



Full wwPDB EM Validation Report ⓘ

Mar 31, 2025 – 06:28 PM JST

PDB ID : 5ZET / pdb_00005zet
EMDB ID : EMD-6922
Title : M. smegmatis P/P state 50S ribosomal subunit
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-28
Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
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) : 2.42

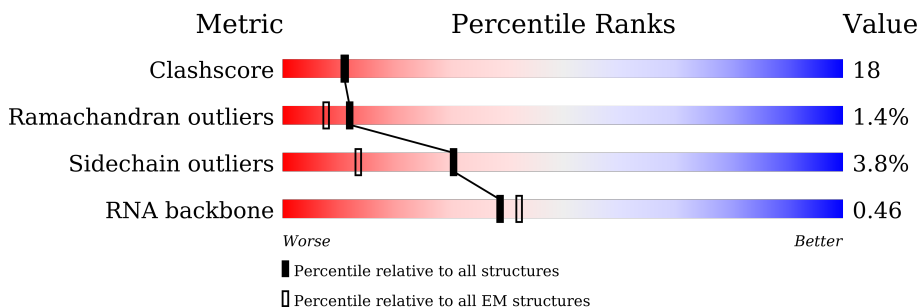
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	278	
2	D	217	
3	E	215	
4	F	187	
5	G	179	
6	H	151	
7	I	175	

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Mol	Chain	Length	Quality of chain
8	J	142	
9	K	147	
10	L	122	
11	M	147	
12	N	138	
13	O	199	
14	P	127	
15	Q	113	
16	R	129	
17	S	103	
18	T	153	
19	U	100	
20	V	105	
21	W	215	
22	X	88	
23	Y	64	
24	Z	77	
25	B	118	
26	A	3120	
27	1	61	
28	2	75	
29	3	57	
30	4	55	
31	5	47	
32	6	64	

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Mol	Chain	Length	Quality of chain
33	7	37	<div><div></div><div>51%</div><div>46%</div><div></div></div>
34	8	24	<div><div></div><div>79%</div><div>17%</div><div></div></div>

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 97374 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

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

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	147	Total	C	N	O	S	0	0
			1138	727	208	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 11 is a protein called 50S ribosomal protein L15.

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

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	134	Total	C	N	O	S	0	0
			1074	680	211	181	2		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	S	102	Total	C	N	O	0	0
			768	487	140	141		

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	97	Total	C	N	O	S	0	0
			731	456	137	136	2		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	W	188	Total	C	N	O	0	0
			1407	869	251	287		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 25 is a RNA chain called P-tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	1	60	Total	C	N	O	0	0
			483	298	97	88		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	6	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	7	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

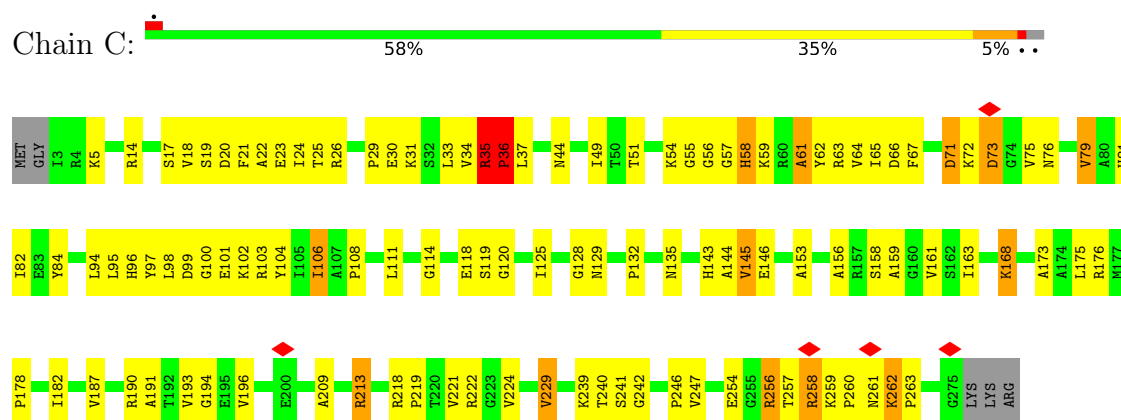
- Molecule 34 is a protein called Uncharacterized protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	8	23	Total	C	N	O	0	0
			189	111	50	28		

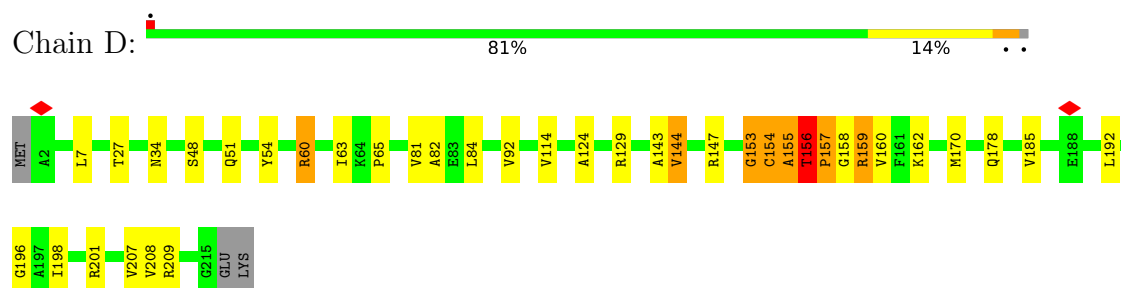
3 Residue-property plots

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.

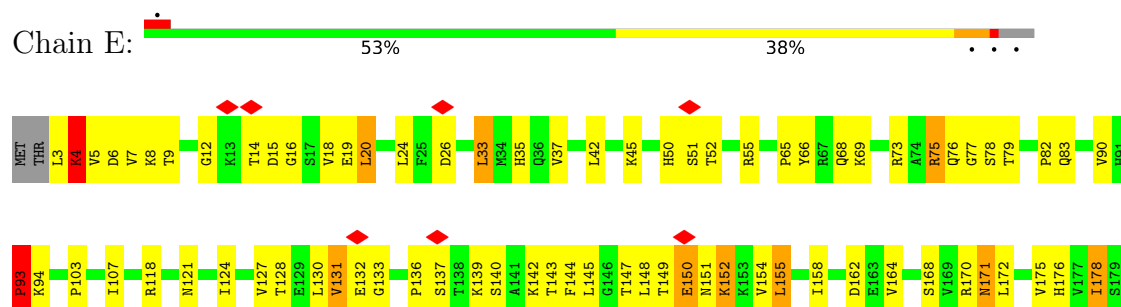
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3



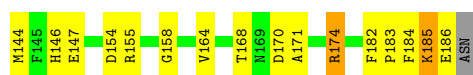
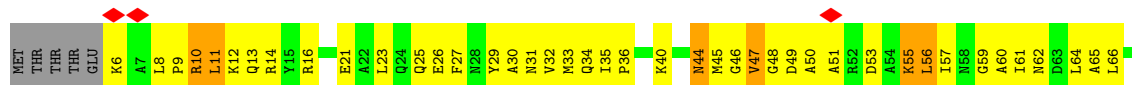
• Molecule 3: 50S ribosomal protein L4





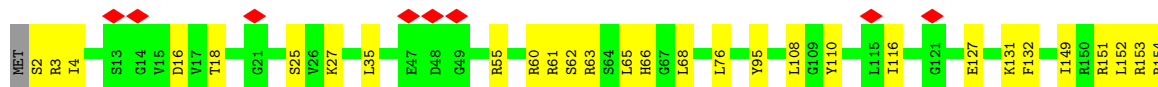
• Molecule 4: 50S ribosomal protein L5

Chain F: 43% 47% 7%



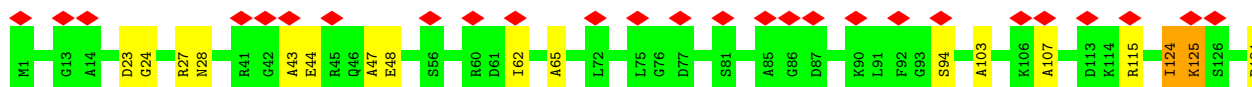
• Molecule 5: 50S ribosomal protein L6

Chain G: 77% 21%



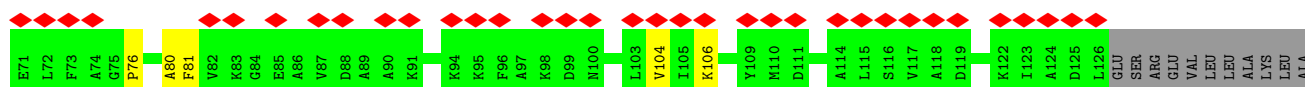
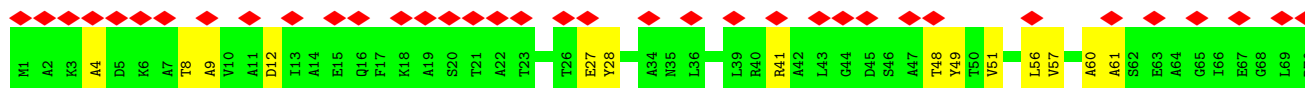
• Molecule 6: 50S ribosomal protein L9

Chain H: 20% 88% 11%



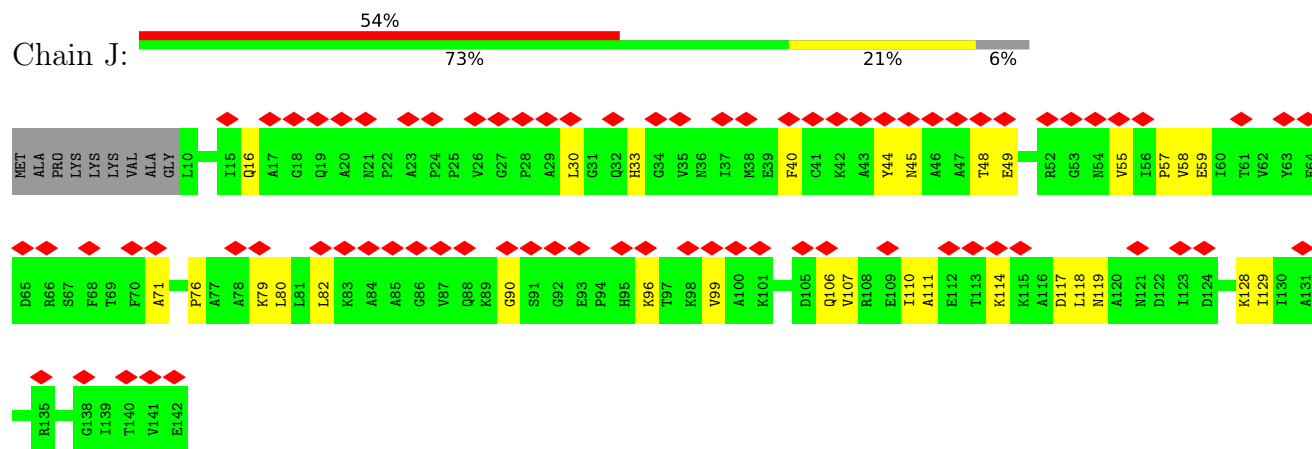
• Molecule 7: 50S ribosomal protein L10

Chain I: 41% 61% 11% 28%

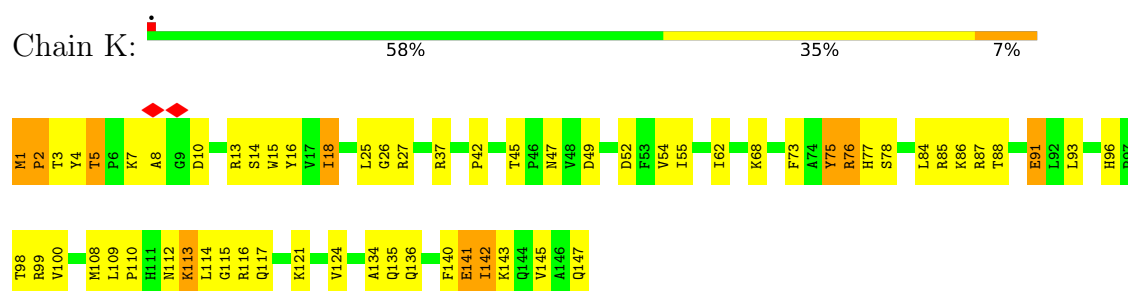


GLY
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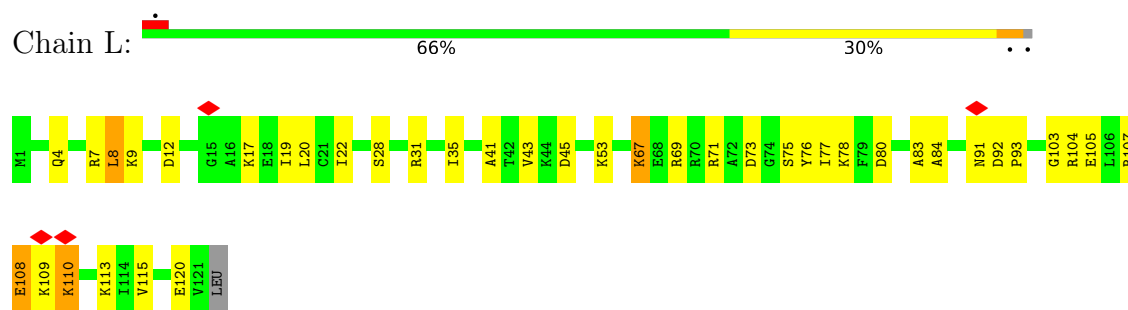
• Molecule 8: 50S ribosomal protein L11



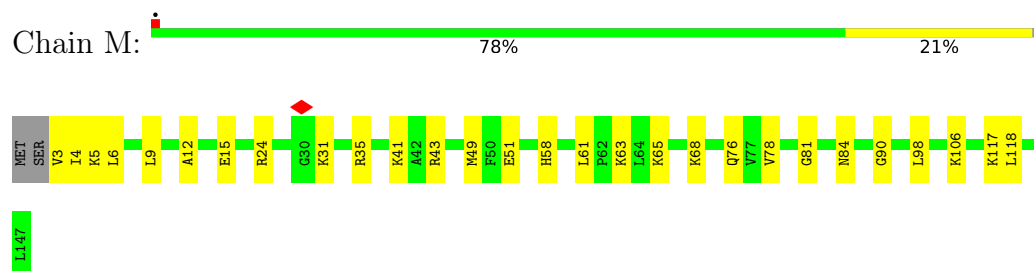
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

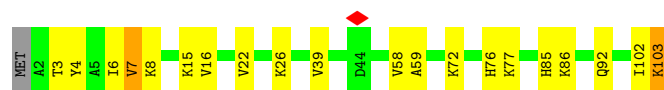


• Molecule 11: 50S ribosomal protein L15

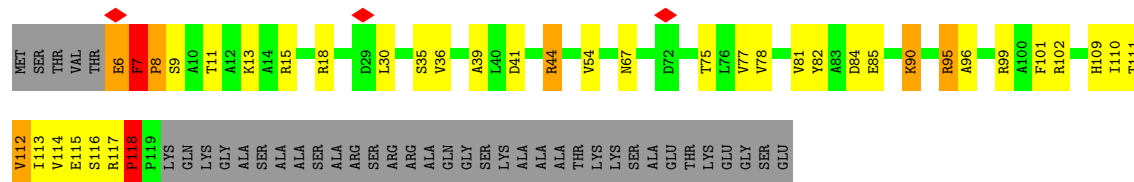


• Molecule 12: 50S ribosomal protein L16

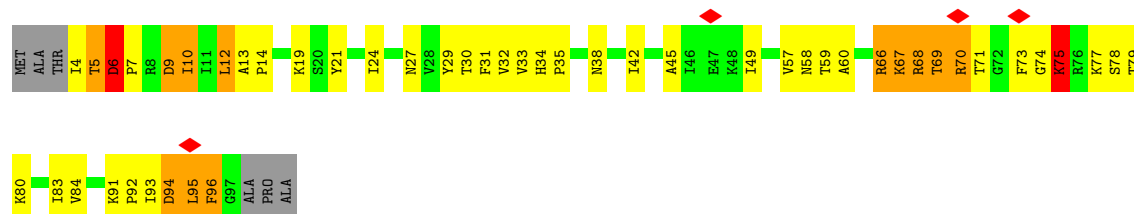




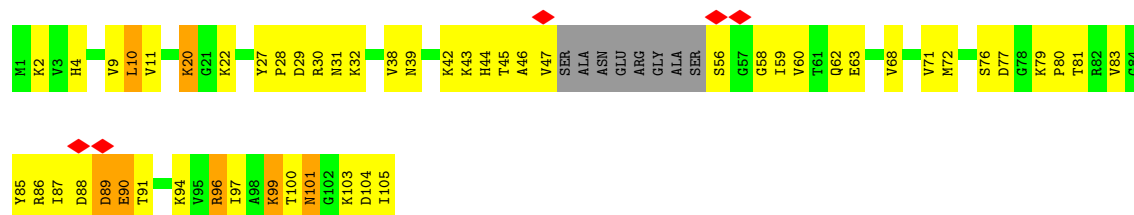
- Molecule 18: 50S ribosomal protein L22



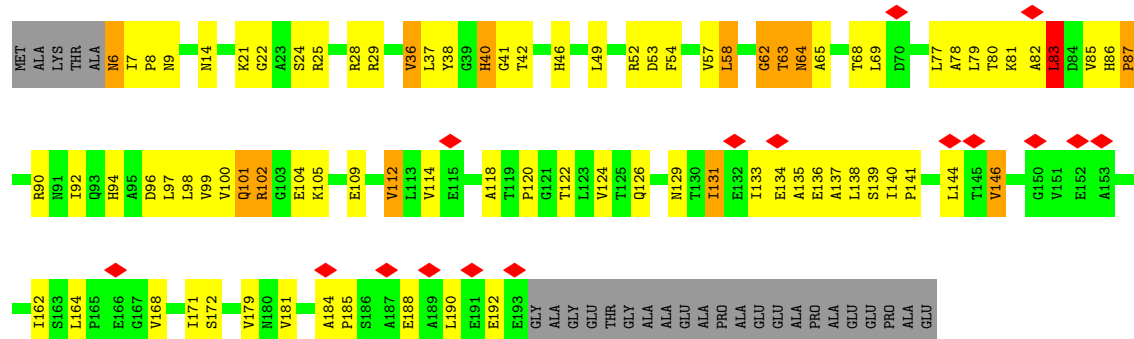
- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24

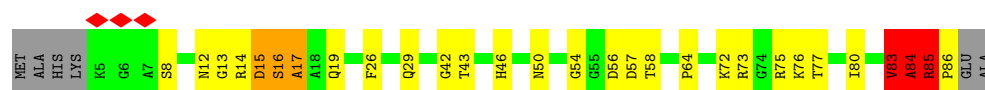


- Molecule 21: 50S ribosomal protein L25




- Molecule 22: 50S ribosomal protein L27

Chain X: 



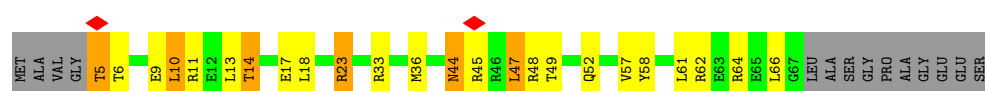
- Molecule 23: 50S ribosomal protein L28

Chain Y: 




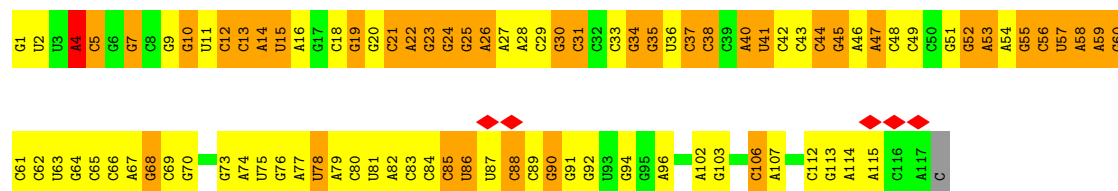
- Molecule 24: 50S ribosomal protein L29

Chain Z: 



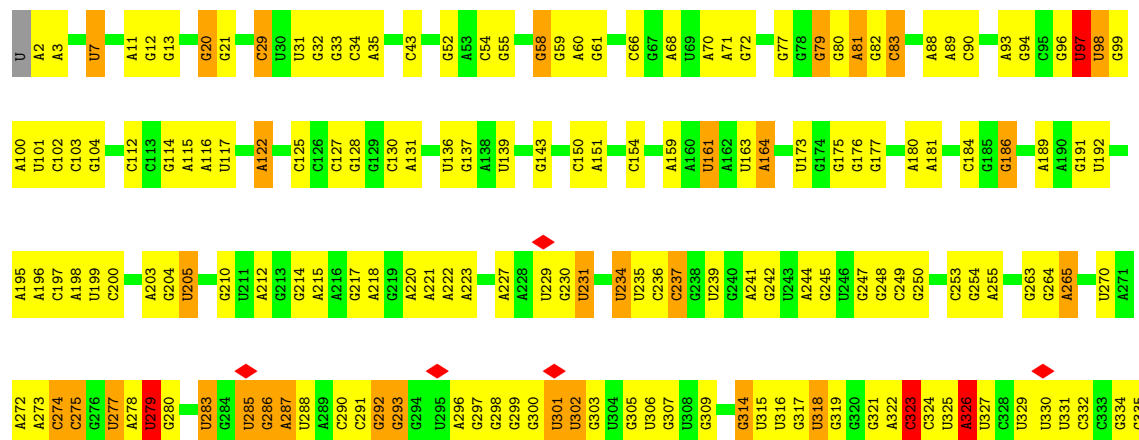
- Molecule 25: P-tRNA^{fMet}

Chain B: 



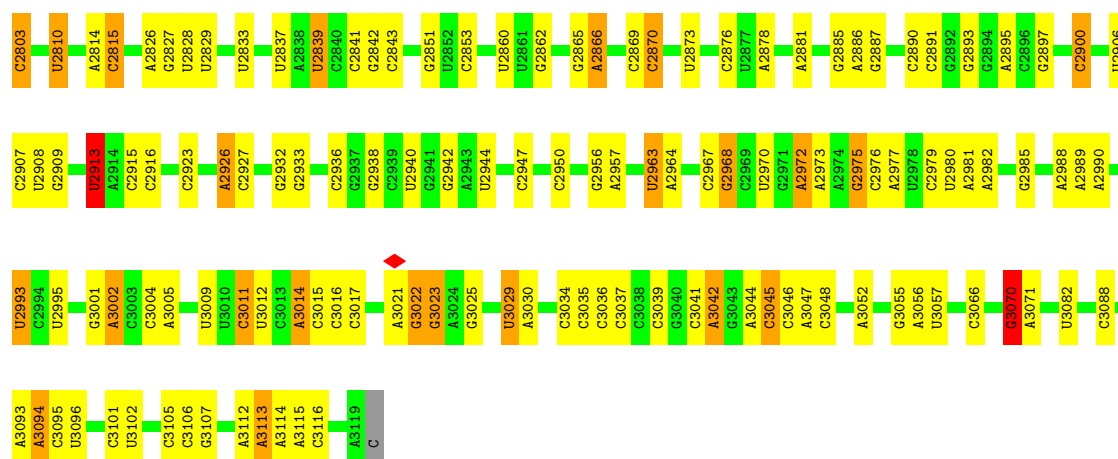
- Molecule 26: 23S rRNA

Chain A: 

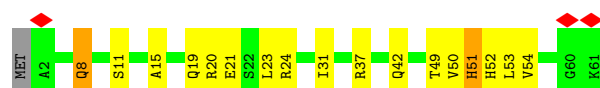


G1522	U1428	U1325	G1225	C1068	U981	U905	C802	G718	A623	G534	U438	C336
U1523	C1429	G1332	A1229	G1069	A982	A908	C805	G719	G624	A535	U442	U337
U1524	C1436	G1330	G1230	G1070	U983	C806	C807	C720	A625	U443	U444	U338
A1526	G1439	A1336	U1231	A1074	G989	U911	A808	A721	A633	G541	C	A
U1529	C1440	G1337	A1233	A1075	G993	C912	C813	A725	C	U	C	C
C1530	C1441	G1343	U1237	A1076	A994	U915	G828	G728	G	A545	U445	U
C1531	U1444	A1344	G1238	A1077	U995	G916	G829	G729	G	A546	G446	G
U1533	C1239	G1345	U1238	C1082	G996	A917	U828	C729	U638	G449	G345	G345
C1534	U1346	G1240	G1240	U1083	G997	U918	G830	G731	C639	G450	G346	G346
C1535	G1347	G1243	U1243	U1084	C1000	A919	A831	G732	G640	U451	U347	U347
A1536	U1244	G1245	U1245	G1085	C1001	G920	G832	U733	U641	G452	G348	G348
U1537	A1244	U1245	U1245	G1086	C1002	C921	A833	C734	G642	U453	G351	G351
G1538	A1246	U1246	A1246	U1088	C1003	U922	G838	A737	G643	U454	G352	G352
A1539	G1359	G1249	G1249	A1091	C	G924	U839	A740	G644	G458	U357	U357
U1540	A1362	U1250	U1250	A1092	A	C927	G844	G741	U646	A459	U358	U358
G1541	G1363	A1178	U1178	A1093	G1006	U928	C845	G742	U647	U461	A361	A361
A1542	U1370	G1181	G1181	G1094	G1007	C929	C846	A747	U648	G468	A364	A364
U1543	G1365	U1184	U1184	A1098	G1008	C930	A849	A753	G650	C471	U365	U365
C1545	A1366	A1185	A1185	U1099	U1010	C931	C853	G757	G655	C472	G366	G366
A1546	G1367	G1186	G1186	A1100	A1011	C932	A854	A758	C856	C474	U370	U370
G1547	U1259	U1187	U1187	C1101	U1012	U937	C855	G759	C857	A478	C377	C377
C1548	G1260	A1188	A1188	A1102	U1013	G938	U856	G761	U658	A479	G378	G378
G1549	U1261	G1189	G1189	G1103	G1014	C939	U857	G762	C674	U489	U383	U383
U1550	A1262	C1190	C1190	C1104	A1015	U942	U858	G763	U674	A490	G384	G384
U1551	G1375	A1191	A1191	A1105	C1016	U943	G859	G764	C675	U491	G385	G385
A1552	U1267	G1192	G1192	A1106	C1022	A944	U861	G765	U676	C492	C386	C386
C1553	C1287	C1193	C1193	G1107	A1025	G945	U862	G766	U677	U493	U387	U387
U1554	U1289	C1194	C1194	C1110	C1029	U947	G863	G767	A678	C494	U393	U393
A1555	G1270	C1197	C1197	G1111	C1030	G948	U864	G768	G679	U498	U403	U403
U1556	U1271	C1198	C1198	C1112	U1034	C952	A865	A770	U680	A404	A404	A404
U1560	G1272	G1201	G1201	C1113	A1033	C957	G866	G771	C881	G405	G405	G405
C1561	A1273	A1202	A1202	G1114	U1040	U951	U867	G772	A682	A406	A406	A406
A1562	U1274	A1203	A1203	A1118	A1041	U952	C868	G773	G683	C407	C407	C407
A1563	G1275	G1204	G1204	C1122	A1042	C963	A871	G774	G684	G805	C416	C416
A1564	U1276	A1205	A1205	C1123	G1043	U964	G872	A785	G685	U509	C417	C417
A1565	G1281	A1206	A1206	C1124	U1044	U965	G878	C786	G689	G512	G420	G420
A1566	U1283	G1207	G1207	C1125	C1045	C966	A879	G787	U689	C513	U421	U421
C1567	C1283	U1208	U1208	A1126	U1046	U967	G880	A790	G694	C514	A422	A422
A1568	G1291	G1209	G1209	A1127	C1047	G967	G889	G794	U699	U515	C423	C423
C1569	U1292	U1212	U1212	A1128	A1048	G971	G890	G795	G706	G516	G424	G424
A1570	G1293	A1213	A1213	C1130	G1049	U976	G891	A888	G707	A517	U425	U425
U1571	U1296	A1214	A1214	G1131	C1057	G977	G894	G799	G708	C521	G426	G426
G1572	G1297	U1215	U1215	A1140	A1058	C980	U894	A800	G709	G530	A427	A427
U1573	C1298	A1216	A1216	U1141	C1062	G978	G895	G800	G710	U531	G434	G434
G1574	G1411	U1219	U1219	G1142	A1063	U979	A896	G809	U709	G512	U428	U428
A1575	U1414	C1220	C1220	G1143	A1064	U976	A897	G610	G711	C513	U429	U429
C1576	A1415	A1221	A1221	A1144	U1065	G977	A888	G611	G712	C514	A430	A430
U1577	U1416	C1222	C1222	A1151	C1065	C980	G899	G612	G713	C515	U431	U431
G1578	A1417	U1223	U1223	U1151	C1065	C980	A904	G613	U714	C516	U432	U432
C1579	G1521	G1224	G1224	U1151	C1065	C980	A904	G614	U715	C517	U433	U433

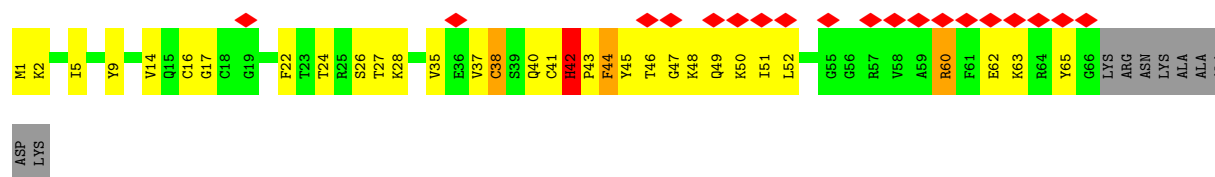
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G2714	A2635	A2546	U2457	G2379	U2309	A2212	U2112	G2016	G1917	C1819	A1731	C1651	G1587
U2715	G2640	U2548	G2458	G2380	U2315	U2215	C2116	C2017	G1921	C1822	C1734	G1654	G1588
U2717	U2643	G2549	G2462	A2381	G2316	G2216	C2117	G2018	G1922	A1826	G1734	G1658	G1589
G2718	C2644	U2550	G2463	U2382	G2317	U2217	C2118	A2019	G1923	A1826	A1737	U1658	G1590
G2726		A2551	U2467	G2385	G2319	C2220	A2120	A2020	C1926	C1830	A1744	A1660	U1591
G2729	U2647	C2556	U2468	U2386	U2321	A2221	G2121	G2025	G1933	A1836	A1744	C1662	G1592
U2730	C2648	A2557	G2471	U2387	C2322	A2221	U2122	A2027	G1933	G1837	C1747	U1665	U1593
U2739	A2649	C2558	A2471	G2387	G2323	C2224	G2127	G2028	G1938	A1843	A1748	A1666	G1594
A2650	A2650	A2559	U2473	G2388	A2324	U2225		G2031	U1939	A1844	C1753	A1666	G1595
C2734	G2651	A2560	U2472	U2389	U2325	U2226	G2130	A2032	A1940	G1845	G1754	C1667	C1596
U2735	G2652	G2562	G2476	U2390	C2327	C2230	G2131	U2033	C1943	G1846	A1755	C1668	G1597
G2736	G2653	U2567		G2391	G2327	C2230	U2130	A2033	C1944	U1847	A1755		G1597
A2654	U2654			A2392	G2328	A2238	A2137	C2043	U1945	U	G	C1672	U1598
G2737	U2655	C2571	U2482	A2393	G2329	A2239	C2138	U2046	U	A1852	U	A1673	U1599
A2742	A2658	C2574	U2485	U2395	U2334	A2239	C2138	A2046	U	A1853	G1758	G1674	G1600
U2743	A2659	G2575	U2486	U2395	G2335	C2243	A2140	U2046	A	U1854	A1759	U1675	G1601
C2745	G2745	A2578	C2487	A2396	U2336	A2244	U2141	G2052	C1949	A1855	G1761	G1677	U1602
U2746	C2665		A2490	C2402	U2336	C2245	A2142	G2059	C1953	U1857	C1762	U1678	G1603
G2747	C2666	U2582	A2497	U2403	G2337	U2246	G2143	C2060	C1954	A1858	G1763	A1679	G1604
G2750	G2668		A2497	U2403	G2338	A2247	C2144	U2061	C1954	A1858	A1764	U1681	G1605
C2751	G2669	U2585	A2498	G2405	U2338	C2247	U2147	G2062	A1956	G1862	A1765		G1606
U2752	G2670	G2586	G2499	U2406	A2337	U2246	A2142	G2063	G1957	G1863	U1766	U1689	C1607
G2753	G2671	G2586	G2500	U2407	A2338	C2248	G2144	U2061	C1958	U1864	C1768	A1690	U1608
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G2756	G2595	G2596	G2503	U2409	G2343	A2256	G2153	A2070			C1775	C1693	A1611
C2757	G2596		G2503	A2410	G2346	A2257	U2155	G2072	G1970	G1869	U1778	U1695	G1613
A2677	A2601	A2601	G2506	U2411	G2347	C2260	C2158	A2073	C1971	U1870	A1778	C1694	U1612
G2758	G2678	A2602	C2507	U2412	G2348	U2261	G2159	G2074	A1972	G1871	U1778	U1695	G1613
G2759	G2679	A2602	G2508	G2413	A2349	C2262	A2160	G2075	C1973	A1872	U1779	G1696	G1614
C2764	C2680		C2509	G2414	G2350	G2263	A2161	A2076	A1974	A1872	G1780	U1697	G1615
	U2681	G2607	A2510	U2418	A2351	C2267	A2162	C2077	A1975	U1875		G1703	A1616
G2780	G2682	G2608	A2511	C2419	U2352	G2268	U2163	U2081	C1976	A1876	C1785	G1703	A1616
G2781		A2609	A2512	U2420	U2353	C2269	G2163	U2082	C1977	U1877	G1786	U1704	C1617
C2782	U2686	C2610	A2512	U2421	G2354	C2269	C2166	A2083	U1981	G1878	A1787	C1705	U1618
U2786	U2687	U2611	U2515	A2421	U2355	C2274	U2167	C2084	A1981	A1882	G1788	A1710	U1619
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A2789	G2690	G2615	C2521	G2424	A2357	C2276	U2179	U2088	U1992	A1886	A1791	G1713	G1622
G2790	A2693	A2616	A2522	G2427	G2358	G2279	U2180	C2089	U1996	A1887	A1792	U1713	U1623
G2791	G2694	C2618	G2527	C2430	C2360	G2280	C2181	U2090	A1996	U1892	U1798	A1715	G1624
C2792			G2527	G2431	U2361	A2284	C2181	U2090	A1997	G1892	U1798	A1716	G1625
G2793	U2697	C2622	G2528	C2432	U2362	G2284	A2190	U2091	C1998	C1893	C1801	U1717	G1626
G2794	C2698	G2530	A2530	U2433	A2363	G2285	C2191	U2092	C1998	G1802	C1801	U1717	U1627
C2795	U2698	G2531	G2531	A2434	G2364	C2287	G2093	G2093	A2000	U1898	A1803	C1718	A1628
A2796	G2699	G2525	G2532	U2435	A2365	C2287	G2094	G2094	A2001	U1898	G1804	C1719	G1629
G2797	A2700	U2626	G2532	U2436	A2365	C2288	A2194	G2095	C1903	C1903	G1805	G1720	G1629
U2701	G2627	G2627	U2536	A2436	G2366	C2289	U2195	G2096	C2005	C1903	G1805	U1721	U1630
G2798	U2701	U2627	U2536	U2437	G2367	C2290	G2196	G2096	A2006	G1905	A1806		A1631
G2799	A2702	U2628	C2537	G2438	G2367	C2290	G2197	G2097	C2007	U1906	A1806	G1724	G1632
G2800		A2630	A2538	G2446	C2368	C2295	C2198	A2106	C2007	C1813	A1806	G1725	U1633
A2801	G2705	G2631	G2539	G2446	C2368	C2295	C2198	G2107	C2012	G1913	C1816	A1727	C1634
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				A2451	U2374								A1636
					G2375								G1637
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					G2376								G1639
													A1640
													U1641
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													A1643



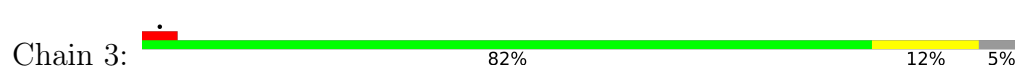
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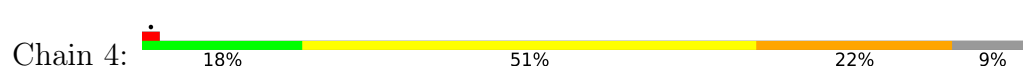
- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33 1



- Molecule 31: 50S ribosomal protein L34

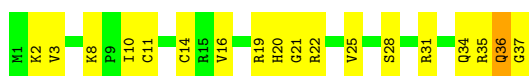




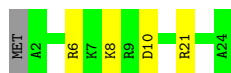
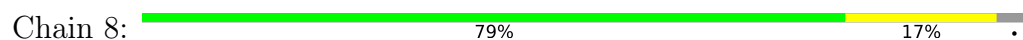
- Molecule 32: 50S ribosomal protein L35



- Molecule 33: 50S ribosomal protein L36



- Molecule 34: Uncharacterized protein bL37



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.781	Depositor
Minimum map value	-0.495	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	361.19998, 361.19998, 361.19998	wwPDB
Map dimensions	344, 344, 344	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	C	1.01	5/2140 (0.2%)	0.94	5/2879 (0.2%)
2	D	0.55	0/1609	0.66	2/2165 (0.1%)
3	E	0.84	1/1576 (0.1%)	0.87	4/2132 (0.2%)
4	F	0.59	0/1459	0.79	0/1962
5	G	0.36	0/1369	0.57	0/1848
6	H	0.33	0/1027	0.61	1/1398 (0.1%)
7	I	0.29	0/925	0.52	0/1246
8	J	0.29	0/1006	0.60	0/1364
9	K	0.76	1/1165 (0.1%)	0.88	4/1578 (0.3%)
10	L	0.92	0/938	0.95	4/1257 (0.3%)
11	M	0.53	0/1091	0.65	0/1457
12	N	0.91	1/1100 (0.1%)	0.91	2/1482 (0.1%)
13	O	0.75	0/936	0.94	4/1256 (0.3%)
14	P	0.43	0/966	0.57	0/1298
15	Q	0.51	0/921	0.60	1/1236 (0.1%)
16	R	0.55	0/1000	0.58	0/1341
17	S	0.48	0/778	0.57	0/1048
18	T	0.96	1/887 (0.1%)	0.93	3/1204 (0.2%)
19	U	0.74	0/749	0.83	2/1006 (0.2%)
20	V	0.65	0/737	0.78	1/987 (0.1%)
21	W	0.53	0/1422	0.81	4/1941 (0.2%)
22	X	0.94	0/613	0.85	1/821 (0.1%)
23	Y	0.55	0/478	0.70	0/641
24	Z	0.69	0/530	0.75	0/708
25	B	0.56	1/2797 (0.0%)	1.13	18/4357 (0.4%)
26	A	1.00	1/74597 (0.0%)	1.24	633/116386 (0.5%)
27	1	0.80	0/486	0.89	0/651
28	2	0.37	0/520	0.60	1/698 (0.1%)
29	3	0.55	0/427	0.61	0/572
30	4	0.73	1/424 (0.2%)	0.78	2/567 (0.4%)
31	5	0.85	0/375	1.00	1/493 (0.2%)
32	6	0.91	0/507	0.94	2/672 (0.3%)
33	7	0.83	0/302	0.80	0/401
34	8	0.44	0/191	0.60	0/247

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.92	12/106048 (0.0%)	1.14	695/159299 (0.4%)

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
1	C	0	4
2	D	0	2
3	E	0	5
4	F	0	1
9	K	0	1
12	N	0	1
13	O	0	1
18	T	0	1
22	X	0	2
All	All	0	18

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	B	1	G	OP3-P	-10.43	1.48	1.61
1	C	79	VAL	CB-CG2	-6.92	1.38	1.52
18	T	112	VAL	CB-CG2	-6.68	1.38	1.52
1	C	224	VAL	CB-CG2	-6.23	1.39	1.52
12	N	92	TRP	CB-CG	-6.01	1.39	1.50
30	4	42	CYS	CB-SG	-5.59	1.72	1.81
1	C	247	VAL	CB-CG1	-5.48	1.41	1.52
26	A	1099	A	N7-C5	-5.34	1.36	1.39
9	K	54	VAL	CB-CG2	-5.15	1.42	1.52
1	C	224	VAL	CB-CG1	-5.12	1.42	1.52
3	E	37	VAL	CB-CG1	-5.10	1.42	1.52
1	C	187	VAL	CB-CG1	-5.04	1.42	1.52

All (695) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	323	C	N1-C2-O2	11.55	125.83	118.90
26	A	1130	C	N1-C2-O2	11.20	125.62	118.90
26	A	2245	C	N1-C2-O2	11.08	125.55	118.90
26	A	2245	C	C2-N1-C1'	10.64	130.51	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	323	C	C2-N1-C1'	10.56	130.42	118.80
26	A	2025	C	N3-C2-O2	-10.31	114.68	121.90
26	A	619	C	N1-C2-O2	10.28	125.06	118.90
26	A	3046	C	C2-N1-C1'	10.18	130.00	118.80
26	A	1012	C	C2-N1-C1'	9.93	129.72	118.80
26	A	237	C	C6-N1-C2	-9.92	116.33	120.30
26	A	2245	C	N3-C2-O2	-9.69	115.12	121.90
26	A	1630	U	C5-C4-O4	9.60	131.66	125.90
26	A	1012	C	N1-C2-O2	9.56	124.64	118.90
26	A	619	C	C2-N1-C1'	9.54	129.30	118.80
26	A	1694	C	N1-C2-O2	9.51	124.61	118.90
26	A	1130	C	C2-N1-C1'	9.50	129.25	118.80
26	A	1694	C	N3-C2-O2	-9.47	115.27	121.90
26	A	2025	C	N1-C2-O2	9.43	124.56	118.90
26	A	2407	C	N1-C2-O2	9.39	124.53	118.90
26	A	1001	C	C6-N1-C2	-9.37	116.55	120.30
26	A	1428	U	C2-N1-C1'	9.35	128.92	117.70
26	A	323	C	N3-C2-O2	-9.32	115.38	121.90
26	A	912	C	C5-C6-N1	9.26	125.63	121.00
26	A	2025	C	C2-N1-C1'	9.23	128.96	118.80
26	A	336	C	C2-N1-C1'	9.20	128.92	118.80
26	A	2407	C	C2-N1-C1'	9.18	128.90	118.80
26	A	3046	C	N3-C2-O2	-9.18	115.47	121.90
26	A	1428	U	N1-C2-O2	8.94	129.06	122.80
26	A	1694	C	C6-N1-C2	-8.89	116.74	120.30
26	A	709	U	N3-C2-O2	-8.88	115.98	122.20
26	A	1130	C	N3-C2-O2	-8.86	115.70	121.90
19	U	12	LEU	CA-CB-CG	8.81	135.56	115.30
26	A	237	C	C5-C6-N1	8.76	125.38	121.00
26	A	417	C	C6-N1-C2	-8.69	116.82	120.30
26	A	1428	U	N3-C2-O2	-8.68	116.12	122.20
26	A	2697	U	N1-C2-O2	8.63	128.84	122.80
26	A	2870	C	C6-N1-C2	-8.61	116.86	120.30
26	A	3046	C	N1-C2-O2	8.52	124.01	118.90
26	A	3011	C	N1-C2-O2	8.42	123.95	118.90
13	O	45	ARG	C-N-CD	8.41	146.07	128.40
26	A	709	U	N1-C2-O2	8.41	128.69	122.80
26	A	622	C	C5-C6-N1	8.31	125.16	121.00
21	W	62	GLY	N-CA-C	8.28	133.80	113.10
26	A	905	U	C2-N1-C1'	8.27	127.62	117.70
26	A	2521	C	C2-N1-C1'	8.21	127.83	118.80
26	A	2005	C	C6-N1-C2	-8.19	117.02	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	703	C	C2-N1-C1'	8.15	127.77	118.80
26	A	845	C	N1-C2-O2	8.07	123.74	118.90
25	B	31	C	N1-C2-O2	8.06	123.73	118.90
26	A	275	C	C2-N1-C1'	8.00	127.60	118.80
26	A	619	C	C6-N1-C1'	-8.00	111.20	120.80
26	A	962	U	C2-N1-C1'	7.99	127.29	117.70
26	A	2870	C	C5-C6-N1	7.99	124.99	121.00
26	A	975	U	C2-N1-C1'	7.94	127.23	117.70
26	A	1521	C	C2-N1-C1'	7.93	127.53	118.80
26	A	2947	C	C6-N1-C2	-7.93	117.13	120.30
26	A	323	C	C6-N1-C2	-7.91	117.14	120.30
26	A	2689	C	C5-C6-N1	7.90	124.95	121.00
26	A	1429	C	C2-N1-C1'	7.88	127.47	118.80
26	A	905	U	N1-C2-O2	7.88	128.31	122.80
26	A	2267	C	C6-N1-C2	-7.83	117.17	120.30
26	A	1535	C	C6-N1-C2	-7.82	117.17	120.30
18	T	118	PRO	CA-N-CD	-7.80	100.58	111.50
26	A	275	C	C6-N1-C2	-7.78	117.19	120.30
26	A	275	C	N1-C2-O2	7.78	123.57	118.90
26	A	543	U	N3-C2-O2	-7.78	116.76	122.20
26	A	1535	C	C2-N1-C1'	7.78	127.35	118.80
26	A	2325	U	N1-C2-O2	7.76	128.23	122.80
26	A	1403	C	N3-C2-O2	-7.75	116.48	121.90
26	A	1302	G	C6-C5-N7	-7.73	125.76	130.40
26	A	1694	C	C2-N1-C1'	7.73	127.31	118.80
26	A	2289	C	C5-C6-N1	7.70	124.85	121.00
26	A	2322	C	N1-C2-O2	7.68	123.51	118.90
26	A	2944	U	N1-C2-O2	7.66	128.16	122.80
26	A	2245	C	C6-N1-C2	-7.63	117.25	120.30
26	A	2521	C	C6-N1-C2	-7.62	117.25	120.30
26	A	2697	U	C2-N1-C1'	7.61	126.83	117.70
26	A	29	C	C2-N1-C1'	7.60	127.16	118.80
26	A	1044	U	N1-C2-O2	7.60	128.12	122.80
26	A	472	C	C2-N1-C1'	7.59	127.15	118.80
26	A	2180	U	N1-C2-O2	7.59	128.11	122.80
26	A	2267	C	C5-C6-N1	7.58	124.79	121.00
26	A	102	C	C2-N1-C1'	7.58	127.14	118.80
26	A	2287	C	C6-N1-C2	-7.55	117.28	120.30
26	A	1130	C	C6-N1-C2	-7.54	117.28	120.30
26	A	1409	C	C6-N1-C2	-7.50	117.30	120.30
26	A	2180	U	N3-C2-O2	-7.50	116.95	122.20
26	A	932	C	C6-N1-C2	-7.48	117.31	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2288	C	C6-N1-C2	-7.46	117.31	120.30
26	A	1123	C	C5-C6-N1	7.44	124.72	121.00
26	A	2697	U	N3-C2-O2	-7.43	117.00	122.20
26	A	2111	U	N1-C2-O2	7.42	127.99	122.80
26	A	1030	C	C2-N1-C1'	7.40	126.94	118.80
26	A	234	U	N3-C2-O2	-7.39	117.03	122.20
26	A	1429	C	C5-C6-N1	7.38	124.69	121.00
26	A	2841	C	C6-N1-C2	-7.35	117.36	120.30
26	A	619	C	N3-C2-O2	-7.35	116.75	121.90
26	A	905	U	N3-C2-O2	-7.35	117.06	122.20
26	A	1531	C	C2-N1-C1'	7.33	126.86	118.80
25	B	62	C	N1-C2-O2	7.27	123.26	118.90
26	A	1219	U	N3-C2-O2	-7.25	117.12	122.20
26	A	2360	C	N1-C2-O2	7.25	123.25	118.90
26	A	102	C	C6-N1-C2	-7.25	117.40	120.30
26	A	962	U	N1-C2-O2	7.24	127.87	122.80
26	A	1123	C	C6-N1-C2	-7.23	117.41	120.30
26	A	514	C	C2-N1-C1'	7.22	126.75	118.80
26	A	845	C	C6-N1-C2	-7.18	117.43	120.30
26	A	2005	C	C5-C6-N1	7.18	124.59	121.00
26	A	2087	C	C2-N1-C1'	7.18	126.69	118.80
26	A	2325	U	C2-N1-C1'	7.15	126.28	117.70
26	A	2325	U	N3-C2-O2	-7.15	117.19	122.20
26	A	283	U	N3-C2-O2	-7.14	117.20	122.20
26	A	2245	C	C6-N1-C1'	-7.13	112.24	120.80
26	A	1822	C	C6-N1-C2	-7.11	117.46	120.30
26	A	543	U	N1-C2-O2	7.10	127.77	122.80
26	A	3011	C	N3-C2-O2	-7.08	116.94	121.90
26	A	1044	U	N3-C2-O2	-7.08	117.25	122.20
26	A	734	C	C5-C6-N1	7.07	124.53	121.00
26	A	1044	U	C2-N1-C1'	7.07	126.18	117.70
26	A	2320	C	N1-C2-O2	7.07	123.14	118.90
26	A	1219	U	N1-C2-O2	7.06	127.74	122.80
26	A	2086	U	C5-C6-N1	7.05	126.22	122.70
26	A	279	U	N1-C2-O2	7.04	127.73	122.80
26	A	2322	C	C2-N1-C1'	7.04	126.55	118.80
26	A	445	U	P-O3'-C3'	7.03	128.13	119.70
25	B	31	C	N3-C2-O2	-7.02	116.99	121.90
26	A	323	C	C6-N1-C1'	-7.01	112.39	120.80
26	A	3046	C	C6-N1-C1'	-7.01	112.39	120.80
26	A	709	U	C2-N1-C1'	7.00	126.10	117.70
26	A	102	C	N1-C2-O2	7.00	123.10	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2085	C	P-O3'-C3'	6.99	128.09	119.70
26	A	336	C	C5-C6-N1	6.98	124.49	121.00
26	A	2890	C	N1-C2-O2	6.98	123.09	118.90
26	A	2248	C	C5-C6-N1	6.96	124.48	121.00
26	A	2327	C	C6-N1-C2	-6.95	117.52	120.30
26	A	1012	C	C6-N1-C1'	-6.95	112.46	120.80
26	A	2680	C	C5-C6-N1	6.94	124.47	121.00
26	A	910	C	C5-C6-N1	6.93	124.47	121.00
26	A	283	U	N1-C2-O2	6.93	127.65	122.80
26	A	714	U	N1-C2-O2	6.91	127.64	122.80
26	A	2094	G	P-O3'-C3'	6.90	127.98	119.70
26	A	197	C	C5-C6-N1	6.89	124.45	121.00
26	A	1298	C	C5-C6-N1	6.89	124.44	121.00
26	A	703	C	C6-N1-C2	-6.88	117.55	120.30
26	A	514	C	C6-N1-C2	-6.87	117.55	120.30
26	A	7	U	C2-N1-C1'	6.86	125.94	117.70
26	A	962	U	N3-C2-O2	-6.86	117.40	122.20
26	A	910	C	C6-N1-C2	-6.85	117.56	120.30
26	A	275	C	C5-C6-N1	6.85	124.42	121.00
26	A	472	C	N1-C2-O2	6.84	123.01	118.90
26	A	1862	C	C6-N1-C2	-6.84	117.56	120.30
26	A	2327	C	N1-C2-O2	6.83	123.00	118.90
25	B	106	C	N1-C2-O2	6.82	122.99	118.90
26	A	1057	C	C6-N1-C2	-6.81	117.58	120.30
26	A	1303	U	C5-C6-N1	6.80	126.10	122.70
26	A	2407	C	C5-C6-N1	6.80	124.40	121.00
26	A	784	G	C4-N9-C1'	6.79	135.33	126.50
26	A	2671	G	C6-N1-C2	-6.79	121.02	125.10
26	A	729	C	C6-N1-C2	-6.79	117.58	120.30
26	A	2248	C	C6-N1-C2	-6.79	117.59	120.30
26	A	2890	C	N3-C2-O2	-6.79	117.15	121.90
26	A	3046	C	C6-N1-C2	-6.79	117.59	120.30
26	A	714	U	N3-C2-O2	-6.78	117.45	122.20
26	A	1130	C	C5-C6-N1	6.77	124.39	121.00
26	A	1534	C	N1-C2-O2	6.77	122.96	118.90
26	A	1382	U	N1-C2-O2	6.76	127.53	122.80
26	A	764	U	N3-C2-O2	-6.76	117.47	122.20
26	A	656	C	C6-N1-C2	-6.74	117.61	120.30
26	A	975	U	C5-C6-N1	6.71	126.06	122.70
26	A	1667	C	C6-N1-C2	-6.71	117.62	120.30
26	A	2689	C	C2-N1-C1'	6.71	126.18	118.80
26	A	975	U	N1-C2-O2	6.70	127.49	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2289	C	C6-N1-C2	-6.70	117.62	120.30
9	K	108	MET	CA-CB-CG	6.69	124.68	113.30
26	A	2647	U	N1-C2-O2	6.69	127.48	122.80
26	A	1535	C	N3-C2-O2	-6.68	117.22	121.90
26	A	2327	C	C2-N1-C1'	6.67	126.14	118.80
26	A	283	U	C2-N1-C1'	6.67	125.70	117.70
26	A	1239	C	C5-C6-N1	6.67	124.33	121.00
26	A	2111	U	N3-C2-O2	-6.67	117.53	122.20
26	A	192	U	N3-C2-O2	-6.66	117.54	122.20
26	A	1630	U	N3-C4-O4	-6.66	114.74	119.40
26	A	2717	U	C5-C6-N1	6.65	126.03	122.70
26	A	417	C	C5-C6-N1	6.63	124.31	121.00
1	C	106	ILE	CG1-CB-CG2	-6.62	96.84	111.40
26	A	1012	C	N3-C2-O2	-6.61	117.27	121.90
26	A	29	C	N1-C2-O2	6.61	122.86	118.90
26	A	1302	G	N3-C4-N9	6.60	129.96	126.00
26	A	1123	C	C2-N1-C1'	6.58	126.04	118.80
26	A	845	C	C5-C6-N1	6.58	124.29	121.00
26	A	1403	C	N1-C2-O2	6.57	122.84	118.90
26	A	2025	C	C6-N1-C1'	-6.57	112.92	120.80
26	A	2970	U	C5-C6-N1	6.57	125.98	122.70
26	A	2521	C	C5-C6-N1	6.57	124.28	121.00
26	A	2407	C	C6-N1-C1'	-6.56	112.92	120.80
26	A	332	C	N3-C2-O2	-6.55	117.31	121.90
26	A	1219	U	C2-N1-C1'	6.55	125.56	117.70
26	A	7	U	N1-C2-O2	6.53	127.37	122.80
26	A	2913	U	N3-C2-O2	-6.52	117.63	122.20
26	A	1893	C	N1-C2-O2	6.51	122.81	118.90
26	A	1045	C	C2-N1-C1'	6.50	125.96	118.80
26	A	1409	C	C5-C6-N1	6.49	124.25	121.00
26	A	2944	U	N3-C2-O2	-6.48	117.67	122.20
26	A	2689	C	C6-N1-C2	-6.47	117.71	120.30
26	A	1302	G	C4-N9-C1'	6.46	134.90	126.50
26	A	2671	G	C5-C6-O6	-6.46	124.72	128.60
26	A	1991	C	C5-C6-N1	6.45	124.23	121.00
26	A	2290	C	C6-N1-C2	-6.45	117.72	120.30
26	A	336	C	N1-C2-O2	6.44	122.77	118.90
26	A	764	U	N1-C2-O2	6.44	127.31	122.80
26	A	438	U	C2-N1-C1'	6.43	125.42	117.70
26	A	1197	C	C2-N1-C1'	6.42	125.87	118.80
13	O	89	ASP	CB-CG-OD1	6.42	124.08	118.30
26	A	2407	C	N3-C2-O2	-6.41	117.41	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2138	C	N1-C2-O2	6.40	122.74	118.90
26	A	2260	C	C6-N1-C2	-6.39	117.74	120.30
26	A	2269	C	C6-N1-C2	-6.39	117.74	120.30
26	A	336	C	C6-N1-C1'	-6.39	113.13	120.80
26	A	1534	C	C2-N1-C1'	6.39	125.83	118.80
26	A	1088	U	C5-C6-N1	6.38	125.89	122.70
26	A	505	C	C5-C6-N1	6.37	124.18	121.00
26	A	1551	U	C5-C6-N1	6.35	125.88	122.70
26	A	2734	C	N1-C2-O2	6.35	122.71	118.90
26	A	139	U	N3-C2-O2	-6.34	117.76	122.20
26	A	550	C	C6-N1-C2	-6.33	117.77	120.30
26	A	1428	U	C6-N1-C1'	-6.33	112.34	121.20
26	A	608	C	C5-C6-N1	6.33	124.16	121.00
26	A	1837	G	C4-C5-N7	6.33	113.33	110.80
25	B	69	C	N1-C2-O2	6.32	122.69	118.90
26	A	2360	C	C2-N1-C1'	6.32	125.75	118.80
26	A	2869	C	C2-N1-C1'	6.32	125.75	118.80
26	A	102	C	C5-C6-N1	6.31	124.15	121.00
26	A	2076	A	N1-C6-N6	6.30	122.38	118.60
13	O	46	PRO	CA-N-CD	-6.30	102.68	111.50
26	A	514	C	C5-C6-N1	6.30	124.15	121.00
26	A	2947	C	C5-C6-N1	6.30	124.15	121.00
2	D	144	VAL	CG1-CB-CG2	-6.29	100.83	110.90
26	A	336	C	C6-N1-C2	-6.29	117.79	120.30
26	A	839	U	N3-C2-O2	-6.28	117.80	122.20
26	A	1212	U	C5-C6-N1	6.28	125.84	122.70
26	A	461	U	N3-C2-O2	-6.27	117.81	122.20
26	A	1893	C	N3-C2-O2	-6.27	117.51	121.90
26	A	1012	C	C6-N1-C2	-6.27	117.79	120.30
26	A	1441	C	N1-C2-O2	6.26	122.66	118.90
26	A	1816	C	C2-N1-C1'	6.26	125.69	118.80
26	A	2362	C	N1-C2-O2	6.26	122.66	118.90
26	A	1001	C	C5-C6-N1	6.25	124.13	121.00
26	A	2841	C	C5-C6-N1	6.25	124.13	121.00
26	A	2198	C	C5-C6-N1	6.25	124.13	121.00
26	A	1044	U	C5-C6-N1	6.25	125.82	122.70
26	A	323	C	C5-C6-N1	6.24	124.12	121.00
26	A	2916	C	C6-N1-C2	-6.24	117.80	120.30
26	A	1008	G	C4-N9-C1'	6.23	134.59	126.50
9	K	18	ILE	CG1-CB-CG2	-6.22	97.70	111.40
26	A	279	U	N3-C2-O2	-6.22	117.84	122.20
26	A	3070	G	C4-N9-C1'	-6.22	118.41	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	192	U	N1-C2-O2	6.22	127.15	122.80
26	A	1429	C	C6-N1-C2	-6.22	117.81	120.30
26	A	2435	U	N3-C2-O2	-6.21	117.85	122.20
26	A	1012	C	C5-C6-N1	6.21	124.11	121.00
26	A	2841	C	N1-C2-O2	6.21	122.62	118.90
26	A	1197	C	N1-C2-O2	6.21	122.62	118.90
1	C	213	ARG	NE-CZ-NH2	-6.20	117.20	120.30
26	A	898	A	C4-N9-C1'	6.20	137.45	126.30
26	A	2900	C	C6-N1-C2	-6.20	117.82	120.30
26	A	2166	C	C5-C6-N1	6.19	124.10	121.00
26	A	561	G	N3-C4-N9	6.19	129.72	126.00
26	A	1130	C	C6-N1-C1'	-6.18	113.38	120.80
26	A	2900	C	C5-C6-N1	6.17	124.08	121.00
26	A	1697	U	N3-C2-O2	-6.17	117.89	122.20
12	N	61	GLY	N-CA-C	6.16	128.50	113.10
25	B	4	A	C8-N9-C4	-6.16	103.34	105.80
18	T	102	ARG	NE-CZ-NH2	-6.15	117.22	120.30
26	A	2487	C	C6-N1-C2	-6.15	117.84	120.30
26	A	2061	U	C5-C6-N1	6.14	125.77	122.70
26	A	2158	C	N1-C2-O2	6.14	122.58	118.90
26	A	1057	C	C5-C6-N1	6.14	124.07	121.00
26	A	703	C	C5-C6-N1	6.13	124.06	121.00
26	A	918	U	C5-C6-N1	6.13	125.77	122.70
26	A	1531	C	C5-C6-N1	6.12	124.06	121.00
12	N	122	ILE	CG1-CB-CG2	-6.12	97.94	111.40
26	A	2155	U	N1-C2-O2	6.12	127.08	122.80
26	A	2320	C	C2-N1-C1'	6.11	125.52	118.80
31	5	7	THR	N-CA-C	6.11	127.50	111.00
26	A	1302	G	C8-N9-C1'	-6.11	119.06	127.00
26	A	2366	C	N3-C2-O2	-6.11	117.62	121.90
26	A	853	C	C2-N1-C1'	6.10	125.51	118.80
26	A	1813	C	C5-C6-N1	6.09	124.05	121.00
26	A	2025	C	C6-N1-C2	-6.09	117.86	120.30
26	A	3034	C	C6-N1-C2	-6.09	117.86	120.30
1	C	95	LEU	CB-CG-CD1	-6.08	100.66	111.00
25	B	4	A	N7-C8-N9	6.08	116.84	113.80
13	O	88	ALA	C-N-CA	6.07	136.88	121.70
20	V	10	LEU	CA-CB-CG	6.07	129.27	115.30
26	A	957	C	C6-N1-C2	-6.07	117.87	120.30
26	A	3045	C	C6-N1-C2	-6.07	117.87	120.30
26	A	1103	C	C5-C6-N1	6.06	124.03	121.00
26	A	912	C	C6-N1-C2	-6.06	117.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2320	C	N3-C2-O2	-6.06	117.66	121.90
26	A	549	C	C6-N1-C2	-6.06	117.88	120.30
26	A	2680	C	C6-N1-C2	-6.06	117.88	120.30
25	B	106	C	N3-C2-O2	-6.05	117.66	121.90
26	A	1251	A	O4'-C1'-N9	6.05	113.04	108.20
26	A	2782	C	C5-C6-N1	6.04	124.02	121.00
26	A	2438	C	N1-C2-O2	6.03	122.52	118.90
26	A	839	U	N1-C2-O2	6.02	127.01	122.80
26	A	2155	U	N3-C2-O2	-6.01	117.99	122.20
25	B	62	C	N3-C2-O2	-6.01	117.69	121.90
26	A	2689	C	N1-C2-O2	6.01	122.50	118.90
26	A	622	C	C6-N1-C2	-6.00	117.90	120.30
26	A	1410	C	C6-N1-C2	-6.00	117.90	120.30
26	A	387	U	N1-C2-O2	6.00	127.00	122.80
26	A	930	C	C6-N1-C2	-6.00	117.90	120.30
26	A	237	C	C2-N1-C1'	6.00	125.40	118.80
26	A	1535	C	N1-C2-O2	6.00	122.50	118.90
25	B	31	C	C6-N1-C2	-6.00	117.90	120.30
26	A	293	G	N1-C6-O6	-6.00	116.30	119.90
26	A	461	U	N1-C2-O2	6.00	127.00	122.80
26	A	1449	C	C6-N1-C2	-6.00	117.90	120.30
26	A	66	C	C6-N1-C2	-5.99	117.90	120.30
26	A	2940	U	N3-C2-O2	-5.99	118.01	122.20
26	A	2381	A	P-O3'-C3'	5.99	126.88	119.70
26	A	784	G	C8-N9-C1'	-5.98	119.22	127.00
26	A	1158	U	N3-C2-O2	-5.98	118.02	122.20
26	A	1302	G	C4-C5-N7	5.98	113.19	110.80
25	B	106	C	C2-N1-C1'	5.97	125.37	118.80
26	A	845	C	C2-N3-C4	5.97	122.88	119.90
26	A	2116	C	N1-C2-O2	5.97	122.48	118.90
26	A	1531	C	N1-C2-O2	5.96	122.48	118.90
26	A	2602	A	N1-C6-N6	5.96	122.18	118.60
26	A	2622	C	C6-N1-C2	-5.96	117.92	120.30
26	A	1798	U	N3-C2-O2	-5.96	118.03	122.20
26	A	1553	C	N1-C2-O2	5.96	122.47	118.90
26	A	161	U	C2-N1-C1'	5.96	124.85	117.70
3	E	33	LEU	CB-CG-CD2	-5.95	100.88	111.00
26	A	2144	C	C6-N1-C2	-5.95	117.92	120.30
26	A	1801	C	N1-C2-O2	5.95	122.47	118.90
26	A	357	U	P-O3'-C3'	5.94	126.83	119.70
26	A	2734	C	N3-C2-O2	-5.94	117.74	121.90
26	A	1531	C	C6-N1-C2	-5.94	117.92	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2111	U	C2-N1-C1'	5.93	124.82	117.70
26	A	1662	C	C6-N1-C2	-5.93	117.93	120.30
26	A	2407	C	C6-N1-C2	-5.91	117.94	120.30
26	A	279	U	C2-N1-C1'	5.91	124.79	117.70
26	A	2993	U	N1-C2-O2	5.90	126.93	122.80
26	A	617	U	N3-C2-O2	-5.90	118.07	122.20
26	A	2226	U	N1-C2-O2	5.90	126.93	122.80
26	A	1030	C	N1-C2-O2	5.90	122.44	118.90
26	A	1801	C	C2-N1-C1'	5.89	125.28	118.80
26	A	2815	C	C6-N1-C2	-5.89	117.94	120.30
26	A	1467	U	N3-C2-O2	-5.88	118.08	122.20
26	A	2327	C	N3-C2-O2	-5.88	117.78	121.90
26	A	714	U	C2-N1-C1'	5.88	124.75	117.70
26	A	2110	U	C2-N1-C1'	5.85	124.72	117.70
26	A	1529	U	C5-C6-N1	5.85	125.63	122.70
26	A	2419	C	C2-N1-C1'	5.85	125.23	118.80
25	B	31	C	C2-N1-C1'	5.84	125.23	118.80
26	A	930	C	C5-C6-N1	5.84	123.92	121.00
26	A	974	G	P-O3'-C3'	5.84	126.71	119.70
26	A	1816	C	C5-C6-N1	5.84	123.92	121.00
26	A	1167	C	C6-N1-C2	-5.83	117.97	120.30
26	A	2690	C	C6-N1-C2	-5.83	117.97	120.30
26	A	1747	C	C6-N1-C2	-5.82	117.97	120.30
26	A	1625	G	N7-C8-N9	5.82	116.01	113.10
26	A	1082	C	C6-N1-C2	-5.81	117.97	120.30
26	A	2013	C	C6-N1-C2	-5.81	117.97	120.30
26	A	599	G	O4'-C1'-N9	5.81	112.85	108.20
26	A	2430	C	N1-C2-O2	5.81	122.39	118.90
26	A	2138	C	C2-N1-C1'	5.80	125.19	118.80
10	L	67	LYS	CD-CE-NZ	-5.80	98.35	111.70
26	A	504	C	C5-C6-N1	5.78	123.89	121.00
26	A	1521	C	C6-N1-C2	-5.78	117.99	120.30
26	A	7	U	N3-C2-O2	-5.78	118.16	122.20
26	A	1618	C	N1-C2-O2	5.77	122.36	118.90
26	A	2217	U	N3-C2-O2	-5.77	118.16	122.20
21	W	49	LEU	CB-CG-CD2	-5.77	101.19	111.00
26	A	1034	U	N3-C2-O2	-5.76	118.17	122.20
26	A	2744	C	N1-C2-O2	5.76	122.36	118.90
26	A	2927	C	N1-C2-O2	5.75	122.35	118.90
26	A	857	U	C5-C6-N1	5.75	125.58	122.70
26	A	1668	C	C6-N1-C2	-5.75	118.00	120.30
26	A	1045	C	N1-C2-O2	5.75	122.35	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2890	C	C6-N1-C2	-5.75	118.00	120.30
26	A	139	U	C2-N1-C1'	5.74	124.59	117.70
26	A	1321	C	C6-N1-C2	-5.74	118.00	120.30
26	A	200	C	C6-N1-C2	-5.74	118.01	120.30
26	A	2423	C	C5-C6-N1	5.73	123.86	121.00
26	A	1197	C	C6-N1-C2	-5.73	118.01	120.30
26	A	324	C	N3-C2-O2	-5.72	117.89	121.90
26	A	1082	C	C5-C6-N1	5.72	123.86	121.00
26	A	2088	C	N1-C2-O2	5.72	122.33	118.90
26	A	975	U	N3-C2-O2	-5.70	118.21	122.20
26	A	1494	U	N3-C2-O2	-5.69	118.21	122.20
26	A	1560	U	N3-C2-O2	-5.69	118.21	122.20
26	A	1008	G	C6-C5-N7	-5.69	126.99	130.40
26	A	1393	C	C6-N1-C2	-5.69	118.03	120.30
26	A	2350	G	P-O3'-C3'	5.68	126.52	119.70
26	A	2191	C	N1-C2-O2	5.68	122.31	118.90
25	B	69	C	N3-C2-O2	-5.68	117.93	121.90
26	A	1775	C	C5-C6-N1	5.67	123.84	121.00
26	A	417	C	N1-C2-O2	5.67	122.30	118.90
26	A	962	U	C6-N1-C1'	-5.67	113.26	121.20
26	A	939	C	C6-N1-C2	-5.66	118.03	120.30
26	A	1561	C	N1-C2-O2	5.66	122.30	118.90
26	A	332	C	N1-C2-O2	5.66	122.30	118.90
26	A	2144	C	C5-C6-N1	5.65	123.83	121.00
26	A	703	C	N1-C2-O2	5.65	122.29	118.90
26	A	1001	C	N1-C2-O2	5.64	122.29	118.90
26	A	2666	C	N1-C2-O2	5.64	122.29	118.90
26	A	191	G	C4-N9-C1'	5.64	133.84	126.50
26	A	898	A	N7-C8-N9	5.64	116.62	113.80
26	A	2730	U	N3-C2-O2	-5.64	118.25	122.20
26	A	868	C	C6-N1-C2	-5.64	118.04	120.30
26	A	2841	C	N3-C2-O2	-5.64	117.95	121.90
26	A	3035	C	C6-N1-C2	-5.63	118.05	120.30
21	W	49	LEU	CA-CB-CG	5.63	128.25	115.30
26	A	1198	C	C6-N1-C2	-5.63	118.05	120.30
26	A	2632	U	C5-C6-N1	5.63	125.51	122.70
26	A	977	G	N3-C4-N9	5.62	129.37	126.00
26	A	1467	U	C2-N1-C1'	5.62	124.44	117.70
25	B	62	C	C2-N1-C1'	5.61	124.97	118.80
26	A	29	C	C6-N1-C1'	-5.61	114.07	120.80
26	A	1813	C	C6-N1-C2	-5.61	118.06	120.30
26	A	1996	U	C2-N1-C1'	5.61	124.43	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	1045	C	N3-C2-O2	-5.61	117.98	121.90
26	A	3066	C	C6-N1-C2	-5.61	118.06	120.30
26	A	1548	C	N1-C2-O2	5.60	122.26	118.90
26	A	1298	C	C2-N1-C1'	5.59	124.95	118.80
26	A	1386	G	C8-N9-C4	-5.59	104.16	106.40
26	A	2803	C	N1-C2-O2	5.59	122.26	118.90
26	A	937	U	C5-C6-N1	5.59	125.49	122.70
26	A	1651	C	C5-C6-N1	5.59	123.80	121.00
26	A	1775	C	C2-N1-C1'	5.59	124.94	118.80
10	L	110	LYS	N-CA-C	5.58	126.08	111.00
26	A	154	C	C6-N1-C2	-5.58	118.07	120.30
26	A	1429	C	N1-C2-O2	5.58	122.25	118.90
26	A	3048	C	N1-C2-O2	5.58	122.25	118.90
26	A	2245	C	C5-C6-N1	5.57	123.79	121.00
26	A	788	C	C6-N1-C2	-5.57	118.07	120.30
26	A	839	U	C2-N1-C1'	5.57	124.39	117.70
26	A	495	C	C6-N1-C2	-5.57	118.07	120.30
26	A	922	U	N3-C2-O2	-5.57	118.30	122.20
26	A	112	C	C6-N1-C2	-5.57	118.07	120.30
26	A	2290	C	C5-C6-N1	5.56	123.78	121.00
26	A	1212	U	N1-C2-O2	5.55	126.69	122.80
26	A	2842	G	C2-N3-C4	5.55	114.68	111.90
26	A	2842	G	N3-C4-C5	-5.55	125.83	128.60
26	A	234	U	N1-C2-O2	5.55	126.68	122.80
26	A	1862	C	C5-C6-N1	5.55	123.77	121.00
26	A	2181	C	C6-N1-C2	-5.54	118.09	120.30
26	A	2687	U	C5-C6-N1	5.54	125.47	122.70
26	A	1158	U	N1-C2-O2	5.53	126.67	122.80
26	A	929	C	C5-C6-N1	5.53	123.77	121.00
9	K	5	THR	N-CA-C	-5.52	96.09	111.00
26	A	43	C	C6-N1-C2	-5.52	118.09	120.30
26	A	1321	C	C5-C6-N1	5.52	123.76	121.00
26	A	846	C	C6-N1-C2	-5.52	118.09	120.30
26	A	2829	U	N3-C2-O2	-5.51	118.34	122.20
26	A	1816	C	C6-N1-C2	-5.51	118.10	120.30
26	A	1302	G	N9-C4-C5	-5.51	103.20	105.40
26	A	1612	U	N3-C2-O2	-5.51	118.35	122.20
26	A	1843	C	C2-N1-C1'	5.49	124.84	118.80
26	A	2230	C	N1-C2-O2	5.49	122.20	118.90
22	X	85	ARG	C-N-CD	5.49	139.93	128.40
26	A	2752	U	N1-C2-O2	5.49	126.64	122.80
26	A	802	C	N1-C2-O2	5.49	122.19	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2979	C	C5-C6-N1	5.49	123.74	121.00
26	A	3070	G	N3-C4-C5	5.49	131.34	128.60
26	A	2198	C	C6-N1-C2	-5.48	118.11	120.30
15	Q	15	ASP	CB-CG-OD1	5.48	123.23	118.30
26	A	1197	C	C5-C6-N1	5.48	123.74	121.00
26	A	1734	C	C6-N1-C2	-5.48	118.11	120.30
26	A	1801	C	C6-N1-C2	-5.48	118.11	120.30
2	D	156	THR	C-N-CD	5.48	139.90	128.40
26	A	733	U	C5-C6-N1	5.48	125.44	122.70
26	A	2521	C	N1-C2-O2	5.48	122.19	118.90
10	L	12	ASP	CB-CG-OD1	5.46	123.22	118.30
26	A	324	C	C6-N1-C2	-5.46	118.12	120.30
26	A	918	U	C6-N1-C2	-5.46	117.73	121.00
26	A	1816	C	N1-C2-O2	5.45	122.17	118.90
26	A	2625	C	N1-C2-O2	5.45	122.17	118.90
26	A	204	G	O4'-C1'-N9	5.45	112.56	108.20
26	A	1102	G	N3-C4-C5	-5.45	125.88	128.60
26	A	1515	C	C6-N1-C2	-5.45	118.12	120.30
25	B	38	C	N1-C2-O2	5.44	122.16	118.90
26	A	1561	C	N3-C2-O2	-5.43	118.10	121.90
26	A	2665	C	N1-C2-O2	5.43	122.16	118.90
26	A	1991	C	C6-N1-C2	-5.42	118.13	120.30
26	A	1996	U	O4'-C1'-N1	5.42	112.54	108.20
26	A	1366	A	C2-N3-C4	5.42	113.31	110.60
26	A	1766	U	N1-C2-N3	5.42	118.15	114.90
26	A	2116	C	N3-C2-O2	-5.42	118.11	121.90
26	A	1847	U	N1-C2-N3	5.42	118.15	114.90
26	A	2226	U	C5-C6-N1	5.42	125.41	122.70
26	A	2647	U	N3-C2-O2	-5.41	118.41	122.20
26	A	1943	C	N1-C2-O2	5.41	122.14	118.90
26	A	184	C	C6-N1-C2	-5.40	118.14	120.30
26	A	2267	C	N1-C2-O2	5.39	122.13	118.90
26	A	1953	C	C6-N1-C2	-5.39	118.14	120.30
26	A	957	C	C5-C6-N1	5.39	123.69	121.00
26	A	1904	C	N3-C2-O2	-5.39	118.13	121.90
26	A	2362	C	C6-N1-C2	-5.39	118.14	120.30
26	A	845	C	N3-C2-O2	-5.38	118.13	121.90
26	A	1521	C	C6-N1-C1'	-5.38	114.34	120.80
26	A	1694	C	C5-C6-N1	5.38	123.69	121.00
26	A	514	C	N1-C2-O2	5.38	122.13	118.90
26	A	2327	C	C5-C6-N1	5.37	123.69	121.00
26	A	1220	C	C6-N1-C2	-5.37	118.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2360	C	C5-C6-N1	5.37	123.68	121.00
26	A	3016	C	C6-N1-C2	-5.36	118.16	120.30
26	A	905	U	C6-N1-C1'	-5.36	113.69	121.20
26	A	1898	U	N3-C2-O2	-5.36	118.45	122.20
26	A	2571	C	N1-C2-O2	5.36	122.12	118.90
26	A	97	U	P-O3'-C3'	5.35	126.12	119.70
26	A	2886	A	C8-N9-C4	-5.35	103.66	105.80
21	W	58	LEU	CB-CG-CD2	-5.34	101.92	111.00
26	A	2472	C	C2-N1-C1'	5.34	124.68	118.80
26	A	191	G	C8-N9-C1'	-5.34	120.06	127.00
26	A	984	U	C5-C6-N1	5.34	125.37	122.70
26	A	2118	C	N1-C2-O2	5.34	122.10	118.90
26	A	2322	C	C6-N1-C1'	-5.34	114.40	120.80
26	A	2890	C	C2-N1-C1'	5.33	124.67	118.80
26	A	1977	C	C6-N1-C2	-5.33	118.17	120.30
26	A	1926	C	C6-N1-C2	-5.32	118.17	120.30
26	A	1298	C	C6-N1-C2	-5.32	118.17	120.30
26	A	2472	C	C5-C6-N1	5.32	123.66	121.00
32	6	15	ARG	CB-CG-CD	-5.32	97.77	111.60
10	L	108	GLU	N-CA-C	-5.32	96.64	111.00
26	A	2435	U	C2-N1-C1'	5.32	124.08	117.70
26	A	2967	C	C6-N1-C2	-5.32	118.17	120.30
26	A	236	C	C5-C6-N1	5.32	123.66	121.00
26	A	1260	C	C2-N1-C1'	5.32	124.65	118.80
26	A	2736	C	C5-C6-N1	5.32	123.66	121.00
26	A	996	G	C4-N9-C1'	5.31	133.41	126.50
26	A	1276	G	C4-C5-N7	5.31	112.92	110.80
26	A	2698	C	C2-N1-C1'	5.31	124.64	118.80
26	A	425	U	C5-C6-N1	5.31	125.36	122.70
26	A	1651	C	C6-N1-C2	-5.31	118.18	120.30
6	H	124	ILE	C-N-CA	5.31	134.97	121.70
26	A	1409	C	C2-N1-C1'	5.30	124.63	118.80
26	A	2690	C	C5-C6-N1	5.30	123.65	121.00
9	K	1	MET	C-N-CD	5.30	139.53	128.40
26	A	472	C	C6-N1-C2	-5.30	118.18	120.30
3	E	19	GLU	C-N-CA	5.29	134.93	121.70
26	A	505	C	C6-N1-C2	-5.29	118.18	120.30
26	A	231	U	C2-N1-C1'	5.28	124.04	117.70
26	A	192	U	C2-N1-C1'	5.28	124.04	117.70
26	A	929	C	C6-N1-C2	-5.28	118.19	120.30
26	A	1485	C	C5-C6-N1	5.28	123.64	121.00
26	A	205	U	N1-C2-O2	5.28	126.49	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	952	C	C6-N1-C2	-5.28	118.19	120.30
26	A	1008	G	N3-C4-N9	5.28	129.16	126.00
26	A	2375	G	C6-C5-N7	-5.27	127.23	130.40
26	A	472	C	C6-N1-C1'	-5.27	114.47	120.80
30	4	8	ARG	C-N-CD	5.27	139.47	128.40
26	A	2138	C	N3-C2-O2	-5.27	118.21	121.90
26	A	3116	C	C6-N1-C2	-5.26	118.19	120.30
26	A	438	U	N1-C2-O2	5.26	126.48	122.80
26	A	1094	G	C4-C5-N7	5.26	112.90	110.80
26	A	274	C	C2-N1-C1'	5.25	124.58	118.80
26	A	1320	U	C5-C6-N1	5.25	125.33	122.70
26	A	2262	C	C5-C6-N1	5.25	123.62	121.00
26	A	1266	C	C6-N1-C2	-5.25	118.20	120.30
26	A	1008	G	C8-N9-C1'	-5.25	120.18	127.00
26	A	1065	C	C5-C6-N1	5.25	123.62	121.00
26	A	1449	C	C5-C6-N1	5.24	123.62	121.00
26	A	2138	C	C6-N1-C2	-5.24	118.20	120.30
26	A	2087	C	C6-N1-C1'	-5.24	114.51	120.80
26	A	2487	C	N3-C2-O2	-5.24	118.23	121.90
26	A	2780	C	C6-N1-C2	-5.24	118.21	120.30
26	A	277	U	C5-C6-N1	5.23	125.31	122.70
25	B	78	U	N3-C2-O2	-5.23	118.54	122.20
26	A	324	C	N1-C2-O2	5.23	122.04	118.90
26	A	275	C	N3-C2-O2	-5.22	118.25	121.90
26	A	787	C	C6-N1-C2	-5.22	118.21	120.30
26	A	658	U	C2-N1-C1'	5.22	123.96	117.70
26	A	2260	C	N3-C2-O2	-5.21	118.25	121.90
26	A	101	U	N1-C2-O2	5.21	126.45	122.80
26	A	2107	G	C2-N3-C4	-5.21	109.30	111.90
26	A	79	G	C8-N9-C4	-5.21	104.32	106.40
18	T	7	PHE	C-N-CD	5.21	139.33	128.40
26	A	2274	C	C6-N1-C2	-5.21	118.22	120.30
32	6	62	LEU	CA-CB-CG	5.20	127.27	115.30
26	A	2366	C	N1-C2-O2	5.20	122.02	118.90
26	A	547	U	N1-C2-O2	5.20	126.44	122.80
26	A	1467	U	N1-C2-O2	5.20	126.44	122.80
26	A	417	C	N3-C2-O2	-5.19	118.26	121.90
26	A	1553	C	N3-C2-O2	-5.19	118.26	121.90
26	A	2782	C	C6-N1-C2	-5.19	118.22	120.30
26	A	1212	U	C2-N1-C1'	5.19	123.92	117.70
26	A	102	C	N3-C2-O2	-5.19	118.27	121.90
26	A	1662	C	C5-C6-N1	5.18	123.59	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2118	C	N3-C2-O2	-5.18	118.27	121.90
26	A	472	C	C5-C6-N1	5.18	123.59	121.00
26	A	572	C	C5-C6-N1	5.17	123.59	121.00
26	A	197	C	C2-N1-C1'	5.17	124.48	118.80
26	A	407	C	C6-N1-C2	-5.17	118.23	120.30
26	A	1030	C	C6-N1-C1'	-5.17	114.60	120.80
26	A	1478	C	N1-C2-O2	5.17	122.00	118.90
26	A	3048	C	C5-C6-N1	5.17	123.58	121.00
1	C	94	LEU	CB-CG-CD1	-5.17	102.22	111.00
26	A	1382	U	N3-C2-O2	-5.17	118.58	122.20
26	A	1991	C	N3-C2-O2	-5.17	118.28	121.90
26	A	599	G	N1-C6-O6	-5.17	116.80	119.90
26	A	3045	C	C5-C6-N1	5.16	123.58	121.00
26	A	184	C	C5-C6-N1	5.16	123.58	121.00
26	A	608	C	N1-C2-O2	5.16	122.00	118.90
26	A	961	U	C2-N1-C1'	5.16	123.89	117.70
26	A	1102	G	C2-N3-C4	5.16	114.48	111.90
26	A	1429	C	C6-N1-C1'	-5.16	114.61	120.80
26	A	1953	C	C5-C6-N1	5.16	123.58	121.00
26	A	2012	C	C6-N1-C2	-5.16	118.24	120.30
26	A	2147	U	C5-C6-N1	5.16	125.28	122.70
26	A	3034	C	C5-C6-N1	5.16	123.58	121.00
26	A	1276	G	C6-C5-N7	-5.16	127.31	130.40
26	A	1903	C	N1-C2-O2	5.16	121.99	118.90
26	A	2940	U	N1-C2-O2	5.16	126.41	122.80
26	A	927	C	C6-N1-C2	-5.15	118.24	120.30
26	A	2226	U	N3-C2-O2	-5.15	118.59	122.20
26	A	326	A	C8-N9-C4	-5.15	103.74	105.80
26	A	802	C	C2-N1-C1'	5.15	124.46	118.80
26	A	1298	C	N1-C2-O2	5.15	121.99	118.90
26	A	1817	C	C5-C6-N1	5.15	123.58	121.00
26	A	387	U	N3-C2-O2	-5.15	118.60	122.20
26	A	703	C	C6-N1-C1'	-5.15	114.62	120.80
26	A	1001	C	N3-C2-O2	-5.14	118.30	121.90
3	E	93	PRO	C-N-CA	5.14	134.56	121.70
26	A	747	A	C4-C5-N7	5.14	113.27	110.70
26	A	1837	G	N9-C4-C5	-5.14	103.34	105.40
26	A	643	G	C4-C5-N7	5.14	112.86	110.80
26	A	685	G	C4-N9-C1'	5.14	133.18	126.50
26	A	1103	C	C2-N1-C1'	5.14	124.45	118.80
26	A	2697	U	C5-C6-N1	5.13	125.27	122.70
1	C	35	ARG	C-N-CD	5.13	139.18	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	U	6	ASP	C-N-CD	5.13	139.18	128.40
26	A	2077	C	C5-C6-N1	5.13	123.57	121.00
26	A	2780	C	N1-C2-O2	5.13	121.98	118.90
26	A	2158	C	N3-C2-O2	-5.12	118.31	121.90
26	A	472	C	N3-C2-O2	-5.12	118.31	121.90
26	A	1030	C	C5-C6-N1	5.12	123.56	121.00
26	A	1460	C	C2-N1-C1'	5.12	124.43	118.80
26	A	2993	U	N3-C2-O2	-5.12	118.62	122.20
26	A	912	C	C4-C5-C6	-5.11	114.84	117.40
26	A	2913	U	N1-C2-O2	5.11	126.38	122.80
26	A	318	U	N1-C2-O2	5.11	126.38	122.80
26	A	83	C	C5-C6-N1	5.11	123.55	121.00
26	A	127	C	C5-C6-N1	5.11	123.55	121.00
26	A	1521	C	C5-C6-N1	5.11	123.55	121.00
26	A	186	G	C4-C5-N7	5.10	112.84	110.80
26	A	2087	C	C5-C6-N1	5.10	123.55	121.00
26	A	2260	C	N1-C2-O2	5.10	121.96	118.90
26	A	2680	C	C2-N1-C1'	5.09	124.41	118.80
25	B	4	A	N1-C6-N6	5.09	121.65	118.60
26	A	199	U	N1-C2-O2	5.09	126.36	122.80
26	A	2839	U	N1-C2-O2	5.09	126.36	122.80
26	A	2485	C	N3-C2-O2	-5.08	118.34	121.90
26	A	609	G	N3-C4-N9	5.08	129.05	126.00
26	A	1283	C	C6-N1-C2	-5.08	118.27	120.30
26	A	1534	C	N3-C2-O2	-5.08	118.34	121.90
26	A	1862	C	N1-C2-O2	5.08	121.95	118.90
26	A	2430	C	N3-C2-O2	-5.08	118.34	121.90
26	A	1837	G	N3-C4-N9	5.08	129.05	126.00
26	A	2118	C	C6-N1-C2	-5.08	118.27	120.30
26	A	2243	C	C2-N1-C1'	5.08	124.39	118.80
26	A	2419	C	N1-C2-O2	5.08	121.94	118.90
26	A	2717	U	C6-N1-C2	-5.08	117.95	121.00
26	A	1102	G	N3-C4-N9	5.07	129.04	126.00
26	A	3036	C	C6-N1-C2	-5.07	118.27	120.30
28	2	42	HIS	C-N-CD	5.07	139.05	128.40
26	A	2086	U	C6-N1-C2	-5.07	117.96	121.00
26	A	1403	C	C2-N1-C1'	5.07	124.37	118.80
26	A	2923	C	C5-C6-N1	5.07	123.53	121.00
26	A	646	U	N3-C2-O2	-5.07	118.65	122.20
26	A	977	G	N3-C4-C5	-5.06	126.07	128.60
26	A	2005	C	C2-N1-C1'	5.06	124.37	118.80
26	A	759	G	N3-C4-C5	5.06	131.13	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2698	C	N1-C2-O2	5.06	121.94	118.90
26	A	1819	G	N1-C6-O6	-5.05	116.87	119.90
26	A	197	C	N1-C2-O2	5.05	121.93	118.90
26	A	1695	U	N1-C2-O2	5.05	126.34	122.80
26	A	779	U	N1-C2-O2	5.05	126.33	122.80
26	A	2402	C	N1-C2-O2	5.05	121.93	118.90
26	A	3029	U	N1-C2-O2	5.05	126.33	122.80
30	4	32	ASP	C-N-CD	5.04	138.98	128.40
26	A	853	C	C6-N1-C2	-5.03	118.29	120.30
26	A	1485	C	C2-N1-C1'	5.03	124.34	118.80
26	A	2800	G	C4-N9-C1'	5.03	133.04	126.50
25	B	73	G	N3-C4-N9	5.02	129.01	126.00
26	A	2295	C	N3-C2-O2	-5.02	118.38	121.90
26	A	2288	C	N3-C2-O2	-5.02	118.39	121.90
3	E	155	LEU	CB-CG-CD1	-5.01	102.48	111.00
26	A	54	C	C6-N1-C2	-5.01	118.30	120.30
26	A	1239	C	N1-C2-O2	5.01	121.90	118.90
26	A	1467	U	C5-C6-N1	5.00	125.20	122.70
26	A	1753	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	ALA	Peptide
1	C	229	VAL	Peptide
1	C	246	PRO	Peptide
1	C	61	ALA	Peptide
2	D	153	GLY	Peptide
2	D	156	THR	Peptide
3	E	131	VAL	Peptide
3	E	137	SER	Peptide
3	E	158	ILE	Peptide
3	E	162	ASP	Peptide
3	E	93	PRO	Peptide
4	F	81	ILE	Peptide
9	K	91	GLU	Peptide
12	N	78	PRO	Peptide
13	O	61	HIS	Peptide
18	T	95	ARG	Peptide
22	X	83	VAL	Peptide
22	X	84	ALA	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2097	0	2147	211	0
2	D	1587	0	1629	66	0
3	E	1553	0	1586	145	0
4	F	1437	0	1463	210	0
5	G	1348	0	1399	27	0
6	H	1018	0	988	12	0
7	I	918	0	959	14	0
8	J	990	0	1021	28	0
9	K	1138	0	1174	115	0
10	L	930	0	989	57	0
11	M	1078	0	1151	46	0
12	N	1074	0	1116	63	0
13	O	919	0	959	151	0
14	P	956	0	989	41	0
15	Q	907	0	938	30	0
16	R	988	0	1038	19	0
17	S	768	0	820	46	0
18	T	873	0	909	57	0
19	U	739	0	777	119	0
20	V	731	0	782	114	0
21	W	1407	0	1423	155	0
22	X	604	0	622	56	0
23	Y	470	0	484	9	0
24	Z	527	0	537	54	0
25	B	2501	0	1269	297	0
26	A	66623	0	33514	1028	0
27	1	483	0	513	22	0
28	2	510	0	497	61	0
29	3	423	0	463	12	0
30	4	416	0	421	95	0
31	5	372	0	406	41	0
32	6	502	0	541	32	0
33	7	298	0	320	25	0
34	8	189	0	205	4	0
All	All	97374	0	64049	2838	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 18.

All (2838) 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)
17:S:3:THR:CG2	17:S:102:ILE:HD13	1.26	1.66
19:U:83:ILE:HD11	26:A:1456:G:C2	1.14	1.64
26:A:1561:C:C4	26:A:1562:C:C5	1.86	1.62
26:A:1565:A:N3	26:A:1606:G:C5	1.69	1.60
17:S:58:VAL:HG23	17:S:103:LYS:CG	1.24	1.60
26:A:1561:C:C4	26:A:1562:C:H5	1.16	1.59
13:O:29:PHE:CB	13:O:79:LEU:HD12	1.29	1.54
4:F:117:ARG:NH1	4:F:146:HIS:CD2	1.72	1.54
3:E:192:ASP:HB3	11:M:5:LYS:NZ	1.21	1.53
3:E:144:PHE:CG	3:E:148:LEU:HD11	1.42	1.53
20:V:4:HIS:CE1	20:V:96:ARG:NH1	1.75	1.53
26:A:1580:A:N6	26:A:1592:G:C5	1.78	1.51
19:U:83:ILE:CD1	26:A:1456:G:C2	1.85	1.51
33:7:22:ARG:NH2	33:7:37:GLY:HA2	1.25	1.51
17:S:3:THR:CG2	17:S:102:ILE:CD1	1.83	1.51
21:W:77:LEU:HB3	21:W:100:VAL:CG2	1.40	1.48
1:C:25:THR:HG21	1:C:81:HIS:CA	1.44	1.47
17:S:3:THR:HG22	17:S:102:ILE:CD1	1.38	1.47
20:V:4:HIS:CE1	20:V:96:ARG:HH12	1.32	1.45
3:E:144:PHE:CD1	3:E:148:LEU:HD21	1.51	1.44
17:S:58:VAL:CG2	17:S:103:LYS:HG2	1.48	1.43
4:F:132:THR:CG2	14:P:6:VAL:HG21	1.48	1.43
3:E:182:GLN:NE2	26:A:706:G:H8	1.06	1.43
2:D:154:CYS:CB	26:A:2798:G:O3'	1.68	1.42
25:B:20:G:N2	25:B:63:U:H3	1.11	1.42
26:A:1580:A:N6	26:A:1592:G:C4	1.85	1.42
9:K:142:ILE:CG2	26:A:1130:C:H41	1.33	1.41
26:A:1565:A:N3	26:A:1606:G:C6	1.86	1.41
19:U:4:ILE:HD13	24:Z:58:TYR:CE1	1.57	1.40
20:V:2:LYS:HD2	20:V:83:VAL:CG1	1.52	1.39
2:D:155:ALA:CB	26:A:2796:A:C8	2.02	1.39
19:U:19:LYS:HD2	26:A:1508:A:N6	1.30	1.39
25:B:18:C:C2'	25:B:19:G:H5''	1.51	1.37
4:F:51:ALA:O	4:F:85:LYS:NZ	1.58	1.36
25:B:24:G:C5	25:B:56:C:O2	1.75	1.36
1:C:26:ARG:HD2	1:C:81:HIS:CD2	1.61	1.35
19:U:83:ILE:HD11	26:A:1456:G:N2	1.42	1.34
13:O:29:PHE:HB3	13:O:79:LEU:CD1	1.54	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:29:C:N3	25:B:55:G:N2	1.76	1.34
26:A:1578:G:C4	26:A:1592:G:N1	1.97	1.33
13:O:90:ARG:NH2	13:O:118:GLU:HG3	1.41	1.32
13:O:90:ARG:HH22	13:O:118:GLU:CG	1.39	1.32
19:U:4:ILE:HD13	24:Z:58:TYR:CZ	1.63	1.32
4:F:183:PRO:O	4:F:184:PHE:CD2	1.79	1.32
26:A:1580:A:C6	26:A:1592:G:C4	2.17	1.31
25:B:4:A:C2	25:B:25:G:O6	1.84	1.31
3:E:144:PHE:CE1	3:E:148:LEU:HD21	1.66	1.30
13:O:29:PHE:CG	13:O:79:LEU:HD11	1.65	1.30
25:B:24:G:N7	25:B:56:C:O2	1.64	1.29
13:O:29:PHE:CB	13:O:79:LEU:CD1	2.07	1.29
13:O:81:ALA:O	13:O:85:PRO:CD	1.79	1.29
22:X:17:ALA:CB	26:A:2485:C:OP2	1.80	1.29
9:K:142:ILE:CG2	26:A:1130:C:N4	1.94	1.28
26:A:1561:C:C5	26:A:1562:C:H5	1.49	1.28
26:A:1570:C:N4	26:A:1602:U:O2	1.66	1.28
19:U:83:ILE:HD11	26:A:1456:G:N3	1.48	1.28
26:A:1595:G:H5''	26:A:1596:C:C6	1.68	1.27
25:B:18:C:H2'	25:B:19:G:C5'	1.63	1.27
30:4:15:CYS:O	30:4:20:HIS:CB	1.82	1.27
30:4:15:CYS:O	30:4:20:HIS:HB2	1.27	1.27
26:A:1565:A:C2	26:A:1606:G:N7	2.01	1.26
2:D:154:CYS:N	26:A:2798:G:O2'	1.67	1.26
19:U:19:LYS:NZ	26:A:1508:A:H61	1.31	1.26
4:F:73:GLU:HG2	25:B:42:C:C5	1.71	1.26
4:F:183:PRO:O	4:F:184:PHE:HD2	0.92	1.26
19:U:19:LYS:CD	26:A:1508:A:N6	1.98	1.26
25:B:19:G:N2	25:B:65:C:N3	1.83	1.26
13:O:33:ARG:HD3	13:O:114:GLU:OE2	1.19	1.26
13:O:75:VAL:O	13:O:79:LEU:HB3	1.09	1.25
1:C:25:THR:CG2	1:C:81:HIS:HB3	1.66	1.25
13:O:29:PHE:CG	13:O:79:LEU:CD1	2.16	1.25
3:E:151:ASN:O	3:E:152:LYS:CG	1.83	1.25
13:O:33:ARG:CD	13:O:114:GLU:OE2	1.84	1.25
26:A:1595:G:H8	26:A:1596:C:C6	1.54	1.24
13:O:81:ALA:O	13:O:85:PRO:HD2	1.11	1.24
26:A:1580:A:C6	26:A:1591:U:O2	1.91	1.24
4:F:46:GLY:O	4:F:47:VAL:CG2	1.86	1.23
25:B:40:A:N6	28:2:1:MET:H2	1.37	1.23
26:A:1570:C:N4	26:A:1602:U:C2	2.07	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:THR:HG21	1:C:81:HIS:CB	1.69	1.22
17:S:58:VAL:CG2	17:S:103:LYS:CG	2.07	1.22
26:A:1561:C:N3	26:A:1562:C:C5	2.06	1.21
9:K:142:ILE:HG21	26:A:1130:C:N4	1.50	1.21
1:C:96:HIS:CE1	1:C:102:LYS:HZ3	1.57	1.21
2:D:154:CYS:HB2	26:A:2799:C:P	1.80	1.20
14:P:41:ASN:ND2	25:B:7:G:O2'	1.73	1.20
21:W:6:ASN:HB2	21:W:138:LEU:O	1.36	1.20
26:A:1565:A:C2	26:A:1606:G:C5	2.28	1.20
13:O:8:PRO:HG3	26:A:1870:U:C4	1.75	1.20
3:E:144:PHE:CE1	3:E:148:LEU:CD2	2.23	1.20
10:L:7:ARG:NH2	10:L:20:LEU:HD12	1.55	1.20
14:P:50:GLN:NE2	25:B:7:G:H21	1.38	1.20
26:A:1590:G:C5	26:A:1591:U:H5	1.58	1.20
4:F:51:ALA:C	4:F:85:LYS:NZ	1.87	1.20
1:C:72:LYS:HG3	1:C:75:VAL:HG21	1.21	1.19
2:D:154:CYS:SG	26:A:2796:A:H5''	1.80	1.19
21:W:100:VAL:CG1	21:W:137:ALA:HB1	1.71	1.19
25:B:24:G:HO2'	25:B:56:C:N4	1.37	1.19
25:B:25:G:N2	25:B:114:A:N3	1.88	1.19
25:B:24:G:O2'	25:B:56:C:N4	1.74	1.19
1:C:54:LYS:HZ2	26:A:2031:G:C4'	1.55	1.19
3:E:151:ASN:O	3:E:152:LYS:HG3	1.01	1.19
8:J:96:LYS:CE	21:W:120:PRO:HB2	1.73	1.19
2:D:154:CYS:HB3	26:A:2798:G:C3'	1.72	1.18
2:D:155:ALA:CB	26:A:2796:A:N7	2.04	1.18
21:W:105:LYS:HZ1	21:W:136:GLU:CD	1.46	1.18
3:E:182:GLN:NE2	26:A:706:G:C8	1.97	1.17
26:A:1595:G:H5''	26:A:1596:C:C5	1.80	1.17
33:7:22:ARG:NH2	33:7:37:GLY:CA	2.01	1.17
1:C:25:THR:CG2	1:C:81:HIS:CB	2.20	1.17
12:N:85:SER:OG	22:X:8:SER:HB3	1.43	1.16
2:D:154:CYS:HB3	26:A:2798:G:O3'	1.24	1.16
26:A:1580:A:N6	26:A:1591:U:C2	2.13	1.16
1:C:73:ASP:HB3	1:C:120:GLY:CA	1.76	1.16
9:K:142:ILE:HG22	26:A:1130:C:H41	1.03	1.16
21:W:6:ASN:CB	21:W:138:LEU:O	1.93	1.16
4:F:46:GLY:O	4:F:47:VAL:HG22	1.00	1.15
9:K:141:GLU:CD	9:K:143:LYS:HG2	1.66	1.15
22:X:17:ALA:HB2	26:A:2485:C:OP2	1.34	1.15
3:E:144:PHE:CD1	3:E:148:LEU:HD11	1.80	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:7:ARG:HH22	10:L:20:LEU:HD12	1.00	1.15
1:C:258:ARG:HA	26:A:2015:U:H5''	1.28	1.15
13:O:9:ARG:HG2	13:O:14:SER:HB3	1.25	1.15
19:U:91:LYS:HG2	19:U:92:PRO:CD	1.77	1.15
20:V:45:THR:O	26:A:571:A:O2'	1.65	1.15
26:A:1578:G:C4	26:A:1592:G:C2	2.26	1.15
33:7:22:ARG:HH22	33:7:37:GLY:CA	1.49	1.15
3:E:7:VAL:HG23	3:E:16:GLY:C	1.65	1.15
2:D:155:ALA:HB3	26:A:2796:A:H8	1.08	1.14
9:K:3:THR:CG2	26:A:1113:C:O2	1.96	1.14
21:W:105:LYS:CE	21:W:136:GLU:OE2	1.96	1.14
30:4:29:ARG:HH21	30:4:34:ASP:CB	1.58	1.14
19:U:4:ILE:CD1	24:Z:58:TYR:CE1	2.31	1.14
26:A:1601:G:C2'	26:A:1602:U:H5'	1.78	1.14
28:2:41:CYS:HB3	28:2:43:PRO:HD2	1.29	1.14
2:D:154:CYS:HA	26:A:2799:C:H5'	1.17	1.13
4:F:132:THR:HG21	14:P:6:VAL:CG2	1.75	1.13
26:A:1595:G:C8	26:A:1596:C:C6	2.36	1.13
4:F:45:MET:CE	4:F:64:LEU:HD21	1.78	1.13
26:A:1595:G:C8	26:A:1596:C:H6	1.66	1.13
30:4:19:LYS:CD	30:4:44:ASN:HB2	1.77	1.13
19:U:19:LYS:CE	26:A:1508:A:H61	1.60	1.13
26:A:1590:G:C5	26:A:1591:U:C5	2.36	1.12
26:A:1595:G:C5'	26:A:1596:C:C6	2.31	1.13
17:S:3:THR:HG21	17:S:102:ILE:CD1	1.62	1.12
21:W:77:LEU:CB	21:W:100:VAL:HG23	1.79	1.12
25:B:19:G:H2'	25:B:20:G:H5'	1.32	1.12
20:V:4:HIS:CE1	20:V:96:ARG:CZ	2.33	1.12
21:W:105:LYS:NZ	21:W:136:GLU:CD	2.03	1.12
1:C:96:HIS:CE1	1:C:102:LYS:NZ	2.16	1.11
9:K:25:LEU:O	26:A:1258:C:OP1	1.65	1.11
13:O:79:LEU:HG	13:O:83:ILE:HD12	1.27	1.11
26:A:1580:A:N1	26:A:1592:G:C1'	2.14	1.11
9:K:141:GLU:OE1	9:K:143:LYS:HG2	1.50	1.11
13:O:90:ARG:NH2	13:O:118:GLU:CG	2.04	1.11
14:P:42:ARG:NH1	25:B:48:C:OP1	1.83	1.11
2:D:154:CYS:CA	26:A:2799:C:H5'	1.80	1.11
25:B:4:A:H2	25:B:25:G:O6	1.24	1.11
25:B:10:G:N1	25:B:107:A:C2	2.17	1.11
25:B:58:A:C5	25:B:59:A:N7	2.19	1.11
3:E:144:PHE:CD1	3:E:148:LEU:CD2	2.31	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:100:VAL:CG1	21:W:137:ALA:CB	2.27	1.11
21:W:101:GLN:HB3	21:W:104:GLU:HB2	1.30	1.10
13:O:90:ARG:NH2	13:O:118:GLU:CB	2.14	1.10
26:A:1601:G:H2'	26:A:1602:U:H5'	1.31	1.10
2:D:155:ALA:HB2	26:A:2796:A:C8	1.78	1.10
9:K:112:ASN:ND2	26:A:650:G:OP1	1.84	1.10
26:A:1581:C:H42	26:A:1591:U:H1'	1.14	1.10
17:S:103:LYS:HZ3	17:S:103:LYS:HA	1.06	1.10
3:E:192:ASP:CB	11:M:5:LYS:NZ	2.14	1.09
1:C:25:THR:HG23	1:C:81:HIS:HB3	1.17	1.09
21:W:9:ASN:ND2	21:W:57:VAL:HG13	1.66	1.09
24:Z:6:THR:HG22	24:Z:10:LEU:HD11	1.21	1.09
24:Z:13:LEU:HD11	24:Z:17:GLU:HB2	1.34	1.09
30:4:15:CYS:CB	30:4:20:HIS:HA	1.83	1.09
1:C:25:THR:CG2	1:C:81:HIS:CA	2.30	1.09
20:V:28:PRO:HG2	26:A:83:C:OP1	1.49	1.09
25:B:57:U:H2'	25:B:58:A:H5''	1.35	1.09
25:B:78:U:O2	26:A:977:G:O2'	1.71	1.09
26:A:1580:A:N6	26:A:1592:G:N7	1.99	1.09
1:C:26:ARG:CD	1:C:81:HIS:CD2	2.36	1.08
3:E:7:VAL:N	3:E:16:GLY:O	1.84	1.08
26:A:2510:A:P	30:4:31:ASN:OD1	2.10	1.08
30:4:19:LYS:HD2	30:4:44:ASN:HB2	1.10	1.08
25:B:40:A:N6	28:2:1:MET:N	2.01	1.08
26:A:1580:A:N6	26:A:1592:G:C8	2.07	1.08
30:4:15:CYS:HB2	30:4:20:HIS:HA	1.35	1.08
9:K:13:ARG:NH2	9:K:49:ASP:O	1.86	1.08
20:V:4:HIS:ND1	20:V:96:ARG:NH1	2.02	1.08
13:O:75:VAL:O	13:O:79:LEU:CB	2.01	1.08
17:S:59:ALA:O	17:S:103:LYS:NZ	1.87	1.07
21:W:100:VAL:HG12	21:W:137:ALA:CB	1.84	1.07
25:B:58:A:H5'	25:B:58:A:H8	1.17	1.07
1:C:30:GLU:OE1	1:C:33:LEU:HD12	1.54	1.07
4:F:73:GLU:OE1	25:B:41:U:H5	1.35	1.07
19:U:19:LYS:HZ2	26:A:1508:A:N6	1.52	1.07
26:A:1580:A:N6	26:A:1591:U:O2	1.87	1.07
2:D:155:ALA:HB3	26:A:2796:A:C8	1.81	1.07
21:W:100:VAL:HG12	21:W:137:ALA:HB2	1.37	1.07
4:F:46:GLY:C	4:F:47:VAL:HG22	1.74	1.06
10:L:80:ASP:OD2	15:Q:61:ARG:NH1	1.86	1.06
21:W:77:LEU:CB	21:W:100:VAL:CG2	2.33	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:45:MET:HE3	4:F:64:LEU:HD21	1.34	1.06
20:V:62:GLN:HG2	20:V:63:GLU:N	1.53	1.06
26:A:1565:A:C2	26:A:1606:G:C8	2.44	1.06
4:F:132:THR:HG21	14:P:6:VAL:HG21	1.10	1.06
11:M:51:GLU:CG	32:6:57:ARG:NH1	2.19	1.06
14:P:42:ARG:HH12	25:B:48:C:P	1.77	1.06
17:S:6:ILE:O	17:S:7:VAL:HG23	1.54	1.06
3:E:144:PHE:CG	3:E:148:LEU:CD1	2.38	1.06
4:F:99:ARG:HD2	25:B:45:G:C8	1.89	1.06
21:W:37:LEU:CD1	21:W:69:LEU:CD1	2.33	1.06
1:C:55:GLY:HA3	1:C:218:ARG:CD	1.86	1.05
4:F:132:THR:HG22	14:P:6:VAL:HG21	1.37	1.05
26:A:1581:C:H42	26:A:1591:U:C1'	1.69	1.05
26:A:1608:U:H2'	26:A:1609:G:H8	1.16	1.05
26:A:1608:U:H2'	26:A:1609:G:C8	1.90	1.05
21:W:77:LEU:HB3	21:W:100:VAL:HG21	1.30	1.05
20:V:28:PRO:CG	26:A:83:C:OP1	2.03	1.05
30:4:11:ILE:HD13	30:4:27:LYS:HG2	1.37	1.05
20:V:2:LYS:CD	20:V:83:VAL:HG11	1.85	1.05
26:A:1570:C:N4	26:A:1602:U:H3	1.53	1.05
26:A:1570:C:N4	26:A:1602:U:N3	2.03	1.05
4:F:73:GLU:HG2	25:B:42:C:C6	1.91	1.04
21:W:101:GLN:O	21:W:101:GLN:NE2	1.87	1.04
21:W:102:ARG:NH2	21:W:138:LEU:HD11	1.72	1.04
26:A:1580:A:N6	26:A:1592:G:N9	2.03	1.04
26:A:1595:G:C3'	26:A:1596:C:H5'	1.87	1.04
4:F:138:GLY:HA3	26:A:2529:A:H5''	1.38	1.04
19:U:91:LYS:CG	19:U:92:PRO:HD2	1.87	1.04
26:A:1595:G:H3'	26:A:1596:C:H5'	1.07	1.04
3:E:150:GLU:O	3:E:193:ASP:OD2	1.75	1.04
4:F:118:ILE:H	4:F:118:ILE:HD12	1.17	1.04
19:U:19:LYS:CE	26:A:1508:A:N6	2.20	1.04
2:D:154:CYS:HB3	26:A:2798:G:C2'	1.88	1.04
4:F:49:ASP:HB2	4:F:56:LEU:HD11	1.09	1.04
26:A:1572:G:O6	26:A:1600:G:N1	1.91	1.04
1:C:54:LYS:HZ2	26:A:2031:G:H4'	1.10	1.03
9:K:141:GLU:OE2	9:K:143:LYS:CG	2.06	1.03
17:S:58:VAL:HG23	17:S:103:LYS:HG3	1.07	1.03
21:W:105:LYS:NZ	21:W:136:GLU:OE2	1.92	1.03
18:T:18:ARG:NH1	26:A:1436:C:O2'	1.92	1.03
26:A:1580:A:N6	26:A:1591:U:N3	2.06	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:19:G:H5'	25:B:19:G:H8	1.23	1.03
12:N:60:ARG:HH12	26:A:1193:C:H5''	1.18	1.02
25:B:10:G:N1	25:B:107:A:H2	1.52	1.02
10:L:7:ARG:HH22	10:L:20:LEU:CD1	1.72	1.02
13:O:90:ARG:HH22	13:O:118:GLU:HG3	0.87	1.02
21:W:188:GLU:O	21:W:192:GLU:OE1	1.76	1.02
25:B:60:G:O2'	25:B:61:C:H5'	1.55	1.02
26:A:1590:G:C4	26:A:1591:U:C5	2.47	1.02
21:W:100:VAL:HG11	21:W:137:ALA:HB1	1.38	1.02
9:K:141:GLU:OE2	9:K:143:LYS:HG2	1.58	1.02
19:U:5:THR:HG22	19:U:6:ASP:H	1.24	1.02
26:A:1561:C:C2	26:A:1562:C:C6	2.48	1.02
26:A:1565:A:N3	26:A:1606:G:N7	2.04	1.02
2:D:155:ALA:HB1	26:A:2796:A:N7	1.71	1.01
13:O:16:HIS:HD2	26:A:1390:A:C8	1.77	1.01
26:A:2509:C:C5	30:4:8:ARG:NH1	2.28	1.01
4:F:9:PRO:HD2	4:F:12:LYS:NZ	1.75	1.00
4:F:183:PRO:C	4:F:184:PHE:HD2	1.63	1.00
26:A:1563:A:N6	26:A:1607:C:H41	1.59	1.00
21:W:77:LEU:HB3	21:W:100:VAL:HG23	1.01	1.00
26:A:1564:A:H2'	26:A:1565:A:H5''	1.44	1.00
28:2:41:CYS:HB2	28:2:44:PHE:CZ	1.97	1.00
1:C:26:ARG:HD2	1:C:81:HIS:NE2	1.76	1.00
1:C:54:LYS:NZ	26:A:2031:G:O3'	1.94	1.00
25:B:58:A:C4	25:B:59:A:C8	2.49	0.99
26:A:2980:U:OP2	33:7:19:ARG:NH1	1.95	0.99
20:V:62:GLN:CG	20:V:63:GLU:H	1.75	0.99
1:C:25:THR:CG2	1:C:81:HIS:HA	1.90	0.99
10:L:8:LEU:CD1	10:L:19:ILE:HG13	1.92	0.99
20:V:2:LYS:CD	20:V:83:VAL:CG1	2.37	0.99
31:5:5:LYS:HB3	31:5:9:GLN:NE2	1.76	0.99
1:C:55:GLY:HA3	1:C:218:ARG:HD2	1.43	0.99
4:F:10:ARG:HG2	4:F:10:ARG:HH11	1.27	0.99
4:F:49:ASP:HB2	4:F:56:LEU:CD1	1.93	0.99
14:P:108:THR:OG1	25:B:47:A:O2'	1.79	0.99
25:B:40:A:H61	28:2:1:MET:N	1.58	0.99
28:2:44:PHE:O	28:2:48:LYS:HG3	1.61	0.99
25:B:57:U:C2'	25:B:58:A:H5''	1.93	0.99
19:U:19:LYS:NZ	26:A:1508:A:N6	2.09	0.98
20:V:62:GLN:HG2	20:V:63:GLU:H	0.84	0.98
3:E:66:TYR:CD1	3:E:73:ARG:NH1	2.31	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1580:A:C6	26:A:1592:G:N9	2.31	0.98
21:W:105:LYS:HE2	21:W:136:GLU:OE2	1.61	0.98
25:B:60:G:H5'	25:B:60:G:H8	1.25	0.98
26:A:1565:A:C4	26:A:1606:G:C6	2.50	0.98
30:4:15:CYS:CA	30:4:20:HIS:HA	1.93	0.98
18:T:9:SER:HB3	18:T:115:GLU:CB	1.92	0.98
31:5:8:PHE:CE2	31:5:10:PRO:HG3	1.99	0.98
30:4:19:LYS:HD2	30:4:44:ASN:CB	1.93	0.98
4:F:117:ARG:NH1	4:F:146:HIS:HD2	1.24	0.97
12:N:85:SER:OG	22:X:8:SER:CB	2.11	0.97
13:O:90:ARG:CZ	13:O:118:GLU:HG3	1.94	0.97
2:D:154:CYS:SG	26:A:2796:A:H2'	2.04	0.97
3:E:192:ASP:CB	11:M:5:LYS:HZ1	1.75	0.97
17:S:58:VAL:HG22	17:S:103:LYS:HG2	1.45	0.97
26:A:1563:A:H61	26:A:1607:C:H41	1.05	0.97
3:E:7:VAL:CG2	3:E:16:GLY:HA3	1.95	0.97
13:O:8:PRO:CG	26:A:1870:U:C5	2.48	0.97
20:V:46:ALA:HB2	26:A:571:A:O3'	1.65	0.97
1:C:54:LYS:NZ	26:A:2031:G:C4'	2.28	0.97
12:N:111:GLU:OE2	12:N:115:ARG:NE	1.97	0.97
14:P:50:GLN:NE2	25:B:7:G:N2	2.13	0.96
17:S:3:THR:CG2	17:S:102:ILE:HD11	1.93	0.96
13:O:79:LEU:HG	13:O:83:ILE:CD1	1.96	0.96
1:C:54:LYS:HZ2	26:A:2031:G:C5'	1.76	0.96
12:N:61:GLY:O	12:N:108:TYR:CE1	2.17	0.96
8:J:96:LYS:HE3	21:W:120:PRO:HB2	1.48	0.96
21:W:87:PRO:O	21:W:90:ARG:NH2	1.97	0.96
26:A:1595:G:H3'	26:A:1596:C:C5'	1.95	0.96
30:4:11:ILE:CD1	30:4:27:LYS:HG2	1.95	0.96
18:T:75:THR:HB	18:T:118:PRO:HD3	1.46	0.96
20:V:2:LYS:HG2	20:V:83:VAL:HB	1.47	0.96
21:W:21:LYS:NZ	25:B:80:C:H42	1.64	0.96
4:F:66:LEU:HD23	28:2:27:THR:CG2	1.95	0.95
13:O:90:ARG:HH22	13:O:118:GLU:CB	1.75	0.95
26:A:1580:A:N1	26:A:1592:G:H1'	1.78	0.95
1:C:25:THR:HG21	1:C:81:HIS:HA	0.99	0.95
1:C:256:ARG:HA	1:C:256:ARG:HE	1.28	0.95
10:L:8:LEU:HD11	10:L:19:ILE:HG13	1.47	0.95
25:B:54:A:O2'	25:B:55:G:H5'	1.64	0.95
19:U:91:LYS:HG2	19:U:92:PRO:HD2	0.96	0.95
25:B:25:G:H21	25:B:114:A:C2'	1.79	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:109:ARG:HG3	4:F:113:ILE:HD12	1.48	0.95
25:B:96:A:H2	26:A:977:G:N3	1.62	0.95
18:T:44:ARG:HH12	29:3:55:ASP:H	1.09	0.95
4:F:116:PRO:HB2	28:2:37:VAL:HG11	1.48	0.95
25:B:24:G:C8	25:B:56:C:C2	2.55	0.95
10:L:8:LEU:H	10:L:8:LEU:HD12	1.32	0.94
25:B:24:G:O2'	25:B:56:C:C4	2.17	0.94
13:O:8:PRO:HG3	26:A:1870:U:C5	2.02	0.94
13:O:33:ARG:HD3	13:O:114:GLU:CD	1.86	0.94
26:A:1551:U:H3	26:A:1619:U:H3	1.12	0.94
26:A:1570:C:C4	26:A:1602:U:O2	2.20	0.94
17:S:6:ILE:O	17:S:7:VAL:CG2	2.15	0.94
24:Z:13:LEU:HD11	24:Z:17:GLU:CB	1.95	0.94
25:B:58:A:C5	25:B:59:A:C8	2.55	0.94
26:A:1554:U:H3	26:A:1617:C:N4	1.64	0.94
11:M:51:GLU:HG2	32:6:57:ARG:NH1	1.79	0.94
3:E:9:THR:OG1	3:E:12:GLY:O	1.85	0.94
17:S:3:THR:HG21	17:S:102:ILE:HD12	1.46	0.94
18:T:18:ARG:CZ	26:A:1436:C:O2'	2.16	0.94
12:N:60:ARG:HG2	12:N:60:ARG:HH21	1.27	0.94
19:U:4:ILE:HD13	24:Z:58:TYR:OH	1.68	0.94
25:B:82:A:H2	25:B:91:G:H1	1.05	0.94
26:A:1581:C:H2'	26:A:1582:C:C6	2.03	0.94
20:V:96:ARG:HD2	20:V:105:ILE:HG23	1.50	0.93
4:F:66:LEU:HD23	28:2:27:THR:HG21	1.48	0.93
9:K:141:GLU:CD	9:K:143:LYS:CG	2.35	0.93
30:4:36:LEU:HD21	30:4:38:ILE:HD12	1.48	0.93
18:T:9:SER:HB3	18:T:115:GLU:HB2	1.50	0.93
2:D:154:CYS:CB	26:A:2799:C:H5'	1.97	0.93
4:F:49:ASP:CB	4:F:56:LEU:HD11	1.96	0.93
4:F:110:LEU:HD23	4:F:111:ILE:N	1.83	0.93
20:V:2:LYS:CG	20:V:83:VAL:HB	1.99	0.93
26:A:1595:G:OP2	26:A:1596:C:C4	2.22	0.93
4:F:44:ASN:OD1	26:A:2537:C:O4'	1.86	0.93
13:O:9:ARG:HG2	13:O:14:SER:CB	1.99	0.93
3:E:144:PHE:HD1	3:E:148:LEU:HD21	1.33	0.93
22:X:15:ASP:OD2	26:A:2487:C:N4	2.01	0.93
30:4:29:ARG:NH2	30:4:34:ASP:CB	2.31	0.92
26:A:1597:G:N3	26:A:1598:U:C6	2.37	0.92
4:F:109:ARG:HD2	4:F:147:GLU:OE2	1.69	0.92
30:4:12:THR:HG22	30:4:22:ASN:HB3	1.50	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:68:LYS:NZ	26:A:1140:G:O6	2.01	0.92
24:Z:9:GLU:O	24:Z:11:ARG:N	2.03	0.92
4:F:105:GLU:HG3	28:2:24:THR:HG22	1.52	0.92
17:S:58:VAL:HG23	17:S:103:LYS:HG2	0.98	0.92
22:X:64:PRO:HB3	26:A:759:G:H1	1.34	0.92
25:B:58:A:C4	25:B:59:A:H8	1.84	0.92
2:D:154:CYS:SG	26:A:2796:A:OP1	2.28	0.92
3:E:144:PHE:CD1	3:E:148:LEU:CD1	2.52	0.92
19:U:19:LYS:HD2	26:A:1508:A:H62	0.84	0.92
19:U:83:ILE:HD12	26:A:1456:G:C2	2.05	0.92
21:W:87:PRO:HA	21:W:90:ARG:HH22	1.35	0.92
4:F:73:GLU:OE1	25:B:41:U:C5	2.23	0.92
1:C:72:LYS:HG3	1:C:75:VAL:CG2	2.00	0.92
26:A:1580:A:N6	26:A:1591:U:H3	1.66	0.92
26:A:1580:A:N1	26:A:1591:U:O2	2.02	0.91
26:A:1583:U:O2	26:A:1589:G:N1	2.03	0.91
1:C:30:GLU:OE2	1:C:102:LYS:HD3	1.68	0.91
2:D:154:CYS:HB3	26:A:2798:G:O2'	1.71	0.91
2:D:156:THR:HG21	26:A:2256:G:H21	1.36	0.91
19:U:83:ILE:CD1	26:A:1456:G:N2	2.11	0.91
25:B:19:G:N2	25:B:64:G:N1	2.19	0.91
30:4:29:ARG:HH21	30:4:34:ASP:HB3	1.34	0.91
4:F:168:THR:OG1	14:P:4:LYS:O	1.89	0.91
18:T:115:GLU:OE2	18:T:117:ARG:NH1	2.04	0.91
3:E:7:VAL:HB	3:E:16:GLY:HA3	1.52	0.91
3:E:192:ASP:HB3	11:M:5:LYS:HZ3	1.30	0.91
26:A:1561:C:N3	26:A:1562:C:C6	2.39	0.91
19:U:4:ILE:CD1	24:Z:58:TYR:CZ	2.51	0.90
30:4:15:CYS:HB2	30:4:20:HIS:CA	2.01	0.90
21:W:83:LEU:CD1	21:W:92:ILE:HG23	2.01	0.90
1:C:54:LYS:NZ	26:A:2031:G:H4'	1.83	0.90
10:L:108:GLU:HG3	10:L:109:LYS:H	1.36	0.90
9:K:13:ARG:CZ	9:K:121:LYS:HZ3	1.85	0.90
30:4:9:PRO:HD2	30:4:27:LYS:O	1.71	0.90
13:O:9:ARG:CG	13:O:14:SER:HB3	2.01	0.90
26:A:2086:U:H3	26:A:2096:G:H1	0.97	0.90
25:B:4:A:H2	25:B:25:G:C6	1.90	0.90
26:A:2508:C:OP1	30:4:7:VAL:HG11	1.71	0.90
13:O:29:PHE:CD1	13:O:79:LEU:HD11	2.06	0.90
30:4:29:ARG:NH2	30:4:34:ASP:HB2	1.87	0.90
25:B:96:A:C2	26:A:977:G:N3	2.39	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1561:C:N4	26:A:1562:C:N4	2.19	0.90
25:B:58:A:H5'	25:B:58:A:C8	2.07	0.90
26:A:1565:A:H2'	26:A:1566:A:C8	2.05	0.90
26:A:2571:C:O2'	30:4:23:TYR:OH	1.77	0.90
14:P:41:ASN:ND2	25:B:7:G:HO2'	1.66	0.89
26:A:1563:A:N7	26:A:1565:A:N7	2.20	0.89
1:C:256:ARG:O	26:A:2014:G:H4'	1.71	0.89
9:K:112:ASN:CG	26:A:650:G:OP1	2.08	0.89
26:A:1564:A:C2'	26:A:1565:A:H5''	2.02	0.89
1:C:37:LEU:HD23	1:C:62:TYR:HB2	1.54	0.89
1:C:73:ASP:HB3	1:C:120:GLY:HA2	1.50	0.89
3:E:144:PHE:CD2	3:E:148:LEU:HD11	2.07	0.89
21:W:83:LEU:HD11	21:W:92:ILE:HD12	1.55	0.89
1:C:96:HIS:HE1	1:C:102:LYS:NZ	1.70	0.89
1:C:258:ARG:HA	26:A:2015:U:C5'	2.01	0.89
25:B:19:G:C2'	25:B:20:G:H5'	2.03	0.89
25:B:20:G:C2'	25:B:21:C:H5'	2.02	0.89
26:A:325:U:H3	26:A:450:G:H1	0.94	0.89
3:E:7:VAL:O	3:E:14:THR:HA	1.73	0.89
12:N:58:ILE:CG2	12:N:108:TYR:CE1	2.55	0.89
26:A:1597:G:N3	26:A:1598:U:C5	2.41	0.89
13:O:8:PRO:CG	26:A:1870:U:C4	2.55	0.89
20:V:42:LYS:HD2	26:A:586:U:H5''	1.53	0.88
25:B:20:G:N1	25:B:63:U:O4	2.05	0.88
25:B:24:G:C5	25:B:56:C:C2	2.61	0.88
26:A:1571:C:O2'	26:A:1572:G:H5''	1.73	0.88
25:B:19:G:H5'	25:B:19:G:C8	2.07	0.88
26:A:1561:C:C2	26:A:1562:C:H6	1.92	0.88
25:B:58:A:C6	25:B:59:A:N7	2.40	0.88
26:A:1575:A:O2'	26:A:1576:C:H5'	1.72	0.88
26:A:1597:G:C4	26:A:1598:U:H5	1.91	0.88
31:5:22:ARG:O	31:5:26:ARG:HD3	1.73	0.88
25:B:29:C:H42	25:B:55:G:H1	1.18	0.88
30:4:18:CYS:SG	30:4:19:LYS:N	2.47	0.88
20:V:2:LYS:HD2	20:V:83:VAL:HG11	0.88	0.88
2:D:154:CYS:CB	26:A:2799:C:P	2.52	0.88
19:U:83:ILE:CD1	26:A:1456:G:N3	2.20	0.88
22:X:83:VAL:HG13	22:X:85:ARG:HA	1.54	0.88
26:A:1578:G:H22	26:A:1592:G:C2'	1.87	0.88
26:A:1580:A:C6	26:A:1591:U:C2	2.56	0.88
30:4:19:LYS:HB2	30:4:21:ARG:NH2	1.89	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:25:G:H21	25:B:114:A:C1'	1.86	0.87
1:C:256:ARG:HA	1:C:256:ARG:NE	1.88	0.87
13:O:117:ARG:HD3	13:O:118:GLU:H	1.39	0.87
1:C:73:ASP:HB3	1:C:120:GLY:HA3	1.56	0.87
13:O:8:PRO:HG2	26:A:1870:U:C5	2.10	0.87
20:V:83:VAL:HG11	20:V:96:ARG:HG3	1.57	0.87
26:A:1597:G:C4	26:A:1598:U:C5	2.62	0.87
26:A:2509:C:H5	30:4:8:ARG:NH1	1.69	0.87
4:F:45:MET:CE	4:F:64:LEU:CD2	2.52	0.87
11:M:58:HIS:CD2	32:6:7:HIS:HE1	1.93	0.87
17:S:3:THR:HG22	17:S:102:ILE:HD11	1.51	0.87
26:A:1598:U:O4	26:A:1601:G:C6	2.28	0.87
1:C:29:PRO:CG	1:C:34:VAL:HG21	2.05	0.87
8:J:45:ASN:O	8:J:49:GLU:HB2	1.74	0.87
21:W:29:ARG:NH1	25:B:90:G:H5'	1.89	0.87
4:F:99:ARG:CD	25:B:45:G:C8	2.57	0.87
25:B:28:A:H61	25:B:56:C:H42	1.21	0.86
26:A:1561:C:N4	26:A:1562:C:C5	2.41	0.86
3:E:150:GLU:OE1	3:E:193:ASP:OD1	1.92	0.86
28:2:41:CYS:HB3	28:2:43:PRO:CD	2.03	0.86
26:A:1578:G:H22	26:A:1592:G:H2'	1.40	0.86
26:A:1550:G:H1	26:A:1620:U:H3	0.86	0.86
4:F:74:VAL:O	25:B:41:U:O4	1.93	0.86
4:F:99:ARG:CD	25:B:45:G:H8	1.88	0.86
21:W:37:LEU:HD11	21:W:69:LEU:CD1	2.06	0.86
25:B:24:G:N7	25:B:56:C:C2	2.44	0.86
26:A:1582:C:O2'	26:A:1583:U:H5'	1.75	0.86
30:4:11:ILE:HD13	30:4:27:LYS:CG	2.06	0.86
13:O:4:PRO:HG3	26:A:3094:A:C2	2.10	0.85
20:V:29:ASP:OD1	20:V:30:ARG:N	2.09	0.85
21:W:77:LEU:HD22	21:W:100:VAL:HG21	1.57	0.85
26:A:1566:A:O2'	26:A:1567:C:H5'	1.75	0.85
12:N:60:ARG:O	21:W:190:LEU:HD11	1.76	0.85
20:V:4:HIS:HE1	20:V:96:ARG:NH2	1.74	0.85
3:E:7:VAL:CB	3:E:16:GLY:HA3	2.05	0.85
19:U:4:ILE:HD13	24:Z:58:TYR:HE1	1.40	0.85
26:A:1590:G:C6	26:A:1591:U:C5	2.64	0.85
25:B:4:A:C2	25:B:25:G:C6	2.63	0.85
3:E:68:GLN:OE1	26:A:790:A:O2'	1.94	0.85
25:B:20:G:O2'	25:B:21:C:H5'	1.77	0.85
26:A:2510:A:OP2	30:4:31:ASN:OD1	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:45:MET:HE3	4:F:64:LEU:CD2	2.06	0.85
26:A:1601:G:O2'	26:A:1602:U:C5'	2.24	0.85
20:V:97:ILE:HD12	20:V:103:LYS:O	1.77	0.84
24:Z:18:LEU:HD13	24:Z:61:LEU:CD2	2.07	0.84
13:O:29:PHE:CE2	13:O:51:LEU:HD12	2.11	0.84
17:S:103:LYS:HZ3	17:S:103:LYS:CA	1.90	0.84
25:B:19:G:N2	25:B:65:C:C2	2.44	0.84
25:B:19:G:H2'	25:B:20:G:C5'	2.07	0.84
19:U:19:LYS:CD	26:A:1508:A:H61	1.78	0.84
3:E:144:PHE:CE1	3:E:148:LEU:HD22	2.09	0.84
9:K:3:THR:HG21	26:A:1113:C:O2	1.75	0.84
2:D:155:ALA:HB2	26:A:2796:A:N7	1.83	0.84
13:O:20:LEU:HD11	13:O:40:LYS:HZ2	1.41	0.84
21:W:37:LEU:HD12	21:W:69:LEU:HD11	1.59	0.84
19:U:29:TYR:CE1	19:U:93:ILE:CG2	2.60	0.84
24:Z:13:LEU:CD1	24:Z:17:GLU:HB2	2.07	0.84
1:C:55:GLY:CA	1:C:218:ARG:CD	2.54	0.84
26:A:1556:A:H61	26:A:1615:G:H1	1.26	0.84
12:N:58:ILE:HG21	12:N:108:TYR:CE1	2.13	0.84
26:A:2510:A:OP1	30:4:31:ASN:OD1	1.95	0.83
1:C:25:THR:HG22	1:C:82:ILE:N	1.92	0.83
1:C:76:ASN:O	1:C:98:LEU:CD2	2.25	0.83
8:J:96:LYS:HE2	21:W:120:PRO:HB2	1.59	0.83
13:O:96:ARG:NH2	13:O:116:VAL:HG12	1.93	0.83
21:W:37:LEU:HD12	21:W:69:LEU:CD1	2.08	0.83
3:E:90:VAL:HG11	26:A:678:A:O5'	1.77	0.83
4:F:99:ARG:HD2	25:B:45:G:H8	1.40	0.83
21:W:101:GLN:HB3	21:W:104:GLU:CB	2.08	0.83
25:B:59:A:H2'	25:B:60:G:H5'	1.59	0.83
25:B:82:A:C2	25:B:91:G:N1	2.45	0.83
22:X:17:ALA:CB	26:A:2485:C:P	2.66	0.83
30:4:37:GLU:O	30:4:38:ILE:HG13	1.78	0.83
4:F:105:GLU:CG	28:2:24:THR:HG22	2.07	0.83
19:U:19:LYS:HZ2	26:A:1508:A:H61	1.01	0.83
21:W:86:HIS:O	21:W:90:ARG:NH2	2.10	0.83
30:4:29:ARG:HH21	30:4:34:ASP:HB2	1.43	0.83
4:F:108:ASP:O	4:F:111:ILE:HG22	1.76	0.83
25:B:18:C:H2'	25:B:19:G:H5''	0.83	0.83
33:7:22:ARG:CZ	33:7:37:GLY:HA2	2.07	0.83
25:B:25:G:N2	25:B:114:A:H1'	1.94	0.83
4:F:132:THR:CG2	14:P:6:VAL:CG2	2.40	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:2508:C:OP1	30:4:7:VAL:CG1	2.27	0.83
2:D:154:CYS:HB2	26:A:2799:C:OP1	1.79	0.82
3:E:145:LEU:HA	3:E:148:LEU:HD12	1.58	0.82
21:W:83:LEU:CD1	21:W:92:ILE:HD12	2.09	0.82
22:X:83:VAL:HG12	22:X:85:ARG:HB2	1.62	0.82
3:E:14:THR:HG22	3:E:15:ASP:H	1.44	0.82
24:Z:13:LEU:O	24:Z:64:ARG:NH1	2.12	0.82
25:B:20:G:N2	25:B:63:U:N3	1.89	0.82
26:A:1580:A:N1	26:A:1592:G:N9	2.27	0.82
26:A:1595:G:H8	26:A:1596:C:C5	1.96	0.82
19:U:77:LYS:NZ	19:U:79:THR:HG22	1.93	0.82
21:W:8:PRO:HB2	21:W:68:THR:OG1	1.80	0.82
26:A:1580:A:C2	26:A:1592:G:H1'	2.14	0.82
2:D:154:CYS:SG	26:A:2796:A:C5'	2.66	0.82
22:X:15:ASP:CG	26:A:2487:C:H41	1.83	0.82
25:B:36:U:O2'	25:B:37:C:H5'	1.80	0.82
9:K:112:ASN:OD1	9:K:113:LYS:N	2.11	0.82
25:B:85:C:O2'	25:B:86:U:O4'	1.97	0.82
26:A:1561:C:N4	26:A:1562:C:H41	1.76	0.82
4:F:116:PRO:CB	28:2:37:VAL:HG11	2.09	0.82
24:Z:13:LEU:HD11	24:Z:17:GLU:OE1	1.79	0.82
11:M:51:GLU:HG3	32:6:57:ARG:NH1	1.93	0.81
13:O:14:SER:O	13:O:15:SER:OG	1.96	0.81
25:B:19:G:N2	25:B:65:C:C4	2.47	0.81
12:N:60:ARG:NH1	26:A:1193:C:H5''	1.94	0.81
19:U:91:LYS:CG	19:U:92:PRO:CD	2.51	0.81
9:K:141:GLU:OE1	9:K:143:LYS:CG	2.27	0.81
24:Z:6:THR:HG22	24:Z:10:LEU:CD1	2.09	0.81
26:A:1567:C:O2'	26:A:1568:C:OP2	1.96	0.81
26:A:1602:U:H2'	26:A:1603:G:C8	2.16	0.81
1:C:29:PRO:HB2	1:C:34:VAL:CG2	2.09	0.81
3:E:45:LYS:HG3	26:A:709:U:O4	1.80	0.81
4:F:45:MET:HB2	4:F:94:ALA:O	1.81	0.81
13:O:79:LEU:CG	13:O:83:ILE:HD12	2.10	0.81
17:S:103:LYS:HA	17:S:103:LYS:NZ	1.95	0.81
13:O:81:ALA:O	13:O:85:PRO:CG	2.28	0.81
1:C:54:LYS:NZ	26:A:2031:G:H5''	1.94	0.81
26:A:1566:A:N3	26:A:1605:G:C6	2.48	0.81
26:A:1582:C:C2'	26:A:1583:U:H5'	2.10	0.81
28:2:41:CYS:CB	28:2:43:PRO:HD2	2.10	0.81
26:A:1561:C:C5	26:A:1562:C:C5	2.41	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:21:ARG:HG3	30:4:44:ASN:OD1	1.81	0.81
25:B:21:C:H2'	25:B:22:A:O4'	1.81	0.81
3:E:51:SER:OG	26:A:35:A:H5'	1.81	0.80
18:T:6:GLU:C	18:T:8:PRO:HD3	2.01	0.80
26:A:1580:A:H62	26:A:1591:U:H3	1.25	0.80
9:K:113:LYS:HD2	26:A:616:A:OP1	1.81	0.80
26:A:1561:C:C2	26:A:1562:C:C5	2.68	0.80
26:A:1570:C:H42	26:A:1602:U:H3	0.80	0.80
26:A:1570:C:O2'	26:A:1571:C:H5'	1.80	0.80
9:K:26:GLY:O	26:A:1262:A:N6	2.14	0.80
19:U:19:LYS:HE3	26:A:1454:G:H5'	1.62	0.80
22:X:15:ASP:HB2	26:A:2486:U:O4	1.81	0.80
31:5:5:LYS:HB3	31:5:9:GLN:HE21	1.47	0.80
2:D:154:CYS:H	26:A:2798:G:HO2'	1.26	0.80
3:E:24:LEU:HD21	3:E:208:ASN:OD1	1.82	0.80
9:K:3:THR:HG23	26:A:1113:C:N3	1.97	0.80
13:O:4:PRO:HG3	26:A:3094:A:N1	1.97	0.80
13:O:33:ARG:HG3	13:O:114:GLU:CG	2.11	0.80
26:A:1561:C:C4	26:A:1562:C:C4	2.69	0.80
30:4:9:PRO:CD	30:4:27:LYS:O	2.30	0.80
1:C:56:GLY:CA	26:A:807:C:OP1	2.29	0.80
25:B:60:G:H5'	25:B:60:G:C8	2.15	0.80
1:C:30:GLU:OE1	1:C:33:LEU:CD1	2.29	0.80
21:W:40:HIS:O	21:W:42:THR:N	2.14	0.80
26:A:1561:C:N4	26:A:1562:C:C4	2.50	0.80
2:D:154:CYS:HG	26:A:2796:A:P	2.05	0.79
25:B:18:C:C2'	25:B:19:G:C5'	2.40	0.79
26:A:351:G:H1	26:A:444:U:H3	1.27	0.79
26:A:1581:C:N4	26:A:1591:U:C1'	2.45	0.79
26:A:1596:C:O2'	26:A:1597:G:O4'	2.00	0.79
25:B:30:G:N1	25:B:54:A:C2	2.48	0.79
21:W:98:LEU:HD23	21:W:99:VAL:N	1.97	0.79
26:A:1578:G:N7	26:A:1592:G:O6	2.15	0.79
26:A:1600:G:C3'	26:A:1601:G:H5''	2.11	0.79
4:F:55:LYS:HB2	4:F:55:LYS:NZ	1.97	0.79
9:K:112:ASN:HD21	26:A:650:G:P	2.04	0.79
21:W:9:ASN:HD22	21:W:57:VAL:HG13	1.41	0.79
22:X:17:ALA:HB3	26:A:2485:C:OP2	1.82	0.79
18:T:75:THR:HB	18:T:118:PRO:CD	2.12	0.79
25:B:96:A:H2	26:A:977:G:C2	2.00	0.79
5:G:171:ARG:NH2	33:7:28:SER:O	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:120:ASP:OD2	4:F:122:ARG:NH1	2.16	0.79
4:F:182:PHE:CD2	4:F:184:PHE:HE2	2.01	0.79
25:B:19:G:N2	25:B:64:G:H1	1.80	0.79
1:C:54:LYS:NZ	26:A:2031:G:C5'	2.46	0.79
1:C:55:GLY:HA3	1:C:218:ARG:CG	2.13	0.79
3:E:7:VAL:CG2	3:E:16:GLY:CA	2.61	0.79
26:A:1561:C:C2'	26:A:1562:C:H5'	2.13	0.79
1:C:257:THR:HB	26:A:2014:G:O2'	1.82	0.79
2:D:154:CYS:HA	26:A:2799:C:C5'	2.07	0.79
3:E:118:ARG:HH11	11:M:3:VAL:HG13	1.48	0.79
14:P:50:GLN:CD	25:B:7:G:H21	1.86	0.79
26:A:1563:A:C5	26:A:1565:A:N7	2.50	0.78
3:E:8:LYS:O	3:E:127:VAL:HA	1.82	0.78
14:P:42:ARG:NH1	25:B:48:C:P	2.46	0.78
21:W:102:ARG:HH21	21:W:138:LEU:HD21	1.45	0.78
33:7:22:ARG:HD3	33:7:36:GLN:O	1.83	0.78
12:N:61:GLY:O	12:N:108:TYR:HE1	1.59	0.78
20:V:2:LYS:NZ	20:V:85:TYR:CE2	2.51	0.78
22:X:14:ARG:NH2	26:A:2503:G:N7	2.30	0.78
12:N:61:GLY:O	12:N:108:TYR:CD1	2.36	0.78
21:W:37:LEU:CD1	21:W:69:LEU:HD11	2.11	0.78
26:A:1541:G:O6	26:A:1630:U:C4	2.36	0.78
3:E:145:LEU:CA	3:E:148:LEU:HD12	1.98	0.78
12:N:134:ARG:HH21	21:W:129:ASN:HD21	1.30	0.78
13:O:42:ARG:O	13:O:45:ARG:HB3	1.83	0.78
21:W:87:PRO:CA	21:W:90:ARG:HH22	1.96	0.78
26:A:725:A:OP2	32:6:47:ARG:NH2	2.16	0.78
28:2:48:LYS:O	28:2:52:LEU:HG	1.82	0.78
19:U:29:TYR:CE1	19:U:93:ILE:HG22	2.19	0.78
26:A:1578:G:C5	26:A:1592:G:N1	2.18	0.78
2:D:154:CYS:HB2	26:A:2799:C:C5'	2.14	0.78
4:F:117:ARG:NH1	4:F:146:HIS:NE2	2.30	0.78
25:B:25:G:N2	25:B:114:A:C1'	2.47	0.78
10:L:107:ARG:NH1	15:Q:33:GLU:HG3	1.99	0.78
26:A:1541:G:O6	26:A:1630:U:C5	2.36	0.78
13:O:16:HIS:CD2	26:A:1390:A:C8	2.68	0.77
24:Z:5:THR:HG23	24:Z:6:THR:H	1.47	0.77
25:B:59:A:C2'	25:B:60:G:H5'	2.14	0.77
21:W:40:HIS:O	21:W:40:HIS:ND1	2.16	0.77
30:4:36:LEU:HG	30:4:37:GLU:N	1.99	0.77
9:K:3:THR:CG2	26:A:1113:C:C2	2.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:60:ARG:NE	26:A:1194:C:OP2	2.17	0.77
19:U:77:LYS:HG3	26:A:55:G:H5''	1.66	0.77
26:A:1601:G:O2'	26:A:1602:U:H5'	1.82	0.77
28:2:44:PHE:O	28:2:48:LYS:HE3	1.84	0.77
3:E:51:SER:HB3	26:A:34:C:O2'	1.84	0.77
13:O:33:ARG:HG3	13:O:114:GLU:HG3	1.66	0.77
13:O:33:ARG:HD2	13:O:114:GLU:OE2	1.85	0.77
26:A:1595:G:H5'	26:A:1596:C:C6	2.20	0.77
10:L:92:ASP:OD2	10:L:93:PRO:HD2	1.85	0.77
19:U:7:PRO:O	19:U:49:ILE:HD11	1.84	0.77
26:A:1554:U:H3	26:A:1617:C:H42	1.31	0.77
26:A:1566:A:H1'	26:A:1605:G:H1	1.47	0.77
2:D:154:CYS:CB	26:A:2798:G:O2'	2.33	0.77
19:U:69:THR:OG1	19:U:73:PHE:O	2.03	0.77
3:E:107:ILE:CD1	26:A:710:G:OP1	2.33	0.77
11:M:61:LEU:CD2	32:6:24:ARG:HH11	1.96	0.77
20:V:44:HIS:HA	20:V:58:GLY:O	1.84	0.77
26:A:1563:A:N6	26:A:1607:C:N4	2.33	0.77
2:D:154:CYS:HB2	26:A:2799:C:H5'	1.67	0.77
13:O:33:ARG:NH2	13:O:114:GLU:OE2	2.16	0.77
1:C:35:ARG:HG3	1:C:36:PRO:CD	2.14	0.76
4:F:53:ASP:O	4:F:56:LEU:CD2	2.33	0.76
25:B:54:A:C2'	25:B:55:G:H5'	2.15	0.76
25:B:84:C:H2'	25:B:85:C:H5'	1.65	0.76
4:F:78:ARG:NH2	26:A:2522:A:OP1	2.19	0.76
21:W:37:LEU:CD1	21:W:69:LEU:HD13	2.15	0.76
1:C:35:ARG:HD2	1:C:36:PRO:HD3	1.66	0.76
26:A:1600:G:C2'	26:A:1601:G:H5''	2.15	0.76
30:4:15:CYS:O	30:4:20:HIS:HB3	1.80	0.76
17:S:3:THR:HG22	17:S:102:ILE:HD13	0.76	0.76
1:C:57:GLY:O	1:C:58:HIS:O	2.02	0.76
3:E:121:ASN:HD22	11:M:3:VAL:HG22	1.50	0.76
13:O:20:LEU:HD11	13:O:40:LYS:NZ	2.00	0.76
28:2:47:GLY:O	28:2:51:ILE:HG13	1.85	0.76
3:E:7:VAL:HG23	3:E:16:GLY:CA	2.15	0.76
20:V:4:HIS:CE1	20:V:96:ARG:NH2	2.50	0.76
26:A:802:C:H1'	31:5:7:THR:HG22	1.67	0.76
26:A:1597:G:C2	26:A:1598:U:C5	2.73	0.76
30:4:12:THR:CG2	30:4:22:ASN:HB3	2.16	0.76
11:M:63:LYS:HE3	32:6:12:LYS:HG2	1.68	0.76
26:A:860:G:HO2'	26:A:863:G:HO2'	1.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:51:GLU:HG2	32:6:57:ARG:CZ	2.16	0.76
16:R:50:ARG:HG2	16:R:53:ARG:HH21	1.51	0.76
4:F:9:PRO:HD2	4:F:12:LYS:HZ1	1.48	0.75
4:F:182:PHE:HD2	4:F:184:PHE:HE2	1.32	0.75
4:F:51:ALA:HB2	4:F:90:MET:CE	2.15	0.75
8:J:44:TYR:O	8:J:48:THR:HB	1.87	0.75
13:O:95:THR:HG22	13:O:115:LEU:HD23	1.68	0.75
13:O:29:PHE:HE2	13:O:51:LEU:CD1	1.99	0.75
17:S:6:ILE:HG22	17:S:7:VAL:N	1.99	0.75
21:W:29:ARG:HH12	25:B:90:G:C5'	2.00	0.75
31:5:8:PHE:CD2	31:5:10:PRO:HG3	2.21	0.75
22:X:15:ASP:CB	26:A:2487:C:H41	1.98	0.75
26:A:1586:C:H3'	26:A:1587:G:H5''	1.68	0.75
18:T:95:ARG:NH2	26:A:863:G:OP1	2.18	0.75
33:7:35:ARG:HG2	33:7:36:GLN:H	1.50	0.75
1:C:76:ASN:HB2	1:C:98:LEU:HD21	1.68	0.75
6:H:103:ALA:O	6:H:107:ALA:HB3	1.86	0.75
25:B:82:A:H2	25:B:91:G:N1	1.82	0.75
30:4:18:CYS:HG	30:4:45:CYS:HG	1.32	0.75
1:C:239:LYS:HE2	26:A:2196:G:OP2	1.85	0.75
9:K:96:HIS:HB3	9:K:99:ARG:HG2	1.66	0.75
18:T:41:ASP:OD2	29:3:27:LEU:HD13	1.86	0.75
24:Z:13:LEU:HD21	24:Z:17:GLU:CB	2.16	0.75
13:O:16:HIS:CD2	26:A:1390:A:C4	2.75	0.75
13:O:29:PHE:CE2	13:O:51:LEU:CD1	2.69	0.75
26:A:1601:G:O2'	26:A:1602:U:H5''	1.86	0.75
4:F:32:VAL:O	4:F:33:MET:HB2	1.86	0.74
4:F:168:THR:HG21	14:P:3:HIS:CE1	2.21	0.74
18:T:44:ARG:NH1	29:3:55:ASP:H	1.85	0.74
19:U:5:THR:HG22	19:U:6:ASP:N	2.01	0.74
20:V:86:ARG:HD3	20:V:97:ILE:HG13	1.68	0.74
20:V:96:ARG:NH2	20:V:96:ARG:HB2	2.01	0.74
26:A:1590:G:C4	26:A:1591:U:C6	2.74	0.74
24:Z:13:LEU:HD21	24:Z:17:GLU:HB3	1.68	0.74
26:A:1565:A:H2	26:A:1606:G:C8	1.98	0.74
18:T:116:SER:OG	18:T:118:PRO:HG2	1.86	0.74
27:1:51:HIS:H	27:1:51:HIS:CD2	2.03	0.74
30:4:18:CYS:HB2	30:4:45:CYS:SG	2.27	0.74
4:F:45:MET:CB	4:F:94:ALA:O	2.34	0.74
9:K:3:THR:HG23	26:A:1113:C:C2	2.22	0.74
21:W:83:LEU:HD11	21:W:92:ILE:HG23	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:35:ARG:HG2	33:7:36:GLN:N	2.03	0.74
1:C:35:ARG:HG3	1:C:36:PRO:HD2	1.68	0.74
1:C:256:ARG:CZ	1:C:258:ARG:HE	1.99	0.74
18:T:96:ALA:O	26:A:866:G:OP2	2.04	0.74
20:V:97:ILE:CD1	20:V:103:LYS:O	2.36	0.74
30:4:36:LEU:HD21	30:4:38:ILE:CD1	2.17	0.74
22:X:15:ASP:CB	26:A:2486:U:O4	2.35	0.74
1:C:256:ARG:HD3	1:C:258:ARG:CD	2.17	0.74
26:A:2644:C:OP1	32:6:34:GLU:OE2	2.05	0.74
28:2:41:CYS:HB2	28:2:44:PHE:CE2	2.22	0.74
24:Z:18:LEU:HD13	24:Z:61:LEU:HD23	1.68	0.74
25:B:25:G:H21	25:B:114:A:H1'	1.50	0.74
25:B:84:C:C4	25:B:85:C:N3	2.55	0.74
10:L:109:LYS:HD2	10:L:110:LYS:NZ	2.02	0.74
25:B:10:G:H1	25:B:107:A:H2	0.80	0.74
25:B:28:A:H61	25:B:56:C:N4	1.85	0.74
1:C:23:GLU:O	1:C:82:ILE:HB	1.86	0.73
33:7:22:ARG:HH22	33:7:37:GLY:HA2	0.93	0.73
4:F:64:LEU:HB2	4:F:72:PRO:HG3	1.70	0.73
26:A:1563:A:O2'	26:A:1564:A:H5'	1.87	0.73
4:F:11:LEU:HD13	4:F:108:ASP:HB2	1.70	0.73
12:N:60:ARG:HG2	12:N:60:ARG:NH2	2.03	0.73
13:O:90:ARG:NH2	13:O:118:GLU:HB2	2.03	0.73
26:A:1563:A:H61	26:A:1607:C:N4	1.82	0.73
4:F:185:LYS:O	4:F:185:LYS:HE2	1.88	0.73
20:V:47:VAL:C	20:V:56:SER:HA	2.09	0.73
21:W:29:ARG:NH1	25:B:90:G:C5'	2.51	0.73
26:A:1561:C:H41	26:A:1562:C:H41	1.34	0.73
26:A:1703:G:H1	26:A:1726:C:H42	1.33	0.73
1:C:55:GLY:HA3	1:C:218:ARG:HG3	1.71	0.73
4:F:6:LYS:HE2	4:F:6:LYS:HA	1.70	0.73
26:A:801:U:O2'	31:5:7:THR:O	2.05	0.73
1:C:20:ASP:OD2	1:C:22:ALA:HB2	1.89	0.73
20:V:42:LYS:CD	26:A:586:U:H5''	2.18	0.73
26:A:1601:G:C2'	26:A:1602:U:C5'	2.62	0.73
15:Q:51:GLY:HA2	15:Q:56:GLU:HG3	1.71	0.73
19:U:77:LYS:HD3	19:U:79:THR:HG23	1.70	0.73
1:C:262:LYS:CE	26:A:2309:U:OP1	2.37	0.73
1:C:56:GLY:HA3	26:A:807:C:OP1	1.90	0.72
3:E:7:VAL:CG2	3:E:16:GLY:C	2.54	0.72
20:V:86:ARG:HB3	20:V:97:ILE:CG1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:59:ALA:H	17:S:103:LYS:HE2	1.53	0.72
25:B:24:G:N7	25:B:56:C:O2'	2.21	0.72
9:K:96:HIS:CB	9:K:99:ARG:CG	2.68	0.72
17:S:103:LYS:C	17:S:103:LYS:HD3	2.10	0.72
25:B:18:C:O2'	25:B:19:G:H5''	1.89	0.72
12:N:59:LYS:HB2	12:N:59:LYS:NZ	2.05	0.72
12:N:65:TRP:HZ3	26:A:989:G:HO2'	1.36	0.72
13:O:33:ARG:CG	13:O:114:GLU:HG2	2.19	0.72
30:4:15:CYS:HB2	30:4:20:HIS:N	2.05	0.72
1:C:55:GLY:CA	1:C:218:ARG:HD2	2.17	0.72
26:A:1561:C:H2'	26:A:1562:C:H5'	1.71	0.72
26:A:1604:G:H2'	26:A:1605:G:H5''	1.72	0.72
1:C:25:THR:HG22	1:C:82:ILE:H	1.53	0.72
3:E:14:THR:HG22	3:E:15:ASP:N	2.04	0.72
4:F:105:GLU:HG3	28:2:24:THR:CG2	2.20	0.72
10:L:8:LEU:HD12	10:L:8:LEU:N	2.03	0.72
13:O:90:ARG:NH1	13:O:118:GLU:HG3	2.05	0.72
17:S:6:ILE:C	17:S:7:VAL:HG23	2.10	0.72
26:A:1566:A:C2'	26:A:1605:G:O6	2.38	0.72
1:C:257:THR:HG22	26:A:2020:A:O2'	1.90	0.72
4:F:74:VAL:O	25:B:41:U:C4	2.42	0.72
26:A:2363:A:H61	26:A:2374:U:H3	1.36	0.72
22:X:15:ASP:HB2	26:A:2486:U:C4	2.25	0.71
25:B:81:U:H3	25:B:92:G:H22	1.38	0.71
26:A:1581:C:N4	26:A:1591:U:H1'	1.98	0.71
12:N:59:LYS:HB2	12:N:59:LYS:HZ3	1.54	0.71
22:X:26:PHE:H	22:X:29:GLN:HE21	1.38	0.71
25:B:57:U:C3'	25:B:58:A:H5''	2.20	0.71
26:A:1572:G:OP2	26:A:1594:G:OP2	2.08	0.71
31:5:6:ARG:NH1	31:5:6:ARG:HB2	2.05	0.71
3:E:24:LEU:CD2	3:E:208:ASN:OD1	2.38	0.71
4:F:44:ASN:OD1	26:A:2536:U:H2'	1.90	0.71
19:U:66:ARG:HA	19:U:75:LYS:HA	1.72	0.71
26:A:964:C:O2'	27:1:21:GLU:HG2	1.90	0.71
26:A:1600:G:OP1	26:A:1600:G:H4'	1.88	0.71
19:U:73:PHE:HZ	31:5:43:ARG:HH22	1.37	0.71
26:A:1600:G:H3'	26:A:1601:G:H5''	1.70	0.71
13:O:43:ALA:C	13:O:46:PRO:HD2	2.11	0.71
19:U:83:ILE:HD13	26:A:1456:G:C2	2.19	0.71
21:W:87:PRO:O	21:W:90:ARG:CZ	2.39	0.71
2:D:154:CYS:SG	26:A:2798:G:O3'	2.48	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:50:GLN:HE22	25:B:7:G:N2	1.87	0.71
26:A:279:U:H3	26:A:307:G:H1	1.39	0.71
26:A:290:C:H42	26:A:298:G:H1	1.38	0.71
3:E:143:THR:O	3:E:147:THR:OG1	2.09	0.71
13:O:16:HIS:CD2	26:A:1390:A:C5	2.78	0.71
13:O:117:ARG:HD3	13:O:118:GLU:N	2.06	0.71
24:Z:18:LEU:CD1	24:Z:61:LEU:CD2	2.69	0.71
1:C:54:LYS:NZ	26:A:2031:G:C3'	2.54	0.71
2:D:154:CYS:SG	26:A:2796:A:C2'	2.79	0.71
9:K:142:ILE:HG22	9:K:143:LYS:N	2.06	0.71
13:O:4:PRO:CG	26:A:3094:A:C2	2.73	0.71
20:V:96:ARG:O	20:V:97:ILE:HD13	1.91	0.71
26:A:1704:U:H3	26:A:1725:G:H1	1.39	0.70
9:K:112:ASN:ND2	26:A:650:G:P	2.64	0.70
20:V:99:LYS:HZ2	20:V:99:LYS:HB3	1.56	0.70
26:A:1566:A:O2'	26:A:1605:G:O6	2.09	0.70
4:F:9:PRO:HD2	4:F:12:LYS:CE	2.21	0.70
9:K:13:ARG:HH21	9:K:49:ASP:C	1.94	0.70
19:U:68:ARG:O	19:U:69:THR:HG23	1.92	0.70
24:Z:13:LEU:HD21	24:Z:17:GLU:C	2.11	0.70
26:A:2075:G:HO2'	26:A:2107:G:H1	0.77	0.70
30:4:15:CYS:C	30:4:20:HIS:CB	2.59	0.70
25:B:20:G:N2	25:B:63:U:C2	2.52	0.70
26:A:1554:U:N3	26:A:1617:C:N4	2.33	0.70
1:C:33:LEU:O	1:C:64:VAL:HG22	1.91	0.70
1:C:57:GLY:O	1:C:58:HIS:C	2.29	0.70
2:D:156:THR:HG21	26:A:2256:G:N2	2.05	0.70
13:O:29:PHE:CD2	13:O:79:LEU:HD11	2.24	0.70
30:4:15:CYS:CB	30:4:20:HIS:CA	2.63	0.70
2:D:156:THR:O	26:A:2795:C:O2'	2.09	0.70
10:L:109:LYS:HD2	10:L:110:LYS:HZ1	1.55	0.70
20:V:42:LYS:HD3	20:V:59:ILE:HD11	1.73	0.70
25:B:19:G:C5'	25:B:19:G:H8	2.03	0.70
26:A:1580:A:C6	26:A:1592:G:N3	2.58	0.70
4:F:66:LEU:HA	28:2:27:THR:HG21	1.74	0.70
13:O:5:THR:O	13:O:6:LYS:HB3	1.92	0.70
14:P:45:ARG:NH1	25:B:52:G:N7	2.17	0.70
21:W:21:LYS:HZ2	25:B:80:C:H42	1.39	0.70
26:A:1578:G:N3	26:A:1592:G:N2	2.17	0.70
1:C:25:THR:HG1	1:C:81:HIS:CE1	2.06	0.70
13:O:33:ARG:HD3	13:O:114:GLU:CG	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:13:LEU:CD1	24:Z:17:GLU:OE1	2.39	0.70
26:A:802:C:O4'	31:5:7:THR:HA	1.92	0.70
26:A:1566:A:N3	26:A:1605:G:N1	2.39	0.70
1:C:25:THR:CB	1:C:81:HIS:HD1	2.03	0.70
13:O:33:ARG:CG	13:O:114:GLU:CG	2.70	0.70
2:D:154:CYS:CA	26:A:2798:G:O2'	2.39	0.69
9:K:7:LYS:O	9:K:10:ASP:OD1	2.10	0.69
13:O:29:PHE:CZ	13:O:51:LEU:HD12	2.25	0.69
13:O:33:ARG:CD	13:O:114:GLU:CG	2.70	0.69
25:B:29:C:C2	25:B:55:G:N2	2.58	0.69
25:B:60:G:H8	25:B:60:G:C5'	2.02	0.69
26:A:997:G:H1	26:A:1010:U:H3	1.40	0.69
21:W:87:PRO:C	21:W:90:ARG:HH22	1.95	0.69
26:A:1556:A:N6	26:A:1615:G:H1	1.89	0.69
27:1:19:GLN:CG	27:1:50:VAL:HG12	2.21	0.69
9:K:47:ASN:HD21	26:A:623:A:H2	1.39	0.69
13:O:90:ARG:NH2	13:O:118:GLU:HB3	2.07	0.69
21:W:77:LEU:CB	21:W:100:VAL:HG21	2.11	0.69
22:X:83:VAL:HG13	22:X:86:PRO:HD3	1.72	0.69
20:V:62:GLN:CG	20:V:63:GLU:N	2.39	0.69
24:Z:18:LEU:CD1	24:Z:61:LEU:HD23	2.22	0.69
26:A:966:U:H5'	27:1:49:THR:OG1	1.92	0.69
1:C:262:LYS:HE2	26:A:2309:U:OP1	1.93	0.69
21:W:37:LEU:HD11	21:W:69:LEU:HD12	1.73	0.69
28:2:38:CYS:SG	28:2:40:GLN:NE2	2.64	0.69
4:F:182:PHE:HD2	4:F:184:PHE:CE2	2.09	0.69
17:S:58:VAL:CG2	17:S:103:LYS:HG3	1.94	0.69
25:B:24:G:C4	25:B:56:C:N3	2.61	0.69
9:K:25:LEU:HD12	9:K:26:GLY:H	1.56	0.69
30:4:18:CYS:CB	30:4:45:CYS:SG	2.81	0.69
4:F:73:GLU:CG	25:B:42:C:C6	2.73	0.69
9:K:3:THR:HG22	26:A:1113:C:O2	1.92	0.69
25:B:24:G:C6	25:B:56:C:O2	2.42	0.69
26:A:802:C:C4'	31:5:7:THR:HA	2.21	0.69
26:A:1563:A:N1	26:A:1607:C:N4	2.41	0.69
9:K:96:HIS:CB	9:K:99:ARG:HG3	2.23	0.69
13:O:20:LEU:HD23	13:O:20:LEU:C	2.13	0.69
22:X:13:GLY:C	22:X:14:ARG:HG3	2.13	0.69
30:4:15:CYS:N	30:4:20:HIS:HA	2.07	0.69
1:C:26:ARG:CD	1:C:81:HIS:CG	2.76	0.69
10:L:92:ASP:OD2	10:L:93:PRO:CD	2.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:40:A:C8	28:2:2:LYS:HE3	2.27	0.69
25:B:58:A:H8	25:B:58:A:C5'	2.02	0.69
26:A:753:A:H61	26:A:762:U:H3	1.41	0.69
26:A:1566:A:O2'	26:A:1605:G:N1	2.26	0.69
4:F:183:PRO:C	4:F:184:PHE:CD2	2.50	0.68
21:W:24:SER:OG	25:B:76:G:H5''	1.92	0.68
22:X:83:VAL:CG1	22:X:86:PRO:HD3	2.23	0.68
26:A:1566:A:O2'	26:A:1605:G:C6	2.37	0.68
10:L:8:LEU:CD1	10:L:19:ILE:CG1	2.71	0.68
19:U:83:ILE:CD1	26:A:1456:G:N1	2.52	0.68
20:V:46:ALA:HB1	26:A:572:C:OP1	1.94	0.68
25:B:19:G:C2	25:B:65:C:N3	2.59	0.68
26:A:2702:A:OP1	33:7:31:ARG:NH1	2.26	0.68
13:O:20:LEU:HD21	13:O:24:LEU:HD11	1.73	0.68
18:T:81:VAL:HG12	18:T:112:VAL:HG12	1.75	0.68
2:D:155:ALA:CB	26:A:2796:A:H8	1.65	0.68
21:W:64:ASN:ND2	21:W:109:GLU:O	2.27	0.68
21:W:101:GLN:CB	21:W:104:GLU:HB2	2.16	0.68
26:A:1608:U:O2'	26:A:1609:G:H5'	1.93	0.68
1:C:58:HIS:HE1	26:A:1788:G:H21	1.41	0.68
19:U:4:ILE:CD1	24:Z:58:TYR:HE1	2.00	0.68
21:W:22:GLY:HA3	25:B:92:G:OP2	1.93	0.68
25:B:40:A:H61	28:2:1:MET:H3	1.37	0.68
25:B:44:C:OP2	28:2:1:MET:N	2.27	0.68
3:E:7:VAL:HG23	3:E:16:GLY:O	1.92	0.68
9:K:4:TYR:CD2	16:R:100:VAL:HG11	2.29	0.68
26:A:1590:G:C4	26:A:1591:U:H5	1.97	0.68
1:C:73:ASP:OD1	1:C:73:ASP:N	2.26	0.68
13:O:9:ARG:N	13:O:9:ARG:HD2	2.09	0.68
21:W:58:LEU:O	21:W:62:GLY:HA3	1.93	0.68
26:A:1580:A:O2'	26:A:1581:C:H5''	1.94	0.68
4:F:47:VAL:HG21	4:F:93:GLY:N	2.09	0.68
25:B:24:G:C8	25:B:56:C:O2	2.37	0.68
1:C:76:ASN:O	1:C:98:LEU:HD22	1.92	0.68
9:K:96:HIS:HB3	9:K:99:ARG:CG	2.23	0.68
9:K:113:LYS:N	9:K:113:LYS:HD3	2.06	0.68
20:V:43:LYS:O	20:V:59:ILE:HA	1.93	0.68
22:X:19:GLN:N	22:X:19:GLN:OE1	2.26	0.68
22:X:83:VAL:HG12	22:X:85:ARG:CB	2.24	0.68
25:B:25:G:O2'	25:B:26:A:H5'	1.94	0.68
4:F:45:MET:HG2	4:F:60:ALA:HB1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:47:TYR:OH	13:O:69:LYS:HG2	1.92	0.67
26:A:1939:U:H3	26:A:1955:A:H62	1.40	0.67
2:D:114:VAL:HG12	2:D:208:VAL:HG12	1.74	0.67
9:K:142:ILE:O	9:K:143:LYS:HB2	1.95	0.67
13:O:79:LEU:C	13:O:79:LEU:HD23	2.15	0.67
25:B:83:C:H4'	27:1:52:HIS:ND1	2.08	0.67
26:A:1574:G:O6	26:A:1600:G:N7	2.27	0.67
26:A:1609:G:O2'	26:A:1610:C:H5'	1.94	0.67
30:4:11:ILE:HD13	30:4:27:LYS:CD	2.24	0.67
3:E:149:THR:C	3:E:150:GLU:HG3	2.13	0.67
4:F:79:LYS:HE3	4:F:81:ILE:HG12	1.76	0.67
10:L:108:GLU:HG3	10:L:109:LYS:N	2.08	0.67
26:A:1541:G:O6	26:A:1630:U:O4	2.12	0.67
26:A:1572:G:O6	26:A:1600:G:C2	2.47	0.67
26:A:2349:A:H61	26:A:2386:U:H5'	1.58	0.67
30:4:34:ASP:OD2	30:4:35:ARG:HG2	1.95	0.67
1:C:26:ARG:HG3	1:C:81:HIS:CG	2.29	0.67
1:C:29:PRO:CB	1:C:34:VAL:HG21	2.25	0.67
9:K:25:LEU:HD12	9:K:26:GLY:N	2.10	0.67
12:N:58:ILE:HG23	12:N:108:TYR:CZ	2.30	0.67
18:T:9:SER:HB3	18:T:115:GLU:HB3	1.72	0.67
10:L:7:ARG:HG2	10:L:7:ARG:HH21	1.58	0.67
18:T:75:THR:O	18:T:118:PRO:HD3	1.95	0.67
26:A:1567:C:N3	26:A:1603:G:O6	2.27	0.67
26:A:1577:C:H5	26:A:1594:G:O6	1.78	0.67
1:C:35:ARG:NH2	1:C:35:ARG:HG2	2.09	0.67
22:X:75:ARG:HE	26:A:2558:C:N4	1.93	0.67
24:Z:18:LEU:HB3	24:Z:61:LEU:HD21	1.76	0.67
26:A:1568:C:C3'	26:A:1569:A:H8	2.06	0.67
30:4:28:ASN:OD1	30:4:31:ASN:N	2.27	0.67
1:C:25:THR:HG23	1:C:81:HIS:CB	1.98	0.67
25:B:10:G:C6	25:B:107:A:N1	2.62	0.67
26:A:747:A:N6	26:A:768:G:O2'	2.28	0.67
26:A:1540:U:H3	26:A:1632:G:H1	1.43	0.67
26:A:1592:G:O2'	26:A:1593:U:H6	1.77	0.67
1:C:22:ALA:O	1:C:23:GLU:HB2	1.94	0.67
9:K:113:LYS:HD3	9:K:113:LYS:H	1.60	0.67
9:K:142:ILE:HG22	26:A:1130:C:N4	1.78	0.67
25:B:35:G:C2	25:B:36:U:C5	2.83	0.67
3:E:144:PHE:CD1	3:E:148:LEU:CG	2.77	0.67
3:E:151:ASN:C	3:E:152:LYS:HG3	2.06	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:95:THR:HG22	13:O:115:LEU:CD2	2.25	0.67
20:V:30:ARG:O	20:V:31:ASN:HB2	1.95	0.67
25:B:20:G:H2'	25:B:21:C:H5'	1.77	0.67
3:E:107:ILE:HD11	26:A:710:G:OP1	1.95	0.67
18:T:67:ASN:ND2	26:A:574:C:O2'	2.29	0.67
19:U:9:ASP:N	19:U:9:ASP:OD1	2.25	0.67
30:4:36:LEU:HG	30:4:37:GLU:H	1.60	0.67
1:C:29:PRO:HG2	1:C:34:VAL:HG21	1.75	0.66
1:C:222:ARG:NH1	26:A:2006:A:OP2	2.28	0.66
4:F:111:ILE:HD11	4:F:182:PHE:HA	1.76	0.66
6:H:43:ALA:O	6:H:47:ALA:HB3	1.95	0.66
9:K:3:THR:HG23	26:A:1113:C:O2	1.95	0.66
13:O:81:ALA:C	13:O:85:PRO:HD2	2.08	0.66
22:X:76:LYS:NZ	26:A:973:G:OP1	2.27	0.66
25:B:2:U:H3	25:B:115:A:H61	1.43	0.66
26:A:1583:U:O2	26:A:1589:G:C2	2.49	0.66
19:U:69:THR:CG2	19:U:73:PHE:O	2.43	0.66
1:C:56:GLY:HA2	26:A:807:C:OP1	1.95	0.66
19:U:10:ILE:HD13	19:U:10:ILE:N	2.10	0.66
4:F:32:VAL:O	4:F:33:MET:CB	2.43	0.66
26:A:1568:C:H2'	26:A:1569:A:C8	2.30	0.66
13:O:20:LEU:HD21	13:O:24:LEU:CD1	2.24	0.66
20:V:4:HIS:HE1	20:V:96:ARG:HH22	1.39	0.66
20:V:96:ARG:HG3	20:V:96:ARG:HH21	1.61	0.66
21:W:9:ASN:HD21	21:W:57:VAL:HG13	1.59	0.66
25:B:85:C:H2'	25:B:86:U:H5''	1.75	0.66
26:A:1568:C:H3'	26:A:1569:A:C8	2.30	0.66
26:A:1607:C:H6	26:A:1607:C:O5'	1.78	0.66
25:B:12:C:O2'	25:B:13:C:OP2	2.11	0.66
26:A:1578:G:N2	26:A:1592:G:H2'	2.09	0.66
3:E:201:LEU:O	3:E:201:LEU:HD23	1.94	0.66
4:F:51:ALA:HB2	4:F:90:MET:HE1	1.77	0.66
20:V:43:LYS:NZ	20:V:43:LYS:HB3	2.09	0.66
21:W:8:PRO:CB	21:W:68:THR:OG1	2.44	0.66
4:F:87:ARG:HB3	4:F:90:MET:HG3	1.78	0.66
9:K:96:HIS:HB2	9:K:99:ARG:HG3	1.77	0.66
26:A:1577:C:O2'	26:A:1578:G:H5'	1.95	0.66
1:C:100:GLY:O	26:A:1720:G:O2'	2.14	0.66
9:K:27:ARG:HH11	9:K:27:ARG:HG3	1.59	0.66
28:2:14:VAL:HB	28:2:22:PHE:HB2	1.78	0.65
26:A:1568:C:H3'	26:A:1569:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:6:26:LYS:NZ	32:6:45:ASP:O	2.28	0.65
1:C:29:PRO:HB2	1:C:34:VAL:HG21	1.77	0.65
11:M:61:LEU:HD21	32:6:24:ARG:HH11	1.60	0.65
21:W:105:LYS:HZ3	21:W:136:GLU:CD	1.99	0.65
26:A:1830:C:H4'	31:5:10:PRO:HD3	1.79	0.65
31:5:5:LYS:O	31:5:6:ARG:HG2	1.96	0.65
3:E:45:LYS:HG3	26:A:709:U:C4	2.31	0.65
4:F:6:LYS:HE2	4:F:6:LYS:CA	2.26	0.65
20:V:72:MET:HG2	20:V:80:PRO:HB2	1.78	0.65
25:B:70:G:H22	25:B:103:G:H1	1.43	0.65
4:F:110:LEU:HD23	4:F:111:ILE:H	1.60	0.65
21:W:102:ARG:NH2	21:W:138:LEU:HD21	2.12	0.65
1:C:35:ARG:HG2	1:C:35:ARG:HH21	1.59	0.65
2:D:144:VAL:HG22	2:D:147:ARG:HE	1.62	0.65
9:K:25:LEU:HD22	9:K:62:ILE:CD1	2.27	0.65
26:A:1563:A:H8	26:A:1563:A:OP2	1.80	0.65
3:E:192:ASP:HB3	11:M:5:LYS:HZ1	0.83	0.65
9:K:85:ARG:NH2	26:A:2866:A:OP2	2.26	0.65
9:K:116:ARG:NH2	26:A:615:A:H5''	2.12	0.65
9:K:134:ALA:C	9:K:135:GLN:HG2	2.17	0.65
26:A:1573:U:H1'	26:A:1574:G:P	2.37	0.65
3:E:8:LYS:HE3	3:E:148:LEU:HD22	1.79	0.65
3:E:7:VAL:HB	3:E:16:GLY:CA	2.26	0.65
3:E:192:ASP:CB	11:M:5:LYS:HZ3	1.92	0.65
4:F:57:ILE:HG12	4:F:91:PRO:HB2	1.77	0.65
9:K:96:HIS:CB	9:K:99:ARG:HG2	2.25	0.65
13:O:77:HIS:CG	26:A:1674:G:H2'	2.11	0.65
20:V:2:LYS:CE	20:V:83:VAL:HG12	2.27	0.65
22:X:16:SER:O	22:X:17:ALA:HB3	1.96	0.65
21:W:77:LEU:CD2	21:W:100:VAL:HG21	2.26	0.64
4:F:46:GLY:O	4:F:47:VAL:CB	2.46	0.64
25:B:79:A:H2	25:B:94:G:H1	1.42	0.64
30:4:47:THR:OG1	30:4:49:GLN:NE2	2.30	0.64
21:W:9:ASN:ND2	21:W:57:VAL:CG1	2.53	0.64
26:A:1573:U:H1'	26:A:1574:G:OP1	1.97	0.64
30:4:18:CYS:SG	30:4:19:LYS:NZ	2.70	0.64
4:F:10:ARG:HG2	4:F:10:ARG:NH1	2.05	0.64
26:A:1563:A:C6	26:A:1607:C:N4	2.65	0.64
3:E:107:ILE:HD11	26:A:710:G:H5''	1.79	0.64
25:B:96:A:H2	26:A:977:G:N2	1.96	0.64
1:C:108:PRO:HD2	1:C:111:LEU:HD22	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1610:C:O5'	26:A:1610:C:H6	1.80	0.64
4:F:45:MET:HE1	4:F:64:LEU:CD2	2.27	0.64
9:K:13:ARG:NE	9:K:121:LYS:HZ3	1.96	0.64
22:X:17:ALA:HB1	26:A:2485:C:P	2.37	0.64
26:A:1565:A:C2	26:A:1606:G:C4	2.86	0.64
31:5:6:ARG:HB2	31:5:6:ARG:HH11	1.62	0.64
4:F:55:LYS:HB2	4:F:55:LYS:HZ2	1.63	0.64
13:O:29:PHE:CD2	13:O:79:LEU:CD1	2.77	0.64
19:U:75:LYS:O	26:A:61:G:H5'	1.96	0.64
25:B:29:C:N4	25:B:55:G:H1	1.94	0.64
1:C:37:LEU:HD23	1:C:62:TYR:CB	2.27	0.64
13:O:56:LYS:NZ	13:O:94:TYR:OH	2.21	0.64
20:V:99:LYS:HB3	20:V:99:LYS:NZ	2.12	0.64
1:C:256:ARG:CD	1:C:258:ARG:HD2	2.28	0.64
3:E:150:GLU:HB2	3:E:193:ASP:OD2	1.98	0.64
4:F:53:ASP:O	4:F:56:LEU:HD21	1.97	0.64
10:L:80:ASP:OD2	15:Q:61:ARG:CZ	2.46	0.64
13:O:45:ARG:NH1	26:A:3102:U:O2	2.31	0.64
2:D:48:SER:HB2	2:D:92:VAL:HG21	1.80	0.63
4:F:132:THR:HG21	14:P:6:VAL:HG22	1.77	0.63
9:K:1:MET:N	9:K:2:PRO:HD3	2.13	0.63
10:L:91:ASN:OD1	10:L:92:ASP:N	2.30	0.63
12:N:60:ARG:CZ	26:A:1194:C:P	2.86	0.63
20:V:2:LYS:NZ	20:V:85:TYR:CD2	2.62	0.63
20:V:96:ARG:HH21	20:V:96:ARG:CG	2.11	0.63
18:T:44:ARG:HH12	29:3:55:ASP:N	1.90	0.63
18:T:75:THR:CB	18:T:118:PRO:HG3	2.28	0.63
21:W:104:GLU:HA	21:W:104:GLU:OE1	1.98	0.63
26:A:1582:C:H2'	26:A:1583:U:H5'	1.79	0.63
1:C:25:THR:CG2	1:C:82:ILE:N	2.62	0.63
4:F:11:LEU:HD13	4:F:108:ASP:CB	2.27	0.63
11:M:76:GLN:NE2	26:A:720:C:N3	2.46	0.63
19:U:4:ILE:N	19:U:4:ILE:HD12	2.13	0.63
4:F:66:LEU:CD2	28:2:27:THR:CG2	2.73	0.63
4:F:118:ILE:HD12	4:F:118:ILE:N	2.02	0.63
12:N:124:LYS:NZ	26:A:2691:C:O2	2.29	0.63
20:V:89:ASP:N	20:V:89:ASP:OD1	2.31	0.63
25:B:35:G:C2	25:B:36:U:C4	2.85	0.63
3:E:149:THR:HG23	3:E:150:GLU:HG3	1.79	0.63
4:F:49:ASP:CB	4:F:56:LEU:CD1	2.65	0.63
4:F:66:LEU:CD2	28:2:27:THR:HG22	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:55:ARG:HD2	5:G:62:SER:HB3	1.81	0.63
10:L:109:LYS:C	10:L:110:LYS:HG3	2.17	0.63
19:U:5:THR:CG2	19:U:6:ASP:H	2.07	0.63
19:U:69:THR:HG21	26:A:61:G:O2'	1.98	0.63
26:A:1598:U:O4	26:A:1601:G:N1	2.31	0.63
28:2:41:CYS:C	28:2:43:PRO:HD2	2.19	0.63
31:5:26:ARG:HD2	31:5:26:ARG:N	2.12	0.63
1:C:240:THR:HG22	1:C:242:GLY:H	1.64	0.63
3:E:3:LEU:HD11	3:E:26:ASP:OD1	1.99	0.63
20:V:28:PRO:HG3	26:A:83:C:OP1	1.98	0.63
20:V:86:ARG:HB3	20:V:97:ILE:HG12	1.80	0.63
24:Z:48:ARG:O	24:Z:52:GLN:NE2	2.31	0.63
25:B:57:U:H2'	25:B:58:A:C5'	2.21	0.63
26:A:1581:C:C2'	26:A:1582:C:C6	2.79	0.63
26:A:1592:G:HO2'	26:A:1593:U:H6	1.44	0.63
26:A:1604:G:C2'	26:A:1605:G:H5''	2.28	0.63
4:F:11:LEU:HD22	4:F:108:ASP:N	2.13	0.63
3:E:52:THR:OG1	3:E:92:GLY:HA3	1.99	0.63
3:E:118:ARG:NH1	11:M:4:ILE:O	2.31	0.63
9:K:96:HIS:HB2	9:K:99:ARG:CG	2.29	0.63
13:O:26:THR:HG23	13:O:75:VAL:HG21	1.81	0.63
25:B:19:G:C6	25:B:20:G:N7	2.67	0.63
25:B:25:G:N2	25:B:114:A:C4	2.62	0.63
4:F:120:ASP:CG	4:F:122:ARG:HH11	2.01	0.63
10:L:92:ASP:OD2	10:L:93:PRO:N	2.32	0.63
26:A:1564:A:C3'	26:A:1565:A:H5''	2.28	0.63
30:4:22:ASN:OD1	30:4:22:ASN:N	2.32	0.63
1:C:25:THR:HG21	1:C:81:HIS:CG	2.34	0.62
1:C:37:LEU:CD2	1:C:62:TYR:HD1	2.12	0.62
4:F:70:GLN:NE2	25:B:43:C:H4'	2.14	0.62
9:K:25:LEU:HD22	9:K:62:ILE:HD12	1.81	0.62
19:U:6:ASP:OD2	24:Z:23:ARG:HG3	1.98	0.62
25:B:82:A:N1	25:B:91:G:O6	2.32	0.62
25:B:84:C:C2'	25:B:85:C:H5'	2.28	0.62
26:A:1586:C:C3'	26:A:1587:G:H5''	2.28	0.62
28:2:38:CYS:HB2	28:2:40:GLN:NE2	2.14	0.62
31:5:38:ARG:HA	31:5:45:LEU:HD21	1.80	0.62
1:C:35:ARG:HH21	1:C:35:ARG:CG	2.12	0.62
4:F:118:ILE:HG13	4:F:144:MET:HG2	1.79	0.62
10:L:7:ARG:HH21	10:L:7:ARG:CG	2.12	0.62
19:U:29:TYR:CZ	19:U:93:ILE:HB	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:43:LYS:HG2	26:A:568:A:H4'	1.81	0.62
25:B:21:C:C6	25:B:21:C:H3'	2.35	0.62
26:A:1563:A:C5	26:A:1565:A:C5	2.87	0.62
26:A:1571:C:N3	26:A:1601:G:N2	2.47	0.62
30:4:15:CYS:CB	30:4:20:HIS:H	2.12	0.62
3:E:69:LYS:HE2	26:A:2668:G:OP2	1.98	0.62
5:G:154:ARG:HD2	5:G:155:PRO:HD2	1.82	0.62
21:W:101:GLN:HE21	21:W:101:GLN:C	2.01	0.62
25:B:40:A:H8	28:2:2:LYS:HE3	1.63	0.62
26:A:1590:G:C6	26:A:1591:U:C4	2.86	0.62
31:5:6:ARG:O	31:5:7:THR:OG1	2.09	0.62
1:C:96:HIS:HE1	1:C:102:LYS:HZ2	1.45	0.62
1:C:257:THR:CG2	26:A:2020:A:O2'	2.47	0.62
19:U:29:TYR:CD1	19:U:93:ILE:HG21	2.34	0.62
19:U:60:ALA:HB2	26:A:1456:G:H4'	1.81	0.62
20:V:83:VAL:CG1	20:V:96:ARG:HG3	2.27	0.62
1:C:37:LEU:CD2	1:C:62:TYR:CD1	2.81	0.62
13:O:33:ARG:HG3	13:O:114:GLU:HG2	1.78	0.62
17:S:6:ILE:CG2	17:S:7:VAL:N	2.63	0.62
25:B:24:G:C4	25:B:56:C:C2	2.88	0.62
25:B:88:C:H2'	25:B:89:C:C5	2.35	0.62
28:2:44:PHE:O	28:2:48:LYS:CG	2.42	0.62
25:B:21:C:H3'	25:B:21:C:H6	1.65	0.62
25:B:60:G:C2'	25:B:61:C:H5'	2.29	0.62
3:E:118:ARG:HH11	11:M:3:VAL:CG1	2.13	0.62
17:S:6:ILE:HG22	17:S:7:VAL:H	1.64	0.62
19:U:69:THR:HG23	19:U:73:PHE:O	1.98	0.62
26:A:1603:G:C2	26:A:1604:G:C5	2.88	0.62
26:A:1609:G:H2'	26:A:1610:C:C6	2.35	0.62
25:B:79:A:C2	25:B:94:G:N1	2.58	0.62
26:A:1122:C:H2'	26:A:1129:G:H2'	1.82	0.62
4:F:76:ARG:NH1	25:B:41:U:H3	1.98	0.62
13:O:67:MET:HG3	13:O:76:VAL:HG11	1.81	0.62
19:U:29:TYR:CE1	19:U:93:ILE:HG21	2.34	0.62
30:4:19:LYS:HD3	30:4:44:ASN:HB2	1.80	0.62
26:A:1563:A:C8	26:A:1565:A:N7	2.68	0.62
1:C:63:ARG:HH12	26:A:1788:G:P	2.22	0.61
2:D:60:ARG:NH2	26:A:3052:A:OP1	2.33	0.61
4:F:126:PRO:O	4:F:174:ARG:NH1	2.33	0.61
7:I:27:GLU:HB2	7:I:106:LYS:HE3	1.81	0.61
25:B:59:A:H2'	25:B:59:A:N3	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:15:CYS:C	30:4:20:HIS:HA	2.20	0.61
11:M:84:ASN:ND2	11:M:117:LYS:O	2.33	0.61
20:V:2:LYS:CD	20:V:83:VAL:HG12	2.30	0.61
30:4:11:ILE:HD13	30:4:27:LYS:HD3	1.81	0.61
30:4:19:LYS:HG3	30:4:21:ARG:HG2	1.82	0.61
1:C:256:ARG:NE	1:C:258:ARG:HE	1.97	0.61
13:O:7:GLY:O	13:O:9:ARG:NH1	2.33	0.61
25:B:19:G:C8	25:B:19:G:H3'	2.35	0.61
1:C:256:ARG:HD3	1:C:258:ARG:NE	2.14	0.61
1:C:73:ASP:CB	1:C:120:GLY:HA3	2.28	0.61
1:C:158:SER:OG	1:C:159:ALA:N	2.34	0.61
8:J:96:LYS:HE3	21:W:120:PRO:CB	2.27	0.61
10:L:107:ARG:NH1	15:Q:33:GLU:CG	2.63	0.61
11:M:51:GLU:CG	32:6:57:ARG:HH11	2.11	0.61
12:N:60:ARG:CZ	26:A:1194:C:OP2	2.48	0.61
13:O:43:ALA:CA	13:O:46:PRO:HD2	2.30	0.61
20:V:86:ARG:HD3	20:V:97:ILE:CG1	2.30	0.61
21:W:102:ARG:NH2	21:W:138:LEU:CD1	2.57	0.61
28:2:16:CYS:SG	28:2:17:GLY:N	2.74	0.61
20:V:86:ARG:CB	20:V:97:ILE:HG13	2.30	0.61
4:F:45:MET:HB3	4:F:94:ALA:N	2.16	0.61
26:A:1610:C:H2'	26:A:1611:A:H8	1.65	0.61
26:A:1754:G:O6	26:A:1759:A:N1	2.33	0.61
30:4:13:LEU:O	30:4:23:TYR:N	2.34	0.61
4:F:9:PRO:HD2	4:F:12:LYS:HZ2	1.66	0.61
9:K:110:PRO:O	9:K:115:GLY:HA3	2.01	0.61
13:O:8:PRO:HG3	26:A:1870:U:N3	2.14	0.61
4:F:77:ALA:HB2	4:F:92:ILE:HD11	1.82	0.60
18:T:41:ASP:CG	29:3:38:LYS:HB2	2.20	0.60
19:U:57:VAL:HG22	19:U:84:VAL:HG12	1.82	0.60
19:U:68:ARG:HB2	26:A:1450:C:OP1	2.01	0.60
1:C:241:SER:OG	26:A:2127:G:OP1	2.18	0.60
26:A:2256:G:N2	26:A:2796:A:OP2	2.33	0.60
10:L:109:LYS:HG2	10:L:110:LYS:HG3	1.82	0.60
1:C:25:THR:CG2	1:C:81:HIS:CG	2.83	0.60
3:E:121:ASN:ND2	11:M:3:VAL:HG22	2.16	0.60
24:Z:18:LEU:HD13	24:Z:61:LEU:HD21	1.82	0.60
28:2:43:PRO:HA	28:2:46:THR:HG1	1.66	0.60
3:E:35:HIS:HE1	26:A:1359:G:O2'	1.85	0.60
3:E:121:ASN:ND2	11:M:3:VAL:CG2	2.64	0.60
3:E:155:LEU:HB3	3:E:194:VAL:HG12	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:129:ILE:HA	26:A:1198:C:HI'	1.84	0.60
9:K:77:HIS:CD2	9:K:78:SER:O	2.54	0.60
18:T:116:SER:C	18:T:118:PRO:HD2	2.21	0.60
1:C:262:LYS:HD2	1:C:262:LYS:N	2.17	0.60
2:D:27:THR:HG21	2:D:198:ILE:HG12	1.84	0.60
8:J:57:PRO:HD3	8:J:76:PRO:HD3	1.84	0.60
11:M:61:LEU:HD22	32:6:24:ARG:HH11	1.64	0.60
13:O:43:ALA:O	13:O:46:PRO:HD2	2.02	0.60
20:V:59:ILE:O	20:V:59:ILE:HG12	2.02	0.60
26:A:808:A:O2'	26:A:1468:A:N3	2.35	0.60
19:U:4:ILE:O	19:U:4:ILE:HG22	2.01	0.60
25:B:25:G:N2	25:B:114:A:C2'	2.61	0.60
26:A:1562:C:O2'	26:A:1563:A:H5'	2.02	0.60
27:1:51:HIS:H	27:1:51:HIS:HD2	1.46	0.60
1:C:54:LYS:HZ3	26:A:2031:G:H5''	1.65	0.60
3:E:42:LEU:O	26:A:531:A:N6	2.34	0.60
3:E:186:TYR:CE1	11:M:6:LEU:HD11	2.37	0.60
8:J:111:ALA:HA	8:J:114:LYS:HB2	1.83	0.60
10:L:104:ARG:HH12	15:Q:33:GLU:HB2	1.67	0.60
25:B:24:G:C8	25:B:56:C:H2'	2.37	0.60
26:A:2713:G:OP1	34:8:6:ARG:NH2	2.33	0.60
33:7:22:ARG:CD	33:7:36:GLN:O	2.49	0.60
5:G:63:ARG:HB3	26:A:2973:A:H4'	1.84	0.60
20:V:45:THR:C	26:A:571:A:O2'	2.38	0.60
13:O:9:ARG:HG2	13:O:14:SER:CA	2.32	0.59
13:O:16:HIS:CD2	26:A:1390:A:N9	2.70	0.59
25:B:24:G:C2'	25:B:56:C:C4	2.85	0.59
25:B:36:U:O5'	25:B:36:U:H6	1.84	0.59
25:B:60:G:O2'	25:B:61:C:C5'	2.42	0.59
30:4:15:CYS:HB2	30:4:20:HIS:H	1.66	0.59
1:C:261:ASN:O	1:C:262:LYS:HB2	2.03	0.59
3:E:4:LYS:HD3	3:E:5:VAL:N	2.17	0.59
12:N:75:THR:HA	12:N:90:PRO:HA	1.84	0.59
21:W:6:ASN:O	21:W:6:ASN:ND2	2.35	0.59
21:W:36:VAL:HG21	25:B:74:A:H2	1.67	0.59
25:B:34:G:C6	25:B:44:C:C5	2.89	0.59
25:B:84:C:C4	25:B:85:C:C2	2.90	0.59
25:B:87:U:H3'	25:B:88:C:O4'	2.02	0.59
1:C:21:PHE:O	1:C:24:ILE:HG13	2.02	0.59
1:C:73:ASP:O	1:C:119:SER:O	2.19	0.59
1:C:257:THR:HG22	1:C:257:THR:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:262:LYS:HE3	26:A:2309:U:OP1	2.02	0.59
15:Q:5:ASP:O	15:Q:9:GLN:HB3	2.02	0.59
26:A:325:U:O2	26:A:450:G:N2	2.30	0.59
27:1:50:VAL:O	27:1:50:VAL:HG23	2.01	0.59
18:T:75:THR:HB	18:T:118:PRO:CG	2.32	0.59
26:A:2747:G:HO2'	26:A:2988:A:HO2'	1.49	0.59
3:E:45:LYS:CG	26:A:709:U:O4	2.49	0.59
25:B:19:G:C8	25:B:19:G:C3'	2.85	0.59
26:A:1608:U:C2	26:A:1609:G:N7	2.69	0.59
1:C:254:GLU:HG2	1:C:254:GLU:O	2.03	0.59
25:B:4:A:N3	25:B:25:G:O6	2.34	0.59
13:O:90:ARG:HH21	13:O:118:GLU:CB	2.10	0.59
18:T:82:TYR:HD2	18:T:111:THR:HB	1.68	0.59
19:U:4:ILE:CD1	24:Z:58:TYR:OH	2.46	0.59
19:U:73:PHE:HZ	31:5:43:ARG:NH2	2.01	0.59
21:W:29:ARG:HH11	25:B:90:G:H5'	1.65	0.59
26:A:285:U:H3'	26:A:286:G:H4'	1.85	0.59
1:C:37:LEU:HD21	1:C:62:TYR:HD1	1.67	0.59
3:E:107:ILE:HD12	26:A:710:G:OP1	2.02	0.59
3:E:127:VAL:O	3:E:198:VAL:HG23	2.02	0.59
12:N:60:ARG:O	21:W:190:LEU:CD1	2.51	0.59
18:T:75:THR:HB	18:T:118:PRO:HG3	1.83	0.59
18:T:116:SER:HG	18:T:118:PRO:HG2	1.66	0.59
20:V:2:LYS:HD2	20:V:83:VAL:CB	2.32	0.59
24:Z:18:LEU:CD1	24:Z:61:LEU:HD21	2.33	0.59
26:A:993:G:N2	26:A:1015:A:OP2	2.36	0.59
26:A:1552:A:N6	26:A:1616:A:OP2	2.35	0.59
11:M:68:LYS:NZ	26:A:244:A:OP1	2.36	0.59
18:T:84:ASP:OD1	26:A:20:G:N2	2.23	0.59
18:T:85:GLU:O	26:A:21:G:O2'	2.20	0.59
25:B:60:G:C2'	25:B:61:C:C5'	2.80	0.59
26:A:1604:G:H2'	26:A:1605:G:C5'	2.31	0.59
33:7:2:LYS:NZ	33:7:31:ARG:O	2.32	0.59
1:C:62:TYR:CE1	26:A:2033:U:H3'	2.38	0.59
1:C:96:HIS:CE1	1:C:102:LYS:HZ2	2.14	0.59
3:E:144:PHE:CD2	3:E:148:LEU:CD1	2.79	0.59
19:U:77:LYS:HE2	19:U:79:THR:HA	1.84	0.59
19:U:77:LYS:HZ3	19:U:79:THR:HG22	1.67	0.59
20:V:86:ARG:CD	20:V:97:ILE:HG13	2.32	0.59
25:B:55:G:H8	25:B:55:G:O5'	1.86	0.59
26:A:1573:U:O2'	26:A:1574:G:OP1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:LYS:HE3	26:A:1648:A:O2'	2.03	0.58
4:F:70:GLN:OE1	4:F:96:VAL:HG23	2.03	0.58
13:O:33:ARG:CD	13:O:114:GLU:CD	2.58	0.58
15:Q:19:PHE:HA	15:Q:88:ARG:HH12	1.68	0.58
26:A:858:A:O2'	26:A:1877:U:OP1	2.20	0.58
26:A:1174:G:O2'	26:A:1221:A:N6	2.36	0.58
1:C:20:ASP:O	1:C:21:PHE:HB2	2.04	0.58
2:D:154:CYS:CB	26:A:2799:C:C5'	2.72	0.58
13:O:79:LEU:HD23	13:O:80:PHE:N	2.18	0.58
20:V:86:ARG:HB3	20:V:97:ILE:HG13	1.85	0.58
25:B:31:C:H42	25:B:51:G:H1	1.51	0.58
25:B:96:A:C2	26:A:977:G:N2	2.71	0.58
26:A:1568:C:C3'	26:A:1569:A:C8	2.86	0.58
3:E:170:ARG:NH2	26:A:422:A:O2'	2.36	0.58
13:O:52:ILE:HD12	13:O:94:TYR:HB2	1.85	0.58
17:S:72:LYS:NZ	26:A:1337:G:N7	2.51	0.58
26:A:1595:G:O5'	26:A:1596:C:OP2	2.21	0.58
12:N:58:ILE:CG2	12:N:108:TYR:CZ	2.87	0.58
20:V:96:ARG:CZ	20:V:96:ARG:HB2	2.33	0.58
21:W:6:ASN:HB3	21:W:138:LEU:O	1.96	0.58
24:Z:18:LEU:CB	24:Z:61:LEU:HD21	2.33	0.58
26:A:1187:A:H4'	26:A:1188:A:H5''	1.85	0.58
12:N:58:ILE:HG21	12:N:108:TYR:CD1	2.36	0.58
13:O:29:PHE:HB3	13:O:79:LEU:HD12	0.60	0.58
19:U:58:ASN:HD22	26:A:1456:G:H21	1.49	0.58
21:W:82:ALA:O	21:W:83:LEU:HB2	2.04	0.58
28:2:45:TYR:O	28:2:49:GLN:HG3	2.03	0.58
3:E:9:THR:HG22	3:E:128:THR:OG1	2.04	0.58
12:N:85:SER:HG	22:X:8:SER:HB3	1.64	0.58
26:A:1397:U:H3	26:A:1401:A:H62	1.50	0.58
26:A:1568:C:C2'	26:A:1569:A:C8	2.87	0.58
1:C:51:THR:HG21	1:C:54:LYS:HE3	1.86	0.58
1:C:176:ARG:HG3	1:C:182:ILE:HG12	1.86	0.58
14:P:39:VAL:HA	14:P:103:ASP:HB3	1.86	0.58
24:Z:62:ARG:O	24:Z:62:ARG:HD3	2.03	0.58
25:B:4:A:C2	25:B:26:A:N6	2.71	0.58
25:B:84:C:N4	25:B:85:C:N3	2.52	0.58
26:A:1201:G:N2	26:A:1204:A:OP2	2.34	0.58
26:A:1584:U:C5	26:A:1586:C:OP2	2.57	0.58
3:E:90:VAL:CG1	26:A:678:A:O5'	2.51	0.58
5:G:2:SER:N	26:A:2973:A:OP1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:6:GLU:HG3	18:T:6:GLU:O	2.03	0.58
26:A:122:A:OP2	31:5:22:ARG:NH1	2.37	0.58
26:A:1000:C:OP2	26:A:1002:C:N4	2.36	0.58
4:F:11:LEU:HD22	4:F:108:ASP:HB3	1.85	0.58
4:F:53:ASP:O	4:F:56:LEU:HD22	2.02	0.58
13:O:16:HIS:HD2	26:A:1390:A:N9	2.02	0.58
19:U:19:LYS:CD	26:A:1508:A:H62	1.78	0.58
22:X:83:VAL:HG13	22:X:83:VAL:O	2.04	0.58
26:A:1574:G:H5''	26:A:1575:A:OP1	2.04	0.58
26:A:1584:U:C6	26:A:1586:C:OP2	2.57	0.58
10:L:76:TYR:O	15:Q:71:ARG:HD2	2.04	0.57
13:O:29:PHE:HE2	13:O:51:LEU:HD12	1.56	0.57
19:U:94:ASP:O	19:U:96:PHE:N	2.28	0.57
21:W:102:ARG:HH22	21:W:138:LEU:HD11	1.66	0.57
26:A:1703:G:H1	26:A:1726:C:N4	2.01	0.57
1:C:256:ARG:HG3	1:C:258:ARG:HD2	1.86	0.57
1:C:260:PRO:O	1:C:263:PRO:HD3	2.04	0.57
30:4:13:LEU:N	30:4:23:TYR:O	2.34	0.57
1:C:55:GLY:CA	1:C:218:ARG:HD3	2.33	0.57
13:O:11:GLY:O	13:O:12:GLY:C	2.42	0.57
26:A:1249:G:N2	26:A:1250:U:O4	2.35	0.57
26:A:1600:G:H3'	26:A:1601:G:C5'	2.34	0.57
15:Q:13:ARG:NH1	15:Q:80:ILE:O	2.36	0.57
18:T:9:SER:HB2	18:T:114:VAL:O	2.04	0.57
25:B:10:G:C2	25:B:107:A:H2	2.19	0.57
25:B:21:C:C6	25:B:21:C:C3'	2.88	0.57
3:E:144:PHE:HE1	3:E:148:LEU:CD2	2.05	0.57
12:N:134:ARG:HH21	21:W:129:ASN:ND2	2.00	0.57
14:P:50:GLN:NE2	25:B:7:G:C2	2.69	0.57
15:Q:19:PHE:O	15:Q:49:ARG:NH1	2.37	0.57
20:V:4:HIS:CG	20:V:96:ARG:NH1	2.71	0.57
25:B:14:A:OP2	25:B:70:G:O2'	2.22	0.57
4:F:23:LEU:CD2	4:F:29:TYR:OH	2.53	0.57
8:J:44:TYR:O	8:J:48:THR:CB	2.51	0.57
26:A:1518:A:HO2'	26:A:1692:G:HO2'	1.52	0.57
26:A:2508:C:OP2	30:4:8:ARG:HG3	2.04	0.57
1:C:256:ARG:HD3	1:C:258:ARG:HD2	1.85	0.57
3:E:51:SER:HB2	26:A:35:A:H4'	1.87	0.57
9:K:142:ILE:HG21	26:A:1130:C:H42	1.63	0.57
13:O:20:LEU:CD2	13:O:24:LEU:HD12	2.34	0.57
23:Y:19:SER:OG	23:Y:20:HIS:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1573:U:O4	26:A:1596:C:N4	2.28	0.57
26:A:1608:U:O5'	26:A:1608:U:H6	1.87	0.57
26:A:1100:C:O2	34:8:21:ARG:NH2	2.37	0.57
26:A:1996:U:OP2	26:A:2001:A:N6	2.36	0.57
4:F:47:VAL:HG23	4:F:48:GLY:H	1.69	0.57
4:F:109:ARG:O	4:F:113:ILE:HB	2.04	0.57
5:G:95:TYR:HE2	5:G:161:LYS:HB3	1.69	0.57
13:O:20:LEU:CD1	13:O:40:LYS:NZ	2.68	0.57
13:O:24:LEU:HB3	13:O:44:LEU:HD22	1.86	0.57
25:B:24:G:N7	25:B:56:C:C2'	2.68	0.57
1:C:26:ARG:HG3	1:C:81:HIS:ND1	2.19	0.57
8:J:96:LYS:CE	21:W:120:PRO:CB	2.66	0.57
20:V:2:LYS:HD2	20:V:83:VAL:HG12	1.73	0.57
20:V:2:LYS:CE	20:V:85:TYR:CE2	2.88	0.57
26:A:1042:A:H1'	27:1:42:GLN:HE22	1.69	0.57
1:C:25:THR:OG1	1:C:81:HIS:ND1	1.92	0.56
10:L:78:LYS:HD3	15:Q:70:GLU:OE1	2.04	0.56
19:U:83:ILE:HD13	26:A:1456:G:N3	2.19	0.56
26:A:301:U:H5'	26:A:302:U:H4'	1.85	0.56
30:4:13:LEU:O	30:4:22:ASN:HA	2.05	0.56
3:E:75:ARG:NH1	26:A:2669:G:OP1	2.38	0.56
6:H:115:ARG:NH1	26:A:163:U:O2	2.37	0.56
8:J:30:LEU:HA	8:J:33:HIS:HD2	1.69	0.56
13:O:56:LYS:HD3	13:O:87:TYR:O	2.05	0.56
18:T:117:ARG:N	18:T:118:PRO:HD2	2.20	0.56
20:V:42:LYS:O	26:A:568:A:O2'	2.23	0.56
30:4:49:GLN:O	30:4:51:HIS:HD2	1.87	0.56
4:F:64:LEU:HD11	4:F:94:ALA:O	2.05	0.56
4:F:99:ARG:HD3	25:B:45:G:H8	1.66	0.56
4:F:130:ASP:OD2	4:F:134:ASN:ND2	2.38	0.56
17:S:4:TYR:CD2	17:S:15:LYS:HE3	2.41	0.56
20:V:42:LYS:HG3	26:A:586:U:H4'	1.86	0.56
26:A:346:C:H41	26:A:445:U:H3	1.53	0.56
26:A:1530:G:H21	26:A:1805:G:H22	1.54	0.56
26:A:1580:A:N1	26:A:1592:G:O4'	2.38	0.56
26:A:3014:A:H62	26:A:3113:A:H2	1.53	0.56
27:1:19:GLN:HG3	27:1:50:VAL:HG12	1.87	0.56
30:4:15:CYS:CB	30:4:20:HIS:N	2.68	0.56
30:4:32:ASP:HB2	30:4:33:PRO:CD	2.35	0.56
1:C:73:ASP:CB	1:C:120:GLY:CA	2.68	0.56
21:W:40:HIS:C	21:W:42:THR:H	2.09	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:18:LEU:HD22	24:Z:57:VAL:HG13	1.86	0.56
26:A:1882:A:H61	26:A:2220:C:H42	1.52	0.56
1:C:258:ARG:HG2	1:C:259:LYS:N	2.19	0.56
13:O:44:LEU:HD23	13:O:113:ILE:HD12	1.87	0.56
18:T:18:ARG:CZ	26:A:1436:C:HO2'	2.18	0.56
19:U:60:ALA:HB2	26:A:1456:G:C4'	2.36	0.56
25:B:30:G:C6	25:B:54:A:N1	2.74	0.56
25:B:35:G:N3	25:B:35:G:H2'	2.21	0.56
26:A:995:U:O4	26:A:1014:G:N2	2.38	0.56
26:A:1563:A:N6	26:A:1565:A:C6	2.73	0.56
26:A:1601:G:H2'	26:A:1602:U:H6	1.70	0.56
26:A:1602:U:H2'	26:A:1603:G:N7	2.20	0.56
26:A:1607:C:C5	26:A:1608:U:C4	2.93	0.56
26:A:2329:G:O6	26:A:2406:U:O2	2.24	0.56
3:E:51:SER:CB	26:A:35:A:H5'	2.35	0.56
3:E:143:THR:O	3:E:147:THR:CB	2.53	0.56
3:E:184:ASN:ND2	26:A:708:G:N2	2.54	0.56
26:A:1566:A:H2'	26:A:1605:G:O6	2.06	0.56
4:F:10:ARG:HH11	4:F:10:ARG:CG	2.09	0.56
4:F:46:GLY:C	4:F:47:VAL:CG2	2.49	0.56
25:B:30:G:O6	25:B:54:A:N1	2.39	0.56
11:M:58:HIS:CD2	32:6:7:HIS:CE1	2.84	0.56
17:S:4:TYR:CE2	17:S:15:LYS:HE3	2.41	0.56
26:A:1577:C:O2'	26:A:1578:G:O4'	2.24	0.56
30:4:12:THR:HG23	30:4:24:ILE:HG22	1.87	0.56
1:C:132:PRO:HA	1:C:190:ARG:HA	1.87	0.56
3:E:7:VAL:H	3:E:16:GLY:C	1.99	0.56
17:S:6:ILE:CG2	17:S:7:VAL:H	2.19	0.56
20:V:2:LYS:CG	20:V:83:VAL:CB	2.79	0.56
21:W:62:GLY:O	21:W:63:THR:HG23	2.05	0.56
21:W:105:LYS:HZ2	21:W:135:ALA:HA	1.71	0.56
26:A:159:A:OP2	26:A:164:A:N6	2.30	0.56
26:A:1563:A:C5	26:A:1565:A:C8	2.93	0.56
26:A:1565:A:H2'	26:A:1566:A:N7	2.21	0.56
26:A:1603:G:H2'	26:A:1604:G:C8	2.39	0.56
26:A:2086:U:O4	26:A:2096:G:O6	2.23	0.56
27:1:21:GLU:OE2	27:1:24:ARG:NH1	2.39	0.56
28:2:46:THR:O	28:2:50:LYS:HG3	2.05	0.56
30:4:28:ASN:OD1	30:4:31:ASN:HB2	2.06	0.56
4:F:171:ALA:HA	4:F:174:ARG:HD3	1.88	0.56
9:K:75:TYR:N	9:K:75:TYR:CD1	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:12:GLN:HG3	12:N:73:PRO:HD2	1.88	0.56
23:Y:41:ARG:NH1	26:A:164:A:O3'	2.39	0.56
26:A:137:G:H21	26:A:1524:G:H1'	1.70	0.56
9:K:13:ARG:NE	9:K:121:LYS:NZ	2.53	0.55
26:A:640:G:O2'	26:A:642:G:OP2	2.24	0.55
26:A:2509:C:H5	30:4:8:ARG:CZ	2.20	0.55
26:A:2873:U:O4	26:A:2895:A:N1	2.38	0.55
33:7:11:CYS:SG	33:7:14:CYS:N	2.80	0.55
1:C:65:ILE:HG13	1:C:104:TYR:HB3	1.88	0.55
9:K:8:ALA:HB2	26:A:625:A:O2'	2.07	0.55
9:K:15:TRP:N	9:K:15:TRP:CD1	2.73	0.55
19:U:4:ILE:HD11	24:Z:58:TYR:CE1	2.38	0.55
19:U:59:THR:HG23	19:U:80:LYS:HE3	1.86	0.55
25:B:60:G:C2'	25:B:61:C:O5'	2.53	0.55
25:B:86:U:O2	25:B:88:C:H2'	2.06	0.55
26:A:1563:A:C6	26:A:1565:A:C5	2.94	0.55
26:A:1649:C:N4	26:A:1790:A:OP2	2.35	0.55
26:A:2851:G:N2	26:A:3001:G:OP2	2.36	0.55
1:C:35:ARG:CD	1:C:36:PRO:HD3	2.35	0.55
1:C:256:ARG:O	1:C:257:THR:HB	2.07	0.55
15:Q:74:PRO:HB2	15:Q:77:SER:HB2	1.87	0.55
26:A:1659:U:H2'	26:A:1660:A:H8	1.71	0.55
26:A:3017:C:N3	26:A:3025:G:O6	2.39	0.55
3:E:7:VAL:HG21	3:E:16:GLY:HA3	1.86	0.55
13:O:69:LYS:O	13:O:71:ARG:NH1	2.40	0.55
18:T:18:ARG:NH1	26:A:1436:C:C2'	2.69	0.55
25:B:19:G:C5'	25:B:19:G:C8	2.84	0.55
26:A:222:A:O2'	26:A:508:G:N3	2.40	0.55
26:A:263:G:O2'	26:A:517:A:N3	2.39	0.55
26:A:1573:U:C1'	26:A:1574:G:P	2.94	0.55
1:C:257:THR:HG23	26:A:2020:A:O3'	2.06	0.55
9:K:145:VAL:HG23	9:K:145:VAL:O	2.05	0.55
21:W:105:LYS:HZ3	21:W:136:GLU:CG	2.19	0.55
4:F:11:LEU:CD1	4:F:108:ASP:HB2	2.36	0.55
10:L:80:ASP:OD2	15:Q:61:ARG:NH2	2.40	0.55
13:O:81:ALA:O	13:O:85:PRO:HG2	2.05	0.55
20:V:10:LEU:HD23	20:V:20:LYS:HB3	1.88	0.55
25:B:16:A:H2	25:B:68:G:H22	1.55	0.55
26:A:1593:U:O2	26:A:1593:U:H2'	2.07	0.55
4:F:44:ASN:HD22	4:F:44:ASN:C	2.10	0.55
11:M:12:ALA:HB3	11:M:15:GLU:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:11:THR:HG22	18:T:113:ILE:HG23	1.86	0.55
20:V:89:ASP:O	20:V:90:GLU:C	2.43	0.55
26:A:1586:C:O5'	26:A:1586:C:H6	1.89	0.55
1:C:18:VAL:HG21	26:A:1785:C:H5''	1.88	0.55
12:N:34:ILE:HG23	12:N:104:PHE:H	1.71	0.55
26:A:1582:C:O5'	26:A:1582:C:H6	1.88	0.55
26:A:2644:C:OP1	32:6:34:GLU:HG3	2.06	0.55
1:C:256:ARG:CD	1:C:258:ARG:CD	2.85	0.55
2:D:7:LEU:HB2	2:D:34:ASN:HD21	1.71	0.55
22:X:43:THR:OG1	26:A:2560:A:N6	2.33	0.55
26:A:868:C:H5''	31:5:3:LYS:HE2	1.88	0.55
26:A:2691:C:OP1	33:7:8:LYS:NZ	2.39	0.55
6:H:23:ASP:O	6:H:27:ARG:HB3	2.07	0.55
13:O:29:PHE:HB2	13:O:79:LEU:HD12	1.68	0.55
16:R:89:GLU:OE1	17:S:8:LYS:NZ	2.37	0.55
21:W:131:ILE:HD11	21:W:162:ILE:HD12	1.87	0.55
26:A:351:G:O6	26:A:444:U:O2	2.24	0.55
12:N:22:SER:OG	12:N:23:GLY:N	2.40	0.54
13:O:94:TYR:O	13:O:116:VAL:HG22	2.07	0.54
19:U:69:THR:C	19:U:71:THR:H	2.09	0.54
26:A:1583:U:H2'	26:A:1584:U:C5	2.42	0.54
30:4:55:ARG:HG3	30:4:55:ARG:O	2.08	0.54
33:7:22:ARG:HB3	33:7:36:GLN:HB3	1.88	0.54
2:D:84:LEU:HD22	2:D:209:ARG:HD3	1.90	0.54
4:F:29:TYR:O	4:F:30:ALA:HB3	2.08	0.54
6:H:131:PRO:HA	6:H:145:SER:HA	1.89	0.54
20:V:28:PRO:CG	26:A:83:C:P	2.95	0.54
25:B:35:G:N2	25:B:36:U:C2	2.75	0.54
25:B:59:A:H2'	25:B:60:G:C8	2.42	0.54
26:A:1581:C:N4	26:A:1591:U:C6	2.76	0.54
1:C:24:ILE:HD13	1:C:84:TYR:HB2	1.88	0.54
1:C:66:ASP:OD2	1:C:103:ARG:NH1	2.41	0.54
4:F:50:ALA:O	4:F:51:ALA:HB3	2.06	0.54
4:F:118:ILE:H	4:F:118:ILE:CD1	1.96	0.54
5:G:154:ARG:NH1	26:A:2750:G:OP1	2.40	0.54
8:J:79:LYS:HD3	8:J:82:LEU:HD12	1.89	0.54
14:P:73:ILE:HG22	14:P:75:GLY:H	1.72	0.54
18:T:15:ARG:HG2	18:T:109:HIS:CD2	2.43	0.54
22:X:13:GLY:O	22:X:14:ARG:HG3	2.06	0.54
25:B:24:G:N7	25:B:56:C:H2'	2.21	0.54
25:B:57:U:C3'	25:B:58:A:C5'	2.86	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1567:C:HO2'	26:A:1568:C:P	2.28	0.54
26:A:2490:A:N6	26:A:2497:A:OP2	2.39	0.54
1:C:35:ARG:CG	1:C:36:PRO:CD	2.85	0.54
1:C:156:ALA:HB2	1:C:163:ILE:HG13	1.89	0.54
4:F:55:LYS:HB2	4:F:55:LYS:HZ3	1.71	0.54
7:I:41:ARG:HH21	8:J:119:ASN:HA	1.72	0.54
11:M:90:GLY:HA2	11:M:122:VAL:HG22	1.90	0.54
13:O:43:ALA:HA	13:O:46:PRO:HD2	1.89	0.54
13:O:79:LEU:O	13:O:83:ILE:HG13	2.06	0.54
16:R:25:ARG:NH1	26:A:2245:C:OP1	2.41	0.54
20:V:86:ARG:NE	20:V:88:ASP:OD2	2.36	0.54
26:A:541:G:N2	26:A:546:G:OP2	2.40	0.54
26:A:737:A:N1	26:A:2593:A:O2'	2.41	0.54
26:A:1564:A:C3'	26:A:1565:A:C5'	2.86	0.54
26:A:2230:C:O2'	26:A:3044:A:N3	2.38	0.54
4:F:11:LEU:HD22	4:F:108:ASP:CA	2.37	0.54
8:J:107:VAL:O	8:J:111:ALA:HB3	2.07	0.54
9:K:134:ALA:O	9:K:135:GLN:HG2	2.08	0.54
19:U:69:THR:O	19:U:71:THR:N	2.40	0.54
20:V:72:MET:HE3	26:A:383:U:H5'	1.89	0.54
31:5:9:GLN:HA	31:5:9:GLN:OE1	2.07	0.54
3:E:8:LYS:NZ	3:E:148:LEU:HB3	2.23	0.54
9:K:42:PRO:HB3	16:R:68:ALA:HB2	1.89	0.54
9:K:47:ASN:ND2	26:A:649:U:O2	2.40	0.54
13:O:20:LEU:CD2	13:O:24:LEU:CD1	2.85	0.54
19:U:30:THR:HG23	19:U:83:ILE:HG22	1.90	0.54
20:V:28:PRO:HG3	26:A:83:C:P	2.47	0.54
25:B:60:G:H2'	25:B:61:C:C5'	2.37	0.54
26:A:1578:G:H22	26:A:1592:G:C1'	2.21	0.54
26:A:1600:G:C3'	26:A:1601:G:C5'	2.86	0.54
26:A:2755:A:N6	26:A:2885:G:O6	2.41	0.54
30:4:28:ASN:CG	30:4:31:ASN:HB2	2.28	0.54
1:C:97:TYR:HD2	1:C:101:GLU:HG3	1.72	0.54
4:F:79:LYS:HG2	4:F:80:SER:N	2.23	0.54
14:P:104:ARG:HH12	26:A:2517:C:H5''	1.72	0.54
25:B:89:C:H6	25:B:89:C:P	2.30	0.54
3:E:170:ARG:NE	26:A:404:A:OP1	2.38	0.54
4:F:114:ALA:O	4:F:118:ILE:HD11	2.08	0.54
5:G:61:ARG:NH1	26:A:2981:A:O2'	2.40	0.54
12:N:85:SER:O	26:A:2500:G:OP2	2.26	0.54
13:O:90:ARG:HH12	13:O:118:GLU:HG3	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:13:LEU:HD12	24:Z:14:THR:H	1.72	0.54
25:B:19:G:C5	25:B:20:G:N7	2.75	0.54
25:B:60:G:H2'	25:B:61:C:O5'	2.07	0.54
26:A:270:U:O2	26:A:458:G:C6	2.61	0.54
20:V:79:LYS:HG3	20:V:79:LYS:O	2.07	0.54
26:A:2862:G:O2'	26:A:3002:A:N6	2.40	0.54
2:D:159:ARG:H	2:D:159:ARG:HD2	1.73	0.54
4:F:115:LEU:HD23	4:F:183:PRO:HG2	1.89	0.54
8:J:96:LYS:NZ	21:W:120:PRO:HB2	2.22	0.54
9:K:116:ARG:HH22	26:A:615:A:H5''	1.73	0.54
9:K:141:GLU:OE2	9:K:143:LYS:CD	2.56	0.54
12:N:85:SER:OG	22:X:8:SER:OG	2.25	0.54
12:N:103:LEU:HD11	12:N:127:ILE:HD11	1.90	0.54
22:X:83:VAL:CG1	22:X:85:ARG:HA	2.34	0.54
25:B:2:U:H3	25:B:115:A:N6	2.05	0.54
26:A:1580:A:C6	26:A:1591:U:N3	2.62	0.54
32:6:33:LEU:HD23	32:6:36:LYS:HD2	1.89	0.54
18:T:6:GLU:HA	18:T:117:ARG:NH1	2.23	0.53
22:X:83:VAL:O	22:X:84:ALA:HB3	2.07	0.53
24:Z:13:LEU:CG	24:Z:17:GLU:HB2	2.38	0.53
26:A:1561:C:C6	26:A:1562:C:C5	2.95	0.53
26:A:1572:G:O6	26:A:1600:G:C6	2.61	0.53
5:G:116:ILE:HD11	5:G:152:LEU:HD11	1.90	0.53
7:I:9:ALA:HA	7:I:12:ASP:HB2	1.89	0.53
13:O:76:VAL:O	13:O:80:PHE:HB2	2.08	0.53
25:B:58:A:N7	25:B:59:A:N7	2.53	0.53
25:B:60:G:C8	25:B:60:G:C5'	2.85	0.53
26:A:444:U:H5'	26:A:446:G:H4'	1.90	0.53
26:A:944:A:N7	26:A:2471:A:O2'	2.42	0.53
26:A:1583:U:H2'	26:A:1584:U:C4	2.44	0.53
26:A:2337:A:N6	26:A:2342:A:N7	2.56	0.53
4:F:45:MET:HB3	4:F:94:ALA:H	1.74	0.53
9:K:1:MET:HE1	26:A:642:G:OP1	2.09	0.53
12:N:10:ARG:HG3	12:N:90:PRO:HG3	1.91	0.53
16:R:50:ARG:O	16:R:54:LYS:NZ	2.40	0.53
25:B:23:G:H1	25:B:60:G:H1	1.56	0.53
25:B:94:G:N3	26:A:1033:A:H4'	2.23	0.53
4:F:168:THR:CG2	14:P:3:HIS:CE1	2.91	0.53
6:H:94:SER:HA	6:H:125:LYS:HD3	1.90	0.53
1:C:55:GLY:CA	1:C:218:ARG:HG3	2.38	0.53
4:F:8:LEU:HD22	4:F:16:ARG:HD2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:31:ASN:OD1	25:B:57:U:O4'	2.26	0.53
12:N:118:LEU:O	12:N:122:ILE:HB	2.08	0.53
19:U:92:PRO:HG2	19:U:94:ASP:OD1	2.08	0.53
25:B:10:G:O6	25:B:107:A:N1	2.42	0.53
26:A:828:G:H22	26:A:832:G:H5''	1.74	0.53
3:E:55:ARG:NH2	26:A:788:C:OP1	2.42	0.53
7:I:28:TYR:OH	26:A:1224:G:O2'	2.26	0.53
16:R:6:ARG:NH1	26:A:1366:A:OP2	2.41	0.53
26:A:270:U:O2	26:A:458:G:O6	2.27	0.53
26:A:1567:C:O2'	26:A:1568:C:P	2.66	0.53
26:A:2224:C:O2'	26:A:2913:U:OP2	2.26	0.53
26:A:2348:G:O2'	26:A:2396:A:N6	2.41	0.53
3:E:118:ARG:HH22	3:E:189:LEU:HA	1.73	0.53
4:F:168:THR:HG21	14:P:3:HIS:ND1	2.23	0.53
5:G:16:ASP:HB2	5:G:27:LYS:HB3	1.90	0.53
8:J:107:VAL:O	8:J:111:ALA:CB	2.56	0.53
9:K:147:GLN:HG2	26:A:1131:G:H1'	1.90	0.53
12:N:70:PRO:HA	12:N:95:ALA:HB2	1.91	0.53
20:V:9:VAL:HB	20:V:71:VAL:HB	1.90	0.53
21:W:21:LYS:NZ	25:B:80:C:N4	2.46	0.53
25:B:87:U:O2'	25:B:88:C:H4'	2.08	0.53
26:A:189:A:N3	26:A:794:G:O2'	2.37	0.53
26:A:1589:G:O5'	26:A:1589:G:H8	1.91	0.53
1:C:35:ARG:HD2	1:C:36:PRO:CD	2.37	0.53
5:G:62:SER:O	5:G:66:HIS:HB2	2.08	0.53
9:K:98:THR:HG23	9:K:124:VAL:HB	1.90	0.53
12:N:59:LYS:C	12:N:60:ARG:HG3	2.29	0.53
13:O:90:ARG:HH22	13:O:118:GLU:HB3	1.68	0.53
21:W:9:ASN:HD22	21:W:57:VAL:CG1	2.17	0.53
26:A:384:G:H2'	26:A:385:G:H8	1.72	0.53
26:A:1921:G:H2'	26:A:1922:G:H8	1.73	0.53
9:K:112:ASN:ND2	26:A:650:G:H5''	2.24	0.53
10:L:28:SER:HA	26:A:2787:U:H4'	1.90	0.53
24:Z:44:ASN:HD21	26:A:58:G:P	2.31	0.53
25:B:5:C:OP1	25:B:61:C:O2'	2.23	0.53
26:A:1603:G:H2'	26:A:1604:G:H8	1.74	0.53
28:2:42:HIS:O	28:2:46:THR:HG23	2.08	0.53
30:4:15:CYS:O	30:4:20:HIS:CA	2.54	0.53
1:C:256:ARG:O	26:A:2014:G:C4'	2.52	0.53
1:C:257:THR:CG2	26:A:2020:A:O3'	2.57	0.53
2:D:84:LEU:HD21	2:D:207:VAL:HG11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B:89:C:H2'	25:B:90:G:C8	2.44	0.53
1:C:98:LEU:HD22	1:C:98:LEU:N	2.24	0.52
9:K:5:THR:HG21	26:A:624:G:H4'	1.91	0.52
21:W:62:GLY:O	21:W:63:THR:OG1	2.26	0.52
26:A:1627:U:H2'	26:A:1628:A:H2'	1.90	0.52
20:V:4:HIS:CE1	20:V:96:ARG:HH22	2.22	0.52
25:B:11:U:O2	25:B:11:U:H2'	2.08	0.52
25:B:34:G:H8	25:B:34:G:O5'	1.92	0.52
25:B:82:A:N1	25:B:91:G:C6	2.77	0.52
26:A:114:G:OP2	26:A:116:A:O2'	2.26	0.52
26:A:1566:A:C1'	26:A:1605:G:H1	2.21	0.52
6:H:44:GLU:O	6:H:48:GLU:CB	2.57	0.52
19:U:19:LYS:NZ	26:A:1508:A:N1	2.53	0.52
24:Z:13:LEU:CD2	24:Z:17:GLU:C	2.78	0.52
26:A:1044:U:O2'	27:1:24:ARG:O	2.27	0.52
26:A:1540:U:O4	26:A:1632:G:O6	2.27	0.52
26:A:1565:A:C2'	26:A:1566:A:C8	2.85	0.52
26:A:1567:C:C2'	26:A:1568:C:OP2	2.57	0.52
26:A:1570:C:C4	26:A:1602:U:C2	2.84	0.52
26:A:1600:G:O2'	26:A:1601:G:H5''	2.09	0.52
26:A:1830:C:H5'	31:5:10:PRO:HG2	1.91	0.52
26:A:2356:G:H2'	26:A:2380:G:H1	1.74	0.52
1:C:14:ARG:NH2	26:A:1913:G:N7	2.55	0.52
4:F:6:LYS:CA	4:F:6:LYS:CE	2.87	0.52
4:F:46:GLY:O	4:F:47:VAL:HG13	2.09	0.52
4:F:113:ILE:O	4:F:116:PRO:HD2	2.09	0.52
19:U:67:LYS:HZ2	19:U:67:LYS:CB	2.23	0.52
20:V:43:LYS:NZ	20:V:43:LYS:CB	2.73	0.52
20:V:99:LYS:NZ	20:V:99:LYS:CB	2.73	0.52
26:A:239:U:OP1	26:A:684:G:N2	2.42	0.52
9:K:75:TYR:HD2	9:K:86:LYS:HG2	1.73	0.52
12:N:17:GLN:HB2	12:N:39:HIS:HB2	1.91	0.52
16:R:41:HIS:HE1	26:A:655:G:H4'	1.75	0.52
26:A:1544:U:H3	26:A:1626:G:H1	1.58	0.52
26:A:1604:G:C2	26:A:1605:G:C8	2.98	0.52
1:C:262:LYS:N	1:C:263:PRO:CD	2.73	0.52
5:G:127:GLU:OE1	5:G:131:LYS:NZ	2.42	0.52
10:L:109:LYS:HB3	10:L:110:LYS:HE2	1.92	0.52
21:W:98:LEU:HD23	21:W:98:LEU:C	2.29	0.52
26:A:1573:U:O2'	26:A:1573:U:O2	2.27	0.52
26:A:2315:U:OP1	26:A:2422:A:O2'	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:8:ARG:HH21	30:4:28:ASN:HB2	1.74	0.52
33:7:35:ARG:CG	33:7:36:GLN:H	2.21	0.52
11:M:81:GLY:HA2	11:M:84:ASN:HD22	1.75	0.52
11:M:106:LYS:NZ	26:A:714:U:O2'	2.43	0.52
25:B:25:G:C2'	25:B:26:A:H5'	2.40	0.52
26:A:1078:G:O6	34:8:8:LYS:NZ	2.43	0.52
26:A:1885:G:O2'	26:A:2215:U:O4	2.28	0.52
26:A:1938:G:H21	26:A:1956:A:H62	1.58	0.52
26:A:2585:U:OP1	32:6:24:ARG:NH1	2.26	0.52
1:C:26:ARG:CG	1:C:81:HIS:CG	2.92	0.52
13:O:75:VAL:HG12	13:O:79:LEU:HD13	1.92	0.52
27:1:51:HIS:CD2	27:1:51:HIS:N	2.74	0.52
28:2:42:HIS:N	28:2:43:PRO:CD	2.72	0.52
5:G:4:ILE:HD13	26:A:2972:A:H5'	1.91	0.52
9:K:1:MET:N	9:K:2:PRO:CD	2.73	0.52
10:L:109:LYS:CD	10:L:110:LYS:NZ	2.73	0.52
20:V:43:LYS:HB3	20:V:43:LYS:HZ3	1.75	0.52
22:X:16:SER:O	22:X:17:ALA:CB	2.58	0.52
30:4:38:ILE:HG22	30:4:40:LYS:HG2	1.92	0.52
14:P:22:HIS:HE1	25:B:9:G:OP2	1.93	0.52
18:T:35:SER:HA	18:T:77:VAL:HA	1.92	0.52
26:A:1533:U:O2	26:A:1803:A:O2'	2.25	0.52
26:A:1856:C:O3'	26:A:2933:G:N2	2.43	0.52
31:5:6:ARG:CB	31:5:6:ARG:CZ	2.87	0.52
1:C:34:VAL:HG22	1:C:63:ARG:HG2	1.91	0.51
1:C:256:ARG:CG	1:C:258:ARG:HD2	2.39	0.51
9:K:75:TYR:CD2	9:K:86:LYS:HG2	2.43	0.51
10:L:8:LEU:HD13	10:L:19:ILE:CG1	2.40	0.51
13:O:117:ARG:CD	13:O:118:GLU:N	2.73	0.51
19:U:77:LYS:HZ2	19:U:79:THR:HG22	1.73	0.51
25:B:5:C:H42	25:B:112:C:H42	1.57	0.51
25:B:86:U:H2'	25:B:88:C:H1'	1.90	0.51
26:A:1171:C:H2'	26:A:1172:A:H8	1.75	0.51
31:5:21:PHE:O	31:5:25:MET:HG2	2.09	0.51
1:C:145:VAL:HG11	1:C:175:LEU:HD11	1.92	0.51
1:C:259:LYS:HG2	26:A:2016:G:OP1	2.09	0.51
1:C:262:LYS:N	1:C:262:LYS:CD	2.73	0.51
3:E:5:VAL:HG12	3:E:18:VAL:O	2.10	0.51
8:J:128:LYS:HG2	26:A:1198:C:H4'	1.93	0.51
9:K:14:SER:N	9:K:52:ASP:OD1	2.31	0.51
11:M:24:ARG:NH1	26:A:1365:G:OP2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:17:ALA:HB1	26:A:2485:C:OP1	2.10	0.51
22:X:46:HIS:HB2	22:X:77:THR:HG22	1.91	0.51
26:A:1564:A:H3'	26:A:1565:A:C5'	2.41	0.51
26:A:1589:G:C2'	26:A:1590:G:H5'	2.40	0.51
26:A:1589:G:H2'	26:A:1590:G:H5'	1.91	0.51
26:A:2340:A:H61	26:A:2389:U:H3	1.58	0.51
33:7:16:VAL:HG22	33:7:25:VAL:HG22	1.92	0.51
1:C:62:TYR:HE1	26:A:2033:U:H3'	1.75	0.51
1:C:256:ARG:CZ	1:C:258:ARG:NE	2.73	0.51
3:E:139:LYS:HE2	3:E:142:LYS:HD2	1.92	0.51
4:F:138:GLY:HA3	26:A:2529:A:C5'	2.27	0.51
13:O:16:HIS:HD2	26:A:1390:A:N7	2.04	0.51
20:V:96:ARG:NH2	20:V:96:ARG:CB	2.72	0.51
26:A:1755:A:O2'	26:A:1758:G:N2	2.36	0.51
26:A:2571:C:OP1	30:4:40:LYS:NZ	2.36	0.51
28:2:42:HIS:N	28:2:43:PRO:HD2	2.24	0.51
1:C:209:ALA:HB2	26:A:2007:C:O2'	2.10	0.51
4:F:9:PRO:HD2	4:F:12:LYS:HE3	1.91	0.51
13:O:35:LYS:HG3	13:O:112:VAL:HG22	1.93	0.51
19:U:59:THR:CG2	19:U:80:LYS:HE3	2.39	0.51
19:U:69:THR:C	19:U:71:THR:N	2.64	0.51
21:W:102:ARG:HH21	21:W:138:LEU:HD11	1.70	0.51
25:B:24:G:O6	25:B:60:G:C2	2.63	0.51
26:A:1174:G:N1	26:A:1220:C:OP2	2.44	0.51
26:A:1563:A:N7	26:A:1565:A:C5	2.78	0.51
26:A:1599:U:H3'	26:A:1599:U:OP2	2.09	0.51
30:4:9:PRO:HD3	30:4:27:LYS:O	2.09	0.51
2:D:63:ILE:HG22	2:D:65:PRO:HD2	1.93	0.51
12:N:65:TRP:HZ3	26:A:989:G:O2'	1.93	0.51
21:W:87:PRO:HA	21:W:90:ARG:NH2	2.16	0.51
26:A:1584:U:H6	26:A:1584:U:H3'	1.75	0.51
26:A:1595:G:C5'	26:A:1596:C:OP2	2.59	0.51
26:A:1940:A:N6	26:A:1954:C:O2'	2.43	0.51
26:A:2142:A:O2'	26:A:2144:C:N4	2.43	0.51
28:2:44:PHE:O	28:2:48:LYS:CE	2.55	0.51
1:C:108:PRO:HG3	1:C:128:GLY:HA2	1.91	0.51
1:C:145:VAL:HG13	1:C:191:ALA:HB2	1.93	0.51
3:E:45:LYS:CG	26:A:709:U:C4	2.94	0.51
3:E:131:VAL:HG13	3:E:140:SER:HB2	1.91	0.51
19:U:5:THR:O	19:U:6:ASP:HB2	2.10	0.51
20:V:72:MET:CE	26:A:383:U:H5'	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:83:LEU:HD11	21:W:92:ILE:CG2	2.36	0.51
26:A:1597:G:N3	26:A:1598:U:H6	2.02	0.51
26:A:1601:G:H2'	26:A:1602:U:C6	2.46	0.51
8:J:114:LYS:O	8:J:118:LEU:N	2.40	0.51
16:R:48:ARG:NH1	16:R:49:ASP:OD1	2.44	0.51
20:V:2:LYS:HE3	20:V:83:VAL:HG12	1.92	0.51
23:Y:17:SER:HB2	23:Y:27:ARG:HD2	1.91	0.51
23:Y:33:ILE:HA	23:Y:52:CYS:HA	1.91	0.51
26:A:601:A:N3	26:A:673:C:O2'	2.39	0.51
9:K:141:GLU:OE2	9:K:143:LYS:HG3	2.01	0.51
18:T:75:THR:CB	18:T:118:PRO:HD3	2.32	0.51
26:A:1544:U:O4	26:A:1626:G:O6	2.29	0.51
26:A:2279:C:OP1	29:3:5:LYS:NZ	2.44	0.51
26:A:2764:C:O2'	26:A:2964:A:N3	2.34	0.51
28:2:38:CYS:CB	28:2:40:GLN:NE2	2.73	0.51
28:2:43:PRO:HA	28:2:46:THR:OG1	2.09	0.51
31:5:5:LYS:HB3	31:5:9:GLN:HE22	1.67	0.51
3:E:186:TYR:O	3:E:190:ASN:HB2	2.11	0.51
11:M:78:VAL:HG21	11:M:98:LEU:HD13	1.91	0.51
11:M:134:ARG:HH22	11:M:146:GLU:HG2	1.75	0.51
13:O:29:PHE:CE2	13:O:51:LEU:HD13	2.45	0.51
25:B:80:C:O2'	26:A:1033:A:H1'	2.10	0.51
26:A:242:G:OP2	32:6:3:LYS:HE2	2.10	0.51
26:A:854:A:H1'	26:A:855:C:H5	1.75	0.51
26:A:1127:A:N3	26:A:1272:C:O2'	2.39	0.51
1:C:37:LEU:HD23	1:C:62:TYR:CD1	2.45	0.51
4:F:62:ASN:O	4:F:65:ALA:O	2.28	0.51
20:V:2:LYS:HE2	20:V:85:TYR:CE2	2.46	0.51
21:W:81:LYS:HB2	21:W:96:ASP:O	2.10	0.51
22:X:54:GLY:N	22:X:58:THR:O	2.39	0.51
26:A:277:U:H2'	26:A:278:A:C8	2.46	0.51
26:A:1577:C:C5	26:A:1594:G:O6	2.62	0.51
26:A:1598:U:C4	26:A:1601:G:C6	2.99	0.51
1:C:61:ALA:O	1:C:63:ARG:NH2	2.44	0.50
4:F:102:ARG:NH1	28:2:9:TYR:CE1	2.78	0.50
9:K:141:GLU:CD	9:K:143:LYS:HG3	2.25	0.50
9:K:141:GLU:OE1	9:K:142:ILE:C	2.49	0.50
10:L:7:ARG:NH2	10:L:7:ARG:CG	2.73	0.50
26:A:1597:G:HO2'	26:A:1598:U:H6	1.57	0.50
4:F:71:LYS:HG3	28:2:5:ILE:HB	1.93	0.50
5:G:65:LEU:HD12	5:G:68:LEU:HD23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:R:98:LEU:CD2	17:S:4:TYR:OH	2.59	0.50
18:T:75:THR:O	18:T:118:PRO:CD	2.59	0.50
24:Z:62:ARG:NH2	24:Z:66:LEU:HD11	2.26	0.50
1:C:26:ARG:HD3	1:C:81:HIS:CD2	2.38	0.50
11:M:84:ASN:HD21	11:M:118:LEU:HA	1.76	0.50
15:Q:93:ARG:HH21	26:A:1971:C:H5	1.60	0.50
21:W:40:HIS:C	21:W:42:THR:N	2.65	0.50
25:B:24:G:HO2'	25:B:56:C:H41	1.48	0.50
25:B:34:G:O2'	25:B:35:G:N7	2.43	0.50
26:A:2211:C:H2'	26:A:2212:A:H8	1.76	0.50
26:A:2547:G:O6	26:A:2556:C:N3	2.44	0.50
4:F:11:LEU:HD22	4:F:108:ASP:CB	2.41	0.50
6:H:62:ILE:H	6:H:65:ALA:HB3	1.77	0.50
9:K:1:MET:H3	9:K:2:PRO:HD3	1.77	0.50
9:K:13:ARG:CZ	9:K:121:LYS:NZ	2.68	0.50
26:A:2380:G:N2	26:A:2381:A:N1	2.58	0.50
26:A:2756:G:O2'	26:A:2881:A:N1	2.40	0.50
28:2:63:LYS:O	28:2:65:TYR:HD2	1.94	0.50
10:L:31:ARG:NH2	26:A:2900:C:OP1	2.45	0.50
12:N:111:GLU:OE2	12:N:115:ARG:CD	2.59	0.50
20:V:42:LYS:HD2	26:A:586:U:C5'	2.36	0.50
26:A:1592:G:O2'	26:A:1593:U:C6	2.57	0.50
26:A:1673:A:O2'	26:A:2926:A:OP2	2.28	0.50
30:4:15:CYS:C	30:4:20:HIS:CA	2.79	0.50
31:5:6:ARG:NH1	31:5:6:ARG:CB	2.72	0.50
3:E:51:SER:HB2	26:A:35:A:C4'	2.42	0.50
4:F:45:MET:HE3	4:F:64:LEU:CG	2.41	0.50
9:K:1:MET:CE	26:A:642:G:OP1	2.60	0.50
9:K:27:ARG:HH11	9:K:27:ARG:CG	2.25	0.50
13:O:16:HIS:CD2	26:A:1390:A:N7	2.78	0.50
13:O:118:GLU:OE1	13:O:118:GLU:HA	2.11	0.50
25:B:34:G:C6	25:B:44:C:C6	2.99	0.50
26:A:247:G:OP2	26:A:249:C:N4	2.41	0.50
26:A:499:G:OP2	26:A:2630:A:O2'	2.27	0.50
1:C:213:ARG:HH22	1:C:219:PRO:HD3	1.75	0.50
19:U:67:LYS:HE2	26:A:1451:A:OP2	2.10	0.50
22:X:50:ASN:HB2	22:X:80:ILE:HB	1.94	0.50
24:Z:62:ARG:HD2	24:Z:66:LEU:HD22	1.93	0.50
25:B:56:C:O2	25:B:56:C:O2'	2.22	0.50
26:A:813:C:O2'	26:A:849:A:N6	2.41	0.50
26:A:1665:U:H2'	26:A:1666:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:25:VAL:HB	33:7:34:GLN:HG2	1.92	0.50
11:M:65:LYS:HD2	26:A:2640:G:H5''	1.92	0.50
26:A:1596:C:O2'	26:A:1597:G:C8	2.65	0.50
26:A:1606:G:H2'	26:A:1606:G:N3	2.27	0.50
2:D:178:GLN:NE2	26:A:2995:U:O2'	2.37	0.50
9:K:136:GLN:HA	9:K:136:GLN:OE1	2.12	0.50
18:T:7:PHE:O	18:T:7:PHE:HD1	1.95	0.50
25:B:85:C:H3'	25:B:85:C:H6	1.75	0.50
9:K:75:TYR:HB3	9:K:85:ARG:O	2.11	0.49
9:K:113:LYS:HD2	26:A:616:A:P	2.52	0.49
19:U:67:LYS:HB3	19:U:67:LYS:NZ	2.27	0.49
19:U:83:ILE:HD12	26:A:1456:G:N2	2.13	0.49
21:W:52:ARG:NH1	21:W:53:ASP:OD1	2.45	0.49
25:B:58:A:C8	25:B:58:A:C5'	2.86	0.49
26:A:1566:A:C4	26:A:1605:G:C6	3.00	0.49
1:C:34:VAL:HG22	1:C:63:ARG:CG	2.42	0.49
2:D:157:PRO:HD2	2:D:158:GLY:H	1.78	0.49
4:F:115:LEU:O	4:F:118:ILE:HD13	2.11	0.49
13:O:58:GLY:HA2	13:O:62:ASN:HB2	1.94	0.49
21:W:9:ASN:O	21:W:68:THR:N	2.30	0.49
26:A:217:G:H22	26:A:235:U:H4'	1.77	0.49
3:E:136:PRO:HB3	3:E:164:VAL:HA	1.94	0.49
4:F:51:ALA:HB2	4:F:90:MET:HE3	1.94	0.49
4:F:78:ARG:O	4:F:88:GLU:OE1	2.30	0.49
4:F:158:GLY:HA3	26:A:2529:A:C2	2.47	0.49
7:I:27:GLU:HB3	7:I:104:VAL:HB	1.93	0.49
16:R:90:VAL:HG13	17:S:6:ILE:CD1	2.42	0.49
19:U:91:LYS:CG	19:U:92:PRO:HD3	2.40	0.49
21:W:62:GLY:HA2	21:W:65:ALA:HB2	1.95	0.49
26:A:218:A:N3	26:A:234:U:O2'	2.38	0.49
26:A:718:C:O2'	26:A:772:U:OP1	2.26	0.49
26:A:966:U:H2'	26:A:967:G:H8	1.77	0.49
26:A:1590:G:N3	26:A:1591:U:C6	2.79	0.49
1:C:256:ARG:NH1	1:C:258:ARG:NH1	2.60	0.49
4:F:11:LEU:HD21	4:F:108:ASP:HA	1.95	0.49
4:F:47:VAL:HG23	4:F:48:GLY:N	2.26	0.49
17:S:6:ILE:C	17:S:7:VAL:CG2	2.78	0.49
18:T:13:LYS:HG2	18:T:111:THR:HG23	1.93	0.49
19:U:67:LYS:NZ	26:A:1451:A:OP2	2.45	0.49
21:W:46:HIS:HE1	25:B:74:A:O2'	1.96	0.49
21:W:81:LYS:N	21:W:96:ASP:O	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:2963:U:H2'	26:A:2964:A:H8	1.77	0.49
12:N:35:GLN:NE2	21:W:90:ARG:NH1	2.60	0.49
14:P:16:ASN:O	14:P:20:ARG:HB2	2.12	0.49
26:A:242:G:OP2	32:6:3:LYS:CE	2.61	0.49
26:A:280:G:H1	26:A:306:U:H3	1.60	0.49
3:E:118:ARG:HH22	3:E:189:LEU:HD23	1.77	0.49
4:F:32:VAL:CG2	25:B:55:G:H5'	2.43	0.49
4:F:147:GLU:HA	28:2:28:LYS:HD3	1.93	0.49
5:G:61:ARG:O	5:G:65:LEU:HB2	2.13	0.49
17:S:77:LYS:HD3	17:S:86:LYS:HE2	1.94	0.49
26:A:223:A:OP2	26:A:507:G:N2	2.41	0.49
26:A:277:U:H2'	26:A:278:A:H8	1.77	0.49
26:A:403:U:O2'	26:A:422:A:N3	2.45	0.49
4:F:21:GLU:O	4:F:25:GLN:HG3	2.13	0.49
9:K:84:LEU:HD11	26:A:1250:U:H6	1.77	0.49
15:Q:48:ARG:NH1	26:A:2909:G:OP1	2.43	0.49
20:V:81:THR:OG1	20:V:100:THR:HG23	2.12	0.49
26:A:567:A:H1'	26:A:568:A:H5'	1.94	0.49
26:A:1580:A:C5	26:A:1592:G:N3	2.80	0.49
1:C:256:ARG:NE	1:C:258:ARG:NE	2.60	0.49
4:F:11:LEU:CD2	4:F:108:ASP:CA	2.91	0.49
4:F:46:GLY:O	4:F:47:VAL:CG1	2.61	0.49
10:L:19:ILE:HG22	10:L:43:VAL:HA	1.95	0.49
13:O:33:ARG:CB	13:O:114:GLU:HG2	2.43	0.49
25:B:21:C:H2'	25:B:22:A:O5'	2.13	0.49
26:A:610:C:O2	26:A:646:U:O2'	2.31	0.49
26:A:1610:C:H2'	26:A:1611:A:C8	2.46	0.49
26:A:2375:G:H2'	26:A:2376:G:H8	1.77	0.49
26:A:2629:G:O2'	26:A:2635:A:N6	2.42	0.49
10:L:22:ILE:HD12	26:A:2176:A:C5	2.48	0.49
14:P:112:ARG:N	25:B:49:C:OP1	2.40	0.49
21:W:28:ARG:HH12	25:B:77:A:H5'	1.78	0.49
21:W:77:LEU:CG	21:W:100:VAL:HG21	2.43	0.49
25:B:55:G:H2'	25:B:56:C:H6	1.78	0.49
26:A:1543:A:N1	26:A:1628:A:O2'	2.44	0.49
26:A:1581:C:N4	26:A:1591:U:N1	2.61	0.49
26:A:1596:C:O2'	26:A:1597:G:C5'	2.60	0.49
31:5:21:PHE:HB2	31:5:46:THR:HG21	1.95	0.49
7:I:9:ALA:HB3	7:I:56:LEU:HD11	1.95	0.49
9:K:87:ARG:NH1	9:K:91:GLU:OE2	2.46	0.49
12:N:60:ARG:NH1	26:A:1193:C:C5'	2.71	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:38:GLU:O	13:O:42:ARG:HG3	2.13	0.49
19:U:33:VAL:HG11	19:U:42:ILE:HD11	1.93	0.49
19:U:67:LYS:CE	26:A:1451:A:OP2	2.61	0.49
26:A:799:G:OP1	31:5:19:HIS:HD2	1.96	0.49
26:A:1044:U:P	27:1:37:ARG:HH12	2.36	0.49
3:E:5:VAL:HG22	3:E:6:ASP:N	2.27	0.48
4:F:45:MET:HA	4:F:45:MET:HE2	1.95	0.48
19:U:66:ARG:HA	19:U:75:LYS:CA	2.43	0.48
25:B:54:A:H2'	25:B:55:G:C8	2.48	0.48
1:C:99:ASP:O	26:A:1720:G:N2	2.23	0.48
2:D:162:LYS:HG2	26:A:2843:C:H5''	1.95	0.48
4:F:80:SER:OG	4:F:88:GLU:N	2.46	0.48
8:J:96:LYS:HE2	21:W:120:PRO:CB	2.37	0.48
10:L:19:ILE:HB	10:L:41:ALA:HB1	1.95	0.48
18:T:77:VAL:HG22	18:T:117:ARG:HG2	1.96	0.48
19:U:96:PHE:CD2	19:U:96:PHE:C	2.86	0.48
22:X:56:ASP:N	22:X:56:ASP:OD1	2.39	0.48
25:B:19:G:C6	25:B:20:G:C5	3.01	0.48
25:B:88:C:H3'	25:B:88:C:H6	1.79	0.48
26:A:1552:A:H1'	26:A:1618:C:H42	1.78	0.48
26:A:2509:C:C4	30:4:8:ARG:NH1	2.79	0.48
30:4:13:LEU:HA	30:4:53:GLU:HA	1.95	0.48
3:E:144:PHE:CE1	3:E:148:LEU:CD1	2.97	0.48
4:F:8:LEU:CD2	4:F:16:ARG:HD2	2.43	0.48
17:S:16:VAL:HG12	17:S:22:VAL:HG21	1.96	0.48
21:W:87:PRO:C	21:W:90:ARG:NH2	2.60	0.48
26:A:1563:A:N6	26:A:1565:A:C5	2.81	0.48
26:A:1564:A:C2'	26:A:1565:A:C5'	2.86	0.48
26:A:1564:A:H3'	26:A:1565:A:H5''	1.94	0.48
30:4:15:CYS:C	30:4:20:HIS:HB3	2.29	0.48
1:C:25:THR:CG2	1:C:81:HIS:ND1	2.77	0.48
3:E:6:ASP:HA	3:E:16:GLY:O	2.13	0.48
3:E:180:PRO:HG3	3:E:200:ALA:HB1	1.94	0.48
4:F:46:GLY:HA3	26:A:2529:A:H61	1.79	0.48
19:U:6:ASP:OD2	24:Z:23:ARG:CG	2.60	0.48
19:U:67:LYS:CB	19:U:67:LYS:NZ	2.76	0.48
22:X:75:ARG:NH1	26:A:2557:A:OP1	2.45	0.48
24:Z:45:ARG:O	24:Z:49:THR:OG1	2.27	0.48
24:Z:62:ARG:HH21	24:Z:66:LEU:CD1	2.26	0.48
25:B:19:G:C8	25:B:19:G:C4'	2.96	0.48
25:B:37:C:C5	25:B:38:C:C5	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1590:G:C2	26:A:1591:U:C5	3.00	0.48
26:A:1637:G:O2'	26:A:1805:G:O2'	2.31	0.48
26:A:1882:A:N6	26:A:2220:C:H42	2.11	0.48
29:3:27:LEU:HB3	29:3:38:LYS:HB3	1.95	0.48
4:F:35:ILE:CG2	4:F:36:PRO:HD2	2.43	0.48
9:K:45:THR:OG1	16:R:64:ARG:NH2	2.46	0.48
10:L:8:LEU:HD12	10:L:19:ILE:O	2.14	0.48
12:N:60:ARG:NH2	12:N:60:ARG:CG	2.72	0.48
12:N:111:GLU:OE2	12:N:115:ARG:HB2	2.13	0.48
21:W:157:ILE:HB	21:W:179:VAL:HB	1.96	0.48
24:Z:13:LEU:HD21	24:Z:17:GLU:O	2.14	0.48
25:B:86:U:O2'	25:B:87:U:H2'	2.14	0.48
26:A:1569:A:O2'	26:A:1570:C:C6	2.63	0.48
2:D:129:ARG:HG2	2:D:170:MET:HB3	1.96	0.48
3:E:154:VAL:HB	3:E:175:VAL:HG23	1.95	0.48
10:L:107:ARG:HD3	10:L:115:VAL:HG11	1.94	0.48
12:N:134:ARG:HD3	21:W:129:ASN:ND2	2.29	0.48
18:T:30:LEU:HD23	29:3:24:ALA:HB2	1.95	0.48
18:T:99:ARG:HD2	26:A:862:U:O2'	2.12	0.48
24:Z:62:ARG:NH2	24:Z:66:LEU:CD1	2.77	0.48
26:A:1171:C:H2'	26:A:1172:A:C8	2.49	0.48
26:A:2072:G:O6	26:A:2111:U:O4	2.31	0.48
5:G:132:PHE:HZ	5:G:149:ILE:HG21	1.79	0.48
13:O:20:LEU:HD23	13:O:24:LEU:HD12	1.95	0.48
13:O:81:ALA:C	13:O:85:PRO:CD	2.74	0.48
24:Z:48:ARG:HG3	26:A:58:G:OP1	2.13	0.48
25:B:10:G:C6	25:B:11:U:H1'	2.47	0.48
33:7:35:ARG:CG	33:7:36:GLN:N	2.73	0.48
1:C:256:ARG:NH1	1:C:258:ARG:HH11	2.12	0.48
9:K:84:LEU:HD11	26:A:1250:U:C6	2.49	0.48
9:K:112:ASN:OD1	26:A:650:G:OP1	2.31	0.48
12:N:17:GLN:NE2	26:A:1075:U:H5	2.11	0.48
26:A:351:G:N2	26:A:444:U:O4	2.40	0.48
26:A:1411:G:OP1	26:A:2933:G:O2'	2.26	0.48
26:A:1571:C:O2'	26:A:1572:G:C5'	2.54	0.48
28:2:41:CYS:CB	28:2:44:PHE:CZ	2.86	0.48
1:C:76:ASN:C	1:C:98:LEU:CD2	2.82	0.48
10:L:77:ILE:HG12	15:Q:71:ARG:HD3	1.96	0.48
13:O:80:PHE:C	13:O:80:PHE:CD2	2.85	0.48
16:R:57:PHE:HZ	26:A:623:A:H4'	1.78	0.48
16:R:98:LEU:HD21	17:S:4:TYR:OH	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:2:LYS:CD	20:V:83:VAL:CB	2.91	0.48
26:A:79:G:N2	26:A:100:A:OP2	2.44	0.48
26:A:681:C:H2'	26:A:682:A:H8	1.79	0.48
26:A:2374:U:H2'	26:A:2375:G:C8	2.49	0.48
1:C:76:ASN:CB	1:C:98:LEU:HD21	2.42	0.48
4:F:9:PRO:O	4:F:13:GLN:N	2.43	0.48
7:I:48:THR:HB	7:I:81:PHE:HB2	1.96	0.48
15:Q:33:GLU:OE1	15:Q:38:ARG:NH2	2.47	0.48
21:W:87:PRO:O	21:W:90:ARG:NH1	2.46	0.48
26:A:81:A:N1	26:A:96:G:O2'	2.34	0.48
26:A:265:A:N1	26:A:515:U:O2'	2.41	0.48
26:A:2745:C:O2'	26:A:2788:A:N3	2.39	0.48
1:C:5:LYS:HD2	1:C:17:SER:HB3	1.96	0.47
1:C:59:LYS:HG3	26:A:1788:G:H4'	1.96	0.47
1:C:76:ASN:O	1:C:98:LEU:HD23	2.11	0.47
4:F:70:GLN:OE1	4:F:96:VAL:CG2	2.62	0.47
12:N:59:LYS:NZ	12:N:59:LYS:CB	2.73	0.47
13:O:116:VAL:HG23	13:O:116:VAL:O	2.13	0.47
26:A:1581:C:H2'	26:A:1582:C:C5	2.44	0.47
26:A:2163:U:OP1	26:A:2828:U:O2'	2.29	0.47
4:F:73:GLU:HB3	25:B:42:C:C6	2.48	0.47
9:K:37:ARG:NH1	26:A:1125:C:OP1	2.46	0.47
10:L:73:ASP:OD1	10:L:73:ASP:N	2.46	0.47
20:V:46:ALA:HB2	26:A:572:C:P	2.54	0.47
21:W:79:LEU:N	21:W:98:LEU:O	2.48	0.47
26:A:292:G:H2'	26:A:293:G:H8	1.79	0.47
26:A:1554:U:C4	26:A:1617:C:N4	2.82	0.47
26:A:1568:C:H2'	26:A:1569:A:N7	2.29	0.47
26:A:1578:G:N9	26:A:1592:G:N1	2.57	0.47
26:A:2800:G:O2'	26:A:2803:C:OP2	2.28	0.47
1:C:79:VAL:HG23	1:C:114:GLY:H	1.78	0.47
1:C:108:PRO:HA	1:C:196:VAL:HA	1.96	0.47
1:C:256:ARG:CD	1:C:258:ARG:NE	2.76	0.47
4:F:23:LEU:HD22	4:F:36:PRO:HD2	1.95	0.47
11:M:51:GLU:HG3	32:6:57:ARG:HH11	1.70	0.47
21:W:6:ASN:HB2	21:W:138:LEU:C	2.26	0.47
25:B:13:C:O2'	25:B:14:A:H3'	2.14	0.47
25:B:89:C:H2'	25:B:90:G:H8	1.79	0.47
26:A:1830:C:H4'	31:5:10:PRO:CD	2.44	0.47
26:A:1830:C:C5'	31:5:10:PRO:HG2	2.43	0.47
1:C:143:HIS:ND1	1:C:194:GLY:O	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:178:PRO:HG2	26:A:2016:G:O6	2.14	0.47
13:O:49:GLU:OE1	13:O:94:TYR:CD2	2.67	0.47
20:V:43:LYS:O	20:V:60:VAL:N	2.47	0.47
20:V:87:ILE:HG12	20:V:94:LYS:HG3	1.96	0.47
21:W:122:THR:HG23	21:W:181:VAL:HG13	1.96	0.47
22:X:83:VAL:CG1	22:X:85:ARG:CB	2.93	0.47
25:B:34:G:O6	25:B:44:C:C6	2.68	0.47
25:B:35:G:N1	25:B:36:U:C4	2.82	0.47
26:A:860:G:O2'	26:A:863:G:O2'	2.21	0.47
26:A:1551:U:O4	26:A:1619:U:O4	2.32	0.47
4:F:102:ARG:NH1	28:2:9:TYR:CD1	2.82	0.47
9:K:1:MET:H2	9:K:2:PRO:CD	2.27	0.47
15:Q:55:SER:HB2	26:A:2907:C:H5'	1.97	0.47
20:V:11:VAL:HG21	20:V:38:VAL:HG11	1.96	0.47
20:V:27:TYR:HB3	20:V:30:ARG:HB2	1.96	0.47
24:Z:33:ARG:HA	24:Z:36:MET:HG2	1.95	0.47
25:B:58:A:C6	25:B:59:A:C8	2.99	0.47
25:B:59:A:C3'	25:B:60:G:H5'	2.45	0.47
26:A:103:C:H2'	26:A:104:G:H8	1.79	0.47
26:A:325:U:H2'	26:A:326:A:H8	1.79	0.47
26:A:534:G:H4'	26:A:535:A:H5'	1.97	0.47
26:A:2528:G:H22	26:A:2536:U:H3	1.62	0.47
3:E:181:ASP:OD1	3:E:181:ASP:N	2.43	0.47
25:B:4:A:C2	25:B:25:G:N1	2.82	0.47
26:A:1110:C:H2'	26:A:1111:G:H8	1.80	0.47
26:A:1588:G:H3'	26:A:1589:G:H8	1.79	0.47
1:C:67:PHE:HE1	1:C:106:ILE:HD11	1.80	0.47
1:C:262:LYS:N	1:C:263:PRO:HD3	2.30	0.47
4:F:23:LEU:HD21	4:F:29:TYR:OH	2.14	0.47
6:H:23:ASP:O	6:H:27:ARG:CB	2.62	0.47
10:L:107:ARG:HH21	10:L:115:VAL:HG11	1.80	0.47
14:P:50:GLN:NE2	25:B:7:G:N3	2.51	0.47
19:U:29:TYR:CE2	19:U:93:ILE:HB	2.50	0.47
21:W:94:HIS:CE1	25:B:75:U:O2	2.67	0.47
22:X:42:GLY:N	22:X:57:ASP:OD2	2.46	0.47
25:B:34:G:O6	25:B:44:C:H2'	2.13	0.47
26:A:451:U:H2'	26:A:452:G:C8	2.49	0.47
26:A:1414:G:N1	26:A:1858:A:OP2	2.36	0.47
26:A:1550:G:N2	26:A:1620:U:O2	2.35	0.47
26:A:1563:A:O2'	26:A:1564:A:OP2	2.28	0.47
26:A:1597:G:C4	26:A:1598:U:C6	2.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:2255:A:O2'	26:A:2678:G:N2	2.44	0.47
32:6:27:ALA:O	32:6:29:ARG:N	2.46	0.47
1:C:25:THR:CG2	1:C:81:HIS:HD1	2.28	0.47
4:F:115:LEU:HD23	4:F:183:PRO:CD	2.45	0.47
4:F:118:ILE:HB	4:F:121:PHE:HB2	1.97	0.47
7:I:27:GLU:HG3	7:I:76:PRO:HG2	1.97	0.47
16:R:124:PRO:HB3	26:A:1268:C:H4'	1.97	0.47
21:W:164:LEU:HD13	21:W:168:VAL:HG12	1.96	0.47
22:X:56:ASP:HA	26:A:2610:C:H4'	1.95	0.47
22:X:76:LYS:CE	26:A:973:G:OP1	2.63	0.47
26:A:1541:G:C6	26:A:1630:U:O4	2.68	0.47
26:A:1596:C:O2'	26:A:1597:G:P	2.73	0.47
28:2:44:PHE:C	28:2:48:LYS:HE3	2.35	0.47
30:4:35:ARG:HD3	30:4:35:ARG:HA	1.68	0.47
5:G:3:ARG:NH1	26:A:2975:G:OP2	2.43	0.47
9:K:114:LEU:HD12	26:A:650:G:H5'	1.97	0.47
12:N:74:LEU:HD22	26:A:1075:U:OP2	2.15	0.47
13:O:33:ARG:HD3	13:O:114:GLU:HG2	1.95	0.47
21:W:28:ARG:NH1	25:B:76:G:O3'	2.48	0.47
25:B:83:C:H5''	27:1:52:HIS:CE1	2.50	0.47
26:A:347:U:H2'	26:A:348:G:H8	1.80	0.47
26:A:1162:G:O2'	26:A:1229:A:N6	2.44	0.47
26:A:1596:C:O2'	26:A:1597:G:H5'	2.15	0.47
1:C:73:ASP:HB3	1:C:120:GLY:N	2.25	0.47
1:C:132:PRO:HD2	1:C:135:ASN:HD22	1.79	0.47
8:J:40:PHE:O	8:J:44:TYR:HB2	2.15	0.47
11:M:76:GLN:HE22	26:A:720:C:H42	1.63	0.47
15:Q:92:ARG:HG3	26:A:1970:G:H5''	1.95	0.47
20:V:31:ASN:O	20:V:68:VAL:HB	2.16	0.47
21:W:14:ASN:OD1	21:W:14:ASN:N	2.48	0.47
21:W:134:GLU:HB2	21:W:171:ILE:HD11	1.97	0.47
25:B:24:G:N9	25:B:56:C:C2	2.83	0.47
26:A:1535:C:H3'	26:A:1536:A:H8	1.79	0.47
26:A:1562:C:O2'	26:A:1563:A:OP2	2.32	0.47
26:A:1595:G:C8	26:A:1596:C:C5	2.88	0.47
26:A:1717:U:H5''	26:A:1718:C:H5	1.80	0.47
26:A:2753:G:O6	33:7:31:ARG:NH1	2.47	0.47
31:5:6:ARG:C	31:5:7:THR:HG23	2.36	0.47
32:6:48:THR:OG1	32:6:49:THR:N	2.48	0.47
32:6:58:ILE:HD13	32:6:61:LEU:HD12	1.97	0.47
3:E:77:GLY:H	26:A:789:G:H5''	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:S:76:HIS:HE1	17:S:85:HIS:HD2	1.63	0.46
21:W:29:ARG:HH12	25:B:90:G:C4'	2.28	0.46
34:8:6:ARG:O	34:8:10:ASP:HB2	2.14	0.46
1:C:25:THR:CG2	1:C:81:HIS:C	2.83	0.46
4:F:34:GLN:NE2	25:B:57:U:O2'	2.47	0.46
8:J:106:GLN:O	8:J:110:ILE:HB	2.15	0.46
9:K:142:ILE:HG22	9:K:143:LYS:H	1.80	0.46
10:L:35:ILE:HG21	10:L:103:GLY:HA3	1.98	0.46
11:M:35:ARG:NH1	11:M:41:LYS:O	2.47	0.46
20:V:46:ALA:CB	26:A:572:C:OP1	2.62	0.46
20:V:96:ARG:NH2	20:V:96:ARG:CG	2.72	0.46
25:B:84:C:C5	25:B:85:C:C4	3.03	0.46
26:A:1588:G:H3'	26:A:1589:G:C8	2.50	0.46
30:4:18:CYS:SG	30:4:19:LYS:HG2	2.55	0.46
3:E:145:LEU:HA	3:E:148:LEU:CD1	2.38	0.46
4:F:10:ARG:NH1	4:F:10:ARG:CG	2.72	0.46
20:V:79:LYS:HE3	20:V:79:LYS:HB2	1.70	0.46
21:W:77:LEU:HD13	21:W:100:VAL:HB	1.96	0.46
23:Y:34:GLN:NE2	26:A:2453:U:O2	2.43	0.46
25:B:15:U:H3'	25:B:16:A:H8	1.79	0.46
25:B:25:G:H2'	25:B:26:A:H5'	1.97	0.46
25:B:54:A:C2'	25:B:55:G:C5'	2.91	0.46
26:A:1530:G:N2	26:A:1805:G:H1	2.13	0.46
31:5:6:ARG:CZ	31:5:6:ARG:HB3	2.44	0.46
1:C:49:ILE:N	26:A:894:U:OP1	2.33	0.46
2:D:7:LEU:HD11	2:D:82:ALA:HB3	1.97	0.46
3:E:7:VAL:CB	3:E:16:GLY:CA	2.84	0.46
5:G:18:THR:OG1	5:G:25:SER:O	2.32	0.46
5:G:159:LYS:HA	5:G:172:ARG:HH22	1.81	0.46
6:H:124:ILE:HG22	6:H:125:LYS:H	1.81	0.46
7:I:4:ALA:O	7:I:8:THR:OG1	2.23	0.46
10:L:17:LYS:HB3	10:L:45:ASP:HB3	1.96	0.46
19:U:58:ASN:HB3	26:A:1456:G:H1'	1.97	0.46
25:B:59:A:H2'	25:B:60:G:H8	1.80	0.46
26:A:334:G:H2'	26:A:335:G:C8	2.50	0.46
26:A:2515:U:H2'	26:A:2516:U:C6	2.51	0.46
2:D:34:ASN:HD21	2:D:54:TYR:HB2	1.80	0.46
2:D:156:THR:CG2	26:A:2256:G:N2	2.75	0.46
2:D:159:ARG:NH1	2:D:159:ARG:HG2	2.30	0.46
19:U:94:ASP:OD1	19:U:94:ASP:N	2.48	0.46
20:V:77:ASP:N	20:V:77:ASP:OD1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1189:G:H1'	26:A:1207:G:H2'	1.96	0.46
26:A:2509:C:OP2	30:4:28:ASN:ND2	2.48	0.46
30:4:16:GLU:HA	30:4:20:HIS:HB3	1.97	0.46
1:C:57:GLY:C	1:C:58:HIS:O	2.54	0.46
3:E:201:LEU:HD23	3:E:201:LEU:C	2.36	0.46
4:F:76:ARG:HG2	4:F:91:PRO:HA	1.96	0.46
4:F:99:ARG:HD3	25:B:45:G:H5'	1.98	0.46
14:P:43:SER:CB	25:B:28:A:OP1	2.63	0.46
16:R:90:VAL:HG13	17:S:6:ILE:HD13	1.97	0.46
21:W:36:VAL:HG22	21:W:94:HIS:CE1	2.50	0.46
22:X:76:LYS:HD3	26:A:973:G:OP1	2.16	0.46
26:A:1479:G:N2	26:A:1482:A:OP2	2.47	0.46
26:A:1612:U:H2'	26:A:1613:G:H8	1.81	0.46
28:2:38:CYS:SG	28:2:40:GLN:CD	2.94	0.46
1:C:261:ASN:C	1:C:262:LYS:HD3	2.36	0.46
3:E:131:VAL:O	3:E:133:GLY:N	2.49	0.46
3:E:208:ASN:N	3:E:208:ASN:HD22	2.13	0.46
8:J:40:PHE:HZ	8:J:58:VAL:HG11	1.81	0.46
9:K:147:GLN:O	16:R:75:THR:HG21	2.16	0.46
25:B:54:A:H2'	25:B:55:G:H5'	1.93	0.46
25:B:60:G:HO2'	25:B:61:C:H5'	1.72	0.46
26:A:747:A:H2	26:A:768:G:H21	1.63	0.46
26:A:1479:G:H4'	26:A:2025:C:H5	1.79	0.46
2:D:159:ARG:H	2:D:159:ARG:CD	2.28	0.46
9:K:14:SER:O	9:K:52:ASP:HB3	2.16	0.46
13:O:42:ARG:O	13:O:46:PRO:CD	2.63	0.46
13:O:106:ASP:OD1	13:O:106:ASP:N	2.48	0.46
16:R:77:ASN:HD22	26:A:1270:G:H21	1.64	0.46
22:X:83:VAL:O	22:X:85:ARG:HA	2.16	0.46
25:B:24:G:N9	25:B:56:C:N3	2.63	0.46
4:F:64:LEU:HD12	4:F:72:PRO:CB	2.46	0.46
17:S:3:THR:CB	17:S:102:ILE:HD11	2.44	0.46
17:S:6:ILE:O	17:S:7:VAL:HG22	2.12	0.46
20:V:96:ARG:CZ	20:V:96:ARG:CB	2.94	0.46
26:A:2070:A:H2'	26:A:2071:A:C8	2.51	0.46
26:A:2081:U:OP1	26:A:2634:G:O2'	2.26	0.46
1:C:229:VAL:HB	26:A:899:G:O6	2.16	0.46
3:E:24:LEU:HD21	3:E:208:ASN:CB	2.46	0.46
7:I:49:TYR:HD1	7:I:80:ALA:HB2	1.81	0.46
14:P:43:SER:HB2	25:B:28:A:OP1	2.16	0.46
18:T:36:VAL:HG22	18:T:78:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:112:VAL:HG23	21:W:126:GLN:HE21	1.80	0.46
25:B:79:A:N1	25:B:94:G:O6	2.49	0.46
26:A:2394:A:O2'	26:A:2396:A:OP1	2.28	0.46
1:C:73:ASP:HA	1:C:119:SER:HB3	1.98	0.45
3:E:164:VAL:O	3:E:168:SER:OG	2.20	0.45
4:F:44:ASN:HD22	4:F:45:MET:N	2.13	0.45
4:F:99:ARG:HD3	25:B:45:G:O4'	2.16	0.45
10:L:75:SER:HB2	15:Q:71:ARG:HE	1.80	0.45
15:Q:58:PHE:HD1	15:Q:75:VAL:HG22	1.82	0.45
18:T:18:ARG:HH12	26:A:1436:C:C2'	2.28	0.45
21:W:83:LEU:HD12	21:W:92:ILE:HD12	1.95	0.45
26:A:2509:C:C5	30:4:8:ARG:CZ	2.94	0.45
1:C:37:LEU:CD2	1:C:62:TYR:HB2	2.37	0.45
11:M:61:LEU:HD12	32:6:14:PHE:HZ	1.81	0.45
12:N:110:ASP:OD1	12:N:110:ASP:N	2.43	0.45
26:A:1595:G:OP2	26:A:1596:C:C5	2.68	0.45
3:E:140:SER:O	3:E:144:PHE:HB3	2.17	0.45
4:F:183:PRO:O	4:F:184:PHE:CE2	2.55	0.45
8:J:80:LEU:HD13	8:J:110:ILE:HG23	1.97	0.45
19:U:14:PRO:HA	19:U:31:PHE:HA	1.98	0.45
26:A:1040:U:H2'	26:A:1041:A:C8	2.52	0.45
1:C:58:HIS:CE1	26:A:1788:G:H21	2.28	0.45
1:C:221:VAL:HG21	26:A:897:A:C8	2.51	0.45
9:K:114:LEU:HD23	9:K:117:GLN:HE21	1.80	0.45
13:O:26:THR:CG2	13:O:75:VAL:HG21	2.46	0.45
25:B:83:C:C5'	27:1:52:HIS:CE1	2.99	0.45
26:A:273:A:H61	26:A:314:G:H1'	1.81	0.45
26:A:2059:G:H1	26:A:2122:U:H3	1.64	0.45
26:A:2288:C:H2'	26:A:2289:C:C6	2.52	0.45
26:A:2374:U:H2'	26:A:2375:G:H8	1.81	0.45
26:A:2527:G:H1	26:A:2537:C:H42	1.62	0.45
4:F:6:LYS:CE	4:F:6:LYS:N	2.80	0.45
4:F:73:GLU:HG2	25:B:42:C:C4	2.43	0.45
4:F:154:ASP:OD1	4:F:155:ARG:N	2.48	0.45
5:G:165:TYR:HB2	5:G:168:GLU:HB2	1.98	0.45
21:W:78:ALA:HB1	21:W:97:LEU:HB3	1.99	0.45
26:A:314:G:O2'	26:A:321:G:O2'	2.35	0.45
26:A:377:C:H2'	26:A:378:G:H8	1.81	0.45
26:A:1573:U:OP1	26:A:1593:U:OP1	2.34	0.45
26:A:1754:G:C6	26:A:1759:A:N1	2.85	0.45
27:1:15:ALA:HB3	27:1:20:ARG:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:83:GLN:H	3:E:83:GLN:HG2	1.42	0.45
9:K:76:ARG:HG2	9:K:76:ARG:O	2.17	0.45
10:L:76:TYR:HB2	15:Q:72:THR:HB	1.98	0.45
10:L:120:GLU:OE1	15:Q:64:SER:HB3	2.15	0.45
13:O:38:GLU:OE2	13:O:99:LYS:NZ	2.50	0.45
13:O:46:PRO:HG2	13:O:47:TYR:N	2.32	0.45
19:U:13:ALA:O	19:U:32:VAL:N	2.38	0.45
1:C:71:ASP:OD1	1:C:71:ASP:N	2.30	0.45
3:E:7:VAL:O	3:E:14:THR:CA	2.55	0.45
3:E:151:ASN:O	3:E:152:LYS:CB	2.57	0.45
12:N:60:ARG:NH1	26:A:1194:C:OP2	2.49	0.45
12:N:124:LYS:HD2	26:A:2708:G:H1'	1.99	0.45
17:S:76:HIS:HE1	17:S:85:HIS:CD2	2.35	0.45
20:V:83:VAL:CG1	20:V:96:ARG:CG	2.95	0.45
26:A:286:G:N2	26:A:287:A:H62	2.14	0.45
26:A:605:G:OP2	29:3:14:ARG:NH2	2.49	0.45
26:A:624:G:HO2'	26:A:625:A:H8	1.64	0.45
26:A:857:U:H2'	26:A:858:A:C8	2.51	0.45
26:A:1597:G:O2'	26:A:1598:U:C6	2.70	0.45
1:C:97:TYR:CD2	1:C:101:GLU:HG3	2.51	0.45
4:F:170:ASP:OD1	4:F:170:ASP:N	2.41	0.45
8:J:114:LYS:HA	8:J:117:ASP:HB3	1.99	0.45
10:L:71:ARG:NH2	10:L:105:GLU:HG3	2.32	0.45
11:M:51:GLU:OE2	32:6:57:ARG:NE	2.49	0.45
12:N:60:ARG:NE	26:A:1194:C:P	2.89	0.45
12:N:108:TYR:CD2	12:N:110:ASP:OD1	2.70	0.45
19:U:77:LYS:CE	19:U:79:THR:HG22	2.45	0.45
20:V:4:HIS:ND1	20:V:96:ARG:CZ	2.67	0.45
22:X:72:LYS:HG3	22:X:73:ARG:H	1.80	0.45
25:B:22:A:C6	25:B:23:G:O6	2.70	0.45
26:A:805:C:O2'	26:A:895:G:OP1	2.27	0.45
26:A:1550:G:O6	26:A:1620:U:O4	2.34	0.45
28:2:60:ARG:C	28:2:60:ARG:CD	2.86	0.45
1:C:168:LYS:HA	1:C:173:ALA:HA	1.97	0.45
4:F:70:GLN:HE21	25:B:43:C:H4'	1.80	0.45
13:O:20:LEU:HD23	13:O:20:LEU:O	2.17	0.45
13:O:33:ARG:CD	13:O:114:GLU:HG2	2.44	0.45
14:P:88:ILE:O	14:P:92:ALA:CB	2.65	0.45
19:U:83:ILE:HD13	26:A:1456:G:C4	2.51	0.45
21:W:37:LEU:HD21	21:W:99:VAL:CG2	2.47	0.45
24:Z:5:THR:HG23	24:Z:6:THR:N	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:159:A:N3	26:A:2431:C:O2'	2.48	0.45
26:A:1379:G:OP1	29:3:16:ARG:NH2	2.47	0.45
26:A:1537:U:H2'	26:A:1538:G:H8	1.82	0.45
26:A:2375:G:H2'	26:A:2376:G:C8	2.52	0.45
3:E:9:THR:HG22	3:E:128:THR:CG2	2.47	0.45
3:E:201:LEU:C	3:E:201:LEU:CD2	2.85	0.45
4:F:11:LEU:CD2	4:F:108:ASP:N	2.80	0.45
12:N:39:HIS:HB3	12:N:99:PRO:HD3	1.99	0.45
13:O:9:ARG:CD	13:O:14:SER:HB3	2.47	0.45
15:Q:50:GLN:HB2	15:Q:57:THR:HG22	1.99	0.45
20:V:100:THR:O	20:V:101:ASN:HB2	2.17	0.45
21:W:38:TYR:O	21:W:38:TYR:CD1	2.69	0.45
21:W:124:VAL:HG12	21:W:181:VAL:HG22	1.99	0.45
26:A:249:C:OP2	26:A:2618:C:O2'	2.33	0.45
26:A:857:U:H2'	26:A:858:A:H8	1.81	0.45
26:A:1098:A:N3	26:A:2261:U:O2'	2.42	0.45
26:A:1512:U:OP2	26:A:1513:C:N4	2.44	0.45
27:1:19:GLN:HG2	27:1:50:VAL:HG12	1.98	0.45
1:C:63:ARG:NH1	26:A:1788:G:OP2	2.50	0.44
1:C:261:ASN:C	1:C:262:LYS:CD	2.86	0.44
2:D:60:ARG:HH22	26:A:3055:G:H5'	1.82	0.44
3:E:51:SER:OG	26:A:35:A:C5'	2.58	0.44
4:F:27:PHE:HB2	4:F:29:TYR:CE1	2.51	0.44
19:U:74:GLY:HA2	26:A:61:G:O2'	2.18	0.44
25:B:20:G:N1	25:B:63:U:C4	2.73	0.44
25:B:34:G:O2'	25:B:35:G:C5	2.70	0.44
25:B:58:A:H2'	25:B:59:A:O5'	2.17	0.44
26:A:130:C:H2'	26:A:131:A:C8	2.53	0.44
26:A:478:A:H4'	26:A:479:A:H5'	1.99	0.44
26:A:2238:A:H2'	26:A:2239:A:C8	2.53	0.44
27:1:8:GLN:HG2	27:1:31:ILE:HA	1.99	0.44
10:L:7:ARG:NH2	10:L:20:LEU:CD1	2.43	0.44
11:M:61:LEU:HD12	32:6:14:PHE:CZ	2.52	0.44
14:P:108:THR:CB	25:B:47:A:O2'	2.64	0.44
20:V:86:ARG:CB	20:V:97:ILE:CG1	2.89	0.44
22:X:83:VAL:HG13	22:X:85:ARG:CA	2.37	0.44
25:B:89:C:C5	25:B:89:C:OP2	2.70	0.44
26:A:681:C:H2'	26:A:682:A:C8	2.53	0.44
26:A:1580:A:C2	26:A:1592:G:C1'	2.87	0.44
28:2:41:CYS:CA	28:2:43:PRO:HD2	2.47	0.44
30:4:20:HIS:CD2	30:4:20:HIS:O	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:158:GLY:O	26:A:2276:G:N3	2.50	0.44
18:T:41:ASP:OD2	29:3:38:LYS:HB2	2.17	0.44
20:V:83:VAL:HG11	20:V:96:ARG:CG	2.39	0.44
20:V:97:ILE:HD13	20:V:103:LYS:O	2.16	0.44
26:A:944:A:C8	26:A:2472:C:H5'	2.52	0.44
26:A:1296:G:H2'	26:A:1297:G:C8	2.52	0.44
26:A:1515:C:N4	26:A:1516:G:O6	2.50	0.44
26:A:2616:A:H5''	32:6:28:ASN:ND2	2.33	0.44
1:C:256:ARG:O	26:A:2014:G:O3'	2.34	0.44
3:E:14:THR:CG2	3:E:15:ASP:H	2.15	0.44
4:F:26:GLU:OE1	4:F:27:PHE:CE2	2.70	0.44
12:N:74:LEU:HD12	12:N:94:VAL:HG21	1.99	0.44
12:N:108:TYR:CE2	12:N:110:ASP:OD1	2.70	0.44
22:X:83:VAL:HG11	22:X:86:PRO:HD3	1.99	0.44
26:A:176:G:H3'	26:A:177:G:H8	1.83	0.44
26:A:1525:U:H2'	26:A:1526:A:H8	1.83	0.44
26:A:1576:C:O2	26:A:1577:C:C4	2.71	0.44
28:2:62:GLU:O	28:2:65:TYR:CD2	2.70	0.44
31:5:22:ARG:O	31:5:26:ARG:CD	2.58	0.44
1:C:51:THR:HG21	1:C:54:LYS:CE	2.46	0.44
4:F:6:LYS:N	4:F:6:LYS:HE3	2.32	0.44
9:K:5:THR:CG2	26:A:624:G:H4'	2.47	0.44
13:O:52:ILE:HD12	13:O:94:TYR:CB	2.48	0.44
13:O:90:ARG:HH21	13:O:118:GLU:HB2	1.74	0.44
14:P:37:ARG:HD2	14:P:103:ASP:HB2	1.98	0.44
14:P:43:SER:OG	25:B:29:C:OP2	2.19	0.44
19:U:74:GLY:O	26:A:61:G:O3'	2.35	0.44
26:A:1569:A:C8	26:A:1569:A:OP2	2.70	0.44
26:A:2323:G:H2'	26:A:2324:A:H8	1.83	0.44
26:A:3070:G:H4'	26:A:3071:A:H5'	1.99	0.44
30:4:19:LYS:O	30:4:20:HIS:CG	2.70	0.44
5:G:108:LEU:HD13	5:G:153:ARG:HG2	1.98	0.44
13:O:29:PHE:HE2	13:O:51:LEU:HD13	1.79	0.44
16:R:26:GLY:O	16:R:30:ARG:NH1	2.51	0.44
21:W:37:LEU:HD13	21:W:69:LEU:HD13	1.95	0.44
26:A:742:G:O2'	26:A:2575:G:OP1	2.36	0.44
26:A:947:U:H2'	26:A:948:G:C8	2.53	0.44
5:G:60:ARG:HA	5:G:63:ARG:HH21	1.82	0.44
13:O:72:ASP:O	13:O:76:VAL:HG23	2.18	0.44
21:W:102:ARG:HH21	21:W:138:LEU:CD2	2.22	0.44
26:A:947:U:H2'	26:A:948:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1562:C:O2'	26:A:1563:A:O4'	2.35	0.44
26:A:1562:C:O2'	26:A:1563:A:C8	2.70	0.44
26:A:1586:C:H2'	26:A:1587:G:O4'	2.18	0.44
26:A:2339:G:H3'	26:A:2340:A:H8	1.83	0.44
30:4:19:LYS:O	30:4:21:ARG:NH2	2.51	0.44
9:K:18:ILE:HD13	9:K:18:ILE:HG21	1.80	0.44
13:O:33:ARG:HB2	13:O:114:GLU:HG2	2.00	0.44
14:P:43:SER:HB3	14:P:46:HIS:H	1.83	0.44
20:V:58:GLY:HA2	26:A:571:A:HO2'	1.83	0.44
26:A:254:G:H4'	26:A:472:C:H4'	1.99	0.44
26:A:351:G:N1	26:A:444:U:N3	2.45	0.44
26:A:1159:C:H2'	26:A:1160:G:H8	1.82	0.44
28:2:41:CYS:HB2	28:2:44:PHE:HZ	1.74	0.44
30:4:15:CYS:HB3	30:4:20:HIS:H	1.81	0.44
31:5:40:LYS:O	31:5:40:LYS:HG3	2.18	0.44
4:F:120:ASP:O	4:F:122:ARG:HD3	2.17	0.44
7:I:57:VAL:HA	7:I:60:ALA:HB3	2.00	0.44
10:L:93:PRO:HD2	10:L:113:LYS:HD3	2.00	0.44
20:V:76:SER:C	20:V:77:ASP:OD1	2.56	0.44
24:Z:48:ARG:HD2	26:A:58:G:OP1	2.18	0.44
25:B:89:C:P	25:B:89:C:C6	3.10	0.44
26:A:325:U:H2'	26:A:326:A:C8	2.52	0.44
26:A:325:U:O4	26:A:450:G:O6	2.36	0.44
26:A:569:G:O2'	26:A:594:U:O4	2.35	0.44
26:A:621:U:H2'	26:A:622:C:C6	2.53	0.44
26:A:1439:G:H3'	26:A:1440:C:H4'	2.00	0.44
26:A:1551:U:C4	26:A:1619:U:O4	2.71	0.44
26:A:1575:A:C8	26:A:1575:A:OP2	2.70	0.44
26:A:2325:U:O4	26:A:2410:A:N1	2.51	0.44
4:F:56:LEU:O	4:F:59:GLY:N	2.51	0.43
4:F:66:LEU:HD23	28:2:27:THR:HG22	1.81	0.43
10:L:4:GLN:HE22	26:A:2176:A:H61	1.66	0.43
18:T:7:PHE:N	18:T:8:PRO:CD	2.81	0.43
21:W:6:ASN:CG	21:W:138:LEU:O	2.51	0.43
21:W:105:LYS:HZ3	21:W:136:GLU:HG3	1.83	0.43
25:B:27:A:H2'	25:B:28:A:H8	1.83	0.43
26:A:2:A:H2'	26:A:3:A:C8	2.52	0.43
26:A:406:A:N6	26:A:420:G:O2'	2.50	0.43
26:A:1551:U:H3'	26:A:1552:A:H8	1.83	0.43
3:E:14:THR:CG2	3:E:15:ASP:N	2.73	0.43
13:O:68:LYS:HB2	26:A:2932:G:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Z:44:ASN:ND2	26:A:58:G:OP1	2.50	0.43
25:B:18:C:H2'	25:B:19:G:H5'	1.81	0.43
26:A:196:A:H2	26:A:2658:A:H62	1.66	0.43
26:A:922:U:O2'	26:A:2284:A:N1	2.48	0.43
26:A:1621:C:H2'	26:A:1622:G:H8	1.83	0.43
26:A:1668:C:O2'	26:A:1764:A:N3	2.41	0.43
26:A:1921:G:H2'	26:A:1922:G:C8	2.53	0.43
26:A:2585:U:P	32:6:24:ARG:HH12	2.36	0.43
4:F:118:ILE:HD11	4:F:144:MET:HE2	2.01	0.43
5:G:61:ARG:O	5:G:65:LEU:CB	2.67	0.43
12:N:14:HIS:HA	12:N:15:PRO:HD2	1.80	0.43
13:O:56:LYS:CD	13:O:87:TYR:O	2.67	0.43
15:Q:49:ARG:NE	15:Q:56:GLU:OE2	2.50	0.43
17:S:26:LYS:NZ	26:A:1281:G:O3'	2.51	0.43
18:T:7:PHE:O	18:T:7:PHE:CD1	2.70	0.43
19:U:4:ILE:O	19:U:5:THR:HB	2.18	0.43
19:U:58:ASN:HB2	19:U:83:ILE:HG12	1.99	0.43
20:V:97:ILE:CD1	20:V:104:ASP:HA	2.49	0.43
23:Y:34:GLN:OE1	26:A:2452:G:N2	2.44	0.43
26:A:1566:A:H1'	26:A:1605:G:N1	2.24	0.43
26:A:1590:G:O2'	26:A:1591:U:O4'	2.20	0.43
26:A:1595:G:H5'	26:A:1596:C:N1	2.32	0.43
28:2:41:CYS:O	28:2:44:PHE:CE2	2.70	0.43
3:E:118:ARG:NH2	3:E:189:LEU:HA	2.34	0.43
3:E:121:ASN:ND2	11:M:3:VAL:HG23	2.33	0.43
3:E:171:ASN:ND2	3:E:171:ASN:O	2.51	0.43
4:F:40:LYS:HG2	4:F:164:VAL:HB	2.00	0.43
5:G:151:ARG:HH21	26:A:2968:G:H4'	1.84	0.43
7:I:51:VAL:N	26:A:1202:A:OP1	2.51	0.43
8:J:59:GLU:HB3	8:J:71:ALA:HB3	2.00	0.43
13:O:25:ALA:O	13:O:29:PHE:CD2	2.70	0.43
13:O:29:PHE:CZ	13:O:51:LEU:CD1	2.99	0.43
13:O:48:ALA:O	13:O:52:ILE:HG13	2.18	0.43
23:Y:48:ARG:NH2	26:A:2424:C:OP1	2.36	0.43
26:A:334:G:H2'	26:A:335:G:H8	1.84	0.43
26:A:1106:A:H3'	27:1:11:SER:HB2	2.00	0.43
26:A:1583:U:C2	26:A:1584:U:O4	2.71	0.43
26:A:1590:G:C6	26:A:1591:U:O4	2.70	0.43
26:A:1597:G:C2	26:A:1598:U:C6	3.01	0.43
26:A:1597:G:C5	26:A:1598:U:H5	2.33	0.43
27:1:23:LEU:HD11	27:1:53:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:27:THR:OG1	2:D:196:GLY:O	2.28	0.43
2:D:143:ALA:HB1	26:A:1875:U:H4'	2.00	0.43
9:K:1:MET:H2	9:K:2:PRO:HD3	1.80	0.43
9:K:5:THR:HG21	26:A:624:G:O3'	2.18	0.43
10:L:109:LYS:HE3	10:L:109:LYS:HB2	1.74	0.43
18:T:117:ARG:HA	18:T:117:ARG:HD2	1.78	0.43
19:U:73:PHE:CZ	31:5:43:ARG:NH2	2.80	0.43
21:W:6:ASN:HD22	21:W:6:ASN:C	2.22	0.43
21:W:100:VAL:HG11	21:W:137:ALA:CB	2.16	0.43
21:W:133:ILE:HD11	21:W:144:LEU:HD11	2.00	0.43
25:B:21:C:H6	25:B:21:C:C3'	2.29	0.43
26:A:1189:G:O2'	26:A:1207:G:OP2	2.35	0.43
26:A:1561:C:C3'	26:A:1562:C:H5'	2.48	0.43
26:A:1581:C:N4	26:A:1590:G:N3	2.66	0.43
26:A:1621:C:H2'	26:A:1622:G:C8	2.54	0.43
33:7:3:VAL:CG1	33:7:37:GLY:HA3	2.49	0.43
2:D:185:VAL:HG22	2:D:192:LEU:HG	2.01	0.43
3:E:77:GLY:N	26:A:789:G:H5''	2.33	0.43
3:E:124:ILE:H	3:E:124:ILE:HG13	1.48	0.43
3:E:149:THR:C	3:E:150:GLU:CG	2.85	0.43
4:F:45:MET:CE	4:F:45:MET:HA	2.49	0.43
4:F:185:LYS:O	4:F:185:LYS:HG3	2.18	0.43
19:U:83:ILE:HD11	26:A:1456:G:H21	1.63	0.43
20:V:28:PRO:HG3	26:A:82:G:O3'	2.19	0.43
26:A:334:G:H1	26:A:347:U:H3	1.66	0.43
26:A:802:C:OP1	31:5:9:GLN:HG3	2.19	0.43
26:A:1525:U:H2'	26:A:1526:A:C8	2.53	0.43
26:A:1898:U:N3	26:A:1981:U:OP2	2.46	0.43
26:A:3022:G:H2'	26:A:3023:G:C8	2.53	0.43
20:V:4:HIS:CD2	20:V:96:ARG:NH1	2.86	0.43
20:V:97:ILE:HD12	20:V:103:LYS:C	2.38	0.43
21:W:105:LYS:NZ	21:W:136:GLU:N	2.66	0.43
26:A:2693:A:N6	26:A:2705:G:O2'	2.51	0.43
30:4:19:LYS:HB2	30:4:21:ARG:CZ	2.48	0.43
5:G:35:LEU:HD13	5:G:76:LEU:HD22	2.00	0.43
11:M:49:MET:HB2	11:M:58:HIS:CE1	2.54	0.43
21:W:21:LYS:O	21:W:25:ARG:HG2	2.19	0.43
24:Z:44:ASN:O	24:Z:47:LEU:N	2.51	0.43
26:A:241:A:H61	26:A:255:A:H5''	1.83	0.43
26:A:286:G:H21	26:A:287:A:H62	1.66	0.43
26:A:895:G:O2'	26:A:898:A:N6	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1118:A:OP2	26:A:1273:G:N1	2.37	0.43
26:A:1291:G:N2	26:A:1292:U:O3'	2.52	0.43
26:A:3012:U:O2'	26:A:3030:A:N3	2.39	0.43
7:I:57:VAL:O	7:I:61:ALA:N	2.51	0.43
9:K:15:TRP:H	9:K:15:TRP:HD1	1.64	0.43
9:K:15:TRP:CE3	9:K:55:ILE:HD11	2.54	0.43
10:L:67:LYS:HA	10:L:67:LYS:HD2	1.83	0.43
18:T:18:ARG:HH12	26:A:1436:C:H2'	1.84	0.43
25:B:84:C:C5	25:B:85:C:N3	2.86	0.43
26:A:1581:C:O2'	26:A:1582:C:H6	2.02	0.43
33:7:21:GLY:C	33:7:22:ARG:HG3	2.39	0.43
1:C:241:SER:N	26:A:2195:U:O2	2.52	0.43
4:F:9:PRO:HG2	4:F:12:LYS:HE3	2.00	0.43
4:F:146:HIS:CE1	28:2:35:VAL:HG23	2.53	0.43
15:Q:1:MET:N	26:A:3096:U:O2	2.44	0.43
18:T:35:SER:O	18:T:39:ALA:N	2.51	0.43
26:A:1567:C:O2'	26:A:1568:C:H5'	2.19	0.43
28:2:63:LYS:O	28:2:65:TYR:CD2	2.70	0.43
1:C:67:PHE:HB3	1:C:153:ALA:HB3	2.01	0.42
3:E:103:PRO:HG3	26:A:773:G:O2'	2.18	0.42
5:G:160:GLY:HA3	5:G:164:ARG:HH21	1.84	0.42
13:O:9:ARG:HG2	13:O:14:SER:HA	2.01	0.42
19:U:69:THR:CG2	19:U:73:PHE:C	2.87	0.42
21:W:21:LYS:HZ1	25:B:80:C:H42	1.57	0.42
21:W:77:LEU:HD13	21:W:100:VAL:CB	2.49	0.42
26:A:721:A:N3	26:A:730:G:N2	2.63	0.42
26:A:832:G:H3'	26:A:833:A:H8	1.83	0.42
26:A:1573:U:C6	26:A:1573:U:OP2	2.72	0.42
26:A:2510:A:N6	30:4:25:THR:OG1	2.52	0.42
26:A:2539:G:H2'	26:A:2540:G:C8	2.54	0.42
30:4:29:ARG:NH2	30:4:34:ASP:CG	2.72	0.42
2:D:7:LEU:HG	2:D:207:VAL:HG22	2.01	0.42
4:F:45:MET:HB2	4:F:64:LEU:HD11	2.01	0.42
4:F:45:MET:HB3	4:F:94:ALA:O	2.15	0.42
13:O:4:PRO:HG2	26:A:3094:A:C2	2.51	0.42
20:V:99:LYS:HA	20:V:99:LYS:HD2	1.64	0.42
21:W:8:PRO:O	21:W:8:PRO:HG2	2.19	0.42
21:W:24:SER:HG	25:B:76:G:H5''	1.80	0.42
25:B:33:C:H2'	25:B:34:G:O4'	2.19	0.42
26:A:1574:G:C5'	26:A:1575:A:OP1	2.66	0.42
26:A:1665:U:H2'	26:A:1666:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:2643:U:H4'	30:4:24:ILE:HD13	2.01	0.42
1:C:23:GLU:OE2	1:C:23:GLU:HA	2.18	0.42
1:C:132:PRO:HD2	1:C:135:ASN:ND2	2.34	0.42
4:F:121:PHE:CD2	4:F:121:PHE:O	2.72	0.42
10:L:8:LEU:HD22	10:L:84:ALA:HB2	2.01	0.42
19:U:34:HIS:HA	19:U:35:PRO:HD3	1.86	0.42
24:Z:57:VAL:O	24:Z:61:LEU:HG	2.18	0.42
25:B:29:C:N4	25:B:55:G:H22	2.15	0.42
26:A:961:U:O2'	26:A:963:U:O4	2.32	0.42
26:A:1000:C:H2'	26:A:1001:C:H5''	2.00	0.42
26:A:1188:A:N7	26:A:1214:A:O2'	2.44	0.42
26:A:1601:G:C4	26:A:1602:U:C5	3.08	0.42
26:A:2814:A:H2'	26:A:2815:C:C6	2.55	0.42
4:F:45:MET:HE1	4:F:64:LEU:HD23	2.00	0.42
10:L:108:GLU:CG	10:L:109:LYS:N	2.73	0.42
14:P:90:GLU:O	14:P:94:ALA:CB	2.68	0.42
21:W:38:TYR:CZ	21:W:96:ASP:OD2	2.65	0.42
21:W:38:TYR:OH	21:W:81:LYS:HD3	2.19	0.42
21:W:80:THR:HG21	21:W:83:LEU:CD2	2.48	0.42
25:B:85:C:C6	25:B:85:C:C3'	3.02	0.42
25:B:85:C:O2	25:B:86:U:N3	2.52	0.42
26:A:13:G:H5''	29:3:14:ARG:HB3	2.00	0.42
26:A:760:U:H2'	26:A:761:G:C8	2.55	0.42
26:A:1174:G:H4'	26:A:1204:A:H8	1.84	0.42
26:A:2467:U:H2'	26:A:2468:U:C6	2.54	0.42
30:4:34:ASP:O	30:4:35:ARG:HB2	2.18	0.42
2:D:51:GLN:HE21	2:D:81:VAL:HG11	1.84	0.42
3:E:76:GLN:HE22	3:E:83:GLN:NE2	2.18	0.42
9:K:73:PHE:CE1	9:K:88:THR:HG22	2.54	0.42
14:P:88:ILE:O	14:P:92:ALA:HB2	2.19	0.42
25:B:58:A:C8	25:B:58:A:C4'	3.02	0.42
26:A:1007:G:H2'	26:A:1008:G:H8	1.83	0.42
26:A:2482:U:O2'	26:A:2651:C:OP2	2.35	0.42
4:F:44:ASN:C	4:F:44:ASN:ND2	2.73	0.42
7:I:48:THR:N	7:I:81:PHE:O	2.47	0.42
19:U:74:GLY:HA2	26:A:61:G:H4'	2.02	0.42
20:V:89:ASP:O	20:V:91:THR:N	2.53	0.42
21:W:37:LEU:HD21	21:W:99:VAL:HG22	2.01	0.42
21:W:146:VAL:HG21	21:W:157:ILE:HG21	2.01	0.42
22:X:64:PRO:CB	26:A:759:G:H1	2.18	0.42
22:X:83:VAL:O	22:X:83:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1586:C:H2'	26:A:1587:G:C4'	2.50	0.42
26:A:1594:G:H8	26:A:1594:G:O5'	2.02	0.42
26:A:1791:A:H2'	26:A:1792:A:C8	2.54	0.42
26:A:2422:A:N1	26:A:2450:C:N4	2.64	0.42
28:2:41:CYS:O	28:2:44:PHE:CD2	2.73	0.42
28:2:62:GLU:O	28:2:65:TYR:CE2	2.73	0.42
3:E:24:LEU:HD21	3:E:208:ASN:HB3	2.01	0.42
4:F:56:LEU:N	4:F:56:LEU:HD23	2.34	0.42
4:F:64:LEU:HD12	4:F:72:PRO:HB2	2.00	0.42
12:N:108:TYR:HB3	12:N:114:ALA:HB2	2.01	0.42
19:U:77:LYS:HE2	19:U:79:THR:CA	2.49	0.42
21:W:36:VAL:HG21	25:B:74:A:C2	2.52	0.42
22:X:26:PHE:N	22:X:29:GLN:HE21	2.12	0.42
23:Y:37:ARG:HB3	23:Y:46:LYS:HD3	2.00	0.42
26:A:1571:C:HO2'	26:A:1572:G:H8	1.64	0.42
26:A:1571:C:HO2'	26:A:1572:G:H5''	1.78	0.42
26:A:1690:A:H2'	26:A:1691:A:C8	2.55	0.42
1:C:125:ILE:HG23	1:C:193:VAL:HG11	2.01	0.42
3:E:3:LEU:O	3:E:4:LYS:HG3	2.20	0.42
3:E:9:THR:HG22	3:E:128:THR:HG23	2.01	0.42
18:T:7:PHE:N	18:T:8:PRO:HD3	2.34	0.42
25:B:59:A:H3'	25:B:60:G:C8	2.55	0.42
26:A:210:G:OP2	31:5:28:ARG:NH2	2.51	0.42
26:A:1586:C:O5'	26:A:1586:C:C6	2.70	0.42
26:A:2616:A:H5''	32:6:28:ASN:HD22	1.84	0.42
26:A:2665:C:OP2	26:A:2810:U:O2'	2.37	0.42
4:F:56:LEU:CD2	4:F:56:LEU:N	2.83	0.42
9:K:7:LYS:HG3	26:A:626:G:OP1	2.20	0.42
9:K:112:ASN:CG	9:K:113:LYS:N	2.73	0.42
13:O:21:LEU:HD23	13:O:21:LEU:HA	1.89	0.42
19:U:45:ALA:O	19:U:49:ILE:HG12	2.20	0.42
21:W:54:PHE:HE2	21:W:92:ILE:HG21	1.84	0.42
22:X:75:ARG:NE	26:A:2558:C:N4	2.63	0.42
23:Y:28:ARG:NH1	23:Y:30:ASN:OD1	2.53	0.42
25:B:40:A:N6	28:2:1:MET:H3	1.98	0.42
26:A:1565:A:H2	26:A:1606:G:C4	2.35	0.42
31:5:15:ARG:NH1	31:5:47:ALA:HB1	2.35	0.42
1:C:37:LEU:HD23	1:C:62:TYR:CG	2.55	0.42
3:E:176:HIS:CE1	26:A:708:G:O6	2.73	0.42
3:E:189:LEU:HD13	11:M:9:LEU:HD11	2.02	0.42
12:N:21:ALA:HB2	12:N:98:LYS:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:95:ARG:HG3	18:T:101:PHE:CD2	2.55	0.42
19:U:38:ASN:OD1	19:U:38:ASN:N	2.46	0.42
19:U:94:ASP:O	19:U:95:LEU:HB3	2.19	0.42
24:Z:48:ARG:CG	26:A:58:G:OP1	2.68	0.42
26:A:1678:U:H3	26:A:2926:A:H61	1.68	0.42
1:C:29:PRO:CB	1:C:34:VAL:CG2	2.84	0.41
4:F:44:ASN:ND2	4:F:45:MET:O	2.53	0.41
20:V:30:ARG:HD2	20:V:32:LYS:HD2	2.02	0.41
25:B:59:A:C2'	25:B:60:G:C5'	2.94	0.41
26:A:97:U:OP1	26:A:98:U:O2'	2.32	0.41
26:A:253:C:P	32:6:5:LYS:HZ3	2.44	0.41
26:A:2457:U:H2'	26:A:2458:G:C8	2.55	0.41
3:E:176:HIS:HE1	26:A:708:G:O6	2.03	0.41
4:F:11:LEU:HD12	4:F:11:LEU:HA	1.88	0.41
4:F:47:VAL:HG23	4:F:92:ILE:HG22	2.02	0.41
20:V:2:LYS:CD	20:V:83:VAL:HB	2.49	0.41
22:X:15:ASP:CB	26:A:2487:C:N4	2.75	0.41
26:A:844:G:H5'	26:A:845:C:H5''	2.01	0.41
26:A:1567:C:C2	26:A:1603:G:O6	2.73	0.41
26:A:1882:A:H61	26:A:2220:C:N4	2.17	0.41
26:A:2364:C:H2'	26:A:2365:A:C8	2.55	0.41
26:A:2497:A:H2'	26:A:2498:A:C8	2.55	0.41
4:F:23:LEU:HD22	4:F:35:ILE:HG23	2.02	0.41
4:F:56:LEU:HD23	4:F:57:ILE:H	1.85	0.41
12:N:134:ARG:HD3	21:W:129:ASN:HD21	1.85	0.41
14:P:77:LYS:HB3	14:P:112:ARG:HD3	2.01	0.41
17:S:92:GLN:HE22	26:A:1281:G:H21	1.67	0.41
21:W:118:ALA:HB1	21:W:122:THR:HG21	2.02	0.41
27:1:50:VAL:O	27:1:54:VAL:HG22	2.19	0.41
4:F:57:ILE:O	4:F:61:ILE:HG13	2.21	0.41
9:K:15:TRP:O	9:K:16:TYR:CD1	2.74	0.41
14:P:68:ALA:HA	14:P:71:ARG:HB2	2.01	0.41
26:A:150:C:H2'	26:A:151:A:C8	2.55	0.41
26:A:1243:G:OP1	33:7:22:ARG:NH1	2.53	0.41
28:2:26:SER:OG	28:2:27:THR:N	2.53	0.41
31:5:38:ARG:CA	31:5:45:LEU:HD21	2.50	0.41
1:C:98:LEU:HD22	1:C:98:LEU:H	1.84	0.41
6:H:24:GLY:O	6:H:28:ASN:HB2	2.21	0.41
8:J:90:GLY:HA2	8:J:99:VAL:HG11	2.01	0.41
9:K:93:LEU:HG	9:K:100:VAL:HG21	2.01	0.41
25:B:27:A:H2'	25:B:28:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:1499:A:O2'	26:A:1519:C:O2	2.39	0.41
26:A:1574:G:N2	26:A:1599:U:H5''	2.35	0.41
26:A:1584:U:C6	26:A:1584:U:C3'	3.03	0.41
26:A:1854:U:H2'	26:A:1855:A:H8	1.85	0.41
4:F:45:MET:CG	4:F:60:ALA:HB1	2.49	0.41
25:B:52:G:O2'	25:B:53:A:N7	2.45	0.41
26:A:210:G:P	31:5:28:ARG:HH22	2.43	0.41
26:A:1597:G:O2'	26:A:1598:U:P	2.78	0.41
26:A:2781:G:H2'	26:A:2782:C:C6	2.56	0.41
30:4:19:LYS:HD2	30:4:44:ASN:CG	2.39	0.41
1:C:118:GLU:O	1:C:129:ASN:HB2	2.20	0.41
3:E:155:LEU:HD11	3:E:178:ILE:HD11	2.01	0.41
8:J:16:GLN:HG2	8:J:55:VAL:HG12	2.02	0.41
10:L:9:LYS:O	10:L:83:ALA:HA	2.20	0.41
13:O:99:LYS:HE2	26:A:3037:C:H5''	2.03	0.41
19:U:83:ILE:CD1	26:A:1456:G:C4	2.97	0.41
25:B:24:G:H2'	25:B:56:C:C4	2.56	0.41
25:B:56:C:O2	25:B:56:C:C2'	2.69	0.41
25:B:96:A:C2	26:A:977:G:C2	2.91	0.41
26:A:442:U:H2'	26:A:443:C:C6	2.56	0.41
26:A:600:A:H2	26:A:674:U:H4'	1.86	0.41
26:A:1224:G:H2'	26:A:1225:G:H8	1.86	0.41
26:A:1562:C:O2'	26:A:1563:A:P	2.79	0.41
26:A:1569:A:N3	26:A:1570:C:H5	2.18	0.41
26:A:2644:C:OP1	32:6:34:GLU:CD	2.57	0.41
31:5:14:ARG:HH11	31:5:14:ARG:HD2	1.75	0.41
1:C:19:SER:O	1:C:21:PHE:CD2	2.74	0.41
4:F:185:LYS:HE2	4:F:185:LYS:C	2.40	0.41
9:K:27:ARG:CG	9:K:27:ARG:NH1	2.82	0.41
19:U:21:TYR:HA	19:U:24:ILE:HG12	2.00	0.41
20:V:47:VAL:C	20:V:56:SER:CA	2.86	0.41
21:W:37:LEU:HA	21:W:97:LEU:O	2.21	0.41
26:A:1501:C:H2'	26:A:1502:G:C8	2.56	0.41
26:A:1551:U:O4	26:A:1618:C:N4	2.54	0.41
26:A:1576:C:O2'	26:A:1577:C:P	2.79	0.41
26:A:1633:U:H2'	26:A:1634:C:C6	2.56	0.41
1:C:35:ARG:CD	1:C:36:PRO:CD	2.97	0.41
1:C:161:VAL:HG13	1:C:178:PRO:HB3	2.02	0.41
1:C:261:ASN:C	1:C:263:PRO:HD3	2.41	0.41
4:F:10:ARG:O	4:F:13:GLN:HB3	2.21	0.41
4:F:76:ARG:HH12	25:B:41:U:H3	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:182:PHE:HA	4:F:183:PRO:HD3	1.90	0.41
5:G:110:TYR:HD1	26:A:2891:C:H1'	1.85	0.41
12:N:17:GLN:HB3	12:N:96:ASN:HD21	1.86	0.41
13:O:16:HIS:ND1	13:O:16:HIS:C	2.73	0.41
13:O:87:TYR:OH	13:O:115:LEU:HB3	2.21	0.41
14:P:14:ARG:HH21	25:B:46:A:H5''	1.86	0.41
15:Q:28:HIS:ND1	15:Q:41:VAL:HG12	2.36	0.41
19:U:69:THR:CB	19:U:73:PHE:O	2.68	0.41
21:W:140:ILE:HA	21:W:141:PRO:HD3	1.89	0.41
22:X:15:ASP:CA	26:A:2486:U:O4	2.68	0.41
25:B:34:G:N1	25:B:44:C:C4	2.88	0.41
25:B:79:A:N1	25:B:94:G:C6	2.88	0.41
26:A:176:G:OP2	26:A:176:G:N2	2.42	0.41
26:A:658:U:O2'	26:A:924:G:OP2	2.37	0.41
26:A:683:G:H1'	32:6:2:PRO:HD2	2.02	0.41
26:A:733:U:H2'	26:A:734:C:C6	2.56	0.41
26:A:1086:C:H2'	26:A:1087:G:H8	1.86	0.41
26:A:1565:A:H2	26:A:1606:G:N9	2.19	0.41
26:A:1579:C:O2'	26:A:1580:A:P	2.79	0.41
26:A:1590:G:N1	26:A:1591:U:C5	2.89	0.41
26:A:1602:U:C2'	26:A:1603:G:C8	2.96	0.41
26:A:1627:U:H2'	26:A:1628:A:H8	1.86	0.41
26:A:1704:U:H2'	26:A:1705:C:C6	2.56	0.41
26:A:2043:C:O2'	26:A:2195:U:OP2	2.38	0.41
26:A:2096:G:H2'	26:A:2097:G:H8	1.86	0.41
26:A:2106:A:H3'	26:A:2107:G:H5''	2.02	0.41
26:A:2593:A:H2'	26:A:2594:G:H8	1.84	0.41
27:1:49:THR:HG22	27:1:50:VAL:HG13	2.03	0.41
30:4:13:LEU:HD23	30:4:53:GLU:HB3	2.02	0.41
3:E:78:SER:OG	3:E:79:THR:N	2.53	0.41
3:E:150:GLU:OE1	3:E:193:ASP:CG	2.58	0.41
11:M:31:LYS:HE3	11:M:31:LYS:HB3	1.94	0.41
21:W:29:ARG:HH12	25:B:90:G:H4'	1.85	0.41
22:X:83:VAL:CG1	22:X:85:ARG:HB2	2.42	0.41
26:A:181:A:N3	26:A:521:C:O2'	2.47	0.41
26:A:323:C:H42	26:A:453:U:H3	1.69	0.41
26:A:1591:U:O2	26:A:1591:U:C2'	2.69	0.41
26:A:3041:C:OP2	26:A:3042:A:N6	2.50	0.41
3:E:24:LEU:HD21	3:E:208:ASN:CG	2.38	0.40
9:K:3:THR:HG21	26:A:1113:C:C2	2.46	0.40
9:K:109:LEU:HD23	9:K:109:LEU:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:O:64:ARG:NH1	26:A:1675:U:O2	2.55	0.40
15:Q:99:LEU:HD11	15:Q:109:ILE:HD11	2.02	0.40
18:T:90:LYS:NZ	26:A:1375:G:OP1	2.37	0.40
26:A:1688:G:N2	26:A:1748:A:H1'	2.36	0.40
26:A:1761:G:H2'	26:A:1762:C:C6	2.56	0.40
26:A:2701:U:O4	33:7:10:ILE:HG12	2.21	0.40
2:D:124:ALA:HB3	2:D:129:ARG:HG3	2.02	0.40
3:E:172:LEU:HD12	3:E:172:LEU:HA	1.93	0.40
6:H:43:ALA:O	6:H:47:ALA:CB	2.68	0.40
10:L:69:ARG:HD2	10:L:69:ARG:HA	1.91	0.40
12:N:60:ARG:HB2	12:N:61:GLY:H	1.62	0.40
18:T:54:VAL:HG22	18:T:110:ILE:HD13	2.03	0.40
19:U:67:LYS:NZ	26:A:1451:A:P	2.93	0.40
26:A:1624:U:O2'	26:A:1625:G:H8	2.04	0.40
26:A:2350:G:H2'	26:A:2351:A:C8	2.56	0.40
26:A:2649:A:H4'	26:A:2650:A:H5''	2.03	0.40
26:A:2686:U:H2'	26:A:2687:U:C6	2.56	0.40
30:4:39:LYS:HA	30:4:50:PRO:HA	2.03	0.40
1:C:26:ARG:HD2	1:C:81:HIS:CE1	2.49	0.40
1:C:44:ASN:OD1	1:C:44:ASN:N	2.50	0.40
1:C:54:LYS:NZ	26:A:2032:A:P	2.94	0.40
2:D:157:PRO:CD	2:D:158:GLY:H	2.34	0.40
9:K:75:TYR:H	9:K:75:TYR:HD1	1.68	0.40
15:Q:48:ARG:NE	15:Q:59:THR:OG1	2.50	0.40
17:S:6:ILE:O	17:S:39:VAL:HG13	2.21	0.40
19:U:58:ASN:HD22	26:A:1456:G:N2	2.18	0.40
19:U:71:THR:HB	26:A:544:U:C2	2.56	0.40
19:U:77:LYS:HE2	19:U:78:SER:C	2.41	0.40
21:W:99:VAL:HG12	21:W:101:GLN:H	1.86	0.40
25:B:20:G:C2	25:B:63:U:N3	2.68	0.40
25:B:20:G:C6	25:B:63:U:O4	2.74	0.40
25:B:88:C:C3'	25:B:88:C:C6	3.03	0.40
26:A:937:U:H2'	26:A:938:G:C8	2.56	0.40
26:A:937:U:H2'	26:A:938:G:H8	1.87	0.40
2:D:153:GLY:O	2:D:155:ALA:N	2.55	0.40
3:E:4:LYS:CA	3:E:20:LEU:HD21	2.52	0.40
3:E:55:ARG:HD2	3:E:82:PRO:HD3	2.04	0.40
4:F:44:ASN:ND2	4:F:45:MET:N	2.70	0.40
13:O:96:ARG:CZ	13:O:116:VAL:HG12	2.48	0.40
18:T:6:GLU:O	18:T:7:PHE:CB	2.70	0.40
21:W:184:ALA:HA	21:W:185:PRO:HD3	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A:845:C:OP1	26:A:1992:U:O2'	2.27	0.40
26:A:860:G:H21	26:A:865:A:H61	1.70	0.40
26:A:1805:G:H2'	26:A:1806:A:H8	1.85	0.40
26:A:1922:G:H2'	26:A:1923:G:H8	1.86	0.40
4:F:35:ILE:HG23	4:F:36:PRO:HD2	2.03	0.40
9:K:134:ALA:O	9:K:135:GLN:CB	2.70	0.40
19:U:4:ILE:CG1	24:Z:58:TYR:HE1	2.34	0.40
21:W:40:HIS:ND1	21:W:40:HIS:C	2.72	0.40
25:B:79:A:H2	25:B:94:G:N1	2.10	0.40
26:A:55:G:O2'	26:A:70:A:N1	2.53	0.40
26:A:1105:C:O2'	26:A:1118:A:N3	2.44	0.40
26:A:1393:C:H2'	26:A:1394:A:H8	1.85	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	C	271/278 (98%)	233 (86%)	33 (12%)	5 (2%)	7	35
2	D	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	14	49
3	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	24
4	F	179/187 (96%)	162 (90%)	15 (8%)	2 (1%)	12	44
5	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
6	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	19	54
7	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
8	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
9	K	145/147 (99%)	133 (92%)	9 (6%)	3 (2%)	5	31
10	L	119/122 (98%)	107 (90%)	12 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
12	N	132/138 (96%)	113 (86%)	19 (14%)	0	100	100
13	O	115/199 (58%)	102 (89%)	10 (9%)	3 (3%)	4	27
14	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
15	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
16	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
17	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	13	47
18	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	26
19	U	92/100 (92%)	70 (76%)	16 (17%)	6 (6%)	1	8
20	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	30
21	W	186/215 (86%)	171 (92%)	10 (5%)	5 (3%)	4	26
22	X	80/88 (91%)	61 (76%)	13 (16%)	6 (8%)	1	6
23	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
24	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	8	37
27	1	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
28	2	64/75 (85%)	61 (95%)	2 (3%)	1 (2%)	8	37
29	3	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
30	4	48/55 (87%)	37 (77%)	7 (15%)	4 (8%)	0	4
31	5	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
32	6	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
33	7	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	8	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	3623/3991 (91%)	3287 (91%)	285 (8%)	51 (1%)	12	40

All (51) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	58	HIS
1	C	145	VAL
1	C	262	LYS
3	E	94	LYS
3	E	152	LYS
4	F	47	VAL
9	K	142	ILE

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Mol	Chain	Res	Type
18	T	7	PHE
18	T	118	PRO
21	W	41	GLY
21	W	83	LEU
24	Z	10	LEU
1	C	146	GLU
2	D	155	ALA
3	E	65	PRO
4	F	142	GLN
9	K	140	PHE
13	O	15	SER
13	O	115	LEU
19	U	68	ARG
21	W	63	THR
22	X	12	ASN
22	X	16	SER
22	X	17	ALA
1	C	36	PRO
9	K	2	PRO
19	U	70	ARG
19	U	75	LYS
21	W	85	VAL
22	X	85	ARG
30	4	34	ASP
3	E	4	LYS
3	E	93	PRO
6	H	125	LYS
13	O	60	LEU
18	T	8	PRO
19	U	6	ASP
20	V	90	GLU
20	V	101	ASN
21	W	87	PRO
22	X	84	ALA
30	4	7	VAL
2	D	157	PRO
3	E	132	GLU
19	U	5	THR
17	S	7	VAL
19	U	10	ILE
22	X	83	VAL
28	2	42	HIS

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Mol	Chain	Res	Type
30	4	33	PRO
30	4	9	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	214/218 (98%)	207 (97%)	7 (3%)	33	64
2	D	160/163 (98%)	155 (97%)	5 (3%)	35	66
3	E	167/173 (96%)	158 (95%)	9 (5%)	18	51
4	F	150/156 (96%)	137 (91%)	13 (9%)	8	32
5	G	148/150 (99%)	148 (100%)	0	100	100
6	H	90/116 (78%)	90 (100%)	0	100	100
7	I	89/120 (74%)	89 (100%)	0	100	100
8	J	102/108 (94%)	102 (100%)	0	100	100
9	K	120/120 (100%)	116 (97%)	4 (3%)	33	64
10	L	99/100 (99%)	97 (98%)	2 (2%)	50	75
11	M	112/114 (98%)	111 (99%)	1 (1%)	75	89
12	N	112/116 (97%)	107 (96%)	5 (4%)	23	56
13	O	96/158 (61%)	91 (95%)	5 (5%)	19	52
14	P	93/94 (99%)	93 (100%)	0	100	100
15	Q	100/100 (100%)	99 (99%)	1 (1%)	73	87
16	R	97/99 (98%)	96 (99%)	1 (1%)	73	87
17	S	82/83 (99%)	81 (99%)	1 (1%)	67	85
18	T	90/117 (77%)	86 (96%)	4 (4%)	24	57
19	U	82/85 (96%)	71 (87%)	11 (13%)	3	15
20	V	81/86 (94%)	75 (93%)	6 (7%)	11	40
21	W	154/168 (92%)	139 (90%)	15 (10%)	6	27
22	X	59/63 (94%)	58 (98%)	1 (2%)	56	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	Y	50/51 (98%)	50 (100%)	0	100	100
24	Z	58/66 (88%)	53 (91%)	5 (9%)	8	33
27	1	53/54 (98%)	51 (96%)	2 (4%)	28	60
28	2	57/63 (90%)	54 (95%)	3 (5%)	19	52
29	3	43/46 (94%)	43 (100%)	0	100	100
30	4	48/52 (92%)	40 (83%)	8 (17%)	2	9
31	5	35/36 (97%)	33 (94%)	2 (6%)	17	50
32	6	53/54 (98%)	53 (100%)	0	100	100
33	7	35/35 (100%)	33 (94%)	2 (6%)	17	50
34	8	18/19 (95%)	18 (100%)	0	100	100
All	All	2947/3183 (93%)	2834 (96%)	113 (4%)	30	60

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	35	ARG
1	C	36	PRO
1	C	71	ASP
1	C	73	ASP
1	C	168	LYS
1	C	256	ARG
1	C	258	ARG
2	D	60	ARG
2	D	154	CYS
2	D	159	ARG
2	D	160	VAL
2	D	201	ARG
3	E	4	LYS
3	E	20	LEU
3	E	33	LEU
3	E	50	HIS
3	E	75	ARG
3	E	130	LEU
3	E	150	GLU
3	E	171	ASN
3	E	178	ILE
4	F	10	ARG
4	F	11	LEU

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Mol	Chain	Res	Type
4	F	14	ARG
4	F	44	ASN
4	F	55	LYS
4	F	56	LEU
4	F	108	ASP
4	F	110	LEU
4	F	118	ILE
4	F	122	ARG
4	F	174	ARG
4	F	185	LYS
4	F	186	GLU
9	K	75	TYR
9	K	76	ARG
9	K	113	LYS
9	K	141	GLU
10	L	8	LEU
10	L	53	LYS
11	M	43	ARG
12	N	34	ILE
12	N	59	LYS
12	N	60	ARG
12	N	92	TRP
12	N	96	ASN
13	O	5	THR
13	O	9	ARG
13	O	14	SER
13	O	79	LEU
13	O	117	ARG
15	Q	38	ARG
16	R	34	LYS
17	S	103	LYS
18	T	6	GLU
18	T	44	ARG
18	T	90	LYS
18	T	118	PRO
19	U	9	ASP
19	U	12	LEU
19	U	27	ASN
19	U	66	ARG
19	U	67	LYS
19	U	69	THR
19	U	70	ARG

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Mol	Chain	Res	Type
19	U	75	LYS
19	U	94	ASP
19	U	95	LEU
19	U	96	PHE
20	V	20	LYS
20	V	22	LYS
20	V	39	ASN
20	V	89	ASP
20	V	96	ARG
20	V	99	LYS
21	W	6	ASN
21	W	7	ILE
21	W	36	VAL
21	W	40	HIS
21	W	64	ASN
21	W	83	LEU
21	W	101	GLN
21	W	102	ARG
21	W	112	VAL
21	W	114	VAL
21	W	131	ILE
21	W	139	SER
21	W	146	VAL
21	W	158	THR
21	W	172	SER
22	X	15	ASP
24	Z	5	THR
24	Z	14	THR
24	Z	23	ARG
24	Z	44	ASN
24	Z	47	LEU
27	1	8	GLN
27	1	51	HIS
28	2	38	CYS
28	2	44	PHE
28	2	60	ARG
30	4	22	ASN
30	4	23	TYR
30	4	26	LYS
30	4	27	LYS
30	4	30	ARG
30	4	36	LEU

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Mol	Chain	Res	Type
30	4	37	GLU
30	4	42	CYS
31	5	6	ARG
31	5	27	THR
33	7	20	HIS
33	7	36	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	58	HIS
1	C	96	HIS
1	C	130	ASN
1	C	135	ASN
1	C	205	ASN
2	D	34	ASN
3	E	35	HIS
3	E	76	GLN
3	E	121	ASN
3	E	176	HIS
3	E	184	ASN
3	E	202	ASN
4	F	31	ASN
4	F	34	GLN
4	F	44	ASN
4	F	142	GLN
4	F	146	HIS
5	G	66	HIS
6	H	118	GLN
8	J	33	HIS
8	J	119	ASN
9	K	47	ASN
9	K	132	HIS
9	K	135	GLN
10	L	4	GLN
11	M	58	HIS
11	M	76	GLN
11	M	84	ASN
11	M	127	ASN
12	N	96	ASN
13	O	16	HIS
13	O	77	HIS

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Mol	Chain	Res	Type
14	P	3	HIS
14	P	41	ASN
16	R	38	GLN
16	R	41	HIS
17	S	76	HIS
17	S	85	HIS
17	S	92	GLN
18	T	67	ASN
18	T	68	ASN
19	U	27	ASN
19	U	58	ASN
21	W	6	ASN
21	W	9	ASN
21	W	46	HIS
21	W	101	GLN
22	X	29	GLN
22	X	46	HIS
22	X	79	ASN
23	Y	22	HIS
24	Z	44	ASN
24	Z	52	GLN
27	1	8	GLN
27	1	42	GLN
27	1	51	HIS
28	2	40	GLN
30	4	20	HIS
30	4	48	HIS
30	4	49	GLN
31	5	11	ASN
31	5	19	HIS
32	6	7	HIS
32	6	28	ASN
32	6	31	HIS
34	8	17	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	B	116/118 (98%)	42 (36%)	3 (2%)
26	A	3096/3120 (99%)	788 (25%)	44 (1%)
All	All	3212/3238 (99%)	830 (25%)	47 (1%)

All (830) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	B	4	A
25	B	5	C
25	B	7	G
25	B	10	G
25	B	12	C
25	B	13	C
25	B	14	A
25	B	15	U
25	B	19	G
25	B	21	C
25	B	22	A
25	B	23	G
25	B	24	G
25	B	25	G
25	B	26	A
25	B	30	G
25	B	34	G
25	B	35	G
25	B	37	C
25	B	40	A
25	B	41	U
25	B	44	C
25	B	45	G
25	B	47	A
25	B	52	G
25	B	53	A
25	B	55	G
25	B	56	C
25	B	57	U
25	B	58	A
25	B	59	A
25	B	60	G
25	B	66	C
25	B	67	A
25	B	68	G
25	B	85	C
25	B	86	U
25	B	88	C
25	B	90	G
25	B	102	A
25	B	106	C
25	B	113	G

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Mol	Chain	Res	Type
26	A	7	U
26	A	11	A
26	A	12	G
26	A	20	G
26	A	29	C
26	A	31	U
26	A	32	G
26	A	33	G
26	A	52	G
26	A	58	G
26	A	59	G
26	A	60	A
26	A	68	A
26	A	71	A
26	A	72	G
26	A	77	G
26	A	80	G
26	A	81	A
26	A	88	A
26	A	89	A
26	A	90	C
26	A	93	A
26	A	94	G
26	A	98	U
26	A	99	G
26	A	115	A
26	A	117	U
26	A	122	A
26	A	125	C
26	A	128	G
26	A	136	U
26	A	143	G
26	A	161	U
26	A	164	A
26	A	173	U
26	A	175	G
26	A	180	A
26	A	186	G
26	A	195	A
26	A	198	A
26	A	203	A
26	A	205	U

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Mol	Chain	Res	Type
26	A	212	A
26	A	214	G
26	A	215	A
26	A	220	A
26	A	221	A
26	A	227	A
26	A	229	U
26	A	230	G
26	A	231	U
26	A	237	C
26	A	245	G
26	A	248	G
26	A	250	G
26	A	264	G
26	A	265	A
26	A	272	A
26	A	274	C
26	A	275	C
26	A	279	U
26	A	283	U
26	A	285	U
26	A	286	G
26	A	287	A
26	A	288	U
26	A	291	C
26	A	292	G
26	A	296	A
26	A	297	G
26	A	299	G
26	A	300	G
26	A	301	U
26	A	302	U
26	A	303	G
26	A	305	G
26	A	309	G
26	A	314	G
26	A	315	U
26	A	317	G
26	A	318	U
26	A	319	G
26	A	322	A
26	A	323	C

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Mol	Chain	Res	Type
26	A	326	A
26	A	327	U
26	A	329	U
26	A	330	U
26	A	331	U
26	A	336	C
26	A	337	U
26	A	338	C
26	A	346	C
26	A	351	G
26	A	352	G
26	A	357	U
26	A	358	G
26	A	361	A
26	A	364	A
26	A	366	G
26	A	370	U
26	A	384	G
26	A	393	U
26	A	404	A
26	A	412	A
26	A	416	C
26	A	417	C
26	A	424	G
26	A	425	U
26	A	427	A
26	A	434	G
26	A	438	U
26	A	445	U
26	A	446	G
26	A	449	G
26	A	450	G
26	A	452	G
26	A	453	U
26	A	454	U
26	A	459	A
26	A	460	G
26	A	468	G
26	A	471	C
26	A	472	C
26	A	474	G
26	A	489	A

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Mol	Chain	Res	Type
26	A	491	U
26	A	493	U
26	A	498	G
26	A	505	C
26	A	509	U
26	A	512	G
26	A	530	G
26	A	543	U
26	A	544	U
26	A	547	U
26	A	555	G
26	A	561	G
26	A	562	G
26	A	566	A
26	A	567	A
26	A	568	A
26	A	569	G
26	A	585	G
26	A	589	A
26	A	591	G
26	A	592	A
26	A	594	U
26	A	595	A
26	A	596	C
26	A	605	G
26	A	617	U
26	A	618	C
26	A	619	C
26	A	620	G
26	A	639	C
26	A	640	G
26	A	641	U
26	A	642	G
26	A	643	G
26	A	644	G
26	A	647	G
26	A	649	U
26	A	655	G
26	A	665	G
26	A	666	A
26	A	667	A
26	A	678	A

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Mol	Chain	Res	Type
26	A	679	G
26	A	684	G
26	A	685	G
26	A	689	U
26	A	696	A
26	A	706	G
26	A	707	G
26	A	708	G
26	A	709	U
26	A	712	G
26	A	721	A
26	A	725	A
26	A	728	G
26	A	730	G
26	A	731	A
26	A	740	A
26	A	747	A
26	A	753	A
26	A	757	G
26	A	758	A
26	A	760	U
26	A	763	G
26	A	765	G
26	A	766	G
26	A	768	G
26	A	769	U
26	A	770	A
26	A	774	G
26	A	784	G
26	A	785	A
26	A	794	G
26	A	801	U
26	A	830	A
26	A	832	G
26	A	838	G
26	A	845	C
26	A	862	U
26	A	863	G
26	A	868	C
26	A	871	A
26	A	872	G
26	A	878	G

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Mol	Chain	Res	Type
26	A	879	A
26	A	880	G
26	A	890	G
26	A	891	G
26	A	897	A
26	A	899	G
26	A	904	A
26	A	908	A
26	A	915	U
26	A	917	A
26	A	919	A
26	A	920	G
26	A	921	C
26	A	927	C
26	A	942	U
26	A	944	A
26	A	945	G
26	A	960	G
26	A	961	U
26	A	966	U
26	A	971	G
26	A	973	G
26	A	974	G
26	A	975	U
26	A	981	U
26	A	982	A
26	A	994	A
26	A	995	U
26	A	996	G
26	A	1001	C
26	A	1002	C
26	A	1003	A
26	A	1007	G
26	A	1009	U
26	A	1011	A
26	A	1012	C
26	A	1013	U
26	A	1014	G
26	A	1016	C
26	A	1022	C
26	A	1025	A
26	A	1029	C

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Mol	Chain	Res	Type
26	A	1030	C
26	A	1042	A
26	A	1044	U
26	A	1046	C
26	A	1047	A
26	A	1048	A
26	A	1049	G
26	A	1058	A
26	A	1062	A
26	A	1063	G
26	A	1068	C
26	A	1070	G
26	A	1074	A
26	A	1076	A
26	A	1078	G
26	A	1085	G
26	A	1091	A
26	A	1092	G
26	A	1098	A
26	A	1100	C
26	A	1101	A
26	A	1107	G
26	A	1114	G
26	A	1130	C
26	A	1131	G
26	A	1140	G
26	A	1141	U
26	A	1143	G
26	A	1144	A
26	A	1151	U
26	A	1163	A
26	A	1164	A
26	A	1169	A
26	A	1171	C
26	A	1173	G
26	A	1175	A
26	A	1178	U
26	A	1181	G
26	A	1184	U
26	A	1185	A
26	A	1186	G
26	A	1187	A

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Mol	Chain	Res	Type
26	A	1188	A
26	A	1189	G
26	A	1190	C
26	A	1191	A
26	A	1192	G
26	A	1201	G
26	A	1202	A
26	A	1205	G
26	A	1206	A
26	A	1207	G
26	A	1209	G
26	A	1212	U
26	A	1213	A
26	A	1215	U
26	A	1216	A
26	A	1224	G
26	A	1229	A
26	A	1230	G
26	A	1232	G
26	A	1233	A
26	A	1237	U
26	A	1238	G
26	A	1239	C
26	A	1240	G
26	A	1244	A
26	A	1246	A
26	A	1250	U
26	A	1251	A
26	A	1253	C
26	A	1260	C
26	A	1261	A
26	A	1270	G
26	A	1275	A
26	A	1292	U
26	A	1293	G
26	A	1303	U
26	A	1325	U
26	A	1332	G
26	A	1335	G
26	A	1343	G
26	A	1344	A
26	A	1345	G

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Mol	Chain	Res	Type
26	A	1347	G
26	A	1353	G
26	A	1362	A
26	A	1363	G
26	A	1365	G
26	A	1368	A
26	A	1369	A
26	A	1371	G
26	A	1372	C
26	A	1386	G
26	A	1389	U
26	A	1404	C
26	A	1409	C
26	A	1415	A
26	A	1416	A
26	A	1417	A
26	A	1440	C
26	A	1444	U
26	A	1448	C
26	A	1456	G
26	A	1462	G
26	A	1465	C
26	A	1467	U
26	A	1480	A
26	A	1493	A
26	A	1494	U
26	A	1499	A
26	A	1501	C
26	A	1507	G
26	A	1510	A
26	A	1521	C
26	A	1522	G
26	A	1529	U
26	A	1531	C
26	A	1532	G
26	A	1533	U
26	A	1534	C
26	A	1539	A
26	A	1540	U
26	A	1546	A
26	A	1549	G
26	A	1550	G

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Mol	Chain	Res	Type
26	A	1551	U
26	A	1552	A
26	A	1553	C
26	A	1554	U
26	A	1555	A
26	A	1556	A
26	A	1562	C
26	A	1563	A
26	A	1564	A
26	A	1565	A
26	A	1566	A
26	A	1567	C
26	A	1568	C
26	A	1569	A
26	A	1570	C
26	A	1571	C
26	A	1572	G
26	A	1574	G
26	A	1575	A
26	A	1576	C
26	A	1577	C
26	A	1578	G
26	A	1579	C
26	A	1580	A
26	A	1581	C
26	A	1582	C
26	A	1584	U
26	A	1585	U
26	A	1586	C
26	A	1587	G
26	A	1588	G
26	A	1589	G
26	A	1590	G
26	A	1591	U
26	A	1592	G
26	A	1593	U
26	A	1594	G
26	A	1595	G
26	A	1596	C
26	A	1597	G
26	A	1598	U
26	A	1599	U

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Mol	Chain	Res	Type
26	A	1600	G
26	A	1601	G
26	A	1602	U
26	A	1603	G
26	A	1605	G
26	A	1606	G
26	A	1625	G
26	A	1629	G
26	A	1630	U
26	A	1632	G
26	A	1633	U
26	A	1636	A
26	A	1637	G
26	A	1638	C
26	A	1639	G
26	A	1640	A
26	A	1641	U
26	A	1642	G
26	A	1648	A
26	A	1649	C
26	A	1654	G
26	A	1658	G
26	A	1672	C
26	A	1674	G
26	A	1676	G
26	A	1678	U
26	A	1679	A
26	A	1680	A
26	A	1681	U
26	A	1688	G
26	A	1703	G
26	A	1710	A
26	A	1711	G
26	A	1713	U
26	A	1715	A
26	A	1717	U
26	A	1721	U
26	A	1724	G
26	A	1727	A
26	A	1728	U
26	A	1731	A
26	A	1737	A

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Mol	Chain	Res	Type
26	A	1744	A
26	A	1748	A
26	A	1753	C
26	A	1754	G
26	A	1767	U
26	A	1768	C
26	A	1769	G
26	A	1774	U
26	A	1778	A
26	A	1780	G
26	A	1786	G
26	A	1787	A
26	A	1789	A
26	A	1792	A
26	A	1798	U
26	A	1803	A
26	A	1813	C
26	A	1826	A
26	A	1836	A
26	A	1837	G
26	A	1845	G
26	A	1852	A
26	A	1863	G
26	A	1864	U
26	A	1866	C
26	A	1869	G
26	A	1870	U
26	A	1871	G
26	A	1872	A
26	A	1878	G
26	A	1887	A
26	A	1892	G
26	A	1893	C
26	A	1903	C
26	A	1906	U
26	A	1916	A
26	A	1917	G
26	A	1933	G
26	A	1958	C
26	A	1967	G
26	A	1973	C
26	A	1974	A

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Mol	Chain	Res	Type
26	A	1975	A
26	A	1981	U
26	A	1990	A
26	A	1998	C
26	A	1999	U
26	A	2017	C
26	A	2018	G
26	A	2026	A
26	A	2028	G
26	A	2033	U
26	A	2046	A
26	A	2052	G
26	A	2062	G
26	A	2064	A
26	A	2074	G
26	A	2075	G
26	A	2083	A
26	A	2085	C
26	A	2086	U
26	A	2088	C
26	A	2089	C
26	A	2090	U
26	A	2091	U
26	A	2092	U
26	A	2093	G
26	A	2094	G
26	A	2095	G
26	A	2096	G
26	A	2106	A
26	A	2107	G
26	A	2111	U
26	A	2112	U
26	A	2118	C
26	A	2120	A
26	A	2130	G
26	A	2131	G
26	A	2137	A
26	A	2138	C
26	A	2140	A
26	A	2142	A
26	A	2151	A
26	A	2153	G

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Mol	Chain	Res	Type
26	A	2154	G
26	A	2160	A
26	A	2161	A
26	A	2163	U
26	A	2167	U
26	A	2179	U
26	A	2190	A
26	A	2191	C
26	A	2194	A
26	A	2195	U
26	A	2196	G
26	A	2206	C
26	A	2215	U
26	A	2217	U
26	A	2221	A
26	A	2244	A
26	A	2247	A
26	A	2251	G
26	A	2255	A
26	A	2256	G
26	A	2257	A
26	A	2263	G
26	A	2267	C
26	A	2276	G
26	A	2279	C
26	A	2280	G
26	A	2284	A
26	A	2285	G
26	A	2286	A
26	A	2299	C
26	A	2315	U
26	A	2316	G
26	A	2317	G
26	A	2319	G
26	A	2320	C
26	A	2322	C
26	A	2323	G
26	A	2325	U
26	A	2328	G
26	A	2334	U
26	A	2335	G
26	A	2337	A

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Mol	Chain	Res	Type
26	A	2338	G
26	A	2339	G
26	A	2340	A
26	A	2341	U
26	A	2342	A
26	A	2343	G
26	A	2346	G
26	A	2348	G
26	A	2349	A
26	A	2351	A
26	A	2353	U
26	A	2354	G
26	A	2355	U
26	A	2356	G
26	A	2357	A
26	A	2362	C
26	A	2368	C
26	A	2371	G
26	A	2380	G
26	A	2382	G
26	A	2383	U
26	A	2384	C
26	A	2385	G
26	A	2386	U
26	A	2387	U
26	A	2388	G
26	A	2390	U
26	A	2392	A
26	A	2393	A
26	A	2394	A
26	A	2395	U
26	A	2396	A
26	A	2404	G
26	A	2407	C
26	A	2408	G
26	A	2409	U
26	A	2410	A
26	A	2411	U
26	A	2413	G
26	A	2414	G
26	A	2418	U
26	A	2421	A

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Mol	Chain	Res	Type
26	A	2427	G
26	A	2433	U
26	A	2434	A
26	A	2436	A
26	A	2446	G
26	A	2449	A
26	A	2462	G
26	A	2463	G
26	A	2467	U
26	A	2473	U
26	A	2476	G
26	A	2490	A
26	A	2502	A
26	A	2506	G
26	A	2507	C
26	A	2510	A
26	A	2511	A
26	A	2512	A
26	A	2529	A
26	A	2531	G
26	A	2532	G
26	A	2545	G
26	A	2546	A
26	A	2549	G
26	A	2551	A
26	A	2558	C
26	A	2559	A
26	A	2567	U
26	A	2571	C
26	A	2574	C
26	A	2578	A
26	A	2582	A
26	A	2585	U
26	A	2586	G
26	A	2596	G
26	A	2601	A
26	A	2607	G
26	A	2608	G
26	A	2609	A
26	A	2612	A
26	A	2614	U
26	A	2615	G

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Mol	Chain	Res	Type
26	A	2616	A
26	A	2626	U
26	A	2627	C
26	A	2630	A
26	A	2631	G
26	A	2640	G
26	A	2643	U
26	A	2647	U
26	A	2648	C
26	A	2649	A
26	A	2650	A
26	A	2651	C
26	A	2653	G
26	A	2654	A
26	A	2655	U
26	A	2659	A
26	A	2665	C
26	A	2669	G
26	A	2671	G
26	A	2672	A
26	A	2673	U
26	A	2676	C
26	A	2677	A
26	A	2682	G
26	A	2694	G
26	A	2698	C
26	A	2700	A
26	A	2702	A
26	A	2705	G
26	A	2715	U
26	A	2718	G
26	A	2726	G
26	A	2729	G
26	A	2737	G
26	A	2742	A
26	A	2744	C
26	A	2753	G
26	A	2758	A
26	A	2759	G
26	A	2786	U
26	A	2788	A
26	A	2790	A

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Mol	Chain	Res	Type
26	A	2791	G
26	A	2793	G
26	A	2796	A
26	A	2797	C
26	A	2802	G
26	A	2810	U
26	A	2826	A
26	A	2827	G
26	A	2833	U
26	A	2837	U
26	A	2839	U
26	A	2853	C
26	A	2860	U
26	A	2865	G
26	A	2866	A
26	A	2870	C
26	A	2876	C
26	A	2878	A
26	A	2887	G
26	A	2893	G
26	A	2897	G
26	A	2906	U
26	A	2908	U
26	A	2913	U
26	A	2915	C
26	A	2926	A
26	A	2936	C
26	A	2938	G
26	A	2942	G
26	A	2950	C
26	A	2956	G
26	A	2957	A
26	A	2963	U
26	A	2968	G
26	A	2972	A
26	A	2975	G
26	A	2976	C
26	A	2977	A
26	A	2982	A
26	A	2985	G
26	A	2989	A
26	A	2990	A

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Mol	Chain	Res	Type
26	A	2993	U
26	A	3002	A
26	A	3004	C
26	A	3005	A
26	A	3009	U
26	A	3011	C
26	A	3014	A
26	A	3015	C
26	A	3021	A
26	A	3022	G
26	A	3023	G
26	A	3029	U
26	A	3039	C
26	A	3042	A
26	A	3045	C
26	A	3047	A
26	A	3056	A
26	A	3057	U
26	A	3070	G
26	A	3082	U
26	A	3088	C
26	A	3093	A
26	A	3094	A
26	A	3095	C
26	A	3101	C
26	A	3105	C
26	A	3106	C
26	A	3107	G
26	A	3112	A
26	A	3113	A
26	A	3114	A
26	A	3115	A

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	B	12	C
25	B	60	G
25	B	66	C
26	A	89	A
26	A	97	U
26	A	316	U

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Mol	Chain	Res	Type
26	A	336	C
26	A	357	U
26	A	445	U
26	A	567	A
26	A	974	G
26	A	980	C
26	A	981	U
26	A	1002	C
26	A	1010	U
26	A	1084	U
26	A	1186	G
26	A	1562	C
26	A	1563	A
26	A	1564	A
26	A	1565	A
26	A	1566	A
26	A	1567	C
26	A	1568	C
26	A	1569	A
26	A	1570	C
26	A	1571	C
26	A	1573	U
26	A	1575	A
26	A	1576	C
26	A	1577	C
26	A	1578	G
26	A	1579	C
26	A	1580	A
26	A	1581	C
26	A	1590	G
26	A	1591	U
26	A	1596	C
26	A	1597	G
26	A	1598	U
26	A	1730	U
26	A	2085	C
26	A	2088	C
26	A	2094	G
26	A	2350	G
26	A	2381	A
26	A	2435	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

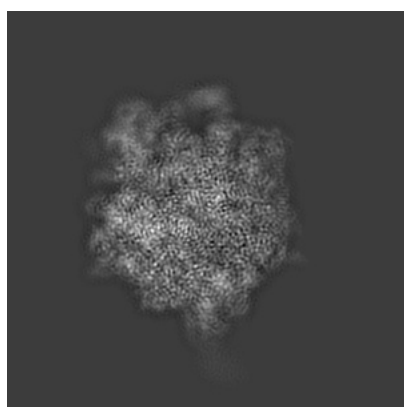
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6922. These allow visual inspection of the internal detail of the map and identification of artifacts.

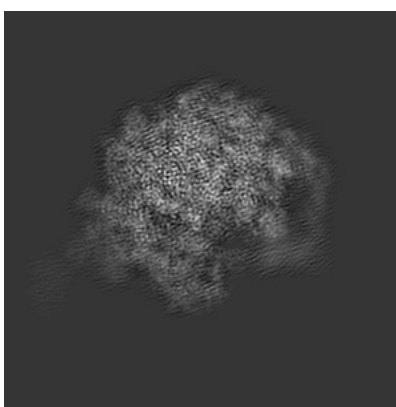
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

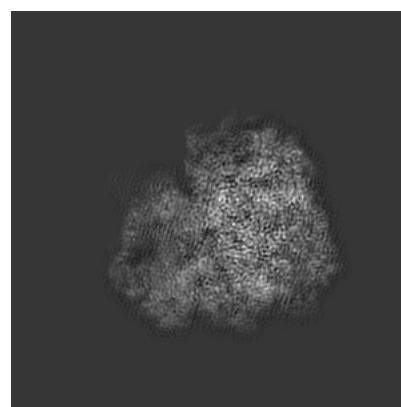
6.1.1 Primary map



X



Y

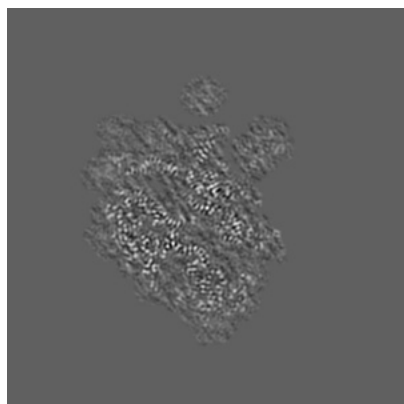


Z

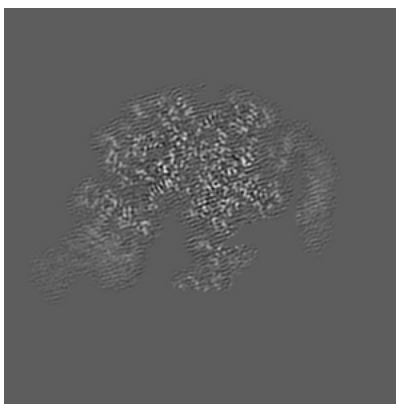
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

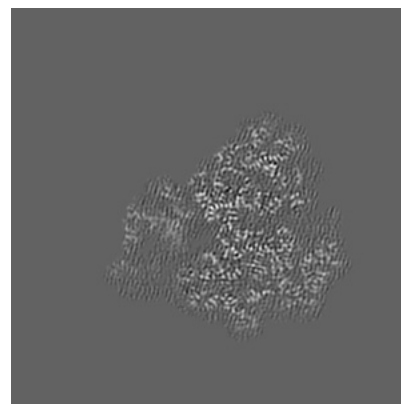
6.2.1 Primary map



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Y Index: 172

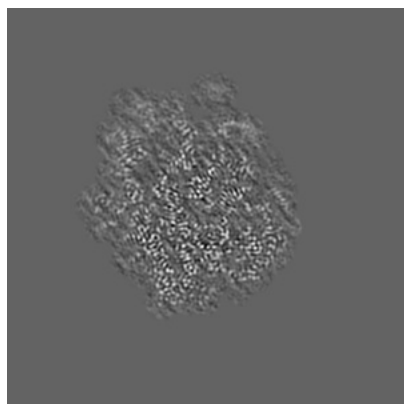


Z Index: 172

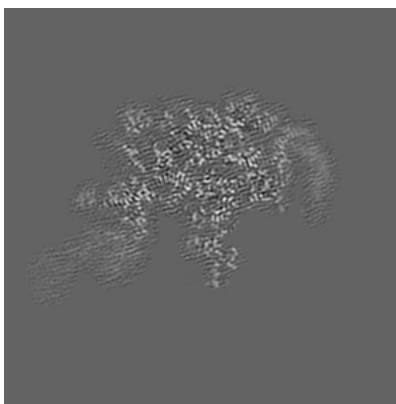
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

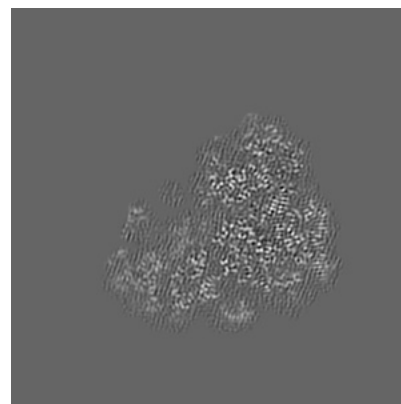
6.3.1 Primary map



X Index: 205



Y Index: 181

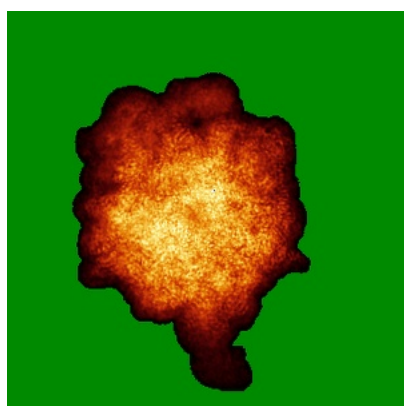


Z Index: 154

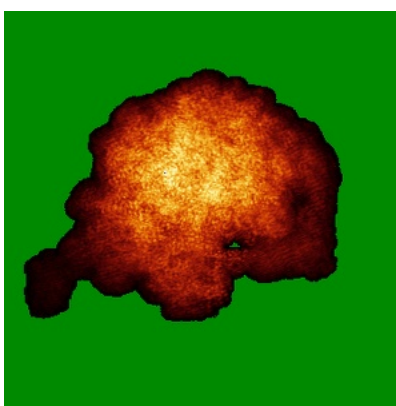
The images above show the largest variance slices of the map in three orthogonal directions.

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

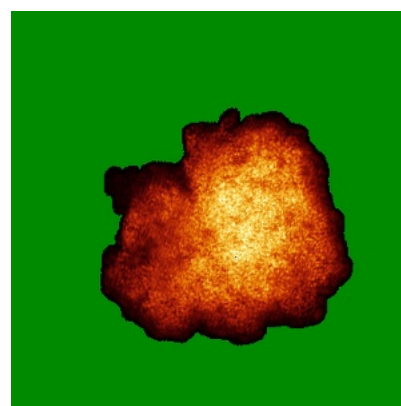
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

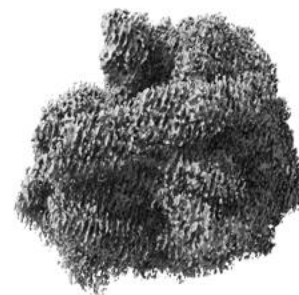
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

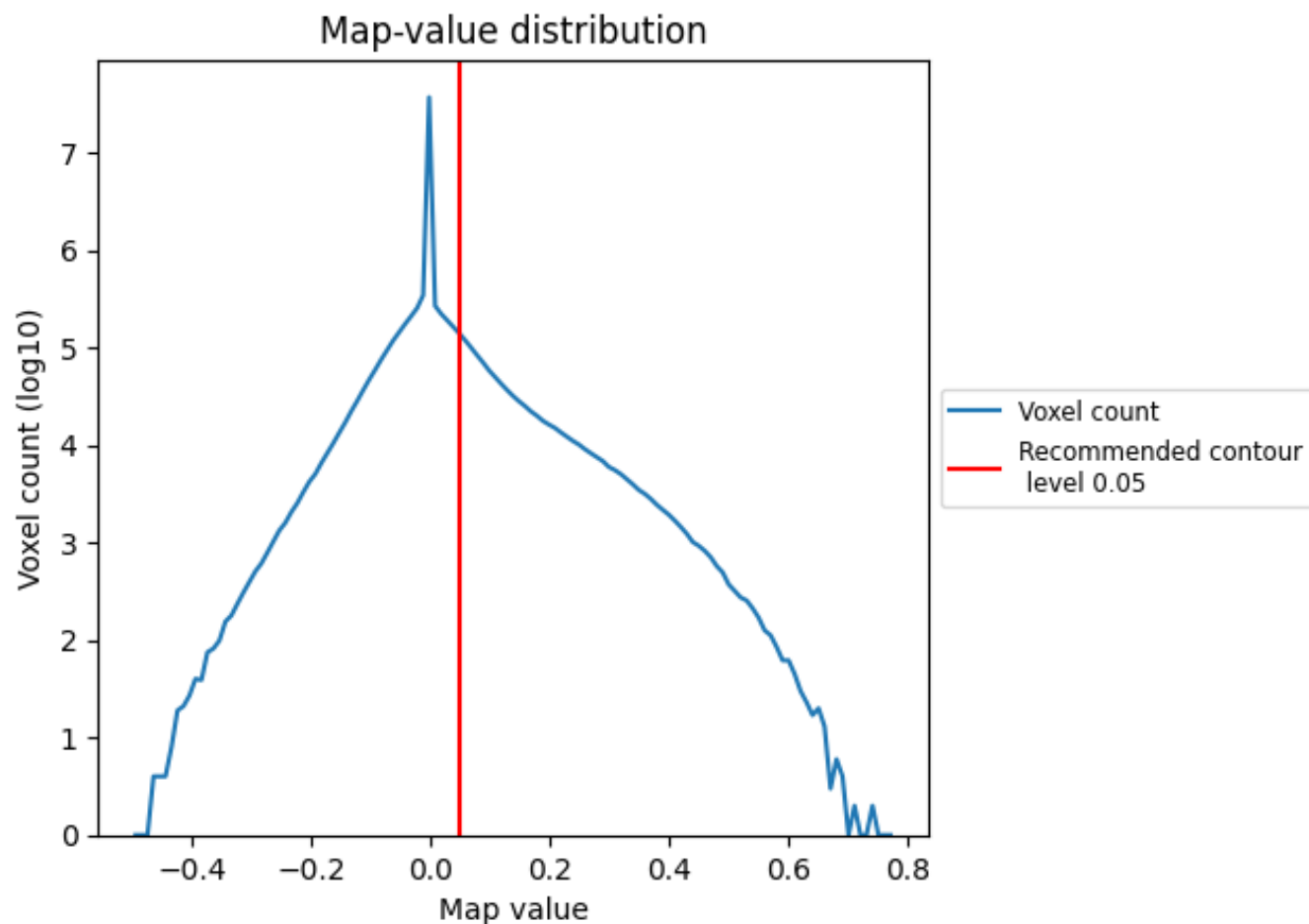
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

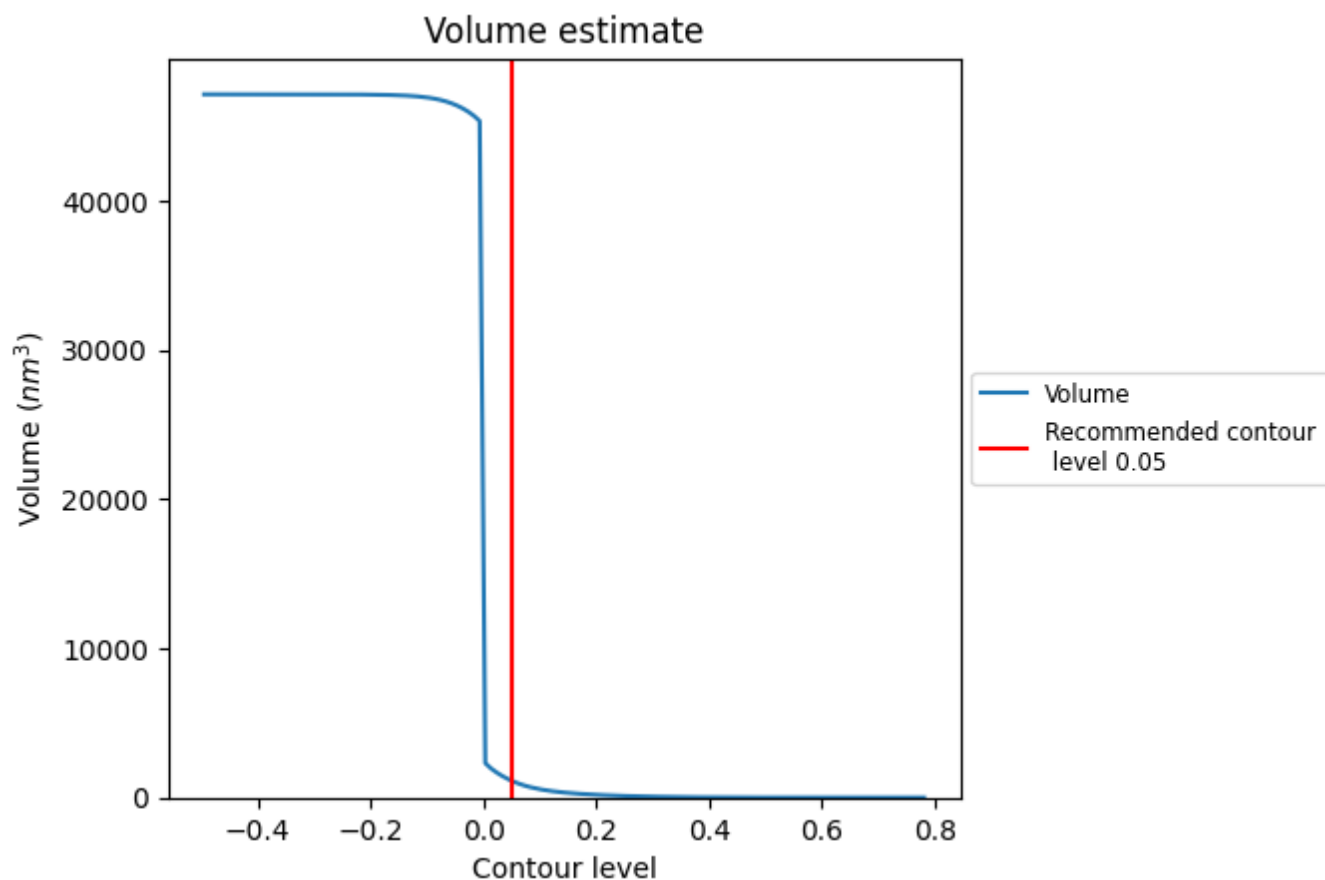
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

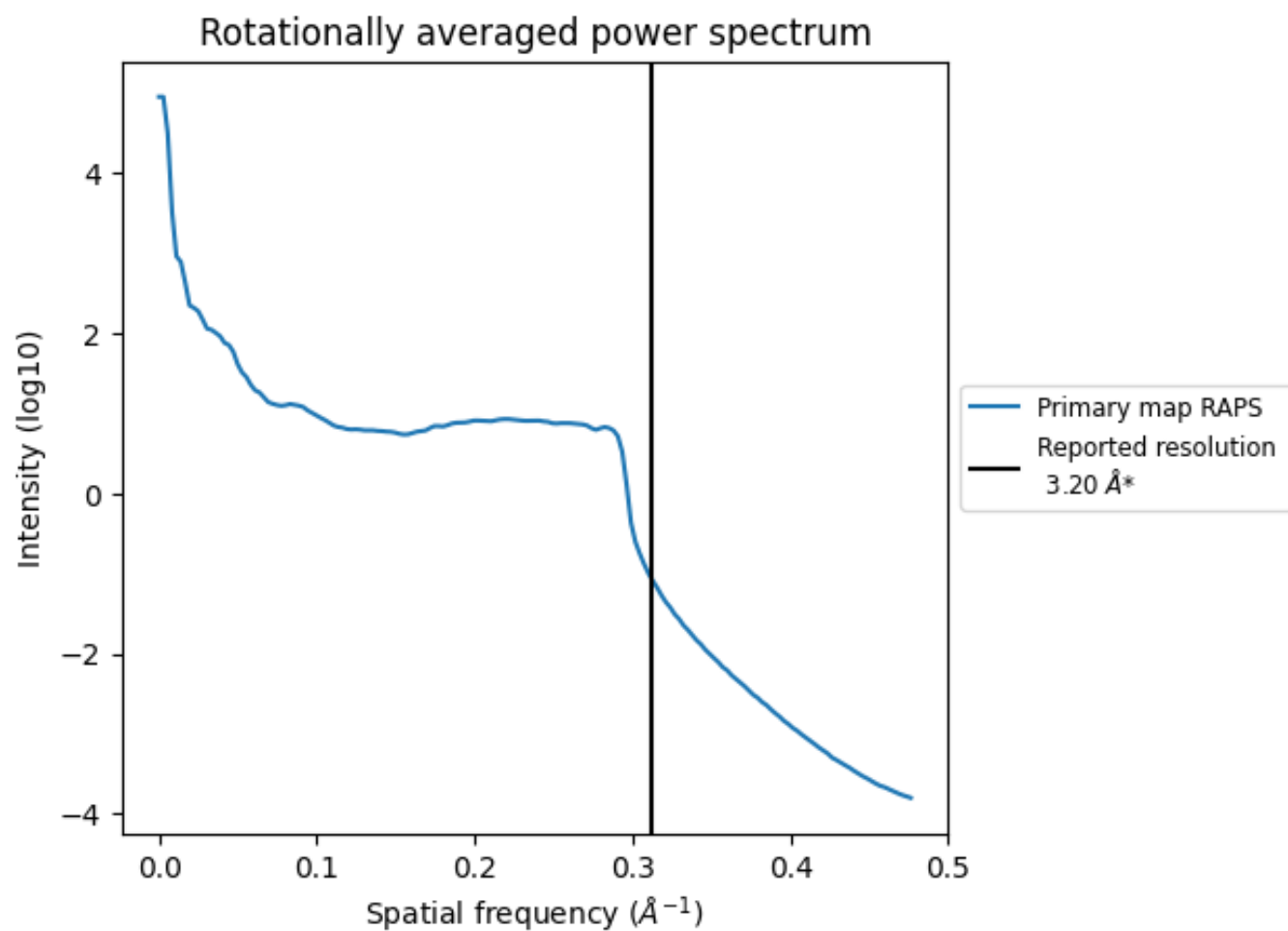
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1134 nm^3 ; this corresponds to an approximate mass of 1024 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 0.312 Å⁻¹

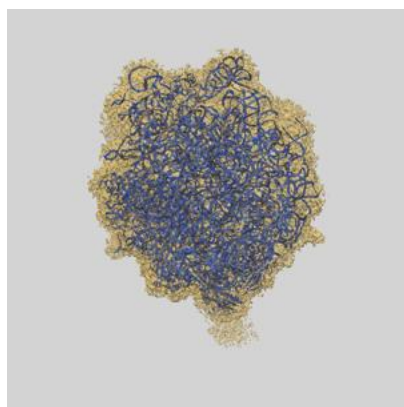
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

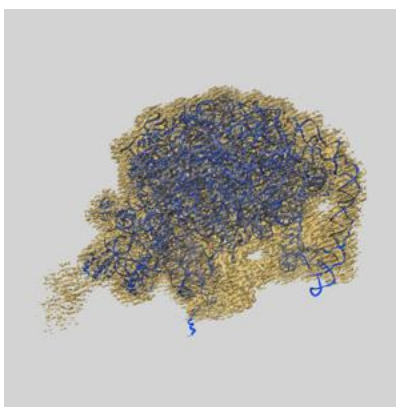
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6922 and PDB model 5ZET. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

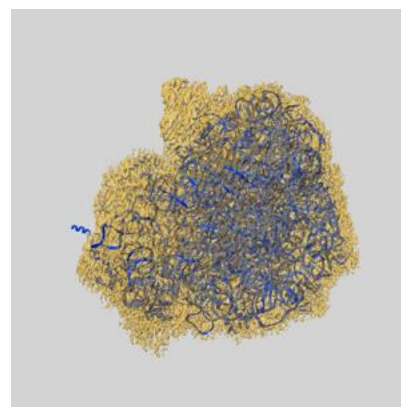
9.1 Map-model overlay [i](#)



X



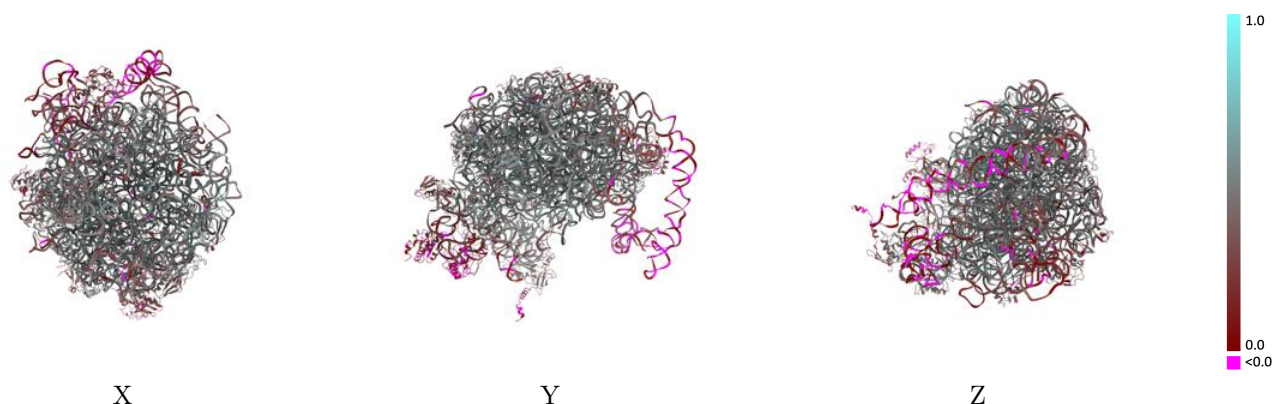
Y



Z

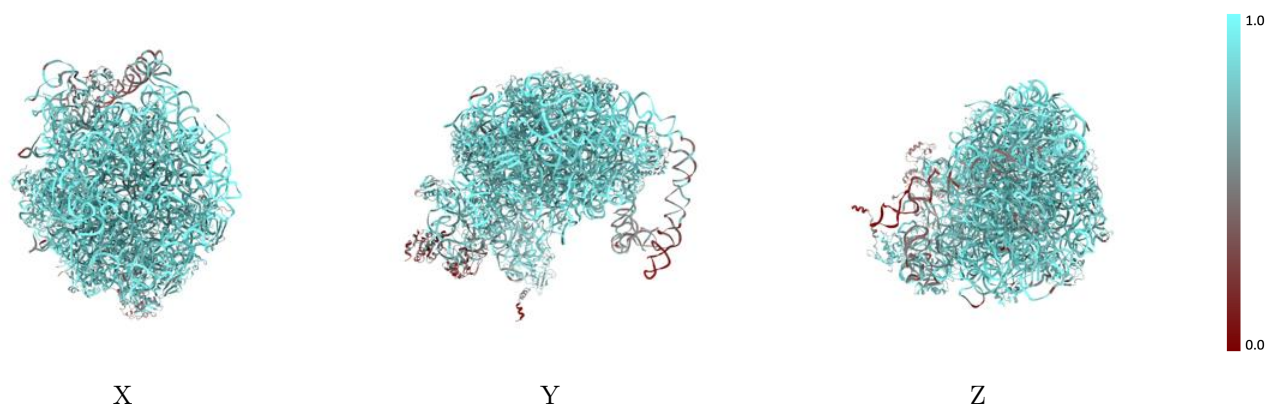
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



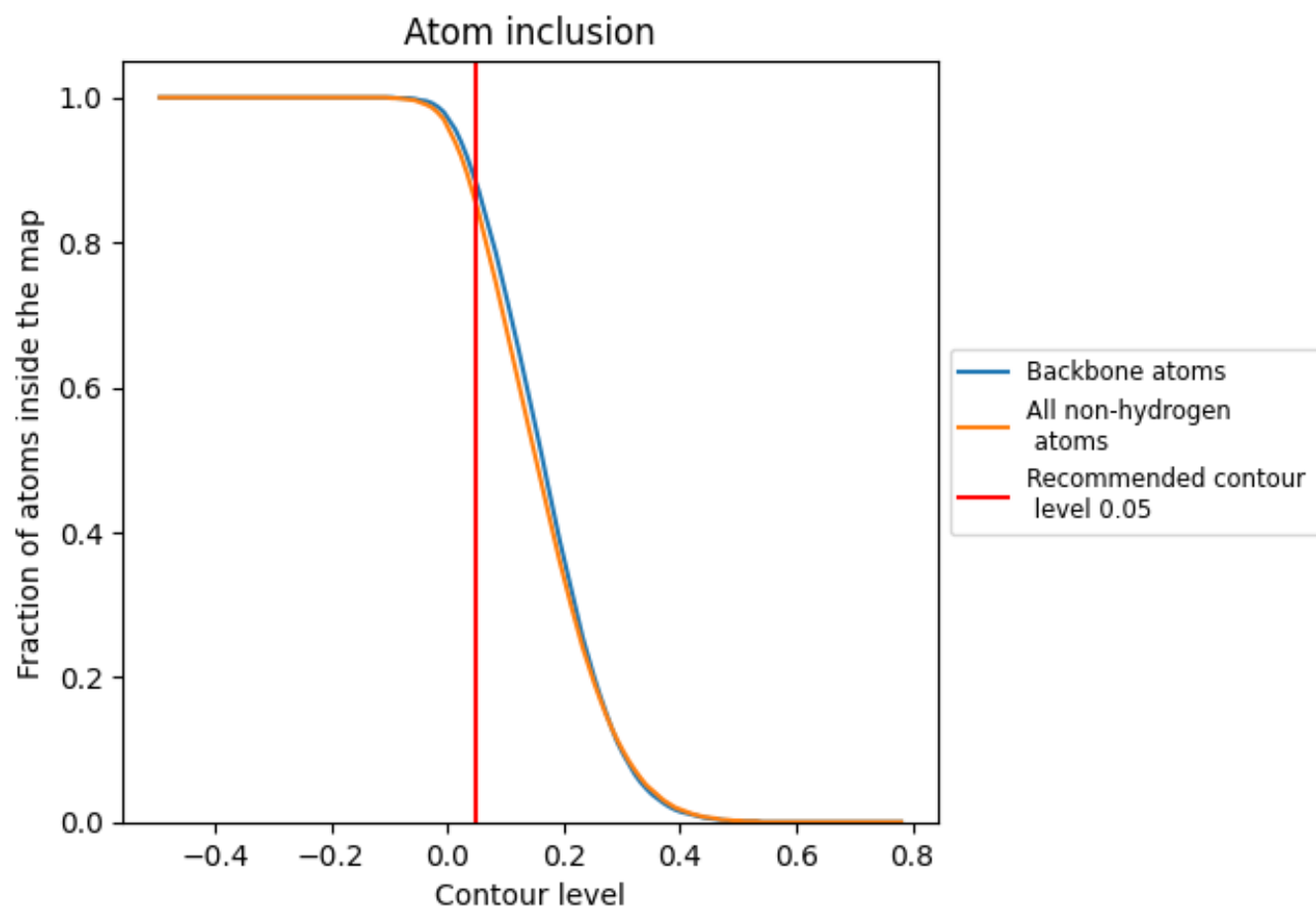
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.4220
1	 0.8210	 0.4500
2	 0.5390	 0.1850
3	 0.8360	 0.4500
4	 0.8040	 0.3790
5	 0.8610	 0.4740
6	 0.8690	 0.4850
7	 0.8810	 0.4790
8	 0.7930	 0.4410
A	 0.8820	 0.4320
B	 0.8620	 0.3920
C	 0.8530	 0.4810
D	 0.8520	 0.4720
E	 0.8200	 0.4230
F	 0.7930	 0.3790
G	 0.7670	 0.3570
H	 0.6300	 0.3000
I	 0.3450	 0.1310
J	 0.3720	 0.0990
K	 0.8400	 0.4650
L	 0.8260	 0.4500
M	 0.8220	 0.4320
N	 0.8410	 0.4600
O	 0.8220	 0.4380
P	 0.8330	 0.4300
Q	 0.8040	 0.4390
R	 0.8670	 0.4750
S	 0.8390	 0.4340
T	 0.8120	 0.4440
U	 0.7910	 0.4080
V	 0.7680	 0.3650
W	 0.6950	 0.3140
X	 0.8340	 0.4650
Y	 0.8370	 0.4520
Z	 0.8180	 0.4000

