



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:01 PM GMT

PDB ID : 1VQ4
Title : The structure of the transition state analogue "DAA" bound to the large ribosomal subunit of *Haloarcula marismortui*
Authors : Schmeing, T.M.; Steitz, T.A.
Deposited on : 2004-12-16
Resolution : 2.70 Å(reported)

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

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

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

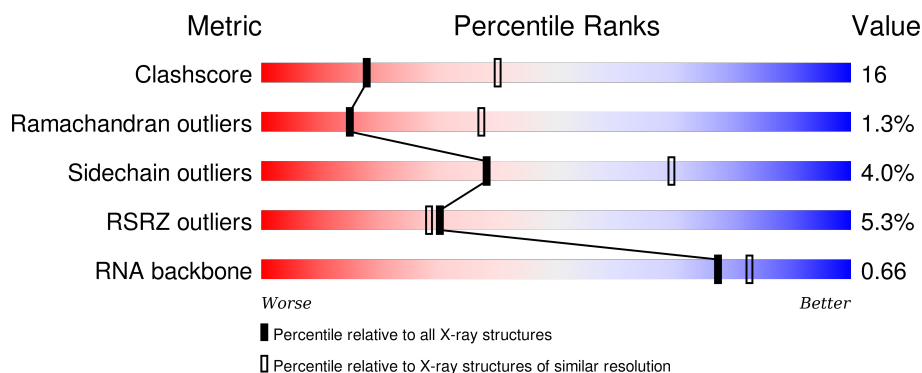
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)
RNA backbone	2183	1069 (3.10-2.30)

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

Mol	Chain	Length	Quality of chain
1	0	2922	<div> <div>2%</div> <div>59% 30% 5% • 6%</div> </div>
2	9	122	<div> <div>3%</div> <div>53% 34% 11% •</div> </div>
3	4	8	<div> <div>50% 38% 13%</div> </div>
4	A	240	<div> <div>4%</div> <div>56% 38% • •</div> </div>
5	B	338	<div> <div>2%</div> <div>52% 42% 6%</div> </div>

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Mol	Chain	Length	Quality of chain
6	C	246	
7	D	177	
8	E	178	
9	F	120	
10	G	348	
11	H	171	
12	J	145	
13	K	132	
14	L	165	
15	M	194	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	155	
21	S	85	
22	T	120	
23	U	66	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	83	
29	1	57	
30	2	50	

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Mol	Chain	Length	Quality of chain
31	3	92	
32	I	162	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	MG	0	8053	-	-	-	X
33	MG	0	8060	-	-	-	X
34	K	0	9001	-	-	-	X
35	NA	0	9102	-	-	-	X
35	NA	0	9121	-	-	-	X
35	NA	0	9125	-	-	-	X
35	NA	0	9126	-	-	-	X
35	NA	0	9129	-	-	-	X
35	NA	0	9135	-	-	-	X
35	NA	0	9150	-	-	-	X
35	NA	0	9155	-	-	-	X
35	NA	0	9156	-	-	-	X
35	NA	0	9161	-	-	-	X
35	NA	0	9162	-	-	-	X
35	NA	0	9168	-	-	-	X
35	NA	0	9171	-	-	-	X
35	NA	0	9172	-	-	-	X
35	NA	0	9173	-	-	-	X
35	NA	0	9174	-	-	-	X
35	NA	0	9177	-	-	-	X
35	NA	0	9178	-	-	-	X
35	NA	0	9182	-	-	-	X
35	NA	L	9180	-	-	-	X
35	NA	M	9147	-	-	-	X
35	NA	Q	9148	-	-	-	X
35	NA	R	9186	-	-	-	X
36	CL	0	9315	-	-	-	X

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 98999 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal rna.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2754	Total	C	N	O	P	0	0	0
			59021	26350	10878	19048	2745			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	628	1MA	A	modified residue	GB 3377779
0	2587	OMU	U	modified residue	GB 3377779
0	2588	OMG	G	modified residue	GB 3377779
0	2619	UR3	U	modified residue	GB 3377779
0	2621	PSU	U	modified residue	GB 3377779

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

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

- Molecule 3 is a RNA chain called 5'-R(*CP*CP*(5AA)P*(2OP)P*(PO2)P*(DA)P*C*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	8	Total	C	N	O	P	0	0	0
			127	61	23	38	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

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

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

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

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

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

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

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

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

- Molecule 9 is a protein called 50S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 10 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG.

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

- Molecule 11 is a protein called 50S RIBOSOMAL PROTEIN L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	H	160	Total	C	N	O	S	0	0	0
			1266	785	237	238	6			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	CONFLICT	UNP P22450

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

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

- Molecule 15 is a protein called 50S Ribosomal Protein L15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1560	943	332	284	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	CONFLICT	GB 55231501
M	194	ALA	GLY	CONFLICT	GB 55231501

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	CONFLICT	GB 55231162

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	I	70	Total	C	N	O	S	0	0	0
			519	323	81	114	1			

- Molecule 33 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	108	Total	Mg	0	0
			108	108		
33	Y	1	Total	Mg	0	0
			1	1		
33	K	1	Total	Mg	0	0
			1	1		
33	B	1	Total	Mg	0	0
			1	1		
33	A	2	Total	Mg	0	0
			2	2		
33	T	1	Total	Mg	0	0
			1	1		
33	9	2	Total	Mg	0	0
			2	2		
33	3	1	Total	Mg	0	0
			1	1		

- Molecule 34 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	3	Total	K	0	0
			3	3		

- Molecule 35 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	0	72	Total Na 72 72	0	0
35	J	1	Total Na 1 1	0	0
35	Q	1	Total Na 1 1	0	0
35	H	2	Total Na 2 2	0	0
35	C	1	Total Na 1 1	0	0
35	A	1	Total Na 1 1	0	0
35	R	3	Total Na 3 3	0	0
35	9	2	Total Na 2 2	0	0
35	L	1	Total Na 1 1	0	0
35	S	1	Total Na 1 1	0	0
35	M	1	Total Na 1 1	0	0

- Molecule 36 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	0	10	Total Cl 10 10	0	0
36	J	3	Total Cl 3 3	0	0
36	K	1	Total Cl 1 1	0	0
36	B	1	Total Cl 1 1	0	0
36	A	1	Total Cl 1 1	0	0
36	N	1	Total Cl 1 1	0	0
36	O	1	Total Cl 1 1	0	0
36	R	1	Total Cl 1 1	0	0
36	L	1	Total Cl 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	3	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	O	1	Total 1	Cd 1	0	0
37	Z	1	Total 1	Cd 1	0	0
37	1	1	Total 1	Cd 1	0	0
37	3	1	Total 1	Cd 1	0	0
37	U	1	Total 1	Cd 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	0	5764	Total 5764	O 5764	0	0
38	9	133	Total 133	O 133	0	0
38	4	3	Total 3	O 3	0	0
38	A	116	Total 116	O 116	0	0
38	B	143	Total 143	O 143	0	0
38	C	173	Total 173	O 173	0	0
38	D	44	Total 44	O 44	0	0
38	E	43	Total 43	O 43	0	0
38	F	24	Total 24	O 24	0	0
38	G	17	Total 17	O 17	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	H	66	Total 66	O 66	0	0
38	J	52	Total 52	O 52	0	0
38	K	57	Total 57	O 57	0	0
38	L	81	Total 81	O 81	0	0
38	M	115	Total 115	O 115	0	0
38	N	61	Total 61	O 61	0	0
38	O	45	Total 45	O 45	0	0
38	P	63	Total 63	O 63	0	0
38	Q	52	Total 52	O 52	0	0
38	R	89	Total 89	O 89	0	0
38	S	31	Total 31	O 31	0	0
38	T	36	Total 36	O 36	0	0
38	U	26	Total 26	O 26	0	0
38	V	13	Total 13	O 13	0	0
38	W	70	Total 70	O 70	0	0
38	X	31	Total 31	O 31	0	0
38	Y	93	Total 93	O 93	0	0
38	Z	31	Total 31	O 31	0	0
38	1	61	Total 61	O 61	0	0
38	2	42	Total 42	O 42	0	0
38	3	71	Total 71	O 71	0	0

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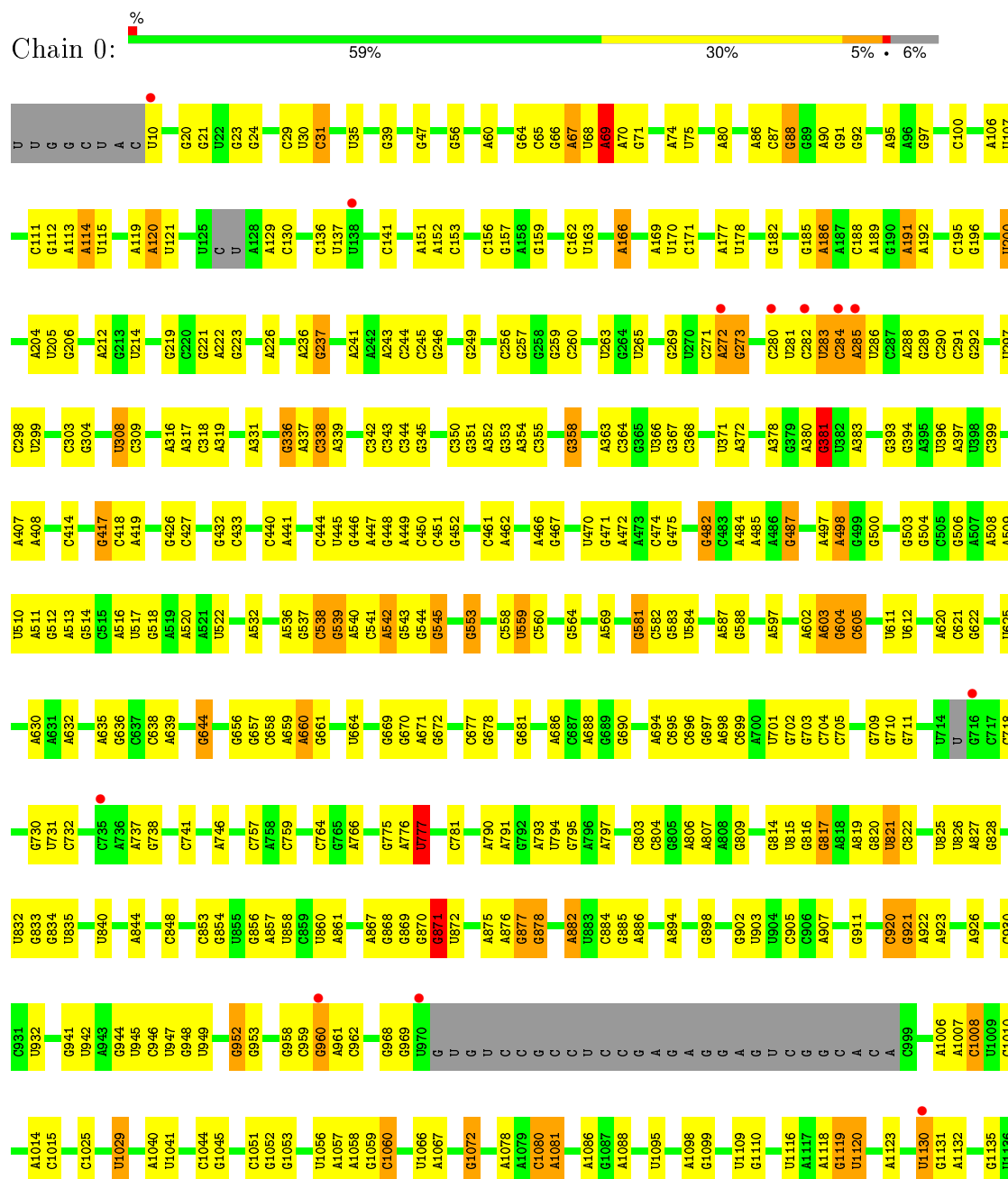
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	I	9	Total	O	0	0
			9	9		

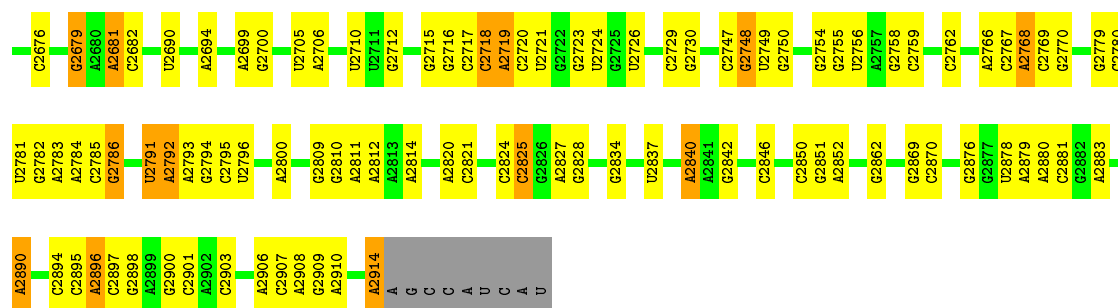
3 Residue-property plots

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

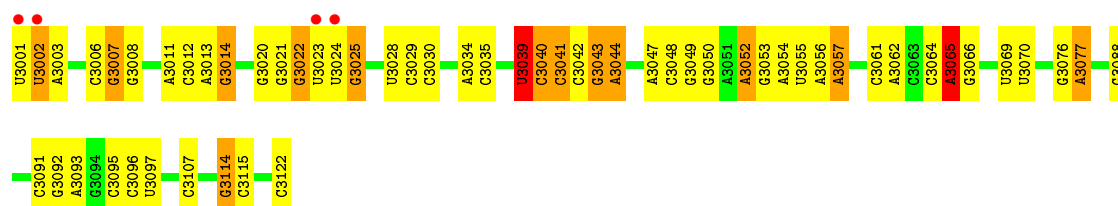
- Molecule 1: 23S ribosomal rna



C2561	A2469	C2241	A2353	G2094	U1984	C1862	G1765	G1666	G1557	C1439	A1329	C1229	G1137
G2562	C2472	U2242	A2354	A2095	A1969	G1863	U1766	A1867	C1558	U1440	U1333	A1230	G1151
G2563	U2473	C2243	G2564	A2096	G1970	G1867	A1767	U1668	U1559	G1441	C1334	A1230	
C2565	A2474	G2249	A2361	A2101	G1971	G1868	C1769	A1669	U1561	C1335	U1234	G1235	G1156
G2570	C2476	G2250	G2275	G2102	U1972	U1874	C1772	G1670	C1562	G1340	G1235	A1236	C1157
	U2477	A2252	C2363	C2105	A1973	G1877	G1773	C1675	G1563	A1341	U1237	A1236	G1158
G2578	A2478	G2253	G2365	C2106	U1978	G1877	G1774	G1676	C1564	C1342	G1238	U1237	G1159
U2586	U2479	U	A2369	G2110	U1980	U1879	A1778	U1677	U1568	A1343	G1239	G1239	A1161
U2587	G2480	C	A2369	G2111	U1980	U1879	A1778	C1677	U1568	A1344	G1239	G1239	G1162
G2588	A2483	G	G2379	G2112	U1986	U1880	A1779	A1681	A1572	A1242	A1242	A1242	G1163
U2589	G2489	C	A2380	G2113	U1986	U1880	A1779	A1682	A1572	G1351	G1243	G1243	G1163
C2590	U2590	G	C2381	G2113	U1986	U1880	A1779	G1683	A1573	A1352	U1244	U1244	U1164
C2591	A2490	G	A2382	U2003	U2003	U1903	A1783	A1684	C1574	A1353	U1244	U1244	G1165
G2592	U2491	C	A2382	U2004	U2004	A1904	U1784	A1685	C1574	A1246	A1246	A1246	A1166
	U2492	C	A2395	G2136	U1980	U1905	C1787	C1686	G1589	C1360	G1252	A1252	G1167
C2597	C2493	C	A2395	A	U2008	U1905	C1787	C1687	G1589	A1477	A1252	A1252	G1168
U2598		C	C2403	C	U2009	A1909	C1790	C1687	G1592	C1366	C1253	C1253	U1169
	C2502	C	G2404	U	G2009	A1940	U1791	C1692	C1593	U1170	U1278	U1278	U1170
A2601	A2503	G	C2404	G	A2011	A1940	U1791	C1692	C1593	A1372	U1266	U1266	U1171
G2602	A2504	G	U2012	U	U2012	U1915	C1798	A1701	U1595	A1375	G1267	G1267	G1172
C2603	G2505	G	G2013	G	G2013	C1916	C1798	U1702	U1596	G1376	G1268	G1268	A1173
U2607	A2506	G	G2014	C	G2014	A1919	C1803	U1702	A1597	C1377	G1273	G1273	A1174
C2608	G2507	C	A2015	C	A2015	G1920	A1804	C1705	A1598				G1175
	U2609	C	U2016	C	U2016	C1920	G1805	C1705	A1598				G1176
G2613	A2508	A	A2030	C	A2030	A1921	A1811	A1710	A1603	G1385	A1278	A1278	U1180
C2614	U2509	C	A2030	C	A2030	A1922	A1811	A1711	G1604	U1279	U1279	U1279	U1181
A2619	A2511	C	U2034	A	U2034	G1925	U1813	A1712	G1605	U1285	U1285	U1285	C1182
	C2515	G	G2035	C	G2035	G1926	C1818	A1717	A1606	G1389	U1285	U1285	C1183
C2626	U2418	G	C2036	U	C2036	A1927	G1819	U1722	A1607	C1391	G1289	G1289	C1184
G2627	G2420	G	U2421	G	U2421	U1937	G1820	G1723	U1506	A1392	G1290	G1290	U1185
G2630	U2422	A	A2039	C	A2039	G1938	U1825	C1725	U1507	C1394	U1293	U1293	U1186
G2634	U2424	U	G2044	C	G2044	U1939	U1826	C1725	U1507	G1398	A1294	A1294	U1187
	A2425	A	G2045	C	G2045	A1941	C1826	C1725	U1507	A1399	G1295	G1295	U1188
G2637	G2426	C	G2046	U	G2046	C1942	A1629	G1730	U1626	U1298	U1298	U1298	A1189
G2638	C2427	U	C2047	C	C2047	G1943	A1629	G1731	A1626	A1406	A1191	A1191	G1190
	U2428	C	G2050	C	G2050	G1944	C1834	A1733	A1630	A1407	A1192	A1192	A1193
G2642	A2434	C	G2050	C	G2050	G1945	U1835	C1735	A1631	U1304	U1304	U1304	U1198
G2643	U2435	C	A2054	U	A2054	G1946	U1838	C1735	G1523	C1305	C1305	C1305	A1199
C2644	U2436	G	U2064	G	U2064	G1947	A1839	U1741	U1524	U1306	U1306	U1306	A1200
A2649	U2441	C	U2064	G	U2064	G1948	A1840	U1742	G1525	G1415	A1307	A1307	G1208
	G2442	C	G2070	C	G2070	G1949	U1845	A1743	A1527	G1416	A1308	A1308	C1209
U2652	C2443	G	G2071	C	G2071	G1951	A1846	G1744	G1528	U1418	G1311	G1311	G1210
	U2541	U	C2072	C	C2072	U	U1847	A1747	G1529	U1419	G1312	G1312	
A2664	C2542	G	G2073	A	G2073	A	A1847	A1747	G1535	U1422	A1313	A1313	U1205
U	U2545	G	A2074	C	A2074	C	G1848	G1751	C1536	C1423	U1314	U1314	U1206
G2667	U2546	C	G2074	C	G2074	C	U1849	G1752	C1537	A1424	G1315	G1315	A1207
G2668	C2547	U	U2081	U	U2081	U	U1850	G1752	G1543	G1425	G1316	G1316	C1208
U2669	G2548	C	A2089	C	A2089	U	G1851	A1755	U1654	C1426	A1321	A1321	G1210
G2670	U2671	C	G2090	C	G2090	A	A1852	G1756	G1655	A1427	G1322	G1322	
U2671	C2672	A	G2091	C	G2091	A	G1855	A1759	A1656	A1434	G1325	G1325	C1213
C2673	U2673	G	G2092	C	G2092	C	C1856	A1759	A1657	U1435	G1325	G1325	G1214
			G2093	C	G2093	C	C1856	A1759	A1658	C1436	G1325	G1325	G1215
				C		C	C1861	C1764	G1660		A1328	A1328	G1216



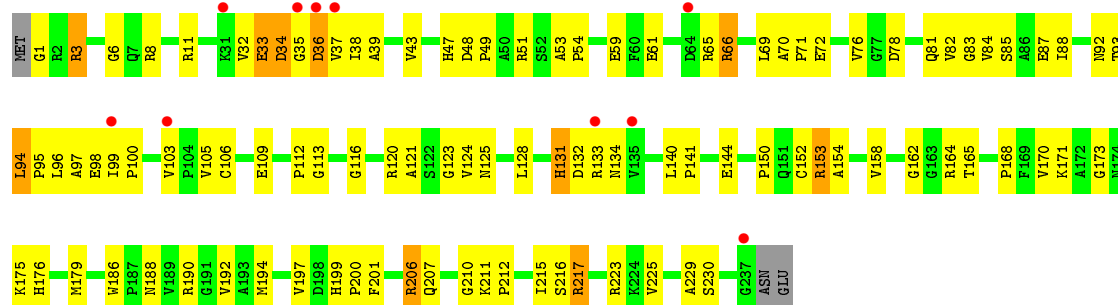
• Molecule 2: 5S ribosomal RNA



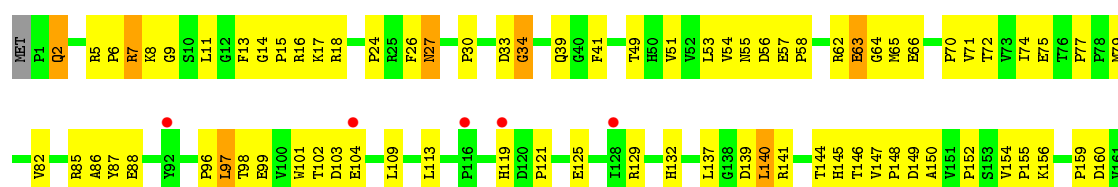
• Molecule 3: 5'-R(*CP*CP*(5AA)P*(2OP)P*(PO2)P*(DA)P*C*C)-3'

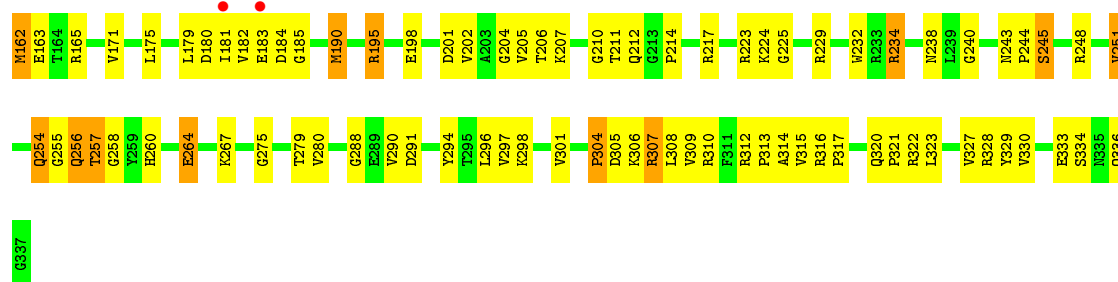


• Molecule 4: 50S ribosomal protein L2P

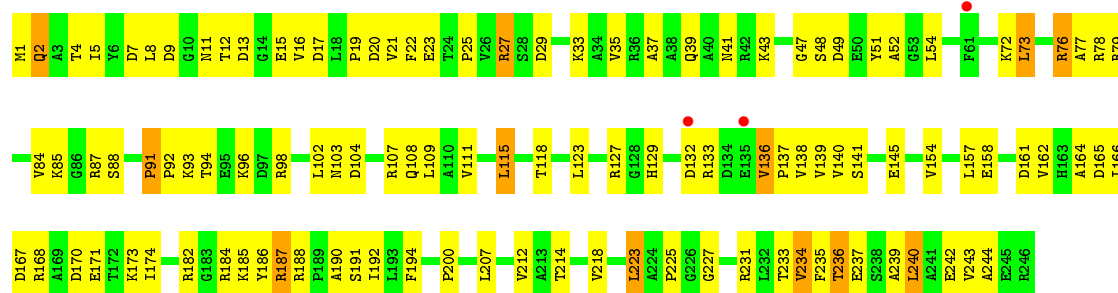


• Molecule 5: 50S ribosomal protein L3P

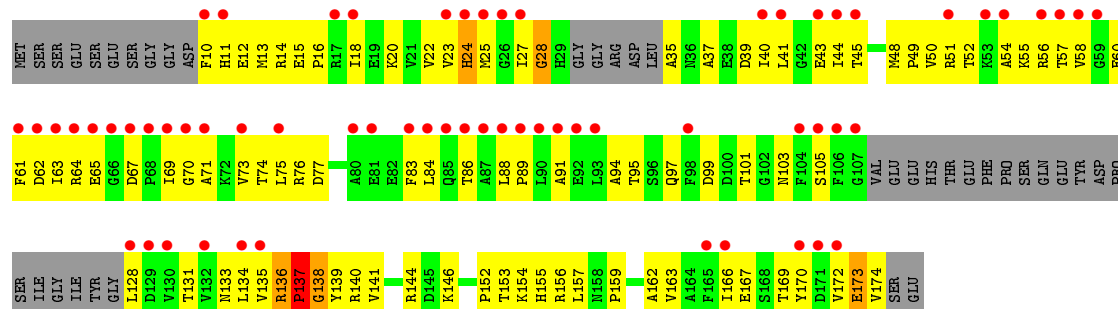




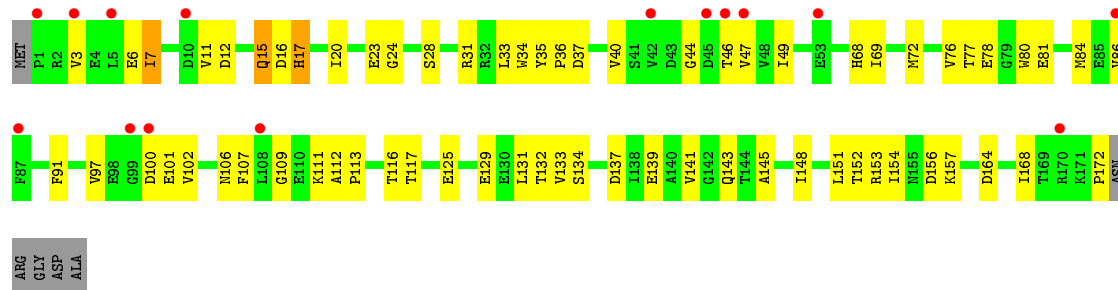
- Molecule 6: 50S ribosomal protein L4E



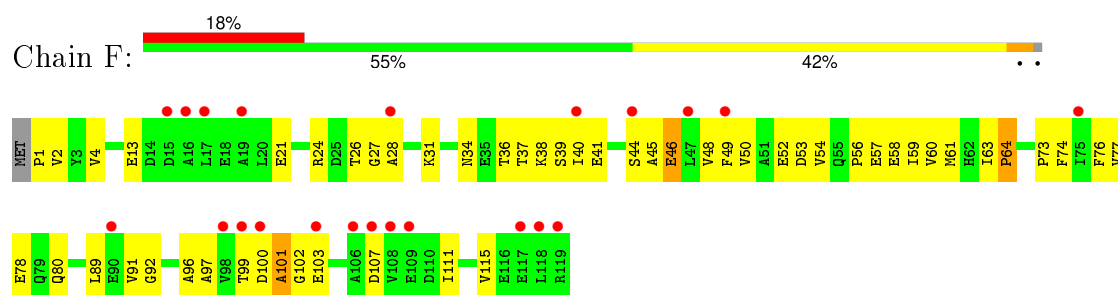
- Molecule 7: 50S ribosomal protein L5P



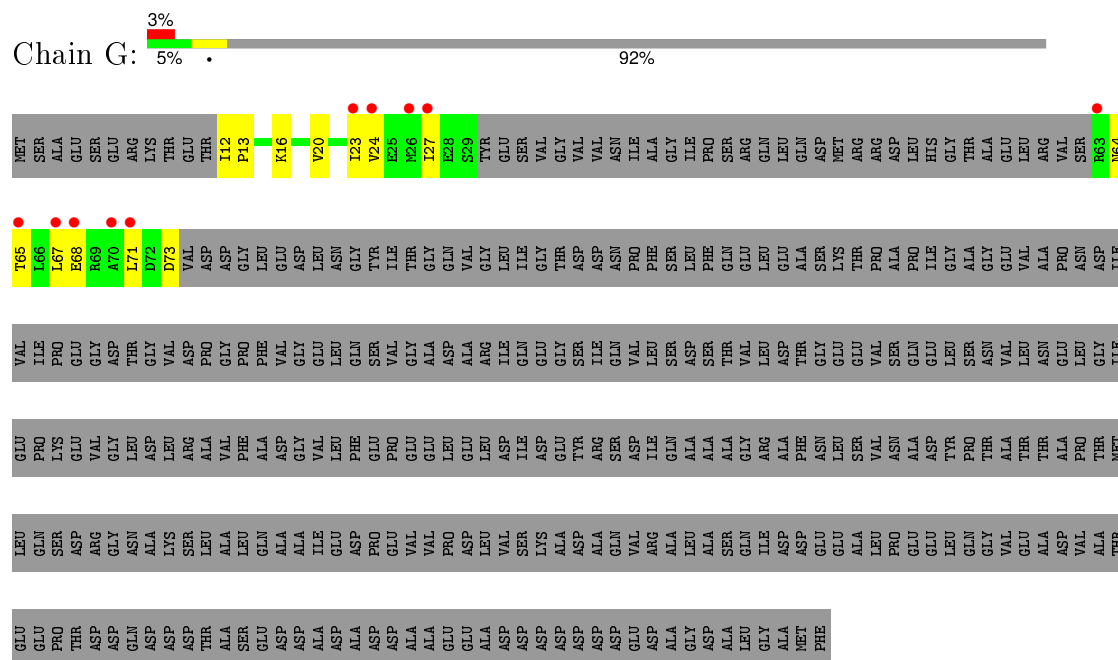
- Molecule 8: 50S ribosomal protein L6P



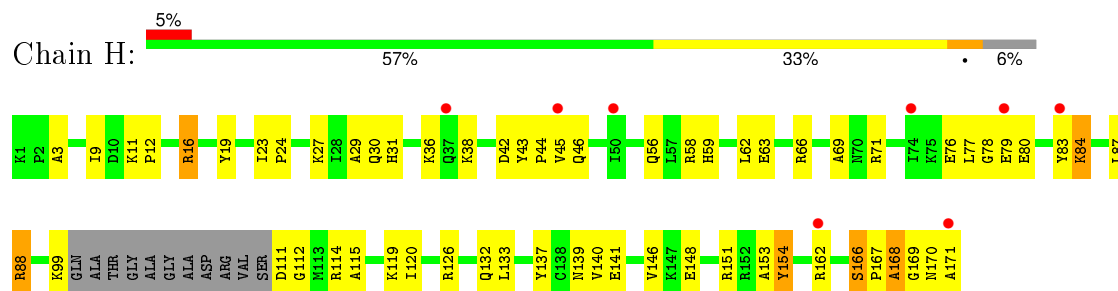
- Molecule 9: 50S ribosomal protein L7AE



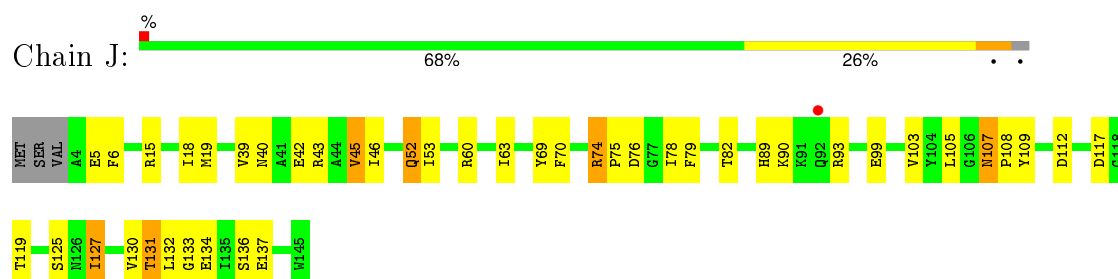
- Molecule 10: ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG



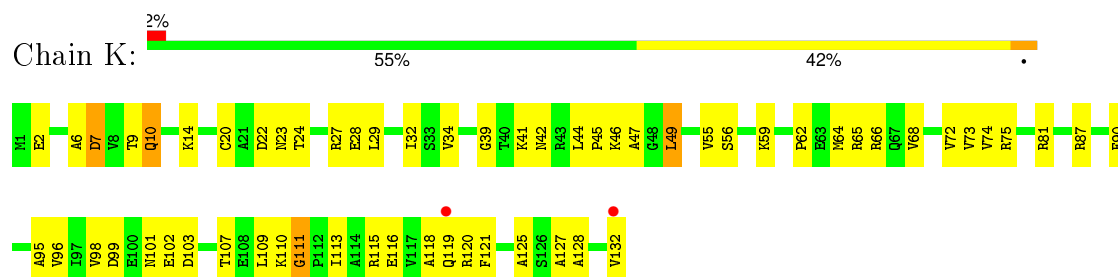
- Molecule 11: 50S RIBOSOMAL PROTEIN L10E



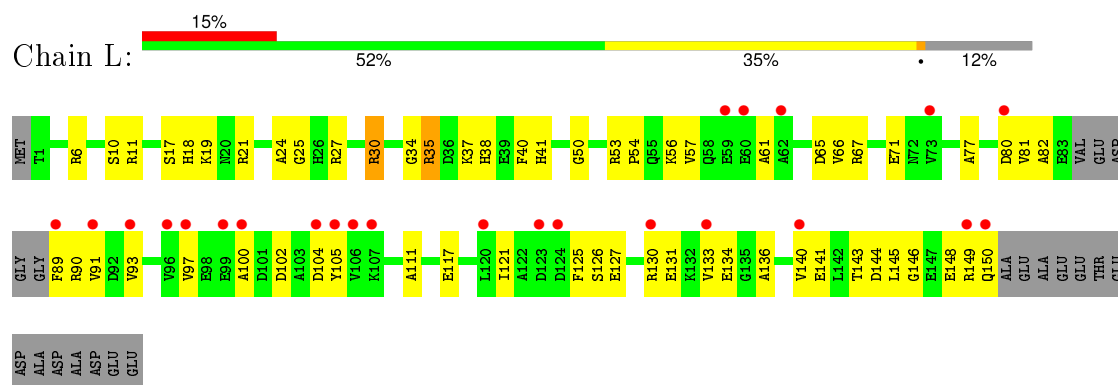
- Molecule 12: 50S ribosomal protein L13P



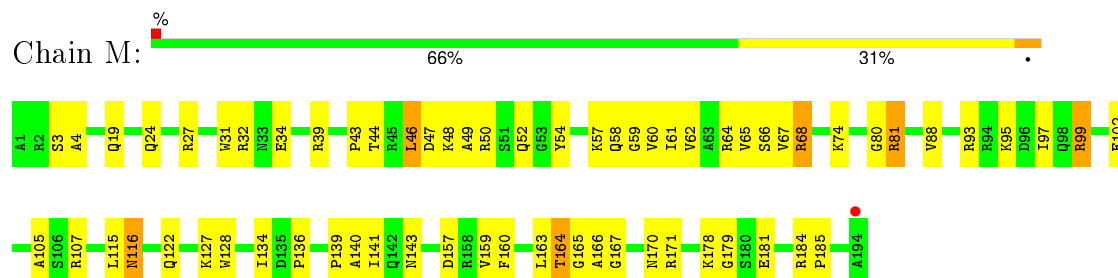
- Molecule 13: 50S ribosomal protein L14P



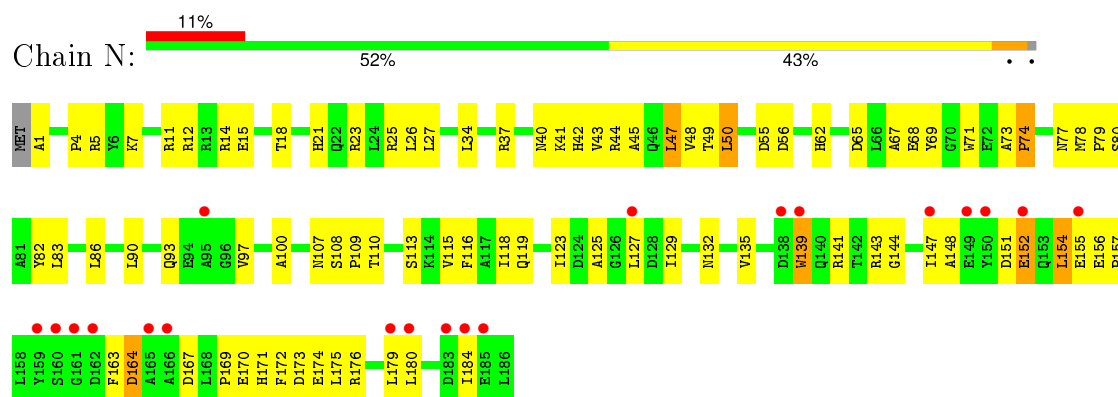
- Molecule 14: 50S ribosomal protein L15P



- Molecule 15: 50S Ribosomal Protein L15E



- Molecule 16: 50S ribosomal protein L18P



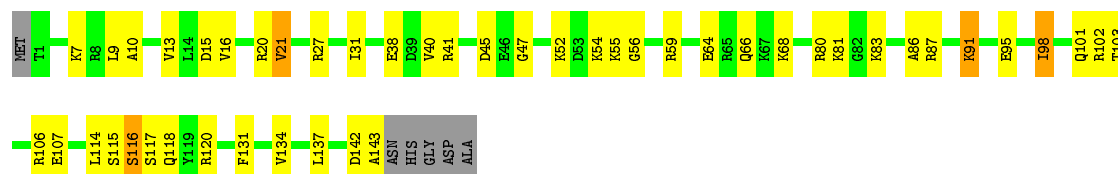
- Molecule 17: 50S ribosomal protein L18e





- Molecule 18: 50S ribosomal protein L19E

Chain P: 64% 29%



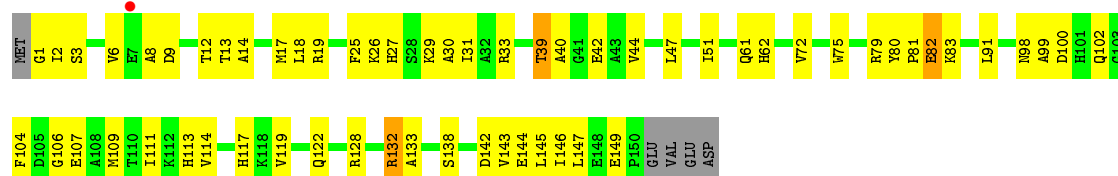
- Molecule 19: 50S ribosomal protein L21e

Chain Q: 72% 25%



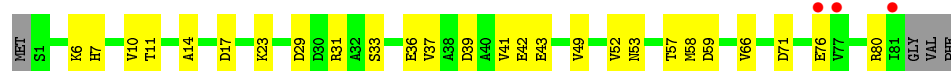
- Molecule 20: 50S ribosomal protein L22P

Chain R: 58% 37%



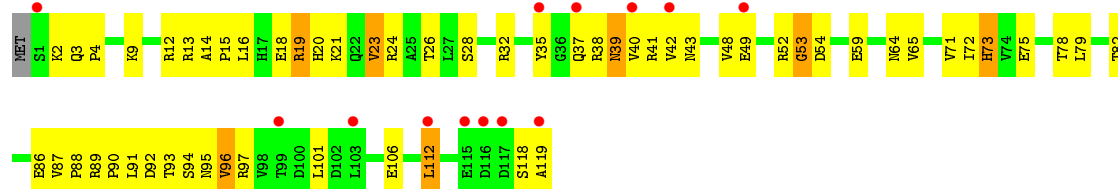
- Molecule 21: 50S ribosomal protein L23P

Chain S: 4% 65% 31% 5%

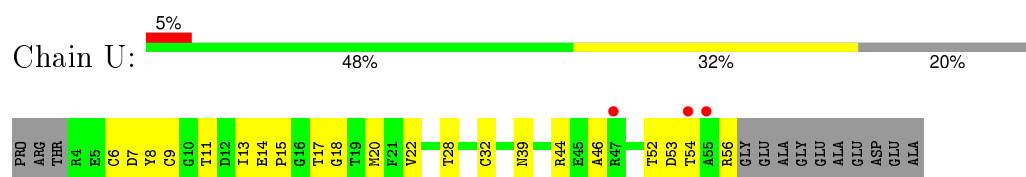


- Molecule 22: 50S ribosomal protein L24P

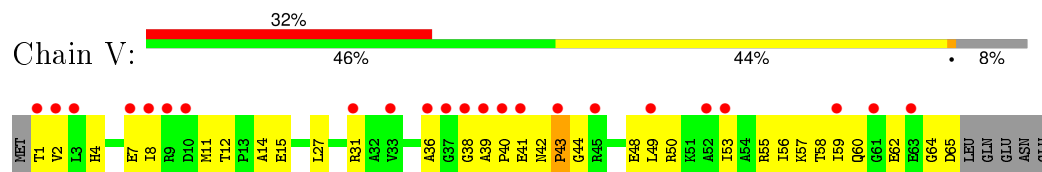
Chain T: 11% 51% 43% 6%



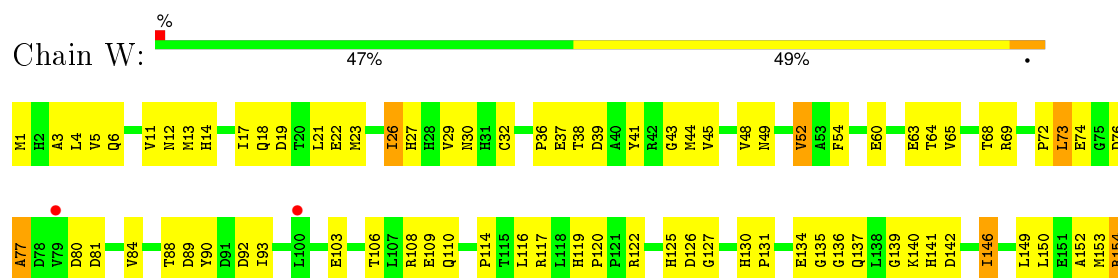
- Molecule 23: 50S ribosomal protein L24E



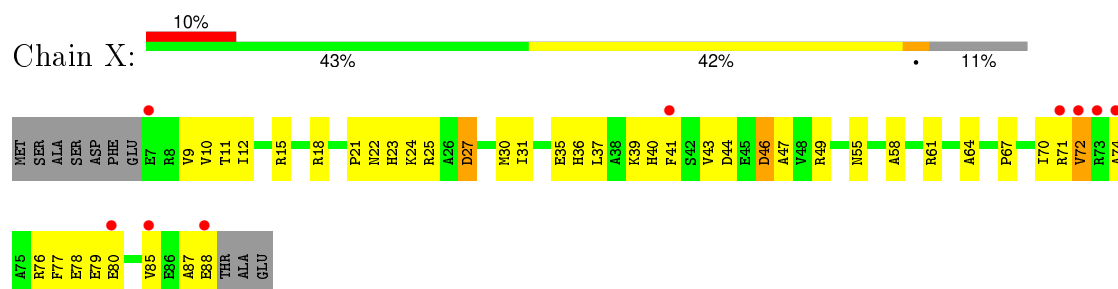
- Molecule 24: 50S ribosomal protein L29P



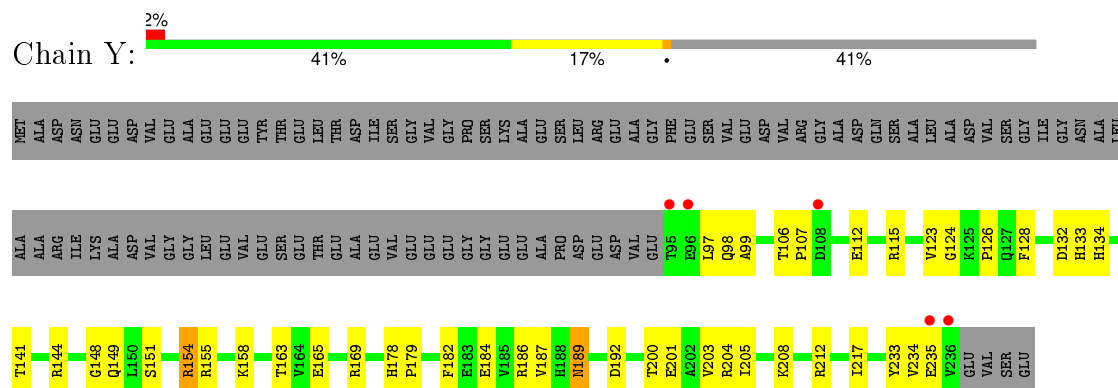
- Molecule 25: 50S ribosomal protein L30P



- Molecule 26: 50S ribosomal protein L31e

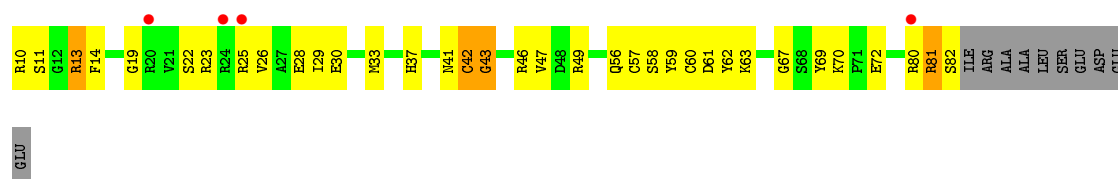


- Molecule 27: 50S ribosomal protein L32E



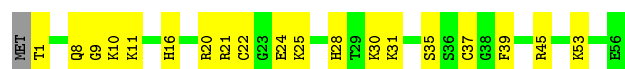
- Molecule 28: 50S ribosomal protein L37Ae





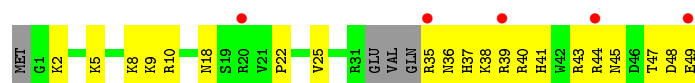
- Molecule 29: 50S ribosomal protein L37e

Chain 1: 65% 33%



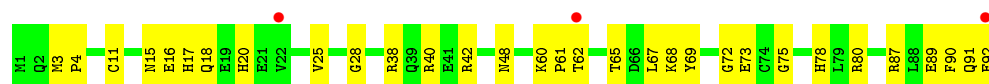
- Molecule 30: 50S ribosomal protein L39e

Chain 2: 10% 50% 42% 8%



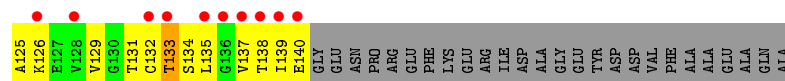
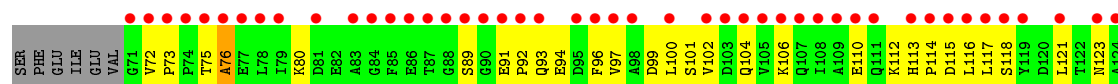
- Molecule 31: 50S ribosomal protein L44E

Chain 3: 3% 66% 34%



- Molecule 32: 50S RIBOSOMAL PROTEIN L11P

Chain I: 19% 35% 23% 57%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.00Å 301.03Å 575.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 49.83 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.70) 94.8 (49.83-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.230 0.183 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.309	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 505940 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	98999	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 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, NA, K, PO2, CD, 5AA, OMU, UR3, 2OP, 1MA, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.38	0/65959	0.69	20/102870 (0.0%)
2	9	0.35	0/2905	0.71	2/4528 (0.0%)
3	4	0.46	0/102	0.73	0/149
4	A	0.31	0/1786	0.65	0/2408
5	B	0.34	0/2690	0.65	0/3652
6	C	0.37	0/1884	0.65	1/2551 (0.0%)
7	D	0.30	0/1111	0.53	0/1498
8	E	0.33	0/1382	0.58	0/1880
9	F	0.30	0/901	0.54	0/1224
10	G	0.30	0/241	0.49	0/324
11	H	0.35	0/1287	0.67	0/1725
12	J	0.37	0/1136	0.63	0/1530
13	K	0.36	0/1001	0.69	0/1347
14	L	0.33	0/1130	0.64	0/1509
15	M	0.33	0/1584	0.61	0/2119
16	N	0.30	0/1474	0.63	0/1999
17	O	0.31	0/874	0.56	0/1181
18	P	0.33	0/1147	0.54	0/1528
19	Q	0.36	0/749	0.72	0/1005
20	R	0.36	0/1172	0.65	0/1578
21	S	0.32	0/648	0.57	0/875
22	T	0.32	0/958	0.61	0/1289
23	U	0.34	0/417	0.58	0/562
24	V	0.27	0/502	0.54	0/675
25	W	0.36	0/1219	0.63	0/1655
26	X	0.36	0/664	0.58	0/895
27	Y	0.37	0/1146	0.64	0/1536
28	Z	0.36	0/589	0.67	0/787
29	1	0.36	0/438	0.62	0/578
30	2	0.33	0/401	0.52	0/529
31	3	0.38	0/771	0.58	0/1024
32	I	0.30	0/526	0.54	0/716

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.37	0/98794	0.67	23/147726 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	47
2	9	0	2
3	4	0	1
25	W	0	1
All	All	0	51

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1563	G	C2'-C3'-O3'	8.54	128.28	109.50
1	0	1942	A	C5'-C4'-C3'	8.16	129.06	116.00
1	0	1979	G	C2'-C3'-O3'	6.72	124.45	113.70
1	0	871	G	C5'-C4'-O4'	-6.61	101.17	109.10
2	9	3039	U	N1-C1'-C2'	6.29	122.18	114.00
1	0	2313	C	C5'-C4'-O4'	6.29	116.65	109.10
1	0	2291	A	N9-C1'-C2'	6.28	122.16	114.00
2	9	3065	A	N9-C1'-C2'	6.26	122.14	114.00
1	0	1504	A	C1'-O4'-C4'	-6.11	105.01	109.90
1	0	2467	A	C1'-O4'-C4'	-5.87	105.21	109.90
1	0	2541	U	C2'-C3'-O3'	5.70	122.83	113.70
1	0	206	G	C5'-C4'-C3'	-5.49	107.22	116.00
1	0	1504	A	N9-C1'-C2'	5.34	120.94	114.00
1	0	1979	G	N9-C1'-C2'	5.28	120.87	114.00
1	0	2526	C	N1-C1'-C2'	5.21	120.77	114.00
1	0	777	U	O4'-C1'-N1	5.16	112.33	108.20
1	0	2313	C	C1'-O4'-C4'	-5.14	105.79	109.90
1	0	2313	C	C5'-C4'-C3'	5.10	124.15	116.00
6	C	73	LEU	CA-CB-CG	-5.09	103.58	115.30
1	0	2607	U	N1-C1'-C2'	5.09	120.62	114.00
1	0	1942	A	C5'-C4'-O4'	5.07	115.19	109.10
1	0	381	G	N9-C1'-C2'	5.07	120.59	114.00
1	0	69	A	C5'-C4'-O4'	-5.07	103.02	109.10

There are no chirality outliers.

All (51) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1078	A	Sidechain
1	0	1340	G	Sidechain
1	0	1342	C	Sidechain
1	0	1351	G	Sidechain
1	0	1377	C	Sidechain
1	0	1417	G	Sidechain
1	0	1614	G	Sidechain
1	0	1681	G	Sidechain
1	0	1744	G	Sidechain
1	0	1829	A	Sidechain
1	0	1835	U	Sidechain
1	0	1845	A	Sidechain
1	0	1861	C	Sidechain
1	0	1863	G	Sidechain
1	0	1867	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	191	A	Sidechain
1	0	1970	G	Sidechain
1	0	221	G	Sidechain
1	0	2312	G	Sidechain
1	0	2316	G	Sidechain
1	0	2395	A	Sidechain
1	0	24	G	Sidechain
1	0	2412	G	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2526	C	Sidechain
1	0	2552	C	Sidechain
1	0	2564	G	Sidechain
1	0	2607	U	Sidechain
1	0	2630	G	Sidechain
1	0	2673	U	Sidechain
1	0	2679	G	Sidechain
1	0	2840	A	Sidechain
1	0	2842	G	Sidechain
1	0	417	G	Sidechain
1	0	471	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	781	C	Sidechain
1	0	817	G	Sidechain
1	0	867	A	Sidechain
1	0	882	A	Sidechain
1	0	952	G	Sidechain
3	4	176	DA	Sidechain
2	9	3039	U	Sidechain
2	9	3065	A	Sidechain
25	W	90	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59021	0	29812	849	0
2	9	2600	0	1326	65	0
3	4	127	0	75	4	0
4	A	1753	0	1766	119	0
5	B	2625	0	2533	159	0
6	C	1859	0	1816	127	0
7	D	1094	0	1085	91	0
8	E	1357	0	1266	64	0
9	F	890	0	843	56	0
10	G	240	0	231	13	0
11	H	1266	0	1268	70	0
12	J	1120	0	1098	55	0
13	K	992	0	1031	65	0
14	L	1118	0	1076	55	0
15	M	1560	0	1568	70	0
16	N	1445	0	1401	107	0
17	O	865	0	873	39	0
18	P	1136	0	1123	44	0
19	Q	735	0	729	23	0
20	R	1149	0	1122	62	0
21	S	641	0	605	21	0
22	T	950	0	923	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	U	410	0	364	24	0
24	V	499	0	511	33	0
25	W	1196	0	1137	95	0
26	X	654	0	653	50	0
27	Y	1130	0	1133	55	0
28	Z	578	0	539	27	0
29	1	431	0	426	30	0
30	2	396	0	413	27	0
31	3	755	0	728	31	0
32	I	519	0	500	54	0
33	0	108	0	0	0	0
33	3	1	0	0	0	0
33	9	2	0	0	0	0
33	A	2	0	0	0	0
33	B	1	0	0	0	0
33	K	1	0	0	0	0
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	3	0	0	0	0
35	0	72	0	0	0	0
35	9	2	0	0	0	0
35	A	1	0	0	0	0
35	C	1	0	0	0	0
35	H	2	0	0	0	0
35	J	1	0	0	0	0
35	L	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	3	0	0	0	0
35	S	1	0	0	0	0
36	0	10	0	0	1	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	1	0
36	K	1	0	0	0	0
36	L	1	0	0	0	0
36	M	1	0	0	1	0
36	N	1	0	0	1	0
36	O	1	0	0	0	0
36	R	1	0	0	0	0
37	1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5764	0	0	97	0
38	1	61	0	0	3	0
38	2	42	0	0	3	0
38	3	71	0	0	5	0
38	4	3	0	0	0	0
38	9	133	0	0	4	0
38	A	116	0	0	18	0
38	B	143	0	0	23	0
38	C	173	0	0	21	0
38	D	44	0	0	8	0
38	E	43	0	0	5	0
38	F	24	0	0	4	0
38	G	17	0	0	0	0
38	H	66	0	0	9	0
38	I	9	0	0	2	0
38	J	52	0	0	3	0
38	K	57	0	0	8	0
38	L	81	0	0	11	0
38	M	115	0	0	4	0
38	N	61	0	0	10	0
38	O	45	0	0	6	0
38	P	63	0	0	3	0
38	Q	52	0	0	1	0
38	R	89	0	0	5	0
38	S	31	0	0	2	0
38	T	36	0	0	2	0
38	U	26	0	0	0	0
38	V	13	0	0	1	0
38	W	70	0	0	5	0
38	X	31	0	0	5	0
38	Y	93	0	0	7	0
38	Z	31	0	0	1	0
All	All	98999	0	59974	2378	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (2378) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3006:C:H5"	16:N:37:ARG:NH1	1.64	1.13
6:C:236:THR:HG22	6:C:239:ALA:H	1.11	1.13
11:H:46:GLN:HB3	11:H:167:PRO:HD2	1.32	1.11
2:9:3006:C:H5"	16:N:37:ARG:HH12	1.08	1.07
1:0:1160:G:H5'	1:0:1161:A:H5'	1.34	1.04
6:C:127:ARG:NH2	6:C:225:PRO:HG2	1.71	1.04
1:0:156:C:H5"	15:M:171:ARG:HD3	1.38	1.03
12:J:19:MET:HE3	12:J:132:LEU:HD21	1.37	1.03
1:0:1242:A:H5'	12:J:82:THR:HG23	1.40	1.03
26:X:37:LEU:HD13	26:X:85:VAL:HG21	1.39	1.02
11:H:56:GLN:HE21	11:H:126:ARG:HE	1.02	1.01
28:Z:10:ARG:HA	38:Z:9216:HOH:O	1.57	1.01
5:B:238:ASN:HD22	5:B:240:GLY:H	1.06	1.00
13:K:10:GLN:H	13:K:10:GLN:HE21	1.05	1.00
4:A:211:LYS:HB3	4:A:212:PRO:HD2	1.43	0.99
1:0:2364:A:H5"	19:Q:15:LYS:HD3	1.45	0.98
1:0:871:G:H8	1:0:871:G:H5'	1.27	0.97
22:T:71:VAL:HG11	22:T:90:PRO:HB3	1.44	0.97
8:E:36:PRO:HD3	12:J:127:ILE:HD12	1.45	0.96
1:0:871:G:C8	1:0:871:G:H5'	1.99	0.96
7:D:134:LEU:HD11	7:D:166:ILE:HD11	1.46	0.96
1:0:56:G:H5"	24:V:50:ARG:HH12	1.31	0.95
1:0:1751:G:H2'	1:0:1752:G:H5"	1.46	0.95
24:V:12:THR:HG22	24:V:15:GLU:HG3	1.47	0.95
1:0:870:G:H2'	1:0:871:G:H5"	1.45	0.94
2:9:3056:A:H2'	2:9:3057:A:H5"	1.48	0.94
18:P:115:SER:H	18:P:118:GLN:HE21	0.96	0.94
9:F:91:VAL:HG12	9:F:92:GLY:H	1.32	0.92
7:D:154:LYS:HD2	7:D:154:LYS:H	1.31	0.92
1:0:1187:U:HO2'	1:0:1189:A:H2	1.10	0.91
20:R:39:THR:HG22	20:R:42:GLU:H	1.35	0.91
1:0:1474:C:H6	1:0:1474:C:H5'	1.36	0.91
13:K:39:GLY:HA2	38:K:4183:HOH:O	1.71	0.91
1:0:1835:U:H5	1:0:1840:A:N7	1.69	0.90
2:9:3076:G:H3'	2:9:3077:A:H5"	1.52	0.90
26:X:76:ARG:HH11	26:X:76:ARG:HG3	1.33	0.90
21:S:57:THR:HG22	21:S:59:ASP:H	1.37	0.90
1:0:2717:C:H2'	1:0:2718:C:H5"	1.53	0.90
15:M:164:THR:HG22	15:M:167:GLY:H	1.36	0.89
13:K:10:GLN:H	13:K:10:GLN:NE2	1.70	0.89
1:0:2717:C:C2'	1:0:2718:C:H5"	2.03	0.88
8:E:81:GLU:HG2	8:E:134:SER:HB3	1.56	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1116:U:HO2'	1:0:1118:A:H2	0.89	0.88
5:B:212:GLN:HB2	5:B:257:THR:HG21	1.55	0.88
22:T:9:LYS:HE3	22:T:13:ARG:NH1	1.89	0.88
11:H:46:GLN:HE21	11:H:137:TYR:HE2	1.15	0.88
1:0:2812:A:H2	1:0:2814:A:H62	1.22	0.88
1:0:2506:A:HO2'	1:0:2507:G:H8	0.89	0.87
13:K:74:VAL:HG11	13:K:113:ILE:HG12	1.53	0.87
24:V:1:THR:HG23	24:V:2:VAL:H	1.36	0.87
20:R:8:ALA:HB1	20:R:13:THR:HG21	1.56	0.87
6:C:1:MET:HG2	6:C:2:GLN:H	1.38	0.87
1:0:506:G:H22	1:0:509:A:H5'	1.40	0.87
1:0:56:G:H5''	24:V:50:ARG:NH1	1.90	0.87
20:R:99:ALA:HB1	20:R:109:MET:HE1	1.56	0.86
18:P:115:SER:N	18:P:118:GLN:HE21	1.74	0.85
14:L:121:ILE:HG12	14:L:141:GLU:HB2	1.56	0.85
7:D:25:MET:HE3	7:D:37:ALA:HB1	1.59	0.85
5:B:179:LEU:O	5:B:183:GLU:HG2	1.75	0.85
1:0:282:C:H1'	1:0:368:C:N4	1.91	0.85
16:N:144:GLY:O	16:N:147:ILE:HG22	1.76	0.85
1:0:2533:C:H6	1:0:2533:C:H5'	1.42	0.84
1:0:1162:G:H1'	32:I:117:LEU:HD11	1.59	0.84
25:W:88:THR:HG22	25:W:89:ASP:H	1.41	0.84
6:C:236:THR:HG22	6:C:239:ALA:N	1.90	0.84
1:0:1667:A:H8	1:0:1667:A:H5'	1.42	0.84
5:B:18:ARG:HG3	5:B:256:GLN:HG3	1.59	0.83
13:K:62:PRO:HG3	13:K:65:ARG:HH21	1.42	0.83
12:J:74:ARG:HB3	12:J:74:ARG:HH11	1.44	0.83
1:0:1160:G:C5'	1:0:1161:A:H5'	2.08	0.83
32:I:99:ASP:OD1	32:I:138:THR:HB	1.77	0.83
1:0:21:G:H5'	20:R:2:ILE:HA	1.61	0.83
1:0:545:G:H8	1:0:545:G:H5'	1.44	0.83
25:W:6:GLN:HB2	25:W:26:ILE:HD12	1.59	0.82
5:B:264:GLU:HG2	5:B:267:LYS:HE2	1.61	0.82
30:2:41:HIS:H	30:2:45:ASN:HD22	1.23	0.82
6:C:78:ARG:HG3	6:C:78:ARG:HH11	1.44	0.82
1:0:2506:A:O2'	1:0:2507:G:H8	1.61	0.82
1:0:2890:A:H1'	23:U:56:ARG:NH2	1.94	0.82
25:W:4:LEU:HD23	25:W:54:PHE:HB3	1.60	0.82
15:M:99:ARG:HD2	15:M:167:GLY:HA2	1.62	0.82
31:3:60:LYS:HG3	31:3:61:PRO:HD2	1.62	0.82
18:P:115:SER:H	18:P:118:GLN:NE2	1.76	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:88:THR:HB	38:W:6679:HOH:O	1.80	0.81
11:H:56:GLN:NE2	11:H:126:ARG:HE	1.79	0.81
13:K:10:GLN:N	13:K:10:GLN:HE21	1.79	0.81
24:V:57:LYS:HA	24:V:60:GLN:HE21	1.46	0.81
1:0:1372:A:H3'	38:0:7376:HOH:O	1.81	0.80
11:H:29:ALA:HB3	11:H:66:ARG:HH12	1.44	0.80
15:M:102:GLU:OE1	15:M:164:THR:HG21	1.81	0.80
4:A:36:ASP:OD2	4:A:85:SER:HB2	1.79	0.80
2:9:3006:C:C5'	16:N:37:ARG:NH1	2.45	0.80
1:0:1593:C:H5'	18:P:116:SER:O	1.81	0.80
25:W:88:THR:HG23	25:W:110:GLN:HE21	1.46	0.79
1:0:559:U:H5'	1:0:559:U:H6	1.47	0.79
1:0:870:G:C2'	1:0:871:G:H5''	2.11	0.79
5:B:62:ARG:HA	5:B:65:MET:HE3	1.62	0.79
1:0:2270:G:H4'	4:A:223:ARG:HH12	1.48	0.79
13:K:32:ILE:HD11	13:K:56:SER:HB3	1.64	0.79
4:A:88:ILE:HD13	4:A:100:PRO:HD3	1.63	0.79
9:F:46:GLU:O	9:F:73:PRO:HD2	1.83	0.79
1:0:1116:U:O2'	1:0:1118:A:H2	1.66	0.79
25:W:72:PRO:HG2	25:W:77:ALA:HB3	1.64	0.79
29:1:8:GLN:HE22	29:1:11:LYS:NZ	1.81	0.78
1:0:506:G:H22	1:0:509:A:C5'	1.95	0.78
16:N:176:ARG:HE	16:N:180:LEU:HD21	1.48	0.78
1:0:542:A:H5'	1:0:542:A:H8	1.48	0.78
13:K:14:LYS:HB2	13:K:45:PRO:HG2	1.65	0.78
16:N:48:VAL:CG1	16:N:55:ASP:HB3	2.13	0.78
12:J:93:ARG:HH11	12:J:93:ARG:HB3	1.49	0.78
4:A:100:PRO:HG2	4:A:103:VAL:HG21	1.66	0.78
7:D:99:ASP:HB3	7:D:103:ASN:H	1.47	0.78
1:0:21:G:C5'	20:R:2:ILE:HA	2.14	0.77
1:0:1116:U:H3	1:0:1246:A:H62	1.32	0.77
1:0:1180:U:H4'	32:I:91:GLU:HG2	1.64	0.77
1:0:1450:C:H4'	1:0:1451:C:OP2	1.82	0.77
20:R:106:GLY:HA2	20:R:109:MET:HE3	1.65	0.77
8:E:6:GLU:HA	8:E:46:THR:HG22	1.67	0.77
5:B:238:ASN:HD22	5:B:240:GLY:N	1.83	0.77
13:K:74:VAL:HG13	13:K:113:ILE:HG23	1.66	0.77
1:0:541:C:H2'	1:0:542:A:H5''	1.65	0.77
22:T:48:VAL:HG11	22:T:96:VAL:HG13	1.66	0.77
13:K:29:LEU:HB3	13:K:55:VAL:HG11	1.66	0.76
1:0:541:C:C2'	1:0:542:A:H5''	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:132:CYS:HB3	32:I:137:VAL:HB	1.67	0.76
28:Z:26:VAL:O	28:Z:30:GLU:HG3	1.85	0.76
6:C:182:ARG:HB2	6:C:184:ARG:NH1	1.99	0.76
25:W:68:THR:HG23	25:W:69:ARG:HG2	1.68	0.76
28:Z:46:ARG:HD2	28:Z:59:TYR:HB2	1.66	0.76
1:0:2908:A:H2'	1:0:2909:G:O4'	1.86	0.76
2:9:3014:G:H8	2:9:3014:G:H5'	1.50	0.76
29:1:21:ARG:HD2	29:1:39:PHE:HB2	1.68	0.76
1:0:1603:A:H5'	1:0:1605:G:O4'	1.86	0.76
1:0:188:C:H5''	15:M:163:LEU:HD21	1.68	0.76
2:9:3039:U:H1'	2:9:3044:A:H61	1.50	0.76
1:0:871:G:H8	1:0:871:G:C5'	1.99	0.76
1:0:1118:A:H3'	1:0:1118:A:C8	2.21	0.76
1:0:1120:U:H6	1:0:1120:U:H5'	1.51	0.75
1:0:2716:G:H5''	5:B:206:THR:HG21	1.66	0.75
1:0:2291:A:C8	1:0:2309:C:H5'	2.21	0.75
1:0:1474:C:C6	1:0:1474:C:H5'	2.21	0.75
16:N:113:SER:HB2	38:N:9357:HOH:O	1.86	0.75
9:F:63:ILE:HB	9:F:64:PRO:HD3	1.69	0.75
4:A:153:ARG:HH11	4:A:153:ARG:HB2	1.52	0.75
16:N:83:LEU:HD13	16:N:175:LEU:HD23	1.66	0.75
25:W:6:GLN:HB2	25:W:26:ILE:CD1	2.16	0.74
32:I:75:THR:HA	32:I:112:LYS:HZ1	1.51	0.74
8:E:3:VAL:HG22	8:E:49:ILE:HB	1.69	0.74
1:0:236:A:H4'	1:0:237:G:H5'	1.69	0.74
1:0:1118:A:H3'	1:0:1118:A:H8	1.51	0.74
8:E:31:ARG:HH12	8:E:68:HIS:CG	2.04	0.74
13:K:74:VAL:CG1	13:K:113:ILE:HG12	2.17	0.74
1:0:111:C:O2'	29:1:20:ARG:HG2	1.87	0.74
1:0:1181:A:H5'	32:I:94:GLU:OE2	1.88	0.74
20:R:17:MET:HE1	20:R:19:ARG:NH2	2.02	0.74
32:I:102:VAL:HG12	32:I:106:LYS:HE3	1.69	0.74
1:0:1684:A:H1'	30:2:43:ARG:HH22	1.52	0.74
5:B:320:GLN:HE21	5:B:321:PRO:HD2	1.53	0.74
5:B:320:GLN:NE2	5:B:321:PRO:HD2	2.03	0.74
6:C:236:THR:H	6:C:239:ALA:HB3	1.53	0.73
2:9:3056:A:C2'	2:9:3057:A:H5''	2.18	0.73
1:0:1189:A:H1'	1:0:1209:C:O4'	1.89	0.73
25:W:21:LEU:HD22	25:W:26:ILE:CD1	2.18	0.73
1:0:1160:G:H5'	1:0:1161:A:C5'	2.15	0.73
31:3:17:HIS:O	31:3:18:GLN:HG3	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:88:THR:HG23	25:W:110:GLN:NE2	2.03	0.73
16:N:164:ASP:CG	16:N:167:ASP:HA	2.09	0.73
5:B:238:ASN:ND2	5:B:240:GLY:H	1.86	0.73
1:O:657:G:OP1	6:C:27:ARG:NH2	2.21	0.73
5:B:98:THR:HG22	5:B:99:GLU:H	1.53	0.73
1:O:1328:A:OP1	27:Y:169:ARG:HD2	1.89	0.73
1:O:2548:C:OP2	5:B:5:ARG:NH2	2.22	0.73
13:K:62:PRO:HG3	13:K:65:ARG:NH2	2.04	0.72
6:C:27:ARG:HG3	6:C:29:ASP:OD1	1.88	0.72
1:O:1234:U:N3	5:B:244:PRO:HB3	2.03	0.72
22:T:9:LYS:HE3	22:T:13:ARG:HH11	1.54	0.72
1:O:396:U:H1'	38:O:7793:HOH:O	1.90	0.72
1:O:289:G:H22	1:O:363:A:H2	1.38	0.72
10:G:16:LYS:O	10:G:20:VAL:HG23	1.90	0.72
1:O:1206:U:H6	1:O:1206:U:H5'	1.55	0.72
16:N:132:ASN:O	16:N:135:VAL:HG12	1.89	0.72
31:3:25:VAL:HG22	31:3:68:LYS:HG3	1.72	0.72
1:O:877:G:H5'	1:O:878:G:OP1	1.89	0.72
25:W:137:GLN:HE21	25:W:141:HIS:HE1	1.36	0.72
1:O:272:A:H5'	1:O:273:G:OP2	1.90	0.72
4:A:36:ASP:HB2	4:A:83:GLY:HA3	1.72	0.72
1:O:2524:G:H21	1:O:2526:C:N4	1.88	0.72
21:S:57:THR:HG22	21:S:59:ASP:N	2.04	0.72
11:H:99:LYS:HD3	11:H:119:LYS:HD3	1.71	0.72
9:F:38:LYS:NZ	15:M:3:SER:HA	2.04	0.72
13:K:98:VAL:CG1	13:K:102:GLU:HA	2.20	0.72
15:M:164:THR:CG2	15:M:167:GLY:H	2.02	0.71
5:B:125:GLU:O	5:B:129:ARG:HG3	1.90	0.71
26:X:78:GLU:HG2	26:X:79:GLU:H	1.55	0.71
1:O:541:C:H2'	1:O:542:A:C5'	2.19	0.71
26:X:37:LEU:CD1	26:X:85:VAL:HG21	2.18	0.71
1:O:2426:G:H1'	38:O:6331:HOH:O	1.89	0.71
8:E:100:ASP:HB2	38:E:2789:HOH:O	1.89	0.71
9:F:2:VAL:HG22	9:F:57:GLU:OE1	1.91	0.71
1:O:1167:G:H4'	32:I:135:LEU:HD22	1.72	0.71
1:O:2769:C:H2'	1:O:2770:G:O4'	1.90	0.71
16:N:7:LYS:HE3	19:Q:21:ARG:O	1.90	0.71
1:O:1165:G:H4'	1:O:1174:A:O2'	1.89	0.71
1:O:1119:G:N2	1:O:1246:A:C2	2.58	0.71
4:A:43:VAL:HG21	4:A:59:GLU:HG3	1.71	0.71
1:O:2524:G:H21	1:O:2526:C:H41	1.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:962:C:H1'	16:N:5:ARG:NH1	2.06	0.71
20:R:14:ALA:HB3	20:R:147:LEU:HB2	1.70	0.71
14:L:133:VAL:HA	38:L:9372:HOH:O	1.91	0.71
20:R:39:THR:HG23	20:R:107:GLU:O	1.90	0.71
17:O:73:ASP:HA	17:O:92:VAL:O	1.91	0.71
11:H:169:GLY:HA3	38:H:9187:HOH:O	1.91	0.70
6:C:139:VAL:HG13	38:C:9249:HOH:O	1.89	0.70
1:0:2533:C:C6	1:0:2533:C:H5'	2.25	0.70
29:1:8:GLN:HE22	29:1:11:LYS:HZ2	1.38	0.70
1:0:1058:A:H2'	1:0:1060:C:H5''	1.71	0.70
7:D:136:ARG:HD2	7:D:155:HIS:O	1.91	0.70
1:0:1751:G:C2'	1:0:1752:G:H5''	2.20	0.70
7:D:28:GLY:HA2	7:D:69:ILE:HG23	1.71	0.70
27:Y:187:VAL:HG23	27:Y:192:ASP:HB2	1.72	0.70
25:W:21:LEU:HD22	25:W:26:ILE:HD13	1.74	0.70
27:Y:187:VAL:HG23	27:Y:192:ASP:CB	2.22	0.70
26:X:72:VAL:HG22	26:X:85:VAL:HG12	1.72	0.70
11:H:9:ILE:HG23	11:H:126:ARG:CZ	2.21	0.70
24:V:56:ILE:O	24:V:60:GLN:HG3	1.90	0.70
15:M:164:THR:HG22	15:M:167:GLY:N	2.07	0.70
1:0:2587:OMU:H2'	1:0:2589:U:H5''	1.74	0.70
7:D:146:LYS:NZ	16:N:107:ASN:HD21	1.90	0.70
1:0:1119:G:H2'	12:J:52:GLN:NE2	2.06	0.70
30:2:39:ARG:HG2	38:2:3143:HOH:O	1.92	0.70
1:0:2586:U:H3	1:0:2592:G:H22	1.38	0.69
1:0:553:G:P	27:Y:204:ARG:HH22	2.16	0.69
4:A:94:LEU:HG	4:A:99:ILE:HD11	1.73	0.69
1:0:1118:A:H62	1:0:1244:U:H3	1.39	0.69
1:0:1201:C:H2'	1:0:1202:A:H5'	1.74	0.69
18:P:103:THR:HA	18:P:106:ARG:NH1	2.06	0.69
13:K:81:ARG:HB2	13:K:87:ARG:NH1	2.07	0.69
11:H:166:SER:HB2	11:H:167:PRO:CD	2.22	0.69
1:0:544:G:H2'	1:0:545:G:H5''	1.73	0.69
27:Y:189:ASN:HA	27:Y:217:ILE:HD11	1.74	0.69
23:U:52:THR:CG2	23:U:54:THR:HB	2.23	0.69
24:V:12:THR:HG22	24:V:15:GLU:CG	2.23	0.69
13:K:14:LYS:CB	13:K:45:PRO:HG2	2.23	0.69
18:P:59:ARG:NH2	18:P:66:GLN:HE22	1.91	0.69
9:F:53:ASP:OD1	9:F:80:GLN:HB2	1.93	0.69
1:0:1205:U:H2'	1:0:1206:U:C5'	2.23	0.68
27:Y:144:ARG:CZ	38:Y:8197:HOH:O	2.40	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:44:GLY:O	24:V:48:GLU:HG2	1.94	0.68
6:C:115:LEU:HD21	6:C:243:VAL:HG13	1.75	0.68
1:O:1351:G:OP1	6:C:96:LYS:NZ	2.25	0.68
1:O:797:A:H4'	28:Z:10:ARG:N	2.08	0.68
12:J:76:ASP:HA	38:J:9361:HOH:O	1.92	0.68
17:O:32:ARG:HE	17:O:35:LYS:HD2	1.57	0.68
20:R:99:ALA:HB1	20:R:109:MET:CE	2.22	0.68
6:C:78:ARG:HG3	6:C:78:ARG:NH1	2.09	0.68
1:O:1205:U:H2'	1:O:1206:U:H5''	1.75	0.68
1:O:2768:A:H5''	38:O:4707:HOH:O	1.94	0.68
1:O:2768:A:H2'	1:O:2769:C:O4'	1.93	0.68
12:J:131:THR:HG22	12:J:134:GLU:H	1.57	0.68
16:N:154:LEU:HD11	16:N:157:PRO:HA	1.75	0.68
26:X:76:ARG:NH1	26:X:76:ARG:HG3	2.06	0.68
32:I:138:THR:HG22	32:I:139:ILE:H	1.58	0.68
24:V:39:ALA:N	24:V:40:PRO:HD2	2.09	0.68
12:J:90:LYS:HB2	36:J:9302:CL:CL	2.31	0.68
32:I:93:GLN:HA	32:I:96:PHE:HE2	1.58	0.68
11:H:58:ARG:HG3	11:H:58:ARG:HH11	1.57	0.68
2:9:3039:U:H1'	2:9:3044:A:N6	2.08	0.68
17:O:32:ARG:HD3	17:O:32:ARG:O	1.94	0.68
14:L:37:LYS:HG2	38:L:9334:HOH:O	1.92	0.68
7:D:37:ALA:O	7:D:40:ILE:HG12	1.94	0.68
5:B:201:ASP:HB2	5:B:312:ARG:HD2	1.76	0.68
2:9:3064:C:H2'	2:9:3065:A:H5'	1.76	0.68
30:2:41:HIS:HD2	30:2:44:ARG:H	1.41	0.68
1:O:656:G:OP2	17:O:37:ARG:HD2	1.94	0.68
9:F:58:GLU:HA	9:F:61:MET:HG3	1.75	0.67
30:2:36:ASN:O	30:2:39:ARG:HG3	1.93	0.67
5:B:202:VAL:HG11	5:B:301:VAL:HG13	1.77	0.67
1:O:2468:A:H61	31:3:48:ASN:HD21	1.41	0.67
22:T:38:ARG:HG3	22:T:38:ARG:HH11	1.57	0.67
25:W:4:LEU:HD22	25:W:52:VAL:HG21	1.76	0.67
7:D:50:VAL:O	7:D:71:ALA:HA	1.95	0.67
1:O:157:G:H4'	15:M:95:LYS:HE2	1.77	0.67
24:V:64:GLY:O	24:V:65:ASP:HB2	1.94	0.67
5:B:304:PRO:HD2	5:B:307:ARG:HD2	1.76	0.67
1:O:2252:A:C5	1:O:2253:G:H1'	2.30	0.67
21:S:33:SER:O	21:S:37:VAL:HG23	1.93	0.67
25:W:81:ASP:OD1	25:W:92:ASP:HB2	1.95	0.67
22:T:52:ARG:HB2	22:T:95:ASN:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1119:G:H2'	12:J:52:GLN:HE22	1.58	0.67
1:0:871:G:C5'	1:0:871:G:C8	2.76	0.67
1:0:1666:C:O2'	1:0:1667:A:H5''	1.95	0.67
4:A:192:VAL:HG12	4:A:207:GLN:HB3	1.75	0.67
1:0:1819:G:H5'	38:0:4985:HOH:O	1.93	0.67
1:0:2054:A:N3	20:R:128:ARG:NH2	2.42	0.67
5:B:41:PHE:CD1	5:B:79:MET:HE2	2.29	0.67
9:F:46:GLU:OE1	9:F:100:ASP:HA	1.95	0.67
1:0:1701:A:H5'	38:0:6518:HOH:O	1.93	0.67
1:0:1080:C:H4'	1:0:1081:A:OP1	1.94	0.67
6:C:16:VAL:HG12	6:C:17:ASP:H	1.59	0.66
6:C:236:THR:CG2	6:C:239:ALA:H	1.99	0.66
10:G:20:VAL:O	10:G:24:VAL:HG23	1.96	0.66
6:C:7:ASP:OD2	6:C:9:ASP:HB2	1.95	0.66
1:0:1244:U:OP1	12:J:18:ILE:HD13	1.95	0.66
32:I:129:VAL:HG13	32:I:139:ILE:HD11	1.75	0.66
15:M:59:GLY:HA3	15:M:141:ILE:HD11	1.77	0.66
29:1:25:LYS:HD2	30:2:49:GLU:H	1.59	0.66
25:W:88:THR:HG22	25:W:89:ASP:N	2.10	0.66
5:B:5:ARG:HD2	5:B:8:LYS:NZ	2.10	0.66
13:K:81:ARG:HB2	13:K:87:ARG:HH11	1.59	0.66
22:T:101:LEU:HD13	22:T:112:LEU:HD11	1.77	0.66
38:0:5785:HOH:O	15:M:58:GLN:HG3	1.95	0.66
1:0:2649:A:H5'	1:0:2649:A:H8	1.60	0.66
1:0:1641:A:H2'	1:0:1642:A:H5'	1.76	0.66
1:0:1666:C:H2'	1:0:1667:A:H5'	1.77	0.66
25:W:88:THR:HG23	25:W:110:GLN:HB3	1.78	0.66
25:W:4:LEU:CD2	25:W:54:PHE:HB3	2.26	0.66
25:W:65:VAL:HA	25:W:68:THR:HG22	1.78	0.66
20:R:6:VAL:HG21	20:R:113:HIS:CD2	2.31	0.66
38:0:7598:HOH:O	22:T:9:LYS:HB2	1.93	0.66
9:F:52:GLU:HG3	9:F:77:VAL:O	1.96	0.66
1:0:2851:G:O2'	1:0:2852:A:H5'	1.96	0.66
32:I:110:GLU:HA	32:I:113:HIS:CD2	2.31	0.65
7:D:135:VAL:HG21	7:D:139:TYR:CD1	2.31	0.65
32:I:125:ALA:O	32:I:129:VAL:HG23	1.96	0.65
7:D:54:ALA:HB2	7:D:69:ILE:HD12	1.78	0.65
1:0:1130:U:H2'	1:0:1131:G:O4'	1.97	0.65
7:D:88:LEU:HB2	7:D:89:PRO:HD3	1.78	0.65
2:9:3029:C:O3'	7:D:138:GLY:HA2	1.97	0.65
1:0:470:U:O2'	29:1:16:HIS:HD2	1.80	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1189:A:H1'	1:0:1209:C:C1'	2.27	0.65
1:0:870:G:OP2	4:A:3:ARG:HD3	1.97	0.65
1:0:558:C:O2'	1:0:559:U:H5''	1.96	0.65
2:9:3029:C:H2'	2:9:3030:C:H5'	1.78	0.65
11:H:166:SER:CB	11:H:167:PRO:HD3	2.26	0.65
1:0:560:C:H42	1:0:597:A:H61	1.43	0.65
10:G:27:ILE:HD13	10:G:71:LEU:HD23	1.78	0.65
5:B:162:MET:CE	5:B:308:LEU:HD21	2.27	0.65
1:0:820:G:C6	4:A:171:LYS:HB2	2.32	0.65
22:T:71:VAL:HG11	22:T:90:PRO:CB	2.26	0.65
1:0:1681:G:H5''	1:0:1682:A:H5'	1.78	0.65
14:L:67:ARG:O	14:L:71:GLU:HG3	1.96	0.65
23:U:39:ASN:ND2	23:U:44:ARG:HH11	1.95	0.65
27:Y:186:ARG:HG2	27:Y:186:ARG:HH11	1.62	0.65
32:I:118:SER:HB2	32:I:123:ASN:HB2	1.78	0.65
12:J:52:GLN:HG3	12:J:53:ILE:N	2.11	0.64
12:J:74:ARG:NH1	12:J:76:ASP:HB2	2.12	0.64
1:0:777:U:O2'	29:1:11:LYS:HG2	1.97	0.64
27:Y:99:ALA:HB2	27:Y:233:TYR:CZ	2.32	0.64
1:0:1701:A:H4'	1:0:1702:U:H5''	1.78	0.64
10:G:64:ASN:N	10:G:64:ASN:HD22	1.95	0.64
22:T:48:VAL:HG11	22:T:96:VAL:CG1	2.27	0.64
13:K:98:VAL:HG11	13:K:102:GLU:HA	1.78	0.64
19:Q:18:PRO:O	19:Q:21:ARG:HB2	1.97	0.64
16:N:119:GLN:O	16:N:123:ILE:HG13	1.97	0.64
20:R:18:LEU:HB2	20:R:143:VAL:HG12	1.79	0.64
1:0:2827:A:H2'	1:0:2828:G:O4'	1.98	0.64
12:J:75:PRO:HG2	12:J:105:LEU:HD21	1.79	0.64
1:0:545:G:C8	1:0:545:G:H5'	2.31	0.64
20:R:111:ILE:HG23	20:R:145:LEU:HD11	1.78	0.64
4:A:81:GLN:HB2	4:A:92:ASN:ND2	2.12	0.64
8:E:69:ILE:HA	8:E:72:MET:HE3	1.79	0.64
20:R:18:LEU:HD12	20:R:143:VAL:HG11	1.80	0.64
1:0:538:C:OP2	27:Y:134:HIS:HE1	1.81	0.64
6:C:5:ILE:HD11	6:C:16:VAL:HG23	1.78	0.64
25:W:21:LEU:HD21	25:W:48:VAL:HG11	1.78	0.64
12:J:93:ARG:NH1	12:J:93:ARG:HB3	2.12	0.64
2:9:3014:G:C8	2:9:3014:G:H5'	2.32	0.64
1:0:2690:U:O2'	8:E:111:LYS:HE3	1.98	0.64
1:0:380:A:H2'	38:0:7412:HOH:O	1.97	0.64
1:0:2491:G:H1'	38:0:7076:HOH:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1667:A:C8	1:0:1667:A:H5'	2.31	0.64
1:0:558:C:H2'	1:0:559:U:H5'	1.79	0.64
8:E:69:ILE:HA	8:E:72:MET:CE	2.28	0.63
1:0:1060:C:H6	1:0:1060:C:H5'	1.63	0.63
1:0:1819:G:H2'	1:0:1820:G:H4'	1.79	0.63
7:D:57:THR:HG23	7:D:63:ILE:HA	1.79	0.63
7:D:105:SER:HB2	7:D:131:THR:HG23	1.80	0.63
11:H:27:LYS:H	11:H:59:HIS:HD2	1.46	0.63
1:0:281:U:H2'	1:0:282:C:O4'	1.98	0.63
18:P:134:VAL:O	18:P:137:LEU:HB3	1.98	0.63
16:N:169:PRO:O	16:N:172:PHE:HB3	1.99	0.63
1:0:2896:A:H5''	38:0:6338:HOH:O	1.98	0.63
1:0:285:A:H2'	1:0:286:U:O4'	1.98	0.63
14:L:143:THR:HG22	14:L:144:ASP:N	2.14	0.63
14:L:149:ARG:O	14:L:150:GLN:HB2	1.98	0.63
1:0:2570:G:H5''	38:0:5188:HOH:O	1.99	0.63
7:D:99:ASP:HA	38:D:5675:HOH:O	1.97	0.63
18:P:91:LYS:O	18:P:95:GLU:HG3	1.99	0.63
8:E:145:ALA:HB1	8:E:168:ILE:HD11	1.81	0.63
1:0:447:A:OP1	22:T:2:LYS:HG2	1.98	0.63
25:W:125:HIS:HD2	25:W:127:GLY:H	1.46	0.63
38:0:7629:HOH:O	6:C:188:ARG:HD2	1.96	0.63
7:D:54:ALA:CB	7:D:69:ILE:HD12	2.28	0.63
7:D:57:THR:HG23	7:D:63:ILE:HG22	1.80	0.63
1:0:2414:A:H2'	1:0:2415:A:C8	2.34	0.63
32:I:75:THR:HA	32:I:112:LYS:NZ	2.14	0.63
5:B:41:PHE:CD2	5:B:190:MET:HE3	2.34	0.63
16:N:170:GLU:HA	16:N:173:ASP:OD2	1.98	0.63
1:0:1377:C:H6	1:0:1377:C:H5'	1.64	0.63
38:0:4132:HOH:O	11:H:11:LYS:HE2	1.99	0.63
1:0:1741:U:H5'	1:0:1742:A:OP1	1.98	0.63
21:S:11:THR:H	21:S:14:ALA:HB3	1.64	0.63
1:0:1184:C:H1'	38:0:7636:HOH:O	1.99	0.63
1:0:1130:U:H5'	38:0:7834:HOH:O	1.98	0.62
1:0:1299:G:O6	14:L:6:ARG:HD3	1.98	0.62
16:N:43:VAL:HG13	16:N:118:ILE:HD11	1.81	0.62
4:A:65:ARG:C	4:A:66:ARG:HG3	2.19	0.62
1:0:1159:G:H21	1:0:1189:A:H8	1.45	0.62
1:0:1834:C:H2'	1:0:1840:A:N6	2.14	0.62
16:N:47:LEU:HD11	16:N:127:LEU:HD21	1.81	0.62
26:X:41:PHE:O	26:X:43:VAL:HG23	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:134:ILE:HG23	15:M:141:ILE:HD13	1.81	0.62
1:0:2756:U:H3	1:0:2896:A:H2	1.47	0.62
1:0:564:G:H1'	38:0:6543:HOH:O	1.99	0.62
22:T:9:LYS:CE	22:T:13:ARG:NH1	2.61	0.62
2:9:3114:G:O6	16:N:11:ARG:HD3	1.98	0.62
1:0:2320:U:H4'	1:0:2321:A:O4'	1.98	0.62
6:C:145:GLU:HG3	38:C:9175:HOH:O	1.99	0.62
1:0:1187:U:O2'	1:0:1189:A:H2	1.80	0.62
7:D:41:LEU:HA	7:D:44:ILE:HG22	1.82	0.62
1:0:797:A:C4'	28:Z:10:ARG:N	2.62	0.62
26:X:30:MET:HE1	26:X:55:ASN:HA	1.81	0.62
4:A:200:PRO:HG2	4:A:225:VAL:HG21	1.82	0.62
38:0:7228:HOH:O	4:A:211:LYS:HG2	2.00	0.62
1:0:2251:G:H2'	1:0:2252:A:C8	2.34	0.62
7:D:58:VAL:CG1	7:D:60:GLU:HG2	2.28	0.62
16:N:154:LEU:O	16:N:155:GLU:HB3	2.00	0.62
22:T:32:ARG:NH1	22:T:38:ARG:HH12	1.97	0.62
1:0:2004:U:H4'	38:0:5568:HOH:O	1.99	0.62
7:D:95:THR:OG1	7:D:174:VAL:HG22	1.99	0.62
20:R:9:ASP:O	20:R:13:THR:HB	1.99	0.62
22:T:48:VAL:CG1	22:T:96:VAL:HG13	2.30	0.62
2:9:3002:U:OP2	2:9:3003:A:H5'	1.99	0.62
32:I:134:SER:O	32:I:135:LEU:HD23	2.00	0.62
16:N:110:THR:HB	16:N:113:SER:OG	2.00	0.62
5:B:254:GLN:HG2	5:B:255:GLY:N	2.15	0.62
13:K:118:ALA:HA	13:K:125:ALA:HB2	1.82	0.62
6:C:127:ARG:HH21	6:C:225:PRO:HG2	1.61	0.61
1:0:544:G:C2'	1:0:545:G:H5''	2.30	0.61
16:N:23:ARG:HD3	38:N:9346:HOH:O	1.99	0.61
8:E:31:ARG:NH1	8:E:68:HIS:CG	2.68	0.61
15:M:24:GLN:NE2	15:M:27:ARG:HH11	1.98	0.61
14:L:143:THR:HG21	38:L:9336:HOH:O	1.99	0.61
1:0:926:A:O2'	14:L:41:HIS:HD2	1.81	0.61
9:F:21:GLU:O	9:F:24:ARG:HG3	2.00	0.61
1:0:1086:A:C6	25:W:11:VAL:HG11	2.35	0.61
1:0:2840:A:OP1	5:B:211:THR:HG23	2.00	0.61
27:Y:189:ASN:HD22	27:Y:189:ASN:C	2.03	0.61
26:X:25:ARG:HD2	38:X:3861:HOH:O	1.99	0.61
31:3:62:THR:HB	38:3:9349:HOH:O	2.00	0.61
5:B:5:ARG:NH1	5:B:8:LYS:HE2	2.16	0.61
1:0:399:C:H5'	15:M:179:GLY:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:11:VAL:HG12	8:E:12:ASP:N	2.16	0.61
2:9:3055:U:H4'	2:9:3056:A:C8	2.36	0.61
25:W:149:LEU:HG	25:W:153:MET:HE2	1.81	0.61
16:N:48:VAL:HG11	16:N:55:ASP:HB3	1.82	0.61
22:T:48:VAL:HG13	22:T:97:ARG:O	2.00	0.61
1:0:2256:G:C2'	1:0:2257:G:H5'	2.31	0.61
38:0:7081:HOH:O	15:M:178:LYS:HB2	2.00	0.61
1:0:1625:U:H4'	38:0:4940:HOH:O	2.00	0.61
22:T:71:VAL:CG1	22:T:90:PRO:HB3	2.24	0.61
13:K:74:VAL:HG12	13:K:75:ARG:HG3	1.83	0.61
4:A:88:ILE:HG22	4:A:88:ILE:O	1.99	0.61
32:I:131:THR:O	32:I:135:LEU:HG	2.01	0.61
16:N:143:ARG:HA	16:N:172:PHE:CD2	2.36	0.61
25:W:125:HIS:CD2	25:W:127:GLY:H	2.19	0.61
1:0:902:G:N7	14:L:18:HIS:HD2	1.98	0.61
15:M:60:VAL:C	15:M:61:ILE:HD12	2.20	0.61
5:B:297:VAL:HB	38:B:9406:HOH:O	2.00	0.61
8:E:137:ASP:O	8:E:141:VAL:HG23	2.01	0.61
1:0:1166:A:H1'	1:0:1192:A:C2	2.36	0.61
27:Y:235:GLU:H	27:Y:235:GLU:CD	2.03	0.61
12:J:6:PHE:HB3	12:J:109:TYR:OH	2.01	0.61
6:C:16:VAL:HG12	6:C:17:ASP:N	2.16	0.60
4:A:66:ARG:HH11	4:A:66:ARG:HB2	1.66	0.60
38:0:7626:HOH:O	5:B:211:THR:HG21	2.01	0.60
1:0:848:C:H5'	38:0:7455:HOH:O	1.99	0.60
5:B:140:LEU:HD23	38:B:9378:HOH:O	1.99	0.60
1:0:2346:C:O5'	1:0:2346:C:H6	1.84	0.60
15:M:64:ARG:HD2	38:M:9378:HOH:O	2.00	0.60
1:0:1189:A:O2'	1:0:1208:C:H2'	2.00	0.60
22:T:38:ARG:HG3	22:T:38:ARG:NH1	2.17	0.60
6:C:104:ASP:HA	6:C:107:ARG:HH12	1.65	0.60
25:W:38:THR:HG22	25:W:39:ASP:H	1.67	0.60
11:H:166:SER:CB	11:H:167:PRO:CD	2.78	0.60
9:F:50:VAL:HG21	9:F:63:ILE:HG21	1.83	0.60
12:J:99:GLU:HA	38:J:9371:HOH:O	2.01	0.60
1:0:1266:U:H4'	27:Y:115:ARG:HH21	1.65	0.60
1:0:282:C:O2'	1:0:283:U:H5'	2.01	0.60
16:N:152:GLU:C	16:N:154:LEU:H	2.03	0.60
1:0:2256:G:H2'	1:0:2257:G:H5'	1.83	0.60
11:H:23:ILE:HA	11:H:120:ILE:HG21	1.82	0.60
25:W:13:MET:HE3	25:W:17:ILE:HG22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:63:GLU:HA	38:H:9177:HOH:O	2.00	0.60
1:0:2502:C:C2'	1:0:2503:A:H5'	2.32	0.60
1:0:449:A:N7	6:C:43:LYS:HG2	2.16	0.60
16:N:11:ARG:HG3	16:N:14:ARG:NH1	2.16	0.60
1:0:2504:A:H4'	11:H:71:ARG:HH11	1.67	0.60
1:0:793:A:H5''	18:P:83:LYS:HG2	1.83	0.60
7:D:13:MET:HA	7:D:137:PRO:HG2	1.83	0.60
11:H:45:VAL:HA	11:H:167:PRO:O	2.01	0.60
9:F:91:VAL:HG12	9:F:92:GLY:N	2.09	0.60
25:W:4:LEU:HD22	25:W:52:VAL:CG2	2.32	0.60
25:W:5:VAL:HG22	25:W:32:CYS:HB2	1.83	0.60
4:A:210:GLY:HA3	38:A:9380:HOH:O	2.02	0.60
4:A:194:MET:CE	4:A:199:HIS:HB2	2.31	0.60
6:C:33:LYS:HE2	38:C:9160:HOH:O	2.01	0.60
4:A:105:VAL:HG11	4:A:154:ALA:HB1	1.83	0.60
28:Z:57:CYS:SG	28:Z:59:TYR:HB3	2.42	0.60
1:0:1119:G:H8	12:J:52:GLN:HE22	1.48	0.60
1:0:2837:U:H1'	5:B:307:ARG:HH12	1.67	0.60
6:C:233:THR:HG22	6:C:234:VAL:N	2.17	0.60
17:O:14:LEU:CD2	17:O:102:ILE:HD11	2.32	0.60
1:0:338:C:H4'	6:C:174:ILE:CD1	2.32	0.60
16:N:27:LEU:HD13	16:N:50:LEU:HD21	1.82	0.59
14:L:136:ALA:HB3	38:L:9372:HOH:O	2.01	0.59
23:U:46:ALA:HB1	23:U:52:THR:HG21	1.84	0.59
4:A:192:VAL:CG1	4:A:207:GLN:HB3	2.32	0.59
4:A:211:LYS:HB3	4:A:212:PRO:CD	2.25	0.59
10:G:64:ASN:O	10:G:68:GLU:HG3	2.02	0.59
5:B:150:ALA:O	5:B:152:PRO:HD3	2.02	0.59
2:9:3055:U:H4'	2:9:3056:A:H8	1.67	0.59
15:M:164:THR:HG23	15:M:165:GLY:N	2.17	0.59
1:0:485:A:N3	1:0:487:G:H5''	2.17	0.59
29:1:10:LYS:HG3	38:1:9236:HOH:O	2.01	0.59
1:0:120:A:H5'	29:1:20:ARG:HH21	1.68	0.59
5:B:329:TYR:CE2	23:U:15:PRO:HG2	2.36	0.59
1:0:1926:G:H2'	1:0:1927:A:C8	2.36	0.59
14:L:61:ALA:HA	38:L:9363:HOH:O	2.03	0.59
1:0:1441:G:O2'	1:0:1442:A:H5'	2.02	0.59
26:X:43:VAL:HG12	26:X:44:ASP:N	2.17	0.59
1:0:1118:A:H2'	1:0:1120:U:H5''	1.84	0.59
8:E:23:GLU:HG2	8:E:28:SER:HB3	1.84	0.59
13:K:34:VAL:HG22	13:K:47:ALA:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:22:VAL:HG22	7:D:74:THR:HG22	1.84	0.59
1:0:2748:G:H5'	38:0:7705:HOH:O	2.02	0.59
2:9:3064:C:C2'	2:9:3065:A:H5'	2.33	0.59
1:0:121:U:OP2	30:2:10:ARG:NH2	2.32	0.59
1:0:1299:G:N7	14:L:6:ARG:NH1	2.50	0.59
25:W:38:THR:HG22	25:W:39:ASP:N	2.18	0.59
21:S:52:VAL:C	21:S:53:ASN:HD22	2.06	0.59
4:A:94:LEU:HG	4:A:99:ILE:CD1	2.31	0.59
4:A:94:LEU:N	4:A:94:LEU:HD23	2.18	0.59
4:A:194:MET:HE2	4:A:199:HIS:HB2	1.85	0.59
1:0:65:C:O2'	1:0:66:G:H5'	2.02	0.59
1:0:625:U:H5''	1:0:1044:C:N4	2.17	0.59
1:0:2668:G:H2'	1:0:2669:U:C6	2.38	0.59
7:D:10:PHE:CG	7:D:11:HIS:N	2.71	0.59
8:E:35:TYR:HA	12:J:127:ILE:HD12	1.84	0.59
7:D:166:ILE:HB	38:D:6326:HOH:O	2.03	0.59
12:J:74:ARG:CB	12:J:74:ARG:HH11	2.13	0.59
2:9:3028:U:H5''	16:N:40:ASN:HD21	1.67	0.59
32:I:76:ALA:O	32:I:80:LYS:HG3	2.01	0.59
30:2:5:LYS:O	30:2:9:LYS:HG3	2.03	0.59
18:P:80:ARG:HG2	18:P:87:ARG:CZ	2.33	0.59
1:0:1733:A:H4'	5:B:212:GLN:HA	1.84	0.59
16:N:139:TRP:HA	16:N:139:TRP:CE3	2.38	0.59
14:L:143:THR:HG22	14:L:145:LEU:H	1.66	0.59
1:0:1213:C:O2'	1:0:1214:G:H5'	2.03	0.59
1:0:1813:U:O2'	18:P:81:LYS:HE3	2.03	0.59
4:A:39:ALA:HB3	4:A:61:GLU:OE2	2.02	0.59
27:Y:212:ARG:HD2	38:Y:8187:HOH:O	2.02	0.59
1:0:88:G:H5'	1:0:88:G:H8	1.68	0.59
5:B:16:ARG:NH1	38:B:9416:HOH:O	2.36	0.59
4:A:105:VAL:CG1	4:A:154:ALA:HB1	2.33	0.59
31:3:73:GLU:HB3	38:3:9360:HOH:O	2.02	0.59
26:X:25:ARG:HD3	26:X:64:ALA:O	2.01	0.59
5:B:16:ARG:HB3	5:B:217:ARG:NH2	2.18	0.58
38:0:7333:HOH:O	29:1:1:THR:HB	2.01	0.58
20:R:25:PHE:CE2	20:R:29:LYS:HE2	2.38	0.58
28:Z:42:CYS:SG	28:Z:43:GLY:N	2.76	0.58
1:0:2649:A:H5'	1:0:2649:A:C8	2.38	0.58
1:0:2779:G:H21	8:E:143:GLN:NE2	2.01	0.58
1:0:2502:C:H2'	1:0:2503:A:H5'	1.84	0.58
1:0:381:G:H5''	38:0:4603:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:106:THR:HG23	27:Y:107:PRO:HD2	1.84	0.58
4:A:217:ARG:HH11	4:A:217:ARG:HG3	1.67	0.58
2:9:3092:G:H2'	2:9:3093:A:C8	2.38	0.58
4:A:8:ARG:HG2	38:A:9349:HOH:O	2.03	0.58
2:9:3069:U:OP1	16:N:4:PRO:HG3	2.03	0.58
11:H:167:PRO:O	11:H:168:ALA:HB2	2.02	0.58
12:J:75:PRO:HG2	12:J:105:LEU:CD2	2.32	0.58
20:R:40:ALA:O	20:R:44:VAL:HG23	2.03	0.58
1:0:2717:C:H2'	1:0:2718:C:C5'	2.31	0.58
1:0:1450:C:O2'	1:0:1494:A:H5'	2.03	0.58
5:B:312:ARG:HD3	5:B:315:VAL:HG13	1.84	0.58
5:B:307:ARG:HB2	5:B:307:ARG:HH11	1.68	0.58
5:B:41:PHE:HB3	5:B:190:MET:HE3	1.84	0.58
27:Y:107:PRO:HB3	27:Y:182:PHE:CE2	2.38	0.58
2:9:3048:C:H4'	16:N:141:ARG:HH21	1.67	0.58
1:0:2546:U:H5	5:B:2:GLN:HE22	1.50	0.58
20:R:132:ARG:HG2	20:R:133:ALA:N	2.17	0.58
1:0:1730:G:H5'	1:0:1731:C:C5	2.38	0.58
7:D:25:MET:HE3	7:D:37:ALA:CB	2.31	0.58
1:0:2524:G:N2	1:0:2526:C:H41	2.01	0.58
1:0:2094:G:H4'	5:B:245:SER:HB3	1.84	0.58
1:0:2365:G:H4'	19:Q:45:PRO:O	2.03	0.58
6:C:154:VAL:O	6:C:158:GLU:HG3	2.03	0.58
1:0:31:C:H4'	38:0:7598:HOH:O	2.03	0.58
16:N:163:PHE:HZ	16:N:171:HIS:HD1	1.51	0.58
1:0:1741:U:O2'	1:0:2723:G:H4'	2.04	0.58
32:I:139:ILE:HG22	32:I:140:GLU:N	2.19	0.58
22:T:48:VAL:HG12	22:T:49:GLU:N	2.18	0.58
4:A:190:ARG:NH2	4:A:207:GLN:OE1	2.37	0.58
25:W:13:MET:HE1	25:W:18:GLN:HA	1.86	0.58
1:0:2578:G:H5'	1:0:2578:G:H8	1.69	0.58
1:0:2241:C:H2'	1:0:2242:U:C6	2.39	0.58
32:I:72:VAL:HG13	32:I:73:PRO:HD2	1.85	0.58
26:X:31:ILE:O	26:X:35:GLU:HG3	2.03	0.58
28:Z:11:SER:CB	28:Z:23:ARG:HB2	2.34	0.58
13:K:62:PRO:CG	13:K:65:ARG:HH21	2.16	0.58
6:C:182:ARG:HB2	6:C:184:ARG:HH12	1.68	0.58
1:0:1527:A:H1'	1:0:1528:A:C8	2.38	0.58
25:W:4:LEU:O	25:W:32:CYS:HA	2.04	0.58
20:R:145:LEU:HD12	20:R:146:ILE:N	2.19	0.58
1:0:447:A:O2'	1:0:448:G:H5'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:120:ILE:N	11:H:120:ILE:HD12	2.19	0.58
1:O:1180:U:H1'	38:O:3528:HOH:O	2.03	0.58
8:E:31:ARG:HH12	8:E:68:HIS:CD2	2.22	0.58
1:O:962:C:H1'	16:N:5:ARG:HH12	1.68	0.58
17:O:37:ARG:HG3	38:O:3002:HOH:O	2.03	0.58
1:O:1790:C:H2'	1:O:1791:U:H6	1.69	0.58
15:M:31:TRP:HA	15:M:34:GLU:HG3	1.84	0.58
1:O:182:G:H5'	38:O:5426:HOH:O	2.03	0.58
1:O:1835:U:C5	1:O:1840:A:N7	2.61	0.57
9:F:50:VAL:HG13	9:F:60:VAL:HG11	1.86	0.57
6:C:168:ARG:NH2	6:C:190:ALA:O	2.37	0.57
12:J:19:MET:HE2	12:J:132:LEU:HD11	1.85	0.57
25:W:84:VAL:HG12	38:W:6679:HOH:O	2.03	0.57
32:I:138:THR:HG22	32:I:139:ILE:N	2.19	0.57
23:U:17:THR:HG22	23:U:18:GLY:N	2.19	0.57
1:O:644:G:N3	1:O:644:G:H5'	2.18	0.57
25:W:108:ARG:HE	25:W:114:PRO:CG	2.17	0.57
1:O:2256:G:H2'	1:O:2257:G:C5'	2.35	0.57
20:R:47:LEU:O	20:R:51:ILE:HG13	2.04	0.57
5:B:55:ASN:HB3	5:B:63:GLU:HA	1.86	0.57
18:P:9:LEU:O	18:P:13:VAL:HG12	2.03	0.57
7:D:39:ASP:O	7:D:43:GLU:HG3	2.03	0.57
25:W:122:ARG:HH11	25:W:122:ARG:HG2	1.70	0.57
4:A:121:ALA:O	4:A:124:VAL:HG22	2.04	0.57
4:A:109:GLU:HG2	4:A:116:GLY:N	2.18	0.57
15:M:61:ILE:N	15:M:61:ILE:HD12	2.19	0.57
27:Y:151:SER:HB3	27:Y:154:ARG:HB3	1.87	0.57
1:O:1008:C:H5''	11:H:16:ARG:HH12	1.70	0.57
27:Y:200:THR:HG22	27:Y:201:GLU:HG2	1.86	0.57
1:O:2878:U:H2'	1:O:2879:A:O4'	2.04	0.57
25:W:88:THR:CG2	25:W:110:GLN:NE2	2.68	0.57
13:K:55:VAL:HG12	13:K:56:SER:N	2.20	0.57
1:O:1182:C:H1'	1:O:1192:A:H8	1.68	0.57
13:K:81:ARG:HD3	13:K:87:ARG:NH1	2.19	0.57
1:O:2508:C:H2'	38:O:6966:HOH:O	2.04	0.57
18:P:64:GLU:HG2	38:P:170:HOH:O	2.05	0.57
1:O:2679:G:H2'	1:O:2681:A:OP2	2.05	0.57
4:A:153:ARG:CB	4:A:153:ARG:HH11	2.18	0.57
16:N:80:SER:HB2	38:N:9336:HOH:O	2.04	0.57
1:O:703:G:O2'	1:O:704:C:H5'	2.05	0.57
5:B:275:GLY:O	5:B:291:ASP:HA	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:80:TRP:O	8:E:134:SER:HA	2.05	0.57
30:2:36:ASN:HB3	30:2:39:ARG:HE	1.70	0.57
29:1:25:LYS:HD2	30:2:48:ASP:HA	1.87	0.57
20:R:18:LEU:HB2	20:R:143:VAL:CG1	2.34	0.57
1:0:1163:G:H5'	32:I:115:ASP:O	2.05	0.57
17:O:87:THR:O	17:O:91:GLN:HG3	2.04	0.57
1:0:1118:A:C8	1:0:1118:A:C3'	2.85	0.57
1:0:1926:G:H2'	1:0:1927:A:H8	1.70	0.57
1:0:960:G:H2'	1:0:960:G:N3	2.20	0.57
21:S:17:ASP:HB3	21:S:23:LYS:HB2	1.87	0.57
6:C:35:VAL:HG21	6:C:227:GLY:HA2	1.86	0.57
5:B:280:VAL:CG1	5:B:334:SER:HA	2.35	0.57
20:R:145:LEU:HD12	20:R:146:ILE:H	1.70	0.56
1:0:256:C:H2'	1:0:257:G:O4'	2.05	0.56
14:L:77:ALA:HB3	38:L:9329:HOH:O	2.05	0.56
1:0:1189:A:H3'	38:0:7842:HOH:O	2.04	0.56
4:A:82:VAL:HG13	4:A:93:THR:HB	1.87	0.56
9:F:38:LYS:HZ1	15:M:3:SER:HA	1.68	0.56
29:1:25:LYS:O	29:1:25:LYS:HG2	2.05	0.56
1:0:2346:C:O2'	7:D:52:THR:HG21	2.04	0.56
9:F:96:ALA:HA	38:F:3111:HOH:O	2.04	0.56
2:9:3041:C:H4'	7:D:48:MET:HB2	1.87	0.56
1:0:2265:U:H2'	1:0:2266:A:C8	2.40	0.56
1:0:1462:C:H2'	1:0:1463:A:C8	2.41	0.56
1:0:280:C:H2'	1:0:281:U:O4'	2.05	0.56
9:F:58:GLU:OE1	15:M:27:ARG:NH2	2.34	0.56
7:D:135:VAL:HG22	7:D:136:ARG:N	2.20	0.56
24:V:39:ALA:N	24:V:40:PRO:CD	2.69	0.56
1:0:2256:G:O2'	1:0:2257:G:H5'	2.05	0.56
1:0:1657:A:H2'	1:0:1658:A:C8	2.40	0.56
2:9:3054:A:O2'	2:9:3055:U:H5'	2.06	0.56
23:U:9:CYS:HA	23:U:52:THR:HG23	1.87	0.56
21:S:33:SER:OG	21:S:36:GLU:HG3	2.06	0.56
1:0:2415:A:C2	16:N:25:ARG:HB3	2.41	0.56
13:K:34:VAL:CG2	13:K:47:ALA:HB2	2.35	0.56
5:B:305:ASP:O	5:B:306:LYS:HB2	2.06	0.56
1:0:2563:U:H2'	1:0:2565:C:O5'	2.05	0.56
38:0:4274:HOH:O	22:T:82:THR:HA	2.06	0.56
1:0:1314:U:H2'	38:0:6124:HOH:O	2.03	0.56
22:T:35:TYR:CD2	22:T:112:LEU:HD22	2.40	0.56
1:0:1682:A:H5''	38:0:9763:HOH:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:602:A:O2'	1:0:605:C:H4'	2.04	0.56
1:0:1535:G:H2'	1:0:1536:C:C6	2.41	0.56
32:I:75:THR:CA	32:I:112:LYS:HZ1	2.19	0.56
1:0:119:A:H2'	1:0:120:A:H5''	1.88	0.56
23:U:14:GLU:O	23:U:17:THR:HB	2.05	0.56
22:T:24:ARG:HH21	22:T:39:ASN:ND2	2.04	0.56
30:2:22:PRO:HG2	30:2:25:VAL:HG23	1.88	0.56
1:0:820:G:OP2	4:A:171:LYS:NZ	2.37	0.56
22:T:24:ARG:HH21	22:T:39:ASN:HD22	1.52	0.56
25:W:22:GLU:HG2	25:W:27:HIS:CD2	2.40	0.56
18:P:7:LYS:HD3	18:P:21:VAL:CG2	2.36	0.56
1:0:709:G:O2'	17:O:25:VAL:HG12	2.05	0.56
31:3:87:ARG:HD2	31:3:89:GLU:OE2	2.06	0.56
23:U:52:THR:HG21	23:U:54:THR:HB	1.87	0.56
11:H:77:LEU:HD12	11:H:83:TYR:CD2	2.41	0.56
2:9:3049:G:O2'	2:9:3050:G:H5'	2.05	0.56
1:0:136:C:H2'	1:0:137:U:O4'	2.06	0.56
1:0:2271:G:H5'	38:0:5025:HOH:O	2.06	0.56
24:V:1:THR:HG23	24:V:2:VAL:N	2.15	0.55
23:U:52:THR:HG22	23:U:54:THR:N	2.21	0.55
16:N:143:ARG:NH1	16:N:173:ASP:OD2	2.39	0.55
1:0:1778:A:H2'	1:0:1779:A:H5'	1.88	0.55
7:D:51:ARG:HD3	38:D:7636:HOH:O	2.06	0.55
20:R:3:SER:HA	38:R:9348:HOH:O	2.06	0.55
18:P:115:SER:O	18:P:117:SER:N	2.36	0.55
2:9:3013:A:O2'	2:9:3014:G:H5''	2.05	0.55
1:0:2769:C:C2'	1:0:2770:G:H5'	2.36	0.55
8:E:137:ASP:OD1	8:E:139:GLU:HB2	2.06	0.55
8:E:23:GLU:HG2	8:E:28:SER:CB	2.35	0.55
6:C:109:LEU:O	6:C:109:LEU:HD12	2.05	0.55
26:X:30:MET:HE1	26:X:58:ALA:HB3	1.88	0.55
22:T:92:ASP:OD1	22:T:94:SER:HB3	2.06	0.55
1:0:426:G:H2'	1:0:427:C:O4'	2.07	0.55
2:9:3006:C:OP1	16:N:37:ARG:NH1	2.39	0.55
1:0:2718:C:H6	1:0:2718:C:H5'	1.71	0.55
4:A:35:GLY:O	4:A:36:ASP:HB3	2.06	0.55
5:B:198:GLU:HA	38:B:9454:HOH:O	2.06	0.55
1:0:290:C:H1'	38:0:6342:HOH:O	2.05	0.55
4:A:76:VAL:HG23	28:Z:63:LYS:HB3	1.87	0.55
8:E:20:ILE:HD11	8:E:40:VAL:HG11	1.88	0.55
1:0:1766:U:O2	1:0:1778:A:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:660:A:H4'	1:0:661:G:O5'	2.07	0.55
3:4:176:DA:O4'	3:4:175:C:H2'	2.06	0.55
13:K:115:ARG:HG3	13:K:116:GLU:N	2.20	0.55
1:0:2755:G:H1'	38:0:4956:HOH:O	2.06	0.55
1:0:1909:A:H2'	1:0:1910:A:C8	2.40	0.55
7:D:86:THR:C	7:D:89:PRO:HD2	2.27	0.55
25:W:73:LEU:O	25:W:74:GLU:HG3	2.06	0.55
4:A:153:ARG:NH1	4:A:153:ARG:HB2	2.20	0.55
6:C:111:VAL:HB	38:C:9123:HOH:O	2.07	0.55
1:0:968:G:O2'	1:0:969:G:H5'	2.07	0.55
25:W:119:HIS:HD2	25:W:120:PRO:O	1.89	0.55
1:0:1506:U:H6	1:0:1506:U:H5'	1.72	0.55
20:R:39:THR:HB	20:R:42:GLU:HG3	1.89	0.55
1:0:2505:G:O2'	1:0:2506:A:H5'	2.07	0.55
20:R:104:PHE:HB2	20:R:109:MET:HE1	1.88	0.55
5:B:71:VAL:HG11	5:B:296:LEU:HD22	1.88	0.55
5:B:88:GLU:HB3	5:B:97:LEU:HG	1.89	0.55
1:0:1687:C:O2	29:1:9:GLY:HA2	2.06	0.55
1:0:1972:U:H2'	1:0:1973:A:H5'	1.88	0.55
12:J:19:MET:HE1	12:J:78:ILE:HG22	1.89	0.55
1:0:1242:A:C5'	12:J:82:THR:HG23	2.25	0.55
1:0:2768:A:O2'	1:0:2769:C:H5'	2.07	0.55
21:S:37:VAL:O	21:S:41:VAL:HG23	2.06	0.55
28:Z:11:SER:HB3	28:Z:23:ARG:HB2	1.88	0.55
1:0:681:G:N3	1:0:681:G:H5'	2.22	0.55
1:0:1505:U:H6	1:0:1505:U:H5'	1.70	0.55
11:H:9:ILE:O	11:H:9:ILE:HG22	2.07	0.55
25:W:80:ASP:O	25:W:84:VAL:HG23	2.06	0.55
17:O:21:SER:OG	17:O:106:PRO:HB2	2.07	0.55
1:0:2613:G:O2'	1:0:2614:C:H5'	2.07	0.55
28:Z:13:ARG:NH1	28:Z:14:PHE:CZ	2.75	0.55
28:Z:25:ARG:O	28:Z:29:ILE:HG13	2.06	0.55
18:P:143:ALA:HA	38:P:190:HOH:O	2.07	0.55
9:F:107:ASP:O	9:F:111:ILE:HG13	2.07	0.55
11:H:166:SER:HB2	11:H:167:PRO:HD3	1.86	0.54
26:X:78:GLU:HG2	26:X:79:GLU:N	2.20	0.54
6:C:107:ARG:NH1	6:C:107:ARG:HB3	2.22	0.54
32:I:89:SER:HB3	32:I:97:VAL:CG2	2.37	0.54
1:0:2630:G:O6	4:A:206:ARG:NH2	2.41	0.54
38:0:4897:HOH:O	4:A:6:GLY:HA3	2.07	0.54
25:W:139:GLY:O	25:W:141:HIS:CD2	2.59	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2526:C:O2'	1:0:2527:U:H5'	2.07	0.54
27:Y:187:VAL:CG2	27:Y:192:ASP:HB2	2.36	0.54
1:0:2783:A:H3'	38:0:5494:HOH:O	2.07	0.54
17:O:47:ARG:HG3	17:O:47:ARG:HH11	1.72	0.54
1:0:2509:A:H2'	1:0:2510:C:O4'	2.08	0.54
25:W:21:LEU:HD13	25:W:26:ILE:HD11	1.88	0.54
1:0:1234:U:C4	5:B:244:PRO:HB3	2.43	0.54
26:X:22:ASN:O	26:X:25:ARG:HG3	2.07	0.54
1:0:2676:C:H4'	12:J:70:PHE:CE1	2.42	0.54
1:0:1289:C:H3'	38:0:6638:HOH:O	2.06	0.54
7:D:25:MET:SD	7:D:40:ILE:HD11	2.48	0.54
1:0:282:C:H1'	1:0:368:C:H42	1.68	0.54
32:I:139:ILE:HG22	32:I:140:GLU:H	1.71	0.54
1:0:21:G:H4'	20:R:2:ILE:HG22	1.87	0.54
6:C:77:ALA:O	6:C:78:ARG:HG3	2.07	0.54
1:0:92:G:H4'	24:V:44:GLY:HA3	1.89	0.54
2:9:3028:U:H5''	16:N:40:ASN:ND2	2.22	0.54
27:Y:99:ALA:HB2	27:Y:233:TYR:CE2	2.42	0.54
10:G:64:ASN:N	10:G:64:ASN:ND2	2.54	0.54
8:E:84:MET:HB2	8:E:131:LEU:HB2	1.90	0.54
2:9:3001:U:H5''	2:9:3003:A:OP1	2.08	0.54
5:B:51:VAL:HG13	5:B:53:LEU:HD13	1.89	0.54
4:A:217:ARG:CG	4:A:217:ARG:HH11	2.20	0.54
2:9:3091:C:H2'	2:9:3092:G:O4'	2.07	0.54
5:B:119:HIS:O	5:B:121:PRO:HD3	2.08	0.54
1:0:2862:G:H4'	5:B:336:GLN:O	2.07	0.54
26:X:80:GLU:HB3	38:X:5564:HOH:O	2.07	0.54
1:0:2717:C:O2'	1:0:2718:C:H5''	2.06	0.54
12:J:103:VAL:HG12	38:J:9361:HOH:O	2.07	0.54
27:Y:184:GLU:OE1	27:Y:204:ARG:NH1	2.39	0.54
6:C:1:MET:HG2	6:C:2:GLN:N	2.15	0.54
1:0:776:A:OP1	29:1:28:HIS:HE1	1.91	0.54
20:R:17:MET:CE	20:R:19:ARG:CZ	2.85	0.54
27:Y:189:ASN:ND2	27:Y:192:ASP:H	2.05	0.54
6:C:235:PHE:HE2	6:C:243:VAL:HG21	1.72	0.54
16:N:151:ASP:OD1	16:N:154:LEU:HD13	2.08	0.54
32:I:72:VAL:CG1	32:I:73:PRO:HD2	2.37	0.54
27:Y:112:GLU:OE1	27:Y:112:GLU:HA	2.07	0.54
13:K:27:ARG:HD2	38:K:4747:HOH:O	2.07	0.54
1:0:583:G:H2'	1:0:584:U:C6	2.42	0.54
9:F:27:GLY:HA3	9:F:101:ALA:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:140:VAL:HB	38:C:9252:HOH:O	2.07	0.54
16:N:139:TRP:HA	16:N:139:TRP:HE3	1.72	0.54
24:V:38:GLY:C	24:V:40:PRO:HD2	2.27	0.54
1:O:1847:A:OP1	4:A:175:LYS:HG3	2.08	0.54
5:B:146:THR:O	5:B:159:PRO:HB3	2.08	0.54
25:W:106:THR:OG1	25:W:109:GLU:HG3	2.07	0.54
32:I:92:PRO:C	32:I:94:GLU:H	2.10	0.54
23:U:52:THR:HG22	23:U:54:THR:HB	1.90	0.54
25:W:122:ARG:HG3	25:W:152:ALA:O	2.07	0.54
27:Y:133:HIS:HD2	38:Y:8168:HOH:O	1.90	0.54
1:O:1342:C:O2'	1:O:1343:C:H5'	2.08	0.54
1:O:1278:A:H4'	1:O:1279:U:C4	2.43	0.54
1:O:1116:U:O2'	1:O:1118:A:C2	2.51	0.54
5:B:162:MET:HG3	5:B:310:ARG:CZ	2.38	0.54
2:9:3003:A:N6	2:9:3022:G:H1'	2.23	0.54
14:L:104:ASP:O	14:L:105:TYR:HB3	2.06	0.54
19:Q:28:ARG:HD2	19:Q:92:ARG:NH1	2.23	0.54
1:O:371:U:H2'	1:O:372:A:H8	1.73	0.54
1:O:56:G:C5'	24:V:50:ARG:HH12	2.12	0.53
6:C:2:GLN:HB3	38:C:9186:HOH:O	2.07	0.53
16:N:164:ASP:OD2	16:N:167:ASP:HA	2.08	0.53
1:O:2720:C:O2	13:K:87:ARG:NH2	2.41	0.53
16:N:100:ALA:O	16:N:129:ILE:HG23	2.08	0.53
22:T:16:LEU:HA	22:T:19:ARG:HG3	1.90	0.53
1:O:2300:A:H4'	1:O:2301:A:O5'	2.09	0.53
32:I:75:THR:CA	32:I:112:LYS:NZ	2.71	0.53
17:O:14:LEU:HD23	17:O:102:ILE:HD11	1.90	0.53
16:N:37:ARG:NE	38:N:9334:HOH:O	2.41	0.53
1:O:1942:A:O2'	1:O:1943:C:H5'	2.09	0.53
7:D:25:MET:HE1	7:D:41:LEU:HG	1.91	0.53
27:Y:144:ARG:NH1	38:Y:8163:HOH:O	2.41	0.53
25:W:108:ARG:HE	25:W:114:PRO:HG3	1.73	0.53
6:C:127:ARG:HG2	6:C:127:ARG:NH1	2.24	0.53
4:A:36:ASP:HB2	4:A:83:GLY:CA	2.39	0.53
12:J:45:VAL:HG22	12:J:130:VAL:O	2.09	0.53
2:9:3042:C:H5'	2:9:3043:G:OP2	2.08	0.53
16:N:23:ARG:O	16:N:27:LEU:HG	2.08	0.53
1:O:1164:U:H3	1:O:1192:A:H2	1.56	0.53
9:F:50:VAL:CG2	9:F:63:ILE:HG21	2.37	0.53
1:O:657:G:H2'	1:O:658:C:C6	2.43	0.53
38:C:9168:HOH:O	22:T:2:LYS:HE2	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:O:9668:HOH:O	29:I:1:THR:HA	2.07	0.53
1:O:407:A:H2'	1:O:408:A:C8	2.43	0.53
1:O:2064:U:H5'	1:O:2652:U:H4'	1.90	0.53
5:B:294:TYR:HE2	38:B:9446:HOH:O	1.90	0.53
1:O:1014:A:H2'	1:O:1015:C:H5'	1.91	0.53
1:O:2597:U:H2'	1:O:2598:U:H5'	1.90	0.53
25:W:63:GLU:HG2	25:W:93:ILE:HG22	1.89	0.53
1:O:1667:A:H2'	1:O:1668:U:C6	2.44	0.53
25:W:21:LEU:HB3	25:W:26:ILE:HG12	1.91	0.53
32:I:102:VAL:CG1	32:I:106:LYS:HE3	2.37	0.53
27:Y:186:ARG:HG2	27:Y:186:ARG:NH1	2.23	0.53
9:F:48:VAL:HG12	9:F:97:ALA:CB	2.39	0.53
7:D:153:THR:HA	7:D:156:ARG:HG3	1.91	0.53
5:B:212:GLN:HB2	5:B:257:THR:CG2	2.34	0.53
9:F:38:LYS:HZ2	15:M:3:SER:HA	1.70	0.53
1:O:2769:C:O2'	1:O:2770:G:H5'	2.09	0.53
1:O:1377:C:H5'	1:O:1377:C:C6	2.44	0.53
6:C:133:ARG:NE	6:C:138:VAL:HG22	2.23	0.53
1:O:90:A:H2'	1:O:91:G:O4'	2.09	0.53
1:O:539:G:H2'	1:O:540:A:C8	2.43	0.53
1:O:289:G:N2	1:O:363:A:H2	2.04	0.53
5:B:41:PHE:CZ	5:B:79:MET:HG3	2.44	0.53
11:H:76:GLU:C	11:H:77:LEU:HD23	2.29	0.53
9:F:101:ALA:HA	38:F:5413:HOH:O	2.09	0.53
38:9:4707:HOH:O	16:N:147:ILE:HB	2.08	0.53
25:W:21:LEU:HD21	25:W:48:VAL:CG1	2.39	0.53
25:W:6:GLN:CB	25:W:26:ILE:HD12	2.35	0.53
2:9:3044:A:O4'	7:D:76:ARG:NE	2.42	0.53
15:M:46:LEU:HG	38:M:9411:HOH:O	2.09	0.53
5:B:27:ASN:H	5:B:27:ASN:HD22	1.57	0.53
12:J:19:MET:CE	12:J:132:LEU:HD11	2.38	0.52
6:C:184:ARG:CZ	38:C:9216:HOH:O	2.57	0.52
26:X:30:MET:CE	26:X:58:ALA:HB3	2.39	0.52
25:W:122:ARG:CZ	38:W:5817:HOH:O	2.57	0.52
8:E:15:GLN:HG3	8:E:20:ILE:HG12	1.91	0.52
12:J:39:VAL:HG12	12:J:40:ASN:ND2	2.25	0.52
22:T:78:THR:OG1	22:T:86:GLU:HG2	2.08	0.52
1:O:2324:G:H4'	1:O:2418:G:O2'	2.09	0.52
5:B:17:LYS:O	5:B:260:HIS:HD2	1.92	0.52
1:O:1175:G:H1'	1:O:1193:A:H2'	1.91	0.52
16:N:37:ARG:HD3	36:N:9307:CL:CL	2.47	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:U:11:THR:HG22	23:U:53:ASP:OD2	2.10	0.52
15:M:59:GLY:HA3	15:M:141:ILE:CD1	2.38	0.52
20:R:114:VAL:HG13	20:R:114:VAL:O	2.09	0.52
1:0:338:C:H4'	6:C:174:ILE:HD11	1.91	0.52
31:3:3:MET:HG3	31:3:4:PRO:HD2	1.90	0.52
6:C:139:VAL:HG21	6:C:240:LEU:HD12	1.92	0.52
18:P:114:LEU:HA	18:P:118:GLN:NE2	2.25	0.52
20:R:106:GLY:HA2	20:R:109:MET:CE	2.35	0.52
16:N:176:ARG:O	16:N:180:LEU:HD13	2.09	0.52
1:0:2909:G:H2'	1:0:2910:A:H8	1.74	0.52
25:W:139:GLY:O	25:W:141:HIS:HD2	1.92	0.52
22:T:28:SER:O	22:T:32:ARG:HG3	2.08	0.52
11:H:24:PRO:HD3	11:H:120:ILE:HG22	1.90	0.52
18:P:83:LYS:O	18:P:86:ALA:HB3	2.09	0.52
17:O:4:ASN:HB3	17:O:7:LEU:HB3	1.92	0.52
11:H:31:HIS:HD2	11:H:87:LEU:O	1.93	0.52
1:0:814:G:H4'	38:0:3429:HOH:O	2.09	0.52
12:J:93:ARG:HH11	12:J:93:ARG:CB	2.20	0.52
1:0:120:A:H2'	1:0:120:A:N3	2.25	0.52
25:W:13:MET:CE	25:W:17:ILE:HG22	2.39	0.52
1:0:1342:C:C2'	1:0:1343:C:H5'	2.40	0.52
38:0:4516:HOH:O	30:2:38:LYS:HE3	2.10	0.52
1:0:475:G:H5'	6:C:73:LEU:HD23	1.91	0.52
28:Z:56:GLN:HA	28:Z:62:TYR:O	2.10	0.52
1:0:553:G:O4'	1:0:1325:G:H5'	2.09	0.52
8:E:11:VAL:CG1	8:E:12:ASP:N	2.72	0.52
12:J:107:ASN:HD22	12:J:107:ASN:C	2.13	0.52
5:B:51:VAL:CG2	5:B:327:VAL:HG13	2.40	0.52
1:0:1634:G:H3'	38:0:4181:HOH:O	2.09	0.52
1:0:2758:G:H2'	1:0:2759:C:C6	2.45	0.52
6:C:127:ARG:HG2	6:C:127:ARG:HH11	1.75	0.52
25:W:5:VAL:HG11	25:W:153:MET:CE	2.40	0.52
6:C:132:ASP:HB3	38:C:9162:HOH:O	2.09	0.52
26:X:9:VAL:HG13	26:X:88:GLU:OE2	2.10	0.52
1:0:2364:A:OP1	19:Q:11:ARG:NH1	2.42	0.52
1:0:1119:G:H8	12:J:52:GLN:NE2	2.08	0.52
26:X:21:PRO:HD3	38:X:6179:HOH:O	2.09	0.52
1:0:503:G:H2'	1:0:504:G:H8	1.75	0.52
1:0:1423:C:O2'	1:0:1424:A:H5'	2.10	0.52
22:T:71:VAL:HG13	22:T:91:LEU:O	2.10	0.52
38:0:7598:HOH:O	22:T:9:LYS:HD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:542:A:H2'	1:0:543:G:O4'	2.10	0.52
2:9:3003:A:OP2	2:9:3025:G:N2	2.42	0.52
25:W:11:VAL:O	25:W:12:ASN:HB2	2.10	0.52
1:0:816:G:H5'	1:0:1598:A:H4'	1.91	0.52
1:0:1654:U:H2'	4:A:47:HIS:HD2	1.75	0.52
5:B:54:VAL:HB	38:B:9412:HOH:O	2.09	0.52
6:C:115:LEU:HD13	6:C:223:LEU:HD21	1.90	0.52
1:0:259:G:O2'	1:0:260:C:H5'	2.10	0.52
4:A:66:ARG:HH11	4:A:66:ARG:CB	2.22	0.52
26:X:25:ARG:HG2	38:X:5356:HOH:O	2.10	0.52
15:M:66:SER:HB3	15:M:128:TRP:CD1	2.45	0.52
1:0:69:A:H5'	1:0:69:A:C8	2.45	0.52
16:N:179:LEU:HD23	16:N:184:ILE:CD1	2.40	0.52
1:0:1874:U:OP1	4:A:51:ARG:HD2	2.10	0.52
8:E:34:TRP:O	12:J:127:ILE:HD11	2.10	0.52
7:D:146:LYS:NZ	16:N:107:ASN:ND2	2.56	0.52
28:Z:37:HIS:HB2	28:Z:47:VAL:HB	1.92	0.52
27:Y:126:PRO:HG2	27:Y:128:PHE:CE1	2.45	0.52
1:0:960:G:H4'	38:0:7605:HOH:O	2.10	0.51
8:E:20:ILE:CD1	8:E:40:VAL:HG11	2.40	0.51
26:X:71:ARG:HB3	26:X:88:GLU:OE1	2.09	0.51
16:N:78:MET:HB2	16:N:79:PRO:HD3	1.91	0.51
12:J:15:ARG:NH1	12:J:43:ARG:NH1	2.57	0.51
1:0:1855:G:H8	4:A:144:GLU:OE2	1.93	0.51
5:B:214:PRO:HD2	38:B:9321:HOH:O	2.09	0.51
31:3:69:TYR:CZ	31:3:80:ARG:HD2	2.45	0.51
4:A:88:ILE:HD13	4:A:100:PRO:CD	2.35	0.51
16:N:11:ARG:O	16:N:15:GLU:HG3	2.10	0.51
1:0:1205:U:C2'	1:0:1206:U:H5''	2.40	0.51
25:W:137:GLN:HE21	25:W:141:HIS:CE1	2.22	0.51
11:H:3:ALA:HA	11:H:58:ARG:NH1	2.25	0.51
5:B:162:MET:HG3	5:B:310:ARG:HD3	1.92	0.51
14:L:145:LEU:O	14:L:148:GLU:HG3	2.10	0.51
5:B:258:GLY:H	5:B:260:HIS:CE1	2.27	0.51
1:0:67:A:H5''	1:0:69:A:C8	2.46	0.51
15:M:107:ARG:HD2	38:M:9370:HOH:O	2.09	0.51
15:M:65:VAL:HG21	15:M:105:ALA:HB2	1.90	0.51
5:B:62:ARG:CA	5:B:65:MET:HE3	2.35	0.51
29:1:8:GLN:NE2	29:1:11:LYS:NZ	2.55	0.51
28:Z:46:ARG:HD3	28:Z:58:SER:OG	2.11	0.51
27:Y:107:PRO:HB3	27:Y:182:PHE:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1850:U:H2'	1:0:1851:G:H8	1.74	0.51
1:0:2894:C:O2'	1:0:2895:C:H5'	2.10	0.51
1:0:2081:A:H4'	12:J:69:TYR:CE1	2.45	0.51
1:0:512:G:O3'	1:0:513:A:H8	1.94	0.51
4:A:36:ASP:CB	4:A:83:GLY:HA3	2.41	0.51
22:T:35:TYR:CG	22:T:112:LEU:HD22	2.46	0.51
20:R:111:ILE:HG23	20:R:145:LEU:CD1	2.40	0.51
5:B:310:ARG:HD2	38:B:9444:HOH:O	2.08	0.51
4:A:199:HIS:CD2	4:A:201:PHE:H	2.28	0.51
24:V:27:LEU:HA	24:V:49:LEU:HD13	1.92	0.51
30:2:48:ASP:O	30:2:49:GLU:HB2	2.10	0.51
1:0:159:G:OP1	15:M:74:LYS:HE3	2.10	0.51
5:B:141:ARG:HD2	5:B:163:GLU:OE2	2.11	0.51
11:H:148:GLU:HA	11:H:148:GLU:OE1	2.10	0.51
14:L:90:ARG:NH2	14:L:121:ILE:HD11	2.26	0.51
1:0:1180:U:H2'	1:0:1181:A:C8	2.46	0.51
1:0:775:G:OP1	29:1:16:HIS:HE1	1.94	0.51
10:G:23:ILE:O	10:G:27:ILE:HG13	2.10	0.51
1:0:2897:C:H2'	1:0:2898:G:H8	1.74	0.51
31:3:40:ARG:HD2	38:3:9357:HOH:O	2.10	0.51
11:H:166:SER:HB3	11:H:167:PRO:HD3	1.93	0.51
20:R:132:ARG:CZ	38:R:9385:HOH:O	2.59	0.51
27:Y:126:PRO:HG2	27:Y:128:PHE:CZ	2.46	0.51
32:I:101:SER:OG	32:I:104:GLN:HG3	2.11	0.51
26:X:10:VAL:HG11	26:X:36:HIS:HE1	1.75	0.51
17:O:42:GLU:HB2	38:O:2176:HOH:O	2.09	0.51
4:A:179:MET:HG3	4:A:186:TRP:CG	2.46	0.51
21:S:43:GLU:HB3	38:S:9141:HOH:O	2.10	0.51
1:0:1500:U:P	18:P:41:ARG:HH22	2.33	0.51
1:0:638:C:H2'	1:0:639:A:C8	2.46	0.51
15:M:59:GLY:CA	15:M:141:ILE:HD11	2.41	0.51
23:U:39:ASN:HD22	23:U:44:ARG:HH11	1.57	0.51
1:0:474:C:O3'	6:C:73:LEU:CD2	2.59	0.51
1:0:2036:C:O4'	13:K:44:LEU:HG	2.11	0.51
15:M:157:ASP:HB3	15:M:160:PHE:HD1	1.75	0.51
1:0:419:A:H1'	1:0:1921:A:C2	2.45	0.51
1:0:1252:A:H2'	1:0:1253:C:O4'	2.11	0.51
25:W:5:VAL:HG11	25:W:153:MET:HE3	1.93	0.51
1:0:1167:G:H2'	1:0:1168:C:O4'	2.11	0.51
32:I:91:GLU:HB3	32:I:94:GLU:OE2	2.11	0.51
16:N:151:ASP:O	16:N:154:LEU:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:233:THR:HG22	6:C:234:VAL:H	1.76	0.51
1:0:702:G:O2'	1:0:703:G:H5'	2.11	0.51
18:P:7:LYS:HD3	18:P:21:VAL:HG21	1.92	0.51
38:0:9863:HOH:O	25:W:119:HIS:HE1	1.93	0.51
1:0:583:G:H2'	1:0:584:U:H6	1.76	0.51
1:0:1422:U:H2'	1:0:1423:C:C6	2.46	0.51
11:H:36:LYS:HA	11:H:84:LYS:NZ	2.26	0.51
1:0:694:A:H2'	1:0:695:C:H5'	1.93	0.51
1:0:790:A:H2'	1:0:791:A:O4'	2.10	0.51
25:W:130:HIS:O	25:W:136:GLY:HA3	2.10	0.51
1:0:263:U:C4	9:F:54:VAL:HG13	2.45	0.51
4:A:105:VAL:HG12	4:A:106:CYS:N	2.26	0.51
24:V:42:ASN:O	24:V:44:GLY:N	2.43	0.51
21:S:53:ASN:N	21:S:53:ASN:HD22	2.09	0.51
4:A:217:ARG:HG2	4:A:229:ALA:HB2	1.93	0.51
1:0:1528:A:H2'	1:0:1529:G:O4'	2.11	0.51
6:C:13:ASP:OD1	6:C:13:ASP:O	2.27	0.51
25:W:36:PRO:HD2	25:W:41:TYR:CE1	2.46	0.51
1:0:1555:G:H4'	1:0:1630:A:H2	1.75	0.51
1:0:2361:A:H5'	1:0:2361:A:H8	1.76	0.51
4:A:211:LYS:HB2	38:A:9412:HOH:O	2.10	0.50
1:0:2533:C:H6	1:0:2533:C:C5'	2.20	0.50
1:0:1730:G:H5''	1:0:1731:C:H6	1.76	0.50
13:K:6:ALA:CB	13:K:116:GLU:HG2	2.41	0.50
1:0:945:U:H2'	1:0:946:C:C6	2.46	0.50
18:P:55:LYS:HG2	18:P:56:GLY:N	2.25	0.50
1:0:1189:A:H1'	1:0:1209:C:H1'	1.92	0.50
13:K:109:LEU:HD13	13:K:113:ILE:HD11	1.94	0.50
32:I:106:LYS:O	32:I:110:GLU:HG3	2.12	0.50
1:0:289:G:O2'	1:0:290:C:H5'	2.11	0.50
16:N:170:GLU:O	16:N:174:GLU:HG3	2.10	0.50
17:O:53:GLN:HG2	17:O:56:GLU:OE1	2.12	0.50
6:C:242:GLU:HG3	38:C:9183:HOH:O	2.11	0.50
9:F:56:PRO:HG2	15:M:43:PRO:O	2.11	0.50
1:0:243:A:H61	1:0:269:G:H1'	1.76	0.50
1:0:366:U:H2'	1:0:367:G:O4'	2.11	0.50
5:B:315:VAL:HG23	5:B:316:ARG:HG2	1.94	0.50
38:0:3252:HOH:O	26:X:23:HIS:HD2	1.93	0.50
6:C:136:VAL:HG22	6:C:137:PRO:HA	1.92	0.50
1:0:2453:G:H4'	14:L:50:GLY:C	2.31	0.50
1:0:1904:A:H2'	1:0:1905:U:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:451:C:O2'	1:0:452:G:H5'	2.11	0.50
23:U:13:ILE:HG12	23:U:32:CYS:HB3	1.93	0.50
4:A:164:ARG:CZ	38:A:9383:HOH:O	2.59	0.50
5:B:7:ARG:HG2	5:B:7:ARG:HH11	1.76	0.50
1:0:559:U:H2'	1:0:560:C:O4'	2.11	0.50
1:0:657:G:H2'	1:0:658:C:H6	1.75	0.50
11:H:170:ASN:N	11:H:170:ASN:HD22	2.08	0.50
5:B:304:PRO:CG	5:B:307:ARG:NH1	2.74	0.50
14:L:148:GLU:HA	38:L:9371:HOH:O	2.10	0.50
13:K:22:ASP:HB2	38:K:5264:HOH:O	2.10	0.50
1:0:2419:U:H5''	1:0:2420:G:H5'	1.94	0.50
7:D:23:VAL:HG11	7:D:83:PHE:CZ	2.46	0.50
1:0:1594:C:OP2	18:P:120:ARG:HD2	2.11	0.50
1:0:1236:A:H2'	1:0:1237:U:O4'	2.11	0.50
1:0:241:A:C2	1:0:378:A:H4'	2.46	0.50
14:L:54:PRO:HG2	14:L:57:VAL:CG2	2.41	0.50
1:0:2507:G:H2'	1:0:2510:C:H42	1.77	0.50
20:R:18:LEU:HD12	20:R:143:VAL:CG1	2.42	0.50
5:B:145:HIS:HD2	5:B:146:THR:O	1.94	0.50
1:0:263:U:O4'	9:F:59:ILE:HD13	2.11	0.50
4:A:33:GLU:O	4:A:34:ASP:HB2	2.11	0.50
6:C:237:GLU:HB2	38:C:9234:HOH:O	2.11	0.50
2:9:3057:A:O2'	7:D:152:PRO:HD2	2.12	0.50
25:W:21:LEU:HD22	25:W:26:ILE:HD11	1.92	0.50
22:T:49:GLU:OE2	22:T:97:ARG:HD2	2.11	0.50
6:C:104:ASP:HA	6:C:107:ARG:NH1	2.27	0.50
1:0:113:A:OP2	1:0:114:A:H2'	2.11	0.50
9:F:99:THR:HA	38:F:3461:HOH:O	2.11	0.50
17:O:38:ARG:HD3	38:O:7674:HOH:O	2.10	0.50
1:0:1641:A:C2'	1:0:1642:A:H5'	2.42	0.50
1:0:1289:C:O2'	1:0:1290:G:H5'	2.11	0.50
14:L:54:PRO:HG2	14:L:57:VAL:HG21	1.93	0.50
26:X:18:ARG:NH1	38:X:4132:HOH:O	2.41	0.50
8:E:24:GLY:HA3	8:E:76:VAL:HB	1.93	0.50
1:0:1304:U:H2'	1:0:1305:C:C6	2.47	0.50
1:0:1563:G:O2'	1:0:1564:C:OP2	2.25	0.50
12:J:117:ASP:O	12:J:119:THR:HG23	2.12	0.50
1:0:189:A:OP1	15:M:171:ARG:NH2	2.45	0.50
6:C:72:LYS:HG2	6:C:77:ALA:HA	1.94	0.50
1:0:1205:U:H2'	1:0:1206:U:H5'	1.92	0.50
1:0:2851:G:C2'	1:0:2852:A:H5'	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:104:ASP:O	6:C:108:GLN:HG3	2.11	0.50
16:N:77:ASN:OD1	16:N:79:PRO:HD2	2.12	0.50
16:N:73:ALA:HB1	16:N:74:PRO:HD2	1.93	0.50
15:M:122:GLN:OE1	15:M:127:LYS:HE2	2.11	0.50
1:O:2353:A:H4'	1:O:2354:A:O5'	2.12	0.50
38:K:7438:HOH:O	23:U:20:MET:HE1	2.12	0.50
3:4:74:C:H2'	3:4:75:C:H5'	1.93	0.50
15:M:99:ARG:HD2	15:M:167:GLY:CA	2.39	0.50
1:O:2509:A:OP2	1:O:2510:C:H5	1.94	0.50
29:1:25:LYS:HD2	30:2:49:GLU:N	2.26	0.50
7:D:84:LEU:C	7:D:86:THR:H	2.16	0.50
1:O:1183:C:N4	1:O:1184:C:H41	2.09	0.50
7:D:52:THR:N	7:D:70:GLY:O	2.45	0.50
25:W:41:TYR:HA	25:W:44:MET:HE3	1.94	0.50
4:A:97:ALA:HB2	4:A:150:PRO:HB2	1.94	0.50
13:K:72:VAL:HG11	13:K:121:PHE:CD1	2.46	0.50
16:N:49:THR:HG22	16:N:56:ASP:HB2	1.94	0.50
22:T:65:VAL:HG22	22:T:72:ILE:HG22	1.94	0.49
24:V:64:GLY:O	24:V:65:ASP:CB	2.60	0.49
5:B:147:VAL:HG12	5:B:150:ALA:H	1.76	0.49
6:C:129:HIS:HD2	6:C:165:ASP:OD2	1.95	0.49
1:O:475:G:OP1	6:C:73:LEU:HD22	2.12	0.49
9:F:31:LYS:HD3	9:F:89:LEU:HG	1.94	0.49
22:T:106:GLU:HG3	38:T:4913:HOH:O	2.12	0.49
12:J:75:PRO:HB3	12:J:132:LEU:HB3	1.95	0.49
1:O:1593:C:OP1	18:P:117:SER:HB3	2.12	0.49
1:O:1180:U:H2'	1:O:1181:A:O4'	2.12	0.49
20:R:17:MET:HE1	20:R:19:ARG:CZ	2.42	0.49
1:O:396:U:O2'	1:O:418:C:H4'	2.12	0.49
5:B:79:MET:HE3	5:B:144:THR:HG21	1.93	0.49
1:O:1730:G:C5'	1:O:1731:C:C6	2.95	0.49
1:O:69:A:H5'	1:O:69:A:H8	1.77	0.49
1:O:944:G:H21	25:W:44:MET:CE	2.25	0.49
16:N:49:THR:CG2	16:N:56:ASP:HB2	2.42	0.49
22:T:53:GLY:HA3	38:T:6384:HOH:O	2.11	0.49
6:C:139:VAL:CG2	6:C:240:LEU:HD12	2.43	0.49
13:K:20:CYS:HB2	13:K:29:LEU:HG	1.94	0.49
31:3:18:GLN:OE1	31:3:73:GLU:HB3	2.13	0.49
16:N:154:LEU:O	16:N:155:GLU:CB	2.60	0.49
18:P:38:GLU:HA	18:P:41:ARG:NH1	2.27	0.49
22:T:79:LEU:HG	22:T:89:ARG:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:75:GLU:C	5:B:77:PRO:HD3	2.33	0.49
1:0:1406:A:H4'	1:0:1407:A:H5''	1.93	0.49
1:0:316:A:H5'	22:T:54:ASP:OD2	2.12	0.49
1:0:2506:A:O2'	1:0:2507:G:O5'	2.30	0.49
22:T:48:VAL:CG1	22:T:49:GLU:N	2.74	0.49
4:A:99:ILE:O	4:A:131:HIS:HE1	1.95	0.49
38:0:5245:HOH:O	11:H:58:ARG:HG3	2.12	0.49
1:0:1701:A:H4'	1:0:1702:U:C5'	2.42	0.49
16:N:47:LEU:CD1	16:N:97:VAL:HG11	2.42	0.49
26:X:30:MET:CE	26:X:55:ASN:HA	2.41	0.49
1:0:2241:C:O2'	1:0:2242:U:H5'	2.12	0.49
17:O:25:VAL:HG23	17:O:26:TRP:N	2.26	0.49
16:N:67:ALA:C	16:N:69:TYR:H	2.14	0.49
19:Q:3:SER:HB3	38:Q:5998:HOH:O	2.13	0.49
15:M:80:GLY:O	15:M:81:ARG:HD3	2.12	0.49
1:0:1735:C:OP2	5:B:234:ARG:HG3	2.12	0.49
1:0:500:G:H21	20:R:98:ASN:HD21	1.58	0.49
1:0:317:A:OP1	22:T:52:ARG:O	2.30	0.49
18:P:55:LYS:CG	18:P:56:GLY:N	2.75	0.49
15:M:57:LYS:HE2	15:M:140:ALA:O	2.12	0.49
1:0:1537:C:H1'	38:0:6807:HOH:O	2.12	0.49
8:E:125:GLU:HB2	8:E:132:THR:CG2	2.43	0.49
6:C:170:ASP:O	6:C:171:GLU:HG3	2.12	0.49
27:Y:123:VAL:HG12	27:Y:124:GLY:O	2.12	0.49
7:D:159:PRO:O	7:D:163:VAL:HG23	2.13	0.49
16:N:86:LEU:HD12	16:N:125:ALA:HB2	1.94	0.49
1:0:1166:A:H61	1:0:1180:U:H3	1.61	0.49
2:9:3008:G:O6	16:N:11:ARG:NH1	2.46	0.49
13:K:101:ASN:HB2	13:K:103:ASP:OD2	2.13	0.49
27:Y:178:HIS:CG	27:Y:179:PRO:HD2	2.48	0.49
32:I:123:ASN:HA	32:I:126:LYS:HD2	1.94	0.49
12:J:107:ASN:ND2	12:J:109:TYR:H	2.11	0.49
25:W:60:GLU:O	25:W:63:GLU:HB2	2.13	0.49
6:C:118:THR:HG22	6:C:137:PRO:HB3	1.94	0.49
4:A:132:ASP:OD1	4:A:133:ARG:N	2.45	0.49
1:0:2793:A:H2'	1:0:2794:G:H5'	1.94	0.49
1:0:80:A:H3'	22:T:43:ASN:OD1	2.11	0.49
8:E:106:ASN:ND2	8:E:109:GLY:HA2	2.27	0.49
31:3:65:THR:HG23	31:3:67:LEU:HG	1.94	0.49
1:0:1804:A:H2'	1:0:1805:G:C8	2.48	0.49
1:0:542:A:H5'	1:0:542:A:C8	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:134:ILE:O	15:M:136:PRO:HD3	2.13	0.49
1:0:1086:A:N6	25:W:11:VAL:HG11	2.28	0.49
2:9:3034:A:H2'	2:9:3035:C:O4'	2.12	0.49
1:0:2834:G:OP1	26:X:39:LYS:HE2	2.12	0.49
17:O:96:VAL:CG1	17:O:100:GLN:HB2	2.43	0.49
5:B:248:ARG:O	5:B:251:VAL:HG13	2.13	0.49
25:W:126:ASP:HB3	25:W:135:GLY:O	2.12	0.49
1:0:2587:OMU:H6	1:0:2587:OMU:O5'	2.13	0.49
1:0:2721:U:H4'	13:K:87:ARG:HG3	1.95	0.49
23:U:17:THR:CG2	23:U:18:GLY:N	2.75	0.49
27:Y:200:THR:HG22	27:Y:201:GLU:CG	2.42	0.49
1:0:371:U:H2'	1:0:372:A:C8	2.48	0.49
1:0:894:A:C2	6:C:87:ARG:NH2	2.80	0.49
1:0:1787:C:H4'	1:0:2883:A:O4'	2.12	0.49
1:0:1311:G:O6	6:C:173:LYS:HE3	2.13	0.49
1:0:569:A:H5''	1:0:587:A:N1	2.27	0.49
38:0:9527:HOH:O	4:A:11:ARG:HD3	2.13	0.49
21:S:10:VAL:HG11	24:V:36:ALA:HA	1.94	0.49
20:R:72:VAL:CG1	20:R:75:TRP:HB3	2.43	0.49
6:C:25:PRO:HG2	38:C:9124:HOH:O	2.11	0.49
29:1:22:CYS:SG	29:1:24:GLU:HB2	2.53	0.49
6:C:39:GLN:O	6:C:43:LYS:HD3	2.13	0.49
7:D:23:VAL:HG23	7:D:23:VAL:O	2.13	0.49
1:0:1393:A:H2'	1:0:1394:C:C6	2.48	0.49
1:0:603:A:H5''	1:0:604:G:OP1	2.12	0.49
1:0:432:G:O2'	1:0:433:C:H5'	2.12	0.49
1:0:2073:G:OP2	1:0:2490:A:H5'	2.13	0.49
1:0:2619:UR3:H6	1:0:2619:UR3:O5'	2.13	0.49
1:0:541:C:H2'	1:0:542:A:H5'	1.95	0.49
6:C:118:THR:O	6:C:136:VAL:HG13	2.13	0.49
1:0:1878:G:H1'	38:0:6359:HOH:O	2.13	0.49
4:A:168:PRO:O	4:A:170:VAL:HG23	2.12	0.49
14:L:81:VAL:HG12	14:L:82:ALA:N	2.28	0.49
11:H:46:GLN:CB	11:H:167:PRO:HD2	2.22	0.48
20:R:39:THR:HG22	20:R:42:GLU:N	2.16	0.48
1:0:506:G:N2	1:0:509:A:H5'	2.20	0.48
5:B:132:HIS:CE1	5:B:171:VAL:HG21	2.48	0.48
9:F:111:ILE:O	9:F:115:VAL:HG23	2.12	0.48
11:H:80:GLU:HA	38:H:9182:HOH:O	2.13	0.48
38:0:6921:HOH:O	27:Y:165:GLU:HB3	2.11	0.48
1:0:482:G:H4'	1:0:508:A:N1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:383:A:H4'	38:0:5588:HOH:O	2.13	0.48
6:C:47:GLY:HA2	6:C:92:PRO:HB2	1.94	0.48
8:E:101:GLU:HB2	8:E:116:THR:O	2.13	0.48
4:A:211:LYS:CB	4:A:212:PRO:HD2	2.28	0.48
30:2:41:HIS:CD2	30:2:44:ARG:H	2.27	0.48
1:0:2890:A:C1'	23:U:56:ARG:NH2	2.72	0.48
1:0:2269:C:H2'	1:0:2270:G:H5'	1.94	0.48
1:0:1206:U:H2'	1:0:1207:A:O4'	2.13	0.48
11:H:120:ILE:CD1	11:H:120:ILE:N	2.76	0.48
20:R:29:LYS:NZ	38:R:9341:HOH:O	2.47	0.48
5:B:85:ARG:NH1	38:B:9431:HOH:O	2.45	0.48
1:0:1636:G:O2'	1:0:1637:A:H5'	2.12	0.48
32:I:135:LEU:HB2	32:I:137:VAL:HG23	1.95	0.48
27:Y:184:GLU:OE2	27:Y:204:ARG:HD2	2.13	0.48
17:O:32:ARG:HH21	17:O:35:LYS:NZ	2.11	0.48
1:0:926:A:O2'	14:L:41:HIS:CD2	2.65	0.48
5:B:74:ILE:HD13	5:B:309:VAL:HG21	1.95	0.48
1:0:214:U:H5'	38:0:6378:HOH:O	2.13	0.48
1:0:1507:C:H4'	38:0:3891:HOH:O	2.14	0.48
1:0:440:C:H2'	1:0:441:A:C8	2.48	0.48
18:P:115:SER:OG	18:P:118:GLN:HG3	2.13	0.48
7:D:39:ASP:HB2	38:D:5583:HOH:O	2.14	0.48
8:E:31:ARG:NH1	38:E:5919:HOH:O	2.46	0.48
1:0:2780:C:H1'	8:E:143:GLN:HE21	1.77	0.48
25:W:14:HIS:HB2	25:W:17:ILE:HG13	1.95	0.48
22:T:26:THR:HA	22:T:39:ASN:HB3	1.94	0.48
4:A:164:ARG:HA	28:Z:69:TYR:CE1	2.48	0.48
1:0:1053:G:OP1	11:H:12:PRO:HG3	2.12	0.48
13:K:75:ARG:CZ	38:K:4172:HOH:O	2.61	0.48
1:0:2428:G:N7	31:3:60:LYS:HE2	2.29	0.48
20:R:17:MET:HE3	20:R:19:ARG:CZ	2.43	0.48
5:B:98:THR:HG22	5:B:99:GLU:N	2.26	0.48
5:B:132:HIS:HB2	5:B:137:LEU:HD22	1.95	0.48
4:A:194:MET:HE2	4:A:199:HIS:CB	2.44	0.48
4:A:53:ALA:HB3	38:A:9401:HOH:O	2.12	0.48
8:E:116:THR:HG22	8:E:151:LEU:HD22	1.94	0.48
1:0:920:C:H5''	1:0:921:G:O5'	2.13	0.48
24:V:55:ARG:O	24:V:59:ILE:HG12	2.14	0.48
4:A:72:GLU:OE1	28:Z:72:GLU:HA	2.13	0.48
22:T:41:ARG:HH11	22:T:41:ARG:HG2	1.79	0.48
1:0:1029:U:O2'	1:0:1273:C:OP1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:185:LYS:HD3	6:C:186:TYR:CE1	2.49	0.48
6:C:236:THR:HG21	38:C:9175:HOH:O	2.13	0.48
4:A:32:VAL:HG22	4:A:38:ILE:HG13	1.95	0.48
4:A:105:VAL:HG11	4:A:154:ALA:CB	2.43	0.48
5:B:5:ARG:HD2	5:B:8:LYS:HZ1	1.79	0.48
9:F:58:GLU:CD	15:M:27:ARG:HH22	2.17	0.48
30:2:22:PRO:HG2	30:2:25:VAL:CG2	2.42	0.48
24:V:58:THR:O	24:V:62:GLU:HG3	2.13	0.48
1:0:1132:A:N6	1:0:1229:C:H2'	2.29	0.48
1:0:1333:U:H2'	1:0:1334:C:C6	2.49	0.48
1:0:152:A:O2'	1:0:153:C:H5'	2.13	0.48
1:0:2561:C:OP1	8:E:153:ARG:NH2	2.46	0.48
14:L:125:PHE:CZ	14:L:140:VAL:HG13	2.47	0.48
1:0:2362:A:H2'	1:0:2363:G:C8	2.48	0.48
7:D:163:VAL:HA	38:D:6326:HOH:O	2.13	0.48
1:0:558:C:H2'	1:0:559:U:C5'	2.41	0.48
27:Y:187:VAL:HG23	27:Y:192:ASP:HB3	1.92	0.48
8:E:20:ILE:HD11	8:E:40:VAL:CG1	2.44	0.48
9:F:99:THR:O	9:F:99:THR:HG23	2.13	0.48
1:0:1878:G:O2'	1:0:1879:U:C6	2.64	0.48
27:Y:155:ARG:NH1	38:Y:8147:HOH:O	2.47	0.48
1:0:1168:C:H4'	38:I:5128:HOH:O	2.13	0.48
14:L:133:VAL:HB	38:L:9357:HOH:O	2.13	0.48
1:0:319:A:H4'	1:0:338:C:C5	2.49	0.48
22:T:24:ARG:NH2	22:T:39:ASN:HD22	2.12	0.48
1:0:2898:G:H4'	5:B:288:GLY:HA2	1.95	0.48
16:N:73:ALA:HB1	16:N:74:PRO:CD	2.43	0.48
6:C:102:LEU:HD12	38:C:9117:HOH:O	2.14	0.48
1:0:2541:U:H4'	1:0:2542:C:OP1	2.13	0.48
1:0:2015:A:H2'	1:0:2016:U:O4'	2.13	0.48
2:9:3012:C:H5'	2:9:3070:U:O4'	2.12	0.48
19:Q:30:VAL:HG12	19:Q:30:VAL:O	2.13	0.48
6:C:236:THR:O	6:C:237:GLU:C	2.52	0.48
11:H:9:ILE:HG12	11:H:56:GLN:CG	2.44	0.48
24:V:11:MET:HB3	24:V:15:GLU:HB2	1.94	0.48
12:J:52:GLN:HG3	12:J:53:ILE:H	1.77	0.48
1:0:2783:A:H2'	1:0:2784:A:C8	2.49	0.48
26:X:12:ILE:HB	26:X:70:ILE:HG22	1.95	0.48
1:0:2478:U:O2'	1:0:2479:A:H5'	2.14	0.48
1:0:1352:A:N1	6:C:48:SER:HB3	2.28	0.48
8:E:16:ASP:O	8:E:17:HIS:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:3:ALA:O	25:W:54:PHE:HA	2.14	0.48
1:0:2269:C:C2'	1:0:2270:G:H5'	2.43	0.48
1:0:1849:G:H1'	1:0:2011:A:N1	2.28	0.48
1:0:1942:A:H3'	38:0:7527:HOH:O	2.15	0.47
7:D:159:PRO:O	7:D:162:ALA:HB3	2.14	0.47
31:3:16:GLU:HG3	31:3:18:GLN:HE21	1.79	0.47
1:0:396:U:OP2	31:3:38:ARG:HD2	2.13	0.47
1:0:157:G:H4'	15:M:95:LYS:CE	2.43	0.47
5:B:72:THR:HB	38:B:9406:HOH:O	2.13	0.47
7:D:153:THR:HA	7:D:156:ARG:CG	2.43	0.47
1:0:832:U:H2'	1:0:833:G:C8	2.49	0.47
1:0:1568:G:O2'	1:0:1569:U:H5'	2.14	0.47
17:O:45:LEU:HD12	17:O:88:LYS:HD2	1.95	0.47
1:0:2472:C:O2'	1:0:2634:G:H4'	2.13	0.47
1:0:2846:C:H4'	5:B:156:LYS:HB3	1.96	0.47
27:Y:151:SER:HB3	27:Y:154:ARG:CB	2.44	0.47
1:0:1634:G:H2'	1:0:1635:U:C6	2.49	0.47
8:E:132:THR:HB	38:E:2227:HOH:O	2.15	0.47
7:D:128:LEU:C	7:D:128:LEU:HD23	2.35	0.47
18:P:20:ARG:NH1	18:P:54:LYS:HD3	2.28	0.47
1:0:1940:C:H4'	38:0:7527:HOH:O	2.13	0.47
22:T:71:VAL:HG12	22:T:72:ILE:N	2.28	0.47
1:0:558:C:C2'	1:0:559:U:C5'	2.92	0.47
20:R:119:VAL:HG12	20:R:119:VAL:O	2.14	0.47
1:0:1307:A:H2'	1:0:1308:A:C8	2.49	0.47
1:0:1120:U:H5'	1:0:1120:U:C6	2.40	0.47
7:D:135:VAL:HG22	7:D:136:ARG:H	1.79	0.47
2:9:3028:U:H2'	2:9:3029:C:C6	2.48	0.47
1:0:2694:A:H4'	8:E:91:PHE:CE1	2.48	0.47
32:I:133:THR:N	38:I:5371:HOH:O	2.47	0.47
1:0:1613:C:H2'	1:0:1614:G:O4'	2.14	0.47
1:0:343:C:O2'	1:0:344:C:H5'	2.14	0.47
15:M:48:LYS:HE3	15:M:52:GLN:NE2	2.29	0.47
32:I:129:VAL:HG13	32:I:139:ILE:CD1	2.41	0.47
2:9:3114:G:H2'	2:9:3115:C:C6	2.50	0.47
24:V:39:ALA:O	24:V:41:GLU:N	2.42	0.47
7:D:138:GLY:N	38:D:7597:HOH:O	2.47	0.47
25:W:125:HIS:HE1	38:W:3071:HOH:O	1.97	0.47
5:B:141:ARG:HG2	5:B:165:ARG:HA	1.97	0.47
1:0:621:C:H5'	27:Y:132:ASP:OD2	2.15	0.47
9:F:26:THR:HG21	9:F:102:GLY:C	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1825:U:O2'	1:0:1826:C:H5'	2.14	0.47
7:D:25:MET:CE	7:D:41:LEU:HG	2.44	0.47
7:D:28:GLY:CA	7:D:69:ILE:HG23	2.42	0.47
18:P:103:THR:O	18:P:106:ARG:HB3	2.15	0.47
24:V:39:ALA:C	24:V:41:GLU:H	2.18	0.47
14:L:145:LEU:O	14:L:145:LEU:HD23	2.15	0.47
7:D:58:VAL:HG12	7:D:60:GLU:HG2	1.96	0.47
1:0:1925:G:O2'	1:0:1926:G:H5'	2.15	0.47
28:Z:19:GLY:O	28:Z:23:ARG:HG2	2.15	0.47
8:E:37:ASP:OD1	12:J:125:SER:HB3	2.14	0.47
5:B:14:GLY:HA2	5:B:15:PRO:C	2.35	0.47
1:0:2379:G:H5'	1:0:2381:C:O4'	2.14	0.47
13:K:132:VAL:HG11	23:U:22:VAL:HG22	1.96	0.47
1:0:731:U:H2'	1:0:732:C:C6	2.50	0.47
16:N:37:ARG:CZ	38:N:9334:HOH:O	2.62	0.47
12:J:19:MET:HE3	12:J:132:LEU:CD2	2.27	0.47
22:T:73:HIS:CD2	22:T:88:PRO:HG3	2.49	0.47
30:2:40:ARG:HD2	30:2:47:THR:HG22	1.95	0.47
32:I:132:CYS:O	32:I:135:LEU:N	2.47	0.47
32:I:92:PRO:O	32:I:94:GLU:HG3	2.14	0.47
1:0:2547:C:OP2	5:B:5:ARG:NH1	2.47	0.47
4:A:192:VAL:HG13	38:A:9354:HOH:O	2.15	0.47
15:M:134:ILE:CG2	15:M:141:ILE:HD13	2.45	0.47
1:0:1010:C:H4'	16:N:4:PRO:HB2	1.97	0.47
38:0:4353:HOH:O	5:B:27:ASN:HB2	2.14	0.47
31:3:69:TYR:HB2	31:3:78:HIS:CE1	2.49	0.47
1:0:2694:A:H4'	8:E:91:PHE:HE1	1.80	0.47
21:S:42:GLU:HG2	21:S:49:VAL:HG23	1.95	0.47
28:Z:33:MET:SD	28:Z:49:ARG:HD2	2.54	0.47
1:0:1427:A:H61	1:0:1440:U:C1'	2.27	0.47
6:C:5:ILE:HD11	6:C:16:VAL:CG2	2.45	0.47
1:0:1118:A:H8	1:0:1119:G:H5''	1.79	0.47
4:A:36:ASP:HB2	4:A:84:VAL:N	2.30	0.47
32:I:112:LYS:C	32:I:114:PRO:HD2	2.35	0.47
13:K:99:ASP:OD1	13:K:101:ASN:N	2.43	0.47
4:A:217:ARG:NH1	4:A:217:ARG:CG	2.77	0.47
1:0:1730:G:H5'	1:0:1731:C:H5	1.78	0.47
1:0:1462:C:H2'	1:0:1463:A:H8	1.78	0.47
1:0:705:C:H2'	1:0:705:C:O2	2.15	0.47
1:0:1503:U:H2'	1:0:1504:A:O4'	2.15	0.47
1:0:1890:U:H4'	1:0:2010:A:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:76:ARG:HH11	6:C:76:ARG:CG	2.28	0.47
2:9:3076:G:C3'	2:9:3077:A:H5''	2.36	0.47
12:J:74:ARG:HH12	12:J:76:ASP:HB2	1.76	0.47
25:W:76:ASP:O	25:W:77:ALA:C	2.52	0.47
1:0:1701:A:H5''	1:0:1702:U:H3'	1.97	0.47
2:9:3029:C:C2'	2:9:3030:C:H5'	2.44	0.47
5:B:162:MET:HE3	5:B:308:LEU:HD21	1.96	0.47
2:9:3001:U:O3'	2:9:3003:A:H5'	2.14	0.47
1:0:945:U:O2'	25:W:43:GLY:HA3	2.14	0.47
9:F:56:PRO:HG2	15:M:44:THR:HA	1.95	0.47
5:B:279:THR:OG1	5:B:290:VAL:HB	2.14	0.47
6:C:20:ASP:O	6:C:23:GLU:HB2	2.15	0.47
8:E:97:VAL:HG12	38:E:4191:HOH:O	2.15	0.47
1:0:2869:G:H2'	1:0:2870:C:C6	2.50	0.47
4:A:211:LYS:NZ	38:A:9413:HOH:O	2.46	0.47
2:9:3056:A:H1'	7:D:14:ARG:HG2	1.97	0.47
1:0:284:C:H4'	1:0:285:A:O5'	2.15	0.47
5:B:210:GLY:HA2	5:B:256:GLN:HE22	1.80	0.47
9:F:50:VAL:CG1	9:F:60:VAL:HG11	2.45	0.47
9:F:61:MET:HB3	15:M:19:GLN:OE1	2.14	0.47
16:N:5:ARG:HG3	19:Q:18:PRO:CB	2.44	0.47
8:E:84:MET:HG2	8:E:168:ILE:HD13	1.97	0.47
1:0:2748:G:H2'	38:0:7705:HOH:O	2.15	0.47
1:0:2668:G:H2'	1:0:2669:U:H6	1.77	0.47
1:0:952:G:N3	1:0:2302:A:H2'	2.30	0.47
4:A:48:ASP:HB3	38:A:9401:HOH:O	2.15	0.47
1:0:659:A:N1	17:O:42:GLU:OE2	2.48	0.47
7:D:91:ALA:HB1	38:D:5198:HOH:O	2.15	0.47
2:9:3107:C:H5	38:9:3167:HOH:O	1.97	0.47
11:H:154:TYR:C	11:H:154:TYR:CD1	2.87	0.47
21:S:57:THR:CG2	21:S:58:MET:N	2.78	0.46
2:9:3013:A:N3	16:N:14:ARG:NH2	2.57	0.46
5:B:5:ARG:HD2	5:B:8:LYS:HZ3	1.79	0.46
5:B:41:PHE:HB3	5:B:190:MET:CE	2.45	0.46
15:M:59:GLY:C	15:M:141:ILE:HD11	2.35	0.46
30:2:10:ARG:HD2	30:2:49:GLU:OE2	2.15	0.46
20:R:113:HIS:O	20:R:145:LEU:HD12	2.15	0.46
1:0:2545:U:OP2	5:B:2:GLN:HG2	2.14	0.46
17:O:47:ARG:HA	17:O:50:ARG:NH1	2.30	0.46
1:0:100:C:H4'	22:T:16:LEU:HB2	1.98	0.46
1:0:1787:C:OP1	18:P:68:LYS:HE2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:947:U:H2'	1:0:948:G:C8	2.50	0.46
9:F:37:THR:O	9:F:41:GLU:HG3	2.14	0.46
1:0:1419:U:H2'	1:0:1685:A:C2	2.51	0.46
9:F:4:VAL:HG13	9:F:76:PHE:CE1	2.50	0.46
1:0:1162:G:H1'	32:I:117:LEU:CD1	2.37	0.46
11:H:66:ARG:HD3	38:H:9177:HOH:O	2.14	0.46
20:R:19:ARG:HA	20:R:142:ASP:OD1	2.15	0.46
13:K:81:ARG:HD3	13:K:87:ARG:CZ	2.45	0.46
1:0:1285:U:H4'	25:W:74:GLU:OE1	2.15	0.46
11:H:162:ARG:HD3	38:H:9180:HOH:O	2.14	0.46
1:0:352:A:H2'	1:0:353:G:C8	2.49	0.46
15:M:164:THR:HG23	15:M:166:ALA:N	2.30	0.46
7:D:18:ILE:HD13	7:D:84:LEU:CD1	2.45	0.46
14:L:146:GLY:C	14:L:148:GLU:H	2.18	0.46
1:0:2840:A:H3'	38:0:7810:HOH:O	2.14	0.46
16:N:69:TYR:CE2	16:N:184:ILE:HD11	2.51	0.46
26:X:10:VAL:HG12	26:X:11:THR:N	2.29	0.46
4:A:164:ARG:NE	38:A:9383:HOH:O	2.47	0.46
6:C:76:ARG:HH11	6:C:76:ARG:HG2	1.81	0.46
1:0:669:G:O2'	1:0:670:G:H5'	2.16	0.46
1:0:2534:C:H1'	38:0:3787:HOH:O	2.14	0.46
1:0:1434:A:H2'	1:0:1436:C:C5	2.50	0.46
6:C:4:THR:HA	6:C:15:GLU:HB3	1.96	0.46
1:0:1187:U:H2'	38:0:7102:HOH:O	2.16	0.46
16:N:164:ASP:OD1	16:N:167:ASP:HA	2.15	0.46
1:0:2591:C:H2'	1:0:2592:G:O4'	2.15	0.46
13:K:87:ARG:NH1	38:K:4066:HOH:O	2.48	0.46
17:O:96:VAL:HG12	17:O:97:SER:N	2.30	0.46
18:P:101:GLN:HG3	38:P:164:HOH:O	2.16	0.46
20:R:30:ALA:HA	20:R:33:ARG:HH12	1.81	0.46
14:L:35:ARG:O	14:L:40:PHE:HA	2.15	0.46
1:0:2820:A:H2'	1:0:2821:C:C6	2.51	0.46
5:B:24:PRO:HG2	5:B:204:GLY:HA2	1.98	0.46
31:3:72:GLY:HA2	38:3:9373:HOH:O	2.15	0.46
6:C:166:ILE:CD1	6:C:207:LEU:HD13	2.45	0.46
5:B:30:PRO:HB2	5:B:39:GLN:NE2	2.29	0.46
1:0:1759:A:N3	1:0:1818:C:H2'	2.31	0.46
5:B:66:GLU:OE1	5:B:328:ARG:HD2	2.15	0.46
17:O:39:THR:O	17:O:115:ARG:NH2	2.48	0.46
1:0:466:A:H2'	1:0:467:G:O4'	2.15	0.46
1:0:506:G:H22	1:0:509:A:H5''	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:132:CYS:O	32:I:134:SER:N	2.49	0.46
1:0:308:U:C4	1:0:342:C:H1'	2.51	0.46
23:U:53:ASP:O	23:U:54:THR:C	2.54	0.46
1:0:259:G:H21	15:M:58:GLN:NE2	2.14	0.46
10:G:67:LEU:O	10:G:71:LEU:HG	2.16	0.46
1:0:945:U:H2'	1:0:946:C:H6	1.80	0.46
23:U:6:CYS:HB2	23:U:32:CYS:HB3	1.97	0.46
15:M:139:PRO:O	15:M:143:ASN:ND2	2.49	0.46
1:0:1521:C:H2'	1:0:1522:A:H8	1.80	0.46
1:0:20:G:H21	20:R:117:HIS:HD2	1.62	0.46
26:X:43:VAL:CG1	26:X:47:ALA:HB3	2.45	0.46
2:9:3014:G:O2'	16:N:1:ALA:HB2	2.15	0.46
1:0:1603:A:H5'	1:0:1605:G:C4'	2.45	0.46
1:0:1058:A:H2'	1:0:1060:C:C5'	2.43	0.46
1:0:1185:U:H5'	38:0:7636:HOH:O	2.16	0.46
16:N:34:LEU:HD22	16:N:129:ILE:HD13	1.97	0.46
15:M:61:ILE:HG22	15:M:62:VAL:N	2.31	0.46
29:1:28:HIS:HD2	29:1:30:LYS:H	1.62	0.46
15:M:159:VAL:HG13	15:M:160:PHE:N	2.30	0.46
1:0:2421:G:H4'	38:0:5056:HOH:O	2.15	0.46
27:Y:97:LEU:C	27:Y:98:GLN:HG2	2.36	0.46
1:0:853:C:H2'	1:0:854:G:O4'	2.15	0.46
1:0:226:A:H1'	1:0:393:G:C5	2.50	0.46
1:0:1329:A:N1	36:0:9313:CL:CL	2.85	0.46
1:0:166:A:N7	14:L:25:GLY:HA2	2.30	0.46
15:M:49:ALA:C	15:M:54:TYR:HB3	2.35	0.46
1:0:1545:C:H2'	1:0:1546:G:O4'	2.16	0.46
1:0:1919:A:H5'	38:0:6245:HOH:O	2.16	0.46
1:0:2715:G:N2	5:B:264:GLU:OE1	2.45	0.46
1:0:2521:A:OP2	11:H:3:ALA:HB3	2.15	0.46
1:0:820:G:H5'	1:0:821:U:H5'	1.96	0.46
1:0:821:U:H2'	1:0:822:C:H6	1.80	0.46
32:I:123:ASN:HA	32:I:126:LYS:CD	2.46	0.46
9:F:56:PRO:CG	15:M:44:THR:HA	2.45	0.46
1:0:1804:A:H2'	1:0:1805:G:H8	1.80	0.46
1:0:74:A:H2'	1:0:75:U:C6	2.51	0.46
6:C:88:SER:O	6:C:91:PRO:HD3	2.15	0.46
1:0:2900:G:H2'	1:0:2901:C:O4'	2.16	0.46
1:0:522:U:O2'	1:0:1366:C:H5'	2.15	0.46
38:9:3472:HOH:O	16:N:41:LYS:HD3	2.15	0.46
25:W:149:LEU:HG	25:W:153:MET:CE	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:182:ARG:HD2	6:C:184:ARG:HH12	1.81	0.46
7:D:146:LYS:HZ3	16:N:107:ASN:HD21	1.63	0.46
12:J:131:THR:HB	12:J:134:GLU:OE1	2.15	0.46
13:K:23:ASN:HD21	13:K:107:THR:HB	1.81	0.46
1:O:1517:U:C2	1:O:1670:G:N2	2.84	0.46
1:O:1385:G:O3'	26:X:49:ARG:NH1	2.49	0.46
6:C:12:THR:HB	38:C:9244:HOH:O	2.15	0.46
1:O:911:G:H5'	1:O:932:U:OP1	2.16	0.46
7:D:67:ASP:O	7:D:69:ILE:HG13	2.16	0.46
16:N:34:LEU:HD13	16:N:47:LEU:HD21	1.97	0.46
12:J:108:PRO:HG2	12:J:109:TYR:CD1	2.51	0.46
6:C:129:HIS:CE1	6:C:231:ARG:HA	2.50	0.46
2:9:3049:G:H2'	2:9:3050:G:O4'	2.15	0.46
1:O:497:A:H2'	1:O:498:A:C5'	2.46	0.46
14:L:17:SER:C	14:L:19:LYS:H	2.18	0.46
6:C:93:LYS:O	6:C:98:ARG:NH2	2.49	0.46
4:A:188:ASN:HA	38:A:9363:HOH:O	2.16	0.46
8:E:77:THR:OG1	8:E:78:GLU:N	2.48	0.46
18:P:15:ASP:O	18:P:16:VAL:HG23	2.16	0.46
26:X:27:ASP:OD2	26:X:27:ASP:N	2.48	0.46
31:3:42:ARG:HH11	31:3:42:ARG:HG3	1.80	0.46
22:T:88:PRO:O	22:T:90:PRO:HD3	2.16	0.46
25:W:64:THR:O	25:W:68:THR:HG22	2.16	0.46
5:B:195:ARG:N	5:B:198:GLU:OE1	2.50	0.46
7:D:64:ARG:CD	7:D:67:ASP:HB3	2.46	0.46
13:K:7:ASP:OD2	13:K:81:ARG:NH2	2.49	0.46
29:1:25:LYS:HD2	30:2:48:ASP:CA	2.45	0.46
10:G:23:ILE:HD13	10:G:67:LEU:HD23	1.97	0.46
1:O:1072:G:P	27:Y:154:ARG:HH22	2.39	0.46
1:O:960:G:N3	1:O:960:G:C2'	2.79	0.46
11:H:84:LYS:NZ	11:H:84:LYS:HB2	2.31	0.46
14:L:35:ARG:HD3	14:L:35:ARG:C	2.36	0.46
25:W:154:ARG:HE	25:W:154:ARG:HB3	1.53	0.46
1:O:671:A:O2'	1:O:672:G:H2'	2.16	0.46
12:J:133:GLY:O	12:J:137:GLU:HG3	2.16	0.46
1:O:2338:G:OP1	7:D:97:GLN:HG2	2.15	0.46
25:W:131:PRO:HD2	25:W:134:GLU:OE1	2.15	0.46
4:A:96:LEU:HD22	4:A:128:LEU:HD13	1.97	0.46
5:B:56:ASP:OD1	5:B:322:ARG:HB3	2.15	0.46
11:H:9:ILE:HG12	11:H:56:GLN:HG3	1.98	0.45
7:D:35:ALA:C	7:D:37:ALA:H	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1184:C:O2'	1:0:1185:U:OP2	2.24	0.45
29:1:28:HIS:CE1	29:1:31:LYS:HE2	2.51	0.45
28:Z:60:CYS:O	28:Z:61:ASP:HB2	2.17	0.45
1:0:2420:G:O2'	1:0:2421:G:H5'	2.17	0.45
17:O:45:LEU:CD1	17:O:88:LYS:HD2	2.45	0.45
4:A:70:ALA:HA	4:A:71:PRO:HD3	1.80	0.45
29:1:45:ARG:NH2	38:1:9232:HOH:O	2.43	0.45
14:L:10:SER:O	14:L:11:ARG:HB3	2.16	0.45
5:B:314:ALA:HB3	5:B:317:PRO:HG3	1.98	0.45
9:F:1:PRO:HB2	38:F:5897:HOH:O	2.16	0.45
6:C:19:PRO:CB	6:C:244:ALA:HB2	2.45	0.45
1:0:1666:C:C2'	1:0:1667:A:C5'	2.94	0.45
1:0:553:G:O2'	27:Y:179:PRO:HG3	2.16	0.45
11:H:58:ARG:HG3	11:H:58:ARG:NH1	2.27	0.45
14:L:143:THR:CG2	14:L:144:ASP:N	2.79	0.45
25:W:38:THR:HG22	38:W:3580:HOH:O	2.16	0.45
16:N:67:ALA:C	16:N:69:TYR:N	2.69	0.45
15:M:122:GLN:HG3	15:M:122:GLN:O	2.15	0.45
1:0:316:A:N3	1:0:336:G:O2'	2.45	0.45
13:K:66:ARG:HD3	38:K:2777:HOH:O	2.16	0.45
11:H:171:ALA:HA	38:H:9168:HOH:O	2.17	0.45
11:H:38:LYS:HE2	11:H:42:ASP:HB2	1.97	0.45
1:0:2506:A:H1'	38:O:4035:HOH:O	2.15	0.45
13:K:6:ALA:HB2	13:K:116:GLU:HG2	1.98	0.45
19:Q:94:GLN:HG2	19:Q:95:GLU:OE1	2.17	0.45
19:Q:94:GLN:O	19:Q:95:GLU:HB2	2.16	0.45
1:0:285:A:C2	1:0:368:C:H4'	2.51	0.45
16:N:43:VAL:CG1	16:N:118:ILE:HD11	2.44	0.45
1:0:86:A:C2	30:2:25:VAL:HG13	2.51	0.45
31:3:3:MET:O	31:3:90:PHE:HA	2.16	0.45
6:C:136:VAL:HA	6:C:137:PRO:C	2.37	0.45
1:0:1406:A:H4'	1:0:1407:A:C5'	2.46	0.45
22:T:20:HIS:ND1	22:T:41:ARG:NE	2.60	0.45
19:Q:25:PRO:HA	19:Q:26:PRO:HD3	1.83	0.45
7:D:101:THR:O	7:D:157:LEU:HB3	2.16	0.45
6:C:200:PRO:HB3	6:C:212:VAL:HG23	1.97	0.45
5:B:149:ASP:HB2	38:B:9379:HOH:O	2.15	0.45
6:C:236:THR:O	6:C:239:ALA:N	2.50	0.45
2:9:3052:A:H2'	2:9:3053:G:O4'	2.17	0.45
25:W:65:VAL:HA	25:W:68:THR:CG2	2.46	0.45
1:0:2589:U:H2'	1:0:2590:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:32:ARG:HH21	17:O:35:LYS:HD2	1.81	0.45
1:O:1641:A:H2'	1:O:1642:A:C5'	2.45	0.45
2:9:3020:G:O2'	2:9:3021:G:H5'	2.16	0.45
4:A:109:GLU:CD	4:A:113:GLY:H	2.20	0.45
16:N:67:ALA:O	16:N:69:TYR:N	2.50	0.45
5:B:7:ARG:HD3	5:B:9:GLY:O	2.16	0.45
1:O:35:U:H5'	6:C:47:GLY:O	2.17	0.45
20:R:30:ALA:HA	20:R:33:ARG:NH1	2.31	0.45
14:L:34:GLY:HA3	14:L:38:HIS:CE1	2.51	0.45
1:O:2404:G:OP1	19:Q:68:GLY:HA3	2.16	0.45
1:O:1155:G:H2'	1:O:1156:C:C6	2.52	0.45
16:N:44:ARG:HG3	16:N:45:ALA:N	2.32	0.45
5:B:320:GLN:NE2	5:B:321:PRO:CD	2.79	0.45
32:I:93:GLN:HA	32:I:96:PHE:CE2	2.45	0.45
5:B:145:HIS:HA	5:B:160:ASP:O	2.17	0.45
26:X:36:HIS:CE1	26:X:40:HIS:CD2	3.05	0.45
5:B:82:VAL:HG12	5:B:101:TRP:CE3	2.51	0.45
15:M:32:ARG:NH2	38:M:9391:HOH:O	2.49	0.45
1:O:710:G:O2'	1:O:711:G:H5'	2.16	0.45
2:9:3056:A:C3'	2:9:3057:A:H5''	2.45	0.45
25:W:4:LEU:HD23	25:W:4:LEU:HA	1.75	0.45
4:A:103:VAL:O	4:A:105:VAL:HG23	2.16	0.45
17:O:32:ARG:HG2	38:O:2336:HOH:O	2.16	0.45
1:O:1185:U:O2'	1:O:1186:C:H5'	2.17	0.45
1:O:1298:U:H2'	1:O:1299:G:C8	2.51	0.45
6:C:138:VAL:O	6:C:234:VAL:HA	2.16	0.45
4:A:8:ARG:NH1	38:A:9349:HOH:O	2.45	0.45
1:O:1279:U:O2	1:O:1279:U:H2'	2.17	0.45
17:O:44:ASN:OD1	17:O:65:LEU:HB2	2.17	0.45
1:O:2050:G:H5''	20:R:80:TYR:O	2.17	0.45
19:Q:64:GLU:HA	19:Q:64:GLU:OE1	2.17	0.45
12:J:75:PRO:HD3	12:J:136:SER:OG	2.16	0.45
1:O:2812:A:C2	1:O:2814:A:N6	2.72	0.45
16:N:152:GLU:C	16:N:154:LEU:N	2.70	0.45
1:O:2781:U:H1'	8:E:139:GLU:OE2	2.16	0.45
1:O:1874:U:P	4:A:51:ARG:HD2	2.57	0.45
11:H:36:LYS:HA	11:H:84:LYS:HZ1	1.82	0.45
23:U:6:CYS:C	23:U:8:TYR:H	2.20	0.45
1:O:2039:A:OP2	5:B:234:ARG:NH2	2.50	0.45
5:B:248:ARG:NH2	38:B:9325:HOH:O	2.49	0.45
14:L:89:PHE:CD1	14:L:89:PHE:N	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:97:VAL:O	14:L:100:ALA:HB2	2.16	0.45
1:O:1573:A:H2'	1:O:1574:C:O4'	2.16	0.45
19:Q:32:GLU:HA	19:Q:71:TYR:OH	2.17	0.45
1:O:2424:U:H1'	19:Q:7:LEU:HD12	1.99	0.45
1:O:2045:G:H2'	1:O:2046:G:O4'	2.17	0.45
26:X:43:VAL:CG1	26:X:44:ASP:N	2.79	0.45
1:O:1666:C:H2'	1:O:1667:A:C5'	2.46	0.45
32:I:113:HIS:NE2	32:I:121:LEU:HD22	2.32	0.45
16:N:163:PHE:O	16:N:164:ASP:OD1	2.35	0.45
7:D:167:GLU:OE2	7:D:173:GLU:HG2	2.17	0.45
15:M:61:ILE:CG2	15:M:62:VAL:N	2.80	0.45
21:S:52:VAL:HG22	21:S:66:VAL:HG13	1.98	0.45
1:O:1730:G:C5'	1:O:1731:C:H6	2.30	0.45
1:O:1790:C:H2'	1:O:1791:U:C6	2.50	0.45
9:F:48:VAL:HG12	9:F:97:ALA:HB2	1.99	0.45
1:O:1855:G:H4'	1:O:1856:C:O5'	2.16	0.45
20:R:33:ARG:NH1	38:R:9344:HOH:O	2.49	0.45
6:C:218:VAL:HG12	38:C:9228:HOH:O	2.16	0.45
7:D:15:GLU:HA	7:D:16:PRO:HD3	1.83	0.45
22:T:64:ASN:HB3	22:T:73:HIS:HB2	1.98	0.45
1:O:21:G:H5''	20:R:1:GLY:O	2.17	0.45
5:B:62:ARG:HG2	5:B:65:MET:CE	2.47	0.45
10:G:64:ASN:H	10:G:64:ASN:ND2	2.15	0.45
1:O:1185:U:H2'	1:O:1186:C:C6	2.51	0.45
1:O:902:G:N7	14:L:18:HIS:CD2	2.83	0.45
4:A:53:ALA:HB1	4:A:54:PRO:HD2	1.99	0.45
1:O:746:A:C6	17:O:65:LEU:HD13	2.52	0.45
1:O:222:A:H2'	1:O:223:G:O4'	2.17	0.45
1:O:1293:U:O2'	27:Y:149:GLN:NE2	2.46	0.45
1:O:1425:G:O2'	1:O:1426:C:H5'	2.17	0.45
7:D:170:TYR:CD1	7:D:170:TYR:N	2.85	0.45
25:W:110:GLN:NE2	25:W:110:GLN:HA	2.32	0.44
5:B:243:ASN:HA	5:B:244:PRO:C	2.37	0.44
38:O:6984:HOH:O	16:N:5:ARG:HB2	2.17	0.44
6:C:115:LEU:CD2	6:C:243:VAL:HG13	2.45	0.44
5:B:137:LEU:HD21	5:B:140:LEU:HD21	1.98	0.44
6:C:132:ASP:HB2	6:C:161:ASP:HB3	1.98	0.44
9:F:28:ALA:CB	9:F:99:THR:HG23	2.47	0.44
2:9:3035:C:H5''	38:9:4078:HOH:O	2.16	0.44
1:O:2404:G:OP1	19:Q:69:ASP:N	2.46	0.44
19:Q:37:GLU:OE1	19:Q:93:ARG:NE	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:110:LYS:O	13:K:111:GLY:O	2.34	0.44
1:0:1098:A:H2'	1:0:1099:G:O4'	2.17	0.44
1:0:1209:C:H2'	1:0:1210:G:H8	1.82	0.44
1:0:558:C:C2'	1:0:559:U:H5''	2.46	0.44
1:0:877:G:H1'	38:0:9479:HOH:O	2.17	0.44
9:F:48:VAL:CG2	9:F:74:PHE:HB3	2.47	0.44
31:3:69:TYR:CE1	31:3:80:ARG:HD2	2.52	0.44
1:0:694:A:H4'	1:0:2441:U:OP1	2.18	0.44
13:K:68:VAL:O	13:K:68:VAL:HG12	2.17	0.44
1:0:2699:A:H2'	1:0:2700:G:O4'	2.16	0.44
1:0:303:C:H2'	1:0:304:G:O4'	2.17	0.44
1:0:949:U:O2'	19:Q:40:HIS:HE1	2.00	0.44
1:0:1486:A:C5	30:2:2:LYS:HG3	2.52	0.44
22:T:18:GLU:O	22:T:21:LYS:HE2	2.17	0.44
1:0:170:U:H2'	1:0:171:C:H5'	1.99	0.44
1:0:1589:G:N2	1:0:1605:G:H1'	2.33	0.44
1:0:1205:U:C2'	1:0:1206:U:C5'	2.95	0.44
11:H:170:ASN:N	11:H:170:ASN:ND2	2.66	0.44
12:J:42:GLU:O	12:J:131:THR:HG23	2.18	0.44
5:B:207:LYS:HG2	5:B:304:PRO:HB3	1.99	0.44
2:9:3002:U:P	2:9:3003:A:H5'	2.58	0.44
17:O:26:TRP:HA	17:O:26:TRP:CE3	2.53	0.44
18:P:142:ASP:O	18:P:143:ALA:O	2.35	0.44
1:0:2301:A:H5''	1:0:2302:A:H5'	1.98	0.44
1:0:2044:G:OP1	26:X:23:HIS:HE1	2.00	0.44
4:A:33:GLU:OE1	4:A:33:GLU:N	2.47	0.44
1:0:1803:C:H2'	1:0:1804:A:C8	2.52	0.44
1:0:1496:G:H5'	1:0:1572:A:H1'	1.98	0.44
38:0:4497:HOH:O	13:K:2:GLU:HA	2.17	0.44
16:N:115:VAL:HG23	16:N:116:PHE:N	2.31	0.44
13:K:96:VAL:HG21	13:K:109:LEU:HD22	1.99	0.44
1:0:2781:U:C2'	1:0:2782:G:H5'	2.47	0.44
32:I:89:SER:HB3	32:I:97:VAL:HG23	1.98	0.44
16:N:179:LEU:HD23	16:N:184:ILE:HD12	1.99	0.44
1:0:604:G:H2'	38:0:7912:HOH:O	2.17	0.44
1:0:920:C:H5'	1:0:921:G:C4	2.53	0.44
22:T:41:ARG:NH1	22:T:42:VAL:O	2.51	0.44
1:0:1398:G:O2'	1:0:1399:A:H5'	2.18	0.44
6:C:103:ASN:HB3	38:C:9109:HOH:O	2.18	0.44
1:0:2795:C:O2'	1:0:2796:U:H5'	2.18	0.44
1:0:1477:C:H5'	1:0:1868:G:H5''	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:14:ALA:HA	22:T:15:PRO:HD3	1.87	0.44
1:0:162:C:H2'	1:0:163:U:H5'	2.00	0.44
1:0:299:U:H5'	38:0:7516:HOH:O	2.16	0.44
1:0:827:A:H2'	1:0:828:G:O4'	2.17	0.44
4:A:212:PRO:HB2	38:A:9357:HOH:O	2.17	0.44
1:0:290:C:O2'	1:0:291:C:H5'	2.17	0.44
31:3:25:VAL:HG13	31:3:68:LYS:HE3	2.00	0.44
5:B:125:GLU:OE2	5:B:129:ARG:NH1	2.51	0.44
17:O:32:ARG:HH21	17:O:35:LYS:CD	2.31	0.44
1:0:1131:G:C6	1:0:1230:A:C4	3.05	0.44
4:A:194:MET:HE3	4:A:199:HIS:HB2	1.99	0.44
4:A:199:HIS:HD2	4:A:201:PHE:H	1.65	0.44
18:P:38:GLU:HA	18:P:41:ARG:HH11	1.82	0.44
1:0:958:G:H2'	1:0:959:C:C6	2.53	0.44
1:0:794:U:H3	1:0:819:A:H61	1.66	0.44
5:B:102:THR:CG2	5:B:182:VAL:HG12	2.48	0.44
6:C:19:PRO:HB3	6:C:244:ALA:HB2	2.00	0.44
1:0:1119:G:C8	12:J:52:GLN:NE2	2.85	0.44
1:0:484:A:N1	1:0:506:G:H4'	2.33	0.44
32:I:99:ASP:O	32:I:100:LEU:HG	2.18	0.44
25:W:6:GLN:HA	25:W:52:VAL:HG23	1.99	0.44
13:K:125:ALA:C	13:K:127:ALA:H	2.21	0.44
8:E:7:ILE:HD11	8:E:11:VAL:C	2.37	0.44
1:0:2271:G:N3	1:0:2271:G:H2'	2.33	0.44
1:0:2092:G:H2'	1:0:2613:G:OP1	2.18	0.44
5:B:175:LEU:HD23	5:B:175:LEU:O	2.18	0.44
4:A:87:GLU:HB3	38:A:9415:HOH:O	2.16	0.44
24:V:31:ARG:NE	38:V:2682:HOH:O	2.51	0.44
1:0:825:U:H5''	1:0:826:U:OP1	2.18	0.44
16:N:37:ARG:NH2	38:N:9334:HOH:O	2.51	0.44
24:V:12:THR:HG23	24:V:14:ALA:H	1.83	0.44
2:9:3053:G:O2'	2:9:3054:A:H5'	2.18	0.44
4:A:36:ASP:O	4:A:38:ILE:N	2.50	0.44
5:B:62:ARG:HA	5:B:65:MET:CE	2.40	0.44
29:1:8:GLN:NE2	29:1:11:LYS:HZ2	2.11	0.44
29:1:8:GLN:HE22	29:1:11:LYS:HZ1	1.60	0.44
1:0:2769:C:H2'	1:0:2770:G:C5'	2.48	0.44
5:B:310:ARG:HB3	38:B:9444:HOH:O	2.16	0.44
22:T:78:THR:HB	22:T:87:VAL:O	2.18	0.44
15:M:159:VAL:HG12	36:M:9318:CL:CL	2.54	0.44
15:M:47:ASP:CG	15:M:48:LYS:N	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:106:A:H2'	1:0:107:U:O4'	2.18	0.44
1:0:1525:G:H5'	1:0:1526:A:OP2	2.17	0.44
38:0:5004:HOH:O	16:N:21:HIS:HD2	2.01	0.44
5:B:180:ASP:O	5:B:181:ILE:C	2.55	0.44
20:R:82:GLU:HG3	20:R:83:LYS:N	2.32	0.44
1:0:2670:G:O2'	1:0:2671:U:H5'	2.17	0.44
6:C:19:PRO:HG2	6:C:22:PHE:CE1	2.53	0.44
13:K:113:ILE:HD12	13:K:128:ALA:HB2	2.00	0.44
7:D:35:ALA:C	7:D:37:ALA:N	2.71	0.44
16:N:147:ILE:HG23	16:N:148:ALA:N	2.33	0.44
1:0:2451:G:O2'	31:3:38:ARG:NH2	2.51	0.44
1:0:64:G:H2'	1:0:65:C:O4'	2.18	0.44
6:C:54:LEU:HD23	6:C:79:ARG:HG3	1.98	0.44
19:Q:32:GLU:O	19:Q:93:ARG:NH2	2.51	0.44
1:0:1135:G:H5'	38:0:6173:HOH:O	2.18	0.44
1:0:2312:G:H2'	1:0:2313:C:H5'	1.99	0.44
1:0:2314:G:C2'	1:0:2315:C:H5'	2.47	0.44
1:0:2112:A:H2'	1:0:2113:G:C8	2.53	0.44
1:0:2467:A:O2'	1:0:2468:A:H2'	2.17	0.44
4:A:192:VAL:HB	38:A:9387:HOH:O	2.18	0.44
1:0:820:G:C5	4:A:171:LYS:HB2	2.53	0.44
11:H:83:TYR:C	11:H:83:TYR:CD1	2.91	0.44
1:0:1596:U:H2'	1:0:1598:A:OP2	2.17	0.44
1:0:1334:C:H2'	1:0:1335:C:H6	1.83	0.44
1:0:1711:A:O2'	1:0:1712:A:H5'	2.18	0.44
14:L:91:VAL:HB	38:L:9358:HOH:O	2.17	0.44
4:A:165:THR:O	4:A:165:THR:HG22	2.17	0.44
26:X:76:ARG:NH1	26:X:76:ARG:CG	2.74	0.43
16:N:86:LEU:HD21	16:N:180:LEU:CD1	2.48	0.43
16:N:86:LEU:O	16:N:90:LEU:HG	2.18	0.43
32:I:132:CYS:C	32:I:134:SER:H	2.21	0.43
14:L:134:GLU:HG3	38:L:9357:HOH:O	2.18	0.43
38:0:4890:HOH:O	17:O:35:LYS:HD3	2.18	0.43
8:E:145:ALA:HB1	8:E:168:ILE:CD1	2.47	0.43
16:N:127:LEU:HB2	38:N:9356:HOH:O	2.17	0.43
23:U:14:GLU:OE1	23:U:15:PRO:HD2	2.17	0.43
1:0:816:G:C6	1:0:817:G:N1	2.86	0.43
17:O:38:ARG:NH1	38:O:7674:HOH:O	2.51	0.43
1:0:794:U:H2'	1:0:795:G:H5'	2.00	0.43
15:M:68:ARG:O	15:M:68:ARG:HD3	2.17	0.43
1:0:2326:U:H4'	1:0:2412:G:H4'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:941:G:C5	1:0:942:U:C4	3.06	0.43
16:N:42:HIS:CG	16:N:62:HIS:HE1	2.36	0.43
16:N:62:HIS:O	16:N:65:ASP:OD1	2.35	0.43
6:C:84:VAL:O	6:C:85:LYS:HB2	2.17	0.43
22:T:23:VAL:C	22:T:93:THR:HG21	2.38	0.43
1:0:445:U:H2'	1:0:446:G:H8	1.82	0.43
8:E:107:PHE:CE1	8:E:152:THR:HB	2.52	0.43
6:C:236:THR:HA	38:C:9252:HOH:O	2.18	0.43
26:X:74:ALA:HB2	26:X:85:VAL:HG13	1.99	0.43
7:D:76:ARG:O	7:D:77:ASP:HB2	2.18	0.43
16:N:71:TRP:HE3	16:N:175:LEU:HD22	1.82	0.43
18:P:59:ARG:NH2	18:P:66:GLN:NE2	2.62	0.43
20:R:18:LEU:HG	20:R:91:LEU:HD13	1.99	0.43
1:0:474:C:O3'	6:C:73:LEU:HD21	2.17	0.43
1:0:2050:G:OP1	20:R:79:ARG:HB3	2.18	0.43
14:L:93:VAL:HG12	14:L:97:VAL:HG23	2.00	0.43
1:0:757:C:OP1	14:L:27:ARG:HD2	2.16	0.43
26:X:43:VAL:HG12	26:X:47:ALA:HB3	2.00	0.43
11:H:9:ILE:HG23	11:H:126:ARG:NE	2.33	0.43
14:L:121:ILE:HA	14:L:141:GLU:O	2.18	0.43
32:I:110:GLU:HA	32:I:113:HIS:NE2	2.34	0.43
27:Y:187:VAL:HG12	27:Y:205:ILE:HA	2.00	0.43
11:H:59:HIS:HA	11:H:62:LEU:HD23	1.98	0.43
8:E:20:ILE:HD12	8:E:33:LEU:HD12	2.00	0.43
1:0:1850:U:H2'	1:0:1851:G:C8	2.53	0.43
11:H:154:TYR:C	11:H:154:TYR:HD1	2.22	0.43
4:A:128:LEU:HG	38:A:9366:HOH:O	2.18	0.43
5:B:109:LEU:CG	5:B:113:LEU:HD12	2.49	0.43
30:2:35:ARG:HB2	38:2:2691:HOH:O	2.18	0.43
14:L:21:ARG:N	38:L:9330:HOH:O	2.51	0.43
11:H:146:VAL:HG22	38:H:9174:HOH:O	2.19	0.43
6:C:49:ASP:HB3	6:C:52:ALA:HB2	1.99	0.43
18:P:27:ARG:O	18:P:31:ILE:HG13	2.18	0.43
6:C:5:ILE:HG23	38:C:9234:HOH:O	2.18	0.43
24:V:7:GLU:O	24:V:11:MET:HG3	2.18	0.43
1:0:541:C:O2'	1:0:542:A:H5"	2.19	0.43
6:C:184:ARG:NE	38:C:9216:HOH:O	2.51	0.43
25:W:65:VAL:HG12	25:W:116:LEU:HD13	1.99	0.43
7:D:49:PRO:HA	7:D:73:VAL:HG22	2.00	0.43
17:O:26:TRP:HA	17:O:26:TRP:HE3	1.82	0.43
1:0:136:C:P	15:M:39:ARG:HH22	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:3:65:THR:CG2	31:3:67:LEU:HG	2.48	0.43
6:C:79:ARG:O	6:C:87:ARG:HG2	2.17	0.43
1:0:690:G:H4'	1:0:741:C:O2	2.19	0.43
1:0:1768:C:H2'	1:0:1769:C:H5'	2.00	0.43
9:F:36:THR:O	9:F:40:ILE:HG13	2.19	0.43
11:H:43:TYR:HA	11:H:44:PRO:HD3	1.76	0.43
1:0:1375:A:C2'	1:0:1376:G:H5'	2.48	0.43
6:C:19:PRO:HD2	6:C:240:LEU:CD2	2.49	0.43
5:B:13:PHE:N	38:B:9416:HOH:O	2.47	0.43
25:W:88:THR:CG2	25:W:89:ASP:H	2.22	0.43
30:2:40:ARG:HG3	30:2:45:ASN:CB	2.48	0.43
8:E:47:VAL:HG11	8:E:69:ILE:HD13	2.01	0.43
5:B:147:VAL:O	5:B:147:VAL:HG12	2.19	0.43
1:0:2719:A:C2	5:B:70:PRO:HG3	2.53	0.43
9:F:34:ASN:HA	15:M:4:ALA:HB2	2.01	0.43
1:0:922:A:N7	1:0:2281:C:H5'	2.33	0.43
13:K:29:LEU:HB3	13:K:55:VAL:CG1	2.42	0.43
1:0:2909:G:H2'	1:0:2910:A:C8	2.52	0.43
16:N:163:PHE:O	16:N:164:ASP:CG	2.56	0.43
1:0:244:C:OP2	9:F:38:LYS:HE3	2.19	0.43
1:0:2781:U:H2'	1:0:2782:G:H5'	1.99	0.43
1:0:661:G:C5	1:0:686:A:C2	3.07	0.43
1:0:2754:G:H2'	1:0:2755:G:O4'	2.18	0.43
26:X:21:PRO:HG2	26:X:24:LYS:HD3	1.99	0.43
5:B:148:PRO:HD2	38:B:9379:HOH:O	2.18	0.43
1:0:1398:G:H2'	1:0:1399:A:C8	2.53	0.43
1:0:1772:C:H5'	1:0:1773:G:C5	2.53	0.43
15:M:184:ARG:HG3	15:M:185:PRO:HA	2.01	0.43
13:K:49:LEU:HA	13:K:73:VAL:HG12	2.00	0.43
1:0:737:A:H2'	1:0:738:G:O4'	2.18	0.43
14:L:130:ARG:O	14:L:131:GLU:C	2.57	0.43
13:K:9:THR:O	13:K:10:GLN:C	2.57	0.43
8:E:81:GLU:O	8:E:172:PRO:HD3	2.18	0.43
8:E:3:VAL:CG2	8:E:49:ILE:HB	2.44	0.43
1:0:363:A:O2'	1:0:364:C:H5'	2.18	0.43
25:W:146:ILE:HG23	25:W:150:LEU:HD12	2.00	0.43
5:B:26:PHE:HE1	38:B:9444:HOH:O	2.00	0.43
26:X:12:ILE:HB	26:X:70:ILE:CG2	2.48	0.43
11:H:84:LYS:HB2	11:H:84:LYS:HZ2	1.84	0.43
1:0:1151:G:OP2	10:G:65:THR:HG21	2.19	0.43
4:A:35:GLY:O	4:A:36:ASP:CB	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1174:A:C5	1:0:1201:C:H4'	2.53	0.43
12:J:130:VAL:HG12	12:J:131:THR:H	1.84	0.43
5:B:41:PHE:CB	5:B:190:MET:HE3	2.48	0.43
6:C:7:ASP:C	6:C:9:ASP:H	2.22	0.43
1:0:470:U:O2'	29:1:16:HIS:CD2	2.68	0.43
7:D:58:VAL:HB	7:D:62:ASP:HB3	2.01	0.43
1:0:2241:C:H2'	1:0:2242:U:H6	1.81	0.43
1:0:2264:A:H2'	1:0:2265:U:C6	2.54	0.43
9:F:48:VAL:HG23	9:F:74:PHE:CB	2.49	0.43
1:0:1594:C:O2'	1:0:1607:A:H4'	2.19	0.43
13:K:72:VAL:O	13:K:95:ALA:HA	2.18	0.43
8:E:132:THR:O	8:E:132:THR:HG23	2.19	0.43
1:0:204:A:C2'	1:0:205:U:H5'	2.49	0.43
1:0:766:A:H5'	38:0:4926:HOH:O	2.18	0.43
1:0:1852:A:H4'	4:A:230:SER:HB2	2.00	0.43
25:W:1:MET:N	25:W:103:GLU:OE2	2.47	0.43
1:0:2531:U:O2'	1:0:2532:A:H5'	2.19	0.43
6:C:162:VAL:CG1	6:C:192:ILE:HD11	2.49	0.43
1:0:1007:A:H2'	11:H:19:TYR:CZ	2.54	0.43
1:0:2382:A:H5'	38:0:5017:HOH:O	2.18	0.43
1:0:635:A:H2'	1:0:636:G:H5''	2.01	0.43
11:H:112:GLY:N	38:H:9185:HOH:O	2.52	0.43
1:0:1943:C:O4'	4:A:212:PRO:HA	2.18	0.43
38:0:3098:HOH:O	13:K:39:GLY:HA3	2.18	0.43
25:W:54:PHE:CZ	25:W:140:LYS:HB2	2.54	0.43
32:I:113:HIS:N	32:I:114:PRO:HD2	2.33	0.43
27:Y:144:ARG:HG3	27:Y:144:ARG:HH11	1.84	0.43
17:O:47:ARG:HG3	17:O:47:ARG:NH1	2.32	0.43
7:D:169:THR:C	7:D:170:TYR:HD1	2.22	0.43
16:N:62:HIS:HB3	16:N:65:ASP:OD1	2.19	0.43
28:Z:81:ARG:O	28:Z:82:SER:C	2.56	0.43
1:0:677:C:O2'	1:0:678:G:H5'	2.18	0.43
4:A:140:LEU:HB3	4:A:141:PRO:HD2	2.00	0.43
7:D:140:ARG:O	7:D:144:ARG:HG2	2.19	0.43
5:B:217:ARG:CD	5:B:257:THR:HG22	2.49	0.43
1:0:2070:G:H2'	1:0:2072:G:OP1	2.18	0.43
1:0:553:G:P	27:Y:204:ARG:NH2	2.89	0.43
1:0:1080:C:H6	1:0:1080:C:O5'	2.01	0.43
6:C:107:ARG:CZ	6:C:107:ARG:HB3	2.49	0.43
25:W:73:LEU:HA	25:W:73:LEU:HD12	1.76	0.43
28:Z:56:GLN:HG3	28:Z:62:TYR:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2785:C:H4'	1:0:2786:G:OP2	2.18	0.43
5:B:103:ASP:HB2	38:B:9395:HOH:O	2.19	0.43
1:0:1123:A:C6	1:0:1238:C:H5'	2.54	0.43
1:0:10:U:O4	1:0:532:A:OP2	2.37	0.43
8:E:156:ASP:OD2	8:E:157:LYS:NZ	2.46	0.43
6:C:5:ILE:HA	6:C:139:VAL:HG12	2.01	0.42
1:0:1603:A:H5''	1:0:1605:G:H5'	2.00	0.42
1:0:288:A:H61	1:0:364:C:H42	1.67	0.42
20:R:114:VAL:HA	20:R:144:GLU:O	2.19	0.42
7:D:11:HIS:CG	7:D:12:GLU:N	2.87	0.42
1:0:1675:C:H5''	30:2:5:LYS:HD2	2.01	0.42
1:0:2265:U:H2'	1:0:2266:A:H8	1.84	0.42
1:0:1095:U:O2	25:W:120:PRO:HG2	2.19	0.42
5:B:66:GLU:HG2	38:B:9443:HOH:O	2.18	0.42
1:0:2791:U:H1'	1:0:2792:A:H5''	2.00	0.42
6:C:37:ALA:O	6:C:41:ASN:ND2	2.51	0.42
1:0:1617:C:C4	1:0:1643:C:H4'	2.54	0.42
4:A:123:GLY:HA3	4:A:162:GLY:HA2	2.01	0.42
31:3:75:GLY:HA2	38:3:9358:HOH:O	2.18	0.42
1:0:177:A:H2'	1:0:178:U:O4'	2.18	0.42
13:K:14:LYS:HD2	13:K:45:PRO:HG3	2.01	0.42
32:I:132:CYS:C	32:I:134:SER:N	2.72	0.42
27:Y:144:ARG:HH11	27:Y:144:ARG:CG	2.32	0.42
8:E:84:MET:HE1	8:E:148:ILE:HD12	2.00	0.42
28:Z:60:CYS:SG	28:Z:62:TYR:HB2	2.59	0.42
1:0:451:C:C2'	1:0:452:G:H5'	2.49	0.42
1:0:1236:A:C8	12:J:63:ILE:HD11	2.53	0.42
5:B:154:VAL:HA	5:B:155:PRO:HD3	1.84	0.42
1:0:2489:G:H1'	38:0:7457:HOH:O	2.19	0.42
1:0:1829:A:H5''	38:0:3377:HOH:O	2.18	0.42
20:R:39:THR:HB	20:R:42:GLU:CG	2.48	0.42
1:0:1306:U:OP1	6:C:184:ARG:HD2	2.19	0.42
1:0:907:A:H4'	1:0:1328:A:C2	2.54	0.42
17:O:26:TRP:HB2	38:O:3062:HOH:O	2.18	0.42
1:0:1903:U:O2'	1:0:1904:A:N7	2.50	0.42
1:0:2869:G:H2'	1:0:2870:C:H6	1.84	0.42
1:0:2326:U:H4'	1:0:2412:G:C4'	2.49	0.42
13:K:28:GLU:HB3	13:K:59:LYS:HB2	2.02	0.42
1:0:1051:C:H2'	1:0:1052:G:O4'	2.20	0.42
1:0:23:G:H1'	1:0:520:A:N6	2.35	0.42
1:0:1158:G:O2'	1:0:1159:G:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:58:MET:SD	30:2:8:LYS:HE3	2.59	0.42
7:D:40:ILE:HG23	38:D:5583:HOH:O	2.18	0.42
1:0:1603:A:C5'	1:0:1605:G:H5'	2.50	0.42
16:N:151:ASP:HB3	38:N:9328:HOH:O	2.19	0.42
1:0:1299:G:H5'	38:0:4362:HOH:O	2.19	0.42
4:A:65:ARG:O	4:A:66:ARG:HG3	2.18	0.42
4:A:199:HIS:HD2	4:A:201:PHE:HB2	1.85	0.42
2:9:3047:A:C2	2:9:3048:C:C2	3.07	0.42
14:L:57:VAL:O	14:L:57:VAL:HG12	2.19	0.42
1:0:2664:A:H8	1:0:2664:A:OP1	2.02	0.42
25:W:19:ASP:O	25:W:23:MET:HG3	2.19	0.42
1:0:2434:A:O3'	31:3:28:GLY:HA3	2.19	0.42
1:0:2809:G:H2'	1:0:2810:G:O4'	2.19	0.42
1:0:297:U:H2'	1:0:298:C:H6	1.84	0.42
21:S:76:GLU:HB3	38:S:9143:HOH:O	2.19	0.42
21:S:57:THR:C	21:S:59:ASP:H	2.22	0.42
1:0:2269:C:H2'	1:0:2270:G:C5'	2.48	0.42
2:9:3007:G:H5'	38:N:9346:HOH:O	2.18	0.42
11:H:169:GLY:C	11:H:170:ASN:HD22	2.23	0.42
25:W:122:ARG:HH11	25:W:122:ARG:CG	2.33	0.42
9:F:28:ALA:HB3	9:F:99:THR:O	2.19	0.42
3:4:74:C:C2'	3:4:75:C:H5'	2.49	0.42
1:0:95:A:H5''	1:0:97:G:O4'	2.19	0.42
16:N:12:ARG:HD3	16:N:18:THR:OG1	2.20	0.42
1:0:292:G:H2'	1:0:358:G:N2	2.34	0.42
8:E:112:ALA:HA	8:E:113:PRO:HD3	1.88	0.42
8:E:86:VAL:CG1	8:E:129:GLU:HA	2.48	0.42
1:0:2672:C:O2'	1:0:2673:U:H5'	2.20	0.42
1:0:156:C:H5''	15:M:171:ARG:CD	2.27	0.42
7:D:41:LEU:HA	7:D:44:ILE:CG2	2.48	0.42
25:W:29:VAL:O	25:W:30:ASN:HB2	2.19	0.42
5:B:62:ARG:HG2	5:B:65:MET:HE3	2.02	0.42
5:B:195:ARG:HG2	5:B:323:LEU:HD22	2.02	0.42
1:0:1201:C:C2'	1:0:1202:A:H5'	2.46	0.42
7:D:173:GLU:O	7:D:174:VAL:C	2.58	0.42
13:K:34:VAL:HG21	13:K:46:LYS:O	2.20	0.42
20:R:25:PHE:CZ	20:R:29:LYS:HE2	2.55	0.42
1:0:2323:G:H5'	38:0:7221:HOH:O	2.19	0.42
7:D:20:LYS:HA	7:D:75:LEU:O	2.20	0.42
1:0:1676:G:O2'	1:0:1677:U:H5'	2.20	0.42
11:H:139:ASN:O	11:H:141:GLU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:55:LYS:O	7:D:56:ARG:HB2	2.19	0.42
1:0:245:C:H2'	1:0:246:G:H5'	2.02	0.42
1:0:2443:C:O3'	14:L:56:LYS:HE3	2.20	0.42
6:C:164:ALA:O	6:C:167:ASP:HB2	2.20	0.42
5:B:238:ASN:ND2	5:B:240:GLY:N	2.56	0.42
24:V:60:GLN:O	24:V:65:ASP:N	2.47	0.42
1:0:1166:A:N3	1:0:1166:A:H2'	2.35	0.42
32:I:112:LYS:HB3	32:I:116:LEU:HG	2.02	0.42
1:0:111:C:H2'	1:0:112:G:O4'	2.20	0.42
5:B:195:ARG:CG	5:B:323:LEU:HD22	2.50	0.42
7:D:64:ARG:HG2	7:D:67:ASP:HB3	2.02	0.42
24:V:42:ASN:N	24:V:43:PRO:HD3	2.34	0.42
20:R:61:GLN:CD	38:R:9341:HOH:O	2.58	0.42
1:0:1314:U:H5''	1:0:1316:G:O4'	2.19	0.42
1:0:2064:U:H5'	1:0:2652:U:O3'	2.20	0.42
5:B:17:LYS:O	5:B:260:HIS:CD2	2.73	0.42
26:X:70:ILE:O	26:X:70:ILE:HG23	2.20	0.42
1:0:2541:U:H3'	1:0:2541:U:H6	1.84	0.42
1:0:794:U:C2'	1:0:795:G:H5'	2.50	0.42
1:0:1025:C:H5'	25:W:23:MET:O	2.20	0.42
1:0:394:G:H1	15:M:181:GLU:CD	2.23	0.42
10:G:12:ILE:N	10:G:13:PRO:HD3	2.34	0.42
1:0:1979:G:H2'	38:0:3589:HOH:O	2.19	0.42
1:0:2638:G:H1'	38:0:4856:HOH:O	2.19	0.42
1:0:517:U:H1'	38:0:7742:HOH:O	2.17	0.42
1:0:2824:C:H5''	1:0:2825:C:H5'	2.00	0.42
21:S:6:LYS:O	21:S:7:HIS:HB3	2.20	0.42
1:0:1631:A:H2'	1:0:1632:A:C8	2.54	0.42
6:C:187:ARG:NH2	38:C:9164:HOH:O	2.51	0.42
18:P:115:SER:OG	18:P:118:GLN:CG	2.68	0.42
1:0:2506:A:O2'	1:0:2507:G:P	2.78	0.42
27:Y:187:VAL:HB	38:Y:8158:HOH:O	2.19	0.42
1:0:656:G:H3'	17:O:37:ARG:HH12	1.84	0.42
5:B:86:ALA:HA	38:B:9378:HOH:O	2.19	0.42
18:P:10:ALA:HA	18:P:13:VAL:CG1	2.50	0.42
4:A:51:ARG:HB2	38:A:9401:HOH:O	2.19	0.42
1:0:947:U:O2'	1:0:948:G:H5'	2.19	0.42
38:0:6519:HOH:O	27:Y:158:LYS:HD3	2.19	0.42
1:0:472:A:H5'	29:I:35:SER:OG	2.19	0.42
19:Q:75:ILE:CD1	19:Q:84:ILE:HD11	2.50	0.42
11:H:69:ALA:HB2	11:H:153:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:39:G:N2	1:0:444:C:C2	2.88	0.42
15:M:115:LEU:HD13	15:M:116:ASN:HB2	2.02	0.42
1:0:2425:A:H5'	1:0:2426:G:OP2	2.20	0.42
30:2:49:GLU:HB2	38:2:719:HOH:O	2.20	0.42
1:0:1878:G:O2'	1:0:1879:U:OP2	2.37	0.42
5:B:104:GLU:HG3	38:B:9395:HOH:O	2.20	0.42
14:L:24:ALA:HB2	14:L:30:ARG:HD2	2.02	0.42
6:C:115:LEU:HA	6:C:115:LEU:HD12	1.92	0.42
10:G:71:LEU:C	10:G:73:ASP:N	2.73	0.42
21:S:39:ASP:HB3	21:S:43:GLU:OE2	2.20	0.42
1:0:790:A:H1'	1:0:1710:A:H2'	2.02	0.42
14:L:53:ARG:NH2	14:L:57:VAL:HG12	2.35	0.42
1:0:1878:G:O2'	1:0:1879:U:P	2.78	0.42
8:E:101:GLU:HB3	8:E:117:THR:HA	2.01	0.42
1:0:462:A:C8	30:2:37:HIS:CE1	3.08	0.42
4:A:95:PRO:HG2	4:A:98:GLU:HG2	2.02	0.42
1:0:1562:C:N4	38:0:6115:HOH:O	2.51	0.42
38:0:9421:HOH:O	5:B:229:ARG:HD2	2.20	0.42
1:0:611:U:H2'	1:0:612:U:C6	2.55	0.42
22:T:37:GLN:OE1	22:T:118:SER:HA	2.19	0.42
22:T:3:GLN:HA	22:T:4:PRO:HD3	1.88	0.42
1:0:195:C:H2'	1:0:196:G:H5'	2.02	0.42
1:0:1242:A:OP2	12:J:60:ARG:NH2	2.49	0.41
22:T:49:GLU:HB3	22:T:59:GLU:HG3	2.02	0.41
28:Z:22:SER:O	28:Z:26:VAL:HG23	2.19	0.41
16:N:71:TRP:CE3	16:N:175:LEU:HD22	2.55	0.41
25:W:141:HIS:HB2	25:W:146:ILE:HG12	2.02	0.41
4:A:99:ILE:O	4:A:131:HIS:CE1	2.72	0.41
14:L:143:THR:HG22	14:L:144:ASP:H	1.83	0.41
22:T:12:ARG:O	22:T:19:ARG:NH2	2.53	0.41
1:0:1921:A:C6	1:0:1922:A:C2	3.08	0.41
31:3:11:CYS:HB2	31:3:20:HIS:CE1	2.55	0.41
1:0:2642:G:H2'	1:0:2643:G:O4'	2.20	0.41
1:0:249:G:H1'	1:0:265:U:O2	2.20	0.41
9:F:91:VAL:CG1	9:F:92:GLY:H	2.15	0.41
16:N:50:LEU:HD12	16:N:55:ASP:OD1	2.20	0.41
1:0:1192:A:N6	32:I:134:SER:CB	2.82	0.41
29:1:21:ARG:HD2	29:1:37:CYS:SG	2.59	0.41
18:P:131:PHE:CD1	18:P:137:LEU:HD13	2.56	0.41
1:0:2003:U:H4'	1:0:2004:U:H5	1.85	0.41
1:0:2780:C:H2'	1:0:2781:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:22:VAL:HA	7:D:73:VAL:O	2.19	0.41
1:O:1163:G:H5''	32:I:115:ASP:HB3	2.03	0.41
11:H:76:GLU:O	11:H:77:LEU:HD23	2.20	0.41
24:V:49:LEU:O	24:V:53:ILE:HG13	2.20	0.41
5:B:82:VAL:O	5:B:82:VAL:HG12	2.19	0.41
1:O:711:G:C2	1:O:718:C:C2	3.08	0.41
7:D:169:THR:HG22	7:D:169:THR:O	2.19	0.41
1:O:886:A:OP2	1:O:2113:G:H5'	2.20	0.41
6:C:51:TYR:CE2	29:1:53:LYS:HB3	2.55	0.41
1:O:2515:C:H2'	1:O:2516:G:O4'	2.20	0.41
13:K:24:THR:HB	13:K:64:MET:HE2	2.01	0.41
21:S:29:ASP:OD1	21:S:31:ARG:NH1	2.53	0.41
1:O:806:A:H2'	1:O:807:A:O4'	2.20	0.41
2:9:3096:C:O2'	2:9:3097:U:H5'	2.21	0.41
28:Z:67:GLY:N	28:Z:70:LYS:O	2.52	0.41
26:X:44:ASP:HB3	26:X:46:ASP:OD2	2.20	0.41
26:X:72:VAL:HG22	26:X:85:VAL:CG1	2.45	0.41
1:O:1474:C:C5'	1:O:1474:C:H6	2.20	0.41
4:A:36:ASP:HA	4:A:83:GLY:HA3	2.01	0.41
8:E:68:HIS:O	8:E:72:MET:HG3	2.19	0.41
9:F:58:GLU:HG3	9:F:61:MET:HE1	2.02	0.41
5:B:205:VAL:O	5:B:307:ARG:NE	2.53	0.41
20:R:114:VAL:HB	20:R:145:LEU:HD13	2.01	0.41
14:L:66:VAL:HG23	14:L:67:ARG:N	2.35	0.41
5:B:51:VAL:HG23	5:B:330:VAL:HG22	2.01	0.41
6:C:165:ASP:O	6:C:168:ARG:HB3	2.19	0.41
5:B:280:VAL:HG13	5:B:333:GLU:O	2.19	0.41
1:O:664:U:O4	1:O:681:G:H5''	2.19	0.41
1:O:2676:C:H4'	12:J:70:PHE:HE1	1.85	0.41
7:D:153:THR:O	7:D:156:ARG:HB2	2.20	0.41
2:9:3095:C:O2'	2:9:3096:C:H5'	2.20	0.41
1:O:1481:G:H2'	1:O:1482:A:O4'	2.21	0.41
13:K:41:LYS:O	13:K:42:ASN:HB2	2.20	0.41
1:O:2363:G:O2'	19:Q:11:ARG:HG3	2.20	0.41
25:W:6:GLN:HG2	25:W:29:VAL:HA	2.01	0.41
1:O:559:U:O2'	1:O:560:C:H5'	2.20	0.41
4:A:93:THR:HG23	4:A:154:ALA:O	2.21	0.41
22:T:48:VAL:O	22:T:59:GLU:HG2	2.20	0.41
9:F:58:GLU:HA	9:F:61:MET:HE2	2.00	0.41
27:Y:189:ASN:HD22	27:Y:192:ASP:H	1.67	0.41
1:O:1730:G:H5''	1:O:1731:C:C6	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:3049:G:C2'	2:9:3050:G:H5'	2.51	0.41
1:0:1343:C:H2'	1:0:1344:G:O5'	2.20	0.41
1:0:815:U:O2'	1:0:1598:A:H4'	2.20	0.41
2:9:3088:G:OP1	25:W:130:HIS:NE2	2.49	0.41
1:0:200:U:H2'	38:0:3736:HOH:O	2.20	0.41
1:0:1945:G:O2'	1:0:1946:C:H5'	2.20	0.41
1:0:1764:C:H2'	1:0:1765:G:O4'	2.20	0.41
1:0:1414:A:H2'	1:0:1415:G:O4'	2.20	0.41
1:0:1041:U:H4'	1:0:1295:G:H5'	2.03	0.41
5:B:33:ASP:O	5:B:34:GLY:O	2.38	0.41
6:C:123:LEU:HA	6:C:123:LEU:HD23	1.94	0.41
6:C:140:VAL:HG12	6:C:141:SER:N	2.34	0.41
1:0:2712:G:H5'	38:K:4183:HOH:O	2.21	0.41
13:K:109:LEU:HD13	13:K:113:ILE:CD1	2.51	0.41
1:0:656:G:H5'	17:O:3:THR:HB	2.02	0.41
1:0:2252:A:H2'	1:0:2253:G:H5'	2.02	0.41
6:C:7:ASP:OD1	6:C:11:ASN:O	2.37	0.41
1:0:88:G:C8	1:0:88:G:H5'	2.53	0.41
1:0:2474:A:N6	3:4:176:DA:OP2	2.53	0.41
12:J:70:PHE:CD2	12:J:70:PHE:O	2.74	0.41
4:A:134:ASN:O	4:A:150:PRO:HD3	2.20	0.41
15:M:50:ARG:N	15:M:54:TYR:HB3	2.34	0.41
14:L:17:SER:C	14:L:19:LYS:N	2.74	0.41
1:0:1477:C:H4'	1:0:1868:G:H5''	2.01	0.41
1:0:1056:U:H2'	1:0:1057:A:O4'	2.20	0.41
20:R:122:GLN:HB3	20:R:138:SER:HB2	2.03	0.41
1:0:2766:A:O2'	1:0:2767:C:H5'	2.20	0.41
38:0:5775:HOH:O	5:B:298:LYS:HD3	2.19	0.41
16:N:82:TYR:C	16:N:82:TYR:CD2	2.94	0.41
1:0:870:G:C3'	1:0:871:G:H5''	2.50	0.41
8:E:35:TYR:HA	12:J:127:ILE:CD1	2.48	0.41
1:0:1188:A:C6	1:0:1189:A:C6	3.09	0.41
7:D:41:LEU:CA	7:D:44:ILE:HG22	2.48	0.41
9:F:63:ILE:HB	9:F:64:PRO:CD	2.47	0.41
5:B:5:ARG:HA	5:B:6:PRO:HD3	1.97	0.41
1:0:2436:U:H5'	31:3:68:LYS:HE2	2.01	0.41
26:X:78:GLU:CG	26:X:79:GLU:H	2.27	0.41
16:N:154:LEU:C	16:N:156:GLU:H	2.22	0.41
1:0:2781:U:H2'	1:0:2782:G:C5'	2.51	0.41
5:B:280:VAL:HG13	5:B:334:SER:HA	2.03	0.41
4:A:76:VAL:CG2	28:Z:63:LYS:HB3	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:27:ASN:HB3	38:B:9425:HOH:O	2.20	0.41
11:H:78:GLY:C	11:H:80:GLU:H	2.24	0.41
1:0:947:U:H2'	1:0:948:G:H8	1.83	0.41
1:0:711:G:H1'	38:0:7290:HOH:O	2.20	0.41
1:0:1773:G:N2	1:0:1774:G:C8	2.88	0.41
1:0:1755:A:H2'	1:0:1756:G:O4'	2.20	0.41
18:P:45:ASP:C	18:P:47:GLY:H	2.24	0.41
1:0:1838:U:O2'	1:0:2644:C:H5'	2.21	0.41
5:B:224:LYS:HD3	5:B:224:LYS:HA	1.93	0.41
26:X:74:ALA:CB	26:X:85:VAL:HG22	2.51	0.41
2:9:3057:A:C8	7:D:141:VAL:HG21	2.56	0.41
1:0:1328:A:C8	27:Y:169:ARG:HD3	2.56	0.41
1:0:820:G:O2'	1:0:856:G:H4'	2.21	0.41
11:H:27:LYS:H	11:H:59:HIS:CD2	2.32	0.41
4:A:66:ARG:NH1	4:A:66:ARG:CB	2.84	0.41
1:0:695:C:H2'	1:0:696:C:C6	2.56	0.41
23:U:20:MET:CG	23:U:28:THR:HG23	2.51	0.41
1:0:212:A:O4'	1:0:214:U:C6	2.74	0.41
2:9:3011:A:O2'	2:9:3012:C:H3'	2.21	0.41
1:0:1717:A:H5''	18:P:54:LYS:HB2	2.03	0.41
28:Z:80:ARG:O	28:Z:81:ARG:O	2.39	0.41
1:0:1937:U:O2'	1:0:1938:G:H5'	2.20	0.41
1:0:844:A:C6	1:0:882:A:C5	3.09	0.41
4:A:173:GLY:O	4:A:176:HIS:HB3	2.21	0.41
1:0:2090:G:H2'	1:0:2091:G:C8	2.55	0.41
20:R:26:LYS:HB3	20:R:62:HIS:CD2	2.56	0.41
1:0:1915:U:O2'	1:0:1916:C:H5'	2.20	0.41
11:H:114:ARG:O	11:H:115:ALA:C	2.59	0.41
1:0:876:A:H2'	1:0:876:A:N3	2.36	0.41
6:C:140:VAL:CG1	6:C:141:SER:N	2.84	0.41
7:D:44:ILE:HG23	7:D:45:THR:HG23	2.02	0.41
1:0:2416:G:O2'	16:N:25:ARG:HG2	2.21	0.41
4:A:200:PRO:HD3	38:A:9319:HOH:O	2.21	0.41
1:0:903:U:O4	14:L:18:HIS:HB2	2.21	0.41
27:Y:106:THR:CG2	27:Y:107:PRO:HD2	2.51	0.41
1:0:47:G:N3	1:0:114:A:C2	2.89	0.41
1:0:1333:U:H2'	1:0:1334:C:H6	1.86	0.41
6:C:76:ARG:NH1	6:C:76:ARG:CG	2.81	0.41
1:0:1439:C:H6	1:0:1439:C:O5'	2.04	0.41
1:0:1659:A:H2'	1:0:1660:G:O4'	2.20	0.41
26:X:61:ARG:HH12	26:X:67:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:350:C:O2'	1:0:351:G:H5'	2.21	0.41
22:T:40:VAL:HG23	22:T:119:ALA:C	2.41	0.41
8:E:81:GLU:HA	8:E:133:VAL:O	2.21	0.41
24:V:4:HIS:O	24:V:8:ILE:HG13	2.20	0.41
24:V:1:THR:O	24:V:4:HIS:CE1	2.74	0.41
22:T:48:VAL:CG1	22:T:96:VAL:HG22	2.50	0.41
2:9:3039:U:H3'	2:9:3040:C:H5''	2.02	0.41
23:U:9:CYS:O	23:U:52:THR:HG23	2.20	0.41
1:0:1820:G:C6	1:0:2030:A:C2	3.09	0.41
29:1:25:LYS:HE2	38:1:9262:HOH:O	2.20	0.41
1:0:1543:G:N1	1:0:1641:A:OP2	2.39	0.41
16:N:47:LEU:HD13	16:N:97:VAL:HG11	2.02	0.41
16:N:93:GLN:HG2	38:N:9356:HOH:O	2.21	0.41
7:D:172:VAL:HG12	7:D:173:GLU:N	2.35	0.41
2:9:3003:A:H2	2:9:3021:G:N3	2.19	0.41
8:E:12:ASP:HA	38:E:1750:HOH:O	2.19	0.41
26:X:9:VAL:HG22	26:X:88:GLU:OE2	2.20	0.41
1:0:1654:U:H2'	4:A:47:HIS:CD2	2.54	0.41
1:0:638:C:H2'	1:0:639:A:H8	1.85	0.41
1:0:1747:A:C8	13:K:44:LEU:HD13	2.56	0.41
5:B:7:ARG:CG	5:B:7:ARG:HH11	2.33	0.41
1:0:1406:A:H5'	1:0:1407:A:C8	2.56	0.41
1:0:764:C:OP1	6:C:87:ARG:NH1	2.54	0.41
1:0:2403:C:H2'	1:0:2404:G:O5'	2.20	0.41
1:0:1477:C:O2'	1:0:1478:U:H5'	2.21	0.41
1:0:2435:U:OP1	31:3:28:GLY:HA3	2.20	0.41
1:0:1839:A:H5'	1:0:2643:G:H4'	2.02	0.41
5:B:33:ASP:HB3	5:B:34:GLY:H	1.76	0.41
26:X:61:ARG:NH1	26:X:67:PRO:HD3	2.36	0.41
13:K:90:PHE:N	13:K:90:PHE:CD1	2.89	0.41
5:B:225:GLY:HA3	38:B:9367:HOH:O	2.21	0.41
1:0:318:C:H5'	1:0:339:A:C4	2.55	0.41
1:0:2626:C:H2'	1:0:2627:G:C8	2.56	0.41
1:0:697:G:H4'	1:0:730:G:O3'	2.21	0.41
20:R:12:THR:HG22	20:R:149:GLU:OE1	2.21	0.41
11:H:88:ARG:HG2	11:H:133:LEU:O	2.20	0.41
20:R:27:HIS:O	20:R:31:ILE:HG13	2.21	0.41
1:0:1313:A:H5'	27:Y:208:LYS:O	2.21	0.41
1:0:930:C:N3	1:0:1040:A:N6	2.68	0.41
1:0:1321:A:H2'	1:0:1322:G:C8	2.56	0.41
1:0:1811:A:H2'	1:0:1812:G:H5'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2724:U:O5'	1:0:2724:U:H6	2.03	0.41
6:C:19:PRO:HD2	6:C:240:LEU:HD21	2.03	0.41
7:D:154:LYS:H	7:D:154:LYS:CD	2.09	0.41
20:R:39:THR:O	20:R:40:ALA:C	2.59	0.41
26:X:76:ARG:O	26:X:77:PHE:HB3	2.20	0.41
15:M:99:ARG:HE	15:M:170:ASN:ND2	2.19	0.41
1:0:396:U:P	31:3:38:ARG:HH11	2.44	0.41
1:0:1173:A:H4'	1:0:1174:A:C8	2.56	0.41
7:D:24:HIS:HB2	7:D:71:ALA:O	2.21	0.41
25:W:92:ASP:OD1	25:W:92:ASP:N	2.54	0.41
1:0:1130:U:H4'	38:0:6364:HOH:O	2.20	0.41
5:B:55:ASN:HB3	5:B:64:GLY:H	1.85	0.41
17:O:50:ARG:HD2	17:O:51:TYR:CE1	2.56	0.41
25:W:1:MET:N	25:W:37:GLU:HG3	2.36	0.41
9:F:49:PHE:CD1	9:F:49:PHE:N	2.89	0.41
1:0:2880:A:H2'	1:0:2881:C:H5'	2.03	0.41
1:0:1471:A:H2'	1:0:1472:C:C6	2.55	0.41
1:0:2705:U:O2'	1:0:2706:A:H5'	2.20	0.41
2:9:3061:C:H2'	2:9:3062:A:H8	1.85	0.41
1:0:414:C:H5'	38:0:9961:HOH:O	2.20	0.41
4:A:215:ILE:HG13	4:A:216:SER:N	2.36	0.41
1:0:185:G:H4'	1:0:186:A:H4'	2.03	0.41
1:0:29:C:O2'	1:0:30:U:H5'	2.21	0.41
6:C:21:VAL:HG23	6:C:22:PHE:CD1	2.56	0.40
4:A:211:LYS:CB	38:A:9412:HOH:O	2.68	0.40
4:A:36:ASP:HB2	4:A:83:GLY:C	2.41	0.40
1:0:1705:C:C5'	18:P:59:ARG:HH12	2.34	0.40
9:F:102:GLY:O	9:F:103:GLU:HB2	2.21	0.40
1:0:1969:A:N7	1:0:1970:G:C6	2.89	0.40
14:L:65:ASP:CG	14:L:111:ALA:HB3	2.41	0.40
1:0:2408:A:H4'	31:3:15:ASN:O	2.21	0.40
4:A:1:GLY:HA2	4:A:197:VAL:HG23	2.02	0.40
5:B:57:GLU:HA	5:B:58:PRO:HD2	1.96	0.40
19:Q:16:ASN:HD22	19:Q:16:ASN:HA	1.70	0.40
11:H:167:PRO:O	11:H:168:ALA:CB	2.67	0.40
1:0:1160:G:O2'	1:0:1190:G:H1'	2.21	0.40
24:V:12:THR:H	24:V:15:GLU:HB2	1.86	0.40
15:M:99:ARG:HE	15:M:170:ASN:HD22	1.69	0.40
1:0:2072:G:N2	38:0:7076:HOH:O	2.46	0.40
1:0:2072:G:C6	1:0:2533:C:H1'	2.57	0.40
11:H:66:ARG:HB3	38:H:9177:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:I:92:PRO:C	32:I:94:GLU:N	2.74	0.40
1:O:450:C:OP1	6:C:184:ARG:NH2	2.55	0.40
25:W:69:ARG:HD2	25:W:117:ARG:O	2.21	0.40
5:B:321:PRO:HA	38:B:9454:HOH:O	2.21	0.40
1:O:1268:C:O2'	27:Y:169:ARG:HB2	2.22	0.40
7:D:146:LYS:HZ1	16:N:107:ASN:ND2	2.19	0.40
18:P:103:THR:O	18:P:107:GLU:HG3	2.21	0.40
27:Y:234:VAL:HG12	27:Y:235:GLU:N	2.37	0.40
5:B:132:HIS:CE1	5:B:171:VAL:CG2	3.05	0.40
1:O:2503:A:OP1	11:H:151:ARG:NH2	2.50	0.40
5:B:51:VAL:HG23	5:B:329:TYR:O	2.21	0.40
1:O:1634:G:H2'	1:O:1635:U:H6	1.86	0.40
7:D:94:ALA:HB3	7:D:97:GLN:NE2	2.35	0.40
1:O:1477:C:H5'	1:O:1868:G:C5'	2.51	0.40
6:C:191:SER:OG	6:C:192:ILE:N	2.54	0.40
8:E:154:ILE:HD11	8:E:157:LYS:HE2	2.03	0.40
21:S:29:ASP:OD1	21:S:31:ARG:HG3	2.21	0.40
27:Y:141:THR:HG23	38:Y:8175:HOH:O	2.19	0.40
1:O:803:C:O2'	1:O:804:C:H5'	2.21	0.40
1:O:354:A:H2'	1:O:355:C:C6	2.56	0.40
9:F:13:GLU:OE2	9:F:78:GLU:HG2	2.21	0.40
4:A:112:PRO:HD3	4:A:152:CYS:SG	2.61	0.40
1:O:2047:C:H5'	38:O:3119:HOH:O	2.20	0.40
26:X:41:PHE:CZ	26:X:74:ALA:HB3	2.57	0.40
1:O:1118:A:C8	1:O:1119:G:H5''	2.56	0.40
1:O:308:U:H5'	22:T:97:ARG:NH2	2.37	0.40
8:E:69:ILE:HA	8:E:72:MET:HE2	2.00	0.40
13:K:98:VAL:CG1	13:K:99:ASP:N	2.85	0.40
1:O:1819:G:H2'	1:O:1820:G:C4'	2.48	0.40
13:K:118:ALA:O	13:K:120:ARG:N	2.54	0.40
18:P:13:VAL:HG11	18:P:40:VAL:CG1	2.51	0.40
4:A:48:ASP:HA	4:A:49:PRO:HD3	1.82	0.40
1:O:2281:C:C2'	1:O:2282:U:H5'	2.50	0.40
1:O:622:G:P	27:Y:148:GLY:HA3	2.60	0.40
1:O:860:U:H2'	1:O:861:A:C8	2.56	0.40
17:O:80:ASP:OD1	17:O:81:PHE:N	2.54	0.40
1:O:2710:U:H1'	38:O:7786:HOH:O	2.21	0.40
1:O:2906:A:H5'	1:O:2907:C:O4'	2.21	0.40
1:O:2105:C:H2'	1:O:2106:C:C6	2.56	0.40
14:L:126:SER:O	14:L:127:GLU:C	2.57	0.40
15:M:67:VAL:HB	15:M:97:ILE:HG23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:3:91:GLN:O	31:3:92:GLU:HB2	2.21	0.40
16:N:108:SER:HA	16:N:109:PRO:HD3	1.79	0.40
15:M:164:THR:HG23	15:M:166:ALA:H	1.85	0.40
12:J:74:ARG:HH12	12:J:76:ASP:CB	2.34	0.40
9:F:57:GLU:O	9:F:61:MET:HG3	2.22	0.40
11:H:27:LYS:N	11:H:59:HIS:HD2	2.14	0.40
7:D:13:MET:CA	7:D:137:PRO:HG2	2.51	0.40
1:0:475:G:C5'	6:C:73:LEU:HD23	2.52	0.40
1:0:694:A:C2'	1:0:695:C:H5'	2.51	0.40
5:B:24:PRO:CG	5:B:204:GLY:HA2	2.51	0.40
5:B:313:PRO:O	5:B:314:ALA:C	2.59	0.40
1:0:1375:A:H2'	1:0:1376:G:H5'	2.03	0.40
8:E:154:ILE:HG13	8:E:156:ASP:OD1	2.21	0.40
1:0:2089:A:O2'	1:0:2090:G:H5'	2.21	0.40
1:0:318:C:H5'	1:0:339:A:C2	2.57	0.40
1:0:581:G:O2'	1:0:582:C:H5'	2.21	0.40
5:B:87:TYR:CE2	5:B:96:PRO:HG3	2.56	0.40
1:0:1783:A:O2'	1:0:1784:U:H5'	2.20	0.40
5:B:223:ARG:HG3	5:B:232:TRP:O	2.22	0.40
1:0:2729:C:O2'	1:0:2730:G:H5'	2.22	0.40
9:F:39:SER:HB3	9:F:45:ALA:HB2	2.04	0.40
1:0:536:A:H3'	38:0:5321:HOH:O	2.21	0.40
1:0:1556:G:O2'	1:0:1557:G:H5'	2.21	0.40
16:N:139:TRP:CZ2	16:N:176:ARG:NH1	2.90	0.40
15:M:24:GLN:HE22	15:M:27:ARG:HH11	1.67	0.40
5:B:162:MET:HE1	5:B:308:LEU:HD21	2.03	0.40
7:D:57:THR:CG2	7:D:63:ILE:HG22	2.49	0.40
4:A:109:GLU:HG2	4:A:116:GLY:H	1.85	0.40
1:0:68:U:O2'	1:0:69:A:H5''	2.22	0.40
26:X:12:ILE:HD13	26:X:36:HIS:CE1	2.56	0.40
1:0:1311:G:C2	1:0:1312:G:C8	3.09	0.40
9:F:26:THR:CG2	9:F:102:GLY:HA3	2.52	0.40
1:0:1391:G:H2'	1:0:1392:A:H5'	2.03	0.40
18:P:98:ILE:HD12	18:P:102:ARG:NE	2.37	0.40
4:A:125:ASN:HB3	4:A:158:VAL:HG12	2.03	0.40
1:0:1388:U:H2'	1:0:1389:G:O4'	2.22	0.40
1:0:1066:U:H2'	1:0:1067:A:C8	2.57	0.40
1:0:2667:G:H1'	1:0:2914:A:N3	2.36	0.40
20:R:100:ASP:C	20:R:102:GLN:N	2.74	0.40
6:C:157:LEU:HD11	6:C:194:PHE:HZ	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	235/240 (98%)	205 (87%)	28 (12%)	2 (1%)	21	49
5	B	335/338 (99%)	303 (90%)	27 (8%)	5 (2%)	13	32
6	C	244/246 (99%)	223 (91%)	20 (8%)	1 (0%)	39	69
7	D	134/177 (76%)	94 (70%)	34 (25%)	6 (4%)	3	6
8	E	170/178 (96%)	161 (95%)	7 (4%)	2 (1%)	16	39
9	F	117/120 (98%)	101 (86%)	13 (11%)	3 (3%)	7	16
10	G	25/348 (7%)	24 (96%)	1 (4%)	0	100	100
11	H	156/171 (91%)	144 (92%)	7 (4%)	5 (3%)	5	12
12	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	14	35
13	K	130/132 (98%)	116 (89%)	12 (9%)	2 (2%)	13	32
14	L	141/165 (86%)	118 (84%)	23 (16%)	0	100	100
15	M	192/194 (99%)	178 (93%)	13 (7%)	1 (0%)	34	63
16	N	184/187 (98%)	167 (91%)	12 (6%)	5 (3%)	6	16
17	O	113/116 (97%)	107 (95%)	6 (5%)	0	100	100
18	P	141/149 (95%)	131 (93%)	9 (6%)	1 (1%)	26	55
19	Q	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
20	R	148/155 (96%)	133 (90%)	14 (10%)	1 (1%)	26	55
21	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
22	T	117/120 (98%)	108 (92%)	8 (7%)	1 (1%)	21	49
23	U	51/66 (77%)	47 (92%)	3 (6%)	1 (2%)	9	24
24	V	63/71 (89%)	55 (87%)	7 (11%)	1 (2%)	12	30
25	W	152/154 (99%)	144 (95%)	6 (4%)	2 (1%)	15	37
26	X	80/92 (87%)	72 (90%)	7 (9%)	1 (1%)	15	37
27	Y	140/241 (58%)	134 (96%)	6 (4%)	0	100	100
28	Z	71/83 (86%)	57 (80%)	9 (13%)	5 (7%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	1	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
30	2	42/50 (84%)	40 (95%)	2 (5%)	0	100	100
31	3	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
32	I	68/162 (42%)	55 (81%)	11 (16%)	2 (3%)	6	14
All	All	3705/4430 (84%)	3348 (90%)	308 (8%)	49 (1%)	15	37

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	D	27	ILE
7	D	137	PRO
7	D	173	GLU
9	F	101	ALA
11	H	140	VAL
11	H	166	SER
11	H	168	ALA
16	N	154	LEU
28	Z	42	CYS
28	Z	81	ARG
5	B	34	GLY
6	C	8	LEU
7	D	65	GLU
7	D	138	GLY
12	J	5	GLU
13	K	111	GLY
16	N	139	TRP
24	V	43	PRO
4	A	34	ASP
5	B	139	ASP
5	B	184	ASP
11	H	16	ARG
12	J	89	HIS
16	N	68	GLU
16	N	164	ASP
18	P	116	SER
25	W	49	ASN
25	W	77	ALA
26	X	87	ALA
28	Z	41	ASN
32	I	76	ALA
32	I	133	THR

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Mol	Chain	Res	Type
5	B	185	GLY
8	E	17	HIS
9	F	44	SER
13	K	119	GLN
28	Z	43	GLY
4	A	37	VAL
7	D	28	GLY
23	U	7	ASP
28	Z	28	GLU
8	E	44	GLY
9	F	64	PRO
11	H	79	GLU
22	T	53	GLY
5	B	2	GLN
15	M	88	VAL
20	R	81	PRO
16	N	74	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	179/182 (98%)	167 (93%)	12 (7%)	20	44
5	B	282/283 (100%)	263 (93%)	19 (7%)	20	44
6	C	193/193 (100%)	180 (93%)	13 (7%)	20	44
7	D	117/148 (79%)	112 (96%)	5 (4%)	35	66
8	E	152/156 (97%)	148 (97%)	4 (3%)	54	83
9	F	93/94 (99%)	92 (99%)	1 (1%)	80	94
10	G	27/283 (10%)	27 (100%)	0	100	100
11	H	132/138 (96%)	126 (96%)	6 (4%)	34	65
12	J	118/121 (98%)	109 (92%)	9 (8%)	16	37
13	K	106/106 (100%)	103 (97%)	3 (3%)	51	81
14	L	113/127 (89%)	108 (96%)	5 (4%)	35	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	M	158/158 (100%)	151 (96%)	7 (4%)	35	65
16	N	149/150 (99%)	145 (97%)	4 (3%)	52	82
17	O	93/94 (99%)	92 (99%)	1 (1%)	80	94
18	P	113/117 (97%)	109 (96%)	4 (4%)	43	74
19	Q	79/80 (99%)	76 (96%)	3 (4%)	40	71
20	R	117/122 (96%)	114 (97%)	3 (3%)	54	83
21	S	71/74 (96%)	69 (97%)	2 (3%)	51	81
22	T	105/106 (99%)	98 (93%)	7 (7%)	20	44
23	U	44/52 (85%)	44 (100%)	0	100	100
24	V	51/57 (90%)	51 (100%)	0	100	100
25	W	130/130 (100%)	123 (95%)	7 (5%)	27	56
26	X	66/74 (89%)	62 (94%)	4 (6%)	23	49
27	Y	120/196 (61%)	116 (97%)	4 (3%)	45	76
28	Z	60/68 (88%)	59 (98%)	1 (2%)	68	90
29	1	46/47 (98%)	46 (100%)	0	100	100
30	2	42/46 (91%)	41 (98%)	1 (2%)	57	85
31	3	79/79 (100%)	79 (100%)	0	100	100
32	I	58/130 (45%)	58 (100%)	0	100	100
All	All	3093/3611 (86%)	2968 (96%)	125 (4%)	38	69

All (125) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	3	ARG
4	A	33	GLU
4	A	36	ASP
4	A	66	ARG
4	A	69	LEU
4	A	78	ASP
4	A	94	LEU
4	A	120	ARG
4	A	131	HIS
4	A	153	ARG
4	A	206	ARG
4	A	217	ARG
5	B	7	ARG

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Mol	Chain	Res	Type
5	B	11	LEU
5	B	27	ASN
5	B	49	THR
5	B	63	GLU
5	B	97	LEU
5	B	140	LEU
5	B	162	MET
5	B	190	MET
5	B	195	ARG
5	B	234	ARG
5	B	245	SER
5	B	251	VAL
5	B	254	GLN
5	B	256	GLN
5	B	257	THR
5	B	264	GLU
5	B	304	PRO
5	B	307	ARG
6	C	2	GLN
6	C	27	ARG
6	C	76	ARG
6	C	91	PRO
6	C	94	THR
6	C	115	LEU
6	C	136	VAL
6	C	187	ARG
6	C	214	THR
6	C	223	LEU
6	C	234	VAL
6	C	236	THR
6	C	240	LEU
7	D	24	HIS
7	D	61	PHE
7	D	133	ASN
7	D	136	ARG
7	D	137	PRO
8	E	7	ILE
8	E	15	GLN
8	E	102	VAL
8	E	164	ASP
9	F	46	GLU
11	H	30	GLN

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Mol	Chain	Res	Type
11	H	84	LYS
11	H	88	ARG
11	H	111	ASP
11	H	132	GLN
11	H	154	TYR
12	J	45	VAL
12	J	46	ILE
12	J	52	GLN
12	J	74	ARG
12	J	79	PHE
12	J	107	ASN
12	J	112	ASP
12	J	127	ILE
12	J	131	THR
13	K	7	ASP
13	K	10	GLN
13	K	49	LEU
14	L	30	ARG
14	L	35	ARG
14	L	80	ASP
14	L	102	ASP
14	L	117	GLU
15	M	46	LEU
15	M	68	ARG
15	M	81	ARG
15	M	93	ARG
15	M	99	ARG
15	M	116	ASN
15	M	164	THR
16	N	26	LEU
16	N	47	LEU
16	N	50	LEU
16	N	152	GLU
17	O	43	VAL
18	P	21	VAL
18	P	52	LYS
18	P	91	LYS
18	P	98	ILE
19	Q	11	ARG
19	Q	16	ASN
19	Q	57	ASP
20	R	39	THR

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Mol	Chain	Res	Type
20	R	82	GLU
20	R	132	ARG
21	S	71	ASP
21	S	80	ARG
22	T	19	ARG
22	T	23	VAL
22	T	39	ASN
22	T	73	HIS
22	T	75	GLU
22	T	96	VAL
22	T	112	LEU
25	W	26	ILE
25	W	45	VAL
25	W	52	VAL
25	W	73	LEU
25	W	142	ASP
25	W	146	ILE
25	W	154	ARG
26	X	15	ARG
26	X	27	ASP
26	X	46	ASP
26	X	72	VAL
27	Y	154	ARG
27	Y	163	THR
27	Y	189	ASN
27	Y	203	VAL
28	Z	13	ARG
30	2	18	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	29	HIS
4	A	47	HIS
4	A	92	ASN
4	A	125	ASN
4	A	127	GLN
4	A	199	HIS
5	B	27	ASN
5	B	145	HIS
5	B	238	ASN
5	B	256	GLN

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Mol	Chain	Res	Type
5	B	260	HIS
5	B	320	GLN
5	B	332	ASN
6	C	2	GLN
6	C	39	GLN
6	C	129	HIS
6	C	163	HIS
7	D	47	GLN
7	D	97	GLN
7	D	103	ASN
7	D	133	ASN
8	E	74	HIS
8	E	106	ASN
8	E	119	HIS
8	E	143	GLN
10	G	64	ASN
11	H	31	HIS
11	H	56	GLN
11	H	59	HIS
11	H	70	ASN
11	H	132	GLN
12	J	52	GLN
12	J	107	ASN
13	K	10	GLN
14	L	18	HIS
14	L	41	HIS
14	L	58	GLN
15	M	24	GLN
15	M	58	GLN
15	M	137	ASN
15	M	143	ASN
15	M	170	ASN
16	N	40	ASN
16	N	107	ASN
18	P	50	GLN
18	P	66	GLN
18	P	118	GLN
19	Q	16	ASN
19	Q	40	HIS
20	R	61	GLN
20	R	94	ASN
20	R	98	ASN

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Mol	Chain	Res	Type
20	R	113	HIS
20	R	117	HIS
20	R	123	GLN
21	S	25	GLN
21	S	53	ASN
22	T	39	ASN
22	T	73	HIS
23	U	39	ASN
23	U	48	ASN
24	V	60	GLN
25	W	12	ASN
25	W	27	HIS
25	W	28	HIS
25	W	87	HIS
25	W	110	GLN
25	W	119	HIS
25	W	125	HIS
25	W	141	HIS
26	X	23	HIS
26	X	36	HIS
27	Y	133	HIS
27	Y	134	HIS
27	Y	149	GLN
27	Y	189	ASN
29	1	8	GLN
29	1	16	HIS
29	1	28	HIS
30	2	16	ASN
30	2	18	ASN
30	2	41	HIS
30	2	45	ASN
31	3	15	ASN
31	3	30	GLN
31	3	48	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2745/2922 (93%)	237 (8%)	34 (1%)
2	9	121/122 (99%)	17 (14%)	1 (0%)
3	4	1/8 (12%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	2867/3052 (93%)	254 (8%)	35 (1%)

All (254) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	31	C
1	0	60	A
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	141	C
1	0	151	A
1	0	166	A
1	0	186	A
1	0	191	A
1	0	192	A
1	0	200	U
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	331	A
1	0	336	G
1	0	337	A
1	0	345	G
1	0	358	G
1	0	381	G
1	0	397	A
1	0	417	G

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Mol	Chain	Res	Type
1	0	461	C
1	0	487	G
1	0	498	A
1	0	510	U
1	0	511	A
1	0	514	G
1	0	516	A
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G
1	0	553	G
1	0	559	U
1	0	581	G
1	0	588	G
1	0	604	G
1	0	605	C
1	0	620	A
1	0	630	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	688	A
1	0	698	A
1	0	701	U
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	871	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	884	C

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Mol	Chain	Res	Type
1	0	885	G
1	0	898	G
1	0	905	C
1	0	920	C
1	0	921	G
1	0	923	A
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1088	A
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1120	U
1	0	1130	U
1	0	1137	G
1	0	1164	U
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1193	A
1	0	1206	U
1	0	1208	C
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1289	C
1	0	1342	C
1	0	1353	C
1	0	1360	C

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Mol	Chain	Res	Type
1	0	1377	C
1	0	1407	A
1	0	1451	C
1	0	1474	C
1	0	1485	A
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1528	A
1	0	1563	G
1	0	1564	C
1	0	1592	G
1	0	1625	U
1	0	1626	A
1	0	1633	C
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1731	C
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U
1	0	1919	A
1	0	1942	A
1	0	1971	G
1	0	1973	A
1	0	1978	A

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Mol	Chain	Res	Type
1	0	1980	U
1	0	1996	U
1	0	2004	U
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2332	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2467	A
1	0	2469	A
1	0	2476	C
1	0	2480	G
1	0	2483	A
1	0	2507	G
1	0	2509	A
1	0	2511	A
1	0	2533	C
1	0	2537	G
1	0	2541	U

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Mol	Chain	Res	Type
1	0	2542	C
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2637	A
1	0	2649	A
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2719	A
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2792	A
1	0	2800	A
1	0	2811	A
1	0	2825	C
1	0	2850	C
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U
2	9	3007	G
2	9	3014	G
2	9	3022	G
2	9	3023	U
2	9	3024	U
2	9	3025	G
2	9	3040	C
2	9	3041	C
2	9	3043	G

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Mol	Chain	Res	Type
2	9	3044	A
2	9	3052	A
2	9	3057	A
2	9	3066	G
2	9	3077	A
2	9	3114	G
2	9	3122	C

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	69	A
1	0	129	A
1	0	169	A
1	0	338	C
1	0	603	A
1	0	604	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	869	G
1	0	871	G
1	0	877	G
1	0	898	G
1	0	1080	C
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1377	C
1	0	1450	C
1	0	1506	U
1	0	1563	G
1	0	1692	C
1	0	1730	G
1	0	1856	C
1	0	1942	A
1	0	1979	G
1	0	2011	A
1	0	2313	C
1	0	2467	A
1	0	2536	C
1	0	2541	U

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Mol	Chain	Res	Type
1	0	2649	A
1	0	2718	C
1	0	2791	U
2	9	3065	A

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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$
1	OMU	0	2587	1	12,22,23	0.98	1 (8%)	19,31,34	3.19	2 (10%)
1	OMG	0	2588	1,3	17,26,27	1.09	1 (5%)	21,38,41	2.50	3 (14%)
1	UR3	0	2619	1	12,22,23	0.96	0	16,32,35	0.77	0
1	PSU	0	2621	1	13,21,22	1.56	2 (15%)	18,30,33	6.09	3 (16%)
1	1MA	0	628	1	14,25,26	1.00	1 (7%)	15,37,40	1.21	1 (6%)
3	5AA	4	76	1,3	16,26,27	0.65	0	15,38,41	1.22	2 (13%)

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
1	OMU	0	2587	1	-	0/5/27/28	0/2/2/2
1	OMG	0	2588	1,3	-	0/5/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/3/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2
1	1MA	0	628	1	-	0/3/25/26	0/3/3/3
3	5AA	4	76	1,3	-	0/7/29/30	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C5-C1'	-4.49	1.48	1.52
1	0	2587	OMU	C4-N3	2.32	1.37	1.33
1	0	2621	PSU	C4-N3	2.75	1.38	1.33
1	0	628	1MA	C6-N6	2.78	1.34	1.29
1	0	2588	OMG	C6-N1	3.37	1.39	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	N1-C2-N3	-21.29	114.75	128.33
1	0	2588	OMG	C5-C6-N1	-8.61	111.81	123.59
1	0	628	1MA	C2-N3-C4	-3.62	110.80	116.40
1	0	2587	OMU	C5-C4-N3	-3.28	114.70	123.12
1	0	2588	OMG	N3-C2-N1	-2.32	123.91	127.44
3	4	76	5AA	C9-N6-C6	2.13	126.20	119.48
1	0	2621	PSU	C6-N1-C2	2.55	119.57	115.47
3	4	76	5AA	C2-N1-C6	3.58	119.04	111.43
1	0	2588	OMG	C6-N1-C2	6.56	125.05	115.94
1	0	2587	OMU	C4-N3-C2	13.32	127.33	114.14
1	0	2621	PSU	C4-N3-C2	13.97	127.33	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	2	0
1	0	2619	UR3	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 233 ligands modelled in this entry, 233 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.49	34 (1%) 81 81	29, 51, 94, 161	0
2	9	122/122 (100%)	-0.46	4 (3%) 50 50	39, 62, 91, 152	0
3	4	5/8 (62%)	-0.44	0 100 100	41, 43, 47, 47	0
4	A	237/240 (98%)	0.18	10 (4%) 40 39	33, 57, 95, 119	0
5	B	337/338 (99%)	0.05	7 (2%) 67 68	29, 57, 80, 94	0
6	C	246/246 (100%)	-0.07	3 (1%) 81 81	27, 53, 75, 84	0
7	D	140/177 (79%)	2.21	63 (45%) 0 0	58, 101, 127, 137	0
8	E	172/178 (96%)	0.67	15 (8%) 13 10	47, 67, 87, 93	0
9	F	119/120 (99%)	0.96	22 (18%) 2 1	60, 82, 104, 119	0
10	G	29/348 (8%)	1.80	10 (34%) 0 0	65, 90, 102, 105	0
11	H	160/171 (93%)	0.30	8 (5%) 32 31	41, 59, 90, 99	0
12	J	142/145 (97%)	-0.01	1 (0%) 89 90	37, 52, 72, 90	0
13	K	132/132 (100%)	0.04	2 (1%) 76 76	34, 56, 77, 87	0
14	L	145/165 (87%)	0.68	24 (16%) 2 2	30, 72, 118, 132	0
15	M	194/194 (100%)	-0.08	1 (0%) 91 93	34, 50, 67, 74	0
16	N	186/187 (99%)	0.63	20 (10%) 8 6	38, 66, 115, 121	0
17	O	115/116 (99%)	0.13	0 100 100	45, 61, 77, 85	0
18	P	143/149 (95%)	0.29	0 100 100	45, 60, 77, 85	0
19	Q	95/96 (98%)	-0.03	1 (1%) 82 83	40, 48, 60, 75	0
20	R	150/155 (96%)	-0.15	1 (0%) 89 90	37, 48, 68, 75	0
21	S	81/85 (95%)	0.29	3 (3%) 45 45	49, 67, 85, 94	0
22	T	119/120 (99%)	0.75	13 (10%) 7 5	46, 63, 91, 110	0
23	U	53/66 (80%)	0.23	3 (5%) 27 26	43, 57, 74, 85	0
24	V	65/71 (91%)	1.79	23 (35%) 0 0	63, 86, 117, 121	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.04	2 (1%) 79 79	39, 50, 67, 76	0
26	X	82/92 (89%)	0.48	9 (10%) 7 5	45, 59, 77, 95	0
27	Y	142/241 (58%)	0.03	5 (3%) 48 48	30, 49, 71, 86	0
28	Z	73/83 (87%)	0.20	4 (5%) 29 27	44, 63, 77, 97	0
29	1	56/57 (98%)	-0.40	0 100 100	33, 40, 46, 54	0
30	2	46/50 (92%)	0.56	5 (10%) 7 5	41, 65, 97, 109	0
31	3	92/92 (100%)	0.33	3 (3%) 50 50	37, 59, 73, 84	0
32	I	70/162 (43%)	3.69	56 (80%) 0 0	99, 121, 143, 145	0
All	All	6651/7482 (88%)	0.01	352 (5%) 30 28	27, 56, 102, 161	0

All (352) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
24	V	1	THR	12.2
32	I	133	THR	10.4
32	I	71	GLY	10.2
7	D	63	ILE	9.5
32	I	93	GLN	8.7
32	I	96	PHE	8.3
7	D	88	LEU	7.9
32	I	88	GLY	7.8
32	I	113	HIS	7.5
7	D	90	LEU	7.3
7	D	57	THR	7.2
32	I	79	ILE	7.1
32	I	76	ALA	6.9
16	N	166	ALA	6.7
22	T	119	ALA	6.7
24	V	39	ALA	6.7
24	V	40	PRO	6.6
32	I	137	VAL	6.6
7	D	128	LEU	6.5
7	D	69	ILE	6.4
1	0	1173	A	6.3
24	V	38	GLY	6.2
32	I	117	LEU	6.2
32	I	109	ALA	6.2
2	9	3023	U	6.1
30	2	49	GLU	6.1

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Mol	Chain	Res	Type	RSRZ
32	I	97	VAL	6.0
32	I	91	GLU	5.8
7	D	130	VAL	5.8
32	I	102	VAL	5.8
7	D	106	PHE	5.6
24	V	43	PRO	5.6
7	D	93	LEU	5.5
7	D	66	GLY	5.5
2	9	3024	U	5.4
21	S	81	ILE	5.4
16	N	183	ASP	5.3
26	X	88	GLU	5.3
22	T	112	LEU	5.3
7	D	87	ALA	5.2
7	D	18	ILE	5.2
7	D	85	GLN	5.2
9	F	119	ARG	5.2
32	I	98	ALA	5.1
1	0	2237	G	5.1
7	D	64	ARG	5.0
32	I	111	GLN	5.0
7	D	65	GLU	4.9
7	D	84	LEU	4.9
30	2	35	ARG	4.9
7	D	89	PRO	4.9
32	I	118	SER	4.8
1	0	1199	A	4.8
32	I	87	THR	4.8
10	G	27	ILE	4.7
32	I	116	LEU	4.7
14	L	105	TYR	4.7
4	A	37	VAL	4.7
7	D	44	ILE	4.7
14	L	60	GLU	4.6
7	D	56	ARG	4.6
7	D	170	TYR	4.6
7	D	25	MET	4.5
8	E	45	ASP	4.5
7	D	62	ASP	4.5
14	L	80	ASP	4.5
1	0	1198	U	4.4
1	0	1171	A	4.4

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Mol	Chain	Res	Type	RSRZ
7	D	58	VAL	4.4
32	I	77	GLU	4.4
1	0	282	C	4.4
7	D	26	GLY	4.4
7	D	68	PRO	4.4
2	9	3001	U	4.3
24	V	41	GLU	4.2
7	D	83	PHE	4.2
1	0	1172	G	4.1
32	I	85	PHE	4.1
7	D	41	LEU	4.0
1	0	1177	A	4.0
24	V	8	ILE	4.0
27	Y	235	GLU	3.9
32	I	107	GLN	3.9
10	G	23	ILE	3.9
8	E	170	ARG	3.9
7	D	165	PHE	3.9
32	I	95	ASP	3.9
32	I	110	GLU	3.9
31	3	22	VAL	3.8
7	D	27	ILE	3.8
7	D	92	GLU	3.8
14	L	106	VAL	3.8
16	N	147	ILE	3.8
7	D	10	PHE	3.8
16	N	179	LEU	3.8
32	I	89	SER	3.8
1	0	2238	A	3.7
30	2	39	ARG	3.7
7	D	61	PHE	3.7
7	D	86	THR	3.7
9	F	47	LEU	3.7
24	V	3	LEU	3.7
7	D	104	PHE	3.7
9	F	107	ASP	3.7
7	D	129	ASP	3.6
32	I	75	THR	3.6
32	I	135	LEU	3.6
32	I	128	VAL	3.6
7	D	172	VAL	3.6
16	N	165	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
7	D	23	VAL	3.6
32	I	114	PRO	3.6
24	V	52	ALA	3.6
32	I	121	LEU	3.5
1	0	284	C	3.5
32	I	81	ASP	3.5
23	U	47	ARG	3.5
14	L	96	VAL	3.5
22	T	40	VAL	3.5
22	T	42	VAL	3.5
14	L	104	ASP	3.4
9	F	106	ALA	3.4
1	0	735	C	3.4
1	0	970	U	3.4
1	0	1279	U	3.4
1	0	960	G	3.4
7	D	134	LEU	3.3
7	D	166	ILE	3.3
16	N	138	ASP	3.3
32	I	103	ASP	3.3
32	I	139	ILE	3.3
1	0	1951	G	3.3
9	F	17	LEU	3.3
9	F	28	ALA	3.3
26	X	85	VAL	3.3
11	H	45	VAL	3.2
8	E	100	ASP	3.2
14	L	124	ASP	3.2
8	E	5	LEU	3.2
7	D	45	THR	3.2
7	D	17	ARG	3.2
9	F	117	GLU	3.2
27	Y	108	ASP	3.2
9	F	16	ALA	3.2
1	0	1202	A	3.2
14	L	130	ARG	3.2
32	I	106	LYS	3.1
19	Q	95	GLU	3.1
11	H	171	ALA	3.1
23	U	55	ALA	3.1
9	F	90	GLU	3.1
10	G	24	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
7	D	171	ASP	3.1
24	V	37	GLY	3.1
26	X	41	PHE	3.1
32	I	124	ALA	3.0
14	L	100	ALA	3.0
14	L	150	GLN	3.0
6	C	132	ASP	3.0
9	F	108	VAL	3.0
9	F	49	PHE	3.0
22	T	49	GLU	3.0
32	I	105	VAL	3.0
16	N	127	LEU	2.9
7	D	98	PHE	2.9
22	T	116	ASP	2.9
4	A	135	VAL	2.9
24	V	49	LEU	2.9
9	F	100	ASP	2.9
6	C	135	GLU	2.9
15	M	194	ALA	2.9
28	Z	20	ARG	2.9
22	T	1	SER	2.9
11	H	37	GLN	2.9
32	I	104	GLN	2.9
32	I	83	ALA	2.9
16	N	159	TYR	2.9
24	V	45	ARG	2.8
1	0	2239	C	2.8
7	D	24	HIS	2.8
32	I	123	ASN	2.8
9	F	103	GLU	2.8
5	B	128	ILE	2.8
32	I	78	LEU	2.8
9	F	98	VAL	2.8
31	3	62	THR	2.8
7	D	40	ILE	2.8
8	E	3	VAL	2.8
24	V	59	ILE	2.8
8	E	42	VAL	2.8
1	0	1525	G	2.8
14	L	89	PHE	2.8
1	0	1170	U	2.7
14	L	91	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
9	F	109	GLU	2.7
7	D	75	LEU	2.7
16	N	161	GLY	2.7
28	Z	24	ARG	2.7
4	A	237	GLY	2.7
1	0	1950	G	2.7
7	D	54	ALA	2.7
4	A	35	GLY	2.7
10	G	71	LEU	2.7
32	I	72	VAL	2.7
26	X	73	ARG	2.7
7	D	70	GLY	2.7
1	0	138	U	2.6
5	B	119	HIS	2.6
9	F	15	ASP	2.6
32	I	132	CYS	2.6
24	V	36	ALA	2.6
4	A	36	ASP	2.6
9	F	99	THR	2.6
22	T	99	THR	2.6
32	I	140	GLU	2.6
16	N	95	ALA	2.6
14	L	107	LYS	2.6
7	D	43	GLU	2.6
10	G	65	THR	2.5
14	L	123	ASP	2.5
32	I	138	THR	2.5
26	X	71	ARG	2.5
24	V	63	GLU	2.5
32	I	126	LYS	2.5
32	I	73	PRO	2.5
5	B	104	GLU	2.5
4	A	64	ASP	2.5
32	I	108	ILE	2.5
23	U	54	THR	2.5
7	D	107	GLY	2.5
14	L	73	VAL	2.5
7	D	80	ALA	2.5
13	K	132	VAL	2.5
8	E	46	THR	2.5
32	I	119	TYR	2.5
32	I	115	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
7	D	132	VAL	2.5
9	F	118	LEU	2.5
9	F	19	ALA	2.5
2	9	3002	U	2.5
16	N	149	GLU	2.4
32	I	86	GLU	2.4
25	W	79	VAL	2.4
13	K	119	GLN	2.4
11	H	79	GLU	2.4
16	N	155	GLU	2.4
32	I	92	PRO	2.4
22	T	37	GLN	2.4
7	D	11	HIS	2.4
22	T	115	GLU	2.4
24	V	33	VAL	2.4
16	N	185	GLU	2.4
1	0	1200	A	2.4
14	L	140	VAL	2.4
10	G	67	LEU	2.3
21	S	76	GLU	2.3
5	B	181	ILE	2.3
1	0	280	C	2.3
1	0	1180	U	2.3
20	R	7	GLU	2.3
1	0	716	G	2.3
16	N	139	TRP	2.3
12	J	92	GLN	2.3
7	D	59	GLY	2.3
1	0	2250	G	2.3
9	F	44	SER	2.3
24	V	9	ARG	2.3
7	D	67	ASP	2.3
4	A	99	ILE	2.3
8	E	87	PHE	2.3
5	B	183	GLU	2.3
7	D	135	VAL	2.3
24	V	61	GLY	2.3
32	I	84	GLY	2.3
14	L	99	GLU	2.3
27	Y	96	GLU	2.3
24	V	2	VAL	2.3
1	0	1948	G	2.3

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Mol	Chain	Res	Type	RSRZ
9	F	75	ILE	2.3
7	D	91	ALA	2.2
9	F	40	ILE	2.2
1	0	10	U	2.2
10	G	68	GLU	2.2
26	X	7	GLU	2.2
25	W	100	LEU	2.2
30	2	20	ARG	2.2
1	0	272	A	2.2
7	D	53	LYS	2.2
7	D	81	GLU	2.2
11	H	74	ILE	2.2
22	T	117	ASP	2.2
30	2	44	ARG	2.2
26	X	72	VAL	2.2
4	A	31	LYS	2.2
8	E	1	PRO	2.2
8	E	53	GLU	2.2
10	G	26	MET	2.2
1	0	285	A	2.2
16	N	160	SER	2.2
24	V	10	ASP	2.2
16	N	150	TYR	2.2
22	T	35	TYR	2.2
7	D	71	ALA	2.2
28	Z	25	ARG	2.2
4	A	103	VAL	2.2
8	E	108	LEU	2.2
1	0	1169	U	2.2
10	G	70	ALA	2.2
7	D	73	VAL	2.2
14	L	97	VAL	2.2
14	L	133	VAL	2.2
24	V	53	ILE	2.1
11	H	83	TYR	2.1
4	A	133	ARG	2.1
14	L	149	ARG	2.1
14	L	93	VAL	2.1
16	N	180	LEU	2.1
7	D	105	SER	2.1
32	I	136	GLY	2.1
24	V	31	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
26	X	80	GLU	2.1
6	C	61	PHE	2.1
16	N	162	ASP	2.1
8	E	99	GLY	2.1
11	H	162	ARG	2.1
16	N	184	ILE	2.1
31	3	92	GLU	2.1
1	0	2344	G	2.1
8	E	86	VAL	2.1
27	Y	95	THR	2.1
32	I	74	PRO	2.1
26	X	74	ALA	2.1
32	I	100	LEU	2.1
7	D	51	ARG	2.1
22	T	103	LEU	2.1
8	E	47	VAL	2.1
32	I	90	GLY	2.1
11	H	50	ILE	2.0
14	L	59	GLU	2.0
24	V	7	GLU	2.0
14	L	62	ALA	2.0
14	L	120	LEU	2.0
16	N	152	GLU	2.0
1	0	2249	G	2.0
5	B	92	TYR	2.0
10	G	63	ARG	2.0
27	Y	236	VAL	2.0
28	Z	80	ARG	2.0
8	E	10	ASP	2.0
1	0	1130	U	2.0
21	S	77	VAL	2.0
5	B	116	PRO	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	OMG	0	2588	24/25	0.98	0.13	-	32,36,39,40	0
3	5AA	4	76	24/25	0.98	0.14	-	38,44,48,48	0
1	1MA	0	628	23/24	0.99	0.15	-	29,32,34,36	0
1	UR3	0	2619	21/22	0.99	0.15	-	32,39,41,42	0
1	PSU	0	2621	20/21	0.99	0.14	-	30,33,37,38	0
1	OMU	0	2587	21/22	0.99	0.13	-	35,37,39,42	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
36	CL	0	9315	1/1	0.93	0.41	65.34	84,84,84,84	0
35	NA	0	9174	1/1	0.86	0.89	41.97	64,64,64,64	0
35	NA	0	9171	1/1	0.73	0.41	31.45	64,64,64,64	0
35	NA	R	9186	1/1	0.30	0.75	22.47	84,84,84,84	0
35	NA	0	9156	1/1	0.95	0.45	21.62	51,51,51,51	0
35	NA	0	9177	1/1	0.80	0.41	18.69	73,73,73,73	0
35	NA	0	9182	1/1	0.73	0.45	18.48	84,84,84,84	0
35	NA	L	9180	1/1	0.93	0.52	17.97	72,72,72,72	0
35	NA	0	9150	1/1	0.88	0.29	15.99	48,48,48,48	0
35	NA	0	9135	1/1	0.93	0.28	15.22	50,50,50,50	0
35	NA	0	9125	1/1	0.93	0.26	15.15	69,69,69,69	0
35	NA	0	9172	1/1	0.93	0.38	12.80	61,61,61,61	0
35	NA	0	9155	1/1	0.92	0.54	12.49	78,78,78,78	0
33	MG	0	8060	1/1	0.99	0.31	11.35	49,49,49,49	0
35	NA	0	9161	1/1	0.90	0.30	7.75	56,56,56,56	0
35	NA	0	9121	1/1	0.96	0.33	7.27	58,58,58,58	0
35	NA	0	9178	1/1	0.97	0.21	6.37	57,57,57,57	0
35	NA	0	9162	1/1	0.95	0.23	6.02	72,72,72,72	0
34	K	0	9001	1/1	0.96	0.25	5.43	74,74,74,74	0
35	NA	0	9129	1/1	0.69	0.17	4.72	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9168	1/1	0.84	0.15	3.77	56,56,56,56	0
35	NA	0	9173	1/1	0.90	0.24	3.45	58,58,58,58	0
35	NA	0	9102	1/1	0.96	0.16	3.26	44,44,44,44	0
33	MG	0	8053	1/1	0.98	0.17	3.13	58,58,58,58	0
35	NA	Q	9148	1/1	0.93	0.29	2.96	43,43,43,43	0
35	NA	M	9147	1/1	0.98	0.21	2.31	33,33,33,33	0
35	NA	0	9126	1/1	0.85	0.18	2.16	44,44,44,44	0
35	NA	0	9176	1/1	0.97	0.18	1.84	42,42,42,42	0
33	MG	0	8080	1/1	0.95	0.15	1.73	46,46,46,46	0
36	CL	0	9305	1/1	0.85	0.18	1.60	71,71,71,71	0
33	MG	0	8054	1/1	0.91	0.15	1.47	39,39,39,39	0
33	MG	0	8013	1/1	0.98	0.19	1.45	41,41,41,41	0
35	NA	0	9110	1/1	0.92	0.16	1.29	38,38,38,38	0
33	MG	A	8065	1/1	0.98	0.21	1.22	52,52,52,52	0
33	MG	0	8038	1/1	0.99	0.16	1.06	26,26,26,26	0
33	MG	0	8012	1/1	0.97	0.16	1.04	32,32,32,32	0
35	NA	0	9124	1/1	0.86	0.17	0.83	67,67,67,67	0
36	CL	0	9316	1/1	0.96	0.16	0.62	61,61,61,61	0
33	MG	0	8018	1/1	0.99	0.15	0.47	47,47,47,47	0
36	CL	O	9308	1/1	0.97	0.22	0.40	81,81,81,81	0
35	NA	0	9103	1/1	0.97	0.15	0.35	39,39,39,39	0
35	NA	0	9165	1/1	0.93	0.21	0.22	42,42,42,42	0
35	NA	9	9183	1/1	0.89	0.13	-0.23	49,49,49,49	0
35	NA	A	9145	1/1	0.96	0.17	-0.28	45,45,45,45	0
36	CL	0	9313	1/1	0.98	0.14	-0.28	61,61,61,61	0
33	MG	0	8044	1/1	0.94	0.12	-0.38	49,49,49,49	0
35	NA	R	9137	1/1	0.85	0.12	-0.46	50,50,50,50	0
36	CL	L	9310	1/1	0.98	0.15	-0.48	61,61,61,61	0
35	NA	H	9109	1/1	0.95	0.13	-0.60	36,36,36,36	0
35	NA	C	9104	1/1	0.89	0.15	-0.62	41,41,41,41	0
33	MG	B	8055	1/1	0.98	0.14	-0.67	52,52,52,52	0
36	CL	M	9318	1/1	0.98	0.15	-0.78	50,50,50,50	0
33	MG	0	8077	1/1	0.99	0.13	-0.82	35,35,35,35	0
35	NA	0	9123	1/1	0.96	0.17	-0.86	43,43,43,43	0
33	MG	0	8057	1/1	0.95	0.14	-0.93	45,45,45,45	0
35	NA	0	9166	1/1	0.84	0.11	-0.96	68,68,68,68	0
35	NA	0	9133	1/1	0.92	0.11	-1.00	32,32,32,32	0
33	MG	0	8107	1/1	0.98	0.09	-1.06	38,38,38,38	0
35	NA	0	9144	1/1	0.97	0.10	-1.08	27,27,27,27	0
33	MG	0	8033	1/1	0.99	0.13	-1.11	32,32,32,32	0
36	CL	J	9321	1/1	0.97	0.13	-1.12	54,54,54,54	0
35	NA	0	9114	1/1	0.96	0.12	-1.18	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
37	CD	Z	9203	1/1	0.99	0.09	-1.21	68,68,68,68	0
37	CD	U	9201	1/1	0.99	0.09	-1.21	69,69,69,69	0
33	MG	0	8017	1/1	0.98	0.10	-1.25	33,33,33,33	0
33	MG	0	8064	1/1	0.96	0.12	-1.27	33,33,33,33	0
36	CL	B	9319	1/1	0.99	0.14	-1.37	60,60,60,60	0
35	NA	0	9117	1/1	0.92	0.11	-1.44	46,46,46,46	0
33	MG	0	8015	1/1	0.99	0.11	-1.48	31,31,31,31	0
33	MG	0	8086	1/1	0.97	0.06	-1.61	47,47,47,47	0
35	NA	0	9139	1/1	0.99	0.13	-1.75	22,22,22,22	0
33	MG	0	8058	1/1	0.98	0.12	-1.76	57,57,57,57	0
33	MG	0	8074	1/1	0.99	0.09	-1.82	40,40,40,40	0
33	MG	0	8101	1/1	0.92	0.11	-1.86	74,74,74,74	0
36	CL	3	9304	1/1	0.93	0.15	-1.96	70,70,70,70	0
33	MG	T	8073	1/1	0.90	0.09	-1.97	66,66,66,66	0
36	CL	K	9312	1/1	0.97	0.10	-1.98	55,55,55,55	0
37	CD	1	9202	1/1	1.00	0.05	-2.07	68,68,68,68	0
33	MG	0	8112	1/1	0.95	0.11	-2.17	47,47,47,47	0
35	NA	J	9146	1/1	0.98	0.10	-2.22	35,35,35,35	0
33	MG	0	8056	1/1	0.97	0.12	-2.42	51,51,51,51	0
35	NA	0	9127	1/1	0.95	0.10	-2.44	35,35,35,35	0
33	MG	0	8070	1/1	0.98	0.04	-2.47	45,45,45,45	0
33	MG	0	8062	1/1	0.96	0.10	-2.66	57,57,57,57	0
33	MG	0	8003	1/1	0.99	0.14	-2.68	40,40,40,40	0
33	MG	0	8108	1/1	0.97	0.10	-2.71	75,75,75,75	0
33	MG	0	8008	1/1	0.99	0.08	-2.82	37,37,37,37	0
33	MG	3	8078	1/1	0.93	0.05	-2.89	55,55,55,55	0
33	MG	0	8010	1/1	0.99	0.11	-2.99	29,29,29,29	0
35	NA	0	9131	1/1	0.97	0.08	-3.01	36,36,36,36	0
33	MG	0	8020	1/1	0.99	0.12	-3.27	24,24,24,24	0
33	MG	0	8096	1/1	0.96	0.07	-3.33	51,51,51,51	0
35	NA	R	9138	1/1	0.91	0.06	-3.47	61,61,61,61	0
35	NA	0	9153	1/1	0.98	0.10	-3.56	25,25,25,25	0
35	NA	0	9132	1/1	0.94	0.09	-3.71	35,35,35,35	0
33	MG	0	8001	1/1	0.99	0.10	-3.74	38,38,38,38	0
33	MG	0	8019	1/1	0.99	0.09	-3.95	38,38,38,38	0
33	MG	0	8004	1/1	0.98	0.05	-3.97	27,27,27,27	0
33	MG	0	8091	1/1	0.99	0.07	-4.38	57,57,57,57	0
33	MG	0	8007	1/1	0.99	0.07	-4.69	24,24,24,24	0
33	MG	0	8032	1/1	0.98	0.05	-4.78	35,35,35,35	0
33	MG	0	8022	1/1	0.98	0.07	-4.85	35,35,35,35	0
33	MG	0	8084	1/1	0.94	0.10	-5.05	51,51,51,51	0
33	MG	0	8067	1/1	0.98	0.09	-5.20	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	MG	0	8118	1/1	0.99	0.09	-5.30	40,40,40,40	0
34	K	0	9002	1/1	0.98	0.08	-5.34	54,54,54,54	0
33	MG	0	8006	1/1	0.99	0.05	-5.51	33,33,33,33	0
33	MG	Y	8109	1/1	0.99	0.09	-5.73	39,39,39,39	0
35	NA	0	9120	1/1	0.99	0.10	-5.81	43,43,43,43	0
35	NA	0	9105	1/1	0.97	0.08	-6.61	39,39,39,39	0
33	MG	0	8035	1/1	0.98	0.07	-6.80	51,51,51,51	0
35	NA	0	9143	1/1	0.98	0.07	-8.25	36,36,36,36	0
33	MG	0	8002	1/1	0.99	0.05	-8.54	39,39,39,39	0
33	MG	0	8110	1/1	0.99	0.07	-10.22	40,40,40,40	0
33	MG	9	8052	1/1	0.98	0.05	-12.56	47,47,47,47	0
33	MG	0	8023	1/1	0.98	0.18	-	48,48,48,48	0
33	MG	0	8029	1/1	0.99	0.17	-	36,36,36,36	0
33	MG	0	8117	1/1	0.98	0.10	-	40,40,40,40	0
35	NA	0	9185	1/1	0.90	0.65	-	54,54,54,54	0
33	MG	0	8102	1/1	0.97	0.14	-	67,67,67,67	0
33	MG	0	8104	1/1	0.96	0.21	-	73,73,73,73	0
35	NA	0	9163	1/1	0.91	0.41	-	63,63,63,63	0
35	NA	0	9128	1/1	0.97	0.07	-	35,35,35,35	0
33	MG	0	8094	1/1	0.95	0.12	-	86,86,86,86	0
33	MG	0	8089	1/1	0.92	0.09	-	60,60,60,60	0
33	MG	0	8011	1/1	0.98	0.16	-	23,23,23,23	0
35	NA	0	9152	1/1	0.86	0.41	-	65,65,65,65	0
35	NA	0	9136	1/1	0.98	0.07	-	56,56,56,56	0
35	NA	0	9184	1/1	0.94	0.53	-	96,96,96,96	0
36	CL	0	9322	1/1	0.83	0.54	-	92,92,92,92	0
33	MG	9	8095	1/1	0.85	0.14	-	75,75,75,75	0
33	MG	0	8100	1/1	0.99	0.18	-	82,82,82,82	0
37	CD	3	9204	1/1	0.95	0.09	-	66,66,66,66	0
35	NA	0	9149	1/1	0.90	0.14	-	42,42,42,42	0
33	MG	0	8043	1/1	0.91	0.08	-	53,53,53,53	0
33	MG	0	8082	1/1	0.86	0.20	-	65,65,65,65	0
33	MG	0	8114	1/1	0.94	0.18	-	56,56,56,56	0
35	NA	0	9160	1/1	0.94	0.33	-	49,49,49,49	0
35	NA	0	9181	1/1	0.95	0.12	-	48,48,48,48	0
33	MG	0	8016	1/1	0.98	0.21	-	44,44,44,44	0
33	MG	0	8045	1/1	0.97	0.11	-	62,62,62,62	0
33	MG	0	8115	1/1	0.96	0.12	-	49,49,49,49	0
34	K	0	9003	1/1	0.90	0.13	-	66,66,66,66	0
33	MG	0	8093	1/1	0.84	0.11	-	52,52,52,52	0
33	MG	0	8081	1/1	0.96	0.18	-	54,54,54,54	0
35	NA	0	9101	1/1	0.92	0.21	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9167	1/1	0.93	0.08	-	47,47,47,47	0
33	MG	0	8090	1/1	0.76	0.60	-	69,69,69,69	0
33	MG	0	8088	1/1	0.93	0.06	-	36,36,36,36	0
36	CL	0	9317	1/1	0.97	0.08	-	64,64,64,64	0
36	CL	0	9311	1/1	0.99	0.09	-	52,52,52,52	0
36	CL	J	9302	1/1	0.94	0.06	-	61,61,61,61	0
35	NA	0	9164	1/1	0.92	0.23	-	55,55,55,55	0
35	NA	0	9106	1/1	0.95	0.80	-	51,51,51,51	0
33	MG	0	8026	1/1	0.99	0.13	-	31,31,31,31	0
33	MG	0	8009	1/1	0.99	0.11	-	35,35,35,35	0
35	NA	0	9157	1/1	0.95	0.09	-	69,69,69,69	0
33	MG	0	8014	1/1	0.95	0.11	-	41,41,41,41	0
33	MG	0	8042	1/1	0.94	0.08	-	39,39,39,39	0
35	NA	0	9113	1/1	0.94	0.16	-	66,66,66,66	0
36	CL	R	9306	1/1	0.96	0.12	-	48,48,48,48	0
33	MG	0	8025	1/1	0.99	0.11	-	35,35,35,35	0
33	MG	0	8027	1/1	0.95	0.13	-	55,55,55,55	0
33	MG	0	8036	1/1	0.99	0.13	-	35,35,35,35	0
33	MG	0	8103	1/1	0.97	0.11	-	81,81,81,81	0
35	NA	0	9130	1/1	0.98	0.08	-	44,44,44,44	0
36	CL	J	9301	1/1	0.98	0.19	-	73,73,73,73	0
33	MG	0	8113	1/1	0.96	0.12	-	45,45,45,45	0
33	MG	0	8051	1/1	0.96	0.07	-	61,61,61,61	0
33	MG	0	8034	1/1	0.98	0.10	-	32,32,32,32	0
33	MG	0	8068	1/1	0.96	0.08	-	59,59,59,59	0
33	MG	0	8021	1/1	0.99	0.17	-	30,30,30,30	0
35	NA	0	9154	1/1	0.97	0.19	-	38,38,38,38	0
33	MG	0	8111	1/1	0.94	0.15	-	77,77,77,77	0
33	MG	0	8031	1/1	1.00	0.08	-	37,37,37,37	0
35	NA	0	9175	1/1	0.97	0.45	-	56,56,56,56	0
33	MG	0	8071	1/1	0.94	0.13	-	72,72,72,72	0
36	CL	0	9320	1/1	0.96	0.11	-	48,48,48,48	0
36	CL	N	9307	1/1	0.94	0.20	-	66,66,66,66	0
35	NA	0	9111	1/1	0.92	0.11	-	59,59,59,59	0
35	NA	0	9169	1/1	0.93	0.38	-	79,79,79,79	0
33	MG	K	8069	1/1	0.84	0.15	-	49,49,49,49	0
33	MG	0	8075	1/1	0.96	0.06	-	43,43,43,43	0
35	NA	0	9159	1/1	0.94	0.23	-	56,56,56,56	0
35	NA	0	9108	1/1	0.97	0.09	-	61,61,61,61	0
33	MG	0	8116	1/1	0.97	0.06	-	47,47,47,47	0
33	MG	0	8085	1/1	0.80	0.24	-	74,74,74,74	0
36	CL	A	9309	1/1	0.89	0.19	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	MG	0	8040	1/1	0.97	0.18	-	52,52,52,52	0
35	NA	0	9158	1/1	0.90	0.59	-	84,84,84,84	0
33	MG	0	8049	1/1	0.87	0.29	-	80,80,80,80	0
33	MG	0	8106	1/1	0.91	0.08	-	63,63,63,63	0
36	CL	0	9303	1/1	0.94	0.13	-	64,64,64,64	0
33	MG	0	8076	1/1	0.93	0.06	-	70,70,70,70	0
36	CL	0	9314	1/1	0.97	0.07	-	53,53,53,53	0
33	MG	0	8092	1/1	0.72	0.66	-	115,115,115,115	0
35	NA	S	9112	1/1	0.86	0.51	-	75,75,75,75	0
35	NA	0	9141	1/1	0.96	0.07	-	47,47,47,47	0
35	NA	0	9142	1/1	0.91	0.17	-	53,53,53,53	0
33	MG	0	8046	1/1	0.96	0.09	-	54,54,54,54	0
33	MG	0	8028	1/1	0.97	0.12	-	44,44,44,44	0
33	MG	0	8059	1/1	0.96	0.07	-	44,44,44,44	0
33	MG	0	8005	1/1	1.00	0.14	-	37,37,37,37	0
33	MG	A	8066	1/1	0.92	0.05	-	66,66,66,66	0
35	NA	0	9140	1/1	0.94	0.20	-	45,45,45,45	0
35	NA	0	9134	1/1	0.98	0.10	-	37,37,37,37	0
33	MG	0	8048	1/1	0.97	0.16	-	62,62,62,62	0
33	MG	0	8087	1/1	0.95	0.14	-	54,54,54,54	0
33	MG	0	8047	1/1	0.92	0.18	-	78,78,78,78	0
33	MG	0	8039	1/1	0.93	0.06	-	51,51,51,51	0
35	NA	0	9115	1/1	0.96	0.15	-	39,39,39,39	0
33	MG	0	8072	1/1	0.99	0.24	-	55,55,55,55	0
37	CD	O	9205	1/1	0.04	0.30	-	200,200,200,200	0
33	MG	0	8030	1/1	1.00	0.15	-	26,26,26,26	0
33	MG	0	8061	1/1	0.98	0.08	-	45,45,45,45	0
35	NA	0	9118	1/1	0.98	0.20	-	47,47,47,47	0
33	MG	0	8041	1/1	0.90	0.24	-	72,72,72,72	0
35	NA	0	9116	1/1	0.95	0.11	-	36,36,36,36	0
33	MG	0	8079	1/1	0.99	0.12	-	38,38,38,38	0
35	NA	9	9151	1/1	0.63	0.36	-	87,87,87,87	0
33	MG	0	8099	1/1	0.95	0.10	-	63,63,63,63	0
33	MG	0	8050	1/1	0.91	0.08	-	61,61,61,61	0
35	NA	0	9170	1/1	0.85	0.48	-	97,97,97,97	0
33	MG	0	8063	1/1	0.95	0.15	-	84,84,84,84	0
33	MG	0	8097	1/1	0.95	0.15	-	40,40,40,40	0
33	MG	0	8083	1/1	0.94	0.08	-	42,42,42,42	0
33	MG	0	8024	1/1	0.83	0.65	-	83,83,83,83	0
35	NA	0	9119	1/1	0.98	0.08	-	36,36,36,36	0
33	MG	0	8037	1/1	0.98	0.06	-	44,44,44,44	0
35	NA	0	9179	1/1	0.95	0.18	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	9107	1/1	0.91	0.20	-	50,50,50,50	0
33	MG	0	8098	1/1	0.93	0.24	-	40,40,40,40	0
35	NA	H	9122	1/1	0.96	0.13	-	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.