



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:32 PM UTC

PDB ID : 3CXC / pdb_00003cxc
Title : The structure of an enhanced oxazolidinone inhibitor bound to the 50S ribosomal subunit of *H. marismortui*
Authors : Ippolito, J.A.; Wang, D.; Kanyo, Z.F.; Duffy, E.M.
Deposited on : 2008-04-24
Resolution : 3.00 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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

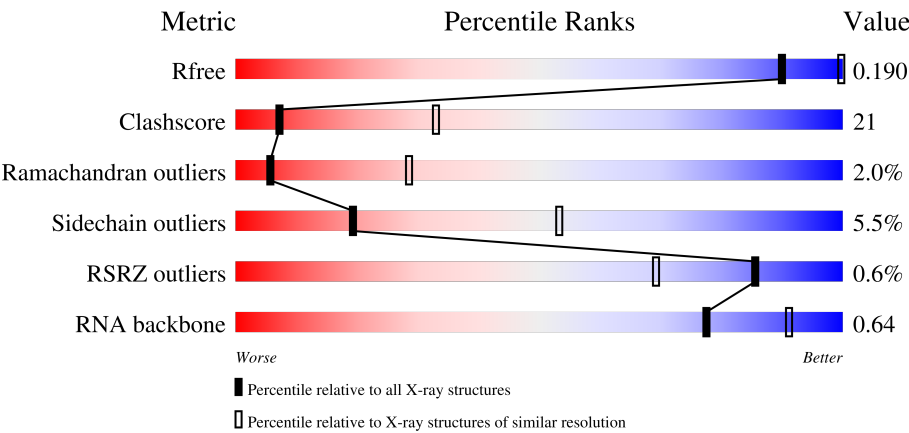
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)
RNA backbone	3983	1109 (3.20-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	2922	47% 41% 6% 6%
2	9	122	4% 38% 49% 11% .
3	4	3	33% 33% 33%
4	A	239	50% 40% 8% ..

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Mol	Chain	Length	Quality of chain
5	B	337	
6	C	246	
7	D	176	
8	E	177	
9	F	119	
10	G	348	
11	H	167	
12	I	145	
13	J	132	
14	K	164	
15	L	194	
16	M	186	
17	N	115	
18	O	148	
19	P	95	
20	Q	154	
21	R	84	
22	S	119	
23	T	66	
24	U	70	
25	V	154	
26	W	91	
27	X	240	
28	Y	73	
29	Z	56	

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Mol	Chain	Length	Quality of chain
30	1	48	
31	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
34	K	0	8201	-	-	-	X
37	CD	2	8404	-	-	X	-

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 98635 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 RIBOSOMAL RNA.

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 RIBOSOMAL RNA.

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 RNA chain called 5'-R(*CP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	3	Total	C	N	O	P	0	0	0
			59	28	11	18	2			

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L2.

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

- Molecule 5 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	310	ARG	PRO	conflict	UNP P20279

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L5.

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

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L6.

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

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	F	119	Total	C	N	O	S	0	0	0
			886	552	141	192	1			

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L10.

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

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	H	156	Total	C	N	O	S	0	0	0
			1216	766	233	213	4			

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	I	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	J	132	Total	C	N	O	S	0	0	0
			994	609	189	192	4			

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	K	145	Total	C	N	O	S	0	0	0
			1118	670	222	226				

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	L	194	Total	C	N	O	S	0	0	0
			1606	988	346	267	5			

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	M	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L18E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	N	115	Total	C	N	O	S	0	0	0
			865	529	161	175				

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L19E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	O	143	Total	C	N	O	S	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 19 is a protein called RIBOSOMAL PROTEIN L21E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	P	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L22.

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

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L23.

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

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
22	S	119	Total	C	N	O	0	0	0
			950	568	180	202			

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L24E.

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

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L29.

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

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	V	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L31E.

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

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L32E.

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

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L37AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Y	73	Total	C	N	O	S	0	0	0
			564	359	111	87	7			

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	Z	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	1	46	Total	C	N	O	S	0	0	0
			394	238	86	69	1			

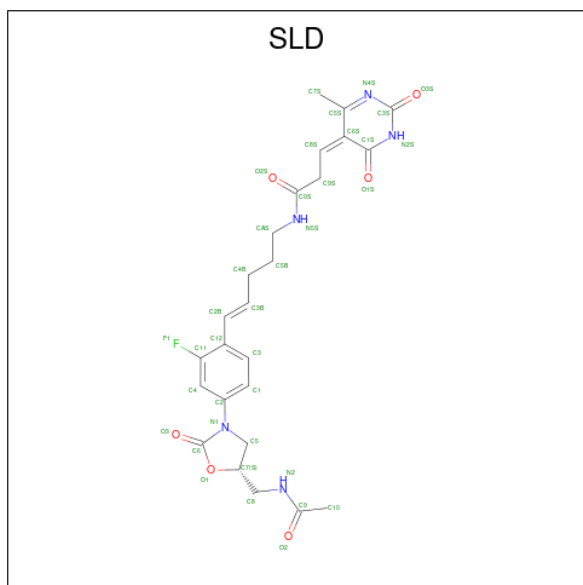
There is a discrepancy between the modelled and reference sequences:

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

- Molecule 31 is a protein called RIBOSOMAL PROTEIN L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	2	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is (3Z)-N-[(4E)-5-(4-{(5S)-5-[(acetylamino)methyl]-2-oxo-1,3-oxazolidin-3-yl}-2-fluorophenyl)pent-4-en-1-yl]-3-(4-methyl-2,6-dioxo-1,6-dihydropyrimidin-5(2H)-ylidene)propanamide (CCD ID: SLD) (formula: C₂₅H₂₈FN₅O₆).



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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	X	1	Total	Mg	0	0
			1	1		
33	2	1	Total	Mg	0	0
			1	1		

- Molecule 34 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	2	Total	K	0	0
			2	2		

- Molecule 35 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	73	Total	Na	0	0
			73	73		
35	9	2	Total	Na	0	0
			2	2		
35	A	1	Total	Na	0	0
			1	1		
35	C	1	Total	Na	0	0
			1	1		
35	H	2	Total	Na	0	0
			2	2		
35	I	1	Total	Na	0	0
			1	1		
35	K	1	Total	Na	0	0
			1	1		
35	L	1	Total	Na	0	0
			1	1		
35	P	1	Total	Na	0	0
			1	1		
35	Q	2	Total	Na	0	0
			2	2		
35	R	1	Total	Na	0	0
			1	1		

- Molecule 36 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	8	Total	Cl	0	0
			8	8		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	A	1	Total 1	Cl 1	0	0
36	B	1	Total 1	Cl 1	0	0
36	I	3	Total 3	Cl 3	0	0
36	J	1	Total 1	Cl 1	0	0
36	K	1	Total 1	Cl 1	0	0
36	L	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0
36	N	1	Total 1	Cl 1	0	0
36	P	1	Total 1	Cl 1	0	0
36	Q	1	Total 1	Cl 1	0	0
36	X	1	Total 1	Cl 1	0	0
36	2	1	Total 1	Cl 1	0	0

- Molecule 37 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	N	1	Total 1	Cd 1	0	0
37	T	1	Total 1	Cd 1	0	0
37	Y	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0
37	2	1	Total 1	Cd 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	0	5806	Total 5806	O 5806	0	0
38	9	147	Total 147	O 147	0	0
38	4	1	Total 1	O 1	0	0
38	A	136	Total 136	O 136	0	0
38	B	160	Total 160	O 160	0	0
38	C	180	Total 180	O 180	0	0
38	D	49	Total 49	O 49	0	0
38	E	47	Total 47	O 47	0	0
38	F	26	Total 26	O 26	0	0
38	G	21	Total 21	O 21	0	0
38	H	82	Total 82	O 82	0	0
38	I	61	Total 61	O 61	0	0
38	J	63	Total 63	O 63	0	0
38	K	85	Total 85	O 85	0	0
38	L	130	Total 130	O 130	0	0
38	M	69	Total 69	O 69	0	0
38	N	45	Total 45	O 45	0	0
38	O	70	Total 70	O 70	0	0
38	P	56	Total 56	O 56	0	0
38	Q	92	Total 92	O 92	0	0
38	R	40	Total 40	O 40	0	0
38	S	37	Total 37	O 37	0	0

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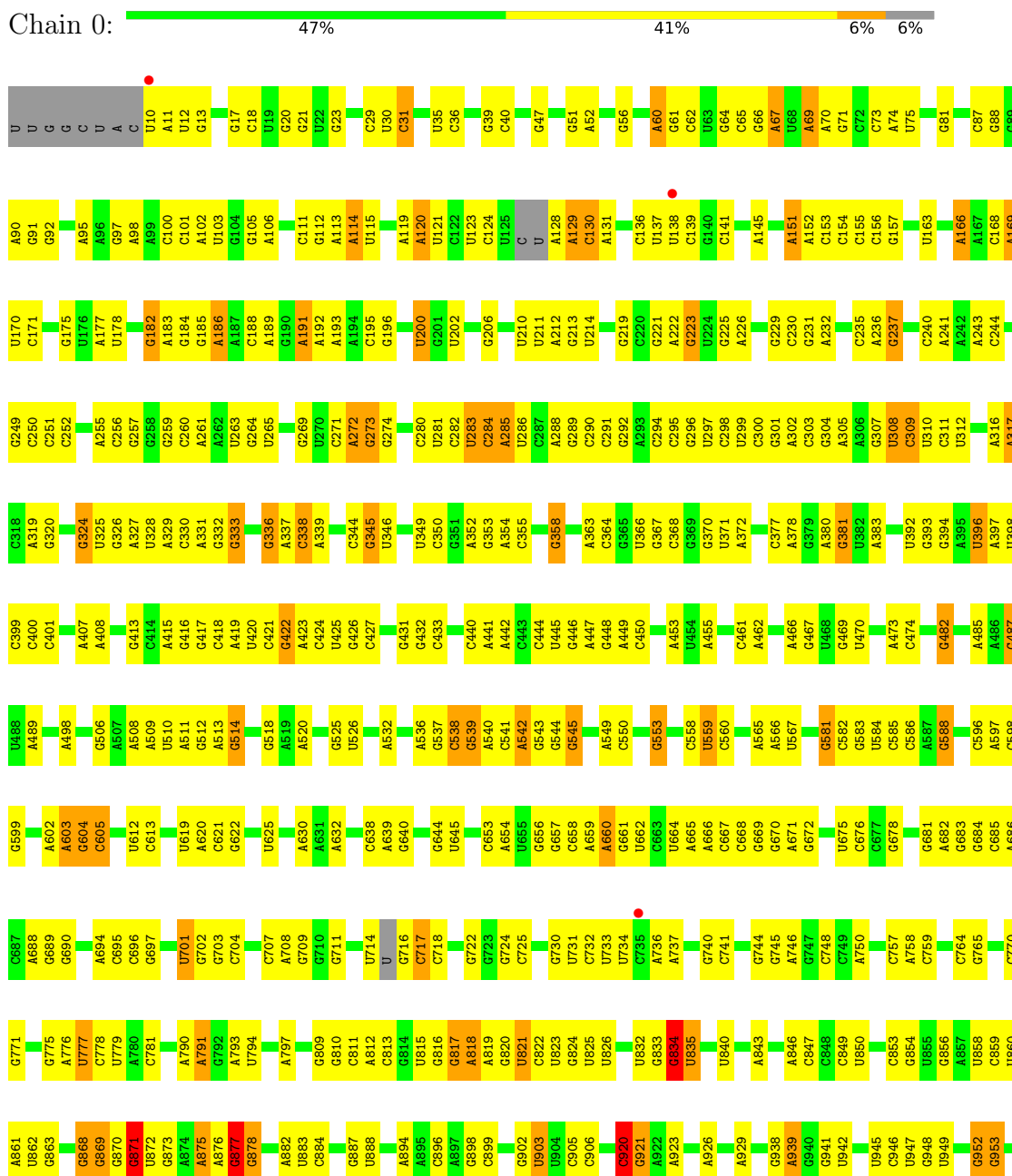
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	T	27	Total 27	O 27	0	0
38	U	13	Total 13	O 13	0	0
38	V	74	Total 74	O 74	0	0
38	W	29	Total 29	O 29	0	0
38	X	105	Total 105	O 105	0	0
38	Y	41	Total 41	O 41	0	0
38	Z	57	Total 57	O 57	0	0
38	1	45	Total 45	O 45	0	0
38	2	76	Total 76	O 76	0	0

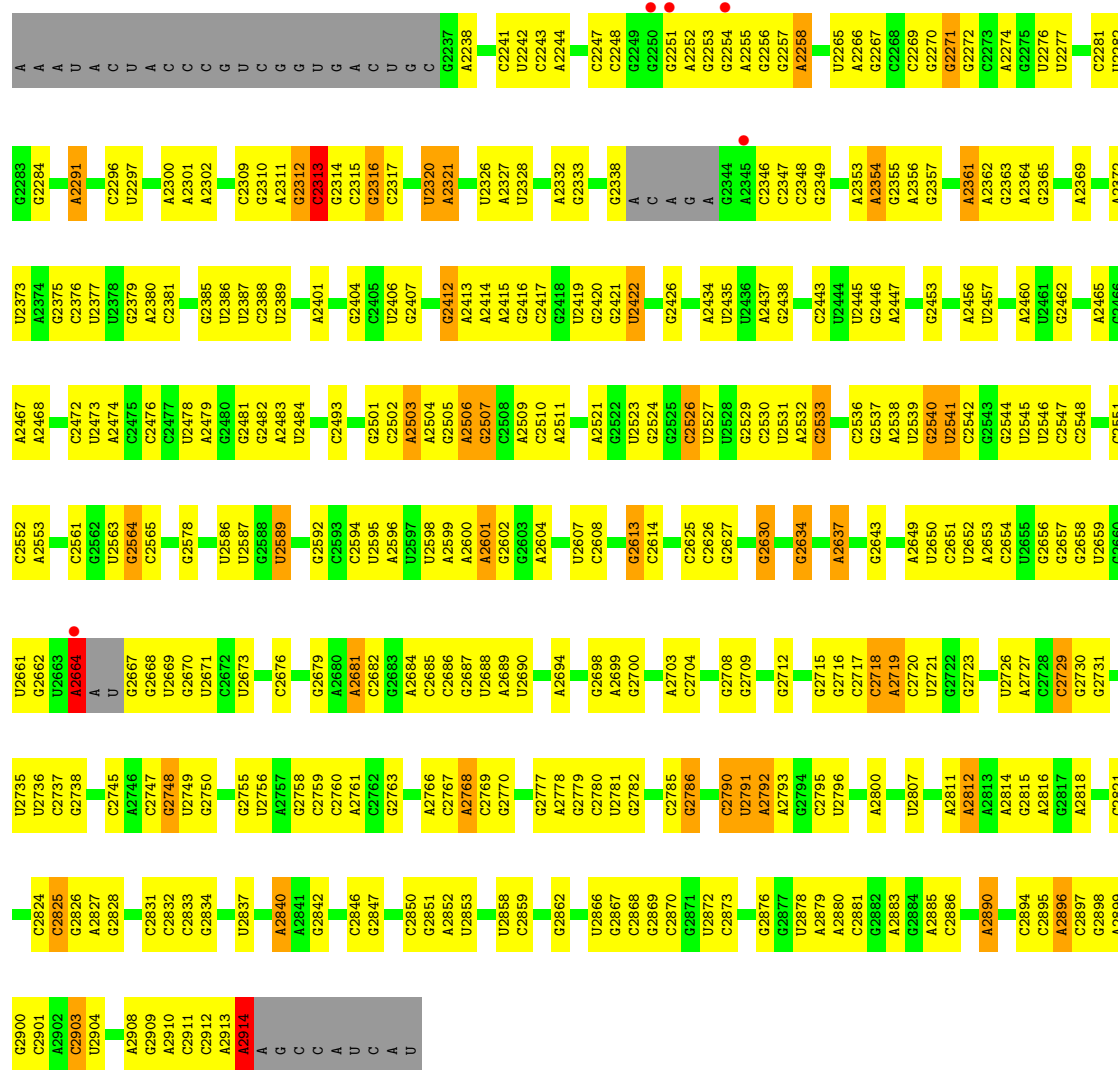
3 Residue-property plots

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

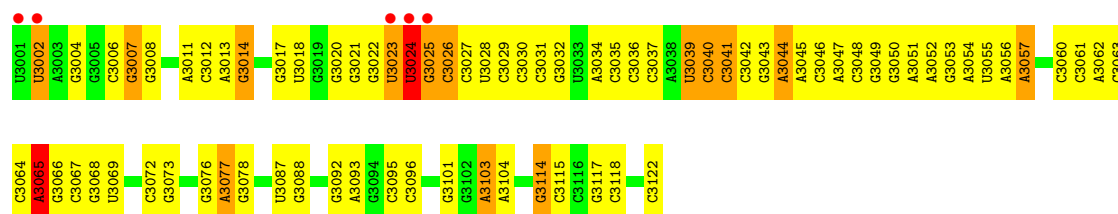
• Molecule 1: 23S RIBOSOMAL RNA



C	G2072	C1988	A1909	G1819	A1746	U1654	A1572	G1497	U1418	G1312	U1219	G1151	U1028	G958
A	G2073	C1989	A1910	G1820	A1747	G1655	A1573	G1498	U1419	A1313	G1223	A1154	U1029	C959
G	A2074	C1990	A1911	A1821	U1748	A1656	C1574	U1499	C1421	U1314	G1224	A1155	U1030	A960
C	G2075	C1991	A1912	A1822	G1751	A1657	C1575	U1500	C1422	G1320	G1225	C1156	G1031	A961
A	A2083	G1992	U1917	G1823	G1752	A1658	A1580	A1501	U1423	A1321	G1226	G1157	G1044	C962
A	A2084	G1993	U1918	G1824	G1753	C1686	C1584	A1502	C1424	G1322	G1227	G1158	G1045	C963
G	A2085	G1994	U1919	U1825	A1755	A1687	C1585	U1503	A1425	G1323	C1229	G1159	G1046	G964
G	A2086	G1995	U1920	C1826	G1756	A1688	C1586	A1504	G1426	U1324	G1230	G1160	G1052	G965
G	A2087	G1996	U1921	G1827	U1757	A1689	C1587	U1505	A1427	G1325	U1234	G1161	G1053	G966
A	G2091	G2000	A1922	G1828	U1758	C1670	U1587	U1506	G1428	A1326	G1235	G1162	G1054	G967
A	G2092	G2001	A1923	A1829	U1759	A1678	C1588	G1511	G1429	A1327	G1236	G1163	G1055	G968
G	G2093	G2002	U1924	C1830	G1760	C1679	G1589	U1512	G1430	A1328	G1237	G1164	G1056	U970
G	G2094	G2003	U1925	G1831	U1761	C1675	G1590	C1513	U1431	A1329	G1238	G1165	G1057	G
A	A2095	U2004	A1926	C1832	C1762	G1676	C1591	C1514	U1432	A1330	G1239	G1166	G1058	G
G	A2096	G2005	U1927	U1835	C1763	A1677	G1592	A1515	G1433	A1331	G1240	G1167	G1059	U
A	A2101	G2006	U1928	A1840	C1764	C1678	U1593	C1516	G1434	C1332	G1241	G1168	C1060	C
C	G2102	U2008	A1930	A1841	U1766	A1682	U1594	U1517	C1435	A1333	G1242	U1170	U1064	C
A	A2103	A2009	U1931	A1842	U1767	G1683	G1600	U1518	U1440	C1334	G1243	U1171	U1065	C
C	G2104	G2010	U1932	U1843	C1768	G1684	G1601	U1519	G1441	A1335	G1244	G1172	G1066	C
C	G2105	U2012	G1933	U1844	C1769	G1685	G1602	U1520	G1442	A1336	G1245	G1173	C1069	C
A	C2106	A2013	U1934	G1845	U1770	A1686	A1603	A1521	G1443	A1337	G1246	A1174	A1070	C
A	U2107	G2014	C1935	G1846	U1771	C1687	G1604	A1522	G1444	A1338	G1247	G1175	G1071	C
C	A2015	A2016	U1936	G1847	U1772	C1688	G1605	U1523	G1445	A1339	G1248	G1176	G1072	C
A	G2110	G2017	U1937	G1848	G1773	C1689	G1606	U1524	G1446	A1340	G1249	U1180	A1073	A
C	G2111	G2018	U1938	G1849	G1774	C1690	G1607	U1525	G1447	A1341	G1250	U1181	A1074	G
G	A2112	G2019	U1939	U1851	U1775	C1691	G1608	U1526	G1448	A1342	G1251	U1182	A1075	G
G	G2113	U2020	A1940	A1852	U1776	G1692	G1609	A1527	C1450	A1343	G1252	U1183	A1076	A
U	C2114	G2021	U1941	C1853	U1777	G1693	G1610	A1528	C1451	A1344	G1253	U1184	A1077	A
A	G2115	A2022	U1942	G1854	U1778	U1694	G1611	A1529	G1452	A1345	G1254	U1185	A1078	G
C	U2116	A2023	C1943	G1855	U1779	A1695	A1612	G1529	U1453	A1346	G1255	U1186	A1079	A
C	U2117	G2024	U1944	A1856	U1780	C1696	A1613	U1530	U1454	U1347	G1256	U1187	A1080	A
C	G2118	G2025	U1945	A1857	G1781	U1702	G1614	G1531	G1455	U1348	G1257	U1188	A1081	G
C	C2119	G2026	U1946	C1858	G1782	U1703	A1615	G1532	G1456	U1349	G1258	U1189	A1082	G
G	U2120	U2027	U1947	C1859	U1783	U1704	A1616	C1533	U1457	U1350	G1259	U1190	A1083	U
G	G2121	C2035	G1951	G1860	U1784	A1711	C1617	U1534	U1458	U1351	G1260	U1191	U1109	C
C	C2122	G2036	U1952	G1861	U1785	G1712	G1618	U1535	G1459	U1352	G1261	U1192	G1110	G
C	G2123	U2037	U1953	C1862	C1786	G1713	G1619	G1536	U1460	A1372	G1262	U1193	A1114	A
C	U2124	A2038	A	C1863	U1787	U1714	G1620	G1537	C1461	U1373	G1263	U1194	U1115	C
U	G2125	C2039	A	U1864	U1788	C1715	U1621	G1538	U1462	U1374	G1264	U1195	U1116	A
C	A	G2040	C	C1865	G1789	G1716	U1622	U1539	U1463	U1375	G1265	U1196	U1117	G
A	G2126	G2041	U	C1866	U1790	U1717	U1623	G1540	U1464	U1376	G1266	U1197	U1118	G
G	U2127	U2042	A	G1877	U1791	A1718	U1624	U1541	A1470	U1377	G1267	U1198	U1119	G
G	A2135	G2043	U	U1878	C1792	U1719	G1625	C1542	C1471	U1378	G1268	U1199	U1120	G
C	G2136	G2044	G	U1879	C1793	U1720	G1626	U1543	C1472	U1379	G1269	U1200	G1121	C
C	A	G2050	A	C1882	C1794	U1721	U1627	U1544	A1473	U1380	G1270	U1201	G1122	A
C	C	G2051	C	U1883	G1795	U1722	G1628	U1545	C1474	U1381	G1271	U1202	G1123	C
C	A	G2052	C	G1884	U1796	U1723	U1629	G1546	U1475	U1382	G1272	U1203	C999	A
C	U2053	A2054	U	U1885	A1801	C1725	U1630	U1547	U1476	U1383	G1273	U1204	U1000	G
C	G2054	G2055	C	C1886	U1802	U1726	U1631	U1548	C1477	U1384	G1274	U1205	U1001	G
C	A	A2056	A	U1887	G1803	U1727	U1632	U1549	U1478	U1385	G1275	U1206	U1002	G
C	U2057	G2056	U	G1888	U1804	U1728	U1633	U1550	U1479	U1386	G1276	U1207	U1003	G
A	A2058	G2057	C	U1889	A1805	U1729	U1634	U1551	C1480	U1387	G1277	U1208	A1006	A
G	C2059	U2059	G	G1890	G1806	U1730	U1635	U1552	U1481	U1388	G1278	U1209	A1007	C
G	A2060	G2060	U	U1891	U1807	U1731	U1636	U1553	U1482	U1389	G1279	U1210	U1008	G
C	U2061	U2062	U	U1892	U1808	U1732	U1637	U1554	U1483	U1390	G1280	U1211	U1009	G
C	C2062	G2063	C	U1893	U1809	U1733	U1638	U1555	U1484	U1391	G1281	U1212	A1014	G
A	U2064	U2065	A	U1894	U1810	U1734	U1639	U1556	U1485	U1392	G1282	U1213	U1015	G
A	G2065	G2066	G	U1895	C1810	U1735	U1640	U1557	U1486	U1393	G1283	U1214	U1016	G
C	A	U2067	C	G1896	U1811	U1736	U1641	U1558	U1487	U1394	G1284	U1215	G1019	G
C	U2068	G2068	U	U1897	U1812	U1737	U1642	U1559	U1488	U1395	G1285	U1216	G1020	G
A	A2069	U2069	A	U1898	U1813	U1738	U1643	U1560	U1489	U1396	G1286	U1217	G1021	G
G	G2070	G2070	G	U1899	U1814	U1739	U1644	U1561	U1490	U1397	G1287	U1218	U1022	G
U	U2071	C2071	G	U1900	U1815	U1740	U1645	U1562	U1491	U1398	G1288	G1219	A1150	G
G	A	A	A	U1901	U1816	U1741	U1646	U1563	U1492	U1399	G1289	U1220	G1138	G
G	C	C	C	U1902	U1817	U1742	U1647	U1564	U1493	U1400	G1290	U1221	G1139	G
G	C	C	C	U1903	U1818	U1743	U1648	U1565	U1494	U1401	G1291	U1222	C1140	G
G	C	C	C	U1904	U1819	U1744	U1649	U1566	U1495	U1402	G1292	U1223	G1141	G
G	C	C	C	U1905	U1820	U1745	U1650	U1567	U1496	U1403	G1293	U1224	G1142	G
G	C	C	C	U1906	U1821	U1746	U1651	U1568	U1497	U1404	G1294	U1225	G1143	G
G	C	C	C	U1907	U1822	U1747	U1652	U1569	U1498	U1405	G1295	U1226	G1144	G
G	C	C	C	U1908	U1823	U1748	U1653	U1570	U1499	U1406	G1296	U1227	G1145	G
G	C	C	C	U1909	U1824	U1749	U1654	U1571	U1500	U1407	G1297	U1228	G1146	G
G	C	C	C	U1910	U1825	U1750	U1655	U1572	U1501	U1408	G1298	U1229	G1147	G
G	C	C	C	U1911	U1826	U1751	U1656	U1573	U1502	U1409	G1299	U1230	G1148	G
G	C	C	C	U1912	U1827	U1752	U1657	U1574	U1503	U1410	G1300	U1231	G1149	G
G	C	C	C	U1913	U1828	U1753	U1658	U1575	U1504	U1411	G1301	U1232	G1150	G
G	C	C	C	U1914	U1829	U1754	U1659	U1576	U1505	U1412	G1302	U1233	G1151	G
G	C	C	C	U1915	U1830	U1755	U1660	U1577	U1506	U1413	G1303	U1234	G1152	G
G	C	C	C	U1916	U1831	U1756	U1661	U1578	U1507	U1414	G1304	U1235	G1153	G
G	C	C	C	U1917	U1832	U1757	U1662	U1579	U1508	U1415	G1305	U1236	G1154	G
G	C	C	C	U1918	U1833	U1758	U1663	U1580	U1509	U1416	G1306	U1237	G1155	G
G	C	C	C	U1919	U1834	U1759	U1664	U1581	U1510	U1417	G1307	U1238	G1156	G
G	C	C	C	U1920	U1835	U1760	U1665	U1582	U1511	U1418	G1308	U1239	G1157	G
G	C	C	C	U1921	U1836	U1761	U1666	U1583	U1512	U1419	G1309	U1240	G1158	G
G	C	C	C	U1922	U1837	U1762	U1667	U1584	U1513	U1420	G1310	U1241	G1159	G
G	C	C	C	U1923	U1838	U1763	U1668	U1585	U1514	U1421	G1311	U1242	G1160	G
G	C	C	C	U1924	U1839	U1764	U1669	U1586	U1515	U1422	G1312	U1243	G1161	G
G	C	C	C	U1925	U1840	U1765	U1670	U1587	U1516	U1423	G1313	U1244	G1162	G
G	C	C	C	U1926	U1841	U1766	U1671	U1588	U1517	U1424	G1314	U1245	G1163	G
G	C	C	C	U1927	U1842	U1767	U1672	U1589	U1518	U1425	G1315	U1246	G1164	G
G	C	C	C	U1928	U1843	U1768	U1673	U1590	U1519	U1426	G1316	U1247	G1165	G
G	C	C												



• Molecule 2: 5S RIBOSOMAL RNA

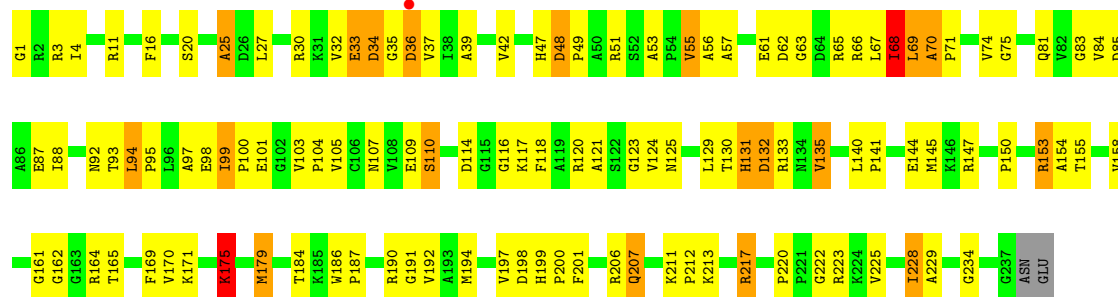


• Molecule 3: 5'-R(*CP*CP*A)-3'



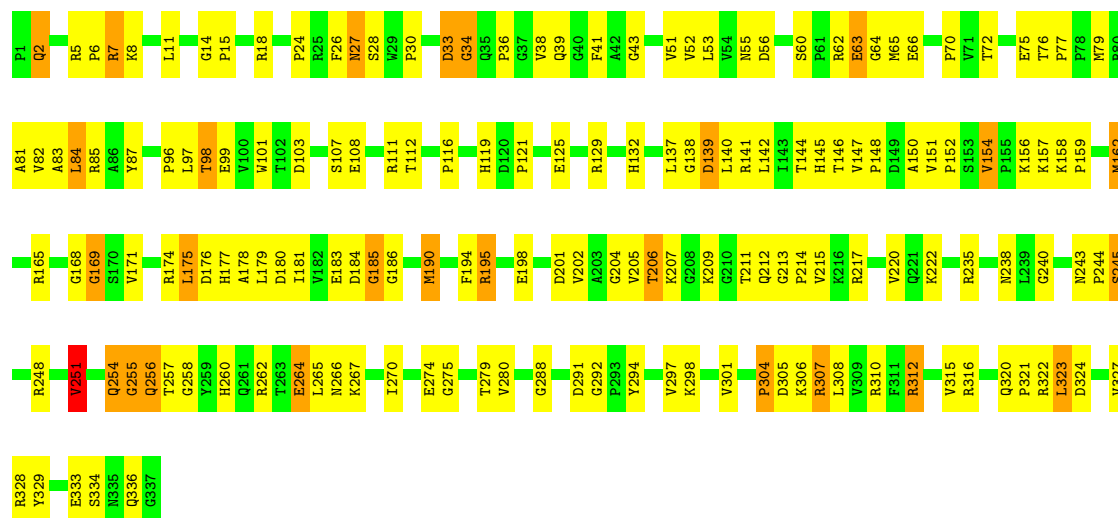
• Molecule 4: RIBOSOMAL PROTEIN L2

Chain A: 



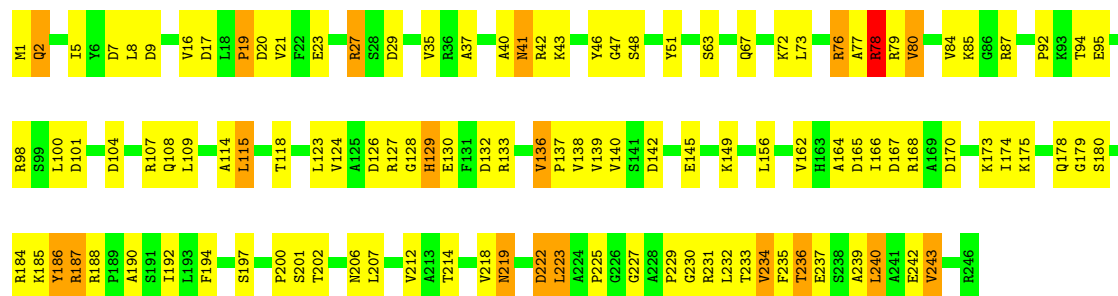
• Molecule 5: RIBOSOMAL PROTEIN L3

Chain B: 

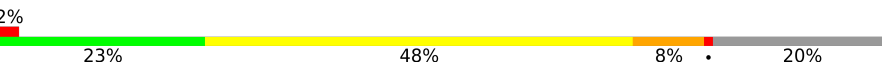


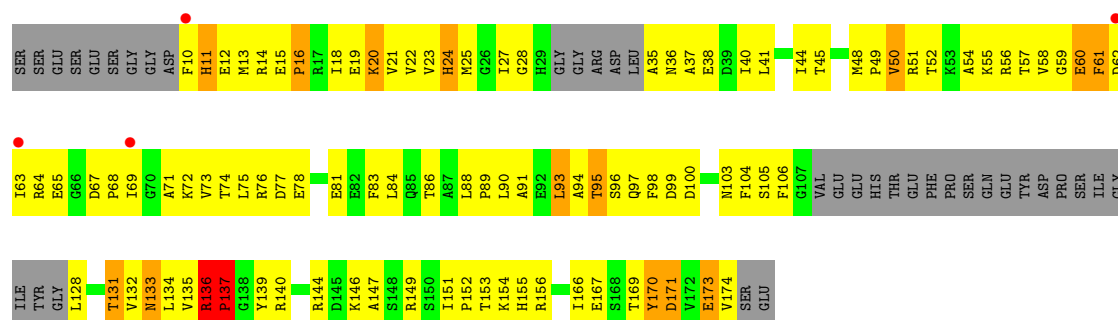
• Molecule 6: RIBOSOMAL PROTEIN L4

Chain C: 

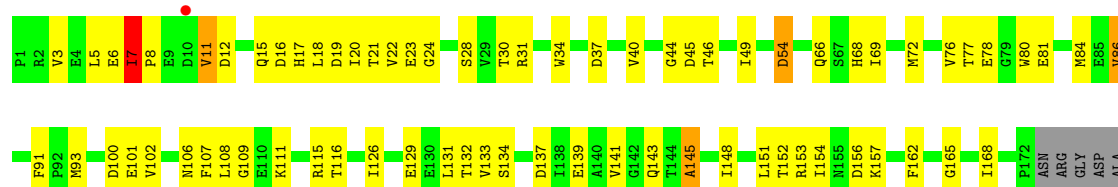


• Molecule 7: RIBOSOMAL PROTEIN L5

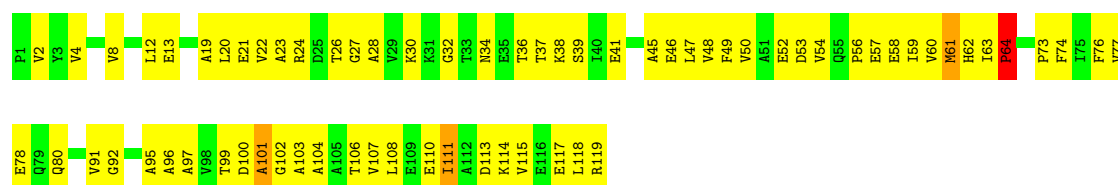
Chain D: 



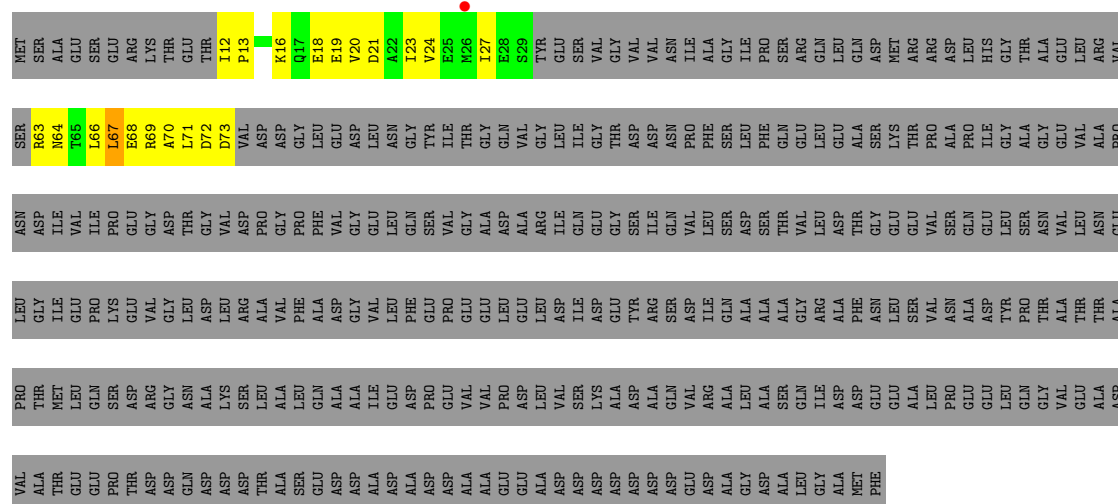
• Molecule 8: RIBOSOMAL PROTEIN L6



• Molecule 9: RIBOSOMAL PROTEIN L7AE

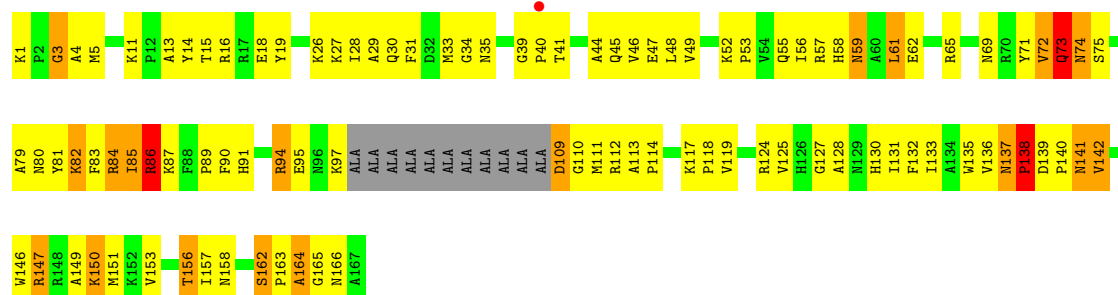


• Molecule 10: RIBOSOMAL PROTEIN L10



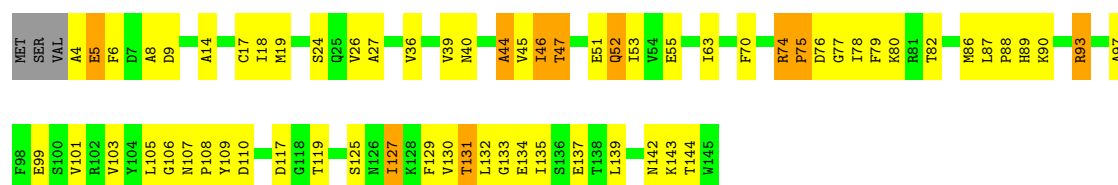
- Molecule 11: RIBOSOMAL PROTEIN L10E

Chain H: 



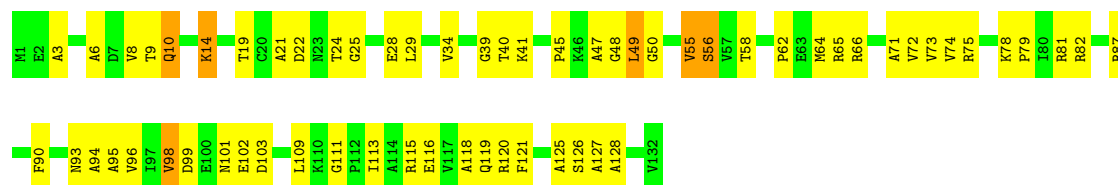
- Molecule 12: RIBOSOMAL PROTEIN L13

Chain I: 



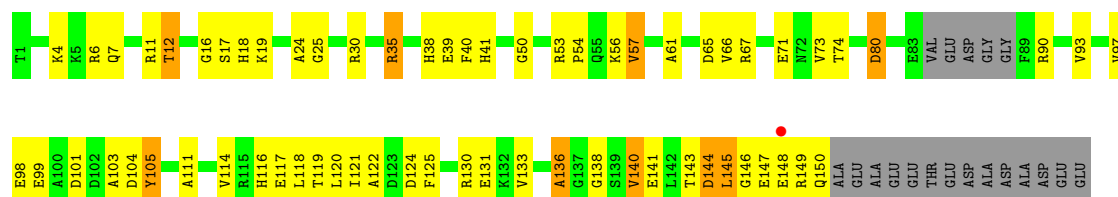
- Molecule 13: RIBOSOMAL PROTEIN L14

Chain J: 



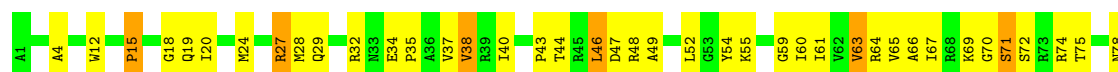
- Molecule 14: RIBOSOMAL PROTEIN L15

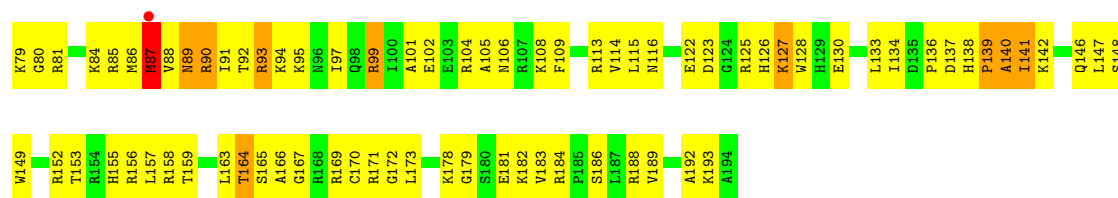
Chain K: 



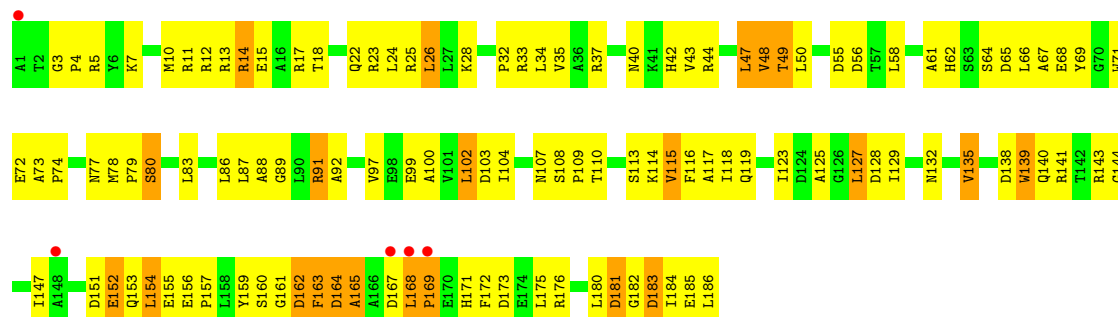
- Molecule 15: RIBOSOMAL PROTEIN L15E

Chain L: 

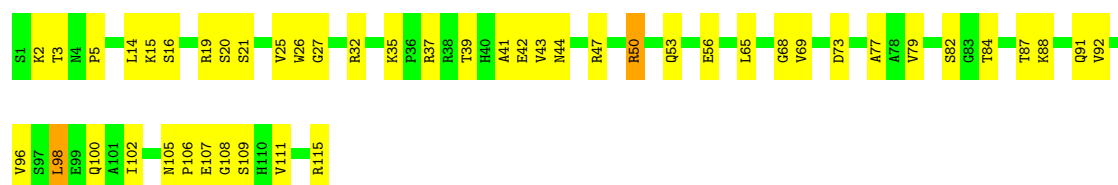




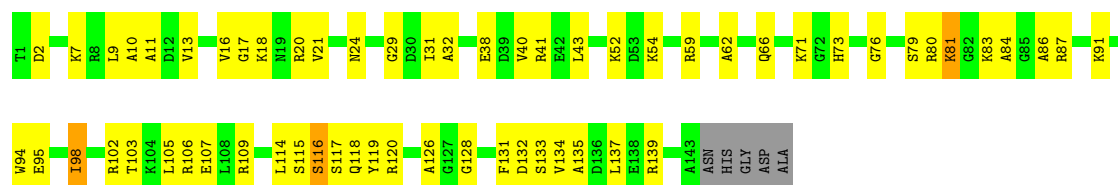
• Molecule 16: RIBOSOMAL PROTEIN L18



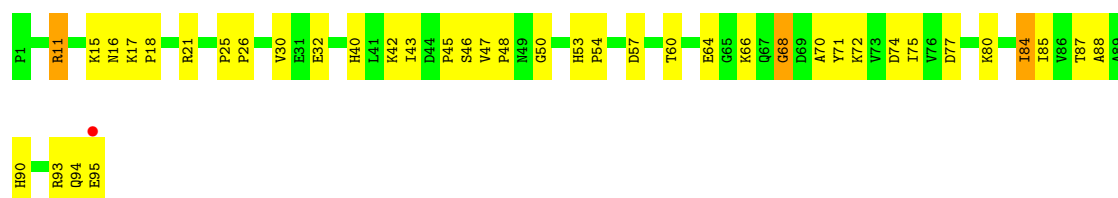
• Molecule 17: RIBOSOMAL PROTEIN L18E



• Molecule 18: RIBOSOMAL PROTEIN L19E

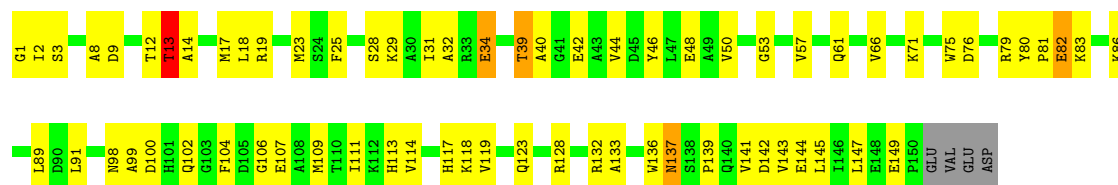


• Molecule 19: RIBOSOMAL PROTEIN L21E



- Molecule 20: RIBOSOMAL PROTEIN L22

Chain Q:  53% 41%



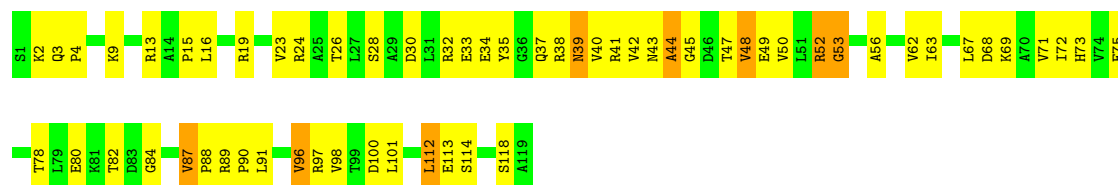
- Molecule 21: RIBOSOMAL PROTEIN L23

Chain R:  60% 35%

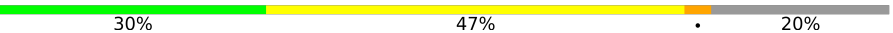


- Molecule 22: RIBOSOMAL PROTEIN L24

Chain S:  50% 44% 7%



- Molecule 23: RIBOSOMAL PROTEIN L24E

Chain T:  30% 47% 20%



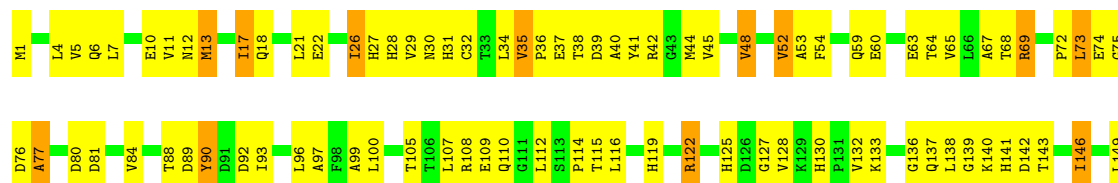
- Molecule 24: RIBOSOMAL PROTEIN L29

Chain U:  3% 39% 49% 6% 7%



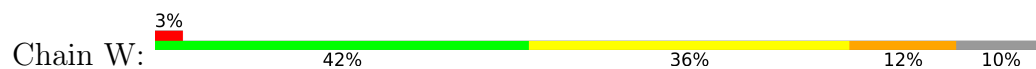
- Molecule 25: RIBOSOMAL PROTEIN L30

Chain V:  40% 52% 8%



L150
E151
A152
M153
R154

• Molecule 26: RIBOSOMAL PROTEIN L31E



SER
ALA
SER
ASP
PHE
GLU
E7
R8
V9
L14
R15
R18
A19
E20
P21
N22
H23
K24
R25
A26
D27
M30
I31
E35
H36
L37
F41
S42
V43
D44
A47
V48
R49
L50
D51
P52
N55
A58
A64
N65
T66
P67
I70
R71
G72
V73
R74
A75
R76
F77

E78
E79
A83
I84
V85
E86
A87
E88
THR
ALA
GLU

• Molecule 27: RIBOSOMAL PROTEIN L32E



ALA
ASP
ASN
GLU
ASP
VAL
GLU
ALA
GLU
GLU
TYR
THR
LEU
THR
ASP
ILE
SER
GLY
VAL
GLY
PRO
SER
LYS
ALA
GLU
SER
LEU
ARG
GLU
ALA
PHE
GLU
SER
VAL
ASP
VAL
ARG
GLY
ALA
ASP
GLN
SER
LEU
ALA
ASP
VAL
SER
GLY
ILE
GLY
ASN
ALA
LEU
ALA

ALA
ARG
ILE
LYS
ALA
ASP
VAL
GLY
GLY
LEU
GLU
VAL
GLU
SER
THR
THR
GLU
ALA
GLU
VAL
GLY
GLU
GLY
GLY
GLY
GLU
GLU
ALA
PRO
ASP
GLU
ASP
VAL
T95
A99
R100
T103
E104
K105
T106
P107
D108
E112
R115
L116
L117
P126
Q127
F128
N129
R130
Q131
D132

T141
S142
W143
R144
R147
G148
Q149
S150
S151
R154
K158
T163
R169
T172
A173
V174
H178
P179
F182
E183
E184
V185
R186
V187
H188
M189
D192
D197
G198
D199
T200
E201
A202
V203
R204
I205
A206
S207
R212
E219
E220
V228
Y233
V234
E235
V236

GLU
VAL
SER
GLU

• Molecule 28: RIBOSOMAL PROTEIN L37AE



R10
T11
G12
R13
F14
G19
L20
K21
I22
R23
V26
A27
D28
V29
E30
I31
K32
H33
K34
H37
K38
C39
P40
V41
C42
G43
F44
K45
K46
L47
K48
R49
A50
G53
I54
W55
M56
C57
G58
H59
Y62
K63
A64
G67
C68
Y69
T73
V74
K77
M80
K81

A82

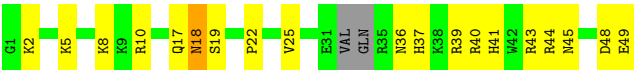
• Molecule 29: RIBOSOMAL PROTEIN L37E



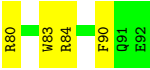
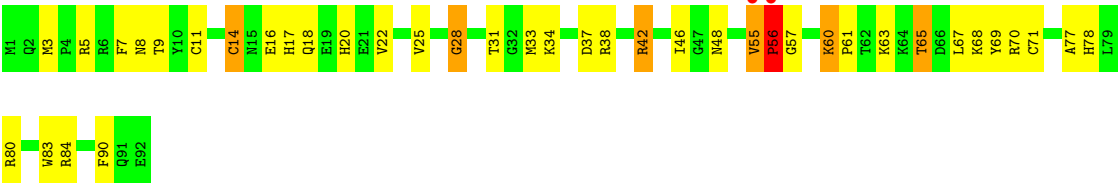
T1
T5
P6
S7
Q8
G9
K10
K11
T14
T15
H16
R20
R21
K25
H28
I29
K30
K31
K32
S36
F39
A43
Q51
S52
K53
E56

• Molecule 30: RIBOSOMAL PROTEIN L39E





• Molecule 31: 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	213.66Å 300.71Å 575.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	91.4 (20.00-3.00) 90.9 (20.00-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.98Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.186 , 0.229 0.186 , 0.190	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	66.9	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 61.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	98635	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.82% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, K, CD, SLD, 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	0.43	0/66076	0.64	26/103052 (0.0%)
2	9	0.40	0/2905	0.69	4/4528 (0.1%)
3	4	0.65	0/65	1.05	1/99 (1.0%)
4	A	0.49	0/1787	1.09	13/2409 (0.5%)
5	B	0.51	0/2690	1.07	16/3652 (0.4%)
6	C	0.55	0/1884	1.07	7/2551 (0.3%)
7	D	0.43	0/1111	0.94	4/1498 (0.3%)
8	E	0.48	0/1382	0.93	3/1880 (0.2%)
9	F	0.45	0/897	0.94	2/1219 (0.2%)
10	G	0.52	0/241	0.86	1/324 (0.3%)
11	H	0.56	0/1247	1.28	14/1686 (0.8%)
12	I	0.53	0/1136	1.00	5/1530 (0.3%)
13	J	0.52	0/1004	1.07	6/1351 (0.4%)
14	K	0.45	0/1130	1.07	7/1509 (0.5%)
15	L	0.56	0/1634	1.07	10/2180 (0.5%)
16	M	0.48	1/1474 (0.1%)	1.12	12/1999 (0.6%)
17	N	0.50	0/874	1.02	8/1181 (0.7%)
18	O	0.51	0/1143	0.96	2/1521 (0.1%)
19	P	0.53	0/749	1.17	5/1005 (0.5%)
20	Q	0.59	0/1172	1.03	6/1578 (0.4%)
21	R	0.44	0/648	0.91	2/875 (0.2%)
22	S	0.47	0/958	0.99	4/1289 (0.3%)
23	T	0.56	0/417	1.08	4/562 (0.7%)
24	U	0.45	0/502	1.04	3/675 (0.4%)
25	V	0.60	1/1219 (0.1%)	1.01	4/1655 (0.2%)
26	W	0.55	0/664	1.06	4/895 (0.4%)
27	X	0.54	0/1146	1.01	3/1536 (0.2%)
28	Y	0.59	0/576	1.10	2/763 (0.3%)
29	Z	0.55	0/438	1.06	3/578 (0.5%)
30	1	0.48	0/399	0.82	0/527
31	2	0.65	1/771 (0.1%)	1.07	4/1024 (0.4%)
All	All	0.46	3/98339 (0.0%)	0.77	185/147131 (0.1%)

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	0	70
2	9	0	2
25	V	0	1
All	All	0	73

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	V	13	MET	SD-CE	-6.45	1.63	1.79
31	2	14	CYS	CB-SG	-6.16	1.60	1.81
16	M	115	VAL	CA-CB	5.63	1.60	1.54

All (185) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	H	74	ASN	N-CA-C	-15.10	92.50	114.39
11	H	141	ASN	N-CA-C	-14.65	95.47	113.50
2	9	3024	U	C2'-C3'-O3'	12.44	128.16	109.50
1	0	1979	G	C2'-C3'-O3'	10.16	124.75	109.50
1	0	1563	G	C2'-C3'-O3'	9.96	124.45	109.50
16	M	135	VAL	N-CA-C	-9.28	104.10	113.10
19	P	47	VAL	CA-C-N	9.17	128.50	118.97
19	P	47	VAL	C-N-CA	9.17	128.50	118.97
5	B	157	LYS	N-CA-C	-8.89	103.02	114.04
11	H	156	THR	N-CA-C	-8.67	97.65	110.48
4	A	222	GLY	N-CA-C	-8.41	104.58	113.58
2	9	3024	U	C4'-C3'-O3'	8.24	121.76	109.40
8	E	11	VAL	N-CA-C	8.20	120.94	109.29
6	C	80	VAL	CA-C-N	7.91	128.34	119.32
6	C	80	VAL	C-N-CA	7.91	128.34	119.32
5	B	323	LEU	N-CA-C	7.88	120.49	110.24
5	B	265	LEU	N-CA-C	7.63	121.78	110.48
14	K	7	GLN	N-CA-C	7.51	120.35	111.71
11	H	137	ASN	N-CA-C	-7.46	100.69	110.39
5	B	154	VAL	CA-C-N	7.29	126.83	119.24
5	B	154	VAL	C-N-CA	7.29	126.83	119.24
16	M	153	GLN	N-CA-C	-7.08	103.58	113.20
6	C	78	ARG	N-CA-C	7.04	118.89	108.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	175	LEU	N-CA-C	-7.03	103.55	111.07
7	D	136	ARG	CA-C-N	7.03	128.62	119.84
7	D	136	ARG	C-N-CA	7.03	128.62	119.84
20	Q	137	ASN	N-CA-C	7.01	120.45	110.14
14	K	57	VAL	N-CA-C	-6.98	106.50	113.20
11	H	147	ARG	N-CA-C	-6.98	103.68	111.71
6	C	219	ASN	N-CA-C	6.95	119.05	109.18
23	T	34	SER	N-CA-C	-6.93	103.81	111.36
5	B	222	LYS	N-CA-C	-6.93	100.27	110.52
1	0	834	G	C2'-C3'-O3'	-6.89	103.37	113.70
4	A	213	LYS	N-CA-C	6.86	120.91	112.54
14	K	145	LEU	N-CA-C	-6.83	103.84	111.28
27	X	143	TRP	N-CA-C	6.82	120.19	109.96
5	B	213	GLY	CA-C-N	6.72	126.68	119.28
5	B	213	GLY	C-N-CA	6.72	126.68	119.28
13	J	8	VAL	N-CA-C	6.64	118.05	108.48
24	U	42	ASN	CA-C-N	6.59	128.08	119.84
24	U	42	ASN	C-N-CA	6.59	128.08	119.84
15	L	127	LYS	N-CA-C	-6.57	97.55	108.32
7	D	100	ASP	N-CA-C	-6.51	105.34	113.28
11	H	86	ARG	N-CA-C	6.49	120.80	113.01
12	I	9	ASP	N-CA-C	-6.49	104.29	111.82
16	M	48	VAL	N-CA-C	6.48	118.37	108.71
1	0	1559	A	C2'-C3'-O3'	6.48	123.42	113.70
17	N	82	SER	N-CA-C	-6.45	102.01	110.53
20	Q	13	THR	N-CA-C	6.44	119.76	108.75
20	Q	3	SER	N-CA-C	-6.42	99.66	109.41
19	P	68	GLY	N-CA-C	-6.41	97.98	113.18
15	L	141	ILE	N-CA-C	-6.39	104.80	111.58
25	V	75	GLY	N-CA-C	6.38	120.06	112.33
9	F	111	ILE	N-CA-C	-6.38	104.29	110.42
1	0	1120	U	C5'-C4'-C3'	-6.34	106.48	116.00
15	L	87	MET	N-CA-C	6.33	119.17	110.24
5	B	206	THR	N-CA-C	6.33	118.50	110.33
21	R	57	THR	N-CA-C	6.33	119.43	110.50
20	Q	34	GLU	N-CA-C	6.31	117.82	111.07
17	N	79	VAL	N-CA-C	-6.30	104.19	110.62
13	J	14	LYS	N-CA-C	-6.26	100.77	110.10
1	0	2338	G	C2'-C3'-O3'	6.24	123.06	113.70
29	Z	43	ALA	N-CA-C	-6.24	104.56	111.36
5	B	151	VAL	CA-C-N	6.23	125.45	118.97
5	B	151	VAL	C-N-CA	6.23	125.45	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1942	A	C5'-C4'-C3'	6.20	125.30	116.00
4	A	110	SER	N-CA-C	-6.17	104.48	111.14
4	A	228	ILE	N-CA-C	6.17	116.98	108.84
1	0	2664	A	N9-C1'-C2'	6.15	121.22	112.00
7	D	170	TYR	N-CA-C	6.14	120.34	111.56
16	M	13	ARG	N-CA-C	-6.13	105.46	113.12
13	J	111	GLY	CA-C-N	6.12	126.09	120.21
13	J	111	GLY	C-N-CA	6.12	126.09	120.21
14	K	136	ALA	N-CA-C	-6.09	105.16	112.59
23	T	50	GLU	N-CA-C	6.09	118.70	111.33
16	M	165	ALA	N-CA-C	-6.08	105.77	113.43
12	I	75	PRO	N-CA-C	-6.07	106.56	114.03
31	2	28	GLY	N-CA-C	-6.06	104.46	112.82
2	9	3039	U	N1-C1'-C2'	6.01	121.02	112.00
31	2	60	LYS	N-CA-C	-6.00	102.02	110.29
2	9	3039	U	C4'-C3'-O3'	-5.97	104.04	113.00
17	N	69	VAL	N-CA-C	5.97	117.07	108.48
1	0	1819	G	C5'-C4'-C3'	5.95	124.92	116.00
31	2	22	VAL	N-CA-C	5.94	117.14	108.58
12	I	88	PRO	N-CA-C	-5.94	104.46	112.48
1	0	714	U	C2'-C3'-O3'	-5.94	100.59	109.50
29	Z	51	GLN	N-CA-C	-5.92	106.10	113.15
1	0	2914	A	C2'-C3'-O3'	5.90	122.55	113.70
1	0	1592	G	N9-C1'-C2'	5.88	120.82	112.00
1	0	2011	A	C5'-C4'-C3'	5.85	123.98	115.20
4	A	207	GLN	N-CA-C	5.84	118.18	109.25
16	M	14	ARG	N-CA-C	-5.84	104.83	111.07
16	M	102	LEU	N-CA-C	5.82	117.69	108.67
19	P	17	LYS	N-CA-C	-5.77	101.02	109.50
25	V	69	ARG	N-CA-C	5.76	120.14	112.30
26	W	79	GLU	N-CA-C	5.75	119.91	113.01
16	M	169	PRO	N-CA-C	-5.75	106.96	114.03
1	0	206	G	C5'-C4'-C3'	-5.75	107.38	116.00
11	H	110	GLY	N-CA-C	-5.72	99.61	113.18
8	E	7	ILE	N-CA-C	5.72	113.55	108.63
11	H	3	GLY	N-CA-C	-5.71	106.68	113.99
28	Y	39	CYS	CA-C-N	5.71	125.07	118.85
28	Y	39	CYS	C-N-CA	5.71	125.07	118.85
16	M	91	ARG	N-CA-C	-5.70	104.43	111.33
20	Q	141	VAL	N-CA-C	5.68	117.52	108.89
4	A	48	ASP	CA-C-N	5.66	125.33	119.05
4	A	48	ASP	C-N-CA	5.66	125.33	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	K	144	ASP	N-CA-C	-5.65	105.12	111.28
16	M	168	LEU	N-CA-C	5.64	120.93	108.64
27	X	202	ALA	N-CA-C	-5.63	101.86	110.14
24	U	64	GLY	N-CA-C	-5.62	105.86	115.08
17	N	43	VAL	N-CA-C	5.61	115.97	108.11
21	R	27	ALA	N-CA-C	-5.60	100.05	108.96
15	L	70	GLY	N-CA-C	5.60	119.11	112.33
6	C	186	TYR	N-CA-C	5.60	118.37	110.14
13	J	25	GLY	N-CA-C	-5.58	106.97	115.00
16	M	3	GLY	CA-C-N	5.56	125.17	119.56
16	M	3	GLY	C-N-CA	5.56	125.17	119.56
17	N	2	LYS	N-CA-C	-5.56	102.66	110.50
17	N	50	ARG	N-CA-C	5.56	118.27	111.82
1	0	871	G	C5'-C4'-O4'	-5.55	101.48	109.80
14	K	12	THR	N-CA-C	5.53	119.87	113.18
22	S	52	ARG	N-CA-C	5.52	122.56	110.80
4	A	99	ILE	N-CA-C	5.49	113.92	107.77
11	H	1	LYS	CA-C-N	5.48	125.39	119.85
11	H	1	LYS	C-N-CA	5.48	125.39	119.85
4	A	70	ALA	N-CA-C	5.46	116.53	109.65
6	C	41	ASN	N-CA-C	5.46	119.42	112.87
23	T	18	GLY	N-CA-C	5.46	119.56	112.68
1	0	920	C	C2'-C3'-O3'	-5.45	105.53	113.70
27	X	173	ALA	N-CA-C	5.44	119.41	112.34
5	B	255	GLY	N-CA-C	5.41	117.49	110.45
1	0	2291	A	N9-C1'-C2'	5.41	120.12	112.00
1	0	2313	C	C5'-C4'-C3'	5.41	124.11	116.00
9	F	62	HIS	N-CA-C	5.39	118.07	111.82
5	B	251	VAL	CA-C-N	5.39	126.23	119.98
5	B	251	VAL	C-N-CA	5.39	126.23	119.98
11	H	73	GLN	N-CA-C	-5.38	103.87	110.65
15	L	4	ALA	N-CA-C	-5.38	105.58	111.82
1	0	877	G	C2'-C3'-O3'	-5.37	105.65	113.70
1	0	1942	A	C5'-C4'-O4'	-5.36	101.76	109.80
6	C	129	HIS	N-CA-C	5.35	117.99	110.23
25	V	17	ILE	N-CA-C	-5.35	105.63	110.82
26	W	22	ASN	N-CA-C	5.35	120.19	111.37
25	V	143	THR	N-CA-C	-5.33	105.64	111.82
3	4	76	A	C2'-C3'-O3'	-5.31	101.53	109.50
13	J	71	ALA	N-CA-C	5.31	116.07	108.74
4	A	135	VAL	N-CA-C	5.29	116.94	108.89
1	0	2316	G	C5'-C4'-C3'	-5.27	107.29	115.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	T	16	GLY	N-CA-C	-5.27	105.80	114.76
19	P	84	ILE	N-CA-C	5.23	115.50	108.17
1	0	1615	A	C5'-C4'-C3'	5.22	123.84	116.00
12	I	110	ASP	N-CA-C	-5.22	105.74	112.68
18	O	24	ASN	CA-C-N	5.21	125.52	119.47
18	O	24	ASN	C-N-CA	5.21	125.52	119.47
29	Z	9	GLY	N-CA-C	5.21	120.46	114.16
4	A	175	LYS	N-CA-C	-5.20	105.50	111.07
31	2	55	VAL	N-CA-C	5.18	113.78	107.61
15	L	89	ASN	N-CA-C	5.17	117.31	111.11
11	H	84	ARG	N-CA-C	5.16	116.83	108.26
14	K	80	ASP	N-CA-C	5.16	121.79	110.80
15	L	139	PRO	N-CA-C	-5.15	101.86	112.47
15	L	27	ARG	N-CA-C	5.15	117.31	111.02
12	I	44	ALA	N-CA-C	-5.15	104.08	110.41
15	L	90	ARG	N-CA-C	5.14	119.41	113.18
1	0	2291	A	C4'-C3'-O3'	-5.11	105.34	113.00
20	Q	71	LYS	N-CA-C	5.11	117.58	111.71
22	S	87	VAL	CA-C-N	5.10	124.86	119.76
22	S	87	VAL	C-N-CA	5.10	124.86	119.76
1	0	1723	G	C4'-C3'-O3'	-5.10	105.36	113.00
1	0	1504	A	N9-C1'-C2'	5.07	119.61	112.00
4	A	68	ILE	N-CA-C	5.07	115.95	108.45
26	W	51	ASP	CA-C-N	5.06	126.17	119.84
26	W	51	ASP	C-N-CA	5.06	126.17	119.84
22	S	34	GLU	N-CA-C	5.05	116.79	111.28
5	B	266	ASN	N-CA-C	5.05	117.33	111.02
17	N	27	GLY	N-CA-C	-5.04	106.61	113.37
11	H	52	LYS	CA-C-N	-5.04	114.61	119.90
11	H	52	LYS	C-N-CA	-5.04	114.61	119.90
10	G	67	LEU	N-CA-C	-5.03	105.71	111.14
17	N	41	ALA	N-CA-C	5.03	118.41	109.96
1	0	1419	U	N1-C1'-C2'	5.02	119.53	112.00
8	E	145	ALA	N-CA-C	-5.02	105.46	111.03
4	A	25	ALA	N-CA-C	5.02	116.87	108.99
15	L	63	VAL	N-CA-C	5.00	114.95	108.35

There are no chirality outliers.

All (73) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1055	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1226	G	Sidechain
1	0	1236	A	Sidechain
1	0	1309	U	Sidechain
1	0	1342	C	Sidechain
1	0	1417	G	Sidechain
1	0	1430	G	Sidechain
1	0	1595	G	Sidechain
1	0	1635	U	Sidechain
1	0	1744	G	Sidechain
1	0	1809	G	Sidechain
1	0	1819	G	Sidechain
1	0	182	G	Sidechain
1	0	1822	A	Sidechain
1	0	1829	A	Sidechain
1	0	1835	U	Sidechain
1	0	1845	A	Sidechain
1	0	1848	G	Sidechain
1	0	1861	C	Sidechain
1	0	1863	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1933	G	Sidechain
1	0	1978	A	Sidechain
1	0	202	U	Sidechain
1	0	2023	G	Sidechain
1	0	223	G	Sidechain
1	0	2312	G	Sidechain
1	0	2313	C	Sidechain
1	0	2316	G	Sidechain
1	0	2412	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	2564	G	Sidechain
1	0	2607	U	Sidechain
1	0	261	A	Sidechain
1	0	2630	G	Sidechain
1	0	2637	A	Sidechain
1	0	2643	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	2673	U	Sidechain
1	0	2727	A	Sidechain
1	0	2729	C	Sidechain
1	0	2790	C	Sidechain
1	0	2793	A	Sidechain
1	0	2840	A	Sidechain
1	0	2853	U	Sidechain
1	0	324	G	Sidechain
1	0	333	G	Sidechain
1	0	396	U	Sidechain
1	0	422	G	Sidechain
1	0	469	G	Sidechain
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	532	A	Sidechain
1	0	619	U	Sidechain
1	0	664	U	Sidechain
1	0	722	G	Sidechain
1	0	781	C	Sidechain
1	0	791	A	Sidechain
1	0	815	U	Sidechain
1	0	817	G	Sidechain
1	0	818	A	Sidechain
1	0	868	G	Sidechain
1	0	903	U	Sidechain
1	0	939	A	Sidechain
1	0	952	G	Sidechain
2	9	3065	A	Sidechain
2	9	3087	U	Sidechain
25	V	90	TYR	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	29800	1230	0
2	9	2600	0	1326	88	0
3	4	59	0	35	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1754	0	1763	135	0
5	B	2625	0	2533	174	0
6	C	1859	0	1816	116	0
7	D	1094	0	1085	132	0
8	E	1357	0	1266	74	0
9	F	886	0	854	71	0
10	G	240	0	231	24	0
11	H	1216	0	1215	160	0
12	I	1120	0	1098	69	0
13	J	994	0	1027	62	0
14	K	1118	0	1076	67	0
15	L	1606	0	1676	148	0
16	M	1445	0	1401	143	0
17	N	865	0	873	37	0
18	O	1133	0	1127	60	0
19	P	735	0	729	30	0
20	Q	1149	0	1122	67	0
21	R	641	0	605	25	0
22	S	950	0	923	54	0
23	T	410	0	364	35	0
24	U	499	0	511	38	0
25	V	1196	0	1137	101	0
26	W	654	0	653	49	0
27	X	1130	0	1133	55	0
28	Y	564	0	598	58	0
29	Z	431	0	426	24	0
30	1	394	0	406	31	0
31	2	755	0	729	54	0
32	0	37	0	28	4	0
33	0	107	0	0	0	0
33	2	1	0	0	0	0
33	4	1	0	0	0	0
33	9	2	0	0	0	0
33	A	2	0	0	0	0
33	B	1	0	0	0	0
33	J	1	0	0	0	0
33	S	1	0	0	0	0
33	X	1	0	0	0	0
34	0	2	0	0	0	0
35	0	73	0	0	0	0
35	9	2	0	0	0	0
35	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	C	1	0	0	0	0
35	H	2	0	0	0	0
35	I	1	0	0	0	0
35	K	1	0	0	0	0
35	L	1	0	0	0	0
35	P	1	0	0	0	0
35	Q	2	0	0	0	0
35	R	1	0	0	0	0
36	0	8	0	0	1	0
36	2	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	I	3	0	0	1	0
36	J	1	0	0	0	0
36	K	1	0	0	0	0
36	L	1	0	0	1	0
36	M	1	0	0	1	0
36	N	1	0	0	0	0
36	P	1	0	0	0	0
36	Q	1	0	0	0	0
36	X	1	0	0	0	0
37	2	1	0	0	2	0
37	N	1	0	0	0	0
37	T	1	0	0	0	0
37	Y	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5806	0	0	71	0
38	1	45	0	0	1	0
38	2	76	0	0	4	0
38	4	1	0	0	0	0
38	9	147	0	0	5	0
38	A	136	0	0	12	0
38	B	160	0	0	16	0
38	C	180	0	0	11	0
38	D	49	0	0	8	0
38	E	47	0	0	1	0
38	F	26	0	0	6	0
38	G	21	0	0	2	0
38	H	82	0	0	9	0
38	I	61	0	0	3	0
38	J	63	0	0	4	0
38	K	85	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	L	130	0	0	4	0
38	M	69	0	0	8	0
38	N	45	0	0	5	0
38	O	70	0	0	0	0
38	P	56	0	0	1	0
38	Q	92	0	0	4	0
38	R	40	0	0	1	0
38	S	37	0	0	3	0
38	T	27	0	0	2	0
38	U	13	0	0	1	0
38	V	74	0	0	6	0
38	W	29	0	0	3	0
38	X	105	0	0	4	0
38	Y	41	0	0	5	0
38	Z	57	0	0	1	0
All	All	98635	0	59566	3095	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 21.

All (3095) 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)
24:U:12:THR:HG22	24:U:15:GLU:HG3	1.24	1.14
13:J:10:GLN:NE2	13:J:10:GLN:H	1.47	1.13
20:Q:99:ALA:HB1	20:Q:109:MET:HE1	1.29	1.12
7:D:25:MET:HE2	7:D:41:LEU:HG	1.31	1.10
1:O:871:G:H5'	1:O:871:G:H8	1.13	1.10
11:H:86:ARG:NH1	11:H:133:ILE:HG13	1.66	1.08
15:L:87:MET:HB3	31:2:46:ILE:HD13	1.31	1.07
6:C:236:THR:HG22	6:C:239:ALA:H	1.17	1.07
15:L:164:THR:HG22	15:L:167:GLY:H	1.20	1.06
1:O:1160:G:H5'	1:O:1161:A:H5'	1.33	1.06
1:O:871:G:H5'	1:O:871:G:C8	1.90	1.06
5:B:162:MET:HE1	5:B:308:LEU:HD21	1.35	1.06
13:J:10:GLN:HE21	13:J:10:GLN:N	1.54	1.05
22:S:71:VAL:HG11	22:S:90:PRO:HB3	1.37	1.05
12:I:19:MET:HE3	12:I:132:LEU:HD11	1.37	1.03
25:V:149:LEU:HG	25:V:153:MET:HE2	1.37	1.03
6:C:127:ARG:NH2	6:C:225:PRO:HG2	1.74	1.03
1:O:156:C:H5''	15:L:171:ARG:HD3	1.36	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3023:U:H3'	2:9:3024:U:H5''	1.39	1.03
11:H:86:ARG:HH11	11:H:133:ILE:HG13	0.87	1.02
2:9:3056:A:H2'	2:9:3057:A:H5''	1.40	1.02
1:0:1119:G:H2'	12:I:52:GLN:HE22	1.25	1.02
15:L:106:ASN:ND2	36:L:8518:CL:CL	2.30	1.02
6:C:5:ILE:HD11	6:C:16:VAL:HG23	1.43	1.01
4:A:194:MET:HE3	4:A:199:HIS:HB2	1.39	1.00
11:H:45:GLN:HB3	11:H:163:PRO:HD2	1.42	0.99
1:0:1751:G:H2'	1:0:1752:G:H5''	1.44	0.99
2:9:3076:G:H3'	2:9:3077:A:H5''	1.44	0.99
5:B:238:ASN:HD22	5:B:240:GLY:H	1.08	0.98
13:J:62:PRO:HG3	13:J:65:ARG:HH21	1.29	0.96
1:0:1134:G:H4'	11:H:151:MET:HE1	1.44	0.96
11:H:162:SER:HB2	11:H:163:PRO:HD3	1.46	0.95
7:D:105:SER:HB2	7:D:131:THR:HG23	1.49	0.95
6:C:115:LEU:HD13	6:C:223:LEU:HD21	1.49	0.95
11:H:86:ARG:HH11	11:H:133:ILE:CG1	1.80	0.94
1:0:1164:U:H4'	1:0:1165:G:OP1	1.68	0.94
1:0:289:G:H22	1:0:363:A:H2	1.14	0.93
16:M:47:LEU:HD11	16:M:127:LEU:HD21	1.49	0.93
7:D:134:LEU:HD11	7:D:166:ILE:HD11	1.50	0.93
11:H:29:ALA:HB3	11:H:65:ARG:HH12	1.31	0.92
1:0:545:G:H5'	1:0:545:G:H8	1.34	0.92
1:0:870:G:H2'	1:0:871:G:H5''	1.51	0.92
1:0:1242:A:H5'	12:I:82:THR:HG23	1.51	0.92
2:9:3006:C:H5''	16:M:37:ARG:NH1	1.85	0.92
11:H:26:LYS:HD2	11:H:28:ILE:HD12	1.50	0.91
28:Y:46:LYS:HD3	28:Y:59:HIS:HB2	1.52	0.91
26:W:37:LEU:HD13	26:W:85:VAL:HG21	1.50	0.90
1:0:2812:A:H2	1:0:2814:A:H62	1.14	0.90
20:Q:106:GLY:HA2	20:Q:109:MET:HE3	1.51	0.90
31:2:71:CYS:SG	37:2:8404:CD:CD	1.79	0.90
18:O:115:SER:H	18:O:118:GLN:HE21	0.96	0.89
1:0:182:G:H4'	15:L:157:LEU:HD13	1.51	0.89
11:H:55:GLN:HE21	11:H:124:ARG:HE	1.14	0.89
28:Y:38:LYS:HG2	28:Y:45:LYS:HG2	1.54	0.89
2:9:3024:U:O2'	2:9:3025:G:H4'	1.73	0.88
1:0:1120:U:H6	1:0:1120:U:H5''	1.39	0.88
15:L:102:GLU:OE1	15:L:164:THR:HG21	1.72	0.88
27:X:187:VAL:HG23	27:X:192:ASP:HB2	1.56	0.88
26:W:15:ARG:HB3	26:W:15:ARG:HH11	1.37	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:264:GLU:HG2	5:B:267:LYS:HE2	1.57	0.87
7:D:154:LYS:H	7:D:154:LYS:HD2	1.38	0.87
7:D:27:ILE:HG22	7:D:28:GLY:H	1.37	0.87
11:H:139:ASP:N	11:H:140:PRO:HD3	1.90	0.87
1:0:1116:U:O2'	1:0:1118:A:H2	1.56	0.86
16:M:49:THR:HG22	16:M:56:ASP:HB2	1.56	0.86
25:V:5:VAL:HG11	25:V:153:MET:HE1	1.54	0.86
25:V:72:PRO:HG2	25:V:77:ALA:HB3	1.57	0.86
1:0:1835:U:H5	1:0:1840:A:N7	1.74	0.86
11:H:162:SER:HB2	11:H:163:PRO:CD	2.06	0.85
25:V:4:LEU:HD22	25:V:52:VAL:HG21	1.59	0.85
25:V:88:THR:HG23	25:V:110:GLN:NE2	1.91	0.85
31:2:71:CYS:HG	37:2:8404:CD:CD	1.07	0.85
11:H:26:LYS:HG2	11:H:28:ILE:H	1.42	0.84
1:0:2717:C:C2'	1:0:2718:C:H5''	2.07	0.84
30:1:41:HIS:H	30:1:45:ASN:HD22	1.24	0.84
1:0:506:G:H22	1:0:509:A:H5'	1.42	0.84
18:O:103:THR:HA	18:O:106:ARG:NH1	1.91	0.84
25:V:6:GLN:HB2	25:V:26:ILE:HD12	1.58	0.84
15:L:35:PRO:CG	15:L:38:VAL:HG23	2.06	0.83
1:0:56:G:H5''	24:U:50:ARG:HH12	1.43	0.83
1:0:2506:A:HO2'	1:0:2507:G:H8	0.85	0.83
8:E:6:GLU:HA	8:E:46:THR:HG22	1.58	0.83
28:Y:38:LYS:HE2	28:Y:45:LYS:HE2	1.60	0.83
12:I:131:THR:HG22	12:I:134:GLU:H	1.44	0.83
1:0:1771:U:H4'	28:Y:20:LEU:HD21	1.61	0.83
1:0:2717:C:H2'	1:0:2718:C:H5''	1.57	0.83
9:F:63:ILE:HB	9:F:64:PRO:HD3	1.57	0.83
1:0:2502:C:C2'	1:0:2503:A:H5'	2.09	0.83
5:B:212:GLN:HB2	5:B:257:THR:HG21	1.61	0.83
18:O:115:SER:N	18:O:118:GLN:HE21	1.76	0.83
25:V:122:ARG:HG2	25:V:122:ARG:HH11	1.42	0.83
25:V:88:THR:HG22	25:V:89:ASP:H	1.44	0.83
5:B:62:ARG:HA	5:B:65:MET:HE3	1.59	0.82
8:E:23:GLU:HG2	8:E:28:SER:HB3	1.62	0.82
11:H:27:LYS:H	11:H:58:HIS:HD2	1.23	0.82
15:L:106:ASN:HD22	15:L:114:VAL:HG23	1.44	0.82
26:W:76:ARG:HH11	26:W:76:ARG:HG3	1.44	0.82
7:D:37:ALA:O	7:D:40:ILE:HG12	1.80	0.82
1:0:2274:A:N3	15:L:86:MET:HE1	1.95	0.82
1:0:2502:C:H2'	1:0:2503:A:H5'	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:21:G:H5'	20:Q:2:ILE:HA	1.61	0.82
1:0:1450:C:H4'	1:0:1451:C:OP2	1.78	0.82
2:9:3023:U:H3'	2:9:3024:U:C5'	2.10	0.82
13:J:74:VAL:HG11	13:J:113:ILE:HG12	1.62	0.82
28:Y:28:ASP:O	28:Y:31:ILE:HG22	1.79	0.82
15:L:87:MET:HB2	15:L:91:ILE:HD11	1.61	0.81
5:B:27:ASN:HD22	5:B:27:ASN:H	1.25	0.81
1:0:2506:A:O2'	1:0:2507:G:H8	1.64	0.81
12:I:19:MET:HE1	12:I:78:ILE:HG22	1.63	0.81
1:0:506:G:H22	1:0:509:A:C5'	1.93	0.81
6:C:142:ASP:OD1	6:C:237:GLU:HB3	1.81	0.81
1:0:1603:A:H5'	1:0:1605:G:O4'	1.80	0.81
6:C:162:VAL:HG12	6:C:192:ILE:HD11	1.62	0.81
1:0:870:G:C2'	1:0:871:G:H5''	2.11	0.81
22:S:9:LYS:HE3	22:S:13:ARG:NH1	1.95	0.81
1:0:2533:C:H5'	1:0:2533:C:H6	1.46	0.81
13:J:39:GLY:HA2	38:J:4183:HOH:O	1.78	0.80
24:U:1:THR:HG23	24:U:2:VAL:H	1.46	0.80
25:V:137:GLN:HE21	25:V:141:HIS:HE1	1.26	0.80
12:I:74:ARG:HB3	12:I:74:ARG:HH11	1.44	0.80
28:Y:37:HIS:HB2	28:Y:47:LEU:HB2	1.63	0.80
15:L:60:ILE:C	15:L:61:ILE:HD12	2.07	0.80
1:0:450:C:OP1	6:C:184:ARG:NH2	2.15	0.80
2:9:3056:A:C2'	2:9:3057:A:H5''	2.12	0.80
23:T:20:MET:HE2	23:T:30:HIS:NE2	1.97	0.79
20:Q:39:THR:HG22	20:Q:42:GLU:H	1.47	0.79
11:H:45:GLN:HE21	11:H:135:TRP:HE1	1.31	0.79
1:0:2586:U:H3	1:0:2592:G:H22	1.30	0.79
4:A:36:ASP:OD2	4:A:85:ASP:HB2	1.83	0.79
11:H:139:ASP:H	11:H:140:PRO:HD3	1.47	0.79
26:W:30:MET:HE1	26:W:58:ALA:HB3	1.65	0.79
1:0:2526:C:O2'	1:0:2527:U:H5'	1.82	0.79
4:A:194:MET:CE	4:A:199:HIS:HB2	2.13	0.79
16:M:87:LEU:HD12	16:M:186:LEU:HD21	1.65	0.79
5:B:190:MET:HE2	5:B:194:PHE:CD1	2.18	0.79
5:B:304:PRO:HD2	5:B:307:ARG:HD2	1.64	0.79
5:B:18:ARG:HG3	5:B:256:GLN:HG3	1.64	0.79
5:B:195:ARG:HG2	5:B:323:LEU:HD22	1.63	0.79
2:9:3025:G:H3'	2:9:3026:C:C5'	2.13	0.78
31:2:70:ARG:HG2	31:2:77:ALA:HB2	1.65	0.78
1:0:1201:C:H5''	38:0:7119:HOH:O	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:20:ILE:HD11	8:E:40:VAL:HG11	1.64	0.78
1:O:2420:G:O2'	1:O:2421:G:H5'	1.82	0.78
4:A:69:LEU:HD21	4:A:120:ARG:HB3	1.65	0.78
5:B:201:ASP:HB2	5:B:312:ARG:HD2	1.64	0.78
8:E:107:PHE:CE2	8:E:108:LEU:HD13	2.19	0.78
15:L:139:PRO:O	15:L:140:ALA:HB3	1.81	0.78
1:O:2679:G:H2'	1:O:2681:A:OP2	1.82	0.78
24:U:12:THR:HG22	24:U:15:GLU:CG	2.12	0.78
1:O:1474:C:H6	1:O:1474:C:H5'	1.49	0.78
1:O:1164:U:H3	1:O:1192:A:H2	1.32	0.77
9:F:46:GLU:O	9:F:73:PRO:HD2	1.85	0.77
1:O:542:A:H5'	1:O:542:A:H8	1.48	0.77
4:A:191:GLY:HA2	4:A:194:MET:HE2	1.66	0.77
13:J:14:LYS:HB2	13:J:45:PRO:HG2	1.65	0.77
21:R:33:SER:O	21:R:37:VAL:HG23	1.84	0.77
9:F:2:VAL:HG22	9:F:57:GLU:OE1	1.85	0.77
11:H:151:MET:HA	11:H:151:MET:HE3	1.67	0.77
1:O:1119:G:H2'	12:I:52:GLN:NE2	1.98	0.77
6:C:236:THR:HG22	6:C:239:ALA:N	1.98	0.77
18:O:115:SER:OG	18:O:118:GLN:HG3	1.84	0.77
26:W:41:PHE:O	26:W:43:VAL:HG23	1.83	0.77
20:Q:8:ALA:HB1	20:Q:13:THR:HG21	1.66	0.77
26:W:72:VAL:HG22	26:W:85:VAL:HG12	1.64	0.77
20:Q:44:VAL:O	20:Q:48:GLU:HG3	1.85	0.77
2:9:3025:G:H3'	2:9:3026:C:H5'	1.64	0.77
1:O:240:C:H4'	15:L:146:GLN:NE2	2.00	0.76
1:O:1166:A:H1'	1:O:1192:A:C2	2.19	0.76
1:O:1116:U:H3	1:O:1246:A:H62	1.30	0.76
1:O:1134:G:C4'	11:H:151:MET:HE1	2.16	0.76
1:O:2094:G:H4'	5:B:245:SER:HB3	1.66	0.76
13:J:29:LEU:HB3	13:J:55:VAL:HG11	1.65	0.76
25:V:88:THR:HB	38:V:6679:HOH:O	1.83	0.76
1:O:282:C:H1'	1:O:368:C:N4	2.00	0.76
1:O:1119:G:N2	1:O:1246:A:C2	2.52	0.76
25:V:21:LEU:HD22	25:V:26:ILE:HD11	1.67	0.76
5:B:238:ASN:ND2	5:B:240:GLY:H	1.81	0.76
7:D:19:GLU:O	7:D:20:LYS:HG2	1.85	0.76
25:V:4:LEU:HD23	25:V:54:PHE:HB3	1.67	0.76
4:A:211:LYS:HB3	4:A:212:PRO:HD2	1.66	0.76
16:M:7:LYS:HE3	19:P:21:ARG:O	1.86	0.76
11:H:75:SER:O	11:H:79:ALA:HB2	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1751:G:C2'	1:0:1752:G:H5''	2.15	0.76
2:9:3069:U:OP1	16:M:4:PRO:HG3	1.86	0.76
4:A:35:GLY:O	4:A:36:ASP:HB3	1.86	0.76
1:0:794:U:H3	1:0:819:A:H61	1.34	0.76
12:I:52:GLN:HG3	12:I:53:ILE:N	1.99	0.76
15:L:164:THR:HG23	15:L:165:SER:N	2.00	0.75
1:0:656:G:OP2	17:N:37:ARG:HD2	1.87	0.75
1:0:2694:A:H4'	8:E:91:PHE:HE1	1.50	0.75
14:K:136:ALA:HB3	38:K:8579:HOH:O	1.86	0.75
1:0:871:G:H8	1:0:871:G:C5'	1.95	0.75
11:H:55:GLN:NE2	11:H:124:ARG:HE	1.85	0.75
1:0:1206:U:H5'	1:0:1206:U:H6	1.50	0.75
18:O:59:ARG:NH2	18:O:66:GLN:HE22	1.85	0.75
1:0:1116:U:HO2'	1:0:1118:A:H2	0.77	0.75
1:0:2502:C:H4'	11:H:151:MET:HG2	1.67	0.75
1:0:2890:A:H1'	23:T:56:ARG:NH2	2.02	0.75
5:B:125:GLU:O	5:B:129:ARG:HG3	1.86	0.75
8:E:15:GLN:HG3	8:E:20:ILE:HG12	1.68	0.75
11:H:162:SER:CB	11:H:163:PRO:HD3	2.16	0.75
27:X:189:ASN:HD22	27:X:189:ASN:C	1.95	0.75
6:C:139:VAL:HG13	38:C:8461:HOH:O	1.85	0.75
27:X:187:VAL:HG23	27:X:192:ASP:CB	2.17	0.75
16:M:113:SER:HB2	38:M:8559:HOH:O	1.86	0.74
31:2:25:VAL:HG22	31:2:68:LYS:HG3	1.68	0.74
20:Q:99:ALA:HB1	20:Q:109:MET:CE	2.14	0.74
1:0:21:G:C5'	20:Q:2:ILE:HA	2.17	0.74
10:G:12:ILE:N	10:G:13:PRO:HD3	2.01	0.74
1:0:962:C:H1'	16:M:5:ARG:NH1	2.03	0.74
1:0:1120:U:H5''	1:0:1120:U:C6	2.22	0.74
16:M:11:ARG:HG3	16:M:14:ARG:NH1	2.03	0.74
6:C:162:VAL:HG13	6:C:232:LEU:HD21	1.70	0.74
21:R:51:GLN:HE21	21:R:53:ASN:HD21	1.34	0.74
1:0:1160:G:H5'	1:0:1161:A:C5'	2.16	0.74
7:D:146:LYS:NZ	16:M:107:ASN:HD21	1.86	0.74
17:N:32:ARG:O	17:N:32:ARG:HD3	1.87	0.74
6:C:78:ARG:HH11	6:C:78:ARG:HG3	1.52	0.73
1:0:284:C:H4'	1:0:285:A:O5'	1.87	0.73
16:M:86:LEU:HD12	16:M:125:ALA:HB2	1.71	0.73
7:D:22:VAL:HG22	7:D:74:THR:HG22	1.70	0.73
9:F:91:VAL:HG12	9:F:92:GLY:N	2.03	0.73
11:H:47:GLU:HB3	11:H:133:ILE:HD13	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:62:PRO:HG3	13:J:65:ARG:NH2	2.03	0.73
1:O:56:G:H5''	24:U:50:ARG:NH1	2.02	0.73
5:B:119:HIS:O	5:B:121:PRO:HD3	1.89	0.73
5:B:297:VAL:HB	38:B:8619:HOH:O	1.88	0.73
1:O:1834:C:H2'	1:O:1840:A:N6	2.03	0.73
1:O:2507:G:H2'	1:O:2510:C:H42	1.52	0.73
11:H:53:PRO:HG3	11:H:127:GLY:H	1.52	0.73
15:L:104:ARG:O	15:L:108:LYS:HE2	1.88	0.73
1:O:2851:G:O2'	1:O:2852:A:H5'	1.87	0.73
7:D:57:THR:HG23	7:D:63:ILE:HG22	1.71	0.73
13:J:24:THR:HB	13:J:64:MET:HE2	1.71	0.73
1:O:1080:C:H4'	1:O:1081:A:OP1	1.87	0.73
7:D:135:VAL:HG21	7:D:139:TYR:CD1	2.24	0.72
11:H:59:ASN:HD22	11:H:59:ASN:N	1.87	0.72
16:M:164:ASP:CG	16:M:167:ASP:HA	2.14	0.72
2:9:3092:G:H2'	2:9:3093:A:C8	2.24	0.72
11:H:130:HIS:CD2	11:H:133:ILE:HD11	2.24	0.72
11:H:56:ILE:HG22	11:H:61:LEU:HD22	1.70	0.72
1:O:541:C:C2'	1:O:542:A:H5''	2.20	0.72
1:O:545:G:H5'	1:O:545:G:C8	2.23	0.72
7:D:41:LEU:HA	7:D:44:ILE:HG22	1.72	0.72
7:D:88:LEU:HB2	7:D:89:PRO:HD3	1.71	0.72
16:M:184:ILE:HG22	16:M:185:GLU:HG3	1.70	0.72
1:O:603:A:H5''	1:O:604:G:OP1	1.88	0.72
10:G:16:LYS:O	10:G:20:VAL:HG23	1.89	0.72
1:O:447:A:OP1	22:S:2:LYS:HG2	1.90	0.72
14:K:143:THR:HG22	14:K:145:LEU:H	1.54	0.72
16:M:89:GLY:O	16:M:92:ALA:HB3	1.89	0.72
16:M:159:TYR:HB3	16:M:162:ASP:HB2	1.72	0.72
20:Q:9:ASP:O	20:Q:13:THR:HB	1.90	0.72
8:E:23:GLU:HG2	8:E:28:SER:CB	2.20	0.72
1:O:121:U:OP2	30:1:10:ARG:NH2	2.23	0.71
8:E:11:VAL:HG12	8:E:12:ASP:N	2.04	0.71
1:O:289:G:N2	1:O:363:A:H2	1.86	0.71
1:O:1118:A:C8	1:O:1118:A:H3'	2.25	0.71
7:D:99:ASP:HB3	7:D:103:ASN:H	1.56	0.71
13:J:109:LEU:HD13	13:J:113:ILE:HD11	1.72	0.71
25:V:21:LEU:HD22	25:V:26:ILE:CD1	2.21	0.71
1:O:541:C:H2'	1:O:542:A:H5''	1.71	0.71
7:D:105:SER:CB	7:D:131:THR:HG23	2.19	0.71
1:O:1160:G:C5'	1:O:1161:A:H5'	2.14	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2827:A:H2'	1:0:2828:G:O4'	1.89	0.71
2:9:3048:C:H4'	16:M:141:ARG:HH21	1.55	0.71
4:A:217:ARG:HG2	4:A:229:ALA:HB2	1.71	0.71
11:H:28:ILE:HA	11:H:62:GLU:OE1	1.90	0.71
20:Q:14:ALA:HB3	20:Q:147:LEU:HB2	1.72	0.71
25:V:88:THR:HG22	25:V:89:ASP:N	2.05	0.71
25:V:4:LEU:HD22	25:V:52:VAL:CG2	2.20	0.71
24:U:39:ALA:N	24:U:40:PRO:HD2	2.06	0.71
4:A:179:MET:HA	4:A:179:MET:HE3	1.72	0.71
16:M:144:GLY:O	16:M:147:ILE:HG22	1.90	0.71
6:C:127:ARG:HG2	6:C:127:ARG:HH11	1.56	0.71
12:I:93:ARG:HB3	12:I:93:ARG:HH11	1.56	0.71
23:T:9:CYS:HA	23:T:52:THR:HG23	1.72	0.71
5:B:24:PRO:CG	5:B:204:GLY:HA2	2.21	0.71
11:H:137:ASN:O	11:H:139:ASP:N	2.23	0.71
20:Q:17:MET:HE1	20:Q:19:ARG:NH2	2.06	0.71
31:2:17:HIS:O	31:2:18:GLN:HG3	1.90	0.71
1:0:1328:A:OP1	27:X:169:ARG:HD2	1.90	0.70
7:D:64:ARG:HG2	7:D:67:ASP:HB3	1.73	0.70
11:H:55:GLN:HE21	11:H:124:ARG:NE	1.89	0.70
26:W:78:GLU:HG2	26:W:79:GLU:H	1.56	0.70
1:0:1185:U:H2'	1:0:1186:C:C6	2.27	0.70
1:0:2256:G:O2'	1:0:2257:G:H5'	1.89	0.70
25:V:88:THR:HG23	25:V:110:GLN:HE21	1.54	0.70
1:0:31:C:H4'	38:S:7242:HOH:O	1.90	0.70
5:B:175:LEU:C	5:B:175:LEU:HD23	2.17	0.70
15:L:34:GLU:HB3	15:L:35:PRO:HD2	1.74	0.70
1:0:1805:G:H2'	1:0:1806:G:H8	1.56	0.70
1:0:2716:G:H5''	5:B:206:THR:HG21	1.72	0.70
4:A:88:ILE:HD13	4:A:100:PRO:HD3	1.74	0.70
11:H:35:ASN:ND2	11:H:80:ASN:HA	2.07	0.70
28:Y:40:PRO:HD3	28:Y:47:LEU:HD11	1.73	0.70
1:0:1535:G:H2'	1:0:1536:C:C6	2.27	0.70
20:Q:18:LEU:HB2	20:Q:143:VAL:HG12	1.72	0.70
1:0:1684:A:H1'	30:1:43:ARG:HH22	1.55	0.70
5:B:41:PHE:CD1	5:B:79:MET:HE2	2.26	0.70
29:Z:25:LYS:HD2	30:1:49:GLU:H	1.55	0.70
16:M:138:ASP:O	16:M:140:GLN:N	2.23	0.70
1:0:371:U:H2'	1:0:372:A:H8	1.57	0.70
7:D:27:ILE:HG22	7:D:28:GLY:N	2.07	0.70
9:F:58:GLU:HA	9:F:61:MET:HG3	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:52:THR:HG22	23:T:54:THR:H	1.57	0.70
4:A:190:ARG:NH2	4:A:207:GLN:OE1	2.24	0.70
23:T:39:ASN:ND2	23:T:44:ARG:HH11	1.89	0.70
4:A:94:LEU:HG	4:A:99:ILE:HD11	1.73	0.69
26:W:71:ARG:HB3	26:W:88:GLU:OE1	1.92	0.69
1:O:2694:A:H4'	8:E:91:PHE:CE1	2.26	0.69
6:C:115:LEU:O	6:C:118:THR:HB	1.92	0.69
1:O:1165:G:H4'	1:O:1174:A:O2'	1.91	0.69
4:A:51:ARG:HB2	38:A:8617:HOH:O	1.91	0.69
15:L:139:PRO:O	15:L:140:ALA:CB	2.39	0.69
5:B:177:HIS:O	5:B:181:ILE:HG13	1.93	0.69
16:M:48:VAL:CG1	16:M:55:ASP:HB3	2.22	0.69
16:M:132:ASN:O	16:M:135:VAL:HG12	1.92	0.69
6:C:107:ARG:NH1	6:C:107:ARG:HB3	2.07	0.69
16:M:119:GLN:O	16:M:123:ILE:HG13	1.93	0.69
6:C:236:THR:CG2	6:C:239:ALA:H	2.01	0.69
14:K:133:VAL:HA	38:K:8579:HOH:O	1.91	0.69
11:H:45:GLN:HG3	11:H:135:TRP:NE1	2.08	0.69
1:O:236:A:H4'	1:O:237:G:H5'	1.75	0.69
1:O:1130:U:H2'	1:O:1131:G:O4'	1.93	0.69
1:O:1926:G:H2'	1:O:1927:A:H8	1.58	0.69
5:B:55:ASN:HB3	5:B:63:GLU:HA	1.73	0.69
26:W:15:ARG:HB3	26:W:15:ARG:NH1	2.06	0.69
1:O:1942:A:H3'	38:O:8223:HOH:O	1.92	0.69
8:E:20:ILE:CD1	8:E:40:VAL:HG11	2.22	0.69
20:Q:39:THR:HG23	20:Q:107:GLU:O	1.93	0.69
25:V:13:MET:HE2	25:V:18:GLN:CA	2.22	0.69
1:O:560:C:H42	1:O:597:A:H61	1.41	0.68
5:B:321:PRO:HA	38:B:8672:HOH:O	1.92	0.68
15:L:35:PRO:HG2	15:L:38:VAL:HG23	1.75	0.68
22:S:32:ARG:NH1	22:S:38:ARG:HH12	1.90	0.68
1:O:1118:A:H3'	1:O:1118:A:H8	1.57	0.68
1:O:2908:A:H2'	1:O:2909:G:O4'	1.94	0.68
1:O:285:A:H2'	1:O:286:U:O4'	1.94	0.68
4:A:153:ARG:HB2	4:A:153:ARG:HH11	1.57	0.68
17:N:47:ARG:HA	17:N:50:ARG:NH1	2.08	0.68
24:U:12:THR:CG2	24:U:15:GLU:HG3	2.14	0.68
1:O:1790:C:H2'	1:O:1791:U:H6	1.59	0.68
4:A:131:HIS:O	4:A:132:ASP:HB2	1.92	0.68
12:I:19:MET:HE2	12:I:79:PHE:HA	1.73	0.68
1:O:188:C:H5''	15:L:163:LEU:HD21	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2414:A:H2'	1:O:2415:A:C8	2.29	0.68
22:S:71:VAL:HG11	22:S:90:PRO:CB	2.20	0.68
27:X:187:VAL:CG2	27:X:192:ASP:HB2	2.23	0.68
1:O:2346:C:O2'	7:D:52:THR:HG21	1.93	0.68
6:C:219:ASN:O	6:C:222:ASP:OD1	2.12	0.68
15:L:164:THR:CG2	15:L:165:SER:N	2.56	0.68
16:M:169:PRO:O	16:M:172:PHE:HB3	1.93	0.68
22:S:47:THR:HB	22:S:100:ASP:HB3	1.75	0.68
26:W:72:VAL:HG22	26:W:85:VAL:CG1	2.24	0.68
7:D:20:LYS:HA	7:D:75:LEU:O	1.93	0.68
8:E:37:ASP:OD1	12:I:125:SER:HB3	1.94	0.68
8:E:84:MET:HE1	8:E:148:ILE:CD1	2.23	0.68
1:O:1450:C:O2'	1:O:1494:A:H5'	1.93	0.68
5:B:258:GLY:H	5:B:260:HIS:CE1	2.11	0.68
15:L:12:TRP:CE2	15:L:20:ILE:HD11	2.28	0.68
15:L:164:THR:HG22	15:L:167:GLY:N	2.02	0.68
1:O:1209:C:H2'	1:O:1210:G:H8	1.56	0.67
13:J:74:VAL:HG13	13:J:113:ILE:HG23	1.76	0.67
15:L:37:VAL:HG21	15:L:108:LYS:HG3	1.75	0.67
6:C:1:MET:HG2	6:C:2:GLN:H	1.58	0.67
17:N:47:ARG:HA	17:N:50:ARG:HH12	1.59	0.67
5:B:168:GLY:H	5:B:174:ARG:HD3	1.57	0.67
1:O:1191:A:H3'	1:O:1192:A:H5''	1.76	0.67
1:O:1244:U:OP1	12:I:18:ILE:HD13	1.94	0.67
1:O:2274:A:H1'	15:L:86:MET:SD	2.34	0.67
1:O:2768:A:H2'	1:O:2769:C:O4'	1.93	0.67
7:D:50:VAL:O	7:D:71:ALA:HA	1.95	0.67
12:I:133:GLY:O	12:I:137:GLU:HG3	1.95	0.67
14:K:67:ARG:O	14:K:71:GLU:HG3	1.94	0.67
15:L:55:LYS:O	15:L:60:ILE:HD12	1.95	0.67
17:N:44:ASN:OD1	17:N:65:LEU:HB2	1.95	0.67
1:O:288:A:H61	1:O:364:C:H42	1.42	0.67
1:O:1666:C:H2'	1:O:1667:A:H5'	1.77	0.67
1:O:2897:C:H2'	1:O:2898:G:H8	1.59	0.67
4:A:36:ASP:HA	4:A:83:GLY:HA3	1.77	0.67
4:A:192:VAL:HB	38:A:8604:HOH:O	1.94	0.67
15:L:65:VAL:HG21	15:L:105:ALA:HB2	1.75	0.67
22:S:50:VAL:HG12	22:S:56:ALA:HA	1.76	0.67
1:O:2769:C:O2'	1:O:2770:G:H5'	1.94	0.67
5:B:254:GLN:HG2	5:B:255:GLY:N	2.08	0.67
14:K:73:VAL:HG23	14:K:74:THR:H	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:U:64:GLY:O	24:U:65:ASP:HB2	1.93	0.67
1:O:2780:C:H1'	8:E:143:GLN:HE21	1.59	0.67
1:O:1008:C:H5''	11:H:16:ARG:HH12	1.59	0.67
1:O:1930:A:H2'	1:O:1931:A:C8	2.30	0.67
1:O:2265:U:H2'	1:O:2266:A:C8	2.30	0.67
5:B:24:PRO:HG2	5:B:204:GLY:HA2	1.76	0.67
28:Y:53:GLY:HA2	28:Y:67:GLY:O	1.94	0.67
1:O:1299:G:O6	14:K:6:ARG:HD3	1.95	0.67
9:F:107:VAL:O	9:F:111:ILE:HG13	1.95	0.67
1:O:820:G:OP2	4:A:171:LYS:NZ	2.27	0.67
1:O:559:U:H6	1:O:559:U:H5'	1.59	0.66
1:O:1134:G:C5'	11:H:151:MET:HE1	2.25	0.66
2:9:3023:U:C3'	2:9:3024:U:H5''	2.20	0.66
25:V:6:GLN:HB2	25:V:26:ILE:CD1	2.25	0.66
17:N:73:ASP:HA	17:N:92:VAL:O	1.95	0.66
1:O:1926:G:H2'	1:O:1927:A:C8	2.29	0.66
1:O:2256:G:C2'	1:O:2257:G:H5'	2.25	0.66
6:C:233:THR:HG22	6:C:234:VAL:H	1.60	0.66
12:I:117:ASP:O	12:I:119:THR:HG23	1.96	0.66
25:V:122:ARG:NH2	25:V:154:ARG:OXT	2.26	0.66
1:O:2769:C:H2'	1:O:2770:G:O4'	1.95	0.66
2:9:3039:U:H1'	2:9:3044:A:H61	1.61	0.66
7:D:64:ARG:CG	7:D:67:ASP:HB3	2.26	0.66
11:H:26:LYS:HD2	11:H:28:ILE:CD1	2.25	0.66
20:Q:18:LEU:HB2	20:Q:143:VAL:CG1	2.26	0.66
27:X:203:VAL:HG12	27:X:228:VAL:HG22	1.78	0.66
1:O:2421:G:H3'	1:O:2422:U:H5''	1.76	0.66
5:B:7:ARG:HG2	5:B:7:ARG:HH11	1.61	0.66
11:H:47:GLU:HB3	11:H:133:ILE:CD1	2.26	0.66
23:T:14:GLU:O	23:T:17:THR:HB	1.95	0.66
28:Y:30:GLU:O	28:Y:33:HIS:HB3	1.95	0.66
1:O:2506:A:O2'	1:O:2507:G:O5'	2.14	0.66
1:O:2594:C:O2'	1:O:2595:U:H5'	1.95	0.66
7:D:135:VAL:HG22	7:D:136:ARG:H	1.61	0.66
11:H:150:LYS:HB2	11:H:157:ILE:HD12	1.78	0.66
16:M:152:GLU:C	16:M:154:LEU:H	2.03	0.66
11:H:33:MET:HB2	11:H:83:PHE:HB3	1.77	0.66
13:J:81:ARG:HB2	13:J:87:ARG:NH1	2.11	0.66
10:G:71:LEU:C	10:G:73:ASP:H	2.04	0.65
28:Y:11:THR:OG1	28:Y:23:ARG:HB2	1.96	0.65
5:B:195:ARG:HD2	5:B:324:ASP:OD1	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:238:ASN:HD22	5:B:240:GLY:N	1.87	0.65
11:H:147:ARG:HA	11:H:150:LYS:HZ2	1.61	0.65
24:U:39:ALA:C	24:U:41:GLU:H	2.04	0.65
5:B:280:VAL:CG1	5:B:334:SER:HA	2.27	0.65
15:L:72:SER:HB2	15:L:93:ARG:HG2	1.77	0.65
1:O:2269:C:C2'	1:O:2270:G:H5'	2.26	0.65
1:O:1641:A:H2'	1:O:1642:A:H5'	1.78	0.65
1:O:2578:G:H5'	1:O:2578:G:H8	1.61	0.65
1:O:1771:U:C4'	28:Y:20:LEU:HD21	2.26	0.65
8:E:11:VAL:HG12	8:E:12:ASP:H	1.61	0.65
1:O:2271:G:H5'	38:A:8579:HOH:O	1.95	0.65
11:H:13:ALA:HA	11:H:91:HIS:HE1	1.62	0.65
28:Y:38:LYS:HE2	28:Y:45:LYS:CE	2.27	0.65
31:2:55:VAL:O	31:2:56:PRO:O	2.15	0.65
1:O:111:C:O2'	29:Z:20:ARG:HG2	1.96	0.65
1:O:877:G:H5'	1:O:878:G:OP1	1.96	0.65
1:O:1505:U:H6	1:O:1505:U:H5'	1.60	0.65
1:O:1835:U:C5	1:O:1840:A:N7	2.61	0.65
5:B:168:GLY:N	5:B:174:ARG:HD3	2.11	0.65
5:B:312:ARG:HD3	5:B:315:VAL:HG13	1.78	0.65
16:M:154:LEU:O	16:M:155:GLU:HB3	1.96	0.65
21:R:37:VAL:O	21:R:41:VAL:HG23	1.96	0.65
16:M:163:PHE:HE1	16:M:171:HIS:HD1	1.44	0.65
20:Q:29:LYS:HD3	38:Q:8542:HOH:O	1.96	0.65
1:O:544:G:H2'	1:O:545:G:H5''	1.79	0.65
1:O:1234:U:N3	5:B:244:PRO:HB3	2.12	0.65
2:9:3054:A:O2'	2:9:3055:U:H5'	1.97	0.65
11:H:140:PRO:HA	11:H:142:VAL:HG12	1.78	0.65
15:L:37:VAL:HG21	15:L:108:LYS:CG	2.27	0.65
1:O:2717:C:O2'	1:O:2718:C:H5''	1.97	0.64
1:O:2878:U:H2'	1:O:2879:A:O4'	1.97	0.64
9:F:50:VAL:HG13	9:F:60:VAL:HG11	1.77	0.64
29:Z:28:HIS:CE1	29:Z:31:LYS:HE2	2.32	0.64
2:9:3006:C:OP1	16:M:37:ARG:NH1	2.29	0.64
14:K:54:PRO:HG2	14:K:57:VAL:HG21	1.78	0.64
23:T:52:THR:HG22	23:T:54:THR:N	2.13	0.64
28:Y:29:VAL:O	28:Y:33:HIS:HB2	1.97	0.64
5:B:275:GLY:O	5:B:291:ASP:HA	1.97	0.64
6:C:235:PHE:HE2	6:C:243:VAL:HG21	1.62	0.64
8:E:84:MET:HE1	8:E:148:ILE:HD13	1.79	0.64
1:O:184:G:H5''	15:L:153:THR:HG22	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3028:U:H5''	16:M:40:ASN:HD21	1.63	0.64
5:B:36:PRO:HA	5:B:168:GLY:CA	2.27	0.64
5:B:307:ARG:HH11	5:B:307:ARG:HB2	1.63	0.64
26:W:25:ARG:HD3	26:W:64:ALA:O	1.97	0.64
1:0:2094:G:C4'	5:B:245:SER:HB3	2.27	0.64
2:9:3049:G:O2'	2:9:3050:G:H5'	1.96	0.64
9:F:53:ASP:OD1	9:F:80:GLN:HB2	1.96	0.64
24:U:49:LEU:O	24:U:53:ILE:HG13	1.97	0.64
28:Y:33:HIS:CE1	28:Y:49:ARG:HD2	2.33	0.64
1:0:407:A:H2'	1:0:408:A:C8	2.33	0.64
1:0:541:C:H2'	1:0:542:A:C5'	2.26	0.64
1:0:1803:C:H2'	1:0:1804:A:C8	2.33	0.64
4:A:140:LEU:HB3	4:A:141:PRO:HD2	1.77	0.64
12:I:74:ARG:HH11	12:I:74:ARG:CB	2.10	0.64
13:J:74:VAL:CG1	13:J:113:ILE:HG12	2.26	0.64
20:Q:25:PHE:CE2	20:Q:29:LYS:HE2	2.32	0.64
21:R:57:THR:HG22	21:R:59:ASP:N	2.12	0.64
17:N:32:ARG:HE	17:N:35:LYS:HD2	1.63	0.64
20:Q:18:LEU:HD12	20:Q:143:VAL:HG11	1.80	0.64
27:X:235:GLU:H	27:X:235:GLU:CD	2.03	0.64
11:H:44:ALA:HA	11:H:163:PRO:O	1.98	0.64
14:K:104:ASP:O	14:K:105:TYR:HB3	1.96	0.64
22:S:101:LEU:HD13	22:S:112:LEU:HD11	1.79	0.64
31:2:31:THR:HB	31:2:33:MET:HE3	1.80	0.64
1:0:2613:G:O2'	1:0:2614:C:H5'	1.98	0.64
23:T:52:THR:CG2	23:T:54:THR:HB	2.28	0.64
7:D:64:ARG:CD	7:D:67:ASP:HB3	2.28	0.64
11:H:27:LYS:N	11:H:58:HIS:HD2	1.94	0.64
12:I:27:ALA:HB1	12:I:87:LEU:HD21	1.80	0.64
1:0:1972:U:H2'	1:0:1973:A:H5'	1.80	0.63
14:K:143:THR:HG22	14:K:144:ASP:N	2.13	0.63
1:0:157:G:H4'	15:L:95:LYS:HE3	1.80	0.63
4:A:48:ASP:HB3	38:A:8617:HOH:O	1.97	0.63
11:H:14:TYR:H	11:H:91:HIS:CE1	2.15	0.63
12:I:107:ASN:ND2	12:I:109:TYR:H	1.96	0.63
13:J:55:VAL:HG12	13:J:56:SER:H	1.62	0.63
1:0:871:G:C8	1:0:871:G:C5'	2.74	0.63
1:0:1595:G:O2'	1:0:1596:U:H5'	1.99	0.63
4:A:88:ILE:HD13	4:A:100:PRO:CD	2.28	0.63
15:L:87:MET:HB3	31:2:46:ILE:HG21	1.80	0.63
23:T:14:GLU:OE1	23:T:15:PRO:HD2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:23:VAL:HG22	7:D:73:VAL:HB	1.80	0.63
16:M:183:ASP:OD2	16:M:186:LEU:HD12	1.99	0.63
22:S:49:GLU:OE2	22:S:97:ARG:HD2	1.98	0.63
1:O:2690:U:O2'	8:E:111:LYS:HE3	1.98	0.63
10:G:64:ASN:HD22	10:G:64:ASN:N	1.94	0.63
11:H:84:ARG:NH2	11:H:135:TRP:HH2	1.96	0.63
11:H:147:ARG:HA	11:H:150:LYS:NZ	2.14	0.63
14:K:24:ALA:HB2	14:K:30:ARG:HD2	1.81	0.63
1:O:136:C:H2'	1:O:137:U:O4'	1.98	0.63
1:O:960:G:N3	1:O:960:G:H2'	2.14	0.63
1:O:1596:U:H2'	1:O:1598:A:OP2	1.99	0.63
5:B:202:VAL:HG11	5:B:301:VAL:HG13	1.81	0.63
10:G:64:ASN:O	10:G:68:GLU:HG3	1.98	0.63
12:I:45:VAL:HG21	12:I:129:PHE:CD1	2.34	0.63
15:L:52:LEU:HD13	15:L:116:ASN:HB3	1.80	0.63
26:W:15:ARG:HH11	26:W:15:ARG:CB	2.10	0.63
1:O:1474:C:H5'	1:O:1474:C:C6	2.33	0.63
11:H:26:LYS:HD3	11:H:89:PRO:HG3	1.80	0.63
1:O:2270:G:H4'	4:A:223:ARG:HH12	1.64	0.63
6:C:46:TYR:CE2	6:C:98:ARG:NH1	2.67	0.63
6:C:104:ASP:HA	6:C:107:ARG:HH12	1.63	0.63
1:O:1741:U:H5'	1:O:1742:A:OP1	1.99	0.62
32:O:9500:SLD:C6S	3:4:76:A:H5''	2.29	0.62
4:A:94:LEU:HD23	4:A:94:LEU:N	2.14	0.62
4:A:129:LEU:CD1	4:A:145:MET:HE1	2.28	0.62
11:H:13:ALA:HA	11:H:91:HIS:CE1	2.33	0.62
13:J:10:GLN:H	13:J:10:GLN:HE21	0.75	0.62
14:K:114:VAL:HG11	38:K:8579:HOH:O	1.99	0.62
1:O:553:G:P	27:X:204:ARG:HH22	2.22	0.62
4:A:164:ARG:HB2	28:Y:68:CYS:SG	2.39	0.62
15:L:81:ARG:O	15:L:86:MET:HE2	1.99	0.62
1:O:2070:G:H2'	1:O:2072:G:OP1	2.00	0.62
1:O:2265:U:H2'	1:O:2266:A:H8	1.64	0.62
2:9:3020:G:O2'	2:9:3021:G:H5'	1.99	0.62
2:9:3040:C:N4	7:D:51:ARG:HB2	2.13	0.62
21:R:57:THR:HG22	21:R:59:ASP:H	1.65	0.62
27:X:186:ARG:HH11	27:X:186:ARG:HG2	1.64	0.62
1:O:1667:A:H5'	1:O:1667:A:H8	1.64	0.62
2:9:3051:A:H5'	16:M:160:SER:HB3	1.81	0.62
5:B:56:ASP:HB3	5:B:322:ARG:HH21	1.65	0.62
24:U:8:ILE:HA	24:U:11:MET:HE3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:731:U:H2'	1:0:732:C:C6	2.35	0.62
1:0:1636:G:O2'	1:0:1637:A:H5'	1.98	0.62
1:0:2780:C:H2'	1:0:2781:U:C6	2.34	0.62
28:Y:62:TYR:CE2	28:Y:64:ILE:HG23	2.34	0.62
31:2:65:THR:HG23	31:2:67:LEU:HG	1.80	0.62
1:0:2256:G:H2'	1:0:2257:G:H5'	1.82	0.62
1:0:2456:A:H2'	1:0:2457:U:C6	2.34	0.62
9:F:21:GLU:O	9:F:24:ARG:HG3	1.99	0.62
22:S:32:ARG:NH1	22:S:38:ARG:NH1	2.47	0.62
25:V:68:THR:HG23	25:V:69:ARG:HG2	1.79	0.62
1:0:2054:A:N3	20:Q:128:ARG:NH2	2.47	0.62
1:0:2269:C:O2'	1:0:2270:G:H5'	2.00	0.62
2:9:3006:C:H5''	16:M:37:ARG:HH12	1.63	0.62
5:B:162:MET:CE	5:B:308:LEU:HD21	2.22	0.62
11:H:71:TYR:C	11:H:73:GLN:H	2.08	0.62
14:K:138:GLY:HA3	38:K:8558:HOH:O	2.00	0.62
25:V:137:GLN:HE21	25:V:141:HIS:CE1	2.13	0.62
1:0:2421:G:H3'	1:0:2422:U:C5'	2.27	0.62
4:A:81:GLN:HB2	4:A:92:ASN:ND2	2.14	0.62
9:F:117:GLU:C	9:F:119:ARG:H	2.08	0.62
11:H:48:LEU:HG	11:H:157:ILE:HG21	1.82	0.62
18:O:76:GLY:O	18:O:79:SER:N	2.32	0.62
4:A:129:LEU:HD12	4:A:145:MET:HE1	1.80	0.62
1:0:638:C:H2'	1:0:639:A:C8	2.35	0.62
1:0:702:G:O2'	1:0:703:G:H5'	2.00	0.62
29:Z:21:ARG:HD2	29:Z:39:PHE:HB2	1.82	0.62
1:0:558:C:O2'	1:0:559:U:H5''	1.99	0.61
1:0:2505:G:O2'	1:0:2506:A:H5'	2.00	0.61
2:9:3030:C:OP1	7:D:137:PRO:O	2.18	0.61
4:A:101:GLU:OE2	4:A:131:HIS:HB2	2.00	0.61
13:J:98:VAL:HG13	13:J:102:GLU:HA	1.82	0.61
18:O:7:LYS:HD3	18:O:21:VAL:CG2	2.30	0.61
4:A:121:ALA:O	4:A:124:VAL:HG22	1.99	0.61
11:H:29:ALA:HB3	11:H:65:ARG:NH1	2.09	0.61
22:S:9:LYS:CE	22:S:13:ARG:NH1	2.62	0.61
28:Y:30:GLU:HA	28:Y:33:HIS:HB3	1.81	0.61
1:0:470:U:O2'	29:Z:16:HIS:HD2	1.82	0.61
1:0:2375:G:H2'	1:0:2376:C:C6	2.35	0.61
2:9:3044:A:O4'	7:D:76:ARG:NE	2.33	0.61
9:F:96:ALA:HA	38:F:3111:HOH:O	2.00	0.61
20:Q:40:ALA:O	20:Q:44:VAL:HG23	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1850:U:H2'	1:0:1851:G:H8	1.65	0.61
1:0:1909:A:H2'	1:0:1910:A:C8	2.35	0.61
1:0:2533:C:H5'	1:0:2533:C:C6	2.33	0.61
1:0:2795:C:O2'	1:0:2796:U:H5'	2.00	0.61
6:C:5:ILE:HD11	6:C:16:VAL:CG2	2.24	0.61
15:L:48:ARG:HH11	15:L:52:LEU:HD21	1.64	0.61
16:M:48:VAL:HG11	16:M:55:ASP:HB3	1.82	0.61
16:M:91:ARG:HG3	16:M:186:LEU:HD23	1.81	0.61
23:T:11:THR:HG22	23:T:53:ASP:OD2	2.01	0.61
1:0:281:U:H2'	1:0:282:C:O4'	2.01	0.61
1:0:696:C:O2'	1:0:697:G:H5'	2.00	0.61
1:0:1250:C:O2'	1:0:1251:C:H5'	2.01	0.61
1:0:669:G:O2'	1:0:670:G:H5'	2.00	0.61
1:0:1422:U:H2'	1:0:1423:C:C6	2.35	0.61
12:I:74:ARG:O	12:I:78:ILE:HG12	2.00	0.61
1:0:1882:C:H2'	1:0:1883:U:H6	1.64	0.61
1:0:2502:C:C4'	11:H:151:MET:HG2	2.30	0.61
2:9:3013:A:O2'	2:9:3014:G:H5''	2.00	0.61
8:E:31:ARG:HH12	8:E:68:HIS:CG	2.19	0.61
10:G:23:ILE:HD13	10:G:67:LEU:HD23	1.83	0.61
27:X:200:THR:HG22	27:X:201:GLU:HG3	1.83	0.61
1:0:657:G:OP1	6:C:27:ARG:NH2	2.28	0.61
1:0:1170:U:O2'	1:0:1172:G:N7	2.32	0.61
1:0:2840:A:OP1	5:B:211:THR:HG23	2.01	0.61
5:B:145:HIS:HD2	5:B:146:THR:O	1.84	0.61
9:F:56:PRO:HG2	15:L:44:THR:HA	1.82	0.61
6:C:47:GLY:HA2	6:C:92:PRO:HB2	1.81	0.61
25:V:84:VAL:HG12	38:V:6679:HOH:O	1.99	0.61
4:A:199:HIS:HD2	4:A:201:PHE:HB2	1.66	0.61
25:V:122:ARG:NH1	25:V:152:ALA:O	2.34	0.61
1:0:1666:C:O2'	1:0:1667:A:H5''	2.00	0.60
7:D:25:MET:CE	7:D:37:ALA:HB1	2.31	0.60
26:W:9:VAL:HG22	26:W:88:GLU:OE2	2.01	0.60
1:0:1003:U:HO2'	11:H:90:PHE:HE1	1.49	0.60
1:0:1393:A:H2'	1:0:1394:C:C6	2.36	0.60
1:0:1666:C:C2'	1:0:1667:A:H5'	2.31	0.60
2:9:3025:G:C3'	2:9:3026:C:H5'	2.31	0.60
4:A:27:LEU:HD21	4:A:55:VAL:HG21	1.83	0.60
6:C:27:ARG:HD2	17:N:5:PRO:HD2	1.81	0.60
9:F:56:PRO:CG	15:L:44:THR:HA	2.32	0.60
1:0:777:U:O2'	29:Z:11:LYS:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1119:G:H22	1:0:1246:A:H2	1.48	0.60
12:I:75:PRO:HG2	12:I:105:LEU:HD21	1.82	0.60
31:2:42:ARG:HG3	31:2:42:ARG:HH11	1.65	0.60
11:H:95:GLU:HB3	11:H:119:VAL:HG11	1.82	0.60
25:V:13:MET:HE2	25:V:18:GLN:HA	1.81	0.60
1:0:241:A:C2	1:0:378:A:H4'	2.36	0.60
1:0:645:U:OP2	14:K:4:LYS:HE2	2.00	0.60
1:0:2001:G:O2'	1:0:2002:C:H5'	2.01	0.60
12:I:52:GLN:HG3	12:I:53:ILE:H	1.64	0.60
23:T:49:LEU:HG	38:T:3805:HOH:O	2.00	0.60
1:0:1158:G:O2'	1:0:1159:G:H5'	2.01	0.60
1:0:2291:A:C8	1:0:2309:C:H5'	2.37	0.60
28:Y:30:GLU:HA	28:Y:33:HIS:CB	2.32	0.60
31:2:60:LYS:HG3	31:2:61:PRO:HD2	1.84	0.60
1:0:2028:U:H2'	1:0:2029:C:C6	2.36	0.60
1:0:2266:A:H2'	1:0:2267:G:C8	2.36	0.60
12:I:45:VAL:HG23	12:I:130:VAL:O	2.01	0.60
13:J:28:GLU:HG2	13:J:58:THR:HB	1.84	0.60
1:0:2415:A:N3	16:M:26:LEU:HD13	2.17	0.60
1:0:2598:U:O2	1:0:2600:A:H8	1.83	0.60
4:A:164:ARG:HA	28:Y:69:TYR:CE1	2.36	0.60
6:C:78:ARG:HG3	6:C:78:ARG:NH1	2.13	0.60
6:C:118:THR:O	6:C:136:VAL:HG13	2.01	0.60
11:H:27:LYS:H	11:H:58:HIS:CD2	2.13	0.60
1:0:256:C:H2'	1:0:257:G:O4'	2.02	0.60
1:0:2241:C:H2'	1:0:2242:U:C6	2.37	0.60
16:M:165:ALA:HB1	38:M:8526:HOH:O	2.02	0.60
20:Q:18:LEU:HG	20:Q:91:LEU:HD13	1.84	0.60
1:0:29:C:O2'	1:0:30:U:H5'	2.02	0.60
1:0:2720:C:O2	13:J:87:ARG:NH2	2.35	0.60
1:0:2779:G:H21	8:E:143:GLN:NE2	2.00	0.60
5:B:5:ARG:HD2	5:B:8:LYS:NZ	2.17	0.60
7:D:44:ILE:HG23	7:D:45:THR:HG23	1.83	0.60
7:D:135:VAL:HG22	7:D:136:ARG:N	2.17	0.60
11:H:139:ASP:N	11:H:140:PRO:CD	2.65	0.60
18:O:59:ARG:HH22	18:O:66:GLN:HE22	1.48	0.60
1:0:2320:U:H4'	1:0:2321:A:O4'	2.02	0.59
1:0:2361:A:H2'	1:0:2362:A:C8	2.37	0.59
8:E:86:VAL:CG1	8:E:129:GLU:HA	2.31	0.59
11:H:31:PHE:CD2	11:H:85:ILE:HG23	2.37	0.59
15:L:47:ASP:CG	15:L:48:ARG:H	2.09	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:74:ARG:HH11	15:L:74:ARG:HG3	1.66	0.59
25:V:64:THR:O	25:V:68:THR:HG22	2.02	0.59
1:O:902:G:N7	14:K:18:HIS:HD2	1.99	0.59
1:O:2256:G:H2'	1:O:2257:G:C5'	2.31	0.59
5:B:51:VAL:HG13	5:B:53:LEU:HD13	1.83	0.59
7:D:95:THR:O	7:D:97:GLN:N	2.31	0.59
15:L:48:ARG:NH1	15:L:52:LEU:HD21	2.17	0.59
20:Q:61:GLN:NE2	38:Q:8542:HOH:O	2.35	0.59
1:O:1790:C:H2'	1:O:1791:U:C6	2.37	0.59
2:9:3014:G:H5'	2:9:3014:G:H8	1.67	0.59
9:F:58:GLU:OE1	15:L:27:ARG:NH2	2.34	0.59
14:K:35:ARG:O	14:K:40:PHE:HA	2.02	0.59
8:E:11:VAL:HG13	8:E:23:GLU:O	2.03	0.59
10:G:12:ILE:N	10:G:13:PRO:CD	2.64	0.59
31:2:84:ARG:HD3	38:2:8554:HOH:O	2.02	0.59
1:O:2507:G:H2'	1:O:2510:C:N4	2.17	0.59
6:C:1:MET:HG2	6:C:2:GLN:NE2	2.16	0.59
13:J:115:ARG:HG3	13:J:116:GLU:N	2.18	0.59
30:1:40:ARG:HH11	30:1:40:ARG:HG2	1.67	0.59
1:O:947:U:H2'	1:O:948:G:C8	2.37	0.59
1:O:1461:U:H2'	1:O:1462:C:C6	2.37	0.59
16:M:155:GLU:O	16:M:156:GLU:HG3	2.02	0.59
1:O:303:C:O2'	1:O:304:G:H5'	2.03	0.59
1:O:2356:A:H2'	1:O:2357:G:O4'	2.03	0.59
1:O:2413:A:N7	16:M:109:PRO:HB3	2.17	0.59
7:D:86:THR:O	7:D:90:LEU:HG	2.02	0.59
15:L:138:HIS:ND1	15:L:139:PRO:O	2.31	0.59
20:Q:12:THR:HG22	20:Q:149:GLU:OE1	2.03	0.59
26:W:43:VAL:HG12	26:W:44:ASP:N	2.17	0.59
27:X:112:GLU:OE1	27:X:112:GLU:HA	2.00	0.59
1:O:449:A:N7	6:C:43:LYS:HG2	2.18	0.59
11:H:46:VAL:HG12	11:H:146:TRP:HZ3	1.68	0.59
14:K:54:PRO:HG2	14:K:57:VAL:CG2	2.32	0.59
16:M:33:ARG:NH1	16:M:103:ASP:OD2	2.26	0.59
16:M:151:ASP:O	16:M:154:LEU:HB2	2.01	0.59
1:O:1855:G:H8	4:A:144:GLU:OE2	1.85	0.59
2:9:3039:U:H1'	2:9:3044:A:N6	2.17	0.59
16:M:164:ASP:OD2	16:M:167:ASP:HA	2.02	0.59
26:W:76:ARG:O	26:W:77:PHE:HB3	2.01	0.59
1:O:1552:G:H2'	1:O:1553:C:C6	2.38	0.59
8:E:84:MET:HE2	8:E:133:VAL:CG2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:57:THR:C	21:R:59:ASP:H	2.11	0.59
23:T:52:THR:HG22	23:T:54:THR:HB	1.85	0.59
25:V:110:GLN:NE2	25:V:110:GLN:HA	2.18	0.59
26:W:76:ARG:HG3	26:W:76:ARG:NH1	2.16	0.59
1:0:95:A:H5''	1:0:97:G:O4'	2.03	0.58
1:0:282:C:O2'	1:0:283:U:H5'	2.03	0.58
1:0:2363:G:O2'	19:P:11:ARG:HG3	2.03	0.58
6:C:233:THR:HG22	6:C:234:VAL:N	2.17	0.58
30:1:41:HIS:HD2	30:1:44:ARG:H	1.51	0.58
1:0:338:C:H4'	6:C:174:ILE:CD1	2.32	0.58
1:0:1187:U:O2'	1:0:1189:A:H2	1.86	0.58
9:F:91:VAL:HG12	9:F:92:GLY:H	1.64	0.58
14:K:149:ARG:O	14:K:150:GLN:HB2	2.03	0.58
1:0:694:A:H2'	1:0:695:C:H5'	1.84	0.58
4:A:110:SER:HA	4:A:118:PHE:HE1	1.68	0.58
16:M:143:ARG:HA	16:M:172:PHE:CD2	2.38	0.58
17:N:14:LEU:HG	17:N:102:ILE:HD11	1.85	0.58
1:0:625:U:H5''	1:0:1044:C:N4	2.18	0.58
2:9:3055:U:H4'	2:9:3056:A:C8	2.37	0.58
7:D:94:ALA:HB3	7:D:174:VAL:CA	2.33	0.58
16:M:25:ARG:HA	16:M:28:LYS:HG3	1.84	0.58
27:X:200:THR:HG22	27:X:201:GLU:CG	2.32	0.58
1:0:292:G:H2'	1:0:358:G:N2	2.17	0.58
5:B:36:PRO:HA	5:B:168:GLY:HA3	1.85	0.58
7:D:99:ASP:HA	38:D:5675:HOH:O	2.04	0.58
9:F:110:GLU:HA	9:F:113:ASP:OD2	2.03	0.58
14:K:65:ASP:CG	14:K:111:ALA:HB3	2.28	0.58
15:L:74:ARG:HG3	15:L:74:ARG:NH1	2.17	0.58
15:L:80:GLY:O	15:L:81:ARG:HD2	2.04	0.58
5:B:144:THR:HG22	5:B:145:HIS:N	2.18	0.58
7:D:44:ILE:HG12	7:D:83:PHE:HE1	1.68	0.58
11:H:166:ASN:HD22	11:H:166:ASN:N	1.99	0.58
17:N:87:THR:O	17:N:91:GLN:HG3	2.04	0.58
18:O:9:LEU:O	18:O:13:VAL:HG12	2.03	0.58
24:U:56:ILE:O	24:U:60:GLN:HG3	2.03	0.58
1:0:1643:C:O2'	1:0:1644:C:H5'	2.04	0.58
7:D:49:PRO:HA	7:D:73:VAL:HG22	1.86	0.58
11:H:127:GLY:O	11:H:128:ALA:HB3	2.03	0.58
14:K:145:LEU:O	14:K:148:GLU:HG3	2.03	0.58
18:O:115:SER:H	18:O:118:GLN:NE2	1.82	0.58
1:0:21:G:H4'	20:Q:2:ILE:HG22	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2300:A:H4'	1:0:2301:A:O5'	2.03	0.58
5:B:96:PRO:HG2	38:B:8648:HOH:O	2.03	0.58
15:L:37:VAL:HG13	15:L:63:VAL:HG11	1.86	0.58
25:V:65:VAL:HG12	25:V:116:LEU:HD13	1.86	0.58
25:V:122:ARG:HH11	25:V:122:ARG:CG	2.14	0.58
1:0:812:A:H2'	1:0:813:C:C6	2.39	0.58
1:0:1164:U:C4'	1:0:1165:G:OP1	2.48	0.58
1:0:1864:C:OP1	15:L:75:THR:HG23	2.03	0.58
14:K:93:VAL:HG12	14:K:97:VAL:HG23	1.85	0.58
1:0:862:U:H2'	1:0:863:G:H8	1.68	0.58
1:0:1444:G:O2'	1:0:1445:G:H5'	2.02	0.58
1:0:2668:G:H2'	1:0:2669:U:C6	2.38	0.58
1:0:2894:C:O2'	1:0:2895:C:H5'	2.04	0.58
5:B:141:ARG:HG2	5:B:165:ARG:HA	1.85	0.58
23:T:17:THR:HG22	23:T:18:GLY:N	2.18	0.58
31:2:11:CYS:HB2	31:2:20:HIS:CE1	2.38	0.58
1:0:544:G:C2'	1:0:545:G:H5''	2.34	0.57
7:D:19:GLU:O	7:D:133:ASN:HB3	2.03	0.57
11:H:46:VAL:O	11:H:146:TRP:HH2	1.87	0.57
12:I:39:VAL:HG12	12:I:40:ASN:ND2	2.18	0.57
22:S:73:HIS:CD2	22:S:88:PRO:HG3	2.38	0.57
28:Y:77:LYS:HA	28:Y:80:MET:HE2	1.86	0.57
1:0:566:A:H2'	1:0:567:U:O4'	2.04	0.57
1:0:1804:A:H2'	1:0:1805:G:C8	2.39	0.57
2:9:3048:C:H4'	16:M:141:ARG:NH2	2.17	0.57
4:A:66:ARG:HH11	4:A:66:ARG:HB2	1.67	0.57
13:J:72:VAL:HG11	13:J:121:PHE:CD1	2.39	0.57
16:M:97:VAL:HG12	16:M:127:LEU:HD11	1.86	0.57
21:R:6:LYS:HB2	21:R:27:ALA:O	2.04	0.57
1:0:394:G:H1	15:L:181:GLU:CD	2.12	0.57
1:0:820:G:C6	4:A:171:LYS:HB2	2.39	0.57
1:0:1441:G:O2'	1:0:1442:A:H5'	2.03	0.57
4:A:33:GLU:O	4:A:34:ASP:HB2	2.03	0.57
11:H:26:LYS:HE3	11:H:28:ILE:HB	1.86	0.57
11:H:47:GLU:CB	11:H:133:ILE:HD13	2.35	0.57
17:N:77:ALA:HB1	17:N:98:LEU:HD12	1.86	0.57
23:T:13:ILE:HG12	23:T:32:CYS:HB3	1.85	0.57
1:0:1496:G:H5'	1:0:1572:A:H1'	1.86	0.57
1:0:2756:U:H3	1:0:2896:A:H2	1.53	0.57
7:D:95:THR:C	7:D:97:GLN:H	2.13	0.57
13:J:55:VAL:HG12	13:J:56:SER:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:13:VAL:HG11	18:O:40:VAL:HG11	1.86	0.57
1:O:297:U:H2'	1:O:298:C:H6	1.69	0.57
1:O:1783:A:O2'	1:O:1784:U:H5'	2.04	0.57
7:D:64:ARG:HB3	7:D:67:ASP:OD2	2.04	0.57
12:I:39:VAL:HG13	12:I:106:GLY:O	2.03	0.57
16:M:78:MET:HB2	16:M:79:PRO:HD3	1.87	0.57
24:U:44:GLY:O	24:U:48:GLU:HG2	2.04	0.57
1:O:832:U:H2'	1:O:833:G:C8	2.39	0.57
2:9:3028:U:H2'	2:9:3029:C:C6	2.40	0.57
8:E:132:THR:HG23	8:E:132:THR:O	2.03	0.57
11:H:53:PRO:HA	11:H:125:VAL:O	2.05	0.57
27:X:99:ALA:HB2	27:X:233:TYR:CZ	2.40	0.57
1:O:1827:G:H2'	1:O:1828:G:C8	2.39	0.57
13:J:99:ASP:OD1	13:J:101:ASN:N	2.36	0.57
15:L:186:SER:O	15:L:189:VAL:HG12	2.04	0.57
25:V:38:THR:HG22	25:V:39:ASP:N	2.20	0.57
28:Y:19:GLY:O	28:Y:23:ARG:HG2	2.05	0.57
1:O:797:A:H4'	28:Y:10:ARG:N	2.19	0.57
1:O:962:C:H1'	16:M:5:ARG:HH12	1.69	0.57
1:O:1333:U:H2'	1:O:1334:C:C6	2.40	0.57
1:O:1667:A:H2'	1:O:1668:U:C6	2.40	0.57
4:A:199:HIS:CD2	4:A:201:PHE:H	2.23	0.57
11:H:83:PHE:HZ	11:H:146:TRP:HE1	1.47	0.57
12:I:107:ASN:HD21	12:I:109:TYR:HB2	1.70	0.57
24:U:11:MET:HB3	24:U:15:GLU:HB2	1.87	0.57
25:V:151:GLU:O	25:V:154:ARG:HB3	2.04	0.57
28:Y:50:ALA:HB3	28:Y:54:ILE:HG22	1.85	0.57
1:O:170:U:H2'	1:O:171:C:H5'	1.87	0.57
1:O:1189:A:H3'	38:O:8560:HOH:O	2.05	0.57
1:O:1205:U:C2'	1:O:1206:U:H5''	2.35	0.57
1:O:1803:C:H2'	1:O:1804:A:H8	1.68	0.57
1:O:2717:C:H2'	1:O:2718:C:C5'	2.30	0.57
38:O:6828:HOH:O	11:H:4:ALA:HB3	2.05	0.57
4:A:87:GLU:HB3	38:A:8635:HOH:O	2.04	0.57
5:B:140:LEU:HA	38:B:8592:HOH:O	2.04	0.57
6:C:162:VAL:CG1	6:C:192:ILE:HD11	2.34	0.57
11:H:49:VAL:O	11:H:157:ILE:HG23	2.05	0.57
28:Y:57:CYS:SG	28:Y:59:HIS:HB3	2.45	0.57
1:O:371:U:H2'	1:O:372:A:C8	2.40	0.57
1:O:1234:U:C4	5:B:244:PRO:HB3	2.40	0.57
1:O:2456:A:H2'	1:O:2457:U:H6	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:39:ALA:HB3	4:A:61:GLU:OE2	2.04	0.57
8:E:31:ARG:HH12	8:E:68:HIS:CD2	2.23	0.57
28:Y:10:ARG:HA	38:Y:8416:HOH:O	2.03	0.57
1:O:12:U:H2'	1:O:13:G:H5'	1.86	0.56
1:O:2729:C:O2'	1:O:2730:G:H5'	2.05	0.56
1:O:2780:C:H2'	1:O:2781:U:H6	1.68	0.56
9:F:19:ALA:O	9:F:22:VAL:HG22	2.04	0.56
18:O:80:ARG:HG2	18:O:87:ARG:CZ	2.35	0.56
1:O:290:C:O2'	1:O:291:C:H5'	2.05	0.56
1:O:1398:G:H2'	1:O:1399:A:C8	2.41	0.56
4:A:1:GLY:HA2	4:A:197:VAL:HG23	1.87	0.56
10:G:23:ILE:O	10:G:27:ILE:HG13	2.04	0.56
15:L:52:LEU:HD13	15:L:116:ASN:CG	2.30	0.56
25:V:13:MET:HE2	25:V:18:GLN:N	2.20	0.56
29:Z:25:LYS:HD2	30:1:49:GLU:N	2.19	0.56
1:O:392:U:O2'	15:L:182:LYS:HE2	2.05	0.56
1:O:431:G:P	15:L:48:ARG:HH12	2.28	0.56
1:O:1209:C:H2'	1:O:1210:G:C8	2.39	0.56
1:O:1352:A:N1	6:C:48:SER:HB3	2.20	0.56
1:O:1766:U:O2	1:O:1778:A:H5'	2.06	0.56
1:O:1829:A:H2'	1:O:1830:C:H5'	1.88	0.56
1:O:2404:G:O5'	19:P:68:GLY:HA3	2.04	0.56
2:9:3023:U:H6	2:9:3023:U:H5''	1.69	0.56
6:C:104:ASP:HA	6:C:107:ARG:NH1	2.19	0.56
7:D:41:LEU:HA	7:D:44:ILE:CG2	2.35	0.56
11:H:35:ASN:HD21	11:H:80:ASN:HA	1.69	0.56
12:I:26:VAL:HG13	12:I:36:VAL:HG11	1.88	0.56
14:K:90:ARG:NH2	14:K:121:ILE:HD11	2.21	0.56
15:L:47:ASP:CG	15:L:48:ARG:N	2.64	0.56
15:L:172:GLY:O	15:L:183:VAL:HG11	2.04	0.56
16:M:143:ARG:NH1	16:M:173:ASP:OD2	2.36	0.56
17:N:47:ARG:HG3	17:N:47:ARG:HH11	1.70	0.56
20:Q:82:GLU:HG3	20:Q:83:LYS:N	2.20	0.56
21:R:52:VAL:HG22	21:R:66:VAL:HG22	1.88	0.56
22:S:28:SER:O	22:S:32:ARG:HG3	2.05	0.56
24:U:39:ALA:N	24:U:40:PRO:CD	2.67	0.56
26:W:78:GLU:HG2	26:W:79:GLU:N	2.18	0.56
1:O:64:G:H2'	1:O:65:C:C6	2.40	0.56
1:O:2269:C:H2'	1:O:2270:G:H5'	1.86	0.56
2:9:3055:U:H4'	2:9:3056:A:H8	1.71	0.56
5:B:24:PRO:HG3	5:B:204:GLY:HA2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:47:LEU:HB2	9:F:108:LEU:HD11	1.88	0.56
15:L:155:HIS:CE1	15:L:158:ARG:HE	2.23	0.56
16:M:71:TRP:HE3	16:M:175:LEU:HD22	1.71	0.56
24:U:58:THR:O	24:U:62:GLU:HG3	2.05	0.56
25:V:21:LEU:HD21	25:V:48:VAL:HG11	1.88	0.56
1:0:445:U:H2'	1:0:446:G:H8	1.69	0.56
1:0:558:C:H2'	1:0:559:U:H5'	1.86	0.56
1:0:960:G:H4'	38:0:8921:HOH:O	2.05	0.56
1:0:1139:U:H2'	1:0:1140:C:C6	2.40	0.56
1:0:2011:A:H4'	1:0:2012:U:O5'	2.06	0.56
2:9:3028:U:H5''	16:M:40:ASN:ND2	2.20	0.56
19:P:64:GLU:HG3	19:P:74:ASP:OD2	2.05	0.56
1:0:732:C:H2'	1:0:733:U:C6	2.40	0.56
1:0:1669:A:H2'	1:0:1670:G:C8	2.41	0.56
1:0:2364:A:H5''	19:P:15:LYS:HD3	1.87	0.56
2:9:3025:G:H5''	2:9:3026:C:C6	2.40	0.56
5:B:175:LEU:HD23	5:B:175:LEU:O	2.05	0.56
6:C:27:ARG:HG3	6:C:29:ASP:OD1	2.06	0.56
11:H:97:LYS:HD3	11:H:117:LYS:HD3	1.86	0.56
12:I:74:ARG:NH1	12:I:76:ASP:HB2	2.20	0.56
18:O:16:VAL:HG12	18:O:17:GLY:N	2.20	0.56
26:W:37:LEU:CD1	26:W:85:VAL:HG21	2.32	0.56
1:0:862:U:H2'	1:0:863:G:C8	2.39	0.56
1:0:1586:G:O2'	1:0:1587:U:H5'	2.06	0.56
1:0:2054:A:C2	20:Q:128:ARG:NH2	2.74	0.56
1:0:2768:A:O2'	1:0:2769:C:H5'	2.05	0.56
38:0:6414:HOH:O	5:B:298:LYS:HD3	2.06	0.56
2:9:3029:C:H2'	2:9:3030:C:H5'	1.87	0.56
4:A:51:ARG:NH1	4:A:120:ARG:O	2.38	0.56
12:I:19:MET:HE3	12:I:132:LEU:CD1	2.24	0.56
12:I:19:MET:CE	12:I:132:LEU:HD11	2.25	0.56
1:0:2310:G:OP2	11:H:114:PRO:HD2	2.05	0.56
7:D:25:MET:SD	7:D:40:ILE:HD11	2.46	0.56
7:D:69:ILE:HG22	7:D:69:ILE:O	2.05	0.56
8:E:31:ARG:NH1	8:E:68:HIS:CG	2.73	0.56
15:L:134:ILE:O	15:L:136:PRO:HD3	2.05	0.56
1:0:1154:A:H2'	1:0:1155:G:C8	2.40	0.56
1:0:1453:G:H2'	1:0:1454:U:O4'	2.06	0.56
1:0:2119:C:O2'	1:0:2120:U:H5'	2.06	0.56
1:0:2426:G:H1'	38:0:6980:HOH:O	2.05	0.56
1:0:2435:U:OP1	31:2:28:GLY:HA3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2909:G:O2'	1:O:2910:A:H5'	2.06	0.56
5:B:162:MET:HE2	5:B:310:ARG:HD3	1.88	0.56
6:C:20:ASP:O	6:C:23:GLU:HB2	2.06	0.56
7:D:10:PHE:CG	7:D:11:HIS:N	2.73	0.56
11:H:165:GLY:C	11:H:166:ASN:HD22	2.14	0.56
12:I:27:ALA:HB1	12:I:87:LEU:CD2	2.36	0.56
1:O:485:A:N3	1:O:487:G:H5''	2.21	0.56
1:O:1733:A:H4'	5:B:212:GLN:HA	1.88	0.56
4:A:100:PRO:HG2	4:A:103:VAL:HG21	1.87	0.56
5:B:56:ASP:OD1	5:B:322:ARG:HB3	2.05	0.56
6:C:72:LYS:HG2	6:C:77:ALA:HA	1.86	0.56
12:I:99:GLU:HA	38:I:7377:HOH:O	2.06	0.56
13:J:81:ARG:HB2	13:J:87:ARG:HH11	1.70	0.56
26:W:66:THR:HG23	26:W:67:PRO:HD2	1.88	0.56
1:O:1882:C:H2'	1:O:1883:U:C6	2.42	0.55
4:A:192:VAL:O	4:A:192:VAL:HG12	2.05	0.55
16:M:77:ASN:OD1	16:M:79:PRO:HD2	2.05	0.55
23:T:44:ARG:HB3	38:T:3805:HOH:O	2.06	0.55
1:O:1657:A:H2'	1:O:1658:A:C8	2.41	0.55
2:9:3023:U:H4'	2:9:3024:U:OP2	2.05	0.55
17:N:53:GLN:HG2	17:N:56:GLU:OE1	2.07	0.55
30:1:18:ASN:ND2	30:1:40:ARG:H	2.04	0.55
1:O:596:C:H2'	1:O:597:A:C8	2.41	0.55
38:O:7746:HOH:O	15:L:178:LYS:HB2	2.06	0.55
4:A:125:ASN:CB	4:A:158:VAL:HG12	2.36	0.55
5:B:75:GLU:C	5:B:77:PRO:HD3	2.32	0.55
5:B:280:VAL:HG13	5:B:334:SER:HA	1.88	0.55
11:H:46:VAL:HG21	38:H:8387:HOH:O	2.05	0.55
16:M:64:SER:C	16:M:66:LEU:H	2.12	0.55
18:O:7:LYS:HD3	18:O:21:VAL:HG21	1.87	0.55
25:V:21:LEU:HD21	25:V:48:VAL:CG1	2.36	0.55
1:O:671:A:O2'	1:O:672:G:H2'	2.07	0.55
1:O:1223:G:O2'	1:O:1224:G:H5'	2.06	0.55
6:C:168:ARG:NH2	6:C:190:ALA:O	2.39	0.55
9:F:61:MET:HB3	15:L:19:GLN:OE1	2.05	0.55
14:K:66:VAL:HG23	14:K:67:ARG:N	2.21	0.55
27:X:103:THR:HG22	27:X:104:GLU:OE2	2.07	0.55
31:2:3:MET:O	31:2:90:PHE:HA	2.05	0.55
1:O:319:A:H4'	1:O:338:C:C4	2.41	0.55
1:O:542:A:H2'	1:O:543:G:O4'	2.07	0.55
1:O:793:A:H5''	18:O:83:LYS:HG2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:1789:G:O6	18:O:73:HIS:HE1	1.89	0.55
4:A:105:VAL:CG1	4:A:154:ALA:HB1	2.36	0.55
7:D:99:ASP:HB2	7:D:103:ASN:HB2	1.88	0.55
8:E:81:GLU:HG2	8:E:134:SER:HB3	1.88	0.55
9:F:56:PRO:HG2	15:L:43:PRO:O	2.06	0.55
21:R:32:ALA:HA	21:R:36:GLU:OE1	2.06	0.55
26:W:31:ILE:O	26:W:35:GLU:HG3	2.06	0.55
28:Y:42:CYS:SG	28:Y:44:PHE:HB2	2.47	0.55
28:Y:56:MET:HA	28:Y:62:TYR:O	2.06	0.55
1:O:67:A:H5''	1:O:69:A:C8	2.41	0.55
1:O:420:U:H2'	1:O:421:C:C6	2.42	0.55
1:O:1249:U:H2'	1:O:1250:C:C6	2.41	0.55
1:O:2715:G:O2'	5:B:262:ARG:HD2	2.06	0.55
6:C:124:VAL:HA	6:C:230:GLY:O	2.07	0.55
9:F:37:THR:O	9:F:41:GLU:HG3	2.07	0.55
5:B:82:VAL:O	5:B:82:VAL:HG12	2.06	0.55
6:C:139:VAL:CG2	6:C:240:LEU:HD12	2.37	0.55
7:D:86:THR:C	7:D:89:PRO:HD2	2.31	0.55
15:L:12:TRP:O	15:L:15:PRO:HD3	2.07	0.55
1:O:432:G:O2'	1:O:433:C:H5'	2.07	0.55
4:A:36:ASP:HB2	4:A:84:VAL:N	2.22	0.55
7:D:23:VAL:HG21	7:D:45:THR:HG21	1.87	0.55
7:D:146:LYS:HZ1	16:M:107:ASN:HD21	1.53	0.55
10:G:71:LEU:O	10:G:73:ASP:N	2.40	0.55
15:L:134:ILE:HG23	15:L:141:ILE:HD13	1.89	0.55
22:S:71:VAL:HG13	22:S:91:LEU:O	2.07	0.55
4:A:179:MET:HG2	4:A:186:TRP:CG	2.42	0.55
8:E:7:ILE:HG22	8:E:45:ASP:O	2.07	0.55
11:H:31:PHE:HA	11:H:85:ILE:CG2	2.37	0.55
2:9:3114:G:O6	16:M:11:ARG:HD3	2.06	0.55
4:A:125:ASN:HB3	4:A:158:VAL:HG12	1.88	0.55
6:C:218:VAL:N	38:C:8434:HOH:O	2.40	0.55
7:D:54:ALA:HB2	7:D:69:ILE:HD12	1.88	0.55
9:F:91:VAL:CG1	9:F:92:GLY:N	2.70	0.55
13:J:74:VAL:HG12	13:J:75:ARG:HG3	1.89	0.55
15:L:149:TRP:O	15:L:152:ARG:HG2	2.07	0.55
20:Q:106:GLY:HA2	20:Q:109:MET:CE	2.32	0.55
28:Y:27:ALA:HA	38:Y:8416:HOH:O	2.07	0.55
1:O:596:C:H2'	1:O:597:A:H8	1.72	0.54
1:O:832:U:H2'	1:O:833:G:H8	1.72	0.54
1:O:1165:G:H1'	1:O:1174:A:H1'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1942:A:H2'	1:0:1943:C:H6	1.72	0.54
1:0:2600:A:H2'	1:0:2601:A:O4'	2.07	0.54
4:A:170:VAL:HG13	28:Y:22:ILE:HG21	1.89	0.54
21:R:11:THR:H	21:R:14:ALA:HB3	1.71	0.54
1:0:398:U:H2'	1:0:399:C:C6	2.43	0.54
1:0:1943:C:O4'	4:A:212:PRO:HA	2.08	0.54
1:0:2777:G:O2'	1:0:2778:A:H5'	2.07	0.54
9:F:50:VAL:HG21	9:F:63:ILE:HG21	1.89	0.54
11:H:157:ILE:HG22	11:H:158:ASN:N	2.21	0.54
13:J:75:ARG:HG2	13:J:90:PHE:CD2	2.42	0.54
25:V:125:HIS:CD2	25:V:127:GLY:H	2.25	0.54
1:0:506:G:N2	1:0:509:A:H5'	2.19	0.54
1:0:825:U:H5''	1:0:826:U:OP1	2.07	0.54
1:0:1377:C:H5'	1:0:1377:C:H6	1.71	0.54
1:0:2072:G:C6	1:0:2533:C:H1'	2.42	0.54
1:0:2502:C:H2'	1:0:2503:A:C5'	2.36	0.54
1:0:2718:C:H6	1:0:2718:C:H5'	1.71	0.54
1:0:2769:C:C2'	1:0:2770:G:H5'	2.37	0.54
1:0:2885:A:H2'	1:0:2886:C:H6	1.71	0.54
8:E:5:LEU:HD21	8:E:66:GLN:HG3	1.89	0.54
11:H:3:GLY:HA2	11:H:57:ARG:NH1	2.23	0.54
24:U:57:LYS:HA	24:U:60:GLN:HE21	1.71	0.54
25:V:90:TYR:CE2	25:V:99:ALA:HB2	2.41	0.54
1:0:263:U:O4'	9:F:59:ILE:HD13	2.07	0.54
1:0:2419:U:H5''	1:0:2420:G:H5'	1.89	0.54
2:9:3064:C:C2'	2:9:3065:A:H5'	2.37	0.54
6:C:40:ALA:CB	6:C:100:LEU:HD12	2.37	0.54
1:0:1119:G:N2	1:0:1246:A:H2	2.05	0.54
1:0:2050:G:H5''	20:Q:80:TYR:O	2.07	0.54
1:0:2766:A:O2'	1:0:2767:C:H5'	2.07	0.54
9:F:28:ALA:HB3	9:F:99:THR:O	2.07	0.54
14:K:73:VAL:HG23	14:K:74:THR:N	2.22	0.54
25:V:125:HIS:HD2	25:V:127:GLY:H	1.55	0.54
26:W:21:PRO:HG2	26:W:24:LYS:HD3	1.90	0.54
1:0:100:C:H4'	22:S:16:LEU:HB2	1.90	0.54
1:0:1666:C:O2'	1:0:1667:A:C5'	2.55	0.54
1:0:2676:C:H4'	12:I:70:PHE:CE1	2.42	0.54
1:0:2897:C:H2'	1:0:2898:G:C8	2.41	0.54
2:9:3076:G:C3'	2:9:3077:A:H5''	2.28	0.54
4:A:42:VAL:HG21	4:A:74:VAL:CG1	2.38	0.54
15:L:137:ASP:C	15:L:142:LYS:HE3	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:2:69:TYR:HB2	31:2:78:HIS:CE1	2.43	0.54
1:0:263:U:C4	9:F:54:VAL:HG13	2.42	0.54
1:0:282:C:H1'	1:0:368:C:H42	1.70	0.54
1:0:660:A:H4'	1:0:661:G:O5'	2.08	0.54
1:0:1331:A:OP2	27:X:142:SER:OG	2.23	0.54
1:0:2112:A:H2'	1:0:2113:G:C8	2.41	0.54
2:9:3056:A:H1'	7:D:14:ARG:HG2	1.90	0.54
5:B:248:ARG:O	5:B:251:VAL:HG13	2.08	0.54
5:B:305:ASP:O	5:B:306:LYS:HB2	2.08	0.54
6:C:16:VAL:HG12	6:C:17:ASP:N	2.22	0.54
8:E:24:GLY:HA3	8:E:76:VAL:HB	1.90	0.54
11:H:31:PHE:HD2	11:H:85:ILE:O	1.90	0.54
18:O:29:GLY:O	18:O:32:ALA:HB3	2.07	0.54
28:Y:48:LYS:HG2	38:Y:8435:HOH:O	2.08	0.54
1:0:2379:G:H4'	1:0:2380:A:H5''	1.90	0.54
2:9:3006:C:C5'	16:M:37:ARG:NH1	2.67	0.54
7:D:140:ARG:O	7:D:144:ARG:HG2	2.07	0.54
9:F:28:ALA:CB	9:F:99:THR:HG23	2.37	0.54
30:1:39:ARG:HG2	38:1:3143:HOH:O	2.06	0.54
1:0:947:U:H2'	1:0:948:G:H8	1.70	0.54
5:B:62:ARG:CA	5:B:65:MET:HE3	2.33	0.54
11:H:45:GLN:HE21	11:H:135:TRP:NE1	2.02	0.54
16:M:34:LEU:HD22	16:M:129:ILE:HD13	1.88	0.54
20:Q:98:ASN:HD22	20:Q:98:ASN:N	2.04	0.54
1:0:60:A:O2'	1:0:61:G:H5'	2.08	0.54
1:0:512:G:O3'	1:0:513:A:H8	1.91	0.54
1:0:1641:A:C2'	1:0:1642:A:H5'	2.38	0.54
1:0:2437:A:H2'	1:0:2438:G:C8	2.42	0.54
4:A:53:ALA:HB3	38:A:8617:HOH:O	2.08	0.54
11:H:149:ALA:C	11:H:151:MET:H	2.15	0.54
16:M:154:LEU:HD11	38:M:8526:HOH:O	2.08	0.54
1:0:168:C:O2'	1:0:169:A:H5'	2.08	0.53
1:0:249:G:O2'	1:0:250:C:H5'	2.08	0.53
1:0:415:A:O2'	1:0:416:G:H5'	2.09	0.53
1:0:1123:A:C2	1:0:1129:C:H4'	2.43	0.53
5:B:52:VAL:O	5:B:53:LEU:HD12	2.06	0.53
6:C:21:VAL:C	6:C:23:GLU:H	2.16	0.53
8:E:84:MET:HB2	8:E:131:LEU:HB2	1.89	0.53
13:J:28:GLU:OE2	13:J:58:THR:HG21	2.08	0.53
16:M:34:LEU:HA	16:M:47:LEU:HD23	1.89	0.53
16:M:139:TRP:CE3	16:M:139:TRP:HA	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Z:28:HIS:HD2	29:Z:30:LYS:H	1.56	0.53
1:0:316:A:N3	1:0:336:G:O2'	2.39	0.53
1:0:352:A:H2'	1:0:353:G:C8	2.43	0.53
1:0:639:A:H2'	1:0:640:G:C8	2.43	0.53
38:9:8461:HOH:O	19:P:25:PRO:HB2	2.08	0.53
7:D:94:ALA:HB3	7:D:174:VAL:HA	1.89	0.53
9:F:52:GLU:HG3	9:F:77:VAL:O	2.09	0.53
15:L:87:MET:HB2	15:L:91:ILE:CD1	2.36	0.53
20:Q:119:VAL:HG21	20:Q:142:ASP:CG	2.33	0.53
31:2:56:PRO:HA	38:2:8553:HOH:O	2.07	0.53
1:0:381:G:H5''	38:0:5237:HOH:O	2.06	0.53
1:0:447:A:O2'	1:0:448:G:H5'	2.08	0.53
1:0:1528:A:H2'	1:0:1529:G:O4'	2.08	0.53
1:0:1666:C:H2'	1:0:1667:A:H8	1.73	0.53
1:0:1884:G:O6	4:A:190:ARG:HD2	2.07	0.53
1:0:2276:U:H2'	1:0:2277:U:C6	2.43	0.53
1:0:2791:U:H1'	1:0:2792:A:H5''	1.91	0.53
7:D:54:ALA:CB	7:D:69:ILE:HD12	2.38	0.53
14:K:61:ALA:HA	38:K:8569:HOH:O	2.08	0.53
22:S:19:ARG:NH1	22:S:68:ASP:O	2.41	0.53
28:Y:30:GLU:HB2	38:Y:8416:HOH:O	2.07	0.53
1:0:797:A:C4'	28:Y:10:ARG:N	2.72	0.53
1:0:810:G:H2'	1:0:811:C:C6	2.43	0.53
1:0:1182:C:H1'	1:0:1192:A:H8	1.73	0.53
1:0:1471:A:H2'	1:0:1472:C:C6	2.43	0.53
1:0:1805:G:H2'	1:0:1806:G:C8	2.40	0.53
1:0:1825:U:O2'	1:0:1826:C:H5'	2.08	0.53
7:D:59:GLY:O	7:D:61:PHE:N	2.35	0.53
9:F:63:ILE:HB	9:F:64:PRO:CD	2.33	0.53
13:J:34:VAL:HG22	13:J:47:ALA:HB2	1.90	0.53
13:J:98:VAL:CG1	13:J:102:GLU:HA	2.38	0.53
16:M:11:ARG:HG3	16:M:14:ARG:HH12	1.72	0.53
18:O:131:PHE:CD1	18:O:137:LEU:HD13	2.43	0.53
22:S:37:GLN:OE1	22:S:118:SER:HA	2.09	0.53
1:0:1516:C:H2'	1:0:1517:U:C6	2.44	0.53
1:0:2247:C:O2'	1:0:2248:C:H5'	2.07	0.53
1:0:2781:U:O2'	1:0:2782:G:H5'	2.08	0.53
6:C:127:ARG:HG2	6:C:127:ARG:NH1	2.20	0.53
31:2:65:THR:HB	31:2:83:TRP:H	1.73	0.53
1:0:111:C:O2'	1:0:112:G:H5'	2.07	0.53
1:0:462:A:C2	30:1:37:HIS:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:861:A:H2'	1:0:862:U:C6	2.43	0.53
1:0:1058:A:H2'	1:0:1060:C:H5''	1.91	0.53
1:0:1934:A:C8	1:0:1935:C:C5	2.96	0.53
1:0:2353:A:O2'	16:M:7:LYS:HB3	2.08	0.53
7:D:57:THR:HG23	7:D:63:ILE:CG2	2.38	0.53
14:K:133:VAL:HG13	38:K:8558:HOH:O	2.09	0.53
15:L:32:ARG:HH21	15:L:123:ASP:HB3	1.74	0.53
15:L:38:VAL:C	15:L:63:VAL:HG13	2.33	0.53
20:Q:18:LEU:HD12	20:Q:143:VAL:CG1	2.38	0.53
25:V:52:VAL:HG22	25:V:53:ALA:H	1.74	0.53
25:V:81:ASP:OD1	25:V:92:ASP:HB2	2.09	0.53
1:0:120:A:H2'	1:0:120:A:N3	2.23	0.53
1:0:280:C:H2'	1:0:281:U:O4'	2.09	0.53
1:0:1132:A:N6	1:0:1229:C:H2'	2.24	0.53
1:0:1701:A:H4'	1:0:1702:U:H5''	1.89	0.53
1:0:2721:U:H4'	13:J:87:ARG:HG3	1.91	0.53
7:D:41:LEU:CA	7:D:44:ILE:HG22	2.37	0.53
7:D:167:GLU:C	7:D:169:THR:H	2.16	0.53
16:M:167:ASP:O	16:M:168:LEU:HD23	2.08	0.53
1:0:703:G:O2'	1:0:704:C:H5'	2.09	0.53
1:0:2712:G:H5'	38:J:4183:HOH:O	2.09	0.53
38:0:4718:HOH:O	15:L:189:VAL:HG21	2.08	0.53
4:A:220:PRO:HD2	4:A:223:ARG:HD3	1.90	0.53
7:D:23:VAL:HG23	7:D:41:LEU:HD22	1.89	0.53
16:M:71:TRP:CE3	16:M:175:LEU:HD22	2.43	0.53
20:Q:118:LYS:HE3	20:Q:139:PRO:HB3	1.91	0.53
25:V:108:ARG:HE	25:V:114:PRO:HG3	1.74	0.53
1:0:661:G:C5	1:0:686:A:C2	2.96	0.53
1:0:1304:U:H2'	1:0:1305:C:C6	2.44	0.53
38:0:5492:HOH:O	15:L:87:MET:HE1	2.09	0.53
2:9:3060:C:O2'	2:9:3061:C:H5'	2.08	0.53
9:F:117:GLU:C	9:F:119:ARG:N	2.67	0.53
10:G:71:LEU:C	10:G:73:ASP:N	2.66	0.53
12:I:46:ILE:HG12	12:I:53:ILE:HD13	1.91	0.53
20:Q:29:LYS:HB3	38:Q:8533:HOH:O	2.08	0.53
24:U:39:ALA:O	24:U:41:GLU:N	2.42	0.53
25:V:10:GLU:HG3	25:V:11:VAL:N	2.24	0.53
1:0:324:G:O2'	1:0:325:U:H5'	2.09	0.53
1:0:1515:A:H2'	1:0:1516:C:C6	2.43	0.53
1:0:1714:C:O2'	1:0:1715:C:H5'	2.08	0.53
1:0:1878:G:O2'	1:0:1879:U:P	2.67	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3041:C:O4'	7:D:50:VAL:HG23	2.08	0.53
5:B:87:TYR:HD1	38:B:8592:HOH:O	1.91	0.53
11:H:75:SER:C	11:H:79:ALA:HB2	2.34	0.53
22:S:35:TYR:CG	22:S:112:LEU:HD22	2.43	0.53
1:0:1829:A:H5''	38:0:4035:HOH:O	2.09	0.52
1:0:1850:U:H2'	1:0:1851:G:C8	2.44	0.52
6:C:130:GLU:HG2	6:C:168:ARG:HD3	1.91	0.52
6:C:175:LYS:HD3	6:C:184:ARG:O	2.09	0.52
12:I:19:MET:HE1	12:I:78:ILE:CG2	2.37	0.52
15:L:87:MET:CB	31:2:46:ILE:HG21	2.38	0.52
15:L:172:GLY:C	15:L:183:VAL:HG11	2.34	0.52
25:V:1:MET:N	25:V:37:GLU:HG3	2.24	0.52
1:0:470:U:O2'	29:Z:16:HIS:CD2	2.61	0.52
1:0:695:C:O2'	1:0:696:C:H5'	2.08	0.52
1:0:858:U:H2'	1:0:859:C:H6	1.74	0.52
1:0:949:U:O2'	19:P:40:HIS:HE1	1.92	0.52
1:0:1899:C:O2'	1:0:1900:A:H5'	2.09	0.52
1:0:2115:U:H2'	1:0:2116:U:C6	2.44	0.52
1:0:2812:A:C2	1:0:2814:A:N6	2.72	0.52
5:B:14:GLY:HA2	5:B:15:PRO:C	2.35	0.52
1:0:1821:A:O2'	1:0:1822:A:H5'	2.09	0.52
4:A:88:ILE:O	4:A:88:ILE:HG22	2.09	0.52
6:C:236:THR:O	6:C:237:GLU:C	2.52	0.52
8:E:7:ILE:HD11	8:E:11:VAL:C	2.34	0.52
9:F:13:GLU:OE2	9:F:78:GLU:HG2	2.09	0.52
11:H:26:LYS:CD	11:H:28:ILE:HB	2.39	0.52
28:Y:31:ILE:HG23	28:Y:32:LYS:N	2.25	0.52
1:0:332:G:O2'	1:0:333:G:H5'	2.10	0.52
1:0:1055:G:OP2	11:H:94:ARG:NH1	2.43	0.52
1:0:1206:U:H5'	1:0:1206:U:C6	2.37	0.52
1:0:1568:G:O2'	1:0:1569:U:H5'	2.08	0.52
1:0:1634:G:H2'	1:0:1635:U:C6	2.44	0.52
1:0:1638:U:O2'	1:0:1639:U:H5'	2.09	0.52
1:0:2468:A:H61	31:2:48:ASN:HD21	1.58	0.52
4:A:94:LEU:HG	4:A:99:ILE:CD1	2.38	0.52
7:D:154:LYS:H	7:D:154:LYS:CD	2.17	0.52
16:M:151:ASP:OD1	16:M:154:LEU:HD13	2.10	0.52
1:0:621:C:H5'	27:X:132:ASP:OD2	2.10	0.52
1:0:858:U:H2'	1:0:859:C:C6	2.43	0.52
1:0:1268:C:H2'	1:0:1269:G:H8	1.75	0.52
1:0:2346:C:H6	1:0:2346:C:O5'	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2346:C:HO2'	7:D:52:THR:HG21	1.74	0.52
2:9:3064:C:H2'	2:9:3065:A:H5'	1.91	0.52
7:D:23:VAL:HG23	7:D:23:VAL:O	2.09	0.52
9:F:49:PHE:O	9:F:95:ALA:HA	2.09	0.52
25:V:65:VAL:CG1	25:V:116:LEU:HD13	2.38	0.52
1:0:221:G:H2'	1:0:222:A:C8	2.44	0.52
1:0:330:C:H5	6:C:170:ASP:OD2	1.92	0.52
1:0:1191:A:C3'	1:0:1192:A:H5''	2.38	0.52
1:0:1787:C:H4'	1:0:2883:A:O4'	2.10	0.52
1:0:2326:U:H4'	1:0:2412:G:H4'	1.90	0.52
1:0:2781:U:C2'	1:0:2782:G:H5'	2.40	0.52
4:A:65:ARG:C	4:A:66:ARG:HG3	2.35	0.52
4:A:192:VAL:O	4:A:207:GLN:HG2	2.10	0.52
11:H:81:TYR:CD1	11:H:81:TYR:C	2.86	0.52
1:0:240:C:O2	1:0:240:C:H2'	2.10	0.52
1:0:1456:C:H2'	1:0:1457:U:C6	2.44	0.52
1:0:1513:C:O2'	1:0:1514:C:H5'	2.10	0.52
1:0:2266:A:OP2	15:L:90:ARG:NH2	2.42	0.52
5:B:101:TRP:HB2	5:B:119:HIS:CD2	2.45	0.52
1:0:269:G:O3'	1:0:274:G:H4'	2.09	0.52
1:0:1134:G:OP2	11:H:156:THR:HG23	2.09	0.52
1:0:1730:G:H5'	1:0:1731:C:C5	2.45	0.52
1:0:2909:G:H2'	1:0:2910:A:H8	1.75	0.52
6:C:236:THR:O	6:C:239:ALA:N	2.43	0.52
7:D:11:HIS:C	7:D:13:MET:H	2.17	0.52
8:E:15:GLN:HG2	8:E:19:ASP:O	2.10	0.52
16:M:62:HIS:HB3	16:M:65:ASP:OD1	2.09	0.52
22:S:9:LYS:HE3	22:S:13:ARG:HH11	1.70	0.52
22:S:71:VAL:HG12	22:S:72:ILE:N	2.23	0.52
25:V:38:THR:HG22	25:V:39:ASP:H	1.74	0.52
1:0:105:G:O2'	1:0:106:A:H5'	2.10	0.52
1:0:226:A:H1'	1:0:393:G:C5	2.45	0.52
1:0:289:G:O2'	1:0:290:C:H5'	2.10	0.52
1:0:1497:G:H4'	1:0:1627:G:O2'	2.10	0.52
1:0:1878:G:O2'	1:0:1879:U:C6	2.60	0.52
1:0:2269:C:H2'	1:0:2270:G:C5'	2.40	0.52
1:0:2903:C:O2'	1:0:2904:U:H5'	2.10	0.52
5:B:36:PRO:HA	5:B:168:GLY:HA2	1.92	0.52
8:E:15:GLN:HB2	8:E:20:ILE:HG23	1.92	0.52
1:0:155:C:O2'	1:0:156:C:H5'	2.10	0.52
1:0:175:G:H2'	15:L:192:ALA:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:542:A:H5'	1:0:542:A:C8	2.37	0.52
1:0:1345:A:H2'	1:0:1346:U:C6	2.45	0.52
1:0:1527:A:H1'	1:0:1528:A:C8	2.45	0.52
7:D:38:GLU:OE2	7:D:51:ARG:CZ	2.57	0.52
9:F:30:LYS:HB2	9:F:97:ALA:HB3	1.91	0.52
11:H:47:GLU:HG2	11:H:133:ILE:HD12	1.91	0.52
16:M:180:LEU:O	16:M:181:ASP:HB3	2.08	0.52
17:N:84:THR:CG2	17:N:88:LYS:HE3	2.40	0.52
22:S:63:ILE:HD11	22:S:75:GLU:HB2	1.91	0.52
1:0:189:A:OP1	15:L:171:ARG:NH2	2.43	0.51
1:0:255:A:H2'	1:0:256:C:C6	2.45	0.51
1:0:1634:G:H2'	1:0:1635:U:H6	1.74	0.51
13:J:98:VAL:HG13	13:J:99:ASP:N	2.24	0.51
19:P:26:PRO:O	19:P:30:VAL:HG23	2.10	0.51
1:0:820:G:C5	4:A:171:LYS:HB2	2.46	0.51
1:0:1820:G:C6	1:0:2030:A:C2	2.98	0.51
1:0:1909:A:N1	1:0:2128:G:H1'	2.25	0.51
1:0:2531:U:O2'	1:0:2532:A:H5'	2.10	0.51
1:0:2781:U:H1'	8:E:139:GLU:OE2	2.10	0.51
5:B:63:GLU:HG3	5:B:63:GLU:O	2.10	0.51
9:F:48:VAL:CG2	9:F:74:PHE:HB3	2.40	0.51
15:L:52:LEU:HD13	15:L:116:ASN:CB	2.40	0.51
15:L:147:LEU:O	15:L:149:TRP:N	2.43	0.51
19:P:42:LYS:NZ	19:P:43:ILE:O	2.42	0.51
22:S:9:LYS:HB2	38:S:7242:HOH:O	2.10	0.51
25:V:13:MET:CE	25:V:17:ILE:HG22	2.39	0.51
25:V:26:ILE:HG13	25:V:26:ILE:O	2.10	0.51
25:V:73:LEU:O	25:V:74:GLU:HG3	2.11	0.51
27:X:178:HIS:CG	27:X:179:PRO:HD2	2.46	0.51
1:0:419:A:H1'	1:0:1921:A:C2	2.45	0.51
1:0:816:G:H5'	1:0:1598:A:H4'	1.93	0.51
1:0:1218:U:H2'	1:0:1219:U:C6	2.44	0.51
1:0:2121:G:H1'	38:0:5481:HOH:O	2.10	0.51
2:9:3007:G:H5'	38:9:8479:HOH:O	2.09	0.51
5:B:304:PRO:CG	5:B:307:ARG:NH1	2.73	0.51
7:D:170:TYR:O	7:D:171:ASP:HB3	2.09	0.51
17:N:96:VAL:HG13	17:N:100:GLN:HB2	1.93	0.51
23:T:6:CYS:C	23:T:8:TYR:H	2.18	0.51
26:W:30:MET:HE3	26:W:55:ASN:OD1	2.09	0.51
1:0:958:G:H2'	1:0:959:C:C6	2.45	0.51
5:B:72:THR:HB	38:B:8619:HOH:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:175:LEU:C	5:B:175:LEU:CD2	2.83	0.51
5:B:280:VAL:HG13	5:B:333:GLU:O	2.10	0.51
8:E:11:VAL:CG1	8:E:12:ASP:N	2.72	0.51
16:M:115:VAL:HG23	38:M:8559:HOH:O	2.10	0.51
28:Y:81:LYS:O	28:Y:82:ALA:C	2.53	0.51
1:O:1159:G:H21	1:O:1189:A:H8	1.58	0.51
5:B:212:GLN:HB2	5:B:257:THR:CG2	2.38	0.51
6:C:173:LYS:HB3	6:C:187:ARG:HG3	1.90	0.51
16:M:154:LEU:O	16:M:155:GLU:CB	2.58	0.51
19:P:32:GLU:HA	19:P:71:TYR:OH	2.11	0.51
22:S:78:THR:HB	22:S:87:VAL:O	2.11	0.51
24:U:64:GLY:O	24:U:65:ASP:CB	2.58	0.51
1:O:39:G:H2'	1:O:40:C:O4'	2.11	0.51
1:O:1385:G:O3'	26:W:49:ARG:NH1	2.43	0.51
1:O:2241:C:O2'	1:O:2242:U:H5'	2.11	0.51
1:O:2346:C:O2'	1:O:2347:C:H5'	2.11	0.51
8:E:31:ARG:HH12	8:E:68:HIS:CE1	2.29	0.51
12:I:90:LYS:HB2	36:I:8502:CL:CL	2.47	0.51
15:L:38:VAL:O	15:L:38:VAL:HG12	2.11	0.51
17:N:96:VAL:CG1	17:N:100:GLN:HB2	2.41	0.51
1:O:184:G:H5''	15:L:153:THR:CG2	2.41	0.51
1:O:506:G:H22	1:O:509:A:H5''	1.73	0.51
1:O:1332:C:O2'	1:O:1333:U:H5'	2.11	0.51
1:O:1810:C:OP1	23:T:44:ARG:NE	2.32	0.51
1:O:2547:C:OP2	5:B:5:ARG:NH1	2.44	0.51
1:O:2598:U:O2	1:O:2600:A:C8	2.63	0.51
1:O:2785:C:H4'	1:O:2786:G:OP2	2.11	0.51
5:B:294:TYR:HE2	38:B:8665:HOH:O	1.94	0.51
6:C:109:LEU:HD12	6:C:109:LEU:O	2.10	0.51
9:F:58:GLU:CD	15:L:27:ARG:HH22	2.18	0.51
11:H:137:ASN:O	11:H:138:PRO:C	2.53	0.51
12:I:77:GLY:O	12:I:78:ILE:C	2.54	0.51
16:M:87:LEU:CD1	16:M:186:LEU:HD21	2.39	0.51
25:V:4:LEU:CD2	25:V:54:PHE:HB3	2.38	0.51
26:W:9:VAL:HG13	26:W:88:GLU:OE2	2.11	0.51
30:1:36:ASN:HB3	30:1:39:ARG:NE	2.25	0.51
31:2:55:VAL:O	31:2:55:VAL:HG23	2.10	0.51
1:O:222:A:H2'	1:O:223:G:O4'	2.10	0.51
1:O:920:C:H5''	1:O:921:G:O5'	2.11	0.51
1:O:1333:U:H2'	1:O:1334:C:H6	1.76	0.51
15:L:27:ARG:NH2	15:L:44:THR:HG23	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:X:99:ALA:HB2	27:X:233:TYR:CE2	2.45	0.51
31:2:14:CYS:HB3	31:2:16:GLU:HG2	1.93	0.51
1:0:1189:A:H1'	1:0:1209:C:O4'	2.11	0.51
1:0:1654:U:H2'	4:A:47:HIS:CD2	2.46	0.51
1:0:1855:G:H4'	1:0:1856:C:O5'	2.09	0.51
1:0:1920:C:O2'	1:0:1921:A:H5'	2.11	0.51
2:9:3045:A:H2'	2:9:3046:C:H6	1.75	0.51
15:L:155:HIS:ND1	15:L:158:ARG:NE	2.54	0.51
28:Y:22:ILE:O	28:Y:26:VAL:HG23	2.11	0.51
31:2:69:TYR:O	31:2:77:ALA:HA	2.10	0.51
1:0:1494:A:O2'	1:0:1505:U:O2	2.28	0.51
1:0:1819:G:H2'	1:0:1820:G:H4'	1.93	0.51
1:0:1849:G:H1'	1:0:2011:A:N1	2.26	0.51
1:0:1855:G:O6	4:A:141:PRO:HG2	2.11	0.51
1:0:2676:C:H4'	12:I:70:PHE:HE1	1.76	0.51
8:E:11:VAL:CG1	8:E:12:ASP:H	2.24	0.51
11:H:26:LYS:HD3	11:H:89:PRO:CG	2.40	0.51
1:0:195:C:H2'	1:0:196:G:H5'	1.93	0.50
1:0:243:A:H61	1:0:269:G:H1'	1.75	0.50
1:0:1079:A:N1	1:0:2068:G:O2'	2.40	0.50
1:0:2314:G:C2'	1:0:2315:C:H5'	2.41	0.50
1:0:2667:G:H1'	1:0:2914:A:N3	2.25	0.50
4:A:200:PRO:HG2	4:A:225:VAL:HG21	1.94	0.50
11:H:85:ILE:HG23	11:H:85:ILE:O	2.11	0.50
21:R:33:SER:OG	21:R:36:GLU:HG3	2.12	0.50
28:Y:26:VAL:O	28:Y:30:GLU:HG3	2.11	0.50
31:2:70:ARG:HG2	31:2:70:ARG:HH11	1.76	0.50
1:0:426:G:H2'	1:0:427:C:O4'	2.12	0.50
6:C:165:ASP:O	6:C:168:ARG:HB3	2.12	0.50
14:K:90:ARG:NH1	14:K:119:THR:HG21	2.26	0.50
16:M:67:ALA:C	16:M:69:TYR:H	2.20	0.50
19:P:75:ILE:HD13	19:P:84:ILE:HD11	1.94	0.50
24:U:20:LEU:HD22	24:U:60:GLN:HE22	1.75	0.50
26:W:85:VAL:HG12	26:W:86:GLU:N	2.26	0.50
1:0:213:G:N2	1:0:225:G:H2'	2.26	0.50
1:0:283:U:H5	1:0:284:C:N4	2.09	0.50
1:0:288:A:H2'	1:0:289:G:C8	2.45	0.50
1:0:1192:A:O2'	1:0:1193:A:OP1	2.29	0.50
1:0:1197:G:N2	38:0:7119:HOH:O	2.39	0.50
1:0:1654:U:H2'	4:A:47:HIS:HD2	1.75	0.50
1:0:2758:G:H2'	1:0:2759:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:125:PHE:CE1	14:K:140:VAL:HG13	2.47	0.50
16:M:24:LEU:HD13	19:P:26:PRO:HB3	1.93	0.50
16:M:67:ALA:C	16:M:69:TYR:N	2.69	0.50
19:P:46:SER:O	19:P:48:PRO:HD3	2.12	0.50
20:Q:119:VAL:O	20:Q:119:VAL:HG12	2.11	0.50
1:0:182:G:O2'	1:0:183:A:H5'	2.12	0.50
1:0:1398:G:O2'	1:0:1399:A:H5'	2.11	0.50
1:0:1804:A:H2'	1:0:1805:G:H8	1.74	0.50
1:0:2540:G:O2'	1:0:2541:U:H5''	2.11	0.50
1:0:2862:G:H4'	5:B:336:GLN:O	2.12	0.50
2:9:3041:C:C6	7:D:50:VAL:HG21	2.47	0.50
5:B:217:ARG:CD	5:B:257:THR:HG22	2.41	0.50
11:H:165:GLY:HA3	38:H:8403:HOH:O	2.11	0.50
11:H:166:ASN:N	11:H:166:ASN:ND2	2.60	0.50
13:J:82:ARG:NH2	13:J:115:ARG:HG2	2.26	0.50
18:O:134:VAL:O	18:O:137:LEU:HB3	2.11	0.50
20:Q:119:VAL:CG2	20:Q:142:ASP:HB2	2.42	0.50
21:R:51:GLN:HB3	21:R:67:ARG:NH1	2.26	0.50
25:V:22:GLU:HG2	25:V:27:HIS:CD2	2.46	0.50
1:0:559:U:H2'	1:0:560:C:O4'	2.11	0.50
1:0:1822:A:O2'	1:0:1823:G:H5'	2.11	0.50
2:9:3002:U:OP2	2:9:3002:U:H4'	2.11	0.50
4:A:100:PRO:O	4:A:103:VAL:HG23	2.11	0.50
7:D:99:ASP:CB	7:D:103:ASN:HB2	2.41	0.50
8:E:16:ASP:O	8:E:17:HIS:HB2	2.11	0.50
8:E:107:PHE:CD2	8:E:108:LEU:HD13	2.47	0.50
8:E:137:ASP:OD1	8:E:139:GLU:HB2	2.11	0.50
23:T:33:SER:O	23:T:37:GLU:HG3	2.12	0.50
25:V:38:THR:O	25:V:42:ARG:HB2	2.11	0.50
31:2:8:ASN:O	31:2:9:THR:HB	2.10	0.50
1:0:20:G:H21	20:Q:117:HIS:HD2	1.60	0.50
1:0:667:C:H2'	1:0:668:C:H6	1.76	0.50
1:0:1008:C:OP1	11:H:16:ARG:NH2	2.44	0.50
1:0:1762:C:O2'	1:0:1763:C:H5'	2.11	0.50
1:0:2453:G:H4'	14:K:50:GLY:C	2.37	0.50
5:B:207:LYS:HG2	5:B:304:PRO:HB3	1.93	0.50
11:H:86:ARG:HD3	11:H:130:HIS:HD2	1.77	0.50
15:L:24:MET:HE3	15:L:28:MET:HE3	1.93	0.50
20:Q:132:ARG:HG2	20:Q:133:ALA:N	2.26	0.50
26:W:9:VAL:HG13	26:W:88:GLU:OE1	2.12	0.50
1:0:241:A:N1	1:0:378:A:H4'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1538:C:O2'	1:0:1539:U:H5'	2.12	0.50
1:0:2626:C:H2'	1:0:2627:G:C8	2.47	0.50
38:0:5742:HOH:O	12:I:47:THR:HB	2.11	0.50
11:H:59:ASN:HD22	11:H:59:ASN:H	1.59	0.50
14:K:104:ASP:HB3	38:K:8569:HOH:O	2.11	0.50
14:K:148:GLU:HA	38:K:8578:HOH:O	2.10	0.50
15:L:166:ALA:HA	15:L:169:ARG:NH1	2.27	0.50
22:S:71:VAL:CG1	22:S:90:PRO:HB3	2.25	0.50
25:V:122:ARG:NH1	25:V:122:ARG:CG	2.74	0.50
1:0:151:A:C2	1:0:442:A:C8	3.00	0.50
1:0:2101:A:H2'	6:C:63:SER:OG	2.11	0.50
1:0:2251:G:H2'	1:0:2252:A:C8	2.46	0.50
1:0:2699:A:H2'	1:0:2700:G:O4'	2.11	0.50
38:0:5524:HOH:O	17:N:35:LYS:HD3	2.12	0.50
6:C:237:GLU:HB2	38:C:8441:HOH:O	2.11	0.50
7:D:57:THR:HG23	7:D:63:ILE:CB	2.42	0.50
9:F:91:VAL:CG1	9:F:92:GLY:H	2.25	0.50
11:H:130:HIS:CG	11:H:133:ILE:HD11	2.47	0.50
18:O:38:GLU:HA	18:O:41:ARG:NH1	2.27	0.50
20:Q:111:ILE:HG23	20:Q:145:LEU:HD11	1.92	0.50
22:S:48:VAL:HG22	22:S:98:VAL:HA	1.92	0.50
25:V:60:GLU:O	25:V:63:GLU:HB2	2.12	0.50
25:V:63:GLU:HG2	25:V:93:ILE:HG22	1.92	0.50
28:Y:38:LYS:CE	28:Y:45:LYS:HE2	2.38	0.50
1:0:90:A:H2'	1:0:91:G:O4'	2.12	0.50
1:0:154:C:P	15:L:188:ARG:HH12	2.34	0.50
1:0:352:A:H2'	1:0:353:G:H8	1.75	0.50
1:0:353:G:H2'	1:0:354:A:C8	2.46	0.50
1:0:1171:A:H2'	1:0:1172:G:H5'	1.94	0.50
1:0:1463:A:H2'	1:0:1464:U:C6	2.47	0.50
1:0:2541:U:H2'	1:0:2542:C:C6	2.47	0.50
38:0:4491:HOH:O	15:L:152:ARG:HG3	2.12	0.50
4:A:199:HIS:CD2	4:A:201:PHE:HB2	2.47	0.50
5:B:304:PRO:HD2	5:B:307:ARG:NH1	2.27	0.50
7:D:97:GLN:HG2	7:D:97:GLN:O	2.11	0.50
11:H:59:ASN:N	11:H:59:ASN:ND2	2.56	0.50
11:H:112:ARG:O	11:H:113:ALA:C	2.55	0.50
11:H:142:VAL:HG13	38:H:8387:HOH:O	2.12	0.50
13:J:49:LEU:HD21	13:J:74:VAL:O	2.12	0.50
22:S:19:ARG:HD3	22:S:67:LEU:O	2.12	0.50
1:0:281:U:O2'	1:0:282:C:H5'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:354:A:H2'	1:0:355:C:C6	2.47	0.49
1:0:694:A:C2'	1:0:695:C:H5'	2.42	0.49
1:0:962:C:H2'	1:0:963:C:H5'	1.94	0.49
1:0:1266:U:H4'	27:X:115:ARG:HH21	1.76	0.49
1:0:2416:G:H2'	1:0:2417:C:C6	2.47	0.49
1:0:2818:A:H2	38:B:8648:HOH:O	1.93	0.49
6:C:166:ILE:HD13	6:C:207:LEU:HD22	1.93	0.49
12:I:93:ARG:HH11	12:I:93:ARG:CB	2.25	0.49
13:J:22:ASP:C	13:J:22:ASP:OD1	2.55	0.49
16:M:161:GLY:O	16:M:162:ASP:C	2.54	0.49
18:O:71:LYS:HG3	18:O:71:LYS:O	2.12	0.49
18:O:98:ILE:HD12	18:O:102:ARG:NE	2.27	0.49
26:W:14:LEU:HD12	26:W:67:PRO:O	2.12	0.49
1:0:396:U:OP2	31:2:38:ARG:NH1	2.37	0.49
1:0:1174:A:C5	1:0:1201:C:H4'	2.46	0.49
1:0:2547:C:H2'	1:0:2548:C:H6	1.77	0.49
1:0:2911:C:H2'	1:0:2912:C:C6	2.48	0.49
5:B:53:LEU:HD21	5:B:270:ILE:HD12	1.94	0.49
5:B:162:MET:HE2	5:B:310:ARG:CG	2.42	0.49
6:C:126:ASP:C	6:C:128:GLY:N	2.70	0.49
7:D:40:ILE:HG23	38:D:5583:HOH:O	2.11	0.49
12:I:39:VAL:HG11	12:I:107:ASN:HB2	1.92	0.49
14:K:143:THR:CG2	14:K:144:ASP:N	2.76	0.49
1:0:297:U:H2'	1:0:298:C:C6	2.47	0.49
1:0:1425:G:O2'	1:0:1426:C:H5'	2.12	0.49
1:0:1925:G:O2'	1:0:1926:G:H5'	2.12	0.49
1:0:2028:U:H2'	1:0:2029:C:H6	1.78	0.49
1:0:2587:U:H2'	1:0:2589:U:H5''	1.94	0.49
2:9:3017:G:O2'	2:9:3018:U:H5'	2.12	0.49
6:C:164:ALA:O	6:C:167:ASP:HB2	2.12	0.49
8:E:34:TRP:O	12:I:127:ILE:HD11	2.12	0.49
9:F:27:GLY:HA3	9:F:101:ALA:O	2.12	0.49
27:X:189:ASN:C	27:X:189:ASN:ND2	2.67	0.49
29:Z:8:GLN:HE22	29:Z:11:LYS:NZ	2.11	0.49
30:1:41:HIS:N	30:1:45:ASN:HD22	2.02	0.49
1:0:119:A:H2'	1:0:120:A:H5''	1.95	0.49
1:0:214:U:H5'	38:0:7028:HOH:O	2.11	0.49
1:0:657:G:H2'	1:0:658:C:C6	2.48	0.49
1:0:962:C:C2'	1:0:963:C:H5'	2.42	0.49
1:0:1483:C:O2'	1:0:1484:G:H5'	2.12	0.49
1:0:1935:C:H2'	1:0:1936:C:H6	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3023:U:C3'	2:9:3024:U:C5'	2.87	0.49
5:B:243:ASN:HA	5:B:244:PRO:C	2.36	0.49
14:K:101:ASP:C	14:K:103:ALA:H	2.20	0.49
16:M:159:TYR:HE2	16:M:163:PHE:HE2	1.60	0.49
19:P:72:LYS:HG2	19:P:85:ILE:HD13	1.93	0.49
25:V:90:TYR:N	25:V:90:TYR:CD1	2.80	0.49
25:V:107:LEU:O	25:V:112:LEU:HB2	2.11	0.49
1:0:21:G:H5''	20:Q:1:GLY:O	2.12	0.49
1:0:1213:C:O2'	1:0:1214:G:H5'	2.12	0.49
1:0:1687:C:O2	29:Z:9:GLY:HA2	2.13	0.49
1:0:1834:C:H2'	1:0:1840:A:H62	1.75	0.49
1:0:1902:G:O2'	1:0:1903:U:H5'	2.12	0.49
1:0:2478:U:H2'	1:0:2479:A:C8	2.47	0.49
4:A:194:MET:HE1	38:A:8518:HOH:O	2.13	0.49
5:B:329:TYR:CE2	23:T:15:PRO:HG2	2.48	0.49
15:L:87:MET:HG2	31:2:46:ILE:HG21	1.94	0.49
16:M:110:THR:HB	16:M:113:SER:OG	2.12	0.49
18:O:13:VAL:HG21	18:O:41:ARG:HG2	1.94	0.49
20:Q:111:ILE:HG23	20:Q:145:LEU:CD1	2.42	0.49
30:1:40:ARG:HG2	30:1:40:ARG:NH1	2.28	0.49
30:1:41:HIS:O	30:1:45:ASN:HB2	2.11	0.49
1:0:74:A:H2'	1:0:75:U:C6	2.47	0.49
1:0:853:C:H2'	1:0:854:G:O4'	2.12	0.49
1:0:1205:U:H2'	1:0:1206:U:H5''	1.94	0.49
1:0:2446:G:H2'	1:0:2447:A:H8	1.78	0.49
1:0:2563:U:H2'	1:0:2565:C:O5'	2.12	0.49
5:B:304:PRO:CD	5:B:307:ARG:NH1	2.76	0.49
6:C:107:ARG:HB3	6:C:107:ARG:HH11	1.74	0.49
8:E:93:MET:HE1	8:E:165:GLY:N	2.27	0.49
9:F:26:THR:HG21	9:F:103:ALA:CB	2.43	0.49
12:I:6:PHE:HB3	12:I:109:TYR:OH	2.12	0.49
13:J:6:ALA:HB3	13:J:116:GLU:HG2	1.93	0.49
16:M:22:GLN:HG2	16:M:26:LEU:HD22	1.95	0.49
25:V:4:LEU:O	25:V:32:CYS:HA	2.12	0.49
1:0:894:A:C2	6:C:87:ARG:NH2	2.81	0.49
1:0:1563:G:O2'	1:0:1564:C:OP2	2.23	0.49
1:0:1735:C:O2'	1:0:1736:A:H5'	2.13	0.49
38:O:4656:HOH:O	15:L:157:LEU:HD11	2.12	0.49
2:9:3014:G:H5'	2:9:3014:G:C8	2.47	0.49
2:9:3035:C:H5''	38:9:8457:HOH:O	2.12	0.49
11:H:62:GLU:HA	38:H:8390:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:82:GLU:O	20:Q:86:LYS:HG3	2.13	0.49
22:S:71:VAL:CG1	22:S:72:ILE:N	2.75	0.49
25:V:115:THR:HG23	38:V:5420:HOH:O	2.12	0.49
1:0:182:G:H5'	38:0:6059:HOH:O	2.13	0.49
1:0:1994:A:P	13:J:66:ARG:HH22	2.36	0.49
2:9:3041:C:H4'	7:D:48:MET:HB2	1.94	0.49
4:A:99:ILE:O	4:A:131:HIS:HE1	1.96	0.49
5:B:5:ARG:HD2	5:B:8:LYS:HZ3	1.77	0.49
7:D:58:VAL:HG12	7:D:59:GLY:N	2.27	0.49
8:E:137:ASP:O	8:E:141:VAL:HG23	2.13	0.49
11:H:131:ILE:HG23	11:H:132:PHE:CD1	2.48	0.49
11:H:139:ASP:HA	38:H:8375:HOH:O	2.13	0.49
11:H:139:ASP:O	11:H:139:ASP:CG	2.56	0.49
15:L:164:THR:HB	38:L:8519:HOH:O	2.12	0.49
18:O:115:SER:C	18:O:117:SER:H	2.20	0.49
25:V:67:ALA:HB2	25:V:93:ILE:HD13	1.93	0.49
29:Z:28:HIS:O	29:Z:32:LYS:N	2.40	0.49
1:0:612:U:H2'	1:0:613:C:C6	2.48	0.49
1:0:684:G:H2'	1:0:685:C:C6	2.48	0.49
1:0:849:C:O2'	1:0:850:U:H5'	2.12	0.49
1:0:1181:A:O2'	1:0:1182:C:H5'	2.12	0.49
1:0:1768:C:H2'	1:0:1769:C:O4'	2.13	0.49
1:0:2252:A:C5	1:0:2253:G:H1'	2.47	0.49
1:0:2377:U:H6	1:0:2377:U:O5'	1.95	0.49
6:C:84:VAL:O	6:C:85:LYS:HB2	2.13	0.49
6:C:174:ILE:HD13	6:C:185:LYS:HE2	1.94	0.49
9:F:46:GLU:OE1	9:F:100:ASP:HA	2.13	0.49
12:I:93:ARG:HB3	12:I:93:ARG:NH1	2.24	0.49
1:0:682:A:H2'	1:0:683:G:O4'	2.11	0.49
1:0:939:A:N1	1:0:1027:G:O2'	2.46	0.49
1:0:1029:U:O2'	1:0:1273:C:OP1	2.31	0.49
1:0:1086:A:C6	25:V:11:VAL:HG11	2.47	0.49
1:0:1162:G:H2'	1:0:1162:G:N3	2.27	0.49
1:0:1450:C:C4'	1:0:1451:C:OP2	2.55	0.49
1:0:1942:A:O2'	1:0:1943:C:H5'	2.13	0.49
5:B:274:GLU:HA	5:B:292:GLY:O	2.12	0.49
6:C:84:VAL:HG12	6:C:85:LYS:HG2	1.93	0.49
7:D:99:ASP:CB	7:D:103:ASN:H	2.25	0.49
10:G:64:ASN:N	10:G:64:ASN:ND2	2.60	0.49
18:O:13:VAL:HG11	18:O:40:VAL:CG1	2.42	0.49
24:U:1:THR:HG23	24:U:2:VAL:N	2.23	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:X:235:GLU:CD	27:X:235:GLU:N	2.71	0.49
1:O:776:A:OP1	29:Z:28:HIS:HE1	1.95	0.48
1:O:887:G:H2'	1:O:888:U:C6	2.48	0.48
1:O:1203:G:O2'	1:O:1204:C:H5'	2.13	0.48
1:O:1808:C:O2'	1:O:1809:G:H5'	2.13	0.48
1:O:2406:U:O2'	1:O:2407:G:H5'	2.13	0.48
1:O:2504:A:H2'	1:O:2505:G:O4'	2.13	0.48
1:O:2668:G:H2'	1:O:2669:U:H6	1.78	0.48
4:A:200:PRO:HD3	38:A:8522:HOH:O	2.12	0.48
6:C:235:PHE:CE2	6:C:243:VAL:HG21	2.44	0.48
7:D:173:GLU:O	7:D:174:VAL:C	2.56	0.48
8:E:54:ASP:N	8:E:54:ASP:OD1	2.46	0.48
13:J:34:VAL:HB	38:J:7169:HOH:O	2.12	0.48
15:L:37:VAL:CG1	15:L:63:VAL:HG11	2.43	0.48
18:O:59:ARG:HH22	18:O:66:GLN:NE2	2.11	0.48
30:1:18:ASN:HD21	30:1:40:ARG:H	1.61	0.48
1:O:1007:A:H2'	11:H:19:TYR:CZ	2.48	0.48
1:O:1375:A:O2'	1:O:1376:G:H5'	2.12	0.48
1:O:1778:A:H2'	1:O:1779:A:H5'	1.94	0.48
1:O:2296:C:H2'	1:O:2297:U:H6	1.78	0.48
2:9:3042:C:O2	7:D:76:ARG:NH1	2.46	0.48
7:D:93:LEU:HB3	7:D:97:GLN:OE1	2.13	0.48
15:L:164:THR:HG23	15:L:165:SER:H	1.75	0.48
16:M:72:GLU:HB3	16:M:171:HIS:HE1	1.78	0.48
1:O:1210:G:O2'	1:O:1211:G:H5'	2.14	0.48
1:O:1535:G:H2'	1:O:1536:C:H6	1.78	0.48
1:O:2791:U:C1'	1:O:2792:A:H5''	2.43	0.48
2:9:3004:G:O2'	16:M:44:ARG:NH2	2.46	0.48
5:B:52:VAL:C	5:B:53:LEU:HD12	2.38	0.48
7:D:146:LYS:HE2	16:M:107:ASN:ND2	2.28	0.48
19:P:32:GLU:O	19:P:93:ARG:NH2	2.45	0.48
25:V:88:THR:CG2	25:V:89:ASP:H	2.21	0.48
27:X:126:PRO:HG2	27:X:128:PHE:CE1	2.47	0.48
28:Y:56:MET:HE2	28:Y:63:LYS:HG3	1.94	0.48
1:O:120:A:H5'	29:Z:20:ARG:HH21	1.78	0.48
1:O:821:U:H2'	1:O:822:C:H6	1.78	0.48
1:O:1015:C:H2'	1:O:1016:U:C6	2.48	0.48
1:O:1189:A:O2'	1:O:1208:C:H2'	2.12	0.48
1:O:1829:A:C2'	1:O:1830:C:H5'	2.43	0.48
1:O:2089:A:O2'	1:O:2090:G:H5'	2.13	0.48
9:F:32:GLY:N	38:F:3111:HOH:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:107:ASN:HD22	12:I:107:ASN:C	2.20	0.48
13:J:49:LEU:HA	13:J:73:VAL:HG12	1.95	0.48
25:V:11:VAL:O	25:V:12:ASN:HB2	2.14	0.48
1:0:344:C:H2'	1:0:345:G:O4'	2.13	0.48
1:0:638:C:H2'	1:0:639:A:H8	1.77	0.48
1:0:678:G:OP2	6:C:107:ARG:NH2	2.46	0.48
1:0:2387:U:H2'	1:0:2388:C:C6	2.48	0.48
9:F:50:VAL:CG2	9:F:63:ILE:HG21	2.43	0.48
14:K:40:PHE:CD1	14:K:41:HIS:N	2.82	0.48
20:Q:114:VAL:HA	20:Q:144:GLU:O	2.13	0.48
23:T:52:THR:HG21	23:T:54:THR:HB	1.95	0.48
24:U:55:ARG:O	24:U:59:ILE:HG12	2.14	0.48
25:V:13:MET:HE3	25:V:17:ILE:HG22	1.95	0.48
31:2:70:ARG:HG2	31:2:70:ARG:NH1	2.28	0.48
1:0:182:G:O3'	15:L:157:LEU:CD1	2.62	0.48
1:0:229:G:O2'	1:0:230:C:H5'	2.13	0.48
1:0:707:C:C2	1:0:708:A:C8	3.02	0.48
1:0:1166:A:H2'	1:0:1166:A:N3	2.28	0.48
1:0:1422:U:H2'	1:0:1423:C:H6	1.77	0.48
1:0:1882:C:O2'	1:0:2012:U:OP2	2.32	0.48
1:0:2502:C:O2'	1:0:2503:A:H5'	2.13	0.48
1:0:2858:U:H2'	1:0:2859:C:C6	2.48	0.48
2:9:3023:U:H5''	2:9:3023:U:C6	2.49	0.48
2:9:3026:C:O2'	2:9:3027:C:H5'	2.14	0.48
2:9:3063:C:O2'	2:9:3064:C:H5'	2.14	0.48
4:A:194:MET:HE3	4:A:199:HIS:CB	2.29	0.48
5:B:162:MET:HE2	5:B:310:ARG:CD	2.43	0.48
5:B:215:VAL:HA	5:B:220:VAL:HG22	1.94	0.48
7:D:56:ARG:N	38:D:6752:HOH:O	2.46	0.48
7:D:95:THR:CG2	7:D:174:VAL:HG22	2.43	0.48
11:H:157:ILE:CG2	11:H:158:ASN:N	2.77	0.48
15:L:108:LYS:HD3	15:L:108:LYS:N	2.28	0.48
18:O:94:TRP:CZ2	18:O:98:ILE:HG13	2.48	0.48
19:P:30:VAL:O	19:P:30:VAL:HG12	2.13	0.48
21:R:50:GLU:OE2	21:R:69:SER:HB3	2.14	0.48
22:S:40:VAL:HG22	22:S:41:ARG:N	2.28	0.48
25:V:122:ARG:HG2	25:V:152:ALA:O	2.14	0.48
26:W:43:VAL:CG1	26:W:44:ASP:N	2.75	0.48
26:W:51:ASP:OD2	26:W:52:PRO:HD2	2.14	0.48
27:X:117:LEU:HD12	27:X:174:VAL:HG11	1.95	0.48
1:0:272:A:H5'	1:0:273:G:OP2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1321:A:H2'	1:0:1322:G:C8	2.49	0.48
1:0:2270:G:H4'	4:A:223:ARG:NH1	2.29	0.48
1:0:2348:C:H2'	1:0:2349:G:H8	1.78	0.48
1:0:2821:C:H4'	5:B:116:PRO:HB3	1.95	0.48
5:B:146:THR:O	5:B:148:PRO:HD3	2.14	0.48
5:B:179:LEU:O	5:B:183:GLU:HG2	2.13	0.48
6:C:51:TYR:CE2	29:Z:53:LYS:HB3	2.48	0.48
6:C:129:HIS:CE1	6:C:231:ARG:HA	2.49	0.48
7:D:95:THR:C	7:D:97:GLN:N	2.71	0.48
11:H:163:PRO:O	11:H:164:ALA:HB2	2.14	0.48
21:R:73:ASP:OD1	21:R:75:GLN:HB2	2.14	0.48
1:0:549:A:O2'	1:0:550:C:H5'	2.14	0.48
1:0:906:C:OP2	27:X:147:ARG:NH2	2.46	0.48
1:0:1900:A:H2'	1:0:1901:G:H8	1.78	0.48
1:0:1905:U:H2'	1:0:1906:C:H6	1.79	0.48
1:0:1972:U:C2'	1:0:1973:A:H5'	2.43	0.48
38:0:3375:HOH:O	15:L:94:LYS:HE2	2.13	0.48
4:A:135:VAL:HG11	4:A:147:ARG:NH2	2.29	0.48
5:B:87:TYR:O	5:B:138:GLY:N	2.39	0.48
5:B:279:THR:HG22	5:B:280:VAL:N	2.29	0.48
15:L:85:ARG:C	15:L:87:MET:HG3	2.39	0.48
18:O:115:SER:O	18:O:117:SER:N	2.46	0.48
23:T:5:GLU:CG	23:T:10:GLY:O	2.61	0.48
24:U:12:THR:HG23	24:U:14:ALA:H	1.78	0.48
25:V:13:MET:HE3	25:V:17:ILE:CG2	2.43	0.48
1:0:466:A:H2'	1:0:467:G:O4'	2.13	0.48
1:0:1114:A:O2'	1:0:1115:U:H5'	2.12	0.48
1:0:1154:A:H2'	1:0:1155:G:H8	1.77	0.48
1:0:1218:U:H2'	1:0:1219:U:H6	1.79	0.48
1:0:1308:A:H2'	1:0:1309:U:H6	1.78	0.48
5:B:147:VAL:HG12	5:B:150:ALA:H	1.78	0.48
5:B:180:ASP:O	5:B:181:ILE:C	2.57	0.48
7:D:128:LEU:C	7:D:128:LEU:HD23	2.39	0.48
8:E:80:TRP:O	8:E:134:SER:HA	2.13	0.48
26:W:9:VAL:HG13	26:W:88:GLU:CD	2.38	0.48
27:X:187:VAL:HG12	27:X:205:ILE:HA	1.96	0.48
31:2:69:TYR:CB	31:2:78:HIS:CE1	2.97	0.48
1:0:598:C:H2'	1:0:599:G:H8	1.78	0.48
1:0:1268:C:H2'	1:0:1269:G:C8	2.49	0.48
1:0:1462:C:H2'	1:0:1463:A:C8	2.49	0.48
1:0:1573:A:H2'	1:0:1574:C:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:1652:C:O4'	4:A:164:ARG:HG3	2.14	0.48
1:O:2015:A:H2'	1:O:2016:U:O4'	2.13	0.48
5:B:81:ALA:O	5:B:186:GLY:HA3	2.13	0.48
5:B:168:GLY:H	5:B:174:ARG:HH11	1.62	0.48
6:C:21:VAL:C	6:C:23:GLU:N	2.72	0.48
8:E:84:MET:HE1	8:E:148:ILE:HD12	1.96	0.48
14:K:144:ASP:O	14:K:147:GLU:HB2	2.13	0.48
26:W:85:VAL:HG12	26:W:86:GLU:H	1.78	0.48
29:Z:5:THR:HB	29:Z:6:PRO:CD	2.44	0.48
1:O:396:U:O2'	1:O:418:C:H4'	2.13	0.47
1:O:764:C:H2'	1:O:765:G:O4'	2.14	0.47
1:O:1289:C:H3'	38:O:7289:HOH:O	2.14	0.47
1:O:1298:U:H2'	1:O:1299:G:C8	2.49	0.47
1:O:2044:G:OP1	26:W:23:HIS:HE1	1.97	0.47
1:O:2523:U:O2'	1:O:2524:G:H5'	2.13	0.47
1:O:2735:U:H2'	1:O:2736:U:C6	2.49	0.47
38:9:8479:HOH:O	16:M:18:THR:HG21	2.14	0.47
5:B:43:GLY:O	5:B:308:LEU:HD12	2.13	0.47
5:B:76:THR:N	5:B:77:PRO:HD3	2.28	0.47
6:C:118:THR:CG2	6:C:137:PRO:HB3	2.44	0.47
6:C:132:ASP:HB3	38:C:8371:HOH:O	2.14	0.47
11:H:26:LYS:HG2	11:H:28:ILE:N	2.19	0.47
11:H:72:VAL:HG11	11:H:81:TYR:CZ	2.49	0.47
12:I:103:VAL:HG12	38:I:5907:HOH:O	2.13	0.47
13:J:101:ASN:HB2	13:J:103:ASP:OD2	2.14	0.47
14:K:24:ALA:CB	14:K:30:ARG:HD2	2.44	0.47
22:S:41:ARG:NH1	22:S:42:VAL:O	2.47	0.47
31:2:16:GLU:HG3	31:2:18:GLN:HE21	1.79	0.47
1:O:1717:A:H5''	18:O:54:LYS:HB2	1.96	0.47
1:O:1847:A:OP1	4:A:175:LYS:HG3	2.14	0.47
1:O:2503:A:OP1	11:H:147:ARG:NH2	2.44	0.47
1:O:2539:U:C4	32:O:9500:SLD:H7	2.49	0.47
6:C:236:THR:H	6:C:239:ALA:HB3	1.78	0.47
8:E:7:ILE:CG2	8:E:45:ASP:O	2.62	0.47
9:F:28:ALA:HB3	9:F:99:THR:HG23	1.95	0.47
11:H:39:GLY:O	11:H:41:THR:N	2.47	0.47
11:H:69:ASN:O	11:H:72:VAL:HG12	2.14	0.47
14:K:38:HIS:CD2	14:K:39:GLU:HG3	2.49	0.47
14:K:53:ARG:NH2	14:K:57:VAL:HG12	2.29	0.47
1:O:157:G:H4'	15:L:95:LYS:CE	2.43	0.47
1:O:711:G:HI'	38:O:7966:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1266:U:O2'	1:0:1267:C:H5'	2.14	0.47
1:0:1701:A:H5'	38:0:7166:HOH:O	2.13	0.47
1:0:1761:U:H5'	18:O:81:LYS:O	2.14	0.47
4:A:114:ASP:HB2	4:A:117:LYS:HE2	1.96	0.47
4:A:164:ARG:HA	28:Y:69:TYR:HE1	1.78	0.47
5:B:211:THR:HA	5:B:255:GLY:O	2.14	0.47
6:C:240:LEU:HD23	6:C:240:LEU:O	2.13	0.47
25:V:88:THR:CG2	25:V:110:GLN:NE2	2.72	0.47
25:V:119:HIS:CB	38:V:4276:HOH:O	2.62	0.47
1:0:310:U:H2'	1:0:311:C:C6	2.49	0.47
1:0:1851:G:O2'	1:0:1852:A:H5'	2.14	0.47
2:9:3114:G:H2'	2:9:3115:C:C6	2.49	0.47
11:H:26:LYS:HD2	11:H:28:ILE:CG1	2.45	0.47
15:L:64:ARG:HD2	38:L:8587:HOH:O	2.13	0.47
28:Y:27:ALA:O	28:Y:28:ASP:C	2.57	0.47
1:0:431:G:O2'	1:0:432:G:H5'	2.13	0.47
1:0:536:A:N1	1:0:2075:G:O2'	2.47	0.47
1:0:1594:C:OP2	18:O:120:ARG:HD2	2.15	0.47
1:0:1603:A:H5'	1:0:1605:G:C4'	2.45	0.47
1:0:1782:G:O2'	1:0:1783:A:H5'	2.15	0.47
1:0:2255:A:O2'	1:0:2256:G:H5'	2.14	0.47
1:0:2266:A:H2'	1:0:2267:G:H8	1.77	0.47
1:0:2362:A:H2'	1:0:2363:G:C8	2.50	0.47
1:0:2437:A:H2'	1:0:2438:G:H8	1.79	0.47
1:0:2473:U:O3'	1:0:2474:A:H3'	2.13	0.47
2:9:3047:A:C2	2:9:3048:C:C2	3.02	0.47
4:A:99:ILE:O	4:A:131:HIS:CE1	2.68	0.47
6:C:178:GLN:O	6:C:179:GLY:C	2.58	0.47
7:D:153:THR:O	7:D:156:ARG:HB2	2.14	0.47
11:H:140:PRO:HB3	38:H:8387:HOH:O	2.14	0.47
13:J:125:ALA:C	13:J:127:ALA:H	2.21	0.47
14:K:124:ASP:OD1	14:K:125:PHE:N	2.47	0.47
22:S:24:ARG:HH21	22:S:39:ASN:ND2	2.12	0.47
26:W:26:ALA:O	26:W:27:ASP:C	2.57	0.47
1:0:288:A:H2'	1:0:289:G:H8	1.80	0.47
1:0:1592:G:O2'	1:0:1593:C:O5'	2.32	0.47
1:0:1927:A:O2'	1:0:1928:C:H5'	2.14	0.47
4:A:36:ASP:CB	4:A:85:ASP:H	2.27	0.47
4:A:153:ARG:HH11	4:A:153:ARG:CB	2.27	0.47
5:B:82:VAL:HG12	5:B:101:TRP:CE3	2.48	0.47
5:B:320:GLN:HG3	5:B:321:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:182:LYS:HD2	15:L:193:LYS:HB2	1.96	0.47
17:N:39:THR:O	17:N:115:ARG:NH2	2.47	0.47
22:S:24:ARG:HH21	22:S:39:ASN:HD22	1.60	0.47
24:U:39:ALA:C	24:U:41:GLU:N	2.72	0.47
1:0:319:A:H4'	1:0:338:C:C5	2.50	0.47
1:0:326:G:O2'	1:0:327:A:H5'	2.14	0.47
1:0:941:G:C5	1:0:942:U:C4	3.03	0.47
1:0:945:U:H2'	1:0:946:C:C6	2.50	0.47
1:0:1151:G:OP1	10:G:63:ARG:NH1	2.47	0.47
1:0:1593:C:H5'	18:O:116:SER:O	2.14	0.47
1:0:1624:A:H5'	1:0:1626:A:O4'	2.15	0.47
1:0:1741:U:O2'	1:0:2723:G:H4'	2.15	0.47
1:0:1792:C:H2'	1:0:1793:C:H6	1.78	0.47
1:0:1872:C:H5	4:A:20:SER:HB3	1.80	0.47
1:0:2388:C:O2'	1:0:2389:U:H5'	2.15	0.47
2:9:3029:C:C2'	2:9:3030:C:H5'	2.43	0.47
4:A:95:PRO:HA	4:A:153:ARG:HA	1.97	0.47
5:B:51:VAL:CG2	5:B:327:VAL:HG13	2.45	0.47
5:B:175:LEU:O	5:B:178:ALA:HB3	2.14	0.47
6:C:7:ASP:C	6:C:9:ASP:H	2.22	0.47
8:E:84:MET:HE2	8:E:133:VAL:HG23	1.97	0.47
11:H:35:ASN:ND2	11:H:79:ALA:O	2.46	0.47
15:L:49:ALA:C	15:L:54:TYR:HB3	2.40	0.47
16:M:152:GLU:C	16:M:154:LEU:N	2.72	0.47
16:M:154:LEU:HD11	16:M:157:PRO:HA	1.97	0.47
18:O:84:ALA:C	18:O:86:ALA:N	2.73	0.47
26:W:27:ASP:OD2	26:W:27:ASP:N	2.41	0.47
27:X:234:VAL:HG12	27:X:235:GLU:N	2.29	0.47
31:2:7:PHE:HD1	31:2:8:ASN:O	1.97	0.47
1:0:183:A:H5'	15:L:157:LEU:HD12	1.97	0.47
1:0:474:C:O3'	6:C:73:LEU:CD2	2.62	0.47
1:0:820:G:H5'	1:0:821:U:H5'	1.97	0.47
1:0:946:C:H2'	1:0:947:U:C6	2.49	0.47
1:0:1299:G:N7	14:K:6:ARG:NH1	2.62	0.47
1:0:1307:A:H2'	1:0:1308:A:C8	2.50	0.47
1:0:1921:A:C6	1:0:1922:A:C2	3.03	0.47
1:0:2112:A:H2'	1:0:2113:G:H8	1.79	0.47
1:0:2435:U:H1'	38:O:6323:HOH:O	2.13	0.47
1:0:2897:C:O2'	1:0:2898:G:H5'	2.15	0.47
1:0:2898:G:O2'	1:0:2899:A:H5'	2.15	0.47
6:C:242:GLU:HG3	38:C:8390:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:100:ASP:O	9:F:101:ALA:O	2.33	0.47
14:K:40:PHE:CD1	14:K:40:PHE:C	2.92	0.47
14:K:90:ARG:HH11	14:K:119:THR:HG21	1.80	0.47
16:M:61:ALA:HB3	16:M:88:ALA:HB2	1.97	0.47
22:S:48:VAL:CG2	22:S:98:VAL:HA	2.45	0.47
1:O:65:C:O2'	1:O:66:G:H5'	2.15	0.47
1:O:553:G:O4'	1:O:1325:G:H5'	2.15	0.47
1:O:2687:G:O2'	1:O:2688:U:H5'	2.15	0.47
38:O:5858:HOH:O	2:9:3103:A:H4'	2.14	0.47
5:B:177:HIS:NE2	5:B:181:ILE:HD11	2.29	0.47
6:C:139:VAL:HG21	6:C:240:LEU:HD12	1.97	0.47
7:D:25:MET:HE2	7:D:41:LEU:CG	2.22	0.47
11:H:71:TYR:C	11:H:73:GLN:N	2.71	0.47
11:H:72:VAL:CG1	11:H:81:TYR:CZ	2.98	0.47
12:I:39:VAL:CG1	12:I:107:ASN:HB2	2.44	0.47
13:J:49:LEU:HA	13:J:73:VAL:CG1	2.45	0.47
1:O:1217:G:H2'	1:O:1218:U:C6	2.50	0.47
1:O:1701:A:H4'	1:O:1702:U:C5'	2.44	0.47
1:O:1800:G:O2'	1:O:1801:A:H5'	2.14	0.47
1:O:2326:U:H4'	1:O:2412:G:C4'	2.45	0.47
1:O:2729:C:H2'	1:O:2730:G:H8	1.79	0.47
1:O:2858:U:H2'	1:O:2859:C:H6	1.80	0.47
7:D:91:ALA:HB1	38:D:5198:HOH:O	2.13	0.47
7:D:166:ILE:HB	38:D:6326:HOH:O	2.15	0.47
9:F:39:SER:HB3	9:F:45:ALA:HB2	1.97	0.47
9:F:99:THR:O	9:F:99:THR:HG23	2.14	0.47
10:G:67:LEU:O	10:G:71:LEU:HG	2.14	0.47
16:M:42:HIS:CG	16:M:62:HIS:HE1	2.33	0.47
25:V:149:LEU:CG	25:V:153:MET:HE2	2.27	0.47
31:2:70:ARG:CG	31:2:77:ALA:HB2	2.40	0.47
1:O:289:G:N1	1:O:363:A:C2	2.78	0.46
1:O:317:A:OP1	22:S:52:ARG:O	2.32	0.46
1:O:383:A:H4'	38:O:6225:HOH:O	2.15	0.46
1:O:581:G:O2'	1:O:582:C:H5'	2.15	0.46
1:O:1181:A:H2'	1:O:1182:C:O4'	2.14	0.46
1:O:1584:C:O2'	1:O:1585:C:H5'	2.15	0.46
5:B:315:VAL:HG23	5:B:316:ARG:HG2	1.97	0.46
13:J:75:ARG:O	13:J:93:ASN:HA	2.15	0.46
16:M:139:TRP:CH2	16:M:176:ARG:NH1	2.83	0.46
30:1:19:SER:O	30:1:36:ASN:ND2	2.47	0.46
31:2:42:ARG:HH11	31:2:42:ARG:CG	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:665:A:H2'	1:0:666:A:C8	2.51	0.46
1:0:1252:A:H2'	1:0:1253:C:O4'	2.15	0.46
1:0:1269:G:H2'	1:0:1270:U:C6	2.50	0.46
1:0:1787:C:O2'	1:0:1788:U:H5'	2.15	0.46
1:0:1942:A:H1'	38:A:8564:HOH:O	2.15	0.46
1:0:2004:U:H4'	38:0:6205:HOH:O	2.16	0.46
1:0:2090:G:H2'	1:0:2091:G:C8	2.49	0.46
5:B:85:ARG:NH1	38:B:8648:HOH:O	2.47	0.46
7:D:21:VAL:HG13	7:D:131:THR:O	2.14	0.46
9:F:110:GLU:HG2	38:F:6926:HOH:O	2.14	0.46
11:H:109:ASP:HB2	38:H:8349:HOH:O	2.15	0.46
11:H:162:SER:CB	11:H:163:PRO:CD	2.78	0.46
16:M:100:ALA:O	16:M:129:ILE:HG23	2.15	0.46
20:Q:98:ASN:N	20:Q:98:ASN:ND2	2.64	0.46
21:R:51:GLN:NE2	21:R:53:ASN:HD21	2.06	0.46
22:S:30:ASP:O	22:S:33:GLU:HB3	2.15	0.46
1:0:482:G:H4'	1:0:508:A:N1	2.30	0.46
1:0:958:G:O2'	1:0:959:C:H5'	2.16	0.46
1:0:1246:A:O2'	1:0:1247:A:H3'	2.15	0.46
1:0:1600:G:OP2	1:0:1600:G:H8	1.98	0.46
2:9:3095:C:O2'	2:9:3096:C:H5'	2.16	0.46
4:A:55:VAL:HG22	4:A:68:ILE:O	2.15	0.46
5:B:55:ASN:HB3	5:B:64:GLY:H	1.80	0.46
5:B:274:GLU:HG3	5:B:275:GLY:N	2.30	0.46
6:C:127:ARG:HH21	6:C:225:PRO:HG2	1.70	0.46
8:E:126:ILE:HB	8:E:131:LEU:CD2	2.45	0.46
9:F:113:ASP:O	9:F:117:GLU:HG3	2.16	0.46
10:G:63:ARG:HB2	10:G:66:LEU:HG	1.96	0.46
14:K:124:ASP:CG	14:K:125:PHE:N	2.73	0.46
17:N:26:TRP:HB2	38:N:3062:HOH:O	2.15	0.46
21:R:14:ALA:HA	21:R:25:GLN:NE2	2.29	0.46
28:Y:57:CYS:C	28:Y:59:HIS:H	2.23	0.46
1:0:138:U:H5''	1:0:139:C:OP2	2.16	0.46
1:0:259:G:O2'	1:0:260:C:H5'	2.15	0.46
1:0:366:U:H2'	1:0:367:G:O4'	2.15	0.46
1:0:1677:U:OP2	30:1:8:LYS:NZ	2.44	0.46
1:0:1773:G:C2'	1:0:1774:G:H5'	2.46	0.46
1:0:2311:A:O2'	1:0:2312:G:H5'	2.15	0.46
5:B:7:ARG:HB2	5:B:7:ARG:CZ	2.46	0.46
6:C:107:ARG:HH11	6:C:107:ARG:CB	2.27	0.46
7:D:67:ASP:O	7:D:69:ILE:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:50:GLY:O	13:J:120:ARG:NH1	2.43	0.46
16:M:74:PRO:HG2	16:M:159:TYR:CZ	2.51	0.46
21:R:29:ASP:OD1	21:R:31:ARG:HG3	2.16	0.46
23:T:14:GLU:OE1	23:T:15:PRO:CD	2.63	0.46
27:X:107:PRO:HB3	27:X:182:PHE:CD2	2.51	0.46
1:0:170:U:H2'	1:0:171:C:C5'	2.45	0.46
1:0:212:A:O4'	1:0:214:U:C6	2.68	0.46
1:0:2332:A:H5'	1:0:2333:G:OP2	2.15	0.46
1:0:2748:G:H1'	38:0:8782:HOH:O	2.15	0.46
5:B:190:MET:HE2	5:B:194:PHE:HD1	1.77	0.46
7:D:11:HIS:O	7:D:12:GLU:HB3	2.15	0.46
7:D:18:ILE:HG12	7:D:134:LEU:CD2	2.45	0.46
10:G:12:ILE:HG13	38:G:6833:HOH:O	2.15	0.46
14:K:57:VAL:HG12	14:K:57:VAL:O	2.15	0.46
16:M:73:ALA:HB1	16:M:74:PRO:CD	2.45	0.46
16:M:139:TRP:HA	16:M:139:TRP:HE3	1.81	0.46
22:S:43:ASN:C	22:S:45:GLY:H	2.24	0.46
29:Z:28:HIS:ND1	29:Z:31:LYS:HE2	2.29	0.46
31:2:69:TYR:HE1	31:2:80:ARG:HB2	1.79	0.46
1:0:200:U:H2'	38:0:4388:HOH:O	2.15	0.46
1:0:724:G:O2'	1:0:725:C:H5'	2.15	0.46
1:0:745:G:O6	17:N:68:GLY:HA3	2.15	0.46
1:0:960:G:N3	1:0:960:G:C2'	2.77	0.46
1:0:1064:U:H2'	1:0:1065:G:C8	2.51	0.46
1:0:1503:U:H2'	1:0:1504:A:O4'	2.14	0.46
1:0:2761:A:C4	1:0:2763:G:C8	3.04	0.46
1:0:2825:C:H4'	1:0:2826:G:O5'	2.15	0.46
5:B:147:VAL:O	5:B:150:ALA:HB3	2.15	0.46
7:D:60:GLU:C	7:D:62:ASP:N	2.72	0.46
7:D:104:PHE:CE2	7:D:132:VAL:HB	2.51	0.46
15:L:67:ILE:CD1	15:L:104:ARG:HD2	2.46	0.46
15:L:87:MET:HB3	31:2:46:ILE:CD1	2.24	0.46
17:N:14:LEU:CG	17:N:102:ILE:HD11	2.45	0.46
1:0:1118:A:H62	1:0:1244:U:H3	1.63	0.46
1:0:2034:U:H2'	1:0:2035:C:H6	1.80	0.46
1:0:2064:U:H4'	1:0:2653:A:OP1	2.16	0.46
1:0:2786:G:H2'	38:0:8861:HOH:O	2.15	0.46
4:A:199:HIS:HD2	4:A:201:PHE:H	1.61	0.46
7:D:49:PRO:HG3	38:D:5828:HOH:O	2.15	0.46
7:D:91:ALA:HB2	7:D:106:PHE:CD2	2.51	0.46
8:E:68:HIS:O	8:E:72:MET:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:107:PHE:CE1	8:E:152:THR:HB	2.51	0.46
12:I:74:ARG:C	12:I:76:ASP:N	2.74	0.46
14:K:120:LEU:HD12	14:K:133:VAL:HG21	1.97	0.46
16:M:83:LEU:HD13	16:M:175:LEU:HD23	1.98	0.46
18:O:105:LEU:CD2	18:O:137:LEU:HD21	2.45	0.46
22:S:73:HIS:CD2	22:S:88:PRO:CG	2.99	0.46
25:V:59:GLN:NE2	25:V:97:ALA:HB3	2.30	0.46
1:0:399:C:H5'	15:L:179:GLY:O	2.16	0.46
1:0:445:U:H2'	1:0:446:G:C8	2.51	0.46
1:0:1300:G:H1'	38:0:5591:HOH:O	2.15	0.46
1:0:1735:C:H2'	1:0:1736:A:H8	1.80	0.46
1:0:1878:G:O2'	1:0:1879:U:OP2	2.34	0.46
1:0:2035:C:O2'	1:0:2036:C:H5'	2.16	0.46
1:0:2365:G:H4'	19:P:45:PRO:O	2.15	0.46
1:0:2578:G:H5'	1:0:2578:G:C8	2.48	0.46
11:H:15:THR:HG22	11:H:91:HIS:HA	1.98	0.46
11:H:151:MET:HA	11:H:151:MET:CE	2.41	0.46
12:I:135:ILE:O	12:I:139:LEU:HG	2.15	0.46
27:X:184:GLU:OE1	27:X:204:ARG:NH1	2.49	0.46
28:Y:57:CYS:C	28:Y:59:HIS:N	2.73	0.46
1:0:47:G:N3	1:0:114:A:C2	2.84	0.46
1:0:299:U:O2'	1:0:300:C:H5'	2.16	0.46
1:0:453:A:H4'	1:0:455:A:N7	2.31	0.46
1:0:903:U:OP2	14:K:11:ARG:NH1	2.44	0.46
1:0:926:A:O2'	14:K:41:HIS:CD2	2.69	0.46
1:0:1003:U:O2	11:H:90:PHE:CZ	2.69	0.46
1:0:1773:G:H2'	1:0:1774:G:H5'	1.98	0.46
1:0:2453:G:H3'	38:0:6807:HOH:O	2.15	0.46
1:0:2851:G:C2'	1:0:2852:A:H5'	2.46	0.46
1:0:2899:A:O2'	1:0:2900:G:H5'	2.16	0.46
4:A:4:ILE:HG22	4:A:198:ASP:O	2.16	0.46
4:A:105:VAL:HG11	4:A:154:ALA:HB1	1.98	0.46
5:B:279:THR:CG2	5:B:280:VAL:N	2.79	0.46
13:J:62:PRO:CG	13:J:65:ARG:HH21	2.14	0.46
15:L:104:ARG:O	15:L:108:LYS:HG2	2.15	0.46
16:M:62:HIS:O	16:M:65:ASP:OD1	2.34	0.46
16:M:71:TRP:N	38:M:8539:HOH:O	2.49	0.46
20:Q:23:MET:HE3	20:Q:28:SER:OG	2.16	0.46
25:V:41:TYR:CD2	25:V:44:MET:HE3	2.51	0.46
26:W:18:ARG:HA	38:W:5356:HOH:O	2.16	0.46
1:0:101:C:H2'	1:0:102:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:232:A:H4'	38:0:6972:HOH:O	2.16	0.46
1:0:1557:G:O2'	1:0:1558:C:H5'	2.16	0.46
1:0:1641:A:H2'	1:0:1642:A:C5'	2.45	0.46
1:0:2372:A:H2'	1:0:2373:U:C6	2.51	0.46
1:0:2698:G:H2'	1:0:2699:A:C8	2.51	0.46
1:0:2781:U:H2'	1:0:2782:G:H5'	1.97	0.46
7:D:60:GLU:O	7:D:62:ASP:N	2.49	0.46
9:F:26:THR:HB	9:F:102:GLY:HA3	1.98	0.46
15:L:84:LYS:O	15:L:87:MET:HG2	2.16	0.46
16:M:91:ARG:HG3	16:M:186:LEU:CD2	2.44	0.46
18:O:84:ALA:C	18:O:86:ALA:H	2.23	0.46
25:V:34:LEU:CD1	25:V:100:LEU:HD13	2.46	0.46
30:1:41:HIS:H	30:1:45:ASN:ND2	2.04	0.46
31:2:55:VAL:O	31:2:56:PRO:C	2.58	0.46
1:0:128:A:O2'	1:0:129:A:H5'	2.16	0.45
1:0:156:C:H5''	15:L:171:ARG:CD	2.25	0.45
1:0:1305:C:O2'	1:0:1306:U:H5'	2.15	0.45
1:0:1335:C:OP2	27:X:207:SER:CB	2.64	0.45
1:0:1512:G:O2'	1:0:1513:C:H5'	2.16	0.45
1:0:1593:C:OP1	18:O:117:SER:HB3	2.16	0.45
1:0:1626:A:H2'	1:0:1627:G:O4'	2.16	0.45
6:C:123:LEU:HD23	6:C:123:LEU:HA	1.84	0.45
6:C:197:SER:OG	6:C:242:GLU:OE2	2.32	0.45
7:D:10:PHE:CD1	7:D:11:HIS:N	2.84	0.45
9:F:110:GLU:O	9:F:114:LYS:HG3	2.15	0.45
11:H:58:HIS:HA	11:H:61:LEU:HD23	1.98	0.45
11:H:150:LYS:CB	11:H:157:ILE:HD12	2.46	0.45
22:S:15:PRO:O	22:S:19:ARG:HG3	2.16	0.45
23:T:34:SER:HA	23:T:37:GLU:OE1	2.16	0.45
27:X:186:ARG:HG2	27:X:186:ARG:NH1	2.30	0.45
31:2:69:TYR:CE1	31:2:80:ARG:HB2	2.50	0.45
1:0:553:G:H5'	38:0:4440:HOH:O	2.16	0.45
1:0:689:G:O2'	1:0:690:G:H5'	2.17	0.45
1:0:963:C:H2'	1:0:964:G:C8	2.50	0.45
1:0:1058:A:H2'	1:0:1060:C:C5'	2.47	0.45
1:0:1116:U:C2'	1:0:1118:A:H2	2.27	0.45
1:0:1171:A:C2'	1:0:1172:G:H5'	2.46	0.45
1:0:1206:U:H2'	1:0:1207:A:O4'	2.16	0.45
1:0:1421:C:O2'	1:0:1422:U:H5'	2.16	0.45
1:0:1917:G:H2'	1:0:1918:U:C6	2.51	0.45
1:0:2256:G:C2'	1:0:2257:G:C5'	2.93	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2314:G:O2'	1:0:2315:C:H5'	2.16	0.45
1:0:2546:U:H5	5:B:2:GLN:HE22	1.63	0.45
1:0:2885:A:H2'	1:0:2886:C:C6	2.51	0.45
2:9:3061:C:H2'	2:9:3062:A:H8	1.82	0.45
4:A:65:ARG:HG2	4:A:65:ARG:HH11	1.81	0.45
4:A:192:VAL:O	4:A:192:VAL:CG1	2.64	0.45
5:B:132:HIS:CE1	5:B:171:VAL:HG21	2.51	0.45
5:B:146:THR:O	5:B:159:PRO:HB3	2.16	0.45
8:E:77:THR:OG1	8:E:78:GLU:N	2.48	0.45
11:H:34:GLY:HA3	11:H:81:TYR:O	2.16	0.45
12:I:51:GLU:O	12:I:55:GLU:HG3	2.16	0.45
15:L:115:LEU:C	15:L:115:LEU:HD13	2.41	0.45
16:M:139:TRP:HH2	16:M:176:ARG:HH11	1.62	0.45
18:O:31:ILE:HG12	18:O:43:LEU:HD13	1.98	0.45
25:V:4:LEU:HD23	25:V:4:LEU:HA	1.74	0.45
25:V:122:ARG:HG2	25:V:122:ARG:NH1	2.20	0.45
1:0:170:U:C2'	1:0:171:C:H5'	2.47	0.45
1:0:251:C:O2'	1:0:252:C:H5'	2.16	0.45
1:0:489:A:C8	22:S:82:THR:HG22	2.51	0.45
1:0:697:G:H4'	1:0:730:G:O3'	2.17	0.45
1:0:709:G:O2'	17:N:25:VAL:HG12	2.16	0.45
1:0:869:G:OP1	15:L:79:LYS:HE2	2.16	0.45
1:0:1545:C:H2'	1:0:1546:G:O4'	2.16	0.45
1:0:1940:C:H5''	4:A:234:GLY:HA3	1.97	0.45
1:0:2355:G:H5''	1:0:2356:A:OP2	2.16	0.45
1:0:2547:C:H2'	1:0:2548:C:C6	2.51	0.45
1:0:2630:G:O6	4:A:206:ARG:NH2	2.49	0.45
1:0:2846:C:H4'	5:B:156:LYS:HB3	1.97	0.45
1:0:2846:C:OP1	5:B:158:LYS:HD3	2.16	0.45
4:A:30:ARG:HE	4:A:30:ARG:HB3	1.65	0.45
4:A:66:ARG:HH11	4:A:66:ARG:CB	2.29	0.45
7:D:23:VAL:CG2	7:D:73:VAL:HB	2.46	0.45
9:F:60:VAL:O	9:F:61:MET:C	2.59	0.45
9:F:99:THR:O	9:F:100:ASP:HB2	2.15	0.45
9:F:101:ALA:HB2	9:F:108:LEU:HD22	1.97	0.45
11:H:59:ASN:H	11:H:59:ASN:ND2	2.14	0.45
16:M:73:ALA:HB1	16:M:74:PRO:HD2	1.98	0.45
16:M:184:ILE:HG22	16:M:185:GLU:N	2.30	0.45
17:N:21:SER:OG	17:N:106:PRO:HB2	2.17	0.45
18:O:115:SER:C	18:O:117:SER:N	2.74	0.45
20:Q:39:THR:CG2	20:Q:42:GLU:HG3	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:249:G:H1'	1:0:265:U:O2	2.17	0.45
1:0:283:U:H5''	1:0:284:C:P	2.56	0.45
1:0:295:C:H2'	1:0:296:G:O4'	2.16	0.45
1:0:541:C:C2'	1:0:542:A:C5'	2.91	0.45
1:0:711:G:C2	1:0:718:C:C2	3.05	0.45
1:0:1381:A:N3	1:0:1382:G:H1'	2.32	0.45
2:9:3026:C:H2'	2:9:3027:C:H6	1.81	0.45
4:A:70:ALA:HA	4:A:71:PRO:HD3	1.79	0.45
5:B:304:PRO:HD2	5:B:307:ARG:CD	2.40	0.45
7:D:57:THR:HG23	7:D:63:ILE:HA	1.99	0.45
14:K:97:VAL:HG12	14:K:98:GLU:O	2.16	0.45
16:M:115:VAL:HG23	16:M:116:PHE:H	1.81	0.45
16:M:182:GLY:O	16:M:183:ASP:O	2.34	0.45
21:R:51:GLN:HB3	21:R:67:ARG:HH12	1.82	0.45
26:W:70:ILE:HG23	26:W:70:ILE:O	2.16	0.45
27:X:107:PRO:HB3	27:X:182:PHE:CE2	2.51	0.45
1:0:31:C:H2'	38:0:8568:HOH:O	2.15	0.45
1:0:539:G:H2'	1:0:540:A:C8	2.52	0.45
1:0:583:G:H2'	1:0:584:U:C6	2.51	0.45
1:0:1517:U:C2	1:0:1670:G:N2	2.84	0.45
1:0:2000:G:O2'	1:0:2001:G:H5'	2.17	0.45
1:0:2460:A:OP1	31:2:63:LYS:NZ	2.48	0.45
2:9:3117:G:H2'	2:9:3118:C:C6	2.51	0.45
4:A:57:ALA:HA	4:A:67:LEU:HD23	1.98	0.45
4:A:161:GLY:O	28:Y:68:CYS:SG	2.75	0.45
7:D:35:ALA:HB2	38:D:5858:HOH:O	2.16	0.45
7:D:73:VAL:HG21	38:D:5828:HOH:O	2.15	0.45
7:D:95:THR:HG21	7:D:174:VAL:HG22	1.99	0.45
16:M:115:VAL:O	16:M:118:ILE:HB	2.17	0.45
19:P:75:ILE:CD1	19:P:84:ILE:HD11	2.46	0.45
22:S:113:GLU:O	22:S:114:SER:C	2.58	0.45
25:V:130:HIS:O	25:V:136:GLY:HA3	2.17	0.45
29:Z:25:LYS:O	29:Z:25:LYS:HG2	2.17	0.45
1:0:1184:C:H1'	38:0:8953:HOH:O	2.16	0.45
1:0:1500:U:P	18:O:41:ARG:HH22	2.39	0.45
1:0:1735:C:H2'	1:0:1736:A:C8	2.51	0.45
1:0:2346:C:H4'	7:D:52:THR:HG22	1.99	0.45
1:0:2716:G:C5'	5:B:206:THR:HG21	2.45	0.45
5:B:137:LEU:HD11	5:B:140:LEU:HD21	1.99	0.45
5:B:140:LEU:HD13	5:B:175:LEU:HA	1.97	0.45
5:B:248:ARG:O	5:B:251:VAL:CG1	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:145:ALA:HB1	8:E:168:ILE:CD1	2.46	0.45
9:F:99:THR:HA	38:F:3461:HOH:O	2.17	0.45
13:J:118:ALA:HA	13:J:125:ALA:HB2	1.99	0.45
14:K:146:GLY:C	14:K:148:GLU:H	2.25	0.45
16:M:77:ASN:OD1	16:M:80:SER:HB2	2.17	0.45
18:O:16:VAL:CG1	18:O:20:ARG:HB2	2.47	0.45
18:O:59:ARG:HG2	18:O:59:ARG:HH11	1.82	0.45
20:Q:75:TRP:CD1	20:Q:76:ASP:H	2.34	0.45
27:X:172:THR:HG22	27:X:173:ALA:N	2.32	0.45
1:0:243:A:H61	1:0:269:G:C1'	2.29	0.45
1:0:338:C:H4'	6:C:174:ILE:HD11	1.97	0.45
1:0:338:C:H4'	6:C:174:ILE:HD12	1.99	0.45
1:0:514:G:OP1	1:0:514:G:H2'	2.16	0.45
1:0:668:C:H2'	1:0:669:G:H8	1.80	0.45
1:0:820:G:O2'	1:0:856:G:H4'	2.17	0.45
1:0:958:G:H2'	1:0:959:C:H6	1.80	0.45
1:0:1416:G:C2'	1:0:1417:G:H5'	2.46	0.45
1:0:1565:C:O4'	1:0:2738:G:H1'	2.16	0.45
1:0:1813:U:O2'	18:O:81:LYS:HE3	2.17	0.45
5:B:87:TYR:CE2	5:B:96:PRO:HG3	2.51	0.45
10:G:27:ILE:HD12	10:G:70:ALA:HB1	1.98	0.45
15:L:37:VAL:CG2	15:L:108:LYS:HG3	2.45	0.45
22:S:96:VAL:HG13	22:S:97:ARG:N	2.32	0.45
25:V:54:PHE:CZ	25:V:140:LYS:HB2	2.52	0.45
27:X:106:THR:HG23	27:X:107:PRO:HD2	1.99	0.45
27:X:141:THR:HG23	38:X:8599:HOH:O	2.16	0.45
29:Z:8:GLN:HE22	29:Z:11:LYS:HZ2	1.63	0.45
30:1:40:ARG:HG3	30:1:45:ASN:CB	2.46	0.45
1:0:64:G:H2'	1:0:65:C:H6	1.80	0.45
1:0:1156:C:O2'	1:0:1157:C:H5'	2.17	0.45
1:0:1600:G:H4'	38:0:6539:HOH:O	2.17	0.45
1:0:2625:C:O2'	1:0:2626:C:H5'	2.16	0.45
2:9:3047:A:H2'	2:9:3048:C:C6	2.51	0.45
4:A:69:LEU:CD2	4:A:120:ARG:HB3	2.41	0.45
5:B:144:THR:CG2	5:B:145:HIS:N	2.79	0.45
9:F:20:LEU:O	9:F:23:ALA:HB3	2.16	0.45
20:Q:113:HIS:O	20:Q:145:LEU:HD12	2.17	0.45
28:Y:20:LEU:O	28:Y:21:LYS:C	2.59	0.45
1:0:740:G:O2'	1:0:741:C:H5'	2.17	0.45
1:0:790:A:H1'	1:0:1710:A:H2'	1.99	0.45
1:0:953:G:H5'	38:0:8786:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1118:A:C8	1:0:1118:A:C3'	2.87	0.45
1:0:1613:C:H2'	1:0:1614:G:O4'	2.17	0.45
1:0:1973:A:H2'	1:0:1974:G:O4'	2.17	0.45
1:0:2421:G:H4'	38:0:5686:HOH:O	2.17	0.45
5:B:7:ARG:HH11	5:B:7:ARG:CG	2.23	0.45
5:B:38:VAL:HG22	5:B:142:LEU:HD12	1.99	0.45
5:B:84:LEU:HD13	5:B:84:LEU:C	2.41	0.45
7:D:59:GLY:C	7:D:61:PHE:H	2.20	0.45
8:E:162:PHE:N	8:E:162:PHE:CD1	2.84	0.45
11:H:136:VAL:HG22	11:H:137:ASN:O	2.16	0.45
12:I:17:CYS:HA	12:I:119:THR:O	2.17	0.45
15:L:59:GLY:HA3	15:L:141:ILE:HD12	1.99	0.45
15:L:99:ARG:HD2	15:L:167:GLY:HA2	1.98	0.45
15:L:101:ALA:O	15:L:102:GLU:C	2.60	0.45
20:Q:39:THR:HG22	20:Q:42:GLU:HG3	1.98	0.45
20:Q:66:VAL:HG22	20:Q:79:ARG:CZ	2.47	0.45
21:R:58:MET:SD	30:1:8:LYS:HE3	2.57	0.45
22:S:44:ALA:HA	22:S:62:VAL:HG12	1.99	0.45
25:V:40:ALA:O	25:V:44:MET:HG3	2.16	0.45
31:2:11:CYS:HB2	31:2:20:HIS:NE2	2.32	0.45
1:0:538:C:H5''	1:0:539:G:C8	2.52	0.45
1:0:1134:G:H4'	11:H:151:MET:CE	2.32	0.45
1:0:1278:A:H4'	1:0:1279:U:C4	2.52	0.45
1:0:1470:A:OP1	15:L:93:ARG:HD2	2.17	0.45
1:0:1514:C:H2'	1:0:1515:A:H8	1.81	0.45
1:0:1523:G:H2'	1:0:1524:U:C6	2.52	0.45
1:0:1758:U:H2'	1:0:1759:A:O4'	2.17	0.45
5:B:195:ARG:N	5:B:198:GLU:OE1	2.45	0.45
6:C:76:ARG:HD2	38:C:8444:HOH:O	2.17	0.45
6:C:104:ASP:O	6:C:108:GLN:HG3	2.17	0.45
6:C:140:VAL:HB	38:C:8463:HOH:O	2.16	0.45
8:E:126:ILE:HB	8:E:131:LEU:HD23	1.99	0.45
12:I:74:ARG:C	12:I:76:ASP:H	2.25	0.45
15:L:113:ARG:NH2	15:L:156:ARG:HG2	2.31	0.45
17:N:14:LEU:CD2	17:N:102:ILE:HD11	2.47	0.45
27:X:219:GLU:HG3	27:X:220:GLU:N	2.31	0.45
1:0:169:A:H1'	31:2:48:ASN:ND2	2.31	0.44
1:0:653:C:H2'	1:0:654:A:C8	2.51	0.44
1:0:2561:C:OP1	8:E:153:ARG:NH2	2.50	0.44
2:9:3031:C:O2'	2:9:3032:G:H5'	2.17	0.44
5:B:7:ARG:CG	5:B:7:ARG:NH1	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:34:LEU:HD13	16:M:47:LEU:HD21	1.99	0.44
17:N:47:ARG:HG3	17:N:47:ARG:NH1	2.32	0.44
17:N:77:ALA:HA	17:N:96:VAL:O	2.17	0.44
20:Q:75:TRP:CG	20:Q:76:ASP:H	2.35	0.44
22:S:24:ARG:NH2	22:S:39:ASN:HD22	2.15	0.44
23:T:46:ALA:HB1	23:T:52:THR:HG21	2.00	0.44
1:O:812:A:H2'	1:O:813:C:H6	1.80	0.44
1:O:1384:C:H5'	26:W:30:MET:HG2	1.99	0.44
1:O:1548:U:O2'	1:O:1549:C:H5'	2.17	0.44
1:O:1611:G:O2'	1:O:1612:A:H5'	2.18	0.44
1:O:1937:U:O2'	1:O:1938:G:H5'	2.17	0.44
1:O:2106:C:H2'	1:O:2107:U:C6	2.53	0.44
1:O:2709:G:H4'	13:J:3:ALA:CB	2.47	0.44
4:A:101:GLU:HG2	38:A:8580:HOH:O	2.17	0.44
4:A:132:ASP:OD1	4:A:133:ARG:N	2.50	0.44
5:B:98:THR:HG22	5:B:99:GLU:H	1.83	0.44
5:B:154:VAL:HG12	5:B:156:LYS:HG2	1.99	0.44
11:H:74:ASN:HD22	11:H:141:ASN:CG	2.25	0.44
16:M:47:LEU:HD13	16:M:97:VAL:HG11	1.98	0.44
16:M:72:GLU:H	16:M:171:HIS:CE1	2.35	0.44
17:N:96:VAL:HA	38:N:4258:HOH:O	2.17	0.44
18:O:7:LYS:CD	18:O:21:VAL:CG2	2.95	0.44
19:P:77:ASP:N	19:P:80:LYS:O	2.49	0.44
23:T:36:CYS:O	23:T:37:GLU:C	2.60	0.44
28:Y:31:ILE:CG2	28:Y:32:LYS:N	2.80	0.44
1:O:349:U:O2'	1:O:350:C:H5'	2.18	0.44
1:O:1857:A:N6	1:O:2247:C:H1'	2.32	0.44
1:O:1894:C:C2	1:O:1939:U:C4	3.05	0.44
1:O:2481:G:C3'	1:O:2482:G:H5''	2.46	0.44
6:C:223:LEU:HD12	6:C:223:LEU:HA	1.87	0.44
7:D:64:ARG:O	7:D:67:ASP:OD2	2.36	0.44
8:E:156:ASP:OD2	8:E:157:LYS:NZ	2.34	0.44
13:J:21:ALA:O	13:J:96:VAL:HG22	2.17	0.44
14:K:125:PHE:CZ	14:K:140:VAL:HG13	2.52	0.44
14:K:144:ASP:HA	14:K:147:GLU:HG3	1.99	0.44
15:L:88:VAL:HG12	15:L:89:ASN:N	2.32	0.44
16:M:58:LEU:HD12	16:M:58:LEU:N	2.32	0.44
23:T:17:THR:CG2	23:T:18:GLY:N	2.81	0.44
26:W:23:HIS:HB2	38:W:7830:HOH:O	2.16	0.44
1:O:81:G:N3	1:O:98:A:C2	2.85	0.44
1:O:328:U:O4'	6:C:202:THR:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:653:C:H5''	38:N:7674:HOH:O	2.16	0.44
1:0:731:U:H2'	1:0:732:C:H6	1.80	0.44
1:0:1184:C:O2'	1:0:1185:U:P	2.76	0.44
1:0:1372:A:H3'	38:0:8863:HOH:O	2.18	0.44
1:0:1872:C:O2	4:A:25:ALA:HA	2.18	0.44
1:0:2415:A:C2	16:M:25:ARG:HB3	2.52	0.44
1:0:2755:G:H1'	38:0:5590:HOH:O	2.18	0.44
8:E:69:ILE:O	8:E:72:MET:HB2	2.16	0.44
9:F:34:ASN:O	9:F:38:LYS:HG3	2.16	0.44
11:H:117:LYS:O	11:H:119:VAL:HG13	2.18	0.44
16:M:32:PRO:HD2	16:M:99:GLU:O	2.17	0.44
16:M:37:ARG:NE	38:M:8534:HOH:O	2.50	0.44
18:O:10:ALA:HA	18:O:13:VAL:CG1	2.48	0.44
26:W:78:GLU:CG	26:W:79:GLU:H	2.26	0.44
1:0:113:A:OP2	1:0:114:A:H2'	2.18	0.44
1:0:363:A:O2'	1:0:364:C:H5'	2.18	0.44
1:0:622:G:P	27:X:148:GLY:HA3	2.57	0.44
1:0:821:U:H5''	38:0:4004:HOH:O	2.17	0.44
1:0:1164:U:N3	1:0:1192:A:H2	2.07	0.44
1:0:1463:A:H2'	1:0:1464:U:H6	1.82	0.44
1:0:1746:A:O4'	1:0:1747:A:C2	2.70	0.44
1:0:2912:C:O2'	1:0:2913:A:H5'	2.18	0.44
32:0:9500:SLD:N4S	3:4:75:C:OP2	2.50	0.44
2:9:3088:G:OP1	25:V:130:HIS:NE2	2.40	0.44
11:H:86:ARG:H	11:H:86:ARG:HG2	1.44	0.44
13:J:34:VAL:CG2	13:J:47:ALA:HB2	2.48	0.44
18:O:109:ARG:NH1	18:O:119:TYR:CE2	2.85	0.44
19:P:88:ALA:C	19:P:90:HIS:N	2.73	0.44
25:V:80:ASP:O	25:V:84:VAL:HG23	2.17	0.44
25:V:110:GLN:HE21	25:V:110:GLN:HA	1.82	0.44
1:0:101:C:H2'	1:0:102:A:C8	2.53	0.44
1:0:152:A:O2'	1:0:153:C:H5'	2.18	0.44
1:0:283:U:H5	1:0:284:C:H42	1.65	0.44
1:0:659:A:H5''	38:N:6799:HOH:O	2.17	0.44
1:0:1019:C:O2	19:P:94:GLN:NE2	2.51	0.44
1:0:1299:G:N2	38:0:5591:HOH:O	2.50	0.44
1:0:1432:U:H5'	38:0:3181:HOH:O	2.17	0.44
1:0:1514:C:O2'	1:0:1515:A:H5'	2.18	0.44
1:0:2091:G:O3'	5:B:235:ARG:HD3	2.17	0.44
1:0:2241:C:H2'	1:0:2242:U:H6	1.79	0.44
1:0:2509:A:OP2	1:0:2510:C:H5	2.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2815:G:N7	12:I:80:LYS:NZ	2.64	0.44
6:C:236:THR:C	38:C:8461:HOH:O	2.61	0.44
13:J:10:GLN:NE2	13:J:10:GLN:N	2.31	0.44
13:J:113:ILE:HD12	13:J:128:ALA:HB2	2.00	0.44
26:W:43:VAL:CG1	26:W:47:ALA:HB3	2.47	0.44
28:Y:30:GLU:HB3	28:Y:34:LYS:HE3	1.99	0.44
1:0:130:C:O2'	1:0:131:A:N7	2.50	0.44
1:0:377:C:O2'	1:0:378:A:H5'	2.18	0.44
1:0:818:A:O2'	28:Y:13:ARG:HD3	2.17	0.44
1:0:1283:G:O2'	1:0:1284:G:H5'	2.18	0.44
1:0:1759:A:N3	1:0:1818:C:H2'	2.33	0.44
1:0:2064:U:H2'	1:0:2065:C:H6	1.83	0.44
2:9:3078:G:N2	2:9:3103:A:OP2	2.48	0.44
4:A:56:ALA:O	4:A:68:ILE:N	2.49	0.44
8:E:7:ILE:HA	8:E:8:PRO:HD3	1.90	0.44
9:F:50:VAL:CG1	9:F:60:VAL:HG11	2.46	0.44
9:F:104:ALA:C	9:F:106:THR:N	2.75	0.44
11:H:72:VAL:O	11:H:72:VAL:HG13	2.17	0.44
15:L:40:ILE:O	15:L:40:ILE:HG13	2.18	0.44
25:V:7:LEU:HD12	25:V:53:ALA:HB2	2.00	0.44
1:0:541:C:O2'	1:0:542:A:H5''	2.18	0.44
1:0:612:U:H2'	1:0:613:C:H6	1.83	0.44
1:0:1072:G:OP2	27:X:154:ARG:NH2	2.51	0.44
1:0:1118:A:H8	1:0:1119:G:H5''	1.82	0.44
1:0:1180:U:H2'	1:0:1181:A:O4'	2.18	0.44
1:0:1201:C:H2'	1:0:1202:A:H5'	1.99	0.44
1:0:1419:U:H2'	1:0:1685:A:C2	2.53	0.44
1:0:1901:G:O2'	1:0:1902:G:H5'	2.18	0.44
1:0:2252:A:H2'	1:0:2253:G:O4'	2.18	0.44
1:0:2401:A:H5'	38:0:3467:HOH:O	2.17	0.44
1:0:2834:G:C4	1:0:2847:G:N2	2.85	0.44
1:0:2868:C:H2'	1:0:2869:G:O4'	2.18	0.44
1:0:2896:A:OP1	26:W:15:ARG:NH1	2.51	0.44
4:A:190:ARG:O	4:A:191:GLY:C	2.60	0.44
5:B:148:PRO:HD2	38:B:8593:HOH:O	2.18	0.44
10:G:12:ILE:HA	38:G:8806:HOH:O	2.18	0.44
11:H:26:LYS:CG	11:H:28:ILE:H	2.20	0.44
14:K:121:ILE:HG12	14:K:141:GLU:HB2	1.99	0.44
15:L:153:THR:O	15:L:156:ARG:HG3	2.17	0.44
25:V:7:LEU:CD1	25:V:53:ALA:HB2	2.48	0.44
27:X:184:GLU:OE2	27:X:204:ARG:HD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:177:A:H2'	1:0:178:U:O4'	2.18	0.44
1:0:308:U:H5'	22:S:97:ARG:NH2	2.33	0.44
1:0:823:U:H2'	1:0:824:G:O4'	2.17	0.44
1:0:1882:C:OP1	4:A:192:VAL:HG23	2.18	0.44
1:0:1936:C:O2'	1:0:1937:U:H5'	2.18	0.44
1:0:2807:U:OP2	5:B:28:SER:OG	2.28	0.44
1:0:2872:U:H2'	1:0:2873:C:H6	1.83	0.44
38:0:7167:HOH:O	27:X:158:LYS:HD3	2.17	0.44
2:9:3053:G:O2'	2:9:3054:A:H5'	2.18	0.44
5:B:41:PHE:CE1	5:B:79:MET:HG3	2.53	0.44
5:B:66:GLU:OE1	5:B:328:ARG:HD2	2.18	0.44
6:C:133:ARG:NE	6:C:138:VAL:HG22	2.33	0.44
6:C:156:LEU:HD12	6:C:156:LEU:O	2.18	0.44
7:D:27:ILE:CG2	7:D:28:GLY:H	2.18	0.44
7:D:136:ARG:HD2	7:D:155:HIS:O	2.18	0.44
8:E:69:ILE:HA	8:E:72:MET:CE	2.48	0.44
8:E:69:ILE:HA	8:E:72:MET:HE2	1.98	0.44
9:F:26:THR:HB	9:F:102:GLY:O	2.17	0.44
10:G:12:ILE:O	10:G:13:PRO:C	2.59	0.44
11:H:84:ARG:CZ	11:H:135:TRP:CH2	3.00	0.44
38:J:408:HOH:O	23:T:37:GLU:HB3	2.17	0.44
14:K:130:ARG:O	14:K:131:GLU:C	2.59	0.44
16:M:104:ILE:O	16:M:107:ASN:HB2	2.17	0.44
17:N:107:GLU:O	17:N:108:GLY:C	2.61	0.44
24:U:23:LEU:HD22	24:U:49:LEU:HD23	2.00	0.44
25:V:122:ARG:CG	25:V:152:ALA:O	2.66	0.44
28:Y:56:MET:CE	28:Y:63:LYS:HE3	2.48	0.44
1:0:60:A:H5'	30:1:19:SER:OG	2.18	0.43
1:0:102:A:H2'	1:0:103:U:C6	2.53	0.43
1:0:861:A:H2'	1:0:862:U:H6	1.83	0.43
1:0:1052:G:H2'	1:0:1052:G:N3	2.33	0.43
1:0:1311:G:C2	1:0:1312:G:C8	3.05	0.43
1:0:1505:U:H5'	1:0:1505:U:C6	2.48	0.43
1:0:1537:C:H1'	38:0:7461:HOH:O	2.18	0.43
1:0:1852:A:H2'	1:0:1853:C:H6	1.83	0.43
1:0:2004:U:C2'	1:0:2005:G:OP1	2.66	0.43
1:0:2595:U:O2'	1:0:2596:A:H5'	2.18	0.43
1:0:2719:A:C2	5:B:70:PRO:HG3	2.53	0.43
1:0:2880:A:H2'	1:0:2881:C:O4'	2.18	0.43
2:9:3039:U:H3'	2:9:3040:C:H5''	1.99	0.43
6:C:19:PRO:HD2	6:C:240:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:55:LYS:O	7:D:56:ARG:HB2	2.18	0.43
7:D:96:SER:C	7:D:98:PHE:H	2.26	0.43
8:E:93:MET:HE2	8:E:107:PHE:CD1	2.53	0.43
9:F:8:VAL:HG13	9:F:12:LEU:HD13	1.99	0.43
9:F:115:VAL:O	9:F:118:LEU:N	2.51	0.43
13:J:78:LYS:HA	13:J:79:PRO:HD3	1.85	0.43
13:J:81:ARG:HD3	13:J:87:ARG:NH1	2.33	0.43
15:L:87:MET:HG3	15:L:87:MET:H	1.35	0.43
16:M:114:LYS:O	16:M:117:ALA:HB3	2.18	0.43
20:Q:50:VAL:O	20:Q:53:GLY:N	2.51	0.43
31:2:7:PHE:CD1	31:2:7:PHE:C	2.95	0.43
1:0:305:A:C5	1:0:329:A:C2	3.06	0.43
4:A:36:ASP:CA	4:A:83:GLY:HA3	2.47	0.43
4:A:61:GLU:C	4:A:63:GLY:H	2.26	0.43
4:A:95:PRO:HG2	4:A:98:GLU:HG2	2.00	0.43
7:D:59:GLY:C	7:D:61:PHE:N	2.77	0.43
7:D:77:ASP:HB3	7:D:78:GLU:H	1.59	0.43
9:F:104:ALA:O	9:F:108:LEU:HB3	2.18	0.43
20:Q:104:PHE:HB2	20:Q:109:MET:HE2	2.00	0.43
27:X:212:ARG:HD2	38:X:8610:HOH:O	2.17	0.43
1:0:602:A:O2'	1:0:605:C:H4'	2.19	0.43
1:0:1114:A:H2'	1:0:1115:U:H6	1.83	0.43
1:0:1116:U:O2'	1:0:1118:A:C2	2.44	0.43
1:0:1278:A:P	17:N:19:ARG:HH22	2.41	0.43
1:0:1486:A:C5	30:1:2:LYS:HG3	2.53	0.43
1:0:2502:C:H4'	11:H:151:MET:CG	2.43	0.43
1:0:2529:G:O2'	1:0:2530:C:H5'	2.18	0.43
1:0:2837:U:H1'	5:B:307:ARG:HH12	1.83	0.43
1:0:2898:G:H4'	5:B:288:GLY:HA2	1.99	0.43
4:A:66:ARG:CB	4:A:66:ARG:NH1	2.81	0.43
8:E:101:GLU:HB2	8:E:116:THR:O	2.17	0.43
11:H:26:LYS:CE	11:H:28:ILE:HB	2.47	0.43
12:I:97:ALA:O	12:I:101:VAL:HG23	2.17	0.43
16:M:37:ARG:HA	16:M:37:ARG:HD3	1.83	0.43
16:M:49:THR:CG2	16:M:56:ASP:HB2	2.36	0.43
18:O:114:LEU:HA	18:O:118:GLN:NE2	2.34	0.43
19:P:40:HIS:HD2	19:P:60:THR:OG1	2.01	0.43
25:V:122:ARG:NH2	38:V:4276:HOH:O	2.49	0.43
1:0:235:C:O2'	1:0:236:A:H2'	2.18	0.43
1:0:695:C:H2'	1:0:696:C:C6	2.53	0.43
1:0:1805:G:O2'	1:0:1806:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2434:A:O3'	31:2:28:GLY:HA3	2.19	0.43
1:0:2694:A:C4'	8:E:91:PHE:HE1	2.23	0.43
1:0:2758:G:O2'	1:0:2759:C:H5'	2.19	0.43
4:A:109:GLU:HG2	4:A:116:GLY:N	2.33	0.43
5:B:41:PHE:CZ	5:B:79:MET:HG3	2.53	0.43
8:E:7:ILE:HD11	8:E:11:VAL:O	2.19	0.43
11:H:47:GLU:HG2	11:H:133:ILE:CD1	2.49	0.43
11:H:58:HIS:CE1	11:H:59:ASN:ND2	2.86	0.43
15:L:95:LYS:HG2	15:L:99:ARG:HB3	1.99	0.43
16:M:10:MET:O	16:M:11:ARG:C	2.61	0.43
18:O:103:THR:HA	18:O:106:ARG:HH12	1.81	0.43
27:X:100:ARG:HE	27:X:234:VAL:HG21	1.81	0.43
1:0:400:C:O2'	1:0:401:C:H5'	2.19	0.43
1:0:1461:U:H2'	1:0:1462:C:H6	1.80	0.43
1:0:2244:A:H5''	15:L:29:GLN:OE1	2.19	0.43
5:B:55:ASN:CB	5:B:63:GLU:HA	2.46	0.43
5:B:132:HIS:HB2	5:B:137:LEU:HD22	1.99	0.43
10:G:18:GLU:O	10:G:21:ASP:HB2	2.18	0.43
16:M:47:LEU:CD1	16:M:97:VAL:HG11	2.48	0.43
18:O:103:THR:O	18:O:106:ARG:HB3	2.18	0.43
21:R:56:ASN:O	30:1:8:LYS:HE2	2.18	0.43
27:X:144:ARG:NE	38:X:8621:HOH:O	2.50	0.43
27:X:203:VAL:CG1	27:X:228:VAL:HG22	2.46	0.43
31:2:69:TYR:CE1	31:2:80:ARG:HD2	2.53	0.43
1:0:1114:A:H2'	1:0:1115:U:C6	2.54	0.43
1:0:1244:U:H4'	1:0:1246:A:O4'	2.19	0.43
1:0:1276:U:H3'	17:N:19:ARG:HH11	1.83	0.43
1:0:2296:C:H2'	1:0:2297:U:C6	2.53	0.43
8:E:18:LEU:HD13	8:E:34:TRP:CG	2.54	0.43
12:I:107:ASN:ND2	12:I:107:ASN:C	2.76	0.43
15:L:55:LYS:HB2	15:L:60:ILE:CD1	2.49	0.43
15:L:61:ILE:HD12	15:L:61:ILE:N	2.33	0.43
16:M:15:GLU:O	16:M:17:ARG:HG3	2.19	0.43
16:M:64:SER:C	16:M:66:LEU:N	2.77	0.43
27:X:112:GLU:CD	27:X:115:ARG:NH1	2.77	0.43
27:X:200:THR:HG22	27:X:201:GLU:HG2	2.00	0.43
28:Y:58:GLY:HA3	38:Y:8442:HOH:O	2.19	0.43
1:0:353:G:H2'	1:0:354:A:H8	1.82	0.43
1:0:473:A:O2'	1:0:474:C:H5'	2.19	0.43
1:0:797:A:H5'	28:Y:10:ARG:HG2	2.00	0.43
1:0:883:U:O2	1:0:883:U:H2'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:1755:A:H2'	1:O:1756:G:O4'	2.18	0.43
8:E:22:VAL:O	8:E:28:SER:HA	2.19	0.43
9:F:49:PHE:N	9:F:49:PHE:CD1	2.87	0.43
10:G:12:ILE:O	10:G:12:ILE:HG22	2.19	0.43
11:H:28:ILE:HG23	38:H:8390:HOH:O	2.17	0.43
13:J:87:ARG:HB2	23:T:19:THR:HG23	2.01	0.43
22:S:3:GLN:HA	22:S:4:PRO:HD3	1.89	0.43
27:X:151:SER:HB3	27:X:154:ARG:HB3	2.00	0.43
27:X:189:ASN:ND2	27:X:192:ASP:H	2.16	0.43
1:O:440:C:H2'	1:O:441:A:C8	2.54	0.43
1:O:999:C:O2'	1:O:1000:C:H5'	2.19	0.43
1:O:2670:G:O2'	1:O:2671:U:H5'	2.18	0.43
7:D:21:VAL:HA	7:D:131:THR:O	2.18	0.43
12:I:4:ALA:O	12:I:5:GLU:O	2.36	0.43
13:J:90:PHE:N	13:J:90:PHE:CD1	2.87	0.43
15:L:138:HIS:C	15:L:139:PRO:O	2.58	0.43
15:L:184:ARG:NH1	15:L:184:ARG:HB2	2.34	0.43
16:M:143:ARG:HA	16:M:172:PHE:CE2	2.54	0.43
19:P:50:GLY:HA3	19:P:87:THR:OG1	2.19	0.43
22:S:87:VAL:HB	22:S:88:PRO:HD2	2.00	0.43
28:Y:73:THR:O	28:Y:74:VAL:C	2.62	0.43
1:O:111:C:H2'	1:O:112:G:O4'	2.19	0.43
1:O:264:G:H1'	1:O:265:U:H5	1.82	0.43
1:O:559:U:O2'	1:O:560:C:H5'	2.19	0.43
1:O:685:C:O2	1:O:748:C:H4'	2.18	0.43
1:O:790:A:H2'	1:O:791:A:O4'	2.19	0.43
1:O:1008:C:H2'	1:O:1009:U:C6	2.53	0.43
1:O:1205:U:H2'	1:O:1206:U:C5'	2.49	0.43
1:O:1566:C:O2'	1:O:1567:A:H5'	2.19	0.43
1:O:2054:A:H2	20:Q:128:ARG:HH22	1.61	0.43
1:O:2060:A:H2'	1:O:2061:C:C6	2.54	0.43
1:O:2106:C:H1'	1:O:2484:U:O2	2.19	0.43
1:O:2538:A:H4'	1:O:2539:U:OP1	2.19	0.43
1:O:2661:U:H3	1:O:2812:A:H62	1.67	0.43
38:O:3070:HOH:O	5:B:214:PRO:HD2	2.19	0.43
7:D:23:VAL:HG21	7:D:45:THR:CG2	2.49	0.43
7:D:146:LYS:CE	16:M:107:ASN:ND2	2.81	0.43
13:J:29:LEU:HB3	13:J:55:VAL:CG1	2.42	0.43
15:L:122:GLU:HB2	15:L:126:HIS:O	2.19	0.43
15:L:147:LEU:C	15:L:149:TRP:N	2.77	0.43
16:M:138:ASP:O	16:M:138:ASP:CG	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:175:LEU:O	16:M:176:ARG:C	2.62	0.43
18:O:16:VAL:CG1	18:O:17:GLY:N	2.82	0.43
21:R:42:GLU:HG2	21:R:49:VAL:HG23	2.01	0.43
25:V:26:ILE:O	25:V:26:ILE:CG1	2.66	0.43
28:Y:32:LYS:HE2	28:Y:32:LYS:HB3	1.90	0.43
1:0:193:A:N1	1:0:413:G:O2'	2.50	0.43
1:0:250:C:O2'	1:0:251:C:H5'	2.18	0.43
1:0:354:A:H2'	1:0:355:C:H6	1.83	0.43
1:0:392:U:H4'	15:L:193:LYS:HB3	2.00	0.43
1:0:1008:C:O2'	1:0:1009:U:H5'	2.19	0.43
1:0:1377:C:H5'	1:0:1377:C:C6	2.51	0.43
1:0:1853:C:H5'	4:A:228:ILE:O	2.18	0.43
1:0:1947:G:N2	1:0:1966:U:C2	2.87	0.43
1:0:2684:A:H2'	1:0:2685:C:C6	2.54	0.43
2:9:3056:A:O2'	7:D:14:ARG:HD3	2.19	0.43
4:A:97:ALA:HB2	4:A:150:PRO:HB2	2.01	0.43
4:A:103:VAL:HA	4:A:104:PRO:HD3	1.84	0.43
9:F:36:THR:OG1	38:F:3111:HOH:O	2.22	0.43
9:F:104:ALA:C	9:F:106:THR:H	2.27	0.43
11:H:111:MET:O	11:H:114:PRO:HD3	2.19	0.43
15:L:71:SER:HB2	15:L:92:THR:HG22	2.00	0.43
16:M:108:SER:HA	16:M:109:PRO:HD3	1.80	0.43
18:O:135:ALA:HB1	18:O:139:ARG:HH12	1.84	0.43
19:P:93:ARG:HG3	19:P:93:ARG:NH1	2.34	0.43
24:U:11:MET:HE1	24:U:19:GLU:HG2	2.00	0.43
1:0:123:U:H2'	1:0:124:C:C6	2.54	0.42
1:0:152:A:H2'	1:0:153:C:C6	2.54	0.42
1:0:1329:A:N1	36:0:8513:CL:CL	2.88	0.42
1:0:1667:A:H5'	1:0:1667:A:C8	2.50	0.42
1:0:2688:U:H2'	1:0:2689:A:C8	2.54	0.42
5:B:205:VAL:O	5:B:307:ARG:CD	2.67	0.42
6:C:138:VAL:O	6:C:234:VAL:HA	2.19	0.42
7:D:151:ILE:HA	7:D:152:PRO:HD3	1.89	0.42
14:K:133:VAL:HB	38:K:8562:HOH:O	2.19	0.42
20:Q:89:LEU:HD23	20:Q:89:LEU:HA	1.79	0.42
24:U:12:THR:HG23	24:U:14:ALA:N	2.34	0.42
1:0:61:G:C2	1:0:62:C:C2	3.07	0.42
1:0:843:A:C2	1:0:846:A:C8	3.08	0.42
1:0:2105:C:H2'	1:0:2106:C:C6	2.54	0.42
1:0:2544:G:H2'	1:0:2545:U:O4'	2.18	0.42
1:0:2708:G:H2'	1:0:2709:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2730:G:O2'	1:0:2731:G:H5'	2.19	0.42
1:0:2840:A:H3'	38:0:8528:HOH:O	2.18	0.42
38:0:4962:HOH:O	6:C:149:LYS:HE3	2.18	0.42
2:9:3007:G:H4'	16:M:55:ASP:OD2	2.18	0.42
5:B:238:ASN:ND2	5:B:240:GLY:N	2.54	0.42
6:C:194:PHE:HA	6:C:234:VAL:HG13	2.00	0.42
7:D:84:LEU:C	7:D:86:THR:H	2.27	0.42
8:E:106:ASN:ND2	8:E:109:GLY:HA2	2.34	0.42
12:I:6:PHE:O	12:I:8:ALA:N	2.52	0.42
15:L:35:PRO:HD2	15:L:38:VAL:CG2	2.48	0.42
21:R:57:THR:CG2	21:R:58:MET:N	2.82	0.42
25:V:29:VAL:O	25:V:30:ASN:HB2	2.18	0.42
25:V:154:ARG:HB3	25:V:154:ARG:HE	1.50	0.42
31:2:5:ARG:O	31:2:5:ARG:HG3	2.20	0.42
1:0:525:G:H2'	1:0:526:U:O4'	2.18	0.42
1:0:639:A:H2'	1:0:640:G:H8	1.83	0.42
1:0:776:A:H1'	1:0:779:U:O4	2.19	0.42
1:0:1139:U:H2'	1:0:1140:C:H6	1.84	0.42
1:0:1328:A:N7	1:0:1329:A:C5	2.87	0.42
1:0:1342:C:O2'	1:0:1343:C:H5'	2.19	0.42
1:0:1433:G:O2'	1:0:1434:A:H5'	2.19	0.42
1:0:2347:C:H2'	1:0:2348:C:H6	1.85	0.42
1:0:2896:A:N3	1:0:2896:A:H2'	2.34	0.42
38:0:7645:HOH:O	16:M:4:PRO:HD2	2.19	0.42
38:9:8411:HOH:O	7:D:68:PRO:HG3	2.20	0.42
4:A:88:ILE:CD1	4:A:100:PRO:HD3	2.47	0.42
7:D:133:ASN:HD22	7:D:133:ASN:HA	1.66	0.42
8:E:101:GLU:OE2	8:E:115:ARG:HD3	2.19	0.42
11:H:46:VAL:CG1	11:H:146:TRP:HZ3	2.32	0.42
13:J:9:THR:HG22	13:J:78:LYS:HG2	2.01	0.42
16:M:34:LEU:HD22	16:M:129:ILE:CD1	2.49	0.42
21:R:57:THR:C	21:R:59:ASP:N	2.76	0.42
1:0:301:G:O2'	1:0:302:A:H5'	2.19	0.42
1:0:565:A:H2'	1:0:566:A:C8	2.54	0.42
1:0:675:U:O2'	6:C:42:ARG:NH1	2.52	0.42
1:0:1028:U:H5'	1:0:1031:G:O4'	2.19	0.42
1:0:1635:U:O2'	1:0:1636:G:H5'	2.19	0.42
1:0:1649:G:O2'	1:0:1650:C:H5'	2.18	0.42
1:0:1669:A:H2'	1:0:1670:G:H8	1.84	0.42
1:0:2011:A:H5'	1:0:2013:G:H1'	2.00	0.42
1:0:2039:A:H4'	1:0:2760:C:O2'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2053:G:H4'	20:Q:136:TRP:CE2	2.55	0.42
1:O:2353:A:H4'	1:O:2354:A:O5'	2.19	0.42
38:O:5879:HOH:O	11:H:57:ARG:HG3	2.19	0.42
5:B:33:ASP:HB3	5:B:34:GLY:H	1.71	0.42
5:B:62:ARG:HA	5:B:65:MET:CE	2.38	0.42
5:B:152:PRO:HD2	38:B:8645:HOH:O	2.18	0.42
6:C:40:ALA:HB3	6:C:100:LEU:HD12	2.02	0.42
7:D:166:ILE:O	7:D:169:THR:N	2.51	0.42
11:H:31:PHE:HE2	11:H:87:LYS:O	2.02	0.42
12:I:142:ASN:O	12:I:144:THR:N	2.52	0.42
16:M:175:LEU:HA	16:M:175:LEU:HD12	1.75	0.42
24:U:1:THR:C	24:U:3:LEU:N	2.77	0.42
24:U:45:ARG:C	24:U:47:LYS:N	2.74	0.42
27:X:205:ILE:O	27:X:206:ALA:C	2.60	0.42
29:Z:25:LYS:CD	30:1:49:GLU:H	2.28	0.42
1:O:191:A:H2'	1:O:237:G:O6	2.19	0.42
1:O:307:G:C2	1:O:309:C:C4	3.06	0.42
1:O:317:A:H5'	22:S:52:ARG:HD2	2.01	0.42
1:O:370:G:O2'	1:O:371:U:H5'	2.19	0.42
1:O:770:C:O2'	1:O:771:G:H5'	2.18	0.42
1:O:821:U:H2'	1:O:822:C:C6	2.54	0.42
1:O:902:G:N7	14:K:18:HIS:CD2	2.85	0.42
1:O:1517:U:H2'	1:O:1518:A:C8	2.54	0.42
1:O:1714:C:H4'	1:O:2745:C:O2	2.19	0.42
1:O:2039:A:H2'	1:O:2040:C:C6	2.55	0.42
1:O:2651:C:H2'	1:O:2652:U:O4'	2.19	0.42
1:O:2824:C:H5''	1:O:2825:C:H5'	2.01	0.42
5:B:83:ALA:HB2	5:B:101:TRP:CD2	2.54	0.42
7:D:54:ALA:O	7:D:65:GLU:O	2.37	0.42
9:F:4:VAL:HA	9:F:76:PHE:CE1	2.54	0.42
11:H:48:LEU:CG	11:H:157:ILE:HG21	2.48	0.42
12:I:45:VAL:HG22	12:I:46:ILE:N	2.34	0.42
13:J:19:THR:HB	13:J:94:ALA:HB2	2.01	0.42
14:K:124:ASP:OD1	14:K:149:ARG:NH2	2.53	0.42
15:L:137:ASP:O	15:L:142:LYS:HE3	2.19	0.42
1:O:92:G:H4'	24:U:44:GLY:HA3	2.00	0.42
1:O:585:C:H2'	1:O:586:C:C6	2.54	0.42
1:O:709:G:O2'	17:N:25:VAL:CG1	2.67	0.42
1:O:846:A:O2'	1:O:847:C:H5'	2.19	0.42
1:O:920:C:H5'	1:O:921:G:C4	2.55	0.42
1:O:1014:A:H5''	2:9:3101:G:O2'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1200:A:H2'	38:0:6645:HOH:O	2.20	0.42
1:0:1217:G:H2'	1:0:1218:U:H6	1.85	0.42
1:0:1320:U:H2'	1:0:1321:A:C8	2.55	0.42
1:0:1574:C:H2'	1:0:1575:C:C6	2.55	0.42
1:0:1996:U:H6	1:0:2586:U:O2	2.03	0.42
1:0:2413:A:N7	16:M:109:PRO:CB	2.81	0.42
1:0:2670:G:H4'	5:B:112:THR:HG22	2.02	0.42
38:0:4613:HOH:O	15:L:79:LYS:HD3	2.20	0.42
5:B:132:HIS:CE1	5:B:171:VAL:CG2	3.03	0.42
6:C:200:PRO:HB3	6:C:212:VAL:HG23	2.01	0.42
8:E:15:GLN:NE2	8:E:40:VAL:O	2.52	0.42
8:E:116:THR:HG22	8:E:151:LEU:HD22	2.00	0.42
10:G:20:VAL:O	10:G:24:VAL:HG23	2.20	0.42
11:H:149:ALA:C	11:H:151:MET:N	2.77	0.42
12:I:130:VAL:HG12	12:I:131:THR:N	2.32	0.42
14:K:105:TYR:C	14:K:105:TYR:CD1	2.97	0.42
16:M:69:TYR:HE2	16:M:183:ASP:OD2	2.03	0.42
18:O:103:THR:O	18:O:107:GLU:HG3	2.20	0.42
19:P:42:LYS:HA	19:P:42:LYS:HD2	1.93	0.42
29:Z:25:LYS:HD2	30:1:48:ASP:HA	2.02	0.42
1:0:35:U:O2'	1:0:36:C:H5'	2.20	0.42
1:0:169:A:O2'	31:2:48:ASN:ND2	2.53	0.42
1:0:255:A:H2'	1:0:256:C:H6	1.83	0.42
1:0:424:C:H2'	1:0:425:U:H6	1.85	0.42
1:0:424:C:H2'	1:0:425:U:C6	2.53	0.42
1:0:750:A:O3'	6:C:101:ASP:HB2	2.20	0.42
1:0:1236:A:H2'	1:0:1237:U:O4'	2.20	0.42
1:0:1362:U:H5'	38:0:4214:HOH:O	2.19	0.42
1:0:1477:C:O2'	1:0:1478:U:H5'	2.19	0.42
1:0:1511:U:O2'	1:0:1512:G:H5'	2.19	0.42
1:0:1597:A:O4'	18:O:95:GLU:HG2	2.20	0.42
1:0:1976:G:H1'	1:0:2005:G:N2	2.35	0.42
1:0:1992:U:H2'	1:0:1994:A:OP2	2.20	0.42
1:0:2004:U:H2'	1:0:2005:G:OP1	2.19	0.42
1:0:2327:A:H2'	1:0:2328:U:C6	2.55	0.42
1:0:2478:U:H2'	1:0:2479:A:H8	1.85	0.42
4:A:16:PHE:HB3	38:A:8556:HOH:O	2.20	0.42
5:B:183:GLU:OE1	5:B:183:GLU:HA	2.20	0.42
14:K:73:VAL:HG11	14:K:118:LEU:HD21	2.02	0.42
16:M:34:LEU:HA	16:M:47:LEU:CD2	2.50	0.42
16:M:67:ALA:O	16:M:69:TYR:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:80:GLU:OE2	22:S:84:GLY:HA2	2.20	0.42
28:Y:13:ARG:NH1	28:Y:14:PHE:CZ	2.87	0.42
28:Y:42:CYS:SG	28:Y:43:GLY:N	2.93	0.42
30:1:22:PRO:HG2	30:1:25:VAL:HG23	2.02	0.42
1:0:17:G:H2'	1:0:18:C:C6	2.54	0.42
1:0:39:G:N2	1:0:444:C:C2	2.88	0.42
1:0:1056:U:O4'	11:H:5:MET:HE3	2.20	0.42
1:0:1276:U:H3'	17:N:19:ARG:NH1	2.34	0.42
1:0:1666:C:H2'	1:0:1667:A:C8	2.54	0.42
2:9:3031:C:H2'	2:9:3032:G:O4'	2.19	0.42
5:B:27:ASN:HB3	38:B:8641:HOH:O	2.19	0.42
7:D:41:LEU:O	7:D:44:ILE:HG22	2.20	0.42
7:D:81:GLU:O	7:D:84:LEU:N	2.52	0.42
7:D:81:GLU:C	7:D:83:PHE:N	2.76	0.42
8:E:3:VAL:HG22	8:E:49:ILE:HB	2.01	0.42
9:F:21:GLU:O	9:F:24:ARG:CG	2.65	0.42
9:F:23:ALA:HB1	38:F:5413:HOH:O	2.19	0.42
11:H:29:ALA:CB	11:H:65:ARG:HH12	2.18	0.42
11:H:47:GLU:CB	11:H:133:ILE:CD1	2.95	0.42
14:K:12:THR:HG21	14:K:16:GLY:O	2.19	0.42
16:M:154:LEU:HG	16:M:155:GLU:H	1.84	0.42
16:M:157:PRO:HG3	38:M:8526:HOH:O	2.19	0.42
23:T:37:GLU:O	23:T:40:ALA:HB3	2.20	0.42
25:V:65:VAL:HA	25:V:68:THR:HG22	2.01	0.42
28:Y:30:GLU:C	28:Y:33:HIS:HB3	2.44	0.42
1:0:462:A:C8	30:1:37:HIS:CE1	3.08	0.42
1:0:630:A:H5''	38:0:5660:HOH:O	2.19	0.42
1:0:757:C:H2'	1:0:758:A:C8	2.55	0.42
1:0:1069:C:H2'	1:0:1070:A:O4'	2.20	0.42
1:0:1268:C:O2'	1:0:1269:G:H5'	2.19	0.42
1:0:1289:C:O2'	1:0:1290:G:H5'	2.20	0.42
1:0:1769:C:O2'	1:0:1770:U:H5'	2.20	0.42
1:0:1988:C:C2	1:0:2001:G:N2	2.88	0.42
1:0:2055:A:H4'	20:Q:132:ARG:NH2	2.35	0.42
1:0:2406:U:C2	1:0:2407:G:C8	3.08	0.42
1:0:2869:G:H2'	1:0:2870:C:C6	2.54	0.42
1:0:2895:C:H4'	38:W:4132:HOH:O	2.19	0.42
10:G:19:GLU:O	10:G:20:VAL:C	2.63	0.42
11:H:150:LYS:HA	11:H:153:VAL:HG22	2.01	0.42
20:Q:19:ARG:HA	20:Q:142:ASP:OD1	2.20	0.42
25:V:76:ASP:O	25:V:77:ALA:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:73:C:O2'	1:0:74:A:H5'	2.19	0.42
1:0:185:G:H4'	1:0:186:A:H4'	2.01	0.42
1:0:319:A:H2'	1:0:320:G:C8	2.55	0.42
1:0:441:A:H1'	1:0:442:A:N7	2.35	0.42
1:0:660:A:N6	1:0:746:A:O4'	2.53	0.42
1:0:668:C:H2'	1:0:669:G:C8	2.55	0.42
1:0:834:G:H5''	1:0:835:U:O5'	2.19	0.42
1:0:1184:C:O2'	1:0:1185:U:OP2	2.35	0.42
1:0:1352:A:P	6:C:92:PRO:HG3	2.60	0.42
1:0:1520:G:H2'	1:0:1521:C:C6	2.54	0.42
1:0:1905:U:H2'	1:0:1906:C:C6	2.54	0.42
1:0:2381:C:H4'	31:2:80:ARG:NH1	2.34	0.42
1:0:2445:U:H2'	1:0:2446:G:C8	2.55	0.42
1:0:2604:A:H5'	38:0:6679:HOH:O	2.19	0.42
1:0:2782:G:O6	1:0:2790:C:H5''	2.19	0.42
1:0:2866:U:H4'	1:0:2867:G:H5'	2.02	0.42
4:A:65:ARG:HG2	4:A:65:ARG:NH1	2.35	0.42
4:A:130:THR:HG22	4:A:131:HIS:N	2.33	0.42
6:C:95:GLU:H	6:C:95:GLU:CD	2.28	0.42
6:C:114:ALA:HB1	6:C:223:LEU:HB3	2.01	0.42
8:E:15:GLN:HB2	8:E:20:ILE:HA	2.02	0.42
15:L:139:PRO:C	15:L:141:ILE:H	2.28	0.42
18:O:59:ARG:O	18:O:62:ALA:HB3	2.20	0.42
20:Q:29:LYS:CD	38:Q:8542:HOH:O	2.60	0.42
20:Q:99:ALA:CB	20:Q:109:MET:HE1	2.22	0.42
22:S:69:LYS:O	22:S:71:VAL:HG23	2.20	0.42
26:W:30:MET:CE	26:W:58:ALA:HB3	2.44	0.42
1:0:23:G:H1'	1:0:520:A:N6	2.35	0.41
1:0:51:G:O2'	1:0:52:A:H5'	2.20	0.41
1:0:145:A:H4'	15:L:137:ASP:OD2	2.20	0.41
1:0:163:U:O3'	1:0:896:C:H4'	2.19	0.41
1:0:1116:U:C2'	1:0:1118:A:C2	3.03	0.41
1:0:1514:C:H2'	1:0:1515:A:C8	2.55	0.41
1:0:1524:U:O2'	1:0:1525:G:P	2.78	0.41
1:0:2253:G:O2'	1:0:2254:G:H5'	2.21	0.41
1:0:2301:A:H5''	1:0:2302:A:H5'	2.02	0.41
1:0:2389:U:H4'	19:P:53:HIS:CD2	2.54	0.41
5:B:60:SER:C	5:B:62:ARG:H	2.27	0.41
5:B:139:ASP:HB2	38:B:8532:HOH:O	2.19	0.41
5:B:304:PRO:HD2	5:B:307:ARG:HH11	1.83	0.41
6:C:236:THR:HG21	38:C:8382:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:140:ARG:HH11	7:D:140:ARG:HG3	1.84	0.41
11:H:75:SER:HB3	11:H:79:ALA:HB1	2.02	0.41
15:L:133:LEU:O	15:L:134:ILE:HD13	2.20	0.41
16:M:102:LEU:HG	16:M:104:ILE:CG2	2.50	0.41
17:N:15:LYS:O	17:N:16:SER:C	2.61	0.41
18:O:2:ASP:OD1	18:O:2:ASP:C	2.63	0.41
19:P:32:GLU:HA	19:P:71:TYR:HH	1.83	0.41
20:Q:39:THR:O	20:Q:40:ALA:C	2.62	0.41
20:Q:44:VAL:HG13	20:Q:89:LEU:HD22	2.01	0.41
20:Q:123:GLN:HA	20:Q:137:ASN:OD1	2.20	0.41
21:R:8:PRO:HD2	24:U:32:ALA:HA	2.02	0.41
27:X:197:ASP:C	27:X:197:ASP:OD1	2.63	0.41
30:1:36:ASN:HB3	30:1:39:ARG:HG3	2.01	0.41
1:0:689:G:H2'	1:0:690:G:H8	1.84	0.41
1:0:883:U:O2	1:0:883:U:C2'	2.67	0.41
1:0:1044:C:H5''	38:0:3019:HOH:O	2.19	0.41
1:0:1132:A:N3	1:0:2521:A:O2'	2.52	0.41
1:0:1334:C:H2'	1:0:1335:C:H6	1.85	0.41
1:0:1409:G:H5'	38:0:4658:HOH:O	2.19	0.41
1:0:2502:C:C4'	11:H:151:MET:CG	2.98	0.41
2:9:3011:A:O2'	2:9:3012:C:H3'	2.20	0.41
2:9:3036:C:C5	2:9:3037:C:C5	3.08	0.41
6:C:35:VAL:HG21	6:C:227:GLY:HA2	2.02	0.41
12:I:70:PHE:CD2	12:I:70:PHE:O	2.73	0.41
14:K:90:ARG:HA	14:K:119:THR:HB	2.02	0.41
19:P:66:LYS:HB2	19:P:70:ALA:O	2.19	0.41
20:Q:100:ASP:C	20:Q:102:GLN:N	2.78	0.41
22:S:53:GLY:HA3	38:S:6384:HOH:O	2.20	0.41
25:V:28:HIS:HD2	25:V:31:HIS:CE1	2.38	0.41
25:V:34:LEU:HD12	25:V:100:LEU:HD13	2.02	0.41
26:W:74:ALA:HB2	26:W:85:VAL:HG13	2.01	0.41
1:0:251:C:H5'	15:L:140:ALA:HA	2.02	0.41
1:0:294:C:H2'	1:0:295:C:O4'	2.20	0.41
1:0:876:A:N3	1:0:876:A:H2'	2.35	0.41
1:0:1444:G:O2'	1:0:1502:A:N1	2.48	0.41
1:0:1735:C:H5'	5:B:235:ARG:NH2	2.35	0.41
1:0:2737:C:H3'	1:0:2738:G:H5''	2.02	0.41
1:0:2781:U:H2'	1:0:2782:G:C5'	2.50	0.41
2:9:3056:A:C3'	2:9:3057:A:H5''	2.50	0.41
4:A:130:THR:HG22	4:A:131:HIS:O	2.20	0.41
4:A:186:TRP:CG	4:A:187:PRO:HA	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:145:HIS:CD2	5:B:145:HIS:C	2.98	0.41
7:D:95:THR:OG1	7:D:174:VAL:HG22	2.20	0.41
16:M:67:ALA:HA	16:M:71:TRP:HB3	2.02	0.41
16:M:141:ARG:HB3	38:M:8569:HOH:O	2.20	0.41
19:P:88:ALA:O	19:P:90:HIS:N	2.53	0.41
23:T:6:CYS:HA	23:T:13:ILE:HD11	2.02	0.41
26:W:76:ARG:NH1	26:W:76:ARG:CG	2.79	0.41
27:X:197:ASP:OD1	27:X:199:ASP:HB2	2.20	0.41
1:O:213:G:O2'	1:O:214:U:OP2	2.37	0.41
1:O:311:C:H2'	1:O:312:U:C6	2.56	0.41
1:O:474:C:O3'	6:C:73:LEU:HD21	2.20	0.41
1:O:1150:A:N7	10:G:69:ARG:NH2	2.69	0.41
1:O:1150:A:C2	10:G:20:VAL:HG21	2.55	0.41
1:O:1365:C:H2'	1:O:1366:C:H6	1.85	0.41
1:O:1586:G:H2'	1:O:1587:U:H6	1.85	0.41
1:O:1711:A:O2'	1:O:1712:A:H5'	2.20	0.41
1:O:2703:A:H2'	1:O:2704:C:H6	1.85	0.41
1:O:2900:G:H2'	1:O:2901:C:O4'	2.20	0.41
2:9:3008:G:O6	16:M:11:ARG:NH1	2.54	0.41
11:H:82:LYS:NZ	11:H:82:LYS:HB2	2.36	0.41
15:L:46:LEU:HB2	38:L:8611:HOH:O	2.20	0.41
15:L:78:ASN:O	15:L:79:LYS:HG2	2.20	0.41
16:M:24:LEU:O	16:M:28:LYS:HG2	2.21	0.41
16:M:50:LEU:HD12	16:M:50:LEU:HA	1.74	0.41
16:M:71:TRP:CE2	16:M:73:ALA:HB3	2.55	0.41
17:N:42:GLU:HB2	38:N:2176:HOH:O	2.20	0.41
20:Q:34:GLU:HG2	20:Q:46:TYR:CZ	2.56	0.41
25:V:146:ILE:HG23	25:V:150:LEU:HD12	2.02	0.41
31:2:38:ARG:O	31:2:42:ARG:HB2	2.20	0.41
1:O:541:C:H2'	1:O:542:A:H5'	2.01	0.41
1:O:658:C:O2'	1:O:662:U:OP1	2.28	0.41
1:O:734:U:H2'	1:O:736:A:OP2	2.21	0.41
1:O:736:A:H2'	1:O:737:A:O4'	2.20	0.41
1:O:946:C:H2'	1:O:947:U:H6	1.85	0.41
1:O:1003:U:O2'	11:H:90:PHE:HE1	2.03	0.41
1:O:1666:C:C2'	1:O:1667:A:C5'	2.97	0.41
1:O:2135:A:O2'	1:O:2136:G:H5'	2.20	0.41
1:O:2501:G:H1'	38:O:5452:HOH:O	2.20	0.41
38:O:4776:HOH:O	11:H:11:LYS:HE2	2.20	0.41
5:B:176:ASP:O	5:B:177:HIS:C	2.64	0.41
6:C:2:GLN:HB3	38:C:8342:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:79:ARG:O	6:C:80:VAL:C	2.63	0.41
6:C:187:ARG:HD2	6:C:188:ARG:N	2.35	0.41
7:D:166:ILE:O	7:D:167:GLU:C	2.62	0.41
9:F:26:THR:HG21	9:F:102:GLY:C	2.45	0.41
15:L:69:LYS:HD3	15:L:125:ARG:HA	2.02	0.41
15:L:71:SER:CB	15:L:92:THR:HG22	2.51	0.41
15:L:137:ASP:HA	15:L:142:LYS:HE3	2.02	0.41
18:O:76:GLY:O	18:O:79:SER:HB2	2.21	0.41
21:R:23:LYS:HE2	38:R:8333:HOH:O	2.20	0.41
1:0:128:A:C8	1:0:128:A:H3'	2.55	0.41
1:0:168:C:C2'	1:0:169:A:H5'	2.50	0.41
1:0:1192:A:H3'	1:0:1193:A:H5'	2.02	0.41
1:0:1323:G:C2	1:0:1324:G:C8	3.09	0.41
1:0:1375:A:C2'	1:0:1376:G:H5'	2.50	0.41
1:0:1473:U:O2'	1:0:1474:C:H5''	2.20	0.41
1:0:1626:A:C2'	1:0:1627:G:H5'	2.51	0.41
1:0:1780:G:O2'	1:0:1781:G:H5'	2.20	0.41
1:0:2082:G:O2'	1:0:2083:A:H5'	2.20	0.41
1:0:2443:C:O3'	14:K:56:LYS:HE3	2.20	0.41
1:0:2656:G:C2'	1:0:2657:G:H5'	2.50	0.41
1:0:2686:C:O2'	1:0:2687:G:H5'	2.21	0.41
38:0:3197:HOH:O	4:A:11:ARG:HD3	2.20	0.41
9:F:58:GLU:CA	9:F:61:MET:HG3	2.46	0.41
11:H:47:GLU:CG	11:H:133:ILE:CD1	2.99	0.41
12:I:74:ARG:HD3	38:I:5061:HOH:O	2.21	0.41
14:K:122:ALA:HB3	14:K:125:PHE:CZ	2.56	0.41
16:M:180:LEU:O	16:M:181:ASP:CB	2.69	0.41
24:U:38:GLY:C	24:U:40:PRO:HD2	2.46	0.41
25:V:6:GLN:CB	25:V:26:ILE:HD12	2.39	0.41
31:2:70:ARG:HB3	38:2:8576:HOH:O	2.20	0.41
1:0:10:U:O2'	1:0:11:A:H8	2.03	0.41
1:0:166:A:N7	14:K:25:GLY:HA2	2.35	0.41
1:0:345:G:N2	1:0:346:U:H1'	2.35	0.41
1:0:681:G:N3	1:0:681:G:H5'	2.36	0.41
1:0:711:G:N2	1:0:718:C:C2	2.88	0.41
1:0:778:C:C4	1:0:779:U:C4	3.09	0.41
1:0:2478:U:O2'	1:0:2479:A:H5'	2.20	0.41
1:0:2551:C:O2'	1:0:2552:C:H5'	2.21	0.41
1:0:2599:A:C6	1:0:2600:A:N1	2.89	0.41
1:0:2831:C:H2'	1:0:2832:C:H5'	2.02	0.41
1:0:2833:C:H2'	1:0:2834:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2898:G:H2'	1:0:2899:A:H8	1.84	0.41
2:9:3007:G:OP1	16:M:23:ARG:NE	2.53	0.41
2:9:3034:A:H2'	2:9:3035:C:O4'	2.21	0.41
4:A:48:ASP:HA	4:A:49:PRO:HD3	1.85	0.41
4:A:105:VAL:HG13	4:A:155:THR:O	2.20	0.41
4:A:169:PHE:O	4:A:170:VAL:HB	2.21	0.41
4:A:211:LYS:HB3	4:A:212:PRO:CD	2.43	0.41
5:B:320:GLN:HG3	5:B:321:PRO:CD	2.51	0.41
6:C:237:GLU:N	38:C:8461:HOH:O	2.53	0.41
11:H:57:ARG:C	11:H:59:ASN:N	2.77	0.41
13:J:40:THR:O	13:J:41:LYS:C	2.62	0.41
15:L:63:VAL:HG21	15:L:109:PHE:CE1	2.56	0.41
15:L:173:LEU:HD23	15:L:183:VAL:HG12	2.02	0.41
23:T:9:CYS:CA	23:T:52:THR:HG23	2.46	0.41
23:T:14:GLU:HA	23:T:15:PRO:HD2	1.92	0.41
24:U:42:ASN:O	24:U:44:GLY:N	2.53	0.41
1:0:138:U:OP2	1:0:139:C:H5	2.03	0.41
1:0:329:A:OP2	6:C:206:ASN:HB2	2.21	0.41
1:0:380:A:H5''	15:L:48:ARG:NH2	2.35	0.41
1:0:716:G:O2'	1:0:717:C:H5'	2.21	0.41
1:0:952:G:N3	1:0:2302:A:H2'	2.35	0.41
1:0:1003:U:O2	11:H:90:PHE:HZ	2.03	0.41
1:0:1525:G:H5'	1:0:1526:A:OP2	2.20	0.41
1:0:1616:A:H2'	1:0:1618:G:C8	2.55	0.41
1:0:2381:C:H4'	31:2:80:ARG:CZ	2.51	0.41
1:0:2688:U:H2'	1:0:2689:A:H8	1.85	0.41
1:0:2737:C:H3'	1:0:2738:G:C5'	2.51	0.41
4:A:36:ASP:HB2	4:A:85:ASP:H	1.86	0.41
4:A:75:GLY:HA2	28:Y:63:LYS:O	2.21	0.41
4:A:123:GLY:HA3	4:A:162:GLY:HA2	2.03	0.41
5:B:26:PHE:CE1	5:B:310:ARG:HB3	2.55	0.41
12:I:24:SER:HA	12:I:86:MET:SD	2.61	0.41
13:J:49:LEU:HD21	13:J:74:VAL:C	2.45	0.41
14:K:17:SER:C	14:K:19:LYS:H	2.28	0.41
15:L:59:GLY:HA3	15:L:141:ILE:CD1	2.50	0.41
16:M:35:VAL:HG12	16:M:37:ARG:HG2	2.02	0.41
24:U:5:VAL:HG23	38:U:2271:HOH:O	2.20	0.41
25:V:139:GLY:O	25:V:141:HIS:CD2	2.74	0.41
26:W:20:GLU:O	26:W:21:PRO:C	2.61	0.41
26:W:41:PHE:O	26:W:42:SER:C	2.63	0.41
1:0:61:G:OP1	30:1:17:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:291:C:H2'	1:0:292:G:O4'	2.21	0.41
1:0:331:A:C6	1:0:332:G:C4	3.08	0.41
1:0:701:U:C2	1:0:744:G:C2	3.08	0.41
1:0:818:A:H2	28:Y:13:ARG:HA	1.86	0.41
1:0:899:C:H5'	38:0:4153:HOH:O	2.21	0.41
1:0:926:A:H5'	14:K:39:GLU:OE2	2.20	0.41
1:0:1165:G:OP1	1:0:1165:G:H3'	2.21	0.41
1:0:1196:C:C2'	1:0:1197:G:H5'	2.51	0.41
1:0:1224:G:H2'	1:0:1225:C:C6	2.55	0.41
1:0:1269:G:H2'	1:0:1270:U:H6	1.86	0.41
1:0:1562:C:O2	1:0:1562:C:H2'	2.21	0.41
1:0:1697:G:O2'	1:0:1698:U:H5'	2.20	0.41
1:0:1748:U:H4'	38:0:8399:HOH:O	2.21	0.41
1:0:2042:U:H2'	1:0:2043:U:C6	2.56	0.41
1:0:2134:G:C6	1:0:2258:A:C8	3.09	0.41
1:0:2281:C:C2'	1:0:2282:U:H5'	2.49	0.41
1:0:2385:G:H2'	1:0:2386:U:C6	2.55	0.41
1:0:2506:A:O2'	1:0:2507:G:P	2.79	0.41
1:0:2662:G:O2'	1:0:2816:A:N1	2.53	0.41
1:0:2664:A:OP1	1:0:2664:A:H8	2.04	0.41
5:B:168:GLY:O	5:B:169:GLY:O	2.39	0.41
5:B:254:GLN:HG2	5:B:255:GLY:H	1.85	0.41
5:B:310:ARG:HD2	38:B:8663:HOH:O	2.21	0.41
6:C:7:ASP:O	6:C:9:ASP:N	2.54	0.41
7:D:15:GLU:HA	7:D:16:PRO:HD3	1.95	0.41
7:D:23:VAL:O	7:D:23:VAL:CG2	2.69	0.41
7:D:24:HIS:HB2	7:D:72:LYS:CB	2.51	0.41
7:D:25:MET:HE1	7:D:40:ILE:CG1	2.51	0.41
7:D:57:THR:CG2	7:D:63:ILE:HG22	2.48	0.41
11:H:55:GLN:NE2	11:H:124:ARG:NE	2.59	0.41
11:H:127:GLY:O	11:H:128:ALA:CB	2.66	0.41
11:H:140:PRO:HA	11:H:142:VAL:CG1	2.50	0.41
12:I:107:ASN:HD22	12:I:108:PRO:N	2.19	0.41
13:J:48:GLY:C	13:J:73:VAL:HG11	2.45	0.41
14:K:73:VAL:HG21	14:K:116:HIS:CD2	2.56	0.41
14:K:98:GLU:O	14:K:99:GLU:HB2	2.21	0.41
15:L:35:PRO:HD2	15:L:38:VAL:HG21	2.01	0.41
18:O:98:ILE:O	18:O:98:ILE:HD13	2.20	0.41
23:T:31:PHE:CG	23:T:37:GLU:HG2	2.56	0.41
24:U:59:ILE:O	24:U:63:GLU:HG2	2.21	0.41
25:V:35:VAL:HA	25:V:36:PRO:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:V:133:LYS:HG3	38:V:5904:HOH:O	2.20	0.41
25:V:139:GLY:O	25:V:141:HIS:HD2	2.03	0.41
26:W:7:GLU:HA	26:W:75:ALA:HA	2.03	0.41
26:W:22:ASN:C	26:W:24:LYS:H	2.29	0.41
27:X:126:PRO:HG2	27:X:128:PHE:CZ	2.56	0.41
27:X:130:ARG:HB2	27:X:142:SER:O	2.20	0.41
27:X:163:THR:HG23	38:X:8529:HOH:O	2.20	0.41
29:Z:10:LYS:HG3	38:Z:2979:HOH:O	2.20	0.41
1:0:255:A:H2'	1:0:256:C:O4'	2.21	0.41
1:0:968:G:O2'	1:0:969:G:H5'	2.20	0.41
1:0:1021:G:O2'	1:0:1022:A:H5'	2.21	0.41
1:0:1269:G:O2'	1:0:1270:U:H5'	2.21	0.41
1:0:1427:A:H61	1:0:1440:U:H1'	1.85	0.41
1:0:1552:G:H2'	1:0:1553:C:H6	1.84	0.41
1:0:1616:A:H5''	1:0:1617:C:OP1	2.21	0.41
1:0:1679:C:H5'	38:0:3303:HOH:O	2.20	0.41
1:0:1896:G:C6	1:0:1897:U:C4	3.08	0.41
1:0:2284:G:H5'	38:0:3431:HOH:O	2.20	0.41
1:0:2531:U:H2'	1:0:2532:A:O4'	2.20	0.41
1:0:2539:U:C5	32:0:9500:SLD:H7	2.56	0.41
2:9:3103:A:O2'	2:9:3104:A:H5'	2.21	0.41
4:A:93:THR:HG23	4:A:154:ALA:O	2.21	0.41
4:A:217:ARG:HH11	4:A:217:ARG:HG3	1.84	0.41
6:C:37:ALA:O	6:C:41:ASN:ND2	2.54	0.41
6:C:201:SER:O	6:C:202:THR:C	2.63	0.41
12:I:131:THR:CG2	12:I:134:GLU:HG3	2.51	0.41
16:M:25:ARG:O	16:M:28:LYS:HB2	2.21	0.41
16:M:71:TRP:CZ2	16:M:73:ALA:HB3	2.56	0.41
17:N:25:VAL:HG23	17:N:26:TRP:N	2.36	0.41
18:O:132:ASP:O	18:O:133:SER:HB3	2.20	0.41
25:V:96:LEU:O	25:V:97:ALA:C	2.64	0.41
25:V:105:THR:HA	25:V:109:GLU:OE1	2.20	0.41
25:V:108:ARG:HE	25:V:114:PRO:CG	2.33	0.41
25:V:132:VAL:HG23	25:V:138:LEU:O	2.21	0.41
26:W:75:ALA:O	26:W:83:ALA:HA	2.21	0.41
1:0:56:G:C5'	24:U:50:ARG:HH12	2.25	0.40
1:0:210:U:H2'	1:0:211:U:C6	2.56	0.40
1:0:244:C:H6	1:0:244:C:O5'	2.04	0.40
1:0:860:U:H2'	1:0:861:A:C8	2.56	0.40
1:0:1242:A:H5'	12:I:82:THR:CG2	2.37	0.40
1:0:1472:C:H6	1:0:1472:C:O5'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1624:A:H4'	1:0:1626:A:H5''	2.03	0.40
1:0:1853:C:H4'	4:A:217:ARG:HH22	1.87	0.40
1:0:2120:U:H2'	1:0:2121:G:O4'	2.22	0.40
1:0:2472:C:O2'	1:0:2634:G:H4'	2.21	0.40
1:0:2548:C:OP2	5:B:5:ARG:NH2	2.54	0.40
4:A:179:MET:HA	4:A:179:MET:CE	2.43	0.40
5:B:30:PRO:HB2	5:B:39:GLN:NE2	2.35	0.40
6:C:127:ARG:HD2	6:C:229:PRO:O	2.20	0.40
12:I:40:ASN:OD1	12:I:106:GLY:HA2	2.21	0.40
13:J:9:THR:O	13:J:10:GLN:C	2.64	0.40
13:J:82:ARG:HH21	13:J:115:ARG:HG2	1.86	0.40
14:K:125:PHE:CE2	14:K:140:VAL:HG22	2.56	0.40
15:L:67:ILE:HG21	15:L:97:ILE:HG23	2.03	0.40
19:P:11:ARG:HD3	38:P:5620:HOH:O	2.20	0.40
20:Q:57:VAL:HG21	20:Q:81:PRO:HD2	2.03	0.40
22:S:48:VAL:CG1	22:S:96:VAL:HG13	2.51	0.40
22:S:89:ARG:O	22:S:89:ARG:HG3	2.21	0.40
24:U:42:ASN:N	24:U:43:PRO:HD3	2.36	0.40
27:X:150:LEU:O	27:X:151:SER:C	2.65	0.40
1:0:485:A:O2'	1:0:487:G:H5'	2.22	0.40
1:0:558:C:C2'	1:0:559:U:C5'	2.99	0.40
1:0:816:G:C6	1:0:817:G:N1	2.89	0.40
1:0:834:G:H3'	1:0:835:U:H4'	2.04	0.40
1:0:1001:U:O2'	1:0:1002:G:H5'	2.21	0.40
1:0:1159:G:H1	1:0:1208:C:H42	1.69	0.40
1:0:1314:U:H2'	38:0:6761:HOH:O	2.20	0.40
1:0:1767:A:O2'	1:0:1768:C:H5'	2.21	0.40
1:0:1903:U:O2'	1:0:1904:A:N7	2.46	0.40
1:0:2001:G:C2'	1:0:2002:C:H5'	2.52	0.40
1:0:2890:A:H1'	23:T:56:ARG:HH21	1.80	0.40
2:9:3072:C:O2'	2:9:3073:G:H5'	2.21	0.40
4:A:55:VAL:HG11	4:A:67:LEU:HD13	2.02	0.40
6:C:185:LYS:HD3	6:C:186:TYR:CE1	2.56	0.40
11:H:74:ASN:ND2	11:H:141:ASN:OD1	2.55	0.40
11:H:82:LYS:NZ	11:H:82:LYS:CB	2.85	0.40
11:H:118:PRO:HD2	38:H:8341:HOH:O	2.20	0.40
12:I:14:ALA:HB1	12:I:44:ALA:HB2	2.02	0.40
13:J:72:VAL:O	13:J:95:ALA:HA	2.21	0.40
15:L:24:MET:HE3	15:L:28:MET:CE	2.51	0.40
15:L:74:ARG:HD3	15:L:91:ILE:HD12	2.04	0.40
15:L:97:ILE:CD1	15:L:127:LYS:HD2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:154:LEU:CG	16:M:155:GLU:H	2.34	0.40
17:N:105:ASN:HD21	17:N:109:SER:H	1.68	0.40
18:O:17:GLY:O	18:O:18:LYS:C	2.62	0.40
20:Q:31:ILE:O	20:Q:32:ALA:C	2.62	0.40
22:S:41:ARG:O	22:S:42:VAL:C	2.63	0.40
25:V:1:MET:H2	25:V:37:GLU:HG3	1.85	0.40
27:X:117:LEU:HA	27:X:174:VAL:HG11	2.03	0.40
1:O:514:G:O5'	1:O:514:G:H8	2.04	0.40
1:O:873:G:H2'	1:O:875:A:N7	2.37	0.40
1:O:1434:A:H2'	1:O:1436:C:C5	2.56	0.40
1:O:1897:U:O2'	1:O:1898:G:H5'	2.21	0.40
1:O:2050:G:OP1	20:Q:79:ARG:HB3	2.21	0.40
1:O:2852:A:H5''	38:O:6132:HOH:O	2.21	0.40
2:9:3013:A:H3'	2:9:3014:G:H5'	2.02	0.40
2:9:3067:C:H2'	2:9:3068:G:H8	1.86	0.40
4:A:32:VAL:O	4:A:33:GLU:C	2.63	0.40
4:A:107:ASN:OD1	4:A:116:GLY:HA3	2.21	0.40
4:A:179:MET:HE2	4:A:184:THR:HB	2.02	0.40
4:A:211:LYS:HD3	38:A:8623:HOH:O	2.20	0.40
5:B:209:LYS:HE2	38:B:8579:HOH:O	2.21	0.40
6:C:219:ASN:N	6:C:222:ASP:OD1	2.52	0.40
7:D:58:VAL:CG1	7:D:59:GLY:N	2.83	0.40
7:D:94:ALA:O	7:D:95:THR:O	2.39	0.40
8:E:21:THR:HG23	8:E:30:THR:OG1	2.21	0.40
28:Y:50:ALA:HB3	28:Y:54:ILE:CG2	2.49	0.40
30:1:41:HIS:CD2	30:1:44:ARG:H	2.34	0.40
31:2:84:ARG:HH11	31:2:84:ARG:HG3	1.86	0.40
1:O:230:C:H2'	1:O:231:G:C8	2.57	0.40
1:O:422:G:H2'	1:O:423:A:H8	1.85	0.40
1:O:775:G:OP1	29:Z:16:HIS:HE1	2.03	0.40
1:O:929:A:H8	1:O:929:A:O5'	2.04	0.40
1:O:1331:A:O2'	1:O:1332:C:H5'	2.21	0.40
1:O:1497:G:O2'	1:O:1498:G:H5'	2.22	0.40
1:O:1572:A:H2'	1:O:1573:A:C8	2.55	0.40
1:O:1682:A:H5''	38:O:3430:HOH:O	2.21	0.40
1:O:1743:G:H1'	38:O:5797:HOH:O	2.22	0.40
1:O:2124:G:H2'	1:O:2125:G:C8	2.57	0.40
1:O:2134:G:N2	1:O:2242:U:C2	2.90	0.40
1:O:2546:U:H2'	1:O:2547:C:C6	2.57	0.40
1:O:2653:A:H2'	1:O:2654:C:C6	2.57	0.40
1:O:2658:G:H4'	1:O:2842:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3045:A:H2'	2:9:3046:C:C6	2.55	0.40
5:B:108:GLU:HB3	5:B:111:ARG:HD2	2.04	0.40
8:E:100:ASP:HB2	38:E:2789:HOH:O	2.22	0.40
9:F:58:GLU:HA	9:F:61:MET:HE2	2.03	0.40
15:L:66:ALA:HB2	15:L:128:TRP:NE1	2.37	0.40
15:L:183:VAL:HG12	15:L:184:ARG:N	2.37	0.40
17:N:26:TRP:CE3	17:N:26:TRP:HA	2.57	0.40
18:O:126:ALA:C	18:O:128:GLY:H	2.30	0.40
22:S:32:ARG:HH12	22:S:38:ARG:HH12	1.67	0.40
22:S:48:VAL:HG13	22:S:96:VAL:HG13	2.03	0.40
31:2:11:CYS:SG	31:2:14:CYS:HB2	2.61	0.40
31:2:34:LYS:HB2	31:2:37:ASP:OD2	2.20	0.40
1:0:473:A:OP1	29:Z:51:GLN:NE2	2.55	0.40
1:0:588:G:O6	25:V:154:ARG:NH1	2.55	0.40
1:0:675:U:H2'	1:0:676:C:H5'	2.03	0.40
1:0:870:G:C3'	1:0:871:G:H5''	2.52	0.40
1:0:1211:G:O2'	1:0:1212:C:H5'	2.21	0.40
1:0:1235:G:C1'	12:I:63:ILE:HG23	2.51	0.40
1:0:1345:A:H2'	1:0:1346:U:H6	1.85	0.40
1:0:1609:C:H2'	1:0:1610:G:H8	1.87	0.40
1:0:1675:C:H5''	30:1:5:LYS:HD2	2.04	0.40
1:0:1792:C:H2'	1:0:1793:C:C6	2.56	0.40
1:0:2011:A:O4'	1:0:2013:G:C8	2.75	0.40
1:0:2255:A:N1	1:0:2256:G:C4	2.90	0.40
1:0:2659:U:H4'	20:Q:76:ASP:HB3	2.04	0.40
4:A:94:LEU:N	4:A:94:LEU:CD2	2.83	0.40
4:A:105:VAL:HG11	4:A:154:ALA:CB	2.52	0.40
4:A:165:THR:O	4:A:165:THR:HG22	2.20	0.40
5:B:5:ARG:HA	5:B:6:PRO:HD3	2.00	0.40
5:B:185:GLY:HA2	38:B:8647:HOH:O	2.21	0.40
7:D:18:ILE:HG12	7:D:134:LEU:HD21	2.04	0.40
9:F:22:VAL:CG2	9:F:104:ALA:HB2	2.52	0.40
11:H:57:ARG:HG3	11:H:57:ARG:HH11	1.86	0.40
11:H:58:HIS:CE1	11:H:59:ASN:HD21	2.40	0.40
12:I:75:PRO:HG2	12:I:105:LEU:CD2	2.49	0.40
15:L:169:ARG:HD2	38:L:8593:HOH:O	2.21	0.40
16:M:37:ARG:HD3	36:M:8507:CL:CL	2.58	0.40
16:M:119:GLN:HE21	16:M:129:ILE:CG2	2.34	0.40
18:O:11:ALA:HB2	18:O:18:LYS:HA	2.03	0.40
23:T:49:LEU:HD13	23:T:51:TRP:CZ2	2.57	0.40
24:U:12:THR:O	24:U:13:PRO:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:V:72:PRO:C	25:V:74:GLU:N	2.78	0.40
31:2:55:VAL:HG22	38:2:8509:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
4	A	235/239 (98%)	207 (88%)	24 (10%)	4 (2%)	7	32
5	B	335/337 (99%)	300 (90%)	28 (8%)	7 (2%)	5	27
6	C	244/246 (99%)	213 (87%)	28 (12%)	3 (1%)	10	40
7	D	134/176 (76%)	96 (72%)	26 (19%)	12 (9%)	0	3
8	E	170/177 (96%)	157 (92%)	12 (7%)	1 (1%)	21	56
9	F	117/119 (98%)	102 (87%)	12 (10%)	3 (3%)	4	23
10	G	25/348 (7%)	22 (88%)	2 (8%)	1 (4%)	2	14
11	H	152/167 (91%)	132 (87%)	16 (10%)	4 (3%)	4	23
12	I	140/145 (97%)	127 (91%)	10 (7%)	3 (2%)	5	27
13	J	130/132 (98%)	117 (90%)	11 (8%)	2 (2%)	8	35
14	K	141/164 (86%)	116 (82%)	23 (16%)	2 (1%)	9	36
15	L	192/194 (99%)	167 (87%)	20 (10%)	5 (3%)	4	23
16	M	184/186 (99%)	153 (83%)	24 (13%)	7 (4%)	2	15
17	N	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	48
18	O	141/148 (95%)	129 (92%)	11 (8%)	1 (1%)	18	53
19	P	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	26
20	Q	148/154 (96%)	134 (90%)	14 (10%)	0	100	100
21	R	79/84 (94%)	76 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	S	117/119 (98%)	103 (88%)	12 (10%)	2 (2%)	7	32
23	T	51/66 (77%)	47 (92%)	3 (6%)	1 (2%)	6	28
24	U	63/70 (90%)	57 (90%)	4 (6%)	2 (3%)	3	18
25	V	152/154 (99%)	140 (92%)	11 (7%)	1 (1%)	18	53
26	W	80/91 (88%)	71 (89%)	7 (9%)	2 (2%)	4	23
27	X	140/240 (58%)	134 (96%)	6 (4%)	0	100	100
28	Y	71/73 (97%)	58 (82%)	10 (14%)	3 (4%)	2	13
29	Z	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
30	1	42/48 (88%)	40 (95%)	2 (5%)	0	100	100
31	2	90/92 (98%)	82 (91%)	6 (7%)	2 (2%)	5	26
All	All	3633/4235 (86%)	3224 (89%)	338 (9%)	71 (2%)	6	28

All (71) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	139	ASP
7	D	93	LEU
7	D	95	THR
7	D	137	PRO
7	D	173	GLU
9	F	101	ALA
11	H	138	PRO
11	H	162	SER
12	I	5	GLU
16	M	139	TRP
16	M	154	LEU
16	M	162	ASP
16	M	164	ASP
16	M	183	ASP
28	Y	20	LEU
28	Y	81	LYS
31	2	56	PRO
5	B	34	GLY
5	B	107	SER
5	B	169	GLY
6	C	8	LEU
7	D	11	HIS
7	D	16	PRO

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Mol	Chain	Res	Type
7	D	20	LYS
7	D	61	PHE
7	D	147	ALA
10	G	72	ASP
11	H	164	ALA
12	I	89	HIS
12	I	143	LYS
14	K	80	ASP
15	L	148	SER
16	M	181	ASP
18	O	116	SER
22	S	53	GLY
24	U	43	PRO
28	Y	28	ASP
31	2	57	GLY
4	A	34	ASP
4	A	132	ASP
5	B	184	ASP
7	D	171	ASP
11	H	40	PRO
13	J	119	GLN
14	K	105	TYR
15	L	18	GLY
15	L	140	ALA
26	W	77	PHE
4	A	62	ASP
5	B	185	GLY
17	N	20	SER
23	T	7	ASP
26	W	70	ILE
5	B	2	GLN
6	C	145	GLU
7	D	36	ASN
7	D	60	GLU
9	F	61	MET
9	F	64	PRO
13	J	126	SER
15	L	15	PRO
16	M	68	GLU
25	V	77	ALA
4	A	37	VAL
15	L	71	SER

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Mol	Chain	Res	Type
22	S	44	ALA
8	E	44	GLY
24	U	40	PRO
19	P	18	PRO
6	C	19	PRO
19	P	54	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	
4	A	179/181 (99%)	167 (93%)	12 (7%)	15	46
5	B	282/282 (100%)	262 (93%)	20 (7%)	13	43
6	C	193/193 (100%)	176 (91%)	17 (9%)	9	35
7	D	117/147 (80%)	110 (94%)	7 (6%)	17	50
8	E	152/155 (98%)	147 (97%)	5 (3%)	33	67
9	F	92/92 (100%)	91 (99%)	1 (1%)	65	83
10	G	27/283 (10%)	27 (100%)	0	100	100
11	H	122/122 (100%)	108 (88%)	14 (12%)	5	24
12	I	118/121 (98%)	111 (94%)	7 (6%)	18	50
13	J	106/106 (100%)	101 (95%)	5 (5%)	23	58
14	K	113/126 (90%)	110 (97%)	3 (3%)	39	71
15	L	166/166 (100%)	157 (95%)	9 (5%)	20	53
16	M	149/149 (100%)	139 (93%)	10 (7%)	15	46
17	N	93/93 (100%)	90 (97%)	3 (3%)	34	67
18	O	113/116 (97%)	109 (96%)	4 (4%)	32	65
19	P	79/79 (100%)	75 (95%)	4 (5%)	21	55
20	Q	117/121 (97%)	114 (97%)	3 (3%)	40	72
21	R	71/73 (97%)	69 (97%)	2 (3%)	38	70
22	S	105/105 (100%)	99 (94%)	6 (6%)	18	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	T	44/52 (85%)	44 (100%)	0	100	100
24	U	51/56 (91%)	50 (98%)	1 (2%)	48	76
25	V	130/130 (100%)	119 (92%)	11 (8%)	10	36
26	W	66/73 (90%)	59 (89%)	7 (11%)	6	27
27	X	120/195 (62%)	113 (94%)	7 (6%)	18	51
28	Y	56/56 (100%)	52 (93%)	4 (7%)	13	43
29	Z	46/46 (100%)	44 (96%)	2 (4%)	26	60
30	1	42/44 (96%)	41 (98%)	1 (2%)	43	73
31	2	79/79 (100%)	76 (96%)	3 (4%)	29	63
All	All	3028/3441 (88%)	2860 (94%)	168 (6%)	19	53

All (168) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	3	ARG
4	A	33	GLU
4	A	36	ASP
4	A	55	VAL
4	A	68	ILE
4	A	69	LEU
4	A	94	LEU
4	A	131	HIS
4	A	153	ARG
4	A	175	LYS
4	A	179	MET
4	A	217	ARG
5	B	7	ARG
5	B	11	LEU
5	B	27	ASN
5	B	33	ASP
5	B	63	GLU
5	B	84	LEU
5	B	97	LEU
5	B	98	THR
5	B	103	ASP
5	B	162	MET
5	B	190	MET
5	B	195	ARG
5	B	245	SER

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Mol	Chain	Res	Type
5	B	251	VAL
5	B	254	GLN
5	B	256	GLN
5	B	264	GLU
5	B	304	PRO
5	B	307	ARG
5	B	312	ARG
6	C	2	GLN
6	C	27	ARG
6	C	67	GLN
6	C	76	ARG
6	C	78	ARG
6	C	94	THR
6	C	115	LEU
6	C	136	VAL
6	C	180	SER
6	C	187	ARG
6	C	214	THR
6	C	222	ASP
6	C	223	LEU
6	C	234	VAL
6	C	236	THR
6	C	240	LEU
6	C	243	VAL
7	D	24	HIS
7	D	50	VAL
7	D	131	THR
7	D	133	ASN
7	D	136	ARG
7	D	137	PRO
7	D	149	ARG
8	E	7	ILE
8	E	54	ASP
8	E	86	VAL
8	E	102	VAL
8	E	154	ILE
9	F	64	PRO
11	H	18	GLU
11	H	30	GLN
11	H	59	ASN
11	H	61	LEU
11	H	72	VAL

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Mol	Chain	Res	Type
11	H	73	GLN
11	H	82	LYS
11	H	85	ILE
11	H	86	ARG
11	H	94	ARG
11	H	109	ASP
11	H	138	PRO
11	H	142	VAL
11	H	150	LYS
12	I	46	ILE
12	I	47	THR
12	I	52	GLN
12	I	74	ARG
12	I	93	ARG
12	I	127	ILE
12	I	131	THR
13	J	10	GLN
13	J	49	LEU
13	J	55	VAL
13	J	56	SER
13	J	98	VAL
14	K	35	ARG
14	K	117	GLU
14	K	140	VAL
15	L	38	VAL
15	L	46	LEU
15	L	87	MET
15	L	93	ARG
15	L	99	ARG
15	L	130	GLU
15	L	159	THR
15	L	164	THR
15	L	170	CYS
16	M	12	ARG
16	M	26	LEU
16	M	43	VAL
16	M	47	LEU
16	M	49	THR
16	M	80	SER
16	M	127	LEU
16	M	128	ASP
16	M	152	GLU

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Mol	Chain	Res	Type
16	M	163	PHE
17	N	3	THR
17	N	98	LEU
17	N	111	VAL
18	O	52	LYS
18	O	81	LYS
18	O	91	LYS
18	O	98	ILE
19	P	11	ARG
19	P	16	ASN
19	P	57	ASP
19	P	95	GLU
20	Q	13	THR
20	Q	39	THR
20	Q	82	GLU
21	R	10	VAL
21	R	28	VAL
22	S	23	VAL
22	S	26	THR
22	S	39	ASN
22	S	48	VAL
22	S	96	VAL
22	S	112	LEU
24	U	22	ASP
25	V	26	ILE
25	V	35	VAL
25	V	45	VAL
25	V	48	VAL
25	V	52	VAL
25	V	73	LEU
25	V	122	ARG
25	V	128	VAL
25	V	142	ASP
25	V	146	ILE
25	V	154	ARG
26	W	15	ARG
26	W	27	ASP
26	W	49	ARG
26	W	66	THR
26	W	72	VAL
26	W	84	ILE
26	W	85	VAL

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Mol	Chain	Res	Type
27	X	103	THR
27	X	154	ARG
27	X	163	THR
27	X	189	ASN
27	X	200	THR
27	X	203	VAL
27	X	235	GLU
28	Y	11	THR
28	Y	42	CYS
28	Y	64	ILE
28	Y	68	CYS
29	Z	14	THR
29	Z	36	SER
30	1	18	ASN
31	2	42	ARG
31	2	56	PRO
31	2	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	47	HIS
4	A	176	HIS
4	A	199	HIS
4	A	218	ASN
5	B	2	GLN
5	B	27	ASN
5	B	55	ASN
5	B	94	GLN
5	B	145	HIS
5	B	221	GLN
5	B	238	ASN
5	B	260	HIS
5	B	320	GLN
6	C	2	GLN
6	C	39	GLN
6	C	67	GLN
6	C	129	HIS
6	C	163	HIS
7	D	47	GLN
7	D	103	ASN
7	D	133	ASN

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Mol	Chain	Res	Type
8	E	66	GLN
8	E	106	ASN
8	E	143	GLN
9	F	80	GLN
10	G	17	GLN
10	G	64	ASN
11	H	35	ASN
11	H	45	GLN
11	H	55	GLN
11	H	58	HIS
11	H	59	ASN
11	H	69	ASN
11	H	74	ASN
11	H	80	ASN
11	H	91	HIS
11	H	129	ASN
11	H	130	HIS
11	H	137	ASN
11	H	166	ASN
12	I	25	GLN
12	I	29	GLN
12	I	52	GLN
12	I	107	ASN
13	J	10	GLN
13	J	44	HIS
13	J	67	GLN
14	K	18	HIS
14	K	41	HIS
14	K	58	GLN
15	L	26	HIS
15	L	58	GLN
15	L	78	ASN
15	L	89	ASN
16	M	40	ASN
16	M	107	ASN
16	M	119	GLN
16	M	132	ASN
17	N	53	GLN
18	O	50	GLN
18	O	66	GLN
18	O	73	HIS
18	O	118	GLN

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Mol	Chain	Res	Type
19	P	16	ASN
19	P	40	HIS
19	P	94	GLN
20	Q	61	GLN
20	Q	94	ASN
20	Q	98	ASN
20	Q	113	HIS
20	Q	117	HIS
20	Q	140	GLN
21	R	25	GLN
21	R	53	ASN
21	R	55	GLN
22	S	39	ASN
22	S	73	HIS
23	T	39	ASN
24	U	4	HIS
24	U	6	GLN
24	U	60	GLN
25	V	6	GLN
25	V	27	HIS
25	V	28	HIS
25	V	59	GLN
25	V	87	HIS
25	V	110	GLN
25	V	119	HIS
25	V	125	HIS
25	V	141	HIS
26	W	23	HIS
26	W	36	HIS
27	X	119	GLN
27	X	149	GLN
27	X	189	ASN
29	Z	8	GLN
29	Z	16	HIS
29	Z	28	HIS
30	1	16	ASN
30	1	17	GLN
30	1	18	ASN
30	1	37	HIS
30	1	41	HIS
30	1	45	ASN
31	2	13	HIS

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Mol	Chain	Res	Type
31	2	30	GLN
31	2	39	GLN
31	2	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	245 (8%)	25 (0%)
2	9	121/122 (99%)	18 (14%)	3 (2%)
3	4	2/3 (66%)	1 (50%)	0
All	All	2868/3047 (94%)	264 (9%)	28 (0%)

All (264) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
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
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	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	200	U
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U

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Mol	Chain	Res	Type
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	317	A
1	0	336	G
1	0	337	A
1	0	338	C
1	0	339	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
1	0	559	U
1	0	581	G
1	0	588	G
1	0	604	G
1	0	605	C
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

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Mol	Chain	Res	Type
1	0	835	U
1	0	840	U
1	0	868	G
1	0	869	G
1	0	871	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	882	A
1	0	884	C
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	938	G
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
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1137	G
1	0	1151	G
1	0	1162	G
1	0	1164	U
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U

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Mol	Chain	Res	Type
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	1331	A
1	0	1342	C
1	0	1353	C
1	0	1360	C
1	0	1377	C
1	0	1407	A
1	0	1451	C
1	0	1460	G
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	1528	A
1	0	1564	C
1	0	1580	A
1	0	1592	G
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	1722	U
1	0	1723	G

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Mol	Chain	Res	Type
1	0	1725	C
1	0	1731	C
1	0	1732	A
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
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	1971	G
1	0	1973	A
1	0	1974	G
1	0	1978	A
1	0	1979	G
1	0	1980	U
1	0	1996	U
1	0	2005	G
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2063	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	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G

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Mol	Chain	Res	Type
1	0	2317	C
1	0	2320	U
1	0	2321	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2422	U
1	0	2462	G
1	0	2467	A
1	0	2476	C
1	0	2483	A
1	0	2507	G
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2540	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	2634	G
1	0	2637	A
1	0	2649	A
1	0	2650	U
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2718	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	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A

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Mol	Chain	Res	Type
1	0	2811	A
1	0	2812	A
1	0	2825	C
1	0	2850	C
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U
2	9	3007	G
2	9	3014	G
2	9	3022	G
2	9	3023	U
2	9	3024	U
2	9	3025	G
2	9	3026	C
2	9	3040	C
2	9	3041	C
2	9	3043	G
2	9	3044	A
2	9	3052	A
2	9	3057	A
2	9	3066	G
2	9	3077	A
2	9	3114	G
2	9	3122	C
3	4	76	A

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	129	A
1	0	284	C
1	0	338	C
1	0	603	A
1	0	604	G
1	0	834	G
1	0	871	G
1	0	877	G
1	0	1080	C
1	0	1164	U

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Mol	Chain	Res	Type
1	0	1237	U
1	0	1352	A
1	0	1450	C
1	0	1563	G
1	0	1667	A
1	0	1856	C
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2320	U
1	0	2467	A
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2791	U
2	9	3024	U
2	9	3065	A
2	9	3103	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 233 ligands modelled in this entry, 232 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	SLD	0	9500	-	38,39,39	4.86	18 (47%)	47,53,53	2.60	19 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	SLD	0	9500	-	-	4/23/51/51	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	0	9500	SLD	C8S-C6S	17.00	1.58	1.34
32	0	9500	SLD	C9S-C8S	-9.48	1.35	1.50
32	0	9500	SLD	C5S-N4S	9.45	1.45	1.32
32	0	9500	SLD	C12-C11	8.09	1.53	1.39
32	0	9500	SLD	C6-N1	8.07	1.45	1.36
32	0	9500	SLD	C6S-C1S	7.03	1.58	1.45
32	0	9500	SLD	C9S-C0S	-6.62	1.43	1.51
32	0	9500	SLD	C1-C2	5.89	1.50	1.39
32	0	9500	SLD	C3-C1	5.57	1.47	1.38
32	0	9500	SLD	C4-C11	5.18	1.46	1.37
32	0	9500	SLD	C12-C2B	4.37	1.54	1.47
32	0	9500	SLD	C1S-N2S	3.77	1.45	1.38
32	0	9500	SLD	C7S-C5S	3.76	1.57	1.49
32	0	9500	SLD	O1-C6	3.52	1.40	1.35
32	0	9500	SLD	F1-C11	3.25	1.44	1.35
32	0	9500	SLD	O1-C7	-3.25	1.41	1.46
32	0	9500	SLD	C3-C12	2.94	1.46	1.41
32	0	9500	SLD	C4-C2	2.06	1.43	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	0	9500	SLD	O3-C6-N1	-7.30	122.04	128.80
32	0	9500	SLD	O1-C6-O3	6.28	129.77	122.40
32	0	9500	SLD	C3S-N4S-C5S	5.16	123.64	118.86
32	0	9500	SLD	C2-N1-C6	5.13	131.36	125.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	0	9500	SLD	C5-N1-C6	-4.06	108.17	111.17
32	0	9500	SLD	C9S-C0S-N5S	-3.80	109.95	116.23
32	0	9500	SLD	O1-C7-C5	3.53	107.91	104.50
32	0	9500	SLD	O2S-C0S-C9S	3.34	126.61	121.40
32	0	9500	SLD	CAS-C5B-C4B	3.34	122.35	112.82
32	0	9500	SLD	C5B-CAS-N5S	3.28	121.40	112.20
32	0	9500	SLD	C7-O1-C6	-2.84	107.83	110.10
32	0	9500	SLD	C7-C8-N2	-2.81	106.40	111.98
32	0	9500	SLD	F1-C11-C12	2.63	121.61	118.11
32	0	9500	SLD	C8-N2-C9	2.54	126.33	122.64
32	0	9500	SLD	C5-C7-C8	-2.53	110.50	113.38
32	0	9500	SLD	CAS-N5S-C0S	-2.44	118.28	122.82
32	0	9500	SLD	O1-C7-C8	-2.43	106.38	109.13
32	0	9500	SLD	C1-C2-N1	-2.27	116.91	120.18
32	0	9500	SLD	O1-C6-N1	-2.07	108.18	109.92

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	0	9500	SLD	C5-C7-C8-N2
32	0	9500	SLD	C4B-C5B-CAS-N5S
32	0	9500	SLD	O1-C7-C8-N2
32	0	9500	SLD	C6S-C8S-C9S-C0S

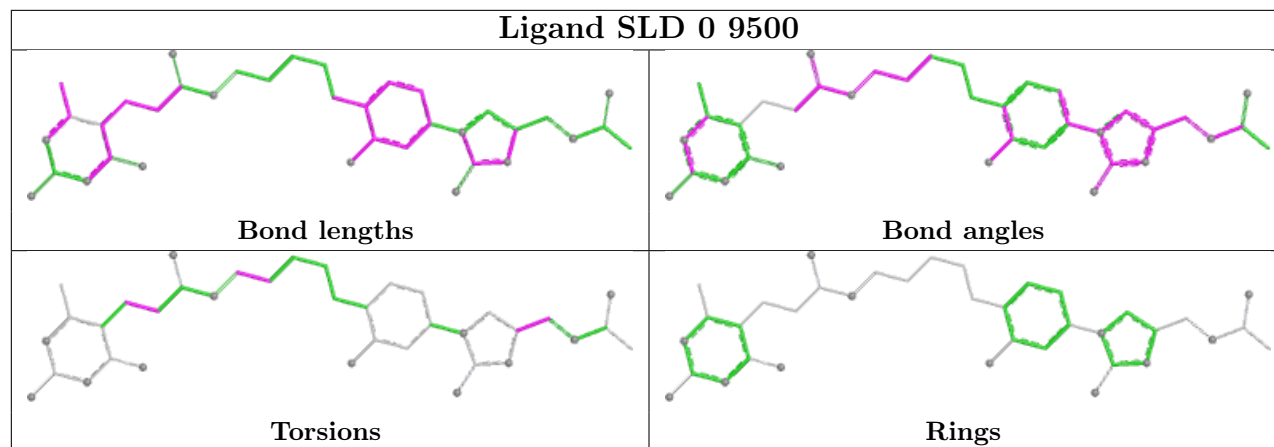
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	0	9500	SLD	4	0

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

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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%)	-0.66	12 (0%) 88 76	35, 63, 107, 150	0
2	9	122/122 (100%)	-0.31	5 (4%) 41 23	52, 80, 106, 150	0
3	4	3/3 (100%)	-0.71	0 100 100	49, 49, 51, 51	0
4	A	237/239 (99%)	-0.44	1 (0%) 88 76	44, 69, 101, 121	0
5	B	337/337 (100%)	-0.36	0 100 100	42, 72, 98, 108	0
6	C	246/246 (100%)	-0.47	0 100 100	36, 63, 87, 99	0
7	D	140/176 (79%)	0.43	4 (2%) 53 31	70, 115, 131, 136	0
8	E	172/177 (97%)	-0.19	1 (0%) 85 69	61, 84, 102, 107	0
9	F	119/119 (100%)	-0.13	0 100 100	70, 88, 112, 118	0
10	G	29/348 (8%)	0.39	1 (3%) 48 27	85, 105, 113, 117	0
11	H	156/167 (93%)	-0.20	1 (0%) 85 69	51, 72, 100, 108	0
12	I	142/145 (97%)	-0.44	0 100 100	50, 66, 85, 102	0
13	J	132/132 (100%)	-0.32	0 100 100	53, 71, 89, 96	0
14	K	145/164 (88%)	-0.24	1 (0%) 84 66	39, 83, 117, 129	0
15	L	194/194 (100%)	-0.40	1 (0%) 87 72	47, 62, 79, 90	0
16	M	186/186 (100%)	0.01	5 (2%) 56 33	58, 81, 120, 133	0
17	N	115/115 (100%)	-0.29	0 100 100	56, 72, 90, 94	0
18	O	143/148 (96%)	-0.42	0 100 100	50, 72, 87, 94	0
19	P	95/95 (100%)	-0.49	1 (1%) 78 57	51, 62, 75, 88	0
20	Q	150/154 (97%)	-0.59	0 100 100	46, 61, 81, 88	0
21	R	81/84 (96%)	-0.47	0 100 100	59, 76, 95, 103	0
22	S	119/119 (100%)	-0.32	0 100 100	55, 74, 97, 113	0
23	T	53/66 (80%)	-0.24	0 100 100	57, 73, 92, 99	0
24	U	65/70 (92%)	-0.01	2 (3%) 51 30	68, 90, 123, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	V	154/154 (100%)	-0.51	0 100 100	51, 64, 82, 94	0
26	W	82/91 (90%)	-0.18	3 (3%) 45 25	58, 75, 99, 117	0
27	X	142/240 (59%)	-0.53	1 (0%) 84 66	43, 61, 82, 101	0
28	Y	73/73 (100%)	0.07	0 100 100	62, 76, 95, 104	0
29	Z	56/56 (100%)	-0.73	0 100 100	42, 52, 58, 68	0
30	1	46/48 (95%)	-0.21	0 100 100	49, 77, 105, 117	0
31	2	92/92 (100%)	-0.15	2 (2%) 62 39	53, 73, 87, 98	0
All	All	6580/7282 (90%)	-0.45	41 (0%) 85 69	35, 69, 108, 150	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
24	U	1	THR	4.0
2	9	3025	G	3.9
31	2	55	VAL	3.4
7	D	10	PHE	3.3
2	9	3001	U	3.2
16	M	148	ALA	3.2
31	2	56	PRO	3.1
1	0	2250	G	3.0
16	M	168	LEU	2.8
1	0	10	U	2.7
1	0	1175	G	2.7
8	E	10	ASP	2.7
26	W	88	GLU	2.6
2	9	3002	U	2.5
1	0	1964	U	2.5
7	D	62	ASP	2.5
7	D	63	ILE	2.5
1	0	2251	G	2.5
19	P	95	GLU	2.5
16	M	167	ASP	2.5
2	9	3024	U	2.4
14	K	148	GLU	2.4
1	0	1173	A	2.4
1	0	1160	G	2.4
4	A	36	ASP	2.3
24	U	2	VAL	2.3
1	0	138	U	2.3
7	D	69	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	0	2254	G	2.3
1	0	2345	A	2.2
15	L	87	MET	2.2
1	0	735	C	2.2
27	X	108	ASP	2.2
1	0	2664	A	2.2
26	W	87	ALA	2.2
16	M	1	ALA	2.1
2	9	3023	U	2.1
10	G	26	MET	2.1
11	H	40	PRO	2.1
16	M	169	PRO	2.1
26	W	83	ALA	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	9	8351	1/1	0.42	0.17	94,94,94,94	0
35	NA	R	8312	1/1	0.51	0.18	84,84,84,84	0
35	NA	0	8341	1/1	0.54	0.10	60,60,60,60	0
35	NA	0	8329	1/1	0.62	0.17	98,98,98,98	0
35	NA	0	8366	1/1	0.66	0.15	82,82,82,82	0
35	NA	0	8368	1/1	0.66	0.24	69,69,69,69	0
35	NA	Q	8386	1/1	0.68	0.36	107,107,107,107	0
35	NA	0	8324	1/1	0.68	0.21	58,58,58,58	0
35	NA	0	8340	1/1	0.71	0.28	69,69,69,69	0
35	NA	0	8384	1/1	0.72	0.10	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8382	1/1	0.73	0.30	89,89,89,89	0
34	K	0	8201	1/1	0.77	0.48	141,141,141,141	0
35	NA	0	8385	1/1	0.80	0.29	73,73,73,73	0
33	MG	9	8095	1/1	0.82	0.26	106,106,106,106	0
33	MG	0	8092	1/1	0.82	0.40	111,111,111,111	0
36	CL	0	8505	1/1	0.82	0.18	99,99,99,99	0
33	MG	0	8046	1/1	0.83	0.08	86,86,86,86	0
35	NA	0	8375	1/1	0.84	0.24	81,81,81,81	0
35	NA	0	8352	1/1	0.84	0.10	61,61,61,61	0
33	MG	0	8102	1/1	0.84	0.12	91,91,91,91	0
33	MG	0	8114	1/1	0.84	0.21	95,95,95,95	0
36	CL	B	8519	1/1	0.84	0.11	95,95,95,95	0
36	CL	N	8508	1/1	0.84	0.15	116,116,116,116	0
33	MG	0	8049	1/1	0.85	0.12	90,90,90,90	0
35	NA	0	8325	1/1	0.85	0.12	64,64,64,64	0
35	NA	9	8383	1/1	0.85	0.09	67,67,67,67	0
35	NA	0	8374	1/1	0.85	0.29	77,77,77,77	0
34	K	0	8202	1/1	0.86	0.29	92,92,92,92	0
35	NA	0	8307	1/1	0.86	0.12	71,71,71,71	0
35	NA	0	8369	1/1	0.86	0.38	96,96,96,96	0
35	NA	0	8308	1/1	0.86	0.20	77,77,77,77	0
35	NA	0	8362	1/1	0.86	0.27	79,79,79,79	0
35	NA	0	8302	1/1	0.87	0.11	55,55,55,55	0
35	NA	0	8360	1/1	0.87	0.62	69,69,69,69	0
35	NA	0	8311	1/1	0.88	0.18	73,73,73,73	0
35	NA	0	8313	1/1	0.88	0.11	89,89,89,89	0
35	NA	0	8326	1/1	0.88	0.18	73,73,73,73	0
35	NA	0	8350	1/1	0.88	0.13	57,57,57,57	0
36	CL	I	8502	1/1	0.88	0.12	93,93,93,93	0
36	CL	K	8510	1/1	0.88	0.11	104,104,104,104	0
35	NA	0	8378	1/1	0.88	0.16	65,65,65,65	0
35	NA	H	8322	1/1	0.89	0.21	78,78,78,78	0
35	NA	0	8377	1/1	0.89	0.26	75,75,75,75	0
35	NA	0	8365	1/1	0.89	0.18	47,47,47,47	0
33	MG	0	8101	1/1	0.89	0.13	94,94,94,94	0
35	NA	0	8330	1/1	0.89	0.08	61,61,61,61	0
33	MG	A	8105	1/1	0.89	0.14	52,52,52,52	0
35	NA	0	8328	1/1	0.89	0.11	55,55,55,55	0
35	NA	0	8363	1/1	0.89	0.22	83,83,83,83	0
33	MG	0	8103	1/1	0.90	0.16	97,97,97,97	0
33	MG	0	8045	1/1	0.90	0.19	91,91,91,91	0
33	MG	0	8022	1/1	0.90	0.14	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8314	1/1	0.90	0.26	53,53,53,53	0
35	NA	0	8361	1/1	0.90	0.15	77,77,77,77	0
35	NA	0	8321	1/1	0.90	0.19	67,67,67,67	0
35	NA	0	8379	1/1	0.90	0.09	48,48,48,48	0
36	CL	I	8501	1/1	0.90	0.11	99,99,99,99	0
35	NA	0	8333	1/1	0.90	0.16	40,40,40,40	0
35	NA	0	8339	1/1	0.90	0.09	33,33,33,33	0
33	MG	0	8024	1/1	0.90	0.23	98,98,98,98	0
35	NA	0	8334	1/1	0.91	0.22	48,48,48,48	0
36	CL	0	8515	1/1	0.91	0.20	100,100,100,100	0
35	NA	0	8335	1/1	0.91	0.22	83,83,83,83	0
35	NA	0	8357	1/1	0.91	0.24	61,61,61,61	0
35	NA	0	8306	1/1	0.91	0.20	59,59,59,59	0
35	NA	0	8323	1/1	0.91	0.14	66,66,66,66	0
35	NA	0	8316	1/1	0.91	0.09	52,52,52,52	0
33	MG	0	8047	1/1	0.92	0.12	90,90,90,90	0
35	NA	0	8370	1/1	0.92	0.33	76,76,76,76	0
33	MG	0	8104	1/1	0.92	0.08	66,66,66,66	0
36	CL	A	8509	1/1	0.92	0.23	89,89,89,89	0
33	MG	0	8050	1/1	0.92	0.04	68,68,68,68	0
33	MG	0	8115	1/1	0.92	0.07	73,73,73,73	0
35	NA	0	8367	1/1	0.92	0.11	85,85,85,85	0
35	NA	Q	8337	1/1	0.92	0.05	64,64,64,64	0
33	MG	0	8067	1/1	0.92	0.09	81,81,81,81	0
37	CD	N	8405	1/1	0.92	0.25	150,150,150,150	0
33	MG	0	8072	1/1	0.93	0.09	78,78,78,78	0
33	MG	0	8111	1/1	0.93	0.05	75,75,75,75	0
35	NA	0	8332	1/1	0.93	0.09	50,50,50,50	0
36	CL	0	8522	1/1	0.93	0.24	92,92,92,92	0
35	NA	0	8371	1/1	0.93	0.35	69,69,69,69	0
35	NA	0	8373	1/1	0.93	0.08	57,57,57,57	0
35	NA	0	8343	1/1	0.93	0.06	48,48,48,48	0
35	NA	A	8345	1/1	0.93	0.06	48,48,48,48	0
35	NA	0	8301	1/1	0.93	0.09	59,59,59,59	0
35	NA	0	8318	1/1	0.93	0.09	48,48,48,48	0
33	MG	S	8073	1/1	0.93	0.05	71,71,71,71	0
33	MG	0	8097	1/1	0.94	0.11	53,53,53,53	0
33	MG	0	8100	1/1	0.94	0.16	97,97,97,97	0
35	NA	0	8359	1/1	0.94	0.18	81,81,81,81	0
33	MG	0	8044	1/1	0.94	0.13	59,59,59,59	0
32	SLD	0	9500	37/37	0.94	0.09	46,50,53,59	0
33	MG	0	8087	1/1	0.94	0.11	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8042	1/1	0.94	0.08	61,61,61,61	0
35	NA	0	8364	1/1	0.94	0.15	66,66,66,66	0
35	NA	P	8348	1/1	0.94	0.05	68,68,68,68	0
36	CL	L	8518	1/1	0.94	0.07	69,69,69,69	0
36	CL	M	8507	1/1	0.94	0.06	86,86,86,86	0
35	NA	0	8349	1/1	0.94	0.11	69,69,69,69	0
36	CL	P	8511	1/1	0.94	0.10	84,84,84,84	0
33	MG	0	8106	1/1	0.94	0.08	78,78,78,78	0
35	NA	0	8303	1/1	0.95	0.08	55,55,55,55	0
33	MG	0	8071	1/1	0.95	0.08	104,104,104,104	0
35	NA	0	8338	1/1	0.95	0.06	66,66,66,66	0
35	NA	0	8376	1/1	0.95	0.34	79,79,79,79	0
33	MG	0	8064	1/1	0.95	0.08	39,39,39,39	0
33	MG	0	8085	1/1	0.95	0.06	92,92,92,92	0
35	NA	0	8310	1/1	0.95	0.07	46,46,46,46	0
35	NA	0	8381	1/1	0.95	0.05	69,69,69,69	0
33	MG	0	8066	1/1	0.95	0.09	105,105,105,105	0
33	MG	0	8088	1/1	0.95	0.13	40,40,40,40	0
33	MG	0	8090	1/1	0.95	0.20	81,81,81,81	0
36	CL	J	8512	1/1	0.95	0.07	67,67,67,67	0
33	MG	0	8013	1/1	0.95	0.07	60,60,60,60	0
35	NA	0	8353	1/1	0.95	0.06	43,43,43,43	0
35	NA	0	8356	1/1	0.95	0.15	73,73,73,73	0
35	NA	H	8309	1/1	0.95	0.09	49,49,49,49	0
33	MG	0	8070	1/1	0.95	0.06	63,63,63,63	0
36	CL	X	8520	1/1	0.95	0.10	57,57,57,57	0
35	NA	L	8347	1/1	0.95	0.04	55,55,55,55	0
36	CL	0	8514	1/1	0.96	0.07	75,75,75,75	0
33	MG	0	8112	1/1	0.96	0.09	64,64,64,64	0
36	CL	0	8516	1/1	0.96	0.21	64,64,64,64	0
36	CL	0	8517	1/1	0.96	0.08	82,82,82,82	0
33	MG	0	8076	1/1	0.96	0.05	102,102,102,102	0
33	MG	0	8041	1/1	0.96	0.08	68,68,68,68	0
33	MG	0	8094	1/1	0.96	0.28	97,97,97,97	0
35	NA	0	8317	1/1	0.96	0.04	57,57,57,57	0
33	MG	0	8096	1/1	0.96	0.07	70,70,70,70	0
36	CL	I	8521	1/1	0.96	0.08	69,69,69,69	0
35	NA	K	8380	1/1	0.96	0.12	85,85,85,85	0
33	MG	B	8055	1/1	0.96	0.06	71,71,71,71	0
33	MG	0	8003	1/1	0.96	0.05	51,51,51,51	0
33	MG	0	8060	1/1	0.96	0.15	63,63,63,63	0
35	NA	0	8354	1/1	0.96	0.17	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
35	NA	0	8355	1/1	0.96	0.12	77,77,77,77	0
36	CL	0	8503	1/1	0.96	0.10	82,82,82,82	0
35	NA	0	8336	1/1	0.96	0.08	63,63,63,63	0
36	CL	0	8513	1/1	0.97	0.06	74,74,74,74	0
33	MG	0	8108	1/1	0.97	0.10	102,102,102,102	0
33	MG	0	8110	1/1	0.97	0.04	56,56,56,56	0
33	MG	0	8043	1/1	0.97	0.05	64,64,64,64	0
35	NA	0	8344	1/1	0.97	0.03	48,48,48,48	0
33	MG	0	8082	1/1	0.97	0.11	79,79,79,79	0
33	MG	0	8098	1/1	0.97	0.07	50,50,50,50	0
33	MG	0	8053	1/1	0.97	0.07	63,63,63,63	0
35	NA	C	8304	1/1	0.97	0.03	51,51,51,51	0
33	MG	9	8052	1/1	0.97	0.04	60,60,60,60	0
33	MG	0	8068	1/1	0.97	0.04	64,64,64,64	0
35	NA	0	8372	1/1	0.97	0.13	72,72,72,72	0
33	MG	4	8063	1/1	0.97	0.08	62,62,62,62	0
33	MG	0	8011	1/1	0.97	0.08	50,50,50,50	0
33	MG	0	8062	1/1	0.97	0.09	90,90,90,90	0
33	MG	J	8069	1/1	0.97	0.04	87,87,87,87	0
33	MG	0	8028	1/1	0.97	0.04	57,57,57,57	0
33	MG	0	8075	1/1	0.97	0.09	77,77,77,77	0
36	CL	2	8504	1/1	0.97	0.11	100,100,100,100	0
35	NA	0	8320	1/1	0.97	0.07	40,40,40,40	0
33	MG	0	8057	1/1	0.98	0.05	53,53,53,53	0
33	MG	0	8006	1/1	0.98	0.10	60,60,60,60	0
33	MG	0	8093	1/1	0.98	0.03	63,63,63,63	0
35	NA	0	8327	1/1	0.98	0.05	46,46,46,46	0
33	MG	0	8008	1/1	0.98	0.06	52,52,52,52	0
35	NA	0	8305	1/1	0.98	0.04	42,42,42,42	0
35	NA	0	8358	1/1	0.98	0.16	109,109,109,109	0
33	MG	0	8113	1/1	0.98	0.04	60,60,60,60	0
35	NA	0	8331	1/1	0.98	0.06	60,60,60,60	0
33	MG	0	8048	1/1	0.98	0.04	66,66,66,66	0
33	MG	0	8077	1/1	0.98	0.04	54,54,54,54	0
33	MG	0	8116	1/1	0.98	0.04	84,84,84,84	0
33	MG	0	8081	1/1	0.98	0.04	67,67,67,67	0
33	MG	0	8099	1/1	0.98	0.07	80,80,80,80	0
33	MG	0	8009	1/1	0.98	0.04	44,44,44,44	0
35	NA	0	8315	1/1	0.98	0.07	70,70,70,70	0
33	MG	0	8025	1/1	0.98	0.06	59,59,59,59	0
33	MG	0	8086	1/1	0.98	0.04	62,62,62,62	0
33	MG	0	8051	1/1	0.98	0.05	97,97,97,97	0

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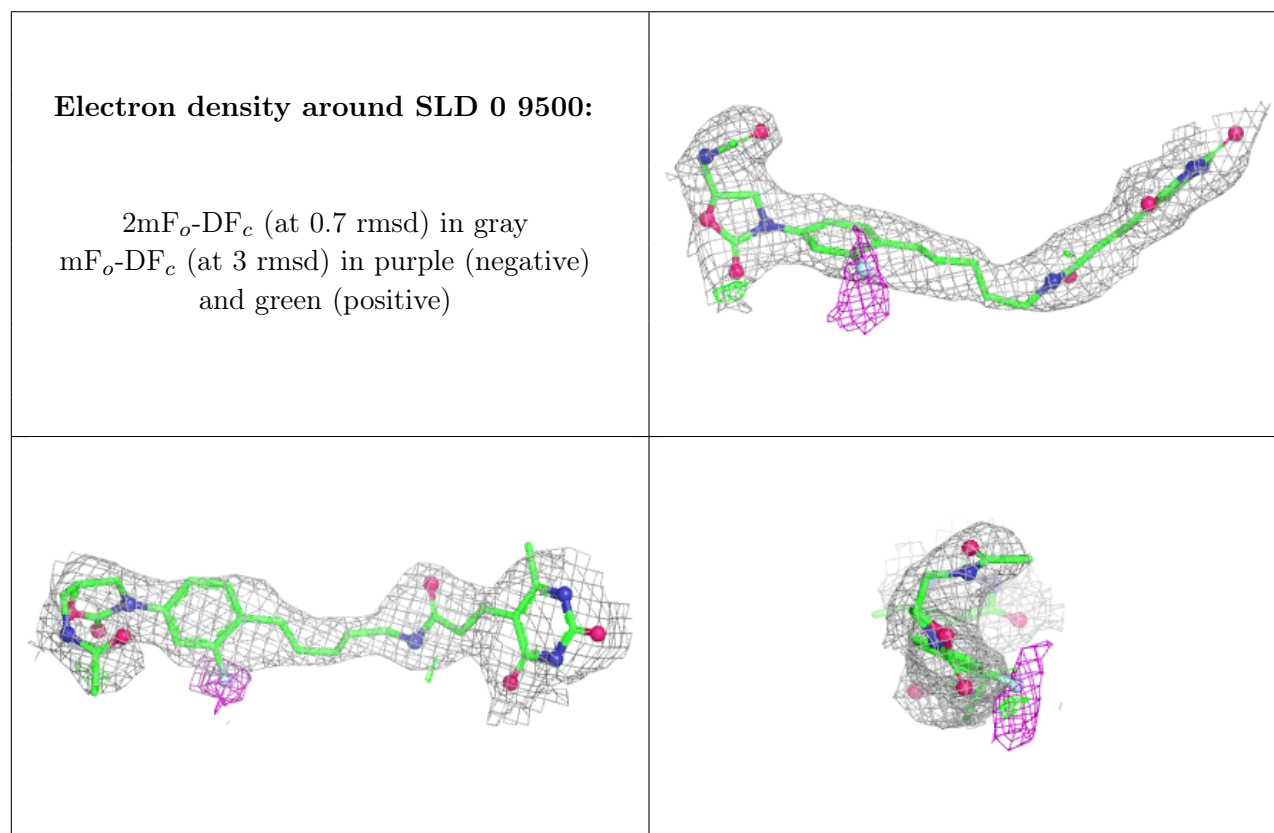
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8004	1/1	0.98	0.05	50,50,50,50	0
33	MG	X	8109	1/1	0.98	0.05	66,66,66,66	0
33	MG	0	8089	1/1	0.98	0.04	82,82,82,82	0
33	MG	0	8074	1/1	0.99	0.04	51,51,51,51	0
33	MG	0	8107	1/1	0.99	0.06	55,55,55,55	0
33	MG	0	8019	1/1	0.99	0.04	43,43,43,43	0
33	MG	0	8020	1/1	0.99	0.08	53,53,53,53	0
33	MG	0	8005	1/1	0.99	0.06	58,58,58,58	0
35	NA	I	8346	1/1	0.99	0.04	45,45,45,45	0
33	MG	0	8079	1/1	0.99	0.04	53,53,53,53	0
33	MG	0	8023	1/1	0.99	0.02	46,46,46,46	0
35	NA	0	8319	1/1	0.99	0.02	41,41,41,41	0
33	MG	0	8001	1/1	0.99	0.06	46,46,46,46	0
33	MG	0	8083	1/1	0.99	0.03	65,65,65,65	0
33	MG	0	8012	1/1	0.99	0.04	42,42,42,42	0
33	MG	0	8117	1/1	0.99	0.03	45,45,45,45	0
33	MG	0	8026	1/1	0.99	0.05	39,39,39,39	0
33	MG	0	8027	1/1	0.99	0.09	65,65,65,65	0
33	MG	0	8002	1/1	0.99	0.03	51,51,51,51	0
33	MG	A	8065	1/1	0.99	0.04	55,55,55,55	0
33	MG	0	8054	1/1	0.99	0.07	45,45,45,45	0
33	MG	0	8056	1/1	0.99	0.03	60,60,60,60	0
33	MG	0	8091	1/1	0.99	0.03	65,65,65,65	0
33	MG	0	8029	1/1	0.99	0.05	60,60,60,60	0
33	MG	0	8059	1/1	0.99	0.03	60,60,60,60	0
33	MG	2	8078	1/1	0.99	0.02	65,65,65,65	0
33	MG	0	8031	1/1	0.99	0.04	54,54,54,54	0
33	MG	0	8061	1/1	0.99	0.05	45,45,45,45	0
33	MG	0	8034	1/1	0.99	0.04	46,46,46,46	0
33	MG	0	8035	1/1	0.99	0.05	69,69,69,69	0
33	MG	0	8036	1/1	0.99	0.04	52,52,52,52	0
33	MG	0	8037	1/1	0.99	0.03	54,54,54,54	0
35	NA	0	8342	1/1	0.99	0.06	42,42,42,42	0
33	MG	0	8039	1/1	0.99	0.06	53,53,53,53	0
36	CL	Q	8506	1/1	0.99	0.07	80,80,80,80	0
33	MG	0	8014	1/1	0.99	0.02	46,46,46,46	0
33	MG	0	8016	1/1	0.99	0.10	71,71,71,71	0
33	MG	0	8018	1/1	0.99	0.04	57,57,57,57	0
37	CD	Y	8403	1/1	0.99	0.02	84,84,84,84	0
37	CD	Z	8402	1/1	0.99	0.04	89,89,89,89	0
37	CD	2	8404	1/1	0.99	0.03	90,90,90,90	0
33	MG	0	8033	1/1	1.00	0.03	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
33	MG	0	8084	1/1	1.00	0.05	70,70,70,70	0
33	MG	0	8021	1/1	1.00	0.06	54,54,54,54	0
33	MG	0	8017	1/1	1.00	0.03	43,43,43,43	0
33	MG	0	8058	1/1	1.00	0.05	61,61,61,61	0
33	MG	0	8010	1/1	1.00	0.03	47,47,47,47	0
33	MG	0	8015	1/1	1.00	0.04	60,60,60,60	0
33	MG	0	8038	1/1	1.00	0.02	56,56,56,56	0
33	MG	0	8030	1/1	1.00	0.07	48,48,48,48	0
33	MG	0	8040	1/1	1.00	0.03	88,88,88,88	0
37	CD	T	8401	1/1	1.00	0.02	83,83,83,83	0
33	MG	0	8080	1/1	1.00	0.02	52,52,52,52	0
33	MG	0	8007	1/1	1.00	0.03	47,47,47,47	0
33	MG	0	8032	1/1	1.00	0.02	52,52,52,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.