



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:23 PM GMT

PDB ID : 1JJ2
Title : Fully Refined Crystal Structure of the Haloarcula marismortui Large Ribosomal Subunit at 2.4 Angstrom Resolution
Authors : Klein, D.J.; Schmeing, T.M.; Moore, P.B.; Steitz, T.A.
Deposited on : 2001-07-03
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

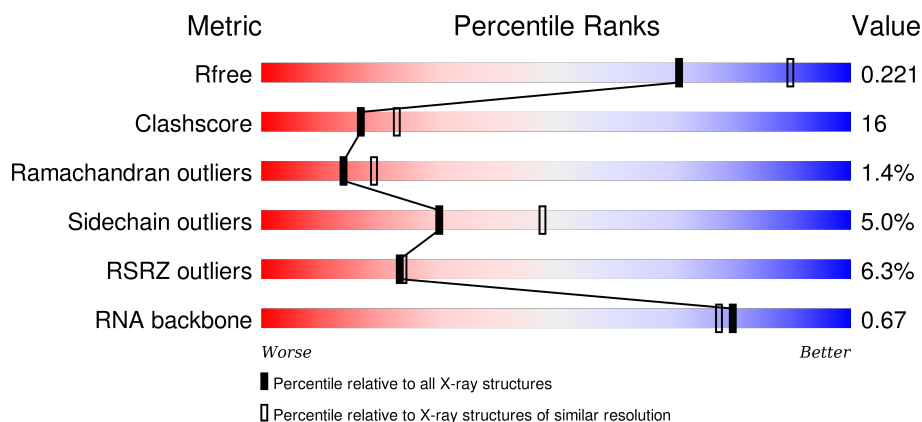
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)
RNA backbone	2183	1073 (2.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	2922	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>24%</div> <div>5%</div> <div>6%</div> </div> </div>
2	9	122	<div> <div>5%</div> <div> <div></div> <div>56%</div> <div>32%</div> <div>9%</div> <div>.</div> </div> </div>
3	A	239	<div> <div>9%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>6%</div> <div>.</div> </div> </div>
4	B	337	<div> <div>5%</div> <div> <div></div> <div>53%</div> <div>41%</div> <div>5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	176	
7	E	177	
8	F	119	
9	G	348	
10	H	167	
11	I	145	
12	J	132	
13	K	164	
14	L	194	
15	M	186	
16	N	115	
17	O	148	
18	P	95	
19	Q	154	
20	R	84	
21	S	119	
22	T	66	
23	U	70	
24	V	154	
25	W	91	
26	X	240	
27	Y	73	
28	Z	56	
29	1	48	

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Mol	Chain	Length	Quality of chain
30	2	92	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
31	MG	0	8060	-	-	-	X
33	NA	0	8302	-	-	-	X
33	NA	0	8303	-	-	-	X
33	NA	0	8305	-	-	-	X
33	NA	0	8314	-	-	-	X
33	NA	0	8320	-	-	-	X
33	NA	0	8321	-	-	-	X
33	NA	0	8325	-	-	-	X
33	NA	0	8327	-	-	-	X
33	NA	0	8331	-	-	-	X
33	NA	0	8340	-	-	-	X
33	NA	0	8350	-	-	-	X
33	NA	0	8361	-	-	-	X
33	NA	0	8362	-	-	-	X
33	NA	0	8364	-	-	-	X
33	NA	0	8366	-	-	-	X
33	NA	0	8371	-	-	-	X
33	NA	0	8372	-	-	-	X
33	NA	0	8374	-	-	-	X
33	NA	0	8376	-	-	-	X
33	NA	K	8380	-	-	-	X
33	NA	Q	8386	-	-	-	X

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 98543 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59017	26346	10878	19048	2745			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	CONFLICT	GB 3377779

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2600	1160	472	847	121			

- Molecule 3 is a protein called RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	237	Total	C	N	O	S	0	0	0
			1754	1072	352	325	5			

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	337	Total	C	N	O	S	0	0	0
			2624	1616	493	510	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	DELETION	UNP P20279
B	310	ARG	PHE	CONFLICT	UNP P20279

- Molecule 5 is a protein called RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1858	1131	344	382	1			

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	119	Total	C	N	O	S	0	0	0
			885	552	141	191	1			

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	29	Total	C	N	O	S	0	0	0
			240	149	39	51	1			

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	156	Total	C	N	O	S	0	0	0
			1215	766	233	212	4			

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	142	Total	C	N	O	S	0	0	0
			1119	696	199	221	3			

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	132	Total	C	N	O	S	0	0	0
			993	609	189	191	4			

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	145	Total	C	N	O		0	0	0
			1114	668	222	224				

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	194	Total	C	N	O	S	0	0	0
			1605	988	346	266	5			

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	186	Total	C	N	O	S	0	0	0
			1444	895	262	285	2			

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L18E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	115	Total	C	N	O		0	0	0
			864	529	161	174				

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L19E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	O	143	Total	C	N	O		0	0	0
			1133	680	230	223				

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	71	LYS	TYR	CONFLICT	UNP P14119

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L21E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	95	Total	C	N	O			
			734	450	141	143	0	0	0

- Molecule 19 is a protein called RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	Q	150	Total	C	N	O	S		
			1149	713	209	223	4	0	0

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	R	81	Total	C	N	O	S		
			641	389	111	138	3	0	0

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	S	119	Total	C	N	O			
			949	568	180	201		0	0

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L24E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	T	53	Total	C	N	O	S		
			410	244	75	86	5	0	0

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	U	65	Total	C	N	O	S		
			499	304	94	100	1	0	0

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	V	154	Total	C	N	O	S		
			1195	737	209	243	6	0	0

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L31E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	W	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L32E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	X	142	Total	C	N	O		0	0	0
			1130	686	228	216				

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y	73	Total	C	N	O	S	0	0	0
			563	359	111	86	7			

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	56	Total	C	N	O	S	0	0	0
			430	258	86	82	4			

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	46	Total	C	N	O	S	0	0	0
			393	238	86	68	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	ARG	DELETION	UNP P22452

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
31	0	109	Total Mg 109 109	0	0
31	J	1	Total Mg 1 1	0	0
31	B	1	Total Mg 1 1	0	0
31	A	2	Total Mg 2 2	0	0
31	X	1	Total Mg 1 1	0	0
31	2	1	Total Mg 1 1	0	0
31	9	1	Total Mg 1 1	0	0
31	S	1	Total Mg 1 1	0	0

- Molecule 32 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	0	2	Total K 2 2	0	0

- Molecule 33 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	0	72	Total Na 72 72	0	0
33	P	1	Total Na 1 1	0	0
33	Q	2	Total Na 2 2	0	0
33	K	1	Total Na 1 1	0	0
33	H	2	Total Na 2 2	0	0
33	I	1	Total Na 1 1	0	0
33	C	1	Total Na 1 1	0	0
33	A	1	Total Na 1 1	0	0
33	R	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	9	2	Total 2	Na 2	0	0
33	L	1	Total 1	Na 1	0	0
33	S	1	Total 1	Na 1	0	0

- Molecule 34 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	10	Total 10	Cl 10	0	0
34	Q	1	Total 1	Cl 1	0	0
34	K	1	Total 1	Cl 1	0	0
34	B	1	Total 1	Cl 1	0	0
34	I	3	Total 3	Cl 3	0	0
34	A	1	Total 1	Cl 1	0	0
34	N	1	Total 1	Cl 1	0	0
34	X	1	Total 1	Cl 1	0	0
34	2	1	Total 1	Cl 1	0	0
34	L	1	Total 1	Cl 1	0	0
34	M	1	Total 1	Cl 1	0	0

- Molecule 35 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	Z	1	Total 1	Cd 1	0	0
35	Y	1	Total 1	Cd 1	0	0
35	T	1	Total 1	Cd 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	2	1	Total	Cd	0	0
			1	1		
35	N	1	Total	Cd	0	0
			1	1		

- Molecule 36 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	5938	Total	O	0	0
			5938	5938		
36	9	135	Total	O	0	0
			135	135		
36	A	126	Total	O	0	0
			126	126		
36	B	150	Total	O	0	0
			150	150		
36	C	172	Total	O	0	0
			172	172		
36	D	53	Total	O	0	0
			53	53		
36	E	46	Total	O	0	0
			46	46		
36	F	28	Total	O	0	0
			28	28		
36	G	21	Total	O	0	0
			21	21		
36	H	74	Total	O	0	0
			74	74		
36	I	56	Total	O	0	0
			56	56		
36	J	62	Total	O	0	0
			62	62		
36	K	80	Total	O	0	0
			80	80		
36	L	127	Total	O	0	0
			127	127		
36	M	70	Total	O	0	0
			70	70		
36	N	43	Total	O	0	0
			43	43		
36	O	68	Total	O	0	0
			68	68		

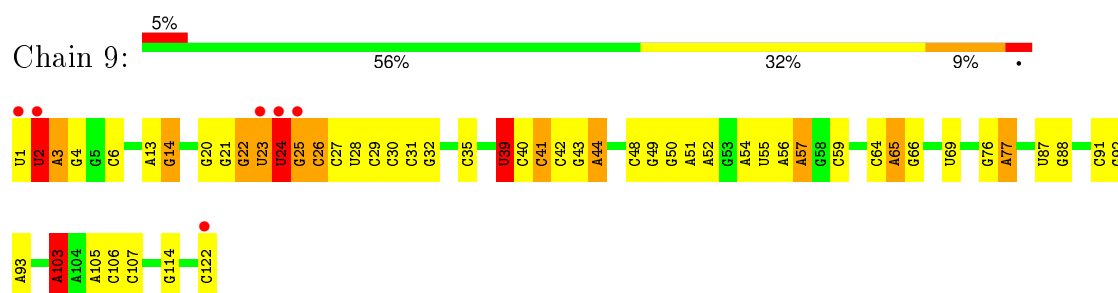
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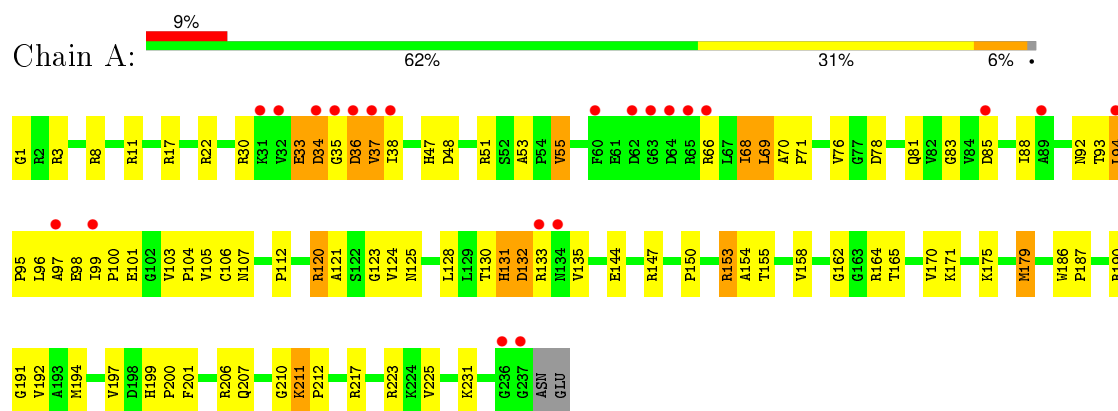
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	P	53	Total 53	O 53	0	0
36	Q	81	Total 81	O 81	0	0
36	R	32	Total 32	O 32	0	0
36	S	39	Total 39	O 39	0	0
36	T	25	Total 25	O 25	0	0
36	U	15	Total 15	O 15	0	0
36	V	67	Total 67	O 67	0	0
36	W	29	Total 29	O 29	0	0
36	X	99	Total 99	O 99	0	0
36	Y	39	Total 39	O 39	0	0
36	Z	53	Total 53	O 53	0	0
36	1	40	Total 40	O 40	0	0
36	2	72	Total 72	O 72	0	0

A2820	G2898	C2591	G2480	C2346	G2250	C	G2102	G1971	G1862	U1724	A1598	C1480	G1299
C2821	U2710	G2592	A2483	A2353	G2251	G	G2110	U1972	G1863	C1725	A1603	C1451	U1306
G2826	U2711	U2597	A2354	A2354	A2252	C	G2111	G1973	G1867	G1730	A1604	C1451	U1314
A2827	G2712	U2598	A2361	A2361	G2253	C	G2112	G1974	G1868	C1731	G1605	A1458	A1328
G2828	A2488	A2601	A2362	A2362	G2254	C	G2113	A1978	G1877	A1732	C1613	C1462	A1329
G2829	G2489	G2602	G2363	G2363	A2255	U	G2114	G1979	G1878	A1733	C1614	A1463	A1333
U2830	A2490	A2603	G2364	G2364	G2256	A	U2115	U1980	U1879	C1734	A1615	A1463	U1333
C2831	C2493	A2604	G2365	G2365	G2257	G	U2116	A1981	U1879	C1735	A1615	A1463	C1334
C2832	C2502	A2607	A2369	A2369	A2258	C	G2128	C1982	A1881	A1736	U1625	C1467	U1333
U2837	A2503	U2608	A2369	A2369	C2259	G	G2136	U1986	U1882	U1741	A1626	A1470	C1334
U2840	A2504	A2613	G2383	G2383	A2265	G	A	A1997	U1883	A1742	G1627	A1474	G1339
A2841	G2505	G2614	C2388	C2388	A2266	C	C	G2001	U1887	G1751	A1630	C1477	G1340
G2842	A2506	U2615	C2388	C2388	G2270	A	G	C2002	U1887	C1752	C1633	C1477	A1341
A2843	G2507	U2615	A2395	A2395	G2271	C	U	U2003	G1902	C1753	C1633	C1477	C1343
C2850	C2508	G2630	A2401	A2401	G2272	C	G	U2004	G1902	G1756	U1635	G1484	G1351
G2852	A2510	A2633	A2412	A2412	C2273	G	U	G2005	U1903	U1766	G1636	A1485	A1352
G2853	A2511	G2634	A2414	A2414	A2274	A	U	U2008	A1904	U1766	A1637	U1488	C1353
G2854	G2526	G2635	A2415	A2415	U2297	G	U	G2009	A1909	U1771	A1641	G1497	C1360
G2855	C2527	G2636	A2416	A2416	U2297	U	U	A2010	C1920	U1771	A1642	U1500	A1367
G2856	G2533	G2637	U2419	U2419	A2300	A	G	U2011	A1919	A1778	U1654	A1501	U1368
G2857	C2534	A2649	G2420	G2420	A2301	A	C	A2012	C1920	A1778	G1655	A1502	A1372
G2858	U2535	U2652	G2421	G2421	A2302	U	A	G2013	A1921	A1779	U1656	A1503	A1372
G2859	C2536	G2654	U2422	U2422	U2303	C	U	A2019	G1926	C1787	G1657	A1504	C1377
G2860	G2537	C2654	G2426	G2426	U2297	G	U	G2033	C1928	U1788	A1657	U1505	U1380
G2861	U2541	A2664	U2426	U2426	U2297	U	U	U2034	G1929	G1789	A1658	U1506	U1380
G2862	C2542	A	A2434	A2434	A2300	A	A	G2044	C1940	G1794	C1666	G1523	U1380
G2863	G2543	U	G2438	G2438	A2301	A	G	A2054	A1941	C1798	A1667	U1524	C1384
G2864	C2547	G2667	G2438	G2438	A2302	U	C	C2061	A1942	A1804	U1668	G1525	G1385
G2865	C2548	U2668	C2443	C2443	G2310	C	U	A2062	C1943	G1805	A1669	A1526	A1393
G2866	C2552	G2670	A2456	A2456	G2311	U	A	U2063	G1947	U1677	A1678	A1527	C1394
G2867	A2553	C2671	U2457	U2457	G2312	U	G	U2064	G1948	G1809	A1679	A1528	A1406
G2868	C2559	U2673	G2462	G2462	G2313	A	G	G2072	G1949	G1819	C1680	C1545	A1407
G2869	U2563	G2676	A2465	A2465	G2314	C	U	A2074	G1950	G1820	G1681	G1546	U1408
G2870	G2564	A2681	G2466	G2466	G2315	G	A	G2073	G1951	A1829	A1682	G1555	G1409
G2871	C2565	C2682	A2467	A2467	C2317	U	C	A2078	U	A	A1683	G1555	A1413
G2872	G2570	U2688	A2468	A2468	U2320	C	A	U2078	A	C	A1684	A1559	A1414
G2873	G2578	A2690	A2470	A2470	U2321	G	C	A2081	C	C	A1685	U	A1417
G2874	U2586	A2691	C2472	C2472	A2322	U	C	G2082	U	U	C1692	G1561	G1417
G2875	U2587	A2694	C2476	C2476	A2323	C	A	A2083	G	A	C1699	C1562	U1418
G2876	G2588	U2697	U2477	U2477	A2324	U	G	A2089	C	A	G1700	G1563	U1419
G2877	U2589	A2699	U2478	U2478	G2344	C	C	G2090	U	C	A1701	C1564	C1423
G2878	U2590	A2699	A2479	A2479	A2345	C	C	G2091	C	C	U1702	A1580	A1424
G2879									U1964	C1853	A1710	G1592	G1430
G2880									C1965	C1854	A1717	G1592	C1439
G2881									U1966	G1855	A1717	C1594	U1440
G2882									U1967	C1856	U1722	G1596	G1441
G2883									G1970	A1857	G1723		A1442

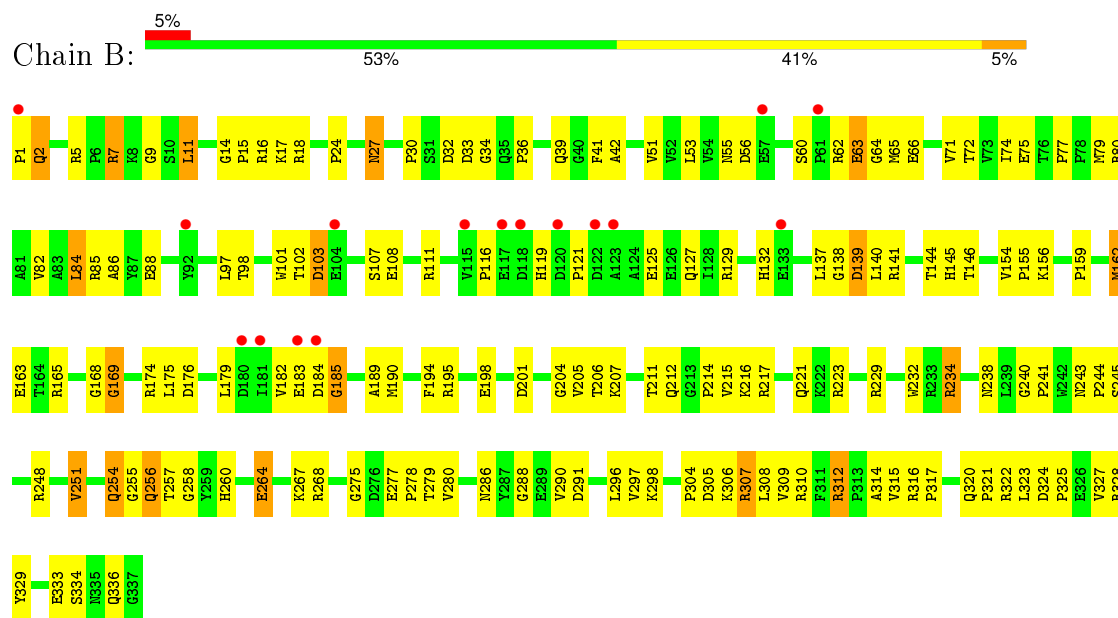
• Molecule 2: 5S rRNA



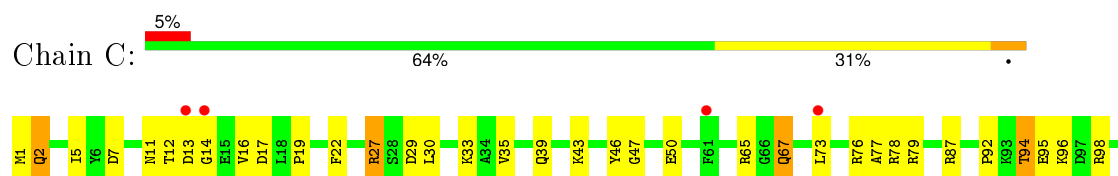
• Molecule 3: RIBOSOMAL PROTEIN L2

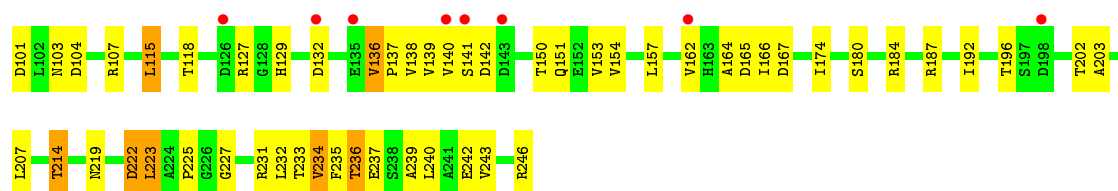


• Molecule 4: RIBOSOMAL PROTEIN L3

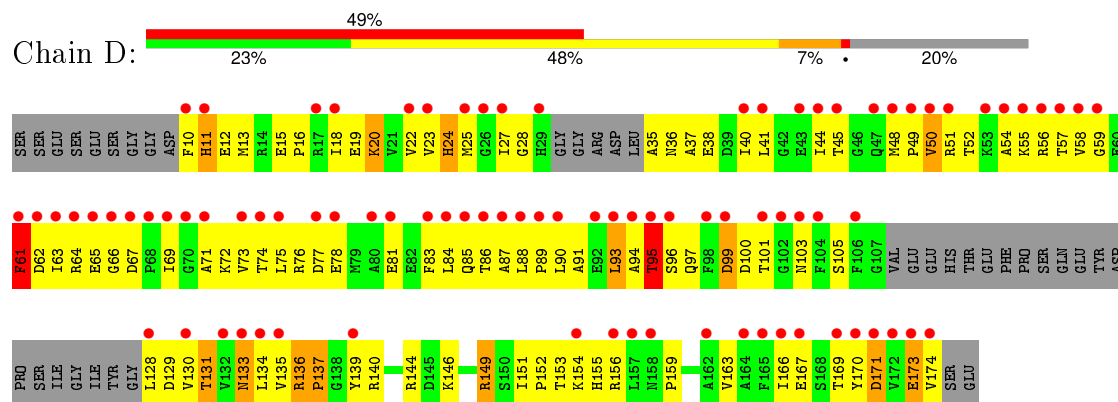


• Molecule 5: RIBOSOMAL PROTEIN L4

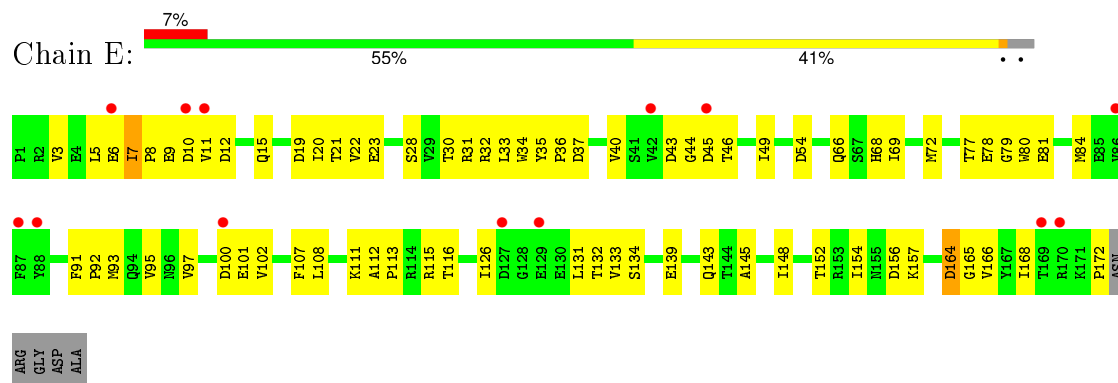




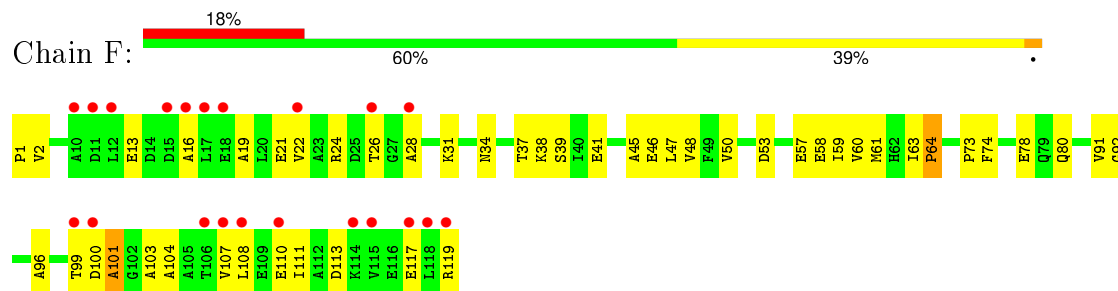
• Molecule 6: RIBOSOMAL PROTEIN L5



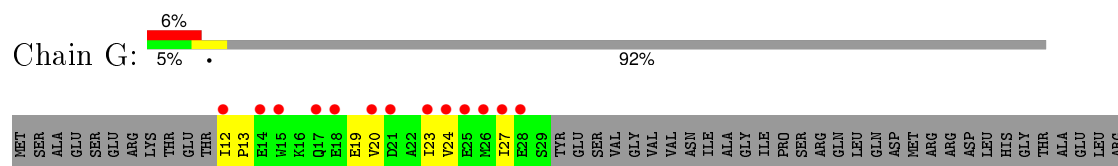
• Molecule 7: RIBOSOMAL PROTEIN L6

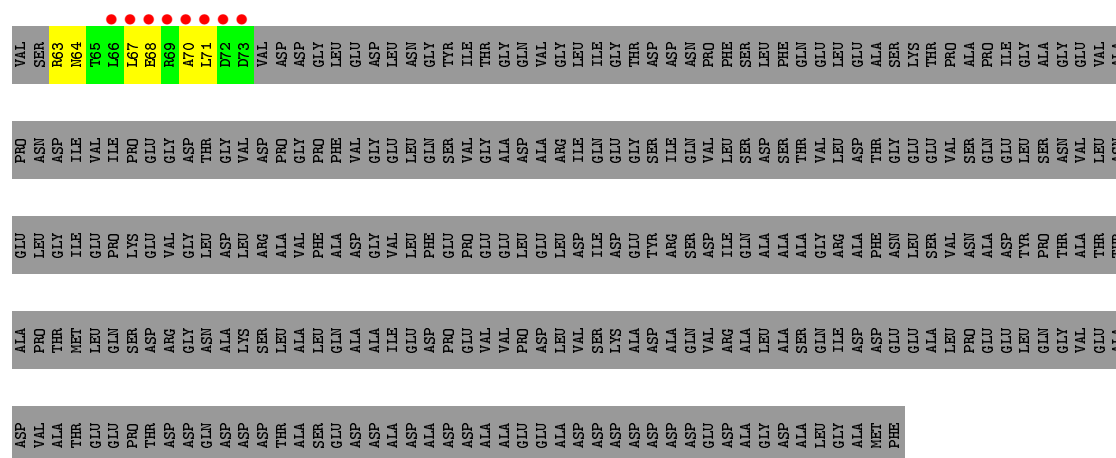


• Molecule 8: RIBOSOMAL PROTEIN L7AE

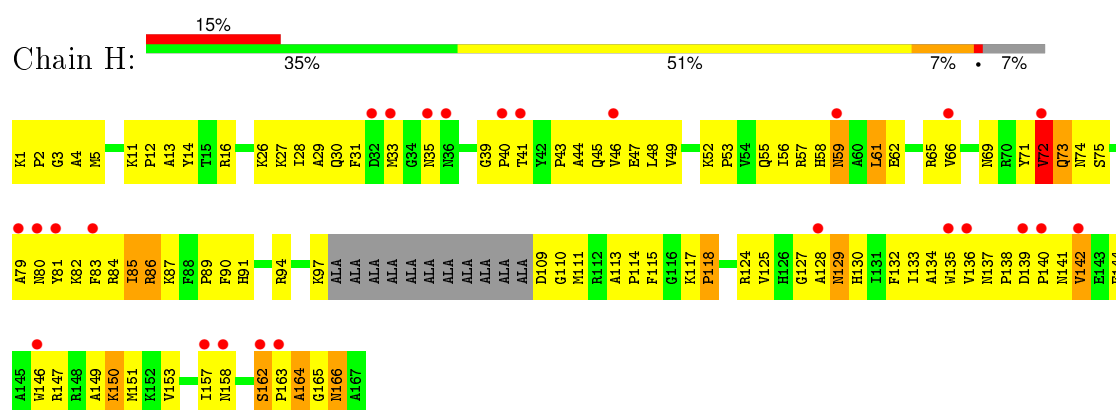


• Molecule 9: RIBOSOMAL PROTEIN L10

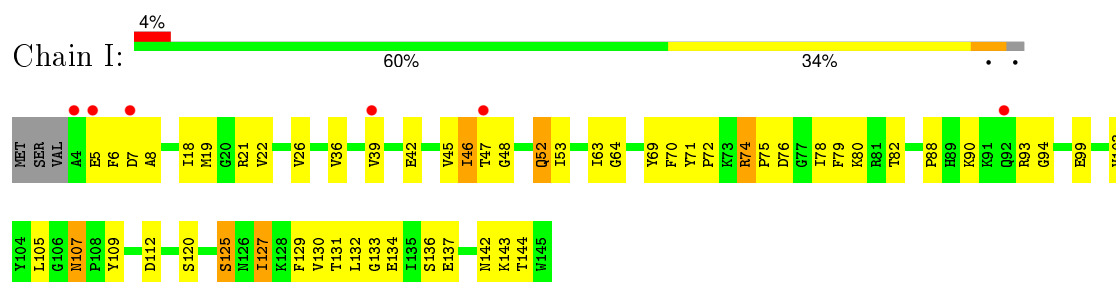




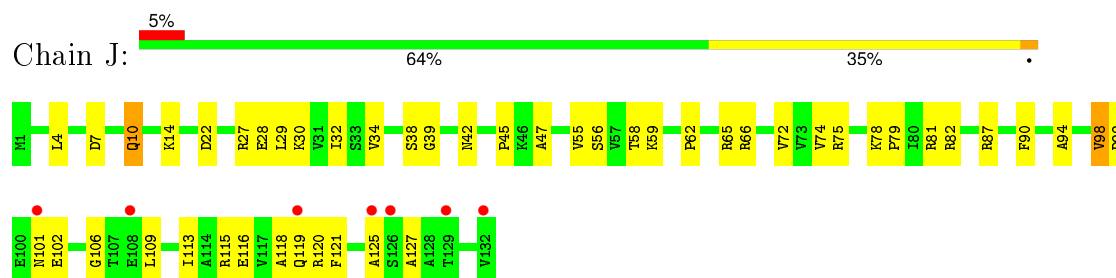
- Molecule 10: RIBOSOMAL PROTEIN L10E



- Molecule 11: RIBOSOMAL PROTEIN L13

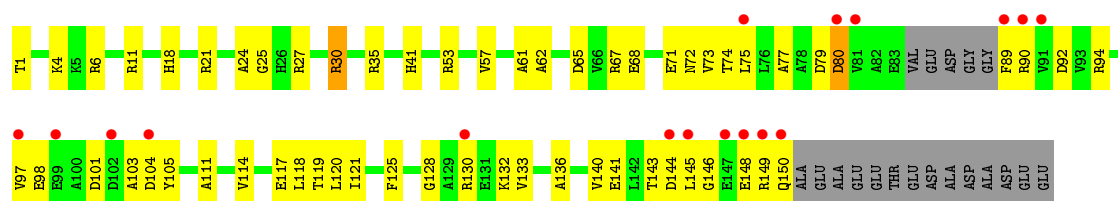


- Molecule 12: RIBOSOMAL PROTEIN L14

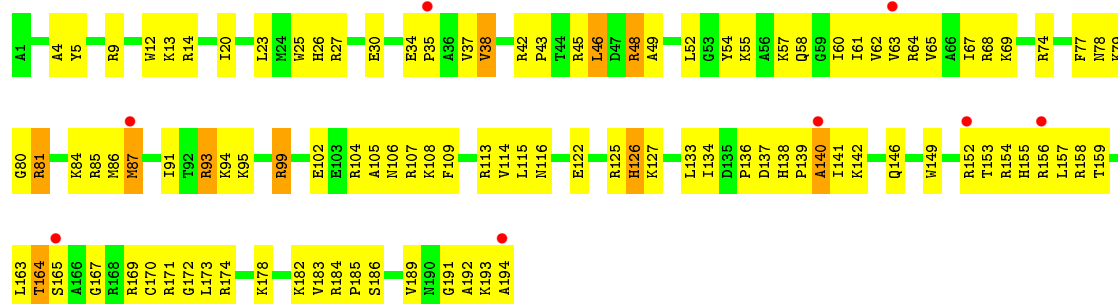


- Molecule 13: RIBOSOMAL PROTEIN L15

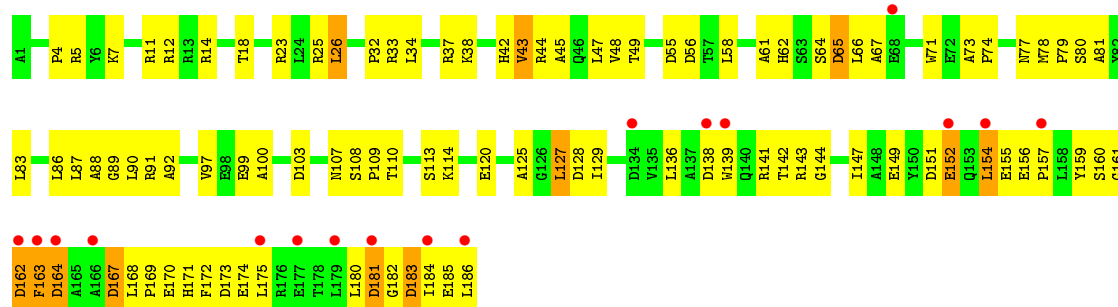




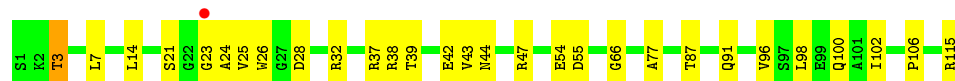
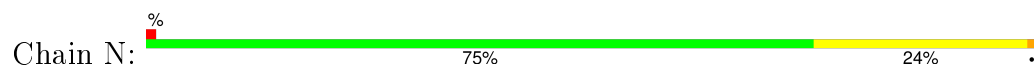
• Molecule 14: RIBOSOMAL PROTEIN L15E



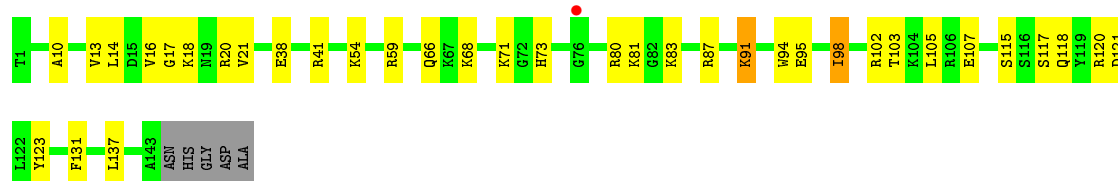
• Molecule 15: RIBOSOMAL PROTEIN L18



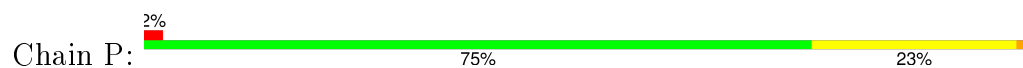
• Molecule 16: RIBOSOMAL PROTEIN L18E



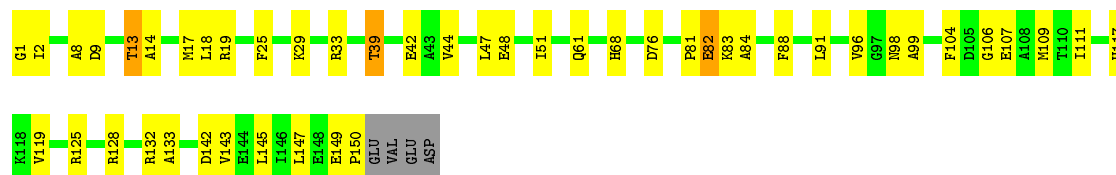
• Molecule 17: RIBOSOMAL PROTEIN L19E



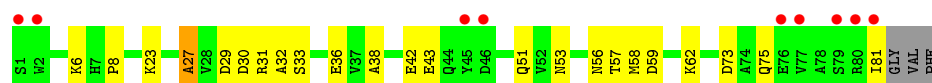
- Molecule 18: RIBOSOMAL PROTEIN L21E



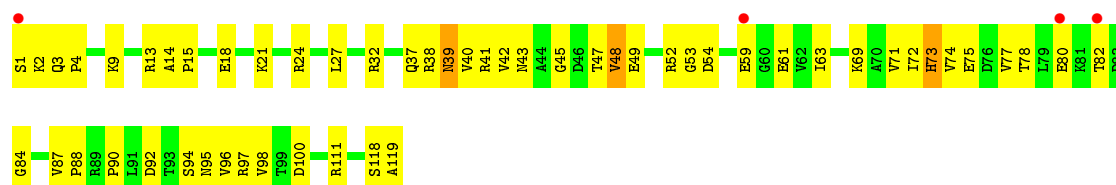
- Molecule 19: RIBOSOMAL PROTEIN L22



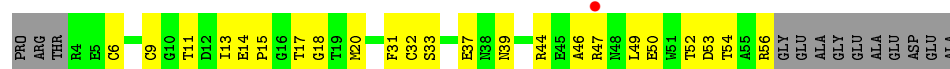
- Molecule 20: RIBOSOMAL PROTEIN L23



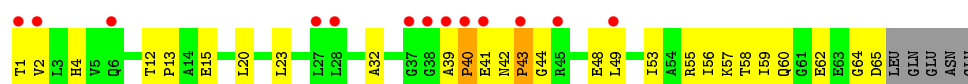
- Molecule 21: RIBOSOMAL PROTEIN L24



- Molecule 22: RIBOSOMAL PROTEIN L24E

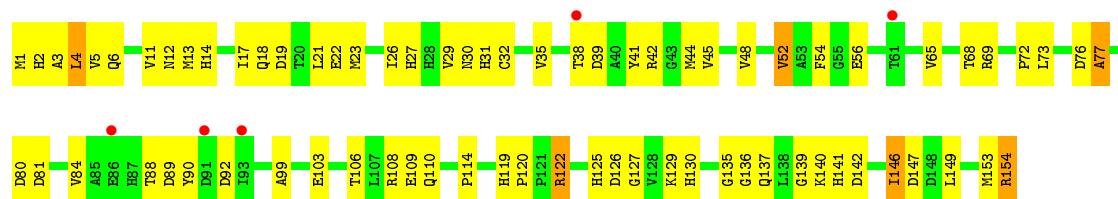


- Molecule 23: RIBOSOMAL PROTEIN L29



- Molecule 24: RIBOSOMAL PROTEIN L30

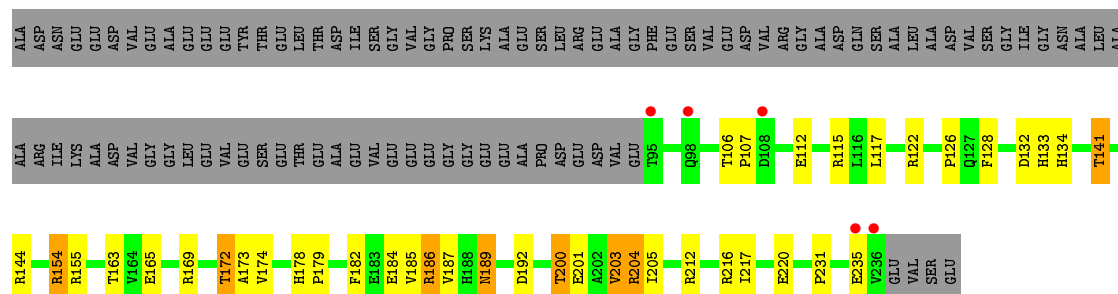




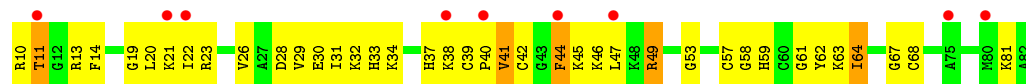
• Molecule 25: RIBOSOMAL PROTEIN L31E



• Molecule 26: RIBOSOMAL PROTEIN L32E



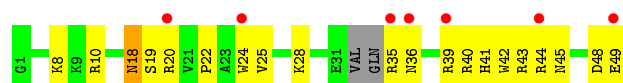
• Molecule 27: RIBOSOMAL PROTEIN L37Ae



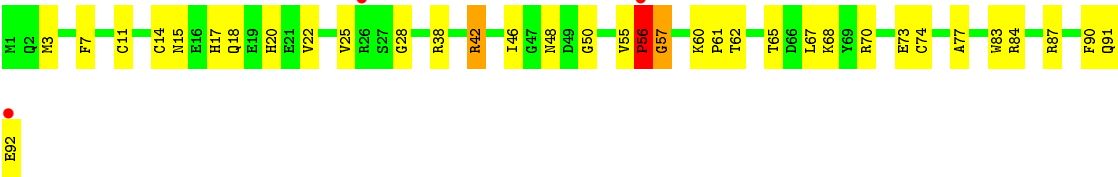
• Molecule 28: RIBOSOMAL PROTEIN L37E



• Molecule 29: RIBOSOMAL PROTEIN L39E



● Molecule 30: RIBOSOMAL PROTEIN L44E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.66Å 299.67Å 573.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 85.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	90.2 (15.00-2.40) 90.6 (85.48-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.189 , 0.222 0.189 , 0.221	Depositor DCC
R_{free} test set	6512 reflections (1.04%)	DCC
Wilson B-factor (Å ²)	38.9	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 666819 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	98543	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MG, CD, K, CL

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	0	0.38	3/66076 (0.0%)	0.71	32/103052 (0.0%)
2	9	0.44	3/2905 (0.1%)	0.85	11/4528 (0.2%)
3	A	0.34	0/1787	0.66	0/2409
4	B	0.34	0/2689	0.64	0/3652
5	C	0.39	0/1883	0.67	0/2551
6	D	0.31	0/1111	0.59	0/1498
7	E	0.31	0/1382	0.57	0/1880
8	F	0.33	0/896	0.56	0/1219
9	G	0.25	0/241	0.47	0/324
10	H	0.38	0/1246	0.74	1/1686 (0.1%)
11	I	0.33	0/1135	0.61	0/1530
12	J	0.33	0/1003	0.65	0/1351
13	K	0.34	0/1126	0.68	0/1504
14	L	0.41	0/1633	0.71	1/2180 (0.0%)
15	M	0.29	0/1473	0.64	0/1999
16	N	0.32	0/873	0.61	1/1181 (0.1%)
17	O	0.33	0/1143	0.54	0/1521
18	P	0.35	0/748	0.68	0/1005
19	Q	0.35	0/1172	0.67	0/1578
20	R	0.32	0/648	0.59	1/875 (0.1%)
21	S	0.31	0/957	0.63	0/1289
22	T	0.32	0/417	0.58	0/562
23	U	0.29	0/502	0.54	0/675
24	V	0.33	0/1218	0.62	0/1655
25	W	0.32	0/664	0.60	0/895
26	X	0.34	0/1146	0.63	0/1536
27	Y	0.37	0/575	0.69	0/763
28	Z	0.42	0/437	0.67	0/578
29	1	0.34	0/398	0.54	0/527
30	2	0.38	0/771	0.62	0/1024
All	All	0.37	6/98255 (0.0%)	0.70	47/147027 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	1	62
2	9	0	2
All	All	1	64

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	9	3	A	C2'-O2'	-7.92	1.31	1.41
1	0	1206	U	P-OP2	6.22	1.59	1.49
2	9	3	A	O5'-C5'	6.21	1.54	1.44
1	0	1206	U	C3'-O3'	-5.28	1.34	1.42
1	0	1205	U	C3'-O3'	-5.23	1.34	1.42
2	9	3	A	C5'-C4'	-5.13	1.45	1.51

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1165	G	O5'-P-OP1	-22.95	83.17	110.70
1	0	1164	U	OP1-P-O3'	-20.79	59.47	105.20
1	0	1165	G	O5'-P-OP2	-15.10	92.11	105.70
2	9	3	A	OP1-P-O3'	-13.36	75.82	105.20
1	0	1164	U	OP2-P-O3'	-13.28	75.98	105.20
2	9	3	A	C5'-C4'-C3'	-11.15	98.16	116.00
2	9	2	U	OP2-P-O3'	-10.56	81.96	105.20
1	0	1563	G	C2'-C3'-O3'	9.58	130.57	109.50
1	0	1942	A	C5'-C4'-C3'	8.93	130.28	116.00
2	9	24	U	C2'-C3'-O3'	8.93	129.14	109.50
1	0	871	G	C5'-C4'-O4'	-8.42	99.00	109.10
1	0	1979	G	C2'-C3'-O3'	8.18	127.49	109.50
2	9	2	U	OP1-P-O3'	7.93	122.65	105.20
1	0	1819	G	C5'-C4'-C3'	7.14	127.43	116.00
2	9	39	U	N1-C1'-C2'	7.07	123.19	114.00
2	9	3	A	OP2-P-O3'	7.00	120.61	105.20
1	0	1206	U	C5'-C4'-C3'	-6.94	104.89	116.00
2	9	103	A	C5'-C4'-O4'	6.87	117.34	109.10
1	0	2316	G	C5'-C4'-C3'	-6.84	105.06	116.00
1	0	1942	A	C5'-C4'-O4'	6.80	117.26	109.10
1	0	1504	A	C1'-O4'-C4'	-6.55	104.66	109.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2467	A	C1'-O4'-C4'	-6.40	104.78	109.90
1	0	206	G	C5'-C4'-C3'	-6.37	105.81	116.00
1	0	2291	A	N9-C1'-C2'	6.26	122.14	114.00
1	0	1504	A	N9-C1'-C2'	6.21	122.08	114.00
1	0	1559	A	C2'-C3'-O3'	5.91	123.16	113.70
10	H	74	ASN	N-CA-C	-5.82	95.28	111.00
1	0	1942	A	C1'-O4'-C4'	-5.80	105.26	109.90
1	0	1942	A	C4'-C3'-C2'	-5.79	96.81	102.60
1	0	777	U	O4'-C1'-N1	5.70	112.76	108.20
1	0	1164	U	O3'-P-O5'	5.68	114.78	104.00
1	0	1205	U	C4'-C3'-O3'	-5.61	97.63	109.40
1	0	169	A	C5'-C4'-O4'	-5.54	102.46	109.10
1	0	1120	U	C5'-C4'-C3'	-5.52	107.17	116.00
1	0	1829	A	N9-C1'-C2'	-5.47	105.98	112.00
14	L	126	HIS	CB-CA-C	-5.44	99.53	110.40
2	9	103	A	C4'-C3'-C2'	-5.38	97.22	102.60
1	0	2313	C	C5'-C4'-O4'	5.31	115.47	109.10
1	0	1819	G	C4'-C3'-C2'	-5.30	97.30	102.60
1	0	1592	G	N9-C1'-C2'	5.27	120.85	114.00
1	0	841	A	C1'-O4'-C4'	-5.21	105.73	109.90
2	9	103	A	C1'-O4'-C4'	-5.15	105.78	109.90
2	9	24	U	C4'-C3'-C2'	5.11	107.71	102.60
1	0	1165	G	OP1-P-OP2	5.11	127.26	119.60
16	N	66	GLY	N-CA-C	5.04	125.70	113.10
20	R	27	ALA	N-CA-C	-5.03	97.41	111.00
1	0	1563	G	C4'-C3'-O3'	5.01	123.03	113.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1563	G	C3'

All (64) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1164	U	Sidechain
1	0	1192	A	Sidechain
1	0	1292	G	Sidechain
1	0	1340	G	Sidechain
1	0	1342	C	Sidechain
1	0	1351	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	1417	G	Sidechain
1	0	1430	G	Sidechain
1	0	1458	A	Sidechain
1	0	1501	A	Sidechain
1	0	1524	U	Sidechain
1	0	1794	G	Sidechain
1	0	1809	G	Sidechain
1	0	182	G	Sidechain
1	0	1829	A	Sidechain
1	0	1845	A	Sidechain
1	0	1848	G	Sidechain
1	0	1863	G	Sidechain
1	0	1867	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	191	A	Sidechain
1	0	1970	G	Sidechain
1	0	1972	U	Sidechain
1	0	1979	G	Sidechain
1	0	2012	U	Sidechain
1	0	2078	U	Sidechain
1	0	22	U	Sidechain
1	0	221	G	Sidechain
1	0	2316	G	Sidechain
1	0	2395	A	Sidechain
1	0	2412	G	Sidechain
1	0	246	G	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2526	C	Sidechain
1	0	2543	G	Sidechain
1	0	2552	C	Sidechain
1	0	2564	G	Sidechain
1	0	2607	U	Sidechain
1	0	2615	U	Sidechain
1	0	2630	G	Sidechain
1	0	270	U	Sidechain
1	0	2842	G	Sidechain
1	0	332	G	Sidechain
1	0	333	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	396	U	Sidechain
1	0	452	G	Sidechain
1	0	469	G	Sidechain
1	0	470	U	Sidechain
1	0	471	G	Sidechain
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	619	U	Sidechain
1	0	639	A	Sidechain
1	0	795	G	Sidechain
1	0	817	G	Sidechain
1	0	867	A	Sidechain
1	0	868	G	Sidechain
2	9	39	U	Sidechain
2	9	87	U	Sidechain

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	0	59017	0	29807	760	0
2	9	2600	0	1326	78	0
3	A	1754	0	1763	109	0
4	B	2624	0	2533	176	0
5	C	1858	0	1816	105	0
6	D	1094	0	1085	130	0
7	E	1357	0	1266	79	0
8	F	885	0	854	59	0
9	G	240	0	231	18	0
10	H	1215	0	1215	150	0
11	I	1119	0	1098	62	0
12	J	993	0	1027	56	0
13	K	1114	0	1072	55	0
14	L	1605	0	1676	141	0
15	M	1444	0	1401	119	0
16	N	864	0	873	31	0
17	O	1133	0	1127	38	0
18	P	734	0	728	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Q	1149	0	1122	49	0
20	R	641	0	605	21	0
21	S	949	0	923	52	0
22	T	410	0	364	31	0
23	U	499	0	511	28	0
24	V	1195	0	1137	91	0
25	W	654	0	653	44	0
26	X	1130	0	1133	52	0
27	Y	563	0	597	53	0
28	Z	430	0	426	22	0
29	1	393	0	406	32	0
30	2	755	0	728	36	0
31	0	109	0	0	0	0
31	2	1	0	0	0	0
31	9	1	0	0	0	0
31	A	2	0	0	0	0
31	B	1	0	0	0	0
31	J	1	0	0	0	0
31	S	1	0	0	0	0
31	X	1	0	0	0	0
32	0	2	0	0	0	0
33	0	72	0	0	0	0
33	9	2	0	0	0	0
33	A	1	0	0	0	0
33	C	1	0	0	0	0
33	H	2	0	0	0	0
33	I	1	0	0	0	0
33	K	1	0	0	0	0
33	L	1	0	0	0	0
33	P	1	0	0	0	0
33	Q	2	0	0	0	0
33	R	1	0	0	0	0
33	S	1	0	0	0	0
34	0	10	0	0	0	0
34	2	1	0	0	0	0
34	A	1	0	0	0	0
34	B	1	0	0	0	0
34	I	3	0	0	1	0
34	K	1	0	0	0	0
34	L	1	0	0	1	0
34	M	1	0	0	0	0
34	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	Q	1	0	0	0	0
34	X	1	0	0	0	0
35	2	1	0	0	0	0
35	N	1	0	0	0	0
35	T	1	0	0	0	0
35	Y	1	0	0	0	0
35	Z	1	0	0	0	0
36	0	5938	0	0	173	0
36	1	40	0	0	6	0
36	2	72	0	0	10	0
36	9	135	0	0	14	0
36	A	126	0	0	20	0
36	B	150	0	0	30	0
36	C	172	0	0	30	0
36	D	53	0	0	18	0
36	E	46	0	0	12	0
36	F	28	0	0	7	0
36	G	21	0	0	4	0
36	H	74	0	0	21	0
36	I	56	0	0	5	0
36	J	62	0	0	13	0
36	K	80	0	0	17	0
36	L	127	0	0	19	0
36	M	70	0	0	16	0
36	N	43	0	0	6	0
36	O	68	0	0	1	0
36	P	53	0	0	1	0
36	Q	81	0	0	9	0
36	R	32	0	0	5	0
36	S	39	0	0	5	0
36	T	25	0	0	6	0
36	U	15	0	0	4	0
36	V	67	0	0	10	0
36	W	29	0	0	3	0
36	X	99	0	0	15	0
36	Y	39	0	0	12	0
36	Z	53	0	0	1	0
All	All	98543	0	59503	2453	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 16.

All (2453) 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)
1:O:1160:G:H5'	1:O:1161:A:H5'	1.26	1.14
10:H:86:ARG:NH1	10:H:133:ILE:HG13	1.62	1.12
5:C:5:ILE:HD11	5:C:16:VAL:HG23	1.35	1.07
25:W:37:LEU:HD13	25:W:85:VAL:HG21	1.29	1.06
1:O:960:G:H4'	36:O:6956:HOH:O	1.54	1.06
5:C:236:THR:HG22	5:C:239:ALA:H	1.02	1.06
1:O:1134:G:H4'	10:H:151:MET:HE1	1.34	1.05
21:S:71:VAL:HG11	21:S:90:PRO:HB3	1.39	1.03
2:9:23:U:H4'	2:9:24:U:OP2	1.54	1.02
10:H:162:SER:HB2	10:H:163:PRO:HD3	1.37	1.02
23:U:12:THR:HG22	23:U:15:GLU:HG3	1.40	1.02
6:D:134:LEU:HD11	6:D:166:ILE:HD11	1.39	1.02
1:O:156:C:H5''	14:L:171:ARG:HD3	1.39	1.01
1:O:1242:A:H5'	11:I:82:THR:HG23	1.42	1.01
1:O:871:G:C8	1:O:871:G:H5'	1.94	1.01
14:L:164:THR:HG22	14:L:167:GLY:H	1.23	1.00
1:O:1751:G:H2'	1:O:1752:G:H5''	1.43	1.00
10:H:26:LYS:HD2	10:H:28:ILE:HD12	1.41	1.00
10:H:45:GLN:HB3	10:H:163:PRO:HD2	1.38	1.00
1:O:21:G:H5'	19:Q:2:ILE:HA	1.45	0.99
2:9:6:C:H5''	15:M:37:ARG:NH1	1.78	0.99
1:O:856:G:H2'	36:O:4940:HOH:O	1.61	0.99
2:9:56:A:H2'	2:9:57:A:H5''	1.45	0.99
10:H:86:ARG:HH11	10:H:133:ILE:HG13	0.84	0.99
27:Y:10:ARG:HA	36:Y:8415:HOH:O	1.62	0.98
10:H:86:ARG:HH11	10:H:133:ILE:CG1	1.77	0.98
12:J:81:ARG:HB2	12:J:87:ARG:HH11	1.24	0.98
2:9:76:G:H3'	2:9:77:A:H5''	1.46	0.98
17:O:115:SER:H	17:O:118:GLN:HE21	1.02	0.97
12:J:10:GLN:NE2	12:J:10:GLN:H	1.60	0.97
12:J:39:GLY:HA2	36:J:4183:HOH:O	1.63	0.97
1:O:870:G:H2'	1:O:871:G:H5''	1.46	0.97
2:9:3:A:O5'	2:9:3:A:H2'	1.62	0.97
4:B:140:LEU:HA	36:B:8583:HOH:O	1.63	0.95
27:Y:38:LYS:HE2	27:Y:45:LYS:HE2	1.46	0.95
24:V:88:THR:HB	36:V:6679:HOH:O	1.66	0.95
2:9:6:C:H5''	15:M:37:ARG:HH12	1.32	0.95
14:L:102:GLU:OE1	14:L:164:THR:HG21	1.67	0.95
11:I:76:ASP:HA	36:I:5907:HOH:O	1.67	0.95
12:J:29:LEU:HB3	12:J:55:VAL:HG11	1.46	0.95
5:C:115:LEU:HD13	5:C:223:LEU:HD21	1.49	0.94
14:L:52:LEU:HD11	36:L:8616:HOH:O	1.65	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:83:LEU:HD13	15:M:175:LEU:HD23	1.48	0.94
26:X:200:THR:HG22	26:X:201:GLU:HG3	1.50	0.93
6:D:154:LYS:HD2	6:D:154:LYS:H	1.34	0.93
1:O:871:G:H8	1:O:871:G:H5'	1.30	0.93
24:V:88:THR:HG22	24:V:89:ASP:H	1.33	0.93
20:R:57:THR:HG22	20:R:59:ASP:H	1.34	0.92
5:C:127:ARG:NH2	5:C:225:PRO:HG2	1.85	0.92
24:V:137:GLN:HE21	24:V:141:HIS:HE1	1.12	0.92
4:B:264:GLU:HG2	4:B:267:LYS:HE2	1.50	0.92
5:C:236:THR:HG22	5:C:239:ALA:N	1.85	0.92
1:O:1835:U:H5	1:O:1840:A:N7	1.68	0.92
36:O:3976:HOH:O	14:L:146:GLN:HG2	1.69	0.91
14:L:106:ASN:ND2	34:L:8518:CL:CL	2.40	0.91
4:B:86:ALA:HA	36:B:8583:HOH:O	1.68	0.91
12:J:10:GLN:N	12:J:10:GLN:HE21	1.67	0.91
10:H:29:ALA:HB3	10:H:65:ARG:HH12	1.33	0.90
1:O:542:A:H5'	1:O:542:A:H8	1.35	0.90
15:M:47:LEU:HD11	15:M:127:LEU:HD21	1.52	0.89
15:M:144:GLY:O	15:M:147:ILE:HG22	1.70	0.89
15:M:23:ARG:HD3	36:M:8549:HOH:O	1.72	0.89
5:C:2:GLN:HB3	36:C:8335:HOH:O	1.73	0.89
36:O:4373:HOH:O	14:L:14:ARG:HG2	1.73	0.89
12:J:81:ARG:HB2	12:J:87:ARG:NH1	1.88	0.88
15:M:87:LEU:HD12	15:M:186:LEU:HD21	1.54	0.88
24:V:6:GLN:HB2	24:V:26:ILE:HD12	1.53	0.88
23:U:42:ASN:HB3	36:U:7247:HOH:O	1.74	0.88
4:B:212:GLN:HB2	4:B:257:THR:HG21	1.53	0.88
3:A:199:HIS:HD2	3:A:201:PHE:H	1.20	0.88
1:O:1116:U:H3	1:O:1246:A:H62	1.20	0.87
1:O:645:U:OP2	13:K:4:LYS:HE2	1.73	0.87
24:V:88:THR:HG23	24:V:110:GLN:NE2	1.89	0.87
1:O:1164:U:H3	1:O:1192:A:H2	1.21	0.87
3:A:211:LYS:HB3	3:A:212:PRO:HD2	1.55	0.87
10:H:27:LYS:H	10:H:58:HIS:HD2	1.22	0.87
10:H:162:SER:HB2	10:H:163:PRO:CD	2.04	0.87
6:D:25:MET:HE2	6:D:41:LEU:HG	1.57	0.87
1:O:1701:A:H4'	1:O:1702:U:H5''	1.55	0.87
27:Y:38:LYS:HG2	27:Y:45:LYS:HG2	1.54	0.86
27:Y:46:LYS:HD3	27:Y:59:HIS:HB2	1.58	0.86
2:9:25:G:H3'	2:9:26:C:H5'	1.57	0.86
5:C:132:ASP:HB3	36:C:8365:HOH:O	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1165:G:H4'	1:0:1174:A:O2'	1.75	0.86
4:B:7:ARG:HG2	4:B:7:ARG:HH11	1.39	0.86
6:D:64:ARG:HG2	6:D:67:ASP:HB3	1.56	0.85
2:9:23:U:H3'	36:9:8474:HOH:O	1.76	0.85
10:H:55:GLN:HE21	10:H:124:ARG:HE	1.22	0.85
1:0:2812:A:H2	1:0:2814:A:H62	1.20	0.85
1:0:2716:G:H5''	4:B:206:THR:HG21	1.59	0.85
5:C:236:THR:CG2	5:C:239:ALA:H	1.88	0.85
12:J:10:GLN:H	12:J:10:GLN:HE21	0.86	0.85
16:N:42:GLU:HB2	36:N:2176:HOH:O	1.74	0.85
1:0:1474:C:H6	1:0:1474:C:H5'	1.42	0.85
6:D:25:MET:HE1	6:D:37:ALA:HB1	1.57	0.85
2:9:24:U:O2'	2:9:25:G:H4'	1.76	0.84
10:H:49:VAL:O	10:H:157:ILE:HG23	1.76	0.84
1:0:1329:A:H2	36:0:4193:HOH:O	1.60	0.84
1:0:381:G:H5''	36:0:3826:HOH:O	1.75	0.84
4:B:238:ASN:HD22	4:B:240:GLY:H	1.26	0.84
5:C:214:THR:HG21	36:C:8403:HOH:O	1.78	0.84
19:Q:99:ALA:HB1	19:Q:109:MET:HE1	1.59	0.84
5:C:78:ARG:HH11	5:C:78:ARG:HG3	1.43	0.84
12:J:74:VAL:HG11	12:J:113:ILE:HG12	1.58	0.84
15:M:7:LYS:HE3	18:P:21:ARG:O	1.77	0.84
2:9:3:A:O5'	2:9:3:A:C2'	2.23	0.83
4:B:321:PRO:HA	36:B:8662:HOH:O	1.78	0.83
19:Q:8:ALA:HB1	19:Q:13:THR:HG21	1.59	0.83
13:K:133:VAL:HA	36:K:8572:HOH:O	1.77	0.83
7:E:97:VAL:HG12	36:E:4191:HOH:O	1.77	0.83
29:1:41:HIS:H	29:1:45:ASN:HD22	1.25	0.83
1:0:560:C:H42	1:0:597:A:H61	1.24	0.83
1:0:2717:C:H2'	1:0:2718:C:H5''	1.60	0.83
1:0:2506:A:HO2'	1:0:2507:G:H8	0.87	0.83
1:0:2717:C:C2'	1:0:2718:C:H5''	2.09	0.83
6:D:105:SER:HB2	6:D:131:THR:HG23	1.59	0.83
15:M:113:SER:HB2	36:M:8562:HOH:O	1.78	0.83
14:L:172:GLY:O	14:L:183:VAL:HG11	1.79	0.82
27:Y:58:GLY:HA3	36:Y:8439:HOH:O	1.80	0.82
8:F:91:VAL:HG12	8:F:92:GLY:H	1.45	0.82
1:0:214:U:H5'	36:0:5660:HOH:O	1.78	0.82
1:0:1184:C:H1'	36:0:6994:HOH:O	1.79	0.82
3:A:100:PRO:HG2	3:A:103:VAL:HG21	1.61	0.82
4:B:201:ASP:HB2	4:B:312:ARG:HD2	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:4:ALA:HB3	36:H:8364:HOH:O	1.80	0.82
1:0:870:G:C2'	1:0:871:G:H5''	2.10	0.82
12:J:14:LYS:HB2	12:J:45:PRO:HG2	1.61	0.82
1:0:962:C:H1'	15:M:5:ARG:NH1	1.93	0.82
7:E:15:GLN:HG3	7:E:20:ILE:HG12	1.60	0.81
13:K:79:ASP:HB3	36:K:8558:HOH:O	1.81	0.81
10:H:139:ASP:N	10:H:140:PRO:HD3	1.95	0.81
3:A:191:GLY:HA2	3:A:194:MET:CE	2.10	0.81
23:U:1:THR:HG23	23:U:2:VAL:H	1.44	0.81
1:0:1372:A:H3'	36:0:6711:HOH:O	1.79	0.81
17:O:115:SER:H	17:O:118:GLN:NE2	1.79	0.81
1:0:541:C:H2'	1:0:542:A:H5''	1.62	0.81
30:2:62:THR:HB	36:2:8550:HOH:O	1.79	0.81
2:9:25:G:H3'	2:9:26:C:C5'	2.10	0.80
1:0:1667:A:H8	1:0:1667:A:H5'	1.45	0.80
29:1:22:PRO:HB2	29:1:24:TRP:CD1	2.17	0.80
13:K:68:GLU:HA	36:K:8543:HOH:O	1.82	0.80
1:0:506:G:H22	1:0:509:A:C5'	1.94	0.80
23:U:12:THR:HG22	23:U:15:GLU:CG	2.11	0.80
14:L:152:ARG:HG3	36:L:8555:HOH:O	1.82	0.80
15:M:164:ASP:CG	15:M:167:ASP:HA	2.02	0.80
1:0:1116:U:O2'	1:0:1118:A:H2	1.65	0.80
1:0:1191:A:N1	1:0:1206:U:O4	2.14	0.80
24:V:88:THR:HG23	24:V:110:GLN:HE21	1.45	0.80
24:V:4:LEU:HD22	24:V:52:VAL:HG21	1.64	0.79
36:0:6394:HOH:O	14:L:178:LYS:HB2	1.81	0.79
1:0:346:U:H4'	36:0:6364:HOH:O	1.82	0.79
5:C:5:ILE:HD11	5:C:16:VAL:CG2	2.10	0.79
6:D:20:LYS:HA	6:D:75:LEU:O	1.82	0.79
30:2:70:ARG:HD3	36:2:8539:HOH:O	1.81	0.79
1:0:288:A:H61	1:0:364:C:H42	1.31	0.79
3:A:192:VAL:HB	36:A:8596:HOH:O	1.81	0.79
36:0:4053:HOH:O	10:H:151:MET:HE2	1.80	0.79
15:M:49:THR:HG22	15:M:56:ASP:HB2	1.64	0.79
1:0:1160:G:H5'	1:0:1161:A:C5'	2.11	0.78
21:S:61:GLU:HG3	36:S:3851:HOH:O	1.81	0.78
24:V:137:GLN:HE21	24:V:141:HIS:CE1	2.01	0.78
1:0:2710:U:H1'	36:0:7157:HOH:O	1.84	0.78
1:0:871:G:H8	1:0:871:G:C5'	1.96	0.78
24:V:88:THR:HG22	24:V:89:ASP:N	1.98	0.78
24:V:122:ARG:HG2	24:V:122:ARG:HH11	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2506:A:O2'	1:0:2507:G:H8	1.65	0.78
27:Y:40:PRO:HD3	27:Y:47:LEU:HD11	1.66	0.78
1:0:1160:G:C5'	1:0:1161:A:H5'	2.10	0.78
1:0:1119:G:H22	1:0:1246:A:H2	1.26	0.78
1:0:1701:A:H5'	36:0:5802:HOH:O	1.84	0.78
29:1:39:ARG:HG2	36:1:3143:HOH:O	1.83	0.78
5:C:236:THR:HG21	36:C:8376:HOH:O	1.82	0.78
1:0:1116:U:HO2'	1:0:1118:A:H2	0.82	0.78
36:0:6950:HOH:O	21:S:9:LYS:HB2	1.82	0.78
3:A:88:ILE:HD13	3:A:100:PRO:HD3	1.65	0.78
14:L:87:MET:HB3	30:2:46:ILE:HG21	1.65	0.78
29:1:24:TRP:CD1	36:1:6863:HOH:O	2.36	0.78
10:H:55:GLN:NE2	10:H:124:ARG:HE	1.80	0.78
1:0:544:G:H2'	1:0:545:G:H5''	1.65	0.78
6:D:27:ILE:HG22	6:D:28:GLY:H	1.48	0.77
7:E:81:GLU:HG2	7:E:134:SER:HB3	1.65	0.77
1:0:559:U:H5'	1:0:559:U:H6	1.49	0.77
36:0:4346:HOH:O	11:I:47:THR:HB	1.83	0.77
36:0:9211:HOH:O	4:B:254:GLN:HG3	1.84	0.77
24:V:149:LEU:HG	24:V:153:MET:HE2	1.67	0.77
30:2:70:ARG:HG2	30:2:77:ALA:HB2	1.65	0.77
26:X:187:VAL:HG23	26:X:192:ASP:HB2	1.65	0.77
1:0:545:G:H8	1:0:545:G:H5'	1.48	0.77
2:9:56:A:C2'	2:9:57:A:H5''	2.14	0.77
2:9:14:G:H5'	2:9:14:G:H8	1.50	0.77
1:0:284:C:H4'	1:0:285:A:O5'	1.83	0.77
36:0:3295:HOH:O	14:L:189:VAL:HG21	1.84	0.77
10:H:33:MET:HB2	10:H:83:PHE:HB3	1.67	0.77
12:J:74:VAL:HG13	12:J:113:ILE:HG23	1.67	0.77
1:0:1625:U:H4'	36:0:4177:HOH:O	1.84	0.77
10:H:59:ASN:HD22	10:H:59:ASN:N	1.82	0.77
7:E:20:ILE:HD11	7:E:40:VAL:HG11	1.66	0.77
1:0:2890:A:H1'	22:T:56:ARG:NH2	2.00	0.77
1:0:536:A:H3'	36:0:4557:HOH:O	1.85	0.77
14:L:87:MET:HB3	30:2:46:ILE:HD13	1.66	0.76
36:0:6291:HOH:O	15:M:4:PRO:HD2	1.85	0.76
24:V:68:THR:HG23	24:V:69:ARG:HG2	1.67	0.76
27:Y:49:ARG:HD2	36:Y:8430:HOH:O	1.84	0.76
3:A:200:PRO:HG2	3:A:225:VAL:HG21	1.67	0.76
8:F:96:ALA:HA	36:F:3111:HOH:O	1.83	0.76
1:0:1130:U:H5'	36:0:7208:HOH:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:190:MET:HE2	4:B:194:PHE:CD1	2.21	0.76
14:L:139:PRO:O	14:L:140:ALA:HB3	1.86	0.76
8:F:91:VAL:HG12	8:F:92:GLY:N	2.01	0.76
5:C:242:GLU:HG3	36:C:8384:HOH:O	1.85	0.76
1:0:1751:G:C2'	1:0:1752:G:H5''	2.15	0.76
15:M:164:ASP:OD2	15:M:167:ASP:HA	1.85	0.76
4:B:62:ARG:HA	4:B:65:MET:HE3	1.67	0.76
14:L:35:PRO:HG2	14:L:38:VAL:HG23	1.67	0.76
8:F:50:VAL:HG13	8:F:60:VAL:HG11	1.68	0.76
36:0:3235:HOH:O	14:L:157:LEU:HD11	1.85	0.76
20:R:51:GLN:HE21	20:R:53:ASN:HD21	1.34	0.76
2:9:23:U:H6	2:9:23:U:H5''	1.50	0.75
2:9:3:A:N6	2:9:22:G:H1'	2.01	0.75
1:0:1191:A:C2	1:0:1206:U:O4	2.40	0.75
16:N:47:ARG:HH11	16:N:47:ARG:HG3	1.51	0.75
3:A:35:GLY:O	3:A:36:ASP:HB3	1.85	0.75
36:0:5814:HOH:O	6:D:99:ASP:HA	1.85	0.75
1:0:871:G:C8	1:0:871:G:C5'	2.70	0.75
10:H:59:ASN:HD22	10:H:59:ASN:H	1.34	0.75
1:0:1209:C:H4'	36:0:4791:HOH:O	1.85	0.75
11:I:93:ARG:HH11	11:I:93:ARG:HB3	1.49	0.75
3:A:105:VAL:HG11	3:A:154:ALA:HB1	1.69	0.75
1:0:541:C:C2'	1:0:542:A:H5''	2.17	0.75
19:Q:9:ASP:O	19:Q:13:THR:HB	1.87	0.74
1:0:2054:A:N3	19:Q:128:ARG:NH2	2.35	0.74
24:V:122:ARG:HH21	24:V:154:ARG:HD2	1.51	0.74
14:L:87:MET:HG2	30:2:46:ILE:HG21	1.69	0.74
26:X:189:ASN:HA	26:X:217:ILE:HD11	1.67	0.74
19:Q:18:LEU:HB2	19:Q:143:VAL:HG12	1.67	0.74
4:B:18:ARG:HG3	4:B:256:GLN:HG3	1.67	0.74
25:W:78:GLU:HG2	25:W:79:GLU:H	1.52	0.74
4:B:41:PHE:CD1	4:B:79:MET:HE2	2.23	0.74
24:V:72:PRO:HG2	24:V:77:ALA:HB3	1.69	0.74
20:R:57:THR:HG22	20:R:59:ASP:N	2.02	0.74
23:U:39:ALA:N	23:U:40:PRO:HD2	2.03	0.74
1:0:2637:A:H5'	36:0:8785:HOH:O	1.88	0.74
1:0:2768:A:H2'	1:0:2769:C:O4'	1.87	0.74
1:0:21:G:C5'	19:Q:2:ILE:HA	2.17	0.74
5:C:115:LEU:HD21	5:C:243:VAL:HG13	1.70	0.74
1:0:289:G:H22	1:0:363:A:H2	1.36	0.74
19:Q:39:THR:HG22	19:Q:42:GLU:H	1.53	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1634:G:H3'	36:0:3402:HOH:O	1.87	0.74
10:H:162:SER:CB	10:H:163:PRO:HD3	2.17	0.73
10:H:150:LYS:HE2	36:H:8381:HOH:O	1.89	0.73
6:D:146:LYS:NZ	15:M:107:ASN:HD21	1.86	0.73
6:D:19:GLU:O	6:D:20:LYS:HG2	1.89	0.73
1:0:2840:A:OP1	4:B:211:THR:HG23	1.88	0.73
1:0:1351:G:OP1	5:C:96:LYS:NZ	2.21	0.73
10:H:165:GLY:HA3	36:H:8394:HOH:O	1.87	0.73
5:C:1:MET:HG2	5:C:2:GLN:H	1.53	0.73
3:A:191:GLY:HA2	3:A:194:MET:HE2	1.67	0.73
8:F:50:VAL:CG1	8:F:60:VAL:HG11	2.19	0.73
17:O:115:SER:OG	17:O:118:GLN:HG3	1.88	0.73
1:0:1328:A:OP1	26:X:169:ARG:HD2	1.87	0.73
6:D:88:LEU:HB2	6:D:89:PRO:HD3	1.71	0.73
30:2:65:THR:HG23	30:2:67:LEU:HG	1.70	0.73
1:0:2586:U:H3	1:0:2592:G:H22	1.35	0.73
10:H:46:VAL:HG12	10:H:146:TRP:HZ3	1.53	0.73
1:0:431:G:P	14:L:48:ARG:HH12	2.11	0.73
13:K:143:THR:HG22	13:K:144:ASP:N	2.03	0.73
5:C:236:THR:HA	36:C:8450:HOH:O	1.89	0.73
6:D:64:ARG:CG	6:D:67:ASP:HB3	2.18	0.73
5:C:104:ASP:HA	5:C:107:ARG:HH12	1.53	0.73
15:M:48:VAL:CG1	15:M:55:ASP:HB3	2.18	0.73
1:0:272:A:H3'	36:0:7061:HOH:O	1.88	0.73
1:0:657:G:OP1	5:C:27:ARG:NH2	2.18	0.73
3:A:131:HIS:O	3:A:132:ASP:HB2	1.89	0.72
1:0:1118:A:H3'	1:0:1118:A:C8	2.24	0.72
27:Y:37:HIS:HB2	27:Y:47:LEU:HB2	1.71	0.72
1:0:1450:C:H4'	1:0:1451:C:OP2	1.88	0.72
9:G:23:ILE:HD13	9:G:67:LEU:HD23	1.69	0.72
14:L:104:ARG:O	14:L:108:LYS:HE2	1.88	0.72
1:0:1118:A:H3'	1:0:1118:A:H8	1.54	0.72
1:0:1194:A:C6	1:0:1206:U:C4	2.78	0.72
1:0:506:G:H22	1:0:509:A:H5'	1.53	0.72
24:V:65:VAL:HA	24:V:68:THR:HG22	1.72	0.72
10:H:14:TYR:H	10:H:91:HIS:CE1	2.07	0.72
10:H:142:VAL:HG13	36:H:8379:HOH:O	1.89	0.72
1:0:1666:C:H2'	1:0:1667:A:H5'	1.71	0.72
14:L:164:THR:HG22	14:L:167:GLY:N	2.03	0.72
1:0:31:C:H2'	36:0:7224:HOH:O	1.89	0.72
1:0:1187:U:HO2'	1:0:1189:A:H2	1.35	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:221:GLN:HE22	12:J:42:ASN:HD22	1.37	0.72
1:O:1594:C:OP2	17:O:120:ARG:HD2	1.89	0.72
24:V:21:LEU:HD22	24:V:26:ILE:HD11	1.72	0.71
3:A:199:HIS:CD2	3:A:201:PHE:H	2.07	0.71
1:O:877:G:H5'	1:O:878:G:OP1	1.89	0.71
17:O:115:SER:N	17:O:118:GLN:HE21	1.84	0.71
1:O:1771:U:H4'	27:Y:20:LEU:HD21	1.71	0.71
10:H:41:THR:HA	36:H:8392:HOH:O	1.88	0.71
36:O:3192:HOH:O	14:L:79:LYS:HD3	1.90	0.71
3:A:153:ARG:HH11	3:A:153:ARG:HB2	1.54	0.71
2:9:6:C:OP1	15:M:37:ARG:NH1	2.23	0.71
14:L:106:ASN:HD22	14:L:114:VAL:HG23	1.53	0.71
22:T:14:GLU:O	22:T:17:THR:HB	1.91	0.71
10:H:26:LYS:HG2	10:H:28:ILE:H	1.55	0.71
14:L:87:MET:HB2	14:L:91:ILE:HD11	1.72	0.71
1:O:183:A:H5'	14:L:157:LEU:HD12	1.73	0.71
1:O:1170:U:O2'	1:O:1172:G:N7	2.21	0.71
10:H:47:GLU:HB3	10:H:133:ILE:CD1	2.20	0.71
14:L:87:MET:CB	30:2:46:ILE:HG21	2.20	0.71
13:K:148:GLU:HA	36:K:8571:HOH:O	1.90	0.71
3:A:210:GLY:HA3	36:A:8590:HOH:O	1.90	0.71
14:L:35:PRO:CG	14:L:38:VAL:HG23	2.20	0.71
3:A:81:GLN:HB2	3:A:92:ASN:ND2	2.05	0.71
1:O:2291:A:C8	1:O:2309:C:H5'	2.25	0.71
1:O:1119:G:N2	1:O:1246:A:C2	2.55	0.71
19:Q:99:ALA:HB1	19:Q:109:MET:CE	2.20	0.71
11:I:107:ASN:HD21	11:I:109:TYR:HB2	1.56	0.71
7:E:101:GLU:HB2	7:E:116:THR:O	1.91	0.71
12:J:81:ARG:HD3	12:J:87:ARG:NH1	2.06	0.71
1:O:281:U:H2'	1:O:282:C:O4'	1.90	0.71
17:O:59:ARG:NH2	17:O:66:GLN:HE22	1.89	0.70
19:Q:18:LEU:HD12	19:Q:143:VAL:HG11	1.71	0.70
9:G:12:ILE:N	9:G:13:PRO:HD3	2.05	0.70
1:O:2896:A:H5''	36:O:5618:HOH:O	1.90	0.70
15:M:80:SER:HB2	36:M:8537:HOH:O	1.90	0.70
1:O:1166:A:H1'	1:O:1192:A:C2	2.26	0.70
29:1:41:HIS:N	29:1:45:ASN:HD22	1.89	0.70
10:H:137:ASN:O	10:H:139:ASP:N	2.25	0.70
4:B:103:ASP:HB2	36:B:8598:HOH:O	1.89	0.70
11:I:45:VAL:HG23	11:I:130:VAL:O	1.91	0.70
16:N:14:LEU:HD23	16:N:102:ILE:HD11	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:187:VAL:HG23	26:X:192:ASP:CB	2.22	0.70
1:0:1973:A:H5'	1:0:1973:A:H8	1.57	0.70
10:H:3:GLY:HA2	10:H:57:ARG:HH12	1.57	0.70
13:K:136:ALA:HB3	36:K:8572:HOH:O	1.90	0.70
14:L:113:ARG:NH2	14:L:156:ARG:HG2	2.07	0.70
30:2:73:GLU:HB3	36:2:8560:HOH:O	1.91	0.70
3:A:105:VAL:CG1	3:A:154:ALA:HB1	2.21	0.70
5:C:139:VAL:HG13	36:C:8447:HOH:O	1.91	0.70
7:E:68:HIS:O	7:E:72:MET:HG3	1.92	0.70
1:0:2468:A:H61	30:2:48:ASN:HD21	1.38	0.70
1:0:1835:U:C5	1:0:1840:A:N7	2.58	0.69
36:C:8359:HOH:O	16:N:3:THR:HG21	1.92	0.69
2:9:39:U:H1'	2:9:44:A:H61	1.56	0.69
1:0:542:A:H5'	1:0:542:A:C8	2.24	0.69
29:1:18:ASN:HD21	29:1:40:ARG:H	1.41	0.69
1:0:1603:A:H5'	1:0:1605:G:O4'	1.92	0.69
7:E:23:GLU:HG2	7:E:28:SER:HB3	1.75	0.69
14:L:164:THR:HG23	14:L:165:SER:N	2.06	0.69
1:0:236:A:H4'	1:0:237:G:H5'	1.75	0.69
11:I:107:ASN:ND2	11:I:109:TYR:H	1.89	0.69
12:J:22:ASP:HB2	36:J:5264:HOH:O	1.91	0.69
6:D:95:THR:O	6:D:97:GLN:N	2.23	0.69
3:A:190:ARG:NH2	3:A:207:GLN:OE1	2.26	0.69
10:H:71:TYR:C	10:H:73:GLN:H	1.96	0.69
10:H:31:PHE:HE2	10:H:87:LYS:O	1.76	0.69
5:C:140:VAL:HB	36:C:8450:HOH:O	1.93	0.69
1:0:1172:G:H1'	36:0:4485:HOH:O	1.91	0.69
2:9:29:C:H2'	2:9:30:C:H5'	1.75	0.69
5:C:162:VAL:HG12	5:C:192:ILE:HD11	1.73	0.69
9:G:12:ILE:HA	36:G:4499:HOH:O	1.93	0.69
25:W:71:ARG:HB3	25:W:88:GLU:OE1	1.93	0.69
30:2:57:GLY:HA2	36:2:8526:HOH:O	1.92	0.69
27:Y:38:LYS:HE2	27:Y:45:LYS:CE	2.22	0.68
1:0:1474:C:C6	1:0:1474:C:H5'	2.28	0.68
1:0:1377:C:H6	1:0:1377:C:H5'	1.58	0.68
1:0:182:G:H5'	36:0:4666:HOH:O	1.94	0.68
7:E:100:ASP:HB2	36:E:2789:HOH:O	1.93	0.68
10:H:47:GLU:HB3	10:H:133:ILE:HD13	1.75	0.68
6:D:37:ALA:O	6:D:40:ILE:HG12	1.94	0.68
21:S:9:LYS:HE3	21:S:13:ARG:NH1	2.09	0.68
1:0:2346:C:O2'	6:D:52:THR:HG21	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:34:VAL:HG22	12:J:47:ALA:HB2	1.76	0.68
36:O:6982:HOH:O	4:B:211:THR:HG21	1.93	0.68
10:H:53:PRO:HG3	10:H:127:GLY:H	1.59	0.68
1:O:1194:A:N6	1:O:1206:U:C4	2.61	0.68
24:V:149:LEU:HG	24:V:153:MET:CE	2.24	0.68
4:B:51:VAL:CG2	4:B:327:VAL:HG13	2.22	0.68
24:V:13:MET:CE	24:V:17:ILE:HG22	2.24	0.68
3:A:192:VAL:HG13	36:A:8558:HOH:O	1.92	0.68
5:C:236:THR:H	5:C:239:ALA:HB3	1.59	0.68
24:V:21:LEU:HB3	24:V:26:ILE:HG12	1.76	0.68
1:O:711:G:H1'	36:O:6617:HOH:O	1.93	0.68
8:F:63:ILE:HB	8:F:64:PRO:HD3	1.74	0.68
6:D:97:GLN:HG2	6:D:97:GLN:O	1.94	0.68
14:L:52:LEU:HD21	36:L:8616:HOH:O	1.93	0.68
36:9:8462:HOH:O	15:M:147:ILE:HB	1.94	0.68
12:J:74:VAL:CG1	12:J:113:ILE:HG12	2.24	0.68
5:C:246:ARG:NE	36:C:8424:HOH:O	2.27	0.68
19:Q:39:THR:HB	19:Q:42:GLU:HG3	1.74	0.67
7:E:69:ILE:HA	7:E:72:MET:CE	2.24	0.67
11:I:74:ARG:HB3	11:I:74:ARG:HH11	1.57	0.67
24:V:21:LEU:HD22	24:V:26:ILE:CD1	2.25	0.67
14:L:139:PRO:O	14:L:140:ALA:CB	2.40	0.67
4:B:71:VAL:HG11	4:B:296:LEU:HB3	1.75	0.67
23:U:12:THR:CG2	23:U:15:GLU:HG3	2.21	0.67
3:A:33:GLU:O	3:A:34:ASP:HB2	1.94	0.67
3:A:96:LEU:HD22	3:A:128:LEU:HD13	1.75	0.67
1:O:396:U:H1'	36:O:7164:HOH:O	1.95	0.67
4:B:125:GLU:O	4:B:129:ARG:HG3	1.94	0.67
19:Q:111:ILE:HG23	19:Q:145:LEU:HD11	1.76	0.67
24:V:21:LEU:HD21	24:V:48:VAL:HG11	1.76	0.67
8:F:58:GLU:OE1	14:L:27:ARG:NH2	2.23	0.67
1:O:1819:G:H2'	1:O:1820:G:H4'	1.76	0.67
1:O:1505:U:H5'	1:O:1505:U:H6	1.58	0.67
1:O:1205:U:C2'	1:O:1206:U:H5''	2.24	0.67
1:O:1701:A:H4'	1:O:1702:U:C5'	2.24	0.67
10:H:136:VAL:HG22	10:H:137:ASN:O	1.94	0.67
1:O:282:C:H1'	1:O:368:C:N4	2.09	0.67
14:L:34:GLU:HB3	14:L:35:PRO:HD2	1.76	0.67
3:A:36:ASP:OD2	3:A:85:ASP:HB2	1.94	0.67
4:B:51:VAL:HG23	4:B:329:TYR:O	1.95	0.67
1:O:2426:G:H1'	36:O:5611:HOH:O	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:62:ARG:HA	4:B:65:MET:CE	2.24	0.67
23:U:64:GLY:O	23:U:65:ASP:HB2	1.93	0.67
4:B:16:ARG:NH1	36:B:8621:HOH:O	2.28	0.67
1:0:1119:G:H8	11:I:52:GLN:HE22	1.41	0.67
1:0:1209:C:H2'	1:0:1210:G:H8	1.59	0.67
24:V:13:MET:HE3	24:V:17:ILE:HG22	1.76	0.67
8:F:39:SER:HB3	8:F:45:ALA:HB2	1.76	0.67
1:0:2748:G:H2'	36:0:7073:HOH:O	1.94	0.67
1:0:1205:U:H2'	1:0:1206:U:H5''	1.75	0.67
14:L:63:VAL:HG21	14:L:109:PHE:CE1	2.30	0.67
10:H:28:ILE:HA	10:H:62:GLU:OE1	1.94	0.66
5:C:162:VAL:HG13	5:C:232:LEU:HD21	1.77	0.66
27:Y:61:GLY:HA3	36:Y:8427:HOH:O	1.95	0.66
10:H:26:LYS:HD2	10:H:28:ILE:CD1	2.22	0.66
24:V:6:GLN:HB2	24:V:26:ILE:CD1	2.25	0.66
10:H:46:VAL:O	10:H:146:TRP:HH2	1.78	0.66
21:S:47:THR:HB	21:S:100:ASP:HB3	1.77	0.66
26:X:185:VAL:HG12	36:X:8572:HOH:O	1.94	0.66
2:9:14:G:H5'	2:9:14:G:C8	2.29	0.66
1:0:2508:C:H2'	36:0:6273:HOH:O	1.94	0.66
26:X:141:THR:HG23	36:X:8591:HOH:O	1.94	0.66
25:W:76:ARG:HG3	25:W:76:ARG:HH11	1.60	0.66
16:N:32:ARG:O	16:N:32:ARG:HD3	1.94	0.66
9:G:12:ILE:HG13	36:G:6833:HOH:O	1.94	0.66
1:0:1058:A:H2'	1:0:1060:C:H5''	1.77	0.66
8:F:53:ASP:OD1	8:F:80:GLN:HB2	1.96	0.66
17:O:18:LYS:O	17:O:21:VAL:HG22	1.95	0.66
1:0:1730:G:H5'	1:0:1731:C:C5	2.31	0.66
2:9:6:C:C5'	15:M:37:ARG:NH1	2.57	0.66
28:Z:25:LYS:HE2	36:1:7213:HOH:O	1.93	0.66
1:0:1766:U:O2	1:0:1778:A:H5'	1.96	0.66
1:0:2908:A:H2'	1:0:2909:G:O4'	1.96	0.66
1:0:1080:C:H4'	1:0:1081:A:OP1	1.95	0.66
6:D:54:ALA:HB2	6:D:69:ILE:HD12	1.78	0.66
14:L:138:HIS:ND1	14:L:139:PRO:O	2.22	0.66
16:N:87:THR:O	16:N:91:GLN:HG3	1.96	0.66
19:Q:44:VAL:O	19:Q:48:GLU:HG3	1.94	0.66
14:L:149:TRP:O	14:L:152:ARG:HG2	1.95	0.66
1:0:2414:A:H2'	1:0:2415:A:C8	2.30	0.66
10:H:85:ILE:HB	10:H:132:PHE:CE2	2.31	0.66
1:0:1684:A:H1'	29:1:43:ARG:HH22	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2635:A:O2'	1:0:2636:C:H5'	1.96	0.66
36:0:4461:HOH:O	2:9:103:A:H4'	1.95	0.66
4:B:307:ARG:HB2	4:B:307:ARG:HH11	1.59	0.66
1:0:69:A:H5'	1:0:69:A:C8	2.31	0.66
10:H:150:LYS:HB2	10:H:157:ILE:HD12	1.78	0.65
17:O:10:ALA:HA	17:O:13:VAL:HG12	1.78	0.65
4:B:36:PRO:HA	4:B:168:GLY:CA	2.26	0.65
1:0:1191:A:H3'	1:0:1192:A:H5''	1.79	0.65
1:0:2533:C:H6	1:0:2533:C:H5'	1.61	0.65
1:0:541:C:H2'	1:0:542:A:C5'	2.26	0.65
29:1:41:HIS:H	29:1:45:ASN:ND2	1.94	0.65
4:B:204:GLY:HA3	36:B:8659:HOH:O	1.95	0.65
5:C:78:ARG:HG3	5:C:78:ARG:NH1	2.11	0.65
1:0:282:C:O2'	1:0:283:U:H5'	1.96	0.65
3:A:69:LEU:HD21	3:A:120:ARG:HB3	1.77	0.65
12:J:32:ILE:HD11	12:J:56:SER:HB3	1.77	0.65
15:M:183:ASP:OD2	15:M:186:LEU:HD12	1.95	0.65
6:D:69:ILE:O	6:D:69:ILE:HG22	1.96	0.65
1:0:2505:G:O2'	1:0:2506:A:H5'	1.97	0.65
27:Y:39:CYS:HA	27:Y:47:LEU:HD11	1.77	0.65
16:N:14:LEU:CD2	16:N:102:ILE:HD11	2.26	0.65
1:0:20:G:H21	19:Q:117:HIS:HD2	1.45	0.65
4:B:162:MET:HE3	4:B:308:LEU:HD21	1.79	0.65
4:B:141:ARG:HD2	4:B:163:GLU:OE2	1.97	0.65
21:S:41:ARG:HH11	21:S:41:ARG:HG2	1.60	0.65
1:0:2878:U:H2'	1:0:2879:A:O4'	1.96	0.65
3:A:191:GLY:HA2	3:A:194:MET:HE3	1.79	0.65
4:B:190:MET:HE2	4:B:194:PHE:HD1	1.60	0.65
14:L:104:ARG:O	14:L:108:LYS:HG2	1.97	0.65
6:D:99:ASP:HB2	6:D:103:ASN:HB2	1.79	0.65
1:0:1666:C:O2'	1:0:1667:A:H5''	1.97	0.65
21:S:9:LYS:HE3	21:S:13:ARG:HH11	1.62	0.65
21:S:53:GLY:HA3	36:S:6384:HOH:O	1.94	0.65
1:0:2690:U:O2'	7:E:111:LYS:HE3	1.97	0.65
10:H:166:ASN:N	10:H:166:ASN:HD22	1.94	0.65
5:C:115:LEU:O	5:C:118:THR:HB	1.97	0.65
2:9:49:G:H5''	36:9:8462:HOH:O	1.97	0.65
24:V:4:LEU:O	24:V:32:CYS:HA	1.97	0.65
1:0:2756:U:H3	1:0:2896:A:H2	1.43	0.65
11:I:131:THR:HG22	11:I:134:GLU:H	1.61	0.65
21:S:32:ARG:NH1	21:S:38:ARG:HH12	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:23:U:H5''	2:9:23:U:C6	2.32	0.65
10:H:3:GLY:HA2	10:H:57:ARG:NH1	2.11	0.65
6:D:23:VAL:HG22	6:D:73:VAL:HB	1.79	0.65
14:L:94:LYS:HE3	36:L:8582:HOH:O	1.95	0.65
36:0:7116:HOH:O	27:Y:31:ILE:HG13	1.96	0.65
1:0:299:U:H5'	36:0:6860:HOH:O	1.97	0.65
4:B:179:LEU:O	4:B:183:GLU:HG2	1.97	0.65
7:E:11:VAL:HG12	7:E:12:ASP:N	2.12	0.64
1:0:2783:A:H3'	36:0:4742:HOH:O	1.96	0.64
8:F:99:THR:HA	36:F:3461:HOH:O	1.96	0.64
6:D:135:VAL:HG22	6:D:136:ARG:H	1.62	0.64
4:B:36:PRO:HA	4:B:168:GLY:HA3	1.79	0.64
1:0:603:A:H5''	1:0:604:G:OP1	1.97	0.64
25:W:72:VAL:HG22	25:W:85:VAL:HG12	1.78	0.64
10:H:27:LYS:N	10:H:58:HIS:HD2	1.92	0.64
2:9:69:U:OP1	15:M:4:PRO:HG3	1.98	0.64
14:L:80:GLY:O	14:L:81:ARG:HD3	1.97	0.64
7:E:6:GLU:HA	7:E:46:THR:HG22	1.80	0.64
23:U:44:GLY:O	23:U:48:GLU:HG2	1.98	0.64
5:C:76:ARG:HD3	36:C:8369:HOH:O	1.95	0.64
1:0:2672:C:H1'	36:B:8639:HOH:O	1.97	0.64
6:D:25:MET:CE	6:D:37:ALA:HB1	2.27	0.64
1:0:1701:A:H5''	1:0:1702:U:H3'	1.80	0.64
7:E:15:GLN:NE2	7:E:40:VAL:O	2.29	0.64
7:E:7:ILE:HD11	7:E:11:VAL:C	2.18	0.64
3:A:223:ARG:HG3	36:A:8604:HOH:O	1.97	0.64
1:0:259:G:H21	14:L:58:GLN:NE2	1.96	0.64
10:H:69:ASN:O	10:H:72:VAL:HG12	1.98	0.64
4:B:185:GLY:HA2	36:B:8638:HOH:O	1.97	0.64
24:V:154:ARG:C	36:V:4276:HOH:O	2.35	0.64
2:9:13:A:O2'	2:9:14:G:H5''	1.98	0.64
1:0:1778:A:H2'	1:0:1779:A:H5'	1.80	0.64
1:0:2676:C:H4'	11:I:70:PHE:CE1	2.33	0.64
1:0:2438:G:H5'	36:0:5690:HOH:O	1.97	0.64
20:R:43:GLU:HB3	36:R:8341:HOH:O	1.97	0.64
24:V:38:THR:HG22	36:V:3580:HOH:O	1.98	0.64
10:H:140:PRO:HB3	36:H:8379:HOH:O	1.98	0.64
1:0:2769:C:H2'	1:0:2770:G:O4'	1.98	0.64
24:V:21:LEU:HD21	24:V:48:VAL:CG1	2.27	0.63
1:0:1189:A:H3'	36:0:7217:HOH:O	1.97	0.63
1:0:1441:G:H1'	36:0:7301:HOH:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:64:ARG:HD2	36:L:8586:HOH:O	1.97	0.63
1:0:902:G:N7	13:K:18:HIS:HD2	1.97	0.63
1:0:506:G:H22	1:0:509:A:H5''	1.62	0.63
14:L:30:GLU:O	14:L:34:GLU:HG3	1.98	0.63
19:Q:39:THR:HG23	19:Q:107:GLU:O	1.99	0.63
5:C:27:ARG:HG3	5:C:29:ASP:OD1	1.99	0.63
1:0:558:C:O2'	1:0:559:U:H5''	1.98	0.63
12:J:62:PRO:HG3	12:J:65:ARG:HH21	1.64	0.63
1:0:1168:C:H2'	1:0:1169:U:O4'	1.99	0.63
5:C:142:ASP:OD1	5:C:237:GLU:HB3	1.99	0.63
1:0:544:G:C2'	1:0:545:G:H5''	2.27	0.63
6:D:55:LYS:HA	36:D:6752:HOH:O	1.99	0.63
1:0:962:C:H1'	15:M:5:ARG:HH12	1.62	0.63
26:X:187:VAL:CG2	26:X:192:ASP:HB2	2.28	0.63
5:C:107:ARG:NE	36:C:8457:HOH:O	2.24	0.63
6:D:99:ASP:CB	6:D:103:ASN:H	2.12	0.63
6:D:57:THR:HG23	6:D:63:ILE:HG22	1.79	0.63
13:K:73:VAL:HG23	13:K:74:THR:H	1.62	0.63
5:C:16:VAL:HG12	5:C:17:ASP:N	2.14	0.63
14:L:87:MET:CG	30:2:46:ILE:HG21	2.29	0.63
14:L:37:VAL:CG1	14:L:63:VAL:HG11	2.28	0.63
1:0:69:A:H5'	1:0:69:A:H8	1.64	0.63
1:0:2830:U:H3'	36:0:4738:HOH:O	1.97	0.63
26:X:212:ARG:HD2	36:X:8605:HOH:O	1.99	0.63
26:X:133:HIS:HD2	36:X:8584:HOH:O	1.80	0.63
10:H:44:ALA:HA	10:H:163:PRO:O	1.99	0.62
3:A:55:VAL:HG22	3:A:68:ILE:O	1.99	0.62
1:0:1741:U:H5'	1:0:1742:A:OP1	1.99	0.62
1:0:2827:A:H2'	1:0:2828:G:O4'	1.98	0.62
4:B:145:HIS:HD2	4:B:146:THR:O	1.83	0.62
15:M:12:ARG:HD3	15:M:18:THR:OG1	1.99	0.62
21:S:24:ARG:HH21	21:S:39:ASN:HD22	1.45	0.62
1:0:2694:A:H4'	7:E:91:PHE:CE1	2.33	0.62
10:H:130:HIS:CD2	10:H:133:ILE:HD11	2.34	0.62
10:H:35:ASN:ND2	10:H:80:ASN:HA	2.13	0.62
3:A:125:ASN:HB3	3:A:158:VAL:HG12	1.80	0.62
1:0:474:C:O3'	5:C:73:LEU:HD21	1.99	0.62
1:0:2547:C:OP2	4:B:5:ARG:NH1	2.32	0.62
25:W:75:ALA:O	25:W:83:ALA:HA	1.99	0.62
1:0:2851:G:O2'	1:0:2852:A:H5'	1.99	0.62
15:M:37:ARG:NE	36:M:8535:HOH:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:76:ARG:HG2	5:C:78:ARG:NH1	2.14	0.62
10:H:2:PRO:HB2	36:H:8364:HOH:O	1.99	0.62
7:E:7:ILE:HD11	7:E:11:VAL:O	1.98	0.62
19:Q:111:ILE:HG23	19:Q:145:LEU:CD1	2.29	0.62
15:M:86:LEU:HD12	15:M:125:ALA:HB2	1.82	0.62
24:V:4:LEU:HD22	24:V:52:VAL:CG2	2.29	0.62
4:B:7:ARG:CG	4:B:7:ARG:HH11	2.10	0.62
1:O:1187:U:O2'	1:O:1189:A:H2	1.83	0.62
1:O:1008:C:H5''	10:H:16:ARG:HH12	1.64	0.62
15:M:155:GLU:O	15:M:156:GLU:HG3	2.00	0.62
1:O:470:U:O2'	28:Z:16:HIS:HD2	1.82	0.62
5:C:79:ARG:O	5:C:87:ARG:HG2	1.99	0.62
1:O:710:G:OP1	16:N:24:ALA:HB3	2.00	0.62
1:O:2587:U:H2'	1:O:2589:U:H5''	1.82	0.62
12:J:55:VAL:HG12	12:J:56:SER:N	2.15	0.62
12:J:75:ARG:CZ	36:J:4172:HOH:O	2.46	0.62
24:V:122:ARG:NH2	24:V:154:ARG:HD2	2.14	0.62
1:O:182:G:O3'	14:L:157:LEU:HD13	1.99	0.62
19:Q:18:LEU:HB2	19:Q:143:VAL:CG1	2.29	0.62
7:E:3:VAL:HG22	7:E:49:ILE:HB	1.81	0.62
7:E:69:ILE:HA	7:E:72:MET:HE3	1.82	0.62
1:O:2638:G:H5'	36:O:4439:HOH:O	2.00	0.62
15:M:159:TYR:HB3	15:M:162:ASP:HB2	1.82	0.62
2:9:39:U:H1'	2:9:44:A:N6	2.14	0.62
26:X:186:ARG:HG2	26:X:186:ARG:HH11	1.65	0.62
1:O:417:G:P	36:O:6944:HOH:O	2.58	0.62
6:D:149:ARG:NH1	36:D:3066:HOH:O	2.23	0.62
1:O:2578:G:H5'	1:O:2578:G:H8	1.64	0.62
2:9:25:G:C3'	2:9:26:C:H5'	2.27	0.61
11:I:103:VAL:HG12	36:I:5907:HOH:O	1.99	0.61
6:D:23:VAL:HG21	6:D:45:THR:HG21	1.81	0.61
1:O:2346:C:O5'	1:O:2346:C:H6	1.83	0.61
1:O:338:C:H5''	36:C:8421:HOH:O	1.97	0.61
15:M:71:TRP:CE3	15:M:175:LEU:HD22	2.35	0.61
1:O:1118:A:H62	1:O:1244:U:H3	1.48	0.61
10:H:139:ASP:HA	36:H:8369:HOH:O	1.99	0.61
6:D:93:LEU:HB3	6:D:97:GLN:OE1	2.01	0.61
1:O:338:C:H4'	5:C:174:ILE:CD1	2.30	0.61
13:K:67:ARG:O	13:K:71:GLU:HG3	1.99	0.61
4:B:195:ARG:HG2	4:B:323:LEU:HD22	1.80	0.61
5:C:237:GLU:HB2	36:C:8430:HOH:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:139:ASP:H	10:H:140:PRO:HD3	1.62	0.61
6:D:35:ALA:N	36:D:5576:HOH:O	2.32	0.61
2:9:48:C:H4'	15:M:141:ARG:HH21	1.66	0.61
6:D:41:LEU:HA	6:D:44:ILE:HG22	1.82	0.61
2:9:42:C:H2'	36:9:8497:HOH:O	2.00	0.61
10:H:127:GLY:O	10:H:128:ALA:HB3	2.00	0.61
13:K:72:ASN:HB2	36:K:8580:HOH:O	2.00	0.61
8:F:107:VAL:O	8:F:111:ILE:HG13	2.00	0.61
1:0:1120:U:H5''	1:0:1120:U:C6	2.36	0.61
7:E:132:THR:HB	36:E:2227:HOH:O	2.01	0.61
20:R:81:ILE:HG23	36:R:8334:HOH:O	2.00	0.61
15:M:23:ARG:NH1	36:M:8549:HOH:O	2.34	0.61
1:0:1299:G:O6	13:K:6:ARG:HD3	2.01	0.61
6:D:23:VAL:O	6:D:23:VAL:HG23	2.01	0.61
1:0:558:C:C2'	1:0:559:U:H5''	2.31	0.61
7:E:20:ILE:CD1	7:E:40:VAL:HG11	2.29	0.61
1:0:2779:G:H21	7:E:143:GLN:NE2	1.98	0.61
14:L:169:ARG:HD2	36:L:8590:HOH:O	2.01	0.61
15:M:184:ILE:HG22	15:M:185:GLU:HG3	1.83	0.61
25:W:74:ALA:CB	25:W:85:VAL:HG22	2.31	0.61
6:D:54:ALA:CB	6:D:69:ILE:HD12	2.30	0.61
1:0:1130:U:H2'	1:0:1131:G:O4'	2.01	0.61
1:0:1189:A:H1'	1:0:1209:C:O4'	2.01	0.61
9:G:23:ILE:O	9:G:27:ILE:HG13	2.01	0.61
36:J:408:HOH:O	22:T:37:GLU:HB3	2.00	0.61
1:0:281:U:O2'	1:0:282:C:H5'	2.01	0.61
6:D:38:GLU:HB3	6:D:49:PRO:HG2	1.83	0.61
1:0:553:G:P	26:X:204:ARG:HH22	2.24	0.61
24:V:21:LEU:HD13	24:V:26:ILE:HD11	1.83	0.60
1:0:1525:G:H5'	1:0:1526:A:OP2	2.01	0.60
7:E:79:GLY:HA3	36:E:7046:HOH:O	2.00	0.60
1:0:1244:U:OP1	11:I:18:ILE:HD13	2.01	0.60
1:0:1667:A:C8	1:0:1667:A:H5'	2.34	0.60
10:H:118:PRO:HD2	36:H:8339:HOH:O	2.00	0.60
1:0:111:C:O2'	28:Z:20:ARG:HG2	2.01	0.60
8:F:110:GLU:HG2	36:F:6926:HOH:O	2.01	0.60
15:M:47:LEU:HD13	15:M:97:VAL:HG11	1.82	0.60
10:H:83:PHE:HZ	10:H:146:TRP:HE1	1.46	0.60
2:9:41:C:O4'	6:D:50:VAL:HG23	2.01	0.60
1:0:2570:G:H5''	36:0:4423:HOH:O	2.02	0.60
6:D:166:ILE:HD12	36:D:6326:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:264:GLU:HG2	4:B:267:LYS:CE	2.27	0.60
1:0:1189:A:H1'	1:0:1209:C:C1'	2.30	0.60
1:0:2780:C:H1'	7:E:143:GLN:HE21	1.66	0.60
27:Y:53:GLY:HA2	27:Y:67:GLY:O	2.00	0.60
4:B:7:ARG:CD	4:B:9:GLY:O	2.50	0.60
3:A:101:GLU:OE2	3:A:131:HIS:HB2	2.02	0.60
14:L:87:MET:CB	30:2:46:ILE:HD13	2.30	0.60
7:E:31:ARG:NH1	7:E:68:HIS:CG	2.70	0.60
7:E:23:GLU:HG2	7:E:28:SER:CB	2.32	0.60
4:B:258:GLY:H	4:B:260:HIS:CE1	2.20	0.60
4:B:140:LEU:HD23	36:B:8583:HOH:O	2.01	0.60
9:G:12:ILE:N	9:G:13:PRO:CD	2.65	0.60
1:0:1641:A:H2'	1:0:1642:A:H5'	1.83	0.60
10:H:5:MET:HG3	36:H:8364:HOH:O	2.01	0.60
3:A:170:VAL:HG22	27:Y:22:ILE:HG23	1.84	0.60
1:0:447:A:OP1	21:S:2:LYS:HG2	2.02	0.60
4:B:238:ASN:HD22	4:B:240:GLY:N	2.00	0.60
23:U:39:ALA:C	23:U:41:GLU:H	2.05	0.60
23:U:55:ARG:O	23:U:59:ILE:HG12	2.02	0.60
24:V:88:THR:CG2	24:V:89:ASP:H	2.09	0.60
5:C:118:THR:O	5:C:136:VAL:HG13	2.02	0.60
7:E:81:GLU:HG2	7:E:134:SER:CB	2.32	0.60
11:I:74:ARG:CB	11:I:74:ARG:HH11	2.14	0.60
25:W:21:PRO:HG2	25:W:24:LYS:HD3	1.83	0.60
4:B:74:ILE:HD13	4:B:309:VAL:HG21	1.84	0.60
3:A:95:PRO:HG2	3:A:98:GLU:HG2	1.84	0.60
14:L:48:ARG:NH2	36:L:8562:HOH:O	2.34	0.59
25:W:15:ARG:HH11	25:W:15:ARG:HB3	1.66	0.59
15:M:151:ASP:O	15:M:154:LEU:HB2	2.02	0.59
13:K:145:LEU:O	13:K:148:GLU:HG3	2.02	0.59
25:W:25:ARG:HD2	36:W:3861:HOH:O	2.02	0.59
11:I:75:PRO:HG2	11:I:105:LEU:HD21	1.84	0.59
13:K:53:ARG:NH2	13:K:57:VAL:HG12	2.16	0.59
1:0:2310:G:OP2	10:H:114:PRO:HD2	2.01	0.59
4:B:307:ARG:CG	4:B:307:ARG:HH11	2.14	0.59
25:W:30:MET:HE1	25:W:58:ALA:HB3	1.84	0.59
15:M:38:LYS:HD2	15:M:114:LYS:HE3	1.84	0.59
5:C:12:THR:HB	36:C:8440:HOH:O	2.00	0.59
6:D:44:ILE:HG23	6:D:45:THR:HG23	1.84	0.59
20:R:38:ALA:O	20:R:42:GLU:HG3	2.03	0.59
10:H:84:ARG:NH2	10:H:135:TRP:HH2	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:58:HIS:HA	10:H:61:LEU:HD23	1.84	0.59
5:C:76:ARG:HG2	5:C:78:ARG:HH12	1.66	0.59
13:K:77:ALA:HB3	36:K:8530:HOH:O	2.00	0.59
1:O:2721:U:H4'	12:J:87:ARG:HG3	1.84	0.59
29:1:22:PRO:HG2	29:1:25:VAL:CG2	2.32	0.59
19:Q:39:THR:HB	19:Q:42:GLU:CG	2.32	0.59
1:O:2270:G:H4'	3:A:223:ARG:HH12	1.67	0.59
14:L:174:ARG:HG3	36:L:8521:HOH:O	2.02	0.59
18:P:64:GLU:HG3	18:P:74:ASP:OD2	2.02	0.59
26:X:126:PRO:HG2	26:X:128:PHE:CE1	2.38	0.59
10:H:27:LYS:H	10:H:58:HIS:CD2	2.12	0.59
10:H:56:ILE:HG22	10:H:61:LEU:HD22	1.84	0.59
15:M:47:LEU:HD12	15:M:92:ALA:HB1	1.85	0.59
3:A:153:ARG:CB	3:A:153:ARG:HH11	2.14	0.59
11:I:131:THR:HG22	11:I:133:GLY:N	2.17	0.59
6:D:95:THR:C	6:D:97:GLN:H	2.06	0.59
36:O:5309:HOH:O	14:L:170:CYS:SG	2.32	0.59
1:O:1159:G:H21	1:O:1189:A:H8	1.50	0.59
1:O:558:C:H5'	36:O:4769:HOH:O	2.03	0.59
6:D:65:GLU:HG3	36:D:6752:HOH:O	2.01	0.59
22:T:9:CYS:HA	22:T:52:THR:HG23	1.83	0.59
24:V:80:ASP:O	24:V:84:VAL:HG23	2.03	0.59
14:L:114:VAL:HG21	14:L:159:THR:HG21	1.85	0.59
1:O:1119:G:N2	1:O:1246:A:H2	1.98	0.59
13:K:133:VAL:HB	36:K:8557:HOH:O	2.02	0.59
1:O:545:G:C8	1:O:545:G:H5'	2.35	0.59
15:M:43:VAL:HG11	15:M:81:ALA:HA	1.85	0.59
1:O:1166:A:H1'	1:O:1192:A:N1	2.17	0.58
1:O:1053:G:OP1	10:H:12:PRO:HG3	2.03	0.58
1:O:2004:U:H4'	36:O:4818:HOH:O	2.03	0.58
1:O:2502:C:C2'	1:O:2503:A:H5'	2.33	0.58
1:O:1329:A:C2	36:O:4193:HOH:O	2.45	0.58
3:A:88:ILE:HG22	3:A:88:ILE:O	2.02	0.58
36:O:3172:HOH:O	14:L:79:LYS:HD2	2.02	0.58
4:B:307:ARG:CB	4:B:307:ARG:HH11	2.16	0.58
27:Y:28:ASP:O	27:Y:31:ILE:HG22	2.03	0.58
1:O:1528:A:H2'	1:O:1529:G:O4'	2.03	0.58
29:1:22:PRO:HG2	29:1:25:VAL:HG23	1.85	0.58
1:O:31:C:H4'	36:O:6950:HOH:O	2.02	0.58
1:O:285:A:H2'	1:O:286:U:O4'	2.03	0.58
7:E:31:ARG:HH12	7:E:68:HIS:CD2	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:316:A:H5'	21:S:54:ASP:OD2	2.02	0.58
3:A:164:ARG:NE	36:A:8591:HOH:O	2.35	0.58
2:9:92:G:H22	10:H:52:LYS:NZ	2.01	0.58
15:M:78:MET:HB2	15:M:79:PRO:HD3	1.86	0.58
30:2:25:VAL:HG22	30:2:68:LYS:HG3	1.84	0.58
6:D:44:ILE:HG12	6:D:83:PHE:HE1	1.67	0.58
28:Z:21:ARG:HD2	28:Z:37:CYS:SG	2.43	0.58
27:Y:62:TYR:CE2	27:Y:64:ILE:HG23	2.38	0.58
13:K:114:VAL:HG11	36:K:8572:HOH:O	2.02	0.58
1:0:2694:A:H4'	7:E:91:PHE:HE1	1.68	0.58
1:0:485:A:N3	1:0:487:G:H5''	2.18	0.58
1:0:1887:U:OP1	27:Y:21:LYS:HE3	2.03	0.58
3:A:175:LYS:HE2	36:A:8579:HOH:O	2.03	0.58
36:0:3353:HOH:O	10:H:11:LYS:HE2	2.03	0.58
1:0:2064:U:H5'	1:0:2652:U:O3'	2.04	0.58
15:M:62:HIS:HB3	15:M:65:ASP:OD1	2.03	0.58
10:H:45:GLN:HE21	10:H:135:TRP:HE1	1.51	0.58
10:H:46:VAL:HG12	10:H:146:TRP:CZ3	2.37	0.58
36:0:3496:HOH:O	21:S:82:THR:HA	2.03	0.58
26:X:144:ARG:NH1	36:X:8578:HOH:O	2.33	0.58
20:R:81:ILE:HG12	36:R:8334:HOH:O	2.03	0.58
1:0:328:U:O4'	5:C:202:THR:HG22	2.03	0.58
1:0:2862:G:H4'	4:B:336:GLN:O	2.03	0.58
14:L:108:LYS:HE3	36:L:8614:HOH:O	2.04	0.58
13:K:143:THR:CG2	13:K:144:ASP:N	2.66	0.58
7:E:172:PRO:HB3	36:E:6931:HOH:O	2.03	0.58
3:A:37:VAL:HG22	36:A:8599:HOH:O	2.04	0.58
4:B:267:LYS:HD3	36:B:8528:HOH:O	2.02	0.58
22:T:52:THR:HG22	22:T:54:THR:N	2.19	0.58
27:Y:13:ARG:NH1	36:Y:8421:HOH:O	2.37	0.58
23:U:58:THR:O	23:U:62:GLU:HG3	2.04	0.58
1:0:1118:A:H8	1:0:1119:G:H5''	1.67	0.57
13:K:143:THR:HG22	13:K:144:ASP:H	1.69	0.57
13:K:73:VAL:HG23	13:K:74:THR:N	2.19	0.57
15:M:154:LEU:O	15:M:155:GLU:HB3	2.04	0.57
1:0:1878:G:H1'	36:0:5640:HOH:O	2.03	0.57
13:K:90:ARG:NH2	13:K:121:ILE:HD11	2.19	0.57
15:M:34:LEU:HA	15:M:47:LEU:HD23	1.86	0.57
1:0:1181:A:H2'	1:0:1182:C:O4'	2.03	0.57
4:B:62:ARG:CA	4:B:65:MET:HE3	2.34	0.57
22:T:13:ILE:HG12	22:T:32:CYS:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1173:A:H2'	36:0:3856:HOH:O	2.04	0.57
7:E:15:GLN:HG2	7:E:19:ASP:O	2.04	0.57
22:T:31:PHE:CG	22:T:37:GLU:HG2	2.39	0.57
22:T:52:THR:CG2	22:T:54:THR:HB	2.34	0.57
4:B:108:GLU:HB3	4:B:111:ARG:HD2	1.86	0.57
1:0:371:U:H2'	1:0:372:A:H8	1.69	0.57
4:B:175:LEU:C	4:B:175:LEU:HD23	2.24	0.57
23:U:39:ALA:N	23:U:40:PRO:CD	2.66	0.57
5:C:104:ASP:HA	5:C:107:ARG:NH1	2.16	0.57
4:B:329:TYR:CE2	22:T:15:PRO:HG2	2.38	0.57
1:0:1120:U:H6	1:0:1120:U:H5''	1.69	0.57
36:0:7216:HOH:O	14:L:154:ARG:HB2	2.04	0.57
36:0:4077:HOH:O	5:C:50:GLU:HG2	2.03	0.57
1:0:1679:C:H5'	36:0:8834:HOH:O	2.05	0.57
8:F:37:THR:O	8:F:41:GLU:HG3	2.04	0.57
1:0:2456:A:H5'	36:0:5210:HOH:O	2.04	0.57
6:D:91:ALA:HB1	36:D:5198:HOH:O	2.03	0.57
4:B:212:GLN:HB2	4:B:257:THR:CG2	2.31	0.57
3:A:164:ARG:HB2	27:Y:68:CYS:SG	2.44	0.57
3:A:53:ALA:HB3	36:A:8608:HOH:O	2.05	0.57
2:9:20:G:O2'	2:9:21:G:H5'	2.05	0.57
1:0:558:C:H2'	1:0:559:U:C5'	2.34	0.57
24:V:122:ARG:CZ	36:V:5817:HOH:O	2.53	0.57
15:M:48:VAL:HG11	15:M:55:ASP:HB3	1.85	0.57
7:E:31:ARG:NH1	36:E:5919:HOH:O	2.36	0.57
11:I:75:PRO:HG2	11:I:105:LEU:CD2	2.33	0.57
1:0:2241:C:O2'	1:0:2242:U:H5'	2.04	0.57
1:0:2630:G:O6	3:A:206:ARG:NH2	2.37	0.57
25:W:31:ILE:O	25:W:35:GLU:HG3	2.05	0.57
24:V:106:THR:OG1	24:V:109:GLU:HG3	2.04	0.57
20:R:33:SER:OG	20:R:36:GLU:HG3	2.05	0.57
12:J:115:ARG:HG3	12:J:116:GLU:N	2.19	0.57
1:0:2866:U:H4'	1:0:2867:G:H5'	1.86	0.57
6:D:86:THR:O	6:D:90:LEU:HG	2.05	0.57
23:U:4:HIS:HB3	36:U:6622:HOH:O	2.05	0.57
15:M:90:LEU:HB2	15:M:186:LEU:HD22	1.85	0.57
10:H:48:LEU:HG	10:H:157:ILE:HG21	1.87	0.57
14:L:38:VAL:C	14:L:63:VAL:HG13	2.24	0.57
9:G:12:ILE:HG22	9:G:12:ILE:O	2.05	0.57
4:B:162:MET:HG3	4:B:310:ARG:NH1	2.19	0.57
22:T:46:ALA:HB1	22:T:52:THR:HG21	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:X:144:ARG:NE	36:X:8615:HOH:O	2.37	0.57
1:O:2420:G:O2'	1:O:2421:G:H5'	2.04	0.57
17:O:121:ASP:HB2	36:O:198:HOH:O	2.05	0.57
1:O:449:A:N7	5:C:43:LYS:HG2	2.18	0.57
2:9:55:U:H4'	2:9:56:A:C8	2.39	0.57
2:9:76:G:C3'	2:9:77:A:H5''	2.28	0.57
1:O:2533:C:C6	1:O:2533:C:H5'	2.39	0.57
4:B:162:MET:HG3	4:B:310:ARG:CZ	2.35	0.57
1:O:1441:G:O2'	1:O:1442:A:H5'	2.05	0.57
1:O:797:A:O4'	27:Y:10:ARG:N	2.37	0.57
5:C:1:MET:HG2	5:C:2:GLN:N	2.18	0.57
12:J:34:VAL:CG2	12:J:47:ALA:HB2	2.33	0.57
8:F:50:VAL:HG21	8:F:63:ILE:HG21	1.87	0.57
3:A:105:VAL:HG12	3:A:106:CYS:N	2.20	0.57
15:M:154:LEU:HG	15:M:155:GLU:H	1.68	0.57
26:X:165:GLU:HB3	36:X:8597:HOH:O	2.04	0.57
14:L:60:ILE:C	14:L:61:ILE:HD12	2.25	0.57
36:J:1387:HOH:O	22:T:20:MET:HE3	2.03	0.57
28:Z:28:HIS:CD2	28:Z:30:LYS:HB2	2.40	0.57
6:D:136:ARG:HD2	6:D:155:HIS:O	2.04	0.56
1:O:2419:U:H5''	1:O:2420:G:H5'	1.87	0.56
14:L:61:ILE:HG13	36:L:8624:HOH:O	2.04	0.56
8:F:101:ALA:HB2	8:F:108:LEU:CD2	2.34	0.56
10:H:14:TYR:N	10:H:91:HIS:CE1	2.74	0.56
5:C:214:THR:HG23	36:C:8436:HOH:O	2.05	0.56
20:R:51:GLN:HE21	20:R:53:ASN:ND2	2.02	0.56
10:H:166:ASN:N	10:H:166:ASN:ND2	2.52	0.56
24:V:125:HIS:CD2	24:V:127:GLY:H	2.23	0.56
8:F:2:VAL:HG22	8:F:57:GLU:OE1	2.04	0.56
6:D:103:ASN:ND2	6:D:134:LEU:H	2.03	0.56
20:R:51:GLN:NE2	20:R:53:ASN:HD21	2.00	0.56
1:O:289:G:N2	1:O:363:A:H2	2.00	0.56
6:D:93:LEU:HG	36:D:3862:HOH:O	2.05	0.56
8:F:99:THR:O	8:F:100:ASP:HB2	2.05	0.56
1:O:2676:C:H4'	11:I:70:PHE:HE1	1.70	0.56
10:H:75:SER:HB3	10:H:79:ALA:HB1	1.88	0.56
4:B:82:VAL:HG12	4:B:82:VAL:O	2.05	0.56
24:V:31:HIS:HB3	36:V:5420:HOH:O	2.05	0.56
24:V:81:ASP:OD1	24:V:92:ASP:HB2	2.04	0.56
26:X:220:GLU:HG2	36:X:8551:HOH:O	2.04	0.56
1:O:738:G:H3'	36:O:6569:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:200:U:H2'	36:O:9957:HOH:O	2.03	0.56
25:W:12:ILE:HD12	25:W:36:HIS:ND1	2.20	0.56
3:A:121:ALA:O	3:A:124:VAL:HG22	2.05	0.56
1:O:2718:C:H6	1:O:2718:C:H5'	1.70	0.56
1:O:183:A:C5'	14:L:157:LEU:HD12	2.36	0.56
1:O:2769:C:C2'	1:O:2770:G:H5'	2.35	0.56
1:O:380:A:H5''	14:L:48:ARG:NH2	2.21	0.56
15:M:64:SER:C	15:M:66:LEU:H	2.09	0.56
21:S:9:LYS:CE	21:S:13:ARG:NH1	2.68	0.56
1:O:280:C:H2'	1:O:281:U:O4'	2.06	0.56
1:O:2890:A:H1'	22:T:56:ARG:HH21	1.70	0.56
11:I:130:VAL:HG12	11:I:131:THR:N	2.19	0.56
17:O:13:VAL:HG21	17:O:41:ARG:HG2	1.87	0.56
1:O:2548:C:OP2	4:B:5:ARG:NH2	2.39	0.56
6:D:49:PRO:HG3	36:D:5828:HOH:O	2.05	0.56
16:N:96:VAL:HA	36:N:4258:HOH:O	2.04	0.56
1:O:1116:U:O2'	1:O:1118:A:C2	2.48	0.56
19:Q:106:GLY:HA2	19:Q:109:MET:HE3	1.87	0.56
17:O:38:GLU:HA	17:O:41:ARG:NH1	2.21	0.56
1:O:2781:U:H1'	7:E:139:GLU:OE2	2.05	0.56
1:O:2815:G:OP2	11:I:99:GLU:HG2	2.06	0.56
22:T:11:THR:HG22	22:T:53:ASP:OD2	2.06	0.56
10:H:109:ASP:HB2	36:H:8345:HOH:O	2.05	0.56
10:H:47:GLU:HG2	10:H:133:ILE:HD12	1.87	0.56
15:M:159:TYR:HE2	15:M:163:PHE:HE2	1.54	0.56
14:L:37:VAL:HG13	14:L:63:VAL:HG11	1.88	0.56
12:J:62:PRO:HG3	12:J:65:ARG:NH2	2.20	0.56
4:B:215:VAL:HB	4:B:234:ARG:HH12	1.70	0.56
24:V:108:ARG:HE	24:V:114:PRO:HG3	1.71	0.56
1:O:797:A:C4'	27:Y:10:ARG:N	2.69	0.56
1:O:1119:G:H8	11:I:52:GLN:NE2	2.04	0.56
25:W:78:GLU:CG	25:W:79:GLU:H	2.18	0.56
9:G:63:ARG:O	9:G:67:LEU:HG	2.05	0.56
10:H:39:GLY:O	10:H:41:THR:N	2.39	0.56
1:O:2081:A:H4'	11:I:69:TYR:CE1	2.41	0.56
18:P:11:ARG:HD3	36:P:5620:HOH:O	2.04	0.56
1:O:1134:G:H4'	10:H:151:MET:CE	2.23	0.56
3:A:212:PRO:HB2	36:A:8562:HOH:O	2.06	0.56
1:O:1209:C:H2'	1:O:1210:G:C8	2.39	0.56
1:O:2821:C:H4'	4:B:116:PRO:HB3	1.88	0.56
36:O:5761:HOH:O	3:A:22:ARG:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:11:HIS:C	6:D:13:MET:H	2.09	0.56
15:M:87:LEU:CD1	15:M:186:LEU:HD21	2.33	0.55
19:Q:18:LEU:HD12	19:Q:143:VAL:CG1	2.36	0.55
6:D:10:PHE:CG	6:D:11:HIS:N	2.74	0.55
29:I:35:ARG:HB2	36:I:2691:HOH:O	2.06	0.55
5:C:16:VAL:HG12	5:C:17:ASP:H	1.69	0.55
1:O:1667:A:H2'	1:O:1668:U:C6	2.41	0.55
4:B:141:ARG:HG2	4:B:165:ARG:HA	1.88	0.55
25:W:25:ARG:HG2	36:W:5356:HOH:O	2.05	0.55
15:M:11:ARG:NH2	36:M:8521:HOH:O	2.39	0.55
5:C:98:ARG:NH1	36:C:8357:HOH:O	2.36	0.55
1:O:1086:A:C6	24:V:11:VAL:HG11	2.41	0.55
36:O:6547:HOH:O	3:A:211:LYS:HG2	2.06	0.55
27:Y:58:GLY:CA	36:Y:8439:HOH:O	2.47	0.55
1:O:567:U:H5'	36:V:5817:HOH:O	2.06	0.55
1:O:1524:U:OP1	1:O:1524:U:H4'	2.06	0.55
1:O:2604:A:H5'	36:O:5307:HOH:O	2.06	0.55
4:B:314:ALA:HB3	4:B:317:PRO:HG3	1.88	0.55
13:K:104:ASP:HB3	36:K:8563:HOH:O	2.07	0.55
1:O:263:U:O4'	8:F:59:ILE:HD13	2.05	0.55
5:C:107:ARG:NH1	5:C:107:ARG:HB3	2.21	0.55
30:2:18:GLN:OE1	30:2:73:GLU:HB3	2.05	0.55
7:E:11:VAL:HG13	7:E:23:GLU:O	2.05	0.55
6:D:135:VAL:HG21	6:D:139:TYR:CD1	2.42	0.55
26:X:144:ARG:CZ	36:X:8615:HOH:O	2.53	0.55
4:B:154:VAL:HG12	4:B:156:LYS:HG2	1.88	0.55
1:O:1185:U:H2'	1:O:1186:C:C6	2.41	0.55
10:H:139:ASP:N	10:H:140:PRO:CD	2.68	0.55
14:L:94:LYS:CE	36:L:8582:HOH:O	2.54	0.55
10:H:97:LYS:HD3	10:H:117:LYS:HE2	1.88	0.55
26:X:216:ARG:HD3	36:X:8571:HOH:O	2.05	0.55
9:G:64:ASN:N	9:G:64:ASN:HD22	2.03	0.55
36:O:5728:HOH:O	4:B:2:GLN:HA	2.05	0.55
14:L:164:THR:HB	36:L:8519:HOH:O	2.07	0.55
6:D:64:ARG:CD	6:D:67:ASP:HB3	2.37	0.55
1:O:558:C:H2'	1:O:559:U:H5'	1.89	0.55
11:I:133:GLY:O	11:I:137:GLU:HG3	2.07	0.55
6:D:174:VAL:HG13	36:D:6555:HOH:O	2.07	0.55
1:O:2064:U:H5'	1:O:2652:U:H4'	1.88	0.55
6:D:36:ASN:HA	36:D:7500:HOH:O	2.07	0.55
6:D:62:ASP:HA	36:D:4233:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:O:8907:HOH:O	14:L:94:LYS:HE2	2.06	0.55
8:F:46:GLU:OE1	8:F:100:ASP:HA	2.06	0.55
1:O:65:C:O2'	1:O:66:G:H5'	2.07	0.55
1:O:1477:C:H5'	1:O:1868:G:C5'	2.36	0.55
15:M:61:ALA:HB3	15:M:88:ALA:HB2	1.89	0.55
21:S:111:ARG:HB3	21:S:119:ALA:HB2	1.89	0.55
14:L:74:ARG:HG3	14:L:74:ARG:HH11	1.72	0.55
2:9:55:U:H4'	2:9:56:A:H8	1.70	0.55
24:V:21:LEU:HB3	24:V:26:ILE:CG1	2.36	0.55
3:A:128:LEU:HD21	3:A:131:HIS:HE1	1.72	0.55
1:O:2898:G:H4'	4:B:288:GLY:HA2	1.88	0.55
25:W:43:VAL:CG1	25:W:47:ALA:HB3	2.37	0.55
6:D:58:VAL:HG12	6:D:59:GLY:N	2.22	0.55
1:O:1299:G:N2	36:O:4193:HOH:O	2.39	0.55
10:H:59:ASN:H	10:H:59:ASN:ND2	2.04	0.55
1:O:1377:C:H5'	1:O:1377:C:C6	2.40	0.55
1:O:1123:A:C6	1:O:1238:C:H5'	2.42	0.55
1:O:1137:G:H1'	36:O:3386:HOH:O	2.06	0.55
1:O:1615:A:H5'	36:O:3690:HOH:O	2.07	0.55
1:O:57:C:H5''	36:O:6278:HOH:O	2.06	0.55
26:X:235:GLU:CD	26:X:235:GLU:H	2.10	0.55
6:D:154:LYS:H	6:D:154:LYS:CD	2.10	0.55
1:O:2717:C:O2'	1:O:2718:C:H5''	2.06	0.55
15:M:49:THR:CG2	15:M:56:ASP:HB2	2.36	0.55
11:I:107:ASN:HD22	11:I:109:TYR:H	1.52	0.55
6:D:51:ARG:HD3	36:D:7636:HOH:O	2.07	0.55
8:F:101:ALA:HB2	8:F:108:LEU:HD22	1.88	0.55
11:I:99:GLU:HA	36:I:7377:HOH:O	2.06	0.55
1:O:1669:A:H2'	1:O:1670:G:C8	2.42	0.55
19:Q:25:PHE:CE2	19:Q:29:LYS:HE2	2.42	0.55
20:R:23:LYS:HE2	36:R:8329:HOH:O	2.06	0.55
17:O:80:ARG:HG2	17:O:87:ARG:CZ	2.37	0.55
15:M:170:GLU:O	15:M:174:GLU:HG3	2.07	0.55
16:N:38:ARG:NH1	36:N:7674:HOH:O	2.40	0.55
26:X:189:ASN:C	26:X:189:ASN:HD22	2.10	0.54
30:2:17:HIS:O	30:2:18:GLN:HG3	2.07	0.54
25:W:74:ALA:HB2	25:W:85:VAL:HG13	1.88	0.54
8:F:58:GLU:CD	14:L:27:ARG:HH22	2.10	0.54
1:O:138:U:H5''	1:O:139:C:OP2	2.08	0.54
26:X:112:GLU:CD	26:X:115:ARG:NH1	2.60	0.54
17:O:16:VAL:HG12	17:O:17:GLY:N	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:7:ARG:NH1	4:B:11:LEU:HD22	2.22	0.54
14:L:55:LYS:HB2	14:L:60:ILE:CD1	2.38	0.54
14:L:61:ILE:HA	36:L:8624:HOH:O	2.07	0.54
19:Q:33:ARG:NH1	36:Q:8541:HOH:O	2.39	0.54
10:H:129:ASN:HD22	10:H:129:ASN:N	2.04	0.54
1:O:2502:C:H2'	1:O:2503:A:H5'	1.89	0.54
1:O:21:G:H5''	19:Q:1:GLY:O	2.07	0.54
1:O:542:A:H2'	1:O:543:G:O4'	2.07	0.54
1:O:1118:A:C8	1:O:1118:A:C3'	2.87	0.54
1:O:283:U:H5''	1:O:284:C:P	2.47	0.54
14:L:37:VAL:HG21	14:L:108:LYS:CG	2.38	0.54
1:O:1189:A:H1'	1:O:1209:C:H1'	1.89	0.54
1:O:1268:C:O2'	26:X:169:ARG:HB2	2.07	0.54
13:K:143:THR:HG22	13:K:145:LEU:H	1.72	0.54
19:Q:119:VAL:HG12	19:Q:119:VAL:O	2.07	0.54
23:U:39:ALA:O	23:U:41:GLU:N	2.41	0.54
25:W:9:VAL:HG22	25:W:88:GLU:OE2	2.07	0.54
1:O:2795:C:O2'	1:O:2796:U:H5'	2.06	0.54
5:C:47:GLY:HA2	5:C:92:PRO:HB2	1.89	0.54
4:B:55:ASN:HB3	4:B:63:GLU:HA	1.89	0.54
2:9:25:G:H2'	36:9:8458:HOH:O	2.08	0.54
12:J:87:ARG:CZ	36:J:4854:HOH:O	2.55	0.54
2:9:49:G:H2'	2:9:50:G:O4'	2.07	0.54
15:M:110:THR:HB	15:M:113:SER:OG	2.07	0.54
1:O:1189:A:O2'	1:O:1208:C:H2'	2.07	0.54
10:H:53:PRO:HA	10:H:125:VAL:O	2.07	0.54
4:B:85:ARG:NH1	36:B:8639:HOH:O	2.41	0.54
36:O:9462:HOH:O	25:W:23:HIS:HD2	1.90	0.54
16:N:39:THR:O	16:N:115:ARG:NH2	2.40	0.54
1:O:2488:A:H61	1:O:2534:C:H42	1.55	0.54
14:L:164:THR:CG2	14:L:165:SER:N	2.71	0.54
24:V:139:GLY:O	24:V:141:HIS:HD2	1.90	0.54
11:I:93:ARG:HB3	11:I:93:ARG:NH1	2.22	0.54
1:O:244:C:OP2	8:F:38:LYS:HE3	2.08	0.54
1:O:2094:G:H4'	4:B:245:SER:HB3	1.89	0.54
1:O:1333:U:H2'	1:O:1334:C:C6	2.43	0.54
1:O:797:A:H5'	27:Y:10:ARG:HG2	1.90	0.54
27:Y:38:LYS:HD3	36:Y:8425:HOH:O	2.06	0.54
3:A:211:LYS:HB3	3:A:212:PRO:CD	2.33	0.54
17:O:103:THR:O	17:O:107:GLU:HG3	2.08	0.54
1:O:2265:U:H2'	1:O:2266:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:7:ARG:HG2	4:B:7:ARG:NH1	2.15	0.54
5:C:77:ALA:O	5:C:78:ARG:HG3	2.07	0.54
3:A:100:PRO:HG2	3:A:103:VAL:CG2	2.34	0.54
1:0:282:C:H1'	1:0:368:C:H42	1.71	0.54
4:B:51:VAL:HG21	4:B:327:VAL:HG13	1.90	0.54
10:H:35:ASN:HD21	10:H:80:ASN:HA	1.73	0.54
1:0:1384:C:H5'	25:W:30:MET:HG2	1.90	0.54
26:X:106:THR:HG23	26:X:107:PRO:HD2	1.90	0.54
12:J:30:LYS:O	12:J:55:VAL:HG13	2.07	0.54
3:A:36:ASP:HA	3:A:83:GLY:HA3	1.90	0.54
1:0:2289:G:H21	1:0:2291:A:H2	1.52	0.54
2:9:44:A:O4'	6:D:76:ARG:NE	2.41	0.54
10:H:71:TYR:C	10:H:73:GLN:N	2.59	0.54
1:0:1730:G:H5'	1:0:1731:C:C6	2.43	0.54
4:B:162:MET:CE	4:B:308:LEU:HD21	2.38	0.54
8:F:47:LEU:HD22	8:F:108:LEU:CD1	2.38	0.54
1:0:2815:G:N7	11:I:80:LYS:NZ	2.55	0.54
1:0:951:A:C2'	1:0:952:G:H5'	2.38	0.54
4:B:248:ARG:O	4:B:251:VAL:CG1	2.56	0.54
10:H:45:GLN:HG3	10:H:135:TRP:NE1	2.23	0.53
6:D:99:ASP:O	6:D:159:PRO:HG3	2.07	0.53
14:L:172:GLY:C	14:L:183:VAL:HG11	2.26	0.53
4:B:297:VAL:HB	36:B:8610:HOH:O	2.08	0.53
1:0:500:G:H21	19:Q:98:ASN:HD21	1.56	0.53
6:D:81:GLU:O	6:D:85:GLN:HG3	2.08	0.53
1:0:1044:C:H3'	1:0:1045:G:H5''	1.90	0.53
1:0:1919:A:H4'	36:0:4360:HOH:O	2.08	0.53
1:0:2301:A:H5''	1:0:2302:A:H5'	1.89	0.53
27:Y:30:GLU:HA	27:Y:33:HIS:CB	2.39	0.53
3:A:105:VAL:HG11	3:A:154:ALA:CB	2.37	0.53
11:I:107:ASN:C	11:I:107:ASN:HD22	2.12	0.53
36:0:8593:HOH:O	4:B:214:PRO:HD2	2.08	0.53
1:0:2812:A:N7	36:0:7048:HOH:O	2.34	0.53
10:H:147:ARG:HA	10:H:150:LYS:NZ	2.24	0.53
29:1:19:SER:HB3	36:1:4479:HOH:O	2.09	0.53
8:F:39:SER:CB	8:F:45:ALA:HB2	2.39	0.53
29:1:48:ASP:O	29:1:49:GLU:HB2	2.08	0.53
15:M:154:LEU:HG	15:M:155:GLU:N	2.22	0.53
1:0:775:G:OP1	28:Z:16:HIS:HE1	1.91	0.53
1:0:2526:C:O2'	1:0:2527:U:H5'	2.08	0.53
2:9:3:A:OP2	2:9:3:A:C8	2.61	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:143:THR:CG2	13:K:144:ASP:H	2.20	0.53
1:0:272:A:H5'	1:0:273:G:OP2	2.08	0.53
9:G:12:ILE:HD12	36:G:692:HOH:O	2.07	0.53
4:B:16:ARG:NE	36:B:8555:HOH:O	2.25	0.53
6:D:57:THR:HG23	6:D:63:ILE:CB	2.38	0.53
12:J:82:ARG:NH2	12:J:115:ARG:HG2	2.23	0.53
8:F:47:LEU:HB2	8:F:108:LEU:HD11	1.90	0.53
7:E:36:PRO:HD3	11:I:127:ILE:HD12	1.90	0.53
17:O:91:LYS:O	17:O:95:GLU:HG3	2.08	0.53
11:I:19:MET:HE3	11:I:132:LEU:HD11	1.89	0.53
24:V:19:ASP:O	24:V:23:MET:HG3	2.09	0.53
8:F:91:VAL:CG1	8:F:92:GLY:H	2.18	0.53
3:A:132:ASP:OD1	3:A:133:ARG:N	2.41	0.53
5:C:246:ARG:NH1	5:C:246:ARG:HB3	2.23	0.53
6:D:38:GLU:OE2	6:D:51:ARG:CZ	2.57	0.53
27:Y:11:THR:OG1	27:Y:23:ARG:HB2	2.09	0.53
30:2:60:LYS:HG3	30:2:61:PRO:HD2	1.90	0.53
1:0:703:G:O2'	1:0:704:C:H5'	2.09	0.53
1:0:2591:C:H2'	1:0:2592:G:O4'	2.09	0.53
5:C:27:ARG:HG2	5:C:30:LEU:HG	1.91	0.53
17:O:105:LEU:HD21	17:O:137:LEU:HD21	1.91	0.53
23:U:56:ILE:O	23:U:60:GLN:HG3	2.08	0.53
12:J:58:THR:HG22	12:J:59:LYS:HG3	1.91	0.53
1:0:920:C:H5''	1:0:921:G:O5'	2.08	0.53
21:S:49:GLU:HB3	21:S:59:GLU:CG	2.38	0.53
3:A:76:VAL:HG23	27:Y:63:LYS:HB3	1.89	0.53
28:Z:8:GLN:HE22	28:Z:11:LYS:NZ	2.07	0.53
24:V:141:HIS:HB2	24:V:146:ILE:HG12	1.89	0.53
1:0:2717:C:H2'	1:0:2718:C:C5'	2.35	0.53
14:L:185:PRO:HG2	14:L:189:VAL:HG11	1.91	0.53
23:U:64:GLY:O	23:U:65:ASP:CB	2.57	0.53
4:B:42:ALA:HB1	4:B:308:LEU:HD11	1.89	0.53
1:0:1523:G:H2'	1:0:1524:U:C6	2.44	0.53
36:0:9045:HOH:O	17:O:81:LYS:HG2	2.08	0.53
8:F:22:VAL:HG21	8:F:104:ALA:HB2	1.90	0.53
19:Q:106:GLY:HA2	19:Q:109:MET:CE	2.39	0.53
27:Y:30:GLU:HA	27:Y:33:HIS:HB3	1.90	0.53
22:T:14:GLU:OE1	22:T:15:PRO:HD2	2.09	0.53
24:V:41:TYR:O	24:V:45:VAL:HG13	2.09	0.53
4:B:119:HIS:O	4:B:121:PRO:HD3	2.09	0.53
19:Q:132:ARG:NH1	36:Q:8580:HOH:O	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:166:VAL:HG12	36:E:3134:HOH:O	2.08	0.53
10:H:144:GLU:OE1	10:H:144:GLU:HA	2.08	0.53
2:9:23:U:H3'	2:9:24:U:H5''	1.91	0.53
1:0:2507:G:H2'	1:0:2510:C:H42	1.74	0.53
1:0:2896:A:OP1	25:W:15:ARG:NH1	2.42	0.53
7:E:49:ILE:HD11	7:E:69:ILE:HD12	1.90	0.53
1:0:2072:G:C6	1:0:2533:C:H1'	2.44	0.53
1:0:2638:G:H1'	36:0:7295:HOH:O	2.08	0.53
8:F:19:ALA:O	8:F:22:VAL:HG22	2.09	0.53
36:0:8627:HOH:O	5:C:103:ASN:HB3	2.08	0.53
26:X:178:HIS:CG	26:X:179:PRO:HD2	2.44	0.53
1:0:1299:G:H5'	36:0:3580:HOH:O	2.09	0.53
19:Q:104:PHE:HB2	19:Q:109:MET:HE1	1.90	0.53
8:F:100:ASP:HB3	36:F:5691:HOH:O	2.09	0.53
8:F:2:VAL:HG11	14:L:23:LEU:HD23	1.89	0.53
1:0:1306:U:OP1	5:C:184:ARG:HD2	2.09	0.53
1:0:1353:C:P	36:0:4189:HOH:O	2.67	0.53
13:K:125:PHE:CZ	13:K:140:VAL:HG13	2.44	0.53
5:C:180:SER:HB2	36:C:8444:HOH:O	2.09	0.53
5:C:246:ARG:NH2	36:C:8424:HOH:O	2.41	0.52
4:B:138:GLY:O	4:B:139:ASP:O	2.26	0.52
1:0:2787:C:H5	36:0:4141:HOH:O	1.91	0.52
6:D:99:ASP:HB2	6:D:103:ASN:H	1.75	0.52
6:D:99:ASP:HB3	6:D:103:ASN:H	1.74	0.52
6:D:163:VAL:HA	36:D:6326:HOH:O	2.09	0.52
5:C:127:ARG:CZ	5:C:225:PRO:HG2	2.36	0.52
12:J:109:LEU:HD13	12:J:113:ILE:HD11	1.91	0.52
11:I:45:VAL:HG21	11:I:129:PHE:CD1	2.45	0.52
1:0:2415:A:C2	15:M:25:ARG:HB3	2.44	0.52
4:B:17:LYS:O	4:B:260:HIS:HD2	1.93	0.52
26:X:184:GLU:OE1	26:X:204:ARG:NH1	2.42	0.52
25:W:30:MET:CE	25:W:58:ALA:HB3	2.39	0.52
3:A:164:ARG:CZ	36:A:8591:HOH:O	2.57	0.52
1:0:317:A:H5''	21:S:52:ARG:HD2	1.91	0.52
16:N:7:LEU:HD22	36:N:5650:HOH:O	2.09	0.52
3:A:211:LYS:HD3	36:A:8613:HOH:O	2.09	0.52
10:H:55:GLN:HE22	10:H:91:HIS:CD2	2.27	0.52
16:N:47:ARG:HG3	16:N:47:ARG:NH1	2.22	0.52
19:Q:39:THR:HB	19:Q:42:GLU:CD	2.30	0.52
1:0:184:G:H5''	14:L:153:THR:HG22	1.91	0.52
1:0:949:U:O2'	18:P:40:HIS:HE1	1.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:56:ASN:O	29:I:8:LYS:HE2	2.09	0.52
1:O:2329:C:O2'	1:O:2330:U:H5'	2.10	0.52
6:D:105:SER:CB	6:D:131:THR:HG23	2.35	0.52
18:P:40:HIS:CE1	18:P:94:GLN:HA	2.45	0.52
1:O:602:A:O2'	1:O:605:C:H4'	2.10	0.52
14:L:77:PHE:HD2	36:L:8526:HOH:O	1.91	0.52
1:O:396:U:O2'	1:O:418:C:H4'	2.10	0.52
27:Y:11:THR:CG2	27:Y:23:ARG:HB2	2.40	0.52
19:Q:17:MET:HE1	19:Q:19:ARG:NH2	2.24	0.52
30:2:87:ARG:NH1	36:2:8525:HOH:O	2.43	0.52
2:9:23:U:C3'	2:9:24:U:H5''	2.39	0.52
6:D:146:LYS:NZ	15:M:107:ASN:ND2	2.56	0.52
1:O:1151:G:OP1	9:G:63:ARG:NH1	2.43	0.52
7:E:22:VAL:O	7:E:28:SER:HA	2.10	0.52
3:A:125:ASN:CB	3:A:158:VAL:HG12	2.40	0.52
1:O:2524:G:H21	1:O:2526:C:N4	2.07	0.52
19:Q:132:ARG:CZ	36:Q:8580:HOH:O	2.57	0.52
3:A:94:LEU:N	3:A:94:LEU:HD23	2.24	0.52
15:M:37:ARG:NH2	36:M:8535:HOH:O	2.43	0.52
1:O:2769:C:O2'	1:O:2770:G:H5'	2.09	0.52
5:C:246:ARG:CZ	36:C:8424:HOH:O	2.56	0.52
4:B:310:ARG:NH2	36:B:8558:HOH:O	2.41	0.52
6:D:22:VAL:HG22	6:D:74:THR:HG22	1.92	0.52
11:I:88:PRO:O	11:I:94:GLY:HA3	2.10	0.52
15:M:169:PRO:O	15:M:172:PHE:HB3	2.10	0.52
1:O:2090:G:H2'	1:O:2091:G:C8	2.44	0.52
3:A:179:MET:HG2	3:A:186:TRP:CB	2.40	0.52
1:O:960:G:H2'	1:O:960:G:N3	2.25	0.52
6:D:23:VAL:HG21	6:D:45:THR:CG2	2.40	0.52
27:Y:29:VAL:O	27:Y:33:HIS:HB2	2.10	0.52
1:O:182:G:O3'	14:L:157:LEU:CD1	2.57	0.52
6:D:94:ALA:O	6:D:95:THR:O	2.27	0.52
8:F:99:THR:HG23	8:F:99:THR:O	2.09	0.52
1:O:1878:G:O2'	1:O:1879:U:C6	2.60	0.52
1:O:1197:G:N2	36:O:5753:HOH:O	2.43	0.52
12:J:10:GLN:NE2	12:J:10:GLN:N	2.42	0.52
1:O:88:G:H5'	1:O:88:G:H8	1.75	0.52
1:O:1497:G:H4'	1:O:1627:G:O2'	2.10	0.52
14:L:12:TRP:CE2	14:L:20:ILE:HD11	2.45	0.52
1:O:1213:C:O2'	1:O:1214:G:H5'	2.10	0.52
14:L:182:LYS:HB2	14:L:194:ALA:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1503:U:H2'	1:0:1504:A:O4'	2.10	0.52
14:L:137:ASP:HA	14:L:142:LYS:HE3	1.91	0.52
1:0:1506:U:H6	1:0:1506:U:H5'	1.75	0.52
20:R:57:THR:CG2	20:R:58:MET:N	2.73	0.52
6:D:27:ILE:HG22	6:D:28:GLY:N	2.20	0.52
3:A:192:VAL:CG1	3:A:207:GLN:HB3	2.40	0.52
1:0:2768:A:O2'	1:0:2769:C:H5'	2.10	0.52
36:9:8514:HOH:O	15:M:107:ASN:HB3	2.09	0.52
1:0:2837:U:H2'	36:0:6360:HOH:O	2.10	0.52
8:F:46:GLU:N	36:F:3461:HOH:O	2.42	0.52
1:0:710:G:P	16:N:24:ALA:HB3	2.50	0.52
4:B:175:LEU:O	4:B:175:LEU:HD23	2.09	0.52
19:Q:29:LYS:HB3	36:Q:8530:HOH:O	2.08	0.52
1:0:2300:A:H4'	1:0:2301:A:O5'	2.10	0.52
7:E:43:ASP:HA	36:E:5864:HOH:O	2.10	0.52
5:C:151:GLN:O	5:C:154:VAL:HB	2.10	0.52
13:K:149:ARG:O	13:K:150:GLN:HB2	2.10	0.52
2:9:1:U:O3'	2:9:3:A:H5'	2.10	0.51
4:B:7:ARG:CG	4:B:7:ARG:NH1	2.71	0.51
1:0:88:G:C6	29:1:24:TRP:CZ3	2.98	0.51
1:0:1450:C:C4'	1:0:1451:C:OP2	2.57	0.51
6:D:135:VAL:HG22	6:D:136:ARG:N	2.25	0.51
22:T:33:SER:O	22:T:37:GLU:HG3	2.10	0.51
6:D:50:VAL:O	6:D:71:ALA:HA	2.10	0.51
4:B:305:ASP:O	4:B:306:LYS:HB2	2.11	0.51
15:M:157:PRO:HA	36:M:8527:HOH:O	2.09	0.51
5:C:129:HIS:HD2	5:C:165:ASP:OD2	1.93	0.51
1:0:1462:C:H2'	1:0:1463:A:C8	2.46	0.51
25:W:37:LEU:CD1	25:W:85:VAL:HG21	2.20	0.51
14:L:114:VAL:HB	14:L:159:THR:HG23	1.90	0.51
1:0:2506:A:O2'	1:0:2507:G:O5'	2.27	0.51
14:L:37:VAL:HG21	14:L:108:LYS:HG3	1.91	0.51
14:L:81:ARG:HG3	14:L:85:ARG:HB2	1.91	0.51
3:A:170:VAL:HG13	27:Y:22:ILE:HG21	1.92	0.51
26:X:144:ARG:NH2	36:X:8615:HOH:O	2.44	0.51
36:0:7089:HOH:O	30:2:60:LYS:HG3	2.11	0.51
18:P:75:ILE:CD1	18:P:84:ILE:HD11	2.41	0.51
1:0:2812:A:C2	1:0:2814:A:N6	2.68	0.51
1:0:283:U:H5''	1:0:284:C:OP2	2.11	0.51
2:9:29:C:C2'	2:9:30:C:H5'	2.40	0.51
1:0:470:U:O2'	28:Z:16:HIS:CD2	2.62	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1878:G:H4'	36:0:3624:HOH:O	2.10	0.51
1:0:538:C:H5''	1:0:539:G:C8	2.45	0.51
2:9:49:G:O2'	2:9:50:G:H5'	2.10	0.51
4:B:217:ARG:HG3	4:B:257:THR:HG22	1.92	0.51
10:H:59:ASN:ND2	10:H:59:ASN:N	2.55	0.51
3:A:34:ASP:OD1	3:A:35:GLY:N	2.40	0.51
21:S:80:GLU:OE2	21:S:84:GLY:HA2	2.11	0.51
26:X:155:ARG:NH1	36:X:8559:HOH:O	2.44	0.51
14:L:84:LYS:HE2	36:L:8576:HOH:O	2.10	0.51
25:W:74:ALA:HB1	25:W:85:VAL:HG22	1.92	0.51
1:0:1118:A:C8	1:0:1119:G:H5''	2.45	0.51
19:Q:18:LEU:HG	19:Q:91:LEU:HD13	1.91	0.51
7:E:69:ILE:HA	7:E:72:MET:HE2	1.92	0.51
6:D:65:GLU:HA	36:D:6752:HOH:O	2.09	0.51
6:D:11:HIS:O	6:D:12:GLU:HB3	2.10	0.51
1:0:1236:A:H2'	1:0:1237:U:O4'	2.11	0.51
36:0:5650:HOH:O	29:1:20:ARG:HB3	2.11	0.51
23:U:49:LEU:O	23:U:53:ILE:HG13	2.11	0.51
2:9:23:U:H6	2:9:23:U:C5'	2.21	0.51
15:M:71:TRP:HE3	15:M:175:LEU:HD22	1.76	0.51
8:F:91:VAL:CG1	8:F:92:GLY:N	2.72	0.51
14:L:87:MET:HB2	14:L:91:ILE:CD1	2.39	0.51
12:J:106:GLY:HA3	36:J:5264:HOH:O	2.09	0.51
24:V:38:THR:HG22	24:V:39:ASP:N	2.26	0.51
6:D:58:VAL:CG1	6:D:59:GLY:N	2.72	0.51
19:Q:132:ARG:HG2	19:Q:133:ALA:N	2.26	0.51
21:S:92:ASP:OD1	21:S:94:SER:HB3	2.11	0.51
1:0:2251:G:H2'	1:0:2252:A:C8	2.46	0.51
1:0:1972:U:H2'	1:0:1973:A:C5'	2.41	0.51
14:L:113:ARG:HH21	14:L:156:ARG:HG2	1.74	0.51
1:0:475:G:OP1	5:C:73:LEU:HD22	2.11	0.51
22:T:52:THR:HG22	22:T:54:THR:HB	1.93	0.51
16:N:96:VAL:HG13	16:N:100:GLN:HB2	1.93	0.51
6:D:170:TYR:O	6:D:171:ASP:HB3	2.10	0.51
6:D:25:MET:CE	6:D:41:LEU:HG	2.34	0.51
7:E:31:ARG:HH12	7:E:68:HIS:CG	2.28	0.51
4:B:139:ASP:HB2	4:B:165:ARG:HE	1.76	0.51
10:H:75:SER:C	10:H:79:ALA:HB2	2.31	0.51
13:K:57:VAL:O	13:K:57:VAL:HG12	2.11	0.51
4:B:156:LYS:HE3	36:B:8635:HOH:O	2.09	0.51
1:0:1470:A:OP1	14:L:93:ARG:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1249:U:H2'	1:0:1250:C:C6	2.46	0.51
2:9:6:C:C5'	15:M:37:ARG:HH12	2.12	0.51
14:L:52:LEU:HD13	14:L:116:ASN:HB3	1.93	0.51
26:X:187:VAL:HB	36:X:8572:HOH:O	2.10	0.51
3:A:93:THR:HG23	3:A:154:ALA:O	2.11	0.51
1:0:1044:C:H5''	36:0:8542:HOH:O	2.10	0.51
1:0:1862:C:H1'	36:0:6742:HOH:O	2.10	0.51
15:M:182:GLY:O	15:M:183:ASP:O	2.28	0.51
17:O:10:ALA:HA	17:O:13:VAL:CG1	2.41	0.51
1:0:2672:C:O2'	1:0:2673:U:H5'	2.11	0.51
10:H:75:SER:O	10:H:79:ALA:HB2	2.11	0.51
15:M:152:GLU:C	15:M:154:LEU:H	2.13	0.51
1:0:1787:C:OP1	17:O:68:LYS:HE2	2.11	0.51
25:W:18:ARG:NH1	36:W:4132:HOH:O	2.41	0.51
1:0:1592:G:O2'	1:0:1593:C:O4'	2.27	0.51
24:V:119:HIS:HD2	24:V:120:PRO:O	1.94	0.51
15:M:180:LEU:O	15:M:181:ASP:HB3	2.10	0.51
24:V:5:VAL:O	24:V:52:VAL:HG22	2.11	0.50
1:0:1180:U:H2'	1:0:1181:A:O4'	2.11	0.50
1:0:1194:A:N6	1:0:1206:U:O4	2.44	0.50
4:B:41:PHE:CE1	4:B:79:MET:HG3	2.45	0.50
10:H:71:TYR:O	10:H:73:GLN:N	2.44	0.50
25:W:43:VAL:HG12	25:W:44:ASP:N	2.25	0.50
4:B:14:GLY:HA2	4:B:15:PRO:C	2.31	0.50
1:0:2842:G:H2'	1:0:2843:A:H5'	1.92	0.50
24:V:122:ARG:HH22	24:V:154:ARG:C	2.15	0.50
1:0:2270:G:H4'	3:A:223:ARG:NH1	2.26	0.50
24:V:38:THR:HG22	24:V:39:ASP:H	1.77	0.50
1:0:2363:G:O3'	18:P:11:ARG:NH1	2.44	0.50
27:Y:19:GLY:O	27:Y:23:ARG:HG2	2.10	0.50
1:0:2361:A:H8	1:0:2361:A:H5'	1.76	0.50
1:0:899:C:H5'	36:0:9711:HOH:O	2.11	0.50
14:L:69:LYS:HG2	14:L:127:LYS:HG3	1.93	0.50
3:A:66:ARG:HH11	3:A:66:ARG:HB2	1.74	0.50
1:0:1733:A:H4'	4:B:212:GLN:HA	1.92	0.50
12:J:74:VAL:HG12	12:J:75:ARG:HG3	1.92	0.50
14:L:63:VAL:HG21	14:L:109:PHE:CZ	2.47	0.50
6:D:146:LYS:HZ3	15:M:107:ASN:HD21	1.57	0.50
4:B:168:GLY:O	4:B:169:GLY:O	2.30	0.50
21:S:49:GLU:OE2	21:S:97:ARG:HD2	2.10	0.50
13:K:97:VAL:HG12	13:K:98:GLU:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:65:ARG:HB3	36:H:8383:HOH:O	2.12	0.50
12:J:87:ARG:NE	36:J:4854:HOH:O	2.44	0.50
10:H:48:LEU:HD13	10:H:146:TRP:HB3	1.93	0.50
11:I:74:ARG:O	11:I:78:ILE:HG12	2.11	0.50
1:O:818:A:O2'	27:Y:13:ARG:HD3	2.11	0.50
13:K:61:ALA:HA	36:K:8563:HOH:O	2.12	0.50
4:B:63:GLU:HG3	4:B:63:GLU:O	2.11	0.50
5:C:129:HIS:CE1	5:C:231:ARG:HA	2.47	0.50
36:O:3572:HOH:O	4:B:27:ASN:HB2	2.10	0.50
10:H:56:ILE:HG21	10:H:61:LEU:HD13	1.94	0.50
4:B:320:GLN:HG3	4:B:321:PRO:HD2	1.94	0.50
24:V:125:HIS:HD2	24:V:127:GLY:H	1.58	0.50
12:J:28:GLU:HB3	12:J:59:LYS:HB2	1.93	0.50
4:B:27:ASN:H	4:B:27:ASN:HD22	1.59	0.50
2:9:35:C:H5''	36:9:8452:HOH:O	2.12	0.50
30:2:56:PRO:N	36:2:8549:HOH:O	2.43	0.50
5:C:233:THR:HG22	5:C:234:VAL:N	2.26	0.50
2:9:54:A:O2'	2:9:55:U:H5'	2.12	0.50
1:O:1834:C:H2'	1:O:1840:A:N6	2.26	0.50
3:A:194:MET:CE	3:A:199:HIS:HB2	2.42	0.50
4:B:333:GLU:HB2	22:T:14:GLU:OE2	2.10	0.50
1:O:2004:U:H2'	1:O:2004:U:O2	2.10	0.50
1:O:371:U:H2'	1:O:372:A:C8	2.45	0.50
3:A:94:LEU:HG	3:A:99:ILE:HD11	1.94	0.50
1:O:188:C:H5''	14:L:163:LEU:HD21	1.94	0.50
15:M:77:ASN:OD1	15:M:80:SER:HB2	2.12	0.50
2:9:92:G:H2'	2:9:93:A:C8	2.47	0.50
15:M:139:TRP:N	36:M:8572:HOH:O	2.45	0.50
5:C:235:PHE:HE2	5:C:243:VAL:HG21	1.77	0.50
26:X:186:ARG:NH1	26:X:186:ARG:HG2	2.26	0.50
4:B:248:ARG:HG2	36:B:8577:HOH:O	2.11	0.50
14:L:43:PRO:HG3	14:L:62:VAL:HG21	1.94	0.50
22:T:39:ASN:ND2	22:T:44:ARG:HH11	2.10	0.50
1:O:1559:A:H1'	36:O:5381:HOH:O	2.11	0.50
1:O:1717:A:H5''	17:O:54:LYS:HB2	1.94	0.50
12:J:29:LEU:HB3	12:J:55:VAL:CG1	2.30	0.50
6:D:41:LEU:HA	6:D:44:ILE:CG2	2.41	0.50
27:Y:30:GLU:O	27:Y:33:HIS:HB3	2.12	0.50
25:W:78:GLU:HG2	25:W:79:GLU:N	2.25	0.50
1:O:2756:U:N3	1:O:2896:A:H2	2.09	0.50
6:D:57:THR:HG23	6:D:63:ILE:CG2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1527:A:H1'	1:0:1528:A:C8	2.46	0.50
26:X:107:PRO:HB3	26:X:182:PHE:CE2	2.47	0.50
10:H:47:GLU:CB	10:H:133:ILE:HD13	2.42	0.49
6:D:99:ASP:CB	6:D:103:ASN:HB2	2.41	0.49
6:D:27:ILE:HD11	6:D:37:ALA:CB	2.42	0.49
10:H:147:ARG:HA	10:H:150:LYS:HZ2	1.77	0.49
25:W:41:PHE:O	25:W:43:VAL:HG23	2.11	0.49
1:0:920:C:H5'	1:0:921:G:C4	2.47	0.49
1:0:2434:A:O3'	30:2:28:GLY:HA3	2.12	0.49
1:0:2320:U:H4'	1:0:2321:A:O4'	2.12	0.49
1:0:175:G:H2'	14:L:192:ALA:HB3	1.94	0.49
1:0:1996:U:O2'	1:0:1997:A:H5'	2.12	0.49
22:T:47:ARG:CG	36:T:4381:HOH:O	2.60	0.49
7:E:10:ASP:HA	36:E:3707:HOH:O	2.11	0.49
4:B:56:ASP:OD1	4:B:322:ARG:HB3	2.12	0.49
17:O:71:LYS:O	17:O:71:LYS:HG3	2.12	0.49
1:0:1164:U:N3	1:0:1192:A:H2	2.02	0.49
1:0:380:A:OP2	14:L:9:ARG:HD2	2.11	0.49
1:0:1972:U:H2'	1:0:1973:A:H5'	1.95	0.49
1:0:1060:C:H6	1:0:1060:C:H5'	1.77	0.49
19:Q:29:LYS:HD3	36:Q:8530:HOH:O	2.11	0.49
1:0:1656:A:H2'	1:0:1657:A:O4'	2.12	0.49
28:Z:10:LYS:HG3	36:Z:8430:HOH:O	2.11	0.49
1:0:344:C:H2'	1:0:345:G:O4'	2.11	0.49
1:0:644:G:N3	1:0:644:G:H5'	2.27	0.49
1:0:1289:C:O2'	1:0:1290:G:H5'	2.12	0.49
1:0:1500:U:P	17:O:41:ARG:HH22	2.35	0.49
1:0:654:A:OP2	16:N:38:ARG:HD3	2.12	0.49
1:0:1266:U:H4'	26:X:115:ARG:HH21	1.76	0.49
26:X:107:PRO:HB3	26:X:182:PHE:CD2	2.48	0.49
1:0:1056:U:H2'	1:0:1057:A:O4'	2.12	0.49
4:B:30:PRO:HB2	4:B:39:GLN:NE2	2.27	0.49
1:0:559:U:H5'	1:0:559:U:C6	2.39	0.49
12:J:45:PRO:HB2	36:J:7169:HOH:O	2.13	0.49
1:0:656:G:OP2	16:N:37:ARG:HD2	2.12	0.49
1:0:407:A:H5'	36:0:5542:HOH:O	2.12	0.49
3:A:123:GLY:HA3	3:A:162:GLY:HA2	1.95	0.49
36:0:6950:HOH:O	21:S:9:LYS:HD2	2.12	0.49
3:A:128:LEU:HG	36:A:8576:HOH:O	2.11	0.49
1:0:396:U:OP2	30:2:38:ARG:NH1	2.44	0.49
1:0:538:C:OP2	26:X:134:HIS:HE1	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:44:ARG:HB3	36:T:3805:HOH:O	2.11	0.49
14:L:155:HIS:CE1	14:L:158:ARG:HE	2.29	0.49
1:O:1595:G:O2'	1:O:1596:U:H5'	2.12	0.49
5:C:219:ASN:O	5:C:222:ASP:OD1	2.30	0.49
21:S:71:VAL:HG11	21:S:90:PRO:CB	2.28	0.49
1:O:1010:C:H4'	15:M:4:PRO:HB2	1.95	0.49
11:I:42:GLU:O	11:I:131:THR:HG23	2.12	0.49
7:E:11:VAL:CG1	7:E:12:ASP:N	2.75	0.49
10:H:130:HIS:CG	10:H:133:ILE:HD11	2.46	0.49
15:M:73:ALA:HB2	15:M:163:PHE:CZ	2.48	0.49
11:I:47:THR:HG22	11:I:48:GLY:N	2.28	0.49
4:B:41:PHE:CZ	4:B:79:MET:HG3	2.47	0.49
13:K:148:GLU:HB2	36:K:8587:HOH:O	2.11	0.49
14:L:78:ASN:C	14:L:79:LYS:HG2	2.33	0.49
4:B:279:THR:OG1	4:B:290:VAL:HB	2.12	0.49
22:T:52:THR:HG22	22:T:54:THR:H	1.77	0.49
30:2:55:VAL:HB	30:2:56:PRO:HD2	1.95	0.49
24:V:126:ASP:HB3	24:V:135:GLY:O	2.12	0.49
22:T:47:ARG:HG3	36:T:4381:HOH:O	2.13	0.49
1:O:2472:C:O2'	1:O:2634:G:H4'	2.12	0.49
1:O:1192:A:N3	36:O:3910:HOH:O	2.45	0.49
1:O:1204:C:C4	1:O:1205:U:C5	3.00	0.49
1:O:558:C:C2'	1:O:559:U:C5'	2.91	0.49
24:V:65:VAL:HA	24:V:68:THR:CG2	2.42	0.49
27:Y:26:VAL:O	27:Y:30:GLU:HG3	2.13	0.49
1:O:1172:G:H5'	36:O:6784:HOH:O	2.13	0.49
1:O:2756:U:N3	1:O:2896:A:C2	2.72	0.49
5:C:246:ARG:NH1	36:C:8372:HOH:O	2.46	0.49
1:O:2316:G:H4'	36:O:5611:HOH:O	2.12	0.49
21:S:38:ARG:NH1	36:S:6217:HOH:O	2.45	0.49
1:O:447:A:O2'	1:O:448:G:H5'	2.13	0.49
4:B:27:ASN:HB3	36:B:8632:HOH:O	2.12	0.49
36:O:5713:HOH:O	29:1:44:ARG:HG2	2.13	0.49
4:B:7:ARG:HD2	4:B:9:GLY:O	2.12	0.49
13:K:120:LEU:HD12	13:K:133:VAL:HG21	1.95	0.49
4:B:41:PHE:CD2	4:B:190:MET:HE3	2.47	0.49
11:I:45:VAL:HG22	11:I:46:ILE:N	2.27	0.49
15:M:139:TRP:HA	15:M:139:TRP:CE3	2.48	0.49
7:E:92:PRO:HB2	36:E:4917:HOH:O	2.12	0.49
2:9:24:U:H4'	2:9:25:G:OP1	2.13	0.48
1:O:820:G:C6	3:A:171:LYS:HB2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:84:VAL:HG12	36:V:6679:HOH:O	2.13	0.48
26:X:189:ASN:ND2	26:X:192:ASP:H	2.11	0.48
1:0:281:U:H3'	36:0:6729:HOH:O	2.13	0.48
27:Y:30:GLU:HB3	27:Y:34:LYS:HE3	1.95	0.48
8:F:50:VAL:CG2	8:F:63:ILE:HG21	2.42	0.48
3:A:130:THR:HG22	3:A:131:HIS:O	2.12	0.48
2:9:41:C:C6	6:D:50:VAL:HG21	2.47	0.48
14:L:182:LYS:HD2	14:L:193:LYS:HB2	1.95	0.48
1:0:256:C:H2'	1:0:257:G:O4'	2.13	0.48
29:1:24:TRP:NE1	36:1:6863:HOH:O	2.43	0.48
3:A:192:VAL:HG12	3:A:207:GLN:HB3	1.96	0.48
1:0:1730:G:C5'	1:0:1731:C:C6	2.96	0.48
21:S:41:ARG:NH1	21:S:41:ARG:HG2	2.28	0.48
1:0:2256:G:H2'	1:0:2257:G:C5'	2.43	0.48
14:L:5:TYR:HE2	14:L:46:LEU:HD13	1.78	0.48
4:B:248:ARG:O	4:B:251:VAL:HG12	2.13	0.48
1:0:1234:U:N3	4:B:244:PRO:HB3	2.29	0.48
19:Q:68:HIS:CD2	19:Q:76:ASP:HB2	2.48	0.48
5:C:150:THR:HA	5:C:203:ALA:O	2.14	0.48
5:C:166:ILE:CD1	5:C:207:LEU:HD13	2.43	0.48
8:F:113:ASP:O	8:F:117:GLU:HG3	2.13	0.48
1:0:681:G:N3	1:0:681:G:H5'	2.29	0.48
14:L:115:LEU:HD13	14:L:116:ASN:HB2	1.95	0.48
1:0:2768:A:H5''	36:0:3935:HOH:O	2.13	0.48
36:0:5044:HOH:O	14:L:58:GLN:HG3	2.13	0.48
28:Z:28:HIS:CD2	28:Z:31:LYS:HG3	2.48	0.48
26:X:172:THR:HG22	26:X:173:ALA:N	2.29	0.48
20:R:73:ASP:OD1	20:R:75:GLN:HB2	2.13	0.48
26:X:200:THR:HG22	26:X:201:GLU:CG	2.33	0.48
26:X:126:PRO:HG2	26:X:128:PHE:CZ	2.47	0.48
6:D:10:PHE:CD1	6:D:11:HIS:N	2.81	0.48
14:L:74:ARG:NH1	14:L:74:ARG:HG3	2.28	0.48
1:0:2044:G:OP1	25:W:23:HIS:HE1	1.97	0.48
1:0:1699:C:H4'	36:0:5960:HOH:O	2.14	0.48
13:K:62:ALA:HB2	13:K:103:ALA:CB	2.43	0.48
10:H:26:LYS:HD3	10:H:89:PRO:CG	2.42	0.48
1:0:1192:A:H3'	1:0:1193:A:H5'	1.94	0.48
21:S:41:ARG:NH1	21:S:42:VAL:O	2.46	0.48
1:0:2256:G:H2'	1:0:2257:G:H5'	1.95	0.48
1:0:1484:G:H2'	36:0:8618:HOH:O	2.13	0.48
1:0:1940:C:H4'	36:0:6871:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:168:C:O2'	1:0:169:A:H5'	2.13	0.48
1:0:278:A:H2'	1:0:279:C:O4'	2.14	0.48
5:C:140:VAL:HG12	5:C:141:SER:N	2.29	0.48
15:M:37:ARG:CZ	36:M:8535:HOH:O	2.62	0.48
27:Y:38:LYS:HG3	36:Y:8431:HOH:O	2.14	0.48
24:V:3:ALA:O	24:V:54:PHE:HA	2.14	0.48
2:9:42:C:O2	6:D:76:ARG:NH1	2.47	0.48
1:0:2420:G:H4'	36:0:3602:HOH:O	2.13	0.48
4:B:207:LYS:HG2	4:B:304:PRO:HB3	1.94	0.48
1:0:121:U:OP2	29:1:10:ARG:NH2	2.39	0.48
7:E:77:THR:OG1	7:E:78:GLU:N	2.45	0.48
10:H:26:LYS:HD3	10:H:89:PRO:HG3	1.95	0.48
27:Y:46:LYS:NZ	36:Y:8442:HOH:O	2.46	0.48
1:0:1666:C:C2'	1:0:1667:A:C5'	2.92	0.48
1:0:2896:A:N3	1:0:2896:A:H2'	2.29	0.48
30:2:48:ASN:ND2	30:2:50:GLY:H	2.11	0.48
1:0:1819:G:H2'	1:0:1820:G:C4'	2.44	0.48
1:0:2837:U:H1'	4:B:307:ARG:HH12	1.79	0.48
2:9:91:C:H2'	2:9:92:G:O4'	2.13	0.48
1:0:2326:U:H4'	1:0:2412:G:H4'	1.96	0.48
26:X:122:ARG:NH2	36:X:8536:HOH:O	2.46	0.48
6:D:67:ASP:OD2	6:D:69:ILE:HD11	2.13	0.48
10:H:55:GLN:HE21	10:H:124:ARG:NE	2.02	0.48
12:J:75:ARG:HG2	12:J:90:PHE:CD2	2.49	0.48
24:V:122:ARG:CG	24:V:122:ARG:HH11	2.19	0.48
17:O:59:ARG:HH22	17:O:66:GLN:HE22	1.60	0.48
21:S:41:ARG:O	21:S:43:ASN:ND2	2.47	0.48
8:F:22:VAL:CG2	8:F:104:ALA:HB2	2.43	0.48
1:0:450:C:OP1	5:C:184:ARG:NH2	2.31	0.48
1:0:1028:U:H1'	36:0:3157:HOH:O	2.14	0.48
6:D:101:THR:HG22	36:D:7400:HOH:O	2.14	0.48
7:E:95:VAL:O	7:E:126:ILE:HD13	2.13	0.48
24:V:130:HIS:O	24:V:136:GLY:HA3	2.14	0.48
1:0:2073:G:OP2	1:0:2490:A:H5'	2.14	0.48
15:M:58:LEU:HD12	15:M:58:LEU:N	2.29	0.48
10:H:46:VAL:O	10:H:146:TRP:CH2	2.63	0.48
4:B:162:MET:CE	4:B:310:ARG:HD3	2.44	0.48
1:0:1477:C:H5'	1:0:1868:G:H5''	1.95	0.48
1:0:941:G:O2'	1:0:942:U:H5'	2.13	0.48
1:0:185:G:H4'	1:0:186:A:H4'	1.96	0.48
21:S:73:HIS:CD2	21:S:88:PRO:HG3	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1003:U:O2'	10:H:90:PHE:HE1	1.96	0.48
1:0:1667:A:H2'	1:0:1668:U:H6	1.78	0.47
15:M:171:HIS:CE1	36:M:8569:HOH:O	2.67	0.47
4:B:144:THR:HG22	4:B:145:HIS:N	2.28	0.47
3:A:36:ASP:O	3:A:38:ILE:N	2.47	0.47
1:0:656:G:H5'	16:N:3:THR:HG22	1.96	0.47
15:M:79:PRO:HG3	15:M:142:THR:O	2.14	0.47
1:0:584:U:H3'	36:0:5614:HOH:O	2.12	0.47
1:0:1132:A:N6	1:0:1229:C:H2'	2.29	0.47
1:0:2443:C:H3'	36:0:9984:HOH:O	2.14	0.47
15:M:32:PRO:HD2	15:M:99:GLU:O	2.14	0.47
6:D:167:GLU:OE2	6:D:173:GLU:HG2	2.13	0.47
1:0:1878:G:O2'	1:0:1879:U:OP2	2.32	0.47
1:0:2791:U:H1'	1:0:2792:A:H5''	1.95	0.47
36:0:6749:HOH:O	14:L:13:LYS:HE2	2.13	0.47
1:0:1409:G:H5'	36:0:3237:HOH:O	2.14	0.47
2:9:64:C:H2'	2:9:65:A:H5'	1.97	0.47
1:0:1909:A:N1	1:0:2128:G:H1'	2.28	0.47
10:H:157:ILE:CG2	10:H:158:ASN:N	2.77	0.47
1:0:182:G:H4'	14:L:157:LEU:HD13	1.96	0.47
6:D:94:ALA:HB3	6:D:174:VAL:HA	1.96	0.47
26:X:154:ARG:HH12	26:X:155:ARG:HG3	1.79	0.47
1:0:482:G:H4'	1:0:508:A:N1	2.29	0.47
1:0:1014:A:H2'	1:0:1015:C:H5'	1.96	0.47
10:H:84:ARG:CZ	10:H:135:TRP:HH2	2.26	0.47
1:0:1166:A:H61	1:0:1180:U:H3	1.61	0.47
6:D:23:VAL:CG2	6:D:73:VAL:HB	2.43	0.47
7:E:31:ARG:HH12	7:E:68:HIS:CE1	2.32	0.47
8:F:58:GLU:HA	8:F:61:MET:HG3	1.96	0.47
1:0:1500:U:OP2	17:O:41:ARG:NH2	2.48	0.47
4:B:195:ARG:HD2	4:B:324:ASP:OD1	2.14	0.47
15:M:184:ILE:HG22	15:M:185:GLU:N	2.27	0.47
1:0:1333:U:H2'	1:0:1334:C:H6	1.79	0.47
21:S:18:GLU:O	21:S:21:LYS:HG2	2.15	0.47
9:G:20:VAL:O	9:G:24:VAL:HG23	2.15	0.47
18:P:30:VAL:O	18:P:30:VAL:HG12	2.14	0.47
10:H:163:PRO:O	10:H:164:ALA:HB2	2.14	0.47
36:0:4483:HOH:O	10:H:57:ARG:HG3	2.14	0.47
1:0:2769:C:H2'	1:0:2770:G:C5'	2.44	0.47
22:T:17:THR:HG22	22:T:18:GLY:N	2.30	0.47
25:W:76:ARG:HG3	25:W:76:ARG:NH1	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:76:ARG:O	25:W:77:PHE:HB3	2.14	0.47
3:A:51:ARG:NH2	3:A:69:LEU:HD13	2.28	0.47
8:F:46:GLU:O	8:F:73:PRO:HD2	2.14	0.47
6:D:59:GLY:C	6:D:61:PHE:H	2.18	0.47
17:O:105:LEU:CD2	17:O:137:LEU:HD21	2.45	0.47
30:2:3:MET:O	30:2:90:PHE:HA	2.14	0.47
17:O:98:ILE:HD12	17:O:102:ARG:NE	2.30	0.47
1:O:432:G:O2'	1:O:433:C:H5'	2.14	0.47
4:B:32:ASP:HA	36:B:8575:HOH:O	2.13	0.47
21:S:63:ILE:HD11	21:S:75:GLU:HB2	1.95	0.47
1:O:2670:G:O2'	1:O:2671:U:H5'	2.15	0.47
10:H:132:PHE:O	10:H:133:ILE:HD13	2.13	0.47
10:H:149:ALA:C	10:H:151:MET:H	2.17	0.47
15:M:90:LEU:CB	15:M:186:LEU:HD22	2.44	0.47
10:H:150:LYS:HG2	36:H:8381:HOH:O	2.14	0.47
7:E:132:THR:O	7:E:132:THR:HG23	2.15	0.47
10:H:111:MET:O	10:H:114:PRO:HD3	2.14	0.47
1:O:2488:A:H2	36:O:6800:HOH:O	1.96	0.47
1:O:621:C:H5'	26:X:132:ASP:OD2	2.15	0.47
25:W:70:ILE:O	25:W:70:ILE:HG23	2.14	0.47
10:H:86:ARG:HD3	10:H:130:HIS:HD2	1.80	0.47
1:O:2720:C:O2	12:J:87:ARG:NH2	2.48	0.47
24:V:110:GLN:NE2	24:V:110:GLN:HA	2.30	0.47
36:9:8462:HOH:O	15:M:147:ILE:HD12	2.14	0.47
10:H:150:LYS:HE2	36:H:8377:HOH:O	2.14	0.47
6:D:146:LYS:HZ1	15:M:107:ASN:HD21	1.60	0.47
5:C:107:ARG:NH2	36:C:8457:HOH:O	2.39	0.47
10:H:127:GLY:O	10:H:128:ALA:CB	2.63	0.47
4:B:168:GLY:N	4:B:174:ARG:HD3	2.29	0.47
13:K:53:ARG:HH22	13:K:57:VAL:HG12	1.79	0.47
1:O:1878:G:O2'	1:O:1879:U:P	2.73	0.47
26:X:115:ARG:NE	36:X:8557:HOH:O	2.47	0.47
1:O:2361:A:H5''	36:O:8523:HOH:O	2.15	0.47
8:F:117:GLU:C	8:F:119:ARG:H	2.18	0.47
1:O:671:A:O2'	1:O:672:G:H2'	2.15	0.47
1:O:581:G:H5'	36:O:7219:HOH:O	2.14	0.47
7:E:21:THR:HG23	7:E:30:THR:OG1	2.15	0.47
1:O:1681:G:H5''	1:O:1682:A:H5'	1.96	0.47
1:O:2724:U:H2'	1:O:2725:G:O4'	2.14	0.47
1:O:119:A:H2'	1:O:120:A:H5''	1.95	0.47
7:E:108:LEU:HB3	36:E:1306:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1181:A:C2	1:0:1192:A:C8	3.03	0.47
14:L:173:LEU:HD23	14:L:183:VAL:HG12	1.97	0.47
29:1:18:ASN:ND2	29:1:40:ARG:H	2.09	0.47
25:W:9:VAL:HG13	25:W:88:GLU:OE2	2.15	0.47
15:M:143:ARG:HA	15:M:172:PHE:CD2	2.50	0.47
1:0:1003:U:O2	10:H:90:PHE:CZ	2.68	0.47
1:0:2563:U:H2'	1:0:2565:C:O5'	2.14	0.47
1:0:2010:A:H2'	36:0:5476:HOH:O	2.15	0.47
14:L:57:LYS:HE2	14:L:140:ALA:O	2.14	0.47
3:A:81:GLN:HB2	3:A:92:ASN:HD22	1.80	0.47
17:O:16:VAL:CG1	17:O:17:GLY:N	2.78	0.47
22:T:49:LEU:HD11	36:T:3805:HOH:O	2.15	0.47
1:0:2353:A:H4'	1:0:2354:A:O5'	2.13	0.47
1:0:291:C:H2'	1:0:292:G:O4'	2.15	0.47
1:0:189:A:OP1	14:L:171:ARG:NH2	2.47	0.47
1:0:1185:U:H5'	36:0:6994:HOH:O	2.15	0.47
10:H:136:VAL:HG23	36:H:8343:HOH:O	2.14	0.47
4:B:79:MET:HE3	4:B:144:THR:HG21	1.97	0.47
4:B:307:ARG:HD3	36:B:8524:HOH:O	2.15	0.47
4:B:82:VAL:HG12	4:B:101:TRP:CE3	2.50	0.47
1:0:1250:C:O2'	1:0:1251:C:H5'	2.15	0.47
13:K:101:ASP:C	13:K:103:ALA:H	2.18	0.47
1:0:1753:C:O2	4:B:229:ARG:NH2	2.46	0.47
4:B:80:ARG:HD3	36:B:8611:HOH:O	2.15	0.47
7:E:145:ALA:HB1	7:E:168:ILE:CD1	2.45	0.47
30:2:7:PHE:HE2	30:2:22:VAL:HG21	1.80	0.47
24:V:21:LEU:CD2	24:V:48:VAL:HG11	2.43	0.46
10:H:150:LYS:NZ	36:H:8377:HOH:O	2.47	0.46
1:0:283:U:H5	1:0:284:C:N4	2.12	0.46
1:0:1741:U:O2'	1:0:2723:G:H4'	2.15	0.46
1:0:1120:U:H5'	1:0:1121:G:OP2	2.15	0.46
5:C:13:ASP:OD1	5:C:13:ASP:O	2.33	0.46
1:0:951:A:O2'	1:0:952:G:H5'	2.15	0.46
7:E:34:TRP:O	11:I:127:ILE:HD11	2.15	0.46
16:N:25:VAL:HG23	16:N:26:TRP:N	2.30	0.46
2:9:24:U:C6	36:9:8477:HOH:O	2.56	0.46
3:A:88:ILE:HD13	3:A:100:PRO:CD	2.39	0.46
1:0:1505:U:C6	1:0:1505:U:H5'	2.46	0.46
1:0:603:A:H4'	1:0:604:G:O5'	2.15	0.46
3:A:223:ARG:NH1	36:A:8518:HOH:O	2.48	0.46
1:0:1167:G:O2'	1:0:1168:C:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:41:TYR:HA	24:V:44:MET:HE3	1.97	0.46
16:N:25:VAL:HG23	16:N:26:TRP:H	1.80	0.46
6:D:153:THR:HG22	36:D:5234:HOH:O	2.15	0.46
10:H:47:GLU:CB	10:H:133:ILE:CD1	2.91	0.46
15:M:37:ARG:HD3	15:M:37:ARG:HA	1.71	0.46
17:O:38:GLU:HA	17:O:41:ARG:HH11	1.78	0.46
6:D:55:LYS:O	6:D:56:ARG:HB2	2.14	0.46
26:X:112:GLU:OE2	26:X:115:ARG:NH1	2.49	0.46
24:V:41:TYR:CD2	24:V:44:MET:HE3	2.50	0.46
13:K:21:ARG:N	36:K:8531:HOH:O	2.48	0.46
1:O:204:A:C2'	1:O:205:U:H5'	2.45	0.46
6:D:23:VAL:HG12	6:D:130:VAL:HG22	1.98	0.46
8:F:60:VAL:HG12	8:F:60:VAL:O	2.16	0.46
11:I:46:ILE:HA	36:I:1123:HOH:O	2.15	0.46
1:O:585:C:H6	36:O:5614:HOH:O	1.97	0.46
7:E:5:LEU:HD21	7:E:66:GLN:HG3	1.97	0.46
5:C:19:PRO:HG2	5:C:22:PHE:CD1	2.50	0.46
12:J:66:ARG:HH11	12:J:66:ARG:HG2	1.80	0.46
5:C:236:THR:HG22	5:C:239:ALA:CB	2.46	0.46
15:M:89:GLY:O	15:M:92:ALA:HB3	2.15	0.46
24:V:4:LEU:HD23	24:V:54:PHE:HB3	1.97	0.46
15:M:7:LYS:HE2	36:M:8514:HOH:O	2.14	0.46
1:O:1439:C:OP1	29:1:41:HIS:HE1	1.97	0.46
14:L:37:VAL:HG12	14:L:63:VAL:HG11	1.97	0.46
11:I:70:PHE:CD2	11:I:70:PHE:O	2.68	0.46
12:J:4:LEU:HD22	12:J:116:GLU:HB3	1.98	0.46
4:B:241:PRO:HD2	36:B:8661:HOH:O	2.14	0.46
15:M:100:ALA:O	15:M:129:ILE:HG23	2.16	0.46
1:O:816:G:C6	1:O:817:G:N1	2.83	0.46
14:L:167:GLY:O	14:L:171:ARG:HG3	2.15	0.46
4:B:217:ARG:HG3	4:B:257:THR:CG2	2.45	0.46
5:C:214:THR:HB	36:C:8325:HOH:O	2.16	0.46
1:O:1419:U:H2'	1:O:1685:A:C2	2.51	0.46
8:F:16:ALA:HA	8:F:111:ILE:HD13	1.97	0.46
21:S:27:LEU:HD23	21:S:98:VAL:HB	1.98	0.46
12:J:101:ASN:O	12:J:102:GLU:HB2	2.15	0.46
18:P:66:LYS:HB2	18:P:70:ALA:O	2.16	0.46
2:9:107:C:H5	36:9:8436:HOH:O	1.97	0.46
1:O:2730:G:O2'	1:O:2731:G:H5'	2.15	0.46
1:O:128:A:H3'	1:O:128:A:C8	2.50	0.46
1:O:2502:C:C4'	10:H:151:MET:HG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3:A:H61	2:9:22:G:H1'	1.75	0.46
10:H:157:ILE:HG22	10:H:158:ASN:N	2.30	0.46
11:I:93:ARG:HH11	11:I:93:ARG:CB	2.23	0.46
1:0:656:G:H5'	16:N:3:THR:CG2	2.46	0.46
25:W:9:VAL:HG13	25:W:88:GLU:OE1	2.16	0.46
8:F:101:ALA:HA	36:F:5413:HOH:O	2.16	0.46
2:9:88:G:OP1	24:V:130:HIS:NE2	2.46	0.46
4:B:75:GLU:C	4:B:77:PRO:HD3	2.35	0.46
6:D:128:LEU:N	36:D:6007:HOH:O	2.49	0.46
20:R:8:PRO:HD2	23:U:32:ALA:HA	1.98	0.46
1:0:2831:C:H2'	1:0:2832:C:H5'	1.98	0.46
4:B:66:GLU:OE1	4:B:328:ARG:HD2	2.15	0.46
1:0:1119:G:H2'	11:I:52:GLN:NE2	2.31	0.46
4:B:7:ARG:NH1	4:B:11:LEU:CD2	2.79	0.46
1:0:88:G:C6	29:1:24:TRP:CE3	3.04	0.46
14:L:38:VAL:HG12	14:L:38:VAL:O	2.15	0.46
1:0:431:G:OP1	14:L:48:ARG:NH1	2.49	0.46
24:V:38:THR:HB	36:V:5390:HOH:O	2.15	0.46
1:0:474:C:O3'	5:C:73:LEU:CD2	2.64	0.46
8:F:107:VAL:HG23	36:F:6617:HOH:O	2.16	0.46
22:T:9:CYS:CA	22:T:52:THR:HG23	2.45	0.46
28:Z:28:HIS:HD2	28:Z:30:LYS:H	1.62	0.46
7:E:107:PHE:CE2	7:E:108:LEU:HD13	2.51	0.46
25:W:66:THR:HG23	25:W:67:PRO:HD2	1.98	0.46
1:0:2403:C:H3'	36:O:4722:HOH:O	2.16	0.46
1:0:2649:A:H5'	1:0:2649:A:H8	1.80	0.46
10:H:134:ALA:HB3	10:H:142:VAL:HG21	1.97	0.46
1:0:1603:A:H5''	1:0:1605:G:H5'	1.97	0.46
1:0:2415:A:H2'	1:0:2416:G:H5'	1.96	0.46
4:B:55:ASN:HB3	4:B:64:GLY:H	1.81	0.46
11:I:19:MET:CE	11:I:132:LEU:HD11	2.46	0.46
1:0:2883:A:H2'	1:0:2884:G:O4'	2.16	0.46
1:0:1592:G:HO2'	1:0:1593:C:C4'	2.29	0.46
1:0:1789:G:O6	17:O:73:HIS:HE1	1.98	0.46
10:H:141:ASN:HA	36:H:8365:HOH:O	2.16	0.46
4:B:102:THR:HG21	4:B:182:VAL:O	2.16	0.46
1:0:1735:C:O2'	1:0:1736:A:H5'	2.15	0.46
2:9:3:A:H2	2:9:21:G:N3	2.14	0.46
15:M:5:ARG:HG3	18:P:18:PRO:CB	2.46	0.46
3:A:81:GLN:CB	3:A:92:ASN:ND2	2.78	0.46
2:9:39:U:H3'	2:9:40:C:H5''	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:475:G:C5'	5:C:73:LEU:HD23	2.46	0.46
2:9:31:C:H2'	2:9:32:G:O4'	2.16	0.46
1:0:2679:G:H2'	1:0:2681:A:OP2	2.16	0.46
8:F:48:VAL:CG2	8:F:74:PHE:HB3	2.45	0.46
1:0:820:G:C5	3:A:171:LYS:HB2	2.51	0.45
1:0:88:G:N7	29:1:28:LYS:HD2	2.30	0.45
1:0:2768:A:H3'	36:0:3935:HOH:O	2.15	0.45
4:B:221:GLN:HE22	12:J:42:ASN:ND2	2.08	0.45
23:U:55:ARG:NH2	36:U:4428:HOH:O	2.40	0.45
4:B:72:THR:HB	36:B:8610:HOH:O	2.15	0.45
3:A:48:ASP:HB3	36:A:8608:HOH:O	2.17	0.45
26:X:154:ARG:NH1	26:X:155:ARG:HG3	2.31	0.45
1:0:1418:U:OP1	29:1:42:TRP:HB3	2.16	0.45
12:J:79:PRO:HB2	36:J:782:HOH:O	2.15	0.45
1:0:2825:C:H4'	1:0:2826:G:O5'	2.16	0.45
4:B:268:ARG:NH2	4:B:325:PRO:HG3	2.31	0.45
10:H:84:ARG:CZ	10:H:135:TRP:CH2	2.99	0.45
5:C:118:THR:CG2	5:C:137:PRO:HB3	2.46	0.45
10:H:150:LYS:HA	10:H:153:VAL:HG22	1.97	0.45
4:B:60:SER:C	4:B:62:ARG:H	2.18	0.45
17:O:120:ARG:NH2	17:O:123:TYR:CD2	2.84	0.45
30:2:73:GLU:HB2	36:2:8527:HOH:O	2.16	0.45
21:S:40:VAL:HG22	21:S:41:ARG:N	2.31	0.45
8:F:28:ALA:HB3	8:F:99:THR:O	2.15	0.45
20:R:32:ALA:HA	20:R:36:GLU:OE1	2.16	0.45
1:0:2559:C:H4'	36:0:6780:HOH:O	2.16	0.45
1:0:2297:U:H1'	36:0:4686:HOH:O	2.17	0.45
22:T:50:GLU:CD	36:T:7349:HOH:O	2.53	0.45
18:P:25:PRO:HA	18:P:26:PRO:HD3	1.84	0.45
1:0:960:G:N3	1:0:960:G:C2'	2.79	0.45
10:H:26:LYS:HA	10:H:58:HIS:CD2	2.51	0.45
15:M:86:LEU:O	15:M:90:LEU:HG	2.16	0.45
1:0:1666:C:C2'	1:0:1667:A:H5'	2.44	0.45
1:0:776:A:OP1	28:Z:28:HIS:HE1	2.00	0.45
1:0:737:A:H2'	1:0:738:G:O4'	2.16	0.45
23:U:57:LYS:HA	23:U:60:GLN:HE21	1.81	0.45
1:0:95:A:H5''	1:0:97:G:O4'	2.16	0.45
11:I:90:LYS:HB2	34:I:8502:CL:CL	2.53	0.45
20:R:6:LYS:HB2	20:R:27:ALA:O	2.15	0.45
1:0:2401:A:H5'	36:0:9000:HOH:O	2.16	0.45
1:0:821:U:H5''	36:0:9559:HOH:O	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:33:LYS:HE2	36:C:8362:HOH:O	2.16	0.45
6:D:166:ILE:O	6:D:169:THR:N	2.49	0.45
15:M:71:TRP:N	36:M:8540:HOH:O	2.49	0.45
30:2:65:THR:HB	30:2:83:TRP:H	1.81	0.45
4:B:280:VAL:HG13	4:B:333:GLU:O	2.17	0.45
4:B:16:ARG:NH2	36:B:8555:HOH:O	2.44	0.45
1:0:1730:G:C5'	1:0:1731:C:H6	2.29	0.45
15:M:154:LEU:CG	15:M:155:GLU:H	2.26	0.45
36:0:6931:HOH:O	21:S:2:LYS:HE2	2.14	0.45
7:E:84:MET:HB2	7:E:131:LEU:HB2	1.97	0.45
1:0:2912:C:H2'	1:0:2913:A:O4'	2.17	0.45
10:H:81:TYR:C	10:H:81:TYR:CD1	2.89	0.45
4:B:205:VAL:O	4:B:307:ARG:NE	2.49	0.45
24:V:11:VAL:O	24:V:12:ASN:HB2	2.16	0.45
4:B:1:PRO:O	4:B:2:GLN:HB2	2.16	0.45
1:0:2361:A:H2'	1:0:2362:A:C8	2.51	0.45
5:C:234:VAL:HG22	5:C:234:VAL:O	2.17	0.45
7:E:84:MET:HE1	7:E:148:ILE:HD12	1.99	0.45
1:0:1218:U:H2'	1:0:1219:U:C6	2.51	0.45
4:B:275:GLY:O	4:B:291:ASP:HA	2.17	0.45
12:J:27:ARG:HD2	36:J:4747:HOH:O	2.17	0.45
1:0:797:A:H4'	27:Y:10:ARG:N	2.31	0.45
2:9:2:U:OP2	2:9:3:A:H5'	2.16	0.45
1:0:1268:C:O2'	1:0:1269:G:H5'	2.15	0.45
1:0:2780:C:H1'	7:E:143:GLN:NE2	2.30	0.45
12:J:98:VAL:HG22	12:J:102:GLU:C	2.36	0.45
12:J:78:LYS:HA	12:J:79:PRO:HD3	1.86	0.45
1:0:1314:U:H2'	36:0:5390:HOH:O	2.16	0.45
3:A:8:ARG:HG2	36:A:8553:HOH:O	2.16	0.45
8:F:50:VAL:HG11	8:F:60:VAL:HG11	1.97	0.45
5:C:162:VAL:HG12	5:C:162:VAL:O	2.17	0.45
1:0:1086:A:N6	24:V:11:VAL:HG11	2.32	0.45
1:0:1853:C:OP1	3:A:231:LYS:HG3	2.17	0.45
4:B:127:GLN:HG3	36:B:8647:HOH:O	2.16	0.45
24:V:129:LYS:HG2	36:V:1990:HOH:O	2.17	0.45
1:0:420:U:H2'	1:0:421:C:C6	2.52	0.45
18:P:31:GLU:CD	18:P:93:ARG:HH12	2.20	0.45
1:0:814:G:H4'	36:0:9643:HOH:O	2.16	0.45
7:E:93:MET:HE1	7:E:165:GLY:N	2.32	0.45
6:D:41:LEU:CA	6:D:44:ILE:HG22	2.46	0.45
21:S:45:GLY:C	36:S:3851:HOH:O	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:307:ARG:HH11	4:B:307:ARG:HG3	1.81	0.45
5:C:39:GLN:O	5:C:43:LYS:HD3	2.17	0.45
7:E:108:LEU:HD11	7:E:164:ASP:HB2	1.99	0.45
1:O:136:C:H2'	1:O:137:U:O4'	2.16	0.45
19:Q:84:ALA:O	19:Q:88:PHE:HD1	1.99	0.45
1:O:1176:C:H1'	36:O:3439:HOH:O	2.16	0.45
1:O:514:G:O5'	1:O:514:G:H8	1.99	0.45
1:O:1183:C:N4	36:O:3910:HOH:O	2.48	0.45
7:E:32:ARG:O	7:E:33:LEU:HD23	2.16	0.45
15:M:167:ASP:O	15:M:168:LEU:HD23	2.17	0.45
1:O:566:A:H2'	1:O:567:U:O4'	2.17	0.45
27:Y:33:HIS:HE1	27:Y:49:ARG:NE	2.15	0.45
14:L:67:ILE:CD1	14:L:104:ARG:HD2	2.47	0.45
1:O:1730:G:H5'	1:O:1731:C:H5	1.81	0.45
1:O:1684:A:O2'	1:O:1685:A:H5''	2.17	0.45
1:O:1168:C:H5	36:O:7027:HOH:O	1.99	0.45
10:H:113:ALA:N	10:H:114:PRO:CD	2.80	0.45
7:E:154:ILE:HG13	7:E:156:ASP:OD1	2.17	0.45
7:E:20:ILE:HD12	7:E:33:LEU:HD12	2.00	0.45
23:U:1:THR:HG23	23:U:2:VAL:N	2.22	0.45
36:O:5586:HOH:O	27:Y:34:LYS:HE2	2.17	0.45
29:1:18:ASN:HD22	29:1:18:ASN:HA	1.59	0.45
23:U:55:ARG:NE	36:U:4428:HOH:O	2.37	0.45
7:E:126:ILE:HB	7:E:131:LEU:CD2	2.47	0.45
1:O:926:A:O2'	13:K:41:HIS:HD2	2.00	0.45
2:9:51:A:H5'	15:M:160:SER:HB3	1.99	0.45
3:A:17:ARG:HD2	36:A:8542:HOH:O	2.17	0.45
11:I:142:ASN:O	11:I:144:THR:N	2.50	0.45
1:O:2642:G:H2'	1:O:2643:G:O4'	2.17	0.45
5:C:153:VAL:O	5:C:157:LEU:HG	2.17	0.45
1:O:1162:G:H2'	36:O:6102:HOH:O	2.17	0.45
5:C:164:ALA:O	5:C:167:ASP:HB2	2.17	0.45
1:O:1636:G:O2'	1:O:1637:A:H5'	2.16	0.45
8:F:13:GLU:OE2	8:F:78:GLU:HG2	2.17	0.45
21:S:74:VAL:HB	21:S:77:VAL:HG21	1.99	0.45
1:O:1182:C:H1'	1:O:1192:A:H8	1.82	0.44
12:J:75:ARG:HE	12:J:94:ALA:HB3	1.82	0.44
24:V:122:ARG:NE	36:V:5817:HOH:O	2.50	0.44
9:G:27:ILE:HD12	9:G:70:ALA:HB1	1.99	0.44
1:O:2467:A:O2'	1:O:2468:A:H2'	2.17	0.44
8:F:28:ALA:CB	8:F:99:THR:HG23	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2781:U:C2'	1:0:2782:G:H5'	2.47	0.44
11:I:63:ILE:HG22	11:I:64:GLY:N	2.31	0.44
1:0:2326:U:H4'	1:0:2412:G:C4'	2.47	0.44
1:0:2777:G:O2'	1:0:2778:A:H5'	2.17	0.44
19:Q:14:ALA:HB3	19:Q:147:LEU:HB2	1.99	0.44
1:0:870:G:C3'	1:0:871:G:H5''	2.47	0.44
2:9:2:U:OP2	2:9:2:U:H4'	2.17	0.44
10:H:14:TYR:N	10:H:91:HIS:HE1	2.16	0.44
1:0:2505:G:H8	36:0:5154:HOH:O	2.00	0.44
30:2:84:ARG:HD3	36:2:8550:HOH:O	2.17	0.44
14:L:186:SER:O	14:L:189:VAL:HG12	2.17	0.44
6:D:76:ARG:O	6:D:77:ASP:HB2	2.18	0.44
24:V:13:MET:HE1	24:V:18:GLN:HA	2.00	0.44
4:B:314:ALA:CB	4:B:317:PRO:HG3	2.47	0.44
1:0:2515:C:H2'	1:0:2516:G:O4'	2.17	0.44
3:A:165:THR:HG22	36:A:8620:HOH:O	2.17	0.44
36:0:7244:HOH:O	5:C:94:THR:HG21	2.16	0.44
19:Q:125:ARG:HG2	36:Q:8540:HOH:O	2.17	0.44
14:L:122:GLU:HB2	14:L:126:HIS:O	2.17	0.44
4:B:198:GLU:HB3	36:B:8601:HOH:O	2.16	0.44
10:H:31:PHE:HA	10:H:85:ILE:CG2	2.48	0.44
15:M:47:LEU:CD1	15:M:97:VAL:HG11	2.47	0.44
4:B:125:GLU:OE2	4:B:129:ARG:NH1	2.50	0.44
4:B:36:PRO:HA	4:B:168:GLY:HA2	1.95	0.44
10:H:35:ASN:ND2	10:H:79:ALA:O	2.51	0.44
21:S:52:ARG:HB2	21:S:95:ASN:HB3	1.99	0.44
1:0:2388:C:H5'	18:P:83:THR:O	2.17	0.44
11:I:22:VAL:O	11:I:26:VAL:HG23	2.16	0.44
27:Y:59:HIS:HA	36:Y:8442:HOH:O	2.18	0.44
28:Z:25:LYS:HD2	29:1:49:GLU:H	1.82	0.44
17:O:10:ALA:CA	17:O:13:VAL:HG12	2.45	0.44
15:M:154:LEU:O	15:M:155:GLU:CB	2.66	0.44
1:0:2456:A:H2'	1:0:2457:U:C6	2.52	0.44
24:V:108:ARG:HE	24:V:114:PRO:CG	2.30	0.44
13:K:125:PHE:CE1	13:K:140:VAL:HG13	2.53	0.44
7:E:152:THR:HG21	7:E:165:GLY:HA2	1.99	0.44
1:0:2338:G:H2'	6:D:129:ASP:OD1	2.17	0.44
1:0:1555:G:H4'	1:0:1630:A:H2	1.83	0.44
1:0:2112:A:H2'	1:0:2113:G:C8	2.52	0.44
5:C:236:THR:O	5:C:237:GLU:C	2.55	0.44
6:D:169:THR:O	6:D:170:TYR:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:57:ARG:O	10:H:61:LEU:HD22	2.18	0.44
15:M:91:ARG:HG3	15:M:186:LEU:HD23	1.99	0.44
10:H:43:PRO:HD2	10:H:137:ASN:HA	1.99	0.44
26:X:187:VAL:HG12	26:X:205:ILE:HA	1.99	0.44
3:A:153:ARG:NH1	3:A:153:ARG:HB2	2.26	0.44
28:Z:25:LYS:O	28:Z:25:LYS:HG2	2.18	0.44
1:O:2781:U:H2'	1:O:2782:G:H5'	2.00	0.44
15:M:11:ARG:HG3	15:M:14:ARG:NH1	2.33	0.44
19:Q:25:PHE:CE2	19:Q:29:LYS:CE	3.00	0.44
24:V:42:ARG:O	24:V:45:VAL:HG22	2.17	0.44
1:O:1006:A:N1	1:O:2311:A:H1'	2.33	0.44
13:K:128:GLY:O	13:K:132:LYS:HG3	2.17	0.44
6:D:140:ARG:O	6:D:144:ARG:HG2	2.17	0.44
10:H:110:GLY:N	36:H:8393:HOH:O	2.50	0.44
1:O:484:A:N1	1:O:506:G:H4'	2.32	0.44
15:M:161:GLY:O	15:M:162:ASP:C	2.55	0.44
6:D:95:THR:C	6:D:97:GLN:N	2.68	0.44
36:O:6063:HOH:O	27:Y:22:ILE:HG13	2.17	0.44
5:C:13:ASP:N	36:C:8440:HOH:O	2.50	0.44
1:O:2314:G:C2'	1:O:2315:C:H5'	2.47	0.44
13:K:92:ASP:OD1	13:K:94:ARG:HB2	2.17	0.44
1:O:1029:U:O2'	1:O:1273:C:OP1	2.31	0.44
12:J:55:VAL:CG1	12:J:56:SER:N	2.81	0.44
15:M:182:GLY:N	36:M:8573:HOH:O	2.51	0.44
1:O:1119:G:C8	11:I:52:GLN:NE2	2.85	0.44
6:D:23:VAL:O	6:D:23:VAL:CG2	2.64	0.44
28:Z:8:GLN:HE22	28:Z:11:LYS:HZ2	1.65	0.44
7:E:126:ILE:HB	7:E:131:LEU:HD23	1.99	0.44
11:I:6:PHE:O	11:I:8:ALA:N	2.51	0.44
1:O:1211:G:O2'	1:O:1212:C:H5'	2.17	0.44
1:O:130:C:H5'	36:O:4724:HOH:O	2.17	0.44
1:O:2005:G:OP2	1:O:2005:G:H3'	2.18	0.44
21:S:71:VAL:CG1	21:S:72:ILE:N	2.80	0.44
24:V:26:ILE:HG13	24:V:26:ILE:O	2.18	0.44
24:V:5:VAL:HG22	24:V:32:CYS:HB2	2.00	0.44
24:V:122:ARG:CG	24:V:122:ARG:NH1	2.80	0.44
4:B:146:THR:O	4:B:159:PRO:HB3	2.17	0.44
26:X:106:THR:CG2	26:X:107:PRO:HD2	2.47	0.44
27:Y:11:THR:HG23	27:Y:11:THR:O	2.17	0.44
7:E:84:MET:HE1	7:E:133:VAL:HG21	1.98	0.44
8:F:48:VAL:HG23	8:F:74:PHE:CB	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:7:ASP:OD1	5:C:11:ASN:O	2.36	0.44
1:0:590:A:H2'	1:0:591:A:H5'	2.00	0.44
36:0:5034:HOH:O	4:B:298:LYS:HD3	2.17	0.44
1:0:2812:A:H1'	36:0:5305:HOH:O	2.18	0.44
14:L:183:VAL:HG12	14:L:184:ARG:N	2.32	0.44
36:0:5789:HOH:O	17:O:59:ARG:HD3	2.17	0.44
1:0:2064:U:H4'	1:0:2653:A:OP1	2.18	0.44
1:0:1980:U:O2	1:0:2008:U:H4'	2.18	0.44
24:V:90:TYR:N	24:V:90:TYR:CD1	2.85	0.44
14:L:107:ARG:NH1	36:L:8577:HOH:O	2.48	0.44
15:M:108:SER:HA	15:M:109:PRO:HD3	1.79	0.44
1:0:1943:C:O4'	3:A:212:PRO:HA	2.18	0.43
1:0:2769:C:H2'	1:0:2770:G:H5'	2.00	0.43
1:0:338:C:H4'	5:C:174:ILE:HD12	1.99	0.43
1:0:314:G:N2	1:0:316:A:H3'	2.33	0.43
13:K:121:ILE:HG12	13:K:141:GLU:HB2	1.99	0.43
1:0:816:G:H5'	1:0:1598:A:H4'	1.98	0.43
11:I:26:VAL:HG13	11:I:36:VAL:HG11	1.99	0.43
3:A:135:VAL:N	36:A:8598:HOH:O	2.50	0.43
8:F:21:GLU:O	8:F:24:ARG:HG3	2.17	0.43
1:0:321:A:H1'	36:0:6554:HOH:O	2.18	0.43
1:0:2383:G:H1'	36:0:6223:HOH:O	2.17	0.43
1:0:1902:G:H2'	1:0:1903:U:O4'	2.18	0.43
14:L:125:ARG:NH1	36:L:8596:HOH:O	2.50	0.43
1:0:40:C:H4'	36:0:6522:HOH:O	2.18	0.43
1:0:42:C:H1'	36:0:4186:HOH:O	2.18	0.43
10:H:26:LYS:HG2	10:H:28:ILE:N	2.29	0.43
27:Y:57:CYS:SG	27:Y:59:HIS:HB3	2.58	0.43
13:K:6:ARG:NH2	36:K:8548:HOH:O	2.47	0.43
7:E:7:ILE:HG22	7:E:45:ASP:O	2.19	0.43
6:D:173:GLU:HG3	6:D:174:VAL:N	2.33	0.43
21:S:38:ARG:HG3	21:S:38:ARG:HH11	1.82	0.43
14:L:55:LYS:O	14:L:60:ILE:HD12	2.18	0.43
1:0:1669:A:H2'	1:0:1670:G:H8	1.82	0.43
3:A:186:TRP:CG	3:A:187:PRO:HA	2.53	0.43
3:A:97:ALA:HB2	3:A:150:PRO:HB2	1.99	0.43
2:9:59:C:H6	2:9:59:C:O5'	2.01	0.43
1:0:1423:C:O2'	1:0:1424:A:H5'	2.18	0.43
3:A:1:GLY:HA2	3:A:197:VAL:HG23	2.00	0.43
2:9:56:A:C3'	2:9:57:A:H5''	2.49	0.43
4:B:254:GLN:HG2	4:B:255:GLY:N	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:53:ARG:NH2	13:K:57:VAL:CG1	2.82	0.43
5:C:14:GLY:N	36:C:8440:HOH:O	2.49	0.43
1:0:2419:U:H5''	1:0:2420:G:C5'	2.47	0.43
1:0:2782:G:O6	1:0:2790:C:H5''	2.18	0.43
1:0:2832:C:H5	36:0:6736:HOH:O	2.01	0.43
2:9:31:C:H1'	36:9:8392:HOH:O	2.18	0.43
1:0:2083:A:N6	11:I:90:LYS:HE2	2.33	0.43
24:V:90:TYR:CE2	24:V:99:ALA:HB2	2.54	0.43
2:9:4:G:OP1	2:9:59:C:O2'	2.33	0.43
20:R:29:ASP:OD1	20:R:31:ARG:HG3	2.19	0.43
1:0:1342:C:O2'	1:0:1343:C:H5'	2.18	0.43
1:0:1109:U:O4	11:I:21:ARG:HA	2.18	0.43
27:Y:38:LYS:CE	27:Y:45:LYS:HE2	2.34	0.43
15:M:67:ALA:HA	15:M:71:TRP:H	1.83	0.43
11:I:39:VAL:CG1	11:I:107:ASN:HB2	2.49	0.43
25:W:15:ARG:NH1	25:W:15:ARG:HB3	2.32	0.43
4:B:307:ARG:NH1	4:B:307:ARG:CG	2.79	0.43
13:K:72:ASN:OD1	13:K:75:LEU:HD12	2.19	0.43
22:T:13:ILE:HG12	22:T:32:CYS:CB	2.47	0.43
25:W:12:ILE:HG23	25:W:36:HIS:CG	2.53	0.43
1:0:653:C:H2'	1:0:654:A:C8	2.53	0.43
3:A:179:MET:HG2	3:A:186:TRP:CG	2.53	0.43
3:A:70:ALA:HA	3:A:71:PRO:HD3	1.78	0.43
1:0:790:A:H2'	1:0:791:A:O4'	2.19	0.43
1:0:426:G:H2'	1:0:427:C:O4'	2.18	0.43
13:K:65:ASP:CG	13:K:111:ALA:HB3	2.38	0.43
24:V:22:GLU:HG2	24:V:27:HIS:CD2	2.54	0.43
10:H:30:GLN:H	10:H:65:ARG:NH1	2.17	0.43
11:I:103:VAL:CG1	36:I:5907:HOH:O	2.64	0.43
1:0:1206:U:H2'	1:0:1207:A:O4'	2.18	0.43
13:K:130:ARG:HA	36:K:8557:HOH:O	2.18	0.43
3:A:105:VAL:CG1	3:A:106:CYS:N	2.81	0.43
4:B:279:THR:CG2	4:B:280:VAL:N	2.81	0.43
1:0:1973:A:H5'	1:0:1973:A:C8	2.44	0.43
21:S:24:ARG:HH21	21:S:39:ASN:ND2	2.13	0.43
13:K:90:ARG:NH1	13:K:119:THR:HG21	2.34	0.43
1:0:1235:G:C1'	11:I:63:ILE:HG23	2.48	0.43
26:X:117:LEU:HD12	26:X:174:VAL:HG11	2.01	0.43
6:D:24:HIS:HB2	6:D:72:LYS:CB	2.49	0.43
36:0:8729:HOH:O	3:A:11:ARG:HD3	2.19	0.43
27:Y:41:VAL:HG12	27:Y:42:CYS:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:2:91:GLN:O	30:2:92:GLU:HB2	2.18	0.43
3:A:194:MET:HE1	3:A:199:HIS:HB2	1.99	0.43
29:1:36:ASN:HB3	29:1:39:ARG:NE	2.34	0.43
1:0:1467:C:OP1	14:L:35:PRO:HB2	2.19	0.43
14:L:38:VAL:O	14:L:63:VAL:HG13	2.18	0.43
13:K:146:GLY:C	13:K:148:GLU:H	2.22	0.43
8:F:28:ALA:HB3	8:F:99:THR:HG23	2.00	0.43
1:0:2851:G:C2'	1:0:2852:A:H5'	2.49	0.43
2:9:92:G:H22	10:H:52:LYS:HZ2	1.65	0.43
14:L:25:TRP:HE3	14:L:26:HIS:HD2	1.66	0.43
23:U:23:LEU:HD12	23:U:56:ILE:HD12	2.00	0.43
1:0:1787:C:H4'	1:0:2883:A:O4'	2.18	0.43
1:0:716:G:C2'	1:0:717:C:O5'	2.67	0.43
1:0:559:U:H2'	1:0:560:C:O4'	2.19	0.43
26:X:187:VAL:HB	26:X:203:VAL:HG22	1.99	0.43
14:L:153:THR:O	14:L:156:ARG:HG3	2.18	0.43
4:B:24:PRO:CG	4:B:204:GLY:HA2	2.49	0.43
10:H:113:ALA:N	10:H:114:PRO:HD3	2.33	0.43
6:D:84:LEU:HA	6:D:87:ALA:HB3	2.01	0.43
1:0:1592:G:O2'	1:0:1593:C:O5'	2.36	0.43
1:0:1657:A:H2'	1:0:1658:A:C8	2.54	0.43
8:F:26:THR:HG21	8:F:103:ALA:HB2	1.99	0.43
6:D:99:ASP:HB2	6:D:103:ASN:CB	2.47	0.43
14:L:146:GLN:NE2	36:L:8643:HOH:O	2.51	0.43
24:V:48:VAL:CG1	24:V:48:VAL:O	2.65	0.43
6:D:23:VAL:HG23	6:D:41:LEU:HD22	1.99	0.43
1:0:88:G:N1	29:1:24:TRP:CE3	2.87	0.43
7:E:80:TRP:O	7:E:134:SER:HA	2.18	0.43
27:Y:34:LYS:HE2	36:Y:8426:HOH:O	2.18	0.43
1:0:1328:A:C8	26:X:169:ARG:HD3	2.54	0.43
15:M:149:GLU:O	15:M:152:GLU:HB2	2.19	0.43
27:Y:13:ARG:NH1	27:Y:14:PHE:CE2	2.87	0.43
5:C:33:LYS:HD2	36:C:8459:HOH:O	2.18	0.43
1:0:716:G:H2'	1:0:717:C:O5'	2.19	0.43
1:0:1857:A:N6	1:0:2247:C:H1'	2.34	0.43
1:0:1613:C:H2'	1:0:1614:G:O4'	2.18	0.43
3:A:103:VAL:HA	3:A:104:PRO:HD3	1.89	0.43
3:A:105:VAL:HG13	3:A:155:THR:O	2.19	0.43
1:0:777:U:O2'	28:Z:11:LYS:HG2	2.19	0.43
2:9:27:C:H1'	36:9:8431:HOH:O	2.19	0.43
1:0:1194:A:C6	1:0:1206:U:N3	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:320:GLN:HG3	4:B:321:PRO:CD	2.48	0.43
15:M:163:PHE:HE1	15:M:171:HIS:HD1	1.67	0.43
6:D:77:ASP:HB3	6:D:78:GLU:H	1.58	0.43
1:O:396:U:H5'	30:2:42:ARG:NH1	2.34	0.43
28:Z:25:LYS:HZ3	28:Z:25:LYS:HG2	1.75	0.43
4:B:24:PRO:HG3	4:B:204:GLY:HA2	2.01	0.43
4:B:74:ILE:HG13	36:B:8610:HOH:O	2.18	0.43
6:D:84:LEU:C	6:D:86:THR:H	2.22	0.43
19:Q:29:LYS:NZ	36:Q:8538:HOH:O	2.52	0.43
21:S:49:GLU:HB3	21:S:59:GLU:HG3	2.01	0.43
8:F:21:GLU:HA	8:F:24:ARG:HE	1.83	0.43
20:R:29:ASP:OD1	20:R:31:ARG:NH1	2.52	0.43
14:L:49:ALA:C	14:L:54:TYR:HB3	2.39	0.43
1:O:2365:G:H4'	18:P:45:PRO:O	2.18	0.43
1:O:2274:A:H1'	14:L:86:MET:SD	2.59	0.43
4:B:277:GLU:N	4:B:278:PRO:HD2	2.33	0.43
16:N:21:SER:OG	16:N:106:PRO:HB2	2.19	0.43
24:V:88:THR:CG2	24:V:89:ASP:N	2.69	0.42
6:D:67:ASP:O	6:D:69:ILE:HG13	2.18	0.42
12:J:34:VAL:HB	36:J:7169:HOH:O	2.19	0.42
4:B:62:ARG:CB	4:B:65:MET:HE3	2.49	0.42
1:O:1634:G:H2'	1:O:1635:U:C6	2.54	0.42
1:O:869:G:OP1	14:L:79:LYS:HE2	2.19	0.42
3:A:107:ASN:OD1	3:A:120:ARG:HD2	2.19	0.42
12:J:99:ASP:OD1	12:J:101:ASN:N	2.51	0.42
4:B:268:ARG:NE	36:B:8612:HOH:O	2.51	0.42
1:O:514:G:OP1	1:O:514:G:H2'	2.19	0.42
21:S:3:GLN:HA	21:S:4:PRO:HD3	1.83	0.42
14:L:134:ILE:HG23	14:L:141:ILE:HD13	2.01	0.42
12:J:55:VAL:HG12	12:J:56:SER:H	1.83	0.42
24:V:139:GLY:O	24:V:141:HIS:CD2	2.71	0.42
11:I:75:PRO:HD3	11:I:136:SER:OG	2.18	0.42
1:O:736:A:H2'	1:O:737:A:O4'	2.19	0.42
23:U:20:LEU:HD22	23:U:60:GLN:HE22	1.84	0.42
1:O:834:G:H3'	1:O:835:U:H4'	2.00	0.42
1:O:834:G:H4'	1:O:835:U:OP2	2.19	0.42
1:O:564:G:H1'	36:O:5829:HOH:O	2.20	0.42
25:W:26:ALA:HB1	25:W:59:TRP:CE2	2.54	0.42
23:U:12:THR:OG1	23:U:13:PRO:HD2	2.20	0.42
11:I:130:VAL:CG1	11:I:131:THR:N	2.81	0.42
1:O:488:U:O2'	21:S:82:THR:HG21	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:9:GLU:HG3	7:E:10:ASP:N	2.33	0.42
1:0:2608:C:H2'	36:0:3085:HOH:O	2.19	0.42
1:0:1406:A:H4'	1:0:1407:A:H5''	2.00	0.42
13:K:1:THR:N	36:K:8540:HOH:O	2.53	0.42
10:H:62:GLU:HA	36:H:8383:HOH:O	2.19	0.42
24:V:54:PHE:CZ	24:V:140:LYS:HB2	2.54	0.42
1:0:1173:A:H4'	1:0:1174:A:C8	2.54	0.42
24:V:76:ASP:O	24:V:77:ALA:C	2.58	0.42
4:B:280:VAL:CG1	4:B:334:SER:HA	2.49	0.42
9:G:64:ASN:N	9:G:64:ASN:ND2	2.66	0.42
25:W:43:VAL:CG1	25:W:44:ASP:N	2.81	0.42
3:A:94:LEU:HG	3:A:99:ILE:CD1	2.48	0.42
15:M:139:TRP:HA	15:M:139:TRP:HE3	1.84	0.42
18:P:32:GLU:O	18:P:93:ARG:NH2	2.53	0.42
12:J:125:ALA:C	12:J:127:ALA:H	2.21	0.42
15:M:33:ARG:NH1	15:M:103:ASP:OD2	2.46	0.42
2:9:20:G:H3'	36:9:8434:HOH:O	2.19	0.42
15:M:47:LEU:HD12	15:M:92:ALA:CB	2.48	0.42
1:0:289:G:O2'	1:0:290:C:H5'	2.20	0.42
1:0:2289:G:N2	1:0:2291:A:C2	2.80	0.42
6:D:57:THR:HA	6:D:63:ILE:HA	2.00	0.42
22:T:52:THR:HG21	22:T:54:THR:HB	2.00	0.42
1:0:1477:C:C5'	1:0:1868:G:H5''	2.50	0.42
1:0:2842:G:C2'	1:0:2843:A:H5'	2.49	0.42
7:E:9:GLU:HA	36:E:5240:HOH:O	2.18	0.42
1:0:661:G:C5	1:0:686:A:C2	3.07	0.42
15:M:44:ARG:HG3	15:M:45:ALA:N	2.35	0.42
1:0:23:G:H1'	1:0:520:A:N6	2.35	0.42
16:N:43:VAL:HG12	16:N:44:ASN:O	2.19	0.42
1:0:37:A:H2'	1:0:38:G:C8	2.55	0.42
1:0:827:A:H2'	1:0:828:G:O4'	2.19	0.42
6:D:19:GLU:O	6:D:133:ASN:HB3	2.20	0.42
10:H:136:VAL:HG22	10:H:137:ASN:N	2.35	0.42
15:M:73:ALA:HB1	15:M:74:PRO:CD	2.49	0.42
15:M:42:HIS:CG	15:M:62:HIS:HE1	2.38	0.42
4:B:154:VAL:HA	4:B:155:PRO:HD3	1.91	0.42
1:0:1123:A:C2	1:0:1129:C:H4'	2.54	0.42
2:9:64:C:C2'	2:9:65:A:H5'	2.49	0.42
16:N:26:TRP:CE3	16:N:26:TRP:HA	2.53	0.42
24:V:1:MET:HB2	24:V:103:GLU:HG2	2.00	0.42
1:0:1367:A:H2'	1:0:1368:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1098:A:H2'	1:0:1099:G:O4'	2.19	0.42
27:Y:32:LYS:HB3	27:Y:32:LYS:HE2	1.76	0.42
5:C:16:VAL:CG1	5:C:17:ASP:N	2.81	0.42
21:S:69:LYS:O	21:S:71:VAL:HG23	2.20	0.42
6:D:44:ILE:HG12	6:D:83:PHE:CE1	2.53	0.42
1:0:545:G:H2'	1:0:546:C:O4'	2.20	0.42
9:G:19:GLU:O	9:G:23:ILE:HG13	2.20	0.42
8:F:58:GLU:HA	8:F:61:MET:HE2	2.01	0.42
1:0:1236:A:C8	11:I:63:ILE:HD11	2.55	0.42
14:L:42:ARG:HA	14:L:43:PRO:HD3	1.85	0.42
14:L:191:GLY:O	14:L:192:ALA:HB3	2.20	0.42
1:0:2061:C:C2'	1:0:2062:A:H5'	2.49	0.42
11:I:71:TYR:CD1	11:I:72:PRO:HD2	2.54	0.42
5:C:35:VAL:HG21	5:C:227:GLY:HA2	2.00	0.42
1:0:2001:G:O2'	1:0:2002:C:H5'	2.20	0.42
1:0:1804:A:H2'	1:0:1805:G:C8	2.54	0.42
1:0:1279:U:H5''	36:0:9100:HOH:O	2.20	0.42
28:Z:2:GLY:O	28:Z:6:PRO:HG2	2.19	0.42
15:M:120:GLU:HG3	15:M:136:LEU:HD13	2.02	0.42
1:0:2502:C:H4'	10:H:151:MET:HG2	2.02	0.42
14:L:99:ARG:HD2	14:L:167:GLY:HA2	2.01	0.42
5:C:1:MET:HG2	5:C:2:GLN:NE2	2.35	0.42
3:A:33:GLU:CD	3:A:33:GLU:H	2.23	0.42
1:0:1158:G:O2'	1:0:1159:G:H5'	2.19	0.42
7:E:31:ARG:NH1	7:E:68:HIS:CD2	2.88	0.42
1:0:2415:A:N3	15:M:26:LEU:HD13	2.35	0.42
10:H:117:LYS:HB2	36:H:8339:HOH:O	2.19	0.42
1:0:2653:A:H2'	1:0:2654:C:C6	2.55	0.42
1:0:1878:G:O2'	1:0:1879:U:H6	2.03	0.42
6:D:86:THR:HG23	36:D:7477:HOH:O	2.20	0.42
1:0:2820:A:H2'	1:0:2821:C:O4'	2.19	0.42
19:Q:132:ARG:NH2	36:Q:8580:HOH:O	2.52	0.42
1:0:2251:G:H2'	1:0:2252:A:H8	1.85	0.42
1:0:644:G:H1'	36:0:5924:HOH:O	2.19	0.42
1:0:2681:A:H4'	1:0:2682:C:H5'	2.02	0.42
10:H:94:ARG:NH2	36:H:8332:HOH:O	2.50	0.42
1:0:1883:U:O2'	1:0:1884:G:H5'	2.19	0.42
1:0:249:G:O2'	1:0:250:C:H5'	2.20	0.42
16:N:54:GLU:O	16:N:55:ASP:HB2	2.20	0.42
5:C:139:VAL:CG1	36:C:8447:HOH:O	2.61	0.42
1:0:306:A:P	21:S:38:ARG:HH21	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:9:CYS:O	22:T:52:THR:HG23	2.20	0.42
1:0:1855:G:H8	3:A:144:GLU:OE2	2.03	0.42
15:M:127:LEU:HA	15:M:127:LEU:HD12	1.85	0.42
1:0:1175:G:H1'	1:0:1193:A:H2'	2.02	0.42
29:1:19:SER:O	29:1:36:ASN:ND2	2.53	0.42
1:0:1524:U:O2'	1:0:1525:G:OP2	2.34	0.42
1:0:2257:G:H4'	1:0:2259:C:C2	2.55	0.42
1:0:2649:A:H5'	1:0:2649:A:C8	2.55	0.42
1:0:324:G:O2'	1:0:325:U:H5'	2.20	0.42
12:J:72:VAL:HG11	12:J:121:PHE:CD1	2.55	0.42
24:V:146:ILE:HA	24:V:146:ILE:HD13	1.88	0.41
10:H:13:ALA:HA	10:H:91:HIS:CE1	2.55	0.41
19:Q:96:VAL:HG13	19:Q:106:GLY:HA3	2.02	0.41
1:0:88:G:H2'	1:0:89:G:C8	2.54	0.41
3:A:200:PRO:HD3	36:A:8521:HOH:O	2.20	0.41
4:B:145:HIS:CD2	4:B:146:THR:O	2.68	0.41
9:G:67:LEU:O	9:G:71:LEU:HG	2.20	0.41
1:0:1058:A:H2'	1:0:1060:C:C5'	2.47	0.41
1:0:2578:G:C8	1:0:2578:G:H5'	2.51	0.41
28:Z:28:HIS:HD2	28:Z:31:LYS:H	1.68	0.41
18:P:40:HIS:HD2	18:P:60:THR:OG1	2.03	0.41
8:F:26:THR:HG21	8:F:103:ALA:CB	2.48	0.41
4:B:315:VAL:HG23	4:B:316:ARG:HG2	2.01	0.41
1:0:1385:G:O3'	25:W:49:ARG:NH1	2.52	0.41
1:0:1139:U:H2'	1:0:1140:C:C6	2.55	0.41
24:V:29:VAL:O	24:V:30:ASN:HB2	2.19	0.41
21:S:37:GLN:OE1	21:S:118:SER:HA	2.19	0.41
1:0:613:C:H2'	1:0:614:U:H6	1.85	0.41
1:0:2115:U:H2'	1:0:2116:U:C6	2.55	0.41
1:0:2601:A:N1	12:J:38:SER:HB2	2.35	0.41
2:9:24:U:C5	36:9:8477:HOH:O	2.72	0.41
1:0:820:G:O2'	1:0:856:G:H4'	2.20	0.41
10:H:83:PHE:HE1	10:H:146:TRP:CZ2	2.39	0.41
15:M:73:ALA:N	36:M:8569:HOH:O	2.53	0.41
2:9:28:U:H2'	2:9:29:C:C6	2.55	0.41
1:0:2821:C:H4'	4:B:116:PRO:CB	2.49	0.41
15:M:61:ALA:CB	15:M:88:ALA:HB2	2.50	0.41
4:B:305:ASP:O	4:B:306:LYS:CB	2.67	0.41
5:C:138:VAL:O	5:C:234:VAL:HA	2.21	0.41
1:0:1003:U:O2	10:H:90:PHE:HZ	2.03	0.41
14:L:125:ARG:CZ	36:L:8596:HOH:O	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:757:C:OP1	13:K:27:ARG:HD2	2.20	0.41
14:L:65:VAL:HG21	14:L:105:ALA:HB2	2.01	0.41
1:0:806:A:H2'	1:0:807:A:O4'	2.20	0.41
1:0:440:C:H2'	1:0:441:A:C8	2.55	0.41
36:0:3538:HOH:O	18:P:13:LYS:HE3	2.19	0.41
3:A:30:ARG:HB3	3:A:30:ARG:HE	1.68	0.41
1:0:2712:G:H5'	36:J:4183:HOH:O	2.19	0.41
10:H:46:VAL:CG1	10:H:146:TRP:HZ3	2.29	0.41
10:H:83:PHE:CE1	10:H:146:TRP:NE1	2.87	0.41
25:W:76:ARG:HA	25:W:82:GLU:O	2.20	0.41
21:S:38:ARG:HG3	21:S:38:ARG:NH1	2.34	0.41
1:0:2589:U:H2'	1:0:2590:U:C6	2.55	0.41
15:M:143:ARG:HH12	15:M:173:ASP:CG	2.21	0.41
5:C:129:HIS:HE1	5:C:231:ARG:HA	1.85	0.41
26:X:154:ARG:HH11	26:X:154:ARG:HB3	1.84	0.41
1:0:1593:C:OP1	17:O:117:SER:CB	2.68	0.41
17:O:94:TRP:CZ2	17:O:98:ILE:HG13	2.55	0.41
1:0:858:U:H2'	1:0:859:C:C6	2.55	0.41
1:0:764:C:H2'	1:0:765:G:O4'	2.21	0.41
1:0:303:C:H2'	1:0:304:G:O4'	2.21	0.41
36:0:3589:HOH:O	8:F:31:LYS:HE3	2.19	0.41
21:S:78:THR:HB	21:S:87:VAL:O	2.21	0.41
2:9:105:A:H2'	2:9:106:C:O4'	2.20	0.41
1:0:2667:G:H1'	1:0:2914:A:N3	2.34	0.41
1:0:162:C:H2'	1:0:163:U:H5'	2.01	0.41
1:0:2668:G:H2'	1:0:2669:U:C6	2.55	0.41
1:0:1881:A:OP1	3:A:199:HIS:HE1	2.04	0.41
15:M:163:PHE:O	15:M:164:ASP:O	2.37	0.41
4:B:41:PHE:HB3	4:B:190:MET:CE	2.50	0.41
4:B:60:SER:C	4:B:62:ARG:N	2.73	0.41
23:U:39:ALA:C	23:U:41:GLU:N	2.74	0.41
4:B:258:GLY:N	4:B:260:HIS:CE1	2.86	0.41
3:A:223:ARG:NE	36:A:8575:HOH:O	2.54	0.41
1:0:553:G:P	26:X:204:ARG:NH2	2.93	0.41
1:0:2820:A:H2'	1:0:2821:C:C6	2.55	0.41
5:C:65:ARG:HG3	5:C:67:GLN:HB2	2.03	0.41
1:0:1413:A:H2'	1:0:1414:A:O4'	2.20	0.41
8:F:34:ASN:HA	14:L:4:ALA:HB2	2.02	0.41
20:R:30:ASP:HA	20:R:62:LYS:HE3	2.03	0.41
1:0:1545:C:H2'	1:0:1546:G:O4'	2.21	0.41
21:S:71:VAL:HG12	21:S:72:ILE:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:146:ILE:HG22	24:V:147:ASP:N	2.35	0.41
23:U:42:ASN:O	23:U:44:GLY:N	2.53	0.41
1:0:1205:U:O2	1:0:1205:U:H2'	2.20	0.41
12:J:90:PHE:CD1	12:J:90:PHE:N	2.89	0.41
1:0:262:A:OP2	8:F:91:VAL:HG11	2.20	0.41
15:M:159:TYR:CE2	15:M:163:PHE:HE2	2.36	0.41
1:0:588:G:O6	24:V:154:ARG:NH1	2.53	0.41
7:E:101:GLU:OE2	7:E:115:ARG:HD3	2.21	0.41
16:N:14:LEU:HD23	16:N:102:ILE:CD1	2.48	0.41
1:0:2346:C:H4'	6:D:52:THR:HG22	2.03	0.41
4:B:71:VAL:CG1	4:B:296:LEU:HB3	2.48	0.41
25:W:30:MET:HE1	25:W:55:ASN:HA	2.03	0.41
1:0:2421:G:H3'	1:0:2422:U:C5'	2.51	0.41
28:Z:28:HIS:CD2	28:Z:31:LYS:H	2.38	0.41
36:0:9135:HOH:O	8:F:38:LYS:HE2	2.20	0.41
7:E:35:TYR:HA	11:I:127:ILE:HD12	2.03	0.41
4:B:243:ASN:HA	4:B:244:PRO:C	2.39	0.41
16:N:26:TRP:HE3	16:N:26:TRP:HA	1.84	0.41
36:0:3919:HOH:O	3:A:11:ARG:CZ	2.69	0.41
1:0:1406:A:N1	36:0:5553:HOH:O	2.37	0.41
1:0:793:A:H5''	17:O:83:LYS:HG2	2.03	0.41
1:0:1926:G:H2'	1:0:1927:A:C8	2.56	0.41
16:N:23:GLY:C	36:N:3062:HOH:O	2.58	0.41
13:K:89:PHE:N	36:K:8570:HOH:O	2.54	0.41
1:0:903:U:OP2	13:K:11:ARG:NH1	2.51	0.41
16:N:98:LEU:HD12	16:N:98:LEU:HA	1.88	0.41
1:0:1752:G:H2'	36:0:7080:HOH:O	2.19	0.41
24:V:6:GLN:HA	24:V:52:VAL:HG23	2.02	0.41
10:H:48:LEU:CD1	10:H:157:ILE:HG21	2.50	0.41
9:G:63:ARG:N	36:G:2569:HOH:O	2.53	0.41
14:L:78:ASN:O	14:L:79:LYS:HG2	2.21	0.41
1:0:2346:C:H4'	6:D:52:THR:CG2	2.50	0.41
36:0:3697:HOH:O	26:X:186:ARG:HD2	2.21	0.41
16:N:77:ALA:HA	16:N:96:VAL:O	2.20	0.41
1:0:513:A:H3'	36:0:3363:HOH:O	2.20	0.41
21:S:1:SER:N	36:S:5837:HOH:O	2.53	0.41
10:H:62:GLU:O	10:H:66:VAL:HG23	2.21	0.41
23:U:1:THR:HG23	23:U:2:VAL:HG23	2.02	0.41
3:A:36:ASP:HB2	3:A:83:GLY:HA3	2.03	0.41
24:V:14:HIS:HB2	24:V:17:ILE:HD12	2.03	0.41
1:0:677:C:H4'	5:C:246:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:205:VAL:HA	4:B:260:HIS:O	2.21	0.41
4:B:307:ARG:NH1	4:B:307:ARG:HG3	2.35	0.41
1:0:1525:G:C5'	1:0:1526:A:OP2	2.68	0.41
21:S:48:VAL:HG22	21:S:97:ARG:O	2.21	0.41
21:S:48:VAL:HG13	21:S:49:GLU:N	2.35	0.41
1:0:660:A:H4'	1:0:661:G:O5'	2.21	0.41
7:E:37:ASP:OD1	11:I:125:SER:HB3	2.21	0.41
1:0:305:A:C5	1:0:329:A:C2	3.09	0.41
18:P:16:ASN:HA	18:P:16:ASN:HD22	1.71	0.41
2:9:3:A:H61	2:9:22:G:C1'	2.34	0.41
1:0:771:G:OP2	14:L:79:LYS:HE3	2.21	0.41
7:E:11:VAL:HG11	7:E:22:VAL:HG13	2.02	0.41
1:0:2346:C:O3'	6:D:52:THR:HG23	2.20	0.41
4:B:129:ARG:NH2	4:B:176:ASP:OD1	2.52	0.41
1:0:2779:G:H21	7:E:143:GLN:HE22	1.69	0.41
1:0:1878:G:H5''	36:0:9307:HOH:O	2.20	0.41
1:0:2241:C:H2'	1:0:2242:U:C6	2.56	0.41
13:K:104:ASP:O	13:K:105:TYR:HB3	2.21	0.41
1:0:40:C:O5'	1:0:40:C:H6	2.04	0.41
27:Y:42:CYS:SG	27:Y:44:PHE:HB2	2.61	0.41
1:0:2597:U:H2'	1:0:2598:U:H5'	2.03	0.41
1:0:412:C:H2'	1:0:413:G:O4'	2.21	0.41
19:Q:149:GLU:HA	19:Q:150:PRO:HD3	1.95	0.41
6:D:15:GLU:HA	6:D:16:PRO:HD3	1.87	0.41
10:H:85:ILE:HB	10:H:132:PHE:HE2	1.84	0.41
25:W:37:LEU:HD21	25:W:72:VAL:HG11	2.02	0.41
6:D:64:ARG:HG2	6:D:66:GLY:O	2.21	0.41
7:E:20:ILE:CD1	7:E:33:LEU:HD12	2.50	0.41
4:B:254:GLN:NE2	36:B:8595:HOH:O	2.51	0.41
14:L:138:HIS:C	14:L:139:PRO:O	2.54	0.41
19:Q:39:THR:CG2	19:Q:42:GLU:HG3	2.50	0.41
7:E:7:ILE:HA	7:E:8:PRO:HD3	1.89	0.41
1:0:2748:G:H5'	36:0:7073:HOH:O	2.21	0.41
28:Z:25:LYS:HD2	29:1:49:GLU:N	2.35	0.41
28:Z:17:THR:HA	29:1:49:GLU:HA	2.03	0.41
6:D:48:MET:HA	6:D:49:PRO:HD3	1.78	0.41
10:H:114:PRO:O	10:H:115:PHE:C	2.58	0.41
15:M:66:LEU:HA	15:M:66:LEU:HD12	1.95	0.41
1:0:1615:A:H4'	36:0:5402:HOH:O	2.20	0.41
1:0:625:U:H5''	1:0:1044:C:N4	2.35	0.41
1:0:1462:C:H2'	1:0:1463:A:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:153:THR:O	6:D:156:ARG:HB2	2.20	0.41
12:J:101:ASN:O	12:J:102:GLU:CB	2.69	0.41
1:0:2413:A:N7	15:M:109:PRO:HB3	2.35	0.41
14:L:134:ILE:O	14:L:136:PRO:HD3	2.20	0.41
36:0:4589:HOH:O	4:B:216:LYS:HA	2.21	0.41
19:Q:47:LEU:O	19:Q:51:ILE:HG13	2.21	0.41
6:D:151:ILE:HA	6:D:152:PRO:HD3	1.93	0.41
4:B:223:ARG:HG3	4:B:232:TRP:O	2.21	0.41
25:W:51:ASP:O	25:W:53:SER:N	2.54	0.41
1:0:694:A:H2'	1:0:695:C:H5'	2.02	0.41
1:0:141:C:P	36:0:3373:HOH:O	2.79	0.41
5:C:95:GLU:HG3	36:C:8475:HOH:O	2.20	0.41
1:0:1339:G:C6	1:0:1340:G:N1	2.88	0.41
1:0:245:C:H2'	1:0:246:G:H5'	2.01	0.41
1:0:2281:C:C2'	1:0:2282:U:H5'	2.50	0.41
1:0:638:C:H2'	1:0:639:A:C8	2.56	0.41
1:0:1242:A:C5'	11:I:82:THR:HG23	2.30	0.41
5:C:115:LEU:HA	5:C:115:LEU:HD12	1.89	0.41
10:H:150:LYS:CB	10:H:157:ILE:HD12	2.46	0.41
1:0:2718:C:H5'	1:0:2718:C:C6	2.52	0.41
1:0:2506:A:H1'	36:0:5574:HOH:O	2.21	0.41
15:M:164:ASP:OD1	15:M:167:ASP:HA	2.19	0.41
30:2:65:THR:HG23	30:2:67:LEU:CG	2.45	0.41
1:0:1524:U:O2'	1:0:1525:G:P	2.78	0.41
6:D:18:ILE:HD13	6:D:84:LEU:HD12	2.03	0.41
17:O:131:PHE:CD1	17:O:137:LEU:HD13	2.55	0.41
22:T:49:LEU:CD1	36:T:3805:HOH:O	2.69	0.41
14:L:133:LEU:O	14:L:134:ILE:HD13	2.21	0.41
30:2:15:ASN:ND2	36:2:8547:HOH:O	2.53	0.41
1:0:1654:U:H2'	3:A:47:HIS:CD2	2.56	0.41
4:B:88:GLU:HG3	4:B:88:GLU:O	2.20	0.41
6:D:103:ASN:ND2	6:D:133:ASN:HD22	2.18	0.40
1:0:157:G:H4'	14:L:95:LYS:HE3	2.04	0.40
24:V:4:LEU:HA	24:V:4:LEU:HD23	1.94	0.40
14:L:45:ARG:CZ	14:L:48:ARG:HG3	2.50	0.40
3:A:128:LEU:HD21	3:A:131:HIS:CE1	2.55	0.40
1:0:1377:C:H1'	36:0:6797:HOH:O	2.19	0.40
1:0:2909:G:H2'	1:0:2910:A:H8	1.86	0.40
1:0:1878:G:H5''	36:0:4675:HOH:O	2.20	0.40
4:B:82:VAL:CG1	4:B:82:VAL:O	2.67	0.40
27:Y:23:ARG:NH1	36:Y:8404:HOH:O	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:317:A:OP1	21:S:52:ARG:O	2.39	0.40
4:B:286:ASN:O	4:B:306:LYS:HE3	2.20	0.40
1:0:204:A:H2'	1:0:205:U:H5'	2.03	0.40
3:A:135:VAL:HG21	3:A:147:ARG:NH1	2.35	0.40
1:0:1654:U:H2'	3:A:47:HIS:HD2	1.85	0.40
1:0:2697:A:H2'	1:0:2698:G:O4'	2.20	0.40
1:0:1393:A:H2'	1:0:1394:C:C6	2.57	0.40
1:0:1947:G:H2'	1:0:1948:G:C8	2.56	0.40
24:V:2:HIS:HD2	24:V:56:GLU:N	2.19	0.40
13:K:24:ALA:HB2	13:K:30:ARG:HD2	2.03	0.40
1:0:708:A:H2'	1:0:709:G:O4'	2.20	0.40
1:0:166:A:N7	13:K:25:GLY:HA2	2.36	0.40
1:0:2478:U:O2'	1:0:2479:A:H5'	2.21	0.40
1:0:377:C:H5	36:0:9820:HOH:O	2.04	0.40
1:0:2691:A:OP1	1:0:2691:A:H8	2.04	0.40
4:B:84:LEU:HD13	4:B:84:LEU:O	2.21	0.40
22:T:6:CYS:HA	22:T:13:ILE:HD11	2.03	0.40
9:G:64:ASN:O	9:G:68:GLU:HG3	2.21	0.40
6:D:59:GLY:O	6:D:61:PHE:N	2.42	0.40
1:0:1677:U:OP2	29:1:8:LYS:NZ	2.51	0.40
36:0:9057:HOH:O	14:L:84:LYS:HD3	2.21	0.40
1:0:2256:G:C2'	1:0:2257:G:H5'	2.51	0.40
7:E:156:ASP:OD2	7:E:157:LYS:HG3	2.19	0.40
1:0:1614:G:H2'	36:0:4136:HOH:O	2.21	0.40
12:J:118:ALA:C	12:J:120:ARG:H	2.24	0.40
5:C:196:THR:HG23	36:C:8400:HOH:O	2.22	0.40
30:2:11:CYS:HB2	30:2:20:HIS:CE1	2.57	0.40
1:0:2471:G:N3	1:0:2633:A:H2	2.18	0.40
6:D:99:ASP:HB2	6:D:103:ASN:CA	2.51	0.40
14:L:95:LYS:HG2	14:L:99:ARG:HB3	2.02	0.40
15:M:175:LEU:HA	15:M:175:LEU:HD12	1.86	0.40
1:0:1194:A:C5	1:0:1206:U:N3	2.90	0.40
11:I:46:ILE:HG12	11:I:53:ILE:HD13	2.03	0.40
30:2:74:CYS:N	36:2:8560:HOH:O	2.54	0.40
13:K:73:VAL:HG11	13:K:118:LEU:HD21	2.01	0.40
6:D:10:PHE:CE1	6:D:11:HIS:HB3	2.55	0.40
19:Q:61:GLN:NE2	36:Q:8538:HOH:O	2.53	0.40
17:O:16:VAL:CG1	17:O:20:ARG:HB2	2.52	0.40
19:Q:119:VAL:HG21	19:Q:142:ASP:CG	2.42	0.40
5:C:46:TYR:CE1	5:C:92:PRO:HB3	2.56	0.40
1:0:2089:A:O2'	1:0:2090:G:H5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:138:ASP:C	36:M:8572:HOH:O	2.60	0.40
1:0:419:A:H1'	1:0:1921:A:C2	2.57	0.40
1:0:151:A:H2'	1:0:152:A:O4'	2.22	0.40
1:0:934:C:H2'	1:0:935:G:C8	2.57	0.40
1:0:1166:A:N3	1:0:1166:A:H2'	2.37	0.40
3:A:192:VAL:O	3:A:207:GLN:HG2	2.22	0.40
14:L:87:MET:HG2	30:2:46:ILE:CG2	2.45	0.40
20:R:53:ASN:ND2	36:R:8320:HOH:O	2.55	0.40
3:A:35:GLY:O	3:A:36:ASP:CB	2.62	0.40
1:0:771:G:P	14:L:79:LYS:HG3	2.61	0.40
6:D:94:ALA:HB3	6:D:174:VAL:CA	2.52	0.40
24:V:13:MET:HE3	24:V:17:ILE:CG2	2.48	0.40
16:N:32:ARG:NE	36:N:3360:HOH:O	2.54	0.40
4:B:275:GLY:C	36:B:8656:HOH:O	2.59	0.40
1:0:1756:G:H1'	36:0:5783:HOH:O	2.21	0.40
1:0:398:U:H2'	1:0:399:C:C6	2.56	0.40
4:B:132:HIS:HB2	4:B:137:LEU:HD22	2.03	0.40
1:0:2289:G:N2	1:0:2291:A:H2	2.19	0.40
17:O:13:VAL:HG13	17:O:14:LEU:N	2.36	0.40
4:B:36:PRO:CA	4:B:168:GLY:HA3	2.49	0.40
1:0:894:A:C2	5:C:87:ARG:NH2	2.90	0.40
2:9:92:G:H22	10:H:52:LYS:HZ1	1.68	0.40
1:0:370:G:O2'	1:0:371:U:H5'	2.22	0.40
14:L:23:LEU:O	14:L:26:HIS:HB2	2.21	0.40
4:B:215:VAL:HB	4:B:234:ARG:NH1	2.35	0.40
1:0:2255:A:H2'	1:0:2256:G:O4'	2.21	0.40
2:9:31:C:O2'	2:9:32:G:H5'	2.21	0.40
21:S:14:ALA:HA	21:S:15:PRO:HD3	1.93	0.40
1:0:517:U:H1'	36:0:7111:HOH:O	2.22	0.40
7:E:112:ALA:HA	7:E:113:PRO:HD3	1.93	0.40
19:Q:82:GLU:HG3	19:Q:83:LYS:N	2.35	0.40
4:B:189:ALA:HB1	36:B:8568:HOH:O	2.21	0.40
1:0:2019:A:H5'	36:0:4048:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	235/239 (98%)	216 (92%)	14 (6%)	5 (2%)	9	10
4	B	335/337 (99%)	314 (94%)	14 (4%)	7 (2%)	9	10
5	C	244/246 (99%)	226 (93%)	18 (7%)	0	100	100
6	D	134/176 (76%)	97 (72%)	28 (21%)	9 (7%)	1	0
7	E	170/177 (96%)	161 (95%)	8 (5%)	1 (1%)	30	43
8	F	117/119 (98%)	106 (91%)	9 (8%)	2 (2%)	11	14
9	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
10	H	152/167 (91%)	135 (89%)	12 (8%)	5 (3%)	5	4
11	I	140/145 (97%)	130 (93%)	7 (5%)	3 (2%)	9	10
12	J	130/132 (98%)	121 (93%)	8 (6%)	1 (1%)	24	35
13	K	141/164 (86%)	121 (86%)	19 (14%)	1 (1%)	26	38
14	L	192/194 (99%)	181 (94%)	10 (5%)	1 (0%)	34	48
15	M	184/186 (99%)	167 (91%)	10 (5%)	7 (4%)	4	3
16	N	113/115 (98%)	109 (96%)	4 (4%)	0	100	100
17	O	141/148 (95%)	138 (98%)	3 (2%)	0	100	100
18	P	93/95 (98%)	89 (96%)	4 (4%)	0	100	100
19	Q	148/154 (96%)	143 (97%)	4 (3%)	1 (1%)	26	38
20	R	79/84 (94%)	75 (95%)	4 (5%)	0	100	100
21	S	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
22	T	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
23	U	63/70 (90%)	58 (92%)	3 (5%)	2 (3%)	5	4
24	V	152/154 (99%)	147 (97%)	4 (3%)	1 (1%)	26	38
25	W	80/91 (88%)	70 (88%)	8 (10%)	2 (2%)	7	7
26	X	140/240 (58%)	140 (100%)	0	0	100	100
27	Y	71/73 (97%)	64 (90%)	5 (7%)	2 (3%)	6	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Z	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
29	1	42/48 (88%)	42 (100%)	0	0	100	100
30	2	90/92 (98%)	86 (96%)	2 (2%)	2 (2%)	8	9
All	All	3633/4235 (86%)	3372 (93%)	209 (6%)	52 (1%)	14	19

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	139	ASP
6	D	93	LEU
6	D	95	THR
6	D	137	PRO
6	D	173	GLU
10	H	162	SER
13	K	80	ASP
15	M	154	LEU
15	M	164	ASP
15	M	183	ASP
23	U	43	PRO
3	A	34	ASP
3	A	37	VAL
3	A	132	ASP
4	B	34	GLY
4	B	169	GLY
6	D	11	HIS
6	D	20	LYS
8	F	101	ALA
10	H	164	ALA
11	I	7	ASP
11	I	143	LYS
15	M	162	ASP
30	2	56	PRO
30	2	57	GLY
4	B	184	ASP
6	D	171	ASP
10	H	40	PRO
10	H	138	PRO
11	I	5	GLU
14	L	140	ALA
15	M	167	ASP
15	M	181	ASP

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Mol	Chain	Res	Type
24	V	77	ALA
25	W	77	PHE
27	Y	81	LYS
4	B	185	GLY
6	D	61	PHE
10	H	72	VAL
15	M	65	ASP
4	B	107	SER
8	F	64	PRO
6	D	96	SER
12	J	119	GLN
23	U	40	PRO
4	B	2	GLN
27	Y	41	VAL
7	E	44	GLY
19	Q	81	PRO
3	A	211	LYS
25	W	52	PRO
3	A	112	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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	179/181 (99%)	166 (93%)	13 (7%)	17	27
4	B	282/282 (100%)	264 (94%)	18 (6%)	22	34
5	C	193/193 (100%)	179 (93%)	14 (7%)	17	27
6	D	117/147 (80%)	106 (91%)	11 (9%)	11	16
7	E	152/155 (98%)	148 (97%)	4 (3%)	54	74
8	F	92/92 (100%)	91 (99%)	1 (1%)	80	92
9	G	27/283 (10%)	27 (100%)	0	100	100
10	H	122/122 (100%)	109 (89%)	13 (11%)	8	11
11	I	118/121 (98%)	109 (92%)	9 (8%)	16	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	J	106/106 (100%)	103 (97%)	3 (3%)	51	72
13	K	112/126 (89%)	108 (96%)	4 (4%)	42	63
14	L	166/166 (100%)	157 (95%)	9 (5%)	27	43
15	M	149/149 (100%)	143 (96%)	6 (4%)	38	58
16	N	93/93 (100%)	91 (98%)	2 (2%)	60	79
17	O	113/116 (97%)	111 (98%)	2 (2%)	66	84
18	P	79/79 (100%)	75 (95%)	4 (5%)	29	46
19	Q	117/121 (97%)	114 (97%)	3 (3%)	54	74
20	R	71/73 (97%)	71 (100%)	0	100	100
21	S	105/105 (100%)	101 (96%)	4 (4%)	40	60
22	T	44/52 (85%)	44 (100%)	0	100	100
23	U	51/56 (91%)	50 (98%)	1 (2%)	63	81
24	V	130/130 (100%)	122 (94%)	8 (6%)	23	35
25	W	66/73 (90%)	62 (94%)	4 (6%)	23	36
26	X	120/195 (62%)	110 (92%)	10 (8%)	14	21
27	Y	56/56 (100%)	52 (93%)	4 (7%)	18	28
28	Z	46/46 (100%)	46 (100%)	0	100	100
29	1	42/44 (96%)	41 (98%)	1 (2%)	57	76
30	2	79/79 (100%)	76 (96%)	3 (4%)	40	60
All	All	3027/3441 (88%)	2876 (95%)	151 (5%)	30	48

All (151) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	3	ARG
3	A	33	GLU
3	A	36	ASP
3	A	55	VAL
3	A	68	ILE
3	A	69	LEU
3	A	78	ASP
3	A	94	LEU
3	A	120	ARG
3	A	131	HIS
3	A	153	ARG

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Mol	Chain	Res	Type
3	A	179	MET
3	A	217	ARG
4	B	7	ARG
4	B	11	LEU
4	B	27	ASN
4	B	33	ASP
4	B	53	LEU
4	B	63	GLU
4	B	84	LEU
4	B	97	LEU
4	B	98	THR
4	B	103	ASP
4	B	162	MET
4	B	234	ARG
4	B	251	VAL
4	B	254	GLN
4	B	256	GLN
4	B	264	GLU
4	B	307	ARG
4	B	312	ARG
5	C	2	GLN
5	C	27	ARG
5	C	67	GLN
5	C	94	THR
5	C	101	ASP
5	C	115	LEU
5	C	136	VAL
5	C	187	ARG
5	C	214	THR
5	C	222	ASP
5	C	223	LEU
5	C	234	VAL
5	C	236	THR
5	C	240	LEU
6	D	24	HIS
6	D	50	VAL
6	D	61	PHE
6	D	95	THR
6	D	99	ASP
6	D	100	ASP
6	D	131	THR
6	D	133	ASN

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Mol	Chain	Res	Type
6	D	136	ARG
6	D	137	PRO
6	D	149	ARG
7	E	7	ILE
7	E	54	ASP
7	E	102	VAL
7	E	164	ASP
8	F	1	PRO
10	H	1	LYS
10	H	59	ASN
10	H	61	LEU
10	H	72	VAL
10	H	73	GLN
10	H	82	LYS
10	H	85	ILE
10	H	86	ARG
10	H	118	PRO
10	H	129	ASN
10	H	142	VAL
10	H	150	LYS
10	H	166	ASN
11	I	46	ILE
11	I	52	GLN
11	I	74	ARG
11	I	79	PHE
11	I	107	ASN
11	I	112	ASP
11	I	120	SER
11	I	125	SER
11	I	127	ILE
12	J	7	ASP
12	J	10	GLN
12	J	98	VAL
13	K	30	ARG
13	K	35	ARG
13	K	80	ASP
13	K	117	GLU
14	L	38	VAL
14	L	46	LEU
14	L	48	ARG
14	L	68	ARG
14	L	81	ARG

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Mol	Chain	Res	Type
14	L	87	MET
14	L	93	ARG
14	L	99	ARG
14	L	164	THR
15	M	26	LEU
15	M	43	VAL
15	M	127	LEU
15	M	128	ASP
15	M	152	GLU
15	M	163	PHE
16	N	3	THR
16	N	28	ASP
17	O	91	LYS
17	O	98	ILE
18	P	11	ARG
18	P	16	ASN
18	P	57	ASP
18	P	95	GLU
19	Q	13	THR
19	Q	39	THR
19	Q	82	GLU
21	S	39	ASN
21	S	48	VAL
21	S	73	HIS
21	S	96	VAL
23	U	43	PRO
24	V	4	LEU
24	V	35	VAL
24	V	52	VAL
24	V	73	LEU
24	V	122	ARG
24	V	142	ASP
24	V	146	ILE
24	V	154	ARG
25	W	15	ARG
25	W	27	ASP
25	W	49	ARG
25	W	72	VAL
26	X	141	THR
26	X	154	ARG
26	X	163	THR
26	X	172	THR

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Mol	Chain	Res	Type
26	X	186	ARG
26	X	189	ASN
26	X	200	THR
26	X	203	VAL
26	X	204	ARG
26	X	231	PRO
27	Y	11	THR
27	Y	44	PHE
27	Y	49	ARG
27	Y	64	ILE
29	1	18	ASN
30	2	14	CYS
30	2	42	ARG
30	2	56	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (87) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	92	ASN
3	A	127	GLN
3	A	199	HIS
4	B	27	ASN
4	B	145	HIS
4	B	221	GLN
4	B	238	ASN
4	B	256	GLN
4	B	260	HIS
4	B	318	ASN
4	B	332	ASN
5	C	2	GLN
5	C	39	GLN
5	C	129	HIS
5	C	163	HIS
6	D	103	ASN
7	E	106	ASN
7	E	119	HIS
7	E	143	GLN
9	G	17	GLN
9	G	64	ASN
10	H	8	ASN
10	H	35	ASN
10	H	55	GLN

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Mol	Chain	Res	Type
10	H	58	HIS
10	H	59	ASN
10	H	69	ASN
10	H	74	ASN
10	H	91	HIS
10	H	129	ASN
10	H	130	HIS
10	H	166	ASN
11	I	52	GLN
11	I	107	ASN
11	I	126	ASN
12	J	10	GLN
13	K	18	HIS
13	K	41	HIS
13	K	42	ASN
13	K	116	HIS
14	L	26	HIS
14	L	58	GLN
14	L	89	ASN
14	L	176	GLN
15	M	21	HIS
15	M	107	ASN
15	M	153	GLN
16	N	53	GLN
17	O	50	GLN
17	O	66	GLN
17	O	73	HIS
17	O	118	GLN
18	P	16	ASN
18	P	40	HIS
19	Q	61	GLN
19	Q	94	ASN
19	Q	98	ASN
19	Q	113	HIS
19	Q	117	HIS
19	Q	122	GLN
20	R	53	ASN
21	S	39	ASN
21	S	73	HIS
22	T	39	ASN
23	U	60	GLN
24	V	27	HIS

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Mol	Chain	Res	Type
24	V	87	HIS
24	V	110	GLN
24	V	119	HIS
24	V	125	HIS
24	V	141	HIS
25	W	23	HIS
26	X	133	HIS
26	X	134	HIS
26	X	149	GLN
26	X	189	ASN
27	Y	33	HIS
27	Y	70	GLN
28	Z	8	GLN
28	Z	16	HIS
28	Z	28	HIS
29	1	16	ASN
29	1	18	ASN
29	1	41	HIS
29	1	45	ASN
30	2	30	GLN
30	2	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2747/2922 (94%)	239 (8%)	35 (1%)
2	9	121/122 (99%)	16 (13%)	5 (4%)
All	All	2868/3044 (94%)	255 (8%)	40 (1%)

All (255) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	11	A
1	0	31	C
1	0	60	A
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	87	C
1	0	88	G

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Mol	Chain	Res	Type
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	139	C
1	0	141	C
1	0	151	A
1	0	166	A
1	0	169	A
1	0	186	A
1	0	191	A
1	0	192	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	318	C
1	0	336	G
1	0	337	A
1	0	345	G
1	0	358	G
1	0	381	G
1	0	397	A
1	0	417	G
1	0	461	C
1	0	487	G
1	0	498	A
1	0	510	U
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G
1	0	553	G

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Mol	Chain	Res	Type
1	0	559	U
1	0	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	688	A
1	0	701	U
1	0	717	C
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	884	C
1	0	898	G
1	0	905	C
1	0	921	G
1	0	923	A
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1088	A
1	0	1109	U

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Mol	Chain	Res	Type
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1161	A
1	0	1162	G
1	0	1164	U
1	0	1165	G
1	0	1166	A
1	0	1171	A
1	0	1174	A
1	0	1175	G
1	0	1177	A
1	0	1185	U
1	0	1192	A
1	0	1193	A
1	0	1206	U
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1289	C
1	0	1342	C
1	0	1353	C
1	0	1360	C
1	0	1377	C
1	0	1380	U
1	0	1407	A
1	0	1409	G
1	0	1451	C
1	0	1474	C
1	0	1485	A
1	0	1488	U
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1564	C
1	0	1580	A
1	0	1592	G
1	0	1603	A

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Mol	Chain	Res	Type
1	0	1625	U
1	0	1626	A
1	0	1633	C
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1710	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1731	C
1	0	1752	G
1	0	1778	A
1	0	1779	A
1	0	1798	C
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U
1	0	1904	A
1	0	1919	A
1	0	1942	A
1	0	1943	C
1	0	1971	G
1	0	1973	A
1	0	1974	G
1	0	1978	A
1	0	1979	G
1	0	1980	U
1	0	1982	C
1	0	1996	U
1	0	2004	U
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G

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Mol	Chain	Res	Type
1	0	2034	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2238	A
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2346	C
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2422	U
1	0	2462	G
1	0	2469	A
1	0	2476	C
1	0	2480	G
1	0	2483	A
1	0	2507	G
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2638	G
1	0	2649	A
1	0	2664	A
1	0	2681	A

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Mol	Chain	Res	Type
1	0	2682	C
1	0	2719	A
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2825	C
1	0	2840	A
1	0	2850	C
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2914	A
2	9	2	U
2	9	14	G
2	9	22	G
2	9	23	U
2	9	24	U
2	9	25	G
2	9	26	C
2	9	41	C
2	9	43	G
2	9	44	A
2	9	52	A
2	9	57	A
2	9	66	G
2	9	77	A
2	9	114	G
2	9	122	C

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	10	U
1	0	69	A

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Mol	Chain	Res	Type
1	0	129	A
1	0	284	C
1	0	338	C
1	0	603	A
1	0	699	C
1	0	716	G
1	0	834	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	1080	C
1	0	1164	U
1	0	1232	A
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1377	C
1	0	1450	C
1	0	1563	G
1	0	1692	C
1	0	1856	C
1	0	1942	A
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2467	A
1	0	2526	C
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2726	U
1	0	2761	A
1	0	2791	U
2	9	2	U
2	9	23	U
2	9	24	U
2	9	65	A
2	9	103	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 232 ligands modelled in this entry, 232 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2754/2922 (94%)	-0.20	67 (2%) 62 61	17, 36, 79, 127	0
2	9	122/122 (100%)	-0.18	6 (4%) 33 34	31, 54, 78, 136	0
3	A	237/239 (99%)	0.45	22 (9%) 11 10	19, 38, 71, 92	0
4	B	337/337 (100%)	0.44	16 (4%) 35 36	21, 45, 71, 82	0
5	C	246/246 (100%)	0.38	12 (4%) 33 34	15, 35, 58, 70	0
6	D	140/176 (79%)	2.69	87 (62%) 0 0	43, 86, 105, 108	0
7	E	172/177 (97%)	0.66	13 (7%) 17 16	37, 59, 77, 81	0
8	F	119/119 (100%)	0.98	21 (17%) 2 2	37, 58, 83, 88	0
9	G	29/348 (8%)	2.70	21 (72%) 0 0	64, 79, 86, 91	0
10	H	156/167 (93%)	0.77	25 (16%) 3 2	30, 47, 75, 79	0
11	I	142/145 (97%)	0.30	6 (4%) 40 41	29, 42, 63, 84	0
12	J	132/132 (100%)	0.22	7 (5%) 30 30	27, 42, 61, 71	0
13	K	145/164 (88%)	0.77	17 (11%) 6 6	18, 54, 90, 102	0
14	L	194/194 (100%)	0.18	8 (4%) 41 42	19, 32, 50, 62	0
15	M	186/186 (100%)	0.67	17 (9%) 11 11	31, 50, 91, 103	0
16	N	115/115 (100%)	0.02	1 (0%) 85 85	27, 44, 60, 69	0
17	O	143/148 (96%)	0.19	1 (0%) 89 88	30, 44, 57, 64	0
18	P	95/95 (100%)	0.13	2 (2%) 67 66	25, 34, 50, 61	0
19	Q	150/154 (97%)	0.02	0 100 100	23, 36, 54, 63	0
20	R	81/84 (96%)	0.53	9 (11%) 7 7	31, 47, 68, 72	0
21	S	119/119 (100%)	0.47	4 (3%) 49 49	28, 45, 69, 81	0
22	T	53/66 (80%)	0.41	1 (1%) 70 69	33, 47, 63, 71	0
23	U	65/70 (92%)	1.73	13 (20%) 1 1	39, 59, 97, 101	0
24	V	154/154 (100%)	0.40	5 (3%) 51 51	27, 40, 57, 65	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	82/91 (90%)	0.52	7 (8%) 13 13	35, 48, 73, 91	0
26	X	142/240 (59%)	0.05	5 (3%) 48 48	22, 35, 59, 74	0
27	Y	73/73 (100%)	0.64	9 (12%) 5 5	36, 49, 63, 77	0
28	Z	56/56 (100%)	0.27	0 100 100	17, 24, 32, 35	0
29	1	46/48 (95%)	0.58	7 (15%) 3 3	27, 49, 77, 86	0
30	2	92/92 (100%)	0.26	3 (3%) 50 50	23, 44, 59, 72	0
All	All	6577/7279 (90%)	0.21	412 (6%) 23 24	15, 41, 80, 136	0

All (412) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
23	U	1	THR	14.4
6	D	63	ILE	10.3
23	U	39	ALA	9.1
6	D	57	THR	7.9
23	U	40	PRO	7.1
25	W	88	GLU	6.8
20	R	81	ILE	6.8
3	A	37	VAL	6.8
15	M	166	ALA	6.6
15	M	186	LEU	6.6
2	9	1	U	6.6
6	D	18	ILE	6.6
6	D	10	PHE	6.5
23	U	38	GLY	6.2
6	D	170	TYR	6.1
1	0	1172	G	5.9
25	W	80	GLU	5.9
8	F	106	THR	5.8
4	B	1	PRO	5.7
3	A	237	GLY	5.6
6	D	69	ILE	5.6
6	D	92	GLU	5.6
6	D	66	GLY	5.5
9	G	23	ILE	5.5
23	U	43	PRO	5.5
6	D	85	GLN	5.4
6	D	61	PHE	5.4
6	D	58	VAL	5.3
6	D	172	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	0	1198	U	5.2
6	D	166	ILE	5.2
1	0	1200	A	5.1
2	9	25	G	5.0
6	D	75	LEU	5.0
3	A	36	ASP	5.0
1	0	282	C	5.0
1	0	1177	A	4.9
15	M	162	ASP	4.9
6	D	165	PHE	4.9
1	0	1202	A	4.9
6	D	88	LEU	4.9
1	0	1174	A	4.8
3	A	35	GLY	4.8
6	D	94	ALA	4.8
1	0	1171	A	4.7
3	A	85	ASP	4.7
9	G	26	MET	4.7
6	D	50	VAL	4.6
2	9	23	U	4.6
1	0	284	C	4.6
26	X	235	GLU	4.5
7	E	87	PHE	4.5
6	D	62	ASP	4.5
9	G	12	ILE	4.4
6	D	102	GLY	4.4
9	G	70	ALA	4.4
6	D	106	PHE	4.3
6	D	67	ASP	4.3
6	D	44	ILE	4.3
6	D	95	THR	4.3
1	0	1169	U	4.3
1	0	1525	G	4.2
6	D	81	GLU	4.2
1	0	1173	A	4.2
6	D	104	PHE	4.2
5	C	135	GLU	4.1
1	0	1199	A	4.1
10	H	146	TRP	4.1
1	0	960	G	4.1
11	I	4	ALA	4.1
1	0	1201	C	4.0

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Mol	Chain	Res	Type	RSRZ
1	0	1170	U	4.0
6	D	64	ARG	4.0
13	K	81	VAL	4.0
13	K	80	ASP	3.9
1	0	970	U	3.9
27	Y	80	MET	3.9
6	D	27	ILE	3.8
2	9	24	U	3.8
6	D	40	ILE	3.8
1	0	1196	C	3.8
6	D	56	ARG	3.8
7	E	45	ASP	3.8
6	D	134	LEU	3.8
9	G	24	VAL	3.7
6	D	132	VAL	3.7
6	D	171	ASP	3.7
23	U	41	GLU	3.7
27	Y	22	ILE	3.7
9	G	73	ASP	3.7
1	0	1951	G	3.7
15	M	163	PHE	3.7
6	D	68	PRO	3.7
6	D	51	ARG	3.7
23	U	2	VAL	3.7
6	D	101	THR	3.6
6	D	11	HIS	3.6
8	F	119	ARG	3.6
1	0	1192	A	3.6
6	D	84	LEU	3.6
6	D	73	VAL	3.6
6	D	17	ARG	3.6
1	0	1165	G	3.6
1	0	2237	G	3.6
6	D	93	LEU	3.6
10	H	83	PHE	3.6
9	G	25	GLU	3.6
10	H	163	PRO	3.6
15	M	152	GLU	3.6
25	W	85	VAL	3.5
13	K	147	GLU	3.5
1	0	1181	A	3.5
4	B	57	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
12	J	132	VAL	3.5
14	L	194	ALA	3.5
8	F	115	VAL	3.5
1	0	1179	C	3.5
8	F	118	LEU	3.5
10	H	32	ASP	3.5
10	H	79	ALA	3.5
6	D	98	PHE	3.5
10	H	135	TRP	3.5
24	V	93	ILE	3.5
6	D	103	ASN	3.4
1	0	1203	G	3.4
22	T	47	ARG	3.4
6	D	173	GLU	3.4
15	M	68	GLU	3.4
1	0	1175	G	3.4
12	J	119	GLN	3.4
15	M	181	ASP	3.4
3	A	31	LYS	3.3
13	K	145	LEU	3.3
1	0	10	U	3.3
6	D	26	GLY	3.3
21	S	1	SER	3.3
8	F	16	ALA	3.3
30	2	92	GLU	3.3
5	C	132	ASP	3.3
6	D	99	ASP	3.3
1	0	1178	G	3.3
14	L	87	MET	3.3
3	A	133	ARG	3.3
1	0	1163	G	3.3
6	D	74	THR	3.2
20	R	77	VAL	3.2
1	0	1168	C	3.2
13	K	102	ASP	3.2
9	G	69	ARG	3.2
16	N	23	GLY	3.2
6	D	96	SER	3.2
6	D	167	GLU	3.2
6	D	23	VAL	3.2
1	0	1195	G	3.2
26	X	108	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
6	D	22	VAL	3.2
4	B	133	GLU	3.1
8	F	108	LEU	3.1
20	R	2	TRP	3.1
1	0	1950	G	3.1
27	Y	38	LYS	3.1
4	B	104	GLU	3.1
3	A	236	GLY	3.1
10	H	81	TYR	3.1
8	F	107	VAL	3.1
6	D	49	PRO	3.0
6	D	157	LEU	3.0
9	G	66	LEU	3.0
3	A	34	ASP	3.0
27	Y	44	PHE	3.0
6	D	78	GLU	3.0
6	D	55	LYS	3.0
5	C	198	ASP	3.0
9	G	15	TRP	3.0
1	0	1180	U	3.0
13	K	150	GLN	3.0
6	D	86	THR	3.0
1	0	1176	C	3.0
11	I	5	GLU	3.0
6	D	89	PRO	3.0
29	1	39	ARG	2.9
8	F	99	THR	2.9
2	9	2	U	2.9
6	D	25	MET	2.9
29	1	24	TRP	2.9
3	A	64	ASP	2.9
9	G	28	GLU	2.9
1	0	1206	U	2.9
4	B	117	GLU	2.9
8	F	117	GLU	2.9
7	E	169	THR	2.9
20	R	80	ARG	2.9
13	K	148	GLU	2.9
8	F	12	LEU	2.9
9	G	71	LEU	2.9
4	B	183	GLU	2.9
6	D	80	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
10	H	157	ILE	2.9
8	F	17	LEU	2.9
1	0	1205	U	2.9
3	A	97	ALA	2.9
6	D	65	GLU	2.8
24	V	38	THR	2.8
27	Y	11	THR	2.8
7	E	88	TYR	2.8
3	A	32	VAL	2.8
9	G	21	ASP	2.8
15	M	164	ASP	2.8
5	C	14	GLY	2.8
29	1	35	ARG	2.8
1	0	1197	G	2.8
9	G	72	ASP	2.8
9	G	20	VAL	2.8
4	B	180	ASP	2.8
6	D	45	THR	2.8
10	H	66	VAL	2.8
9	G	14	GLU	2.8
7	E	10	ASP	2.8
10	H	72	VAL	2.8
6	D	133	ASN	2.8
30	2	56	PRO	2.8
4	B	184	ASP	2.8
1	0	1167	G	2.7
15	M	154	LEU	2.7
14	L	165	SER	2.7
12	J	108	GLU	2.7
13	K	75	LEU	2.7
6	D	158	ASN	2.7
10	H	41	THR	2.7
6	D	77	ASP	2.7
7	E	170	ARG	2.7
9	G	27	ILE	2.7
7	E	100	ASP	2.7
1	0	1162	G	2.7
25	W	71	ARG	2.7
20	R	76	GLU	2.7
4	B	120	ASP	2.7
14	L	152	ARG	2.7
10	H	35	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
5	C	143	ASP	2.7
13	K	91	VAL	2.7
14	L	140	ALA	2.7
1	0	2238	A	2.7
27	Y	21	LYS	2.7
1	0	1948	G	2.6
20	R	1	SER	2.6
1	0	735	C	2.6
12	J	125	ALA	2.6
8	F	110	GLU	2.6
10	H	162	SER	2.6
6	D	48	MET	2.6
4	B	123	ALA	2.6
4	B	181	ILE	2.6
6	D	156	ARG	2.6
13	K	130	ARG	2.6
1	0	1208	C	2.6
8	F	22	VAL	2.6
6	D	53	LYS	2.6
6	D	47	GLN	2.6
6	D	128	LEU	2.6
6	D	130	VAL	2.6
8	F	15	ASP	2.6
23	U	37	GLY	2.6
8	F	10	ALA	2.6
1	0	1204	C	2.5
7	E	129	GLU	2.5
9	G	18	GLU	2.5
29	1	49	GLU	2.5
21	S	82	THR	2.5
6	D	70	GLY	2.5
1	0	1967	U	2.5
13	K	104	ASP	2.5
15	M	138	ASP	2.5
10	H	142	VAL	2.5
23	U	6	GLN	2.5
6	D	90	LEU	2.5
26	X	236	VAL	2.5
1	0	1625	U	2.5
1	0	2769	C	2.5
6	D	54	ALA	2.5
15	M	139	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
5	C	13	ASP	2.5
8	F	28	ALA	2.5
4	B	115	VAL	2.4
5	C	162	VAL	2.4
6	D	71	ALA	2.4
6	D	139	TYR	2.4
8	F	100	ASP	2.4
9	G	17	GLN	2.4
6	D	59	GLY	2.4
5	C	61	PHE	2.4
27	Y	40	PRO	2.4
15	M	177	GLU	2.4
1	0	1207	A	2.4
15	M	184	ILE	2.4
23	U	45	ARG	2.4
29	1	44	ARG	2.4
6	D	162	ALA	2.4
10	H	36	ASN	2.4
1	0	283	U	2.4
13	K	149	ARG	2.4
12	J	126	SER	2.4
3	A	38	ILE	2.4
10	H	158	ASN	2.4
10	H	59	ASN	2.3
1	0	2508	C	2.3
20	R	46	ASP	2.3
6	D	43	GLU	2.3
12	J	129	THR	2.3
1	0	2004	U	2.3
10	H	139	ASP	2.3
6	D	29	HIS	2.3
25	W	73	ARG	2.3
10	H	33	MET	2.3
8	F	18	GLU	2.3
13	K	144	ASP	2.3
1	0	1279	U	2.3
11	I	39	VAL	2.3
9	G	68	GLU	2.3
1	0	1166	A	2.3
4	B	92	TYR	2.3
1	0	1965	C	2.3
6	D	135	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
6	D	169	THR	2.3
1	0	281	U	2.3
1	0	1949	G	2.3
6	D	83	PHE	2.3
20	R	45	TYR	2.3
8	F	26	THR	2.3
14	L	63	VAL	2.3
1	0	2825	C	2.3
15	M	134	ASP	2.3
24	V	91	ASP	2.3
3	A	66	ARG	2.3
6	D	41	LEU	2.3
8	F	114	LYS	2.3
26	X	95	THR	2.3
8	F	11	ASP	2.2
15	M	179	LEU	2.2
24	V	61	THR	2.2
3	A	99	ILE	2.2
11	I	7	ASP	2.2
12	J	101	ASN	2.2
13	K	90	ARG	2.2
15	M	175	LEU	2.2
23	U	49	LEU	2.2
24	V	86	GLU	2.2
1	0	999	C	2.2
1	0	2250	G	2.2
4	B	61	PRO	2.2
10	H	136	VAL	2.2
27	Y	75	ALA	2.2
13	K	89	PHE	2.2
11	I	47	THR	2.2
10	H	80	ASN	2.2
29	1	36	ASN	2.2
3	A	89	ALA	2.2
6	D	164	ALA	2.2
3	A	63	GLY	2.2
20	R	79	SER	2.2
2	9	122	C	2.2
3	A	94	LEU	2.2
23	U	28	LEU	2.2
10	H	128	ALA	2.1
17	O	76	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	0	736	A	2.1
27	Y	47	LEU	2.1
3	A	134	ASN	2.1
1	0	1164	U	2.1
5	C	140	VAL	2.1
7	E	86	VAL	2.1
10	H	46	VAL	2.1
1	0	280	C	2.1
3	A	60	PHE	2.1
7	E	127	ASP	2.1
9	G	67	LEU	2.1
1	0	1194	A	2.1
10	H	40	PRO	2.1
14	L	35	PRO	2.1
18	P	95	GLU	2.1
5	C	141	SER	2.1
4	B	118	ASP	2.1
21	S	59	GLU	2.1
23	U	27	LEU	2.1
1	0	128	A	2.1
14	L	156	ARG	2.1
25	W	10	VAL	2.1
5	C	126	ASP	2.1
21	S	80	GLU	2.1
5	C	73	LEU	2.1
3	A	65	ARG	2.1
1	0	288	A	2.1
25	W	7	GLU	2.1
11	I	92	GLN	2.1
26	X	98	GLN	2.1
29	1	20	ARG	2.1
10	H	140	PRO	2.1
7	E	11	VAL	2.1
7	E	6	GLU	2.1
1	0	2254	G	2.1
15	M	157	PRO	2.1
4	B	122	ASP	2.1
6	D	87	ALA	2.0
30	2	26	ARG	2.0
6	D	174	VAL	2.0
7	E	42	VAL	2.0
13	K	97	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
3	A	62	ASP	2.0
1	0	1929	G	2.0
13	K	99	GLU	2.0
6	D	154	LYS	2.0
18	P	92	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
33	NA	0	8320	1/1	0.99	0.29	31.60	38,38,38,38	0
33	NA	0	8350	1/1	0.93	0.35	29.76	36,36,36,36	0
33	NA	0	8371	1/1	0.76	0.36	23.72	49,49,49,49	0
33	NA	0	8372	1/1	0.92	0.43	23.09	54,54,54,54	0
33	NA	0	8362	1/1	0.94	0.34	18.39	51,51,51,51	0
33	NA	0	8327	1/1	0.92	0.27	17.22	38,38,38,38	0
33	NA	0	8340	1/1	0.90	0.26	15.56	47,47,47,47	0
33	NA	Q	8386	1/1	0.62	0.44	12.93	74,74,74,74	0
33	NA	0	8366	1/1	0.96	0.26	12.64	54,54,54,54	0
33	NA	0	8331	1/1	0.98	0.27	11.15	39,39,39,39	0
33	NA	0	8376	1/1	0.91	0.28	10.71	39,39,39,39	0
33	NA	0	8302	1/1	0.93	0.24	9.87	44,44,44,44	0
33	NA	0	8364	1/1	0.97	0.26	8.74	38,38,38,38	0
33	NA	0	8314	1/1	0.93	0.32	8.45	40,40,40,40	0
33	NA	0	8374	1/1	0.96	0.20	6.89	44,44,44,44	0
33	NA	0	8325	1/1	0.94	0.23	4.93	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	0	8361	1/1	0.93	0.23	4.34	38,38,38,38	0
33	NA	K	8380	1/1	0.97	0.26	4.24	42,42,42,42	0
33	NA	0	8305	1/1	0.98	0.22	4.09	32,32,32,32	0
31	MG	0	8060	1/1	0.99	0.21	3.89	31,31,31,31	0
33	NA	0	8321	1/1	0.94	0.24	2.81	40,40,40,40	0
33	NA	0	8303	1/1	0.98	0.17	2.58	32,32,32,32	0
33	NA	9	8383	1/1	0.89	0.21	1.79	43,43,43,43	0
33	NA	0	8356	1/1	0.93	0.20	1.33	37,37,37,37	0
33	NA	0	8368	1/1	0.94	0.14	1.04	48,48,48,48	0
33	NA	0	8335	1/1	0.96	0.18	0.92	31,31,31,31	0
33	NA	0	8339	1/1	0.98	0.19	0.87	20,20,20,20	0
31	MG	0	8012	1/1	0.95	0.14	0.51	32,32,32,32	0
33	NA	0	8373	1/1	0.90	0.12	0.27	43,43,43,43	0
33	NA	C	8304	1/1	0.85	0.18	-0.09	30,30,30,30	0
33	NA	0	8365	1/1	0.96	0.18	-0.20	28,28,28,28	0
31	MG	0	8067	1/1	0.91	0.14	-0.24	34,34,34,34	0
33	NA	0	8324	1/1	0.95	0.13	-0.25	48,48,48,48	0
31	MG	0	8010	1/1	0.97	0.17	-0.35	24,24,24,24	0
31	MG	0	8007	1/1	0.98	0.17	-0.39	21,21,21,21	0
34	CL	I	8521	1/1	0.94	0.17	-0.39	47,47,47,47	0
34	CL	0	8516	1/1	0.99	0.14	-0.47	42,42,42,42	0
34	CL	L	8518	1/1	0.98	0.15	-0.50	32,32,32,32	0
33	NA	0	8381	1/1	0.98	0.12	-0.54	41,41,41,41	0
35	CD	Y	8403	1/1	0.99	0.14	-0.67	49,49,49,49	0
31	MG	0	8064	1/1	0.94	0.15	-0.72	26,26,26,26	0
33	NA	0	8378	1/1	0.97	0.17	-0.73	39,39,39,39	0
31	MG	0	8013	1/1	0.95	0.15	-0.75	22,22,22,22	0
33	NA	L	8347	1/1	0.97	0.14	-0.82	18,18,18,18	0
31	MG	0	8086	1/1	0.99	0.09	-0.90	33,33,33,33	0
31	MG	0	8015	1/1	0.98	0.18	-1.03	26,26,26,26	0
33	NA	0	8344	1/1	0.97	0.11	-1.11	24,24,24,24	0
33	NA	0	8382	1/1	0.94	0.10	-1.31	64,64,64,64	0
31	MG	0	8038	1/1	0.98	0.13	-1.38	22,22,22,22	0
33	NA	H	8309	1/1	0.99	0.10	-1.47	28,28,28,28	0
34	CL	0	8515	1/1	0.99	0.11	-1.54	48,48,48,48	0
33	NA	0	8332	1/1	0.97	0.12	-1.54	33,33,33,33	0
35	CD	T	8401	1/1	0.99	0.10	-1.62	49,49,49,49	0
33	NA	0	8310	1/1	0.94	0.11	-1.74	27,27,27,27	0
34	CL	B	8519	1/1	0.99	0.14	-1.78	33,33,33,33	0
35	CD	2	8404	1/1	0.99	0.09	-1.86	47,47,47,47	0
34	CL	0	8512	1/1	0.99	0.11	-1.86	34,34,34,34	0
31	MG	0	8054	1/1	0.98	0.16	-1.94	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	I	8346	1/1	0.98	0.09	-2.02	34,34,34,34	0
33	NA	0	8353	1/1	0.99	0.14	-2.14	18,18,18,18	0
33	NA	0	8333	1/1	0.95	0.09	-2.19	23,23,23,23	0
31	MG	0	8004	1/1	0.99	0.13	-2.28	21,21,21,21	0
31	MG	0	8027	1/1	0.98	0.06	-2.39	37,37,37,37	0
33	NA	0	8317	1/1	0.96	0.10	-2.53	27,27,27,27	0
33	NA	0	8334	1/1	0.95	0.09	-2.54	33,33,33,33	0
34	CL	0	8505	1/1	0.98	0.11	-2.66	41,41,41,41	0
32	K	0	8201	1/1	0.95	0.14	-2.72	62,62,62,62	0
34	CL	N	8508	1/1	0.97	0.07	-2.75	52,52,52,52	0
31	MG	2	8078	1/1	0.98	0.10	-2.77	39,39,39,39	0
33	NA	P	8348	1/1	0.95	0.07	-2.80	32,32,32,32	0
31	MG	S	8073	1/1	0.98	0.06	-3.07	39,39,39,39	0
33	NA	A	8345	1/1	0.93	0.09	-3.18	46,46,46,46	0
31	MG	0	8091	1/1	0.96	0.10	-3.21	41,41,41,41	0
33	NA	S	8343	1/1	0.97	0.06	-3.27	29,29,29,29	0
31	MG	0	8003	1/1	0.98	0.11	-3.28	21,21,21,21	0
31	MG	0	8077	1/1	0.92	0.14	-3.29	23,23,23,23	0
31	MG	0	8057	1/1	0.98	0.12	-3.32	35,35,35,35	0
31	MG	0	8074	1/1	0.97	0.06	-3.40	36,36,36,36	0
31	MG	0	8096	1/1	0.97	0.10	-3.50	37,37,37,37	0
31	MG	0	8017	1/1	1.00	0.13	-3.61	12,12,12,12	0
31	MG	0	8112	1/1	0.98	0.10	-3.93	23,23,23,23	0
31	MG	0	8033	1/1	0.97	0.09	-4.00	20,20,20,20	0
35	CD	Z	8402	1/1	0.99	0.04	-4.10	37,37,37,37	0
31	MG	0	8008	1/1	0.99	0.10	-4.16	22,22,22,22	0
31	MG	X	8109	1/1	0.98	0.08	-4.18	25,25,25,25	0
31	MG	0	8080	1/1	0.94	0.07	-4.33	41,41,41,41	0
31	MG	0	8020	1/1	0.97	0.09	-4.47	24,24,24,24	0
31	MG	0	8110	1/1	0.99	0.10	-4.65	24,24,24,24	0
31	MG	B	8055	1/1	0.91	0.07	-4.80	40,40,40,40	0
31	MG	0	8084	1/1	0.98	0.07	-5.01	39,39,39,39	0
33	NA	Q	8337	1/1	0.96	0.07	-5.14	33,33,33,33	0
33	NA	0	8323	1/1	0.99	0.12	-5.40	31,31,31,31	0
31	MG	0	8056	1/1	0.98	0.04	-5.49	31,31,31,31	0
31	MG	A	8065	1/1	0.97	0.07	-5.63	24,24,24,24	0
31	MG	0	8108	1/1	0.97	0.07	-5.64	62,62,62,62	0
33	NA	0	8313	1/1	0.94	0.09	-5.93	48,48,48,48	0
31	MG	0	8001	1/1	0.98	0.11	-6.04	25,25,25,25	0
33	NA	0	8338	1/1	0.99	0.06	-6.32	36,36,36,36	0
31	MG	0	8107	1/1	0.96	0.03	-6.57	30,30,30,30	0
31	MG	0	8035	1/1	0.98	0.07	-6.62	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	0	8044	1/1	0.98	0.09	-6.73	32,32,32,32	0
31	MG	0	8058	1/1	0.97	0.06	-6.73	27,27,27,27	0
34	CL	2	8504	1/1	0.98	0.06	-7.08	45,45,45,45	0
31	MG	0	8059	1/1	0.96	0.07	-7.65	25,25,25,25	0
31	MG	0	8053	1/1	0.99	0.07	-8.20	28,28,28,28	0
31	MG	0	8039	1/1	0.97	0.07	-8.73	32,32,32,32	0
31	MG	0	8018	1/1	0.97	0.06	-8.80	27,27,27,27	0
31	MG	0	8032	1/1	0.96	0.06	-8.82	23,23,23,23	0
31	MG	0	8021	1/1	0.99	0.09	-8.96	24,24,24,24	0
31	MG	0	8019	1/1	0.99	0.05	-9.13	23,23,23,23	0
31	MG	0	8006	1/1	0.94	0.07	-10.10	27,27,27,27	0
31	MG	0	8028	1/1	0.96	0.06	-11.38	25,25,25,25	0
31	MG	0	8071	1/1	0.94	0.04	-11.41	62,62,62,62	0
31	MG	0	8002	1/1	0.96	0.08	-12.77	26,26,26,26	0
31	MG	0	8052	1/1	0.98	0.06	-14.41	45,45,45,45	0
32	K	0	8202	1/1	0.99	0.08	-16.18	37,37,37,37	0
33	NA	0	8349	1/1	0.96	0.18	-	37,37,37,37	0
31	MG	0	8087	1/1	0.62	0.28	-	72,72,72,72	0
31	MG	0	8048	1/1	0.98	0.07	-	39,39,39,39	0
34	CL	K	8510	1/1	0.98	0.08	-	36,36,36,36	0
34	CL	I	8502	1/1	0.96	0.11	-	53,53,53,53	0
33	NA	9	8351	1/1	0.90	0.12	-	42,42,42,42	0
31	MG	0	8014	1/1	0.93	0.09	-	25,25,25,25	0
31	MG	0	8102	1/1	0.84	0.11	-	51,51,51,51	0
33	NA	0	8360	1/1	0.93	0.21	-	41,41,41,41	0
34	CL	A	8509	1/1	0.98	0.12	-	50,50,50,50	0
31	MG	0	8016	1/1	0.94	0.09	-	32,32,32,32	0
31	MG	0	8031	1/1	0.97	0.12	-	24,24,24,24	0
31	MG	0	8043	1/1	0.90	0.07	-	33,33,33,33	0
31	MG	0	8116	1/1	0.97	0.09	-	42,42,42,42	0
31	MG	0	8090	1/1	0.90	0.31	-	53,53,53,53	0
34	CL	0	8522	1/1	0.97	0.15	-	44,44,44,44	0
31	MG	0	8066	1/1	0.95	0.49	-	85,85,85,85	0
33	NA	0	8370	1/1	0.77	0.44	-	61,61,61,61	0
31	MG	0	8076	1/1	0.87	0.04	-	46,46,46,46	0
31	MG	A	8105	1/1	0.97	0.16	-	27,27,27,27	0
31	MG	0	8093	1/1	0.94	0.12	-	35,35,35,35	0
34	CL	0	8517	1/1	0.97	0.09	-	50,50,50,50	0
33	NA	0	8306	1/1	0.98	0.13	-	28,28,28,28	0
31	MG	0	8062	1/1	0.91	0.08	-	41,41,41,41	0
31	MG	0	8045	1/1	0.95	0.07	-	51,51,51,51	0
31	MG	0	8024	1/1	0.99	0.15	-	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	CL	I	8501	1/1	0.98	0.09	-	44,44,44,44	0
31	MG	0	8063	1/1	0.96	0.12	-	62,62,62,62	0
31	MG	0	8022	1/1	0.92	0.12	-	32,32,32,32	0
31	MG	0	8023	1/1	0.97	0.14	-	30,30,30,30	0
31	MG	0	8106	1/1	0.95	0.13	-	42,42,42,42	0
33	NA	0	8330	1/1	0.97	0.07	-	39,39,39,39	0
31	MG	0	8075	1/1	0.98	0.06	-	28,28,28,28	0
31	MG	0	8046	1/1	0.94	0.05	-	38,38,38,38	0
33	NA	0	8307	1/1	0.88	0.13	-	42,42,42,42	0
34	CL	X	8520	1/1	0.96	0.13	-	38,38,38,38	0
31	MG	0	8040	1/1	0.97	0.12	-	38,38,38,38	0
33	NA	0	8355	1/1	0.96	0.38	-	47,47,47,47	0
34	CL	0	8513	1/1	0.99	0.10	-	44,44,44,44	0
31	MG	0	8036	1/1	0.97	0.08	-	35,35,35,35	0
33	NA	0	8326	1/1	0.95	0.21	-	37,37,37,37	0
31	MG	0	8088	1/1	0.99	0.09	-	20,20,20,20	0
34	CL	Q	8506	1/1	0.97	0.12	-	40,40,40,40	0
34	CL	0	8503	1/1	0.98	0.17	-	40,40,40,40	0
31	MG	0	8100	1/1	0.96	0.06	-	64,64,64,64	0
33	NA	0	8358	1/1	0.92	0.35	-	74,74,74,74	0
33	NA	0	8363	1/1	0.88	0.32	-	52,52,52,52	0
31	MG	J	8069	1/1	0.94	0.13	-	46,46,46,46	0
31	MG	0	8083	1/1	0.98	0.07	-	30,30,30,30	0
31	MG	0	8082	1/1	0.94	0.17	-	56,56,56,56	0
31	MG	0	8029	1/1	0.98	0.09	-	35,35,35,35	0
31	MG	0	8047	1/1	0.87	0.10	-	54,54,54,54	0
31	MG	0	8009	1/1	0.97	0.14	-	24,24,24,24	0
33	NA	0	8342	1/1	0.96	0.22	-	33,33,33,33	0
31	MG	0	8030	1/1	0.99	0.07	-	22,22,22,22	0
31	MG	0	8099	1/1	0.93	0.24	-	44,44,44,44	0
31	MG	0	8114	1/1	0.97	0.09	-	35,35,35,35	0
31	MG	0	8049	1/1	0.84	0.12	-	56,56,56,56	0
31	MG	0	8101	1/1	0.88	0.30	-	48,48,48,48	0
33	NA	0	8352	1/1	0.98	0.12	-	40,40,40,40	0
33	NA	0	8316	1/1	0.97	0.22	-	35,35,35,35	0
31	MG	0	8042	1/1	0.97	0.10	-	29,29,29,29	0
33	NA	0	8384	1/1	0.82	0.14	-	52,52,52,52	0
31	MG	0	8113	1/1	0.86	0.13	-	36,36,36,36	0
31	MG	0	8061	1/1	0.97	0.13	-	32,32,32,32	0
33	NA	0	8367	1/1	0.97	0.26	-	45,45,45,45	0
31	MG	0	8041	1/1	0.97	0.10	-	33,33,33,33	0
35	CD	N	8405	1/1	0.98	0.08	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	H	8322	1/1	0.86	0.26	-	52,52,52,52	0
31	MG	0	8092	1/1	0.98	0.10	-	66,66,66,66	0
34	CL	0	8511	1/1	0.98	0.10	-	37,37,37,37	0
31	MG	0	8111	1/1	0.99	0.12	-	32,32,32,32	0
34	CL	0	8514	1/1	0.98	0.20	-	36,36,36,36	0
33	NA	0	8301	1/1	0.97	0.09	-	33,33,33,33	0
31	MG	0	8068	1/1	0.94	0.04	-	44,44,44,44	0
31	MG	0	8115	1/1	0.95	0.07	-	36,36,36,36	0
33	NA	0	8319	1/1	0.96	0.13	-	29,29,29,29	0
31	MG	0	8117	1/1	0.92	0.17	-	36,36,36,36	0
31	MG	9	8095	1/1	0.80	0.15	-	69,69,69,69	0
31	MG	0	8104	1/1	0.94	0.13	-	45,45,45,45	0
33	NA	0	8328	1/1	0.99	0.12	-	28,28,28,28	0
33	NA	0	8336	1/1	0.96	0.06	-	37,37,37,37	0
33	NA	0	8308	1/1	0.89	0.18	-	42,42,42,42	0
33	NA	0	8369	1/1	0.92	0.22	-	40,40,40,40	0
31	MG	0	8070	1/1	0.84	0.15	-	40,40,40,40	0
31	MG	0	8051	1/1	0.94	0.09	-	56,56,56,56	0
31	MG	0	8034	1/1	0.89	0.09	-	31,31,31,31	0
33	NA	0	8341	1/1	0.94	0.11	-	37,37,37,37	0
33	NA	0	8329	1/1	0.80	0.14	-	48,48,48,48	0
31	MG	0	8037	1/1	0.97	0.07	-	35,35,35,35	0
31	MG	0	8005	1/1	0.99	0.12	-	24,24,24,24	0
33	NA	0	8379	1/1	0.97	0.45	-	48,48,48,48	0
31	MG	0	8085	1/1	0.93	0.07	-	35,35,35,35	0
31	MG	0	8081	1/1	0.96	0.11	-	39,39,39,39	0
33	NA	0	8315	1/1	0.95	0.17	-	30,30,30,30	0
33	NA	0	8375	1/1	0.99	0.21	-	39,39,39,39	0
31	MG	0	8025	1/1	0.98	0.10	-	36,36,36,36	0
33	NA	0	8357	1/1	0.94	0.08	-	39,39,39,39	0
33	NA	0	8311	1/1	0.89	0.15	-	48,48,48,48	0
31	MG	0	8050	1/1	0.76	0.12	-	56,56,56,56	0
33	NA	0	8377	1/1	0.94	0.23	-	50,50,50,50	0
31	MG	0	8026	1/1	0.97	0.15	-	26,26,26,26	0
33	NA	0	8385	1/1	0.92	0.40	-	48,48,48,48	0
31	MG	0	8079	1/1	0.95	0.16	-	19,19,19,19	0
33	NA	0	8318	1/1	0.92	0.25	-	49,49,49,49	0
31	MG	0	8103	1/1	0.78	0.23	-	54,54,54,54	0
31	MG	0	8098	1/1	0.95	0.07	-	27,27,27,27	0
31	MG	0	8011	1/1	0.98	0.10	-	23,23,23,23	0
33	NA	0	8359	1/1	0.96	0.26	-	39,39,39,39	0
33	NA	R	8312	1/1	0.93	0.09	-	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	CL	M	8507	1/1	0.99	0.08	-	45,45,45,45	0
31	MG	0	8094	1/1	0.92	0.09	-	59,59,59,59	0
31	MG	0	8089	1/1	0.91	0.06	-	51,51,51,51	0
31	MG	0	8097	1/1	0.96	0.07	-	30,30,30,30	0
33	NA	0	8354	1/1	0.98	0.16	-	25,25,25,25	0
31	MG	0	8072	1/1	0.81	0.09	-	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.