



## Full wwPDB EM Validation Report ⓘ

Feb 10, 2025 – 10:34 AM EST

PDB ID : 8VKI  
EMDB ID : EMD-43317  
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX:50S-HflX-C  
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.  
Deposited on : 2024-01-09  
Resolution : 2.96 Å (reported)  
Based on initial models : 5O61, 6DZI

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

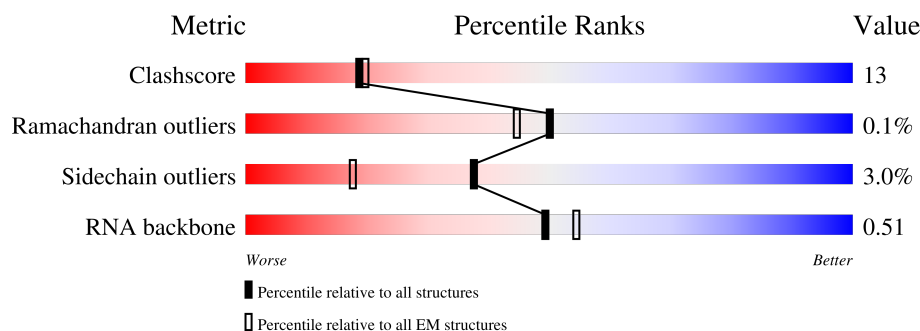
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.96 Å.

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



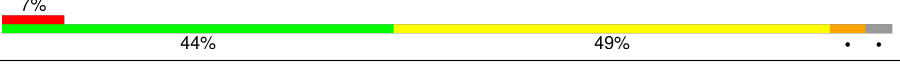

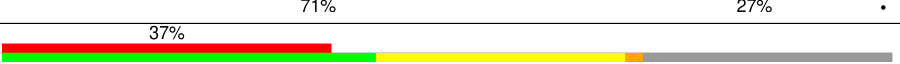
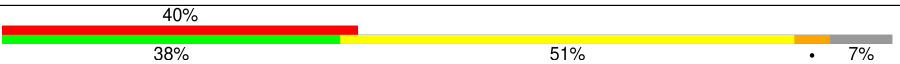


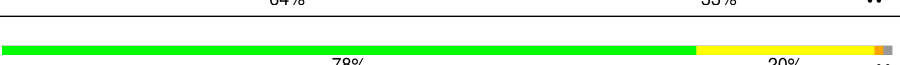
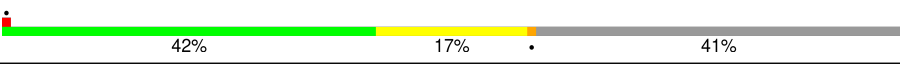
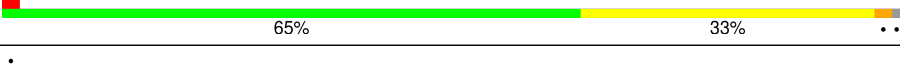




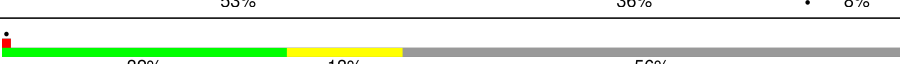

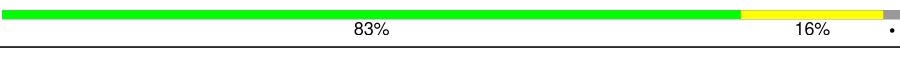

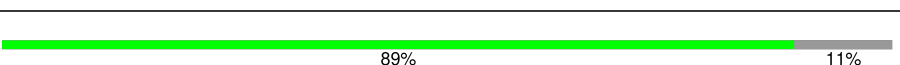
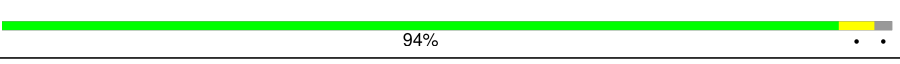
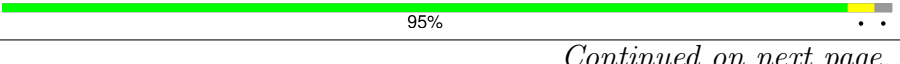



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	2	61	<div> <div>66%</div> <div>30%</div> <div>..</div> </div>
2	3	24	<div> <div>79%</div> <div>17%</div> <div>.</div> </div>
3	4	470	<div> <div>8%</div> <div>55%</div> <div>43%</div> <div>..</div> </div>
4	B	118	<div> <div>47%</div> <div>43%</div> <div>10%</div> </div>
5	C	278	<div> <div>78%</div> <div>21%</div> <div>.</div> </div>
6	D	217	<div> <div>67%</div> <div>30%</div> <div>..</div> </div>
7	E	215	<div> <div>75%</div> <div>20%</div> <div>..</div> </div>

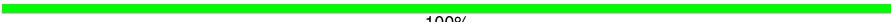

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Mol	Chain	Length	Quality of chain
8	F	187	
9	G	179	
10	H	151	
11	I	175	
12	J	142	
13	K	147	
14	L	122	
15	M	147	
16	N	138	
17	O	199	
18	P	127	
19	Q	113	
20	R	129	
21	S	103	
22	T	153	
23	U	100	
24	V	105	
25	W	215	
26	X	88	
27	Y	64	
28	Z	77	
29	b	57	
30	c	55	
31	d	47	
32	e	64	

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Mol	Chain	Length	Quality of chain
33	f	37	 100%
34	A	3120	 49% 35% 10% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	GCP	4	501	-	-	X	-

## 2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 96565 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	466	Total	C	N	O	S	0	0
			3516	2171	649	689	7		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 7 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 8 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	132	Total	C	N	O	S	0	0
			958	602	172	181	3		

- Molecule 13 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 18 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 20 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 21 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 22 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 23 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	W	95	Total	C	N	O	0	0
			735	452	149	134		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 27 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 28 is a protein called 50S ribosomal protein L29.



Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

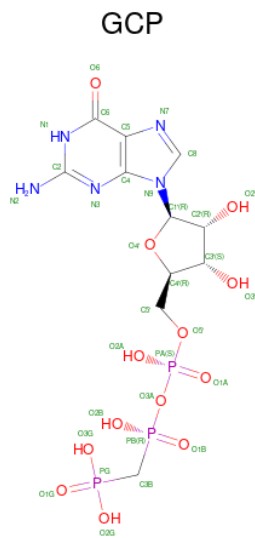
- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	f	37	Total	C	N	O	0	0
			299	181	66	47	5	

- Molecule 34 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A	2952	Total	C	N	O	P	0	0
			63419	28264	11675	20528	2952		

- Molecule 35 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
35	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

### 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: 50S ribosomal protein L30

Chain 2: 



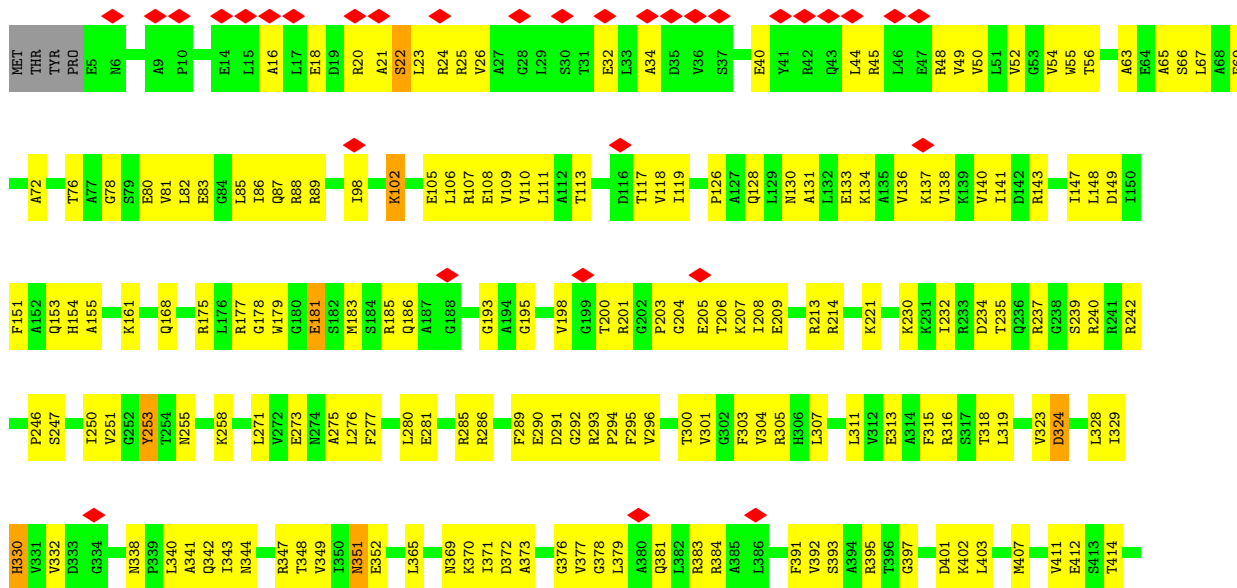
- Molecule 2: 50S Ribosomal Protein L37

Chain 3: 



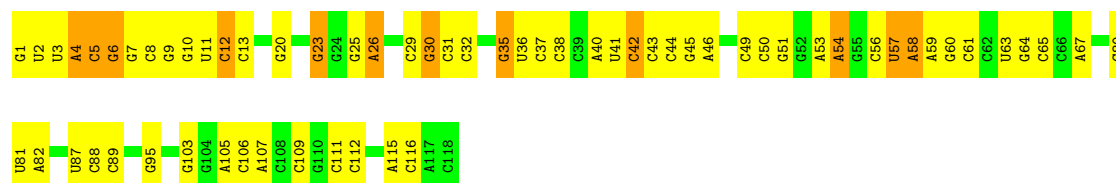
- Molecule 3: GTPase HflX

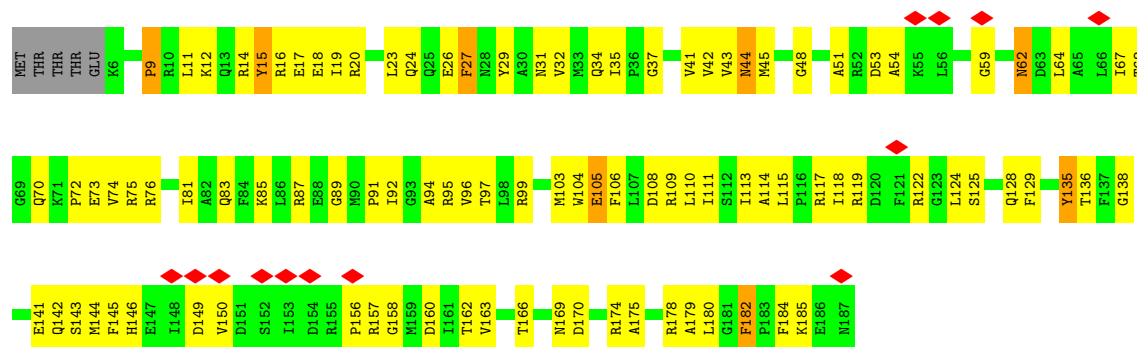
Chain 4: 



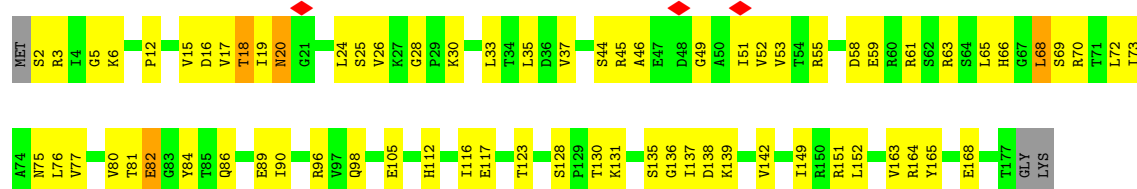


- Molecule 4: 5S ribosomal RNA

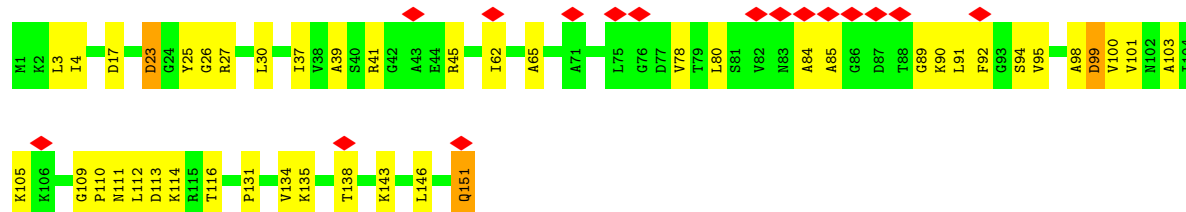




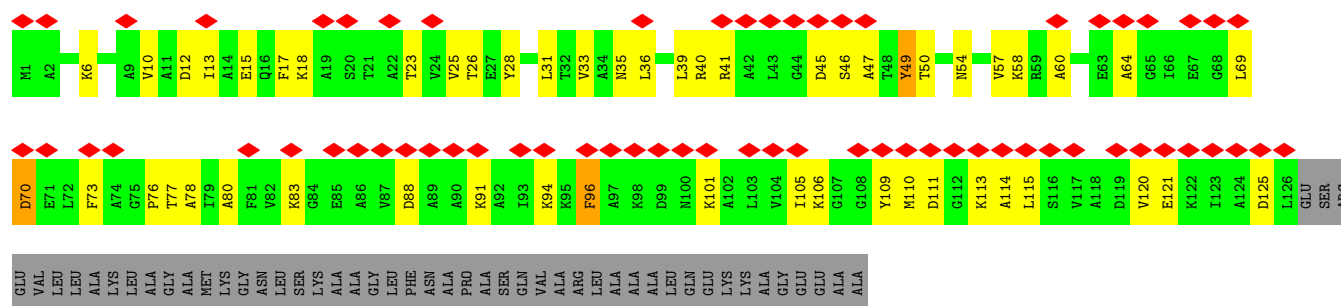
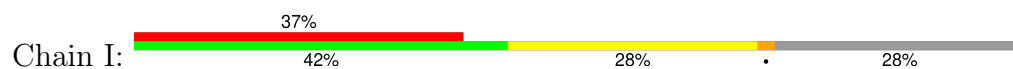
• Molecule 9: 50S ribosomal protein L6



• Molecule 10: 50S ribosomal protein L9

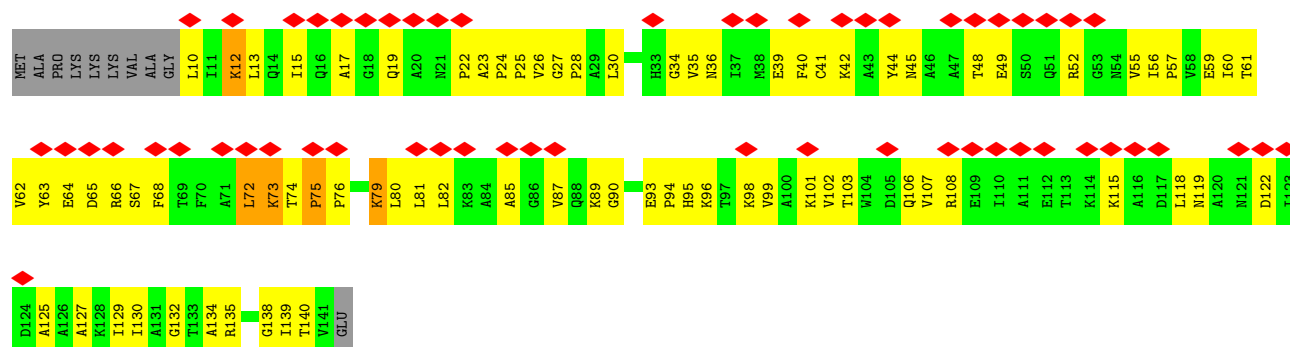


• Molecule 11: 50S ribosomal protein L10



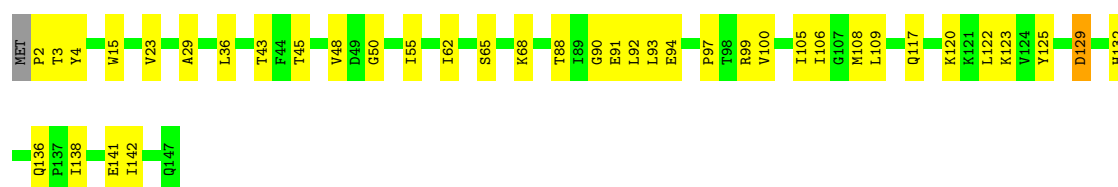
• Molecule 12: 50S ribosomal protein L11





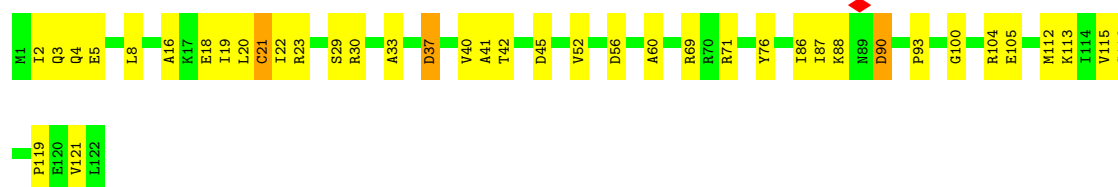
• Molecule 13: 50S Ribosomal Protein L13

Chain K: 73% 26% ..



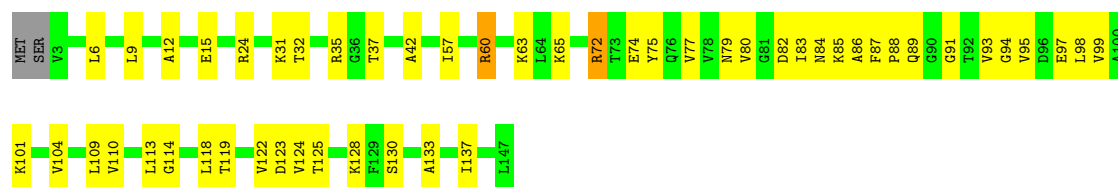
• Molecule 14: 50S ribosomal protein L14

Chain L: 67% 30% .



• Molecule 15: 50S ribosomal protein L15

Chain M: 64% 33% ..



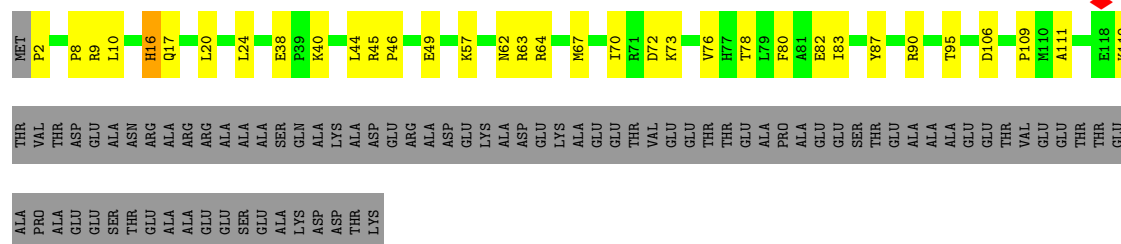
• Molecule 16: Large ribosomal subunit protein uL16

Chain N: 78% 20% ..



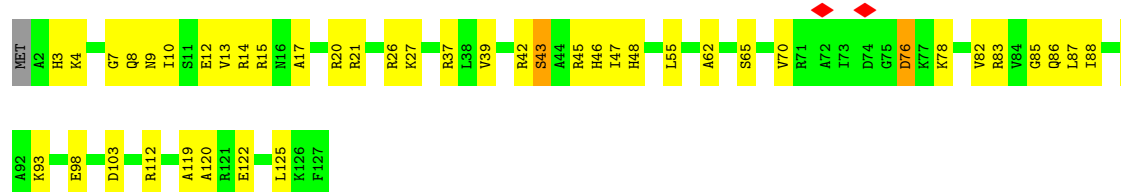
• Molecule 17: 50S ribosomal protein L17

Chain O: 



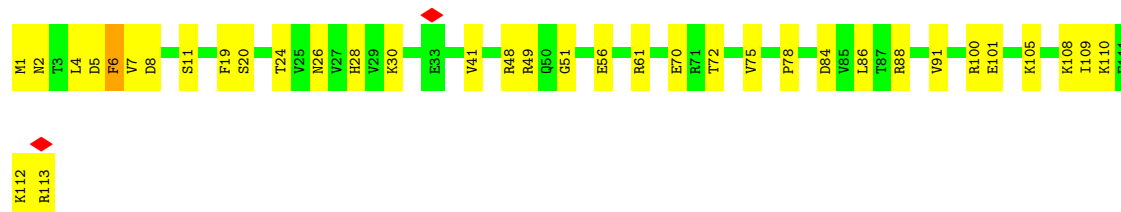
• Molecule 18: 50S Ribosomal Protein L18

Chain P: 



• Molecule 19: 50S ribosomal protein L19

Chain Q: 



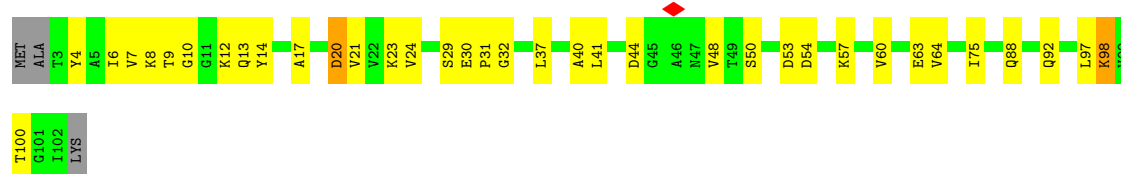
• Molecule 20: 50S Ribosomal Protein L20

Chain R: 



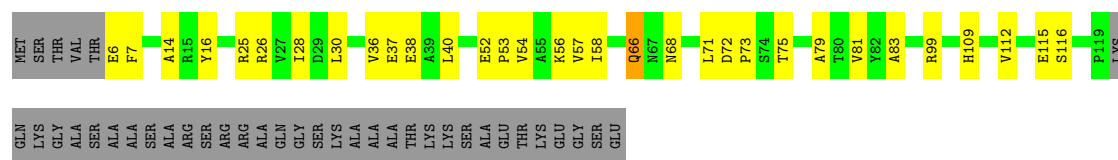
• Molecule 21: 50S Ribosomal Protein L21

Chain S: 



• Molecule 22: 50S Ribosomal Protein L22

Chain T: 



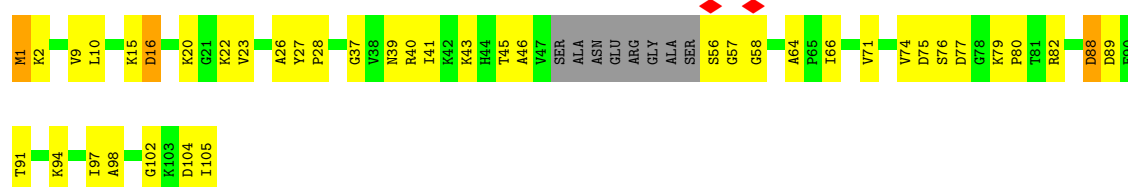
• Molecule 23: 50S Ribosomal Protein L23

Chain U: 




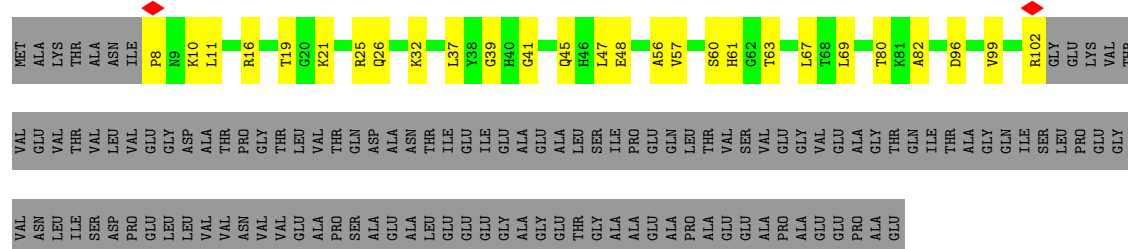
• Molecule 24: 50S ribosomal protein L24

Chain V: 



• Molecule 25: 50S ribosomal protein L25

Chain W: 




• Molecule 26: 50S ribosomal protein L27

Chain X: 



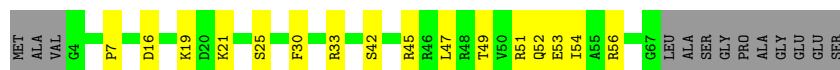
• Molecule 27: 50S Ribosomal Protein L28

Chain Y: 

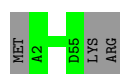




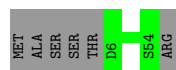
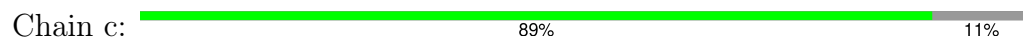
- Molecule 28: 50S ribosomal protein L29



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S Ribosomal Protein L33



- Molecule 31: 50S ribosomal protein L34



- Molecule 32: 50S ribosomal protein L35

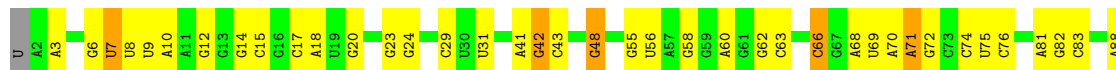


- Molecule 33: 50S ribosomal protein L36



There are no outlier residues recorded for this chain.

- Molecule 34: 23S ribosomal RNA





A2405	U2345	G2276	A	C	G2056	C1843	G1756	C1651	G	U1529	G1425
U2406	G2346	G2277	A	C	G2057	A1844	U1757	A1652	U	G1530	G1426
C2407	A2278	G2279	U	C	U2058	A1852	G1758	G1653	U	G1531	U1427
G2408	G2347	G2280	U	C	G2059	A1853	A1759	G1654	G	G1532	U1428
U2409	G2348	G2281	U	C	G2060	A1854	G1760	C1655	G	U1533	C1429
A2410	A2349	A2282	C	C	C2061	A1855	G1761	C1656	C	U1534	C1430
U2411	G2350	A2283	C	C	U2062	C1856	G1762	U1671	C	C1535	U1431
G2412	A2351	U2284	A	C	G2063	U1860	A1764	C1672	U	A1536	G1434
G2413	C2352	A2285	C	C	A	U1864	U1767	A1673	U	G1541	G1435
G2414	G2353	G2286	C	C	U2064	A1865	G1768	U1674	G	A1542	C1436
G2415	U2354	U2287	U	C	U2065	G1866	G1769	G1675	U	A1543	G1443
C2416	G2354	C2288	G	C	G2066	G1867	G1770	U1676	G	U1544	C1444
C2417	U2355	G2289	C	C	A	A1868	U1771	A1680	U	C1545	G1449
U2418	U2356	A2294	A	C	U2067	U1869	A1778	U1681	G	A	G1456
G2419	G2357	C2295	C	C	U2068	U1870	U1779	G1682	U	G	A1457
U2420	A2358	U2296	U	C	U2069	U1871	G1780	A1690	C	A	G1466
A2421	G2359	U2297	A	C	G2070	A1872	U1781	A1691	U	C	A1467
G2422	C2360	U2298	A	C	U2071	U1873	C1784	G1696	G	C	C1465
G2423	A2361	C2299	A	C	U2072	A1883	C1785	U1709	C	A	G1473
C2424	C2362	A2300	G	C	U2073	G1884	G1786	G1710	C	C	G1475
A2425	A2363	G2197	A	C	U2074	G1885	A1787	G1711	U	C	G1476
G2426	C2364	C2198	C	C	U2075	U1889	G1788	U1712	C	A	C1477
G2427	U2365	G2199	C	C	A2000	G1890	A1789	U1713	U	U	C1478
G2428	G2366	U2200	C	C	A2001	G1891	A1790	U1714	C	C	C1479
U2429	C2367	U2201	C	C	U2002	G1892	A1791	A1715	C	A	G1480
G2430	G2368	C2203	C	C	U2003	G1893	U1792	U1716	C	A	C1481
G2431	U2369	U2204	C	C	U2004	U1894	U1793	U1717	C	A	A1482
G2432	C2370	U2205	C	C	U2005	G1895	U1794	U1718	C	A	U1487
G2433	G2371	U2206	C	C	U2006	G1896	U1795	U1719	C	A	A1488
G2434	U2372	U2207	C	C	U2007	U1897	U1796	G1720	C	C	A1493
U2435	G2373	U2208	C	C	U2008	U1898	A1803	C1722	C	A	A1494
G2436	U2374	U2209	C	C	U2009	G1899	G1804	U1721	C	C	A1499
G2437	G2375	U2210	C	C	U2010	U1900	G1805	U1722	C	C	A1500
U2438	C2376	U2211	C	C	U2011	C1901	A1806	U1723	C	A	G1502
G2439	U2377	U2212	C	C	U2012	U1902	C1807	U1724	C	C	U1509
G2440	G2378	U2213	C	C	U2013	C1903	A1808	U1725	C	C	A1510
U2441	U2379	U2214	C	C	U2014	U1904	U1809	U1726	C	C	U1511
G2442	G2380	U2215	C	C	U2015	A1905	A1810	U1727	C	C	U1512
U2443	A2381	U2216	C	C	U2016	U1906	C1811	U1728	C	C	C1514
G2444	G2382	U2217	C	C	U2017	U1907	A1812	A1729	C	C	G1524
U2445	U2383	U2218	C	C	U2018	U1908	G1815	U1730	C	C	U1525
G2446	C2384	U2219	C	C	U2019	U1909	C1816	U1731	C	C	G1528
G2447	U2385	U2220	C	C	U2020	U1910	U1822	U1732	C	C	
U2448	G2386	U2221	C	C	U2021	U1911	C1823	U1733	C	C	
G2449	U2387	U2222	C	C	U2022	U1912	C1824	U1734	C	C	
G2450	G2388	U2223	C	C	U2023	U1913	C1825	U1735	C	C	
U2451	U2389	U2224	C	C	U2024	U1914	A1826	U1736	C	C	
G2452	C2390	U2225	C	C	U2025	U1915	U1827	U1737	C	C	
G2453	U2391	U2226	C	C	U2026	U1916	A1828	U1738	C	C	
U2454	G2392	U2227	C	C	U2027	U1917	A1829	U1739	C	C	
G2455	A2393	U2228	C	C	U2028	U1918	A1830	U1740	C	C	
U2456	U2394	U2229	C	C	U2029	U1919	C1831	U1741	C	C	
G2457	G2395	U2230	C	C	U2030	U1920	C1832	U1742	C	C	
U2458	U2396	U2231	C	C	U2031	U1921	C1833	U1743	C	C	
G2459	A2397	U2232	C	C	U2032	U1922	C1834	U1744	C	C	
U2460	G2398	U2233	C	C	U2033	U1923	C1835	U1745	C	C	
G2461	U2399	U2234	C	C	U2034	U1924	C1836	U1746	C	C	
U2462	C2400	U2235	C	C	U2035	U1925	C1837	U1747	C	C	
G2463	U2401	U2236	C	C	U2036	U1926	C1838	U1748	C	C	
U2464	G2402	U2237	C	C	U2037	U1927	C1839	U1749	C	C	
G2465	U2403	U2238	C	C	U2038	U1928	C1840	U1750	C	C	
U2466	G2404	U2239	C	C	U2039	U1929	C1841	U1751	C	C	
G2467		U2240	C	C	U2040	U1930	C1842	U1752	C	C	
U2468		U2241	C	C	U2041	U1931	C1843	U1753	C	C	
G2469		U2242	C	C	U2042	U1932	C1844	U1754	C	C	
U2470		U2243	C	C	U2043	U1933	C1845	U1755	C	C	
G2471		U2244	C	C	U2044	U1934	C1846	U1756	C	C	
U2472		U2245	C	C	U2045	U1935	C1847	U1757	C	C	
G2473		U2246	C	C	U2046	U1936	C1848	U1758	C	C	
U2474		U2247	C	C	U2047	U1937	C1849	U1759	C	C	
G2475		U2248	C	C	U2048	U1938	C1850	U1760	C	C	
U2476		U2249	C	C	U2049	U1939	C1851	U1761	C	C	
G2477		U2250	C	C	U2050	U1940	C1852	U1762	C	C	
U2478		U2251	C	C	U2051	U1941	C1853	U1763	C	C	
G2479		U2252	C	C	U2052	U1942	C1854	U1764	C	C	
U2480		U2253	C	C	U2053	U1943	C1855	U1765	C	C	
G2481		U2254	C	C	U2054	U1944	C1856	U1766	C	C	
U2482		U2255	C	C	U2055	U1945	C1857	U1767	C	C	
G2483		U2256	C	C	U2056	U1946	C1858	U1768	C	C	
U2484		U2257	C	C	U2057	U1947	C1859	U1769	C	C	
G2485		U2258	C	C	U2058	U1948	C1860	U1770	C	C	
U2486		U2259	C	C	U2059	U1949	C1861	U1771	C	C	
G2487		U2260	C	C	U2060	U1950	C1862	U1772	C	C	
U2488		U2261	C	C	U2061	U1951	C1863	U1773	C	C	
G2489		U2262	C	C	U2062	U1952	C1864	U1774	C	C	
U2490		U2263	C	C	U2063	U1953	C1865	U1775	C	C	
G2491		U2264	C	C	U2064	U1954	C1866	U1776	C	C	
U2492		U2265	C	C	U2065	U1955	C1867	U1777	C	C	
G2493		U2266	C	C	U2066	U1956	C1868	U1778	C	C	
U2494		U2267	C	C	U2067	U1957	C1869	U1779	C	C	
G2495		U2268	C	C	U2068	U1958	C1870	U1780	C	C	
U2496		U2269	C	C	U2069	U1959	C1871	U1781	C	C	
G2497		U2270	C	C	U2070	U1960	C1872	U1782	C	C	
U2498		U2271	C	C	U2071	U1961	C1873	U1783	C	C	
G2499		U2272	C	C	U2072	U1962	C1874	U1784	C	C	
U2500		U2273	C	C	U2073	U1963	C1875	U1785	C	C	
G2501		U2274	C	C	U2074	U1964	C1876	U1786	C	C	
U2502		U2275	C	C	U2075	U1965	C1877	U1787	C	C	
G2503		U2276	C	C	U2076	U1966	C1878	U1788	C	C	
U2504		U2277	C	C	U2077	U1967	C1879	U1789	C	C	
G2505		U2278	C	C	U2078	U1968	C1880	U1790	C	C	
U2506		U2279	C	C	U2079	U1969	C1881	U1791	C	C	
G2507		U2280	C	C	U2080	U1970	C1882	U1792	C	C	
U2508		U2281	C	C	U2081	U1971	C1883	U1793	C	C	
G2509		U2282	C	C	U2082	U1972	C1884	U1794	C	C	
U2510		U2283	C	C	U2083	U1973	C1885	U1795	C	C	
G2511		U2284	C	C	U2084	U1974	C1886	U1796	C	C	
U2512		U2285	C	C	U2085	U1975	C1887	U1797	C	C	
G2513		U2286	C	C	U2086	U1976	C1888	U1798	C	C	
U2514		U2287	C	C	U2087	U1977	C1889	U1799	C	C	
G2515		U2288	C	C	U2088	U1978	C1890	U1800	C	C	
U2516		U2289	C	C	U2089	U1979	C1891	U1801	C	C	
G2517		U2290	C	C	U2090	U1980	C1892	U1802	C	C	
U2518		U2291	C	C	U2091	U1981	C1893	U1803	C	C	
G2519		U2292	C	C	U2092	U1982	C1894	U1804	C	C	
U2520		U2293	C	C	U2093	U1983	C1895	U1805	C	C	
G2521		U2294	C	C	U2094	U1984	C1896	U1806	C	C	
U2522		U2295	C	C	U2095	U1985	C1897	U1807	C	C	
G2523		U2296	C	C	U2096	U1986	C1898	U1808	C	C	
U2524		U2297	C	C	U2097	U1987	C1899	U1809	C	C	
G2525		U2298	C	C	U2098	U1988	C1900	U1810	C	C	
U2526		U2299	C	C	U2099	U1989	C1901	C1811	C	C	
G2527		U2300	C	C	U2100	U1990	C1902	A1812	C	C	
U2528		U2301	C	C	U2101	U1991	C1903	G1815	C	C	
G2529		U2302	C	C	U2102	U1992	C1904	C1816	C	C	
U2530		U2303	C	C	U2103	U1993	C1905	C1928	C	C	
G2531		U2304	C	C	U2104	U1994	C1906	A1931	C	C	
U2532		U2305	C	C	U2105	U1995	C1907	U1932	C	C	
G2533		U2306	C	C	U2106	U1996	C1908	G1933	C	C	
U2534		U2307	C	C	U2107						

A3113	A2593	A2693	C2795	C2905	U3018	A3113
A3114	A2597	A2694	A2796	C2909	C3019	A3114
A3115	A2598	A2695	C2797	C2913	U3020	A3115
C3116	A2599	A2696	C2798	C2914	A3021	C3116
U3117	A2600	U2697	G2802	U2913	G3022	U3117
U3118	G2603	C2698	G2805	A2914	A3023	U3118
A3119	U2604	C2699	U2809	C2915	A3024	A3119
C3120	U2605	A2700	U2810	C2916	G3025	C3120
	A2522	C2704	U2820	U2922	A3026	
	A2523	C2705		C2923	G3027	
	C2524	A2706		U2926	U3028	
	G2527	G2713	U2833	G2933	A3030	
	A2528	U2714	C2834	C2936	A3031	
	A2529	U2715	U2835	C2948	G3032	
	C2530	C2720	U2836	C2949	C3033	
	G2531	A2727	U2837	C2950	C3034	
	G2532	U2728	A2838	G2956		
	C2533	G2729	U2839	A2957	C3037	
	A2534	U2735	G2842	G2968		
	A2535	C2736		C2969	G3040	
	U2536	G2740	U2847	U2970	C3041	
	C2537	C2741	C2848	C2971	A3042	
	A2538	A2742	G2851	A2972	G3043	
	G2539	U2743	A2854	C2973	A3044	
	U2540	C2744		G2974	G3045	
	G2542	U2753	A2857	C2975	C3046	
	U2544	G2754	C2858	C2976	A3047	
	G2547	A2755	U2859	U2980		
	U2548	G2756	C2860	A2981	G3070	
	U2550	C2757	U2861	G2985	A3071	
	A2551	A2758	G2862	A2989	A3072	
	A2552	G2759	G2865	C2997	G3073	
	G2553	U2760	C2869	C2998	C3074	
	A2557	U2761	C2870	A2999	C3075	
	C2558	C2762	U2871	G3000	G3078	
	A2559	U2771	G2872	A3001	U3079	
	A2560	G2776	U2873	C3002	A3080	
	C2571	U2777	C2874	C3003	A3081	
	G2574	U2778	G2879	G3008	U3082	
	G2575	U2779	G2883	U3009	G3087	
	G2580	C2780	G2885	C3010	C3088	
	G2581	U2781	U2886	C3011	A3093	
	U2585	C2782	G2887	G3012	A3100	
	U2586	A2788	G2888	U3013	C3101	
	U2587	U2789	A2899	C3014		
	C2588	A2790		C3015	A3104	
	G2589	G2791		C3016		
	A2590	C2792		C3017	A3112	

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132147	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	51.85	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.399	Depositor
Minimum map value	-1.560	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.111	Depositor
Recommended contour level	0.35	Depositor
Map size ( $\text{\AA}$ )	430.4, 430.4, 430.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.076, 1.076, 1.076	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	2	0.39	0/477	0.59	0/640
2	3	0.37	0/191	0.66	0/247
3	4	0.40	2/3558 (0.1%)	0.75	4/4822 (0.1%)
4	B	0.70	0/2821	0.85	0/4396
5	C	0.43	0/2153	0.59	0/2895
6	D	0.45	0/1609	0.61	1/2165 (0.0%)
7	E	0.40	0/1592	0.55	0/2153
8	F	0.43	2/1467 (0.1%)	0.76	2/1973 (0.1%)
9	G	0.34	0/1369	0.60	0/1848
10	H	0.33	0/1027	0.60	0/1398
11	I	0.27	0/925	0.52	0/1246
12	J	0.36	0/971	0.79	1/1315 (0.1%)
13	K	0.42	0/1157	0.54	0/1567
14	L	0.42	0/946	0.65	1/1268 (0.1%)
15	M	0.44	1/1091 (0.1%)	0.56	0/1457
16	N	0.42	0/1118	0.57	0/1506
17	O	0.42	0/945	0.57	0/1267
18	P	0.37	0/966	0.61	0/1298
19	Q	0.42	0/921	0.58	0/1236
20	R	0.48	0/1000	0.60	0/1341
21	S	0.45	1/764 (0.1%)	0.56	0/1030
22	T	0.41	0/887	0.57	0/1204
23	U	0.41	0/766	0.54	0/1030
24	V	0.36	0/738	0.58	0/987
25	W	0.33	0/745	0.57	0/1008
26	X	0.41	0/595	0.61	0/798
27	Y	0.46	0/478	0.57	0/641
28	Z	0.35	0/534	0.60	0/713
29	b	0.40	0/427	0.64	0/572
30	c	0.40	0/413	0.55	0/553
31	d	0.44	0/380	0.71	0/500
32	e	0.40	0/507	0.63	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	f	0.42	0/303	0.61	0/401
34	A	0.91	0/71013	0.87	49/110798 (0.0%)
All	All	0.79	6/104854 (0.0%)	0.81	58/156945 (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
12	J	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	458	PRO	CG-CD	-11.45	1.12	1.50
3	4	458	PRO	CB-CG	-6.40	1.18	1.50
15	M	60	ARG	C-N	-5.80	1.20	1.34
8	F	9	PRO	CG-CD	-5.67	1.31	1.50
21	S	29	SER	C-N	-5.35	1.21	1.34
8	F	9	PRO	N-CD	5.05	1.54	1.47

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	458	PRO	N-CD-CG	-21.18	71.43	103.20
3	4	458	PRO	CA-CB-CG	-15.62	74.33	104.00
8	F	9	PRO	CA-N-CD	-12.34	94.22	111.50
8	F	9	PRO	N-CD-CG	-9.26	89.31	103.20
34	A	2245	C	C2-N1-C1'	8.52	128.17	118.80
34	A	342	C	N3-C2-O2	-8.39	116.03	121.90
34	A	2155	U	C2-N1-C1'	8.28	127.63	117.70
3	4	458	PRO	CB-CG-CD	8.24	138.63	106.50
34	A	2521	C	C2-N1-C1'	7.72	127.29	118.80
34	A	617	U	N1-C2-O2	7.61	128.12	122.80
34	A	617	U	C2-N1-C1'	7.49	126.68	117.70
34	A	2245	C	N1-C2-O2	7.09	123.15	118.90
34	A	2025	C	N3-C2-O2	-6.87	117.09	121.90
34	A	617	U	N3-C2-O2	-6.72	117.50	122.20
14	L	90	ASP	CB-CG-OD1	6.65	124.28	118.30
34	A	1753	C	C2-N1-C1'	6.54	126.00	118.80
34	A	1755	A	O4'-C1'-N9	6.45	113.36	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	A	342	C	N1-C2-O2	6.31	122.69	118.90
34	A	1428	U	C2-N1-C1'	6.30	125.26	117.70
34	A	1533	U	C2-N1-C1'	6.21	125.15	117.70
34	A	2245	C	N3-C2-O2	-6.20	117.56	121.90
34	A	619	C	C2-N1-C1'	6.13	125.55	118.80
6	D	113	ASP	CB-CG-OD1	6.08	123.77	118.30
34	A	962	U	N3-C2-O2	-6.08	117.95	122.20
34	A	599	G	O4'-C1'-N9	5.99	112.99	108.20
34	A	2155	U	N1-C2-O2	5.96	126.97	122.80
34	A	962	U	C2-N1-C1'	5.91	124.79	117.70
34	A	2245	C	C6-N1-C1'	-5.87	113.76	120.80
34	A	1758	G	P-O3'-C3'	5.82	126.68	119.70
12	J	73	LYS	N-CA-C	-5.81	95.31	111.00
34	A	905	U	C2-N1-C1'	5.76	124.61	117.70
34	A	1534	C	N1-C2-O2	5.75	122.35	118.90
34	A	1753	C	C6-N1-C1'	-5.75	113.90	120.80
34	A	1638	C	C2-N1-C1'	5.70	125.07	118.80
34	A	2155	U	C5-C6-N1	5.61	125.50	122.70
3	4	458	PRO	CA-N-CD	-5.58	103.68	111.50
34	A	2245	C	C6-N1-C2	-5.58	118.07	120.30
34	A	2195	U	C2-N1-C1'	5.58	124.39	117.70
34	A	2521	C	C6-N1-C1'	-5.56	114.13	120.80
34	A	619	C	N1-C2-O2	5.51	122.21	118.90
34	A	1533	U	N1-C2-O2	5.51	126.66	122.80
34	A	274	C	C2-N1-C1'	5.48	124.83	118.80
34	A	2374	U	C2-N1-C1'	5.45	124.23	117.70
34	A	2025	C	C2-N1-C1'	5.42	124.77	118.80
34	A	1102	G	O4'-C1'-N9	5.37	112.49	108.20
34	A	2230	C	N1-C2-O2	5.36	122.12	118.90
34	A	2320	C	C2-N1-C1'	5.35	124.69	118.80
34	A	2155	U	C6-N1-C1'	-5.30	113.78	121.20
34	A	2025	C	N1-C2-O2	5.28	122.07	118.90
34	A	2025	C	C6-N1-C2	-5.25	118.20	120.30
34	A	2374	U	C5-C4-O4	-5.22	122.77	125.90
34	A	617	U	C6-N1-C1'	-5.13	114.01	121.20
34	A	2155	U	N3-C2-O2	-5.11	118.62	122.20
34	A	1477	C	C2-N1-C1'	5.10	124.41	118.80
34	A	2372	U	C2-N1-C1'	5.06	123.77	117.70
34	A	1429	C	C2-N1-C1'	5.03	124.33	118.80
34	A	2805	G	O4'-C1'-N9	5.02	112.22	108.20
34	A	2698	C	N1-C2-O2	5.02	121.91	118.90

There are no chirality outliers.



All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	J	72	LEU	Mainchain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	474	0	500	16	0
2	3	189	0	205	4	0
3	4	3516	0	3564	198	0
4	B	2522	0	1285	45	0
5	C	2110	0	2165	43	0
6	D	1587	0	1630	58	0
7	E	1569	0	1607	36	0
8	F	1445	0	1476	94	0
9	G	1348	0	1399	58	0
10	H	1018	0	988	34	0
11	I	918	0	959	47	0
12	J	958	0	961	138	0
13	K	1130	0	1167	26	0
14	L	938	0	1000	25	0
15	M	1078	0	1151	36	0
16	N	1092	0	1128	22	0
17	O	928	0	972	25	0
18	P	956	0	991	39	0
19	Q	907	0	938	25	0
20	R	988	0	1038	24	0
21	S	754	0	801	24	0
22	T	873	0	909	22	0
23	U	756	0	802	22	0
24	V	732	0	782	33	0
25	W	735	0	756	18	0
26	X	586	0	601	14	0
27	Y	470	0	484	5	0
28	Z	531	0	541	15	0
29	b	423	0	463	0	0
30	c	405	0	411	0	0
31	d	377	0	411	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	e	502	0	541	0	0
33	f	299	0	324	0	0
34	A	63419	0	31905	1007	0
35	4	32	0	14	11	0
All	All	96565	0	64869	1959	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 (1959) 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)
12:J:56:ILE:CD1	12:J:74:THR:HG22	1.48	1.39
12:J:56:ILE:HD13	12:J:74:THR:CG2	1.49	1.39
12:J:56:ILE:HD12	12:J:74:THR:CA	1.52	1.37
12:J:56:ILE:CD1	12:J:74:THR:HA	1.58	1.31
12:J:24:PRO:HG2	12:J:25:PRO:CD	1.58	1.30
12:J:99:VAL:O	12:J:139:ILE:HG22	1.16	1.28
12:J:59:GLU:HB2	12:J:73:LYS:NZ	1.50	1.25
12:J:24:PRO:O	12:J:28:PRO:HD2	1.36	1.25
12:J:24:PRO:O	12:J:28:PRO:CD	1.84	1.24
3:4:444:HIS:CE1	12:J:24:PRO:CB	2.22	1.22
12:J:56:ILE:CD1	12:J:74:THR:CG2	2.11	1.22
3:4:21:ALA:HB1	3:4:88:ARG:HB3	1.23	1.21
12:J:24:PRO:CG	12:J:25:PRO:HD3	1.69	1.21
3:4:444:HIS:ND1	12:J:24:PRO:HB3	1.56	1.19
12:J:56:ILE:CD1	12:J:74:THR:CA	2.16	1.18
3:4:21:ALA:CB	3:4:88:ARG:HB3	1.75	1.17
12:J:98:LYS:HG2	12:J:138:GLY:O	1.45	1.16
12:J:99:VAL:O	12:J:139:ILE:CG2	1.94	1.15
3:4:444:HIS:CE1	12:J:24:PRO:HB3	1.84	1.11
34:A:273:A:H62	34:A:313:G:N2	1.51	1.06
34:A:2055:C:H41	34:A:2145:C:H5'	1.17	1.04
12:J:24:PRO:HG2	12:J:25:PRO:HD3	1.05	1.02
3:4:21:ALA:HB1	3:4:88:ARG:CB	1.90	1.02
9:G:18:THR:OG1	9:G:25:SER:N	1.93	0.99
34:A:1938:G:H21	34:A:1956:A:H62	1.05	0.98
12:J:98:LYS:CG	12:J:138:GLY:O	2.12	0.97
3:4:18:GLU:HB2	3:4:22:SER:H	1.29	0.97
12:J:24:PRO:CG	12:J:25:PRO:CD	2.34	0.95
12:J:24:PRO:HG2	12:J:25:PRO:HD2	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:24:PRO:CB	12:J:25:PRO:HD3	1.98	0.92
3:4:444:HIS:NE2	12:J:24:PRO:HB2	1.86	0.91
12:J:56:ILE:CD1	12:J:74:THR:CB	2.48	0.90
12:J:59:GLU:HB2	12:J:73:LYS:HZ3	1.37	0.90
12:J:59:GLU:HB2	12:J:73:LYS:HZ1	1.11	0.90
10:H:105:LYS:HD2	10:H:111:ASN:HB2	1.50	0.90
12:J:23:ALA:O	12:J:26:VAL:N	2.07	0.88
3:4:444:HIS:CE1	12:J:24:PRO:HB2	2.06	0.87
12:J:76:PRO:O	12:J:80:LEU:N	2.07	0.87
34:A:2129:C:H4'	34:A:2130:G:H8	1.40	0.86
3:4:444:HIS:CD2	12:J:24:PRO:HB2	2.10	0.86
34:A:2127:G:H3'	34:A:2128:G:H8	1.39	0.86
3:4:255:ASN:H	35:4:501:GCP:H3B1	1.39	0.86
34:A:2129:C:H4'	34:A:2130:G:H5'	1.58	0.85
34:A:2354:G:H5''	34:A:2356:G:H4'	1.55	0.85
34:A:285:U:H3'	34:A:286:G:H4'	1.58	0.85
34:A:273:A:N6	34:A:313:G:H21	1.75	0.85
34:A:273:A:N6	34:A:313:G:N2	2.24	0.85
3:4:201:ARG:HD2	3:4:205:GLU:HG2	1.57	0.84
3:4:198:VAL:HG21	3:4:203:PRO:HD2	1.59	0.84
12:J:79:LYS:HB2	12:J:82:LEU:HB2	1.60	0.84
34:A:297:G:H2'	34:A:298:G:H8	1.40	0.84
9:G:18:THR:HG1	9:G:25:SER:H	1.25	0.83
21:S:7:VAL:HG12	21:S:60:VAL:HG11	1.57	0.83
20:R:6:ARG:HD2	34:A:1365:G:H5''	1.61	0.82
3:4:18:GLU:CB	3:4:22:SER:H	1.92	0.82
34:A:1181:G:N1	34:A:1193:C:N3	2.28	0.82
6:D:119:LYS:NZ	34:A:2905:C:OP2	2.13	0.82
3:4:141:ILE:HG22	3:4:179:TRP:HZ2	1.44	0.82
12:J:23:ALA:O	12:J:27:GLY:N	2.13	0.82
12:J:23:ALA:O	12:J:24:PRO:C	2.17	0.81
12:J:56:ILE:HD11	12:J:74:THR:CG2	2.08	0.81
34:A:329:U:HO2'	34:A:446:G:H1	1.28	0.81
34:A:2133:G:H3'	34:A:2134:G:H8	1.42	0.81
8:F:41:VAL:HG22	8:F:103:MET:HG3	1.63	0.81
12:J:59:GLU:CB	12:J:73:LYS:HZ1	1.93	0.81
3:4:21:ALA:HB2	3:4:88:ARG:HB3	1.63	0.81
14:L:30:ARG:NH1	14:L:37:ASP:OD2	2.14	0.80
34:A:1181:G:N2	34:A:1193:C:O2	2.14	0.80
12:J:17:ALA:HB2	12:J:55:VAL:CA	2.12	0.80
26:X:64:PRO:HB3	34:A:759:G:H1	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:18:THR:HG21	9:G:25:SER:HB3	1.63	0.80
22:T:68:ASN:ND2	34:A:582:G:N3	2.31	0.79
12:J:98:LYS:NZ	12:J:140:THR:HG22	1.97	0.79
5:C:85:ASP:OD2	5:C:88:ARG:NH1	2.16	0.79
3:4:426:ARG:HB3	3:4:429:LEU:HD13	1.65	0.79
24:V:104:ASP:OD2	24:V:105:ILE:N	2.16	0.79
12:J:59:GLU:CB	12:J:73:LYS:NZ	2.42	0.78
6:D:104:GLU:N	6:D:104:GLU:OE1	2.17	0.78
12:J:56:ILE:HD11	12:J:74:THR:N	1.99	0.78
27:Y:18:VAL:HG12	27:Y:24:ARG:HG2	1.65	0.77
34:A:347:U:H2'	34:A:348:G:H8	1.47	0.77
34:A:273:A:H62	34:A:313:G:H21	1.27	0.77
12:J:17:ALA:HB2	12:J:55:VAL:N	1.99	0.77
8:F:142:GLN:HE21	8:F:156:PRO:HA	1.49	0.77
12:J:56:ILE:HD11	12:J:73:LYS:C	2.05	0.77
34:A:293:G:H2'	34:A:294:G:C8	2.20	0.77
9:G:17:VAL:HA	9:G:26:VAL:HG12	1.66	0.76
26:X:14:ARG:NH1	34:A:2503:G:N7	2.32	0.76
12:J:55:VAL:O	12:J:75:PRO:CB	2.34	0.76
34:A:2131:G:H3'	34:A:2132:U:H6	1.50	0.76
7:E:186:TYR:O	7:E:190:ASN:HB2	1.85	0.76
3:4:18:GLU:HB2	3:4:22:SER:N	2.00	0.75
20:R:36:LYS:NZ	34:A:1367:G:N7	2.34	0.75
12:J:24:PRO:O	12:J:28:PRO:HD3	1.86	0.75
12:J:56:ILE:CD1	12:J:74:THR:N	2.50	0.75
3:4:237:ARG:HG2	3:4:240:ARG:HH12	1.51	0.75
34:A:2358:A:HO2'	34:A:2383:U:HO2'	1.35	0.74
9:G:35:LEU:HB2	9:G:76:LEU:HD22	1.70	0.74
10:H:4:ILE:HG13	10:H:45:ARG:HA	1.69	0.74
34:A:297:G:H2'	34:A:298:G:C8	2.22	0.74
3:4:444:HIS:CE1	12:J:24:PRO:CA	2.69	0.74
34:A:960:G:OP2	34:A:960:G:N2	2.15	0.74
22:T:81:VAL:HG12	22:T:112:VAL:HG22	1.68	0.74
34:A:1157:G:O6	34:A:1234:U:O2	2.05	0.73
3:4:444:HIS:ND1	12:J:24:PRO:CB	2.34	0.73
17:O:10:LEU:HD21	17:O:40:LYS:HG2	1.71	0.73
17:O:106:ASP:OD2	34:A:1867:G:O2'	2.06	0.73
34:A:1938:G:N2	34:A:1956:A:H62	1.85	0.73
34:A:2317:G:H1	34:A:2418:U:H3	1.32	0.73
3:4:23:LEU:HA	3:4:102:LYS:HE2	1.70	0.73
3:4:300:THR:HB	3:4:318:THR:HG23	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2055:C:N4	34:A:2145:C:H5'	1.99	0.73
34:A:2361:U:H3	34:A:2376:G:H1	1.36	0.73
21:S:30:GLU:OE2	21:S:32:GLY:N	2.16	0.73
8:F:23:LEU:HD11	8:F:175:ALA:HB1	1.70	0.73
9:G:96:ARG:HH22	9:G:98:GLN:HB3	1.53	0.73
24:V:10:LEU:HD13	24:V:80:PRO:HG3	1.70	0.73
34:A:1996:U:OP2	34:A:2001:A:N6	2.22	0.72
34:A:2255:A:N3	34:A:2679:G:O2'	2.22	0.72
34:A:2055:C:H42	34:A:2122:U:H2'	1.54	0.72
12:J:56:ILE:HD13	12:J:74:THR:CB	2.14	0.72
27:Y:41:ARG:HG2	27:Y:42:PRO:HD2	1.70	0.72
3:4:330:HIS:ND1	3:4:330:HIS:O	2.20	0.72
10:H:84:ALA:HB3	10:H:94:SER:H	1.54	0.72
34:A:2474:G:O2'	34:A:2720:C:OP1	2.08	0.72
34:A:298:G:N2	34:A:300:G:O2'	2.22	0.71
9:G:2:SER:HA	9:G:55:ARG:HH12	1.54	0.71
34:A:2158:C:H4'	34:A:2159:G:H2'	1.70	0.71
3:4:420:VAL:HG11	3:4:463:LEU:HB3	1.71	0.71
34:A:3023:G:H2'	34:A:3024:A:H8	1.55	0.71
25:W:37:LEU:HB3	25:W:45:GLN:HB2	1.71	0.71
3:4:21:ALA:CB	3:4:88:ARG:CB	2.54	0.71
20:R:49:ASP:OD2	34:A:651:G:N2	2.24	0.71
8:F:20:ARG:HG3	8:F:35:ILE:HG21	1.71	0.71
14:L:3:GLN:NE2	34:A:2219:U:O2	2.23	0.71
20:R:92:ARG:NH2	34:A:1272:C:OP1	2.24	0.71
34:A:2123:A:N7	34:A:2145:C:C4	2.59	0.71
18:P:43:SER:O	18:P:112:ARG:NH2	2.24	0.70
3:4:376:GLY:HA3	3:4:379:LEU:HG	1.73	0.70
20:R:37:GLU:OE2	34:A:1367:G:N2	2.19	0.70
3:4:24:ARG:HD2	3:4:88:ARG:HE	1.57	0.70
9:G:2:SER:N	34:A:2973:A:OP1	2.24	0.70
18:P:9:ASN:OD1	18:P:10:ILE:N	2.25	0.70
9:G:12:PRO:HG3	9:G:81:THR:HG22	1.73	0.70
3:4:395:ARG:HB2	35:4:501:GCP:N1	2.07	0.70
34:A:1181:G:O6	34:A:1193:C:N4	2.25	0.70
4:B:26:A:H2	4:B:115:A:H1'	1.57	0.69
8:F:15:TYR:HA	8:F:19:ILE:HG12	1.74	0.69
3:4:76:THR:HG21	3:4:276:LEU:HB2	1.72	0.69
34:A:3023:G:H2'	34:A:3024:A:C8	2.27	0.69
8:F:138:GLY:HA2	8:F:160:ASP:HA	1.74	0.69
34:A:2127:G:H3'	34:A:2128:G:C8	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:29:TYR:CD1	8:F:34:GLN:HB2	2.28	0.69
24:V:15:LYS:NZ	34:A:390:G:O2'	2.25	0.69
12:J:119:ASN:ND2	34:A:1176:G:N3	2.38	0.69
34:A:1415:A:H4'	34:A:1416:A:H5''	1.75	0.69
5:C:175:LEU:HD11	5:C:185:VAL:HG12	1.75	0.69
34:A:2123:A:N7	34:A:2145:C:C5	2.61	0.69
22:T:56:LYS:NZ	34:A:576:G:O2'	2.21	0.68
34:A:2051:U:H4'	34:A:2160:A:H62	1.58	0.68
34:A:7:U:O2'	34:A:8:U:O4'	2.12	0.68
34:A:289:A:H2'	34:A:290:C:H5	1.59	0.68
34:A:2851:G:N2	34:A:3001:G:OP2	2.27	0.68
8:F:53:ASP:OD1	8:F:54:ALA:N	2.27	0.68
34:A:737:A:N1	34:A:2593:A:O2'	2.25	0.68
12:J:56:ILE:CD1	12:J:73:LYS:C	2.61	0.68
12:J:81:LEU:HD21	12:J:102:VAL:HG21	1.74	0.68
9:G:17:VAL:O	9:G:45:ARG:NH1	2.27	0.68
23:U:34:HIS:ND1	23:U:36:ASP:OD1	2.25	0.68
34:A:1411:G:OP1	34:A:2933:G:O2'	2.08	0.68
14:L:69:ARG:HE	14:L:105:GLU:HG2	1.59	0.68
15:M:94:GLY:HA2	15:M:125:THR:HG22	1.76	0.68
34:A:1754:G:H1	34:A:1759:A:H2	1.40	0.68
5:C:257:THR:OG1	34:A:2014:G:O2'	2.12	0.68
3:4:444:HIS:CG	12:J:24:PRO:CB	2.77	0.68
14:L:4:GLN:NE2	14:L:22:ILE:O	2.25	0.68
4:B:3:U:O2'	4:B:5:C:OP2	2.10	0.67
6:D:144:VAL:HA	6:D:147:ARG:HG3	1.76	0.67
20:R:48:ARG:NH1	20:R:49:ASP:OD1	2.26	0.67
34:A:1756:G:H1'	34:A:1758:G:H22	1.59	0.67
3:4:371:ILE:HG21	3:4:391:PHE:HD1	1.57	0.67
34:A:1195:A:H2	34:A:1206:A:H8	1.42	0.67
12:J:56:ILE:HG12	12:J:72:LEU:HB3	1.76	0.67
34:A:499:G:OP2	34:A:2630:A:O2'	2.13	0.67
34:A:587:G:N1	34:A:590:A:OP2	2.28	0.67
8:F:108:ASP:HA	8:F:111:ILE:HG22	1.76	0.67
6:D:27:THR:OG1	6:D:196:GLY:O	2.13	0.67
16:N:118:LEU:HD12	16:N:131:ILE:HG23	1.77	0.67
34:A:978:A:H2'	34:A:979:G:H8	1.58	0.67
13:K:141:GLU:OE1	13:K:142:ILE:N	2.28	0.67
34:A:2527:G:O6	34:A:2538:A:N6	2.27	0.67
17:O:90:ARG:NH2	34:A:3101:C:O2'	2.27	0.67
34:A:2123:A:C8	34:A:2145:C:C2	2.82	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:24:PRO:CB	12:J:25:PRO:CD	2.70	0.67
15:M:99:VAL:HG13	15:M:104:VAL:HG23	1.76	0.67
18:P:8:GLN:HG2	18:P:12:GLU:OE2	1.95	0.67
12:J:129:ILE:HD11	34:A:1199:U:H1'	1.77	0.67
34:A:1864:U:O2	34:A:1865:A:N6	2.27	0.67
34:A:2350:G:H2'	34:A:2351:A:C8	2.30	0.66
6:D:148:PRO:O	34:A:2735:U:O2'	2.13	0.66
18:P:46:HIS:HB3	18:P:65:SER:HB3	1.76	0.66
3:4:21:ALA:HB2	3:4:88:ARG:HD2	1.75	0.66
3:4:291:ASP:OD1	3:4:292:GLY:N	2.29	0.66
8:F:68:THR:HG23	8:F:70:GLN:H	1.58	0.66
26:X:11:ARG:O	26:X:14:ARG:NH2	2.23	0.66
34:A:1478:C:O2'	34:A:2026:A:N3	2.27	0.66
3:4:234:ASP:OD1	3:4:235:THR:N	2.28	0.66
34:A:2399:A:HO2'	34:A:2400:C:H6	1.43	0.66
3:4:85:LEU:HD21	3:4:109:VAL:HG21	1.78	0.66
11:I:69:LEU:HB3	11:I:109:TYR:HB3	1.77	0.66
12:J:23:ALA:HA	12:J:26:VAL:HB	1.78	0.66
34:A:286:G:H2'	34:A:287:A:H8	1.59	0.66
34:A:1758:G:O2'	34:A:1759:A:OP2	2.11	0.66
34:A:1212:U:H3'	34:A:1213:A:H5''	1.78	0.66
6:D:39:ILE:O	6:D:44:ARG:NH2	2.26	0.66
34:A:263:G:O2'	34:A:517:A:N3	2.26	0.66
34:A:289:A:N7	34:A:298:G:N1	2.39	0.66
3:4:195:GLY:HA2	3:4:204:GLY:HA2	1.78	0.65
6:D:39:ILE:HD11	6:D:95:TYR:HB2	1.78	0.65
12:J:22:PRO:HG2	12:J:41:CYS:SG	2.36	0.65
11:I:47:ALA:HB1	11:I:80:ALA:HB1	1.78	0.65
8:F:17:GLU:N	8:F:17:GLU:OE2	2.27	0.65
34:A:137:G:H21	34:A:1524:G:H1'	1.62	0.65
34:A:944:A:N7	34:A:2471:A:O2'	2.29	0.65
34:A:2051:U:O2	34:A:2194:A:O2'	2.13	0.65
34:A:2121:G:H5'	34:A:2145:C:P	2.37	0.65
34:A:2123:A:C8	34:A:2145:C:N3	2.65	0.65
3:4:289:PHE:CE1	3:4:295:PHE:HB3	2.32	0.65
34:A:2394:A:OP1	34:A:2397:C:N4	2.29	0.65
17:O:70:ILE:HG23	17:O:72:ASP:H	1.61	0.65
12:J:24:PRO:O	12:J:28:PRO:CG	2.44	0.65
17:O:38:GLU:HG3	17:O:111:ALA:HB2	1.79	0.65
34:A:1184:U:N3	34:A:1187:A:OP2	2.27	0.65
7:E:105:LYS:NZ	34:A:699:U:OP2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2528:G:H22	34:A:2536:U:H3	1.44	0.65
4:B:53:A:N7	18:P:45:ARG:NH2	2.45	0.64
8:F:14:ARG:O	8:F:18:GLU:HG3	1.96	0.64
9:G:165:TYR:HB2	9:G:168:GLU:HG2	1.79	0.64
24:V:45:THR:O	34:A:571:A:O2'	2.14	0.64
13:K:3:THR:HG21	20:R:61:TRP:HE1	1.62	0.64
34:A:1122:C:H2'	34:A:1129:G:H2'	1.78	0.64
34:A:1202:A:O3'	34:A:1223:U:O2'	2.13	0.64
3:4:444:HIS:CG	12:J:24:PRO:HB3	2.29	0.64
12:J:82:LEU:HD11	12:J:90:GLY:HA2	1.80	0.64
34:A:523:U:H2'	34:A:524:C:H5'	1.79	0.64
3:4:108:GLU:HA	3:4:111:LEU:HG	1.79	0.64
3:4:136:VAL:HG13	3:4:138:VAL:H	1.63	0.64
34:A:2390:U:H2'	34:A:2392:A:N7	2.12	0.64
12:J:56:ILE:HD11	12:J:74:THR:CA	2.24	0.64
20:R:83:LEU:HD22	20:R:88:VAL:HG21	1.79	0.64
34:A:2158:C:H5'	34:A:2159:G:C4	2.33	0.64
1:2:6:ILE:HD11	1:2:54:VAL:HG21	1.80	0.64
3:4:143:ARG:NH1	3:4:305:ARG:O	2.29	0.64
34:A:1696:G:O2'	34:A:1736:G:O6	2.15	0.64
34:A:2054:C:O2	34:A:2145:C:C2	2.51	0.63
8:F:27:PHE:CZ	8:F:35:ILE:HG13	2.33	0.63
12:J:24:PRO:HB2	12:J:25:PRO:HD3	1.80	0.63
34:A:634:C:H3'	34:A:635:G:H5''	1.80	0.63
34:A:2129:C:H4'	34:A:2130:G:C8	2.29	0.63
3:4:178:GLY:O	3:4:181:GLU:HG3	1.98	0.63
8:F:27:PHE:HZ	8:F:35:ILE:HG13	1.63	0.63
34:A:2123:A:C8	34:A:2145:C:C4	2.86	0.63
3:4:286:ARG:HG3	34:A:2697:U:H1'	1.80	0.63
7:E:127:VAL:HG11	7:E:148:LEU:HD11	1.80	0.63
12:J:10:LEU:N	12:J:60:ILE:O	2.32	0.63
3:4:285:ARG:NH2	34:A:2695:A:OP1	2.30	0.63
5:C:124:ASP:OD1	5:C:129:ASN:ND2	2.32	0.63
26:X:15:ASP:OD1	34:A:2487:C:N4	2.31	0.63
34:A:66:C:O2	34:A:70:A:O2'	2.16	0.63
34:A:242:G:O2'	34:A:254:G:O6	2.13	0.63
6:D:40:ARG:HD2	6:D:83:GLU:OE1	1.99	0.63
9:G:20:ASN:N	9:G:20:ASN:OD1	2.30	0.63
34:A:279:U:H2'	34:A:280:G:H8	1.64	0.63
34:A:2575:G:O2'	34:A:2590:A:N6	2.30	0.63
17:O:57:LYS:O	17:O:62:ASN:ND2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:453:U:H1'	34:A:454:U:H5	1.63	0.63
34:A:978:A:H2'	34:A:979:G:C8	2.34	0.63
34:A:2872:G:H2'	34:A:2873:U:C6	2.33	0.63
3:4:107:ARG:NH2	3:4:136:VAL:O	2.32	0.63
5:C:37:LEU:HD13	5:C:62:TYR:HB2	1.81	0.63
10:H:114:LYS:NZ	34:A:282:A:OP1	2.28	0.63
34:A:273:A:N6	34:A:313:G:C2	2.66	0.63
14:L:93:PRO:HD2	14:L:113:LYS:HE3	1.81	0.62
3:4:332:VAL:HB	3:4:343:ILE:HD11	1.81	0.62
4:B:111:C:H2'	4:B:112:C:C6	2.34	0.62
23:U:85:LYS:NZ	34:A:1514:C:OP1	2.27	0.62
34:A:1195:A:H2	34:A:1206:A:C8	2.16	0.62
26:X:19:GLN:NE2	34:A:2486:U:OP2	2.32	0.62
1:2:57:GLU:N	1:2:57:GLU:OE1	2.32	0.62
34:A:1625:G:N1	34:A:1626:G:O6	2.31	0.62
11:I:58:LYS:HA	11:I:73:PHE:HE2	1.64	0.62
22:T:71:LEU:HD21	22:T:116:SER:HB2	1.80	0.62
34:A:1313:U:H2'	34:A:1314:C:H6	1.65	0.62
5:C:208:LYS:HG3	5:C:211:ARG:HB2	1.81	0.62
9:G:35:LEU:HD13	9:G:76:LEU:HD13	1.80	0.62
10:H:131:PRO:HB2	10:H:143:LYS:NZ	2.15	0.62
13:K:90:GLY:O	13:K:94:GLU:HG3	1.99	0.62
34:A:277:U:H2'	34:A:278:A:C8	2.35	0.62
2:3:17:ASN:ND2	34:A:1103:C:O2	2.31	0.62
11:I:58:LYS:HD2	11:I:70:ASP:HB3	1.81	0.62
8:F:111:ILE:HA	8:F:115:LEU:HD12	1.80	0.62
24:V:15:LYS:HZ3	34:A:411:G:H1	1.48	0.62
34:A:2294:A:H2'	34:A:2295:C:C6	2.35	0.62
13:K:125:TYR:OH	13:K:132:HIS:NE2	2.32	0.62
34:A:1201:G:N2	34:A:1204:A:OP2	2.33	0.62
34:A:2131:G:H3'	34:A:2132:U:C6	2.32	0.62
6:D:160:VAL:HG21	34:A:2842:G:H21	1.65	0.62
34:A:1479:G:N2	34:A:1482:A:OP2	2.29	0.62
5:C:89:THR:HG21	34:A:2038:A:H5''	1.82	0.61
6:D:64:LYS:HG2	34:A:3011:C:H4'	1.80	0.61
34:A:2410:A:H2'	34:A:2411:U:C6	2.35	0.61
15:M:65:LYS:NZ	34:A:2641:U:OP1	2.28	0.61
26:X:75:ARG:HD2	34:A:2558:C:H42	1.65	0.61
34:A:326:A:N6	34:A:450:G:H21	1.98	0.61
34:A:823:C:H2'	34:A:824:G:H8	1.65	0.61
12:J:62:VAL:HA	12:J:67:SER:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:997:G:H2'	34:A:998:G:H5'	1.83	0.61
15:M:80:VAL:HG22	15:M:114:GLY:HA2	1.83	0.61
34:A:1199:U:H2'	34:A:1200:U:C6	2.35	0.61
34:A:2055:C:H5''	34:A:2149:C:C5	2.35	0.61
3:4:370:LYS:HG2	35:4:501:GCP:C5	2.31	0.61
12:J:57:PRO:N	12:J:73:LYS:O	2.33	0.61
34:A:450:G:O2'	34:A:451:U:H5'	2.01	0.61
3:4:379:LEU:N	3:4:383:ARG:HB2	2.16	0.61
18:P:42:ARG:HA	18:P:47:ILE:HG13	1.83	0.61
34:A:1770:G:OP1	34:A:1937:U:O2'	2.13	0.61
34:A:2125:A:H2'	34:A:2125:A:N3	2.16	0.61
10:H:100:VAL:HG21	10:H:146:LEU:HD21	1.81	0.61
14:L:115:VAL:HG13	14:L:121:VAL:HG21	1.82	0.61
8:F:125:SER:H	8:F:185:LYS:NZ	1.98	0.61
34:A:742:G:O2'	34:A:2575:G:OP1	2.17	0.61
34:A:1223:U:H2'	34:A:1224:G:H8	1.66	0.61
25:W:21:LYS:O	25:W:25:ARG:HG3	2.01	0.61
34:A:2336:U:O2'	34:A:2337:A:O5'	2.18	0.61
7:E:189:LEU:HD13	15:M:9:LEU:HD11	1.83	0.60
34:A:920:G:N2	34:A:944:A:OP1	2.34	0.60
34:A:1710:A:H62	34:A:1716:A:H5''	1.66	0.60
34:A:2133:G:H5''	34:A:2134:G:N7	2.16	0.60
4:B:59:A:N3	18:P:9:ASN:ND2	2.49	0.60
34:A:2412:U:H2'	34:A:2413:G:C8	2.36	0.60
18:P:62:ALA:O	18:P:91:ARG:NH1	2.34	0.60
25:W:32:LYS:NZ	25:W:48:GLU:OE1	2.30	0.60
34:A:2339:G:O6	34:A:2394:A:N6	2.33	0.60
34:A:2359:G:C2	34:A:2360:C:H1'	2.36	0.60
34:A:3115:A:H2'	34:A:3116:C:C6	2.36	0.60
6:D:83:GLU:OE2	34:A:2860:U:H4'	2.01	0.60
17:O:67:MET:HG2	17:O:76:VAL:HG21	1.84	0.60
34:A:1003:A:N3	34:A:1004:C:O2'	2.30	0.60
24:V:1:MET:HE2	24:V:28:PRO:HB3	1.83	0.60
8:F:29:TYR:HD1	8:F:34:GLN:HB2	1.65	0.60
11:I:88:ASP:OD1	11:I:88:ASP:N	2.32	0.60
34:A:289:A:H2'	34:A:290:C:C5	2.36	0.60
34:A:2062:G:H21	34:A:2119:C:H5	1.49	0.60
34:A:2726:G:H5''	34:A:2727:A:H5''	1.84	0.60
3:4:348:THR:O	3:4:352:GLU:HG2	2.00	0.60
34:A:1728:U:H5'	34:A:1729:A:O5'	2.02	0.60
34:A:2552:A:H2'	34:A:2553:G:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:95:ARG:NH2	34:A:2537:C:OP1	2.34	0.60
22:T:54:VAL:O	22:T:58:ILE:HG13	2.02	0.60
34:A:353:G:H1	34:A:442:U:H3	1.47	0.60
3:4:63:ALA:O	3:4:66:SER:OG	2.15	0.60
3:4:50:VAL:HG12	3:4:83:GLU:HB3	1.84	0.59
11:I:25:VAL:HG12	11:I:106:LYS:HG3	1.84	0.59
12:J:56:ILE:HD13	12:J:74:THR:HG22	0.67	0.59
13:K:129:ASP:OD1	13:K:129:ASP:N	2.34	0.59
14:L:5:GLU:HA	14:L:20:LEU:HD21	1.84	0.59
34:A:292:G:OP1	34:A:344:G:N2	2.35	0.59
34:A:747:A:N6	34:A:768:G:O2'	2.35	0.59
3:4:280:LEU:HA	3:4:301:VAL:HG13	1.83	0.59
14:L:2:ILE:HG13	14:L:8:LEU:HD21	1.84	0.59
34:A:2054:C:O2	34:A:2145:C:C4	2.55	0.59
11:I:26:THR:HG22	11:I:105:ILE:HG23	1.85	0.59
12:J:76:PRO:CB	12:J:79:LYS:HG3	2.32	0.59
14:L:112:MET:O	14:L:116:SER:OG	2.19	0.59
34:A:292:G:H2'	34:A:293:G:C8	2.37	0.59
34:A:747:A:H2'	34:A:748:U:O4'	2.03	0.59
4:B:31:C:OP1	18:P:14:ARG:NH1	2.35	0.59
9:G:19:ILE:O	9:G:19:ILE:HG22	2.02	0.59
20:R:50:ARG:O	20:R:54:LYS:NZ	2.36	0.59
34:A:279:U:H3	34:A:307:G:H1	1.51	0.59
34:A:635:G:O2'	34:A:636:U:O5'	2.20	0.59
13:K:108:MET:SD	34:A:1256:G:N2	2.70	0.59
34:A:1938:G:H21	34:A:1956:A:N6	1.87	0.59
28:Z:25:SER:HB2	28:Z:54:ILE:HD11	1.84	0.59
34:A:1003:A:H1'	34:A:1004:C:H2'	1.84	0.59
34:A:2382:G:O2'	34:A:2383:U:O4'	2.21	0.59
12:J:135:ARG:HH22	34:A:1206:A:N6	2.00	0.59
34:A:1063:G:O6	34:A:1090:G:N2	2.36	0.59
34:A:808:A:O2'	34:A:1468:A:N3	2.31	0.59
34:A:993:G:N2	34:A:1015:A:OP2	2.30	0.59
25:W:37:LEU:HB2	25:W:47:LEU:HD11	1.85	0.58
34:A:271:A:OP2	34:A:314:G:N1	2.27	0.58
34:A:473:C:O2'	34:A:476:G:N2	2.36	0.58
34:A:2331:U:H4'	34:A:2374:U:H5'	1.84	0.58
34:A:1160:G:H1	34:A:1231:U:H3	1.51	0.58
12:J:44:TYR:OH	12:J:56:ILE:O	2.20	0.58
34:A:996:G:C4	34:A:997:G:C8	2.91	0.58
34:A:1530:G:H2'	34:A:1531:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2127:G:H5'	34:A:2153:G:H2'	1.84	0.58
3:4:148:LEU:HB3	3:4:168:GLN:HG2	1.85	0.58
7:E:178:ILE:HD12	34:A:708:G:H1	1.67	0.58
21:S:75:ILE:HB	21:S:88:GLN:HB3	1.84	0.58
34:A:2872:G:H2'	34:A:2873:U:H6	1.69	0.58
3:4:24:ARG:HG3	3:4:26:VAL:HG13	1.84	0.58
7:E:153:LYS:NZ	34:A:1319:A:OP1	2.27	0.58
16:N:47:ILE:HD12	16:N:70:PRO:HG3	1.85	0.58
34:A:2364:C:H2'	34:A:2365:A:H8	1.68	0.58
12:J:26:VAL:HG13	12:J:30:LEU:HD23	1.85	0.58
16:N:44:ASN:OD1	16:N:44:ASN:N	2.37	0.58
34:A:1011:A:C6	34:A:1012:C:H1'	2.39	0.58
34:A:2061:U:H2'	34:A:2062:G:H4'	1.85	0.58
6:D:48:SER:OG	6:D:86:LEU:O	2.18	0.58
8:F:11:LEU:HD11	8:F:111:ILE:HG21	1.86	0.58
34:A:1704:U:H2'	34:A:1705:C:C6	2.38	0.58
34:A:2869:C:H3'	34:A:2870:C:H5'	1.85	0.58
3:4:141:ILE:HG22	3:4:179:TRP:CZ2	2.33	0.58
6:D:135:GLN:HE21	34:A:2802:G:H21	1.52	0.58
9:G:58:ASP:O	9:G:63:ARG:NH1	2.36	0.58
12:J:12:LYS:H	12:J:12:LYS:HD3	1.68	0.58
34:A:1205:G:O2'	34:A:1207:G:O4'	2.21	0.58
4:B:49:C:OP1	18:P:42:ARG:NH1	2.31	0.57
19:Q:101:GLU:N	19:Q:101:GLU:OE1	2.36	0.57
34:A:248:G:H5'	34:A:250:G:N7	2.19	0.57
34:A:389:G:N1	34:A:392:A:OP2	2.31	0.57
12:J:95:HIS:HB2	34:A:1195:A:H4'	1.85	0.57
15:M:82:ASP:HA	15:M:85:LYS:HG2	1.86	0.57
3:4:214:ARG:NH1	34:A:2684:U:O2'	2.37	0.57
3:4:315:PHE:O	3:4:319:LEU:HG	2.04	0.57
12:J:98:LYS:HZ2	12:J:140:THR:HG22	1.65	0.57
34:A:1204:A:O2'	34:A:1205:G:N7	2.37	0.57
18:P:20:ARG:NH1	34:A:2558:C:OP2	2.37	0.57
34:A:3078:G:N2	34:A:3081:A:OP2	2.29	0.57
12:J:129:ILE:HA	34:A:1198:C:H1'	1.87	0.57
28:Z:52:GLN:O	28:Z:56:ARG:HG3	2.04	0.57
34:A:284:G:H21	34:A:286:G:H22	1.50	0.57
34:A:996:G:H3'	34:A:997:G:H8	1.70	0.57
34:A:347:U:H2'	34:A:348:G:C8	2.35	0.57
34:A:1537:U:H2'	34:A:1538:G:C8	2.39	0.57
34:A:2238:A:H2'	34:A:2239:A:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:29:C:N4	34:A:535:A:OP2	2.38	0.57
34:A:2053:C:P	34:A:2134:G:H22	2.28	0.57
34:A:2125:A:H3'	34:A:2126:C:C5	2.39	0.57
34:A:2402:C:H2'	34:A:2403:U:C2	2.39	0.57
16:N:71:ASP:OD1	16:N:71:ASP:N	2.33	0.57
21:S:9:THR:HG21	21:S:37:LEU:HD22	1.86	0.57
5:C:177:MET:HG2	5:C:181:GLU:O	2.05	0.57
9:G:149:ILE:O	9:G:163:VAL:HG11	2.05	0.57
23:U:4:ILE:HD12	28:Z:19:LYS:NZ	2.19	0.57
34:A:757:G:OP2	34:A:757:G:N2	2.23	0.57
3:4:246:PRO:HG3	3:4:293:ARG:HD3	1.86	0.56
3:4:424:TYR:CE1	3:4:444:HIS:HE1	2.23	0.56
12:J:93:GLU:HA	12:J:96:LYS:HE3	1.87	0.56
12:J:129:ILE:HG22	12:J:130:ILE:HD13	1.87	0.56
34:A:995:U:H2'	34:A:996:G:H8	1.69	0.56
34:A:2358:A:H3'	34:A:2359:G:H8	1.70	0.56
34:A:2358:A:O2'	34:A:2383:U:O2'	2.12	0.56
34:A:2362:C:H2'	34:A:2363:A:C8	2.40	0.56
34:A:2761:U:H2'	34:A:2762:C:C6	2.40	0.56
34:A:3115:A:H2'	34:A:3116:C:H6	1.70	0.56
3:4:285:ARG:NH1	34:A:2696:G:OP2	2.38	0.56
3:4:392:VAL:HG21	3:4:403:LEU:HD22	1.87	0.56
8:F:111:ILE:HD11	8:F:182:PHE:HA	1.86	0.56
12:J:89:LYS:NZ	34:A:1183:U:OP1	2.38	0.56
26:X:64:PRO:HB3	34:A:759:G:N1	2.18	0.56
34:A:1671:U:O2	34:A:1673:A:N6	2.37	0.56
34:A:2326:A:C5	34:A:2410:A:C2	2.94	0.56
34:A:2332:U:N3	34:A:2404:G:N3	2.52	0.56
6:D:29:VAL:HG21	6:D:194:ILE:HD12	1.87	0.56
9:G:3:ARG:HB3	34:A:2975:G:C8	2.41	0.56
12:J:107:VAL:HG23	12:J:108:ARG:HD3	1.87	0.56
23:U:57:VAL:HG13	23:U:84:VAL:HG22	1.87	0.56
34:A:327:U:H2'	34:A:328:C:C6	2.40	0.56
11:I:109:TYR:HA	11:I:115:LEU:HA	1.86	0.56
34:A:1000:C:H2'	34:A:1001:C:H6	1.70	0.56
34:A:3014:A:H62	34:A:3113:A:H2	1.53	0.56
3:4:251:VAL:HG12	3:4:300:THR:HG21	1.86	0.56
10:H:62:ILE:H	10:H:65:ALA:HB3	1.69	0.56
34:A:159:A:N3	34:A:2431:C:O2'	2.36	0.56
34:A:2163:U:H1'	34:A:2198:C:H4'	1.87	0.56
3:4:444:HIS:CG	12:J:24:PRO:HB2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:31:LEU:HD23	11:I:35:ASN:ND2	2.21	0.56
11:I:40:ARG:HH21	11:I:50:THR:HA	1.69	0.56
12:J:56:ILE:HD12	12:J:74:THR:HA	0.69	0.56
34:A:1118:A:H2'	34:A:1119:A:C8	2.41	0.56
3:4:381:GLN:HA	3:4:384:ARG:HB2	1.88	0.56
3:4:424:TYR:HB3	12:J:28:PRO:HA	1.86	0.56
7:E:158:ILE:HD13	7:E:197:SER:HB3	1.87	0.56
12:J:59:GLU:CB	12:J:73:LYS:HZ3	2.15	0.56
34:A:2357:A:O2'	34:A:2382:G:N3	2.31	0.56
3:4:55:TRP:N	3:4:87:GLN:O	2.35	0.56
14:L:16:ALA:HB2	14:L:52:VAL:HG21	1.86	0.56
24:V:82:ARG:NH2	34:A:382:A:OP2	2.37	0.56
34:A:1178:U:H3	34:A:1206:A:H2	1.52	0.56
34:A:1188:A:H2'	34:A:1215:U:OP1	2.04	0.56
34:A:1907:A:H2'	34:A:1908:A:C8	2.40	0.56
12:J:23:ALA:O	12:J:25:PRO:N	2.38	0.56
24:V:1:MET:HG2	24:V:2:LYS:O	2.06	0.56
34:A:1203:A:H2'	34:A:1204:A:C4	2.41	0.56
34:A:1755:A:N3	34:A:1755:A:H2'	2.20	0.56
34:A:1825:C:N4	34:A:1840:G:OP2	2.35	0.56
3:4:370:LYS:HE2	35:4:501:GCP:N9	2.21	0.56
9:G:33:LEU:HD11	9:G:137:ILE:HG22	1.87	0.56
9:G:75:ASN:ND2	34:A:2971:G:OP1	2.37	0.55
17:O:8:PRO:HG2	34:A:1870:U:C4	2.41	0.55
19:Q:28:HIS:HD2	19:Q:41:VAL:HG22	1.71	0.55
20:R:28:ARG:NH1	20:R:38:GLN:OE1	2.39	0.55
34:A:2053:C:N4	34:A:2158:C:OP1	2.39	0.55
34:A:2121:G:H8	34:A:2121:G:O5'	1.88	0.55
34:A:2341:U:H5'	34:A:2371:G:O2'	2.06	0.55
34:A:2805:G:OP2	34:A:2805:G:N2	2.33	0.55
5:C:177:MET:HA	5:C:177:MET:HE3	1.87	0.55
13:K:106:ILE:HD12	13:K:109:LEU:HD12	1.89	0.55
22:T:66:GLN:HG3	22:T:73:PRO:HG3	1.88	0.55
34:A:2382:G:H2'	34:A:2383:U:C6	2.40	0.55
3:4:195:GLY:HA2	3:4:204:GLY:CA	2.37	0.55
5:C:141:VAL:HG13	5:C:162:SER:HB2	1.87	0.55
12:J:30:LEU:HD12	12:J:35:VAL:HB	1.86	0.55
14:L:21:CYS:HA	14:L:41:ALA:HA	1.88	0.55
34:A:217:G:H22	34:A:235:U:H4'	1.70	0.55
4:B:5:C:HO2'	4:B:6:G:H8	1.54	0.55
21:S:8:LYS:HG3	21:S:40:ALA:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:79:ALA:HB2	22:T:115:GLU:HB2	1.89	0.55
34:A:1530:G:H21	34:A:1805:G:H1	1.53	0.55
34:A:1536:A:H2'	34:A:1537:U:O4'	2.07	0.55
8:F:14:ARG:HH22	8:F:180:LEU:HD23	1.71	0.55
9:G:55:ARG:HD3	9:G:63:ARG:HA	1.89	0.55
11:I:54:ASN:HA	11:I:57:VAL:HG12	1.88	0.55
11:I:88:ASP:O	11:I:91:LYS:NZ	2.33	0.55
12:J:76:PRO:O	12:J:80:LEU:CA	2.55	0.55
34:A:1305:G:H2'	34:A:1306:G:H8	1.72	0.55
23:U:11:ILE:O	28:Z:33:ARG:NH2	2.40	0.55
34:A:365:U:H2'	34:A:366:G:H8	1.72	0.55
34:A:681:C:H2'	34:A:682:A:C8	2.42	0.55
34:A:858:A:O2'	34:A:1877:U:OP1	2.23	0.55
34:A:965:U:H2'	34:A:966:U:C6	2.42	0.55
34:A:6:G:O2'	34:A:3114:A:N6	2.40	0.55
34:A:2146:A:H3'	34:A:2146:A:OP2	2.07	0.55
34:A:2777:G:N1	34:A:2779:U:C5	2.75	0.55
4:B:26:A:C2	4:B:115:A:H1'	2.41	0.55
5:C:258:ARG:NE	5:C:262:LYS:HZ3	2.05	0.55
7:E:50:HIS:O	7:E:50:HIS:ND1	2.40	0.55
7:E:130:LEU:HD23	7:E:130:LEU:H	1.71	0.55
8:F:19:ILE:HD12	8:F:179:ALA:HB1	1.89	0.55
34:A:2054:C:H4'	34:A:2055:C:OP2	2.06	0.55
1:2:18:LYS:NZ	34:A:1035:G:OP1	2.34	0.55
4:B:42:C:H2'	8:F:73:GLU:HG3	1.89	0.55
12:J:96:LYS:HE2	34:A:1194:C:H4'	1.89	0.55
34:A:56:U:O2'	34:A:71:A:OP2	2.21	0.55
34:A:491:U:H4'	34:A:492:C:H5'	1.89	0.55
34:A:1201:G:N2	34:A:1203:A:H3'	2.22	0.55
3:4:34:ALA:HB2	3:4:80:GLU:HG3	1.89	0.54
3:4:255:ASN:N	35:4:501:GCP:H3B1	2.16	0.54
19:Q:30:LYS:NZ	19:Q:78:PRO:O	2.31	0.54
34:A:1291:G:C2	34:A:1292:U:H1'	2.43	0.54
34:A:3117:U:H2'	34:A:3118:U:C6	2.42	0.54
21:S:10:GLY:O	21:S:12:LYS:NZ	2.39	0.54
34:A:285:U:H2'	34:A:287:A:H5'	1.89	0.54
3:4:379:LEU:H	3:4:383:ARG:HB2	1.72	0.54
11:I:18:LYS:HB3	11:I:64:ALA:HB1	1.89	0.54
13:K:43:THR:HG22	20:R:100:VAL:HG13	1.90	0.54
20:R:9:ASN:HA	20:R:12:LYS:HZ3	1.71	0.54
34:A:2051:U:H4'	34:A:2160:A:N6	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2857:A:H2'	34:A:2858:G:C8	2.43	0.54
9:G:44:SER:HB3	9:G:52:VAL:O	2.07	0.54
34:A:733:U:H2'	34:A:734:C:C6	2.43	0.54
34:A:1955:A:H3'	34:A:1956:A:H8	1.72	0.54
34:A:3024:A:H2'	34:A:3025:G:O4'	2.08	0.54
5:C:133:LEU:HD23	5:C:136:ILE:HD12	1.89	0.54
9:G:53:VAL:HG21	9:G:70:ARG:HB2	1.90	0.54
34:A:823:C:H2'	34:A:824:G:C8	2.43	0.54
34:A:997:G:H3'	34:A:998:G:H8	1.73	0.54
34:A:2054:C:O2	34:A:2145:C:C6	2.60	0.54
34:A:2411:U:H2'	34:A:2412:U:O4'	2.08	0.54
34:A:2780:C:H2'	34:A:2781:G:O4'	2.07	0.54
5:C:258:ARG:HE	5:C:262:LYS:HZ3	1.56	0.54
6:D:30:LYS:HA	6:D:191:VAL:HG12	1.89	0.54
34:A:206:A:H2'	34:A:207:C:O4'	2.08	0.54
34:A:2129:C:C4'	34:A:2130:G:H5'	2.33	0.54
34:A:2532:G:N2	34:A:2534:A:O2'	2.40	0.54
8:F:128:GLN:HB3	8:F:135:TYR:CE1	2.43	0.54
24:V:89:ASP:N	24:V:89:ASP:OD1	2.37	0.54
25:W:63:THR:O	25:W:80:THR:OG1	2.26	0.54
34:A:88:A:H1'	34:A:89:A:C8	2.42	0.54
34:A:998:G:N2	34:A:1010:U:O4	2.40	0.54
34:A:2356:G:H2'	34:A:2380:G:C5	2.42	0.54
6:D:40:ARG:HH21	34:A:3008:C:H1'	1.72	0.54
19:Q:19:PHE:O	19:Q:49:ARG:NH1	2.40	0.54
25:W:11:LEU:HD11	25:W:57:VAL:HG11	1.89	0.54
3:4:148:LEU:HD13	3:4:168:GLN:HA	1.89	0.54
6:D:142:GLN:NE2	34:A:861:U:O4	2.41	0.54
10:H:84:ALA:HB1	10:H:92:PHE:CE2	2.43	0.54
11:I:70:ASP:HA	11:I:73:PHE:CE2	2.42	0.54
22:T:25:ARG:NH1	22:T:83:ALA:O	2.41	0.54
25:W:56:ALA:O	25:W:60:SER:OG	2.21	0.54
34:A:669:G:O2'	34:A:1369:A:OP1	2.24	0.54
34:A:1000:C:H2'	34:A:1001:C:C6	2.43	0.54
34:A:1291:G:H1'	34:A:1293:G:N2	2.23	0.54
8:F:73:GLU:O	8:F:94:ALA:HA	2.08	0.54
12:J:56:ILE:HD11	12:J:74:THR:HG23	1.88	0.54
12:J:103:THR:HB	12:J:106:GLN:HG3	1.89	0.54
3:4:369:ASN:OD1	3:4:370:LYS:N	2.42	0.53
34:A:380:A:N3	34:A:401:C:O2'	2.40	0.53
3:4:271:LEU:HD12	3:4:273:GLU:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:12:ALA:HB3	15:M:15:GLU:HB2	1.89	0.53
18:P:98:GLU:HB3	18:P:125:LEU:HA	1.90	0.53
34:A:1198:C:H2'	34:A:1199:U:H6	1.73	0.53
34:A:1690:A:H2'	34:A:1691:A:C8	2.43	0.53
12:J:101:LYS:HA	12:J:101:LYS:HE2	1.90	0.53
21:S:30:GLU:OE1	21:S:31:PRO:HD2	2.08	0.53
25:W:39:GLY:HA3	25:W:99:VAL:HG12	1.90	0.53
34:A:1430:C:H2'	34:A:1431:U:C6	2.43	0.53
12:J:98:LYS:HG2	12:J:138:GLY:C	2.23	0.53
13:K:93:LEU:HD23	13:K:97:PRO:HA	1.91	0.53
21:S:41:LEU:HD11	21:S:48:VAL:HG13	1.89	0.53
25:W:41:GLY:H	25:W:99:VAL:HG11	1.73	0.53
34:A:678:A:N1	34:A:924:G:O2'	2.36	0.53
12:J:102:VAL:HG12	12:J:106:GLN:HE21	1.73	0.53
34:A:762:U:H2'	34:A:763:G:C8	2.43	0.53
34:A:2470:A:H2'	34:A:2471:A:C8	2.43	0.53
1:2:15:ALA:O	1:2:20:ARG:NH1	2.41	0.53
3:4:377:VAL:HB	3:4:383:ARG:HH21	1.74	0.53
10:H:101:VAL:HG21	10:H:114:LYS:HA	1.90	0.53
12:J:94:PRO:HD2	34:A:1194:C:H1'	1.90	0.53
20:R:91:ASP:OD2	21:S:13:GLN:HG3	2.07	0.53
34:A:1223:U:C2	34:A:1224:G:C8	2.96	0.53
34:A:1758:G:HO2'	34:A:1759:A:P	2.30	0.53
34:A:2497:A:H2'	34:A:2498:A:C8	2.44	0.53
3:4:24:ARG:H	3:4:87:GLN:CD	2.12	0.53
7:E:156:VAL:HG12	7:E:158:ILE:HG12	1.90	0.53
16:N:85:SER:O	16:N:85:SER:OG	2.20	0.53
26:X:50:ASN:HB2	26:X:80:ILE:HB	1.91	0.53
34:A:1146:A:H2'	34:A:1147:A:C8	2.43	0.53
34:A:1473:G:N1	34:A:1487:U:OP2	2.27	0.53
34:A:2054:C:O2	34:A:2145:C:C5	2.61	0.53
34:A:2122:U:H4'	34:A:2125:A:N7	2.23	0.53
34:A:2133:G:H5''	34:A:2134:G:C8	2.44	0.53
34:A:2288:C:H2'	34:A:2289:C:C6	2.44	0.53
3:4:24:ARG:NH1	3:4:86:ILE:HG22	2.24	0.53
5:C:176:ARG:HH12	5:C:182:ILE:HD11	1.73	0.53
9:G:63:ARG:HG2	34:A:2973:A:H4'	1.90	0.53
19:Q:110:LYS:HD3	19:Q:113:ARG:HH22	1.72	0.53
34:A:1198:C:H2'	34:A:1199:U:C6	2.44	0.53
3:4:54:VAL:HB	3:4:56:THR:HG23	1.91	0.53
3:4:67:LEU:HG	3:4:86:ILE:HD11	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:7:GLY:HA2	34:A:2540:G:H5''	1.90	0.53
23:U:31:PHE:CE2	23:U:96:PHE:HZ	2.27	0.53
28:Z:7:PRO:HD3	28:Z:56:ARG:HD2	1.90	0.53
28:Z:51:ARG:NH2	34:A:58:G:OP2	2.42	0.53
34:A:2053:C:H5'	34:A:2134:G:N2	2.24	0.53
34:A:2948:C:H2'	34:A:2949:A:C8	2.44	0.53
3:4:395:ARG:HB2	35:4:501:GCP:C6	2.39	0.53
4:B:81:U:H2'	4:B:82:A:C8	2.44	0.53
11:I:28:TYR:HD2	11:I:78:ALA:HB2	1.73	0.53
18:P:27:LYS:HD3	34:A:2558:C:H1'	1.90	0.53
34:A:388:U:H2'	34:A:389:G:O4'	2.08	0.53
34:A:1165:G:O2'	34:A:1228:A:N6	2.36	0.53
34:A:2123:A:H8	34:A:2145:C:C2	2.26	0.53
34:A:2346:G:H1'	34:A:2347:G:H5'	1.90	0.53
34:A:2407:C:H2'	34:A:2408:G:C8	2.43	0.53
34:A:2626:U:O2'	34:A:2627:C:H5'	2.09	0.53
4:B:56:C:O3'	8:F:31:ASN:ND2	2.42	0.52
6:D:7:LEU:HD22	6:D:207:VAL:HG22	1.90	0.52
6:D:47:TYR:OH	34:A:2860:U:O2'	2.24	0.52
10:H:80:LEU:HD21	10:H:99:ASP:OD2	2.09	0.52
10:H:84:ALA:HB3	10:H:94:SER:N	2.21	0.52
13:K:48:VAL:HG12	13:K:50:GLY:H	1.74	0.52
18:P:26:ARG:HH12	18:P:37:ARG:CD	2.21	0.52
34:A:221:A:N6	34:A:232:G:H1'	2.24	0.52
34:A:365:U:H2'	34:A:366:G:C8	2.44	0.52
34:A:1156:A:H2'	34:A:1157:G:O4'	2.09	0.52
34:A:2756:G:N2	34:A:2887:G:O2'	2.42	0.52
7:E:55:ARG:NH2	34:A:789:G:OP1	2.42	0.52
8:F:142:GLN:NE2	8:F:156:PRO:HA	2.20	0.52
34:A:1889:U:O2'	34:A:1891:G:N7	2.31	0.52
8:F:12:LYS:HG3	8:F:104:TRP:CD1	2.45	0.52
18:P:83:ARG:HD3	18:P:87:LEU:HD23	1.92	0.52
34:A:1201:G:H21	34:A:1203:A:H3'	1.74	0.52
34:A:1287:C:H2'	34:A:1288:A:H8	1.75	0.52
34:A:2146:A:OP2	34:A:2146:A:C8	2.63	0.52
6:D:63:ILE:HG13	6:D:66:VAL:HG22	1.90	0.52
16:N:67:ASN:ND2	16:N:105:GLU:OE2	2.37	0.52
34:A:441:G:H2'	34:A:442:U:C6	2.44	0.52
34:A:448:U:H2'	34:A:449:G:H8	1.74	0.52
3:4:24:ARG:CG	3:4:26:VAL:HG13	2.39	0.52
12:J:24:PRO:CG	12:J:25:PRO:HD2	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:747:A:H61	34:A:768:G:H1'	1.74	0.52
34:A:1001:C:C5	34:A:1002:C:H1'	2.45	0.52
34:A:1343:G:H2'	34:A:1345:G:C8	2.45	0.52
3:4:72:ALA:O	3:4:76:THR:HG22	2.09	0.52
3:4:437:GLY:HA2	3:4:456:PRO:HD3	1.90	0.52
4:B:2:U:H2'	4:B:3:U:C6	2.45	0.52
16:N:74:LEU:HB2	16:N:92:TRP:HB2	1.91	0.52
34:A:196:A:N6	34:A:2654:A:O2'	2.43	0.52
34:A:1291:G:H5'	34:A:1292:U:OP2	2.10	0.52
12:J:132:GLY:O	12:J:135:ARG:NH2	2.43	0.52
20:R:4:VAL:HG22	34:A:1314:C:H1'	1.92	0.52
24:V:88:ASP:OD1	24:V:91:THR:OG1	2.22	0.52
34:A:718:C:O2'	34:A:772:U:OP1	2.26	0.52
34:A:2404:G:H2'	34:A:2405:A:C4	2.45	0.52
3:4:126:PRO:HG3	3:4:175:ARG:HB3	1.92	0.52
9:G:128:SER:HB3	9:G:131:LYS:HB2	1.92	0.52
18:P:76:ASP:OD2	18:P:78:LYS:N	2.35	0.52
34:A:325:U:O4'	34:A:450:G:N2	2.39	0.52
34:A:751:A:H2'	34:A:752:C:C6	2.45	0.52
34:A:2133:G:H3'	34:A:2134:G:C8	2.33	0.52
34:A:2417:C:H2'	34:A:2418:U:O4'	2.10	0.52
34:A:2672:A:HO2'	34:A:2673:U:H5	1.57	0.52
13:K:136:GLN:N	13:K:136:GLN:OE1	2.42	0.52
20:R:14:ARG:HA	20:R:32:TYR:CE1	2.43	0.52
34:A:993:G:O2'	34:A:1015:A:N6	2.43	0.52
34:A:995:U:C2	34:A:996:G:C8	2.98	0.52
1:2:11:SER:OG	34:A:1107:G:OP2	2.11	0.51
3:4:251:VAL:N	3:4:329:ILE:O	2.35	0.51
5:C:228:PRO:HA	5:C:234:GLY:HA3	1.92	0.51
8:F:42:VAL:HG11	34:A:2538:A:H5'	1.90	0.51
34:A:523:U:C2'	34:A:524:C:H5'	2.40	0.51
34:A:1098:A:N3	34:A:2261:U:O2'	2.40	0.51
6:D:10:LYS:NZ	6:D:200:GLY:O	2.36	0.51
8:F:110:LEU:HA	8:F:114:ALA:HB3	1.93	0.51
12:J:66:ARG:HB3	12:J:68:PHE:CZ	2.45	0.51
34:A:502:C:H2'	34:A:503:A:C8	2.45	0.51
34:A:1398:G:O2'	34:A:1400:G:N7	2.37	0.51
34:A:1642:G:O2'	34:A:1713:U:O4	2.22	0.51
34:A:2124:A:N6	34:A:2155:U:O2'	2.43	0.51
9:G:59:GLU:HG3	9:G:61:ARG:H	1.76	0.51
34:A:349:G:H3'	34:A:350:A:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2704:C:H2'	34:A:2705:G:O4'	2.11	0.51
34:A:3055:G:H2'	34:A:3100:A:H61	1.75	0.51
6:D:111:TYR:CD1	6:D:214:ARG:HD3	2.46	0.51
11:I:73:PHE:HD1	11:I:77:THR:HG21	1.75	0.51
34:A:1294:U:H2'	34:A:1295:U:C6	2.45	0.51
34:A:1425:G:N2	34:A:1428:U:C4	2.79	0.51
34:A:2339:G:H1	34:A:2387:U:H3	1.57	0.51
34:A:2345:U:N3	34:A:2346:G:O6	2.44	0.51
34:A:2538:A:H2'	34:A:2539:G:C8	2.46	0.51
3:4:193:GLY:O	3:4:207:LYS:HG3	2.10	0.51
3:4:300:THR:HB	3:4:318:THR:CG2	2.38	0.51
6:D:96:GLU:HG2	6:D:99:GLN:HB2	1.92	0.51
14:L:71:ARG:NH1	14:L:104:ARG:HB3	2.25	0.51
34:A:1195:A:C2	34:A:1206:A:H2'	2.45	0.51
3:4:25:ARG:NH1	3:4:85:LEU:HD11	2.26	0.51
3:4:44:LEU:HD23	3:4:45:ARG:H	1.75	0.51
3:4:106:LEU:HD23	3:4:136:VAL:HB	1.92	0.51
3:4:407:MET:O	3:4:411:VAL:HG23	2.11	0.51
34:A:1076:A:H2'	34:A:1077:A:C8	2.45	0.51
34:A:1174:G:H4'	34:A:1204:A:H8	1.76	0.51
34:A:1199:U:H2'	34:A:1200:U:H6	1.76	0.51
34:A:1223:U:H2'	34:A:1224:G:C8	2.45	0.51
34:A:2778:U:H2'	34:A:2780:C:C4	2.46	0.51
3:4:65:ALA:O	3:4:69:GLU:HG2	2.11	0.51
4:B:25:G:O6	4:B:57:U:O2'	2.28	0.51
11:I:54:ASN:OD1	11:I:77:THR:OG1	2.28	0.51
18:P:12:GLU:OE2	18:P:13:VAL:HG23	2.11	0.51
22:T:52:GLU:HB3	22:T:53:PRO:HD3	1.93	0.51
34:A:1754:G:H2'	34:A:1755:A:O2'	2.11	0.51
3:4:118:VAL:O	3:4:119:ILE:HD12	2.11	0.51
17:O:49:GLU:OE2	17:O:95:THR:OG1	2.28	0.51
34:A:346:C:H2'	34:A:347:U:O4'	2.10	0.51
34:A:681:C:H2'	34:A:682:A:H8	1.75	0.51
34:A:764:U:H3'	34:A:765:G:H8	1.74	0.51
34:A:1284:A:H2'	34:A:1285:G:C8	2.46	0.51
34:A:1729:A:H2'	34:A:1731:A:C8	2.46	0.51
34:A:2007:C:H2'	34:A:2008:A:C8	2.45	0.51
3:4:395:ARG:HB2	35:4:501:GCP:C2	2.41	0.51
12:J:44:TYR:O	12:J:48:THR:HG23	2.10	0.51
22:T:37:GLU:HG3	22:T:38:GLU:N	2.26	0.51
34:A:298:G:H3'	34:A:299:G:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:672:C:H2'	34:A:673:C:C6	2.46	0.51
34:A:980:C:O2'	34:A:981:U:O5'	2.27	0.51
34:A:2127:G:H21	34:A:2150:U:H2'	1.74	0.51
3:4:106:LEU:O	3:4:110:VAL:HG13	2.11	0.51
6:D:108:ASP:OD1	6:D:184:LYS:HA	2.11	0.51
12:J:115:LYS:HG2	12:J:118:LEU:HD12	1.93	0.51
34:A:979:G:H2'	34:A:980:C:C6	2.46	0.51
34:A:2693:A:H2'	34:A:2694:G:O4'	2.11	0.51
34:A:3070:G:H4'	34:A:3071:A:H5'	1.93	0.51
3:4:151:PHE:HE2	3:4:311:LEU:HD13	1.76	0.50
9:G:24:LEU:HD13	9:G:73:ILE:HD12	1.93	0.50
11:I:31:LEU:HD23	11:I:35:ASN:HD22	1.75	0.50
14:L:88:LYS:HG3	14:L:90:ASP:H	1.76	0.50
15:M:87:PHE:CE1	15:M:101:LYS:HE2	2.46	0.50
18:P:87:LEU:HD12	18:P:91:ARG:HH21	1.76	0.50
34:A:2847:G:OP1	34:A:3047:A:O2'	2.22	0.50
34:A:2857:A:H2'	34:A:2858:G:H8	1.75	0.50
3:4:119:ILE:HG13	3:4:141:ILE:HD12	1.93	0.50
9:G:17:VAL:HG11	9:G:51:ILE:HG12	1.92	0.50
12:J:85:ALA:HB3	12:J:87:VAL:HG22	1.93	0.50
19:Q:48:ARG:NH1	34:A:2909:G:OP1	2.45	0.50
34:A:2407:C:N4	34:A:2408:G:O6	2.44	0.50
3:4:45:ARG:HB3	3:4:48:ARG:HH21	1.75	0.50
12:J:56:ILE:CD1	12:J:73:LYS:O	2.60	0.50
34:A:410:U:O2	34:A:414:A:N7	2.45	0.50
34:A:1284:A:H2'	34:A:1285:G:H8	1.76	0.50
34:A:2654:A:N3	34:A:2654:A:H2'	2.26	0.50
34:A:2781:G:H2'	34:A:2782:C:H6	1.76	0.50
8:F:11:LEU:HA	8:F:14:ARG:HH11	1.76	0.50
13:K:92:LEU:HD23	13:K:100:VAL:HG22	1.94	0.50
34:A:1428:U:H2'	34:A:1828:A:C2	2.46	0.50
34:A:2879:G:O2'	34:A:2888:G:O6	2.21	0.50
8:F:44:ASN:ND2	8:F:94:ALA:H	2.09	0.50
24:V:15:LYS:NZ	34:A:411:G:H22	2.09	0.50
25:W:11:LEU:HD11	25:W:57:VAL:HG21	1.94	0.50
34:A:818:U:H2'	34:A:819:G:O4'	2.12	0.50
34:A:1533:U:OP2	34:A:1535:C:N4	2.44	0.50
7:E:24:LEU:HG	7:E:209:SER:HB2	1.92	0.50
25:W:82:ALA:HB3	25:W:96:ASP:HB2	1.94	0.50
34:A:2399:A:O2'	34:A:2400:C:H6	1.94	0.50
34:A:2777:G:N1	34:A:2779:U:C4	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:165:GLY:O	7:E:169:VAL:HG22	2.12	0.50
9:G:65:LEU:O	9:G:68:LEU:HD23	2.12	0.50
34:A:1047:A:OP1	34:A:1297:G:N2	2.30	0.50
34:A:1201:G:H21	34:A:1203:A:H8	1.59	0.50
34:A:1291:G:N2	34:A:1292:U:H1'	2.27	0.50
34:A:1653:G:H2'	34:A:1654:G:O4'	2.12	0.50
34:A:2394:A:P	34:A:2397:C:H41	2.34	0.50
7:E:65:PRO:HG3	7:E:79:THR:HG23	1.93	0.50
8:F:169:ASN:N	8:F:169:ASN:OD1	2.44	0.50
34:A:277:U:H2'	34:A:278:A:H8	1.77	0.50
34:A:928:U:H2'	34:A:929:C:C6	2.46	0.50
34:A:2122:U:H3'	34:A:2122:U:OP2	2.12	0.50
6:D:188:GLU:H	6:D:188:GLU:CD	2.15	0.50
8:F:74:VAL:HG13	8:F:91:PRO:HB3	1.93	0.50
18:P:120:ALA:O	18:P:125:LEU:HB2	2.12	0.50
34:A:633:A:H2'	34:A:634:C:O4'	2.11	0.50
34:A:1529:U:H3'	34:A:1530:G:C8	2.47	0.50
34:A:1815:G:H5''	34:A:1816:C:H5'	1.94	0.50
2:3:15:LYS:HA	4:B:87:U:O2	2.13	0.49
9:G:46:ALA:HB2	9:G:52:VAL:HG23	1.92	0.49
9:G:89:GLU:O	9:G:90:ILE:HD13	2.12	0.49
12:J:57:PRO:CB	12:J:73:LYS:O	2.60	0.49
1:2:2:ALA:HB1	1:2:59:VAL:HG21	1.94	0.49
6:D:76:ASN:N	6:D:76:ASN:OD1	2.45	0.49
8:F:81:ILE:HG13	8:F:83:GLN:HG2	1.94	0.49
8:F:125:SER:H	8:F:185:LYS:HZ3	1.58	0.49
15:M:113:LEU:HD23	15:M:130:SER:HB2	1.94	0.49
34:A:55:G:O2'	34:A:70:A:N1	2.33	0.49
34:A:502:C:H2'	34:A:503:A:H8	1.77	0.49
34:A:981:U:H4'	34:A:982:A:O5'	2.12	0.49
34:A:2156:A:H1'	34:A:2159:G:OP1	2.12	0.49
34:A:2529:A:H2'	34:A:2530:C:C6	2.47	0.49
34:A:644:G:H2'	34:A:645:G:H8	1.77	0.49
34:A:2121:G:C5'	34:A:2121:G:C8	2.95	0.49
34:A:2613:G:H5''	34:A:2614:U:O4'	2.12	0.49
3:4:130:ASN:OD1	3:4:131:ALA:N	2.45	0.49
12:J:15:ILE:O	12:J:44:TYR:OH	2.18	0.49
15:M:72:ARG:HE	15:M:74:GLU:HG2	1.77	0.49
34:A:1675:U:O2'	34:A:1676:G:N7	2.44	0.49
34:A:2121:G:H3'	34:A:2122:U:H6	1.76	0.49
34:A:2343:G:H2'	34:A:2344:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:69:LYS:NZ	34:A:2285:G:OP1	2.38	0.49
9:G:77:VAL:O	9:G:81:THR:HG23	2.11	0.49
16:N:42:ILE:HD12	16:N:97:VAL:HG11	1.94	0.49
34:A:1290:C:H2'	34:A:1291:G:O4'	2.12	0.49
34:A:1703:G:C6	34:A:1727:A:C2	3.00	0.49
3:4:250:ILE:O	3:4:300:THR:HG23	2.13	0.49
3:4:411:VAL:O	3:4:412:GLU:HB3	2.12	0.49
25:W:8:PRO:N	25:W:10:LYS:HZ3	2.11	0.49
34:A:150:C:H2'	34:A:151:A:H8	1.77	0.49
34:A:857:U:H2'	34:A:858:A:C8	2.46	0.49
34:A:2528:G:N2	34:A:2536:U:H3	2.08	0.49
34:A:2580:G:H2'	34:A:2581:G:O4'	2.13	0.49
11:I:111:ASP:O	11:I:113:LYS:NZ	2.33	0.49
28:Z:7:PRO:HD3	28:Z:56:ARG:CD	2.43	0.49
34:A:844:G:O2'	34:A:878:G:H4'	2.13	0.49
34:A:2193:A:O2'	34:A:2196:G:N3	2.36	0.49
34:A:2235:C:H2'	34:A:2236:G:O4'	2.13	0.49
34:A:2404:G:H8	34:A:2405:A:C2	2.30	0.49
3:4:237:ARG:HG2	3:4:240:ARG:NH1	2.25	0.49
3:4:338:ASN:ND2	3:4:341:ALA:HB2	2.28	0.49
8:F:76:ARG:HG3	8:F:89:GLY:HA2	1.94	0.49
8:F:115:LEU:HA	8:F:118:ILE:HG13	1.94	0.49
9:G:5:GLY:HA3	9:G:66:HIS:NE2	2.28	0.49
21:S:30:GLU:HG3	21:S:32:GLY:O	2.13	0.49
34:A:828:G:H2'	34:A:829:U:C6	2.47	0.49
34:A:1735:U:H2'	34:A:1736:G:O4'	2.13	0.49
34:A:2354:G:C5	34:A:2381:A:H1'	2.48	0.49
3:4:247:SER:HA	3:4:296:VAL:HG12	1.95	0.49
8:F:15:TYR:HA	8:F:19:ILE:CG1	2.40	0.49
8:F:48:GLY:H	8:F:92:ILE:HG23	1.76	0.49
10:H:89:GLY:C	10:H:90:LYS:HD3	2.34	0.49
15:M:77:VAL:HG11	34:A:730:G:N1	2.28	0.49
16:N:59:LYS:O	16:N:60:ARG:HD2	2.13	0.49
34:A:729:C:O2'	34:A:733:U:OP1	2.31	0.49
34:A:782:U:H2'	34:A:783:G:O4'	2.13	0.49
34:A:821:A:H2'	34:A:822:G:O4'	2.13	0.49
34:A:1673:A:H2'	34:A:1673:A:N3	2.27	0.49
34:A:3017:C:H2'	34:A:3018:U:C6	2.48	0.49
34:A:3071:A:P	34:A:3087:G:H22	2.35	0.49
8:F:141:GLU:HG3	8:F:143:SER:H	1.78	0.49
8:F:149:ASP:OD1	8:F:150:VAL:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:80:LEU:HD22	10:H:100:VAL:HG23	1.95	0.49
23:U:24:ILE:HG12	23:U:29:TYR:CD1	2.47	0.49
26:X:19:GLN:HB2	26:X:21:LEU:HG	1.93	0.49
34:A:1532:G:H2'	34:A:1533:U:H6	1.78	0.49
34:A:2019:A:H2'	34:A:2020:A:C8	2.47	0.49
34:A:2420:U:H1'	34:A:2421:A:C8	2.48	0.49
4:B:29:C:O2'	4:B:60:G:N2	2.46	0.48
6:D:14:THR:HG22	6:D:15:GLN:H	1.78	0.48
9:G:117:GLU:N	9:G:117:GLU:OE2	2.46	0.48
10:H:131:PRO:HB3	10:H:146:LEU:H	1.77	0.48
12:J:98:LYS:HA	12:J:138:GLY:O	2.13	0.48
34:A:621:U:H2'	34:A:622:C:C6	2.47	0.48
34:A:1529:U:H3'	34:A:1530:G:H8	1.78	0.48
34:A:1532:G:O2'	34:A:1803:A:N1	2.41	0.48
3:4:442:THR:HB	3:4:451:ILE:HA	1.95	0.48
15:M:75:TYR:CD2	15:M:109:LEU:HB3	2.48	0.48
34:A:429:A:H2'	34:A:430:A:C8	2.48	0.48
34:A:443:C:H2'	34:A:444:U:O4'	2.13	0.48
34:A:672:C:H2'	34:A:673:C:H6	1.79	0.48
34:A:1177:G:H2'	34:A:1178:U:C6	2.48	0.48
34:A:1999:U:H1'	34:A:2833:U:H5''	1.95	0.48
34:A:3046:C:H2'	34:A:3047:A:O4'	2.13	0.48
4:B:58:A:H1'	8:F:34:GLN:HG3	1.94	0.48
8:F:129:PHE:HE1	8:F:174:ARG:HG3	1.78	0.48
11:I:28:TYR:CE2	11:I:76:PRO:HB2	2.47	0.48
34:A:193:G:H2'	34:A:194:A:O4'	2.12	0.48
34:A:288:U:O2	34:A:299:G:N2	2.46	0.48
34:A:1334:C:H2'	34:A:1335:G:O4'	2.13	0.48
34:A:1630:U:H2'	34:A:1631:A:O4'	2.13	0.48
34:A:2044:U:H2'	34:A:2045:G:O4'	2.13	0.48
34:A:2054:C:H41	34:A:2135:U:H3	1.61	0.48
5:C:63:ARG:NH1	34:A:1788:G:OP1	2.47	0.48
5:C:268:ILE:HG21	5:C:271:ARG:HE	1.78	0.48
10:H:91:LEU:HD13	10:H:94:SER:HB2	1.94	0.48
12:J:81:LEU:HD13	12:J:134:ALA:HB2	1.95	0.48
17:O:24:LEU:HB3	17:O:44:LEU:HD22	1.96	0.48
34:A:377:C:H2'	34:A:378:G:H8	1.78	0.48
34:A:625:A:H2'	34:A:626:G:O4'	2.14	0.48
34:A:1719:C:C2	34:A:1720:G:C8	3.01	0.48
34:A:2122:U:O2	34:A:2126:C:N4	2.47	0.48
3:4:207:LYS:HG2	3:4:208:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:98:ALA:HB2	10:H:114:LYS:HE3	1.94	0.48
21:S:54:ASP:HA	21:S:57:LYS:HG3	1.95	0.48
24:V:97:ILE:HA	24:V:104:ASP:HA	1.96	0.48
34:A:58:G:C6	34:A:92:G:N2	2.81	0.48
34:A:834:C:H2'	34:A:835:C:C6	2.48	0.48
3:4:45:ARG:NE	3:4:78:GLY:O	2.46	0.48
3:4:423:PRO:HD2	3:4:466:TYR:CE2	2.49	0.48
4:B:49:C:P	18:P:42:ARG:HH12	2.37	0.48
5:C:108:PRO:HA	5:C:196:VAL:HA	1.96	0.48
17:O:72:ASP:OD1	17:O:73:LYS:N	2.47	0.48
34:A:332:C:H2'	34:A:333:C:C6	2.48	0.48
34:A:337:U:H1'	34:A:345:G:C2	2.49	0.48
34:A:994:A:H3'	34:A:995:U:H6	1.79	0.48
34:A:1229:A:H1'	34:A:1230:G:H1'	1.95	0.48
34:A:3037:C:O2	34:A:3104:A:O2'	2.30	0.48
12:J:64:GLU:HG2	12:J:65:ASP:OD1	2.13	0.48
16:N:75:THR:HA	16:N:90:PRO:HA	1.95	0.48
17:O:82:GLU:HG3	17:O:83:ILE:N	2.29	0.48
19:Q:100:ARG:HG2	19:Q:101:GLU:OE1	2.13	0.48
22:T:36:VAL:O	22:T:40:LEU:HG	2.13	0.48
28:Z:16:ASP:N	28:Z:16:ASP:OD1	2.43	0.48
6:D:154:CYS:O	6:D:157:PRO:HD2	2.14	0.48
7:E:160:ARG:HG3	7:E:179:SER:OG	2.14	0.48
10:H:4:ILE:HG23	10:H:17:ASP:O	2.14	0.48
12:J:36:ASN:HB3	12:J:39:GLU:HB3	1.95	0.48
15:M:104:VAL:HG11	15:M:110:VAL:HG12	1.96	0.48
34:A:665:G:N2	34:A:2255:A:OP1	2.43	0.48
34:A:1208:U:C4	34:A:1220:C:C2	3.02	0.48
18:P:4:LYS:HD3	18:P:4:LYS:N	2.28	0.48
34:A:334:G:O6	34:A:347:U:O2	2.31	0.48
34:A:1295:U:H2'	34:A:1296:G:H8	1.77	0.48
34:A:1400:G:N2	34:A:1443:G:H5''	2.29	0.48
34:A:1944:C:H2'	34:A:1945:U:O4'	2.13	0.48
3:4:32:GLU:O	3:4:81:VAL:HG23	2.13	0.48
3:4:444:HIS:CE1	12:J:24:PRO:HA	2.48	0.48
5:C:16:ALA:HB2	5:C:207:GLY:HA3	1.96	0.48
20:R:54:LYS:HE3	34:A:1113:C:OP2	2.13	0.48
34:A:2134:G:C2'	34:A:2135:U:H2'	2.44	0.48
3:4:444:HIS:HA	3:4:449:THR:HG22	1.96	0.47
7:E:186:TYR:O	7:E:190:ASN:CB	2.59	0.47
15:M:89:GLN:H	15:M:89:GLN:CD	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:16:ASP:OD1	24:V:16:ASP:N	2.47	0.47
34:A:2383:U:C4	34:A:2384:C:H1'	2.49	0.47
3:4:154:HIS:ND1	3:4:277:PHE:O	2.46	0.47
3:4:286:ARG:HH21	3:4:294:PRO:HB3	1.79	0.47
14:L:90:ASP:O	14:L:90:ASP:OD1	2.32	0.47
20:R:70:ARG:NH2	34:A:1130:C:OP1	2.48	0.47
34:A:1203:A:O2'	34:A:1204:A:O4'	2.12	0.47
34:A:1535:C:H2'	34:A:1536:A:O4'	2.14	0.47
34:A:1542:A:H1'	34:A:1628:A:C6	2.49	0.47
34:A:2326:A:H2'	34:A:2327:C:H5'	1.96	0.47
3:4:98:ILE:HD11	3:4:106:LEU:HD13	1.95	0.47
3:4:393:SER:O	3:4:397:GLY:N	2.45	0.47
11:I:94:LYS:NZ	11:I:125:ASP:OD2	2.43	0.47
13:K:29:ALA:HA	13:K:105:ILE:HG12	1.97	0.47
15:M:24:ARG:HA	34:A:926:U:H2'	1.96	0.47
24:V:75:ASP:C	24:V:77:ASP:H	2.17	0.47
27:Y:15:GLY:HA3	27:Y:29:TRP:HZ3	1.78	0.47
34:A:997:G:H3'	34:A:998:G:C8	2.50	0.47
34:A:2055:C:H4'	34:A:2056:G:H8	1.80	0.47
34:A:2351:A:H1'	34:A:2396:A:H1'	1.95	0.47
6:D:6:ILE:HD11	6:D:34:ASN:OD1	2.14	0.47
7:E:9:THR:HG21	7:E:13:LYS:HD2	1.96	0.47
24:V:57:GLY:HA3	34:A:571:A:O2'	2.13	0.47
9:G:30:LYS:HE2	9:G:82:GLU:HA	1.96	0.47
9:G:59:GLU:HG3	9:G:61:ARG:N	2.30	0.47
11:I:10:VAL:HG13	11:I:60:ALA:HB2	1.96	0.47
12:J:23:ALA:N	12:J:24:PRO:HD2	2.29	0.47
12:J:98:LYS:HE3	12:J:98:LYS:HB2	1.44	0.47
14:L:76:TYR:HB2	19:Q:72:THR:HB	1.95	0.47
24:V:15:LYS:NZ	34:A:411:G:H1	2.12	0.47
34:A:2791:G:H2'	34:A:2792:C:C6	2.50	0.47
4:B:46:A:H1'	8:F:99:ARG:HH21	1.80	0.47
24:V:74:VAL:HG23	24:V:76:SER:H	1.80	0.47
34:A:76:C:O2'	34:A:428:A:N3	2.40	0.47
34:A:827:G:H2'	34:A:828:G:C8	2.50	0.47
34:A:971:G:H2'	34:A:972:A:C8	2.49	0.47
34:A:2056:G:O2'	34:A:2057:G:O5'	2.32	0.47
34:A:2311:G:H2'	34:A:2312:U:O4'	2.15	0.47
3:4:24:ARG:HH12	3:4:86:ILE:HG22	1.78	0.47
3:4:55:TRP:HB3	3:4:88:ARG:HA	1.97	0.47
3:4:424:TYR:OH	3:4:445:THR:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:7:G:OP1	18:P:15:ARG:NH1	2.41	0.47
4:B:41:U:N3	4:B:45:G:OP2	2.35	0.47
4:B:81:U:O2'	34:A:1033:A:N3	2.45	0.47
8:F:85:LYS:O	8:F:85:LYS:HD3	2.14	0.47
12:J:15:ILE:HB	12:J:44:TYR:CZ	2.50	0.47
14:L:60:ALA:HB2	14:L:86:ILE:HD13	1.95	0.47
15:M:93:VAL:HB	15:M:124:VAL:HA	1.96	0.47
19:Q:51:GLY:HA2	19:Q:56:GLU:CD	2.35	0.47
28:Z:45:ARG:HG2	34:A:94:G:O2'	2.13	0.47
34:A:600:A:H5''	34:A:1330:C:O2'	2.14	0.47
34:A:1798:U:H2'	34:A:1799:A:H8	1.80	0.47
34:A:2322:C:H2'	34:A:2323:G:O4'	2.15	0.47
4:B:29:C:OP1	18:P:48:HIS:NE2	2.35	0.47
4:B:49:C:H2'	4:B:50:C:O4'	2.15	0.47
5:C:245:HIS:HB3	5:C:246:PRO:HD2	1.97	0.47
7:E:7:VAL:O	7:E:15:ASP:N	2.46	0.47
15:M:95:VAL:O	15:M:99:VAL:HG22	2.15	0.47
34:A:994:A:H3'	34:A:995:U:C6	2.50	0.47
34:A:1161:C:H2'	34:A:1162:G:C8	2.50	0.47
34:A:1182:C:H2'	34:A:1183:U:O4'	2.14	0.47
34:A:1326:G:H1'	34:A:1351:G:N2	2.30	0.47
34:A:2058:U:O5'	34:A:2151:A:N6	2.48	0.47
3:4:370:LYS:HG2	35:4:501:GCP:C6	2.44	0.47
3:4:443:GLU:HG3	3:4:450:ARG:HG2	1.97	0.47
6:D:28:VAL:HG11	19:Q:7:VAL:HG21	1.97	0.47
8:F:32:VAL:HA	8:F:35:ILE:HD13	1.97	0.47
8:F:37:GLY:H	8:F:166:THR:HG1	1.60	0.47
8:F:43:VAL:HA	8:F:160:ASP:O	2.15	0.47
16:N:29:PHE:HB2	16:N:105:GLU:OE1	2.15	0.47
16:N:40:ALA:HB2	16:N:127:ILE:HG21	1.97	0.47
16:N:77:LYS:N	34:A:1074:A:OP1	2.46	0.47
21:S:53:ASP:N	21:S:53:ASP:OD1	2.48	0.47
34:A:503:A:H2'	34:A:504:C:C6	2.50	0.47
34:A:1015:A:H2'	34:A:1016:C:O4'	2.14	0.47
34:A:1189:G:H1'	34:A:1207:G:H2'	1.97	0.47
34:A:1900:C:H2'	34:A:1901:C:C6	2.50	0.47
34:A:2055:C:C5	34:A:2146:A:OP1	2.67	0.47
34:A:2298:U:H4'	34:A:2820:U:O2	2.15	0.47
34:A:2414:G:H2'	34:A:2415:G:H8	1.79	0.47
6:D:151:ILE:HG21	6:D:160:VAL:HG22	1.96	0.47
7:E:130:LEU:HD22	7:E:158:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:4:ILE:HG12	10:H:39:ALA:HB2	1.96	0.47
10:H:37:ILE:HD12	10:H:37:ILE:HA	1.79	0.47
11:I:12:ASP:O	11:I:15:GLU:HG3	2.14	0.47
21:S:4:TYR:HA	21:S:17:ALA:HA	1.96	0.47
22:T:53:PRO:O	22:T:57:VAL:HG23	2.15	0.47
24:V:56:SER:HA	34:A:572:C:H4'	1.96	0.47
34:A:1189:G:N3	34:A:1207:G:O2'	2.34	0.47
34:A:1898:U:H2'	34:A:1899:G:O4'	2.15	0.47
34:A:2510:A:H4'	34:A:2511:A:O4'	2.15	0.47
3:4:432:ARG:HH21	3:4:462:THR:HG21	1.78	0.46
34:A:824:G:H2'	34:A:825:C:H6	1.80	0.46
34:A:911:U:H2'	34:A:912:C:C6	2.50	0.46
34:A:993:G:N2	34:A:1014:G:H2'	2.30	0.46
34:A:1278:C:C2	34:A:1279:G:C8	3.04	0.46
34:A:1316:U:H2'	34:A:1317:G:H8	1.80	0.46
20:R:14:ARG:HA	20:R:32:TYR:CD1	2.50	0.46
28:Z:49:THR:O	28:Z:53:GLU:HG3	2.15	0.46
34:A:452:G:H2'	34:A:453:U:N1	2.30	0.46
34:A:979:G:H2'	34:A:980:C:H6	1.79	0.46
34:A:1177:G:H2'	34:A:1178:U:C5	2.50	0.46
34:A:2629:G:O2'	34:A:2635:A:N6	2.41	0.46
3:4:200:THR:HG23	16:N:45:ARG:HH22	1.81	0.46
3:4:232:ILE:HD13	34:A:2704:C:H4'	1.97	0.46
3:4:340:LEU:HD12	3:4:343:ILE:HB	1.98	0.46
12:J:24:PRO:C	12:J:28:PRO:HD2	2.26	0.46
18:P:12:GLU:HA	18:P:15:ARG:HB3	1.96	0.46
21:S:23:LYS:HE3	21:S:23:LYS:HB2	1.59	0.46
34:A:304:U:H2'	34:A:305:G:C8	2.51	0.46
34:A:931:C:H2'	34:A:932:C:H6	1.80	0.46
34:A:1856:C:O2	34:A:2922:U:O2'	2.31	0.46
3:4:183:MET:HB3	3:4:207:LYS:NZ	2.31	0.46
5:C:272:ARG:NH1	34:A:2015:U:OP2	2.45	0.46
6:D:123:PHE:HB2	34:A:3044:A:OP1	2.15	0.46
21:S:97:LEU:HD23	21:S:97:LEU:HA	1.78	0.46
24:V:9:VAL:HB	24:V:71:VAL:HG13	1.97	0.46
34:A:138:A:H2'	34:A:139:U:O2	2.14	0.46
34:A:285:U:O2'	34:A:287:A:OP1	2.31	0.46
34:A:325:U:O2'	34:A:326:A:OP1	2.29	0.46
34:A:2127:G:H2'	34:A:2127:G:N3	2.30	0.46
34:A:2148:C:OP2	34:A:2149:C:N4	2.49	0.46
8:F:119:ARG:NH1	8:F:119:ARG:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:141:GLU:OE1	8:F:143:SER:OG	2.19	0.46
10:H:135:LYS:NZ	10:H:138:THR:O	2.37	0.46
14:L:18:GLU:HG2	14:L:45:ASP:HB2	1.96	0.46
34:A:1169:A:N3	34:A:2975:G:N2	2.62	0.46
34:A:1476:G:H2'	34:A:1477:C:C6	2.50	0.46
34:A:1928:C:H4'	34:A:3079:U:H3	1.80	0.46
3:4:155:ALA:HA	3:4:280:LEU:HD11	1.97	0.46
7:E:205:ILE:O	7:E:209:SER:HB3	2.15	0.46
9:G:17:VAL:HG12	9:G:19:ILE:HG12	1.98	0.46
12:J:98:LYS:HD2	12:J:140:THR:HA	1.97	0.46
13:K:15:TRP:O	13:K:138:ILE:HD12	2.16	0.46
20:R:91:ASP:OD1	20:R:93:LYS:N	2.48	0.46
25:W:60:SER:HB2	25:W:61:HIS:CE1	2.51	0.46
34:A:827:G:C2'	34:A:828:G:H5'	2.45	0.46
34:A:944:A:C8	34:A:2472:C:H5'	2.50	0.46
3:4:242:ARG:NE	34:A:2755:A:OP1	2.49	0.46
8:F:34:GLN:HB3	18:P:3:HIS:CD2	2.50	0.46
8:F:117:ARG:HG3	8:F:144:MET:HA	1.98	0.46
34:A:567:A:N3	34:A:569:G:H5''	2.30	0.46
34:A:752:C:H2'	34:A:753:A:C8	2.51	0.46
34:A:965:U:H2'	34:A:966:U:H6	1.79	0.46
34:A:1138:A:N1	34:A:1259:U:H2'	2.31	0.46
34:A:1175:A:N7	34:A:1204:A:H2'	2.30	0.46
34:A:1313:U:H2'	34:A:1314:C:C6	2.49	0.46
34:A:2686:U:H2'	34:A:2687:U:C6	2.50	0.46
3:4:23:LEU:HG	3:4:102:LYS:HG3	1.97	0.46
3:4:347:ARG:O	3:4:351:ASN:OD1	2.33	0.46
4:B:35:G:N3	4:B:37:C:N4	2.64	0.46
4:B:80:C:H2'	4:B:81:U:O4'	2.15	0.46
5:C:80:ALA:HB2	5:C:96:HIS:CD2	2.51	0.46
6:D:95:TYR:HA	6:D:99:GLN:OE1	2.15	0.46
6:D:157:PRO:HD3	34:A:2795:C:O2'	2.16	0.46
13:K:23:VAL:O	13:K:62:ILE:HG13	2.16	0.46
18:P:17:ALA:O	18:P:21:ARG:HG3	2.15	0.46
34:A:448:U:H2'	34:A:449:G:C8	2.51	0.46
34:A:828:G:N1	34:A:832:G:OP2	2.49	0.46
34:A:1457:A:H2	34:A:1511:U:HO2'	1.64	0.46
34:A:1473:G:O2'	34:A:1488:A:N6	2.48	0.46
34:A:1963:G:H2'	34:A:1964:U:C6	2.51	0.46
34:A:2157:G:H5'	34:A:2158:C:H5''	1.96	0.46
3:4:242:ARG:HH22	34:A:2757:C:N4	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1:G:H2'	4:B:2:U:C6	2.50	0.46
4:B:63:U:H2'	4:B:64:G:H8	1.81	0.46
8:F:118:ILE:HG12	8:F:144:MET:HG2	1.98	0.46
9:G:98:GLN:OE1	9:G:98:GLN:N	2.49	0.46
15:M:72:ARG:HG2	34:A:727:A:OP1	2.16	0.46
34:A:1174:G:H4'	34:A:1204:A:C8	2.51	0.46
34:A:1668:C:O2'	34:A:1764:A:N3	2.45	0.46
34:A:2344:G:H5'	34:A:2392:A:O2'	2.15	0.46
34:A:3022:G:H2'	34:A:3023:G:H1'	1.98	0.46
5:C:212:MET:HG3	34:A:2008:A:H5''	1.98	0.46
34:A:1090:G:OP2	34:A:1091:A:O2'	2.27	0.46
34:A:1296:G:H2'	34:A:1297:G:C8	2.51	0.46
34:A:2331:U:C4'	34:A:2374:U:H5'	2.46	0.46
3:4:253:TYR:CZ	3:4:304:VAL:HA	2.51	0.45
4:B:11:U:H3'	4:B:12:C:H5''	1.98	0.45
34:A:944:A:N7	34:A:2472:C:H5'	2.32	0.45
34:A:2600:A:H8	34:A:2600:A:OP1	1.99	0.45
34:A:2781:G:H2'	34:A:2782:C:C6	2.52	0.45
34:A:2922:U:H2'	34:A:2923:C:C6	2.51	0.45
3:4:149:ASP:OD1	3:4:153:GLN:NE2	2.50	0.45
8:F:12:LYS:HG3	8:F:104:TRP:NE1	2.31	0.45
11:I:57:VAL:HA	11:I:60:ALA:HB3	1.98	0.45
16:N:40:ALA:HB2	16:N:127:ILE:CG2	2.47	0.45
26:X:41:ARG:NE	26:X:41:ARG:HA	2.31	0.45
34:A:328:C:H2'	34:A:329:U:O4'	2.16	0.45
34:A:1157:G:O6	34:A:1234:U:C2	2.69	0.45
34:A:1187:A:H5'	34:A:1188:A:OP1	2.16	0.45
34:A:1524:G:H2'	34:A:1525:U:C6	2.50	0.45
34:A:2873:U:H2'	34:A:2874:C:H6	1.81	0.45
34:A:3017:C:H2'	34:A:3018:U:H6	1.81	0.45
3:4:258:LYS:H	35:4:501:GCP:PB	2.39	0.45
6:D:185:VAL:HG13	6:D:192:LEU:HD23	1.98	0.45
7:E:166:ALA:O	7:E:170:ARG:HB2	2.16	0.45
8:F:11:LEU:O	8:F:15:TYR:HB3	2.16	0.45
9:G:19:ILE:HG23	9:G:19:ILE:HD12	1.66	0.45
12:J:135:ARG:NH2	34:A:1197:C:H1'	2.30	0.45
15:M:35:ARG:NH1	15:M:42:ALA:O	2.47	0.45
15:M:88:PRO:HD2	15:M:89:GLN:NE2	2.31	0.45
19:Q:4:LEU:HD23	19:Q:4:LEU:HA	1.80	0.45
21:S:63:GLU:HB2	21:S:100:THR:HG23	1.97	0.45
24:V:15:LYS:HZ1	34:A:411:G:H22	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:754:C:H2'	34:A:755:A:O4'	2.16	0.45
34:A:1200:U:H3'	34:A:1201:G:H8	1.81	0.45
34:A:1900:C:OP2	34:A:1917:G:N2	2.45	0.45
34:A:2332:U:H2'	34:A:2333:G:C8	2.52	0.45
34:A:3030:A:H2'	34:A:3031:A:C8	2.51	0.45
1:2:39:ASP:OD2	1:2:44:ARG:NH2	2.49	0.45
3:4:16:ALA:HB3	3:4:22:SER:OG	2.16	0.45
3:4:319:LEU:O	3:4:323:VAL:HG23	2.16	0.45
6:D:53:ALA:HB1	6:D:78:ARG:HB2	1.98	0.45
6:D:176:THR:OG1	34:A:2997:C:OP1	2.30	0.45
8:F:16:ARG:HA	8:F:20:ARG:HH21	1.80	0.45
8:F:48:GLY:HA3	34:A:2531:G:O6	2.16	0.45
8:F:72:PRO:HB2	8:F:94:ALA:HB1	1.97	0.45
10:H:23:ASP:O	10:H:27:ARG:HB2	2.17	0.45
34:A:993:G:C6	34:A:1014:G:C6	3.05	0.45
34:A:1015:A:H3'	34:A:1016:C:H6	1.81	0.45
34:A:1089:C:H2'	34:A:1090:G:O4'	2.16	0.45
34:A:1647:G:H3'	34:A:1648:A:H2'	1.98	0.45
34:A:2515:U:O2'	34:A:2598:C:O2	2.34	0.45
14:L:22:ILE:N	14:L:40:VAL:O	2.39	0.45
17:O:9:ARG:HA	17:O:9:ARG:HD3	1.64	0.45
23:U:4:ILE:HD12	28:Z:19:LYS:HZ3	1.82	0.45
34:A:729:C:H2'	34:A:730:G:O4'	2.16	0.45
34:A:999:C:H1'	34:A:1000:C:C5	2.52	0.45
34:A:2528:G:H1	34:A:2536:U:H3	1.63	0.45
3:4:49:VAL:HG13	3:4:81:VAL:HA	1.97	0.45
3:4:414:THR:O	3:4:414:THR:OG1	2.33	0.45
9:G:98:GLN:OE1	9:G:105:GLU:HB3	2.16	0.45
21:S:6:ILE:HD12	21:S:41:LEU:HB3	1.98	0.45
24:V:46:ALA:HA	34:A:571:A:H4'	1.99	0.45
34:A:17:C:H2'	34:A:18:A:C8	2.52	0.45
34:A:377:C:H2'	34:A:378:G:C8	2.50	0.45
34:A:468:G:C2'	34:A:469:G:H5'	2.47	0.45
34:A:543:U:O2'	34:A:560:U:N3	2.43	0.45
34:A:762:U:H2'	34:A:763:G:H8	1.81	0.45
34:A:1200:U:H3'	34:A:1201:G:C8	2.52	0.45
34:A:1533:U:H3'	34:A:1534:C:H5''	1.98	0.45
34:A:2134:G:H4'	34:A:2146:A:N1	2.32	0.45
34:A:2326:A:C2'	34:A:2327:C:H5'	2.46	0.45
34:A:2651:C:H5'	34:A:2653:G:H5'	1.98	0.45
3:4:21:ALA:O	3:4:22:SER:C	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:371:ILE:HG12	3:4:391:PHE:HB3	1.99	0.45
4:B:4:A:H8	4:B:63:U:H1'	1.82	0.45
9:G:12:PRO:HD2	9:G:15:VAL:HG21	1.99	0.45
9:G:136:GLY:HA3	9:G:142:VAL:CG2	2.47	0.45
11:I:33:VAL:HG11	34:A:1175:A:H1'	1.98	0.45
15:M:79:ASN:O	15:M:83:ILE:HG13	2.17	0.45
23:U:53:LYS:HB3	23:U:53:LYS:HE3	1.79	0.45
24:V:98:ALA:HB3	24:V:102:GLY:O	2.16	0.45
34:A:81:A:C2	34:A:100:A:C5	3.04	0.45
34:A:439:C:H2'	34:A:440:U:C6	2.52	0.45
34:A:3118:U:H2'	34:A:3119:A:C8	2.52	0.45
3:4:143:ARG:O	3:4:147:ILE:HG12	2.17	0.45
3:4:370:LYS:HE2	35:4:501:GCP:C4	2.47	0.45
3:4:401:ASP:N	3:4:401:ASP:OD1	2.50	0.45
8:F:41:VAL:HA	8:F:162:THR:O	2.17	0.45
11:I:45:ASP:N	11:I:45:ASP:OD1	2.47	0.45
21:S:14:TYR:HE2	21:S:24:VAL:HG23	1.82	0.45
22:T:72:ASP:O	22:T:75:THR:HG22	2.17	0.45
34:A:410:U:H5''	34:A:411:G:OP2	2.17	0.45
34:A:451:U:H1'	34:A:452:G:N7	2.31	0.45
34:A:688:A:H2'	34:A:689:U:C6	2.52	0.45
34:A:1705:C:H2'	34:A:1706:A:H8	1.81	0.45
34:A:2054:C:N4	34:A:2135:U:H3	2.14	0.45
3:4:253:TYR:HB2	3:4:342:GLN:HB3	1.99	0.45
5:C:93:ALA:HB2	5:C:107:ALA:HB2	1.98	0.45
8:F:109:ARG:O	8:F:113:ILE:HB	2.17	0.45
12:J:132:GLY:CA	12:J:135:ARG:HH21	2.30	0.45
19:Q:28:HIS:CD2	19:Q:41:VAL:HG22	2.51	0.45
34:A:62:G:H2'	34:A:63:C:H6	1.82	0.45
34:A:326:A:H3'	34:A:326:A:N3	2.32	0.45
34:A:620:G:H2'	34:A:621:U:C6	2.52	0.45
34:A:753:A:C2	34:A:763:G:C2	3.05	0.45
34:A:1174:G:H5''	34:A:1175:A:H5'	1.99	0.45
34:A:1180:G:H2'	34:A:1181:G:C8	2.51	0.45
34:A:1288:A:H2'	34:A:1289:A:C8	2.52	0.45
34:A:1305:G:H2'	34:A:1306:G:C8	2.51	0.45
34:A:2351:A:O2'	34:A:2352:C:O5'	2.33	0.45
34:A:2873:U:H2'	34:A:2874:C:C6	2.52	0.45
3:4:203:PRO:O	3:4:207:LYS:N	2.49	0.45
3:4:445:THR:HG22	3:4:446:ASP:H	1.82	0.45
10:H:131:PRO:HB2	10:H:143:LYS:HZ1	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:2:LEU:HD23	16:N:2:LEU:HA	1.79	0.45
22:T:25:ARG:NH2	34:A:604:C:O2'	2.50	0.45
34:A:150:C:H2'	34:A:151:A:C8	2.52	0.45
34:A:429:A:H2'	34:A:430:A:H8	1.81	0.45
34:A:1178:U:N3	34:A:1206:A:H2	2.13	0.45
34:A:1509:U:H2'	34:A:1510:A:O4'	2.17	0.45
34:A:2531:G:H5'	34:A:2532:G:C8	2.52	0.45
3:4:89:ARG:HD2	3:4:89:ARG:HA	1.84	0.44
4:B:4:A:N6	4:B:23:G:O2'	2.47	0.44
6:D:6:ILE:HD12	6:D:6:ILE:HA	1.76	0.44
9:G:65:LEU:HD23	9:G:65:LEU:HA	1.83	0.44
22:T:30:LEU:HD23	22:T:30:LEU:HA	1.84	0.44
23:U:28:VAL:HG22	23:U:85:LYS:HA	1.98	0.44
24:V:23:VAL:HG21	24:V:26:ALA:HB2	1.98	0.44
34:A:137:G:H22	34:A:1812:A:H2	1.65	0.44
34:A:452:G:H2'	34:A:453:U:C2	2.52	0.44
34:A:824:G:H2'	34:A:825:C:C6	2.52	0.44
34:A:1287:C:H2'	34:A:1288:A:C8	2.50	0.44
34:A:2056:G:O2'	34:A:2057:G:O4'	2.35	0.44
34:A:2058:U:H5	34:A:2059:G:C4	2.35	0.44
34:A:2154:G:N3	34:A:2155:U:N3	2.58	0.44
34:A:2523:A:H2'	34:A:2524:C:H6	1.82	0.44
5:C:108:PRO:HD2	5:C:111:LEU:HD22	1.99	0.44
8:F:59:GLY:HA2	8:F:62:ASN:OD1	2.17	0.44
17:O:90:ARG:NH1	17:O:119:LYS:O	2.50	0.44
19:Q:24:THR:HG22	19:Q:86:LEU:HD12	1.98	0.44
22:T:28:ILE:HD12	22:T:83:ALA:HB2	1.98	0.44
34:A:82:G:C6	34:A:96:G:N1	2.85	0.44
34:A:365:U:H3	34:A:437:G:H1	1.66	0.44
34:A:367:U:H2'	34:A:368:U:C6	2.52	0.44
34:A:995:U:H2'	34:A:996:G:C8	2.49	0.44
34:A:3013:C:H5'	34:A:3014:A:O5'	2.17	0.44
1:2:40:ASN:O	1:2:44:ARG:HG2	2.17	0.44
3:4:24:ARG:HB3	3:4:87:GLN:HA	2.00	0.44
5:C:14:ARG:NH1	34:A:1911:U:O2'	2.50	0.44
6:D:60:ARG:NH2	34:A:3052:A:OP1	2.50	0.44
7:E:163:GLU:O	7:E:167:LYS:HG2	2.17	0.44
7:E:179:SER:OG	7:E:180:PRO:HD2	2.17	0.44
12:J:95:HIS:HD2	12:J:138:GLY:HA2	1.82	0.44
12:J:115:LYS:HA	12:J:118:LEU:HG	1.99	0.44
24:V:41:ILE:HG22	24:V:43:LYS:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:837:C:C2	34:A:838:G:C8	3.05	0.44
34:A:2026:A:H8	34:A:2026:A:OP2	2.00	0.44
34:A:3033:G:H2'	34:A:3034:C:C6	2.53	0.44
3:4:423:PRO:HD2	3:4:466:TYR:CD2	2.52	0.44
5:C:212:MET:HE2	5:C:217:LYS:HD2	2.00	0.44
8:F:75:ARG:HD3	8:F:95:ARG:HB2	1.99	0.44
8:F:118:ILE:HA	8:F:144:MET:SD	2.57	0.44
12:J:61:THR:O	12:J:61:THR:OG1	2.31	0.44
12:J:95:HIS:CB	34:A:1195:A:H4'	2.47	0.44
18:P:39:VAL:HA	18:P:103:ASP:HB3	1.98	0.44
25:W:67:LEU:HB3	25:W:69:LEU:HG	1.99	0.44
34:A:131:A:H2'	34:A:132:C:C6	2.53	0.44
34:A:1222:C:H2'	34:A:1223:U:C6	2.52	0.44
34:A:1324:G:O6	34:A:1352:A:H2'	2.17	0.44
34:A:1809:U:H2'	34:A:1810:A:C8	2.52	0.44
34:A:1822:C:H2'	34:A:1823:C:H6	1.82	0.44
2:3:11:ARG:NH1	34:A:1100:C:O2	2.49	0.44
4:B:44:C:O2	8:F:97:THR:OG1	2.36	0.44
4:B:58:A:H1'	8:F:34:GLN:CG	2.48	0.44
5:C:133:LEU:HD23	5:C:133:LEU:HA	1.78	0.44
5:C:176:ARG:NH1	5:C:182:ILE:HD11	2.32	0.44
7:E:55:ARG:HH12	34:A:789:G:P	2.39	0.44
7:E:192:ASP:N	7:E:192:ASP:OD1	2.50	0.44
9:G:84:TYR:CE2	9:G:139:LYS:HB2	2.52	0.44
11:I:13:ILE:HB	11:I:17:PHE:CZ	2.52	0.44
12:J:45:ASN:O	12:J:49:GLU:HG3	2.17	0.44
15:M:88:PRO:HD2	15:M:89:GLN:HE22	1.81	0.44
34:A:489:A:H2'	34:A:490:A:C8	2.53	0.44
34:A:2344:G:C5	34:A:2345:U:H1'	2.52	0.44
3:4:133:GLU:OE2	3:4:134:LYS:HG2	2.18	0.44
3:4:377:VAL:HB	3:4:383:ARG:NH2	2.32	0.44
6:D:85:ARG:NH1	34:A:2861:U:H5''	2.32	0.44
11:I:28:TYR:CD2	11:I:78:ALA:HB2	2.51	0.44
11:I:105:ILE:HD13	11:I:120:VAL:HG21	1.98	0.44
13:K:136:GLN:HE22	34:A:3119:A:H5'	1.82	0.44
34:A:826:G:C2	34:A:827:G:C4	3.05	0.44
34:A:1727:A:H2'	34:A:1728:U:O4'	2.17	0.44
34:A:1900:C:H2'	34:A:1901:C:H6	1.81	0.44
34:A:2056:G:N1	34:A:2151:A:OP2	2.50	0.44
34:A:2869:C:C3'	34:A:2870:C:H5'	2.48	0.44
3:4:161:LYS:HE3	34:A:2706:A:O3'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:324:ASP:N	3:4:324:ASP:OD1	2.50	0.44
3:4:445:THR:HG22	3:4:446:ASP:N	2.33	0.44
6:D:153:GLY:O	34:A:2276:G:H4'	2.18	0.44
9:G:28:GLY:HA3	9:G:80:VAL:HB	1.99	0.44
9:G:123:THR:HG23	9:G:135:SER:OG	2.18	0.44
11:I:73:PHE:CD1	11:I:77:THR:HG21	2.52	0.44
19:Q:105:LYS:HB2	19:Q:105:LYS:HE2	1.74	0.44
34:A:191:G:OP2	34:A:191:G:N2	2.43	0.44
34:A:231:U:H2'	34:A:232:G:O4'	2.18	0.44
34:A:298:G:H3'	34:A:299:G:C8	2.50	0.44
34:A:654:U:H6	34:A:654:U:H2'	1.58	0.44
34:A:857:U:H2'	34:A:858:A:H8	1.82	0.44
34:A:1805:G:H2'	34:A:1806:A:C8	2.53	0.44
34:A:2412:U:H2'	34:A:2413:G:H8	1.82	0.44
3:4:20:ARG:HB3	3:4:88:ARG:NH1	2.32	0.44
8:F:51:ALA:HA	8:F:85:LYS:HD2	1.99	0.44
8:F:105:GLU:HA	8:F:108:ASP:OD2	2.18	0.44
11:I:105:ILE:HG21	11:I:120:VAL:HG13	1.98	0.44
15:M:63:LYS:HE3	34:A:2618:C:H5''	1.99	0.44
22:T:6:GLU:OE2	22:T:7:PHE:N	2.42	0.44
34:A:14:G:H2'	34:A:15:C:C6	2.52	0.44
34:A:564:G:N1	34:A:567:A:OP2	2.47	0.44
34:A:567:A:H1'	34:A:568:A:H5''	1.99	0.44
34:A:1784:C:H2'	34:A:1785:C:C6	2.53	0.44
34:A:2018:G:H1	34:A:2028:G:P	2.41	0.44
34:A:2777:G:C6	34:A:2778:U:H1'	2.52	0.44
1:2:5:LYS:HG3	1:2:5:LYS:O	2.17	0.44
3:4:378:GLY:HA3	3:4:383:ARG:N	2.32	0.44
4:B:32:C:O2'	4:B:54:A:N1	2.44	0.44
5:C:177:MET:HA	5:C:177:MET:CE	2.47	0.44
5:C:245:HIS:O	5:C:247:VAL:HG23	2.18	0.44
6:D:191:VAL:HG21	19:Q:7:VAL:HG11	2.00	0.44
8:F:45:MET:HE3	8:F:64:LEU:HD12	1.99	0.44
11:I:94:LYS:HB2	11:I:120:VAL:HB	1.99	0.44
17:O:10:LEU:HD21	17:O:40:LYS:HA	1.99	0.44
17:O:87:TYR:HD2	17:O:90:ARG:HD3	1.83	0.44
25:W:11:LEU:HD13	25:W:67:LEU:HG	2.00	0.44
34:A:326:A:H2	34:A:449:G:H1	1.62	0.44
34:A:997:G:C5	34:A:998:G:C5	3.06	0.44
34:A:1754:G:O3'	34:A:1755:A:H4'	2.18	0.44
34:A:2131:G:H2'	34:A:2132:U:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2213:A:H2'	34:A:2214:C:O4'	2.17	0.44
34:A:2755:A:C6	34:A:2756:G:N7	2.86	0.44
1:2:38:GLU:HG2	1:2:39:ASP:N	2.32	0.43
2:3:7:LYS:NZ	34:A:1252:G:N3	2.65	0.43
3:4:372:ASP:OD1	3:4:373:ALA:N	2.51	0.43
4:B:40:A:C2	4:B:45:G:C2	3.06	0.43
6:D:161:PHE:O	6:D:164:THR:OG1	2.35	0.43
8:F:124:LEU:O	8:F:184:PHE:HA	2.18	0.43
11:I:28:TYR:OH	34:A:1225:G:OP1	2.21	0.43
13:K:2:PRO:HA	34:A:1113:C:N3	2.33	0.43
14:L:2:ILE:HB	14:L:33:ALA:HB3	1.99	0.43
26:X:49:VAL:HG22	26:X:79:ASN:HB3	2.00	0.43
28:Z:7:PRO:HG3	34:A:74:C:H5''	2.00	0.43
34:A:332:C:H2'	34:A:333:C:H6	1.82	0.43
3:4:105:GLU:O	3:4:109:VAL:HG23	2.18	0.43
6:D:65:PRO:O	34:A:3010:U:O2'	2.34	0.43
11:I:23:THR:HG21	11:I:69:LEU:HD22	2.00	0.43
11:I:110:MET:N	11:I:114:ALA:O	2.27	0.43
12:J:22:PRO:HD2	12:J:41:CYS:SG	2.58	0.43
13:K:65:SER:OG	34:A:1259:U:OP2	2.22	0.43
14:L:100:GLY:O	14:L:119:PRO:HD2	2.18	0.43
15:M:37:THR:O	15:M:42:ALA:HB2	2.19	0.43
23:U:54:VAL:HG13	23:U:84:VAL:HG13	2.00	0.43
24:V:79:LYS:HA	24:V:79:LYS:HD3	1.65	0.43
34:A:150:C:O2'	34:A:151:A:H5'	2.18	0.43
34:A:394:G:H4'	34:A:413:G:C6	2.53	0.43
34:A:1160:G:N2	34:A:1231:U:O2	2.44	0.43
34:A:2134:G:C3'	34:A:2135:U:H2'	2.48	0.43
34:A:2490:A:H4'	34:A:2491:A:N3	2.33	0.43
34:A:2537:C:H2'	34:A:2538:A:H8	1.83	0.43
3:4:16:ALA:HB3	3:4:22:SER:CB	2.48	0.43
3:4:118:VAL:O	3:4:140:VAL:HG23	2.19	0.43
7:E:23:GLU:OE2	7:E:23:GLU:N	2.27	0.43
10:H:112:LEU:HD13	10:H:134:VAL:HG11	2.01	0.43
12:J:59:GLU:N	12:J:73:LYS:HZ1	2.17	0.43
24:V:22:LYS:HE3	24:V:22:LYS:HB2	1.83	0.43
34:A:993:G:H2'	34:A:1014:G:N2	2.33	0.43
34:A:1430:C:H2'	34:A:1431:U:H6	1.82	0.43
34:A:1636:A:H2'	34:A:1637:G:O4'	2.18	0.43
34:A:3014:A:C2	34:A:3015:C:C5	3.06	0.43
5:C:133:LEU:N	5:C:189:CYS:O	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:273:ARG:HE	5:C:276:LYS:HD2	1.82	0.43
6:D:11:LEU:HB3	19:Q:4:LEU:HD21	2.00	0.43
14:L:22:ILE:HD11	14:L:42:THR:OG1	2.19	0.43
25:W:26:GLN:OE1	25:W:26:GLN:HA	2.18	0.43
34:A:1243:G:OP2	34:A:1244:A:O2'	2.22	0.43
34:A:2133:G:OP2	34:A:2133:G:H8	2.02	0.43
34:A:2368:C:H5''	34:A:2369:C:OP1	2.18	0.43
34:A:2380:G:H2'	34:A:2381:A:C2	2.53	0.43
34:A:2514:G:H4'	34:A:2605:C:O2'	2.18	0.43
34:A:2861:U:H2'	34:A:2862:G:O4'	2.17	0.43
34:A:3118:U:H2'	34:A:3119:A:H8	1.83	0.43
3:4:18:GLU:HB2	3:4:22:SER:CA	2.48	0.43
6:D:4:LYS:HE2	6:D:4:LYS:HB2	1.82	0.43
9:G:16:ASP:N	9:G:16:ASP:OD1	2.52	0.43
9:G:35:LEU:HD21	9:G:72:LEU:HB3	2.01	0.43
12:J:122:ASP:CG	12:J:125:ALA:HB3	2.39	0.43
18:P:93:LYS:HB2	18:P:93:LYS:HE3	1.69	0.43
24:V:39:ASN:HD22	24:V:66:ILE:HB	1.83	0.43
34:A:1963:G:H2'	34:A:1964:U:H6	1.84	0.43
34:A:2274:C:H2'	34:A:2275:A:O4'	2.18	0.43
34:A:2538:A:H2'	34:A:2539:G:H8	1.84	0.43
34:A:2757:C:H2'	34:A:2758:A:O4'	2.19	0.43
3:4:133:GLU:O	3:4:137:LYS:N	2.35	0.43
3:4:313:GLU:OE2	3:4:316:ARG:NH1	2.51	0.43
4:B:50:C:H2'	4:B:51:G:C8	2.53	0.43
6:D:40:ARG:NH2	34:A:3008:C:O2	2.52	0.43
6:D:135:GLN:OE1	6:D:135:GLN:N	2.52	0.43
6:D:154:CYS:N	34:A:2798:G:O2'	2.45	0.43
7:E:21:PRO:HB2	7:E:24:LEU:HB2	2.00	0.43
12:J:19:GLN:OE1	12:J:19:GLN:N	2.39	0.43
12:J:135:ARG:O	12:J:135:ARG:HG2	2.17	0.43
34:A:164:A:H2'	34:A:165:U:C6	2.54	0.43
34:A:1543:A:N1	34:A:1628:A:H8	2.16	0.43
34:A:1633:U:H2'	34:A:1634:C:C6	2.53	0.43
34:A:2597:A:H2'	34:A:2598:C:C6	2.54	0.43
3:4:432:ARG:HB3	3:4:459:LEU:HD21	2.00	0.43
8:F:26:GLU:OE1	8:F:26:GLU:N	2.50	0.43
9:G:49:GLY:O	9:G:51:ILE:HG13	2.18	0.43
12:J:94:PRO:O	34:A:1194:C:O2'	2.17	0.43
19:Q:91:VAL:HG13	19:Q:109:ILE:HG23	2.01	0.43
23:U:46:ILE:HG23	23:U:50:PHE:HD2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:16:ARG:NH2	25:W:19:THR:HA	2.34	0.43
27:Y:63:ARG:HH12	34:A:2315:U:P	2.41	0.43
34:A:149:C:H2'	34:A:150:C:C6	2.54	0.43
34:A:281:C:H2'	34:A:282:A:C8	2.54	0.43
34:A:290:C:C5	34:A:303:G:H5''	2.54	0.43
34:A:1202:A:N3	34:A:1224:G:H1'	2.34	0.43
34:A:1425:G:H3'	34:A:1426:G:N2	2.34	0.43
34:A:1545:C:O2'	34:A:1625:G:O6	2.33	0.43
34:A:1961:G:H3'	34:A:1962:A:H8	1.83	0.43
34:A:2124:A:N6	34:A:2157:G:O4'	2.52	0.43
3:4:82:LEU:HD22	3:4:113:THR:HG22	2.00	0.43
7:E:158:ILE:HD13	7:E:158:ILE:HA	1.89	0.43
34:A:1013:U:H2'	34:A:1014:G:O4'	2.17	0.43
34:A:1651:C:H2'	34:A:1652:A:C8	2.53	0.43
34:A:1790:A:H2'	34:A:1791:A:C8	2.54	0.43
34:A:2196:G:O2'	34:A:2197:G:OP2	2.30	0.43
34:A:2261:U:H2'	34:A:2262:C:C6	2.54	0.43
34:A:2375:G:H2'	34:A:2376:G:C8	2.52	0.43
34:A:2383:U:H2'	34:A:2384:C:H4'	2.00	0.43
34:A:2551:A:H2'	34:A:2552:A:C8	2.53	0.43
34:A:2623:A:H2'	34:A:2624:C:C6	2.53	0.43
1:2:46:LEU:O	1:2:50:VAL:HG22	2.18	0.43
5:C:35:ARG:H	5:C:35:ARG:HG2	2.56	0.43
5:C:258:ARG:HD2	34:A:2016:G:OP1	2.19	0.43
8:F:87:ARG:HE	8:F:87:ARG:HB2	1.59	0.43
8:F:117:ARG:O	8:F:117:ARG:NH1	2.37	0.43
9:G:18:THR:OG1	9:G:25:SER:CA	2.65	0.43
12:J:108:ARG:HD2	12:J:127:ALA:HB1	2.00	0.43
23:U:68:ARG:NH2	34:A:1449:C:H5''	2.34	0.43
34:A:42:G:H5'	34:A:43:C:OP1	2.18	0.43
34:A:74:C:H2'	34:A:75:U:C6	2.54	0.43
34:A:82:G:C6	34:A:83:C:C4	3.06	0.43
34:A:431:C:H2'	34:A:432:C:C6	2.54	0.43
34:A:722:G:C6	34:A:730:G:C2	3.07	0.43
34:A:954:U:H2'	34:A:955:C:C6	2.54	0.43
34:A:1214:A:OP2	34:A:1214:A:H8	2.01	0.43
34:A:1622:G:H2'	34:A:1622:G:N3	2.32	0.43
34:A:1843:C:O2'	34:A:1844:A:H5'	2.17	0.43
34:A:2193:A:C4	34:A:2197:G:H1'	2.54	0.43
34:A:2349:A:H1'	34:A:2350:G:C8	2.54	0.43
34:A:2521:C:O2	34:A:2521:C:H2'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:49:VAL:HA	3:4:117:THR:HB	2.01	0.43
3:4:181:GLU:OE1	3:4:185:ARG:NH1	2.52	0.43
3:4:201:ARG:C	3:4:204:GLY:H	2.21	0.43
8:F:108:ASP:OD1	8:F:109:ARG:N	2.52	0.43
10:H:41:ARG:HD2	10:H:41:ARG:HA	1.74	0.43
20:R:43:LEU:HD23	20:R:43:LEU:HA	1.70	0.43
23:U:43:LYS:HB2	23:U:57:VAL:HG21	2.01	0.43
34:A:756:A:H3'	34:A:757:G:C2	2.54	0.43
34:A:946:G:H2'	34:A:947:U:O4'	2.18	0.43
34:A:1087:G:H2'	34:A:1088:U:C6	2.53	0.43
34:A:1178:U:C2	34:A:1180:G:H5'	2.54	0.43
34:A:1316:U:O2'	34:A:1317:G:H5'	2.19	0.43
34:A:1401:A:H1'	34:A:1403:C:OP2	2.19	0.43
34:A:1810:A:H2'	34:A:1811:C:C6	2.53	0.43
34:A:2054:C:O2	34:A:2145:C:N3	2.52	0.43
34:A:2130:G:C2	34:A:2131:G:N7	2.87	0.43
34:A:2133:G:H2'	34:A:2133:G:N3	2.34	0.43
34:A:2300:A:H2'	34:A:2301:C:C6	2.54	0.43
34:A:2366:C:H3'	34:A:2367:G:H8	1.84	0.43
34:A:2374:U:C2	34:A:2375:G:C8	3.07	0.43
34:A:2636:A:H2'	34:A:2637:G:O4'	2.19	0.43
34:A:3018:U:H2'	34:A:3019:C:C6	2.54	0.43
3:4:76:THR:OG1	3:4:275:ALA:HB1	2.19	0.42
3:4:303:PHE:CE2	3:4:349:VAL:HG11	2.53	0.42
3:4:420:VAL:HG12	3:4:467:ALA:HA	2.00	0.42
4:B:40:A:H2'	4:B:41:U:C6	2.53	0.42
7:E:139:LYS:HB2	7:E:139:LYS:HE3	1.77	0.42
8:F:11:LEU:HG	8:F:108:ASP:HB3	2.00	0.42
12:J:98:LYS:HZ1	12:J:140:THR:HG22	1.81	0.42
13:K:93:LEU:HG	13:K:100:VAL:HG21	2.00	0.42
16:N:52:ILE:HD13	16:N:52:ILE:HA	1.82	0.42
17:O:38:GLU:HB2	17:O:109:PRO:HB2	2.01	0.42
18:P:88:ILE:HD12	18:P:88:ILE:HA	1.94	0.42
34:A:295:U:H2'	34:A:296:A:O4'	2.19	0.42
34:A:673:C:H2'	34:A:674:U:C6	2.54	0.42
34:A:1012:C:C4	34:A:1013:U:C4	3.07	0.42
34:A:1202:A:C8	34:A:1203:A:N1	2.87	0.42
34:A:2336:U:H5'	34:A:2338:G:N1	2.33	0.42
34:A:3013:C:O2'	34:A:3113:A:N6	2.46	0.42
1:2:10:ARG:HE	1:2:10:ARG:HB3	1.51	0.42
3:4:128:GLN:OE1	3:4:128:GLN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:41:VAL:HG12	8:F:163:VAL:HA	2.00	0.42
8:F:67:ILE:HG12	8:F:145:PHE:CG	2.53	0.42
8:F:142:GLN:NE2	8:F:157:ARG:H	2.17	0.42
10:H:146:LEU:HD12	10:H:146:LEU:HA	1.93	0.42
11:I:6:LYS:O	11:I:10:VAL:HG23	2.19	0.42
11:I:101:LYS:HA	11:I:101:LYS:HD3	1.82	0.42
24:V:10:LEU:HG	24:V:20:LYS:HG2	2.01	0.42
24:V:82:ARG:NH1	34:A:381:A:OP2	2.52	0.42
34:A:296:A:H2'	34:A:297:G:C8	2.54	0.42
34:A:828:G:H2'	34:A:829:U:O4'	2.19	0.42
34:A:864:A:H4'	34:A:1386:G:N3	2.35	0.42
34:A:1323:G:O2'	34:A:1352:A:N1	2.36	0.42
34:A:1822:C:H2'	34:A:1823:C:C6	2.54	0.42
34:A:2288:C:H2'	34:A:2289:C:H6	1.81	0.42
34:A:2350:G:H2'	34:A:2351:A:H8	1.80	0.42
34:A:2373:G:H2'	34:A:2374:U:C6	2.54	0.42
3:4:52:VAL:HA	3:4:85:LEU:O	2.19	0.42
3:4:304:VAL:HG12	3:4:307:LEU:HD12	2.02	0.42
4:B:4:A:C8	4:B:63:U:H1'	2.54	0.42
4:B:53:A:N7	18:P:45:ARG:CZ	2.82	0.42
4:B:60:G:H3'	4:B:61:C:H6	1.84	0.42
10:H:26:GLY:HA2	10:H:30:LEU:HB2	2.00	0.42
13:K:68:LYS:HE3	34:A:1140:G:N7	2.34	0.42
15:M:94:GLY:H	15:M:97:GLU:HB2	1.84	0.42
18:P:10:ILE:HD13	18:P:10:ILE:HA	1.85	0.42
21:S:92:GLN:OE1	34:A:1111:G:H1'	2.18	0.42
34:A:394:G:H4'	34:A:413:G:C5	2.55	0.42
34:A:401:C:H2'	34:A:402:G:O4'	2.19	0.42
34:A:1064:A:H2'	34:A:1065:C:C6	2.53	0.42
34:A:1378:U:C4	34:A:1379:G:C6	3.08	0.42
34:A:1650:G:H2'	34:A:1651:C:C6	2.54	0.42
34:A:2008:A:N6	34:A:2045:G:O2'	2.39	0.42
1:2:38:GLU:HG2	1:2:39:ASP:H	1.85	0.42
3:4:141:ILE:HD12	3:4:141:ILE:O	2.19	0.42
3:4:206:THR:O	3:4:209:GLU:N	2.46	0.42
3:4:280:LEU:HG	3:4:281:GLU:HG3	2.02	0.42
3:4:328:LEU:O	3:4:365:LEU:N	2.48	0.42
5:C:179:SER:OG	34:A:2016:G:N7	2.52	0.42
10:H:85:ALA:HB3	10:H:151:GLN:HB3	2.01	0.42
11:I:31:LEU:HB3	11:I:36:LEU:HD12	2.01	0.42
11:I:40:ARG:NH1	34:A:1201:G:H4'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:98:LYS:CE	12:J:140:THR:HG22	2.49	0.42
18:P:55:LEU:HD23	18:P:55:LEU:HA	1.72	0.42
18:P:83:ARG:HD3	18:P:83:ARG:O	2.20	0.42
34:A:446:G:OP2	34:A:446:G:H8	2.01	0.42
34:A:948:G:H2'	34:A:949:C:C6	2.55	0.42
34:A:1001:C:H3'	34:A:1002:C:O4'	2.19	0.42
34:A:1202:A:H2'	34:A:1203:A:C4	2.54	0.42
34:A:1721:U:H2'	34:A:1722:C:C6	2.55	0.42
34:A:1733:C:H2'	34:A:1734:C:H6	1.84	0.42
34:A:2364:C:H2'	34:A:2365:A:C8	2.50	0.42
34:A:2713:G:O2'	34:A:2714:G:H5'	2.19	0.42
3:4:193:GLY:HA2	3:4:207:LYS:CE	2.49	0.42
3:4:200:THR:HG23	3:4:200:THR:O	2.19	0.42
3:4:293:ARG:HA	3:4:438:HIS:NE2	2.34	0.42
4:B:30:G:H21	4:B:58:A:N6	2.16	0.42
5:C:78:LYS:HB2	5:C:78:LYS:HE2	1.82	0.42
5:C:273:ARG:CZ	5:C:274:THR:H	2.32	0.42
8:F:14:ARG:HB2	8:F:18:GLU:OE1	2.20	0.42
8:F:105:GLU:O	8:F:109:ARG:HG2	2.20	0.42
8:F:122:ARG:HH11	8:F:122:ARG:HA	1.83	0.42
9:G:37:VAL:HG23	9:G:69:SER:HB3	2.00	0.42
11:I:28:TYR:HB2	11:I:31:LEU:HD12	2.00	0.42
14:L:19:ILE:HB	14:L:41:ALA:HB1	2.01	0.42
15:M:6:LEU:HD23	15:M:6:LEU:HA	1.81	0.42
15:M:118:LEU:HD12	15:M:119:THR:N	2.35	0.42
18:P:85:GLY:O	18:P:88:ILE:HG22	2.19	0.42
22:T:7:PHE:HB3	22:T:116:SER:O	2.20	0.42
34:A:331:U:H2'	34:A:332:C:C6	2.54	0.42
34:A:387:U:H2'	34:A:388:U:C6	2.55	0.42
34:A:689:U:H2'	34:A:690:G:H8	1.84	0.42
34:A:1005:A:H2'	34:A:1006:G:O4'	2.19	0.42
34:A:1197:C:C2	34:A:1198:C:C5	3.08	0.42
34:A:1733:C:H2'	34:A:1734:C:C6	2.54	0.42
34:A:2761:U:H2'	34:A:2762:C:H6	1.84	0.42
34:A:3074:C:H2'	34:A:3075:C:H6	1.83	0.42
6:D:54:TYR:CG	6:D:55:GLY:N	2.87	0.42
6:D:100:GLU:OE2	6:D:100:GLU:HA	2.20	0.42
7:E:30:ASN:O	7:E:34:MET:HG3	2.18	0.42
7:E:48:GLY:O	7:E:95:PRO:HA	2.19	0.42
8:F:9:PRO:HG2	8:F:104:TRP:HB3	2.01	0.42
8:F:24:GLN:HA	8:F:27:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:128:GLN:HA	34:A:2528:G:OP1	2.19	0.42
12:J:89:LYS:HE3	12:J:89:LYS:HB3	1.94	0.42
13:K:36:LEU:HD11	13:K:122:LEU:HD13	2.02	0.42
15:M:91:GLY:HA2	15:M:122:VAL:HG12	2.01	0.42
19:Q:56:GLU:HB3	19:Q:75:VAL:HB	2.01	0.42
21:S:17:ALA:N	21:S:20:ASP:OD1	2.52	0.42
21:S:64:VAL:HG22	21:S:97:LEU:HD21	2.01	0.42
23:U:31:PHE:CE2	23:U:96:PHE:CZ	3.07	0.42
23:U:42:ILE:O	23:U:46:ILE:HG12	2.20	0.42
24:V:39:ASN:ND2	24:V:66:ILE:HB	2.35	0.42
34:A:307:G:H2'	34:A:308:U:C6	2.53	0.42
34:A:380:A:N1	34:A:404:A:O2'	2.38	0.42
34:A:502:C:N4	34:A:503:A:H62	2.18	0.42
34:A:772:U:H2'	34:A:773:G:C8	2.54	0.42
34:A:847:C:H2'	34:A:848:G:O4'	2.19	0.42
34:A:1289:A:H2'	34:A:1290:C:O4'	2.20	0.42
34:A:1935:C:H2'	34:A:1936:G:H8	1.85	0.42
1:2:38:GLU:OE1	1:2:40:ASN:ND2	2.53	0.42
3:4:21:ALA:HB1	3:4:88:ARG:HB2	1.90	0.42
8:F:136:THR:OG1	34:A:2527:G:N2	2.53	0.42
12:J:129:ILE:HG12	34:A:1198:C:O2	2.19	0.42
13:K:117:GLN:O	13:K:120:LYS:HG2	2.20	0.42
20:R:31:LEU:HD13	34:A:672:C:H4'	2.01	0.42
20:R:101:SER:OG	20:R:102:ASP:N	2.53	0.42
22:T:14:ALA:HB2	22:T:57:VAL:HG22	2.01	0.42
34:A:578:G:OP2	34:A:578:G:H8	2.02	0.42
34:A:947:U:H2'	34:A:948:G:C8	2.55	0.42
34:A:1434:G:O2'	34:A:1435:C:H5'	2.19	0.42
34:A:1533:U:O2	34:A:1533:U:H2'	2.19	0.42
34:A:1854:U:O2'	34:A:1977:C:O2'	2.21	0.42
34:A:2324:A:N6	34:A:2413:G:C5	2.88	0.42
34:A:2588:C:H2'	34:A:2589:G:O4'	2.20	0.42
5:C:54:LYS:HE2	34:A:2040:G:OP1	2.19	0.42
8:F:68:THR:HG21	8:F:96:VAL:HG11	2.02	0.42
16:N:76:LYS:HD3	16:N:91:GLU:HG2	2.02	0.42
19:Q:88:ARG:HB2	19:Q:112:LYS:HB2	2.02	0.42
34:A:74:C:H2'	34:A:75:U:H6	1.83	0.42
34:A:1418:G:O6	34:A:1419:A:N6	2.53	0.42
34:A:1951:G:H2'	34:A:1952:C:C6	2.55	0.42
34:A:2321:U:H2'	34:A:2322:C:C6	2.55	0.42
34:A:2870:C:H2'	34:A:2871:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:136:VAL:HG13	3:4:138:VAL:HB	2.02	0.42
6:D:151:ILE:HG23	6:D:160:VAL:HG13	2.02	0.42
7:E:53:LYS:HE2	34:A:539:C:H4'	2.02	0.42
9:G:152:LEU:HD23	9:G:152:LEU:HA	1.91	0.42
11:I:46:SER:HA	11:I:83:LYS:HB2	2.01	0.42
12:J:42:LYS:HA	12:J:42:LYS:HD3	1.64	0.42
15:M:57:ILE:HD13	15:M:60:ARG:HH21	1.84	0.42
34:A:928:U:HO2'	34:A:1339:G:HO2'	1.65	0.42
34:A:1002:C:O2'	34:A:1003:A:OP1	2.26	0.42
34:A:1301:G:H2'	34:A:1302:G:O4'	2.20	0.42
34:A:1542:A:H8	34:A:1543:A:N7	2.18	0.42
34:A:3013:C:H5'	34:A:3014:A:C5'	2.50	0.42
3:4:20:ARG:HB3	3:4:88:ARG:HH12	1.85	0.42
3:4:177:ARG:HD2	3:4:177:ARG:HA	1.86	0.42
3:4:443:GLU:H	3:4:450:ARG:HG3	1.85	0.42
5:C:155:LEU:HD13	5:C:177:MET:HE1	2.02	0.42
6:D:150:SER:O	34:A:2736:C:H1'	2.19	0.42
17:O:16:HIS:CE1	17:O:20:LEU:HD12	2.55	0.42
22:T:99:ARG:HH12	34:A:862:U:H4'	1.85	0.42
34:A:504:C:H2'	34:A:505:C:C6	2.55	0.42
34:A:1278:C:N3	34:A:1279:G:N7	2.68	0.42
34:A:1869:G:H2'	34:A:1870:U:O4'	2.20	0.42
34:A:2127:G:O2'	34:A:2151:A:H4'	2.20	0.42
34:A:2366:C:H3'	34:A:2367:G:C8	2.55	0.42
34:A:2777:G:N2	34:A:2779:U:OP1	2.53	0.42
34:A:2869:C:H4'	34:A:2956:G:O2'	2.20	0.42
34:A:3014:A:N6	34:A:3112:A:H2'	2.35	0.42
34:A:3074:C:H2'	34:A:3075:C:C6	2.55	0.42
3:4:22:SER:HB3	3:4:23:LEU:H	1.59	0.41
4:B:50:C:H2'	4:B:51:G:H8	1.85	0.41
6:D:86:LEU:HD22	6:D:95:TYR:HE2	1.85	0.41
6:D:173:ASP:OD1	6:D:173:ASP:N	2.53	0.41
8:F:178:ARG:HA	8:F:182:PHE:HD2	1.85	0.41
12:J:94:PRO:O	12:J:95:HIS:HB2	2.20	0.41
12:J:102:VAL:HG12	12:J:103:THR:H	1.85	0.41
15:M:31:LYS:HB3	15:M:32:THR:H	1.61	0.41
18:P:82:VAL:HG23	18:P:119:ALA:HB2	2.02	0.41
20:R:91:ASP:OD1	20:R:93:LYS:HB3	2.20	0.41
34:A:24:G:C2	34:A:599:G:N3	2.88	0.41
34:A:183:G:H2'	34:A:184:C:H6	1.85	0.41
34:A:339:U:H2'	34:A:340:A:N7	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:966:U:H2'	34:A:967:G:H8	1.85	0.41
34:A:1001:C:C6	34:A:1002:C:H1'	2.55	0.41
34:A:1652:A:H2'	34:A:1653:G:C8	2.55	0.41
34:A:1833:C:H2'	34:A:1835:C:C5	2.55	0.41
34:A:2134:G:O2'	34:A:2146:A:N6	2.51	0.41
34:A:2396:A:C6	34:A:2397:C:C4	3.09	0.41
4:B:95:G:O2'	34:A:1033:A:H5''	2.20	0.41
8:F:34:GLN:HB3	18:P:3:HIS:HD2	1.84	0.41
8:F:158:GLY:HA3	34:A:2529:A:C6	2.55	0.41
12:J:57:PRO:CB	12:J:73:LYS:HB2	2.50	0.41
13:K:120:LYS:HE2	13:K:120:LYS:HB3	1.75	0.41
15:M:77:VAL:HG11	34:A:730:G:H1	1.85	0.41
23:U:12:LEU:HB2	23:U:32:VAL:HG13	2.03	0.41
34:A:446:G:N2	34:A:447:A:H1'	2.35	0.41
34:A:949:C:C2	34:A:950:A:C8	3.08	0.41
34:A:996:G:C5	34:A:997:G:N7	2.88	0.41
34:A:998:G:H8	34:A:998:G:OP2	2.03	0.41
34:A:1934:G:H2'	34:A:1935:C:H6	1.85	0.41
34:A:2420:U:O2'	34:A:2421:A:H2'	2.20	0.41
34:A:2971:G:H2'	34:A:2972:A:C8	2.55	0.41
1:2:3:GLU:HA	1:2:3:GLU:OE1	2.20	0.41
3:4:383:ARG:NE	3:4:383:ARG:HA	2.36	0.41
3:4:454:ARG:H	3:4:454:ARG:HG2	1.60	0.41
5:C:162:SER:HB3	5:C:195:GLU:HB2	2.03	0.41
6:D:78:ARG:HA	6:D:78:ARG:HD2	1.95	0.41
10:H:78:VAL:HG13	10:H:146:LEU:HD12	2.01	0.41
10:H:80:LEU:HD13	10:H:103:ALA:HB2	2.02	0.41
13:K:88:THR:OG1	13:K:91:GLU:HG3	2.20	0.41
15:M:86:ALA:O	15:M:88:PRO:HD3	2.21	0.41
18:P:70:VAL:HG22	18:P:83:ARG:HG3	2.01	0.41
19:Q:61:ARG:NH1	19:Q:70:GLU:OE1	2.41	0.41
24:V:41:ILE:HG13	24:V:64:ALA:HB2	2.03	0.41
26:X:29:GLN:HE21	26:X:29:GLN:HB3	1.76	0.41
34:A:334:G:C6	34:A:348:G:C5	3.08	0.41
34:A:441:G:H2'	34:A:442:U:H6	1.84	0.41
34:A:479:A:H1'	34:A:499:G:O4'	2.20	0.41
34:A:980:C:HO2'	34:A:981:U:P	2.42	0.41
34:A:1006:G:H2'	34:A:1007:G:O4'	2.21	0.41
34:A:1175:A:N6	34:A:1205:G:OP1	2.53	0.41
34:A:2125:A:N3	34:A:2126:C:N4	2.68	0.41
34:A:2623:A:H2'	34:A:2624:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:24:ARG:H	3:4:87:GLN:NE2	2.18	0.41
3:4:230:LYS:HE3	3:4:316:ARG:NH2	2.35	0.41
8:F:174:ARG:HD3	8:F:178:ARG:HH21	1.86	0.41
11:I:41:ARG:HH22	34:A:1200:U:H4'	1.86	0.41
12:J:76:PRO:O	12:J:79:LYS:C	2.57	0.41
15:M:124:VAL:HG21	15:M:137:ILE:HD13	2.03	0.41
17:O:2:PRO:HG2	34:A:2914:A:C2	2.55	0.41
23:U:30:THR:HA	23:U:82:ALA:O	2.20	0.41
34:A:279:U:H2'	34:A:280:G:C8	2.51	0.41
34:A:680:U:H2'	34:A:681:C:C6	2.55	0.41
34:A:1383:A:H2'	34:A:1384:G:O4'	2.19	0.41
34:A:1931:A:H61	34:A:1962:A:H61	1.67	0.41
34:A:2132:U:HO2'	34:A:2133:G:C1'	2.33	0.41
34:A:2366:C:H2'	34:A:2367:G:O4'	2.20	0.41
34:A:2389:U:H3'	34:A:2390:U:C5	2.54	0.41
34:A:2482:U:O2'	34:A:2651:C:OP2	2.32	0.41
34:A:3033:G:H2'	34:A:3034:C:H6	1.84	0.41
3:4:221:LYS:HD3	34:A:2686:U:OP1	2.21	0.41
9:G:6:LYS:HD3	9:G:6:LYS:HA	1.83	0.41
9:G:116:ILE:HD11	9:G:152:LEU:HD11	2.02	0.41
10:H:113:ASP:O	10:H:116:THR:OG1	2.27	0.41
15:M:133:ALA:O	15:M:137:ILE:HG13	2.20	0.41
20:R:46:ALA:O	20:R:50:ARG:HB2	2.21	0.41
34:A:1091:A:H5'	34:A:1303:U:H1'	2.01	0.41
34:A:1250:U:H2'	34:A:1251:A:C8	2.55	0.41
34:A:1387:A:OP1	34:A:1387:A:H4'	2.20	0.41
34:A:1621:C:H2'	34:A:1622:G:H5'	2.01	0.41
34:A:1622:G:H2'	34:A:1623:U:H5'	2.01	0.41
34:A:2027:A:H2'	34:A:2028:G:O4'	2.21	0.41
34:A:2740:G:H2'	34:A:2741:C:C6	2.55	0.41
34:A:2998:C:H2'	34:A:2999:A:O4'	2.21	0.41
3:4:118:VAL:O	3:4:140:VAL:HA	2.20	0.41
3:4:151:PHE:CE2	3:4:311:LEU:HD13	2.55	0.41
10:H:80:LEU:HD23	10:H:95:VAL:HG22	2.02	0.41
12:J:95:HIS:NE2	12:J:135:ARG:HG2	2.36	0.41
14:L:23:ARG:NH2	34:A:2771:U:O2	2.47	0.41
15:M:84:ASN:HB2	15:M:118:LEU:HD13	2.02	0.41
15:M:98:LEU:HD23	15:M:98:LEU:HA	1.86	0.41
17:O:45:ARG:HB3	17:O:46:PRO:HD3	2.03	0.41
17:O:64:ARG:NH1	34:A:3072:A:O3'	2.54	0.41
17:O:87:TYR:CD2	17:O:90:ARG:HD3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:119:ALA:O	18:P:122:GLU:HG3	2.20	0.41
22:T:26:ARG:HE	22:T:26:ARG:HB3	1.63	0.41
23:U:93:ILE:H	23:U:93:ILE:HG13	1.72	0.41
25:W:16:ARG:HG2	25:W:48:GLU:HB3	2.02	0.41
34:A:287:A:H1'	34:A:300:G:C6	2.55	0.41
34:A:322:A:H2'	34:A:323:C:O4'	2.20	0.41
34:A:376:G:H2'	34:A:377:C:C6	2.55	0.41
34:A:449:G:C6	34:A:450:G:C5	3.09	0.41
34:A:813:C:O2'	34:A:849:A:N6	2.47	0.41
34:A:819:G:O2'	34:A:841:G:N2	2.39	0.41
34:A:1002:C:H2'	34:A:1003:A:H5''	2.03	0.41
34:A:1314:C:H2'	34:A:1315:C:H6	1.84	0.41
3:4:434:HIS:CE1	3:4:439:VAL:HG11	2.55	0.41
8:F:106:PHE:HA	8:F:109:ARG:HG2	2.02	0.41
9:G:90:ILE:HB	9:G:130:THR:HA	2.02	0.41
11:I:49:TYR:HE1	11:I:78:ALA:HB1	1.85	0.41
12:J:34:GLY:C	12:J:66:ARG:HH21	2.24	0.41
34:A:48:G:H1'	34:A:115:A:N6	2.36	0.41
34:A:630:U:H2'	34:A:631:C:C6	2.55	0.41
34:A:2350:G:H4'	34:A:2351:A:OP1	2.20	0.41
34:A:2537:C:H2'	34:A:2538:A:C8	2.56	0.41
34:A:3013:C:H5'	34:A:3014:A:H5'	2.02	0.41
6:D:43:GLU:OE2	6:D:43:GLU:N	2.31	0.41
7:E:182:GLN:HB3	34:A:708:G:H22	1.86	0.41
9:G:19:ILE:HA	9:G:19:ILE:HD13	1.71	0.41
17:O:82:GLU:HG3	17:O:83:ILE:HG13	2.02	0.41
19:Q:4:LEU:HD23	19:Q:6:PHE:HE1	1.84	0.41
19:Q:26:ASN:HB2	19:Q:84:ASP:OD1	2.20	0.41
22:T:16:TYR:H	22:T:109:HIS:CE1	2.39	0.41
34:A:337:U:H2'	34:A:344:G:C6	2.56	0.41
34:A:490:A:C2'	34:A:491:U:H5'	2.51	0.41
34:A:862:U:OP2	34:A:2835:U:O2'	2.37	0.41
34:A:1007:G:C6	34:A:1008:G:C6	3.09	0.41
34:A:1177:G:N1	34:A:1198:C:N3	2.68	0.41
34:A:1226:U:C4	34:A:1227:C:C4	3.09	0.41
34:A:2523:A:H2'	34:A:2524:C:C6	2.55	0.41
34:A:2603:G:H2'	34:A:2604:U:C6	2.56	0.41
34:A:2755:A:C6	34:A:2756:G:C5	3.09	0.41
34:A:3026:G:H2'	34:A:3027:G:O4'	2.21	0.41
1:2:32:ARG:NH1	34:A:1116:C:O2	2.46	0.41
4:B:64:G:H2'	4:B:65:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:23:LEU:HA	8:F:23:LEU:HD12	1.76	0.41
8:F:113:ILE:HG22	8:F:146:HIS:CE1	2.55	0.41
8:F:170:ASP:O	8:F:174:ARG:HB2	2.20	0.41
11:I:39:LEU:HD21	11:I:96:PHE:CG	2.56	0.41
11:I:83:LYS:HB2	11:I:83:LYS:HE3	1.89	0.41
13:K:55:ILE:HA	13:K:123:LYS:O	2.20	0.41
19:Q:2:ASN:HB3	19:Q:5:ASP:OD2	2.20	0.41
23:U:8:ARG:HG2	28:Z:30:PHE:HB2	2.03	0.41
24:V:58:GLY:N	34:A:571:A:N3	2.60	0.41
27:Y:36:VAL:HG11	27:Y:61:VAL:HG11	2.02	0.41
34:A:139:U:H2'	34:A:140:G:O4'	2.21	0.41
34:A:494:G:H2'	34:A:495:C:O4'	2.21	0.41
34:A:940:A:H2'	34:A:941:U:O4'	2.21	0.41
34:A:1105:C:O2'	34:A:1118:A:N3	2.44	0.41
34:A:1139:A:H2'	34:A:1141:U:H5'	2.02	0.41
34:A:1314:C:H2'	34:A:1315:C:C6	2.56	0.41
34:A:1752:C:H2'	34:A:1753:C:O4'	2.21	0.41
34:A:2329:G:H1	34:A:2406:U:H3	1.69	0.41
34:A:2346:G:C2	34:A:2399:A:N7	2.89	0.41
34:A:2469:U:O2'	34:A:2660:G:OP2	2.25	0.41
34:A:2481:U:O2'	34:A:2482:U:H5'	2.21	0.41
3:4:432:ARG:NH2	3:4:459:LEU:HG	2.36	0.41
5:C:182:ILE:HD13	5:C:270:ARG:NH1	2.36	0.41
6:D:174:ARG:NH1	34:A:2997:C:OP1	2.54	0.41
16:N:29:PHE:HZ	34:A:1020:A:H2	1.69	0.41
16:N:45:ARG:H	16:N:45:ARG:HG3	1.64	0.41
16:N:58:ILE:O	16:N:59:LYS:HG2	2.21	0.41
23:U:15:VAL:HB	23:U:30:THR:HG23	2.03	0.41
26:X:8:SER:O	34:A:2479:G:N2	2.41	0.41
34:A:1003:A:OP1	34:A:1003:A:H2'	2.20	0.41
34:A:1195:A:N1	34:A:1206:A:H2'	2.36	0.41
34:A:1295:U:H2'	34:A:1296:G:C8	2.54	0.41
34:A:1337:G:N2	34:A:1340:A:OP2	2.47	0.41
34:A:1417:A:H5'	34:A:1826:A:OP2	2.21	0.41
34:A:1443:G:H2'	34:A:1445:C:C5	2.55	0.41
34:A:1649:C:C5	34:A:1789:A:H5''	2.56	0.41
34:A:1755:A:C2	34:A:1759:A:H1'	2.56	0.41
34:A:1806:A:H2'	34:A:1807:C:C6	2.56	0.41
34:A:1934:G:H2'	34:A:1935:C:C6	2.55	0.41
34:A:2133:G:C8	34:A:2134:G:C8	3.09	0.41
34:A:2335:G:N1	34:A:2390:U:O3'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:2408:G:H2'	34:A:2409:U:O4'	2.21	0.41
34:A:2885:G:H2'	34:A:2886:A:C8	2.55	0.41
3:4:193:GLY:HA2	3:4:207:LYS:HE2	2.01	0.40
3:4:424:TYR:CE2	3:4:447:ALA:HA	2.56	0.40
9:G:164:ARG:HE	9:G:164:ARG:HB2	1.62	0.40
10:H:80:LEU:HD21	10:H:95:VAL:HG13	2.03	0.40
11:I:41:ARG:NH2	34:A:1200:U:H4'	2.35	0.40
12:J:19:GLN:NE2	12:J:52:ARG:NH1	2.69	0.40
13:K:45:THR:HG23	13:K:48:VAL:HB	2.03	0.40
19:Q:110:LYS:CD	19:Q:113:ARG:HH22	2.33	0.40
34:A:6:G:N2	34:A:7:U:O4	2.54	0.40
34:A:155:G:H2'	34:A:156:C:H6	1.84	0.40
34:A:155:G:H2'	34:A:156:C:C6	2.55	0.40
34:A:220:A:H2	34:A:266:U:H4'	1.87	0.40
34:A:1406:U:H2'	34:A:1407:G:H8	1.86	0.40
34:A:2031:G:OP2	34:A:2032:A:O2'	2.30	0.40
34:A:2125:A:N3	34:A:2125:A:C2'	2.83	0.40
34:A:2248:C:H2'	34:A:2249:G:H8	1.85	0.40
34:A:2358:A:C2	34:A:2359:G:H1'	2.56	0.40
34:A:2522:A:H2'	34:A:2523:A:O4'	2.21	0.40
34:A:2543:U:H1'	34:A:2544:U:C5	2.55	0.40
7:E:182:GLN:HB3	34:A:708:G:N2	2.36	0.40
9:G:17:VAL:HB	9:G:45:ARG:CZ	2.51	0.40
10:H:25:TYR:CD1	34:A:2317:G:H5'	2.56	0.40
12:J:40:PHE:CE1	12:J:60:ILE:HD13	2.57	0.40
12:J:101:LYS:HE2	12:J:140:THR:OG1	2.21	0.40
24:V:37:GLY:HA2	24:V:40:ARG:HH22	1.86	0.40
28:Z:21:LYS:HE2	28:Z:21:LYS:HB2	1.77	0.40
28:Z:54:ILE:HA	28:Z:54:ILE:HD13	1.80	0.40
34:A:183:G:H2'	34:A:184:C:C6	2.56	0.40
34:A:468:G:O2'	34:A:469:G:H5'	2.22	0.40
34:A:489:A:H2'	34:A:490:A:H8	1.86	0.40
34:A:545:A:N1	34:A:558:A:H5''	2.36	0.40
34:A:1073:G:O6	34:A:1075:U:O2'	2.38	0.40
34:A:1109:U:H3	34:A:1282:G:H1	1.69	0.40
34:A:1194:C:H2'	34:A:1195:A:O4'	2.21	0.40
34:A:1205:G:C6	34:A:1207:G:C2	3.09	0.40
34:A:1227:C:H2'	34:A:1228:A:C4	2.56	0.40
35:4:501:GCP:O2B	35:4:501:GCP:O3G	2.39	0.40
10:H:109:GLY:N	10:H:110:PRO:HD2	2.37	0.40
11:I:94:LYS:HZ2	11:I:121:GLU:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:29:SER:HB2	34:A:2899:A:H4'	2.03	0.40
17:O:63:ARG:HA	17:O:80:PHE:CZ	2.57	0.40
23:U:10:ILE:H	23:U:10:ILE:HD12	1.86	0.40
34:A:222:A:O2'	34:A:508:G:N3	2.50	0.40
34:A:229:U:H3'	34:A:230:G:C5'	2.51	0.40
34:A:503:A:H2'	34:A:504:C:H6	1.85	0.40
34:A:722:G:H2'	34:A:723:C:C6	2.56	0.40
34:A:931:C:H2'	34:A:932:C:C6	2.57	0.40
34:A:1117:U:O2	34:A:1118:A:C8	2.74	0.40
34:A:1127:A:N3	34:A:1272:C:O2'	2.51	0.40
34:A:2053:C:OP2	34:A:2134:G:N2	2.54	0.40
34:A:2054:C:C6	34:A:2133:G:O6	2.75	0.40
34:A:2054:C:H5''	34:A:2133:G:C6	2.56	0.40
34:A:2059:G:H2'	34:A:2060:C:C6	2.55	0.40
34:A:2359:G:H3'	34:A:2360:C:H5''	2.02	0.40
34:A:2414:G:H2'	34:A:2415:G:C8	2.55	0.40
34:A:3055:G:H1'	34:A:3104:A:N6	2.36	0.40
7:E:126:ALA:HA	7:E:196:PHE:O	2.22	0.40
9:G:138:ASP:O	9:G:142:VAL:HG23	2.21	0.40
14:L:87:ILE:HA	14:L:93:PRO:HA	2.04	0.40
16:N:15:PRO:O	16:N:41:TYR:OH	2.32	0.40
34:A:565:A:H2'	34:A:566:A:C8	2.55	0.40
34:A:1010:U:H2'	34:A:1012:C:C6	2.56	0.40
34:A:1405:U:H2'	34:A:1406:U:H6	1.86	0.40
34:A:2307:C:H2'	34:A:2308:U:O4'	2.21	0.40
34:A:3040:G:H2'	34:A:3042:A:N7	2.36	0.40
34:A:3116:C:H2'	34:A:3117:U:H6	1.87	0.40
4:B:32:C:C2'	4:B:54:A:H61	2.34	0.40
5:C:100:GLY:O	34:A:1720:G:O2'	2.35	0.40
17:O:10:LEU:HB3	17:O:17:GLN:HG3	2.04	0.40
19:Q:1:MET:N	34:A:3064:G:N3	2.69	0.40
21:S:12:LYS:HE3	34:A:1112:C:O2	2.22	0.40
21:S:14:TYR:CE2	21:S:24:VAL:HG23	2.56	0.40
21:S:21:VAL:HG12	21:S:98:LYS:HB2	2.04	0.40
26:X:18:ALA:HB1	34:A:2495:G:OP1	2.21	0.40
34:A:94:G:H2'	34:A:95:C:C6	2.57	0.40
34:A:248:G:N3	34:A:2655:U:H4'	2.36	0.40
34:A:609:G:H2'	34:A:610:C:C6	2.57	0.40
34:A:694:C:H2'	34:A:695:G:O4'	2.22	0.40
34:A:819:G:H1'	34:A:842:A:N6	2.35	0.40
34:A:1162:G:H1'	34:A:1166:A:H1'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:A:1369:A:H5''	34:A:1370:U:H5''	2.04	0.40
34:A:1804:G:H2'	34:A:1805:G:C8	2.56	0.40
34:A:2466:G:H2'	34:A:2467:U:O4'	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
2	3	21/24 (88%)	21 (100%)	0	0	100	100
3	4	464/470 (99%)	396 (85%)	67 (14%)	1 (0%)	44	67
5	C	273/278 (98%)	256 (94%)	17 (6%)	0	100	100
6	D	212/217 (98%)	197 (93%)	15 (7%)	0	100	100
7	E	207/215 (96%)	192 (93%)	15 (7%)	0	100	100
8	F	180/187 (96%)	162 (90%)	18 (10%)	0	100	100
9	G	174/179 (97%)	153 (88%)	21 (12%)	0	100	100
10	H	149/151 (99%)	117 (78%)	32 (22%)	0	100	100
11	I	124/175 (71%)	103 (83%)	21 (17%)	0	100	100
12	J	130/142 (92%)	113 (87%)	16 (12%)	1 (1%)	16	39
13	K	144/147 (98%)	133 (92%)	11 (8%)	0	100	100
14	L	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
15	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
16	N	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
17	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
18	P	124/127 (98%)	112 (90%)	12 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	Q	111/113 (98%)	97 (87%)	14 (13%)	0	100	100
20	R	122/129 (95%)	119 (98%)	3 (2%)	0	100	100
21	S	98/103 (95%)	90 (92%)	8 (8%)	0	100	100
22	T	112/153 (73%)	101 (90%)	11 (10%)	0	100	100
23	U	95/100 (95%)	88 (93%)	7 (7%)	0	100	100
24	V	93/105 (89%)	80 (86%)	13 (14%)	0	100	100
25	W	93/215 (43%)	85 (91%)	8 (9%)	0	100	100
26	X	77/88 (88%)	75 (97%)	2 (3%)	0	100	100
27	Y	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
28	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
29	b	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
30	c	47/55 (86%)	45 (96%)	2 (4%)	0	100	100
31	d	44/47 (94%)	39 (89%)	5 (11%)	0	100	100
32	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
33	f	35/37 (95%)	35 (100%)	0	0	100	100
All	All	3935/4386 (90%)	3566 (91%)	367 (9%)	2 (0%)	50	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	J	75	PRO
3	4	22	SER

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	52/54 (96%)	51 (98%)	1 (2%)	52	73
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	367/372 (99%)	351 (96%)	16 (4%)	24	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	C	215/218 (99%)	211 (98%)	4 (2%)	52	73
6	D	160/163 (98%)	156 (98%)	4 (2%)	42	66
7	E	169/173 (98%)	162 (96%)	7 (4%)	26	51
8	F	151/156 (97%)	144 (95%)	7 (5%)	23	47
9	G	148/150 (99%)	141 (95%)	7 (5%)	22	46
10	H	90/116 (78%)	86 (96%)	4 (4%)	24	49
11	I	89/120 (74%)	86 (97%)	3 (3%)	32	57
12	J	93/108 (86%)	89 (96%)	4 (4%)	25	49
13	K	119/120 (99%)	116 (98%)	3 (2%)	42	66
14	L	100/100 (100%)	97 (97%)	3 (3%)	36	60
15	M	112/114 (98%)	109 (97%)	3 (3%)	40	64
16	N	114/116 (98%)	113 (99%)	1 (1%)	75	86
17	O	97/158 (61%)	95 (98%)	2 (2%)	48	70
18	P	93/94 (99%)	90 (97%)	3 (3%)	34	59
19	Q	100/100 (100%)	95 (95%)	5 (5%)	20	44
20	R	97/99 (98%)	96 (99%)	1 (1%)	73	85
21	S	81/83 (98%)	77 (95%)	4 (5%)	21	45
22	T	90/117 (77%)	89 (99%)	1 (1%)	70	83
23	U	83/85 (98%)	83 (100%)	0	100	100
24	V	81/86 (94%)	76 (94%)	5 (6%)	15	36
25	W	77/168 (46%)	76 (99%)	1 (1%)	65	80
26	X	58/63 (92%)	58 (100%)	0	100	100
27	Y	50/51 (98%)	49 (98%)	1 (2%)	50	72
28	Z	58/66 (88%)	56 (97%)	2 (3%)	32	57
29	b	43/46 (94%)	43 (100%)	0	100	100
30	c	47/52 (90%)	47 (100%)	0	100	100
31	d	35/36 (97%)	33 (94%)	2 (6%)	17	39
32	e	53/54 (98%)	51 (96%)	2 (4%)	28	53
33	f	35/35 (100%)	35 (100%)	0	100	100
All	All	3175/3492 (91%)	3079 (97%)	96 (3%)	37	60

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	39	ASP
3	4	40	GLU
3	4	102	LYS
3	4	181	GLU
3	4	186	GLN
3	4	213	ARG
3	4	239	SER
3	4	253	TYR
3	4	290	GLU
3	4	324	ASP
3	4	330	HIS
3	4	344	ASN
3	4	351	ASN
3	4	402	LYS
3	4	450	ARG
3	4	454	ARG
3	4	469	PHE
5	C	26	ARG
5	C	244	ARG
5	C	248	SER
5	C	265	ASP
6	D	3	ARG
6	D	34	ASN
6	D	78	ARG
6	D	113	ASP
7	E	15	ASP
7	E	121	ASN
7	E	129	GLU
7	E	151	ASN
7	E	163	GLU
7	E	186	TYR
7	E	192	ASP
8	F	15	TYR
8	F	27	PHE
8	F	44	ASN
8	F	62	ASN
8	F	105	GLU
8	F	135	TYR
8	F	182	PHE
9	G	18	THR
9	G	20	ASN
9	G	68	LEU
9	G	82	GLU

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Mol	Chain	Res	Type
9	G	86	GLN
9	G	112	HIS
9	G	151	ARG
10	H	3	LEU
10	H	23	ASP
10	H	99	ASP
10	H	151	GLN
11	I	49	TYR
11	I	70	ASP
11	I	96	PHE
12	J	12	LYS
12	J	13	LEU
12	J	63	TYR
12	J	79	LYS
13	K	4	TYR
13	K	99	ARG
13	K	129	ASP
14	L	21	CYS
14	L	37	ASP
14	L	56	ASP
15	M	72	ARG
15	M	123	ASP
15	M	128	LYS
16	N	71	ASP
17	O	16	HIS
17	O	78	THR
18	P	43	SER
18	P	76	ASP
18	P	86	GLN
19	Q	6	PHE
19	Q	8	ASP
19	Q	11	SER
19	Q	20	SER
19	Q	108	LYS
20	R	36	LYS
21	S	20	ASP
21	S	44	ASP
21	S	50	SER
21	S	98	LYS
22	T	66	GLN
24	V	1	MET
24	V	16	ASP

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Mol	Chain	Res	Type
24	V	27	TYR
24	V	88	ASP
24	V	94	LYS
25	W	102	ARG
27	Y	62	SER
28	Z	42	SER
28	Z	47	LEU
31	d	23	LEU
31	d	39	SER
32	e	31	HIS
32	e	63	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
3	4	444	HIS
6	D	21	ASN
8	F	31	ASN
8	F	44	ASN
8	F	142	GLN
11	I	100	ASN
15	M	89	GLN
19	Q	79	ASN
30	c	44	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	A	2946/3120 (94%)	662 (22%)	23 (0%)
4	B	117/118 (99%)	29 (24%)	0
All	All	3063/3238 (94%)	691 (22%)	23 (0%)

All (691) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	B	4	A
4	B	5	C
4	B	6	G
4	B	8	C
4	B	9	G

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Mol	Chain	Res	Type
4	B	10	G
4	B	12	C
4	B	13	C
4	B	20	G
4	B	23	G
4	B	26	A
4	B	30	G
4	B	35	G
4	B	36	U
4	B	38	C
4	B	42	C
4	B	43	C
4	B	54	A
4	B	57	U
4	B	58	A
4	B	67	A
4	B	88	C
4	B	89	C
4	B	103	G
4	B	105	A
4	B	106	C
4	B	107	A
4	B	109	C
4	B	116	C
34	A	3	A
34	A	7	U
34	A	9	U
34	A	10	A
34	A	12	G
34	A	20	G
34	A	23	G
34	A	31	U
34	A	41	A
34	A	42	G
34	A	48	G
34	A	60	A
34	A	66	C
34	A	68	A
34	A	69	U
34	A	71	A
34	A	72	G
34	A	91	C

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Mol	Chain	Res	Type
34	A	94	G
34	A	96	G
34	A	97	U
34	A	98	U
34	A	99	G
34	A	115	A
34	A	116	A
34	A	117	U
34	A	122	A
34	A	125	C
34	A	128	G
34	A	143	G
34	A	144	U
34	A	145	G
34	A	151	A
34	A	162	A
34	A	164	A
34	A	174	G
34	A	175	G
34	A	180	A
34	A	195	A
34	A	198	A
34	A	212	A
34	A	214	G
34	A	215	A
34	A	218	A
34	A	221	A
34	A	227	A
34	A	229	U
34	A	230	G
34	A	233	A
34	A	246	U
34	A	248	G
34	A	263	G
34	A	264	G
34	A	265	A
34	A	268	G
34	A	274	C
34	A	275	C
34	A	276	G
34	A	278	A
34	A	283	U

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Mol	Chain	Res	Type
34	A	285	U
34	A	286	G
34	A	287	A
34	A	288	U
34	A	289	A
34	A	290	C
34	A	291	C
34	A	292	G
34	A	301	U
34	A	302	U
34	A	303	G
34	A	304	U
34	A	307	G
34	A	315	U
34	A	316	U
34	A	318	U
34	A	319	G
34	A	324	C
34	A	325	U
34	A	326	A
34	A	327	U
34	A	330	U
34	A	331	U
34	A	334	G
34	A	335	G
34	A	336	C
34	A	337	U
34	A	338	C
34	A	340	A
34	A	342	C
34	A	343	U
34	A	349	G
34	A	350	A
34	A	351	G
34	A	353	G
34	A	356	G
34	A	357	U
34	A	363	A
34	A	364	A
34	A	366	G
34	A	367	U
34	A	370	U

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Mol	Chain	Res	Type
34	A	371	G
34	A	384	G
34	A	385	G
34	A	386	C
34	A	387	U
34	A	392	A
34	A	393	U
34	A	411	G
34	A	412	A
34	A	413	G
34	A	434	G
34	A	439	C
34	A	445	U
34	A	446	G
34	A	450	G
34	A	451	U
34	A	452	G
34	A	453	U
34	A	454	U
34	A	455	C
34	A	460	G
34	A	469	G
34	A	474	G
34	A	482	U
34	A	484	C
34	A	489	A
34	A	490	A
34	A	491	U
34	A	494	G
34	A	500	A
34	A	505	C
34	A	512	G
34	A	516	G
34	A	517	A
34	A	519	U
34	A	524	C
34	A	527	A
34	A	528	G
34	A	531	A
34	A	543	U
34	A	545	A
34	A	555	G

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Mol	Chain	Res	Type
34	A	569	G
34	A	578	G
34	A	591	G
34	A	592	A
34	A	594	U
34	A	595	A
34	A	596	C
34	A	597	C
34	A	600	A
34	A	605	G
34	A	614	C
34	A	617	U
34	A	618	C
34	A	619	C
34	A	620	G
34	A	635	G
34	A	636	U
34	A	637	G
34	A	638	U
34	A	642	G
34	A	655	G
34	A	658	U
34	A	665	G
34	A	667	A
34	A	679	G
34	A	684	G
34	A	691	U
34	A	692	C
34	A	696	A
34	A	697	G
34	A	704	C
34	A	706	G
34	A	707	G
34	A	709	U
34	A	721	A
34	A	724	G
34	A	725	A
34	A	731	A
34	A	737	A
34	A	739	U
34	A	741	G
34	A	743	G

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Mol	Chain	Res	Type
34	A	747	A
34	A	755	A
34	A	756	A
34	A	758	A
34	A	759	G
34	A	760	U
34	A	761	G
34	A	762	U
34	A	764	U
34	A	765	G
34	A	766	G
34	A	770	A
34	A	801	U
34	A	826	G
34	A	828	G
34	A	830	A
34	A	836	G
34	A	838	G
34	A	839	U
34	A	840	G
34	A	841	G
34	A	845	C
34	A	862	U
34	A	872	G
34	A	879	A
34	A	890	G
34	A	891	G
34	A	897	A
34	A	899	G
34	A	900	G
34	A	904	A
34	A	907	A
34	A	920	G
34	A	927	C
34	A	942	U
34	A	944	A
34	A	963	U
34	A	972	A
34	A	974	G
34	A	981	U
34	A	982	A
34	A	993	G

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Mol	Chain	Res	Type
34	A	994	A
34	A	998	G
34	A	999	C
34	A	1002	C
34	A	1003	A
34	A	1004	C
34	A	1008	G
34	A	1009	U
34	A	1010	U
34	A	1012	C
34	A	1017	G
34	A	1024	A
34	A	1025	A
34	A	1029	C
34	A	1030	C
34	A	1042	A
34	A	1048	A
34	A	1049	G
34	A	1063	G
34	A	1075	U
34	A	1076	A
34	A	1078	G
34	A	1085	G
34	A	1092	G
34	A	1098	A
34	A	1101	A
34	A	1102	G
34	A	1114	G
34	A	1115	G
34	A	1117	U
34	A	1130	C
34	A	1131	G
34	A	1135	G
34	A	1140	G
34	A	1141	U
34	A	1144	A
34	A	1151	U
34	A	1152	G
34	A	1158	U
34	A	1176	G
34	A	1177	G
34	A	1184	U

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Mol	Chain	Res	Type
34	A	1187	A
34	A	1188	A
34	A	1189	G
34	A	1191	A
34	A	1196	C
34	A	1201	G
34	A	1203	A
34	A	1205	G
34	A	1206	A
34	A	1207	G
34	A	1208	U
34	A	1212	U
34	A	1213	A
34	A	1214	A
34	A	1215	U
34	A	1225	G
34	A	1228	A
34	A	1229	A
34	A	1230	G
34	A	1235	U
34	A	1237	U
34	A	1250	U
34	A	1251	A
34	A	1253	C
34	A	1254	G
34	A	1260	C
34	A	1261	A
34	A	1285	G
34	A	1292	U
34	A	1293	G
34	A	1317	G
34	A	1326	G
34	A	1335	G
34	A	1343	G
34	A	1344	A
34	A	1347	G
34	A	1351	G
34	A	1352	A
34	A	1353	G
34	A	1365	G
34	A	1368	A
34	A	1371	G

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Mol	Chain	Res	Type
34	A	1380	A
34	A	1386	G
34	A	1387	A
34	A	1399	A
34	A	1405	U
34	A	1409	C
34	A	1415	A
34	A	1416	A
34	A	1436	C
34	A	1444	U
34	A	1456	G
34	A	1465	C
34	A	1467	U
34	A	1475	G
34	A	1477	C
34	A	1480	A
34	A	1493	A
34	A	1494	U
34	A	1499	A
34	A	1501	C
34	A	1502	G
34	A	1509	U
34	A	1512	U
34	A	1528	G
34	A	1529	U
34	A	1531	C
34	A	1533	U
34	A	1534	C
34	A	1535	C
34	A	1538	G
34	A	1542	A
34	A	1543	A
34	A	1545	C
34	A	1622	G
34	A	1623	U
34	A	1624	U
34	A	1629	G
34	A	1632	G
34	A	1636	A
34	A	1640	A
34	A	1641	U
34	A	1645	G

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Mol	Chain	Res	Type
34	A	1648	A
34	A	1649	C
34	A	1673	A
34	A	1674	G
34	A	1676	G
34	A	1680	A
34	A	1681	U
34	A	1703	G
34	A	1709	U
34	A	1710	A
34	A	1711	G
34	A	1714	A
34	A	1716	A
34	A	1717	U
34	A	1727	A
34	A	1728	U
34	A	1729	A
34	A	1730	U
34	A	1731	A
34	A	1737	A
34	A	1746	G
34	A	1754	G
34	A	1755	A
34	A	1756	G
34	A	1758	G
34	A	1759	A
34	A	1760	G
34	A	1762	C
34	A	1767	U
34	A	1768	C
34	A	1769	G
34	A	1778	A
34	A	1780	G
34	A	1786	G
34	A	1788	G
34	A	1789	A
34	A	1798	U
34	A	1810	A
34	A	1825	C
34	A	1826	A
34	A	1828	A
34	A	1832	A

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Mol	Chain	Res	Type
34	A	1852	A
34	A	1853	A
34	A	1864	U
34	A	1866	C
34	A	1871	G
34	A	1872	A
34	A	1883	A
34	A	1885	G
34	A	1892	G
34	A	1904	C
34	A	1911	U
34	A	1933	G
34	A	1938	G
34	A	1946	U
34	A	1947	U
34	A	1959	G
34	A	1981	U
34	A	1985	A
34	A	1990	A
34	A	1999	U
34	A	2016	G
34	A	2017	C
34	A	2018	G
34	A	2019	A
34	A	2025	C
34	A	2033	U
34	A	2038	A
34	A	2046	A
34	A	2051	U
34	A	2052	G
34	A	2053	C
34	A	2054	C
34	A	2055	C
34	A	2056	G
34	A	2057	G
34	A	2058	U
34	A	2062	G
34	A	2063	G
34	A	2120	A
34	A	2122	U
34	A	2123	A
34	A	2124	A

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Mol	Chain	Res	Type
34	A	2125	A
34	A	2126	C
34	A	2127	G
34	A	2128	G
34	A	2129	C
34	A	2130	G
34	A	2131	G
34	A	2133	G
34	A	2134	G
34	A	2135	U
34	A	2146	A
34	A	2147	U
34	A	2149	C
34	A	2150	U
34	A	2151	A
34	A	2154	G
34	A	2156	A
34	A	2157	G
34	A	2158	C
34	A	2159	G
34	A	2160	A
34	A	2162	A
34	A	2163	U
34	A	2193	A
34	A	2194	A
34	A	2195	U
34	A	2196	G
34	A	2199	G
34	A	2215	U
34	A	2217	U
34	A	2220	C
34	A	2244	A
34	A	2245	C
34	A	2247	A
34	A	2255	A
34	A	2256	G
34	A	2257	A
34	A	2267	C
34	A	2277	G
34	A	2279	C
34	A	2280	G
34	A	2282	A

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Mol	Chain	Res	Type
34	A	2284	A
34	A	2285	G
34	A	2286	A
34	A	2310	G
34	A	2315	U
34	A	2316	G
34	A	2319	G
34	A	2320	C
34	A	2327	C
34	A	2330	U
34	A	2333	G
34	A	2336	U
34	A	2337	A
34	A	2338	G
34	A	2339	G
34	A	2340	A
34	A	2341	U
34	A	2342	A
34	A	2345	U
34	A	2346	G
34	A	2347	G
34	A	2348	G
34	A	2349	A
34	A	2351	A
34	A	2352	C
34	A	2353	U
34	A	2354	G
34	A	2355	U
34	A	2357	A
34	A	2358	A
34	A	2360	C
34	A	2361	U
34	A	2368	C
34	A	2369	C
34	A	2370	A
34	A	2371	G
34	A	2373	G
34	A	2378	U
34	A	2379	G
34	A	2380	G
34	A	2381	A
34	A	2382	G

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Mol	Chain	Res	Type
34	A	2384	C
34	A	2385	G
34	A	2386	U
34	A	2387	U
34	A	2388	G
34	A	2389	U
34	A	2390	U
34	A	2392	A
34	A	2394	A
34	A	2396	A
34	A	2399	A
34	A	2400	C
34	A	2402	C
34	A	2404	G
34	A	2405	A
34	A	2406	U
34	A	2407	C
34	A	2409	U
34	A	2411	U
34	A	2413	G
34	A	2418	U
34	A	2421	A
34	A	2427	G
34	A	2436	A
34	A	2447	G
34	A	2449	A
34	A	2462	G
34	A	2463	G
34	A	2467	U
34	A	2503	G
34	A	2507	C
34	A	2511	A
34	A	2512	A
34	A	2527	G
34	A	2528	G
34	A	2529	A
34	A	2531	G
34	A	2532	G
34	A	2533	C
34	A	2534	A
34	A	2541	U
34	A	2542	G

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Mol	Chain	Res	Type
34	A	2543	U
34	A	2547	G
34	A	2549	G
34	A	2557	A
34	A	2558	C
34	A	2559	A
34	A	2560	A
34	A	2571	C
34	A	2574	C
34	A	2585	U
34	A	2587	U
34	A	2607	G
34	A	2609	A
34	A	2615	G
34	A	2627	C
34	A	2628	U
34	A	2630	A
34	A	2649	A
34	A	2650	A
34	A	2653	G
34	A	2654	A
34	A	2656	A
34	A	2659	A
34	A	2665	C
34	A	2672	A
34	A	2693	A
34	A	2694	G
34	A	2698	C
34	A	2700	A
34	A	2715	U
34	A	2726	G
34	A	2729	G
34	A	2742	A
34	A	2744	C
34	A	2753	G
34	A	2759	G
34	A	2776	U
34	A	2777	G
34	A	2778	U
34	A	2779	U
34	A	2788	A
34	A	2790	A

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Mol	Chain	Res	Type
34	A	2791	G
34	A	2797	C
34	A	2809	U
34	A	2810	U
34	A	2826	A
34	A	2827	G
34	A	2833	U
34	A	2834	C
34	A	2837	U
34	A	2838	A
34	A	2839	U
34	A	2847	G
34	A	2848	C
34	A	2854	A
34	A	2865	G
34	A	2883	G
34	A	2913	U
34	A	2915	C
34	A	2926	A
34	A	2936	C
34	A	2950	C
34	A	2957	A
34	A	2968	G
34	A	2969	C
34	A	2972	A
34	A	2975	G
34	A	2976	C
34	A	2981	A
34	A	2985	G
34	A	2989	A
34	A	3002	A
34	A	3003	C
34	A	3014	A
34	A	3015	C
34	A	3020	U
34	A	3021	A
34	A	3022	G
34	A	3023	G
34	A	3025	G
34	A	3027	G
34	A	3029	U
34	A	3041	C

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Mol	Chain	Res	Type
34	A	3042	A
34	A	3052	A
34	A	3053	U
34	A	3055	G
34	A	3070	G
34	A	3080	A
34	A	3082	U
34	A	3088	C
34	A	3093	A
34	A	3101	C
34	A	3104	A
34	A	3112	A
34	A	3114	A
34	A	3115	A

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	A	97	U
34	A	161	U
34	A	325	U
34	A	326	A
34	A	980	C
34	A	981	U
34	A	1002	C
34	A	1151	U
34	A	1207	G
34	A	1234	U
34	A	1758	G
34	A	2053	C
34	A	2054	C
34	A	2121	G
34	A	2122	U
34	A	2123	A
34	A	2124	A
34	A	2125	A
34	A	2336	U
34	A	2350	G
34	A	2975	G
34	A	2980	U
34	A	3113	A



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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
35	GCP	4	501	-	27,34,34	1.34	3 (11%)	35,54,54	2.10	9 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	GCP	4	501	-	-	7/15/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	4	501	GCP	C5-C6	4.06	1.48	1.41
35	4	501	GCP	PG-O2G	2.82	1.61	1.55
35	4	501	GCP	PG-O3G	2.75	1.61	1.55

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	4	501	GCP	PB-O3A-PA	-5.08	115.78	132.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	4	501	GCP	C2-N3-C4	4.89	120.76	115.48
35	4	501	GCP	C2-N1-C6	4.65	122.43	115.96
35	4	501	GCP	C5-C6-N1	-4.16	117.85	123.42
35	4	501	GCP	C4'-O4'-C1'	-3.64	106.60	109.92
35	4	501	GCP	N3-C2-N1	-3.35	122.95	127.21
35	4	501	GCP	C4-C5-N7	-2.87	106.30	109.34
35	4	501	GCP	C4-C5-C6	-2.68	117.14	121.23
35	4	501	GCP	O4'-C1'-N9	2.46	112.01	108.75

There are no chirality outliers.

All (7) torsion outliers are listed below:

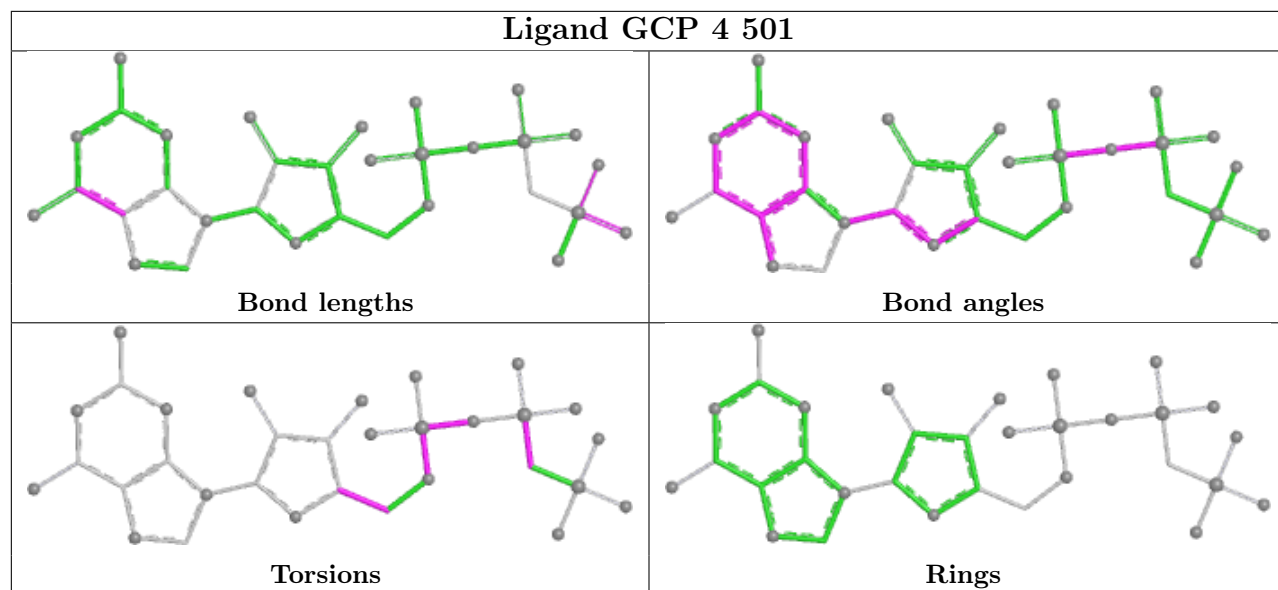
Mol	Chain	Res	Type	Atoms
35	4	501	GCP	C5'-O5'-PA-O3A
35	4	501	GCP	C5'-O5'-PA-O1A
35	4	501	GCP	C5'-O5'-PA-O2A
35	4	501	GCP	O4'-C4'-C5'-O5'
35	4	501	GCP	C3'-C4'-C5'-O5'
35	4	501	GCP	PG-C3B-PB-O1B
35	4	501	GCP	PB-O3A-PA-O1A

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	4	501	GCP	11	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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.

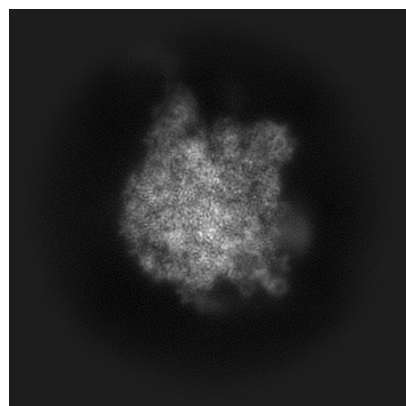
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43317. These allow visual inspection of the internal detail of the map and identification of artifacts.

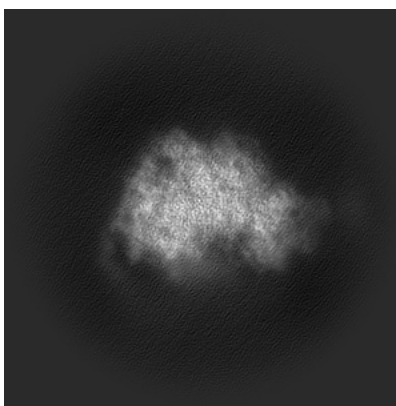
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

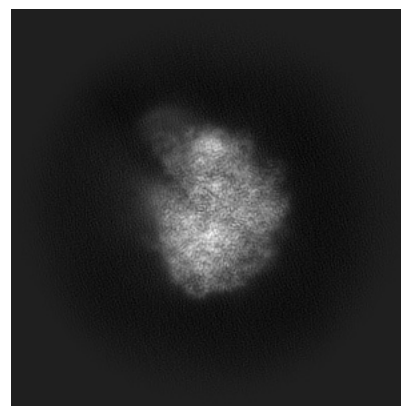
#### 6.1.1 Primary map



X

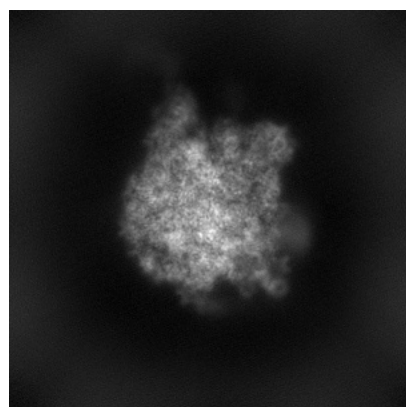


Y

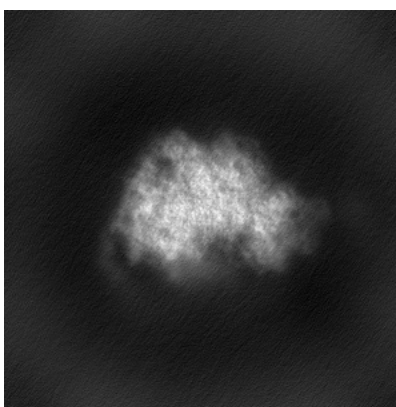


Z

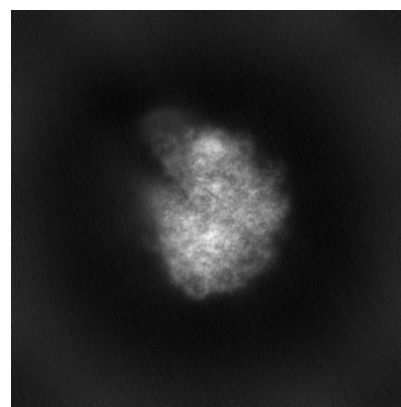
#### 6.1.2 Raw map



X



Y

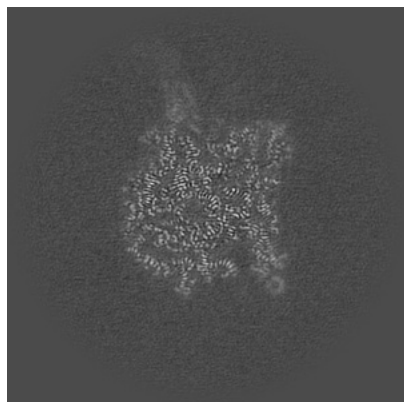


Z

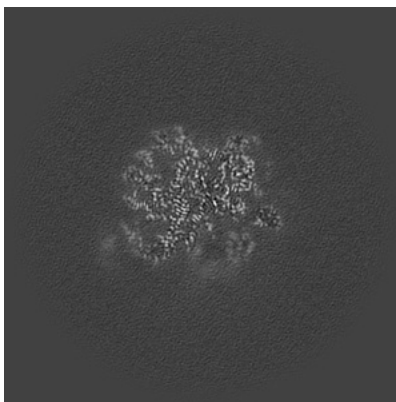
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

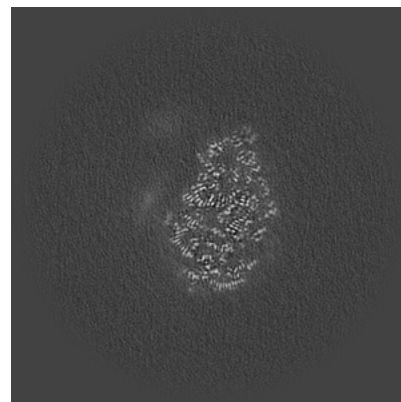
### 6.2.1 Primary map



X Index: 200

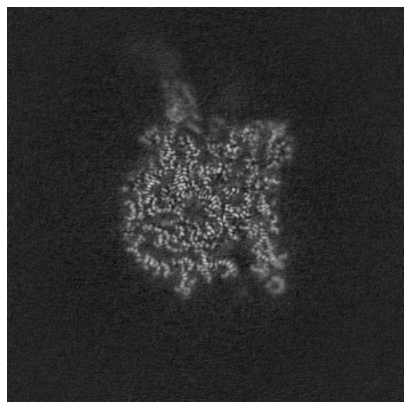


Y Index: 200

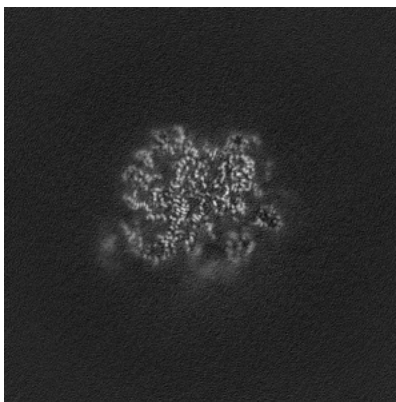


Z Index: 200

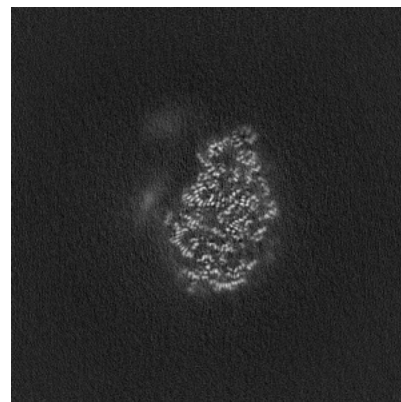
### 6.2.2 Raw map



X Index: 200



Y Index: 200

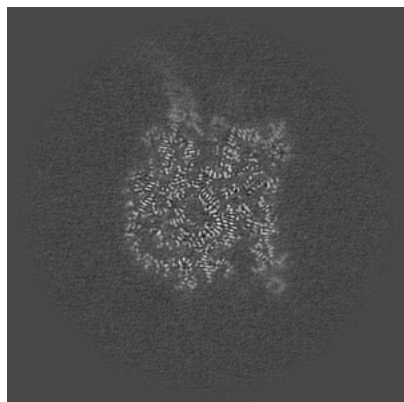


Z Index: 200

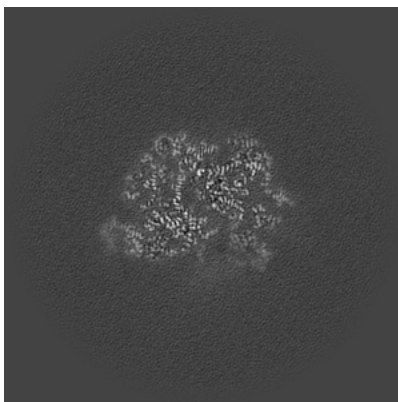
The images above show central slices of the map in three orthogonal directions.

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

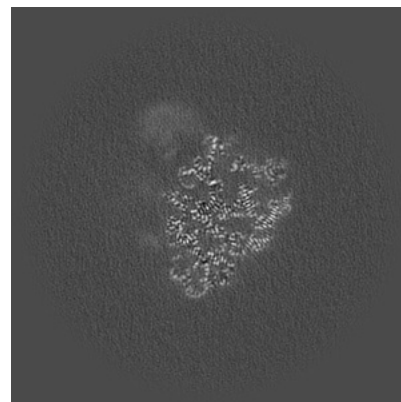
### 6.3.1 Primary map



X Index: 202

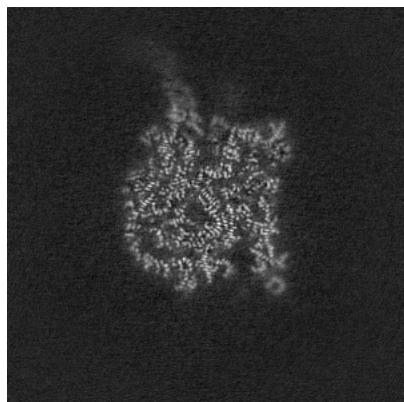


Y Index: 192

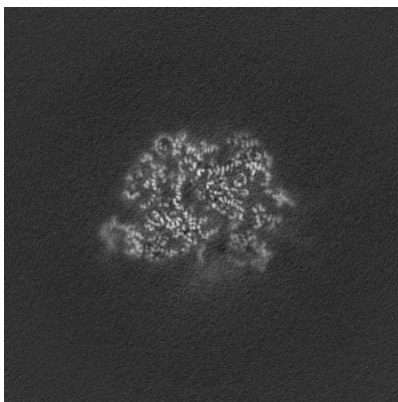


Z Index: 176

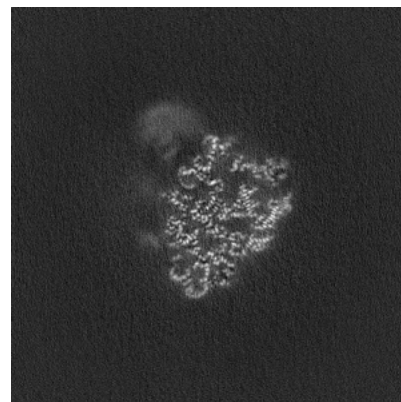
### 6.3.2 Raw map



X Index: 202



Y Index: 192



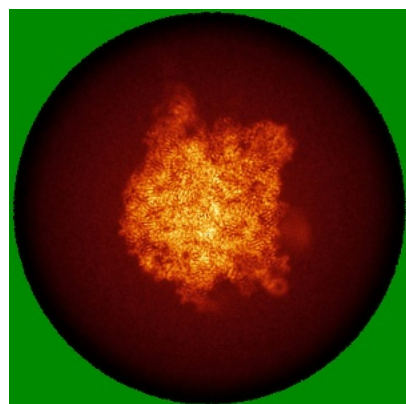
Z Index: 176

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

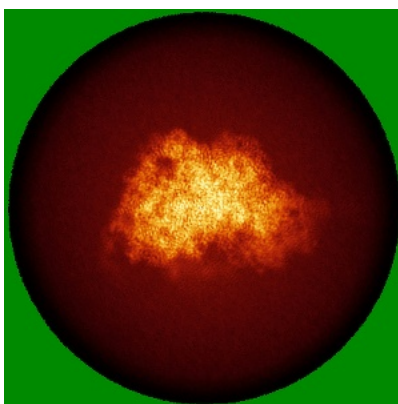


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

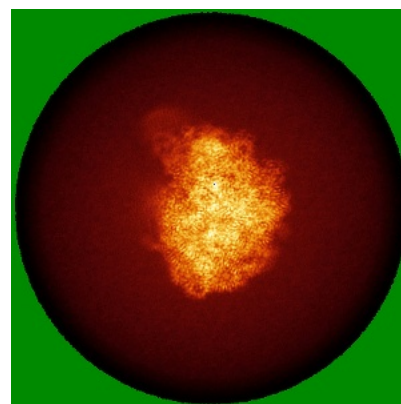
### 6.4.1 Primary map



X

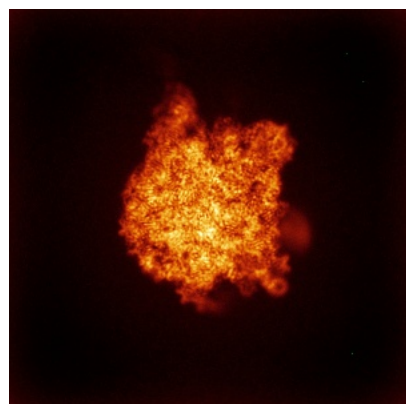


Y

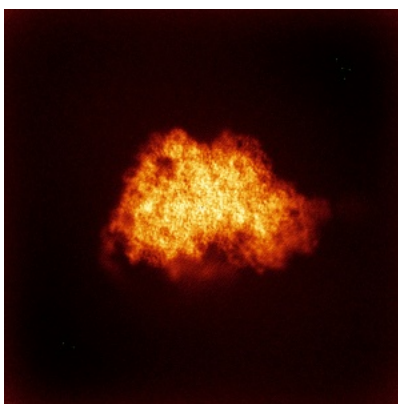


Z

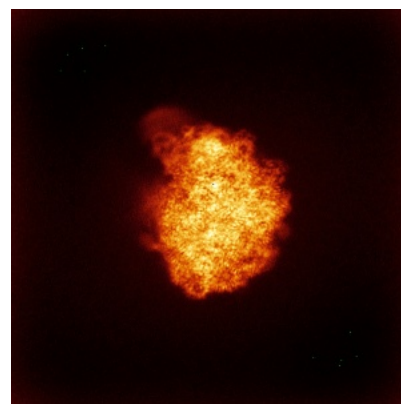
### 6.4.2 Raw map



X



Y



Z

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

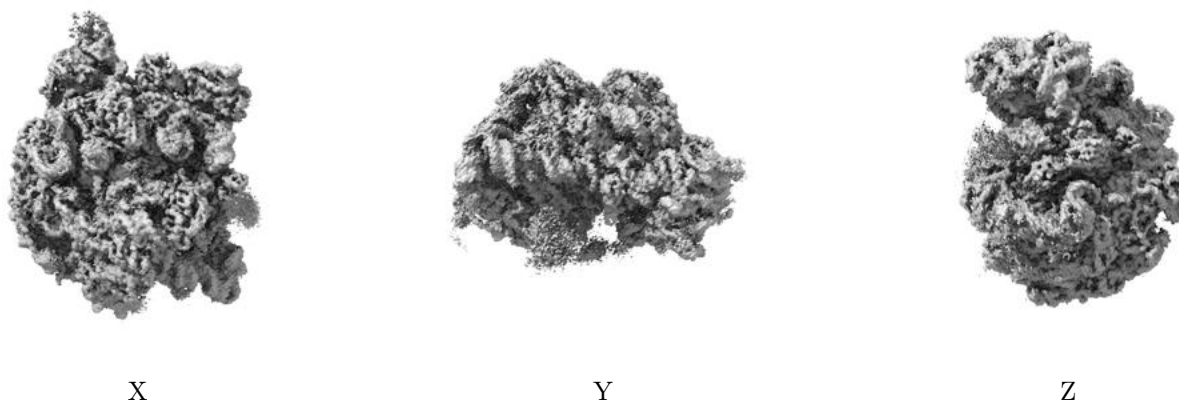
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

## 6.6 Mask visualisation [i](#)

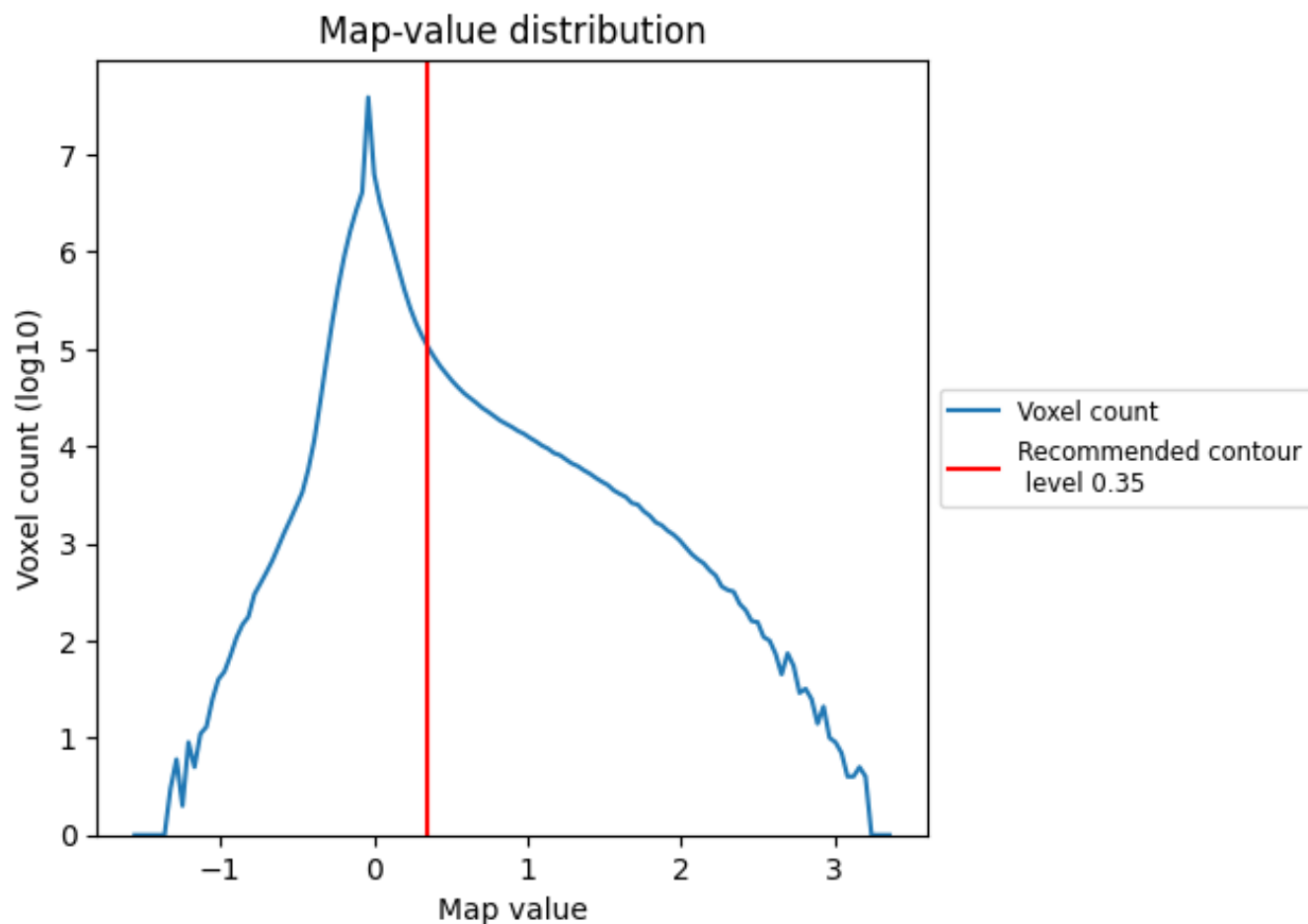
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

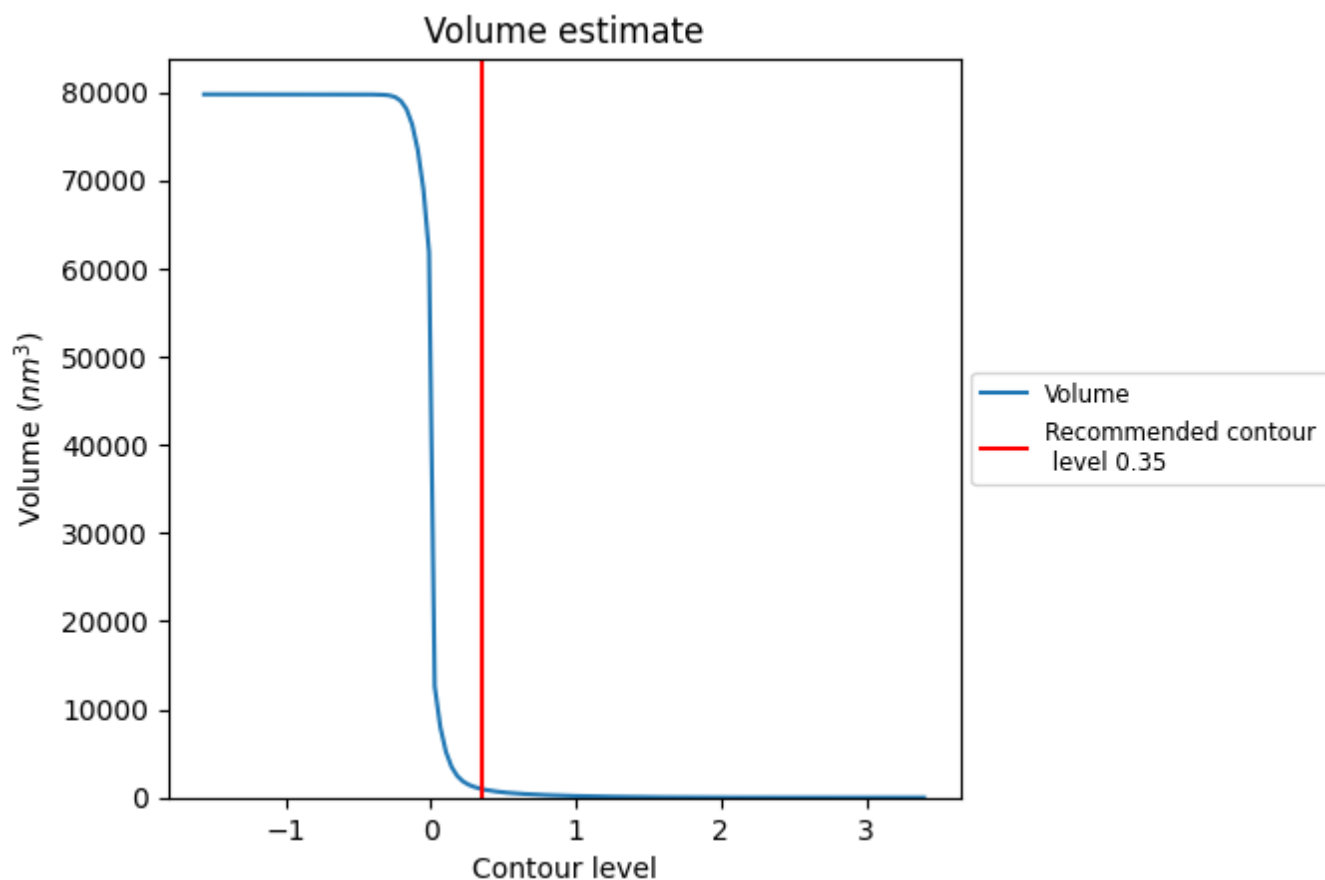
This section contains the results of statistical analysis of the map.

### 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.

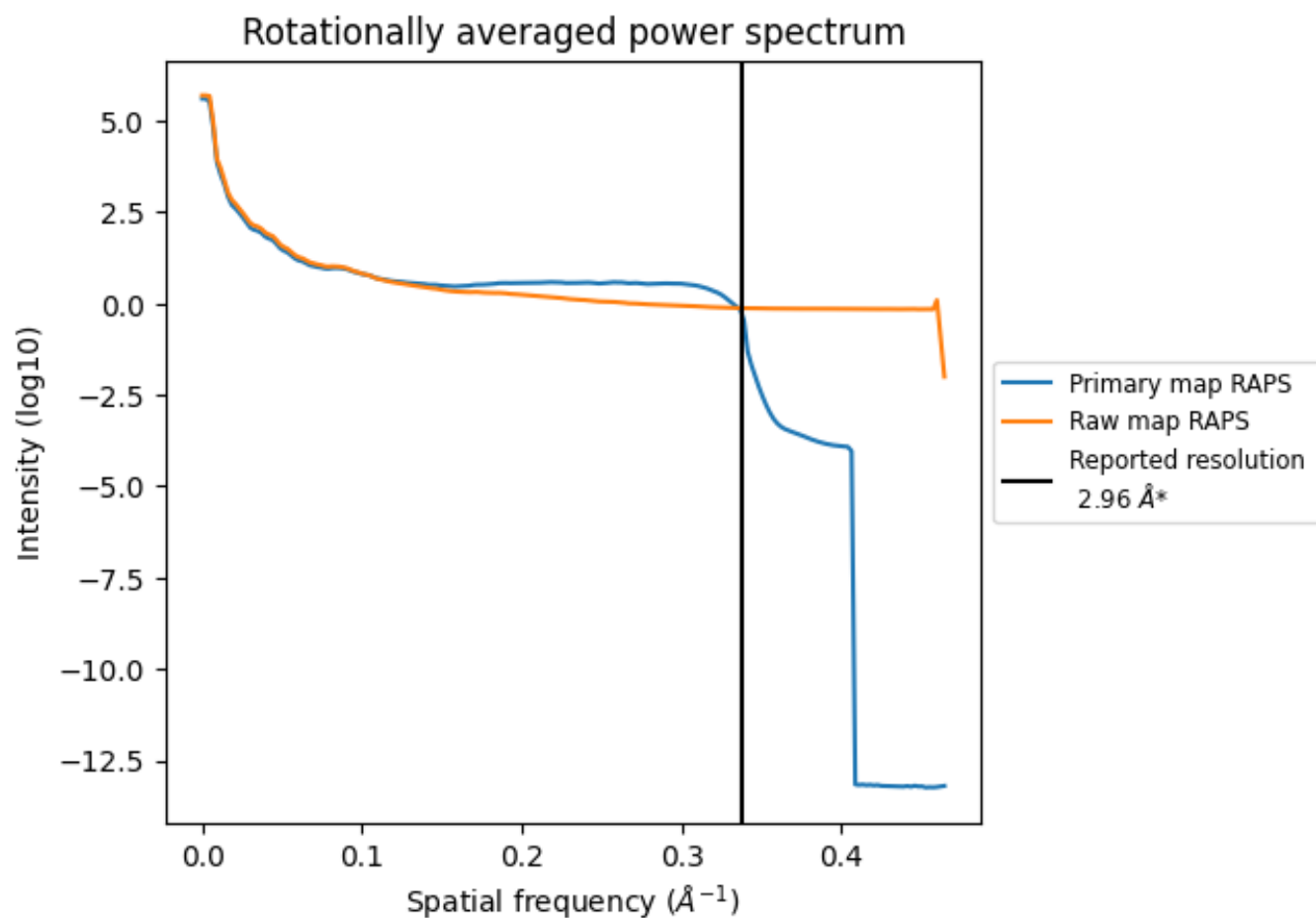
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982  $\text{nm}^3$ ; this corresponds to an approximate mass of 887 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 ⓘ

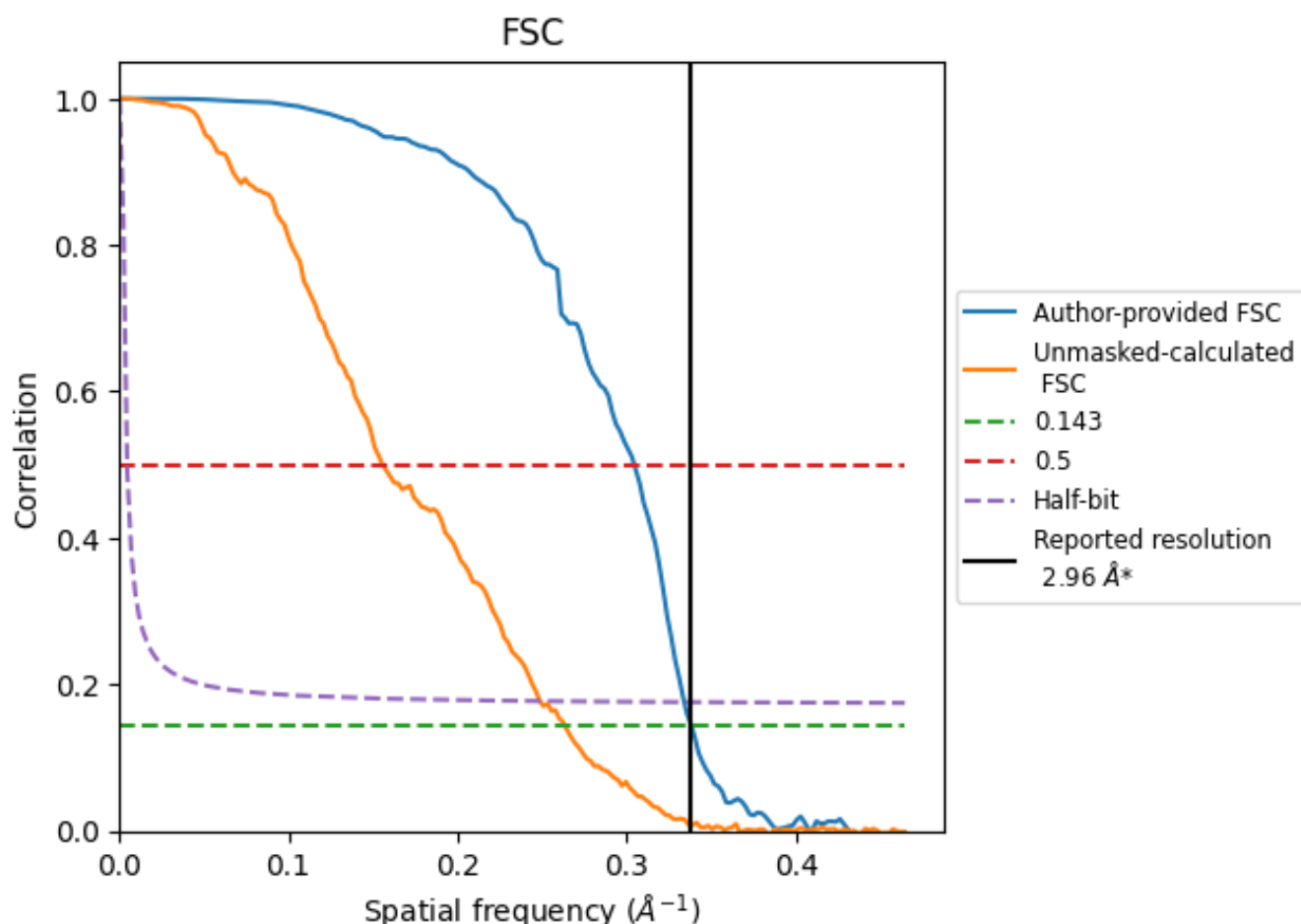


\*Reported resolution corresponds to spatial frequency of 0.338  $\text{\AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.338 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

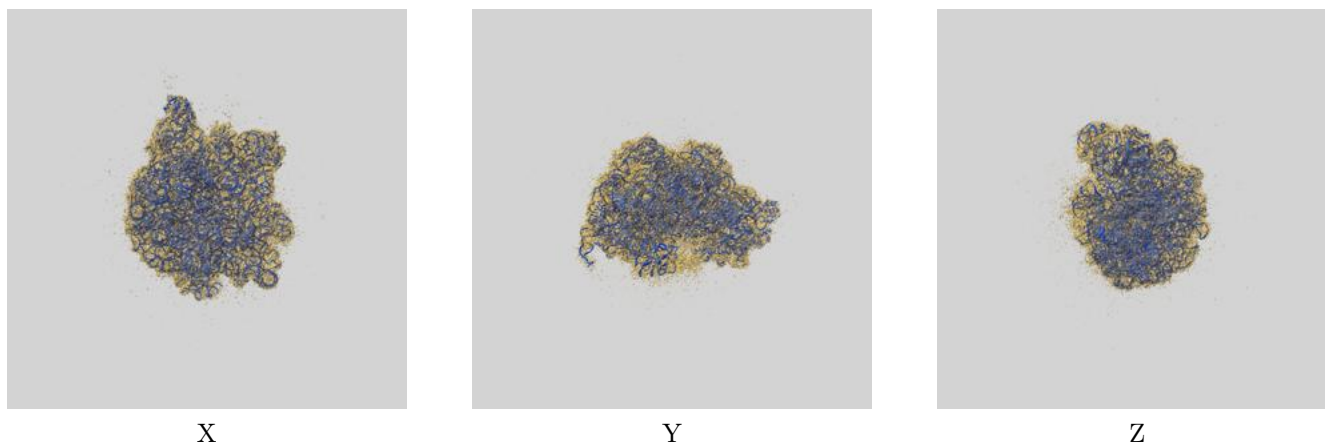
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.28	2.99
Unmasked-calculated*	3.79	6.43	4.02

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.79 differs from the reported value 2.96 by more than 10 %

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

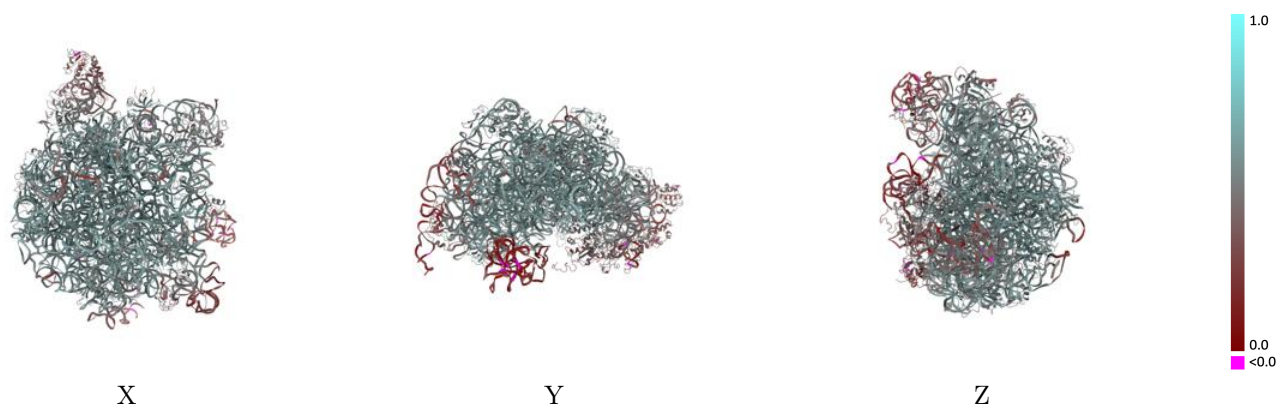
This section contains information regarding the fit between EMDB map EMD-43317 and PDB model 8VKI. Per-residue inclusion information can be found in section [3](#) on page [11](#).

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



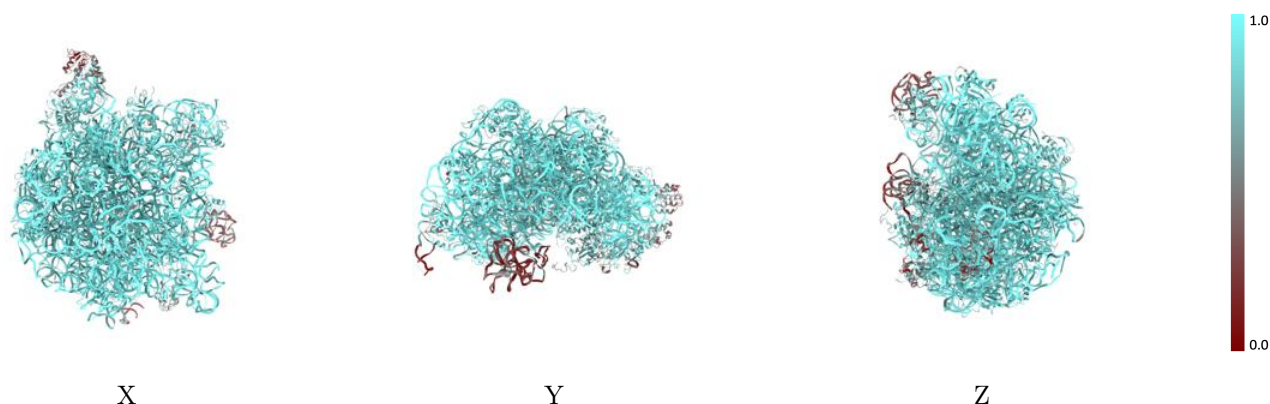
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



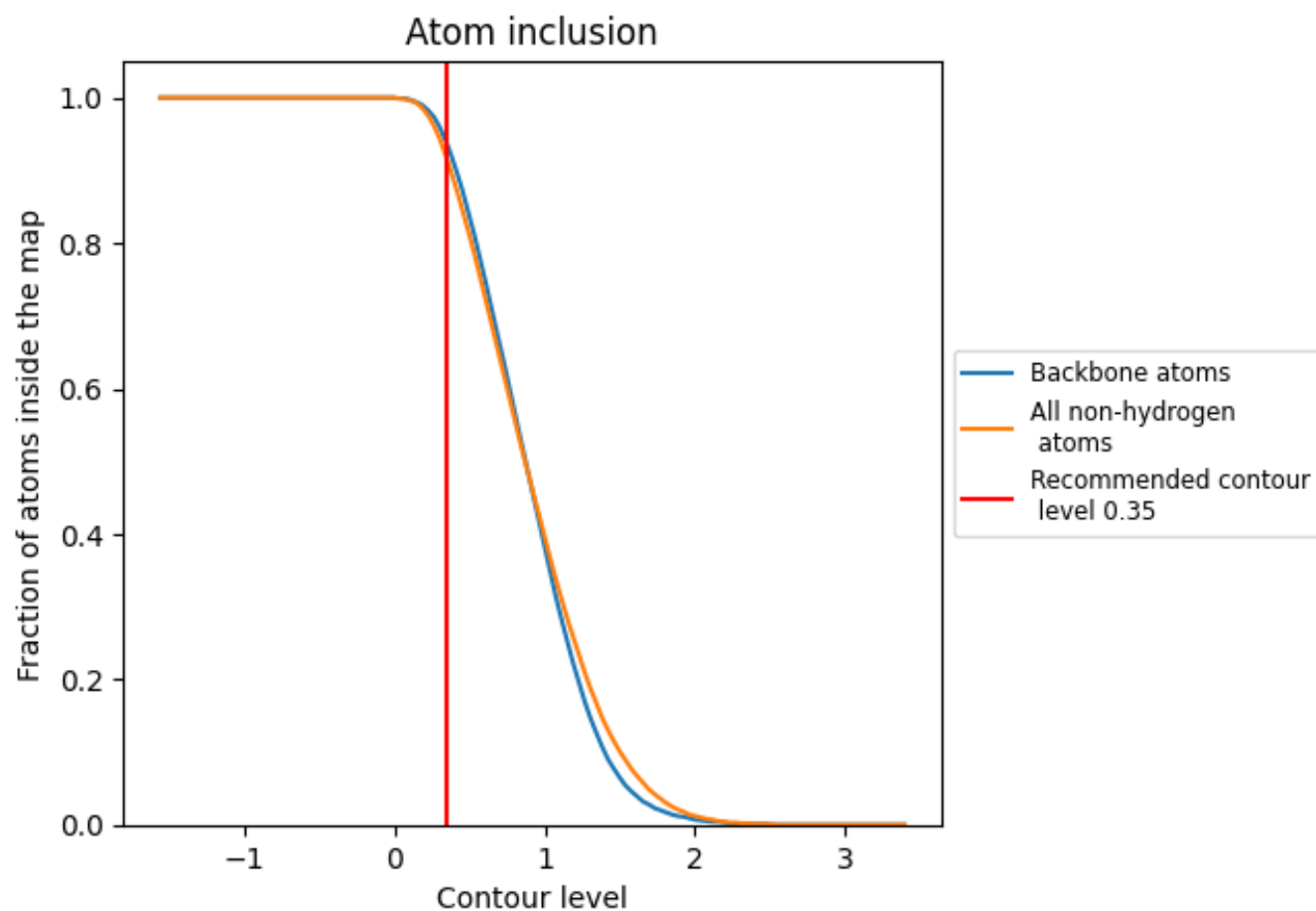
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 94% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9150	 0.5200
2	 0.9350	 0.5680
3	 0.9550	 0.6090
4	 0.7710	 0.4150
A	 0.9370	 0.5250
B	 0.9700	 0.5110
C	 0.9330	 0.5660
D	 0.9530	 0.5670
E	 0.9240	 0.5470
F	 0.7600	 0.3950
G	 0.8260	 0.4740
H	 0.7230	 0.4480
I	 0.4020	 0.3090
J	 0.4590	 0.3130
K	 0.9520	 0.5700
L	 0.9310	 0.5560
M	 0.9350	 0.5590
N	 0.9280	 0.5670
O	 0.9500	 0.5720
P	 0.9050	 0.4960
Q	 0.8870	 0.5250
R	 0.9570	 0.5700
S	 0.9100	 0.5550
T	 0.9490	 0.5720
U	 0.9430	 0.5490
V	 0.8940	 0.5020
W	 0.8450	 0.5210
X	 0.9400	 0.5810
Y	 0.9690	 0.5700
Z	 0.9250	 0.5290
b	 0.9680	 0.5820
c	 0.9570	 0.5620
d	 0.9600	 0.5930
e	 0.9750	 0.5890
f	 0.9650	 0.5780

