



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:54 PM GMT

PDB ID : 2OTJ
Title : 13-deoxytedanolide bound to the large subunit of Haloarcula marismortui
Authors : Blaha, G.; Schroeder, S.J.; Tirado-Rives, J.
Deposited on : 2007-02-08
Resolution : 2.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

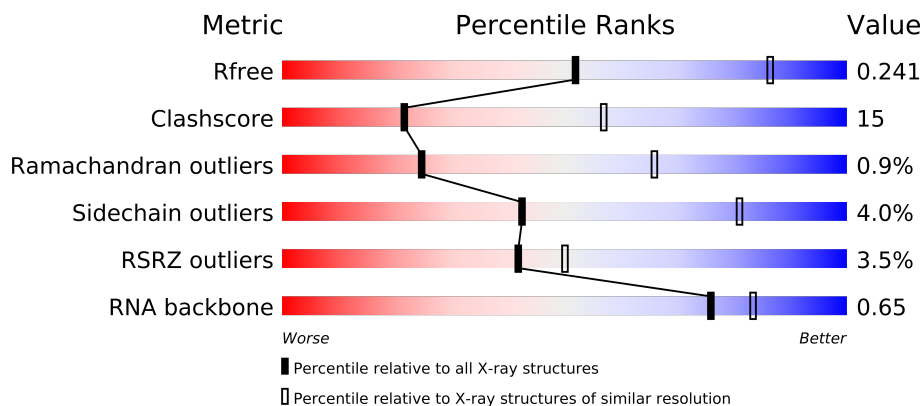
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.90 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}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)
RNA backbone	1838	1055 (3.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	0	2922	
2	9	122	
3	A	240	
4	B	338	
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	171	
11	J	145	

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Mol	Chain	Length	Quality of chain
12	K	132	
13	L	165	
14	M	194	
15	N	187	
16	O	116	
17	P	149	
18	Q	96	
19	R	155	
20	S	85	
21	T	120	
22	U	66	
23	V	71	
24	W	154	
25	X	92	
26	Y	241	
27	Z	73	
28	1	57	
29	2	50	
30	3	92	
31	I	161	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
32	13T	0	9000	-	X
33	MG	0	8011	-	X
33	MG	0	8012	-	X
33	MG	0	8013	-	X
33	MG	0	8023	-	X
33	MG	0	8024	-	X
33	MG	0	8040	-	X
33	MG	0	8041	-	X
33	MG	0	8049	-	X
33	MG	0	8062	-	X
33	MG	0	8070	-	X
33	MG	0	8090	-	X
33	MG	0	8094	-	X
33	MG	0	8099	-	X
33	MG	0	8102	-	X
33	MG	0	8103	-	X
33	MG	0	8104	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
33	MG	0	8114	-	X
34	K	0	8401	-	X
35	NA	0	8502	-	X
35	NA	0	8503	-	X
35	NA	0	8506	-	X
35	NA	0	8507	-	X
35	NA	0	8508	-	X
35	NA	0	8515	-	X
35	NA	0	8516	-	X
35	NA	0	8518	-	X
35	NA	0	8520	-	X
35	NA	0	8521	-	X
35	NA	0	8523	-	X
35	NA	0	8525	-	X
35	NA	0	8526	-	X
35	NA	0	8527	-	X
35	NA	0	8528	-	X
35	NA	0	8531	-	X
35	NA	0	8532	-	X
35	NA	0	8535	-	X
35	NA	0	8539	-	X
35	NA	0	8540	-	X
35	NA	0	8542	-	X
35	NA	0	8543	-	X
35	NA	0	8549	-	X
35	NA	0	8550	-	X
35	NA	0	8555	-	X
35	NA	0	8556	-	X
35	NA	0	8557	-	X
35	NA	0	8558	-	X
35	NA	0	8559	-	X
35	NA	0	8560	-	X
35	NA	0	8561	-	X
35	NA	0	8562	-	X
35	NA	0	8563	-	X
35	NA	0	8564	-	X
35	NA	0	8565	-	X
35	NA	0	8566	-	X
35	NA	0	8567	-	X
35	NA	0	8568	-	X
35	NA	0	8569	-	X
35	NA	0	8570	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
35	NA	0	8571	-	X
35	NA	0	8572	-	X
35	NA	0	8573	-	X
35	NA	0	8574	-	X
35	NA	0	8575	-	X
35	NA	0	8577	-	X
35	NA	0	8579	-	X
35	NA	0	8582	-	X
35	NA	0	8584	-	X
35	NA	0	8585	-	X
35	NA	9	8583	-	X
35	NA	H	8522	-	X
35	NA	L	8580	-	X
35	NA	R	8586	-	X
35	NA	S	8512	-	X
36	CL	0	8803	-	X
36	CL	0	8805	-	X
36	CL	0	8815	-	X
36	CL	0	8822	-	X
36	CL	A	8809	-	X

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 99043 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

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

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	CONFLICT	GB 3377779
0	628	1MA	A	MODIFIED RESIDUE	GB 3377779
0	2587	OMU	U	MODIFIED RESIDUE	GB 3377779
0	2588	OMG	G	MODIFIED RESIDUE	GB 3377779
0	2619	UR3	U	MODIFIED RESIDUE	GB 3377779
0	2621	PSU	U	MODIFIED RESIDUE	GB 3377779

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

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

- Molecule 3 is a protein called 50S ribosomal protein L2P.

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

- Molecule 4 is a protein called 50S ribosomal protein L3P.

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

- Molecule 5 is a protein called 50S ribosomal protein L4P.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	LEU	GLN	CONFLICT	UNP P12735

- Molecule 6 is a protein called 50S ribosomal protein L5P.

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

- Molecule 7 is a protein called 50S ribosomal protein L6P.

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

- Molecule 8 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 9 is a protein called 50S ribosomal protein L10E.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	248	ASP	ALA	CONFLICT	UNP P15825

- Molecule 10 is a protein called 50S ribosomal protein L10e.

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	164	ASP	-	INSERTION	UNP P60617
H	165	SER	-	INSERTION	UNP P60617
H	166	SER	-	INSERTION	UNP P60617
H	167	PRO	-	INSERTION	UNP P60617
H	168	ALA	-	INSERTION	UNP P60617
H	169	GLY	-	INSERTION	UNP P60617
H	170	ASN	-	INSERTION	UNP P60617
H	171	ALA	-	INSERTION	UNP P60617

- Molecule 11 is a protein called 50S ribosomal protein L13P.

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

- Molecule 12 is a protein called 50S ribosomal protein L14P.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 13 is a protein called 50S ribosomal protein L15P.

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

- Molecule 14 is a protein called 50S ribosomal protein L15e.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	CONFLICT	UNP P60618
M	194	ALA	-	INSERTION	UNP P60618

- Molecule 15 is a protein called 50S ribosomal protein L18P.

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

- Molecule 16 is a protein called 50S ribosomal protein L18e.

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

- Molecule 17 is a protein called 50S ribosomal protein L19e.

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

- Molecule 18 is a protein called 50S ribosomal protein L21e.

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

- Molecule 19 is a protein called 50S ribosomal protein L22P.

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

- Molecule 20 is a protein called 50S ribosomal protein L23P.

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

- Molecule 21 is a protein called 50S ribosomal protein L24P.

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

- Molecule 22 is a protein called 50S ribosomal protein L24e.

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

- Molecule 23 is a protein called 50S ribosomal protein L29P.

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

- Molecule 24 is a protein called 50S ribosomal protein L30P.

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

- Molecule 25 is a protein called 50S ribosomal protein L31e.

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

- Molecule 26 is a protein called 50S ribosomal protein L32e.

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

- Molecule 27 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Z	73	Total	C	N	O	S	0	0	0
			579	346	116	112	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	-	INSERTION	UNP P60619

- Molecule 28 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 29 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

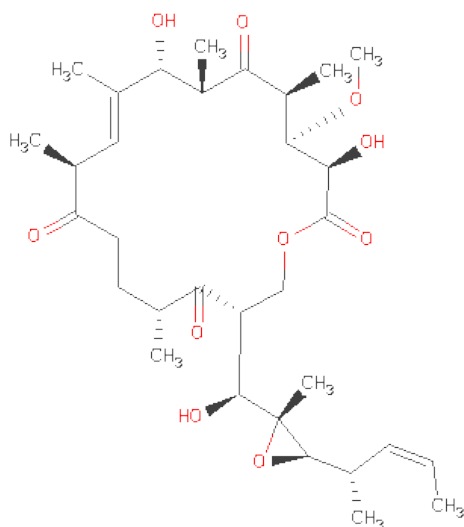
- Molecule 30 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 31 is a protein called 50S ribosomal protein L11P.

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

- Molecule 32 is 13-DEOXYTEDANOLIDE (three-letter code: 13T) (formula: C₃₂H₅₀O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
32	0	1	Total	C	O	0	0
			42	32	10		

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

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

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	74	Total	Na	0	0
			74	74		
35	J	1	Total	Na	0	0
			1	1		
35	Q	1	Total	Na	0	0
			1	1		
35	H	1	Total	Na	0	0
			1	1		
35	C	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	A	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	L	1	Total 1	Na 1	0	0
35	S	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	0	9	Total 9	Cl 9	0	0
36	J	3	Total 3	Cl 3	0	0
36	B	1	Total 1	Cl 1	0	0
36	A	1	Total 1	Cl 1	0	0
36	N	1	Total 1	Cl 1	0	0
36	O	1	Total 1	Cl 1	0	0
36	R	1	Total 1	Cl 1	0	0
36	Y	2	Total 2	Cl 2	0	0
36	L	1	Total 1	Cl 1	0	0
36	3	1	Total 1	Cl 1	0	0
36	M	1	Total 1	Cl 1	0	0

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

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

- Molecule 38 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
38	0	5905	Total O 5905 5905	0	0
38	9	140	Total O 140 140	0	0
38	A	112	Total O 112 112	0	0
38	B	142	Total O 142 142	0	0
38	C	170	Total O 170 170	0	0
38	D	45	Total O 45 45	0	0
38	E	42	Total O 42 42	0	0
38	F	26	Total O 26 26	0	0
38	G	19	Total O 19 19	0	0
38	H	70	Total O 70 70	0	0
38	J	58	Total O 58 58	0	0
38	K	59	Total O 59 59	0	0
38	L	83	Total O 83 83	0	0
38	M	123	Total O 123 123	0	0
38	N	63	Total O 63 63	0	0

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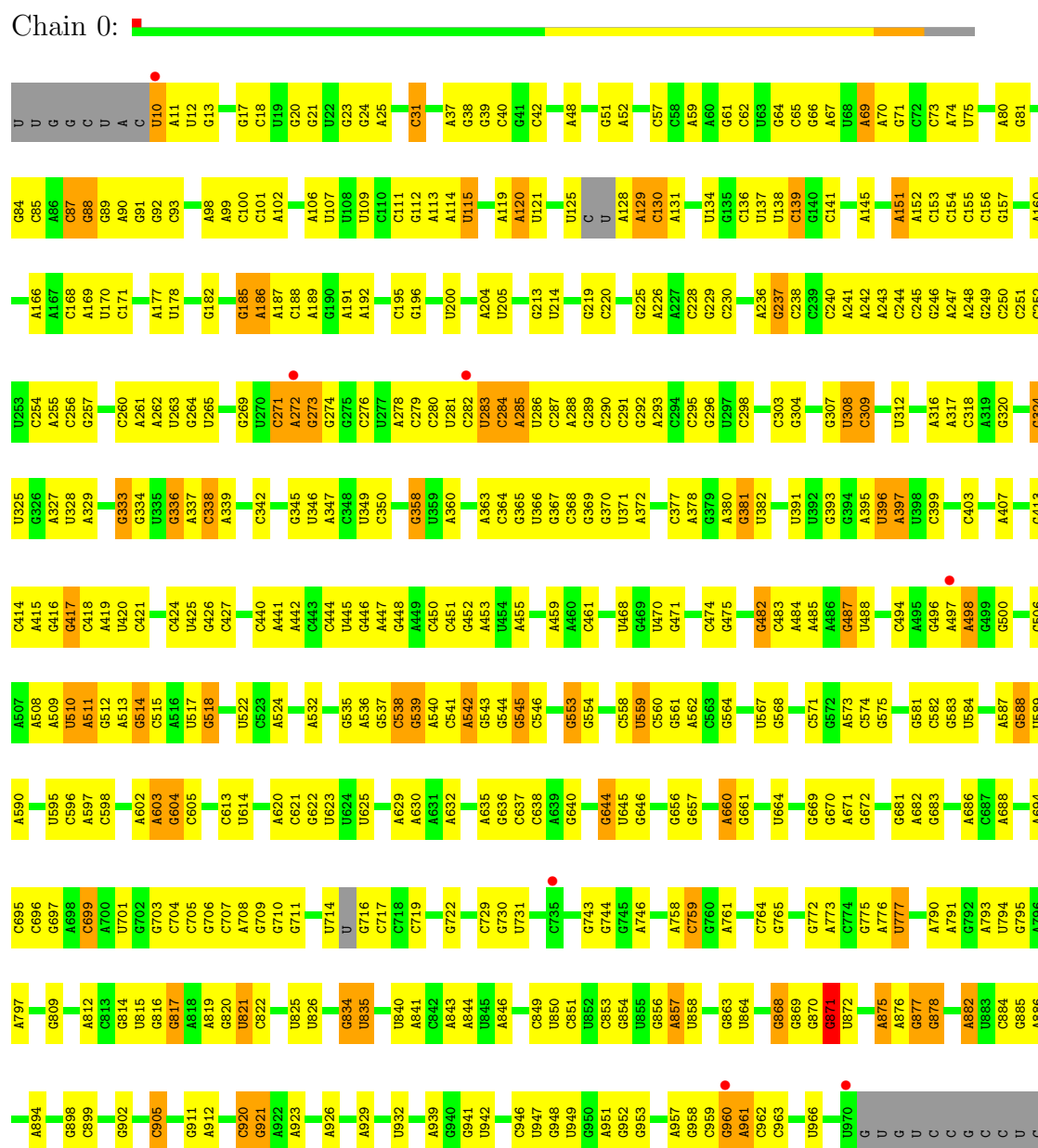
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	O	44	Total 44	O 44	0	0
38	P	56	Total 56	O 56	0	0
38	Q	51	Total 51	O 51	0	0
38	R	80	Total 80	O 80	0	0
38	S	36	Total 36	O 36	0	0
38	T	33	Total 33	O 33	0	0
38	U	26	Total 26	O 26	0	0
38	V	11	Total 11	O 11	0	0
38	W	67	Total 67	O 67	0	0
38	X	21	Total 21	O 21	0	0
38	Y	96	Total 96	O 96	0	0
38	Z	31	Total 31	O 31	0	0
38	1	56	Total 56	O 56	0	0
38	2	45	Total 45	O 45	0	0
38	3	66	Total 66	O 66	0	0
38	I	8	Total 8	O 8	0	0

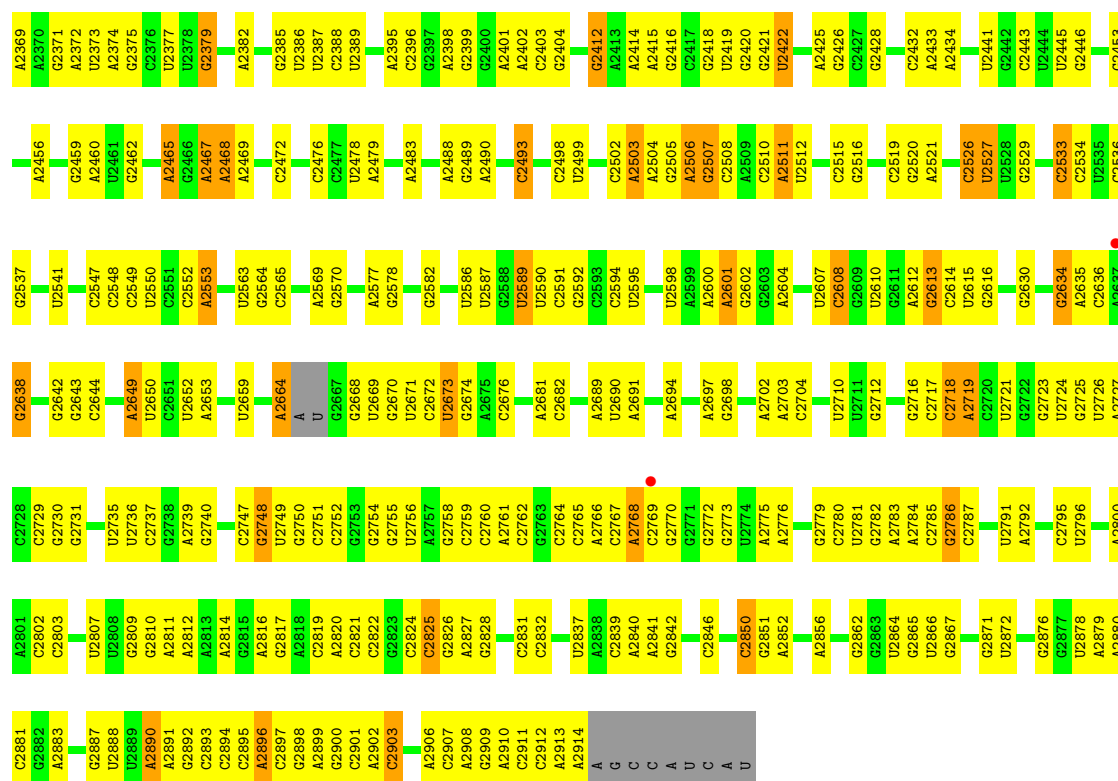
3 Residue-property plots

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

• Molecule 1: 23S ribosomal RNA

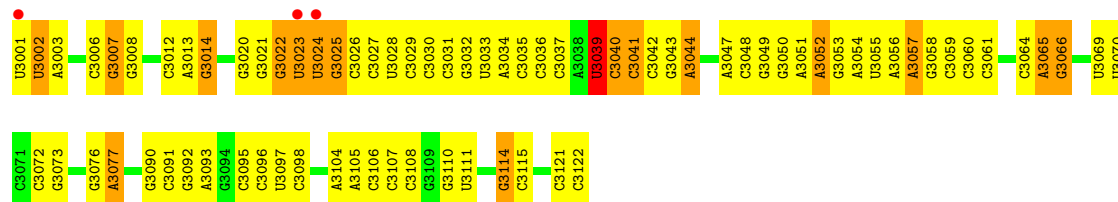


U2297	U2078	U1985	U1879	U1599	U1506	A1414	G1319	C1229	U1164	C1060	C
A2300	G2079	C1993	U1883	G1600	G1523	G1415	U1520	A1230	G1165	A1069	G
A2301	A2080	C1993	U1883	G1601	U1524	U1419	A1321	A1231	A1166	A1070	A
A2302	G2081	C1993	U1883	G1602	U1524	U1419	G1322	A1232	G1167	G1071	G
A2303	A2082	U1996	G1902	A1603	G1525	C1420	G1323	A1233	C1168	G1072	A
U2308	G2083	C	U1903	G1604	A1526	C1421	A1328	U1234	U1169	G	G
U2309	C2087	G2000	A1904	G1605	A1527	U1422	A1329	G1235	U1170	G	G
G2310	C2088	G2001	U1905	C1609	A1528	C1423	A1330	A1236	A1171	G	U
A2311	G2089	U2003	A1909	G1610	G1529	A1424	A1331	U1237	G1172	G	G
G2312	G2090	U2004	U1971	C1616	G1535	A1434	A1332	A1238	A1173	U	U
C2313	G2091	G2005	C1913	A1615	C1536	U1435	U1333	G1239	A1174	C	C
G2314	G2092	C2006	C1914	A1616	C1537	U1436	C1334	A1242	G1175	G	G
G2315	A2096	A2067	A1919	C1617	U1543	C1439	C1335	G1243	A1177	C	C
G2316	A2100	G2009	C1920	G1618	U1544	U1440	G1339	U1244	U1180	A	A
C2317	A2101	A2010	A1921	C1619	G1545	G1441	C1245	A1246	C1182	C999	C
U2320	G2102	A2011	A1922	C1620	C1546	A1442	A1340	A1246	C1183	C1000	C
A2321	U2012	G2013	G1923	G1621	G1546	G1443	C1342	U1249	C1184	U1001	C
C2322	A2103	G2013	A1924	C1622	G1552	G1444	C1343	C1250	U1185	G1002	C
G2324	C2104	G2014	A1815	A1623	C1553	G1445	G1344	C1251	C1186	C1003	C
C2325	C2105	A2015	G1819	U1625	G1556	U1447	U1350	A1252	U1187	U1004	C
U2326	G2106	U2016	G1820	A1626	G1557	U1448	A1351	C1253	A1188	C1005	C
U2327	U2017	U2017	G1820	G1627	C1558	G1449	A1352	C1257	A1189	A1006	C
C2328	G2110	A1930	C1730	A1630	A1559	C1450	C1353	G1258	U1109	A1007	C
C2241	G2111	A1931	A1732	A1631	U	C1451	C1360	U1266	G1110	C1008	C
U2242	A2112	G1932	A1733	A1632	U1561	G1452	C1366	C1267	U1009	C1010	C
C2243	C2113	C2003	A1736	G1633	G1562	U1454	A1114	A1115	A1114	A1013	C
A2244	G2114	A1940	U1741	C1634	G1563	U1454	A1115	U1116	U1116	A1014	C
C2247	C2115	A1941	U1742	U1635	C1564	G1455	A1116	U1117	A1117	C1015	C
C2251	U2116	C2035	U1835	G1636	C1565	U1456	G1196	U1270	U1118	U1016	C
G2252	G2121	C2036	U1838	A1637	C1566	U1457	G1197	C1273	U1198	A1018	C
A2253	C2122	A2039	U1839	A1641	G1567	A1458	A1199	A1200	A1199	A1019	C
G2254	G2128	G2044	C1841	A1642	U1568	C1474	A1201	A1278	A1123	C1020	C
A2255	C2133	C2047	A1845	C1643	U1569	C1477	A1202	U1279	A1123	G1021	C
G2256	G2134	A2055	U1850	U1654	A1573	C1477	G1203	A1280	C1127	A1022	C
U2257	A2135	C2048	C1854	G1655	C1574	A1482	A1205	A1287	U1128	G1023	C
A2258	G2136	C2049	C1855	A1656	G1576	C1483	U1206	U1288	C1129	G1024	C
G2263	C	G2050	U1851	A1657	U1577	G1484	A1207	C1289	U1130	C1025	C
A2264	C	A2054	A1852	A1658	C1578	C1485	C1208	G1290	G1131	U1028	C
U2265	C	C	C1853	A1661	A1580	A1486	A1307	A1291	A1132	U1029	C
A2266	C	U	C1854	A1662	A1580	A1487	A1308	A1294	G1137	U1039	C
G2267	C	C	C1855	C1663	U1583	U1488	C1209	A1294	G1138	G1039	C
C2268	C	C2061	C1856	G1666	U1583	G1489	C1210	G1299	A1150	C1044	C
G2269	C	A2062	A1857	C1667	G1586	A1492	A1398	G1299	G1151	G1045	C
G2270	C	U2063	A1858	A1667	U1587	A1493	A1399	A1307	A1151	G1046	C
G2271	C	U2064	C1965	U1668	U1588	A1494	A1400	A1308	A1151	G1053	C
C2272	C	C2065	C1966	A1669	G1589	C1495	G1401	U1309	G1155	G1054	C
A2274	C	C	U1966	G1670	G1592	G1496	A1406	A1309	C1156	G1055	C
G2275	C	G2070	G1970	U1677	C1593	G1497	A1407	A1307	G1156	G1056	C
C2276	C	G2072	C1971	A1678	C1594	U1500	U1408	A1307	G1157	G1057	C
G2277	C	G2073	U1972	C1679	G1595	U1500	A1409	A1307	G1158	G1058	C
A2278	C	A1973	G1774	C1679	G1595	U1500	G1410	A1307	G1159	U1059	C
G2284	C	G2075	G1873	C1680	U1596	U1500	G1410	A1307	G1160	U1060	C
A2291	C	G1979	G1877	G1681	A1597	U1500	G1410	A1307	A1161	A1067	C
C2296	C	G1979	G1878	A1882	A1598	U1500	G1410	A1307	A1162	A1068	C



• Molecule 2: 5S ribosomal RNA

Chain 9:



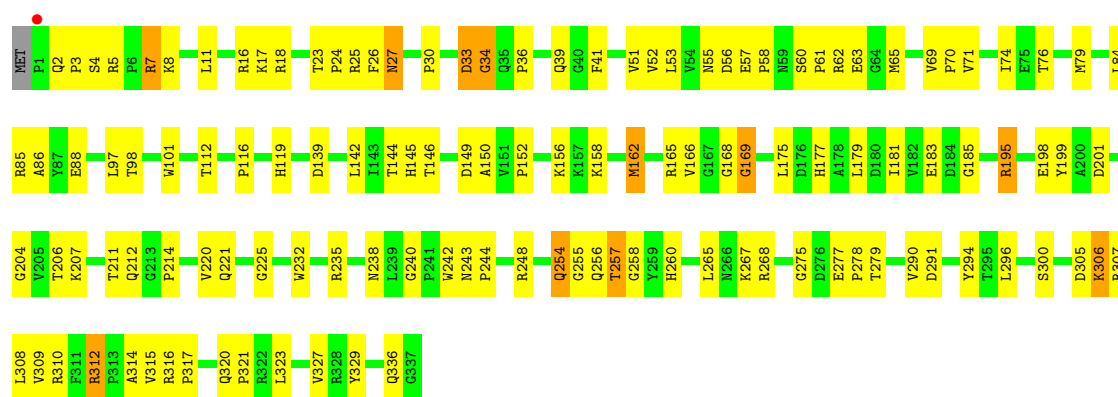
• Molecule 3: 50S ribosomal protein L2P

Chain A:



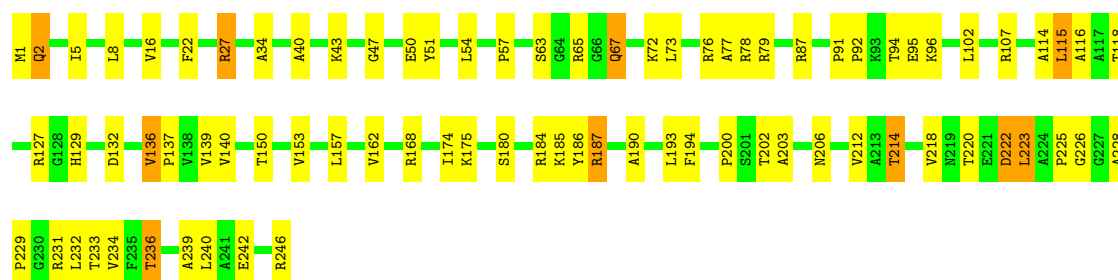
• Molecule 4: 50S ribosomal protein L3P

Chain B:



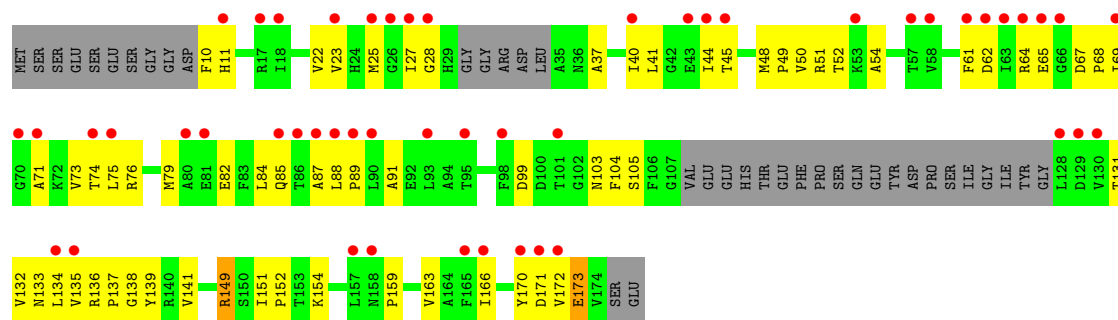
• Molecule 5: 50S ribosomal protein L4P

Chain C:



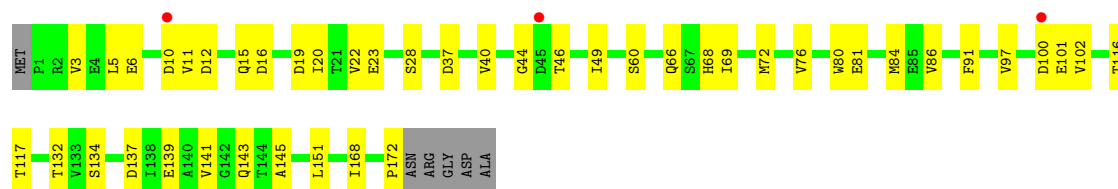
• Molecule 6: 50S ribosomal protein L5P

Chain D:



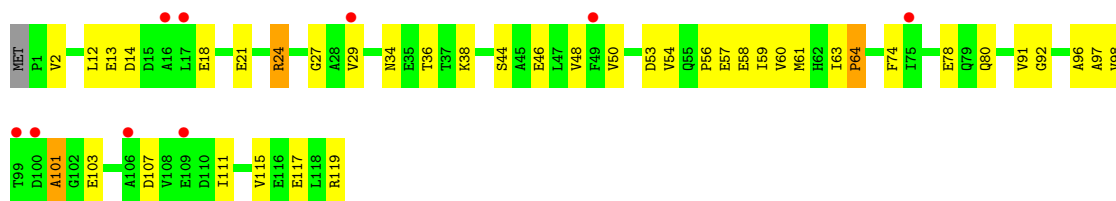
• Molecule 7: 50S ribosomal protein L6P

Chain E:



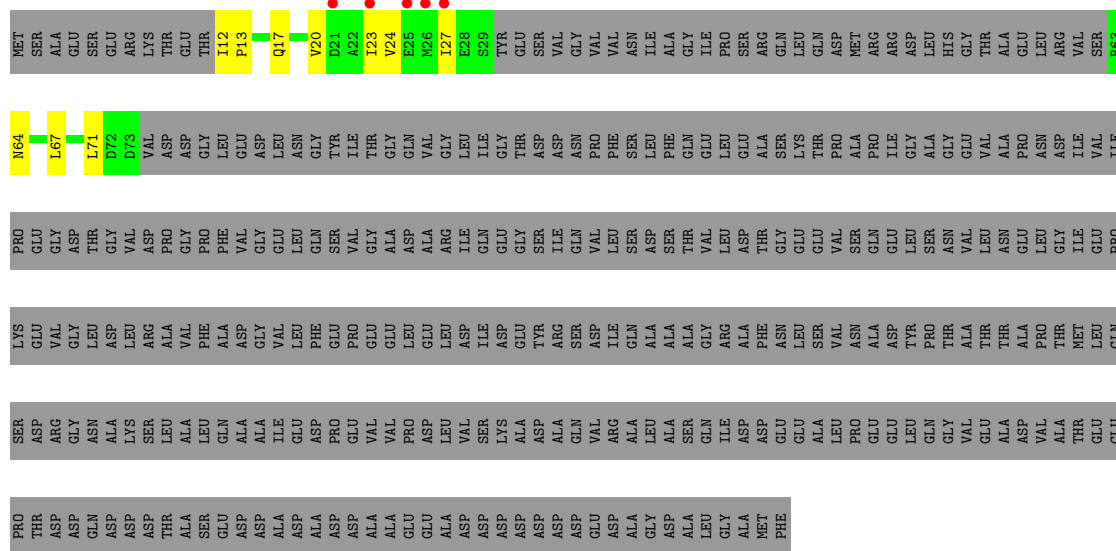
• Molecule 8: 50S ribosomal protein L7Ae

Chain F:



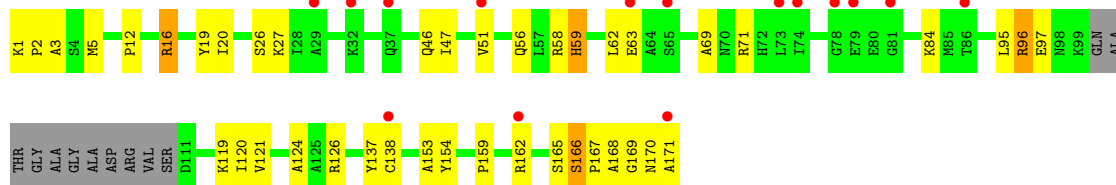
• Molecule 9: 50S ribosomal protein L10E

Chain G:



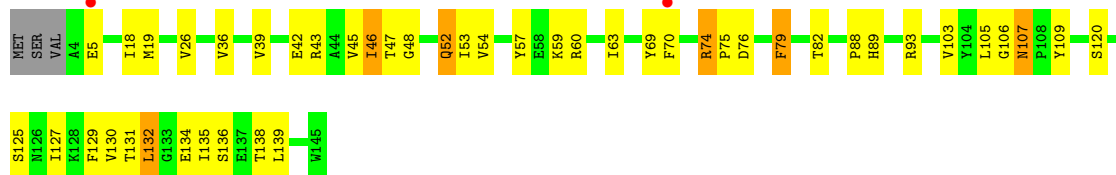
• Molecule 10: 50S ribosomal protein L10e

Chain H:



• Molecule 11: 50S ribosomal protein L13P

Chain J:



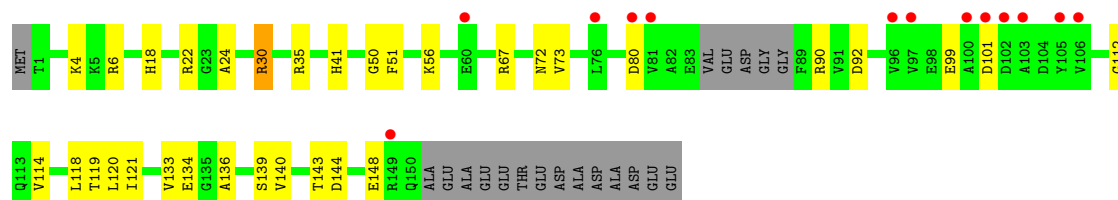
• Molecule 12: 50S ribosomal protein L14P

Chain K:



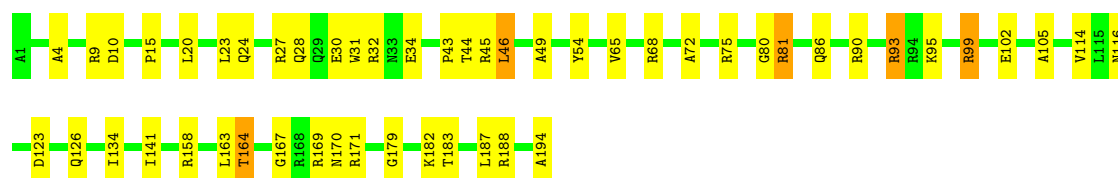
- Molecule 13: 50S ribosomal protein L15P

Chain L:



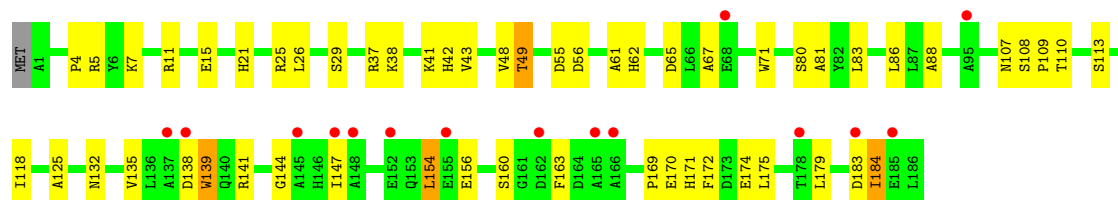
- Molecule 14: 50S ribosomal protein L15e

Chain M:



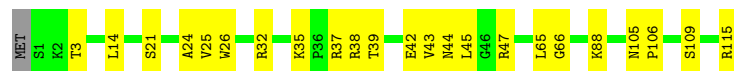
- Molecule 15: 50S ribosomal protein L18P

Chain N:



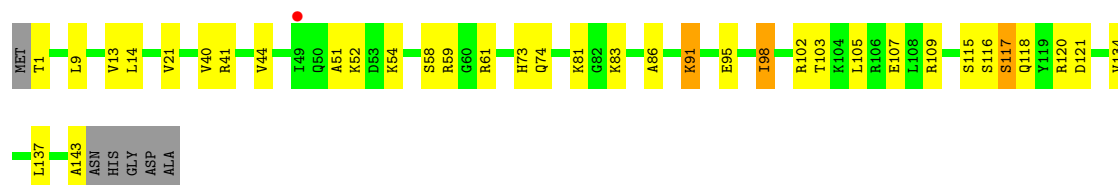
- Molecule 16: 50S ribosomal protein L18e

Chain O:



- Molecule 17: 50S ribosomal protein L19e

Chain P:



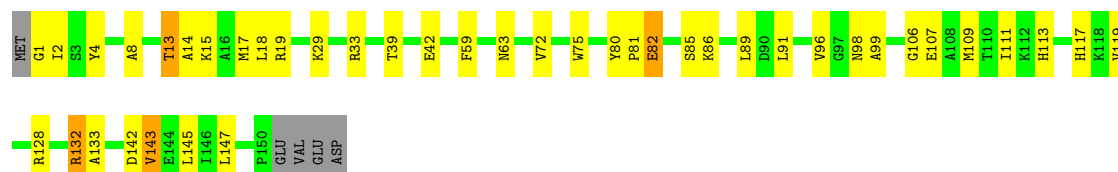
- Molecule 18: 50S ribosomal protein L21e

Chain Q: 



- Molecule 19: 50S ribosomal protein L22P

Chain R: 



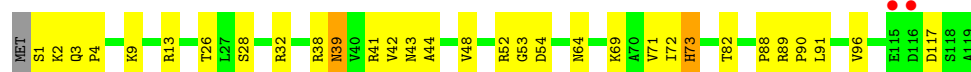
- Molecule 20: 50S ribosomal protein L23P

Chain S: 



- Molecule 21: 50S ribosomal protein L24P

Chain T: 



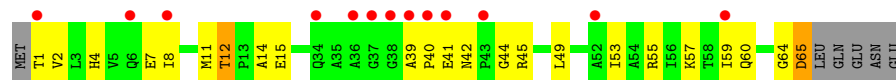
- Molecule 22: 50S ribosomal protein L24e

Chain U: 



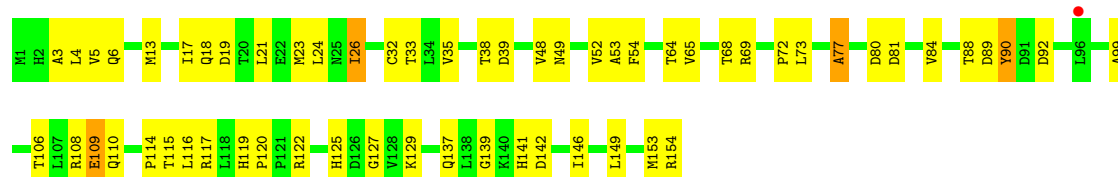
- Molecule 23: 50S ribosomal protein L29P

Chain V: 



- Molecule 24: 50S ribosomal protein L30P

Chain W: 



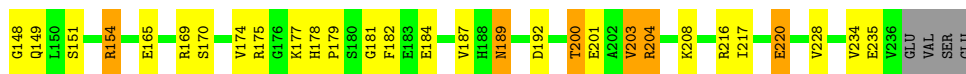
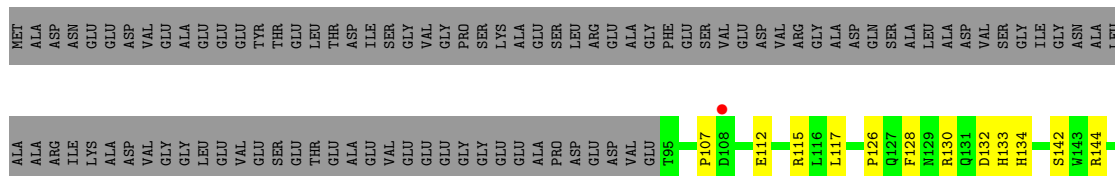
- Molecule 25: 50S ribosomal protein L31e

Chain X:



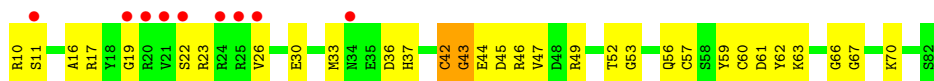
- Molecule 26: 50S ribosomal protein L32e

Chain Y:



- Molecule 27: 50S ribosomal protein L37Ae

Chain Z:



- Molecule 28: 50S ribosomal protein L37e

Chain 1:



- Molecule 29: 50S ribosomal protein L39e

Chain 2:



- Molecule 30: 50S ribosomal protein L44E

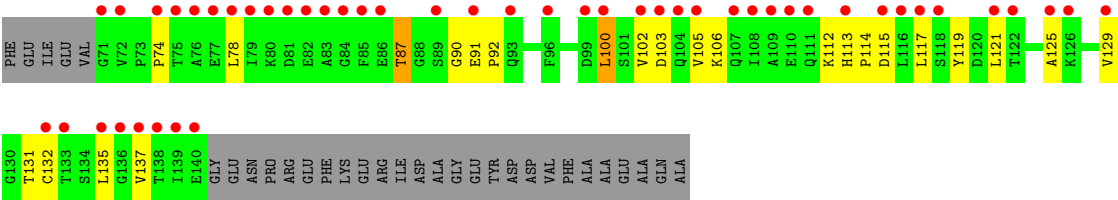
Chain 3:



- Molecule 31: 50S ribosomal protein L11P

Chain I:





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	211.74Å 299.52Å 573.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.70 – 2.90 85.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.70-2.90) 91.7 (85.48-2.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 2.86Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.193 , 0.238 0.212 , 0.241	Depositor DCC
R_{free} test set	3809 reflections (0.99%)	DCC
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 422682 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	99043	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, OMG, CL, NA, K, UR3, CD, OMU, 13T, 1MA, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.39	0/65959	0.69	14/102870 (0.0%)
2	9	0.34	0/2905	0.69	1/4528 (0.0%)
3	A	0.35	0/1786	0.66	0/2408
4	B	0.34	0/2690	0.66	0/3652
5	C	0.39	0/1884	0.66	0/2551
6	D	0.33	0/1111	0.58	0/1498
7	E	0.34	0/1382	0.57	0/1880
8	F	0.38	0/901	0.58	0/1224
9	G	0.33	0/241	0.49	0/324
10	H	0.38	0/1287	0.65	0/1725
11	J	0.36	0/1136	0.61	0/1530
12	K	0.36	0/1001	0.68	0/1347
13	L	0.35	0/1130	0.64	0/1509
14	M	0.37	0/1584	0.63	0/2119
15	N	0.31	0/1474	0.65	1/1999 (0.1%)
16	O	0.36	0/874	0.61	1/1181 (0.1%)
17	P	0.35	0/1147	0.55	0/1528
18	Q	0.37	0/749	0.68	0/1005
19	R	0.36	0/1172	0.64	0/1578
20	S	0.35	0/648	0.59	0/875
21	T	0.34	0/958	0.63	0/1289
22	U	0.36	0/417	0.56	0/562
23	V	0.35	0/502	0.56	0/675
24	W	0.34	0/1219	0.63	0/1655
25	X	0.35	0/664	0.59	0/895
26	Y	0.36	0/1146	0.63	0/1536
27	Z	0.39	0/590	0.64	0/787
28	1	0.40	0/438	0.63	0/578
29	2	0.37	0/401	0.56	0/529
30	3	0.37	0/771	0.57	0/1024
31	I	0.35	0/526	0.57	0/716
All	All	0.38	0/98693	0.67	17/147577 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	1	42
2	9	0	2
24	W	0	1
All	All	1	45

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1563	G	C2'-C3'-O3'	9.37	130.11	109.50
2	9	3039	U	N1-C1'-C2'	6.50	122.45	114.00
1	0	2316	G	C5'-C4'-C3'	-6.49	105.61	116.00
1	0	1504	A	C1'-O4'-C4'	-6.21	104.93	109.90
1	0	1942	A	C5'-C4'-C3'	6.20	125.92	116.00
15	N	163	PHE	N-CA-C	-5.68	95.66	111.00
16	O	66	GLY	N-CA-C	5.59	127.06	113.10
1	0	871	G	C5'-C4'-O4'	-5.54	102.45	109.10
1	0	1504	A	N9-C1'-C2'	5.52	121.17	114.00
1	0	1819	G	C5'-C4'-C3'	5.40	124.64	116.00
1	0	1829	A	N9-C1'-C2'	-5.39	106.07	112.00
1	0	2313	C	C5'-C4'-O4'	5.31	115.47	109.10
1	0	2291	A	N9-C1'-C2'	5.15	120.70	114.00
1	0	1559	A	C2'-C3'-O3'	5.15	121.94	113.70
1	0	2313	C	O4'-C4'-C3'	-5.07	98.93	104.00
1	0	1878	G	N9-C1'-C2'	-5.04	106.46	112.00
1	0	777	U	O4'-C1'-N1	5.03	112.23	108.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1563	G	C3'

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	1039	G	Sidechain
1	0	1078	A	Sidechain
1	0	1131	G	Sidechain

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Mol	Chain	Res	Type	Group
1	0	1309	U	Sidechain
1	0	131	A	Sidechain
1	0	1376	G	Sidechain
1	0	1445	G	Sidechain
1	0	1458	A	Sidechain
1	0	1635	U	Sidechain
1	0	1809	G	Sidechain
1	0	1829	A	Sidechain
1	0	1863	G	Sidechain
1	0	1877	G	Sidechain
1	0	1878	G	Sidechain
1	0	1970	G	Sidechain
1	0	1972	U	Sidechain
1	0	1979	G	Sidechain
1	0	1993	C	Sidechain
1	0	220	C	Sidechain
1	0	2308	U	Sidechain
1	0	2316	G	Sidechain
1	0	2412	G	Sidechain
1	0	2465	A	Sidechain
1	0	2493	C	Sidechain
1	0	2503	A	Sidechain
1	0	2506	A	Sidechain
1	0	2552	C	Sidechain
1	0	2630	G	Sidechain
1	0	2673	U	Sidechain
1	0	2842	G	Sidechain
1	0	324	G	Sidechain
1	0	333	G	Sidechain
1	0	391	U	Sidechain
1	0	396	U	Sidechain
1	0	471	G	Sidechain
1	0	48	A	Sidechain
1	0	482	G	Sidechain
1	0	518	G	Sidechain
1	0	722	G	Sidechain
1	0	795	G	Sidechain
1	0	817	G	Sidechain
1	0	868	G	Sidechain
2	9	3039	U	Sidechain
2	9	3090	G	Sidechain
24	W	90	TYR	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	59021	0	29812	1337	0
2	9	2600	0	1326	95	0
3	A	1753	0	1766	78	0
4	B	2625	0	2533	112	0
5	C	1859	0	1816	74	0
6	D	1094	0	1085	56	0
7	E	1357	0	1266	38	0
8	F	890	0	843	32	0
9	G	240	0	231	9	0
10	H	1266	0	1268	39	0
11	J	1120	0	1098	49	0
12	K	992	0	1031	40	0
13	L	1118	0	1076	28	0
14	M	1560	0	1568	45	0
15	N	1445	0	1401	45	0
16	O	865	0	873	21	0
17	P	1136	0	1123	33	0
18	Q	735	0	728	22	0
19	R	1149	0	1122	41	0
20	S	641	0	605	14	0
21	T	950	0	923	25	0
22	U	410	0	364	21	0
23	V	499	0	511	19	0
24	W	1196	0	1137	57	0
25	X	654	0	653	25	0
26	Y	1130	0	1133	46	0
27	Z	579	0	539	25	0
28	1	431	0	426	21	0
29	2	396	0	413	18	0
30	3	755	0	728	18	0
31	I	519	0	500	23	0
32	0	42	0	50	24	0
33	0	108	0	0	0	0
33	3	2	0	0	0	0
33	9	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	A	2	0	0	0	0
33	B	1	0	0	0	0
33	K	1	0	0	0	0
33	T	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	2	0	0	0	0
35	0	74	0	0	2	0
35	9	2	0	0	0	0
35	A	1	0	0	0	0
35	C	1	0	0	0	0
35	H	1	0	0	0	0
35	J	1	0	0	0	0
35	L	1	0	0	1	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	9	0	0	2	0
36	3	1	0	0	0	0
36	A	1	0	0	0	0
36	B	1	0	0	0	0
36	J	3	0	0	2	0
36	L	1	0	0	0	0
36	M	1	0	0	1	0
36	N	1	0	0	0	0
36	O	1	0	0	0	0
36	R	1	0	0	0	0
36	Y	2	0	0	0	0
37	1	1	0	0	0	0
37	3	1	0	0	0	0
37	O	1	0	0	0	0
37	U	1	0	0	0	0
37	Z	1	0	0	0	0
38	0	5905	0	0	199	0
38	1	56	0	0	1	0
38	2	45	0	0	4	0
38	3	66	0	0	2	0
38	9	140	0	0	10	0
38	A	112	0	0	8	0
38	B	142	0	0	21	0
38	C	170	0	0	16	0
38	D	45	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	E	42	0	0	5	0
38	F	26	0	0	2	0
38	G	19	0	0	0	0
38	H	70	0	0	6	0
38	I	8	0	0	1	0
38	J	58	0	0	3	0
38	K	59	0	0	1	0
38	L	83	0	0	10	0
38	M	123	0	0	4	0
38	N	63	0	0	6	0
38	O	44	0	0	3	0
38	P	56	0	0	2	0
38	Q	51	0	0	5	0
38	R	80	0	0	2	0
38	S	36	0	0	2	0
38	T	33	0	0	1	0
38	U	26	0	0	2	0
38	V	11	0	0	1	0
38	W	67	0	0	6	0
38	X	21	0	0	2	0
38	Y	96	0	0	6	0
38	Z	31	0	0	2	0
All	All	99043	0	59948	2276	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (2276) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:871:G:C8	1:0:871:G:H5'	1.77	1.19
1:0:1160:G:C5'	1:0:1161:A:H5'	1.73	1.18
1:0:1160:G:H5'	1:0:1161:A:C5'	1.79	1.12
1:0:871:G:H8	1:0:871:G:H5'	1.01	1.09
1:0:1002:G:H2'	1:0:1003:U:H5''	1.37	1.07
1:0:1474:C:H6	1:0:1474:C:H5'	1.16	1.06
2:9:3006:C:H5''	15:N:37:ARG:NH1	1.70	1.06
2:9:3056:A:H2'	2:9:3057:A:H5''	1.34	1.05
1:0:1242:A:H5'	11:J:82:THR:HG23	1.34	1.04
1:0:541:C:H2'	1:0:542:A:H5''	1.41	1.03
10:H:46:GLN:HB3	10:H:167:PRO:HD2	1.41	1.02
1:0:542:A:H5'	1:0:542:A:H8	1.25	1.01
1:0:1559:A:H1'	38:0:5876:HOH:O	1.59	1.01

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2717:C:C2'	1:0:2718:C:H5''	1.91	1.01
1:0:381:G:H5''	38:0:4329:HOH:O	1.61	1.00
1:0:1474:C:C6	1:0:1474:C:H5'	1.99	0.98
1:0:1701:A:H4'	1:0:1702:U:H5''	1.44	0.98
1:0:1666:C:O2'	1:0:1667:A:H5''	1.64	0.98
1:0:1162:G:H1'	31:I:117:LEU:HD11	1.45	0.98
1:0:156:C:H5''	14:M:171:ARG:HD3	1.41	0.97
1:0:1118:A:H62	1:0:1244:U:H3	1.09	0.97
1:0:2717:C:H2'	1:0:2718:C:H5''	1.46	0.96
1:0:2460:A:H5'	32:0:9000:13T:C23	1.96	0.96
2:9:3092:G:H2'	2:9:3093:A:C8	2.01	0.96
2:9:3076:G:H3'	2:9:3077:A:H5''	1.43	0.95
5:C:236:THR:HG22	5:C:239:ALA:H	1.28	0.95
1:0:871:G:H8	1:0:871:G:C5'	1.80	0.95
10:H:166:SER:HB2	10:H:167:PRO:HD3	1.49	0.94
1:0:1205:U:H2'	1:0:1206:U:H5''	1.50	0.94
1:0:2460:A:H5'	32:0:9000:13T:H233	1.46	0.93
1:0:1667:A:H8	1:0:1667:A:H5'	1.34	0.93
29:2:41:HIS:H	29:2:45:ASN:HD22	1.16	0.93
26:Y:200:THR:HG22	26:Y:201:GLU:HG3	1.49	0.93
1:0:289:G:H22	1:0:363:A:H2	0.97	0.93
1:0:1172:G:H5''	38:0:7252:HOH:O	1.69	0.93
1:0:877:G:H5'	1:0:878:G:OP1	1.69	0.93
1:0:282:C:H1'	1:0:368:C:N4	1.84	0.93
1:0:2710:U:H1'	38:0:7605:HOH:O	1.68	0.92
1:0:545:G:H8	1:0:545:G:H5'	1.34	0.92
1:0:1372:A:H3'	38:0:7182:HOH:O	1.69	0.92
12:K:10:GLN:H	12:K:10:GLN:HE21	0.93	0.92
1:0:2506:A:HO2'	1:0:2507:G:H8	0.93	0.92
1:0:506:G:H22	1:0:509:A:C5'	1.82	0.91
1:0:1118:A:H3'	1:0:1118:A:C8	2.05	0.91
1:0:1118:A:H3'	1:0:1118:A:H8	1.33	0.91
1:0:2812:A:H2	1:0:2814:A:H62	1.06	0.91
1:0:541:C:C2'	1:0:542:A:H5''	1.99	0.91
1:0:870:G:H2'	1:0:871:G:H5''	1.50	0.90
1:0:1184:C:H1'	38:0:7452:HOH:O	1.70	0.90
1:0:1603:A:H5'	1:0:1605:G:O4'	1.72	0.90
1:0:93:C:H5''	23:V:1:THR:HB	1.51	0.90
25:X:37:LEU:HD13	25:X:85:VAL:HG21	1.54	0.89
24:W:4:LEU:HD22	24:W:52:VAL:HG21	1.53	0.89
12:K:29:LEU:HB3	12:K:55:VAL:HG11	1.54	0.89
1:0:2529:G:H3'	38:0:7177:HOH:O	1.70	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:289:G:N2	1:0:363:A:H2	1.70	0.89
21:T:71:VAL:HG11	21:T:90:PRO:HB3	1.55	0.88
1:0:317:A:H4'	38:0:3775:HOH:O	1.73	0.88
17:P:115:SER:H	17:P:118:GLN:HE21	1.20	0.88
6:D:134:LEU:HD11	6:D:166:ILE:HD11	1.56	0.88
1:0:1209:C:H2'	1:0:1210:G:H8	1.39	0.87
1:0:2508:C:H2'	38:0:6748:HOH:O	1.72	0.87
1:0:1165:G:H4'	1:0:1174:A:O2'	1.74	0.87
1:0:506:G:H22	1:0:509:A:H5''	1.37	0.87
2:9:3049:G:H5''	38:N:8842:HOH:O	1.73	0.87
1:0:1641:A:H2'	1:0:1642:A:H5'	1.55	0.86
1:0:1116:U:H3	1:0:1246:A:H62	1.21	0.86
1:0:2783:A:H3'	38:0:5234:HOH:O	1.75	0.84
1:0:2586:U:H3	1:0:2592:G:H22	1.25	0.84
1:0:1701:A:H5'	38:0:6285:HOH:O	1.77	0.84
12:K:10:GLN:N	12:K:10:GLN:HE21	1.76	0.84
1:0:2769:C:C2'	1:0:2770:G:H5'	2.08	0.84
12:K:10:GLN:H	12:K:10:GLN:NE2	1.76	0.84
1:0:182:G:H5'	38:0:5159:HOH:O	1.78	0.83
1:0:2291:A:C8	1:0:2309:C:H5'	2.13	0.83
1:0:21:G:H5'	19:R:2:ILE:HA	1.61	0.83
15:N:113:SER:HB2	38:N:8855:HOH:O	1.78	0.83
1:0:272:A:H3'	38:0:7515:HOH:O	1.79	0.83
1:0:272:A:H5'	1:0:273:G:OP2	1.79	0.83
24:W:21:LEU:HD21	24:W:48:VAL:HG11	1.61	0.83
1:0:1450:C:H4'	1:0:1451:C:OP2	1.76	0.83
10:H:56:GLN:HE21	10:H:126:ARG:HE	1.25	0.83
1:0:282:C:O2'	1:0:283:U:H5'	1.79	0.83
2:9:3056:A:C2'	2:9:3057:A:H5''	2.09	0.83
5:C:5:ILE:HD11	5:C:16:VAL:HG23	1.59	0.82
4:B:307:ARG:HG3	4:B:307:ARG:HH11	1.42	0.82
4:B:36:PRO:HA	4:B:168:GLY:HA3	1.61	0.82
1:0:559:U:H5'	1:0:559:U:H6	1.44	0.82
1:0:69:A:H5'	1:0:69:A:C8	2.14	0.82
24:W:88:THR:HB	38:W:6679:HOH:O	1.79	0.82
1:0:797:A:H4'	27:Z:10:ARG:N	1.94	0.82
1:0:1183:C:H2'	38:0:6249:HOH:O	1.79	0.81
6:D:54:ALA:HB2	6:D:69:ILE:HD12	1.62	0.81
1:0:1187:U:HO2'	1:0:1189:A:H2	1.26	0.81
4:B:221:GLN:HE22	12:K:42:ASN:HD22	1.23	0.81
38:0:5223:HOH:O	12:K:39:GLY:HA2	1.81	0.81
1:0:236:A:H4'	1:0:237:G:H5'	1.63	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:211:LYS:HB3	3:A:212:PRO:HD2	1.62	0.81
1:0:2717:C:O2'	1:0:2718:C:H5''	1.80	0.81
15:N:83:LEU:HD13	15:N:175:LEU:HD23	1.62	0.80
24:W:137:GLN:HE21	24:W:141:HIS:HE1	1.29	0.80
1:0:515:C:H5''	38:0:5657:HOH:O	1.81	0.80
3:A:199:HIS:HD2	3:A:201:PHE:H	1.27	0.80
1:0:558:C:O2'	1:0:559:U:H5''	1.81	0.80
1:0:1160:G:H5'	1:0:1161:A:H5'	0.88	0.80
19:R:8:ALA:HB1	19:R:13:THR:HG21	1.64	0.80
1:0:541:C:H2'	1:0:542:A:C5'	2.12	0.80
1:0:2533:C:H5'	1:0:2533:C:H6	1.46	0.79
1:0:1835:U:H5	1:0:1840:A:N7	1.79	0.79
1:0:1206:U:H5'	1:0:1206:U:H6	1.47	0.79
4:B:212:GLN:HB2	4:B:257:THR:HG21	1.63	0.79
2:9:3029:C:H2'	2:9:3030:C:H5'	1.61	0.79
1:0:292:G:H2'	1:0:358:G:N2	1.97	0.79
1:0:2716:G:H5''	4:B:206:THR:HG21	1.63	0.79
1:0:1116:U:O2'	1:0:1118:A:H2	1.63	0.79
12:K:98:VAL:HG13	12:K:102:GLU:HA	1.64	0.79
1:0:2054:A:N3	19:R:128:ARG:NH2	2.30	0.79
1:0:1615:A:H5'	38:0:4195:HOH:O	1.83	0.79
1:0:2676:C:H4'	11:J:70:PHE:CE1	2.18	0.79
1:0:1667:A:C8	1:0:1667:A:H5'	2.18	0.79
1:0:1116:U:HO2'	1:0:1118:A:H2	0.83	0.79
1:0:1119:G:N2	1:0:1246:A:C2	2.51	0.79
20:S:57:THR:HG22	20:S:59:ASP:H	1.48	0.79
27:Z:46:ARG:HD3	27:Z:59:TYR:HB2	1.64	0.79
1:0:1002:G:C2'	1:0:1003:U:H5''	2.13	0.78
1:0:1741:U:H5'	1:0:1742:A:OP1	1.83	0.78
1:0:1441:G:H1'	38:0:7748:HOH:O	1.82	0.78
32:0:9000:13T:H2	32:0:9000:13T:H262	1.65	0.78
1:0:514:G:H4'	38:0:5657:HOH:O	1.83	0.78
1:0:1919:A:H4'	38:0:4858:HOH:O	1.83	0.78
1:0:1878:G:H1'	38:0:6128:HOH:O	1.83	0.78
1:0:1666:C:C2'	1:0:1667:A:H5''	2.14	0.78
1:0:2908:A:H2'	1:0:2909:G:O4'	1.83	0.78
1:0:871:G:C8	1:0:871:G:C5'	2.59	0.77
1:0:681:G:N3	1:0:681:G:H5'	1.99	0.77
1:0:1474:C:C5'	1:0:1474:C:H6	1.97	0.77
1:0:21:G:C5'	19:R:2:ILE:HA	2.13	0.77
1:0:130:C:H2'	38:0:3162:HOH:O	1.84	0.77
11:J:75:PRO:HG2	11:J:105:LEU:HD21	1.66	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2426:G:H1'	38:0:6098:HOH:O	1.85	0.77
1:0:1679:C:H5'	38:0:9320:HOH:O	1.85	0.77
1:0:542:A:H5'	1:0:542:A:C8	2.15	0.77
5:C:115:LEU:HD13	5:C:223:LEU:HD21	1.66	0.77
5:C:127:ARG:NH2	5:C:225:PRO:HG2	2.00	0.77
32:0:9000:13T:H21	32:0:9000:13T:C30	2.14	0.76
32:0:9000:13T:C2	32:0:9000:13T:H262	2.14	0.76
1:0:1205:U:H2'	1:0:1206:U:C5'	2.15	0.76
1:0:2769:C:H2'	1:0:2770:G:H5'	1.68	0.76
6:D:154:LYS:HD2	6:D:154:LYS:H	1.50	0.76
1:0:12:U:H2'	1:0:13:G:H5'	1.67	0.76
1:0:1603:A:H5''	1:0:1605:G:H5'	1.67	0.75
1:0:1701:A:H4'	1:0:1702:U:C5'	2.15	0.75
1:0:1058:A:H2'	1:0:1060:C:H5''	1.67	0.75
1:0:2851:G:O2'	1:0:2852:A:H5'	1.87	0.75
19:R:18:LEU:HB2	19:R:143:VAL:HG13	1.66	0.75
24:W:4:LEU:HD23	24:W:54:PHE:HB3	1.68	0.74
1:0:2502:C:C2'	1:0:2503:A:H5'	2.16	0.74
1:0:558:C:C2'	1:0:559:U:H5''	2.17	0.74
1:0:2010:A:H2'	38:0:5968:HOH:O	1.86	0.74
1:0:2570:G:H5''	38:0:4917:HOH:O	1.86	0.74
1:0:2766:A:H5'	38:B:8824:HOH:O	1.87	0.74
1:0:1205:U:C2'	1:0:1206:U:H5''	2.18	0.74
1:0:2756:U:H3	1:0:2896:A:H2	1.31	0.74
1:0:2768:A:O2'	1:0:2769:C:H5'	1.86	0.74
1:0:2005:G:H3'	1:0:2005:G:OP2	1.87	0.74
24:W:84:VAL:HG12	38:W:6679:HOH:O	1.88	0.74
1:0:396:U:H1'	38:0:7612:HOH:O	1.88	0.74
1:0:899:C:H5'	38:0:3205:HOH:O	1.86	0.74
1:0:949:U:H4'	18:Q:95:GLU:HA	1.68	0.74
1:0:69:A:H5'	1:0:69:A:H8	1.52	0.74
7:E:116:THR:HG22	7:E:151:LEU:HD22	1.70	0.74
1:0:2768:A:H2'	1:0:2769:C:O4'	1.87	0.73
10:H:56:GLN:NE2	10:H:126:ARG:HE	1.86	0.73
1:0:797:A:C4'	27:Z:10:ARG:N	2.51	0.73
1:0:711:G:H1'	38:0:7092:HOH:O	1.87	0.73
1:0:1926:G:H2'	1:0:1927:A:H8	1.53	0.73
2:9:3014:G:H8	2:9:3014:G:H5'	1.51	0.73
1:0:2578:G:H5'	1:0:2578:G:H8	1.53	0.73
1:0:961:A:H4'	38:0:6766:HOH:O	1.89	0.73
1:0:2468:A:H61	30:3:48:ASN:HD21	1.35	0.73
3:A:35:GLY:O	3:A:36:ASP:HB3	1.87	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2748:G:H1'	38:0:7883:HOH:O	1.87	0.73
15:N:49:THR:HG22	15:N:56:ASP:HB2	1.71	0.73
3:A:51:ARG:HB2	38:A:8897:HOH:O	1.89	0.73
22:U:14:GLU:O	22:U:17:THR:HB	1.88	0.73
11:J:127:ILE:HG22	36:J:8801:CL:CL	2.25	0.73
1:0:288:A:H61	1:0:364:C:H42	1.36	0.73
1:0:544:G:H2'	1:0:545:G:H5''	1.70	0.72
5:C:233:THR:HG22	5:C:234:VAL:H	1.54	0.72
1:0:545:G:C8	1:0:545:G:H5'	2.22	0.72
1:0:587:A:H5''	38:0:7279:HOH:O	1.89	0.72
1:0:2781:U:C2'	1:0:2782:G:H5'	2.19	0.72
1:0:1926:G:H2'	1:0:1927:A:C8	2.24	0.72
24:W:137:GLN:HE21	24:W:141:HIS:CE1	2.07	0.72
1:0:2781:U:H2'	1:0:2782:G:H5'	1.70	0.72
1:0:1634:G:H3'	38:0:3901:HOH:O	1.89	0.72
1:0:870:G:C2'	1:0:871:G:H5''	2.17	0.72
1:0:1350:U:H4'	38:0:5124:HOH:O	1.88	0.72
1:0:1080:C:H4'	1:0:1081:A:OP1	1.89	0.72
1:0:2505:G:O2'	1:0:2506:A:H5'	1.89	0.71
1:0:2507:G:H2'	1:0:2510:C:H42	1.55	0.71
1:0:1593:C:H5'	17:P:116:SER:O	1.89	0.71
1:0:2243:C:H5''	38:0:3753:HOH:O	1.88	0.71
30:3:25:VAL:HG22	30:3:68:LYS:HG3	1.71	0.71
25:X:76:ARG:HH11	25:X:76:ARG:HG3	1.55	0.71
38:0:3759:HOH:O	21:T:9:LYS:HD3	1.88	0.71
1:0:1189:A:H1'	1:0:1209:C:O4'	1.91	0.71
1:0:1189:A:H1'	1:0:1209:C:C1'	2.19	0.71
19:R:18:LEU:HG	19:R:91:LEU:HD13	1.73	0.71
1:0:2878:U:H2'	1:0:2879:A:O4'	1.90	0.71
1:0:2420:G:O2'	1:0:2421:G:H5'	1.90	0.71
1:0:2862:G:H4'	4:B:336:GLN:O	1.91	0.71
1:0:2827:A:H2'	1:0:2828:G:O4'	1.90	0.71
16:O:32:ARG:HE	16:O:35:LYS:HD2	1.56	0.71
2:9:3039:U:H3'	2:9:3040:C:H5''	1.73	0.71
1:0:156:C:H5''	14:M:171:ARG:CD	2.19	0.71
1:0:308:U:H5'	1:0:309:C:OP1	1.90	0.71
1:0:271:C:H41	1:0:378:A:H2	1.36	0.70
1:0:2717:C:H2'	1:0:2718:C:C5'	2.21	0.70
5:C:236:THR:HG22	5:C:239:ALA:N	2.04	0.70
13:L:133:VAL:HA	38:L:8872:HOH:O	1.90	0.70
1:0:2364:A:H5''	18:Q:15:LYS:HD3	1.73	0.70
1:0:1342:C:C2'	1:0:1343:C:H5'	2.20	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:R:81:PRO:O	19:R:85:SER:HB2	1.91	0.70
6:D:23:VAL:HG22	6:D:73:VAL:HB	1.72	0.70
1:0:214:U:H5'	38:0:6147:HOH:O	1.91	0.70
1:0:2526:C:O2'	1:0:2527:U:H5'	1.91	0.70
1:0:544:G:C2'	1:0:545:G:H5''	2.22	0.70
8:F:58:GLU:HA	8:F:61:MET:HE2	1.74	0.70
3:A:191:GLY:HA2	3:A:194:MET:CE	2.22	0.69
17:P:115:SER:H	17:P:118:GLN:NE2	1.90	0.69
1:0:962:C:H1'	15:N:5:ARG:NH1	2.07	0.69
1:0:2748:G:H2'	38:0:7526:HOH:O	1.91	0.69
24:W:72:PRO:HG2	24:W:77:ALA:HB3	1.74	0.69
17:P:143:ALA:HA	38:P:5521:HOH:O	1.93	0.69
1:0:2748:G:H5'	38:0:7526:HOH:O	1.92	0.69
4:B:201:ASP:HB2	4:B:312:ARG:HD2	1.74	0.69
1:0:338:C:H4'	5:C:174:ILE:CD1	2.21	0.69
1:0:960:G:H4'	38:0:7420:HOH:O	1.92	0.69
1:0:1299:G:O6	13:L:6:ARG:HD3	1.92	0.69
5:C:47:GLY:HA2	5:C:92:PRO:HB2	1.74	0.69
24:W:80:ASP:O	24:W:84:VAL:HG23	1.92	0.69
6:D:103:ASN:ND2	6:D:134:LEU:H	1.90	0.69
1:0:559:U:H5'	1:0:559:U:C6	2.27	0.69
3:A:191:GLY:HA2	3:A:194:MET:HE3	1.75	0.69
4:B:74:ILE:HD13	4:B:309:VAL:HG21	1.73	0.69
24:W:88:THR:HG22	24:W:89:ASP:H	1.58	0.69
1:0:2004:U:H4'	38:0:5313:HOH:O	1.93	0.69
1:0:1119:G:H2'	11:J:52:GLN:NE2	2.08	0.69
1:0:558:C:H2'	1:0:559:U:C5'	2.23	0.69
4:B:238:ASN:HD22	4:B:240:GLY:H	1.41	0.69
1:0:1189:A:H3'	38:0:7666:HOH:O	1.93	0.68
1:0:560:C:H42	1:0:597:A:H61	1.39	0.68
1:0:1242:A:H5'	11:J:82:THR:CG2	2.18	0.68
32:0:9000:13T:H301	32:0:9000:13T:H21	1.74	0.68
1:0:657:G:OP1	5:C:27:ARG:NH2	2.26	0.68
2:9:3054:A:O2'	2:9:3055:U:H5'	1.94	0.68
10:H:166:SER:HB2	10:H:167:PRO:CD	2.21	0.68
1:0:1641:A:C2'	1:0:1642:A:H5'	2.23	0.68
36:0:8813:CL:CL	38:0:4691:HOH:O	2.48	0.68
7:E:97:VAL:HG12	38:E:4191:HOH:O	1.94	0.68
1:0:821:U:H2'	1:0:822:C:H6	1.57	0.68
1:0:1183:C:H42	1:0:1184:C:H41	1.42	0.68
3:A:199:HIS:CD2	3:A:201:PHE:H	2.10	0.68
1:0:2635:A:O2'	1:0:2636:C:H5'	1.94	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:E:81:GLU:HG2	7:E:134:SER:HB3	1.75	0.68
1:O:1244:U:OP1	11:J:18:ILE:HD13	1.93	0.68
1:O:2459:G:H2'	32:O:9000:13T:C23	2.24	0.68
6:D:41:LEU:HA	6:D:44:ILE:HG22	1.76	0.68
3:A:192:VAL:CG1	3:A:207:GLN:HB3	2.22	0.68
1:O:2812:A:C2	1:O:2814:A:N6	2.55	0.68
1:O:603:A:H5''	1:O:604:G:OP1	1.93	0.68
24:W:125:HIS:HD2	24:W:127:GLY:H	1.40	0.68
1:O:1183:C:N4	1:O:1184:C:H41	1.90	0.68
14:M:134:ILE:HG23	14:M:141:ILE:HD13	1.76	0.68
1:O:138:U:H5''	1:O:139:C:OP2	1.95	0.67
1:O:500:G:H21	19:R:98:ASN:HD21	1.41	0.67
1:O:2374:A:H2'	1:O:2375:G:C8	2.29	0.67
1:O:2502:C:H2'	1:O:2503:A:H5'	1.76	0.67
29:2:35:ARG:HB2	38:2:2691:HOH:O	1.95	0.67
1:O:1189:A:O2'	1:O:1208:C:H2'	1.95	0.67
1:O:1213:C:O2'	1:O:1214:G:H5'	1.94	0.67
1:O:1118:A:N6	1:O:1244:U:H3	1.87	0.67
1:O:506:G:H22	1:O:509:A:H5'	1.57	0.67
23:V:57:LYS:HA	23:V:60:GLN:HE21	1.60	0.67
5:C:129:HIS:CE1	5:C:231:ARG:HA	2.29	0.67
1:O:2533:C:C6	1:O:2533:C:H5'	2.28	0.67
11:J:107:ASN:HD22	11:J:109:TYR:H	1.42	0.67
1:O:706:G:HO2'	1:O:707:C:H6	1.43	0.67
1:O:2717:C:OP1	4:B:207:LYS:HG3	1.95	0.67
11:J:76:ASP:HA	38:J:8868:HOH:O	1.94	0.67
23:V:12:THR:HG22	23:V:15:GLU:HG3	1.77	0.67
1:O:1973:A:H5'	1:O:1973:A:H8	1.59	0.67
1:O:280:C:H2'	1:O:281:U:O4'	1.95	0.66
4:B:267:LYS:HD3	38:B:8824:HOH:O	1.95	0.66
1:O:2563:U:H2'	1:O:2565:C:O5'	1.96	0.66
1:O:2100:A:H5'	38:C:8662:HOH:O	1.93	0.66
1:O:2256:G:H2'	1:O:2257:G:C5'	2.25	0.66
27:Z:10:ARG:HA	38:Z:8715:HOH:O	1.96	0.66
11:J:74:ARG:HB3	11:J:74:ARG:HH11	1.61	0.66
1:O:485:A:N3	1:O:487:G:H5''	2.10	0.66
1:O:2256:G:H2'	1:O:2257:G:H5'	1.78	0.66
5:C:1:MET:HG2	5:C:2:GLN:H	1.61	0.66
1:O:2489:G:H1'	38:O:7268:HOH:O	1.95	0.66
1:O:284:C:H4'	1:O:285:A:O5'	1.96	0.66
30:3:73:GLU:HB3	38:3:8854:HOH:O	1.94	0.66
1:O:1162:G:H1'	31:I:117:LEU:CD1	2.24	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2506:A:O2'	1:0:2507:G:H8	1.72	0.66
1:0:1209:C:H2'	1:0:1210:G:C8	2.26	0.66
1:0:2521:A:OP2	10:H:3:ALA:HB3	1.96	0.66
1:0:1524:U:OP1	1:0:1524:U:H4'	1.94	0.66
1:0:1328:A:OP1	26:Y:169:ARG:HD2	1.96	0.66
4:B:162:MET:HG3	4:B:310:ARG:HD3	1.78	0.66
1:0:694:A:H2'	1:0:695:C:H5'	1.77	0.66
19:R:99:ALA:HB1	19:R:109:MET:CE	2.26	0.66
1:0:21:G:H5''	19:R:1:GLY:O	1.97	0.65
1:0:1684:A:H1'	29:2:43:ARG:HH22	1.61	0.65
1:0:2638:G:H1'	38:0:7742:HOH:O	1.96	0.65
15:N:48:VAL:CG1	15:N:55:ASP:HB3	2.25	0.65
2:9:3029:C:C2'	2:9:3030:C:H5'	2.26	0.65
12:K:74:VAL:HG12	12:K:75:ARG:HG3	1.79	0.65
1:0:2460:A:C5'	32:0:9000:13T:H233	2.23	0.65
26:Y:187:VAL:HG23	26:Y:192:ASP:CB	2.26	0.65
5:C:140:VAL:HB	38:C:8651:HOH:O	1.94	0.65
1:0:136:C:H2'	1:0:137:U:O4'	1.97	0.65
1:0:2890:A:H1'	22:U:56:ARG:NH2	2.11	0.65
4:B:179:LEU:O	4:B:183:GLU:HG2	1.95	0.65
1:0:1666:C:H2'	1:0:1667:A:C5'	2.26	0.65
1:0:558:C:H2'	1:0:559:U:H5'	1.79	0.65
1:0:2414:A:H2'	1:0:2415:A:C8	2.31	0.65
1:0:447:A:O2'	1:0:448:G:H5'	1.97	0.65
1:0:1187:U:O2'	1:0:1189:A:H2	1.78	0.65
1:0:2795:C:O2'	1:0:2796:U:H5'	1.96	0.65
1:0:584:U:H3'	38:0:6101:HOH:O	1.96	0.65
12:K:14:LYS:HB2	12:K:45:PRO:HG2	1.79	0.65
1:0:407:A:H8	38:0:4466:HOH:O	1.79	0.65
2:9:3003:A:N6	2:9:3022:G:H1'	2.12	0.65
1:0:1701:A:H5''	1:0:1702:U:H3'	1.77	0.65
1:0:2780:C:H1'	7:E:143:GLN:HE21	1.62	0.64
1:0:2320:U:H4'	1:0:2321:A:O4'	1.97	0.64
10:H:169:GLY:HA3	38:H:8591:HOH:O	1.95	0.64
24:W:88:THR:HG23	24:W:110:GLN:HE21	1.62	0.64
1:0:1342:C:H2'	1:0:1343:C:H5'	1.79	0.64
12:K:74:VAL:CG1	12:K:113:ILE:HG12	2.28	0.64
1:0:2787:C:H5	38:0:4641:HOH:O	1.80	0.64
1:0:403:C:H3'	38:0:6307:HOH:O	1.97	0.64
1:0:2241:C:O2'	1:0:2242:U:H5'	1.96	0.64
1:0:281:U:O2'	1:0:282:C:H5'	1.96	0.64
6:D:99:ASP:HB3	6:D:103:ASN:H	1.62	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2896:A:H5''	38:0:6105:HOH:O	1.97	0.64
1:0:441:A:H1'	1:0:442:A:N7	2.13	0.64
38:0:4678:HOH:O	4:B:300:SER:HB3	1.97	0.64
1:0:958:G:H2'	1:0:959:C:C6	2.32	0.64
6:D:135:VAL:HG21	6:D:139:TYR:CD1	2.32	0.64
1:0:2721:U:H4'	12:K:87:ARG:HG3	1.79	0.64
25:X:72:VAL:HG22	25:X:85:VAL:HG12	1.79	0.64
2:9:3091:C:H2'	2:9:3092:G:O4'	1.97	0.64
12:K:98:VAL:CG1	12:K:102:GLU:HA	2.27	0.64
3:A:121:ALA:O	3:A:124:VAL:HG22	1.97	0.64
1:0:2459:G:H2'	32:0:9000:13T:H233	1.80	0.64
1:0:1185:U:H2'	1:0:1186:C:C6	2.33	0.64
1:0:2769:C:O2'	1:0:2770:G:H5'	1.96	0.64
2:9:3048:C:H4'	15:N:141:ARG:HH21	1.63	0.64
1:0:1044:C:H5	38:0:6599:HOH:O	1.81	0.64
2:9:3039:U:H1'	2:9:3044:A:H61	1.63	0.64
23:V:42:ASN:HB3	38:V:7247:HOH:O	1.95	0.64
14:M:23:LEU:HD13	14:M:27:ARG:NH2	2.12	0.63
1:0:1200:A:H3'	38:0:5765:HOH:O	1.98	0.63
10:H:46:GLN:HE21	10:H:137:TYR:HE2	1.45	0.63
1:0:2769:C:H2'	1:0:2770:G:C5'	2.27	0.63
1:0:1790:C:H2'	1:0:1791:U:H6	1.63	0.63
2:9:3007:G:H5'	38:9:5071:HOH:O	1.98	0.63
5:C:236:THR:HG21	38:C:8571:HOH:O	1.98	0.63
13:L:114:VAL:HG11	38:L:8872:HOH:O	1.99	0.63
10:H:166:SER:CB	10:H:167:PRO:HD3	2.27	0.63
1:0:1165:G:H1'	1:0:1174:A:H1'	1.79	0.63
1:0:1189:A:H1'	1:0:1209:C:H1'	1.79	0.63
4:B:36:PRO:HG3	4:B:169:GLY:H	1.62	0.63
18:Q:26:PRO:O	18:Q:30:VAL:HG23	1.98	0.63
1:0:157:G:H4'	14:M:95:LYS:HE2	1.79	0.63
16:O:47:ARG:HG3	16:O:47:ARG:HH11	1.63	0.63
1:0:1185:U:H5'	38:0:7452:HOH:O	1.98	0.63
1:0:1211:G:H2'	1:0:1212:C:H6	1.63	0.63
1:0:2443:C:H1'	13:L:56:LYS:HE3	1.81	0.63
1:0:1596:U:H2'	1:0:1598:A:OP2	1.99	0.63
27:Z:57:CYS:SG	27:Z:59:TYR:HB3	2.38	0.63
1:0:447:A:P	21:T:1:SER:HB2	2.39	0.63
13:L:148:GLU:HB2	38:L:8889:HOH:O	1.99	0.63
1:0:20:G:H21	19:R:117:HIS:HD2	1.47	0.63
4:B:71:VAL:HG21	4:B:296:LEU:HB3	1.81	0.63
1:0:289:G:O2'	1:0:290:C:H5'	1.99	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1666:C:C2'	1:0:1667:A:C5'	2.77	0.62
1:0:1164:U:H3	1:0:1192:A:H2	1.46	0.62
1:0:1878:G:O2'	1:0:1879:U:C6	2.49	0.62
1:0:567:U:H5''	38:0:6400:HOH:O	1.98	0.62
2:9:3092:G:H2'	2:9:3093:A:H8	1.58	0.62
1:0:1313:A:H5'	26:Y:208:LYS:O	1.99	0.62
1:0:1666:C:H2'	1:0:1667:A:H5'	1.81	0.62
1:0:1307:A:H2'	1:0:1308:A:C8	2.34	0.62
1:0:951:A:C2'	1:0:952:G:H5'	2.29	0.62
5:C:67:GLN:HG2	38:C:8624:HOH:O	2.00	0.62
18:Q:25:PRO:HB2	38:Q:4350:HOH:O	1.99	0.62
1:0:396:U:O2'	1:0:418:C:H4'	1.99	0.62
2:9:3036:C:C5	2:9:3037:C:C5	2.88	0.62
1:0:1537:C:H1'	38:0:6583:HOH:O	1.98	0.62
1:0:1667:A:H2'	1:0:1668:U:C6	2.34	0.62
1:0:292:G:H2'	1:0:358:G:H22	1.65	0.62
15:N:80:SER:HB2	38:N:8832:HOH:O	1.99	0.62
1:0:1377:C:H6	1:0:1377:C:H5'	1.64	0.62
3:A:200:PRO:HG2	3:A:225:VAL:HG21	1.80	0.62
1:0:960:G:H2'	1:0:960:G:N3	2.13	0.62
1:0:1625:U:H4'	38:0:4674:HOH:O	2.00	0.62
25:X:43:VAL:HG12	25:X:44:ASP:N	2.15	0.62
14:M:99:ARG:HH21	14:M:170:ASN:HD22	1.48	0.62
1:0:1441:G:O2'	1:0:1442:A:H5'	2.00	0.62
1:0:2256:G:C2'	1:0:2257:G:H5'	2.29	0.62
29:2:22:PRO:HG2	29:2:25:VAL:HG23	1.82	0.62
1:0:1636:G:O2'	1:0:1637:A:H5'	1.99	0.62
1:0:558:C:C2'	1:0:559:U:C5'	2.78	0.61
2:9:3014:G:C8	2:9:3014:G:H5'	2.34	0.61
23:V:39:ALA:N	23:V:40:PRO:HD2	2.14	0.61
19:R:96:VAL:HG13	19:R:106:GLY:HA3	1.82	0.61
15:N:67:ALA:HA	15:N:71:TRP:HB3	1.82	0.61
1:0:656:G:H5'	16:O:3:THR:HB	1.80	0.61
35:L:8580:NA:NA	38:L:8826:HOH:O	1.71	0.61
1:0:597:A:H2'	1:0:598:C:H6	1.65	0.61
23:V:55:ARG:O	23:V:59:ILE:HG12	1.99	0.61
15:N:61:ALA:HB3	15:N:88:ALA:HB2	1.80	0.61
35:0:8542:NA:NA	38:0:5663:HOH:O	1.71	0.61
1:0:2511:A:H2'	1:0:2512:U:O4'	2.00	0.61
1:0:1603:A:C5'	1:0:1605:G:H5'	2.30	0.61
23:V:1:THR:HG23	23:V:2:VAL:H	1.65	0.61
1:0:308:U:C4	1:0:342:C:H1'	2.35	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1406:A:H4'	1:0:1407:A:H5''	1.81	0.61
1:0:2445:U:H2'	1:0:2446:G:C8	2.36	0.61
1:0:1528:A:H2'	1:0:1529:G:O4'	2.00	0.61
1:0:470:U:O2'	28:1:16:HIS:HD2	1.82	0.61
38:0:7359:HOH:O	12:K:45:PRO:HB2	2.01	0.61
1:0:2338:G:H1'	6:D:105:SER:OG	1.99	0.61
1:0:1234:U:N3	4:B:244:PRO:HB3	2.15	0.61
1:0:538:C:OP2	26:Y:134:HIS:HE1	1.84	0.61
12:K:81:ARG:HD3	12:K:87:ARG:NH2	2.15	0.61
18:Q:21:ARG:HA	38:Q:6597:HOH:O	2.00	0.61
2:9:3041:C:O4'	6:D:50:VAL:HG22	2.00	0.61
24:W:13:MET:HE1	24:W:18:GLN:HA	1.82	0.61
1:0:128:A:O2'	1:0:129:A:H5'	2.01	0.61
6:D:28:GLY:HA2	6:D:69:ILE:HG23	1.82	0.61
1:0:1477:C:H5'	1:0:1868:G:C5'	2.30	0.61
2:9:3064:C:H2'	2:9:3065:A:H5'	1.83	0.61
1:0:281:U:H2'	1:0:282:C:O4'	2.01	0.61
1:0:2507:G:H2'	1:0:2510:C:N4	2.16	0.61
24:W:137:GLN:NE2	24:W:141:HIS:HE1	1.98	0.61
2:9:3064:C:C2'	2:9:3065:A:H5'	2.31	0.61
8:F:50:VAL:HG13	8:F:60:VAL:HG11	1.82	0.61
1:0:1762:C:H2'	1:0:1763:C:H6	1.65	0.61
1:0:2433:A:H2'	1:0:2434:A:C8	2.36	0.61
10:H:27:LYS:H	10:H:59:HIS:CD2	2.19	0.61
1:0:2134:G:N2	1:0:2242:U:C2	2.69	0.60
1:0:656:G:OP2	16:O:37:ARG:HD2	2.00	0.60
3:A:88:ILE:HD13	3:A:100:PRO:HD3	1.81	0.60
2:9:3006:C:H5''	15:N:37:ARG:HH12	1.62	0.60
1:0:1130:U:H2'	1:0:1131:G:O4'	2.01	0.60
1:0:517:U:H1'	38:0:7561:HOH:O	2.00	0.60
1:0:338:C:H4'	5:C:174:ILE:HD11	1.83	0.60
20:S:11:THR:H	20:S:14:ALA:HB3	1.65	0.60
1:0:90:A:H2'	1:0:91:G:O4'	2.01	0.60
32:0:9000:13T:H262	32:0:9000:13T:O3	2.01	0.60
1:0:669:G:O2'	1:0:670:G:H5'	2.01	0.60
30:3:65:THR:HG23	30:3:67:LEU:HG	1.84	0.60
1:0:2659:U:H5''	38:0:4135:HOH:O	2.00	0.60
29:2:20:ARG:HG2	29:2:21:VAL:H	1.66	0.60
1:0:1118:A:C3'	1:0:1118:A:C8	2.70	0.60
27:Z:11:SER:HB3	27:Z:23:ARG:HB2	1.83	0.60
1:0:255:A:H2'	1:0:256:C:C6	2.36	0.60
1:0:602:A:O2'	1:0:605:C:H4'	2.01	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:510:U:H6	38:0:7427:HOH:O	1.85	0.60
1:0:1819:G:H2'	1:0:1820:G:H4'	1.83	0.60
1:0:2359:G:H3'	38:0:5701:HOH:O	2.01	0.60
1:0:512:G:O3'	1:0:513:A:H8	1.85	0.60
14:M:187:LEU:CD2	14:M:194:ALA:HB3	2.32	0.60
3:A:48:ASP:HB3	38:A:8897:HOH:O	2.02	0.60
6:D:103:ASN:ND2	6:D:133:ASN:HA	2.17	0.59
1:0:2301:A:H5''	1:0:2302:A:H5'	1.84	0.59
1:0:255:A:H2'	1:0:256:C:H6	1.66	0.59
4:B:214:PRO:HD2	38:B:8820:HOH:O	2.02	0.59
6:D:65:GLU:HA	38:D:4069:HOH:O	2.02	0.59
27:Z:22:SER:O	27:Z:26:VAL:HG23	2.01	0.59
1:0:1202:A:H2'	1:0:1203:G:H5'	1.85	0.59
6:D:50:VAL:O	6:D:71:ALA:HA	2.02	0.59
1:0:1525:G:H5'	1:0:1526:A:OP2	2.02	0.59
1:0:450:C:OP1	5:C:184:ARG:NH2	2.34	0.59
1:0:1266:U:H4'	26:Y:115:ARG:HH21	1.66	0.59
32:0:9000:13T:H3	30:3:56:PRO:HB2	1.83	0.59
1:0:1741:U:O2'	1:0:2723:G:H4'	2.02	0.59
2:9:3039:U:H3'	2:9:3040:C:C5'	2.32	0.59
4:B:86:ALA:HA	38:B:8876:HOH:O	2.01	0.59
7:E:15:GLN:HG3	7:E:20:ILE:HG12	1.83	0.59
19:R:111:ILE:HG23	19:R:145:LEU:HD11	1.83	0.59
27:Z:42:CYS:SG	27:Z:43:GLY:N	2.75	0.59
14:M:114:VAL:HG23	36:M:8818:CL:CL	2.39	0.59
4:B:212:GLN:HB2	4:B:257:THR:CG2	2.33	0.59
1:0:1504:A:H5'	38:0:4423:HOH:O	2.02	0.59
1:0:1060:C:H6	1:0:1060:C:H5'	1.65	0.59
11:J:45:VAL:HG21	11:J:129:PHE:CD1	2.38	0.59
1:0:966:U:H5'	38:0:3861:HOH:O	2.01	0.59
1:0:2807:U:P	4:B:27:ASN:HD21	2.24	0.59
1:0:1163:G:H2'	1:0:1164:U:C5	2.37	0.59
23:V:12:THR:HG23	23:V:14:ALA:H	1.68	0.59
1:0:249:G:O2'	1:0:250:C:H5'	2.03	0.59
1:0:1183:C:N3	1:0:1184:C:C5	2.71	0.59
8:F:58:GLU:HG3	8:F:61:MET:HE1	1.85	0.59
23:V:49:LEU:O	23:V:53:ILE:HG13	2.01	0.59
7:E:100:ASP:HB2	38:E:2789:HOH:O	2.02	0.59
1:0:1167:G:O2'	1:0:1168:C:H5'	2.02	0.59
1:0:1736:A:H1'	38:0:7569:HOH:O	2.03	0.59
1:0:2781:U:H2'	1:0:2782:G:C5'	2.31	0.59
10:H:3:ALA:HA	10:H:58:ARG:HH12	1.67	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:0:9354:HOH:O	28:1:1:THR:HA	2.03	0.59
1:0:84:G:O2'	1:0:85:C:H5'	2.02	0.59
14:M:30:GLU:O	14:M:34:GLU:HG3	2.02	0.59
1:0:39:G:N2	1:0:444:C:C2	2.71	0.59
27:Z:44:GLU:HG2	27:Z:46:ARG:HD2	1.85	0.59
1:0:2851:G:C2'	1:0:2852:A:H5'	2.32	0.59
1:0:947:U:H2'	1:0:948:G:C8	2.38	0.59
1:0:121:U:OP2	29:2:10:ARG:NH2	2.35	0.59
35:0:8542:NA:NA	38:0:3317:HOH:O	1.75	0.59
1:0:316:A:N3	1:0:336:G:O2'	2.34	0.59
1:0:364:C:H2'	1:0:365:G:O4'	2.03	0.58
15:N:86:LEU:HD12	15:N:125:ALA:HB2	1.85	0.58
8:F:63:ILE:HB	8:F:64:PRO:HD3	1.84	0.58
1:0:2676:C:H4'	11:J:70:PHE:HE1	1.66	0.58
11:J:107:ASN:ND2	11:J:109:TYR:H	2.01	0.58
1:0:1014:A:H2'	1:0:1015:C:H5'	1.85	0.58
1:0:1015:C:H2'	1:0:1016:U:H6	1.67	0.58
12:K:34:VAL:HG22	12:K:47:ALA:HB2	1.85	0.58
31:I:132:CYS:HB3	31:I:137:VAL:HB	1.83	0.58
1:0:1202:A:C2'	1:0:1203:G:H5'	2.33	0.58
1:0:2252:A:C5	1:0:2253:G:H1'	2.36	0.58
25:X:43:VAL:HG12	25:X:44:ASP:H	1.69	0.58
5:C:139:VAL:HG13	38:C:8648:HOH:O	2.02	0.58
19:R:14:ALA:HB3	19:R:147:LEU:HB2	1.86	0.58
1:0:1377:C:H5'	1:0:1377:C:C6	2.38	0.58
3:A:94:LEU:HD12	3:A:98:GLU:HB2	1.84	0.58
5:C:180:SER:HB2	38:C:8645:HOH:O	2.02	0.58
24:W:21:LEU:HD21	24:W:48:VAL:CG1	2.32	0.58
3:A:100:PRO:HG2	3:A:103:VAL:HG21	1.85	0.58
2:9:3035:C:H5''	38:9:4078:HOH:O	2.03	0.58
16:O:42:GLU:HB2	38:O:2176:HOH:O	2.04	0.58
13:L:136:ALA:HB3	38:L:8872:HOH:O	2.03	0.58
1:0:1168:C:H4'	38:I:5128:HOH:O	2.04	0.58
1:0:87:C:H2'	29:2:28:LYS:O	2.04	0.58
1:0:2816:A:H5''	1:0:2817:G:H5'	1.86	0.58
1:0:42:C:H3'	38:0:4179:HOH:O	2.03	0.58
5:C:5:ILE:HD11	5:C:16:VAL:CG2	2.31	0.58
4:B:25:ARG:HA	4:B:310:ARG:HH21	1.68	0.58
13:L:143:THR:HG22	13:L:144:ASP:N	2.18	0.58
1:0:1182:C:H1'	1:0:1192:A:H8	1.69	0.58
1:0:282:C:H1'	1:0:368:C:H42	1.69	0.58
15:N:144:GLY:O	15:N:147:ILE:HG22	2.02	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:J:103:VAL:HG12	38:J:8868:HOH:O	2.03	0.58
1:0:661:G:C5	1:0:686:A:C2	2.92	0.58
6:D:22:VAL:HG22	6:D:74:THR:HG22	1.84	0.58
1:0:2703:A:H2'	1:0:2704:C:H6	1.67	0.58
4:B:195:ARG:HG2	4:B:323:LEU:HD22	1.86	0.58
2:9:3057:A:H8	6:D:141:VAL:HG21	1.69	0.57
1:0:875:A:C2	3:A:194:MET:SD	2.97	0.57
28:1:21:ARG:HD2	28:1:37:CYS:SG	2.44	0.57
1:0:2613:G:O2'	1:0:2614:C:H5'	2.04	0.57
8:F:53:ASP:OD1	8:F:80:GLN:HB2	2.05	0.57
1:0:1183:C:O2	1:0:1183:C:H2'	2.03	0.57
7:E:68:HIS:O	7:E:72:MET:HG3	2.04	0.57
10:H:63:GLU:HA	38:H:8582:HOH:O	2.03	0.57
11:J:107:ASN:HD21	11:J:109:TYR:HB2	1.68	0.57
38:0:7344:HOH:O	26:Y:149:GLN:HG3	2.02	0.57
4:B:320:GLN:HE21	4:B:321:PRO:HD2	1.70	0.57
11:J:131:THR:HB	11:J:134:GLU:HG3	1.85	0.57
1:0:2498:C:O2'	1:0:2499:U:H5'	2.04	0.57
1:0:877:G:C5'	1:0:878:G:OP1	2.49	0.57
4:B:258:GLY:H	4:B:260:HIS:CE1	2.21	0.57
1:0:2478:U:O2'	1:0:2479:A:H5'	2.04	0.57
1:0:1202:A:H2'	1:0:1203:G:C5'	2.34	0.57
1:0:1835:U:C5	1:0:1840:A:N7	2.67	0.57
14:M:24:GLN:NE2	14:M:27:ARG:HH11	2.02	0.57
1:0:1972:U:H2'	1:0:1973:A:C5'	2.35	0.57
1:0:2256:G:O2'	1:0:2257:G:H5'	2.04	0.57
1:0:1226:G:H5'	38:0:4537:HOH:O	2.05	0.57
2:9:3072:C:O2'	2:9:3073:G:H5'	2.05	0.57
7:E:137:ASP:OD1	7:E:139:GLU:HB2	2.05	0.57
1:0:92:G:H4'	23:V:44:GLY:HA3	1.87	0.57
30:3:70:ARG:HG2	30:3:77:ALA:HB2	1.85	0.57
1:0:31:C:H2'	38:0:7673:HOH:O	2.03	0.57
24:W:88:THR:HG23	24:W:110:GLN:HB3	1.85	0.57
1:0:671:A:O2'	1:0:672:G:H2'	2.05	0.57
23:V:64:GLY:O	23:V:65:ASP:HB2	2.03	0.57
1:0:1028:U:H1'	38:0:3649:HOH:O	2.04	0.57
4:B:254:GLN:HG2	4:B:255:GLY:N	2.19	0.57
1:0:1654:U:H2'	3:A:47:HIS:HD2	1.70	0.57
2:9:3095:C:O2'	2:9:3096:C:H5'	2.05	0.57
1:0:1118:A:H8	1:0:1119:G:H5"	1.69	0.57
2:9:3091:C:H1'	38:9:7454:HOH:O	2.04	0.57
1:0:2676:C:H4'	11:J:70:PHE:CD1	2.39	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:O:32:ARG:HH21	16:O:35:LYS:NZ	2.03	0.57
1:O:1015:C:H2'	1:O:1016:U:C6	2.40	0.57
1:O:1393:A:H2'	1:O:1394:C:C6	2.40	0.57
30:3:11:CYS:HB2	30:3:20:HIS:CE1	2.40	0.57
1:O:88:G:H5'	1:O:88:G:H8	1.70	0.57
1:O:1291:A:H2	38:O:5297:HOH:O	1.86	0.57
1:O:2781:U:O2'	1:O:2782:G:H5'	2.05	0.57
10:H:138:CYS:HB2	38:H:8544:HOH:O	2.03	0.57
4:B:152:PRO:HA	38:B:8866:HOH:O	2.04	0.57
1:O:1193:A:C2	1:O:1194:A:N6	2.73	0.56
1:O:2291:A:N9	1:O:2309:C:H5'	2.20	0.56
1:O:820:G:O2'	1:O:856:G:H4'	2.05	0.56
2:9:3052:A:H2'	2:9:3053:G:O4'	2.05	0.56
2:9:3057:A:C8	6:D:141:VAL:HG21	2.40	0.56
10:H:26:SER:HA	10:H:59:HIS:HD2	1.70	0.56
4:B:225:GLY:HA3	38:B:8863:HOH:O	2.05	0.56
1:O:564:G:H1'	38:O:6311:HOH:O	2.03	0.56
3:A:217:ARG:HG2	3:A:229:ALA:HB2	1.87	0.56
1:O:1201:C:H2'	1:O:1202:A:H5'	1.86	0.56
24:W:139:GLY:O	24:W:141:HIS:HD2	1.89	0.56
1:O:2756:U:N3	1:O:2896:A:H2	2.02	0.56
2:9:3044:A:O4'	6:D:76:ARG:NE	2.38	0.56
26:Y:187:VAL:HG23	26:Y:192:ASP:HB3	1.86	0.56
1:O:2445:U:H2'	1:O:2446:G:H8	1.69	0.56
3:A:99:ILE:O	3:A:131:HIS:HE1	1.87	0.56
21:T:64:ASN:HB3	21:T:73:HIS:HB2	1.88	0.56
1:O:2604:A:H5'	38:O:5801:HOH:O	2.05	0.56
1:O:2385:G:H2'	1:O:2386:U:C6	2.40	0.56
15:N:147:ILE:HB	38:N:8842:HOH:O	2.04	0.56
1:O:941:G:O2'	1:O:942:U:H5'	2.04	0.56
2:9:3049:G:O2'	2:9:3050:G:H5'	2.06	0.56
4:B:254:GLN:HG3	38:B:8828:HOH:O	2.06	0.56
8:F:91:VAL:HG12	8:F:92:GLY:N	2.20	0.56
1:O:1154:A:H2'	1:O:1155:G:C8	2.40	0.56
20:S:43:GLU:HB3	38:S:8546:HOH:O	2.04	0.56
1:O:870:G:OP2	3:A:3:ARG:HD3	2.06	0.56
38:O:5467:HOH:O	9:G:12:ILE:HA	2.05	0.56
1:O:1717:A:H5''	17:P:54:LYS:HB2	1.88	0.56
1:O:776:A:OP1	28:1:28:HIS:HE1	1.87	0.56
1:O:1181:A:C2	1:O:1192:A:C8	2.94	0.56
12:K:29:LEU:HB3	12:K:55:VAL:CG1	2.31	0.56
24:W:88:THR:HG23	24:W:110:GLN:NE2	2.21	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:O:32:ARG:HD3	16:O:32:ARG:O	2.05	0.56
1:0:1329:A:H2	38:0:4691:HOH:O	1.89	0.56
1:0:821:U:H5''	38:0:3050:HOH:O	2.05	0.56
25:X:43:VAL:HG11	25:X:82:GLU:HA	1.86	0.56
1:0:111:C:O2'	28:1:20:ARG:HG2	2.06	0.56
8:F:36:THR:HG23	8:F:97:ALA:HB2	1.88	0.56
1:0:2064:U:H5'	1:0:2652:U:O3'	2.06	0.56
1:0:380:A:OP2	14:M:9:ARG:HD2	2.06	0.56
1:0:573:A:O2'	1:0:574:C:H5'	2.06	0.56
1:0:1527:A:H1'	1:0:1528:A:C8	2.41	0.56
1:0:1167:G:H4'	31:I:135:LEU:HD22	1.88	0.56
28:1:8:GLN:HE22	28:1:11:LYS:HZ2	1.54	0.56
24:W:108:ARG:HH21	24:W:114:PRO:HG2	1.71	0.56
1:0:2403:C:H2'	1:0:2404:G:O5'	2.06	0.56
22:U:47:ARG:HG2	38:U:4381:HOH:O	2.05	0.56
21:T:71:VAL:HG11	21:T:90:PRO:CB	2.33	0.56
5:C:114:ALA:HB1	5:C:223:LEU:HB3	1.88	0.56
1:0:2255:A:N1	1:0:2256:G:C4	2.74	0.56
1:0:1167:G:H2'	1:0:1168:C:O4'	2.06	0.56
2:9:3006:C:C5'	15:N:37:ARG:NH1	2.58	0.56
1:0:1172:G:H1'	38:0:4978:HOH:O	2.05	0.56
1:0:21:G:H4'	19:R:2:ILE:HG22	1.88	0.56
12:K:74:VAL:HG11	12:K:113:ILE:HG12	1.88	0.56
10:H:20:ILE:HG23	10:H:120:ILE:HD11	1.87	0.56
38:0:9539:HOH:O	17:P:81:LYS:HG2	2.05	0.56
5:C:65:ARG:HG3	5:C:67:GLN:HB2	1.88	0.55
1:0:1377:C:H2'	1:0:1723:G:O6	2.06	0.55
1:0:1168:C:H5''	31:I:87:THR:HG22	1.88	0.55
3:A:105:VAL:CG1	3:A:154:ALA:HB1	2.36	0.55
2:9:3106:C:O2'	2:9:3107:C:H5'	2.07	0.55
6:D:159:PRO:O	6:D:163:VAL:HG23	2.06	0.55
3:A:192:VAL:HG12	3:A:207:GLN:HB3	1.89	0.55
1:0:333:G:O2'	1:0:334:G:H5'	2.06	0.55
4:B:62:ARG:HA	4:B:65:MET:HE3	1.87	0.55
1:0:2670:G:O2'	1:0:2671:U:H5'	2.05	0.55
25:X:74:ALA:HB2	25:X:85:VAL:HG13	1.88	0.55
38:0:6860:HOH:O	3:A:211:LYS:HD3	2.07	0.55
20:S:57:THR:HG22	20:S:59:ASP:N	2.18	0.55
4:B:79:MET:HE1	38:B:8921:HOH:O	2.06	0.55
1:0:1309:U:O2'	1:0:1310:U:H5'	2.06	0.55
6:D:149:ARG:HH12	15:N:15:GLU:HA	1.72	0.55
22:U:39:ASN:ND2	22:U:44:ARG:HH11	2.05	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:W:6:GLN:HB2	24:W:26:ILE:CD1	2.36	0.55
2:9:3001:U:H5''	2:9:3003:A:OP1	2.07	0.55
1:0:2839:C:H2'	1:0:2840:A:H5''	1.88	0.55
24:W:88:THR:HG22	24:W:89:ASP:N	2.20	0.55
1:0:1873:G:H3'	38:0:5213:HOH:O	2.06	0.55
26:Y:133:HIS:HD2	38:Y:8881:HOH:O	1.88	0.55
1:0:1180:U:H2'	1:0:1181:A:O4'	2.07	0.55
7:E:137:ASP:O	7:E:141:VAL:HG23	2.06	0.55
1:0:926:A:O2'	13:L:41:HIS:CD2	2.60	0.55
5:C:246:ARG:NE	38:C:8623:HOH:O	2.38	0.55
8:F:27:GLY:HA3	8:F:101:ALA:O	2.07	0.55
1:0:1169:U:H2'	1:0:1170:U:O4'	2.07	0.55
22:U:52:THR:CG2	22:U:54:THR:HB	2.37	0.55
1:0:960:G:N3	1:0:960:G:C2'	2.69	0.55
1:0:1687:C:O2	28:1:9:GLY:HA2	2.06	0.55
5:C:72:LYS:HG2	5:C:77:ALA:HA	1.88	0.55
1:0:553:G:P	26:Y:204:ARG:HH22	2.30	0.55
1:0:559:U:C5'	1:0:559:U:H6	2.18	0.55
1:0:958:G:H2'	1:0:959:C:H6	1.72	0.55
29:2:20:ARG:HG2	29:2:21:VAL:N	2.22	0.55
1:0:88:G:H2'	1:0:89:G:C8	2.41	0.55
4:B:62:ARG:HA	4:B:65:MET:CE	2.37	0.55
5:C:77:ALA:O	5:C:78:ARG:HD2	2.06	0.55
1:0:1132:A:N6	1:0:1229:C:H2'	2.22	0.55
1:0:621:C:H5'	26:Y:132:ASP:OD2	2.07	0.55
1:0:1118:A:C8	1:0:1119:G:H5''	2.41	0.55
1:0:947:U:H2'	1:0:948:G:H8	1.70	0.55
1:0:941:G:C5	1:0:942:U:C4	2.95	0.55
5:C:236:THR:H	5:C:239:ALA:HB3	1.72	0.55
1:0:856:G:C8	38:0:5435:HOH:O	2.54	0.55
1:0:902:G:N7	13:L:18:HIS:HD2	2.06	0.55
8:F:58:GLU:CD	14:M:27:ARG:HH22	2.10	0.54
5:C:129:HIS:HE1	5:C:231:ARG:HA	1.69	0.54
1:0:1790:C:H2'	1:0:1791:U:C6	2.40	0.54
1:0:65:C:O2'	1:0:66:G:H5'	2.07	0.54
38:0:4844:HOH:O	11:J:47:THR:HB	2.07	0.54
1:0:2456:A:H5'	38:0:5705:HOH:O	2.06	0.54
24:W:125:HIS:HE1	38:W:3071:HOH:O	1.91	0.54
26:Y:187:VAL:HG23	26:Y:192:ASP:HB2	1.87	0.54
4:B:41:PHE:HA	4:B:79:MET:HE2	1.90	0.54
1:0:120:A:H2'	1:0:120:A:N3	2.22	0.54
1:0:2090:G:H2'	1:0:2091:G:C8	2.41	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1588:G:C6	1:0:1589:G:N1	2.75	0.54
14:M:24:GLN:HE22	14:M:27:ARG:HH11	1.55	0.54
1:0:255:A:C5	1:0:256:C:C4	2.96	0.54
31:I:113:HIS:N	31:I:114:PRO:HD2	2.22	0.54
25:X:21:PRO:HG2	25:X:24:LYS:HD3	1.88	0.54
1:0:1137:G:H1'	38:0:3885:HOH:O	2.07	0.54
3:A:33:GLU:O	3:A:34:ASP:HB2	2.07	0.54
1:0:468:U:H3'	38:0:7553:HOH:O	2.07	0.54
2:9:3076:G:C3'	2:9:3077:A:H5''	2.30	0.54
1:0:2780:C:H1'	7:E:143:GLN:NE2	2.22	0.54
19:R:111:ILE:HG23	19:R:145:LEU:CD1	2.37	0.54
1:0:2266:A:OP2	14:M:90:ARG:NH2	2.41	0.54
1:0:2425:A:H2'	38:0:9228:HOH:O	2.06	0.54
19:R:39:THR:HB	19:R:42:GLU:HG3	1.90	0.54
1:0:2826:G:C6	1:0:2913:A:N6	2.75	0.54
38:9:3472:HOH:O	15:N:41:LYS:HD3	2.08	0.54
1:0:2718:C:H6	1:0:2718:C:H5'	1.73	0.54
5:C:233:THR:HG22	5:C:234:VAL:N	2.21	0.54
8:F:29:VAL:HG12	8:F:98:VAL:HA	1.90	0.54
1:0:226:A:H1'	1:0:393:G:C5	2.43	0.54
1:0:705:C:H2'	1:0:705:C:O2	2.08	0.54
5:C:22:PHE:HA	5:C:116:ALA:HA	1.88	0.54
21:T:53:GLY:HA3	38:T:6384:HOH:O	2.08	0.54
5:C:236:THR:CG2	5:C:239:ALA:H	2.11	0.54
1:0:1171:A:H2'	1:0:1172:G:H5'	1.90	0.54
1:0:506:G:N2	1:0:509:A:H5''	2.16	0.54
1:0:1603:A:H5'	1:0:1605:G:C4'	2.38	0.54
2:9:3003:A:OP2	2:9:3025:G:N2	2.40	0.54
1:0:1595:G:O2'	1:0:1596:U:H5'	2.08	0.54
8:F:21:GLU:O	8:F:24:ARG:HG2	2.07	0.54
1:0:2346:C:O5'	1:0:2346:C:H6	1.90	0.54
1:0:1783:A:O2'	1:0:1784:U:H5'	2.08	0.54
1:0:2001:G:O2'	1:0:2002:C:H5'	2.07	0.54
1:0:2587:OMU:H2'	1:0:2589:U:H5''	1.88	0.54
10:H:46:GLN:HG3	10:H:137:TYR:CE2	2.43	0.54
1:0:1667:A:H2'	1:0:1668:U:H6	1.72	0.54
2:9:3076:G:H3'	2:9:3077:A:C5'	2.28	0.54
5:C:1:MET:HG2	5:C:2:GLN:N	2.21	0.54
12:K:118:ALA:HA	12:K:125:ALA:HB2	1.90	0.54
38:0:4623:HOH:O	16:O:39:THR:HB	2.07	0.54
2:9:3055:U:H4'	2:9:3056:A:C8	2.43	0.54
38:0:4376:HOH:O	3:A:212:PRO:HB2	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:J:75:PRO:HG2	11:J:105:LEU:CD2	2.38	0.54
1:0:1568:G:O2'	1:0:1569:U:H5'	2.07	0.54
1:0:1421:C:H2'	1:0:1422:U:H6	1.73	0.54
1:0:1446:U:H2'	20:S:55:GLN:NE2	2.23	0.54
1:0:1450:C:C4'	1:0:1451:C:OP2	2.53	0.54
1:0:1319:G:H1'	38:0:4701:HOH:O	2.07	0.54
8:F:117:GLU:C	8:F:119:ARG:H	2.10	0.54
1:0:1931:A:H2'	1:0:1932:G:H5'	1.90	0.54
5:C:236:THR:HA	38:C:8651:HOH:O	2.08	0.54
3:A:51:ARG:NH1	3:A:120:ARG:O	2.41	0.54
1:0:1762:C:H2'	1:0:1763:C:C6	2.43	0.54
1:0:2064:U:H4'	1:0:2653:A:OP1	2.08	0.54
1:0:328:U:O4'	5:C:202:THR:HG22	2.07	0.54
5:C:118:THR:O	5:C:136:VAL:HG13	2.08	0.54
1:0:794:U:H3	1:0:819:A:H61	1.54	0.54
17:P:91:LYS:O	17:P:95:GLU:HG3	2.08	0.54
1:0:1173:A:H2	38:0:6282:HOH:O	1.91	0.54
1:0:645:U:OP2	13:L:4:LYS:HE2	2.08	0.54
1:0:820:G:H5'	1:0:821:U:H5'	1.90	0.53
4:B:26:PHE:CE1	4:B:310:ARG:HB3	2.43	0.53
1:0:841:A:H5''	38:0:6906:HOH:O	2.08	0.53
1:0:1396:C:H1'	17:P:1:THR:O	2.08	0.53
1:0:1677:U:OP2	29:2:8:LYS:NZ	2.38	0.53
1:0:125:U:H2'	38:0:3769:HOH:O	2.07	0.53
1:0:1053:G:OP1	10:H:12:PRO:HG3	2.08	0.53
1:0:424:C:H2'	1:0:425:U:C6	2.43	0.53
1:0:349:U:O2'	1:0:350:C:H5'	2.09	0.53
4:B:279:THR:OG1	4:B:290:VAL:HB	2.08	0.53
4:B:74:ILE:HG22	4:B:76:THR:HG23	1.91	0.53
1:0:2488:A:H61	1:0:2534:C:H42	1.54	0.53
1:0:2361:A:H8	1:0:2361:A:H5'	1.73	0.53
19:R:18:LEU:HB2	19:R:143:VAL:CG1	2.36	0.53
23:V:4:HIS:O	23:V:8:ILE:HG13	2.08	0.53
1:0:1444:G:O2'	1:0:1445:G:H5'	2.08	0.53
20:S:57:THR:HG22	20:S:59:ASP:HB2	1.90	0.53
1:0:40:C:H4'	38:0:6998:HOH:O	2.08	0.53
1:0:660:A:H4'	1:0:661:G:O5'	2.08	0.53
22:U:9:CYS:HA	22:U:52:THR:HG23	1.90	0.53
1:0:399:C:H5'	14:M:179:GLY:O	2.09	0.53
1:0:2472:C:O2'	1:0:2634:G:H4'	2.08	0.53
1:0:2784:A:H1'	7:E:60:SER:OG	2.08	0.53
8:F:56:PRO:HG2	14:M:43:PRO:O	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2526:C:H5'	1:0:2526:C:C6	2.43	0.53
4:B:162:MET:CE	4:B:308:LEU:HD21	2.39	0.53
1:0:2064:U:H5'	1:0:2652:U:H4'	1.91	0.53
24:W:64:THR:O	24:W:68:THR:HG22	2.08	0.53
24:W:48:VAL:HG12	24:W:52:VAL:HB	1.90	0.53
1:0:271:C:H4'	1:0:272:A:OP1	2.08	0.53
18:Q:11:ARG:HD3	38:Q:5620:HOH:O	2.08	0.53
4:B:23:THR:HG23	4:B:308:LEU:HD23	1.91	0.53
11:J:46:ILE:HA	38:J:8828:HOH:O	2.09	0.53
24:W:68:THR:HG23	24:W:69:ARG:HG2	1.91	0.53
8:F:96:ALA:HA	38:F:3111:HOH:O	2.09	0.53
5:C:40:ALA:O	5:C:43:LYS:HB2	2.08	0.53
1:0:2735:U:H2'	1:0:2736:U:C6	2.44	0.53
1:0:622:G:O2'	1:0:623:U:H5'	2.08	0.53
1:0:2382:A:H5'	38:3:8831:HOH:O	2.09	0.53
1:0:821:U:H2'	1:0:822:C:C6	2.41	0.53
1:0:420:U:H2'	1:0:421:C:C6	2.44	0.53
31:I:103:ASP:HA	31:I:106:LYS:HD2	1.91	0.53
17:P:14:LEU:HD13	17:P:51:ALA:HB2	1.91	0.53
1:0:1314:U:H2'	38:0:5885:HOH:O	2.09	0.53
1:0:2071:C:H5'	38:0:9529:HOH:O	2.09	0.53
17:P:105:LEU:HD21	17:P:137:LEU:HD11	1.90	0.53
24:W:129:LYS:HG2	38:W:1990:HOH:O	2.07	0.53
20:S:52:VAL:HG22	20:S:66:VAL:HG22	1.90	0.53
1:0:282:C:O2'	1:0:283:U:C5'	2.53	0.53
6:D:163:VAL:HA	38:D:6326:HOH:O	2.07	0.53
6:D:166:ILE:HB	38:D:6326:HOH:O	2.09	0.53
1:0:12:U:C2'	1:0:13:G:H5'	2.38	0.53
1:0:2781:U:H1'	7:E:139:GLU:OE2	2.09	0.53
1:0:1342:C:O2'	1:0:1343:C:H5'	2.09	0.53
1:0:1855:G:H4'	1:0:1856:C:O5'	2.09	0.53
1:0:2081:A:H4'	11:J:69:TYR:CE1	2.44	0.53
1:0:1456:C:H2'	1:0:1457:U:C6	2.44	0.53
1:0:1181:A:N1	1:0:1192:A:O2'	2.38	0.53
1:0:1213:C:C2'	1:0:1214:G:H5'	2.39	0.53
9:G:64:ASN:N	9:G:64:ASN:HD22	2.06	0.53
1:0:2694:A:H4'	7:E:91:PHE:CE1	2.43	0.53
1:0:2548:C:OP2	4:B:5:ARG:NH2	2.42	0.53
21:T:32:ARG:NH1	21:T:38:ARG:HH12	2.07	0.53
1:0:1159:G:H21	1:0:1189:A:H8	1.55	0.53
6:D:135:VAL:HG22	6:D:136:ARG:H	1.74	0.53
28:1:8:GLN:HE22	28:1:11:LYS:NZ	2.06	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1309:U:C2'	1:0:1310:U:H5'	2.40	0.53
1:0:1236:A:H2'	1:0:1237:U:O4'	2.09	0.53
1:0:2269:C:C2'	1:0:2270:G:H5'	2.39	0.53
1:0:1104:C:H4'	11:J:88:PRO:HD3	1.89	0.53
15:N:43:VAL:HG13	15:N:118:ILE:HD11	1.89	0.53
10:H:56:GLN:HE21	10:H:126:ARG:NE	2.00	0.52
1:0:1733:A:H4'	4:B:212:GLN:HA	1.90	0.52
1:0:2251:G:H2'	1:0:2252:A:C8	2.43	0.52
1:0:625:U:H5''	1:0:1044:C:N4	2.24	0.52
12:K:34:VAL:CG2	12:K:47:ALA:HB2	2.39	0.52
22:U:46:ALA:HB1	22:U:52:THR:HG21	1.90	0.52
2:9:3031:C:H2'	2:9:3032:G:O4'	2.10	0.52
1:0:204:A:C2'	1:0:205:U:H5'	2.38	0.52
5:C:57:PRO:HG2	5:C:73:LEU:HD13	1.91	0.52
1:0:2837:U:H2'	38:0:6833:HOH:O	2.08	0.52
2:9:3060:C:O2'	2:9:3061:C:H5'	2.09	0.52
14:M:169:ARG:HD2	38:M:8886:HOH:O	2.09	0.52
4:B:16:ARG:NH1	38:B:8913:HOH:O	2.42	0.52
1:0:2737:C:OP2	17:P:61:ARG:NH2	2.38	0.52
1:0:371:U:H2'	1:0:372:A:H8	1.75	0.52
1:0:1588:G:C6	1:0:1589:G:C6	2.98	0.52
1:0:603:A:H4'	1:0:604:G:O5'	2.09	0.52
10:H:69:ALA:HB2	10:H:153:ALA:HB2	1.90	0.52
20:S:76:GLU:HB3	38:S:8547:HOH:O	2.09	0.52
15:N:38:LYS:HE2	15:N:107:ASN:ND2	2.24	0.52
1:0:544:G:H2'	1:0:545:G:C5'	2.40	0.52
1:0:2601:A:N1	12:K:38:SER:HB2	2.25	0.52
1:0:2894:C:O2'	1:0:2895:C:H5'	2.09	0.52
1:0:1010:C:H4'	15:N:4:PRO:HB2	1.91	0.52
1:0:1972:U:C2'	1:0:1973:A:H5''	2.39	0.52
1:0:1755:A:H2'	1:0:1756:G:O4'	2.09	0.52
1:0:2237:G:H1'	38:0:4862:HOH:O	2.10	0.52
1:0:1766:U:O2	1:0:1778:A:H5'	2.09	0.52
1:0:1384:C:H5'	25:X:30:MET:HG2	1.92	0.52
19:R:33:ARG:NH1	38:R:8838:HOH:O	2.41	0.52
30:3:3:MET:O	30:3:90:PHE:HA	2.10	0.52
1:0:304:G:H1'	1:0:347:A:N6	2.24	0.52
1:0:289:G:N2	1:0:363:A:C2	2.57	0.52
1:0:2769:C:H2'	1:0:2770:G:O4'	2.10	0.52
2:9:3029:C:H2'	2:9:3030:C:C5'	2.36	0.52
14:M:24:GLN:NE2	14:M:27:ARG:NH1	2.57	0.52
1:0:1421:C:H2'	1:0:1422:U:C6	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:D:82:GLU:HA	6:D:85:GLN:HE21	1.74	0.52
21:T:26:THR:HA	21:T:39:ASN:HB3	1.91	0.52
1:0:1641:A:H2'	1:0:1642:A:C5'	2.33	0.52
24:W:88:THR:HG22	24:W:90:TYR:HD1	1.74	0.52
4:B:312:ARG:HD3	4:B:315:VAL:HG13	1.90	0.52
1:0:707:C:C2	1:0:708:A:C8	2.97	0.52
10:H:3:ALA:HA	10:H:58:ARG:NH1	2.25	0.52
13:L:148:GLU:HA	38:L:8871:HOH:O	2.10	0.52
7:E:49:ILE:HD11	7:E:69:ILE:HD12	1.91	0.52
1:0:1169:U:C5	1:0:1170:U:C4	2.97	0.52
1:0:204:A:H2'	1:0:205:U:H5'	1.91	0.52
1:0:346:U:H4'	38:0:6837:HOH:O	2.08	0.52
22:U:37:GLU:HB3	38:U:408:HOH:O	2.09	0.52
24:W:21:LEU:HD22	24:W:26:ILE:CD1	2.40	0.52
1:0:567:U:C5'	38:0:6400:HOH:O	2.57	0.52
1:0:951:A:O2'	1:0:952:G:H5'	2.10	0.52
9:G:23:ILE:O	9:G:27:ILE:HG13	2.10	0.52
1:0:2460:A:H5'	32:0:9000:13T:H231	1.90	0.52
4:B:307:ARG:HG3	4:B:307:ARG:NH1	2.16	0.52
1:0:1878:G:O2'	1:0:1879:U:P	2.68	0.52
1:0:2766:A:O2'	1:0:2767:C:H5'	2.10	0.52
1:0:262:A:OP2	8:F:91:VAL:HG11	2.10	0.52
1:0:1661:A:C8	38:0:5210:HOH:O	2.55	0.52
1:0:59:A:H5'	38:0:4342:HOH:O	2.09	0.52
4:B:162:MET:HE2	4:B:310:ARG:HD3	1.92	0.52
1:0:2880:A:H2'	1:0:2881:C:H5'	1.92	0.52
5:C:95:GLU:HG3	38:C:8673:HOH:O	2.09	0.52
14:M:164:THR:HG22	14:M:167:GLY:H	1.74	0.51
1:0:1119:G:H22	1:0:1246:A:H2	1.48	0.51
24:W:6:GLN:HB2	24:W:26:ILE:HD12	1.92	0.51
1:0:475:G:OP1	5:C:73:LEU:HD22	2.09	0.51
38:0:7541:HOH:O	30:3:60:LYS:HG3	2.10	0.51
2:9:3020:G:O2'	2:9:3021:G:H5'	2.10	0.51
1:0:291:C:H2'	1:0:292:G:O4'	2.10	0.51
1:0:2010:A:C2'	38:0:5968:HOH:O	2.50	0.51
1:0:2467:A:O2'	1:0:2468:A:H2'	2.10	0.51
1:0:2361:A:H5''	38:0:9001:HOH:O	2.08	0.51
38:0:4733:HOH:O	19:R:29:LYS:HD3	2.10	0.51
5:C:242:GLU:HB2	38:C:8579:HOH:O	2.09	0.51
1:0:2388:C:O2'	1:0:2389:U:H5'	2.10	0.51
1:0:285:A:H2'	1:0:286:U:O4'	2.11	0.51
8:F:91:VAL:HG12	8:F:92:GLY:H	1.76	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:64:G:H2'	1:0:65:C:O4'	2.10	0.51
1:0:119:A:H2'	1:0:120:A:H5''	1.93	0.51
1:0:2266:A:H2'	1:0:2267:G:C8	2.45	0.51
1:0:2694:A:H4'	7:E:91:PHE:HE1	1.74	0.51
1:0:254:C:O2	1:0:254:C:H2'	2.09	0.51
1:0:1500:U:P	17:P:41:ARG:HH22	2.33	0.51
1:0:1545:C:H2'	1:0:1546:G:O4'	2.10	0.51
14:M:102:GLU:OE1	14:M:164:THR:HG21	2.09	0.51
2:9:3092:G:C6	2:9:3093:A:C6	2.98	0.51
26:Y:189:ASN:HD22	26:Y:189:ASN:C	2.14	0.51
2:9:3034:A:H2'	2:9:3035:C:O4'	2.11	0.51
1:0:1391:G:H2'	1:0:1392:A:H5'	1.93	0.51
1:0:1398:G:O2'	1:0:1399:A:H5'	2.11	0.51
1:0:2036:C:O4'	12:K:44:LEU:HG	2.10	0.51
1:0:1594:C:OP2	17:P:120:ARG:HD2	2.11	0.51
18:Q:75:ILE:HD13	18:Q:84:ILE:HD11	1.93	0.51
27:Z:37:HIS:HB2	27:Z:47:VAL:HB	1.93	0.51
1:0:2887:G:H2'	1:0:2888:U:C6	2.45	0.51
15:N:132:ASN:O	15:N:135:VAL:HG12	2.09	0.51
1:0:894:A:C2	5:C:87:ARG:NH2	2.78	0.51
1:0:1249:U:H2'	1:0:1250:C:C6	2.46	0.51
1:0:714:U:H3'	38:0:6939:HOH:O	2.09	0.51
13:L:72:ASN:HB2	38:L:8881:HOH:O	2.09	0.51
4:B:85:ARG:NH1	38:B:8930:HOH:O	2.42	0.51
17:P:115:SER:N	17:P:118:GLN:HE21	2.00	0.51
3:A:101:GLU:OE2	3:A:131:HIS:HB2	2.10	0.51
17:P:134:VAL:O	17:P:137:LEU:HB3	2.11	0.51
11:J:54:VAL:HG11	11:J:138:THR:HG21	1.93	0.51
1:0:2379:G:N3	1:0:2418:G:H2'	2.25	0.51
1:0:2871:G:H2'	1:0:2872:U:C6	2.46	0.51
1:0:1559:A:OP2	1:0:1559:A:H8	1.92	0.51
1:0:558:C:H2'	1:0:559:U:H5''	1.88	0.51
2:9:3013:A:O2'	2:9:3014:G:H5''	2.11	0.51
1:0:2578:G:C8	1:0:2578:G:H5'	2.41	0.51
2:9:3039:U:H1'	2:9:3044:A:N6	2.26	0.51
1:0:1819:G:H5'	38:0:4720:HOH:O	2.09	0.51
7:E:69:ILE:HA	7:E:72:MET:CE	2.40	0.51
1:0:1314:U:H5''	1:0:1316:G:O4'	2.11	0.51
6:D:62:ASP:HA	38:D:4233:HOH:O	2.11	0.51
15:N:169:PRO:O	15:N:172:PHE:HB3	2.11	0.51
1:0:1163:G:H5'	31:I:115:ASP:O	2.10	0.51
1:0:1543:G:N1	1:0:1641:A:OP2	2.38	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1856:C:H5'	1:0:1858:A:O4'	2.10	0.51
1:0:589:U:H2'	1:0:590:A:H8	1.74	0.51
1:0:1787:C:H4'	1:0:2883:A:O4'	2.11	0.51
4:B:145:HIS:HD2	4:B:146:THR:O	1.94	0.51
20:S:17:ASP:HB3	20:S:23:LYS:HB2	1.92	0.51
1:0:324:G:C6	1:0:325:U:C5	2.99	0.51
1:0:482:G:H4'	1:0:508:A:N1	2.26	0.51
1:0:1116:U:O2'	1:0:1118:A:C2	2.50	0.51
29:2:40:ARG:HD2	29:2:47:THR:HG22	1.93	0.51
1:0:1878:G:C1'	38:0:6128:HOH:O	2.49	0.51
3:A:105:VAL:HG11	3:A:154:ALA:HB1	1.93	0.51
1:0:2893:C:O2'	1:0:2894:C:H5'	2.11	0.51
1:0:228:C:H2'	1:0:229:G:H5'	1.92	0.51
7:E:101:GLU:HB3	7:E:117:THR:HA	1.92	0.51
1:0:1119:G:H8	11:J:52:GLN:HE22	1.59	0.51
1:0:2765:C:H2'	1:0:2766:A:H8	1.76	0.51
26:Y:189:ASN:ND2	26:Y:192:ASP:H	2.08	0.51
1:0:329:A:OP2	5:C:206:ASN:HB2	2.11	0.51
1:0:1600:G:OP2	1:0:1600:G:H8	1.94	0.51
1:0:168:C:O5'	1:0:168:C:H6	1.93	0.51
5:C:132:ASP:HB3	38:C:8560:HOH:O	2.10	0.51
1:0:1119:G:H8	11:J:52:GLN:NE2	2.08	0.50
1:0:1586:G:O2'	1:0:1587:U:H5'	2.11	0.50
12:K:20:CYS:HB2	12:K:29:LEU:HG	1.93	0.50
1:0:2269:C:O2'	1:0:2270:G:H5'	2.11	0.50
1:0:2106:C:H5'	1:0:2284:G:H21	1.77	0.50
1:0:2135:A:O2'	1:0:2136:G:H5'	2.10	0.50
24:W:4:LEU:HB2	24:W:33:THR:HG22	1.92	0.50
6:D:103:ASN:HD22	6:D:134:LEU:H	1.57	0.50
1:0:710:G:C2'	1:0:711:G:H5'	2.41	0.50
28:1:28:HIS:CE1	28:1:31:LYS:HE2	2.46	0.50
1:0:2515:C:H2'	1:0:2516:G:O4'	2.11	0.50
1:0:1862:C:H1'	38:0:7211:HOH:O	2.10	0.50
4:B:314:ALA:HB3	4:B:317:PRO:HG3	1.93	0.50
26:Y:117:LEU:HD12	26:Y:174:VAL:CG1	2.41	0.50
1:0:17:G:H2'	1:0:18:C:C6	2.47	0.50
1:0:588:G:O6	24:W:154:ARG:NH1	2.43	0.50
1:0:1556:G:O2'	1:0:1557:G:H5'	2.11	0.50
1:0:814:G:H4'	38:0:3133:HOH:O	2.12	0.50
9:G:12:ILE:HG22	9:G:17:GLN:NE2	2.27	0.50
1:0:1413:A:H2'	1:0:1414:A:O4'	2.11	0.50
19:R:119:VAL:HG21	19:R:142:ASP:CG	2.31	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1287:A:O4'	24:W:117:ARG:HD3	2.12	0.50
32:0:9000:13T:C23	32:0:9000:13T:C31	2.90	0.50
1:0:1188:A:H5'	38:0:7415:HOH:O	2.11	0.50
11:J:107:ASN:HD22	11:J:107:ASN:C	2.14	0.50
1:0:1406:A:H4'	1:0:1407:A:C5'	2.42	0.50
31:I:78:LEU:HD12	31:I:112:LYS:NZ	2.26	0.50
12:K:82:ARG:NH2	12:K:115:ARG:HG2	2.26	0.50
2:9:3023:U:O2'	2:9:3024:U:H4'	2.11	0.50
1:0:2717:C:C2'	1:0:2718:C:C5'	2.78	0.50
1:0:2896:A:OP1	25:X:15:ARG:NH1	2.45	0.50
3:A:191:GLY:HA2	3:A:194:MET:HE2	1.94	0.50
1:0:1972:U:H2'	1:0:1973:A:H5'	1.94	0.50
1:0:1853:C:O2'	3:A:217:ARG:NH2	2.44	0.50
2:9:3104:A:O2'	2:9:3105:A:H5'	2.12	0.50
19:R:119:VAL:HG12	19:R:119:VAL:O	2.10	0.50
5:C:102:LEU:HD12	38:C:8515:HOH:O	2.11	0.50
1:0:1985:U:C2	1:0:1996:U:O4'	2.64	0.50
12:K:74:VAL:HG13	12:K:113:ILE:HG12	1.92	0.50
26:Y:189:ASN:HA	26:Y:217:ILE:HD11	1.93	0.50
1:0:84:G:C2'	1:0:85:C:H5'	2.42	0.50
1:0:240:C:O2	1:0:240:C:H2'	2.12	0.50
1:0:2664:A:OP1	1:0:2664:A:H8	1.95	0.50
6:D:172:VAL:HG12	6:D:173:GLU:N	2.27	0.50
13:L:24:ALA:HB2	13:L:30:ARG:HD2	1.93	0.50
4:B:232:TRP:CD1	4:B:235:ARG:HD2	2.46	0.50
1:0:793:A:H5''	17:P:83:LYS:HG2	1.94	0.50
3:A:96:LEU:HD22	3:A:128:LEU:HD13	1.94	0.50
28:1:10:LYS:HG3	38:1:8731:HOH:O	2.11	0.50
21:T:69:LYS:O	21:T:71:VAL:HG23	2.12	0.50
24:W:125:HIS:CD2	24:W:127:GLY:H	2.25	0.50
3:A:217:ARG:HH11	3:A:217:ARG:HG3	1.76	0.50
1:0:370:G:O2'	1:0:371:U:H5'	2.12	0.50
26:Y:203:VAL:HG12	26:Y:228:VAL:HG22	1.94	0.50
4:B:18:ARG:HG3	4:B:256:GLN:HG3	1.94	0.50
19:R:59:PHE:O	19:R:63:ASN:HB3	2.12	0.50
21:T:41:ARG:NH1	21:T:42:VAL:O	2.45	0.50
7:E:23:GLU:HG2	7:E:28:SER:HB3	1.93	0.50
1:0:363:A:O2'	1:0:364:C:H5'	2.12	0.50
1:0:2506:A:N6	1:0:2511:A:O2'	2.44	0.50
1:0:1207:A:C8	1:0:1208:C:C5	3.00	0.50
1:0:1878:G:O2'	1:0:1879:U:H6	1.93	0.50
1:0:2253:G:C2	1:0:2254:G:C8	3.00	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2779:G:H21	7:E:143:GLN:NE2	2.10	0.50
1:0:1130:U:H5'	38:0:7657:HOH:O	2.11	0.50
9:G:12:ILE:N	9:G:13:PRO:HD3	2.27	0.50
3:A:89:ALA:HB3	38:A:8913:HOH:O	2.11	0.50
1:0:2336:G:H1'	38:0:6297:HOH:O	2.12	0.50
3:A:125:ASN:HB3	3:A:158:VAL:HG12	1.93	0.50
5:C:214:THR:HG23	38:C:8636:HOH:O	2.10	0.50
1:0:2668:G:H2'	1:0:2669:U:C6	2.46	0.50
1:0:1163:G:N2	38:0:6056:HOH:O	2.45	0.50
27:Z:19:GLY:O	27:Z:23:ARG:HG2	2.11	0.50
1:0:1154:A:H2'	1:0:1155:G:H8	1.75	0.50
1:0:424:C:H2'	1:0:425:U:H6	1.77	0.50
25:X:25:ARG:HD3	25:X:64:ALA:O	2.12	0.50
10:H:47:ILE:HG12	10:H:165:SER:HA	1.93	0.50
1:0:93:C:H5''	23:V:1:THR:CB	2.33	0.49
21:T:71:VAL:HG12	21:T:72:ILE:N	2.27	0.49
1:0:2764:C:O2'	1:0:2765:C:H5'	2.12	0.49
8:F:48:VAL:CG2	8:F:74:PHE:HB3	2.42	0.49
15:N:43:VAL:HG11	15:N:81:ALA:HA	1.94	0.49
1:0:2831:C:H2'	1:0:2832:C:H5'	1.93	0.49
1:0:2296:C:H2'	1:0:2297:U:C6	2.47	0.49
1:0:635:A:H2'	1:0:636:G:H5''	1.92	0.49
13:L:80:ASP:HB2	13:L:90:ARG:O	2.12	0.49
2:9:3055:U:H4'	2:9:3056:A:H8	1.77	0.49
1:0:2896:A:N3	1:0:2896:A:H2'	2.28	0.49
1:0:710:G:O2'	1:0:711:G:H5'	2.12	0.49
4:B:26:PHE:HE1	4:B:310:ARG:HB3	1.77	0.49
5:C:168:ARG:NH2	5:C:190:ALA:O	2.45	0.49
1:0:1423:C:O2'	1:0:1424:A:H5'	2.12	0.49
10:H:162:ARG:HD3	38:H:8585:HOH:O	2.12	0.49
3:A:179:MET:HG2	3:A:186:TRP:CG	2.46	0.49
3:A:190:ARG:NH2	3:A:207:GLN:OE1	2.45	0.49
1:0:775:G:OP1	28:1:16:HIS:HE1	1.95	0.49
9:G:12:ILE:HG22	9:G:17:GLN:HE21	1.76	0.49
1:0:1497:G:H4'	1:0:1627:G:O2'	2.12	0.49
1:0:415:A:O2'	1:0:416:G:H5'	2.13	0.49
1:0:1909:A:N1	1:0:2128:G:H1'	2.26	0.49
13:L:134:GLU:HG3	38:L:8855:HOH:O	2.12	0.49
1:0:1642:A:C8	1:0:1643:C:C5	3.00	0.49
1:0:2363:G:O2'	18:Q:11:ARG:HG3	2.13	0.49
1:0:2493:C:O2	1:0:2493:C:H2'	2.11	0.49
3:A:153:ARG:HH11	3:A:153:ARG:HB2	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1008:C:H5''	10:H:16:ARG:HH12	1.76	0.49
1:0:2866:U:C5	22:U:50:GLU:HB2	2.47	0.49
1:0:451:C:O2'	1:0:452:G:H5'	2.12	0.49
1:0:2533:C:H6	1:0:2533:C:C5'	2.20	0.49
1:0:2004:U:H2'	1:0:2004:U:O2	2.11	0.49
1:0:1972:U:H2'	1:0:1973:A:H5''	1.93	0.49
10:H:27:LYS:H	10:H:59:HIS:HD2	1.59	0.49
1:0:946:C:H2'	1:0:947:U:C6	2.47	0.49
1:0:494:C:H2'	1:0:496:G:OP2	2.13	0.49
26:Y:107:PRO:HD3	26:Y:182:PHE:CE1	2.47	0.49
11:J:19:MET:HE2	11:J:79:PHE:HA	1.94	0.49
27:Z:53:GLY:HA2	27:Z:67:GLY:O	2.12	0.49
1:0:1474:C:C5'	1:0:1474:C:C6	2.81	0.49
1:0:1119:G:H2'	11:J:52:GLN:HE22	1.78	0.49
4:B:36:PRO:CA	4:B:168:GLY:HA3	2.38	0.49
11:J:75:PRO:HD3	11:J:136:SER:OG	2.13	0.49
4:B:267:LYS:HA	38:B:8824:HOH:O	2.11	0.49
1:0:920:C:H4'	1:0:921:G:C2	2.47	0.49
1:0:318:C:H5'	1:0:339:A:C2	2.48	0.49
1:0:251:C:O2'	1:0:252:C:H5'	2.12	0.49
1:0:2122:C:H3'	38:0:5295:HOH:O	2.13	0.49
1:0:710:G:OP1	16:O:24:ALA:HB3	2.13	0.49
1:0:2270:G:H4'	3:A:223:ARG:NH1	2.27	0.49
1:0:1488:U:H4'	1:0:1489:G:OP1	2.12	0.49
1:0:1681:G:H5''	1:0:1682:A:H5'	1.94	0.49
8:F:2:VAL:HG22	8:F:57:GLU:OE1	2.11	0.49
1:0:1278:A:H4'	1:0:1279:U:C4	2.48	0.49
1:0:645:U:O2	1:0:761:A:H2	1.96	0.49
1:0:2694:A:C6	1:0:2702:A:C8	3.01	0.49
1:0:1331:A:OP2	26:Y:142:SER:OG	2.27	0.49
38:0:5640:HOH:O	17:P:58:SER:HB3	2.11	0.49
10:H:51:VAL:HG13	10:H:159:PRO:HG3	1.95	0.49
4:B:36:PRO:HA	4:B:168:GLY:CA	2.39	0.49
1:0:558:C:H5'	38:0:5262:HOH:O	2.13	0.49
1:0:514:G:OP1	1:0:514:G:H2'	2.12	0.49
1:0:2316:G:H4'	38:0:6098:HOH:O	2.12	0.49
4:B:320:GLN:NE2	4:B:321:PRO:HD2	2.28	0.49
1:0:1422:U:H2'	1:0:1423:C:C6	2.48	0.49
1:0:1484:G:H2'	38:0:9098:HOH:O	2.13	0.49
28:1:25:LYS:O	28:1:25:LYS:HG2	2.13	0.49
1:0:152:A:O2'	1:0:153:C:H5'	2.13	0.49
1:0:2372:A:H2'	1:0:2373:U:C6	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2102:G:C2	1:0:2104:C:C4	3.01	0.49
26:Y:126:PRO:HG2	26:Y:128:PHE:CE1	2.48	0.49
4:B:294:TYR:HE2	38:B:8945:HOH:O	1.95	0.49
1:0:1834:C:H2'	1:0:1840:A:N6	2.27	0.49
1:0:949:U:O2'	18:Q:40:HIS:HE1	1.96	0.49
1:0:2300:A:H4'	1:0:2301:A:O5'	2.13	0.49
3:A:94:LEU:HG	3:A:99:ILE:CD1	2.43	0.49
1:0:1421:C:O2'	1:0:1422:U:H5'	2.13	0.49
38:0:6679:HOH:O	21:T:38:ARG:NH1	2.45	0.49
1:0:2387:U:H2'	1:0:2388:C:C6	2.48	0.49
38:0:6699:HOH:O	26:Y:165:GLU:HB3	2.13	0.49
1:0:1311:G:C2	1:0:1312:G:C8	3.01	0.49
1:0:1333:U:H2'	1:0:1334:C:C6	2.46	0.49
1:0:2453:G:H3'	38:0:5931:HOH:O	2.13	0.49
1:0:23:G:C6	1:0:24:G:N1	2.81	0.49
1:0:1098:A:H2'	1:0:1099:G:O4'	2.12	0.49
1:0:1165:G:C4'	1:0:1174:A:O2'	2.55	0.48
24:W:115:THR:HG23	38:W:5420:HOH:O	2.13	0.48
17:P:115:SER:OG	17:P:118:GLN:HG3	2.12	0.48
1:0:559:U:C3'	1:0:559:U:C6	2.96	0.48
3:A:211:LYS:HB3	3:A:212:PRO:CD	2.39	0.48
1:0:447:A:OP2	21:T:1:SER:HB2	2.12	0.48
1:0:522:U:O2'	1:0:1366:C:H5'	2.13	0.48
2:9:3002:U:OP2	2:9:3003:A:H5'	2.12	0.48
1:0:816:G:C6	1:0:817:G:N1	2.80	0.48
30:3:65:THR:HB	30:3:83:TRP:H	1.78	0.48
5:C:200:PRO:HB3	5:C:212:VAL:HG23	1.95	0.48
1:0:999:C:H2'	1:0:1000:C:O4'	2.14	0.48
13:L:67:ARG:HB2	13:L:112:GLY:HA3	1.94	0.48
14:M:99:ARG:CD	14:M:167:GLY:HA2	2.42	0.48
24:W:4:LEU:HD22	24:W:52:VAL:CG2	2.34	0.48
1:0:292:G:H1'	1:0:360:A:N6	2.28	0.48
1:0:1477:C:H5'	1:0:1868:G:H5'	1.95	0.48
1:0:2703:A:H2'	1:0:2704:C:C6	2.48	0.48
25:X:23:HIS:CD2	25:X:24:LYS:HG3	2.49	0.48
1:0:474:C:O2'	5:C:73:LEU:HD21	2.13	0.48
10:H:170:ASN:N	10:H:170:ASN:HD22	2.10	0.48
5:C:107:ARG:NE	38:C:8657:HOH:O	2.35	0.48
1:0:1947:G:H2'	1:0:1948:G:H8	1.78	0.48
1:0:2349:G:O2'	1:0:2350:G:H5'	2.12	0.48
12:K:130:MET:SD	22:U:25:ASP:O	2.71	0.48
4:B:30:PRO:HB2	4:B:39:GLN:NE2	2.28	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:M:164:THR:CG2	14:M:167:GLY:H	2.27	0.48
1:0:1589:G:N2	1:0:1605:G:H1'	2.28	0.48
3:A:53:ALA:HB3	38:A:8897:HOH:O	2.12	0.48
1:0:2374:A:H2'	1:0:2375:G:H8	1.78	0.48
1:0:441:A:O5'	1:0:441:A:H8	1.96	0.48
1:0:1211:G:O2'	1:0:1212:C:H5'	2.14	0.48
31:I:113:HIS:CE1	31:I:121:LEU:HD22	2.48	0.48
38:0:9792:HOH:O	13:L:30:ARG:NH2	2.44	0.48
1:0:1056:U:H2'	1:0:1057:A:O4'	2.13	0.48
1:0:154:C:H2'	1:0:155:C:H6	1.78	0.48
14:M:49:ALA:C	14:M:54:TYR:HB3	2.34	0.48
1:0:10:U:O4	1:0:532:A:OP2	2.32	0.48
2:9:3054:A:C2	2:9:3055:U:N3	2.81	0.48
1:0:1193:A:H2	1:0:1194:A:N6	2.12	0.48
1:0:597:A:C4	1:0:598:C:C5	3.01	0.48
16:O:47:ARG:HG3	16:O:47:ARG:NH1	2.29	0.48
4:B:17:LYS:O	4:B:260:HIS:HD2	1.95	0.48
19:R:39:THR:HB	19:R:42:GLU:CG	2.43	0.48
1:0:2055:A:H4'	19:R:132:ARG:NH2	2.28	0.48
10:H:97:GLU:HB3	10:H:121:VAL:HG11	1.96	0.48
1:0:188:C:H5''	14:M:163:LEU:HD21	1.95	0.48
1:0:366:U:H2'	1:0:367:G:O4'	2.12	0.48
1:0:597:A:H2'	1:0:598:C:C6	2.46	0.48
1:0:1942:A:O2'	1:0:1943:C:H5'	2.14	0.48
1:0:1081:A:C6	1:0:1082:A:N1	2.82	0.48
1:0:470:U:O2'	28:1:16:HIS:CD2	2.64	0.48
1:0:2616:G:H1'	38:0:9423:HOH:O	2.14	0.48
1:0:2403:C:H3'	38:0:5214:HOH:O	2.13	0.48
10:H:20:ILE:HG23	10:H:120:ILE:CD1	2.44	0.48
2:9:3058:G:C8	2:9:3059:C:C5	3.02	0.48
7:E:11:VAL:HG12	7:E:12:ASP:N	2.29	0.48
1:0:1495:C:H1'	1:0:1573:A:H1'	1.95	0.48
1:0:1118:A:N6	1:0:1244:U:N3	2.57	0.48
29:2:41:HIS:HD2	29:2:44:ARG:H	1.62	0.48
24:W:3:ALA:O	24:W:54:PHE:HA	2.14	0.48
27:Z:33:MET:SD	27:Z:49:ARG:HD2	2.53	0.48
4:B:221:GLN:HE22	12:K:42:ASN:ND2	2.03	0.48
1:0:1878:G:O2'	1:0:1879:U:OP2	2.32	0.48
11:J:74:ARG:NH1	11:J:76:ASP:HB2	2.29	0.48
11:J:42:GLU:O	11:J:131:THR:HG23	2.14	0.48
1:0:2553:A:H2'	1:0:2553:A:N3	2.28	0.48
1:0:2324:G:N2	1:0:2377:U:H1'	2.29	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:963:C:O2	1:0:1005:A:N1	2.46	0.48
1:0:790:A:H2'	1:0:791:A:O4'	2.14	0.48
1:0:613:C:H2'	1:0:614:U:H6	1.79	0.48
1:0:1351:G:OP1	5:C:96:LYS:NZ	2.32	0.48
1:0:1552:G:C6	1:0:1553:C:C4	3.01	0.48
1:0:1942:A:H3'	38:0:7336:HOH:O	2.12	0.48
1:0:2032:U:H2'	1:0:2033:G:C5'	2.44	0.48
15:N:48:VAL:HG11	15:N:55:ASP:HB3	1.93	0.48
3:A:200:PRO:HD3	38:A:8819:HOH:O	2.14	0.48
11:J:45:VAL:HG23	11:J:130:VAL:O	2.14	0.48
1:0:2269:C:H2'	1:0:2270:G:H5'	1.96	0.48
1:0:1217:G:C2	1:0:1218:U:C2	3.02	0.48
1:0:1921:A:O2'	1:0:1922:A:H5'	2.14	0.48
1:0:1842:A:C4	1:0:1979:G:C6	3.01	0.48
3:A:123:GLY:HA3	3:A:162:GLY:HA2	1.95	0.48
8:F:13:GLU:OE2	8:F:78:GLU:HG2	2.14	0.48
1:0:886:A:OP2	1:0:2113:G:H5'	2.14	0.48
4:B:51:VAL:CG2	4:B:327:VAL:HG13	2.42	0.48
5:C:127:ARG:CZ	5:C:225:PRO:HG2	2.43	0.48
1:0:2488:A:H2	38:0:7268:HOH:O	1.96	0.48
1:0:1044:C:H5''	38:0:9021:HOH:O	2.12	0.48
1:0:1789:G:O6	17:P:73:HIS:HE1	1.97	0.48
23:V:39:ALA:C	23:V:41:GLU:H	2.16	0.48
3:A:94:LEU:HG	3:A:99:ILE:HD11	1.95	0.48
1:0:1747:A:C8	12:K:44:LEU:HD13	2.49	0.48
1:0:1573:A:N7	1:0:1574:C:C2	2.82	0.48
5:C:51:TYR:HA	5:C:54:LEU:HD12	1.96	0.48
1:0:1669:A:H2'	1:0:1670:G:C8	2.49	0.48
1:0:2070:G:H5''	38:0:3786:HOH:O	2.14	0.48
1:0:1587:U:H2'	1:0:1588:G:O4'	2.13	0.48
15:N:67:ALA:HA	15:N:71:TRP:CB	2.42	0.48
7:E:3:VAL:HG22	7:E:49:ILE:HB	1.96	0.48
16:O:39:THR:O	16:O:115:ARG:NH2	2.47	0.48
6:D:51:ARG:HH11	6:D:68:PRO:HB3	1.79	0.48
1:0:2353:A:H4'	1:0:2354:A:O5'	2.12	0.48
2:9:3051:A:H5'	15:N:160:SER:HB3	1.96	0.48
1:0:629:A:H2'	1:0:630:A:O4'	2.14	0.48
1:0:664:U:O4	1:0:681:G:H5''	2.14	0.47
7:E:20:ILE:HD11	7:E:40:VAL:CG1	2.44	0.47
1:0:2044:G:OP1	25:X:23:HIS:HE1	1.97	0.47
1:0:324:G:O2'	1:0:325:U:H5'	2.14	0.47
1:0:2831:C:C2'	1:0:2832:C:H5'	2.44	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2689:A:H2'	1:0:2690:U:H5'	1.96	0.47
4:B:84:LEU:HD23	4:B:142:LEU:HD23	1.95	0.47
25:X:66:THR:HG23	25:X:67:PRO:HD2	1.96	0.47
1:0:57:C:H5''	38:0:6753:HOH:O	2.14	0.47
1:0:2114:C:OP1	3:A:1:GLY:HA2	2.13	0.47
1:0:1188:A:C6	1:0:1189:A:C6	3.02	0.47
1:0:2765:C:H2'	1:0:2766:A:C8	2.49	0.47
1:0:1477:C:C5'	1:0:1868:G:H5''	2.43	0.47
1:0:941:G:C6	1:0:942:U:C4	3.02	0.47
28:1:25:LYS:HD2	29:2:48:ASP:HA	1.96	0.47
1:0:2649:A:H5'	1:0:2649:A:H8	1.78	0.47
4:B:139:ASP:HB2	4:B:165:ARG:HE	1.79	0.47
1:0:709:G:O2'	16:O:25:VAL:HG12	2.14	0.47
7:E:10:ASP:HA	38:E:6017:HOH:O	2.14	0.47
1:0:2506:A:O2'	1:0:2507:G:O5'	2.31	0.47
1:0:255:A:C8	1:0:256:C:C5	3.02	0.47
4:B:150:ALA:O	4:B:152:PRO:HD3	2.14	0.47
3:A:217:ARG:CG	3:A:217:ARG:HH11	2.27	0.47
1:0:1398:G:H2'	1:0:1399:A:C8	2.49	0.47
1:0:2297:U:H1'	38:0:5179:HOH:O	2.13	0.47
1:0:2112:A:H2'	1:0:2113:G:C8	2.49	0.47
1:0:2330:U:H4'	1:0:2331:C:OP1	2.15	0.47
1:0:2802:C:H2'	1:0:2803:C:C6	2.50	0.47
1:0:1339:G:C6	1:0:1340:G:N1	2.82	0.47
1:0:264:G:H1'	1:0:265:U:H5	1.79	0.47
2:9:3049:G:H2'	2:9:3050:G:O4'	2.14	0.47
1:0:271:C:C2	1:0:273:G:O4'	2.67	0.47
1:0:293:A:C4	1:0:360:A:C2	3.03	0.47
2:9:3002:U:OP2	2:9:3002:U:H4'	2.15	0.47
21:T:73:HIS:CD2	21:T:88:PRO:HG3	2.49	0.47
1:0:155:C:OP2	14:M:188:ARG:HD3	2.13	0.47
1:0:106:A:O2'	1:0:107:U:H5'	2.14	0.47
4:B:112:THR:OG1	4:B:158:LYS:HG3	2.14	0.47
38:0:9215:HOH:O	3:A:11:ARG:HD3	2.15	0.47
2:9:3114:G:O6	15:N:11:ARG:HD3	2.13	0.47
11:J:135:ILE:O	11:J:139:LEU:HG	2.15	0.47
1:0:1592:G:O2'	1:0:1593:C:O5'	2.33	0.47
1:0:1503:U:H2'	1:0:1504:A:O4'	2.14	0.47
13:L:143:THR:HG21	38:L:8836:HOH:O	2.14	0.47
30:3:3:MET:HG3	30:3:4:PRO:HD2	1.96	0.47
1:0:80:A:H3'	21:T:43:ASN:OD1	2.15	0.47
24:W:52:VAL:HG22	24:W:53:ALA:H	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:69:A:H8	1:0:69:A:C5'	2.25	0.47
26:Y:189:ASN:HD22	26:Y:192:ASP:H	1.63	0.47
1:0:2403:C:C2'	1:0:2404:G:O5'	2.62	0.47
1:0:1574:C:H2'	1:0:1575:C:C6	2.50	0.47
1:0:2115:U:H2'	1:0:2116:U:C6	2.49	0.47
1:0:1562:C:O2	1:0:1562:C:H2'	2.12	0.47
1:0:876:A:N3	1:0:876:A:H2'	2.29	0.47
1:0:247:A:H2'	38:0:3931:HOH:O	2.13	0.47
1:0:2026:C:O2'	1:0:2027:U:H5'	2.15	0.47
15:N:108:SER:HA	15:N:109:PRO:HD3	1.74	0.47
1:0:1202:A:O2'	1:0:1203:G:H5'	2.14	0.47
24:W:21:LEU:HD22	24:W:26:ILE:HD11	1.97	0.47
24:W:90:TYR:CE2	24:W:99:ALA:HB2	2.50	0.47
19:R:18:LEU:HD12	19:R:143:VAL:CG1	2.45	0.47
1:0:2419:U:H5''	1:0:2420:G:H5'	1.97	0.47
1:0:2421:G:H3'	1:0:2422:U:H5''	1.97	0.47
1:0:2421:G:H3'	1:0:2422:U:C5'	2.45	0.47
1:0:1845:A:O3'	3:A:187:PRO:HB2	2.15	0.47
1:0:1845:A:OP2	3:A:190:ARG:NH1	2.47	0.47
2:9:3048:C:H4'	15:N:141:ARG:NH2	2.30	0.47
1:0:2615:U:C5	1:0:2616:G:C6	3.03	0.47
31:I:102:VAL:HG12	31:I:106:LYS:HE3	1.96	0.47
1:0:475:G:H5'	5:C:73:LEU:CD2	2.44	0.47
1:0:524:A:C5'	19:R:29:LYS:HE2	2.45	0.47
1:0:1333:U:H2'	1:0:1334:C:H6	1.79	0.47
1:0:758:A:H2'	1:0:759:C:O4'	2.15	0.47
1:0:1079:A:H4'	1:0:2078:U:H5'	1.97	0.47
1:0:1069:C:C2'	1:0:1070:A:H5'	2.44	0.47
1:0:1007:A:H2'	10:H:19:TYR:CZ	2.50	0.47
1:0:2371:G:H5'	38:0:5013:HOH:O	2.14	0.47
1:0:2274:A:O2'	1:0:2275:G:H5'	2.14	0.47
1:0:644:G:N3	1:0:644:G:H5'	2.30	0.47
1:0:729:C:C2	1:0:743:G:C2	3.03	0.47
12:K:4:LEU:HD22	12:K:116:GLU:HB3	1.97	0.47
4:B:275:GLY:O	4:B:291:ASP:HA	2.15	0.47
1:0:2754:G:O2'	1:0:2755:G:H5'	2.15	0.47
14:M:65:VAL:HG21	14:M:105:ALA:HB2	1.97	0.47
16:O:38:ARG:NH1	38:O:7674:HOH:O	2.47	0.47
10:H:2:PRO:HD2	10:H:5:MET:SD	2.55	0.47
1:0:951:A:H2'	1:0:952:G:H5'	1.96	0.47
1:0:1819:G:H2'	1:0:1820:G:C4'	2.45	0.47
28:1:28:HIS:HD2	28:1:30:LYS:H	1.61	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:U:33:SER:O	22:U:37:GLU:HG3	2.14	0.47
1:0:1746:A:O4'	1:0:1747:A:C2	2.67	0.47
26:Y:117:LEU:HD12	26:Y:174:VAL:HG11	1.97	0.47
4:B:232:TRP:HD1	4:B:235:ARG:HD2	1.79	0.47
1:0:920:C:H5'	1:0:921:G:C4	2.50	0.47
3:A:17:ARG:HD2	38:A:8836:HOH:O	2.13	0.47
1:0:2111:G:H1'	38:0:9044:HOH:O	2.14	0.47
1:0:1731:C:H1'	38:0:6446:HOH:O	2.14	0.47
1:0:1114:A:O2'	1:0:1115:U:H5'	2.15	0.47
1:0:1593:C:OP1	17:P:117:SER:HB3	2.15	0.47
1:0:2768:A:C2'	1:0:2769:C:O4'	2.61	0.47
1:0:2502:C:H2'	1:0:2503:A:C5'	2.43	0.47
1:0:2468:A:H4'	38:0:3550:HOH:O	2.14	0.47
1:0:1268:C:O2'	1:0:1269:G:H5'	2.14	0.47
2:9:3047:A:C2	2:9:3048:C:C2	3.03	0.47
1:0:329:A:C5	1:0:347:A:C2	3.03	0.47
1:0:524:A:H5'	19:R:29:LYS:HE2	1.97	0.47
1:0:1921:A:C6	1:0:1922:A:C2	3.03	0.47
1:0:2274:A:H1'	14:M:86:GLN:NE2	2.30	0.47
1:0:1013:A:H1'	38:0:9156:HOH:O	2.15	0.47
38:0:6273:HOH:O	17:P:59:ARG:HD3	2.15	0.47
1:0:2244:A:H1'	38:M:8866:HOH:O	2.14	0.47
38:0:6996:HOH:O	18:Q:9:GLY:HA2	2.15	0.47
1:0:905:C:H3'	38:0:5188:HOH:O	2.15	0.47
24:W:149:LEU:HG	24:W:153:MET:CE	2.45	0.47
3:A:109:GLU:HG2	3:A:116:GLY:H	1.79	0.47
1:0:1878:G:H5'	38:0:4380:HOH:O	2.15	0.47
6:D:135:VAL:HG22	6:D:136:ARG:N	2.29	0.47
1:0:1015:C:O5'	1:0:1015:C:H6	1.98	0.47
1:0:1857:A:N6	1:0:2247:C:H1'	2.30	0.47
8:F:34:ASN:HA	14:M:4:ALA:HB2	1.97	0.47
1:0:312:U:C2	1:0:320:G:N2	2.83	0.47
7:E:37:ASP:OD1	11:J:125:SER:HB3	2.15	0.47
6:D:84:LEU:HA	6:D:87:ALA:HB3	1.97	0.47
3:A:215:ILE:HG13	3:A:216:SER:N	2.30	0.47
1:0:377:C:H5	38:0:3309:HOH:O	1.98	0.47
21:T:71:VAL:HG13	21:T:91:LEU:O	2.15	0.46
1:0:559:U:H3'	1:0:559:U:C6	2.51	0.46
1:0:1058:A:H2'	1:0:1060:C:C5'	2.43	0.46
1:0:2255:A:C6	1:0:2256:G:C5	3.03	0.46
18:Q:28:ARG:HG2	38:Q:4350:HOH:O	2.15	0.46
1:0:513:A:N3	38:0:3663:HOH:O	2.36	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2047:C:H2'	1:0:2048:C:H6	1.80	0.46
26:Y:144:ARG:NH1	38:Y:8875:HOH:O	2.48	0.46
1:0:851:C:H5	38:0:6802:HOH:O	1.96	0.46
24:W:38:THR:HG22	24:W:39:ASP:N	2.30	0.46
1:0:2063:U:O4	1:0:2083:A:H2	1.98	0.46
1:0:1773:G:N2	1:0:1774:G:C8	2.83	0.46
1:0:2809:G:H2'	1:0:2810:G:O4'	2.15	0.46
2:9:3097:U:H2'	2:9:3098:C:H6	1.79	0.46
1:0:812:A:H1'	38:0:3966:HOH:O	2.14	0.46
4:B:55:ASN:HB3	4:B:63:GLU:HA	1.97	0.46
32:0:9000:13T:C23	32:0:9000:13T:H311	2.46	0.46
1:0:1183:C:C2	1:0:1184:C:C5	3.03	0.46
2:9:3028:U:H2'	2:9:3029:C:C6	2.50	0.46
1:0:2255:A:C2	1:0:2256:G:C4	3.03	0.46
1:0:31:C:H4'	38:0:7414:HOH:O	2.16	0.46
1:0:111:C:O2'	1:0:112:G:H5'	2.16	0.46
1:0:1447:U:H3'	1:0:1506:U:O2	2.15	0.46
1:0:1838:U:O2'	1:0:2644:C:H5'	2.15	0.46
1:0:2087:C:O2'	1:0:2088:C:H5'	2.16	0.46
1:0:1207:A:N6	38:0:5644:HOH:O	2.48	0.46
1:0:1878:G:O2'	1:0:1879:U:C5	2.65	0.46
1:0:2764:C:H1'	38:0:7458:HOH:O	2.16	0.46
1:0:1523:G:C6	1:0:1524:U:O4	2.67	0.46
1:0:694:A:C2'	1:0:695:C:H5'	2.43	0.46
1:0:1198:U:C6	1:0:1200:A:OP2	2.68	0.46
1:0:1211:G:H2'	1:0:1212:C:C6	2.47	0.46
1:0:2269:C:H2'	1:0:2270:G:C5'	2.46	0.46
3:A:126:ALA:HB1	3:A:138:VAL:CG1	2.45	0.46
1:0:1850:U:H2'	1:0:1851:G:H8	1.81	0.46
8:F:111:ILE:O	8:F:115:VAL:HG23	2.15	0.46
1:0:1913:C:H2'	1:0:1914:C:H6	1.80	0.46
2:9:3006:C:OP1	15:N:37:ARG:NH1	2.48	0.46
1:0:2459:G:C2'	32:0:9000:13T:C23	2.94	0.46
1:0:559:U:H2'	1:0:560:C:O4'	2.14	0.46
1:0:704:C:H2'	1:0:705:C:H6	1.81	0.46
1:0:1931:A:C2'	1:0:1932:G:H5'	2.45	0.46
4:B:5:ARG:HD2	4:B:8:LYS:NZ	2.31	0.46
1:0:1913:C:H2'	1:0:1914:C:C6	2.50	0.46
1:0:843:A:C2	1:0:846:A:C8	3.04	0.46
16:O:105:ASN:HD21	16:O:109:SER:H	1.62	0.46
31:I:100:LEU:HD22	31:I:105:VAL:CG2	2.46	0.46
1:0:2459:G:H2'	32:0:9000:13T:H232	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1204:C:H2'	1:0:1205:U:O4'	2.16	0.46
1:0:317:A:OP1	21:T:52:ARG:O	2.33	0.46
1:0:1131:G:C6	1:0:1230:A:C4	3.04	0.46
15:N:65:ASP:HB3	38:N:8821:HOH:O	2.14	0.46
1:0:2821:C:H2'	1:0:2822:C:H6	1.80	0.46
3:A:3:ARG:H	3:A:3:ARG:HG2	1.55	0.46
3:A:179:MET:HG2	3:A:186:TRP:CB	2.45	0.46
14:M:183:THR:HG22	14:M:194:ALA:HB1	1.96	0.46
1:0:39:G:C2	1:0:444:C:C2	3.04	0.46
1:0:1173:A:H3'	38:0:4360:HOH:O	2.16	0.46
1:0:2114:C:O2'	1:0:2115:U:H5'	2.16	0.46
1:0:2332:A:H3'	1:0:2333:G:H8	1.80	0.46
1:0:1619:G:C5	1:0:1620:C:C4	3.03	0.46
22:U:13:ILE:HG12	22:U:32:CYS:HB3	1.97	0.46
1:0:1192:A:H3'	1:0:1193:A:H5'	1.98	0.46
1:0:281:U:C2'	1:0:282:C:H5'	2.46	0.46
19:R:39:THR:HG23	19:R:107:GLU:O	2.16	0.46
1:0:1850:U:H2'	1:0:1851:G:C8	2.50	0.46
3:A:72:GLU:HG3	27:Z:66:GLY:HA2	1.98	0.46
1:0:857:A:H4'	3:A:176:HIS:CD2	2.51	0.46
6:D:88:LEU:HB2	6:D:89:PRO:HD3	1.96	0.46
6:D:10:PHE:CG	6:D:11:HIS:N	2.84	0.46
3:A:36:ASP:O	3:A:38:ILE:N	2.49	0.46
1:0:1684:A:O2'	1:0:1685:A:H5''	2.15	0.46
13:L:56:LYS:NZ	38:L:8873:HOH:O	2.49	0.46
22:U:52:THR:HG22	22:U:54:THR:N	2.31	0.46
1:0:475:G:H5'	5:C:73:LEU:HD23	1.96	0.46
31:I:78:LEU:HD12	31:I:112:LYS:HZ2	1.79	0.46
1:0:2121:G:O2'	1:0:2122:C:H5'	2.16	0.46
1:0:2729:C:O2'	1:0:2730:G:H5'	2.15	0.46
26:Y:216:ARG:HD2	38:Y:8868:HOH:O	2.14	0.46
26:Y:184:GLU:OE2	26:Y:204:ARG:HD2	2.15	0.46
1:0:1218:U:H2'	1:0:1219:U:C6	2.51	0.46
1:0:2329:C:O2'	1:0:2330:U:H5'	2.16	0.46
1:0:2263:G:H1'	38:0:6618:HOH:O	2.16	0.46
1:0:1182:C:O2'	1:0:1183:C:H5	1.99	0.46
1:0:1166:A:H1'	1:0:1192:A:C2	2.50	0.46
20:S:57:THR:CG2	20:S:59:ASP:HB2	2.45	0.46
14:M:134:ILE:CG2	14:M:141:ILE:HD13	2.43	0.46
29:2:22:PRO:HG2	29:2:25:VAL:CG2	2.45	0.46
7:E:69:ILE:HA	7:E:72:MET:HE3	1.98	0.46
1:0:2672:C:H1'	38:B:8930:HOH:O	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:17:G:H2'	1:0:18:C:H6	1.81	0.46
10:H:170:ASN:N	10:H:170:ASN:ND2	2.64	0.46
6:D:51:ARG:NH1	6:D:68:PRO:HB3	2.31	0.46
8:F:107:ASP:O	8:F:111:ILE:HG13	2.15	0.46
1:0:101:C:H2'	1:0:102:A:C8	2.51	0.46
1:0:113:A:H2'	1:0:115:U:O4	2.16	0.46
38:0:7403:HOH:O	31:I:90:GLY:HA2	2.16	0.46
6:D:75:LEU:HD22	6:D:79:MET:HB3	1.98	0.46
1:0:2549:C:H4'	38:0:7504:HOH:O	2.16	0.46
1:0:2911:C:H2'	1:0:2912:C:C6	2.51	0.46
11:J:26:VAL:HG13	11:J:36:VAL:HG11	1.98	0.46
1:0:2050:G:H5''	19:R:80:TYR:O	2.16	0.46
1:0:189:A:OP1	14:M:171:ARG:NH2	2.49	0.45
1:0:1180:U:H4'	31:I:91:GLU:HG2	1.97	0.45
3:A:69:LEU:HD21	3:A:120:ARG:HB3	1.98	0.45
1:0:2253:G:O2'	1:0:2254:G:H5'	2.16	0.45
1:0:583:G:H2'	1:0:584:U:C6	2.51	0.45
11:J:45:VAL:HG22	11:J:46:ILE:N	2.30	0.45
2:9:3107:C:H2'	2:9:3108:C:C6	2.51	0.45
1:0:2000:G:O2'	1:0:2001:G:H5'	2.16	0.45
10:H:1:LYS:HA	10:H:2:PRO:HD3	1.73	0.45
1:0:2730:G:O2'	1:0:2731:G:H5'	2.15	0.45
1:0:1583:U:H1'	38:0:9979:HOH:O	2.15	0.45
20:S:77:VAL:O	20:S:80:ARG:HG2	2.17	0.45
1:0:1741:U:C4	1:0:2033:G:C8	3.04	0.45
1:0:2570:G:H8	38:0:4917:HOH:O	2.00	0.45
16:O:32:ARG:HB2	38:O:4656:HOH:O	2.17	0.45
1:0:2092:G:H5''	1:0:2613:G:OP1	2.15	0.45
1:0:1947:G:N2	1:0:1966:U:C2	2.84	0.45
1:0:2820:A:H2'	1:0:2821:C:O4'	2.17	0.45
1:0:939:A:H5'	38:0:5419:HOH:O	2.16	0.45
23:V:7:GLU:O	23:V:11:MET:HG3	2.15	0.45
1:0:1127:C:C5	1:0:1128:U:C4	3.04	0.45
10:H:95:LEU:HD11	10:H:124:ALA:HB2	1.99	0.45
26:Y:220:GLU:HG3	38:Y:8849:HOH:O	2.16	0.45
1:0:1321:A:H2'	1:0:1322:G:C8	2.51	0.45
18:Q:66:LYS:HB2	18:Q:70:ALA:O	2.17	0.45
1:0:1535:G:H2'	1:0:1536:C:C6	2.51	0.45
27:Z:56:GLN:HA	27:Z:62:TYR:O	2.16	0.45
1:0:541:C:C2'	1:0:542:A:C5'	2.82	0.45
1:0:365:G:C6	1:0:366:U:C4	3.04	0.45
1:0:706:G:O2'	1:0:707:C:H6	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:814:G:N2	1:0:815:U:H1'	2.31	0.45
23:V:39:ALA:N	23:V:40:PRO:CD	2.80	0.45
29:2:20:ARG:HB3	38:2:5444:HOH:O	2.17	0.45
1:0:512:G:O3'	1:0:513:A:C8	2.69	0.45
2:9:3107:C:C5	38:9:3167:HOH:O	2.68	0.45
1:0:1855:G:H8	3:A:144:GLU:OE2	1.99	0.45
25:X:30:MET:HE1	25:X:58:ALA:HB3	1.98	0.45
17:P:83:LYS:O	17:P:86:ALA:HB3	2.16	0.45
1:0:2831:C:H2'	1:0:2832:C:C5'	2.46	0.45
1:0:920:C:H5''	1:0:921:G:O5'	2.17	0.45
1:0:419:A:H1'	1:0:1921:A:C2	2.51	0.45
23:V:45:ARG:HH11	23:V:45:ARG:HG3	1.82	0.45
15:N:139:TRP:HA	15:N:139:TRP:CE3	2.52	0.45
1:0:2314:G:C2'	1:0:2315:C:H5'	2.46	0.45
1:0:2582:G:H5''	4:B:3:PRO:HB3	1.98	0.45
27:Z:60:CYS:O	27:Z:61:ASP:HB2	2.16	0.45
1:0:1588:G:C5	1:0:1589:G:C6	3.05	0.45
1:0:1477:C:H5'	1:0:1868:G:H5''	1.97	0.45
1:0:2237:G:O2'	1:0:2238:A:C8	2.69	0.45
1:0:2428:G:N7	30:3:60:LYS:NZ	2.61	0.45
1:0:229:G:O2'	1:0:230:C:H5'	2.16	0.45
1:0:2105:C:H2'	1:0:2106:C:C6	2.52	0.45
26:Y:130:ARG:HB2	26:Y:142:SER:O	2.16	0.45
1:0:2649:A:C8	1:0:2649:A:H5'	2.52	0.45
1:0:200:U:H2'	38:0:3446:HOH:O	2.15	0.45
3:A:82:VAL:HG13	3:A:93:THR:HB	1.98	0.45
1:0:51:G:O2'	1:0:52:A:H5'	2.16	0.45
4:B:162:MET:CE	4:B:310:ARG:HD3	2.47	0.45
1:0:407:A:H5'	38:0:6034:HOH:O	2.15	0.45
1:0:2871:G:H2'	1:0:2872:U:H6	1.81	0.45
2:9:3008:G:O6	15:N:11:ARG:NH1	2.39	0.45
3:A:109:GLU:HG2	3:A:116:GLY:N	2.31	0.45
1:0:2864:U:C5	1:0:2865:G:C6	3.04	0.45
38:0:9988:HOH:O	13:L:22:ARG:HG2	2.15	0.45
5:C:150:THR:HA	5:C:203:ALA:O	2.17	0.45
2:9:3026:C:O2'	2:9:3027:C:H5'	2.17	0.45
1:0:2016:U:H2'	1:0:2017:U:C6	2.51	0.45
25:X:76:ARG:NH1	25:X:76:ARG:HG3	2.28	0.45
25:X:76:ARG:HH11	25:X:76:ARG:CG	2.28	0.45
26:Y:117:LEU:HA	26:Y:174:VAL:HG11	1.98	0.45
1:0:1730:G:H4'	1:0:1731:C:H6	1.82	0.45
4:B:101:TRP:HB2	4:B:119:HIS:CD2	2.51	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:453:A:H4'	1:0:455:A:N7	2.32	0.45
1:0:1164:U:OP1	31:I:74:PRO:HA	2.17	0.45
1:0:560:C:H2'	1:0:561:G:H8	1.82	0.45
1:0:2110:G:C2	1:0:2478:U:C2	3.04	0.45
1:0:111:C:C2'	1:0:112:G:H5'	2.47	0.45
1:0:1544:U:O2'	1:0:1545:C:H5'	2.17	0.45
1:0:1771:U:O2'	1:0:1773:G:N7	2.48	0.45
1:0:2326:U:H4'	1:0:2412:G:C4'	2.46	0.45
1:0:2891:A:C2	1:0:2892:G:C4	3.05	0.45
1:0:2772:G:O2'	1:0:2773:G:H5'	2.16	0.45
5:C:153:VAL:O	5:C:157:LEU:HG	2.16	0.45
1:0:278:A:H2'	1:0:279:C:O4'	2.16	0.45
1:0:289:G:N1	1:0:363:A:C2	2.81	0.45
15:N:110:THR:HB	15:N:113:SER:OG	2.17	0.45
1:0:1940:C:H4'	38:0:7336:HOH:O	2.17	0.45
1:0:2073:G:OP2	1:0:2490:A:H5'	2.16	0.45
1:0:1973:A:H5'	1:0:1973:A:C8	2.45	0.45
1:0:696:C:O2'	1:0:731:U:OP1	2.33	0.45
1:0:1819:G:H2'	1:0:1820:G:C5'	2.47	0.45
7:E:15:GLN:HG2	7:E:19:ASP:O	2.17	0.45
13:L:143:THR:HG22	13:L:144:ASP:H	1.81	0.45
30:3:69:TYR:O	30:3:77:ALA:HA	2.16	0.45
1:0:1682:A:O2'	1:0:1683:G:H5'	2.17	0.45
24:W:5:VAL:HG11	24:W:153:MET:CE	2.47	0.45
1:0:834:G:H4'	1:0:835:U:OP2	2.16	0.45
1:0:244:C:OP2	8:F:38:LYS:HE3	2.17	0.45
1:0:1123:A:N1	1:0:1238:C:H5'	2.32	0.45
1:0:1150:A:C2	9:G:20:VAL:HG21	2.52	0.45
1:0:1252:A:H2'	1:0:1253:C:O4'	2.17	0.45
1:0:1029:U:O2'	1:0:1273:C:OP1	2.32	0.45
1:0:542:A:C5'	1:0:542:A:C8	2.95	0.45
1:0:2505:G:C2'	1:0:2506:A:H5'	2.46	0.45
1:0:292:G:H1'	1:0:360:A:H61	1.81	0.45
5:C:2:GLN:HB3	38:C:8582:HOH:O	2.15	0.45
1:0:2614:C:O2'	1:0:2615:U:H5'	2.17	0.45
1:0:2075:G:C6	1:0:2076:U:C4	3.05	0.45
1:0:2906:A:H5'	1:0:2907:C:O4'	2.17	0.45
1:0:1076:G:C2	1:0:1084:C:C2	3.05	0.45
4:B:277:GLU:N	4:B:278:PRO:HD2	2.31	0.45
5:C:236:THR:HG22	5:C:239:ALA:CB	2.47	0.45
24:W:139:GLY:O	24:W:141:HIS:CD2	2.70	0.45
1:0:2133:U:H4'	1:0:2134:G:H5'	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:670:G:H2'	1:0:671:A:C8	2.52	0.45
1:0:926:A:O2'	13:L:41:HIS:HD2	2.00	0.45
4:B:8:LYS:HG3	4:B:220:VAL:HG12	1.98	0.45
1:0:1238:C:H5''	1:0:1239:G:OP2	2.17	0.45
1:0:488:U:O2'	21:T:82:THR:HG21	2.17	0.45
17:P:9:LEU:O	17:P:13:VAL:HG23	2.17	0.45
1:0:1188:A:C5	1:0:1189:A:C2	3.05	0.44
1:0:538:C:N4	1:0:2061:C:H1'	2.32	0.44
1:0:248:A:H5'	1:0:249:G:OP2	2.18	0.44
1:0:660:A:N6	1:0:746:A:O4'	2.50	0.44
22:U:52:THR:HG22	22:U:54:THR:HB	1.98	0.44
1:0:703:G:O2'	1:0:704:C:H5'	2.18	0.44
1:0:2346:C:O2'	6:D:52:THR:HG21	2.17	0.44
18:Q:75:ILE:CD1	18:Q:84:ILE:HD11	2.47	0.44
1:0:1279:U:H2'	1:0:1279:U:O2	2.17	0.44
1:0:2354:A:C2	1:0:2367:A:C8	3.04	0.44
26:Y:235:GLU:CD	26:Y:235:GLU:H	2.21	0.44
1:0:2594:C:O2'	1:0:2595:U:H5'	2.17	0.44
6:D:40:ILE:HG23	38:D:5583:HOH:O	2.17	0.44
11:J:53:ILE:O	11:J:57:TYR:HD1	2.00	0.44
1:0:426:G:H2'	1:0:427:C:O4'	2.17	0.44
15:N:179:LEU:HD23	15:N:184:ILE:CD1	2.47	0.44
25:X:78:GLU:HG2	25:X:79:GLU:H	1.82	0.44
1:0:256:C:H2'	1:0:257:G:O4'	2.18	0.44
11:J:45:VAL:CG2	11:J:129:PHE:HD1	2.30	0.44
2:9:3058:G:H1'	38:9:3839:HOH:O	2.16	0.44
1:0:1494:A:O2'	1:0:1505:U:O2	2.34	0.44
3:A:107:ASN:OD1	3:A:116:GLY:HA3	2.17	0.44
2:9:3097:U:H2'	2:9:3098:C:C6	2.51	0.44
1:0:957:A:O5'	1:0:957:A:H8	2.00	0.44
1:0:2719:A:C2	4:B:70:PRO:HG3	2.52	0.44
26:Y:151:SER:HB3	26:Y:154:ARG:HB3	2.00	0.44
12:K:32:ILE:HD11	12:K:56:SER:HB3	1.98	0.44
6:D:104:PHE:CE2	6:D:132:VAL:HB	2.52	0.44
1:0:536:A:H3'	38:0:5051:HOH:O	2.16	0.44
4:B:60:SER:HA	4:B:61:PRO:HD3	1.85	0.44
1:0:2716:G:O2'	1:0:2717:C:H5'	2.18	0.44
1:0:1244:U:H4'	1:0:1246:A:O4'	2.17	0.44
1:0:1174:A:C5	1:0:1201:C:H4'	2.53	0.44
1:0:1972:U:C2'	1:0:1973:A:C5'	2.96	0.44
1:0:1269:G:H2'	1:0:1270:U:C6	2.53	0.44
1:0:2133:U:H4'	1:0:2134:G:C5'	2.47	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:111:C:H2'	1:0:112:G:C5'	2.46	0.44
3:A:95:PRO:HA	3:A:153:ARG:HA	1.98	0.44
26:Y:126:PRO:HG2	26:Y:128:PHE:CZ	2.52	0.44
1:0:1334:C:O2'	1:0:1335:C:H5'	2.18	0.44
1:0:834:G:H3'	1:0:835:U:H4'	1.99	0.44
1:0:2900:G:C2'	1:0:2901:C:H5'	2.47	0.44
15:N:154:LEU:C	15:N:156:GLU:H	2.20	0.44
14:M:15:PRO:HA	14:M:20:LEU:HD23	2.00	0.44
1:0:263:U:C2	8:F:59:ILE:CD1	3.01	0.44
1:0:697:G:H4'	1:0:730:G:O3'	2.17	0.44
4:B:307:ARG:HA	38:B:8850:HOH:O	2.17	0.44
1:0:2256:G:H2'	1:0:2257:G:O5'	2.17	0.44
18:Q:25:PRO:HA	18:Q:26:PRO:HD3	1.85	0.44
4:B:18:ARG:HE	4:B:256:GLN:NE2	2.15	0.44
1:0:2610:U:H4'	38:0:9479:HOH:O	2.18	0.44
5:C:34:ALA:HB3	5:C:220:THR:HG21	2.00	0.44
1:0:1667:A:H8	1:0:1667:A:C5'	2.18	0.44
1:0:710:G:N2	1:0:719:C:C2	2.86	0.44
4:B:144:THR:HB	38:B:8921:HOH:O	2.18	0.44
1:0:1309:U:C4	1:0:1310:U:C5	3.06	0.44
1:0:1748:U:C5	1:0:1749:U:C4	3.06	0.44
1:0:1714:C:O2'	1:0:1715:C:H5'	2.18	0.44
1:0:2846:C:H4'	4:B:156:LYS:HB3	1.98	0.44
1:0:1117:A:C2	1:0:1244:U:C2	3.06	0.44
32:0:9000:13T:H323	32:0:9000:13T:O2	2.18	0.44
1:0:1602:C:OP2	27:Z:46:ARG:NH2	2.51	0.44
1:0:1523:G:H2'	1:0:1524:U:C6	2.53	0.44
19:R:99:ALA:HB1	19:R:109:MET:HE1	1.97	0.44
12:K:14:LYS:CB	12:K:45:PRO:HG2	2.46	0.44
1:0:816:G:H5'	1:0:1598:A:H4'	2.00	0.44
1:0:538:C:H5''	1:0:539:G:C8	2.53	0.44
1:0:1853:C:OP1	3:A:231:LYS:HG3	2.18	0.44
1:0:1500:U:OP2	17:P:41:ARG:NH2	2.51	0.44
1:0:2819:C:H2'	1:0:2820:A:C8	2.53	0.44
23:V:45:ARG:NH1	23:V:45:ARG:HG3	2.32	0.44
1:0:2504:A:H4'	10:H:71:ARG:HH11	1.83	0.44
4:B:199:TYR:CE2	4:B:268:ARG:HB2	2.53	0.44
1:0:170:U:H2'	1:0:171:C:H5'	1.98	0.44
7:E:132:THR:HB	38:E:2227:HOH:O	2.17	0.44
1:0:929:A:O5'	1:0:929:A:H8	2.01	0.44
1:0:2432:C:H1'	32:0:9000:13T:O9	2.17	0.44
24:W:90:TYR:N	24:W:90:TYR:CD1	2.85	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:C:129:HIS:CE1	5:C:232:LEU:H	2.36	0.44
1:0:1419:U:H2'	1:0:1685:A:C2	2.53	0.44
1:0:2416:G:O2'	15:N:25:ARG:HG2	2.17	0.44
24:W:13:MET:CE	24:W:17:ILE:HG22	2.48	0.44
4:B:321:PRO:HA	38:B:8952:HOH:O	2.16	0.44
1:0:500:G:H21	19:R:98:ASN:ND2	2.13	0.44
38:0:7396:HOH:O	21:T:2:LYS:HE2	2.17	0.44
1:0:2361:A:H2'	1:0:2362:A:C8	2.52	0.44
1:0:622:G:P	26:Y:148:GLY:HA3	2.58	0.44
7:E:11:VAL:HG13	7:E:23:GLU:O	2.17	0.44
1:0:920:C:H4'	1:0:921:G:N2	2.32	0.44
1:0:2802:C:H2'	1:0:2803:C:H6	1.81	0.44
1:0:1069:C:O2'	1:0:1070:A:H5'	2.18	0.44
1:0:1730:G:H4'	1:0:1731:C:C6	2.53	0.44
1:0:1773:G:C8	27:Z:16:ALA:HA	2.53	0.44
1:0:2899:A:O2'	1:0:2900:G:H5'	2.18	0.44
1:0:1280:A:H3'	1:0:1280:A:OP1	2.18	0.44
1:0:413:G:H2'	1:0:414:C:C6	2.52	0.44
15:N:171:HIS:CE1	38:N:8862:HOH:O	2.71	0.44
1:0:445:U:H2'	1:0:446:G:H8	1.82	0.44
1:0:2577:A:H5'	38:0:7734:HOH:O	2.17	0.44
1:0:637:C:H2'	1:0:638:C:C6	2.52	0.44
2:9:3039:U:H3	2:9:3042:C:H5''	1.83	0.44
1:0:307:G:C2	1:0:309:C:C4	3.05	0.44
1:0:821:U:H4'	27:Z:17:ARG:NH1	2.33	0.44
4:B:162:MET:HE1	4:B:308:LEU:HD21	1.99	0.44
1:0:2385:G:H2'	1:0:2386:U:H6	1.79	0.44
1:0:1236:A:C8	11:J:63:ILE:HD11	2.53	0.44
1:0:303:C:O2'	1:0:304:G:H5'	2.18	0.44
1:0:2691:A:OP1	1:0:2691:A:H8	2.01	0.44
1:0:276:C:O5'	1:0:276:C:H6	2.01	0.44
4:B:185:GLY:HA2	38:B:8929:HOH:O	2.17	0.44
1:0:238:C:H4'	1:0:287:C:OP1	2.18	0.44
1:0:1191:A:H2'	1:0:1193:A:H5'	2.00	0.43
1:0:1205:U:C2'	1:0:1206:U:C5'	2.87	0.43
1:0:1159:G:H1	1:0:1208:C:H42	1.64	0.43
1:0:1761:U:H5'	17:P:81:LYS:O	2.18	0.43
1:0:699:C:C2	1:0:743:G:N2	2.86	0.43
27:Z:36:ASP:HB3	27:Z:45:ASP:HB3	1.99	0.43
1:0:1183:C:H42	1:0:1184:C:N4	2.12	0.43
1:0:338:C:H4'	5:C:174:ILE:HD12	1.98	0.43
12:K:87:ARG:NH1	38:K:4066:HOH:O	2.51	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:303:C:H2'	1:0:304:G:O4'	2.18	0.43
5:C:51:TYR:CE2	28:1:53:LYS:HB3	2.53	0.43
1:0:106:A:H2'	1:0:107:U:O4'	2.18	0.43
1:0:2821:C:H4'	4:B:116:PRO:HG3	2.00	0.43
1:0:2850:C:H6	1:0:2850:C:H5'	1.83	0.43
1:0:1215:A:O3'	1:0:1216:G:C4'	2.66	0.43
1:0:1923:G:H4'	30:3:31:THR:O	2.18	0.43
1:0:2101:A:H2'	5:C:63:SER:OG	2.18	0.43
1:0:37:A:H2'	1:0:38:G:C8	2.52	0.43
1:0:1829:A:H5''	38:0:3081:HOH:O	2.17	0.43
32:0:9000:13T:C26	32:0:9000:13T:H2	2.42	0.43
1:0:1377:C:C5'	1:0:1377:C:H6	2.28	0.43
38:0:7442:HOH:O	4:B:211:THR:HG21	2.19	0.43
1:0:2089:A:O2'	1:0:2090:G:H5'	2.18	0.43
1:0:1624:A:H5'	1:0:1626:A:O4'	2.17	0.43
1:0:2039:A:H4'	1:0:2760:C:O2'	2.19	0.43
1:0:195:C:H2'	1:0:196:G:H5'	2.00	0.43
1:0:1118:A:N6	1:0:1244:U:C2	2.86	0.43
5:C:115:LEU:HA	5:C:115:LEU:HD12	1.87	0.43
1:0:1343:C:H2'	1:0:1344:G:O5'	2.19	0.43
1:0:2252:A:C6	1:0:2253:G:H1'	2.54	0.43
12:K:34:VAL:HG21	12:K:46:LYS:O	2.19	0.43
8:F:101:ALA:HA	38:F:5413:HOH:O	2.18	0.43
1:0:2002:C:H2'	1:0:2003:U:H5'	2.00	0.43
1:0:304:G:H1'	1:0:347:A:H61	1.83	0.43
7:E:22:VAL:O	7:E:76:VAL:HG11	2.18	0.43
1:0:2326:U:H4'	1:0:2412:G:H4'	2.01	0.43
6:D:170:TYR:O	6:D:171:ASP:HB3	2.18	0.43
1:0:772:G:H2'	1:0:773:A:O4'	2.17	0.43
1:0:99:A:C8	1:0:100:C:C5	3.06	0.43
1:0:1409:G:C2	1:0:1410:G:C8	3.06	0.43
20:S:33:SER:O	20:S:37:VAL:HG23	2.18	0.43
17:P:98:ILE:HD12	17:P:102:ARG:NE	2.34	0.43
12:K:132:VAL:HG21	22:U:22:VAL:HG11	2.00	0.43
1:0:1903:U:O2'	1:0:1904:A:N7	2.49	0.43
27:Z:30:GLU:HG2	27:Z:33:MET:HE2	1.99	0.43
6:D:49:PRO:HA	6:D:73:VAL:HG22	2.01	0.43
7:E:80:TRP:O	7:E:134:SER:HA	2.17	0.43
1:0:137:U:H2'	1:0:139:C:C5	2.53	0.43
15:N:7:LYS:HE3	18:Q:21:ARG:O	2.19	0.43
19:R:132:ARG:HG2	19:R:133:ALA:N	2.32	0.43
1:0:187:A:H3'	1:0:188:C:H6	1.83	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2786:G:H2'	38:0:7180:HOH:O	2.17	0.43
1:0:1768:C:H2'	1:0:1769:C:O4'	2.18	0.43
5:C:193:LEU:HD13	5:C:222:ASP:HB2	2.00	0.43
1:0:242:A:N6	1:0:269:G:H1'	2.34	0.43
5:C:185:LYS:HD3	5:C:186:TYR:CE1	2.53	0.43
2:9:3012:C:H5'	2:9:3070:U:O4'	2.18	0.43
1:0:1183:C:O2	1:0:1183:C:C2'	2.67	0.43
1:0:1186:C:H5''	31:I:119:TYR:CE1	2.53	0.43
1:0:2812:A:H2	1:0:2814:A:N6	1.91	0.43
24:W:26:ILE:HB	38:W:5420:HOH:O	2.18	0.43
1:0:69:A:C8	1:0:69:A:C5'	2.95	0.43
1:0:2779:G:N2	1:0:2796:U:C2	2.87	0.43
1:0:1130:U:H4'	38:0:6133:HOH:O	2.18	0.43
1:0:2840:A:OP1	4:B:211:THR:HG23	2.19	0.43
1:0:645:U:H2'	1:0:646:G:C8	2.54	0.43
8:F:56:PRO:CG	14:M:44:THR:HA	2.48	0.43
4:B:4:SER:O	4:B:5:ARG:HB2	2.19	0.43
9:G:20:VAL:O	9:G:24:VAL:HG23	2.19	0.43
4:B:88:GLU:HG3	4:B:88:GLU:O	2.18	0.43
1:0:1439:C:H6	1:0:1439:C:O5'	2.01	0.43
1:0:1811:A:C2	1:0:2752:C:H1'	2.52	0.43
1:0:1119:G:N2	1:0:1246:A:H2	2.09	0.43
1:0:2460:A:C4	32:0:9000:13T:H20	2.53	0.43
1:0:365:G:C5	1:0:366:U:C5	3.07	0.43
1:0:947:U:O2'	1:0:948:G:H5'	2.18	0.43
11:J:47:THR:HG22	11:J:48:GLY:N	2.34	0.43
1:0:1778:A:H2'	1:0:1779:A:H5'	2.00	0.43
1:0:1772:C:H5'	1:0:1773:G:C5	2.53	0.43
1:0:1215:A:O3'	1:0:1216:G:H4'	2.19	0.43
1:0:1904:A:H2'	1:0:1905:U:O4'	2.19	0.43
3:A:81:GLN:HB2	3:A:92:ASN:ND2	2.34	0.43
24:W:106:THR:OG1	24:W:109:GLU:HB2	2.19	0.43
1:0:1386:G:O2'	1:0:1387:G:H5'	2.19	0.43
1:0:1257:C:O2'	1:0:1258:G:H5'	2.18	0.43
14:M:46:LEU:HG	38:M:8913:HOH:O	2.18	0.43
4:B:24:PRO:CG	4:B:204:GLY:HA2	2.49	0.43
1:0:1883:U:H5'	1:0:2012:U:OP2	2.19	0.43
1:0:2591:C:H2'	1:0:2592:G:O4'	2.19	0.43
1:0:241:A:C2	1:0:378:A:H4'	2.53	0.43
1:0:2856:A:OP1	25:X:15:ARG:NH2	2.51	0.43
11:J:127:ILE:CG2	36:J:8801:CL:CL	3.00	0.43
2:9:3069:U:OP1	15:N:4:PRO:HG3	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2036:C:C4'	12:K:44:LEU:HG	2.48	0.43
26:Y:107:PRO:HB3	26:Y:182:PHE:CD2	2.54	0.43
1:0:1850:U:O4'	1:0:1941:A:C2	2.71	0.43
1:0:445:U:O2'	1:0:446:G:H5'	2.18	0.43
1:0:2697:A:H2'	1:0:2698:G:O4'	2.19	0.43
1:0:1565:C:O2'	1:0:1566:C:H5'	2.19	0.43
31:I:125:ALA:O	31:I:129:VAL:HG23	2.19	0.43
38:0:6721:HOH:O	18:Q:2:SER:HA	2.19	0.43
38:0:9208:HOH:O	4:B:248:ARG:NH2	2.51	0.43
1:0:1434:A:H2'	1:0:1436:C:C5	2.53	0.43
4:B:33:ASP:HB3	4:B:34:GLY:H	1.60	0.43
1:0:1415:G:H5'	28:1:12:ASN:O	2.18	0.43
32:0:9000:13T:H3	30:3:56:PRO:CB	2.48	0.43
1:0:1191:A:H2	1:0:1206:U:H3	1.67	0.43
1:0:1943:C:O4'	3:A:212:PRO:HA	2.18	0.43
1:0:2254:G:C2	1:0:2255:A:C8	3.06	0.43
7:E:20:ILE:HD11	7:E:40:VAL:HG11	2.01	0.43
8:F:48:VAL:HG12	8:F:97:ALA:CB	2.49	0.43
12:K:125:ALA:C	12:K:127:ALA:H	2.22	0.43
1:0:228:C:C2'	1:0:229:G:H5'	2.49	0.43
1:0:2372:A:H2'	1:0:2373:U:H6	1.82	0.43
24:W:5:VAL:HG11	24:W:153:MET:HE3	1.99	0.43
1:0:2088:C:H1'	1:0:2841:A:N1	2.34	0.43
1:0:134:U:C2	1:0:145:A:C2	3.07	0.43
6:D:138:GLY:N	38:D:7597:HOH:O	2.51	0.43
1:0:1825:U:O2'	1:0:1826:C:H5'	2.19	0.43
1:0:1667:A:C2	1:0:1668:U:C2	3.07	0.43
1:0:1114:A:H2'	1:0:1115:U:C6	2.54	0.43
1:0:1163:G:H1	1:0:1184:C:N4	2.17	0.43
29:2:40:ARG:HG3	29:2:45:ASN:CB	2.48	0.43
24:W:4:LEU:O	24:W:32:CYS:HA	2.18	0.43
22:U:17:THR:HG22	22:U:18:GLY:N	2.34	0.43
1:0:1080:C:O5'	1:0:1080:C:H6	2.02	0.43
1:0:2255:A:O2'	1:0:2256:G:H5'	2.18	0.43
1:0:2255:A:H2'	1:0:2256:G:O4'	2.18	0.43
1:0:815:U:O2'	1:0:1598:A:H4'	2.18	0.43
11:J:45:VAL:HG21	11:J:129:PHE:HD1	1.82	0.43
1:0:1654:U:H2'	3:A:47:HIS:CD2	2.52	0.43
26:Y:107:PRO:HD3	26:Y:182:PHE:CD1	2.54	0.43
1:0:2598:U:O2	1:0:2600:A:H8	2.00	0.43
1:0:73:C:O2'	1:0:74:A:H5'	2.18	0.43
1:0:213:G:N2	1:0:225:G:H2'	2.34	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:2348:C:H1'	6:D:131:THR:HG21	2.01	0.43
14:M:80:GLY:O	14:M:81:ARG:HD3	2.18	0.43
4:B:177:HIS:O	4:B:181:ILE:HG13	2.19	0.43
1:0:1805:G:H2'	1:0:1806:G:H8	1.83	0.43
1:0:1242:A:OP2	11:J:60:ARG:NH2	2.47	0.42
32:0:9000:13T:H233	32:0:9000:13T:H311	2.01	0.42
1:0:1181:A:H2'	1:0:1182:C:H5'	2.00	0.42
6:D:103:ASN:HD22	6:D:133:ASN:HA	1.84	0.42
1:0:2291:A:H8	38:0:6467:HOH:O	2.01	0.42
1:0:559:U:C5	1:0:560:C:C5	3.07	0.42
1:0:2712:G:H5'	38:0:5223:HOH:O	2.18	0.42
5:C:194:PHE:HA	5:C:234:VAL:HG13	2.01	0.42
38:0:6400:HOH:O	24:W:122:ARG:NH2	2.45	0.42
1:0:952:G:N3	1:0:2302:A:H2'	2.34	0.42
1:0:1930:A:H2'	1:0:1931:A:C8	2.54	0.42
28:1:53:LYS:HD3	28:1:53:LYS:HA	1.85	0.42
26:Y:234:VAL:HG12	26:Y:235:GLU:N	2.34	0.42
1:0:2504:A:H4'	10:H:71:ARG:NH1	2.34	0.42
1:0:571:C:O5'	1:0:571:C:H6	2.01	0.42
1:0:2519:C:O2'	1:0:2520:G:H5'	2.19	0.42
1:0:2072:G:C6	1:0:2533:C:H1'	2.54	0.42
1:0:169:A:H1'	30:3:48:ASN:ND2	2.34	0.42
2:9:3041:C:C2	6:D:50:VAL:HG21	2.54	0.42
6:D:44:ILE:HG23	6:D:45:THR:HG23	2.00	0.42
1:0:952:G:OP1	18:Q:42:LYS:HE2	2.20	0.42
21:T:28:SER:O	21:T:32:ARG:HG3	2.18	0.42
10:H:47:ILE:HG21	38:H:8579:HOH:O	2.20	0.42
1:0:1552:G:H2'	1:0:1553:C:C6	2.54	0.42
16:O:105:ASN:HD21	16:O:109:SER:N	2.18	0.42
16:O:21:SER:OG	16:O:106:PRO:HB2	2.18	0.42
1:0:682:A:H2'	1:0:683:G:O4'	2.19	0.42
1:0:1138:G:H4'	38:0:5719:HOH:O	2.19	0.42
26:Y:178:HIS:CG	26:Y:179:PRO:HD2	2.54	0.42
19:R:4:TYR:CE1	19:R:15:LYS:HD3	2.53	0.42
1:0:177:A:H2'	1:0:178:U:O4'	2.19	0.42
1:0:284:C:C4'	1:0:285:A:O5'	2.64	0.42
25:X:30:MET:HE1	25:X:55:ASN:HA	2.00	0.42
1:0:1544:U:H2'	1:0:1545:C:C6	2.54	0.42
1:0:151:A:H2'	1:0:152:A:O4'	2.18	0.42
4:B:165:ARG:HG2	4:B:166:VAL:N	2.35	0.42
1:0:644:G:O2'	36:0:8814:CL:CL	2.67	0.42
1:0:2015:A:H2'	1:0:2016:U:O4'	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:S:37:VAL:O	20:S:41:VAL:HG23	2.19	0.42
1:0:2785:C:H4'	1:0:2786:G:OP2	2.19	0.42
4:B:204:GLY:HA3	38:B:8948:HOH:O	2.18	0.42
1:0:1970:G:H2'	1:0:1970:G:N3	2.35	0.42
1:0:2608:C:H3'	38:0:7790:HOH:O	2.18	0.42
38:0:4740:HOH:O	15:N:21:HIS:HD2	2.01	0.42
6:D:91:ALA:HB1	38:D:5198:HOH:O	2.19	0.42
14:M:167:GLY:O	14:M:171:ARG:HG3	2.19	0.42
1:0:2415:A:H2'	1:0:2416:G:H5'	2.00	0.42
2:9:3001:U:H4'	2:9:3003:A:OP1	2.19	0.42
1:0:2296:C:H2'	1:0:2297:U:H6	1.82	0.42
22:U:6:CYS:HB2	22:U:32:CYS:HB3	2.00	0.42
1:0:1486:A:C5	29:2:2:LYS:HG3	2.55	0.42
16:O:44:ASN:HA	16:O:65:LEU:O	2.19	0.42
15:N:71:TRP:CE3	15:N:175:LEU:HD22	2.55	0.42
1:0:2909:G:O2'	1:0:2910:A:H5'	2.20	0.42
1:0:2502:C:O2'	1:0:2503:A:H5'	2.18	0.42
1:0:958:G:O2'	1:0:959:C:H5'	2.19	0.42
2:9:3031:C:H1'	38:9:1137:HOH:O	2.18	0.42
1:0:263:U:C4	8:F:54:VAL:HG13	2.54	0.42
1:0:395:A:H4'	38:0:9964:HOH:O	2.20	0.42
12:K:28:GLU:HB3	12:K:59:LYS:HB2	2.01	0.42
1:0:853:C:H2'	1:0:854:G:O4'	2.19	0.42
17:P:103:THR:O	17:P:107:GLU:HG3	2.20	0.42
28:1:26:SER:HB3	28:1:35:SER:OG	2.20	0.42
13:L:73:VAL:HG11	13:L:118:LEU:HD21	2.01	0.42
1:0:2395:A:C6	1:0:2396:C:C4	3.07	0.42
1:0:2035:C:O5'	1:0:2035:C:H6	2.02	0.42
1:0:1175:G:H1'	1:0:1193:A:H2'	2.01	0.42
1:0:1046:G:N3	1:0:1082:A:H2	2.17	0.42
2:9:3034:A:H8	2:9:3034:A:O5'	2.02	0.42
1:0:2265:U:H2'	1:0:2266:A:C8	2.55	0.42
1:0:475:G:C5'	5:C:73:LEU:HD23	2.50	0.42
1:0:482:G:O4'	1:0:511:A:C2	2.72	0.42
1:0:2105:C:O2'	1:0:2284:G:N2	2.52	0.42
26:Y:151:SER:HB3	26:Y:154:ARG:CB	2.49	0.42
11:J:39:VAL:HG13	11:J:106:GLY:O	2.20	0.42
1:0:764:C:H2'	1:0:765:G:O4'	2.19	0.42
1:0:2607:U:H4'	38:0:9438:HOH:O	2.18	0.42
14:M:28:GLN:O	14:M:32:ARG:HG3	2.18	0.42
15:N:170:GLU:O	15:N:174:GLU:HG3	2.20	0.42
3:A:9:ARG:NH1	38:A:8822:HOH:O	2.53	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:X:80:GLU:HB3	38:X:5564:HOH:O	2.17	0.42
19:R:82:GLU:O	19:R:86:LYS:HG3	2.20	0.42
32:0:9000:13T:H323	32:0:9000:13T:C1	2.49	0.42
1:0:440:C:H2'	1:0:441:A:C8	2.54	0.42
30:3:22:VAL:HG11	30:3:67:LEU:HD13	2.01	0.42
1:0:316:A:H5'	21:T:54:ASP:OD2	2.20	0.42
1:0:535:G:C6	1:0:2064:U:C5	3.08	0.42
38:0:3186:HOH:O	14:M:9:ARG:HG3	2.19	0.42
11:J:59:LYS:O	11:J:63:ILE:HG13	2.19	0.42
2:9:3059:C:H5'	38:9:5233:HOH:O	2.18	0.42
1:0:1323:G:N2	1:0:1335:C:C2	2.88	0.42
1:0:876:A:N3	1:0:876:A:C2'	2.83	0.42
2:9:3110:G:C5	2:9:3111:U:C5	3.07	0.42
4:B:57:GLU:HA	4:B:58:PRO:HD2	1.96	0.42
1:0:1161:A:O5'	1:0:1161:A:H8	2.02	0.42
2:9:3013:A:H3'	2:9:3014:G:H5'	2.02	0.42
13:L:120:LEU:HD12	13:L:133:VAL:HG21	2.02	0.42
1:0:2256:G:C2'	1:0:2257:G:C5'	2.93	0.42
1:0:447:A:OP1	21:T:2:LYS:HG2	2.20	0.42
38:0:3652:HOH:O	16:O:3:THR:HG21	2.19	0.42
4:B:243:ASN:HA	4:B:244:PRO:C	2.40	0.42
5:C:218:VAL:HG12	38:C:8623:HOH:O	2.19	0.42
5:C:118:THR:HG22	5:C:137:PRO:HB3	2.02	0.42
1:0:2078:U:O2'	1:0:2079:G:H5'	2.20	0.42
12:K:4:LEU:HD23	12:K:4:LEU:HA	1.83	0.42
1:0:2900:G:H2'	1:0:2901:C:O4'	2.20	0.42
38:0:4574:HOH:O	5:C:50:GLU:HG2	2.20	0.42
1:0:1579:C:H4'	1:0:1580:A:OP1	2.19	0.42
1:0:595:U:H2'	1:0:596:C:H6	1.85	0.42
1:0:282:C:O2'	1:0:283:U:C4'	2.68	0.42
1:0:856:G:H2'	38:0:5435:HOH:O	2.18	0.42
2:9:3059:C:H2'	2:9:3060:C:C6	2.55	0.42
1:0:589:U:H2'	1:0:590:A:C8	2.54	0.42
1:0:318:C:H5'	1:0:339:A:N3	2.35	0.42
1:0:1069:C:H2'	1:0:1070:A:O4'	2.20	0.42
22:U:6:CYS:C	22:U:8:TYR:H	2.21	0.42
6:D:25:MET:HE1	6:D:37:ALA:O	2.20	0.42
1:0:1923:G:H2'	1:0:1924:A:H8	1.84	0.42
6:D:64:ARG:HD3	6:D:67:ASP:HB3	2.02	0.42
26:Y:170:SER:OG	26:Y:175:ARG:HG3	2.19	0.42
1:0:2758:G:H2'	1:0:2759:C:C6	2.55	0.42
1:0:825:U:H5''	1:0:826:U:OP1	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:561:G:C2	1:0:562:A:C5	3.08	0.42
6:D:23:VAL:HG21	6:D:45:THR:HG21	2.02	0.42
1:0:2521:A:P	10:H:3:ALA:HB3	2.60	0.42
1:0:2240:U:O2'	1:0:2241:C:H5'	2.19	0.42
1:0:1789:G:H2'	1:0:1790:C:O5'	2.20	0.42
4:B:79:MET:HE3	4:B:79:MET:HB2	1.99	0.42
1:0:2824:C:O3'	1:0:2825:C:H6	2.01	0.42
19:R:132:ARG:NH2	38:R:8879:HOH:O	2.52	0.42
2:9:3114:G:H2'	2:9:3115:C:C6	2.55	0.42
4:B:24:PRO:HG3	4:B:204:GLY:HA2	2.01	0.42
1:0:1482:A:O2'	1:0:1483:C:H5'	2.20	0.42
4:B:305:ASP:O	4:B:306:LYS:CB	2.68	0.42
1:0:2612:A:H4'	38:0:3685:HOH:O	2.19	0.42
1:0:1055:G:OP2	10:H:96:ARG:NH1	2.53	0.42
1:0:2032:U:O2'	1:0:2033:G:H5''	2.20	0.41
19:R:18:LEU:HD12	19:R:143:VAL:HG11	2.02	0.41
6:D:48:MET:HA	6:D:49:PRO:HD3	1.87	0.41
1:0:1762:C:H4'	38:0:4662:HOH:O	2.19	0.41
1:0:517:U:C2'	1:0:518:G:H5'	2.50	0.41
1:0:946:C:H2'	1:0:947:U:H6	1.84	0.41
3:A:131:HIS:O	3:A:132:ASP:HB2	2.20	0.41
4:B:260:HIS:HE1	38:B:8883:HOH:O	2.03	0.41
1:0:941:G:C2'	1:0:942:U:H5'	2.50	0.41
2:9:3105:A:C2'	2:9:3106:C:H5'	2.49	0.41
1:0:2589:U:H2'	1:0:2590:U:C6	2.55	0.41
2:9:3059:C:O5'	2:9:3059:C:H6	2.03	0.41
1:0:2389:U:H4'	18:Q:53:HIS:CD2	2.55	0.41
6:D:25:MET:SD	6:D:40:ILE:HD11	2.60	0.41
3:A:76:VAL:HG23	27:Z:63:LYS:HB3	2.00	0.41
1:0:2724:U:H2'	1:0:2725:G:O4'	2.20	0.41
1:0:2401:A:H2'	1:0:2402:A:C8	2.55	0.41
1:0:1019:C:O2	18:Q:94:GLN:NE2	2.53	0.41
1:0:381:G:OP2	14:M:45:ARG:NH2	2.50	0.41
14:M:164:THR:HG22	14:M:167:GLY:N	2.35	0.41
22:U:17:THR:CG2	22:U:18:GLY:N	2.83	0.41
6:D:49:PRO:HG3	38:D:5828:HOH:O	2.21	0.41
1:0:2254:G:O2'	1:0:2255:A:H5'	2.20	0.41
8:F:48:VAL:HG23	8:F:74:PHE:HB3	2.01	0.41
1:0:553:G:H2'	1:0:554:G:H5'	2.02	0.41
28:1:25:LYS:HD2	29:2:49:GLU:H	1.84	0.41
1:0:2112:A:H2'	1:0:2113:G:H8	1.85	0.41
1:0:2689:A:C2'	1:0:2690:U:H5'	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:699:C:C6	1:0:744:G:C4	3.08	0.41
1:0:2754:G:C2'	1:0:2755:G:H5'	2.50	0.41
31:I:100:LEU:HD22	31:I:105:VAL:HG23	2.02	0.41
1:0:1904:A:C8	1:0:1905:U:C5	3.08	0.41
1:0:2402:A:H1'	38:0:3163:HOH:O	2.20	0.41
1:0:497:A:H2'	1:0:498:A:C5'	2.50	0.41
8:F:14:ASP:O	8:F:18:GLU:HG3	2.20	0.41
31:I:91:GLU:HA	31:I:92:PRO:HD2	1.84	0.41
24:W:4:LEU:CD1	24:W:24:LEU:HD13	2.50	0.41
1:0:1158:G:O2'	1:0:1159:G:H5'	2.20	0.41
27:Z:30:GLU:HB2	38:Z:8715:HOH:O	2.20	0.41
21:T:9:LYS:HE3	21:T:13:ARG:NH1	2.35	0.41
2:9:3042:C:O2	6:D:76:ARG:NH1	2.52	0.41
1:0:694:A:H4'	1:0:2441:U:OP1	2.21	0.41
1:0:2434:A:O3'	30:3:28:GLY:HA3	2.20	0.41
26:Y:112:GLU:CD	26:Y:115:ARG:NH1	2.74	0.41
1:0:1225:C:H2'	1:0:1226:G:O4'	2.21	0.41
2:9:3105:A:H2'	2:9:3106:C:H5'	2.03	0.41
1:0:902:G:N7	13:L:18:HIS:CD2	2.85	0.41
1:0:371:U:H2'	1:0:372:A:C8	2.55	0.41
11:J:19:MET:CE	11:J:132:LEU:HD11	2.51	0.41
28:1:25:LYS:HE2	38:2:7213:HOH:O	2.20	0.41
1:0:1576:G:H2'	1:0:1577:U:H6	1.85	0.41
2:9:3033:U:H2'	38:9:3797:HOH:O	2.19	0.41
10:H:171:ALA:HA	38:H:8570:HOH:O	2.20	0.41
1:0:459:A:H5''	38:0:9047:HOH:O	2.20	0.41
1:0:185:G:O3'	1:0:186:A:H4'	2.21	0.41
7:E:84:MET:HG2	7:E:168:ILE:HA	2.02	0.41
1:0:1289:C:O2'	1:0:1290:G:H5'	2.19	0.41
25:X:7:GLU:HA	25:X:74:ALA:O	2.20	0.41
1:0:1943:C:C4'	3:A:212:PRO:HA	2.50	0.41
11:J:74:ARG:HH11	11:J:74:ARG:CB	2.30	0.41
1:0:695:C:H2'	1:0:696:C:C6	2.54	0.41
1:0:2825:C:H4'	1:0:2826:G:O5'	2.20	0.41
1:0:1422:U:H4'	38:0:7732:HOH:O	2.19	0.41
1:0:2634:G:OP2	3:A:204:GLY:N	2.53	0.41
1:0:2270:G:H4'	3:A:223:ARG:HH12	1.86	0.41
11:J:19:MET:HE1	11:J:132:LEU:HD11	2.02	0.41
1:0:81:G:N3	1:0:98:A:C2	2.89	0.41
1:0:1815:A:H4'	1:0:2751:C:O4'	2.21	0.41
15:N:42:HIS:CG	15:N:62:HIS:HE1	2.38	0.41
2:9:3092:G:C6	2:9:3093:A:N6	2.88	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:X:74:ALA:CB	25:X:85:VAL:HG22	2.51	0.41
1:0:308:U:C4	1:0:342:C:C1'	3.03	0.41
2:9:3001:U:H5'	2:9:3121:C:O2	2.20	0.41
2:9:3001:U:O3'	2:9:3003:A:C5'	2.69	0.41
8:F:50:VAL:CG1	8:F:60:VAL:HG11	2.48	0.41
14:M:182:LYS:HB2	14:M:194:ALA:HB2	2.01	0.41
1:0:1024:G:C6	1:0:1025:C:C4	3.08	0.41
27:Z:67:GLY:N	27:Z:70:LYS:O	2.54	0.41
24:W:149:LEU:HG	24:W:153:MET:HE2	2.03	0.41
4:B:69:VAL:HA	4:B:70:PRO:HD3	1.86	0.41
1:0:1923:G:H2'	1:0:1924:A:C8	2.56	0.41
1:0:1052:G:N3	1:0:1052:G:H2'	2.35	0.41
1:0:61:G:C6	1:0:62:C:C4	3.09	0.41
1:0:1020:A:H2'	1:0:1021:G:C8	2.56	0.41
1:0:849:C:O2'	1:0:850:U:H5'	2.21	0.41
1:0:1400:C:O2'	1:0:1401:G:H5'	2.21	0.41
1:0:1206:U:C5'	1:0:1206:U:H6	2.23	0.41
1:0:255:A:C5	1:0:256:C:C5	3.09	0.41
31:I:129:VAL:O	31:I:129:VAL:HG12	2.21	0.41
7:E:145:ALA:HB1	7:E:168:ILE:CD1	2.51	0.41
1:0:2775:A:C6	1:0:2776:A:C6	3.08	0.41
24:W:19:ASP:O	24:W:23:MET:HG3	2.20	0.41
1:0:863:G:C6	1:0:864:U:C4	3.08	0.41
18:Q:16:ASN:OD1	18:Q:45:PRO:HB2	2.20	0.41
1:0:1181:A:C2'	1:0:1182:C:H5'	2.51	0.41
1:0:1224:G:H2'	1:0:1225:C:C6	2.55	0.41
1:0:2549:C:O2'	1:0:2550:U:H5'	2.20	0.41
1:0:298:C:O5'	1:0:298:C:H6	2.04	0.41
4:B:7:ARG:HG2	4:B:7:ARG:HH11	1.85	0.41
7:E:5:LEU:HD21	7:E:66:GLN:HG3	2.01	0.41
14:M:123:ASP:OD1	14:M:126:GLN:HG2	2.19	0.41
24:W:119:HIS:HD2	24:W:120:PRO:O	2.03	0.41
1:0:25:A:O2'	1:0:640:G:H5'	2.21	0.41
1:0:2716:G:H5''	4:B:206:THR:CG2	2.44	0.41
2:9:3003:A:H61	2:9:3022:G:H1'	1.83	0.41
1:0:539:G:H2'	1:0:540:A:C8	2.56	0.41
1:0:2036:C:C1'	12:K:44:LEU:HG	2.51	0.41
14:M:158:ARG:HB2	14:M:163:LEU:HB2	2.03	0.41
1:0:247:A:H1'	38:0:3892:HOH:O	2.21	0.41
26:Y:144:ARG:NH2	38:Y:8912:HOH:O	2.54	0.41
20:S:45:TYR:O	20:S:80:ARG:NH2	2.53	0.41
12:K:132:VAL:HG21	22:U:22:VAL:CG1	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1021:G:O2'	1:0:1022:A:H5'	2.19	0.41
1:0:2365:G:H4'	18:Q:45:PRO:O	2.20	0.41
1:0:912:A:C4	1:0:1294:A:C2	3.09	0.41
1:0:295:C:H2'	1:0:296:G:O4'	2.20	0.41
1:0:1609:C:H2'	1:0:1610:G:H8	1.84	0.41
1:0:1622:G:H2'	1:0:1623:C:H5'	2.02	0.41
19:R:72:VAL:CG1	19:R:75:TRP:HB3	2.50	0.41
13:L:92:ASP:HA	13:L:121:ILE:HB	2.02	0.41
1:0:2303:A:H2	38:Q:5641:HOH:O	2.03	0.41
1:0:1666:C:H2'	1:0:1667:A:H8	1.86	0.41
1:0:1115:U:O2'	1:0:1116:U:H5'	2.20	0.41
1:0:1116:U:C2	1:0:1246:A:N6	2.89	0.41
1:0:1166:A:P	1:0:1174:A:H4'	2.61	0.41
1:0:368:C:H2'	1:0:369:G:H5'	2.02	0.41
1:0:1157:C:O2'	1:0:1158:G:H5'	2.20	0.41
1:0:2768:A:H5''	38:0:4432:HOH:O	2.21	0.41
1:0:2569:A:H2'	1:0:2570:G:O5'	2.20	0.41
1:0:2727:A:N1	1:0:2756:U:C2	2.89	0.41
1:0:169:A:H4'	38:M:8837:HOH:O	2.20	0.41
2:9:3040:C:OP1	2:9:3041:C:H5	2.04	0.41
3:A:186:TRP:CG	3:A:187:PRO:HA	2.56	0.41
4:B:23:THR:HG23	4:B:308:LEU:CD2	2.51	0.41
1:0:2415:A:O2'	15:N:29:SER:HB3	2.21	0.41
2:9:3001:U:C4'	2:9:3003:A:OP1	2.69	0.41
1:0:567:U:O2'	1:0:568:G:H5'	2.20	0.41
2:9:3065:A:O2'	2:9:3066:G:P	2.79	0.41
19:R:113:HIS:O	19:R:145:LEU:HD12	2.20	0.41
31:I:131:THR:O	31:I:135:LEU:HG	2.21	0.41
11:J:42:GLU:HG2	11:J:43:ARG:HG3	2.03	0.41
3:A:105:VAL:HG11	3:A:154:ALA:CB	2.51	0.41
2:9:3104:A:C2'	2:9:3105:A:H5'	2.50	0.41
4:B:41:PHE:CZ	4:B:79:MET:HG3	2.56	0.41
1:0:66:G:C2	1:0:109:U:C4	3.08	0.41
21:T:32:ARG:NH1	21:T:38:ARG:NH1	2.69	0.41
1:0:327:A:H4'	1:0:329:A:C8	2.55	0.41
1:0:1619:G:C6	1:0:1620:C:N3	2.89	0.41
1:0:287:C:H6	1:0:287:C:O5'	2.04	0.41
1:0:1805:G:O2'	1:0:1806:G:H5'	2.21	0.41
1:0:2607:U:C4	4:B:242:TRP:CZ2	3.08	0.41
1:0:1786:C:OP1	17:P:74:GLN:HG2	2.21	0.41
4:B:329:TYR:CE2	22:U:15:PRO:HG2	2.56	0.41
5:C:228:ALA:HA	5:C:229:PRO:HD3	1.90	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:B:265:LEU:HD21	4:B:316:ARG:HD3	2.01	0.41
6:D:151:ILE:HA	6:D:152:PRO:HD3	1.92	0.41
21:T:3:GLN:HA	21:T:4:PRO:HD3	1.76	0.41
4:B:52:VAL:O	4:B:53:LEU:HD12	2.21	0.41
1:0:483:C:C4	1:0:484:A:C6	3.09	0.41
1:0:581:G:O2'	1:0:582:C:H5'	2.21	0.41
24:W:81:ASP:OD1	24:W:92:ASP:HB2	2.20	0.41
1:0:1630:A:O2'	1:0:1631:A:H5'	2.21	0.41
1:0:2398:A:H2'	1:0:2399:G:O4'	2.21	0.41
1:0:911:G:H5'	1:0:932:U:OP1	2.21	0.41
32:0:9000:13T:H261	32:0:9000:13T:H10	1.80	0.41
1:0:1182:C:H6	1:0:1182:C:O5'	2.02	0.41
17:P:115:SER:O	17:P:117:SER:N	2.46	0.41
1:0:2004:U:H5''	1:0:2005:G:C8	2.56	0.41
1:0:2363:G:H2'	1:0:2364:A:O4'	2.21	0.41
1:0:1299:G:N2	38:0:4691:HOH:O	2.53	0.41
1:0:1662:C:H2'	1:0:1663:G:O4'	2.21	0.41
1:0:380:A:O4'	1:0:382:U:H1'	2.21	0.41
1:0:1594:C:OP1	17:P:109:ARG:NH1	2.54	0.41
26:Y:144:ARG:NE	38:Y:8912:HOH:O	2.54	0.41
1:0:397:A:H1'	1:0:417:G:H1'	2.02	0.41
1:0:2791:U:H1'	1:0:2792:A:H5''	2.03	0.41
1:0:2791:U:H4'	1:0:2792:A:OP1	2.21	0.41
1:0:2897:C:O2'	1:0:2898:G:H5'	2.21	0.41
1:0:716:G:C6	1:0:717:C:N4	2.89	0.41
13:L:119:THR:HA	13:L:139:SER:O	2.21	0.41
3:A:68:ILE:HD11	38:A:8863:HOH:O	2.20	0.41
1:0:545:G:H2'	1:0:546:C:O4'	2.21	0.40
1:0:2072:G:H3'	1:0:2073:G:C5'	2.52	0.40
1:0:1925:G:O2'	1:0:1926:G:H5'	2.21	0.40
4:B:336:GLN:NE2	38:B:8822:HOH:O	2.53	0.40
26:Y:189:ASN:ND2	26:Y:192:ASP:N	2.69	0.40
7:E:69:ILE:HA	7:E:72:MET:HE2	2.03	0.40
4:B:198:GLU:HA	38:B:8952:HOH:O	2.20	0.40
3:A:33:GLU:CD	3:A:33:GLU:H	2.24	0.40
1:0:2887:G:H2'	1:0:2888:U:O4'	2.21	0.40
1:0:228:C:H2'	1:0:229:G:C5'	2.51	0.40
7:E:22:VAL:O	7:E:28:SER:HA	2.22	0.40
1:0:2549:C:H2'	1:0:2550:U:O4'	2.22	0.40
1:0:445:U:C1'	38:0:7326:HOH:O	2.68	0.40
1:0:2598:U:O2	1:0:2600:A:C8	2.74	0.40
4:B:305:ASP:O	4:B:306:LYS:HB2	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:1449:G:N3	1:0:1449:G:H2'	2.36	0.40
19:R:89:LEU:HA	19:R:89:LEU:HD23	1.84	0.40
7:E:172:PRO:HB3	38:E:6931:HOH:O	2.21	0.40
1:0:1745:G:H5'	38:0:4341:HOH:O	2.20	0.40
9:G:67:LEU:O	9:G:71:LEU:HG	2.21	0.40
1:0:542:A:H2'	1:0:543:G:O4'	2.21	0.40
1:0:1642:A:N7	1:0:1643:C:C4	2.89	0.40
1:0:567:U:O5'	1:0:567:U:H6	2.04	0.40
26:Y:134:HIS:H	26:Y:134:HIS:CD2	2.38	0.40
1:0:2064:U:H2'	1:0:2065:C:H6	1.86	0.40
1:0:535:G:O6	1:0:2064:U:C6	2.75	0.40
1:0:1310:U:P	5:C:168:ARG:HH11	2.44	0.40
1:0:2361:A:H2'	1:0:2362:A:O4'	2.21	0.40
1:0:1457:U:H5	38:0:7859:HOH:O	2.04	0.40
1:0:2547:C:OP2	4:B:5:ARG:NH1	2.54	0.40
1:0:2453:G:O3'	13:L:50:GLY:HA2	2.21	0.40
1:0:1494:A:H1'	1:0:1495:C:C6	2.56	0.40
1:0:1574:C:H6	1:0:1574:C:O5'	2.04	0.40
1:0:699:C:H6	1:0:744:G:O4'	2.03	0.40
1:0:2344:G:H2'	1:0:2344:G:N3	2.36	0.40
1:0:1657:A:H2'	1:0:1658:A:C8	2.56	0.40
1:0:1268:C:O2'	26:Y:169:ARG:HB2	2.21	0.40
1:0:574:C:H2'	1:0:575:G:O4'	2.21	0.40
24:W:13:MET:CE	24:W:18:GLN:HA	2.49	0.40
3:A:105:VAL:HG12	3:A:106:CYS:N	2.36	0.40
6:D:25:MET:HE3	6:D:37:ALA:HB1	2.04	0.40
1:0:1902:G:H2'	1:0:1903:U:O4'	2.21	0.40
1:0:74:A:H2'	1:0:75:U:C6	2.55	0.40
1:0:844:A:C6	1:0:882:A:C6	3.09	0.40
17:P:121:ASP:HB2	38:P:5891:HOH:O	2.21	0.40
24:W:65:VAL:HG12	24:W:116:LEU:HD13	2.04	0.40
1:0:2902:A:H4'	1:0:2903:C:OP1	2.21	0.40
26:Y:177:LYS:HD3	26:Y:181:GLY:O	2.22	0.40
1:0:2642:G:H2'	1:0:2643:G:O4'	2.22	0.40
14:M:72:ALA:HB2	14:M:93:ARG:HG2	2.03	0.40
1:0:1180:U:O2'	31:I:92:PRO:HD2	2.21	0.40
1:0:1189:A:C3'	38:0:7666:HOH:O	2.62	0.40
1:0:559:U:C4'	1:0:559:U:C6	3.04	0.40
1:0:1741:U:H3'	38:0:9763:HOH:O	2.20	0.40
1:0:485:A:HO2'	1:0:487:G:H8	1.68	0.40
38:9:466:HOH:O	18:Q:25:PRO:HB3	2.21	0.40
1:0:1308:A:O4'	5:C:226:GLY:HA3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:0:517:U:H2'	1:0:518:G:H5'	2.03	0.40
1:0:1309:U:H2'	1:0:1310:U:O4'	2.21	0.40
1:0:705:C:C2'	1:0:705:C:O2	2.70	0.40
1:0:474:C:O3'	5:C:73:LEU:HD21	2.22	0.40
25:X:30:MET:CE	25:X:58:ALA:HB3	2.52	0.40
1:0:2754:G:HO2'	1:0:2755:G:H5'	1.85	0.40
1:0:1705:C:P	17:P:59:ARG:HH12	2.45	0.40
6:D:25:MET:CE	6:D:37:ALA:HB1	2.51	0.40
2:9:3110:G:C2'	2:9:3111:U:H5'	2.51	0.40
6:D:64:ARG:HB3	6:D:67:ASP:OD2	2.22	0.40
1:0:1006:A:N1	1:0:2311:A:H1'	2.37	0.40
16:O:45:LEU:CD1	16:O:88:LYS:HD2	2.51	0.40
12:K:62:PRO:HG3	12:K:65:ARG:NH2	2.37	0.40
1:0:243:A:H2	1:0:274:G:N3	2.19	0.40
16:O:14:LEU:HB3	16:O:26:TRP:O	2.21	0.40
1:0:260:C:C4	1:0:261:A:C5	3.10	0.40
1:0:1087:G:H4'	1:0:1088:A:OP1	2.22	0.40
1:0:2673:U:C4	1:0:2674:G:C6	3.10	0.40
5:C:175:LYS:HD2	5:C:187:ARG:HB3	2.04	0.40
1:0:1617:C:C4	1:0:1643:C:H4'	2.57	0.40
27:Z:49:ARG:NH2	27:Z:52:THR:HA	2.37	0.40
8:F:58:GLU:HA	8:F:61:MET:CE	2.47	0.40
1:0:1329:A:H5''	38:O:3790:HOH:O	2.20	0.40
1:0:820:G:H5'	1:0:821:U:C5'	2.51	0.40
23:V:39:ALA:O	23:V:41:GLU:N	2.51	0.40
1:0:1544:U:H2'	1:0:1545:C:H6	1.87	0.40
29:2:49:GLU:HB2	38:2:131:HOH:O	2.21	0.40
1:0:1334:C:H2'	1:0:1335:C:H6	1.86	0.40
1:0:160:A:C4	1:0:177:A:C2	3.09	0.40
14:M:28:GLN:HA	14:M:31:TRP:HB2	2.03	0.40
17:P:40:VAL:O	17:P:44:VAL:HG23	2.22	0.40
19:R:17:MET:HE3	19:R:19:ARG:HH21	1.86	0.40
7:E:6:GLU:HA	7:E:46:THR:HG22	2.03	0.40
25:X:8:ARG:NH1	38:X:2479:HOH:O	2.49	0.40
1:0:245:C:H2'	1:0:246:G:H5'	2.04	0.40
1:0:2739:A:C6	1:0:2740:G:C5	3.09	0.40
1:0:1453:G:H2'	1:0:1454:U:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	235/240 (98%)	212 (90%)	21 (9%)	2 (1%)	25	66
4	B	335/338 (99%)	310 (92%)	21 (6%)	4 (1%)	19	57
5	C	244/246 (99%)	224 (92%)	18 (7%)	2 (1%)	27	68
6	D	134/177 (76%)	113 (84%)	18 (13%)	3 (2%)	10	37
7	E	170/178 (96%)	163 (96%)	6 (4%)	1 (1%)	33	76
8	F	117/120 (98%)	103 (88%)	11 (9%)	3 (3%)	8	32
9	G	25/348 (7%)	25 (100%)	0	0	100	100
10	H	156/171 (91%)	142 (91%)	11 (7%)	3 (2%)	12	42
11	J	140/145 (97%)	129 (92%)	9 (6%)	2 (1%)	16	52
12	K	130/132 (98%)	122 (94%)	8 (6%)	0	100	100
13	L	141/165 (86%)	121 (86%)	20 (14%)	0	100	100
14	M	192/194 (99%)	183 (95%)	9 (5%)	0	100	100
15	N	184/187 (98%)	167 (91%)	13 (7%)	4 (2%)	10	37
16	O	113/116 (97%)	110 (97%)	3 (3%)	0	100	100
17	P	141/149 (95%)	136 (96%)	4 (3%)	1 (1%)	30	72
18	Q	93/96 (97%)	86 (92%)	6 (6%)	1 (1%)	21	60
19	R	148/155 (96%)	137 (93%)	11 (7%)	0	100	100
20	S	79/85 (93%)	76 (96%)	3 (4%)	0	100	100
21	T	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	25	66
22	U	51/66 (77%)	48 (94%)	3 (6%)	0	100	100
23	V	63/71 (89%)	58 (92%)	5 (8%)	0	100	100
24	W	152/154 (99%)	150 (99%)	0	2 (1%)	18	54
25	X	80/92 (87%)	72 (90%)	7 (9%)	1 (1%)	18	54
26	Y	140/241 (58%)	140 (100%)	0	0	100	100
27	Z	71/73 (97%)	60 (84%)	9 (13%)	2 (3%)	8	29
28	1	54/57 (95%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
30	3	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
31	I	68/161 (42%)	62 (91%)	6 (9%)	0	100	100
All	All	3705/4419 (84%)	3436 (93%)	237 (6%)	32 (1%)	25	66

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	F	101	ALA
10	H	166	SER
11	J	5	GLU
15	N	154	LEU
15	N	183	ASP
15	N	184	ILE
3	A	34	ASP
4	B	34	GLY
4	B	169	GLY
6	D	27	ILE
6	D	137	PRO
6	D	173	GLU
8	F	44	SER
24	W	49	ASN
3	A	37	VAL
15	N	139	TRP
27	Z	42	CYS
5	C	79	ARG
10	H	16	ARG
10	H	168	ALA
17	P	117	SER
25	X	70	ILE
4	B	2	GLN
5	C	8	LEU
8	F	64	PRO
21	T	44	ALA
24	W	77	ALA
4	B	306	LYS
7	E	44	GLY
11	J	89	HIS
18	Q	18	PRO
27	Z	43	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	179/182 (98%)	170 (95%)	9 (5%)	34	73
4	B	282/283 (100%)	268 (95%)	14 (5%)	34	73
5	C	193/193 (100%)	178 (92%)	15 (8%)	18	46
6	D	117/148 (79%)	115 (98%)	2 (2%)	73	94
7	E	152/156 (97%)	149 (98%)	3 (2%)	68	92
8	F	93/94 (99%)	89 (96%)	4 (4%)	40	78
9	G	27/283 (10%)	27 (100%)	0	100	100
10	H	132/138 (96%)	126 (96%)	6 (4%)	38	77
11	J	118/121 (98%)	110 (93%)	8 (7%)	22	55
12	K	106/106 (100%)	104 (98%)	2 (2%)	69	93
13	L	113/127 (89%)	107 (95%)	6 (5%)	32	70
14	M	158/158 (100%)	149 (94%)	9 (6%)	29	66
15	N	149/150 (99%)	146 (98%)	3 (2%)	68	92
16	O	93/94 (99%)	92 (99%)	1 (1%)	84	97
17	P	113/117 (97%)	109 (96%)	4 (4%)	48	85
18	Q	79/80 (99%)	78 (99%)	1 (1%)	80	96
19	R	117/122 (96%)	113 (97%)	4 (3%)	49	86
20	S	71/74 (96%)	70 (99%)	1 (1%)	78	96
21	T	105/106 (99%)	99 (94%)	6 (6%)	29	66
22	U	44/52 (85%)	43 (98%)	1 (2%)	63	92
23	V	51/57 (90%)	49 (96%)	2 (4%)	43	82
24	W	130/130 (100%)	124 (95%)	6 (5%)	37	76
25	X	66/74 (89%)	61 (92%)	5 (8%)	19	48
26	Y	120/196 (61%)	114 (95%)	6 (5%)	34	73
27	Z	60/60 (100%)	60 (100%)	0	100	100
28	1	46/47 (98%)	45 (98%)	1 (2%)	64	92
29	2	42/46 (91%)	40 (95%)	2 (5%)	35	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	3	79/79 (100%)	78 (99%)	1 (1%)	80	96
31	I	58/129 (45%)	56 (97%)	2 (3%)	49	86
All	All	3093/3602 (86%)	2969 (96%)	124 (4%)	42	81

All (124) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	3	ARG
3	A	36	ASP
3	A	69	LEU
3	A	94	LEU
3	A	120	ARG
3	A	131	HIS
3	A	153	ARG
3	A	179	MET
3	A	217	ARG
4	B	7	ARG
4	B	11	LEU
4	B	27	ASN
4	B	33	ASP
4	B	56	ASP
4	B	97	LEU
4	B	98	THR
4	B	149	ASP
4	B	162	MET
4	B	175	LEU
4	B	195	ARG
4	B	254	GLN
4	B	257	THR
4	B	312	ARG
5	C	2	GLN
5	C	27	ARG
5	C	67	GLN
5	C	76	ARG
5	C	91	PRO
5	C	94	THR
5	C	115	LEU
5	C	136	VAL
5	C	162	VAL
5	C	187	ARG
5	C	214	THR

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Mol	Chain	Res	Type
5	C	222	ASP
5	C	223	LEU
5	C	236	THR
5	C	240	LEU
6	D	61	PHE
6	D	149	ARG
7	E	16	ASP
7	E	86	VAL
7	E	102	VAL
8	F	12	LEU
8	F	24	ARG
8	F	46	GLU
8	F	103	GLU
10	H	59	HIS
10	H	62	LEU
10	H	84	LYS
10	H	96	ARG
10	H	119	LYS
10	H	154	TYR
11	J	46	ILE
11	J	52	GLN
11	J	74	ARG
11	J	79	PHE
11	J	93	ARG
11	J	107	ASN
11	J	120	SER
11	J	132	LEU
12	K	10	GLN
12	K	132	VAL
13	L	30	ARG
13	L	35	ARG
13	L	51	PHE
13	L	99	GLU
13	L	101	ASP
13	L	140	VAL
14	M	10	ASP
14	M	46	LEU
14	M	68	ARG
14	M	75	ARG
14	M	81	ARG
14	M	93	ARG
14	M	99	ARG

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Mol	Chain	Res	Type
14	M	116	ASN
14	M	164	THR
15	N	26	LEU
15	N	49	THR
15	N	138	ASP
16	O	43	VAL
17	P	21	VAL
17	P	52	LYS
17	P	91	LYS
17	P	98	ILE
18	Q	95	GLU
19	R	13	THR
19	R	82	GLU
19	R	132	ARG
19	R	143	VAL
20	S	72	ASP
21	T	39	ASN
21	T	48	VAL
21	T	73	HIS
21	T	89	ARG
21	T	96	VAL
21	T	117	ASP
22	U	47	ARG
23	V	12	THR
23	V	65	ASP
24	W	26	ILE
24	W	35	VAL
24	W	73	LEU
24	W	109	GLU
24	W	142	ASP
24	W	146	ILE
25	X	15	ARG
25	X	27	ASP
25	X	52	PRO
25	X	72	VAL
25	X	82	GLU
26	Y	154	ARG
26	Y	189	ASN
26	Y	200	THR
26	Y	203	VAL
26	Y	204	ARG
26	Y	220	GLU

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Mol	Chain	Res	Type
28	1	47	ASP
29	2	18	ASN
29	2	31	ARG
30	3	3	MET
31	I	87	THR
31	I	100	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	47	HIS
3	A	176	HIS
3	A	199	HIS
4	B	27	ASN
4	B	145	HIS
4	B	238	ASN
4	B	256	GLN
4	B	260	HIS
4	B	320	GLN
4	B	332	ASN
5	C	129	HIS
6	D	85	GLN
6	D	103	ASN
6	D	133	ASN
7	E	119	HIS
7	E	143	GLN
9	G	17	GLN
9	G	64	ASN
10	H	46	GLN
10	H	56	GLN
10	H	59	HIS
10	H	170	ASN
11	J	52	GLN
11	J	107	ASN
12	K	10	GLN
12	K	42	ASN
13	L	18	HIS
13	L	41	HIS
13	L	42	ASN
13	L	116	HIS
14	M	24	GLN
14	M	58	GLN

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Mol	Chain	Res	Type
14	M	137	ASN
14	M	170	ASN
15	N	21	HIS
15	N	107	ASN
17	P	50	GLN
17	P	73	HIS
17	P	118	GLN
18	Q	40	HIS
19	R	94	ASN
19	R	98	ASN
19	R	117	HIS
19	R	123	GLN
20	S	9	HIS
20	S	53	ASN
21	T	39	ASN
22	U	39	ASN
22	U	48	ASN
23	V	60	GLN
24	W	28	HIS
24	W	110	GLN
24	W	119	HIS
24	W	125	HIS
24	W	141	HIS
25	X	23	HIS
26	Y	134	HIS
26	Y	149	GLN
26	Y	188	HIS
26	Y	189	ASN
28	1	8	GLN
28	1	16	HIS
28	1	28	HIS
29	2	18	ASN
29	2	41	HIS
29	2	45	ASN
30	3	2	GLN
30	3	30	GLN
30	3	48	ASN
31	I	93	GLN
31	I	107	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2746/2922 (93%)	241 (8%)	33 (1%)
2	9	121/122 (99%)	18 (14%)	1 (0%)
All	All	2867/3044 (94%)	259 (9%)	34 (1%)

All (259) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	11	A
1	0	31	C
1	0	67	A
1	0	69	A
1	0	70	A
1	0	71	G
1	0	87	C
1	0	88	G
1	0	114	A
1	0	115	U
1	0	120	A
1	0	130	C
1	0	139	C
1	0	141	C
1	0	151	A
1	0	166	A
1	0	185	G
1	0	186	A
1	0	191	A
1	0	192	A
1	0	219	G
1	0	237	G
1	0	271	C
1	0	272	A
1	0	273	G
1	0	283	U
1	0	284	C
1	0	285	A
1	0	308	U
1	0	309	C
1	0	336	G
1	0	337	A
1	0	345	G
1	0	358	G
1	0	381	G
1	0	397	A

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Mol	Chain	Res	Type
1	0	417	G
1	0	461	C
1	0	487	G
1	0	498	A
1	0	510	U
1	0	511	A
1	0	514	G
1	0	537	G
1	0	538	C
1	0	539	G
1	0	542	A
1	0	545	G
1	0	553	G
1	0	559	U
1	0	588	G
1	0	604	G
1	0	620	A
1	0	632	A
1	0	644	G
1	0	660	A
1	0	688	A
1	0	701	U
1	0	759	C
1	0	777	U
1	0	809	G
1	0	821	U
1	0	835	U
1	0	840	U
1	0	857	A
1	0	858	U
1	0	868	G
1	0	869	G
1	0	872	U
1	0	875	A
1	0	877	G
1	0	878	G
1	0	882	A
1	0	884	C
1	0	885	G
1	0	898	G
1	0	905	C
1	0	920	C

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Mol	Chain	Res	Type
1	0	921	G
1	0	923	A
1	0	953	G
1	0	960	G
1	0	961	A
1	0	1003	U
1	0	1006	A
1	0	1008	C
1	0	1029	U
1	0	1045	G
1	0	1059	G
1	0	1060	C
1	0	1072	G
1	0	1081	A
1	0	1087	G
1	0	1088	A
1	0	1109	U
1	0	1110	G
1	0	1119	G
1	0	1130	U
1	0	1137	G
1	0	1151	G
1	0	1164	U
1	0	1165	G
1	0	1166	A
1	0	1174	A
1	0	1175	G
1	0	1185	U
1	0	1192	A
1	0	1193	A
1	0	1205	U
1	0	1206	U
1	0	1216	G
1	0	1237	U
1	0	1238	C
1	0	1239	G
1	0	1279	U
1	0	1289	C
1	0	1331	A
1	0	1342	C
1	0	1353	C
1	0	1360	C

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Mol	Chain	Res	Type
1	0	1377	C
1	0	1407	A
1	0	1451	C
1	0	1474	C
1	0	1492	A
1	0	1505	U
1	0	1506	U
1	0	1524	U
1	0	1525	G
1	0	1526	A
1	0	1559	A
1	0	1564	C
1	0	1580	A
1	0	1592	G
1	0	1625	U
1	0	1626	A
1	0	1633	C
1	0	1634	G
1	0	1656	A
1	0	1667	A
1	0	1682	A
1	0	1684	A
1	0	1685	A
1	0	1692	C
1	0	1701	A
1	0	1722	U
1	0	1723	G
1	0	1725	C
1	0	1730	G
1	0	1731	C
1	0	1732	A
1	0	1742	A
1	0	1752	G
1	0	1778	A
1	0	1798	C
1	0	1819	G
1	0	1820	G
1	0	1829	A
1	0	1856	C
1	0	1879	U
1	0	1919	A
1	0	1942	A

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Mol	Chain	Res	Type
1	0	1971	G
1	0	1973	A
1	0	1979	G
1	0	1996	U
1	0	2006	C
1	0	2008	U
1	0	2011	A
1	0	2012	U
1	0	2013	G
1	0	2033	G
1	0	2034	U
1	0	2064	U
1	0	2072	G
1	0	2073	G
1	0	2074	A
1	0	2096	A
1	0	2101	A
1	0	2102	G
1	0	2110	G
1	0	2238	A
1	0	2243	C
1	0	2258	A
1	0	2271	G
1	0	2272	G
1	0	2291	A
1	0	2317	C
1	0	2321	A
1	0	2354	A
1	0	2361	A
1	0	2369	A
1	0	2379	G
1	0	2422	U
1	0	2462	G
1	0	2465	A
1	0	2467	A
1	0	2468	A
1	0	2469	A
1	0	2476	C
1	0	2483	A
1	0	2507	G
1	0	2511	A
1	0	2526	C

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Mol	Chain	Res	Type
1	0	2527	U
1	0	2533	C
1	0	2537	G
1	0	2541	U
1	0	2553	A
1	0	2564	G
1	0	2589	U
1	0	2601	A
1	0	2602	G
1	0	2608	C
1	0	2613	G
1	0	2634	G
1	0	2638	G
1	0	2649	A
1	0	2650	U
1	0	2664	A
1	0	2681	A
1	0	2682	C
1	0	2719	A
1	0	2726	U
1	0	2747	C
1	0	2748	G
1	0	2749	U
1	0	2750	G
1	0	2762	C
1	0	2768	A
1	0	2786	G
1	0	2800	A
1	0	2811	A
1	0	2825	C
1	0	2850	C
1	0	2867	G
1	0	2876	G
1	0	2890	A
1	0	2896	A
1	0	2903	C
1	0	2914	A
2	9	3002	U
2	9	3007	G
2	9	3014	G
2	9	3022	G
2	9	3023	U

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Mol	Chain	Res	Type
2	9	3024	U
2	9	3025	G
2	9	3039	U
2	9	3040	C
2	9	3041	C
2	9	3043	G
2	9	3044	A
2	9	3052	A
2	9	3057	A
2	9	3066	G
2	9	3077	A
2	9	3114	G
2	9	3122	C

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	10	U
1	0	69	A
1	0	129	A
1	0	338	C
1	0	603	A
1	0	644	G
1	0	699	C
1	0	834	G
1	0	857	A
1	0	871	G
1	0	877	G
1	0	1080	C
1	0	1165	G
1	0	1232	A
1	0	1237	U
1	0	1246	A
1	0	1352	A
1	0	1377	C
1	0	1450	C
1	0	1474	C
1	0	1506	U
1	0	1563	G
1	0	1667	A
1	0	1685	A
1	0	1942	A

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Mol	Chain	Res	Type
1	0	2313	C
1	0	2361	A
1	0	2467	A
1	0	2526	C
1	0	2536	C
1	0	2649	A
1	0	2718	C
1	0	2761	A
2	9	3065	A

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

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2754/2922 (94%)	-0.29	26 (0%) 81 88	23, 50, 93, 150	0
2	9	122/122 (100%)	-0.52	3 (2%) 54 64	43, 69, 91, 151	0
3	A	237/240 (98%)	-0.18	6 (2%) 54 64	32, 55, 86, 105	0
4	B	337/338 (99%)	-0.25	1 (0%) 91 95	33, 60, 82, 90	0
5	C	246/246 (100%)	-0.42	0 100 100	30, 50, 73, 82	0
6	D	140/177 (79%)	1.47	50 (35%) 1 1	63, 103, 124, 130	0
7	E	172/178 (96%)	-0.05	3 (1%) 67 76	55, 73, 90, 96	0
8	F	119/120 (99%)	0.47	9 (7%) 14 17	57, 74, 96, 106	0
9	G	29/348 (8%)	0.99	5 (17%) 2 3	81, 94, 103, 103	0
10	H	160/171 (93%)	0.51	15 (9%) 9 11	52, 67, 93, 100	0
11	J	142/145 (97%)	-0.34	2 (1%) 72 80	45, 56, 74, 94	0
12	K	132/132 (100%)	-0.44	1 (0%) 83 89	41, 54, 75, 81	0
13	L	145/165 (87%)	0.34	13 (8%) 10 12	32, 71, 107, 118	0
14	M	194/194 (100%)	-0.50	0 100 100	36, 47, 60, 64	0
15	N	186/187 (99%)	0.18	15 (8%) 12 15	50, 67, 110, 119	0
16	O	115/116 (99%)	-0.24	0 100 100	44, 59, 71, 76	0
17	P	143/149 (95%)	-0.22	1 (0%) 84 90	46, 60, 70, 75	0
18	Q	95/96 (98%)	-0.40	0 100 100	43, 52, 64, 72	0
19	R	150/155 (96%)	-0.35	0 100 100	38, 50, 68, 73	0
20	S	81/85 (95%)	-0.05	3 (3%) 39 47	52, 65, 81, 85	0
21	T	119/120 (99%)	-0.09	2 (1%) 67 76	47, 62, 83, 96	0
22	U	53/66 (80%)	-0.17	1 (1%) 64 72	51, 61, 75, 81	0
23	V	65/71 (91%)	1.31	13 (20%) 2 2	59, 79, 109, 114	0
24	W	154/154 (100%)	-0.35	1 (0%) 86 91	42, 56, 70, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	X	82/92 (89%)	0.23	8 (9%) 8 10	52, 64, 87, 97	0
26	Y	142/241 (58%)	-0.55	1 (0%) 84 90	30, 51, 70, 86	0
27	Z	73/73 (100%)	0.38	9 (12%) 5 6	58, 69, 80, 94	0
28	1	56/57 (98%)	-0.47	0 100 100	31, 37, 43, 51	0
29	2	46/50 (92%)	0.23	3 (6%) 18 22	41, 69, 90, 99	0
30	3	92/92 (100%)	-0.34	0 100 100	42, 60, 71, 82	0
31	I	70/161 (43%)	3.38	48 (68%) 0 0	109, 119, 135, 135	0
All	All	6651/7463 (89%)	-0.12	239 (3%) 42 48	23, 57, 100, 151	0

All (239) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
31	I	118	SER	9.7
31	I	109	ALA	9.1
6	D	63	ILE	9.0
31	I	75	THR	8.6
13	L	100	ALA	8.5
31	I	79	ILE	8.4
23	V	39	ALA	8.3
31	I	71	GLY	8.3
23	V	43	PRO	8.0
23	V	1	THR	7.9
23	V	40	PRO	7.5
31	I	113	HIS	7.5
13	L	97	VAL	7.2
31	I	102	VAL	7.0
15	N	166	ALA	6.7
31	I	137	VAL	6.7
6	D	64	ARG	6.5
31	I	93	GLN	6.3
31	I	96	PHE	6.2
6	D	57	THR	6.2
25	X	88	GLU	5.8
31	I	133	THR	5.7
31	I	76	ALA	5.4
6	D	85	GLN	5.4
27	Z	26	VAL	5.4
23	V	41	GLU	5.2
10	H	73	LEU	5.2
3	A	37	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
31	I	105	VAL	5.1
6	D	90	LEU	5.0
13	L	102	ASP	4.9
31	I	103	ASP	4.9
4	B	1	PRO	4.7
1	0	1172	G	4.7
31	I	85	PHE	4.6
25	X	80	GLU	4.5
20	S	81	ILE	4.5
23	V	38	GLY	4.5
27	Z	11	SER	4.5
27	Z	22	SER	4.4
6	D	18	ILE	4.4
31	I	116	LEU	4.4
8	F	17	LEU	4.4
31	I	77	GLU	4.3
31	I	107	GLN	4.3
31	I	111	GLN	4.3
27	Z	21	VAL	4.2
6	D	66	GLY	4.1
6	D	87	ALA	4.1
9	G	27	ILE	4.1
15	N	183	ASP	4.1
25	X	71	ARG	4.1
26	Y	108	ASP	4.1
6	D	69	ILE	4.0
6	D	88	LEU	4.0
31	I	83	ALA	3.9
31	I	84	GLY	3.8
27	Z	19	GLY	3.8
1	0	1199	A	3.7
6	D	23	VAL	3.7
10	H	79	GLU	3.7
15	N	185	GLU	3.7
31	I	117	LEU	3.7
31	I	104	GLN	3.6
1	0	960	G	3.6
13	L	76	LEU	3.6
13	L	101	ASP	3.6
9	G	25	GLU	3.6
31	I	121	LEU	3.6
31	I	108	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	0	1198	U	3.5
2	9	3024	U	3.5
1	0	497	A	3.5
31	I	115	ASP	3.5
2	9	3001	U	3.4
15	N	165	ALA	3.4
7	E	45	ASP	3.4
23	V	52	ALA	3.4
13	L	105	TYR	3.4
8	F	49	PHE	3.4
29	2	39	ARG	3.4
23	V	37	GLY	3.4
3	A	237	GLY	3.3
31	I	138	THR	3.3
29	2	49	GLU	3.3
31	I	126	LYS	3.3
29	2	35	ARG	3.3
31	I	74	PRO	3.2
31	I	99	ASP	3.2
10	H	138	CYS	3.2
6	D	17	ARG	3.2
13	L	60	GLU	3.2
1	0	1177	A	3.2
6	D	40	ILE	3.1
6	D	128	LEU	3.1
13	L	106	VAL	3.1
6	D	166	ILE	3.0
1	0	1171	A	3.0
3	A	31	LYS	3.0
13	L	80	ASP	3.0
15	N	68	GLU	3.0
10	H	74	ILE	3.0
6	D	89	PRO	3.0
31	I	81	ASP	3.0
6	D	44	ILE	3.0
9	G	23	ILE	3.0
1	0	1169	U	3.0
31	I	132	CYS	2.9
15	N	148	ALA	2.9
31	I	91	GLU	2.9
6	D	45	THR	2.9
25	X	10	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
6	D	157	LEU	2.9
15	N	95	ALA	2.9
31	I	129	VAL	2.9
15	N	155	GLU	2.9
31	I	110	GLU	2.9
6	D	129	ASP	2.9
31	I	72	VAL	2.8
6	D	93	LEU	2.8
6	D	26	GLY	2.8
31	I	122	THR	2.8
27	Z	34	ASN	2.8
7	E	100	ASP	2.8
6	D	58	VAL	2.8
6	D	81	GLU	2.8
1	0	2637	A	2.8
10	H	65	SER	2.8
6	D	86	THR	2.7
13	L	81	VAL	2.7
8	F	16	ALA	2.7
3	A	82	VAL	2.7
1	0	282	C	2.7
10	H	32	LYS	2.7
31	I	86	GLU	2.7
10	H	171	ALA	2.7
23	V	34	GLN	2.7
1	0	970	U	2.6
6	D	171	ASP	2.6
10	H	29	ALA	2.6
6	D	165	PHE	2.6
15	N	147	ILE	2.6
6	D	74	THR	2.6
15	N	178	THR	2.6
27	Z	25	ARG	2.6
6	D	75	LEU	2.6
25	X	74	ALA	2.6
1	0	1951	G	2.5
1	0	10	U	2.5
10	H	78	GLY	2.5
6	D	25	MET	2.5
15	N	137	ALA	2.5
6	D	62	ASP	2.5
27	Z	24	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
8	F	106	ALA	2.5
1	0	1173	A	2.5
1	0	1202	A	2.5
8	F	29	VAL	2.5
9	G	21	ASP	2.5
31	I	100	LEU	2.5
8	F	100	ASP	2.5
27	Z	20	ARG	2.5
6	D	134	LEU	2.5
6	D	27	ILE	2.4
23	V	8	ILE	2.4
6	D	101	THR	2.4
13	L	96	VAL	2.4
2	9	3023	U	2.4
1	0	1170	U	2.4
21	T	116	ASP	2.4
13	L	149	ARG	2.4
24	W	96	LEU	2.4
10	H	37	GLN	2.4
3	A	35	GLY	2.4
22	U	47	ARG	2.4
10	H	63	GLU	2.4
23	V	59	ILE	2.4
6	D	65	GLU	2.3
11	J	5	GLU	2.3
1	0	1200	A	2.3
12	K	119	GLN	2.3
25	X	72	VAL	2.3
25	X	85	VAL	2.3
15	N	162	ASP	2.3
31	I	78	LEU	2.3
10	H	51	VAL	2.3
1	0	2237	G	2.3
31	I	135	LEU	2.3
6	D	170	TYR	2.3
6	D	61	PHE	2.3
3	A	36	ASP	2.3
6	D	80	ALA	2.3
6	D	95	THR	2.3
15	N	152	GLU	2.3
17	P	49	ILE	2.3
1	0	735	C	2.3

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Mol	Chain	Res	Type	RSRZ
31	I	89	SER	2.2
31	I	140	GLU	2.2
1	0	1203	G	2.2
20	S	2	TRP	2.2
31	I	82	GLU	2.2
31	I	125	ALA	2.2
10	H	162	ARG	2.2
6	D	135	VAL	2.2
20	S	78	ALA	2.2
23	V	36	ALA	2.2
10	H	86	THR	2.2
6	D	53	LYS	2.2
31	I	139	ILE	2.2
1	0	1181	A	2.2
6	D	98	PHE	2.2
11	J	70	PHE	2.2
8	F	99	THR	2.2
21	T	115	GLU	2.2
1	0	999	C	2.2
9	G	26	MET	2.2
6	D	11	HIS	2.2
1	0	1196	C	2.2
15	N	145	ALA	2.2
1	0	272	A	2.1
6	D	71	ALA	2.1
13	L	103	ALA	2.1
25	X	65	ASN	2.1
6	D	70	GLY	2.1
6	D	158	ASN	2.1
10	H	81	GLY	2.1
8	F	75	ILE	2.1
31	I	136	GLY	2.1
6	D	130	VAL	2.0
6	D	172	VAL	2.0
15	N	138	ASP	2.0
7	E	10	ASP	2.0
6	D	43	GLU	2.0
1	0	1197	G	2.0
6	D	28	GLY	2.0
31	I	80	LYS	2.0
23	V	6	GLN	2.0
8	F	109	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	0	2769	C	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	UR3	0	2619	21/22	0.14	1.88	36,38,39,40	0
1	1MA	0	628	23/24	0.16	0.60	33,35,36,37	0
1	OMU	0	2587	21/22	0.12	-0.73	38,39,40,41	0
1	OMG	0	2588	24/25	0.13	-0.79	37,38,39,40	0
1	PSU	0	2621	20/21	0.11	-2.06	30,32,39,40	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
35	NA	0	8577	1/1	1.06	95.15	81,81,81,81	0
35	NA	0	8584	1/1	0.78	59.12	90,90,90,90	0
35	NA	0	8558	1/1	0.60	55.99	75,75,75,75	0
34	K	0	8401	1/1	0.68	46.16	84,84,84,84	0
35	NA	0	8575	1/1	0.40	36.84	72,72,72,72	0
35	NA	0	8506	1/1	0.73	35.77	49,49,49,49	0
35	NA	0	8585	1/1	0.36	32.93	65,65,65,65	0
33	MG	0	8024	1/1	1.15	30.81	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	8528	1/1	0.49	27.23	54,54,54,54	0
35	NA	0	8574	1/1	0.42	26.22	67,67,67,67	0
35	NA	0	8531	1/1	0.42	26.09	57,57,57,57	0
35	NA	0	8559	1/1	0.45	25.35	53,53,53,53	0
35	NA	0	8550	1/1	0.50	23.34	65,65,65,65	0
36	CL	0	8822	1/1	0.40	23.21	90,90,90,90	0
35	NA	0	8567	1/1	0.43	21.62	61,61,61,61	0
35	NA	0	8516	1/1	0.41	20.57	49,49,49,49	0
35	NA	0	8502	1/1	0.20	19.88	57,57,57,57	0
35	NA	0	8565	1/1	0.73	18.73	47,47,47,47	0
35	NA	0	8525	1/1	0.34	17.53	59,59,59,59	0
35	NA	0	8562	1/1	0.43	16.70	70,70,70,70	0
35	NA	0	8556	1/1	0.42	16.21	61,61,61,61	0
35	NA	0	8518	1/1	0.34	16.16	58,58,58,58	0
35	NA	0	8563	1/1	0.34	14.96	68,68,68,68	0
35	NA	0	8571	1/1	0.24	14.91	59,59,59,59	0
35	NA	0	8564	1/1	0.33	13.51	49,49,49,49	0
35	NA	0	8570	1/1	0.39	13.40	65,65,65,65	0
35	NA	0	8521	1/1	0.40	13.26	77,77,77,77	0
33	MG	0	8114	1/1	0.33	13.23	54,54,54,54	0
35	NA	0	8579	1/1	0.33	12.31	65,65,65,65	0
35	NA	0	8503	1/1	0.29	11.92	1,1,1,1	0
35	NA	0	8526	1/1	0.25	11.49	70,70,70,70	0
35	NA	0	8555	1/1	1.00	11.36	85,85,85,85	0
35	NA	0	8572	1/1	0.35	11.26	73,73,73,73	0
35	NA	0	8532	1/1	0.23	10.84	44,44,44,44	0
33	MG	0	8102	1/1	0.24	10.70	50,50,50,50	0
35	NA	0	8523	1/1	0.29	10.11	38,38,38,38	0
35	NA	0	8573	1/1	0.22	10.10	56,56,56,56	0
33	MG	0	8040	1/1	0.29	9.92	53,53,53,53	0
35	NA	0	8582	1/1	0.29	9.39	85,85,85,85	0
35	NA	0	8507	1/1	0.23	9.27	69,69,69,69	0
35	NA	0	8540	1/1	0.24	8.52	50,50,50,50	0
33	MG	0	8099	1/1	0.32	8.46	70,70,70,70	0
33	MG	0	8049	1/1	0.16	8.46	36,36,36,36	0
35	NA	0	8535	1/1	0.33	8.36	54,54,54,54	0
35	NA	0	8568	1/1	0.19	8.16	87,87,87,87	0
33	MG	0	8011	1/1	0.18	7.81	39,39,39,39	0
33	MG	0	8103	1/1	0.19	7.56	78,78,78,78	0
33	MG	0	8062	1/1	0.22	6.99	13,13,13,13	0
33	MG	0	8104	1/1	0.35	6.90	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	0	8561	1/1	0.24	6.48	50,50,50,50	0
35	NA	0	8560	1/1	0.25	6.14	60,60,60,60	0
35	NA	0	8539	1/1	0.25	6.13	40,40,40,40	0
35	NA	0	8508	1/1	0.27	6.02	58,58,58,58	0
33	MG	0	8090	1/1	0.33	5.65	73,73,73,73	0
33	MG	0	8041	1/1	0.22	5.61	68,68,68,68	0
35	NA	0	8520	1/1	0.22	5.48	36,36,36,36	0
35	NA	0	8549	1/1	0.23	5.03	53,53,53,53	0
35	NA	0	8566	1/1	0.15	5.03	48,48,48,48	0
35	NA	0	8527	1/1	0.23	4.82	61,61,61,61	0
35	NA	0	8515	1/1	0.21	4.60	49,49,49,49	0
35	NA	L	8580	1/1	0.23	4.17	1,1,1,1	0
35	NA	S	8512	1/1	0.45	4.17	57,57,57,57	0
35	NA	0	8542	1/1	0.29	4.15	15,15,15,15	0
36	CL	0	8815	1/1	0.15	3.76	89,89,89,89	0
32	13T	0	9000	42/42	0.24	3.69	58,67,73,74	0
35	NA	R	8586	1/1	0.34	3.67	23,23,23,23	0
36	CL	A	8809	1/1	0.18	3.41	82,82,82,82	0
33	MG	0	8013	1/1	0.18	3.30	38,38,38,38	0
33	MG	0	8094	1/1	0.14	3.05	59,59,59,59	0
33	MG	0	8070	1/1	0.16	3.00	43,43,43,43	0
35	NA	H	8522	1/1	0.34	2.99	77,77,77,77	0
35	NA	0	8543	1/1	0.18	2.99	35,35,35,35	0
33	MG	0	8023	1/1	0.23	2.92	61,61,61,61	0
35	NA	0	8569	1/1	0.24	2.84	64,64,64,64	0
36	CL	0	8803	1/1	0.17	2.79	56,56,56,56	0
35	NA	0	8557	1/1	0.14	2.63	45,45,45,45	0
36	CL	0	8805	1/1	0.15	2.57	71,71,71,71	0
33	MG	0	8012	1/1	0.15	2.56	39,39,39,39	0
35	NA	9	8583	1/1	0.15	2.17	73,73,73,73	0
33	MG	B	8055	1/1	0.15	1.69	64,64,64,64	0
33	MG	0	8081	1/1	0.16	1.69	43,43,43,43	0
33	MG	0	8050	1/1	0.17	1.58	74,74,74,74	0
33	MG	0	8018	1/1	0.15	1.43	39,39,39,39	0
33	MG	0	8060	1/1	0.17	1.28	45,45,45,45	0
33	MG	0	8084	1/1	0.14	1.14	58,58,58,58	0
33	MG	9	8095	1/1	0.14	1.11	77,77,77,77	0
35	NA	0	8510	1/1	0.14	0.97	45,45,45,45	0
33	MG	0	8058	1/1	0.13	0.93	42,42,42,42	0
33	MG	3	8118	1/1	0.19	0.84	50,50,50,50	0
36	CL	Y	8817	1/1	0.16	0.73	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	J	8546	1/1	0.23	0.63	39,39,39,39	0
35	NA	0	8541	1/1	0.12	0.62	46,46,46,46	0
33	MG	0	8043	1/1	0.12	0.62	47,47,47,47	0
33	MG	Y	8109	1/1	0.18	0.62	44,44,44,44	0
33	MG	0	8054	1/1	0.15	0.60	30,30,30,30	0
33	MG	0	8089	1/1	0.14	0.36	62,62,62,62	0
35	NA	0	8552	1/1	0.12	0.35	68,68,68,68	0
35	NA	0	8533	1/1	0.11	0.22	39,39,39,39	0
35	NA	9	8551	1/1	0.33	0.10	92,92,92,92	0
33	MG	0	8004	1/1	0.16	0.08	37,37,37,37	0
36	CL	J	8821	1/1	0.18	-0.05	77,77,77,77	0
33	MG	0	8007	1/1	0.17	-0.06	26,26,26,26	0
33	MG	0	8079	1/1	0.14	-0.12	27,27,27,27	0
33	MG	0	8098	1/1	0.12	-0.14	42,42,42,42	0
35	NA	0	8530	1/1	0.10	-0.26	45,45,45,45	0
35	NA	0	8519	1/1	0.15	-0.34	17,17,17,17	0
35	NA	0	8524	1/1	0.12	-0.55	48,48,48,48	0
33	MG	0	8107	1/1	0.11	-0.57	38,38,38,38	0
35	NA	Q	8548	1/1	0.13	-0.60	46,46,46,46	0
36	CL	0	8816	1/1	0.12	-0.62	69,69,69,69	0
36	CL	J	8802	1/1	0.14	-0.64	76,76,76,76	0
33	MG	0	8009	1/1	0.15	-0.65	36,36,36,36	0
33	MG	0	8038	1/1	0.12	-0.70	31,31,31,31	0
33	MG	0	8113	1/1	0.15	-0.70	44,44,44,44	0
33	MG	0	8045	1/1	0.12	-0.72	67,67,67,67	0
37	CD	U	8701	1/1	0.09	-0.78	67,67,67,67	0
33	MG	0	8087	1/1	0.08	-0.78	63,63,63,63	0
33	MG	0	8056	1/1	0.12	-0.81	56,56,56,56	0
35	NA	A	8545	1/1	0.12	-0.86	61,61,61,61	0
35	NA	0	8509	1/1	0.12	-0.87	48,48,48,48	0
34	K	0	8402	1/1	0.14	-0.90	61,61,61,61	0
35	NA	0	8505	1/1	0.13	-0.94	37,37,37,37	0
36	CL	3	8804	1/1	0.10	-1.02	56,56,56,56	0
35	NA	0	8534	1/1	0.08	-1.03	40,40,40,40	0
33	MG	0	8001	1/1	0.12	-1.04	44,44,44,44	0
35	NA	0	8576	1/1	0.14	-1.04	33,33,33,33	0
33	MG	0	8017	1/1	0.15	-1.05	31,31,31,31	0
33	MG	0	8077	1/1	0.15	-1.12	36,36,36,36	0
33	MG	0	8052	1/1	0.12	-1.13	68,68,68,68	0
35	NA	R	8537	1/1	0.13	-1.16	45,45,45,45	0
33	MG	0	8047	1/1	0.12	-1.18	57,57,57,57	0
37	CD	O	8705	1/1	0.11	-1.22	186,186,186,186	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	MG	0	8086	1/1	0.05	-1.27	42,42,42,42	0
35	NA	0	8517	1/1	0.12	-1.28	37,37,37,37	0
33	MG	0	8080	1/1	0.14	-1.30	39,39,39,39	0
37	CD	Z	8703	1/1	0.09	-1.35	71,71,71,71	0
33	MG	A	8065	1/1	0.13	-1.35	45,45,45,45	0
36	CL	0	8812	1/1	0.09	-1.36	49,49,49,49	0
36	CL	O	8808	1/1	0.11	-1.43	67,67,67,67	0
36	CL	N	8807	1/1	0.12	-1.52	71,71,71,71	0
33	MG	0	8064	1/1	0.10	-1.56	41,41,41,41	0
37	CD	3	8704	1/1	0.08	-1.58	65,65,65,65	0
33	MG	0	8085	1/1	0.12	-1.59	48,48,48,48	0
36	CL	0	8814	1/1	0.10	-1.60	57,57,57,57	0
33	MG	3	8078	1/1	0.10	-1.60	16,16,16,16	0
36	CL	J	8801	1/1	0.08	-1.61	58,58,58,58	0
33	MG	0	8096	1/1	0.10	-1.67	48,48,48,48	0
33	MG	0	8076	1/1	0.07	-1.67	49,49,49,49	0
33	MG	0	8015	1/1	0.14	-1.69	35,35,35,35	0
35	NA	0	8511	1/1	0.09	-1.79	56,56,56,56	0
33	MG	0	8074	1/1	0.04	-1.81	30,30,30,30	0
33	MG	0	8010	1/1	0.15	-1.84	11,11,11,11	0
33	MG	T	8073	1/1	0.10	-1.85	57,57,57,57	0
37	CD	1	8702	1/1	0.07	-1.88	65,65,65,65	0
36	CL	L	8810	1/1	0.08	-1.95	59,59,59,59	0
33	MG	0	8053	1/1	0.13	-1.96	43,43,43,43	0
35	NA	C	8504	1/1	0.07	-1.97	35,35,35,35	0
35	NA	0	8529	1/1	0.08	-1.98	68,68,68,68	0
33	MG	0	8106	1/1	0.06	-1.98	71,71,71,71	0
33	MG	0	8020	1/1	0.11	-2.04	39,39,39,39	0
33	MG	0	8061	1/1	0.14	-2.04	44,44,44,44	0
33	MG	A	8066	1/1	0.05	-2.09	73,73,73,73	0
35	NA	0	8554	1/1	0.13	-2.10	42,42,42,42	0
33	MG	0	8035	1/1	0.11	-2.13	46,46,46,46	0
36	CL	M	8818	1/1	0.09	-2.14	44,44,44,44	0
33	MG	0	8100	1/1	0.09	-2.43	42,42,42,42	0
33	MG	0	8039	1/1	0.08	-2.52	64,64,64,64	0
33	MG	0	8029	1/1	0.13	-2.54	42,42,42,42	0
33	MG	0	8117	1/1	0.10	-2.54	34,34,34,34	0
36	CL	Y	8820	1/1	0.05	-2.55	44,44,44,44	0
35	NA	0	8514	1/1	0.11	-2.61	38,38,38,38	0
33	MG	0	8028	1/1	0.06	-2.63	33,33,33,33	0
35	NA	0	8538	1/1	0.09	-2.65	55,55,55,55	0
33	MG	0	8051	1/1	0.11	-2.90	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
35	NA	M	8547	1/1	0.08	-2.92	41,41,41,41	0
33	MG	0	8083	1/1	0.08	-2.98	41,41,41,41	0
33	MG	0	8032	1/1	0.06	-3.01	35,35,35,35	0
36	CL	0	8811	1/1	0.07	-3.03	58,58,58,58	0
33	MG	0	8042	1/1	0.06	-3.04	33,33,33,33	0
36	CL	B	8819	1/1	0.08	-3.08	53,53,53,53	0
33	MG	0	8006	1/1	0.08	-3.19	36,36,36,36	0
33	MG	0	8101	1/1	0.08	-3.21	45,45,45,45	0
36	CL	0	8813	1/1	0.07	-3.39	54,54,54,54	0
33	MG	0	8003	1/1	0.10	-3.40	36,36,36,36	0
33	MG	0	8037	1/1	0.06	-3.60	42,42,42,42	0
33	MG	0	8092	1/1	0.09	-3.74	72,72,72,72	0
35	NA	0	8578	1/1	0.10	-3.74	57,57,57,57	0
33	MG	0	8034	1/1	0.09	-3.80	25,25,25,25	0
35	NA	0	8581	1/1	0.06	-3.93	42,42,42,42	0
33	MG	K	8069	1/1	0.06	-3.98	51,51,51,51	0
33	MG	0	8116	1/1	0.08	-4.08	56,56,56,56	0
33	MG	0	8008	1/1	0.06	-4.17	29,29,29,29	0
33	MG	0	8068	1/1	0.08	-4.22	56,56,56,56	0
33	MG	0	8072	1/1	0.09	-4.24	57,57,57,57	0
33	MG	0	8097	1/1	0.08	-4.28	45,45,45,45	0
35	NA	0	8513	1/1	0.07	-4.38	72,72,72,72	0
33	MG	0	8059	1/1	0.06	-4.41	39,39,39,39	0
33	MG	0	8048	1/1	0.07	-4.63	49,49,49,49	0
33	MG	0	8026	1/1	0.08	-4.82	33,33,33,33	0
33	MG	0	8005	1/1	0.10	-4.89	32,32,32,32	0
33	MG	0	8014	1/1	0.06	-4.93	41,41,41,41	0
33	MG	0	8091	1/1	0.08	-5.05	65,65,65,65	0
33	MG	0	8088	1/1	0.10	-5.14	33,33,33,33	0
33	MG	0	8112	1/1	0.07	-5.15	39,39,39,39	0
33	MG	0	8046	1/1	0.07	-5.18	56,56,56,56	0
33	MG	0	8067	1/1	0.06	-5.22	37,37,37,37	0
35	NA	0	8536	1/1	0.07	-5.33	54,54,54,54	0
33	MG	0	8057	1/1	0.05	-5.34	41,41,41,41	0
33	MG	0	8021	1/1	0.08	-5.53	37,37,37,37	0
33	MG	0	8093	1/1	0.10	-5.56	61,61,61,61	0
33	MG	0	8022	1/1	0.08	-5.62	37,37,37,37	0
36	CL	R	8806	1/1	0.02	-5.73	49,49,49,49	0
33	MG	0	8027	1/1	0.02	-5.79	40,40,40,40	0
33	MG	0	8075	1/1	0.04	-5.89	56,56,56,56	0
35	NA	0	8553	1/1	0.08	-5.99	44,44,44,44	0
33	MG	0	8016	1/1	0.07	-6.20	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
33	MG	0	8044	1/1	0.08	-6.38	55,55,55,55	0
33	MG	0	8111	1/1	0.07	-6.57	46,46,46,46	0
33	MG	0	8036	1/1	0.05	-6.71	41,41,41,41	0
33	MG	0	8110	1/1	0.10	-6.72	53,53,53,53	0
33	MG	0	8108	1/1	0.05	-6.79	77,77,77,77	0
33	MG	0	8033	1/1	0.04	-7.10	38,38,38,38	0
33	MG	0	8002	1/1	0.03	-7.11	40,40,40,40	0
33	MG	0	8030	1/1	0.05	-7.27	35,35,35,35	0
33	MG	0	8063	1/1	0.09	-8.53	63,63,63,63	0
33	MG	0	8071	1/1	0.06	-8.79	50,50,50,50	0
33	MG	0	8025	1/1	0.08	-12.68	43,43,43,43	0
35	NA	0	8544	1/1	0.06	-13.08	29,29,29,29	0
33	MG	0	8019	1/1	0.05	-15.18	34,34,34,34	0
35	NA	0	8501	1/1	0.04	-15.46	50,50,50,50	0
33	MG	0	8031	1/1	0.10	-22.32	30,30,30,30	0
33	MG	0	8115	1/1	0.07	-29.00	45,45,45,45	0
33	MG	0	8082	1/1	0.36	-	84,84,84,84	0

6.5 Other polymers ⓘ

There are no such residues in this entry.