



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 12:15 pm BST

PDB ID : 3CCR
Title : Structure of Anisomycin resistant 50S Ribosomal Subunit: 23S rRNA mutation A2488C. Density for anisomycin is visible but not included in the model.
Authors : Blaha, G.; Gurel, G.
Deposited on : 2008-02-26
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

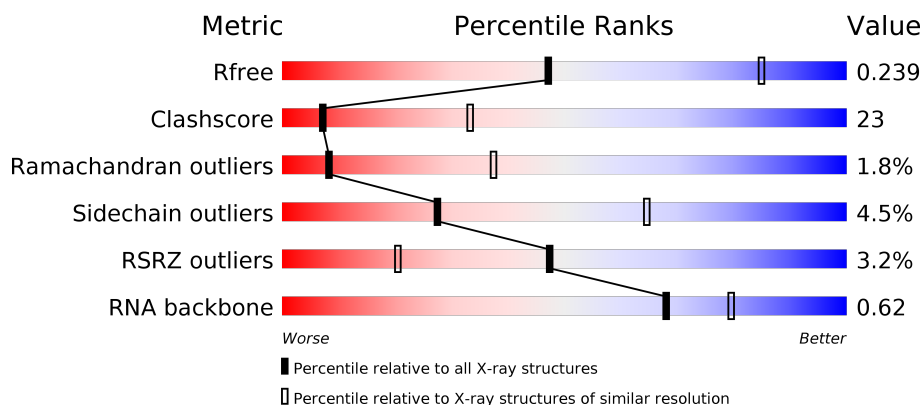
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	<div> <div>8%</div> <div>62%</div> <div>33%</div> <div>..</div> </div>
2	B	338	<div> <div>58%</div> <div>37%</div> <div>.</div> </div>
3	C	246	<div> <div>68%</div> <div>27%</div> <div>5%</div> </div>
4	D	177	<div> <div>8%</div> <div>42%</div> <div>35%</div> <div>..</div> <div>21%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	178	
6	F	120	
7	G	348	
8	H	177	
9	I	162	
10	J	145	
11	K	132	
12	L	165	
13	M	196	
14	N	187	
15	O	116	
16	P	149	
17	Q	96	
18	R	155	
19	S	85	
20	T	120	
21	U	67	
22	V	71	
23	W	154	
24	X	92	
25	Y	241	
26	Z	116	
27	1	57	
28	2	50	
29	3	92	

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Mol	Chain	Length	Quality of chain
30	0	2923	
31	9	122	

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	CL	3	8804	-	-	X	-
33	CL	B	8819	-	-	X	-
33	CL	M	8818	-	-	X	-
34	SR	0	8957	-	-	-	X
34	SR	0	8982	-	-	-	X
34	SR	0	8986	-	-	-	X
34	SR	0	8997	-	-	-	X
34	SR	0	9004	-	-	-	X
34	SR	0	9006	-	-	-	X
35	NA	0	8528	-	-	-	X
35	NA	0	8559	-	-	-	X
35	NA	0	8563	-	-	-	X

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99120 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 protein called 50S ribosomal protein L2P.

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

- Molecule 2 is a protein called 50S ribosomal protein L3P.

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

- Molecule 3 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	246	Total	C	N	O	S	0	0	0
			1860	1130	345	384	1			

- Molecule 4 is a protein called 50S ribosomal protein L5P.

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

- Molecule 5 is a protein called 50S ribosomal protein L6P.

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

- Molecule 6 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 7 is a protein called 50S ribosomal protein L10E.

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

- Molecule 8 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	160	Total	C	N	O	S	0	0	0
			1282	798	240	238	6			

- Molecule 9 is a protein called 50S ribosomal protein L11P.

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

- Molecule 10 is a protein called 50S ribosomal protein L13P.

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

- Molecule 11 is a protein called 50S ribosomal protein L14P.

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

- Molecule 12 is a protein called 50S ribosomal protein L15P.

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

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	194	Total	C	N	O	S	0	0	0
			1558	943	333	281	1			

- Molecule 14 is a protein called 50S ribosomal protein L18P.

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

- Molecule 15 is a protein called 50S ribosomal protein L18e.

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

- Molecule 16 is a protein called 50S ribosomal protein L19e.

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

- Molecule 17 is a protein called 50S ribosomal protein L21e.

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

- Molecule 18 is a protein called 50S ribosomal protein L22P.

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

- Molecule 19 is a protein called 50S ribosomal protein L23P.

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

- Molecule 20 is a protein called 50S ribosomal protein L24P.

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

- Molecule 21 is a protein called 50S ribosomal protein L24e.

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

- Molecule 22 is a protein called 50S ribosomal protein L29P.

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

- Molecule 23 is a protein called 50S ribosomal protein L30P.

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

- Molecule 24 is a protein called 50S ribosomal protein L31e.

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

- Molecule 25 is a protein called 50S ribosomal protein L32e.

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

- Molecule 26 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	73	Total	C	N	O	S	0	0	0
			573	343	113	112	5			

- Molecule 27 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 28 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 29 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 30 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59018	26348	10871	19054	2745			

- Molecule 31 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	84	Total	Mg	0	0
			84	84		
32	9	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	B	2	Total	Mg	0	0
			2	2		
32	A	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	2	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	9	Total 9	Cl 9	0	0
33	J	3	Total 3	Cl 3	0	0
33	K	1	Total 1	Cl 1	0	0
33	B	1	Total 1	Cl 1	0	0
33	A	1	Total 1	Cl 1	0	0
33	N	1	Total 1	Cl 1	0	0
33	O	1	Total 1	Cl 1	0	0
33	R	1	Total 1	Cl 1	0	0
33	Y	1	Total 1	Cl 1	0	0
33	L	1	Total 1	Cl 1	0	0
33	3	1	Total 1	Cl 1	0	0
33	M	1	Total 1	Cl 1	0	0

- Molecule 34 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	93	Total 93	Sr 93	0	0
34	1	2	Total 2	Sr 2	0	0
34	B	2	Total 2	Sr 2	0	0
34	3	2	Total 2	Sr 2	0	0
34	A	3	Total 3	Sr 3	0	0
34	R	1	Total 1	Sr 1	0	0
34	9	3	Total 3	Sr 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	S	1	Total 1	Sr 1	0	0
34	F	1	Total 1	Sr 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	66	Total 66	Na 66	0	0
35	J	1	Total 1	Na 1	0	0
35	Q	1	Total 1	Na 1	0	0
35	C	1	Total 1	Na 1	0	0
35	R	2	Total 2	Na 2	0	0
35	9	2	Total 2	Na 2	0	0
35	S	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0

- Molecule 36 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	1	Total 1	K 1	0	0
36	M	1	Total 1	K 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

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

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	A	121	Total	O	0	0
			121	121		
38	B	145	Total	O	0	0
			145	145		
38	C	166	Total	O	0	0
			166	166		
38	D	46	Total	O	0	0
			46	46		
38	E	43	Total	O	0	0
			43	43		
38	F	31	Total	O	0	0
			31	31		
38	G	17	Total	O	0	0
			17	17		
38	H	72	Total	O	0	0
			72	72		
38	I	5	Total	O	0	0
			5	5		
38	J	52	Total	O	0	0
			52	52		
38	K	52	Total	O	0	0
			52	52		
38	L	81	Total	O	0	0
			81	81		
38	M	133	Total	O	0	0
			133	133		
38	N	56	Total	O	0	0
			56	56		
38	O	41	Total	O	0	0
			41	41		
38	P	63	Total	O	0	0
			63	63		
38	Q	52	Total	O	0	0
			52	52		

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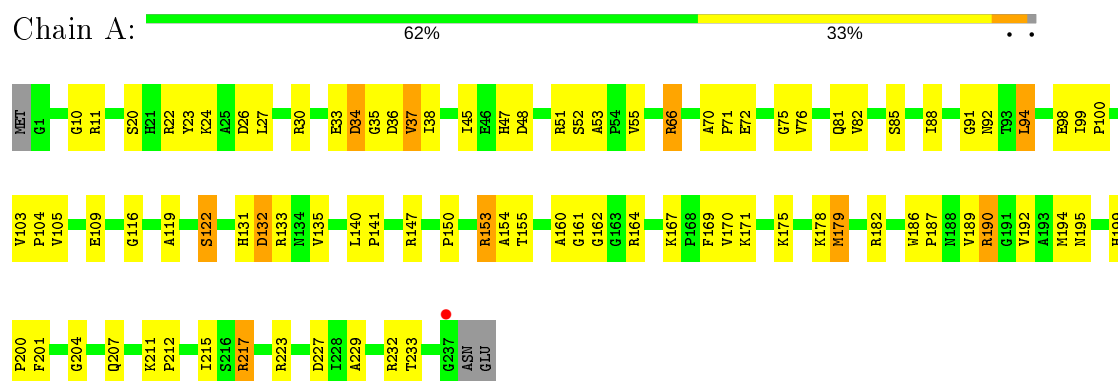
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	R	75	Total 75	O 75	0	0
38	S	37	Total 37	O 37	0	0
38	T	40	Total 40	O 40	0	0
38	U	28	Total 28	O 28	0	0
38	V	15	Total 15	O 15	0	0
38	W	69	Total 69	O 69	0	0
38	X	22	Total 22	O 22	0	0
38	Y	100	Total 100	O 100	0	0
38	Z	28	Total 28	O 28	0	0
38	1	61	Total 61	O 61	0	0
38	2	45	Total 45	O 45	0	0
38	3	76	Total 76	O 76	0	0
38	0	5897	Total 5897	O 5897	0	0
38	9	154	Total 154	O 154	0	0

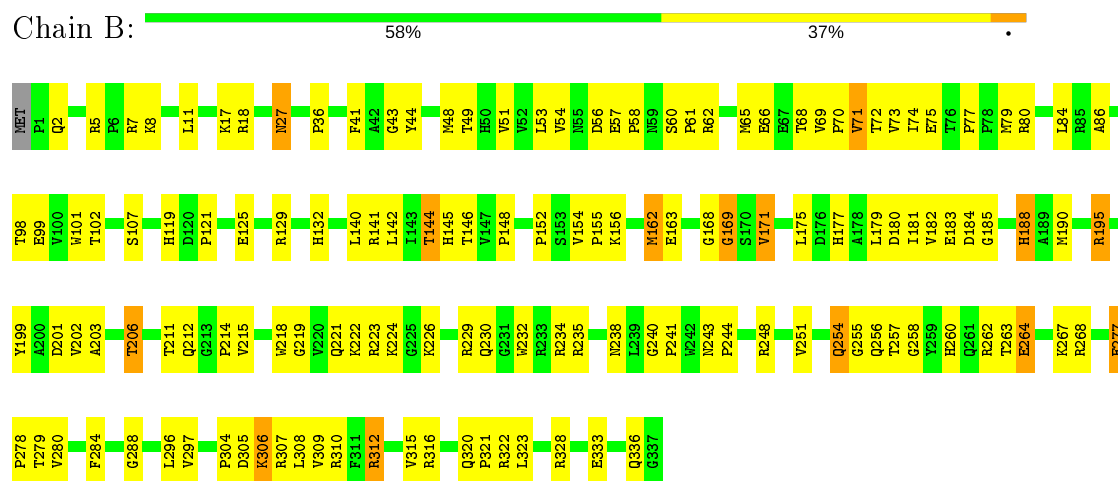
3 Residue-property plots

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

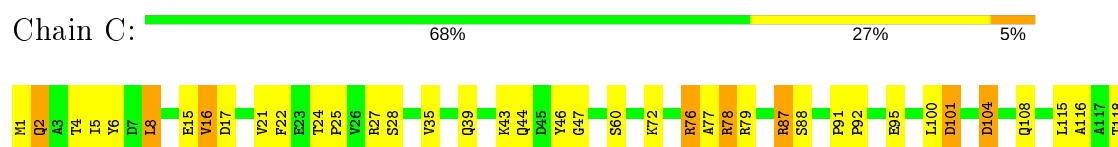
• Molecule 1: 50S ribosomal protein L2P

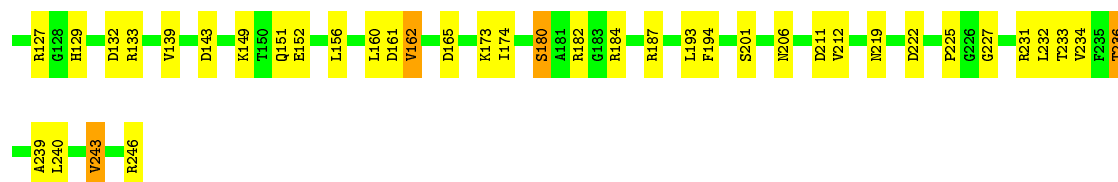


• Molecule 2: 50S ribosomal protein L3P

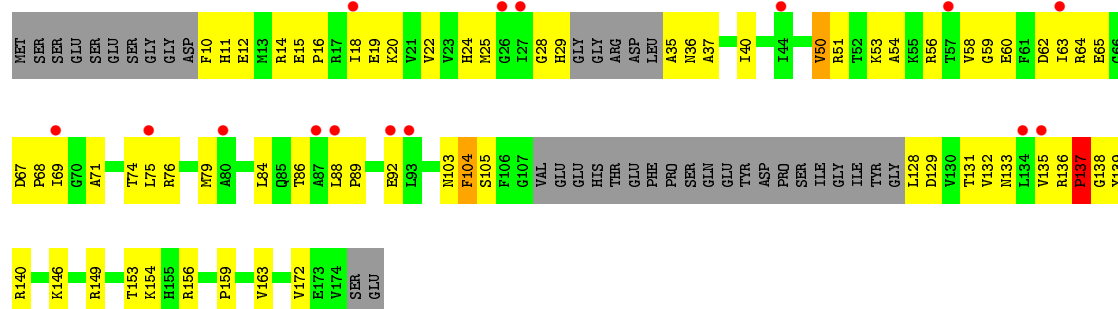
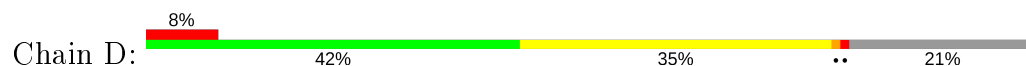


• Molecule 3: 50S ribosomal protein L4P

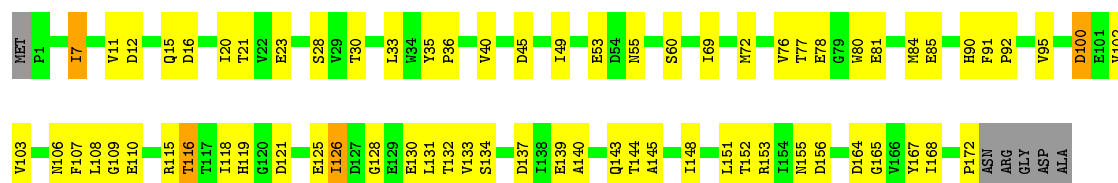




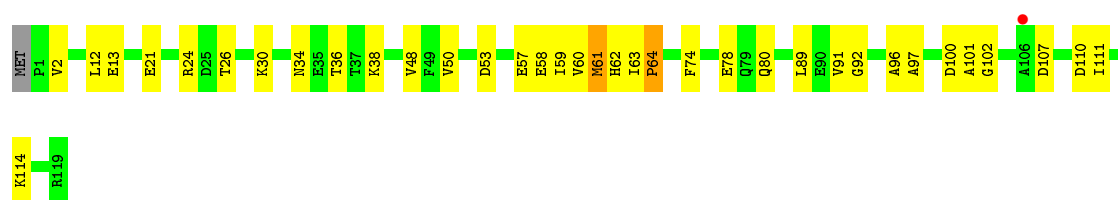
• Molecule 4: 50S ribosomal protein L5P



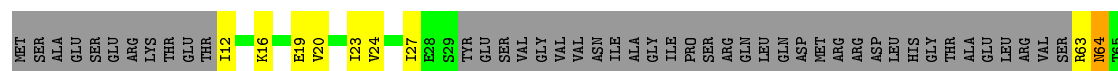
• Molecule 5: 50S ribosomal protein L6P



• Molecule 6: 50S ribosomal protein L7Ae



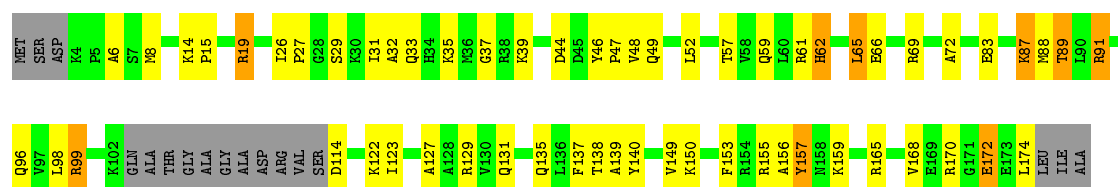
• Molecule 7: 50S ribosomal protein L10E





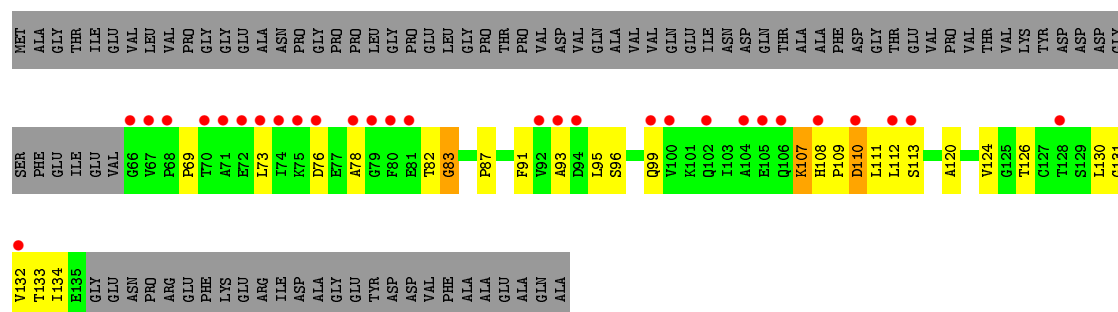
• Molecule 8: 50S ribosomal protein L10e

Chain H: 57% 28% 5% 10%



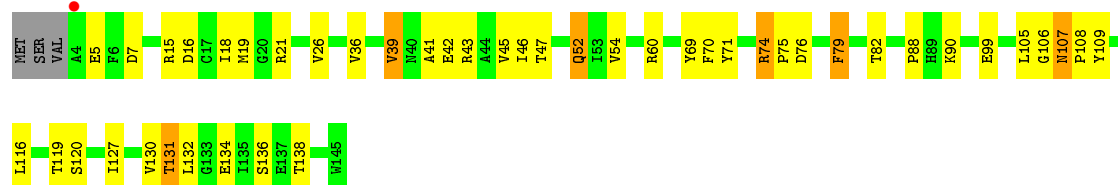
• Molecule 9: 50S ribosomal protein L11P

Chain I: 18% 27% 15% 57%



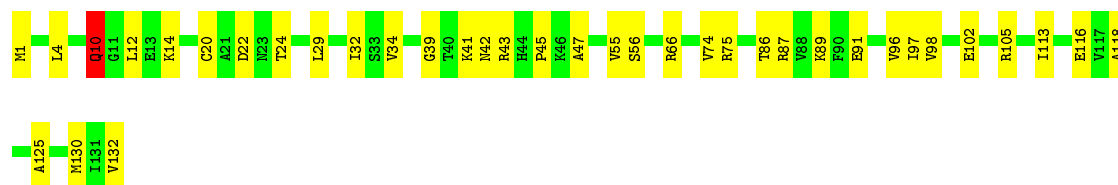
• Molecule 10: 50S ribosomal protein L13P

Chain J: 67% 27% 6%

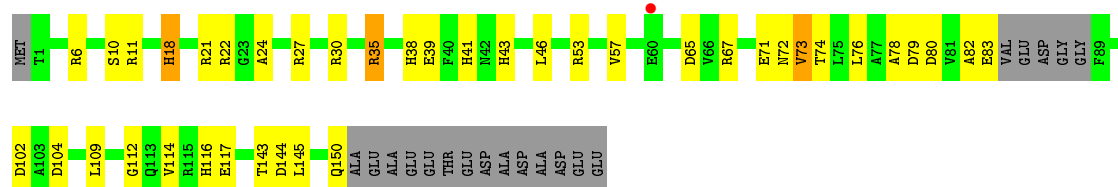


• Molecule 11: 50S ribosomal protein L14P

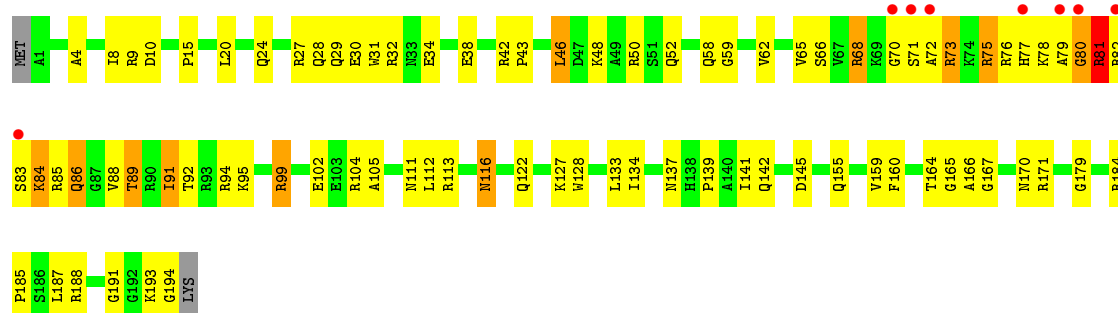
Chain K: 72% 27% 1%



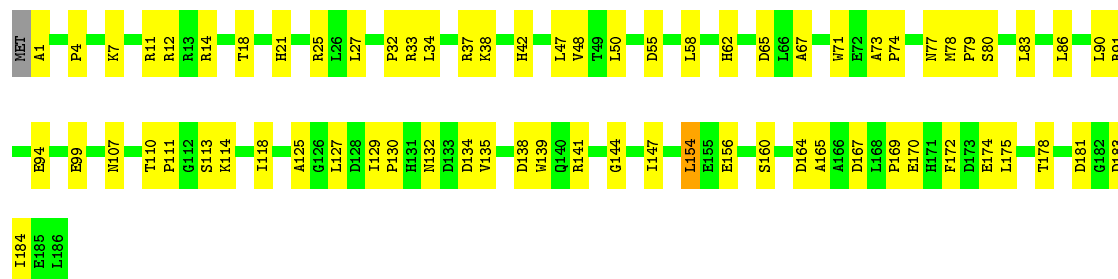
- Molecule 12: 50S ribosomal protein L15P



- Molecule 13: 50S ribosomal protein L15e

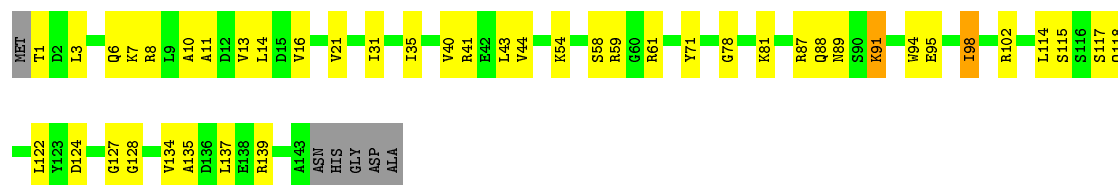


- Molecule 14: 50S ribosomal protein L18P



- Molecule 16: 50S ribosomal protein L19e

Chain P: 



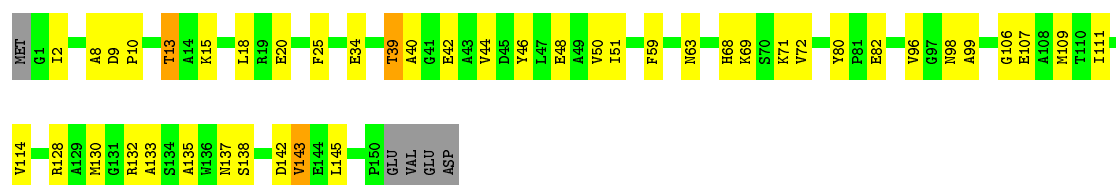
- Molecule 17: 50S ribosomal protein L21e

Chain Q: 



- Molecule 18: 50S ribosomal protein L22P

Chain R: 



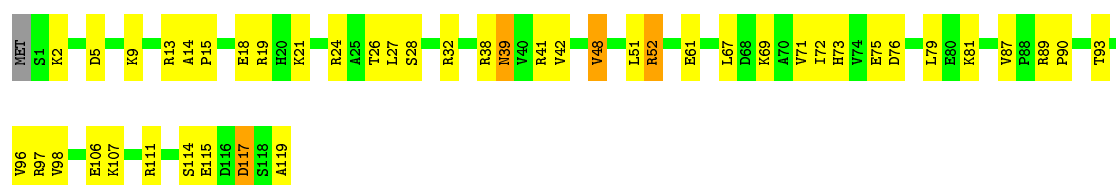
- Molecule 19: 50S ribosomal protein L23P

Chain S: 



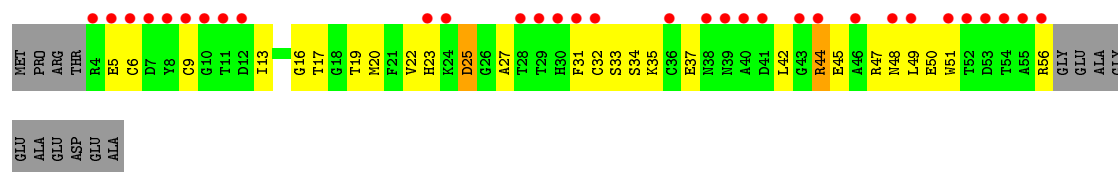
- Molecule 20: 50S ribosomal protein L24P

Chain T: 

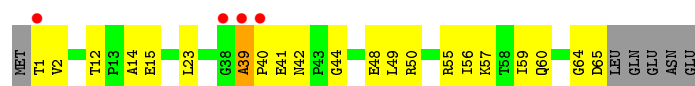


- Molecule 21: 50S ribosomal protein L24e

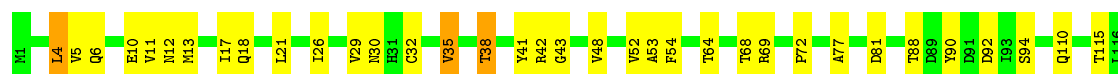
Chain U: 



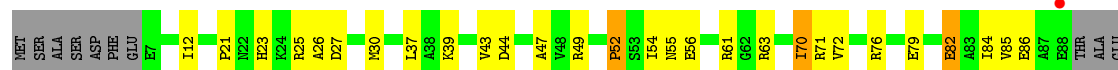
- Molecule 22: 50S ribosomal protein L29P



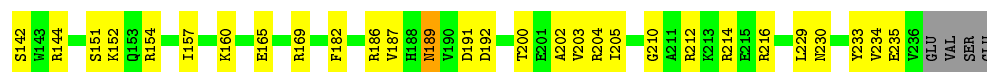
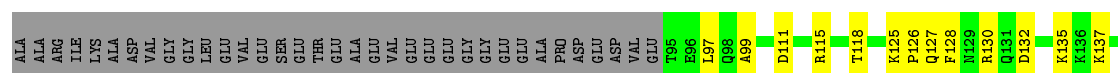
- Molecule 23: 50S ribosomal protein L30P



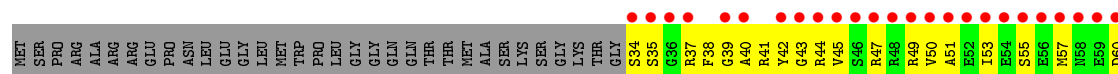
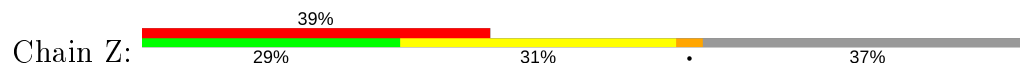
- Molecule 24: 50S ribosomal protein L31e



- Molecule 25: 50S ribosomal protein L32e

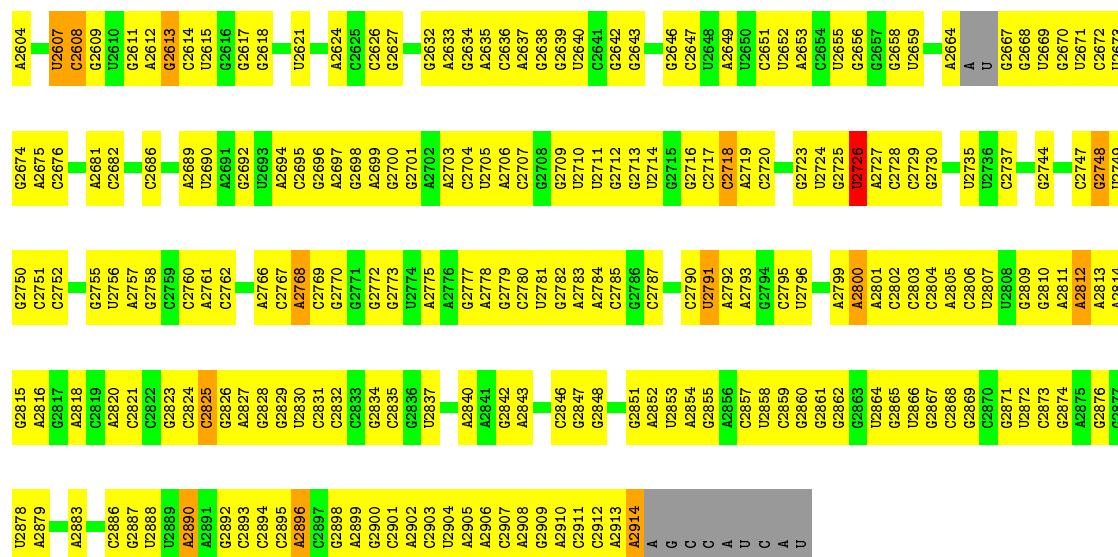


- Molecule 26: 50S ribosomal protein L37Ae

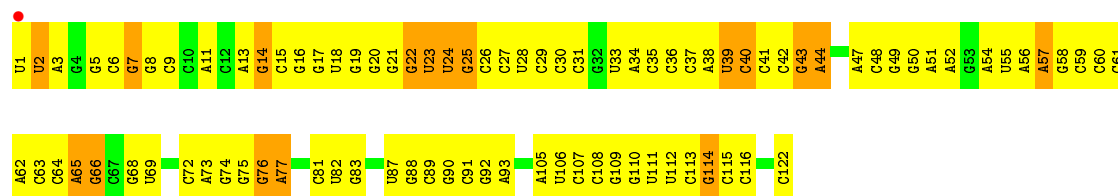


G1475	U1405	C1251	G1186	G1112	C1025	G964	G887	G814	C735	A591	G514	A441
A1476	A1406	A1255	U1187	U1115	U1026	A965	U888	U815	A736	G	G517	A442
C1477	A1407	C1256	A1188	U1116	G1027	U966	C889	G816	A737	C594	U517	C443
U1478	U1408	G1257	U1189	U1117	U1028	U967	C890	G817	U518	U595	G518	C444
G1484	G1409	G1260	A1190	A1117	U1029	G968	G	A818	C741	C596	A519	U445
A1485	A1410	G1337	U1191	U1118	U1030	G969	A894	A819	G742	A520	A520	G446
		G1339	A1192	U1119	G1031	U970	A895	G820	G743	A521	A521	A447
		G1340	A1193	U1120	A1032	G	C896	C821	G744	C598	U522	G448
A1413	A1413	U1264	A1194	G1121	U1041	U	A897	C822	G745	G600	A524	A449
G1415	A1414	G1265	A1195	C1127	U1042	U	G898	G823	A746	A603	A532	C450
C1495	G1416	C1267	G1196	U1128	C1043	C	G899	U824	G747	G604	U611	C451
A1496	G1417	G1268	A1197	U1129	G1044	U	G902	U825	C748	C605	U612	G452
G1497	U1418	G1269	U1198	U1130	G1045	C	U903	A827	C749	G	U613	A453
		U1270	A1199	G1131	U1046	C	U904	G828	A750	U614	C532	U457
U1419	A1420	A1271	A1200	A1132	U1047	C	G905	A829	A751	U615	U615	G458
C1420	C1421	C1272	C1201	A1133	U1048	U	G	G830	U752	U616	C533	A459
G1421	C1422	C1273	A1202	A1134	U1049	U	G	G831	G753	U617	C534	A460
U1503	G1423	A1274	G1203	G1137	G1052	C	G910	U831	U754	U618	C535	U461
U1504	C1424	C1275	G1204	U1138	G1053	C	G911	G834	C759	U619	A540	C461
U1505	A1355	U1276	U1205	G1139	G1054	A	A912	U835	G	U620	C541	A462
U1506	G1425	C1277	U1206	U1140	U1055	G	A913	U836	C763	U621	C542	A466
C1507	A1426	U1278	U1207	A1150	G1056	U	G	U837	C764	U622	A543	G467
	C1427	A1279	C1208	G1151	A1057	A	A916	C838	U765	U623	G544	U468
	C1428	U1279	C1209	C1140	U1058	G	U917	C839	G766	U624	G545	U469
			G1210	U1149	G1059	G	C920	U840	A767	G625	G546	G469
G1430	U1429	G1361	G1211	A1150	C1060	A	G921	A841	A768	G626	A547	U470
		G1362	G1212	G1151	U1061	U	A922	C842	G772	U627	A549	G
A1434	U1430	U1285	C1213	A1154	G1062	U	A923	A843	G773	U628	C550	A473
U1435	U1435	A1286	G1214	A1155	G1063	G	G	A844	C774	U629	A551	C474
U1436	C1366	A1287	G1215	A1156	U1066	C	G924	C848	G775	U630	A552	A477
C1437	C1367	U1288	G1216	C1157	U1067	C	A925	G	A776	A628	G553	G478
G1438	U1437	G1289	G1217	U1158	U1068	A	U927	C853	U777	A629	C556	G479
U1439	U1368	U1290	G1218	G1159	C1069	C	G854	U855	A780	G706	C557	G482
C1440	U1440	A1291	U1219	G1160	A1070	U	U856	G857	A781	A631	C558	C483
U1441	G1441	U1292	U1219	G1161	G1071	A	A929	A857	C781	A632	U560	A484
G1442	A1442	A1294	U1220	A1162	G1072	C	C999	A858	G789	A633	U561	A485
U1443	G1443	G1303	G1224	G1163	U1073	C1000	G938	U859	A790	A634	A562	A486
G1444	U1444	U1298	C1225	G1164	A1074	U1003	A939	C859	A791	G635	C563	G487
G1445	G1378	G1299	G1226	U1165	G1074	C1004	G940	U862	U793	G644	U564	U488
U1446	A1379	G1300	C1227	G1166	U1075	U1005	G941	U863	U794	G	U567	C491
U1447	U1380	C1227	U1227	A1167	C1080	A1006	U942	G863	U795	G652	U568	C492
A1448	G1381	U1304	C1229	C1168	A1081	C1007	U945	G864	A796	U653	A569	U493
G1449	U1382	G1305	U1234	U1169	U1087	C1008	C946	G865	U797	A654	C571	C494
C1451	C1384	G1305	G1235	U1170	A1088	U1009	U947	G870	G798	U655	C571	A495
G1452	G1385	U1309	A1236	A1171	G1089	C1010	G948	U871	C799	G656	G577	G496
U1453	G1389	U1310	U1237	G1172	U1095	A1012	U949	U872	A721	G657	G577	A497
U1454	G1390	G1312	G1238	A1173	U1096	A1013	G950	U873	G724	C658	G581	A498
G1460	A1391	A1313	G1239	A1174	A1095	A1014	A951	A874	C725	A659	G582	G506
U1461	A1392	U1314	G1240	G1175	U1096	C1015	G952	A875	A660	G590	U582	A507
C1462	A1393	G1315	G1241	C1176	A1097	U1016	G953	A876	G726	A659	C583	A508
U1463	C1394	U1316	A1242	U1177	U1098	U1017	G956	G877	G727	G661	U584	A509
C1464	C1395	G1316	U1243	G1178	C1102	A1018	U957	G878	C728	U662	C585	U510
U1469	G1397	G1324	U1244	C1179	C1103	C1019	G958	U879	C729	C663	C586	A507
A1470	U1398	G1325	G1245	U1180	C1104	A1020	U959	G880	G730	U664	C587	A508
A1471	A1399	C1326	A1246	A1181	C1104	G1021	G960	G881	G731	A665	A587	A509
C1472	G1400	G1327	A1247	C1182	U1109	A1022	A961	C884	C732	A666	G588	U511
U1473	U1473	A1328	U1248	C1183	U1110	C1023	G962	G885	U733	G	U589	G
C1474	C1474	A1330	C1250	U1185	U1111	G1024	C963	A886	U734	G669	A590	G





● Molecule 31: 5S RIBOSOMAL RNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	212.41Å 299.52Å 574.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.00 85.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.81-3.00) 77.4 (85.66-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 2.40Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.180 , 0.247 0.177 , 0.239	Depositor DCC
R_{free} test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å ²)	52.9	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 82.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	99120	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, SR, NA, K, CD, OMU, UR3, 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	A	0.34	0/1786	0.65	0/2408
2	B	0.34	0/2690	0.64	0/3652
3	C	0.38	0/1885	0.65	0/2552
4	D	0.32	0/1111	0.56	0/1498
5	E	0.34	0/1382	0.59	0/1880
6	F	0.34	0/901	0.58	0/1224
7	G	0.33	0/241	0.48	0/324
8	H	0.34	0/1302	0.65	0/1743
9	I	0.31	0/526	0.51	0/716
10	J	0.38	0/1136	0.62	0/1530
11	K	0.36	0/1004	0.67	0/1351
12	L	0.33	0/1130	0.62	0/1509
13	M	0.38	0/1582	0.63	0/2116
14	N	0.32	0/1474	0.63	0/1999
15	O	0.37	0/874	0.60	0/1181
16	P	0.34	0/1147	0.53	0/1528
17	Q	0.33	0/749	0.69	0/1005
18	R	0.37	0/1172	0.63	0/1578
19	S	0.38	0/648	0.60	0/875
20	T	0.34	0/958	0.66	1/1289 (0.1%)
21	U	0.45	0/417	0.67	0/562
22	V	0.32	0/502	0.55	0/675
23	W	0.36	0/1219	0.64	0/1655
24	X	0.35	0/664	0.61	0/895
25	Y	0.36	0/1146	0.62	0/1536
26	Z	0.45	0/584	0.63	0/781
27	1	0.43	0/438	0.57	0/578
28	2	0.35	0/401	0.60	0/529
29	3	0.48	0/771	0.66	0/1024
30	0	0.41	0/65954	0.68	4/102862 (0.0%)
31	9	0.35	0/2904	0.68	0/4526
All	All	0.39	0/98698	0.67	5/147581 (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
23	W	0	1
30	0	0	18
31	9	0	1
All	All	0	20

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	1819	G	C5'-C4'-C3'	5.99	125.59	116.00
30	0	871	G	C5'-C4'-O4'	-5.85	102.08	109.10
30	0	1504	A	C1'-O4'-C4'	-5.36	105.62	109.90
20	T	52	ARG	N-CA-C	5.08	124.73	111.00
30	0	2726	U	N1-C1'-C2'	5.01	120.52	114.00

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1266	U	Sidechain
30	0	1430	G	Sidechain
30	0	2076	U	Sidechain
30	0	2078	U	Sidechain
30	0	214	U	Sidechain
30	0	2412	G	Sidechain
30	0	2465	A	Sidechain
30	0	2552	C	Sidechain
30	0	2607	U	Sidechain
30	0	2726	U	Sidechain
30	0	324	G	Sidechain
30	0	393	G	Sidechain
30	0	435	A	Sidechain
30	0	436	A	Sidechain
30	0	462	A	Sidechain
30	0	518	G	Sidechain
30	0	664	U	Sidechain
30	0	868	G	Sidechain

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Mol	Chain	Res	Type	Group
31	9	76	G	Sidechain
23	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	A	1753	0	1766	97	0
2	B	2625	0	2532	127	0
3	C	1860	0	1813	70	0
4	D	1094	0	1085	50	0
5	E	1357	0	1266	55	0
6	F	890	0	843	27	0
7	G	240	0	231	11	0
8	H	1282	0	1292	55	0
9	I	519	0	500	26	0
10	J	1120	0	1098	44	0
11	K	994	0	1027	39	0
12	L	1118	0	1076	29	0
13	M	1558	0	1573	98	0
14	N	1445	0	1401	59	0
15	O	865	0	873	32	0
16	P	1136	0	1123	44	0
17	Q	735	0	729	21	0
18	R	1149	0	1122	37	0
19	S	641	0	605	16	0
20	T	950	0	924	33	0
21	U	410	0	368	38	0
22	V	499	0	511	19	0
23	W	1196	0	1137	52	0
24	X	654	0	653	24	0
25	Y	1130	0	1133	44	0
26	Z	573	0	535	64	0
27	1	431	0	426	20	0
28	2	396	0	413	21	0
29	3	755	0	732	90	0
30	0	59018	0	29810	2239	0
31	9	2599	0	1325	161	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	0	84	0	0	0	0
32	2	1	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	2	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	9	0	0	2	0
33	3	1	0	0	3	0
33	A	1	0	0	1	0
33	B	1	0	0	2	0
33	J	3	0	0	2	0
33	K	1	0	0	0	0
33	L	1	0	0	1	0
33	M	1	0	0	2	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	93	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	3	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	66	0	0	0	0
35	9	2	0	0	0	0
35	C	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	2	0	0	0	0
35	S	1	0	0	0	0
36	0	1	0	0	0	0
36	M	1	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5897	0	0	323	0
38	1	61	0	0	3	0
38	2	45	0	0	1	0
38	3	76	0	0	7	0
38	9	154	0	0	11	0
38	A	121	0	0	3	0
38	B	145	0	0	20	0
38	C	166	0	0	13	0
38	D	46	0	0	7	0
38	E	43	0	0	4	0
38	F	31	0	0	1	0
38	G	17	0	0	0	0
38	H	72	0	0	10	0
38	I	5	0	0	2	0
38	J	52	0	0	4	0
38	K	52	0	0	3	0
38	L	81	0	0	4	0
38	M	133	0	0	12	0
38	N	56	0	0	6	0
38	O	41	0	0	2	0
38	P	63	0	0	5	0
38	Q	52	0	0	1	0
38	R	75	0	0	2	0
38	S	37	0	0	0	0
38	T	40	0	0	3	0
38	U	28	0	0	5	0
38	V	15	0	0	1	0
38	W	69	0	0	7	0
38	X	22	0	0	4	0
38	Y	100	0	0	5	0
38	Z	28	0	0	5	0
All	All	99120	0	59922	3377	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 23.

All (3377) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:871:G:C8	30:0:871:G:H5'	1.74	1.22
30:0:1160:G:H5'	30:0:1161:A:C5'	1.70	1.20
30:0:1160:G:C5'	30:0:1161:A:H5'	1.73	1.18
30:0:1278:A:H4'	30:0:1279:U:C4	1.81	1.16
13:M:171:ARG:HD3	30:0:156:C:H5''	1.15	1.13
14:N:37:ARG:NH1	31:9:6:C:H5''	1.65	1.12
30:0:1559:A:H1'	38:0:5836:HOH:O	1.48	1.11
10:J:82:THR:HG23	30:0:1242:A:H5'	1.30	1.10
30:0:236:A:H4'	30:0:237:G:H5'	1.26	1.09
14:N:37:ARG:HH12	31:9:6:C:H5''	1.04	1.08
30:0:1205:U:H2'	30:0:1206:U:C5'	1.83	1.07
30:0:1205:U:H2'	30:0:1206:U:H5'	1.32	1.06
2:B:264:GLU:HG2	2:B:267:LYS:HE2	1.35	1.06
30:0:545:G:H8	30:0:545:G:H5'	1.18	1.05
29:3:88:LEU:HD22	33:3:8804:CL:CL	1.95	1.03
30:0:871:G:H5'	30:0:871:G:H8	0.89	1.02
31:9:54:A:O2'	31:9:55:U:H5'	1.58	1.02
30:0:2506:A:HO2'	30:0:2507:G:H8	1.04	1.01
30:0:1118:A:H3'	30:0:1118:A:H8	1.24	1.01
31:9:14:G:H5'	31:9:14:G:H8	1.25	1.01
22:V:50:ARG:HH12	30:0:56:G:H5''	1.25	1.01
30:0:960:G:H4'	38:0:7414:HOH:O	1.61	0.99
30:0:558:C:C2'	30:0:559:U:H5''	1.92	0.99
30:0:2372:A:H2'	30:0:2373:U:H6	1.28	0.99
29:3:68:LYS:HD3	29:3:70:ARG:HH21	1.28	0.99
30:0:1603:A:H5'	30:0:1605:G:O4'	1.61	0.98
30:0:1834:C:H2'	30:0:1840:A:N6	1.78	0.98
31:9:76:G:H3'	31:9:77:A:H5''	1.44	0.98
29:3:47:GLY:HA2	30:0:2121:G:H4'	1.43	0.98
30:0:1666:C:O2'	30:0:1667:A:H5''	1.62	0.98
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.46	0.97
30:0:694:A:H2'	30:0:695:C:H5'	1.44	0.97
30:0:877:G:H5'	30:0:878:G:OP1	1.65	0.97
2:B:238:ASN:HD22	2:B:240:GLY:H	1.09	0.97
30:0:2717:C:C2'	30:0:2718:C:H5''	1.95	0.96
21:U:51:TRP:HD1	30:0:2865:G:HO2'	1.07	0.96
30:0:1118:A:H3'	30:0:1118:A:C8	1.99	0.96
30:0:1305:C:H5'	38:0:9833:HOH:O	1.66	0.96
30:0:1209:C:H2'	30:0:1210:G:H8	1.31	0.95
31:9:29:C:H2'	31:9:30:C:H5'	1.49	0.95
30:0:2717:C:O2'	30:0:2718:C:H5''	1.65	0.95
30:0:363:C:H1'	38:0:5247:HOH:O	1.67	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:545:G:C8	30:0:545:G:H5'	2.01	0.95
15:O:3:THR:HG22	30:0:656:G:H5'	1.46	0.95
38:M:8869:HOH:O	30:0:381:G:H5''	1.67	0.95
26:Z:44:ARG:HH21	30:0:1771:U:H5'	1.31	0.95
30:0:2420:G:O2'	30:0:2421:G:H5'	1.64	0.94
31:9:59:C:H2'	31:9:60:C:H6	1.33	0.94
30:0:1118:A:H62	30:0:1244:U:H3	1.14	0.93
30:0:2321:A:H2	30:0:2378:U:H3	1.12	0.93
30:0:871:G:C5'	30:0:871:G:H8	1.81	0.93
3:C:127:ARG:NH2	3:C:225:PRO:HG2	1.82	0.93
30:0:2748:G:H2'	38:0:7523:HOH:O	1.68	0.93
30:0:559:U:H6	30:0:559:U:H5'	1.34	0.92
31:9:54:A:C2'	31:9:55:U:H5'	1.99	0.92
30:0:1116:U:H3	30:0:1246:A:H62	1.17	0.92
30:0:2586:U:H3	30:0:2592:G:H22	1.18	0.91
30:0:2710:U:H1'	38:0:7601:HOH:O	1.69	0.91
30:0:2649:A:H3'	38:0:9829:HOH:O	1.70	0.91
30:0:1856:C:H1'	38:0:5846:HOH:O	1.70	0.91
30:0:1170:U:H2'	30:0:1172:G:OP2	1.71	0.91
30:0:1835:U:H5	30:0:1840:A:N7	1.68	0.91
30:0:1595:G:O2'	30:0:1596:U:H5'	1.71	0.91
30:0:2769:C:C2'	30:0:2770:G:H5'	2.01	0.90
8:H:49:GLN:HE21	8:H:140:TYR:HE2	1.18	0.90
30:0:870:G:H2'	30:0:871:G:H5''	1.51	0.90
13:M:58:GLN:HE22	30:0:259:G:H21	1.13	0.90
30:0:963:C:H2'	30:0:964:G:C8	2.05	0.90
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.37	0.90
30:0:615:G:H1'	38:0:5221:HOH:O	1.72	0.90
23:W:4:LEU:HD13	23:W:52:VAL:HG21	1.51	0.90
30:0:1835:U:H2'	38:0:3618:HOH:O	1.72	0.90
30:0:625:U:H5''	30:0:1044:C:N4	1.87	0.89
30:0:969:G:H1	30:0:999:C:N4	1.71	0.89
30:0:1701:A:H4'	30:0:1702:U:H5''	1.55	0.89
16:P:115:SER:H	16:P:118:GLN:HE21	0.89	0.89
10:J:52:GLN:NE2	30:0:1119:G:H2'	1.88	0.88
13:M:73:ARG:NH2	30:0:2263:G:H5''	1.87	0.88
1:A:199:HIS:HD2	1:A:201:PHE:H	1.21	0.88
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.37	0.87
30:0:542:A:H5'	30:0:542:A:H8	1.39	0.87
30:0:2502:C:H2'	30:0:2503:A:H5'	1.57	0.87
30:0:814:G:H4'	38:0:3128:HOH:O	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1666:C:H2'	30:0:1667:A:H5'	1.55	0.87
30:0:2005:G:OP2	30:0:2005:G:H3'	1.75	0.87
25:Y:187:VAL:HG23	25:Y:192:ASP:HB2	1.57	0.87
30:0:506:G:H22	30:0:509:A:C5'	1.87	0.86
31:9:56:A:H2'	31:9:57:A:H5''	1.57	0.86
30:0:2637:A:H4'	38:0:6039:HOH:O	1.75	0.86
30:0:2908:A:H2'	30:0:2909:G:O4'	1.75	0.86
30:0:506:G:H22	30:0:509:A:H5''	1.40	0.86
30:0:2248:C:H3'	38:0:5403:HOH:O	1.76	0.86
30:0:2372:A:H2'	30:0:2373:U:C6	2.09	0.86
13:M:71:SER:HB2	13:M:92:THR:HG22	1.56	0.86
11:K:10:GLN:HE21	11:K:10:GLN:H	1.18	0.86
30:0:553:G:H3'	38:0:4066:HOH:O	1.76	0.86
30:0:969:G:H1	30:0:999:C:H42	1.24	0.86
16:P:115:SER:H	16:P:118:GLN:NE2	1.73	0.86
6:F:63:ILE:HB	6:F:64:PRO:HD3	1.57	0.86
30:0:1183:C:H2'	38:0:6223:HOH:O	1.75	0.85
30:0:558:C:H2'	30:0:559:U:H5''	1.57	0.85
13:M:99:ARG:HE	13:M:170:ASN:HD22	1.19	0.85
30:0:2419:U:H5''	30:0:2420:G:H5'	1.57	0.85
29:3:20:HIS:CD2	29:3:69:TYR:HB3	2.12	0.85
30:0:2421:G:H1'	38:0:7004:HOH:O	1.75	0.85
30:0:2505:G:O2'	30:0:2506:A:H5'	1.76	0.85
30:0:308:U:H5'	30:0:309:C:OP1	1.75	0.85
30:0:1474:C:H6	30:0:1474:C:H5'	1.40	0.85
30:0:200:C:H2'	38:0:3433:HOH:O	1.75	0.84
30:0:2345:A:H3'	30:0:2346:C:H6	1.43	0.84
30:0:1474:C:C6	30:0:1474:C:H5'	2.13	0.84
30:0:870:G:C2'	30:0:871:G:H5''	2.07	0.84
31:9:13:A:O2'	31:9:14:G:H5''	1.77	0.84
30:0:1080:C:H4'	30:0:1081:A:OP1	1.76	0.84
11:K:39:GLY:HA2	38:0:5187:HOH:O	1.75	0.84
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.23	0.83
31:9:73:A:H2'	31:9:74:G:H8	1.43	0.83
16:P:115:SER:N	16:P:118:GLN:HE21	1.74	0.83
30:0:12:U:H2'	30:0:13:G:H5'	1.57	0.83
30:0:2717:C:H2'	30:0:2718:C:H5''	1.59	0.83
30:0:558:C:H2'	30:0:559:U:C5'	2.08	0.83
31:9:92:G:H2'	31:9:93:A:C8	2.14	0.83
30:0:2570:G:H5''	38:0:4880:HOH:O	1.78	0.83
13:M:68:ARG:NH2	13:M:73:ARG:HD3	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2896:A:H5''	38:0:6075:HOH:O	1.77	0.83
31:9:14:G:C8	31:9:14:G:H5'	2.14	0.83
30:0:271:C:H41	30:0:378:A:H2	1.22	0.82
30:0:1644:C:H2'	30:0:1645:U:H6	1.44	0.82
30:0:810:G:H2'	30:0:811:C:C6	2.13	0.82
30:0:2437:A:H2'	30:0:2438:G:C8	2.14	0.82
22:V:12:THR:HG22	22:V:15:GLU:HG3	1.60	0.82
30:0:1205:U:C2'	30:0:1206:U:C5'	2.57	0.82
30:0:1206:U:H5'	30:0:1206:U:H6	1.43	0.82
30:0:236:A:C4'	30:0:237:G:H5'	2.09	0.82
4:D:25:MET:SD	4:D:40:ILE:HD11	2.19	0.82
15:O:3:THR:CG2	30:0:656:G:H5'	2.09	0.82
3:C:236:THR:HG22	3:C:239:ALA:H	1.44	0.82
30:0:2345:A:H3'	30:0:2346:C:C6	2.15	0.82
30:0:2426:G:H1'	38:0:6068:HOH:O	1.79	0.82
30:0:2502:C:C2'	30:0:2503:A:H5'	2.10	0.82
13:M:134:ILE:HG23	13:M:141:ILE:HD13	1.62	0.81
30:0:1116:U:O2'	30:0:1118:A:H2	1.62	0.81
30:0:1191:A:H2'	30:0:1193:A:H5'	1.62	0.81
30:0:1278:A:H4'	30:0:1279:U:C5	2.15	0.81
30:0:614:U:O2'	30:0:615:G:H5'	1.80	0.81
30:0:2604:A:H5'	38:0:5760:HOH:O	1.79	0.81
30:0:185:G:H4'	30:0:186:A:OP1	1.78	0.81
26:Z:42:TYR:HA	30:0:1829:A:H61	1.45	0.81
30:0:282:C:O2'	30:0:283:U:H5'	1.79	0.81
14:N:67:ALA:HA	14:N:71:TRP:HB3	1.62	0.81
18:R:39:THR:HG22	18:R:42:GLU:H	1.44	0.80
13:M:171:ARG:CD	30:0:156:C:H5''	2.06	0.80
31:9:56:A:C2'	31:9:57:A:H5''	2.11	0.80
30:0:1632:A:H2'	30:0:1633:C:H5'	1.61	0.80
29:3:2:GLN:O	30:0:2320:U:H2'	1.80	0.80
6:F:91:VAL:HG12	6:F:92:GLY:H	1.47	0.80
30:0:1119:G:N2	30:0:1246:A:C2	2.48	0.80
30:0:2467:A:H3'	38:0:5416:HOH:O	1.82	0.80
31:9:59:C:H2'	31:9:60:C:C6	2.16	0.80
30:0:558:C:O2'	30:0:559:U:H5''	1.81	0.80
30:0:1185:U:H2'	30:0:1186:C:H6	1.46	0.80
22:V:50:ARG:NH1	30:0:56:G:H5''	1.95	0.80
11:K:14:LYS:HB2	11:K:45:PRO:HG2	1.63	0.80
31:9:29:C:C2'	31:9:30:C:H5'	2.12	0.79
19:S:55:GLN:NE2	30:0:1446:U:H2'	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LYS:HE2	26:Z:50:VAL:HG13	1.63	0.79
30:0:1116:U:HO2'	30:0:1118:A:H2	0.80	0.79
30:0:1603:A:H5''	30:0:1605:G:H5'	1.65	0.79
28:2:41:HIS:H	28:2:45:ASN:HD22	1.31	0.79
21:U:56:ARG:HD2	30:0:2890:A:N9	1.97	0.79
13:M:58:GLN:NE2	30:0:259:G:H21	1.81	0.79
30:0:2506:A:O2'	30:0:2507:G:H8	1.66	0.79
1:A:199:HIS:CD2	1:A:201:PHE:H	2.00	0.79
13:M:159:VAL:HG12	33:M:8818:CL:CL	2.20	0.79
30:0:2717:C:H2'	30:0:2718:C:C5'	2.13	0.79
31:9:73:A:H2'	31:9:74:G:C8	2.17	0.79
30:0:2604:A:H4'	38:0:7586:HOH:O	1.83	0.79
30:0:282:C:H1'	30:0:368:C:H41	1.46	0.79
30:0:282:C:H1'	30:0:368:C:N4	1.98	0.79
30:0:2783:A:H3'	38:0:5197:HOH:O	1.82	0.78
30:0:2769:C:O2'	30:0:2770:G:H5'	1.84	0.78
30:0:1829:A:H2'	30:0:1830:C:H5'	1.65	0.78
30:0:2533:C:H5'	30:0:2533:C:H6	1.47	0.78
30:0:2906:A:H5'	30:0:2907:C:O4'	1.83	0.78
31:9:55:U:H5''	38:9:9146:HOH:O	1.82	0.78
30:0:541:C:C2'	30:0:542:A:H5''	2.13	0.78
30:0:853:C:H3'	38:0:4528:HOH:O	1.83	0.78
30:0:2416:G:H2'	30:0:2417:C:H6	1.49	0.78
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.32	0.78
10:J:74:ARG:HB3	10:J:74:ARG:HH11	1.48	0.78
13:M:70:GLY:HA3	13:M:73:ARG:NH2	1.99	0.78
30:0:2237:G:H1'	38:0:4824:HOH:O	1.83	0.78
30:0:297:U:H2'	30:0:298:C:H6	1.49	0.78
31:9:56:A:C3'	31:9:57:A:H5''	2.12	0.78
30:0:1189:A:H1'	30:0:1209:C:O4'	1.84	0.77
30:0:1426:C:H2'	38:0:9600:HOH:O	1.83	0.77
30:0:1617:C:C4	30:0:1643:C:H4'	2.19	0.77
30:0:1741:U:H5'	30:0:1742:A:OP1	1.83	0.77
13:M:171:ARG:HD3	30:0:156:C:C5'	2.07	0.77
30:0:1942:A:H5'	38:0:7329:HOH:O	1.84	0.77
30:0:2440:C:H5''	38:0:3808:HOH:O	1.83	0.77
30:0:603:A:H1'	30:0:605:C:C2	2.19	0.77
30:0:1118:A:C3'	30:0:1118:A:C8	2.66	0.77
4:D:105:SER:OG	30:0:2338:G:H1'	1.83	0.77
30:0:2769:C:H2'	30:0:2770:G:O4'	1.82	0.77
10:J:70:PHE:CE1	30:0:2676:C:H4'	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2578:G:H5'	30:0:2578:G:H8	1.49	0.77
8:H:91:ARG:O	30:0:1003:U:H4'	1.84	0.77
30:0:2335:C:H2'	30:0:2336:G:C8	2.20	0.76
30:0:2469:A:H1'	38:0:3231:HOH:O	1.85	0.76
30:0:247:A:H2'	38:0:3913:HOH:O	1.85	0.76
29:3:64:LYS:HA	29:3:84:ARG:HA	1.67	0.76
11:K:10:GLN:NE2	11:K:10:GLN:H	1.83	0.76
30:0:1205:U:H2'	30:0:1206:U:H5''	1.66	0.76
30:0:1834:C:H2'	30:0:1840:A:H62	1.48	0.76
20:T:71:VAL:HG11	20:T:90:PRO:HB3	1.65	0.76
30:0:1249:U:H2'	30:0:1250:C:H6	1.51	0.76
30:0:1170:U:H1'	30:0:1172:G:N7	2.00	0.76
30:0:136:C:H2'	30:0:137:U:O4'	1.86	0.76
30:0:960:G:N3	30:0:960:G:H3'	2.00	0.76
31:9:36:C:H4'	38:9:9029:HOH:O	1.85	0.76
30:0:1634:G:H3'	38:0:3885:HOH:O	1.85	0.76
30:0:146:U:O2'	30:0:147:G:H5'	1.86	0.76
30:0:541:C:H2'	30:0:542:A:C5'	2.15	0.75
31:9:75:G:H1	31:9:106:U:H3	1.33	0.75
30:0:2083:A:H3'	38:0:7559:HOH:O	1.86	0.75
30:0:564:G:H1'	38:0:6290:HOH:O	1.85	0.75
2:B:18:ARG:HE	2:B:256:GLN:HE21	1.31	0.75
13:M:88:VAL:HG21	30:0:2122:C:O2'	1.86	0.75
26:Z:63:CYS:SG	26:Z:81:CYS:HB2	2.26	0.75
30:0:1434:A:HO2'	30:0:1435:U:H6	1.32	0.75
30:0:1189:A:H3'	38:0:7661:HOH:O	1.86	0.75
30:0:297:U:H2'	30:0:298:C:C6	2.21	0.75
30:0:1524:U:H4'	30:0:1524:U:OP1	1.87	0.75
30:0:281:U:O2'	30:0:282:C:H5'	1.85	0.75
30:0:1184:C:H1'	38:0:7447:HOH:O	1.86	0.75
30:0:40:C:H4'	38:0:6986:HOH:O	1.86	0.75
30:0:1377:C:H6	30:0:1377:C:H5'	1.52	0.74
30:0:69:A:H5'	30:0:69:A:C8	2.22	0.74
30:0:718:C:H2'	30:0:718:C:O2	1.87	0.74
8:H:44:ASP:HA	8:H:170:ARG:HH12	1.50	0.74
30:0:1279:U:O2	30:0:1279:U:H2'	1.85	0.74
30:0:1787:C:O2'	30:0:1788:U:H5'	1.87	0.74
30:0:279:C:O2'	30:0:280:C:H5'	1.87	0.74
30:0:635:A:H2'	30:0:636:G:H5''	1.68	0.74
30:0:1972:U:H2'	30:0:1973:A:C5'	2.18	0.74
1:A:223:ARG:NH2	30:0:2271:G:H5'	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:848:C:H5'	38:0:7257:HOH:O	1.87	0.74
10:J:26:VAL:HG13	10:J:36:VAL:HG11	1.69	0.74
30:0:1589:G:N2	30:0:1605:G:H1'	2.02	0.74
30:0:1165:G:O3'	30:0:1174:A:H4'	1.88	0.74
30:0:2831:C:C2'	30:0:2832:C:H5'	2.18	0.74
30:0:629:A:H4'	38:0:4498:HOH:O	1.88	0.74
30:0:694:A:C2'	30:0:695:C:H5'	2.18	0.74
1:A:47:HIS:CD2	30:0:1654:U:H2'	2.22	0.74
30:0:1185:U:H5'	38:0:7447:HOH:O	1.88	0.73
30:0:2100:A:H5'	38:0:7373:HOH:O	1.88	0.73
30:0:2703:A:H2'	30:0:2704:C:H6	1.52	0.73
21:U:44:ARG:HD3	21:U:49:LEU:HD11	1.70	0.73
30:0:2011:A:H5''	38:0:4388:HOH:O	1.87	0.73
29:3:68:LYS:CD	29:3:70:ARG:HH21	2.01	0.73
30:0:1603:A:C5'	30:0:1605:G:H5'	2.19	0.73
30:0:254:C:H2'	30:0:254:C:O2	1.88	0.73
30:0:1855:G:H4'	30:0:1856:C:O5'	1.88	0.73
30:0:2769:C:H2'	30:0:2770:G:H5'	1.69	0.73
31:9:1:U:H4'	31:9:3:A:OP1	1.88	0.73
2:B:18:ARG:HE	2:B:256:GLN:NE2	1.86	0.73
30:0:137:U:H2'	30:0:139:C:C5	2.23	0.73
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.70	0.73
30:0:1589:G:H22	30:0:1605:G:H1'	1.53	0.73
30:0:1835:U:C5	30:0:1840:A:N7	2.53	0.73
30:0:2505:G:C2'	30:0:2506:A:H5'	2.19	0.73
30:0:69:A:H5'	30:0:69:A:H8	1.54	0.73
31:9:3:A:N6	31:9:22:G:H1'	2.03	0.73
10:J:47:THR:HG21	30:0:1244:U:H2'	1.69	0.73
30:0:2472:C:O2'	30:0:2634:G:H4'	1.89	0.73
30:0:2064:U:H5'	30:0:2652:U:O3'	1.89	0.73
30:0:871:G:C8	30:0:871:G:C5'	2.63	0.73
30:0:2635:A:O2'	30:0:2636:C:H5'	1.88	0.72
38:B:9106:HOH:O	30:0:2672:C:H1'	1.87	0.72
30:0:1625:U:H6	30:0:1625:U:H3'	1.54	0.72
30:0:1666:C:H2'	30:0:1667:A:C5'	2.19	0.72
30:0:283:U:H5	30:0:284:C:N3	1.87	0.72
1:A:109:GLU:HG2	1:A:116:GLY:H	1.53	0.72
30:0:1733:A:C6	30:0:1734:C:C2	2.77	0.72
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.71	0.72
1:A:48:ASP:HB3	38:A:9085:HOH:O	1.90	0.72
13:M:79:ALA:HB1	38:0:4442:HOH:O	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:VAL:HB	4:D:62:ASP:HB3	1.72	0.72
13:M:76:ARG:HB2	13:M:88:VAL:HG13	1.72	0.72
30:0:1372:A:H3'	38:0:7172:HOH:O	1.88	0.72
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.05	0.72
30:0:2467:A:H1'	38:0:9049:HOH:O	1.89	0.72
30:0:2898:G:O2'	30:0:2899:A:H5'	1.89	0.72
30:0:1316:G:H5''	38:0:5285:HOH:O	1.88	0.72
30:0:2831:C:O2'	30:0:2832:C:H5'	1.88	0.72
30:0:1178:G:H2'	30:0:1179:C:C6	2.25	0.72
30:0:1713:G:H1'	38:0:5039:HOH:O	1.89	0.72
30:0:2297:U:H1'	38:0:5144:HOH:O	1.88	0.72
30:0:272:A:H5'	30:0:273:G:OP2	1.90	0.72
30:0:2253:G:H2'	30:0:2254:G:H8	1.55	0.72
30:0:595:U:O2'	30:0:596:C:H5'	1.90	0.71
30:0:603:A:H5''	30:0:604:G:OP1	1.89	0.71
31:9:26:C:O2'	31:9:27:C:H5'	1.91	0.71
30:0:1979:G:H3'	38:0:3283:HOH:O	1.88	0.71
30:0:958:G:H2'	30:0:959:C:C6	2.24	0.71
30:0:1477:C:H5'	30:0:1868:G:H5'	1.72	0.71
18:R:2:ILE:HG22	30:0:21:G:H4'	1.71	0.71
30:0:1801:A:H3'	38:0:7596:HOH:O	1.90	0.71
30:0:2321:A:H2	30:0:2378:U:N3	1.88	0.71
27:1:25:LYS:HD2	28:2:49:GLU:H	1.55	0.71
23:W:125:HIS:CE1	30:0:1097:A:H5''	2.25	0.71
25:Y:187:VAL:HG23	25:Y:192:ASP:CB	2.21	0.71
30:0:1197:G:H1'	30:0:1203:G:N2	2.06	0.71
30:0:1398:G:H2'	30:0:1399:A:C8	2.25	0.71
30:0:2769:C:H2'	30:0:2770:G:C5'	2.20	0.71
5:E:143:GLN:NE2	30:0:2779:G:H21	1.89	0.71
30:0:2780:C:H2'	30:0:2781:U:C6	2.26	0.71
30:0:920:C:H4'	30:0:921:G:C2	2.26	0.71
14:N:33:ARG:HH21	14:N:48:VAL:HG11	1.55	0.71
26:Z:84:CYS:HB3	30:0:1604:G:H22	1.56	0.71
31:9:55:U:H4'	31:9:56:A:C8	2.25	0.71
21:U:56:ARG:HG3	21:U:56:ARG:HH11	1.56	0.71
30:0:1666:C:C2'	30:0:1667:A:C5'	2.69	0.71
3:C:139:VAL:HG13	38:C:8645:HOH:O	1.91	0.70
30:0:1185:U:H2'	30:0:1186:C:C6	2.25	0.70
30:0:2321:A:C2	30:0:2378:U:N3	2.55	0.70
30:0:2524:G:H21	30:0:2526:C:N4	1.88	0.70
30:0:1118:A:N6	30:0:1244:U:H3	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2416:G:H2'	30:0:2417:C:C6	2.26	0.70
3:C:78:ARG:HH11	3:C:78:ARG:HG3	1.56	0.70
30:0:1972:U:H2'	30:0:1973:A:H5'	1.73	0.70
30:0:2312:G:H2'	30:0:2313:C:H5'	1.72	0.70
30:0:2717:C:C2'	30:0:2718:C:C5'	2.68	0.70
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.57	0.70
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.73	0.70
30:0:1596:U:H2'	30:0:1598:A:OP2	1.90	0.70
30:0:2565:C:H4'	38:0:4806:HOH:O	1.91	0.70
26:Z:43:GLY:O	26:Z:47:ARG:HG2	1.91	0.70
30:0:1829:A:C2'	30:0:1830:C:H5'	2.21	0.70
30:0:2539:U:H1'	38:0:7770:HOH:O	1.90	0.70
13:M:164:THR:HG22	13:M:166:ALA:H	1.57	0.70
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.55	0.70
14:N:11:ARG:HD3	31:9:114:G:O6	1.90	0.70
38:C:8565:HOH:O	20:T:2:LYS:HE3	1.92	0.70
29:3:40:ARG:HA	29:3:52:PHE:CE1	2.26	0.70
30:0:1226:G:H2'	30:0:1227:C:H6	1.57	0.70
31:9:59:C:O5'	31:9:59:C:H6	1.74	0.69
30:0:1589:G:H5'	38:0:6843:HOH:O	1.91	0.69
30:0:2415:A:H2'	30:0:2416:G:H5'	1.74	0.69
30:0:522:U:O2'	30:0:1366:C:H5'	1.92	0.69
30:0:1181:A:C2'	30:0:1182:C:H5'	2.22	0.69
30:0:2404:G:H5''	38:0:5177:HOH:O	1.91	0.69
30:0:714:U:H4'	38:0:5705:HOH:O	1.93	0.69
1:A:135:VAL:HG11	1:A:147:ARG:NH2	2.07	0.69
7:G:64:ASN:N	7:G:64:ASN:HD22	1.90	0.69
10:J:70:PHE:CD1	30:0:2676:C:H4'	2.27	0.69
30:0:2667:G:H1'	30:0:2914:A:N3	2.08	0.69
8:H:168:VAL:HG13	38:H:218:HOH:O	1.91	0.69
29:3:20:HIS:HD2	29:3:69:TYR:HB3	1.56	0.69
26:Z:37:ARG:HB3	38:0:4665:HOH:O	1.91	0.69
30:0:1205:U:C2'	30:0:1206:U:H5''	2.23	0.69
30:0:545:G:C5'	30:0:545:G:H8	1.99	0.69
14:N:37:ARG:NH1	31:9:6:C:C5'	2.50	0.69
30:0:735:C:H2'	30:0:736:A:O4'	1.93	0.69
2:B:258:GLY:H	2:B:260:HIS:CE1	2.10	0.69
3:C:76:ARG:HH11	3:C:76:ARG:HB3	1.57	0.69
30:0:1741:U:O2'	30:0:2723:G:H4'	1.91	0.69
15:O:32:ARG:HE	15:O:35:LYS:HD2	1.58	0.69
30:0:2705:U:H2'	30:0:2706:A:C8	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2827:A:H2'	30:0:2828:G:O4'	1.92	0.69
13:M:81:ARG:HD2	13:M:85:ARG:HG3	1.74	0.69
18:R:128:ARG:NH2	30:0:2054:A:N3	2.41	0.69
30:0:596:C:H2'	30:0:597:A:H8	1.58	0.69
30:0:1632:A:C2'	30:0:1633:C:H5'	2.22	0.68
30:0:2795:C:O2'	30:0:2796:U:H5'	1.93	0.68
21:U:56:ARG:HB2	30:0:2890:A:C8	2.27	0.68
18:R:138:SER:HB3	30:0:2053:G:OP1	1.94	0.68
11:K:74:VAL:HG21	11:K:96:VAL:HG23	1.75	0.68
16:P:117:SER:HB3	30:0:1593:C:OP1	1.92	0.68
30:0:1702:U:H5'	38:0:3414:HOH:O	1.92	0.68
26:Z:47:ARG:NH2	30:0:1771:U:H1'	2.08	0.68
30:0:2111:G:H1'	38:0:9052:HOH:O	1.94	0.68
30:0:2635:A:C2'	30:0:2636:C:H5'	2.23	0.68
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.10	0.68
30:0:2637:A:H5'	38:0:4897:HOH:O	1.94	0.68
30:0:333:G:O2'	30:0:334:G:H5'	1.94	0.68
2:B:264:GLU:HG2	2:B:267:LYS:CE	2.19	0.68
23:W:125:HIS:NE2	30:0:1097:A:H5''	2.09	0.68
30:0:1197:G:H1'	30:0:1203:G:C2	2.28	0.68
29:3:50:GLY:HA3	30:0:170:U:H1'	1.75	0.68
30:0:585:C:H5''	38:0:4840:HOH:O	1.94	0.68
30:0:1209:C:H2'	30:0:1210:G:C8	2.23	0.68
26:Z:42:TYR:CA	30:0:1829:A:H61	2.07	0.68
30:0:685:C:O2	30:0:748:C:H4'	1.94	0.68
2:B:267:LYS:HD3	38:B:8996:HOH:O	1.93	0.68
30:0:1151:G:H2'	38:0:5713:HOH:O	1.92	0.68
2:B:206:THR:HG21	30:0:2716:G:H5''	1.76	0.68
30:0:2840:A:H3'	38:0:7629:HOH:O	1.94	0.68
10:J:18:ILE:HD13	30:0:1244:U:OP1	1.94	0.68
10:J:74:ARG:CB	10:J:74:ARG:HH11	2.07	0.68
13:M:95:LYS:HE2	30:0:157:G:H4'	1.76	0.67
30:0:1625:U:C6	30:0:1625:U:H3'	2.29	0.67
18:R:98:ASN:HD21	30:0:500:G:H21	1.40	0.67
29:3:90:PHE:HD1	29:3:90:PHE:H	1.42	0.67
3:C:76:ARG:NH1	3:C:76:ARG:HB3	2.09	0.67
10:J:39:VAL:HG22	10:J:106:GLY:O	1.94	0.67
30:0:1118:A:C8	30:0:1119:G:H5''	2.29	0.67
30:0:1813:U:H2'	38:0:6701:HOH:O	1.94	0.67
13:M:70:GLY:HA2	30:0:2263:G:H4'	1.76	0.67
21:U:42:LEU:HD22	30:0:1810:C:H1'	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1528:A:H2'	30:0:1529:G:O4'	1.95	0.67
30:0:541:C:H2'	30:0:542:A:H5''	1.74	0.67
8:H:57:THR:HG23	8:H:131:GLN:HA	1.76	0.67
30:0:2524:G:H5''	38:0:4698:HOH:O	1.94	0.67
30:0:1787:C:H4'	30:0:2883:A:O4'	1.94	0.67
13:M:91:ILE:HG23	38:0:7530:HOH:O	1.94	0.67
30:0:2894:C:O2'	30:0:2895:C:H5'	1.95	0.67
28:2:28:LYS:HE2	30:0:86:A:H1'	1.77	0.67
13:M:73:ARG:HH22	30:0:2263:G:H5''	1.58	0.67
21:U:19:THR:HG22	21:U:20:MET:H	1.59	0.67
30:0:119:A:H2'	30:0:120:A:H5''	1.77	0.67
30:0:370:G:O2'	30:0:371:U:H5'	1.93	0.67
31:9:76:G:C3'	31:9:77:A:H5''	2.23	0.67
30:0:2780:C:H2'	30:0:2781:U:H6	1.59	0.67
30:0:2829:G:N2	30:0:2912:C:C2	2.63	0.67
12:L:46:LEU:O	30:0:2430:A:H4'	1.95	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.77	0.67
30:0:256:C:H2'	30:0:257:G:O4'	1.95	0.67
30:0:810:G:H2'	30:0:811:C:H6	1.56	0.67
29:3:60:LYS:HG3	29:3:61:PRO:HD2	1.77	0.67
4:D:154:LYS:HD2	4:D:154:LYS:H	1.60	0.67
5:E:91:PHE:HE1	30:0:2694:A:H4'	1.58	0.67
10:J:75:PRO:HG2	10:J:105:LEU:HD21	1.77	0.67
11:K:20:CYS:HB2	11:K:29:LEU:HG	1.77	0.67
16:P:59:ARG:HD3	38:0:6249:HOH:O	1.95	0.66
1:A:135:VAL:HG21	1:A:147:ARG:HB3	1.77	0.66
30:0:2785:C:H5'	38:0:7694:HOH:O	1.95	0.66
30:0:596:C:H2'	30:0:597:A:C8	2.29	0.66
14:N:33:ARG:NH2	14:N:48:VAL:HG11	2.10	0.66
30:0:468:U:H3'	38:0:7549:HOH:O	1.93	0.66
29:3:68:LYS:HD3	29:3:70:ARG:NH2	2.07	0.66
15:O:14:LEU:HD23	15:O:102:ILE:HD11	1.77	0.66
30:0:1041:U:H2'	30:0:1042:U:H5'	1.78	0.66
30:0:869:G:H1'	38:0:3302:HOH:O	1.95	0.66
13:M:48:LYS:HE3	13:M:52:GLN:HE21	1.60	0.66
30:0:1120:U:H5'	30:0:1121:G:OP2	1.95	0.66
11:K:12:LEU:HB2	11:K:47:ALA:HB3	1.77	0.66
30:0:1205:U:C2'	30:0:1206:U:H5'	2.18	0.66
30:0:123:U:H5'	38:0:6635:HOH:O	1.96	0.66
30:0:1942:A:H3'	38:0:7329:HOH:O	1.95	0.66
30:0:2329:C:O2'	30:0:2330:U:H5'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:113:SER:HB2	38:N:8852:HOH:O	1.94	0.66
30:0:1063:G:H5''	38:0:9856:HOH:O	1.94	0.66
30:0:1167:G:H2'	30:0:1168:C:C6	2.31	0.66
28:2:43:ARG:NH2	30:0:1684:A:H1'	2.10	0.66
30:0:2032:U:H2'	30:0:2033:G:C5'	2.26	0.66
30:0:2760:C:H5''	38:0:5294:HOH:O	1.95	0.66
30:0:318:U:H5'	30:0:339:A:C2	2.31	0.66
30:0:704:C:H2'	30:0:705:C:H6	1.60	0.66
31:9:7:G:H5'	38:9:9102:HOH:O	1.95	0.66
2:B:27:ASN:H	2:B:27:ASN:HD22	1.44	0.66
30:0:2533:C:C6	30:0:2533:C:H5'	2.31	0.66
3:C:184:ARG:NH2	30:0:450:C:OP1	2.29	0.66
30:0:559:U:C6	30:0:559:U:H5'	2.23	0.66
30:0:921:G:H4'	30:0:924:G:N1	2.11	0.66
30:0:1249:U:H2'	30:0:1250:C:C6	2.30	0.65
30:0:1603:A:H5'	30:0:1605:G:C4'	2.26	0.65
30:0:449:A:H3'	38:0:6214:HOH:O	1.95	0.65
26:Z:44:ARG:NH2	30:0:1771:U:H5'	2.09	0.65
30:0:2851:G:H2'	30:0:2902:A:H61	1.60	0.65
30:0:559:U:H6	30:0:559:U:C5'	2.09	0.65
2:B:179:LEU:O	2:B:183:GLU:HG2	1.96	0.65
12:L:143:THR:HG22	12:L:144:ASP:H	1.61	0.65
14:N:80:SER:HB2	38:N:8833:HOH:O	1.95	0.65
20:T:9:LYS:HE3	20:T:13:ARG:NH1	2.12	0.65
30:0:368:C:H2'	30:0:369:G:H5'	1.77	0.65
31:9:29:C:C5	31:9:30:C:C6	2.84	0.65
26:Z:78:ILE:HG21	26:Z:87:LYS:HE2	1.78	0.65
30:0:2707:C:H2'	30:0:2707:C:O2	1.96	0.65
38:D:7597:HOH:O	31:9:56:A:H2	1.79	0.65
16:P:88:GLN:NE2	30:0:1800:G:H1'	2.10	0.65
1:A:122:SER:HB2	1:A:164:ARG:NH1	2.11	0.65
21:U:56:ARG:HD2	30:0:2890:A:C1'	2.25	0.65
30:0:1061:C:H3'	38:0:5051:HOH:O	1.97	0.65
30:0:1132:A:N6	30:0:1229:C:H2'	2.12	0.65
30:0:1666:C:C2'	30:0:1667:A:H5''	2.27	0.65
30:0:213:G:N2	30:0:225:G:H2'	2.11	0.65
30:0:2597:U:H2'	30:0:2598:U:H5'	1.77	0.65
30:0:416:G:H5''	38:0:7402:HOH:O	1.96	0.65
30:0:696:C:H4'	38:0:7263:HOH:O	1.96	0.65
5:E:91:PHE:CE1	30:0:2694:A:H4'	2.32	0.65
9:I:110:ASP:O	30:0:1163:G:H5'	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.60	0.65
30:0:1385:G:H1'	38:0:4024:HOH:O	1.97	0.65
30:0:290:C:O2'	30:0:291:C:H5'	1.96	0.65
30:0:42:C:H1'	38:0:4645:HOH:O	1.97	0.65
38:O:1484:HOH:O	30:0:710:G:H1'	1.97	0.65
30:0:812:A:H2'	30:0:813:C:C6	2.31	0.65
2:B:238:ASN:HD22	2:B:240:GLY:N	1.90	0.65
30:0:2119:C:O2'	30:0:2120:U:H5'	1.97	0.65
16:P:81:LYS:O	30:0:1761:U:H5'	1.97	0.65
30:0:1586:G:O2'	30:0:1587:U:H5'	1.97	0.64
30:0:2892:G:C6	30:0:2893:C:C4	2.85	0.64
30:0:696:C:O2'	30:0:697:G:H5'	1.97	0.64
31:9:61:C:H2'	31:9:62:A:H8	1.62	0.64
30:0:1377:C:H5'	30:0:1377:C:C6	2.33	0.64
30:0:1422:U:H2'	30:0:1423:C:C6	2.32	0.64
30:0:1735:C:O2'	30:0:1736:A:H5'	1.97	0.64
30:0:1862:C:H1'	38:0:7203:HOH:O	1.96	0.64
38:B:8996:HOH:O	30:0:2766:A:H5'	1.97	0.64
30:0:441:A:H1'	30:0:442:A:N7	2.13	0.64
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.61	0.64
30:0:1819:G:H5'	38:0:4680:HOH:O	1.96	0.64
30:0:1972:U:C2'	30:0:1973:A:H5''	2.27	0.64
30:0:671:A:O2'	30:0:672:G:H2'	1.97	0.64
2:B:36:PRO:HA	2:B:168:GLY:HA3	1.78	0.64
21:U:56:ARG:HD2	30:0:2890:A:C8	2.33	0.64
27:1:9:GLY:HA2	30:0:1687:C:O2	1.98	0.64
30:0:281:U:H2'	30:0:282:C:O4'	1.98	0.64
30:0:693:A:H2'	30:0:694:A:C8	2.33	0.64
2:B:312:ARG:HD3	2:B:315:VAL:HG13	1.80	0.64
30:0:1706:G:H1'	30:0:1712:A:H61	1.61	0.64
30:0:2768:A:O2'	30:0:2769:C:H5'	1.97	0.64
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.38	0.64
5:E:143:GLN:HE22	30:0:2779:G:H21	1.44	0.64
5:E:20:ILE:HD11	5:E:40:VAL:HG11	1.79	0.64
23:W:6:GLN:HB2	23:W:26:ILE:HD11	1.79	0.64
26:Z:70:ARG:HH11	26:Z:83:TYR:HD1	1.46	0.64
3:C:78:ARG:HG3	3:C:78:ARG:NH1	2.13	0.64
30:0:1181:A:H2'	30:0:1182:C:H5'	1.80	0.64
30:0:1973:A:H2'	30:0:1974:G:O4'	1.96	0.64
30:0:2088:C:H2'	30:0:2089:A:H8	1.62	0.64
25:Y:154:ARG:HH22	30:0:1071:G:H4'	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:169:ARG:HD2	30:0:1328:A:OP1	1.98	0.64
30:0:459:A:H5''	38:0:9055:HOH:O	1.96	0.64
3:C:16:VAL:HG12	3:C:17:ASP:H	1.62	0.64
14:N:86:LEU:HD12	14:N:125:ALA:HB2	1.78	0.64
30:0:1748:U:C5	30:0:1749:U:C5	2.85	0.63
11:K:66:ARG:HH22	30:0:1994:A:P	2.21	0.63
8:H:27:PRO:HD3	8:H:123:ILE:HG22	1.79	0.63
21:U:23:HIS:HD2	21:U:27:ALA:HB3	1.63	0.63
30:0:2867:G:H2'	30:0:2868:C:C6	2.33	0.63
30:0:541:C:H2'	30:0:542:A:H5'	1.77	0.63
3:C:132:ASP:O	3:C:133:ARG:HG3	1.98	0.63
3:C:236:THR:HG21	38:C:8571:HOH:O	1.97	0.63
11:K:98:VAL:CG1	11:K:102:GLU:HA	2.28	0.63
18:R:40:ALA:O	18:R:44:VAL:HG23	1.99	0.63
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.63	0.63
30:0:1116:U:O2'	30:0:1118:A:C2	2.40	0.63
30:0:2727:A:H2'	30:0:2728:C:H5'	1.80	0.63
30:0:541:C:O2'	30:0:542:A:H5''	1.97	0.63
31:9:17:G:O2'	31:9:18:U:H5'	1.97	0.63
17:Q:26:PRO:O	17:Q:30:VAL:HG23	1.97	0.63
30:0:1835:U:H3'	38:0:5539:HOH:O	1.97	0.63
30:0:2032:U:O2'	30:0:2033:G:H5''	1.98	0.63
13:M:66:SER:HB3	13:M:128:TRP:CD1	2.33	0.63
13:M:164:THR:HG22	13:M:166:ALA:N	2.13	0.63
30:0:2659:U:H5''	38:0:4112:HOH:O	1.98	0.63
30:0:506:G:H22	30:0:509:A:H5'	1.63	0.63
23:W:88:THR:HG22	23:W:110:GLN:HB3	1.81	0.63
30:0:1985:U:H1'	38:0:4497:HOH:O	1.98	0.63
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.63
29:3:65:THR:O	29:3:82:GLY:HA3	1.99	0.63
31:9:91:C:H2'	31:9:92:G:O4'	1.99	0.63
1:A:211:LYS:HB3	1:A:212:PRO:HD2	1.79	0.63
26:Z:38:PHE:HB3	26:Z:42:TYR:CD1	2.33	0.63
30:0:1149:U:H5''	30:0:1151:G:O4'	1.98	0.63
30:0:1644:C:H2'	30:0:1645:U:C6	2.31	0.63
30:0:2291:A:H8	38:0:6453:HOH:O	1.81	0.63
30:0:2675:A:H1'	30:0:2813:A:C2	2.34	0.63
30:0:2824:C:H5''	30:0:2825:C:H5'	1.80	0.63
14:N:164:ASP:OD1	14:N:167:ASP:HA	1.98	0.63
14:N:37:ARG:HH12	31:9:6:C:C5'	1.95	0.63
30:0:2250:G:H2'	30:0:2251:G:O4'	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2766:A:O2'	30:0:2767:C:H5'	1.99	0.63
29:3:59:ASP:HB3	29:3:63:LYS:NZ	2.13	0.63
29:3:2:GLN:HB3	29:3:91:GLN:CD	2.19	0.63
2:B:280:VAL:HG13	2:B:333:GLU:O	1.99	0.63
4:D:131:THR:HG21	30:0:2348:C:H1'	1.79	0.63
22:V:42:ASN:HB3	38:V:7247:HOH:O	1.98	0.63
30:0:2782:G:H3'	38:0:5004:HOH:O	1.98	0.63
5:E:60:SER:OG	30:0:2784:A:H1'	1.98	0.63
30:0:279:C:C2'	30:0:280:C:H5'	2.29	0.63
30:0:630:A:H5''	38:0:4722:HOH:O	1.99	0.63
30:0:956:G:C8	38:0:9387:HOH:O	2.50	0.63
28:2:41:HIS:HB3	28:2:44:ARG:HB2	1.80	0.63
11:K:74:VAL:CG1	11:K:113:ILE:HG12	2.29	0.63
30:0:1165:G:H21	30:0:1173:A:C5'	2.12	0.62
30:0:2349:G:H2'	30:0:2350:G:H8	1.62	0.62
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.80	0.62
27:1:2:GLY:O	27:1:6:PRO:HG2	1.99	0.62
20:T:72:ILE:HD13	20:T:93:THR:HG22	1.81	0.62
26:Z:34:SER:HB2	38:0:7481:HOH:O	1.99	0.62
26:Z:41:ARG:HD2	30:0:1830:C:O2	1.98	0.62
30:0:1921:A:O2'	30:0:1922:A:H5'	1.98	0.62
29:3:54:LYS:HE2	30:0:2468:A:N7	2.14	0.62
30:0:1527:A:H1'	30:0:1528:A:C8	2.34	0.62
30:0:1351:G:H5'	38:0:3619:HOH:O	1.99	0.62
30:0:1878:G:H1'	38:0:6097:HOH:O	2.00	0.62
30:0:1889:C:H2'	30:0:1890:U:O4'	2.00	0.62
4:D:54:ALA:HB2	4:D:69:ILE:HD12	1.80	0.62
14:N:160:SER:HB3	31:9:51:A:H5'	1.82	0.62
21:U:49:LEU:HD12	38:U:3805:HOH:O	1.99	0.62
30:0:1477:C:H5'	30:0:1868:G:C5'	2.29	0.62
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.00	0.62
30:0:790:A:H1'	30:0:1710:A:O2'	1.99	0.62
30:0:229:G:O2'	30:0:230:C:H5'	2.00	0.62
5:E:153:ARG:HH12	30:0:2778:A:H1'	1.65	0.62
20:T:61:GLU:HG2	38:T:3851:HOH:O	1.99	0.62
30:0:1226:G:H5'	38:0:4509:HOH:O	1.98	0.62
29:3:68:LYS:NZ	30:0:2436:U:H5'	2.14	0.62
3:C:246:ARG:NH2	30:0:677:C:H4'	2.14	0.62
30:0:2510:C:H5'	30:0:2511:A:OP2	1.99	0.62
15:O:51:TYR:CE2	30:0:721:A:H5''	2.35	0.62
30:0:920:C:H4'	30:0:921:G:N2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:2:22:PRO:HG2	28:2:25:VAL:HG23	1.82	0.62
22:V:39:ALA:H	22:V:40:PRO:HD2	1.65	0.62
26:Z:53:ILE:O	26:Z:57:MET:HB2	2.00	0.62
30:0:1752:G:H2'	38:0:7531:HOH:O	2.00	0.62
30:0:303:C:O2'	30:0:304:G:H5'	2.00	0.62
30:0:630:A:H5'	38:0:9372:HOH:O	1.98	0.62
17:Q:14:LEU:HD21	17:Q:43:ILE:HD12	1.82	0.62
30:0:1131:G:H1'	38:0:3907:HOH:O	1.99	0.61
30:0:1279:U:C2'	30:0:1279:U:O2	2.48	0.61
30:0:2251:G:H2'	30:0:2252:A:C8	2.35	0.61
30:0:2300:A:H4'	30:0:2301:A:O5'	2.00	0.61
30:0:236:A:H4'	30:0:237:G:C5'	2.17	0.61
30:0:2439:C:H5'	38:0:5449:HOH:O	1.99	0.61
30:0:2775:A:C6	30:0:2799:A:C8	2.88	0.61
31:9:91:C:H1'	38:9:9149:HOH:O	1.98	0.61
3:C:129:HIS:CE1	3:C:231:ARG:HA	2.35	0.61
23:W:64:THR:O	23:W:68:THR:HG22	2.00	0.61
30:0:1477:C:O2'	30:0:1478:U:H5'	1.99	0.61
30:0:2576:A:H2'	38:0:7732:HOH:O	2.00	0.61
30:0:825:U:H5''	30:0:826:U:OP1	2.00	0.61
9:I:130:LEU:CD2	30:0:1167:G:H4'	2.29	0.61
22:V:55:ARG:O	22:V:59:ILE:HG12	2.01	0.61
30:0:2314:G:C2'	30:0:2315:C:H5'	2.30	0.61
25:Y:186:ARG:HG2	25:Y:186:ARG:HH11	1.65	0.61
30:0:1711:A:O2'	30:0:1712:A:H5'	2.00	0.61
30:0:2912:C:O5'	30:0:2912:C:H6	1.83	0.61
30:0:301:C:O2'	30:0:302:A:H5'	2.00	0.61
2:B:262:ARG:HG3	30:0:2716:G:H5'	1.83	0.61
7:G:12:ILE:HG23	38:0:5418:HOH:O	1.98	0.61
13:M:75:ARG:NH2	13:M:78:LYS:HE2	2.16	0.61
23:W:52:VAL:HG22	23:W:53:ALA:H	1.63	0.61
24:X:71:ARG:HD2	38:X:7542:HOH:O	1.99	0.61
30:0:1118:A:H8	30:0:1119:G:H5''	1.64	0.61
1:A:20:SER:HB3	30:0:1872:C:H5	1.65	0.61
2:B:336:GLN:O	30:0:2862:G:H4'	2.00	0.61
30:0:39:G:N2	30:0:444:C:C2	2.68	0.61
2:B:320:GLN:HE21	2:B:321:PRO:HD2	1.65	0.61
9:I:91:PHE:HD2	9:I:131:GLY:HA2	1.66	0.61
12:L:67:ARG:HB2	12:L:112:GLY:HA3	1.83	0.61
30:0:2526:C:H3'	30:0:2526:C:H6	1.65	0.61
30:0:705:C:H2'	30:0:705:C:O2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.81	0.61
23:W:13:MET:HE1	23:W:18:GLN:HA	1.81	0.61
30:0:1774:G:O2'	30:0:1775:A:H5'	2.01	0.61
30:0:228:C:H2'	30:0:229:G:H5'	1.80	0.61
30:0:877:G:C5'	30:0:878:G:OP1	2.46	0.61
31:9:20:G:H3'	38:9:9057:HOH:O	2.00	0.61
22:V:12:THR:HG22	22:V:15:GLU:CG	2.31	0.61
30:0:1676:G:O2'	30:0:1677:U:H5'	2.01	0.61
30:0:1856:C:H5'	30:0:1858:A:O4'	2.01	0.61
30:0:282:C:O2	30:0:282:C:H2'	2.00	0.61
30:0:2834:G:C2	30:0:2835:C:H1'	2.35	0.61
23:W:145:GLY:HA3	38:W:6373:HOH:O	2.00	0.61
30:0:1398:G:H2'	30:0:1399:A:H8	1.64	0.61
30:0:283:U:C5	30:0:284:C:C4	2.88	0.61
30:0:807:A:H2'	30:0:808:A:C8	2.36	0.61
31:9:39:U:HO2'	31:9:42:C:H5	1.48	0.61
30:0:1701:A:H4'	30:0:1702:U:C5'	2.30	0.61
30:0:558:C:H2'	30:0:559:U:H5'	1.81	0.61
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.82	0.61
11:K:10:GLN:N	11:K:10:GLN:HE21	1.96	0.61
30:0:1878:G:HO2'	30:0:1879:U:H6	1.42	0.60
38:3:9025:HOH:O	30:0:2468:A:H5'	2.00	0.60
30:0:31:C:H4'	38:0:7408:HOH:O	2.00	0.60
1:A:140:LEU:HB3	1:A:141:PRO:HD2	1.83	0.60
10:J:47:THR:HB	38:0:4807:HOH:O	2.01	0.60
30:0:1175:G:H1'	30:0:1193:A:C2'	2.31	0.60
30:0:1697:G:H4'	38:0:9347:HOH:O	2.02	0.60
30:0:2281:C:H2'	30:0:2282:U:H5'	1.82	0.60
29:3:9:THR:HG23	29:3:20:HIS:ND1	2.15	0.60
2:B:102:THR:HG23	2:B:182:VAL:HG12	1.81	0.60
2:B:320:GLN:HE21	2:B:321:PRO:CD	2.14	0.60
3:C:27:ARG:NH2	30:0:657:G:OP1	2.34	0.60
30:0:2071:C:H5'	38:0:9540:HOH:O	2.00	0.60
30:0:2312:G:C2'	30:0:2313:C:H5'	2.30	0.60
30:0:282:C:O2'	30:0:283:U:C5'	2.49	0.60
30:0:2872:U:H2'	30:0:2873:C:O4'	2.02	0.60
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.83	0.60
30:0:1201:C:H5''	38:0:6211:HOH:O	2.00	0.60
30:0:1495:C:H1'	30:0:1573:A:H1'	1.83	0.60
26:Z:84:CYS:HB3	30:0:1604:G:N2	2.15	0.60
30:0:38:G:O2'	30:0:39:G:H5'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:407:A:H3'	38:0:4438:HOH:O	2.01	0.60
25:Y:126:PRO:HG2	25:Y:128:PHE:CE1	2.36	0.60
30:0:1205:U:O2'	30:0:1206:U:H5''	2.01	0.60
30:0:1398:G:O2'	30:0:1399:A:H5'	2.02	0.60
30:0:1407:A:O2'	30:0:1408:U:H3'	2.01	0.60
30:0:1972:U:C2'	30:0:1973:A:C5'	2.80	0.60
30:0:2420:G:C2'	30:0:2421:G:H5'	2.30	0.60
30:0:51:G:H1'	38:0:9033:HOH:O	2.01	0.60
30:0:947:U:H2'	30:0:948:G:C8	2.36	0.60
2:B:72:THR:HB	38:B:9076:HOH:O	2.02	0.60
11:K:74:VAL:HG13	11:K:113:ILE:HG12	1.82	0.60
20:T:48:VAL:HG22	20:T:97:ARG:O	2.01	0.60
30:0:146:U:C2'	30:0:147:G:H5'	2.31	0.60
16:P:41:ARG:HH22	30:0:1500:U:P	2.24	0.60
30:0:2893:C:O2'	30:0:2894:C:H5'	2.01	0.60
31:9:18:U:H2'	31:9:19:G:C8	2.37	0.60
31:9:23:U:O2'	31:9:24:U:H4'	2.01	0.60
7:G:16:LYS:HE2	7:G:63:ARG:HH12	1.67	0.60
13:M:102:GLU:OE1	13:M:164:THR:HG21	2.01	0.60
30:0:2353:A:H4'	30:0:2354:A:O5'	2.01	0.60
29:3:31:THR:OG1	29:3:34:LYS:HD3	2.01	0.60
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.81	0.60
15:O:14:LEU:CD2	15:O:102:ILE:HD11	2.32	0.60
18:R:135:ALA:HB1	18:R:137:ASN:HD21	1.67	0.60
30:0:1844:C:H6	30:0:1844:C:O5'	1.84	0.60
30:0:2608:C:H3'	38:0:7790:HOH:O	2.02	0.60
31:9:26:C:H2'	31:9:27:C:C6	2.36	0.60
31:9:29:C:H2'	31:9:30:C:C5'	2.28	0.60
31:9:3:A:C6	31:9:22:G:H1'	2.36	0.60
33:B:8819:CL:CL	38:B:8997:HOH:O	2.54	0.60
13:M:188:ARG:HD3	30:0:155:C:OP2	2.02	0.60
10:J:82:THR:CG2	30:0:1242:A:H5'	2.20	0.60
30:0:307:G:H3'	38:0:6667:HOH:O	2.01	0.60
30:0:567:U:H5''	38:0:5254:HOH:O	2.02	0.60
2:B:79:MET:HB2	2:B:188:HIS:CE1	2.36	0.60
18:R:46:TYR:O	18:R:50:VAL:HG23	2.00	0.60
30:0:74:G:H2'	30:0:75:U:C6	2.37	0.60
30:0:947:U:H2'	30:0:948:G:H8	1.65	0.60
29:3:43:ASN:HB2	29:3:52:PHE:CE1	2.36	0.60
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.05	0.60
30:0:1878:G:O2'	30:0:1879:U:C6	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:319:A:H4'	30:0:338:C:C4	2.37	0.59
30:0:324:G:O2'	30:0:325:U:H5'	2.02	0.59
31:9:63:C:O2'	31:9:64:C:H5'	2.01	0.59
2:B:235:ARG:HD3	30:0:2091:G:H5''	1.83	0.59
16:P:91:LYS:O	16:P:95:GLU:HG3	2.02	0.59
30:0:1590:A:H1'	30:0:1606:A:C2	2.36	0.59
30:0:2686:C:C2	30:0:2709:G:N2	2.70	0.59
27:1:20:ARG:HG2	30:0:111:C:O2'	2.01	0.59
31:9:65:A:N6	31:9:112:U:C6	2.71	0.59
11:K:130:MET:SD	21:U:25:ASP:O	2.60	0.59
13:M:82:ARG:HH22	13:M:85:ARG:HH21	1.49	0.59
30:0:2403:C:H5'	38:0:6001:HOH:O	2.01	0.59
30:0:2718:C:H6	30:0:2718:C:H5'	1.67	0.59
30:0:2820:A:H2'	30:0:2821:C:C6	2.36	0.59
1:A:94:LEU:HG	1:A:99:ILE:HD11	1.84	0.59
3:C:236:THR:HA	38:C:8648:HOH:O	2.01	0.59
5:E:145:ALA:HB1	5:E:168:ILE:HD11	1.85	0.59
30:0:2867:G:H2'	30:0:2868:C:H6	1.67	0.59
30:0:653:U:H2'	30:0:654:A:C8	2.37	0.59
30:0:834:G:H4'	30:0:835:U:OP2	2.02	0.59
2:B:101:TRP:HB2	2:B:119:HIS:CD2	2.38	0.59
2:B:156:LYS:HB3	30:0:2846:C:H4'	1.84	0.59
12:L:79:ASP:HB3	38:L:8859:HOH:O	2.03	0.59
14:N:86:LEU:O	14:N:90:LEU:HG	2.02	0.59
30:0:1585:C:H2'	30:0:1586:G:C8	2.37	0.59
30:0:2809:G:H2'	30:0:2810:G:C8	2.37	0.59
30:0:2831:C:H2'	30:0:2832:C:H5'	1.82	0.59
30:0:2874:G:H3'	38:0:9586:HOH:O	2.02	0.59
30:0:652:G:C2	30:0:653:U:H1'	2.37	0.59
1:A:179:MET:HG2	1:A:186:TRP:CB	2.32	0.59
1:A:33:GLU:H	1:A:33:GLU:CD	2.06	0.59
2:B:62:ARG:HG2	2:B:65:MET:HE3	1.85	0.59
6:F:13:GLU:OE2	6:F:78:GLU:HG2	2.01	0.59
38:B:8993:HOH:O	30:0:2549:C:H1'	2.03	0.59
4:D:58:VAL:HG12	4:D:60:GLU:HG2	1.83	0.59
30:0:1702:U:H5''	38:0:7201:HOH:O	2.01	0.59
30:0:2846:C:H4'	38:0:5047:HOH:O	2.03	0.59
30:0:812:A:H2'	30:0:813:C:H6	1.68	0.59
8:H:37:GLY:HA3	8:H:87:LYS:HA	1.85	0.59
30:0:1380:U:C4	30:0:2748:G:C4	2.91	0.59
30:0:2065:C:O2'	30:0:2066:C:H5'	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:542:A:H5'	30:0:542:A:C8	2.29	0.59
30:0:590:A:H2'	30:0:591:A:H5'	1.83	0.59
2:B:215:VAL:HB	38:B:9089:HOH:O	2.02	0.59
8:H:155:ARG:NH1	30:0:2503:A:H5''	2.18	0.59
30:0:1563:G:H4'	38:0:4215:HOH:O	2.01	0.59
30:0:1566:C:O2'	30:0:1567:G:H5'	2.03	0.59
30:0:1972:U:H2'	30:0:1973:A:H5''	1.83	0.59
30:0:499:G:O2'	30:0:500:G:H5'	2.02	0.59
30:0:702:G:O2'	30:0:703:G:H5'	2.02	0.59
30:0:921:G:H4'	30:0:924:G:C6	2.37	0.59
31:9:54:A:C2	31:9:55:U:C2	2.91	0.59
2:B:145:HIS:HD2	2:B:146:THR:O	1.85	0.59
4:D:159:PRO:O	4:D:163:VAL:HG23	2.02	0.59
11:K:41:LYS:HA	30:0:2582:G:O3'	2.03	0.59
16:P:7:LYS:HD3	16:P:21:VAL:HG22	1.85	0.59
18:R:39:THR:HG23	18:R:107:GLU:O	2.03	0.59
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.84	0.59
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.85	0.59
13:M:137:ASN:ND2	30:0:145:A:H4'	2.18	0.59
30:0:255:A:H2'	30:0:256:C:H6	1.67	0.59
30:0:281:U:C2'	30:0:282:C:H5'	2.33	0.59
6:F:30:LYS:HB2	6:F:97:ALA:HB3	1.84	0.59
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.38	0.59
30:0:1568:G:O2'	30:0:1569:U:H5'	2.03	0.58
30:0:2563:U:H2'	30:0:2565:C:O5'	2.02	0.58
30:0:2724:U:H2'	30:0:2725:G:O4'	2.03	0.58
30:0:2826:G:C6	30:0:2913:A:C6	2.90	0.58
30:0:925:C:H3'	38:0:3826:HOH:O	2.02	0.58
26:Z:40:ALA:HA	30:0:1773:G:C8	2.38	0.58
30:0:1245:C:O5'	30:0:1245:C:H6	1.85	0.58
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.38	0.58
30:0:2825:C:H4'	30:0:2826:G:O5'	2.03	0.58
30:0:28:G:H1'	38:0:4650:HOH:O	2.03	0.58
29:3:47:GLY:HA2	30:0:2121:G:C4'	2.25	0.58
2:B:243:ASN:HB3	38:0:6624:HOH:O	2.02	0.58
2:B:297:VAL:HB	38:B:9076:HOH:O	2.03	0.58
8:H:98:LEU:HD11	8:H:127:ALA:HB2	1.85	0.58
30:0:1158:G:O2'	30:0:1159:G:H5'	2.03	0.58
9:I:83:GLY:H	30:0:1168:C:H5''	1.68	0.58
30:0:1187:U:H2'	38:0:6880:HOH:O	2.01	0.58
30:0:1290:G:H4'	38:0:7465:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2467:A:H5''	38:0:4285:HOH:O	2.03	0.58
30:0:951:A:C2'	30:0:952:G:H5'	2.33	0.58
3:C:79:ARG:O	3:C:87:ARG:HG2	2.04	0.58
4:D:28:GLY:HA2	4:D:69:ILE:HG23	1.85	0.58
12:L:145:LEU:HB2	38:L:8836:HOH:O	2.03	0.58
13:M:28:GLN:HA	13:M:31:TRP:HB2	1.85	0.58
26:Z:34:SER:HA	30:0:797:A:H4'	1.83	0.58
30:0:1186:C:H42	30:0:1190:G:H22	1.48	0.58
30:0:2590:U:H2'	30:0:2591:C:H5'	1.85	0.58
30:0:293:A:C4	30:0:360:A:C2	2.91	0.58
20:T:52:ARG:HD2	30:0:317:A:H5''	1.85	0.58
30:0:1711:A:C2'	30:0:1712:A:H5'	2.33	0.58
30:0:204:A:H2'	30:0:205:U:H5'	1.85	0.58
30:0:2784:A:H8	30:0:2784:A:O5'	1.87	0.58
3:C:182:ARG:HH12	30:0:450:C:H3'	1.67	0.58
12:L:18:HIS:HD2	30:0:902:G:N7	2.01	0.58
25:Y:234:VAL:HG12	25:Y:235:GLU:H	1.66	0.58
30:0:1520:G:C6	30:0:1521:C:C4	2.92	0.58
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.40	0.58
26:Z:70:ARG:HB2	26:Z:81:CYS:SG	2.44	0.58
30:0:1503:U:C2'	30:0:1504:A:H5'	2.34	0.58
30:0:164:G:H3'	38:0:3636:HOH:O	2.03	0.58
30:0:368:C:C2'	30:0:369:G:H5'	2.34	0.58
30:0:271:C:N4	30:0:378:A:C2	2.66	0.58
31:9:39:U:H1'	31:9:44:A:N6	2.19	0.58
2:B:162:MET:HG3	2:B:310:ARG:HD3	1.84	0.58
5:E:100:ASP:HB3	38:E:2789:HOH:O	2.02	0.58
30:0:1662:C:H2'	30:0:1663:G:O4'	2.03	0.58
30:0:2073:G:OP2	30:0:2490:A:H5'	2.03	0.58
30:0:2493:C:O2	30:0:2493:C:H2'	2.02	0.58
30:0:2505:G:H2'	30:0:2506:A:H5'	1.86	0.58
30:0:2624:A:H1'	38:0:9769:HOH:O	2.04	0.58
30:0:482:G:H4'	30:0:508:A:N1	2.19	0.58
30:0:951:A:O2'	30:0:952:G:H5'	2.03	0.58
31:9:54:A:C2	31:9:55:U:N3	2.72	0.58
2:B:267:LYS:HA	38:B:8996:HOH:O	2.04	0.58
17:Q:11:ARG:NH2	30:0:2363:G:H5''	2.19	0.58
26:Z:42:TYR:HA	30:0:1829:A:N6	2.16	0.58
30:0:1585:C:H2'	30:0:1586:G:H8	1.68	0.58
30:0:1634:G:H2'	30:0:1635:U:C6	2.38	0.58
30:0:1973:A:H5'	30:0:1973:A:H8	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2511:A:H2'	30:0:2512:U:O4'	2.03	0.58
30:0:2581:U:H1'	38:0:4452:HOH:O	2.03	0.58
30:0:412:C:O2'	30:0:413:G:H5'	2.02	0.58
30:0:544:G:H2'	30:0:545:G:H5''	1.85	0.58
30:0:625:U:H3'	38:0:3244:HOH:O	2.03	0.58
8:H:172:GLU:HB2	38:H:248:HOH:O	2.04	0.58
22:V:1:THR:HG23	22:V:2:VAL:H	1.69	0.58
30:0:1041:U:C2'	30:0:1042:U:H5'	2.34	0.58
30:0:1160:G:H5'	30:0:1161:A:H5'	0.78	0.58
30:0:1300:G:H1'	38:0:4652:HOH:O	2.03	0.58
30:0:2812:A:N7	38:0:7497:HOH:O	2.32	0.58
30:0:51:G:O2'	30:0:52:A:H5'	2.03	0.58
30:0:1057:A:H1'	30:0:2492:U:O2'	2.03	0.57
30:0:12:U:C2'	30:0:13:G:H5'	2.32	0.57
4:D:76:ARG:CZ	31:9:44:A:H1'	2.34	0.57
1:A:75:GLY:HA2	26:Z:88:PHE:HA	1.86	0.57
2:B:125:GLU:O	2:B:129:ARG:HG3	2.03	0.57
3:C:236:THR:CG2	3:C:239:ALA:H	2.16	0.57
11:K:20:CYS:SG	11:K:22:ASP:OD1	2.62	0.57
15:O:10:LEU:HD13	15:O:99:GLU:HG3	1.84	0.57
30:0:2705:U:H2'	30:0:2706:A:H8	1.68	0.57
30:0:2748:G:H5'	38:0:7523:HOH:O	2.04	0.57
30:0:820:G:H5'	30:0:821:U:H5'	1.86	0.57
10:J:70:PHE:HE1	30:0:2676:C:H4'	1.68	0.57
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.85	0.57
30:0:1166:A:H61	30:0:1180:U:H3	1.51	0.57
30:0:1216:G:H2'	30:0:1217:G:O4'	2.03	0.57
30:0:1256:C:H6	38:0:7140:HOH:O	1.87	0.57
30:0:1342:C:C2'	30:0:1343:C:H5'	2.34	0.57
30:0:590:A:C2'	30:0:591:A:H5'	2.33	0.57
30:0:821:U:H3'	38:0:3764:HOH:O	2.03	0.57
1:A:53:ALA:HB2	1:A:122:SER:OG	2.05	0.57
14:N:48:VAL:HG13	14:N:55:ASP:HB3	1.86	0.57
26:Z:90:GLY:HA3	26:Z:95:PRO:O	2.04	0.57
30:0:1503:U:O2'	30:0:1504:A:H5'	2.04	0.57
30:0:2712:G:H5'	38:0:5187:HOH:O	2.02	0.57
30:0:283:U:H5	30:0:284:C:C4	2.22	0.57
30:0:916:A:C2	30:0:928:G:C4	2.93	0.57
3:C:236:THR:HG22	3:C:239:ALA:N	2.15	0.57
20:T:18:GLU:O	20:T:21:LYS:HG2	2.03	0.57
30:0:1552:G:H2'	30:0:1553:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1555:G:H4'	30:0:1630:A:H2	1.69	0.57
30:0:1883:U:C2'	30:0:1884:G:H5'	2.34	0.57
30:0:694:A:H2'	30:0:695:C:C5'	2.27	0.57
30:0:727:G:H3'	30:0:728:C:H6	1.68	0.57
29:3:51:LYS:HG3	29:3:52:PHE:CD2	2.40	0.57
11:K:14:LYS:CB	11:K:45:PRO:HG2	2.35	0.57
30:0:1754:A:H5''	38:0:9757:HOH:O	2.04	0.57
30:0:1819:G:H2'	30:0:1820:G:H4'	1.85	0.57
30:0:2078:U:O2'	30:0:2079:G:H5'	2.05	0.57
30:0:2240:U:O2'	30:0:2241:C:H5'	2.04	0.57
30:0:2335:C:H2'	30:0:2336:G:H8	1.67	0.57
30:0:2828:G:H8	30:0:2828:G:O5'	1.87	0.57
30:0:544:G:C2'	30:0:545:G:H5''	2.35	0.57
3:C:8:LEU:HD11	3:C:143:ASP:O	2.04	0.57
5:E:125:GLU:HB2	5:E:132:THR:HG23	1.86	0.57
30:0:1189:A:H1'	30:0:1209:C:C1'	2.35	0.57
30:0:1577:U:O2'	30:0:1578:C:H5'	2.05	0.57
30:0:2001:G:O2'	30:0:2002:C:H5'	2.04	0.57
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.70	0.57
21:U:56:ARG:HG3	21:U:56:ARG:NH1	2.19	0.57
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.20	0.57
30:0:138:U:OP2	30:0:139:C:C5	2.58	0.57
30:0:1718:G:O2'	30:0:1719:G:H5'	2.04	0.57
30:0:2010:A:H2'	38:0:5933:HOH:O	2.03	0.57
18:R:68:HIS:O	30:0:2842:G:H5'	2.05	0.57
30:0:371:U:O2'	30:0:372:A:H5'	2.05	0.57
30:0:403:C:H3'	38:0:6286:HOH:O	2.05	0.57
1:A:153:ARG:HD3	38:A:9011:HOH:O	2.04	0.57
2:B:214:PRO:HD2	38:B:8989:HOH:O	2.05	0.57
5:E:153:ARG:NH1	30:0:2778:A:H1'	2.19	0.57
14:N:160:SER:CB	31:9:51:A:H5'	2.34	0.57
15:O:19:ARG:NH1	30:0:1276:U:H3'	2.19	0.57
21:U:13:ILE:HG12	21:U:32:CYS:HB3	1.86	0.57
21:U:33:SER:O	21:U:37:GLU:HG3	2.04	0.57
25:Y:216:ARG:HD2	38:Y:8871:HOH:O	2.03	0.57
26:Z:45:VAL:HG13	26:Z:49:ARG:HE	1.70	0.57
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.57
30:0:1971:G:H5'	38:0:7053:HOH:O	2.05	0.57
30:0:2407:G:O2'	30:0:2408:A:H5'	2.05	0.57
31:9:23:U:H2'	31:9:24:U:H4'	1.87	0.57
31:9:64:C:C2'	31:9:65:A:H5'	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ARG:HD2	30:0:1884:G:O6	2.03	0.57
2:B:41:PHE:CZ	2:B:79:MET:HG3	2.40	0.57
13:M:68:ARG:HD3	13:M:68:ARG:O	2.05	0.57
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.53	0.57
24:X:30:MET:HE1	24:X:55:ASN:HA	1.86	0.57
30:0:1079:A:OP2	30:0:1080:C:N4	2.36	0.56
30:0:10:U:C4	30:0:532:A:C8	2.94	0.56
30:0:2251:G:H2'	30:0:2252:A:H8	1.70	0.56
30:0:2769:C:C2'	30:0:2770:G:C5'	2.78	0.56
30:0:312:U:O2'	30:0:313:U:H5'	2.05	0.56
30:0:407:A:H2'	30:0:408:A:C8	2.40	0.56
10:J:116:LEU:HB2	10:J:119:THR:HG21	1.87	0.56
30:0:1020:A:H2'	30:0:1021:G:C8	2.40	0.56
30:0:1173:A:H4'	30:0:1174:A:C8	2.40	0.56
13:M:82:ARG:HD2	30:0:170:U:OP2	2.05	0.56
30:0:2110:G:O2'	30:0:2111:G:H5'	2.05	0.56
30:0:2265:U:H2'	30:0:2266:A:C8	2.40	0.56
30:0:2698:G:H2'	30:0:2699:A:O4'	2.05	0.56
30:0:2700:G:H3'	38:0:3575:HOH:O	2.05	0.56
31:9:54:A:HO2'	31:9:55:U:H5'	1.67	0.56
11:K:32:ILE:HD11	11:K:56:SER:HB2	1.86	0.56
30:0:1616:A:H5''	30:0:1617:C:OP1	2.05	0.56
30:0:1948:G:O2'	30:0:1949:G:H5'	2.05	0.56
30:0:2011:A:H5'	30:0:2013:G:H1'	1.87	0.56
30:0:695:C:O2'	30:0:696:C:H5'	2.04	0.56
30:0:947:U:O2'	30:0:948:G:H5'	2.05	0.56
14:N:48:VAL:CG1	14:N:55:ASP:HB3	2.35	0.56
23:W:38:THR:O	23:W:42:ARG:HB2	2.04	0.56
30:0:1183:C:N4	30:0:1184:C:H41	2.03	0.56
30:0:1928:C:H2'	30:0:1929:G:O4'	2.05	0.56
30:0:280:C:H2'	30:0:281:U:O4'	2.06	0.56
28:2:40:ARG:HG3	28:2:45:ASN:HB2	1.85	0.56
29:3:34:LYS:HB3	38:3:9001:HOH:O	2.05	0.56
11:K:98:VAL:HG13	11:K:102:GLU:HA	1.85	0.56
14:N:141:ARG:NH2	31:9:48:C:H4'	2.21	0.56
30:0:162:C:H2'	30:0:163:U:H5'	1.87	0.56
30:0:1735:C:H2'	30:0:1736:A:C8	2.40	0.56
13:M:171:ARG:NH2	30:0:189:A:OP1	2.38	0.56
30:0:2659:U:H3'	38:0:4379:HOH:O	2.05	0.56
31:9:33:U:H2'	38:9:9068:HOH:O	2.04	0.56
2:B:17:LYS:O	2:B:260:HIS:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:49:GLN:NE2	8:H:140:TYR:HE2	1.95	0.56
15:O:24:ALA:HB3	30:0:710:G:OP1	2.05	0.56
17:Q:45:PRO:O	30:0:2365:G:H4'	2.06	0.56
13:M:68:ARG:HG3	30:0:1469:C:OP1	2.05	0.56
30:0:1904:A:H2'	30:0:1905:U:O4'	2.05	0.56
30:0:2289:G:O2'	30:0:2290:U:H5'	2.06	0.56
30:0:2349:G:H2'	30:0:2350:G:C8	2.38	0.56
30:0:2064:U:H4'	30:0:2653:A:OP1	2.05	0.56
30:0:26:U:H5	38:0:3099:HOH:O	1.89	0.56
30:0:1042:U:O2'	30:0:1043:C:H5'	2.05	0.56
30:0:113:A:OP2	30:0:114:A:H2'	2.06	0.56
30:0:1434:A:O2'	30:0:1435:U:H2'	2.05	0.56
30:0:2502:C:H2'	30:0:2503:A:C5'	2.34	0.56
30:0:473:A:O2'	30:0:474:C:H5'	2.06	0.56
30:0:799:C:O2'	30:0:800:G:H5'	2.05	0.56
29:3:65:THR:HG23	33:3:8804:CL:CL	2.43	0.56
2:B:223:ARG:HD3	33:B:8819:CL:CL	2.43	0.56
30:0:1127:C:C5	30:0:1128:U:C4	2.94	0.56
30:0:138:U:OP2	30:0:139:C:H5	1.88	0.56
30:0:2595:U:O2'	30:0:2596:A:H5'	2.05	0.56
26:Z:34:SER:HA	30:0:797:A:C4'	2.36	0.56
29:3:18:GLN:HB3	38:3:9013:HOH:O	2.06	0.56
31:9:54:A:H2'	31:9:55:U:H5'	1.82	0.56
2:B:199:TYR:HE2	2:B:268:ARG:HB2	1.71	0.56
12:L:27:ARG:NH2	12:L:30:ARG:HD3	2.21	0.56
16:P:127:GLY:HA3	38:P:152:HOH:O	2.05	0.56
25:Y:165:GLU:HB3	38:0:6689:HOH:O	2.05	0.56
30:0:1292:G:HO2'	30:0:1293:U:H6	1.52	0.56
13:M:94:ARG:HD2	30:0:158:A:OP2	2.06	0.56
30:0:2241:C:O2'	30:0:2242:U:H5'	2.05	0.56
30:0:2514:U:OP1	30:0:2572:G:H1'	2.04	0.56
21:U:56:ARG:HD2	30:0:2890:A:H1'	1.87	0.56
27:1:28:HIS:HE1	30:0:776:A:OP1	1.88	0.56
30:0:473:A:O2'	30:0:890:C:H5'	2.05	0.56
1:A:27:LEU:HD21	1:A:55:VAL:HG21	1.88	0.56
3:C:4:THR:HA	3:C:15:GLU:HB3	1.88	0.56
13:M:24:GLN:HE22	13:M:27:ARG:HH11	1.53	0.56
21:U:44:ARG:HD3	21:U:49:LEU:CD1	2.35	0.56
30:0:1679:C:H5'	38:0:9332:HOH:O	2.06	0.56
30:0:1788:U:C2	30:0:1805:G:N2	2.73	0.56
30:0:2673:U:C4	30:0:2674:G:C6	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:18:U:H2'	31:9:19:G:H8	1.71	0.56
15:O:47:ARG:HG3	15:O:47:ARG:HH11	1.71	0.56
30:0:1020:A:H2'	30:0:1021:G:H8	1.71	0.56
30:0:1181:A:H2'	30:0:1182:C:O4'	2.06	0.56
30:0:2314:G:H2'	30:0:2315:C:H5'	1.87	0.56
30:0:2578:G:C8	30:0:2578:G:H5'	2.36	0.56
30:0:2911:C:H2'	30:0:2912:C:C6	2.42	0.56
3:C:174:ILE:HD11	30:0:338:C:H4'	1.89	0.56
30:0:660:A:H4'	30:0:661:G:O5'	2.06	0.56
12:L:41:HIS:HD2	30:0:926:A:O2'	1.89	0.56
31:9:49:G:H2'	31:9:50:G:O4'	2.06	0.56
2:B:68:THR:HG21	21:U:16:GLY:HA3	1.87	0.56
21:U:23:HIS:CD2	21:U:27:ALA:HB3	2.40	0.56
25:Y:142:SER:HB2	38:Y:8902:HOH:O	2.05	0.56
30:0:1116:U:H3	30:0:1246:A:N6	1.96	0.55
1:A:47:HIS:HD2	30:0:1654:U:C2'	2.18	0.55
30:0:1878:G:C1'	38:0:6097:HOH:O	2.53	0.55
30:0:558:C:C2'	30:0:559:U:C5'	2.68	0.55
30:0:1613:C:H2'	30:0:1614:G:O4'	2.06	0.55
29:3:33:MET:HG2	30:0:1922:A:H2'	1.88	0.55
30:0:2271:G:N3	30:0:2271:G:H2'	2.20	0.55
30:0:2325:U:O2'	30:0:2411:C:H1'	2.06	0.55
30:0:2852:A:H5''	38:0:5199:HOH:O	2.05	0.55
30:0:339:A:H2'	38:0:4203:HOH:O	2.06	0.55
30:0:684:G:H5''	38:0:4053:HOH:O	2.06	0.55
30:0:858:U:H2'	30:0:859:C:H6	1.71	0.55
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.88	0.55
25:Y:99:ALA:HB2	25:Y:233:TYR:CZ	2.42	0.55
30:0:1165:G:H21	30:0:1173:A:H5''	1.72	0.55
30:0:1172:G:H1'	38:0:4940:HOH:O	2.05	0.55
30:0:1183:C:H41	30:0:1192:A:H5'	1.72	0.55
30:0:1512:G:O2'	30:0:1513:C:H5'	2.05	0.55
30:0:2113:G:C6	30:0:2114:C:C4	2.94	0.55
30:0:735:C:C6	30:0:736:A:C8	2.94	0.55
3:C:115:LEU:HD21	3:C:243:VAL:HG13	1.86	0.55
23:W:52:VAL:HG22	23:W:53:ALA:N	2.20	0.55
30:0:2668:G:H2'	30:0:2669:U:C6	2.42	0.55
30:0:913:A:O5'	30:0:913:A:H8	1.90	0.55
30:0:920:C:H5'	30:0:921:G:C4	2.41	0.55
3:C:1:MET:HG2	3:C:2:GLN:H	1.72	0.55
25:Y:210:GLY:HA2	38:0:5285:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:44:ARG:HB2	30:0:1886:A:O2'	2.05	0.55
30:0:1625:U:C6	30:0:1625:U:C3'	2.85	0.55
2:B:229:ARG:NH2	30:0:1753:C:O2	2.39	0.55
30:0:2250:G:N2	30:0:2251:G:H1'	2.21	0.55
30:0:310:U:H2'	30:0:311:C:C6	2.41	0.55
29:3:59:ASP:HB3	29:3:63:LYS:HZ3	1.72	0.55
3:C:21:VAL:HG13	38:C:8594:HOH:O	2.05	0.55
7:G:16:LYS:HE2	7:G:63:ARG:NH1	2.21	0.55
24:X:76:ARG:HH11	24:X:76:ARG:HG3	1.72	0.55
38:Y:8879:HOH:O	30:0:1355:A:H5''	2.06	0.55
30:0:1562:C:N4	38:0:5836:HOH:O	2.38	0.55
30:0:1909:A:H2'	30:0:1910:A:C8	2.42	0.55
29:3:47:GLY:CA	30:0:2121:G:H4'	2.29	0.55
30:0:956:G:H3'	38:0:9387:HOH:O	2.06	0.55
3:C:149:LYS:HB2	3:C:152:GLU:HG3	1.89	0.55
3:C:162:VAL:HG22	3:C:232:LEU:HD21	1.87	0.55
10:J:19:MET:HE1	10:J:132:LEU:HD21	1.87	0.55
26:Z:63:CYS:SG	26:Z:81:CYS:CB	2.94	0.55
30:0:1691:A:H5''	38:0:3140:HOH:O	2.06	0.55
30:0:1736:A:H1'	38:0:7566:HOH:O	2.07	0.55
30:0:212:A:O4'	30:0:214:U:C6	2.59	0.55
30:0:545:G:C5'	30:0:545:G:C8	2.81	0.55
30:0:571:C:O5'	30:0:571:C:H6	1.90	0.55
30:0:822:C:C2	30:0:823:U:C5	2.94	0.55
30:0:835:U:H3'	38:0:9381:HOH:O	2.06	0.55
2:B:36:PRO:HA	2:B:168:GLY:CA	2.36	0.55
23:W:119:HIS:HD2	23:W:120:PRO:O	1.89	0.55
30:0:2274:A:H2'	30:0:2275:G:C8	2.42	0.55
30:0:2868:C:H1'	38:0:7107:HOH:O	2.07	0.55
30:0:401:C:H2'	30:0:402:U:H6	1.72	0.55
30:0:696:C:HO2'	30:0:697:G:H5'	1.71	0.55
29:3:90:PHE:CD1	29:3:90:PHE:N	2.75	0.55
31:9:59:C:C2	31:9:60:C:C5	2.94	0.55
2:B:102:THR:HG21	2:B:182:VAL:O	2.07	0.55
4:D:140:ARG:HG3	4:D:140:ARG:HH11	1.72	0.55
13:M:111:ASN:HB2	38:M:8852:HOH:O	2.07	0.55
30:0:1156:C:O2'	30:0:1157:C:H5'	2.07	0.55
30:0:1175:G:H2'	30:0:1176:C:C6	2.42	0.55
30:0:1166:A:C6	30:0:1181:A:C2	2.95	0.55
30:0:1200:A:N1	30:0:1201:C:C2	2.75	0.55
30:0:130:C:O2'	30:0:131:A:N7	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:291:C:H2'	30:0:292:G:O4'	2.07	0.55
28:2:43:ARG:HH22	30:0:1684:A:C1'	2.16	0.55
5:E:132:THR:HB	38:E:2227:HOH:O	2.06	0.55
13:M:70:GLY:CA	30:0:2263:G:H4'	2.37	0.55
19:S:37:VAL:O	19:S:41:VAL:HG23	2.05	0.55
30:0:1905:U:H2'	30:0:1906:C:H6	1.72	0.55
30:0:1849:G:H1'	30:0:2011:A:N1	2.22	0.55
30:0:2584:G:H4'	38:0:7102:HOH:O	2.07	0.55
30:0:2689:A:C2'	30:0:2690:U:H5'	2.37	0.55
30:0:2790:C:HO2'	30:0:2791:U:H6	1.55	0.55
30:0:777:U:OP2	30:0:777:U:H4'	2.07	0.55
5:E:118:ILE:HG23	5:E:144:THR:HG21	1.89	0.55
5:E:53:GLU:HB3	5:E:55:ASN:ND2	2.21	0.55
30:0:1377:C:H6	30:0:1377:C:C5'	2.20	0.54
30:0:1903:U:O2'	30:0:1904:A:N7	2.40	0.54
30:0:1909:A:N1	30:0:2128:G:H1'	2.22	0.54
30:0:2782:G:N2	30:0:2783:A:N6	2.55	0.54
30:0:690:G:H4'	30:0:741:C:O2	2.06	0.54
30:0:820:G:H5'	30:0:821:U:C5'	2.37	0.54
30:0:941:G:C5	30:0:942:U:C4	2.95	0.54
3:C:132:ASP:HB2	3:C:161:ASP:HB3	1.89	0.54
3:C:2:GLN:HB3	38:C:8581:HOH:O	2.07	0.54
14:N:110:THR:HB	14:N:113:SER:OG	2.07	0.54
1:A:76:VAL:HG23	26:Z:87:LYS:HB3	1.88	0.54
30:0:1593:C:H1'	38:0:6083:HOH:O	2.06	0.54
30:0:363:C:O2'	30:0:364:U:H5'	2.07	0.54
30:0:814:G:H2'	30:0:815:U:O4'	2.07	0.54
30:0:960:G:H8	38:0:5945:HOH:O	1.89	0.54
29:3:12:PRO:HG2	29:3:13:HIS:HD2	1.71	0.54
31:9:58:G:N7	31:9:59:C:C4	2.75	0.54
2:B:232:TRP:CZ3	30:0:2614:C:H5''	2.41	0.54
5:E:108:LEU:HD11	5:E:164:ASP:HB2	1.88	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
30:0:1015:C:H4'	38:0:6566:HOH:O	2.06	0.54
30:0:1175:G:H4'	38:0:6842:HOH:O	2.07	0.54
30:0:2032:U:C2'	30:0:2033:G:C5'	2.86	0.54
30:0:2032:U:C2'	30:0:2033:G:H5''	2.38	0.54
30:0:2524:G:H21	30:0:2526:C:H41	1.55	0.54
30:0:2869:G:H5'	38:0:5457:HOH:O	2.07	0.54
27:1:28:HIS:HD2	27:1:30:LYS:H	1.53	0.54
2:B:140:LEU:HA	38:B:9051:HOH:O	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:PHE:CE1	2:B:79:MET:HG3	2.43	0.54
9:I:78:ALA:HB2	9:I:95:LEU:HD21	1.89	0.54
14:N:114:LYS:O	14:N:118:ILE:HG13	2.07	0.54
14:N:130:PRO:HA	38:N:8837:HOH:O	2.06	0.54
30:0:1447:U:OP1	30:0:1506:U:N3	2.39	0.54
30:0:1876:C:H4'	30:0:1877:G:OP2	2.08	0.54
30:0:2281:C:C2'	30:0:2282:U:H5'	2.38	0.54
31:9:27:C:H2'	31:9:28:U:O4'	2.08	0.54
5:E:85:GLU:HG2	5:E:130:GLU:HG2	1.89	0.54
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.08	0.54
13:M:59:GLY:HA3	13:M:141:ILE:HD12	1.90	0.54
30:0:1139:U:H2'	30:0:1140:C:H6	1.72	0.54
15:O:19:ARG:HH22	30:0:1278:A:P	2.31	0.54
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.22	0.54
30:0:2477:C:O2'	30:0:2478:U:H5'	2.07	0.54
31:9:36:C:C5	31:9:37:C:C5	2.96	0.54
1:A:192:VAL:CG1	1:A:207:GLN:HB3	2.38	0.54
9:I:87:PRO:HD2	30:0:1180:U:H1'	1.89	0.54
9:I:91:PHE:CD2	9:I:131:GLY:HA2	2.42	0.54
12:L:143:THR:HG22	12:L:144:ASP:N	2.22	0.54
13:M:99:ARG:HE	13:M:170:ASN:ND2	1.96	0.54
30:0:1697:G:H5'	38:0:5475:HOH:O	2.08	0.54
30:0:2081:A:H2'	30:0:2082:G:O4'	2.08	0.54
30:0:2107:U:O2'	30:0:2108:A:H5'	2.07	0.54
30:0:2321:A:C4	30:0:2323:G:C8	2.95	0.54
30:0:236:A:H4'	30:0:237:G:OP1	2.08	0.54
30:0:2831:C:H3'	38:0:7197:HOH:O	2.07	0.54
30:0:312:U:C2	30:0:320:G:N2	2.76	0.54
30:0:710:G:O2'	30:0:711:G:H5'	2.08	0.54
1:A:195:ASN:ND2	30:0:877:G:C8	2.76	0.54
30:0:963:C:O2	30:0:1005:A:N1	2.40	0.54
29:3:60:LYS:HB3	29:3:62:THR:O	2.07	0.54
12:L:67:ARG:O	12:L:71:GLU:HG3	2.08	0.54
30:0:1617:C:C5	30:0:1643:C:H4'	2.42	0.54
30:0:2078:U:H2'	30:0:2079:G:C8	2.42	0.54
30:0:2892:G:C5	30:0:2893:C:C5	2.95	0.54
30:0:461:C:N3	30:0:479:G:H5'	2.22	0.54
30:0:623:U:O2'	30:0:624:U:H5'	2.08	0.54
30:0:661:G:C5	30:0:686:A:C2	2.96	0.54
30:0:706:G:HO2'	30:0:707:C:H6	1.53	0.54
30:0:960:G:N3	30:0:960:G:C3'	2.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:19:ARG:HH21	31:9:11:A:P	2.30	0.54
16:P:35:ILE:HD13	38:P:171:HOH:O	2.08	0.54
30:0:1175:G:H1'	30:0:1193:A:H2'	1.89	0.54
30:0:1676:G:H1'	38:0:9441:HOH:O	2.08	0.54
30:0:1850:U:H2'	30:0:1851:G:H8	1.73	0.54
30:0:2045:G:H5''	38:0:7204:HOH:O	2.06	0.54
30:0:2256:G:O2'	30:0:2257:G:H5'	2.08	0.54
30:0:2670:G:O2'	30:0:2671:U:H5'	2.08	0.54
27:1:16:HIS:HD2	30:0:470:U:O2'	1.91	0.54
31:9:30:C:O2	31:9:30:C:H2'	2.08	0.54
2:B:62:ARG:HA	2:B:65:MET:HE3	1.88	0.54
4:D:135:VAL:HG21	4:D:139:TYR:CD1	2.43	0.54
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.90	0.54
18:R:99:ALA:HB1	18:R:109:MET:CE	2.37	0.54
15:O:19:ARG:HH11	30:0:1276:U:H3'	1.73	0.54
30:0:1625:U:H5''	38:0:5995:HOH:O	2.07	0.54
30:0:2487:C:H5	38:0:4858:HOH:O	1.91	0.54
30:0:2787:C:H5	38:0:4605:HOH:O	1.90	0.54
30:0:2908:A:H8	30:0:2908:A:O5'	1.91	0.54
30:0:334:G:C4	30:0:335:U:C6	2.96	0.54
13:M:164:THR:CG2	13:M:165:GLY:N	2.70	0.54
30:0:2831:C:H2'	30:0:2832:C:C5'	2.38	0.54
30:0:541:C:C2'	30:0:542:A:C5'	2.78	0.54
30:0:853:C:H2'	30:0:854:G:O4'	2.08	0.54
28:2:13:LYS:O	28:2:17:GLN:HG3	2.07	0.54
31:9:23:U:C2'	31:9:24:U:H4'	2.38	0.54
30:0:1453:G:H2'	30:0:1454:U:O4'	2.07	0.53
30:0:1525:G:H5'	30:0:1526:A:OP2	2.08	0.53
30:0:2106:C:H2'	30:0:2107:U:C6	2.43	0.53
30:0:2599:A:H5''	38:0:3367:HOH:O	2.08	0.53
30:0:30:U:H5''	38:0:5777:HOH:O	2.08	0.53
30:0:338:C:H5''	38:0:3793:HOH:O	2.07	0.53
30:0:354:A:H2'	30:0:355:C:H6	1.73	0.53
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.91	0.53
2:B:238:ASN:ND2	2:B:240:GLY:H	1.92	0.53
8:H:99:ARG:NH1	30:0:1055:G:OP2	2.41	0.53
14:N:132:ASN:HD22	30:0:2413:A:H4'	1.72	0.53
25:Y:97:LEU:HA	25:Y:234:VAL:O	2.08	0.53
30:0:1268:C:H2'	30:0:1269:G:H8	1.73	0.53
30:0:2321:A:C5	30:0:2323:G:C8	2.96	0.53
30:0:2379:G:N3	30:0:2418:G:H2'	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2553:A:N3	30:0:2553:A:H2'	2.23	0.53
30:0:2563:U:O2'	30:0:2564:G:H3'	2.08	0.53
30:0:2769:C:H2'	30:0:2770:G:C4'	2.37	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.90	0.53
15:O:105:ASN:HD21	15:O:109:SER:H	1.56	0.53
16:P:7:LYS:HD3	16:P:21:VAL:CG2	2.38	0.53
30:0:1226:G:C4	30:0:1227:C:C5	2.96	0.53
30:0:1311:G:C2	30:0:1312:G:C8	2.97	0.53
2:B:212:GLN:HA	30:0:1733:A:H4'	1.89	0.53
30:0:2465:A:H5'	38:0:6910:HOH:O	2.07	0.53
30:0:421:C:H2'	30:0:422:G:H8	1.74	0.53
31:9:73:A:H61	31:9:108:C:H42	1.57	0.53
1:A:33:GLU:O	1:A:34:ASP:HB2	2.08	0.53
18:R:25:PHE:HB3	38:R:8914:HOH:O	2.07	0.53
23:W:35:VAL:HG23	23:W:41:TYR:CD2	2.43	0.53
30:0:1754:A:H2'	30:0:1755:A:O4'	2.09	0.53
1:A:20:SER:HB3	30:0:1872:C:C5	2.44	0.53
30:0:2703:A:H2'	30:0:2704:C:C6	2.40	0.53
30:0:491:C:O2'	30:0:492:C:H5'	2.09	0.53
30:0:869:G:OP2	30:0:869:G:C8	2.62	0.53
31:9:114:G:H2'	31:9:115:C:C6	2.43	0.53
12:L:11:ARG:O	30:0:903:U:C2	2.61	0.53
23:W:5:VAL:HG22	23:W:32:CYS:HB2	1.91	0.53
30:0:1271:A:H2'	30:0:1272:C:C6	2.43	0.53
30:0:1741:U:C4	30:0:2033:G:C8	2.96	0.53
30:0:1762:C:O2'	30:0:1763:C:H5'	2.08	0.53
30:0:2119:C:C2'	30:0:2120:U:H5'	2.38	0.53
30:0:213:G:H22	30:0:225:G:H2'	1.72	0.53
30:0:2831:C:C2	30:0:2910:A:C2	2.96	0.53
30:0:2895:C:H2'	38:0:9579:HOH:O	2.08	0.53
30:0:549:A:C2	30:0:550:C:C2	2.97	0.53
30:0:597:A:O2'	30:0:598:C:H5'	2.08	0.53
30:0:718:C:C2'	30:0:718:C:O2	2.55	0.53
8:H:49:GLN:HG3	8:H:140:TYR:CE2	2.43	0.53
16:P:71:TYR:CE2	30:0:1790:C:H5	2.26	0.53
30:0:1278:A:C4'	30:0:1279:U:C4	2.74	0.53
30:0:2078:U:H2'	30:0:2079:G:H8	1.74	0.53
30:0:2321:A:H2'	30:0:2321:A:N3	2.24	0.53
30:0:2501:G:H1	30:0:2519:C:H42	1.56	0.53
21:U:56:ARG:CD	30:0:2890:A:H1'	2.38	0.53
30:0:466:A:H2'	30:0:467:G:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:535:G:C5	30:0:2063:U:C4	2.96	0.53
29:3:68:LYS:HZ1	30:0:2436:U:H5'	1.73	0.53
31:9:58:G:C8	31:9:59:C:C5	2.97	0.53
8:H:69:ARG:HD3	38:H:239:HOH:O	2.08	0.53
11:K:89:LYS:HA	38:K:7064:HOH:O	2.08	0.53
30:0:1706:G:C6	30:0:1707:G:C6	2.97	0.53
30:0:1806:G:C5	30:0:1807:U:C5	2.97	0.53
30:0:1819:G:H5'	38:0:5785:HOH:O	2.07	0.53
29:3:31:THR:O	30:0:1923:G:H4'	2.09	0.53
30:0:195:C:H2'	30:0:196:G:H5'	1.91	0.53
30:0:1972:U:O2'	30:0:1973:A:H5''	2.09	0.53
30:0:2321:A:H4'	30:0:2322:U:OP1	2.08	0.53
30:0:398:U:H2'	30:0:399:C:C6	2.44	0.53
30:0:561:G:N3	30:0:562:A:C8	2.77	0.53
2:B:305:ASP:O	2:B:306:LYS:HB2	2.09	0.53
14:N:11:ARG:HG3	14:N:14:ARG:NH1	2.23	0.53
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.23	0.53
30:0:1167:G:H2'	30:0:1168:C:H6	1.71	0.53
30:0:1769:C:O2'	30:0:1770:U:H5'	2.09	0.53
30:0:191:A:H61	30:0:435:A:N6	2.06	0.53
30:0:2250:G:C2	30:0:2251:G:H1'	2.44	0.53
30:0:2613:G:O2'	30:0:2614:C:H5'	2.09	0.53
30:0:2864:U:C2'	30:0:2865:G:H5'	2.38	0.53
13:M:179:GLY:O	30:0:399:C:H5'	2.08	0.53
30:0:424:C:H2'	30:0:425:U:C6	2.44	0.53
23:W:154:ARG:NH1	30:0:588:G:O6	2.40	0.53
30:0:69:A:H2'	30:0:70:A:OP2	2.09	0.53
30:0:735:C:C5	30:0:736:A:C5	2.97	0.53
1:A:164:ARG:HB3	1:A:164:ARG:HH11	1.73	0.53
1:A:199:HIS:HD2	1:A:201:PHE:N	2.00	0.53
2:B:141:ARG:HD2	2:B:163:GLU:OE2	2.08	0.53
10:J:39:VAL:HG22	10:J:107:ASN:HA	1.91	0.53
11:K:41:LYS:O	11:K:42:ASN:HB2	2.09	0.53
13:M:187:LEU:CD2	13:M:194:GLY:HA3	2.38	0.53
14:N:154:LEU:C	14:N:156:GLU:H	2.11	0.53
22:V:44:GLY:O	22:V:48:GLU:HG2	2.08	0.53
30:0:1158:G:C2'	30:0:1159:G:H5'	2.39	0.53
30:0:1913:C:H2'	30:0:1914:C:H6	1.73	0.53
30:0:1922:A:N1	30:0:2449:G:O2'	2.38	0.53
30:0:1968:A:H2'	30:0:1969:A:C8	2.44	0.53
30:0:2336:G:H2'	38:0:6275:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:334:G:H2'	30:0:335:U:O4'	2.08	0.53
2:B:62:ARG:HA	2:B:65:MET:CE	2.38	0.53
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.74	0.53
10:J:41:ALA:HB3	38:J:8863:HOH:O	2.09	0.53
16:P:115:SER:OG	16:P:118:GLN:HG3	2.08	0.53
30:0:74:G:H1	30:0:103:C:H42	1.55	0.53
30:0:1844:C:O2'	30:0:1845:A:H5'	2.08	0.53
30:0:2642:G:H2'	30:0:2643:G:O4'	2.09	0.53
9:I:108:HIS:H	9:I:109:PRO:HD2	1.74	0.53
14:N:38:LYS:HE2	14:N:107:ASN:ND2	2.24	0.53
30:0:1014:A:H2'	30:0:1015:C:H5'	1.90	0.52
30:0:1188:A:C6	30:0:1189:A:C6	2.97	0.52
30:0:1244:U:H4'	30:0:1246:A:O4'	2.09	0.52
30:0:1451:C:H5'	30:0:1505:U:C5	2.44	0.52
30:0:2037:C:H3'	38:0:6684:HOH:O	2.09	0.52
30:0:216:A:O2'	30:0:217:C:H5'	2.09	0.52
30:0:2719:A:H2'	30:0:2720:C:H5'	1.90	0.52
30:0:488:U:H2'	38:0:3993:HOH:O	2.08	0.52
31:9:20:G:O2'	31:9:21:G:H5'	2.09	0.52
31:9:37:C:O2	31:9:47:A:H1'	2.09	0.52
31:9:58:G:C6	31:9:59:C:C2	2.97	0.52
1:A:105:VAL:HG13	1:A:155:THR:O	2.09	0.52
1:A:45:ILE:HG22	26:Z:78:ILE:HG12	1.89	0.52
8:H:26:ILE:HA	8:H:123:ILE:HG21	1.91	0.52
8:H:159:LYS:HG2	30:0:2519:C:O2	2.09	0.52
30:0:1164:U:H5	38:0:6024:HOH:O	1.91	0.52
30:0:675:U:H2'	30:0:676:C:H5'	1.90	0.52
15:O:25:VAL:HG13	30:0:709:G:O3'	2.10	0.52
23:W:4:LEU:HD22	23:W:54:PHE:HB3	1.90	0.52
30:0:125:U:H2'	38:0:3760:HOH:O	2.10	0.52
30:0:1515:A:H2'	30:0:1516:U:C6	2.44	0.52
30:0:1557:G:O2'	30:0:1558:C:H5'	2.09	0.52
30:0:1684:A:O2'	30:0:1685:A:H5''	2.10	0.52
13:M:73:ARG:HH21	30:0:2263:G:H5''	1.70	0.52
30:0:271:C:C2	30:0:273:G:O4'	2.61	0.52
30:0:2901:C:H6	30:0:2901:C:O5'	1.93	0.52
3:C:43:LYS:HG2	30:0:449:A:N7	2.24	0.52
30:0:622:G:O2'	30:0:623:U:H5'	2.10	0.52
31:9:1:U:C4'	31:9:3:A:OP1	2.58	0.52
5:E:126:ILE:HA	5:E:131:LEU:HD23	1.91	0.52
13:M:24:GLN:NE2	13:M:27:ARG:HH11	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:33:SER:O	19:S:37:VAL:HG23	2.10	0.52
30:0:1359:U:O5'	30:0:1360:C:H5''	2.10	0.52
30:0:1664:A:OP1	30:0:1664:A:H8	1.92	0.52
30:0:1865:A:H2'	30:0:1866:A:C8	2.44	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.09	0.52
30:0:2407:G:H2'	30:0:2408:A:O4'	2.09	0.52
30:0:249:G:N2	30:0:250:C:C2	2.77	0.52
30:0:2783:A:O2'	30:0:2784:A:H5'	2.09	0.52
30:0:40:C:H6	30:0:40:C:O5'	1.93	0.52
30:0:24:G:N2	30:0:518:G:H1'	2.24	0.52
28:2:49:GLU:HB2	38:2:131:HOH:O	2.08	0.52
31:9:38:A:C2	31:9:39:U:C4	2.97	0.52
11:K:66:ARG:HH12	30:0:1992:U:H3'	1.75	0.52
20:T:26:THR:HG23	20:T:97:ARG:HG3	1.90	0.52
23:W:130:HIS:NE2	31:9:88:G:OP1	2.42	0.52
30:0:1590:A:C2	30:0:1606:A:H1'	2.44	0.52
30:0:204:A:C2'	30:0:205:U:H5'	2.39	0.52
30:0:916:A:C2	30:0:928:G:N3	2.78	0.52
29:3:68:LYS:HG2	29:3:77:ALA:HB3	1.91	0.52
14:N:55:ASP:OD2	31:9:7:G:H4'	2.09	0.52
2:B:226:LYS:HG2	2:B:230:GLN:NE2	2.25	0.52
6:F:53:ASP:OD1	6:F:80:GLN:HB2	2.10	0.52
13:M:81:ARG:HB3	13:M:86:GLN:HG2	1.91	0.52
30:0:1139:U:H2'	30:0:1140:C:C6	2.45	0.52
30:0:1180:U:O2'	30:0:1181:A:H5'	2.10	0.52
30:0:1641:A:C2'	30:0:1642:A:H5'	2.40	0.52
30:0:1649:G:H1'	38:0:5498:HOH:O	2.09	0.52
30:0:1087:G:O2'	33:0:8822:CL:CL	2.55	0.52
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.52
1:A:66:ARG:HH11	1:A:66:ARG:HB2	1.74	0.52
4:D:18:ILE:HD13	4:D:84:LEU:HD12	1.91	0.52
5:E:153:ARG:HH12	30:0:2778:A:C1'	2.22	0.52
18:R:111:ILE:HG23	18:R:145:LEU:HD11	1.90	0.52
18:R:132:ARG:HH22	30:0:2055:A:H4'	1.74	0.52
20:T:106:GLU:HG3	38:T:4913:HOH:O	2.09	0.52
30:0:1052:G:H2'	30:0:1052:G:N3	2.24	0.52
30:0:1886:A:H4'	38:0:9333:HOH:O	2.09	0.52
30:0:1890:U:H4'	30:0:2010:A:C6	2.44	0.52
30:0:1930:A:H2'	30:0:1931:A:C8	2.44	0.52
30:0:2041:G:O2'	30:0:2042:U:H5'	2.10	0.52
30:0:228:C:C2'	30:0:229:G:H5'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:C6	30:0:2526:C:C3'	2.93	0.52
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.10	0.52
28:2:18:ASN:HD21	28:2:40:ARG:HB3	1.74	0.52
31:9:58:G:C5	31:9:59:C:C2	2.98	0.52
2:B:223:ARG:HG3	2:B:232:TRP:O	2.10	0.52
38:I:1549:HOH:O	30:0:1180:U:H1'	2.10	0.52
30:0:2637:A:C5'	38:0:4897:HOH:O	2.55	0.52
30:0:2651:C:H2'	30:0:2652:U:O4'	2.10	0.52
30:0:506:G:N2	30:0:509:A:H5''	2.18	0.52
30:0:595:U:H3'	38:0:6474:HOH:O	2.09	0.52
30:0:734:U:O2'	30:0:736:A:N7	2.33	0.52
30:0:800:G:H2'	30:0:801:U:C6	2.45	0.52
27:1:11:LYS:HG2	30:0:777:U:O2'	2.10	0.52
31:9:34:A:H2'	31:9:35:C:O4'	2.10	0.52
18:R:18:LEU:HB2	18:R:143:VAL:HG13	1.91	0.52
30:0:1183:C:C4	30:0:1184:C:N4	2.78	0.52
30:0:1522:A:C2'	30:0:1523:G:H5'	2.40	0.52
30:0:2672:C:H2'	30:0:2673:U:H6	1.74	0.52
30:0:599:G:H2'	30:0:600:G:H8	1.74	0.52
30:0:615:G:H2'	30:0:616:U:C6	2.44	0.52
30:0:793:A:C5	30:0:794:U:C5	2.98	0.52
2:B:243:ASN:HB2	30:0:2607:U:OP2	2.10	0.52
6:F:91:VAL:HG12	6:F:92:GLY:N	2.20	0.52
7:G:63:ARG:O	7:G:67:LEU:HG	2.10	0.52
12:L:73:VAL:HG23	12:L:74:THR:H	1.75	0.52
30:0:1154:A:H2'	30:0:1155:G:C8	2.44	0.52
30:0:1422:U:H2'	30:0:1423:C:H6	1.72	0.52
30:0:1504:A:H5'	38:0:4396:HOH:O	2.10	0.52
30:0:2088:C:H2'	30:0:2089:A:C8	2.44	0.52
30:0:308:U:C4	30:0:342:C:H1'	2.45	0.52
30:0:818:A:C6	30:0:819:A:N1	2.78	0.52
29:3:4:PRO:HA	29:3:91:GLN:O	2.09	0.52
13:M:73:ARG:HD2	13:M:73:ARG:N	2.25	0.52
30:0:1175:G:N7	30:0:1176:C:C4	2.78	0.51
30:0:1191:A:C2'	30:0:1193:A:H5'	2.38	0.51
30:0:1309:U:O2'	30:0:1310:U:H5'	2.10	0.51
30:0:1743:G:H2'	30:0:1744:G:O4'	2.10	0.51
30:0:2872:U:H2'	30:0:2873:C:H6	1.76	0.51
30:0:818:A:C6	30:0:819:A:C2	2.98	0.51
12:L:78:ALA:HB3	38:L:8860:HOH:O	2.11	0.51
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:49:ARG:HD3	24:X:84:ILE:HG12	1.92	0.51
30:0:1395:C:H2'	30:0:1396:C:C6	2.46	0.51
30:0:2498:C:O2'	30:0:2499:U:H5'	2.10	0.51
30:0:2900:G:H2'	30:0:2901:C:O4'	2.10	0.51
30:0:395:A:H2'	30:0:397:A:H62	1.74	0.51
2:B:144:THR:HB	38:B:9096:HOH:O	2.10	0.51
14:N:7:LYS:HE3	17:Q:21:ARG:O	2.09	0.51
17:Q:87:THR:HB	38:Q:1295:HOH:O	2.10	0.51
20:T:52:ARG:HH12	30:0:308:U:H2'	1.75	0.51
26:Z:38:PHE:HB3	26:Z:42:TYR:CE1	2.46	0.51
30:0:1667:A:H8	30:0:1667:A:H5'	1.75	0.51
30:0:1992:U:H2'	30:0:1994:A:OP2	2.10	0.51
30:0:2544:G:H5'	38:0:3418:HOH:O	2.10	0.51
30:0:20:G:H5''	30:0:510:U:O4	2.09	0.51
25:Y:205:ILE:HB	25:Y:230:ASN:HD21	1.75	0.51
30:0:1641:A:H2'	30:0:1642:A:C5'	2.40	0.51
30:0:2032:U:H2'	30:0:2033:G:H5''	1.92	0.51
29:3:54:LYS:HE2	30:0:2468:A:C8	2.45	0.51
30:0:2614:C:O2'	30:0:2615:U:H5'	2.10	0.51
9:I:120:ALA:O	9:I:124:VAL:HG23	2.09	0.51
30:0:1160:G:H2'	38:0:5597:HOH:O	2.11	0.51
30:0:1167:G:H2'	30:0:1168:C:O4'	2.11	0.51
30:0:1395:C:H2'	30:0:1396:C:H6	1.76	0.51
31:9:56:A:H3'	31:9:57:A:H5''	1.89	0.51
1:A:175:LYS:HE2	33:A:8809:CL:CL	2.48	0.51
15:O:65:LEU:HD13	30:0:746:A:C6	2.45	0.51
17:Q:7:LEU:HD12	30:0:2424:U:H1'	1.93	0.51
30:0:254:C:C2'	30:0:254:C:O2	2.57	0.51
30:0:2700:G:O2'	30:0:2701:G:H5'	2.09	0.51
30:0:2846:C:H3'	38:0:7070:HOH:O	2.11	0.51
30:0:2851:G:H2'	30:0:2902:A:N6	2.26	0.51
30:0:660:A:N6	30:0:746:A:O4'	2.43	0.51
30:0:702:G:C2	30:0:703:G:C8	2.98	0.51
31:9:58:G:H3'	31:9:59:C:C5	2.45	0.51
3:C:127:ARG:HD3	3:C:129:HIS:CE1	2.45	0.51
10:J:21:ARG:HH21	30:0:1244:U:H5''	1.76	0.51
11:K:91:GLU:HG3	38:U:151:HOH:O	2.11	0.51
30:0:1019:C:O2'	30:0:1020:A:H5'	2.11	0.51
30:0:128:A:O2'	30:0:129:A:H5'	2.10	0.51
2:B:234:ARG:HG3	30:0:1735:C:OP2	2.11	0.51
30:0:1947:G:N2	30:0:1966:U:C2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2032:U:H2'	30:0:2033:G:H5'	1.93	0.51
30:0:2719:A:C2'	30:0:2720:C:H5'	2.41	0.51
30:0:37:A:H2'	30:0:38:G:C8	2.46	0.51
30:0:633:C:O2'	30:0:634:G:H5'	2.10	0.51
29:3:40:ARG:HA	29:3:52:PHE:HE1	1.73	0.51
29:3:83:TRP:NE1	30:0:2380:A:H2	2.09	0.51
5:E:137:ASP:OD1	5:E:139:GLU:HB2	2.11	0.51
8:H:114:ASP:HA	38:H:204:HOH:O	2.11	0.51
17:Q:94:GLN:O	17:Q:95:GLU:HB2	2.11	0.51
24:X:56:GLU:HG2	30:0:1400:C:H4'	1.92	0.51
30:0:1236:A:O2'	30:0:1237:U:H5'	2.11	0.51
30:0:2047:C:H5'	38:0:9814:HOH:O	2.10	0.51
30:0:210:U:O2'	30:0:211:U:H5'	2.11	0.51
30:0:2456:A:O2'	30:0:2457:U:H5'	2.10	0.51
30:0:2689:A:H2'	30:0:2690:U:H5'	1.92	0.51
15:O:37:ARG:HD2	30:0:656:G:OP2	2.11	0.51
30:0:727:G:H3'	30:0:728:C:C6	2.45	0.51
30:0:822:C:N3	30:0:823:U:C5	2.79	0.51
3:C:149:LYS:HE3	38:0:4023:HOH:O	2.10	0.51
3:C:219:ASN:O	3:C:222:ASP:HB2	2.11	0.51
6:F:91:VAL:HG11	30:0:262:A:OP2	2.10	0.51
6:F:36:THR:HG23	6:F:97:ALA:HB2	1.93	0.51
7:G:64:ASN:HD22	7:G:64:ASN:H	1.58	0.51
13:M:28:GLN:O	13:M:32:ARG:HG3	2.10	0.51
20:T:32:ARG:NH1	20:T:38:ARG:NH1	2.58	0.51
26:Z:53:ILE:HG23	38:Z:8719:HOH:O	2.10	0.51
26:Z:78:ILE:HD12	38:Z:8715:HOH:O	2.11	0.51
30:0:1890:U:H1'	30:0:2013:G:N2	2.26	0.51
11:K:66:ARG:NH2	30:0:1994:A:OP1	2.44	0.51
30:0:2589:U:H2'	30:0:2590:U:C6	2.46	0.51
30:0:2712:G:C5'	38:0:5187:HOH:O	2.58	0.51
30:0:523:C:H2'	30:0:524:A:C8	2.46	0.51
16:P:128:GLY:HA3	30:0:801:U:O4'	2.11	0.51
8:H:61:ARG:HH11	8:H:61:ARG:HG3	1.75	0.51
24:X:61:ARG:O	30:0:2744:G:H5''	2.11	0.51
25:Y:127:GLN:HA	38:Y:8909:HOH:O	2.11	0.51
30:0:1186:C:N4	30:0:1187:U:C4	2.79	0.51
30:0:1568:G:H2'	30:0:1569:U:O4'	2.10	0.51
30:0:1819:G:H2'	30:0:1820:G:C5'	2.41	0.51
30:0:2526:C:O2'	30:0:2527:U:H5'	2.10	0.51
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:39:G:C2	30:0:444:C:C2	2.99	0.51
30:0:617:C:H2'	30:0:618:G:O4'	2.11	0.51
29:3:22:VAL:HG12	29:3:90:PHE:CE2	2.46	0.51
2:B:80:ARG:HB2	2:B:145:HIS:CE1	2.45	0.51
8:H:31:ILE:HD11	8:H:65:LEU:HB3	1.93	0.51
16:P:118:GLN:O	16:P:122:LEU:HG	2.11	0.51
9:I:83:GLY:HA3	30:0:1168:C:H5'	1.93	0.50
30:0:1226:G:C5	30:0:1227:C:C5	2.99	0.50
30:0:553:G:O4'	30:0:1325:G:H5'	2.10	0.50
30:0:1441:G:O2'	30:0:1442:A:H5'	2.11	0.50
30:0:1511:U:O2'	30:0:1512:G:H5'	2.11	0.50
30:0:1642:A:C8	30:0:1643:C:C5	2.99	0.50
30:0:1796:A:H8	30:0:1796:A:O5'	1.94	0.50
30:0:1805:G:O2'	30:0:1806:G:H5'	2.11	0.50
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.93	0.50
30:0:560:U:H2'	30:0:561:G:H8	1.75	0.50
2:B:71:VAL:HG21	2:B:296:LEU:HB3	1.92	0.50
7:G:20:VAL:O	7:G:24:VAL:HG23	2.11	0.50
11:K:97:ILE:HG22	11:K:98:VAL:N	2.25	0.50
22:V:12:THR:HG23	22:V:14:ALA:H	1.76	0.50
26:Z:102:THR:HG23	26:Z:105:ARG:HD2	1.93	0.50
30:0:1167:G:N2	30:0:1180:U:C2	2.79	0.50
30:0:134:U:O2	30:0:145:A:C2	2.63	0.50
30:0:2087:C:O2'	30:0:2088:C:H5'	2.11	0.50
30:0:2672:C:C2	30:0:2673:U:C6	3.00	0.50
30:0:2847:G:O2'	30:0:2848:G:H5'	2.11	0.50
3:C:127:ARG:HH21	3:C:225:PRO:HG2	1.71	0.50
25:Y:210:GLY:N	30:0:1313:A:H5''	2.27	0.50
30:0:1087:G:H4'	30:0:1088:A:OP1	2.12	0.50
30:0:1216:G:N2	30:0:1217:G:H1'	2.26	0.50
30:0:1461:U:H2'	30:0:1462:C:C6	2.46	0.50
30:0:1735:C:H2'	30:0:1736:A:H8	1.75	0.50
30:0:2899:A:O2'	30:0:2900:G:H5'	2.12	0.50
30:0:523:C:H2'	30:0:524:A:H8	1.76	0.50
30:0:876:A:H2'	30:0:876:A:N3	2.26	0.50
27:1:16:HIS:CD2	30:0:470:U:O2'	2.64	0.50
29:3:29:ARG:HA	38:3:9012:HOH:O	2.11	0.50
2:B:248:ARG:O	2:B:251:VAL:HG22	2.11	0.50
3:C:193:LEU:HA	3:C:211:ASP:O	2.10	0.50
3:C:236:THR:HG22	3:C:239:ALA:CB	2.41	0.50
5:E:7:ILE:HG13	5:E:11:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:35:LYS:HA	30:0:2755:G:OP1	2.11	0.50
30:0:1181:A:H2'	30:0:1182:C:C5'	2.41	0.50
30:0:1463:U:H2'	30:0:1464:C:C6	2.47	0.50
30:0:1474:C:H6	30:0:1474:C:C5'	2.17	0.50
30:0:1522:A:H2'	30:0:1523:G:H5'	1.92	0.50
30:0:2564:G:OP2	30:0:2565:C:H5''	2.11	0.50
30:0:2635:A:HO2'	30:0:2636:C:H5'	1.76	0.50
30:0:1811:A:C2	30:0:2752:C:H1'	2.46	0.50
30:0:40:C:H2'	30:0:41:G:C8	2.46	0.50
29:3:10:TYR:CE1	30:0:2408:A:H1'	2.46	0.50
29:3:10:TYR:HB2	29:3:17:HIS:HE1	1.76	0.50
10:J:107:ASN:HD22	10:J:107:ASN:C	2.15	0.50
12:L:65:ASP:HA	12:L:109:LEU:O	2.11	0.50
30:0:1015:C:O5'	30:0:1015:C:H6	1.94	0.50
30:0:105:G:O2'	30:0:106:A:H5'	2.11	0.50
30:0:1187:U:O2'	30:0:1189:A:H2	1.94	0.50
30:0:1149:U:C5	30:0:1215:A:C5	3.00	0.50
30:0:73:U:H2'	30:0:74:G:C8	2.46	0.50
17:Q:95:GLU:HA	30:0:949:U:H4'	1.94	0.50
2:B:235:ARG:HH11	30:0:2092:G:P	2.33	0.50
7:G:16:LYS:O	7:G:20:VAL:HG23	2.11	0.50
13:M:71:SER:HB2	13:M:92:THR:CG2	2.35	0.50
30:0:119:A:H2'	30:0:120:A:C5'	2.42	0.50
38:B:8995:HOH:O	30:0:2093:G:H5''	2.11	0.50
30:0:2344:G:N3	30:0:2344:G:H2'	2.26	0.50
30:0:2295:G:N3	30:0:2361:A:C2	2.80	0.50
30:0:2506:A:C1'	38:0:6031:HOH:O	2.58	0.50
30:0:372:A:C2	30:0:373:G:C4	2.99	0.50
30:0:451:C:O2'	30:0:452:G:H5'	2.12	0.50
30:0:556:C:O2'	30:0:557:C:H5'	2.11	0.50
30:0:738:G:O5'	30:0:738:G:H8	1.95	0.50
30:0:819:A:C4	30:0:821:U:C5	3.00	0.50
30:0:929:A:H5''	38:0:7060:HOH:O	2.11	0.50
8:H:59:GLN:NE2	8:H:129:ARG:HE	2.10	0.50
14:N:37:ARG:NH1	31:9:6:C:OP1	2.44	0.50
16:P:114:LEU:HD22	16:P:118:GLN:HB3	1.93	0.50
16:P:135:ALA:O	16:P:139:ARG:HG3	2.11	0.50
30:0:10:U:O4	30:0:532:A:H8	1.95	0.50
30:0:1666:C:H42	30:0:1667:A:N6	2.10	0.50
26:Z:42:TYR:N	30:0:1829:A:H61	2.10	0.50
30:0:2415:A:C2'	30:0:2416:G:H5'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1705:C:O2	30:0:2735:U:H5''	2.11	0.50
30:0:2803:C:H2'	30:0:2804:C:H6	1.77	0.50
30:0:2823:G:O2'	30:0:2824:C:H5'	2.12	0.50
30:0:69:A:C5'	30:0:69:A:H8	2.24	0.50
30:0:716:G:C6	30:0:717:C:N4	2.80	0.50
30:0:79:G:N2	30:0:97:G:H1'	2.26	0.50
29:3:3:MET:O	29:3:90:PHE:HA	2.11	0.50
31:9:75:G:N2	31:9:106:U:O2	2.36	0.50
31:9:92:G:H2'	31:9:93:A:H8	1.73	0.50
1:A:132:ASP:CG	1:A:133:ARG:H	2.15	0.50
1:A:178:LYS:HA	30:0:1653:A:H5'	1.94	0.50
30:0:74:G:H1	30:0:103:C:N4	2.10	0.50
30:0:1878:G:C4'	38:0:6097:HOH:O	2.60	0.50
30:0:282:C:O2'	30:0:283:U:C4'	2.60	0.50
30:0:59:A:C5'	38:0:4313:HOH:O	2.60	0.50
30:0:764:C:H2'	30:0:765:G:O4'	2.12	0.50
29:3:10:TYR:HB2	29:3:17:HIS:CE1	2.47	0.50
31:9:23:U:H2'	31:9:23:U:O2	2.12	0.50
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.94	0.50
3:C:22:PHE:HA	3:C:116:ALA:HA	1.94	0.50
13:M:82:ARG:HH22	13:M:85:ARG:NH2	2.08	0.50
13:M:77:HIS:CE1	13:M:86:GLN:HG2	2.47	0.50
14:N:38:LYS:HE2	14:N:107:ASN:HD21	1.75	0.50
22:V:56:ILE:O	22:V:60:GLN:HG3	2.12	0.50
30:0:2253:G:O2'	30:0:2254:G:H5'	2.11	0.50
30:0:2465:A:H3'	38:0:3637:HOH:O	2.12	0.50
30:0:561:G:C2	30:0:562:A:C8	3.00	0.50
3:C:101:ASP:HB2	30:0:750:A:O3'	2.12	0.50
30:0:814:G:H2'	30:0:815:U:H6	1.77	0.50
29:3:3:MET:SD	29:3:88:LEU:HD23	2.52	0.50
31:9:42:C:H5'	31:9:43:G:OP2	2.12	0.50
1:A:141:PRO:HG2	30:0:1855:G:O6	2.12	0.50
2:B:18:ARG:HG3	2:B:256:GLN:HG3	1.93	0.50
12:L:24:ALA:HB2	12:L:30:ARG:HE	1.76	0.50
13:M:145:ASP:HB2	38:M:8865:HOH:O	2.11	0.50
20:T:71:VAL:HG11	20:T:90:PRO:CB	2.38	0.50
23:W:130:HIS:O	23:W:136:GLY:HA3	2.12	0.50
23:W:6:GLN:CB	23:W:26:ILE:HD11	2.40	0.50
24:X:26:ALA:HB2	24:X:63:ARG:HA	1.93	0.50
30:0:47:G:N3	30:0:114:A:C2	2.80	0.49
30:0:1165:G:H21	30:0:1173:A:H5'	1.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1268:C:H2'	30:0:1269:G:C8	2.46	0.49
30:0:1393:A:H2'	30:0:1394:C:C6	2.47	0.49
30:0:1601:G:H1'	38:0:9891:HOH:O	2.11	0.49
30:0:1933:G:O2'	30:0:1934:A:H5'	2.12	0.49
30:0:2854:A:C6	30:0:2905:A:C6	3.00	0.49
30:0:952:G:N3	30:0:2302:A:H2'	2.26	0.49
31:9:28:U:O2	31:9:57:A:N6	2.44	0.49
31:9:39:U:H1'	31:9:44:A:H61	1.77	0.49
2:B:66:GLU:OE1	2:B:328:ARG:HD2	2.12	0.49
4:D:58:VAL:CG1	4:D:60:GLU:HG2	2.41	0.49
13:M:159:VAL:CG1	33:M:8818:CL:CL	2.95	0.49
16:P:87:ARG:HG2	38:0:5919:HOH:O	2.10	0.49
30:0:1226:G:H2'	30:0:1227:C:C6	2.44	0.49
30:0:134:U:C2	30:0:145:A:C2	2.99	0.49
30:0:1662:C:H6	30:0:1662:C:O5'	1.94	0.49
30:0:1902:G:N2	30:0:1936:C:C2	2.80	0.49
30:0:589:U:H2'	30:0:590:A:H8	1.76	0.49
30:0:873:G:N2	38:0:9173:HOH:O	2.43	0.49
29:3:60:LYS:C	29:3:62:THR:H	2.15	0.49
31:9:55:U:H4'	31:9:56:A:H8	1.71	0.49
4:D:35:ALA:HB2	38:D:5576:HOH:O	2.11	0.49
8:H:32:ALA:HB3	8:H:69:ARG:HH12	1.77	0.49
16:P:98:ILE:HD12	16:P:102:ARG:NE	2.27	0.49
18:R:18:LEU:O	18:R:142:ASP:HA	2.12	0.49
30:0:1194:A:C2	30:0:1206:U:H1'	2.47	0.49
25:Y:212:ARG:HB2	30:0:1315:G:C4	2.47	0.49
30:0:1800:G:H2'	30:0:1801:A:H8	1.77	0.49
30:0:2291:A:N3	30:0:2291:A:H2'	2.28	0.49
30:0:2617:G:C2	30:0:2618:G:C8	3.00	0.49
30:0:2846:C:H2'	30:0:2847:G:H8	1.77	0.49
30:0:1787:C:C4'	30:0:2883:A:O4'	2.59	0.49
30:0:316:A:N3	30:0:336:G:O2'	2.41	0.49
30:0:400:C:H2'	30:0:401:C:C6	2.47	0.49
10:J:131:THR:HG22	10:J:134:GLU:H	1.77	0.49
11:K:34:VAL:HB	38:K:7169:HOH:O	2.12	0.49
30:0:1206:U:C5'	30:0:1206:U:H6	2.21	0.49
30:0:1255:A:H1'	38:0:7741:HOH:O	2.11	0.49
25:Y:115:ARG:NH2	30:0:1266:U:H4'	2.27	0.49
30:0:1339:G:C6	30:0:1340:G:N1	2.81	0.49
30:0:1381:A:N3	30:0:1382:G:H1'	2.28	0.49
1:A:47:HIS:CD2	30:0:1654:U:C2'	2.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1947:G:N2	30:0:1966:U:N3	2.60	0.49
30:0:2133:U:H4'	30:0:2134:G:H5'	1.93	0.49
30:0:2632:G:C6	30:0:2633:A:N6	2.81	0.49
30:0:2632:G:H2'	30:0:2633:A:C8	2.46	0.49
30:0:36:C:C2	30:0:447:A:C2	3.00	0.49
30:0:814:G:H2'	30:0:815:U:C6	2.47	0.49
30:0:816:G:H5'	30:0:1598:A:H4'	1.94	0.49
29:3:79:LEU:CD1	30:0:2456:A:H2	2.25	0.49
29:3:79:LEU:HD22	38:0:7515:HOH:O	2.13	0.49
2:B:44:TYR:OH	2:B:148:PRO:HG3	2.11	0.49
2:B:215:VAL:O	2:B:219:GLY:HA2	2.13	0.49
6:F:110:ASP:O	6:F:114:LYS:HG3	2.12	0.49
9:I:93:ALA:HB3	9:I:132:VAL:HG22	1.95	0.49
17:Q:66:LYS:HB2	17:Q:70:ALA:O	2.13	0.49
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.92	0.49
30:0:1370:G:H5''	38:0:5497:HOH:O	2.12	0.49
30:0:1559:A:HO2'	30:0:1561:U:H5	1.60	0.49
30:0:1555:G:H4'	30:0:1630:A:C2	2.47	0.49
30:0:1733:A:C5	30:0:1734:C:C2	3.00	0.49
30:0:1878:G:O2'	30:0:1879:U:H6	1.90	0.49
30:0:2118:A:H5'	38:0:3996:HOH:O	2.13	0.49
30:0:2366:C:O5'	30:0:2366:C:H6	1.95	0.49
30:0:1787:C:O4'	30:0:2883:A:H1'	2.11	0.49
30:0:494:C:H1'	30:0:498:A:N6	2.27	0.49
2:B:304:PRO:HD2	2:B:307:ARG:HE	1.78	0.49
14:N:58:LEU:HD12	14:N:58:LEU:N	2.27	0.49
30:0:1189:A:O2'	30:0:1208:C:H2'	2.12	0.49
30:0:1174:A:C5	30:0:1201:C:H4'	2.47	0.49
30:0:1626:A:O2'	30:0:1627:G:H5'	2.13	0.49
30:0:1517:C:O2	30:0:1670:A:C2	2.66	0.49
30:0:1682:A:O2'	30:0:1683:G:H5''	2.12	0.49
30:0:1871:U:O4'	30:0:1873:G:C8	2.66	0.49
30:0:2335:C:C2	30:0:2350:G:C2	3.01	0.49
30:0:29:C:O2'	30:0:30:U:H5'	2.12	0.49
20:T:107:LYS:HD2	30:0:97:G:C2	2.47	0.49
8:H:27:PRO:HD3	8:H:123:ILE:CG2	2.43	0.49
10:J:130:VAL:HG12	10:J:131:THR:H	1.78	0.49
14:N:37:ARG:HG3	14:N:37:ARG:HH11	1.77	0.49
30:0:1226:G:N3	30:0:1227:C:C6	2.81	0.49
29:3:33:MET:HG2	30:0:1922:A:C2'	2.42	0.49
30:0:2478:U:H2'	30:0:2479:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:71:LYS:HE2	30:0:2831:C:O3'	2.13	0.49
30:0:285:A:H2'	30:0:286:U:O4'	2.13	0.49
30:0:316:A:H1'	30:0:336:G:N3	2.27	0.49
30:0:549:A:C6	30:0:550:C:C4	3.00	0.49
30:0:862:U:H2'	30:0:863:G:H8	1.77	0.49
30:0:889:C:H4'	38:0:6368:HOH:O	2.13	0.49
29:3:12:PRO:HB3	30:0:2382:A:O2'	2.12	0.49
2:B:307:ARG:HD2	38:B:9123:HOH:O	2.12	0.49
6:F:110:ASP:O	6:F:114:LYS:N	2.44	0.49
21:U:9:CYS:HB2	38:U:6796:HOH:O	2.11	0.49
30:0:1183:C:N4	30:0:1184:C:N4	2.60	0.49
30:0:1583:U:O2'	30:0:1584:C:H5'	2.13	0.49
30:0:1706:G:C5	30:0:1707:G:C6	3.00	0.49
30:0:1760:G:H5'	30:0:1818:C:O2'	2.12	0.49
30:0:1921:A:C6	30:0:1922:A:C2	3.00	0.49
30:0:2326:C:H4'	30:0:2412:G:H4'	1.94	0.49
30:0:2826:G:H1'	30:0:2914:A:N6	2.28	0.49
30:0:447:A:O2'	30:0:448:G:H5'	2.13	0.49
31:9:110:G:N2	31:9:111:U:H1'	2.28	0.49
1:A:109:GLU:HG2	1:A:116:GLY:N	2.25	0.49
2:B:162:MET:CE	2:B:308:LEU:HD21	2.42	0.49
2:B:98:THR:HG22	2:B:99:GLU:N	2.28	0.49
3:C:233:THR:HG22	3:C:234:VAL:N	2.26	0.49
8:H:29:SER:HA	8:H:62:HIS:HD2	1.77	0.49
26:Z:47:ARG:HH22	30:0:1771:U:H1'	1.77	0.49
30:0:1116:U:C2	30:0:1246:A:N6	2.81	0.49
30:0:1343:C:H2'	30:0:1344:G:O5'	2.12	0.49
30:0:1453:G:C2	30:0:1675:C:C2	3.00	0.49
30:0:2103:A:N3	30:0:2103:A:H2'	2.28	0.49
30:0:2269:C:H2'	30:0:2270:G:O4'	2.12	0.49
30:0:717:C:H2'	30:0:718:C:H6	1.78	0.49
30:0:731:U:O2'	30:0:732:C:H5'	2.13	0.49
29:3:1:MET:HG2	29:3:87:ARG:O	2.11	0.49
31:9:105:A:H2'	31:9:106:U:O4'	2.12	0.49
1:A:36:ASP:HB2	1:A:85:SER:H	1.77	0.49
14:N:25:ARG:HB3	30:0:2415:A:C2	2.47	0.49
25:Y:235:GLU:CD	25:Y:235:GLU:H	2.16	0.49
30:0:1119:G:H22	30:0:1246:A:H2	1.46	0.49
30:0:1351:G:H1'	38:0:4648:HOH:O	2.13	0.49
30:0:1607:A:C4	30:0:1608:G:C8	3.01	0.49
30:0:1615:A:H5'	38:0:4169:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2497:A:C2	30:0:2524:G:C2	3.01	0.49
30:0:2536:C:H6	38:0:4998:HOH:O	1.95	0.49
30:0:271:C:N4	30:0:378:A:H2	2.01	0.49
27:1:21:ARG:HD2	27:1:39:PHE:HB2	1.95	0.49
31:9:60:C:O2'	31:9:61:C:H5'	2.13	0.49
31:9:8:G:C6	31:9:9:C:C4	3.00	0.49
14:N:178:THR:O	14:N:181:ASP:HB3	2.13	0.49
20:T:69:LYS:O	20:T:71:VAL:HG23	2.13	0.49
30:0:1063:G:H4'	30:0:2307:A:H1'	1.95	0.48
30:0:1240:G:H1'	38:0:9360:HOH:O	2.12	0.48
30:0:1586:G:C2'	30:0:1587:U:H5'	2.43	0.48
30:0:1644:C:C2	30:0:1645:U:C5	3.01	0.48
30:0:191:A:H2'	30:0:237:G:O6	2.12	0.48
30:0:419:A:H1'	30:0:1921:A:C2	2.48	0.48
30:0:2297:U:H2'	30:0:2298:C:H6	1.78	0.48
30:0:2639:G:C5	30:0:2640:U:C5	3.01	0.48
30:0:788:A:H4'	38:0:7005:HOH:O	2.12	0.48
29:3:88:LEU:HB3	29:3:90:PHE:CE1	2.48	0.48
3:C:173:LYS:HE3	30:0:1311:G:O6	2.12	0.48
4:D:92:GLU:HB2	38:D:3862:HOH:O	2.13	0.48
6:F:63:ILE:HB	6:F:64:PRO:CD	2.37	0.48
13:M:52:GLN:OE1	13:M:116:ASN:HB3	2.13	0.48
25:Y:137:LYS:HD2	38:0:7590:HOH:O	2.11	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.48	0.48
30:0:106:A:C6	30:0:107:U:C4	3.00	0.48
30:0:1765:G:O2'	30:0:1766:U:H5'	2.12	0.48
30:0:1916:C:O2'	30:0:1917:G:H5'	2.14	0.48
30:0:2646:G:C4	30:0:2647:C:C5	3.02	0.48
30:0:2713:G:O2'	30:0:2714:U:H5'	2.12	0.48
30:0:2864:U:O2'	30:0:2865:G:H5'	2.14	0.48
31:9:19:G:C2	31:9:20:G:C8	3.00	0.48
31:9:2:U:H4'	38:9:9107:HOH:O	2.13	0.48
4:D:22:VAL:HG22	4:D:74:THR:HG22	1.95	0.48
5:E:11:VAL:HG12	5:E:12:ASP:N	2.28	0.48
11:K:98:VAL:HG11	11:K:102:GLU:HA	1.94	0.48
13:M:134:ILE:CG2	13:M:141:ILE:HD13	2.36	0.48
20:T:28:SER:O	20:T:32:ARG:HG3	2.14	0.48
21:U:19:THR:HG22	21:U:20:MET:N	2.28	0.48
30:0:1832:G:C2	30:0:1833:U:C6	3.00	0.48
30:0:1883:U:H2'	30:0:1884:G:H5'	1.94	0.48
30:0:2480:G:O2'	30:0:2481:G:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2526:C:H3'	30:0:2526:C:C6	2.47	0.48
30:0:2827:A:C2	30:0:2914:A:C2	3.01	0.48
30:0:2898:G:H1'	38:0:7555:HOH:O	2.13	0.48
30:0:334:G:C5	30:0:335:U:C5	3.00	0.48
30:0:595:U:O4'	33:0:8817:CL:CL	2.69	0.48
30:0:681:G:N3	30:0:681:G:H5'	2.28	0.48
31:9:3:A:H2	31:9:21:G:N3	2.12	0.48
8:H:52:LEU:HD13	8:H:153:PHE:HB3	1.95	0.48
16:P:124:ASP:O	30:0:801:U:H4'	2.13	0.48
30:0:1015:C:H2'	30:0:1016:U:C6	2.48	0.48
30:0:120:A:H2'	30:0:120:A:N3	2.29	0.48
30:0:1557:G:H2'	30:0:1558:C:H6	1.78	0.48
30:0:1632:A:C3'	30:0:1633:C:H5'	2.43	0.48
26:Z:42:TYR:H	30:0:1829:A:H61	1.61	0.48
30:0:2700:G:H2'	30:0:2701:G:C5'	2.43	0.48
8:H:35:LYS:HE3	30:0:968:G:H1'	1.95	0.48
2:B:152:PRO:HD2	38:B:9102:HOH:O	2.12	0.48
13:M:84:LYS:HA	29:3:46:ILE:O	2.12	0.48
16:P:31:ILE:HG12	16:P:43:LEU:HD13	1.96	0.48
30:0:100:C:C4	30:0:101:C:C5	3.01	0.48
30:0:1434:A:O2'	30:0:1435:U:H6	1.92	0.48
30:0:1496:A:H5'	30:0:1572:A:H1'	1.94	0.48
30:0:1634:G:H2'	30:0:1635:U:H6	1.76	0.48
30:0:222:A:H2'	30:0:223:G:O4'	2.13	0.48
30:0:2255:A:C2	30:0:2256:G:C4	3.02	0.48
30:0:2505:G:C2'	30:0:2506:A:C5'	2.91	0.48
30:0:2672:C:H2'	30:0:2673:U:O4'	2.14	0.48
11:K:43:ARG:NH1	30:0:2712:G:OP1	2.46	0.48
30:0:2755:G:H1'	38:0:4651:HOH:O	2.13	0.48
30:0:2772:G:O2'	30:0:2773:G:H5'	2.13	0.48
30:0:2854:A:H2'	30:0:2855:G:H8	1.78	0.48
30:0:2860:G:H2'	30:0:2861:G:C8	2.48	0.48
30:0:677:C:H2'	30:0:678:G:H8	1.77	0.48
30:0:707:C:C2	30:0:708:A:C8	3.02	0.48
29:3:64:LYS:HE2	38:0:7638:HOH:O	2.12	0.48
4:D:37:ALA:O	4:D:40:ILE:HG12	2.13	0.48
12:L:117:GLU:HG3	12:L:117:GLU:O	2.13	0.48
14:N:78:MET:HB2	14:N:79:PRO:HD3	1.95	0.48
18:R:132:ARG:HG2	18:R:133:ALA:N	2.27	0.48
19:S:6:LYS:HB2	19:S:27:ALA:O	2.13	0.48
20:T:27:LEU:HB2	20:T:32:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1182:C:C1'	30:0:1192:A:H8	2.26	0.48
30:0:1207:A:OP2	30:0:1208:C:H5	1.96	0.48
30:0:1970:G:H1'	38:0:3662:HOH:O	2.13	0.48
30:0:1970:G:H4'	30:0:1971:G:C5'	2.43	0.48
30:0:200:C:H6	38:0:3433:HOH:O	1.96	0.48
30:0:2133:U:H4'	30:0:2134:G:C5'	2.44	0.48
30:0:2598:U:O2	30:0:2600:A:C8	2.66	0.48
30:0:2617:G:H4'	38:0:4487:HOH:O	2.13	0.48
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.13	0.48
30:0:611:U:H2'	30:0:612:U:C6	2.48	0.48
29:3:43:ASN:HB2	29:3:52:PHE:CD1	2.48	0.48
2:B:36:PRO:HG3	2:B:169:GLY:H	1.77	0.48
4:D:51:ARG:HH11	4:D:68:PRO:HB3	1.78	0.48
10:J:60:ARG:HD3	10:J:71:TYR:CE1	2.47	0.48
15:O:88:LYS:HB3	38:O:7061:HOH:O	2.13	0.48
30:0:1224:G:H2'	30:0:1225:C:C6	2.48	0.48
30:0:1520:G:H2'	30:0:1521:C:C6	2.49	0.48
30:0:1878:G:C2	30:0:1879:U:C2	3.02	0.48
30:0:1908:G:N1	30:0:1930:A:OP2	2.46	0.48
30:0:627:G:H2'	30:0:2071:C:C4	2.49	0.48
30:0:2569:A:O5'	30:0:2569:A:H8	1.96	0.48
30:0:2707:C:C2'	30:0:2707:C:O2	2.59	0.48
30:0:31:C:H2'	38:0:7668:HOH:O	2.13	0.48
30:0:705:C:C2'	30:0:705:C:O2	2.62	0.48
27:1:25:LYS:CD	28:2:49:GLU:H	2.25	0.48
5:E:80:TRP:O	5:E:134:SER:HA	2.12	0.48
6:F:107:ASP:O	6:F:111:ILE:HG13	2.13	0.48
13:M:139:PRO:HA	13:M:142:GLN:HB2	1.95	0.48
16:P:94:TRP:CZ2	16:P:98:ILE:HG13	2.49	0.48
17:Q:28:ARG:HG2	38:9:9083:HOH:O	2.12	0.48
18:R:138:SER:HB2	38:0:5570:HOH:O	2.14	0.48
23:W:26:ILE:HB	38:W:5420:HOH:O	2.14	0.48
30:0:1023:C:O2'	30:0:1024:G:H5'	2.14	0.48
30:0:1063:G:H8	38:0:9856:HOH:O	1.96	0.48
28:2:10:ARG:NH2	30:0:121:U:OP2	2.44	0.48
30:0:1029:U:O2'	30:0:1273:C:OP1	2.27	0.48
30:0:2354:A:C2	30:0:2367:A:C8	3.02	0.48
30:0:2717:C:H2'	30:0:2718:C:H5'	1.93	0.48
30:0:808:A:C5	30:0:809:G:H1'	2.48	0.48
30:0:858:U:H2'	30:0:859:C:C6	2.47	0.48
30:0:99:A:C8	30:0:100:C:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:1:THR:HB	38:1:2852:HOH:O	2.12	0.48
29:3:25:VAL:HA	38:3:9036:HOH:O	2.12	0.48
29:3:40:ARG:C	29:3:42:ARG:H	2.16	0.48
9:I:133:THR:HG22	9:I:134:ILE:N	2.28	0.48
16:P:11:ALA:HB1	16:P:16:VAL:O	2.14	0.48
23:W:117:ARG:HH22	30:0:1264:U:P	2.36	0.48
1:A:162:GLY:N	26:Z:91:GLY:HA2	2.29	0.48
30:0:1177:A:N3	30:0:1177:A:H2'	2.28	0.48
30:0:1204:C:H2'	30:0:1205:U:O4'	2.14	0.48
30:0:2254:G:C2	30:0:2255:A:C8	3.01	0.48
30:0:2281:C:H5	38:0:3756:HOH:O	1.97	0.48
30:0:2505:G:H2'	30:0:2506:A:C5'	2.43	0.48
30:0:2587:OMU:H5	38:0:7464:HOH:O	2.13	0.48
30:0:2777:G:O2'	30:0:2778:A:H5'	2.13	0.48
30:0:432:G:H5''	38:0:6860:HOH:O	2.12	0.48
30:0:69:A:C2'	30:0:70:A:OP2	2.62	0.48
30:0:763:C:O2'	30:0:764:C:H5'	2.14	0.48
30:0:842:C:H4'	38:0:3427:HOH:O	2.13	0.48
30:0:920:C:C4'	30:0:921:G:C2	2.95	0.48
31:9:39:U:C2'	31:9:40:C:OP1	2.62	0.48
1:A:71:PRO:HG2	1:A:91:GLY:HA2	1.95	0.48
4:D:51:ARG:NH1	4:D:68:PRO:HB3	2.28	0.48
8:H:157:TYR:C	8:H:157:TYR:HD1	2.18	0.48
30:0:1186:C:C4	30:0:1187:U:C4	3.02	0.48
30:0:1626:A:H2'	30:0:1627:G:O4'	2.14	0.48
30:0:202:U:C4	30:0:203:G:C6	3.01	0.48
11:K:1:MET:N	30:0:2686:C:O2'	2.38	0.48
13:M:9:ARG:HD2	30:0:380:A:OP2	2.14	0.48
29:3:51:LYS:HG3	29:3:52:PHE:HD2	1.76	0.48
29:3:83:TRP:HB2	38:0:5759:HOH:O	2.14	0.48
14:N:4:PRO:HG3	31:9:69:U:OP1	2.13	0.48
1:A:161:GLY:HA3	38:Z:8705:HOH:O	2.13	0.48
1:A:217:ARG:HG2	1:A:229:ALA:HB2	1.95	0.48
2:B:226:LYS:HG2	2:B:230:GLN:HE21	1.78	0.48
6:F:58:GLU:HA	6:F:61:MET:SD	2.54	0.48
9:I:69:PRO:HA	30:0:1164:U:OP1	2.14	0.47
30:0:1188:A:C5	30:0:1189:A:C2	3.02	0.47
30:0:1337:G:C6	30:0:1338:U:C4	3.01	0.47
30:0:1337:G:C5	30:0:1338:U:C5	3.02	0.47
30:0:1471:A:H2'	30:0:1472:C:C6	2.48	0.47
30:0:151:A:H2'	30:0:152:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:50:GLY:CA	30:0:170:U:H1'	2.43	0.47
30:0:1745:G:H5'	38:0:4312:HOH:O	2.14	0.47
30:0:2458:U:H3'	38:0:3241:HOH:O	2.13	0.47
30:0:2474:A:H5'	30:0:2476:C:O5'	2.14	0.47
30:0:2474:A:N7	30:0:2621:PSU:H4'	2.29	0.47
30:0:2598:U:O2	30:0:2600:A:H8	1.96	0.47
30:0:2830:U:H2'	30:0:2831:C:H6	1.79	0.47
30:0:2848:G:O4'	30:0:2906:A:C2	2.66	0.47
30:0:625:U:H5''	30:0:1044:C:H42	1.71	0.47
30:0:870:G:H2'	30:0:871:G:C5'	2.34	0.47
3:C:162:VAL:HG13	3:C:162:VAL:O	2.13	0.47
18:R:15:LYS:HE3	38:R:8976:HOH:O	2.14	0.47
30:0:2385:G:H2'	30:0:2386:U:C6	2.49	0.47
21:U:50:GLU:OE1	30:0:2866:U:H2'	2.13	0.47
30:0:2855:G:C2	30:0:2904:U:N3	2.82	0.47
30:0:373:G:O2'	30:0:374:U:H5'	2.14	0.47
30:0:968:G:O2'	30:0:969:G:H5'	2.14	0.47
1:A:27:LEU:HD21	1:A:55:VAL:CG2	2.44	0.47
2:B:84:LEU:O	2:B:99:GLU:HA	2.14	0.47
30:0:1947:G:OP1	30:0:1971:G:N7	2.47	0.47
30:0:2087:C:H2'	30:0:2088:C:H6	1.80	0.47
30:0:361:C:H2'	30:0:362:G:O4'	2.13	0.47
30:0:834:G:H3'	30:0:835:U:H4'	1.97	0.47
11:K:132:VAL:HG11	21:U:22:VAL:HG22	1.96	0.47
25:Y:234:VAL:HG12	25:Y:235:GLU:N	2.28	0.47
26:Z:40:ALA:HA	30:0:1773:G:H8	1.79	0.47
30:0:1275:C:H2'	30:0:1276:U:H5'	1.96	0.47
30:0:1389:G:N2	30:0:1391:G:H3'	2.29	0.47
30:0:1619:G:H2'	30:0:1620:C:C6	2.49	0.47
30:0:2379:G:H4'	30:0:2380:A:O5'	2.13	0.47
30:0:2719:A:H2'	30:0:2720:C:C5'	2.44	0.47
30:0:2724:U:H6	30:0:2724:U:O5'	1.96	0.47
30:0:2857:C:H1'	38:0:5328:HOH:O	2.15	0.47
30:0:407:A:H5'	38:0:6000:HOH:O	2.14	0.47
30:0:681:G:N3	30:0:681:G:H2'	2.30	0.47
30:0:699:C:C2	30:0:744:G:C2	3.03	0.47
30:0:965:A:H5'	30:0:966:U:OP2	2.14	0.47
1:A:70:ALA:HB1	26:Z:89:THR:HG21	1.97	0.47
2:B:162:MET:HE1	2:B:308:LEU:HD21	1.96	0.47
2:B:74:ILE:HD13	2:B:309:VAL:HG21	1.95	0.47
2:B:201:ASP:CB	2:B:312:ARG:HD2	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:88:MET:HA	8:H:139:ALA:HA	1.96	0.47
21:U:56:ARG:HB2	30:0:2890:A:N7	2.29	0.47
22:V:12:THR:CG2	22:V:15:GLU:HG3	2.40	0.47
24:X:85:VAL:HG12	24:X:86:GLU:N	2.29	0.47
30:0:1210:G:N2	30:0:1211:G:H1'	2.29	0.47
30:0:1226:G:C4	30:0:1227:C:C6	3.02	0.47
30:0:1503:U:H2'	30:0:1504:A:C5'	2.45	0.47
30:0:1733:A:N7	30:0:1734:C:C4	2.82	0.47
30:0:1477:C:H4'	30:0:1868:G:OP1	2.15	0.47
30:0:2265:U:H2'	30:0:2266:A:H8	1.80	0.47
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.47
30:0:287:C:H6	30:0:287:C:O5'	1.97	0.47
30:0:371:U:C4	30:0:372:A:N7	2.83	0.47
30:0:558:C:HO2'	30:0:559:U:H5''	1.78	0.47
30:0:699:C:C6	30:0:744:G:N3	2.82	0.47
30:0:820:G:O2'	30:0:856:G:H4'	2.14	0.47
28:2:15:ASP:O	28:2:18:ASN:HB2	2.15	0.47
29:3:68:LYS:HG2	29:3:77:ALA:CB	2.44	0.47
29:3:88:LEU:CD2	33:3:8804:CL:CL	2.86	0.47
31:9:73:A:H61	31:9:108:C:N4	2.13	0.47
31:9:39:U:H3	31:9:42:C:H5''	1.79	0.47
8:H:59:GLN:HE22	8:H:96:GLN:HG2	1.79	0.47
11:K:118:ALA:HA	11:K:125:ALA:HB2	1.96	0.47
17:Q:11:ARG:HD3	38:0:6238:HOH:O	2.13	0.47
30:0:625:U:C5'	30:0:1044:C:N4	2.71	0.47
13:M:68:ARG:HD2	30:0:1469:C:OP2	2.15	0.47
30:0:1667:A:H5'	30:0:1667:A:C8	2.50	0.47
30:0:1760:G:C5	30:0:1761:U:C4	3.03	0.47
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.47	0.47
30:0:2375:A:H2'	30:0:2376:C:C6	2.50	0.47
30:0:2597:U:C2'	30:0:2598:U:H5'	2.45	0.47
30:0:724:G:O2'	30:0:725:C:H5'	2.15	0.47
30:0:731:U:H2'	30:0:732:C:C6	2.50	0.47
26:Z:34:SER:CA	30:0:797:A:H4'	2.44	0.47
29:3:9:THR:HG23	29:3:20:HIS:CE1	2.49	0.47
31:9:5:G:C2'	31:9:6:C:H5'	2.45	0.47
1:A:135:VAL:HA	1:A:150:PRO:HD3	1.96	0.47
7:G:64:ASN:ND2	7:G:64:ASN:N	2.62	0.47
11:K:97:ILE:HG22	11:K:98:VAL:H	1.79	0.47
20:T:71:VAL:CG1	20:T:90:PRO:HB3	2.40	0.47
30:0:1181:A:N1	30:0:1192:A:O2'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1210:G:O2'	30:0:1211:G:H5'	2.14	0.47
30:0:2509:A:H2'	30:0:2510:C:O4'	2.14	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
30:0:2781:U:H2'	30:0:2782:G:H5'	1.95	0.47
30:0:2860:G:H2'	30:0:2861:G:H8	1.80	0.47
30:0:432:G:H2'	30:0:433:C:H6	1.80	0.47
1:A:94:LEU:HG	1:A:99:ILE:CD1	2.44	0.47
8:H:123:ILE:HD12	8:H:123:ILE:N	2.30	0.47
10:J:39:VAL:CG2	10:J:107:ASN:HA	2.44	0.47
15:O:42:GLU:HB2	38:0:3736:HOH:O	2.15	0.47
20:T:41:ARG:NH1	20:T:42:VAL:O	2.47	0.47
20:T:51:LEU:HD11	20:T:97:ARG:HB2	1.97	0.47
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.96	0.47
25:Y:151:SER:HB3	25:Y:154:ARG:HB3	1.97	0.47
30:0:1333:U:H2'	30:0:1334:C:H6	1.80	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.97	0.47
30:0:1858:A:H2'	30:0:1859:A:C8	2.50	0.47
30:0:1988:C:H2'	30:0:1989:G:O4'	2.15	0.47
30:0:2727:A:C2'	30:0:2728:C:H5'	2.45	0.47
30:0:2837:U:H2'	38:0:6824:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:C6	2.49	0.47
30:0:711:G:O2'	30:0:712:C:H5'	2.15	0.47
2:B:171:VAL:O	2:B:175:LEU:HB2	2.15	0.47
3:C:180:SER:HB2	38:C:8643:HOH:O	2.14	0.47
4:D:59:GLY:HA3	38:D:4886:HOH:O	2.14	0.47
13:M:15:PRO:HA	13:M:20:LEU:HD23	1.95	0.47
14:N:71:TRP:HZ2	38:N:8833:HOH:O	1.97	0.47
16:P:13:VAL:HG13	16:P:14:LEU:N	2.29	0.47
23:W:129:LYS:HE3	31:9:87:U:H2'	1.97	0.47
23:W:77:ALA:HB3	38:W:5763:HOH:O	2.14	0.47
30:0:1168:C:H2'	30:0:1169:U:H5'	1.96	0.47
30:0:1446:U:H4'	30:0:1447:U:OP2	2.14	0.47
30:0:1857:A:N6	30:0:2247:C:H1'	2.30	0.47
30:0:2059:U:H1'	38:0:4439:HOH:O	2.14	0.47
30:0:2460:A:C2	30:0:2461:U:C2	3.02	0.47
30:0:800:G:H8	30:0:800:G:O5'	1.98	0.47
30:0:835:U:H5''	38:0:9381:HOH:O	2.14	0.47
31:9:22:G:N7	31:9:55:U:C6	2.82	0.47
1:A:105:VAL:CG1	1:A:154:ALA:HB1	2.44	0.47
3:C:28:SER:HB2	38:C:8659:HOH:O	2.14	0.47
14:N:27:LEU:HD22	14:N:50:LEU:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:3:LEU:HA	16:P:6:GLN:OE1	2.14	0.47
22:V:64:GLY:O	22:V:65:ASP:HB2	2.15	0.47
23:W:128:VAL:HG22	30:0:1098:A:OP1	2.15	0.47
30:0:1889:C:O2'	30:0:1890:U:H5'	2.15	0.47
30:0:2490:A:H5''	38:0:7023:HOH:O	2.15	0.47
30:0:2858:U:H2'	30:0:2859:C:H6	1.80	0.47
30:0:2878:U:H2'	30:0:2879:A:O4'	2.14	0.47
30:0:292:G:H2'	30:0:358:G:N2	2.30	0.47
30:0:561:G:H2'	30:0:562:A:H8	1.79	0.47
1:A:171:LYS:HB2	30:0:820:G:C5	2.50	0.47
2:B:212:GLN:HB2	2:B:257:THR:OG1	2.15	0.47
6:F:21:GLU:O	6:F:24:ARG:HG2	2.15	0.47
16:P:1:THR:O	30:0:1396:C:H1'	2.15	0.47
18:R:69:LYS:HB2	18:R:72:VAL:HG23	1.97	0.47
22:V:1:THR:HG23	22:V:2:VAL:N	2.29	0.47
23:W:72:PRO:HG2	38:W:5763:HOH:O	2.15	0.47
30:0:1056:U:H2'	30:0:1057:A:O4'	2.14	0.47
23:W:125:HIS:CE1	30:0:1097:A:C5'	2.95	0.47
16:P:41:ARG:NH2	30:0:1500:U:OP2	2.47	0.47
30:0:1806:G:C4	30:0:1807:U:C6	3.03	0.47
30:0:1928:C:O2'	30:0:1929:G:H5'	2.15	0.47
30:0:2301:A:H5''	30:0:2302:A:H5'	1.96	0.47
30:0:249:G:O2'	30:0:250:C:H5'	2.15	0.47
13:M:193:LYS:HB3	30:0:392:U:C5'	2.45	0.47
14:N:170:GLU:O	14:N:174:GLU:HG3	2.14	0.47
17:Q:34:ASP:O	17:Q:37:GLU:HB2	2.15	0.47
30:0:1177:A:N1	30:0:1178:G:C4	2.82	0.46
30:0:1159:G:H1	30:0:1208:C:H42	1.63	0.46
30:0:137:U:OP1	30:0:259:G:O2'	2.33	0.46
24:X:30:MET:HG2	30:0:1384:C:H5'	1.96	0.46
30:0:1760:G:C6	30:0:1761:U:C4	3.03	0.46
30:0:1854:C:H2'	30:0:1875:A:H61	1.80	0.46
30:0:1942:A:O2'	30:0:1943:C:H5'	2.15	0.46
30:0:2019:A:H2'	30:0:2020:C:C6	2.49	0.46
4:D:22:VAL:HG21	30:0:2348:C:C5'	2.45	0.46
30:0:2379:G:H4'	30:0:2380:A:C5'	2.45	0.46
30:0:2388:C:O2'	30:0:2389:U:H5'	2.14	0.46
30:0:40:C:H5'	38:0:3836:HOH:O	2.14	0.46
30:0:589:U:H2'	30:0:590:A:C8	2.50	0.46
30:0:737:A:H2'	30:0:738:G:C8	2.49	0.46
30:0:806:A:H2'	30:0:807:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:54:A:C2'	31:9:55:U:C5'	2.85	0.46
13:M:184:ARG:HG3	13:M:185:PRO:HA	1.97	0.46
16:P:13:VAL:HG13	16:P:14:LEU:H	1.80	0.46
19:S:6:LYS:HE3	19:S:29:ASP:HA	1.97	0.46
30:0:11:A:N3	30:0:11:A:H2'	2.30	0.46
30:0:1409:G:C2	30:0:1410:G:C8	3.03	0.46
30:0:154:C:O2'	30:0:155:C:H5'	2.14	0.46
30:0:1925:G:O2'	30:0:1926:G:H5'	2.15	0.46
29:3:79:LEU:HD12	30:0:2456:A:C2	2.50	0.46
30:0:2461:U:O2	30:0:2466:G:H1'	2.14	0.46
30:0:703:G:C6	30:0:704:C:N4	2.83	0.46
30:0:61:G:C6	30:0:86:A:N6	2.83	0.46
27:1:10:LYS:HG3	38:1:2979:HOH:O	2.14	0.46
2:B:162:MET:CE	2:B:310:ARG:HD3	2.45	0.46
10:J:42:GLU:HG2	10:J:43:ARG:N	2.30	0.46
21:U:47:ARG:HG3	38:U:4381:HOH:O	2.15	0.46
26:Z:70:ARG:NH1	26:Z:83:TYR:HD1	2.11	0.46
30:0:1016:U:H1'	38:0:3652:HOH:O	2.15	0.46
38:W:7804:HOH:O	30:0:1286:A:H5''	2.15	0.46
30:0:1398:G:H4'	38:0:6650:HOH:O	2.15	0.46
30:0:1415:G:O2'	30:0:1416:G:H5'	2.15	0.46
30:0:168:C:H6	30:0:168:C:O5'	1.98	0.46
30:0:1790:C:H2'	30:0:1791:U:H6	1.80	0.46
30:0:1825:U:O2'	30:0:1826:C:H5'	2.15	0.46
30:0:214:U:H5'	38:0:6117:HOH:O	2.15	0.46
30:0:2259:C:C2	30:0:2260:A:C8	3.04	0.46
30:0:2658:G:C2	30:0:2659:U:C6	3.03	0.46
30:0:2871:G:C6	30:0:2887:G:N1	2.83	0.46
30:0:400:C:H2'	30:0:401:C:H6	1.80	0.46
30:0:432:G:C2	30:0:433:C:C5	3.02	0.46
30:0:604:G:H4'	30:0:605:C:O5'	2.15	0.46
12:L:38:HIS:O	30:0:926:A:H1'	2.15	0.46
29:3:67:LEU:HD13	29:3:69:TYR:HE1	1.81	0.46
1:A:88:ILE:HD13	1:A:100:PRO:HD3	1.97	0.46
2:B:5:ARG:HD2	2:B:8:LYS:NZ	2.31	0.46
13:M:92:THR:HB	30:0:401:C:O2'	2.15	0.46
30:0:100:C:H2'	30:0:101:C:H6	1.81	0.46
30:0:10:U:C4	30:0:532:A:N7	2.84	0.46
30:0:128:A:O2'	30:0:129:A:C5'	2.64	0.46
30:0:1484:G:H2'	38:0:9110:HOH:O	2.16	0.46
30:0:1603:A:C5'	30:0:1605:G:C5'	2.91	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1806:G:H2'	30:0:1807:U:H6	1.78	0.46
30:0:247:A:C2	30:0:265:U:C2	3.03	0.46
30:0:2520:G:O2'	30:0:2521:A:H5'	2.16	0.46
30:0:440:C:C4	30:0:441:A:C6	3.04	0.46
30:0:732:C:O2'	30:0:733:U:H5'	2.14	0.46
30:0:959:C:H1'	30:0:961:A:C6	2.50	0.46
27:1:42:SER:HB3	30:0:1473:U:C1'	2.45	0.46
29:3:64:LYS:HD3	29:3:82:GLY:O	2.14	0.46
4:D:138:GLY:HA2	31:9:29:C:O3'	2.15	0.46
31:9:3:A:H2'	38:9:9044:HOH:O	2.14	0.46
1:A:36:ASP:CB	1:A:85:SER:HB2	2.45	0.46
3:C:72:LYS:HG2	3:C:77:ALA:HA	1.96	0.46
10:J:90:LYS:HB2	33:J:8802:CL:CL	2.53	0.46
23:W:81:ASP:OD1	23:W:92:ASP:HB2	2.16	0.46
30:0:1477:C:C5'	30:0:1868:G:C5'	2.94	0.46
30:0:1590:A:C2	30:0:1606:A:C1'	2.99	0.46
30:0:1626:A:H2'	30:0:1627:G:C5'	2.45	0.46
30:0:2004:U:H4'	38:0:5274:HOH:O	2.14	0.46
30:0:2355:G:N3	30:0:2355:G:H2'	2.31	0.46
30:0:2356:A:H2'	30:0:2357:G:O4'	2.16	0.46
30:0:2911:C:O2'	30:0:2912:C:H5'	2.15	0.46
30:0:364:U:H2'	30:0:365:G:O4'	2.15	0.46
30:0:780:A:H2'	30:0:781:C:C6	2.50	0.46
30:0:815:U:H5	38:0:7423:HOH:O	1.98	0.46
1:A:212:PRO:HB2	38:0:4344:HOH:O	2.16	0.46
2:B:199:TYR:CE2	2:B:268:ARG:HB2	2.49	0.46
30:0:1215:A:O3'	30:0:1216:G:H4'	2.16	0.46
30:0:1524:U:H5''	30:0:1524:U:H6	1.81	0.46
30:0:2626:C:H2'	30:0:2627:G:C8	2.51	0.46
30:0:307:G:N2	30:0:309:C:C2	2.84	0.46
30:0:396:U:O2'	30:0:397:A:P	2.73	0.46
30:0:39:G:O6	30:0:441:A:C2	2.68	0.46
1:A:94:LEU:HD12	1:A:98:GLU:HB2	1.96	0.46
2:B:304:PRO:HD2	2:B:307:ARG:NE	2.31	0.46
4:D:64:ARG:HB3	4:D:67:ASP:OD2	2.15	0.46
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.30	0.46
9:I:87:PRO:HD3	38:0:7103:HOH:O	2.14	0.46
10:J:130:VAL:HG12	10:J:131:THR:N	2.31	0.46
14:N:147:ILE:HD12	38:9:9091:HOH:O	2.15	0.46
18:R:48:GLU:HA	18:R:51:ILE:HD12	1.98	0.46
23:W:68:THR:HG23	23:W:69:ARG:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1187:U:C2	30:0:1189:A:OP2	2.68	0.46
30:0:1200:A:H3'	38:0:5722:HOH:O	2.15	0.46
30:0:1427:A:O2'	30:0:1428:C:H5'	2.16	0.46
30:0:1773:G:H2'	30:0:1774:G:H5'	1.98	0.46
30:0:1829:A:H2'	30:0:1830:C:C5'	2.41	0.46
30:0:2017:U:O2'	30:0:2018:A:C8	2.53	0.46
30:0:2100:A:C5'	38:0:7373:HOH:O	2.57	0.46
30:0:2314:G:O2'	30:0:2315:C:H5'	2.15	0.46
30:0:2397:G:N2	38:0:6910:HOH:O	2.49	0.46
30:0:2471:G:C5	30:0:2472:C:C5	3.03	0.46
30:0:2828:G:O5'	30:0:2828:G:C8	2.68	0.46
30:0:421:C:H2'	30:0:422:G:C8	2.50	0.46
30:0:497:A:H5''	38:0:3588:HOH:O	2.16	0.46
30:0:662:U:H1'	30:0:748:C:H1'	1.98	0.46
6:F:89:LEU:HD21	30:0:262:A:C6	2.51	0.46
9:I:112:LEU:CD1	30:0:1162:G:H1'	2.45	0.46
14:N:42:HIS:HB3	14:N:62:HIS:HE1	1.80	0.46
15:O:51:TYR:CD2	30:0:721:A:H5''	2.51	0.46
24:X:43:VAL:HG12	24:X:47:ALA:HB3	1.98	0.46
30:0:1187:U:O2'	30:0:1188:A:C8	2.69	0.46
30:0:1209:C:C2	30:0:1210:G:C8	3.03	0.46
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.46
30:0:2401:A:H2'	30:0:2402:A:C8	2.51	0.46
30:0:2326:C:H4'	30:0:2412:G:C4'	2.46	0.46
30:0:2612:A:H4'	38:0:3676:HOH:O	2.15	0.46
30:0:277:U:O2'	30:0:278:A:H5'	2.16	0.46
30:0:282:C:HO2'	30:0:368:C:N4	2.13	0.46
30:0:2912:C:C6	30:0:2912:C:O5'	2.66	0.46
30:0:334:G:H2'	30:0:335:U:H6	1.81	0.46
30:0:567:U:C5'	38:0:5254:HOH:O	2.62	0.46
30:0:920:C:H5''	30:0:921:G:O5'	2.16	0.46
30:0:969:G:N1	30:0:999:C:N4	2.53	0.46
9:I:124:VAL:C	9:I:126:THR:H	2.18	0.46
18:R:135:ALA:HB1	18:R:137:ASN:ND2	2.29	0.46
30:0:1058:A:H2'	30:0:1060:C:H5''	1.97	0.46
30:0:1157:C:H2'	30:0:1158:G:H8	1.80	0.46
19:S:12:GLU:OE1	30:0:1444:G:H4'	2.15	0.46
30:0:1790:C:H2'	30:0:1791:U:C6	2.51	0.46
30:0:1812:G:H4'	30:0:1814:G:O4'	2.15	0.46
30:0:2038:A:C2	30:0:2039:A:C5	3.04	0.46
30:0:2241:C:H2'	30:0:2242:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2456:A:H1'	38:0:6579:HOH:O	2.16	0.46
30:0:488:U:C2'	38:0:3993:HOH:O	2.64	0.46
30:0:562:A:H2'	30:0:563:C:O4'	2.15	0.46
30:0:735:C:C5	30:0:736:A:C4	3.03	0.46
26:Z:34:SER:CB	30:0:797:A:H4'	2.46	0.46
30:0:897:A:H2'	30:0:899:C:C5	2.50	0.46
31:9:15:C:N4	31:9:16:G:C6	2.84	0.46
31:9:47:A:C2	31:9:48:C:C2	3.03	0.46
10:J:131:THR:HG22	10:J:134:GLU:HG3	1.97	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
15:O:38:ARG:HD3	30:0:654:A:OP2	2.16	0.46
20:T:48:VAL:HG23	20:T:98:VAL:HA	1.97	0.46
23:W:29:VAL:O	23:W:30:ASN:HB2	2.16	0.46
30:0:1119:G:N2	30:0:1246:A:H2	2.04	0.46
30:0:1236:A:C2'	30:0:1237:U:H5'	2.46	0.46
30:0:1504:A:C5'	38:0:4396:HOH:O	2.63	0.46
30:0:1512:G:H4'	38:0:4618:HOH:O	2.15	0.46
30:0:1707:G:H1'	30:0:1711:A:N6	2.31	0.46
30:0:1809:G:H2'	30:0:1811:A:OP2	2.16	0.46
30:0:1902:G:H2'	30:0:1903:U:O4'	2.16	0.46
30:0:2011:A:H5'	30:0:2013:G:C1'	2.46	0.46
30:0:212:A:H5'	30:0:214:U:H1'	1.98	0.46
30:0:2694:A:H3'	30:0:2695:C:H6	1.81	0.46
30:0:2831:C:C2	30:0:2910:A:N1	2.84	0.46
30:0:2860:G:H1'	38:0:6785:HOH:O	2.15	0.46
30:0:938:G:C4	30:0:1031:G:N2	2.84	0.46
29:3:20:HIS:CE1	29:3:71:CYS:SG	3.09	0.46
13:M:164:THR:HG22	13:M:165:GLY:N	2.30	0.46
13:M:94:ARG:NH2	30:0:175:G:O6	2.49	0.46
20:T:79:LEU:HG	20:T:89:ARG:HB2	1.98	0.46
24:X:21:PRO:HD3	38:X:6179:HOH:O	2.16	0.46
25:Y:214:ARG:HH12	25:Y:230:ASN:ND2	2.13	0.46
30:0:1217:G:C2	30:0:1218:U:C2	3.04	0.45
30:0:1516:U:H2'	30:0:1517:C:O4'	2.17	0.45
30:0:1490:G:H4'	30:0:1533:A:OP1	2.16	0.45
30:0:1864:C:H2'	30:0:1865:A:O4'	2.16	0.45
30:0:56:G:H1'	38:0:5300:HOH:O	2.16	0.45
3:C:35:VAL:HG21	3:C:227:GLY:HA2	1.98	0.45
4:D:63:ILE:HG13	4:D:64:ARG:N	2.32	0.45
5:E:103:VAL:HG22	5:E:115:ARG:HB3	1.96	0.45
13:M:133:LEU:O	13:M:134:ILE:HD13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:64:GLU:HG3	17:Q:74:ASP:CG	2.36	0.45
30:0:1018:A:H8	30:0:1018:A:O5'	1.99	0.45
30:0:940:G:C5	30:0:1027:G:C2	3.04	0.45
30:0:1074:G:H4'	30:0:1260:G:C6	2.52	0.45
30:0:1362:U:O2'	30:0:1363:G:H5'	2.17	0.45
30:0:1400:C:C2'	30:0:1401:G:H5'	2.46	0.45
30:0:1444:G:C6	30:0:1445:G:C5	3.05	0.45
30:0:1503:U:H2'	30:0:1504:A:H5'	1.98	0.45
30:0:1831:U:H2'	30:0:1832:G:H5'	1.98	0.45
30:0:1908:G:H1'	30:0:1931:A:N6	2.31	0.45
30:0:1987:C:O2'	30:0:1988:C:H5'	2.16	0.45
30:0:2134:G:N2	30:0:2242:U:C2	2.85	0.45
30:0:2577:A:H8	38:0:9606:HOH:O	1.99	0.45
30:0:2812:A:C2	30:0:2814:A:N7	2.85	0.45
30:0:369:G:O2'	30:0:370:G:H5'	2.16	0.45
30:0:743:G:O2'	30:0:744:G:H5'	2.16	0.45
31:9:39:U:N3	31:9:42:C:H5''	2.31	0.45
4:D:76:ARG:HD2	31:9:42:C:O2	2.16	0.45
1:A:186:TRP:CG	1:A:187:PRO:HA	2.50	0.45
1:A:35:GLY:O	1:A:37:VAL:HG22	2.17	0.45
1:A:94:LEU:N	1:A:94:LEU:HD23	2.31	0.45
2:B:320:GLN:HA	2:B:321:PRO:HD3	1.83	0.45
8:H:157:TYR:CD1	8:H:157:TYR:C	2.89	0.45
9:I:83:GLY:H	30:0:1168:C:C5'	2.28	0.45
11:K:132:VAL:HG21	21:U:22:VAL:HG13	1.97	0.45
15:O:32:ARG:HH21	15:O:35:LYS:NZ	2.14	0.45
30:0:99:A:C8	30:0:100:C:C5	3.05	0.45
9:I:113:SER:HA	30:0:1186:C:H5'	1.98	0.45
30:0:1213:C:O2'	30:0:1214:G:H5'	2.17	0.45
30:0:1116:U:N3	30:0:1246:A:N6	2.60	0.45
30:0:154:C:H2'	30:0:155:C:H6	1.82	0.45
30:0:1603:A:H5'	30:0:1605:G:C5'	2.46	0.45
30:0:1670:A:H2'	30:0:1671:U:O4'	2.16	0.45
30:0:1759:A:N3	30:0:1818:C:H2'	2.31	0.45
30:0:1948:G:H2'	30:0:1949:G:O4'	2.16	0.45
30:0:2293:G:C6	30:0:2294:C:C5	3.04	0.45
30:0:2757:A:H2'	30:0:2758:G:O4'	2.16	0.45
30:0:360:A:H2'	30:0:361:C:O4'	2.16	0.45
30:0:400:C:O2'	30:0:401:C:H5'	2.17	0.45
30:0:191:A:N6	30:0:435:A:H62	2.14	0.45
30:0:595:U:H2'	30:0:596:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:793:A:H2'	30:0:794:U:H6	1.81	0.45
29:3:12:PRO:HG2	29:3:13:HIS:CD2	2.49	0.45
31:9:59:C:O5'	31:9:59:C:C6	2.63	0.45
1:A:51:ARG:O	1:A:52:SER:HB2	2.16	0.45
8:H:46:TYR:HA	8:H:47:PRO:HD3	1.81	0.45
20:T:114:SER:OG	20:T:117:ASP:HB2	2.16	0.45
30:0:1178:G:C6	30:0:1179:C:N4	2.84	0.45
30:0:912:A:C4	30:0:1294:A:C2	3.04	0.45
30:0:790:A:H1'	30:0:1710:A:C2'	2.46	0.45
30:0:1819:G:H2'	30:0:1820:G:C4'	2.46	0.45
30:0:1964:U:O2	30:0:1964:U:H2'	2.15	0.45
30:0:1970:G:N3	30:0:1970:G:H2'	2.31	0.45
30:0:2005:G:P	30:0:2005:G:H3'	2.55	0.45
30:0:2438:G:H2'	30:0:2439:C:C6	2.51	0.45
30:0:2092:G:H2'	30:0:2613:G:OP1	2.17	0.45
30:0:304:G:O5'	30:0:304:G:H8	2.00	0.45
30:0:734:U:H2'	30:0:736:A:OP2	2.16	0.45
30:0:876:A:C2'	30:0:876:A:N3	2.79	0.45
31:9:29:C:C5	31:9:30:C:C5	3.04	0.45
2:B:254:GLN:HG2	2:B:255:GLY:N	2.30	0.45
13:M:122:GLN:HB2	13:M:127:LYS:HG2	1.98	0.45
13:M:30:GLU:HG2	38:M:8864:HOH:O	2.17	0.45
14:N:144:GLY:O	14:N:147:ILE:HG23	2.15	0.45
17:Q:15:LYS:HG3	30:0:2364:A:O3'	2.16	0.45
18:R:96:VAL:HG13	18:R:106:GLY:HA3	1.98	0.45
25:Y:144:ARG:CZ	38:Y:8916:HOH:O	2.65	0.45
26:Z:70:ARG:O	26:Z:81:CYS:SG	2.74	0.45
30:0:940:G:N3	30:0:1032:A:C2	2.84	0.45
30:0:1524:U:H5''	30:0:1524:U:C6	2.51	0.45
30:0:1547:A:H2'	30:0:1548:U:C6	2.52	0.45
30:0:1940:C:H1'	38:0:9382:HOH:O	2.17	0.45
30:0:2697:A:H2'	30:0:2697:A:N3	2.32	0.45
30:0:2718:C:C6	30:0:2718:C:H5'	2.50	0.45
30:0:2728:C:O5'	30:0:2728:C:H6	1.99	0.45
30:0:420:U:O4'	30:0:1920:C:C4	2.70	0.45
30:0:659:A:H5''	38:0:7082:HOH:O	2.17	0.45
38:C:8558:HOH:O	30:0:751:U:H5'	2.16	0.45
28:2:40:ARG:HG3	28:2:45:ASN:CB	2.45	0.45
29:3:59:ASP:OD1	30:0:2460:A:H5''	2.16	0.45
2:B:162:MET:HE2	2:B:310:ARG:HD3	1.97	0.45
5:E:152:THR:HG21	5:E:165:GLY:HA2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:72:ASN:O	12:L:76:LEU:HG	2.17	0.45
18:R:18:LEU:HB2	18:R:143:VAL:CG1	2.46	0.45
23:W:5:VAL:HG11	23:W:153:MET:HE1	1.99	0.45
30:0:1151:G:N2	30:0:1214:G:C4	2.85	0.45
9:I:82:THR:HG22	30:0:1168:C:H5''	1.97	0.45
30:0:1149:U:C5	30:0:1215:A:N7	2.84	0.45
30:0:1406:A:H4'	30:0:1407:A:H5''	1.98	0.45
30:0:1434:A:H4'	30:0:1435:U:H5	1.82	0.45
30:0:1523:G:C6	30:0:1524:U:C4	3.05	0.45
30:0:1883:U:H5''	30:0:2013:G:OP2	2.17	0.45
30:0:2475:C:H5'	38:0:3664:HOH:O	2.16	0.45
30:0:418:C:H2'	30:0:419:A:C8	2.52	0.45
30:0:790:A:H8	38:0:6078:HOH:O	1.98	0.45
30:0:960:G:N3	30:0:960:G:C2'	2.79	0.45
31:9:61:C:H2'	31:9:62:A:C8	2.46	0.45
1:A:11:ARG:HD3	38:0:9222:HOH:O	2.16	0.45
1:A:204:GLY:N	30:0:2634:G:OP2	2.49	0.45
6:F:34:ASN:HA	13:M:4:ALA:HB2	1.98	0.45
12:L:57:VAL:O	12:L:57:VAL:HG12	2.17	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.99	0.45
14:N:33:ARG:HG3	38:N:8841:HOH:O	2.17	0.45
15:O:27:GLY:O	15:O:31:GLU:HG3	2.17	0.45
1:A:189:VAL:HA	30:0:1845:A:OP1	2.16	0.45
30:0:2385:G:H2'	30:0:2386:U:H6	1.81	0.45
30:0:2515:C:H2'	30:0:2516:G:O4'	2.16	0.45
27:1:16:HIS:HE1	30:0:775:G:OP1	1.99	0.45
30:0:92:G:H2'	30:0:93:C:H6	1.82	0.45
29:3:35:TRP:HZ3	30:0:2432:C:OP1	2.00	0.45
2:B:119:HIS:O	2:B:121:PRO:HD3	2.16	0.45
30:0:1405:U:H4'	30:0:1406:A:H5''	1.98	0.45
30:0:1902:G:O2'	30:0:1903:U:H5'	2.16	0.45
30:0:2361:A:H2'	30:0:2362:A:C8	2.51	0.45
30:0:2887:G:H2'	30:0:2888:U:O4'	2.17	0.45
30:0:342:C:N4	30:0:343:C:H41	2.15	0.45
30:0:343:C:O2'	30:0:344:C:H5'	2.17	0.45
30:0:387:G:C2'	30:0:388:G:H5'	2.46	0.45
30:0:916:A:C6	30:0:917:U:C4	3.05	0.45
31:9:30:C:C2'	31:9:30:C:O2	2.65	0.45
31:9:72:C:O2'	31:9:73:A:H5'	2.15	0.45
2:B:43:GLY:O	2:B:308:LEU:HD12	2.16	0.45
4:D:50:VAL:O	4:D:71:ALA:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:96:ALA:HA	38:F:3111:HOH:O	2.15	0.45
10:J:43:ARG:HD3	38:J:8858:HOH:O	2.17	0.45
30:0:1576:G:C2	30:0:1577:U:C2	3.05	0.45
30:0:1626:A:C2'	30:0:1627:G:H5'	2.46	0.45
30:0:1850:U:H2'	30:0:1851:G:C8	2.52	0.45
30:0:228:C:H2'	30:0:229:G:C5'	2.46	0.45
30:0:281:U:H5	38:0:7575:HOH:O	1.99	0.45
30:0:2842:G:H2'	30:0:2843:A:H5'	1.98	0.45
30:0:862:U:H2'	30:0:863:G:C8	2.52	0.45
30:0:957:A:H8	30:0:957:A:O5'	2.00	0.45
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.82	0.45
2:B:86:ALA:HA	38:B:9051:HOH:O	2.16	0.45
3:C:95:GLU:HG3	38:C:8669:HOH:O	2.16	0.45
5:E:121:ASP:HB2	38:E:5899:HOH:O	2.16	0.45
5:E:102:VAL:HG11	5:E:148:ILE:HG12	1.98	0.45
21:U:6:CYS:SG	21:U:31:PHE:HA	2.56	0.45
26:Z:35:SER:HB3	26:Z:47:ARG:HB2	1.98	0.45
30:0:1041:U:H2'	30:0:1042:U:C5'	2.46	0.45
30:0:1543:G:N1	30:0:1641:A:OP2	2.36	0.45
30:0:1801:A:C2	30:0:1802:G:C4	3.04	0.45
30:0:1477:C:C5'	30:0:1868:G:H5''	2.47	0.45
30:0:2311:A:O2'	30:0:2312:G:H5'	2.17	0.45
30:0:2511:A:H2'	30:0:2512:U:H6	1.82	0.45
30:0:958:G:H2'	30:0:959:C:H6	1.75	0.45
30:0:969:G:N2	30:0:1000:C:C2	2.85	0.45
31:9:33:U:C6	31:9:43:G:C8	3.05	0.45
3:C:88:SER:O	3:C:91:PRO:HD3	2.17	0.45
13:M:86:GLN:NE2	38:M:8882:HOH:O	2.50	0.45
30:0:1181:A:O2'	30:0:1182:C:H5'	2.17	0.44
30:0:1392:A:C6	30:0:1395:C:C2	3.05	0.44
30:0:1524:U:C5'	30:0:1524:U:H6	2.29	0.44
30:0:1584:C:O2'	30:0:1585:C:H5'	2.17	0.44
30:0:1748:U:C5	30:0:1749:U:C4	3.06	0.44
30:0:2293:G:C6	30:0:2294:C:C4	3.05	0.44
30:0:198:A:C2	30:0:2444:U:H1'	2.53	0.44
30:0:2826:G:O6	30:0:2913:A:N6	2.50	0.44
30:0:283:U:H5''	30:0:284:C:OP2	2.17	0.44
30:0:339:A:C6	30:0:342:C:N3	2.85	0.44
30:0:581:G:H5'	38:0:7663:HOH:O	2.17	0.44
30:0:163:U:O3'	30:0:896:C:H4'	2.16	0.44
31:9:107:C:O2'	31:9:108:C:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:3:A:OP2	31:9:25:G:N2	2.50	0.44
1:A:164:ARG:NH1	1:A:164:ARG:HB3	2.31	0.44
4:D:128:LEU:HD23	4:D:129:ASP:N	2.32	0.44
5:E:153:ARG:NH1	30:0:2778:A:C1'	2.81	0.44
8:H:83:GLU:HA	38:H:243:HOH:O	2.18	0.44
10:J:107:ASN:HD21	10:J:109:TYR:HB2	1.82	0.44
16:P:81:LYS:HE3	30:0:1813:U:O2'	2.18	0.44
18:R:34:GLU:HG2	18:R:46:TYR:OH	2.17	0.44
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.98	0.44
26:Z:47:ARG:O	26:Z:51:ALA:HB2	2.16	0.44
30:0:1246:A:O2'	30:0:1247:A:H3'	2.17	0.44
30:0:1362:U:H2'	30:0:1363:G:C8	2.52	0.44
30:0:1434:A:H2'	30:0:1436:C:C5	2.52	0.44
30:0:440:C:O5'	30:0:440:C:H6	2.00	0.44
18:R:98:ASN:ND2	30:0:500:G:H21	2.12	0.44
30:0:711:G:C2'	30:0:712:C:H5'	2.47	0.44
2:B:51:VAL:HG13	2:B:53:LEU:HD13	1.98	0.44
3:C:129:HIS:HD2	3:C:165:ASP:OD2	2.01	0.44
3:C:60:SER:HA	38:C:8575:HOH:O	2.17	0.44
10:J:15:ARG:HG2	10:J:16:ASP:OD1	2.17	0.44
12:L:41:HIS:CD2	30:0:926:A:O2'	2.69	0.44
13:M:76:ARG:HG3	38:M:8827:HOH:O	2.17	0.44
14:N:1:ALA:HB2	31:9:14:G:O2'	2.18	0.44
20:T:81:LYS:HD2	20:T:87:VAL:HG11	1.98	0.44
23:W:10:GLU:O	23:W:13:MET:HB3	2.18	0.44
30:0:1069:C:H2'	30:0:1070:A:O4'	2.18	0.44
30:0:1132:A:H2'	30:0:1133:A:C8	2.52	0.44
30:0:1202:A:C2'	30:0:1203:G:H5'	2.48	0.44
30:0:1391:G:N2	30:0:1434:A:H5''	2.32	0.44
30:0:1649:G:H1'	38:0:5049:HOH:O	2.17	0.44
30:0:1680:C:H2'	30:0:1681:G:O4'	2.17	0.44
30:0:1701:A:H5''	30:0:1702:U:H3'	1.99	0.44
30:0:2276:U:H2'	30:0:2277:U:C6	2.52	0.44
29:3:10:TYR:CD1	30:0:2408:A:H1'	2.52	0.44
30:0:372:A:O2'	30:0:373:G:H5'	2.17	0.44
30:0:57:C:H42	30:0:89:G:H1	1.64	0.44
30:0:729:C:C2	30:0:743:G:C2	3.05	0.44
30:0:877:G:N7	30:0:885:G:C5	2.85	0.44
9:I:130:LEU:HD21	30:0:1167:G:C4'	2.46	0.44
11:K:86:THR:HG22	11:K:87:ARG:N	2.32	0.44
13:M:71:SER:OG	13:M:72:ALA:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:59:PHE:O	18:R:63:ASN:HB3	2.18	0.44
22:V:12:THR:CG2	22:V:15:GLU:H	2.30	0.44
2:B:244:PRO:HB3	30:0:1234:U:N3	2.32	0.44
30:0:1415:G:C2'	30:0:1416:G:H5'	2.47	0.44
30:0:1556:G:O2'	30:0:1557:G:H5'	2.17	0.44
30:0:2507:G:H2'	30:0:2510:C:H42	1.81	0.44
30:0:2509:A:OP2	30:0:2510:C:H5	2.00	0.44
30:0:2775:A:N6	30:0:2799:A:C8	2.86	0.44
30:0:2911:C:H2'	30:0:2912:C:H6	1.82	0.44
30:0:625:U:H5'	38:0:3177:HOH:O	2.16	0.44
29:3:5:ARG:HD2	29:3:21:GLU:HG2	1.98	0.44
4:D:153:THR:O	4:D:156:ARG:HB2	2.16	0.44
5:E:20:ILE:O	5:E:30:THR:HA	2.17	0.44
8:H:14:LYS:HG3	38:H:183:HOH:O	2.17	0.44
12:L:22:ARG:HG2	38:0:3223:HOH:O	2.15	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.81	0.44
25:Y:182:PHE:HD2	25:Y:200:THR:O	2.00	0.44
25:Y:189:ASN:HD22	25:Y:189:ASN:C	2.21	0.44
26:Z:69:ASP:O	26:Z:71:VAL:N	2.45	0.44
30:0:1043:C:H2'	38:0:3185:HOH:O	2.18	0.44
18:R:80:TYR:O	30:0:2050:G:H5''	2.16	0.44
30:0:2345:A:C3'	30:0:2346:C:H6	2.23	0.44
23:W:5:VAL:HG11	23:W:153:MET:CE	2.48	0.44
30:0:1112:G:H1	30:0:1251:C:H42	1.65	0.44
30:0:1330:A:H2	38:0:4652:HOH:O	2.00	0.44
30:0:1519:U:O2'	30:0:1520:G:H5'	2.16	0.44
30:0:1706:G:C6	30:0:1707:G:N1	2.86	0.44
30:0:1711:A:H2'	30:0:1712:A:H5'	1.99	0.44
30:0:1762:C:H2'	30:0:1763:C:H6	1.82	0.44
1:A:233:THR:HB	30:0:1942:A:H5''	1.99	0.44
30:0:2005:G:OP2	30:0:2006:C:C5'	2.66	0.44
30:0:1016:U:O2'	30:0:2303:A:N7	2.40	0.44
30:0:2377:U:O2'	30:0:2378:U:H5'	2.17	0.44
30:0:2457:U:H1'	38:0:7515:HOH:O	2.17	0.44
30:0:2552:C:C6	30:0:2577:A:N7	2.85	0.44
30:0:2781:U:H2'	30:0:2782:G:C5'	2.48	0.44
30:0:2834:G:H2'	30:0:2835:C:O5'	2.17	0.44
30:0:2872:U:C2	30:0:2873:C:C6	3.05	0.44
30:0:2854:A:C6	30:0:2905:A:N1	2.86	0.44
30:0:569:A:H5''	30:0:587:A:N1	2.32	0.44
30:0:821:U:H2'	30:0:822:C:H6	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:40:HIS:HE1	30:0:949:U:O2'	2.01	0.44
27:1:20:ARG:HB2	38:1:513:HOH:O	2.18	0.44
23:W:129:LYS:CD	31:9:87:U:H2'	2.47	0.44
3:C:6:TYR:N	3:C:6:TYR:CD1	2.86	0.44
5:E:69:ILE:HA	5:E:72:MET:CE	2.48	0.44
8:H:8:MET:CE	30:0:2494:G:H4'	2.48	0.44
9:I:87:PRO:HG2	30:0:1181:A:O4'	2.18	0.44
13:M:66:SER:HB3	13:M:128:TRP:NE1	2.32	0.44
20:T:97:ARG:NH2	30:0:309:C:OP1	2.51	0.44
25:Y:99:ALA:HB2	25:Y:233:TYR:CE2	2.52	0.44
30:0:1309:U:C2'	30:0:1310:U:H5'	2.48	0.44
25:Y:204:ARG:NH2	30:0:1324:G:N2	2.65	0.44
30:0:1427:A:C2'	30:0:1428:C:H5'	2.47	0.44
19:S:55:GLN:CD	30:0:1446:U:H2'	2.37	0.44
1:A:192:VAL:HG23	30:0:1882:C:OP1	2.17	0.44
30:0:2250:G:N1	30:0:2251:G:N3	2.66	0.44
2:B:5:ARG:NH1	30:0:2547:C:OP2	2.51	0.44
30:0:2541:U:H5'	30:0:2611:G:O6	2.18	0.44
30:0:2566:A:C2	30:0:2696:G:O4'	2.71	0.44
38:T:2151:HOH:O	30:0:317:A:H5'	2.17	0.44
30:0:929:A:H8	30:0:929:A:O5'	2.01	0.44
2:B:241:PRO:HB3	30:0:2609:G:N3	2.33	0.44
4:D:62:ASP:HA	38:D:4233:HOH:O	2.18	0.44
4:D:86:THR:O	4:D:89:PRO:HD2	2.18	0.44
21:U:45:GLU:HB2	21:U:48:ASN:ND2	2.32	0.44
30:0:1202:A:H2'	30:0:1203:G:H5'	2.00	0.44
30:0:157:G:H3'	38:0:3945:HOH:O	2.18	0.44
30:0:1789:G:H2'	30:0:1790:C:O5'	2.17	0.44
30:0:1950:G:H2'	30:0:1951:G:C8	2.53	0.44
30:0:1986:G:C6	30:0:1987:C:N4	2.86	0.44
30:0:2061:C:H2'	30:0:2062:A:H5'	1.99	0.44
30:0:2104:C:O2	30:0:2485:A:N1	2.50	0.44
30:0:304:G:H1'	30:0:347:A:N6	2.32	0.44
30:0:582:U:H2'	30:0:583:C:C6	2.53	0.44
30:0:703:G:C6	30:0:704:C:C4	3.06	0.44
30:0:821:U:O2'	30:0:822:C:H5'	2.18	0.44
30:0:868:G:C4	30:0:887:G:C8	3.06	0.44
31:9:26:C:H2'	31:9:27:C:H6	1.79	0.44
31:9:31:C:C2	31:9:50:G:C2	3.05	0.44
31:9:81:C:C2'	31:9:82:U:H5'	2.48	0.44
1:A:103:VAL:HA	1:A:104:PRO:HD3	1.89	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:MET:SD	30:0:875:A:C2	3.11	0.44
2:B:195:ARG:HE	2:B:323:LEU:HD13	1.83	0.44
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.65	0.44
8:H:87:LYS:HG3	8:H:140:TYR:HD1	1.83	0.44
8:H:66:GLU:HA	38:H:239:HOH:O	2.17	0.44
13:M:80:GLY:O	13:M:81:ARG:HB2	2.18	0.44
14:N:47:LEU:HA	14:N:47:LEU:HD13	1.86	0.44
16:P:13:VAL:HG11	16:P:40:VAL:CG1	2.48	0.44
20:T:19:ARG:HD3	20:T:67:LEU:O	2.18	0.44
30:0:1522:A:H2'	30:0:1523:G:C5'	2.48	0.44
16:P:54:LYS:HB2	30:0:1717:A:H5''	1.98	0.44
30:0:1937:U:O2'	30:0:1938:G:H5'	2.18	0.44
30:0:2250:G:C2	30:0:2251:G:C4	3.06	0.44
29:3:10:TYR:CE2	30:0:2382:A:H1'	2.53	0.44
30:0:2431:C:H2'	30:0:2432:C:C6	2.53	0.44
5:E:90:HIS:CE1	30:0:2694:A:H5''	2.53	0.44
30:0:2729:C:O2'	30:0:2730:G:H5'	2.18	0.44
30:0:483:C:H2'	30:0:484:A:O4'	2.18	0.44
30:0:727:G:C2	30:0:728:C:C2	3.06	0.44
1:A:182:ARG:HB3	38:0:5133:HOH:O	2.18	0.44
2:B:279:THR:HG22	2:B:280:VAL:N	2.33	0.44
2:B:54:VAL:HB	38:B:9083:HOH:O	2.17	0.44
8:H:39:LYS:O	30:0:969:G:H4'	2.18	0.44
10:J:75:PRO:HD3	10:J:136:SER:OG	2.18	0.44
16:P:88:GLN:HB3	38:P:185:HOH:O	2.16	0.44
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.78	0.44
30:0:1166:A:C6	30:0:1167:G:C5	3.06	0.43
30:0:1167:G:O2'	30:0:1168:C:H5'	2.18	0.43
30:0:1185:U:C5'	38:0:7447:HOH:O	2.59	0.43
30:0:634:G:O2'	30:0:1358:A:OP1	2.31	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.18	0.43
30:0:1544:U:H2'	30:0:1545:C:H6	1.82	0.43
30:0:1592:G:O2'	30:0:1593:C:O4'	2.36	0.43
30:0:1642:A:N7	30:0:1643:C:C4	2.86	0.43
30:0:175:G:O2'	30:0:176:U:OP2	2.36	0.43
30:0:2090:G:H2'	30:0:2091:G:C8	2.53	0.43
30:0:2435:U:H4'	38:0:9269:HOH:O	2.17	0.43
30:0:2851:G:O2'	30:0:2852:A:H5'	2.17	0.43
30:0:324:G:C6	30:0:325:U:C5	3.06	0.43
30:0:293:A:C5	30:0:360:A:C2	3.06	0.43
30:0:39:G:O2'	30:0:40:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:533:U:H3'	38:0:3742:HOH:O	2.18	0.43
30:0:838:C:H4'	38:0:9187:HOH:O	2.18	0.43
31:9:74:G:O2'	31:9:75:G:H5'	2.18	0.43
3:C:174:ILE:CD1	30:0:338:C:H4'	2.48	0.43
4:D:103:ASN:ND2	4:D:133:ASN:HA	2.33	0.43
13:M:104:ARG:HG3	38:M:8866:HOH:O	2.18	0.43
14:N:12:ARG:HD3	14:N:18:THR:OG1	2.18	0.43
23:W:119:HIS:HE1	38:0:9568:HOH:O	2.00	0.43
25:Y:182:PHE:CG	25:Y:202:ALA:HB2	2.53	0.43
26:Z:45:VAL:O	26:Z:49:ARG:HG3	2.18	0.43
30:0:1130:U:C2'	30:0:1131:G:H5'	2.48	0.43
30:0:117:A:H2'	30:0:118:G:C8	2.53	0.43
30:0:1706:G:H1'	30:0:1712:A:N6	2.30	0.43
30:0:1916:C:C2	30:0:1924:A:C2	3.06	0.43
30:0:2135:A:O4'	30:0:2243:C:N4	2.51	0.43
30:0:2871:G:C4	30:0:2887:G:N2	2.86	0.43
30:0:692:A:N6	30:0:693:A:C2	2.86	0.43
30:0:827:A:H2'	30:0:828:G:O4'	2.18	0.43
31:9:2:U:OP2	31:9:3:A:H5'	2.18	0.43
1:A:215:ILE:HG22	1:A:227:ASP:O	2.18	0.43
1:A:94:LEU:HD12	1:A:98:GLU:CB	2.48	0.43
2:B:84:LEU:HD23	2:B:142:LEU:HD23	2.00	0.43
2:B:202:VAL:HA	2:B:310:ARG:O	2.18	0.43
3:C:193:LEU:HD12	3:C:211:ASP:O	2.18	0.43
4:D:10:PHE:CG	4:D:11:HIS:N	2.86	0.43
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.00	0.43
23:W:115:THR:HG23	38:W:5420:HOH:O	2.18	0.43
23:W:142:ASP:HB3	23:W:145:GLY:H	1.83	0.43
23:W:13:MET:HE2	23:W:17:ILE:HG22	2.00	0.43
24:X:39:LYS:HE2	30:0:2834:G:OP1	2.17	0.43
26:Z:61:HIS:O	26:Z:69:ASP:HA	2.17	0.43
30:0:1210:G:C2	30:0:1211:G:C8	3.06	0.43
30:0:1298:U:H2'	30:0:1299:G:C8	2.53	0.43
30:0:1363:G:H2'	30:0:1364:G:C8	2.54	0.43
30:0:1816:C:H2'	30:0:1817:U:O4'	2.17	0.43
30:0:1949:G:N2	30:0:1964:U:C2	2.87	0.43
30:0:2112:A:H2'	30:0:2113:G:C8	2.53	0.43
30:0:219:G:O5'	30:0:220:C:H5''	2.18	0.43
30:0:2277:U:H1'	30:0:2469:A:N3	2.33	0.43
30:0:2429:A:C4'	38:0:7716:HOH:O	2.66	0.43
30:0:2594:C:O2'	30:0:2595:U:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1815:A:H4'	30:0:2751:C:O4'	2.19	0.43
30:0:2793:A:N6	38:0:5853:HOH:O	2.50	0.43
30:0:2847:G:C2'	30:0:2848:G:H5'	2.48	0.43
30:0:385:C:O5'	30:0:385:C:H6	2.02	0.43
30:0:665:A:C6	30:0:666:A:C6	3.06	0.43
30:0:820:G:H3'	30:0:820:G:N3	2.33	0.43
1:A:38:ILE:HB	1:A:82:VAL:O	2.18	0.43
3:C:44:GLN:HA	38:C:8605:HOH:O	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
4:D:75:LEU:HD22	4:D:79:MET:HB3	2.00	0.43
20:T:14:ALA:HA	20:T:15:PRO:HD3	1.90	0.43
25:Y:154:ARG:HH21	30:0:1293:U:H5'	1.83	0.43
30:0:152:A:O2'	30:0:153:C:H5'	2.18	0.43
30:0:1537:C:H2'	30:0:1538:C:H6	1.83	0.43
30:0:1878:G:O2'	30:0:1879:U:OP2	2.36	0.43
30:0:1980:U:O2	30:0:2008:U:H4'	2.18	0.43
30:0:234:A:H4'	30:0:437:A:O4'	2.18	0.43
30:0:36:C:H1'	38:0:3051:HOH:O	2.17	0.43
30:0:41:G:H8	30:0:41:G:O5'	2.00	0.43
31:9:115:C:C4	31:9:116:C:C5	3.06	0.43
3:C:6:TYR:HD1	3:C:6:TYR:N	2.17	0.43
5:E:126:ILE:HA	5:E:131:LEU:CD2	2.47	0.43
5:E:84:MET:SD	38:E:3134:HOH:O	2.61	0.43
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.89	0.43
11:K:4:LEU:HD22	11:K:116:GLU:HB3	2.00	0.43
14:N:139:TRP:CE3	14:N:139:TRP:HA	2.53	0.43
30:0:1024:G:C6	30:0:1025:C:C4	3.07	0.43
30:0:148:A:O2'	30:0:149:G:H5'	2.19	0.43
30:0:1503:U:H2'	30:0:1504:A:O4'	2.19	0.43
30:0:1520:G:C2	30:0:1521:C:C2	3.07	0.43
30:0:2070:G:H2'	30:0:2072:G:OP1	2.18	0.43
30:0:2354:A:H5'	30:0:2355:G:N7	2.33	0.43
30:0:2361:A:H5'	38:0:9191:HOH:O	2.19	0.43
30:0:2429:A:H4'	38:0:7716:HOH:O	2.16	0.43
30:0:2445:U:H2'	30:0:2446:G:C8	2.54	0.43
30:0:2451:G:N3	30:0:2451:G:H2'	2.32	0.43
30:0:2531:U:H2'	30:0:2532:A:O4'	2.19	0.43
30:0:2748:G:H1'	38:0:7881:HOH:O	2.18	0.43
30:0:2768:A:H3'	30:0:2768:A:N3	2.33	0.43
30:0:772:G:H2'	30:0:773:A:O4'	2.18	0.43
31:9:39:U:O2'	31:9:42:C:H5	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:VAL:HA	2:B:155:PRO:HD3	1.88	0.43
3:C:39:GLN:O	3:C:43:LYS:HD3	2.18	0.43
9:I:73:LEU:HD12	9:I:107:LYS:NZ	2.33	0.43
16:P:8:ARG:HG3	38:P:188:HOH:O	2.17	0.43
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.48	0.43
30:0:1167:G:C2	30:0:1168:C:C2	3.06	0.43
30:0:1175:G:N3	30:0:1193:A:C6	2.86	0.43
30:0:1275:C:C2'	30:0:1276:U:H5'	2.49	0.43
30:0:1284:G:O2'	30:0:1285:U:H5'	2.18	0.43
30:0:1421:C:C2	30:0:1444:G:N2	2.87	0.43
30:0:1985:U:C2	30:0:1996:U:O4'	2.72	0.43
30:0:2429:A:N6	38:0:3326:HOH:O	2.51	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.19	0.43
30:0:2668:G:H2'	30:0:2669:U:H6	1.81	0.43
30:0:2692:G:N2	30:0:2701:G:C8	2.87	0.43
30:0:2886:C:O2'	30:0:2887:G:H5'	2.18	0.43
30:0:629:A:C2	30:0:2074:A:C2	3.07	0.43
29:3:59:ASP:HB3	29:3:63:LYS:HZ1	1.83	0.43
29:3:67:LEU:CD1	29:3:69:TYR:HE1	2.31	0.43
31:9:108:C:H2'	31:9:109:G:H8	1.82	0.43
31:9:65:A:C4	31:9:113:C:C4	3.07	0.43
31:9:5:G:O2'	31:9:6:C:H5'	2.18	0.43
1:A:71:PRO:O	1:A:160:ALA:HB2	2.18	0.43
4:D:104:PHE:CE2	4:D:132:VAL:HB	2.54	0.43
4:D:128:LEU:HB2	38:D:6007:HOH:O	2.18	0.43
5:E:107:PHE:CE2	5:E:108:LEU:HD13	2.54	0.43
6:F:60:VAL:O	6:F:62:HIS:N	2.52	0.43
10:J:70:PHE:HE1	30:0:2676:C:C4'	2.32	0.43
13:M:164:THR:HB	38:M:8820:HOH:O	2.17	0.43
14:N:77:ASN:OD1	14:N:79:PRO:HD2	2.18	0.43
14:N:32:PRO:HD2	14:N:99:GLU:O	2.18	0.43
17:Q:11:ARG:NH2	30:0:2363:G:C5'	2.81	0.43
26:Z:55:SER:HA	38:0:7562:HOH:O	2.19	0.43
30:0:102:A:C6	30:0:103:C:C4	3.06	0.43
30:0:1178:G:C5	30:0:1179:C:C4	3.07	0.43
30:0:1333:U:H2'	30:0:1334:C:C6	2.53	0.43
30:0:1519:U:H1'	38:0:3898:HOH:O	2.18	0.43
30:0:1602:C:H5'	38:0:6467:HOH:O	2.18	0.43
30:0:1552:G:C6	30:0:1634:G:C6	3.07	0.43
30:0:1665:G:C2	30:0:1666:C:C6	3.07	0.43
13:M:29:GLN:OE1	30:0:2244:A:H5''	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2473:U:H2'	30:0:2476:C:H5	1.84	0.43
30:0:2507:G:H22	30:0:2512:U:H5''	1.84	0.43
30:0:1705:C:O2	30:0:2735:U:C5'	2.65	0.43
30:0:273:G:H2'	30:0:274:G:O4'	2.18	0.43
30:0:2803:C:H2'	30:0:2804:C:C6	2.54	0.43
2:B:27:ASN:HD21	30:0:2807:U:P	2.41	0.43
30:0:284:C:OP2	30:0:284:C:H6	2.01	0.43
30:0:2855:G:C2	30:0:2904:U:C2	3.06	0.43
30:0:624:U:O4	30:0:628:1MA:H8	2.01	0.43
26:Z:41:ARG:HD2	30:0:820:G:H22	1.83	0.43
30:0:85:C:H3'	30:0:86:A:H2'	2.01	0.43
30:0:877:G:H3'	38:0:3106:HOH:O	2.19	0.43
31:9:111:U:O2'	31:9:112:U:H5'	2.19	0.43
13:M:70:GLY:HA3	13:M:73:ARG:HH21	1.77	0.43
14:N:91:ARG:O	14:N:94:GLU:HB2	2.19	0.43
30:0:1159:G:C6	30:0:1160:G:C4	3.07	0.43
30:0:1202:A:H2'	30:0:1203:G:O4'	2.19	0.43
30:0:1255:A:H2'	30:0:1256:C:O5'	2.18	0.43
30:0:1703:G:C2	30:0:1716:A:C4	3.06	0.43
30:0:1788:U:C2	30:0:1805:G:C2	3.07	0.43
30:0:2510:C:H42	30:0:2564:G:H22	1.66	0.43
30:0:2094:G:C2	30:0:2652:U:O2	2.71	0.43
30:0:2727:A:C6	30:0:2756:U:N3	2.87	0.43
30:0:2780:C:C4	30:0:2781:U:C4	3.06	0.43
30:0:2812:A:H2	30:0:2814:A:H62	1.63	0.43
30:0:432:G:C2	30:0:433:C:C6	3.07	0.43
30:0:79:G:H22	30:0:97:G:H1'	1.82	0.43
30:0:816:G:C6	30:0:817:G:N1	2.87	0.43
29:3:22:VAL:HG12	29:3:90:PHE:HE2	1.83	0.43
14:N:65:ASP:HB3	38:N:8820:HOH:O	2.19	0.43
16:P:58:SER:HB3	38:0:5593:HOH:O	2.18	0.43
21:U:6:CYS:HB2	21:U:13:ILE:CG1	2.49	0.43
25:Y:144:ARG:HB3	38:0:4369:HOH:O	2.18	0.43
1:A:167:LYS:CE	26:Z:50:VAL:HG13	2.42	0.43
30:0:1399:A:H2'	30:0:1400:C:C6	2.54	0.43
30:0:1667:A:H2'	30:0:1668:U:O4'	2.19	0.43
30:0:1697:G:H1'	38:0:7261:HOH:O	2.19	0.43
30:0:1712:A:H2'	30:0:1713:G:O4'	2.19	0.43
30:0:1882:C:H2'	30:0:1883:U:C6	2.53	0.43
30:0:191:A:H61	30:0:435:A:H62	1.67	0.43
30:0:2080:G:H2'	30:0:2081:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2328:U:C4	30:0:2329:C:C5	3.07	0.43
30:0:2332:A:H3'	30:0:2333:G:H8	1.84	0.43
29:3:17:HIS:ND1	30:0:2408:A:O2'	2.48	0.43
29:3:54:LYS:HE3	38:0:3005:HOH:O	2.18	0.43
31:9:11:A:H2	31:9:68:G:N3	2.17	0.43
31:9:39:U:H2'	31:9:40:C:OP1	2.18	0.43
1:A:105:VAL:HG11	1:A:154:ALA:HB1	2.00	0.43
2:B:305:ASP:O	2:B:306:LYS:CB	2.66	0.43
5:E:95:VAL:O	5:E:126:ILE:HD12	2.18	0.43
5:E:7:ILE:HG23	5:E:45:ASP:O	2.19	0.43
10:J:99:GLU:HA	38:J:8871:HOH:O	2.19	0.43
16:P:134:VAL:O	16:P:137:LEU:HB3	2.19	0.43
18:R:18:LEU:HD12	18:R:143:VAL:CG1	2.49	0.43
18:R:39:THR:HB	18:R:42:GLU:CD	2.39	0.43
25:Y:235:GLU:CD	25:Y:235:GLU:N	2.72	0.43
30:0:1192:A:H4'	38:0:4383:HOH:O	2.18	0.43
12:L:6:ARG:HD3	30:0:1299:G:O6	2.18	0.43
30:0:1342:C:H2'	30:0:1343:C:H5'	1.99	0.43
30:0:1383:U:H2'	30:0:1384:C:C6	2.54	0.43
30:0:135:G:C2	30:0:144:A:N3	2.86	0.43
30:0:1504:A:H4'	30:0:1506:U:C5	2.53	0.43
30:0:1600:G:H8	30:0:1600:G:OP2	2.02	0.43
30:0:1933:G:C2'	30:0:1934:A:H5'	2.48	0.43
30:0:2095:A:OP1	30:0:2096:A:H4'	2.19	0.43
30:0:2293:G:C5	30:0:2294:C:C5	3.07	0.43
30:0:2476:C:H2'	30:0:2476:C:O2	2.19	0.43
30:0:2779:G:N7	30:0:2790:C:C2	2.86	0.43
30:0:2896:A:H2'	30:0:2896:A:N3	2.34	0.43
30:0:393:G:C2	30:0:394:G:C4	3.06	0.43
30:0:435:A:O2'	30:0:436:A:H5'	2.19	0.43
30:0:67:A:H5''	30:0:69:A:C8	2.54	0.43
30:0:699:C:C2	30:0:744:G:N2	2.87	0.43
30:0:793:A:C2	30:0:822:C:C2	3.06	0.43
30:0:816:G:H8	30:0:816:G:O5'	2.02	0.43
31:9:11:A:H4'	31:9:13:A:C8	2.54	0.43
4:D:12:GLU:O	4:D:15:GLU:HG2	2.18	0.43
6:F:58:GLU:HB3	13:M:8:ILE:HG23	2.01	0.43
13:M:48:LYS:HE3	13:M:52:GLN:NE2	2.28	0.43
19:S:57:THR:C	19:S:59:ASP:H	2.21	0.43
20:T:28:SER:HA	20:T:97:ARG:HD3	1.99	0.43
1:A:72:GLU:HG2	26:Z:100:GLY:HA3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1287:A:H8	38:0:7887:HOH:O	2.02	0.42
30:0:248:A:H5'	30:0:249:G:OP2	2.19	0.42
30:0:349:U:O5'	30:0:349:U:H6	2.02	0.42
30:0:577:G:C2	30:0:581:G:C6	3.07	0.42
30:0:729:C:C2	30:0:743:G:N2	2.87	0.42
30:0:877:G:N7	30:0:885:G:C6	2.87	0.42
30:0:970:U:H2'	38:0:6308:HOH:O	2.18	0.42
31:9:110:G:C6	31:9:111:U:C5	3.07	0.42
31:9:16:G:C2	31:9:66:G:O6	2.72	0.42
1:A:23:TYR:HB2	30:0:1872:C:C5	2.54	0.42
1:A:81:GLN:H	1:A:92:ASN:ND2	2.17	0.42
3:C:156:LEU:O	3:C:160:LEU:HG	2.19	0.42
4:D:67:ASP:HA	4:D:68:PRO:HD3	1.92	0.42
5:E:81:GLU:O	5:E:172:PRO:HD3	2.19	0.42
13:M:42:ARG:HA	13:M:43:PRO:HD3	1.86	0.42
15:O:57:THR:O	15:O:111:VAL:HG23	2.19	0.42
19:S:42:GLU:O	19:S:46:ASP:HA	2.19	0.42
21:U:34:SER:HB3	38:0:3126:HOH:O	2.17	0.42
30:0:1183:C:N3	30:0:1184:C:N4	2.67	0.42
30:0:1184:C:O2'	30:0:1185:U:OP2	2.32	0.42
24:X:49:ARG:NH1	30:0:1385:G:O3'	2.51	0.42
30:0:1568:G:C2'	30:0:1569:U:H5'	2.49	0.42
30:0:188:C:O5'	30:0:188:C:H6	2.02	0.42
30:0:1970:G:H4'	30:0:1971:G:O5'	2.19	0.42
30:0:1981:A:C6	30:0:2005:G:H4'	2.54	0.42
30:0:2005:G:OP2	30:0:2006:C:H5''	2.19	0.42
30:0:2512:U:H4'	30:0:2514:U:O4	2.19	0.42
30:0:2531:U:H4'	38:0:9596:HOH:O	2.17	0.42
30:0:2600:A:H2'	30:0:2601:A:O4'	2.19	0.42
30:0:2853:U:C4	30:0:2906:A:N6	2.87	0.42
30:0:726:C:C2	30:0:727:G:C8	3.07	0.42
30:0:95:A:H5''	30:0:97:G:O4'	2.19	0.42
27:1:44:LYS:HG2	30:0:148:A:H5''	2.01	0.42
3:C:24:THR:HG23	3:C:25:PRO:HD2	2.02	0.42
4:D:137:PRO:O	31:9:30:C:OP1	2.37	0.42
13:M:112:LEU:HB3	13:M:133:LEU:HB3	2.02	0.42
23:W:11:VAL:O	23:W:12:ASN:HB2	2.19	0.42
24:X:43:VAL:HG12	24:X:44:ASP:N	2.34	0.42
30:0:107:U:H2'	30:0:108:U:H5'	2.01	0.42
30:0:1115:U:H5''	30:0:1140:C:O2'	2.20	0.42
30:0:111:C:H2'	30:0:112:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1474:C:O2'	30:0:1475:G:H5'	2.18	0.42
30:0:2248:C:O2'	30:0:2249:G:H5'	2.19	0.42
30:0:2374:G:H2'	30:0:2375:A:C8	2.53	0.42
30:0:314:G:N2	30:0:317:A:C8	2.87	0.42
30:0:354:A:H2'	30:0:355:C:C6	2.52	0.42
30:0:752:G:H2'	30:0:753:U:O4'	2.19	0.42
26:Z:34:SER:HB3	30:0:797:A:H4'	2.00	0.42
30:0:830:G:O2'	30:0:831:U:H5'	2.19	0.42
4:D:76:ARG:NE	31:9:44:A:O4'	2.52	0.42
3:C:151:GLN:HA	3:C:151:GLN:HE21	1.84	0.42
3:C:194:PHE:HB2	3:C:212:VAL:HG12	2.00	0.42
3:C:46:TYR:CE1	30:0:450:C:H4'	2.54	0.42
5:E:21:THR:HG23	5:E:30:THR:OG1	2.19	0.42
8:H:65:LEU:HA	8:H:65:LEU:HD12	1.80	0.42
30:0:1195:G:N2	30:0:1205:U:C2	2.87	0.42
30:0:1350:U:H5''	38:0:5090:HOH:O	2.20	0.42
30:0:1789:G:C2'	30:0:1790:C:O5'	2.67	0.42
30:0:2362:A:H2'	30:0:2363:G:C8	2.54	0.42
30:0:2502:C:O2'	30:0:2503:A:H5'	2.19	0.42
30:0:2655:U:C4	30:0:2656:G:N7	2.87	0.42
30:0:282:C:O2'	30:0:368:C:N4	2.52	0.42
30:0:2893:C:C2'	30:0:2894:C:H5'	2.49	0.42
30:0:652:G:H2'	30:0:653:U:O4'	2.20	0.42
30:0:877:G:C6	30:0:885:G:C4	3.08	0.42
28:2:22:PRO:HG2	28:2:25:VAL:CG2	2.49	0.42
29:3:80:ARG:HH22	30:0:2381:C:H4'	1.84	0.42
31:9:36:C:C5	31:9:37:C:C4	3.08	0.42
31:9:57:A:N3	31:9:57:A:H5'	2.34	0.42
31:9:65:A:C2'	31:9:66:G:OP2	2.68	0.42
2:B:57:GLU:HA	2:B:58:PRO:HD2	1.85	0.42
2:B:60:SER:HA	2:B:61:PRO:HD3	1.90	0.42
5:E:106:ASN:ND2	5:E:109:GLY:HA2	2.34	0.42
5:E:35:TYR:CD2	5:E:36:PRO:HD2	2.55	0.42
5:E:72:MET:O	5:E:76:VAL:HG22	2.19	0.42
12:L:38:HIS:CD2	12:L:39:GLU:HG3	2.54	0.42
19:S:57:THR:HG22	19:S:58:MET:N	2.34	0.42
20:T:24:ARG:HH21	20:T:39:ASN:ND2	2.17	0.42
26:Z:66:CYS:SG	26:Z:67:GLY:N	2.93	0.42
30:0:1342:C:O2'	30:0:1343:C:H5'	2.18	0.42
30:0:138:U:P	30:0:139:C:H5	2.42	0.42
30:0:161:A:H2'	30:0:162:C:C6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:165:A:H2'	30:0:166:A:OP1	2.19	0.42
30:0:1754:A:O5'	30:0:1754:A:H8	2.02	0.42
30:0:1757:U:H5	38:0:3214:HOH:O	2.02	0.42
30:0:1848:G:O2'	30:0:1849:G:H5'	2.19	0.42
30:0:1998:G:O2'	30:0:2026:C:H1'	2.20	0.42
30:0:2346:C:O2	30:0:2346:C:H2'	2.18	0.42
29:3:10:TYR:CD2	30:0:2382:A:H1'	2.55	0.42
30:0:2470:A:H2'	30:0:2471:G:O5'	2.19	0.42
30:0:265:U:C2	30:0:266:G:C8	3.07	0.42
30:0:690:G:H1'	30:0:731:U:O2'	2.20	0.42
30:0:776:A:C2	30:0:780:A:C6	3.08	0.42
31:9:22:G:C6	31:9:55:U:C2	3.07	0.42
1:A:223:ARG:HH12	30:0:2270:G:C4'	2.27	0.42
1:A:81:GLN:HB2	1:A:92:ASN:ND2	2.35	0.42
2:B:162:MET:HG3	2:B:310:ARG:NH1	2.35	0.42
2:B:177:HIS:O	2:B:181:ILE:HG13	2.19	0.42
2:B:307:ARG:HG2	2:B:308:LEU:N	2.34	0.42
3:C:211:ASP:HB2	3:C:231:ARG:HH12	1.85	0.42
4:D:88:LEU:HB2	4:D:89:PRO:HD3	2.00	0.42
8:H:91:ARG:NH2	8:H:135:GLN:NE2	2.68	0.42
12:L:10:SER:O	12:L:11:ARG:HB3	2.19	0.42
15:O:105:ASN:HD21	15:O:109:SER:N	2.18	0.42
16:P:10:ALA:HA	16:P:13:VAL:HG12	2.02	0.42
24:X:12:ILE:HB	24:X:70:ILE:CG2	2.49	0.42
26:Z:38:PHE:HB3	26:Z:42:TYR:HD1	1.82	0.42
30:0:1047:U:O5'	30:0:1047:U:H6	2.03	0.42
30:0:1097:A:H2'	30:0:1098:A:C8	2.54	0.42
30:0:1367:A:H2'	30:0:1368:U:O4'	2.20	0.42
30:0:1391:G:H2'	30:0:1392:A:H5'	2.01	0.42
30:0:1573:A:C8	30:0:1574:C:C6	3.08	0.42
30:0:1603:A:H5'	30:0:1605:G:H5'	1.99	0.42
30:0:1643:C:O2'	30:0:1644:C:H5'	2.19	0.42
30:0:1680:C:H5'	30:0:1685:A:N6	2.34	0.42
30:0:1709:G:C6	30:0:1711:A:C5	3.07	0.42
13:M:191:GLY:O	30:0:175:G:H3'	2.19	0.42
1:A:10:GLY:HA2	30:0:1861:C:O2	2.20	0.42
29:3:33:MET:CG	30:0:1922:A:H2'	2.50	0.42
30:0:221:G:H2'	30:0:222:A:C8	2.55	0.42
30:0:2499:U:H2'	30:0:2500:C:O4'	2.20	0.42
30:0:2805:A:C8	30:0:2806:C:C5	3.07	0.42
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:453:A:C4	30:0:479:G:N7	2.87	0.42
30:0:685:C:O2'	30:0:748:C:H5''	2.19	0.42
27:1:37:CYS:SG	27:1:39:PHE:HB2	2.59	0.42
31:9:108:C:H2'	31:9:109:G:C8	2.55	0.42
2:B:48:MET:O	30:0:2719:A:H5'	2.20	0.42
8:H:48:VAL:HG13	38:H:218:HOH:O	2.18	0.42
9:I:133:THR:HG22	9:I:134:ILE:H	1.83	0.42
13:M:185:PRO:HD3	38:0:9800:HOH:O	2.19	0.42
24:X:71:ARG:HD3	38:X:2171:HOH:O	2.20	0.42
30:0:1060:C:H5'	30:0:1060:C:H6	1.85	0.42
30:0:1255:A:C2'	30:0:1256:C:O5'	2.68	0.42
30:0:1523:G:C6	30:0:1524:U:O4	2.73	0.42
30:0:1965:C:H6	30:0:1965:C:O5'	2.02	0.42
30:0:2492:U:C4	30:0:2493:C:C4	3.07	0.42
30:0:2812:A:H2	30:0:2814:A:N7	2.17	0.42
30:0:2864:U:H2'	30:0:2865:G:H5'	2.02	0.42
30:0:462:A:N6	30:0:477:A:C2	2.88	0.42
30:0:583:C:H2'	30:0:584:U:H6	1.85	0.42
30:0:590:A:H2'	30:0:591:A:C5'	2.48	0.42
30:0:669:G:C4	30:0:670:G:C8	3.07	0.42
30:0:795:G:H2'	38:0:9823:HOH:O	2.20	0.42
1:A:26:ASP:HB2	38:0:7291:HOH:O	2.18	0.42
2:B:223:ARG:HG3	2:B:232:TRP:C	2.40	0.42
8:H:59:GLN:HE21	8:H:129:ARG:HG2	1.85	0.42
10:J:116:LEU:HB2	10:J:119:THR:CG2	2.49	0.42
10:J:131:THR:O	10:J:134:GLU:HB2	2.19	0.42
13:M:159:VAL:HG13	13:M:160:PHE:N	2.35	0.42
13:M:70:GLY:HA3	13:M:73:ARG:CZ	2.50	0.42
14:N:169:PRO:O	14:N:172:PHE:HB3	2.20	0.42
20:T:75:GLU:O	20:T:76:ASP:HB2	2.19	0.42
30:0:1241:G:H2'	30:0:1242:A:O4'	2.19	0.42
30:0:1537:C:O2'	30:0:1538:C:H5'	2.18	0.42
30:0:1541:G:O2'	30:0:1542:G:H5'	2.18	0.42
30:0:2256:G:H2'	30:0:2257:G:C5'	2.50	0.42
38:C:8619:HOH:O	30:0:338:C:H5'	2.19	0.42
30:0:451:C:C2'	30:0:452:G:H5'	2.50	0.42
30:0:711:G:N2	30:0:718:C:N1	2.67	0.42
30:0:802:G:N2	30:0:812:A:C4	2.88	0.42
30:0:877:G:C2	30:0:885:G:O4'	2.73	0.42
4:D:104:PHE:N	4:D:104:PHE:CD2	2.88	0.42
13:M:30:GLU:O	13:M:34:GLU:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:92:ASP:OD2	23:W:94:SER:HB2	2.20	0.42
24:X:25:ARG:HD2	38:X:5356:HOH:O	2.19	0.42
26:Z:37:ARG:HG3	26:Z:38:PHE:CD2	2.54	0.42
1:A:160:ALA:CB	26:Z:89:THR:HB	2.49	0.42
30:0:1187:U:O2	30:0:1189:A:H5''	2.20	0.42
30:0:1183:C:H1'	30:0:1192:A:N6	2.35	0.42
30:0:1413:A:H2'	30:0:1414:A:O4'	2.20	0.42
30:0:1819:G:H2'	30:0:1820:G:H5'	2.01	0.42
30:0:1840:A:H4'	30:0:1841:C:O5'	2.20	0.42
30:0:2355:G:N3	30:0:2355:G:C2'	2.83	0.42
30:0:2523:U:O2'	30:0:2524:G:H5'	2.19	0.42
30:0:325:U:H3'	38:0:5512:HOH:O	2.19	0.42
30:0:387:G:O2'	30:0:388:G:H5'	2.20	0.42
30:0:473:A:C2'	30:0:474:C:H5'	2.49	0.42
30:0:485:A:N3	30:0:487:G:H5''	2.34	0.42
31:9:74:G:C2	31:9:75:G:C8	3.08	0.42
31:9:92:G:C6	31:9:93:A:N6	2.88	0.42
1:A:169:PHE:O	1:A:170:VAL:HB	2.20	0.42
2:B:8:LYS:HB3	2:B:218:TRP:O	2.19	0.42
2:B:316:ARG:HB2	30:0:2768:A:C8	2.55	0.42
3:C:87:ARG:NH2	30:0:894:A:C2	2.88	0.42
30:0:1015:C:H2'	30:0:1016:U:H6	1.82	0.42
30:0:2700:G:C2'	30:0:2701:G:H5'	2.49	0.42
30:0:2909:G:N2	30:0:2910:A:C5	2.88	0.42
30:0:293:A:C2	30:0:294:C:C6	3.08	0.42
30:0:59:A:H5''	38:0:4313:HOH:O	2.18	0.42
30:0:67:A:H3'	30:0:67:A:OP2	2.20	0.42
30:0:868:G:H2'	38:0:3039:HOH:O	2.18	0.42
28:2:41:HIS:CE1	30:0:1439:C:H5''	2.54	0.42
29:3:14:CYS:SG	38:3:9063:HOH:O	2.62	0.42
29:3:83:TRP:O	29:3:85:ALA:N	2.53	0.42
31:9:114:G:C6	31:9:115:C:N4	2.88	0.42
5:E:77:THR:OG1	5:E:78:GLU:N	2.50	0.42
8:H:149:VAL:HG13	8:H:150:LYS:N	2.35	0.42
11:K:105:ARG:HD2	38:K:3385:HOH:O	2.19	0.42
16:P:40:VAL:O	16:P:44:VAL:HG23	2.20	0.42
17:Q:27:GLN:HB3	38:9:9083:HOH:O	2.20	0.42
23:W:10:GLU:HB3	38:W:1223:HOH:O	2.20	0.42
24:X:70:ILE:O	24:X:70:ILE:HG23	2.18	0.42
26:Z:61:HIS:CG	26:Z:95:PRO:HG3	2.55	0.42
30:0:1006:A:N3	30:0:2298:C:O2'	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:I:3512:HOH:O	30:0:1163:G:N2	2.53	0.41
30:0:1182:C:H4'	30:0:1192:A:N7	2.35	0.41
30:0:1210:G:C2	30:0:1211:G:N9	2.88	0.41
30:0:1588:G:C6	30:0:1589:G:C6	3.08	0.41
30:0:1624:A:O4'	30:0:1626:A:C8	2.73	0.41
30:0:1789:G:N2	30:0:1790:C:H1'	2.35	0.41
30:0:1919:A:H4'	38:0:4820:HOH:O	2.19	0.41
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.41
30:0:2478:U:H2'	30:0:2479:A:H8	1.85	0.41
30:0:2799:A:H5'	30:0:2800:A:P	2.59	0.41
21:U:56:ARG:NH1	30:0:2890:A:C2	2.88	0.41
30:0:314:G:C2	30:0:317:A:C8	3.08	0.41
30:0:335:U:C2'	30:0:336:G:OP1	2.68	0.41
30:0:371:U:H2'	30:0:372:A:H8	1.85	0.41
30:0:628:1MA:H4'	38:0:3136:HOH:O	2.19	0.41
15:O:68:GLY:HA3	30:0:745:G:O6	2.20	0.41
30:0:887:G:H2'	30:0:888:U:C6	2.54	0.41
28:2:48:ASP:O	28:2:49:GLU:HB2	2.20	0.41
29:3:62:THR:CG2	29:3:63:LYS:N	2.83	0.41
2:B:203:ALA:HA	2:B:263:THR:HA	2.02	0.41
2:B:224:LYS:HA	2:B:224:LYS:HD3	1.83	0.41
12:L:35:ARG:HB2	12:L:43:HIS:CD2	2.55	0.41
12:L:73:VAL:HG21	12:L:116:HIS:CE1	2.54	0.41
12:L:53:ARG:N	33:L:8810:CL:CL	2.66	0.41
13:M:89:THR:HA	38:M:8950:HOH:O	2.19	0.41
15:O:39:THR:HB	38:0:4589:HOH:O	2.19	0.41
22:V:39:ALA:C	22:V:41:GLU:H	2.23	0.41
30:0:102:A:C6	30:0:103:C:N4	2.88	0.41
30:0:1163:G:C2	30:0:1184:C:N3	2.87	0.41
30:0:1178:G:H2'	30:0:1179:C:H6	1.79	0.41
30:0:1449:G:H4'	38:0:9213:HOH:O	2.20	0.41
30:0:1507:C:H4'	38:0:3595:HOH:O	2.20	0.41
30:0:1519:U:H6	30:0:1519:U:O5'	2.04	0.41
30:0:1915:U:O2	30:0:1925:G:C2	2.73	0.41
30:0:2004:U:H2'	30:0:2004:U:O2	2.20	0.41
30:0:201:G:H1'	38:0:4539:HOH:O	2.19	0.41
30:0:2020:C:O2'	30:0:2021:C:H5'	2.20	0.41
30:0:2061:C:C2'	30:0:2062:A:H5'	2.51	0.41
30:0:272:A:N1	30:0:369:G:H5''	2.34	0.41
30:0:2912:C:C2'	30:0:2913:A:H5'	2.50	0.41
30:0:412:C:C2'	30:0:413:G:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:446:G:H3'	38:0:9539:HOH:O	2.20	0.41
30:0:495:A:O4'	30:0:1390:A:H1'	2.20	0.41
27:1:31:LYS:O	27:1:33:VAL:HG23	2.20	0.41
29:3:5:ARG:HA	29:3:22:VAL:HG23	2.02	0.41
31:9:50:G:C6	31:9:51:A:C6	3.08	0.41
31:9:56:A:C3'	31:9:57:A:C5'	2.93	0.41
1:A:199:HIS:CD2	1:A:200:PRO:HD2	2.55	0.41
1:A:51:ARG:NH2	1:A:53:ALA:HB3	2.35	0.41
4:D:76:ARG:CZ	31:9:44:A:C1'	2.98	0.41
9:I:96:SER:H	9:I:99:GLN:CD	2.22	0.41
10:J:19:MET:HE2	10:J:79:PHE:HA	2.02	0.41
11:K:4:LEU:HD23	11:K:4:LEU:HA	1.84	0.41
16:P:94:TRP:CH2	16:P:98:ILE:HG13	2.55	0.41
18:R:99:ALA:HB1	18:R:109:MET:HE2	2.01	0.41
22:V:23:LEU:HD22	22:V:49:LEU:HD23	2.01	0.41
23:W:13:MET:CE	23:W:17:ILE:HG22	2.50	0.41
26:Z:78:ILE:HB	38:Z:8715:HOH:O	2.19	0.41
30:0:1079:A:N1	30:0:2068:G:O2'	2.43	0.41
30:0:1212:C:C5	30:0:1213:C:C5	3.09	0.41
30:0:1303:C:O2	30:0:1353:C:H1'	2.20	0.41
30:0:1419:U:H5'	30:0:1420:C:OP2	2.21	0.41
30:0:1554:C:O2'	30:0:1631:A:H1'	2.19	0.41
30:0:1804:A:H2'	30:0:1805:G:C8	2.55	0.41
30:0:1826:C:O2'	30:0:1827:G:H5'	2.21	0.41
30:0:1878:G:O2'	30:0:1879:U:P	2.78	0.41
30:0:2256:G:C2'	30:0:2257:G:H5'	2.51	0.41
30:0:236:A:H8	30:0:236:A:OP1	2.03	0.41
38:H:216:HOH:O	30:0:2517:A:H2	1.99	0.41
30:0:2474:A:C8	30:0:2621:PSU:H4'	2.55	0.41
30:0:2782:G:O6	30:0:2790:C:H5''	2.19	0.41
30:0:2795:C:O2'	30:0:2796:U:C5'	2.65	0.41
30:0:2799:A:N6	30:0:2801:A:C2	2.89	0.41
30:0:38:G:C2'	30:0:39:G:H5'	2.50	0.41
26:Z:34:SER:HA	30:0:797:A:C5'	2.50	0.41
2:B:211:THR:HG21	38:0:7438:HOH:O	2.20	0.41
2:B:75:GLU:C	2:B:77:PRO:HD3	2.40	0.41
4:D:84:LEU:HD23	4:D:84:LEU:HA	1.92	0.41
5:E:69:ILE:HA	5:E:72:MET:HE3	2.02	0.41
8:H:59:GLN:NE2	8:H:96:GLN:HG2	2.35	0.41
12:L:150:GLN:HB3	38:L:8869:HOH:O	2.19	0.41
21:U:31:PHE:CG	21:U:37:GLU:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:54:ILE:HD11	24:X:85:VAL:HG12	2.03	0.41
25:Y:157:ILE:HD13	38:0:4836:HOH:O	2.20	0.41
30:0:107:U:C2'	30:0:108:U:H5'	2.50	0.41
30:0:1607:A:C5	30:0:1608:G:C8	3.09	0.41
30:0:1757:U:H6	30:0:1757:U:O5'	2.04	0.41
30:0:1769:C:C2'	30:0:1770:U:H5'	2.51	0.41
30:0:1819:G:C2'	30:0:1820:G:H5'	2.50	0.41
30:0:1894:C:N4	30:0:1939:U:H2'	2.34	0.41
30:0:1928:C:C2'	30:0:1929:G:H5'	2.50	0.41
30:0:1942:A:C1'	38:0:9045:HOH:O	2.69	0.41
30:0:1997:A:H2	30:0:2026:C:O2'	2.04	0.41
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.03	0.41
30:0:2710:U:H2'	30:0:2711:U:C6	2.55	0.41
30:0:2723:G:H1'	38:0:4812:HOH:O	2.19	0.41
30:0:2815:G:H4'	30:0:2816:A:OP2	2.20	0.41
30:0:281:U:C2'	30:0:282:C:C5'	2.98	0.41
30:0:517:U:H2'	30:0:518:G:H5'	2.02	0.41
30:0:552:A:H5'	38:0:5878:HOH:O	2.19	0.41
31:9:110:G:C6	31:9:111:U:C4	3.08	0.41
31:9:58:G:C8	31:9:59:C:C4	3.08	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.77	0.41
5:E:107:PHE:O	5:E:110:GLU:HG3	2.20	0.41
15:O:26:TRP:CE3	15:O:26:TRP:HA	2.55	0.41
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.01	0.41
26:Z:34:SER:HA	30:0:797:A:H5'	2.02	0.41
30:0:1063:G:O5'	30:0:2307:A:H1'	2.21	0.41
30:0:10:U:O4	30:0:532:A:OP2	2.38	0.41
30:0:1271:A:H2'	30:0:1272:C:H6	1.84	0.41
30:0:1423:C:O2'	30:0:1424:A:H5'	2.20	0.41
30:0:1882:C:H2'	30:0:1883:U:H6	1.86	0.41
30:0:1898:G:H2'	30:0:1899:C:C6	2.55	0.41
1:A:212:PRO:HA	30:0:1943:C:O4'	2.20	0.41
11:K:66:ARG:NH1	30:0:1992:U:H3'	2.35	0.41
30:0:2470:A:C2'	30:0:2471:G:O5'	2.68	0.41
30:0:2511:A:H2'	30:0:2512:U:C6	2.56	0.41
30:0:2854:A:N6	30:0:2905:A:N6	2.69	0.41
30:0:343:C:H1'	38:0:5552:HOH:O	2.19	0.41
30:0:594:C:C4	30:0:595:U:C4	3.08	0.41
30:0:910:C:H2'	30:0:911:G:O4'	2.21	0.41
2:B:222:LYS:HG3	30:0:2038:A:H5''	2.01	0.41
2:B:320:GLN:HE21	2:B:321:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:ILE:HG12	3:C:139:VAL:CG1	2.50	0.41
6:F:26:THR:HB	6:F:102:GLY:HA3	2.02	0.41
7:G:23:ILE:O	7:G:27:ILE:HG13	2.20	0.41
8:H:165:ARG:HD2	38:H:241:HOH:O	2.21	0.41
10:J:54:VAL:HG11	10:J:138:THR:HG21	2.02	0.41
10:J:76:ASP:HA	38:J:8863:HOH:O	2.20	0.41
14:N:132:ASN:O	14:N:135:VAL:HG12	2.21	0.41
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.67	0.41
21:U:5:GLU:HG2	21:U:6:CYS:N	2.36	0.41
25:Y:130:ARG:HB2	25:Y:142:SER:O	2.20	0.41
25:Y:152:LYS:CB	25:Y:160:LYS:HG3	2.51	0.41
25:Y:189:ASN:HD22	25:Y:191:ASP:N	2.19	0.41
30:0:1278:A:O2'	30:0:1279:U:C2	2.65	0.41
30:0:1540:G:C4	30:0:1541:G:C8	3.09	0.41
30:0:1666:C:C2'	30:0:1667:A:H5'	2.32	0.41
30:0:165:A:C2'	30:0:166:A:OP1	2.67	0.41
30:0:1679:C:O2	30:0:1685:A:C2	2.73	0.41
30:0:2057:U:O5'	30:0:2057:U:H6	2.03	0.41
30:0:2255:A:H2'	30:0:2256:G:O4'	2.20	0.41
30:0:2692:G:N2	30:0:2701:G:C5	2.88	0.41
30:0:307:G:C2	30:0:309:C:C4	3.08	0.41
31:9:60:C:O2	31:9:60:C:H2'	2.19	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.82	0.41
2:B:241:PRO:HD2	38:B:9125:HOH:O	2.20	0.41
18:R:9:ASP:HA	18:R:10:PRO:HD2	1.90	0.41
19:S:52:VAL:HG22	19:S:66:VAL:HG13	2.03	0.41
23:W:122:ARG:NH2	38:0:5254:HOH:O	2.52	0.41
30:0:1012:A:H8	30:0:1012:A:O5'	2.04	0.41
30:0:1191:A:O5'	30:0:1191:A:C8	2.74	0.41
30:0:1196:C:H2'	30:0:1197:G:H5'	2.02	0.41
30:0:1438:G:N3	30:0:1438:G:H2'	2.35	0.41
30:0:1544:U:O2'	30:0:1545:C:H5'	2.20	0.41
30:0:1798:C:OP2	30:0:1799:G:H5''	2.20	0.41
21:U:42:LEU:HB3	30:0:1810:C:O4'	2.21	0.41
30:0:213:G:O2'	30:0:214:U:OP2	2.39	0.41
30:0:2325:U:C2	30:0:2326:C:C6	3.09	0.41
30:0:2383:G:C6	30:0:2384:U:C4	3.08	0.41
30:0:2668:G:N2	30:0:2669:U:C2	2.88	0.41
30:0:268:U:O4	30:0:269:G:N1	2.54	0.41
30:0:2668:G:O4'	30:0:2827:A:C2	2.73	0.41
30:0:393:G:C6	30:0:394:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:631:A:C6	30:0:2074:A:H5'	2.56	0.41
30:0:677:C:H6	30:0:677:C:O5'	2.03	0.41
30:0:69:A:C3'	30:0:69:A:C8	3.04	0.41
30:0:812:A:H1'	38:0:3946:HOH:O	2.20	0.41
30:0:862:U:O2'	30:0:863:G:H5'	2.20	0.41
30:0:870:G:C3'	30:0:871:G:H5''	2.51	0.41
29:3:91:GLN:O	29:3:92:GLU:HB2	2.21	0.41
8:H:89:THR:O	8:H:137:PHE:HD2	2.04	0.41
21:U:17:THR:HG21	38:U:2221:HOH:O	2.21	0.41
26:Z:70:ARG:HB2	26:Z:81:CYS:HG	1.86	0.41
30:0:1173:A:H2'	30:0:1177:A:H62	1.85	0.41
30:0:1209:C:O2'	30:0:1210:G:H5'	2.20	0.41
30:0:1621:G:H2'	30:0:1622:G:H8	1.86	0.41
30:0:1774:G:C2'	30:0:1775:A:H5'	2.51	0.41
30:0:1803:C:H2'	30:0:1804:A:C8	2.56	0.41
30:0:189:A:H2	30:0:205:U:O2	2.04	0.41
30:0:1913:C:H2'	30:0:1914:C:C6	2.54	0.41
1:A:232:ARG:CZ	30:0:1939:U:H4'	2.50	0.41
30:0:1977:U:OP1	30:0:1977:U:H3'	2.20	0.41
30:0:2039:A:H2'	30:0:2040:C:C6	2.56	0.41
30:0:2324:G:H2'	30:0:2325:U:C6	2.56	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:2700:G:H2'	30:0:2701:G:O5'	2.21	0.41
30:0:383:A:H2'	30:0:384:G:O4'	2.21	0.41
23:W:43:GLY:HA3	30:0:945:U:O2'	2.20	0.41
31:9:82:U:H2'	31:9:83:G:C8	2.56	0.41
1:A:199:HIS:HE1	30:0:1881:A:OP1	2.04	0.41
1:A:47:HIS:HD2	30:0:1654:U:O2'	2.03	0.41
2:B:195:ARG:HG2	2:B:323:LEU:HD22	2.03	0.41
4:D:20:LYS:HG2	4:D:133:ASN:HB3	2.02	0.41
8:H:91:ARG:NH1	8:H:138:THR:OG1	2.53	0.41
10:J:107:ASN:HA	10:J:108:PRO:HD2	1.98	0.41
14:N:83:LEU:HD13	14:N:175:LEU:HD23	2.03	0.41
16:P:89:ASN:HA	38:P:165:HOH:O	2.20	0.41
18:R:114:VAL:HG13	18:R:114:VAL:O	2.20	0.41
30:0:51:G:C2	30:0:111:C:C2	3.08	0.41
30:0:1193:A:C2	30:0:1194:A:N6	2.89	0.41
30:0:1089:G:H1'	30:0:1290:G:N2	2.36	0.41
30:0:1476:A:H1'	30:0:1867:G:O2'	2.21	0.41
30:0:1596:U:O2'	30:0:1598:A:N7	2.46	0.41
30:0:1973:A:C8	30:0:1973:A:H5'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:20:G:H2'	30:0:21:G:O5'	2.21	0.41
30:0:2453:G:H2'	30:0:2454:C:C6	2.55	0.41
30:0:2599:A:C6	30:0:2600:A:N1	2.89	0.41
30:0:2695:C:N4	30:0:2701:G:N2	2.69	0.41
30:0:2801:A:C4	30:0:2802:C:C5	3.08	0.41
21:U:56:ARG:NH1	30:0:2890:A:C4	2.89	0.41
30:0:844:A:C6	30:0:882:A:C6	3.09	0.41
31:9:29:C:C6	31:9:30:C:C6	3.08	0.41
1:A:171:LYS:HB2	30:0:820:G:C6	2.55	0.41
5:E:119:HIS:O	5:E:140:ALA:HB1	2.21	0.41
5:E:145:ALA:HB1	5:E:168:ILE:CD1	2.49	0.41
5:E:20:ILE:HD12	5:E:33:LEU:HD12	2.03	0.41
6:F:61:MET:O	6:F:64:PRO:HD2	2.21	0.41
19:S:73:ASP:OD1	19:S:76:GLU:HG3	2.21	0.41
26:Z:47:ARG:HD2	38:Z:8718:HOH:O	2.20	0.41
30:0:1024:G:C5	30:0:1025:C:C4	3.09	0.41
23:W:120:PRO:HG2	30:0:1095:U:O2	2.20	0.41
30:0:1168:C:C2'	30:0:1169:U:H5'	2.51	0.41
30:0:1207:A:H5'	30:0:1208:C:OP2	2.21	0.41
30:0:1226:G:C2	30:0:1227:C:C6	3.08	0.41
30:0:1339:G:C5	30:0:1340:G:C6	3.09	0.41
30:0:1362:U:H2'	30:0:1363:G:H8	1.86	0.41
30:0:1416:G:C2'	30:0:1417:G:H5'	2.51	0.41
30:0:1543:G:H2'	30:0:1544:U:C5	2.56	0.41
30:0:1553:C:H6	30:0:1553:C:O5'	2.04	0.41
30:0:1619:G:H2'	30:0:1620:C:O4'	2.21	0.41
30:0:1748:U:C6	30:0:1749:U:C5	3.09	0.41
30:0:2366:C:P	38:0:6939:HOH:O	2.79	0.41
30:0:265:U:C4	30:0:266:G:N7	2.89	0.41
16:P:61:ARG:NH2	30:0:2737:C:OP2	2.40	0.41
30:0:279:C:H2'	30:0:280:C:H5'	2.01	0.41
30:0:61:G:C2	30:0:62:C:C2	3.09	0.41
2:B:74:ILE:HG13	38:B:9076:HOH:O	2.20	0.41
4:D:36:ASN:HA	38:D:7500:HOH:O	2.20	0.41
5:E:15:GLN:HG2	5:E:16:ASP:N	2.36	0.41
14:N:73:ALA:HB1	14:N:74:PRO:CD	2.51	0.41
17:Q:41:LEU:HB3	17:Q:52:PHE:CZ	2.56	0.41
25:Y:152:LYS:HB3	25:Y:160:LYS:HG3	2.02	0.41
30:0:1195:G:N1	30:0:1205:U:N3	2.69	0.41
30:0:1208:C:H2'	30:0:1208:C:O2	2.19	0.41
30:0:1103:C:C2	30:0:1241:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:123:U:O2'	30:0:124:C:H5'	2.21	0.41
30:0:1591:A:H5'	30:0:1603:A:H61	1.86	0.41
30:0:1634:G:C4	30:0:1635:U:C5	3.08	0.41
30:0:2016:U:H2'	30:0:2017:U:O4'	2.21	0.41
30:0:2098:C:O5'	30:0:2098:C:H6	2.04	0.41
30:0:2269:C:C4	30:0:2270:G:C5	3.08	0.41
30:0:23:G:H1'	30:0:520:A:N6	2.35	0.41
30:0:2526:C:H5'	30:0:2526:C:C6	2.56	0.41
30:0:2617:G:H5''	38:0:3896:HOH:O	2.20	0.41
38:B:9106:HOH:O	30:0:2818:A:H2	2.04	0.41
30:0:282:C:O2	30:0:282:C:C2'	2.62	0.41
30:0:714:U:O4'	30:0:716:G:C2	2.74	0.41
30:0:736:A:H5''	38:0:4253:HOH:O	2.21	0.41
30:0:965:A:H2'	30:0:965:A:N3	2.36	0.41
31:9:110:G:H2'	31:9:110:G:N3	2.35	0.41
31:9:14:G:C5'	31:9:14:G:H8	2.13	0.41
1:A:37:VAL:HG13	38:A:9088:HOH:O	2.21	0.41
2:B:288:GLY:HA2	30:0:2898:G:H4'	2.02	0.41
5:E:81:GLU:HA	5:E:133:VAL:O	2.21	0.41
5:E:23:GLU:HG2	5:E:28:SER:CB	2.51	0.41
13:M:68:ARG:HB2	38:M:8932:HOH:O	2.19	0.41
18:R:130:MET:HG3	38:0:7551:HOH:O	2.21	0.41
23:W:132:VAL:HG21	23:W:140:LYS:O	2.21	0.41
30:0:1170:U:O2	30:0:1172:G:H8	2.04	0.40
30:0:1177:A:C6	30:0:1178:G:C5	3.09	0.40
30:0:1175:G:C5	30:0:1193:A:C2	3.10	0.40
28:2:42:TRP:HZ2	30:0:1438:G:H1'	1.87	0.40
30:0:1832:G:N3	30:0:1833:U:C6	2.89	0.40
30:0:2330:U:H4'	30:0:2331:C:OP1	2.20	0.40
30:0:2414:A:N1	30:0:2415:A:C6	2.90	0.40
6:F:38:LYS:HE3	30:0:244:C:OP2	2.21	0.40
30:0:257:G:N2	30:0:258:G:C4	2.89	0.40
30:0:2635:A:H2'	30:0:2636:C:H5'	1.98	0.40
30:0:2692:G:N2	30:0:2701:G:C4	2.88	0.40
30:0:797:A:H2'	30:0:798:G:O4'	2.21	0.40
29:3:86:GLY:HA2	38:3:9032:HOH:O	2.21	0.40
3:C:118:THR:HG21	3:C:233:THR:HB	2.03	0.40
4:D:28:GLY:CA	4:D:69:ILE:HG23	2.51	0.40
13:M:72:ALA:HB3	38:M:8950:HOH:O	2.21	0.40
13:M:75:ARG:HG3	38:M:8868:HOH:O	2.20	0.40
14:N:110:THR:HA	14:N:111:PRO:HD3	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:11:THR:CG2	30:0:1444:G:H5''	2.50	0.40
23:W:48:VAL:HG12	23:W:48:VAL:O	2.21	0.40
23:W:4:LEU:CD2	23:W:54:PHE:HB3	2.51	0.40
25:Y:125:LYS:HB2	25:Y:126:PRO:HD2	2.03	0.40
30:0:1634:G:C6	30:0:1635:U:C4	3.10	0.40
30:0:1681:G:H5''	30:0:1682:A:H5'	2.03	0.40
30:0:1774:G:H2'	30:0:1775:A:C5'	2.51	0.40
30:0:2121:G:C2'	30:0:2122:C:H5'	2.51	0.40
30:0:2245:C:O5'	30:0:2245:C:H6	2.04	0.40
30:0:2300:A:H4'	30:0:2301:A:N3	2.37	0.40
30:0:2335:C:N3	30:0:2350:G:C2	2.89	0.40
30:0:2501:G:H1	30:0:2519:C:N4	2.18	0.40
30:0:2831:C:C2'	30:0:2832:C:C5'	2.93	0.40
30:0:2834:G:C2'	30:0:2835:C:O5'	2.69	0.40
30:0:312:U:O2	30:0:320:G:C2	2.75	0.40
30:0:366:U:H2'	30:0:367:G:O4'	2.20	0.40
30:0:534:C:H2'	30:0:2083:A:C2	2.57	0.40
30:0:594:C:H2'	30:0:595:U:C6	2.56	0.40
30:0:596:C:H6	30:0:596:C:O5'	2.03	0.40
30:0:69:A:C5'	30:0:69:A:C8	2.98	0.40
30:0:962:C:H2'	30:0:963:C:H5'	2.03	0.40
3:C:206:ASN:HB2	30:0:329:A:OP2	2.20	0.40
6:F:48:VAL:CG2	6:F:74:PHE:HB3	2.51	0.40
13:M:113:ARG:NH1	13:M:155:GLN:HB2	2.36	0.40
15:O:32:ARG:HD3	15:O:32:ARG:O	2.22	0.40
24:X:26:ALA:HB3	24:X:63:ARG:HG3	2.03	0.40
30:0:1133:A:H2'	30:0:1134:G:H5'	2.03	0.40
30:0:1325:G:O2'	30:0:1326:C:H5'	2.21	0.40
30:0:1474:C:C6	30:0:1474:C:C5'	2.94	0.40
30:0:1521:C:O2'	30:0:1522:A:H5'	2.22	0.40
30:0:1613:C:C6	30:0:1613:C:H3'	2.57	0.40
30:0:2311:A:H3'	38:0:7660:HOH:O	2.20	0.40
30:0:2325:U:H5''	30:0:2417:C:O2'	2.22	0.40
30:0:238:C:H4'	30:0:287:C:OP1	2.22	0.40
30:0:2493:C:C2'	30:0:2493:C:O2	2.67	0.40
30:0:2510:C:H42	30:0:2564:G:N2	2.19	0.40
2:B:5:ARG:NH2	30:0:2548:C:OP2	2.55	0.40
30:0:249:G:O2'	30:0:266:G:H5'	2.21	0.40
30:0:462:A:H2'	38:0:4853:HOH:O	2.21	0.40
30:0:568:G:H21	30:0:590:A:H62	1.69	0.40
30:0:603:A:H4'	30:0:604:G:O5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:822:C:H2'	30:0:823:U:H6	1.86	0.40
29:3:39:GLN:O	29:3:52:PHE:HE1	2.04	0.40
2:B:188:HIS:ND1	2:B:188:HIS:N	2.69	0.40
2:B:277:GLU:N	2:B:278:PRO:CD	2.84	0.40
6:F:50:VAL:HG11	6:F:60:VAL:HG11	2.03	0.40
13:M:46:LEU:O	13:M:50:ARG:HG3	2.21	0.40
22:V:12:THR:HG23	22:V:15:GLU:H	1.86	0.40
24:X:43:VAL:HG11	24:X:82:GLU:HA	2.04	0.40
30:0:1102:C:H5	38:0:3479:HOH:O	2.04	0.40
30:0:1159:G:C2	30:0:1209:C:N3	2.89	0.40
30:0:1520:G:C6	30:0:1521:C:N4	2.89	0.40
30:0:192:A:N6	30:0:194:A:C2	2.89	0.40
30:0:1979:G:H1'	38:0:3061:HOH:O	2.21	0.40
30:0:2102:G:N2	30:0:2103:A:N1	2.69	0.40
30:0:2532:A:OP2	30:0:2532:A:H8	2.05	0.40
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.40
31:9:81:C:O2'	31:9:82:U:H5'	2.21	0.40
31:9:89:C:O2'	31:9:90:G:H5'	2.22	0.40
1:A:33:GLU:CD	1:A:33:GLU:N	2.75	0.40
2:B:73:VAL:HG21	2:B:284:PHE:HZ	1.86	0.40
3:C:100:LEU:HD22	30:0:751:U:H5''	2.03	0.40
4:D:14:ARG:HD3	31:9:56:A:O2'	2.22	0.40
5:E:23:GLU:HG2	5:E:28:SER:HB3	2.03	0.40
7:G:19:GLU:HG2	7:G:66:LEU:HD13	2.03	0.40
8:H:91:ARG:H	8:H:91:ARG:HG2	1.43	0.40
15:O:96:VAL:HG13	15:O:100:GLN:OE1	2.21	0.40
15:O:47:ARG:NH1	15:O:47:ARG:HG3	2.36	0.40
15:O:49:GLU:OE1	15:O:72:LYS:HG3	2.22	0.40
25:Y:132:ASP:OD1	25:Y:135:LYS:HD2	2.20	0.40
30:0:1016:U:H2'	30:0:1017:U:O4'	2.21	0.40
28:2:41:HIS:HE1	30:0:1439:C:OP1	2.05	0.40
30:0:146:U:C4	30:0:147:G:C6	3.09	0.40
30:0:1525:G:OP1	30:0:1525:G:H4'	2.21	0.40
30:0:1557:G:H2'	30:0:1558:C:C6	2.57	0.40
30:0:2004:U:H5''	30:0:2005:G:C8	2.57	0.40
30:0:2273:C:O2'	30:0:2274:A:H5'	2.22	0.40
30:0:295:C:H2'	30:0:296:G:O4'	2.22	0.40
30:0:37:A:H2'	30:0:38:G:H8	1.84	0.40
25:Y:229:LEU:O	30:0:552:A:H5''	2.22	0.40
30:0:766:A:HO2'	30:0:767:A:H8	1.68	0.40
30:0:920:C:H5'	30:0:921:G:N3	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:3:17:HIS:CG	30:0:2409:C:H4'	2.57	0.40
31:9:2:U:OP2	31:9:2:U:H4'	2.22	0.40
1:A:20:SER:C	1:A:22:ARG:H	2.25	0.40
2:B:201:ASP:N	2:B:312:ARG:O	2.53	0.40
3:C:104:ASP:O	3:C:108:GLN:HG3	2.22	0.40
3:C:1:MET:HG2	3:C:2:GLN:N	2.34	0.40
4:D:135:VAL:HG22	4:D:136:ARG:N	2.36	0.40
5:E:84:MET:HA	5:E:167:TYR:O	2.22	0.40
6:F:59:ILE:CD1	30:0:263:U:C2	3.04	0.40
14:N:127:LEU:HD12	14:N:127:LEU:HA	1.93	0.40
15:O:32:ARG:NE	15:O:32:ARG:HA	2.35	0.40
16:P:13:VAL:HG21	16:P:41:ARG:HG2	2.03	0.40
16:P:78:GLY:O	30:0:1813:U:H4'	2.22	0.40
20:T:26:THR:HA	20:T:39:ASN:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	235/240 (98%)	200 (85%)	30 (13%)	5 (2%)	7	33
2	B	335/338 (99%)	305 (91%)	23 (7%)	7 (2%)	7	33
3	C	244/246 (99%)	216 (88%)	26 (11%)	2 (1%)	19	57
4	D	134/177 (76%)	105 (78%)	23 (17%)	6 (4%)	2	14
5	E	170/178 (96%)	158 (93%)	11 (6%)	1 (1%)	25	64
6	F	117/120 (98%)	97 (83%)	16 (14%)	4 (3%)	3	20
7	G	25/348 (7%)	22 (88%)	3 (12%)	0	100	100
8	H	156/177 (88%)	139 (89%)	16 (10%)	1 (1%)	25	64
9	I	68/162 (42%)	49 (72%)	16 (24%)	3 (4%)	2	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	140/145 (97%)	128 (91%)	10 (7%)	2 (1%)	11	43
11	K	130/132 (98%)	120 (92%)	9 (7%)	1 (1%)	19	57
12	L	141/165 (86%)	116 (82%)	22 (16%)	3 (2%)	7	33
13	M	192/196 (98%)	171 (89%)	17 (9%)	4 (2%)	7	33
14	N	184/187 (98%)	163 (89%)	17 (9%)	4 (2%)	6	31
15	O	113/116 (97%)	106 (94%)	7 (6%)	0	100	100
16	P	141/149 (95%)	133 (94%)	8 (6%)	0	100	100
17	Q	93/96 (97%)	86 (92%)	5 (5%)	2 (2%)	6	31
18	R	148/155 (96%)	138 (93%)	9 (6%)	1 (1%)	22	60
19	S	79/85 (93%)	75 (95%)	4 (5%)	0	100	100
20	T	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
21	U	51/67 (76%)	44 (86%)	6 (12%)	1 (2%)	7	34
22	V	63/71 (89%)	58 (92%)	4 (6%)	1 (2%)	9	40
23	W	152/154 (99%)	142 (93%)	9 (6%)	1 (1%)	22	60
24	X	80/92 (87%)	72 (90%)	6 (8%)	2 (2%)	5	28
25	Y	140/241 (58%)	132 (94%)	7 (5%)	1 (1%)	22	60
26	Z	71/116 (61%)	55 (78%)	12 (17%)	4 (6%)	2	10
27	1	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
28	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
29	3	90/92 (98%)	64 (71%)	17 (19%)	9 (10%)	0	2
All	All	3705/4472 (83%)	3292 (89%)	348 (9%)	65 (2%)	8	37

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	206	THR
2	B	306	LYS
4	D	137	PRO
6	F	61	MET
6	F	101	ALA
10	J	5	GLU
12	L	80	ASP
13	M	75	ARG
14	N	154	LEU
14	N	183	ASP

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Mol	Chain	Res	Type
14	N	184	ILE
21	U	44	ARG
26	Z	70	ARG
29	3	56	PRO
29	3	64	LYS
29	3	84	ARG
1	A	34	ASP
3	C	8	LEU
3	C	201	SER
5	E	128	GLY
12	L	21	ARG
12	L	82	ALA
13	M	81	ARG
17	Q	21	ARG
23	W	139	GLY
24	X	70	ILE
26	Z	39	GLY
29	3	4	PRO
29	3	68	LYS
29	3	72	GLY
29	3	73	GLU
2	B	169	GLY
4	D	56	ARG
9	I	83	GLY
9	I	107	LYS
11	K	10	GLN
14	N	165	ALA
26	Z	83	TYR
29	3	90	PHE
1	A	119	ALA
2	B	107	SER
2	B	184	ASP
4	D	65	GLU
10	J	7	ASP
13	M	86	GLN
17	Q	18	PRO
18	R	20	GLU
1	A	24	LYS
1	A	122	SER
1	A	132	ASP
2	B	2	GLN
2	B	185	GLY

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Mol	Chain	Res	Type
4	D	172	VAL
6	F	100	ASP
9	I	76	ASP
13	M	80	GLY
24	X	52	PRO
26	Z	105	ARG
29	3	62	THR
4	D	16	PRO
4	D	53	LYS
6	F	64	PRO
8	H	19	ARG
22	V	39	ALA
25	Y	111	ASP

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	
1	A	179/182 (98%)	170 (95%)	9 (5%)	24	60
2	B	282/283 (100%)	263 (93%)	19 (7%)	16	49
3	C	193/193 (100%)	180 (93%)	13 (7%)	16	49
4	D	117/148 (79%)	110 (94%)	7 (6%)	19	53
5	E	152/156 (97%)	146 (96%)	6 (4%)	32	69
6	F	93/94 (99%)	92 (99%)	1 (1%)	73	90
7	G	27/282 (10%)	25 (93%)	2 (7%)	13	44
8	H	134/145 (92%)	124 (92%)	10 (8%)	13	43
9	I	58/130 (45%)	57 (98%)	1 (2%)	60	85
10	J	118/121 (98%)	109 (92%)	9 (8%)	13	43
11	K	106/106 (100%)	103 (97%)	3 (3%)	43	77
12	L	113/127 (89%)	106 (94%)	7 (6%)	18	52
13	M	158/160 (99%)	147 (93%)	11 (7%)	15	47
14	N	149/150 (99%)	146 (98%)	3 (2%)	55	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	O	93/94 (99%)	93 (100%)	0	100	100
16	P	113/117 (97%)	111 (98%)	2 (2%)	59	85
17	Q	79/80 (99%)	74 (94%)	5 (6%)	18	51
18	R	117/122 (96%)	113 (97%)	4 (3%)	37	72
19	S	71/74 (96%)	70 (99%)	1 (1%)	67	88
20	T	105/106 (99%)	98 (93%)	7 (7%)	16	49
21	U	44/53 (83%)	43 (98%)	1 (2%)	50	80
22	V	51/57 (90%)	51 (100%)	0	100	100
23	W	130/130 (100%)	126 (97%)	4 (3%)	40	75
24	X	66/74 (89%)	61 (92%)	5 (8%)	13	43
25	Y	120/196 (61%)	117 (98%)	3 (2%)	47	79
26	Z	60/94 (64%)	60 (100%)	0	100	100
27	1	46/47 (98%)	46 (100%)	0	100	100
28	2	42/46 (91%)	41 (98%)	1 (2%)	49	79
29	3	79/79 (100%)	73 (92%)	6 (8%)	13	43
All	All	3095/3646 (85%)	2955 (96%)	140 (4%)	27	64

All (140) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	37	VAL
1	A	66	ARG
1	A	94	LEU
1	A	131	HIS
1	A	153	ARG
1	A	179	MET
1	A	190	ARG
1	A	217	ARG
2	B	7	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	56	ASP
2	B	71	VAL
2	B	132	HIS
2	B	144	THR

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Mol	Chain	Res	Type
2	B	162	MET
2	B	171	VAL
2	B	180	ASP
2	B	188	HIS
2	B	190	MET
2	B	195	ARG
2	B	254	GLN
2	B	264	GLU
2	B	277	GLU
2	B	312	ARG
2	B	322	ARG
3	C	2	GLN
3	C	16	VAL
3	C	76	ARG
3	C	78	ARG
3	C	87	ARG
3	C	101	ASP
3	C	104	ASP
3	C	162	VAL
3	C	180	SER
3	C	187	ARG
3	C	236	THR
3	C	240	LEU
3	C	243	VAL
4	D	19	GLU
4	D	24	HIS
4	D	29	HIS
4	D	50	VAL
4	D	104	PHE
4	D	137	PRO
4	D	149	ARG
5	E	7	ILE
5	E	100	ASP
5	E	116	THR
5	E	126	ILE
5	E	155	ASN
5	E	156	ASP
6	F	12	LEU
7	G	64	ASN
7	G	72	ASP
8	H	33	GLN
8	H	62	HIS

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Mol	Chain	Res	Type
8	H	65	LEU
8	H	87	LYS
8	H	89	THR
8	H	91	ARG
8	H	99	ARG
8	H	122	LYS
8	H	157	TYR
8	H	172	GLU
9	I	110	ASP
10	J	39	VAL
10	J	45	VAL
10	J	46	ILE
10	J	52	GLN
10	J	74	ARG
10	J	79	PHE
10	J	107	ASN
10	J	120	SER
10	J	131	THR
11	K	10	GLN
11	K	24	THR
11	K	55	VAL
12	L	18	HIS
12	L	35	ARG
12	L	73	VAL
12	L	83	GLU
12	L	102	ASP
12	L	104	ASP
12	L	114	VAL
13	M	10	ASP
13	M	46	LEU
13	M	68	ARG
13	M	73	ARG
13	M	81	ARG
13	M	83	SER
13	M	84	LYS
13	M	89	THR
13	M	91	ILE
13	M	99	ARG
13	M	116	ASN
14	N	21	HIS
14	N	134	ASP
14	N	138	ASP

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Mol	Chain	Res	Type
16	P	91	LYS
16	P	98	ILE
17	Q	16	ASN
17	Q	18	PRO
17	Q	54	PRO
17	Q	75	ILE
17	Q	95	GLU
18	R	13	THR
18	R	39	THR
18	R	82	GLU
18	R	143	VAL
19	S	30	ASP
20	T	5	ASP
20	T	39	ASN
20	T	48	VAL
20	T	73	HIS
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	25	ASP
23	W	4	LEU
23	W	35	VAL
23	W	38	THR
23	W	146	ILE
24	X	27	ASP
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
24	X	82	GLU
25	Y	118	THR
25	Y	189	ASN
25	Y	203	VAL
28	2	18	ASN
29	3	7	PHE
29	3	15	ASN
29	3	17	HIS
29	3	56	PRO
29	3	71	CYS
29	3	90	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	92	ASN
1	A	176	HIS
1	A	177	HIS
1	A	199	HIS
2	B	27	ASN
2	B	106	HIS
2	B	145	HIS
2	B	238	ASN
2	B	256	GLN
2	B	260	HIS
2	B	320	GLN
2	B	332	ASN
3	C	73	GLN
3	C	129	HIS
4	D	103	ASN
4	D	133	ASN
5	E	55	ASN
5	E	68	HIS
5	E	74	HIS
5	E	90	HIS
5	E	106	ASN
5	E	143	GLN
7	G	64	ASN
8	H	59	GLN
8	H	135	GLN
9	I	106	GLN
10	J	25	GLN
10	J	52	GLN
10	J	107	ASN
10	J	126	ASN
11	K	10	GLN
11	K	42	ASN
11	K	44	HIS
11	K	119	GLN
12	L	18	HIS
12	L	38	HIS
12	L	41	HIS
12	L	43	HIS
12	L	116	HIS
13	M	24	GLN
13	M	58	GLN
13	M	77	HIS

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Mol	Chain	Res	Type
13	M	86	GLN
13	M	137	ASN
13	M	142	GLN
13	M	170	ASN
14	N	107	ASN
14	N	132	ASN
16	P	50	GLN
16	P	66	GLN
16	P	88	GLN
16	P	118	GLN
17	Q	27	GLN
17	Q	40	HIS
18	R	61	GLN
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
19	S	9	HIS
19	S	44	GLN
19	S	53	ASN
20	T	39	ASN
20	T	43	ASN
21	U	39	ASN
22	V	34	GLN
22	V	60	GLN
23	W	12	ASN
23	W	110	GLN
23	W	119	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	129	ASN
25	Y	134	HIS
25	Y	149	GLN
25	Y	189	ASN
27	1	16	HIS
27	1	28	HIS
28	2	16	ASN
28	2	18	ASN
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	13	HIS
29	3	18	GLN

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Mol	Chain	Res	Type
29	3	20	HIS
29	3	30	GLN
29	3	78	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	243 (8%)	22 (0%)
31	9	121/122 (99%)	19 (15%)	2 (1%)
All	All	2866/3045 (94%)	262 (9%)	24 (0%)

All (262) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	138	U
30	0	141	C
30	0	151	A
30	0	166	A
30	0	185	G
30	0	186	A
30	0	191	A
30	0	192	A
30	0	198	A
30	0	200	C
30	0	219	G
30	0	237	G
30	0	271	C
30	0	272	A
30	0	273	G

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Mol	Chain	Res	Type
30	0	283	U
30	0	284	C
30	0	285	A
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	342	C
30	0	358	G
30	0	368	C
30	0	381	G
30	0	397	A
30	0	417	G
30	0	457	U
30	0	461	C
30	0	487	G
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	588	G
30	0	604	G
30	0	605	C
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	698	A
30	0	701	U
30	0	702	G
30	0	746	A
30	0	759	C
30	0	777	U

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Mol	Chain	Res	Type
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A
30	0	1006	A
30	0	1008	C
30	0	1011	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1080	C
30	0	1081	A
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1137	G
30	0	1151	G
30	0	1161	A
30	0	1166	A

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Mol	Chain	Res	Type
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1205	U
30	0	1206	U
30	0	1208	C
30	0	1216	G
30	0	1238	C
30	0	1239	G
30	0	1279	U
30	0	1289	C
30	0	1342	C
30	0	1353	C
30	0	1354	G
30	0	1360	C
30	0	1377	C
30	0	1378	G
30	0	1407	A
30	0	1460	G
30	0	1474	C
30	0	1485	A
30	0	1505	U
30	0	1506	U
30	0	1524	U
30	0	1525	G
30	0	1526	A
30	0	1528	A
30	0	1562	C
30	0	1592	G
30	0	1605	G
30	0	1617	C
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C

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Mol	Chain	Res	Type
30	0	1701	A
30	0	1710	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1730	G
30	0	1731	C
30	0	1752	G
30	0	1778	A
30	0	1798	C
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1967	U
30	0	1968	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1996	U
30	0	2006	C
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2110	G
30	0	2238	A
30	0	2243	C
30	0	2258	A
30	0	2271	G

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Mol	Chain	Res	Type
30	0	2272	G
30	0	2317	C
30	0	2321	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2422	U
30	0	2462	G
30	0	2465	A
30	0	2469	A
30	0	2476	C
30	0	2480	G
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2613	G
30	0	2638	G
30	0	2664	A
30	0	2681	A
30	0	2682	C
30	0	2718	C
30	0	2726	U
30	0	2747	C
30	0	2748	G
30	0	2749	U
30	0	2750	G
30	0	2762	C
30	0	2768	A
30	0	2792	A
30	0	2800	A
30	0	2811	A
30	0	2812	A

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Mol	Chain	Res	Type
30	0	2825	C
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	39	U
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	65	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	0	129	A
30	0	341	C
30	0	396	U
30	0	545	G
30	0	603	A
30	0	604	G
30	0	644	G
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C

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Mol	Chain	Res	Type
30	0	1237	U
30	0	1352	A
30	0	1685	A
30	0	1970	G
30	0	2011	A
30	0	2536	C
30	0	2718	C
30	0	2761	A
30	0	2791	U
31	9	43	G
31	9	65	A

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

5 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	$\# Z > 2$
30	UR3	0	2619	30	14,22,23	0.70	0	15,32,35	0.56	0
30	PSU	0	2621	30	17,21,22	1.65	3 (17%)	20,30,33	5.40	4 (20%)
30	OMG	0	2588	30	18,26,27	1.12	2 (11%)	20,38,41	2.58	4 (20%)
30	OMU	0	2587	30,35	14,22,23	0.98	1 (7%)	14,31,34	1.17	1 (7%)
30	1MA	0	628	30,35	15,25,26	0.78	0	15,37,40	1.39	1 (6%)

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
30	UR3	0	2619	30	-	0/5/25/26	0/2/2/2
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3
30	OMU	0	2587	30,35	-	0/7/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	1MA	0	628	30,35	-	0/3/25/26	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C5-C1'	-5.19	1.47	1.52
30	0	2588	OMG	C6-N1	3.72	1.39	1.33
30	0	2587	OMU	C4-N3	2.72	1.37	1.33
30	0	2621	PSU	C4-N3	2.67	1.37	1.33
30	0	2621	PSU	C2-N1	2.59	1.43	1.38
30	0	2588	OMG	C8-N7	-2.17	1.30	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	N1-C2-N3	-17.23	114.73	128.43
30	0	2621	PSU	C4-N3-C2	14.24	127.16	115.14
30	0	2588	OMG	C5-C6-N1	-8.58	111.69	123.43
30	0	2621	PSU	C5-C4-N3	-8.09	114.94	125.36
30	0	2588	OMG	C6-N1-C2	5.76	125.08	115.93
30	0	628	1MA	C2-N3-C4	-4.70	110.71	116.58
30	0	2587	OMU	C5-C4-N3	-3.99	114.53	123.31
30	0	2588	OMG	C2-N3-C4	-3.15	111.76	115.36
30	0	2621	PSU	C6-N1-C2	2.69	119.80	115.36
30	0	2588	OMG	N3-C2-N1	-2.49	123.89	127.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2621	PSU	2	0
30	0	2587	OMU	2	0
30	0	628	1MA	2	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 305 ligands modelled in this entry, 305 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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	237/240 (98%)	-0.60	1 (0%) 92 79	29, 65, 98, 115	0
2	B	337/338 (99%)	-0.73	0 100 100	31, 59, 87, 97	0
3	C	246/246 (100%)	-0.82	0 100 100	23, 47, 69, 80	0
4	D	140/177 (79%)	0.45	15 (10%) 6 2	74, 109, 132, 140	0
5	E	172/178 (96%)	-0.64	0 100 100	50, 74, 97, 103	0
6	F	119/120 (99%)	-0.30	1 (0%) 86 65	50, 73, 106, 113	0
7	G	29/348 (8%)	0.08	0 100 100	75, 96, 105, 109	0
8	H	160/177 (90%)	-0.49	0 100 100	48, 67, 99, 109	0
9	I	70/162 (43%)	1.80	29 (41%) 0 0	134, 152, 167, 169	0
10	J	142/145 (97%)	-0.79	1 (0%) 87 69	40, 58, 75, 97	0
11	K	132/132 (100%)	-0.87	0 100 100	39, 55, 81, 86	0
12	L	145/165 (87%)	-0.24	1 (0%) 87 69	35, 72, 113, 129	0
13	M	194/196 (98%)	-0.51	8 (4%) 37 14	31, 46, 99, 106	0
14	N	186/187 (99%)	-0.33	0 100 100	60, 80, 126, 132	0
15	O	115/116 (99%)	-0.86	0 100 100	43, 56, 74, 80	0
16	P	143/149 (95%)	-0.75	0 100 100	40, 59, 79, 85	0
17	Q	95/96 (98%)	-0.71	0 100 100	44, 56, 72, 88	0
18	R	150/155 (96%)	-0.83	0 100 100	33, 49, 70, 83	0
19	S	81/85 (95%)	-0.67	1 (1%) 79 54	40, 62, 82, 92	0
20	T	119/120 (99%)	-0.55	0 100 100	40, 59, 87, 116	0
21	U	53/67 (79%)	2.66	32 (60%) 0 0	107, 117, 125, 126	0
22	V	65/71 (91%)	-0.02	4 (6%) 20 7	47, 74, 118, 123	0
23	W	154/154 (100%)	-0.69	0 100 100	39, 54, 73, 87	0
24	X	82/92 (89%)	-0.45	1 (1%) 79 54	46, 65, 94, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	Y	142/241 (58%)	-0.88	0 100 100	30, 49, 71, 92	0
26	Z	73/116 (62%)	3.62	45 (61%) 0 0	98, 116, 126, 130	0
27	1	56/57 (98%)	-0.78	0 100 100	28, 36, 43, 48	0
28	2	46/50 (92%)	-0.57	1 (2%) 62 33	31, 66, 97, 104	0
29	3	92/92 (100%)	4.21	71 (77%) 0 0	104, 119, 130, 134	0
30	0	2749/2923 (94%)	-0.83	2 (0%) 95 89	23, 51, 96, 175	0
31	9	122/122 (100%)	-0.97	1 (0%) 86 65	45, 75, 103, 154	0
All	All	6646/7517 (88%)	-0.53	214 (3%) 47 20	23, 57, 116, 175	0

All (214) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
26	Z	46	SER	17.2
26	Z	58	ASN	13.1
29	3	39	GLN	12.1
26	Z	36	GLY	11.6
29	3	34	LYS	11.4
26	Z	55	SER	11.0
29	3	38	ARG	10.8
29	3	35	TRP	10.6
29	3	41	GLU	10.3
26	Z	35	SER	10.1
26	Z	50	VAL	9.9
29	3	37	ASP	9.8
29	3	20	HIS	9.0
29	3	33	MET	9.0
29	3	42	ARG	8.9
26	Z	43	GLY	8.8
29	3	36	ILE	8.3
26	Z	59	GLU	8.3
29	3	82	GLY	8.2
26	Z	69	ASP	7.8
29	3	19	GLU	7.5
29	3	31	THR	7.5
13	M	71	SER	7.5
21	U	54	THR	7.4
26	Z	49	ARG	7.3
13	M	70	GLY	7.2
29	3	14	CYS	7.2
29	3	15	ASN	7.1

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Mol	Chain	Res	Type	RSRZ
29	3	11	CYS	7.0
29	3	40	ARG	6.7
29	3	32	GLY	6.7
26	Z	53	ILE	6.4
26	Z	54	GLU	6.4
26	Z	44	ARG	6.3
26	Z	34	SER	6.2
21	U	46	ALA	6.1
29	3	62	THR	6.0
29	3	43	ASN	6.0
29	3	71	CYS	5.8
26	Z	42	TYR	5.7
26	Z	48	ARG	5.6
26	Z	57	MET	5.5
29	3	56	PRO	5.5
21	U	9	CYS	5.4
13	M	80	GLY	5.4
21	U	11	THR	5.4
29	3	16	GLU	5.4
29	3	78	HIS	5.4
26	Z	47	ARG	5.3
29	3	48	ASN	5.3
21	U	39	ASN	5.2
26	Z	60	ASP	5.1
29	3	51	LYS	5.1
29	3	47	GLY	5.1
26	Z	82	SER	5.1
9	I	74	ILE	5.0
29	3	44	SER	5.0
26	Z	45	VAL	4.9
26	Z	81	CYS	4.9
29	3	81	GLU	4.9
26	Z	77	GLY	4.8
26	Z	51	ALA	4.7
29	3	12	PRO	4.7
29	3	18	GLN	4.7
26	Z	67	GLY	4.7
26	Z	56	GLU	4.6
21	U	55	ALA	4.5
9	I	93	ALA	4.5
29	3	85	ALA	4.5
29	3	21	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
21	U	40	ALA	4.4
29	3	28	GLY	4.3
29	3	53	SER	4.3
9	I	71	ALA	4.3
21	U	32	CYS	4.3
9	I	92	VAL	4.2
29	3	30	GLN	4.2
1	A	237	GLY	4.1
29	3	59	ASP	4.1
9	I	106	GLN	4.1
29	3	27	SER	4.1
21	U	53	ASP	4.1
29	3	13	HIS	4.1
4	D	57	THR	4.1
9	I	66	GLY	4.0
21	U	6	CYS	4.0
9	I	100	VAL	4.0
21	U	5	GLU	4.0
21	U	12	ASP	4.0
29	3	23	GLU	4.0
29	3	74	CYS	4.0
21	U	48	ASN	3.9
29	3	10	TYR	3.8
22	V	1	THR	3.8
9	I	102	GLN	3.8
29	3	29	ARG	3.7
29	3	84	ARG	3.7
26	Z	63	CYS	3.7
9	I	70	THR	3.7
29	3	76	LYS	3.7
29	3	45	GLY	3.7
31	9	1	U	3.6
26	Z	71	VAL	3.6
29	3	75	GLY	3.5
21	U	52	THR	3.5
29	3	60	LYS	3.5
21	U	10	GLY	3.5
9	I	67	VAL	3.5
9	I	112	LEU	3.4
4	D	18	ILE	3.4
21	U	36	CYS	3.3
29	3	77	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
29	3	91	GLN	3.3
29	3	83	TRP	3.3
26	Z	61	HIS	3.3
29	3	9	THR	3.3
29	3	61	PRO	3.3
9	I	78	ALA	3.2
26	Z	52	GLU	3.2
9	I	99	GLN	3.2
21	U	29	THR	3.2
9	I	104	ALA	3.2
21	U	31	PHE	3.2
4	D	69	ILE	3.2
22	V	38	GLY	3.2
29	3	17	HIS	3.2
9	I	132	VAL	3.1
29	3	63	LYS	3.1
4	D	88	LEU	3.1
29	3	58	GLY	3.1
21	U	56	ARG	3.1
9	I	72	GLU	3.1
29	3	25	VAL	3.1
26	Z	80	GLN	3.0
26	Z	65	ASN	3.0
29	3	69	TYR	3.0
29	3	64	LYS	3.0
26	Z	68	GLU	2.9
29	3	72	GLY	2.9
9	I	76	ASP	2.9
24	X	88	GLU	2.9
21	U	28	THR	2.9
9	I	73	LEU	2.9
26	Z	70	ARG	2.9
9	I	128	THR	2.9
22	V	39	ALA	2.9
9	I	110	ASP	2.9
4	D	92	GLU	2.8
13	M	82	ARG	2.8
22	V	40	PRO	2.8
26	Z	104	ARG	2.8
26	Z	40	ALA	2.8
4	D	63	ILE	2.8
26	Z	39	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
21	U	30	HIS	2.7
29	3	49	ASP	2.7
13	M	79	ALA	2.7
21	U	8	TYR	2.7
21	U	24	LYS	2.7
29	3	73	GLU	2.7
29	3	8	ASN	2.7
29	3	1	MET	2.7
21	U	43	GLY	2.6
29	3	6	ARG	2.6
21	U	51	TRP	2.6
26	Z	37	ARG	2.6
29	3	65	THR	2.6
10	J	4	ALA	2.6
4	D	26	GLY	2.6
29	3	70	ARG	2.5
30	0	1198	U	2.5
21	U	4	ARG	2.5
26	Z	83	TYR	2.5
29	3	3	MET	2.5
9	I	105	GLU	2.5
4	D	93	LEU	2.4
4	D	44	ILE	2.4
13	M	72	ALA	2.4
26	Z	62	ALA	2.4
9	I	68	PRO	2.4
12	L	60	GLU	2.4
21	U	23	HIS	2.4
9	I	108	HIS	2.4
21	U	7	ASP	2.4
29	3	46	ILE	2.4
26	Z	92	SER	2.3
29	3	68	LYS	2.3
21	U	41	ASP	2.3
30	0	1172	G	2.3
21	U	49	LEU	2.3
4	D	135	VAL	2.3
29	3	88	LEU	2.3
9	I	79	GLY	2.3
4	D	87	ALA	2.3
9	I	94	ASP	2.2
9	I	75	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
9	I	113	SER	2.2
4	D	80	ALA	2.2
26	Z	85	ASP	2.2
26	Z	78	ILE	2.1
13	M	83	SER	2.1
19	S	81	ILE	2.1
9	I	80	PHE	2.1
9	I	81	GLU	2.1
28	2	39	ARG	2.1
6	F	106	ALA	2.1
4	D	27	ILE	2.1
26	Z	103	VAL	2.0
13	M	77	HIS	2.0
4	D	134	LEU	2.0
21	U	44	ARG	2.0
4	D	75	LEU	2.0
21	U	38	ASN	2.0
26	Z	66	CYS	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
30	OMG	0	2588	24/25	0.98	0.13	39,41,42,45	0
30	UR3	0	2619	21/22	0.98	0.14	39,43,45,48	0
30	1MA	0	628	23/24	0.98	0.14	31,36,38,38	0
30	PSU	0	2621	20/21	0.98	0.18	40,43,44,44	0
30	OMU	0	2587	21/22	0.98	0.12	41,44,50,50	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. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
34	SR	0	9006	1/1	0.31	0.83	180,180,180,180	0
35	NA	0	8557	1/1	0.41	0.08	59,59,59,59	0
34	SR	0	9004	1/1	0.44	1.01	200,200,200,200	0
34	SR	0	8985	1/1	0.45	0.12	182,182,182,182	0
35	NA	0	8567	1/1	0.50	0.30	68,68,68,68	0
35	NA	0	8563	1/1	0.53	0.68	65,65,65,65	0
34	SR	0	8971	1/1	0.54	0.11	170,170,170,170	0
34	SR	0	8997	1/1	0.54	0.83	194,194,194,194	0
33	CL	J	8802	1/1	0.54	0.08	76,76,76,76	0
34	SR	0	9001	1/1	0.55	0.08	166,166,166,166	0
34	SR	0	8959	1/1	0.56	0.28	200,200,200,200	0
34	SR	0	8974	1/1	0.57	0.14	164,164,164,164	0
34	SR	0	8957	1/1	0.57	0.73	200,200,200,200	0
34	SR	0	8979	1/1	0.61	0.18	198,198,198,198	0
35	NA	0	8553	1/1	0.62	0.33	70,70,70,70	0
35	NA	0	8528	1/1	0.63	0.91	83,83,83,83	0
34	SR	0	8986	1/1	0.63	0.45	200,200,200,200	0
34	SR	0	8975	1/1	0.64	0.11	171,171,171,171	0
34	SR	0	8962	1/1	0.67	0.08	179,179,179,179	0
34	SR	0	8977	1/1	0.72	0.11	181,181,181,181	0
32	MG	0	8091	1/1	0.73	0.07	58,58,58,58	0
37	CD	U	8701	1/1	0.74	0.35	200,200,200,200	0
34	SR	0	8998	1/1	0.75	0.30	184,184,184,184	0
34	SR	0	8922	1/1	0.75	0.29	169,169,169,169	0
34	SR	9	8980	1/1	0.75	0.14	182,182,182,182	0
36	K	0	8401	1/1	0.75	0.15	156,156,156,156	0
34	SR	0	8919	1/1	0.76	0.32	200,200,200,200	0
34	SR	0	8960	1/1	0.76	0.05	152,152,152,152	0
34	SR	0	8982	1/1	0.78	1.88	200,200,200,200	0
33	CL	0	8814	1/1	0.78	0.18	72,72,72,72	0
34	SR	0	8969	1/1	0.78	0.31	192,192,192,192	0
32	MG	0	8063	1/1	0.78	0.22	86,86,86,86	0
35	NA	0	8518	1/1	0.79	0.26	75,75,75,75	0
35	NA	0	8559	1/1	0.79	0.46	122,122,122,122	0
34	SR	0	8973	1/1	0.80	0.14	112,112,112,112	0
34	SR	0	8944	1/1	0.80	0.08	165,165,165,165	0
34	SR	0	8967	1/1	0.81	0.05	133,133,133,133	0
35	NA	0	8566	1/1	0.81	0.32	62,62,62,62	0
34	SR	0	8988	1/1	0.81	0.13	170,170,170,170	0
35	NA	0	8571	1/1	0.82	0.17	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	9007	1/1	0.82	0.24	179,179,179,179	0
35	NA	0	8556	1/1	0.82	0.44	63,63,63,63	0
34	SR	0	8968	1/1	0.82	0.15	177,177,177,177	0
34	SR	3	8932	1/1	0.82	0.09	158,158,158,158	0
35	NA	9	8572	1/1	0.82	0.17	71,71,71,71	0
35	NA	0	8573	1/1	0.82	0.28	55,55,55,55	0
34	SR	0	8947	1/1	0.83	0.30	194,194,194,194	0
35	NA	0	8535	1/1	0.83	0.20	64,64,64,64	0
32	MG	A	8051	1/1	0.83	0.22	101,101,101,101	0
34	SR	0	8931	1/1	0.83	0.07	110,110,110,110	0
33	CL	0	8815	1/1	0.83	0.09	87,87,87,87	0
35	NA	0	8541	1/1	0.83	0.24	54,54,54,54	0
34	SR	0	9002	1/1	0.83	0.06	157,157,157,157	0
34	SR	0	8946	1/1	0.85	0.12	123,123,123,123	0
34	SR	0	8955	1/1	0.85	0.17	200,200,200,200	0
35	NA	0	8548	1/1	0.85	0.12	68,68,68,68	0
35	NA	0	8515	1/1	0.86	0.15	44,44,44,44	0
32	MG	0	8081	1/1	0.86	0.32	80,80,80,80	0
35	NA	0	8564	1/1	0.86	0.34	57,57,57,57	0
35	NA	0	8546	1/1	0.86	0.47	80,80,80,80	0
34	SR	A	8993	1/1	0.86	0.08	159,159,159,159	0
37	CD	Z	8703	1/1	0.86	0.28	200,200,200,200	0
35	NA	0	8507	1/1	0.86	0.16	32,32,32,32	0
34	SR	0	8989	1/1	0.86	0.18	200,200,200,200	0
32	MG	2	8060	1/1	0.86	0.10	35,35,35,35	0
35	NA	0	8525	1/1	0.87	0.25	85,85,85,85	0
32	MG	0	8093	1/1	0.87	0.05	28,28,28,28	0
34	SR	B	8987	1/1	0.87	0.39	200,200,200,200	0
34	SR	0	8953	1/1	0.88	0.07	200,200,200,200	0
35	NA	0	8562	1/1	0.88	0.53	89,89,89,89	0
35	NA	0	8530	1/1	0.88	0.37	49,49,49,49	0
34	SR	0	8942	1/1	0.88	0.07	130,130,130,130	0
34	SR	0	8915	1/1	0.88	0.07	118,118,118,118	0
34	SR	0	8964	1/1	0.88	0.08	129,129,129,129	0
34	SR	0	8939	1/1	0.88	0.08	152,152,152,152	0
35	NA	0	8545	1/1	0.88	0.24	33,33,33,33	0
34	SR	0	8991	1/1	0.88	0.35	193,193,193,193	0
33	CL	3	8804	1/1	0.89	0.19	120,120,120,120	0
32	MG	0	8071	1/1	0.89	0.13	31,31,31,31	0
37	CD	3	8704	1/1	0.89	0.71	200,200,200,200	0
35	NA	0	8570	1/1	0.89	0.07	25,25,25,25	0
34	SR	0	8928	1/1	0.89	0.09	146,146,146,146	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
35	NA	0	8549	1/1	0.90	0.17	77,77,77,77	0
32	MG	0	8047	1/1	0.90	0.15	67,67,67,67	0
34	SR	0	8976	1/1	0.90	0.23	197,197,197,197	0
35	NA	0	8522	1/1	0.90	0.21	45,45,45,45	0
32	MG	B	8042	1/1	0.90	0.08	56,56,56,56	0
32	MG	0	8036	1/1	0.90	0.05	37,37,37,37	0
32	MG	0	8069	1/1	0.90	0.19	55,55,55,55	0
35	NA	0	8552	1/1	0.90	0.26	58,58,58,58	0
34	SR	0	8981	1/1	0.91	0.13	157,157,157,157	0
32	MG	0	8052	1/1	0.91	0.04	51,51,51,51	0
35	NA	0	8505	1/1	0.91	1.13	53,53,53,53	0
34	SR	0	8965	1/1	0.91	0.07	127,127,127,127	0
34	SR	9	9003	1/1	0.91	0.09	177,177,177,177	0
34	SR	0	8956	1/1	0.91	0.05	151,151,151,151	0
32	MG	0	8032	1/1	0.91	0.05	27,27,27,27	0
32	MG	0	8050	1/1	0.91	0.08	52,52,52,52	0
34	SR	3	8999	1/1	0.91	0.28	172,172,172,172	0
32	MG	0	8075	1/1	0.92	0.09	83,83,83,83	0
34	SR	F	9005	1/1	0.92	0.09	131,131,131,131	0
32	MG	0	8049	1/1	0.92	0.38	74,74,74,74	0
35	NA	0	8565	1/1	0.92	0.94	70,70,70,70	0
34	SR	0	8984	1/1	0.92	0.07	105,105,105,105	0
35	NA	0	8509	1/1	0.92	0.14	54,54,54,54	0
34	SR	0	9000	1/1	0.92	0.31	200,200,200,200	0
32	MG	0	8068	1/1	0.92	0.11	49,49,49,49	0
32	MG	K	8054	1/1	0.92	0.15	40,40,40,40	0
32	MG	0	8046	1/1	0.92	0.13	26,26,26,26	0
35	NA	0	8519	1/1	0.92	0.27	51,51,51,51	0
34	SR	0	8937	1/1	0.93	0.17	100,100,100,100	0
32	MG	0	8016	1/1	0.93	0.22	48,48,48,48	0
32	MG	0	8010	1/1	0.93	0.17	24,24,24,24	0
34	SR	0	8994	1/1	0.93	0.24	200,200,200,200	0
35	NA	0	8511	1/1	0.93	0.09	48,48,48,48	0
33	CL	L	8810	1/1	0.93	0.10	64,64,64,64	0
35	NA	0	8521	1/1	0.93	0.20	53,53,53,53	0
32	MG	0	8039	1/1	0.94	0.18	71,71,71,71	0
35	NA	0	8547	1/1	0.94	0.67	47,47,47,47	0
33	CL	J	8821	1/1	0.94	0.11	66,66,66,66	0
35	NA	0	8560	1/1	0.94	0.76	74,74,74,74	0
34	SR	0	8970	1/1	0.94	0.04	131,131,131,131	0
35	NA	J	8538	1/1	0.94	0.08	49,49,49,49	0
34	SR	0	8910	1/1	0.94	0.08	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	MG	0	8037	1/1	0.94	0.17	76,76,76,76	0
32	MG	0	8088	1/1	0.94	0.16	35,35,35,35	0
32	MG	0	8033	1/1	0.94	0.13	40,40,40,40	0
35	NA	0	8544	1/1	0.94	0.11	41,41,41,41	0
33	CL	N	8807	1/1	0.94	0.35	99,99,99,99	0
35	NA	R	8532	1/1	0.94	0.14	37,37,37,37	0
34	SR	0	8916	1/1	0.94	0.10	114,114,114,114	0
33	CL	Y	8820	1/1	0.94	0.11	47,47,47,47	0
34	SR	0	8927	1/1	0.94	0.20	196,196,196,196	0
35	NA	0	8506	1/1	0.95	0.51	58,58,58,58	0
35	NA	0	8526	1/1	0.95	0.13	33,33,33,33	0
34	SR	0	8983	1/1	0.95	0.27	191,191,191,191	0
33	CL	K	8812	1/1	0.95	0.07	48,48,48,48	0
34	SR	0	8914	1/1	0.95	0.20	105,105,105,105	0
35	NA	0	8508	1/1	0.95	0.56	61,61,61,61	0
32	MG	0	8082	1/1	0.95	0.12	66,66,66,66	0
32	MG	0	8065	1/1	0.95	0.12	50,50,50,50	0
33	CL	0	8803	1/1	0.95	0.14	69,69,69,69	0
33	CL	R	8806	1/1	0.95	0.11	47,47,47,47	0
32	MG	0	8062	1/1	0.95	0.20	57,57,57,57	0
35	NA	0	8504	1/1	0.95	0.09	27,27,27,27	0
34	SR	0	8945	1/1	0.95	0.06	107,107,107,107	0
32	MG	0	8080	1/1	0.95	0.28	68,68,68,68	0
33	CL	0	8822	1/1	0.95	0.60	97,97,97,97	0
35	NA	0	8501	1/1	0.96	0.14	43,43,43,43	0
35	NA	0	8561	1/1	0.96	0.36	57,57,57,57	0
35	NA	0	8554	1/1	0.96	0.55	65,65,65,65	0
35	NA	Q	8540	1/1	0.96	0.11	67,67,67,67	0
32	MG	0	8004	1/1	0.96	0.18	21,21,21,21	0
33	CL	0	8817	1/1	0.96	0.20	69,69,69,69	0
33	CL	0	8816	1/1	0.96	0.39	94,94,94,94	0
34	SR	0	8917	1/1	0.96	0.10	109,109,109,109	0
32	MG	B	8043	1/1	0.96	0.11	53,53,53,53	0
34	SR	0	8972	1/1	0.96	0.10	150,150,150,150	0
34	SR	0	8943	1/1	0.96	0.09	72,72,72,72	0
35	NA	S	8510	1/1	0.96	0.04	26,26,26,26	0
35	NA	0	8527	1/1	0.96	0.15	54,54,54,54	0
32	MG	0	8041	1/1	0.96	0.31	36,36,36,36	0
34	SR	0	8990	1/1	0.96	0.15	125,125,125,125	0
35	NA	0	8513	1/1	0.96	0.34	66,66,66,66	0
35	NA	0	8533	1/1	0.96	0.08	53,53,53,53	0
33	CL	J	8801	1/1	0.96	0.13	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	8996	1/1	0.96	0.22	199,199,199,199	0
32	MG	3	8090	1/1	0.96	0.12	80,80,80,80	0
35	NA	M	8539	1/1	0.96	0.09	32,32,32,32	0
35	NA	0	8574	1/1	0.96	0.35	54,54,54,54	0
35	NA	0	8516	1/1	0.96	0.08	20,20,20,20	0
32	MG	0	8035	1/1	0.96	0.10	61,61,61,61	0
32	MG	0	8040	1/1	0.96	0.21	54,54,54,54	0
34	SR	A	8929	1/1	0.96	0.04	117,117,117,117	0
34	SR	0	8948	1/1	0.97	0.08	103,103,103,103	0
35	NA	0	8536	1/1	0.97	0.06	40,40,40,40	0
32	MG	0	8020	1/1	0.97	0.14	29,29,29,29	0
34	SR	0	8995	1/1	0.97	0.14	140,140,140,140	0
32	MG	0	8055	1/1	0.97	0.10	45,45,45,45	0
32	MG	0	8089	1/1	0.97	0.17	59,59,59,59	0
35	NA	0	8550	1/1	0.97	0.27	47,47,47,47	0
32	MG	0	8029	1/1	0.97	0.07	68,68,68,68	0
32	MG	0	8025	1/1	0.97	0.10	30,30,30,30	0
34	SR	0	8924	1/1	0.97	0.17	133,133,133,133	0
32	MG	0	8064	1/1	0.97	0.06	33,33,33,33	0
32	MG	Y	8086	1/1	0.97	0.06	37,37,37,37	0
33	CL	A	8809	1/1	0.97	0.35	100,100,100,100	0
32	MG	T	8057	1/1	0.97	0.04	63,63,63,63	0
34	SR	0	8920	1/1	0.97	0.05	106,106,106,106	0
35	NA	0	8529	1/1	0.97	0.18	41,41,41,41	0
35	NA	0	8534	1/1	0.97	0.18	37,37,37,37	0
32	MG	0	8083	1/1	0.97	0.12	71,71,71,71	0
32	MG	0	8027	1/1	0.97	0.12	26,26,26,26	0
32	MG	0	8067	1/1	0.98	0.13	32,32,32,32	0
32	MG	0	8021	1/1	0.98	0.11	25,25,25,25	0
34	SR	0	8940	1/1	0.98	0.11	77,77,77,77	0
34	SR	0	8963	1/1	0.98	0.05	123,123,123,123	0
32	MG	0	8078	1/1	0.98	0.23	51,51,51,51	0
34	SR	0	8926	1/1	0.98	0.09	109,109,109,109	0
34	SR	S	8961	1/1	0.98	0.05	126,126,126,126	0
32	MG	0	8002	1/1	0.98	0.08	29,29,29,29	0
35	NA	0	8555	1/1	0.98	0.34	50,50,50,50	0
32	MG	0	8018	1/1	0.98	0.14	34,34,34,34	0
32	MG	0	8092	1/1	0.98	0.02	44,44,44,44	0
32	MG	0	8005	1/1	0.98	0.22	34,34,34,34	0
35	NA	R	8575	1/1	0.98	0.34	89,89,89,89	0
32	MG	0	8024	1/1	0.98	0.12	96,96,96,96	0
35	NA	0	8551	1/1	0.98	0.15	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	8908	1/1	0.98	0.13	77,77,77,77	0
32	MG	0	8053	1/1	0.98	0.05	45,45,45,45	0
32	MG	0	8014	1/1	0.98	0.19	21,21,21,21	0
32	MG	0	8009	1/1	0.98	0.21	24,24,24,24	0
32	MG	0	8087	1/1	0.98	0.09	26,26,26,26	0
34	SR	0	8936	1/1	0.98	0.08	87,87,87,87	0
32	MG	0	8034	1/1	0.98	0.13	53,53,53,53	0
34	SR	0	8901	1/1	0.98	0.14	63,63,63,63	0
32	MG	0	8006	1/1	0.98	0.13	20,20,20,20	0
34	SR	B	8950	1/1	0.98	0.16	113,113,113,113	0
34	SR	0	8958	1/1	0.98	0.07	114,114,114,114	0
34	SR	0	8921	1/1	0.98	0.09	75,75,75,75	0
37	CD	O	8705	1/1	0.98	0.08	93,93,93,93	0
34	SR	0	8923	1/1	0.98	0.12	85,85,85,85	0
36	K	M	8402	1/1	0.98	0.11	60,60,60,60	0
34	SR	0	8992	1/1	0.98	0.08	130,130,130,130	0
35	NA	0	8568	1/1	0.98	0.10	38,38,38,38	0
34	SR	0	8951	1/1	0.98	0.09	139,139,139,139	0
34	SR	0	8938	1/1	0.98	0.07	164,164,164,164	0
34	SR	0	8941	1/1	0.98	0.18	122,122,122,122	0
32	MG	0	8073	1/1	0.98	0.06	51,51,51,51	0
35	NA	0	8542	1/1	0.98	0.16	51,51,51,51	0
34	SR	0	8935	1/1	0.98	0.09	87,87,87,87	0
35	NA	0	8520	1/1	0.98	0.10	39,39,39,39	0
35	NA	0	8558	1/1	0.98	0.22	44,44,44,44	0
32	MG	0	8023	1/1	0.98	0.18	24,24,24,24	0
34	SR	0	8911	1/1	0.98	0.06	79,79,79,79	0
32	MG	0	8017	1/1	0.98	0.10	20,20,20,20	0
32	MG	0	8066	1/1	0.98	0.31	75,75,75,75	0
34	SR	0	8909	1/1	0.98	0.13	89,89,89,89	0
34	SR	0	8918	1/1	0.99	0.09	71,71,71,71	0
32	MG	0	8019	1/1	0.99	0.15	23,23,23,23	0
32	MG	0	8038	1/1	0.99	0.05	61,61,61,61	0
32	MG	0	8084	1/1	0.99	0.14	24,24,24,24	0
32	MG	0	8072	1/1	0.99	0.08	47,47,47,47	0
32	MG	0	8030	1/1	0.99	0.34	86,86,86,86	0
32	MG	0	8070	1/1	0.99	0.10	40,40,40,40	0
32	MG	0	8077	1/1	0.99	0.10	43,43,43,43	0
32	MG	0	8045	1/1	0.99	0.10	24,24,24,24	0
32	MG	0	8044	1/1	0.99	0.14	52,52,52,52	0
35	NA	0	8512	1/1	0.99	0.08	36,36,36,36	0
32	MG	0	8056	1/1	0.99	0.08	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	8905	1/1	0.99	0.23	62,62,62,62	0
32	MG	0	8085	1/1	0.99	0.12	67,67,67,67	0
34	SR	0	9008	1/1	0.99	0.17	97,97,97,97	0
32	MG	0	8012	1/1	0.99	0.14	15,15,15,15	0
34	SR	0	8902	1/1	0.99	0.16	67,67,67,67	0
34	SR	0	8966	1/1	0.99	0.07	97,97,97,97	0
32	MG	0	8061	1/1	0.99	0.18	19,19,19,19	0
35	NA	0	8524	1/1	0.99	0.40	54,54,54,54	0
32	MG	0	8048	1/1	0.99	0.21	20,20,20,20	0
32	MG	0	8058	1/1	0.99	0.06	22,22,22,22	0
33	CL	B	8819	1/1	0.99	0.15	59,59,59,59	0
33	CL	M	8818	1/1	0.99	0.05	39,39,39,39	0
33	CL	0	8813	1/1	0.99	0.03	46,46,46,46	0
34	SR	A	8930	1/1	0.99	0.07	125,125,125,125	0
32	MG	0	8013	1/1	0.99	0.04	24,24,24,24	0
32	MG	0	8031	1/1	0.99	0.23	52,52,52,52	0
32	MG	0	8001	1/1	0.99	0.12	26,26,26,26	0
32	MG	0	8079	1/1	0.99	0.11	36,36,36,36	0
35	NA	0	8502	1/1	0.99	0.05	56,56,56,56	0
34	SR	0	8934	1/1	0.99	0.09	99,99,99,99	0
34	SR	1	8913	1/1	0.99	0.11	100,100,100,100	0
32	MG	0	8022	1/1	0.99	0.12	17,17,17,17	0
35	NA	0	8569	1/1	0.99	0.20	67,67,67,67	0
32	MG	0	8003	1/1	0.99	0.17	22,22,22,22	0
35	NA	0	8517	1/1	0.99	0.15	21,21,21,21	0
32	MG	0	8015	1/1	0.99	0.13	25,25,25,25	0
34	SR	0	8933	1/1	0.99	0.07	126,126,126,126	0
35	NA	0	8523	1/1	0.99	0.11	51,51,51,51	0
34	SR	0	8949	1/1	0.99	0.05	102,102,102,102	0
35	NA	0	8514	1/1	0.99	0.19	17,17,17,17	0
32	MG	9	8074	1/1	0.99	0.05	63,63,63,63	0
35	NA	9	8543	1/1	0.99	0.11	38,38,38,38	0
33	CL	0	8811	1/1	0.99	0.38	79,79,79,79	0
35	NA	C	8503	1/1	0.99	0.17	45,45,45,45	0
32	MG	0	8008	1/1	0.99	0.14	26,26,26,26	0
33	CL	O	8808	1/1	0.99	0.11	87,87,87,87	0
32	MG	0	8076	1/1	0.99	0.11	27,27,27,27	0
32	MG	0	8059	1/1	0.99	0.12	53,53,53,53	0
35	NA	0	8531	1/1	0.99	0.10	15,15,15,15	0
33	CL	0	8805	1/1	0.99	0.14	70,70,70,70	0
34	SR	0	8925	1/1	0.99	0.15	94,94,94,94	0
34	SR	0	8906	1/1	1.00	0.20	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	SR	0	8903	1/1	1.00	0.13	46,46,46,46	0
32	MG	0	8028	1/1	1.00	0.13	19,19,19,19	0
35	NA	0	8537	1/1	1.00	0.17	29,29,29,29	0
34	SR	1	8952	1/1	1.00	0.11	72,72,72,72	0
32	MG	0	8011	1/1	1.00	0.21	24,24,24,24	0
32	MG	0	8007	1/1	1.00	0.19	18,18,18,18	0
34	SR	0	8907	1/1	1.00	0.12	40,40,40,40	0
34	SR	0	8904	1/1	1.00	0.17	58,58,58,58	0
37	CD	1	8702	1/1	1.00	0.13	61,61,61,61	0
34	SR	0	8954	1/1	1.00	0.12	103,103,103,103	0
32	MG	0	8026	1/1	1.00	0.04	27,27,27,27	0
34	SR	R	8912	1/1	1.00	0.12	86,86,86,86	0
34	SR	9	8978	1/1	1.00	0.07	125,125,125,125	0

6.5 Other polymers [i](#)

There are no such residues in this entry.