



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 08:11 PM UTC

PDB ID : 7BL2 / pdb_00007bl2
EMDB ID : EMD-12215
Title : pre-50S-ObgE particle state 1
Authors : Hilal, T.; Nikolay, R.; Schmidt, S.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 3.70 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

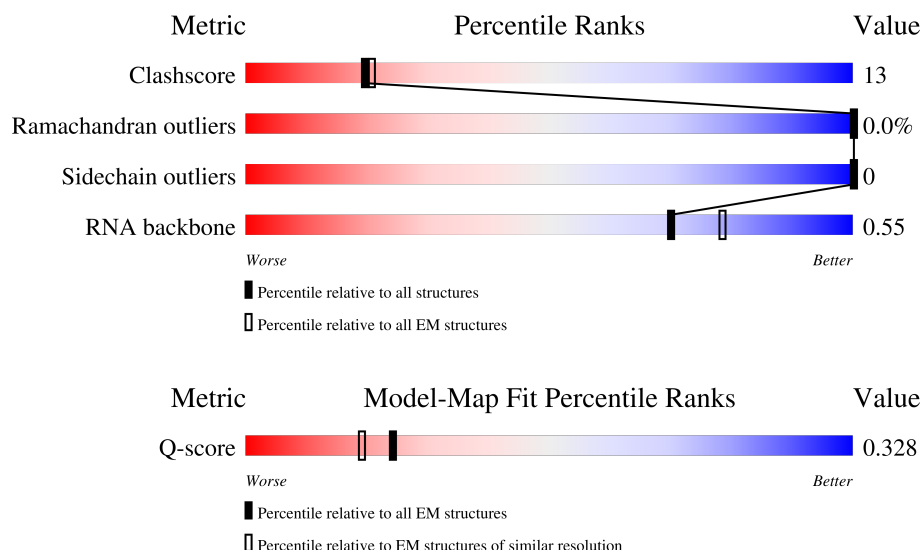
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	2919	 15% (red), 46% (green), 47% (yellow), 7% (grey)
2	B	120	 50% (red), 42% (green), 51% (yellow), 7% (grey)
3	9P1	390	 61% (red), 60% (green), 27% (yellow), 13% (grey)

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Mol	Chain	Length	Quality of chain
4	C	273	
5	D	209	
6	E	201	
7	G	177	
8	J	142	
9	L	144	
10	N	127	
11	O	117	
12	Q	118	
13	R	103	
14	S	110	
15	T	100	
16	U	104	
17	V	94	
18	W	85	
19	X	78	
20	Y	63	
21	Z	59	
22	0	57	
23	1	55	
24	2	46	
25	I	142	
26	K	123	
27	P	115	
28	6	105	

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Mol	Chain	Length	Quality of chain
29	H	149	89% 69%31%
30	F	179	94% 62%36%..
31	b	70	67% 47%20%33%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 92831 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2902	Total	C	N	O	P	0	0
			62301	27793	11465	20141	2902		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 3 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	9P1	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 7 is a protein called 50S ribosomal protein L6.

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

- Molecule 8 is a protein called 50S ribosomal protein L13.

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

- Molecule 9 is a protein called 50S ribosomal protein L15.

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

- Molecule 10 is a protein called 50S ribosomal protein L17.

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

- Molecule 11 is a protein called 50S ribosomal protein L18.

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

- Molecule 12 is a protein called 50S ribosomal protein L20.

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

- Molecule 13 is a protein called 50S ribosomal protein L21.

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

- Molecule 14 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 15 is a protein called 50S ribosomal protein L23.

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

- Molecule 16 is a protein called 50S ribosomal protein L24.

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

- Molecule 17 is a protein called 50S ribosomal protein L25.

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

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	76	Total	C	N	O	S	0	0
			575	356	117	101	1		

- Molecule 19 is a protein called 50S ribosomal protein L28.

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

- Molecule 20 is a protein called 50S ribosomal protein L29.

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

- Molecule 21 is a protein called 50S ribosomal protein L30.

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

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 23 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 25 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 26 is a protein called 50S ribosomal protein L14.

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

- Molecule 27 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 28 is a protein called Ribosomal silencing factor RsfS.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	102	Total	C	N	O	S	0	0
			780	485	133	157	5		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	Q	1	Total	Mg	0
			1	1	

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
33	b	1	Total	Zn	0
			1	1	

- Molecule 34 is water.

Mol	Chain	Residues	Atoms		AltConf
34	A	15	Total	O	0
			15	15	
34	B	1	Total	O	0
			1	1	
34	C	4	Total	O	0
			4	4	

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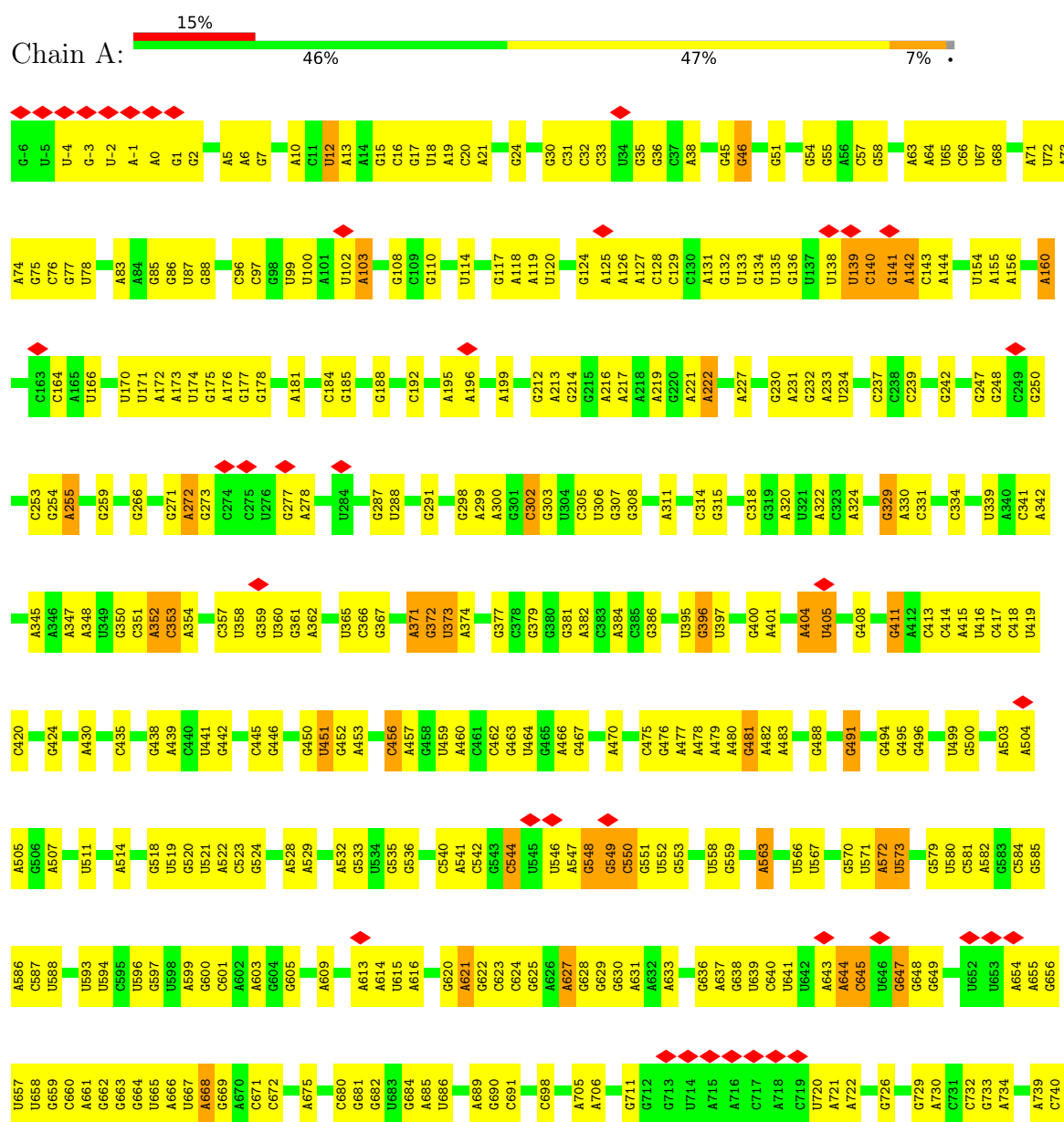
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Mol	Chain	Residues	Atoms		AltConf
34	L	4	Total 4	O 4	0
34	N	2	Total 2	O 2	0
34	F	1	Total 1	O 1	0

3 Residue-property plots

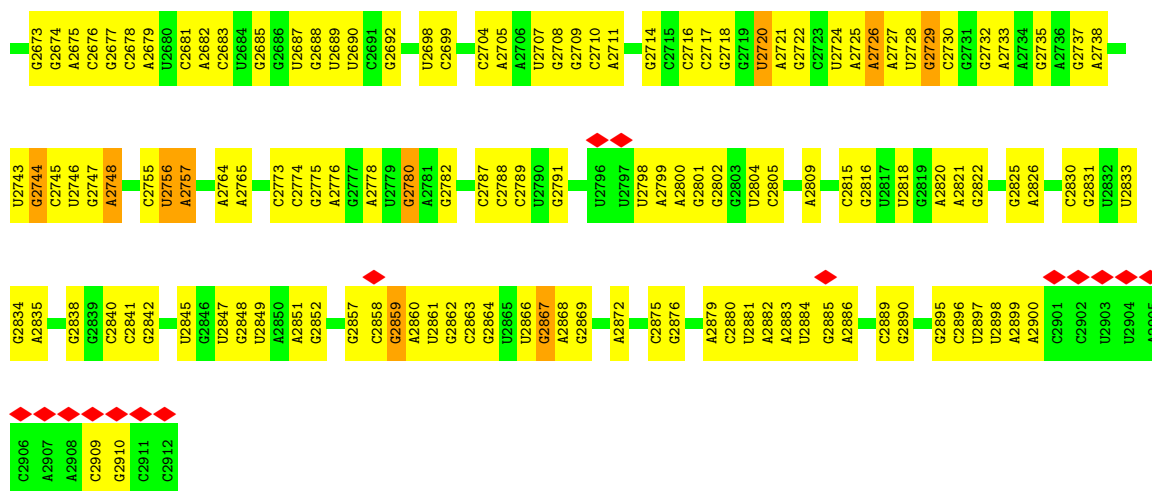
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S ribosomal RNA

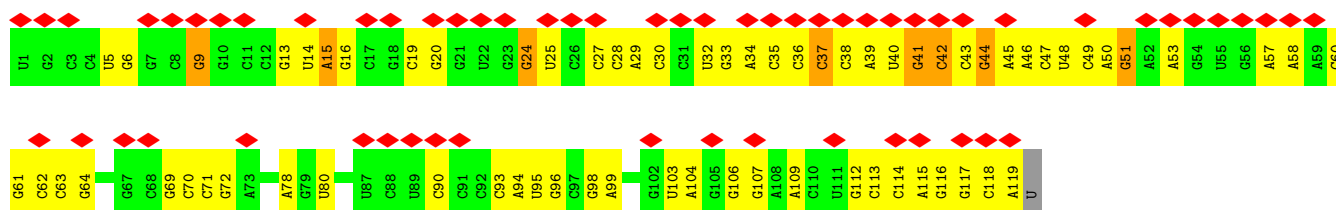




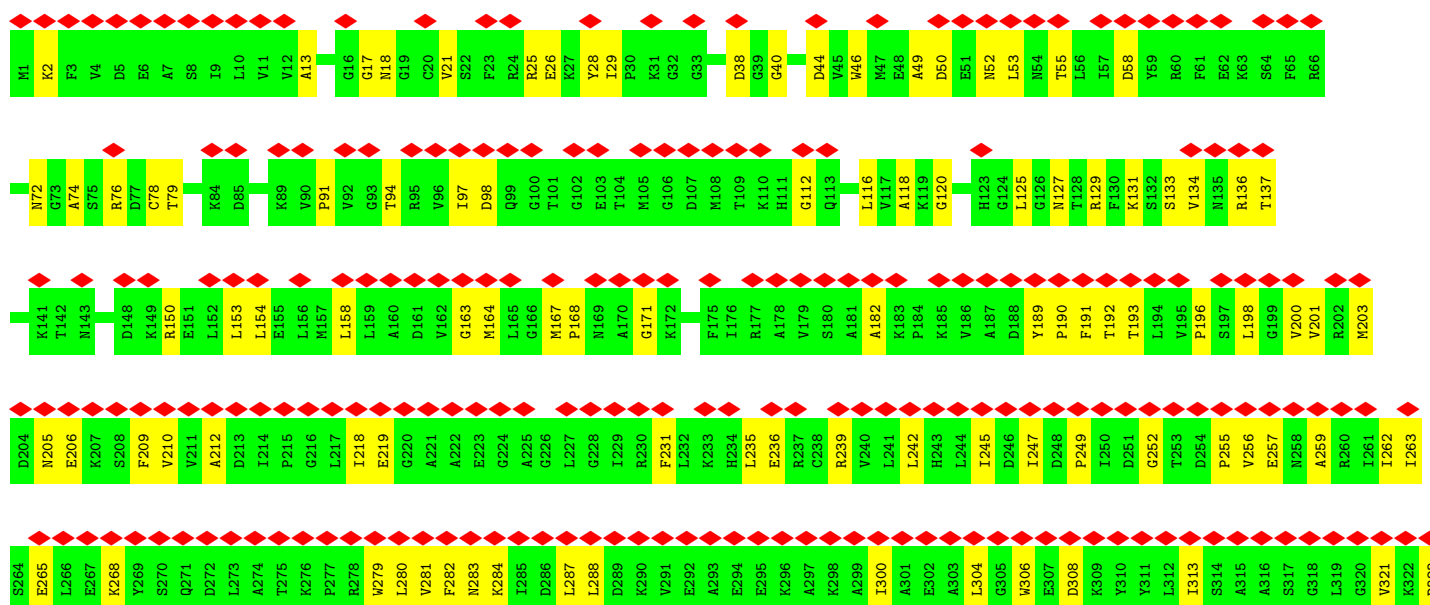
U2593	C2594	G2595	A2598	C2599	A2600	C2601	A2602	C2603	U2604	U2605	C2606	G2607	C2608	U2609	C2610	U2613	U2614	U2615	C2616	U2617	U2618	C2619	C2620	G2623	G2624	G2625	C2626	G2627	C2628	U2629	A2635	C2636	U2637	C2642	G2643	G2644	G2645	C2646	U2647	C2648	C2649	U2650	C2651	C2652	U2656	A2660	A2661	A2662	C2667	G2668	G2669								
U2522	C2523	G2526	C2529	A2530	A2531	C2532	G2535	C2536	U2537	C2538	G2543	C2544	C2545	U2546	A2547	U2548	C2549	U2550	C2551	U2552	C2553	U2554	U2555	C2556	C2557	C2558	C2559	A2560	U2561	A2564	A2565	C2566	C2567	A2568	C2569	C2572	C2573	C2574	C2575	C2576	C2579	U2580	C2581	C2582	C2583	U2584	U2585	U2586	A2587	G2592									
C2462	C2463	G2464	C2465	C2466	C2467	A2468	A2469	C2470	A2471	C2472	U2473	U2474	C2475	A2476	U2477	A2478	U2479	C2480	G2481	A2482	C2483	G2484	G2485	C2486	G2487	G2488	C2489	A2490	U2491	U2492	U2493	G	G	C	A	C	C	U	C	G	A	U	G2505	U2506	C2507	G2508	G2509	C2510	U2511	C2512	A2513	U2514	C2515	A2516	C2517	U2518	U2519	C2520	C2521
C2395	G2396	C2397	U2398	G2399	U2402	U2403	U2404	C2405	A2406	G2410	A2411	A2412	G2413	G2414	G2415	C2416	C2417	A2418	U2423	C2424	A2425	A2426	C2427	C2428	G2429	A2430	U2431	A2432	A2433	A2434	A2435	G2436	G2437	U2438	U2441	C2442	C2443	G2444	G2445	G2446	G2447	A2448	U2449	A2450	A2451	C2452	A2453	G2454	G2455	C2456	U2457	G2458	A2459	U2460	A2461				
G2316	A2317	G2318	G2319	U2320	U2321	A2322	G2325	C2326	A2327	C2328	U2329	G2330	A2333	U2334	A2335	A2336	G2337	C2338	C2339	A2340	G2341	G2345	A2346	C2347	U2348	G2349	C2350	G2351	G2357	A2358	G2361	C2364	G2365	G2371	C2374	G2375	A2376	G2377	A2378	G2379	C2380	A2381	G2382	C2383	U2384	C2385	A2386	U2387	U2393	C2394									
G2250	G2251	G2252	G2253	C2254	G2255	G2256	U2257	C2258	C2261	U2262	C2263	C2264	U2265	A2266	A2267	G2271	U2272	A2273	A2274	C2275	G2276	G2277	A2278	C2283	A2284	C2285	G2286	A2287	G2288	C2289	G2290	U2291	U2292	G2293	U2294	C2295	U2296	A2297	A2298	U2299	C2300	C2301	U2302	G2303	G2304	U2305	G2306	C2307	G2308	A2309	C2310	A2311	U2312	C2313	A2314	G2315			
A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2192	G2193	U2194	U2195	C2196	A2199	G2200	G2201	G2204	A2205	G2208	G2209	U2210	A2211	A2212	G2215	G2216	G2223	G2224	A2225	G2226	G2228	U2229	G2230	U2231	G2232	U2233	G2234	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	U2249									
G2116	A2117	U2118	A2119	G2120	G2121	U2122	A2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	G2143	G2144	G2145	C2146	A2147	G2148	U2149	G2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	C2159	G2160	C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	G2175
C2047	G2048	A2052	G2055	G2056	G2057	A2058	A2059	A2060	G2061	A2062	C2063	G2064	C2065	G2066	G2067	U2068	G2069	C2072	C2073	U2074	U2075	U2076	A2077	U2081	A2082	U2086	G2087	A2088	C2091	U2092	G2093	A2094	A2095	G2096	A2097	U2098	U2099	G2100	A2101	G2102	C2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115						
C1967	G1968	A1969	U1970	U1971	G1972	G1975	U1976	A1977	A1987	G1988	G1989	C1990	U1991	A1992	U1993	C1994	U1995	C1996	A1997	A1998	C1999	C2000	C2001	G2002	C2006	A2009	G2010	U2011	G2012	A2013	A2014	A2015	U2022	G2023	G2024	C2025	G2029	A2030	A2031	G2032	U2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040	C2043	C2044	C2045	G2046							
U1886	C1887	A1889	G1903	G1904	G1907	C1908	C1909	G1910	U1911	U1912	A1913	U1915	A1916	U1917	A1918	A1919	C1920	U1921	G1922	U1923	C1924	C1925	U1926	A1927	A1928	G1929	G1930	U1931	G1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942	U1943	U1944	G1945	A1952	A1953	G1954	U1955	U1956	C1957	C1958	G1959	C1962	U1963	G1964	C1965	A1966							
C1804	A1805	C1806	G1807	A1808	A1809	A1810	G1813	A1814	A1815	C1816	G1817	U1818	A1819	U1820	G1821	C1822	G1823	U1824	A1825	U1826	U1827	A1828	G1829	C1830	G1831	U1834	G1835	C1836	C1837	G1845	G1846	A1847	A1848	G1849	G1850	A1853	U1856	G1862	G1863	U1864	C1868	G1869	C1870	A1871	A1872	G1873	A1874	G1875	U1880	A1885									
A1722	G1723	G1724	U1725	C1726	C1727	C1728	U1729	C1730	A1731	G1732	C1733	G1734	A1735	U1736	G1737	G1738	G1743	A1744	A1745	U1746	U1747	C1748	U1751	C1752	G1753	A1754	A1755	G1756	A1759	C1760	A1761	A1762	G1763	C1764	C1771	A1772	A1773	U1779	A1784	G1862	G1863	U1864	C1790	A1791	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803					

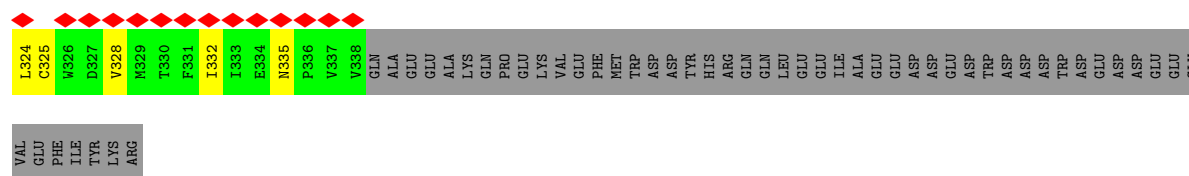


• Molecule 2: 5S ribosomal RNA

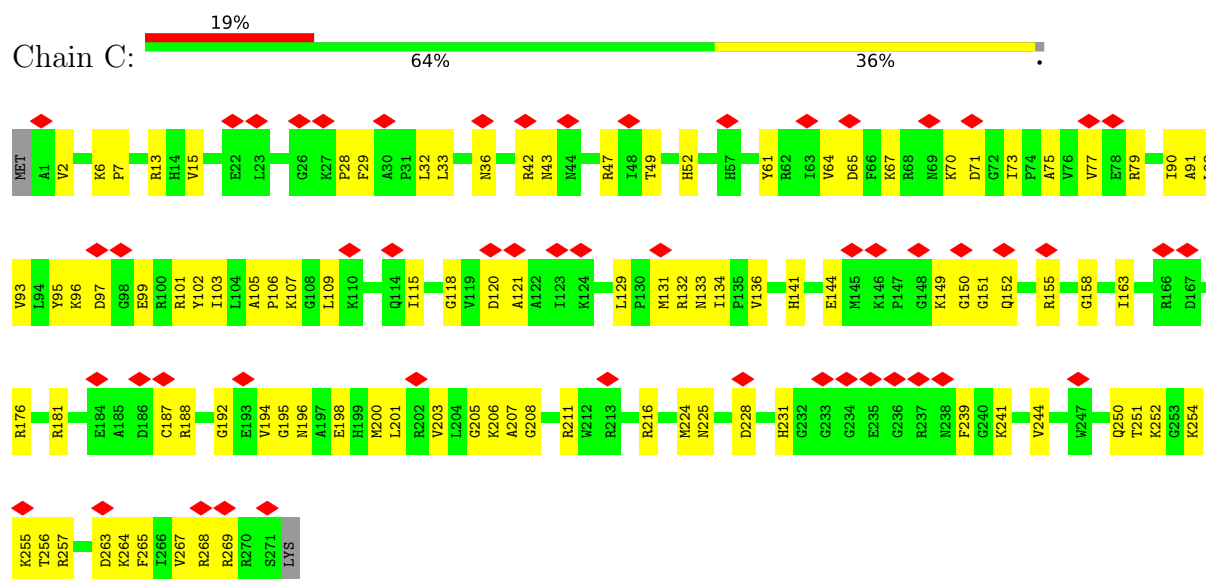


• Molecule 3: GTPase ObgE/CgtA

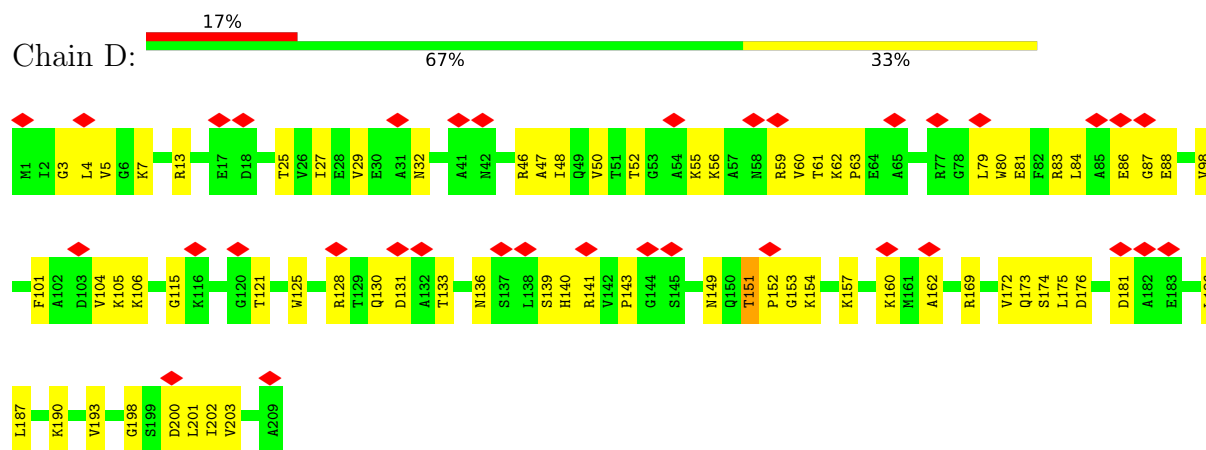




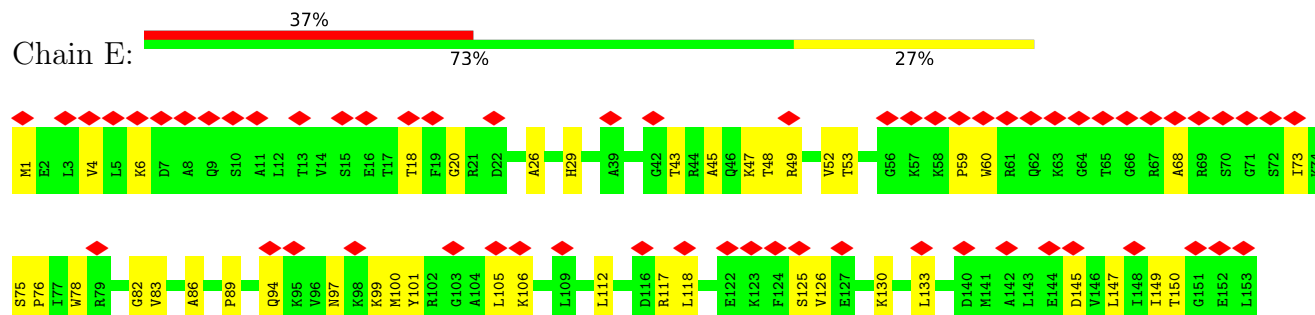
• Molecule 4: 50S ribosomal protein L2

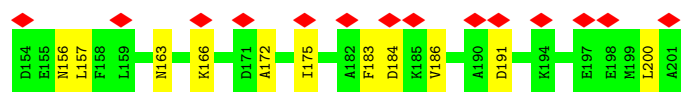


• Molecule 5: 50S ribosomal protein L3

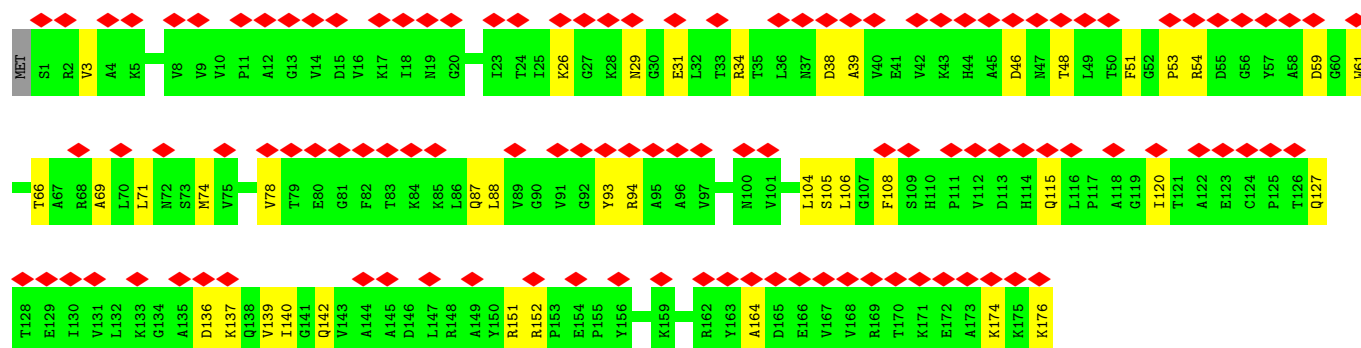
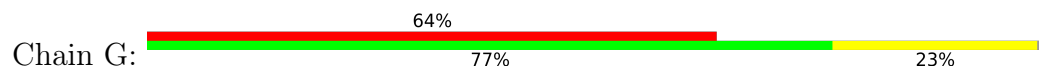


• Molecule 6: 50S ribosomal protein L4

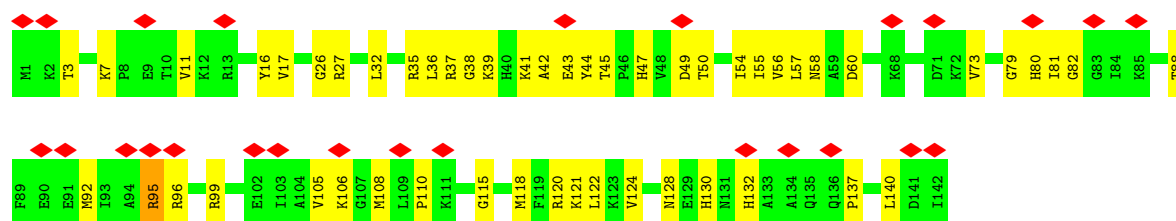




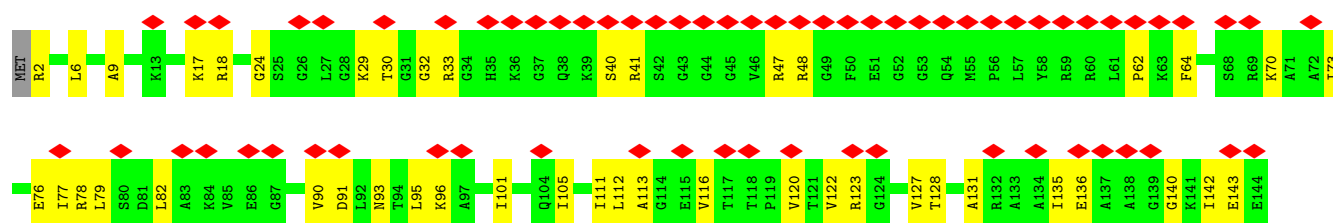
• Molecule 7: 50S ribosomal protein L6



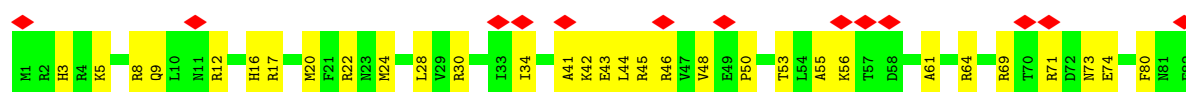
• Molecule 8: 50S ribosomal protein L13

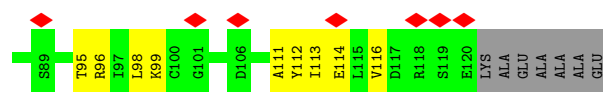


• Molecule 9: 50S ribosomal protein L15

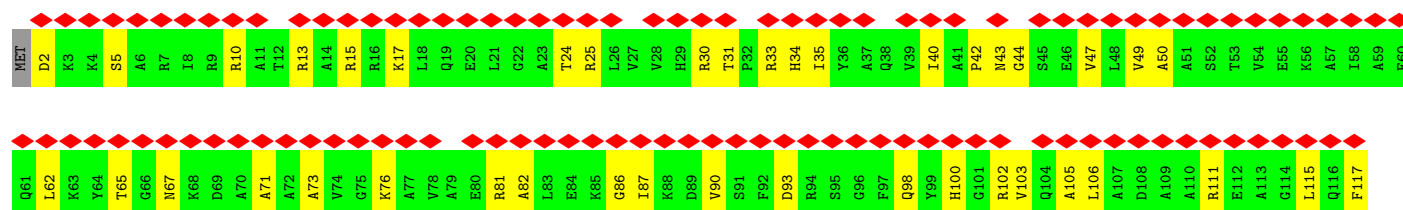
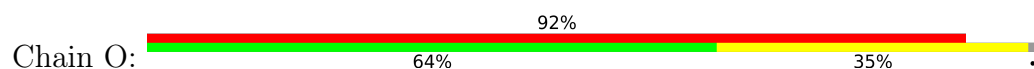


• Molecule 10: 50S ribosomal protein L17

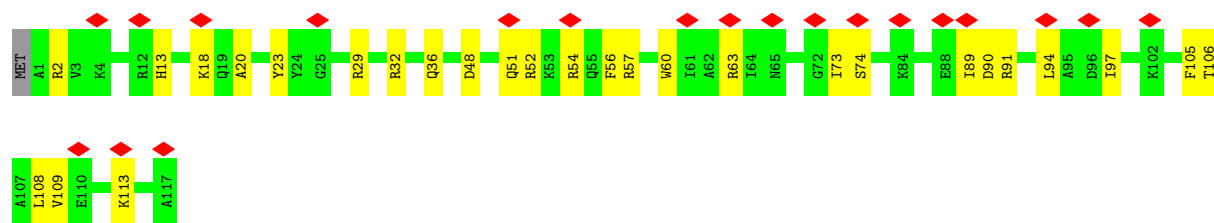
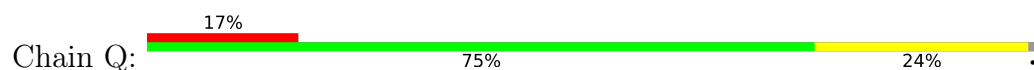




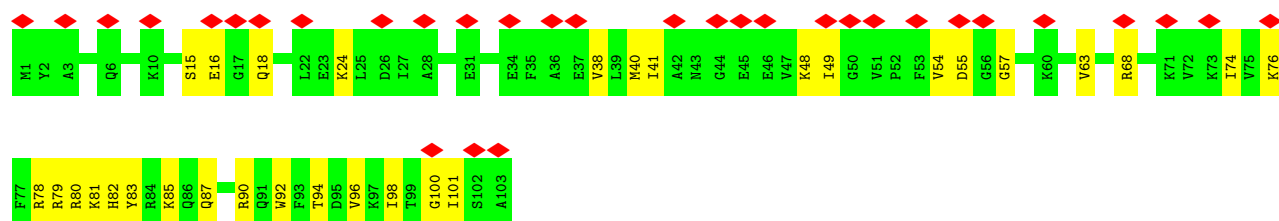
- Molecule 11: 50S ribosomal protein L18



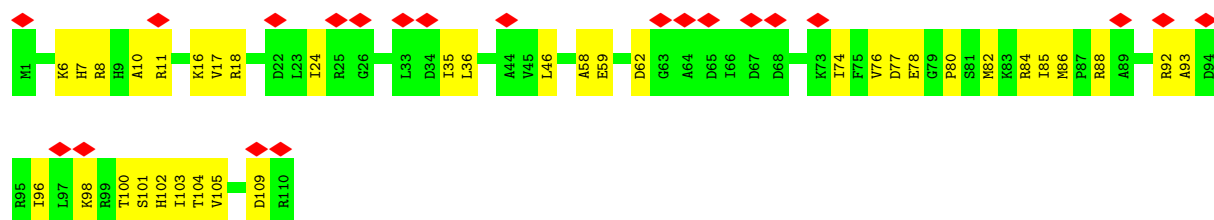
- Molecule 12: 50S ribosomal protein L20



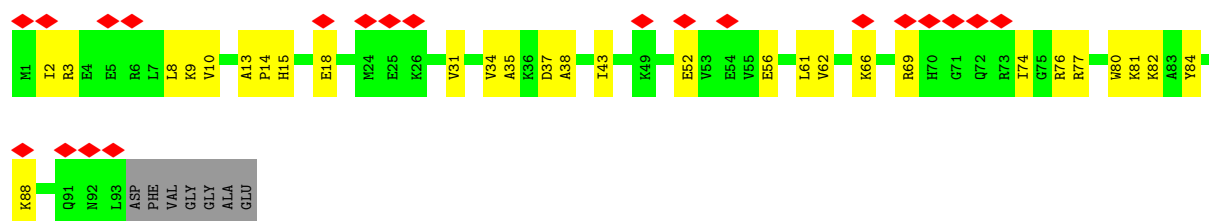
- Molecule 13: 50S ribosomal protein L21



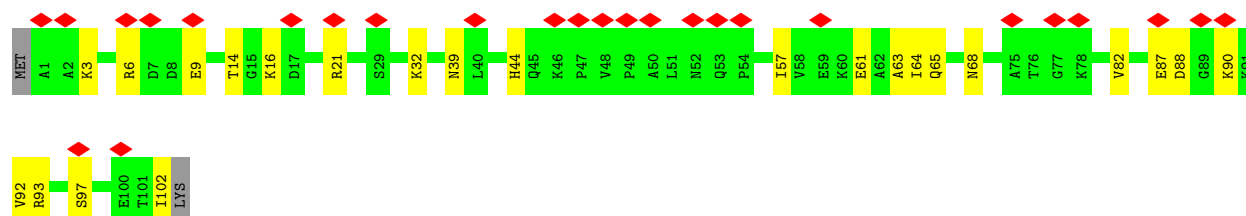
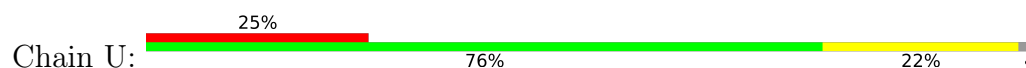
- Molecule 14: 50S ribosomal protein L22



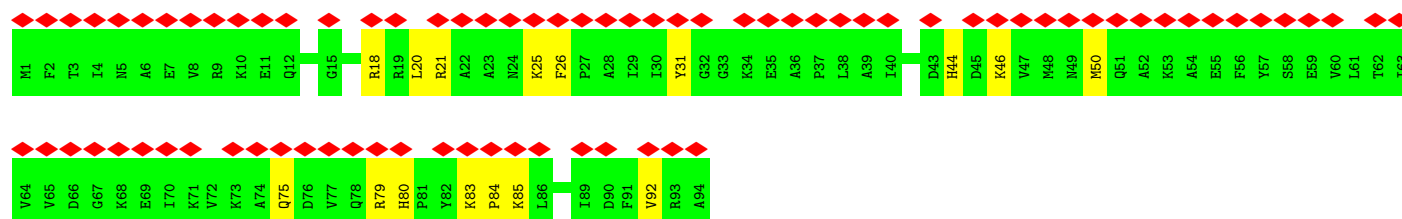
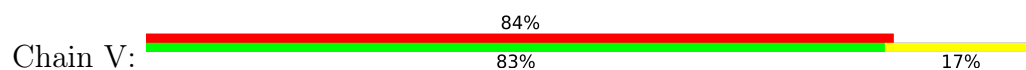
- Molecule 15: 50S ribosomal protein L23



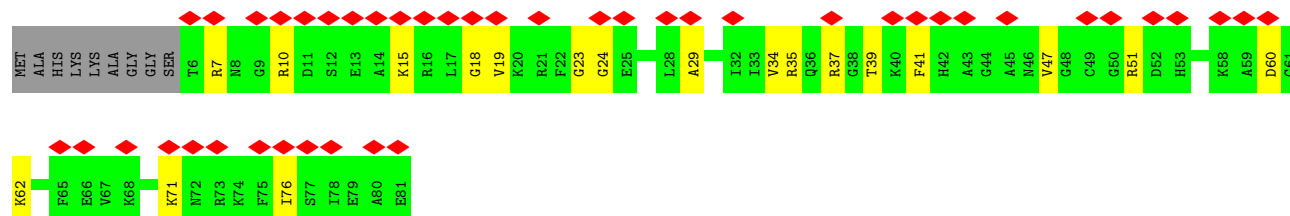
- Molecule 16: 50S ribosomal protein L24



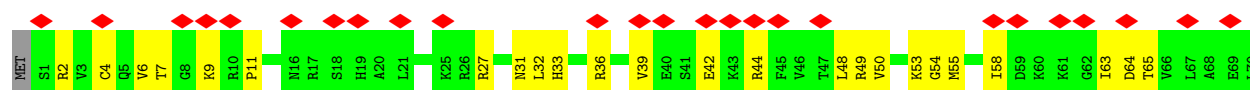
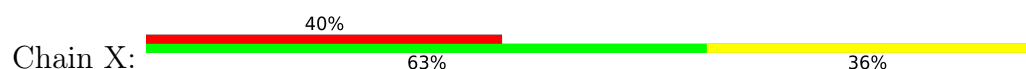
- Molecule 17: 50S ribosomal protein L25



- Molecule 18: 50S ribosomal protein L27

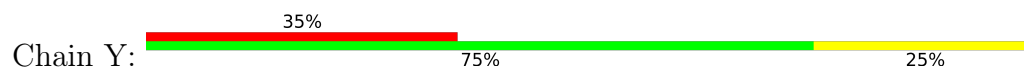


- Molecule 19: 50S ribosomal protein L28

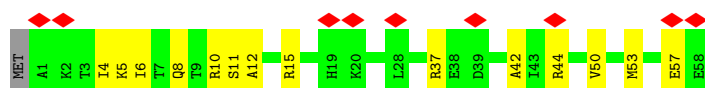




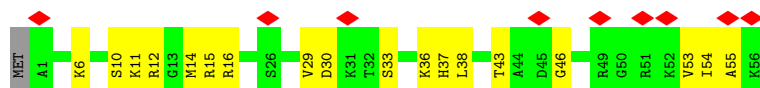
- Molecule 20: 50S ribosomal protein L29



- Molecule 21: 50S ribosomal protein L30



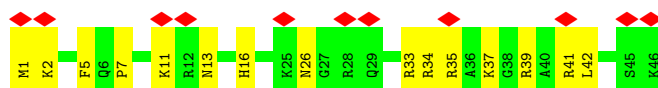
- Molecule 22: 50S ribosomal protein L32



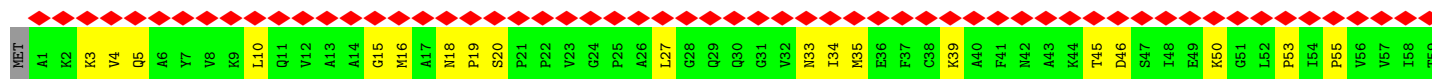
- Molecule 23: 50S ribosomal protein L33

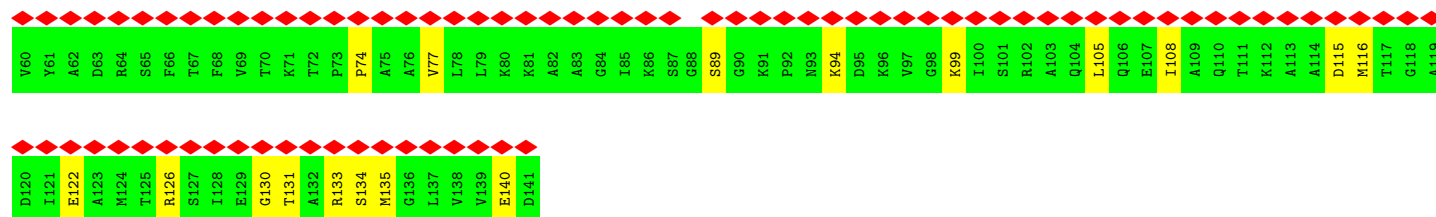


- Molecule 24: 50S ribosomal protein L34

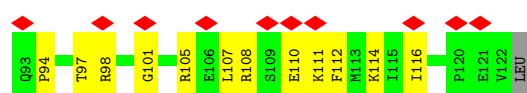
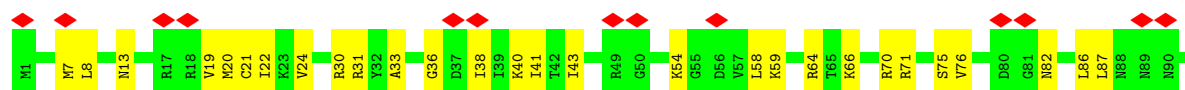


- Molecule 25: 50S ribosomal protein L11

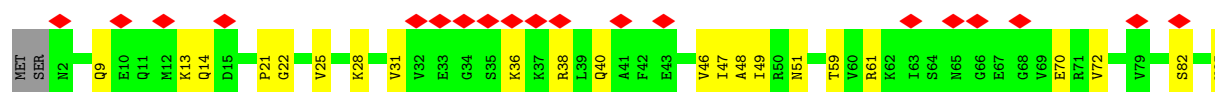




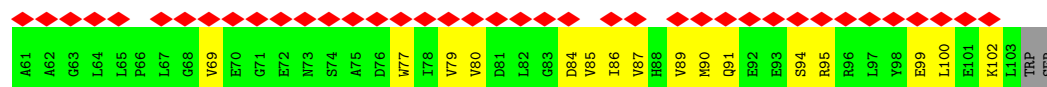
• Molecule 26: 50S ribosomal protein L14



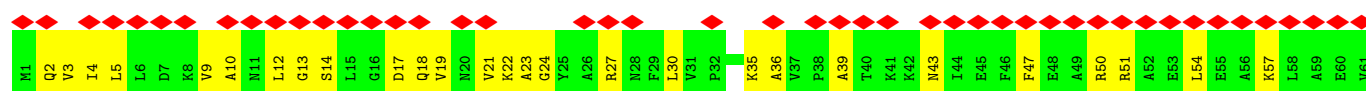
• Molecule 27: 50S ribosomal protein L19

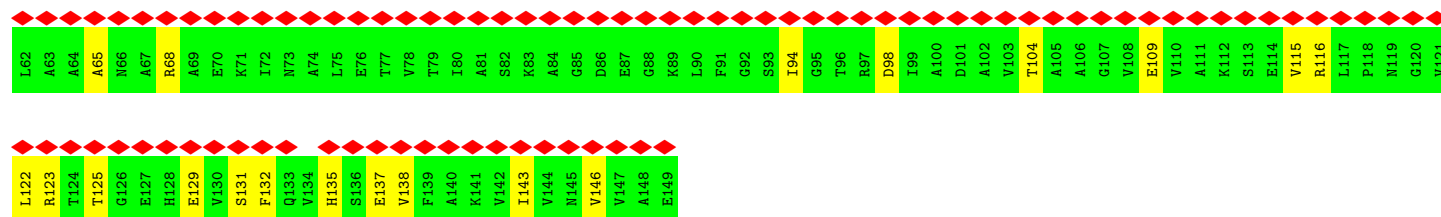


• Molecule 28: Ribosomal silencing factor RsfS



• Molecule 29: 50S ribosomal protein L9





• Molecule 30: 50S ribosomal protein L5



• Molecule 31: 50S ribosomal protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16873	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.453	Depositor
Minimum map value	-6.939	Depositor
Average map value	0.035	Depositor
Map value standard deviation	0.777	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	334.8, 334.8, 334.8	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.24, 1.24, 1.24	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.08	0/69777	0.20	0/108853
2	B	0.07	0/2847	0.18	0/4440
3	9P1	0.15	0/2626	0.47	0/3542
4	C	0.14	0/2121	0.40	0/2852
5	D	0.15	0/1586	0.42	0/2134
6	E	0.11	0/1571	0.34	0/2113
7	G	0.12	0/1343	0.36	0/1816
8	J	0.13	0/1152	0.38	2/1551 (0.1%)
9	L	0.14	0/1054	0.42	0/1403
10	N	0.14	0/973	0.45	0/1301
11	O	0.15	0/902	0.44	0/1209
12	Q	0.12	0/960	0.36	0/1278
13	R	0.13	0/829	0.42	0/1107
14	S	0.13	0/864	0.35	0/1156
15	T	0.13	0/744	0.41	0/994
16	U	0.17	0/787	0.52	2/1051 (0.2%)
17	V	0.12	0/766	0.34	0/1025
18	W	0.11	0/582	0.32	0/769
19	X	0.13	0/635	0.38	0/848
20	Y	0.13	0/510	0.46	0/677
21	Z	0.12	0/453	0.37	0/605
22	0	0.12	0/450	0.36	0/599
23	1	0.11	0/416	0.31	0/554
24	2	0.15	0/380	0.45	0/498
25	I	0.14	0/1046	0.43	0/1410
26	K	0.17	0/947	0.46	0/1268
27	P	0.13	0/923	0.38	0/1234
28	6	0.13	0/787	0.37	0/1062
29	H	0.14	0/1121	0.40	0/1515
30	F	0.15	0/1434	0.43	0/1926
31	b	0.10	0/371	0.28	0/496
All	All	0.10	0/100957	0.27	4/151286 (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
5	D	0	1
30	F	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	U	97	SER	CA-C-N	6.59	134.14	121.54
16	U	97	SER	C-N-CA	6.59	134.14	121.54
8	J	95	ARG	CA-C-N	-5.06	115.86	122.74
8	J	95	ARG	C-N-CA	-5.06	115.86	122.74

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	D	151	THR	Peptide
30	F	174	PHE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62301	0	31334	1167	0
2	B	2548	0	1292	64	0
3	9P1	2582	0	2607	77	0
4	C	2082	0	2157	90	0
5	D	1565	0	1616	65	0
6	E	1552	0	1619	42	0
7	G	1323	0	1374	37	0
8	J	1129	0	1162	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	L	1045	0	1117	42	0
10	N	960	0	1000	36	0
11	O	892	0	923	33	0
12	Q	947	0	1022	34	0
13	R	816	0	839	25	0
14	S	857	0	922	32	0
15	T	738	0	807	31	0
16	U	779	0	834	16	0
17	V	753	0	780	13	0
18	W	575	0	589	16	0
19	X	625	0	655	26	0
20	Y	509	0	543	12	0
21	Z	449	0	491	11	0
22	0	444	0	461	16	0
23	1	409	0	440	9	0
24	2	377	0	418	15	0
25	I	1032	0	1088	26	0
26	K	938	0	1012	38	0
27	P	911	0	957	23	0
28	6	780	0	783	32	0
29	H	1110	0	1148	31	0
30	F	1410	0	1447	50	0
31	b	364	0	362	9	0
32	Q	1	0	0	0	0
33	b	1	0	0	0	0
34	A	15	0	0	1	0
34	B	1	0	0	0	0
34	C	4	0	0	0	0
34	F	1	0	0	0	0
34	L	4	0	0	0	0
34	N	2	0	0	0	0
All	All	92831	0	61799	1884	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 13.

All (1884) 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)
2:B:78:A:H62	2:B:98:G:H21	0.97	0.96
2:B:78:A:H62	2:B:98:G:N2	1.69	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1039:A:H61	1:A:1116:G:H1	1.22	0.88
1:A:1800:C:H42	1:A:1817:G:H22	1.15	0.88
1:A:954:G:H1	1:A:963:U:H3	1.18	0.88
1:A:2514:U:H5''	8:J:81:ILE:HD11	1.55	0.87
4:C:144:GLU:HB3	4:C:187:CYS:HB3	1.59	0.84
1:A:1800:C:H42	1:A:1817:G:N2	1.76	0.84
2:B:78:A:N6	2:B:98:G:H21	1.77	0.83
1:A:1800:C:N4	1:A:1817:G:H22	1.79	0.81
13:R:68:ARG:HB3	13:R:90:ARG:HG2	1.63	0.81
1:A:2458:G:H22	1:A:2491:U:H3	1.28	0.80
1:A:594:U:H3	1:A:663:G:H1	1.30	0.79
1:A:408:G:H1	1:A:419:U:H3	1.28	0.79
1:A:600:G:H1'	6:E:100:MET:HE1	1.65	0.78
3:9P1:201:VAL:HB	3:9P1:209:PHE:HB3	1.64	0.77
26:K:108:ARG:HD2	26:K:116:ILE:HD13	1.66	0.77
20:Y:32:ALA:HB2	20:Y:37:LEU:HD23	1.65	0.77
5:D:121:THR:HG21	5:D:143:PRO:HG3	1.67	0.77
17:V:79:ARG:NH2	17:V:85:LYS:O	2.19	0.76
1:A:2305:U:H1'	30:F:132:ARG:HA	1.68	0.76
1:A:2619:C:H5''	5:D:157:LYS:HB3	1.67	0.75
5:D:61:THR:HG22	5:D:63:PRO:HD2	1.67	0.75
20:Y:31:GLN:HG3	20:Y:37:LEU:HB2	1.66	0.75
29:H:3:VAL:HG12	29:H:21:VAL:HG11	1.69	0.75
1:A:2092:U:O4	1:A:2227:A:N6	2.17	0.75
1:A:463:G:N2	1:A:466:A:OP2	2.20	0.74
1:A:2848:G:O2'	1:A:2867:G:N2	2.18	0.74
1:A:572:A:N6	1:A:2029:G:H21	1.85	0.74
1:A:1190:G:H5''	9:L:32:GLY:HA2	1.69	0.74
4:C:224:MET:HG3	4:C:225:ASN:H	1.52	0.74
1:A:572:A:H61	1:A:2029:G:H21	1.33	0.74
1:A:698:C:O2'	1:A:734:A:N6	2.20	0.74
11:O:40:ILE:HG13	11:O:47:VAL:HG12	1.70	0.73
1:A:1288:G:OP2	1:A:1288:G:N2	2.20	0.73
1:A:2312:U:O2	30:F:36:ASN:ND2	2.21	0.72
2:B:42:C:H5	30:F:65:LEU:HD23	1.53	0.72
10:N:9:GLN:HA	10:N:17:ARG:HD3	1.70	0.72
1:A:2857:G:N2	1:A:2860:A:OP2	2.23	0.72
1:A:935:C:H2'	1:A:936:A:H8	1.53	0.72
1:A:1063:G:H21	25:I:135:MET:HA	1.55	0.72
7:G:106:LEU:HD23	7:G:151:ARG:HB2	1.70	0.72
1:A:629:G:N3	1:A:639:U:O2'	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2451:A:H2'	3:9P1:25:ARG:HB2	1.71	0.72
2:B:30:C:H1'	2:B:57:A:H61	1.55	0.72
1:A:1807:G:N2	1:A:1810:A:OP2	2.22	0.72
28:6:11:ILE:HD12	28:6:14:ILE:HD11	1.72	0.72
3:9P1:21:VAL:HG12	3:9P1:127:ASN:HB3	1.71	0.71
21:Z:4:ILE:HD13	21:Z:44:ARG:HH12	1.55	0.71
1:A:994:C:OP1	12:Q:52:ARG:NH2	2.23	0.71
26:K:105:ARG:NH2	27:P:40:GLN:OE1	2.23	0.71
1:A:78:U:H3	1:A:108:G:H1	1.38	0.71
1:A:1363:C:O2'	1:A:1809:A:N3	2.22	0.71
1:A:830:G:H1	1:A:2446:G:H4'	1.56	0.71
3:9P1:256:VAL:HB	3:9P1:300:ILE:HG23	1.72	0.71
1:A:177:G:OP2	1:A:177:G:N2	2.19	0.71
1:A:2506:U:O2	1:A:2583:G:O6	2.09	0.70
1:A:2065:C:H5'	1:A:2251:G:H21	1.56	0.70
1:A:1155:A:H5''	12:Q:54:ARG:HD3	1.71	0.70
1:A:2637:U:OP1	5:D:83:ARG:NH2	2.24	0.70
1:A:2581:G:N2	1:A:2581:G:OP2	2.23	0.70
12:Q:108:LEU:HD22	13:R:48:LYS:HZ3	1.54	0.70
30:F:3:LEU:HB2	30:F:96:TRP:HB3	1.73	0.70
25:I:4:VAL:HG12	25:I:5:GLN:H	1.54	0.70
11:O:35:ILE:HD13	11:O:102:ARG:HH11	1.57	0.70
30:F:109:ARG:HH11	31:b:36:VAL:HG22	1.56	0.70
1:A:1668:A:N3	1:A:1670:C:N4	2.38	0.69
31:b:16:CYS:SG	31:b:17:SER:N	2.65	0.69
13:R:74:ILE:HB	13:R:87:GLN:HB3	1.73	0.69
1:A:1287:A:N6	1:A:1649:G:O2'	2.25	0.69
1:A:2120:G:H2'	1:A:2121:G:H8	1.57	0.69
4:C:250:GLN:NE2	4:C:251:THR:O	2.26	0.69
11:O:73:ALA:HA	11:O:76:LYS:HE2	1.74	0.69
1:A:1830:C:H2'	1:A:1831:G:H8	1.56	0.69
1:A:2131:U:H5'	1:A:2132:U:H5''	1.75	0.69
1:A:172:A:H2'	1:A:173:A:H8	1.57	0.68
1:A:627:A:N6	9:L:112:LEU:O	2.26	0.68
1:A:1393:A:N6	15:T:18:GLU:OE2	2.26	0.68
1:A:2298:A:H62	1:A:2318:G:H21	1.40	0.68
5:D:4:LEU:HB3	5:D:29:VAL:HG21	1.75	0.68
1:A:475:C:O2	1:A:479:A:N6	2.27	0.68
13:R:76:LYS:HB2	13:R:85:LYS:HB2	1.74	0.68
21:Z:10:ARG:HB2	21:Z:53:MET:HG2	1.74	0.68
1:A:593:U:H3	1:A:664:G:H1	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:U:H3	1:A:144:A:H61	1.39	0.68
1:A:2602:A:OP1	3:9P1:136:ARG:NH1	2.27	0.68
1:A:1966:A:N1	3:9P1:133:SER:OG	2.26	0.68
1:A:2374:C:N4	1:A:2375:G:O6	2.26	0.68
1:A:2743:U:OP2	1:A:2755:C:N4	2.26	0.68
3:9P1:200:VAL:HG12	3:9P1:210:VAL:HG12	1.75	0.68
4:C:257:ARG:NH1	4:C:263:ASP:OD1	2.27	0.68
25:I:15:GLY:HA2	25:I:50:LYS:HB3	1.74	0.68
27:P:38:ARG:NH1	28:6:32:SER:O	2.27	0.68
1:A:1926:U:H3	1:A:1929:G:H1	1.41	0.68
1:A:38:A:N3	6:E:43:THR:OG1	2.26	0.67
29:H:116:ARG:NH1	29:H:131:SER:OG	2.27	0.67
1:A:807:U:OP2	9:L:41:ARG:NH1	2.27	0.67
1:A:72:U:OP2	20:Y:54:LYS:NZ	2.27	0.67
2:B:34:A:N6	2:B:44:G:O2'	2.28	0.67
30:F:104:THR:HG23	30:F:105:ILE:HG23	1.77	0.67
1:A:1992:G:N2	1:A:1996:C:O2'	2.27	0.67
9:L:77:ILE:HD11	9:L:101:ILE:HD11	1.76	0.67
1:A:411:G:OP2	1:A:2406:A:O2'	2.13	0.67
9:L:78:ARG:HB3	9:L:113:ALA:HB3	1.75	0.67
1:A:54:G:O2'	24:2:35:ARG:NH1	2.28	0.67
1:A:1607:C:N4	1:A:1622:G:OP2	2.27	0.67
8:J:96:ARG:HD2	8:J:99:ARG:HG3	1.77	0.67
3:9P1:235:LEU:HG	3:9P1:236:GLU:H	1.60	0.67
25:I:35:MET:SD	25:I:39:LYS:NZ	2.67	0.67
26:K:111:LYS:HE3	28:6:69:VAL:H	1.60	0.66
1:A:1837:C:O2'	1:A:1927:A:N3	2.27	0.66
8:J:37:ARG:NH1	8:J:44:TYR:OH	2.27	0.66
1:A:2336:A:H61	18:W:39:THR:HG21	1.60	0.66
5:D:131:ASP:O	5:D:136:ASN:ND2	2.20	0.66
1:A:690:G:H21	4:C:42:ARG:HH12	1.42	0.66
1:A:1039:A:N6	1:A:1116:G:H1	1.93	0.66
1:A:1999:C:O2	1:A:2687:U:O2'	2.12	0.66
2:B:49:C:OP2	11:O:30:ARG:NH1	2.28	0.66
1:A:125:A:O4'	24:2:13:ASN:ND2	2.28	0.66
6:E:126:VAL:O	6:E:156:ASN:ND2	2.28	0.66
1:A:2210:U:H4'	1:A:2211:A:H5'	1.77	0.66
1:A:2683:C:H4'	5:D:13:ARG:HH11	1.60	0.66
7:G:46:ASP:O	7:G:48:THR:N	2.29	0.66
1:A:213:A:H2'	1:A:214:G:C8	2.31	0.65
6:E:45:ALA:HB2	6:E:89:PRO:HD3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:42:ALA:O	12:Q:63:ARG:NH1	2.29	0.65
12:Q:90:ASP:OD1	12:Q:91:ARG:N	2.29	0.65
14:S:6:LYS:HB3	14:S:104:THR:HG23	1.78	0.65
18:W:7:ARG:O	18:W:10:ARG:NH1	2.30	0.65
1:A:212:G:H2'	1:A:213:A:C8	2.32	0.65
1:A:518:G:O5'	14:S:18:ARG:NH1	2.30	0.65
9:L:30:THR:HB	9:L:33:ARG:HB2	1.78	0.65
25:I:122:GLU:O	25:I:126:ARG:NH1	2.30	0.65
28:6:41:THR:OG1	28:6:95:ARG:NH2	2.29	0.65
1:A:2335:A:OP1	11:O:13:ARG:NH1	2.29	0.65
1:A:1213:A:H2'	1:A:1214:A:H8	1.62	0.65
1:A:1779:U:OP2	1:A:1784:A:N6	2.29	0.65
1:A:2303:G:N2	30:F:152:ASP:OD1	2.29	0.65
1:A:2200:C:OP2	19:X:36:ARG:NH2	2.30	0.65
1:A:188:G:O2'	1:A:1365:A:N6	2.30	0.64
1:A:1062:G:H21	25:I:134:SER:HB3	1.62	0.64
1:A:2199:A:N1	1:A:2226:C:N4	2.44	0.64
14:S:10:ALA:HB3	14:S:101:SER:HB2	1.78	0.64
25:I:55:PRO:HD3	25:I:74:PRO:HD3	1.78	0.64
1:A:1966:A:N3	1:A:2592:G:O2'	2.30	0.64
3:9P1:17:GLY:HA3	3:9P1:40:GLY:H	1.62	0.64
1:A:1386:C:H2'	1:A:1387:A:H8	1.61	0.64
1:A:2009:A:H2'	1:A:2010:G:H8	1.63	0.64
1:A:2885:G:N2	22:0:30:ASP:OD1	2.29	0.64
3:9P1:26:GLU:HB3	3:9P1:29:ILE:HB	1.79	0.64
21:Z:8:GLN:NE2	21:Z:10:ARG:O	2.29	0.64
1:A:645:C:N4	1:A:2349:G:N3	2.44	0.64
7:G:87:GLN:HE22	7:G:164:ALA:HA	1.63	0.64
5:D:105:LYS:HD2	5:D:106:LYS:HG3	1.79	0.64
1:A:397:U:OP2	19:X:9:LYS:NZ	2.25	0.64
1:A:1006:C:H1'	8:J:108:MET:HE1	1.79	0.64
7:G:26:LYS:HG3	7:G:31:GLU:HG3	1.80	0.64
1:A:99:U:H5''	1:A:100:U:H5'	1.78	0.64
1:A:2788:C:O2'	1:A:2809:A:N3	2.30	0.64
1:A:601:C:O2'	6:E:99:LYS:NZ	2.31	0.64
1:A:950:G:H1	1:A:967:U:H3	1.46	0.64
1:A:1153:C:OP1	12:Q:91:ARG:NH2	2.31	0.64
1:A:1629:U:O4	1:A:1630:A:N6	2.31	0.64
28:6:25:LEU:HB2	28:6:37:MET:HB3	1.80	0.64
1:A:466:A:OP1	24:2:34:ARG:NH1	2.29	0.64
13:R:63:VAL:HG12	13:R:96:VAL:HG12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1930:G:N2	1:A:1931:U:O4	2.29	0.63
1:A:1862:G:H1	1:A:1880:U:H3	1.46	0.63
1:A:1927:A:H2'	1:A:1928:A:C8	2.33	0.63
29:H:104:THR:HG22	29:H:109:GLU:HA	1.79	0.63
1:A:1073:A:H3'	1:A:1074:G:H5''	1.81	0.63
1:A:1443:U:H2'	1:A:1444:G:H8	1.63	0.63
1:A:2848:G:HO2'	1:A:2867:G:H22	1.44	0.63
6:E:83:VAL:HB	6:E:86:ALA:HB2	1.80	0.63
19:X:32:LEU:HD11	19:X:49:ARG:HG2	1.80	0.63
1:A:1035:U:H2'	1:A:1036:G:H8	1.63	0.63
1:A:1997:C:H2'	1:A:1998:A:H8	1.63	0.63
11:O:31:THR:OG1	11:O:34:HIS:O	2.15	0.63
26:K:94:PRO:HD2	26:K:114:LYS:NZ	2.14	0.63
27:P:87:ARG:NH2	27:P:109:ILE:O	2.31	0.63
1:A:848:C:H2'	1:A:849:A:H8	1.64	0.63
1:A:377:G:H1	1:A:397:U:H3	1.46	0.63
1:A:932:U:O2'	1:A:934:U:O4	2.15	0.63
1:A:2046:G:OP1	22:O:11:LYS:NZ	2.25	0.63
27:P:28:LYS:HD2	27:P:82:SER:HB3	1.80	0.63
1:A:467:G:OP1	24:2:33:ARG:NH2	2.32	0.63
1:A:956:G:N2	1:A:960:A:OP2	2.31	0.63
25:I:46:ASP:HA	25:I:50:LYS:HD2	1.81	0.62
1:A:584:C:N4	1:A:585:G:O6	2.33	0.62
1:A:2002:G:OP1	10:N:17:ARG:NH1	2.32	0.62
1:A:2081:U:H2'	1:A:2082:A:H8	1.64	0.62
6:E:145:ASP:HB2	6:E:166:LYS:HE3	1.81	0.62
1:A:1649:G:H2'	1:A:1650:A:H8	1.65	0.62
1:A:2838:G:O2'	10:N:45:ARG:NH1	2.30	0.62
10:N:44:LEU:HD22	10:N:113:ILE:HD13	1.81	0.62
26:K:94:PRO:HD2	26:K:114:LYS:HG3	1.81	0.62
1:A:572:A:H61	1:A:2029:G:N2	1.97	0.62
2:B:51:G:OP1	11:O:67:ASN:ND2	2.33	0.62
1:A:2773:C:OP1	5:D:169:ARG:NH2	2.32	0.62
5:D:181:ASP:HB2	5:D:186:LEU:HB2	1.80	0.62
26:K:105:ARG:HD2	28:6:33:ILE:HD13	1.81	0.62
1:A:1059:G:O2'	25:I:131:THR:OG1	2.14	0.62
1:A:2645:G:OP2	1:A:2645:G:N2	2.28	0.62
2:B:78:A:OP2	17:V:18:ARG:NH2	2.32	0.62
7:G:38:ASP:O	7:G:54:ARG:NH1	2.29	0.62
19:X:53:LYS:HA	19:X:53:LYS:HE3	1.82	0.62
30:F:12:VAL:HG12	30:F:16:MET:HE2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:50:ALA:O	11:O:81:ARG:NH2	2.32	0.62
8:J:44:TYR:O	12:Q:63:ARG:NH2	2.33	0.61
28:6:33:ILE:HG23	28:6:34:THR:HG23	1.82	0.61
1:A:970:U:O2	1:A:984:A:O2'	2.17	0.61
1:A:451:U:H4'	6:E:47:LYS:HE3	1.82	0.61
1:A:1040:A:H61	1:A:1115:G:H1	1.48	0.61
1:A:1278:C:H5''	10:N:34:ILE:HD11	1.82	0.61
1:A:1826:G:O2'	1:A:1971:U:OP2	2.18	0.61
1:A:2674:G:H4'	26:K:30:ARG:HD3	1.82	0.61
2:B:9:G:OP1	11:O:15:ARG:NE	2.33	0.61
5:D:157:LYS:HE2	8:J:80:HIS:CD2	2.35	0.61
1:A:818:G:N1	1:A:1188:U:OP2	2.24	0.61
1:A:1518:C:H2'	1:A:1519:G:H8	1.65	0.61
1:A:2223:G:O2'	4:C:264:LYS:NZ	2.33	0.61
4:C:64:VAL:HA	4:C:102:TYR:HB2	1.82	0.61
1:A:630:G:N2	1:A:633:A:OP2	2.33	0.61
1:A:1636:U:O2'	1:A:1760:C:O2	2.18	0.61
1:A:1696:G:N2	1:A:1977:A:O2'	2.30	0.61
1:A:2040:G:OP1	8:J:106:LYS:NZ	2.33	0.61
1:A:2861:U:H2'	1:A:2862:G:H8	1.65	0.61
1:A:100:U:O2'	16:U:90:LYS:NZ	2.34	0.61
7:G:88:LEU:HD23	7:G:93:TYR:HB3	1.83	0.61
1:A:1600:C:OP1	15:T:81:LYS:NZ	2.28	0.61
3:9P1:38:ASP:OD2	3:9P1:129:ARG:NH1	2.33	0.61
1:A:1079:C:O2	25:I:133:ARG:NH2	2.34	0.61
1:A:1315:C:O2'	1:A:1392:A:N3	2.32	0.61
1:A:1665:A:H5''	26:K:66:LYS:HG2	1.83	0.61
1:A:76:C:H5''	20:Y:48:ARG:HD2	1.83	0.61
1:A:1597:A:H5''	1:A:1598:A:H5'	1.83	0.61
1:A:2575:C:H5'	5:D:149:ASN:HB3	1.82	0.61
14:S:35:ILE:HG23	14:S:36:LEU:HD12	1.81	0.61
20:Y:23:ARG:O	20:Y:27:ASN:ND2	2.33	0.61
1:A:1164:C:H2'	1:A:1165:A:H8	1.66	0.60
5:D:172:VAL:HG12	5:D:175:LEU:HD21	1.83	0.60
14:S:85:ILE:HD11	14:S:93:ALA:HB1	1.82	0.60
19:X:4:CYS:SG	19:X:7:THR:OG1	2.57	0.60
29:H:14:SER:N	29:H:17:ASP:OD1	2.32	0.60
1:A:1386:C:H2'	1:A:1387:A:C8	2.37	0.60
1:A:1820:U:OP1	4:C:176:ARG:NE	2.32	0.60
1:A:1952:A:C4	26:K:22:ILE:HD11	2.36	0.60
1:A:536:G:H21	8:J:47:HIS:CD2	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1036:G:O6	1:A:1119:U:O2	2.20	0.60
8:J:44:TYR:HA	8:J:50:THR:HG21	1.84	0.60
1:A:1668:A:N1	1:A:1676:A:N6	2.50	0.60
30:F:60:SER:HB2	30:F:94:ARG:HH22	1.64	0.60
1:A:453:A:N3	1:A:457:A:O2'	2.35	0.60
1:A:767:U:H2'	1:A:768:G:H8	1.65	0.60
1:A:136:G:H1	1:A:143:C:H42	1.49	0.60
1:A:544:C:N4	1:A:548:G:OP1	2.34	0.60
1:A:764:A:H5'	4:C:208:GLY:HA2	1.83	0.60
1:A:2333:A:H4'	1:A:2334:U:H3'	1.82	0.60
6:E:117:ARG:NE	6:E:184:ASP:O	2.34	0.60
8:J:17:VAL:HG23	8:J:137:PRO:HB2	1.83	0.60
13:R:78:ARG:HG3	13:R:83:TYR:HD1	1.66	0.60
1:A:1258:U:H2'	1:A:1259:G:H8	1.67	0.60
30:F:35:LEU:HB2	30:F:88:VAL:HB	1.84	0.60
4:C:151:GLY:O	4:C:155:ARG:NH1	2.35	0.60
14:S:80:PRO:O	14:S:100:THR:OG1	2.16	0.60
1:A:13:A:O2'	1:A:15:G:N7	2.35	0.60
1:A:860:U:H2'	1:A:861:A:H8	1.67	0.60
1:A:1322:A:N1	1:A:1333:G:O2'	2.29	0.60
6:E:149:ILE:HD11	6:E:175:ILE:HG22	1.83	0.60
29:H:9:VAL:HG22	29:H:35:LYS:HD2	1.82	0.60
1:A:959:A:H2'	1:A:960:A:C8	2.36	0.60
1:A:2139:U:H2'	1:A:2140:G:H8	1.67	0.59
5:D:29:VAL:HG13	5:D:98:VAL:HG22	1.84	0.59
9:L:82:LEU:HD21	9:L:120:VAL:HG21	1.83	0.59
11:O:90:VAL:HG12	11:O:115:LEU:HD11	1.83	0.59
1:A:1995:U:OP1	5:D:128:ARG:NH1	2.35	0.59
1:A:2233:U:H2'	1:A:2234:G:H8	1.66	0.59
14:S:8:ARG:HA	14:S:102:HIS:HA	1.83	0.59
25:I:99:LYS:NZ	25:I:140:GLU:OE2	2.35	0.59
29:H:30:LEU:HB3	29:H:36:ALA:HB3	1.84	0.59
1:A:705:A:H4'	4:C:6:LYS:HD2	1.84	0.59
1:A:1277:G:H4'	10:N:20:MET:HE1	1.84	0.59
1:A:1682:G:OP2	1:A:1699:G:N2	2.30	0.59
1:A:2313:C:H2'	1:A:2314:A:C8	2.37	0.59
1:A:2532:G:H22	3:9P1:52:ASN:HD21	1.50	0.59
9:L:111:ILE:HD12	9:L:128:THR:HG21	1.83	0.59
1:A:2076:U:OP2	1:A:2238:G:N2	2.35	0.59
1:A:2320:U:O2'	1:A:2322:A:N6	2.36	0.59
1:A:2595:G:N2	1:A:2598:A:OP2	2.23	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:U:H2'	1:A:19:A:C8	2.37	0.59
1:A:2151:U:H2'	1:A:2152:G:H8	1.68	0.59
29:H:39:ALA:HA	29:H:43:ASN:HB2	1.84	0.59
1:A:2866:U:H5'	1:A:2868:A:H5'	1.84	0.59
1:A:1071:G:N2	1:A:1089:A:H2'	2.18	0.59
1:A:1447:C:H2'	1:A:1448:G:H8	1.67	0.59
1:A:2062:A:H3'	1:A:2063:C:H5''	1.85	0.59
1:A:126:A:H61	24:2:42:LEU:HB2	1.68	0.59
1:A:174:U:H2'	1:A:175:G:H8	1.66	0.59
1:A:1223:G:N2	1:A:1226:A:OP2	2.27	0.59
3:9P1:13:ALA:HB2	3:9P1:118:ALA:HB1	1.85	0.59
1:A:1420:A:O2'	1:A:2211:A:N7	2.33	0.58
1:A:1736:U:H3'	1:A:1737:G:C8	2.38	0.58
1:A:1791:A:N1	1:A:1829:A:H4'	2.17	0.58
1:A:2340:A:H2'	1:A:2341:G:H8	1.67	0.58
3:9P1:158:LEU:HD13	3:9P1:198:LEU:HD11	1.84	0.58
19:X:6:VAL:HG23	19:X:7:THR:HG23	1.85	0.58
29:H:54:LEU:HA	29:H:57:LYS:HG2	1.85	0.58
1:A:1024:G:HO2'	1:A:1144:A:HO2'	1.50	0.58
1:A:1734:G:H2'	1:A:1735:A:H8	1.67	0.58
29:H:22:LYS:HD2	29:H:24:GLY:H	1.68	0.58
31:b:28:VAL:HG11	31:b:32:LEU:HD13	1.84	0.58
1:A:272:A:H2'	1:A:273:G:H8	1.68	0.58
1:A:645:C:H5'	1:A:647:G:N7	2.18	0.58
24:2:34:ARG:NH2	24:2:41:ARG:O	2.35	0.58
1:A:1615:C:OP2	1:A:1617:C:N4	2.35	0.58
1:A:2561:U:O3'	26:K:40:LYS:NZ	2.27	0.58
21:Z:4:ILE:HG23	21:Z:6:ILE:HD11	1.84	0.58
19:X:39:VAL:HG12	19:X:42:GLU:H	1.69	0.58
1:A:2163:A:OP1	1:A:2170:A:O2'	2.22	0.58
1:A:2505:G:N2	1:A:2610:C:O2	2.36	0.58
11:O:25:ARG:HB2	11:O:93:ASP:HB2	1.86	0.58
1:A:117:G:OP2	1:A:119:A:O2'	2.16	0.58
1:A:160:A:N3	1:A:2208:C:O2'	2.34	0.58
1:A:599:A:H2'	1:A:600:G:H8	1.69	0.58
1:A:1123:C:H2'	1:A:1124:G:H8	1.67	0.58
15:T:61:LEU:HB3	15:T:82:LYS:HB2	1.85	0.58
3:9P1:281:VAL:HG21	3:9P1:324:LEU:HD21	1.86	0.58
8:J:95:ARG:HH22	8:J:96:ARG:HH22	1.52	0.58
10:N:44:LEU:HD13	10:N:113:ILE:HG21	1.86	0.58
14:S:86:MET:HE3	14:S:96:ILE:HG21	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2286:G:H4'	1:A:2287:A:C4	2.39	0.57
1:A:2579:C:O2'	5:D:136:ASN:OD1	2.21	0.57
1:A:302:C:H2'	1:A:303:G:H8	1.70	0.57
5:D:47:ALA:HA	5:D:84:LEU:HD23	1.85	0.57
6:E:130:LYS:HB2	6:E:133:LEU:HD13	1.86	0.57
11:O:24:THR:HG22	11:O:42:PRO:HD3	1.86	0.57
29:H:65:ALA:HA	29:H:68:ARG:HE	1.68	0.57
1:A:629:G:H1'	1:A:639:U:H1'	1.86	0.57
1:A:1649:G:H2'	1:A:1650:A:C8	2.38	0.57
1:A:2414:G:H2'	1:A:2415:G:H8	1.70	0.57
1:A:345:A:N3	1:A:347:A:N6	2.52	0.57
1:A:874:G:H2'	1:A:875:G:H8	1.68	0.57
1:A:2673:G:H2'	1:A:2674:G:H8	1.68	0.57
1:A:971:G:OP2	1:A:974:G:N2	2.38	0.57
1:A:1936:A:OP2	1:A:1962:C:N4	2.38	0.57
1:A:2705:A:O2'	1:A:2852:G:OP1	2.17	0.57
1:A:690:G:O3'	4:C:216:ARG:NH1	2.37	0.57
26:K:94:PRO:HD2	26:K:114:LYS:HZ3	1.70	0.57
1:A:937:C:H2'	1:A:938:G:H8	1.69	0.57
1:A:1064:C:H4'	25:I:89:SER:H	1.69	0.57
1:A:1154:G:OP2	12:Q:57:ARG:NH1	2.37	0.57
1:A:1270:C:H5''	1:A:1271:G:H5'	1.87	0.57
1:A:1539:U:H2'	1:A:1540:G:H8	1.70	0.57
1:A:2511:U:H1'	5:D:130:GLN:HE21	1.70	0.57
1:A:2636:C:H4'	5:D:81:GLU:OE2	2.05	0.57
9:L:135:ILE:HG22	9:L:140:GLY:HA3	1.86	0.57
1:A:239:C:O2'	1:A:622:G:O2'	2.22	0.57
1:A:1249:U:O4	9:L:18:ARG:NH2	2.37	0.57
1:A:2127:G:O2'	1:A:2128:G:O5'	2.23	0.57
30:F:39:VAL:HG23	30:F:40:GLY:H	1.70	0.57
1:A:184:C:H2'	1:A:185:G:H8	1.69	0.57
1:A:2024:G:O2'	5:D:154:LYS:NZ	2.37	0.57
1:A:2074:U:H2'	1:A:2075:U:C6	2.40	0.57
2:B:40:U:H5''	2:B:41:G:H4'	1.86	0.57
3:9P1:55:THR:HG21	7:G:174:LYS:HG3	1.86	0.57
28:6:37:MET:HE1	28:6:86:ILE:HB	1.87	0.57
1:A:171:U:H2'	1:A:172:A:C8	2.40	0.57
1:A:1123:C:H2'	1:A:1124:G:C8	2.40	0.57
1:A:446:G:P	12:Q:2:ARG:HG3	2.45	0.56
1:A:960:A:H2'	1:A:962:G:H5'	1.87	0.56
1:A:1070:A:H61	25:I:10:LEU:HD21	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1258:U:H2'	1:A:1259:G:C8	2.39	0.56
1:A:1358:G:O2'	1:A:1373:A:N6	2.38	0.56
1:A:2529:G:O2'	3:9P1:58:ASP:OD1	2.20	0.56
8:J:92:MET:O	8:J:96:ARG:N	2.38	0.56
15:T:8:LEU:HD12	15:T:9:LYS:HD3	1.87	0.56
16:U:39:ASN:HD21	16:U:64:ILE:HB	1.69	0.56
1:A:788:A:OP1	1:A:791:C:N4	2.28	0.56
1:A:1299:G:H5''	1:A:1300:G:H5''	1.87	0.56
1:A:2377:A:O2'	11:O:117:PHE:O	2.21	0.56
2:B:114:C:H2'	2:B:115:A:H8	1.70	0.56
3:9P1:259:ALA:HA	3:9P1:262:ILE:HG12	1.87	0.56
5:D:104:VAL:O	5:D:105:LYS:HG3	2.05	0.56
30:F:48:LEU:HD21	30:F:147:ARG:HH21	1.69	0.56
1:A:535:G:H1	1:A:558:U:H3	1.51	0.56
1:A:675:A:N3	1:A:2443:C:O2'	2.39	0.56
1:A:832:U:H2'	1:A:833:A:H8	1.70	0.56
1:A:918:A:N3	2:B:80:U:O2'	2.38	0.56
1:A:1429:G:H2'	1:A:1430:G:H8	1.69	0.56
1:A:1808:A:H62	19:X:27:ARG:HH11	1.53	0.56
1:A:2821:A:OP2	5:D:115:GLY:N	2.35	0.56
5:D:5:VAL:HG22	5:D:202:ILE:HG22	1.86	0.56
7:G:104:LEU:HB3	7:G:106:LEU:CD1	2.36	0.56
8:J:56:VAL:HB	8:J:124:VAL:HG12	1.87	0.56
11:O:111:ARG:NH2	11:O:117:PHE:OXT	2.38	0.56
1:A:742:A:H2'	1:A:743:A:C8	2.41	0.56
1:A:851:C:O2'	21:Z:42:ALA:O	2.23	0.56
1:A:1322:A:OP1	14:S:11:ARG:NH1	2.38	0.56
1:A:1709:U:H2'	1:A:1710:G:C8	2.41	0.56
14:S:82:MET:HB2	14:S:98:LYS:HB2	1.86	0.56
30:F:33:ILE:HB	30:F:95:MET:HE3	1.87	0.56
1:A:1311:G:H21	1:A:1603:A:H62	1.54	0.56
1:A:2635:A:H4'	5:D:79:LEU:O	2.04	0.56
1:A:371:A:H61	1:A:401:A:H5''	1.68	0.56
1:A:571:U:O2'	1:A:573:U:OP2	2.24	0.56
1:A:1291:C:H2'	1:A:1292:G:C8	2.41	0.56
1:A:2851:A:O2'	10:N:64:ARG:NH2	2.39	0.56
3:9P1:203:MET:HE2	3:9P1:325:CYS:HB3	1.88	0.56
4:C:52:HIS:HA	4:C:216:ARG:HB2	1.88	0.56
6:E:97:ASN:HB2	6:E:100:MET:HG2	1.87	0.56
1:A:746:U:H5''	1:A:748:G:H5''	1.88	0.56
1:A:1681:G:N2	1:A:1763:G:OP2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2074:U:H2'	1:A:2075:U:H6	1.71	0.56
22:O:12:ARG:HE	22:O:16:ARG:HH12	1.54	0.56
30:F:11:VAL:HG22	30:F:171:ALA:HB1	1.88	0.56
1:A:222:A:H61	1:A:232:G:H1'	1.71	0.56
1:A:464:U:O2	24:2:16:HIS:NE2	2.39	0.56
1:A:395:U:O2'	1:A:396:G:N7	2.31	0.55
1:A:705:A:H2'	1:A:706:A:H8	1.72	0.55
1:A:1400:U:H2'	1:A:1401:G:C8	2.42	0.55
1:A:174:U:H2'	1:A:175:G:C8	2.41	0.55
1:A:2011:U:OP2	14:S:16:LYS:NZ	2.29	0.55
26:K:107:LEU:HD21	26:K:112:PHE:HB2	1.87	0.55
30:F:146:ASP:C	30:F:147:ARG:HD3	2.32	0.55
1:A:558:U:H2'	1:A:559:G:C8	2.42	0.55
1:A:843:G:H2'	1:A:844:A:C8	2.42	0.55
1:A:908:C:H2'	1:A:909:A:C8	2.41	0.55
1:A:1131:G:N2	1:A:1132:U:O4	2.36	0.55
1:A:2511:U:H5''	5:D:128:ARG:HB3	1.88	0.55
1:A:2730:C:O3'	5:D:174:SER:OG	2.25	0.55
21:Z:5:LYS:HB2	21:Z:57:GLU:HB3	1.88	0.55
1:A:1295:C:H2'	1:A:1296:G:H8	1.71	0.55
1:A:796:C:H2'	1:A:797:G:H8	1.70	0.55
1:A:1958:C:H2'	1:A:1959:G:H8	1.71	0.55
1:A:2787:C:O3'	5:D:62:LYS:NZ	2.40	0.55
6:E:125:SER:HA	6:E:157:LEU:HD21	1.89	0.55
1:A:16:C:H2'	1:A:17:G:H8	1.70	0.55
1:A:2566:A:H4'	1:A:2567:G:H5''	1.87	0.55
4:C:141:HIS:ND1	4:C:192:GLY:O	2.32	0.55
4:C:131:MET:HE1	4:C:187:CYS:HB2	1.89	0.55
28:6:40:CYS:HB2	28:6:89:VAL:HG12	1.89	0.55
1:A:2730:C:O2'	5:D:173:GLN:O	2.24	0.55
4:C:244:VAL:HG12	4:C:250:GLN:HA	1.89	0.55
5:D:151:THR:O	5:D:153:GLY:N	2.40	0.55
15:T:61:LEU:O	15:T:82:LYS:N	2.33	0.55
1:A:739:A:N3	1:A:740:C:N4	2.51	0.55
3:9P1:189:TYR:HB2	3:9P1:190:PRO:HD2	1.89	0.55
27:P:59:THR:HG22	27:P:72:VAL:HG12	1.89	0.55
1:A:1987:A:H2'	1:A:1988:G:H8	1.71	0.55
1:A:2119:A:H61	1:A:2167:U:H1'	1.71	0.55
1:A:2258:C:O2'	1:A:2427:C:OP2	2.25	0.55
1:A:2345:G:H4'	1:A:2346:A:H3'	1.89	0.55
1:A:2727:A:O2'	26:K:70:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:29:PHE:HE2	4:C:32:LEU:HD23	1.72	0.55
5:D:46:ARG:NH2	5:D:86:GLU:OE2	2.40	0.55
10:N:98:LEU:HB2	10:N:112:TYR:HB2	1.89	0.55
1:A:1863:G:H4'	1:A:2411:A:H4'	1.88	0.54
1:A:2646:C:OP2	1:A:2732:G:O2'	2.25	0.54
6:E:18:THR:HG22	6:E:106:LYS:HE3	1.89	0.54
31:b:12:ILE:HD12	31:b:26:SER:HB3	1.88	0.54
1:A:2047:C:H2'	1:A:2048:G:H8	1.72	0.54
3:9P1:167:MET:HE2	3:9P1:167:MET:HA	1.88	0.54
15:T:2:ILE:HA	15:T:3:ARG:C	2.32	0.54
1:A:272:A:H2'	1:A:273:G:C8	2.42	0.54
1:A:1114:C:N4	1:A:1115:G:O6	2.40	0.54
1:A:2652:C:H5''	28:6:60:ARG:HH12	1.73	0.54
1:A:2822:G:O2'	1:A:2825:G:N1	2.41	0.54
12:Q:57:ARG:HG2	12:Q:57:ARG:HH11	1.72	0.54
1:A:1491:G:O2'	4:C:99:GLU:OE2	2.23	0.54
1:A:1500:G:N2	4:C:97:ASP:O	2.31	0.54
3:9P1:125:LEU:HD12	3:9P1:129:ARG:HG2	1.89	0.54
1:A:2128:G:N3	1:A:2173:A:O2'	2.40	0.54
2:B:37:C:H42	2:B:49:C:H1'	1.73	0.54
1:A:660:C:H2'	1:A:661:A:H8	1.72	0.54
1:A:685:A:O2'	1:A:772:C:N4	2.41	0.54
1:A:2229:U:H2'	1:A:2230:G:H8	1.73	0.54
1:A:2459:A:H2'	1:A:2460:U:O4'	2.07	0.54
26:K:24:VAL:HG23	26:K:33:ALA:HB2	1.89	0.54
30:F:91:ARG:HA	30:F:95:MET:HB2	1.89	0.54
1:A:219:A:N3	1:A:234:U:O2'	2.38	0.54
1:A:1011:G:OP1	12:Q:74:SER:OG	2.25	0.54
1:A:1306:C:N4	1:A:1607:C:OP2	2.41	0.54
19:X:39:VAL:HG22	19:X:63:ILE:HG21	1.89	0.54
1:A:1437:C:O2'	1:A:1516:G:O2'	2.26	0.54
1:A:740:C:H5'	1:A:1784:A:H2'	1.89	0.54
1:A:741:U:H2'	1:A:742:A:H8	1.72	0.54
1:A:2099:U:H2'	1:A:2100:G:H8	1.72	0.54
19:X:64:ASP:OD1	19:X:65:THR:N	2.41	0.54
25:I:45:THR:HG22	25:I:50:LYS:HG3	1.88	0.54
1:A:1501:G:H2'	1:A:1502:A:H8	1.73	0.54
1:A:2046:G:H5'	22:O:15:ARG:HG3	1.90	0.54
1:A:2522:U:O2'	1:A:2647:U:OP1	2.25	0.54
1:A:2724:U:H2'	1:A:2725:A:C8	2.43	0.54
4:C:129:LEU:HD12	4:C:133:ASN:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:I:115:ASP:O	25:I:116:MET:HE2	2.08	0.54
27:P:36:LYS:HZ2	27:P:38:ARG:HD3	1.73	0.54
1:A:45:G:H5'	1:A:46:G:H5'	1.90	0.53
1:A:1444:G:H2'	1:A:1445:G:H8	1.73	0.53
1:A:2559:C:H2'	1:A:2560:A:H8	1.73	0.53
29:H:47:PHE:HA	29:H:50:ARG:HB2	1.90	0.53
29:H:135:HIS:HB3	29:H:138:VAL:HB	1.89	0.53
1:A:30:G:O2'	1:A:1214:A:N3	2.34	0.53
1:A:298:G:N1	1:A:339:U:OP2	2.36	0.53
1:A:796:C:H2'	1:A:797:G:C8	2.42	0.53
1:A:1322:A:O3'	14:S:84:ARG:NH1	2.41	0.53
1:A:2091:C:H4'	19:X:55:MET:HE1	1.90	0.53
14:S:24:ILE:HD13	14:S:36:LEU:HD11	1.89	0.53
1:A:514:A:N3	1:A:581:C:O2'	2.36	0.53
1:A:876:C:H42	1:A:902:C:H42	1.56	0.53
2:B:42:C:O2	30:F:62:GLN:NE2	2.41	0.53
6:E:60:TRP:NE1	6:E:68:ALA:O	2.33	0.53
10:N:99:LYS:HA	10:N:111:ALA:HA	1.90	0.53
1:A:580:U:H2'	1:A:581:C:H6	1.72	0.53
1:A:1038:G:H2'	1:A:1039:A:C8	2.44	0.53
15:T:38:ALA:HB1	15:T:43:ILE:HD11	1.91	0.53
1:A:18:U:H2'	1:A:19:A:H8	1.72	0.53
1:A:1612:C:O2'	24:2:5:PHE:O	2.26	0.53
2:B:14:U:OP2	2:B:70:C:O2'	2.27	0.53
7:G:136:ASP:HB3	7:G:139:VAL:HG22	1.90	0.53
9:L:96:LYS:NZ	9:L:105:ILE:O	2.41	0.53
15:T:76:ARG:HH11	15:T:76:ARG:HG3	1.72	0.53
1:A:83:A:O2'	1:A:103:A:N6	2.42	0.53
1:A:1715:G:N2	1:A:1744:A:OP2	2.36	0.53
1:A:1798:U:O2'	1:A:1802:A:N3	2.36	0.53
1:A:2045:C:H5''	22:0:14:MET:HE2	1.89	0.53
8:J:73:VAL:HG22	8:J:88:THR:HG22	1.90	0.53
1:A:605:G:OP1	6:E:99:LYS:NZ	2.42	0.53
1:A:807:U:H2'	1:A:808:G:H8	1.73	0.53
1:A:1353:A:OP2	1:A:1377:G:N1	2.38	0.53
1:A:1869:G:O2'	1:A:1872:A:N6	2.42	0.53
1:A:2543:G:H2'	1:A:2544:G:C8	2.44	0.53
1:A:2599:G:H2'	1:A:2600:A:H8	1.73	0.53
5:D:84:LEU:HD12	5:D:88:GLU:HG2	1.91	0.53
10:N:20:MET:HE3	10:N:24:MET:HE3	1.90	0.53
22:0:10:SER:O	22:0:14:MET:HG3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:C:O2'	1:A:1000:A:N3	2.39	0.53
1:A:1450:G:N2	1:A:1452:G:O6	2.30	0.53
1:A:2526:G:H1	1:A:2537:U:H3	1.57	0.53
1:A:2737:G:H2'	1:A:2738:A:C8	2.44	0.53
7:G:51:PHE:HZ	7:G:71:LEU:HD22	1.74	0.53
10:N:22:ARG:HD2	10:N:71:ARG:HB2	1.91	0.53
17:V:79:ARG:NH2	17:V:83:LYS:O	2.42	0.53
19:X:54:GLY:O	19:X:58:ILE:HG12	2.09	0.53
1:A:581:C:H2'	1:A:582:A:H8	1.74	0.53
5:D:5:VAL:HG11	5:D:80:TRP:CZ3	2.43	0.53
26:K:105:ARG:HH12	27:P:31:VAL:HG21	1.73	0.53
1:A:580:U:H2'	1:A:581:C:C6	2.44	0.53
1:A:837:C:N3	1:A:941:A:N6	2.57	0.53
1:A:1313:U:H4'	1:A:1332:G:H4'	1.91	0.53
1:A:2909:C:H2'	1:A:2910:G:H8	1.74	0.53
28:6:28:GLN:NE2	28:6:35:ASP:OD1	2.33	0.53
30:F:157:THR:HG22	30:F:159:ALA:H	1.74	0.53
1:A:76:C:H2'	1:A:77:G:H8	1.74	0.52
1:A:171:U:H2'	1:A:172:A:H8	1.73	0.52
1:A:1048:A:H1'	1:A:1112:G:N2	2.24	0.52
1:A:1518:C:H2'	1:A:1519:G:C8	2.42	0.52
1:A:2314:A:H2'	1:A:2315:G:C8	2.44	0.52
3:9P1:38:ASP:H	3:9P1:79:THR:HG22	1.74	0.52
15:T:14:PRO:HD3	20:Y:30:MET:SD	2.49	0.52
1:A:1219:U:OP2	12:Q:18:LYS:NZ	2.23	0.52
1:A:813:U:OP2	9:L:24:GLY:N	2.37	0.52
1:A:237:C:O2	1:A:609:A:O2'	2.27	0.52
1:A:1539:U:H2'	1:A:1540:G:C8	2.44	0.52
1:A:184:C:H2'	1:A:185:G:C8	2.44	0.52
1:A:499:U:H2'	1:A:500:G:O4'	2.10	0.52
1:A:2637:U:H5''	5:D:83:ARG:HH12	1.74	0.52
1:A:2543:G:H2'	1:A:2544:G:H8	1.74	0.52
2:B:63:C:H2'	2:B:64:G:C8	2.45	0.52
5:D:157:LYS:HE2	8:J:80:HIS:HD2	1.72	0.52
9:L:90:VAL:O	9:L:123:ARG:N	2.40	0.52
12:Q:20:ALA:HA	12:Q:23:TYR:HE1	1.75	0.52
14:S:8:ARG:HG2	14:S:8:ARG:HH11	1.74	0.52
30:F:37:MET:HB2	30:F:56:LEU:HD21	1.91	0.52
1:A:720:U:H2'	1:A:721:A:C8	2.45	0.52
1:A:742:A:H2'	1:A:743:A:H8	1.73	0.52
1:A:931:U:O2	1:A:1167:C:O2'	2.21	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1528:A:N6	1:A:1543:G:O2'	2.43	0.52
1:A:1816:C:H5''	4:C:61:TYR:HE2	1.74	0.52
7:G:34:ARG:HB2	7:G:74:MET:HE1	1.92	0.52
8:J:49:ASP:OD1	8:J:121:LYS:NZ	2.43	0.52
13:R:68:ARG:HG2	13:R:92:TRP:HA	1.91	0.52
1:A:65:U:H2'	1:A:66:C:H6	1.73	0.52
1:A:667:U:H2'	1:A:668:A:O4'	2.10	0.52
1:A:743:A:O2'	1:A:1659:G:OP1	2.27	0.52
1:A:1057:A:N6	1:A:1087:G:OP2	2.43	0.52
1:A:1323:C:H5'	14:S:84:ARG:HH11	1.75	0.52
3:9P1:44:ASP:OD1	3:9P1:120:GLY:N	2.41	0.52
1:A:1287:A:N1	1:A:1649:G:H4'	2.25	0.52
1:A:1715:G:O2'	1:A:1743:G:O6	2.23	0.52
1:A:1903:G:H2'	1:A:1904:G:H8	1.75	0.52
1:A:2544:G:H2'	1:A:2545:G:C8	2.45	0.52
1:A:2898:U:H2'	1:A:2899:A:C8	2.45	0.52
28:6:95:ARG:HD3	28:6:100:LEU:HD13	1.91	0.52
1:A:620:G:H4'	1:A:621:A:H5'	1.92	0.52
1:A:781:A:OP1	4:C:216:ARG:NH2	2.43	0.52
1:A:805:G:N2	1:A:829:A:OP1	2.43	0.52
1:A:1164:C:H2'	1:A:1165:A:C8	2.45	0.52
1:A:1798:U:OP1	4:C:255:LYS:NZ	2.40	0.52
1:A:1800:C:N3	1:A:1817:G:N1	2.53	0.52
1:A:1801:A:N6	1:A:2201:G:O2'	2.30	0.52
23:1:36:LYS:HD3	23:1:47:ILE:HG13	1.91	0.52
1:A:1357:C:H2'	1:A:1358:G:O4'	2.10	0.51
4:C:120:ASP:OD1	4:C:121:ALA:N	2.38	0.51
7:G:93:TYR:OH	7:G:151:ARG:NH1	2.42	0.51
15:T:52:GLU:N	15:T:52:GLU:OE1	2.43	0.51
1:A:242:G:N2	1:A:255:A:OP2	2.37	0.51
1:A:828:U:H4'	1:A:831:G:C6	2.45	0.51
1:A:1440:U:H2'	1:A:1441:G:H8	1.75	0.51
1:A:1443:U:H2'	1:A:1444:G:C8	2.45	0.51
2:B:27:C:OP1	11:O:33:ARG:NH1	2.44	0.51
3:9P1:265:GLU:HA	3:9P1:268:LYS:HB3	1.93	0.51
11:O:33:ARG:O	11:O:65:THR:OG1	2.23	0.51
15:T:37:ASP:O	15:T:81:LYS:NZ	2.39	0.51
30:F:135:ILE:H	30:F:135:ILE:HD12	1.75	0.51
1:A:1252:G:H1	12:Q:36:GLN:HG3	1.75	0.51
1:A:1806:C:H4'	4:C:47:ARG:HG2	1.93	0.51
1:A:2454:G:H5'	1:A:2572:A:C4	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:5:U:OP1	2:B:61:G:O2'	2.21	0.51
4:C:106:PRO:HD2	4:C:109:LEU:HD22	1.93	0.51
17:V:20:LEU:HD12	17:V:25:LYS:HB2	1.93	0.51
26:K:36:GLY:HA3	26:K:110:GLU:HG3	1.92	0.51
28:6:77:TRP:CH2	28:6:79:VAL:HB	2.46	0.51
1:A:302:C:H2'	1:A:303:G:C8	2.46	0.51
1:A:2063:C:O2	1:A:2063:C:H2'	2.10	0.51
2:B:13:G:O2'	2:B:15:A:OP2	2.26	0.51
2:B:57:A:H2'	2:B:58:A:H8	1.75	0.51
1:A:373:U:H2'	1:A:374:A:H8	1.74	0.51
1:A:859:G:O2'	1:A:916:G:O6	2.25	0.51
1:A:1141:U:H5''	8:J:27:ARG:HH22	1.75	0.51
1:A:1681:G:H21	1:A:1762:A:H3'	1.76	0.51
1:A:1997:C:H2'	1:A:1998:A:C8	2.45	0.51
2:B:29:A:O2'	2:B:58:A:N1	2.40	0.51
2:B:41:G:OP1	2:B:43:C:N4	2.33	0.51
5:D:125:TRP:CD2	5:D:160:LYS:HB3	2.46	0.51
6:E:112:LEU:HB3	6:E:118:LEU:HB2	1.92	0.51
8:J:105:VAL:HA	8:J:108:MET:HB2	1.91	0.51
22:0:53:VAL:HG22	22:0:54:ILE:H	1.75	0.51
26:K:21:CYS:HA	26:K:41:ILE:HG22	1.92	0.51
30:F:15:LEU:HG	30:F:28:PRO:HD2	1.93	0.51
1:A:133:U:H2'	1:A:134:G:C8	2.46	0.51
1:A:1016:G:O6	1:A:1147:A:N6	2.44	0.51
1:A:1636:U:H2'	1:A:1637:A:C8	2.46	0.51
1:A:2567:G:H2'	1:A:2568:U:C6	2.44	0.51
15:T:61:LEU:HD12	15:T:62:VAL:H	1.76	0.51
1:A:65:U:O2'	1:A:456:C:N3	2.39	0.51
1:A:747:U:O3'	14:S:88:ARG:NH1	2.44	0.51
1:A:1428:C:N4	1:A:1570:A:OP2	2.41	0.51
4:C:194:VAL:HG22	4:C:195:GLY:H	1.75	0.51
4:C:231:HIS:HA	4:C:241:LYS:HD2	1.92	0.51
19:X:48:LEU:HB3	19:X:50:VAL:HG23	1.92	0.51
22:0:37:HIS:ND1	22:0:38:LEU:O	2.39	0.51
30:F:110:ILE:HD11	30:F:131:VAL:HG12	1.92	0.51
1:A:87:U:H5''	1:A:88:G:H5'	1.92	0.51
1:A:633:A:O2'	1:A:2404:U:OP1	2.27	0.51
1:A:1199:U:H1'	12:Q:2:ARG:O	2.11	0.51
1:A:1753:G:H5''	27:P:92:ARG:HD3	1.93	0.51
1:A:2508:G:H1	1:A:2580:U:H3	1.59	0.51
4:C:224:MET:HG3	4:C:225:ASN:N	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:V:79:ARG:HE	17:V:80:HIS:N	2.07	0.51
27:P:90:ALA:HB2	27:P:112:ARG:HA	1.92	0.51
28:6:43:THR:H	28:6:47:HIS:CE1	2.29	0.51
1:A:523:C:H2'	1:A:524:G:H8	1.76	0.51
1:A:599:A:H2'	1:A:600:G:C8	2.46	0.51
1:A:935:C:H2'	1:A:936:A:C8	2.41	0.51
1:A:1709:U:H2'	1:A:1710:G:H8	1.75	0.51
1:A:1791:A:C2	1:A:1829:A:H4'	2.45	0.51
1:A:2039:U:H2'	1:A:2040:G:C8	2.46	0.51
1:A:2228:G:H2'	1:A:2229:U:H6	1.73	0.51
24:2:37:LYS:HE2	24:2:37:LYS:HA	1.91	0.51
1:A:175:G:H2'	1:A:176:A:C8	2.46	0.51
2:B:116:G:H2'	2:B:117:G:H8	1.76	0.51
3:9P1:196:PRO:HD3	3:9P1:231:PHE:HE1	1.76	0.51
3:9P1:245:ILE:HD11	3:9P1:280:LEU:HD22	1.93	0.51
3:9P1:263:ILE:HD11	3:9P1:304:LEU:HD21	1.92	0.51
8:J:55:ILE:HD13	8:J:130:HIS:HD2	1.76	0.51
8:J:96:ARG:HG3	8:J:99:ARG:HB2	1.93	0.51
25:I:16:MET:HG2	25:I:19:PRO:HD3	1.92	0.51
1:A:329:G:H1	16:U:16:LYS:HE2	1.76	0.50
5:D:7:LYS:HD3	5:D:198:GLY:HA2	1.92	0.50
12:Q:105:PHE:HA	12:Q:108:LEU:HD23	1.93	0.50
14:S:74:ILE:HG13	14:S:105:VAL:HG12	1.93	0.50
26:K:22:ILE:HG22	26:K:40:LYS:C	2.35	0.50
27:P:104:GLY:O	27:P:108:ARG:NH2	2.44	0.50
1:A:729:G:O2'	1:A:763:G:H4'	2.11	0.50
1:A:1805:A:H2'	1:A:1806:C:C6	2.47	0.50
1:A:2086:U:H2'	1:A:2087:G:C8	2.46	0.50
1:A:2626:C:H2'	1:A:2627:G:C8	2.46	0.50
3:9P1:50:ASP:HB2	3:9P1:91:PRO:HA	1.92	0.50
4:C:121:ALA:HB3	4:C:129:LEU:HD13	1.93	0.50
26:K:98:ARG:NH2	28:6:99:GLU:OE1	2.44	0.50
1:A:1688:U:O2'	1:A:1700:A:N7	2.42	0.50
1:A:2127:G:H21	1:A:2173:A:H1'	1.77	0.50
1:A:2128:G:H2'	1:A:2129:C:C6	2.45	0.50
4:C:136:VAL:HA	4:C:163:ILE:HG23	1.93	0.50
1:A:926:G:H2'	1:A:927:A:H8	1.75	0.50
1:A:973:A:H5'	1:A:1188:U:H1'	1.93	0.50
1:A:995:C:O2	8:J:3:THR:OG1	2.25	0.50
1:A:998:C:OP2	12:Q:57:ARG:NH2	2.45	0.50
1:A:1102:C:H2'	1:A:1103:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:91:ASP:HB3	9:L:123:ARG:HB3	1.93	0.50
15:T:69:ARG:HB3	15:T:74:ILE:HA	1.93	0.50
1:A:320:A:N3	6:E:163:ASN:ND2	2.59	0.50
1:A:828:U:H4'	1:A:831:G:N1	2.27	0.50
1:A:1874:C:H2'	1:A:1875:G:O4'	2.12	0.50
1:A:2036:C:H2'	1:A:2037:A:H8	1.75	0.50
3:9P1:239:ARG:HE	3:9P1:332:ILE:HG13	1.75	0.50
3:9P1:283:ASN:OD1	3:9P1:284:LYS:N	2.37	0.50
6:E:48:THR:O	6:E:52:VAL:HG23	2.12	0.50
6:E:117:ARG:NH2	6:E:183:PHE:O	2.41	0.50
10:N:98:LEU:N	10:N:112:TYR:O	2.42	0.50
30:F:116:LEU:HD11	30:F:174:PHE:CE2	2.47	0.50
1:A:24:G:O2'	14:S:78:GLU:O	2.24	0.50
1:A:855:G:N2	18:W:23:GLY:O	2.41	0.50
1:A:1752:C:H2'	1:A:1753:G:C8	2.47	0.50
1:A:2262:U:H5''	18:W:37:ARG:HH21	1.76	0.50
6:E:101:TYR:OH	6:E:175:ILE:O	2.29	0.50
10:N:28:LEU:HD22	10:N:44:LEU:HD21	1.94	0.50
17:V:44:HIS:CE1	17:V:85:LYS:HB3	2.47	0.50
26:K:43:ILE:HD11	26:K:58:LEU:HD21	1.94	0.50
1:A:126:A:O2'	1:A:127:A:O4'	2.24	0.50
1:A:139:U:O2'	1:A:141:G:N1	2.36	0.50
1:A:397:U:H5''	19:X:31:ASN:HB2	1.92	0.50
1:A:953:G:O2'	1:A:2266:A:OP2	2.30	0.50
1:A:1637:A:H2'	1:A:1638:C:C6	2.46	0.50
1:A:2057:G:H2'	1:A:2058:A:C8	2.47	0.50
1:A:2335:A:P	11:O:13:ARG:HH12	2.35	0.50
1:A:2728:U:O2'	1:A:2729:G:H8	1.94	0.50
1:A:2868:A:H2'	1:A:2869:G:C8	2.46	0.50
34:A:3008:HOH:O	5:D:140:HIS:NE2	2.34	0.50
1:A:300:A:H2'	1:A:334:C:H1'	1.94	0.50
1:A:660:C:OP1	6:E:94:GLN:NE2	2.44	0.50
1:A:744:U:H2'	1:A:745:G:O4'	2.11	0.50
1:A:1435:G:H2'	1:A:1436:G:C8	2.47	0.50
1:A:2514:U:H3	1:A:2570:G:H1	1.59	0.50
1:A:2692:G:H1'	1:A:2847:U:H1'	1.94	0.50
1:A:2898:U:H2'	1:A:2899:A:H8	1.77	0.50
15:T:88:LYS:HG3	15:T:88:LYS:O	2.12	0.50
30:F:79:ARG:HE	30:F:82:TYR:HD2	1.59	0.50
1:A:1352:U:H1'	1:A:1570:A:H2	1.76	0.50
30:F:120:SER:HB2	30:F:127:TYR:CE1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:A:H2'	1:A:6:A:C8	2.47	0.49
1:A:680:C:H2'	1:A:681:G:H8	1.77	0.49
1:A:1538:G:H2'	1:A:1539:U:C6	2.47	0.49
3:9P1:50:ASP:HB3	3:9P1:53:LEU:HG	1.92	0.49
5:D:136:ASN:ND2	5:D:139:SER:O	2.45	0.49
1:A:133:U:H2'	1:A:134:G:H8	1.77	0.49
1:A:813:U:H2'	1:A:814:C:C6	2.47	0.49
1:A:926:G:H2'	1:A:927:A:C8	2.48	0.49
1:A:1696:G:H21	1:A:1977:A:HO2'	1.57	0.49
1:A:2616:C:H2'	1:A:2617:U:C6	2.47	0.49
1:A:2707:U:H2'	1:A:2708:G:H8	1.77	0.49
1:A:2831:G:N7	5:D:59:ARG:NH1	2.60	0.49
13:R:38:VAL:HG11	13:R:57:GLY:HA3	1.94	0.49
24:2:34:ARG:NE	24:2:39:ARG:HD2	2.27	0.49
25:I:105:LEU:HD12	25:I:108:ILE:HB	1.93	0.49
1:A:58:G:O2'	1:A:73:A:N1	2.37	0.49
1:A:1463:C:H2'	1:A:1464:G:C8	2.46	0.49
1:A:1849:G:H2'	1:A:1850:G:H8	1.78	0.49
1:A:2295:C:OP2	11:O:10:ARG:NE	2.46	0.49
1:A:2840:C:H2'	1:A:2841:C:H6	1.77	0.49
16:U:87:GLU:HG3	16:U:92:VAL:HG11	1.94	0.49
1:A:835:C:H2'	1:A:836:G:H8	1.77	0.49
1:A:1266:G:OP1	22:O:15:ARG:NH1	2.43	0.49
1:A:1943:U:O4'	1:A:1945:G:H5'	2.12	0.49
1:A:2086:U:H2'	1:A:2087:G:H8	1.78	0.49
1:A:2127:G:H4'	1:A:2128:G:OP1	2.12	0.49
12:Q:97:ILE:HG22	12:Q:105:PHE:HB2	1.95	0.49
1:A:404:A:H4'	1:A:405:U:O5'	2.11	0.49
1:A:552:U:H2'	1:A:553:G:H8	1.77	0.49
1:A:739:A:H1'	1:A:740:C:H5	1.76	0.49
1:A:908:C:H2'	1:A:909:A:H8	1.78	0.49
1:A:1092:C:H2'	1:A:1093:G:O4'	2.13	0.49
1:A:1320:C:H2'	1:A:1329:U:OP1	2.12	0.49
1:A:1337:G:OP2	15:T:77:ARG:NH2	2.36	0.49
1:A:1412:U:H2'	1:A:1413:A:H8	1.77	0.49
1:A:1563:U:H2'	1:A:1564:C:C6	2.48	0.49
1:A:2564:A:H2'	1:A:2565:A:C8	2.48	0.49
1:A:2756:U:H1'	1:A:2757:A:H5''	1.93	0.49
1:A:2787:C:H1'	5:D:63:PRO:HG3	1.93	0.49
2:B:33:G:H2'	2:B:34:A:C8	2.48	0.49
3:9P1:206:GLU:HG3	28:6:46:ARG:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:70:LYS:HA	9:L:73:ILE:HG22	1.93	0.49
10:N:73:ASN:OD1	10:N:74:GLU:N	2.45	0.49
10:N:96:ARG:O	10:N:113:ILE:HA	2.12	0.49
21:Z:12:ALA:HA	21:Z:15:ARG:HG3	1.92	0.49
1:A:144:A:H4'	15:T:3:ARG:HH22	1.76	0.49
1:A:170:U:H2'	1:A:171:U:C6	2.48	0.49
1:A:305:C:H2'	1:A:306:U:C6	2.46	0.49
1:A:1013:C:H2'	1:A:1014:A:H8	1.76	0.49
1:A:1614:A:N6	14:S:92:ARG:O	2.37	0.49
1:A:1727:C:N3	1:A:1734:G:N1	2.61	0.49
1:A:2223:G:O3'	4:C:264:LYS:NZ	2.44	0.49
3:9P1:164:MET:HE1	3:9P1:242:LEU:HD12	1.94	0.49
11:O:15:ARG:NH1	11:O:93:ASP:OD2	2.45	0.49
28:6:36:CYS:HB2	28:6:85:VAL:HG12	1.95	0.49
1:A:372:G:O2'	1:A:400:G:O6	2.29	0.49
1:A:813:U:O2'	1:A:1225:G:O2'	2.21	0.49
1:A:2087:G:H2'	1:A:2088:A:H8	1.77	0.49
1:A:2606:C:H2'	1:A:2607:G:C8	2.46	0.49
1:A:2678:C:H2'	1:A:2679:A:C8	2.48	0.49
2:B:49:C:H2'	2:B:50:A:C8	2.48	0.49
3:9P1:98:ASP:HB3	3:9P1:150:ARG:HH21	1.76	0.49
3:9P1:218:ILE:HG22	3:9P1:219:GLU:HG2	1.95	0.49
14:S:58:ALA:O	14:S:62:ASP:HB3	2.13	0.49
15:T:34:VAL:HG23	15:T:81:LYS:HB3	1.95	0.49
26:K:8:LEU:HD23	26:K:82:ASN:HB3	1.95	0.49
26:K:40:LYS:HB2	26:K:59:LYS:HD3	1.94	0.49
1:A:466:A:N1	1:A:795:C:O2'	2.41	0.49
1:A:1447:C:H2'	1:A:1448:G:C8	2.48	0.49
1:A:1592:C:H2'	1:A:1593:A:C8	2.48	0.49
1:A:2515:C:H2'	1:A:2516:A:H8	1.78	0.49
4:C:65:ASP:OD1	4:C:101:ARG:HD3	2.12	0.49
9:L:128:THR:HG23	9:L:131:ALA:H	1.76	0.49
1:A:566:U:H2'	1:A:567:U:C6	2.47	0.49
1:A:865:C:H42	1:A:909:A:H62	1.61	0.49
1:A:1262:A:H2	22:0:6:LYS:HD2	1.77	0.49
1:A:1266:G:P	22:0:16:ARG:HE	2.36	0.49
1:A:1592:C:H2'	1:A:1593:A:H8	1.78	0.49
5:D:25:THR:HG21	5:D:193:VAL:HG22	1.95	0.49
8:J:16:TYR:HE2	8:J:35:ARG:HH21	1.61	0.49
15:T:15:HIS:HB3	15:T:31:VAL:HG12	1.95	0.49
19:X:32:LEU:HD12	19:X:33:HIS:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:2:GLN:NE2	29:H:19:VAL:O	2.46	0.49
1:A:550:C:H2'	1:A:551:G:C8	2.48	0.49
1:A:974:G:O2'	1:A:989:G:N2	2.46	0.49
1:A:1361:G:H2'	1:A:1362:C:C6	2.47	0.49
1:A:1407:G:H2'	1:A:1408:G:H8	1.76	0.49
1:A:1463:C:H2'	1:A:1464:G:H8	1.77	0.49
1:A:2615:U:H2'	1:A:2616:C:C6	2.48	0.49
3:9P1:255:PRO:O	3:9P1:257:GLU:N	2.46	0.49
18:W:18:GLY:N	18:W:35:ARG:O	2.46	0.49
1:A:144:A:O2'	15:T:3:ARG:NH2	2.46	0.48
1:A:813:U:H2'	1:A:814:C:H6	1.78	0.48
1:A:1071:G:H21	1:A:1089:A:H2'	1.78	0.48
1:A:1072:C:N4	1:A:1093:G:H1	2.11	0.48
1:A:1140:C:H5'	8:J:26:GLY:HA3	1.94	0.48
1:A:1440:U:H2'	1:A:1441:G:C8	2.48	0.48
1:A:1441:G:H2'	1:A:1442:U:C6	2.48	0.48
1:A:417:C:H2'	1:A:418:C:H6	1.78	0.48
1:A:639:U:H3	1:A:649:G:H1	1.61	0.48
1:A:820:A:H2	1:A:943:A:H4'	1.78	0.48
1:A:1005:C:H2'	1:A:1006:C:C6	2.47	0.48
1:A:1361:G:H2'	1:A:1362:C:H6	1.78	0.48
1:A:2065:C:H2'	1:A:2066:C:H6	1.77	0.48
1:A:2604:U:OP1	3:9P1:131:LYS:NZ	2.31	0.48
3:9P1:287:LEU:HG	3:9P1:288:LEU:HD12	1.94	0.48
4:C:75:ALA:HB3	4:C:115:ILE:HG13	1.95	0.48
23:1:32:LYS:HG2	23:1:50:GLU:HA	1.94	0.48
27:P:25:VAL:HG12	27:P:85:VAL:HG22	1.94	0.48
1:A:227:A:H2	1:A:418:C:H1'	1.78	0.48
1:A:832:U:H2'	1:A:833:A:C8	2.48	0.48
1:A:1710:G:H2'	1:A:1711:A:C8	2.48	0.48
1:A:2092:U:OP2	29:H:27:ARG:NH2	2.46	0.48
1:A:2183:A:H2'	1:A:2184:A:C8	2.48	0.48
4:C:144:GLU:OE2	4:C:150:GLY:N	2.46	0.48
6:E:191:ASP:OD2	6:E:191:ASP:N	2.45	0.48
11:O:15:ARG:HH22	11:O:25:ARG:CZ	2.26	0.48
30:F:151:LEU:HD13	30:F:153:ILE:HG23	1.94	0.48
1:A:131:A:H2'	1:A:132:G:H8	1.78	0.48
1:A:479:A:H1'	1:A:481:G:H5'	1.95	0.48
1:A:657:U:H2'	1:A:658:U:C6	2.49	0.48
1:A:980:A:N1	1:A:1136:G:H4'	2.28	0.48
1:A:1447:C:O2'	1:A:1544:A:N3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1820:U:N3	4:C:158:GLY:HA3	2.28	0.48
1:A:2011:U:H2'	1:A:2012:G:O4'	2.13	0.48
1:A:2868:A:H2'	1:A:2869:G:H8	1.79	0.48
2:B:38:C:N3	2:B:39:A:N6	2.61	0.48
8:J:49:ASP:HA	8:J:118:MET:HE1	1.96	0.48
19:X:31:ASN:OD1	19:X:33:HIS:NE2	2.46	0.48
21:Z:50:VAL:O	21:Z:50:VAL:HG12	2.13	0.48
1:A:306:U:H2'	1:A:307:G:O4'	2.13	0.48
1:A:414:C:H2'	1:A:415:A:C8	2.49	0.48
1:A:639:U:H2'	1:A:640:C:C6	2.49	0.48
1:A:664:G:H2'	1:A:665:U:H6	1.78	0.48
1:A:2087:G:H2'	1:A:2088:A:C8	2.49	0.48
1:A:2116:G:O6	1:A:2171:A:N6	2.46	0.48
1:A:2144:G:O2'	1:A:2147:A:N6	2.45	0.48
2:B:44:G:H3'	30:F:91:ARG:NH1	2.27	0.48
16:U:9:GLU:CD	16:U:21:ARG:HH21	2.22	0.48
24:2:1:MET:HE3	24:2:2:LYS:H	1.79	0.48
1:A:1143:A:H62	8:J:27:ARG:HG3	1.78	0.48
2:B:70:C:H2'	2:B:71:C:H6	1.79	0.48
9:L:62:PRO:HG2	9:L:64:PHE:CZ	2.48	0.48
14:S:10:ALA:HB1	14:S:46:LEU:HD21	1.94	0.48
15:T:56:GLU:CD	15:T:88:LYS:HD3	2.39	0.48
1:A:141:G:OP2	1:A:142:A:N6	2.46	0.48
1:A:582:A:OP1	12:Q:13:HIS:ND1	2.38	0.48
1:A:690:G:N2	4:C:42:ARG:HH22	2.11	0.48
1:A:711:G:O6	1:A:721:A:N6	2.47	0.48
1:A:2623:G:H2'	1:A:2624:G:H8	1.78	0.48
1:A:2840:C:H5''	10:N:53:THR:HG21	1.94	0.48
10:N:50:PRO:HA	10:N:53:THR:HG22	1.96	0.48
1:A:155:A:H2'	1:A:156:A:C8	2.49	0.48
1:A:884:U:O4	1:A:892:A:N6	2.46	0.48
1:A:1059:G:H21	25:I:130:GLY:HA3	1.78	0.48
1:A:1365:A:OP1	19:X:27:ARG:NH2	2.46	0.48
2:B:95:U:H2'	2:B:96:G:C8	2.49	0.48
1:A:76:C:OP1	20:Y:48:ARG:NH1	2.46	0.48
1:A:192:C:O2'	1:A:802:A:N3	2.45	0.48
1:A:494:G:H2'	1:A:495:G:C8	2.48	0.48
1:A:769:U:H2'	1:A:770:G:C8	2.49	0.48
1:A:1129:A:O2'	1:A:2515:C:O2	2.30	0.48
1:A:2380:C:H2'	1:A:2381:A:C8	2.48	0.48
1:A:2698:U:H2'	1:A:2699:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2799:A:O2'	1:A:2800:A:H5''	2.14	0.48
2:B:24:G:H4'	2:B:25:U:H5	1.79	0.48
1:A:1918:A:O2'	1:A:1919:A:N7	2.44	0.48
1:A:2514:U:H2'	1:A:2515:C:C6	2.48	0.48
1:A:2816:G:N3	1:A:2883:A:O2'	2.41	0.48
2:B:62:C:H2'	2:B:63:C:C6	2.48	0.48
4:C:255:LYS:NZ	4:C:269:ARG:HH12	2.12	0.48
8:J:35:ARG:HB2	8:J:54:ILE:HD11	1.94	0.48
1:A:347:A:H2'	1:A:348:A:C8	2.49	0.47
1:A:381:G:H2'	1:A:382:A:C8	2.48	0.47
1:A:1907:G:O6	1:A:1923:U:O2	2.31	0.47
1:A:2773:C:H2'	1:A:2774:C:H6	1.79	0.47
12:Q:20:ALA:HA	12:Q:23:TYR:CE1	2.49	0.47
25:I:53:PRO:HD2	25:I:77:VAL:HG21	1.96	0.47
27:P:61:ARG:HH22	27:P:100:ARG:HA	1.78	0.47
1:A:85:G:OP2	16:U:6:ARG:NH1	2.43	0.47
1:A:949:G:H2'	1:A:950:G:H8	1.79	0.47
1:A:1654:A:N1	1:A:2048:G:O2'	2.48	0.47
1:A:1734:G:H2'	1:A:1735:A:C8	2.46	0.47
1:A:1952:A:C5	26:K:22:ILE:HD11	2.49	0.47
1:A:2093:G:C8	1:A:2225:A:H2'	2.49	0.47
5:D:157:LYS:NZ	8:J:79:GLY:O	2.47	0.47
20:Y:9:LYS:HB2	20:Y:11:VAL:HG12	1.96	0.47
1:A:155:A:H2'	1:A:156:A:H8	1.80	0.47
1:A:172:A:H2'	1:A:173:A:C8	2.43	0.47
1:A:669:G:N1	1:A:801:G:O6	2.47	0.47
1:A:741:U:H2'	1:A:742:A:C8	2.48	0.47
1:A:1291:C:H2'	1:A:1292:G:H8	1.79	0.47
1:A:1656:C:OP1	5:D:141:ARG:HD2	2.14	0.47
1:A:1924:C:N4	1:A:1926:U:O4	2.47	0.47
1:A:2215:C:H2'	1:A:2216:G:C8	2.49	0.47
1:A:2490:G:O2'	1:A:2491:U:H5''	2.14	0.47
1:A:2625:G:H2'	1:A:2626:C:C6	2.49	0.47
1:A:2881:U:H2'	1:A:2882:A:C8	2.49	0.47
3:9P1:17:GLY:N	3:9P1:40:GLY:O	2.47	0.47
26:K:13:ASN:ND2	26:K:97:THR:OG1	2.36	0.47
31:b:18:CYS:SG	31:b:40:CYS:HB3	2.53	0.47
1:A:7:G:H5'	8:J:132:HIS:CE1	2.49	0.47
1:A:648:G:O2'	1:A:2351:G:OP1	2.30	0.47
1:A:1028:A:OP2	1:A:1126:A:N6	2.31	0.47
1:A:1564:C:H2'	1:A:1565:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1753:G:N2	1:A:1756:G:O5'	2.46	0.47
3:9P1:97:ILE:HB	3:9P1:153:LEU:HB2	1.95	0.47
5:D:3:GLY:HA2	5:D:101:PHE:HZ	1.79	0.47
12:Q:73:ILE:HD13	12:Q:113:LYS:HD3	1.95	0.47
1:A:415:A:H2'	1:A:416:U:C6	2.49	0.47
1:A:682:G:H5'	24:2:26:ASN:ND2	2.29	0.47
1:A:747:U:O2'	14:S:88:ARG:NE	2.47	0.47
1:A:1059:G:H2'	1:A:1060:U:C5	2.49	0.47
1:A:1223:G:OP2	13:R:90:ARG:NH2	2.47	0.47
1:A:1276:A:N6	1:A:1645:G:O6	2.47	0.47
1:A:2623:G:OP1	1:A:2826:A:O2'	2.23	0.47
4:C:70:LYS:HB3	4:C:73:ILE:HG13	1.96	0.47
1:A:141:G:H5''	1:A:142:A:N7	2.30	0.47
1:A:417:C:H2'	1:A:418:C:C6	2.50	0.47
1:A:671:C:OP2	9:L:33:ARG:NH1	2.37	0.47
1:A:937:C:H2'	1:A:938:G:C8	2.48	0.47
1:A:1912:A:H62	1:A:1917:U:H3	1.62	0.47
1:A:2318:G:H2'	1:A:2319:G:C4	2.50	0.47
1:A:2599:G:H2'	1:A:2600:A:C8	2.50	0.47
1:A:2652:C:N3	1:A:2669:G:N1	2.63	0.47
1:A:2776:A:O2'	1:A:2782:G:N7	2.37	0.47
4:C:71:ASP:HB3	4:C:118:GLY:HA2	1.96	0.47
15:T:61:LEU:HD23	15:T:82:LYS:HD3	1.95	0.47
17:V:75:GLN:NE2	17:V:92:VAL:HG22	2.30	0.47
1:A:57:C:H2'	1:A:58:G:H8	1.78	0.47
1:A:563:A:OP2	13:R:79:ARG:NH2	2.47	0.47
1:A:666:A:H4'	9:L:48:ARG:HG3	1.96	0.47
1:A:843:G:H2'	1:A:844:A:H8	1.79	0.47
1:A:1013:C:H2'	1:A:1014:A:C8	2.49	0.47
1:A:1654:A:H2'	1:A:1655:A:H8	1.80	0.47
1:A:2009:A:H2'	1:A:2010:G:C8	2.48	0.47
1:A:2075:U:O2'	1:A:2076:U:O2	2.27	0.47
1:A:2290:G:H2'	1:A:2291:U:C6	2.50	0.47
1:A:2418:A:O2'	23:1:31:GLU:OE1	2.29	0.47
8:J:81:ILE:HG23	8:J:82:GLY:H	1.80	0.47
12:Q:57:ARG:HA	12:Q:60:TRP:CE3	2.50	0.47
15:T:13:ALA:HA	20:Y:30:MET:HE1	1.97	0.47
15:T:38:ALA:HB3	15:T:81:LYS:HD3	1.97	0.47
15:T:69:ARG:HB3	15:T:74:ILE:HG22	1.97	0.47
17:V:84:PRO:C	17:V:85:LYS:HD3	2.40	0.47
30:F:34:THR:HG23	30:F:153:ILE:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:G:OP1	1:A:1376:C:O2'	2.28	0.47
1:A:541:A:N6	1:A:553:G:O6	2.48	0.47
1:A:1182:G:H2'	1:A:1183:U:O4'	2.15	0.47
1:A:1306:C:H41	1:A:1606:C:H2'	1.80	0.47
1:A:1808:A:H3'	1:A:1809:A:C8	2.49	0.47
1:A:2329:U:H2'	1:A:2330:G:C8	2.50	0.47
1:A:2347:C:N3	1:A:2371:G:N2	2.62	0.47
1:A:2896:C:H2'	1:A:2897:U:C6	2.50	0.47
2:B:49:C:H2'	2:B:50:A:H8	1.78	0.47
2:B:63:C:H2'	2:B:64:G:H8	1.78	0.47
28:6:42:GLY:N	28:6:90:MET:O	2.44	0.47
1:A:141:G:H3'	1:A:142:A:C8	2.49	0.47
1:A:997:G:H5''	12:Q:91:ARG:HH11	1.80	0.47
1:A:1040:A:N6	1:A:1115:G:H1	2.12	0.47
1:A:1197:G:H2'	1:A:1198:U:C6	2.50	0.47
1:A:2075:U:H2'	1:A:2077:A:OP2	2.14	0.47
1:A:2199:A:OP1	19:X:36:ARG:NH1	2.32	0.47
1:A:2291:U:H2'	1:A:2292:U:C6	2.49	0.47
1:A:2395:C:H2'	1:A:2396:G:H8	1.79	0.47
1:A:2417:C:H2'	1:A:2418:A:C8	2.50	0.47
1:A:2425:A:H4'	1:A:2426:A:O5'	2.14	0.47
1:A:2774:C:H2'	1:A:2775:G:O4'	2.15	0.47
2:B:42:C:H42	30:F:89:THR:H	1.61	0.47
3:9P1:168:PRO:HG3	3:9P1:191:PHE:CE1	2.49	0.47
18:W:19:VAL:HA	18:W:34:VAL:HG23	1.97	0.47
23:1:8:ILE:HG22	23:1:52:LYS:HB2	1.96	0.47
1:A:341:C:H2'	1:A:342:A:C8	2.49	0.47
1:A:358:U:H2'	1:A:359:G:H8	1.79	0.47
1:A:580:U:OP1	12:Q:32:ARG:NH2	2.48	0.47
1:A:1751:U:H2'	1:A:1752:C:C6	2.50	0.47
1:A:2398:U:H2'	1:A:2399:G:C8	2.50	0.47
25:I:3:LYS:HG3	25:I:4:VAL:H	1.80	0.47
26:K:64:ARG:HH12	26:K:101:GLY:HA3	1.78	0.47
27:P:48:ALA:HB1	27:P:95:LYS:HZ3	1.80	0.47
1:A:20:C:H2'	1:A:21:A:C8	2.50	0.46
1:A:64:A:H2'	1:A:65:U:C6	2.50	0.46
1:A:848:C:H2'	1:A:849:A:C8	2.48	0.46
1:A:934:U:H2'	1:A:935:C:C6	2.51	0.46
1:A:1424:G:H2'	1:A:1425:G:C8	2.50	0.46
1:A:1570:A:H2'	1:A:1571:A:C8	2.51	0.46
1:A:2329:U:H2'	1:A:2330:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2707:U:H2'	1:A:2708:G:C8	2.51	0.46
6:E:26:ALA:HB2	9:L:9:ALA:HB2	1.97	0.46
8:J:16:TYR:CD2	8:J:140:LEU:HD22	2.50	0.46
8:J:88:THR:O	8:J:92:MET:HG3	2.15	0.46
22:O:30:ASP:OD2	22:O:33:SER:N	2.38	0.46
29:H:2:GLN:HB3	29:H:18:GLN:NE2	2.29	0.46
30:F:9:ASP:OD1	30:F:10:GLU:N	2.48	0.46
1:A:459:U:H2'	1:A:460:A:H8	1.79	0.46
1:A:1802:A:H2'	1:A:1803:A:C8	2.50	0.46
1:A:2250:G:H5''	1:A:2251:G:H5''	1.97	0.46
1:A:2417:C:H2'	1:A:2418:A:H8	1.79	0.46
1:A:2861:U:H2'	1:A:2862:G:C8	2.49	0.46
2:B:60:C:H2'	2:B:61:G:H8	1.80	0.46
22:O:46:GLY:HA3	22:O:55:ALA:HA	1.97	0.46
1:A:5:A:H2'	1:A:6:A:H8	1.79	0.46
1:A:154:U:H2'	1:A:155:A:H8	1.80	0.46
1:A:365:U:H2'	1:A:366:C:C6	2.49	0.46
1:A:419:U:H2'	1:A:420:C:C6	2.49	0.46
1:A:550:C:H2'	1:A:551:G:H8	1.80	0.46
1:A:660:C:H2'	1:A:661:A:C8	2.50	0.46
1:A:1130:U:O2'	1:A:1131:G:H2'	2.15	0.46
1:A:1278:C:H2'	1:A:1279:G:C8	2.49	0.46
1:A:2414:G:H2'	1:A:2415:G:C8	2.50	0.46
1:A:2626:C:H2'	1:A:2627:G:H8	1.80	0.46
2:B:44:G:H4'	2:B:46:A:H62	1.79	0.46
30:F:3:LEU:HD22	30:F:172:PHE:CE2	2.50	0.46
1:A:1400:U:H2'	1:A:1401:G:H8	1.77	0.46
1:A:1830:C:H2'	1:A:1831:G:C8	2.44	0.46
1:A:2298:A:H62	1:A:2318:G:N2	2.08	0.46
1:A:2425:A:OP2	1:A:2426:A:O2'	2.26	0.46
1:A:2587:A:H61	1:A:2608:G:H1'	1.79	0.46
1:A:2780:G:OP2	8:J:120:ARG:NE	2.48	0.46
3:9P1:287:LEU:H	3:9P1:287:LEU:HD23	1.80	0.46
19:X:32:LEU:HD12	19:X:33:HIS:H	1.80	0.46
20:Y:56:LEU:O	20:Y:57:LEU:HG	2.15	0.46
30:F:146:ASP:O	30:F:147:ARG:HD3	2.15	0.46
1:A:57:C:H2'	1:A:58:G:C8	2.51	0.46
1:A:96:C:H2'	1:A:97:C:C6	2.51	0.46
1:A:903:C:H2'	1:A:904:G:C8	2.51	0.46
1:A:1062:G:H2'	1:A:1063:G:C8	2.51	0.46
1:A:1173:U:O2'	1:A:1177:G:N2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2205:A:OP1	4:C:67:LYS:NZ	2.48	0.46
1:A:2642:G:H5'	8:J:80:HIS:ND1	2.31	0.46
1:A:32:C:H2'	1:A:33:C:C6	2.51	0.46
1:A:1329:U:OP2	1:A:1330:C:N4	2.31	0.46
1:A:1441:G:H2'	1:A:1442:U:H6	1.79	0.46
1:A:1614:A:N6	14:S:88:ARG:H	2.13	0.46
1:A:2508:G:H2'	1:A:2509:G:H8	1.81	0.46
4:C:36:ASN:HB2	4:C:61:TYR:HB2	1.96	0.46
4:C:90:ILE:HD12	4:C:102:TYR:HD2	1.80	0.46
4:C:255:LYS:HZ1	4:C:269:ARG:HH12	1.64	0.46
5:D:101:PHE:HE2	5:D:203:VAL:HG13	1.81	0.46
6:E:97:ASN:HD22	6:E:100:MET:HG2	1.80	0.46
9:L:90:VAL:HB	9:L:122:VAL:HA	1.97	0.46
9:L:123:ARG:HH12	9:L:143:GLU:HB2	1.81	0.46
15:T:66:LYS:H	15:T:77:ARG:HB2	1.79	0.46
19:X:11:PRO:HG2	19:X:27:ARG:HH21	1.81	0.46
28:6:42:GLY:O	28:6:91:GLN:HA	2.16	0.46
29:H:5:LEU:HD23	29:H:36:ALA:HB2	1.98	0.46
1:A:494:G:H2'	1:A:495:G:H8	1.80	0.46
1:A:558:U:H2'	1:A:559:G:H8	1.81	0.46
1:A:680:C:H2'	1:A:681:G:C8	2.50	0.46
1:A:1035:U:H2'	1:A:1036:G:C8	2.48	0.46
1:A:1309:G:H4'	24:2:7:PRO:HB2	1.97	0.46
1:A:1710:G:H1'	1:A:2859:G:H21	1.80	0.46
1:A:1796:U:H2'	1:A:1797:G:C8	2.51	0.46
1:A:2047:C:H2'	1:A:2048:G:C8	2.51	0.46
1:A:2398:U:H2'	1:A:2399:G:H8	1.81	0.46
1:A:2606:C:H2'	1:A:2607:G:H8	1.81	0.46
3:9P1:249:PRO:HB2	3:9P1:252:GLY:H	1.80	0.46
5:D:48:ILE:HG23	5:D:84:LEU:HD21	1.98	0.46
10:N:98:LEU:O	10:N:112:TYR:N	2.41	0.46
11:O:62:LEU:HD11	11:O:65:THR:HA	1.98	0.46
17:V:21:ARG:HH22	17:V:26:PHE:HB3	1.81	0.46
1:A:353:C:H2'	1:A:354:A:C8	2.51	0.46
1:A:685:A:O2'	1:A:773:U:O4	2.26	0.46
1:A:1022:G:N7	1:A:1140:C:N4	2.64	0.46
1:A:1219:U:H2'	1:A:1220:G:C8	2.50	0.46
1:A:1335:C:H2'	1:A:1336:A:H8	1.80	0.46
1:A:1696:G:N2	1:A:1977:A:HO2'	2.12	0.46
1:A:1722:A:H2'	1:A:1723:G:H8	1.80	0.46
1:A:2153:C:C2	1:A:2154:A:C8	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2312:U:H1'	30:F:36:ASN:HD21	1.80	0.46
1:A:2725:A:O2'	1:A:2726:A:H2'	2.15	0.46
1:A:2822:G:HO2'	1:A:2825:G:H1	1.64	0.46
2:B:39:A:H2'	2:B:40:U:C6	2.51	0.46
2:B:50:A:N6	2:B:51:G:O6	2.49	0.46
21:Z:5:LYS:HE2	21:Z:5:LYS:HA	1.97	0.46
1:A:86:G:H2'	1:A:87:U:C6	2.51	0.46
1:A:351:C:H2'	1:A:352:A:H8	1.81	0.46
1:A:541:A:H2'	1:A:542:C:C6	2.51	0.46
1:A:663:G:H4'	9:L:17:LYS:HE3	1.97	0.46
1:A:857:G:H4'	18:W:41:PHE:HZ	1.80	0.46
1:A:1442:U:H2'	1:A:1443:U:C6	2.51	0.46
1:A:1510:G:H2'	1:A:1511:G:H8	1.80	0.46
1:A:2616:C:H2'	1:A:2617:U:H6	1.80	0.46
19:X:4:CYS:HB3	19:X:9:LYS:H	1.80	0.46
29:H:2:GLN:HE22	29:H:19:VAL:C	2.24	0.46
1:A:419:U:H2'	1:A:420:C:H6	1.81	0.46
1:A:523:C:H5''	1:A:540:C:O2'	2.17	0.46
1:A:581:C:H2'	1:A:582:A:C8	2.51	0.46
1:A:964:C:H2'	1:A:965:C:O4'	2.16	0.46
1:A:988:A:H5''	21:Z:11:SER:HB3	1.98	0.46
1:A:1709:U:O2'	1:A:2859:G:O2'	2.29	0.46
1:A:1935:G:N2	1:A:1964:G:O4'	2.49	0.46
1:A:2193:G:H2'	1:A:2194:U:H6	1.81	0.46
1:A:2788:C:H2'	1:A:2789:C:C6	2.51	0.46
10:N:41:ALA:HB1	10:N:113:ILE:HB	1.97	0.46
26:K:59:LYS:HB2	26:K:87:LEU:HB2	1.98	0.46
28:6:43:THR:N	28:6:47:HIS:HE1	2.13	0.46
29:H:5:LEU:HD12	29:H:13:GLY:HA3	1.97	0.46
30:F:23:SER:HB3	30:F:26:GLN:HG2	1.97	0.46
1:A:18:U:OP1	12:Q:29:ARG:NH2	2.49	0.45
1:A:1306:C:H2'	1:A:1307:A:H8	1.82	0.45
1:A:1505:A:H2'	1:A:1506:U:C6	2.51	0.45
1:A:2249:U:O4	1:A:2256:G:N2	2.50	0.45
1:A:2339:C:H2'	1:A:2340:A:C8	2.51	0.45
9:L:29:LYS:O	9:L:30:THR:OG1	2.29	0.45
10:N:8:ARG:HH12	10:N:42:LYS:HD3	1.80	0.45
13:R:24:LYS:HA	13:R:94:THR:HG23	1.98	0.45
14:S:18:ARG:HE	14:S:18:ARG:HB2	1.51	0.45
16:U:88:ASP:O	16:U:90:LYS:N	2.48	0.45
27:P:22:GLY:H	27:P:46:VAL:HG13	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:P:36:LYS:NZ	27:P:38:ARG:HD3	2.30	0.45
1:A:457:A:N1	1:A:470:A:H5''	2.32	0.45
1:A:639:U:C2	1:A:640:C:C5	3.05	0.45
1:A:769:U:H2'	1:A:770:G:H8	1.81	0.45
1:A:1417:C:H2'	1:A:1418:G:O4'	2.16	0.45
1:A:1754:A:N1	1:A:2716:C:O2'	2.49	0.45
1:A:1825:U:H2'	1:A:1826:G:H8	1.80	0.45
3:9P1:205:ASN:O	3:9P1:206:GLU:HB2	2.16	0.45
10:N:28:LEU:HD23	10:N:48:VAL:HG21	1.98	0.45
13:R:15:SER:O	13:R:98:ILE:HG21	2.17	0.45
16:U:93:ARG:HB2	16:U:102:ILE:HD12	1.97	0.45
19:X:71:ARG:HD3	19:X:77:TYR:HE1	1.82	0.45
30:F:105:ILE:C	30:F:108:PRO:HD2	2.41	0.45
1:A:500:G:N1	1:A:503:A:OP2	2.30	0.45
1:A:820:A:C2	1:A:943:A:H4'	2.51	0.45
1:A:1279:G:H2'	1:A:1280:G:C8	2.51	0.45
1:A:1683:U:H2'	1:A:1684:G:C8	2.52	0.45
1:A:2364:C:H2'	1:A:2365:G:O4'	2.16	0.45
1:A:2620:C:O2'	5:D:162:ALA:O	2.34	0.45
1:A:2660:A:N6	3:9P1:198:LEU:HD12	2.31	0.45
1:A:2743:U:O2'	7:G:152:ARG:NH2	2.46	0.45
9:L:79:LEU:HD12	9:L:112:LEU:HG	1.99	0.45
13:R:24:LYS:HD3	13:R:92:TRP:HB3	1.98	0.45
26:K:7:MET:HA	26:K:20:MET:HA	1.99	0.45
29:H:94:ILE:HB	29:H:122:LEU:HB2	1.97	0.45
30:F:175:PRO:O	30:F:176:PHE:HB3	2.17	0.45
1:A:16:C:H2'	1:A:17:G:C8	2.50	0.45
1:A:299:A:N1	1:A:322:A:O2'	2.38	0.45
1:A:438:G:H2'	1:A:439:A:C8	2.52	0.45
1:A:858:G:H3'	1:A:859:G:C8	2.52	0.45
1:A:966:G:H4'	1:A:2271:G:H22	1.82	0.45
1:A:2387:U:OP1	18:W:51:ARG:NH1	2.49	0.45
1:A:2567:G:H2'	1:A:2568:U:H6	1.80	0.45
1:A:2834:G:H2'	1:A:2879:A:H61	1.81	0.45
1:A:2863:C:H2'	1:A:2864:G:H8	1.81	0.45
3:9P1:242:LEU:HD23	3:9P1:279:TRP:HB2	1.98	0.45
4:C:93:VAL:HG11	4:C:103:ILE:HD11	1.99	0.45
6:E:126:VAL:HG12	6:E:157:LEU:HD22	1.98	0.45
10:N:30:ARG:HH11	10:N:30:ARG:HG3	1.81	0.45
11:O:2:ASP:N	11:O:5:SER:HG	2.15	0.45
14:S:59:GLU:OE1	14:S:59:GLU:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:47:VAL:HG21	18:W:76:ILE:HG22	1.98	0.45
1:A:221:A:C4	1:A:233:A:H1'	2.51	0.45
1:A:523:C:H2'	1:A:524:G:C8	2.52	0.45
1:A:951:C:N4	1:A:952:G:O6	2.50	0.45
9:L:79:LEU:HD13	9:L:116:VAL:HB	1.99	0.45
14:S:109:ASP:OD1	14:S:109:ASP:N	2.48	0.45
29:H:22:LYS:HD2	29:H:24:GLY:N	2.31	0.45
1:A:231:A:H2'	1:A:232:G:O4'	2.17	0.45
1:A:1219:U:H2'	1:A:1220:G:H8	1.82	0.45
1:A:2345:G:H5'	1:A:2347:C:H5'	1.98	0.45
4:C:107:LYS:HE3	4:C:194:VAL:O	2.16	0.45
4:C:144:GLU:OE2	4:C:149:LYS:N	2.50	0.45
5:D:56:LYS:O	5:D:60:VAL:HG23	2.17	0.45
1:A:928:A:H2'	1:A:929:U:C6	2.51	0.45
1:A:1322:A:P	14:S:11:ARG:HH22	2.39	0.45
1:A:1928:A:H2'	1:A:1929:G:C4	2.52	0.45
1:A:2063:C:H1'	3:9P1:28:TYR:O	2.17	0.45
1:A:2233:U:H2'	1:A:2234:G:C8	2.48	0.45
3:9P1:313:ILE:HD12	3:9P1:321:VAL:HG12	1.98	0.45
3:9P1:313:ILE:HD13	3:9P1:324:LEU:HD13	1.99	0.45
4:C:91:ALA:HB2	4:C:105:ALA:HB2	1.99	0.45
7:G:39:ALA:HA	7:G:54:ARG:HH12	1.82	0.45
10:N:43:GLU:OE2	10:N:46:ARG:HG3	2.16	0.45
13:R:16:GLU:OE2	13:R:101:ILE:HG12	2.17	0.45
1:A:357:C:H2'	1:A:358:U:C6	2.52	0.45
1:A:1000:A:OP2	1:A:1154:G:N1	2.29	0.45
1:A:1296:G:OP1	1:A:2709:G:O2'	2.29	0.45
1:A:1800:C:O2'	4:C:152:GLN:OE1	2.28	0.45
1:A:1920:C:H2'	1:A:1921:G:H8	1.81	0.45
1:A:2263:C:H2'	1:A:2264:C:C6	2.51	0.45
1:A:2340:A:H2'	1:A:2341:G:C8	2.50	0.45
1:A:2437:G:H2'	1:A:2438:U:C6	2.51	0.45
1:A:2815:C:H2'	1:A:2816:G:H8	1.81	0.45
3:9P1:74:ALA:HB3	3:9P1:78:CYS:HB2	1.99	0.45
4:C:251:THR:HG22	4:C:252:LYS:N	2.32	0.45
1:A:177:G:H3'	1:A:178:G:H8	1.81	0.45
1:A:587:C:H42	9:L:30:THR:HA	1.82	0.45
1:A:1952:A:H2'	1:A:1953:A:C8	2.52	0.45
1:A:2229:U:H2'	1:A:2230:G:C8	2.52	0.45
1:A:2592:G:H2'	1:A:2593:U:H6	1.82	0.45
2:B:93:C:H2'	2:B:94:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:70:LYS:HZ3	4:C:95:TYR:HD2	1.64	0.45
8:J:36:LEU:HD11	8:J:122:LEU:HB2	1.99	0.45
9:L:123:ARG:NH1	9:L:143:GLU:HB2	2.32	0.45
30:F:56:LEU:HD13	30:F:59:ILE:HD11	1.99	0.45
1:A:1141:U:H4'	1:A:1142:A:O4'	2.17	0.45
1:A:1837:C:H2'	1:A:1899:A:H61	1.80	0.45
1:A:2532:G:H1	3:9P1:52:ASN:CG	2.25	0.45
1:A:2676:C:H2'	1:A:2677:G:H8	1.81	0.45
1:A:2804:U:H2'	1:A:2805:C:H6	1.82	0.45
6:E:1:MET:HE1	6:E:20:GLY:HA3	1.99	0.45
1:A:521:U:H2'	1:A:522:A:H8	1.82	0.44
1:A:732:C:H2'	1:A:733:G:O4'	2.16	0.44
1:A:957:C:H5'	1:A:2459:A:C2	2.51	0.44
1:A:1190:G:H2'	1:A:1191:G:H8	1.81	0.44
1:A:1630:A:H2'	1:A:1631:G:O4'	2.17	0.44
1:A:1638:C:O2	1:A:2698:U:O2'	2.35	0.44
1:A:1745:A:H2'	1:A:1746:A:H8	1.83	0.44
1:A:2058:A:H2'	1:A:2059:A:C8	2.52	0.44
7:G:137:LYS:HA	7:G:140:ILE:HG22	1.99	0.44
8:J:38:GLY:O	8:J:44:TYR:HB2	2.16	0.44
8:J:95:ARG:HH22	8:J:96:ARG:NH2	2.14	0.44
16:U:32:LYS:HB3	16:U:63:ALA:HB1	1.98	0.44
22:0:29:VAL:HA	22:0:36:LYS:HA	1.98	0.44
1:A:166:U:H1'	19:X:44:ARG:HH21	1.82	0.44
1:A:528:A:H2'	1:A:529:A:H5''	2.00	0.44
1:A:873:C:H2'	1:A:874:G:C8	2.52	0.44
1:A:1864:U:OP1	1:A:2410:G:O2'	2.30	0.44
1:A:2623:G:H2'	1:A:2624:G:C8	2.52	0.44
1:A:2845:U:H5''	27:P:51:ASN:O	2.18	0.44
6:E:59:PRO:HG3	6:E:73:ILE:HG12	1.99	0.44
6:E:117:ARG:HH12	9:L:2:ARG:HB2	1.82	0.44
7:G:106:LEU:O	7:G:151:ARG:NH2	2.50	0.44
8:J:55:ILE:HD13	8:J:130:HIS:CD2	2.51	0.44
10:N:12:ARG:HD2	10:N:16:HIS:CD2	2.53	0.44
30:F:108:PRO:HB3	31:b:41:HIS:CD2	2.52	0.44
1:A:690:G:H21	4:C:42:ARG:NH1	2.13	0.44
1:A:753:A:H2'	1:A:754:U:C6	2.52	0.44
1:A:1190:G:H2'	1:A:1191:G:C8	2.52	0.44
1:A:1693:U:O4	1:A:1976:U:O2'	2.31	0.44
3:9P1:191:PHE:O	3:9P1:193:THR:N	2.50	0.44
3:9P1:323:ASP:OD1	3:9P1:324:LEU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:2:VAL:HG21	4:C:201:LEU:HD13	1.99	0.44
4:C:239:PHE:O	4:C:241:LYS:HG2	2.17	0.44
11:O:82:ALA:O	11:O:86:GLY:N	2.49	0.44
18:W:41:PHE:CD1	18:W:76:ILE:HD11	2.52	0.44
26:K:40:LYS:HA	26:K:59:LYS:HA	1.98	0.44
1:A:128:C:H2'	1:A:129:C:H6	1.83	0.44
1:A:227:A:C2	1:A:418:C:H1'	2.52	0.44
1:A:521:U:H2'	1:A:522:A:C8	2.53	0.44
1:A:987:C:O2'	1:A:988:A:OP1	2.35	0.44
1:A:1364:G:H5''	19:X:2:ARG:CZ	2.48	0.44
1:A:1965:C:C2	3:9P1:134:VAL:HG11	2.53	0.44
1:A:2643:G:H2'	1:A:2644:G:C8	2.53	0.44
2:B:19:C:H2'	2:B:20:G:C8	2.52	0.44
2:B:70:C:H2'	2:B:71:C:C6	2.53	0.44
4:C:158:GLY:H	4:C:194:VAL:HG13	1.82	0.44
11:O:43:ASN:OD1	11:O:44:GLY:N	2.50	0.44
26:K:54:LYS:C	26:K:54:LYS:HD3	2.43	0.44
28:6:99:GLU:HG3	28:6:102:LYS:HB2	2.00	0.44
1:A:170:U:H2'	1:A:171:U:H6	1.83	0.44
1:A:666:A:H2'	1:A:667:U:C6	2.52	0.44
1:A:1405:U:H2'	1:A:1406:U:C6	2.52	0.44
1:A:1435:G:H2'	1:A:1436:G:H8	1.83	0.44
1:A:1515:A:H1'	1:A:1557:C:H1'	2.00	0.44
1:A:1726:C:H2'	1:A:1727:C:C6	2.53	0.44
1:A:2127:G:H2'	1:A:2128:G:C8	2.52	0.44
1:A:2520:C:H2'	1:A:2521:C:C6	2.52	0.44
1:A:2556:C:H2'	1:A:2557:G:O4'	2.16	0.44
1:A:2678:C:H2'	1:A:2679:A:H8	1.82	0.44
11:O:71:ALA:HB3	11:O:105:ALA:HB3	2.00	0.44
13:R:49:ILE:HG22	13:R:54:VAL:HG23	2.00	0.44
30:F:119:LYS:O	30:F:121:PHE:N	2.48	0.44
1:A:247:G:O2'	1:A:250:G:O6	2.33	0.44
1:A:1614:A:N6	14:S:88:ARG:O	2.51	0.44
1:A:1813:G:H1'	4:C:49:THR:HG21	1.98	0.44
1:A:1826:G:H2'	1:A:1827:U:H6	1.82	0.44
1:A:2848:G:H1'	1:A:2868:A:H61	1.82	0.44
2:B:116:G:H2'	2:B:117:G:C8	2.52	0.44
3:9P1:205:ASN:ND2	28:6:43:THR:HB	2.32	0.44
4:C:67:LYS:O	4:C:188:ARG:NH2	2.51	0.44
5:D:125:TRP:CG	5:D:160:LYS:HB3	2.53	0.44
9:L:101:ILE:HG22	9:L:105:ILE:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:49:VAL:HG13	11:O:81:ARG:HG3	1.99	0.44
29:H:4:ILE:HD11	29:H:51:ARG:HH22	1.82	0.44
29:H:135:HIS:CE1	29:H:137:GLU:HG2	2.53	0.44
1:A:128:C:H2'	1:A:129:C:C6	2.52	0.44
1:A:638:G:H2'	1:A:639:U:H6	1.82	0.44
1:A:656:G:H2'	1:A:657:U:C6	2.52	0.44
1:A:790:U:N3	1:A:794:A:O2'	2.51	0.44
1:A:963:U:H2'	1:A:964:C:C6	2.52	0.44
1:A:1576:U:H2'	1:A:1577:C:C6	2.53	0.44
4:C:29:PHE:CE2	4:C:32:LEU:HD23	2.53	0.44
4:C:224:MET:CG	4:C:225:ASN:H	2.27	0.44
7:G:106:LEU:HD23	7:G:151:ARG:CB	2.45	0.44
26:K:22:ILE:HG22	26:K:40:LYS:O	2.18	0.44
28:6:80:VAL:O	28:6:87:VAL:HG12	2.18	0.44
28:6:84:ASP:OD1	28:6:84:ASP:N	2.51	0.44
1:A:571:U:H3'	13:R:80:ARG:NH2	2.32	0.44
1:A:690:G:H2'	1:A:691:C:C6	2.53	0.44
1:A:998:C:P	12:Q:91:ARG:HH12	2.41	0.44
1:A:1494:A:H2'	1:A:1495:A:C8	2.52	0.44
1:A:2081:U:H2'	1:A:2082:A:C8	2.48	0.44
8:J:57:LEU:HD21	8:J:130:HIS:HB3	2.00	0.44
12:Q:106:THR:O	12:Q:109:VAL:HG22	2.18	0.44
13:R:98:ILE:HG13	13:R:100:GLY:H	1.82	0.44
15:T:31:VAL:HG13	15:T:84:TYR:HE1	1.82	0.44
20:Y:39:GLN:OE1	20:Y:41:HIS:ND1	2.50	0.44
1:A:779:U:O2	1:A:785:G:O6	2.36	0.44
1:A:991:C:H5'	1:A:1185:G:H2'	2.00	0.44
1:A:1028:A:H2'	1:A:1029:A:C8	2.53	0.44
1:A:1048:A:H1'	1:A:1112:G:H21	1.81	0.44
1:A:1365:A:P	19:X:27:ARG:HH22	2.41	0.44
1:A:1366:A:H2'	1:A:1367:A:O4'	2.18	0.44
1:A:1496:A:H2'	1:A:1498:C:C5	2.53	0.44
1:A:1806:C:H1'	4:C:43:ASN:HD21	1.83	0.44
3:9P1:2:LYS:HB2	7:G:176:LYS:H	1.82	0.44
11:O:17:LYS:HD2	11:O:17:LYS:HA	1.85	0.44
13:R:40:MET:O	13:R:41:ILE:HD13	2.18	0.44
1:A:1853:A:N3	1:A:2233:U:O2'	2.42	0.43
1:A:2615:U:H2'	1:A:2616:C:H6	1.83	0.43
1:A:2687:U:H2'	1:A:2688:G:O4'	2.18	0.43
1:A:2875:C:H2'	1:A:2876:G:H8	1.83	0.43
2:B:19:C:H2'	2:B:20:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:C:H2'	2:B:94:A:C8	2.52	0.43
3:9P1:25:ARG:HG2	3:9P1:26:GLU:O	2.16	0.43
3:9P1:239:ARG:NH2	3:9P1:335:ASN:O	2.44	0.43
3:9P1:252:GLY:HA2	25:I:20:SER:HB3	1.99	0.43
5:D:52:THR:HG22	5:D:80:TRP:HZ3	1.83	0.43
9:L:77:ILE:HG21	9:L:82:LEU:HD12	2.00	0.43
18:W:71:LYS:HD2	18:W:71:LYS:HA	1.78	0.43
28:6:20:GLN:OE1	28:6:20:GLN:N	2.51	0.43
29:H:22:LYS:HD2	29:H:23:ALA:N	2.32	0.43
1:A:291:G:N1	1:A:350:G:N7	2.65	0.43
1:A:811:U:N3	1:A:1250:G:OP1	2.51	0.43
1:A:1954:G:O2'	1:A:1956:U:O4	2.27	0.43
1:A:2034:U:H2'	1:A:2035:G:C8	2.53	0.43
1:A:2443:C:H2'	1:A:2444:G:C8	2.53	0.43
1:A:2650:U:H2'	1:A:2651:C:H6	1.82	0.43
1:A:2851:A:N3	10:N:61:ALA:HB2	2.33	0.43
2:B:28:C:H2'	2:B:29:A:C8	2.53	0.43
2:B:38:C:H2'	2:B:39:A:C8	2.53	0.43
7:G:93:TYR:HA	7:G:105:SER:O	2.19	0.43
30:F:107:VAL:CG1	30:F:108:PRO:HD3	2.48	0.43
1:A:684:G:O3'	1:A:788:A:N6	2.51	0.43
1:A:1130:U:C2	1:A:2025:C:H5'	2.53	0.43
1:A:1341:G:C2	15:T:84:TYR:HD2	2.36	0.43
1:A:1438:U:H2'	1:A:1439:A:C8	2.53	0.43
1:A:1720:U:H2'	1:A:1721:G:O4'	2.17	0.43
1:A:1825:U:C2	1:A:1826:G:C8	3.05	0.43
1:A:1873:G:H2'	1:A:1874:C:C6	2.54	0.43
1:A:2395:C:H2'	1:A:2396:G:C8	2.53	0.43
1:A:2555:U:N3	3:9P1:76:ARG:O	2.45	0.43
1:A:2710:C:H2'	1:A:2711:A:C8	2.54	0.43
1:A:2889:C:H2'	1:A:2890:G:O4'	2.19	0.43
5:D:176:ASP:HB3	5:D:190:LYS:HB3	2.01	0.43
23:1:37:LYS:HB2	23:1:48:TYR:CE2	2.53	0.43
26:K:21:CYS:HA	26:K:41:ILE:HA	2.00	0.43
27:P:70:GLU:OE2	27:P:100:ARG:NH1	2.32	0.43
30:F:101:ARG:HH11	30:F:138:PRO:HD2	1.84	0.43
1:A:721:A:H2'	1:A:722:A:H8	1.82	0.43
1:A:743:A:H2'	1:A:744:U:C6	2.53	0.43
1:A:807:U:H2'	1:A:808:G:C8	2.52	0.43
1:A:954:G:H21	1:A:2274:A:H2	1.66	0.43
1:A:969:G:H2'	1:A:970:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1215:G:H1	1:A:1234:U:H3	1.65	0.43
1:A:1614:A:H61	14:S:88:ARG:H	1.66	0.43
3:9P1:247:ILE:H	3:9P1:284:LYS:HE2	1.84	0.43
4:C:79:ARG:HE	4:C:92:LEU:HD23	1.83	0.43
4:C:181:ARG:NH2	4:C:265:PHE:HB3	2.33	0.43
6:E:29:HIS:HA	9:L:6:LEU:HD21	2.00	0.43
9:L:33:ARG:HD3	9:L:40:SER:HA	2.00	0.43
9:L:136:GLU:OE1	9:L:136:GLU:N	2.43	0.43
14:S:17:VAL:HG23	14:S:76:VAL:HG11	1.99	0.43
26:K:38:ILE:HG13	26:K:112:PHE:HZ	1.83	0.43
1:A:195:A:H4'	9:L:47:ARG:HH22	1.83	0.43
1:A:1279:G:H2'	1:A:1280:G:H8	1.83	0.43
1:A:1324:G:H1'	1:A:1616:A:N6	2.34	0.43
1:A:1394:U:H5'	1:A:1603:A:H4'	2.00	0.43
1:A:2215:C:H2'	1:A:2216:G:H8	1.82	0.43
1:A:2338:C:H2'	1:A:2339:C:C6	2.54	0.43
1:A:2899:A:H2'	1:A:2900:A:C8	2.53	0.43
17:V:79:ARG:HE	17:V:80:HIS:H	1.66	0.43
28:6:43:THR:H	28:6:47:HIS:HE1	1.66	0.43
1:A:483:A:N3	16:U:57:ILE:HD11	2.33	0.43
1:A:1058:U:N3	1:A:1059:G:O6	2.51	0.43
1:A:1687:G:H21	1:A:1701:A:H62	1.66	0.43
1:A:2747:G:H5''	7:G:69:ALA:HB1	2.00	0.43
1:A:2875:C:H2'	1:A:2876:G:C8	2.54	0.43
2:B:5:U:H2'	2:B:6:G:C8	2.54	0.43
2:B:114:C:H2'	2:B:115:A:C8	2.53	0.43
4:C:28:PRO:HG2	4:C:33:LEU:HD11	2.00	0.43
6:E:100:MET:N	6:E:100:MET:HE2	2.34	0.43
7:G:39:ALA:HA	7:G:54:ARG:NH1	2.34	0.43
9:L:127:VAL:HG11	9:L:142:ILE:HD13	2.01	0.43
29:H:129:GLU:HG2	29:H:143:ILE:HG22	2.00	0.43
30:F:46:LYS:HA	30:F:46:LYS:HE2	2.01	0.43
30:F:129:MET:SD	30:F:131:VAL:HG13	2.59	0.43
1:A:372:G:N2	1:A:401:A:OP2	2.36	0.43
1:A:478:A:N6	1:A:500:G:O2'	2.48	0.43
1:A:1316:U:H2'	1:A:1317:G:H8	1.84	0.43
1:A:1571:A:H2'	1:A:1572:A:C8	2.54	0.43
1:A:2292:U:H2'	1:A:2293:G:C8	2.53	0.43
1:A:2320:U:HO2'	1:A:2322:A:N6	2.16	0.43
1:A:2704:C:H2'	1:A:2705:A:O4'	2.19	0.43
1:A:2863:C:H2'	1:A:2864:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:48:THR:HG22	6:E:86:ALA:HB3	2.00	0.43
6:E:49:ARG:HA	6:E:82:GLY:HA3	2.00	0.43
7:G:59:ASP:N	7:G:59:ASP:OD1	2.51	0.43
13:R:55:ASP:OD1	13:R:55:ASP:N	2.49	0.43
25:I:16:MET:SD	25:I:16:MET:N	2.73	0.43
1:A:360:U:H2'	1:A:361:G:O4'	2.19	0.43
1:A:418:C:H2'	1:A:419:U:H6	1.83	0.43
1:A:860:U:H2'	1:A:861:A:C8	2.49	0.43
1:A:1341:G:N3	15:T:84:TYR:HD2	2.15	0.43
1:A:1730:C:O2	1:A:1731:G:N1	2.52	0.43
1:A:1797:G:O2'	4:C:256:THR:OG1	2.36	0.43
1:A:1917:U:H2'	1:A:1918:A:O4'	2.18	0.43
1:A:2307:G:H4'	1:A:2308:G:O4'	2.18	0.43
1:A:2637:U:H5''	5:D:83:ARG:HH22	1.84	0.43
2:B:62:C:H2'	2:B:63:C:H6	1.83	0.43
4:C:132:ARG:HH12	29:H:123:ARG:HG2	1.84	0.43
6:E:105:LEU:HD12	6:E:200:LEU:HD21	2.01	0.43
7:G:29:ASN:HB2	7:G:78:VAL:HA	1.99	0.43
17:V:46:LYS:O	17:V:50:MET:HG3	2.19	0.43
20:Y:18:LEU:HD11	20:Y:22:LEU:HD22	2.00	0.43
1:A:596:U:H2'	1:A:597:G:H8	1.84	0.43
1:A:1531:C:H2'	1:A:1532:A:C8	2.54	0.43
1:A:1680:U:H2'	1:A:1681:G:O4'	2.19	0.43
1:A:1747:U:H2'	1:A:1748:C:C6	2.54	0.43
1:A:1796:U:H2'	1:A:1797:G:H8	1.83	0.43
1:A:2243:U:H2'	1:A:2244:U:C6	2.54	0.43
1:A:2347:C:H2'	1:A:2348:U:C6	2.54	0.43
1:A:2347:C:H2'	1:A:2348:U:H6	1.84	0.43
1:A:2721:A:C4	1:A:2722:G:C8	3.07	0.43
5:D:55:LYS:HD3	5:D:60:VAL:HG22	2.00	0.43
8:J:60:ASP:OD1	8:J:60:ASP:N	2.51	0.43
9:L:76:GLU:OE2	9:L:78:ARG:HG3	2.18	0.43
1:A:214:G:H1'	1:A:217:A:H5'	2.00	0.43
1:A:239:C:N3	1:A:259:G:N1	2.66	0.43
1:A:413:C:H2'	1:A:414:C:C6	2.54	0.43
1:A:1282:U:H3	1:A:1286:A:H62	1.65	0.43
1:A:1341:G:C2	1:A:1398:C:H4'	2.54	0.43
1:A:1444:G:H2'	1:A:1445:G:C8	2.52	0.43
1:A:1794:A:H2'	1:A:1795:C:H6	1.83	0.43
1:A:1967:C:H2'	1:A:1968:G:O4'	2.19	0.43
1:A:1993:U:H4'	5:D:133:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2036:C:H2'	1:A:2037:A:C8	2.54	0.43
1:A:2062:A:H3'	1:A:2063:C:C5'	2.49	0.43
1:A:2523:G:O2'	1:A:2764:A:O2'	2.32	0.43
1:A:2537:U:H2'	1:A:2538:C:C6	2.54	0.43
1:A:2545:G:H2'	1:A:2546:U:O4'	2.19	0.43
1:A:2660:A:H1'	3:9P1:182:ALA:HB2	2.00	0.43
2:B:113:C:O2'	11:O:47:VAL:HG22	2.19	0.43
12:Q:48:ASP:HA	12:Q:51:GLN:HB3	2.01	0.43
16:U:65:GLN:HB2	16:U:68:ASN:ND2	2.34	0.43
28:6:47:HIS:O	28:6:51:ILE:HG12	2.18	0.43
1:A:-4:U:H2'	1:A:-3:G:C8	2.53	0.42
1:A:669:G:C2	1:A:801:G:C6	3.07	0.42
1:A:1045:C:O2	1:A:1047:G:N1	2.52	0.42
1:A:1528:A:OP2	1:A:1543:G:N2	2.41	0.42
1:A:1818:U:OP2	4:C:155:ARG:HG3	2.18	0.42
1:A:2801:G:H2'	1:A:2802:G:H8	1.83	0.42
1:A:2815:C:H2'	1:A:2816:G:C8	2.54	0.42
2:B:47:C:H2'	2:B:48:U:O4'	2.19	0.42
6:E:147:LEU:HB2	6:E:183:PHE:HD2	1.84	0.42
29:H:10:ALA:O	29:H:12:LEU:N	2.41	0.42
31:b:11:GLU:HG3	31:b:25:ARG:HD2	2.01	0.42
1:A:414:C:H2'	1:A:415:A:H8	1.83	0.42
1:A:488:G:N2	1:A:491:G:H5''	2.34	0.42
1:A:1585:C:H2'	1:A:1586:A:O4'	2.19	0.42
1:A:1670:C:H2'	1:A:1671:U:O4'	2.19	0.42
1:A:1822:C:H2'	1:A:1823:G:H8	1.82	0.42
1:A:2231:U:H2'	1:A:2232:C:C6	2.53	0.42
1:A:2602:A:C2	3:9P1:137:THR:HG23	2.54	0.42
1:A:2603:G:H1'	3:9P1:133:SER:HB3	2.01	0.42
1:A:2717:C:H2'	1:A:2718:G:O4'	2.19	0.42
25:I:33:ASN:OD1	25:I:34:ILE:N	2.52	0.42
1:A:624:C:H2'	1:A:625:G:C8	2.54	0.42
1:A:666:A:H2'	1:A:667:U:H6	1.84	0.42
1:A:1321:A:H2'	1:A:1322:A:H5'	2.02	0.42
1:A:1333:G:C2	1:A:1334:G:N7	2.87	0.42
1:A:1431:A:H2'	1:A:1432:G:C8	2.55	0.42
1:A:1912:A:N7	1:A:1917:U:O4	2.53	0.42
2:B:37:C:O2	11:O:100:HIS:ND1	2.51	0.42
3:9P1:163:GLY:O	3:9P1:164:MET:HE2	2.19	0.42
8:J:32:LEU:HD22	8:J:54:ILE:HG21	2.01	0.42
10:N:96:ARG:HH11	10:N:116:VAL:HG13	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:18:GLN:OE1	13:R:18:GLN:N	2.52	0.42
1:A:1229:C:H2'	1:A:1230:A:C8	2.54	0.42
1:A:1280:G:H2'	1:A:1281:G:H8	1.83	0.42
1:A:1873:G:H2'	1:A:1874:C:H6	1.85	0.42
4:C:255:LYS:HE3	4:C:257:ARG:HB3	2.00	0.42
5:D:200:ASP:OD1	5:D:200:ASP:N	2.51	0.42
7:G:53:PRO:HG3	7:G:61:TRP:HD1	1.84	0.42
7:G:94:ARG:HB2	7:G:105:SER:HB3	2.02	0.42
8:J:110:PRO:O	8:J:115:GLY:HA3	2.20	0.42
1:A:549:G:H5''	1:A:550:C:C6	2.54	0.42
1:A:1476:U:H2'	1:A:1477:A:H8	1.83	0.42
1:A:1987:A:H2'	1:A:1988:G:C8	2.52	0.42
1:A:2241:A:H2'	1:A:2242:G:C8	2.55	0.42
1:A:2667:C:H1'	7:G:108:PHE:HD1	1.85	0.42
10:N:55:ALA:HA	10:N:80:PHE:CE1	2.54	0.42
18:W:24:GLY:HA2	18:W:62:LYS:HD3	2.01	0.42
23:1:33:LEU:H	23:1:51:ALA:HB3	1.85	0.42
25:I:94:LYS:HA	25:I:94:LYS:HD3	1.86	0.42
26:K:41:ILE:HD11	26:K:86:LEU:HD22	2.00	0.42
1:A:1406:U:H2'	1:A:1407:G:C8	2.54	0.42
1:A:1424:G:O6	1:A:1575:C:N4	2.53	0.42
1:A:1724:G:O6	1:A:1737:G:N2	2.49	0.42
1:A:2245:U:H5''	1:A:2246:G:H5'	2.01	0.42
1:A:2306:C:C4	30:F:150:GLY:HA3	2.55	0.42
3:9P1:171:GLY:HA3	3:9P1:283:ASN:ND2	2.34	0.42
3:9P1:256:VAL:HG11	3:9P1:300:ILE:HA	2.01	0.42
4:C:224:MET:HE2	4:C:228:ASP:HB2	2.01	0.42
23:1:49:LYS:O	23:1:50:GLU:HG3	2.20	0.42
27:P:13:LYS:HB2	27:P:13:LYS:HE3	1.84	0.42
29:H:94:ILE:HG23	29:H:98:ASP:HB2	2.01	0.42
1:A:154:U:H2'	1:A:155:A:C8	2.53	0.42
1:A:308:G:N2	1:A:477:A:N7	2.67	0.42
1:A:475:C:H2'	1:A:476:G:O4'	2.20	0.42
1:A:511:U:H4'	1:A:1235:G:H4'	2.02	0.42
1:A:1502:A:C2	1:A:1503:A:C8	3.08	0.42
1:A:1942:C:P	1:A:1943:U:H2'	2.59	0.42
1:A:2000:C:OP1	10:N:5:LYS:NZ	2.51	0.42
1:A:2131:U:H1'	1:A:2158:A:H61	1.85	0.42
1:A:2148:G:H2'	1:A:2149:U:C6	2.54	0.42
1:A:2313:C:H2'	1:A:2314:A:H8	1.83	0.42
1:A:2416:C:C2	1:A:2417:C:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:C:H2'	2:B:119:A:C8	2.55	0.42
3:9P1:18:ASN:HB2	3:9P1:72:ASN:OD1	2.20	0.42
3:9P1:164:MET:N	3:9P1:212:ALA:O	2.52	0.42
5:D:169:ARG:HH12	5:D:202:ILE:HD11	1.84	0.42
8:J:81:ILE:HG23	8:J:82:GLY:N	2.34	0.42
27:P:47:ILE:HD13	27:P:61:ARG:HD3	2.01	0.42
29:H:125:THR:HA	29:H:146:VAL:HG23	2.02	0.42
1:A:36:G:N3	1:A:450:G:O2'	2.53	0.42
1:A:481:G:N1	1:A:507:A:H1'	2.35	0.42
1:A:1321:A:C2'	1:A:1322:A:H5'	2.50	0.42
1:A:1538:G:H2'	1:A:1539:U:H6	1.85	0.42
1:A:1684:G:O6	1:A:1705:A:N6	2.52	0.42
1:A:2064:C:H2'	1:A:2065:C:C6	2.55	0.42
1:A:2228:G:H2'	1:A:2229:U:C6	2.53	0.42
1:A:2529:G:H4'	7:G:174:LYS:HD3	2.01	0.42
5:D:27:ILE:HD12	5:D:201:LEU:HD11	2.02	0.42
9:L:93:ASN:C	9:L:95:LEU:H	2.28	0.42
10:N:8:ARG:NH1	10:N:42:LYS:HD3	2.35	0.42
12:Q:89:ILE:HG22	12:Q:94:LEU:HG	2.01	0.42
29:H:22:LYS:HZ1	29:H:24:GLY:HA3	1.85	0.42
1:A:418:C:H2'	1:A:419:U:C6	2.55	0.42
1:A:765:C:H2'	1:A:766:U:C6	2.55	0.42
1:A:1105:U:H2'	1:A:1106:G:H8	1.85	0.42
1:A:1278:C:H5''	10:N:34:ILE:CD1	2.50	0.42
1:A:1335:C:H2'	1:A:1336:A:C8	2.55	0.42
1:A:1389:G:H2'	1:A:1390:U:C6	2.55	0.42
1:A:1418:G:O6	1:A:1578:U:H5''	2.20	0.42
1:A:1590:A:H2'	1:A:1591:A:H8	1.84	0.42
1:A:1835:G:H1'	1:A:1931:U:H1'	2.02	0.42
1:A:2192:U:H2'	1:A:2193:G:C8	2.55	0.42
1:A:2529:G:H5'	7:G:174:LYS:N	2.35	0.42
1:A:2720:U:C2	1:A:2721:A:C8	3.08	0.42
3:9P1:94:THR:HG21	3:9P1:154:LEU:HD23	2.01	0.42
4:C:250:GLN:OE1	4:C:254:LYS:HB2	2.18	0.42
5:D:27:ILE:HB	5:D:187:LEU:HB3	2.02	0.42
5:D:46:ARG:HH22	5:D:86:GLU:HA	1.84	0.42
5:D:151:THR:OG1	5:D:152:PRO:HD3	2.20	0.42
10:N:69:ARG:C	10:N:71:ARG:H	2.28	0.42
16:U:61:GLU:N	16:U:61:GLU:OE2	2.53	0.42
1:A:452:G:C8	6:E:53:THR:HG21	2.55	0.42
1:A:639:U:H2'	1:A:640:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1286:A:H1'	1:A:1288:G:P	2.60	0.42
1:A:1385:A:H1'	1:A:1386:C:C6	2.55	0.42
1:A:2287:A:C5	1:A:2289:G:C8	3.07	0.42
1:A:2841:C:H2'	1:A:2842:G:C8	2.54	0.42
2:B:104:A:H1'	17:V:31:TYR:HE2	1.85	0.42
8:J:7:LYS:O	8:J:11:VAL:HG13	2.20	0.42
16:U:14:THR:OG1	16:U:68:ASN:OD1	2.37	0.42
26:K:76:VAL:H	27:P:72:VAL:CG2	2.33	0.42
28:6:13:LYS:HD2	28:6:58:GLU:HG3	2.02	0.42
1:A:570:G:N2	1:A:2030:A:O4'	2.53	0.41
1:A:720:U:H2'	1:A:721:A:H8	1.85	0.41
1:A:1257:C:C2	1:A:1258:U:C5	3.08	0.41
1:A:1430:G:H2'	1:A:1431:A:C8	2.55	0.41
1:A:1929:G:N2	1:A:1929:G:OP2	2.53	0.41
1:A:2326:C:O2'	1:A:2327:A:H5''	2.20	0.41
1:A:2576:G:O2'	1:A:2579:C:OP2	2.26	0.41
1:A:2773:C:H2'	1:A:2774:C:C6	2.55	0.41
3:9P1:306:TRP:CZ2	3:9P1:308:ASP:HB3	2.55	0.41
6:E:75:SER:HB2	6:E:78:TRP:CD1	2.55	0.41
10:N:95:THR:HA	10:N:114:GLU:O	2.20	0.41
15:T:80:TRP:CZ3	15:T:82:LYS:HG2	2.55	0.41
26:K:71:ARG:HB2	26:K:75:SER:HB2	2.02	0.41
1:A:628:G:H2'	1:A:629:G:H8	1.85	0.41
1:A:748:G:O6	1:A:751:A:H5'	2.21	0.41
1:A:771:G:OP2	24:2:11:LYS:NZ	2.48	0.41
1:A:1063:G:N2	25:I:135:MET:HA	2.29	0.41
1:A:1167:C:H2'	1:A:1168:G:C8	2.55	0.41
1:A:1270:C:N4	1:A:1648:U:O4	2.53	0.41
1:A:1442:U:H2'	1:A:1443:U:H6	1.85	0.41
1:A:1759:A:H1'	1:A:2711:A:C2	2.54	0.41
1:A:1790:C:O2'	4:C:207:ALA:HB2	2.20	0.41
1:A:1820:U:C2	4:C:200:MET:HE1	2.56	0.41
4:C:99:GLU:OE1	4:C:101:ARG:NE	2.51	0.41
4:C:198:GLU:OE2	4:C:198:GLU:N	2.42	0.41
13:R:68:ARG:NH1	13:R:90:ARG:HH21	2.18	0.41
1:A:-1:A:H2'	1:A:0:A:H8	1.85	0.41
1:A:518:G:H2'	1:A:519:U:C6	2.55	0.41
1:A:579:G:C5	1:A:1262:A:N6	2.88	0.41
1:A:623:C:H2'	1:A:624:C:C6	2.55	0.41
1:A:1100:C:H2'	1:A:1101:U:C6	2.55	0.41
1:A:1201:U:H2'	1:A:1202:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1668:A:H1'	1:A:1670:C:H41	1.86	0.41
1:A:1712:U:OP2	1:A:1713:A:O2'	2.36	0.41
1:A:1954:G:H5''	1:A:2550:G:H21	1.85	0.41
1:A:2097:A:H2'	1:A:2098:U:C6	2.56	0.41
1:A:2487:G:C2	1:A:2488:G:N7	2.88	0.41
1:A:2559:C:H2'	1:A:2560:A:C8	2.53	0.41
2:B:32:U:H2'	2:B:33:G:C8	2.55	0.41
4:C:131:MET:HA	4:C:134:ILE:HD12	2.02	0.41
7:G:94:ARG:HA	7:G:127:GLN:NE2	2.35	0.41
11:O:15:ARG:HH12	11:O:25:ARG:NH2	2.18	0.41
11:O:87:ILE:HG22	11:O:90:VAL:HB	2.02	0.41
15:T:37:ASP:OD1	15:T:37:ASP:N	2.50	0.41
23:1:26:LYS:HB3	23:1:27:ARG:NH2	2.35	0.41
30:F:28:PRO:HB2	30:F:168:LEU:HD22	2.03	0.41
1:A:67:U:C2	1:A:68:G:C8	3.08	0.41
1:A:379:G:N1	1:A:396:G:C6	2.89	0.41
1:A:660:C:C2	1:A:661:A:C8	3.09	0.41
1:A:690:G:H21	4:C:42:ARG:HH22	1.67	0.41
1:A:924:G:H2'	1:A:925:A:H8	1.85	0.41
1:A:1130:U:N3	1:A:2025:C:H5'	2.35	0.41
1:A:1295:C:H2'	1:A:1296:G:C8	2.55	0.41
1:A:1398:C:H2'	1:A:1399:C:C6	2.56	0.41
1:A:1771:C:H2'	1:A:1772:A:C8	2.55	0.41
1:A:1794:A:H2'	1:A:1795:C:C6	2.55	0.41
1:A:2151:U:H2'	1:A:2152:G:C8	2.54	0.41
1:A:2306:C:H3'	1:A:2307:G:C8	2.55	0.41
1:A:2326:C:HO2'	1:A:2327:A:H8	1.69	0.41
1:A:2737:G:H2'	1:A:2738:A:H8	1.84	0.41
1:A:2744:G:H21	7:G:142:GLN:CD	2.28	0.41
3:9P1:49:ALA:HB3	3:9P1:112:GLY:H	1.85	0.41
12:Q:57:ARG:NH1	12:Q:57:ARG:HG2	2.34	0.41
15:T:10:VAL:O	15:T:35:ALA:N	2.54	0.41
28:6:54:HIS:O	28:6:58:GLU:HG2	2.20	0.41
29:H:115:VAL:HG22	29:H:132:PHE:CE1	2.56	0.41
1:A:242:G:O2'	1:A:254:G:O6	2.38	0.41
1:A:441:U:H2'	1:A:442:G:C8	2.54	0.41
1:A:662:G:C2	1:A:663:G:C8	3.08	0.41
1:A:1039:A:N1	1:A:1116:G:N2	2.53	0.41
1:A:1174:U:O2'	1:A:1176:U:O2	2.29	0.41
1:A:1316:U:H2'	1:A:1317:G:C8	2.56	0.41
1:A:1695:G:H1'	4:C:7:PRO:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1826:G:H2'	1:A:1827:U:C6	2.55	0.41
1:A:2066:C:H2'	1:A:2067:G:C8	2.55	0.41
1:A:2514:U:H2'	1:A:2515:C:H6	1.85	0.41
1:A:2722:G:O2'	10:N:3:HIS:O	2.35	0.41
1:A:2801:G:H2'	1:A:2802:G:C8	2.56	0.41
3:9P1:46:TRP:CE2	3:9P1:116:LEU:HD13	2.55	0.41
7:G:104:LEU:HB3	7:G:106:LEU:HD13	2.00	0.41
19:X:73:ARG:HE	19:X:75:GLU:HG3	1.84	0.41
26:K:19:VAL:HB	26:K:41:ILE:HD12	2.02	0.41
30:F:101:ARG:HH12	30:F:137:PHE:HD2	1.67	0.41
30:F:116:LEU:HD23	30:F:116:LEU:H	1.86	0.41
1:A:31:C:H4'	1:A:1238:G:H4'	2.02	0.41
1:A:287:G:H2'	1:A:288:U:C6	2.56	0.41
1:A:329:G:O6	16:U:16:LYS:HG2	2.21	0.41
1:A:520:G:H2'	1:A:521:U:C6	2.55	0.41
1:A:743:A:H2'	1:A:744:U:H6	1.85	0.41
1:A:851:C:H2'	1:A:852:U:H6	1.85	0.41
1:A:857:G:H4'	18:W:41:PHE:CZ	2.55	0.41
1:A:929:U:H4'	21:Z:37:ARG:NH2	2.36	0.41
1:A:1790:C:O3'	1:A:1791:A:H8	2.03	0.41
1:A:1824:G:H2'	1:A:1825:U:H6	1.86	0.41
1:A:2014:A:O2'	1:A:2015:A:O4'	2.26	0.41
1:A:2230:G:H2'	1:A:2231:U:C6	2.55	0.41
1:A:2387:U:H1'	18:W:37:ARG:CZ	2.50	0.41
1:A:2636:C:H2'	1:A:2637:U:C6	2.56	0.41
4:C:96:LYS:HE2	4:C:96:LYS:HB2	1.78	0.41
7:G:104:LEU:HD12	7:G:106:LEU:HD11	2.01	0.41
9:L:62:PRO:HG2	9:L:64:PHE:CE1	2.55	0.41
13:R:15:SER:OG	13:R:18:GLN:NE2	2.34	0.41
1:A:1019:U:H3	1:A:1142:A:H62	1.67	0.41
1:A:1252:G:N2	12:Q:32:ARG:O	2.54	0.41
1:A:1262:A:C5	1:A:1263:U:C4	3.09	0.41
1:A:1510:G:H2'	1:A:1511:G:C8	2.56	0.41
1:A:2195:U:H2'	1:A:2196:C:H6	1.85	0.41
1:A:2347:C:H1'	23:1:5:ARG:HH22	1.86	0.41
2:B:72:G:H21	2:B:104:A:H62	1.69	0.41
2:B:112:G:H2'	2:B:113:C:H6	1.86	0.41
6:E:147:LEU:HB3	6:E:186:VAL:HG22	2.02	0.41
12:Q:56:PHE:HB3	12:Q:60:TRP:CZ2	2.56	0.41
14:S:7:HIS:O	14:S:103:ILE:N	2.53	0.41
17:V:79:ARG:HH22	17:V:85:LYS:N	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:6:11:ILE:HD11	28:6:22:ILE:HD12	2.02	0.41
28:6:91:GLN:HB2	28:6:94:SER:HB2	2.01	0.41
1:A:300:A:O2'	1:A:318:C:O2	2.36	0.41
1:A:314:C:H2'	1:A:315:G:C8	2.56	0.41
1:A:324:A:OP2	1:A:1205:A:N6	2.53	0.41
1:A:581:C:C2	1:A:582:A:C8	3.09	0.41
1:A:671:C:H2'	1:A:672:C:C6	2.54	0.41
1:A:1791:A:O2'	4:C:203:VAL:O	2.34	0.41
1:A:1814:G:OP2	1:A:1815:A:O2'	2.32	0.41
1:A:1834:U:H5''	1:A:1835:G:H5'	2.02	0.41
1:A:2039:U:H2'	1:A:2040:G:H8	1.85	0.41
1:A:2312:U:OP1	30:F:70:ARG:HG3	2.21	0.41
1:A:2511:U:H5''	5:D:128:ARG:CB	2.50	0.41
8:J:45:THR:HG22	8:J:47:HIS:H	1.86	0.41
13:R:68:ARG:CZ	13:R:90:ARG:HH21	2.33	0.41
16:U:3:LYS:HD3	16:U:82:VAL:HB	2.03	0.41
1:A:-2:U:H2'	1:A:-1:A:C8	2.56	0.41
1:A:1:G:H2'	1:A:2:G:H8	1.84	0.41
1:A:96:C:H2'	1:A:97:C:H6	1.85	0.41
1:A:596:U:H2'	1:A:597:G:C8	2.56	0.41
1:A:638:G:H2'	1:A:639:U:C6	2.56	0.41
1:A:640:C:H2'	1:A:641:U:C6	2.56	0.41
1:A:664:G:H2'	1:A:665:U:C6	2.55	0.41
1:A:790:U:H3	1:A:795:C:H5'	1.86	0.41
1:A:996:A:H2'	1:A:997:G:C8	2.56	0.41
1:A:1346:G:N1	1:A:1601:G:C6	2.89	0.41
1:A:1352:U:H1'	1:A:1570:A:C2	2.55	0.41
1:A:1372:U:H2'	1:A:1373:A:C8	2.56	0.41
1:A:1683:U:H2'	1:A:1684:G:H8	1.86	0.41
1:A:1886:U:H2'	1:A:1887:C:H6	1.86	0.41
1:A:2241:A:H2'	1:A:2242:G:H8	1.85	0.41
1:A:2290:G:H2'	1:A:2291:U:H6	1.85	0.41
1:A:2315:G:H2'	1:A:2316:G:H8	1.84	0.41
1:A:2379:G:H2'	1:A:2380:C:C6	2.56	0.41
1:A:2411:A:H2'	1:A:2412:A:H8	1.86	0.41
1:A:2414:G:N3	1:A:2415:G:C8	2.89	0.41
1:A:2649:C:H2'	1:A:2650:U:H6	1.86	0.41
1:A:2650:U:H2'	1:A:2651:C:C6	2.56	0.41
1:A:2748:A:H5'	7:G:3:VAL:HG21	2.03	0.41
1:A:2830:C:OP2	5:D:59:ARG:HD2	2.20	0.41
4:C:77:VAL:HB	4:C:93:VAL:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:196:ASN:OD1	4:C:196:ASN:N	2.54	0.41
6:E:49:ARG:HD3	6:E:76:PRO:HD3	2.03	0.41
7:G:120:ILE:HD11	7:G:139:VAL:HG23	2.03	0.41
8:J:58:ASN:ND2	8:J:128:ASN:OD1	2.48	0.41
10:N:71:ARG:HA	10:N:71:ARG:HD2	1.78	0.41
11:O:98:GLN:OE1	11:O:98:GLN:N	2.53	0.41
11:O:103:VAL:HA	11:O:106:LEU:HD12	2.02	0.41
22:O:14:MET:HG3	22:O:14:MET:H	1.70	0.41
27:P:9:GLN:HA	27:P:9:GLN:OE1	2.20	0.41
27:P:14:GLN:H	27:P:14:GLN:CD	2.28	0.41
1:A:140:C:H4'	1:A:141:G:C2	2.56	0.41
1:A:324:A:N6	1:A:339:U:O4'	2.54	0.41
1:A:373:U:H2'	1:A:374:A:C8	2.54	0.41
1:A:636:G:H2'	9:L:111:ILE:HD11	2.03	0.41
1:A:643:A:H2'	1:A:644:A:C4	2.56	0.41
1:A:689:A:N3	1:A:779:U:O2'	2.43	0.41
1:A:764:A:OP1	4:C:206:LYS:NZ	2.54	0.41
1:A:810:U:H3	9:L:30:THR:HG23	1.86	0.41
1:A:817:C:O2'	1:A:839:U:H5''	2.21	0.41
1:A:817:C:H2'	1:A:818:G:O4'	2.20	0.41
1:A:973:A:OP2	13:R:81:LYS:NZ	2.40	0.41
1:A:1266:G:O2'	1:A:2012:G:O6	2.33	0.41
1:A:1281:G:H2'	1:A:1282:U:C6	2.56	0.41
1:A:1501:G:C2	1:A:1502:A:N7	2.90	0.41
1:A:1520:U:H2'	1:A:1521:G:O4'	2.21	0.41
1:A:2064:C:O2'	1:A:2251:G:N2	2.54	0.41
1:A:2077:A:N3	1:A:2434:A:O2'	2.46	0.41
1:A:2257:U:H2'	1:A:2258:C:C6	2.56	0.41
1:A:2261:C:H5''	18:W:15:LYS:NZ	2.36	0.41
1:A:2756:U:H4'	1:A:2757:A:OP1	2.21	0.41
18:W:29:ALA:N	18:W:60:ASP:OD1	2.52	0.41
25:I:18:ASN:HD21	25:I:27:LEU:HD21	1.85	0.41
1:A:865:C:N4	1:A:909:A:H62	2.19	0.40
1:A:922:C:H2'	1:A:923:G:H8	1.86	0.40
1:A:1139:G:H2'	1:A:1140:C:C6	2.56	0.40
1:A:1351:C:N4	1:A:1381:G:O6	2.54	0.40
1:A:1587:G:H2'	1:A:1588:G:H8	1.86	0.40
1:A:1745:A:H2'	1:A:1746:A:C8	2.56	0.40
1:A:1823:G:H2'	1:A:1824:G:H8	1.86	0.40
1:A:2304:G:N2	1:A:2312:U:H3	2.19	0.40
1:A:2643:G:H2'	1:A:2644:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2748:A:H1'	7:G:66:THR:HG22	2.02	0.40
4:C:7:PRO:HB3	4:C:13:ARG:HG3	2.03	0.40
4:C:211:ARG:HA	4:C:211:ARG:HD2	1.89	0.40
8:J:37:ARG:HH11	8:J:39:LYS:HE2	1.86	0.40
8:J:41:LYS:HZ3	8:J:43:GLU:HB2	1.85	0.40
26:K:94:PRO:CD	26:K:114:LYS:HG3	2.49	0.40
28:6:57:GLN:HG3	28:6:58:GLU:OE2	2.20	0.40
29:H:47:PHE:O	29:H:51:ARG:N	2.54	0.40
1:A:-1:A:H2'	1:A:0:A:C8	2.56	0.40
1:A:445:C:H5''	12:Q:2:ARG:HG2	2.01	0.40
1:A:462:C:H2'	1:A:463:G:C8	2.57	0.40
1:A:773:U:H1'	4:C:42:ARG:HH21	1.85	0.40
1:A:864:G:H21	1:A:866:A:N6	2.20	0.40
1:A:1595:C:H2'	1:A:1596:A:C8	2.56	0.40
1:A:1595:C:H2'	1:A:1596:A:H8	1.86	0.40
1:A:1821:A:H2'	1:A:1822:C:C6	2.56	0.40
1:A:1975:G:H2'	1:A:1976:U:O4'	2.20	0.40
1:A:2393:U:H2'	1:A:2394:C:H6	1.86	0.40
1:A:2675:A:OP1	26:K:31:ARG:NH2	2.55	0.40
1:A:2745:C:H2'	1:A:2746:U:H6	1.86	0.40
2:B:40:U:H1'	2:B:45:A:H62	1.86	0.40
3:9P1:2:LYS:NZ	7:G:174:LYS:O	2.40	0.40
4:C:251:THR:HG22	4:C:252:LYS:H	1.86	0.40
5:D:46:ARG:HH12	5:D:87:GLY:H	1.68	0.40
22:0:37:HIS:CD2	22:0:43:THR:HG22	2.56	0.40
24:2:34:ARG:CZ	24:2:39:ARG:HD2	2.52	0.40
30:F:129:MET:SD	30:F:130:GLY:N	2.95	0.40
1:A:-2:U:H2'	1:A:-1:A:H8	1.86	0.40
1:A:12:U:O2	1:A:2626:C:H4'	2.21	0.40
1:A:253:C:H2'	1:A:254:G:O4'	2.20	0.40
1:A:482:A:H4'	16:U:44:HIS:ND1	2.37	0.40
1:A:659:G:H1'	6:E:97:ASN:HD21	1.86	0.40
1:A:665:U:C2	1:A:666:A:C8	3.09	0.40
1:A:721:A:H2'	1:A:722:A:C8	2.55	0.40
1:A:843:G:O6	1:A:936:A:N6	2.55	0.40
1:A:997:G:OP1	12:Q:91:ARG:HD3	2.21	0.40
1:A:1462:C:H2'	1:A:1463:C:C6	2.56	0.40
1:A:1707:G:C8	1:A:1756:G:C5	3.10	0.40
1:A:1800:C:O2	1:A:1817:G:O6	2.40	0.40
1:A:1816:C:H3'	4:C:61:TYR:OH	2.21	0.40
1:A:1817:G:OP2	4:C:155:ARG:NH2	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1988:G:H2'	1:A:1989:G:C8	2.56	0.40
1:A:2291:U:O2	1:A:2374:C:O2'	2.39	0.40
1:A:2489:U:H2'	1:A:2490:G:C8	2.56	0.40
1:A:2564:A:C6	1:A:2647:U:H4'	2.56	0.40
1:A:2649:C:H2'	1:A:2650:U:C6	2.56	0.40
2:B:103:U:H2'	2:B:104:A:C8	2.57	0.40
2:B:106:G:H2'	2:B:107:G:O4'	2.22	0.40
3:9P1:247:ILE:HD11	3:9P1:282:PHE:CD1	2.57	0.40
4:C:29:PHE:HB3	4:C:102:TYR:OH	2.21	0.40
5:D:32:ASN:HB3	5:D:50:VAL:HG21	2.02	0.40
5:D:121:THR:HG22	5:D:162:ALA:N	2.36	0.40
10:N:53:THR:HA	10:N:56:LYS:HG2	2.02	0.40
30:F:109:ARG:NH1	31:b:35:ASP:HB2	2.37	0.40
1:A:415:A:H2'	1:A:416:U:H6	1.87	0.40
1:A:549:G:H5''	1:A:550:C:C5	2.56	0.40
1:A:851:C:H2'	1:A:852:U:C6	2.56	0.40
1:A:1635:A:H2'	1:A:1636:U:O4'	2.21	0.40
1:A:1637:A:H2'	1:A:1638:C:H6	1.84	0.40
2:B:16:G:N2	2:B:69:G:H1'	2.37	0.40
2:B:45:A:H2'	2:B:45:A:N3	2.37	0.40
2:B:71:C:H2'	2:B:72:G:O4'	2.21	0.40
3:9P1:209:PHE:HE1	3:9P1:328:VAL:HG11	1.85	0.40
4:C:15:VAL:HG22	4:C:205:GLY:HA3	2.04	0.40
4:C:267:VAL:HG12	4:C:268:ARG:HG3	2.03	0.40
6:E:4:VAL:HG22	6:E:6:LYS:H	1.86	0.40
6:E:150:THR:O	6:E:172:ALA:N	2.54	0.40
7:G:115:GLN:OE1	7:G:115:GLN:HA	2.22	0.40
9:L:29:LYS:HD3	13:R:82:HIS:ND1	2.36	0.40
27:P:21:PRO:HG3	27:P:49:ILE:HD12	2.04	0.40
31:b:20:ASN:OD1	31:b:20:ASN:N	2.55	0.40
1:A:24:G:H1'	14:S:77:ASP:HB3	2.04	0.40
1:A:819:A:OP2	1:A:1187:G:N2	2.43	0.40
1:A:1007:C:OP2	1:A:1008:A:O2'	2.33	0.40
1:A:2006:C:H4'	1:A:2048:G:H4'	2.02	0.40
1:A:2821:A:H2'	1:A:2822:G:C8	2.55	0.40
1:A:2895:G:H2'	1:A:2896:C:C6	2.57	0.40
8:J:16:TYR:HD2	8:J:140:LEU:HD22	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	9P1	336/390 (86%)	307 (91%)	28 (8%)	1 (0%)	36	65
4	C	269/273 (98%)	251 (93%)	18 (7%)	0	100	100
5	D	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
6	E	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
7	G	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
8	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
9	L	141/144 (98%)	122 (86%)	19 (14%)	0	100	100
10	N	118/127 (93%)	113 (96%)	5 (4%)	0	100	100
11	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
12	Q	115/118 (98%)	110 (96%)	5 (4%)	0	100	100
13	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
14	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
15	T	91/100 (91%)	79 (87%)	12 (13%)	0	100	100
16	U	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
17	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
18	W	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
19	X	75/78 (96%)	75 (100%)	0	0	100	100
20	Y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
21	Z	56/59 (95%)	56 (100%)	0	0	100	100
22	0	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
23	1	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
24	2	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
25	I	139/142 (98%)	113 (81%)	26 (19%)	0	100	100
26	K	120/123 (98%)	107 (89%)	13 (11%)	0	100	100
27	P	111/115 (96%)	106 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	6	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
29	H	147/149 (99%)	131 (89%)	16 (11%)	0	100	100
30	F	175/179 (98%)	160 (91%)	15 (9%)	0	100	100
31	b	45/70 (64%)	42 (93%)	3 (7%)	0	100	100
All	All	3554/3735 (95%)	3298 (93%)	255 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	9P1	192	THR

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	
3	9P1	273/321 (85%)	273 (100%)	0	100	100
4	C	216/218 (99%)	216 (100%)	0	100	100
5	D	164/164 (100%)	164 (100%)	0	100	100
6	E	165/165 (100%)	165 (100%)	0	100	100
7	G	137/138 (99%)	137 (100%)	0	100	100
8	J	116/116 (100%)	116 (100%)	0	100	100
9	L	102/103 (99%)	102 (100%)	0	100	100
10	N	100/103 (97%)	100 (100%)	0	100	100
11	O	86/87 (99%)	86 (100%)	0	100	100
12	Q	89/90 (99%)	89 (100%)	0	100	100
13	R	84/84 (100%)	84 (100%)	0	100	100
14	S	93/93 (100%)	93 (100%)	0	100	100
15	T	80/84 (95%)	80 (100%)	0	100	100
16	U	83/85 (98%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	V	78/78 (100%)	78 (100%)	0	100	100
18	W	56/63 (89%)	56 (100%)	0	100	100
19	X	67/68 (98%)	67 (100%)	0	100	100
20	Y	55/55 (100%)	55 (100%)	0	100	100
21	Z	48/49 (98%)	48 (100%)	0	100	100
22	0	47/48 (98%)	47 (100%)	0	100	100
23	1	45/49 (92%)	45 (100%)	0	100	100
24	2	38/38 (100%)	38 (100%)	0	100	100
25	I	109/110 (99%)	109 (100%)	0	100	100
26	K	103/104 (99%)	103 (100%)	0	100	100
27	P	98/100 (98%)	98 (100%)	0	100	100
28	6	88/91 (97%)	88 (100%)	0	100	100
29	H	114/114 (100%)	114 (100%)	0	100	100
30	F	148/150 (99%)	148 (100%)	0	100	100
31	b	43/62 (69%)	43 (100%)	0	100	100
All	All	2925/3030 (96%)	2925 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
4	C	133	ASN
4	C	250	GLN
5	D	94	GLN
5	D	130	GLN
5	D	134	HIS
6	E	136	GLN
6	E	195	GLN
7	G	29	ASN
7	G	127	GLN
8	J	47	HIS
9	L	104	GLN
15	T	28	ASN
16	U	68	ASN
17	V	75	GLN

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Mol	Chain	Res	Type
24	2	26	ASN
25	I	18	ASN
26	K	29	HIS
29	H	2	GLN
29	H	28	ASN
30	F	134	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2899/2919 (99%)	455 (15%)	15 (0%)
2	B	118/120 (98%)	14 (11%)	0
All	All	3017/3039 (99%)	469 (15%)	15 (0%)

All (469) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	12	U
1	A	35	G
1	A	46	G
1	A	51	G
1	A	55	G
1	A	63	A
1	A	71	A
1	A	74	A
1	A	75	G
1	A	102	U
1	A	103	A
1	A	110	G
1	A	114	U
1	A	118	A
1	A	120	U
1	A	138	U
1	A	139	U
1	A	140	C
1	A	141	G
1	A	142	A
1	A	160	A
1	A	164	C
1	A	181	A

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Mol	Chain	Res	Type
1	A	196	A
1	A	199	A
1	A	216	A
1	A	222	A
1	A	230	G
1	A	248	G
1	A	255	A
1	A	266	G
1	A	272	A
1	A	277	G
1	A	278	A
1	A	302	C
1	A	311	A
1	A	329	G
1	A	330	A
1	A	331	C
1	A	352	A
1	A	353	C
1	A	362	A
1	A	367	G
1	A	371	A
1	A	372	G
1	A	373	U
1	A	384	A
1	A	386	G
1	A	396	G
1	A	404	A
1	A	405	U
1	A	411	G
1	A	424	G
1	A	430	A
1	A	435	C
1	A	451	U
1	A	456	C
1	A	480	A
1	A	481	G
1	A	491	G
1	A	496	G
1	A	504	A
1	A	505	A
1	A	532	A
1	A	533	G

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Mol	Chain	Res	Type
1	A	544	C
1	A	546	U
1	A	547	A
1	A	548	G
1	A	549	G
1	A	550	C
1	A	563	A
1	A	572	A
1	A	573	U
1	A	586	A
1	A	588	U
1	A	603	A
1	A	613	A
1	A	614	A
1	A	615	U
1	A	616	A
1	A	621	A
1	A	627	A
1	A	631	A
1	A	637	A
1	A	644	A
1	A	645	C
1	A	647	G
1	A	654	A
1	A	655	A
1	A	668	A
1	A	686	U
1	A	726	G
1	A	730	A
1	A	747	U
1	A	748	G
1	A	751	A
1	A	764	A
1	A	775	G
1	A	776	G
1	A	782	A
1	A	784	G
1	A	785	G
1	A	789	A
1	A	792	A
1	A	805	G
1	A	812	C

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Mol	Chain	Res	Type
1	A	819	A
1	A	827	U
1	A	830	G
1	A	845	A
1	A	846	U
1	A	858	G
1	A	878	A
1	A	879	G
1	A	885	C
1	A	896	A
1	A	901	C
1	A	907	G
1	A	910	A
1	A	931	U
1	A	934	U
1	A	941	A
1	A	945	A
1	A	959	A
1	A	961	C
1	A	965	C
1	A	973	A
1	A	974	G
1	A	980	A
1	A	983	A
1	A	985	C
1	A	988	A
1	A	989	G
1	A	995	C
1	A	996	A
1	A	999	U
1	A	1009	A
1	A	1012	U
1	A	1013	C
1	A	1017	G
1	A	1022	G
1	A	1026	G
1	A	1033	U
1	A	1040	A
1	A	1046	A
1	A	1047	G
1	A	1059	G
1	A	1061	U

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Mol	Chain	Res	Type
1	A	1062	G
1	A	1063	G
1	A	1065	U
1	A	1066	U
1	A	1068	G
1	A	1070	A
1	A	1071	G
1	A	1072	C
1	A	1073	A
1	A	1074	G
1	A	1075	C
1	A	1083	U
1	A	1089	A
1	A	1092	C
1	A	1096	A
1	A	1098	A
1	A	1099	G
1	A	1104	C
1	A	1112	G
1	A	1116	G
1	A	1130	U
1	A	1132	U
1	A	1133	A
1	A	1135	C
1	A	1136	G
1	A	1142	A
1	A	1151	A
1	A	1157	G
1	A	1168	G
1	A	1170	C
1	A	1171	G
1	A	1173	U
1	A	1174	U
1	A	1175	A
1	A	1176	U
1	A	1179	G
1	A	1180	U
1	A	1181	U
1	A	1182	G
1	A	1195	G
1	A	1212	G
1	A	1225	G

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Mol	Chain	Res	Type
1	A	1236	G
1	A	1238	G
1	A	1253	A
1	A	1256	G
1	A	1262	A
1	A	1266	G
1	A	1271	G
1	A	1272	A
1	A	1300	G
1	A	1301	A
1	A	1314	C
1	A	1322	A
1	A	1325	U
1	A	1329	U
1	A	1332	G
1	A	1341	G
1	A	1345	C
1	A	1347	A
1	A	1365	A
1	A	1378	A
1	A	1379	U
1	A	1386	C
1	A	1416	G
1	A	1419	A
1	A	1420	A
1	A	1428	C
1	A	1434	A
1	A	1435	G
1	A	1437	C
1	A	1451	C
1	A	1452	G
1	A	1458	U
1	A	1482	G
1	A	1491	G
1	A	1493	C
1	A	1497	U
1	A	1504	A
1	A	1509	A
1	A	1510	G
1	A	1515	A
1	A	1523	U
1	A	1532	A

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Mol	Chain	Res	Type
1	A	1533	C
1	A	1534	U
1	A	1535	A
1	A	1555	G
1	A	1569	A
1	A	1578	U
1	A	1583	A
1	A	1585	C
1	A	1603	A
1	A	1607	C
1	A	1608	A
1	A	1619	G
1	A	1634	A
1	A	1646	C
1	A	1647	U
1	A	1648	U
1	A	1667	G
1	A	1674	G
1	A	1714	U
1	A	1715	G
1	A	1729	U
1	A	1730	C
1	A	1732	C
1	A	1736	U
1	A	1737	G
1	A	1738	G
1	A	1764	C
1	A	1773	A
1	A	1800	C
1	A	1808	A
1	A	1816	C
1	A	1820	U
1	A	1829	A
1	A	1835	G
1	A	1845	G
1	A	1870	C
1	A	1885	A
1	A	1903	G
1	A	1908	C
1	A	1909	C
1	A	1912	A
1	A	1914	C

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Mol	Chain	Res	Type
1	A	1925	C
1	A	1926	U
1	A	1929	G
1	A	1930	G
1	A	1931	U
1	A	1937	A
1	A	1938	A
1	A	1941	C
1	A	1943	U
1	A	1944	U
1	A	1955	U
1	A	1965	C
1	A	1967	C
1	A	1970	A
1	A	1972	G
1	A	1991	U
1	A	1992	G
1	A	1993	U
1	A	2022	U
1	A	2023	C
1	A	2031	A
1	A	2033	A
1	A	2036	C
1	A	2043	C
1	A	2052	A
1	A	2055	C
1	A	2059	A
1	A	2061	G
1	A	2063	C
1	A	2069	G
1	A	2072	C
1	A	2093	G
1	A	2095	A
1	A	2096	C
1	A	2102	G
1	A	2107	G
1	A	2110	G
1	A	2111	U
1	A	2112	G
1	A	2114	A
1	A	2116	G
1	A	2117	A

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Mol	Chain	Res	Type
1	A	2118	U
1	A	2119	A
1	A	2120	G
1	A	2122	U
1	A	2123	G
1	A	2126	A
1	A	2128	G
1	A	2131	U
1	A	2132	U
1	A	2133	G
1	A	2136	G
1	A	2146	C
1	A	2147	A
1	A	2148	G
1	A	2154	A
1	A	2157	G
1	A	2158	A
1	A	2159	G
1	A	2161	C
1	A	2162	G
1	A	2164	C
1	A	2165	C
1	A	2170	A
1	A	2171	A
1	A	2172	U
1	A	2173	A
1	A	2178	C
1	A	2183	A
1	A	2199	A
1	A	2200	C
1	A	2204	G
1	A	2211	A
1	A	2212	A
1	A	2225	A
1	A	2226	C
1	A	2238	G
1	A	2239	G
1	A	2252	G
1	A	2267	A
1	A	2274	A
1	A	2275	C
1	A	2278	A

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Mol	Chain	Res	Type
1	A	2283	C
1	A	2285	C
1	A	2286	G
1	A	2287	A
1	A	2288	A
1	A	2297	A
1	A	2305	U
1	A	2306	C
1	A	2319	G
1	A	2321	U
1	A	2322	A
1	A	2325	G
1	A	2333	A
1	A	2334	U
1	A	2357	G
1	A	2361	G
1	A	2376	A
1	A	2383	G
1	A	2385	C
1	A	2402	U
1	A	2406	A
1	A	2425	A
1	A	2426	A
1	A	2429	G
1	A	2430	A
1	A	2434	A
1	A	2435	A
1	A	2441	U
1	A	2448	A
1	A	2449	U
1	A	2450	A
1	A	2453	A
1	A	2456	C
1	A	2458	G
1	A	2459	A
1	A	2476	A
1	A	2491	U
1	A	2513	A
1	A	2518	A
1	A	2520	C
1	A	2529	G
1	A	2535	G

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Mol	Chain	Res	Type
1	A	2547	A
1	A	2552	U
1	A	2554	U
1	A	2564	A
1	A	2566	A
1	A	2567	G
1	A	2572	A
1	A	2573	C
1	A	2574	G
1	A	2582	G
1	A	2585	U
1	A	2586	U
1	A	2602	A
1	A	2603	G
1	A	2609	U
1	A	2610	C
1	A	2613	U
1	A	2615	U
1	A	2629	U
1	A	2642	G
1	A	2646	C
1	A	2656	U
1	A	2662	A
1	A	2681	C
1	A	2682	A
1	A	2685	G
1	A	2689	U
1	A	2690	U
1	A	2714	G
1	A	2720	U
1	A	2726	A
1	A	2729	G
1	A	2733	A
1	A	2735	G
1	A	2744	G
1	A	2748	A
1	A	2757	A
1	A	2765	A
1	A	2778	A
1	A	2780	G
1	A	2791	G
1	A	2798	U

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Mol	Chain	Res	Type
1	A	2818	U
1	A	2820	A
1	A	2833	U
1	A	2835	A
1	A	2849	U
1	A	2859	G
1	A	2867	G
1	A	2872	A
1	A	2880	C
1	A	2884	U
1	A	2886	A
2	B	9	G
2	B	15	A
2	B	24	G
2	B	35	C
2	B	36	C
2	B	37	C
2	B	41	G
2	B	42	C
2	B	44	G
2	B	51	G
2	B	53	A
2	B	90	C
2	B	99	A
2	B	109	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	271	G
1	A	404	A
1	A	987	C
1	A	1224	U
1	A	1328	A
1	A	1378	A
1	A	1606	C
1	A	2058	A
1	A	2127	G
1	A	2211	A
1	A	2273	A
1	A	2425	A
1	A	2573	C

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Mol	Chain	Res	Type
1	A	2756	U
1	A	2858	C

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

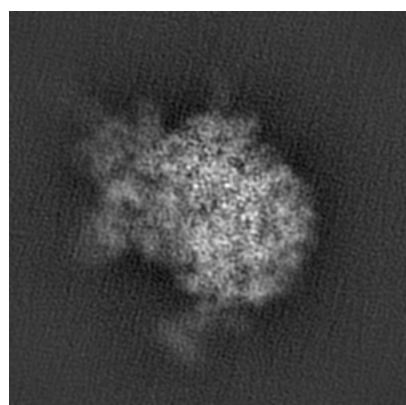
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12215. These allow visual inspection of the internal detail of the map and identification of artifacts.

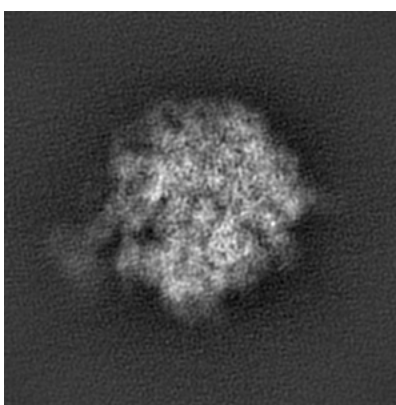
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

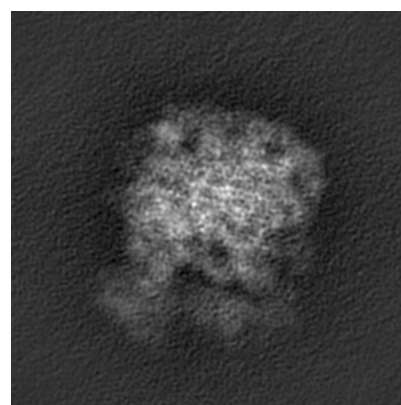
6.1.1 Primary map



X



Y

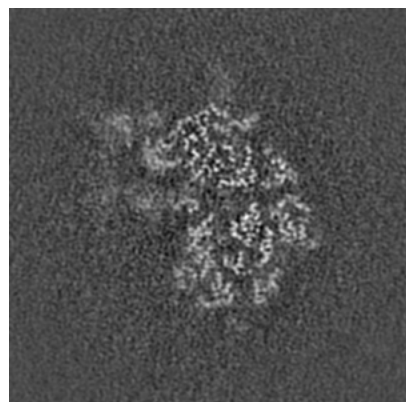


Z

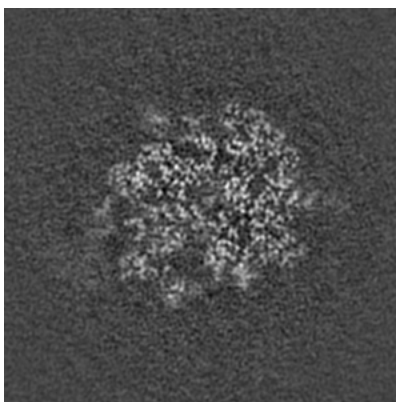
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

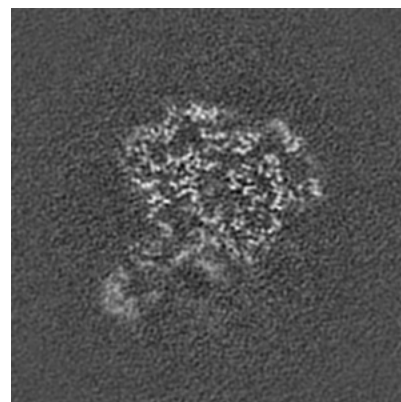
6.2.1 Primary map



X Index: 135



Y Index: 135

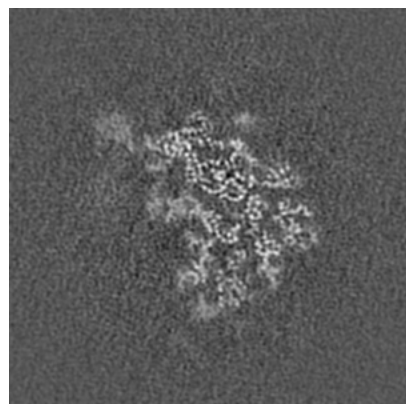


Z Index: 135

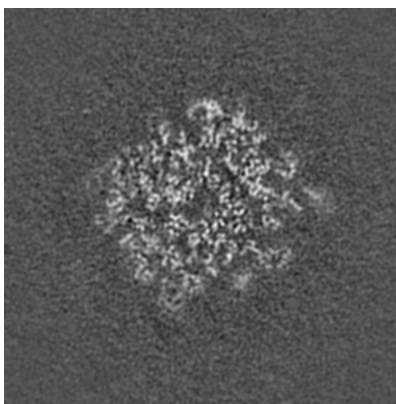
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

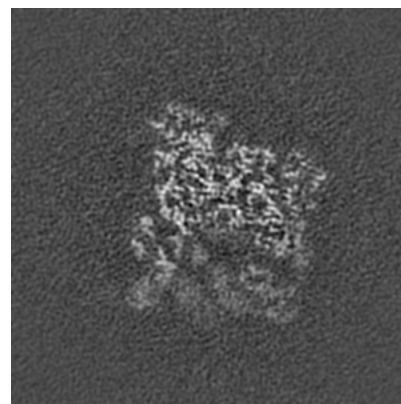
6.3.1 Primary map



X Index: 130



Y Index: 145

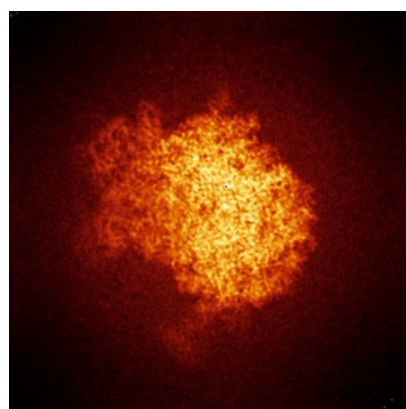


Z Index: 151

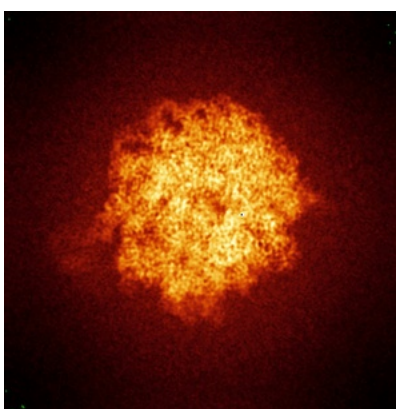
The images above show the largest variance slices of the map in three orthogonal directions.

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

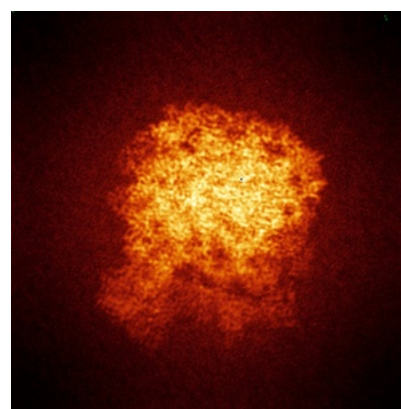
6.4.1 Primary map



X



Y



Z

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

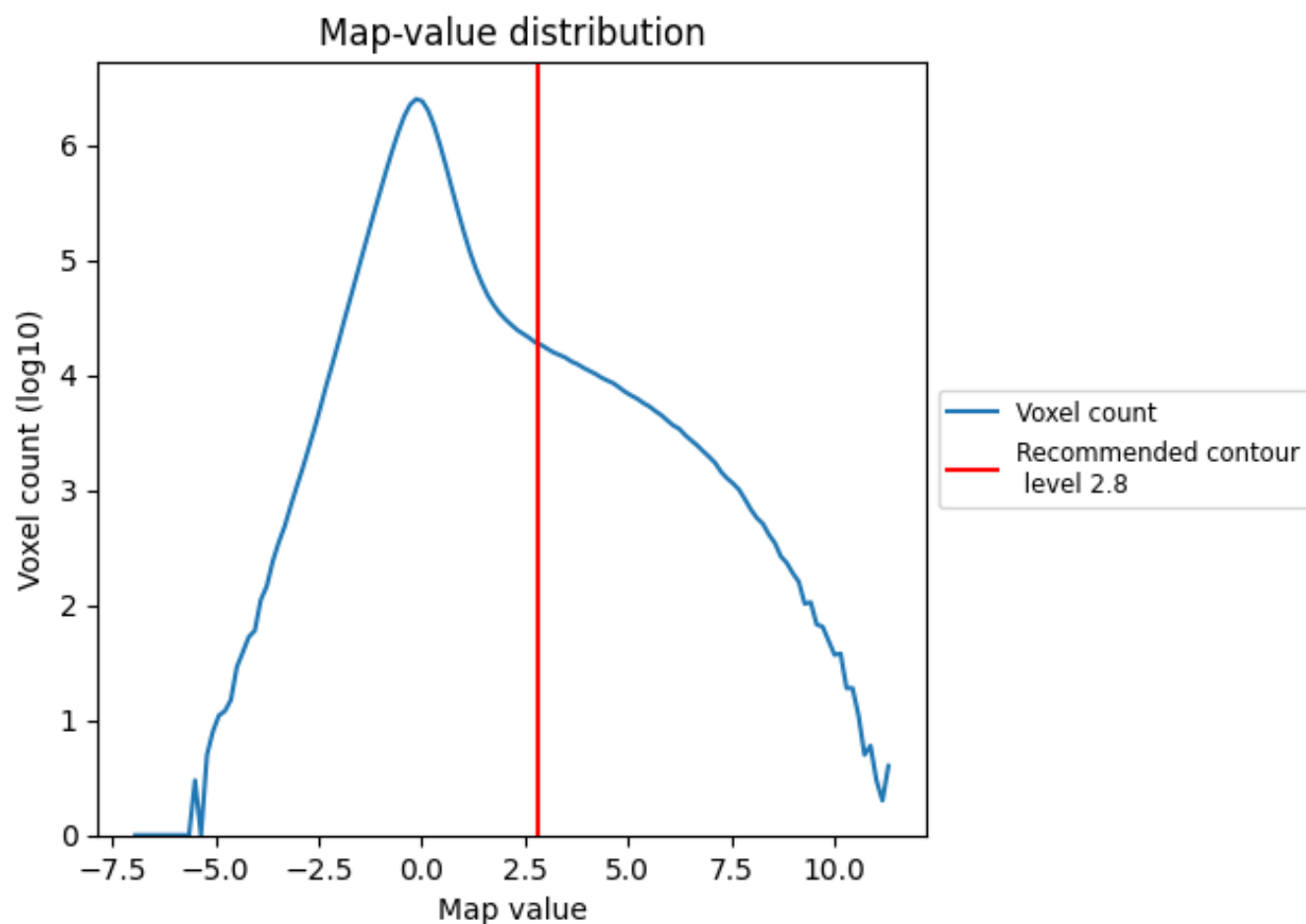
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

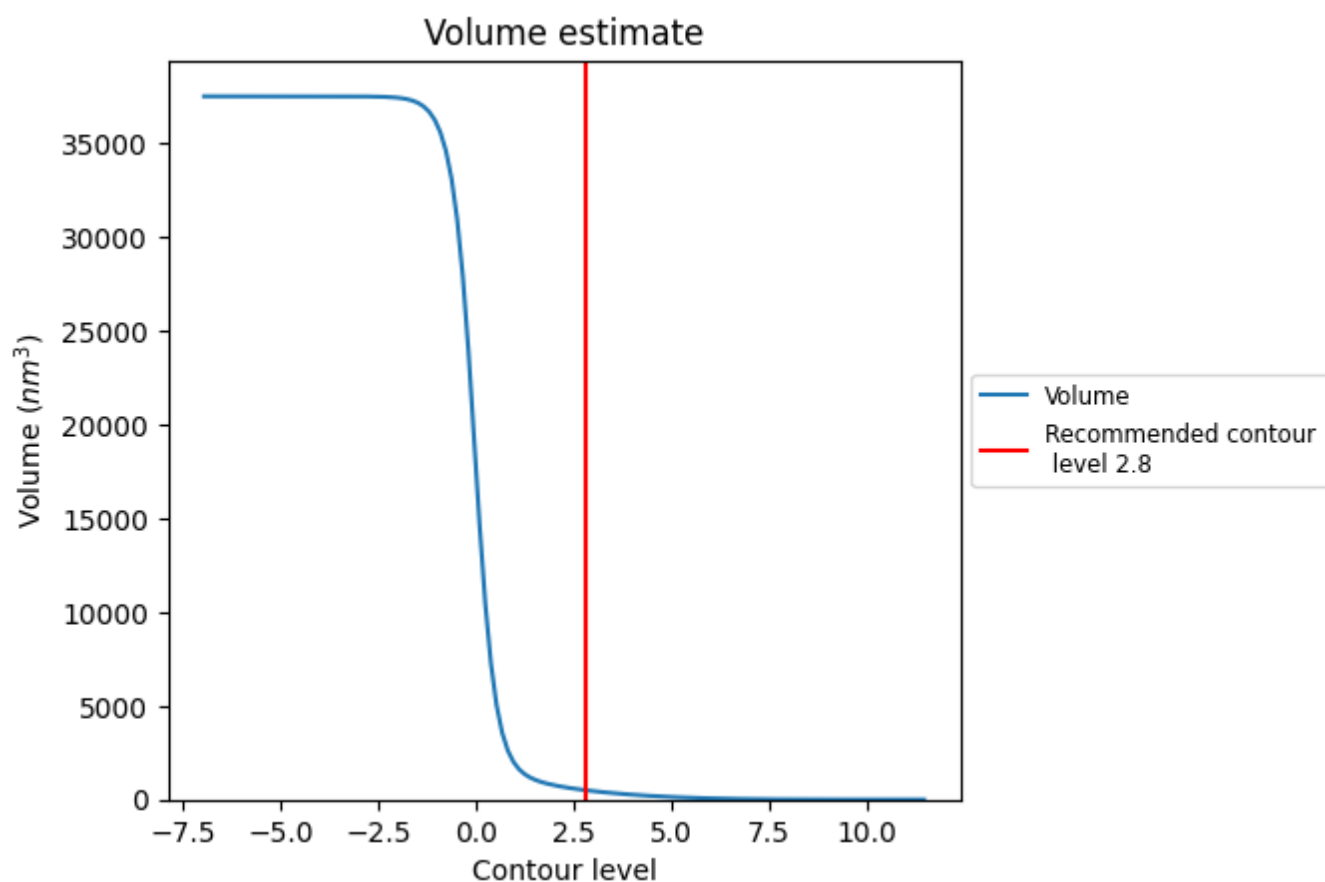
This section contains the results of statistical analysis of the map.

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.

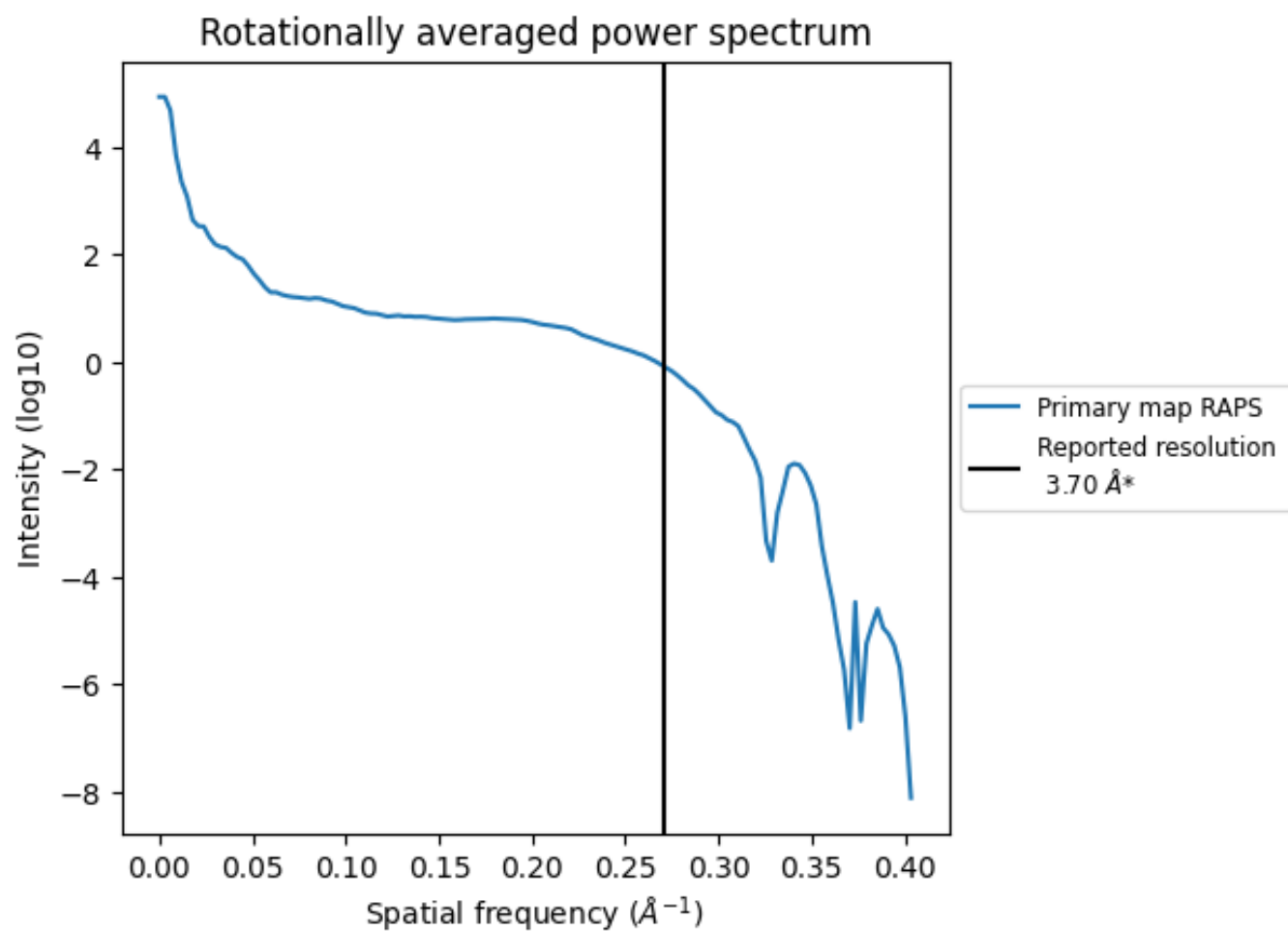
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 501 nm³; this corresponds to an approximate mass of 453 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 ⓘ

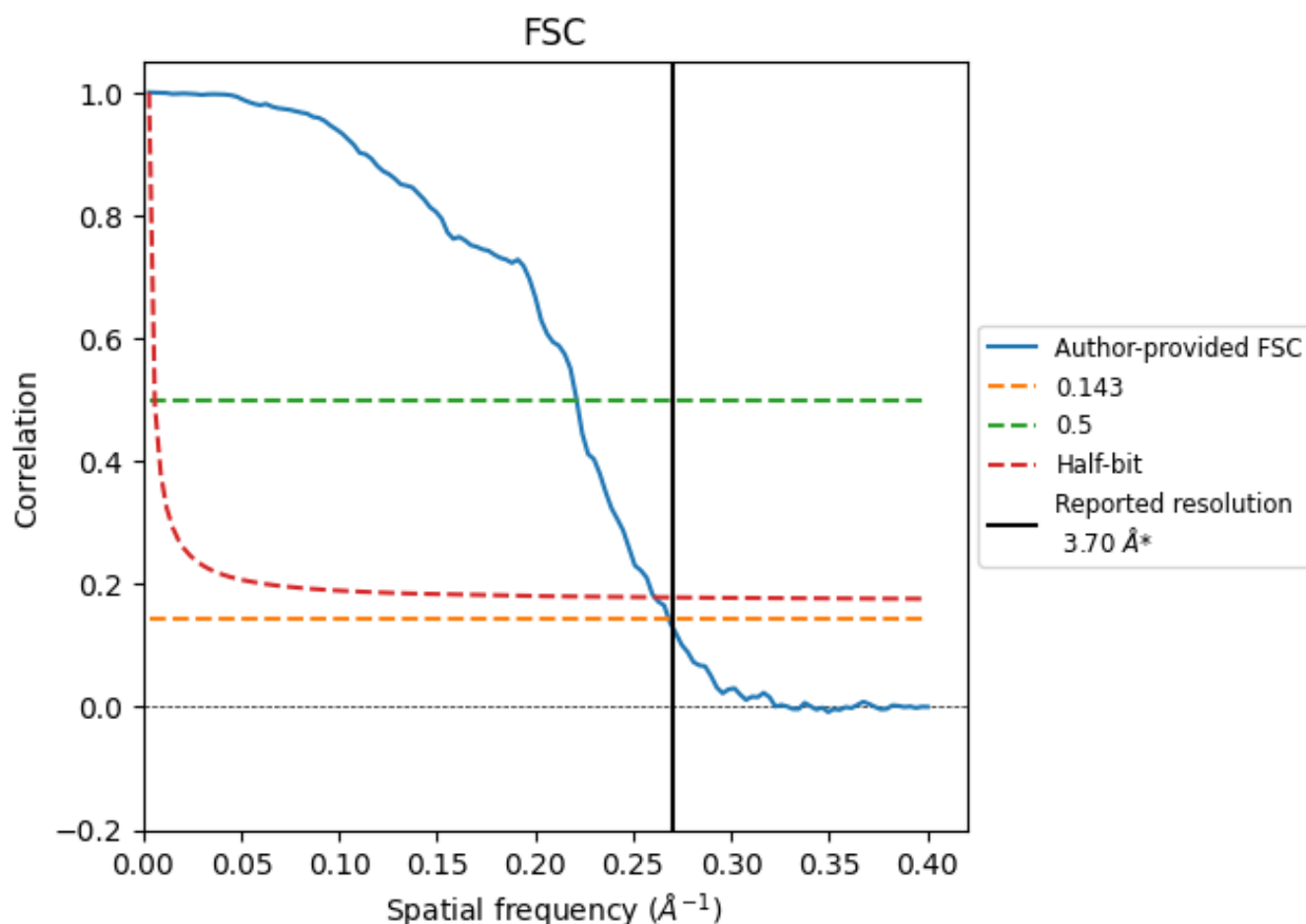


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

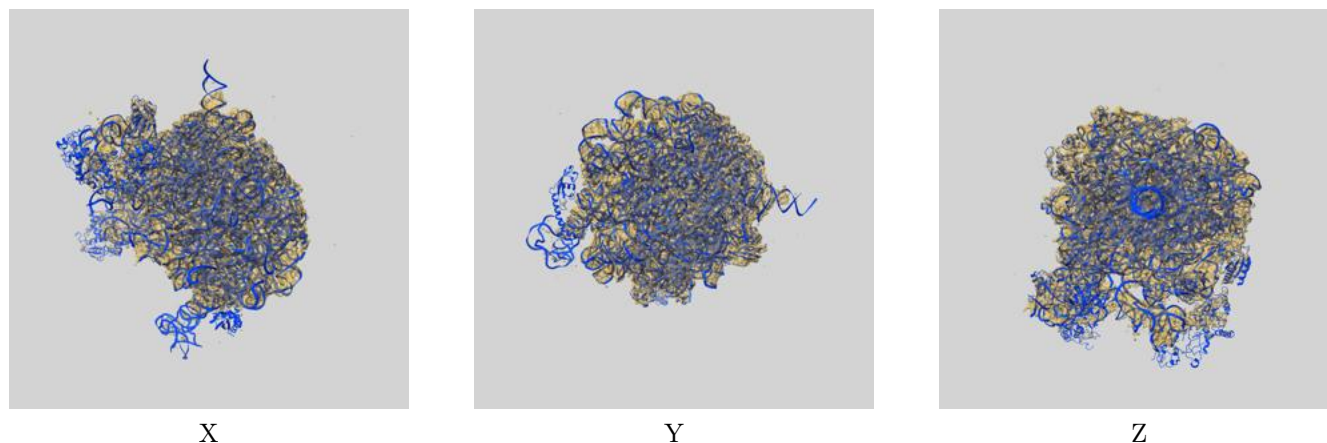
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	4.52	3.83
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

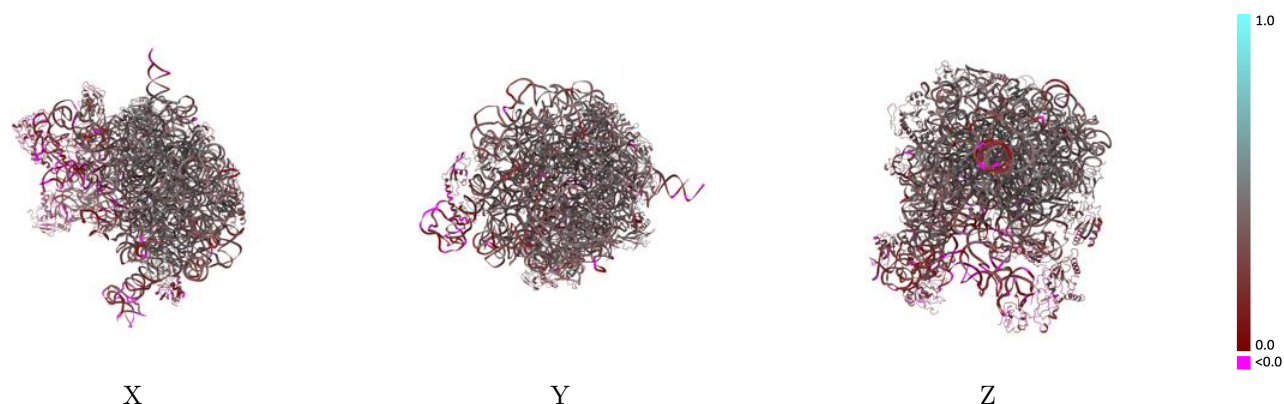
This section contains information regarding the fit between EMDB map EMD-12215 and PDB model 7BL2. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



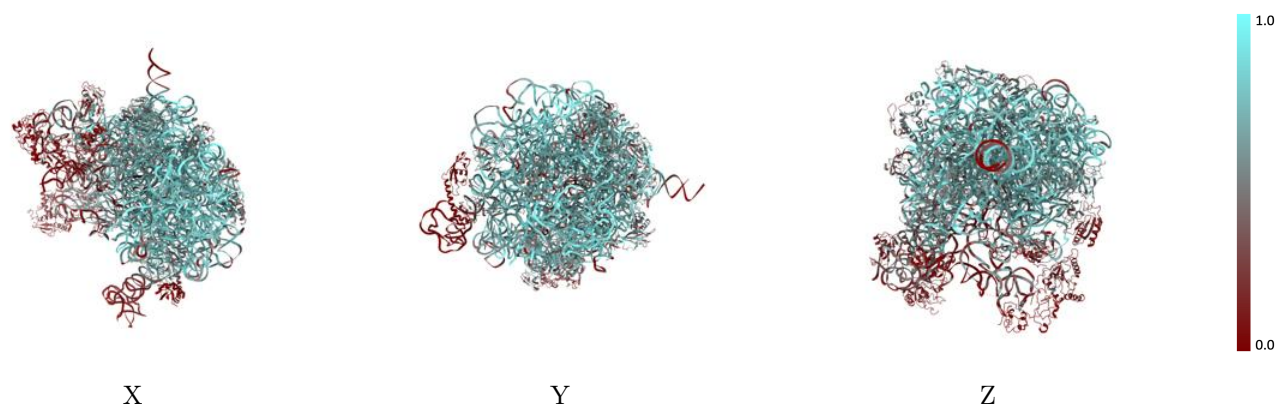
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



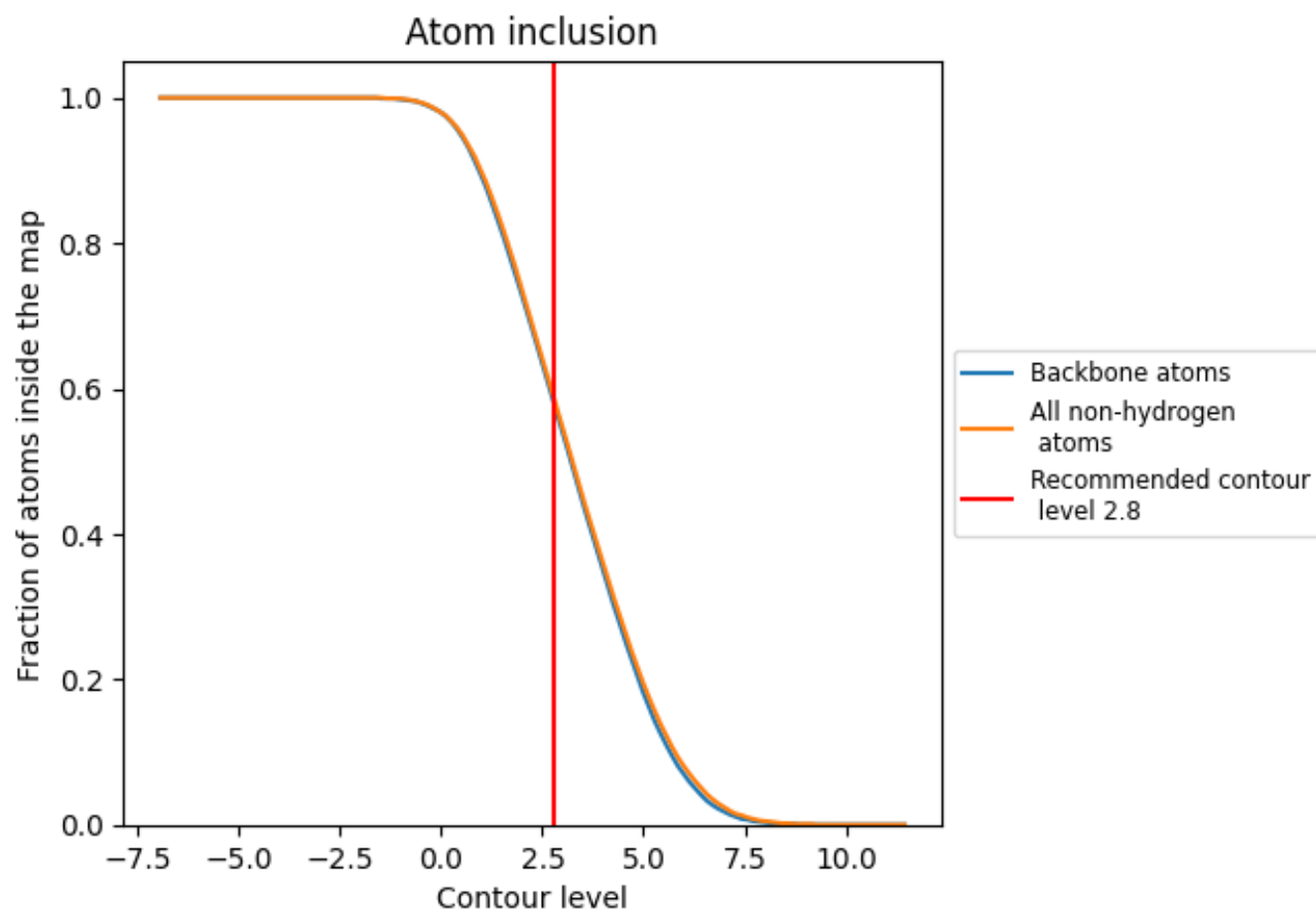
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 58% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5850	 0.3280
0	 0.5890	 0.3900
1	 0.0180	 0.1500
2	 0.5890	 0.4250
6	 0.1430	 0.2700
9P1	 0.2630	 0.2510
A	 0.6800	 0.3350
B	 0.4190	 0.2200
C	 0.5840	 0.4050
D	 0.5820	 0.4190
E	 0.4770	 0.3470
F	 0.0630	 0.1630
G	 0.3080	 0.2960
H	 0.1030	 0.1940
I	 0.0060	 0.1190
J	 0.5840	 0.4150
K	 0.5490	 0.3940
L	 0.4050	 0.2910
N	 0.6010	 0.4030
O	 0.1520	 0.2180
P	 0.5270	 0.4000
Q	 0.5930	 0.4030
R	 0.5290	 0.3840
S	 0.5920	 0.4290
T	 0.5250	 0.3910
U	 0.5360	 0.3930
V	 0.1690	 0.2400
W	 0.3450	 0.3140
X	 0.4860	 0.3770
Y	 0.4750	 0.3130
Z	 0.5220	 0.4040
b	 0.0000	 0.1500

