	1.87	0.40
27:a:68:THR:O	27:a:72:LEU:N	2.52	0.40
34:h:72:SER:HA	34:h:75:THR:HG23	2.03	0.40
34:h:85:ALA:O	34:h:89:GLY:N	2.54	0.40
35:i:30:ARG:N	35:i:88:GLU:O	2.42	0.40
38:l:79:GLY:N	38:l:100:THR:O	2.45	0.40
39:m:51:VAL:HA	39:m:83:LEU:HD23	2.03	0.40
1:A:443:U:H2'	1:A:444:C:H6	1.87	0.40
1:A:930:U:H2'	1:A:931:U:H6	1.87	0.40
13:M:79:ARG:O	13:M:83:ILE:N	2.52	0.40
21:U:18:C:H2'	21:U:19:G:H8	1.87	0.40
21:U:1129:U:C2	21:U:1131:A:H5''	2.57	0.40
21:U:1196:C:H2'	21:U:1197:A:C8	2.56	0.40
21:U:1619:A:H2'	21:U:1620:A:C8	2.56	0.40
21:U:2708:A:H2	24:X:191:ASN:HD22	1.68	0.40
21:U:2847:G:O3'	24:X:163:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:260:ARG:NH1	23:W:266:SER:OG	2.55	0.40
28:b:59:MET:HB2	28:b:62:ARG:HB2	2.04	0.40
34:h:35:ARG:HB3	34:h:100:TYR:CZ	2.56	0.40
51:x:3:TYR:CZ	51:x:24:ILE:HG23	2.56	0.40
21:U:553:A:H4'	21:U:554:U:H5''	2.04	0.40
21:U:565:U:H5''	38:l:25:ARG:NH1	2.37	0.40
21:U:1528:U:H4'	21:U:1529:G:H5'	2.03	0.40
21:U:1618:A:H5'	23:W:36:PRO:HB3	2.03	0.40
21:U:2049:A:H5'	42:p:9:SER:HB3	2.02	0.40
21:U:2054:C:H2'	21:U:2055:U:C6	2.56	0.40
21:U:2213:U:H2'	21:U:2214:G:C8	2.56	0.40
21:U:2759:C:H2'	21:U:2760:G:C8	2.57	0.40
25:Y:118:VAL:HG22	25:Y:123:ILE:HD13	2.04	0.40
26:Z:176:PRO:HB3	50:y:42:PHE:HE2	1.87	0.40
35:i:95:VAL:HG11	35:i:100:LEU:HD11	2.02	0.40
38:l:20:VAL:HG11	38:l:44:SER:HA	2.04	0.40
42:p:29:GLU:HG2	42:p:36:MET:HG2	2.04	0.40
51:x:57:ILE:HG23	51:x:64:LEU:HG	2.04	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	
2	B	222/224 (99%)	195 (88%)	27 (12%)	0	100	100
3	C	208/210 (99%)	180 (86%)	25 (12%)	3 (1%)	9	37
4	D	197/199 (99%)	169 (86%)	28 (14%)	0	100	100
5	E	163/165 (99%)	133 (82%)	30 (18%)	0	100	100
6	F	93/95 (98%)	77 (83%)	16 (17%)	0	100	100
7	G	151/153 (99%)	121 (80%)	30 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	129/131 (98%)	102 (79%)	24 (19%)	3 (2%)	5	30
9	I	128/130 (98%)	95 (74%)	32 (25%)	1 (1%)	16	48
10	J	100/102 (98%)	80 (80%)	20 (20%)	0	100	100
11	K	116/118 (98%)	97 (84%)	19 (16%)	0	100	100
12	L	135/137 (98%)	111 (82%)	24 (18%)	0	100	100
13	M	109/111 (98%)	86 (79%)	23 (21%)	0	100	100
14	N	58/60 (97%)	46 (79%)	12 (21%)	0	100	100
15	O	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
16	P	87/89 (98%)	64 (74%)	23 (26%)	0	100	100
17	Q	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
18	R	69/71 (97%)	54 (78%)	14 (20%)	1 (1%)	9	37
19	S	78/80 (98%)	58 (74%)	20 (26%)	0	100	100
20	T	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
23	W	273/275 (99%)	234 (86%)	36 (13%)	3 (1%)	11	41
24	X	205/207 (99%)	188 (92%)	17 (8%)	0	100	100
25	Y	203/205 (99%)	177 (87%)	24 (12%)	2 (1%)	12	43
26	Z	176/178 (99%)	150 (85%)	26 (15%)	0	100	100
27	a	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
28	b	121/123 (98%)	96 (79%)	22 (18%)	3 (2%)	4	28
29	c	140/142 (99%)	125 (89%)	15 (11%)	0	100	100
30	d	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
31	e	144/146 (99%)	128 (89%)	15 (10%)	1 (1%)	18	51
32	f	136/138 (99%)	120 (88%)	16 (12%)	0	100	100
33	g	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
34	h	118/120 (98%)	104 (88%)	13 (11%)	1 (1%)	16	48
35	i	112/114 (98%)	93 (83%)	19 (17%)	0	100	100
36	j	115/117 (98%)	107 (93%)	6 (5%)	2 (2%)	7	34
37	k	99/101 (98%)	72 (73%)	22 (22%)	5 (5%)	1	17
38	l	107/109 (98%)	88 (82%)	18 (17%)	1 (1%)	14	45
39	m	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
40	n	98/100 (98%)	80 (82%)	18 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	o	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
42	p	52/54 (96%)	46 (88%)	6 (12%)	0	100	100
43	q	46/48 (96%)	42 (91%)	4 (9%)	0	100	100
44	r	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
45	s	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
46	t	34/36 (94%)	30 (88%)	4 (12%)	0	100	100
47	u	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
48	v	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
49	w	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
50	y	62/64 (97%)	56 (90%)	4 (6%)	2 (3%)	3	24
51	x	102/104 (98%)	79 (78%)	20 (20%)	3 (3%)	3	25
All	All	5500/5596 (98%)	4688 (85%)	781 (14%)	31 (1%)	23	54

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	5	VAL
3	C	6	ASN
8	H	98	LEU
23	W	154	LEU
25	Y	80	SER
28	b	108	ILE
28	b	112	VAL
31	e	38	GLN
34	h	26	ALA
37	k	25	LEU
37	k	51	PRO
51	x	94	LYS
8	H	99	ASN
25	Y	81	PRO
36	j	98	LEU
37	k	27	ALA
50	y	49	PHE
3	C	4	LYS
23	W	248	SER
36	j	99	ALA
37	k	54	GLU
8	H	100	GLY

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Mol	Chain	Res	Type
18	R	17	TYR
23	W	246	PRO
37	k	52	THR
38	l	42	ALA
50	y	60	ASN
51	x	32	ASP
51	x	93	THR
28	b	90	VAL
9	I	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	223/223 (100%)	222 (100%)	1 (0%)	84	83
24	X	168/168 (100%)	167 (99%)	1 (1%)	78	79
25	Y	169/169 (100%)	165 (98%)	4 (2%)	43	62
26	Z	153/153 (100%)	151 (99%)	2 (1%)	61	71
27	a	148/148 (100%)	148 (100%)	0	100	100
28	b	105/105 (100%)	100 (95%)	5 (5%)	23	47
29	c	120/120 (100%)	118 (98%)	2 (2%)	53	67
30	d	101/101 (100%)	97 (96%)	4 (4%)	28	52
31	e	110/110 (100%)	108 (98%)	2 (2%)	51	67
32	f	111/111 (100%)	109 (98%)	2 (2%)	51	67
33	g	99/99 (100%)	96 (97%)	3 (3%)	36	57
34	h	93/93 (100%)	90 (97%)	3 (3%)	34	56
35	i	99/99 (100%)	99 (100%)	0	100	100
36	j	96/96 (100%)	95 (99%)	1 (1%)	68	74
37	k	83/83 (100%)	81 (98%)	2 (2%)	43	62
38	l	90/90 (100%)	89 (99%)	1 (1%)	65	73
39	m	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	n	84/84 (100%)	81 (96%)	3 (4%)	31	54
41	o	64/64 (100%)	63 (98%)	1 (2%)	55	68
42	p	48/48 (100%)	48 (100%)	0	100	100
43	q	46/46 (100%)	46 (100%)	0	100	100
44	r	39/39 (100%)	39 (100%)	0	100	100
45	s	54/54 (100%)	54 (100%)	0	100	100
46	t	34/34 (100%)	34 (100%)	0	100	100
47	u	47/47 (100%)	46 (98%)	1 (2%)	47	64
48	v	56/56 (100%)	55 (98%)	1 (2%)	51	67
49	w	52/52 (100%)	52 (100%)	0	100	100
50	y	53/53 (100%)	53 (100%)	0	100	100
51	x	97/97 (100%)	93 (96%)	4 (4%)	27	51
All	All	2726/2726 (100%)	2683 (98%)	43 (2%)	54	68

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	W	154	LEU
24	X	77	LYS
25	Y	80	SER
25	Y	119	ILE
25	Y	125	VAL
25	Y	194	ILE
26	Z	12	ILE
26	Z	117	VAL
28	b	50	VAL
28	b	89	VAL
28	b	106	LEU
28	b	107	GLU
28	b	108	ILE
29	c	58	ILE
29	c	65	LEU
30	d	3	GLN
30	d	10	VAL
30	d	35	ILE
30	d	87	ILE
31	e	3	LEU
31	e	36	LYS

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Mol	Chain	Res	Type
32	f	27	VAL
32	f	94	VAL
33	g	56	LEU
33	g	87	ILE
33	g	104	LEU
34	h	22	LEU
34	h	27	GLU
34	h	58	THR
36	j	98	LEU
37	k	25	LEU
37	k	48	VAL
38	l	35	ILE
40	n	86	GLU
40	n	87	ASP
40	n	89	LYS
41	o	51	THR
47	u	56	SER
48	v	32	LEU
51	x	35	VAL
51	x	44	LYS
51	x	55	VAL
51	x	92	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
23	W	86	ASN
24	X	14	GLN
24	X	33	ASN
24	X	152	ASN
25	Y	49	HIS
25	Y	75	GLN
26	Z	2	ASN
26	Z	27	GLN
26	Z	63	GLN
27	a	20	ASN
27	a	23	ASN
27	a	66	HIS
27	a	75	ASN
27	a	148	ASN
28	b	34	ASN
28	b	70	ASN

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Mol	Chain	Res	Type
28	b	73	ASN
28	b	80	ASN
29	c	80	GLN
29	c	81	HIS
29	c	131	HIS
30	d	3	GLN
31	e	68	ASN
31	e	126	ASN
33	g	27	ASN
33	g	61	GLN
34	h	64	ASN
36	j	36	ASN
36	j	38	GLN
37	k	65	GLN
38	l	28	GLN
38	l	37	ASN
38	l	102	HIS
39	m	35	ASN
40	n	58	ASN
40	n	64	HIS
40	n	67	ASN
40	n	99	GLN
41	o	37	GLN
42	p	19	HIS
42	p	50	ASN
43	q	26	ASN
46	t	36	GLN
47	u	17	ASN
49	w	52	HIS
50	y	20	ASN
50	y	60	ASN
51	x	33	HIS
51	x	75	ASN
51	x	96	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1543/1544 (99%)	367 (23%)	17 (1%)
21	U	2922/2923 (99%)	1021 (34%)	60 (2%)
22	V	111/112 (99%)	46 (41%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4576/4579 (99%)	1434 (31%)	79 (1%)

All (1434) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	G
1	A	18	A
1	A	24	G
1	A	34	A
1	A	41	G
1	A	46	G
1	A	49	C
1	A	50	C
1	A	53	A
1	A	62	A
1	A	63	G
1	A	66	G
1	A	81	A
1	A	83	C
1	A	85	U
1	A	87	C
1	A	88	U
1	A	99	A
1	A	113	G
1	A	114	A
1	A	118	A
1	A	119	C
1	A	120	A
1	A	127	U
1	A	129	A
1	A	130	C
1	A	137	G
1	A	141	G
1	A	142	A
1	A	143	C
1	A	148	A
1	A	151	A
1	A	153	U
1	A	154	C
1	A	157	G
1	A	158	G
1	A	162	C

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Mol	Chain	Res	Type
1	A	163	C
1	A	167	G
1	A	172	U
1	A	181	G
1	A	182	U
1	A	183	U
1	A	184	G
1	A	186	U
1	A	189	A
1	A	194	C
1	A	195	A
1	A	197	G
1	A	204	A
1	A	205	C
1	A	206	A
1	A	207	U
1	A	210	A
1	A	211	A
1	A	212	G
1	A	215	G
1	A	216	G
1	A	222	G
1	A	228	A
1	A	234	A
1	A	238	G
1	A	239	G
1	A	249	G
1	A	253	U
1	A	255	G
1	A	259	G
1	A	274	G
1	A	275	C
1	A	287	A
1	A	288	C
1	A	297	G
1	A	306	A
1	A	314	A
1	A	327	G
1	A	332	G
1	A	336	C
1	A	337	A
1	A	338	C

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Mol	Chain	Res	Type
1	A	340	G
1	A	353	C
1	A	355	G
1	A	359	G
1	A	360	C
1	A	362	G
1	A	364	A
1	A	375	U
1	A	380	C
1	A	385	G
1	A	388	G
1	A	390	A
1	A	396	G
1	A	400	G
1	A	401	A
1	A	406	C
1	A	414	G
1	A	419	A
1	A	420	U
1	A	421	G
1	A	423	A
1	A	429	U
1	A	430	C
1	A	431	G
1	A	432	G
1	A	437	U
1	A	441	G
1	A	447	U
1	A	456	A
1	A	457	A
1	A	466	G
1	A	472	C
1	A	474	A
1	A	476	U
1	A	477	A
1	A	487	C
1	A	490	G
1	A	491	A
1	A	493	G
1	A	494	G
1	A	495	U
1	A	505	G

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Mol	Chain	Res	Type
1	A	506	A
1	A	517	U
1	A	519	A
1	A	520	C
1	A	527	C
1	A	530	G
1	A	533	G
1	A	536	G
1	A	540	U
1	A	541	A
1	A	542	A
1	A	546	G
1	A	556	A
1	A	568	A
1	A	571	U
1	A	572	A
1	A	573	U
1	A	575	G
1	A	581	A
1	A	582	A
1	A	584	G
1	A	585	G
1	A	586	G
1	A	588	U
1	A	591	C
1	A	597	G
1	A	605	A
1	A	606	G
1	A	632	C
1	A	638	A
1	A	641	G
1	A	642	U
1	A	643	C
1	A	651	A
1	A	659	A
1	A	683	G
1	A	696	A
1	A	702	G
1	A	704	A
1	A	712	G
1	A	726	C
1	A	727	A

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Mol	Chain	Res	Type
1	A	728	C
1	A	729	C
1	A	730	A
1	A	732	U
1	A	733	G
1	A	740	G
1	A	756	U
1	A	757	A
1	A	764	G
1	A	769	G
1	A	778	G
1	A	785	G
1	A	786	A
1	A	787	G
1	A	790	A
1	A	802	U
1	A	803	A
1	A	808	G
1	A	820	C
1	A	822	U
1	A	824	A
1	A	826	C
1	A	827	G
1	A	828	A
1	A	829	U
1	A	830	G
1	A	837	A
1	A	843	U
1	A	845	G
1	A	849	G
1	A	850	U
1	A	852	U
1	A	853	C
1	A	856	C
1	A	861	U
1	A	865	G
1	A	874	A
1	A	882	A
1	A	883	A
1	A	886	A
1	A	899	A
1	A	901	U

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Mol	Chain	Res	Type
1	A	905	G
1	A	910	A
1	A	912	G
1	A	924	A
1	A	925	A
1	A	932	G
1	A	936	G
1	A	944	C
1	A	945	A
1	A	949	G
1	A	968	A
1	A	970	U
1	A	971	U
1	A	978	A
1	A	979	A
1	A	981	G
1	A	984	A
1	A	985	A
1	A	986	G
1	A	987	A
1	A	992	U
1	A	993	A
1	A	1003	G
1	A	1014	A
1	A	1018	U
1	A	1028	A
1	A	1030	G
1	A	1034	U
1	A	1036	C
1	A	1039	U
1	A	1040	U
1	A	1041	C
1	A	1042	G
1	A	1043	G
1	A	1044	G
1	A	1046	G
1	A	1053	G
1	A	1060	G
1	A	1064	C
1	A	1066	U
1	A	1074	G
1	A	1075	U

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Mol	Chain	Res	Type
1	A	1076	C
1	A	1077	A
1	A	1090	A
1	A	1099	G
1	A	1104	G
1	A	1105	U
1	A	1109	G
1	A	1110	C
1	A	1111	A
1	A	1112	A
1	A	1118	G
1	A	1129	U
1	A	1130	C
1	A	1134	G
1	A	1135	U
1	A	1137	G
1	A	1143	A
1	A	1148	G
1	A	1149	U
1	A	1150	U
1	A	1151	G
1	A	1155	A
1	A	1161	A
1	A	1163	G
1	A	1166	A
1	A	1168	U
1	A	1169	G
1	A	1173	G
1	A	1176	A
1	A	1177	C
1	A	1186	G
1	A	1190	G
1	A	1191	G
1	A	1192	U
1	A	1193	G
1	A	1200	A
1	A	1205	A
1	A	1206	A
1	A	1209	C
1	A	1210	A
1	A	1211	U
1	A	1221	U

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Mol	Chain	Res	Type
1	A	1222	A
1	A	1223	U
1	A	1233	U
1	A	1234	A
1	A	1236	A
1	A	1237	C
1	A	1247	A
1	A	1249	U
1	A	1266	A
1	A	1267	G
1	A	1269	G
1	A	1278	A
1	A	1289	A
1	A	1294	A
1	A	1296	A
1	A	1302	G
1	A	1307	C
1	A	1308	A
1	A	1309	G
1	A	1313	G
1	A	1314	G
1	A	1325	G
1	A	1328	A
1	A	1329	C
1	A	1331	C
1	A	1332	G
1	A	1333	A
1	A	1343	G
1	A	1344	C
1	A	1345	U
1	A	1349	A
1	A	1351	C
1	A	1355	A
1	A	1367	U
1	A	1368	C
1	A	1373	U
1	A	1374	G
1	A	1377	G
1	A	1382	G
1	A	1387	C
1	A	1403	A
1	A	1406	C

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Mol	Chain	Res	Type
1	A	1407	A
1	A	1409	C
1	A	1428	G
1	A	1434	A
1	A	1442	A
1	A	1451	A
1	A	1455	A
1	A	1461	U
1	A	1462	U
1	A	1463	A
1	A	1464	G
1	A	1465	G
1	A	1485	G
1	A	1494	U
1	A	1499	G
1	A	1502	A
1	A	1504	G
1	A	1507	G
1	A	1512	A
1	A	1513	A
1	A	1514	G
1	A	1515	G
1	A	1516	U
1	A	1517	A
1	A	1518	G
1	A	1527	G
1	A	1529	A
1	A	1530	G
1	A	1539	G
1	A	1540	G
1	A	1541	A
1	A	1543	C
1	A	1544	A
1	A	1547	U
1	A	1548	C
1	A	1551	U
21	U	7	G
21	U	8	U
21	U	9	U
21	U	12	A
21	U	13	A
21	U	23	G

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Mol	Chain	Res	Type
21	U	25	U
21	U	27	G
21	U	28	A
21	U	30	G
21	U	31	C
21	U	33	U
21	U	35	G
21	U	36	G
21	U	39	C
21	U	42	G
21	U	43	G
21	U	44	A
21	U	45	G
21	U	46	C
21	U	49	A
21	U	51	G
21	U	55	G
21	U	56	A
21	U	58	G
21	U	59	G
21	U	60	G
21	U	61	A
21	U	62	C
21	U	63	G
21	U	71	A
21	U	75	G
21	U	76	C
21	U	83	G
21	U	87	U
21	U	89	U
21	U	90	A
21	U	91	A
21	U	92	G
21	U	96	G
21	U	98	U
21	U	100	U
21	U	101	G
21	U	117	A
21	U	118	A
21	U	119	U
21	U	124	A
21	U	125	A

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Mol	Chain	Res	Type
21	U	126	A
21	U	127	C
21	U	130	A
21	U	131	C
21	U	147	G
21	U	150	A
21	U	156	A
21	U	159	U
21	U	161	A
21	U	162	A
21	U	163	U
21	U	175	G
21	U	176	A
21	U	177	G
21	U	180	G
21	U	183	A
21	U	184	G
21	U	197	G
21	U	198	A
21	U	199	A
21	U	200	A
21	U	202	A
21	U	203	U
21	U	207	A
21	U	215	G
21	U	216	A
21	U	218	G
21	U	219	A
21	U	224	A
21	U	225	A
21	U	226	A
21	U	227	G
21	U	230	A
21	U	231	A
21	U	232	U
21	U	233	G
21	U	235	G
21	U	236	A
21	U	244	A
21	U	245	G
21	U	248	G
21	U	251	G

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Mol	Chain	Res	Type
21	U	252	C
21	U	253	G
21	U	258	A
21	U	260	A
21	U	267	C
21	U	268	A
21	U	270	C
21	U	271	C
21	U	272	C
21	U	275	A
21	U	282	G
21	U	286	U
21	U	287	G
21	U	289	C
21	U	290	U
21	U	291	C
21	U	298	U
21	U	299	U
21	U	300	G
21	U	301	U
21	U	302	A
21	U	310	C
21	U	312	G
21	U	313	U
21	U	314	A
21	U	315	C
21	U	320	U
21	U	321	U
21	U	322	A
21	U	324	A
21	U	327	G
21	U	328	G
21	U	329	A
21	U	331	C
21	U	337	A
21	U	338	G
21	U	345	A
21	U	346	G
21	U	348	U
21	U	351	G
21	U	354	A
21	U	355	A

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Mol	Chain	Res	Type
21	U	360	C
21	U	366	A
21	U	367	G
21	U	368	G
21	U	373	A
21	U	374	A
21	U	375	C
21	U	376	A
21	U	377	G
21	U	378	C
21	U	379	C
21	U	382	G
21	U	386	U
21	U	388	A
21	U	389	A
21	U	390	A
21	U	393	U
21	U	395	C
21	U	405	U
21	U	406	G
21	U	410	G
21	U	412	A
21	U	413	U
21	U	414	C
21	U	417	G
21	U	418	A
21	U	419	G
21	U	420	U
21	U	430	C
21	U	433	G
21	U	434	U
21	U	435	G
21	U	437	A
21	U	438	A
21	U	443	G
21	U	446	G
21	U	451	C
21	U	452	C
21	U	453	G
21	U	459	A
21	U	471	G
21	U	474	U

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Mol	Chain	Res	Type
21	U	478	U
21	U	481	U
21	U	483	C
21	U	489	G
21	U	490	A
21	U	491	C
21	U	495	U
21	U	498	U
21	U	502	C
21	U	503	C
21	U	504	A
21	U	511	U
21	U	514	G
21	U	520	G
21	U	526	A
21	U	527	A
21	U	528	G
21	U	529	C
21	U	538	A
21	U	539	G
21	U	547	A
21	U	550	G
21	U	551	A
21	U	552	G
21	U	554	U
21	U	555	C
21	U	556	C
21	U	558	G
21	U	559	A
21	U	563	C
21	U	564	G
21	U	567	U
21	U	568	G
21	U	571	U
21	U	572	A
21	U	574	A
21	U	575	A
21	U	576	G
21	U	577	U
21	U	578	A
21	U	579	G
21	U	584	A

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Mol	Chain	Res	Type
21	U	591	U
21	U	592	A
21	U	594	C
21	U	595	G
21	U	598	U
21	U	599	G
21	U	600	A
21	U	606	U
21	U	607	G
21	U	619	A
21	U	631	G
21	U	632	U
21	U	634	A
21	U	637	A
21	U	647	A
21	U	648	G
21	U	649	G
21	U	650	U
21	U	651	U
21	U	657	G
21	U	658	A
21	U	659	A
21	U	660	G
21	U	665	G
21	U	666	G
21	U	667	A
21	U	673	A
21	U	674	G
21	U	676	G
21	U	680	G
21	U	683	A
21	U	684	G
21	U	687	U
21	U	688	G
21	U	691	U
21	U	696	C
21	U	700	U
21	U	701	G
21	U	711	U
21	U	716	G
21	U	718	C
21	U	719	C

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Mol	Chain	Res	Type
21	U	722	A
21	U	723	A
21	U	733	U
21	U	758	A
21	U	764	C
21	U	765	A
21	U	769	A
21	U	773	G
21	U	774	A
21	U	775	G
21	U	777	C
21	U	781	A
21	U	783	C
21	U	785	C
21	U	786	A
21	U	788	G
21	U	790	A
21	U	792	G
21	U	794	U
21	U	795	G
21	U	804	G
21	U	811	A
21	U	812	G
21	U	819	G
21	U	822	G
21	U	823	G
21	U	824	G
21	U	829	A
21	U	831	U
21	U	832	G
21	U	835	A
21	U	836	A
21	U	837	U
21	U	838	C
21	U	840	A
21	U	843	C
21	U	844	U
21	U	847	A
21	U	848	G
21	U	852	G
21	U	853	C
21	U	857	U

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Mol	Chain	Res	Type
21	U	858	U
21	U	859	C
21	U	864	C
21	U	866	A
21	U	872	C
21	U	874	U
21	U	875	U
21	U	879	G
21	U	882	A
21	U	892	U
21	U	896	A
21	U	899	C
21	U	900	U
21	U	903	G
21	U	905	G
21	U	907	U
21	U	908	A
21	U	911	G
21	U	912	C
21	U	913	A
21	U	914	C
21	U	922	A
21	U	924	U
21	U	925	A
21	U	927	G
21	U	931	C
21	U	932	C
21	U	933	C
21	U	934	U
21	U	935	A
21	U	937	C
21	U	938	G
21	U	940	G
21	U	942	U
21	U	943	A
21	U	944	C
21	U	948	A
21	U	951	C
21	U	952	A
21	U	957	A
21	U	959	C
21	U	960	U

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Mol	Chain	Res	Type
21	U	961	C
21	U	962	C
21	U	964	A
21	U	966	U
21	U	970	A
21	U	972	U
21	U	974	A
21	U	975	C
21	U	977	U
21	U	978	A
21	U	980	C
21	U	981	C
21	U	987	A
21	U	988	G
21	U	992	G
21	U	998	G
21	U	1003	A
21	U	1005	A
21	U	1007	G
21	U	1020	A
21	U	1027	A
21	U	1028	C
21	U	1029	A
21	U	1030	G
21	U	1031	C
21	U	1039	G
21	U	1043	G
21	U	1047	A
21	U	1051	C
21	U	1055	A
21	U	1058	U
21	U	1059	A
21	U	1063	G
21	U	1068	G
21	U	1069	U
21	U	1071	G
21	U	1072	A
21	U	1079	U
21	U	1091	U
21	U	1092	A
21	U	1093	G
21	U	1094	A

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Mol	Chain	Res	Type
21	U	1099	C
21	U	1100	A
21	U	1102	G
21	U	1103	A
21	U	1104	U
21	U	1106	U
21	U	1107	U
21	U	1108	G
21	U	1111	U
21	U	1113	A
21	U	1114	G
21	U	1115	A
21	U	1116	A
21	U	1117	G
21	U	1118	C
21	U	1120	G
21	U	1121	C
21	U	1122	C
21	U	1123	A
21	U	1124	C
21	U	1126	A
21	U	1127	U
21	U	1128	U
21	U	1130	A
21	U	1131	A
21	U	1134	A
21	U	1135	G
21	U	1136	U
21	U	1137	G
21	U	1141	A
21	U	1148	C
21	U	1152	G
21	U	1157	A
21	U	1158	G
21	U	1168	G
21	U	1172	A
21	U	1173	A
21	U	1174	A
21	U	1176	U
21	U	1177	G
21	U	1178	U
21	U	1179	A

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Mol	Chain	Res	Type
21	U	1180	C
21	U	1181	C
21	U	1182	G
21	U	1185	G
21	U	1187	U
21	U	1188	A
21	U	1189	A
21	U	1193	U
21	U	1194	A
21	U	1198	C
21	U	1201	A
21	U	1208	G
21	U	1209	G
21	U	1214	U
21	U	1217	U
21	U	1218	U
21	U	1219	C
21	U	1220	G
21	U	1222	A
21	U	1244	A
21	U	1245	G
21	U	1246	G
21	U	1247	G
21	U	1248	C
21	U	1251	U
21	U	1258	A
21	U	1259	G
21	U	1263	G
21	U	1267	G
21	U	1271	U
21	U	1276	G
21	U	1278	G
21	U	1280	G
21	U	1284	A
21	U	1289	U
21	U	1290	G
21	U	1293	A
21	U	1294	A
21	U	1295	U
21	U	1296	G
21	U	1302	A
21	U	1305	A

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Mol	Chain	Res	Type
21	U	1308	A
21	U	1311	G
21	U	1312	A
21	U	1313	A
21	U	1314	A
21	U	1315	G
21	U	1318	G
21	U	1319	G
21	U	1327	U
21	U	1333	C
21	U	1339	A
21	U	1340	A
21	U	1344	C
21	U	1345	U
21	U	1346	A
21	U	1350	U
21	U	1351	U
21	U	1352	U
21	U	1353	C
21	U	1360	A
21	U	1363	G
21	U	1364	C
21	U	1365	U
21	U	1367	G
21	U	1369	C
21	U	1374	C
21	U	1378	G
21	U	1380	U
21	U	1381	A
21	U	1384	C
21	U	1388	A
21	U	1398	A
21	U	1404	A
21	U	1405	A
21	U	1417	A
21	U	1418	U
21	U	1423	A
21	U	1424	A
21	U	1425	C
21	U	1426	A
21	U	1429	U
21	U	1432	A

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Mol	Chain	Res	Type
21	U	1433	U
21	U	1434	A
21	U	1435	U
21	U	1436	U
21	U	1437	C
21	U	1439	U
21	U	1440	G
21	U	1441	U
21	U	1442	A
21	U	1448	U
21	U	1449	C
21	U	1450	C
21	U	1456	A
21	U	1458	U
21	U	1459	U
21	U	1460	G
21	U	1461	A
21	U	1464	A
21	U	1467	G
21	U	1472	G
21	U	1473	A
21	U	1474	C
21	U	1481	G
21	U	1482	G
21	U	1486	G
21	U	1490	A
21	U	1493	C
21	U	1495	C
21	U	1496	G
21	U	1497	G
21	U	1498	U
21	U	1499	A
21	U	1501	U
21	U	1502	G
21	U	1503	G
21	U	1504	A
21	U	1505	U
21	U	1507	U
21	U	1512	G
21	U	1513	U
21	U	1516	A
21	U	1517	A

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Mol	Chain	Res	Type
21	U	1519	C
21	U	1520	A
21	U	1521	G
21	U	1524	A
21	U	1526	G
21	U	1527	C
21	U	1528	U
21	U	1529	G
21	U	1530	G
21	U	1537	G
21	U	1539	C
21	U	1540	A
21	U	1543	U
21	U	1544	C
21	U	1553	A
21	U	1555	A
21	U	1560	U
21	U	1564	C
21	U	1567	U
21	U	1570	U
21	U	1571	G
21	U	1572	G
21	U	1573	C
21	U	1578	G
21	U	1581	A
21	U	1582	U
21	U	1584	U
21	U	1585	A
21	U	1586	G
21	U	1587	U
21	U	1596	U
21	U	1602	U
21	U	1607	C
21	U	1613	C
21	U	1615	A
21	U	1616	G
21	U	1617	A
21	U	1619	A
21	U	1626	U
21	U	1630	G
21	U	1631	A
21	U	1632	G

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Mol	Chain	Res	Type
21	U	1634	U
21	U	1636	A
21	U	1638	A
21	U	1641	U
21	U	1645	C
21	U	1647	U
21	U	1651	G
21	U	1652	C
21	U	1653	A
21	U	1655	A
21	U	1657	C
21	U	1660	C
21	U	1662	C
21	U	1663	A
21	U	1664	G
21	U	1667	A
21	U	1674	G
21	U	1687	G
21	U	1690	G
21	U	1691	A
21	U	1692	U
21	U	1693	C
21	U	1694	G
21	U	1695	A
21	U	1696	G
21	U	1697	A
21	U	1699	A
21	U	1705	C
21	U	1708	U
21	U	1709	A
21	U	1712	G
21	U	1713	A
21	U	1714	A
21	U	1719	G
21	U	1724	A
21	U	1726	G
21	U	1727	A
21	U	1739	C
21	U	1743	A
21	U	1744	G
21	U	1745	A
21	U	1751	U

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Mol	Chain	Res	Type
21	U	1752	G
21	U	1756	U
21	U	1757	G
21	U	1758	U
21	U	1759	U
21	U	1763	G
21	U	1765	G
21	U	1770	C
21	U	1771	C
21	U	1774	A
21	U	1776	A
21	U	1777	G
21	U	1778	A
21	U	1779	G
21	U	1780	C
21	U	1781	C
21	U	1782	G
21	U	1785	G
21	U	1786	U
21	U	1787	G
21	U	1790	U
21	U	1792	G
21	U	1793	G
21	U	1802	A
21	U	1803	C
21	U	1809	A
21	U	1810	G
21	U	1811	C
21	U	1814	A
21	U	1819	C
21	U	1820	A
21	U	1823	U
21	U	1829	C
21	U	1830	G
21	U	1831	A
21	U	1832	A
21	U	1834	C
21	U	1835	C
21	U	1836	G
21	U	1838	A
21	U	1839	A
21	U	1844	A

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Mol	Chain	Res	Type
21	U	1846	G
21	U	1848	A
21	U	1858	A
21	U	1862	C
21	U	1864	G
21	U	1876	A
21	U	1882	A
21	U	1885	A
21	U	1887	G
21	U	1893	U
21	U	1895	A
21	U	1898	G
21	U	1899	U
21	U	1901	A
21	U	1902	G
21	U	1905	A
21	U	1910	G
21	U	1912	G
21	U	1913	A
21	U	1918	A
21	U	1919	A
21	U	1926	G
21	U	1929	A
21	U	1930	A
21	U	1932	G
21	U	1935	G
21	U	1942	A
21	U	1943	C
21	U	1944	U
21	U	1945	A
21	U	1958	G
21	U	1959	G
21	U	1960	U
21	U	1966	A
21	U	1967	A
21	U	1968	U
21	U	1969	U
21	U	1970	C
21	U	1971	C
21	U	1972	U
21	U	1973	U
21	U	1981	A

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Mol	Chain	Res	Type
21	U	1984	U
21	U	1989	A
21	U	1992	C
21	U	1993	G
21	U	1995	A
21	U	1996	C
21	U	1999	A
21	U	2000	A
21	U	2001	G
21	U	2006	A
21	U	2009	G
21	U	2010	A
21	U	2011	U
21	U	2020	U
21	U	2021	G
21	U	2022	U
21	U	2024	U
21	U	2026	A
21	U	2027	A
21	U	2033	G
21	U	2049	A
21	U	2050	G
21	U	2052	A
21	U	2059	A
21	U	2060	A
21	U	2062	A
21	U	2064	G
21	U	2065	C
21	U	2072	C
21	U	2084	C
21	U	2085	G
21	U	2088	A
21	U	2089	A
21	U	2090	G
21	U	2091	A
21	U	2092	C
21	U	2098	G
21	U	2109	G
21	U	2111	A
21	U	2116	G
21	U	2119	A
21	U	2121	U

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Mol	Chain	Res	Type
21	U	2122	G
21	U	2123	A
21	U	2124	A
21	U	2125	U
21	U	2128	U
21	U	2131	U
21	U	2139	G
21	U	2140	U
21	U	2141	A
21	U	2142	C
21	U	2143	A
21	U	2146	A
21	U	2147	U
21	U	2148	A
21	U	2149	G
21	U	2150	G
21	U	2155	A
21	U	2156	G
21	U	2157	C
21	U	2160	U
21	U	2161	G
21	U	2162	G
21	U	2164	A
21	U	2165	A
21	U	2166	C
21	U	2168	G
21	U	2170	A
21	U	2171	G
21	U	2174	C
21	U	2175	C
21	U	2176	A
21	U	2177	G
21	U	2179	U
21	U	2181	C
21	U	2187	A
21	U	2188	G
21	U	2189	G
21	U	2195	G
21	U	2196	U
21	U	2197	G
21	U	2198	G
21	U	2200	A

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Mol	Chain	Res	Type
21	U	2202	A
21	U	2205	A
21	U	2208	C
21	U	2218	U
21	U	2221	C
21	U	2222	C
21	U	2223	U
21	U	2227	A
21	U	2231	C
21	U	2232	G
21	U	2233	C
21	U	2240	U
21	U	2241	A
21	U	2243	C
21	U	2246	G
21	U	2252	A
21	U	2254	A
21	U	2265	U
21	U	2267	G
21	U	2268	G
21	U	2272	U
21	U	2279	G
21	U	2295	A
21	U	2300	G
21	U	2308	G
21	U	2309	G
21	U	2311	G
21	U	2312	C
21	U	2315	A
21	U	2317	A
21	U	2328	G
21	U	2334	U
21	U	2335	U
21	U	2336	G
21	U	2337	G
21	U	2340	A
21	U	2341	U
21	U	2343	A
21	U	2344	U
21	U	2346	C
21	U	2347	G
21	U	2352	G

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Mol	Chain	Res	Type
21	U	2354	G
21	U	2356	A
21	U	2357	A
21	U	2362	A
21	U	2363	C
21	U	2364	A
21	U	2365	A
21	U	2367	G
21	U	2372	U
21	U	2374	G
21	U	2376	C
21	U	2377	U
21	U	2379	C
21	U	2387	A
21	U	2390	A
21	U	2394	G
21	U	2400	G
21	U	2406	A
21	U	2408	G
21	U	2411	G
21	U	2412	G
21	U	2414	C
21	U	2420	G
21	U	2425	G
21	U	2431	U
21	U	2432	C
21	U	2434	G
21	U	2435	C
21	U	2436	A
21	U	2438	G
21	U	2439	G
21	U	2451	C
21	U	2452	U
21	U	2453	C
21	U	2454	A
21	U	2455	A
21	U	2456	C
21	U	2458	G
21	U	2459	A
21	U	2460	U
21	U	2464	A
21	U	2468	A

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Mol	Chain	Res	Type
21	U	2470	C
21	U	2476	G
21	U	2477	A
21	U	2478	U
21	U	2479	A
21	U	2482	A
21	U	2483	G
21	U	2497	A
21	U	2499	G
21	U	2505	A
21	U	2509	C
21	U	2513	G
21	U	2523	G
21	U	2527	C
21	U	2528	C
21	U	2529	U
21	U	2530	C
21	U	2531	G
21	U	2532	A
21	U	2533	U
21	U	2534	G
21	U	2535	U
21	U	2536	C
21	U	2539	C
21	U	2542	A
21	U	2543	U
21	U	2546	C
21	U	2547	A
21	U	2548	U
21	U	2549	C
21	U	2555	G
21	U	2556	C
21	U	2557	U
21	U	2558	G
21	U	2559	U
21	U	2569	C
21	U	2571	A
21	U	2572	G
21	U	2575	U
21	U	2577	G
21	U	2578	G
21	U	2583	U

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Mol	Chain	Res	Type
21	U	2593	A
21	U	2594	A
21	U	2595	A
21	U	2596	G
21	U	2597	C
21	U	2611	G
21	U	2614	U
21	U	2619	A
21	U	2631	A
21	U	2635	C
21	U	2638	U
21	U	2639	C
21	U	2642	U
21	U	2648	U
21	U	2652	G
21	U	2658	A
21	U	2659	G
21	U	2661	A
21	U	2665	U
21	U	2668	A
21	U	2671	G
21	U	2676	U
21	U	2680	C
21	U	2683	A
21	U	2685	U
21	U	2692	G
21	U	2699	G
21	U	2703	G
21	U	2711	G
21	U	2712	C
21	U	2714	G
21	U	2717	G
21	U	2718	U
21	U	2720	C
21	U	2730	U
21	U	2731	G
21	U	2743	G
21	U	2745	U
21	U	2754	A
21	U	2755	U
21	U	2762	A
21	U	2766	G

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Mol	Chain	Res	Type
21	U	2771	G
21	U	2773	G
21	U	2776	G
21	U	2777	A
21	U	2779	A
21	U	2780	G
21	U	2784	C
21	U	2785	U
21	U	2786	A
21	U	2787	A
21	U	2794	A
21	U	2795	G
21	U	2798	C
21	U	2803	C
21	U	2807	A
21	U	2808	U
21	U	2813	U
21	U	2818	C
21	U	2819	A
21	U	2820	U
21	U	2825	C
21	U	2826	A
21	U	2830	A
21	U	2832	G
21	U	2836	G
21	U	2837	A
21	U	2843	G
21	U	2846	A
21	U	2855	G
21	U	2856	G
21	U	2858	U
21	U	2859	G
21	U	2860	A
21	U	2869	A
21	U	2873	G
21	U	2874	G
21	U	2892	G
21	U	2897	G
21	U	2899	C
21	U	2900	A
21	U	2903	U
21	U	2904	A

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Mol	Chain	Res	Type
21	U	2905	C
21	U	2908	A
21	U	2910	C
21	U	2911	G
21	U	2918	G
21	U	2919	A
21	U	2921	U
22	V	8	G
22	V	10	G
22	V	11	A
22	V	12	U
22	V	13	A
22	V	14	G
22	V	19	G
22	V	20	A
22	V	21	G
22	V	22	G
22	V	23	U
22	V	26	C
22	V	28	C
22	V	31	G
22	V	32	U
22	V	33	U
22	V	35	C
22	V	38	U
22	V	39	A
22	V	40	C
22	V	41	C
22	V	42	G
22	V	43	A
22	V	47	C
22	V	48	G
22	V	49	G
22	V	51	A
22	V	53	U
22	V	54	U
22	V	55	A
22	V	59	U
22	V	60	C
22	V	61	U
22	V	62	U
22	V	63	C

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Mol	Chain	Res	Type
22	V	64	A
22	V	84	G
22	V	85	U
22	V	86	U
22	V	87	U
22	V	88	C
22	V	91	C
22	V	96	G
22	V	97	A
22	V	107	G
22	V	110	G

All (79) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	98	U
1	A	113	G
1	A	119	C
1	A	126	G
1	A	456	A
1	A	727	A
1	A	842	U
1	A	848	G
1	A	855	G
1	A	864	U
1	A	873	U
1	A	1111	A
1	A	1154	C
1	A	1210	A
1	A	1461	U
1	A	1501	G
1	A	1503	A
21	U	43	G
21	U	58	G
21	U	90	A
21	U	124	A
21	U	175	G
21	U	183	A
21	U	229	A
21	U	252	C
21	U	267	C
21	U	271	C

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Mol	Chain	Res	Type
21	U	288	C
21	U	377	G
21	U	389	A
21	U	405	U
21	U	419	G
21	U	437	A
21	U	537	A
21	U	549	A
21	U	558	G
21	U	649	G
21	U	666	G
21	U	683	A
21	U	717	A
21	U	785	C
21	U	837	U
21	U	899	C
21	U	936	C
21	U	980	C
21	U	1092	A
21	U	1093	G
21	U	1103	A
21	U	1107	U
21	U	1117	G
21	U	1245	G
21	U	1289	U
21	U	1294	A
21	U	1339	A
21	U	1351	U
21	U	1362	G
21	U	1438	C
21	U	1455	C
21	U	1518	G
21	U	1527	C
21	U	1595	U
21	U	1615	A
21	U	1630	G
21	U	1652	C
21	U	1755	C
21	U	1779	G
21	U	1784	A
21	U	1813	A
21	U	2334	U

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Mol	Chain	Res	Type
21	U	2351	A
21	U	2454	A
21	U	2504	C
21	U	2625	U
21	U	2716	U
21	U	2784	C
21	U	2785	U
21	U	2812	A
22	V	47	C
22	V	59	U

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

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

5.5 Carbohydrates [i](#)

There are no 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.

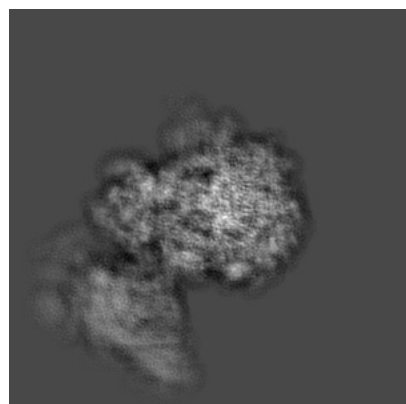
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3656. These allow visual inspection of the internal detail of the map and identification of artifacts.

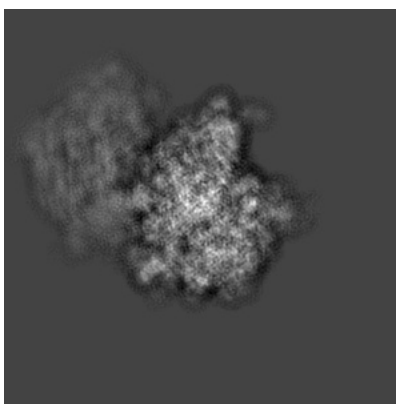
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

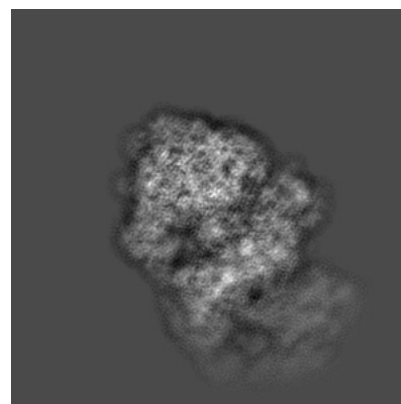
6.1.1 Primary map



X

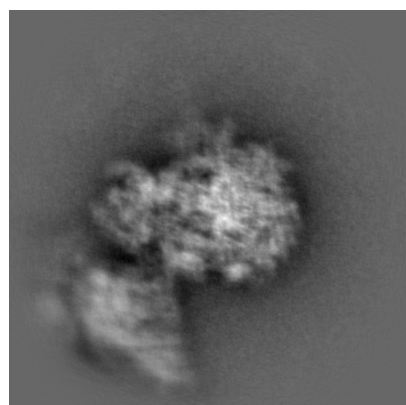


Y

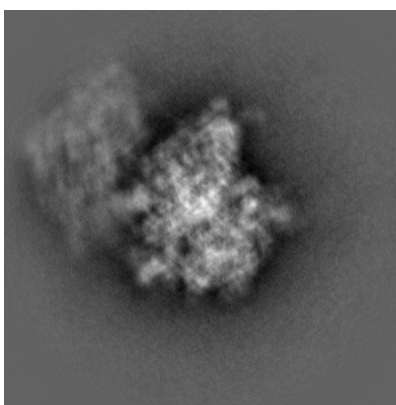


Z

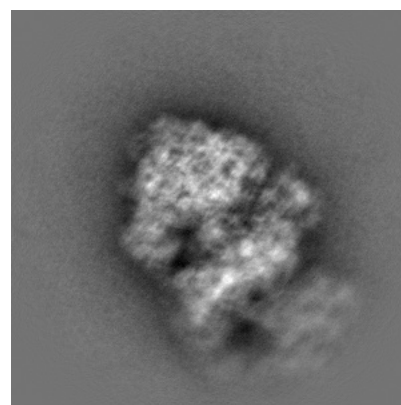
6.1.2 Raw map



X



Y

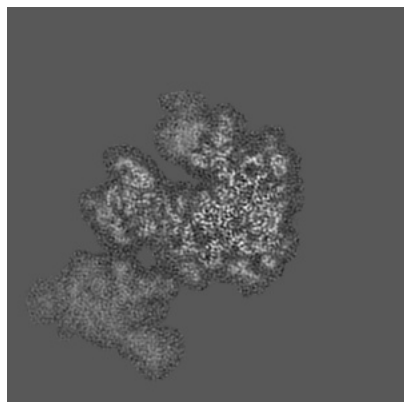


Z

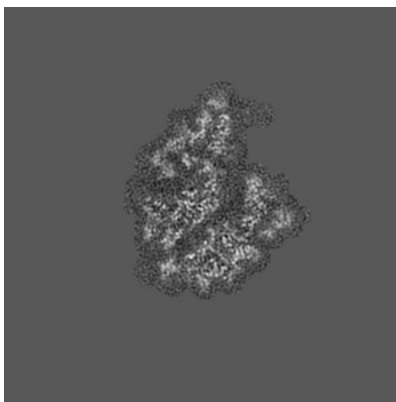
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

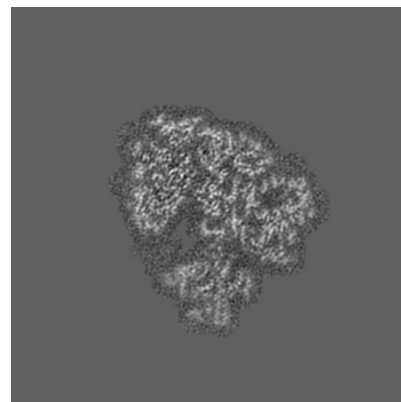
6.2.1 Primary map



X Index: 225

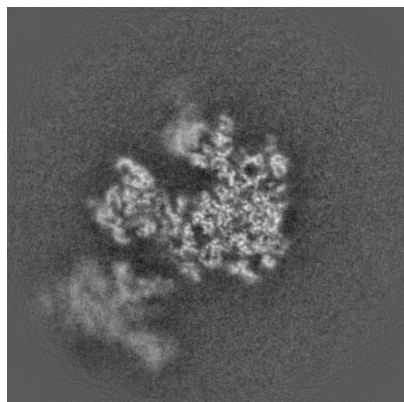


Y Index: 225

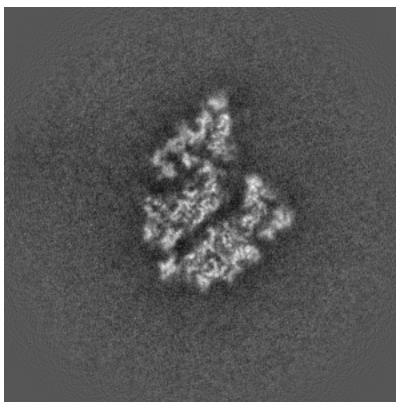


Z Index: 225

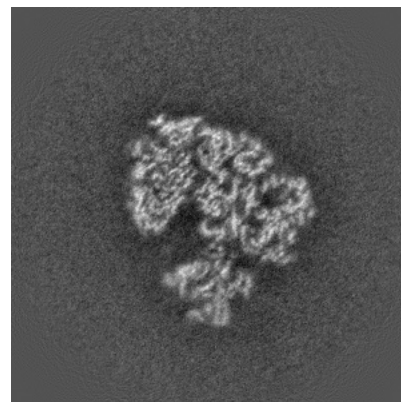
6.2.2 Raw map



X Index: 225



Y Index: 225

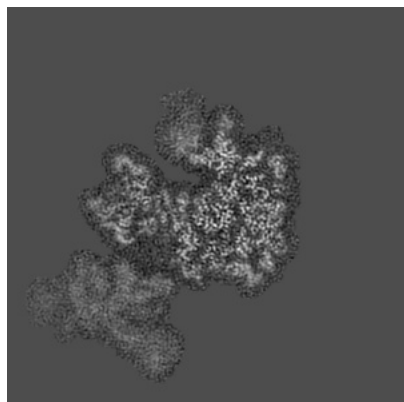


Z Index: 225

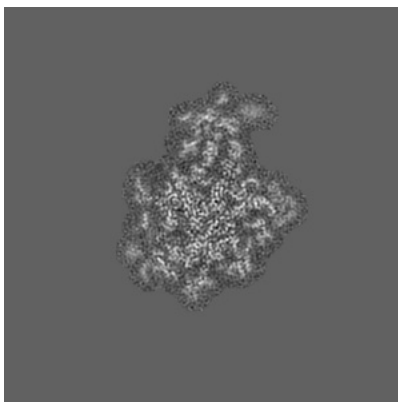
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

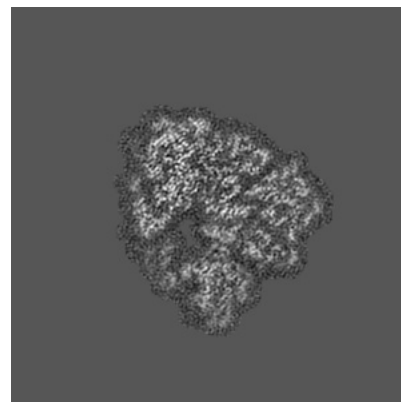
6.3.1 Primary map



X Index: 229

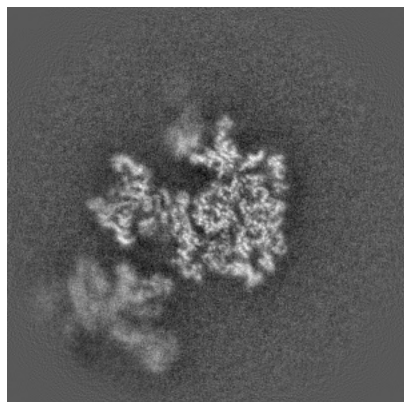


Y Index: 245

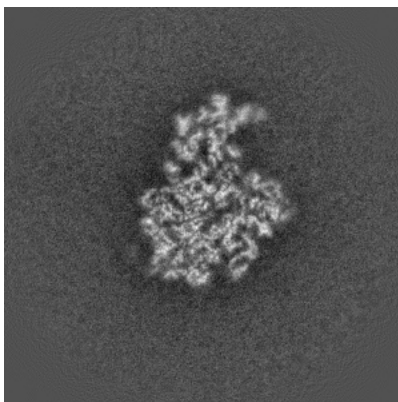


Z Index: 231

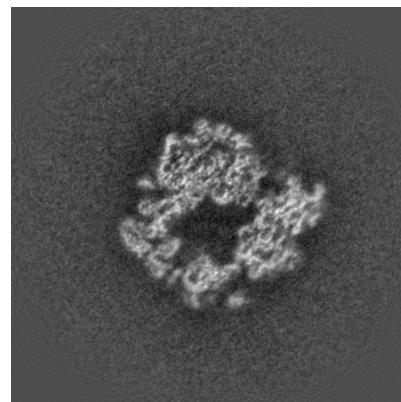
6.3.2 Raw map



X Index: 230



Y Index: 236

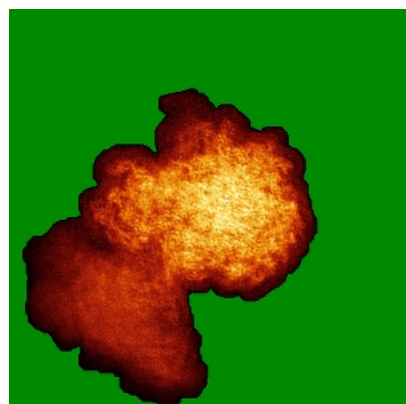


Z Index: 248

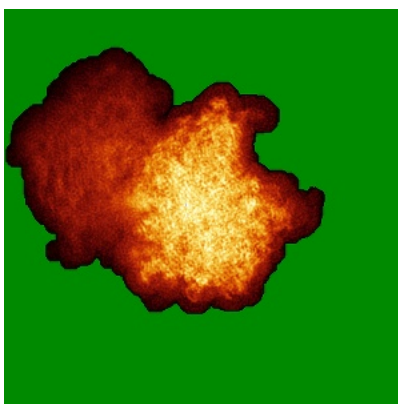
The images above show the largest variance slices of the map in three orthogonal directions.

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

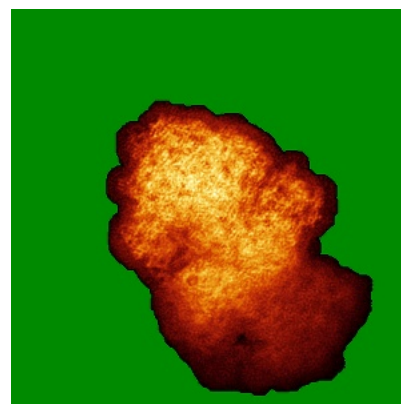
6.4.1 Primary map



X

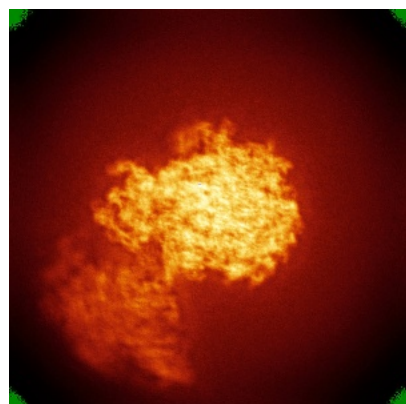


Y

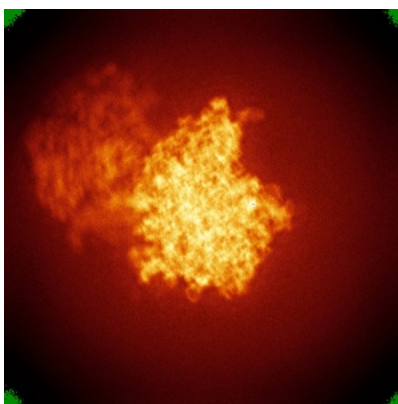


Z

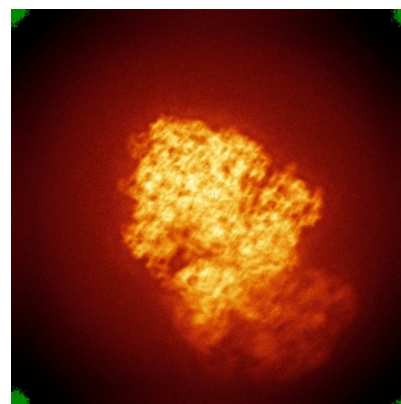
6.4.2 Raw map



X



Y

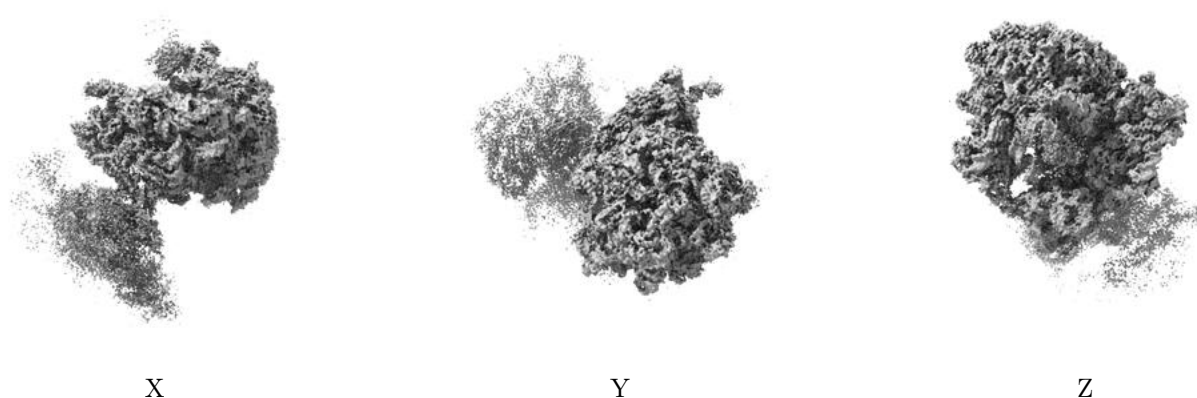


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 11.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

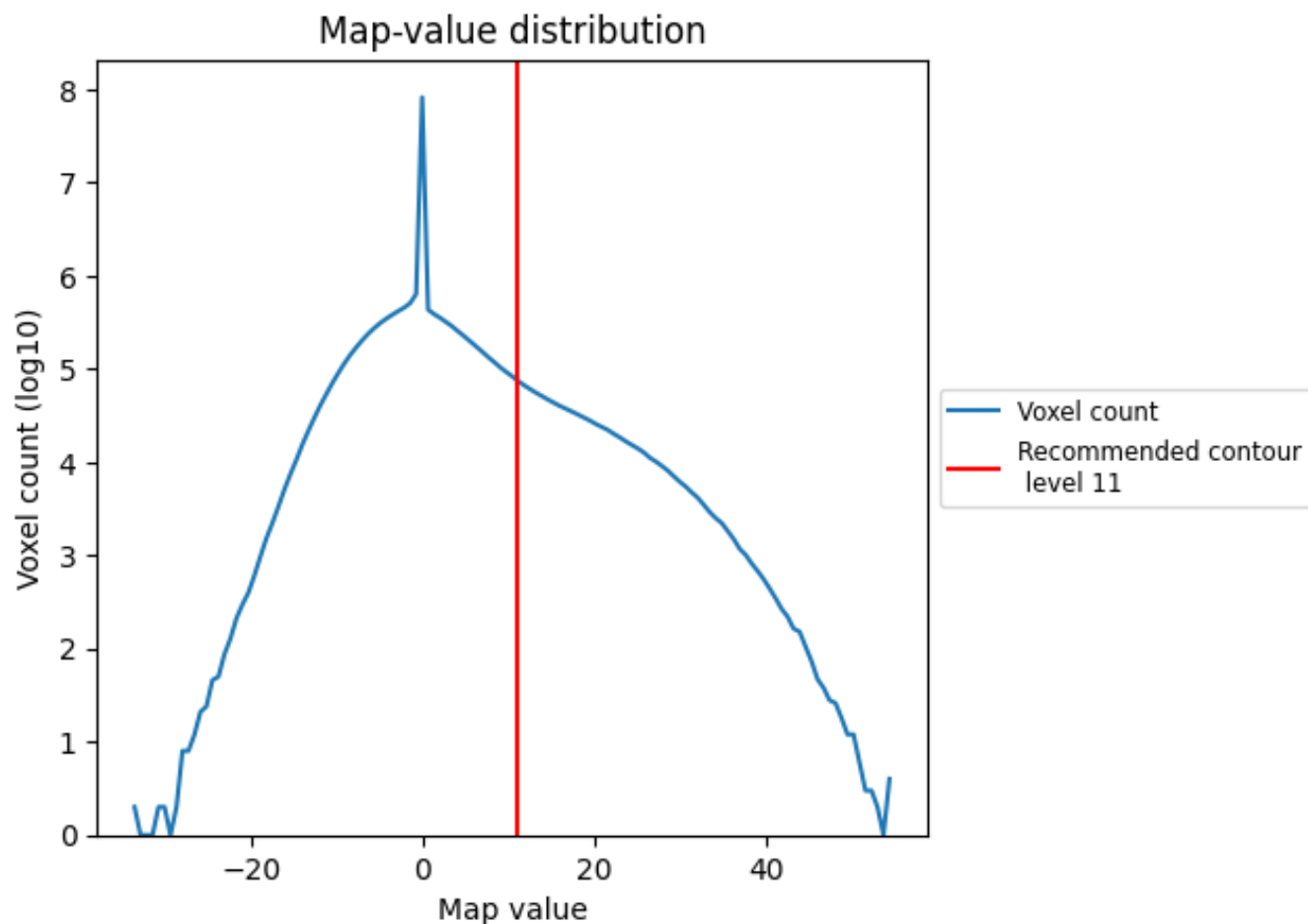
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

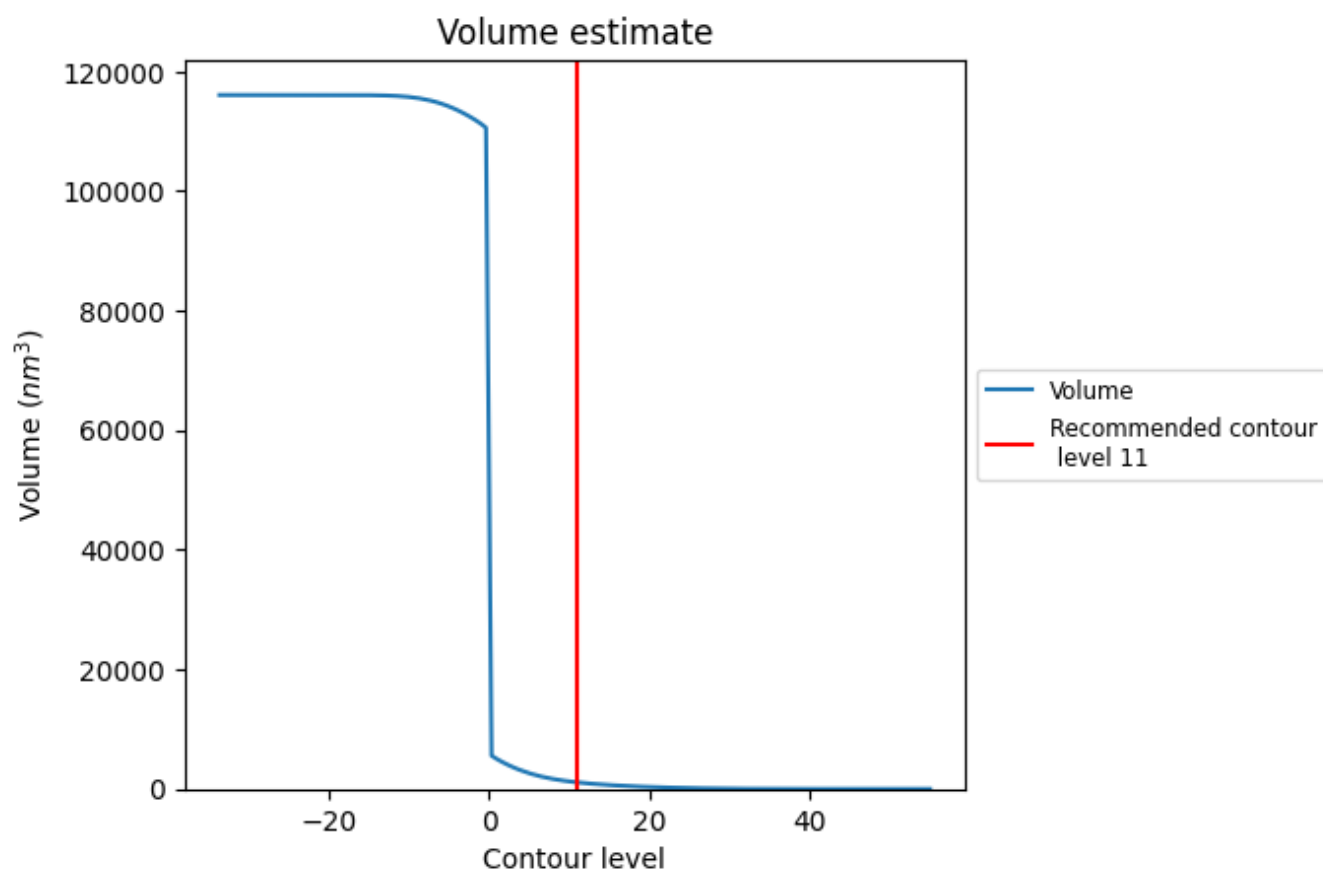
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

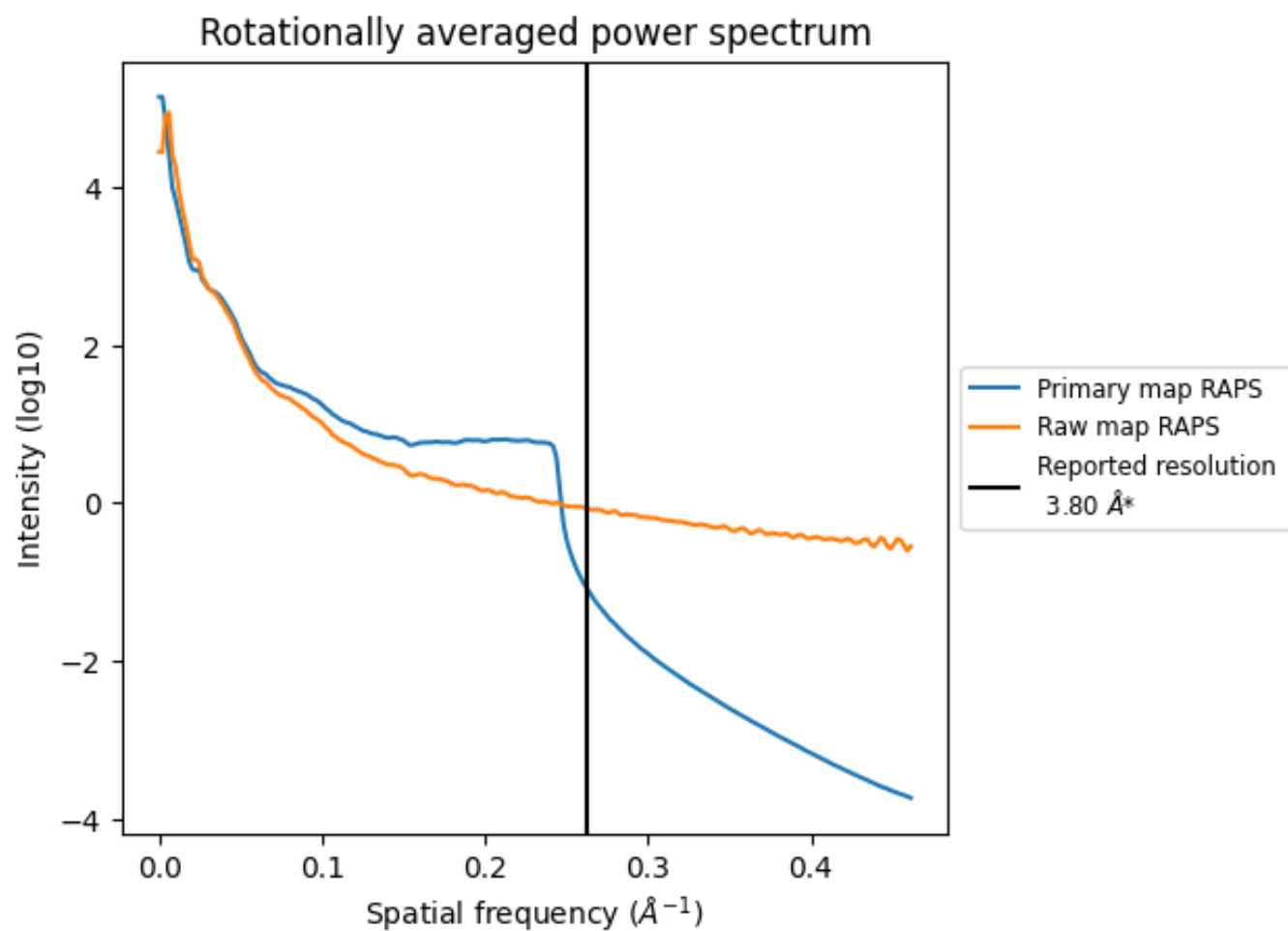
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1108 nm³; this corresponds to an approximate mass of 1001 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 ⓘ

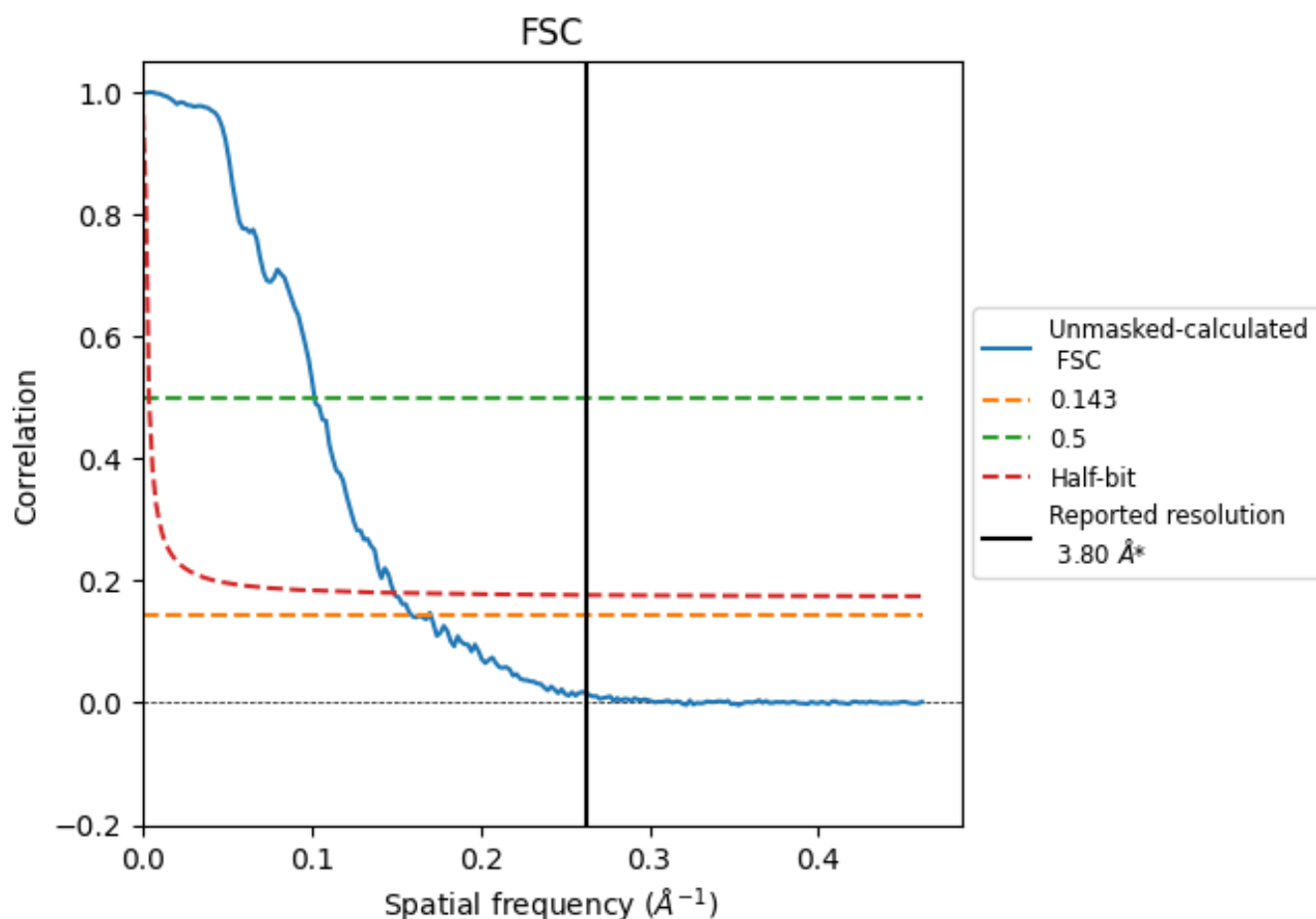


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

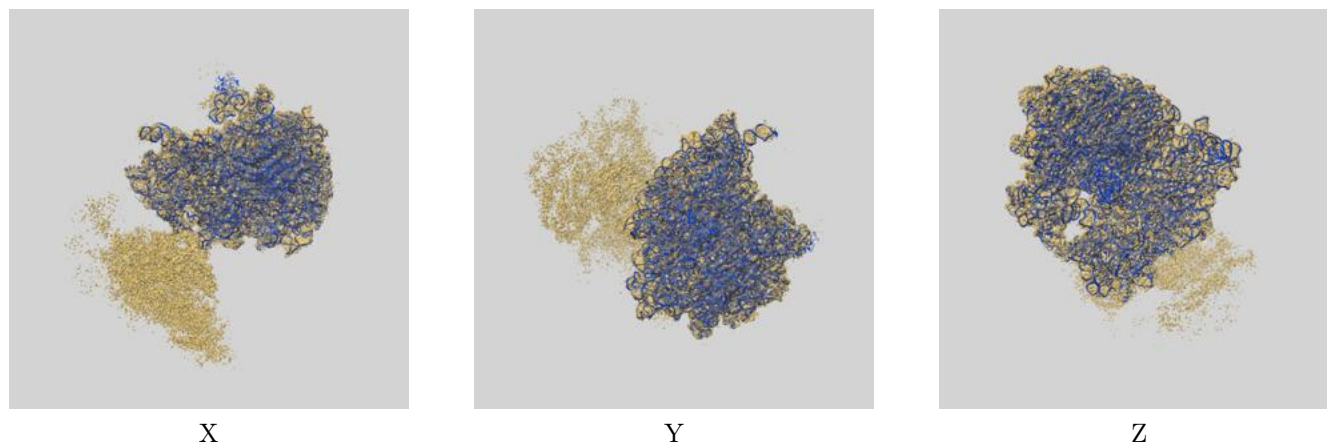
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.27	9.81	6.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.27 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

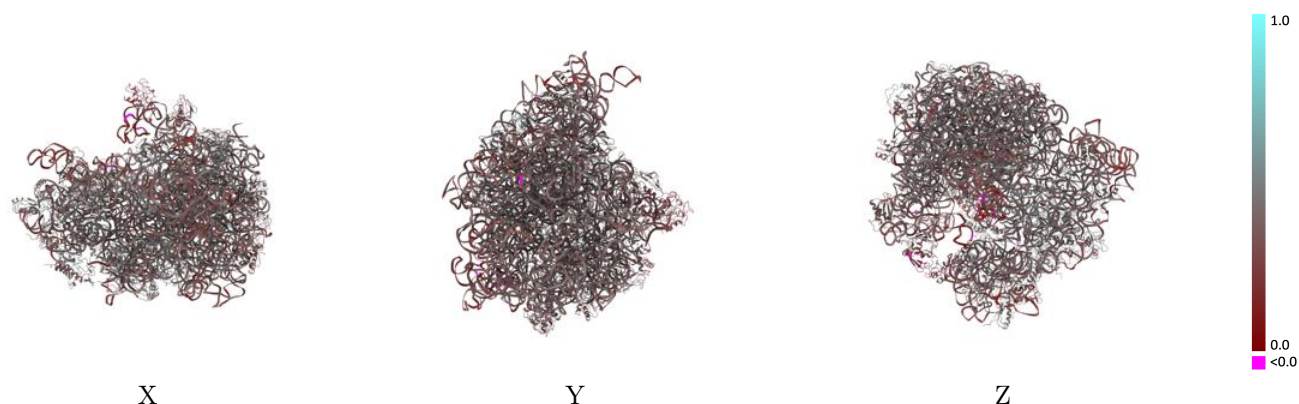
This section contains information regarding the fit between EMDB map EMD-3656 and PDB model 5NJT. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



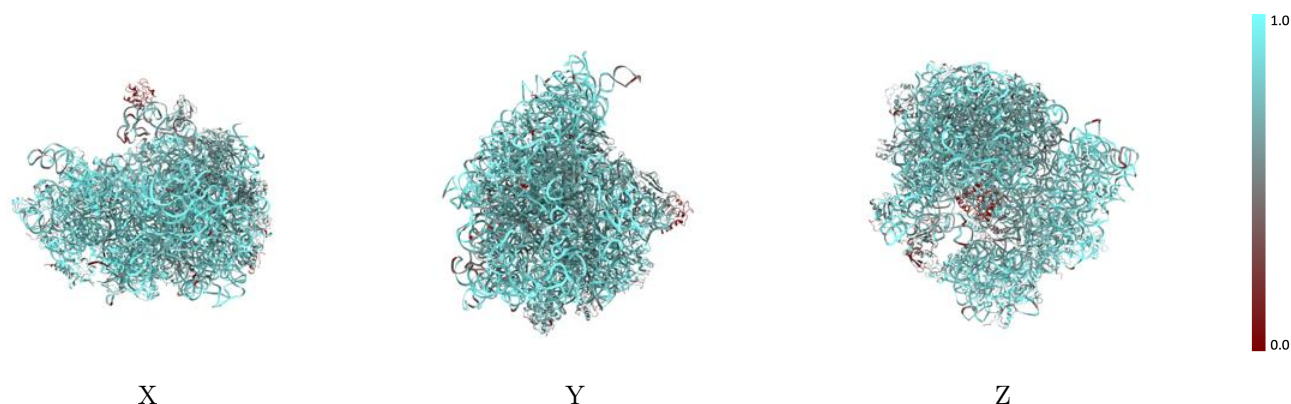
The images above show the 3D surface view of the map at the recommended contour level 11.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



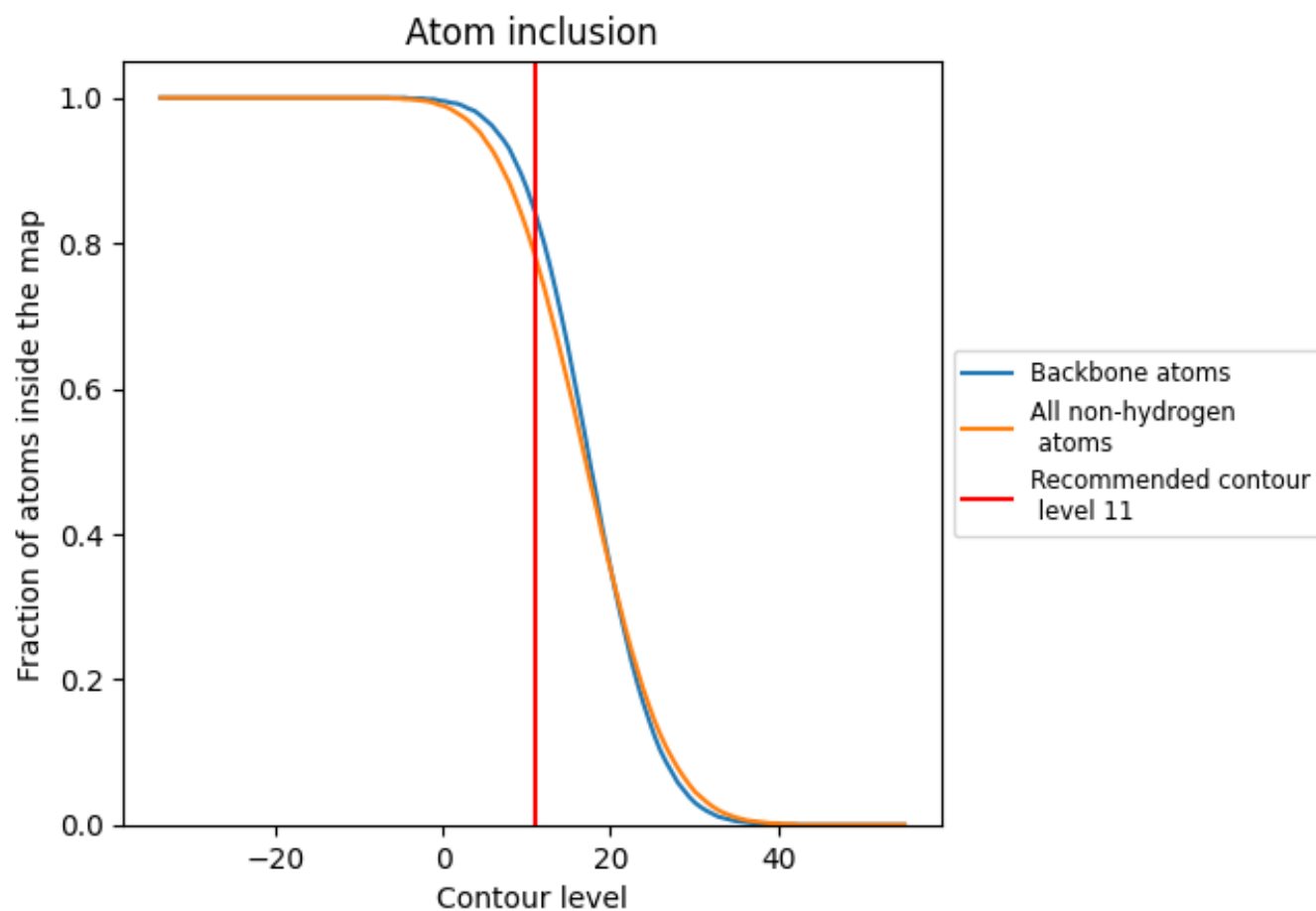
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% 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 (11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.3810
A	 0.8280	 0.3670
B	 0.8020	 0.4200
C	 0.8240	 0.4520
D	 0.8780	 0.4510
E	 0.8610	 0.4810
F	 0.8840	 0.4740
G	 0.7760	 0.4020
H	 0.8990	 0.4820
I	 0.6770	 0.3890
J	 0.7600	 0.4540
K	 0.8180	 0.4350
L	 0.8600	 0.4900
M	 0.7990	 0.3680
N	 0.8920	 0.4450
O	 0.9090	 0.4310
P	 0.8880	 0.4800
Q	 0.8410	 0.4890
R	 0.7720	 0.4560
S	 0.8660	 0.4170
T	 0.8640	 0.3850
U	 0.8320	 0.3800
V	 0.8610	 0.3620
W	 0.6430	 0.4270
X	 0.6230	 0.4240
Y	 0.6510	 0.4010
Z	 0.4920	 0.3010
a	 0.5830	 0.3550
b	 0.0720	 0.2130
c	 0.6590	 0.4140
d	 0.5920	 0.4290
e	 0.6290	 0.4030
f	 0.6470	 0.4150
g	 0.6250	 0.3870
h	 0.5760	 0.3360



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Chain	Atom inclusion	Q-score
i	 0.5760	 0.3920
j	 0.6800	 0.3950
k	 0.6580	 0.4030
l	 0.6140	 0.4220
m	 0.5550	 0.3880
n	 0.6060	 0.3660
o	 0.6030	 0.4050
p	 0.7000	 0.4330
q	 0.6280	 0.3760
r	 0.6580	 0.4320
s	 0.6310	 0.4270
t	 0.6240	 0.4370
u	 0.3800	 0.3920
v	 0.5560	 0.3260
w	 0.5890	 0.4030
x	 0.3900	 0.3300
y	 0.2520	 0.0930