



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 24, 2018 – 07:12 AM EST

PDB ID : 1Q81
Title : Crystal Structure of minihelix with 3' puromycin bound to A-site of the 50S ribosomal subunit.
Authors : Hansen, J.L.; Schmeing, T.M.; Moore, P.B.; Steitz, T.A.
Deposited on : 2003-08-20
Resolution : 2.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

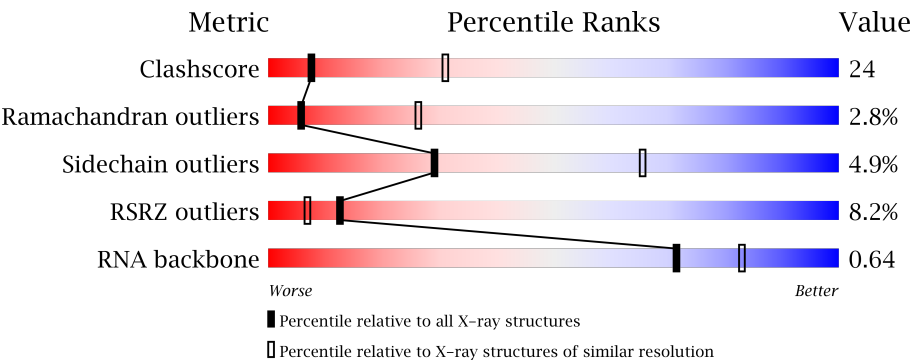
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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))
Clashscore	112137	2773 (3.00-2.92)
Ramachandran outliers	110173	2680 (3.00-2.92)
Sidechain outliers	110143	2683 (3.00-2.92)
RSRZ outliers	101464	2421 (3.00-2.92)
RNA backbone	2435	1008 (3.30-2.62)

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

Mol	Chain	Length	Quality of chain
1	A	2922	<div><div>2%</div><div>48%39%7%6%</div></div>
2	B	122	<div><div>5%</div><div>39%48%11%</div></div>
3	5	2	<div><div>100%</div><div>100%</div></div>
4	C	239	<div><div>9%</div><div>52%41%6%</div></div>
5	D	337	<div><div>%</div><div>45%50%6%</div></div>

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Mol	Chain	Length	Quality of chain
6	E	246	
7	F	176	
8	G	177	
9	H	119	
10	I	348	
11	J	167	
12	K	145	
13	L	132	
14	M	164	
15	N	194	
16	O	186	
17	P	115	
18	Q	148	
19	R	95	
20	S	154	
21	T	84	
22	U	119	
23	V	66	
24	W	70	
25	X	154	
26	Y	91	
27	Z	240	
28	1	73	
29	2	56	
30	3	48	

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Mol	Chain	Length	Quality of chain
31	4	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
32	MG	1	8105	-	-	-	X
32	MG	4	8078	-	-	-	X
32	MG	4	8114	-	-	-	X
32	MG	A	8044	-	-	-	X
32	MG	A	8070	-	-	-	X
32	MG	A	8112	-	-	-	X
34	NA	A	8303	-	-	-	X
34	NA	A	8308	-	-	-	X
34	NA	A	8321	-	-	-	X
34	NA	A	8323	-	-	-	X
34	NA	A	8325	-	-	-	X
34	NA	A	8327	-	-	-	X
34	NA	A	8340	-	-	-	X
34	NA	A	8350	-	-	-	X
34	NA	A	8355	-	-	-	X
34	NA	A	8359	-	-	-	X
34	NA	A	8361	-	-	-	X
34	NA	A	8371	-	-	-	X
34	NA	A	8377	-	-	-	X
34	NA	A	8382	-	-	-	X
34	NA	B	8383	-	-	-	X
34	NA	S	8386	-	-	-	X
35	CL	A	8515	-	-	-	X
35	CL	A	8516	-	-	-	X
35	CL	D	8519	-	-	-	X
36	PPU	5	76	-	-	-	X
37	CD	4	8404	-	-	-	X

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 98596 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	A	2754	Total	C	N	O	P	0	0	0
			59017	26346	10878	19048	2745			

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

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

- Molecule 3 is a RNA chain called minihelix-puromycin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	5	2	Total	C	N	O	P	0	0	0
			40	18	6	14	2			

- Molecule 4 is a protein called 50S ribosomal protein L2P.

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

- Molecule 5 is a protein called 50S ribosomal protein L3P.

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

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 6 is a protein called 50S ribosomal protein L4E.

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

- Molecule 7 is a protein called 50S ribosomal protein L5P.

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

- Molecule 8 is a protein called 50S ribosomal protein L6P.

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

- Molecule 9 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 10 is a protein called Acidic ribosomal protein P0 homolog.

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

- Molecule 11 is a protein called L10 Ribosomal Protein.

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

- Molecule 12 is a protein called 50S ribosomal protein L13P.

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

- Molecule 13 is a protein called 50S ribosomal protein L14P.

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

- Molecule 14 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	M	145	Total	C	N	O	S	0	0	0
			1114	668	222	224				

- Molecule 15 is a protein called L15 Ribosomal Protein.

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

- Molecule 16 is a protein called 50S ribosomal protein L18P.

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

- Molecule 17 is a protein called 50S ribosomal protein L18e.

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

- Molecule 18 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	Q	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
Q	71	LYS	TYR	CONFLICT	UNP P14119

- Molecule 19 is a protein called 50S ribosomal protein L21e.

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

- Molecule 20 is a protein called 50S ribosomal protein L22P.

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

- Molecule 21 is a protein called 50S ribosomal protein L23P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24P.

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

- Molecule 23 is a protein called 50S ribosomal protein L24E.

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

- Molecule 24 is a protein called 50S ribosomal protein L29P.

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

- Molecule 25 is a protein called 50S ribosomal protein L30P.

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

- Molecule 26 is a protein called 50S ribosomal protein L31e.

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

- Molecule 27 is a protein called 50S ribosomal protein L32E.

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

- Molecule 28 is a protein called L37Ae 50S ribosomal protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	1	73	Total	C	N	O	S	0	0	0
			563	359	111	86	7			

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	2	56	Total	C	N	O	S	0	0	0
			430	258	86	82	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	3	46	Total	C	N	O	S	0	0	0
			393	238	86	68	1			

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	4	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
32	1	1	Total Mg 1 1	0	0
32	D	1	Total Mg 1 1	0	0
32	B	1	Total Mg 1 1	0	0
32	C	1	Total Mg 1 1	0	0
32	Z	1	Total Mg 1 1	0	0
32	A	108	Total Mg 108 108	0	0
32	4	2	Total Mg 2 2	0	0
32	U	1	Total Mg 1 1	0	0
32	L	1	Total Mg 1 1	0	0

- Molecule 33 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	A	2	Total K 2 2	0	0

- Molecule 34 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	J	1	Total Na 1 1	0	0
34	K	1	Total Na 1 1	0	0
34	E	1	Total Na 1 1	0	0
34	B	2	Total Na 2 2	0	0
34	C	1	Total Na 1 1	0	0
34	A	73	Total Na 73 73	0	0
34	T	1	Total Na 1 1	0	0
34	N	1	Total Na 1 1	0	0

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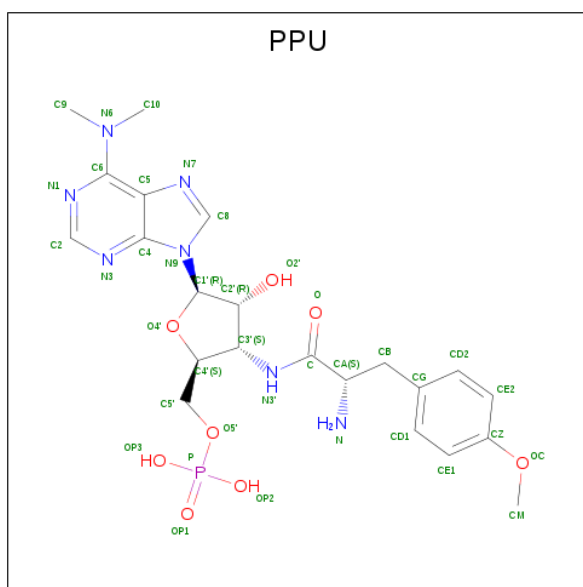
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	R	1	Total 1	Na 1	0	0
34	S	3	Total 3	Na 3	0	0
34	M	1	Total 1	Na 1	0	0

- Molecule 35 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	P	1	Total 1	Cl 1	0	0
35	D	1	Total 1	Cl 1	0	0
35	K	3	Total 3	Cl 3	0	0
35	C	1	Total 1	Cl 1	0	0
35	Z	1	Total 1	Cl 1	0	0
35	A	11	Total 11	Cl 11	0	0
35	4	1	Total 1	Cl 1	0	0
35	N	1	Total 1	Cl 1	0	0
35	O	1	Total 1	Cl 1	0	0
35	S	1	Total 1	Cl 1	0	0

- Molecule 36 is PUROMYCIN-5'-MONOPHOSPHATE (three-letter code: PPU) (formula: C₂₂H₃₀N₇O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
36	5	1	Total	C	N	O	P	0	0
			37	22	7	7	1		

- Molecule 37 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	P	1	Total	Cd	0	0
			1	1		
37	2	1	Total	Cd	0	0
			1	1		
37	1	1	Total	Cd	0	0
			1	1		
37	4	1	Total	Cd	0	0
			1	1		
37	V	1	Total	Cd	0	0
			1	1		

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	A	5871	Total	O	0	0
			5871	5871		
38	B	147	Total	O	0	0
			147	147		
38	C	135	Total	O	0	0
			135	135		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	D	155	Total 155	O 155	0	0
38	E	171	Total 171	O 171	0	0
38	F	51	Total 51	O 51	0	0
38	G	44	Total 44	O 44	0	0
38	H	26	Total 26	O 26	0	0
38	I	20	Total 20	O 20	0	0
38	J	77	Total 77	O 77	0	0
38	K	55	Total 55	O 55	0	0
38	L	63	Total 63	O 63	0	0
38	M	90	Total 90	O 90	0	0
38	N	125	Total 125	O 125	0	0
38	O	64	Total 64	O 64	0	0
38	P	44	Total 44	O 44	0	0
38	Q	68	Total 68	O 68	0	0
38	R	54	Total 54	O 54	0	0
38	S	83	Total 83	O 83	0	0
38	T	31	Total 31	O 31	0	0
38	U	39	Total 39	O 39	0	0
38	V	26	Total 26	O 26	0	0
38	W	15	Total 15	O 15	0	0
38	X	70	Total 70	O 70	0	0

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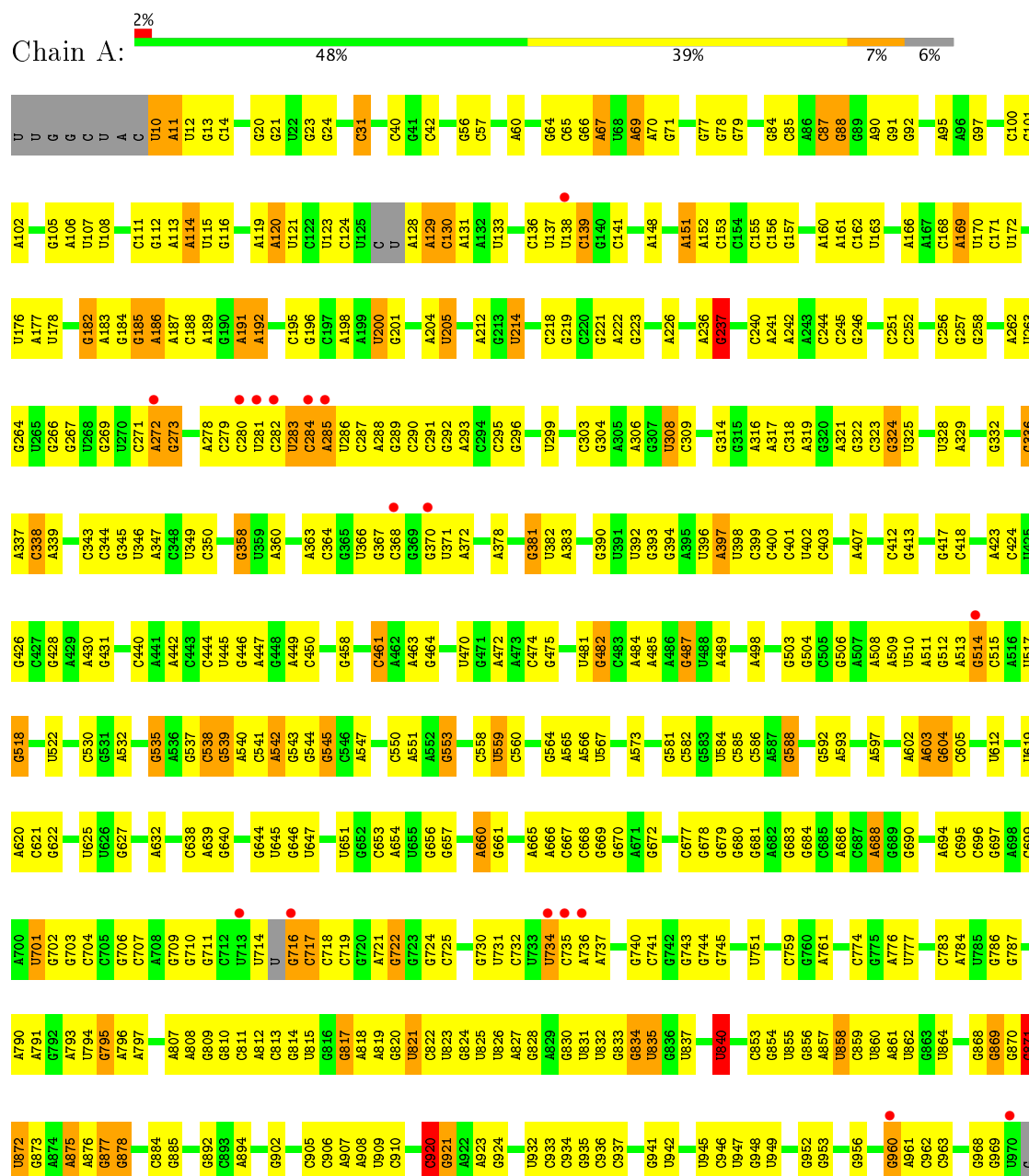
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	Y	30	Total 30	O 30	0	0
38	Z	102	Total 102	O 102	0	0
38	1	38	Total 38	O 38	0	0
38	2	56	Total 56	O 56	0	0
38	3	47	Total 47	O 47	0	0
38	4	72	Total 72	O 72	0	0

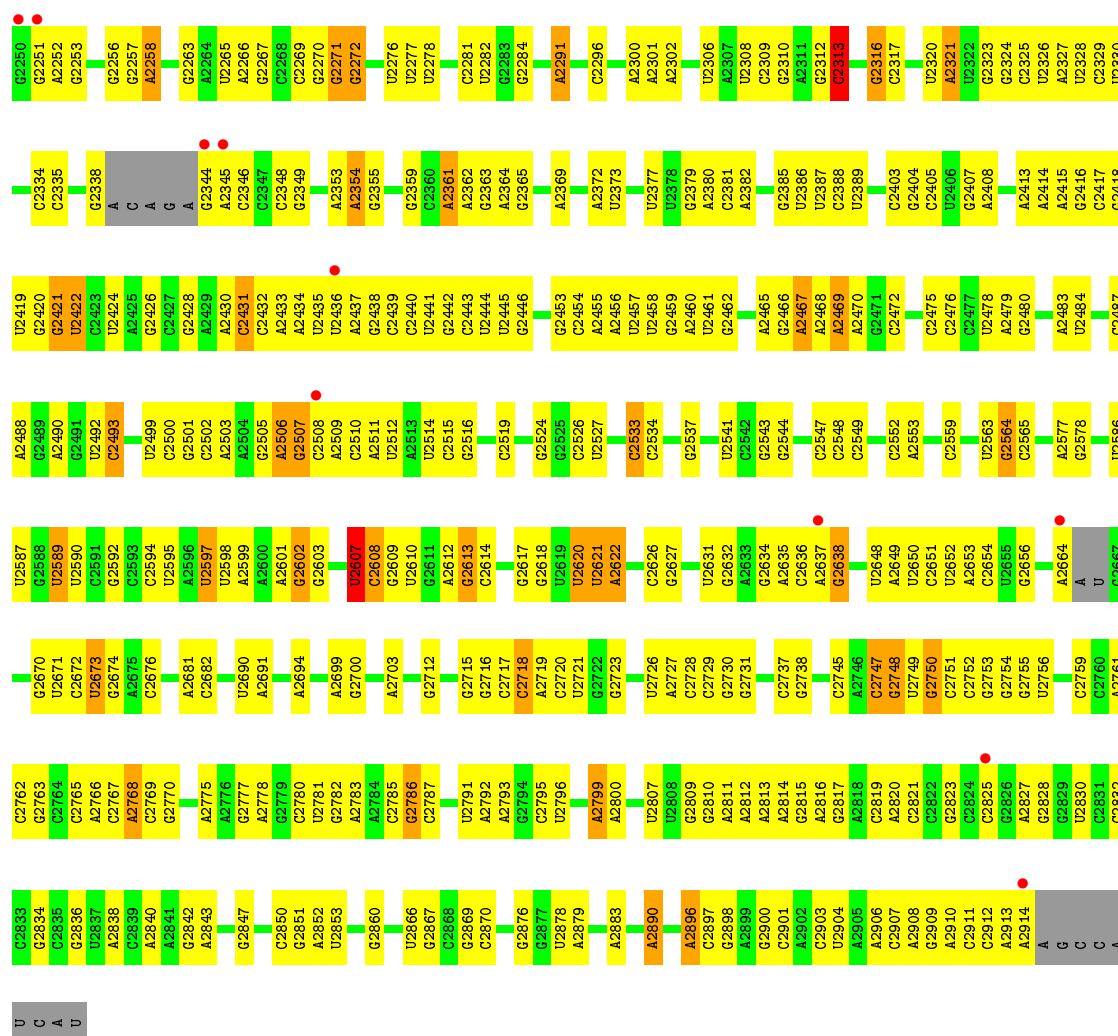
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

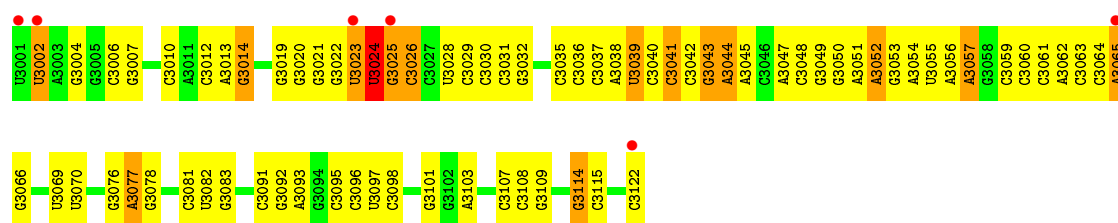
- Molecule 1: 23S ribosomal rna



G	G2025	G1948	G1856	C1772	A1685	U1599	A1515	A1424	G1316	A1215	G1155	U1064	U
C	C2026	G1949	A1857	G1773	G1686	G1600	C1516	G1425	A1321	G1216	C1156	G1065	G
U	U2027	G1950	C1861	A1778	G1688	G1601	U1517	C1426			C1157	U1066	U
A	U2028	G1951	C1862	A1779		C1602	A1522	G1430	G1325	G1226	G1158	C1067	C
C	A2030	U	G1863	A1783	A1691	A1603	G1523		G1326	G1228	G1160	G1068	G
G	C2031	A	C1864	U1784	C1692	G1604	U1824	A1434	G1327	C1229	G1161	C1069	C
G	U2032	C	A1865	G1785	A1696	G1605	G1525	U1435	A1328		G1162	A1070	C
G	G2033	U	A1866	C1786	A1701	A1607	G1526	C1436	A1329	U1234	G1163	G1071	C
C	U2034	A	G1867	G1787	U1702	G1608	A1527		A1330	G1235	G1164	G1072	C
C	C2035	U	G1868	C1788	U1705	G1610	A1528	C1439	A1331	A1236	G1165	A1073	C
A		G	U1788	U1789	G1705		G1529	U1440	G1332	U1237	G1166		G
U	A2038	A	G1873	G1789	G1706			U1441	U1333	G1238	G1167	G1080	A
U	C2039	C	U1874	C1790	G1707	A1635	C1584	A1442	C1334	G1239	C1168	A1081	G
G	G2040	C		U1791	G1708	A1624	G1535	G1443	G1335		U1169	A1082	A
U	G2041	C	G1878		C1709	U1625	C1536	G1444		A1242	U1170	C1083	G
A		C	U1879	A1796	A1710	A1626	G1540	G1445	G1340	C1243	A1171	C1084	G
G	G2044	U	A1797	A1798	A1717		G1541		A1341	U1244	G1172	C1085	A
U		G	C1798			G1629	G1542	C1450	G1342	C1245	A1173	A1086	C
C	G2050	U	C1803	C1803	U1722	A1630		G1451	C1343	A1246	G1174	C1087	U
A	A2054	C	A1804	G1805	G1723	A1631	C1545	U1457	G1344		G1175	A1088	C
C	A2055	U	G1806	G1806	U1724	A1632	G1546		A1345	C1250	C1176	G1094	G
G	U2064	U	U1887	G1807	G1725	G1633	A1547	C1457	U1346		G1177	U1095	C
U	C2065	G	U1887	U1807	G1726	G1634	U1548			G1253	G1178	U1096	A
G	U2066	U	U1890	C1808	G1727	U1635		C1462	G1351		U1179	A1097	C
A	C2066	C		G1809		G1636	G1552	U1463	A1352	U1266	U1180	A1098	A
A	A2071	C	G1901	G1810	G1730	A1637	C1553	U1464	C1353	C1267	A1181	G1099	C
C	C2072	U	U1903	A1811	C1731		U1554	A1465	C1360	G1268	C1182		U1003
C	G2073	C	G1908	A1815	A1732	A1641	G1555		G1363	G1269	C1183	U1109	U1004
A	A2074	U	A1909	C1816	A1733	A1642	G1557	A1471	G1366	U1270	C1184	U1110	A1005
U		A	A1910	G1819	C1734	C1643	G1558	C1472	C1366	G1272	U1187	U1111	A1006
U	A2081	C	G1910	G1820	C1735	U1645	A1559	U1473	A1372	C1274	A1188	U1115	A1007
G	C2084	C	U1915	U1823	U1741	G1652	U1561	G1475	G1376	G1275	A1189	U1116	C1008
C	A2085	U	G1916	C1824	A1742	A1653	G1562	A1476	G1377	U1276	G1190	A1117	A1013
G	U2086	C	G1917	U1825	G1743	U1654	G1563	C1477	C1377	G1277	A1191	A1118	A1014
U	G2094	G	U1918	G1826		G1655	C1564	U1478	G1378	A1278	A1192	G1119	C1015
C	A2095	A	A1919	C1826	G1743	G1655	C1565		G1379	U1279	A1193	U1120	U1016
G	A2096	G	G1920	G1827	A1747	A1656	C1566		U1380		G1194		
G		A	A1921	G1828		A1657	A1567	C1483		U1285	G1195	A1123	C1019
U	A2100	C	A1922	A1829	G1751	A1658		A1494	C1395		G1197		
A	G2101	G	G1923	C1834	U1752	A1659	C1573		C1396	G1289	U1198	G1127	G1023
C	U2102	C	G1925	U1835	C1753	G1660	C1574	G1497	G1397		A1199	U1128	G1024
C	C2105	U	G1925	U1835	A1754		C1575	G1498	G1398	U1298	A1200	C1129	C1025
U	C2106	A	G1925	U1835	A1755	G1666	U1577	U1499	A1399	G1300	C1201	U1130	U1029
G		C	G1929	U1838	G1756	A1667		U1500	A1406	C1305	A1202	A1132	G1044
A	G2110	C	A1930	A1840	U1761	U1668	A1580	A1501	A1407	U1306	G1203	A1133	G1045
C	G2111	A	A1931	C1841	C1762	A1669		A1502	U1408	A1307	U1206	U1134	
A		G	A1934		C1763	G1670	G1589	U1503	G1409		U1207	G1139	G1052
G	U2115	U	C1935	A1845	G1764			U1504	A1416	A1308	C1208	C1140	U1055
U	U2116	U	G1936	U1846	G1765	C1675	G1592	U1505	G1417	U1309	C1209	U1149	U1056
U	U2117	C	A1847		U1766	C1679	C1593	U1506		U1310	G1210	A1150	A1057
C	G2014	C	A1847		A1767		G1595	C1507		G1311	G1211	G1151	A1058
C	A2015	C	A1852	A1852	C1768		U1596		C1420	G1312	G1212		
C	C2119	C	A1941	A1853	C1769	A1682	U1597	G1512	C1421	A1313	C1213		
C	U2120	C	A1942	C1854	U1770	G1683	A1597	C1513	U1422	G1314	G1214		
G	G2121	C	C1943		U1771	A1684	A1598	C1514	C1423			A1154	
C		C											
G	G2237	C	A2238										
C	C2239		U2240										
U	C2241		U2242										
U	C2243												
C													
G	C2247												
C	G2249												



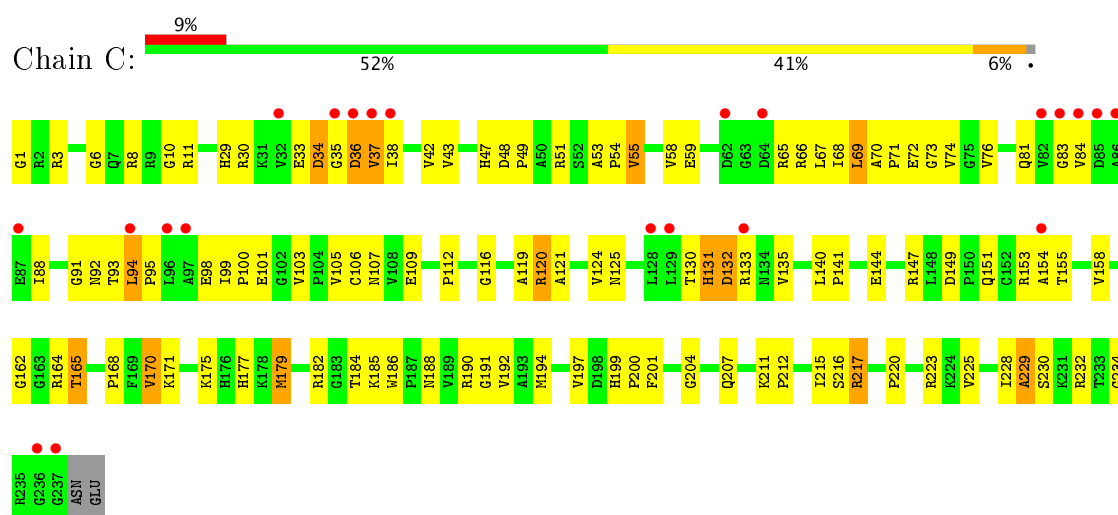
• Molecule 2: 5S ribosomal RNA



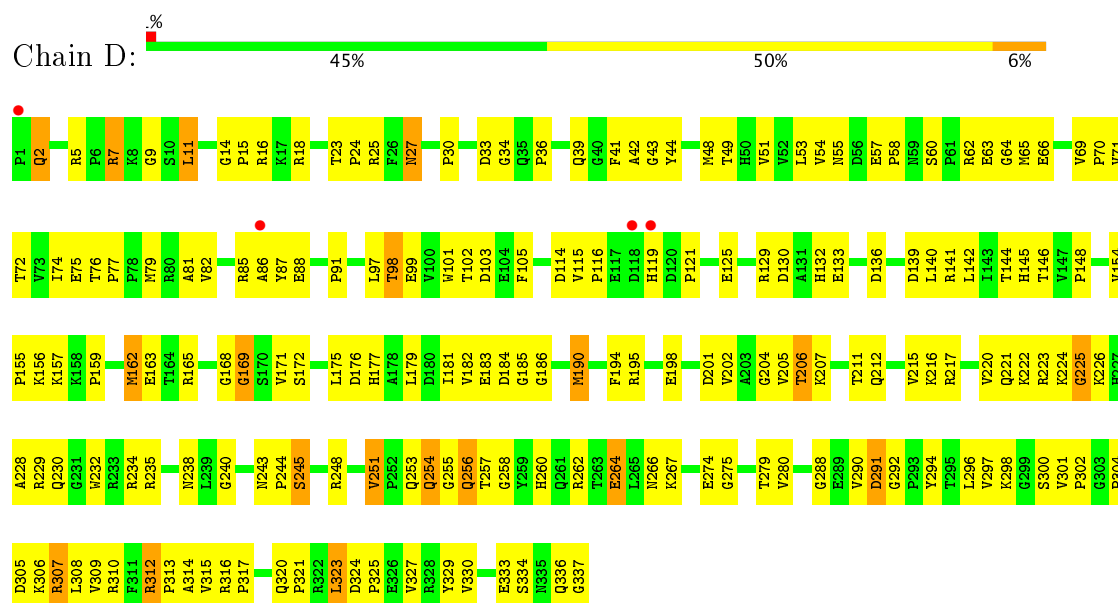
• Molecule 3: minihelix-puromycin



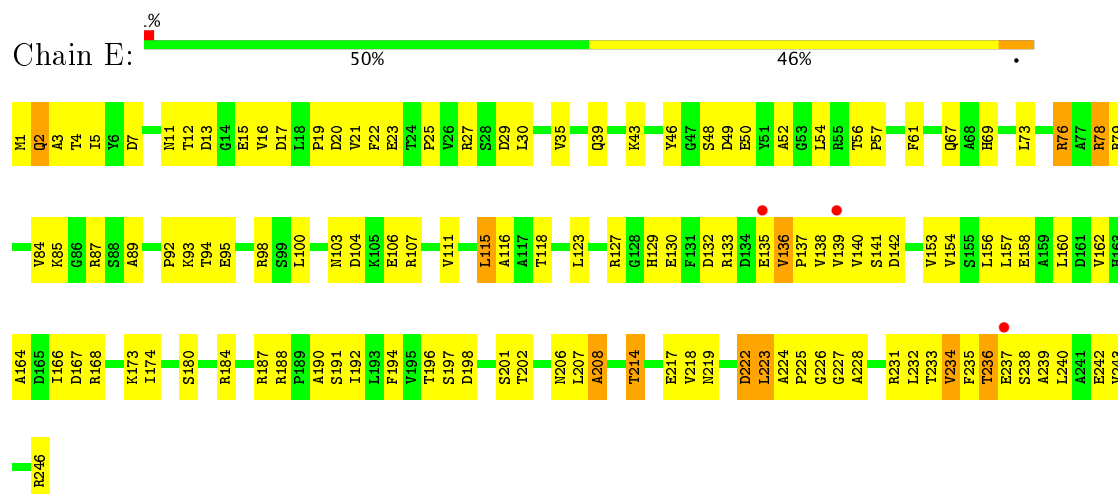
• Molecule 4: 50S ribosomal protein L2P

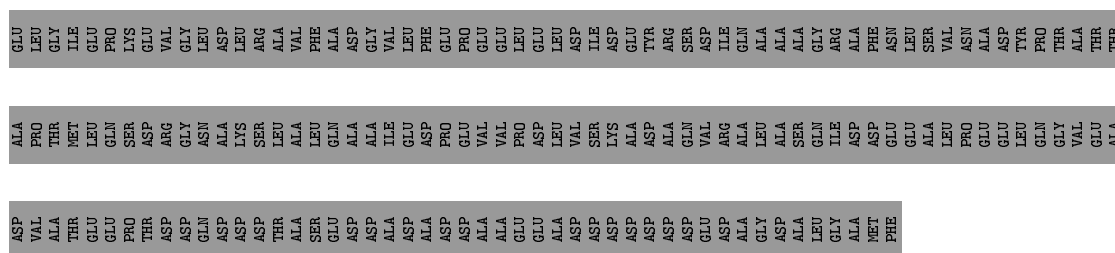


• Molecule 5: 50S ribosomal protein L3P

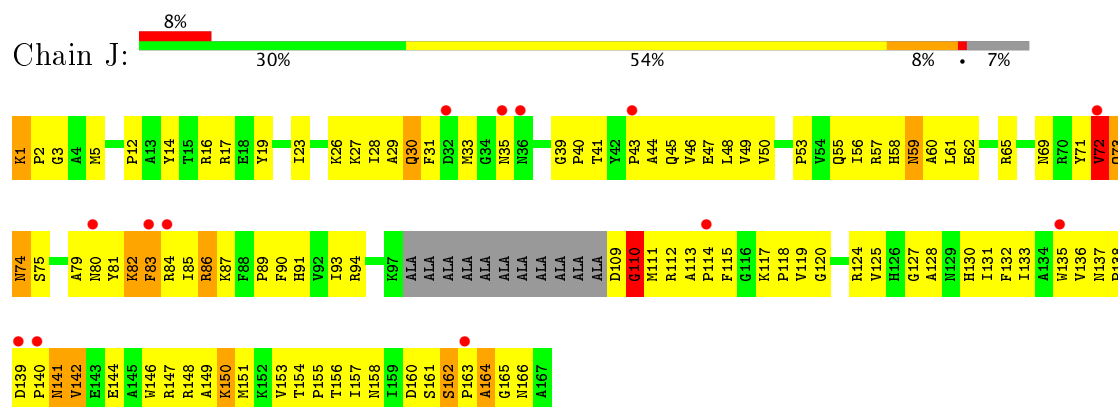


• Molecule 6: 50S ribosomal protein L4E

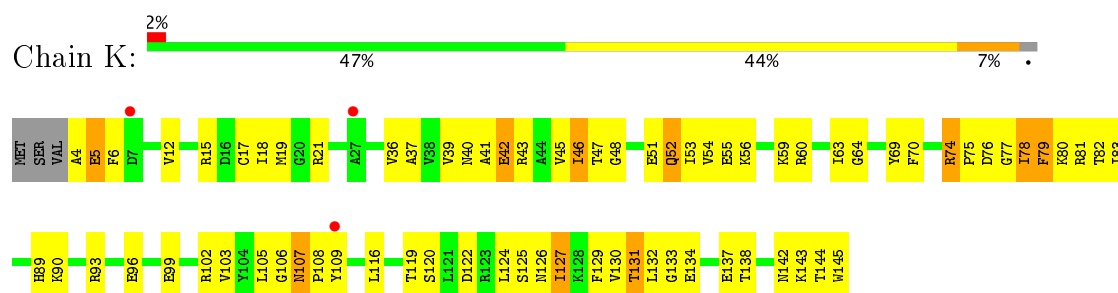




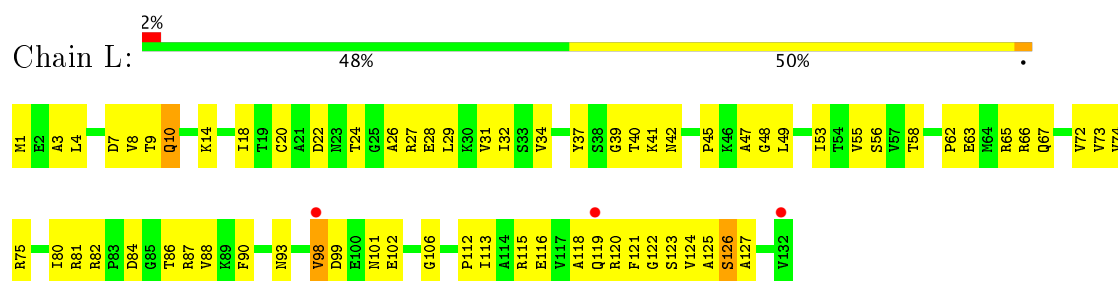
- Molecule 11: L10 Ribosomal Protein



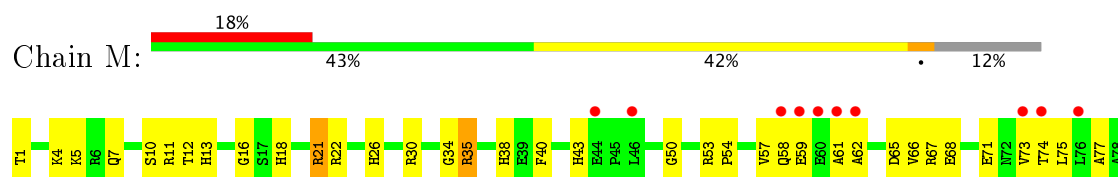
- Molecule 12: 50S ribosomal protein L13P

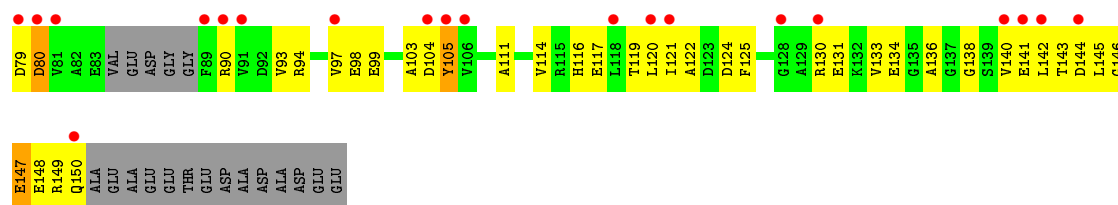


- Molecule 13: 50S ribosomal protein L14P

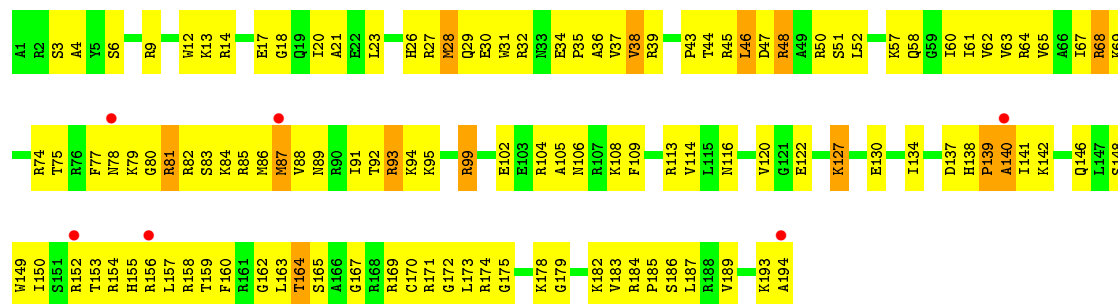


- Molecule 14: 50S ribosomal protein L15P

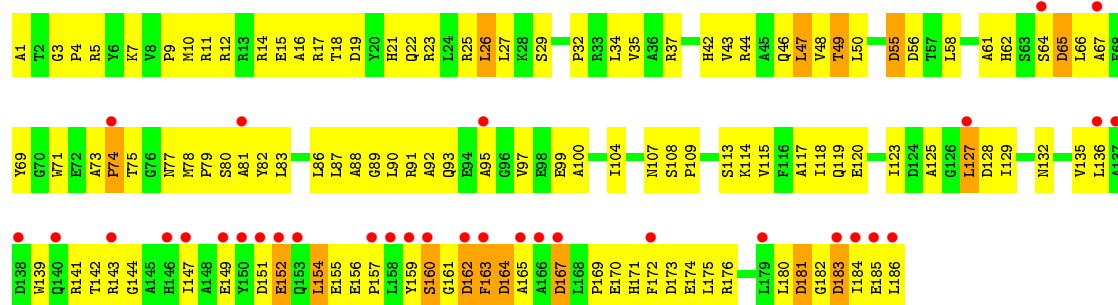




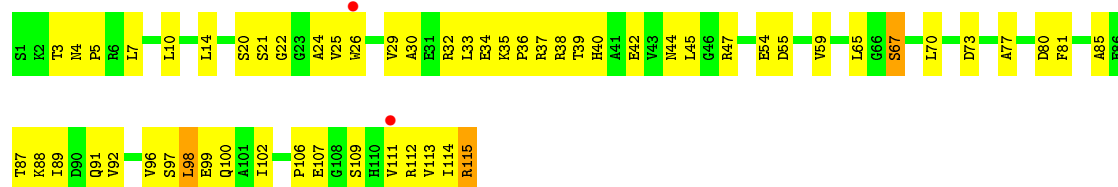
• Molecule 15: L15 Ribosomal Protein



• Molecule 16: 50S ribosomal protein L18P

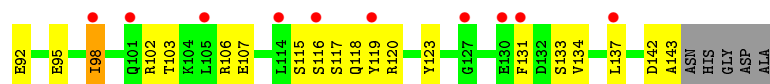


• Molecule 17: 50S ribosomal protein L18e



• Molecule 18: 50S ribosomal protein L19E





- Molecule 19: 50S ribosomal protein L21e



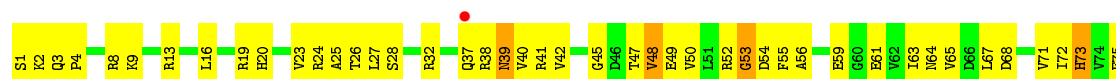
- Molecule 20: 50S ribosomal protein L22P



- Molecule 21: 50S ribosomal protein L23P



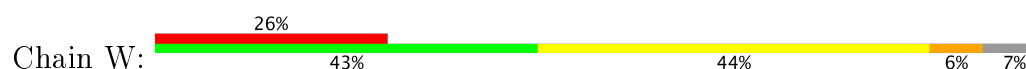
- Molecule 22: 50S ribosomal protein L24P

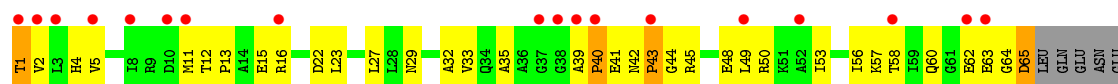


- Molecule 23: 50S ribosomal protein L24E



- Molecule 24: 50S ribosomal protein L29P





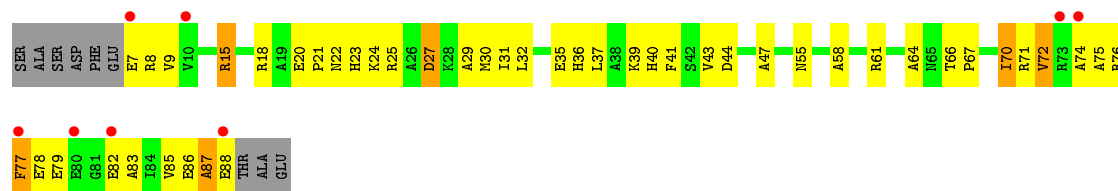
• Molecule 25: 50S ribosomal protein L30P

Chain X: 44% 49% 6%



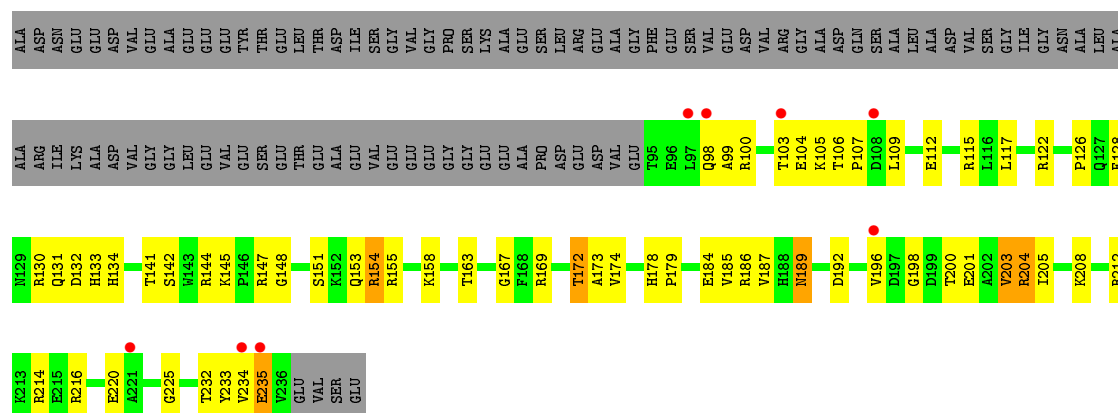
• Molecule 26: 50S ribosomal protein L31e

Chain Y: 9% 40% 44% 7% 10%



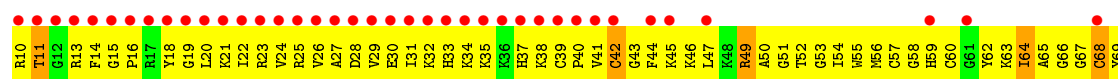
• Molecule 27: 50S ribosomal protein L32E

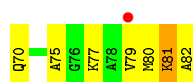
Chain Z: 3% 33% 23% 41%



• Molecule 28: L37Ae 50S ribosomal protein

Chain 1: 15% 55% 77% 8%

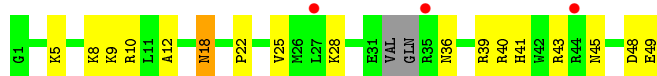




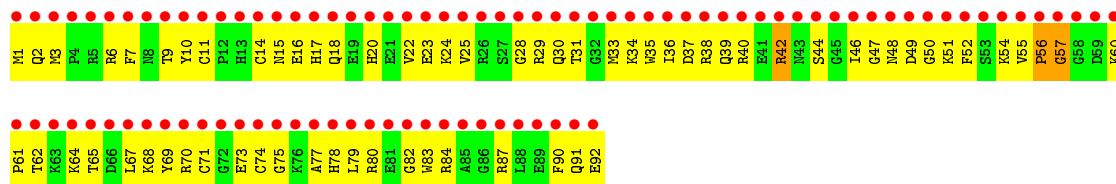
- Molecule 29: 50S ribosomal protein L37e



- Molecule 30: 50S ribosomal protein L39e



- Molecule 31: 50S 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	213.16Å 301.29Å 575.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.95 53.80 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.1 (20.00-2.95) 90.6 (53.80-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.81Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.210 , 0.259 0.209 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	98596	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% 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: MG, CL, NA, K, CD, PPU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.53	6/66076 (0.0%)	0.72	18/103052 (0.0%)
2	B	0.49	0/2905	0.78	3/4528 (0.1%)
3	5	1.19	0/43	0.77	0/64
4	C	0.40	0/1787	0.71	0/2409
5	D	0.39	0/2689	0.69	0/3652
6	E	0.44	0/1883	0.68	0/2551
7	F	0.37	0/1111	0.62	0/1498
8	G	0.38	0/1382	0.62	0/1880
9	H	0.46	1/896 (0.1%)	0.73	3/1219 (0.2%)
10	I	0.42	0/241	0.62	0/324
11	J	0.44	0/1246	0.76	3/1686 (0.2%)
12	K	0.41	0/1135	0.67	0/1530
13	L	0.40	0/1003	0.73	0/1351
14	M	0.41	0/1126	0.72	0/1504
15	N	0.45	0/1633	0.74	2/2180 (0.1%)
16	O	0.36	0/1473	0.69	0/1999
17	P	0.41	0/873	0.71	0/1181
18	Q	0.41	0/1143	0.62	0/1521
19	R	0.42	0/748	0.74	1/1005 (0.1%)
20	S	0.42	0/1172	0.65	0/1578
21	T	0.39	0/648	0.63	0/875
22	U	0.36	0/957	0.66	0/1289
23	V	0.46	0/417	0.65	0/562
24	W	0.33	0/502	0.63	0/675
25	X	0.37	0/1218	0.67	0/1655
26	Y	0.40	0/664	0.66	0/895
27	Z	0.41	0/1146	0.67	0/1536
28	1	0.57	0/575	0.72	0/763
29	2	0.48	0/437	0.69	0/578
30	3	0.35	0/398	0.60	0/527
31	4	0.84	0/771	0.70	0/1024
All	All	0.50	7/98298 (0.0%)	0.71	30/147091 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	58
2	B	1	0
All	All	1	58

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2617	G	C3'-O3'	12.86	1.60	1.42
1	A	2617	G	C4'-O4'	-6.15	1.37	1.45
9	H	3	TYR	CG-CD1	6.05	1.47	1.39
1	A	2618	G	P-OP2	-5.70	1.39	1.49
1	A	2617	G	N9-C8	5.65	1.41	1.37
1	A	2617	G	C2'-C1'	-5.40	1.47	1.53
1	A	2617	G	C4'-C3'	-5.38	1.47	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1165	G	O5'-P-OP2	10.73	123.58	110.70
1	A	1563	G	C2'-C3'-O3'	9.26	129.87	109.50
2	B	3024	U	C2'-C3'-O3'	9.18	129.70	109.50
9	H	3	TYR	CB-CG-CD2	9.11	126.47	121.00
1	A	1164	U	OP1-P-O3'	-8.57	86.34	105.20
1	A	1942	A	C5'-C4'-C3'	7.36	127.77	116.00
1	A	1164	U	OP2-P-O3'	-7.20	89.35	105.20
9	H	3	TYR	CG-CD2-CE2	6.82	126.76	121.30
1	A	871	G	C5'-C4'-O4'	-6.41	101.41	109.10
1	A	1504	A	N9-C1'-C2'	6.34	122.25	114.00
1	A	2617	G	C3'-C2'-C1'	-6.14	96.59	101.50
9	H	3	TYR	CB-CG-CD1	-6.13	117.32	121.00
1	A	1979	G	C2'-C3'-O3'	6.10	123.46	113.70
1	A	381	G	N9-C1'-C2'	5.82	121.57	114.00
1	A	535	G	N9-C1'-C2'	5.82	121.56	114.00
11	J	74	ASN	N-CA-C	-5.75	95.48	111.00
1	A	2291	A	N9-C1'-C2'	5.74	121.47	114.00
1	A	1504	A	C1'-O4'-C4'	-5.64	105.39	109.90
15	N	127	LYS	N-CA-C	-5.56	95.99	111.00
19	R	68	GLY	N-CA-C	-5.42	99.55	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3024	U	C4'-C3'-O3'	5.34	123.69	113.00
2	B	3039	U	N1-C1'-C2'	5.32	120.91	114.00
1	A	2313	C	C5'-C4'-O4'	5.31	115.47	109.10
11	J	141	ASN	N-CA-C	-5.30	96.70	111.00
1	A	2431	C	C5'-C4'-C3'	-5.22	107.64	116.00
1	A	2607	U	N1-C1'-C2'	5.11	120.64	114.00
1	A	237	G	O4'-C4'-C3'	-5.10	98.90	104.00
11	J	110	GLY	N-CA-C	-5.07	100.42	113.10
1	A	1450	C	N1-C1'-C2'	-5.01	106.48	112.00
15	N	139	PRO	N-CA-C	-5.01	99.08	112.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	3024	U	C3'

All (58) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1055	G	Sidechain
1	A	1191	A	Sidechain
1	A	1309	U	Sidechain
1	A	1316	G	Sidechain
1	A	1351	G	Sidechain
1	A	1376	G	Sidechain
1	A	1380	U	Sidechain
1	A	1417	G	Sidechain
1	A	1430	G	Sidechain
1	A	1464	U	Sidechain
1	A	148	A	Sidechain
1	A	1635	U	Sidechain
1	A	1641	A	Sidechain
1	A	1707	G	Sidechain
1	A	176	U	Sidechain
1	A	1772	C	Sidechain
1	A	1819	G	Sidechain
1	A	182	G	Sidechain
1	A	1825	U	Sidechain
1	A	1835	U	Sidechain
1	A	1839	A	Sidechain
1	A	1845	A	Sidechain
1	A	1861	C	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1878	G	Sidechain
1	A	1887	U	Sidechain
1	A	1903	U	Sidechain
1	A	1996	U	Sidechain
1	A	205	U	Sidechain
1	A	214	U	Sidechain
1	A	2308	U	Sidechain
1	A	2313	C	Sidechain
1	A	2316	G	Sidechain
1	A	2421	G	Sidechain
1	A	2493	C	Sidechain
1	A	2506	A	Sidechain
1	A	2552	C	Sidechain
1	A	2564	G	Sidechain
1	A	2597	U	Sidechain
1	A	2599	A	Sidechain
1	A	2607	U	Sidechain
1	A	2622	A	Sidechain
1	A	264	G	Sidechain
1	A	2673	U	Sidechain
1	A	2753	G	Sidechain
1	A	2793	A	Sidechain
1	A	2799	A	Sidechain
1	A	324	G	Sidechain
1	A	482	G	Sidechain
1	A	518	G	Sidechain
1	A	535	G	Sidechain
1	A	619	U	Sidechain
1	A	651	U	Sidechain
1	A	722	G	Sidechain
1	A	734	U	Sidechain
1	A	795	G	Sidechain
1	A	817	G	Sidechain
1	A	840	U	Sidechain
1	A	920	C	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	A	59017	0	29805	1413	0
2	B	2600	0	1326	101	0
3	5	40	0	22	7	0
4	C	1754	0	1763	136	0
5	D	2624	0	2533	221	0
6	E	1858	0	1816	138	0
7	F	1094	0	1085	149	0
8	G	1357	0	1266	101	0
9	H	885	0	854	76	0
10	I	240	0	231	24	0
11	J	1215	0	1215	172	0
12	K	1119	0	1098	86	0
13	L	993	0	1027	73	0
14	M	1114	0	1072	76	0
15	N	1605	0	1676	178	0
16	O	1444	0	1401	159	0
17	P	864	0	873	74	0
18	Q	1133	0	1127	64	0
19	R	734	0	728	36	0
20	S	1149	0	1122	76	0
21	T	641	0	605	23	0
22	U	949	0	923	76	0
23	V	410	0	367	46	0
24	W	499	0	511	37	0
25	X	1195	0	1137	111	0
26	Y	654	0	653	53	0
27	Z	1130	0	1133	77	0
28	1	563	0	600	89	0
29	2	430	0	426	24	0
30	3	393	0	406	17	0
31	4	755	0	732	108	0
32	1	1	0	0	0	0
32	4	2	0	0	0	0
32	A	108	0	0	0	0
32	B	1	0	0	0	0
32	C	1	0	0	0	0
32	D	1	0	0	0	0
32	L	1	0	0	0	0
32	U	1	0	0	0	0
32	Z	1	0	0	0	0
33	A	2	0	0	0	0
34	A	73	0	0	0	0
34	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	C	1	0	0	0	0
34	E	1	0	0	0	0
34	J	1	0	0	0	0
34	K	1	0	0	0	0
34	M	1	0	0	0	0
34	N	1	0	0	0	0
34	R	1	0	0	0	0
34	S	3	0	0	0	0
34	T	1	0	0	0	0
35	4	1	0	0	1	0
35	A	11	0	0	3	0
35	C	1	0	0	0	0
35	D	1	0	0	0	0
35	K	3	0	0	2	0
35	N	1	0	0	1	0
35	O	1	0	0	0	0
35	P	1	0	0	0	0
35	S	1	0	0	0	0
35	Z	1	0	0	0	0
36	5	37	0	28	4	0
37	1	1	0	0	0	0
37	2	1	0	0	0	0
37	4	1	0	0	0	0
37	P	1	0	0	0	0
37	V	1	0	0	0	0
38	1	38	0	0	14	0
38	2	56	0	0	9	0
38	3	47	0	0	2	0
38	4	72	0	0	13	0
38	A	5871	0	0	307	0
38	B	147	0	0	14	0
38	C	135	0	0	24	0
38	D	155	0	0	28	0
38	E	171	0	0	31	0
38	F	51	0	0	25	0
38	G	44	0	0	14	0
38	H	26	0	0	12	0
38	I	20	0	0	6	0
38	J	77	0	0	27	0
38	K	55	0	0	5	0
38	L	63	0	0	14	0
38	M	90	0	0	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	125	0	0	27	0
38	O	64	0	0	26	0
38	P	44	0	0	13	0
38	Q	68	0	0	10	0
38	R	54	0	0	5	0
38	S	83	0	0	9	0
38	T	31	0	0	4	0
38	U	39	0	0	8	0
38	V	26	0	0	7	0
38	W	15	0	0	5	0
38	X	70	0	0	14	0
38	Y	30	0	0	5	0
38	Z	102	0	0	19	0
All	All	98596	0	59561	3672	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 24.

All (3672) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3006:C:H5"	16:O:37:ARG:NH1	1.56	1.19
24:W:12:THR:HG22	24:W:15:GLU:HG3	1.28	1.14
6:E:236:THR:HG22	6:E:239:ALA:H	1.10	1.10
11:J:86:ARG:HH11	11:J:133:ILE:HG13	0.99	1.10
6:E:115:LEU:HD13	6:E:223:LEU:HD21	1.30	1.09
15:N:87:MET:HB3	31:4:46:ILE:HD13	1.30	1.08
2:B:3006:C:H5"	16:O:37:ARG:HH12	0.91	1.05
2:B:3056:A:H2'	2:B:3057:A:H5"	1.35	1.05
26:Y:37:LEU:HD13	26:Y:85:VAL:HG21	1.39	1.04
11:J:162:SER:HB2	11:J:163:PRO:HD3	1.34	1.04
28:1:46:LYS:HD3	28:1:59:HIS:HB2	1.40	1.03
25:X:5:VAL:HG22	25:X:32:CYS:HB2	1.40	1.03
11:J:86:ARG:NH1	11:J:133:ILE:HG13	1.73	1.02
10:I:23:ILE:HD13	10:I:67:LEU:HD23	1.42	1.02
1:A:1679:C:H5'	38:A:8832:HOH:O	1.59	1.02
2:B:3006:C:C5'	16:O:37:ARG:HH12	1.72	1.02
1:A:1119:G:H2'	12:K:52:GLN:HE22	1.22	1.02
22:U:71:VAL:HG11	22:U:90:PRO:HB3	1.38	1.01
1:A:541:C:H2'	1:A:542:A:H5"	1.41	1.00
7:F:134:LEU:HD11	7:F:166:ILE:HD11	1.38	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:162:MET:HE3	5:D:308:LEU:HD21	1.45	0.99
15:N:87:MET:HG2	31:4:46:ILE:HG21	1.45	0.99
1:A:1165:G:H3'	1:A:1165:G:OP1	1.62	0.98
25:X:72:PRO:HG2	25:X:77:ALA:HB3	1.45	0.98
5:D:248:ARG:O	5:D:251:VAL:HG12	1.62	0.98
1:A:1160:G:H5'	1:A:1161:A:H5'	1.45	0.98
1:A:962:C:H1'	16:O:5:ARG:NH1	1.79	0.98
5:D:238:ASN:HD22	5:D:240:GLY:H	1.12	0.97
11:J:27:LYS:H	11:J:58:HIS:HD2	1.08	0.97
13:L:10:GLN:NE2	13:L:10:GLN:H	1.61	0.97
20:S:8:ALA:HB1	20:S:13:THR:HG21	1.43	0.96
28:1:37:HIS:HB2	28:1:47:LEU:HB2	1.48	0.96
1:A:156:C:H5''	15:N:171:ARG:HD3	1.48	0.96
1:A:1751:G:H2'	1:A:1752:G:H5''	1.48	0.95
11:J:45:GLN:HB3	11:J:163:PRO:HD2	1.48	0.95
28:1:39:CYS:SG	28:1:47:LEU:HD21	2.07	0.94
1:A:2717:C:H2'	1:A:2718:C:H5''	1.49	0.94
1:A:856:G:H2'	38:A:4907:HOH:O	1.66	0.94
2:B:3006:C:C5'	16:O:37:ARG:NH1	2.29	0.94
18:Q:115:SER:H	18:Q:118:GLN:HE21	1.14	0.94
1:A:960:G:H4'	38:A:6895:HOH:O	1.68	0.94
18:Q:115:SER:OG	18:Q:118:GLN:HG3	1.68	0.94
12:K:74:ARG:HB3	12:K:74:ARG:HH11	1.33	0.93
5:D:140:LEU:HA	38:D:8587:HOH:O	1.66	0.93
8:G:97:VAL:HG12	38:G:4191:HOH:O	1.66	0.93
1:A:2716:G:H5''	5:D:206:THR:HG21	1.47	0.93
27:Z:220:GLU:HG2	38:Z:8551:HOH:O	1.67	0.93
6:E:127:ARG:NH2	6:E:225:PRO:HG2	1.83	0.93
6:E:61:PHE:HB3	38:E:8444:HOH:O	1.66	0.93
1:A:1242:A:H5'	12:K:82:THR:HG23	1.50	0.93
2:B:3076:G:H3'	2:B:3077:A:H5''	1.52	0.92
14:M:68:GLU:HA	38:M:8419:HOH:O	1.68	0.92
2:B:3056:A:C2'	2:B:3057:A:H5''	1.98	0.92
26:Y:71:ARG:HB3	26:Y:88:GLU:OE1	1.69	0.92
1:A:1134:G:H4'	11:J:151:MET:HE1	1.51	0.92
7:F:25:MET:HE2	7:F:41:LEU:HG	1.52	0.91
17:P:32:ARG:HB2	38:P:4656:HOH:O	1.71	0.91
1:A:871:G:H5'	1:A:871:G:C8	2.06	0.91
7:F:105:SER:HB2	7:F:131:THR:HG23	1.53	0.91
8:G:15:GLN:HG3	8:G:20:ILE:HG12	1.53	0.90
30:3:41:HIS:H	30:3:45:ASN:HD22	1.16	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1625:U:H4'	38:A:4147:HOH:O	1.70	0.90
1:A:1119:G:H2'	12:K:52:GLN:NE2	1.87	0.90
2:B:3023:U:H3'	38:B:8484:HOH:O	1.72	0.90
15:N:35:PRO:CG	15:N:38:VAL:HG23	2.02	0.90
23:V:30:HIS:HB3	38:V:6215:HOH:O	1.72	0.89
4:C:211:LYS:HB3	4:C:212:PRO:HD2	1.53	0.89
1:A:21:G:H5'	20:S:2:ILE:HA	1.53	0.89
1:A:1667:A:H5'	1:A:1667:A:H8	1.34	0.89
5:D:321:PRO:HA	38:D:8666:HOH:O	1.72	0.89
11:J:26:LYS:HD2	11:J:28:ILE:HD12	1.54	0.89
11:J:162:SER:HB2	11:J:163:PRO:CD	2.00	0.89
1:A:1702:U:H5''	38:A:6683:HOH:O	1.72	0.89
1:A:711:G:H1'	38:A:6564:HOH:O	1.72	0.89
16:O:86:LEU:HD12	16:O:125:ALA:HB2	1.54	0.89
15:N:35:PRO:HG2	15:N:38:VAL:HG23	1.52	0.89
4:C:69:LEU:HD21	4:C:120:ARG:HB3	1.54	0.89
1:A:1166:A:H1'	1:A:1192:A:C2	2.08	0.88
11:J:5:MET:HG3	38:J:8354:HOH:O	1.71	0.88
26:Y:78:GLU:HG2	26:Y:79:GLU:H	1.36	0.88
1:A:289:G:H22	1:A:363:A:H2	1.20	0.88
16:O:87:LEU:HD12	16:O:186:LEU:HD21	1.55	0.88
1:A:2812:A:H2	1:A:2814:A:H62	1.20	0.88
12:K:19:MET:HE2	12:K:79:PHE:HA	1.55	0.88
15:N:87:MET:CB	31:4:46:ILE:HD13	2.04	0.88
11:J:55:GLN:HE21	11:J:124:ARG:HE	1.20	0.88
38:B:8478:HOH:O	16:O:23:ARG:HD3	1.74	0.88
11:J:86:ARG:HH11	11:J:133:ILE:CG1	1.87	0.87
1:A:541:C:C2'	1:A:542:A:H5''	2.04	0.87
5:D:86:ALA:HA	38:D:8587:HOH:O	1.75	0.87
20:S:99:ALA:HB1	20:S:109:MET:HE1	1.56	0.87
1:A:346:U:H4'	38:A:6311:HOH:O	1.74	0.87
15:N:64:ARG:HD2	38:N:8580:HOH:O	1.73	0.87
1:A:214:U:H5'	38:A:5630:HOH:O	1.75	0.87
1:A:2506:A:HO2'	1:A:2507:G:H8	0.89	0.86
9:H:107:VAL:HG23	38:H:6617:HOH:O	1.76	0.86
13:L:29:LEU:HB3	13:L:55:VAL:HG11	1.56	0.86
1:A:542:A:H8	1:A:542:A:H5'	1.40	0.86
26:Y:25:ARG:HD2	38:Y:3861:HOH:O	1.74	0.86
2:B:3048:C:H4'	16:O:141:ARG:HH21	1.40	0.86
16:O:144:GLY:O	16:O:147:ILE:HG22	1.76	0.86
12:K:52:GLN:HG3	12:K:53:ILE:N	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:14:GLU:OE1	23:V:15:PRO:HD2	1.76	0.86
1:A:1191:A:H3'	1:A:1192:A:H5''	1.57	0.85
8:G:20:ILE:HD11	8:G:40:VAL:HG11	1.56	0.85
25:X:21:LEU:HD22	25:X:26:ILE:HD11	1.58	0.85
1:A:2459:G:OP1	31:4:64:LYS:N	2.08	0.85
16:O:47:LEU:HD11	16:O:127:LEU:HD21	1.58	0.85
25:X:68:THR:HG23	25:X:69:ARG:HG2	1.58	0.85
14:M:148:GLU:HA	38:M:8448:HOH:O	1.75	0.85
28:1:59:HIS:HA	38:1:8441:HOH:O	1.77	0.85
38:A:3220:HOH:O	15:N:157:LEU:HD11	1.76	0.85
13:L:74:VAL:HG12	13:L:75:ARG:HG3	1.58	0.85
1:A:1164:U:C4'	1:A:1165:G:OP1	2.21	0.84
6:E:235:PHE:HE2	6:E:243:VAL:HG21	1.42	0.84
11:J:165:GLY:HA3	38:J:8384:HOH:O	1.77	0.84
2:B:3023:U:H4'	2:B:3024:U:OP2	1.77	0.84
6:E:180:SER:HB2	38:E:8445:HOH:O	1.77	0.84
38:A:4706:HOH:O	13:L:39:GLY:HA2	1.77	0.84
9:H:63:ILE:HB	9:H:64:PRO:HD3	1.59	0.84
25:X:122:ARG:HH21	25:X:154:ARG:HD2	1.43	0.84
11:J:150:LYS:HB2	11:J:157:ILE:HD12	1.59	0.84
13:L:10:GLN:HE21	13:L:10:GLN:H	1.25	0.84
5:D:55:ASN:HB3	5:D:63:GLU:HA	1.58	0.84
31:4:60:LYS:HD2	31:4:61:PRO:HD2	1.60	0.84
1:A:506:G:H22	1:A:509:A:H5'	1.43	0.84
6:E:242:GLU:HG3	38:E:8382:HOH:O	1.77	0.84
25:X:122:ARG:NH2	25:X:154:ARG:HD2	1.93	0.84
1:A:1702:U:H5'	38:A:9923:HOH:O	1.77	0.84
23:V:9:CYS:HA	23:V:52:THR:HG23	1.58	0.83
1:A:2435:U:OP1	31:4:28:GLY:HA3	1.79	0.83
1:A:1634:G:H3'	38:A:3391:HOH:O	1.76	0.83
4:C:35:GLY:O	4:C:36:ASP:HB3	1.78	0.83
16:O:159:TYR:HB3	16:O:162:ASP:HB2	1.61	0.83
1:A:1120:U:H6	1:A:1120:U:H5''	1.44	0.83
1:A:2586:U:H3	1:A:2592:G:H22	1.22	0.83
1:A:2256:G:H2'	1:A:2257:G:H5'	1.61	0.83
1:A:1835:U:H5	1:A:1840:A:N7	1.76	0.83
26:Y:31:ILE:O	26:Y:35:GLU:HG3	1.79	0.83
1:A:1164:U:H4'	1:A:1165:G:OP1	1.79	0.83
1:A:2004:U:H4'	38:A:4789:HOH:O	1.79	0.83
15:N:164:THR:HG22	15:N:167:GLY:H	1.41	0.83
38:A:5274:HOH:O	15:N:170:CYS:SG	2.37	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:18:LEU:HD12	20:S:143:VAL:HG11	1.61	0.83
28:1:30:GLU:HB3	28:1:34:LYS:HE3	1.60	0.82
5:D:179:LEU:O	5:D:183:GLU:HG2	1.79	0.82
1:A:962:C:H1'	16:O:5:ARG:HH12	1.42	0.82
5:D:258:GLY:H	5:D:260:HIS:CE1	1.97	0.82
6:E:76:ARG:HD2	38:E:8432:HOH:O	1.78	0.82
11:J:2:PRO:HB2	38:J:8354:HOH:O	1.78	0.82
6:E:237:GLU:HB2	38:E:8429:HOH:O	1.80	0.82
24:W:56:ILE:O	24:W:60:GLN:HG3	1.78	0.82
1:A:1773:G:C8	28:1:16:PRO:HA	2.15	0.82
6:E:5:ILE:HD11	6:E:16:VAL:HG23	1.61	0.82
15:N:106:ASN:ND2	35:N:8518:CL:CL	2.50	0.82
6:E:236:THR:HA	38:E:8450:HOH:O	1.78	0.82
38:A:3049:HOH:O	15:N:152:ARG:HG3	1.78	0.82
18:Q:80:ARG:HG2	18:Q:87:ARG:CZ	2.09	0.82
1:A:1164:U:H3	1:A:1192:A:H2	1.27	0.82
7:F:22:VAL:HG22	7:F:74:THR:HG22	1.60	0.82
11:J:139:ASP:N	11:J:140:PRO:HD3	1.95	0.82
31:4:22:VAL:HG11	31:4:67:LEU:HD13	1.63	0.81
7:F:25:MET:HE1	7:F:37:ALA:HB1	1.62	0.81
1:A:877:G:H5'	1:A:878:G:OP1	1.81	0.81
5:D:162:MET:CE	5:D:308:LEU:HD21	2.10	0.81
20:S:9:ASP:O	20:S:13:THR:HB	1.80	0.81
14:M:148:GLU:HB2	38:M:8467:HOH:O	1.81	0.81
1:A:545:G:H5'	1:A:545:G:H8	1.46	0.81
11:J:162:SER:CB	11:J:163:PRO:HD3	2.09	0.81
1:A:2256:G:C2'	1:A:2257:G:H5'	2.11	0.81
15:N:104:ARG:O	15:N:108:LYS:HG2	1.81	0.81
1:A:1116:U:HO2'	1:A:1118:A:H2	0.83	0.81
11:J:59:ASN:HD22	11:J:59:ASN:H	1.27	0.81
16:O:90:LEU:HB2	16:O:186:LEU:HD22	1.63	0.81
26:Y:15:ARG:HH11	26:Y:15:ARG:HB3	1.45	0.81
38:A:7028:HOH:O	31:4:60:LYS:HG3	1.80	0.81
31:4:70:ARG:HG2	31:4:77:ALA:HB2	1.62	0.81
15:N:87:MET:CG	31:4:46:ILE:HG21	2.10	0.80
1:A:1474:C:H6	1:A:1474:C:H5'	1.46	0.80
18:Q:103:THR:HA	18:Q:106:ARG:NH1	1.95	0.80
22:U:19:ARG:HD3	22:U:67:LEU:O	1.81	0.80
11:J:142:VAL:HG13	38:J:8369:HOH:O	1.81	0.80
15:N:52:LEU:HD11	38:N:8610:HOH:O	1.81	0.80
25:X:6:GLN:HB2	25:X:26:ILE:HD12	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2830:U:H3'	38:A:4713:HOH:O	1.80	0.80
9:H:91:VAL:HG12	9:H:92:GLY:N	1.96	0.80
7:F:27:ILE:HG22	7:F:28:GLY:H	1.45	0.80
4:C:6:GLY:HA3	38:C:8578:HOH:O	1.81	0.79
21:T:51:GLN:HE21	21:T:53:ASN:HD21	1.27	0.79
12:K:76:ASP:HA	38:K:5907:HOH:O	1.81	0.79
7:F:154:LYS:H	7:F:154:LYS:HD2	1.47	0.79
11:J:137:ASN:O	11:J:139:ASP:N	2.15	0.79
15:N:94:LYS:HE3	38:N:8578:HOH:O	1.80	0.79
1:A:1923:G:H4'	31:4:31:THR:O	1.83	0.79
1:A:513:A:N3	38:A:3157:HOH:O	2.16	0.79
1:A:560:C:H42	1:A:597:A:H61	1.31	0.79
2:B:3042:C:H2'	38:B:8506:HOH:O	1.80	0.79
5:D:71:VAL:HG11	5:D:296:LEU:HB3	1.62	0.79
25:X:88:THR:HB	38:X:6679:HOH:O	1.81	0.79
3:5:74:C:C2'	3:5:75:C:H5'	2.12	0.79
14:M:133:VAL:HA	38:M:8449:HOH:O	1.81	0.79
5:D:238:ASN:ND2	5:D:240:GLY:H	1.79	0.79
6:E:236:THR:HG22	6:E:239:ALA:N	1.95	0.79
1:A:1878:G:H1'	38:A:5611:HOH:O	1.81	0.78
5:D:119:HIS:O	5:D:121:PRO:HD3	1.83	0.78
13:L:14:LYS:HB2	13:L:45:PRO:HG2	1.66	0.78
1:A:870:G:H2'	1:A:871:G:H5''	1.64	0.78
8:G:3:VAL:HG22	8:G:49:ILE:HB	1.66	0.78
14:M:35:ARG:O	14:M:40:PHE:HA	1.83	0.78
5:D:125:GLU:O	5:D:129:ARG:HG3	1.82	0.78
6:E:1:MET:HG2	6:E:2:GLN:H	1.47	0.78
1:A:2717:C:C2'	1:A:2718:C:H5''	2.14	0.78
1:A:871:G:C5'	1:A:871:G:H8	1.95	0.78
38:A:4346:HOH:O	15:N:14:ARG:HG2	1.84	0.78
16:O:83:LEU:HD13	16:O:175:LEU:HD23	1.66	0.78
38:A:6242:HOH:O	16:O:4:PRO:HD2	1.83	0.78
31:4:31:THR:HB	31:4:33:MET:CE	2.14	0.78
5:D:141:ARG:HD2	5:D:163:GLU:OE2	1.83	0.78
1:A:1886:A:N3	38:A:4306:HOH:O	2.17	0.78
13:L:22:ASP:HB2	38:L:5264:HOH:O	1.83	0.78
23:V:14:GLU:O	23:V:17:THR:HB	1.84	0.78
1:A:1185:U:H2'	1:A:1186:C:C6	2.19	0.78
2:B:3025:G:H3'	2:B:3026:C:C5'	2.14	0.78
2:B:3029:C:H2'	2:B:3030:C:H5'	1.66	0.78
26:Y:72:VAL:HG22	26:Y:85:VAL:HG12	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:30:GLU:HA	28:1:33:HIS:HB3	1.65	0.78
12:K:75:PRO:HG2	12:K:105:LEU:HD21	1.66	0.78
1:A:2432:C:O2'	1:A:2433:A:H5'	1.83	0.77
1:A:1474:C:C6	1:A:1474:C:H5'	2.20	0.77
1:A:1936:C:H3'	38:A:6641:HOH:O	1.83	0.77
2:B:3025:G:H3'	2:B:3026:C:H5'	1.64	0.77
1:A:1372:A:H3'	38:A:6654:HOH:O	1.84	0.77
4:C:121:ALA:O	4:C:124:VAL:HG22	1.83	0.77
5:D:41:PHE:CD2	5:D:190:MET:HE3	2.18	0.77
5:D:264:GLU:HG2	5:D:267:LYS:HE2	1.64	0.77
1:A:1507:C:H4'	38:A:3100:HOH:O	1.84	0.77
15:N:99:ARG:HD2	15:N:167:GLY:HA2	1.66	0.77
4:C:192:VAL:HB	38:C:8607:HOH:O	1.85	0.77
1:A:871:G:H5'	1:A:871:G:H8	1.46	0.77
21:T:6:LYS:HB2	21:T:27:ALA:O	1.85	0.77
27:Z:109:LEU:HD23	38:Z:8573:HOH:O	1.84	0.77
2:B:3107:C:H5	38:B:8439:HOH:O	1.68	0.77
5:D:42:ALA:HB1	5:D:308:LEU:HD11	1.66	0.77
8:G:37:ASP:OD1	12:K:125:SER:HB3	1.85	0.77
24:W:16:ARG:NH2	24:W:63:GLU:HG3	2.00	0.77
25:X:141:HIS:HB2	25:X:146:ILE:HG12	1.64	0.77
1:A:1328:A:OP1	27:Z:169:ARG:HD2	1.85	0.77
11:J:59:ASN:N	11:J:59:ASN:HD22	1.82	0.77
1:A:871:G:C5'	1:A:871:G:C8	2.69	0.76
9:H:46:GLU:O	9:H:73:PRO:HD2	1.85	0.76
15:N:60:ILE:C	15:N:61:ILE:HD12	2.06	0.76
27:Z:187:VAL:HG23	27:Z:192:ASP:HB2	1.66	0.76
29:2:25:LYS:O	29:2:25:LYS:HG2	1.84	0.76
1:A:1450:C:H4'	1:A:1451:C:OP2	1.84	0.76
9:H:99:THR:HA	38:H:3461:HOH:O	1.84	0.76
15:N:172:GLY:O	15:N:183:VAL:HG11	1.86	0.76
1:A:1377:C:H5'	1:A:1377:C:H6	1.51	0.76
4:C:94:LEU:HG	4:C:99:ILE:HD11	1.66	0.76
6:E:111:VAL:HB	38:E:8321:HOH:O	1.85	0.76
7:F:19:GLU:O	7:F:20:LYS:HG2	1.85	0.76
1:A:1187:U:H2'	38:A:6366:HOH:O	1.84	0.76
8:G:166:VAL:HG12	38:G:3134:HOH:O	1.86	0.76
26:Y:76:ARG:HH11	26:Y:76:ARG:HG3	1.48	0.76
1:A:1213:C:O2'	1:A:1214:G:H5'	1.85	0.76
1:A:157:G:H4'	15:N:95:LYS:HE3	1.67	0.76
1:A:1701:A:H4'	1:A:1702:U:H5"	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2291:A:C8	1:A:2309:C:H5'	2.21	0.76
1:A:559:U:H6	1:A:559:U:H5'	1.51	0.76
15:N:80:GLY:O	15:N:81:ARG:HD3	1.86	0.76
5:D:62:ARG:HA	5:D:65:MET:HE3	1.67	0.75
15:N:164:THR:CG2	15:N:167:GLY:H	2.00	0.75
22:U:9:LYS:HE3	22:U:13:ARG:NH1	2.01	0.75
23:V:46:ALA:HB1	23:V:52:THR:HG21	1.66	0.75
1:A:1160:G:H5'	1:A:1161:A:C5'	2.16	0.75
1:A:2533:C:H5'	1:A:2533:C:H6	1.52	0.75
15:N:164:THR:HG22	15:N:167:GLY:N	2.01	0.75
1:A:236:A:H4'	1:A:237:G:H5'	1.69	0.75
1:A:2433:A:O4'	38:A:5776:HOH:O	2.03	0.75
1:A:92:G:H5'	38:W:7247:HOH:O	1.85	0.75
31:4:51:LYS:HA	31:4:54:LYS:HE3	1.67	0.75
1:A:1116:U:H3	1:A:1246:A:H62	1.35	0.75
1:A:2578:G:H5'	1:A:2578:G:H8	1.51	0.75
1:A:2780:C:H1'	8:G:143:GLN:HE21	1.50	0.75
1:A:2768:A:H2'	1:A:2769:C:O4'	1.87	0.75
24:W:1:THR:HG23	24:W:2:VAL:H	1.49	0.75
5:D:275:GLY:O	5:D:291:ASP:HA	1.86	0.75
18:Q:115:SER:H	18:Q:118:GLN:NE2	1.83	0.75
8:G:7:ILE:HG22	8:G:45:ASP:O	1.86	0.74
1:A:2420:G:O2'	1:A:2421:G:H5'	1.87	0.74
1:A:272:A:H5'	1:A:273:G:OP2	1.87	0.74
1:A:338:C:H4'	6:E:174:ILE:HD11	1.68	0.74
1:A:2506:A:O2'	1:A:2507:G:H8	1.68	0.74
22:U:9:LYS:HE3	22:U:13:ARG:HH11	1.51	0.74
1:A:1735:C:O2'	1:A:1736:A:H5'	1.86	0.74
1:A:2526:C:O2'	1:A:2527:U:H5'	1.86	0.74
14:M:67:ARG:O	14:M:71:GLU:HG3	1.88	0.74
2:B:3014:G:H8	2:B:3014:G:H5'	1.51	0.74
9:H:91:VAL:HG12	9:H:92:GLY:H	1.48	0.74
15:N:139:PRO:O	15:N:140:ALA:HB3	1.88	0.74
1:A:1080:C:H4'	1:A:1081:A:OP1	1.87	0.74
15:N:30:GLU:O	15:N:34:GLU:HG3	1.87	0.74
1:A:1160:G:N3	38:A:5114:HOH:O	2.20	0.74
1:A:506:G:H22	1:A:509:A:C5'	2.01	0.74
16:O:61:ALA:HB3	16:O:88:ALA:HB2	1.68	0.74
19:R:23:THR:HA	38:R:4792:HOH:O	1.88	0.74
1:A:544:G:H2'	1:A:545:G:H5''	1.70	0.74
30:3:41:HIS:H	30:3:45:ASN:ND2	1.85	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:22:VAL:CG1	31:4:67:LEU:HD13	2.18	0.74
1:A:282:C:O2'	1:A:283:U:H5'	1.88	0.74
18:Q:115:SER:N	18:Q:118:GLN:HE21	1.86	0.74
7:F:20:LYS:HA	7:F:75:LEU:O	1.88	0.73
1:A:553:G:P	27:Z:204:ARG:HH22	2.11	0.73
1:A:2896:A:H5''	38:A:5590:HOH:O	1.87	0.73
5:D:238:ASN:HD22	5:D:240:GLY:N	1.84	0.73
11:J:55:GLN:NE2	11:J:124:ARG:HE	1.86	0.73
11:J:47:GLU:HB3	11:J:133:ILE:CD1	2.18	0.73
28:1:46:LYS:O	28:1:57:CYS:HA	1.88	0.73
28:1:39:CYS:SG	28:1:57:CYS:HB2	2.29	0.73
1:A:2426:G:H1'	38:A:5583:HOH:O	1.87	0.73
16:O:113:SER:HB2	38:O:8556:HOH:O	1.89	0.73
17:P:47:ARG:HH11	17:P:47:ARG:HG3	1.54	0.73
1:A:2786:G:H2'	38:A:6652:HOH:O	1.88	0.73
6:E:39:GLN:O	6:E:43:LYS:HD3	1.87	0.73
1:A:1864:C:OP1	15:N:75:THR:HG23	1.89	0.73
1:A:1909:A:N1	1:A:2128:G:H1'	2.03	0.73
4:C:88:ILE:HD13	4:C:100:PRO:HD3	1.70	0.73
5:D:211:THR:HA	5:D:255:GLY:O	1.88	0.73
14:M:79:ASP:HB3	38:M:8434:HOH:O	1.87	0.73
4:C:135:VAL:HG21	4:C:147:ARG:NH1	2.03	0.73
6:E:132:ASP:HB3	38:E:8365:HOH:O	1.89	0.73
19:R:46:SER:O	19:R:48:PRO:HD3	1.88	0.73
20:S:18:LEU:HB2	20:S:143:VAL:CG1	2.18	0.73
30:3:39:ARG:HG2	38:3:3143:HOH:O	1.87	0.73
1:A:1119:G:N2	1:A:1246:A:C2	2.57	0.73
2:B:3049:G:H5''	38:B:8469:HOH:O	1.89	0.73
13:L:81:ARG:HB2	13:L:87:ARG:NH1	2.04	0.73
14:M:26:HIS:HB2	38:M:8381:HOH:O	1.88	0.73
28:1:42:CYS:SG	28:1:43:GLY:N	2.62	0.73
3:5:74:C:H2'	3:5:75:C:H5'	1.68	0.73
7:F:54:ALA:HB2	7:F:69:ILE:HD12	1.69	0.73
8:G:81:GLU:HG2	8:G:134:SER:HB3	1.71	0.73
9:H:53:ASP:OD1	9:H:80:GLN:HB2	1.89	0.73
12:K:93:ARG:HH11	12:K:93:ARG:HB3	1.53	0.73
1:A:20:G:H21	20:S:117:HIS:HD2	1.37	0.73
28:1:22:ILE:O	28:1:26:VAL:HG23	1.88	0.72
7:F:25:MET:CE	7:F:41:LEU:HG	2.18	0.72
11:J:75:SER:O	11:J:79:ALA:HB2	1.89	0.72
1:A:1165:G:H4'	1:A:1174:A:O2'	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:201:ASP:HB2	5:D:312:ARG:HD2	1.70	0.72
11:J:132:PHE:O	11:J:133:ILE:HD13	1.89	0.72
15:N:87:MET:CB	31:4:46:ILE:HG21	2.19	0.72
1:A:1266:U:H4'	27:Z:115:ARG:HH21	1.54	0.72
1:A:1751:G:C2'	1:A:1752:G:H5''	2.18	0.72
1:A:2320:U:H4'	1:A:2321:A:O4'	1.90	0.72
1:A:2780:C:H2'	1:A:2781:U:H6	1.54	0.72
38:A:6343:HOH:O	15:N:178:LYS:HB2	1.88	0.72
15:N:61:ILE:HG13	38:N:8619:HOH:O	1.89	0.72
1:A:1120:U:C6	1:A:1120:U:H5''	2.25	0.72
7:F:19:GLU:HG3	38:F:6165:HOH:O	1.87	0.72
1:A:2432:C:H4'	31:4:36:ILE:HG12	1.72	0.72
1:A:584:U:H3'	38:A:5586:HOH:O	1.88	0.72
11:J:26:LYS:HG2	11:J:28:ILE:H	1.53	0.72
12:K:39:VAL:HG13	12:K:106:GLY:O	1.90	0.72
19:R:93:ARG:HG3	19:R:93:ARG:HH11	1.54	0.72
1:A:288:A:H61	1:A:364:C:H42	1.36	0.72
24:W:39:ALA:N	24:W:40:PRO:HD2	2.05	0.72
26:Y:37:LEU:CD1	26:Y:85:VAL:HG21	2.15	0.72
1:A:1160:G:C5'	1:A:1161:A:H5'	2.18	0.72
1:A:195:C:H2'	1:A:196:G:H5'	1.70	0.72
22:U:37:GLN:HB3	38:U:6711:HOH:O	1.90	0.72
20:S:99:ALA:HB1	20:S:109:MET:CE	2.19	0.72
25:X:4:LEU:HD23	25:X:54:PHE:HB3	1.72	0.72
1:A:21:G:C5'	20:S:2:ILE:HA	2.18	0.72
2:B:3023:U:H3'	2:B:3024:U:H5''	1.72	0.72
11:J:41:THR:HA	38:J:8382:HOH:O	1.89	0.72
12:K:74:ARG:HD3	38:K:5061:HOH:O	1.88	0.72
16:O:49:THR:HG22	16:O:56:ASP:HB2	1.72	0.72
17:P:87:THR:O	17:P:91:GLN:HG3	1.90	0.72
27:Z:235:GLU:CD	27:Z:235:GLU:H	1.93	0.72
28:1:38:LYS:HG2	28:1:45:LYS:HG2	1.72	0.72
1:A:1667:A:H5'	1:A:1667:A:C8	2.23	0.72
1:A:1666:C:O2'	1:A:1667:A:H5''	1.90	0.71
1:A:1887:U:OP1	28:1:21:LYS:HG3	1.90	0.71
22:U:48:VAL:HG23	22:U:98:VAL:HA	1.72	0.71
1:A:2382:A:H1'	31:4:10:TYR:CE2	2.25	0.71
1:A:2780:C:H2'	1:A:2781:U:C6	2.25	0.71
1:A:444:C:H1'	38:A:3535:HOH:O	1.88	0.71
6:E:154:VAL:O	6:E:158:GLU:HG3	1.90	0.71
22:U:50:VAL:HG12	22:U:56:ALA:HA	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Z:187:VAL:HG23	27:Z:192:ASP:CB	2.20	0.71
1:A:2851:G:O2'	1:A:2852:A:H5'	1.91	0.71
23:V:13:ILE:HG12	23:V:32:CYS:HB3	1.71	0.71
28:1:40:PRO:HD3	28:1:47:LEU:HD11	1.71	0.71
15:N:87:MET:HG2	31:4:46:ILE:CG2	2.19	0.71
1:A:1116:U:O2'	1:A:1118:A:H2	1.66	0.71
13:L:81:ARG:HB2	13:L:87:ARG:HH11	1.54	0.71
1:A:1170:U:O2'	1:A:1172:G:N7	2.24	0.71
12:K:131:THR:HG22	12:K:134:GLU:H	1.52	0.71
1:A:1118:A:H3'	1:A:1118:A:H8	1.56	0.71
12:K:52:GLN:HG3	12:K:53:ILE:H	1.51	0.71
31:4:31:THR:HB	31:4:33:MET:HE2	1.70	0.71
1:A:681:G:N3	1:A:681:G:H5'	2.06	0.71
1:A:2256:G:H2'	1:A:2257:G:C5'	2.21	0.71
6:E:235:PHE:CE2	6:E:243:VAL:HG21	2.25	0.71
38:B:8469:HOH:O	16:O:147:ILE:HD12	1.90	0.71
27:Z:212:ARG:HD2	38:Z:8606:HOH:O	1.89	0.71
1:A:2727:A:H2'	1:A:2728:C:H5'	1.72	0.71
7:F:53:LYS:HA	7:F:67:ASP:O	1.90	0.71
25:X:81:ASP:OD1	25:X:92:ASP:HB2	1.90	0.71
5:D:175:LEU:C	5:D:175:LEU:HD23	2.12	0.70
8:G:107:PHE:CE2	8:G:108:LEU:HD13	2.26	0.70
15:N:139:PRO:O	15:N:140:ALA:CB	2.39	0.70
31:4:65:THR:HG23	31:4:67:LEU:HG	1.73	0.70
11:J:140:PRO:HB3	38:J:8369:HOH:O	1.89	0.70
15:N:74:ARG:HH11	15:N:74:ARG:HG3	1.56	0.70
8:G:7:ILE:HD11	8:G:11:VAL:C	2.11	0.70
15:N:84:LYS:HE2	38:N:8572:HOH:O	1.90	0.70
16:O:48:VAL:CG1	16:O:55:ASP:HB3	2.22	0.70
1:A:1123:A:C6	1:A:1238:C:H5'	2.26	0.70
1:A:272:A:H3'	38:A:7000:HOH:O	1.90	0.70
38:A:9065:HOH:O	5:D:267:LYS:HD3	1.90	0.70
1:A:2637:A:H5'	38:A:8783:HOH:O	1.91	0.70
1:A:1771:U:H4'	28:1:20:LEU:HD21	1.72	0.70
6:E:162:VAL:HG13	6:E:232:LEU:HD21	1.74	0.70
1:A:2815:G:N7	12:K:80:LYS:NZ	2.39	0.70
15:N:39:ARG:HA	15:N:63:VAL:HG22	1.74	0.70
7:F:95:THR:O	7:F:97:GLN:N	2.21	0.70
16:O:7:LYS:HE3	19:R:21:ARG:O	1.91	0.70
1:A:1773:G:H8	28:1:16:PRO:HA	1.56	0.70
23:V:6:CYS:HA	23:V:13:ILE:HD11	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:110:GLN:HA	25:X:110:GLN:HE21	1.56	0.70
29:2:1:THR:HB	38:2:6858:HOH:O	1.92	0.69
5:D:212:GLN:HB2	5:D:257:THR:HG21	1.72	0.69
26:Y:43:VAL:CG1	26:Y:47:ALA:HB3	2.21	0.69
1:A:1127:C:H2'	1:A:1128:U:H5'	1.74	0.69
1:A:2502:C:H4'	11:J:151:MET:HG2	1.74	0.69
12:K:74:ARG:CB	12:K:74:ARG:HH11	2.04	0.69
15:N:12:TRP:CE2	15:N:20:ILE:HD11	2.28	0.69
1:A:119:A:H2'	1:A:120:A:H5''	1.74	0.69
1:A:2414:A:H2'	1:A:2415:A:C8	2.26	0.69
5:D:7:ARG:HG2	5:D:7:ARG:HH11	1.55	0.69
15:N:134:ILE:HG23	15:N:141:ILE:HD13	1.75	0.69
1:A:694:A:H2'	1:A:695:C:H5'	1.74	0.69
11:J:27:LYS:H	11:J:58:HIS:CD2	2.01	0.69
11:J:48:LEU:HG	11:J:157:ILE:HG21	1.75	0.69
13:L:106:GLY:HA3	38:L:5264:HOH:O	1.91	0.69
2:B:3092:G:H2'	2:B:3093:A:C8	2.27	0.69
4:C:105:VAL:HG12	4:C:106:CYS:N	2.08	0.69
38:A:9470:HOH:O	6:E:174:ILE:HD12	1.93	0.69
12:K:74:ARG:O	12:K:78:ILE:HG12	1.92	0.69
15:N:153:THR:O	15:N:156:ARG:HG3	1.93	0.69
16:O:183:ASP:OD2	16:O:186:LEU:HD12	1.92	0.69
1:A:2054:A:N3	20:S:128:ARG:NH2	2.41	0.69
4:C:153:ARG:HB2	4:C:153:ARG:HH11	1.58	0.69
8:G:137:ASP:O	8:G:141:VAL:HG23	1.93	0.69
1:A:284:C:H4'	1:A:285:A:O5'	1.90	0.69
1:A:541:C:H2'	1:A:542:A:C5'	2.20	0.69
6:E:93:LYS:O	6:E:98:ARG:NH2	2.26	0.69
1:A:2346:C:O2'	7:F:52:THR:HG21	1.92	0.69
20:S:39:THR:HG22	20:S:42:GLU:H	1.56	0.69
10:I:64:ASN:N	10:I:64:ASN:HD22	1.91	0.69
16:O:151:ASP:HB3	38:O:8528:HOH:O	1.93	0.69
25:X:35:VAL:HG23	25:X:41:TYR:CD2	2.27	0.69
1:A:1603:A:H5'	1:A:1605:G:O4'	1.92	0.69
1:A:1666:C:H2'	1:A:1667:A:H5'	1.73	0.69
11:J:29:ALA:HB3	11:J:65:ARG:HH12	1.58	0.69
38:A:8962:HOH:O	20:S:83:LYS:HD3	1.90	0.69
28:1:42:CYS:SG	28:1:44:PHE:N	2.65	0.68
1:A:1118:A:C8	1:A:1118:A:H3'	2.27	0.68
8:G:7:ILE:HD11	8:G:11:VAL:O	1.93	0.68
12:K:103:VAL:HG12	38:K:5907:HOH:O	1.91	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:A:H62	1:A:1244:U:H3	1.39	0.68
1:A:2638:G:H1'	38:A:7228:HOH:O	1.93	0.68
1:A:2795:C:O2'	1:A:2796:U:H5'	1.92	0.68
13:L:115:ARG:HG3	13:L:116:GLU:N	2.08	0.68
28:1:28:ASP:O	28:1:31:ILE:HG22	1.93	0.68
1:A:289:G:N2	1:A:363:A:H2	1.90	0.68
38:A:4434:HOH:O	2:B:3103:A:H4'	1.93	0.68
5:D:16:ARG:HB3	5:D:217:ARG:NH2	2.09	0.68
27:Z:185:VAL:HA	38:Z:8565:HOH:O	1.91	0.68
2:B:3020:G:O2'	2:B:3021:G:H5'	1.93	0.68
2:B:3069:U:OP1	16:O:4:PRO:HG3	1.92	0.68
7:F:23:VAL:HG23	7:F:23:VAL:O	1.93	0.68
15:N:14:ARG:HB3	15:N:17:GLU:HG3	1.75	0.68
25:X:129:LYS:HG2	38:X:1990:HOH:O	1.93	0.68
4:C:223:ARG:HG3	38:C:8617:HOH:O	1.94	0.68
12:K:45:VAL:HG23	12:K:130:VAL:O	1.92	0.68
38:A:8899:HOH:O	15:N:94:LYS:HE2	1.94	0.68
23:V:9:CYS:CA	23:V:52:THR:HG23	2.24	0.68
27:Z:185:VAL:HG12	38:Z:8572:HOH:O	1.92	0.68
1:A:603:A:H5''	1:A:604:G:OP1	1.92	0.68
2:B:3023:U:H6	2:B:3023:U:H5''	1.58	0.68
8:G:11:VAL:HG12	8:G:12:ASP:N	2.08	0.68
38:A:3178:HOH:O	15:N:79:LYS:HD3	1.93	0.68
17:P:25:VAL:O	17:P:29:VAL:HG23	1.94	0.68
1:A:1819:G:H2'	1:A:1820:G:H4'	1.76	0.68
38:A:4999:HOH:O	5:D:298:LYS:HD3	1.92	0.68
7:F:62:ASP:HA	38:F:4233:HOH:O	1.93	0.68
16:O:5:ARG:HG3	19:R:18:PRO:CB	2.24	0.68
38:A:8896:HOH:O	28:1:34:LYS:HD3	1.93	0.68
1:A:1333:U:H2'	1:A:1334:C:C6	2.29	0.68
1:A:1919:A:H4'	38:A:4333:HOH:O	1.94	0.68
5:D:41:PHE:HA	5:D:79:MET:HE2	1.76	0.68
18:Q:16:VAL:HG12	18:Q:17:GLY:N	2.07	0.68
18:Q:18:LYS:O	18:Q:21:VAL:HG22	1.92	0.68
20:S:18:LEU:HD12	20:S:143:VAL:CG1	2.23	0.68
1:A:2890:A:H1'	23:V:56:ARG:NH2	2.08	0.68
8:G:149:GLU:OE1	8:G:168:ILE:HG12	1.94	0.68
1:A:2382:A:H1'	31:4:10:TYR:CD2	2.29	0.68
1:A:1187:U:O2'	1:A:1189:A:H2	1.77	0.67
1:A:2421:G:H3'	1:A:2422:U:C5'	2.24	0.67
16:O:143:ARG:HA	16:O:172:PHE:CD2	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:39:ALA:O	24:W:41:GLU:N	2.27	0.67
29:2:25:LYS:HE2	38:2:7213:HOH:O	1.93	0.67
1:A:1886:A:H4'	38:1:8405:HOH:O	1.93	0.67
1:A:2508:C:H2'	38:A:6224:HOH:O	1.93	0.67
1:A:1857:A:N6	1:A:2247:C:H1'	2.09	0.67
4:C:94:LEU:N	4:C:94:LEU:HD23	2.09	0.67
5:D:333:GLU:HB2	38:V:3564:HOH:O	1.93	0.67
6:E:139:VAL:HG13	38:E:8448:HOH:O	1.95	0.67
20:S:40:ALA:O	20:S:44:VAL:HG23	1.95	0.67
7:F:97:GLN:O	7:F:97:GLN:HG2	1.94	0.67
11:J:33:MET:HB2	11:J:83:PHE:HB3	1.76	0.67
13:L:22:ASP:OD1	13:L:24:THR:HG23	1.95	0.67
26:Y:15:ARG:NH1	26:Y:15:ARG:HB3	2.09	0.67
1:A:2265:U:H2'	1:A:2266:A:C8	2.30	0.67
25:X:21:LEU:HD22	25:X:26:ILE:CD1	2.23	0.67
4:C:179:MET:HG2	4:C:186:TRP:CB	2.25	0.67
4:C:8:ARG:HG2	38:C:8559:HOH:O	1.94	0.67
5:D:175:LEU:O	5:D:175:LEU:HD23	1.95	0.67
1:A:2278:U:H2'	38:A:7073:HOH:O	1.95	0.67
7:F:38:GLU:OE2	7:F:51:ARG:CZ	2.42	0.67
16:O:73:ALA:HB2	16:O:163:PHE:CZ	2.30	0.67
28:1:20:LEU:O	28:1:24:VAL:HG23	1.94	0.67
1:A:2081:A:H4'	12:K:69:TYR:CE1	2.30	0.67
1:A:2506:A:H1'	38:A:3244:HOH:O	1.94	0.67
6:E:214:THR:HG21	38:E:8402:HOH:O	1.95	0.67
6:E:236:THR:CG2	6:E:239:ALA:H	2.00	0.67
5:D:221:GLN:HE22	13:L:42:ASN:HD22	1.43	0.67
27:Z:187:VAL:CG2	27:Z:192:ASP:HB2	2.24	0.67
1:A:1163:G:N2	38:A:5536:HOH:O	2.24	0.66
5:D:11:LEU:HA	38:D:8622:HOH:O	1.94	0.66
25:X:122:ARG:HG2	25:X:122:ARG:HH11	1.60	0.66
1:A:1161:A:O5'	1:A:1161:A:H8	1.78	0.66
1:A:21:G:H4'	20:S:2:ILE:HG22	1.75	0.66
1:A:821:U:H2'	1:A:822:C:H6	1.60	0.66
4:C:33:GLU:O	4:C:34:ASP:HB2	1.93	0.66
13:L:10:GLN:HE21	13:L:10:GLN:N	1.92	0.66
15:N:157:LEU:HB3	15:N:160:PHE:HD1	1.60	0.66
20:S:44:VAL:O	20:S:48:GLU:HG3	1.95	0.66
1:A:317:A:H5''	22:U:52:ARG:HD2	1.77	0.66
1:A:157:G:H4'	15:N:95:LYS:CE	2.26	0.66
1:A:639:A:H2'	1:A:640:G:C8	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:2:ARG:HH21	8:G:48:VAL:HG21	1.59	0.66
10:I:12:ILE:N	10:I:13:PRO:HD3	2.09	0.66
10:I:63:ARG:N	38:I:2569:HOH:O	2.28	0.66
15:N:45:ARG:HB3	15:N:48:ARG:HB2	1.76	0.66
24:W:44:GLY:O	24:W:48:GLU:HG2	1.95	0.66
31:4:64:LYS:HE3	31:4:84:ARG:NH1	2.10	0.66
1:A:1589:G:N2	1:A:1605:G:H1'	2.09	0.66
1:A:2415:A:C2	16:O:25:ARG:HB3	2.29	0.66
5:D:18:ARG:HG3	5:D:256:GLN:HG3	1.78	0.66
5:D:75:GLU:C	5:D:77:PRO:HD3	2.14	0.66
6:E:246:ARG:NH1	6:E:246:ARG:HB3	2.10	0.66
9:H:104:ALA:HA	38:H:6617:HOH:O	1.96	0.66
23:V:52:THR:HG22	23:V:54:THR:H	1.61	0.66
11:J:140:PRO:O	38:J:8355:HOH:O	2.13	0.66
11:J:150:LYS:HA	11:J:153:VAL:HG22	1.77	0.66
31:4:69:TYR:HB2	31:4:78:HIS:CE1	2.30	0.66
1:A:2421:G:H3'	1:A:2422:U:H5''	1.76	0.66
1:A:450:C:OP1	6:E:184:ARG:NH2	2.25	0.66
5:D:144:THR:HG22	5:D:145:HIS:N	2.11	0.66
5:D:51:VAL:HG23	5:D:330:VAL:HG22	1.78	0.66
6:E:198:ASP:O	38:E:8471:HOH:O	2.14	0.66
11:J:49:VAL:O	11:J:157:ILE:HG23	1.96	0.66
25:X:88:THR:HG23	25:X:110:GLN:NE2	2.11	0.66
38:A:8729:HOH:O	4:C:11:ARG:HD3	1.94	0.66
8:G:132:THR:HB	38:G:2227:HOH:O	1.96	0.66
12:K:99:GLU:HA	38:K:7377:HOH:O	1.94	0.66
14:M:1:THR:HA	38:M:8395:HOH:O	1.96	0.66
26:Y:41:PHE:O	26:Y:43:VAL:HG23	1.95	0.66
1:A:2911:C:H3'	38:A:5034:HOH:O	1.95	0.66
8:G:84:MET:HE3	8:G:148:ILE:HG21	1.78	0.66
22:U:106:GLU:HG3	38:U:4913:HOH:O	1.95	0.66
31:4:60:LYS:CD	31:4:61:PRO:HD2	2.25	0.66
1:A:2252:A:C5	1:A:2253:G:H1'	2.31	0.66
15:N:120:VAL:HG11	15:N:130:GLU:OE2	1.97	0.66
9:H:38:LYS:NZ	15:N:3:SER:HA	2.10	0.66
22:U:38:ARG:NH1	38:U:6217:HOH:O	2.29	0.66
27:Z:103:THR:HG22	27:Z:104:GLU:OE2	1.95	0.66
4:C:105:VAL:HG13	4:C:155:THR:O	1.96	0.65
7:F:54:ALA:CB	7:F:69:ILE:HD12	2.26	0.65
8:G:20:ILE:CD1	8:G:40:VAL:HG11	2.26	0.65
15:N:38:VAL:O	15:N:63:VAL:HG13	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:89:GLY:O	16:O:92:ALA:HB3	1.96	0.65
28:1:21:LYS:O	28:1:25:ARG:HG3	1.96	0.65
1:A:1675:C:H5''	30:3:5:LYS:HD2	1.77	0.65
31:4:39:GLN:HA	31:4:42:ARG:NH2	2.12	0.65
1:A:2908:A:H2'	1:A:2909:G:O4'	1.96	0.65
9:H:50:VAL:HG13	9:H:60:VAL:HG11	1.77	0.65
9:H:28:ALA:HB3	9:H:99:THR:O	1.95	0.65
1:A:162:C:H2'	1:A:163:U:H5'	1.78	0.65
1:A:2382:A:H5'	38:4:8535:HOH:O	1.95	0.65
5:D:62:ARG:HA	5:D:65:MET:CE	2.26	0.65
1:A:2717:C:OP1	5:D:207:LYS:HG3	1.96	0.65
1:A:710:G:O2'	1:A:711:G:H5'	1.95	0.65
5:D:74:ILE:HD13	5:D:309:VAL:HG21	1.78	0.65
7:F:57:THR:HG23	7:F:63:ILE:HG22	1.76	0.65
15:N:74:ARG:CD	15:N:91:ILE:HD12	2.26	0.65
1:A:282:C:H1'	1:A:368:C:N4	2.11	0.65
1:A:522:U:O2'	1:A:1366:C:H5'	1.96	0.65
7:F:49:PRO:HG3	38:F:5828:HOH:O	1.96	0.65
7:F:64:ARG:HG2	7:F:67:ASP:HB3	1.77	0.65
11:J:50:VAL:HA	11:J:157:ILE:HG12	1.78	0.65
15:N:138:HIS:ND1	15:N:139:PRO:O	2.26	0.65
23:V:6:CYS:SG	23:V:31:PHE:HA	2.37	0.65
25:X:106:THR:OG1	25:X:109:GLU:HG3	1.97	0.65
1:A:407:A:H5'	38:A:5513:HOH:O	1.96	0.65
1:A:56:G:H5''	24:W:50:ARG:NH1	2.11	0.65
14:M:114:VAL:HG11	38:M:8449:HOH:O	1.96	0.65
15:N:186:SER:O	15:N:189:VAL:HG12	1.95	0.65
16:O:80:SER:HB2	38:O:8534:HOH:O	1.96	0.65
24:W:4:HIS:HB3	38:W:6622:HOH:O	1.95	0.65
1:A:1416:G:H1'	38:A:8527:HOH:O	1.95	0.65
1:A:1909:A:H2'	1:A:1910:A:C8	2.31	0.65
4:C:55:VAL:HG13	4:C:67:LEU:HD22	1.77	0.65
7:F:88:LEU:HB2	7:F:89:PRO:HD3	1.79	0.65
11:J:84:ARG:NH2	11:J:135:TRP:HH2	1.94	0.65
31:4:44:SER:HA	31:4:49:ASP:OD1	1.97	0.65
1:A:2243:C:H5''	38:A:3248:HOH:O	1.97	0.65
1:A:2346:C:O3'	7:F:52:THR:HG23	1.97	0.65
2:B:3029:C:C2'	2:B:3030:C:H5'	2.27	0.65
6:E:5:ILE:HD11	6:E:16:VAL:CG2	2.27	0.65
1:A:514:G:O5'	1:A:514:G:H8	1.80	0.65
7:F:44:ILE:HG12	7:F:83:PHE:HE1	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:645:U:OP2	14:M:4:LYS:HE2	1.96	0.65
7:F:140:ARG:N	38:F:3723:HOH:O	2.27	0.64
12:K:74:ARG:NH1	12:K:76:ASP:HB2	2.12	0.64
16:O:170:GLU:O	16:O:174:GLU:HG3	1.97	0.64
1:A:2359:G:H3'	38:A:5173:HOH:O	1.97	0.64
14:M:143:THR:HG21	38:M:8413:HOH:O	1.97	0.64
20:S:39:THR:HG23	20:S:107:GLU:O	1.97	0.64
1:A:1191:A:C3'	1:A:1192:A:H5''	2.28	0.64
4:C:105:VAL:HG11	4:C:154:ALA:HB1	1.78	0.64
1:A:316:A:H5'	22:U:54:ASP:OD2	1.96	0.64
38:A:6888:HOH:O	22:U:9:LYS:HB2	1.96	0.64
26:Y:78:GLU:CG	26:Y:79:GLU:H	2.09	0.64
28:1:11:THR:CG2	28:1:23:ARG:HB2	2.28	0.64
6:E:162:VAL:HG12	6:E:192:ILE:HD11	1.80	0.64
31:4:3:MET:O	31:4:90:PHE:HA	1.96	0.64
1:A:2597:U:H2'	1:A:2598:U:H5'	1.79	0.64
17:P:42:GLU:HB2	38:P:2176:HOH:O	1.97	0.64
18:Q:143:ALA:HA	38:Q:5521:HOH:O	1.97	0.64
22:U:52:ARG:HB2	22:U:95:ASN:HB3	1.80	0.64
27:Z:186:ARG:HH11	27:Z:186:ARG:HG2	1.62	0.64
28:1:38:LYS:HE2	28:1:45:LYS:HE2	1.79	0.64
1:A:1829:A:H5''	38:A:9585:HOH:O	1.97	0.64
1:A:2549:C:H1'	5:D:248:ARG:NH2	2.13	0.64
15:N:34:GLU:HB3	15:N:35:PRO:HD2	1.80	0.64
17:P:26:TRP:HB2	38:P:3062:HOH:O	1.98	0.64
25:X:72:PRO:O	38:X:7874:HOH:O	2.15	0.64
1:A:2608:C:H3'	38:A:7277:HOH:O	1.98	0.64
16:O:154:LEU:O	16:O:155:GLU:HB3	1.96	0.64
31:4:7:PHE:HE2	31:4:22:VAL:CG2	2.11	0.64
1:A:1162:G:H2'	38:A:6057:HOH:O	1.97	0.64
1:A:138:U:H5''	1:A:139:C:OP2	1.97	0.64
1:A:1929:G:H1'	38:A:4641:HOH:O	1.98	0.64
1:A:2310:G:OP2	11:J:114:PRO:HD2	1.98	0.64
25:X:6:GLN:HB2	25:X:26:ILE:CD1	2.27	0.64
1:A:2281:C:C2'	1:A:2282:U:H5'	2.27	0.64
1:A:339:A:H2'	38:A:3705:HOH:O	1.98	0.64
2:B:3064:C:C2'	2:B:3065:A:H5'	2.28	0.64
28:1:42:CYS:SG	28:1:44:PHE:HB2	2.38	0.64
31:4:57:GLY:HA2	38:4:8528:HOH:O	1.97	0.64
7:F:27:ILE:HG22	7:F:28:GLY:N	2.13	0.64
16:O:78:MET:HB2	16:O:79:PRO:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2265:U:H2'	1:A:2266:A:H8	1.61	0.63
1:A:2415:A:H2'	1:A:2416:G:H5'	1.78	0.63
1:A:2524:G:H21	1:A:2526:C:N4	1.95	0.63
2:B:3024:U:O2'	2:B:3025:G:H4'	1.97	0.63
4:C:179:MET:HG2	4:C:186:TRP:HB2	1.79	0.63
15:N:69:LYS:HG2	15:N:127:LYS:HG3	1.80	0.63
25:X:65:VAL:HA	25:X:68:THR:HG22	1.80	0.63
28:1:10:ARG:HA	38:1:8414:HOH:O	1.98	0.63
1:A:1942:A:O2'	1:A:1943:C:H5'	1.98	0.63
1:A:281:U:H2'	1:A:282:C:O4'	1.98	0.63
4:C:43:VAL:HG21	4:C:59:GLU:HG3	1.78	0.63
5:D:51:VAL:HG13	5:D:53:LEU:HD13	1.79	0.63
8:G:20:ILE:HD11	8:G:40:VAL:CG1	2.28	0.63
13:L:10:GLN:NE2	13:L:10:GLN:N	2.43	0.63
16:O:164:ASP:CG	16:O:167:ASP:HA	2.19	0.63
20:S:18:LEU:HB2	20:S:143:VAL:HG12	1.78	0.63
28:1:46:LYS:HB3	38:1:8436:HOH:O	1.97	0.63
2:B:3023:U:H5''	2:B:3023:U:C6	2.33	0.63
4:C:100:PRO:HG2	4:C:103:VAL:HG21	1.79	0.63
38:A:9125:HOH:O	9:H:38:LYS:HD2	1.97	0.63
10:I:16:LYS:O	10:I:20:VAL:HG23	1.97	0.63
13:L:32:ILE:HD11	13:L:56:SER:HB3	1.79	0.63
16:O:71:TRP:CE3	16:O:175:LEU:HD22	2.33	0.63
17:P:21:SER:CB	17:P:106:PRO:O	2.47	0.63
38:O:8540:HOH:O	19:R:19:ARG:HD3	1.97	0.63
30:3:41:HIS:N	30:3:45:ASN:HD22	1.92	0.63
1:A:1185:U:H5'	38:A:6934:HOH:O	1.99	0.63
1:A:1210:G:O2'	1:A:1211:G:H5'	1.98	0.63
1:A:2325:C:H1'	38:A:3637:HOH:O	1.97	0.63
1:A:656:G:OP2	17:P:37:ARG:HD2	1.98	0.63
5:D:154:VAL:CG1	5:D:156:LYS:HG2	2.28	0.63
5:D:217:ARG:HG3	5:D:257:THR:HG22	1.81	0.63
8:G:133:VAL:HG12	8:G:141:VAL:HG13	1.80	0.63
9:H:110:GLU:O	9:H:114:LYS:HG3	1.99	0.63
1:A:1641:A:H2'	1:A:1642:A:H5'	1.81	0.63
2:B:3047:A:H4'	38:O:8549:HOH:O	1.98	0.63
1:A:1701:A:H5'	38:A:5769:HOH:O	1.97	0.63
1:A:95:A:H5''	1:A:97:G:O4'	1.98	0.63
38:A:6922:HOH:O	5:D:211:THR:HG21	1.97	0.63
7:F:136:ARG:HD2	7:F:155:HIS:O	1.98	0.63
8:G:11:VAL:HG11	8:G:22:VAL:HG13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:74:ARG:HD3	15:N:91:ILE:HD12	1.81	0.63
1:A:182:G:H4'	15:N:157:LEU:HD13	1.81	0.63
1:A:195:C:H5''	38:N:8599:HOH:O	1.97	0.63
7:F:81:GLU:O	7:F:85:GLN:HG3	1.98	0.63
12:K:133:GLY:O	12:K:137:GLU:HG3	1.99	0.63
1:A:218:C:P	31:4:39:GLN:HE21	2.20	0.63
1:A:2501:G:N7	38:A:9280:HOH:O	2.31	0.63
25:X:110:GLN:HA	25:X:110:GLN:NE2	2.13	0.63
25:X:154:ARG:C	38:X:4276:HOH:O	2.37	0.63
31:4:73:GLU:HB3	38:4:8561:HOH:O	1.98	0.62
4:C:101:GLU:OE2	4:C:131:HIS:HB2	1.99	0.62
11:J:26:LYS:HD3	11:J:89:PRO:HG3	1.81	0.62
12:K:39:VAL:HG12	12:K:40:ASN:ND2	2.13	0.62
16:O:82:TYR:C	16:O:82:TYR:CD2	2.73	0.62
1:A:1741:U:H5'	1:A:1742:A:OP1	1.99	0.62
5:D:314:ALA:HB3	5:D:317:PRO:HG3	1.80	0.62
7:F:64:ARG:CD	7:F:67:ASP:HB3	2.28	0.62
17:P:4:ASN:HB2	38:P:6939:HOH:O	1.98	0.62
24:W:12:THR:HG22	24:W:15:GLU:CG	2.18	0.62
14:M:66:VAL:HG23	14:M:67:ARG:N	2.14	0.62
24:W:39:ALA:C	24:W:41:GLU:H	2.01	0.62
1:A:12:U:H2'	1:A:13:G:H5'	1.81	0.62
1:A:2365:G:H4'	19:R:45:PRO:O	2.00	0.62
8:G:23:GLU:HG2	8:G:28:SER:HB3	1.81	0.62
9:H:58:GLU:OE1	15:N:27:ARG:NH2	2.32	0.62
14:M:12:THR:HG21	14:M:16:GLY:O	1.99	0.62
22:U:38:ARG:HG3	22:U:38:ARG:HH11	1.63	0.62
4:C:73:GLY:N	28:1:65:ALA:O	2.21	0.62
1:A:2459:G:P	31:4:64:LYS:HB2	2.40	0.62
7:F:37:ALA:O	7:F:40:ILE:HG12	1.99	0.62
22:U:48:VAL:HG22	22:U:97:ARG:C	2.20	0.62
9:H:47:LEU:HB2	9:H:108:LEU:HD11	1.81	0.62
16:O:91:ARG:HG3	16:O:186:LEU:HD23	1.82	0.62
16:O:32:PRO:HD2	16:O:99:GLU:O	2.00	0.62
25:X:1:MET:HB2	25:X:103:GLU:HG2	1.80	0.62
31:4:11:CYS:HB2	31:4:20:HIS:CE1	2.35	0.62
11:J:26:LYS:HD3	11:J:89:PRO:CG	2.30	0.62
17:P:35:LYS:HD3	38:P:3360:HOH:O	1.99	0.62
21:T:51:GLN:HE21	21:T:53:ASN:ND2	1.97	0.62
1:A:2256:G:O2'	1:A:2257:G:H5'	1.98	0.62
1:A:2470:A:H5''	38:A:9742:HOH:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:224:LYS:NZ	38:D:8551:HOH:O	2.33	0.62
6:E:166:ILE:HG23	6:E:208:ALA:HB3	1.82	0.62
22:U:20:HIS:ND1	22:U:41:ARG:NE	2.38	0.62
26:Y:15:ARG:HH11	26:Y:15:ARG:CB	2.12	0.62
1:A:1165:G:C3'	1:A:1165:G:OP1	2.43	0.62
1:A:855:U:H5''	38:A:3129:HOH:O	1.98	0.62
5:D:24:PRO:CG	5:D:204:GLY:HA2	2.30	0.62
13:L:34:VAL:HG22	13:L:47:ALA:HB2	1.81	0.62
16:O:73:ALA:N	38:O:8563:HOH:O	2.32	0.62
25:X:88:THR:HG22	25:X:89:ASP:H	1.64	0.62
25:X:54:PHE:CZ	25:X:140:LYS:HB2	2.35	0.62
1:A:1316:G:H1'	1:A:1340:G:N2	2.15	0.61
11:J:26:LYS:HD2	11:J:28:ILE:CD1	2.29	0.61
14:M:143:THR:HG22	14:M:144:ASP:N	2.15	0.61
15:N:60:ILE:HG12	15:N:134:ILE:HD12	1.81	0.61
1:A:2031:C:O3'	38:A:3995:HOH:O	2.16	0.61
1:A:2432:C:C1'	38:A:3570:HOH:O	2.47	0.61
1:A:669:G:O2'	1:A:670:G:H5'	2.00	0.61
1:A:338:C:H4'	6:E:174:ILE:CD1	2.30	0.61
7:F:50:VAL:O	7:F:71:ALA:HA	2.00	0.61
9:H:46:GLU:N	38:H:3461:HOH:O	2.33	0.61
16:O:11:ARG:HG3	16:O:14:ARG:NH1	2.15	0.61
1:A:1901:G:O2'	1:A:1902:G:H5'	2.00	0.61
1:A:2635:A:O2'	1:A:2636:C:H5'	2.00	0.61
1:A:2712:G:H5'	38:A:4706:HOH:O	2.01	0.61
24:W:57:LYS:HA	24:W:60:GLN:HE21	1.66	0.61
1:A:316:A:N3	1:A:336:G:O2'	2.33	0.61
1:A:57:C:H5''	38:A:6229:HOH:O	1.99	0.61
2:B:3014:G:H5'	2:B:3014:G:C8	2.34	0.61
16:O:61:ALA:CB	16:O:88:ALA:HB2	2.31	0.61
1:A:960:G:N3	1:A:960:G:H2'	2.16	0.61
8:G:81:GLU:HB3	38:G:4761:HOH:O	2.00	0.61
38:A:7028:HOH:O	31:4:61:PRO:HG2	2.00	0.61
1:A:1766:U:O2	1:A:1778:A:H5'	2.00	0.61
1:A:2106:C:H5'	1:A:2284:G:H21	1.64	0.61
4:C:131:HIS:O	4:C:132:ASP:HB2	1.98	0.61
8:G:3:VAL:CG2	8:G:49:ILE:HB	2.29	0.61
12:K:48:GLY:HA3	12:K:53:ILE:HD11	1.81	0.61
15:N:74:ARG:HG3	15:N:74:ARG:NH1	2.14	0.61
31:4:7:PHE:HE2	31:4:22:VAL:HG21	1.64	0.61
1:A:1209:C:H2'	1:A:1210:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1528:A:H2'	1:A:1529:G:O4'	2.00	0.61
1:A:2748:G:H2'	38:A:7012:HOH:O	2.01	0.61
1:A:544:G:C2'	1:A:545:G:H5''	2.30	0.61
2:B:3048:C:H4'	16:O:141:ARG:NH2	2.14	0.61
2:B:3054:A:O2'	2:B:3055:U:H5'	2.01	0.61
23:V:9:CYS:HA	23:V:52:THR:CG2	2.28	0.61
25:X:131:PRO:HB2	38:X:5904:HOH:O	1.98	0.61
17:P:73:ASP:HA	17:P:92:VAL:O	2.01	0.61
27:Z:155:ARG:NH1	38:Z:8560:HOH:O	2.34	0.61
15:N:154:ARG:HG3	38:N:8607:HOH:O	2.01	0.61
31:4:25:VAL:HG22	31:4:68:LYS:HG3	1.82	0.61
1:A:2900:G:H2'	1:A:2901:C:O4'	2.01	0.61
2:B:3039:U:H1'	2:B:3044:A:H61	1.66	0.61
38:A:6692:HOH:O	15:N:13:LYS:HE2	2.00	0.61
16:O:37:ARG:NE	38:O:8532:HOH:O	2.34	0.61
1:A:2548:C:OP2	5:D:5:ARG:NH2	2.34	0.60
5:D:7:ARG:HD3	5:D:9:GLY:O	2.01	0.60
6:E:76:ARG:HD3	38:E:8368:HOH:O	2.00	0.60
1:A:2338:G:H1'	7:F:105:SER:OG	2.01	0.60
8:G:100:ASP:HB2	38:G:2789:HOH:O	2.01	0.60
8:G:77:THR:OG1	8:G:78:GLU:N	2.34	0.60
10:I:23:ILE:CD1	10:I:67:LEU:HD23	2.23	0.60
16:O:159:TYR:HE2	16:O:163:PHE:HE2	1.49	0.60
17:P:106:PRO:HG2	17:P:107:GLU:OE2	2.01	0.60
23:V:6:CYS:HB2	23:V:32:CYS:HB3	1.82	0.60
1:A:1211:G:O2'	1:A:1212:C:H5'	2.00	0.60
1:A:2827:A:H2'	1:A:2828:G:O4'	2.00	0.60
1:A:314:G:N2	1:A:316:A:H3'	2.16	0.60
4:C:191:GLY:HA2	4:C:194:MET:CE	2.31	0.60
1:A:1669:A:H2	38:A:3200:HOH:O	1.84	0.60
1:A:88:G:H8	1:A:88:G:H5'	1.66	0.60
2:B:3064:C:H2'	2:B:3065:A:H5'	1.81	0.60
4:C:179:MET:HG2	4:C:186:TRP:CG	2.36	0.60
17:P:39:THR:HB	38:P:3360:HOH:O	2.00	0.60
25:X:137:GLN:HE21	25:X:141:HIS:HE1	1.49	0.60
4:C:211:LYS:HB2	38:C:8632:HOH:O	2.02	0.60
7:F:95:THR:C	7:F:97:GLN:H	2.05	0.60
11:J:141:ASN:HA	38:J:8355:HOH:O	2.01	0.60
14:M:104:ASP:HB2	38:M:8452:HOH:O	2.00	0.60
14:M:90:ARG:NH2	14:M:121:ILE:HD11	2.16	0.60
28:1:46:LYS:HE2	38:1:8436:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2433:A:O3'	31:4:30:GLN:OE1	2.19	0.60
7:F:10:PHE:CD1	7:F:11:HIS:N	2.69	0.60
7:F:45:THR:HG22	7:F:75:LEU:HD11	1.84	0.60
11:J:30:GLN:H	11:J:65:ARG:NH1	1.98	0.60
15:N:87:MET:HB3	31:4:46:ILE:HG21	1.81	0.60
38:L:408:HOH:O	23:V:37:GLU:HB3	2.01	0.60
5:D:24:PRO:HG3	5:D:204:GLY:HA2	1.82	0.60
5:D:36:PRO:HA	5:D:168:GLY:CA	2.32	0.60
6:E:219:ASN:O	6:E:222:ASP:OD1	2.20	0.60
6:E:129:HIS:CE1	6:E:231:ARG:HA	2.37	0.60
9:H:58:GLU:HA	9:H:61:MET:HE2	1.83	0.60
10:I:71:LEU:C	10:I:73:ASP:H	2.05	0.60
11:J:14:TYR:H	11:J:91:HIS:CE1	2.20	0.60
13:L:55:VAL:HG12	13:L:56:SER:H	1.67	0.60
17:P:97:SER:OG	17:P:100:GLN:HG3	2.01	0.60
21:T:22:ASN:ND2	21:T:68:LEU:HB2	2.17	0.60
26:Y:30:MET:HE1	26:Y:55:ASN:HA	1.82	0.60
1:A:1182:C:H1'	1:A:1192:A:H8	1.67	0.60
1:A:1804:A:H2'	1:A:1805:G:C8	2.36	0.60
1:A:558:C:O2'	1:A:559:U:H5"	2.02	0.60
1:A:935:G:H4'	17:P:38:ARG:HH12	1.66	0.60
4:C:105:VAL:CG1	4:C:154:ALA:HB1	2.32	0.60
17:P:14:LEU:HD23	17:P:102:ILE:HD11	1.83	0.60
25:X:122:ARG:HG2	25:X:152:ALA:O	2.02	0.60
27:Z:151:SER:HB3	27:Z:154:ARG:HB3	1.84	0.60
31:4:64:LYS:HE3	31:4:84:ARG:HH12	1.66	0.60
1:A:1130:U:H2'	1:A:1131:G:O4'	2.01	0.60
1:A:1434:A:H2'	1:A:1436:C:C5	2.36	0.60
1:A:2832:C:H5'	38:A:6221:HOH:O	2.00	0.60
1:A:31:C:H4'	38:A:6888:HOH:O	2.02	0.60
7:F:64:ARG:CG	7:F:67:ASP:HB3	2.32	0.60
10:I:64:ASN:O	10:I:68:GLU:HG3	2.02	0.60
27:Z:99:ALA:HB2	27:Z:233:TYR:CZ	2.37	0.60
1:A:1353:C:P	38:A:4159:HOH:O	2.60	0.60
1:A:1535:G:H2'	1:A:1536:C:C6	2.37	0.60
1:A:188:C:H5"	15:N:163:LEU:HD21	1.84	0.60
1:A:280:C:H2'	1:A:281:U:O4'	2.02	0.60
2:B:3028:U:H2'	2:B:3029:C:C6	2.36	0.60
12:K:54:VAL:HG11	12:K:138:THR:HG21	1.84	0.60
1:A:558:C:H2'	1:A:559:U:C5'	2.32	0.60
1:A:665:A:H2'	1:A:666:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:199:HIS:HD2	4:C:201:PHE:HB2	1.67	0.60
6:E:115:LEU:HD21	6:E:243:VAL:HG13	1.83	0.60
1:A:2348:C:H5'	7:F:22:VAL:HG21	1.84	0.60
1:A:1151:G:OP1	10:I:63:ARG:NH1	2.35	0.60
23:V:52:THR:HG22	23:V:54:THR:N	2.17	0.60
1:A:2381:C:O2'	31:4:10:TYR:HB3	2.02	0.59
1:A:538:C:OP2	27:Z:134:HIS:HE1	1.84	0.59
9:H:91:VAL:CG1	9:H:92:GLY:H	2.15	0.59
11:J:47:GLU:HG2	11:J:133:ILE:HD12	1.83	0.59
22:U:38:ARG:HG3	22:U:38:ARG:NH1	2.16	0.59
25:X:122:ARG:NH1	25:X:152:ALA:O	2.35	0.59
25:X:13:MET:CE	25:X:17:ILE:HG22	2.32	0.59
1:A:1015:C:H2'	1:A:1016:U:C6	2.37	0.59
1:A:2475:C:O2	38:A:9234:HOH:O	2.15	0.59
5:D:48:MET:N	38:D:8564:HOH:O	2.32	0.59
6:E:127:ARG:HG2	6:E:127:ARG:HH11	1.68	0.59
8:G:145:ALA:HB1	8:G:168:ILE:CD1	2.32	0.59
14:M:149:ARG:O	14:M:150:GLN:HB2	2.02	0.59
16:O:164:ASP:OD2	16:O:167:ASP:HA	2.02	0.59
26:Y:66:THR:HG23	26:Y:67:PRO:HD2	1.84	0.59
31:4:64:LYS:CE	31:4:84:ARG:HH12	2.16	0.59
1:A:1805:G:O2'	1:A:1806:G:H5'	2.02	0.59
1:A:2502:C:C2'	1:A:2503:A:H5'	2.32	0.59
1:A:1845:A:OP2	4:C:190:ARG:NH1	2.35	0.59
7:F:128:LEU:N	38:F:5495:HOH:O	2.35	0.59
8:G:127:ASP:HB3	38:G:6772:HOH:O	2.01	0.59
1:A:182:G:H5'	38:A:4640:HOH:O	2.01	0.59
1:A:2472:C:O2'	1:A:2634:G:H4'	2.02	0.59
1:A:2866:U:H4'	1:A:2867:G:H5'	1.83	0.59
1:A:383:A:H4'	38:A:4810:HOH:O	2.01	0.59
1:A:399:C:H5'	15:N:179:GLY:O	2.02	0.59
5:D:195:ARG:HG2	5:D:323:LEU:HD22	1.84	0.59
11:J:27:LYS:N	11:J:58:HIS:HD2	1.91	0.59
17:P:30:ALA:O	17:P:34:GLU:HG3	2.02	0.59
25:X:84:VAL:HG12	38:X:6679:HOH:O	2.02	0.59
26:Y:72:VAL:HG22	26:Y:85:VAL:CG1	2.31	0.59
1:A:1209:C:H4'	38:A:4763:HOH:O	2.00	0.59
1:A:31:C:H2'	38:A:7160:HOH:O	2.02	0.59
9:H:28:ALA:CB	9:H:99:THR:HG23	2.31	0.59
11:J:136:VAL:HG23	38:J:8331:HOH:O	2.01	0.59
11:J:71:TYR:C	11:J:73:GLN:H	2.06	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:136:ALA:HB3	38:M:8449:HOH:O	2.02	0.59
23:V:6:CYS:HG	23:V:31:PHE:HA	1.68	0.59
1:A:2434:A:OP1	31:4:30:GLN:HG2	2.02	0.59
1:A:1470:A:OP1	15:N:93:ARG:HD2	2.03	0.59
1:A:709:G:O2'	17:P:25:VAL:HG12	2.03	0.59
6:E:115:LEU:HD13	6:E:223:LEU:CD2	2.19	0.59
6:E:127:ARG:HH21	6:E:225:PRO:HG2	1.65	0.59
12:K:19:MET:CE	12:K:132:LEU:HD11	2.32	0.59
25:X:13:MET:HE3	25:X:17:ILE:HG22	1.84	0.59
25:X:65:VAL:HG12	25:X:116:LEU:HD13	1.85	0.59
1:A:1773:G:O2'	28:1:15:GLY:HA2	2.03	0.59
28:1:38:LYS:HG3	38:1:8426:HOH:O	2.02	0.59
29:2:21:ARG:HD2	29:2:37:CYS:SG	2.42	0.59
31:4:35:TRP:HA	31:4:38:ARG:NH1	2.18	0.59
1:A:119:A:H2'	1:A:120:A:C5'	2.33	0.59
1:A:821:U:H2'	1:A:822:C:C6	2.37	0.59
2:B:3107:C:C5	38:B:8439:HOH:O	2.49	0.59
1:A:328:U:O4'	6:E:202:THR:HG22	2.03	0.59
7:F:23:VAL:HG21	7:F:45:THR:HG21	1.84	0.59
16:O:154:LEU:HD11	16:O:157:PRO:HA	1.84	0.59
20:S:82:GLU:HG3	20:S:83:LYS:N	2.18	0.59
28:1:62:TYR:CE2	28:1:64:ILE:HG23	2.37	0.59
1:A:1771:U:O3'	28:1:23:ARG:NH2	2.35	0.59
11:J:75:SER:C	11:J:79:ALA:HB2	2.23	0.59
12:K:15:ARG:NH1	12:K:43:ARG:NH1	2.50	0.59
15:N:184:ARG:HB2	15:N:184:ARG:NH1	2.18	0.59
9:H:38:LYS:HZ1	15:N:3:SER:HA	1.68	0.59
23:V:52:THR:CG2	23:V:54:THR:HB	2.32	0.59
26:Y:85:VAL:HG12	26:Y:86:GLU:H	1.67	0.59
1:A:1652:C:O2	4:C:164:ARG:HD2	2.02	0.59
4:C:199:HIS:CD2	4:C:201:PHE:H	2.20	0.59
5:D:258:GLY:HA2	38:D:8563:HOH:O	2.03	0.59
29:2:10:LYS:HG3	38:2:2979:HOH:O	2.03	0.59
1:A:2620:U:O4	36:5:76:PPU:C	2.51	0.59
1:A:2524:G:H21	1:A:2526:C:H41	1.50	0.59
1:A:2578:G:H5'	1:A:2578:G:C8	2.37	0.59
38:A:5781:HOH:O	7:F:99:ASP:HA	2.03	0.59
9:H:91:VAL:CG1	9:H:92:GLY:N	2.65	0.59
11:J:59:ASN:ND2	11:J:59:ASN:H	2.01	0.59
22:U:61:GLU:HG3	38:U:3851:HOH:O	2.02	0.59
1:A:1119:G:H22	1:A:1246:A:H2	1.46	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2445:U:H2'	1:A:2446:G:C8	2.38	0.58
1:A:2897:C:H2'	1:A:2898:G:H8	1.66	0.58
1:A:625:U:H5''	1:A:1044:C:N4	2.18	0.58
1:A:661:G:C5	1:A:686:A:C2	2.91	0.58
5:D:145:HIS:HD2	5:D:146:THR:O	1.85	0.58
7:F:128:LEU:HD23	7:F:128:LEU:C	2.24	0.58
7:F:140:ARG:O	7:F:144:ARG:HG2	2.02	0.58
8:G:166:VAL:HB	38:G:6341:HOH:O	2.03	0.58
13:L:28:GLU:OE2	13:L:58:THR:HG21	2.02	0.58
15:N:57:LYS:HE2	15:N:140:ALA:O	2.03	0.58
23:V:52:THR:HA	38:V:6796:HOH:O	2.02	0.58
38:A:3966:HOH:O	31:4:51:LYS:HB2	2.02	0.58
1:A:1596:U:H2'	1:A:1598:A:OP2	2.02	0.58
1:A:2507:G:H2'	1:A:2510:C:H42	1.67	0.58
1:A:329:A:OP2	6:E:206:ASN:HB2	2.03	0.58
1:A:2443:C:H3'	38:A:9967:HOH:O	2.03	0.58
1:A:245:C:H2'	38:A:5052:HOH:O	2.04	0.58
1:A:426:G:H5''	38:A:7097:HOH:O	2.02	0.58
6:E:236:THR:HG21	38:E:8374:HOH:O	2.03	0.58
7:F:146:LYS:NZ	16:O:107:ASN:HD21	2.02	0.58
13:L:55:VAL:HG12	13:L:56:SER:N	2.18	0.58
20:S:44:VAL:HG13	20:S:89:LEU:HD22	1.85	0.58
22:U:48:VAL:CG2	22:U:98:VAL:HA	2.33	0.58
1:A:2387:U:H2'	1:A:2388:C:C6	2.37	0.58
1:A:2912:C:OP2	38:A:5034:HOH:O	2.16	0.58
1:A:869:G:H1'	38:A:9812:HOH:O	2.01	0.58
5:D:14:GLY:HA2	5:D:15:PRO:C	2.23	0.58
15:N:102:GLU:OE1	15:N:164:THR:HG21	2.04	0.58
19:R:93:ARG:NH1	19:R:93:ARG:HG3	2.18	0.58
1:A:120:A:H2'	1:A:120:A:N3	2.19	0.58
1:A:2469:A:OP2	38:A:6942:HOH:O	2.17	0.58
6:E:1:MET:HG2	6:E:2:GLN:N	2.18	0.58
8:G:12:ASP:HA	38:G:1750:HOH:O	2.03	0.58
11:J:45:GLN:HG3	11:J:135:TRP:NE1	2.18	0.58
14:M:90:ARG:NH1	14:M:119:THR:HG21	2.19	0.58
15:N:48:ARG:NH1	38:N:8610:HOH:O	2.36	0.58
22:U:47:THR:HB	22:U:100:ASP:HB3	1.85	0.58
1:A:2094:G:H4'	5:D:245:SER:HB3	1.85	0.58
1:A:2727:A:C2'	1:A:2728:C:H5'	2.32	0.58
5:D:36:PRO:HA	5:D:168:GLY:HA3	1.86	0.58
8:G:114:ARG:HA	38:G:3388:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:57:ARG:HG3	11:J:57:ARG:HH11	1.69	0.58
16:O:58:LEU:HD12	16:O:58:LEU:N	2.17	0.58
28:1:30:GLU:HA	28:1:33:HIS:CB	2.31	0.58
31:4:87:ARG:HD2	38:4:8526:HOH:O	2.04	0.58
1:A:1763:C:O2'	1:A:1764:C:H5'	2.03	0.58
1:A:2419:U:H5''	1:A:2420:G:H5'	1.85	0.58
1:A:660:A:H4'	1:A:661:G:O5'	2.03	0.58
5:D:238:ASN:ND2	5:D:240:GLY:N	2.49	0.58
14:M:145:LEU:O	14:M:148:GLU:HG3	2.04	0.58
15:N:106:ASN:HD22	15:N:114:VAL:HG23	1.67	0.58
20:S:119:VAL:O	20:S:119:VAL:HG12	2.03	0.58
1:A:2834:G:OP1	26:Y:39:LYS:HE2	2.04	0.58
11:J:117:LYS:O	11:J:119:VAL:HG13	2.03	0.58
12:K:142:ASN:O	12:K:144:THR:N	2.36	0.58
15:N:14:ARG:HB3	15:N:17:GLU:CG	2.34	0.58
16:O:62:HIS:HB3	16:O:65:ASP:OD1	2.04	0.58
17:P:59:VAL:HG23	17:P:111:VAL:HG23	1.85	0.58
22:U:2:LYS:HE2	38:U:7214:HOH:O	2.03	0.58
31:4:64:LYS:CE	31:4:84:ARG:NH1	2.67	0.58
1:A:1497:G:H2'	1:A:1498:G:H8	1.69	0.58
4:C:95:PRO:HG2	4:C:98:GLU:HG2	1.86	0.58
5:D:217:ARG:HG3	5:D:257:THR:CG2	2.33	0.58
7:F:166:ILE:HD12	38:F:6326:HOH:O	2.03	0.58
10:I:12:ILE:HB	38:I:4714:HOH:O	2.04	0.58
11:J:127:GLY:O	11:J:128:ALA:HB3	2.03	0.58
17:P:77:ALA:HB1	17:P:98:LEU:HD12	1.85	0.58
28:1:29:VAL:O	28:1:33:HIS:HB2	2.04	0.58
1:A:1827:G:H2'	1:A:1828:G:C8	2.38	0.58
1:A:251:C:H1'	15:N:58:GLN:HE22	1.67	0.58
6:E:16:VAL:HG12	6:E:17:ASP:N	2.18	0.58
8:G:108:LEU:HD11	8:G:164:ASP:HB2	1.85	0.58
1:A:263:U:O4'	9:H:59:ILE:HD13	2.03	0.58
15:N:186:SER:OG	15:N:189:VAL:HG12	2.03	0.58
27:Z:178:HIS:CG	27:Z:179:PRO:HD2	2.39	0.58
1:A:2382:A:OP1	31:4:80:ARG:HG2	2.03	0.57
2:B:3064:C:O2'	2:B:3065:A:H5'	2.03	0.57
4:C:72:GLU:HG3	28:1:66:GLY:HA2	1.86	0.57
5:D:253:GLN:HA	38:D:8629:HOH:O	2.04	0.57
13:L:34:VAL:CG2	13:L:47:ALA:HB2	2.33	0.57
16:O:34:LEU:HA	16:O:47:LEU:HD23	1.86	0.57
27:Z:133:HIS:HD2	38:Z:8584:HOH:O	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:A:H1'	1:A:1209:C:C1'	2.35	0.57
1:A:558:C:H2'	1:A:559:U:H5'	1.87	0.57
1:A:1874:U:H2'	4:C:120:ARG:HG3	1.85	0.57
5:D:55:ASN:HB3	5:D:63:GLU:CA	2.33	0.57
6:E:27:ARG:HD2	6:E:29:ASP:OD1	2.04	0.57
7:F:102:GLY:O	7:F:134:LEU:HD12	2.04	0.57
7:F:170:TYR:O	7:F:171:ASP:HB3	2.04	0.57
10:I:16:LYS:NZ	38:I:5575:HOH:O	2.20	0.57
14:M:73:VAL:HG23	14:M:74:THR:N	2.20	0.57
15:N:113:ARG:NH2	15:N:156:ARG:HG2	2.19	0.57
38:B:8391:HOH:O	16:O:7:LYS:HE2	2.02	0.57
25:X:88:THR:HG22	25:X:89:ASP:N	2.19	0.57
1:A:1456:C:H2'	1:A:1457:U:C6	2.38	0.57
1:A:2898:G:H4'	5:D:288:GLY:HA2	1.84	0.57
6:E:7:ASP:OD1	6:E:11:ASN:O	2.23	0.57
8:G:101:GLU:HB2	8:G:116:THR:O	2.04	0.57
25:X:13:MET:HE1	25:X:18:GLN:HA	1.85	0.57
29:2:45:ARG:NH2	38:2:2086:HOH:O	2.18	0.57
1:A:121:U:OP2	30:3:10:ARG:NH2	2.36	0.57
1:A:2349:G:OP1	7:F:20:LYS:NZ	2.32	0.57
1:A:2526:C:C2'	1:A:2527:U:H5'	2.34	0.57
1:A:1733:A:H4'	5:D:212:GLN:HA	1.85	0.57
6:E:191:SER:OG	6:E:192:ILE:N	2.36	0.57
8:G:118:ILE:HG23	8:G:144:THR:HG21	1.85	0.57
8:G:81:GLU:HG2	8:G:134:SER:CB	2.34	0.57
1:A:793:A:H5''	18:Q:83:LYS:HG2	1.86	0.57
31:4:70:ARG:HD3	38:4:8541:HOH:O	2.05	0.57
1:A:1624:A:H5'	1:A:1626:A:O4'	2.05	0.57
1:A:2672:C:P	5:D:25:ARG:NH1	2.77	0.57
1:A:2729:C:H2'	1:A:2730:G:H8	1.69	0.57
1:A:484:A:N1	1:A:506:G:H4'	2.18	0.57
1:A:542:A:H5'	1:A:542:A:C8	2.31	0.57
5:D:162:MET:CE	5:D:310:ARG:HD3	2.34	0.57
7:F:10:PHE:CE1	7:F:11:HIS:HB3	2.39	0.57
15:N:164:THR:HG23	15:N:165:SER:N	2.20	0.57
38:A:5395:HOH:O	15:N:189:VAL:HG23	2.03	0.57
15:N:52:LEU:HD21	38:N:8610:HOH:O	2.05	0.57
26:Y:9:VAL:HG13	26:Y:88:GLU:OE2	2.04	0.57
3:5:74:C:H2'	3:5:75:C:C5'	2.34	0.57
1:A:2385:G:H2'	1:A:2386:U:C6	2.40	0.57
7:F:11:HIS:C	7:F:13:MET:H	2.08	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2781:U:H1'	8:G:139:GLU:OE2	2.05	0.57
17:P:25:VAL:HG23	17:P:26:TRP:N	2.19	0.57
26:Y:23:HIS:HA	26:Y:64:ALA:HB2	1.86	0.57
26:Y:76:ARG:HG3	26:Y:76:ARG:NH1	2.18	0.57
1:A:2769:C:H2'	1:A:2770:G:O4'	2.04	0.57
1:A:542:A:H2'	1:A:543:G:O4'	2.05	0.57
1:A:656:G:H5'	17:P:3:THR:HB	1.86	0.57
6:E:118:THR:HG22	6:E:137:PRO:HB3	1.86	0.57
11:J:163:PRO:HG2	38:J:8326:HOH:O	2.03	0.57
17:P:44:ASN:OD1	17:P:65:LEU:HB2	2.05	0.57
22:U:64:ASN:HA	38:U:5927:HOH:O	2.04	0.57
23:V:13:ILE:HG12	23:V:32:CYS:CB	2.34	0.57
26:Y:78:GLU:HG2	26:Y:79:GLU:N	2.14	0.57
1:A:1206:U:H5'	1:A:1206:U:H6	1.67	0.57
1:A:1328:A:C8	27:Z:169:ARG:HD3	2.39	0.57
1:A:2015:A:H2'	1:A:2016:U:O4'	2.04	0.57
1:A:449:A:N7	6:E:43:LYS:HG2	2.19	0.57
5:D:49:THR:HG21	5:D:280:VAL:HG23	1.87	0.57
5:D:274:GLU:HA	5:D:292:GLY:O	2.04	0.57
8:G:15:GLN:HG2	8:G:19:ASP:O	2.05	0.57
9:H:101:ALA:HB2	9:H:108:LEU:HD22	1.87	0.57
14:M:7:GLN:HB3	14:M:13:HIS:ND1	2.20	0.57
1:A:2135:A:O2'	1:A:2136:G:H5'	2.04	0.57
1:A:2445:U:H2'	1:A:2446:G:H8	1.69	0.57
1:A:283:U:H5''	1:A:284:C:P	2.44	0.57
5:D:74:ILE:HG22	5:D:76:THR:HG23	1.87	0.57
11:J:39:GLY:O	11:J:41:THR:N	2.38	0.57
16:O:64:SER:C	16:O:66:LEU:H	2.09	0.57
19:R:25:PRO:HB2	38:R:4350:HOH:O	2.04	0.57
1:A:1441:G:O2'	1:A:1442:A:H5'	2.05	0.57
1:A:1701:A:H4'	38:A:6683:HOH:O	2.05	0.57
1:A:187:A:H3'	1:A:188:C:H6	1.69	0.57
1:A:2502:C:H2'	1:A:2503:A:H5'	1.85	0.57
1:A:2769:C:C2'	1:A:2770:G:H5'	2.35	0.57
9:H:50:VAL:HG21	9:H:63:ILE:HG21	1.87	0.57
15:N:23:LEU:O	15:N:26:HIS:HB2	2.04	0.57
2:B:3051:A:H5'	16:O:160:SER:HB3	1.87	0.57
16:O:5:ARG:HG3	19:R:18:PRO:HB3	1.86	0.57
21:T:57:THR:C	21:T:59:ASP:H	2.08	0.57
3:5:74:C:H2'	3:5:75:C:O4'	2.05	0.56
1:A:447:A:OP1	22:U:2:LYS:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:870:G:C2'	1:A:871:G:H5''	2.33	0.56
5:D:307:ARG:HH11	5:D:307:ARG:HB2	1.70	0.56
5:D:55:ASN:CB	5:D:63:GLU:HA	2.32	0.56
14:M:34:GLY:HA3	14:M:38:HIS:CE1	2.40	0.56
20:S:33:ARG:NH1	38:S:8543:HOH:O	2.37	0.56
24:W:12:THR:CG2	24:W:15:GLU:HG3	2.18	0.56
31:4:48:ASN:ND2	31:4:50:GLY:H	2.03	0.56
1:A:2783:A:H3'	38:A:4717:HOH:O	2.05	0.56
1:A:241:A:C2	1:A:378:A:H4'	2.39	0.56
5:D:162:MET:HE2	5:D:310:ARG:HD3	1.88	0.56
6:E:15:GLU:HG3	38:E:8336:HOH:O	2.05	0.56
9:H:96:ALA:HA	38:H:3111:HOH:O	2.04	0.56
18:Q:115:SER:O	18:Q:117:SER:N	2.39	0.56
23:V:52:THR:HG22	23:V:54:THR:HB	1.86	0.56
31:4:75:GLY:HA2	38:4:8560:HOH:O	2.05	0.56
1:A:1173:A:H4'	1:A:1174:A:C8	2.40	0.56
1:A:2777:G:O2'	1:A:2778:A:H5'	2.06	0.56
1:A:2911:C:H2'	1:A:2912:C:C6	2.41	0.56
1:A:646:G:H2'	1:A:647:U:H6	1.71	0.56
1:A:69:A:H8	1:A:69:A:H5'	1.70	0.56
1:A:702:G:O2'	1:A:703:G:H5'	2.05	0.56
4:C:188:ASN:HA	38:C:8580:HOH:O	2.05	0.56
4:C:94:LEU:HG	4:C:99:ILE:CD1	2.34	0.56
1:A:2840:A:OP1	5:D:211:THR:HG23	2.06	0.56
7:F:86:THR:C	7:F:89:PRO:HD2	2.24	0.56
8:G:116:THR:HG22	8:G:151:LEU:HD22	1.86	0.56
11:J:35:ASN:ND2	11:J:80:ASN:HA	2.21	0.56
12:K:75:PRO:HG2	12:K:105:LEU:CD2	2.33	0.56
13:L:37:TYR:CE2	13:L:45:PRO:HA	2.40	0.56
13:L:74:VAL:CG1	13:L:113:ILE:HG12	2.35	0.56
13:L:49:LEU:HD12	13:L:80:ILE:HD13	1.87	0.56
2:B:3010:C:C2	16:O:10:MET:HG2	2.40	0.56
16:O:169:PRO:O	16:O:172:PHE:HB3	2.04	0.56
1:A:1151:G:OP1	10:I:16:LYS:NZ	2.30	0.56
1:A:1189:A:H1'	1:A:1209:C:O4'	2.05	0.56
1:A:155:C:O2'	1:A:156:C:H5'	2.05	0.56
1:A:1654:U:H5''	38:A:6885:HOH:O	2.04	0.56
1:A:2786:G:O2'	1:A:2787:C:H5'	2.04	0.56
1:A:319:A:H4'	1:A:338:C:C5	2.40	0.56
6:E:246:ARG:HH11	6:E:246:ARG:HB3	1.69	0.56
1:A:2346:C:H4'	7:F:52:THR:CG2	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:107:PHE:CZ	8:G:152:THR:HB	2.39	0.56
11:J:69:ASN:O	11:J:72:VAL:HG12	2.04	0.56
14:M:134:GLU:HA	14:M:138:GLY:O	2.05	0.56
15:N:149:TRP:O	15:N:152:ARG:HG2	2.05	0.56
1:A:1835:U:C5	1:A:1840:A:N7	2.67	0.56
1:A:2435:U:P	31:4:28:GLY:HA3	2.45	0.56
1:A:553:G:H5'	38:A:9992:HOH:O	2.04	0.56
1:A:654:A:H4'	38:A:5065:HOH:O	2.05	0.56
1:A:699:C:C2	1:A:744:G:C2	2.93	0.56
2:B:3031:C:O2'	2:B:3032:G:H5'	2.06	0.56
5:D:16:ARG:HB3	5:D:217:ARG:HH21	1.71	0.56
5:D:51:VAL:CG2	5:D:327:VAL:HG13	2.35	0.56
6:E:236:THR:H	6:E:239:ALA:HB3	1.70	0.56
10:I:64:ASN:ND2	10:I:64:ASN:N	2.53	0.56
15:N:169:ARG:HD2	38:N:8584:HOH:O	2.06	0.56
15:N:38:VAL:C	15:N:63:VAL:HG13	2.25	0.56
31:4:69:TYR:CB	31:4:78:HIS:CE1	2.89	0.56
1:A:1305:C:O2'	1:A:1306:U:H5'	2.04	0.56
1:A:236:A:H8	1:A:236:A:OP1	1.88	0.56
1:A:2533:C:H5'	1:A:2533:C:C6	2.37	0.56
13:L:87:ARG:NH1	38:L:4066:HOH:O	2.39	0.56
16:O:159:TYR:CE2	16:O:163:PHE:HE2	2.24	0.56
16:O:80:SER:CB	38:O:8534:HOH:O	2.53	0.56
1:A:1184:C:H1'	38:A:6934:HOH:O	2.04	0.56
1:A:2316:G:H2'	38:A:4394:HOH:O	2.04	0.56
1:A:2324:G:H4'	1:A:2418:G:O2'	2.05	0.56
5:D:129:ARG:NH2	5:D:176:ASP:OD1	2.38	0.56
7:F:11:HIS:O	7:F:12:GLU:HB3	2.05	0.56
11:J:56:ILE:HG22	11:J:61:LEU:HD22	1.87	0.56
16:O:71:TRP:HE3	16:O:175:LEU:HD22	1.70	0.56
16:O:73:ALA:HB1	16:O:74:PRO:HD2	1.87	0.56
27:Z:142:SER:OG	38:Z:8618:HOH:O	2.18	0.56
1:A:1829:A:N6	28:1:18:TYR:HA	2.21	0.56
28:1:31:ILE:O	28:1:35:LYS:HG3	2.05	0.56
29:2:28:HIS:HD2	29:2:30:LYS:H	1.54	0.56
1:A:1701:A:H4'	1:A:1702:U:C5'	2.35	0.56
1:A:69:A:H5'	1:A:69:A:C8	2.40	0.56
4:C:132:ASP:OD1	4:C:133:ARG:N	2.38	0.56
7:F:105:SER:CB	7:F:131:THR:HG23	2.31	0.56
1:A:2780:C:C1'	8:G:143:GLN:HE21	2.17	0.56
16:O:114:LYS:O	16:O:117:ALA:HB3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:107:GLU:N	17:P:107:GLU:OE1	2.39	0.56
21:T:51:GLN:NE2	21:T:53:ASN:HD21	1.99	0.56
22:U:23:VAL:HG23	22:U:41:ARG:HG3	1.87	0.56
1:A:1829:A:H61	28:1:18:TYR:HA	1.70	0.56
28:1:39:CYS:HA	28:1:47:LEU:HD11	1.88	0.56
1:A:1395:C:H2'	1:A:1396:C:C6	2.41	0.56
1:A:1753:C:O2	5:D:229:ARG:NH2	2.34	0.56
1:A:1773:G:C8	28:1:16:PRO:CA	2.89	0.56
1:A:42:C:H1'	38:A:4156:HOH:O	2.05	0.56
4:C:51:ARG:HB2	38:C:8621:HOH:O	2.05	0.56
5:D:144:THR:HG22	5:D:145:HIS:H	1.71	0.56
6:E:54:LEU:HD21	6:E:87:ARG:HD2	1.86	0.56
11:J:86:ARG:HD3	11:J:130:HIS:HD2	1.71	0.56
16:O:151:ASP:O	16:O:154:LEU:HB2	2.06	0.56
1:A:1168:C:O2'	38:A:5850:HOH:O	2.18	0.56
1:A:195:C:C2'	1:A:196:G:H5'	2.35	0.56
11:J:3:GLY:HA2	11:J:57:ARG:HH12	1.71	0.56
12:K:79:PHE:O	12:K:83:ILE:HG13	2.06	0.56
38:A:3943:HOH:O	15:N:146:GLN:HG2	2.05	0.56
16:O:87:LEU:CD1	16:O:186:LEU:HD21	2.32	0.56
1:A:1717:A:H5''	18:Q:54:LYS:HB2	1.87	0.56
1:A:113:A:OP2	1:A:114:A:H5''	2.06	0.56
4:C:199:HIS:CD2	4:C:201:PHE:HB2	2.41	0.56
5:D:254:GLN:HG2	5:D:255:GLY:N	2.21	0.56
5:D:336:GLN:NE2	38:D:8526:HOH:O	2.38	0.56
12:K:19:MET:HE3	12:K:132:LEU:HD11	1.87	0.56
16:O:141:ARG:HB3	38:O:8566:HOH:O	2.06	0.56
18:Q:120:ARG:NH2	18:Q:123:TYR:CD2	2.74	0.56
18:Q:16:VAL:CG1	18:Q:17:GLY:N	2.69	0.56
23:V:6:CYS:CA	23:V:13:ILE:HD11	2.34	0.56
26:Y:9:VAL:HG22	26:Y:88:GLU:OE2	2.05	0.56
1:A:1118:A:H8	1:A:1119:G:H5''	1.71	0.55
1:A:1127:C:C2'	1:A:1128:U:H5'	2.36	0.55
1:A:2124:G:H2'	1:A:2125:G:C8	2.41	0.55
1:A:2612:A:H4'	38:A:3180:HOH:O	2.06	0.55
1:A:299:U:H5'	38:A:6805:HOH:O	2.05	0.55
1:A:201:G:N2	35:A:8505:CL:CL	2.72	0.55
5:D:55:ASN:HB3	5:D:64:GLY:H	1.72	0.55
1:A:218:C:P	31:4:39:GLN:NE2	2.79	0.55
1:A:1330:A:H5''	1:A:1331:A:OP2	2.05	0.55
1:A:776:A:OP1	29:2:28:HIS:HE1	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3025:G:C3'	2:B:3026:C:H5'	2.32	0.55
16:O:141:ARG:N	38:O:8566:HOH:O	2.38	0.55
16:O:71:TRP:N	38:O:8537:HOH:O	2.38	0.55
22:U:72:ILE:HD13	22:U:93:THR:HG22	1.88	0.55
1:A:2453:G:H4'	14:M:50:GLY:C	2.27	0.55
1:A:545:G:C8	1:A:545:G:H5'	2.34	0.55
1:A:876:A:H2'	1:A:876:A:N3	2.21	0.55
5:D:49:THR:HG21	5:D:280:VAL:CG2	2.36	0.55
7:F:10:PHE:CG	7:F:11:HIS:N	2.74	0.55
13:L:62:PRO:HG3	13:L:65:ARG:HH21	1.72	0.55
15:N:37:VAL:HG21	15:N:108:LYS:HG3	1.87	0.55
27:Z:126:PRO:HG2	27:Z:128:PHE:CZ	2.42	0.55
1:A:1116:U:O2'	1:A:1118:A:C2	2.50	0.55
5:D:7:ARG:HH11	5:D:7:ARG:CG	2.20	0.55
6:E:49:ASP:HB3	6:E:52:ALA:HB2	1.87	0.55
31:4:24:LYS:HE2	35:4:8504:CL:CL	2.42	0.55
3:5:75:C:N4	36:5:76:PPU:H102	2.22	0.55
1:A:1134:G:H4'	11:J:151:MET:CE	2.29	0.55
1:A:1331:A:OP2	27:Z:142:SER:OG	2.25	0.55
1:A:1379:A:H3'	38:A:8730:HOH:O	2.05	0.55
1:A:2346:C:H6	1:A:2346:C:O5'	1.90	0.55
8:G:81:GLU:HA	8:G:133:VAL:O	2.07	0.55
9:H:34:ASN:O	9:H:38:LYS:HG3	2.06	0.55
17:P:45:LEU:CD1	17:P:88:LYS:HD2	2.37	0.55
38:A:8836:HOH:O	25:X:9:GLY:HA3	2.05	0.55
27:Z:130:ARG:HD2	38:Z:8554:HOH:O	2.07	0.55
31:4:31:THR:HB	31:4:33:MET:HE3	1.85	0.55
1:A:1191:A:H3'	1:A:1192:A:C5'	2.35	0.55
7:F:69:ILE:O	7:F:69:ILE:HG22	2.07	0.55
8:G:114:ARG:HB3	8:G:151:LEU:HD11	1.89	0.55
11:J:149:ALA:C	11:J:151:MET:H	2.08	0.55
14:M:77:ALA:HB3	38:M:8403:HOH:O	2.06	0.55
1:A:240:C:C5'	15:N:146:GLN:NE2	2.70	0.55
1:A:2421:G:H1'	38:A:6491:HOH:O	2.05	0.55
1:A:721:A:H2'	1:A:722:G:H5'	1.87	0.55
7:F:23:VAL:HG12	7:F:130:VAL:HG22	1.87	0.55
7:F:58:VAL:HG12	7:F:59:GLY:N	2.22	0.55
38:A:4026:HOH:O	11:J:151:MET:HE2	2.06	0.55
13:L:40:THR:O	13:L:41:LYS:C	2.45	0.55
16:O:143:ARG:NH1	16:O:173:ASP:OD2	2.37	0.55
16:O:73:ALA:HB1	16:O:74:PRO:CD	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1395:C:H2'	1:A:1396:C:H6	1.72	0.55
1:A:2100:A:H5'	38:E:8461:HOH:O	2.07	0.55
4:C:105:VAL:HG12	4:C:106:CYS:H	1.72	0.55
5:D:258:GLY:H	5:D:260:HIS:HE1	1.51	0.55
6:E:142:ASP:OD1	6:E:237:GLU:HB3	2.07	0.55
14:M:104:ASP:O	14:M:105:TYR:HB3	2.07	0.55
18:Q:134:VAL:O	18:Q:137:LEU:HB3	2.07	0.55
38:A:3782:HOH:O	27:Z:208:LYS:HD2	2.06	0.55
1:A:2385:G:H2'	1:A:2386:U:H6	1.72	0.55
4:C:168:PRO:O	4:C:170:VAL:HG23	2.06	0.55
5:D:85:ARG:NH1	38:D:8642:HOH:O	2.40	0.55
7:F:169:THR:C	7:F:170:TYR:HD1	2.10	0.55
18:Q:41:ARG:O	18:Q:44:VAL:HB	2.07	0.55
20:S:132:ARG:CZ	38:S:8582:HOH:O	2.54	0.55
20:S:132:ARG:HG2	20:S:133:ALA:N	2.22	0.55
20:S:39:THR:CG2	20:S:42:GLU:HG3	2.36	0.55
27:Z:145:LYS:NZ	38:Z:8570:HOH:O	2.35	0.55
1:A:1589:G:H22	1:A:1605:G:H1'	1.70	0.55
1:A:1942:A:H3'	38:A:6813:HOH:O	2.07	0.55
1:A:2301:A:H5''	1:A:2302:A:H5'	1.89	0.55
1:A:283:U:H5''	1:A:284:C:OP2	2.07	0.55
1:A:332:G:H4'	22:U:2:LYS:O	2.07	0.55
4:C:170:VAL:HG11	28:1:14:PHE:CZ	2.42	0.55
6:E:233:THR:HG22	6:E:234:VAL:N	2.22	0.55
17:P:4:ASN:HB3	17:P:7:LEU:HB3	1.87	0.55
38:A:3481:HOH:O	22:U:82:THR:HA	2.07	0.55
25:X:80:ASP:O	25:X:84:VAL:HG23	2.07	0.55
26:Y:75:ALA:O	26:Y:83:ALA:HA	2.07	0.55
27:Z:189:ASN:ND2	27:Z:192:ASP:H	2.05	0.55
28:1:13:ARG:NH1	38:1:8418:HOH:O	2.40	0.54
31:4:60:LYS:CG	31:4:61:PRO:HD2	2.37	0.54
1:A:1269:G:H2'	1:A:1270:U:C6	2.42	0.54
1:A:1641:A:C2'	1:A:1642:A:H5'	2.37	0.54
1:A:2276:U:H2'	1:A:2277:U:C6	2.42	0.54
1:A:245:C:C2'	1:A:246:G:H5'	2.37	0.54
1:A:295:C:O2'	1:A:296:G:H5'	2.07	0.54
5:D:62:ARG:CA	5:D:65:MET:HE3	2.36	0.54
7:F:55:LYS:HA	38:F:6752:HOH:O	2.06	0.54
9:H:36:THR:HG23	9:H:97:ALA:HB2	1.89	0.54
13:L:87:ARG:CZ	38:L:4854:HOH:O	2.55	0.54
15:N:46:LEU:HB2	38:N:8601:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:119:GLN:O	16:O:123:ILE:HG13	2.06	0.54
2:B:3006:C:OP1	16:O:37:ARG:NH1	2.40	0.54
25:X:73:LEU:O	25:X:74:GLU:HG3	2.07	0.54
29:2:20:ARG:HB2	38:2:513:HOH:O	2.05	0.54
1:A:1321:A:N3	38:A:9722:HOH:O	2.33	0.54
1:A:2421:G:H4'	38:A:4264:HOH:O	2.06	0.54
1:A:2763:G:H5'	38:A:8916:HOH:O	2.07	0.54
1:A:558:C:C2'	1:A:559:U:H5''	2.37	0.54
9:H:101:ALA:HB2	9:H:108:LEU:CD2	2.37	0.54
11:J:83:PHE:HZ	11:J:146:TRP:HE1	1.55	0.54
17:P:21:SER:OG	17:P:106:PRO:HB2	2.07	0.54
20:S:34:GLU:OE1	20:S:34:GLU:HA	2.07	0.54
5:D:329:TYR:CE2	23:V:15:PRO:HG2	2.42	0.54
24:W:49:LEU:O	24:W:53:ILE:HG13	2.07	0.54
25:X:88:THR:HG23	25:X:110:GLN:HB3	1.88	0.54
28:1:53:GLY:HA2	28:1:67:GLY:O	2.07	0.54
1:A:1165:G:O2'	1:A:1166:A:OP1	2.23	0.54
1:A:1783:A:O2'	1:A:1784:U:H5'	2.07	0.54
1:A:1804:A:H2'	1:A:1805:G:H8	1.71	0.54
1:A:2011:A:H4'	1:A:2012:U:O5'	2.08	0.54
1:A:2765:C:H2'	1:A:2766:A:H8	1.71	0.54
1:A:714:U:H3'	38:A:6414:HOH:O	2.08	0.54
1:A:78:G:C6	1:A:79:G:C6	2.96	0.54
4:C:105:VAL:CG1	4:C:106:CYS:N	2.70	0.54
11:J:139:ASP:N	11:J:140:PRO:CD	2.69	0.54
11:J:58:HIS:HA	11:J:61:LEU:HD23	1.89	0.54
22:U:25:ALA:O	22:U:39:ASN:CB	2.55	0.54
24:W:64:GLY:O	24:W:65:ASP:HB2	2.07	0.54
26:Y:61:ARG:HH12	26:Y:67:PRO:HD3	1.71	0.54
1:A:1803:C:O2'	1:A:1804:A:H5'	2.06	0.54
2:B:3076:G:C3'	2:B:3077:A:H5''	2.32	0.54
2:B:3096:C:H2'	2:B:3097:U:C6	2.43	0.54
1:A:2338:G:P	7:F:97:GLN:HG3	2.48	0.54
13:L:74:VAL:HG11	13:L:113:ILE:HG12	1.88	0.54
38:A:8540:HOH:O	29:2:15:THR:HG21	2.08	0.54
31:4:38:ARG:O	31:4:42:ARG:HB2	2.08	0.54
1:A:1308:A:O4'	6:E:226:GLY:HA3	2.07	0.54
1:A:1855:G:H8	4:C:144:GLU:OE2	1.90	0.54
1:A:2252:A:C6	1:A:2253:G:H1'	2.41	0.54
8:G:23:GLU:HG2	8:G:28:SER:CB	2.38	0.54
1:A:2044:G:OP1	26:Y:23:HIS:HE1	1.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:36:HIS:CE1	26:Y:40:HIS:CD2	2.96	0.54
29:2:22:CYS:HB2	38:2:1159:HOH:O	2.08	0.54
1:A:1181:A:N1	1:A:1192:A:O2'	2.40	0.54
1:A:2415:A:C2'	1:A:2416:G:H5'	2.38	0.54
12:K:131:THR:HB	12:K:134:GLU:HG3	1.89	0.54
13:L:75:ARG:CZ	38:L:4172:HOH:O	2.55	0.54
15:N:162:GLY:HA2	38:N:8520:HOH:O	2.07	0.54
15:N:45:ARG:CZ	15:N:48:ARG:HG3	2.37	0.54
24:W:39:ALA:N	24:W:40:PRO:CD	2.71	0.54
1:A:920:C:H5''	1:A:921:G:O5'	2.07	0.54
6:E:138:VAL:O	6:E:234:VAL:HA	2.08	0.54
7:F:163:VAL:HA	38:F:6326:HOH:O	2.08	0.54
11:J:118:PRO:HD2	38:J:8327:HOH:O	2.07	0.54
1:A:2502:C:C4'	11:J:151:MET:HG2	2.37	0.54
20:S:8:ALA:CB	20:S:13:THR:HG21	2.29	0.54
21:T:11:THR:H	21:T:14:ALA:HB3	1.71	0.54
26:Y:27:ASP:OD2	26:Y:27:ASP:N	2.40	0.54
1:A:1687:C:O2	29:2:9:GLY:HA2	2.07	0.54
1:A:2442:G:H3'	38:A:6100:HOH:O	2.07	0.54
1:A:2745:C:H5	38:A:5370:HOH:O	1.90	0.54
1:A:485:A:O2'	1:A:487:G:H5'	2.07	0.54
2:B:3040:C:N4	7:F:51:ARG:HB2	2.22	0.54
5:D:202:VAL:HG11	5:D:301:VAL:HG13	1.88	0.54
1:A:2547:C:OP2	5:D:5:ARG:NH1	2.41	0.54
7:F:94:ALA:O	7:F:95:THR:O	2.25	0.54
16:O:47:LEU:HD13	16:O:97:VAL:HG11	1.88	0.54
19:R:32:GLU:O	19:R:93:ARG:NH2	2.41	0.54
27:Z:117:LEU:HD12	27:Z:174:VAL:HG11	1.90	0.54
1:A:1058:A:H2'	1:A:1060:C:H5''	1.89	0.54
1:A:1060:C:H6	1:A:1060:C:H5'	1.73	0.54
1:A:1752:G:H2'	38:A:7018:HOH:O	2.07	0.54
1:A:2408:A:H2	38:4:8518:HOH:O	1.90	0.54
1:A:2769:C:O2'	1:A:2770:G:H5'	2.08	0.54
5:D:81:ALA:HB1	5:D:142:LEU:HD13	1.90	0.54
14:M:146:GLY:C	14:M:148:GLU:H	2.12	0.54
1:A:840:U:H2'	20:S:128:ARG:NH1	2.23	0.54
8:G:125:GLU:O	8:G:132:THR:HG22	2.08	0.54
11:J:53:PRO:HG3	11:J:127:GLY:H	1.73	0.54
17:P:106:PRO:HG2	17:P:107:GLU:OE1	2.08	0.54
18:Q:103:THR:HB	38:Q:4563:HOH:O	2.08	0.54
22:U:41:ARG:HG2	22:U:41:ARG:HH11	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:14:HIS:HA	38:X:2978:HOH:O	2.07	0.54
27:Z:106:THR:HG23	27:Z:107:PRO:HD2	1.90	0.54
1:A:10:U:H3'	38:A:9833:HOH:O	2.08	0.53
1:A:1972:U:H2'	1:A:1973:A:H5'	1.90	0.53
1:A:2501:G:H1'	38:A:4026:HOH:O	2.08	0.53
1:A:706:G:HO2'	1:A:707:C:H6	1.55	0.53
1:A:830:G:H2'	1:A:831:U:C6	2.43	0.53
4:C:153:ARG:CB	4:C:153:ARG:HH11	2.20	0.53
5:D:43:GLY:O	5:D:308:LEU:HD12	2.07	0.53
7:F:16:PRO:HB2	7:F:165:PHE:CG	2.43	0.53
9:H:46:GLU:OE1	9:H:100:ASP:HA	2.08	0.53
9:H:99:THR:HG23	9:H:99:THR:O	2.07	0.53
18:Q:103:THR:O	18:Q:107:GLU:HG3	2.08	0.53
18:Q:13:VAL:HG21	18:Q:41:ARG:HG2	1.89	0.53
22:U:40:VAL:HG23	22:U:119:ALA:C	2.28	0.53
1:A:1187:U:H5''	38:A:5672:HOH:O	2.07	0.53
1:A:1594:C:O2'	1:A:1607:A:H4'	2.08	0.53
1:A:1787:C:H4'	1:A:2883:A:O4'	2.09	0.53
1:A:2729:C:O2'	1:A:2730:G:H5'	2.08	0.53
1:A:514:G:O5'	1:A:514:G:C8	2.61	0.53
6:E:22:PHE:HA	6:E:116:ALA:HA	1.90	0.53
15:N:46:LEU:HD22	15:N:50:ARG:HG3	1.90	0.53
31:4:11:CYS:HB2	31:4:20:HIS:HE1	1.72	0.53
1:A:1423:C:O2'	1:A:1424:A:H5'	2.07	0.53
1:A:2272:G:H5''	38:C:8519:HOH:O	2.08	0.53
1:A:245:C:H2'	1:A:246:G:H5'	1.90	0.53
1:A:646:G:H2'	1:A:647:U:C6	2.44	0.53
1:A:67:A:H5''	1:A:69:A:C8	2.43	0.53
5:D:175:LEU:C	5:D:175:LEU:CD2	2.76	0.53
38:A:6925:HOH:O	6:E:188:ARG:HD2	2.08	0.53
7:F:45:THR:CG2	7:F:75:LEU:HD11	2.38	0.53
20:S:106:GLY:HA2	20:S:109:MET:CE	2.38	0.53
24:W:58:THR:O	24:W:62:GLU:HG3	2.08	0.53
25:X:90:TYR:CD1	25:X:90:TYR:N	2.75	0.53
1:A:1086:A:C6	25:X:11:VAL:HG11	2.42	0.53
1:A:1305:C:H5'	38:A:9338:HOH:O	2.09	0.53
1:A:1484:G:H2'	38:A:8623:HOH:O	2.08	0.53
1:A:1552:G:H2'	1:A:1553:C:C6	2.42	0.53
1:A:1589:G:C2	1:A:1605:G:N3	2.77	0.53
1:A:2263:G:H5'	38:N:8617:HOH:O	2.07	0.53
1:A:820:G:O2'	1:A:856:G:H4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:145:ALA:HB1	8:G:168:ILE:HD11	1.89	0.53
8:G:31:ARG:HH12	8:G:68:HIS:CE1	2.27	0.53
12:K:45:VAL:HG21	12:K:129:PHE:CD1	2.43	0.53
16:O:139:TRP:O	16:O:142:THR:HB	2.09	0.53
16:O:82:TYR:HD2	16:O:83:LEU:N	2.06	0.53
25:X:72:PRO:O	25:X:74:GLU:N	2.42	0.53
27:Z:131:GLN:HB3	27:Z:153:GLN:OE1	2.07	0.53
1:A:111:C:O2'	1:A:112:G:H5'	2.09	0.53
1:A:1161:A:O5'	1:A:1161:A:C8	2.60	0.53
1:A:1209:C:C2	1:A:1210:G:C8	2.96	0.53
1:A:1730:G:H5'	1:A:1731:C:C5	2.44	0.53
2:B:3031:C:H2'	2:B:3032:G:O4'	2.08	0.53
4:C:29:HIS:CE1	4:C:107:ASN:ND2	2.77	0.53
5:D:41:PHE:HB3	5:D:190:MET:HE3	1.89	0.53
6:E:141:SER:HA	38:E:8380:HOH:O	2.07	0.53
10:I:12:ILE:N	10:I:13:PRO:CD	2.72	0.53
1:A:902:G:N7	14:M:18:HIS:HD2	2.07	0.53
15:N:89:ASN:HA	38:N:8549:HOH:O	2.07	0.53
16:O:48:VAL:HG11	16:O:55:ASP:HB3	1.90	0.53
20:S:4:TYR:HA	20:S:144:GLU:OE2	2.09	0.53
20:S:91:LEU:HD21	20:S:145:LEU:HB2	1.90	0.53
25:X:38:THR:HG22	38:X:3580:HOH:O	2.09	0.53
1:A:751:U:H5''	6:E:100:LEU:HD22	1.90	0.53
6:E:133:ARG:HD2	38:E:8409:HOH:O	2.08	0.53
6:E:196:THR:HG23	38:E:8399:HOH:O	2.09	0.53
7:F:101:THR:HG22	38:F:7400:HOH:O	2.08	0.53
11:J:111:MET:O	11:J:114:PRO:HD3	2.08	0.53
11:J:85:ILE:HB	11:J:132:PHE:CE2	2.43	0.53
13:L:1:MET:HE1	38:L:6646:HOH:O	2.07	0.53
13:L:37:TYR:HE2	13:L:45:PRO:HA	1.72	0.53
15:N:77:PHE:CE2	15:N:86:MET:HG2	2.43	0.53
16:O:15:GLU:HB2	16:O:17:ARG:HG3	1.90	0.53
16:O:75:THR:HA	16:O:80:SER:OG	2.08	0.53
1:A:1834:C:H2'	1:A:1840:A:N6	2.24	0.53
1:A:515:C:H3'	38:A:5127:HOH:O	2.09	0.53
1:A:695:C:H2'	1:A:696:C:C6	2.44	0.53
1:A:932:U:H2'	1:A:933:C:C6	2.44	0.53
1:A:945:U:H2'	1:A:946:C:H6	1.74	0.53
2:B:3035:C:H5''	38:B:8458:HOH:O	2.06	0.53
5:D:177:HIS:O	5:D:181:ILE:HG13	2.09	0.53
11:J:26:LYS:HD2	11:J:28:ILE:HB	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1890:U:H4'	1:A:2010:A:C6	2.44	0.53
1:A:204:A:C2'	1:A:205:U:H5'	2.39	0.53
1:A:2607:U:O5'	1:A:2609:G:H4'	2.08	0.53
2:B:3013:A:O2'	2:B:3014:G:H5''	2.08	0.53
7:F:84:LEU:C	7:F:86:THR:H	2.12	0.53
9:H:33:THR:HG21	9:H:59:ILE:O	2.09	0.53
18:Q:59:ARG:NH2	18:Q:66:GLN:HE22	2.05	0.53
38:A:7053:HOH:O	28:1:31:ILE:HG13	2.08	0.53
1:A:1462:C:H2'	1:A:1463:A:C8	2.44	0.53
1:A:1516:C:H2'	1:A:1517:U:C6	2.44	0.53
6:E:127:ARG:HG2	6:E:127:ARG:NH1	2.22	0.53
1:A:1007:A:H2'	11:J:19:TYR:CZ	2.44	0.53
38:A:7151:HOH:O	15:N:154:ARG:HB2	2.08	0.53
38:A:8917:HOH:O	15:N:52:LEU:HD23	2.08	0.53
22:U:20:HIS:HB3	22:U:41:ARG:HD2	1.91	0.53
28:1:19:GLY:O	28:1:23:ARG:HG2	2.09	0.53
1:A:2001:G:O2'	1:A:2002:C:H5'	2.09	0.53
1:A:1930:A:H1'	1:A:2128:G:H5'	1.91	0.53
1:A:2281:C:H2'	1:A:2282:U:H5'	1.89	0.53
1:A:2379:G:H4'	1:A:2380:A:H5''	1.91	0.53
1:A:666:A:H2'	1:A:667:C:O4'	2.09	0.53
6:E:156:LEU:HD12	6:E:156:LEU:O	2.08	0.53
8:G:11:VAL:HG11	8:G:22:VAL:CG1	2.39	0.53
9:H:99:THR:O	9:H:100:ASP:HB2	2.08	0.53
12:K:19:MET:HE2	12:K:79:PHE:CA	2.35	0.53
1:A:2815:G:OP2	12:K:99:GLU:HG2	2.10	0.53
16:O:114:LYS:O	16:O:118:ILE:HG13	2.08	0.53
22:U:25:ALA:O	22:U:39:ASN:HB2	2.09	0.53
25:X:130:HIS:O	25:X:136:GLY:HA3	2.09	0.53
1:A:1269:G:H2'	1:A:1270:U:H6	1.74	0.52
1:A:1029:U:O2'	1:A:1273:C:OP1	2.25	0.52
1:A:1908:G:N1	1:A:1930:A:OP2	2.39	0.52
1:A:2755:G:H1'	38:A:4163:HOH:O	2.09	0.52
1:A:431:G:P	15:N:48:ARG:HH12	2.31	0.52
4:C:93:THR:C	4:C:94:LEU:HD23	2.28	0.52
5:D:232:TRP:CD1	5:D:235:ARG:HD2	2.44	0.52
8:G:7:ILE:CG2	8:G:45:ASP:O	2.56	0.52
12:K:59:LYS:O	12:K:63:ILE:HG13	2.08	0.52
13:L:18:ILE:HG22	13:L:93:ASN:HB2	1.91	0.52
17:P:106:PRO:HG2	17:P:107:GLU:CD	2.28	0.52
1:A:21:G:H5''	20:S:1:GLY:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:C:H2'	1:A:669:G:H8	1.73	0.52
7:F:153:THR:HG22	38:F:5234:HOH:O	2.09	0.52
8:G:146:ALA:O	8:G:150:GLN:HG2	2.10	0.52
12:K:60:ARG:HA	12:K:63:ILE:HD12	1.90	0.52
16:O:86:LEU:HD12	16:O:125:ALA:CB	2.33	0.52
17:P:107:GLU:CD	17:P:107:GLU:N	2.63	0.52
18:Q:50:GLN:HB3	38:Q:5440:HOH:O	2.09	0.52
20:S:18:LEU:HB2	20:S:143:VAL:HG13	1.91	0.52
1:A:2316:G:H8	38:A:5135:HOH:O	1.91	0.52
4:C:51:ARG:NH2	38:C:8555:HOH:O	2.43	0.52
5:D:87:TYR:OH	5:D:163:GLU:OE2	2.15	0.52
6:E:156:LEU:HD11	6:E:160:LEU:HD11	1.92	0.52
11:J:139:ASP:HA	38:J:8359:HOH:O	2.08	0.52
13:L:29:LEU:HB3	13:L:55:VAL:CG1	2.33	0.52
25:X:6:GLN:HA	25:X:52:VAL:HG23	1.90	0.52
1:A:2904:U:H4'	26:Y:8:ARG:NH1	2.24	0.52
1:A:1377:C:C6	1:A:1377:C:H5'	2.38	0.52
1:A:2433:A:H2	38:A:7393:HOH:O	1.92	0.52
1:A:2768:A:H3'	38:A:3906:HOH:O	2.09	0.52
1:A:2270:G:H4'	4:C:223:ARG:HH12	1.74	0.52
5:D:304:PRO:HD2	5:D:307:ARG:HD2	1.91	0.52
17:P:21:SER:HB3	17:P:106:PRO:O	2.09	0.52
19:R:42:LYS:NZ	19:R:43:ILE:O	2.36	0.52
20:S:82:GLU:O	20:S:86:LYS:HG3	2.09	0.52
21:T:22:ASN:HD21	21:T:68:LEU:HB2	1.75	0.52
25:X:60:GLU:O	25:X:63:GLU:HB2	2.09	0.52
28:1:39:CYS:HB2	28:1:57:CYS:SG	2.50	0.52
1:A:1555:G:H4'	1:A:1630:A:H2	1.74	0.52
1:A:256:C:H2'	1:A:257:G:O4'	2.10	0.52
1:A:2691:A:OP1	1:A:2691:A:H8	1.92	0.52
1:A:668:C:H2'	1:A:669:G:C8	2.44	0.52
2:B:3056:A:H2'	2:B:3057:A:C5'	2.25	0.52
5:D:51:VAL:HG23	5:D:329:TYR:O	2.09	0.52
6:E:84:VAL:O	6:E:85:LYS:HB2	2.09	0.52
10:I:69:ARG:NH1	38:I:3513:HOH:O	2.43	0.52
11:J:47:GLU:HB3	11:J:133:ILE:HD13	1.91	0.52
38:A:4456:HOH:O	11:J:57:ARG:HG3	2.09	0.52
14:M:90:ARG:HA	14:M:119:THR:HB	1.91	0.52
15:N:94:LYS:CE	38:N:8578:HOH:O	2.50	0.52
22:U:19:ARG:NH1	22:U:68:ASP:O	2.43	0.52
27:Z:154:ARG:NH1	27:Z:155:ARG:HG3	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1159:G:H1	1:A:1208:C:H42	1.56	0.52
4:C:164:ARG:NE	38:C:8602:HOH:O	2.43	0.52
1:A:2348:C:H5'	7:F:22:VAL:HG11	1.92	0.52
8:G:157:LYS:NZ	38:G:2401:HOH:O	2.42	0.52
12:K:126:ASN:HA	35:K:8501:CL:CL	2.47	0.52
23:V:6:CYS:SG	23:V:32:CYS:N	2.81	0.52
1:A:2389:U:OP1	19:R:82:LYS:NZ	2.38	0.52
1:A:2407:G:O2'	1:A:2408:A:H5'	2.10	0.52
1:A:2543:G:H2'	1:A:2544:G:O4'	2.09	0.52
1:A:840:U:H2'	20:S:128:ARG:HH12	1.74	0.52
2:B:3056:A:N1	7:F:13:MET:HE3	2.25	0.52
5:D:266:ASN:OD1	5:D:317:PRO:HA	2.10	0.52
11:J:47:GLU:OE2	11:J:162:SER:OG	2.28	0.52
1:A:1003:U:O2'	11:J:90:PHE:HE1	1.92	0.52
15:N:36:ALA:HB1	38:N:8546:HOH:O	2.09	0.52
20:S:39:THR:HG22	20:S:42:GLU:HG3	1.92	0.52
27:Z:187:VAL:HB	27:Z:203:VAL:CG2	2.40	0.52
1:A:1025:C:H5'	25:X:23:MET:O	2.10	0.52
1:A:1169:U:C5	1:A:1170:U:C4	2.98	0.52
1:A:1192:A:H3'	1:A:1193:A:H5'	1.92	0.52
1:A:1205:U:H2'	1:A:1206:U:H5'	1.91	0.52
1:A:1442:A:H1'	38:A:6486:HOH:O	2.09	0.52
1:A:1505:U:H6	1:A:1505:U:H5'	1.74	0.52
1:A:2466:G:H5''	38:A:3142:HOH:O	2.10	0.52
2:B:3023:U:C3'	2:B:3024:U:H5''	2.39	0.52
6:E:140:VAL:HB	38:E:8450:HOH:O	2.09	0.52
38:A:5805:HOH:O	7:F:55:LYS:HB2	2.10	0.52
13:L:86:THR:HG22	13:L:87:ARG:N	2.25	0.52
15:N:61:ILE:N	15:N:61:ILE:HD12	2.24	0.52
16:O:155:GLU:O	16:O:156:GLU:HG3	2.10	0.52
20:S:119:VAL:HG21	20:S:142:ASP:CG	2.30	0.52
22:U:101:LEU:HD13	22:U:112:LEU:HD11	1.91	0.52
1:A:1095:U:O2	25:X:120:PRO:HG2	2.10	0.52
26:Y:29:ALA:O	26:Y:32:LEU:N	2.42	0.52
27:Z:189:ASN:HD22	27:Z:189:ASN:C	2.13	0.52
28:I:50:ALA:HB3	28:I:54:ILE:HG22	1.92	0.52
21:T:58:MET:SD	30:3:8:LYS:HE3	2.50	0.52
1:A:1162:G:N3	1:A:1162:G:H2'	2.24	0.52
1:A:2121:G:O2'	31:4:47:GLY:HA2	2.10	0.52
1:A:407:A:H3'	38:A:3938:HOH:O	2.09	0.52
5:D:195:ARG:HD2	5:D:324:ASP:OD1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:82:VAL:HG12	5:D:82:VAL:O	2.10	0.52
8:G:15:GLN:HG3	8:G:20:ILE:CG1	2.34	0.52
11:J:48:LEU:CG	11:J:157:ILE:HG21	2.40	0.52
16:O:154:LEU:HD12	16:O:156:GLU:O	2.09	0.52
31:4:39:GLN:CA	31:4:42:ARG:NH2	2.73	0.52
1:A:1015:C:H2'	1:A:1016:U:H6	1.74	0.52
1:A:1422:U:H2'	1:A:1423:C:C6	2.45	0.52
1:A:1635:U:O2'	1:A:1636:G:H5'	2.10	0.52
1:A:2878:U:H2'	1:A:2879:A:O4'	2.09	0.52
5:D:41:PHE:HD2	5:D:190:MET:HE3	1.71	0.52
27:Z:117:LEU:HA	27:Z:174:VAL:HG11	1.91	0.52
1:A:1189:A:O2'	1:A:1208:C:H2'	2.10	0.51
1:A:1189:A:H1'	1:A:1209:C:H1'	1.92	0.51
1:A:2013:G:C2	1:A:2014:G:N7	2.78	0.51
1:A:853:C:H2'	1:A:854:G:O4'	2.10	0.51
1:A:945:U:H2'	1:A:946:C:C6	2.44	0.51
2:B:3057:A:H5'	2:B:3057:A:N3	2.25	0.51
5:D:79:MET:HE1	38:D:8631:HOH:O	2.09	0.51
6:E:25:PRO:HD2	38:E:8427:HOH:O	2.10	0.51
14:M:54:PRO:HG2	14:M:57:VAL:HG21	1.92	0.51
14:M:73:VAL:HG23	14:M:74:THR:H	1.75	0.51
17:P:7:LEU:HD22	38:P:5650:HOH:O	2.09	0.51
20:S:29:LYS:HD3	38:S:8540:HOH:O	2.09	0.51
20:S:39:THR:HB	20:S:42:GLU:OE1	2.10	0.51
24:W:64:GLY:O	24:W:65:ASP:CB	2.58	0.51
25:X:121:PRO:CA	25:X:153:MET:HG2	2.40	0.51
1:A:2432:C:O5'	1:A:2432:C:H6	1.93	0.51
2:B:3044:A:O4'	7:F:76:ARG:NE	2.44	0.51
7:F:86:THR:O	7:F:90:LEU:HG	2.11	0.51
10:I:12:ILE:HD12	38:I:692:HOH:O	2.09	0.51
26:Y:85:VAL:HG12	26:Y:86:GLU:N	2.24	0.51
1:A:1878:G:O2'	1:A:1879:U:C6	2.62	0.51
1:A:2467:A:H2'	38:A:4937:HOH:O	2.09	0.51
4:C:191:GLY:HA2	4:C:194:MET:HE3	1.90	0.51
7:F:70:GLY:N	38:F:5576:HOH:O	2.44	0.51
9:H:50:VAL:CG2	9:H:63:ILE:HG21	2.39	0.51
9:H:57:GLU:O	9:H:61:MET:HG3	2.10	0.51
12:K:107:ASN:ND2	12:K:109:TYR:H	2.09	0.51
16:O:69:TYR:HE2	16:O:183:ASP:OD2	1.93	0.51
18:Q:7:LYS:HD2	18:Q:21:VAL:HG21	1.93	0.51
28:I:49:ARG:HD2	38:I:8425:HOH:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1979:G:O2'	1:A:1980:U:OP1	2.24	0.51
1:A:2499:U:O2'	1:A:2500:C:H5'	2.09	0.51
1:A:810:G:H2'	1:A:811:C:C6	2.45	0.51
2:B:3055:U:H4'	2:B:3056:A:H8	1.75	0.51
4:C:192:VAL:O	4:C:192:VAL:HG12	2.11	0.51
7:F:57:THR:HG23	7:F:63:ILE:CG2	2.40	0.51
11:J:44:ALA:HB3	11:J:136:VAL:O	2.11	0.51
11:J:44:ALA:HA	11:J:163:PRO:O	2.10	0.51
15:N:155:HIS:CE1	15:N:158:ARG:HE	2.27	0.51
15:N:172:GLY:C	15:N:183:VAL:HG11	2.31	0.51
9:H:56:PRO:CG	15:N:44:THR:HA	2.40	0.51
18:Q:131:PHE:CD1	18:Q:137:LEU:HD13	2.45	0.51
1:A:1377:C:H1'	38:A:6740:HOH:O	2.11	0.51
1:A:1513:C:O2'	1:A:1514:C:H5'	2.10	0.51
1:A:24:G:N2	1:A:518:G:H1'	2.25	0.51
1:A:396:U:H2'	1:A:397:A:N7	2.26	0.51
2:B:3039:U:H3	2:B:3042:C:H5''	1.74	0.51
4:C:211:LYS:HB3	4:C:212:PRO:CD	2.32	0.51
1:A:474:C:O3'	6:E:73:LEU:HD21	2.10	0.51
6:E:95:GLU:H	6:E:95:GLU:CD	2.13	0.51
1:A:2346:C:O3'	7:F:52:THR:CG2	2.59	0.51
11:J:93:ILE:HG12	11:J:120:GLY:O	2.11	0.51
26:Y:22:ASN:O	26:Y:25:ARG:HG3	2.10	0.51
1:A:1235:G:C1'	12:K:63:ILE:HG23	2.41	0.51
1:A:2890:A:H2'	38:A:4674:HOH:O	2.10	0.51
1:A:371:U:H2'	1:A:372:A:H8	1.75	0.51
7:F:144:ARG:NH2	38:F:3839:HOH:O	2.38	0.51
7:F:64:ARG:O	7:F:67:ASP:OD2	2.28	0.51
9:H:104:ALA:O	9:H:108:LEU:HB3	2.10	0.51
16:O:184:ILE:HG22	16:O:185:GLU:HG3	1.92	0.51
22:U:49:GLU:OE2	22:U:97:ARG:HD2	2.11	0.51
25:X:122:ARG:NH2	38:X:4276:HOH:O	2.43	0.51
30:3:48:ASP:O	30:3:49:GLU:HB2	2.10	0.51
1:A:428:G:H5'	38:A:7116:HOH:O	2.11	0.51
4:C:149:ASP:OD1	4:C:151:GLN:HB2	2.11	0.51
7:F:52:THR:HG22	7:F:52:THR:O	2.09	0.51
11:J:31:PHE:HE2	11:J:87:LYS:O	1.93	0.51
38:A:4320:HOH:O	12:K:47:THR:HB	2.10	0.51
19:R:32:GLU:HA	19:R:71:TYR:OH	2.11	0.51
20:S:29:LYS:HD2	20:S:62:HIS:NE2	2.26	0.51
26:Y:43:VAL:HG12	26:Y:44:ASP:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:47:LEU:HA	28:1:56:MET:O	2.11	0.51
1:A:101:C:H2'	1:A:102:A:H8	1.75	0.51
1:A:2506:A:C1'	38:A:3244:HOH:O	2.57	0.51
1:A:2768:A:C2'	1:A:2769:C:O4'	2.58	0.51
2:B:3078:G:N2	2:B:3103:A:OP2	2.38	0.51
4:C:125:ASN:HB3	4:C:158:VAL:HG12	1.93	0.51
11:J:144:GLU:HG3	38:J:8333:HOH:O	2.10	0.51
11:J:154:THR:HB	11:J:155:PRO:HD3	1.93	0.51
16:O:104:ILE:O	16:O:107:ASN:HB2	2.11	0.51
24:W:50:ARG:HD3	38:W:2826:HOH:O	2.10	0.51
27:Z:115:ARG:NE	38:Z:8558:HOH:O	2.44	0.51
1:A:1657:A:H2'	1:A:1658:A:C8	2.45	0.51
1:A:1684:A:H1'	30:3:43:ARG:HH22	1.76	0.51
1:A:1805:G:H2'	1:A:1806:G:H8	1.76	0.51
1:A:2010:A:H2'	38:A:5444:HOH:O	2.11	0.51
1:A:2329:C:O2'	1:A:2330:U:H5'	2.11	0.51
1:A:2064:U:H5'	1:A:2652:U:O3'	2.11	0.51
1:A:2768:A:O2'	1:A:2769:C:H5'	2.11	0.51
1:A:514:G:OP1	1:A:514:G:H2'	2.11	0.51
2:B:3049:G:O2'	2:B:3050:G:H5'	2.11	0.51
4:C:153:ARG:HB2	4:C:153:ARG:NH1	2.24	0.51
7:F:57:THR:HG23	7:F:63:ILE:CB	2.40	0.51
15:N:99:ARG:CD	15:N:167:GLY:HA2	2.38	0.51
17:P:99:GLU:HG2	38:P:6044:HOH:O	2.10	0.51
20:S:17:MET:HE1	20:S:19:ARG:NH2	2.26	0.51
20:S:34:GLU:HG2	20:S:46:TYR:OH	2.10	0.51
25:X:4:LEU:HD22	25:X:52:VAL:HG21	1.92	0.51
26:Y:43:VAL:HG12	26:Y:44:ASP:N	2.25	0.51
1:A:2073:G:OP2	1:A:2490:A:H5'	2.11	0.51
1:A:2597:U:C2'	1:A:2598:U:H5'	2.40	0.51
1:A:282:C:H1'	1:A:368:C:H42	1.74	0.51
1:A:818:A:H5''	38:A:6062:HOH:O	2.10	0.51
2:B:3002:U:H4'	2:B:3002:U:OP2	2.11	0.51
6:E:16:VAL:HG12	6:E:17:ASP:H	1.75	0.51
1:A:450:C:H4'	6:E:46:TYR:CE1	2.46	0.51
7:F:93:LEU:HB2	38:F:5198:HOH:O	2.10	0.51
17:P:39:THR:O	17:P:115:ARG:NH2	2.44	0.51
38:A:6114:HOH:O	17:P:24:ALA:N	2.43	0.51
20:S:96:VAL:HG13	20:S:106:GLY:HA3	1.93	0.51
27:Z:200:THR:HG22	27:Z:201:GLU:HG2	1.92	0.51
1:A:1132:A:H2'	1:A:1133:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1209:C:O2'	1:A:1210:G:H5'	2.11	0.50
1:A:2437:A:H2'	1:A:2438:G:C8	2.46	0.50
1:A:544:G:H2'	1:A:545:G:C5'	2.41	0.50
2:B:3039:U:H1'	2:B:3044:A:N6	2.24	0.50
5:D:41:PHE:CE1	5:D:79:MET:HG3	2.45	0.50
7:F:40:ILE:HG23	38:F:5583:HOH:O	2.12	0.50
8:G:11:VAL:CG1	8:G:12:ASP:N	2.74	0.50
8:G:84:MET:HB2	8:G:131:LEU:HB2	1.92	0.50
14:M:22:ARG:HG2	38:M:8397:HOH:O	2.11	0.50
18:Q:27:ARG:HA	38:Q:3969:HOH:O	2.11	0.50
25:X:137:GLN:NE2	25:X:141:HIS:HE1	2.09	0.50
1:A:1180:U:H2'	1:A:1181:A:O4'	2.12	0.50
1:A:2039:A:H2'	1:A:2040:C:C6	2.46	0.50
1:A:2505:G:O2'	1:A:2506:A:H5'	2.11	0.50
2:B:3025:G:H5''	2:B:3026:C:C6	2.47	0.50
4:C:105:VAL:CG1	4:C:106:CYS:H	2.24	0.50
5:D:146:THR:C	5:D:148:PRO:HD3	2.31	0.50
6:E:194:PHE:HA	6:E:234:VAL:HG13	1.93	0.50
16:O:163:PHE:HA	38:O:8564:HOH:O	2.11	0.50
26:Y:18:ARG:HA	38:Y:5356:HOH:O	2.10	0.50
38:A:8694:HOH:O	31:4:48:ASN:HB2	2.11	0.50
1:A:2754:G:O2'	1:A:2755:G:H5'	2.11	0.50
1:A:559:U:H2'	1:A:560:C:O4'	2.11	0.50
5:D:132:HIS:CE1	5:D:171:VAL:HG21	2.46	0.50
6:E:233:THR:HG21	6:E:235:PHE:CE1	2.47	0.50
13:L:20:CYS:HB3	13:L:26:ALA:O	2.12	0.50
16:O:115:VAL:HG22	38:O:8551:HOH:O	2.10	0.50
16:O:120:GLU:HG3	16:O:136:LEU:HD13	1.92	0.50
1:A:1785:G:OP1	18:Q:76:GLY:HA3	2.11	0.50
1:A:1166:A:H2'	1:A:1166:A:N3	2.26	0.50
1:A:1666:C:C2'	1:A:1667:A:C5'	2.90	0.50
1:A:2456:A:H5'	38:A:5177:HOH:O	2.11	0.50
1:A:285:A:H2'	1:A:286:U:O4'	2.11	0.50
1:A:518:G:H4'	38:A:5551:HOH:O	2.10	0.50
1:A:820:G:C6	4:C:171:LYS:HB2	2.46	0.50
1:A:825:U:H5''	1:A:826:U:OP1	2.11	0.50
1:A:952:G:OP1	19:R:42:LYS:HE2	2.11	0.50
4:C:190:ARG:NH2	4:C:207:GLN:OE1	2.45	0.50
1:A:1352:A:N1	6:E:48:SER:HB3	2.26	0.50
8:G:86:VAL:CG1	8:G:129:GLU:HA	2.42	0.50
16:O:35:VAL:HB	16:O:46:GLN:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:1:MET:N	25:X:103:GLU:OE2	2.39	0.50
4:C:55:VAL:CG1	4:C:67:LEU:HD22	2.40	0.50
20:S:39:THR:HB	20:S:42:GLU:CD	2.32	0.50
22:U:4:PRO:O	22:U:8:ARG:HG3	2.11	0.50
24:W:29:ASN:O	24:W:33:VAL:HG23	2.11	0.50
25:X:8:ARG:HD3	25:X:51:PHE:HA	1.94	0.50
1:A:1052:G:H2'	1:A:1052:G:N3	2.26	0.50
1:A:1666:C:H2'	1:A:1667:A:C5'	2.41	0.50
1:A:2115:U:H2'	1:A:2116:U:C6	2.47	0.50
1:A:960:G:N3	1:A:960:G:C2'	2.74	0.50
4:C:65:ARG:C	4:C:66:ARG:HG3	2.31	0.50
5:D:190:MET:HE2	5:D:194:PHE:HD1	1.75	0.50
1:A:2715:G:O2'	5:D:262:ARG:HD2	2.12	0.50
5:D:55:ASN:HB3	5:D:64:GLY:N	2.26	0.50
7:F:92:GLU:O	7:F:93:LEU:O	2.29	0.50
38:A:9955:HOH:O	12:K:46:ILE:HD12	2.11	0.50
15:N:169:ARG:HB3	38:N:8584:HOH:O	2.11	0.50
38:A:4213:HOH:O	16:O:21:HIS:HD2	1.94	0.50
22:U:37:GLN:OE1	22:U:118:SER:HA	2.12	0.50
30:3:9:LYS:O	30:3:12:ALA:HB3	2.11	0.50
30:3:36:ASN:O	30:3:39:ARG:HG3	2.12	0.50
31:4:7:PHE:CE2	31:4:22:VAL:CG2	2.93	0.50
31:4:91:GLN:O	31:4:92:GLU:HB2	2.11	0.50
1:A:1545:C:H2'	1:A:1546:G:O4'	2.12	0.50
1:A:2440:C:H5''	38:A:3313:HOH:O	2.12	0.50
1:A:2676:C:H4'	12:K:70:PHE:HE1	1.77	0.50
1:A:2869:G:H2'	1:A:2870:C:C6	2.46	0.50
1:A:530:C:H4'	1:A:612:U:H4'	1.92	0.50
5:D:54:VAL:O	5:D:55:ASN:C	2.49	0.50
7:F:25:MET:CE	7:F:37:ALA:HB1	2.38	0.50
11:J:48:LEU:CD1	11:J:157:ILE:HG21	2.42	0.50
12:K:42:GLU:HG3	12:K:145:TRP:CD1	2.47	0.50
16:O:37:ARG:CZ	38:O:8532:HOH:O	2.59	0.50
17:P:47:ARG:HG3	17:P:47:ARG:NH1	2.24	0.50
17:P:96:VAL:HA	38:P:4258:HOH:O	2.12	0.50
22:U:48:VAL:HG22	22:U:97:ARG:O	2.12	0.50
27:Z:112:GLU:HA	27:Z:112:GLU:OE1	2.12	0.50
28:1:11:THR:OG1	28:1:23:ARG:HB2	2.12	0.50
28:1:81:LYS:O	28:1:82:ALA:O	2.30	0.50
1:A:2348:C:C5'	7:F:22:VAL:HG21	2.42	0.50
1:A:2737:C:H3'	1:A:2738:G:H5''	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:512:G:O3'	1:A:513:A:H8	1.94	0.50
1:A:585:C:H5''	38:A:4353:HOH:O	2.10	0.50
1:A:602:A:O2'	1:A:605:C:H4'	2.12	0.50
1:A:832:U:H2'	1:A:833:G:C8	2.47	0.50
1:A:956:G:H5'	2:B:3081:C:H4'	1.94	0.50
5:D:49:THR:CG2	5:D:280:VAL:CG2	2.89	0.50
38:A:6925:HOH:O	6:E:188:ARG:CD	2.60	0.50
11:J:26:LYS:CD	11:J:28:ILE:HB	2.42	0.50
15:N:63:VAL:HG21	15:N:109:PHE:CZ	2.46	0.50
15:N:46:LEU:CD2	15:N:50:ARG:HG3	2.41	0.50
18:Q:7:LYS:HD2	18:Q:21:VAL:CG2	2.42	0.50
25:X:83:TRP:CZ3	25:X:112:LEU:HD21	2.46	0.50
28:1:30:GLU:HB2	38:1:8414:HOH:O	2.12	0.50
31:4:23:GLU:HG2	31:4:24:LYS:N	2.27	0.50
1:A:1629:G:N2	1:A:1632:A:OP2	2.43	0.50
1:A:1762:C:H4'	38:A:4135:HOH:O	2.12	0.50
1:A:177:A:H2'	1:A:178:U:O4'	2.12	0.50
1:A:1885:A:H2'	1:A:1886:A:H5'	1.94	0.50
1:A:2815:G:H2'	38:A:5199:HOH:O	2.12	0.50
1:A:283:U:H5	1:A:284:C:N4	2.10	0.50
1:A:860:U:H2'	1:A:861:A:C8	2.47	0.50
11:J:136:VAL:HG22	11:J:137:ASN:O	2.12	0.50
11:J:150:LYS:O	11:J:150:LYS:HG2	2.10	0.50
13:L:75:ARG:NH1	13:L:112:PRO:HD2	2.27	0.50
38:A:6763:HOH:O	15:N:152:ARG:HB3	2.12	0.50
16:O:182:GLY:O	16:O:183:ASP:O	2.30	0.50
16:O:43:VAL:HG11	16:O:81:ALA:HA	1.94	0.50
18:Q:38:GLU:HA	18:Q:41:ARG:HH11	1.77	0.50
19:R:35:ASP:HA	19:R:63:VAL:O	2.12	0.50
1:A:1086:A:N6	25:X:11:VAL:HG11	2.27	0.50
25:X:3:ALA:O	25:X:54:PHE:HA	2.12	0.50
1:A:621:C:H5'	27:Z:132:ASP:OD2	2.11	0.50
1:A:1139:U:H2'	1:A:1140:C:C6	2.47	0.49
1:A:1159:G:P	38:A:3777:HOH:O	2.69	0.49
1:A:1190:G:H5'	1:A:1208:C:O2'	2.12	0.49
1:A:1289:C:H3'	38:A:5891:HOH:O	2.11	0.49
1:A:1565:C:O4'	1:A:2738:G:H1'	2.12	0.49
1:A:2626:C:H2'	1:A:2627:G:C8	2.47	0.49
1:A:286:U:H2'	1:A:287:C:C6	2.46	0.49
1:A:832:U:H2'	1:A:833:G:H8	1.76	0.49
5:D:226:LYS:HG2	5:D:230:GLN:HE21	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:103:ASN:ND2	7:F:134:LEU:H	2.09	0.49
7:F:44:ILE:HG23	7:F:45:THR:HG23	1.93	0.49
9:H:28:ALA:HB3	9:H:99:THR:HG23	1.94	0.49
16:O:139:TRP:HA	16:O:139:TRP:CE3	2.47	0.49
1:A:962:C:C1'	16:O:5:ARG:NH1	2.65	0.49
18:Q:38:GLU:HA	18:Q:41:ARG:NH1	2.27	0.49
25:X:47:LYS:NZ	38:X:3920:HOH:O	2.26	0.49
28:1:58:GLY:HA3	38:1:8436:HOH:O	2.12	0.49
1:A:2719:A:H2'	1:A:2720:C:H5'	1.94	0.49
1:A:701:U:OP2	1:A:701:U:H2'	2.13	0.49
1:A:2672:C:P	5:D:25:ARG:HH11	2.35	0.49
5:D:315:VAL:HG23	5:D:316:ARG:HG2	1.93	0.49
15:N:32:ARG:NH2	38:N:8590:HOH:O	2.44	0.49
16:O:67:ALA:HA	16:O:71:TRP:HB3	1.94	0.49
21:T:80:ARG:NH1	38:T:8342:HOH:O	2.44	0.49
21:T:8:PRO:HD2	24:W:32:ALA:HA	1.94	0.49
22:U:53:GLY:HA3	38:U:6384:HOH:O	2.11	0.49
25:X:21:LEU:HD21	25:X:48:VAL:CG1	2.42	0.49
1:A:1986:G:H2'	1:A:1987:C:C6	2.47	0.49
1:A:2433:A:H4'	31:4:30:GLN:OE1	2.12	0.49
1:A:2064:U:H5'	1:A:2652:U:H4'	1.94	0.49
1:A:370:G:O2'	1:A:371:U:H5'	2.12	0.49
2:B:3108:C:O2'	2:B:3109:G:H5'	2.13	0.49
4:C:84:VAL:O	4:C:98:GLU:HG3	2.13	0.49
7:F:169:THR:O	7:F:170:TYR:HB2	2.12	0.49
9:H:63:ILE:HB	9:H:64:PRO:CD	2.39	0.49
11:J:45:GLN:HE21	11:J:135:TRP:HE1	1.58	0.49
14:M:93:VAL:HG21	14:M:122:ALA:HB2	1.94	0.49
15:N:48:ARG:NH1	15:N:52:LEU:HD21	2.26	0.49
17:P:54:GLU:O	17:P:55:ASP:HB2	2.12	0.49
21:T:81:ILE:HG12	38:T:8334:HOH:O	2.13	0.49
22:U:71:VAL:CG1	22:U:90:PRO:HB3	2.28	0.49
23:V:8:TYR:CD2	23:V:36:CYS:HB3	2.48	0.49
26:Y:71:ARG:HB2	38:Y:6590:HOH:O	2.12	0.49
28:1:11:THR:HG21	28:1:23:ARG:HB2	1.93	0.49
1:A:1416:G:H2'	1:A:1417:G:H5'	1.94	0.49
1:A:2125:G:O6	38:A:9913:HOH:O	2.20	0.49
1:A:2325:C:H2'	1:A:2326:U:C6	2.47	0.49
1:A:65:C:O2'	1:A:66:G:H5'	2.12	0.49
1:A:820:G:H5'	1:A:821:U:H5'	1.93	0.49
1:A:872:U:O2'	1:A:873:G:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3052:A:N7	38:B:8492:HOH:O	2.35	0.49
6:E:130:GLU:HA	6:E:130:GLU:OE1	2.13	0.49
8:G:69:ILE:HA	8:G:72:MET:CE	2.42	0.49
11:J:59:ASN:N	11:J:59:ASN:ND2	2.55	0.49
1:A:240:C:H5'	15:N:146:GLN:NE2	2.27	0.49
20:S:18:LEU:HG	20:S:91:LEU:HD13	1.94	0.49
27:Z:184:GLU:OE1	27:Z:204:ARG:NH1	2.45	0.49
1:A:100:C:H4'	22:U:16:LEU:HB2	1.95	0.49
1:A:107:U:C2'	1:A:108:U:H5'	2.43	0.49
1:A:1114:A:H2'	1:A:1115:U:H6	1.77	0.49
1:A:1166:A:H61	1:A:1180:U:H3	1.60	0.49
1:A:1512:G:N2	1:A:1513:C:H1'	2.26	0.49
1:A:2134:G:N2	1:A:2242:U:C2	2.81	0.49
1:A:2506:A:O2'	1:A:2507:G:O5'	2.30	0.49
1:A:2587:U:H2'	1:A:2589:U:H5''	1.94	0.49
1:A:677:C:O2'	1:A:678:G:H5'	2.13	0.49
1:A:87:C:H2'	30:3:28:LYS:O	2.13	0.49
4:C:188:ASN:HB3	38:C:8613:HOH:O	2.13	0.49
7:F:158:ASN:HB2	7:F:161:ASP:OD2	2.11	0.49
7:F:86:THR:HG23	38:F:7477:HOH:O	2.12	0.49
9:H:117:GLU:C	9:H:119:ARG:H	2.15	0.49
9:H:49:PHE:HE1	9:H:98:VAL:HG23	1.78	0.49
16:O:154:LEU:O	16:O:155:GLU:CB	2.61	0.49
18:Q:63:ARG:NH2	38:Q:5642:HOH:O	2.40	0.49
20:S:106:GLY:HA2	20:S:109:MET:HE3	1.95	0.49
31:4:34:LYS:HB2	31:4:37:ASP:OD2	2.13	0.49
1:A:1073:A:H1'	1:A:1088:A:C2	2.47	0.49
1:A:1209:C:O2	1:A:1210:G:C8	2.65	0.49
1:A:1918:U:OP2	38:A:3514:HOH:O	2.20	0.49
38:A:4838:HOH:O	4:C:215:ILE:HD12	2.12	0.49
5:D:223:ARG:O	5:D:228:ALA:HB2	2.13	0.49
8:G:45:ASP:OD2	8:G:46:THR:HG23	2.13	0.49
13:L:9:THR:HA	38:L:1611:HOH:O	2.11	0.49
1:A:1353:C:N3	14:M:5:LYS:NZ	2.60	0.49
15:N:137:ASP:HA	15:N:142:LYS:HE3	1.93	0.49
16:O:152:GLU:C	16:O:154:LEU:H	2.15	0.49
1:A:1787:C:OP1	18:Q:68:LYS:HE2	2.13	0.49
1:A:1118:A:C8	1:A:1118:A:C3'	2.90	0.49
1:A:1407:A:O2'	1:A:1408:U:H3'	2.13	0.49
1:A:1464:U:O2'	1:A:1465:A:H5'	2.13	0.49
1:A:1747:A:H1'	38:A:3600:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2124:G:H2'	1:A:2125:G:H8	1.77	0.49
1:A:2577:A:H5'	38:A:7221:HOH:O	2.12	0.49
1:A:281:U:O2'	1:A:282:C:H5'	2.12	0.49
5:D:148:PRO:HD2	38:D:8588:HOH:O	2.11	0.49
5:D:2:GLN:HA	38:D:8626:HOH:O	2.12	0.49
7:F:152:PRO:O	7:F:156:ARG:HG2	2.12	0.49
11:J:110:GLY:HA2	38:J:8379:HOH:O	2.12	0.49
1:A:2676:C:H4'	12:K:70:PHE:CE1	2.48	0.49
1:A:2860:G:H1'	38:A:6055:HOH:O	2.13	0.49
4:C:153:ARG:HD3	38:C:8534:HOH:O	2.12	0.49
8:G:126:ILE:HB	8:G:131:LEU:CD2	2.43	0.49
9:H:100:ASP:O	9:H:101:ALA:O	2.31	0.49
11:J:148:ARG:NE	38:J:8333:HOH:O	2.37	0.49
15:N:77:PHE:HD2	38:N:8528:HOH:O	1.96	0.49
19:R:66:LYS:HB2	19:R:70:ALA:O	2.13	0.49
20:S:39:THR:O	20:S:42:GLU:N	2.46	0.49
23:V:39:ASN:ND2	23:V:44:ARG:HH11	2.11	0.49
27:Z:189:ASN:HD22	27:Z:192:ASP:H	1.60	0.49
1:A:2382:A:C1'	31:4:10:TYR:CD2	2.95	0.49
1:A:1815:A:H4'	1:A:2751:C:O4'	2.13	0.49
1:A:338:C:H5''	38:A:5320:HOH:O	2.11	0.49
4:C:188:ASN:HA	38:C:8564:HOH:O	2.13	0.49
5:D:314:ALA:CB	5:D:317:PRO:HG3	2.43	0.49
1:A:2694:A:H4'	8:G:91:PHE:CE1	2.48	0.49
15:N:173:LEU:HD23	15:N:183:VAL:HG12	1.94	0.49
27:Z:187:VAL:HB	38:Z:8572:HOH:O	2.11	0.49
1:A:1186:C:N4	1:A:1187:U:C4	2.81	0.49
1:A:138:U:OP2	1:A:139:C:H5	1.96	0.49
1:A:292:G:H2'	1:A:358:G:N2	2.28	0.49
1:A:97:G:C2	22:U:107:LYS:HD2	2.48	0.49
4:C:69:LEU:HB3	38:C:8588:HOH:O	2.13	0.49
7:F:84:LEU:HA	7:F:87:ALA:HB3	1.94	0.49
9:H:32:GLY:N	38:H:3111:HOH:O	2.45	0.49
11:J:75:SER:HB3	11:J:79:ALA:HB1	1.94	0.49
14:M:35:ARG:HB2	14:M:43:HIS:CD2	2.47	0.49
38:A:5430:HOH:O	18:Q:87:ARG:HG2	2.13	0.49
38:A:9645:HOH:O	31:4:46:ILE:HG12	2.11	0.48
1:A:170:U:H5'	31:4:48:ASN:HB3	1.95	0.48
1:A:1123:A:N6	1:A:1238:C:H5'	2.28	0.48
1:A:2403:C:H2'	1:A:2404:G:O5'	2.12	0.48
1:A:696:C:O2'	1:A:697:G:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:690:G:H4'	1:A:741:C:O2	2.13	0.48
2:B:3023:U:H6	2:B:3023:U:C5'	2.26	0.48
2:B:3053:G:O2'	2:B:3054:A:H5'	2.13	0.48
5:D:141:ARG:HG2	5:D:165:ARG:HA	1.95	0.48
5:D:205:VAL:O	5:D:307:ARG:NE	2.45	0.48
5:D:24:PRO:HG2	5:D:204:GLY:HA2	1.95	0.48
6:E:197:SER:OG	6:E:242:GLU:OE2	2.28	0.48
8:G:5:LEU:HD21	8:G:66:GLN:HG3	1.93	0.48
11:J:72:VAL:HG11	11:J:81:TYR:CZ	2.48	0.48
12:K:45:VAL:HG22	12:K:46:ILE:N	2.28	0.48
1:A:2121:G:O2'	15:N:83:SER:HB2	2.13	0.48
25:X:14:HIS:HB2	25:X:17:ILE:HG13	1.94	0.48
1:A:1187:U:C3'	38:A:6366:HOH:O	2.61	0.48
1:A:1192:A:O2'	1:A:1193:A:OP1	2.31	0.48
1:A:1278:A:H4'	1:A:1279:U:C4	2.48	0.48
1:A:1477:C:O2'	1:A:1478:U:H5'	2.13	0.48
1:A:1852:A:H4'	4:C:230:SER:HB2	1.95	0.48
1:A:2492:U:H5	38:A:6490:HOH:O	1.95	0.48
1:A:2721:U:H4'	13:L:87:ARG:HG3	1.94	0.48
1:A:10:U:H1'	1:A:532:A:H62	1.78	0.48
1:A:585:C:H2'	1:A:586:C:C6	2.47	0.48
1:A:639:A:H2'	1:A:640:G:H8	1.73	0.48
1:A:734:U:O2'	1:A:737:A:N6	2.46	0.48
4:C:200:PRO:HG2	4:C:225:VAL:HG21	1.95	0.48
11:J:57:ARG:HG3	11:J:57:ARG:NH1	2.29	0.48
1:A:1244:U:OP1	12:K:18:ILE:HD13	2.13	0.48
13:L:118:ALA:HA	13:L:125:ALA:HB2	1.94	0.48
13:L:63:GLU:HG3	38:L:6344:HOH:O	2.12	0.48
14:M:133:VAL:HB	38:M:8433:HOH:O	2.12	0.48
15:N:14:ARG:CB	15:N:17:GLU:HG3	2.41	0.48
38:A:5966:HOH:O	15:N:189:VAL:HA	2.11	0.48
1:A:1396:C:H1'	18:Q:1:THR:O	2.13	0.48
1:A:1500:U:P	18:Q:41:ARG:HH22	2.36	0.48
25:X:11:VAL:O	25:X:12:ASN:HB2	2.13	0.48
25:X:52:VAL:HG13	25:X:53:ALA:N	2.27	0.48
31:4:55:VAL:HG22	38:4:8511:HOH:O	2.13	0.48
38:A:5527:HOH:O	31:4:62:THR:HB	2.13	0.48
1:A:1084:C:H6	1:A:1084:C:O5'	1.95	0.48
1:A:1743:G:H1'	38:A:4373:HOH:O	2.13	0.48
1:A:2084:C:H2'	1:A:2085:A:H8	1.78	0.48
4:C:105:VAL:HG11	4:C:154:ALA:CB	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1654:U:H2'	4:C:47:HIS:CD2	2.48	0.48
6:E:214:THR:HG23	38:E:8436:HOH:O	2.12	0.48
7:F:41:LEU:HA	7:F:44:ILE:HG22	1.95	0.48
11:J:46:VAL:HG12	11:J:146:TRP:HZ3	1.78	0.48
15:N:184:ARG:HB2	15:N:184:ARG:CZ	2.44	0.48
15:N:63:VAL:HG21	15:N:109:PHE:CE1	2.48	0.48
17:P:22:GLY:O	38:P:2823:HOH:O	2.20	0.48
1:A:710:G:P	17:P:24:ALA:HB3	2.53	0.48
25:X:122:ARG:HH22	25:X:154:ARG:C	2.16	0.48
25:X:19:ASP:O	25:X:23:MET:HG3	2.13	0.48
27:Z:186:ARG:NH1	27:Z:186:ARG:HG2	2.28	0.48
27:Z:187:VAL:HG23	27:Z:192:ASP:HB3	1.94	0.48
30:3:18:ASN:ND2	30:3:40:ARG:H	2.11	0.48
31:4:11:CYS:SG	31:4:71:CYS:HB2	2.53	0.48
1:A:2460:A:OP1	31:4:60:LYS:CB	2.62	0.48
1:A:412:C:O2'	1:A:413:G:H5'	2.14	0.48
1:A:481:U:H5'	38:A:5127:HOH:O	2.13	0.48
1:A:894:A:H1'	38:A:4712:HOH:O	2.13	0.48
2:B:3026:C:H1'	38:B:8421:HOH:O	2.12	0.48
5:D:41:PHE:CZ	5:D:79:MET:HG3	2.48	0.48
2:B:3056:A:C4	7:F:13:MET:HB3	2.49	0.48
11:J:26:LYS:HG2	11:J:28:ILE:N	2.27	0.48
18:Q:10:ALA:HA	18:Q:13:VAL:HG12	1.95	0.48
28:1:55:TRP:CZ2	28:1:70:GLN:C	2.87	0.48
1:A:1333:U:H2'	1:A:1334:C:H6	1.78	0.48
1:A:2346:C:H4'	7:F:52:THR:HG22	1.94	0.48
1:A:716:G:H2'	1:A:717:C:O5'	2.14	0.48
1:A:735:C:OP1	1:A:735:C:C6	2.66	0.48
2:B:3055:U:H4'	2:B:3056:A:C8	2.49	0.48
5:D:81:ALA:CB	5:D:142:LEU:HD13	2.43	0.48
5:D:82:VAL:HG12	5:D:101:TRP:CE3	2.49	0.48
6:E:103:ASN:HB2	6:E:106:GLU:HB2	1.96	0.48
6:E:12:THR:HB	38:E:8440:HOH:O	2.13	0.48
1:A:2338:G:OP1	7:F:97:GLN:HG3	2.12	0.48
15:N:37:VAL:HG21	15:N:108:LYS:CG	2.43	0.48
16:O:180:LEU:O	16:O:181:ASP:HB3	2.12	0.48
22:U:52:ARG:O	22:U:53:GLY:O	2.32	0.48
23:V:20:MET:HE1	38:V:7438:HOH:O	2.14	0.48
31:4:69:TYR:O	31:4:77:ALA:HA	2.13	0.48
1:A:101:C:H2'	1:A:102:A:C8	2.48	0.48
1:A:1555:G:H4'	1:A:1630:A:C2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1675:C:H3'	38:A:7279:HOH:O	2.12	0.48
1:A:1768:C:H2'	1:A:1769:C:O4'	2.12	0.48
1:A:1772:C:O4'	1:A:1773:G:C2	2.67	0.48
1:A:1873:G:H2'	1:A:1874:U:H5'	1.96	0.48
1:A:2638:G:H5'	38:A:4413:HOH:O	2.13	0.48
1:A:2737:C:H2'	38:A:5632:HOH:O	2.14	0.48
1:A:319:A:H4'	1:A:338:C:C4	2.49	0.48
4:C:135:VAL:N	38:C:8609:HOH:O	2.45	0.48
4:C:66:ARG:HB2	4:C:66:ARG:HH11	1.78	0.48
5:D:144:THR:CG2	5:D:145:HIS:N	2.77	0.48
5:D:305:ASP:O	5:D:306:LYS:HB2	2.14	0.48
6:E:153:VAL:O	6:E:157:LEU:HG	2.14	0.48
6:E:20:ASP:O	6:E:23:GLU:HB2	2.12	0.48
7:F:159:PRO:O	7:F:163:VAL:HG23	2.13	0.48
7:F:16:PRO:HB2	7:F:165:PHE:CD1	2.48	0.48
9:H:79:GLN:HB2	9:H:82:ASP:OD2	2.13	0.48
13:L:125:ALA:C	13:L:127:ALA:H	2.16	0.48
13:L:62:PRO:HG3	13:L:65:ARG:NH2	2.28	0.48
9:H:58:GLU:CD	15:N:27:ARG:HH22	2.15	0.48
15:N:48:ARG:NH2	38:N:8556:HOH:O	2.45	0.48
38:A:4225:HOH:O	16:O:21:HIS:HB2	2.14	0.48
38:A:3146:HOH:O	17:P:3:THR:HG21	2.12	0.48
22:U:45:GLY:HA3	22:U:102:ASP:CB	2.44	0.48
25:X:72:PRO:CG	25:X:77:ALA:HB3	2.32	0.48
26:Y:7:GLU:HA	26:Y:74:ALA:O	2.13	0.48
28:1:46:LYS:HB2	28:1:57:CYS:SG	2.53	0.48
1:A:1554:U:O2'	1:A:1631:A:N3	2.43	0.48
1:A:1741:U:O2'	1:A:2723:G:H4'	2.13	0.48
1:A:1878:G:C1'	38:A:5611:HOH:O	2.53	0.48
1:A:2106:C:H1'	1:A:2484:U:O2	2.14	0.48
1:A:2812:A:H1'	38:A:5270:HOH:O	2.13	0.48
1:A:2913:A:OP2	38:A:5856:HOH:O	2.20	0.48
4:C:48:ASP:HB3	38:C:8621:HOH:O	2.14	0.48
6:E:218:VAL:HG12	38:E:8422:HOH:O	2.13	0.48
6:E:5:ILE:HG23	38:E:8429:HOH:O	2.14	0.48
8:G:11:VAL:HG12	8:G:12:ASP:H	1.77	0.48
8:G:132:THR:HG23	8:G:132:THR:O	2.13	0.48
8:G:156:ASP:OD2	8:G:157:LYS:NZ	2.37	0.48
13:L:22:ASP:CG	13:L:24:THR:HG23	2.34	0.48
14:M:125:PHE:CZ	14:M:140:VAL:HG13	2.49	0.48
1:A:187:A:OP1	15:N:154:ARG:NE	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1483:C:O2'	1:A:1484:G:H5'	2.14	0.48
1:A:1598:A:N6	35:A:8515:CL:CL	2.84	0.48
1:A:2029:C:O2'	1:A:2030:A:H5'	2.14	0.48
1:A:2468:A:H61	31:4:48:ASN:HD21	1.62	0.48
1:A:2716:G:H5''	5:D:206:THR:CG2	2.32	0.48
9:H:58:GLU:HG3	9:H:61:MET:HE1	1.95	0.48
10:I:71:LEU:C	10:I:73:ASP:N	2.66	0.48
12:K:40:ASN:HA	12:K:106:GLY:H	1.79	0.48
13:L:28:GLU:HG2	13:L:58:THR:HB	1.94	0.48
1:A:2765:C:H2'	1:A:2766:A:C8	2.48	0.48
1:A:349:U:O2'	1:A:350:C:H5'	2.14	0.48
1:A:485:A:N3	1:A:487:G:H5''	2.29	0.48
1:A:539:G:H2'	1:A:540:A:C8	2.49	0.48
4:C:36:ASP:HB2	4:C:83:GLY:HA3	1.96	0.48
1:A:1874:U:P	4:C:51:ARG:HD2	2.54	0.48
5:D:294:TYR:HE2	38:D:8659:HOH:O	1.96	0.48
1:A:894:A:C2	6:E:87:ARG:NH2	2.82	0.48
7:F:140:ARG:HG3	7:F:140:ARG:HH11	1.78	0.48
11:J:166:ASN:N	11:J:166:ASN:HD22	2.11	0.48
11:J:17:ARG:HD3	11:J:23:ILE:CD1	2.43	0.48
12:K:36:VAL:HG12	12:K:37:ALA:N	2.29	0.48
16:O:75:THR:CG2	38:O:8536:HOH:O	2.61	0.48
16:O:78:MET:CB	16:O:79:PRO:HD3	2.44	0.48
25:X:35:VAL:CG2	25:X:41:TYR:CD2	2.96	0.48
1:A:1266:U:O3'	27:Z:115:ARG:NH2	2.46	0.48
31:4:84:ARG:HB2	38:4:8514:HOH:O	2.13	0.48
1:A:1342:C:C2'	1:A:1343:C:H5'	2.44	0.48
1:A:184:G:H5''	15:N:153:THR:HG22	1.96	0.48
1:A:2852:A:H5''	38:A:4718:HOH:O	2.14	0.48
1:A:694:A:C2'	1:A:695:C:H5'	2.42	0.48
1:A:1654:U:H2'	4:C:47:HIS:HD2	1.78	0.48
5:D:325:PRO:HD2	38:D:8570:HOH:O	2.14	0.48
11:J:161:SER:HB3	38:J:8351:HOH:O	2.14	0.48
12:K:12:VAL:HG11	12:K:116:LEU:HD11	1.96	0.48
12:K:77:GLY:O	12:K:78:ILE:C	2.52	0.48
14:M:54:PRO:HG2	14:M:57:VAL:CG2	2.44	0.48
28:1:75:ALA:O	28:1:79:VAL:HG23	2.14	0.47
1:A:1023:C:O2'	1:A:1024:G:H5'	2.15	0.47
1:A:1517:U:C2	1:A:1670:G:N2	2.82	0.47
1:A:968:G:O2'	1:A:969:G:H5'	2.14	0.47
5:D:81:ALA:O	5:D:186:GLY:HA3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A:5661:HOH:O	5:D:216:LYS:HB2	2.12	0.47
9:H:26:THR:HG21	9:H:103:ALA:CB	2.43	0.47
11:J:82:LYS:CB	11:J:82:LYS:NZ	2.77	0.47
14:M:65:ASP:CG	14:M:111:ALA:HB3	2.34	0.47
15:N:81:ARG:HG3	15:N:85:ARG:HB2	1.96	0.47
2:B:3114:G:O6	16:O:11:ARG:HD3	2.13	0.47
17:P:33:LEU:HA	17:P:40:HIS:CE1	2.49	0.47
19:R:21:ARG:HG2	19:R:22:GLY:N	2.29	0.47
24:W:16:ARG:NH1	24:W:65:ASP:O	2.47	0.47
1:A:1097:A:H5''	25:X:125:HIS:NE2	2.29	0.47
1:A:1132:A:N6	1:A:1229:C:H2'	2.29	0.47
1:A:1994:A:P	13:L:66:ARG:HH22	2.37	0.47
1:A:251:C:O2'	1:A:252:C:H5'	2.14	0.47
1:A:2650:U:O2'	1:A:2651:C:H5'	2.15	0.47
1:A:242:A:N6	1:A:269:G:H1'	2.29	0.47
1:A:558:C:H5'	38:A:4742:HOH:O	2.13	0.47
1:A:661:G:C4	1:A:686:A:C2	3.02	0.47
4:C:112:PRO:HB3	4:C:151:GLN:HB3	1.96	0.47
13:L:14:LYS:NZ	13:L:32:ILE:O	2.42	0.47
13:L:82:ARG:NH2	13:L:115:ARG:HG2	2.29	0.47
13:L:87:ARG:NE	38:L:4854:HOH:O	2.46	0.47
14:M:94:ARG:NH1	14:M:143:THR:HG21	2.29	0.47
38:A:9998:HOH:O	18:Q:133:SER:HA	2.13	0.47
1:A:2363:G:O3'	19:R:11:ARG:NH1	2.47	0.47
1:A:622:G:P	27:Z:148:GLY:HA3	2.54	0.47
1:A:1751:G:C3'	1:A:1752:G:H5''	2.44	0.47
1:A:2362:A:H2'	1:A:2363:G:C8	2.49	0.47
1:A:2488:A:H61	1:A:2534:C:H42	1.62	0.47
4:C:171:LYS:HE3	38:C:8570:HOH:O	2.14	0.47
5:D:195:ARG:NH1	5:D:324:ASP:OD1	2.41	0.47
15:N:47:ASP:O	15:N:51:SER:HB2	2.15	0.47
1:A:1808:C:O2'	1:A:1809:G:H5'	2.14	0.47
1:A:1823:G:C2	1:A:2027:U:C2	3.02	0.47
1:A:2327:A:H2'	1:A:2328:U:C6	2.48	0.47
1:A:2334:C:O2'	1:A:2335:C:H5'	2.14	0.47
1:A:581:G:O2'	1:A:582:C:H5'	2.14	0.47
9:H:22:VAL:HG21	9:H:104:ALA:HB2	1.96	0.47
12:K:93:ARG:O	12:K:96:GLU:HB2	2.15	0.47
20:S:111:ILE:O	20:S:111:ILE:HG22	2.14	0.47
22:U:71:VAL:HG12	22:U:72:ILE:N	2.29	0.47
27:Z:187:VAL:HB	27:Z:203:VAL:HG22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1352:A:H5''	1:A:1353:C:OP2	2.14	0.47
1:A:1450:C:O2'	1:A:1494:A:H5'	2.14	0.47
1:A:1754:A:H2'	1:A:1755:A:O4'	2.14	0.47
1:A:2111:G:H5''	38:A:4327:HOH:O	2.14	0.47
1:A:2424:U:H5'	38:A:6755:HOH:O	2.15	0.47
1:A:2775:A:C6	1:A:2799:A:C8	3.02	0.47
4:C:36:ASP:O	4:C:38:ILE:N	2.47	0.47
8:G:126:ILE:HB	8:G:131:LEU:HD21	1.95	0.47
14:M:93:VAL:CG2	14:M:122:ALA:HB2	2.44	0.47
23:V:4:ARG:N	38:V:5334:HOH:O	2.48	0.47
28:1:44:PHE:HD2	28:1:46:LYS:HD2	1.80	0.47
29:2:30:LYS:HD3	38:2:3205:HOH:O	2.15	0.47
1:A:2431:C:O2'	1:A:2432:C:H5'	2.15	0.47
1:A:2502:C:H4'	11:J:151:MET:CG	2.42	0.47
1:A:2526:C:HO2'	1:A:2527:U:H5'	1.79	0.47
1:A:2866:U:C5	23:V:50:GLU:HB2	2.49	0.47
1:A:371:U:H2'	1:A:372:A:C8	2.50	0.47
1:A:790:A:H1'	1:A:1710:A:H2'	1.96	0.47
1:A:875:A:H5'	1:A:876:A:N7	2.29	0.47
5:D:243:ASN:HA	5:D:244:PRO:C	2.34	0.47
5:D:297:VAL:HB	38:D:8611:HOH:O	2.14	0.47
1:A:392:U:C5'	15:N:193:LYS:HB3	2.44	0.47
16:O:58:LEU:CD1	16:O:58:LEU:N	2.78	0.47
28:1:56:MET:CE	28:1:63:LYS:HG3	2.44	0.47
1:A:1204:C:O5'	1:A:1204:C:H6	1.98	0.47
1:A:1329:A:H2	38:A:4164:HOH:O	1.97	0.47
1:A:161:A:OP1	15:N:81:ARG:HA	2.14	0.47
1:A:1997:A:N1	38:A:6441:HOH:O	2.35	0.47
1:A:716:G:C2'	1:A:717:C:O5'	2.63	0.47
1:A:819:A:H5''	38:1:8418:HOH:O	2.15	0.47
2:B:3012:C:H5'	2:B:3070:U:O4'	2.14	0.47
1:A:1014:A:H5''	2:B:3101:G:O2'	2.14	0.47
6:E:140:VAL:HG12	6:E:141:SER:N	2.29	0.47
6:E:162:VAL:HG12	6:E:192:ILE:CD1	2.44	0.47
7:F:45:THR:HB	7:F:75:LEU:HD21	1.95	0.47
10:I:64:ASN:ND2	10:I:64:ASN:H	2.13	0.47
11:J:140:PRO:HA	11:J:142:VAL:HG12	1.95	0.47
1:A:2415:A:N3	16:O:26:LEU:HD13	2.30	0.47
22:U:63:ILE:HD11	22:U:75:GLU:HB2	1.97	0.47
26:Y:76:ARG:O	26:Y:77:PHE:HB3	2.14	0.47
27:Z:154:ARG:HH12	27:Z:155:ARG:HG3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:70:ARG:HB3	38:4:8571:HOH:O	2.14	0.47
3:5:74:C:O2'	3:5:75:C:H5'	2.14	0.47
1:A:111:C:O2'	29:2:20:ARG:HG2	2.15	0.47
1:A:1565:C:O2'	1:A:1566:C:H5'	2.14	0.47
1:A:1819:G:H2'	1:A:1820:G:C4'	2.41	0.47
1:A:1882:C:H2'	1:A:1883:U:H6	1.78	0.47
1:A:721:A:C2'	1:A:722:G:H5'	2.45	0.47
1:A:947:U:H2'	1:A:948:G:C8	2.50	0.47
4:C:191:GLY:HA2	4:C:194:MET:HE2	1.95	0.47
4:C:215:ILE:HG13	4:C:216:SER:N	2.29	0.47
7:F:95:THR:C	7:F:97:GLN:N	2.66	0.47
8:G:101:GLU:OE2	8:G:115:ARG:HD3	2.14	0.47
8:G:167:TYR:CD1	8:G:167:TYR:N	2.83	0.47
8:G:22:VAL:O	8:G:28:SER:HA	2.15	0.47
8:G:58:THR:O	8:G:59:MET:C	2.53	0.47
12:K:93:ARG:HH11	12:K:93:ARG:CB	2.23	0.47
17:P:85:ALA:O	17:P:89:ILE:HG13	2.14	0.47
18:Q:5:ALA:HB3	38:Q:1715:HOH:O	2.15	0.47
23:V:8:TYR:O	23:V:46:ALA:CB	2.63	0.47
31:4:17:HIS:O	31:4:18:GLN:HG3	2.15	0.47
1:A:111:C:C2'	1:A:112:G:H5'	2.44	0.47
1:A:1734:C:OP1	5:D:234:ARG:NH1	2.46	0.47
1:A:2842:G:H2'	1:A:2843:A:H5'	1.96	0.47
1:A:517:U:H2'	1:A:518:G:H5'	1.97	0.47
1:A:934:C:H1'	38:A:9848:HOH:O	2.15	0.47
6:E:21:VAL:C	6:E:23:GLU:H	2.18	0.47
7:F:155:HIS:NE2	38:F:7597:HOH:O	2.36	0.47
7:F:65:GLU:HG3	38:F:6752:HOH:O	2.14	0.47
11:J:112:ARG:O	11:J:113:ALA:C	2.52	0.47
11:J:74:ASN:ND2	11:J:141:ASN:OD1	2.48	0.47
22:U:27:LEU:HD21	22:U:40:VAL:CG1	2.45	0.47
29:2:29:THR:O	29:2:32:LYS:HE2	2.15	0.47
1:A:1191:A:C2	1:A:1207:A:C2	3.03	0.47
1:A:1730:G:H5'	1:A:1731:C:C6	2.50	0.47
1:A:1804:A:O2'	1:A:1805:G:H5'	2.15	0.47
1:A:2432:C:H1'	38:A:3570:HOH:O	2.14	0.47
1:A:2072:G:C6	1:A:2533:C:H1'	2.50	0.47
1:A:262:A:OP2	9:H:91:VAL:HG11	2.15	0.47
1:A:797:A:C4'	28:1:10:ARG:N	2.78	0.47
1:A:820:G:H5'	1:A:821:U:C5'	2.45	0.47
2:B:3114:G:H2'	2:B:3115:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:154:VAL:HG12	5:D:156:LYS:HG2	1.96	0.47
5:D:190:MET:HE2	5:D:194:PHE:CD1	2.50	0.47
14:M:73:VAL:HG21	14:M:116:HIS:CD2	2.50	0.47
15:N:63:VAL:O	15:N:130:GLU:HA	2.15	0.47
16:O:163:PHE:O	16:O:164:ASP:O	2.32	0.47
17:P:25:VAL:HG23	17:P:26:TRP:H	1.79	0.47
18:Q:91:LYS:O	18:Q:95:GLU:HG3	2.15	0.47
20:S:6:VAL:HG23	20:S:113:HIS:CE1	2.50	0.47
25:X:121:PRO:HA	25:X:153:MET:HG2	1.96	0.47
25:X:40:ALA:O	25:X:44:MET:HG3	2.14	0.47
25:X:90:TYR:CE2	25:X:99:ALA:HB2	2.50	0.47
26:Y:78:GLU:CG	26:Y:79:GLU:N	2.77	0.47
31:4:65:THR:HB	31:4:83:TRP:H	1.79	0.47
1:A:1187:U:H3'	38:A:6366:HOH:O	2.14	0.47
1:A:1314:U:H5''	1:A:1316:G:O4'	2.14	0.47
1:A:136:C:H2'	1:A:137:U:O4'	2.15	0.47
1:A:1477:C:H5'	1:A:1868:G:C5'	2.45	0.47
1:A:1527:A:H1'	1:A:1528:A:C8	2.49	0.47
1:A:1878:G:HO2'	1:A:1879:U:H6	1.57	0.47
1:A:218:C:OP1	31:4:39:GLN:NE2	2.36	0.47
1:A:2432:C:H2'	1:A:2433:A:H8	1.80	0.47
1:A:697:G:H4'	1:A:730:G:O3'	2.15	0.47
6:E:115:LEU:HD12	6:E:115:LEU:HA	1.74	0.47
11:J:113:ALA:N	11:J:114:PRO:HD3	2.29	0.47
11:J:43:PRO:HD2	11:J:137:ASN:HA	1.97	0.47
38:G:2512:HOH:O	12:K:127:ILE:HD11	2.14	0.47
14:M:121:ILE:HG12	14:M:141:GLU:HB2	1.96	0.47
38:A:9682:HOH:O	15:N:9:ARG:HG3	2.14	0.47
16:O:165:ALA:HA	38:O:8518:HOH:O	2.14	0.47
20:S:114:VAL:O	20:S:114:VAL:HG13	2.14	0.47
1:A:1023:C:H2'	1:A:1024:G:O4'	2.14	0.46
1:A:1855:G:H4'	1:A:1856:C:O5'	2.15	0.46
1:A:2748:G:H1'	38:A:7371:HOH:O	2.15	0.46
4:C:211:LYS:NZ	38:C:8584:HOH:O	2.43	0.46
5:D:157:LYS:HG2	38:D:8668:HOH:O	2.15	0.46
11:J:112:ARG:HB3	38:J:8383:HOH:O	2.15	0.46
11:J:141:ASN:CA	38:J:8355:HOH:O	2.62	0.46
11:J:84:ARG:CZ	11:J:135:TRP:HH2	2.28	0.46
12:K:37:ALA:HA	12:K:102:ARG:O	2.15	0.46
14:M:75:LEU:N	14:M:75:LEU:HD23	2.30	0.46
14:M:93:VAL:HG12	14:M:97:VAL:HG23	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A:4192:HOH:O	19:R:48:PRO:HG3	2.15	0.46
25:X:122:ARG:NE	38:X:5817:HOH:O	2.48	0.46
28:1:41:VAL:HG12	28:1:42:CYS:N	2.28	0.46
1:A:1309:U:O2'	1:A:1310:U:H5'	2.15	0.46
1:A:185:G:H4'	1:A:186:A:OP1	2.15	0.46
1:A:2039:A:H2'	1:A:2040:C:H6	1.80	0.46
1:A:2241:C:O2'	1:A:2242:U:H5'	2.15	0.46
1:A:2353:A:H4'	1:A:2354:A:O5'	2.15	0.46
1:A:2819:C:H2'	1:A:2820:A:C8	2.50	0.46
1:A:558:C:C2'	1:A:559:U:C5'	2.92	0.46
1:A:830:G:O2'	1:A:831:U:H5'	2.16	0.46
8:G:36:PRO:HD3	12:K:127:ILE:HD12	1.97	0.46
9:H:26:THR:HG21	9:H:103:ALA:HB2	1.96	0.46
11:J:56:ILE:HG22	11:J:61:LEU:CD2	2.45	0.46
12:K:90:LYS:HB2	35:K:8502:CL:CL	2.53	0.46
16:O:184:ILE:HG22	16:O:185:GLU:N	2.30	0.46
18:Q:6:GLN:OE1	18:Q:6:GLN:N	2.35	0.46
22:U:92:ASP:C	22:U:94:SER:H	2.18	0.46
1:A:2430:A:H2'	1:A:2431:C:C6	2.50	0.46
1:A:2670:G:O2'	1:A:2671:U:H5'	2.16	0.46
1:A:396:U:H4'	38:A:3916:HOH:O	2.14	0.46
1:A:834:G:H4'	1:A:835:U:OP2	2.15	0.46
1:A:861:A:H2'	1:A:862:U:C6	2.50	0.46
2:B:3019:G:O2'	2:B:3020:G:H5'	2.16	0.46
5:D:44:TYR:OH	5:D:148:PRO:HG3	2.14	0.46
5:D:51:VAL:CG2	5:D:330:VAL:HG22	2.45	0.46
7:F:64:ARG:HB3	7:F:67:ASP:OD2	2.15	0.46
9:H:21:GLU:O	9:H:24:ARG:HG3	2.14	0.46
9:H:56:PRO:HG2	15:N:44:THR:HA	1.95	0.46
11:J:65:ARG:CZ	38:J:8373:HOH:O	2.62	0.46
11:J:82:LYS:HB2	11:J:82:LYS:HZ2	1.81	0.46
12:K:122:ASP:OD1	12:K:124:LEU:HB2	2.15	0.46
13:L:32:ILE:CD1	13:L:56:SER:HB3	2.43	0.46
13:L:98:VAL:HG13	13:L:99:ASP:N	2.29	0.46
19:R:40:HIS:CE1	19:R:94:GLN:HA	2.51	0.46
20:S:47:LEU:O	20:S:51:ILE:HG13	2.16	0.46
22:U:20:HIS:CE1	22:U:67:LEU:HD11	2.50	0.46
1:A:107:U:H2'	1:A:108:U:H5'	1.97	0.46
1:A:1416:G:C2'	1:A:1417:G:H5'	2.45	0.46
1:A:710:G:OP1	17:P:24:ALA:HB3	2.16	0.46
1:A:731:U:H2'	1:A:732:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:858:U:H2'	1:A:859:C:H6	1.79	0.46
4:C:199:HIS:HD2	4:C:201:PHE:H	1.62	0.46
5:D:98:THR:HG22	5:D:99:GLU:H	1.81	0.46
6:E:129:HIS:HE1	6:E:231:ARG:HA	1.80	0.46
7:F:154:LYS:H	7:F:154:LYS:CD	2.21	0.46
9:H:34:ASN:ND2	9:H:38:LYS:HE2	2.30	0.46
12:K:48:GLY:CA	12:K:53:ILE:HD11	2.45	0.46
12:K:56:LYS:HE2	12:K:60:ARG:NH2	2.30	0.46
14:M:66:VAL:CG2	14:M:67:ARG:N	2.77	0.46
18:Q:98:ILE:HD12	18:Q:102:ARG:NE	2.30	0.46
26:Y:25:ARG:HG2	38:Y:5356:HOH:O	2.13	0.46
27:Z:106:THR:HG22	27:Z:107:PRO:O	2.15	0.46
38:A:3833:HOH:O	27:Z:214:ARG:CZ	2.62	0.46
1:A:1044:C:H5''	38:A:8543:HOH:O	2.15	0.46
1:A:1187:U:C2'	38:A:6366:HOH:O	2.53	0.46
1:A:1669:A:C2	38:A:3200:HOH:O	2.56	0.46
1:A:1827:G:C6	1:A:1828:G:C6	3.04	0.46
1:A:567:U:O5'	1:A:567:U:H6	1.99	0.46
1:A:573:A:P	38:A:6516:HOH:O	2.74	0.46
1:A:936:C:O2'	1:A:937:C:H5'	2.16	0.46
1:A:941:G:O2'	1:A:942:U:H5'	2.15	0.46
5:D:171:VAL:HG23	5:D:172:SER:N	2.30	0.46
8:G:20:ILE:O	8:G:30:THR:HA	2.16	0.46
9:H:48:VAL:HG23	9:H:74:PHE:CB	2.45	0.46
11:J:12:PRO:HD2	38:J:8341:HOH:O	2.16	0.46
14:M:7:GLN:HB3	14:M:13:HIS:CE1	2.51	0.46
9:H:34:ASN:HA	15:N:4:ALA:HB2	1.98	0.46
16:O:157:PRO:HA	38:O:8526:HOH:O	2.15	0.46
17:P:32:ARG:HE	17:P:35:LYS:HD2	1.79	0.46
17:P:96:VAL:CG1	17:P:100:GLN:HB2	2.45	0.46
1:A:1594:C:OP2	18:Q:120:ARG:HD2	2.15	0.46
21:T:81:ILE:HG23	38:T:8334:HOH:O	2.16	0.46
1:A:306:A:P	22:U:38:ARG:HH21	2.38	0.46
24:W:42:ASN:HB3	38:W:7247:HOH:O	2.16	0.46
26:Y:86:GLU:O	26:Y:87:ALA:O	2.32	0.46
1:A:151:A:C2	1:A:442:A:C8	3.04	0.46
1:A:221:G:H2'	1:A:222:A:C8	2.50	0.46
1:A:2291:A:N9	1:A:2309:C:H5'	2.30	0.46
1:A:2906:A:H5'	1:A:2907:C:O4'	2.15	0.46
1:A:322:G:O2'	1:A:323:C:H5'	2.16	0.46
1:A:645:U:O2	1:A:761:A:H2	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:100:PRO:HG2	4:C:103:VAL:CG2	2.46	0.46
4:C:36:ASP:HA	4:C:83:GLY:HA3	1.96	0.46
1:A:1151:G:P	10:I:16:LYS:HZ1	2.34	0.46
13:L:72:VAL:HG11	13:L:121:PHE:CD1	2.51	0.46
16:O:149:GLU:O	16:O:152:GLU:HB2	2.16	0.46
16:O:48:VAL:HG12	16:O:49:THR:N	2.30	0.46
30:3:18:ASN:HD21	30:3:40:ARG:H	1.64	0.46
31:4:40:ARG:HA	31:4:52:PHE:CE1	2.51	0.46
1:A:1215:A:O3'	1:A:1216:G:C4'	2.63	0.46
1:A:1426:C:H2'	38:A:9094:HOH:O	2.16	0.46
1:A:1659:A:H2'	1:A:1660:G:O4'	2.16	0.46
1:A:2256:G:C2'	1:A:2257:G:C5'	2.87	0.46
1:A:2364:A:H5''	19:R:15:LYS:HD3	1.97	0.46
1:A:2493:C:H2'	38:A:4158:HOH:O	2.16	0.46
1:A:2507:G:H2'	1:A:2510:C:N4	2.30	0.46
1:A:2673:U:C2	1:A:2817:G:N2	2.84	0.46
1:A:514:G:P	1:A:514:G:H2'	2.56	0.46
2:B:3095:C:O2'	2:B:3096:C:H5'	2.15	0.46
5:D:76:THR:N	5:D:77:PRO:HD3	2.30	0.46
6:E:136:VAL:HG22	6:E:137:PRO:HA	1.98	0.46
6:E:27:ARG:HG3	6:E:29:ASP:OD1	2.15	0.46
8:G:69:ILE:O	8:G:72:MET:HB2	2.15	0.46
11:J:130:HIS:CD2	11:J:133:ILE:HD11	2.50	0.46
11:J:163:PRO:O	11:J:164:ALA:HB2	2.15	0.46
15:N:104:ARG:O	15:N:108:LYS:HE2	2.16	0.46
17:P:99:GLU:CG	38:P:6044:HOH:O	2.63	0.46
28:1:47:LEU:HD23	28:1:57:CYS:CB	2.46	0.46
1:A:1168:C:H2'	1:A:1169:U:O4'	2.15	0.46
1:A:1497:G:O2'	1:A:1498:G:H5'	2.16	0.46
1:A:1592:G:O2'	1:A:1593:C:O4'	2.32	0.46
1:A:2717:C:H5'	5:D:302:PRO:HA	1.97	0.46
1:A:506:G:N2	1:A:509:A:H5'	2.21	0.46
2:B:3049:G:H2'	2:B:3050:G:O4'	2.16	0.46
4:C:101:GLU:HG2	4:C:131:HIS:ND1	2.31	0.46
9:H:101:ALA:HA	38:H:5413:HOH:O	2.15	0.46
11:J:74:ASN:HD22	11:J:141:ASN:CG	2.18	0.46
15:N:184:ARG:HG3	15:N:185:PRO:HA	1.98	0.46
15:N:35:PRO:HD2	15:N:38:VAL:CG2	2.46	0.46
16:O:34:LEU:HD22	16:O:129:ILE:HD13	1.98	0.46
18:Q:115:SER:O	18:Q:118:GLN:N	2.48	0.46
27:Z:100:ARG:HE	27:Z:234:VAL:HG21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1299:G:N2	38:A:4164:HOH:O	2.48	0.46
1:A:204:A:H2'	1:A:205:U:H5'	1.96	0.46
1:A:20:G:H21	20:S:117:HIS:CD2	2.25	0.46
1:A:2416:G:H2'	1:A:2417:C:C6	2.51	0.46
1:A:2453:G:H2'	1:A:2454:C:C6	2.51	0.46
1:A:2457:U:H1'	31:4:79:LEU:HD13	1.98	0.46
1:A:282:C:H2'	1:A:283:U:O4'	2.15	0.46
2:B:3036:C:C5	2:B:3037:C:C5	3.04	0.46
4:C:228:ILE:HG13	38:C:8516:HOH:O	2.16	0.46
5:D:27:ASN:HD22	5:D:27:ASN:H	1.64	0.46
8:G:118:ILE:HG23	8:G:144:THR:CG2	2.46	0.46
10:I:23:ILE:HG22	10:I:70:ALA:CB	2.46	0.46
11:J:157:ILE:CG2	11:J:158:ASN:N	2.79	0.46
11:J:53:PRO:HA	11:J:125:VAL:O	2.14	0.46
12:K:40:ASN:OD1	12:K:106:GLY:HA2	2.16	0.46
13:L:115:ARG:HG3	13:L:116:GLU:H	1.81	0.46
15:N:35:PRO:CD	15:N:38:VAL:HG23	2.45	0.46
38:B:8478:HOH:O	16:O:23:ARG:NH1	2.49	0.46
17:P:113:VAL:O	17:P:114:ILE:HD13	2.15	0.46
20:S:100:ASP:O	20:S:102:GLN:N	2.49	0.46
23:V:31:PHE:CE2	23:V:37:GLU:HA	2.51	0.46
25:X:4:LEU:HD23	25:X:4:LEU:HA	1.79	0.46
28:1:58:GLY:CA	38:1:8436:HOH:O	2.64	0.46
1:A:1314:U:C2	1:A:1316:G:N2	2.84	0.46
1:A:1380:U:OP2	1:A:2747:C:N4	2.49	0.46
1:A:1512:G:O2'	1:A:1513:C:H5'	2.16	0.46
1:A:2269:C:H2'	1:A:2270:G:O4'	2.15	0.46
1:A:2434:A:H4'	31:4:28:GLY:O	2.16	0.46
1:A:2438:G:H2'	1:A:2439:C:C6	2.50	0.46
1:A:2514:U:O5'	1:A:2514:U:H6	2.00	0.46
1:A:257:G:O2'	1:A:258:G:H5'	2.15	0.46
1:A:2897:C:H2'	1:A:2898:G:C8	2.50	0.46
1:A:821:U:H5''	38:A:9553:HOH:O	2.14	0.46
2:B:3057:A:N6	38:B:8447:HOH:O	2.49	0.46
4:C:217:ARG:CG	4:C:217:ARG:HH11	2.28	0.46
5:D:215:VAL:HG11	5:D:234:ARG:NH2	2.31	0.46
6:E:15:GLU:CG	38:E:8336:HOH:O	2.64	0.46
6:E:224:ALA:HB1	6:E:228:ALA:O	2.15	0.46
7:F:99:ASP:CB	7:F:103:ASN:H	2.29	0.46
13:L:118:ALA:O	13:L:120:ARG:N	2.49	0.46
24:W:11:MET:HB3	24:W:15:GLU:HB2	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:30:GLU:HB3	28:1:34:LYS:CE	2.40	0.45
1:A:1245:C:H5''	1:A:1246:A:H8	1.80	0.45
1:A:1771:U:O2'	28:1:23:ARG:NH2	2.44	0.45
1:A:1825:U:O4'	1:A:1999:C:H5''	2.16	0.45
1:A:245:C:C3'	1:A:246:G:H5'	2.46	0.45
1:A:2673:U:C2'	1:A:2674:G:H5'	2.46	0.45
1:A:2694:A:H4'	8:G:91:PHE:HE1	1.81	0.45
5:D:305:ASP:O	5:D:306:LYS:CB	2.63	0.45
6:E:246:ARG:NH2	38:E:8422:HOH:O	2.49	0.45
8:G:107:PHE:CD2	8:G:108:LEU:HD13	2.51	0.45
8:G:11:VAL:CG1	8:G:22:VAL:HG13	2.45	0.45
9:H:23:ALA:O	9:H:27:GLY:N	2.49	0.45
11:J:127:GLY:O	11:J:128:ALA:CB	2.63	0.45
11:J:151:MET:HA	11:J:151:MET:CE	2.46	0.45
12:K:6:PHE:CD1	12:K:102:ARG:HD2	2.51	0.45
12:K:51:GLU:O	12:K:55:GLU:HG3	2.16	0.45
14:M:124:ASP:OD1	14:M:149:ARG:NH2	2.49	0.45
38:A:9101:HOH:O	15:N:165:SER:HB3	2.16	0.45
28:1:77:LYS:HA	28:1:80:MET:CE	2.46	0.45
28:1:77:LYS:HA	28:1:80:MET:HE3	1.98	0.45
31:4:14:CYS:SG	31:4:18:GLN:NE2	2.89	0.45
1:A:1245:C:H5''	1:A:1246:A:C8	2.51	0.45
1:A:942:U:O4	38:A:9250:HOH:O	2.20	0.45
9:H:37:THR:O	9:H:41:GLU:HG3	2.15	0.45
15:N:67:ILE:HD13	15:N:104:ARG:HH11	1.81	0.45
17:P:21:SER:HB2	17:P:106:PRO:O	2.17	0.45
22:U:79:LEU:HG	22:U:89:ARG:HB2	1.97	0.45
27:Z:216:ARG:NH1	38:Z:8532:HOH:O	2.48	0.45
1:A:797:A:O4'	28:1:10:ARG:N	2.49	0.45
29:2:21:ARG:HD2	29:2:39:PHE:HB2	1.97	0.45
3:5:75:C:H42	36:5:76:PPU:H102	1.79	0.45
1:A:1253:C:H5'	38:A:7201:HOH:O	2.15	0.45
1:A:1767:A:O2'	1:A:1768:C:H5'	2.16	0.45
1:A:627:G:H2'	1:A:2071:C:C5	2.51	0.45
1:A:212:A:O4'	1:A:214:U:C6	2.69	0.45
1:A:2239:C:H6	38:A:6143:HOH:O	1.99	0.45
1:A:2718:C:H6	1:A:2718:C:H5'	1.82	0.45
1:A:394:G:O6	15:N:182:LYS:NZ	2.44	0.45
1:A:40:C:O5'	1:A:40:C:H6	1.99	0.45
1:A:482:G:H4'	1:A:508:A:N1	2.32	0.45
5:D:190:MET:CE	5:D:194:PHE:CD1	2.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:95:GLU:HG3	38:E:8474:HOH:O	2.15	0.45
12:K:4:ALA:O	12:K:5:GLU:O	2.34	0.45
13:L:3:ALA:HB1	38:L:581:HOH:O	2.17	0.45
14:M:146:GLY:O	14:M:148:GLU:N	2.48	0.45
16:O:139:TRP:HH2	16:O:176:ARG:HH11	1.64	0.45
17:P:80:ASP:CG	17:P:81:PHE:N	2.69	0.45
19:R:93:ARG:CG	19:R:93:ARG:NH1	2.80	0.45
22:U:9:LYS:CE	22:U:13:ARG:NH1	2.77	0.45
13:L:84:ASP:O	23:V:16:GLY:HA2	2.16	0.45
1:A:588:G:O6	25:X:154:ARG:NH1	2.49	0.45
27:Z:117:LEU:HD12	27:Z:174:VAL:CG1	2.46	0.45
28:1:27:ALA:HA	38:1:8414:HOH:O	2.17	0.45
1:A:2436:U:H5'	31:4:68:LYS:HE2	1.98	0.45
1:A:162:C:C2'	1:A:163:U:H5'	2.46	0.45
1:A:2251:G:H2'	1:A:2252:A:C8	2.52	0.45
1:A:2355:G:H2'	38:A:5117:HOH:O	2.15	0.45
1:A:2433:A:C2	1:A:2459:G:C2	3.04	0.45
1:A:2607:U:H4'	38:A:8940:HOH:O	2.16	0.45
1:A:2766:A:H5'	38:A:9065:HOH:O	2.15	0.45
1:A:2815:G:H4'	1:A:2816:A:OP2	2.16	0.45
1:A:2860:G:N2	1:A:2898:G:C4	2.84	0.45
1:A:475:G:C5'	6:E:73:LEU:HD23	2.47	0.45
1:A:661:G:C6	1:A:686:A:C2	3.05	0.45
1:A:876:A:C2'	1:A:876:A:N3	2.80	0.45
4:C:192:VAL:HG13	38:C:8563:HOH:O	2.16	0.45
4:C:212:PRO:HB2	38:C:8568:HOH:O	2.15	0.45
5:D:132:HIS:CE1	5:D:171:VAL:CG2	3.00	0.45
6:E:79:ARG:O	6:E:87:ARG:HG2	2.15	0.45
11:J:140:PRO:HA	11:J:142:VAL:CG1	2.45	0.45
11:J:166:ASN:N	11:J:166:ASN:ND2	2.65	0.45
13:L:122:GLY:O	13:L:125:ALA:N	2.49	0.45
15:N:18:GLY:O	15:N:21:ALA:HB3	2.15	0.45
18:Q:143:ALA:CA	38:Q:5521:HOH:O	2.60	0.45
24:W:23:LEU:HD12	24:W:56:ILE:HD12	1.98	0.45
27:Z:154:ARG:HH12	27:Z:155:ARG:CG	2.30	0.45
27:Z:174:VAL:HG12	27:Z:174:VAL:O	2.16	0.45
31:4:84:ARG:HH11	31:4:84:ARG:HG3	1.81	0.45
1:A:1652:C:H5''	28:1:52:THR:OG1	2.16	0.45
1:A:1656:A:H2'	1:A:1657:A:O4'	2.16	0.45
1:A:2361:A:H5''	38:A:8523:HOH:O	2.15	0.45
1:A:23:G:C6	1:A:24:G:N1	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:280:VAL:C	38:D:8567:HOH:O	2.53	0.45
5:D:30:PRO:HB2	5:D:39:GLN:NE2	2.31	0.45
38:A:3280:HOH:O	15:N:189:VAL:HG21	2.16	0.45
16:O:86:LEU:O	16:O:90:LEU:HG	2.17	0.45
22:U:71:VAL:CG1	22:U:72:ILE:N	2.78	0.45
25:X:122:ARG:HG2	25:X:122:ARG:NH1	2.31	0.45
1:A:566:A:H2	1:A:1094:G:O4'	1.99	0.45
1:A:1557:G:O2'	1:A:1558:C:H5'	2.17	0.45
1:A:1636:G:O2'	1:A:1637:A:H5'	2.17	0.45
1:A:1921:A:C6	1:A:1922:A:C2	3.04	0.45
1:A:1934:A:C8	1:A:1935:C:C5	3.05	0.45
1:A:2272:G:H5'	4:C:223:ARG:HB2	1.98	0.45
1:A:236:A:H4'	1:A:237:G:OP1	2.16	0.45
1:A:2405:C:H5'	38:A:6070:HOH:O	2.16	0.45
1:A:240:C:H4'	15:N:146:GLN:NE2	2.30	0.45
1:A:2699:A:H2'	1:A:2700:G:O4'	2.17	0.45
1:A:724:G:O2'	1:A:725:C:H5'	2.17	0.45
4:C:95:PRO:HA	4:C:153:ARG:HA	1.99	0.45
5:D:129:ARG:O	5:D:133:GLU:HG3	2.17	0.45
1:A:2338:G:H2'	7:F:129:ASP:OD1	2.16	0.45
7:F:99:ASP:HB2	7:F:103:ASN:HB2	1.98	0.45
11:J:72:VAL:HG13	11:J:72:VAL:O	2.15	0.45
13:L:49:LEU:HD21	13:L:74:VAL:O	2.16	0.45
16:O:43:VAL:HG13	16:O:118:ILE:HD11	1.97	0.45
20:S:17:MET:HG2	20:S:144:GLU:HA	1.98	0.45
25:X:41:TYR:O	25:X:45:VAL:HG13	2.16	0.45
25:X:65:VAL:HA	25:X:68:THR:CG2	2.46	0.45
1:A:1615:A:H5'	38:A:3673:HOH:O	2.17	0.45
1:A:1768:C:C2'	1:A:1769:C:H5'	2.46	0.45
1:A:1796:A:H2'	1:A:1797:A:C8	2.51	0.45
1:A:1983:C:O5'	1:A:1983:C:H6	2.00	0.45
1:A:2381:C:H2'	1:A:2382:A:H8	1.82	0.45
1:A:481:U:C5'	38:A:5127:HOH:O	2.65	0.45
1:A:585:C:H6	38:A:5586:HOH:O	1.98	0.45
1:A:871:G:H8	1:A:871:G:H5''	1.74	0.45
5:D:279:THR:OG1	5:D:290:VAL:HB	2.16	0.45
5:D:88:GLU:HA	5:D:136:ASP:O	2.17	0.45
6:E:246:ARG:NE	38:E:8422:HOH:O	2.50	0.45
7:F:19:GLU:O	7:F:133:ASN:HB3	2.17	0.45
11:J:3:GLY:HA2	11:J:57:ARG:NH1	2.32	0.45
11:J:45:GLN:NE2	11:J:135:TRP:HE1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:39:ALA:C	24:W:41:GLU:N	2.70	0.45
28:1:38:LYS:HA	28:1:45:LYS:HA	1.99	0.45
4:C:76:VAL:HG23	28:1:63:LYS:HB3	1.99	0.45
1:A:10:U:O4	1:A:532:A:OP2	2.35	0.45
1:A:2524:G:N2	1:A:2526:C:H41	2.13	0.45
1:A:710:G:N2	1:A:719:C:C2	2.84	0.45
1:A:795:G:N3	1:A:817:G:C2	2.85	0.45
1:A:936:C:C2'	1:A:937:C:H5'	2.47	0.45
2:B:3025:G:N2	38:B:8513:HOH:O	2.49	0.45
2:B:3063:C:O2'	2:B:3064:C:H5'	2.17	0.45
5:D:248:ARG:O	5:D:251:VAL:CG1	2.49	0.45
8:G:38:ILE:HG21	8:G:65:PHE:CE1	2.51	0.45
11:J:65:ARG:NH1	38:J:8373:HOH:O	2.50	0.45
15:N:113:ARG:NH1	15:N:150:ILE:O	2.48	0.45
17:P:10:LEU:HD13	17:P:99:GLU:HG3	1.98	0.45
22:U:24:ARG:HH21	22:U:39:ASN:ND2	2.14	0.45
25:X:5:VAL:O	25:X:52:VAL:HG22	2.16	0.45
27:Z:184:GLU:OE2	27:Z:204:ARG:HD2	2.17	0.45
38:A:6071:HOH:O	31:4:79:LEU:HD12	2.17	0.45
1:A:1183:C:N4	38:A:3883:HOH:O	2.50	0.45
1:A:1878:G:O2'	1:A:1879:U:H6	1.98	0.45
1:A:2608:C:H2'	38:A:3069:HOH:O	2.15	0.45
1:A:2730:G:O2'	1:A:2731:G:H5'	2.17	0.45
1:A:1811:A:C2	1:A:2752:C:H1'	2.52	0.45
1:A:2759:C:O5'	1:A:2759:C:H6	2.00	0.45
1:A:2912:C:H3'	38:A:5856:HOH:O	2.15	0.45
38:A:6107:HOH:O	4:C:1:GLY:N	2.50	0.45
38:A:9199:HOH:O	5:D:254:GLN:HG3	2.16	0.45
7:F:36:ASN:HA	38:F:7500:HOH:O	2.15	0.45
9:H:110:GLU:HG2	38:H:6926:HOH:O	2.16	0.45
9:H:28:ALA:HB1	9:H:99:THR:HG23	1.99	0.45
11:J:82:LYS:HB2	11:J:82:LYS:NZ	2.31	0.45
12:K:93:ARG:HB3	12:K:93:ARG:NH1	2.26	0.45
17:P:39:THR:CB	38:P:3360:HOH:O	2.61	0.45
25:X:65:VAL:CG1	25:X:116:LEU:HD13	2.46	0.45
25:X:48:VAL:O	25:X:48:VAL:CG1	2.63	0.45
27:Z:214:ARG:NH2	27:Z:232:THR:OG1	2.49	0.45
1:A:892:G:H5''	29:2:54:ALA:HB2	1.98	0.45
1:A:1925:G:OP1	31:4:29:ARG:NH2	2.50	0.45
1:A:2276:U:H2'	1:A:2277:U:H6	1.81	0.45
1:A:2781:U:O2'	1:A:2782:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:G:OP1	6:E:73:LEU:HD22	2.16	0.45
1:A:656:G:H2'	1:A:657:G:H8	1.82	0.45
7:F:169:THR:C	7:F:170:TYR:CD1	2.91	0.45
7:F:23:VAL:HG21	7:F:45:THR:CG2	2.47	0.45
8:G:15:GLN:NE2	8:G:40:VAL:O	2.50	0.45
11:J:71:TYR:C	11:J:73:GLN:N	2.69	0.45
12:K:131:THR:HG22	12:K:133:GLY:N	2.31	0.45
15:N:84:LYS:O	15:N:87:MET:HG2	2.17	0.45
16:O:181:ASP:HA	38:O:8568:HOH:O	2.17	0.45
16:O:47:LEU:HD23	16:O:47:LEU:HA	1.70	0.45
17:P:112:ARG:HG3	17:P:114:ILE:HD11	1.99	0.45
17:P:112:ARG:CG	17:P:114:ILE:HD11	2.47	0.45
20:S:16:ALA:HB2	20:S:95:ALA:HB2	1.99	0.45
27:Z:187:VAL:HG12	27:Z:205:ILE:HA	1.98	0.45
1:A:1736:A:H8	1:A:1736:A:O5'	2.00	0.44
1:A:1234:U:O2	1:A:2066:C:H5''	2.17	0.44
1:A:2118:A:H2'	1:A:2119:C:H6	1.82	0.44
1:A:2271:G:P	38:A:8934:HOH:O	2.75	0.44
1:A:2910:A:H5''	38:A:3620:HOH:O	2.16	0.44
1:A:324:G:O2'	1:A:325:U:H5'	2.17	0.44
1:A:736:A:H2'	1:A:737:A:O4'	2.17	0.44
38:A:4048:HOH:O	6:E:50:GLU:HG2	2.16	0.44
1:A:1109:U:O4	12:K:21:ARG:HA	2.17	0.44
14:M:10:SER:O	14:M:11:ARG:HB3	2.17	0.44
16:O:139:TRP:HA	16:O:139:TRP:HE3	1.82	0.44
16:O:82:TYR:CD2	16:O:83:LEU:N	2.84	0.44
17:P:32:ARG:O	17:P:35:LYS:HB2	2.16	0.44
27:Z:105:LYS:NZ	27:Z:225:GLY:O	2.48	0.44
31:4:87:ARG:HG3	38:4:8572:HOH:O	2.16	0.44
1:A:1162:G:C2	1:A:1163:G:C8	3.06	0.44
1:A:1803:C:H2'	1:A:1804:A:C8	2.52	0.44
1:A:1815:A:H5'	38:A:3652:HOH:O	2.16	0.44
1:A:1853:C:H5'	4:C:228:ILE:O	2.18	0.44
1:A:1902:G:H2'	1:A:1903:U:O4'	2.17	0.44
4:C:29:HIS:HB2	4:C:153:ARG:HH12	1.82	0.44
4:C:182:ARG:O	4:C:184:THR:N	2.51	0.44
4:C:184:THR:HG22	4:C:185:LYS:N	2.32	0.44
4:C:1:GLY:HA2	4:C:197:VAL:HG23	1.99	0.44
5:D:280:VAL:CG1	5:D:334:SER:HA	2.47	0.44
7:F:154:LYS:HD3	38:F:1796:HOH:O	2.17	0.44
14:M:90:ARG:HH11	14:M:119:THR:HG21	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:164:THR:HG22	15:N:167:GLY:CA	2.46	0.44
16:O:132:ASN:O	16:O:135:VAL:HG12	2.17	0.44
16:O:3:GLY:HA3	38:O:8512:HOH:O	2.17	0.44
1:A:2403:C:O2'	19:R:67:GLN:O	2.29	0.44
20:S:89:LEU:HA	20:S:89:LEU:HD23	1.87	0.44
38:L:1387:HOH:O	23:V:20:MET:HE3	2.16	0.44
28:1:47:LEU:CD2	28:1:57:CYS:HB2	2.47	0.44
30:3:22:PRO:HG2	30:3:25:VAL:HG23	1.99	0.44
1:A:1497:G:H2'	1:A:1498:G:C8	2.50	0.44
1:A:1500:U:OP2	18:Q:41:ARG:NH2	2.49	0.44
1:A:1603:A:C5'	1:A:1605:G:H5'	2.47	0.44
1:A:1819:G:H2'	1:A:1820:G:C5'	2.47	0.44
1:A:182:G:O2'	1:A:183:A:H5'	2.18	0.44
1:A:2769:C:H2'	1:A:2770:G:C5'	2.46	0.44
1:A:553:G:O4'	1:A:1325:G:H5'	2.17	0.44
1:A:711:G:N2	1:A:718:C:C2	2.86	0.44
2:B:3056:A:C3'	2:B:3057:A:H5''	2.44	0.44
5:D:171:VAL:HG23	5:D:172:SER:H	1.83	0.44
5:D:66:GLU:HG2	38:D:8656:HOH:O	2.17	0.44
14:M:35:ARG:HH12	14:M:43:HIS:HB3	1.82	0.44
15:N:122:GLU:OE2	15:N:127:LYS:HE2	2.17	0.44
15:N:37:VAL:HG13	15:N:63:VAL:HG11	1.98	0.44
16:O:19:ASP:OD1	16:O:22:GLN:N	2.31	0.44
16:O:47:LEU:HD12	16:O:92:ALA:HB1	1.99	0.44
16:O:77:ASN:OD1	16:O:80:SER:HB2	2.17	0.44
16:O:92:ALA:O	16:O:95:ALA:HB3	2.17	0.44
25:X:122:ARG:CG	25:X:152:ALA:O	2.66	0.44
27:Z:189:ASN:ND2	27:Z:192:ASP:N	2.64	0.44
27:Z:198:GLY:HA3	27:Z:225:GLY:O	2.17	0.44
1:A:1380:U:H5'	38:A:8730:HOH:O	2.16	0.44
1:A:1503:U:H2'	1:A:1504:A:O4'	2.18	0.44
1:A:152:A:C2	1:A:153:C:C2	3.05	0.44
1:A:168:C:C2'	1:A:169:A:H5'	2.47	0.44
1:A:1790:C:H2'	1:A:1791:U:H6	1.83	0.44
1:A:1931:A:O5'	1:A:1931:A:H8	2.00	0.44
1:A:2281:C:O2'	1:A:2282:U:H5'	2.18	0.44
1:A:2382:A:C1'	31:4:10:TYR:HD2	2.31	0.44
1:A:2431:C:N3	38:A:3182:HOH:O	2.36	0.44
1:A:2515:C:H2'	1:A:2516:G:O4'	2.18	0.44
1:A:814:G:H2'	1:A:815:U:O4'	2.17	0.44
1:A:840:U:C5	1:A:2648:U:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3081:C:O5'	2:B:3081:C:H6	2.01	0.44
4:C:58:VAL:O	4:C:65:ARG:HD2	2.18	0.44
5:D:115:VAL:HA	5:D:116:PRO:HD3	1.90	0.44
5:D:224:LYS:HD3	5:D:224:LYS:HA	1.88	0.44
5:D:7:ARG:CD	5:D:9:GLY:O	2.66	0.44
13:L:123:SER:HA	13:L:126:SER:OG	2.18	0.44
14:M:59:GLU:HG2	14:M:104:ASP:OD2	2.17	0.44
38:A:4433:HOH:O	15:N:82:ARG:HD3	2.17	0.44
15:N:82:ARG:NH2	38:N:8615:HOH:O	2.51	0.44
17:P:44:ASN:HA	17:P:65:LEU:O	2.17	0.44
22:U:96:VAL:CG1	22:U:97:ARG:N	2.81	0.44
28:1:18:TYR:HB3	28:1:22:ILE:HG21	1.98	0.44
38:A:4909:HOH:O	31:4:25:VAL:HG21	2.18	0.44
1:A:1215:A:O3'	1:A:1216:G:H4'	2.17	0.44
1:A:1574:C:O5'	1:A:1574:C:H6	2.00	0.44
1:A:1862:C:H1'	38:A:6685:HOH:O	2.16	0.44
1:A:2408:A:O2'	31:4:16:GLU:HA	2.18	0.44
1:A:2413:A:H2'	1:A:2414:A:O4'	2.18	0.44
1:A:2769:C:H2'	1:A:2770:G:H5'	2.00	0.44
1:A:402:U:H2'	1:A:403:C:C6	2.52	0.44
8:G:57:LYS:O	8:G:60:SER:HB2	2.18	0.44
8:G:61:THR:O	8:G:64:THR:N	2.51	0.44
11:J:57:ARG:O	11:J:60:ALA:N	2.51	0.44
13:L:82:ARG:HD2	13:L:88:VAL:HG21	1.99	0.44
14:M:114:VAL:N	38:M:8440:HOH:O	2.46	0.44
14:M:40:PHE:CD1	14:M:40:PHE:C	2.90	0.44
16:O:79:PRO:HB3	16:O:172:PHE:CD1	2.53	0.44
17:P:97:SER:HB3	17:P:100:GLN:HE21	1.82	0.44
17:P:25:VAL:HG23	17:P:26:TRP:CD2	2.53	0.44
25:X:38:THR:HB	38:X:5390:HOH:O	2.16	0.44
1:A:1118:A:C8	1:A:1119:G:H5''	2.52	0.44
1:A:1189:A:N3	38:A:7152:HOH:O	2.48	0.44
1:A:1311:G:C2	1:A:1312:G:C8	3.06	0.44
1:A:1552:G:H2'	1:A:1553:C:H6	1.82	0.44
1:A:1562:C:N4	38:A:5350:HOH:O	2.39	0.44
1:A:603:A:H4'	1:A:604:G:O5'	2.17	0.44
1:A:2821:C:O2'	5:D:114:ASP:O	2.34	0.44
6:E:168:ARG:NH2	6:E:190:ALA:O	2.51	0.44
2:B:3041:C:O4'	7:F:50:VAL:HG23	2.18	0.44
7:F:58:VAL:CG1	7:F:59:GLY:N	2.79	0.44
12:K:17:CYS:HA	12:K:119:THR:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:130:ARG:O	14:M:131:GLU:C	2.54	0.44
15:N:174:ARG:HG3	38:N:8522:HOH:O	2.18	0.44
16:O:74:PRO:HD3	16:O:159:TYR:CE2	2.52	0.44
25:X:21:LEU:HD21	25:X:48:VAL:HG11	1.99	0.44
25:X:79:VAL:HG13	25:X:83:TRP:CE3	2.53	0.44
4:C:74:VAL:H	28:1:65:ALA:HB3	1.83	0.44
30:3:49:GLU:HB2	38:3:719:HOH:O	2.18	0.44
1:A:1164:U:N3	1:A:1192:A:H2	2.06	0.44
1:A:1609:C:H2'	1:A:1610:G:C8	2.53	0.44
1:A:1840:A:H4'	1:A:1841:C:O5'	2.18	0.44
1:A:2385:G:C4	1:A:2386:U:C5	3.06	0.44
1:A:2610:U:H4'	38:D:8531:HOH:O	2.16	0.44
1:A:2064:U:H4'	1:A:2653:A:OP1	2.17	0.44
1:A:827:A:H2'	1:A:828:G:O4'	2.17	0.44
1:A:864:U:H4'	38:A:8869:HOH:O	2.17	0.44
4:C:217:ARG:HG2	4:C:229:ALA:HB2	1.99	0.44
7:F:95:THR:OG1	7:F:174:VAL:HG22	2.18	0.44
11:J:131:ILE:HG23	11:J:132:PHE:CD1	2.53	0.44
11:J:139:ASP:H	11:J:140:PRO:HD3	1.78	0.44
13:L:90:PHE:CD1	13:L:90:PHE:N	2.86	0.44
15:N:137:ASP:C	15:N:142:LYS:HE3	2.38	0.44
15:N:157:LEU:HD22	15:N:160:PHE:CD1	2.53	0.44
15:N:65:VAL:HG21	15:N:105:ALA:HB2	2.00	0.44
15:N:87:MET:HG3	15:N:87:MET:H	1.38	0.44
7:F:147:ALA:HA	16:O:15:GLU:O	2.18	0.44
17:P:70:LEU:O	17:P:92:VAL:HG21	2.16	0.44
22:U:38:ARG:CG	22:U:38:ARG:HH11	2.27	0.44
38:A:3254:HOH:O	22:U:9:LYS:HD2	2.16	0.44
24:W:12:THR:O	24:W:13:PRO:C	2.56	0.44
27:Z:115:ARG:CZ	38:Z:8558:HOH:O	2.65	0.44
27:Z:99:ALA:HB2	27:Z:233:TYR:CE1	2.53	0.44
28:1:37:HIS:O	28:1:45:LYS:HA	2.17	0.44
1:A:1273:C:O2'	1:A:1274:A:H5'	2.18	0.44
1:A:1398:G:O2'	1:A:1399:A:H5'	2.17	0.44
1:A:1985:U:H5''	38:A:4682:HOH:O	2.18	0.44
1:A:2133:U:H4'	1:A:2134:G:H5'	2.00	0.44
1:A:366:U:H2'	1:A:367:G:O4'	2.18	0.44
1:A:517:U:C2'	1:A:518:G:H5'	2.47	0.44
1:A:795:G:H1'	1:A:817:G:N2	2.32	0.44
6:E:219:ASN:O	6:E:223:LEU:HB2	2.18	0.44
7:F:174:VAL:HG21	38:F:2195:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:80:TRP:O	8:G:134:SER:HA	2.17	0.44
11:J:57:ARG:C	11:J:59:ASN:N	2.69	0.44
11:J:81:TYR:CD1	11:J:81:TYR:C	2.91	0.44
12:K:52:GLN:CG	12:K:53:ILE:N	2.70	0.44
19:R:21:ARG:HG2	19:R:22:GLY:H	1.83	0.44
20:S:39:THR:O	20:S:40:ALA:C	2.56	0.44
5:D:329:TYR:HE2	23:V:15:PRO:HG2	1.82	0.44
25:X:48:VAL:O	25:X:48:VAL:HG12	2.16	0.44
25:X:54:PHE:C	25:X:146:ILE:HD11	2.38	0.44
26:Y:30:MET:CE	26:Y:58:ALA:HB3	2.48	0.44
1:A:1008:C:OP1	11:J:16:ARG:NH2	2.47	0.44
1:A:1195:G:C2	1:A:1205:U:O2	2.71	0.44
1:A:226:A:H1'	1:A:393:G:C5	2.53	0.44
1:A:2909:G:H2'	1:A:2910:A:H8	1.82	0.44
1:A:290:C:O2'	1:A:291:C:H5'	2.16	0.44
1:A:316:A:H1'	1:A:336:G:N3	2.33	0.44
1:A:553:G:P	27:Z:204:ARG:NH2	2.86	0.44
1:A:564:G:H1'	38:A:5796:HOH:O	2.18	0.44
1:A:1852:A:H5''	4:C:232:ARG:O	2.18	0.44
38:A:4739:HOH:O	6:E:73:LEU:HD11	2.17	0.44
7:F:44:ILE:HG12	7:F:83:PHE:CE1	2.48	0.44
7:F:55:LYS:O	7:F:56:ARG:HB2	2.18	0.44
9:H:79:GLN:HB2	9:H:82:ASP:CG	2.39	0.44
11:J:84:ARG:CZ	11:J:135:TRP:CH2	3.01	0.44
15:N:38:VAL:HG12	15:N:38:VAL:O	2.17	0.44
15:N:61:ILE:HA	38:N:8619:HOH:O	2.18	0.44
16:O:113:SER:HB3	38:O:8551:HOH:O	2.18	0.44
16:O:42:HIS:HD1	16:O:75:THR:HG1	1.64	0.44
19:R:3:SER:HB3	38:R:5998:HOH:O	2.18	0.44
26:Y:76:ARG:NH1	26:Y:76:ARG:CG	2.81	0.44
1:A:2434:A:O3'	31:4:28:GLY:HA3	2.17	0.43
1:A:1226:G:H2'	1:A:1227:C:H6	1.83	0.43
1:A:1603:A:H5''	1:A:1605:G:H5'	2.00	0.43
1:A:2505:G:C2'	1:A:2506:A:H5'	2.47	0.43
1:A:263:U:C2	9:H:59:ILE:CD1	3.01	0.43
1:A:558:C:H2'	1:A:559:U:H5''	1.98	0.43
1:A:920:C:H4'	1:A:921:G:N2	2.33	0.43
1:A:963:C:O5'	1:A:963:C:H6	2.01	0.43
5:D:101:TRP:HB2	5:D:119:HIS:CD2	2.53	0.43
5:D:130:ASP:HB2	38:D:8603:HOH:O	2.18	0.43
5:D:72:THR:HB	38:D:8611:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:162:VAL:HG12	6:E:162:VAL:O	2.18	0.43
8:G:118:ILE:HG22	8:G:119:HIS:N	2.32	0.43
9:H:39:SER:HB3	9:H:45:ALA:HB2	1.99	0.43
11:J:150:LYS:HE2	38:J:8371:HOH:O	2.17	0.43
11:J:55:GLN:HE21	11:J:124:ARG:NE	2.01	0.43
21:T:17:ASP:HB3	21:T:23:LYS:HB2	1.99	0.43
25:X:72:PRO:C	25:X:74:GLU:N	2.70	0.43
1:A:1566:C:O2'	1:A:1567:A:H5'	2.17	0.43
1:A:1682:A:H5''	38:A:8955:HOH:O	2.18	0.43
1:A:1789:G:H2'	1:A:1790:C:O5'	2.18	0.43
1:A:1878:G:O2'	1:A:1879:U:P	2.76	0.43
1:A:2312:G:H2'	1:A:2313:C:H5'	2.00	0.43
1:A:683:G:O2'	1:A:684:G:H5'	2.18	0.43
1:A:77:G:O2'	1:A:78:G:H5'	2.17	0.43
1:A:821:U:O2'	1:A:822:C:H5'	2.18	0.43
4:C:81:GLN:H	4:C:92:ASN:ND2	2.16	0.43
6:E:2:GLN:HB3	38:E:8336:HOH:O	2.18	0.43
9:H:107:VAL:O	9:H:111:ILE:HG13	2.17	0.43
11:J:31:PHE:CD2	11:J:85:ILE:HG23	2.54	0.43
17:P:36:PRO:O	17:P:39:THR:OG1	2.32	0.43
22:U:41:ARG:NH1	22:U:42:VAL:O	2.51	0.43
23:V:31:PHE:CG	23:V:37:GLU:HG2	2.53	0.43
25:X:13:MET:HE3	25:X:17:ILE:CG2	2.47	0.43
26:Y:41:PHE:CZ	26:Y:74:ALA:HB3	2.53	0.43
1:A:1069:C:H2'	1:A:1070:A:O4'	2.18	0.43
1:A:1149:U:H5''	1:A:1151:G:O4'	2.19	0.43
1:A:1942:A:HO2'	1:A:1943:C:H5'	1.83	0.43
1:A:794:U:H3	1:A:819:A:H61	1.65	0.43
38:A:6475:HOH:O	4:C:220:PRO:HB3	2.17	0.43
6:E:115:LEU:O	6:E:118:THR:HB	2.18	0.43
6:E:35:VAL:HG21	6:E:227:GLY:HA2	2.00	0.43
8:G:61:THR:O	8:G:62:ILE:C	2.56	0.43
11:J:26:LYS:HD2	11:J:28:ILE:CG1	2.48	0.43
15:N:39:ARG:NH2	38:N:8619:HOH:O	2.51	0.43
15:N:48:ARG:O	15:N:52:LEU:HG	2.19	0.43
17:P:26:TRP:HA	17:P:26:TRP:HE3	1.83	0.43
20:S:132:ARG:NH1	38:S:8582:HOH:O	2.51	0.43
20:S:33:ARG:HA	38:S:8548:HOH:O	2.17	0.43
24:W:42:ASN:N	24:W:43:PRO:HD3	2.33	0.43
25:X:108:ARG:HE	25:X:114:PRO:HG3	1.82	0.43
1:A:1066:U:H2'	1:A:1067:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1420:C:C2	1:A:1445:G:N2	2.87	0.43
1:A:1803:C:H2'	1:A:1804:A:H8	1.83	0.43
1:A:2323:G:H5'	38:A:6491:HOH:O	2.18	0.43
1:A:2634:G:OP2	4:C:204:GLY:N	2.37	0.43
1:A:2756:U:H3	1:A:2896:A:H2	1.64	0.43
38:A:6825:HOH:O	4:C:177:HIS:HE1	2.02	0.43
5:D:41:PHE:CG	5:D:190:MET:HE3	2.53	0.43
5:D:41:PHE:HB3	5:D:190:MET:CE	2.48	0.43
5:D:98:THR:C	5:D:99:GLU:HG3	2.38	0.43
9:H:31:LYS:HG3	38:H:5719:HOH:O	2.19	0.43
15:N:137:ASP:O	15:N:142:LYS:HE3	2.19	0.43
15:N:74:ARG:CD	15:N:91:ILE:CD1	2.96	0.43
20:S:72:VAL:CG1	20:S:75:TRP:HB3	2.48	0.43
20:S:92:LEU:HD23	20:S:145:LEU:HD21	2.00	0.43
21:T:73:ASP:O	21:T:77:VAL:HG23	2.18	0.43
22:U:92:ASP:O	22:U:94:SER:N	2.52	0.43
25:X:4:LEU:CD2	25:X:54:PHE:HB3	2.46	0.43
28:1:33:HIS:HA	28:1:69:TYR:O	2.18	0.43
1:A:1439:C:O5'	1:A:1439:C:H6	2.01	0.43
1:A:1829:A:C8	1:A:1885:A:C8	3.06	0.43
1:A:2120:U:H2'	1:A:2121:G:O4'	2.18	0.43
1:A:2300:A:C2	1:A:2306:U:C5	3.07	0.43
1:A:2458:U:OP1	31:4:82:GLY:N	2.47	0.43
1:A:2548:C:H2'	1:A:2549:C:H6	1.84	0.43
1:A:638:C:H2'	1:A:639:A:C8	2.53	0.43
5:D:23:THR:HA	5:D:24:PRO:HD3	1.73	0.43
6:E:13:ASP:O	6:E:13:ASP:OD1	2.36	0.43
2:B:3045:A:H4'	7:F:143:LYS:O	2.19	0.43
10:I:67:LEU:O	10:I:71:LEU:HG	2.18	0.43
11:J:56:ILE:O	11:J:61:LEU:HD21	2.18	0.43
12:K:108:PRO:HG2	12:K:109:TYR:CD1	2.54	0.43
15:N:175:GLY:O	15:N:184:ARG:NH2	2.46	0.43
38:A:4730:HOH:O	15:N:29:GLN:HA	2.19	0.43
16:O:165:ALA:HB1	38:O:8526:HOH:O	2.19	0.43
16:O:18:THR:HA	38:O:8525:HOH:O	2.17	0.43
1:A:2424:U:H1'	19:R:7:LEU:HD12	1.99	0.43
21:T:10:VAL:CG1	24:W:35:ALA:O	2.66	0.43
26:Y:47:ALA:HB1	26:Y:82:GLU:HA	1.99	0.43
27:Z:133:HIS:HE1	38:Z:8617:HOH:O	2.02	0.43
29:2:28:HIS:O	29:2:32:LYS:N	2.48	0.43
1:A:1213:C:C2'	1:A:1214:G:H5'	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:A:H2'	1:A:223:G:O4'	2.18	0.43
1:A:2296:C:H5	38:R:5998:HOH:O	2.00	0.43
1:A:2719:A:H5''	38:A:3181:HOH:O	2.18	0.43
1:A:2761:A:C4	1:A:2763:G:C8	3.05	0.43
1:A:278:A:H2'	1:A:279:C:O4'	2.19	0.43
1:A:909:U:H2'	1:A:910:C:O4'	2.19	0.43
5:D:168:GLY:O	5:D:169:GLY:O	2.36	0.43
6:E:3:ALA:N	6:E:16:VAL:O	2.51	0.43
6:E:3:ALA:O	6:E:15:GLU:HB2	2.19	0.43
8:G:20:ILE:HD12	8:G:33:LEU:HD12	2.00	0.43
11:J:154:THR:HB	11:J:155:PRO:CD	2.48	0.43
12:K:77:GLY:O	12:K:80:LYS:N	2.51	0.43
14:M:98:GLU:O	14:M:99:GLU:CB	2.67	0.43
15:N:48:ARG:HH11	15:N:52:LEU:HD21	1.82	0.43
15:N:78:ASN:ND2	38:N:8640:HOH:O	2.44	0.43
18:Q:31:ILE:HG12	18:Q:43:LEU:HD13	2.01	0.43
22:U:55:PHE:CD2	22:U:77:VAL:HG13	2.52	0.43
24:W:5:VAL:HG23	38:W:2271:HOH:O	2.18	0.43
31:4:1:MET:HE2	31:4:83:TRP:HZ2	1.83	0.43
1:A:1044:C:C5'	38:A:8543:HOH:O	2.66	0.43
1:A:1175:G:H1'	1:A:1193:A:H2'	2.01	0.43
1:A:1209:C:H2'	1:A:1210:G:C8	2.50	0.43
1:A:200:U:O2'	1:A:201:G:H5'	2.18	0.43
1:A:2382:A:H1'	31:4:10:TYR:HE2	1.82	0.43
1:A:2519:C:H5''	11:J:59:ASN:HB3	2.01	0.43
1:A:283:U:H5	1:A:284:C:H42	1.67	0.43
1:A:458:G:H4'	38:A:9202:HOH:O	2.18	0.43
1:A:475:G:H5'	6:E:73:LEU:HD23	1.99	0.43
1:A:593:A:H1'	38:A:3303:HOH:O	2.19	0.43
1:A:877:G:H1'	38:C:8513:HOH:O	2.19	0.43
2:B:3091:C:H2'	2:B:3092:G:O4'	2.18	0.43
4:C:42:VAL:HG21	4:C:74:VAL:CG1	2.49	0.43
5:D:41:PHE:N	38:D:8657:HOH:O	2.52	0.43
9:H:48:VAL:CG2	9:H:74:PHE:HB3	2.49	0.43
11:J:47:GLU:CB	11:J:133:ILE:CD1	2.94	0.43
12:K:19:MET:HE1	12:K:132:LEU:HD11	1.99	0.43
14:M:21:ARG:N	38:M:8404:HOH:O	2.52	0.43
1:A:183:A:H5'	15:N:157:LEU:HD12	2.01	0.43
15:N:187:LEU:CD2	15:N:194:ALA:HB3	2.48	0.43
17:P:26:TRP:HA	17:P:26:TRP:CE3	2.54	0.43
17:P:96:VAL:HG12	17:P:97:SER:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:41:ARG:NH1	22:U:41:ARG:HG2	2.33	0.43
23:V:6:CYS:CB	23:V:13:ILE:HD11	2.48	0.43
25:X:128:VAL:O	25:X:138:LEU:HD11	2.18	0.43
1:A:1067:A:O2'	25:X:12:ASN:OD1	2.35	0.43
31:4:22:VAL:HG12	31:4:90:PHE:HE2	1.84	0.43
1:A:1164:U:O4'	1:A:1165:G:OP1	2.36	0.43
1:A:1973:A:H5'	1:A:1973:A:H8	1.83	0.43
1:A:2589:U:H2'	1:A:2590:U:C6	2.53	0.43
1:A:390:G:H5''	38:A:9051:HOH:O	2.17	0.43
1:A:401:C:P	38:A:5274:HOH:O	2.76	0.43
1:A:445:U:H2'	1:A:446:G:H8	1.84	0.43
1:A:567:U:H5''	38:X:5817:HOH:O	2.19	0.43
38:A:5661:HOH:O	5:D:216:LYS:HD2	2.18	0.43
6:E:123:LEU:HA	6:E:123:LEU:HD23	1.88	0.43
1:A:672:G:O6	6:E:217:GLU:HG3	2.18	0.43
7:F:11:HIS:C	7:F:13:MET:N	2.71	0.43
7:F:104:PHE:CE2	7:F:132:VAL:HB	2.53	0.43
7:F:56:ARG:N	38:F:6752:HOH:O	2.50	0.43
13:L:27:ARG:HD2	38:L:4747:HOH:O	2.18	0.43
14:M:143:THR:CG2	14:M:144:ASP:N	2.79	0.43
17:P:37:ARG:HG2	38:P:3002:HOH:O	2.19	0.43
18:Q:59:ARG:O	18:Q:63:ARG:HG3	2.19	0.43
23:V:9:CYS:SG	23:V:11:THR:HG23	2.59	0.43
24:W:16:ARG:CZ	24:W:63:GLU:HG3	2.47	0.43
25:X:125:HIS:CD2	25:X:127:GLY:H	2.37	0.43
27:Z:141:THR:HG23	38:Z:8592:HOH:O	2.17	0.43
31:4:6:ARG:HG2	31:4:6:ARG:HH11	1.84	0.43
1:A:1200:A:H4'	38:A:6809:HOH:O	2.19	0.43
1:A:1600:G:H8	1:A:1600:G:OP2	2.02	0.43
1:A:1603:A:H5''	1:A:1604:G:H3'	2.01	0.43
1:A:1707:G:N1	1:A:1710:A:OP2	2.47	0.43
1:A:952:G:N3	1:A:2302:A:H2'	2.34	0.43
1:A:2434:A:C1'	38:A:3009:HOH:O	2.65	0.43
1:A:2559:C:H4'	38:A:6723:HOH:O	2.18	0.43
1:A:2719:A:C2'	1:A:2720:C:H5'	2.49	0.43
1:A:2869:G:H2'	1:A:2870:C:H6	1.83	0.43
1:A:818:A:C5'	38:A:6062:HOH:O	2.67	0.43
1:A:830:G:H2'	1:A:831:U:H6	1.83	0.43
7:F:169:THR:HG22	7:F:169:THR:O	2.19	0.43
7:F:67:ASP:HA	7:F:68:PRO:HD3	1.86	0.43
12:K:19:MET:HE1	12:K:132:LEU:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:74:ARG:HH12	12:K:76:ASP:HB2	1.82	0.43
15:N:63:VAL:HG12	15:N:64:ARG:N	2.32	0.43
16:O:162:ASP:HB3	16:O:163:PHE:H	1.63	0.43
18:Q:28:GLN:O	18:Q:32:ALA:HB2	2.19	0.43
24:W:12:THR:O	24:W:15:GLU:N	2.52	0.43
1:A:1110:G:O2'	1:A:1111:U:H5'	2.18	0.43
1:A:1163:G:H3'	1:A:1164:U:H2'	2.01	0.43
1:A:133:U:H5'	1:A:1465:A:OP1	2.19	0.43
1:A:1865:A:H2'	1:A:1866:A:C8	2.54	0.43
1:A:2038:A:O2'	1:A:2039:A:H5'	2.19	0.43
1:A:2487:C:C1'	36:5:76:PPU:HD2	2.49	0.43
2:B:3097:U:H2'	2:B:3098:C:C6	2.54	0.43
4:C:125:ASN:CB	4:C:158:VAL:HG12	2.49	0.43
7:F:146:LYS:NZ	16:O:107:ASN:ND2	2.64	0.43
11:J:162:SER:CB	11:J:163:PRO:CD	2.75	0.43
13:L:124:VAL:O	13:L:127:ALA:HB3	2.19	0.43
14:M:145:LEU:HD23	14:M:145:LEU:O	2.19	0.43
15:N:67:ILE:CD1	15:N:104:ARG:HD2	2.49	0.43
9:H:38:LYS:HZ3	15:N:3:SER:HA	1.81	0.43
19:R:41:LEU:HB3	19:R:52:PHE:CZ	2.54	0.43
20:S:39:THR:N	20:S:42:GLU:OE1	2.50	0.43
25:X:88:THR:HG23	25:X:110:GLN:HE21	1.83	0.43
26:Y:70:ILE:HG23	26:Y:70:ILE:O	2.19	0.43
1:A:116:G:H5''	1:A:131:A:H5'	2.01	0.42
1:A:1593:C:O2'	1:A:1594:C:H5'	2.19	0.42
1:A:1942:A:OP1	4:C:234:GLY:N	2.49	0.42
1:A:2055:A:H4'	20:S:132:ARG:NH2	2.34	0.42
1:A:2243:C:C5'	38:A:3248:HOH:O	2.60	0.42
1:A:2512:U:H3'	38:A:4829:HOH:O	2.19	0.42
1:A:2656:G:H1'	38:A:6842:HOH:O	2.19	0.42
1:A:396:U:H2'	1:A:397:A:C8	2.54	0.42
1:A:508:A:H2'	1:A:509:A:H5''	2.00	0.42
1:A:653:C:H2'	1:A:654:A:C8	2.54	0.42
6:E:104:ASP:HA	6:E:107:ARG:HH12	1.83	0.42
6:E:98:ARG:NH1	38:E:8358:HOH:O	2.44	0.42
7:F:94:ALA:HB3	7:F:174:VAL:HA	2.01	0.42
7:F:29:HIS:C	38:F:5858:HOH:O	2.57	0.42
7:F:57:THR:CG2	7:F:63:ILE:HG22	2.46	0.42
13:L:80:ILE:HG13	13:L:80:ILE:O	2.19	0.42
9:H:56:PRO:HG2	15:N:43:PRO:O	2.19	0.42
2:B:3048:C:OP1	16:O:114:LYS:HG3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:16:VAL:CG1	18:Q:20:ARG:HB2	2.49	0.42
18:Q:27:ARG:CD	38:Q:5262:HOH:O	2.67	0.42
19:R:86:VAL:HG13	19:R:91:LEU:HD11	2.01	0.42
20:S:39:THR:HB	20:S:42:GLU:HG3	2.01	0.42
21:T:23:LYS:HE2	38:T:8329:HOH:O	2.19	0.42
21:T:33:SER:O	21:T:37:VAL:HG23	2.19	0.42
1:A:317:A:OP1	22:U:52:ARG:O	2.37	0.42
23:V:47:ARG:HG3	38:V:4381:HOH:O	2.18	0.42
31:4:9:THR:OG1	31:4:80:ARG:NH2	2.43	0.42
1:A:1182:C:H1'	1:A:1192:A:C8	2.52	0.42
1:A:1525:G:H5'	1:A:1526:A:OP2	2.19	0.42
1:A:1609:C:H2'	1:A:1610:G:H8	1.84	0.42
1:A:1755:A:O2'	1:A:1756:G:H5'	2.18	0.42
1:A:1878:G:O2'	1:A:1879:U:OP2	2.36	0.42
1:A:2809:G:H2'	1:A:2810:G:O4'	2.19	0.42
1:A:2823:G:H4'	1:A:2827:A:O4'	2.19	0.42
1:A:2896:A:H2'	1:A:2896:A:N3	2.34	0.42
2:B:3020:G:C2'	2:B:3021:G:H5'	2.49	0.42
4:C:81:GLN:HB2	4:C:92:ASN:ND2	2.34	0.42
6:E:27:ARG:HG2	6:E:30:LEU:HG	2.00	0.42
38:A:9457:HOH:O	6:E:78:ARG:HD3	2.19	0.42
16:O:75:THR:HG21	38:O:8536:HOH:O	2.18	0.42
25:X:13:MET:CE	25:X:17:ILE:CG2	2.97	0.42
25:X:4:LEU:O	25:X:32:CYS:HA	2.19	0.42
1:A:2320:U:OP2	31:4:2:GLN:N	2.51	0.42
31:4:70:ARG:CA	38:4:8571:HOH:O	2.67	0.42
1:A:1013:A:C2	1:A:1014:A:H1'	2.55	0.42
1:A:1505:U:C6	1:A:1505:U:H5'	2.54	0.42
1:A:160:A:C4	1:A:177:A:C2	3.08	0.42
1:A:1771:U:O2'	1:A:1773:G:N7	2.49	0.42
1:A:2025:G:C6	1:A:2026:C:C4	3.08	0.42
1:A:2690:U:H2'	1:A:2703:A:N6	2.34	0.42
1:A:2836:G:C6	1:A:2838:A:C2	3.06	0.42
1:A:293:A:C4	1:A:360:A:C2	3.07	0.42
1:A:329:A:C5	1:A:347:A:C2	3.08	0.42
1:A:401:C:H2'	1:A:402:U:C6	2.54	0.42
1:A:470:U:O2'	29:2:16:HIS:HD2	2.02	0.42
1:A:921:G:H4'	1:A:924:G:C6	2.53	0.42
2:B:3041:C:H2'	2:B:3042:C:H6	1.84	0.42
2:B:3059:C:H2'	2:B:3060:C:C6	2.55	0.42
2:B:3096:C:H2'	2:B:3097:U:H6	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:307:ARG:HH11	5:D:307:ARG:CG	2.33	0.42
5:D:48:MET:O	5:D:49:THR:HG23	2.20	0.42
7:F:59:GLY:O	7:F:61:PHE:N	2.42	0.42
8:G:64:THR:HG22	8:G:68:HIS:CD2	2.54	0.42
10:I:23:ILE:O	10:I:27:ILE:HG13	2.19	0.42
11:J:156:THR:C	11:J:157:ILE:HG13	2.39	0.42
16:O:108:SER:HA	16:O:109:PRO:HD3	1.82	0.42
16:O:74:PRO:HG2	16:O:159:TYR:CZ	2.53	0.42
16:O:171:HIS:HA	16:O:174:GLU:OE1	2.18	0.42
16:O:50:LEU:HA	16:O:50:LEU:HD12	1.85	0.42
16:O:71:TRP:HB2	38:O:8537:HOH:O	2.17	0.42
16:O:93:GLN:HG2	38:O:8554:HOH:O	2.19	0.42
23:V:6:CYS:C	23:V:8:TYR:H	2.23	0.42
24:W:45:ARG:O	24:W:48:GLU:N	2.52	0.42
25:X:119:HIS:HD2	25:X:120:PRO:O	2.02	0.42
29:2:5:THR:N	29:2:6:PRO:HD2	2.33	0.42
1:A:1098:A:H2'	1:A:1099:G:O4'	2.20	0.42
1:A:1154:A:H2'	1:A:1155:G:C8	2.54	0.42
1:A:1345:A:H2'	1:A:1346:U:C6	2.54	0.42
1:A:151:A:H2'	1:A:152:A:O4'	2.19	0.42
1:A:169:A:HO2'	1:A:170:U:H6	1.65	0.42
1:A:1787:C:O2'	1:A:1788:U:H5'	2.20	0.42
1:A:2134:G:C6	1:A:2258:A:C8	3.08	0.42
1:A:324:G:C6	1:A:325:U:C5	3.07	0.42
1:A:706:G:H4'	38:A:6853:HOH:O	2.19	0.42
1:A:797:A:H4'	28:1:10:ARG:N	2.35	0.42
1:A:90:A:H2'	1:A:91:G:O4'	2.19	0.42
4:C:94:LEU:N	4:C:94:LEU:CD2	2.80	0.42
5:D:144:THR:CG2	5:D:145:HIS:H	2.32	0.42
5:D:146:THR:O	5:D:148:PRO:HD3	2.19	0.42
5:D:195:ARG:O	5:D:198:GLU:HG3	2.19	0.42
5:D:224:LYS:O	5:D:225:GLY:C	2.57	0.42
12:K:107:ASN:HD22	12:K:108:PRO:HD2	1.84	0.42
13:L:115:ARG:CG	13:L:116:GLU:N	2.80	0.42
16:O:163:PHE:H	16:O:163:PHE:HD2	1.66	0.42
20:S:100:ASP:C	20:S:102:GLN:H	2.21	0.42
23:V:49:LEU:O	23:V:55:ALA:CB	2.68	0.42
26:Y:43:VAL:CG1	26:Y:44:ASP:N	2.82	0.42
27:Z:144:ARG:CZ	38:Z:8618:HOH:O	2.66	0.42
27:Z:172:THR:HG22	27:Z:173:ALA:N	2.33	0.42
27:Z:235:GLU:CD	27:Z:235:GLU:N	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A:4185:HOH:O	28:1:51:GLY:HA3	2.19	0.42
1:A:1242:A:OP2	12:K:60:ARG:NH1	2.51	0.42
1:A:639:A:C2	1:A:1363:G:C2	3.07	0.42
1:A:13:G:O2'	1:A:14:C:H5'	2.19	0.42
1:A:2004:U:H2'	1:A:2004:U:O2	2.19	0.42
1:A:2084:C:H2'	1:A:2085:A:C8	2.54	0.42
1:A:382:U:O2'	1:A:430:A:H1'	2.20	0.42
5:D:226:LYS:HG2	5:D:230:GLN:NE2	2.34	0.42
8:G:31:ARG:HH12	8:G:68:HIS:CG	2.37	0.42
9:H:26:THR:HB	9:H:102:GLY:O	2.20	0.42
11:J:139:ASP:HB3	38:J:8380:HOH:O	2.17	0.42
12:K:6:PHE:CZ	12:K:102:ARG:HG3	2.53	0.42
1:A:401:C:O2'	15:N:92:THR:HB	2.19	0.42
16:O:161:GLY:O	16:O:162:ASP:C	2.57	0.42
16:O:12:ARG:HD3	16:O:18:THR:OG1	2.19	0.42
20:S:16:ALA:CB	20:S:95:ALA:HB2	2.49	0.42
22:U:26:THR:HA	22:U:39:ASN:HB3	2.00	0.42
1:A:1174:A:C5	1:A:1201:C:H4'	2.54	0.42
1:A:1471:A:H2'	1:A:1472:C:C6	2.55	0.42
1:A:1562:C:H2'	1:A:1562:C:O2	2.19	0.42
1:A:171:C:C2'	1:A:172:U:H5'	2.50	0.42
1:A:2408:A:H4'	31:4:15:ASN:O	2.20	0.42
1:A:2430:A:H2'	1:A:2431:C:H6	1.83	0.42
1:A:2909:G:O2'	1:A:2910:A:H5'	2.19	0.42
1:A:398:U:H2'	1:A:399:C:C6	2.53	0.42
1:A:740:G:C6	1:A:741:C:C4	3.08	0.42
1:A:745:G:H4'	38:A:4633:HOH:O	2.19	0.42
5:D:51:VAL:CG2	5:D:329:TYR:O	2.68	0.42
5:D:62:ARG:CB	5:D:65:MET:HE3	2.50	0.42
11:J:26:LYS:NZ	11:J:31:PHE:CZ	2.85	0.42
13:L:98:VAL:HG13	13:L:102:GLU:HA	2.01	0.42
13:L:31:VAL:HG22	13:L:53:ILE:HD12	2.01	0.42
17:P:32:ARG:HD3	17:P:32:ARG:O	2.19	0.42
21:T:29:ASP:OD1	21:T:31:ARG:HG3	2.19	0.42
23:V:49:LEU:HD13	23:V:51:TRP:HE1	1.84	0.42
31:4:60:LYS:HG3	31:4:61:PRO:HD2	2.00	0.42
1:A:1573:A:H2'	1:A:1574:C:O4'	2.19	0.42
1:A:1602:C:H5'	38:A:5962:HOH:O	2.20	0.42
1:A:1778:A:H2'	1:A:1779:A:H5'	2.00	0.42
1:A:1819:G:H5'	38:A:4194:HOH:O	2.18	0.42
1:A:2105:C:H2'	1:A:2106:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2133:U:H4'	1:A:2134:G:C5'	2.50	0.42
1:A:2478:U:O2'	1:A:2479:A:H5'	2.19	0.42
1:A:2673:U:H2'	1:A:2674:G:H5'	2.01	0.42
2:B:3092:G:H2'	2:B:3093:A:H8	1.81	0.42
2:B:3092:G:C6	2:B:3093:A:C6	3.08	0.42
5:D:162:MET:HE3	5:D:308:LEU:CD2	2.31	0.42
7:F:156:ARG:HH11	7:F:156:ARG:HG3	1.83	0.42
8:G:11:VAL:CG1	8:G:12:ASP:H	2.33	0.42
8:G:1:PRO:HG2	8:G:59:MET:SD	2.60	0.42
8:G:81:GLU:N	38:G:6931:HOH:O	2.45	0.42
11:J:60:ALA:CB	38:J:8338:HOH:O	2.67	0.42
15:N:27:ARG:O	15:N:30:GLU:N	2.53	0.42
19:R:16:ASN:HA	19:R:16:ASN:HD22	1.66	0.42
29:2:13:THR:HG22	29:2:14:THR:N	2.34	0.42
1:A:1276:U:H2'	1:A:1278:A:OP2	2.20	0.42
1:A:1474:C:O2'	1:A:1475:G:H5'	2.19	0.42
1:A:1810:C:N3	1:A:1811:A:C5	2.88	0.42
1:A:1885:A:O5'	1:A:1885:A:H8	2.02	0.42
1:A:1915:U:C2	1:A:1925:G:N2	2.88	0.42
1:A:2387:U:H2'	1:A:2388:C:H6	1.84	0.42
1:A:2634:G:H2'	1:A:2635:A:H8	1.85	0.42
1:A:2766:A:O2'	1:A:2767:C:H5'	2.20	0.42
1:A:2812:A:C2	1:A:2814:A:N6	2.72	0.42
1:A:290:C:N3	1:A:363:A:C2	2.87	0.42
1:A:665:A:C6	1:A:666:A:C6	3.08	0.42
1:A:807:A:H2'	1:A:808:A:C8	2.54	0.42
1:A:869:G:OP1	15:N:79:LYS:HE2	2.18	0.42
1:A:947:U:H2'	1:A:948:G:H8	1.81	0.42
2:B:3004:G:O2'	16:O:44:ARG:NH2	2.53	0.42
4:C:170:VAL:HG22	28:1:22:ILE:HG23	2.01	0.42
1:A:1847:A:OP1	4:C:175:LYS:HG3	2.20	0.42
5:D:156:LYS:HE3	38:D:8638:HOH:O	2.19	0.42
6:E:4:THR:HB	6:E:135:GLU:OE1	2.20	0.42
9:H:105:ALA:HB2	38:H:5522:HOH:O	2.19	0.42
13:L:101:ASN:O	13:L:102:GLU:HB2	2.20	0.42
13:L:48:GLY:O	13:L:73:VAL:HB	2.20	0.42
18:Q:59:ARG:HH11	18:Q:59:ARG:HG2	1.85	0.42
19:R:23:THR:HG23	38:R:4792:HOH:O	2.19	0.42
22:U:64:ASN:HB3	22:U:73:HIS:HB2	2.00	0.42
38:A:3094:HOH:O	27:Z:115:ARG:HB2	2.19	0.42
1:A:1157:C:H2'	1:A:1158:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1119:G:N2	1:A:1246:A:H2	2.11	0.42
1:A:1789:G:C2'	1:A:1790:C:O5'	2.68	0.42
1:A:1916:C:N4	1:A:1917:G:C6	2.88	0.42
1:A:2247:C:C5'	38:A:6811:HOH:O	2.67	0.42
1:A:1857:A:C6	1:A:2247:C:H1'	2.55	0.42
1:A:2526:C:H6	1:A:2526:C:H3'	1.85	0.42
1:A:2613:G:O2'	1:A:2614:C:H5'	2.20	0.42
1:A:2672:C:OP2	5:D:25:ARG:NH1	2.53	0.42
1:A:2853:U:C4	1:A:2906:A:N6	2.87	0.42
1:A:695:C:H2'	1:A:696:C:H6	1.82	0.42
2:B:3038:A:H2	2:B:3043:G:H5''	1.85	0.42
4:C:95:PRO:O	4:C:99:ILE:HG12	2.20	0.42
7:F:11:HIS:O	7:F:13:MET:N	2.44	0.42
8:G:158:ASP:HA	38:G:2712:HOH:O	2.20	0.42
9:H:48:VAL:HG23	9:H:74:PHE:HB3	2.01	0.42
11:J:151:MET:HA	11:J:151:MET:HE3	2.01	0.42
11:J:47:GLU:N	11:J:160:ASP:O	2.42	0.42
12:K:130:VAL:HG12	12:K:131:THR:N	2.33	0.42
25:X:132:VAL:C	25:X:134:GLU:H	2.22	0.42
28:1:10:ARG:HG3	28:1:11:THR:N	2.35	0.42
38:A:6071:HOH:O	31:4:79:LEU:HB2	2.19	0.42
1:A:1181:A:H2'	1:A:1182:C:O4'	2.19	0.42
1:A:1188:A:C5	1:A:1189:A:C2	3.08	0.42
1:A:1325:G:O2'	1:A:1326:U:H5'	2.19	0.42
1:A:1494:A:C6	1:A:1512:G:C6	3.08	0.42
1:A:1524:U:O2'	1:A:1525:G:P	2.78	0.42
1:A:1666:C:C2'	1:A:1667:A:H5''	2.49	0.42
1:A:1702:U:H1'	38:A:5255:HOH:O	2.20	0.42
1:A:171:C:H2'	1:A:172:U:H5'	2.02	0.42
1:A:1820:G:C6	1:A:2030:A:C2	3.08	0.42
1:A:1477:C:H4'	1:A:1868:G:OP1	2.19	0.42
1:A:1922:A:H3'	1:A:1923:G:H8	1.84	0.42
1:A:2005:G:OP2	1:A:2005:G:H3'	2.19	0.42
1:A:2035:C:H6	1:A:2035:C:O5'	2.03	0.42
1:A:212:A:C8	1:A:214:U:C2	3.08	0.42
1:A:2813:A:H2'	38:A:3400:HOH:O	2.18	0.42
1:A:472:A:O4'	1:A:774:C:H4'	2.20	0.42
1:A:678:G:OP2	6:E:107:ARG:NH2	2.53	0.42
4:C:37:VAL:HG22	38:C:8610:HOH:O	2.18	0.42
5:D:154:VAL:HA	5:D:155:PRO:HD3	1.89	0.42
5:D:316:ARG:N	5:D:317:PRO:HD3	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:54:VAL:HB	38:D:8618:HOH:O	2.20	0.42
2:B:3029:C:H5''	7:F:140:ARG:HD3	2.02	0.42
8:G:112:ALA:HA	8:G:113:PRO:HD3	1.92	0.42
8:G:69:ILE:HA	8:G:72:MET:HE2	2.01	0.42
10:I:71:LEU:O	10:I:73:ASP:N	2.53	0.42
11:J:31:PHE:HD2	11:J:85:ILE:O	2.03	0.42
11:J:58:HIS:CE1	11:J:59:ASN:ND2	2.87	0.42
15:N:169:ARG:CB	38:N:8584:HOH:O	2.67	0.42
18:Q:16:VAL:CG1	18:Q:17:GLY:H	2.33	0.42
20:S:100:ASP:C	20:S:102:GLN:N	2.73	0.42
22:U:48:VAL:HG13	22:U:49:GLU:N	2.34	0.42
1:A:489:A:C8	22:U:82:THR:HG22	2.55	0.42
38:A:5734:HOH:O	23:V:56:ARG:HB3	2.19	0.42
24:W:27:LEU:HA	24:W:49:LEU:HD13	2.01	0.42
25:X:7:LEU:HD12	25:X:53:ALA:HB2	2.01	0.42
26:Y:20:GLU:O	26:Y:21:PRO:C	2.57	0.42
1:A:1886:A:O2'	28:1:20:LEU:HB2	2.20	0.41
1:A:1056:U:H2'	1:A:1057:A:O4'	2.20	0.41
1:A:1086:A:P	25:X:9:GLY:H	2.42	0.41
1:A:1308:A:H5'	38:A:6406:HOH:O	2.20	0.41
1:A:1409:G:H5'	38:A:3222:HOH:O	2.19	0.41
1:A:1665:G:C6	1:A:1666:C:C4	3.08	0.41
1:A:1727:G:H1'	38:A:4153:HOH:O	2.20	0.41
1:A:1755:A:H2'	1:A:1756:G:O4'	2.20	0.41
1:A:1838:U:H2'	1:A:1839:A:H5'	2.01	0.41
1:A:2433:A:H2'	1:A:2434:A:C8	2.55	0.41
1:A:2694:A:H5''	8:G:90:HIS:CE1	2.55	0.41
1:A:2761:A:H4'	38:A:3968:HOH:O	2.19	0.41
1:A:2673:U:C2	1:A:2817:G:C2	3.08	0.41
1:A:2821:C:H4'	5:D:116:PRO:HG3	2.01	0.41
2:B:3097:U:H2'	2:B:3098:C:H6	1.85	0.41
4:C:109:GLU:HG2	4:C:116:GLY:N	2.35	0.41
1:A:820:G:C5	4:C:171:LYS:HB2	2.54	0.41
4:C:83:GLY:O	4:C:94:LEU:HB3	2.19	0.41
5:D:105:PHE:CD1	5:D:115:VAL:CG1	3.03	0.41
5:D:329:TYR:CE2	23:V:15:PRO:CG	3.02	0.41
5:D:57:GLU:HA	5:D:58:PRO:HD2	1.92	0.41
7:F:101:THR:HG22	7:F:101:THR:O	2.19	0.41
7:F:170:TYR:N	7:F:170:TYR:CD1	2.88	0.41
9:H:78:GLU:HG3	38:H:5966:HOH:O	2.21	0.41
12:K:41:ALA:O	12:K:43:ARG:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:170:GLU:HA	16:O:173:ASP:OD2	2.20	0.41
21:T:39:ASP:O	21:T:43:GLU:HG3	2.20	0.41
24:W:27:LEU:CA	24:W:49:LEU:HD13	2.50	0.41
25:X:125:HIS:HE1	38:X:3071:HOH:O	2.02	0.41
1:A:1474:C:H6	1:A:1474:C:C5'	2.26	0.41
1:A:1483:C:C2'	1:A:1484:G:H5'	2.49	0.41
1:A:1523:G:H2'	1:A:1524:U:C6	2.55	0.41
1:A:1667:A:H2'	1:A:1668:U:C6	2.55	0.41
1:A:1687:C:H2'	1:A:1688:G:O4'	2.20	0.41
1:A:2324:G:C2	1:A:2377:U:O2	2.73	0.41
1:A:2455:A:H2'	1:A:2456:A:O4'	2.19	0.41
1:A:2594:C:O2'	1:A:2595:U:H5'	2.20	0.41
1:A:2785:C:H4'	1:A:2786:G:OP2	2.21	0.41
1:A:418:C:O5'	1:A:418:C:H6	2.03	0.41
1:A:445:U:C1'	38:A:6805:HOH:O	2.68	0.41
1:A:449:A:C8	6:E:43:LYS:HG2	2.54	0.41
1:A:858:U:H2'	1:A:859:C:C6	2.54	0.41
1:A:84:G:O2'	1:A:85:C:H5'	2.21	0.41
1:A:902:G:N7	14:M:18:HIS:CD2	2.87	0.41
5:D:215:VAL:HA	5:D:220:VAL:HG22	2.03	0.41
1:A:1352:A:P	6:E:92:PRO:HG3	2.60	0.41
7:F:173:GLU:O	7:F:174:VAL:C	2.59	0.41
7:F:73:VAL:HG21	38:F:5828:HOH:O	2.20	0.41
14:M:120:LEU:HD12	14:M:133:VAL:HG21	2.00	0.41
14:M:62:ALA:HB2	14:M:103:ALA:CB	2.50	0.41
15:N:37:VAL:CB	15:N:108:LYS:HG3	2.50	0.41
18:Q:103:THR:O	18:Q:106:ARG:HB3	2.20	0.41
1:A:1705:C:P	18:Q:59:ARG:HH12	2.42	0.41
19:R:35:ASP:N	19:R:35:ASP:OD1	2.53	0.41
21:T:57:THR:HG22	21:T:58:MET:N	2.35	0.41
23:V:20:MET:HE2	23:V:30:HIS:CD2	2.55	0.41
26:Y:23:HIS:CD2	26:Y:24:LYS:HG3	2.55	0.41
28:1:56:MET:HE3	28:1:63:LYS:HG3	2.01	0.41
1:A:1174:A:C8	1:A:1201:C:OP1	2.73	0.41
1:A:1342:C:O2'	1:A:1343:C:H5'	2.20	0.41
1:A:1425:G:O2'	1:A:1426:C:H5'	2.20	0.41
1:A:1542:G:C2	1:A:1644:C:C2	3.08	0.41
1:A:791:A:H4'	1:A:1709:G:H4'	2.02	0.41
1:A:2437:A:C6	1:A:2438:G:C6	3.09	0.41
1:A:2503:A:OP1	11:J:147:ARG:NH2	2.48	0.41
1:A:699:C:C2	1:A:743:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:812:A:H2'	1:A:813:C:C6	2.56	0.41
1:A:1452:G:H1'	35:A:8503:CL:CL	2.56	0.41
5:D:204:GLY:HA3	38:D:8662:HOH:O	2.20	0.41
5:D:320:GLN:HG3	5:D:321:PRO:HD2	2.01	0.41
6:E:39:GLN:O	6:E:43:LYS:CD	2.62	0.41
7:F:23:VAL:HG22	7:F:73:VAL:HB	2.02	0.41
9:H:72:VAL:HA	9:H:73:PRO:HD3	1.84	0.41
14:M:53:ARG:O	14:M:58:GLN:NE2	2.54	0.41
1:A:1761:U:H5'	18:Q:81:LYS:O	2.20	0.41
1:A:793:A:C5'	18:Q:83:LYS:HG2	2.51	0.41
23:V:8:TYR:HD2	23:V:36:CYS:HB3	1.85	0.41
25:X:29:VAL:O	25:X:30:ASN:HB2	2.20	0.41
27:Z:98:GLN:HA	38:Z:8538:HOH:O	2.21	0.41
1:A:13:G:H2'	1:A:14:C:H6	1.85	0.41
1:A:1516:C:H2'	1:A:1517:U:H6	1.85	0.41
1:A:1730:G:C5'	1:A:1731:C:C6	3.03	0.41
1:A:1815:A:O2'	1:A:2750:G:H1'	2.20	0.41
1:A:240:C:O2	1:A:240:C:H2'	2.21	0.41
1:A:2820:A:H2'	1:A:2821:C:O4'	2.21	0.41
1:A:401:C:C5'	38:A:5274:HOH:O	2.67	0.41
1:A:550:C:H2'	1:A:551:A:O4'	2.20	0.41
1:A:56:G:H5''	24:W:50:ARG:HH12	1.82	0.41
1:A:796:A:H5'	38:A:5989:HOH:O	2.20	0.41
2:B:3023:U:H3'	2:B:3024:U:C5'	2.47	0.41
2:B:3082:U:H2'	2:B:3083:G:C8	2.55	0.41
1:A:2038:A:H5''	5:D:222:LYS:HG3	2.02	0.41
5:D:307:ARG:HH11	5:D:307:ARG:CB	2.34	0.41
5:D:337:GLY:C	38:D:8558:HOH:O	2.59	0.41
7:F:99:ASP:HB3	7:F:103:ASN:H	1.85	0.41
7:F:27:ILE:CG2	38:F:5858:HOH:O	2.68	0.41
8:G:71:ASN:HA	8:G:80:TRP:HZ2	1.84	0.41
8:G:92:PRO:HB2	38:G:4917:HOH:O	2.19	0.41
11:J:75:SER:O	11:J:79:ALA:CB	2.65	0.41
15:N:186:SER:OG	15:N:189:VAL:CG1	2.69	0.41
15:N:52:LEU:HD13	15:N:116:ASN:HB3	2.02	0.41
17:P:44:ASN:HB3	17:P:67:SER:O	2.20	0.41
20:S:61:GLN:CD	38:S:8540:HOH:O	2.59	0.41
25:X:110:GLN:CA	25:X:110:GLN:HE21	2.23	0.41
25:X:65:VAL:CA	25:X:68:THR:HG22	2.49	0.41
1:A:1064:U:H2'	1:A:1065:G:C8	2.56	0.41
1:A:1500:U:C2	1:A:1503:U:O4	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1576:G:H2'	1:A:1577:U:O4'	2.20	0.41
1:A:1730:G:C5'	1:A:1731:C:H6	2.33	0.41
1:A:1816:C:H6	1:A:1816:C:O5'	2.04	0.41
1:A:192:A:H5''	38:A:5708:HOH:O	2.19	0.41
1:A:2372:A:H2'	1:A:2373:U:C6	2.56	0.41
1:A:2408:A:O2'	31:4:17:HIS:N	2.53	0.41
1:A:2428:G:H1'	1:A:2461:U:O4	2.21	0.41
1:A:2621:U:H2'	1:A:2622:A:O4'	2.21	0.41
1:A:400:C:O2'	1:A:401:C:H5'	2.20	0.41
1:A:152:A:H1'	1:A:440:C:O2'	2.20	0.41
1:A:445:U:H2'	1:A:446:G:C8	2.56	0.41
1:A:463:A:O3'	1:A:464:G:H4'	2.20	0.41
1:A:694:A:H4'	1:A:2441:U:OP1	2.20	0.41
1:A:786:G:O2'	1:A:787:G:H5'	2.21	0.41
4:C:109:GLU:HG3	4:C:153:ARG:O	2.21	0.41
4:C:30:ARG:HB3	4:C:30:ARG:HE	1.71	0.41
4:C:37:VAL:HG13	38:C:8624:HOH:O	2.20	0.41
5:D:7:ARG:NH1	5:D:7:ARG:CG	2.79	0.41
6:E:118:THR:CG2	6:E:137:PRO:HB3	2.48	0.41
7:F:52:THR:N	7:F:70:GLY:O	2.53	0.41
11:J:109:ASP:HB2	38:J:8334:HOH:O	2.20	0.41
11:J:62:GLU:HA	38:J:8373:HOH:O	2.21	0.41
12:K:54:VAL:CG1	12:K:138:THR:HG21	2.48	0.41
38:F:3066:HOH:O	16:O:15:GLU:HB3	2.21	0.41
17:P:59:VAL:CG2	17:P:111:VAL:HG23	2.50	0.41
1:A:1398:G:C4'	18:Q:25:PRO:HG3	2.51	0.41
1:A:1019:C:O2	19:R:94:GLN:NE2	2.54	0.41
1:A:123:U:O2'	1:A:124:C:H5'	2.20	0.41
1:A:1285:U:H4'	25:X:74:GLU:OE1	2.21	0.41
1:A:1548:U:H5''	18:Q:59:ARG:CZ	2.50	0.41
1:A:1683:G:N2	1:A:1723:G:H2'	2.36	0.41
1:A:191:A:N1	1:A:236:A:O2'	2.47	0.41
1:A:2024:A:C2	1:A:2025:G:C8	3.09	0.41
1:A:266:G:C2	1:A:267:G:C8	3.09	0.41
1:A:295:C:C2'	1:A:296:G:H5'	2.50	0.41
1:A:503:G:H2'	1:A:504:G:H8	1.86	0.41
1:A:906:C:C2	1:A:1300:G:N2	2.88	0.41
1:A:1940:C:H5''	4:C:234:GLY:HA3	2.01	0.41
5:D:177:HIS:NE2	5:D:181:ILE:HD11	2.36	0.41
6:E:160:LEU:O	6:E:162:VAL:HG23	2.21	0.41
7:F:135:VAL:HG22	7:F:136:ARG:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:21:GLU:HA	9:H:24:ARG:HE	1.85	0.41
11:J:144:GLU:HA	11:J:144:GLU:OE1	2.20	0.41
11:J:35:ASN:HD21	11:J:80:ASN:HA	1.83	0.41
12:K:42:GLU:O	12:K:131:THR:HG23	2.20	0.41
12:K:81:ARG:HB2	38:K:5750:HOH:O	2.20	0.41
13:L:63:GLU:O	13:L:67:GLN:NE2	2.51	0.41
17:P:59:VAL:HG21	17:P:111:VAL:HG21	2.02	0.41
18:Q:119:TYR:O	18:Q:120:ARG:C	2.57	0.41
18:Q:143:ALA:HA	38:Q:2178:HOH:O	2.19	0.41
20:S:61:GLN:NE2	38:S:8540:HOH:O	2.53	0.41
20:S:76:ASP:OD1	20:S:76:ASP:N	2.53	0.41
26:Y:43:VAL:HG12	26:Y:47:ALA:HB3	1.97	0.41
27:Z:122:ARG:NH2	38:Z:8535:HOH:O	2.52	0.41
1:A:1268:C:O2'	27:Z:169:ARG:HB2	2.21	0.41
1:A:1249:U:H2'	1:A:1250:C:C6	2.55	0.41
1:A:1422:U:H2'	1:A:1423:C:H6	1.83	0.41
1:A:1643:C:O2'	1:A:1644:C:H5'	2.19	0.41
1:A:1534:C:O2'	1:A:1656:A:OP1	2.35	0.41
1:A:64:G:H2'	1:A:65:C:O4'	2.21	0.41
1:A:679:G:C6	1:A:680:G:C4	3.09	0.41
1:A:823:U:H2'	1:A:824:G:O4'	2.20	0.41
2:B:3061:C:H2'	2:B:3062:A:H8	1.85	0.41
4:C:140:LEU:HB3	4:C:141:PRO:HD2	2.03	0.41
4:C:53:ALA:HB1	4:C:54:PRO:HD2	2.02	0.41
5:D:91:PRO:O	12:K:144:THR:HG21	2.21	0.41
11:J:114:PRO:O	11:J:115:PHE:C	2.59	0.41
11:J:149:ALA:C	11:J:151:MET:N	2.74	0.41
14:M:144:ASP:HA	14:M:147:GLU:HG3	2.02	0.41
15:N:37:VAL:CG1	15:N:63:VAL:HG11	2.50	0.41
1:A:2415:A:O2'	16:O:29:SER:HB3	2.20	0.41
1:A:949:U:O2'	19:R:40:HIS:HE1	2.04	0.41
1:A:2404:G:H4'	19:R:68:GLY:CA	2.51	0.41
20:S:56:PRO:HB3	20:S:80:TYR:CE2	2.55	0.41
20:S:98:ASN:N	20:S:98:ASN:ND2	2.69	0.41
22:U:65:VAL:HG22	22:U:72:ILE:HG22	2.02	0.41
25:X:122:ARG:HH11	25:X:122:ARG:CG	2.31	0.41
27:Z:145:LYS:O	27:Z:147:ARG:HG2	2.20	0.41
38:A:4185:HOH:O	28:I:54:ILE:HD12	2.20	0.41
29:2:28:HIS:CD2	29:2:30:LYS:HB2	2.56	0.41
1:A:1158:G:O2'	1:A:1159:G:H5'	2.20	0.41
1:A:2240:U:H5''	38:A:5865:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2267:G:H5'	38:A:3022:HOH:O	2.21	0.41
1:A:2631:U:H2'	1:A:2632:G:O4'	2.21	0.41
1:A:2834:G:C4	1:A:2847:G:N2	2.89	0.41
1:A:396:U:H3'	38:A:3417:HOH:O	2.21	0.41
1:A:461:C:H2'	38:A:3492:HOH:O	2.20	0.41
4:C:29:HIS:CE1	4:C:107:ASN:HD22	2.39	0.41
4:C:164:ARG:HB2	28:1:68:CYS:SG	2.61	0.41
5:D:102:THR:CG2	5:D:182:VAL:HG12	2.51	0.41
5:D:14:GLY:HA2	5:D:15:PRO:O	2.21	0.41
5:D:146:THR:O	5:D:159:PRO:HB3	2.20	0.41
5:D:280:VAL:HG13	5:D:333:GLU:O	2.21	0.41
5:D:313:PRO:O	5:D:314:ALA:C	2.58	0.41
5:D:69:VAL:HA	5:D:70:PRO:HD3	1.94	0.41
5:D:88:GLU:HG3	5:D:88:GLU:O	2.21	0.41
6:E:233:THR:CG2	6:E:234:VAL:N	2.84	0.41
8:G:31:ARG:NH1	8:G:68:HIS:CG	2.88	0.41
11:J:113:ALA:N	11:J:114:PRO:CD	2.84	0.41
11:J:154:THR:N	11:J:155:PRO:HD2	2.35	0.41
11:J:162:SER:HB3	38:J:8330:HOH:O	2.19	0.41
13:L:90:PHE:HB3	38:L:6115:HOH:O	2.20	0.41
14:M:57:VAL:HG12	14:M:57:VAL:O	2.21	0.41
14:M:61:ALA:HA	38:M:8439:HOH:O	2.20	0.41
1:A:189:A:OP1	15:N:171:ARG:NH2	2.53	0.41
15:N:85:ARG:NH1	38:N:8533:HOH:O	2.50	0.41
16:O:74:PRO:CD	16:O:159:TYR:CE2	3.03	0.41
16:O:47:LEU:CD1	16:O:97:VAL:HG11	2.50	0.41
17:P:98:LEU:O	17:P:102:ILE:HG13	2.21	0.41
18:Q:37:ARG:O	18:Q:40:VAL:HB	2.20	0.41
19:R:64:GLU:HG3	19:R:74:ASP:OD2	2.20	0.41
20:S:119:VAL:HG11	38:S:8583:HOH:O	2.21	0.41
20:S:29:LYS:HB3	38:S:8532:HOH:O	2.20	0.41
22:U:32:ARG:NH1	22:U:38:ARG:HH12	2.19	0.41
22:U:3:GLN:HA	22:U:4:PRO:HD3	1.81	0.41
1:A:1073:A:H1'	1:A:1088:A:N1	2.36	0.41
1:A:1298:U:H2'	1:A:1299:G:C8	2.56	0.41
1:A:1316:G:H1'	1:A:1340:G:H22	1.81	0.41
1:A:1883:U:H5''	1:A:2013:G:OP2	2.21	0.41
1:A:2442:G:H2'	38:A:8708:HOH:O	2.21	0.41
1:A:2807:U:OP1	5:D:312:ARG:NH2	2.47	0.41
1:A:321:A:O2'	1:A:322:G:H5'	2.21	0.41
4:C:130:THR:HG22	4:C:131:HIS:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:51:VAL:HG13	5:D:53:LEU:CD1	2.50	0.41
7:F:156:ARG:NH1	7:F:156:ARG:HG3	2.36	0.41
38:A:3188:HOH:O	8:G:143:GLN:CG	2.68	0.41
9:H:17:LEU:O	9:H:21:GLU:HG3	2.20	0.41
9:H:58:GLU:HA	9:H:61:MET:HG3	2.03	0.41
13:L:8:VAL:HG12	13:L:9:THR:N	2.36	0.41
14:M:134:GLU:HG3	38:M:8433:HOH:O	2.21	0.41
16:O:154:LEU:HG	16:O:155:GLU:H	1.85	0.41
38:A:7364:HOH:O	16:O:1:ALA:CB	2.69	0.41
18:Q:142:ASP:O	18:Q:143:ALA:O	2.38	0.41
22:U:16:LEU:HD23	22:U:16:LEU:HA	1.68	0.41
38:A:5770:HOH:O	27:Z:158:LYS:HD3	2.20	0.41
29:2:1:THR:HA	38:2:435:HOH:O	2.21	0.41
1:A:2434:A:O3'	31:4:28:GLY:CA	2.69	0.41
1:A:1819:G:O2'	1:A:1820:G:H5'	2.21	0.41
1:A:1885:A:C2'	1:A:1886:A:H5'	2.50	0.41
1:A:2512:U:H2'	38:A:4829:HOH:O	2.21	0.41
1:A:2602:G:H2'	1:A:2603:G:O4'	2.20	0.41
1:A:2737:C:H3'	1:A:2738:G:C5'	2.51	0.41
1:A:688:A:H62	14:M:111:ALA:HB2	1.85	0.41
4:C:165:THR:O	4:C:165:THR:HG22	2.21	0.41
4:C:48:ASP:HA	4:C:49:PRO:HD3	1.80	0.41
5:D:105:PHE:CD1	5:D:115:VAL:HG11	2.56	0.41
1:A:2715:G:N2	5:D:264:GLU:OE1	2.53	0.41
7:F:99:ASP:O	7:F:159:PRO:HG3	2.20	0.41
7:F:59:GLY:C	7:F:61:PHE:H	2.20	0.41
38:A:3188:HOH:O	8:G:143:GLN:HG2	2.20	0.41
8:G:84:MET:CE	8:G:148:ILE:HG21	2.48	0.41
8:G:93:MET:HE1	8:G:165:GLY:N	2.36	0.41
14:M:145:LEU:HB2	38:M:8413:HOH:O	2.21	0.41
15:N:28:MET:HA	15:N:31:TRP:HB2	2.03	0.41
15:N:68:ARG:O	15:N:68:ARG:HD3	2.21	0.41
16:O:143:ARG:HA	16:O:172:PHE:CE2	2.55	0.41
17:P:14:LEU:CD2	17:P:102:ILE:HD11	2.49	0.41
20:S:14:ALA:HB3	20:S:147:LEU:HB2	2.03	0.41
22:U:49:GLU:HB3	22:U:59:GLU:CG	2.50	0.41
23:V:53:ASP:N	38:V:6796:HOH:O	2.40	0.41
27:Z:100:ARG:HE	27:Z:234:VAL:CG2	2.34	0.41
28:1:45:LYS:HE2	38:1:8409:HOH:O	2.21	0.41
1:A:10:U:HO2'	1:A:11:A:P	2.44	0.41
1:A:1187:U:HO2'	1:A:1188:A:H8	1.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1733:A:C6	1:A:1734:C:C2	3.09	0.41
1:A:2613:G:H2'	1:A:2614:C:H6	1.86	0.41
1:A:2842:G:C2'	1:A:2843:A:H5'	2.51	0.41
5:D:16:ARG:NH2	38:D:8559:HOH:O	2.48	0.41
6:E:166:ILE:CD1	6:E:207:LEU:HD13	2.51	0.41
11:J:157:ILE:HG22	11:J:158:ASN:N	2.35	0.41
12:K:6:PHE:HB3	12:K:109:TYR:OH	2.21	0.41
16:O:154:LEU:HG	16:O:155:GLU:N	2.36	0.41
21:T:50:GLU:OE2	21:T:69:SER:HB3	2.21	0.41
25:X:76:ASP:O	25:X:77:ALA:C	2.59	0.41
31:4:70:ARG:CB	38:4:8571:HOH:O	2.69	0.40
1:A:105:G:O2'	1:A:106:A:H5'	2.21	0.40
1:A:1154:A:H2'	1:A:1155:G:H8	1.87	0.40
1:A:1444:G:O2'	1:A:1502:A:N1	2.47	0.40
1:A:1641:A:H2'	1:A:1642:A:C5'	2.49	0.40
1:A:1768:C:H2'	1:A:1769:C:H5'	2.03	0.40
1:A:2345:A:H3'	1:A:2346:C:C5	2.56	0.40
1:A:2438:G:H2'	1:A:2439:C:O4'	2.21	0.40
1:A:198:A:C2	1:A:2444:U:H1'	2.56	0.40
1:A:244:C:O5'	1:A:244:C:H6	2.03	0.40
1:A:303:C:H2'	1:A:304:G:O4'	2.21	0.40
4:C:70:ALA:HA	4:C:71:PRO:HD3	1.61	0.40
2:B:3042:C:O2	7:F:76:ARG:HD2	2.21	0.40
10:I:12:ILE:HA	38:I:4499:HOH:O	2.19	0.40
13:L:4:LEU:HD22	13:L:116:GLU:HB3	2.02	0.40
15:N:61:ILE:HG22	15:N:62:VAL:N	2.36	0.40
16:O:32:PRO:O	16:O:100:ALA:HA	2.21	0.40
22:U:1:SER:N	38:U:5837:HOH:O	2.55	0.40
25:X:139:GLY:O	25:X:141:HIS:HD2	2.04	0.40
27:Z:196:VAL:HG13	27:Z:201:GLU:OE1	2.20	0.40
28:1:13:ARG:NH1	28:1:14:PHE:CE2	2.89	0.40
28:1:81:LYS:O	28:1:82:ALA:C	2.60	0.40
30:3:48:ASP:O	30:3:49:GLU:CB	2.69	0.40
1:A:1006:A:H4'	38:A:4382:HOH:O	2.21	0.40
1:A:129:A:O2'	1:A:130:C:OP1	2.33	0.40
1:A:1641:A:C8	1:A:1702:U:O4	2.74	0.40
1:A:1886:A:H1'	38:A:4306:HOH:O	2.21	0.40
1:A:1973:A:O2'	38:A:6330:HOH:O	2.22	0.40
1:A:2004:U:H5''	1:A:2005:G:C8	2.56	0.40
1:A:2040:C:H2'	1:A:2041:G:O4'	2.21	0.40
1:A:2249:G:C2	1:A:2253:G:C6	3.08	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:C:O2'	1:A:344:C:H5'	2.20	0.40
1:A:711:G:C2	1:A:718:C:C2	3.09	0.40
1:A:837:U:H4'	38:A:9892:HOH:O	2.21	0.40
2:B:3024:U:H3'	2:B:3025:G:C5'	2.51	0.40
5:D:36:PRO:HA	5:D:168:GLY:HA2	2.01	0.40
1:A:2502:C:C4'	11:J:151:MET:CG	2.99	0.40
12:K:63:ILE:HG22	12:K:64:GLY:N	2.35	0.40
16:O:10:MET:O	16:O:11:ARG:C	2.59	0.40
18:Q:115:SER:C	18:Q:117:SER:N	2.75	0.40
18:Q:5:ALA:CB	38:Q:1715:HOH:O	2.69	0.40
1:A:1307:A:H2'	1:A:1308:A:C8	2.56	0.40
1:A:1334:C:O2'	1:A:1335:C:H5'	2.21	0.40
1:A:1540:G:N2	1:A:1646:G:H1'	2.36	0.40
1:A:1691:A:H5''	38:A:9642:HOH:O	2.19	0.40
1:A:1754:A:N7	38:A:7328:HOH:O	2.37	0.40
1:A:1810:C:H2'	1:A:1811:A:O4'	2.22	0.40
1:A:2321:A:OP1	31:4:91:GLN:NE2	2.42	0.40
1:A:2563:U:H2'	1:A:2565:C:O5'	2.22	0.40
1:A:1838:U:C4	1:A:2622:A:N1	2.89	0.40
1:A:2653:A:H2'	1:A:2654:C:O4'	2.21	0.40
1:A:703:G:O2'	1:A:704:C:H5'	2.21	0.40
1:A:710:G:C2'	1:A:711:G:H5'	2.51	0.40
1:A:783:C:O2'	1:A:784:A:H5'	2.21	0.40
2:B:3107:C:O2'	2:B:3108:C:H5'	2.21	0.40
5:D:294:TYR:C	5:D:294:TYR:CD1	2.94	0.40
6:E:133:ARG:NH1	38:E:8409:HOH:O	2.31	0.40
6:E:236:THR:HG23	6:E:238:SER:H	1.86	0.40
6:E:29:ASP:OD1	17:P:5:PRO:HD3	2.21	0.40
8:G:9:GLU:HG3	8:G:10:ASP:N	2.36	0.40
9:H:27:GLY:HA3	38:H:5413:HOH:O	2.21	0.40
16:O:164:ASP:OD1	16:O:167:ASP:HA	2.21	0.40
1:A:2050:G:H5''	20:S:80:TYR:O	2.21	0.40
22:U:45:GLY:HA3	22:U:102:ASP:HB2	2.03	0.40
25:X:38:THR:O	25:X:42:ARG:HB2	2.21	0.40
26:Y:21:PRO:HD3	38:Y:6179:HOH:O	2.21	0.40
26:Y:72:VAL:C	26:Y:88:GLU:OE2	2.60	0.40
1:A:1004:C:O2'	1:A:1005:A:H5'	2.21	0.40
1:A:128:A:H3'	1:A:128:A:C8	2.57	0.40
1:A:1992:U:H2'	1:A:1994:A:OP2	2.21	0.40
1:A:2334:C:H6	1:A:2334:C:O5'	2.04	0.40
1:A:293:A:C5	1:A:360:A:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:A:H2'	1:A:424:C:O4'	2.22	0.40
1:A:547:A:H3'	38:A:4429:HOH:O	2.22	0.40
1:A:565:A:OP2	1:A:592:G:N1	2.48	0.40
1:A:814:G:H4'	38:A:9631:HOH:O	2.22	0.40
5:D:60:SER:C	5:D:62:ARG:H	2.25	0.40
6:E:11:ASN:O	6:E:12:THR:C	2.60	0.40
6:E:164:ALA:O	6:E:167:ASP:HB2	2.21	0.40
1:A:1311:G:O6	6:E:173:LYS:HE3	2.21	0.40
11:J:49:VAL:C	11:J:157:ILE:HG23	2.42	0.40
11:J:1:LYS:HA	11:J:2:PRO:HD3	1.88	0.40
11:J:28:ILE:HA	11:J:62:GLU:OE1	2.21	0.40
14:M:142:LEU:HG	14:M:146:GLY:HA3	2.04	0.40
38:A:4889:HOH:O	14:M:34:GLY:HA2	2.21	0.40
14:M:66:VAL:HG23	14:M:67:ARG:H	1.83	0.40
14:M:98:GLU:O	14:M:99:GLU:HB2	2.21	0.40
16:O:16:ALA:HB2	38:O:8569:HOH:O	2.22	0.40
17:P:115:ARG:HH11	17:P:115:ARG:HG3	1.86	0.40
6:E:29:ASP:OD1	17:P:5:PRO:CD	2.69	0.40
18:Q:89:ASN:OD1	18:Q:92:GLU:HB2	2.22	0.40
21:T:10:VAL:O	21:T:10:VAL:HG22	2.21	0.40
1:A:56:G:C5'	24:W:50:ARG:HH12	2.34	0.40
28:1:56:MET:HA	28:1:62:TYR:O	2.21	0.40
29:2:10:LYS:CG	38:2:2979:HOH:O	2.65	0.40
1:A:1161:A:C6	1:A:1162:G:N7	2.89	0.40
1:A:1162:G:N1	1:A:1163:G:C5	2.90	0.40
1:A:1204:C:H1'	38:A:4228:HOH:O	2.21	0.40
1:A:1270:U:H2'	1:A:1271:A:C8	2.56	0.40
1:A:1882:C:H2'	1:A:1883:U:C6	2.56	0.40
1:A:2344:G:H8	38:A:6133:HOH:O	2.02	0.40
1:A:2432:C:H2'	1:A:2433:A:C8	2.57	0.40
1:A:282:C:C2'	1:A:283:U:H5'	2.51	0.40
1:A:308:U:H5'	22:U:97:ARG:NH2	2.37	0.40
1:A:907:A:H2'	1:A:908:A:C8	2.57	0.40
1:A:945:U:O2'	1:A:946:C:H5'	2.21	0.40
4:C:71:PRO:HG2	4:C:91:GLY:HA2	2.03	0.40
5:D:162:MET:HE2	5:D:310:ARG:CD	2.50	0.40
6:E:57:PRO:HG2	6:E:73:LEU:CD1	2.51	0.40
1:A:2778:A:H1'	8:G:153:ARG:NH1	2.36	0.40
11:J:93:ILE:HG12	11:J:120:GLY:C	2.42	0.40
18:Q:89:ASN:O	18:Q:89:ASN:OD1	2.40	0.40
22:U:24:ARG:HH21	22:U:39:ASN:HD22	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:96:VAL:HG13	22:U:97:ARG:N	2.36	0.40
23:V:37:GLU:O	23:V:40:ALA:HB3	2.21	0.40
25:X:132:VAL:C	25:X:134:GLU:N	2.74	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	C	235/239 (98%)	199 (85%)	27 (12%)	9 (4%)	4	18
5	D	335/337 (99%)	297 (89%)	28 (8%)	10 (3%)	5	24
6	E	244/246 (99%)	208 (85%)	31 (13%)	5 (2%)	9	36
7	F	134/176 (76%)	98 (73%)	25 (19%)	11 (8%)	1	4
8	G	170/177 (96%)	156 (92%)	13 (8%)	1 (1%)	28	67
9	H	117/119 (98%)	103 (88%)	9 (8%)	5 (4%)	3	15
10	I	25/348 (7%)	23 (92%)	1 (4%)	1 (4%)	3	17
11	J	152/167 (91%)	128 (84%)	18 (12%)	6 (4%)	3	17
12	K	140/145 (97%)	124 (89%)	11 (8%)	5 (4%)	4	19
13	L	130/132 (98%)	113 (87%)	15 (12%)	2 (2%)	12	45
14	M	141/164 (86%)	114 (81%)	23 (16%)	4 (3%)	6	26
15	N	192/194 (99%)	177 (92%)	10 (5%)	5 (3%)	6	28
16	O	184/186 (99%)	153 (83%)	19 (10%)	12 (6%)	1	6
17	P	113/115 (98%)	105 (93%)	7 (6%)	1 (1%)	20	58
18	Q	141/148 (95%)	129 (92%)	11 (8%)	1 (1%)	25	64
19	R	93/95 (98%)	84 (90%)	9 (10%)	0	100	100
20	S	148/154 (96%)	130 (88%)	14 (10%)	4 (3%)	6	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	T	79/84 (94%)	75 (95%)	3 (4%)	1 (1%)	14	48
22	U	117/119 (98%)	106 (91%)	8 (7%)	3 (3%)	6	28
23	V	51/66 (77%)	48 (94%)	1 (2%)	2 (4%)	3	17
24	W	63/70 (90%)	57 (90%)	4 (6%)	2 (3%)	5	22
25	X	152/154 (99%)	142 (93%)	6 (4%)	4 (3%)	6	28
26	Y	80/91 (88%)	69 (86%)	8 (10%)	3 (4%)	4	18
27	Z	140/240 (58%)	134 (96%)	5 (4%)	1 (1%)	25	64
28	1	71/73 (97%)	61 (86%)	9 (13%)	1 (1%)	13	46
29	2	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
30	3	42/48 (88%)	42 (100%)	0	0	100	100
31	4	90/92 (98%)	82 (91%)	6 (7%)	2 (2%)	8	33
All	All	3633/4235 (86%)	3205 (88%)	327 (9%)	101 (3%)	6	26

All (101) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	D	139	ASP
5	D	206	THR
7	F	93	LEU
7	F	95	THR
7	F	173	GLU
9	H	101	ALA
11	J	162	SER
12	K	143	LYS
14	M	80	ASP
16	O	154	LEU
16	O	164	ASP
16	O	183	ASP
26	Y	87	ALA
4	C	10	GLY
4	C	34	ASP
4	C	37	VAL
4	C	119	ALA
5	D	34	GLY
5	D	169	GLY
5	D	184	ASP
6	E	208	ALA
7	F	11	HIS

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Mol	Chain	Res	Type
7	F	171	ASP
9	H	61	MET
11	J	40	PRO
11	J	164	ALA
12	K	5	GLU
13	L	119	GLN
18	Q	116	SER
20	S	106	GLY
22	U	28	SER
22	U	53	GLY
24	W	43	PRO
25	X	14	HIS
25	X	73	LEU
25	X	77	ALA
28	1	81	LYS
31	4	57	GLY
4	C	132	ASP
5	D	323	LEU
6	E	19	PRO
7	F	16	PRO
7	F	170	TYR
11	J	138	PRO
14	M	21	ARG
14	M	147	GLU
15	N	28	MET
15	N	140	ALA
15	N	148	SER
16	O	55	ASP
16	O	160	SER
16	O	162	ASP
16	O	181	ASP
17	P	20	SER
22	U	93	THR
23	V	7	ASP
4	C	165	THR
4	C	229	ALA
5	D	291	ASP
6	E	201	SER
7	F	20	LYS
7	F	85	GLN
12	K	42	GLU
12	K	89	HIS

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Mol	Chain	Res	Type
13	L	126	SER
16	O	65	ASP
20	S	101	HIS
20	S	136	TRP
23	V	46	ALA
24	W	40	PRO
26	Y	77	PHE
5	D	2	GLN
5	D	185	GLY
6	E	69	HIS
6	E	89	ALA
7	F	137	PRO
8	G	66	GLN
9	H	64	PRO
9	H	71	GLY
9	H	104	ALA
10	I	72	ASP
14	M	105	TYR
21	T	58	MET
25	X	49	ASN
31	4	56	PRO
4	C	170	VAL
7	F	61	PHE
15	N	6	SER
16	O	27	LEU
16	O	167	ASP
11	J	72	VAL
16	O	9	PRO
11	J	110	GLY
4	C	162	GLY
12	K	78	ILE
16	O	74	PRO
20	S	56	PRO
26	Y	70	ILE
5	D	225	GLY
15	N	88	VAL
27	Z	167	GLY

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	C	179/181 (99%)	169 (94%)	10 (6%)	25	60
5	D	282/282 (100%)	265 (94%)	17 (6%)	22	57
6	E	193/193 (100%)	178 (92%)	15 (8%)	15	44
7	F	117/147 (80%)	108 (92%)	9 (8%)	15	45
8	G	152/155 (98%)	149 (98%)	3 (2%)	60	86
9	H	92/92 (100%)	90 (98%)	2 (2%)	57	85
10	I	27/283 (10%)	26 (96%)	1 (4%)	39	74
11	J	122/122 (100%)	111 (91%)	11 (9%)	11	37
12	K	118/121 (98%)	110 (93%)	8 (7%)	18	51
13	L	106/106 (100%)	103 (97%)	3 (3%)	49	80
14	M	112/126 (89%)	108 (96%)	4 (4%)	40	75
15	N	166/166 (100%)	156 (94%)	10 (6%)	22	57
16	O	149/149 (100%)	142 (95%)	7 (5%)	30	67
17	P	93/93 (100%)	89 (96%)	4 (4%)	33	70
18	Q	113/116 (97%)	110 (97%)	3 (3%)	50	81
19	R	79/79 (100%)	75 (95%)	4 (5%)	28	64
20	S	117/121 (97%)	114 (97%)	3 (3%)	51	82
21	T	71/73 (97%)	71 (100%)	0	100	100
22	U	105/105 (100%)	102 (97%)	3 (3%)	48	80
23	V	44/52 (85%)	44 (100%)	0	100	100
24	W	51/56 (91%)	48 (94%)	3 (6%)	23	58
25	X	130/130 (100%)	122 (94%)	8 (6%)	21	56
26	Y	66/73 (90%)	63 (96%)	3 (4%)	32	69
27	Z	120/195 (62%)	113 (94%)	7 (6%)	23	59
28	1	56/56 (100%)	49 (88%)	7 (12%)	5	20
29	2	46/46 (100%)	46 (100%)	0	100	100
30	3	42/44 (96%)	41 (98%)	1 (2%)	54	83
31	4	79/79 (100%)	76 (96%)	3 (4%)	38	73
All	All	3027/3441 (88%)	2878 (95%)	149 (5%)	29	65

All (149) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	C	3	ARG
4	C	36	ASP
4	C	55	VAL
4	C	68	ILE
4	C	69	LEU
4	C	94	LEU
4	C	120	ARG
4	C	131	HIS
4	C	179	MET
4	C	217	ARG
5	D	7	ARG
5	D	11	LEU
5	D	27	ASN
5	D	33	ASP
5	D	97	LEU
5	D	98	THR
5	D	103	ASP
5	D	162	MET
5	D	190	MET
5	D	245	SER
5	D	251	VAL
5	D	254	GLN
5	D	256	GLN
5	D	264	GLU
5	D	300	SER
5	D	307	ARG
5	D	312	ARG
6	E	2	GLN
6	E	56	THR
6	E	67	GLN
6	E	76	ARG
6	E	78	ARG
6	E	94	THR
6	E	115	LEU
6	E	136	VAL
6	E	187	ARG
6	E	214	THR
6	E	222	ASP
6	E	223	LEU
6	E	234	VAL
6	E	236	THR
6	E	240	LEU

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Mol	Chain	Res	Type
7	F	24	HIS
7	F	61	PHE
7	F	99	ASP
7	F	100	ASP
7	F	131	THR
7	F	133	ASN
7	F	136	ARG
7	F	137	PRO
7	F	149	ARG
8	G	7	ILE
8	G	12	ASP
8	G	102	VAL
9	H	1	PRO
9	H	100	ASP
10	I	64	ASN
11	J	1	LYS
11	J	30	GLN
11	J	59	ASN
11	J	72	VAL
11	J	73	GLN
11	J	82	LYS
11	J	83	PHE
11	J	86	ARG
11	J	94	ARG
11	J	142	VAL
11	J	150	LYS
12	K	46	ILE
12	K	52	GLN
12	K	74	ARG
12	K	79	PHE
12	K	107	ASN
12	K	120	SER
12	K	127	ILE
12	K	131	THR
13	L	7	ASP
13	L	10	GLN
13	L	98	VAL
14	M	30	ARG
14	M	35	ARG
14	M	80	ASP
14	M	117	GLU
15	N	38	VAL

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Mol	Chain	Res	Type
15	N	46	LEU
15	N	48	ARG
15	N	68	ARG
15	N	81	ARG
15	N	87	MET
15	N	93	ARG
15	N	99	ARG
15	N	159	THR
15	N	164	THR
16	O	26	LEU
16	O	47	LEU
16	O	49	THR
16	O	127	LEU
16	O	128	ASP
16	O	152	GLU
16	O	163	PHE
17	P	67	SER
17	P	98	LEU
17	P	109	SER
17	P	115	ARG
18	Q	52	LYS
18	Q	91	LYS
18	Q	98	ILE
19	R	11	ARG
19	R	16	ASN
19	R	57	ASP
19	R	95	GLU
20	S	13	THR
20	S	39	THR
20	S	82	GLU
22	U	39	ASN
22	U	48	VAL
22	U	73	HIS
24	W	1	THR
24	W	22	ASP
24	W	65	ASP
25	X	26	ILE
25	X	32	CYS
25	X	35	VAL
25	X	52	VAL
25	X	122	ARG
25	X	142	ASP

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Mol	Chain	Res	Type
25	X	146	ILE
25	X	154	ARG
26	Y	15	ARG
26	Y	27	ASP
26	Y	72	VAL
27	Z	154	ARG
27	Z	163	THR
27	Z	172	THR
27	Z	189	ASN
27	Z	203	VAL
27	Z	204	ARG
27	Z	235	GLU
28	1	11	THR
28	1	32	LYS
28	1	42	CYS
28	1	49	ARG
28	1	60	CYS
28	1	64	ILE
28	1	68	CYS
30	3	18	ASN
31	4	42	ARG
31	4	56	PRO
31	4	74	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
4	C	29	HIS
4	C	92	ASN
4	C	125	ASN
4	C	188	ASN
4	C	199	HIS
5	D	27	ASN
5	D	94	GLN
5	D	145	HIS
5	D	191	ASN
5	D	221	GLN
5	D	238	ASN
5	D	260	HIS
5	D	332	ASN
6	E	2	GLN
6	E	39	GLN

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Mol	Chain	Res	Type
6	E	129	HIS
6	E	163	HIS
7	F	47	GLN
7	F	103	ASN
7	F	133	ASN
8	G	71	ASN
8	G	106	ASN
8	G	143	GLN
9	H	80	GLN
10	I	17	GLN
10	I	64	ASN
11	J	35	ASN
11	J	55	GLN
11	J	58	HIS
11	J	59	ASN
11	J	69	ASN
11	J	74	ASN
11	J	80	ASN
11	J	91	HIS
11	J	129	ASN
11	J	130	HIS
11	J	137	ASN
11	J	166	ASN
12	K	25	GLN
12	K	52	GLN
12	K	107	ASN
13	L	10	GLN
14	M	18	HIS
14	M	41	HIS
14	M	116	HIS
15	N	58	GLN
15	N	176	GLN
16	O	107	ASN
16	O	119	GLN
16	O	153	GLN
17	P	100	GLN
18	Q	50	GLN
18	Q	66	GLN
18	Q	73	HIS
18	Q	118	GLN
19	R	16	ASN
19	R	40	HIS

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Mol	Chain	Res	Type
20	S	61	GLN
20	S	94	ASN
20	S	98	ASN
20	S	113	HIS
20	S	117	HIS
20	S	123	GLN
21	T	53	ASN
21	T	55	GLN
22	U	39	ASN
23	V	38	ASN
23	V	39	ASN
24	W	60	GLN
25	X	2	HIS
25	X	12	ASN
25	X	14	HIS
25	X	110	GLN
25	X	119	HIS
25	X	125	HIS
25	X	141	HIS
26	Y	23	HIS
27	Z	133	HIS
27	Z	134	HIS
27	Z	149	GLN
27	Z	189	ASN
29	2	8	GLN
29	2	16	HIS
29	2	28	HIS
30	3	16	ASN
30	3	18	ASN
30	3	41	HIS
30	3	45	ASN
31	4	18	GLN
31	4	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2747/2922 (94%)	246 (8%)	27 (0%)
2	B	121/122 (99%)	17 (14%)	4 (3%)
3	5	1/2 (50%)	0	0
All	All	2869/3046 (94%)	263 (9%)	31 (1%)

All (263) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	31	C
1	A	60	A
1	A	67	A
1	A	69	A
1	A	70	A
1	A	71	G
1	A	87	C
1	A	88	G
1	A	114	A
1	A	115	U
1	A	120	A
1	A	130	C
1	A	139	C
1	A	141	C
1	A	151	A
1	A	166	A
1	A	169	A
1	A	185	G
1	A	186	A
1	A	191	A
1	A	192	A
1	A	200	U
1	A	219	G
1	A	237	G
1	A	271	C
1	A	272	A
1	A	273	G
1	A	283	U
1	A	284	C
1	A	285	A
1	A	308	U
1	A	309	C
1	A	318	C
1	A	336	G
1	A	337	A
1	A	345	G
1	A	358	G
1	A	381	G
1	A	397	A
1	A	417	G
1	A	461	C

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Mol	Chain	Res	Type
1	A	487	G
1	A	498	A
1	A	510	U
1	A	511	A
1	A	514	G
1	A	537	G
1	A	538	C
1	A	539	G
1	A	542	A
1	A	545	G
1	A	553	G
1	A	559	U
1	A	588	G
1	A	604	G
1	A	620	A
1	A	632	A
1	A	644	G
1	A	660	A
1	A	688	A
1	A	701	U
1	A	717	C
1	A	759	C
1	A	777	U
1	A	809	G
1	A	821	U
1	A	835	U
1	A	840	U
1	A	858	U
1	A	868	G
1	A	869	G
1	A	871	G
1	A	872	U
1	A	875	A
1	A	877	G
1	A	878	G
1	A	884	C
1	A	885	G
1	A	905	C
1	A	920	C
1	A	921	G
1	A	923	A
1	A	953	G

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Mol	Chain	Res	Type
1	A	960	G
1	A	961	A
1	A	1006	A
1	A	1008	C
1	A	1029	U
1	A	1045	G
1	A	1059	G
1	A	1060	C
1	A	1072	G
1	A	1081	A
1	A	1083	C
1	A	1087	G
1	A	1088	A
1	A	1109	U
1	A	1110	G
1	A	1119	G
1	A	1120	U
1	A	1127	C
1	A	1129	C
1	A	1130	U
1	A	1151	G
1	A	1161	A
1	A	1162	G
1	A	1164	U
1	A	1165	G
1	A	1166	A
1	A	1171	A
1	A	1174	A
1	A	1175	G
1	A	1177	A
1	A	1185	U
1	A	1192	A
1	A	1193	A
1	A	1206	U
1	A	1216	G
1	A	1238	C
1	A	1239	G
1	A	1242	A
1	A	1279	U
1	A	1289	C
1	A	1331	A
1	A	1342	C

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Mol	Chain	Res	Type
1	A	1353	C
1	A	1360	C
1	A	1377	C
1	A	1406	A
1	A	1407	A
1	A	1409	G
1	A	1451	C
1	A	1474	C
1	A	1505	U
1	A	1506	U
1	A	1524	U
1	A	1525	G
1	A	1526	A
1	A	1564	C
1	A	1580	A
1	A	1592	G
1	A	1625	U
1	A	1626	A
1	A	1633	C
1	A	1634	G
1	A	1656	A
1	A	1667	A
1	A	1682	A
1	A	1684	A
1	A	1685	A
1	A	1692	C
1	A	1701	A
1	A	1710	A
1	A	1722	U
1	A	1723	G
1	A	1725	C
1	A	1731	C
1	A	1737	A
1	A	1752	G
1	A	1778	A
1	A	1798	C
1	A	1819	G
1	A	1820	G
1	A	1829	A
1	A	1856	C
1	A	1879	U
1	A	1919	A

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Mol	Chain	Res	Type
1	A	1942	A
1	A	1971	G
1	A	1973	A
1	A	1974	G
1	A	1978	A
1	A	1980	U
1	A	1996	U
1	A	2004	U
1	A	2006	C
1	A	2008	U
1	A	2011	A
1	A	2012	U
1	A	2013	G
1	A	2033	G
1	A	2034	U
1	A	2064	U
1	A	2072	G
1	A	2073	G
1	A	2074	A
1	A	2096	A
1	A	2101	A
1	A	2102	G
1	A	2110	G
1	A	2238	A
1	A	2258	A
1	A	2271	G
1	A	2272	G
1	A	2317	C
1	A	2321	A
1	A	2354	A
1	A	2361	A
1	A	2369	A
1	A	2422	U
1	A	2462	G
1	A	2465	A
1	A	2467	A
1	A	2469	A
1	A	2476	C
1	A	2480	G
1	A	2483	A
1	A	2507	G
1	A	2509	A

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Mol	Chain	Res	Type
1	A	2511	A
1	A	2533	C
1	A	2537	G
1	A	2541	U
1	A	2553	A
1	A	2564	G
1	A	2589	U
1	A	2601	A
1	A	2602	G
1	A	2608	C
1	A	2613	G
1	A	2620	U
1	A	2621	U
1	A	2638	G
1	A	2649	A
1	A	2664	A
1	A	2681	A
1	A	2682	C
1	A	2726	U
1	A	2747	C
1	A	2748	G
1	A	2749	U
1	A	2750	G
1	A	2762	C
1	A	2768	A
1	A	2786	G
1	A	2792	A
1	A	2800	A
1	A	2811	A
1	A	2825	C
1	A	2850	C
1	A	2876	G
1	A	2890	A
1	A	2896	A
1	A	2903	C
1	A	2914	A
2	B	3002	U
2	B	3007	G
2	B	3014	G
2	B	3022	G
2	B	3023	U
2	B	3024	U

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Mol	Chain	Res	Type
2	B	3025	G
2	B	3026	C
2	B	3041	C
2	B	3043	G
2	B	3044	A
2	B	3052	A
2	B	3057	A
2	B	3066	G
2	B	3077	A
2	B	3114	G
2	B	3122	C

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	10	U
1	A	69	A
1	A	129	A
1	A	284	C
1	A	338	C
1	A	603	A
1	A	716	G
1	A	834	G
1	A	857	A
1	A	871	G
1	A	877	G
1	A	1080	C
1	A	1164	U
1	A	1237	U
1	A	1352	A
1	A	1377	C
1	A	1450	C
1	A	1474	C
1	A	1563	G
1	A	1685	A
1	A	1942	A
1	A	1979	G
1	A	2011	A
1	A	2313	C
1	A	2467	A
1	A	2718	C
1	A	2791	U

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Mol	Chain	Res	Type
2	B	3023	U
2	B	3024	U
2	B	3043	G
2	B	3065	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 carbohydrates 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
36	PPU	5	76	3	31,40,41	2.41	6 (19%)	34,57,60	1.20	3 (8%)

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
36	PPU	5	76	3	-	2/21/43/44	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	5	76	PPU	C10-N6	-4.17	1.35	1.45
36	5	76	PPU	C9-N6	-4.09	1.35	1.45
36	5	76	PPU	CE2-CZ	2.80	1.44	1.38
36	5	76	PPU	CE2-CD2	3.58	1.45	1.38
36	5	76	PPU	CE1-CZ	3.80	1.46	1.38
36	5	76	PPU	C-N3'	9.48	1.55	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	5	76	PPU	C3'-N3'-C	-3.76	117.55	123.21
36	5	76	PPU	CM-OC-CZ	2.09	122.08	117.50
36	5	76	PPU	C2-N1-C6	2.90	118.94	111.82

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	5	76	PPU	O-C-CA-CB
36	5	76	PPU	CB-CA-C-N3'

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	5	76	PPU	4	0

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	A	2754/2922 (94%)	0.08	70 (2%) 58 39	24, 52, 101, 153	0
2	B	122/122 (100%)	0.27	6 (4%) 30 18	42, 71, 102, 149	0
3	5	2/2 (100%)	2.86	2 (100%) 0 0	96, 96, 96, 111	0
4	C	237/239 (99%)	0.52	22 (9%) 9 5	28, 62, 98, 116	0
5	D	337/337 (100%)	0.26	4 (1%) 79 61	29, 60, 88, 96	0
6	E	246/246 (100%)	0.04	3 (1%) 79 61	27, 53, 76, 87	0
7	F	140/176 (79%)	2.24	70 (50%) 0 0	69, 108, 125, 135	0
8	G	172/177 (97%)	1.03	26 (15%) 3 1	50, 75, 99, 106	0
9	H	119/119 (100%)	0.92	21 (17%) 2 1	59, 82, 106, 110	0
10	I	29/348 (8%)	2.95	19 (65%) 0 0	81, 104, 108, 109	0
11	J	156/167 (93%)	0.50	13 (8%) 12 6	40, 61, 92, 97	0
12	K	142/145 (97%)	0.23	3 (2%) 64 45	40, 55, 75, 83	0
13	L	132/132 (100%)	0.12	3 (2%) 61 41	37, 59, 85, 88	0
14	M	145/164 (88%)	1.09	30 (20%) 1 1	27, 83, 118, 124	0
15	N	194/194 (100%)	0.21	6 (3%) 49 31	34, 54, 73, 81	0
16	O	186/186 (100%)	0.95	33 (17%) 2 1	46, 74, 114, 127	0
17	P	115/115 (100%)	0.34	2 (1%) 70 51	47, 63, 86, 91	0
18	Q	143/148 (96%)	0.59	12 (8%) 12 6	43, 63, 82, 90	0
19	R	95/95 (100%)	0.00	1 (1%) 80 63	40, 52, 61, 75	0
20	S	150/154 (97%)	0.04	1 (0%) 87 74	33, 49, 68, 76	0
21	T	81/84 (96%)	0.36	2 (2%) 58 39	55, 69, 88, 92	0
22	U	119/119 (100%)	0.55	9 (7%) 15 8	45, 61, 82, 91	0
23	V	53/66 (80%)	1.55	15 (28%) 1 0	73, 83, 98, 119	0
24	W	65/70 (92%)	1.52	18 (27%) 1 0	58, 84, 111, 115	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	X	154/154 (100%)	0.06	0 100 100	43, 55, 73, 83	0
26	Y	82/91 (90%)	0.48	8 (9%) 8 5	43, 64, 88, 102	0
27	Z	142/240 (59%)	0.21	8 (5%) 25 14	33, 51, 74, 92	0
28	1	73/73 (100%)	3.16	40 (54%) 0 0	76, 107, 118, 119	0
29	2	56/56 (100%)	-0.25	0 100 100	29, 37, 45, 48	0
30	3	46/48 (95%)	0.26	3 (6%) 20 11	41, 62, 83, 97	0
31	4	92/92 (100%)	8.53	92 (100%) 0 0	110, 126, 134, 137	0
All	All	6579/7281 (90%)	0.48	542 (8%) 12 7	24, 59, 111, 153	0

All (542) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
31	4	82	GLY	21.1
31	4	65	THR	20.2
31	4	83	TRP	18.4
31	4	85	ALA	15.1
31	4	62	THR	14.6
28	1	11	THR	14.3
31	4	38	ARG	14.1
31	4	35	TRP	14.0
31	4	3	MET	13.7
31	4	37	ASP	13.6
31	4	84	ARG	13.4
31	4	36	ILE	12.8
31	4	71	CYS	12.3
31	4	22	VAL	12.2
31	4	81	GLU	12.2
31	4	43	ASN	11.9
31	4	88	LEU	11.6
31	4	11	CYS	11.0
31	4	42	ARG	10.6
31	4	64	LYS	10.6
24	W	1	THR	10.5
31	4	4	PRO	10.5
31	4	74	CYS	10.5
31	4	78	HIS	10.4
31	4	72	GLY	10.3
31	4	19	GLU	10.3
31	4	25	VAL	10.1
31	4	9	THR	9.9

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Mol	Chain	Res	Type	RSRZ
31	4	63	LYS	9.8
10	I	27	ILE	9.8
31	4	59	ASP	9.8
31	4	23	GLU	9.7
31	4	40	ARG	9.6
31	4	80	ARG	9.6
31	4	67	LEU	9.5
31	4	33	MET	9.4
28	1	19	GLY	9.3
31	4	53	SER	9.2
31	4	17	HIS	9.1
31	4	1	MET	9.0
31	4	18	GLN	9.0
31	4	91	GLN	9.0
16	O	186	LEU	8.8
31	4	86	GLY	8.8
28	1	20	LEU	8.6
31	4	69	TYR	8.6
31	4	24	LYS	8.5
31	4	32	GLY	8.5
31	4	8	ASN	8.4
31	4	7	PHE	8.4
31	4	34	LYS	8.4
31	4	12	PRO	8.2
28	1	30	GLU	8.1
10	I	24	VAL	8.0
28	1	12	GLY	7.9
31	4	20	HIS	7.9
31	4	14	CYS	7.7
7	F	26	GLY	7.7
31	4	39	GLN	7.7
28	1	26	VAL	7.6
31	4	44	SER	7.6
10	I	23	ILE	7.5
7	F	88	LEU	7.5
31	4	41	GLU	7.5
31	4	13	HIS	7.5
31	4	48	ASN	7.5
31	4	47	GLY	7.5
31	4	66	ASP	7.5
31	4	10	TYR	7.4
31	4	52	PHE	7.4

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Mol	Chain	Res	Type	RSRZ
31	4	2	GLN	7.3
31	4	68	LYS	7.2
31	4	50	GLY	7.1
7	F	44	ILE	7.1
31	4	51	LYS	6.9
31	4	29	ARG	6.9
31	4	61	PRO	6.8
10	I	20	VAL	6.7
31	4	21	GLU	6.7
31	4	60	LYS	6.6
31	4	26	ARG	6.5
28	1	35	LYS	6.4
31	4	46	ILE	6.4
28	1	16	PRO	6.4
31	4	49	ASP	6.3
2	B	3001	U	6.2
31	4	92	GLU	6.2
5	D	1	PRO	6.2
31	4	70	ARG	6.2
31	4	58	GLY	6.1
1	A	1173	A	6.1
28	1	18	TYR	6.1
28	1	44	PHE	6.1
31	4	6	ARG	6.0
28	1	24	VAL	6.0
7	F	18	ILE	5.9
28	1	31	ILE	5.9
28	1	33	HIS	5.8
31	4	76	LYS	5.7
4	C	236	GLY	5.7
31	4	87	ARG	5.7
4	C	37	VAL	5.7
31	4	31	THR	5.7
28	1	14	PHE	5.7
16	O	166	ALA	5.7
28	1	22	ILE	5.6
31	4	75	GLY	5.6
31	4	15	ASN	5.6
7	F	57	THR	5.5
28	1	10	ARG	5.4
16	O	158	LEU	5.4
28	1	36	LYS	5.4

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Mol	Chain	Res	Type	RSRZ
7	F	80	ALA	5.4
23	V	4	ARG	5.3
16	O	147	ILE	5.3
28	1	17	ARG	5.2
28	1	34	LYS	5.2
7	F	24	HIS	5.1
7	F	63	ILE	5.1
1	A	735	C	5.1
16	O	179	LEU	5.1
10	I	71	LEU	5.1
28	1	45	LYS	5.1
16	O	160	SER	5.1
2	B	3025	G	5.1
7	F	69	ILE	5.0
23	V	54	THR	5.0
7	F	58	VAL	5.0
14	M	73	VAL	4.9
14	M	104	ASP	4.9
7	F	87	ALA	4.8
28	1	40	PRO	4.8
31	4	16	GLU	4.8
31	4	56	PRO	4.8
28	1	25	ARG	4.8
31	4	77	ALA	4.8
28	1	37	HIS	4.8
1	A	1172	G	4.7
1	A	1951	G	4.7
7	F	62	ASP	4.7
7	F	10	PHE	4.6
28	1	39	CYS	4.6
28	1	13	ARG	4.6
14	M	59	GLU	4.6
7	F	41	LEU	4.6
10	I	65	THR	4.6
7	F	40	ILE	4.6
1	A	2237	G	4.5
1	A	1175	G	4.5
7	F	84	LEU	4.5
1	A	1177	A	4.5
4	C	36	ASP	4.5
31	4	79	LEU	4.4
1	A	2344	G	4.4

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Mol	Chain	Res	Type	RSRZ
14	M	105	TYR	4.4
16	O	162	ASP	4.4
28	1	28	ASP	4.4
14	M	61	ALA	4.4
31	4	57	GLY	4.3
16	O	150	TYR	4.3
28	1	29	VAL	4.3
7	F	27	ILE	4.3
22	U	119	ALA	4.3
28	1	23	ARG	4.3
7	F	75	LEU	4.3
7	F	45	THR	4.2
7	F	25	MET	4.2
7	F	61	PHE	4.2
31	4	5	ARG	4.2
14	M	97	VAL	4.2
7	F	12	GLU	4.1
28	1	15	GLY	4.1
14	M	91	VAL	4.1
16	O	157	PRO	4.0
28	1	27	ALA	4.0
31	4	28	GLY	4.0
14	M	81	VAL	4.0
9	H	103	ALA	3.9
14	M	76	LEU	3.9
28	1	47	LEU	3.9
9	H	108	LEU	3.9
23	V	52	THR	3.9
14	M	80	ASP	3.9
1	A	1171	A	3.9
7	F	96	SER	3.9
7	F	28	GLY	3.9
10	I	12	ILE	3.9
24	W	8	ILE	3.9
31	4	30	GLN	3.9
1	A	282	C	3.9
7	F	17	ARG	3.8
10	I	72	ASP	3.8
23	V	51	TRP	3.8
9	H	102	GLY	3.8
1	A	1188	A	3.8
9	H	106	THR	3.8

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Mol	Chain	Res	Type	RSRZ
23	V	9	CYS	3.7
10	I	16	LYS	3.7
16	O	167	ASP	3.7
10	I	17	GLN	3.7
31	4	89	GLU	3.7
7	F	56	ARG	3.7
7	F	166	ILE	3.6
14	M	106	VAL	3.6
14	M	118	LEU	3.6
28	1	32	LYS	3.6
28	1	41	VAL	3.6
31	4	55	VAL	3.6
4	C	64	ASP	3.6
1	A	1525	G	3.6
28	1	38	LYS	3.6
16	O	137	ALA	3.6
1	A	1192	A	3.5
2	B	3002	U	3.5
24	W	38	GLY	3.5
24	W	52	ALA	3.5
7	F	73	VAL	3.5
4	C	32	VAL	3.5
16	O	165	ALA	3.5
26	Y	80	GLU	3.5
2	B	3065	A	3.5
14	M	60	GLU	3.5
4	C	38	ILE	3.4
14	M	144	ASP	3.4
31	4	73	GLU	3.4
7	F	90	LEU	3.4
3	5	74	C	3.4
1	A	736	A	3.4
7	F	50	VAL	3.4
14	M	89	PHE	3.4
28	1	59	HIS	3.4
23	V	6	CYS	3.4
7	F	19	GLU	3.3
23	V	55	ALA	3.3
2	B	3023	U	3.3
31	4	90	PHE	3.3
7	F	49	PRO	3.3
24	W	11	MET	3.3

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Mol	Chain	Res	Type	RSRZ
14	M	142	LEU	3.3
23	V	47	ARG	3.3
4	C	237	GLY	3.3
16	O	152	GLU	3.3
11	J	83	PHE	3.3
9	H	16	ALA	3.3
9	H	101	ALA	3.3
7	F	86	THR	3.3
16	O	159	TYR	3.2
10	I	64	ASN	3.2
28	1	79	VAL	3.2
8	G	122	THR	3.2
14	M	58	GLN	3.2
7	F	104	PHE	3.2
19	R	95	GLU	3.2
1	A	970	U	3.2
7	F	170	TYR	3.2
28	1	21	LYS	3.2
1	A	2436	U	3.2
4	C	85	ASP	3.2
7	F	171	ASP	3.2
7	F	72	LYS	3.1
14	M	120	LEU	3.1
11	J	163	PRO	3.1
26	Y	88	GLU	3.1
9	H	19	ALA	3.1
21	T	81	ILE	3.1
7	F	37	ALA	3.1
16	O	183	ASP	3.1
7	F	85	GLN	3.1
10	I	28	GLU	3.1
22	U	82	THR	3.1
8	G	86	VAL	3.1
1	A	1168	C	3.1
1	A	1167	G	3.1
31	4	27	SER	3.1
1	A	2004	U	3.1
9	H	20	LEU	3.1
1	A	960	G	3.0
1	A	1950	G	3.0
7	F	83	PHE	3.0
11	J	135	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
14	M	79	ASP	3.0
16	O	184	ILE	3.0
7	F	106	PHE	3.0
1	A	2345	A	3.0
17	P	111	VAL	3.0
1	A	1198	U	2.9
9	H	119	ARG	2.9
1	A	2637	A	2.9
1	A	1169	U	2.9
24	W	10	ASP	2.9
1	A	1180	U	2.9
7	F	70	GLY	2.9
7	F	92	GLU	2.9
24	W	43	PRO	2.9
30	3	35	ARG	2.9
1	A	2249	G	2.9
4	C	62	ASP	2.9
14	M	46	LEU	2.9
9	H	15	ASP	2.9
4	C	94	LEU	2.9
10	I	15	TRP	2.8
8	G	124	VAL	2.8
18	Q	28	GLN	2.8
1	A	1182	C	2.8
14	M	90	ARG	2.8
23	V	19	THR	2.8
16	O	138	ASP	2.8
31	4	54	LYS	2.8
1	A	716	G	2.8
7	F	60	GLU	2.8
10	I	26	MET	2.8
8	G	131	LEU	2.8
7	F	128	LEU	2.8
7	F	89	PRO	2.8
18	Q	127	GLY	2.8
11	J	43	PRO	2.8
4	C	97	ALA	2.8
8	G	100	ASP	2.7
8	G	82	TYR	2.7
7	F	22	VAL	2.7
23	V	56	ARG	2.7
7	F	16	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	2250	G	2.7
2	B	3122	C	2.7
8	G	126	ILE	2.7
1	A	1166	A	2.7
4	C	129	LEU	2.7
7	F	74	THR	2.7
7	F	165	PHE	2.7
1	A	1204	C	2.7
18	Q	105	LEU	2.7
1	A	1203	G	2.7
1	A	1181	A	2.7
8	G	170	ARG	2.7
28	1	42	CYS	2.7
1	A	1190	G	2.7
1	A	1948	G	2.7
26	Y	10	VAL	2.6
8	G	1	PRO	2.6
22	U	80	GLU	2.6
7	F	93	LEU	2.6
11	J	36	ASN	2.6
16	O	151	ASP	2.6
31	4	45	GLY	2.6
1	A	1162	G	2.6
28	1	68	CYS	2.6
7	F	59	GLY	2.6
4	C	86	ALA	2.6
16	O	67	ALA	2.6
5	D	119	HIS	2.6
17	P	26	TRP	2.6
24	W	63	GLU	2.6
4	C	128	LEU	2.6
7	F	38	GLU	2.6
9	H	90	GLU	2.6
10	I	67	LEU	2.6
9	H	22	VAL	2.6
18	Q	130	GLU	2.5
14	M	150	GLN	2.5
18	Q	131	PHE	2.5
24	W	62	GLU	2.5
24	W	3	LEU	2.5
7	F	11	HIS	2.5
12	K	7	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
7	F	47	GLN	2.5
1	A	2251	G	2.5
16	O	95	ALA	2.5
1	A	2238	A	2.5
7	F	13	MET	2.5
22	U	83	ASP	2.5
7	F	43	GLU	2.5
9	H	117	GLU	2.5
14	M	128	GLY	2.5
1	A	272	A	2.5
8	G	96	ASN	2.5
8	G	10	ASP	2.5
1	A	1193	A	2.5
26	Y	82	GLU	2.5
18	Q	1	THR	2.5
14	M	130	ARG	2.4
22	U	115	GLU	2.4
7	F	97	GLN	2.4
8	G	125	GLU	2.4
16	O	136	LEU	2.4
1	A	1949	G	2.4
1	A	713	U	2.4
7	F	161	ASP	2.4
23	V	12	ASP	2.4
27	Z	108	ASP	2.4
4	C	96	LEU	2.4
21	T	45	TYR	2.4
4	C	83	GLY	2.4
16	O	146	HIS	2.4
7	F	137	PRO	2.4
27	Z	196	VAL	2.4
1	A	1186	C	2.4
16	O	185	GLU	2.4
26	Y	7	GLU	2.4
8	G	88	TYR	2.4
8	G	166	VAL	2.4
24	W	40	PRO	2.4
14	M	141	GLU	2.4
20	S	8	ALA	2.4
24	W	39	ALA	2.4
7	F	76	ARG	2.4
4	C	84	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
6	E	237	GLU	2.4
14	M	44	GLU	2.4
24	W	5	VAL	2.4
5	D	118	ASP	2.4
16	O	163	PHE	2.4
8	G	42	VAL	2.3
16	O	153	GLN	2.3
8	G	157	LYS	2.3
1	A	1199	A	2.3
1	A	1522	A	2.3
4	C	82	VAL	2.3
13	L	132	VAL	2.3
18	Q	101	GLN	2.3
1	A	1205	U	2.3
8	G	127	ASP	2.3
9	H	26	THR	2.3
18	Q	137	LEU	2.3
1	A	370	G	2.3
1	A	1178	G	2.3
1	A	285	A	2.3
1	A	2508	C	2.3
3	5	75	C	2.3
7	F	71	ALA	2.3
1	A	514	G	2.3
1	A	1184	C	2.3
1	A	281	U	2.3
18	Q	119	TYR	2.3
1	A	1526	A	2.3
11	J	32	ASP	2.3
9	H	99	THR	2.3
27	Z	103	THR	2.3
8	G	118	ILE	2.3
16	O	127	LEU	2.3
10	I	13	PRO	2.3
1	A	280	C	2.3
16	O	143	ARG	2.3
7	F	134	LEU	2.3
1	A	368	C	2.3
1	A	1165	G	2.3
16	O	172	PHE	2.2
6	E	135	GLU	2.2
7	F	64	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
18	Q	116	SER	2.2
22	U	103	LEU	2.2
18	Q	98	ILE	2.2
24	W	2	VAL	2.2
1	A	1279	U	2.2
9	H	118	LEU	2.2
10	I	68	GLU	2.2
16	O	149	GLU	2.2
27	Z	235	GLU	2.2
11	J	72	VAL	2.2
1	A	2664	A	2.2
8	G	98	GLU	2.2
14	M	74	THR	2.2
16	O	74	PRO	2.2
23	V	15	PRO	2.2
11	J	84	ARG	2.2
15	N	152	ARG	2.2
8	G	91	PHE	2.2
11	J	140	PRO	2.2
9	H	115	VAL	2.2
8	G	81	GLU	2.2
23	V	10	GLY	2.2
30	3	44	ARG	2.2
8	G	108	LEU	2.2
23	V	53	ASP	2.2
24	W	49	LEU	2.2
9	H	23	ALA	2.2
9	H	28	ALA	2.2
14	M	121	ILE	2.2
15	N	140	ALA	2.2
4	C	35	GLY	2.2
4	C	87	GLU	2.2
9	H	100	ASP	2.1
11	J	139	ASP	2.1
7	F	91	ALA	2.1
14	M	62	ALA	2.1
11	J	35	ASN	2.1
11	J	80	ASN	2.1
15	N	156	ARG	2.1
8	G	117	THR	2.1
1	A	2914	A	2.1
7	F	77	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	138	U	2.1
4	C	133	ARG	2.1
7	F	51	ARG	2.1
1	A	734	U	2.1
13	L	119	GLN	2.1
26	Y	73	ARG	2.1
1	A	1527	A	2.1
15	N	194	ALA	2.1
15	N	78	ASN	2.1
28	1	61	GLY	2.1
16	O	64	SER	2.1
16	O	140	GLN	2.1
15	N	87	MET	2.1
1	A	2825	C	2.1
8	G	76	VAL	2.1
24	W	16	ARG	2.1
22	U	112	LEU	2.1
24	W	58	THR	2.1
8	G	148	ILE	2.1
13	L	98	VAL	2.1
1	A	284	C	2.1
23	V	49	LEU	2.1
7	F	129	ASP	2.1
5	D	86	ALA	2.1
16	O	81	ALA	2.1
11	J	114	PRO	2.1
1	A	1626	A	2.1
18	Q	114	LEU	2.1
4	C	154	ALA	2.1
22	U	108	ARG	2.1
9	H	49	PHE	2.1
26	Y	77	PHE	2.1
1	A	2248	C	2.0
27	Z	98	GLN	2.0
10	I	21	ASP	2.0
12	K	27	ALA	2.0
14	M	140	VAL	2.0
7	F	154	LYS	2.0
10	I	19	GLU	2.0
12	K	109	TYR	2.0
6	E	139	VAL	2.0
1	A	1176	C	2.0

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Mol	Chain	Res	Type	RSRZ
24	W	37	GLY	2.0
26	Y	74	ALA	2.0
27	Z	221	ALA	2.0
22	U	37	GLN	2.0
30	3	27	LEU	2.0
7	F	81	GLU	2.0
1	A	1197	G	2.0
8	G	80	TRP	2.0
27	Z	234	VAL	2.0
27	Z	97	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
32	MG	A	8070	1/1	0.55	1.21	26.41	98,98,98,98	0
34	NA	A	8377	1/1	0.79	0.55	20.13	72,72,72,72	0
35	CL	A	8515	1/1	0.66	0.51	19.92	108,108,108,108	0
34	NA	A	8340	1/1	0.94	0.37	14.08	37,37,37,37	0
34	NA	A	8359	1/1	0.71	0.41	12.20	53,53,53,53	0
34	NA	A	8323	1/1	0.91	0.29	12.06	55,55,55,55	0
34	NA	S	8386	1/1	0.51	0.52	11.77	77,77,77,77	0
34	NA	A	8327	1/1	0.97	0.25	11.70	18,18,18,18	0
34	NA	A	8350	1/1	0.85	0.23	8.27	21,21,21,21	0
32	MG	A	8112	1/1	0.91	0.26	8.06	70,70,70,70	0
34	NA	A	8308	1/1	0.94	0.23	7.25	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
34	NA	A	8361	1/1	0.89	0.28	7.02	48,48,48,48	0
35	CL	D	8519	1/1	0.94	0.32	6.65	68,68,68,68	0
34	NA	A	8355	1/1	0.75	0.41	4.97	88,88,88,88	0
34	NA	A	8321	1/1	0.98	0.23	4.48	53,53,53,53	0
34	NA	B	8383	1/1	0.89	0.20	4.41	52,52,52,52	0
32	MG	4	8114	1/1	0.68	0.74	3.98	111,111,111,111	0
36	PPU	5	76	37/38	0.85	0.36	3.54	90,95,100,100	0
34	NA	A	8382	1/1	0.72	0.24	3.41	44,44,44,44	0
35	CL	A	8516	1/1	0.95	0.23	3.22	57,57,57,57	0
32	MG	A	8044	1/1	0.83	0.21	2.92	64,64,64,64	0
34	NA	A	8371	1/1	0.81	0.18	2.67	35,35,35,35	0
34	NA	A	8303	1/1	0.96	0.18	2.64	33,33,33,33	0
34	NA	A	8325	1/1	0.94	0.17	2.11	56,56,56,56	0
34	NA	A	8331	1/1	0.91	0.19	1.63	37,37,37,37	0
34	NA	A	8332	1/1	0.96	0.17	0.91	38,38,38,38	0
37	CD	V	8401	1/1	0.83	0.37	0.79	202,202,202,202	0
35	CL	A	8510	1/1	0.63	0.30	0.64	83,83,83,83	0
32	MG	1	8105	1/1	0.82	0.45	0.55	80,80,80,80	0
32	MG	A	8053	1/1	0.97	0.16	0.51	86,86,86,86	0
34	NA	S	8338	1/1	0.83	0.19	0.21	84,84,84,84	0
32	MG	4	8078	1/1	0.54	0.62	0.11	117,117,117,117	0
32	MG	A	8049	1/1	0.93	0.17	0.07	61,61,61,61	0
32	MG	A	8003	1/1	0.98	0.19	0.04	36,36,36,36	0
32	MG	A	8077	1/1	0.96	0.16	-0.06	37,37,37,37	0
34	NA	A	8372	1/1	0.93	0.15	-0.31	30,30,30,30	0
35	CL	K	8521	1/1	0.94	0.15	-0.41	49,49,49,49	0
34	NA	A	8366	1/1	0.88	0.15	-0.47	38,38,38,38	0
34	NA	A	8369	1/1	0.88	0.15	-0.49	41,41,41,41	0
35	CL	A	8505	1/1	0.89	0.14	-0.55	68,68,68,68	0
35	CL	P	8508	1/1	0.84	0.16	-0.85	99,99,99,99	0
35	CL	A	8513	1/1	0.97	0.13	-0.98	74,74,74,74	0
34	NA	A	8365	1/1	0.92	0.12	-1.13	21,21,21,21	0
34	NA	C	8345	1/1	0.98	0.15	-1.13	30,30,30,30	0
34	NA	A	8339	1/1	0.90	0.13	-1.14	15,15,15,15	0
37	CD	2	8402	1/1	0.92	0.11	-1.20	67,67,67,67	0
34	NA	A	8367	1/1	0.92	0.14	-1.29	40,40,40,40	0
34	NA	M	8380	1/1	0.98	0.15	-1.48	43,43,43,43	0
32	MG	A	8052	1/1	0.87	0.14	-1.71	42,42,42,42	0
32	MG	A	8074	1/1	0.99	0.08	-1.80	24,24,24,24	0
35	CL	A	8512	1/1	0.93	0.11	-1.98	43,43,43,43	0
32	MG	C	8065	1/1	0.96	0.13	-2.04	62,62,62,62	0
32	MG	U	8073	1/1	0.88	0.13	-2.05	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8013	1/1	0.95	0.15	-2.06	27,27,27,27	0
34	NA	J	8309	1/1	0.93	0.10	-2.09	23,23,23,23	0
32	MG	A	8056	1/1	0.96	0.12	-2.11	53,53,53,53	0
34	NA	A	8333	1/1	0.89	0.09	-2.16	25,25,25,25	0
32	MG	A	8096	1/1	0.93	0.14	-2.17	55,55,55,55	0
34	NA	A	8317	1/1	0.93	0.12	-2.22	25,25,25,25	0
32	MG	A	8015	1/1	0.98	0.08	-2.24	35,35,35,35	0
34	NA	S	8337	1/1	0.94	0.12	-2.26	57,57,57,57	0
34	NA	A	8335	1/1	0.95	0.15	-2.27	50,50,50,50	0
32	MG	A	8067	1/1	0.98	0.15	-2.29	41,41,41,41	0
34	NA	A	8379	1/1	0.95	0.13	-2.32	30,30,30,30	0
37	CD	1	8403	1/1	0.97	0.14	-2.34	187,187,187,187	0
32	MG	A	8107	1/1	0.95	0.05	-2.48	64,64,64,64	0
34	NA	A	8362	1/1	0.98	0.13	-2.60	45,45,45,45	0
34	NA	A	8374	1/1	0.95	0.12	-2.88	36,36,36,36	0
32	MG	A	8060	1/1	0.98	0.12	-2.92	39,39,39,39	0
32	MG	D	8055	1/1	0.94	0.08	-2.98	50,50,50,50	0
34	NA	A	8343	1/1	0.97	0.09	-3.04	17,17,17,17	0
34	NA	A	8324	1/1	0.97	0.06	-3.11	26,26,26,26	0
34	NA	A	8378	1/1	0.96	0.12	-3.17	28,28,28,28	0
34	NA	R	8348	1/1	0.97	0.11	-3.17	20,20,20,20	0
32	MG	A	8004	1/1	0.97	0.08	-3.25	18,18,18,18	0
34	NA	A	8353	1/1	0.98	0.07	-3.31	15,15,15,15	0
34	NA	K	8346	1/1	1.00	0.06	-3.42	19,19,19,19	0
32	MG	A	8014	1/1	0.98	0.13	-3.51	20,20,20,20	0
32	MG	A	8027	1/1	0.93	0.09	-3.53	56,56,56,56	0
32	MG	A	8032	1/1	0.95	0.11	-3.60	24,24,24,24	0
32	MG	A	8064	1/1	0.99	0.11	-3.72	18,18,18,18	0
34	NA	A	8368	1/1	0.92	0.08	-3.81	22,22,22,22	0
32	MG	A	8001	1/1	0.94	0.12	-4.00	33,33,33,33	0
37	CD	4	8404	1/1	0.79	0.46	-4.00	202,202,202,202	0
34	NA	A	8305	1/1	0.94	0.14	-4.22	22,22,22,22	0
35	CL	N	8518	1/1	0.98	0.08	-4.22	36,36,36,36	0
32	MG	A	8017	1/1	0.99	0.05	-4.24	17,17,17,17	0
34	NA	A	8373	1/1	0.96	0.07	-4.28	40,40,40,40	0
34	NA	A	8376	1/1	0.98	0.12	-4.58	35,35,35,35	0
32	MG	Z	8109	1/1	0.94	0.08	-4.71	31,31,31,31	0
34	NA	A	8344	1/1	0.87	0.10	-4.86	20,20,20,20	0
33	K	A	8201	1/1	0.96	0.09	-4.91	53,53,53,53	0
32	MG	A	8091	1/1	0.93	0.07	-5.27	53,53,53,53	0
32	MG	A	8002	1/1	0.98	0.11	-5.32	26,26,26,26	0
34	NA	A	8381	1/1	0.90	0.08	-5.39	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8058	1/1	0.94	0.11	-5.49	47,47,47,47	0
32	MG	A	8033	1/1	0.97	0.09	-5.60	26,26,26,26	0
32	MG	A	8022	1/1	0.98	0.05	-5.63	22,22,22,22	0
32	MG	A	8010	1/1	0.96	0.06	-5.66	37,37,37,37	0
34	NA	N	8347	1/1	0.99	0.05	-5.69	21,21,21,21	0
33	K	A	8202	1/1	0.96	0.07	-5.77	43,43,43,43	0
32	MG	A	8062	1/1	0.92	0.08	-5.83	32,32,32,32	0
32	MG	A	8057	1/1	0.98	0.10	-6.00	16,16,16,16	0
32	MG	A	8008	1/1	0.90	0.08	-6.26	50,50,50,50	0
32	MG	A	8080	1/1	0.98	0.09	-6.44	35,35,35,35	0
32	MG	A	8038	1/1	0.98	0.10	-6.46	30,30,30,30	0
32	MG	A	8054	1/1	0.98	0.09	-7.60	43,43,43,43	0
32	MG	A	8071	1/1	0.91	0.08	-7.72	65,65,65,65	0
32	MG	A	8034	1/1	0.97	0.06	-7.83	32,32,32,32	0
32	MG	A	8108	1/1	0.96	0.10	-7.94	44,44,44,44	0
32	MG	A	8110	1/1	0.99	0.06	-8.12	26,26,26,26	0
34	NA	A	8302	1/1	0.94	0.10	-8.60	36,36,36,36	0
34	NA	A	8320	1/1	0.95	0.10	-9.14	16,16,16,16	0
32	MG	A	8006	1/1	0.96	0.09	-9.66	33,33,33,33	0
32	MG	A	8007	1/1	0.98	0.09	-9.89	22,22,22,22	0
32	MG	A	8020	1/1	0.95	0.09	-11.46	38,38,38,38	0
32	MG	A	8035	1/1	0.98	0.04	-11.88	64,64,64,64	0
32	MG	A	8019	1/1	0.97	0.06	-12.97	27,27,27,27	0
32	MG	A	8084	1/1	0.97	0.09	-15.41	65,65,65,65	0
32	MG	L	8069	1/1	0.96	0.07	-	65,65,65,65	0
35	CL	O	8507	1/1	0.84	0.18	-	72,72,72,72	0
32	MG	A	8068	1/1	0.83	0.08	-	59,59,59,59	0
32	MG	A	8046	1/1	0.64	0.13	-	74,74,74,74	0
34	NA	A	8375	1/1	0.86	0.34	-	44,44,44,44	0
32	MG	A	8104	1/1	0.98	0.09	-	40,40,40,40	0
34	NA	A	8349	1/1	0.94	0.18	-	27,27,27,27	0
32	MG	A	8023	1/1	0.97	0.07	-	47,47,47,47	0
34	NA	E	8304	1/1	0.86	0.12	-	23,23,23,23	0
32	MG	A	8066	1/1	0.88	0.16	-	76,76,76,76	0
34	NA	A	8307	1/1	0.97	0.11	-	28,28,28,28	0
32	MG	A	8041	1/1	0.93	0.31	-	72,72,72,72	0
34	NA	A	8328	1/1	0.96	0.13	-	39,39,39,39	0
35	CL	K	8501	1/1	0.99	0.10	-	61,61,61,61	0
32	MG	A	8005	1/1	0.96	0.12	-	39,39,39,39	0
32	MG	A	8081	1/1	0.99	0.13	-	30,30,30,30	0
34	NA	A	8301	1/1	0.97	0.25	-	27,27,27,27	0
32	MG	A	8087	1/1	0.94	0.29	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	CL	A	8503	1/1	0.96	0.12	-	65,65,65,65	0
34	NA	A	8318	1/1	0.96	0.22	-	62,62,62,62	0
32	MG	A	8021	1/1	0.99	0.10	-	45,45,45,45	0
35	CL	S	8506	1/1	0.91	0.16	-	60,60,60,60	0
32	MG	A	8086	1/1	0.98	0.13	-	49,49,49,49	0
34	NA	A	8370	1/1	0.79	0.41	-	82,82,82,82	0
34	NA	A	8342	1/1	0.93	0.15	-	31,31,31,31	0
32	MG	A	8090	1/1	0.95	0.20	-	81,81,81,81	0
32	MG	A	8116	1/1	0.85	0.32	-	117,117,117,117	0
34	NA	A	8326	1/1	0.96	0.10	-	31,31,31,31	0
32	MG	A	8037	1/1	0.95	0.07	-	40,40,40,40	0
32	MG	A	8072	1/1	0.96	0.22	-	64,64,64,64	0
34	NA	A	8364	1/1	0.94	0.16	-	32,32,32,32	0
32	MG	A	8045	1/1	0.93	0.11	-	69,69,69,69	0
32	MG	A	8051	1/1	0.87	0.16	-	97,97,97,97	0
32	MG	A	8113	1/1	0.97	0.10	-	40,40,40,40	0
32	MG	A	8115	1/1	0.96	0.09	-	41,41,41,41	0
34	NA	A	8329	1/1	0.95	0.08	-	47,47,47,47	0
32	MG	A	8059	1/1	0.95	0.12	-	70,70,70,70	0
35	CL	K	8502	1/1	0.91	0.21	-	83,83,83,83	0
34	NA	A	8360	1/1	0.97	0.15	-	42,42,42,42	0
34	NA	A	8336	1/1	0.94	0.15	-	72,72,72,72	0
34	NA	A	8352	1/1	0.96	0.20	-	36,36,36,36	0
34	NA	A	8330	1/1	0.98	0.10	-	37,37,37,37	0
32	MG	A	8025	1/1	0.99	0.04	-	57,57,57,57	0
32	MG	A	8079	1/1	0.98	0.07	-	19,19,19,19	0
32	MG	A	8082	1/1	0.93	0.10	-	35,35,35,35	0
32	MG	A	8039	1/1	0.92	0.09	-	66,66,66,66	0
32	MG	A	8085	1/1	0.93	0.18	-	60,60,60,60	0
32	MG	A	8040	1/1	0.91	0.17	-	86,86,86,86	0
32	MG	A	8061	1/1	0.97	0.07	-	40,40,40,40	0
35	CL	A	8517	1/1	0.95	0.29	-	75,75,75,75	0
32	MG	A	8076	1/1	0.53	0.37	-	123,123,123,123	0
32	MG	A	8031	1/1	0.97	0.07	-	14,14,14,14	0
32	MG	A	8050	1/1	0.94	0.12	-	62,62,62,62	0
34	NA	A	8322	1/1	0.79	0.26	-	76,76,76,76	0
32	MG	A	8047	1/1	0.92	0.22	-	76,76,76,76	0
34	NA	A	8313	1/1	0.95	0.46	-	76,76,76,76	0
34	NA	A	8354	1/1	0.95	0.13	-	20,20,20,20	0
32	MG	A	8009	1/1	0.97	0.08	-	15,15,15,15	0
34	NA	T	8312	1/1	-0.45	0.48	-	163,163,163,163	0
35	CL	C	8509	1/1	0.88	0.26	-	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8048	1/1	0.95	0.10	-	51,51,51,51	0
32	MG	A	8016	1/1	0.99	0.10	-	26,26,26,26	0
32	MG	A	8088	1/1	0.96	0.07	-	11,11,11,11	0
32	MG	A	8094	1/1	0.95	0.12	-	77,77,77,77	0
32	MG	A	8097	1/1	0.69	0.45	-	80,80,80,80	0
32	MG	A	8030	1/1	0.98	0.13	-	31,31,31,31	0
34	NA	A	8384	1/1	0.66	0.75	-	105,105,105,105	0
32	MG	A	8093	1/1	0.97	0.19	-	91,91,91,91	0
34	NA	A	8341	1/1	0.88	0.10	-	28,28,28,28	0
34	NA	A	8306	1/1	0.91	0.39	-	38,38,38,38	0
35	CL	A	8522	1/1	0.93	0.48	-	72,72,72,72	0
32	MG	A	8026	1/1	0.96	0.09	-	19,19,19,19	0
34	NA	A	8315	1/1	0.97	0.11	-	15,15,15,15	0
32	MG	A	8011	1/1	0.96	0.09	-	36,36,36,36	0
32	MG	A	8117	1/1	0.99	0.06	-	8,8,8,8	0
32	MG	A	8102	1/1	0.91	0.73	-	106,106,106,106	0
34	NA	A	8357	1/1	0.79	0.13	-	43,43,43,43	0
32	MG	A	8029	1/1	0.95	0.10	-	58,58,58,58	0
34	NA	A	8319	1/1	0.89	0.11	-	41,41,41,41	0
32	MG	A	8089	1/1	0.74	0.26	-	89,89,89,89	0
32	MG	A	8075	1/1	0.94	0.08	-	44,44,44,44	0
34	NA	A	8356	1/1	0.90	0.37	-	46,46,46,46	0
37	CD	P	8405	1/1	0.77	0.44	-	202,202,202,202	0
34	NA	A	8358	1/1	0.95	0.57	-	75,75,75,75	0
32	MG	A	8103	1/1	0.96	0.11	-	45,45,45,45	0
32	MG	A	8043	1/1	0.87	0.13	-	67,67,67,67	0
35	CL	4	8504	1/1	0.34	0.55	-	114,114,114,114	0
35	CL	A	8511	1/1	0.88	0.21	-	73,73,73,73	0
35	CL	A	8514	1/1	0.88	0.19	-	62,62,62,62	0
34	NA	B	8351	1/1	0.46	0.42	-	90,90,90,90	0
34	NA	A	8334	1/1	0.97	0.05	-	36,36,36,36	0
32	MG	A	8028	1/1	0.96	0.06	-	60,60,60,60	0
32	MG	A	8092	1/1	0.84	0.28	-	105,105,105,105	0
32	MG	A	8106	1/1	0.81	0.09	-	101,101,101,101	0
35	CL	Z	8520	1/1	0.92	0.15	-	49,49,49,49	0
34	NA	A	8385	1/1	0.95	0.40	-	29,29,29,29	0
32	MG	A	8063	1/1	0.93	0.09	-	82,82,82,82	0
32	MG	A	8101	1/1	0.94	0.09	-	42,42,42,42	0
32	MG	B	8095	1/1	0.94	0.16	-	90,90,90,90	0
32	MG	A	8024	1/1	0.58	1.06	-	84,84,84,84	0
34	NA	A	8316	1/1	0.97	0.11	-	31,31,31,31	0
32	MG	A	8100	1/1	0.95	0.11	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8098	1/1	0.94	0.25	-	53,53,53,53	0
32	MG	A	8036	1/1	0.96	0.06	-	36,36,36,36	0
32	MG	A	8012	1/1	0.98	0.14	-	41,41,41,41	0
32	MG	A	8111	1/1	0.88	0.25	-	69,69,69,69	0
32	MG	A	8083	1/1	0.98	0.07	-	40,40,40,40	0
34	NA	A	8363	1/1	0.68	0.36	-	56,56,56,56	0
34	NA	A	8314	1/1	0.91	0.25	-	35,35,35,35	0
32	MG	A	8042	1/1	0.99	0.05	-	17,17,17,17	0
34	NA	A	8310	1/1	0.95	0.17	-	35,35,35,35	0
34	NA	A	8311	1/1	0.97	0.12	-	68,68,68,68	0
32	MG	A	8099	1/1	0.86	0.19	-	55,55,55,55	0
32	MG	A	8018	1/1	0.94	0.12	-	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.