



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 08:18 am GMT

PDB ID : 1KD1
Title : Co-crystal Structure of Spiramycin bound to the 50S Ribosomal Subunit of *Haloarcula marismortui*
Authors : Hansen, J.L.; Ippolito, J.A.; Ban, N.; Nissen, P.; Moore, P.B.; Steitz, T.A.
Deposited on : 2001-11-12
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

<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 : trunk28620
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) : recalc28949

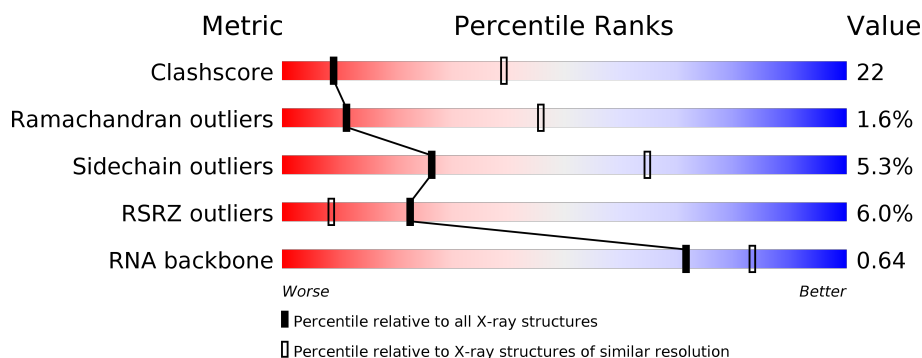
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)
RNA backbone	2435	1007 (3.34-2.66)

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> <div>47%</div> <div>39%</div> <div>7%</div> <div>6%</div> </div> </div>
2	B	122	<div> <div>5%</div> <div> <div>46%</div> <div>37%</div> <div>15%</div> </div> </div>
3	C	239	<div> <div>4%</div> <div> <div>54%</div> <div>39%</div> <div>6%</div> </div> </div>
4	D	337	<div> <div>%</div> <div> <div>51%</div> <div>43%</div> <div>6%</div> </div> </div>
5	E	246	<div> <div>53%</div> <div>41%</div> <div>6%</div> </div>
6	F	176	<div> <div>27%</div> <div> <div>28%</div> <div>43%</div> <div>6%</div> <div>20%</div> </div> </div>

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

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
31	SPR	A	9001	-	-	-	X
32	MG	A	8054	-	-	X	-
32	MG	A	8067	-	-	-	X
32	MG	Z	8109	-	-	-	X
33	NA	A	8303	-	-	-	X
33	NA	A	8308	-	-	-	X
33	NA	A	8310	-	-	-	X
33	NA	A	8321	-	-	-	X
33	NA	A	8323	-	-	-	X
33	NA	A	8331	-	-	-	X
33	NA	A	8332	-	-	-	X
33	NA	A	8335	-	-	-	X
33	NA	A	8356	-	-	-	X
33	NA	A	8362	-	-	-	X
33	NA	A	8365	-	-	-	X
33	NA	A	8366	-	-	-	X
33	NA	A	8371	-	-	-	X
33	NA	A	8372	-	-	-	X
33	NA	A	8373	-	-	-	X
33	NA	A	8374	-	-	-	X
33	NA	A	8376	-	-	-	X
33	NA	A	8378	-	-	-	X
33	NA	A	8379	-	-	-	X
33	NA	A	8381	-	-	-	X
33	NA	A	8382	-	-	-	X
33	NA	B	8383	-	-	-	X
33	NA	S	8337	-	-	-	X
33	NA	S	8386	-	-	-	X
34	CL	4	8504	-	-	-	X
34	CL	A	8505	-	-	-	X
34	CL	A	8515	-	-	-	X
34	CL	D	8519	-	-	-	X
34	CL	O	8507	-	-	X	-
36	CD	4	8404	-	-	-	X
36	CD	V	8401	-	-	-	X

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 98587 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	560	C	U	CONFLICT	? 3377779

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

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 protein called RIBOSOMAL PROTEIN L2.

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

- Molecule 4 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	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 5 is a protein called RIBOSOMAL PROTEIN L4.

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

- Molecule 6 is a protein called RIBOSOMAL PROTEIN L5.

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

- Molecule 7 is a protein called RIBOSOMAL PROTEIN L6.

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

- Molecule 8 is a protein called RIBOSOMAL PROTEIN L7AE.

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

- Molecule 9 is a protein called RIBOSOMAL PROTEIN L10.

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

- Molecule 10 is a protein called RIBOSOMAL PROTEIN L10E.

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

- Molecule 11 is a protein called RIBOSOMAL PROTEIN L13.

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

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L14.

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

- Molecule 13 is a protein called RIBOSOMAL PROTEIN L15.

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

- Molecule 14 is a protein called RIBOSOMAL PROTEIN L15E.

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

- Molecule 15 is a protein called RIBOSOMAL PROTEIN L18.

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

- Molecule 16 is a protein called RIBOSOMAL PROTEIN L18E.

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

- Molecule 17 is a protein called RIBOSOMAL PROTEIN L19E.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 18 is a protein called RIBOSOMAL PROTEIN L21E.

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

- Molecule 19 is a protein called RIBOSOMAL PROTEIN L22.

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

- Molecule 20 is a protein called RIBOSOMAL PROTEIN L23.

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

- Molecule 21 is a protein called RIBOSOMAL PROTEIN L24.

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

- Molecule 22 is a protein called RIBOSOMAL PROTEIN L24E.

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

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L29.

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

- Molecule 24 is a protein called RIBOSOMAL PROTEIN L30.

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

- Molecule 25 is a protein called RIBOSOMAL PROTEIN L31E.

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

- Molecule 26 is a protein called RIBOSOMAL PROTEIN L32E.

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

- Molecule 27 is a protein called RIBOSOMAL PROTEIN L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	73	Total	C	N	O	S	0	0	0
			563	359	111	86	7			

- Molecule 28 is a protein called RIBOSOMAL PROTEIN L37E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	56	Total	C	N	O	S	0	0	0
			430	258	86	82	4			

- Molecule 29 is a protein called RIBOSOMAL PROTEIN L39E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	46	Total	C	N	O	S	0	0	0
			393	238	86	68	1			

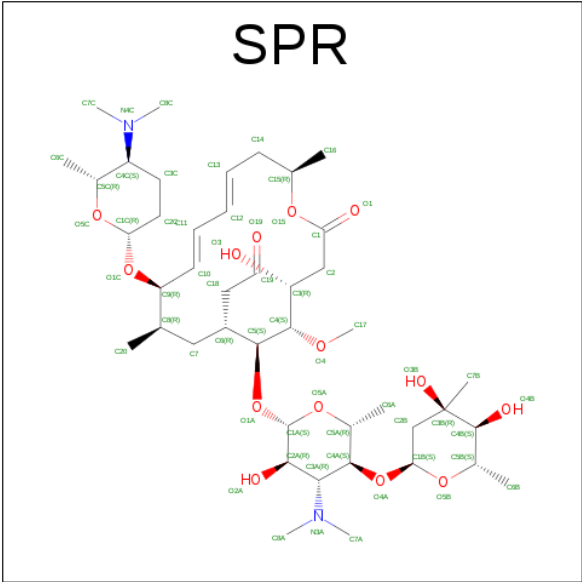
There is a discrepancy between the modelled and reference sequences:

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

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	4	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is SPIRAMYCIN I (three-letter code: SPR) (formula: C₄₃H₇₄N₂O₁₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
31	A	1	Total	C	N	O	0	0
			59	43	2	14		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	1	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	C	1	Total	Mg	0	0
			1	1		
32	Z	1	Total	Mg	0	0
			1	1		
32	A	112	Total	Mg	0	0
			112	112		
32	4	1	Total	Mg	0	0
			1	1		
32	U	1	Total	Mg	0	0
			1	1		
32	L	1	Total	Mg	0	0
			1	1		

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

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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	P	1	Total Cl 1 1	0	0
34	D	1	Total Cl 1 1	0	0
34	K	3	Total Cl 3 3	0	0
34	C	1	Total Cl 1 1	0	0
34	Z	1	Total Cl 1 1	0	0
34	A	9	Total Cl 9 9	0	0
34	4	1	Total Cl 1 1	0	0
34	N	1	Total Cl 1 1	0	0
34	O	1	Total Cl 1 1	0	0

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

- Molecule 35 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	A	3	Total 3	K 3	0	0

- Molecule 36 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	P	1	Total 1	Cd 1	0	0
36	2	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	4	1	Total 1	Cd 1	0	0
36	V	1	Total 1	Cd 1	0	0

- Molecule 37 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	A	5910	Total 5910	O 5910	0	0
37	B	142	Total 142	O 142	0	0
37	C	126	Total 126	O 126	0	0
37	D	150	Total 150	O 150	0	0
37	E	169	Total 169	O 169	0	0
37	F	51	Total 51	O 51	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	G	42	Total 42	O 42	0	0
37	H	26	Total 26	O 26	0	0
37	I	21	Total 21	O 21	0	0
37	J	78	Total 78	O 78	0	0
37	K	54	Total 54	O 54	0	0
37	L	65	Total 65	O 65	0	0
37	M	79	Total 79	O 79	0	0
37	N	132	Total 132	O 132	0	0
37	O	69	Total 69	O 69	0	0
37	P	45	Total 45	O 45	0	0
37	Q	65	Total 65	O 65	0	0
37	R	55	Total 55	O 55	0	0
37	S	83	Total 83	O 83	0	0
37	T	35	Total 35	O 35	0	0
37	U	39	Total 39	O 39	0	0
37	V	25	Total 25	O 25	0	0
37	W	15	Total 15	O 15	0	0
37	X	70	Total 70	O 70	0	0
37	Y	25	Total 25	O 25	0	0
37	Z	94	Total 94	O 94	0	0
37	1	41	Total 41	O 41	0	0

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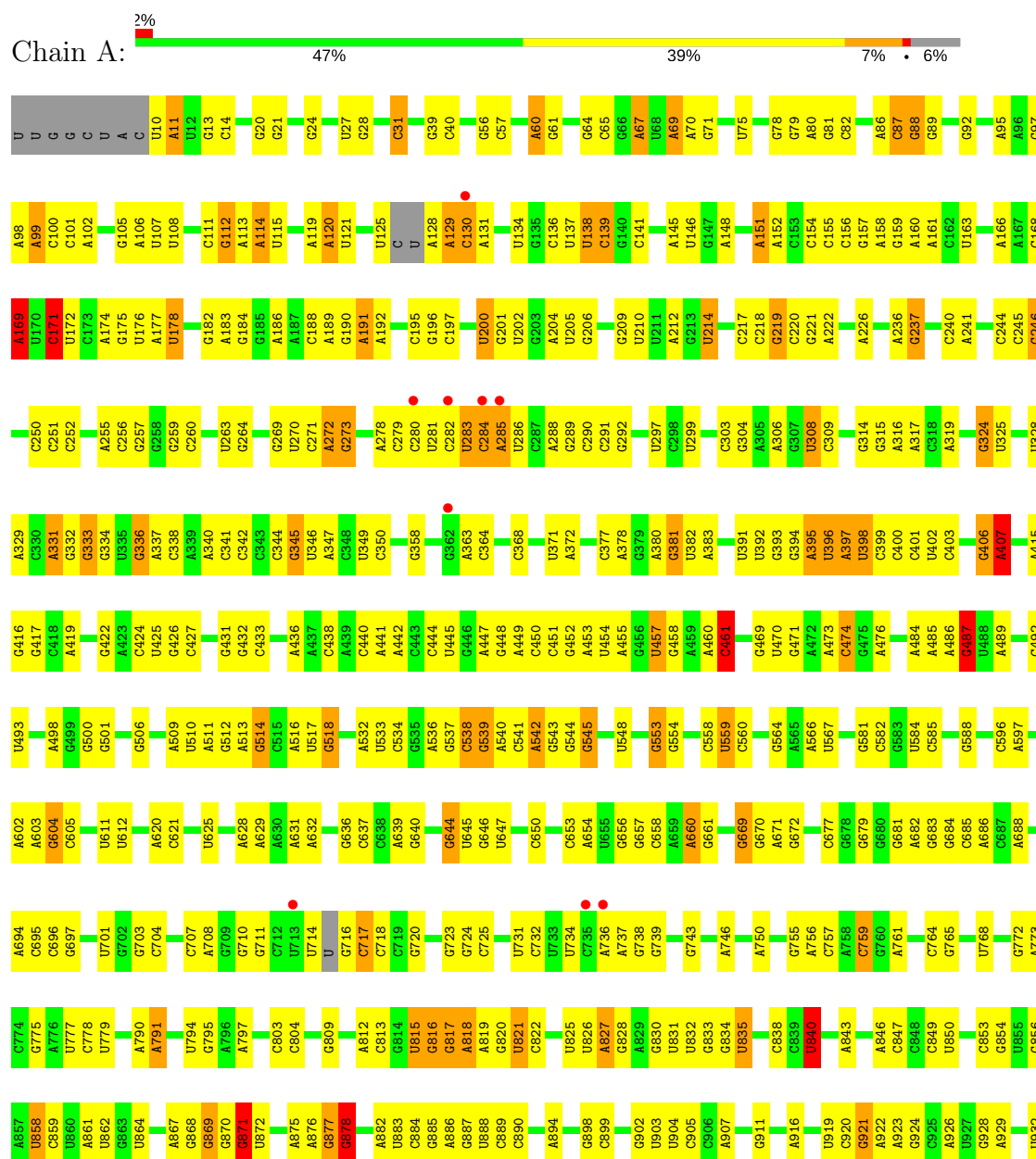
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	2	55	Total 55	O 55	0	0
37	3	42	Total 42	O 42	0	0
37	4	73	Total 73	O 73	0	0

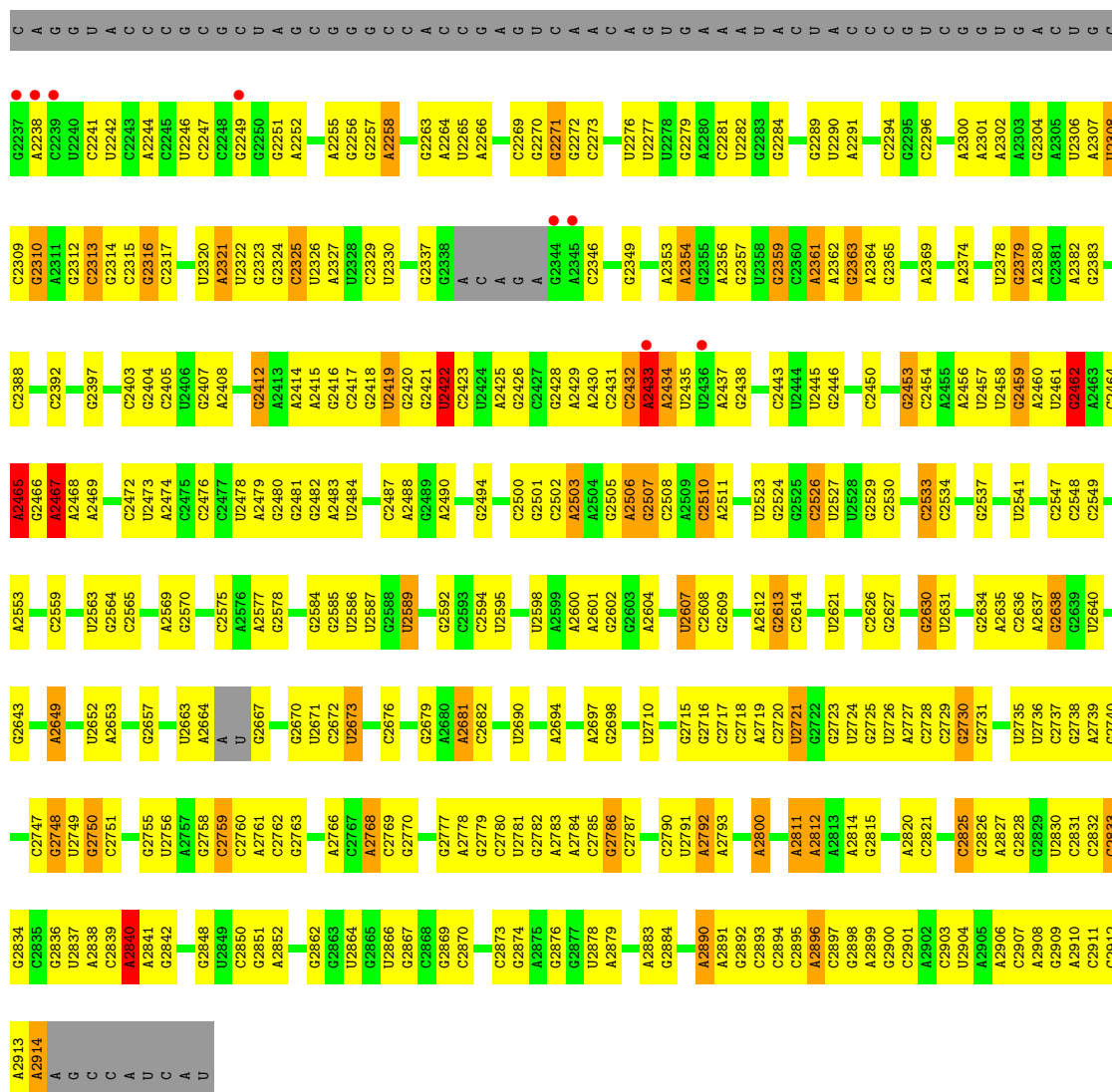
3 Residue-property plots

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.

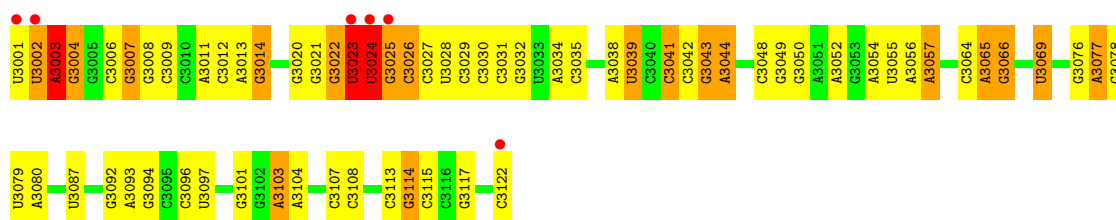
• Molecule 1: 23S rRNA



G2111	A2038	A	U1879	G1707	A1626	A1533	C1450	U1368	C1263	U1180	A1097	G940
A2112	A2039	C	C1880	A1710	G1627	A1534	C1451	A1369	U1264	A1181	A1098	G941
G2113	G1805	C	A1881	A1711	G1628	G1535	C1456	G1370	U1265	C1182	G1099	U942
C2114	G2044	C	C1882	A1712	G1629	C1536	U1457	U1371	C1267	C1183	C1103	
U2115	G2045	U1964	A1886	C1720	C1633	G1543	U1458	A1372	U1268	U1185	U109	C946
U2116	G2046	C1965	U1887	C1721	G1634	U1544	U1459	A1375	G1269	C1186	U109	U947
U2117	C2047	U1966	C1888	C1722	G1635	U1545	C1462	G1376	U1270	U1187	G1110	G948
A2118	G2050	U1967	A1889	C1723	G1636	G1546	U1463	C1377	U1278	A1188	U1110	G949
C2119	G2051	A1968	U1890	G1724	A1637	G1547	U1464	U1380	U1279	U1115	A1114	U948
U2120	G2052	A1969	U1891	C1725	A1641	G1552	G1468	U1381	U1280	U1116	U1116	G950
G2121	G2053	U1970	U1892	U1726	A1642	U1553	C1469	G1377	U1281	U1117	U1117	G951
A2054	A2054	G1971	G1818	C1727	A1643	U1554	U1470	U1382	U1282	U1118	U1118	G952
A2055	G2055	U1972	G1819	C1728	A1644	U1555	U1471	U1383	U1283	U1119	U1119	U954
		A1973	G1820	C1729	A1645	U1556	U1472	C1384	U1284	U1120	U1120	A955
U2059	U2059	G1974	G1821	C1730	A1646	U1557	U1473	U1385	U1285	U1121	U1121	G958
		U1975	G1822	C1731	A1647	U1558	U1474	U1386	U1286	U1122	U1122	G959
U2060	U2060	U1976	G1823	C1732	A1648	U1559	U1475	U1387	U1287	U1123	U1123	G960
U2061	U2061	A1977	U1824	A1733	A1649	U1560	U1476	U1388	U1288	U1124	U1124	A961
U2062	U2062	G1978	U1825	C1734	A1650	U1561	U1477	U1389	U1289	U1125	U1125	C962
U2063	U2063	U1979	U1826	C1735	A1651	U1562	U1478	U1390	U1290	U1126	U1126	C963
G2064	G2064	A1980	U1827	C1736	U1652	G1563	U1479	U1391	U1291	U1127	U1127	
G2065	G2065	U1981	G1828	A1737	U1653	U1564	U1480	U1392	U1292	U1128	U1128	
U2066	U2066	A1982	U1829	C1738	U1654	U1565	U1481	U1393	U1293	U1129	U1129	
U2067	U2067	G1983	U1830	C1739	U1655	U1566	U1482	U1394	U1294	U1130	U1130	
G2068	G2068	U1984	U1831	C1740	U1656	U1567	U1483	U1395	U1295	U1131	U1131	
U2069	U2069	A1985	U1832	C1741	U1657	U1568	U1484	U1396	U1296	U1132	U1132	
G2070	G2070	U1986	U1833	C1742	U1658	U1569	U1485	U1397	U1297	U1133	U1133	
G2071	G2071	U1987	U1834	C1743	U1659	U1570	U1486	U1398	U1298	U1134	U1134	
G2072	G2072	U1988	U1835	C1744	U1660	U1571	U1487	U1399	U1299	U1135	U1135	
G2073	G2073	U1989	U1836	C1745	U1661	U1572	U1488	U1400	U1300	U1136	U1136	
A2074	A2074	U1990	U1837	C1746	U1662	U1573	U1489	U1401	U1301	U1137	U1137	
U2075	U2075	U1991	U1838	C1747	U1663	U1574	U1490	U1402	U1302	U1138	U1138	
U2076	U2076	U1992	U1839	C1748	U1664	U1575	U1491	U1403	U1303	U1139	U1139	
G2077	G2077	U1993	U1840	C1749	U1665	U1576	U1492	U1404	U1304	U1140	U1140	
G2078	G2078	U1994	U1841	C1750	U1666	U1577	U1493	U1405	U1305	U1141	U1141	
G2079	G2079	U1995	U1842	C1751	U1667	U1578	U1494	U1406	U1306	U1142	U1142	
G2080	G2080	U1996	U1843	C1752	U1668	U1579	U1495	U1407	U1307	U1143	U1143	
A2081	A2081	U1997	U1844	C1753	U1669	U1580	U1496	U1408	U1308	U1144	U1144	
G2082	G2082	U1998	U1845	C1754	U1670	U1581	U1497	U1409	U1309	U1145	U1145	
A2083	A2083	U1999	U1846	C1755	U1671	U1582	U1498	U1410	U1310	U1146	U1146	
C2084	C2084	U2000	U1847	C1756	U1672	U1583	U1499	U1411	U1311	U1147	U1147	
A2085	A2085	G2001	U1848	C1757	U1673	U1584	U1500	U1412	U1312	U1148	U1148	
		U2002	U1849	C1758	U1674	U1585	U1501	U1413	U1313	U1149	U1149	
U2086	U2086	U2003	U1850	C1759	U1675	U1586	U1502	U1414	U1314	U1150	U1150	
G2087	G2087	U2004	U1851	C1760	U1676	U1587	U1503	U1415	U1315	U1151	U1151	
U2088	U2088	U2005	U1852	C1761	U1677	U1588	U1504	U1416	U1316	U1152	U1152	
		U2006	U1853	C1762	U1678	U1589	U1505	U1417	U1317	U1153	U1153	
A2089	A2089	U2007	U1854	C1763	U1679	U1590	U1506	U1418	U1318	U1154	U1154	
G2090	G2090	U2008	U1855	C1764	U1680	U1591	U1507	U1419	U1319	U1155	U1155	
G2091	G2091	U2009	U1856	C1765	U1681	U1592	U1508	U1420	U1320	U1156	U1156	
G2092	G2092	U2010	U1857	C1766	U1682	U1593	U1509	U1421	U1321	U1157	U1157	
U2093	U2093	A2011	U1858	C1767	U1683	U1594	U1510	U1422	U1322	U1158	U1158	
U2094	U2094	U2012	U1859	C1768	U1684	U1595	U1511	U1423	U1323	U1159	U1159	
G2095	G2095	U2013	U1860	C1769	U1685	U1596	U1512	U1424	U1324	U1160	U1160	
A2096	A2096	U2014	U1861	C1770	U1686	U1597	U1513	U1425	U1325	U1161	U1161	
U2097	U2097	U2015	U1862	C1771	U1687	U1598	U1514	U1426	U1326	U1162	U1162	
G2098	G2098	U2016	U1863	C1772	U1688	U1599	U1515	U1427	U1327	U1163	U1163	
A2100	A2100	U2017	U1864	C1773	U1689	U1600	U1516	U1428	U1328	U1164	U1164	
G2101	G2101	A2019	U1865	C1774	U1690	U1601	U1517	U1429	U1329	U1165	U1165	
A2102	A2102	U2020	U1866	C1775	U1691	U1602	U1518	U1430	U1330	U1166	U1166	
C2103	C2103	U2021	U1867	C1776	U1692	U1603	U1519	U1431	U1331	U1167	U1167	
C2104	C2104	U2022	U1868	C1777	U1693	U1604	U1520	U1432	U1332	U1168	U1168	
C2105	C2105	U2023	U1869	C1778	U1694	U1605	U1521	U1433	U1333	U1169	U1169	
C2106	C2106	U2024	U1870	C1779	U1695	U1606	U1522	U1434	U1334	U1170	U1170	
C2107	C2107	U2025	U1871	C1780	U1696	U1607	U1523	U1435	U1335	U1171	U1171	
C2108	C2108	U2026	U1872	C1781	U1697	U1608	U1524	U1436	U1336	U1172	U1172	
C2109	C2109	U2027	U1873	C1782	U1698	U1609	U1525	U1437	U1337	U1173	U1173	
C2110	C2110	U2028	U1874	C1783	U1699	U1610	U1526	U1438	U1338	U1174	U1174	
		U2029	U1875	C1784	U1700	U1611	U1527	U1439	U1339	U1175	U1175	
		U2030	U1876	C1785	U1701	U1612	U1528	U1440	U1340	U1176	U1176	
		U2031	U1877	C1786	U1702	U1613	U1529	U1441	U1341	U1177	U1177	
		U2032	U1878	C1787	U1703	U1614	U1530	U1442	U1342	U1178	U1178	
		U2033	U1879	C1788	U1704	U1615	U1531	U1443	U1343	U1179	U1179	
		U2034	U1880	C1789	U1705	U1616	U1532	U1444	U1344	U1180	U1180	
		U2035	U1881	C1790	U1706	U1617	U1533	U1445	U1345	U1181	U1181	
		U2036	U1882	C1791	U1707	U1618	U1534	U1446	U1346	U1182	U1182	
		U2037	U1883	C1792	U1708	U1619	U1535	U1447	U1347	U1183	U1183	
		U2038	U1884	C1793	U1709	U1620	U1536	U1448	U1348	U1184	U1184	
		U2039	U1885	C1794	U1710	U1621	U1537	U1449	U1349	U1185	U1185	
		U2040	U1886	C1795	U1711	U1622	U1538	U1450	U1350	U1186	U1186	
		U2041	U1887	C1796	U1712	U1623	U1539	U1451	U1351	U1187	U1187	
		U2042	U1888	C1797	U1713	U1624	U1540	U1452	U1352	U1188	U1188	
		U2043	U1889	C1798	U1714	U1625	U1541	U1453	U1353	U1189	U1189	
		U2044	U1890	C1799	U1715	U1626	U1542	U1454	U1354	U1190	U1190	
		U2045	U1891	C1800	U1716	U1627	U1543	U1455	U1355	U1191	U1191	
		U2046	U1892	C1801	U1717	U1628	U1544	U1456	U1356	U1192	U1192	
		U2047	U1893	C1802	U1718	U1629	U1545	U1457	U1357	U1193	U1193	
		U2048	U1894	C1803	U1719	U1630	U1546	U1458	U1358	U1194	U1194	
		U2049	U1895	C1804	U1720	U1631	U1547	U1459	U1359	U1195	U1195	
		U2050	U1896	C1805	U1721	U1632	U1548	U1460	U1360	U1196	U1196	
		U2051	U1897	C1806	U1722	U1633	U1549	U1461	U1361	U1197	U1197	
		U2052	U1898	C1807	U1723	U1634	U1550	U1462	U1362	U1198	U1198	
		U2053	U1899	C1808	U1724	U1635	U1551	U1463	U1363	U1199	U1199	
		U2054	U1900	C1809	U1725	U1636	U1552	U1464	U1364	U1200	U1200	
		U2055	U1901	C1810	U1726	U1637	U1553	U1465	U1365	U1201	U1201	
		U2056	U1902	C1811	U1727	U1638	U1554	U1466	U1366	U1202	U1202	
		U2057	U1903	C1812	U1728	U1639	U1555	U1467	U1367	U1203	U1203	
		U2058	U1904	C1813	U1729	U1640	U1556	U1468	U1368	U1204	U1204	
		U2059	U1905	C1814	U1730	U1641	U1557	U1469	U1369	U1205	U1205	
		U2060										

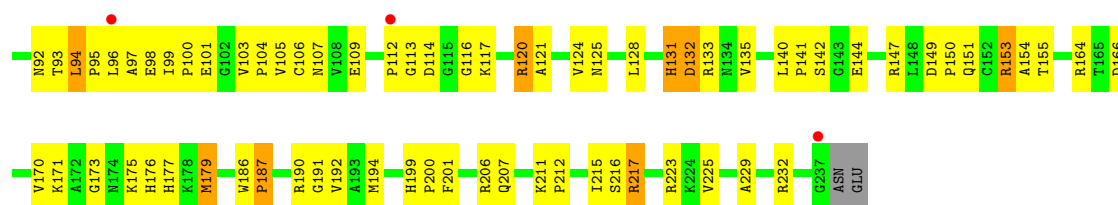


• Molecule 2: 5S rRNA

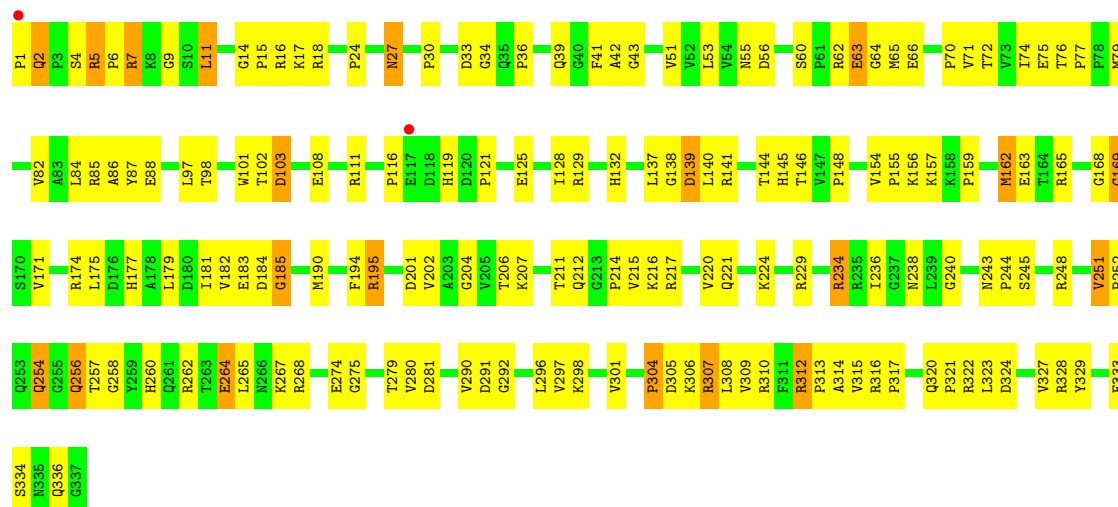


• Molecule 3: RIBOSOMAL PROTEIN L2

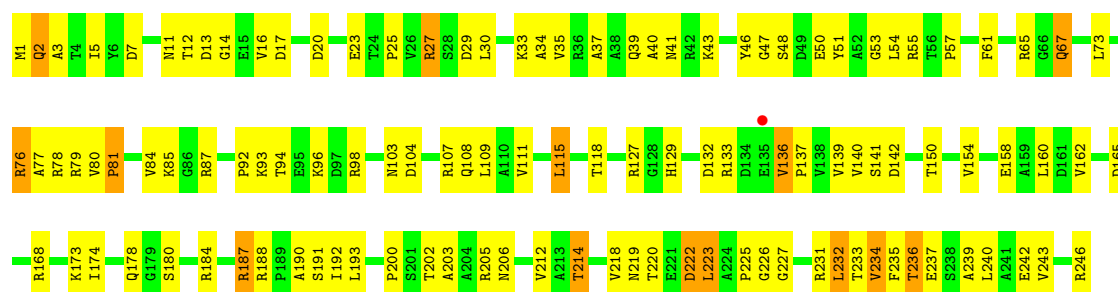




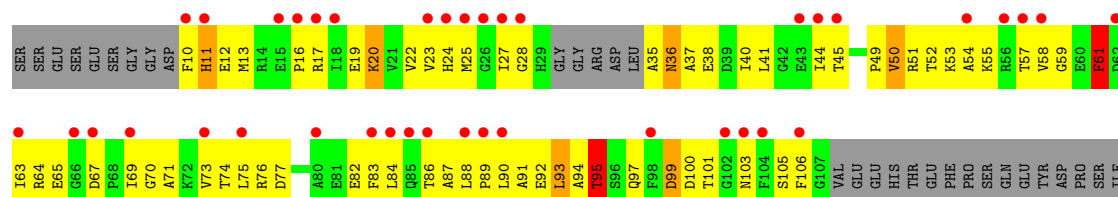
• Molecule 4: RIBOSOMAL PROTEIN L3



• Molecule 5: RIBOSOMAL PROTEIN L4



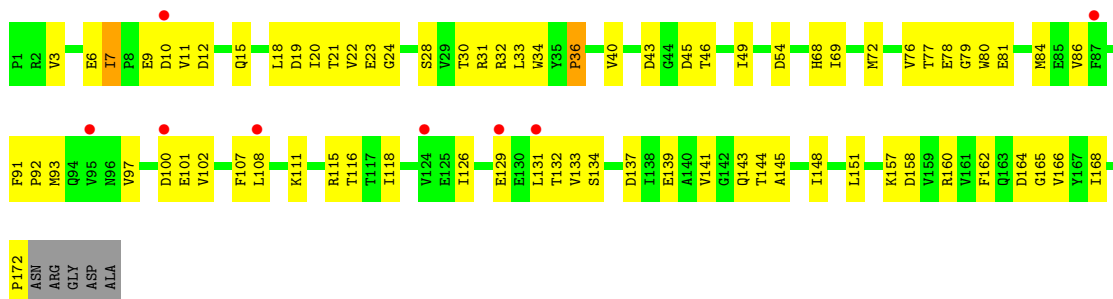
• Molecule 6: RIBOSOMAL PROTEIN L5





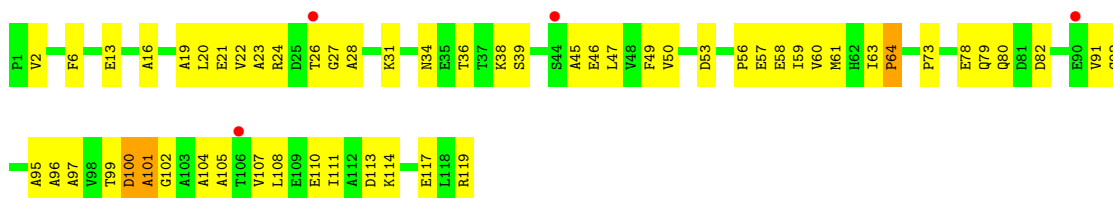
- Molecule 7: RIBOSOMAL PROTEIN L6

Chain G:  5% 55% 41% ..



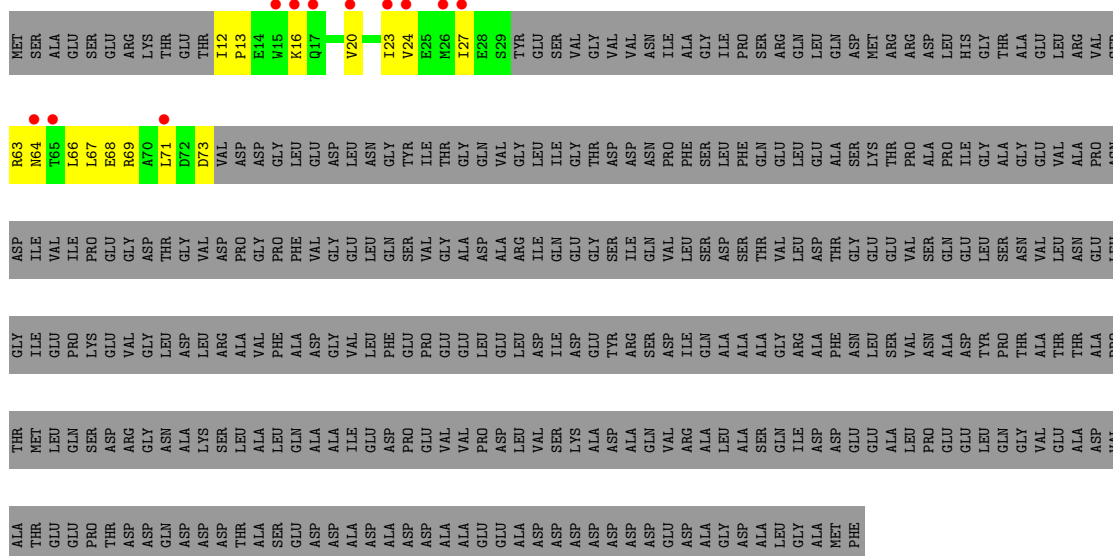
- Molecule 8: RIBOSOMAL PROTEIN L7AE

Chain H: 



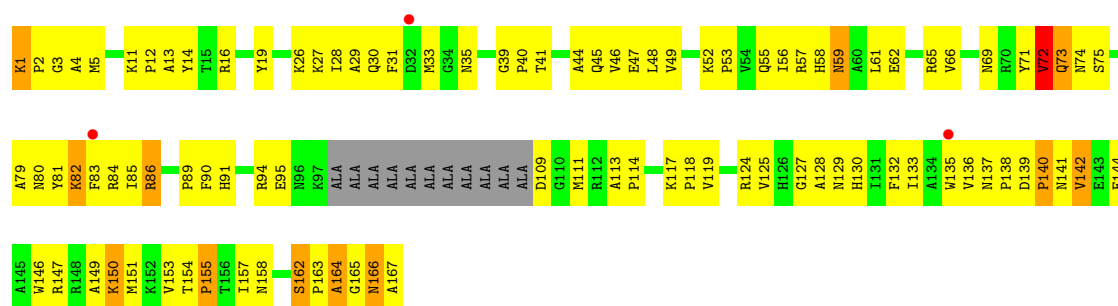
- Molecule 9: RIBOSOMAL PROTEIN L10

Chain I:  3% 92%

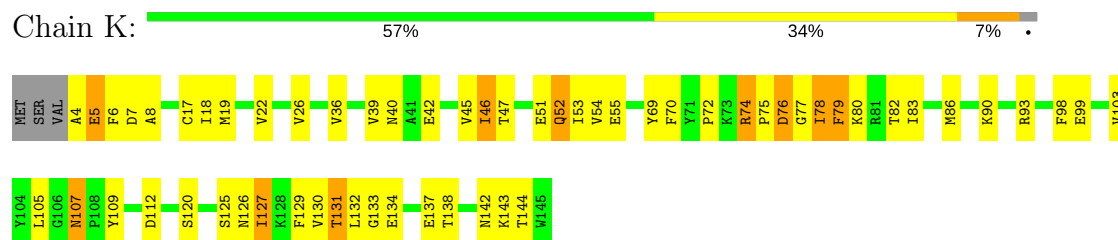


- Molecule 10: RIBOSOMAL PROTEIN L10E

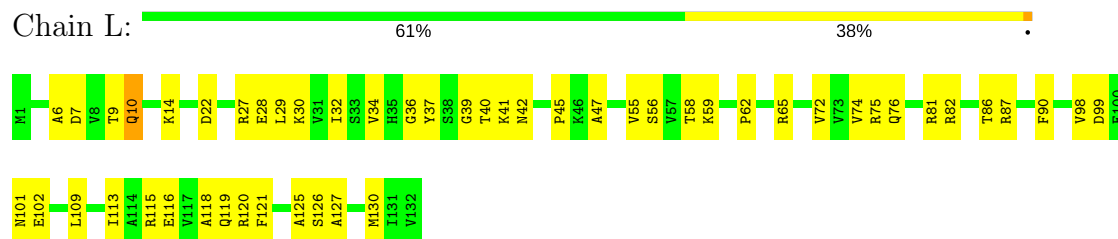
Chain J:  2% 35% 51% 7% 7%



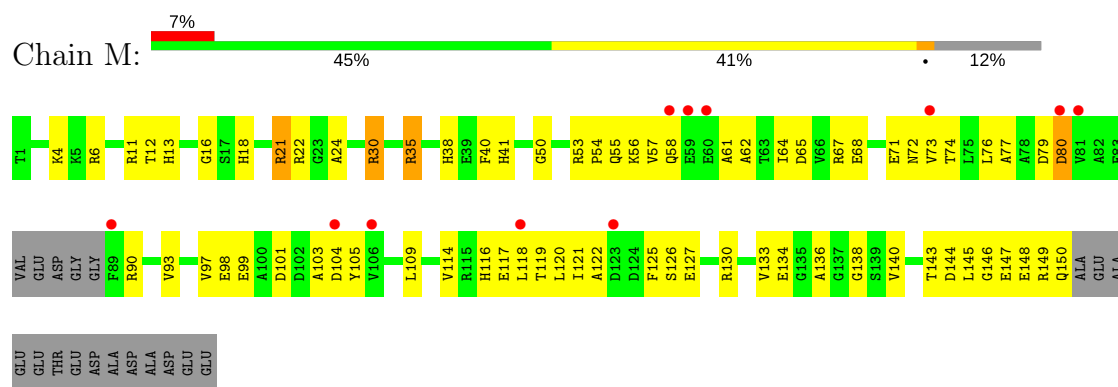
• Molecule 11: RIBOSOMAL PROTEIN L13



• Molecule 12: RIBOSOMAL PROTEIN L14

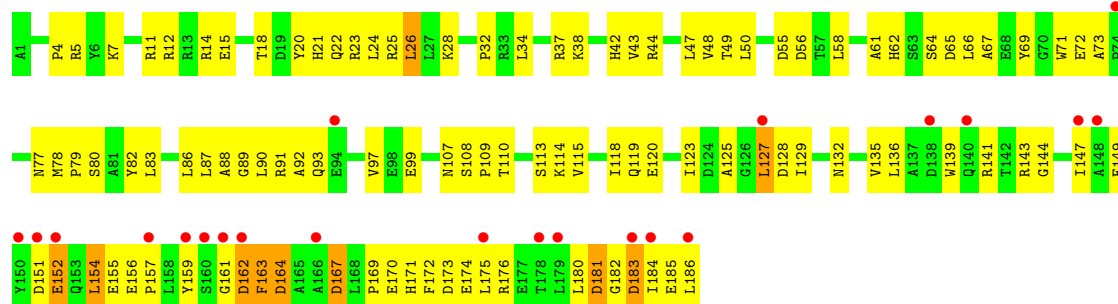


• Molecule 13: RIBOSOMAL PROTEIN L15

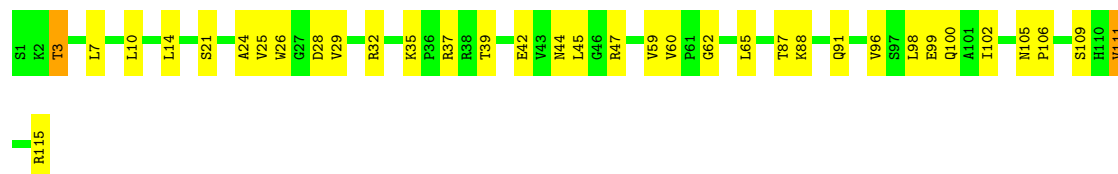




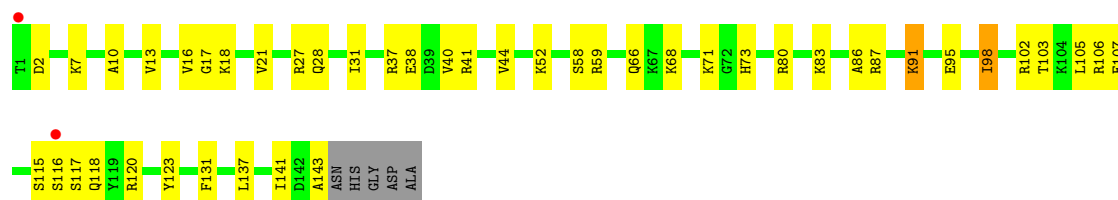
• Molecule 15: RIBOSOMAL PROTEIN L18



• Molecule 16: RIBOSOMAL PROTEIN L18E



• Molecule 17: RIBOSOMAL PROTEIN L19E

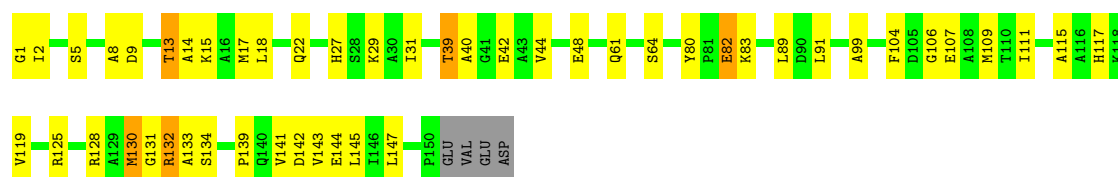


• Molecule 18: RIBOSOMAL PROTEIN L21E

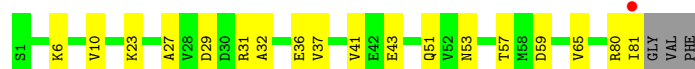
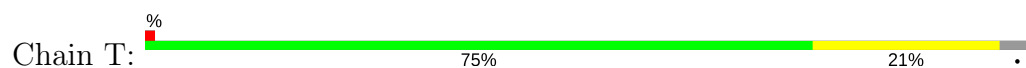


• Molecule 19: RIBOSOMAL PROTEIN L22

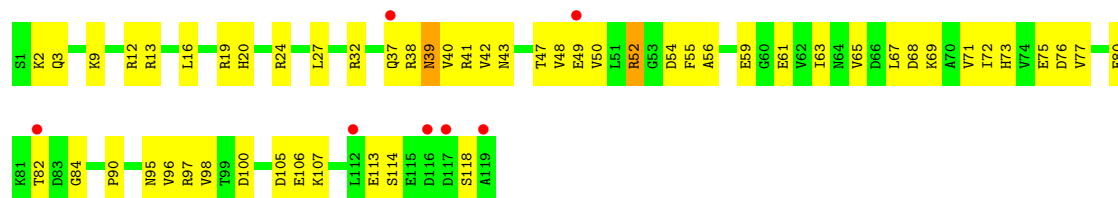




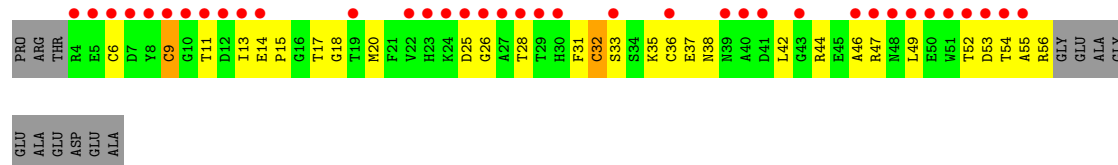
- Molecule 20: RIBOSOMAL PROTEIN L23



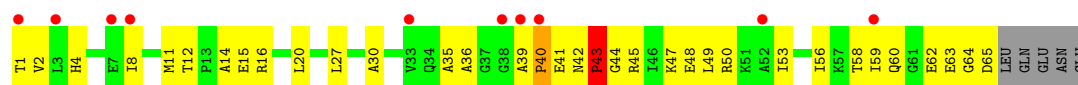
- Molecule 21: RIBOSOMAL PROTEIN L24



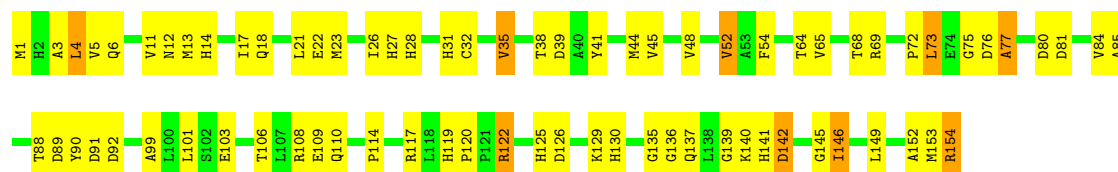
- Molecule 22: RIBOSOMAL PROTEIN L24E



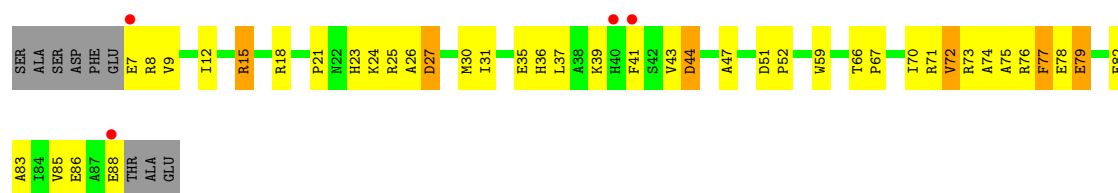
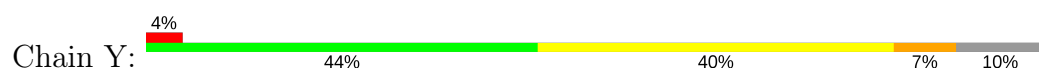
- Molecule 23: RIBOSOMAL PROTEIN L29



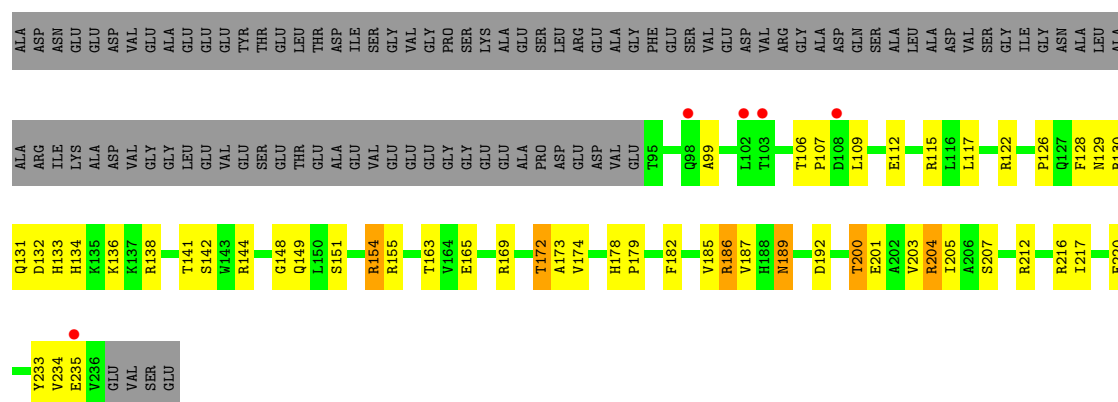
- Molecule 24: RIBOSOMAL PROTEIN L30



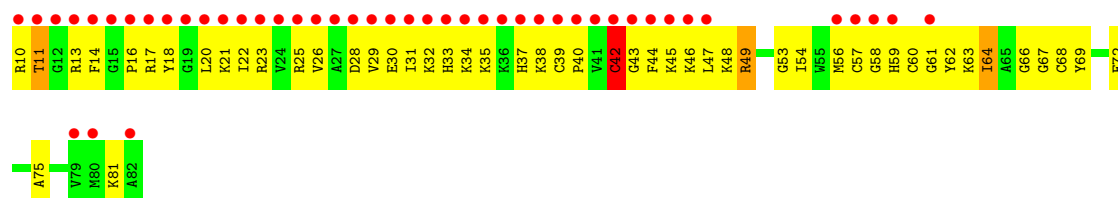
- Molecule 25: RIBOSOMAL PROTEIN L31E



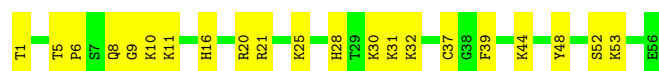
• Molecule 26: RIBOSOMAL PROTEIN L32E



• Molecule 27: RIBOSOMAL PROTEIN L37Ae



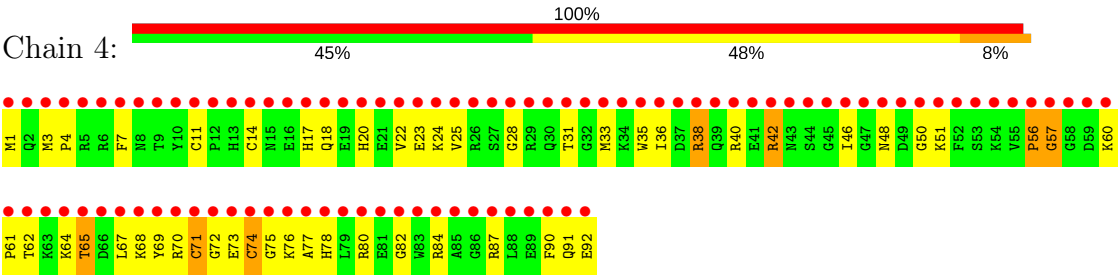
• Molecule 28: RIBOSOMAL PROTEIN L37E



• Molecule 29: RIBOSOMAL PROTEIN L39E



• Molecule 30: RIBOSOMAL PROTEIN L44E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.90Å 300.47Å 575.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 3.00 50.07 – 2.99	Depositor EDS
% Data completeness (in resolution range)	91.7 (19.99-3.00) 91.1 (50.07-2.99)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 3.01Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.220 , 0.269 0.220 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	50.9	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 65.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	98587	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% 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, SPR, CD, K

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	0.62	12/66076 (0.0%)	0.79	45/103052 (0.0%)
2	B	0.90	12/2905 (0.4%)	0.98	17/4528 (0.4%)
3	C	0.53	0/1787	0.79	0/2409
4	D	0.52	0/2689	0.75	0/3652
5	E	0.54	0/1883	0.78	0/2551
6	F	0.43	0/1111	0.65	0/1498
7	G	0.47	0/1382	0.66	0/1880
8	H	0.44	0/896	0.64	0/1219
9	I	0.41	0/241	0.58	0/324
10	J	0.53	0/1246	0.83	1/1686 (0.1%)
11	K	0.52	0/1135	0.70	0/1530
12	L	0.51	0/1003	0.80	0/1351
13	M	0.49	0/1126	0.74	0/1504
14	N	0.67	0/1633	0.86	1/2180 (0.0%)
15	O	0.48	0/1473	0.76	0/1999
16	P	0.53	0/873	0.76	0/1181
17	Q	0.52	0/1143	0.67	0/1521
18	R	0.52	0/748	0.80	1/1005 (0.1%)
19	S	0.66	1/1172 (0.1%)	0.84	2/1578 (0.1%)
20	T	0.45	0/648	0.69	0/875
21	U	0.47	0/957	0.73	1/1289 (0.1%)
22	V	0.77	0/417	0.86	2/562 (0.4%)
23	W	0.42	0/502	0.63	0/675
24	X	0.54	0/1218	0.76	0/1655
25	Y	0.50	0/664	0.72	0/895
26	Z	0.53	0/1146	0.73	0/1536
27	1	0.85	0/575	0.87	1/763 (0.1%)
28	2	0.56	0/437	0.84	0/578
29	3	0.47	0/398	0.64	0/527
30	4	1.04	0/771	0.83	1/1024 (0.1%)
All	All	0.62	25/98255 (0.0%)	0.79	72/147027 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	198
2	B	0	6
28	2	0	1
All	All	1	205

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2103	A	C5-C6	13.31	1.53	1.41
2	B	3025	G	O3'-P	11.56	1.75	1.61
2	B	3026	C	P-OP2	-10.89	1.30	1.49
2	B	3026	C	P-O5'	-9.81	1.50	1.59
2	B	3023	U	C2'-O2'	8.99	1.53	1.41
2	B	3025	G	P-OP2	-8.40	1.34	1.49
1	A	2103	A	N7-C5	8.09	1.44	1.39
2	B	3025	G	C4'-O4'	7.84	1.55	1.45
2	B	3023	U	O5'-C5'	7.80	1.56	1.44
1	A	2104	C	O5'-C5'	-6.97	1.31	1.42
1	A	2106	C	O3'-P	-6.78	1.53	1.61
19	S	130	MET	CB-CG	-6.69	1.29	1.51
1	A	2103	A	C5-C4	6.64	1.43	1.38
1	A	2103	A	C3'-C2'	6.43	1.60	1.52
1	A	2103	A	C8-N7	6.38	1.36	1.31
2	B	3025	G	N9-C4	-6.27	1.32	1.38
1	A	2433	A	C5-C6	6.25	1.46	1.41
1	A	2103	A	N9-C4	6.24	1.41	1.37
1	A	2106	C	N1-C2	6.05	1.46	1.40
2	B	3024	U	P-OP2	-5.48	1.39	1.49
1	A	2104	C	P-O5'	5.38	1.65	1.59
2	B	3026	C	O3'-P	5.25	1.67	1.61
2	B	3024	U	C3'-C2'	5.18	1.58	1.52
1	A	2105	C	O3'-P	5.04	1.67	1.61
2	B	3025	G	C2'-C1'	5.01	1.58	1.53

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1164	U	OP2-P-O3'	-18.78	63.89	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1164	U	OP1-P-O3'	-18.34	64.85	105.20
1	A	2104	C	O5'-P-OP1	-14.12	92.99	105.70
2	B	3024	U	O5'-P-OP2	11.53	124.53	110.70
2	B	3026	C	O5'-P-OP2	-11.17	95.65	105.70
1	A	2103	A	C5'-C4'-O4'	11.13	122.46	109.10
1	A	1165	G	O5'-P-OP1	-11.05	95.75	105.70
1	A	2103	A	OP2-P-O3'	9.79	126.73	105.20
2	B	3026	C	O5'-P-OP1	-9.30	97.33	105.70
2	B	3026	C	OP1-P-OP2	9.15	133.32	119.60
1	A	1942	A	C5'-C4'-C3'	9.01	130.41	116.00
1	A	1942	A	C5'-C4'-O4'	9.01	119.91	109.10
1	A	1563	G	C2'-C3'-O3'	8.94	129.18	109.50
1	A	2106	C	N1-C1'-C2'	-8.05	103.14	112.00
2	B	3004	G	O5'-P-OP1	-7.73	98.74	105.70
1	A	2103	A	O4'-C1'-N9	7.48	114.19	108.20
1	A	2099	G	OP2-P-O3'	7.11	120.84	105.20
1	A	1979	G	C2'-C3'-O3'	6.88	124.71	113.70
2	B	3026	C	C5'-C4'-O4'	6.87	117.35	109.10
22	V	36	CYS	CA-CB-SG	-6.58	102.16	114.00
2	B	3027	C	O5'-P-OP1	-6.45	99.89	105.70
1	A	1165	G	O5'-P-OP2	-6.25	100.07	105.70
19	S	130	MET	CB-CG-SD	6.22	131.06	112.40
1	A	171	C	OP2-P-O3'	6.21	118.86	105.20
1	A	1165	G	OP1-P-OP2	6.09	128.74	119.60
2	B	3023	U	P-O5'-C5'	6.08	130.62	120.90
1	A	2465	A	N9-C1'-C2'	-5.91	105.50	112.00
27	1	42	CYS	CA-CB-SG	5.91	124.63	114.00
1	A	2103	A	C4'-C3'-O3'	-5.87	97.08	109.40
1	A	1738	C	C5'-C4'-C3'	5.86	125.38	116.00
1	A	2313	C	C5'-C4'-O4'	5.76	116.02	109.10
2	B	3024	U	OP1-P-O3'	5.76	117.88	105.20
2	B	3103	A	C5'-C4'-O4'	5.74	115.98	109.10
10	J	74	ASN	N-CA-C	-5.74	95.51	111.00
14	N	73	ARG	N-CA-C	-5.67	95.69	111.00
1	A	129	A	C2'-C3'-O3'	5.65	122.74	113.70
2	B	3039	U	N1-C1'-C2'	5.64	121.33	114.00
2	B	3024	U	C5'-C4'-O4'	5.61	115.83	109.10
1	A	2419	U	N1-C1'-C2'	5.59	121.27	114.00
2	B	3025	G	O5'-P-OP2	-5.56	100.70	105.70
1	A	1342	C	N1-C1'-C2'	-5.50	105.95	112.00
1	A	1878	G	O4'-C1'-N9	5.49	112.59	108.20
18	R	68	GLY	N-CA-C	-5.47	99.41	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2122	C	OP2-P-O3'	5.44	117.17	105.20
1	A	2467	A	C1'-O4'-C4'	-5.44	105.55	109.90
1	A	1563	G	C4'-C3'-O3'	5.43	123.86	113.00
1	A	1504	A	C1'-O4'-C4'	-5.41	105.57	109.90
21	U	52	ARG	N-CA-C	5.40	125.59	111.00
19	S	131	GLY	CA-C-O	-5.40	110.88	120.60
1	A	1504	A	N9-C1'-C2'	5.33	120.93	114.00
1	A	2106	C	O5'-P-OP2	-5.33	100.90	105.70
2	B	3023	U	OP2-P-O3'	-5.33	93.48	105.20
2	B	3003	A	C4'-C3'-C2'	-5.32	97.28	102.60
30	4	71	CYS	CA-CB-SG	-5.32	104.43	114.00
22	V	6	CYS	CA-CB-SG	-5.26	104.53	114.00
1	A	1683	G	N9-C1'-C2'	5.26	120.83	114.00
2	B	3025	G	O3'-P-O5'	5.26	113.99	104.00
1	A	2432	C	N1-C1'-C2'	5.25	120.82	114.00
1	A	2102	G	O4'-C1'-N9	5.22	112.38	108.20
1	A	407	A	O4'-C4'-C3'	-5.13	98.87	104.00
1	A	2105	C	OP2-P-O3'	5.11	116.45	105.20
1	A	928	G	N9-C1'-C2'	-5.10	106.39	112.00
2	B	3113	C	N1-C1'-C2'	5.10	120.63	114.00
1	A	324	G	N9-C1'-C2'	-5.08	106.41	112.00
1	A	2316	G	C5'-C4'-C3'	-5.08	107.87	116.00
1	A	2467	A	O5'-P-OP1	-5.07	101.14	105.70
1	A	2607	U	N1-C1'-C2'	5.05	120.57	114.00
1	A	1829	A	N9-C1'-C2'	-5.05	106.44	112.00
1	A	1051	C	N1-C1'-C2'	-5.04	106.45	112.00
1	A	2106	C	N1-C2-O2	5.04	121.92	118.90
1	A	1119	G	N9-C1'-C2'	5.01	120.52	114.00
1	A	2842	G	N9-C1'-C2'	-5.00	106.50	112.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1563	G	C3'

All (205) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
28	2	48	TYR	Sidechain
1	A	1005	A	Sidechain
1	A	1023	C	Sidechain
1	A	1027	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1039	G	Sidechain
1	A	1042	U	Sidechain
1	A	1055	G	Sidechain
1	A	112	G	Sidechain
1	A	1127	C	Sidechain
1	A	1134	G	Sidechain
1	A	1136	U	Sidechain
1	A	1156	C	Sidechain
1	A	1206	U	Sidechain
1	A	1237	U	Sidechain
1	A	1260	G	Sidechain
1	A	1264	U	Sidechain
1	A	1288	U	Sidechain
1	A	1298	U	Sidechain
1	A	1300	G	Sidechain
1	A	1309	U	Sidechain
1	A	1339	G	Sidechain
1	A	1347	U	Sidechain
1	A	1368	U	Sidechain
1	A	1376	G	Sidechain
1	A	1377	C	Sidechain
1	A	138	U	Sidechain
1	A	1389	G	Sidechain
1	A	1402	G	Sidechain
1	A	1408	U	Sidechain
1	A	1417	G	Sidechain
1	A	1418	U	Sidechain
1	A	1421	C	Sidechain
1	A	1430	G	Sidechain
1	A	1433	G	Sidechain
1	A	1447	U	Sidechain
1	A	1458	A	Sidechain
1	A	146	U	Sidechain
1	A	1468	G	Sidechain
1	A	1487	A	Sidechain
1	A	1501	A	Sidechain
1	A	1503	U	Sidechain
1	A	1614	G	Sidechain
1	A	1621	G	Sidechain
1	A	1628	G	Sidechain
1	A	163	U	Sidechain
1	A	1647	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1677	U	Sidechain
1	A	1683	G	Sidechain
1	A	1684	A	Sidechain
1	A	1688	G	Sidechain
1	A	1689	A	Sidechain
1	A	169	A	Sidechain
1	A	171	C	Sidechain
1	A	1720	C	Sidechain
1	A	1736	A	Sidechain
1	A	174	A	Sidechain
1	A	1747	A	Sidechain
1	A	1748	U	Sidechain
1	A	176	U	Sidechain
1	A	1761	U	Sidechain
1	A	1771	U	Sidechain
1	A	178	U	Sidechain
1	A	1809	G	Sidechain
1	A	1816	C	Sidechain
1	A	1819	G	Sidechain
1	A	1823	G	Sidechain
1	A	1826	C	Sidechain
1	A	1833	U	Sidechain
1	A	1835	U	Sidechain
1	A	1839	A	Sidechain
1	A	1848	G	Sidechain
1	A	1860	U	Sidechain
1	A	1861	C	Sidechain
1	A	1867	G	Sidechain
1	A	1878	G	Sidechain
1	A	1882	C	Sidechain
1	A	1908	G	Sidechain
1	A	191	A	Sidechain
1	A	1933	G	Sidechain
1	A	197	C	Sidechain
1	A	1972	U	Sidechain
1	A	2000	G	Sidechain
1	A	2001	G	Sidechain
1	A	2002	C	Sidechain
1	A	2035	C	Sidechain
1	A	2045	G	Sidechain
1	A	2053	G	Sidechain
1	A	2063	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	2068	G	Sidechain
1	A	2070	G	Sidechain
1	A	2076	U	Sidechain
1	A	2092	G	Sidechain
1	A	2101	A	Sidechain
1	A	2106	C	Sidechain
1	A	2120	U	Sidechain
1	A	2123	A	Sidechain
1	A	2128	G	Sidechain
1	A	2133	U	Sidechain
1	A	214	U	Sidechain
1	A	2244	A	Sidechain
1	A	2273	C	Sidechain
1	A	2294	C	Sidechain
1	A	2304	G	Sidechain
1	A	2308	U	Sidechain
1	A	2310	G	Sidechain
1	A	2312	G	Sidechain
1	A	2313	C	Sidechain
1	A	2325	C	Sidechain
1	A	2337	G	Sidechain
1	A	2359	G	Sidechain
1	A	2363	G	Sidechain
1	A	2364	A	Sidechain
1	A	2378	U	Sidechain
1	A	2412	G	Sidechain
1	A	2422	U	Sidechain
1	A	2423	C	Sidechain
1	A	2433	A	Sidechain
1	A	2434	A	Sidechain
1	A	2453	G	Sidechain
1	A	2458	U	Sidechain
1	A	2459	G	Sidechain
1	A	246	G	Sidechain
1	A	2462	G	Sidechain
1	A	2503	A	Sidechain
1	A	2506	A	Sidechain
1	A	2526	C	Sidechain
1	A	2575	C	Sidechain
1	A	2630	G	Sidechain
1	A	2631	U	Sidechain
1	A	264	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	2640	U	Sidechain
1	A	2643	G	Sidechain
1	A	2663	U	Sidechain
1	A	2673	U	Sidechain
1	A	2720	C	Sidechain
1	A	2721	U	Sidechain
1	A	2727	A	Sidechain
1	A	2730	G	Sidechain
1	A	2759	C	Sidechain
1	A	2790	C	Sidechain
1	A	2793	A	Sidechain
1	A	2800	A	Sidechain
1	A	2811	A	Sidechain
1	A	2833	C	Sidechain
1	A	2840	A	Sidechain
1	A	2864	U	Sidechain
1	A	2891	A	Sidechain
1	A	331	A	Sidechain
1	A	333	G	Sidechain
1	A	395	A	Sidechain
1	A	396	U	Sidechain
1	A	398	U	Sidechain
1	A	406	G	Sidechain
1	A	407	A	Sidechain
1	A	436	A	Sidechain
1	A	458	G	Sidechain
1	A	461	C	Sidechain
1	A	474	C	Sidechain
1	A	476	A	Sidechain
1	A	486	A	Sidechain
1	A	487	G	Sidechain
1	A	518	G	Sidechain
1	A	548	U	Sidechain
1	A	554	G	Sidechain
1	A	650	C	Sidechain
1	A	669	G	Sidechain
1	A	720	G	Sidechain
1	A	723	G	Sidechain
1	A	743	G	Sidechain
1	A	75	U	Sidechain
1	A	750	A	Sidechain
1	A	755	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	756	A	Sidechain
1	A	757	C	Sidechain
1	A	759	C	Sidechain
1	A	761	A	Sidechain
1	A	768	U	Sidechain
1	A	791	A	Sidechain
1	A	815	U	Sidechain
1	A	816	G	Sidechain
1	A	817	G	Sidechain
1	A	818	A	Sidechain
1	A	827	A	Sidechain
1	A	838	C	Sidechain
1	A	840	U	Sidechain
1	A	864	U	Sidechain
1	A	867	A	Sidechain
1	A	871	G	Sidechain
1	A	878	G	Sidechain
1	A	882	A	Sidechain
1	A	887	G	Sidechain
1	A	888	U	Sidechain
1	A	889	C	Sidechain
1	A	904	U	Sidechain
1	A	916	A	Sidechain
1	A	919	U	Sidechain
1	A	946	C	Sidechain
1	A	954	U	Sidechain
1	A	99	A	Sidechain
2	B	3023	U	Sidechain
2	B	3025	G	Sidechain
2	B	3065	A	Sidechain
2	B	3069	U	Sidechain
2	B	3087	U	Sidechain
2	B	3094	G	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	29802	1290	0
2	B	2600	0	1326	80	0
3	C	1754	0	1763	132	0
4	D	2624	0	2533	190	0
5	E	1858	0	1816	149	0
6	F	1094	0	1085	135	0
7	G	1357	0	1266	85	0
8	H	885	0	854	63	0
9	I	240	0	231	21	0
10	J	1215	0	1215	175	0
11	K	1119	0	1098	70	0
12	L	993	0	1027	67	0
13	M	1114	0	1072	72	0
14	N	1605	0	1676	194	0
15	O	1444	0	1401	143	0
16	P	864	0	873	37	0
17	Q	1133	0	1127	53	0
18	R	734	0	727	30	0
19	S	1149	0	1122	60	0
20	T	641	0	605	23	0
21	U	949	0	923	59	0
22	V	410	0	368	45	0
23	W	499	0	511	33	0
24	X	1195	0	1137	99	0
25	Y	654	0	653	51	0
26	Z	1130	0	1133	71	0
27	1	563	0	601	80	0
28	2	430	0	426	27	0
29	3	393	0	406	27	0
30	4	755	0	732	58	0
31	A	59	0	73	9	0
32	1	1	0	0	0	0
32	4	1	0	0	0	0
32	A	112	0	0	5	0
32	B	1	0	0	0	0
32	C	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	73	0	0	1	0
33	B	2	0	0	0	0
33	C	1	0	0	0	0
33	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	J	1	0	0	0	0
33	K	1	0	0	0	0
33	M	1	0	0	0	0
33	N	1	0	0	0	0
33	R	1	0	0	0	0
33	S	2	0	0	0	0
33	T	1	0	0	0	0
34	4	1	0	0	0	0
34	A	9	0	0	2	0
34	C	1	0	0	0	0
34	D	1	0	0	0	0
34	K	3	0	0	2	0
34	M	1	0	0	0	0
34	N	1	0	0	1	0
34	O	1	0	0	3	0
34	P	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
34	Z	1	0	0	0	0
35	A	3	0	0	0	0
36	1	1	0	0	0	0
36	2	1	0	0	0	0
36	4	1	0	0	0	0
36	P	1	0	0	0	0
36	V	1	0	0	0	0
37	1	41	0	0	13	0
37	2	55	0	0	5	0
37	3	42	0	0	5	0
37	4	73	0	0	7	0
37	A	5910	0	0	300	0
37	B	142	0	0	16	0
37	C	126	0	0	23	0
37	D	150	0	0	28	0
37	E	169	0	0	40	0
37	F	51	0	0	22	0
37	G	42	0	0	13	0
37	H	26	0	0	9	0
37	I	21	0	0	5	0
37	J	78	0	0	26	0
37	K	54	0	0	8	0
37	L	65	0	0	12	0
37	M	79	0	0	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	N	132	0	0	36	0
37	O	69	0	0	23	0
37	P	45	0	0	9	0
37	Q	65	0	0	4	0
37	R	55	0	0	6	0
37	S	83	0	0	11	0
37	T	35	0	0	3	0
37	U	39	0	0	4	0
37	V	25	0	0	8	0
37	W	15	0	0	2	0
37	X	70	0	0	10	0
37	Y	25	0	0	11	0
37	Z	94	0	0	18	0
All	All	98587	0	59582	3325	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 22.

All (3325) 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)
30:4:33:MET:SD	30:4:33:MET:CE	2.03	1.47
5:E:236:THR:HG22	5:E:239:ALA:H	1.09	1.15
1:A:2121:G:OP2	37:A:3494:HOH:O	1.64	1.15
1:A:2122:C:OP2	37:A:6549:HOH:O	1.64	1.15
1:A:1134:G:H4'	10:J:151:MET:HE1	1.28	1.12
14:N:87:MET:HG2	30:4:46:ILE:HG21	1.23	1.10
10:J:86:ARG:NH1	10:J:133:ILE:HG13	1.64	1.09
27:1:46:LYS:HD3	27:1:59:HIS:HB2	1.37	1.07
10:J:165:GLY:HA3	37:J:8386:HOH:O	1.54	1.07
1:A:1160:G:H5'	1:A:1161:A:H5'	1.31	1.06
1:A:871:G:H5'	1:A:871:G:H8	1.15	1.06
10:J:45:GLN:HB3	10:J:163:PRO:HD2	1.32	1.06
14:N:164:THR:HG22	14:N:167:GLY:H	1.14	1.06
21:U:71:VAL:HG11	21:U:90:PRO:HB3	1.38	1.04
6:F:25:MET:HE2	6:F:41:LEU:HG	1.40	1.04
31:A:9001:SPR:H6A3	31:A:9001:SPR:H2B1	1.32	1.03
10:J:86:ARG:HH11	10:J:133:ILE:HG13	0.89	1.02
6:F:134:LEU:HD11	6:F:166:ILE:HD11	1.38	1.02
12:L:10:GLN:NE2	12:L:10:GLN:H	1.58	1.01
23:W:12:THR:HG22	23:W:15:GLU:HG3	1.41	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:871:G:H5'	1:A:871:G:C8	1.95	1.00
27:1:40:PRO:HD3	27:1:47:LEU:HD11	1.42	1.00
4:D:62:ARG:HA	4:D:65:MET:HE3	1.43	1.00
1:A:856:G:H2'	37:A:5401:HOH:O	1.62	1.00
5:E:127:ARG:NH2	5:E:225:PRO:HG2	1.77	0.99
14:N:87:MET:CG	30:4:46:ILE:HG21	1.92	0.99
1:A:2432:C:O4'	37:A:9718:HOH:O	1.80	0.99
5:E:5:ILE:HD11	5:E:16:VAL:HG23	1.39	0.99
1:A:2717:C:H2'	1:A:2718:C:H5''	1.45	0.99
17:Q:115:SER:H	17:Q:118:GLN:HE21	1.00	0.98
24:X:88:THR:HB	37:X:6679:HOH:O	1.63	0.98
10:J:26:LYS:HD2	10:J:28:ILE:HD12	1.41	0.98
12:L:29:LEU:HB3	12:L:55:VAL:HG11	1.41	0.98
12:L:74:VAL:HG11	12:L:113:ILE:HG12	1.46	0.98
1:A:156:C:H5''	14:N:171:ARG:HD3	1.43	0.97
1:A:2123:A:OP2	37:A:5266:HOH:O	1.81	0.97
1:A:962:C:H1'	15:O:5:ARG:NH1	1.79	0.97
14:N:35:PRO:HG2	14:N:38:VAL:HG23	1.46	0.97
2:B:3023:U:H5''	2:B:3024:U:OP2	1.62	0.97
4:D:86:ALA:HA	37:D:8581:HOH:O	1.63	0.97
10:J:162:SER:HB2	10:J:163:PRO:HD3	1.43	0.97
1:A:542:A:H8	1:A:542:A:H5'	1.29	0.97
2:B:3056:A:H2'	2:B:3057:A:H5''	1.47	0.96
1:A:1474:C:H6	1:A:1474:C:H5'	1.31	0.95
14:N:52:LEU:HD11	37:N:8616:HOH:O	1.65	0.94
27:1:42:CYS:SG	27:1:44:PHE:HB2	2.06	0.94
10:J:29:ALA:HB3	10:J:65:ARG:HH12	1.33	0.94
10:J:86:ARG:HH11	10:J:133:ILE:CG1	1.78	0.94
11:K:76:ASP:HA	37:K:8565:HOH:O	1.66	0.94
24:X:122:ARG:HH21	24:X:154:ARG:HD2	1.28	0.94
27:1:39:CYS:SG	27:1:47:LEU:HD21	2.08	0.94
4:D:264:GLU:HG2	4:D:267:LYS:HE2	1.49	0.93
1:A:870:G:H2'	1:A:871:G:H5''	1.46	0.93
4:D:140:LEU:HA	37:D:8581:HOH:O	1.67	0.93
13:M:68:GLU:HA	37:M:8546:HOH:O	1.67	0.93
26:Z:187:VAL:HG23	26:Z:192:ASP:HB2	1.50	0.93
1:A:1667:A:H5'	1:A:1667:A:H8	1.34	0.92
10:J:55:GLN:HE21	10:J:124:ARG:HE	1.15	0.92
2:B:3006:C:H5''	15:O:37:ARG:NH1	1.83	0.92
4:D:41:PHE:CD1	4:D:79:MET:HE2	2.03	0.92
1:A:1751:G:H2'	1:A:1752:G:H5''	1.52	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:200:THR:HG22	26:Z:201:GLU:HG3	1.51	0.92
14:N:87:MET:HG2	30:4:46:ILE:CG2	2.00	0.92
6:F:105:SER:HB2	6:F:131:THR:HG23	1.50	0.92
1:A:1835:U:H5	1:A:1840:A:N7	1.66	0.91
5:E:140:VAL:HB	37:E:8450:HOH:O	1.69	0.91
10:J:2:PRO:HB2	37:J:8354:HOH:O	1.69	0.91
5:E:78:ARG:HG3	5:E:78:ARG:HH11	1.36	0.91
12:L:10:GLN:HE21	12:L:10:GLN:H	1.08	0.91
13:M:67:ARG:O	13:M:71:GLU:HG3	1.71	0.91
20:T:57:THR:HG22	20:T:59:ASP:H	1.36	0.91
37:A:3764:HOH:O	14:N:189:VAL:HG21	1.72	0.90
4:D:238:ASN:HD22	4:D:240:GLY:H	1.19	0.90
1:A:871:G:C5'	1:A:871:G:H8	1.83	0.90
12:L:81:ARG:HB2	12:L:87:ARG:HH11	1.36	0.90
15:O:47:LEU:HD11	15:O:127:LEU:HD21	1.50	0.90
15:O:87:LEU:HD12	15:O:186:LEU:HD21	1.51	0.90
26:Z:216:ARG:HD3	37:Z:8569:HOH:O	1.70	0.90
1:A:541:C:H2'	1:A:542:A:H5''	1.52	0.90
14:N:102:GLU:OE1	14:N:164:THR:HG21	1.72	0.90
30:4:70:ARG:HG2	30:4:77:ALA:HB2	1.53	0.89
22:V:9:CYS:SG	22:V:11:THR:HG23	2.13	0.89
5:E:2:GLN:HB3	37:E:8337:HOH:O	1.71	0.89
19:S:99:ALA:HB1	19:S:109:MET:HE1	1.53	0.89
10:J:27:LYS:H	10:J:58:HIS:HD2	1.19	0.88
15:O:83:LEU:HD13	15:O:175:LEU:HD23	1.54	0.88
1:A:1205:U:H2'	1:A:1206:U:H5'	1.54	0.88
1:A:2426:G:H1'	37:A:6061:HOH:O	1.73	0.88
2:B:3076:G:H3'	2:B:3077:A:H5''	1.56	0.88
19:S:9:ASP:O	19:S:13:THR:HB	1.74	0.88
1:A:2466:G:OP1	37:A:3625:HOH:O	1.90	0.88
7:G:100:ASP:HB2	37:G:2789:HOH:O	1.74	0.88
1:A:2533:C:H5'	1:A:2533:C:H6	1.39	0.87
1:A:962:C:H1'	15:O:5:ARG:HH12	1.38	0.87
15:O:144:GLY:O	15:O:147:ILE:HG22	1.75	0.87
1:A:1120:U:H6	1:A:1120:U:H5''	1.39	0.87
1:A:2506:A:HO2'	1:A:2507:G:H8	0.91	0.87
1:A:2812:A:H2	1:A:2814:A:H62	1.22	0.87
37:A:6265:HOH:O	6:F:99:ASP:HA	1.73	0.87
13:M:79:ASP:HB3	37:M:8559:HOH:O	1.75	0.87
5:E:236:THR:HG21	37:E:8372:HOH:O	1.74	0.87
1:A:1184:C:H1'	37:A:7445:HOH:O	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:37:LEU:HD13	25:Y:85:VAL:HG21	1.56	0.87
1:A:541:C:C2'	1:A:542:A:H5''	2.05	0.86
6:F:154:LYS:H	6:F:154:LYS:HD2	1.39	0.86
37:A:3703:HOH:O	14:N:157:LEU:HD11	1.74	0.86
14:N:35:PRO:CG	14:N:38:VAL:HG23	2.05	0.86
1:A:1886:A:N3	37:A:4796:HOH:O	2.07	0.86
1:A:1242:A:H5'	11:K:82:THR:HG23	1.55	0.86
2:B:3069:U:OP1	15:O:4:PRO:HG3	1.75	0.86
17:Q:115:SER:H	17:Q:118:GLN:NE2	1.74	0.85
1:A:960:G:H4'	37:A:7406:HOH:O	1.77	0.85
10:J:150:LYS:HE2	37:J:8372:HOH:O	1.75	0.85
15:O:7:LYS:HE3	18:R:21:ARG:O	1.75	0.85
1:A:1116:U:HO2'	1:A:1118:A:H2	0.88	0.85
5:E:5:ILE:HD11	5:E:16:VAL:CG2	2.06	0.85
13:M:133:VAL:HA	37:M:8572:HOH:O	1.74	0.85
24:X:88:THR:HG22	24:X:89:ASP:H	1.41	0.85
14:N:69:LYS:O	14:N:73:ARG:NH2	2.10	0.85
19:S:8:ALA:HB1	19:S:13:THR:HG21	1.56	0.85
23:W:1:THR:HG23	23:W:2:VAL:H	1.41	0.85
37:A:4928:HOH:O	2:B:3103:A:H4'	1.75	0.85
10:J:162:SER:HB2	10:J:163:PRO:CD	2.06	0.85
8:H:91:VAL:HG12	8:H:92:GLY:H	1.42	0.84
17:Q:115:SER:OG	17:Q:118:GLN:HG3	1.76	0.84
24:X:122:ARG:NH2	24:X:154:ARG:HD2	1.91	0.84
1:A:1166:A:H1'	1:A:1192:A:C2	2.12	0.84
16:P:7:LEU:HD22	37:P:5650:HOH:O	1.76	0.84
1:A:2468:A:H61	30:4:48:ASN:HD21	1.26	0.84
7:G:166:VAL:HG12	37:G:3134:HOH:O	1.76	0.84
37:A:3661:HOH:O	14:N:79:LYS:HD3	1.77	0.84
30:4:25:VAL:HG22	30:4:68:LYS:HG3	1.58	0.83
6:F:20:LYS:HA	6:F:75:LEU:O	1.78	0.83
7:G:107:PHE:CE2	7:G:108:LEU:HD13	2.13	0.83
8:H:96:ALA:HA	37:H:3111:HOH:O	1.76	0.83
10:J:47:GLU:HB3	10:J:133:ILE:CD1	2.08	0.83
1:A:2586:U:H3	1:A:2592:G:H22	1.26	0.83
3:C:211:LYS:HB3	3:C:212:PRO:HD2	1.59	0.83
26:Z:141:THR:HG23	37:Z:8589:HOH:O	1.78	0.83
4:D:321:PRO:HA	37:D:8659:HOH:O	1.79	0.83
1:A:544:G:H2'	1:A:545:G:H5''	1.60	0.83
2:B:3023:U:C5'	2:B:3024:U:OP2	2.26	0.83
12:L:10:GLN:HE21	12:L:10:GLN:N	1.77	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:88:THR:HG23	24:X:110:GLN:NE2	1.95	0.82
19:S:17:MET:SD	37:S:8548:HOH:O	2.37	0.82
15:O:37:ARG:HD3	34:O:8507:CL:CL	2.17	0.82
1:A:2717:C:C2'	1:A:2718:C:H5''	2.10	0.82
10:J:142:VAL:HG13	37:J:8370:HOH:O	1.80	0.82
26:Z:133:HIS:HD2	37:Z:8583:HOH:O	1.63	0.82
10:J:47:GLU:HB3	10:J:133:ILE:HD13	1.61	0.81
10:J:26:LYS:HG2	10:J:28:ILE:H	1.44	0.81
3:C:199:HIS:HD2	3:C:201:PHE:H	1.28	0.81
12:L:74:VAL:HG13	12:L:113:ILE:HG23	1.61	0.81
24:X:122:ARG:HG2	24:X:122:ARG:HH11	1.44	0.81
5:E:104:ASP:HA	5:E:107:ARG:HH12	1.45	0.81
1:A:338:C:H4'	5:E:174:ILE:CD1	2.09	0.81
2:B:3006:C:OP1	15:O:37:ARG:NH1	2.14	0.81
10:J:139:ASP:HA	37:J:8360:HOH:O	1.79	0.81
1:A:1474:C:C6	1:A:1474:C:H5'	2.16	0.81
1:A:1701:A:H5'	37:A:6253:HOH:O	1.81	0.81
22:V:9:CYS:HA	22:V:52:THR:HG23	1.59	0.81
1:A:2716:G:H5''	4:D:206:THR:HG21	1.63	0.81
30:4:74:CYS:SG	30:4:76:LYS:HB2	2.21	0.81
12:L:14:LYS:HB2	12:L:45:PRO:HG2	1.61	0.81
37:A:6840:HOH:O	14:N:178:LYS:HB2	1.81	0.81
1:A:1120:U:C6	1:A:1120:U:H5''	2.16	0.80
26:Z:187:VAL:HG23	26:Z:192:ASP:CB	2.11	0.80
1:A:2467:A:OP1	37:A:9038:HOH:O	1.98	0.80
27:1:38:LYS:HG2	27:1:45:LYS:HG2	1.61	0.80
1:A:1735:C:O2'	1:A:1736:A:H5'	1.81	0.80
1:A:1372:A:H3'	37:A:7165:HOH:O	1.81	0.80
10:J:139:ASP:N	10:J:140:PRO:HD3	1.97	0.80
4:D:212:GLN:HB2	4:D:257:THR:HG21	1.64	0.80
5:E:236:THR:HG22	5:E:239:ALA:N	1.93	0.80
14:N:164:THR:HG23	14:N:165:SER:N	1.94	0.80
25:Y:78:GLU:HG2	25:Y:79:GLU:H	1.47	0.80
5:E:115:LEU:HD13	5:E:223:LEU:HD21	1.63	0.80
7:G:97:VAL:HG12	37:G:4191:HOH:O	1.80	0.80
25:Y:71:ARG:HB3	25:Y:88:GLU:OE1	1.81	0.80
1:A:288:A:H61	1:A:364:C:H42	1.29	0.80
14:N:164:THR:HG22	14:N:167:GLY:N	1.96	0.80
25:Y:25:ARG:HD2	37:Y:3861:HOH:O	1.80	0.80
4:D:201:ASP:HB2	4:D:312:ARG:HD2	1.65	0.79
1:A:1603:A:H5'	1:A:1605:G:O4'	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1209:C:H4'	37:A:5257:HOH:O	1.83	0.79
7:G:15:GLN:HG3	7:G:20:ILE:HG12	1.63	0.79
15:O:4:PRO:HD2	37:O:8558:HOH:O	1.80	0.79
1:A:1118:A:H3'	1:A:1118:A:H8	1.47	0.79
1:A:2064:U:H4'	1:A:2653:A:OP1	1.83	0.79
27:1:30:GLU:HA	27:1:33:HIS:HB3	1.64	0.79
1:A:1835:U:C5	1:A:1840:A:N7	2.51	0.79
10:J:163:PRO:HG2	37:J:8325:HOH:O	1.81	0.79
1:A:1116:U:H3	1:A:1246:A:H62	1.31	0.79
1:A:2420:G:O2'	1:A:2421:G:H5'	1.81	0.79
1:A:272:A:H3'	37:A:7510:HOH:O	1.82	0.79
24:X:4:LEU:HD22	24:X:52:VAL:HG21	1.63	0.79
1:A:1119:G:H2'	11:K:52:GLN:NE2	1.97	0.78
1:A:282:C:H1'	1:A:368:C:N4	1.98	0.78
2:B:3014:G:H8	2:B:3014:G:H5'	1.49	0.78
34:K:8501:CL:CL	37:K:8548:HOH:O	2.38	0.78
1:A:1118:A:C8	1:A:1118:A:H3'	2.18	0.78
1:A:1116:U:O2'	1:A:1118:A:H2	1.67	0.78
27:1:39:CYS:HA	27:1:47:LEU:HD11	1.66	0.78
13:M:53:ARG:NH2	13:M:57:VAL:HG12	1.98	0.78
19:S:106:GLY:HA2	19:S:109:MET:HE3	1.65	0.78
27:1:23:ARG:NH1	37:1:8404:HOH:O	2.17	0.78
37:A:7536:HOH:O	30:4:60:LYS:HG3	1.83	0.78
29:3:39:ARG:HG2	37:3:3143:HOH:O	1.82	0.78
3:C:223:ARG:HG3	37:C:8606:HOH:O	1.84	0.78
24:X:88:THR:HG23	24:X:110:GLN:HE21	1.48	0.78
1:A:545:G:H5'	1:A:545:G:H8	1.49	0.77
1:A:711:G:H1'	37:A:7067:HOH:O	1.82	0.77
15:O:49:THR:HG22	15:O:56:ASP:HB2	1.67	0.77
22:V:35:LYS:NZ	37:V:6621:HOH:O	2.17	0.77
1:A:111:C:O2'	28:2:20:ARG:HG2	1.84	0.77
1:A:1165:G:H4'	1:A:1174:A:O2'	1.84	0.77
24:X:6:GLN:HB2	24:X:26:ILE:HD12	1.67	0.77
1:A:2004:U:H4'	37:A:5284:HOH:O	1.82	0.77
6:F:64:ARG:HG2	6:F:67:ASP:HB3	1.66	0.77
10:J:136:VAL:HG23	37:J:8330:HOH:O	1.84	0.77
1:A:559:U:H6	1:A:559:U:H5'	1.49	0.77
37:A:4837:HOH:O	14:N:14:ARG:HG2	1.83	0.77
1:A:645:U:OP2	13:M:4:LYS:HE2	1.85	0.77
1:A:2508:C:H2'	37:A:6723:HOH:O	1.85	0.77
10:J:33:MET:HB2	10:J:83:PHE:HB3	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:74:ARG:HB3	11:K:74:ARG:HH11	1.49	0.77
15:O:48:VAL:CG1	15:O:55:ASP:HB3	2.14	0.77
3:C:199:HIS:CD2	3:C:201:PHE:H	2.02	0.77
24:X:4:LEU:HD22	24:X:52:VAL:CG2	2.14	0.77
13:M:53:ARG:HH22	13:M:57:VAL:HG12	1.49	0.76
1:A:1187:U:H2'	37:A:6864:HOH:O	1.85	0.76
1:A:542:A:H5'	1:A:542:A:C8	2.19	0.76
14:N:64:ARG:HD2	37:N:8586:HOH:O	1.84	0.76
1:A:1450:C:H4'	1:A:1451:C:OP2	1.86	0.76
1:A:870:G:C2'	1:A:871:G:H5''	2.15	0.76
15:O:86:LEU:HD12	15:O:125:ALA:HB2	1.66	0.76
1:A:797:A:C4'	27:1:10:ARG:N	2.48	0.76
29:3:41:HIS:H	29:3:45:ASN:HD22	1.30	0.76
1:A:289:G:H22	1:A:363:A:H2	1.33	0.76
2:B:3039:U:H1'	2:B:3044:A:H61	1.51	0.76
2:B:3056:A:C2'	2:B:3057:A:H5''	2.15	0.76
3:C:164:ARG:HB2	27:1:68:CYS:SG	2.24	0.76
8:H:91:VAL:HG12	8:H:92:GLY:N	1.99	0.76
14:N:84:LYS:HE2	37:N:8577:HOH:O	1.85	0.76
27:1:38:LYS:HE2	27:1:45:LYS:HE2	1.67	0.76
1:A:1160:G:C5'	1:A:1161:A:H5'	2.11	0.76
1:A:797:A:H4'	27:1:10:ARG:N	2.01	0.76
28:2:21:ARG:HD2	28:2:37:CYS:SG	2.26	0.76
10:J:55:GLN:NE2	10:J:124:ARG:HE	1.84	0.76
1:A:1666:C:O2'	1:A:1667:A:H5''	1.86	0.76
10:J:137:ASN:O	10:J:139:ASP:N	2.19	0.76
21:U:61:GLU:HG3	37:U:3851:HOH:O	1.85	0.76
26:Z:220:GLU:HG2	37:Z:8550:HOH:O	1.85	0.76
9:I:12:ILE:N	9:I:13:PRO:HD3	2.01	0.76
19:S:99:ALA:HB1	19:S:109:MET:CE	2.16	0.76
25:Y:25:ARG:NH1	37:Y:3861:HOH:O	2.19	0.76
1:A:541:C:H2'	1:A:542:A:C5'	2.15	0.75
1:A:1684:A:H1'	29:3:43:ARG:HH22	1.49	0.75
10:J:14:TYR:H	10:J:91:HIS:CE1	2.04	0.75
14:N:87:MET:CB	30:4:46:ILE:HG21	2.16	0.75
14:N:61:ILE:HG13	37:N:8623:HOH:O	1.85	0.75
25:Y:76:ARG:HH11	25:Y:76:ARG:HG3	1.50	0.75
1:A:236:A:H4'	1:A:237:G:H5'	1.69	0.75
1:A:450:C:OP1	5:E:184:ARG:NH2	2.16	0.75
1:A:506:G:H22	1:A:509:A:C5'	1.98	0.75
6:F:27:ILE:HG22	6:F:28:GLY:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2363:G:O3'	18:R:11:ARG:NH1	2.19	0.75
17:Q:143:ALA:HA	37:Q:2178:HOH:O	1.87	0.75
9:I:23:ILE:HD13	9:I:67:LEU:HD23	1.67	0.75
1:A:2506:A:O2'	1:A:2507:G:H8	1.68	0.75
5:E:162:VAL:HG12	5:E:192:ILE:HD11	1.68	0.75
37:A:4432:HOH:O	14:N:146:GLN:HG2	1.86	0.75
4:D:62:ARG:CA	4:D:65:MET:HE3	2.16	0.74
1:A:1594:C:OP2	17:Q:120:ARG:HD2	1.85	0.74
3:C:88:ILE:HD13	3:C:100:PRO:HD3	1.70	0.74
6:F:135:VAL:HG22	6:F:136:ARG:H	1.51	0.74
3:C:35:GLY:O	3:C:36:ASP:HB3	1.86	0.74
16:P:32:ARG:O	16:P:32:ARG:HD3	1.85	0.74
21:U:32:ARG:NH1	21:U:38:ARG:HH12	1.85	0.74
27:I:49:ARG:HD2	37:I:8431:HOH:O	1.87	0.74
1:A:346:U:H4'	37:A:6811:HOH:O	1.87	0.74
5:E:76:ARG:HD2	37:E:8432:HOH:O	1.87	0.74
10:J:41:THR:HA	37:J:8384:HOH:O	1.87	0.74
1:A:1160:G:H5'	1:A:1161:A:C5'	2.15	0.74
1:A:1701:A:H4'	1:A:1702:U:H5''	1.68	0.74
1:A:2466:G:H5''	37:A:3625:HOH:O	1.87	0.74
5:E:178:GLN:OE1	37:E:8465:HOH:O	2.04	0.74
26:Z:185:VAL:HA	37:Z:8564:HOH:O	1.86	0.74
1:A:21:G:H5'	19:S:2:ILE:HA	1.70	0.74
37:A:9110:HOH:O	14:N:82:ARG:HD2	1.88	0.74
15:O:71:TRP:CE3	15:O:175:LEU:HD22	2.23	0.74
1:A:1329:A:H2	37:A:4655:HOH:O	1.69	0.74
10:J:26:LYS:HD2	10:J:28:ILE:CD1	2.15	0.74
13:M:143:THR:HG22	13:M:144:ASP:N	2.02	0.74
1:A:1058:A:H2'	1:A:1060:C:H5''	1.68	0.74
4:D:221:GLN:HE22	12:L:42:ASN:HD22	1.36	0.74
12:L:22:ASP:HB2	37:L:5264:HOH:O	1.88	0.74
14:N:48:ARG:NH2	37:N:8563:HOH:O	2.21	0.74
22:V:13:ILE:HG12	22:V:32:CYS:CB	2.17	0.73
5:E:78:ARG:HG3	5:E:78:ARG:NH1	2.03	0.73
14:N:172:GLY:O	14:N:183:VAL:HG11	1.89	0.73
1:A:2100:A:N1	31:A:9001:SPR:H2A	2.03	0.73
11:K:99:GLU:HA	37:K:8573:HOH:O	1.88	0.73
20:T:51:GLN:HE21	20:T:53:ASN:HD21	1.35	0.73
17:Q:115:SER:N	17:Q:118:GLN:HE21	1.83	0.73
1:A:1130:U:H2'	1:A:1131:G:O4'	1.89	0.73
2:B:3029:C:H2'	2:B:3030:C:H5'	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:59:ASN:HD22	10:J:59:ASN:N	1.87	0.73
19:S:39:THR:HG22	19:S:42:GLU:H	1.54	0.73
25:Y:15:ARG:HH11	25:Y:15:ARG:HB3	1.54	0.73
5:E:132:ASP:HB3	37:E:8361:HOH:O	1.88	0.73
7:G:11:VAL:HG12	7:G:12:ASP:N	2.04	0.73
9:I:12:ILE:HA	37:I:4499:HOH:O	1.89	0.73
17:Q:80:ARG:HG2	17:Q:87:ARG:CZ	2.19	0.73
24:X:130:HIS:O	24:X:136:GLY:HA3	1.89	0.73
1:A:2271:G:OP2	37:A:9415:HOH:O	2.07	0.73
4:D:62:ARG:HA	4:D:65:MET:CE	2.17	0.72
24:X:137:GLN:HE21	24:X:141:HIS:HE1	1.34	0.72
1:A:1667:A:H5'	1:A:1667:A:C8	2.21	0.72
1:A:172:U:OP2	37:A:6180:HOH:O	2.06	0.72
1:A:1743:G:N7	37:A:9244:HOH:O	2.21	0.72
27:1:11:THR:CG2	27:1:23:ARG:HB2	2.19	0.72
7:G:20:ILE:HD11	7:G:40:VAL:HG11	1.71	0.72
1:A:31:C:H4'	37:A:7400:HOH:O	1.89	0.72
14:N:52:LEU:HD13	14:N:116:ASN:HB3	1.71	0.72
5:E:214:THR:HG21	37:E:8399:HOH:O	1.87	0.72
10:J:130:HIS:CD2	10:J:133:ILE:HD11	2.24	0.72
11:K:133:GLY:O	11:K:137:GLU:HG3	1.90	0.72
14:N:35:PRO:O	37:N:8539:HOH:O	2.06	0.72
19:S:132:ARG:NH2	37:S:8582:HOH:O	2.22	0.72
22:V:46:ALA:HB1	22:V:52:THR:HG21	1.71	0.72
1:A:1834:C:H2'	1:A:1840:A:N6	2.04	0.72
13:M:136:ALA:HB3	37:M:8572:HOH:O	1.89	0.72
25:Y:31:ILE:O	25:Y:35:GLU:HG3	1.90	0.72
1:A:1118:A:H62	1:A:1244:U:H3	1.37	0.72
12:L:39:GLY:HA2	37:L:4183:HOH:O	1.89	0.72
14:N:87:MET:HB2	14:N:91:ILE:HD11	1.71	0.72
20:T:57:THR:HG22	20:T:59:ASP:N	2.05	0.72
1:A:1353:C:P	37:A:4650:HOH:O	2.48	0.72
6:F:88:LEU:HB2	6:F:89:PRO:HD3	1.72	0.72
23:W:42:ASN:HB3	37:W:7247:HOH:O	1.90	0.72
24:X:21:LEU:HD22	24:X:26:ILE:HD11	1.71	0.72
26:Z:212:ARG:HD2	37:Z:8600:HOH:O	1.89	0.72
1:A:1164:U:H3	1:A:1192:A:H2	1.35	0.72
8:H:63:ILE:HB	8:H:64:PRO:HD3	1.71	0.72
1:A:506:G:H22	1:A:509:A:H5'	1.53	0.71
3:C:76:VAL:HG23	27:1:63:LYS:HB3	1.72	0.71
1:A:560:C:H42	1:A:597:A:H61	1.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:C:H4'	1:A:285:A:O5'	1.89	0.71
4:D:7:ARG:NH1	4:D:11:LEU:CD2	2.53	0.71
25:Y:18:ARG:NH1	37:Y:4132:HOH:O	2.13	0.71
1:A:2301:A:H5''	1:A:2302:A:H5'	1.71	0.71
1:A:2467:A:H2'	37:A:5431:HOH:O	1.90	0.71
15:O:113:SER:HB2	37:O:8560:HOH:O	1.89	0.71
2:B:3013:A:O2'	2:B:3014:G:H5''	1.90	0.71
2:B:3020:G:O2'	2:B:3021:G:H5'	1.91	0.71
1:A:1003:U:HO2'	10:J:90:PHE:HE1	1.36	0.71
14:N:152:ARG:HG3	37:N:8557:HOH:O	1.91	0.71
1:A:2421:G:H3'	1:A:2422:U:H5''	1.71	0.71
18:R:25:PRO:HB2	37:R:4350:HOH:O	1.91	0.71
1:A:1771:U:H4'	27:1:20:LEU:HD21	1.71	0.71
1:A:1918:U:OP2	37:A:3997:HOH:O	2.07	0.71
1:A:214:U:H5'	37:A:6109:HOH:O	1.91	0.71
26:Z:186:ARG:HH11	26:Z:186:ARG:HG2	1.56	0.71
27:1:10:ARG:HA	37:1:8416:HOH:O	1.89	0.71
27:1:42:CYS:SG	27:1:44:PHE:N	2.59	0.71
1:A:1209:C:H2'	1:A:1210:G:H8	1.55	0.71
10:J:59:ASN:HD22	10:J:59:ASN:H	1.38	0.71
10:J:56:ILE:HG22	10:J:61:LEU:HD22	1.72	0.71
11:K:131:THR:HG22	11:K:134:GLU:H	1.53	0.71
11:K:19:MET:HE3	11:K:132:LEU:HD11	1.73	0.71
24:X:13:MET:HE3	24:X:17:ILE:HG22	1.73	0.71
1:A:338:C:H4'	5:E:174:ILE:HD11	1.71	0.71
3:C:69:LEU:HD21	3:C:120:ARG:HB3	1.72	0.70
5:E:104:ASP:HA	5:E:107:ARG:NH1	2.06	0.70
12:L:55:VAL:HG12	12:L:56:SER:N	2.06	0.70
4:D:18:ARG:HG3	4:D:256:GLN:HG3	1.72	0.70
18:R:23:THR:HA	37:R:4792:HOH:O	1.91	0.70
1:A:1019:C:OP1	37:A:3922:HOH:O	2.08	0.70
1:A:1119:G:H2'	11:K:52:GLN:HE22	1.54	0.70
3:C:88:ILE:O	3:C:88:ILE:HG22	1.90	0.70
1:A:2119:C:O2'	1:A:2120:U:H5'	1.91	0.70
2:B:3006:C:H5''	15:O:37:ARG:HH12	1.54	0.70
3:C:100:PRO:HG2	3:C:103:VAL:HG21	1.73	0.70
4:D:41:PHE:CD2	4:D:190:MET:HE3	2.25	0.70
5:E:85:LYS:NZ	37:E:8328:HOH:O	2.13	0.70
6:F:23:VAL:HG23	6:F:23:VAL:O	1.91	0.70
1:A:2276:U:H2'	1:A:2277:U:C6	2.26	0.70
1:A:2638:G:H1'	37:A:7742:HOH:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2768:A:H2'	1:A:2769:C:O4'	1.90	0.70
5:E:39:GLN:O	5:E:43:LYS:HD3	1.92	0.70
23:W:39:ALA:N	23:W:40:PRO:HD2	2.07	0.70
27:1:37:HIS:HB2	27:1:47:LEU:HB2	1.72	0.70
8:H:50:VAL:HG21	8:H:63:ILE:HG21	1.72	0.70
1:A:544:G:C2'	1:A:545:G:H5''	2.21	0.70
32:A:8054:MG:MG	37:A:7819:HOH:O	1.33	0.70
2:B:3048:C:H4'	15:O:141:ARG:HH21	1.57	0.70
3:C:53:ALA:HB3	37:C:8610:HOH:O	1.91	0.70
12:L:74:VAL:CG1	12:L:113:ILE:HG12	2.20	0.70
18:R:24:SER:O	37:R:2847:HOH:O	2.10	0.70
1:A:877:G:H5'	1:A:878:G:OP1	1.92	0.70
3:C:121:ALA:O	3:C:124:VAL:HG22	1.90	0.70
4:D:179:LEU:O	4:D:183:GLU:HG2	1.92	0.70
8:H:2:VAL:HG22	8:H:57:GLU:OE1	1.92	0.70
15:O:183:ASP:OD2	15:O:186:LEU:HD12	1.91	0.70
19:S:132:ARG:CZ	37:S:8582:HOH:O	2.40	0.70
26:Z:187:VAL:CG2	26:Z:192:ASP:HB2	2.22	0.70
1:A:1191:A:H3'	1:A:1192:A:H5''	1.72	0.69
1:A:2827:A:H2'	1:A:2828:G:O4'	1.91	0.69
6:F:19:GLU:O	6:F:20:LYS:HG2	1.92	0.69
14:N:89:ASN:HA	37:N:8554:HOH:O	1.91	0.69
27:1:30:GLU:HA	27:1:33:HIS:CB	2.22	0.69
1:A:1406:A:N1	37:A:6004:HOH:O	2.25	0.69
1:A:1810:C:OP1	22:V:44:ARG:NE	2.16	0.69
1:A:603:A:H5''	1:A:604:G:OP1	1.92	0.69
3:C:36:ASP:OD2	3:C:85:ASP:HB2	1.91	0.69
1:A:1080:C:H4'	1:A:1081:A:OP1	1.91	0.69
4:D:145:HIS:HD2	4:D:146:THR:O	1.76	0.69
9:I:63:ARG:N	37:I:2569:HOH:O	2.25	0.69
15:O:159:TYR:HB3	15:O:162:ASP:HB2	1.75	0.69
24:X:154:ARG:C	37:X:4276:HOH:O	2.30	0.69
25:Y:72:VAL:HG22	25:Y:85:VAL:HG12	1.75	0.69
5:E:115:LEU:O	5:E:118:THR:HB	1.90	0.69
8:H:99:THR:HA	37:H:3461:HOH:O	1.93	0.69
14:N:59:GLY:HA3	14:N:141:ILE:CD1	2.22	0.69
10:J:57:ARG:HG3	37:J:8341:HOH:O	1.92	0.69
12:L:62:PRO:HG3	12:L:65:ARG:HH21	1.57	0.69
1:A:134:U:C2	1:A:145:A:C2	2.81	0.69
6:F:64:ARG:CG	6:F:67:ASP:HB3	2.22	0.69
7:G:81:GLU:HG2	7:G:134:SER:HB3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:71:TYR:C	10:J:73:GLN:H	1.96	0.69
23:W:12:THR:HG22	23:W:15:GLU:CG	2.22	0.69
1:A:821:U:H2'	1:A:822:C:H6	1.58	0.69
11:K:45:VAL:HG23	11:K:130:VAL:O	1.93	0.69
1:A:31:C:H2'	37:A:7669:HOH:O	1.92	0.69
4:D:85:ARG:NH1	37:D:8637:HOH:O	2.26	0.69
19:S:18:LEU:HD12	19:S:143:VAL:HG11	1.75	0.69
1:A:1625:U:H4'	37:A:4637:HOH:O	1.90	0.68
1:A:2291:A:C8	1:A:2309:C:H5'	2.28	0.68
6:F:55:LYS:HA	37:F:6752:HOH:O	1.93	0.68
11:K:107:ASN:ND2	11:K:109:TYR:H	1.91	0.68
16:P:47:ARG:HH11	16:P:47:ARG:HG3	1.57	0.68
5:E:1:MET:HG2	5:E:2:GLN:H	1.57	0.68
22:V:9:CYS:CA	22:V:52:THR:HG23	2.22	0.68
1:A:1119:G:H22	1:A:1246:A:H2	1.39	0.68
1:A:281:U:H2'	1:A:282:C:O4'	1.93	0.68
1:A:516:A:OP2	37:A:5618:HOH:O	2.12	0.68
14:N:60:ILE:C	14:N:61:ILE:HD12	2.14	0.68
6:F:69:ILE:O	6:F:69:ILE:HG22	1.92	0.68
11:K:75:PRO:HG2	11:K:105:LEU:HD21	1.73	0.68
12:L:81:ARG:HB2	12:L:87:ARG:NH1	2.05	0.68
1:A:2434:A:O3'	30:4:28:GLY:HA3	1.92	0.68
3:C:101:GLU:OE2	3:C:131:HIS:HB2	1.94	0.68
4:D:138:GLY:O	4:D:139:ASP:O	2.11	0.68
6:F:38:GLU:HB3	6:F:49:PRO:HG2	1.75	0.68
10:J:162:SER:CB	10:J:163:PRO:HD3	2.22	0.68
17:Q:59:ARG:NH2	17:Q:66:GLN:HE22	1.91	0.68
1:A:1086:A:N6	24:X:11:VAL:HG11	2.08	0.68
1:A:2748:G:H2'	37:A:7521:HOH:O	1.94	0.68
1:A:2862:G:H4'	4:D:336:GLN:O	1.93	0.68
14:N:113:ARG:NH2	14:N:156:ARG:HG2	2.09	0.68
37:A:4639:HOH:O	20:T:23:LYS:HE2	1.94	0.68
27:1:18:TYR:HB3	27:1:22:ILE:HG21	1.76	0.68
1:A:1185:U:H2'	1:A:1186:C:C6	2.29	0.68
1:A:2054:A:N3	19:S:128:ARG:NH2	2.42	0.68
4:D:42:ALA:HB1	4:D:308:LEU:HD11	1.75	0.68
30:4:65:THR:HG23	30:4:67:LEU:HG	1.75	0.68
1:A:1422:U:H2'	1:A:1423:C:C6	2.28	0.68
1:A:2533:C:H5'	1:A:2533:C:C6	2.26	0.68
1:A:1151:G:OP1	9:I:16:LYS:NZ	2.25	0.68
1:A:20:G:H21	19:S:117:HIS:HD2	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:115:ARG:HG3	12:L:116:GLU:N	2.09	0.68
24:X:88:THR:HG22	24:X:89:ASP:N	2.09	0.68
26:Z:189:ASN:ND2	26:Z:192:ASP:H	1.92	0.68
1:A:677:C:H4'	5:E:246:ARG:NH2	2.09	0.67
2:B:3006:C:C5'	15:O:37:ARG:NH1	2.56	0.67
15:O:61:ALA:HB3	15:O:88:ALA:HB2	1.76	0.67
1:A:1170:U:O2'	1:A:1172:G:N7	2.23	0.67
1:A:1666:C:H2'	1:A:1667:A:H5'	1.74	0.67
11:K:107:ASN:HD21	11:K:109:TYR:HB2	1.59	0.67
37:A:3737:HOH:O	21:U:9:LYS:CD	2.42	0.67
1:A:1041:U:H2'	1:A:1042:U:H5'	1.76	0.67
27:1:34:LYS:HE2	37:1:8428:HOH:O	1.94	0.67
1:A:1187:U:HO2'	1:A:1189:A:H2	1.41	0.67
34:A:8514:CL:CL	37:A:7720:HOH:O	2.50	0.67
3:C:190:ARG:NH2	3:C:207:GLN:OE1	2.26	0.67
12:L:62:PRO:HG3	12:L:65:ARG:NH2	2.09	0.67
19:S:29:LYS:HB3	37:S:8532:HOH:O	1.93	0.67
24:X:65:VAL:HA	24:X:68:THR:HG22	1.76	0.67
1:A:1459:A:OP2	37:A:9224:HOH:O	2.12	0.67
37:A:6996:HOH:O	3:C:211:LYS:HG2	1.94	0.67
4:D:7:ARG:NH1	4:D:11:LEU:HD22	2.10	0.67
10:J:84:ARG:NH2	10:J:135:TRP:HH2	1.92	0.67
11:K:75:PRO:HG2	11:K:105:LEU:CD2	2.24	0.67
15:O:169:PRO:O	15:O:172:PHE:HB3	1.94	0.67
21:U:52:ARG:HB2	21:U:95:ASN:HB3	1.77	0.67
6:F:105:SER:CB	6:F:131:THR:HG23	2.24	0.67
10:J:28:ILE:HA	10:J:62:GLU:OE1	1.95	0.67
14:N:173:LEU:HD23	14:N:183:VAL:HG12	1.77	0.67
15:O:89:GLY:O	15:O:92:ALA:HB3	1.95	0.67
37:A:3737:HOH:O	21:U:9:LYS:HD2	1.92	0.67
3:C:135:VAL:HG21	3:C:147:ARG:NH1	2.09	0.67
12:L:81:ARG:HD3	12:L:87:ARG:NH1	2.10	0.67
23:W:4:HIS:HB3	37:W:6622:HOH:O	1.95	0.67
10:J:127:GLY:O	10:J:128:ALA:HB3	1.92	0.67
10:J:46:VAL:HG12	10:J:146:TRP:HZ3	1.59	0.67
11:K:74:ARG:O	11:K:78:ILE:HG12	1.95	0.67
28:2:10:LYS:HG3	37:2:8432:HOH:O	1.93	0.67
1:A:871:G:C5'	1:A:871:G:C8	2.67	0.67
3:C:2:ARG:NH1	37:C:8515:HOH:O	2.08	0.67
1:A:2780:C:H1'	7:G:143:GLN:HE21	1.59	0.67
1:A:447:A:OP1	21:U:2:LYS:HG2	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:A:7400:HOH:O	21:U:9:LYS:HB2	1.94	0.67
27:1:47:LEU:HD23	27:1:57:CYS:HB2	1.76	0.67
4:D:162:MET:CE	4:D:308:LEU:HD21	2.23	0.67
5:E:139:VAL:HG13	37:E:8447:HOH:O	1.94	0.67
1:A:2346:C:O2'	6:F:52:THR:HG21	1.95	0.67
14:N:164:THR:CG2	14:N:165:SER:N	2.57	0.67
1:A:1244:U:OP1	11:K:18:ILE:HD13	1.95	0.66
1:A:1751:G:C2'	1:A:1752:G:H5''	2.25	0.66
4:D:51:VAL:CG2	4:D:327:VAL:HG13	2.25	0.66
1:A:2548:C:OP2	4:D:5:ARG:NH2	2.28	0.66
10:J:5:MET:HG3	37:J:8354:HOH:O	1.94	0.66
13:M:53:ARG:NH2	13:M:57:VAL:CG1	2.58	0.66
21:U:47:THR:HB	21:U:100:ASP:HB3	1.75	0.66
1:A:1160:G:N3	37:A:5605:HOH:O	2.28	0.66
14:N:139:PRO:O	14:N:140:ALA:HB3	1.93	0.66
15:O:107:ASN:OD1	34:O:8507:CL:CL	2.50	0.66
27:1:46:LYS:HB2	27:1:57:CYS:SG	2.34	0.66
2:B:3026:C:OP2	37:B:3472:HOH:O	2.13	0.66
4:D:162:MET:HE3	4:D:308:LEU:HD21	1.76	0.66
11:K:103:VAL:HG12	37:K:8565:HOH:O	1.96	0.66
14:N:87:MET:HB3	30:4:46:ILE:HD13	1.77	0.66
1:A:154:C:H2'	1:A:155:C:H6	1.60	0.66
1:A:157:G:H4'	14:N:95:LYS:HE3	1.78	0.66
1:A:2000:G:O2'	1:A:2001:G:H5'	1.96	0.66
1:A:2578:G:H5'	1:A:2578:G:H8	1.60	0.66
14:N:74:ARG:NH2	37:N:8631:HOH:O	2.27	0.66
17:Q:105:LEU:HD21	17:Q:137:LEU:HD21	1.77	0.66
1:A:2710:U:H1'	37:A:7602:HOH:O	1.96	0.66
2:B:3049:G:H5''	37:B:4707:HOH:O	1.94	0.66
1:A:2890:A:H1'	22:V:56:ARG:NH2	2.11	0.66
8:H:50:VAL:HG13	8:H:60:VAL:HG11	1.77	0.66
10:J:27:LYS:N	10:J:58:HIS:HD2	1.91	0.66
19:S:132:ARG:HG2	19:S:133:ALA:N	2.10	0.66
4:D:329:TYR:CE2	22:V:15:PRO:HG2	2.30	0.66
1:A:400:C:O3'	37:A:5766:HOH:O	2.13	0.66
2:B:3001:U:O3'	2:B:3003:A:H5''	1.96	0.66
2:B:3039:U:H1'	2:B:3044:A:N6	2.09	0.66
11:K:93:ARG:HH11	11:K:93:ARG:HB3	1.58	0.66
1:A:553:G:P	26:Z:204:ARG:HH22	2.19	0.66
1:A:739:G:C5	37:A:7523:HOH:O	2.49	0.66
5:E:12:THR:HB	37:E:8440:HOH:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:141:ASN:HA	37:J:8356:HOH:O	1.94	0.66
3:C:94:LEU:N	3:C:94:LEU:HD23	2.10	0.66
1:A:396:U:H4'	37:A:4403:HOH:O	1.96	0.66
6:F:97:GLN:O	6:F:97:GLN:HG2	1.95	0.66
10:J:140:PRO:HB3	37:J:8370:HOH:O	1.95	0.66
29:3:22:PRO:HG2	29:3:25:VAL:HG23	1.78	0.65
24:X:68:THR:HG23	24:X:69:ARG:HG2	1.77	0.65
1:A:1909:A:N1	1:A:2128:G:H1'	2.11	0.65
6:F:25:MET:HE1	6:F:37:ALA:HB1	1.77	0.65
9:I:12:ILE:N	9:I:13:PRO:CD	2.60	0.65
26:Z:155:ARG:NH1	37:Z:8558:HOH:O	2.27	0.65
28:2:25:LYS:O	28:2:25:LYS:HG2	1.96	0.65
1:A:2472:C:O2'	1:A:2634:G:H4'	1.96	0.65
32:A:8034:MG:MG	37:A:4868:HOH:O	1.37	0.65
25:Y:41:PHE:O	25:Y:43:VAL:HG23	1.96	0.65
1:A:2036:C:OP1	37:A:6671:HOH:O	2.14	0.65
5:E:129:HIS:CE1	5:E:231:ARG:HA	2.31	0.65
23:W:64:GLY:O	23:W:65:ASP:HB2	1.96	0.65
2:B:3003:A:H2'	37:B:2430:HOH:O	1.95	0.65
2:B:3023:U:C4'	2:B:3024:U:OP2	2.41	0.65
6:F:174:VAL:HG13	37:F:6555:HOH:O	1.96	0.65
21:U:37:GLN:OE1	21:U:118:SER:HA	1.95	0.65
25:Y:25:ARG:CZ	37:Y:3861:HOH:O	2.42	0.65
1:A:1634:G:H3'	37:A:3869:HOH:O	1.96	0.65
6:F:44:ILE:HG23	6:F:45:THR:HG23	1.79	0.65
1:A:282:C:H1'	1:A:368:C:H42	1.60	0.65
6:F:23:VAL:HG22	6:F:73:VAL:HB	1.78	0.65
1:A:188:C:H5''	14:N:163:LEU:HD21	1.77	0.65
37:A:3754:HOH:O	22:V:17:THR:CG2	2.44	0.65
30:4:69:TYR:HB2	30:4:78:HIS:CE1	2.32	0.65
1:A:2320:U:H4'	1:A:2321:A:O4'	1.96	0.65
2:B:3014:G:H5'	2:B:3014:G:C8	2.30	0.65
6:F:95:THR:O	6:F:97:GLN:N	2.27	0.65
24:X:141:HIS:HB2	24:X:146:ILE:HG12	1.77	0.65
1:A:1477:C:O2'	1:A:1478:U:H5'	1.96	0.65
1:A:2769:C:H2'	1:A:2770:G:O4'	1.97	0.65
1:A:2908:A:H2'	1:A:2909:G:O4'	1.96	0.65
4:D:36:PRO:HA	4:D:168:GLY:HA3	1.79	0.65
24:X:110:GLN:HA	24:X:110:GLN:NE2	2.12	0.65
26:Z:200:THR:HG22	26:Z:201:GLU:CG	2.26	0.65
1:A:1741:U:H5'	1:A:1742:A:OP1	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1878:G:H1'	37:A:6090:HOH:O	1.97	0.65
2:B:3028:U:H2'	2:B:3029:C:C6	2.32	0.65
6:F:135:VAL:HG22	6:F:136:ARG:N	2.11	0.65
6:F:140:ARG:O	6:F:144:ARG:HG2	1.96	0.65
13:M:148:GLU:HA	37:M:8571:HOH:O	1.96	0.65
1:A:338:C:H5''	37:E:8419:HOH:O	1.97	0.64
3:C:33:GLU:O	3:C:34:ASP:HB2	1.96	0.64
5:E:236:THR:H	5:E:239:ALA:HB3	1.62	0.64
14:N:138:HIS:ND1	14:N:139:PRO:O	2.23	0.64
1:A:2323:G:H5'	37:A:6990:HOH:O	1.98	0.64
1:A:485:A:N3	1:A:487:G:H5''	2.12	0.64
4:D:238:ASN:HD22	4:D:240:GLY:N	1.95	0.64
8:H:110:GLU:HG2	37:H:6926:HOH:O	1.96	0.64
11:K:46:ILE:HA	37:K:8528:HOH:O	1.97	0.64
13:M:143:THR:HG22	13:M:145:LEU:H	1.60	0.64
15:O:163:PHE:HA	37:O:8519:HOH:O	1.96	0.64
5:E:103:ASN:HB3	37:E:8309:HOH:O	1.97	0.64
6:F:54:ALA:HB2	6:F:69:ILE:HD12	1.79	0.64
1:A:539:G:H2'	1:A:540:A:C8	2.32	0.64
7:G:79:GLY:HA3	37:G:7046:HOH:O	1.98	0.64
11:K:19:MET:CE	11:K:132:LEU:HD11	2.28	0.64
14:N:74:ARG:HH11	14:N:74:ARG:HG3	1.62	0.64
1:A:1329:A:C2	37:A:4655:HOH:O	2.48	0.64
1:A:282:C:O2'	1:A:283:U:H5'	1.98	0.64
4:D:7:ARG:HG2	4:D:7:ARG:HH11	1.62	0.64
6:F:57:THR:HG23	6:F:63:ILE:HG22	1.79	0.64
1:A:1303:C:OP2	37:A:4492:HOH:O	2.14	0.64
1:A:182:G:H4'	14:N:157:LEU:HD13	1.78	0.64
4:D:24:PRO:CG	4:D:204:GLY:HA2	2.28	0.64
5:E:162:VAL:HG13	5:E:232:LEU:HD21	1.79	0.64
1:A:240:C:H4'	14:N:146:GLN:NE2	2.13	0.64
1:A:2421:G:H3'	1:A:2422:U:C5'	2.28	0.64
14:N:81:ARG:HG3	14:N:85:ARG:HB2	1.80	0.64
15:O:141:ARG:N	37:O:8571:HOH:O	2.31	0.64
22:V:14:GLU:O	22:V:17:THR:HB	1.96	0.64
2:B:3009:C:OP2	37:B:466:HOH:O	2.15	0.64
10:J:27:LYS:H	10:J:58:HIS:CD2	2.09	0.64
14:N:106:ASN:HD22	14:N:114:VAL:HG23	1.63	0.64
37:L:1387:HOH:O	22:V:20:MET:HE3	1.98	0.64
26:Z:189:ASN:HD22	26:Z:189:ASN:C	2.01	0.64
28:2:8:GLN:HE22	28:2:11:LYS:NZ	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:A:C4	1:A:177:A:C2	2.86	0.63
3:C:131:HIS:O	3:C:132:ASP:HB2	1.96	0.63
11:K:74:ARG:CB	11:K:74:ARG:HH11	2.11	0.63
19:S:104:PHE:HB2	19:S:109:MET:HE1	1.80	0.63
20:T:43:GLU:HB3	37:T:8344:HOH:O	1.98	0.63
1:A:1086:A:C6	24:X:11:VAL:HG11	2.33	0.63
1:A:2050:G:H5''	19:S:80:TYR:O	1.98	0.63
1:A:1857:A:N6	1:A:2247:C:H1'	2.13	0.63
1:A:263:U:O4'	8:H:59:ILE:HD13	1.98	0.63
1:A:926:A:O2'	13:M:41:HIS:HD2	1.81	0.63
3:C:81:GLN:HB2	3:C:92:ASN:ND2	2.13	0.63
6:F:41:LEU:HA	6:F:44:ILE:HG22	1.81	0.63
1:A:2123:A:H5'	14:N:89:ASN:HD21	1.63	0.63
37:A:5493:HOH:O	4:D:298:LYS:HD3	1.98	0.63
30:4:74:CYS:SG	30:4:76:LYS:CB	2.86	0.63
1:A:2432:C:O2'	1:A:2433:A:H5'	1.98	0.63
1:A:558:C:H5'	37:A:5235:HOH:O	1.99	0.63
32:A:8023:MG:MG	37:A:7787:HOH:O	1.41	0.63
12:L:82:ARG:NH2	12:L:115:ARG:HG2	2.13	0.63
26:Z:235:GLU:CD	26:Z:235:GLU:H	2.01	0.63
1:A:2281:C:C2'	1:A:2282:U:H5'	2.27	0.63
1:A:2676:C:H4'	11:K:70:PHE:CE1	2.34	0.63
37:A:6676:HOH:O	26:Z:165:GLU:HB3	1.98	0.63
1:A:1213:C:O2'	1:A:1214:G:H5'	1.98	0.63
14:N:12:TRP:CE2	14:N:20:ILE:HD11	2.33	0.63
15:O:154:LEU:O	15:O:155:GLU:HB3	1.99	0.63
15:O:48:VAL:HG11	15:O:55:ASP:HB3	1.81	0.63
1:A:1766:U:O2	1:A:1778:A:H5'	1.98	0.63
10:J:46:VAL:O	10:J:146:TRP:HH2	1.82	0.63
29:3:41:HIS:N	29:3:45:ASN:HD22	1.94	0.63
1:A:2637:A:H5'	37:A:9260:HOH:O	1.98	0.63
1:A:299:U:H5'	37:A:7314:HOH:O	1.98	0.63
1:A:952:G:H4'	37:A:4003:HOH:O	1.99	0.63
5:E:16:VAL:HG12	5:E:17:ASP:N	2.13	0.63
6:F:99:ASP:CB	6:F:103:ASN:H	2.12	0.63
1:A:2690:U:O2'	7:G:111:LYS:HE3	1.99	0.63
14:N:34:GLU:HB3	14:N:35:PRO:HD2	1.81	0.63
15:O:61:ALA:CB	15:O:88:ALA:HB2	2.28	0.63
18:R:32:GLU:HA	18:R:71:TYR:OH	1.99	0.63
20:T:51:GLN:HE21	20:T:53:ASN:ND2	1.97	0.63
25:Y:25:ARG:HG2	37:Y:5356:HOH:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1679:C:H5'	37:A:9311:HOH:O	1.99	0.63
1:A:113:A:H3'	1:A:114:A:H5''	1.82	0.62
4:D:307:ARG:HH11	4:D:307:ARG:HB2	1.63	0.62
5:E:233:THR:HG22	5:E:234:VAL:N	2.12	0.62
13:M:145:LEU:O	13:M:148:GLU:HG3	1.98	0.62
17:Q:120:ARG:NH2	17:Q:123:TYR:CD2	2.67	0.62
19:S:18:LEU:HB2	19:S:143:VAL:HG12	1.79	0.62
37:L:408:HOH:O	22:V:37:GLU:HB3	1.99	0.62
1:A:926:A:O2'	13:M:41:HIS:CD2	2.51	0.62
5:E:25:PRO:HG2	37:E:8325:HOH:O	1.98	0.62
15:O:73:ALA:N	37:O:8568:HOH:O	2.32	0.62
20:T:51:GLN:NE2	20:T:53:ASN:HD21	1.97	0.62
30:4:40:ARG:HD2	37:4:8552:HOH:O	1.99	0.62
1:A:1159:G:P	37:A:4266:HOH:O	2.57	0.62
1:A:1377:C:H5'	1:A:1377:C:H6	1.63	0.62
1:A:21:G:C5'	19:S:2:ILE:HA	2.28	0.62
1:A:2314:G:C2'	1:A:2315:C:H5'	2.29	0.62
1:A:631:A:N3	1:A:2073:G:O2'	2.32	0.62
32:A:8054:MG:MG	37:A:7765:HOH:O	1.42	0.62
27:1:62:TYR:CE2	27:1:64:ILE:HG23	2.34	0.62
37:A:6162:HOH:O	29:3:44:ARG:HG2	2.00	0.62
1:A:1119:G:N2	1:A:1246:A:C2	2.61	0.62
2:B:3003:A:N6	2:B:3022:G:H1'	2.15	0.62
5:E:236:THR:HA	37:E:8450:HOH:O	1.99	0.62
1:A:1293:U:O2'	26:Z:149:GLN:NE2	2.29	0.62
1:A:2346:C:H6	1:A:2346:C:O5'	1.82	0.62
1:A:2635:A:O2'	1:A:2636:C:H5'	2.00	0.62
15:O:164:ASP:CG	15:O:167:ASP:HA	2.20	0.62
16:P:87:THR:O	16:P:91:GLN:HG3	1.99	0.62
19:S:39:THR:HG23	19:S:107:GLU:O	2.00	0.62
4:D:258:GLY:H	4:D:260:HIS:CE1	2.17	0.62
6:F:25:MET:HE1	6:F:37:ALA:O	1.99	0.62
23:W:39:ALA:C	23:W:41:GLU:H	2.03	0.62
24:X:26:ILE:O	24:X:26:ILE:HG13	1.99	0.62
14:N:87:MET:CB	30:4:46:ILE:HD13	2.30	0.62
1:A:2324:G:H4'	1:A:2418:G:O2'	2.00	0.62
4:D:175:LEU:C	4:D:175:LEU:HD23	2.20	0.62
6:F:101:THR:HG22	37:F:7400:HOH:O	1.99	0.62
24:X:4:LEU:HD23	24:X:54:PHE:HB3	1.81	0.62
1:A:2878:U:H2'	1:A:2879:A:O4'	2.00	0.62
3:C:153:ARG:HB2	3:C:153:ARG:HH11	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:A:7432:HOH:O	4:D:211:THR:HG21	1.99	0.62
5:E:107:ARG:NH1	5:E:107:ARG:HB3	2.15	0.62
14:N:91:ILE:HA	37:N:8645:HOH:O	1.98	0.62
37:B:5071:HOH:O	15:O:23:ARG:HD3	1.99	0.62
21:U:55:PHE:HB2	37:U:6384:HOH:O	1.99	0.62
27:1:29:VAL:O	27:1:33:HIS:HB2	2.00	0.62
1:A:251:C:O2'	1:A:252:C:H5'	2.00	0.62
14:N:74:ARG:HG3	14:N:74:ARG:NH1	2.15	0.62
21:U:9:LYS:HE3	21:U:13:ARG:NH1	2.15	0.62
1:A:714:U:H3'	37:A:6912:HOH:O	1.99	0.62
6:F:64:ARG:CD	6:F:67:ASP:HB3	2.30	0.62
1:A:2779:G:H21	7:G:143:GLN:NE2	1.98	0.62
15:O:184:ILE:HG22	15:O:185:GLU:HG3	1.81	0.62
37:B:5071:HOH:O	15:O:20:TYR:CE2	2.50	0.62
18:R:75:ILE:CD1	18:R:84:ILE:HD11	2.29	0.62
5:E:242:GLU:HG3	37:E:8380:HOH:O	1.99	0.61
14:N:72:SER:OG	14:N:74:ARG:HB2	1.99	0.61
1:A:1919:A:H4'	37:A:4823:HOH:O	1.99	0.61
1:A:2094:G:H4'	4:D:245:SER:HB3	1.81	0.61
10:J:75:SER:O	10:J:79:ALA:HB2	2.00	0.61
1:A:1119:G:H8	11:K:52:GLN:NE2	1.98	0.61
17:Q:98:ILE:HD12	17:Q:102:ARG:NE	2.15	0.61
3:C:211:LYS:NZ	37:C:8623:HOH:O	2.32	0.61
3:C:72:GLU:HG3	27:1:66:GLY:HA2	1.82	0.61
4:D:154:VAL:HG12	4:D:156:LYS:HG2	1.82	0.61
14:N:68:ARG:HD3	14:N:68:ARG:O	2.00	0.61
6:F:146:LYS:NZ	15:O:107:ASN:HD21	1.98	0.61
27:1:53:GLY:HA2	27:1:67:GLY:O	2.00	0.61
1:A:1441:G:O2'	1:A:1442:A:H5'	2.00	0.61
1:A:2502:C:C2'	1:A:2503:A:H5'	2.31	0.61
1:A:2729:C:O2'	1:A:2730:G:H5'	2.00	0.61
1:A:2780:C:H2'	1:A:2781:U:C6	2.35	0.61
1:A:56:G:H5''	23:W:50:ARG:NH1	2.15	0.61
23:W:58:THR:O	23:W:62:GLU:HG3	2.01	0.61
1:A:281:U:H3'	37:A:7182:HOH:O	2.00	0.61
13:M:114:VAL:HG11	37:M:8572:HOH:O	2.01	0.61
15:O:80:SER:HB2	37:O:8537:HOH:O	2.00	0.61
24:X:21:LEU:HD21	24:X:48:VAL:HG11	1.80	0.61
27:1:31:ILE:O	27:1:35:LYS:HG3	2.00	0.61
1:A:1151:G:OP1	9:I:63:ARG:NH1	2.34	0.61
1:A:2419:U:H5''	1:A:2420:G:H5'	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2502:C:H2'	1:A:2503:A:H5'	1.82	0.61
4:D:36:PRO:HA	4:D:168:GLY:CA	2.31	0.61
15:O:12:ARG:HD3	15:O:18:THR:OG1	2.01	0.61
4:D:55:ASN:HB3	4:D:63:GLU:HA	1.81	0.61
7:G:6:GLU:HA	7:G:46:THR:HG22	1.82	0.61
27:1:28:ASP:O	27:1:31:ILE:HG22	2.01	0.61
1:A:1505:U:H6	1:A:1505:U:H5'	1.63	0.61
5:E:118:THR:O	5:E:136:VAL:HG13	2.00	0.61
1:A:121:U:OP2	29:3:10:ARG:NH2	2.33	0.61
29:3:35:ARG:HB2	37:3:2691:HOH:O	1.99	0.61
1:A:2281:C:H2'	1:A:2282:U:H5'	1.82	0.61
1:A:820:G:O2'	1:A:856:G:H4'	2.01	0.61
3:C:179:MET:HG2	3:C:186:TRP:CB	2.30	0.61
4:D:248:ARG:HG2	37:K:8541:HOH:O	1.99	0.61
6:F:25:MET:CE	6:F:37:ALA:HB1	2.31	0.61
14:N:59:GLY:HA3	14:N:141:ILE:HD11	1.83	0.61
25:Y:75:ALA:O	25:Y:83:ALA:HA	2.01	0.61
1:A:1393:A:H2'	1:A:1394:C:C6	2.36	0.61
10:J:166:ASN:N	10:J:166:ASN:HD22	1.98	0.61
10:J:86:ARG:HD3	10:J:130:HIS:HD2	1.66	0.61
11:K:90:LYS:HB2	34:K:8502:CL:CL	2.38	0.61
24:X:5:VAL:HG22	24:X:32:CYS:HB2	1.83	0.61
26:Z:99:ALA:HB2	26:Z:233:TYR:CZ	2.36	0.61
1:A:1773:G:C8	27:1:16:PRO:HA	2.35	0.60
2:B:3054:A:O2'	2:B:3055:U:H5'	2.01	0.60
6:F:99:ASP:HB2	6:F:103:ASN:HB2	1.83	0.60
12:L:74:VAL:HG12	12:L:75:ARG:HG3	1.83	0.60
1:A:431:G:P	14:N:48:ARG:HH12	2.24	0.60
24:X:22:GLU:HG2	24:X:27:HIS:CD2	2.35	0.60
1:A:2432:C:C4'	37:A:9718:HOH:O	2.43	0.60
1:A:383:A:H4'	37:A:5304:HOH:O	2.00	0.60
1:A:929:A:O5'	1:A:929:A:H8	1.84	0.60
1:A:1847:A:OP1	3:C:175:LYS:HG3	2.00	0.60
5:E:237:GLU:HB2	37:E:8429:HOH:O	2.00	0.60
6:F:36:ASN:HA	37:F:7500:HOH:O	2.00	0.60
14:N:186:SER:O	14:N:189:VAL:HG12	2.01	0.60
14:N:87:MET:HB3	30:4:46:ILE:HG21	1.84	0.60
29:3:22:PRO:HG2	29:3:25:VAL:CG2	2.30	0.60
1:A:69:A:H5'	1:A:69:A:C8	2.36	0.60
4:D:305:ASP:O	4:D:306:LYS:HB2	2.02	0.60
10:J:3:GLY:HA2	10:J:57:ARG:HH12	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:37:ARG:CD	34:O:8507:CL:CL	2.86	0.60
17:Q:10:ALA:HA	17:Q:13:VAL:HG12	1.83	0.60
17:Q:13:VAL:HG21	17:Q:41:ARG:HG2	1.83	0.60
19:S:119:VAL:HG21	19:S:142:ASP:CG	2.21	0.60
30:4:73:GLU:HB3	37:4:8564:HOH:O	2.00	0.60
1:A:2241:C:O2'	1:A:2242:U:H5'	2.01	0.60
1:A:2310:G:OP2	10:J:114:PRO:HD2	2.00	0.60
1:A:797:A:O4'	27:1:10:ARG:N	2.33	0.60
6:F:136:ARG:HD2	6:F:155:HIS:O	2.01	0.60
8:H:46:GLU:O	8:H:73:PRO:HD2	2.02	0.60
14:N:30:GLU:O	14:N:34:GLU:HG3	2.01	0.60
19:S:39:THR:HB	19:S:42:GLU:HG3	1.83	0.60
24:X:4:LEU:O	24:X:32:CYS:HA	2.01	0.60
1:A:125:U:H2'	37:A:3747:HOH:O	2.02	0.60
1:A:1311:G:C2	1:A:1312:G:C8	2.90	0.60
1:A:2249:G:OP2	37:A:5416:HOH:O	2.16	0.60
1:A:821:U:O2'	1:A:822:C:H5'	2.01	0.60
6:F:35:ALA:N	37:F:5576:HOH:O	2.35	0.60
1:A:1205:U:H2'	1:A:1206:U:C5'	2.30	0.60
1:A:2388:C:OP1	37:A:4572:HOH:O	2.16	0.60
1:A:280:C:H2'	1:A:281:U:O4'	2.02	0.60
1:A:941:G:O2'	1:A:942:U:H5'	2.01	0.60
1:A:948:G:N7	37:A:5820:HOH:O	2.31	0.60
37:A:4037:HOH:O	4:D:27:ASN:HB2	2.01	0.60
7:G:11:VAL:HG13	7:G:23:GLU:O	2.01	0.60
27:1:75:ALA:HB3	37:1:8440:HOH:O	2.01	0.60
1:A:886:A:OP1	37:A:3652:HOH:O	2.17	0.60
2:B:3035:C:H5''	37:B:4078:HOH:O	2.00	0.60
4:D:2:GLN:CD	37:D:8622:HOH:O	2.40	0.60
7:G:3:VAL:HG22	7:G:49:ILE:HB	1.84	0.60
15:O:141:ARG:HB3	37:O:8571:HOH:O	2.00	0.60
15:O:71:TRP:HE3	15:O:175:LEU:HD22	1.67	0.60
22:V:49:LEU:HD11	37:V:3805:HOH:O	2.02	0.60
23:W:39:ALA:O	23:W:41:GLU:N	2.35	0.60
24:X:149:LEU:HG	24:X:153:MET:HE2	1.84	0.60
1:A:1982:C:OP2	37:A:4252:HOH:O	2.16	0.60
1:A:1741:U:O2'	1:A:2723:G:H4'	2.01	0.60
15:O:119:GLN:O	15:O:123:ILE:HG13	2.01	0.60
33:A:8313:NA:NA	37:A:5123:HOH:O	1.74	0.60
12:L:32:ILE:HD11	12:L:56:SER:HB3	1.84	0.60
24:X:21:LEU:HD21	24:X:48:VAL:CG1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:78:GLU:CG	25:Y:79:GLU:H	2.13	0.60
26:Z:216:ARG:CD	37:Z:8569:HOH:O	2.39	0.60
1:A:1165:G:H3'	1:A:1165:G:OP1	2.02	0.59
4:D:195:ARG:HD2	4:D:324:ASP:OD1	2.01	0.59
5:E:246:ARG:NH1	5:E:246:ARG:HB3	2.16	0.59
11:K:26:VAL:HG13	11:K:36:VAL:HG11	1.82	0.59
14:N:139:PRO:O	14:N:140:ALA:CB	2.50	0.59
14:N:185:PRO:HG2	14:N:189:VAL:HG11	1.84	0.59
26:Z:115:ARG:NE	37:Z:8556:HOH:O	2.34	0.59
15:O:164:ASP:OD2	15:O:167:ASP:HA	2.02	0.59
22:V:47:ARG:HG3	37:V:4381:HOH:O	2.01	0.59
24:X:38:THR:HG22	37:X:3580:HOH:O	2.01	0.59
1:A:558:C:C2'	1:A:559:U:H5''	2.33	0.59
10:J:111:MET:O	10:J:114:PRO:HD3	2.02	0.59
1:A:182:G:H5'	37:A:5135:HOH:O	2.02	0.59
1:A:2505:G:O2'	1:A:2506:A:H5'	2.01	0.59
1:A:349:U:O2'	1:A:350:C:H5'	2.02	0.59
2:B:3055:U:H4'	2:B:3056:A:C8	2.38	0.59
4:D:312:ARG:HD3	4:D:315:VAL:HG13	1.84	0.59
6:F:95:THR:C	6:F:97:GLN:H	2.05	0.59
24:X:21:LEU:HD22	24:X:26:ILE:CD1	2.31	0.59
1:A:1119:G:H8	11:K:52:GLN:HE22	1.49	0.59
1:A:1523:G:H2'	1:A:1524:U:C6	2.38	0.59
1:A:703:G:O2'	1:A:704:C:H5'	2.02	0.59
3:C:166:ASP:OD1	37:C:8621:HOH:O	2.16	0.59
29:3:1:GLY:HA3	37:3:5969:HOH:O	2.02	0.59
1:A:1187:U:O2'	1:A:1189:A:H2	1.85	0.59
1:A:1669:A:H2'	1:A:1670:G:C8	2.38	0.59
1:A:1134:G:C4'	10:J:151:MET:HE1	2.17	0.59
25:Y:15:ARG:NH1	25:Y:15:ARG:HB3	2.16	0.59
3:C:94:LEU:HG	3:C:99:ILE:HD11	1.84	0.59
37:A:9678:HOH:O	4:D:254:GLN:HG3	2.02	0.59
1:A:1972:U:H2'	1:A:1973:A:H5'	1.85	0.59
1:A:2001:G:O2'	1:A:2002:C:H5'	2.03	0.59
1:A:2783:A:H3'	37:A:5210:HOH:O	2.00	0.59
1:A:820:G:OP1	27:1:17:ARG:NH2	2.31	0.59
2:B:3002:U:H4'	2:B:3002:U:OP2	2.01	0.59
4:D:207:LYS:HG2	4:D:304:PRO:HB3	1.83	0.59
5:E:84:VAL:O	5:E:85:LYS:HB2	2.02	0.59
15:O:151:ASP:O	15:O:154:LEU:HB2	2.03	0.59
26:Z:144:ARG:NE	37:Z:8610:HOH:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:4:7:PHE:HE2	30:4:22:VAL:HG21	1.67	0.59
1:A:2382:A:OP1	30:4:80:ARG:HG2	2.03	0.59
1:A:2064:U:OP1	37:A:3329:HOH:O	2.17	0.59
1:A:681:G:N3	1:A:681:G:H5'	2.18	0.59
7:G:69:ILE:HA	7:G:72:MET:CE	2.33	0.59
8:H:58:GLU:HA	8:H:61:MET:HG3	1.85	0.59
1:A:962:C:C1'	15:O:5:ARG:NH1	2.63	0.59
1:A:960:G:N3	1:A:960:G:H2'	2.18	0.59
4:D:217:ARG:HG3	4:D:257:THR:HG22	1.84	0.59
6:F:54:ALA:CB	6:F:69:ILE:HD12	2.32	0.59
16:P:26:TRP:N	37:P:3062:HOH:O	2.34	0.59
27:1:11:THR:OG1	27:1:23:ARG:HB2	2.04	0.58
32:A:8011:MG:MG	37:A:3953:HOH:O	1.45	0.58
2:B:3041:C:O4'	6:F:50:VAL:HG23	2.03	0.58
4:D:190:MET:HE2	4:D:194:PHE:CD1	2.38	0.58
1:A:1053:G:OP1	10:J:12:PRO:HG3	2.02	0.58
21:U:49:GLU:OE2	21:U:97:ARG:HD2	2.03	0.58
1:A:2064:U:H5'	1:A:2652:U:H4'	1.85	0.58
6:F:166:ILE:HD12	37:F:6326:HOH:O	2.03	0.58
19:S:14:ALA:HB3	19:S:147:LEU:HB2	1.86	0.58
1:A:1923:G:H4'	30:4:31:THR:O	2.03	0.58
1:A:2748:G:H5'	37:A:7521:HOH:O	2.03	0.58
1:A:2851:G:O2'	1:A:2852:A:H5'	2.03	0.58
4:D:141:ARG:HG2	4:D:165:ARG:HA	1.85	0.58
5:E:168:ARG:NH2	5:E:190:ALA:O	2.36	0.58
5:E:219:ASN:O	5:E:222:ASP:OD1	2.21	0.58
12:L:27:ARG:HD2	37:L:4747:HOH:O	2.03	0.58
16:P:39:THR:O	16:P:115:ARG:NH2	2.36	0.58
26:Z:189:ASN:HA	26:Z:217:ILE:HD11	1.84	0.58
1:A:1183:C:N4	37:A:4371:HOH:O	2.32	0.58
1:A:131:A:OP2	37:A:3142:HOH:O	2.17	0.58
1:A:2121:G:O2'	1:A:2122:C:H5'	2.04	0.58
1:A:2279:G:N3	37:A:9807:HOH:O	2.32	0.58
1:A:2507:G:H2'	1:A:2510:C:H42	1.68	0.58
3:C:11:ARG:HD3	37:C:8518:HOH:O	2.02	0.58
3:C:211:LYS:NZ	37:C:8575:HOH:O	2.37	0.58
6:F:37:ALA:O	6:F:40:ILE:HG12	2.03	0.58
10:J:48:LEU:HG	10:J:157:ILE:HG21	1.85	0.58
27:1:25:ARG:O	27:1:29:VAL:HG23	2.03	0.58
1:A:113:A:OP2	1:A:114:A:H2'	2.02	0.58
8:H:110:GLU:O	8:H:114:LYS:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:163:PRO:O	10:J:164:ALA:HB2	2.03	0.58
13:M:143:THR:CG2	13:M:144:ASP:N	2.66	0.58
15:O:43:VAL:HG13	15:O:118:ILE:HD11	1.83	0.58
19:S:44:VAL:O	19:S:48:GLU:HG3	2.03	0.58
26:Z:112:GLU:HA	26:Z:112:GLU:OE1	2.04	0.58
1:A:407:A:H5'	37:A:5994:HOH:O	2.03	0.58
3:C:95:PRO:HG2	3:C:98:GLU:HG2	1.86	0.58
10:J:65:ARG:CZ	37:J:8374:HOH:O	2.50	0.58
10:J:13:ALA:HA	10:J:91:HIS:CE1	2.39	0.58
1:A:1134:G:H4'	10:J:151:MET:CE	2.19	0.58
1:A:285:A:H2'	1:A:286:U:O4'	2.04	0.58
1:A:371:U:H2'	1:A:372:A:H8	1.68	0.58
4:D:74:ILE:HG13	37:D:8606:HOH:O	2.03	0.58
14:N:154:ARG:CZ	37:N:8643:HOH:O	2.51	0.58
25:Y:43:VAL:CG1	25:Y:47:ALA:HB3	2.33	0.58
1:A:1127:C:H2'	1:A:1128:U:H5'	1.85	0.58
1:A:2081:A:H4'	11:K:69:TYR:CE1	2.38	0.58
2:B:3055:U:H4'	2:B:3056:A:H8	1.68	0.58
5:E:43:LYS:NZ	37:E:8387:HOH:O	2.36	0.58
6:F:99:ASP:HB3	6:F:103:ASN:H	1.68	0.58
10:J:150:LYS:HA	10:J:153:VAL:HG22	1.86	0.58
10:J:3:GLY:HA2	10:J:57:ARG:NH1	2.19	0.58
14:N:59:GLY:HA3	14:N:141:ILE:HD12	1.85	0.58
17:Q:105:LEU:CD2	17:Q:137:LEU:HD21	2.34	0.58
1:A:2329:C:O2'	1:A:2330:U:H5'	2.04	0.58
1:A:2359:G:N7	37:A:3681:HOH:O	2.32	0.58
1:A:2594:C:O2'	1:A:2595:U:H5'	2.03	0.58
1:A:2718:C:H6	1:A:2718:C:H5'	1.69	0.58
5:E:27:ARG:HG3	5:E:29:ASP:OD1	2.03	0.58
10:J:147:ARG:HA	10:J:150:LYS:NZ	2.19	0.58
37:A:9380:HOH:O	14:N:94:LYS:HE2	2.03	0.58
22:V:9:CYS:HA	22:V:52:THR:CG2	2.30	0.58
1:A:1829:A:H5''	37:A:3062:HOH:O	2.02	0.58
1:A:2694:A:H4'	7:G:91:PHE:CE1	2.39	0.58
1:A:469:G:O2'	37:A:3035:HOH:O	2.16	0.58
1:A:489:A:C8	21:U:82:THR:HG22	2.39	0.58
13:M:143:THR:HG22	13:M:144:ASP:H	1.69	0.58
37:A:4491:HOH:O	14:N:94:LYS:HE3	2.03	0.58
26:Z:107:PRO:HB3	26:Z:182:PHE:CE2	2.39	0.58
1:A:1474:C:H6	1:A:1474:C:C5'	2.11	0.57
1:A:1535:G:H2'	1:A:1536:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1559:A:H1'	37:A:5836:HOH:O	2.03	0.57
1:A:815:U:OP1	37:A:3037:HOH:O	2.17	0.57
2:B:3026:C:P	37:B:3472:HOH:O	2.62	0.57
2:B:3107:C:H5	37:B:3167:HOH:O	1.87	0.57
4:D:30:PRO:HB2	4:D:39:GLN:NE2	2.18	0.57
6:F:86:THR:O	6:F:90:LEU:HG	2.04	0.57
8:H:46:GLU:N	37:H:3461:HOH:O	2.37	0.57
8:H:53:ASP:OD1	8:H:80:GLN:HB2	2.03	0.57
1:A:558:C:O2'	1:A:559:U:H5''	2.05	0.57
4:D:125:GLU:O	4:D:129:ARG:HG3	2.03	0.57
37:A:7435:HOH:O	5:E:188:ARG:CD	2.51	0.57
10:J:49:VAL:O	10:J:157:ILE:HG23	2.04	0.57
10:J:58:HIS:HA	10:J:61:LEU:HD23	1.86	0.57
24:X:72:PRO:HG2	24:X:77:ALA:HB3	1.85	0.57
1:A:2729:C:H2'	1:A:2730:G:H8	1.68	0.57
1:A:474:C:O3'	5:E:73:LEU:HD21	2.04	0.57
15:O:157:PRO:HA	37:O:8526:HOH:O	2.03	0.57
1:A:1422:U:H2'	1:A:1423:C:H6	1.67	0.57
1:A:272:A:H5'	1:A:273:G:OP2	2.04	0.57
1:A:920:C:H5'	1:A:921:G:C4	2.40	0.57
7:G:31:ARG:NH1	37:G:5919:HOH:O	2.36	0.57
9:I:64:ASN:N	9:I:64:ASN:HD22	2.01	0.57
10:J:127:GLY:O	10:J:128:ALA:CB	2.52	0.57
14:N:114:VAL:HG21	14:N:159:THR:HG21	1.87	0.57
14:N:165:SER:HB3	37:N:8534:HOH:O	2.04	0.57
15:O:143:ARG:HA	15:O:172:PHE:CD2	2.39	0.57
30:4:18:GLN:OE1	30:4:73:GLU:HB3	2.05	0.57
30:4:74:CYS:SG	30:4:76:LYS:CG	2.93	0.57
1:A:1819:G:H2'	1:A:1820:G:H4'	1.85	0.57
1:A:183:A:H5'	14:N:157:LEU:HD12	1.85	0.57
1:A:2433:A:H2'	1:A:2434:A:C8	2.40	0.57
4:D:221:GLN:HE22	12:L:42:ASN:ND2	2.02	0.57
4:D:238:ASN:ND2	4:D:240:GLY:H	1.96	0.57
6:F:25:MET:CE	6:F:41:LEU:HG	2.26	0.57
22:V:52:THR:HG22	22:V:54:THR:HB	1.87	0.57
25:Y:15:ARG:HH11	25:Y:15:ARG:CB	2.16	0.57
1:A:1351:G:OP1	5:E:96:LYS:NZ	2.37	0.57
1:A:2577:A:O2'	37:A:5373:HOH:O	2.18	0.57
17:Q:13:VAL:HG11	17:Q:40:VAL:CG1	2.34	0.57
19:S:18:LEU:HD12	19:S:143:VAL:CG1	2.35	0.57
25:Y:78:GLU:HG2	25:Y:79:GLU:N	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2015:A:H2'	1:A:2016:U:O4'	2.04	0.57
1:A:2382:A:H5'	37:A:4715:HOH:O	2.04	0.57
1:A:2769:C:C2'	1:A:2770:G:H5'	2.35	0.57
1:A:951:A:C2'	1:A:952:G:H5'	2.35	0.57
23:W:39:ALA:N	23:W:40:PRO:CD	2.67	0.57
1:A:1126:C:OP2	37:A:3619:HOH:O	2.18	0.57
1:A:2256:G:H2'	1:A:2257:G:H5'	1.87	0.57
1:A:2766:A:O2'	4:D:265:LEU:O	2.22	0.57
5:E:7:ASP:OD1	5:E:11:ASN:O	2.22	0.57
8:H:19:ALA:O	8:H:22:VAL:HG22	2.04	0.57
37:A:4810:HOH:O	11:K:47:THR:HB	2.04	0.57
14:N:172:GLY:C	14:N:183:VAL:HG11	2.25	0.57
1:A:1118:A:C8	1:A:1118:A:C3'	2.83	0.57
1:A:1192:A:O2'	1:A:1193:A:OP1	2.22	0.57
1:A:2506:A:O2'	1:A:2507:G:O5'	2.23	0.57
1:A:69:A:H8	1:A:69:A:H5'	1.70	0.57
1:A:816:G:H5'	1:A:1598:A:H4'	1.87	0.57
4:D:7:ARG:NH1	4:D:11:LEU:HD21	2.20	0.57
6:F:38:GLU:OE2	6:F:51:ARG:CZ	2.53	0.57
7:G:7:ILE:HD11	7:G:11:VAL:C	2.25	0.57
8:H:28:ALA:HB3	8:H:99:THR:O	2.03	0.57
10:J:86:ARG:NH1	10:J:130:HIS:CD2	2.73	0.57
37:A:5504:HOH:O	14:N:58:GLN:HG3	2.03	0.57
20:T:29:ASP:OD1	20:T:31:ARG:HG3	2.04	0.57
21:U:38:ARG:HG3	21:U:38:ARG:HH11	1.69	0.57
1:A:1687:C:O2	28:2:9:GLY:HA2	2.05	0.57
29:3:41:HIS:H	29:3:45:ASN:ND2	2.03	0.57
1:A:1060:C:H6	1:A:1060:C:H5'	1.70	0.57
8:H:107:VAL:O	8:H:111:ILE:HG13	2.04	0.57
1:A:21:G:H4'	19:S:2:ILE:HG22	1.87	0.57
29:3:22:PRO:HB2	29:3:24:TRP:CD1	2.40	0.56
1:A:1677:U:OP2	29:3:8:LYS:NZ	2.35	0.56
1:A:1528:A:H2'	1:A:1529:G:O4'	2.05	0.56
1:A:1820:G:C6	1:A:2030:A:C2	2.93	0.56
1:A:2270:G:H4'	3:C:223:ARG:HH12	1.70	0.56
3:C:192:VAL:O	3:C:207:GLN:HG2	2.05	0.56
10:J:14:TYR:N	10:J:91:HIS:CE1	2.72	0.56
13:M:149:ARG:O	13:M:150:GLN:HB2	2.05	0.56
14:N:169:ARG:HD2	37:N:8590:HOH:O	2.05	0.56
19:S:106:GLY:HA2	19:S:109:MET:CE	2.35	0.56
1:A:315:G:C6	1:A:316:A:C6	2.93	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:U:C6	1:A:559:U:H5'	2.37	0.56
3:C:109:GLU:HG2	3:C:116:GLY:H	1.70	0.56
12:L:74:VAL:O	12:L:74:VAL:HG12	2.05	0.56
14:N:18:GLY:O	14:N:21:ALA:HB3	2.05	0.56
15:O:58:LEU:HD12	15:O:58:LEU:N	2.20	0.56
20:T:6:LYS:HB2	20:T:27:ALA:O	2.03	0.56
21:U:63:ILE:HD11	21:U:75:GLU:HB2	1.85	0.56
22:V:13:ILE:HG12	22:V:32:CYS:HB3	1.86	0.56
1:A:184:G:H5''	14:N:153:THR:HG22	1.87	0.56
1:A:1925:G:O2'	1:A:1926:G:H5'	2.05	0.56
1:A:2570:G:H5''	37:A:4890:HOH:O	2.06	0.56
3:C:217:ARG:HG2	3:C:229:ALA:HB2	1.87	0.56
8:H:50:VAL:CG1	8:H:60:VAL:HG11	2.34	0.56
10:J:48:LEU:CD1	10:J:157:ILE:HG21	2.34	0.56
10:J:26:LYS:HD3	10:J:89:PRO:HG3	1.87	0.56
1:A:1887:U:OP1	27:I:21:LYS:HE3	2.05	0.56
1:A:1056:U:H2'	1:A:1057:A:O4'	2.06	0.56
1:A:1595:G:O2'	1:A:1596:U:H5'	2.05	0.56
1:A:2276:U:H2'	1:A:2277:U:H6	1.69	0.56
2:B:3103:A:O2'	2:B:3104:A:H5'	2.04	0.56
4:D:168:GLY:N	4:D:174:ARG:HD3	2.20	0.56
4:D:24:PRO:HG3	4:D:204:GLY:HA2	1.87	0.56
4:D:214:PRO:HD2	37:D:8521:HOH:O	2.05	0.56
4:D:27:ASN:HB3	37:D:8630:HOH:O	2.05	0.56
7:G:20:ILE:CD1	7:G:33:LEU:HD12	2.36	0.56
2:B:3006:C:P	15:O:37:ARG:NH1	2.79	0.56
15:O:49:THR:CG2	15:O:56:ASP:HB2	2.35	0.56
1:A:1450:C:O2'	1:A:1494:A:H5'	2.06	0.56
1:A:1641:A:H2'	1:A:1642:A:H5'	1.87	0.56
1:A:816:G:C6	1:A:817:G:N1	2.73	0.56
2:B:3064:C:H2'	2:B:3065:A:H5'	1.87	0.56
3:C:105:VAL:CG1	3:C:154:ALA:HB1	2.35	0.56
5:E:47:GLY:HA2	5:E:92:PRO:HB2	1.88	0.56
37:A:3822:HOH:O	10:J:11:LYS:HE2	2.04	0.56
10:J:85:ILE:HB	10:J:132:PHE:CE2	2.40	0.56
1:A:2502:C:H4'	10:J:151:MET:HG2	1.88	0.56
10:J:56:ILE:HG22	10:J:61:LEU:CD2	2.33	0.56
14:N:104:ARG:O	14:N:108:LYS:HG2	2.04	0.56
14:N:87:MET:CE	37:N:8531:HOH:O	2.53	0.56
15:O:34:LEU:HA	15:O:47:LEU:HD23	1.87	0.56
24:X:13:MET:CE	24:X:17:ILE:HG22	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1483:C:O2'	1:A:1484:G:H5'	2.05	0.56
1:A:484:A:N1	1:A:506:G:H4'	2.21	0.56
1:A:558:C:H2'	1:A:559:U:C5'	2.35	0.56
4:D:148:PRO:HD2	37:D:8582:HOH:O	2.05	0.56
4:D:240:GLY:HA3	37:D:8528:HOH:O	2.05	0.56
4:D:333:GLU:HB2	22:V:14:GLU:OE2	2.06	0.56
4:D:41:PHE:CG	4:D:190:MET:HE3	2.41	0.56
37:A:4513:HOH:O	10:J:151:MET:HE2	2.05	0.56
14:N:74:ARG:O	14:N:88:VAL:HG13	2.04	0.56
21:U:48:VAL:HG22	21:U:97:ARG:C	2.25	0.56
30:4:3:MET:O	30:4:90:PHE:HA	2.06	0.56
1:A:1116:U:O2'	1:A:1118:A:C2	2.50	0.56
1:A:1701:A:H4'	1:A:1702:U:C5'	2.35	0.56
1:A:2587:U:H2'	1:A:2589:U:H5''	1.86	0.56
1:A:289:G:N2	1:A:363:A:H2	2.01	0.56
1:A:778:C:C4	1:A:779:U:C4	2.94	0.56
4:D:304:PRO:HD2	4:D:307:ARG:HD2	1.86	0.56
8:H:100:ASP:O	8:H:101:ALA:O	2.24	0.56
1:A:710:G:OP1	16:P:24:ALA:HB3	2.04	0.56
26:Z:112:GLU:OE1	26:Z:115:ARG:NH1	2.38	0.56
1:A:88:G:N7	29:3:28:LYS:HD2	2.20	0.56
30:4:71:CYS:SG	30:4:72:GLY:N	2.78	0.56
1:A:134:U:O2	1:A:145:A:C2	2.58	0.56
1:A:2361:A:H2'	1:A:2362:A:C8	2.40	0.56
1:A:2547:C:OP2	4:D:5:ARG:NH1	2.39	0.56
1:A:1174:A:C5	1:A:1201:C:H4'	2.40	0.56
1:A:1711:A:O2'	1:A:1712:A:H5'	2.05	0.56
1:A:2064:U:H5'	1:A:2652:U:O3'	2.06	0.56
1:A:2432:C:H4'	30:4:36:ILE:HG12	1.86	0.56
8:H:107:VAL:HG23	37:H:6617:HOH:O	2.06	0.56
9:I:12:ILE:HG22	9:I:12:ILE:O	2.05	0.56
11:K:52:GLN:HG3	11:K:53:ILE:N	2.21	0.56
24:X:81:ASP:OD1	24:X:92:ASP:HB2	2.04	0.56
24:X:80:ASP:O	24:X:84:VAL:HG23	2.05	0.56
1:A:1362:U:H5'	37:E:8342:HOH:O	2.06	0.56
1:A:1730:G:H5'	1:A:1731:C:C5	2.41	0.56
1:A:2011:A:P	37:A:5928:HOH:O	2.64	0.56
4:D:16:ARG:NH2	37:D:8556:HOH:O	2.28	0.56
1:A:1234:U:N3	4:D:244:PRO:HB3	2.21	0.56
2:B:3044:A:O4'	6:F:76:ARG:NE	2.39	0.56
10:J:53:PRO:HA	10:J:125:VAL:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:C:H2'	1:A:137:U:O4'	2.04	0.56
1:A:1733:A:H4'	4:D:212:GLN:HA	1.87	0.56
1:A:1874:U:H2'	3:C:120:ARG:HG3	1.88	0.56
1:A:2433:A:H2'	1:A:2434:A:H8	1.70	0.56
1:A:2526:C:O2'	1:A:2527:U:H5'	2.05	0.56
4:D:141:ARG:HD2	4:D:163:GLU:OE2	2.05	0.56
5:E:133:ARG:HD2	37:E:8408:HOH:O	2.06	0.56
10:J:83:PHE:HZ	10:J:146:TRP:HE1	1.50	0.56
12:L:101:ASN:O	12:L:102:GLU:HB2	2.06	0.56
14:N:39:ARG:NH2	37:N:8623:HOH:O	2.38	0.56
14:N:52:LEU:HD21	37:N:8616:HOH:O	2.06	0.56
21:U:24:ARG:HH21	21:U:39:ASN:HD22	1.53	0.56
1:A:1654:U:H2'	3:C:47:HIS:HD2	1.71	0.55
1:A:1688:G:H4'	28:2:8:GLN:HG3	1.87	0.55
1:A:2256:G:C2'	1:A:2257:G:H5'	2.36	0.55
1:A:2314:G:H2'	1:A:2315:C:H5'	1.87	0.55
1:A:2791:U:H1'	1:A:2792:A:H5''	1.88	0.55
1:A:821:U:H2'	1:A:822:C:C6	2.39	0.55
4:D:195:ARG:HG2	4:D:323:LEU:HD22	1.88	0.55
7:G:23:GLU:HG2	7:G:28:SER:HB3	1.88	0.55
10:J:44:ALA:HA	10:J:163:PRO:O	2.07	0.55
14:N:91:ILE:HG23	37:N:8645:HOH:O	2.05	0.55
18:R:75:ILE:HD13	18:R:84:ILE:HD11	1.88	0.55
26:Z:117:LEU:HD12	26:Z:174:VAL:HG11	1.88	0.55
1:A:1168:C:H2'	1:A:1169:U:O4'	2.05	0.55
1:A:542:A:H2'	1:A:543:G:O4'	2.05	0.55
3:C:96:LEU:HD22	3:C:128:LEU:HD13	1.88	0.55
13:M:54:PRO:HG2	13:M:57:VAL:CG2	2.37	0.55
23:W:56:ILE:O	23:W:60:GLN:HG3	2.05	0.55
1:A:111:C:H2'	1:A:112:G:O4'	2.06	0.55
1:A:1181:A:H2'	1:A:1182:C:O4'	2.05	0.55
1:A:1123:A:C6	1:A:1238:C:H5'	2.42	0.55
2:B:3042:C:O2	6:F:76:ARG:NH1	2.38	0.55
1:A:820:G:C6	3:C:171:LYS:HB2	2.41	0.55
10:J:69:ASN:O	10:J:72:VAL:HG12	2.07	0.55
24:X:106:THR:OG1	24:X:109:GLU:HG3	2.06	0.55
1:A:2316:G:H8	37:A:5626:HOH:O	1.89	0.55
1:A:2464:C:P	37:A:9912:HOH:O	2.64	0.55
1:A:639:A:H2'	1:A:640:G:C8	2.40	0.55
7:G:20:ILE:CD1	7:G:40:VAL:HG11	2.35	0.55
12:L:30:LYS:O	12:L:55:VAL:HG13	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:155:HIS:CE1	14:N:158:ARG:HE	2.24	0.55
15:O:86:LEU:O	15:O:90:LEU:HG	2.06	0.55
23:W:44:GLY:O	23:W:48:GLU:HG2	2.06	0.55
1:A:1182:C:H1'	1:A:1192:A:H8	1.72	0.55
1:A:283:U:H5''	1:A:284:C:P	2.47	0.55
2:B:3029:C:C2'	2:B:3030:C:H5'	2.36	0.55
4:D:7:ARG:HD3	4:D:9:GLY:O	2.06	0.55
5:E:16:VAL:HG12	5:E:17:ASP:H	1.71	0.55
6:F:140:ARG:O	6:F:140:ARG:HG2	2.06	0.55
7:G:81:GLU:HG2	7:G:134:SER:CB	2.37	0.55
15:O:159:TYR:HE2	15:O:163:PHE:HE2	1.55	0.55
24:X:108:ARG:HE	24:X:114:PRO:HG3	1.70	0.55
25:Y:76:ARG:HG3	25:Y:76:ARG:NH1	2.21	0.55
1:A:2271:G:P	37:A:9415:HOH:O	2.65	0.55
1:A:2349:G:OP1	6:F:20:LYS:NZ	2.39	0.55
1:A:2897:C:H2'	1:A:2898:G:H8	1.71	0.55
1:A:57:C:H5''	37:A:6728:HOH:O	2.06	0.55
13:M:57:VAL:HG12	13:M:57:VAL:O	2.05	0.55
15:O:152:GLU:C	15:O:154:LEU:H	2.08	0.55
26:Z:126:PRO:HG2	26:Z:128:PHE:CE1	2.42	0.55
1:A:2649:A:H8	1:A:2649:A:H5'	1.71	0.55
1:A:506:G:H22	1:A:509:A:H5''	1.68	0.55
1:A:516:A:P	37:A:5618:HOH:O	2.64	0.55
1:A:545:G:C8	1:A:545:G:H5'	2.37	0.55
1:A:671:A:O2'	1:A:672:G:H2'	2.07	0.55
37:A:6996:HOH:O	3:C:211:LYS:CG	2.52	0.55
4:D:24:PRO:HG2	4:D:204:GLY:HA2	1.88	0.55
4:D:280:VAL:CG1	4:D:334:SER:HA	2.36	0.55
10:J:75:SER:C	10:J:79:ALA:HB2	2.27	0.55
14:N:149:TRP:O	14:N:152:ARG:HG2	2.06	0.55
15:O:82:TYR:CD2	15:O:82:TYR:C	2.80	0.55
23:W:64:GLY:O	23:W:65:ASP:CB	2.55	0.55
25:Y:43:VAL:HG12	25:Y:44:ASP:N	2.22	0.55
26:Z:99:ALA:HB2	26:Z:233:TYR:CE2	2.42	0.55
28:2:25:LYS:HE2	37:3:7213:HOH:O	2.06	0.55
1:A:1825:U:O4'	1:A:1999:C:H5''	2.06	0.55
1:A:1862:C:H1'	37:A:7195:HOH:O	2.07	0.55
1:A:2897:C:O2'	1:A:2898:G:H5'	2.07	0.55
4:D:320:GLN:HG3	4:D:321:PRO:HD2	1.88	0.55
10:J:71:TYR:C	10:J:73:GLN:N	2.58	0.55
15:O:22:GLN:HG2	15:O:26:LEU:HD22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:44:ASN:OD1	16:P:65:LEU:HB2	2.07	0.55
37:A:3051:HOH:O	19:S:83:LYS:HB3	2.06	0.55
26:Z:144:ARG:CZ	37:Z:8610:HOH:O	2.54	0.55
1:A:2326:U:H4'	1:A:2412:G:C4'	2.37	0.55
4:D:140:LEU:HD23	37:D:8581:HOH:O	2.07	0.55
8:H:100:ASP:HB3	37:H:5691:HOH:O	2.07	0.55
1:A:2365:G:H4'	18:R:45:PRO:O	2.06	0.55
1:A:1205:U:C2'	1:A:1206:U:H5'	2.32	0.55
1:A:1653:A:N6	37:A:4237:HOH:O	2.40	0.55
1:A:694:A:H2'	1:A:695:C:H5'	1.89	0.55
4:D:190:MET:HE2	4:D:194:PHE:HD1	1.72	0.55
4:D:1:PRO:O	4:D:2:GLN:HB2	2.07	0.55
7:G:11:VAL:CG1	7:G:12:ASP:N	2.69	0.55
1:A:2404:G:O3'	37:A:6569:HOH:O	2.18	0.54
1:A:2679:G:H2'	1:A:2681:A:OP2	2.07	0.54
3:C:105:VAL:HG12	3:C:106:CYS:N	2.22	0.54
4:D:314:ALA:HB3	4:D:317:PRO:HG3	1.89	0.54
4:D:66:GLU:OE1	4:D:328:ARG:HD2	2.07	0.54
12:L:37:TYR:CD2	37:L:7169:HOH:O	2.53	0.54
1:A:902:G:N7	13:M:18:HIS:HD2	2.05	0.54
17:Q:13:VAL:HG11	17:Q:40:VAL:HG11	1.87	0.54
26:Z:107:PRO:HB3	26:Z:182:PHE:CD2	2.43	0.54
29:3:18:ASN:HD21	29:3:40:ARG:H	1.53	0.54
1:A:2760:C:H5''	37:A:5303:HOH:O	2.07	0.54
1:A:2821:C:H4'	4:D:116:PRO:HB3	1.88	0.54
8:H:91:VAL:CG1	8:H:92:GLY:H	2.17	0.54
14:N:154:ARG:HG3	37:N:8613:HOH:O	2.07	0.54
1:A:1159:G:H21	1:A:1189:A:H8	1.53	0.54
1:A:1269:G:H2'	1:A:1270:U:C6	2.43	0.54
1:A:1562:C:O2	1:A:1562:C:H2'	2.07	0.54
1:A:1882:C:O2'	1:A:2012:U:OP2	2.23	0.54
1:A:281:U:O2'	1:A:282:C:H5'	2.08	0.54
1:A:401:C:P	37:A:5766:HOH:O	2.66	0.54
1:A:739:G:N7	37:A:7523:HOH:O	2.38	0.54
31:A:9001:SPR:H6A3	31:A:9001:SPR:C2B	2.22	0.54
5:E:115:LEU:HD21	5:E:243:VAL:HG13	1.88	0.54
6:F:50:VAL:O	6:F:71:ALA:HA	2.07	0.54
8:H:21:GLU:O	8:H:24:ARG:HG3	2.06	0.54
21:U:106:GLU:HG3	37:U:4913:HOH:O	2.06	0.54
23:W:49:LEU:O	23:W:53:ILE:HG13	2.06	0.54
1:A:1164:U:O4'	1:A:1165:G:OP1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:G:H2'	14:N:192:ALA:HB3	1.88	0.54
5:E:235:PHE:HE2	5:E:243:VAL:HG21	1.72	0.54
1:A:1470:A:OP1	14:N:93:ARG:HD2	2.08	0.54
15:O:91:ARG:HG3	15:O:186:LEU:HD23	1.89	0.54
27:1:39:CYS:HA	27:1:47:LEU:CD1	2.34	0.54
1:A:2359:G:H3'	37:A:5662:HOH:O	2.08	0.54
4:D:305:ASP:O	4:D:306:LYS:CB	2.55	0.54
5:E:129:HIS:HE1	5:E:231:ARG:HA	1.72	0.54
6:F:170:TYR:O	6:F:171:ASP:HB3	2.06	0.54
10:J:147:ARG:HA	10:J:150:LYS:HZ2	1.73	0.54
10:J:71:TYR:O	10:J:73:GLN:N	2.40	0.54
14:N:37:VAL:HG13	14:N:63:VAL:HG11	1.90	0.54
1:A:2894:C:O2'	1:A:2895:C:H5'	2.07	0.54
7:G:69:ILE:HA	7:G:72:MET:HE3	1.90	0.54
10:J:136:VAL:HG22	10:J:137:ASN:O	2.07	0.54
13:M:104:ASP:O	13:M:105:TYR:HB3	2.05	0.54
15:O:155:GLU:O	15:O:156:GLU:HG3	2.08	0.54
24:X:6:GLN:HB2	24:X:26:ILE:CD1	2.36	0.54
28:2:8:GLN:HE22	28:2:11:LYS:HZ2	1.56	0.54
1:A:1330:A:H5''	1:A:1331:A:OP2	2.08	0.54
1:A:1847:A:OP1	3:C:175:LYS:NZ	2.41	0.54
1:A:204:A:H2'	1:A:205:U:H5'	1.89	0.54
1:A:661:G:C5	1:A:686:A:C2	2.95	0.54
4:D:75:GLU:C	4:D:77:PRO:HD3	2.28	0.54
5:E:154:VAL:O	5:E:158:GLU:HG3	2.07	0.54
7:G:32:ARG:O	7:G:33:LEU:HD23	2.07	0.54
10:J:13:ALA:HA	10:J:91:HIS:HE1	1.72	0.54
19:S:111:ILE:HG23	19:S:145:LEU:HD11	1.90	0.54
22:V:13:ILE:HG12	22:V:32:CYS:HB2	1.89	0.54
22:V:52:THR:CG2	22:V:54:THR:HB	2.38	0.54
26:Z:112:GLU:CD	26:Z:115:ARG:NH1	2.61	0.54
1:A:1887:U:OP1	27:1:21:LYS:HG3	2.07	0.54
1:A:470:U:O2'	28:2:16:HIS:HD2	1.90	0.54
1:A:1878:G:C1'	37:A:6090:HOH:O	2.54	0.54
1:A:2082:G:O2'	1:A:2083:A:H5'	2.07	0.54
1:A:541:C:O2'	1:A:542:A:H5''	2.07	0.54
1:A:775:G:OP1	28:2:16:HIS:HE1	1.91	0.54
3:C:175:LYS:HE2	37:C:8579:HOH:O	2.07	0.54
4:D:56:ASP:OD1	4:D:322:ARG:HB3	2.07	0.54
1:A:338:C:H4'	5:E:174:ILE:HD12	1.86	0.54
6:F:163:VAL:HA	37:F:6326:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:139:ASP:N	10:J:140:PRO:CD	2.69	0.54
14:N:123:ASP:C	14:N:123:ASP:OD1	2.46	0.54
1:A:1268:C:H2'	1:A:1269:G:H8	1.73	0.54
6:F:10:PHE:CG	6:F:11:HIS:N	2.76	0.54
10:J:26:LYS:HD3	10:J:89:PRO:CG	2.38	0.54
14:N:154:ARG:HD3	37:N:8643:HOH:O	2.07	0.54
37:A:5766:HOH:O	14:N:170:CYS:SG	2.59	0.54
15:O:182:GLY:N	37:O:8572:HOH:O	2.39	0.54
1:A:1266:U:H4'	26:Z:115:ARG:HH21	1.71	0.54
30:4:48:ASN:ND2	30:4:50:GLY:H	2.06	0.54
1:A:1695:G:C6	1:A:1696:U:C4	2.96	0.54
1:A:921:G:H4'	1:A:924:G:N1	2.23	0.54
1:A:963:C:O5'	1:A:963:C:H6	1.91	0.54
3:C:105:VAL:HG11	3:C:154:ALA:HB1	1.88	0.54
3:C:171:LYS:NZ	37:C:8526:HOH:O	2.23	0.54
4:D:251:VAL:HG23	4:D:252:PRO:HD2	1.89	0.54
4:D:55:ASN:HB3	4:D:64:GLY:H	1.73	0.54
6:F:154:LYS:H	6:F:154:LYS:CD	2.15	0.54
11:K:22:VAL:O	11:K:26:VAL:HG23	2.08	0.54
22:V:11:THR:HG22	22:V:53:ASP:OD2	2.08	0.54
8:H:47:LEU:HB2	8:H:108:LEU:HD11	1.91	0.53
10:J:139:ASP:H	10:J:140:PRO:HD3	1.68	0.53
13:M:104:ASP:HB3	37:M:8564:HOH:O	2.08	0.53
14:N:122:GLU:OE2	14:N:127:LYS:HE2	2.08	0.53
24:X:26:ILE:O	24:X:26:ILE:CG1	2.56	0.53
26:Z:187:VAL:HB	37:Z:8570:HOH:O	2.08	0.53
1:A:1007:A:H2'	10:J:19:TYR:CZ	2.44	0.53
1:A:119:A:H2'	1:A:120:A:H5''	1.89	0.53
1:A:558:C:H2'	1:A:559:U:H5'	1.90	0.53
1:A:922:A:N7	1:A:2281:C:H5'	2.23	0.53
8:H:99:THR:O	8:H:99:THR:HG23	2.07	0.53
10:J:130:HIS:CG	10:J:133:ILE:HD11	2.43	0.53
10:J:26:LYS:HD2	10:J:28:ILE:CG1	2.37	0.53
11:K:107:ASN:C	11:K:107:ASN:HD22	2.11	0.53
13:M:133:VAL:HB	37:M:8558:HOH:O	2.08	0.53
22:V:49:LEU:CD1	37:V:3805:HOH:O	2.56	0.53
27:1:39:CYS:CB	27:1:47:LEU:HD21	2.37	0.53
1:A:1176:C:H1'	37:A:3905:HOH:O	2.08	0.53
1:A:1636:G:O2'	1:A:1637:A:H5'	2.08	0.53
1:A:39:G:N2	1:A:444:C:C2	2.77	0.53
2:B:3041:C:C6	6:F:50:VAL:HG21	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:117:LYS:HB2	37:J:8326:HOH:O	2.08	0.53
11:K:4:ALA:N	37:K:8572:HOH:O	2.41	0.53
16:P:59:VAL:HG23	16:P:111:VAL:HG23	1.89	0.53
22:V:47:ARG:CG	37:V:4381:HOH:O	2.55	0.53
27:1:46:LYS:O	27:1:57:CYS:HA	2.08	0.53
1:A:1308:A:H5'	37:A:6904:HOH:O	2.08	0.53
1:A:154:C:H2'	1:A:155:C:C6	2.42	0.53
1:A:2073:G:OP2	1:A:2490:A:H5'	2.08	0.53
1:A:553:G:O4'	1:A:1325:G:H5'	2.08	0.53
4:D:275:GLY:O	4:D:291:ASP:HA	2.08	0.53
6:F:93:LEU:HB3	6:F:97:GLN:OE1	2.09	0.53
1:A:2055:A:H5'	19:S:134:SER:HB2	1.90	0.53
20:T:81:ILE:HG23	37:T:8336:HOH:O	2.07	0.53
21:U:38:ARG:HG3	21:U:38:ARG:NH1	2.23	0.53
24:X:122:ARG:HH22	24:X:154:ARG:C	2.12	0.53
1:A:2459:G:OP2	30:4:64:LYS:HD2	2.07	0.53
1:A:657:G:OP1	5:E:27:ARG:NH2	2.29	0.53
37:A:9544:HOH:O	4:D:267:LYS:HD3	2.07	0.53
37:A:6290:HOH:O	6:F:55:LYS:HB2	2.08	0.53
7:G:21:THR:HG23	7:G:30:THR:OG1	2.09	0.53
8:H:39:SER:HB3	8:H:45:ALA:HB2	1.89	0.53
8:H:13:GLU:OE2	8:H:78:GLU:HG2	2.09	0.53
10:J:45:GLN:HG3	10:J:135:TRP:NE1	2.23	0.53
11:K:107:ASN:HD22	11:K:109:TYR:H	1.54	0.53
14:N:154:ARG:NE	37:N:8643:HOH:O	2.42	0.53
14:N:87:MET:SD	37:N:8533:HOH:O	2.58	0.53
1:A:396:U:OP2	30:4:38:ARG:NH1	2.42	0.53
1:A:1189:A:H1'	1:A:1209:C:C1'	2.39	0.53
1:A:1209:C:H2'	1:A:1210:G:C8	2.40	0.53
1:A:1250:C:O2'	1:A:1251:C:H5'	2.08	0.53
1:A:2121:G:C2'	1:A:2122:C:H5'	2.38	0.53
1:A:2414:A:H2'	1:A:2415:A:C8	2.43	0.53
3:C:217:ARG:CG	3:C:217:ARG:HH11	2.21	0.53
6:F:23:VAL:CG2	6:F:23:VAL:O	2.55	0.53
14:N:87:MET:HB2	14:N:91:ILE:CD1	2.39	0.53
17:Q:103:THR:O	17:Q:107:GLU:HG3	2.09	0.53
17:Q:115:SER:O	17:Q:117:SER:N	2.42	0.53
1:A:1527:A:H1'	1:A:1528:A:C8	2.43	0.53
1:A:2613:G:O2'	1:A:2614:C:H5'	2.08	0.53
1:A:2676:C:H4'	11:K:70:PHE:HE1	1.71	0.53
3:C:109:GLU:HG2	3:C:116:GLY:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:140:LEU:HB3	3:C:141:PRO:HD2	1.91	0.53
3:C:200:PRO:HG2	3:C:225:VAL:HG21	1.90	0.53
8:H:50:VAL:CG2	8:H:63:ILE:HG21	2.39	0.53
1:A:1164:U:C4'	1:A:1165:G:OP1	2.50	0.53
1:A:1166:A:H1'	1:A:1192:A:N1	2.23	0.53
1:A:1947:G:N2	1:A:1966:U:C2	2.77	0.53
1:A:329:A:OP1	5:E:205:ARG:NE	2.37	0.53
5:E:236:THR:O	5:E:237:GLU:C	2.47	0.53
7:G:20:ILE:HD12	7:G:33:LEU:HD12	1.90	0.53
14:N:61:ILE:N	14:N:61:ILE:HD12	2.24	0.53
22:V:14:GLU:OE1	22:V:15:PRO:HD2	2.09	0.53
25:Y:73:ARG:O	25:Y:85:VAL:HG13	2.09	0.53
1:A:2634:G:O2'	1:A:2635:A:H5'	2.09	0.53
3:C:191:GLY:HA2	3:C:194:MET:HE3	1.90	0.53
37:A:7435:HOH:O	5:E:188:ARG:HD2	2.09	0.53
1:A:449:A:N7	5:E:43:LYS:HG2	2.23	0.53
19:S:115:ALA:O	19:S:143:VAL:HG23	2.09	0.53
19:S:18:LEU:HG	19:S:91:LEU:HD13	1.90	0.53
21:U:48:VAL:HG22	21:U:97:ARG:O	2.09	0.53
1:A:1185:U:H5'	37:A:7445:HOH:O	2.08	0.53
1:A:1525:G:H5'	1:A:1526:A:OP2	2.09	0.53
1:A:2405:C:P	37:A:6569:HOH:O	2.66	0.53
4:D:82:VAL:HG12	4:D:82:VAL:O	2.09	0.53
4:D:7:ARG:CD	4:D:9:GLY:O	2.57	0.53
7:G:15:GLN:HG2	7:G:19:ASP:O	2.09	0.53
15:O:47:LEU:HD13	15:O:97:VAL:HG11	1.91	0.53
17:Q:58:SER:HB3	37:Q:4744:HOH:O	2.08	0.53
24:X:90:TYR:CE2	24:X:99:ALA:HB2	2.44	0.53
1:A:1667:A:H2'	1:A:1668:U:C6	2.44	0.52
1:A:2326:U:H4'	1:A:2412:G:H4'	1.90	0.52
3:C:164:ARG:NE	37:C:8593:HOH:O	2.41	0.52
7:G:43:ASP:HA	37:G:5864:HOH:O	2.08	0.52
1:A:1733:A:C6	1:A:1734:C:C2	2.97	0.52
1:A:88:G:H8	1:A:88:G:H5'	1.74	0.52
3:C:37:VAL:HG22	37:C:8600:HOH:O	2.09	0.52
14:N:115:LEU:C	14:N:115:LEU:HD13	2.30	0.52
1:A:656:G:OP2	16:P:37:ARG:HD2	2.09	0.52
17:Q:18:LYS:O	17:Q:21:VAL:HG22	2.08	0.52
17:Q:38:GLU:HA	17:Q:41:ARG:HH11	1.73	0.52
24:X:38:THR:HG22	24:X:39:ASP:N	2.25	0.52
30:4:11:CYS:HB2	30:4:20:HIS:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1041:U:C2'	1:A:1042:U:H5'	2.39	0.52
1:A:1200:A:C4'	37:A:7318:HOH:O	2.57	0.52
1:A:1375:A:O2'	1:A:1376:G:H5'	2.10	0.52
1:A:1490:G:OP2	37:A:3628:HOH:O	2.18	0.52
1:A:2735:U:H2'	1:A:2736:U:C6	2.45	0.52
1:A:820:G:H5'	1:A:821:U:H5'	1.91	0.52
2:B:3020:G:H3'	37:B:2984:HOH:O	2.09	0.52
2:B:3092:G:H2'	2:B:3093:A:C8	2.45	0.52
5:E:1:MET:HG2	5:E:2:GLN:N	2.23	0.52
6:F:64:ARG:O	6:F:67:ASP:OD2	2.26	0.52
10:J:117:LYS:O	10:J:119:VAL:HG13	2.09	0.52
14:N:39:ARG:HA	14:N:63:VAL:HG22	1.92	0.52
15:O:170:GLU:O	15:O:174:GLU:HG3	2.09	0.52
15:O:5:ARG:HG3	18:R:18:PRO:CB	2.39	0.52
37:A:3737:HOH:O	21:U:9:LYS:HD3	2.09	0.52
24:X:137:GLN:HE21	24:X:141:HIS:CE1	2.20	0.52
28:2:37:CYS:SG	28:2:39:PHE:HB2	2.49	0.52
1:A:1197:G:N2	37:A:6202:HOH:O	2.42	0.52
1:A:628:A:C8	1:A:2071:C:N4	2.78	0.52
1:A:256:C:H2'	1:A:257:G:O4'	2.09	0.52
1:A:2787:C:H5	37:A:4602:HOH:O	1.91	0.52
1:A:738:G:H3'	37:A:7019:HOH:O	2.08	0.52
4:D:307:ARG:HH11	4:D:307:ARG:CG	2.22	0.52
10:J:65:ARG:NH1	37:J:8374:HOH:O	2.42	0.52
12:L:34:VAL:HG22	12:L:47:ALA:HB2	1.90	0.52
27:1:30:GLU:HB3	27:1:34:LYS:HE3	1.92	0.52
1:A:1079:A:N1	1:A:2068:G:O2'	2.39	0.52
1:A:1127:C:C5	1:A:1128:U:C4	2.97	0.52
1:A:1166:A:H61	1:A:1180:U:H3	1.55	0.52
2:B:3044:A:H1'	6:F:76:ARG:NH2	2.24	0.52
1:A:2780:C:H1'	7:G:143:GLN:NE2	2.24	0.52
7:G:23:GLU:HG2	7:G:28:SER:CB	2.40	0.52
7:G:7:ILE:HD11	7:G:11:VAL:O	2.09	0.52
13:M:143:THR:CG2	13:M:144:ASP:H	2.22	0.52
37:A:9079:HOH:O	14:N:172:GLY:HA2	2.09	0.52
27:1:59:HIS:HA	37:1:8444:HOH:O	2.10	0.52
1:A:381:G:H5''	37:A:4291:HOH:O	2.08	0.52
1:A:82:C:OP1	21:U:67:LEU:HB2	2.09	0.52
1:A:1861:C:H4'	3:C:6:GLY:O	2.10	0.52
6:F:19:GLU:HG3	37:F:6165:HOH:O	2.09	0.52
7:G:11:VAL:HG12	7:G:12:ASP:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:101:ASN:O	12:L:102:GLU:CB	2.58	0.52
13:M:24:ALA:HB2	13:M:30:ARG:HD2	1.91	0.52
14:N:38:VAL:C	14:N:63:VAL:HG13	2.30	0.52
37:A:4332:HOH:O	16:P:37:ARG:HG3	2.10	0.52
1:A:2768:A:O2'	1:A:2769:C:H5'	2.10	0.52
1:A:432:G:O2'	1:A:433:C:H5'	2.09	0.52
1:A:921:G:H4'	1:A:924:G:C6	2.45	0.52
6:F:91:ALA:HB1	37:F:5198:HOH:O	2.10	0.52
8:H:28:ALA:CB	8:H:99:THR:HG23	2.40	0.52
10:J:132:PHE:O	10:J:133:ILE:HD13	2.10	0.52
10:J:46:VAL:HG12	10:J:146:TRP:CZ3	2.43	0.52
24:X:13:MET:HE1	24:X:18:GLN:HA	1.90	0.52
29:3:48:ASP:O	29:3:49:GLU:HB2	2.10	0.52
30:4:51:LYS:NZ	37:4:8531:HOH:O	2.41	0.52
1:A:1180:U:H2'	1:A:1181:A:O4'	2.10	0.52
1:A:1205:U:C2'	1:A:1206:U:C5'	2.88	0.52
1:A:2123:A:H5'	14:N:89:ASN:ND2	2.25	0.52
1:A:2435:U:H1'	37:A:5404:HOH:O	2.09	0.52
1:A:316:A:N3	1:A:336:G:O2'	2.41	0.52
2:B:3006:C:C5'	15:O:37:ARG:HH12	2.19	0.52
5:E:104:ASP:O	5:E:108:GLN:HG3	2.09	0.52
6:F:49:PRO:HG3	37:F:5828:HOH:O	2.08	0.52
8:H:91:VAL:CG1	8:H:92:GLY:N	2.70	0.52
10:J:53:PRO:HG3	10:J:127:GLY:H	1.75	0.52
14:N:115:LEU:HD13	14:N:116:ASN:HB2	1.91	0.52
15:O:110:THR:HB	15:O:113:SER:OG	2.10	0.52
17:Q:98:ILE:HD13	17:Q:98:ILE:O	2.10	0.52
27:1:47:LEU:CD2	27:1:57:CYS:HB2	2.40	0.52
1:A:1398:G:H2'	1:A:1399:A:C8	2.45	0.52
1:A:564:G:H1'	37:A:6280:HOH:O	2.10	0.52
4:D:27:ASN:HD22	4:D:27:ASN:H	1.57	0.52
6:F:23:VAL:HG21	6:F:45:THR:HG21	1.91	0.52
14:N:59:GLY:CA	14:N:141:ILE:HD11	2.39	0.52
1:A:105:G:O2'	1:A:106:A:H5'	2.10	0.52
1:A:1189:A:O2'	1:A:1208:C:H2'	2.10	0.52
1:A:2256:G:H2'	1:A:2257:G:C5'	2.40	0.52
1:A:151:A:C2	1:A:442:A:C8	2.98	0.52
1:A:820:G:C5	3:C:171:LYS:HB2	2.45	0.52
3:C:88:ILE:HD13	3:C:100:PRO:CD	2.40	0.52
10:J:47:GLU:CB	10:J:133:ILE:HD13	2.34	0.52
10:J:56:ILE:HG21	10:J:61:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:A:4675:HOH:O	27:1:54:ILE:HD12	2.09	0.51
1:A:2638:G:H5'	37:A:4906:HOH:O	2.09	0.51
1:A:283:U:H5''	1:A:284:C:OP2	2.11	0.51
4:D:14:GLY:HA2	4:D:15:PRO:C	2.30	0.51
5:E:109:LEU:HD12	5:E:109:LEU:O	2.10	0.51
9:I:16:LYS:O	9:I:20:VAL:HG23	2.10	0.51
12:L:10:GLN:NE2	12:L:10:GLN:N	2.40	0.51
15:O:87:LEU:CD1	15:O:186:LEU:HD21	2.34	0.51
17:Q:143:ALA:HA	37:Q:5521:HOH:O	2.08	0.51
18:R:40:HIS:HD2	18:R:60:THR:OG1	1.93	0.51
24:X:28:HIS:HD2	24:X:31:HIS:CE1	2.27	0.51
1:A:2468:A:H61	30:4:48:ASN:ND2	2.03	0.51
1:A:2672:C:H1'	37:D:8637:HOH:O	2.10	0.51
1:A:2812:A:C2	1:A:2814:A:N6	2.74	0.51
10:J:150:LYS:HE2	37:J:8368:HOH:O	2.09	0.51
10:J:39:GLY:O	10:J:41:THR:N	2.44	0.51
12:L:55:VAL:CG1	12:L:56:SER:N	2.74	0.51
14:N:59:GLY:C	14:N:141:ILE:HD11	2.31	0.51
14:N:67:ILE:HG21	14:N:97:ILE:HG23	1.93	0.51
16:P:42:GLU:HB2	37:P:2176:HOH:O	2.09	0.51
1:A:2429:A:H2'	1:A:2430:A:C8	2.45	0.51
1:A:514:G:OP1	1:A:514:G:H2'	2.10	0.51
3:C:8:ARG:NH1	37:C:8554:HOH:O	2.30	0.51
4:D:79:MET:HE3	4:D:144:THR:HG21	1.93	0.51
5:E:246:ARG:HH11	5:E:246:ARG:HB3	1.73	0.51
5:E:85:LYS:CE	37:E:8328:HOH:O	2.55	0.51
21:U:69:LYS:O	21:U:71:VAL:HG23	2.11	0.51
25:Y:9:VAL:HG13	25:Y:88:GLU:OE2	2.10	0.51
37:A:4163:HOH:O	26:Z:186:ARG:HD2	2.10	0.51
26:Z:186:ARG:NH1	26:Z:186:ARG:HG2	2.22	0.51
1:A:371:U:H2'	1:A:372:A:C8	2.44	0.51
1:A:603:A:H4'	1:A:604:G:O5'	2.09	0.51
3:C:132:ASP:OD1	3:C:133:ARG:N	2.42	0.51
4:D:307:ARG:HH11	4:D:307:ARG:CB	2.23	0.51
5:E:162:VAL:HG12	5:E:162:VAL:O	2.09	0.51
22:V:9:CYS:SG	37:V:6796:HOH:O	2.59	0.51
24:X:119:HIS:HD2	24:X:120:PRO:O	1.92	0.51
26:Z:142:SER:OG	37:Z:8610:HOH:O	2.18	0.51
27:1:61:GLY:HA3	37:1:8429:HOH:O	2.09	0.51
37:A:7116:HOH:O	28:2:1:THR:HB	2.09	0.51
1:A:1450:C:C4'	1:A:1451:C:OP2	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1654:U:H2'	3:C:47:HIS:CD2	2.46	0.51
1:A:2284:G:H5'	37:A:9437:HOH:O	2.11	0.51
1:A:2392:C:N3	37:A:4825:HOH:O	2.34	0.51
1:A:2408:A:H2	37:A:3080:HOH:O	1.92	0.51
1:A:2466:G:C5'	37:A:3625:HOH:O	2.50	0.51
1:A:2478:U:O2'	1:A:2479:A:H5'	2.10	0.51
1:A:2724:U:H2'	1:A:2725:G:O4'	2.10	0.51
1:A:424:C:H2'	1:A:425:U:C6	2.44	0.51
3:C:36:ASP:HA	3:C:83:GLY:HA3	1.93	0.51
4:D:63:GLU:HG3	4:D:63:GLU:O	2.11	0.51
6:F:11:HIS:C	6:F:13:MET:H	2.13	0.51
37:A:4543:HOH:O	14:N:83:SER:HA	2.10	0.51
16:P:96:VAL:HA	37:P:4258:HOH:O	2.10	0.51
20:T:29:ASP:OD1	20:T:31:ARG:NH1	2.44	0.51
21:U:48:VAL:CG1	21:U:96:VAL:HG13	2.41	0.51
25:Y:25:ARG:CD	37:Y:3861:HOH:O	2.50	0.51
1:A:1850:U:H2'	1:A:1851:G:H8	1.75	0.51
1:A:2269:C:H2'	1:A:2270:G:H5'	1.92	0.51
4:D:119:HIS:O	4:D:121:PRO:HD3	2.10	0.51
4:D:144:THR:HG22	4:D:145:HIS:N	2.25	0.51
6:F:65:GLU:HG3	37:F:6752:HOH:O	2.10	0.51
12:L:75:ARG:CZ	37:L:4172:HOH:O	2.58	0.51
14:N:114:VAL:HB	14:N:159:THR:HG23	1.93	0.51
14:N:55:LYS:HB2	14:N:60:ILE:CD1	2.41	0.51
17:Q:7:LYS:CD	17:Q:21:VAL:CG2	2.89	0.51
1:A:538:C:OP2	26:Z:134:HIS:HE1	1.93	0.51
1:A:1669:A:H2'	1:A:1670:G:H8	1.75	0.51
1:A:2315:C:H4'	1:A:2425:A:C6	2.46	0.51
4:D:43:GLY:O	4:D:308:LEU:HD12	2.11	0.51
8:H:101:ALA:HB2	8:H:108:LEU:HD22	1.92	0.51
17:Q:115:SER:HG	17:Q:118:GLN:HG3	1.74	0.51
1:A:56:G:H5''	23:W:50:ARG:HH12	1.74	0.51
27:1:26:VAL:O	27:1:30:GLU:HG3	2.10	0.51
27:1:42:CYS:SG	27:1:43:GLY:N	2.84	0.51
1:A:1189:A:H1'	1:A:1209:C:O4'	2.11	0.51
1:A:1299:G:O6	13:M:6:ARG:HD3	2.11	0.51
1:A:1329:A:N1	34:A:8513:CL:CL	2.81	0.51
4:D:103:ASP:HB2	37:D:8593:HOH:O	2.10	0.51
4:D:146:THR:O	4:D:159:PRO:HB3	2.10	0.51
6:F:59:GLY:C	6:F:61:PHE:H	2.14	0.51
11:K:6:PHE:O	11:K:8:ALA:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:13:HIS:NE2	37:M:8522:HOH:O	2.35	0.51
17:Q:21:VAL:O	17:Q:21:VAL:HG23	2.09	0.51
1:A:2247:C:H5'	37:A:7322:HOH:O	2.11	0.51
1:A:2769:C:O2'	1:A:2770:G:H5'	2.11	0.51
1:A:2756:U:H3	1:A:2896:A:H2	1.55	0.51
1:A:382:U:C5	1:A:406:G:N2	2.78	0.51
1:A:489:A:C8	21:U:82:THR:CG2	2.94	0.51
4:D:2:GLN:NE2	37:D:8622:HOH:O	2.44	0.51
5:E:212:VAL:HG23	5:E:212:VAL:O	2.11	0.51
6:F:57:THR:HG23	6:F:63:ILE:CB	2.41	0.51
7:G:68:HIS:O	7:G:72:MET:HG3	2.11	0.51
13:M:21:ARG:N	37:M:8535:HOH:O	2.44	0.51
24:X:122:ARG:HH11	24:X:122:ARG:CG	2.15	0.51
26:Z:154:ARG:NH1	26:Z:155:ARG:HG3	2.26	0.51
1:A:113:A:H3'	1:A:114:A:C5'	2.41	0.51
1:A:1192:A:H3'	1:A:1193:A:H5'	1.92	0.51
1:A:461:C:H2'	37:A:3974:HOH:O	2.11	0.51
4:D:297:VAL:HB	37:D:8606:HOH:O	2.11	0.51
7:G:157:LYS:NZ	37:G:2401:HOH:O	2.44	0.51
10:J:57:ARG:HG3	10:J:57:ARG:HH11	1.76	0.51
10:J:35:ASN:ND2	10:J:80:ASN:HA	2.26	0.51
1:A:1119:G:C8	11:K:52:GLN:NE2	2.79	0.51
12:L:29:LEU:HB3	12:L:55:VAL:CG1	2.28	0.51
12:L:45:PRO:HB2	37:L:7169:HOH:O	2.11	0.51
29:3:40:ARG:HH11	29:3:40:ARG:HG2	1.76	0.50
1:A:1209:C:C2	1:A:1210:G:C8	2.99	0.50
1:A:154:C:P	14:N:188:ARG:HH12	2.34	0.50
1:A:2321:A:O2'	1:A:2322:U:H3'	2.11	0.50
1:A:639:A:C2	1:A:1363:G:C2	2.99	0.50
3:C:191:GLY:HA2	3:C:194:MET:CE	2.41	0.50
4:D:16:ARG:NE	37:D:8556:HOH:O	2.28	0.50
4:D:162:MET:CE	4:D:310:ARG:HD3	2.41	0.50
6:F:44:ILE:HG12	6:F:83:PHE:HE1	1.74	0.50
8:H:47:LEU:HD22	8:H:108:LEU:CD1	2.41	0.50
12:L:109:LEU:HD13	12:L:113:ILE:HD11	1.93	0.50
12:L:34:VAL:HB	37:L:7169:HOH:O	2.11	0.50
16:P:98:LEU:O	16:P:102:ILE:HG13	2.11	0.50
21:U:75:GLU:O	21:U:76:ASP:HB2	2.10	0.50
24:X:48:VAL:O	24:X:48:VAL:CG1	2.58	0.50
1:A:1041:U:H2'	1:A:1042:U:C5'	2.41	0.50
1:A:1200:A:H4'	37:A:7318:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:A:H1'	1:A:1209:C:H1'	1.93	0.50
1:A:790:A:H1'	1:A:1710:A:H2'	1.92	0.50
1:A:2912:C:OP2	37:A:5528:HOH:O	2.20	0.50
1:A:344:C:H2'	1:A:345:G:O4'	2.10	0.50
1:A:445:U:H1'	37:A:7314:HOH:O	2.12	0.50
8:H:58:GLU:OE1	14:N:27:ARG:NH2	2.41	0.50
11:K:130:VAL:HG12	11:K:131:THR:N	2.24	0.50
24:X:38:THR:HG22	24:X:39:ASP:H	1.77	0.50
1:A:1353:C:OP2	37:A:4516:HOH:O	2.19	0.50
1:A:1690:C:C5	1:A:1692:C:C4	2.99	0.50
1:A:1700:C:OP2	37:A:6004:HOH:O	2.19	0.50
1:A:204:A:C2'	1:A:205:U:H5'	2.41	0.50
1:A:2064:U:H4'	1:A:2653:A:P	2.51	0.50
3:C:211:LYS:HB3	3:C:212:PRO:CD	2.35	0.50
5:E:46:TYR:CE2	5:E:98:ARG:NH1	2.79	0.50
7:G:84:MET:HE1	7:G:148:ILE:HD12	1.93	0.50
7:G:15:GLN:NE2	7:G:40:VAL:O	2.44	0.50
1:A:244:C:OP2	8:H:38:LYS:HE3	2.12	0.50
37:A:3641:HOH:O	14:N:79:LYS:HD2	2.11	0.50
21:U:20:HIS:ND1	21:U:41:ARG:NE	2.54	0.50
25:Y:71:ARG:CD	37:Y:2171:HOH:O	2.59	0.50
30:4:57:GLY:HA2	37:4:8528:HOH:O	2.10	0.50
1:A:1370:G:OP1	19:S:64:SER:OG	2.29	0.50
1:A:1787:C:H4'	1:A:2883:A:O4'	2.11	0.50
1:A:2271:G:H2'	1:A:2271:G:N3	2.27	0.50
1:A:2314:G:O2'	1:A:2315:C:H5'	2.10	0.50
1:A:2361:A:H5''	37:A:9002:HOH:O	2.11	0.50
1:A:454:U:O4	37:A:9151:HOH:O	2.19	0.50
1:A:778:C:OP1	37:A:5516:HOH:O	2.20	0.50
3:C:51:ARG:HB2	37:C:8610:HOH:O	2.11	0.50
5:E:234:VAL:HG22	5:E:234:VAL:O	2.11	0.50
6:F:58:VAL:HG12	6:F:59:GLY:N	2.26	0.50
10:J:47:GLU:CB	10:J:133:ILE:CD1	2.86	0.50
10:J:166:ASN:N	10:J:166:ASN:ND2	2.59	0.50
14:N:84:LYS:O	14:N:87:MET:HG2	2.10	0.50
15:O:37:ARG:NH2	37:O:8534:HOH:O	2.44	0.50
28:2:28:HIS:CE1	28:2:31:LYS:HE2	2.47	0.50
1:A:2464:C:H5''	1:A:2465:A:OP1	2.11	0.50
1:A:2694:A:H4'	7:G:91:PHE:HE1	1.76	0.50
5:E:118:THR:CG2	5:E:137:PRO:HB3	2.42	0.50
6:F:40:ILE:HG23	37:F:5583:HOH:O	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:134:GLU:HA	13:M:138:GLY:O	2.12	0.50
14:N:134:ILE:O	14:N:136:PRO:HD3	2.12	0.50
15:O:34:LEU:HD22	15:O:129:ILE:HD13	1.93	0.50
15:O:64:SER:C	15:O:66:LEU:H	2.15	0.50
27:1:59:HIS:CE1	37:1:8441:HOH:O	2.64	0.50
1:A:88:G:C8	29:3:28:LYS:HB2	2.46	0.50
1:A:1666:C:C2'	1:A:1667:A:C5'	2.90	0.50
3:C:36:ASP:O	3:C:38:ILE:N	2.45	0.50
6:F:11:HIS:O	6:F:12:GLU:HB3	2.10	0.50
6:F:27:ILE:HD11	6:F:37:ALA:CB	2.41	0.50
17:Q:38:GLU:HA	17:Q:41:ARG:NH1	2.27	0.50
26:Z:106:THR:HG23	26:Z:107:PRO:HD2	1.93	0.50
1:A:1834:C:H2'	1:A:1840:A:H62	1.75	0.50
1:A:424:C:H2'	1:A:425:U:H6	1.77	0.50
1:A:559:U:H2'	1:A:560:C:O4'	2.12	0.50
3:C:149:ASP:OD1	3:C:151:GLN:HB2	2.11	0.50
4:D:248:ARG:NH2	37:D:8525:HOH:O	2.44	0.50
10:J:118:PRO:HD2	37:J:8326:HOH:O	2.10	0.50
10:J:72:VAL:HG11	10:J:81:TYR:CZ	2.47	0.50
19:S:29:LYS:NZ	37:S:8541:HOH:O	2.44	0.50
24:X:88:THR:CG2	24:X:110:GLN:NE2	2.70	0.50
1:A:1845:A:OP2	3:C:190:ARG:NH1	2.43	0.50
1:A:2099:G:H1	31:A:9001:SPR:HO2A	1.54	0.50
1:A:2265:U:H2'	1:A:2266:A:C8	2.47	0.50
1:A:2505:G:C2'	1:A:2506:A:H5'	2.41	0.50
1:A:415:A:O2'	1:A:416:G:H5'	2.12	0.50
5:E:192:ILE:CG2	5:E:234:VAL:HG12	2.42	0.50
8:H:99:THR:O	8:H:100:ASP:HB2	2.11	0.50
14:N:85:ARG:NE	37:N:8519:HOH:O	2.14	0.50
21:U:19:ARG:NH1	21:U:68:ASP:O	2.44	0.50
1:A:402:U:H2'	1:A:403:C:C6	2.47	0.50
3:C:199:HIS:CD2	3:C:201:PHE:HB2	2.46	0.50
3:C:199:HIS:HD2	3:C:201:PHE:HB2	1.77	0.50
4:D:217:ARG:HG3	4:D:257:THR:CG2	2.42	0.50
7:G:80:TRP:O	7:G:134:SER:HA	2.11	0.50
10:J:62:GLU:O	10:J:66:VAL:HG23	2.11	0.50
14:N:157:LEU:HB3	14:N:160:PHE:HD1	1.77	0.50
20:T:29:ASP:CG	20:T:31:ARG:NH1	2.65	0.50
21:U:48:VAL:HG23	21:U:98:VAL:HA	1.93	0.50
21:U:9:LYS:HE3	21:U:13:ARG:HH11	1.77	0.50
1:A:1008:C:H5''	10:J:16:ARG:HH12	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1123:A:C2	1:A:1129:C:H4'	2.47	0.49
1:A:1589:G:N2	1:A:1605:G:H1'	2.27	0.49
1:A:1682:A:H5''	37:A:9436:HOH:O	2.11	0.49
1:A:2763:G:OP1	12:L:9:THR:OG1	2.16	0.49
5:E:133:ARG:NH2	37:E:8424:HOH:O	2.45	0.49
10:J:95:GLU:HB3	10:J:119:VAL:HG11	1.93	0.49
1:A:1003:U:O2	10:J:90:PHE:CZ	2.65	0.49
16:P:25:VAL:HG23	16:P:26:TRP:N	2.27	0.49
20:T:80:ARG:HG2	37:T:8336:HOH:O	2.11	0.49
37:L:7438:HOH:O	22:V:20:MET:HE1	2.12	0.49
30:4:74:CYS:SG	30:4:76:LYS:HG3	2.51	0.49
1:A:1804:A:H2'	1:A:1805:G:C8	2.46	0.49
1:A:2506:A:H1'	37:A:6024:HOH:O	2.13	0.49
1:A:2563:U:H2'	1:A:2565:C:O5'	2.11	0.49
1:A:2094:G:C2	1:A:2652:U:O2	2.65	0.49
1:A:2906:A:H5'	1:A:2907:C:O4'	2.12	0.49
1:A:453:A:H4'	1:A:455:A:N7	2.27	0.49
1:A:2719:A:C2	4:D:70:PRO:HG3	2.48	0.49
8:H:57:GLU:O	8:H:61:MET:HG3	2.12	0.49
11:K:80:LYS:HE2	11:K:98:PHE:CZ	2.47	0.49
14:N:107:ARG:NH1	37:N:8579:HOH:O	2.45	0.49
14:N:25:TRP:HE3	14:N:26:HIS:HD2	1.59	0.49
14:N:39:ARG:NE	37:N:8623:HOH:O	2.45	0.49
18:R:33:PHE:N	18:R:71:TYR:OH	2.38	0.49
20:T:57:THR:HG22	20:T:59:ASP:HB2	1.94	0.49
24:X:88:THR:CG2	24:X:89:ASP:H	2.21	0.49
26:Z:148:GLY:O	26:Z:154:ARG:HD3	2.12	0.49
29:3:18:ASN:ND2	29:3:40:ARG:H	2.10	0.49
1:A:221:G:H2'	1:A:222:A:C8	2.46	0.49
1:A:241:A:C2	1:A:378:A:H4'	2.47	0.49
1:A:92:G:H4'	23:W:44:GLY:HA3	1.93	0.49
4:D:248:ARG:O	4:D:251:VAL:CG1	2.60	0.49
4:D:88:GLU:HG3	4:D:88:GLU:O	2.11	0.49
5:E:184:ARG:HB3	37:E:8362:HOH:O	2.12	0.49
13:M:73:VAL:HG21	13:M:116:HIS:CD2	2.47	0.49
15:O:67:ALA:C	15:O:69:TYR:H	2.15	0.49
17:Q:103:THR:HA	17:Q:106:ARG:NH1	2.27	0.49
19:S:27:HIS:O	19:S:31:ILE:HG13	2.11	0.49
4:D:329:TYR:HE2	22:V:15:PRO:HG2	1.75	0.49
24:X:11:VAL:O	24:X:12:ASN:HB2	2.12	0.49
25:Y:71:ARG:HD3	37:Y:2171:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:G:H2'	1:A:175:G:N2	2.27	0.49
1:A:2559:C:H4'	37:A:7232:HOH:O	2.12	0.49
1:A:539:G:H2'	1:A:540:A:H8	1.76	0.49
2:B:3031:C:H2'	2:B:3032:G:O4'	2.12	0.49
4:D:4:SER:O	4:D:5:ARG:HB2	2.13	0.49
7:G:132:THR:HB	37:G:2227:HOH:O	2.11	0.49
7:G:31:ARG:HH12	7:G:68:HIS:CE1	2.30	0.49
10:J:144:GLU:HA	10:J:144:GLU:OE1	2.12	0.49
12:L:99:ASP:OD1	12:L:101:ASN:N	2.44	0.49
13:M:122:ALA:HB3	13:M:125:PHE:CZ	2.48	0.49
21:U:19:ARG:HD3	21:U:67:LEU:O	2.12	0.49
24:X:65:VAL:HA	24:X:68:THR:CG2	2.41	0.49
1:A:1699:C:H4'	37:A:6415:HOH:O	2.12	0.49
1:A:1768:C:H2'	1:A:1769:C:O4'	2.12	0.49
1:A:1827:G:C6	1:A:1828:G:C6	3.01	0.49
1:A:2251:G:H2'	1:A:2252:A:C8	2.48	0.49
4:D:16:ARG:NH1	37:D:8617:HOH:O	2.45	0.49
5:E:127:ARG:HG2	5:E:127:ARG:HH11	1.77	0.49
12:L:125:ALA:C	12:L:127:ALA:H	2.15	0.49
37:A:6218:HOH:O	22:V:56:ARG:HB3	2.11	0.49
1:A:1840:A:H4'	1:A:1841:C:O5'	2.13	0.49
1:A:2353:A:H4'	1:A:2354:A:O5'	2.12	0.49
6:F:86:THR:C	6:F:89:PRO:HD2	2.32	0.49
8:H:113:ASP:O	8:H:117:GLU:HG3	2.12	0.49
12:L:74:VAL:O	12:L:74:VAL:CG1	2.60	0.49
13:M:72:ASN:HB2	37:M:8580:HOH:O	2.12	0.49
37:A:7661:HOH:O	14:N:154:ARG:HB2	2.12	0.49
17:Q:27:ARG:O	17:Q:31:ILE:HG13	2.12	0.49
24:X:122:ARG:HG2	24:X:122:ARG:NH1	2.21	0.49
1:A:2577:A:H5'	37:A:7734:HOH:O	2.13	0.49
1:A:333:G:O2'	1:A:334:G:H5'	2.12	0.49
13:M:120:LEU:HD12	13:M:133:VAL:HG21	1.93	0.49
13:M:125:PHE:CZ	13:M:140:VAL:HG13	2.47	0.49
1:A:710:G:P	16:P:24:ALA:HB3	2.53	0.49
19:S:39:THR:HB	19:S:42:GLU:CG	2.41	0.49
24:X:28:HIS:CD2	24:X:31:HIS:CE1	3.01	0.49
24:X:69:ARG:HD2	24:X:117:ARG:O	2.12	0.49
1:A:470:U:H2'	1:A:471:G:O4'	2.13	0.49
1:A:536:A:H3'	37:A:5025:HOH:O	2.13	0.49
2:B:3064:C:C2'	2:B:3065:A:H5'	2.43	0.49
4:D:315:VAL:HG23	4:D:316:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:110:GLU:HA	8:H:113:ASP:OD2	2.13	0.49
9:I:64:ASN:O	9:I:68:GLU:HG3	2.13	0.49
10:J:59:ASN:ND2	10:J:59:ASN:H	2.10	0.49
1:A:926:A:H1'	13:M:38:HIS:O	2.13	0.49
13:M:65:ASP:HA	13:M:109:LEU:O	2.12	0.49
16:P:10:LEU:HD13	16:P:99:GLU:HG3	1.95	0.49
18:R:28:ARG:NH1	37:R:6206:HOH:O	2.39	0.49
19:S:39:THR:CG2	19:S:42:GLU:HG3	2.42	0.49
1:A:107:U:H2'	1:A:108:U:H5'	1.95	0.49
1:A:1609:C:H2'	1:A:1610:G:H8	1.77	0.49
1:A:2780:C:H2'	1:A:2781:U:H6	1.76	0.49
1:A:660:A:H4'	1:A:661:G:O5'	2.13	0.49
1:A:669:G:O2'	1:A:670:G:H5'	2.13	0.49
5:E:111:VAL:HB	37:E:8324:HOH:O	2.13	0.49
6:F:94:ALA:HB3	6:F:174:VAL:HA	1.95	0.49
7:G:20:ILE:HD12	7:G:33:LEU:CD1	2.43	0.49
7:G:18:LEU:HD13	7:G:34:TRP:CG	2.47	0.49
8:H:28:ALA:HB3	8:H:99:THR:HG23	1.95	0.49
10:J:129:ASN:N	10:J:129:ASN:HD22	2.10	0.49
14:N:78:ASN:ND2	37:N:8647:HOH:O	2.40	0.49
15:O:38:LYS:HD2	15:O:114:LYS:HE3	1.95	0.49
17:Q:16:VAL:HG12	17:Q:17:GLY:N	2.27	0.49
19:S:18:LEU:HB2	19:S:143:VAL:CG1	2.41	0.49
27:1:38:LYS:HE2	27:1:45:LYS:CE	2.39	0.49
1:A:1477:C:H5'	1:A:1868:G:C5'	2.43	0.49
1:A:1593:C:O2'	1:A:1594:C:H5'	2.13	0.49
1:A:159:G:H2'	1:A:175:G:H22	1.77	0.49
1:A:2649:A:C8	1:A:2649:A:H5'	2.48	0.49
1:A:2896:A:H2'	1:A:2896:A:N3	2.28	0.49
1:A:538:C:H5''	1:A:539:G:C8	2.48	0.49
1:A:737:A:H2'	1:A:738:G:O4'	2.13	0.49
4:D:279:THR:CG2	4:D:280:VAL:N	2.75	0.49
4:D:202:VAL:HG11	4:D:301:VAL:HG13	1.95	0.49
4:D:41:PHE:CB	4:D:190:MET:HE3	2.43	0.49
6:F:57:THR:HG23	6:F:63:ILE:CG2	2.42	0.49
10:J:75:SER:HB3	10:J:79:ALA:HB1	1.95	0.49
1:A:380:A:C2	14:N:13:LYS:HB3	2.48	0.49
27:1:11:THR:HG21	27:1:23:ARG:HB2	1.94	0.48
27:1:57:CYS:O	27:1:61:GLY:N	2.44	0.48
1:A:1209:C:O2	1:A:1210:G:C8	2.66	0.48
1:A:13:G:H2'	1:A:14:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1787:C:OP1	17:Q:68:LYS:HE2	2.13	0.48
1:A:2004:U:H1'	37:A:3178:HOH:O	2.12	0.48
1:A:2421:G:HO2'	1:A:2422:U:P	2.36	0.48
1:A:2502:C:C4'	10:J:151:MET:HG2	2.42	0.48
4:D:243:ASN:HA	4:D:244:PRO:C	2.32	0.48
6:F:27:ILE:HG22	6:F:28:GLY:N	2.22	0.48
10:J:154:THR:HB	10:J:155:PRO:HD3	1.95	0.48
13:M:72:ASN:O	13:M:76:LEU:HG	2.13	0.48
1:A:182:G:O3'	14:N:157:LEU:HD13	2.13	0.48
15:O:77:ASN:OD1	15:O:80:SER:HB2	2.13	0.48
20:T:29:ASP:OD2	20:T:31:ARG:NH1	2.45	0.48
1:A:584:U:H3'	37:A:6064:HOH:O	2.12	0.48
1:A:734:U:O2'	1:A:737:A:N6	2.45	0.48
1:A:2781:U:H1'	7:G:139:GLU:OE2	2.13	0.48
7:G:18:LEU:HD13	7:G:34:TRP:CD1	2.49	0.48
10:J:31:PHE:HA	10:J:85:ILE:CG2	2.43	0.48
13:M:73:VAL:HG23	13:M:74:THR:H	1.76	0.48
16:P:47:ARG:NH1	16:P:47:ARG:HG3	2.27	0.48
1:A:101:C:H2'	1:A:102:A:H8	1.78	0.48
1:A:1044:C:H5''	37:A:9022:HOH:O	2.13	0.48
1:A:625:U:H5''	1:A:1044:C:N4	2.28	0.48
1:A:1268:C:O2'	1:A:1269:G:H5'	2.13	0.48
1:A:1383:U:H5''	37:A:6631:HOH:O	2.12	0.48
1:A:2584:G:C2	1:A:2585:G:N7	2.81	0.48
1:A:81:G:N3	1:A:98:A:C2	2.81	0.48
3:C:18:ALA:O	3:C:20:SER:N	2.43	0.48
3:C:93:THR:C	3:C:94:LEU:HD23	2.33	0.48
5:E:214:THR:HG23	37:E:8436:HOH:O	2.12	0.48
7:G:31:ARG:NH1	7:G:68:HIS:CG	2.82	0.48
10:J:84:ARG:CZ	10:J:135:TRP:HH2	2.25	0.48
14:N:52:LEU:HD13	14:N:116:ASN:CB	2.42	0.48
15:O:62:HIS:HB3	15:O:65:ASP:OD1	2.12	0.48
17:Q:83:LYS:O	17:Q:86:ALA:HB3	2.12	0.48
24:X:90:TYR:N	24:X:90:TYR:CD1	2.80	0.48
1:A:1743:G:H1'	37:A:4867:HOH:O	2.12	0.48
1:A:2256:G:O2'	1:A:2257:G:H5'	2.12	0.48
1:A:581:G:H5'	37:A:7664:HOH:O	2.13	0.48
2:B:3042:C:H5'	2:B:3043:G:OP2	2.13	0.48
1:A:2657:G:OP1	4:D:17:LYS:HB2	2.13	0.48
4:D:76:THR:N	4:D:77:PRO:HD3	2.29	0.48
5:E:218:VAL:HG12	37:E:8422:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:101:GLU:HB2	7:G:116:THR:O	2.13	0.48
15:O:139:TRP:HA	15:O:139:TRP:CE3	2.47	0.48
24:X:110:GLN:HE21	24:X:110:GLN:HA	1.78	0.48
30:4:62:THR:HB	37:4:8554:HOH:O	2.12	0.48
30:4:69:TYR:CB	30:4:78:HIS:CE1	2.96	0.48
1:A:1333:U:H2'	1:A:1334:C:C6	2.48	0.48
1:A:1850:U:H2'	1:A:1851:G:C8	2.48	0.48
1:A:2019:A:H5'	37:A:4508:HOH:O	2.13	0.48
1:A:2459:G:P	30:4:64:LYS:HB2	2.54	0.48
1:A:2866:U:H4'	1:A:2867:G:H5'	1.95	0.48
1:A:485:A:O2'	1:A:487:G:H5'	2.13	0.48
1:A:832:U:H2'	1:A:833:G:C8	2.49	0.48
5:E:184:ARG:NE	37:E:8409:HOH:O	2.41	0.48
5:E:236:THR:CG2	5:E:239:ALA:H	2.00	0.48
6:F:84:LEU:C	6:F:86:THR:H	2.16	0.48
6:F:84:LEU:HA	6:F:87:ALA:HB3	1.96	0.48
8:H:117:GLU:C	8:H:119:ARG:H	2.16	0.48
10:J:35:ASN:ND2	10:J:79:ALA:O	2.46	0.48
10:J:48:LEU:CG	10:J:157:ILE:HG21	2.43	0.48
17:Q:10:ALA:HA	17:Q:13:VAL:CG1	2.43	0.48
19:S:82:GLU:HG3	19:S:83:LYS:N	2.28	0.48
37:A:7382:HOH:O	21:U:2:LYS:HE2	2.13	0.48
21:U:41:ARG:HG2	21:U:41:ARG:HH11	1.79	0.48
24:X:122:ARG:CG	24:X:122:ARG:NH1	2.74	0.48
24:X:4:LEU:HD22	24:X:52:VAL:HG22	1.93	0.48
26:Z:151:SER:HB3	26:Z:154:ARG:HB3	1.96	0.48
26:Z:187:VAL:HG23	26:Z:192:ASP:HB3	1.94	0.48
1:A:2251:G:H4'	37:A:7385:HOH:O	2.14	0.48
2:B:3038:A:H2	2:B:3043:G:H5''	1.78	0.48
2:B:3080:A:C2	2:B:3103:A:C4	3.02	0.48
1:A:1361:C:O3'	5:E:77:ALA:HB3	2.14	0.48
6:F:51:ARG:HD3	37:F:7636:HOH:O	2.14	0.48
10:J:59:ASN:ND2	10:J:59:ASN:N	2.59	0.48
1:A:2730:G:O2'	1:A:2731:G:H5'	2.14	0.48
1:A:288:A:H2'	1:A:289:G:C8	2.49	0.48
1:A:380:A:H5''	14:N:48:ARG:NH2	2.29	0.48
10:J:157:ILE:CG2	10:J:158:ASN:N	2.76	0.48
10:J:26:LYS:HG2	10:J:28:ILE:N	2.23	0.48
37:A:4700:HOH:O	15:O:21:HIS:HD2	1.96	0.48
17:Q:7:LYS:HD2	17:Q:21:VAL:CG2	2.43	0.48
23:W:1:THR:HG23	23:W:2:VAL:N	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:75:GLY:HA3	37:X:5763:HOH:O	2.13	0.48
25:Y:27:ASP:OD2	25:Y:27:ASP:N	2.47	0.48
1:A:1380:U:H5'	37:A:9206:HOH:O	2.14	0.48
1:A:639:A:H2'	1:A:640:G:H8	1.79	0.48
1:A:2837:U:H1'	4:D:307:ARG:HH12	1.78	0.48
5:E:79:ARG:O	5:E:87:ARG:N	2.42	0.48
11:K:19:MET:HE1	11:K:132:LEU:HD21	1.94	0.48
11:K:19:MET:HE1	11:K:132:LEU:CD2	2.43	0.48
11:K:93:ARG:HB3	11:K:93:ARG:NH1	2.27	0.48
1:A:1075:G:C2	1:A:1085:C:C2	3.02	0.48
1:A:1316:G:H1'	1:A:1340:G:N2	2.29	0.48
1:A:1666:C:H2'	1:A:1667:A:C5'	2.44	0.48
1:A:2073:G:C6	1:A:2607:U:C2	3.01	0.48
1:A:2269:C:C2'	1:A:2270:G:H5'	2.44	0.48
1:A:2755:G:H1'	37:A:4654:HOH:O	2.13	0.48
3:C:212:PRO:HB2	37:C:8562:HOH:O	2.14	0.48
4:D:84:LEU:HD13	4:D:84:LEU:O	2.13	0.48
10:J:45:GLN:HE21	10:J:135:TRP:HE1	1.62	0.48
14:N:154:ARG:CD	37:N:8643:HOH:O	2.62	0.48
37:A:4849:HOH:O	14:N:174:ARG:HG2	2.13	0.48
25:Y:66:THR:HG23	25:Y:67:PRO:HD2	1.95	0.48
1:A:1377:C:C6	1:A:1377:C:H5'	2.45	0.48
1:A:138:U:H5''	1:A:139:C:OP2	2.14	0.48
1:A:244:C:O5'	1:A:244:C:H6	1.96	0.48
1:A:2781:U:C2'	1:A:2782:G:H5'	2.44	0.48
2:B:3092:G:H22	10:J:52:LYS:NZ	2.12	0.48
7:G:92:PRO:HB2	37:G:4917:HOH:O	2.13	0.48
10:J:57:ARG:C	10:J:59:ASN:N	2.65	0.48
11:K:131:THR:HG22	11:K:133:GLY:N	2.29	0.48
37:A:3147:HOH:O	14:N:87:MET:HE3	2.13	0.48
1:A:1052:G:H2'	1:A:1052:G:N3	2.28	0.47
1:A:1249:U:H2'	1:A:1250:C:C6	2.49	0.47
1:A:1407:A:O2'	1:A:1408:U:H3'	2.14	0.47
1:A:182:G:O3'	14:N:157:LEU:CD1	2.62	0.47
1:A:2001:G:C2'	1:A:2002:C:H5'	2.44	0.47
1:A:212:A:O4'	1:A:214:U:C6	2.67	0.47
1:A:861:A:H2'	1:A:862:U:C6	2.48	0.47
1:A:894:A:C2	5:E:87:ARG:NH2	2.82	0.47
31:A:9001:SPR:C7C	31:A:9001:SPR:H6C3	2.43	0.47
5:E:107:ARG:HH11	5:E:107:ARG:HB3	1.77	0.47
1:A:1352:A:N1	5:E:48:SER:HB3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:41:LEU:HA	6:F:44:ILE:CG2	2.44	0.47
14:N:104:ARG:O	14:N:108:LYS:HE2	2.14	0.47
1:A:2055:A:H4'	19:S:132:ARG:NH2	2.29	0.47
1:A:1164:U:C1'	1:A:1165:G:OP1	2.62	0.47
1:A:1934:A:C8	1:A:1935:C:C5	3.01	0.47
1:A:2670:G:O2'	1:A:2671:U:H5'	2.14	0.47
1:A:682:A:H2'	1:A:683:G:O4'	2.14	0.47
4:D:168:GLY:O	4:D:169:GLY:O	2.32	0.47
37:A:7435:HOH:O	5:E:188:ARG:HD3	2.12	0.47
6:F:22:VAL:HG22	6:F:74:THR:HG22	1.96	0.47
11:K:77:GLY:O	11:K:78:ILE:C	2.52	0.47
15:O:34:LEU:HD13	15:O:47:LEU:HD21	1.96	0.47
19:S:39:THR:HB	19:S:42:GLU:CD	2.34	0.47
21:U:32:ARG:NH1	21:U:38:ARG:NH1	2.56	0.47
22:V:44:ARG:HB3	37:V:3805:HOH:O	2.13	0.47
1:A:2443:C:H3'	37:A:3456:HOH:O	2.14	0.47
1:A:558:C:C2'	1:A:559:U:C5'	2.92	0.47
1:A:920:C:H4'	1:A:921:G:C2	2.49	0.47
4:D:279:THR:OG1	4:D:290:VAL:HB	2.14	0.47
5:E:65:ARG:HG3	5:E:67:GLN:HB2	1.97	0.47
7:G:93:MET:HE1	7:G:165:GLY:N	2.29	0.47
9:I:23:ILE:O	9:I:27:ILE:HG13	2.13	0.47
11:K:142:ASN:O	11:K:144:THR:N	2.47	0.47
12:L:55:VAL:HG12	12:L:56:SER:H	1.77	0.47
15:O:154:LEU:HG	15:O:155:GLU:H	1.78	0.47
1:A:952:G:OP1	18:R:42:LYS:HE2	2.14	0.47
23:W:16:ARG:NH2	23:W:63:GLU:HG3	2.28	0.47
1:A:1097:A:H5''	24:X:125:HIS:NE2	2.30	0.47
1:A:1119:G:N2	1:A:1246:A:H2	2.08	0.47
1:A:1504:A:H5'	37:A:4384:HOH:O	2.14	0.47
1:A:1659:A:H2'	1:A:1660:G:O4'	2.15	0.47
4:D:177:HIS:O	4:D:181:ILE:HG13	2.15	0.47
4:D:82:VAL:HG12	4:D:101:TRP:CE3	2.50	0.47
5:E:127:ARG:CZ	5:E:225:PRO:HG2	2.44	0.47
6:F:10:PHE:CD1	6:F:11:HIS:N	2.82	0.47
6:F:86:THR:HG23	37:F:7477:HOH:O	2.14	0.47
6:F:99:ASP:HB2	6:F:103:ASN:H	1.80	0.47
10:J:150:LYS:HB2	10:J:157:ILE:HD12	1.95	0.47
37:A:9776:HOH:O	12:L:39:GLY:HA3	2.13	0.47
14:N:35:PRO:HD2	14:N:38:VAL:HG21	1.96	0.47
17:Q:71:LYS:O	17:Q:71:LYS:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:39:THR:O	19:S:40:ALA:C	2.51	0.47
26:Z:187:VAL:O	26:Z:187:VAL:HG13	2.14	0.47
27:1:58:GLY:HA3	37:1:8442:HOH:O	2.13	0.47
1:A:1503:U:H2'	1:A:1504:A:O4'	2.14	0.47
1:A:2430:A:H8	1:A:2430:A:O5'	1.97	0.47
1:A:2524:G:H21	1:A:2526:C:N4	2.12	0.47
1:A:2830:U:H3'	37:A:5206:HOH:O	2.13	0.47
1:A:2883:A:H2'	1:A:2884:G:O4'	2.15	0.47
1:A:625:U:H5'	37:A:3169:HOH:O	2.14	0.47
1:A:637:C:OP1	26:Z:136:LYS:NZ	2.33	0.47
5:E:118:THR:HG22	5:E:137:PRO:HB3	1.96	0.47
5:E:223:LEU:HD12	5:E:223:LEU:HA	1.77	0.47
6:F:128:LEU:HD23	6:F:128:LEU:C	2.35	0.47
6:F:99:ASP:CB	6:F:103:ASN:HB2	2.43	0.47
37:A:3180:HOH:O	13:M:4:LYS:HG3	2.13	0.47
14:N:113:ARG:HH21	14:N:156:ARG:HG2	1.77	0.47
15:O:113:SER:C	37:O:8560:HOH:O	2.53	0.47
12:L:130:MET:SD	22:V:26:GLY:HA3	2.54	0.47
24:X:149:LEU:HG	24:X:153:MET:CE	2.45	0.47
27:1:13:ARG:NH1	27:1:14:PHE:CZ	2.82	0.47
1:A:1127:C:C2'	1:A:1128:U:H5'	2.44	0.47
1:A:151:A:H2'	1:A:152:A:O4'	2.14	0.47
1:A:2093:G:H5''	37:A:9462:HOH:O	2.13	0.47
1:A:2133:U:H4'	1:A:2134:G:H5'	1.97	0.47
1:A:2416:G:H2'	1:A:2417:C:C6	2.50	0.47
1:A:2488:A:H61	1:A:2534:C:H42	1.62	0.47
1:A:2812:A:H1'	37:A:5763:HOH:O	2.14	0.47
3:C:192:VAL:O	3:C:192:VAL:HG12	2.13	0.47
10:J:48:LEU:HD13	10:J:146:TRP:HB3	1.96	0.47
15:O:182:GLY:O	15:O:183:ASP:O	2.32	0.47
18:R:21:ARG:NH2	37:R:5853:HOH:O	2.29	0.47
24:X:65:VAL:CA	24:X:68:THR:HG22	2.44	0.47
1:A:1019:C:P	37:A:3922:HOH:O	2.73	0.47
1:A:1023:C:H2'	1:A:1024:G:O4'	2.14	0.47
1:A:1463:A:C6	1:A:1464:U:O4	2.68	0.47
1:A:1694:G:H1'	37:A:9177:HOH:O	2.14	0.47
1:A:1858:A:H2'	1:A:1859:A:C8	2.50	0.47
1:A:1878:G:O2'	1:A:1879:U:C6	2.65	0.47
1:A:2089:A:O2'	1:A:2090:G:H5'	2.15	0.47
1:A:2456:A:H5'	37:A:5666:HOH:O	2.14	0.47
1:A:2781:U:O2'	1:A:2782:G:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:U:O2'	28:2:16:HIS:CD2	2.67	0.47
1:A:790:A:H2'	1:A:791:A:O4'	2.14	0.47
3:C:217:ARG:NH1	3:C:217:ARG:CG	2.76	0.47
4:D:139:ASP:HB2	4:D:165:ARG:HE	1.80	0.47
4:D:51:VAL:HG23	4:D:329:TYR:O	2.14	0.47
11:K:42:GLU:O	11:K:131:THR:HG23	2.14	0.47
13:M:73:VAL:HG23	13:M:74:THR:N	2.29	0.47
15:O:11:ARG:O	15:O:15:GLU:HG3	2.14	0.47
15:O:154:LEU:O	15:O:155:GLU:CB	2.63	0.47
15:O:67:ALA:C	15:O:69:TYR:N	2.68	0.47
20:T:32:ALA:HA	20:T:36:GLU:OE1	2.14	0.47
27:1:13:ARG:NH1	27:1:14:PHE:CE2	2.83	0.47
1:A:1555:G:H4'	1:A:1630:A:H2	1.80	0.47
1:A:2005:G:O2'	1:A:2008:U:OP2	2.25	0.47
1:A:2533:C:H6	1:A:2533:C:C5'	2.20	0.47
2:B:3031:C:O2'	2:B:3032:G:H5'	2.14	0.47
2:B:3049:G:O2'	2:B:3050:G:H5'	2.15	0.47
6:F:76:ARG:O	6:F:77:ASP:HB2	2.15	0.47
8:H:20:LEU:O	8:H:23:ALA:HB3	2.15	0.47
14:N:37:VAL:HG21	14:N:108:LYS:HG3	1.97	0.47
15:O:37:ARG:NE	37:O:8534:HOH:O	2.47	0.47
24:X:129:LYS:HG2	37:X:1990:HOH:O	2.15	0.47
1:A:2834:G:OP1	25:Y:39:LYS:HE2	2.15	0.47
1:A:168:C:O2'	1:A:169:A:H5'	2.15	0.47
1:A:2383:G:N3	37:A:6675:HOH:O	2.35	0.47
1:A:2723:G:H1'	37:A:4815:HOH:O	2.14	0.47
1:A:646:G:H2'	1:A:647:U:C6	2.50	0.47
5:E:1:MET:HG2	5:E:2:GLN:NE2	2.30	0.47
37:A:7202:HOH:O	14:N:13:LYS:HE2	2.14	0.47
14:N:65:VAL:HG21	14:N:105:ALA:HB2	1.96	0.47
37:A:5324:HOH:O	21:U:3:GLN:HG2	2.14	0.47
26:Z:172:THR:HG22	26:Z:173:ALA:N	2.29	0.47
29:3:40:ARG:NH1	29:3:40:ARG:HG2	2.30	0.47
1:A:1702:U:H5''	37:A:7193:HOH:O	2.14	0.47
1:A:1759:A:N3	1:A:1818:C:H2'	2.30	0.47
1:A:2421:G:H4'	37:A:4754:HOH:O	2.15	0.47
1:A:2431:C:O2'	1:A:2432:C:H5'	2.15	0.47
1:A:2481:G:C3'	1:A:2482:G:H5''	2.44	0.47
1:A:825:U:H5''	1:A:826:U:OP1	2.15	0.47
1:A:843:A:C2	1:A:846:A:C8	3.03	0.47
3:C:217:ARG:HG3	3:C:217:ARG:HH11	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:73:VAL:HG11	13:M:118:LEU:HD21	1.97	0.47
2:B:3008:G:O6	15:O:11:ARG:NH1	2.47	0.47
15:O:154:LEU:HD12	15:O:156:GLU:O	2.15	0.47
37:A:5995:HOH:O	18:R:50:GLY:HA2	2.15	0.47
24:X:76:ASP:O	24:X:77:ALA:C	2.53	0.47
1:A:1268:C:H2'	1:A:1269:G:C8	2.49	0.47
1:A:128:A:H3'	1:A:128:A:C8	2.50	0.47
1:A:13:G:H2'	1:A:14:C:C6	2.50	0.47
1:A:1609:C:H2'	1:A:1610:G:C8	2.50	0.47
1:A:2072:G:C6	1:A:2533:C:H1'	2.50	0.47
1:A:2840:A:OP1	4:D:211:THR:HG23	2.15	0.47
1:A:283:U:H5	1:A:284:C:N4	2.13	0.47
1:A:426:G:H2'	1:A:427:C:O4'	2.14	0.47
1:A:512:G:O3'	1:A:513:A:H8	1.98	0.47
1:A:581:G:O2'	1:A:582:C:H5'	2.15	0.47
3:C:192:VAL:HB	37:C:8598:HOH:O	2.14	0.47
8:H:34:ASN:O	8:H:38:LYS:HG3	2.15	0.47
10:J:84:ARG:CZ	10:J:135:TRP:CH2	2.98	0.47
7:G:34:TRP:O	11:K:127:ILE:HD11	2.14	0.47
15:O:67:ALA:HA	15:O:71:TRP:H	1.80	0.47
16:P:32:ARG:HE	16:P:35:LYS:HD2	1.80	0.47
22:V:33:SER:O	22:V:37:GLU:HG3	2.15	0.47
24:X:1:MET:HB2	24:X:103:GLU:HG2	1.97	0.47
24:X:126:ASP:HB3	24:X:135:GLY:O	2.15	0.47
1:A:1114:A:H2'	1:A:1115:U:H6	1.80	0.46
1:A:1130:U:H5'	37:A:7653:HOH:O	2.15	0.46
3:C:153:ARG:CB	3:C:153:ARG:HH11	2.27	0.46
4:D:162:MET:HE1	4:D:308:LEU:HD21	1.94	0.46
4:D:74:ILE:HD13	4:D:309:VAL:HG21	1.97	0.46
5:E:107:ARG:CB	5:E:107:ARG:HH11	2.28	0.46
6:F:19:GLU:O	6:F:133:ASN:HB3	2.15	0.46
10:J:29:ALA:N	10:J:62:GLU:OE1	2.45	0.46
11:K:131:THR:HB	11:K:134:GLU:HG3	1.97	0.46
1:A:2598:U:H5''	12:L:36:GLY:HA2	1.96	0.46
1:A:869:G:OP1	14:N:79:LYS:HE2	2.13	0.46
20:T:57:THR:C	20:T:59:ASP:H	2.17	0.46
21:U:41:ARG:NH1	21:U:42:VAL:O	2.49	0.46
1:A:317:A:H5''	21:U:52:ARG:HD2	1.97	0.46
24:X:122:ARG:CG	24:X:152:ALA:O	2.63	0.46
25:Y:72:VAL:HG22	25:Y:85:VAL:CG1	2.44	0.46
26:Z:189:ASN:HD22	26:Z:192:ASP:H	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1334:C:H2'	1:A:1335:C:H6	1.79	0.46
1:A:1506:U:H6	1:A:1506:U:H5'	1.80	0.46
1:A:2010:A:H5''	37:A:4144:HOH:O	2.14	0.46
1:A:2089:A:C2'	1:A:2090:G:H5'	2.45	0.46
1:A:308:U:C4	1:A:342:C:H1'	2.50	0.46
1:A:514:G:O5'	1:A:514:G:H8	1.98	0.46
1:A:832:U:H2'	1:A:833:G:H8	1.80	0.46
7:G:158:ASP:OD1	7:G:160:ARG:HB2	2.14	0.46
8:H:60:VAL:O	8:H:61:MET:C	2.53	0.46
37:A:9966:HOH:O	13:M:22:ARG:HG2	2.14	0.46
14:N:138:HIS:C	14:N:139:PRO:O	2.47	0.46
37:E:8355:HOH:O	16:P:3:THR:HG21	2.14	0.46
19:S:22:GLN:HA	19:S:139:PRO:O	2.15	0.46
21:U:48:VAL:CG2	21:U:98:VAL:HA	2.44	0.46
22:V:9:CYS:HG	22:V:11:THR:HG23	1.79	0.46
30:4:23:GLU:HG2	30:4:24:LYS:O	2.15	0.46
1:A:1162:G:H2'	37:A:6556:HOH:O	2.15	0.46
1:A:200:U:H2'	37:A:3428:HOH:O	2.14	0.46
1:A:2090:G:H2'	1:A:2091:G:C8	2.49	0.46
1:A:2494:G:H4'	10:J:5:MET:SD	2.55	0.46
1:A:2898:G:O2'	1:A:2899:A:H5'	2.16	0.46
1:A:447:A:O2'	1:A:448:G:H5'	2.16	0.46
1:A:60:A:C2	1:A:61:G:C8	3.04	0.46
3:C:97:ALA:HB2	3:C:150:PRO:HB2	1.97	0.46
4:D:234:ARG:NH1	37:D:8620:HOH:O	2.37	0.46
4:D:41:PHE:CZ	4:D:79:MET:HG3	2.50	0.46
5:E:33:LYS:HE2	37:E:8358:HOH:O	2.14	0.46
11:K:45:VAL:HG22	11:K:46:ILE:N	2.30	0.46
15:O:180:LEU:O	15:O:181:ASP:HB3	2.15	0.46
16:P:25:VAL:O	16:P:29:VAL:HG23	2.14	0.46
17:Q:41:ARG:O	17:Q:44:VAL:HB	2.15	0.46
18:R:50:GLY:HA3	18:R:87:THR:OG1	2.15	0.46
27:1:30:GLU:CA	27:1:33:HIS:HB3	2.41	0.46
27:1:39:CYS:SG	27:1:40:PRO:HD2	2.55	0.46
1:A:1513:C:O2'	1:A:1514:C:H5'	2.15	0.46
1:A:160:A:C5	1:A:177:A:C2	3.03	0.46
1:A:2010:A:H2'	37:A:5928:HOH:O	2.15	0.46
1:A:2445:U:H2'	1:A:2446:G:C8	2.50	0.46
1:A:2506:A:C1'	37:A:6024:HOH:O	2.62	0.46
1:A:396:U:H1'	37:A:7610:HOH:O	2.14	0.46
1:A:500:G:O2'	1:A:501:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2630:G:O6	3:C:206:ARG:NH2	2.49	0.46
3:C:29:HIS:CE1	3:C:107:ASN:ND2	2.84	0.46
4:D:204:GLY:HA3	37:D:8655:HOH:O	2.15	0.46
5:E:115:LEU:HA	5:E:115:LEU:HD12	1.80	0.46
6:F:59:GLY:O	6:F:61:PHE:N	2.37	0.46
10:J:157:ILE:HG22	10:J:158:ASN:N	2.30	0.46
4:D:221:GLN:NE2	12:L:42:ASN:HD22	2.09	0.46
13:M:12:THR:HG21	13:M:16:GLY:O	2.16	0.46
14:N:169:ARG:NH1	37:N:8573:HOH:O	2.49	0.46
14:N:57:LYS:HE2	14:N:140:ALA:O	2.15	0.46
14:N:95:LYS:HG2	14:N:99:ARG:HB3	1.97	0.46
24:X:88:THR:O	37:X:2374:HOH:O	2.21	0.46
25:Y:43:VAL:CG1	25:Y:44:ASP:N	2.78	0.46
28:2:10:LYS:CG	37:2:8432:HOH:O	2.58	0.46
1:A:1064:U:H2'	1:A:1065:G:C8	2.51	0.46
1:A:2099:G:O6	31:A:9001:SPR:H8A2	2.16	0.46
1:A:858:U:H2'	1:A:859:C:C6	2.49	0.46
2:B:3065:A:O2'	2:B:3066:G:P	2.72	0.46
3:C:186:TRP:CG	3:C:187:PRO:HA	2.51	0.46
3:C:8:ARG:HG2	37:C:8554:HOH:O	2.14	0.46
7:G:7:ILE:HG22	7:G:45:ASP:O	2.15	0.46
14:N:69:LYS:O	14:N:73:ARG:CZ	2.64	0.46
21:U:9:LYS:CE	21:U:13:ARG:NH1	2.79	0.46
27:1:38:LYS:HG3	37:1:8432:HOH:O	2.14	0.46
1:A:1218:U:H2'	1:A:1219:U:C6	2.50	0.46
1:A:278:A:H2'	1:A:279:C:O4'	2.16	0.46
1:A:79:G:H22	1:A:97:G:H1'	1.80	0.46
1:A:820:G:H5'	1:A:821:U:C5'	2.45	0.46
1:A:849:C:O2'	1:A:850:U:H5'	2.16	0.46
5:E:61:PHE:HD1	37:E:8377:HOH:O	1.98	0.46
21:U:48:VAL:HG13	21:U:49:GLU:N	2.30	0.46
25:Y:12:ILE:HG23	25:Y:36:HIS:CG	2.50	0.46
26:Z:130:ARG:HB2	26:Z:142:SER:O	2.16	0.46
1:A:1015:C:H2'	1:A:1016:U:C6	2.51	0.46
1:A:101:C:O2'	1:A:102:A:H5'	2.15	0.46
1:A:1855:G:H8	3:C:144:GLU:OE2	1.99	0.46
1:A:319:A:H4'	1:A:338:C:C4	2.51	0.46
1:A:679:G:OP2	37:A:4409:HOH:O	2.20	0.46
3:C:192:VAL:O	3:C:192:VAL:CG1	2.63	0.46
6:F:167:GLU:OE2	6:F:173:GLU:HG2	2.15	0.46
7:G:86:VAL:CG1	7:G:129:GLU:HA	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:A:4055:HOH:O	8:H:31:LYS:HE3	2.16	0.46
12:L:37:TYR:HD2	37:L:7169:HOH:O	1.96	0.46
13:M:146:GLY:C	13:M:148:GLU:H	2.19	0.46
13:M:77:ALA:HB3	37:M:8534:HOH:O	2.15	0.46
15:O:115:VAL:O	15:O:118:ILE:HB	2.14	0.46
19:S:111:ILE:HG23	19:S:145:LEU:CD1	2.46	0.46
24:X:14:HIS:HB2	24:X:17:ILE:HG13	1.98	0.46
26:Z:187:VAL:HG12	26:Z:205:ILE:HA	1.97	0.46
1:A:1534:C:N3	37:A:9465:HOH:O	2.36	0.46
1:A:1613:C:H2'	1:A:1614:G:O4'	2.15	0.46
1:A:190:G:OP2	37:A:3713:HOH:O	2.21	0.46
1:A:2016:U:H6	1:A:2016:U:O5'	1.99	0.46
1:A:331:A:C6	1:A:332:G:C4	3.03	0.46
2:B:3057:A:C8	6:F:141:VAL:HG21	2.51	0.46
10:J:141:ASN:CA	37:J:8356:HOH:O	2.59	0.46
14:N:133:LEU:O	14:N:134:ILE:HD13	2.16	0.46
14:N:68:ARG:O	14:N:68:ARG:CG	2.61	0.46
16:P:105:ASN:HD21	16:P:109:SER:H	1.62	0.46
19:S:15:LYS:HE3	37:S:8578:HOH:O	2.16	0.46
1:A:2873:C:N4	1:A:2874:G:C6	2.84	0.46
1:A:450:C:H4'	5:E:46:TYR:CE1	2.51	0.46
2:B:3078:G:O2'	2:B:3079:U:P	2.74	0.46
4:D:154:VAL:CG1	4:D:156:LYS:HG2	2.46	0.46
7:G:11:VAL:CG1	7:G:12:ASP:H	2.29	0.46
1:A:1003:U:O2	10:J:90:PHE:HZ	1.99	0.46
1:A:2453:G:H4'	13:M:50:GLY:C	2.36	0.46
37:A:7400:HOH:O	21:U:9:LYS:HD2	2.16	0.46
25:Y:76:ARG:O	25:Y:77:PHE:HB3	2.16	0.46
28:2:25:LYS:NZ	37:2:8433:HOH:O	2.45	0.46
37:A:9939:HOH:O	30:4:84:ARG:HB2	2.16	0.46
1:A:1497:G:H4'	1:A:1627:G:O2'	2.16	0.46
1:A:1603:A:H5'	1:A:1605:G:C4'	2.46	0.46
1:A:1657:A:H2'	1:A:1658:A:C8	2.51	0.46
1:A:1909:A:H2'	1:A:1910:A:C8	2.51	0.46
1:A:2045:G:H2'	1:A:2046:G:O4'	2.16	0.46
1:A:2604:A:H5'	37:A:5764:HOH:O	2.16	0.46
1:A:289:G:O2'	1:A:290:C:H5'	2.15	0.46
4:D:132:HIS:CE1	4:D:171:VAL:HG21	2.50	0.46
4:D:41:PHE:HB3	4:D:190:MET:CE	2.46	0.46
5:E:191:SER:OG	5:E:192:ILE:N	2.49	0.46
5:E:142:ASP:OD1	5:E:236:THR:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:35:ALA:HB1	37:F:3279:HOH:O	2.15	0.46
6:F:94:ALA:O	6:F:95:THR:O	2.33	0.46
10:J:4:ALA:HB3	37:J:8354:HOH:O	2.16	0.46
12:L:118:ALA:C	12:L:120:ARG:H	2.19	0.46
14:N:155:HIS:O	14:N:158:ARG:HG2	2.16	0.46
1:A:392:U:C5'	14:N:193:LYS:HB3	2.46	0.46
15:O:50:LEU:HB2	37:O:8523:HOH:O	2.16	0.46
15:O:78:MET:HB2	15:O:79:PRO:HD3	1.98	0.46
1:A:1004:C:O2'	1:A:1005:A:H5'	2.16	0.45
1:A:1191:A:C3'	1:A:1192:A:H5''	2.42	0.45
1:A:1420:C:C2	1:A:1445:G:N2	2.84	0.45
1:A:1603:A:C5'	1:A:1605:G:H5'	2.46	0.45
1:A:1624:A:H5'	1:A:1626:A:O4'	2.17	0.45
1:A:2460:A:OP1	30:4:60:LYS:N	2.46	0.45
1:A:2697:A:H2'	1:A:2698:G:O4'	2.15	0.45
1:A:1562:C:H42	1:A:2738:G:H1	1.63	0.45
1:A:2833:C:C2	1:A:2848:G:N2	2.84	0.45
1:A:566:A:H2'	1:A:567:U:O4'	2.16	0.45
2:B:3042:C:H2'	37:B:6700:HOH:O	2.14	0.45
3:C:57:ALA:HA	3:C:67:LEU:HD23	1.97	0.45
4:D:320:GLN:HG3	4:D:321:PRO:CD	2.46	0.45
5:E:142:ASP:OD1	5:E:237:GLU:HB3	2.16	0.45
6:F:93:LEU:HG	37:F:3862:HOH:O	2.16	0.45
7:G:101:GLU:OE2	7:G:115:ARG:NH1	2.49	0.45
7:G:145:ALA:HB1	7:G:168:ILE:CD1	2.46	0.45
13:M:35:ARG:O	13:M:35:ARG:NH1	2.49	0.45
28:2:28:HIS:CD2	28:2:30:LYS:HB2	2.51	0.45
29:3:49:GLU:CD	37:3:719:HOH:O	2.54	0.45
1:A:1057:A:C6	1:A:1058:A:C6	3.04	0.45
1:A:1753:C:O2	4:D:229:ARG:NH2	2.47	0.45
1:A:2478:U:H2'	1:A:2479:A:C8	2.51	0.45
1:A:2821:C:H4'	4:D:116:PRO:CB	2.46	0.45
1:A:960:G:N3	1:A:960:G:C2'	2.78	0.45
3:C:94:LEU:N	3:C:94:LEU:CD2	2.79	0.45
5:E:200:PRO:HB3	5:E:212:VAL:HG23	1.98	0.45
25:Y:30:MET:HE3	25:Y:59:TRP:HE1	1.81	0.45
37:N:8533:HOH:O	30:4:46:ILE:HB	2.16	0.45
1:A:1552:G:H2'	1:A:1553:C:C6	2.50	0.45
1:A:1603:A:H5''	1:A:1605:G:H5'	1.97	0.45
1:A:1730:G:C5'	1:A:1731:C:C6	2.99	0.45
1:A:2004:U:H2'	1:A:2004:U:O2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2467:A:P	37:A:9038:HOH:O	2.73	0.45
1:A:316:A:H5'	21:U:54:ASP:OD2	2.16	0.45
1:A:920:C:N4	1:A:2467:A:C8	2.84	0.45
1:A:949:U:O2'	18:R:40:HIS:HE1	1.99	0.45
1:A:970:U:H2'	37:A:6298:HOH:O	2.16	0.45
4:D:53:LEU:HD11	4:D:327:VAL:HG22	1.99	0.45
5:E:233:THR:CG2	5:E:234:VAL:N	2.77	0.45
5:E:34:ALA:HB3	5:E:220:THR:HG21	1.99	0.45
13:M:30:ARG:NH2	37:M:8524:HOH:O	2.37	0.45
1:A:1172:G:H1'	37:A:4951:HOH:O	2.15	0.45
1:A:2107:U:O2'	1:A:2108:A:H5'	2.16	0.45
1:A:2300:A:C2	1:A:2306:U:C5	3.03	0.45
1:A:2450:C:O5'	1:A:2450:C:H6	2.00	0.45
1:A:2487:C:H5	37:A:4863:HOH:O	2.00	0.45
1:A:2533:C:O2'	1:A:2534:C:H5'	2.17	0.45
1:A:558:C:H2'	1:A:559:U:H5''	1.97	0.45
1:A:695:C:H2'	1:A:696:C:C6	2.51	0.45
1:A:716:G:H2'	1:A:717:C:O5'	2.17	0.45
2:B:3006:C:P	15:O:37:ARG:HH11	2.40	0.45
8:H:46:GLU:OE1	8:H:100:ASP:HA	2.15	0.45
11:K:39:VAL:CG1	11:K:107:ASN:HB2	2.47	0.45
37:A:3444:HOH:O	11:K:46:ILE:HD12	2.16	0.45
13:M:101:ASP:C	13:M:103:ALA:H	2.18	0.45
1:A:1500:U:P	17:Q:41:ARG:HH22	2.38	0.45
18:R:25:PRO:HA	18:R:26:PRO:HD3	1.80	0.45
24:X:88:THR:CG2	24:X:89:ASP:N	2.79	0.45
26:Z:109:LEU:HA	37:Z:8571:HOH:O	2.16	0.45
1:A:1328:A:OP1	26:Z:169:ARG:HD2	2.17	0.45
1:A:1593:C:OP1	17:Q:117:SER:CB	2.65	0.45
1:A:1778:A:H2'	1:A:1779:A:H5'	1.98	0.45
1:A:1805:G:H2'	1:A:1806:G:H8	1.81	0.45
1:A:1896:G:H1'	37:A:4232:HOH:O	2.15	0.45
1:A:2437:A:H2'	1:A:2438:G:C8	2.52	0.45
1:A:2769:C:H2'	1:A:2770:G:C5'	2.46	0.45
1:A:711:G:C2	1:A:718:C:C2	3.04	0.45
2:B:3057:A:N6	37:B:3535:HOH:O	2.44	0.45
4:D:274:GLU:HA	4:D:292:GLY:O	2.16	0.45
6:F:65:GLU:HA	37:F:6752:HOH:O	2.16	0.45
10:J:109:ASP:HB2	37:J:8333:HOH:O	2.15	0.45
10:J:58:HIS:CE1	10:J:59:ASN:ND2	2.84	0.45
12:L:14:LYS:HD2	12:L:45:PRO:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:143:THR:HG21	37:M:8542:HOH:O	2.17	0.45
15:O:154:LEU:HG	15:O:155:GLU:N	2.30	0.45
15:O:5:ARG:HG3	18:R:18:PRO:HB3	1.98	0.45
1:A:21:G:H5'	19:S:1:GLY:O	2.17	0.45
1:A:1008:C:OP1	10:J:16:ARG:NH2	2.47	0.45
1:A:1161:A:O5'	1:A:1161:A:H8	2.00	0.45
1:A:2038:A:OP2	4:D:224:LYS:NZ	2.43	0.45
1:A:328:U:O4'	5:E:202:THR:HG22	2.17	0.45
2:B:3049:G:H2'	2:B:3050:G:O4'	2.16	0.45
3:C:211:LYS:HD3	37:C:8615:HOH:O	2.16	0.45
4:D:72:THR:HB	37:D:8606:HOH:O	2.15	0.45
5:E:85:LYS:HE2	37:E:8328:HOH:O	2.16	0.45
6:F:25:MET:SD	6:F:40:ILE:HD11	2.57	0.45
7:G:69:ILE:HA	7:G:72:MET:HE2	1.97	0.45
10:J:46:VAL:O	10:J:146:TRP:CH2	2.66	0.45
14:N:77:PHE:CD2	14:N:86:MET:HA	2.52	0.45
37:A:5657:HOH:O	15:O:21:HIS:HE1	1.99	0.45
30:4:7:PHE:HE2	30:4:22:VAL:CG2	2.27	0.45
1:A:1188:A:C5	1:A:1189:A:C2	3.05	0.45
1:A:1745:G:H5'	37:A:4303:HOH:O	2.17	0.45
1:A:1827:G:H2'	1:A:1828:G:C8	2.51	0.45
1:A:1862:C:O2'	1:A:1863:G:H5'	2.16	0.45
1:A:2428:G:O6	1:A:2464:C:H1'	2.17	0.45
1:A:422:G:C6	1:A:2446:G:C6	3.04	0.45
1:A:2909:G:H2'	1:A:2910:A:H8	1.82	0.45
1:A:457:U:H5	1:A:460:A:OP2	2.00	0.45
1:A:920:C:H5'	1:A:921:G:N3	2.31	0.45
2:B:3008:G:C6	2:B:3009:C:C4	3.04	0.45
4:D:55:ASN:HB3	4:D:64:GLY:N	2.31	0.45
4:D:7:ARG:HH12	4:D:11:LEU:HD21	1.81	0.45
5:E:187:ARG:O	5:E:187:ARG:HG3	2.15	0.45
5:E:80:VAL:HA	5:E:81:PRO:HD3	1.82	0.45
11:K:126:ASN:O	11:K:129:PHE:HE2	1.99	0.45
14:N:173:LEU:HD23	14:N:183:VAL:CG1	2.46	0.45
14:N:38:VAL:O	14:N:63:VAL:HG13	2.17	0.45
23:W:42:ASN:O	23:W:44:GLY:N	2.49	0.45
25:Y:21:PRO:HD3	37:Y:6179:HOH:O	2.16	0.45
26:Z:126:PRO:HG2	26:Z:128:PHE:CZ	2.50	0.45
5:E:51:TYR:CE2	28:2:53:LYS:HB3	2.52	0.45
1:A:1301:C:O2'	1:A:1331:A:H4'	2.17	0.45
1:A:158:A:O2'	1:A:159:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1614:G:H2'	37:A:4597:HOH:O	2.16	0.45
1:A:168:C:C2'	1:A:169:A:H5'	2.46	0.45
1:A:2032:U:O2'	1:A:2033:G:H5''	2.15	0.45
1:A:2290:U:H4'	1:A:2291:A:OP1	2.17	0.45
1:A:2379:G:H4'	1:A:2380:A:H5''	1.99	0.45
1:A:2420:G:H4'	37:A:4068:HOH:O	2.17	0.45
1:A:2667:G:H1'	1:A:2914:A:N3	2.31	0.45
1:A:426:G:C2	1:A:427:C:C2	3.05	0.45
1:A:958:G:H2'	1:A:959:C:C6	2.51	0.45
3:C:164:ARG:HA	27:1:69:TYR:CE1	2.52	0.45
7:G:12:ASP:HA	37:G:1750:HOH:O	2.17	0.45
8:H:58:GLU:HA	8:H:61:MET:HE2	1.99	0.45
16:P:60:VAL:O	16:P:62:GLY:N	2.39	0.45
17:Q:28:GLN:N	37:Q:6051:HOH:O	2.50	0.45
19:S:89:LEU:HD23	19:S:89:LEU:HA	1.82	0.45
24:X:122:ARG:HG2	24:X:152:ALA:O	2.15	0.45
24:X:142:ASP:HB3	24:X:145:GLY:H	1.81	0.45
24:X:64:THR:O	24:X:68:THR:HG22	2.16	0.45
1:A:2904:U:H4'	25:Y:8:ARG:NH1	2.32	0.45
26:Z:129:ASN:OD1	26:Z:141:THR:OG1	2.35	0.45
1:A:1335:C:OP2	26:Z:207:SER:CB	2.64	0.45
27:1:47:LEU:HD23	27:1:57:CYS:CB	2.45	0.45
1:A:1656:A:H2'	1:A:1657:A:O4'	2.17	0.45
1:A:1706:G:C5	1:A:1707:G:C6	3.05	0.45
1:A:2547:C:H2'	1:A:2548:C:H6	1.81	0.45
1:A:2569:A:O5'	1:A:2569:A:H8	2.00	0.45
1:A:2761:A:C4	1:A:2763:G:C8	3.05	0.45
1:A:644:G:H5'	1:A:644:G:N3	2.32	0.45
1:A:653:C:H2'	1:A:654:A:C8	2.51	0.45
3:C:109:GLU:CD	3:C:113:GLY:H	2.20	0.45
7:G:126:ILE:HB	7:G:131:LEU:CD2	2.46	0.45
7:G:162:PHE:CD1	7:G:162:PHE:N	2.84	0.45
15:O:58:LEU:CD1	15:O:58:LEU:N	2.80	0.45
15:O:71:TRP:N	37:O:8540:HOH:O	2.49	0.45
22:V:31:PHE:CG	22:V:37:GLU:HG2	2.52	0.45
27:1:11:THR:O	27:1:14:PHE:HB2	2.17	0.45
1:A:1477:C:H5'	1:A:1868:G:H5''	1.98	0.45
1:A:1880:C:C2	1:A:1881:A:C8	3.05	0.45
1:A:2011:A:H4'	1:A:2012:U:O5'	2.17	0.45
1:A:2434:A:O3'	30:4:28:GLY:CA	2.65	0.45
1:A:2909:G:O2'	1:A:2910:A:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:846:A:O2'	1:A:847:C:H5'	2.17	0.45
2:B:3114:G:H2'	2:B:3115:C:C6	2.52	0.45
3:C:125:ASN:ND2	37:C:8538:HOH:O	2.41	0.45
3:C:105:VAL:HG13	3:C:155:THR:O	2.16	0.45
5:E:27:ARG:HD2	5:E:29:ASP:OD1	2.16	0.45
6:F:58:VAL:CG1	6:F:59:GLY:N	2.78	0.45
10:J:30:GLN:H	10:J:65:ARG:NH1	2.15	0.45
10:J:81:TYR:CD1	10:J:81:TYR:C	2.89	0.45
11:K:70:PHE:O	11:K:70:PHE:CD2	2.70	0.45
12:L:14:LYS:CB	12:L:45:PRO:HG2	2.41	0.45
15:O:11:ARG:HG3	15:O:14:ARG:NH1	2.32	0.45
15:O:25:ARG:HA	15:O:28:LYS:HG3	1.98	0.45
25:Y:51:ASP:OD2	25:Y:52:PRO:HD2	2.17	0.45
26:Z:144:ARG:NH2	37:Z:8610:HOH:O	2.50	0.45
1:A:2435:U:P	30:4:28:GLY:HA3	2.56	0.44
1:A:2325:C:H1'	37:A:4120:HOH:O	2.18	0.44
1:A:2362:A:H2'	1:A:2363:G:C8	2.52	0.44
1:A:401:C:H2'	1:A:402:U:C6	2.52	0.44
1:A:596:C:H2'	1:A:597:A:C8	2.52	0.44
1:A:711:G:N2	1:A:718:C:C2	2.85	0.44
4:D:316:ARG:N	4:D:317:PRO:HD3	2.33	0.44
5:E:173:LYS:NZ	37:E:8319:HOH:O	2.49	0.44
10:J:1:LYS:HA	10:J:2:PRO:HD3	1.68	0.44
14:N:37:VAL:HG21	14:N:108:LYS:CG	2.47	0.44
15:O:143:ARG:NH1	15:O:173:ASP:OD2	2.40	0.44
19:S:29:LYS:HD3	37:S:8532:HOH:O	2.15	0.44
24:X:48:VAL:O	24:X:48:VAL:HG12	2.16	0.44
26:Z:117:LEU:HD12	26:Z:174:VAL:CG1	2.46	0.44
1:A:1886:A:O2'	27:1:20:LEU:HB2	2.17	0.44
1:A:1384:C:H5'	25:Y:30:MET:HG2	1.99	0.44
1:A:1434:A:H2'	1:A:1436:C:C5	2.51	0.44
1:A:1592:G:O2'	1:A:1593:C:O5'	2.35	0.44
1:A:1596:U:H2'	1:A:1598:A:OP2	2.16	0.44
1:A:1543:G:N1	1:A:1641:A:OP2	2.39	0.44
1:A:1701:A:H5''	1:A:1702:U:H3'	1.99	0.44
1:A:1771:U:O2'	27:1:23:ARG:NH2	2.49	0.44
1:A:2044:G:OP1	25:Y:23:HIS:HE1	1.99	0.44
1:A:2467:A:O2'	1:A:2468:A:H2'	2.17	0.44
1:A:2598:U:O2	1:A:2600:A:H8	2.00	0.44
1:A:746:A:C6	16:P:65:LEU:HD13	2.52	0.44
2:B:3076:G:C3'	2:B:3077:A:H5''	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:105:VAL:CG1	3:C:106:CYS:N	2.80	0.44
5:E:13:ASP:N	37:E:8440:HOH:O	2.51	0.44
5:E:173:LYS:HB3	5:E:187:ARG:HG3	1.98	0.44
5:E:20:ASP:O	5:E:23:GLU:HB2	2.17	0.44
7:G:77:THR:OG1	7:G:78:GLU:N	2.49	0.44
15:O:113:SER:CB	37:O:8560:HOH:O	2.58	0.44
15:O:120:GLU:HG3	15:O:136:LEU:HD13	1.99	0.44
17:Q:59:ARG:HH22	17:Q:66:GLN:HE22	1.62	0.44
23:W:12:THR:HG23	23:W:14:ALA:H	1.81	0.44
27:1:10:ARG:HG3	27:1:11:THR:N	2.33	0.44
28:2:28:HIS:HD2	28:2:30:LYS:H	1.64	0.44
1:A:1114:A:H2'	1:A:1115:U:C6	2.53	0.44
1:A:1269:G:O2'	1:A:1270:U:H5'	2.17	0.44
1:A:240:C:H2'	1:A:240:C:O2	2.17	0.44
1:A:2715:G:N2	4:D:264:GLU:OE1	2.51	0.44
1:A:2791:U:C1'	1:A:2792:A:H5''	2.47	0.44
1:A:533:U:C5	1:A:2084:C:H5'	2.53	0.44
1:A:818:A:C2	27:1:13:ARG:HA	2.52	0.44
1:A:920:C:H5''	1:A:921:G:O5'	2.17	0.44
1:A:958:G:O2'	1:A:959:C:H5'	2.17	0.44
5:E:55:ARG:HB2	37:E:8311:HOH:O	2.16	0.44
6:F:101:THR:HG22	6:F:101:THR:O	2.17	0.44
6:F:41:LEU:CA	6:F:44:ILE:HG22	2.46	0.44
7:G:81:GLU:HA	7:G:133:VAL:O	2.17	0.44
37:A:3671:HOH:O	7:G:143:GLN:HG2	2.17	0.44
10:J:82:LYS:HB2	10:J:82:LYS:NZ	2.32	0.44
20:T:37:VAL:O	20:T:41:VAL:HG23	2.18	0.44
25:Y:74:ALA:CB	25:Y:85:VAL:HG22	2.47	0.44
30:4:38:ARG:O	30:4:42:ARG:HB2	2.17	0.44
1:A:10:U:H5'	37:A:6007:HOH:O	2.17	0.44
1:A:1236:A:H2'	1:A:1237:U:O4'	2.17	0.44
1:A:1353:C:O5'	37:A:4650:HOH:O	2.19	0.44
1:A:1423:C:O2'	1:A:1424:A:H5'	2.17	0.44
1:A:1440:U:OP2	37:A:4435:HOH:O	2.21	0.44
1:A:157:G:H4'	14:N:95:LYS:CE	2.44	0.44
1:A:1685:A:H4'	1:A:1686:C:OP2	2.17	0.44
1:A:195:C:H2'	1:A:196:G:H5'	1.99	0.44
1:A:1979:G:O2'	1:A:1980:U:OP1	2.32	0.44
1:A:2284:G:H1'	37:A:9552:HOH:O	2.18	0.44
1:A:2851:G:C2'	1:A:2852:A:H5'	2.48	0.44
1:A:226:A:H1'	1:A:393:G:C5	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:602:A:O2'	1:A:605:C:H4'	2.17	0.44
4:D:41:PHE:CE1	4:D:79:MET:HG3	2.51	0.44
7:G:126:ILE:HB	7:G:131:LEU:HD23	1.98	0.44
10:J:72:VAL:CG1	10:J:81:TYR:CZ	3.01	0.44
18:R:64:GLU:HG3	18:R:74:ASP:OD2	2.18	0.44
21:U:50:VAL:HG12	21:U:56:ALA:HA	1.99	0.44
26:Z:136:LYS:HE2	26:Z:138:ARG:NH1	2.31	0.44
27:1:22:ILE:O	27:1:26:VAL:HG23	2.18	0.44
1:A:1517:U:C2	1:A:1670:G:N2	2.85	0.44
1:A:2428:G:C6	1:A:2464:C:H1'	2.53	0.44
1:A:2503:A:OP1	10:J:147:ARG:NH2	2.44	0.44
1:A:2777:G:O2'	1:A:2778:A:H5'	2.17	0.44
4:D:195:ARG:NH1	4:D:324:ASP:OD1	2.48	0.44
5:E:84:VAL:O	5:E:85:LYS:CB	2.65	0.44
6:F:36:ASN:CA	37:F:7500:HOH:O	2.62	0.44
7:G:22:VAL:O	7:G:28:SER:HA	2.18	0.44
9:I:12:ILE:HD12	37:I:692:HOH:O	2.16	0.44
10:J:150:LYS:HG2	37:J:8372:HOH:O	2.17	0.44
13:M:62:ALA:HB2	13:M:103:ALA:CB	2.48	0.44
13:M:93:VAL:HG12	13:M:97:VAL:HG23	2.00	0.44
15:O:132:ASN:O	15:O:135:VAL:HG12	2.18	0.44
24:X:54:PHE:CZ	24:X:140:LYS:HB2	2.53	0.44
30:4:69:TYR:O	30:4:77:ALA:HA	2.17	0.44
1:A:1414:A:H2'	1:A:1415:G:O4'	2.17	0.44
1:A:160:A:C8	1:A:177:A:C6	3.05	0.44
1:A:2443:C:O3'	13:M:56:LYS:HE3	2.17	0.44
1:A:534:C:N4	37:A:7556:HOH:O	2.47	0.44
1:A:818:A:H2	27:1:13:ARG:HA	1.81	0.44
1:A:920:C:C4	1:A:2467:A:C5	3.05	0.44
4:D:248:ARG:NH1	37:D:8616:HOH:O	2.49	0.44
7:G:36:PRO:HD3	11:K:127:ILE:HD12	1.99	0.44
17:Q:2:ASP:OD1	17:Q:2:ASP:C	2.55	0.44
1:A:2363:G:O2'	18:R:11:ARG:HG3	2.18	0.44
1:A:100:C:H4'	21:U:16:LEU:HB2	2.00	0.44
23:W:39:ALA:C	23:W:41:GLU:N	2.71	0.44
37:A:6516:HOH:O	27:1:22:ILE:HG13	2.16	0.44
1:A:1137:G:H1'	37:A:3854:HOH:O	2.18	0.44
1:A:1158:G:O2'	1:A:1159:G:H5'	2.17	0.44
1:A:1992:U:H2'	1:A:1994:A:OP2	2.17	0.44
1:A:236:A:O5'	1:A:236:A:H2'	2.17	0.44
4:D:2:GLN:HA	37:D:8622:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:304:PRO:HD2	4:D:307:ARG:CD	2.48	0.44
8:H:101:ALA:HB2	8:H:108:LEU:CD2	2.48	0.44
9:I:64:ASN:ND2	9:I:64:ASN:N	2.65	0.44
10:J:85:ILE:O	10:J:85:ILE:HG23	2.18	0.44
12:L:22:ASP:OD1	12:L:22:ASP:C	2.56	0.44
12:L:28:GLU:OE2	12:L:58:THR:HG21	2.17	0.44
24:X:4:LEU:HD21	24:X:52:VAL:HG11	1.99	0.44
1:A:1135:G:H5'	37:A:5898:HOH:O	2.17	0.44
1:A:2265:U:H2'	1:A:2266:A:H8	1.83	0.44
1:A:236:A:H4'	1:A:237:G:OP1	2.18	0.44
1:A:2547:C:C2	1:A:2548:C:C5	3.05	0.44
1:A:628:A:C4	1:A:2071:C:C4	3.06	0.44
1:A:731:U:O2'	1:A:732:C:H5'	2.18	0.44
1:A:920:C:H4'	1:A:921:G:N2	2.32	0.44
5:E:150:THR:HA	5:E:203:ALA:O	2.17	0.44
5:E:35:VAL:HG21	5:E:227:GLY:HA2	1.99	0.44
9:I:63:ARG:O	9:I:67:LEU:HG	2.18	0.44
12:L:40:THR:O	12:L:41:LYS:C	2.55	0.44
1:A:2721:U:H4'	12:L:87:ARG:HG3	1.99	0.44
13:M:54:PRO:HG2	13:M:57:VAL:HG21	1.99	0.44
18:R:93:ARG:HH11	18:R:93:ARG:HG3	1.82	0.44
24:X:5:VAL:O	24:X:52:VAL:HG22	2.17	0.44
24:X:6:GLN:HA	24:X:52:VAL:HG23	1.98	0.44
24:X:85:ALA:HB2	24:X:91:ASP:O	2.18	0.44
1:A:797:A:H5'	27:1:10:ARG:HG2	2.00	0.44
37:A:7559:HOH:O	27:1:31:ILE:HG13	2.18	0.44
1:A:148:A:H5''	28:2:44:LYS:HG2	2.00	0.44
30:4:17:HIS:O	30:4:18:GLN:HG3	2.18	0.44
1:A:1819:G:H2'	1:A:1820:G:C5'	2.48	0.44
1:A:1855:G:O6	3:C:142:SER:HB3	2.18	0.44
1:A:2010:A:C2'	37:A:5928:HOH:O	2.66	0.44
1:A:513:A:N3	37:A:3639:HOH:O	2.36	0.44
1:A:716:G:C2'	1:A:717:C:O5'	2.66	0.44
1:A:834:G:H5''	1:A:835:U:O5'	2.18	0.44
3:C:99:ILE:O	3:C:131:HIS:CE1	2.71	0.44
6:F:23:VAL:CG2	6:F:73:VAL:HB	2.47	0.44
13:M:126:SER:O	13:M:127:GLU:C	2.54	0.44
14:N:114:VAL:HG21	14:N:159:THR:CG2	2.47	0.44
14:N:61:ILE:HA	37:N:8623:HOH:O	2.18	0.44
15:O:171:HIS:CE1	37:O:8568:HOH:O	2.70	0.44
19:S:39:THR:CB	19:S:42:GLU:HG3	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:49:LEU:O	22:V:55:ALA:CB	2.66	0.44
24:X:154:ARG:HE	24:X:154:ARG:HB3	1.59	0.44
1:A:1348:A:N3	37:A:9951:HOH:O	2.36	0.43
1:A:1375:A:C2'	1:A:1376:G:H5'	2.48	0.43
1:A:1594:C:O2'	1:A:1607:A:H4'	2.18	0.43
1:A:1730:G:C5'	1:A:1731:C:H6	2.30	0.43
1:A:1878:G:C4'	37:A:6090:HOH:O	2.65	0.43
1:A:1881:A:OP1	3:C:199:HIS:HE1	2.01	0.43
1:A:2453:G:H5'	37:A:4663:HOH:O	2.17	0.43
1:A:2715:G:O2'	4:D:262:ARG:HD2	2.18	0.43
1:A:585:C:H6	37:A:6064:HOH:O	1.99	0.43
3:C:103:VAL:HA	3:C:104:PRO:HD3	1.85	0.43
3:C:81:GLN:CB	3:C:92:ASN:ND2	2.80	0.43
4:D:132:HIS:HB2	4:D:137:LEU:HD22	2.00	0.43
4:D:314:ALA:CB	4:D:317:PRO:HG3	2.48	0.43
5:E:165:ASP:O	5:E:168:ARG:HB3	2.18	0.43
6:F:99:ASP:O	6:F:159:PRO:HG3	2.17	0.43
7:G:107:PHE:CZ	7:G:108:LEU:HD13	2.52	0.43
9:I:71:LEU:C	9:I:73:ASP:H	2.21	0.43
10:J:113:ALA:N	10:J:114:PRO:CD	2.81	0.43
10:J:65:ARG:HD3	37:J:8374:HOH:O	2.17	0.43
15:O:24:LEU:HD13	18:R:26:PRO:HB3	2.00	0.43
19:S:125:ARG:HG2	37:S:8543:HOH:O	2.18	0.43
20:T:10:VAL:HG11	23:W:36:ALA:HA	1.99	0.43
27:1:56:MET:HA	27:1:62:TYR:O	2.18	0.43
30:4:3:MET:HG3	30:4:4:PRO:HD2	2.00	0.43
1:A:1185:U:C5'	37:A:7445:HOH:O	2.65	0.43
1:A:1545:C:O2'	1:A:1546:G:H5'	2.18	0.43
1:A:177:A:H2'	1:A:178:U:O4'	2.18	0.43
1:A:1819:G:H2'	1:A:1820:G:C4'	2.48	0.43
1:A:920:C:N4	1:A:2467:A:C4	2.86	0.43
1:A:707:C:H2'	1:A:708:A:H8	1.82	0.43
3:C:199:HIS:HD2	3:C:201:PHE:N	2.06	0.43
5:E:140:VAL:HG12	5:E:141:SER:N	2.33	0.43
5:E:180:SER:HB2	37:E:8444:HOH:O	2.18	0.43
7:G:139:GLU:CG	37:G:5919:HOH:O	2.65	0.43
7:G:20:ILE:O	7:G:30:THR:HA	2.18	0.43
8:H:79:GLN:HG3	8:H:82:ASP:OD2	2.17	0.43
11:K:130:VAL:CG1	11:K:131:THR:N	2.81	0.43
11:K:39:VAL:HG12	11:K:40:ASN:ND2	2.33	0.43
12:L:14:LYS:HB2	12:L:45:PRO:CG	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:148:GLU:HB2	37:M:8587:HOH:O	2.17	0.43
17:Q:10:ALA:CA	17:Q:13:VAL:HG12	2.45	0.43
20:T:57:THR:CG2	20:T:59:ASP:HB2	2.49	0.43
22:V:17:THR:HG22	22:V:18:GLY:N	2.33	0.43
26:Z:189:ASN:ND2	26:Z:189:ASN:C	2.71	0.43
27:1:47:LEU:HA	27:1:56:MET:O	2.18	0.43
29:3:36:ASN:HB3	29:3:39:ARG:NE	2.33	0.43
1:A:1215:A:O3'	1:A:1216:G:C4'	2.66	0.43
1:A:1973:A:H2'	1:A:1974:G:O4'	2.18	0.43
1:A:2004:U:H5''	1:A:2005:G:C8	2.53	0.43
1:A:2084:C:O2'	1:A:2085:A:H5'	2.18	0.43
1:A:255:A:H2'	1:A:256:C:C6	2.53	0.43
1:A:303:C:H2'	1:A:304:G:O4'	2.19	0.43
1:A:340:A:C2	1:A:341:C:C6	3.06	0.43
1:A:394:G:H1	14:N:181:GLU:CD	2.22	0.43
1:A:694:A:C2'	1:A:695:C:H5'	2.48	0.43
1:A:827:A:H2'	1:A:828:G:O4'	2.17	0.43
2:B:3007:G:OP1	15:O:23:ARG:HD2	2.18	0.43
3:C:179:MET:HG2	3:C:186:TRP:HB3	1.99	0.43
3:C:58:VAL:O	3:C:65:ARG:HD2	2.18	0.43
5:E:5:ILE:CD1	5:E:16:VAL:HG23	2.28	0.43
6:F:52:THR:N	6:F:70:GLY:O	2.51	0.43
11:K:45:VAL:HG21	11:K:129:PHE:CD1	2.54	0.43
12:L:72:VAL:HG11	12:L:121:PHE:CD1	2.53	0.43
13:M:98:GLU:O	13:M:99:GLU:CB	2.66	0.43
14:N:139:PRO:HA	14:N:142:LYS:HB2	2.00	0.43
14:N:158:ARG:N	34:N:8518:CL:CL	2.88	0.43
15:O:184:ILE:HG22	15:O:185:GLU:N	2.33	0.43
17:Q:141:ILE:C	17:Q:143:ALA:H	2.22	0.43
26:Z:107:PRO:HD3	26:Z:182:PHE:CE1	2.54	0.43
30:4:1:MET:N	30:4:87:ARG:O	2.47	0.43
1:A:1069:C:H4'	1:A:1081:A:O2'	2.18	0.43
1:A:10:U:HO2'	1:A:11:A:P	2.42	0.43
1:A:907:A:H4'	1:A:1328:A:C2	2.53	0.43
1:A:2419:U:H5''	1:A:2420:G:C5'	2.48	0.43
1:A:392:U:H4'	14:N:193:LYS:HB3	2.00	0.43
1:A:621:C:H5'	26:Z:132:ASP:OD2	2.19	0.43
1:A:629:A:N7	37:A:9835:HOH:O	2.37	0.43
1:A:911:G:H5'	1:A:932:U:OP1	2.18	0.43
1:A:95:A:H5''	1:A:97:G:O4'	2.18	0.43
3:C:93:THR:HG23	3:C:154:ALA:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:108:GLU:HB3	4:D:111:ARG:HD2	2.00	0.43
5:E:136:VAL:HG22	5:E:137:PRO:HA	1.99	0.43
7:G:107:PHE:CD2	7:G:108:LEU:HD13	2.51	0.43
8:H:105:ALA:HB2	37:H:5522:HOH:O	2.19	0.43
11:K:72:PRO:O	11:K:78:ILE:CD1	2.67	0.43
37:B:4707:HOH:O	15:O:147:ILE:HB	2.19	0.43
16:P:96:VAL:HG13	16:P:100:GLN:HB2	2.01	0.43
17:Q:115:SER:C	17:Q:117:SER:H	2.22	0.43
20:T:23:LYS:HD3	20:T:65:VAL:HG12	2.00	0.43
21:U:96:VAL:HG13	21:U:97:ARG:N	2.33	0.43
23:W:20:LEU:HD22	23:W:60:GLN:HE22	1.82	0.43
24:X:35:VAL:HG23	24:X:41:TYR:CD2	2.53	0.43
27:1:48:LYS:HG2	37:1:8434:HOH:O	2.18	0.43
1:A:1894:C:C2	1:A:1939:U:C4	3.05	0.43
1:A:2478:U:H2'	1:A:2479:A:H8	1.83	0.43
1:A:2484:U:C2	37:A:9600:HOH:O	2.57	0.43
1:A:2783:A:O2'	1:A:2784:A:H5'	2.18	0.43
1:A:297:U:H1'	37:A:3911:HOH:O	2.17	0.43
1:A:299:U:C5'	37:A:7314:HOH:O	2.62	0.43
1:A:440:C:C4	1:A:441:A:C6	3.06	0.43
1:A:899:C:OP2	13:M:22:ARG:NH1	2.51	0.43
3:C:94:LEU:HG	3:C:99:ILE:CD1	2.48	0.43
6:F:92:GLU:O	6:F:93:LEU:O	2.36	0.43
1:A:1003:U:O2'	10:J:90:PHE:HE1	1.97	0.43
1:A:183:A:C5'	14:N:157:LEU:HD12	2.48	0.43
14:N:186:SER:OG	14:N:189:VAL:HG12	2.19	0.43
16:P:14:LEU:CD2	16:P:102:ILE:HD11	2.48	0.43
20:T:10:VAL:HG13	23:W:35:ALA:O	2.18	0.43
1:A:1098:A:H2'	1:A:1099:G:O4'	2.19	0.43
1:A:1730:G:H5'	1:A:1731:C:C6	2.54	0.43
1:A:2769:C:H2'	1:A:2770:G:H5'	2.01	0.43
1:A:282:C:H2'	1:A:283:U:O4'	2.17	0.43
1:A:628:A:C4	1:A:2071:C:N4	2.86	0.43
1:A:772:G:H2'	1:A:773:A:O4'	2.19	0.43
4:D:185:GLY:HA2	37:D:8636:HOH:O	2.19	0.43
37:A:5056:HOH:O	4:D:216:LYS:HA	2.18	0.43
4:D:280:VAL:HG13	4:D:334:SER:HA	1.99	0.43
4:D:86:ALA:HB2	4:D:128:ILE:HD13	2.01	0.43
5:E:218:VAL:CG1	37:E:8422:HOH:O	2.67	0.43
5:E:54:LEU:HD21	5:E:87:ARG:HD2	1.99	0.43
7:G:9:GLU:HG3	7:G:10:ASP:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:104:ALA:HA	37:H:6617:HOH:O	2.18	0.43
8:H:27:GLY:HA3	37:H:5413:HOH:O	2.18	0.43
8:H:36:THR:HG23	8:H:97:ALA:HB2	2.00	0.43
13:M:90:ARG:NH1	13:M:119:THR:HG21	2.34	0.43
14:N:115:LEU:O	14:N:115:LEU:HD13	2.19	0.43
14:N:47:ASP:CG	14:N:48:ARG:N	2.72	0.43
15:O:73:ALA:CB	37:O:8568:HOH:O	2.66	0.43
21:U:48:VAL:HG11	21:U:96:VAL:CG1	2.48	0.43
26:Z:115:ARG:CZ	37:Z:8556:HOH:O	2.67	0.43
29:3:19:SER:O	29:3:36:ASN:ND2	2.52	0.43
1:A:1066:U:H2'	1:A:1067:A:C8	2.53	0.43
1:A:1159:G:H1	1:A:1208:C:H42	1.67	0.43
1:A:1495:C:H1'	1:A:1573:A:H1'	2.01	0.43
1:A:1545:C:H2'	1:A:1546:G:O4'	2.18	0.43
1:A:1666:C:C2'	1:A:1667:A:H5'	2.46	0.43
1:A:1732:A:O5'	1:A:1732:A:H8	2.02	0.43
1:A:1790:C:H2'	1:A:1791:U:H6	1.83	0.43
1:A:2269:C:H2'	1:A:2270:G:C5'	2.49	0.43
1:A:2403:C:H5'	37:A:5995:HOH:O	2.19	0.43
1:A:2405:C:H5'	37:A:6569:HOH:O	2.19	0.43
1:A:245:C:H2'	1:A:246:G:H5'	1.99	0.43
1:A:2728:C:O5'	1:A:2728:C:H6	2.01	0.43
1:A:1815:A:H4'	1:A:2751:C:O4'	2.18	0.43
1:A:2781:U:H2'	1:A:2782:G:H5'	2.00	0.43
4:D:258:GLY:N	4:D:260:HIS:CE1	2.86	0.43
37:A:9185:HOH:O	5:E:107:ARG:NH2	2.51	0.43
1:A:1308:A:O4'	5:E:226:GLY:HA3	2.19	0.43
6:F:23:VAL:HG23	6:F:41:LEU:HD22	2.00	0.43
10:J:149:ALA:C	10:J:151:MET:H	2.21	0.43
10:J:26:LYS:HG3	10:J:58:HIS:HB2	2.01	0.43
10:J:62:GLU:OE2	10:J:66:VAL:CG2	2.67	0.43
12:L:37:TYR:CE2	12:L:45:PRO:HA	2.54	0.43
14:N:68:ARG:CD	14:N:68:ARG:O	2.65	0.43
15:O:67:ALA:HA	15:O:71:TRP:HB3	2.01	0.43
1:A:2737:C:OP2	17:Q:58:SER:HB2	2.19	0.43
22:V:52:THR:HG22	22:V:54:THR:H	1.84	0.43
28:2:52:SER:HA	37:2:8442:HOH:O	2.19	0.43
1:A:1187:U:C2'	37:A:6864:HOH:O	2.55	0.43
1:A:1221:G:C8	37:A:5958:HOH:O	2.69	0.43
1:A:1332:C:O2'	1:A:1333:U:H5'	2.19	0.43
1:A:1773:G:H2'	1:A:1774:G:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1862:C:C2'	1:A:1863:G:H5'	2.49	0.43
1:A:2246:U:N3	1:A:2256:G:C2	2.87	0.43
1:A:2300:A:H4'	1:A:2301:A:O5'	2.19	0.43
1:A:2456:A:H2'	1:A:2457:U:C6	2.54	0.43
1:A:2911:C:H2'	1:A:2912:C:C6	2.54	0.43
1:A:377:C:H5	37:A:3291:HOH:O	2.01	0.43
1:A:830:G:O2'	1:A:831:U:H5'	2.19	0.43
1:A:962:C:H5''	37:A:4892:HOH:O	2.18	0.43
3:C:1:GLY:N	37:C:8612:HOH:O	2.29	0.43
1:A:890:C:OP1	5:E:57:PRO:HG3	2.18	0.43
6:F:94:ALA:HB3	6:F:174:VAL:CA	2.48	0.43
10:J:14:TYR:N	10:J:91:HIS:HE1	2.15	0.43
13:M:130:ARG:NH2	37:M:8547:HOH:O	2.51	0.43
14:N:84:LYS:O	14:N:87:MET:CG	2.67	0.43
19:S:141:VAL:HG12	19:S:142:ASP:O	2.19	0.43
19:S:40:ALA:O	19:S:44:VAL:HG23	2.18	0.43
19:S:82:GLU:HG3	19:S:83:LYS:H	1.84	0.43
21:U:105:ASP:OD1	21:U:107:LYS:N	2.51	0.43
21:U:12:ARG:NH1	37:U:3035:HOH:O	2.51	0.43
24:X:41:TYR:CD2	24:X:44:MET:HE3	2.53	0.43
1:A:101:C:H2'	1:A:102:A:C8	2.53	0.43
1:A:1262:C:H1'	24:X:120:PRO:HG3	2.00	0.43
1:A:1299:G:N2	37:A:4655:HOH:O	2.51	0.43
1:A:1463:A:C6	1:A:1464:U:C4	3.07	0.43
1:A:1940:C:H4'	37:A:7324:HOH:O	2.18	0.43
1:A:201:G:N2	1:A:202:U:C2	2.87	0.43
1:A:2296:C:H5	37:R:5998:HOH:O	2.02	0.43
1:A:2415:A:N3	15:O:26:LEU:HD13	2.33	0.43
1:A:2672:C:O2'	1:A:2673:U:H5'	2.19	0.43
1:A:451:C:N4	1:A:452:G:C6	2.87	0.43
1:A:684:G:H2'	1:A:685:C:C6	2.53	0.43
1:A:696:C:O2'	1:A:697:G:H5'	2.18	0.43
2:B:3056:A:C3'	2:B:3057:A:H5''	2.49	0.43
3:C:55:VAL:HG22	3:C:68:ILE:O	2.19	0.43
4:D:279:THR:HG22	4:D:280:VAL:N	2.32	0.43
5:E:193:LEU:O	5:E:233:THR:HG23	2.18	0.43
5:E:78:ARG:HG2	37:E:8307:HOH:O	2.19	0.43
7:G:132:THR:HG23	7:G:132:THR:O	2.19	0.43
10:J:136:VAL:CG2	37:J:8330:HOH:O	2.56	0.43
12:L:90:PHE:CD1	12:L:90:PHE:N	2.87	0.43
14:N:69:LYS:HG2	14:N:127:LYS:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:41:LEU:HD12	18:R:41:LEU:N	2.33	0.43
25:Y:76:ARG:HA	25:Y:82:GLU:O	2.19	0.43
27:1:38:LYS:HA	27:1:45:LYS:HA	2.01	0.43
1:A:1044:C:C5'	37:A:9022:HOH:O	2.66	0.43
1:A:1634:G:H2'	1:A:1635:U:C6	2.53	0.43
1:A:217:C:OP1	1:A:395:A:O2'	2.25	0.43
1:A:794:U:H3	1:A:819:A:H61	1.66	0.43
1:A:812:A:H2'	1:A:813:C:O4'	2.18	0.43
5:E:127:ARG:HG2	5:E:127:ARG:NH1	2.33	0.43
6:F:23:VAL:HG21	6:F:45:THR:CG2	2.49	0.43
11:K:17:CYS:O	11:K:45:VAL:HG12	2.18	0.43
1:A:1103:C:O2'	11:K:86:MET:HB3	2.19	0.43
14:N:42:ARG:HA	14:N:43:PRO:HD3	1.75	0.43
18:R:40:HIS:CE1	18:R:94:GLN:HA	2.54	0.43
21:U:48:VAL:HG13	21:U:96:VAL:HG13	2.01	0.43
1:A:2460:A:OP1	30:4:60:LYS:HB2	2.19	0.42
1:A:1279:U:H5''	37:A:9572:HOH:O	2.19	0.42
1:A:1391:G:H2'	1:A:1392:A:H5'	2.01	0.42
1:A:2500:C:O2'	1:A:2501:G:H5'	2.18	0.42
1:A:2621:U:H5	37:A:9961:HOH:O	2.01	0.42
1:A:290:C:H2'	1:A:291:C:O4'	2.19	0.42
1:A:445:U:C1'	37:A:7314:HOH:O	2.66	0.42
1:A:517:U:H1'	37:A:7554:HOH:O	2.19	0.42
1:A:80:A:H3'	21:U:43:ASN:OD1	2.19	0.42
2:B:3048:C:H4'	15:O:141:ARG:NH2	2.29	0.42
5:E:77:ALA:O	5:E:78:ARG:HG3	2.19	0.42
6:F:166:ILE:O	6:F:169:THR:N	2.52	0.42
6:F:173:GLU:HG3	6:F:174:VAL:N	2.34	0.42
6:F:35:ALA:C	6:F:37:ALA:N	2.72	0.42
12:L:130:MET:SD	22:V:25:ASP:O	2.77	0.42
12:L:86:THR:HG22	12:L:87:ARG:N	2.34	0.42
14:N:88:VAL:O	14:N:88:VAL:HG12	2.19	0.42
15:O:143:ARG:NH1	15:O:173:ASP:OD1	2.52	0.42
15:O:24:LEU:O	15:O:28:LYS:HG2	2.19	0.42
15:O:32:PRO:HD2	15:O:99:GLU:O	2.19	0.42
21:U:55:PHE:CD2	21:U:77:VAL:HG13	2.54	0.42
25:Y:21:PRO:HG2	25:Y:24:LYS:HD3	2.01	0.42
1:A:1706:G:C6	1:A:1707:G:C6	3.07	0.42
1:A:1968:A:H2'	1:A:1969:A:C8	2.54	0.42
1:A:636:G:H5'	1:A:2059:U:OP2	2.19	0.42
1:A:2526:C:H5'	1:A:2526:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:C:H2'	1:A:292:G:O4'	2.19	0.42
1:A:567:U:H5''	37:A:6375:HOH:O	2.19	0.42
1:A:724:G:O2'	1:A:725:C:H5'	2.19	0.42
2:B:3034:A:H2'	2:B:3035:C:O4'	2.19	0.42
3:C:70:ALA:HA	3:C:71:PRO:HD3	1.80	0.42
5:E:13:ASP:O	5:E:13:ASP:OD1	2.37	0.42
5:E:79:ARG:O	5:E:87:ARG:HG2	2.19	0.42
13:M:148:GLU:HG2	37:M:8553:HOH:O	2.20	0.42
13:M:35:ARG:O	13:M:40:PHE:HA	2.18	0.42
14:N:27:ARG:O	14:N:30:GLU:N	2.51	0.42
14:N:35:PRO:HD2	14:N:38:VAL:CG2	2.49	0.42
14:N:63:VAL:HG21	14:N:109:PHE:CE1	2.54	0.42
16:P:47:ARG:NH2	37:P:510:HOH:O	2.51	0.42
1:A:1789:G:O6	17:Q:73:HIS:HE1	2.03	0.42
19:S:132:ARG:NH1	37:S:8582:HOH:O	2.51	0.42
24:X:73:LEU:HD12	24:X:73:LEU:HA	1.86	0.42
30:4:73:GLU:HB2	37:4:8529:HOH:O	2.18	0.42
1:A:1117:A:C2	1:A:1244:U:C2	3.07	0.42
1:A:1166:A:H2'	1:A:1166:A:N3	2.34	0.42
1:A:1215:A:O3'	1:A:1216:G:H4'	2.19	0.42
1:A:1611:G:O2'	1:A:1612:A:H5'	2.20	0.42
1:A:1902:G:H2'	1:A:1903:U:O4'	2.19	0.42
1:A:2247:C:C5'	37:A:7322:HOH:O	2.67	0.42
37:A:7336:HOH:O	3:C:177:HIS:HE1	2.01	0.42
6:F:144:ARG:NH2	37:F:3839:HOH:O	2.49	0.42
6:F:169:THR:O	6:F:170:TYR:HB2	2.19	0.42
6:F:59:GLY:C	6:F:61:PHE:N	2.73	0.42
13:M:55:GLN:HA	13:M:58:GLN:NE2	2.33	0.42
14:N:87:MET:HG3	14:N:87:MET:H	1.42	0.42
14:N:74:ARG:HD3	14:N:91:ILE:HD12	2.00	0.42
15:O:47:LEU:CD1	15:O:97:VAL:HG11	2.49	0.42
19:S:119:VAL:O	19:S:119:VAL:HG12	2.18	0.42
30:4:75:GLY:HA2	37:4:8563:HOH:O	2.19	0.42
1:A:120:A:H5'	28:2:20:ARG:HH21	1.84	0.42
1:A:1681:G:H5''	1:A:1682:A:H5'	2.00	0.42
1:A:2241:C:H2'	1:A:2242:U:C6	2.54	0.42
1:A:259:G:H21	14:N:58:GLN:NE2	2.17	0.42
1:A:2088:C:H1'	1:A:2841:A:N1	2.34	0.42
1:A:553:G:P	26:Z:204:ARG:NH2	2.91	0.42
1:A:707:C:C2	1:A:708:A:C8	3.06	0.42
1:A:795:G:N3	1:A:817:G:C2	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:876:A:H2'	1:A:876:A:N3	2.35	0.42
2:B:3030:C:OP1	6:F:137:PRO:O	2.37	0.42
6:F:53:LYS:HA	6:F:67:ASP:O	2.20	0.42
10:J:57:ARG:C	10:J:59:ASN:H	2.21	0.42
10:J:65:ARG:NH2	10:J:66:VAL:HG22	2.35	0.42
17:Q:7:LYS:CD	17:Q:21:VAL:HG21	2.49	0.42
37:A:9535:HOH:O	24:X:119:HIS:HE1	2.02	0.42
1:A:1586:G:O2'	1:A:1587:U:H5'	2.19	0.42
1:A:1886:A:H4'	37:1:8405:HOH:O	2.19	0.42
1:A:2270:G:H4'	3:C:223:ARG:NH1	2.34	0.42
1:A:2307:A:C2	1:A:2308:U:N3	2.87	0.42
1:A:473:A:O2'	1:A:474:C:H5'	2.19	0.42
3:C:211:LYS:HB2	37:C:8622:HOH:O	2.18	0.42
4:D:84:LEU:HD13	4:D:84:LEU:C	2.40	0.42
5:E:27:ARG:HG2	5:E:30:LEU:HG	2.02	0.42
5:E:78:ARG:CG	5:E:78:ARG:NH1	2.76	0.42
6:F:153:THR:HG22	37:F:5234:HOH:O	2.19	0.42
8:H:49:PHE:O	8:H:95:ALA:HA	2.19	0.42
10:J:58:HIS:CE1	10:J:59:ASN:HD21	2.37	0.42
14:N:71:SER:O	14:N:73:ARG:NH1	2.51	0.42
18:R:10:THR:O	18:R:11:ARG:C	2.58	0.42
18:R:41:LEU:HB3	18:R:52:PHE:CZ	2.55	0.42
26:Z:133:HIS:CD2	37:Z:8583:HOH:O	2.52	0.42
28:2:5:THR:HB	28:2:6:PRO:CD	2.50	0.42
1:A:1450:C:O2'	1:A:1493:A:H2'	2.19	0.42
1:A:1616:A:H5''	1:A:1617:C:OP1	2.20	0.42
1:A:161:A:OP1	14:N:82:ARG:HG2	2.20	0.42
1:A:1666:C:H2'	1:A:1667:A:H8	1.84	0.42
1:A:1972:U:C2'	1:A:1973:A:H5'	2.48	0.42
1:A:2134:G:C6	1:A:2258:A:C8	3.08	0.42
1:A:269:G:C2	1:A:270:U:O4	2.72	0.42
1:A:2900:G:H2'	1:A:2901:C:O4'	2.20	0.42
1:A:2911:C:H3'	37:A:5528:HOH:O	2.19	0.42
1:A:657:G:H2'	1:A:658:C:C6	2.55	0.42
5:E:53:GLY:O	5:E:79:ARG:HA	2.19	0.42
11:K:54:VAL:HG11	11:K:138:THR:HG21	2.01	0.42
13:M:90:ARG:NH2	13:M:121:ILE:HD11	2.34	0.42
8:H:56:PRO:CG	14:N:44:THR:HA	2.49	0.42
37:B:4707:HOH:O	15:O:147:ILE:HD12	2.20	0.42
16:P:14:LEU:HD23	16:P:102:ILE:HD11	2.01	0.42
17:Q:115:SER:C	17:Q:117:SER:N	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:5:SER:OG	19:S:144:GLU:OE1	2.33	0.42
21:U:96:VAL:CG1	21:U:97:ARG:N	2.80	0.42
26:Z:122:ARG:NH2	37:Z:8535:HOH:O	2.52	0.42
3:C:72:GLU:OE1	27:1:72:GLU:HA	2.19	0.42
30:4:91:GLN:O	30:4:92:GLU:HB2	2.19	0.42
1:A:1139:U:H2'	1:A:1140:C:C6	2.54	0.42
1:A:1185:U:O4'	37:A:7445:HOH:O	2.22	0.42
1:A:1456:C:H2'	1:A:1457:U:C6	2.55	0.42
1:A:1593:C:OP1	17:Q:117:SER:HB3	2.20	0.42
1:A:219:G:O5'	1:A:220:C:H5''	2.20	0.42
1:A:2820:A:H2'	1:A:2821:C:C6	2.55	0.42
1:A:2836:G:C6	1:A:2838:A:C2	3.07	0.42
1:A:324:G:O2'	1:A:325:U:H5'	2.19	0.42
1:A:88:G:H2'	1:A:89:G:C8	2.53	0.42
4:D:312:ARG:HG2	4:D:313:PRO:N	2.33	0.42
12:L:34:VAL:CG2	12:L:47:ALA:HB2	2.48	0.42
15:O:181:ASP:HA	37:O:8572:HOH:O	2.19	0.42
15:O:90:LEU:HB2	15:O:186:LEU:HD22	2.00	0.42
16:P:21:SER:OG	16:P:106:PRO:HB2	2.20	0.42
20:T:10:VAL:CG1	23:W:35:ALA:O	2.68	0.42
1:A:97:G:C2	21:U:107:LYS:HD2	2.54	0.42
24:X:139:GLY:O	24:X:141:HIS:HD2	2.01	0.42
25:Y:79:GLU:OE2	37:Y:5564:HOH:O	2.21	0.42
1:A:1829:A:N6	27:1:18:TYR:HA	2.34	0.42
1:A:1741:U:HO2'	1:A:2723:G:H4'	1.84	0.42
1:A:24:G:N2	1:A:518:G:H1'	2.34	0.42
1:A:736:A:H2'	1:A:737:A:O4'	2.19	0.42
1:A:87:C:H2'	29:3:28:LYS:O	2.19	0.42
3:C:43:VAL:O	3:C:44:ASP:HB2	2.20	0.42
4:D:71:VAL:HG11	4:D:296:LEU:HB3	2.01	0.42
4:D:87:TYR:O	4:D:138:GLY:N	2.39	0.42
6:F:35:ALA:O	6:F:37:ALA:N	2.53	0.42
6:F:95:THR:C	6:F:97:GLN:N	2.70	0.42
14:N:39:ARG:CZ	37:N:8623:HOH:O	2.66	0.42
14:N:87:MET:SD	37:N:8531:HOH:O	2.62	0.42
17:Q:91:LYS:O	17:Q:95:GLU:HG3	2.19	0.42
21:U:65:VAL:HG22	21:U:72:ILE:HG22	2.02	0.42
24:X:101:LEU:HA	24:X:101:LEU:HD23	1.89	0.42
25:Y:76:ARG:NH1	25:Y:76:ARG:CG	2.82	0.42
1:A:86:A:C2	29:3:25:VAL:HG13	2.55	0.42
1:A:1089:G:C8	1:A:1290:G:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1559:A:C1'	37:A:5836:HOH:O	2.67	0.42
1:A:1890:U:H4'	1:A:2010:A:C6	2.55	0.42
1:A:629:A:C2	1:A:2074:A:C2	3.08	0.42
1:A:2785:C:H4'	1:A:2786:G:OP2	2.20	0.42
1:A:2852:A:OP1	4:D:157:LYS:HE2	2.19	0.42
1:A:391:U:OP2	14:N:84:LYS:NZ	2.48	0.42
1:A:67:A:H5''	1:A:69:A:C8	2.55	0.42
11:K:51:GLU:O	11:K:55:GLU:HG3	2.20	0.42
14:N:162:GLY:HA2	37:N:8520:HOH:O	2.20	0.42
15:O:176:ARG:O	15:O:180:LEU:HG	2.19	0.42
23:W:27:LEU:O	23:W:30:ALA:N	2.52	0.42
24:X:31:HIS:HB3	37:X:5420:HOH:O	2.20	0.42
24:X:84:VAL:HG12	37:X:6679:HOH:O	2.20	0.42
24:X:90:TYR:N	37:X:6679:HOH:O	2.53	0.42
1:A:99:A:H3'	1:A:100:C:C6	2.55	0.42
1:A:1051:C:H2'	1:A:1052:G:O4'	2.20	0.42
1:A:10:U:H1'	1:A:532:A:H62	1.85	0.42
1:A:1187:U:C3'	37:A:6864:HOH:O	2.67	0.42
1:A:1132:A:N6	1:A:1229:C:H2'	2.35	0.42
1:A:1444:G:O2'	1:A:1445:G:H5'	2.20	0.42
1:A:2453:G:H2'	1:A:2454:C:C6	2.55	0.42
1:A:245:C:C2'	1:A:246:G:H5'	2.50	0.42
1:A:2529:G:O2'	1:A:2530:C:H5'	2.20	0.42
1:A:1705:C:O2	1:A:2735:U:H5''	2.20	0.42
1:A:803:C:O2'	1:A:804:C:H5'	2.20	0.42
1:A:870:G:C3'	1:A:871:G:H5''	2.50	0.42
4:D:264:GLU:HG2	4:D:267:LYS:CE	2.34	0.42
5:E:160:LEU:O	5:E:162:VAL:HG23	2.19	0.42
6:F:41:LEU:O	6:F:44:ILE:HG22	2.20	0.42
7:G:84:MET:HB2	7:G:131:LEU:HB2	2.01	0.42
10:J:57:ARG:HG3	10:J:57:ARG:NH1	2.35	0.42
11:K:72:PRO:O	11:K:78:ILE:HD11	2.20	0.42
11:K:79:PHE:O	11:K:83:ILE:HG13	2.19	0.42
12:L:58:THR:HG22	12:L:59:LYS:HG3	2.00	0.42
14:N:45:ARG:CZ	14:N:48:ARG:HG3	2.50	0.42
15:O:80:SER:CB	37:O:8537:HOH:O	2.63	0.42
28:2:21:ARG:HD2	28:2:39:PHE:HB2	2.02	0.41
1:A:940:G:C5	1:A:1027:G:C2	3.07	0.41
1:A:1947:G:N2	1:A:1966:U:O2	2.52	0.41
1:A:236:A:O5'	1:A:236:A:C2'	2.68	0.41
1:A:250:C:O2'	1:A:251:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:G:O2'	1:A:260:C:H5'	2.20	0.41
1:A:2758:G:H2'	1:A:2759:C:C6	2.55	0.41
1:A:2815:G:N7	11:K:80:LYS:NZ	2.66	0.41
1:A:314:G:N2	1:A:316:A:H3'	2.35	0.41
3:C:192:VAL:HG12	3:C:207:GLN:HB3	2.02	0.41
3:C:30:ARG:HB3	3:C:30:ARG:HE	1.65	0.41
3:C:46:GLU:O	3:C:55:VAL:N	2.49	0.41
4:D:102:THR:HG23	4:D:182:VAL:CG1	2.50	0.41
6:F:140:ARG:HG3	6:F:140:ARG:HH11	1.85	0.41
37:A:3671:HOH:O	7:G:143:GLN:CG	2.68	0.41
14:N:77:PHE:HD2	37:N:8527:HOH:O	2.02	0.41
16:P:32:ARG:HG2	37:P:2336:HOH:O	2.20	0.41
16:P:44:ASN:HA	16:P:65:LEU:O	2.19	0.41
17:Q:131:PHE:CD1	17:Q:137:LEU:HD13	2.55	0.41
18:R:31:GLU:CD	18:R:93:ARG:HH12	2.24	0.41
22:V:52:THR:HG22	22:V:54:THR:N	2.35	0.41
25:Y:7:GLU:HA	25:Y:74:ALA:O	2.20	0.41
26:Z:154:ARG:HH12	26:Z:155:ARG:HG3	1.84	0.41
26:Z:178:HIS:CG	26:Z:179:PRO:HD2	2.55	0.41
27:1:42:CYS:SG	27:1:44:PHE:CB	2.94	0.41
1:A:1921:A:C6	1:A:1922:A:C2	3.07	0.41
1:A:1985:U:C5	1:A:1996:U:C2	3.07	0.41
1:A:2047:C:H5'	37:A:9799:HOH:O	2.19	0.41
1:A:2523:U:O2'	1:A:2524:G:H5'	2.20	0.41
1:A:2549:C:H1'	4:D:248:ARG:NH2	2.34	0.41
1:A:2739:A:N6	1:A:2740:G:C6	2.88	0.41
1:A:951:A:H2'	1:A:952:G:H5'	2.00	0.41
2:B:3057:A:H8	6:F:141:VAL:HG21	1.85	0.41
2:B:3096:C:H2'	2:B:3097:U:C6	2.55	0.41
3:C:100:PRO:HG2	3:C:103:VAL:CG2	2.48	0.41
3:C:101:GLU:HG2	3:C:131:HIS:ND1	2.34	0.41
3:C:36:ASP:CB	3:C:85:ASP:H	2.32	0.41
5:E:3:ALA:HA	37:E:8451:HOH:O	2.20	0.41
37:A:4537:HOH:O	5:E:50:GLU:HG2	2.20	0.41
6:F:101:THR:CG2	37:F:7400:HOH:O	2.65	0.41
8:H:21:GLU:HA	8:H:24:ARG:HE	1.84	0.41
10:J:48:LEU:HD11	10:J:157:ILE:HG21	2.01	0.41
10:J:56:ILE:HG21	10:J:61:LEU:CD1	2.50	0.41
11:K:4:ALA:O	11:K:5:GLU:O	2.38	0.41
11:K:46:ILE:HG12	11:K:53:ILE:HD13	2.02	0.41
14:N:49:ALA:C	14:N:54:TYR:HB3	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:96:ASN:ND2	37:N:8541:HOH:O	2.48	0.41
15:O:127:LEU:HA	15:O:127:LEU:HD12	1.84	0.41
15:O:159:TYR:CE2	15:O:163:PHE:HE2	2.34	0.41
16:P:26:TRP:HB2	37:P:3062:HOH:O	2.21	0.41
22:V:20:MET:CG	22:V:28:THR:HG23	2.50	0.41
22:V:31:PHE:CE2	22:V:37:GLU:HA	2.54	0.41
28:2:10:LYS:CB	37:2:8432:HOH:O	2.68	0.41
1:A:1014:A:H5'	2:B:3101:G:O2'	2.20	0.41
1:A:1865:A:H2'	1:A:1866:A:C8	2.55	0.41
1:A:2255:A:C6	1:A:2256:G:C5	3.08	0.41
1:A:2626:C:H2'	1:A:2627:G:C8	2.55	0.41
1:A:382:U:C5	1:A:406:G:C2	3.07	0.41
1:A:645:U:H2'	1:A:646:G:C8	2.55	0.41
1:A:883:U:O2	1:A:883:U:C2'	2.68	0.41
3:C:194:MET:HE1	37:C:8517:HOH:O	2.20	0.41
4:D:132:HIS:CE1	4:D:171:VAL:CG2	3.03	0.41
6:F:95:THR:HG21	6:F:174:VAL:HG22	2.02	0.41
10:J:154:THR:HB	10:J:155:PRO:CD	2.50	0.41
10:J:73:GLN:OE1	10:J:73:GLN:CA	2.68	0.41
15:O:143:ARG:HH12	15:O:173:ASP:CG	2.21	0.41
15:O:163:PHE:O	15:O:164:ASP:O	2.38	0.41
16:P:25:VAL:HG23	16:P:26:TRP:H	1.85	0.41
1:A:1265:G:H1'	37:A:4979:HOH:O	2.19	0.41
1:A:1653:A:N7	37:A:6918:HOH:O	2.37	0.41
1:A:1825:U:O2'	1:A:1826:C:H5'	2.21	0.41
1:A:419:A:H1'	1:A:1921:A:C2	2.56	0.41
1:A:306:A:H2'	1:A:341:C:O2'	2.20	0.41
1:A:764:C:H2'	1:A:765:G:O4'	2.20	0.41
4:D:60:SER:C	4:D:62:ARG:H	2.23	0.41
5:E:200:PRO:HB3	5:E:212:VAL:CG2	2.50	0.41
5:E:40:ALA:O	5:E:43:LYS:HB2	2.20	0.41
6:F:95:THR:OG1	6:F:174:VAL:HG22	2.20	0.41
7:G:49:ILE:HD11	7:G:69:ILE:HD12	2.02	0.41
10:J:136:VAL:HG22	10:J:137:ASN:N	2.36	0.41
23:W:11:MET:HB3	23:W:15:GLU:HB2	2.02	0.41
1:A:130:C:H5'	37:A:5192:HOH:O	2.19	0.41
3:C:232:ARG:NE	37:C:8586:HOH:O	2.54	0.41
3:C:66:ARG:HB2	3:C:66:ARG:HH11	1.85	0.41
3:C:36:ASP:HB2	3:C:84:VAL:N	2.36	0.41
4:D:154:VAL:HA	4:D:155:PRO:HD3	1.89	0.41
5:E:93:LYS:O	5:E:98:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:12:ILE:O	9:I:13:PRO:C	2.58	0.41
15:O:34:LEU:HD22	15:O:129:ILE:CD1	2.51	0.41
17:Q:13:VAL:HG11	17:Q:40:VAL:HG12	2.02	0.41
24:X:122:ARG:NH2	37:X:4276:HOH:O	2.53	0.41
24:X:122:ARG:NH1	24:X:152:ALA:O	2.53	0.41
25:Y:25:ARG:NE	37:Y:3861:HOH:O	2.52	0.41
1:A:1025:C:H5'	24:X:23:MET:O	2.20	0.41
1:A:1278:A:H4'	1:A:1279:U:C4	2.56	0.41
1:A:1462:C:H2'	1:A:1463:A:C8	2.56	0.41
1:A:1751:G:C3'	1:A:1752:G:H5''	2.50	0.41
1:A:155:C:H4'	1:A:188:C:H4'	2.03	0.41
1:A:2079:G:H2'	1:A:2080:G:O4'	2.20	0.41
1:A:2505:G:H8	37:A:5611:HOH:O	2.04	0.41
1:A:2607:U:O5'	1:A:2609:G:H4'	2.20	0.41
1:A:2739:A:C6	1:A:2740:G:C5	3.08	0.41
1:A:40:C:O5'	1:A:40:C:H6	2.04	0.41
1:A:492:C:O2'	1:A:493:U:H5'	2.21	0.41
1:A:661:G:C4	1:A:686:A:C2	3.09	0.41
1:A:849:C:C2'	1:A:850:U:H5'	2.51	0.41
3:C:29:HIS:HB2	3:C:153:ARG:HH12	1.86	0.41
4:D:5:ARG:HA	4:D:6:PRO:HD3	1.94	0.41
6:F:170:TYR:N	6:F:170:TYR:CD1	2.88	0.41
6:F:17:ARG:NH2	37:F:3723:HOH:O	2.43	0.41
8:H:16:ALA:HA	8:H:111:ILE:HD13	2.01	0.41
10:J:26:LYS:HD2	10:J:28:ILE:HB	2.02	0.41
12:L:9:THR:O	12:L:10:GLN:C	2.59	0.41
14:N:94:LYS:CE	37:N:8646:HOH:O	2.69	0.41
15:O:108:SER:HA	15:O:109:PRO:HD3	1.79	0.41
22:V:38:ASN:O	22:V:42:LEU:HG	2.21	0.41
22:V:44:ARG:CB	37:V:3805:HOH:O	2.67	0.41
24:X:21:LEU:HB3	24:X:26:ILE:HG12	2.02	0.41
26:Z:189:ASN:ND2	26:Z:192:ASP:N	2.65	0.41
1:A:1116:U:H3	1:A:1246:A:N6	2.09	0.41
1:A:1167:G:O2'	1:A:1168:C:H5'	2.21	0.41
1:A:1377:C:C5'	1:A:1377:C:H6	2.33	0.41
1:A:1515:A:H2'	1:A:1516:C:C6	2.56	0.41
1:A:1888:C:N4	1:A:1889:C:C4	2.89	0.41
1:A:1912:A:O5'	1:A:1912:A:H8	2.03	0.41
1:A:209:G:C6	1:A:210:U:N3	2.89	0.41
1:A:2327:A:C2	1:A:2374:A:C2	3.08	0.41
1:A:329:A:OP2	5:E:206:ASN:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:G:H1'	1:A:347:A:N6	2.35	0.41
1:A:398:U:H2'	1:A:399:C:C6	2.56	0.41
1:A:542:A:H1'	37:A:4648:HOH:O	2.21	0.41
1:A:812:A:H2'	1:A:813:C:C6	2.55	0.41
4:D:138:GLY:O	4:D:139:ASP:C	2.58	0.41
4:D:268:ARG:NE	37:D:8608:HOH:O	2.53	0.41
4:D:280:VAL:CG1	4:D:281:ASP:N	2.83	0.41
6:F:57:THR:HA	6:F:63:ILE:HA	2.01	0.41
8:H:26:THR:HB	8:H:102:GLY:HA3	2.03	0.41
9:I:12:ILE:HB	37:I:4714:HOH:O	2.19	0.41
10:J:113:ALA:N	10:J:114:PRO:HD3	2.36	0.41
12:L:99:ASP:OD1	12:L:99:ASP:C	2.58	0.41
14:N:63:VAL:O	14:N:130:GLU:HA	2.21	0.41
15:O:149:GLU:O	15:O:152:GLU:HB2	2.20	0.41
15:O:37:ARG:CZ	37:O:8534:HOH:O	2.69	0.41
15:O:37:ARG:HD3	15:O:37:ARG:HA	1.84	0.41
16:P:47:ARG:NH1	37:P:4564:HOH:O	2.53	0.41
19:S:132:ARG:NH1	37:S:8558:HOH:O	2.53	0.41
21:U:27:LEU:HD21	21:U:40:VAL:CG1	2.51	0.41
21:U:80:GLU:OE2	21:U:84:GLY:HA2	2.20	0.41
25:Y:12:ILE:HD12	25:Y:36:HIS:ND1	2.36	0.41
1:A:1471:A:H2'	1:A:1472:C:C6	2.56	0.41
1:A:1490:G:H4'	1:A:1533:A:OP1	2.20	0.41
1:A:1666:C:O2'	1:A:1667:A:C5'	2.65	0.41
1:A:183:A:O2'	1:A:184:G:H5'	2.21	0.41
1:A:1871:U:O4'	1:A:1873:G:C8	2.74	0.41
1:A:2118:A:H2'	1:A:2119:C:H6	1.85	0.41
1:A:2456:A:H2'	1:A:2457:U:H6	1.86	0.41
1:A:2481:G:H3'	1:A:2482:G:H5''	2.02	0.41
1:A:542:A:C8	1:A:542:A:C5'	2.99	0.41
1:A:955:A:C2	1:A:1013:A:C4	3.08	0.41
2:B:3107:C:H2'	2:B:3108:C:C6	2.55	0.41
4:D:168:GLY:H	4:D:174:ARG:HD3	1.84	0.41
4:D:236:ILE:HG21	4:D:236:ILE:HD13	1.80	0.41
4:D:307:ARG:CG	4:D:307:ARG:NH1	2.84	0.41
5:E:14:GLY:N	37:E:8440:HOH:O	2.54	0.41
7:G:34:TRP:HA	37:G:4572:HOH:O	2.20	0.41
10:J:47:GLU:HG2	10:J:133:ILE:HD12	2.02	0.41
10:J:57:ARG:O	10:J:61:LEU:HD22	2.21	0.41
1:A:171:C:OP2	14:N:84:LYS:HG3	2.20	0.41
1:A:2123:A:P	14:N:89:ASN:HD22	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:37:ARG:O	17:Q:41:ARG:HG3	2.20	0.41
1:A:1021:G:O2'	1:A:1022:A:H5'	2.20	0.41
1:A:1589:G:H4'	37:A:6824:HOH:O	2.21	0.41
1:A:2246:U:C2	1:A:2256:G:N2	2.89	0.41
1:A:858:U:H2'	1:A:859:C:H6	1.85	0.41
1:A:903:U:OP2	13:M:11:ARG:NH1	2.50	0.41
2:B:3011:A:O2'	2:B:3012:C:H3'	2.21	0.41
2:B:3042:C:N4	2:B:3044:A:N1	2.68	0.41
3:C:170:VAL:HG13	27:1:22:ILE:HG21	2.02	0.41
4:D:102:THR:HG23	4:D:182:VAL:HG12	2.03	0.41
4:D:240:GLY:HA3	37:D:8657:HOH:O	2.21	0.41
7:G:116:THR:HG22	7:G:151:LEU:HD22	2.03	0.41
7:G:172:PRO:HB3	37:G:6931:HOH:O	2.20	0.41
8:H:59:ILE:HG22	8:H:59:ILE:O	2.20	0.41
11:K:6:PHE:HB3	11:K:109:TYR:OH	2.21	0.41
15:O:72:GLU:H	15:O:171:HIS:CE1	2.38	0.41
25:Y:85:VAL:HG12	25:Y:86:GLU:N	2.36	0.41
26:Z:136:LYS:HG3	26:Z:138:ARG:HG2	2.02	0.41
27:1:13:ARG:NH1	37:1:8422:HOH:O	2.54	0.41
29:3:11:LEU:HD23	29:3:11:LEU:HA	1.78	0.41
30:4:35:TRP:HA	30:4:38:ARG:NH1	2.36	0.41
1:A:1744:G:N7	1:A:1745:G:C5	2.89	0.41
1:A:2111:G:H1'	37:A:9042:HOH:O	2.20	0.41
1:A:2122:C:H3'	37:A:5266:HOH:O	2.20	0.41
1:A:2263:G:C6	1:A:2264:A:C5	3.09	0.41
1:A:2473:U:O3'	1:A:2474:A:H3'	2.20	0.41
1:A:2825:C:H4'	1:A:2826:G:O5'	2.21	0.41
1:A:396:U:HO2'	1:A:397:A:P	2.44	0.41
1:A:64:G:H2'	1:A:65:C:O4'	2.21	0.41
1:A:834:G:H4'	1:A:835:U:OP2	2.20	0.41
1:A:853:C:H2'	1:A:854:G:O4'	2.20	0.41
3:C:192:VAL:CG1	3:C:207:GLN:HB3	2.51	0.41
37:A:7107:HOH:O	5:E:107:ARG:NE	2.46	0.41
8:H:6:PHE:CD1	8:H:6:PHE:O	2.74	0.41
10:J:65:ARG:HB3	37:J:8374:HOH:O	2.21	0.41
13:M:64:ILE:O	13:M:64:ILE:HG23	2.20	0.41
13:M:98:GLU:O	13:M:99:GLU:HB2	2.21	0.41
14:N:69:LYS:HD3	14:N:125:ARG:HA	2.02	0.41
14:N:87:MET:HE1	37:N:8531:HOH:O	2.20	0.41
15:O:93:GLN:HG2	37:O:8557:HOH:O	2.21	0.41
16:P:35:LYS:HD3	37:P:3360:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:49:GLU:HB3	21:U:59:GLU:CG	2.51	0.41
23:W:45:ARG:C	23:W:47:LYS:N	2.74	0.41
25:Y:26:ALA:HB1	25:Y:59:TRP:CE2	2.56	0.41
26:Z:234:VAL:HG12	26:Z:235:GLU:N	2.36	0.41
30:4:22:VAL:HG11	30:4:67:LEU:HD13	2.02	0.41
1:A:1421:C:O2'	1:A:1422:U:H5'	2.20	0.41
1:A:1440:U:P	37:A:4435:HOH:O	2.79	0.41
1:A:1447:U:OP2	1:A:1503:U:O2'	2.35	0.41
1:A:1896:G:C6	1:A:1897:U:C4	3.08	0.41
1:A:1942:A:H3'	37:A:7324:HOH:O	2.21	0.41
1:A:1969:A:O2'	1:A:1970:G:H5'	2.21	0.41
1:A:2113:G:C6	1:A:2114:C:C4	3.09	0.41
1:A:2289:G:H21	1:A:2291:A:H2	1.65	0.41
1:A:2428:G:C4	1:A:2461:U:C5	3.09	0.41
1:A:2781:U:H2'	1:A:2782:G:C5'	2.51	0.41
1:A:2831:C:H2'	1:A:2832:C:H5'	2.03	0.41
1:A:2826:G:C6	1:A:2913:A:N6	2.89	0.41
1:A:431:G:OP1	14:N:48:ARG:NH1	2.53	0.41
1:A:902:G:N7	13:M:18:HIS:CD2	2.87	0.41
3:C:190:ARG:NH2	37:C:8598:HOH:O	2.53	0.41
4:D:215:VAL:HA	4:D:220:VAL:HG22	2.02	0.41
5:E:236:THR:C	37:E:8447:HOH:O	2.59	0.41
7:G:137:ASP:O	7:G:141:VAL:HG23	2.21	0.41
8:H:21:GLU:O	8:H:24:ARG:CG	2.68	0.41
9:I:66:LEU:O	9:I:69:ARG:HB3	2.21	0.41
10:J:45:GLN:NE2	10:J:135:TRP:HE1	2.19	0.41
12:L:6:ALA:HB3	12:L:116:GLU:HG2	2.02	0.41
12:L:76:GLN:HB2	37:L:1433:HOH:O	2.21	0.41
1:A:1299:G:N7	13:M:6:ARG:NH1	2.68	0.41
14:N:108:LYS:N	14:N:108:LYS:HD3	2.36	0.41
15:O:139:TRP:HA	15:O:139:TRP:HE3	1.86	0.41
16:P:45:LEU:HD12	16:P:88:LYS:HD2	2.02	0.41
19:S:119:VAL:CG2	19:S:142:ASP:HB2	2.51	0.41
24:X:41:TYR:O	24:X:45:VAL:HG13	2.21	0.41
25:Y:78:GLU:CG	25:Y:79:GLU:N	2.76	0.41
1:A:1044:C:H3'	1:A:1045:G:H5''	2.03	0.40
1:A:1161:A:O5'	1:A:1161:A:C8	2.74	0.40
1:A:1790:C:H2'	1:A:1791:U:C6	2.55	0.40
1:A:1804:A:H2'	1:A:1805:G:H8	1.86	0.40
1:A:1992:U:C2	1:A:1994:A:OP2	2.75	0.40
1:A:1827:G:C2	1:A:2023:G:C6	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:C:C5	1:A:220:C:C4	3.09	0.40
1:A:2116:U:C4	1:A:2271:G:C6	3.09	0.40
1:A:2356:A:H2'	1:A:2357:G:O4'	2.20	0.40
1:A:2780:C:C4	1:A:2781:U:C4	3.10	0.40
1:A:27:U:H2'	1:A:28:G:O4'	2.20	0.40
1:A:2869:G:H2'	1:A:2870:C:C6	2.56	0.40
1:A:78:G:C6	1:A:79:G:C6	3.10	0.40
1:A:941:G:C2'	1:A:942:U:H5'	2.51	0.40
3:C:114:ASP:HB2	3:C:117:LYS:HE2	2.02	0.40
5:E:76:ARG:HD3	37:E:8365:HOH:O	2.21	0.40
7:G:118:ILE:HG23	7:G:144:THR:HG21	2.03	0.40
10:J:150:LYS:CG	37:J:8372:HOH:O	2.69	0.40
11:K:80:LYS:NZ	37:K:8573:HOH:O	2.50	0.40
12:L:30:LYS:C	12:L:55:VAL:HG13	2.42	0.40
12:L:6:ALA:CB	12:L:116:GLU:HG2	2.51	0.40
1:A:240:C:C5'	14:N:146:GLN:NE2	2.84	0.40
14:N:14:ARG:HB3	14:N:17:GLU:HG3	2.02	0.40
14:N:12:TRP:CZ2	14:N:20:ILE:HD11	2.56	0.40
15:O:141:ARG:CB	37:O:8571:HOH:O	2.66	0.40
15:O:175:LEU:HD12	15:O:175:LEU:HA	1.91	0.40
15:O:48:VAL:HG12	37:O:8555:HOH:O	2.21	0.40
16:P:26:TRP:HA	16:P:26:TRP:CE3	2.55	0.40
22:V:9:CYS:O	22:V:52:THR:HG23	2.20	0.40
24:X:3:ALA:O	24:X:54:PHE:HA	2.22	0.40
1:A:2106:C:H2'	1:A:2107:U:C6	2.57	0.40
1:A:2407:G:O2'	1:A:2408:A:H5'	2.21	0.40
1:A:2415:A:H2'	1:A:2416:G:H5'	2.02	0.40
1:A:2690:U:H4'	7:G:111:LYS:CE	2.51	0.40
1:A:2750:G:H8	1:A:2750:G:O5'	2.05	0.40
1:A:380:A:OP2	14:N:9:ARG:HD2	2.22	0.40
2:B:3117:G:C2'	37:B:2118:HOH:O	2.69	0.40
3:C:36:ASP:HB2	3:C:83:GLY:HA3	2.03	0.40
6:F:159:PRO:O	6:F:163:VAL:HG23	2.20	0.40
7:G:24:GLY:HA3	7:G:76:VAL:HB	2.03	0.40
15:O:43:VAL:CG1	15:O:118:ILE:HD11	2.50	0.40
15:O:50:LEU:HA	15:O:50:LEU:HD12	1.87	0.40
23:W:42:ASN:N	23:W:43:PRO:HD3	2.36	0.40
23:W:4:HIS:O	23:W:8:ILE:HG13	2.21	0.40
30:4:65:THR:O	30:4:82:GLY:HA3	2.22	0.40
1:A:1206:U:H2'	1:A:1207:A:O4'	2.22	0.40
1:A:1213:C:C2'	1:A:1214:G:H5'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:A:O2'	1:A:129:A:H5'	2.21	0.40
1:A:189:A:OP1	14:N:171:ARG:NH2	2.55	0.40
1:A:2115:U:H2'	1:A:2116:U:C6	2.57	0.40
1:A:2123:A:P	14:N:89:ASN:ND2	2.94	0.40
1:A:2838:A:H2'	1:A:2839:C:O4'	2.21	0.40
1:A:2892:G:C6	1:A:2893:C:N3	2.90	0.40
1:A:397:A:P	37:A:4317:HOH:O	2.79	0.40
1:A:2099:G:N1	31:A:9001:SPR:O2A	2.47	0.40
2:B:3008:G:P	37:B:5071:HOH:O	2.79	0.40
3:C:173:GLY:O	3:C:176:HIS:HB3	2.20	0.40
3:C:215:ILE:HG13	3:C:216:SER:N	2.37	0.40
8:H:22:VAL:HG21	8:H:104:ALA:HB2	2.02	0.40
9:I:20:VAL:O	9:I:24:VAL:HG23	2.21	0.40
11:K:79:PHE:HB3	11:K:103:VAL:HG11	2.02	0.40
13:M:61:ALA:HA	37:M:8564:HOH:O	2.21	0.40
14:N:61:ILE:CG2	14:N:62:VAL:N	2.84	0.40
15:O:161:GLY:O	15:O:162:ASP:C	2.59	0.40
19:S:61:GLN:CD	37:S:8541:HOH:O	2.59	0.40
23:W:8:ILE:HG21	23:W:59:ILE:HG13	2.03	0.40
26:Z:131:GLN:O	26:Z:132:ASP:HB2	2.21	0.40
29:3:18:ASN:HD22	29:3:18:ASN:HA	1.64	0.40
1:A:1164:U:H6	1:A:1164:U:O5'	2.05	0.40
1:A:1494:A:C4	1:A:1495:C:C5	3.10	0.40
1:A:1562:C:C2'	1:A:1562:C:O2	2.69	0.40
1:A:1592:G:C5	1:A:1593:C:C4	3.09	0.40
1:A:2034:U:H2'	1:A:2035:C:H6	1.87	0.40
1:A:2038:A:O2'	1:A:2039:A:H5'	2.21	0.40
1:A:2502:C:H2'	1:A:2503:A:C5'	2.50	0.40
1:A:611:U:H2'	1:A:612:U:C6	2.57	0.40
31:A:9001:SPR:H6	31:A:9001:SPR:H3	1.84	0.40
31:A:9001:SPR:C8A	31:A:9001:SPR:O2A	2.70	0.40
3:C:36:ASP:HB2	3:C:85:ASP:H	1.86	0.40
4:D:41:PHE:HB3	4:D:190:MET:HE3	2.03	0.40
6:F:95:THR:CG2	6:F:174:VAL:HG22	2.51	0.40
6:F:91:ALA:HB2	6:F:106:PHE:CD2	2.56	0.40
7:G:11:VAL:HG11	7:G:22:VAL:HG13	2.04	0.40
7:G:91:PHE:HA	7:G:92:PRO:HD3	1.91	0.40
9:I:12:ILE:HG13	37:I:6833:HOH:O	2.21	0.40
10:J:167:ALA:HA	37:J:8362:HOH:O	2.20	0.40
10:J:26:LYS:CG	10:J:28:ILE:H	2.25	0.40
10:J:82:LYS:CB	10:J:82:LYS:NZ	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:38:LYS:HE2	15:O:107:ASN:ND2	2.36	0.40
15:O:163:PHE:CZ	15:O:164:ASP:OD2	2.73	0.40
15:O:42:HIS:CG	15:O:62:HIS:HE1	2.40	0.40
2:B:3004:G:O2'	15:O:44:ARG:NH2	2.55	0.40
22:V:14:GLU:HA	22:V:15:PRO:HD2	1.93	0.40
27:1:30:GLU:O	27:1:33:HIS:HB3	2.21	0.40
28:2:28:HIS:O	28:2:32:LYS:N	2.48	0.40
1:A:2462:G:O6	30:4:61:PRO:HG3	2.21	0.40
1:A:2397:G:C5	1:A:2465:A:C6	3.10	0.40
1:A:255:A:C5	1:A:256:C:C4	3.10	0.40
1:A:2612:A:H2'	1:A:2649:A:N6	2.37	0.40
1:A:206:G:O2'	1:A:438:C:N3	2.48	0.40
2:B:3065:A:C2'	2:B:3066:G:OP2	2.69	0.40
3:C:149:ASP:OD1	3:C:151:GLN:CB	2.69	0.40
3:C:51:ARG:NH1	3:C:51:ARG:HB3	2.36	0.40
4:D:156:LYS:HE3	37:D:8633:HOH:O	2.21	0.40
5:E:37:ALA:O	5:E:41:ASN:ND2	2.54	0.40
6:F:103:ASN:ND2	6:F:134:LEU:H	2.19	0.40
1:A:263:U:C2	8:H:59:ILE:HD12	2.57	0.40
11:K:39:VAL:HG11	11:K:107:ASN:HB2	2.04	0.40
14:N:69:LYS:O	14:N:73:ARG:NH1	2.55	0.40
18:R:53:HIS:O	18:R:55:ARG:N	2.55	0.40
1:A:840:U:H2'	19:S:128:ARG:NH1	2.37	0.40
21:U:113:GLU:O	21:U:114:SER:C	2.59	0.40
25:Y:73:ARG:C	25:Y:85:VAL:HG13	2.42	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
3	C	235/239 (98%)	205 (87%)	26 (11%)	4 (2%)	11 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	335/337 (99%)	307 (92%)	21 (6%)	7 (2%)	8	38
5	E	244/246 (99%)	225 (92%)	18 (7%)	1 (0%)	38	78
6	F	134/176 (76%)	95 (71%)	27 (20%)	12 (9%)	1	4
7	G	170/177 (96%)	158 (93%)	12 (7%)	0	100	100
8	H	117/119 (98%)	103 (88%)	12 (10%)	2 (2%)	11	44
9	I	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
10	J	152/167 (91%)	129 (85%)	17 (11%)	6 (4%)	3	20
11	K	140/145 (97%)	131 (94%)	5 (4%)	4 (3%)	5	28
12	L	130/132 (98%)	117 (90%)	11 (8%)	2 (2%)	12	48
13	M	141/164 (86%)	118 (84%)	20 (14%)	3 (2%)	8	38
14	N	192/194 (99%)	172 (90%)	18 (9%)	2 (1%)	18	59
15	O	184/186 (99%)	165 (90%)	13 (7%)	6 (3%)	4	25
16	P	113/115 (98%)	110 (97%)	3 (3%)	0	100	100
17	Q	141/148 (95%)	138 (98%)	2 (1%)	1 (1%)	25	67
18	R	93/95 (98%)	87 (94%)	5 (5%)	1 (1%)	17	56
19	S	148/154 (96%)	138 (93%)	10 (7%)	0	100	100
20	T	79/84 (94%)	72 (91%)	7 (9%)	0	100	100
21	U	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
22	V	51/66 (77%)	47 (92%)	4 (8%)	0	100	100
23	W	63/70 (90%)	57 (90%)	4 (6%)	2 (3%)	5	26
24	X	152/154 (99%)	145 (95%)	6 (4%)	1 (1%)	25	67
25	Y	80/91 (88%)	71 (89%)	7 (9%)	2 (2%)	6	32
26	Z	140/240 (58%)	138 (99%)	2 (1%)	0	100	100
27	1	71/73 (97%)	63 (89%)	7 (10%)	1 (1%)	13	49
28	2	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
29	3	42/48 (88%)	41 (98%)	1 (2%)	0	100	100
30	4	90/92 (98%)	85 (94%)	3 (3%)	2 (2%)	8	36
All	All	3633/4235 (86%)	3299 (91%)	275 (8%)	59 (2%)	11	46

All (59) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	139	ASP

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Mol	Chain	Res	Type
6	F	93	LEU
6	F	95	THR
6	F	137	PRO
6	F	173	GLU
8	H	101	ALA
10	J	162	SER
10	J	164	ALA
13	M	80	ASP
15	O	154	LEU
15	O	164	ASP
15	O	183	ASP
3	C	34	ASP
3	C	37	VAL
4	D	34	GLY
4	D	169	GLY
6	F	11	HIS
6	F	16	PRO
10	J	138	PRO
11	K	5	GLU
11	K	7	ASP
11	K	143	LYS
12	L	119	GLN
17	Q	116	SER
23	W	43	PRO
30	4	57	GLY
3	C	132	ASP
4	D	184	ASP
6	F	20	LYS
6	F	171	ASP
8	H	64	PRO
10	J	40	PRO
10	J	72	VAL
14	N	140	ALA
15	O	162	ASP
15	O	181	ASP
24	X	77	ALA
25	Y	77	PHE
30	4	56	PRO
6	F	36	ASN
6	F	147	ALA
12	L	126	SER
13	M	21	ARG

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Mol	Chain	Res	Type
15	O	167	ASP
27	1	81	LYS
4	D	2	GLN
4	D	185	GLY
5	E	232	LEU
6	F	61	PHE
14	N	18	GLY
18	R	54	PRO
6	F	82	GLU
10	J	140	PRO
13	M	147	GLU
23	W	40	PRO
4	D	5	ARG
11	K	78	ILE
25	Y	70	ILE
3	C	112	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	179/181 (99%)	166 (93%)	13 (7%)	16	50
4	D	282/282 (100%)	264 (94%)	18 (6%)	20	57
5	E	193/193 (100%)	178 (92%)	15 (8%)	15	47
6	F	117/147 (80%)	106 (91%)	11 (9%)	10	37
7	G	152/155 (98%)	147 (97%)	5 (3%)	43	79
8	H	92/92 (100%)	91 (99%)	1 (1%)	78	93
9	I	27/283 (10%)	27 (100%)	0	100	100
10	J	122/122 (100%)	111 (91%)	11 (9%)	11	40
11	K	118/121 (98%)	107 (91%)	11 (9%)	10	38
12	L	106/106 (100%)	103 (97%)	3 (3%)	49	82
13	M	112/126 (89%)	108 (96%)	4 (4%)	40	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	166/166 (100%)	157 (95%)	9 (5%)	26	64
15	O	149/149 (100%)	144 (97%)	5 (3%)	42	78
16	P	93/93 (100%)	90 (97%)	3 (3%)	44	79
17	Q	113/116 (97%)	110 (97%)	3 (3%)	50	82
18	R	79/79 (100%)	75 (95%)	4 (5%)	28	66
19	S	117/121 (97%)	112 (96%)	5 (4%)	33	72
20	T	71/73 (97%)	71 (100%)	0	100	100
21	U	105/105 (100%)	103 (98%)	2 (2%)	62	88
22	V	44/52 (85%)	42 (96%)	2 (4%)	32	71
23	W	51/56 (91%)	50 (98%)	1 (2%)	60	87
24	X	130/130 (100%)	122 (94%)	8 (6%)	21	58
25	Y	66/73 (90%)	61 (92%)	5 (8%)	15	48
26	Z	120/195 (62%)	112 (93%)	8 (7%)	19	54
27	1	56/56 (100%)	50 (89%)	6 (11%)	8	29
28	2	46/46 (100%)	46 (100%)	0	100	100
29	3	42/44 (96%)	41 (98%)	1 (2%)	54	85
30	4	79/79 (100%)	73 (92%)	6 (8%)	15	48
All	All	3027/3441 (88%)	2867 (95%)	160 (5%)	26	65

All (160) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	3	ARG
3	C	33	GLU
3	C	36	ASP
3	C	55	VAL
3	C	68	ILE
3	C	69	LEU
3	C	94	LEU
3	C	120	ARG
3	C	131	HIS
3	C	153	ARG
3	C	179	MET
3	C	187	PRO
3	C	217	ARG
4	D	7	ARG

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Mol	Chain	Res	Type
4	D	11	LEU
4	D	27	ASN
4	D	33	ASP
4	D	63	GLU
4	D	97	LEU
4	D	98	THR
4	D	103	ASP
4	D	162	MET
4	D	195	ARG
4	D	234	ARG
4	D	251	VAL
4	D	254	GLN
4	D	256	GLN
4	D	264	GLU
4	D	304	PRO
4	D	307	ARG
4	D	312	ARG
5	E	2	GLN
5	E	27	ARG
5	E	67	GLN
5	E	76	ARG
5	E	81	PRO
5	E	94	THR
5	E	115	LEU
5	E	136	VAL
5	E	187	ARG
5	E	214	THR
5	E	222	ASP
5	E	223	LEU
5	E	234	VAL
5	E	236	THR
5	E	240	LEU
6	F	24	HIS
6	F	50	VAL
6	F	61	PHE
6	F	95	THR
6	F	99	ASP
6	F	100	ASP
6	F	131	THR
6	F	133	ASN
6	F	136	ARG
6	F	137	PRO

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Mol	Chain	Res	Type
6	F	149	ARG
7	G	7	ILE
7	G	36	PRO
7	G	54	ASP
7	G	102	VAL
7	G	164	ASP
8	H	100	ASP
10	J	1	LYS
10	J	59	ASN
10	J	72	VAL
10	J	73	GLN
10	J	82	LYS
10	J	86	ARG
10	J	94	ARG
10	J	142	VAL
10	J	150	LYS
10	J	155	PRO
10	J	166	ASN
11	K	46	ILE
11	K	52	GLN
11	K	74	ARG
11	K	76	ASP
11	K	79	PHE
11	K	107	ASN
11	K	112	ASP
11	K	120	SER
11	K	125	SER
11	K	127	ILE
11	K	131	THR
12	L	7	ASP
12	L	10	GLN
12	L	98	VAL
13	M	30	ARG
13	M	35	ARG
13	M	80	ASP
13	M	117	GLU
14	N	46	LEU
14	N	48	ARG
14	N	68	ARG
14	N	81	ARG
14	N	87	MET
14	N	93	ARG

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Mol	Chain	Res	Type
14	N	99	ARG
14	N	120	VAL
14	N	164	THR
15	O	26	LEU
15	O	127	LEU
15	O	128	ASP
15	O	152	GLU
15	O	163	PHE
16	P	3	THR
16	P	28	ASP
16	P	111	VAL
17	Q	52	LYS
17	Q	91	LYS
17	Q	98	ILE
18	R	11	ARG
18	R	16	ASN
18	R	57	ASP
18	R	95	GLU
19	S	13	THR
19	S	39	THR
19	S	82	GLU
19	S	130	MET
19	S	132	ARG
21	U	39	ASN
21	U	73	HIS
22	V	9	CYS
22	V	32	CYS
23	W	43	PRO
24	X	4	LEU
24	X	35	VAL
24	X	52	VAL
24	X	73	LEU
24	X	122	ARG
24	X	142	ASP
24	X	146	ILE
24	X	154	ARG
25	Y	15	ARG
25	Y	27	ASP
25	Y	44	ASP
25	Y	72	VAL
25	Y	79	GLU
26	Z	154	ARG

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Mol	Chain	Res	Type
26	Z	163	THR
26	Z	172	THR
26	Z	186	ARG
26	Z	189	ASN
26	Z	200	THR
26	Z	203	VAL
26	Z	204	ARG
27	1	11	THR
27	1	32	LYS
27	1	42	CYS
27	1	49	ARG
27	1	60	CYS
27	1	64	ILE
29	3	18	ASN
30	4	14	CYS
30	4	38	ARG
30	4	42	ARG
30	4	56	PRO
30	4	65	THR
30	4	74	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	47	HIS
3	C	92	ASN
3	C	127	GLN
3	C	199	HIS
4	D	27	ASN
4	D	145	HIS
4	D	238	ASN
4	D	260	HIS
4	D	318	ASN
4	D	332	ASN
5	E	2	GLN
5	E	39	GLN
5	E	129	HIS
6	F	103	ASN
6	F	133	ASN
7	G	106	ASN
7	G	143	GLN
9	I	17	GLN

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Mol	Chain	Res	Type
9	I	64	ASN
10	J	8	ASN
10	J	35	ASN
10	J	55	GLN
10	J	58	HIS
10	J	59	ASN
10	J	69	ASN
10	J	74	ASN
10	J	91	HIS
10	J	129	ASN
10	J	130	HIS
10	J	166	ASN
11	K	52	GLN
11	K	107	ASN
12	L	10	GLN
12	L	42	ASN
13	M	18	HIS
13	M	41	HIS
13	M	58	GLN
13	M	116	HIS
14	N	26	HIS
14	N	58	GLN
14	N	89	ASN
14	N	106	ASN
14	N	176	GLN
15	O	107	ASN
15	O	140	GLN
17	Q	50	GLN
17	Q	66	GLN
17	Q	73	HIS
17	Q	118	GLN
18	R	16	ASN
18	R	40	HIS
19	S	61	GLN
19	S	94	ASN
19	S	98	ASN
19	S	113	HIS
19	S	117	HIS
19	S	122	GLN
19	S	123	GLN
20	T	53	ASN
21	U	39	ASN

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Mol	Chain	Res	Type
22	V	39	ASN
23	W	60	GLN
24	X	27	HIS
24	X	28	HIS
24	X	31	HIS
24	X	87	HIS
24	X	110	GLN
24	X	119	HIS
24	X	125	HIS
24	X	141	HIS
25	Y	23	HIS
26	Z	134	HIS
26	Z	149	GLN
26	Z	189	ASN
27	1	33	HIS
27	1	70	GLN
28	2	8	GLN
28	2	16	HIS
28	2	28	HIS
29	3	16	ASN
29	3	18	ASN
29	3	41	HIS
29	3	45	ASN
30	4	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2745/2922 (93%)	248 (9%)	0
2	B	121/122 (99%)	15 (12%)	0
All	All	2866/3044 (94%)	263 (9%)	0

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

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Mol	Chain	Res	Type
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	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	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	457	U
1	A	461	C
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

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Mol	Chain	Res	Type
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	898	G
1	A	905	C
1	A	921	G
1	A	923	A
1	A	953	G
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

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Mol	Chain	Res	Type
1	A	1060	C
1	A	1072	G
1	A	1081	A
1	A	1083	C
1	A	1088	A
1	A	1109	U
1	A	1110	G
1	A	1119	G
1	A	1127	C
1	A	1130	U
1	A	1137	G
1	A	1151	G
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	1208	C
1	A	1216	G
1	A	1234	U
1	A	1238	C
1	A	1239	G
1	A	1279	U
1	A	1289	C
1	A	1331	A
1	A	1342	C
1	A	1353	C
1	A	1360	C
1	A	1377	C
1	A	1407	A
1	A	1451	C
1	A	1474	C
1	A	1485	A
1	A	1488	U
1	A	1505	U

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Mol	Chain	Res	Type
1	A	1506	U
1	A	1507	C
1	A	1524	U
1	A	1525	G
1	A	1526	A
1	A	1562	C
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	1752	G
1	A	1778	A
1	A	1798	C
1	A	1820	G
1	A	1829	A
1	A	1856	C
1	A	1879	U
1	A	1904	A
1	A	1919	A
1	A	1942	A
1	A	1943	C
1	A	1971	G
1	A	1973	A
1	A	1974	G
1	A	1978	A
1	A	1979	G
1	A	1980	U

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Mol	Chain	Res	Type
1	A	1996	U
1	A	2004	U
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	2097	G
1	A	2101	A
1	A	2102	G
1	A	2103	A
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	2379	G
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	2510	C
1	A	2511	A
1	A	2533	C
1	A	2537	G
1	A	2541	U

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Mol	Chain	Res	Type
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	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	2812	A
1	A	2825	C
1	A	2840	A
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	3003	A
2	B	3007	G
2	B	3014	G
2	B	3022	G
2	B	3024	U
2	B	3041	C
2	B	3043	G
2	B	3044	A
2	B	3052	A

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Mol	Chain	Res	Type
2	B	3057	A
2	B	3066	G
2	B	3077	A
2	B	3114	G
2	B	3122	C

There are no RNA pucker outliers to report.

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 235 ligands modelled in this entry, 234 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	$\# Z > 2$
31	SPR	A	9001	1	61,62,62	2.99	28 (45%)	76,89,89	3.12	31 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	SPR	A	9001	1	-	0/61/113/113	0/3/4/4

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	A	9001	SPR	C6-C5	-5.40	1.42	1.52
31	A	9001	SPR	O5A-C5A	-4.76	1.33	1.44
31	A	9001	SPR	O15-C1	-4.46	1.21	1.34
31	A	9001	SPR	O4A-C1B	-4.02	1.31	1.41
31	A	9001	SPR	O1C-C1C	-3.82	1.31	1.41
31	A	9001	SPR	O3B-C3B	-2.31	1.40	1.44
31	A	9001	SPR	C3C-C2C	-2.07	1.47	1.52
31	A	9001	SPR	C9-C10	2.00	1.57	1.50
31	A	9001	SPR	C7C-N4C	2.01	1.53	1.46
31	A	9001	SPR	C2B-C3B	2.23	1.58	1.53
31	A	9001	SPR	C2B-C1B	2.24	1.56	1.51
31	A	9001	SPR	C3-C4	2.25	1.57	1.52
31	A	9001	SPR	O15-C15	2.26	1.51	1.47
31	A	9001	SPR	O5B-C5B	2.31	1.50	1.44
31	A	9001	SPR	C14-C13	2.39	1.57	1.50
31	A	9001	SPR	O19-C19	2.65	1.36	1.19
31	A	9001	SPR	C12-C13	3.16	1.43	1.32
31	A	9001	SPR	C6B-C5B	3.43	1.59	1.51
31	A	9001	SPR	O1C-C9	3.47	1.52	1.44
31	A	9001	SPR	C5C-C4C	3.86	1.64	1.53
31	A	9001	SPR	C2C-C1C	4.01	1.63	1.50
31	A	9001	SPR	C2A-C3A	4.38	1.61	1.53
31	A	9001	SPR	C7-C6	5.56	1.65	1.53
31	A	9001	SPR	O1A-C5	5.90	1.58	1.43
31	A	9001	SPR	C4A-C5A	6.18	1.64	1.52
31	A	9001	SPR	C4C-N4C	6.30	1.63	1.48
31	A	9001	SPR	C3C-C4C	6.58	1.68	1.52
31	A	9001	SPR	C14-C15	8.90	1.60	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	A	9001	SPR	C8A-N3A-C7A	-9.17	82.41	110.41
31	A	9001	SPR	C5A-C4A-C3A	-7.41	93.97	110.55
31	A	9001	SPR	O19-C19-C18	-7.19	102.19	125.48
31	A	9001	SPR	O1C-C1C-O5C	-5.98	90.45	110.05
31	A	9001	SPR	C15-C14-C13	-5.86	102.86	113.88
31	A	9001	SPR	C4A-C3A-N3A	-5.33	98.69	111.70
31	A	9001	SPR	C7A-N3A-C3A	-4.59	102.98	113.57
31	A	9001	SPR	C6A-C5A-C4A	-4.32	106.71	113.36
31	A	9001	SPR	C14-C13-C12	-3.71	120.26	125.40
31	A	9001	SPR	C17-O4-C4	-3.71	104.40	114.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	A	9001	SPR	C1C-O5C-C5C	-3.42	105.82	114.19
31	A	9001	SPR	O2A-C2A-C1A	-3.29	103.15	110.03
31	A	9001	SPR	C3-C4-C5	-2.94	106.85	113.19
31	A	9001	SPR	C1A-C2A-C3A	-2.52	105.06	109.33
31	A	9001	SPR	O15-C15-C16	-2.42	102.36	107.95
31	A	9001	SPR	O1-C1-C2	-2.32	119.46	124.70
31	A	9001	SPR	C3C-C2C-C1C	-2.14	105.90	110.85
31	A	9001	SPR	O3B-C3B-C4B	2.08	110.97	107.24
31	A	9001	SPR	O5C-C1C-C2C	2.51	116.75	111.27
31	A	9001	SPR	C1A-O1A-C5	2.55	124.20	118.00
31	A	9001	SPR	O5B-C1B-C2B	2.61	117.21	112.21
31	A	9001	SPR	C3C-C4C-N4C	2.68	121.20	115.05
31	A	9001	SPR	O4A-C1B-C2B	2.89	114.06	108.94
31	A	9001	SPR	C15-O15-C1	2.92	121.59	117.90
31	A	9001	SPR	C3C-C4C-C5C	3.66	117.89	110.14
31	A	9001	SPR	O15-C15-C14	3.78	113.83	107.21
31	A	9001	SPR	O4A-C4A-C5A	3.87	117.19	106.72
31	A	9001	SPR	O5A-C5A-C4A	4.16	117.00	109.14
31	A	9001	SPR	O1C-C9-C8	6.98	124.98	108.19
31	A	9001	SPR	C7C-N4C-C4C	7.52	135.04	113.08
31	A	9001	SPR	C16-C15-C14	7.56	123.58	113.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	A	9001	SPR	9	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%)	-0.07	48 (1%) 70 42	23, 51, 96, 143	0
2	B	122/122 (100%)	0.26	6 (4%) 30 12	37, 70, 100, 150	0
3	C	237/239 (99%)	0.12	10 (4%) 37 15	32, 63, 96, 110	0
4	D	337/337 (100%)	-0.14	2 (0%) 89 71	28, 57, 84, 95	0
5	E	246/246 (100%)	-0.20	1 (0%) 92 77	24, 50, 74, 85	0
6	F	140/176 (79%)	1.53	48 (34%) 0 0	60, 103, 122, 127	0
7	G	172/177 (97%)	0.47	8 (4%) 32 13	43, 68, 92, 98	0
8	H	119/119 (100%)	0.41	4 (3%) 46 20	59, 79, 102, 107	0
9	I	29/348 (8%)	1.84	11 (37%) 0 0	76, 94, 102, 104	0
10	J	156/167 (93%)	0.18	3 (1%) 67 37	35, 58, 85, 93	0
11	K	142/145 (97%)	-0.13	0 100 100	36, 50, 76, 84	0
12	L	132/132 (100%)	-0.01	0 100 100	35, 56, 78, 82	0
13	M	145/164 (88%)	0.50	11 (7%) 15 6	31, 74, 108, 117	0
14	N	194/194 (100%)	0.22	16 (8%) 12 5	37, 55, 91, 98	0
15	O	186/186 (100%)	0.69	22 (11%) 5 2	48, 74, 112, 122	0
16	P	115/115 (100%)	-0.05	0 100 100	39, 59, 75, 79	0
17	Q	143/148 (96%)	0.15	2 (1%) 75 49	38, 60, 76, 84	0
18	R	95/95 (100%)	-0.12	1 (1%) 80 55	38, 51, 64, 79	0
19	S	150/154 (97%)	-0.19	0 100 100	32, 45, 66, 75	0
20	T	81/84 (96%)	0.03	1 (1%) 79 53	47, 65, 84, 89	0
21	U	119/119 (100%)	0.38	7 (5%) 23 9	44, 62, 86, 97	0
22	V	53/66 (80%)	3.18	37 (69%) 0 0	85, 94, 102, 110	0
23	W	65/70 (92%)	1.12	10 (15%) 2 1	55, 81, 112, 118	0
24	X	154/154 (100%)	-0.20	0 100 100	32, 49, 66, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	82/91 (90%)	0.24	4 (4%) 30 12	42, 58, 84, 99	0
26	Z	142/240 (59%)	-0.10	5 (3%) 44 19	25, 46, 70, 85	0
27	1	73/73 (100%)	3.49	46 (63%) 0 0	79, 98, 103, 104	0
28	2	56/56 (100%)	-0.42	0 100 100	30, 39, 45, 49	0
29	3	46/48 (95%)	0.06	1 (2%) 62 33	40, 66, 90, 102	0
30	4	92/92 (100%)	6.46	92 (100%) 0 0	91, 103, 108, 111	0
All	All	6577/7279 (90%)	0.22	396 (6%) 23 9	23, 57, 102, 150	0

All (396) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
30	4	37	ASP	15.5
30	4	65	THR	13.0
30	4	82	GLY	12.9
30	4	84	ARG	12.4
30	4	83	TRP	11.9
30	4	62	THR	11.7
30	4	11	CYS	10.8
30	4	38	ARG	10.7
14	N	71	SER	10.6
27	1	11	THR	9.9
30	4	14	CYS	9.6
30	4	1	MET	9.5
30	4	59	ASP	9.5
27	1	30	GLU	9.5
23	W	1	THR	9.5
30	4	35	TRP	9.1
30	4	33	MET	9.0
30	4	56	PRO	8.6
30	4	8	ASN	8.5
30	4	91	GLN	8.5
27	1	31	ILE	8.4
30	4	85	ALA	8.4
30	4	34	LYS	8.2
30	4	39	GLN	8.1
30	4	71	CYS	8.1
30	4	76	LYS	8.1
30	4	58	GLY	7.9
27	1	26	VAL	7.9
30	4	31	THR	7.9

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Mol	Chain	Res	Type	RSRZ
27	1	20	LEU	7.9
27	1	16	PRO	7.8
14	N	89	ASN	7.6
22	V	51	TRP	7.5
14	N	70	GLY	7.5
27	1	12	GLY	7.4
30	4	77	ALA	7.4
30	4	53	SER	7.4
27	1	44	PHE	7.3
27	1	34	LYS	7.2
27	1	15	GLY	7.2
30	4	75	GLY	7.1
30	4	20	HIS	7.1
30	4	81	GLU	7.1
30	4	2	GLN	7.1
30	4	42	ARG	7.1
2	B	3001	U	7.0
30	4	9	THR	7.0
30	4	22	VAL	7.0
30	4	10	TYR	6.9
30	4	32	GLY	6.8
30	4	4	PRO	6.8
30	4	3	MET	6.8
27	1	35	LYS	6.7
27	1	19	GLY	6.6
30	4	27	SER	6.6
27	1	22	ILE	6.5
30	4	60	LYS	6.5
30	4	48	ASN	6.5
30	4	41	GLU	6.5
30	4	18	GLN	6.5
27	1	45	LYS	6.4
30	4	43	ASN	6.4
30	4	88	LEU	6.3
1	A	1198	U	6.3
30	4	30	GLN	6.2
30	4	86	GLY	6.2
22	V	9	CYS	6.2
30	4	16	GLU	6.2
1	A	1173	A	6.2
30	4	74	CYS	6.2
30	4	78	HIS	6.2

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Mol	Chain	Res	Type	RSRZ
30	4	15	ASN	6.1
27	1	25	ARG	6.1
30	4	68	LYS	6.1
30	4	44	SER	6.0
30	4	61	PRO	6.0
14	N	80	GLY	6.0
30	4	67	LEU	6.0
1	A	735	C	5.8
27	1	23	ARG	5.7
27	1	21	LYS	5.7
22	V	11	THR	5.7
27	1	28	ASP	5.6
22	V	39	ASN	5.6
22	V	52	THR	5.5
27	1	32	LYS	5.5
22	V	54	THR	5.4
6	F	57	THR	5.4
9	I	27	ILE	5.4
22	V	55	ALA	5.4
30	4	55	VAL	5.4
30	4	57	GLY	5.4
30	4	17	HIS	5.3
30	4	21	GLU	5.3
30	4	12	PRO	5.2
9	I	23	ILE	5.2
6	F	69	ILE	5.2
27	1	39	CYS	5.2
15	O	160	SER	5.2
6	F	88	LEU	5.2
30	4	80	ARG	5.2
30	4	36	ILE	5.2
27	1	13	ARG	5.2
22	V	6	CYS	5.1
22	V	53	ASP	5.1
30	4	40	ARG	5.1
27	1	24	VAL	5.0
27	1	18	TYR	5.0
30	4	72	GLY	4.9
1	A	1175	G	4.9
27	1	33	HIS	4.8
27	1	14	PHE	4.8
30	4	24	LYS	4.8

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Mol	Chain	Res	Type	RSRZ
30	4	19	GLU	4.8
30	4	6	ARG	4.8
15	O	179	LEU	4.8
30	4	23	GLU	4.7
30	4	49	ASP	4.7
30	4	52	PHE	4.7
30	4	26	ARG	4.7
30	4	51	LYS	4.6
30	4	47	GLY	4.6
27	1	27	ALA	4.6
3	C	64	ASP	4.6
1	A	1172	G	4.6
30	4	87	ARG	4.6
30	4	66	ASP	4.6
14	N	83	SER	4.5
22	V	40	ALA	4.5
22	V	48	ASN	4.5
30	4	63	LYS	4.5
27	1	40	PRO	4.5
27	1	36	LYS	4.5
15	O	186	LEU	4.4
30	4	45	GLY	4.4
30	4	89	GLU	4.4
27	1	42	CYS	4.4
22	V	36	CYS	4.3
30	4	64	LYS	4.3
22	V	12	ASP	4.3
30	4	13	HIS	4.3
1	A	1171	A	4.3
27	1	37	HIS	4.2
27	1	29	VAL	4.2
1	A	1177	A	4.2
23	W	40	PRO	4.2
6	F	18	ILE	4.2
22	V	4	ARG	4.1
30	4	79	LEU	4.1
14	N	74	ARG	4.1
27	1	10	ARG	4.1
2	B	3024	U	4.1
30	4	5	ARG	4.1
6	F	89	PRO	4.0
6	F	63	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
30	4	25	VAL	4.0
30	4	92	GLU	4.0
27	1	41	VAL	4.0
14	N	81	ARG	4.0
22	V	50	GLU	3.9
22	V	10	GLY	3.9
1	A	1199	A	3.9
27	1	17	ARG	3.9
22	V	43	GLY	3.9
1	A	2237	G	3.9
22	V	29	THR	3.8
27	1	58	GLY	3.8
22	V	25	ASP	3.8
27	1	57	CYS	3.8
30	4	69	TYR	3.8
15	O	162	ASP	3.8
22	V	41	ASP	3.8
23	W	39	ALA	3.7
22	V	49	LEU	3.7
6	F	10	PHE	3.7
14	N	90	ARG	3.7
14	N	77	PHE	3.6
1	A	1168	C	3.6
6	F	75	LEU	3.6
30	4	29	ARG	3.6
14	N	73	ARG	3.6
6	F	66	GLY	3.6
30	4	7	PHE	3.5
15	O	147	ILE	3.5
21	U	119	ALA	3.5
6	F	102	GLY	3.5
21	U	112	LEU	3.5
14	N	72	SER	3.5
6	F	85	GLN	3.4
1	A	1192	A	3.4
27	1	38	LYS	3.4
22	V	28	THR	3.4
6	F	128	LEU	3.4
22	V	13	ILE	3.4
30	4	54	LYS	3.4
6	F	27	ILE	3.4
22	V	19	THR	3.4

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Mol	Chain	Res	Type	RSRZ
20	T	81	ILE	3.3
1	A	736	A	3.3
15	O	184	ILE	3.3
15	O	157	PRO	3.3
22	V	5	GLU	3.3
14	N	78	ASN	3.2
22	V	23	HIS	3.2
6	F	16	PRO	3.1
27	1	43	GLY	3.1
30	4	70	ARG	3.1
13	M	80	ASP	3.1
1	A	1176	C	3.1
1	A	284	C	3.1
1	A	285	A	3.1
23	W	8	ILE	3.1
22	V	22	VAL	3.1
10	J	135	TRP	3.1
1	A	1167	G	3.0
17	Q	1	THR	3.0
15	O	178	THR	3.0
2	B	3002	U	3.0
22	V	27	ALA	3.0
30	4	28	GLY	3.0
30	4	50	GLY	3.0
30	4	73	GLU	3.0
1	A	2344	G	3.0
9	I	24	VAL	3.0
27	1	79	VAL	3.0
6	F	26	GLY	3.0
22	V	8	TYR	3.0
2	B	3023	U	3.0
6	F	170	TYR	3.0
1	A	1169	U	2.9
6	F	90	LEU	2.9
22	V	24	LYS	2.9
4	D	1	PRO	2.9
6	F	62	ASP	2.9
27	1	82	ALA	2.9
3	C	85	ASP	2.9
6	F	23	VAL	2.9
3	C	83	GLY	2.9
22	V	47	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
8	H	106	THR	2.8
13	M	73	VAL	2.8
1	A	1948	G	2.8
1	A	1913	C	2.8
30	4	46	ILE	2.8
6	F	56	ARG	2.8
9	I	65	THR	2.8
1	A	1166	A	2.8
22	V	46	ALA	2.8
1	A	1181	A	2.8
9	I	71	LEU	2.8
15	O	161	GLY	2.8
3	C	36	ASP	2.8
1	A	1190	G	2.7
6	F	130	VAL	2.7
10	J	32	ASP	2.7
1	A	2345	A	2.7
13	M	60	GLU	2.7
22	V	7	ASP	2.7
27	1	47	LEU	2.7
15	O	148	ALA	2.7
9	I	17	GLN	2.6
15	O	138	ASP	2.6
6	F	58	VAL	2.6
6	F	134	LEU	2.6
17	Q	116	SER	2.6
27	1	80	MET	2.6
6	F	17	ARG	2.6
1	A	2433	A	2.6
3	C	62	ASP	2.6
7	G	10	ASP	2.6
8	H	26	THR	2.6
1	A	1180	U	2.6
1	A	960	G	2.6
1	A	2238	A	2.6
5	E	135	GLU	2.6
15	O	127	LEU	2.6
15	O	150	TYR	2.6
15	O	159	TYR	2.6
14	N	82	ARG	2.6
25	Y	41	PHE	2.5
1	A	362	G	2.5

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Mol	Chain	Res	Type	RSRZ
7	G	108	LEU	2.5
23	W	7	GLU	2.5
2	B	3122	C	2.5
13	M	89	PHE	2.5
1	A	1193	A	2.5
6	F	132	VAL	2.5
1	A	1197	G	2.5
1	A	1951	G	2.5
30	4	90	PHE	2.5
22	V	33	SER	2.5
9	I	26	MET	2.5
6	F	171	ASP	2.5
14	N	69	LYS	2.5
26	Z	108	ASP	2.5
9	I	15	TRP	2.5
1	A	970	U	2.5
6	F	104	PHE	2.5
15	O	183	ASP	2.5
6	F	106	PHE	2.4
6	F	84	LEU	2.4
23	W	52	ALA	2.4
9	I	64	ASN	2.4
1	A	2436	U	2.4
6	F	15	GLU	2.4
1	A	1182	C	2.4
13	M	81	VAL	2.4
3	C	237	GLY	2.4
1	A	1525	G	2.4
6	F	103	ASN	2.4
15	O	166	ALA	2.4
27	1	59	HIS	2.4
23	W	3	LEU	2.4
6	F	28	GLY	2.4
13	M	59	GLU	2.4
6	F	24	HIS	2.4
6	F	172	VAL	2.4
15	O	175	LEU	2.4
3	C	82	VAL	2.4
6	F	166	ILE	2.4
6	F	44	ILE	2.3
13	M	118	LEU	2.3
10	J	83	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
6	F	98	PHE	2.3
6	F	11	HIS	2.3
26	Z	103	THR	2.3
9	I	16	LYS	2.3
1	A	282	C	2.3
1	A	2239	C	2.3
1	A	713	U	2.3
21	U	37	GLN	2.3
1	A	1170	U	2.3
8	H	90	GLU	2.3
7	G	95	VAL	2.3
6	F	25	MET	2.3
26	Z	98	GLN	2.3
13	M	104	ASP	2.3
6	F	83	PHE	2.3
15	O	74	PRO	2.2
27	1	46	LYS	2.2
6	F	67	ASP	2.2
26	Z	102	LEU	2.2
1	A	2249	G	2.2
15	O	140	GLN	2.2
22	V	26	GLY	2.2
13	M	58	GLN	2.2
15	O	152	GLU	2.2
6	F	43	GLU	2.2
6	F	86	THR	2.2
1	A	280	C	2.2
1	A	1174	A	2.2
25	Y	88	GLU	2.2
22	V	30	HIS	2.2
21	U	49	GLU	2.1
21	U	117	ASP	2.1
6	F	80	ALA	2.1
1	A	130	C	2.1
7	G	124	VAL	2.1
18	R	95	GLU	2.1
23	W	59	ILE	2.1
7	G	131	LEU	2.1
1	A	1914	C	2.1
7	G	100	ASP	2.1
6	F	45	THR	2.1
6	F	73	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
22	V	14	GLU	2.1
27	1	56	MET	2.1
3	C	37	VAL	2.1
7	G	129	GLU	2.1
14	N	76	ARG	2.1
25	Y	40	HIS	2.1
21	U	116	ASP	2.1
1	A	1200	A	2.1
6	F	54	ALA	2.1
14	N	75	THR	2.1
15	O	151	ASP	2.1
7	G	87	PHE	2.1
4	D	117	GLU	2.1
8	H	44	SER	2.1
6	F	137	PRO	2.1
15	O	94	GLU	2.0
3	C	112	PRO	2.0
9	I	20	VAL	2.0
3	C	96	LEU	2.0
2	B	3025	G	2.0
1	A	1912	A	2.0
23	W	33	VAL	2.0
21	U	82	THR	2.0
23	W	38	GLY	2.0
1	A	1947	G	2.0
25	Y	7	GLU	2.0
29	3	36	ASN	2.0
26	Z	235	GLU	2.0
13	M	123	ASP	2.0
27	1	61	GLY	2.0
13	M	106	VAL	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 ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
33	NA	A	8356	1/1	0.83	0.69	40.87	58,58,58,58	0
34	CL	A	8515	1/1	0.87	0.59	24.89	100,100,100,100	0
33	NA	A	8372	1/1	0.83	0.67	22.22	55,55,55,55	0
33	NA	A	8382	1/1	0.55	0.38	19.39	62,62,62,62	0
33	NA	B	8383	1/1	0.71	0.65	17.47	63,63,63,63	0
33	NA	A	8371	1/1	0.69	0.34	15.47	54,54,54,54	0
34	CL	D	8519	1/1	0.93	0.50	15.14	65,65,65,65	0
33	NA	A	8374	1/1	0.90	0.60	14.99	63,63,63,63	0
33	NA	A	8362	1/1	0.82	0.39	14.68	69,69,69,69	0
33	NA	A	8373	1/1	0.74	0.52	12.99	59,59,59,59	0
33	NA	A	8321	1/1	0.91	0.42	12.17	39,39,39,39	0
34	CL	A	8505	1/1	0.92	0.65	10.79	88,88,88,88	0
33	NA	A	8331	1/1	0.72	0.36	10.11	61,61,61,61	0
33	NA	A	8379	1/1	0.94	0.24	9.22	41,41,41,41	0
33	NA	A	8378	1/1	0.91	0.43	8.21	37,37,37,37	0
33	NA	A	8323	1/1	0.91	0.25	7.91	50,50,50,50	0
31	SPR	A	9001	59/59	0.83	0.36	7.31	78,88,95,95	0
33	NA	A	8376	1/1	0.96	0.28	7.04	78,78,78,78	0
33	NA	A	8308	1/1	0.88	0.22	6.51	69,69,69,69	0
33	NA	S	8386	1/1	0.83	0.27	6.29	53,53,53,53	0
33	NA	A	8335	1/1	0.98	0.23	5.87	52,52,52,52	0
33	NA	A	8365	1/1	0.74	0.40	5.32	49,49,49,49	0
33	NA	S	8337	1/1	0.70	0.32	3.42	49,49,49,49	0
33	NA	A	8310	1/1	0.91	0.23	3.29	29,29,29,29	0
32	MG	Z	8109	1/1	0.86	0.22	3.04	53,53,53,53	0
33	NA	A	8303	1/1	0.96	0.20	2.78	51,51,51,51	0
33	NA	A	8332	1/1	0.81	0.23	2.52	58,58,58,58	0
32	MG	A	8067	1/1	0.93	0.23	2.42	50,50,50,50	0
33	NA	A	8366	1/1	0.90	0.27	2.41	49,49,49,49	0
33	NA	A	8381	1/1	0.95	0.20	2.07	51,51,51,51	0
34	CL	A	8512	1/1	0.92	0.20	1.35	32,32,32,32	0
33	NA	A	8368	1/1	0.92	0.16	1.10	47,47,47,47	0
33	NA	A	8326	1/1	0.89	0.27	0.56	46,46,46,46	0
33	NA	A	8314	1/1	0.97	0.17	0.47	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	K	A	8602	1/1	0.83	0.29	0.38	68,68,68,68	0
32	MG	A	8064	1/1	0.95	0.16	0.18	24,24,24,24	0
32	MG	A	8101	1/1	0.94	0.16	0.11	55,55,55,55	0
33	NA	A	8361	1/1	0.97	0.14	0.09	53,53,53,53	0
34	CL	N	8518	1/1	0.82	0.22	-0.12	56,56,56,56	0
34	CL	P	8508	1/1	0.95	0.19	-0.23	93,93,93,93	0
32	MG	1	8105	1/1	0.86	0.29	-0.33	44,44,44,44	0
33	NA	A	8350	1/1	0.96	0.14	-0.39	34,34,34,34	0
33	NA	A	8305	1/1	0.89	0.15	-0.47	34,34,34,34	0
33	NA	A	8324	1/1	0.81	0.15	-0.48	51,51,51,51	0
32	MG	A	8044	1/1	0.98	0.14	-0.56	52,52,52,52	0
34	CL	O	8507	1/1	0.88	0.24	-0.60	62,62,62,62	0
36	CD	4	8404	1/1	0.59	0.79	-0.72	156,156,156,156	0
33	NA	J	8309	1/1	0.95	0.14	-0.79	21,21,21,21	0
36	CD	V	8401	1/1	0.79	0.48	-1.03	142,142,142,142	0
34	CL	K	8521	1/1	0.94	0.14	-1.04	46,46,46,46	0
33	NA	A	8333	1/1	0.88	0.13	-1.14	33,33,33,33	0
34	CL	4	8504	1/1	0.66	0.69	-1.16	95,95,95,95	0
33	NA	M	8380	1/1	0.98	0.15	-1.30	55,55,55,55	0
33	NA	A	8338	1/1	0.98	0.13	-1.32	67,67,67,67	0
32	MG	A	8086	1/1	0.98	0.07	-1.33	50,50,50,50	0
33	NA	A	8353	1/1	0.94	0.12	-1.53	38,38,38,38	0
32	MG	A	8112	1/1	0.98	0.15	-1.65	44,44,44,44	0
33	NA	A	8317	1/1	0.95	0.12	-1.88	27,27,27,27	0
32	MG	A	8074	1/1	0.95	0.08	-1.90	31,31,31,31	0
32	MG	U	8073	1/1	0.93	0.19	-2.03	42,42,42,42	0
32	MG	A	8018	1/1	0.95	0.11	-2.03	61,61,61,61	0
33	NA	A	8327	1/1	0.95	0.13	-2.09	32,32,32,32	0
36	CD	1	8403	1/1	0.85	0.28	-2.12	138,138,138,138	0
32	MG	A	8055	1/1	0.96	0.08	-2.36	71,71,71,71	0
32	MG	A	8107	1/1	0.99	0.04	-2.39	47,47,47,47	0
32	MG	C	8065	1/1	0.94	0.11	-2.49	57,57,57,57	0
36	CD	2	8402	1/1	0.98	0.06	-2.56	59,59,59,59	0
33	NA	A	8339	1/1	0.98	0.14	-2.57	16,16,16,16	0
33	NA	A	8320	1/1	0.93	0.12	-2.77	33,33,33,33	0
32	MG	A	8012	1/1	0.98	0.11	-2.79	52,52,52,52	0
32	MG	A	8058	1/1	0.98	0.09	-2.82	43,43,43,43	0
33	NA	K	8346	1/1	0.96	0.08	-2.84	27,27,27,27	0
33	NA	R	8348	1/1	0.93	0.11	-2.99	37,37,37,37	0
32	MG	A	8027	1/1	0.95	0.05	-3.10	63,63,63,63	0
32	MG	A	8060	1/1	0.96	0.12	-3.20	45,45,45,45	0
32	MG	A	8071	1/1	0.96	0.13	-3.26	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8057	1/1	0.95	0.11	-3.28	49,49,49,49	0
32	MG	A	8108	1/1	0.97	0.09	-3.29	88,88,88,88	0
32	MG	A	8001	1/1	0.79	0.12	-3.43	39,39,39,39	0
32	MG	A	8002	1/1	0.99	0.10	-3.52	31,31,31,31	0
32	MG	A	8015	1/1	0.93	0.10	-3.59	57,57,57,57	0
32	MG	A	8038	1/1	0.97	0.10	-3.61	35,35,35,35	0
32	MG	A	8056	1/1	0.98	0.09	-3.83	53,53,53,53	0
33	NA	A	8344	1/1	0.89	0.09	-3.95	30,30,30,30	0
33	NA	A	8343	1/1	0.89	0.09	-4.27	16,16,16,16	0
33	NA	C	8345	1/1	0.97	0.10	-4.43	42,42,42,42	0
32	MG	A	8062	1/1	0.90	0.11	-4.51	72,72,72,72	0
32	MG	A	8004	1/1	0.97	0.07	-4.53	48,48,48,48	0
32	MG	A	8096	1/1	0.92	0.09	-4.60	53,53,53,53	0
32	MG	A	8003	1/1	0.97	0.10	-4.67	24,24,24,24	0
32	MG	A	8053	1/1	0.94	0.11	-4.69	52,52,52,52	0
32	MG	A	8033	1/1	0.95	0.07	-4.82	30,30,30,30	0
32	MG	A	8006	1/1	0.94	0.08	-4.86	48,48,48,48	0
32	MG	A	8039	1/1	0.89	0.06	-5.21	50,50,50,50	0
32	MG	4	8078	1/1	0.90	0.26	-5.57	74,74,74,74	0
32	MG	A	8032	1/1	0.98	0.05	-5.63	34,34,34,34	0
32	MG	A	8017	1/1	0.98	0.03	-5.72	27,27,27,27	0
32	MG	A	8054	1/1	0.98	0.08	-6.47	48,48,48,48	0
32	MG	A	8019	1/1	0.99	0.07	-6.51	35,35,35,35	0
32	MG	A	8059	1/1	0.95	0.08	-6.53	31,31,31,31	0
32	MG	A	8008	1/1	0.97	0.07	-6.79	49,49,49,49	0
32	MG	A	8013	1/1	0.99	0.12	-7.34	46,46,46,46	0
32	MG	A	8010	1/1	0.96	0.05	-7.69	40,40,40,40	0
32	MG	A	8035	1/1	0.97	0.06	-7.73	54,54,54,54	0
32	MG	A	8014	1/1	0.97	0.06	-7.81	30,30,30,30	0
33	NA	N	8347	1/1	0.99	0.05	-7.92	21,21,21,21	0
32	MG	A	8091	1/1	0.96	0.07	-8.24	48,48,48,48	0
32	MG	A	8034	1/1	0.94	0.06	-8.99	39,39,39,39	0
32	MG	A	8020	1/1	0.98	0.05	-9.64	51,51,51,51	0
32	MG	A	8080	1/1	0.97	0.05	-10.62	50,50,50,50	0
33	NA	A	8325	1/1	0.97	0.09	-10.69	52,52,52,52	0
32	MG	A	8084	1/1	0.97	0.08	-10.93	48,48,48,48	0
32	MG	A	8077	1/1	0.97	0.07	-12.37	31,31,31,31	0
32	MG	A	8007	1/1	0.99	0.04	-12.43	23,23,23,23	0
32	MG	A	8052	1/1	0.99	0.05	-31.47	45,45,45,45	0
32	MG	A	8100	1/1	0.97	0.12	-	69,69,69,69	0
32	MG	A	8023	1/1	0.90	0.07	-	42,42,42,42	0
32	MG	A	8099	1/1	0.96	0.08	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	K	A	8603	1/1	0.84	0.36	-	88,88,88,88	0
33	NA	A	8354	1/1	0.90	0.16	-	40,40,40,40	0
33	NA	A	8336	1/1	0.89	0.19	-	49,49,49,49	0
34	CL	A	8517	1/1	0.87	0.31	-	55,55,55,55	0
32	MG	A	8119	1/1	0.88	0.36	-	71,71,71,71	0
32	MG	A	8037	1/1	0.99	0.10	-	48,48,48,48	0
34	CL	R	8511	1/1	0.81	0.44	-	63,63,63,63	0
32	MG	A	8005	1/1	0.98	0.10	-	44,44,44,44	0
32	MG	A	8009	1/1	0.98	0.06	-	20,20,20,20	0
33	NA	A	8315	1/1	0.97	0.14	-	30,30,30,30	0
33	NA	A	8330	1/1	0.93	0.19	-	43,43,43,43	0
33	NA	A	8370	1/1	0.86	0.35	-	49,49,49,49	0
33	NA	A	8318	1/1	0.95	0.17	-	34,34,34,34	0
33	NA	A	8355	1/1	0.85	0.36	-	55,55,55,55	0
33	NA	A	8334	1/1	0.97	0.06	-	36,36,36,36	0
32	MG	A	8022	1/1	0.96	0.09	-	41,41,41,41	0
32	MG	A	8081	1/1	0.93	0.18	-	58,58,58,58	0
33	NA	A	8306	1/1	0.92	0.51	-	56,56,56,56	0
34	CL	A	8522	1/1	0.89	0.43	-	75,75,75,75	0
34	CL	C	8509	1/1	0.94	0.28	-	86,86,86,86	0
33	NA	A	8385	1/1	0.88	0.39	-	41,41,41,41	0
33	NA	A	8377	1/1	0.85	0.25	-	60,60,60,60	0
33	NA	A	8307	1/1	0.94	0.10	-	39,39,39,39	0
32	MG	A	8049	1/1	0.50	0.60	-	89,89,89,89	0
34	CL	A	8513	1/1	0.94	0.12	-	56,56,56,56	0
32	MG	A	8087	1/1	0.96	0.06	-	48,48,48,48	0
32	MG	A	8011	1/1	0.98	0.10	-	52,52,52,52	0
32	MG	A	8040	1/1	0.88	0.19	-	78,78,78,78	0
32	MG	A	8110	1/1	0.89	0.13	-	47,47,47,47	0
32	MG	A	8090	1/1	0.74	0.29	-	36,36,36,36	0
32	MG	A	8066	1/1	0.95	0.13	-	83,83,83,83	0
32	MG	A	8051	1/1	0.94	0.09	-	56,56,56,56	0
32	MG	A	8068	1/1	0.94	0.13	-	58,58,58,58	0
32	MG	A	8043	1/1	0.95	0.08	-	39,39,39,39	0
36	CD	P	8405	1/1	0.74	0.44	-	169,169,169,169	0
32	MG	A	8113	1/1	0.90	0.11	-	45,45,45,45	0
33	NA	A	8316	1/1	0.94	0.34	-	51,51,51,51	0
33	NA	A	8357	1/1	0.89	0.17	-	67,67,67,67	0
33	NA	A	8364	1/1	0.79	0.32	-	40,40,40,40	0
33	NA	E	8304	1/1	0.88	0.12	-	35,35,35,35	0
33	NA	A	8342	1/1	0.94	0.24	-	47,47,47,47	0
33	NA	B	8351	1/1	0.79	0.23	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	NA	A	8329	1/1	0.40	0.52	-	70,70,70,70	0
32	MG	A	8116	1/1	0.88	0.17	-	67,67,67,67	0
33	NA	A	8367	1/1	0.92	0.20	-	52,52,52,52	0
33	NA	A	8375	1/1	0.91	0.34	-	53,53,53,53	0
33	NA	A	8313	1/1	0.90	0.23	-	63,63,63,63	0
32	MG	A	8115	1/1	0.89	0.10	-	59,59,59,59	0
32	MG	A	8063	1/1	0.97	0.06	-	78,78,78,78	0
34	CL	A	8503	1/1	0.83	0.33	-	50,50,50,50	0
33	NA	A	8311	1/1	0.96	0.09	-	42,42,42,42	0
32	MG	A	8030	1/1	0.99	0.09	-	26,26,26,26	0
32	MG	L	8069	1/1	0.95	0.05	-	50,50,50,50	0
32	MG	A	8094	1/1	0.98	0.14	-	85,85,85,85	0
33	NA	A	8341	1/1	0.56	0.19	-	43,43,43,43	0
32	MG	A	8098	1/1	0.97	0.20	-	50,50,50,50	0
32	MG	A	8048	1/1	0.97	0.09	-	45,45,45,45	0
32	MG	A	8026	1/1	0.99	0.04	-	11,11,11,11	0
33	NA	A	8322	1/1	0.93	0.42	-	46,46,46,46	0
32	MG	A	8046	1/1	0.95	0.08	-	79,79,79,79	0
32	MG	A	8025	1/1	0.99	0.08	-	60,60,60,60	0
32	MG	A	8093	1/1	0.87	0.23	-	56,56,56,56	0
32	MG	A	8070	1/1	0.88	0.59	-	66,66,66,66	0
32	MG	A	8114	1/1	0.94	0.46	-	92,92,92,92	0
34	CL	A	8514	1/1	0.93	0.21	-	61,61,61,61	0
32	MG	A	8061	1/1	0.92	0.09	-	44,44,44,44	0
33	NA	A	8328	1/1	0.88	0.19	-	45,45,45,45	0
33	NA	A	8352	1/1	0.86	0.43	-	52,52,52,52	0
33	NA	A	8384	1/1	0.40	2.03	-	114,114,114,114	0
32	MG	A	8117	1/1	0.84	0.12	-	31,31,31,31	0
32	MG	A	8072	1/1	0.94	0.13	-	80,80,80,80	0
32	MG	A	8036	1/1	0.99	0.06	-	45,45,45,45	0
32	MG	A	8076	1/1	0.76	0.17	-	71,71,71,71	0
32	MG	A	8104	1/1	0.81	0.23	-	40,40,40,40	0
34	CL	A	8516	1/1	0.90	0.19	-	44,44,44,44	0
34	CL	M	8510	1/1	0.52	0.46	-	87,87,87,87	0
32	MG	A	8029	1/1	0.95	0.07	-	51,51,51,51	0
33	NA	A	8360	1/1	0.85	0.86	-	55,55,55,55	0
32	MG	A	8089	1/1	0.91	0.19	-	84,84,84,84	0
33	NA	A	8319	1/1	0.96	0.10	-	52,52,52,52	0
32	MG	A	8031	1/1	0.94	0.05	-	31,31,31,31	0
32	MG	B	8095	1/1	0.82	0.07	-	67,67,67,67	0
34	CL	S	8506	1/1	0.96	0.18	-	46,46,46,46	0
32	MG	A	8050	1/1	0.89	0.13	-	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
32	MG	A	8079	1/1	0.96	0.14	-	39,39,39,39	0
33	NA	A	8302	1/1	0.97	0.13	-	40,40,40,40	0
32	MG	A	8047	1/1	0.96	0.18	-	62,62,62,62	0
34	CL	K	8501	1/1	0.94	0.13	-	56,56,56,56	0
32	MG	A	8082	1/1	0.81	0.21	-	52,52,52,52	0
34	CL	Z	8520	1/1	0.90	0.18	-	35,35,35,35	0
32	MG	A	8103	1/1	0.90	0.29	-	55,55,55,55	0
32	MG	A	8021	1/1	0.98	0.07	-	27,27,27,27	0
32	MG	A	8075	1/1	0.93	0.08	-	57,57,57,57	0
32	MG	A	8111	1/1	0.98	0.07	-	69,69,69,69	0
32	MG	A	8028	1/1	0.98	0.07	-	44,44,44,44	0
33	NA	A	8301	1/1	0.89	0.20	-	43,43,43,43	0
32	MG	A	8097	1/1	0.98	0.22	-	44,44,44,44	0
33	NA	A	8369	1/1	0.72	0.38	-	52,52,52,52	0
32	MG	A	8042	1/1	0.96	0.09	-	44,44,44,44	0
32	MG	A	8106	1/1	0.96	0.08	-	47,47,47,47	0
33	NA	A	8363	1/1	0.84	0.41	-	66,66,66,66	0
32	MG	A	8045	1/1	0.92	0.08	-	54,54,54,54	0
32	MG	A	8102	1/1	0.89	1.19	-	87,87,87,87	0
32	MG	A	8085	1/1	0.91	0.14	-	72,72,72,72	0
32	MG	A	8016	1/1	0.96	0.09	-	41,41,41,41	0
35	K	A	8601	1/1	0.93	0.16	-	73,73,73,73	0
33	NA	T	8312	1/1	0.39	0.82	-	124,124,124,124	0
33	NA	A	8340	1/1	0.93	0.31	-	31,31,31,31	0
32	MG	A	8083	1/1	0.97	0.05	-	47,47,47,47	0
34	CL	K	8502	1/1	0.88	0.08	-	52,52,52,52	0
33	NA	A	8349	1/1	0.99	0.14	-	53,53,53,53	0
32	MG	A	8092	1/1	0.91	0.20	-	91,91,91,91	0
32	MG	A	8041	1/1	0.92	0.07	-	46,46,46,46	0
32	MG	A	8024	1/1	0.45	0.69	-	116,116,116,116	0
33	NA	A	8359	1/1	0.93	0.44	-	61,61,61,61	0
32	MG	A	8118	1/1	0.87	0.33	-	62,62,62,62	0
32	MG	A	8088	1/1	0.90	0.15	-	45,45,45,45	0

6.5 Other polymers ⓘ

There are no such residues in this entry.