



Full wwPDB X-ray Structure Validation Report

Jun 16, 2014 – 09:38 PM BST

PDB ID : 4V9S
Title : Crystal structure of antibiotic GE82832 bound to 70S ribosome
Authors : Bulkley, D.P.; Brandi, L.; Polikanov, Y.S.; Fabbretti, A.; O'Connor, M.;
Gualerzi, C.O.; Steitz, T.A.
Deposited on : 2013-12-05
Resolution : 3.10 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>

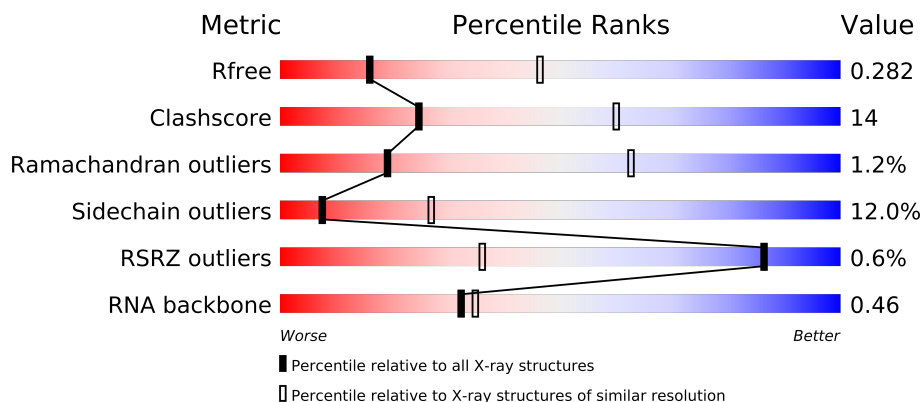
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : stable23397
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) : stable23397

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)
RNA backbone	1838	1047 (3.60-2.60)

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	AA	1522	
1	CA	1522	
2	AB	256	
2	CB	256	
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	

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Mol	Chain	Length	Quality of chain
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AX	77	
23	CX	77	
24	AW	10	
24	CW	10	
25	BA	2915	
25	DA	2915	
26	BB	122	
26	DB	122	
27	BD	276	
27	DD	276	

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Mol	Chain	Length	Quality of chain
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	
38	DS	112	
39	BT	146	
39	DT	146	
40	BU	118	
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	

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Mol	Chain	Length	Quality of chain
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	
51	D5	60	
52	B6	54	
52	D6	54	
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 286321 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1498	Total	C	N	O	P	0	0	0
			32196	14328	5966	10404	1498			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O		0	0	0
			983	623	193	167				
9	CI	127	Total	C	N	O		0	0	0
			978	619	190	169				

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O		0	0	0
			709	440	138	131				

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O			
			714	445	138	131	0	0	0

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	AK	114	Total	C	N	O	S		
			829	516	155	155	3	0	0
11	CK	114	Total	C	N	O	S		
			833	519	156	155	3	0	0

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0
12	CL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	AM	123	Total	C	N	O	S		
			958	592	198	166	2	0	0
13	CM	122	Total	C	N	O	S		
			950	586	197	165	2	0	0

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0
14	CN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0
15	CO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	7	Total	C	N	O	P	0	0	1
			114	49	22	37	6			
22	CV	6	Total	C	N	O	P	0	0	0
			113	49	22	36	6			

- Molecule 23 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			
23	CX	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			

- Molecule 24 is a protein called GE82832.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	AW	10	Total	C	N	O	0	0	0
			93	67	10	16			
24	CW	10	Total	C	N	O	0	0	0
			93	67	10	16			

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2731	Total	C	N	O	P	0	0	0
			58834	26185	11020	18899	2730			
25	DA	2714	Total	C	N	O	P	0	0	0
			58458	26018	10942	18786	2712			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 27 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
27	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 28 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
28	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
29	DF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
30	DG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 31 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
31	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 32 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
32	DI	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 33 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
33	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 34 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
34	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
35	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 36 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
36	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 37 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
37	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 38 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O	S	0	0	0
			877	553	175	149				
38	DS	110	Total	C	N	O	S	0	0	0
			870	549	173	148				

- Molecule 39 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
39	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 40 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
40	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 41 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
41	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 42 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 43 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
43	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 44 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
44	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 45 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BZ	171	Total	C	N	O	S	0	0	0
			1349	862	243	242	2			
45	DZ	174	Total	C	N	O	S	0	0	0
			1360	870	243	245	2			

- Molecule 46 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
46	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 47 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
47	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 48 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
48	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 49 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 50 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			551	348	99	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			531	338	97	91	5			

- Molecule 51 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
51	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 52 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
52	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 53 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
53	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 54 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B8	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
54	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 55 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B4	1	Total	Mg	0	0
			1	1		
56	BA	738	Total	Mg	0	0
			738	738		
56	AK	1	Total	Mg	0	0
			1	1		
56	DQ	5	Total	Mg	0	0
			5	5		
56	D3	1	Total	Mg	0	0
			1	1		
56	DF	6	Total	Mg	0	0
			6	6		
56	B8	3	Total	Mg	0	0
			3	3		
56	BE	10	Total	Mg	0	0
			10	10		
56	B1	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AN	2	Total 2	Mg 2	0	0
56	BP	4	Total 4	Mg 4	0	0
56	AX	9	Total 9	Mg 9	0	0
56	DN	1	Total 1	Mg 1	0	0
56	CA	172	Total 172	Mg 172	0	0
56	B5	1	Total 1	Mg 1	0	0
56	BB	18	Total 18	Mg 18	0	0
56	D8	1	Total 1	Mg 1	0	0
56	DG	1	Total 1	Mg 1	0	0
56	B9	1	Total 1	Mg 1	0	0
56	BF	8	Total 8	Mg 8	0	0
56	AV	1	Total 1	Mg 1	0	0
56	BX	1	Total 1	Mg 1	0	0
56	B2	1	Total 1	Mg 1	0	0
56	AA	221	Total 221	Mg 221	0	0
56	BQ	5	Total 5	Mg 5	0	0
56	CQ	1	Total 1	Mg 1	0	0
56	CX	3	Total 3	Mg 3	0	0
56	DV	4	Total 4	Mg 4	0	0
56	AM	1	Total 1	Mg 1	0	0
56	BU	8	Total 8	Mg 8	0	0

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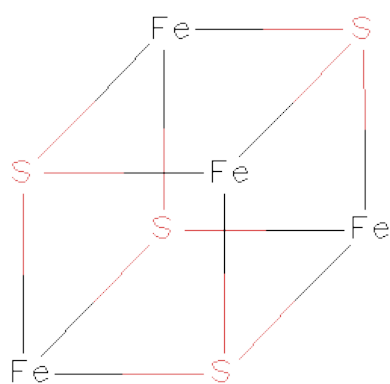
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	DR	2	Total 2	Mg 2	0	0
56	AD	1	Total 1	Mg 1	0	0
56	BN	6	Total 6	Mg 6	0	0
56	CT	1	Total 1	Mg 1	0	0
56	D0	1	Total 1	Mg 1	0	0
56	BG	4	Total 4	Mg 4	0	0
56	BY	1	Total 1	Mg 1	0	0
56	DE	6	Total 6	Mg 6	0	0
56	B3	3	Total 3	Mg 3	0	0
56	BR	4	Total 4	Mg 4	0	0
56	DA	653	Total 653	Mg 653	0	0
56	DW	2	Total 2	Mg 2	0	0
56	B7	4	Total 4	Mg 4	0	0
56	CF	1	Total 1	Mg 1	0	0
56	BV	4	Total 4	Mg 4	0	0
56	DO	1	Total 1	Mg 1	0	0
56	BO	1	Total 1	Mg 1	0	0
56	BZ	1	Total 1	Mg 1	0	0
56	DY	1	Total 1	Mg 1	0	0
56	D5	2	Total 2	Mg 2	0	0
56	BD	12	Total 12	Mg 12	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B0	4	Total	Mg	0	0
			4	4		
56	CE	2	Total	Mg	0	0
			2	2		
56	BW	5	Total	Mg	0	0
			5	5		
56	DD	8	Total	Mg	0	0
			8	8		
56	AF	1	Total	Mg	0	0
			1	1		
56	DB	12	Total	Mg	0	0
			12	12		

- Molecule 57 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	AD	1	Total	Fe	S	0	0
			8	4	4		
57	CD	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

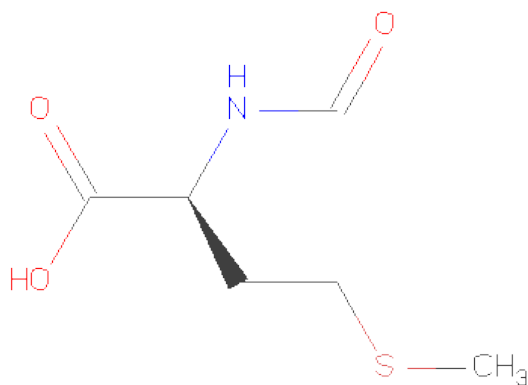
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	B5	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	B4	1	Total	Zn	0	0
			1	1		
58	CN	1	Total	Zn	0	0
			1	1		
58	BY	1	Total	Zn	0	0
			1	1		
58	B9	1	Total	Zn	0	0
			1	1		
58	DY	1	Total	Zn	0	0
			1	1		
58	D5	1	Total	Zn	0	0
			1	1		
58	D4	1	Total	Zn	0	0
			1	1		
58	AN	1	Total	Zn	0	0
			1	1		
58	D6	1	Total	Zn	0	0
			1	1		
58	D9	1	Total	Zn	0	0
			1	1		
58	B6	1	Total	Zn	0	0
			1	1		

- Molecule 59 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
59	AX	1	Total	C	N	O	S	0	0
			10	6	1	2	1		
59	CX	1	Total	C	N	O	S	0	0
			10	6	1	2	1		

- Molecule 60 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	BA	1	Total	K	0	0
			1	1		
60	DA	1	Total	K	0	0
			1	1		

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	148	Total	O	0	0
			148	148		
61	AD	1	Total	O	0	0
			1	1		
61	AE	3	Total	O	0	0
			3	3		
61	AJ	1	Total	O	0	0
			1	1		
61	AL	1	Total	O	0	0
			1	1		
61	AP	1	Total	O	0	0
			1	1		
61	AU	1	Total	O	0	0
			1	1		
61	AV	1	Total	O	0	0
			1	1		
61	AX	1	Total	O	0	0
			1	1		
61	BA	1092	Total	O	0	0
			1092	1092		
61	BB	26	Total	O	0	0
			26	26		
61	BD	8	Total	O	0	0
			8	8		
61	BE	9	Total	O	0	0
			9	9		
61	BF	4	Total	O	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BG	1	Total 1	O 1	0	0
61	BN	3	Total 3	O 3	0	0
61	BO	2	Total 2	O 2	0	0
61	BP	15	Total 15	O 15	0	0
61	BQ	3	Total 3	O 3	0	0
61	BR	1	Total 1	O 1	0	0
61	BT	1	Total 1	O 1	0	0
61	BU	4	Total 4	O 4	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	2	Total 2	O 2	0	0
61	BX	4	Total 4	O 4	0	0
61	B0	4	Total 4	O 4	0	0
61	B1	2	Total 2	O 2	0	0
61	B5	3	Total 3	O 3	0	0
61	B7	1	Total 1	O 1	0	0
61	B8	8	Total 8	O 8	0	0
61	CA	187	Total 187	O 187	0	0
61	CE	2	Total 2	O 2	0	0
61	CN	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CX	2	Total 2	O 2	0	0

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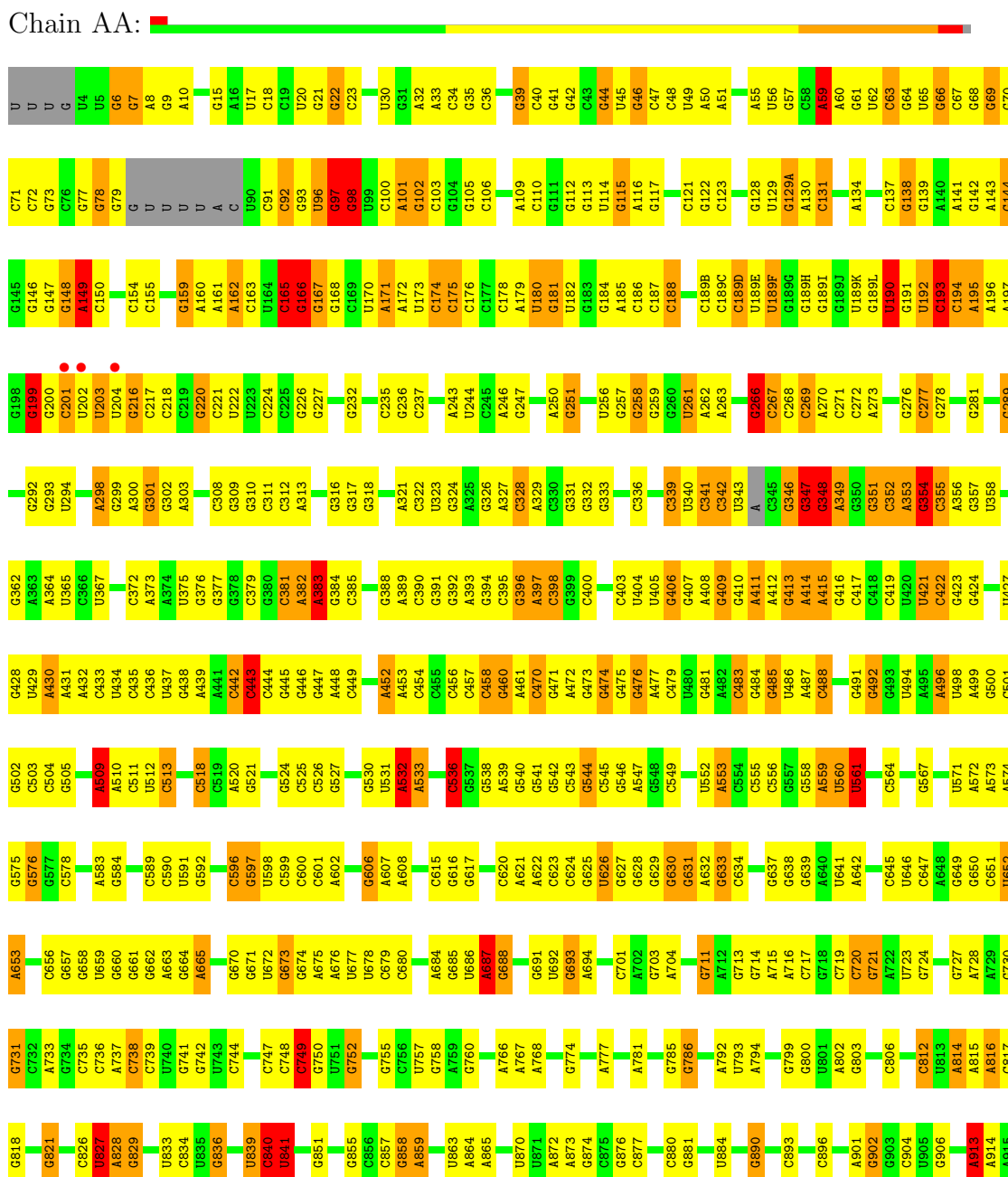
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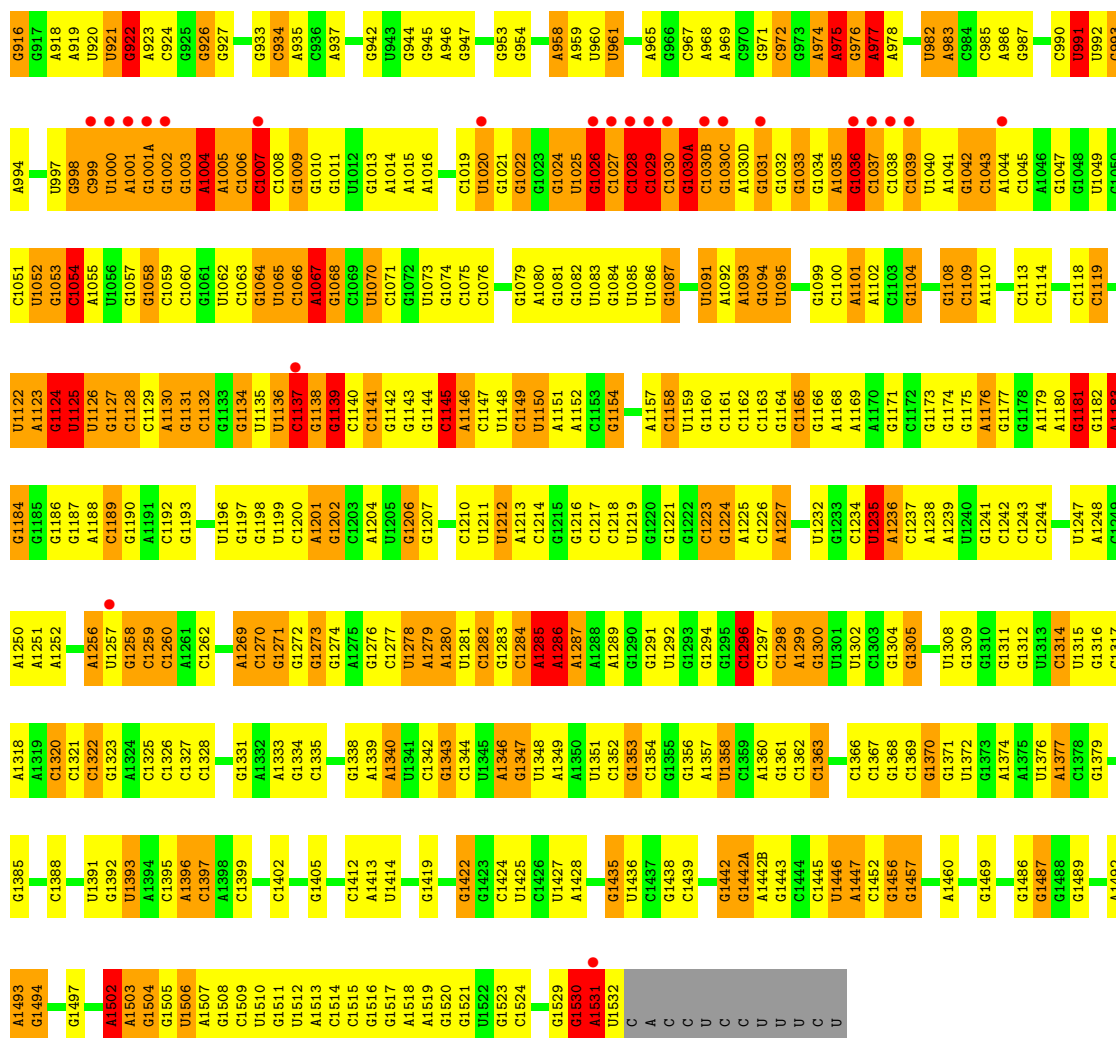
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	DA	902	Total 902	O 902	0	0
61	DB	7	Total 7	O 7	0	0
61	DD	8	Total 8	O 8	0	0
61	DE	13	Total 13	O 13	0	0
61	DF	5	Total 5	O 5	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	14	Total 14	O 14	0	0
61	DQ	3	Total 3	O 3	0	0
61	DU	4	Total 4	O 4	0	0
61	DV	1	Total 1	O 1	0	0
61	DX	2	Total 2	O 2	0	0
61	DY	2	Total 2	O 2	0	0
61	D0	5	Total 5	O 5	0	0
61	D1	1	Total 1	O 1	0	0
61	D7	2	Total 2	O 2	0	0
61	D8	4	Total 4	O 4	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.

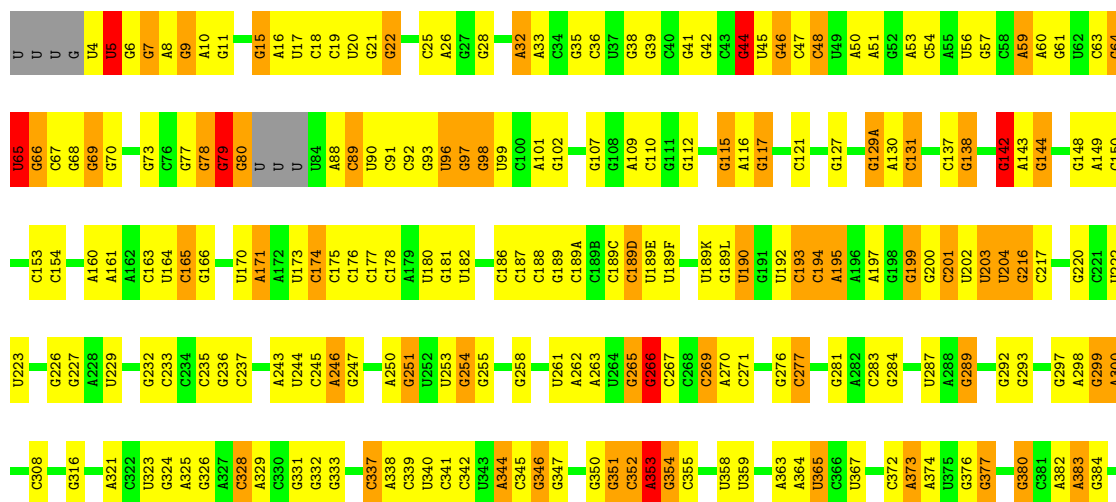
• Molecule 1: 16S Ribosomal RNA





Molecule 1: 16S Ribosomal RNA

Chain CA:

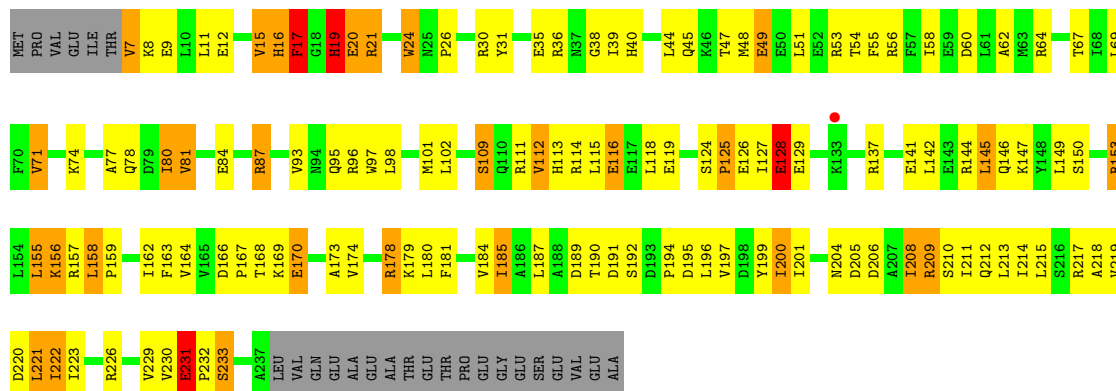


C1445	C1362	C1297	C1228	A1168	A1105	A1041	C985	A919	C934	G752	C680	A608	G538	C454	G388
U1446	C1363	C1298	C1233	A1169	G1106	G1042	A986	U920	U835	A753	C683	A609	A539	C455	A389
A1447	C1366	A1299	G1234	A1170	G1107	G1043	C989	U921	G836	G754	G684	G610	G540	C456	C390
G1452	C1367	G1300	C1235	G1171	G1108	A1044	C990	G922	G837	G755	G685	G611	G541	C457	G391
G1456	C1368	C1303	A1236	G1173	A1110	G1047	U991	G923	G838	G756	G686	G616	C543	C460	G392
G1457	C1369	G1304	U1237	G1174	A1111	G1048	U992	G924	U839	U757	U687	G461	G544	A461	A393
G1458	G1370	A1306	A1238	G1175	C1112	C1051	G993	G926	C940	G758	G688	U619	C545	C470	G396
C1459	A1239	G1307	A1176	A1176	C1113	U1051	A994	G927	U841	G759	G689	C620	C546	G471	A397
A1460	U1240	U1307	G1177	C1116	C1117	G1052	A995	G928	U850	G760	G690	A621	A547	A472	C398
G1372	G1241	U1308	G1178	G1117	G1118	G1053	A996	C931	G851	A767	G691	G622	G551	G473	G399
A1374	C1242	G1309	G1179	A1180	G1118	A1054	U997	C932	G852	A768	U692	C623	U551	C400	C400
A1375	C1243	G1310	A1181	A1180	C1119	U1055	C999	C933	G855	A769	U693	C624	U552	C401	C401
U1376	A1245	G1312	G1182	G1181	C1120	G1056	C999	G934	C940	G774	A694	G625	A553	G475	G402
A1377	C1246	A1314	U1121	G1182	G1120	G1057	U1000	A935	G858	G775	C701	U626	C554	G484	C403
G1378	A1246	U1315	A1183	A1183	A1122	C1058	A1001	A936	A859	G776	A704	G627	C555	G485	U404
G1379	G1249	U1316	G1184	G1184	A1123	C1059	A1001	C937	A860	A777	U705	G628	C556	U486	U405
U1380	A1250	G1317	G1185	G1185	G1124	G1060	G1001A	G938	G861	G778	A706	G629	G557	A487	G406
G1385	A1251	A1318	G1186	G1186	U1125	G1061	G1003	A938	G861	C783	U706	G630	G558	C488	G407
G1386	A1252	G1317	G1187	G1187	U1126	U1062	A1004	C939	A865	G784	A707	G631	A559	C489	A408
G1387	C1321	A1319	A1188	A1188	G1127	U1063	A1005	C940	A866	G785	C707	A632	U560	G490	G409
G1388	C1320	G1320	G1189	G1189	C1128	U1064	C1006	G941	C968	G786	G708	G634	C562	G491	G410
G1389	A1257	C1321	G1190	G1190	G1129	U1065	C1007	G942	G869	G790	G710	G635	A563	G492	A411
U1390	A1258	C1322	A1191	A1191	A1130	A1066	G1008	G947	A872	A791	G711	G638	C564	U494	A412
U1391	G1259	G1323	C1192	G1193	G1131	A1067	G1009	C948	A873	G792	A712	G639	U565	A495	A413
U1392	C1260	A1324	G1194	G1194	C1132	G1068	G1010	G948	A874	A793	G713	A640	C566	A496	A414
U1393	A1261	C1325	U1194	C1195	G1133	C1069	G1011	G951	G874	A794	G714	U641	G568	U498	A415
G1396	C1262	G1326	G1195	G1196	G1134	C1071	G1012	U952	G875	G795	A715	U642	U571	A499	C418
C1397	C1263	C1327	G1197	G1197	U1135	G1072	A1014	G953	G876	G796	A716	A642	C577	G500	C419
C1397	C1264	C1328	G1198	G1198	G1136	U1073	A1015	G954	C877	C797	G719	U646	A573	C501	C422
A1398	G1265	A1329	U1199	U1199	C1137	G1074	A1016	U955	G878	G798	G720	C647	A573	G502	G423
A1399	G1266	U1330	C1200	C1200	G1138	C1075	G1017	U956	G879	G799	G721	A648	C576	C503	G424
C1400	C1267	G1331	A1201	A1201	G1139	U1076	C1018	U957	C880	G800	A722	G650	C578	C504	G425
A1401	A1268	A1332	G1202	G1202	C1140	G1077	C1019	A958	C881	U801	G723	G651	C579	G505	G426
C1402	A1269	A1333	C1203	C1203	G1141	U1078	A1020	A959	C882	A802	U724	C652	C579	A509	U427
A1403	C1270	G1334	A1204	A1204	C1142	U1079	G1021	U960	G885	U804	G725	U652	C579	A510	G428
C1385	G1271	C1335	U1205	U1205	G1143	A1080	G1022	U961	C885	C805	G726	A653	U580	C511	U429
C1336	G1272	C1336	G1206	G1206	G1144	G1081	G1023	A964	G890	C806	G727	A654	U582	C512	U430
C1337	G1273	G1337	C1207	C1207	C1145	G1082	U1024	A965	U891	C811	G730	A655	U583	C513	A431
G1338	G1274	A1413	C1208	C1208	A1146	U1085	G1025	A966	A892	C812	G731	A656	G584	C518	A432
A1339	C1275	U1414	C1209	C1209	C1147	G1086	C1026	G967	C893	C812	G732	C656	G585	C519	C433
A1340	U1276	U1341	C1210	C1210	U1148	G1087	C1027	A968	G894	U813	A733	G660	C586	U434	U434
U1341	G1277	C1342	U1211	U1211	U1150	G1088	C1028	A969	C899	A814	A733	G661	G587	A520	C435
C1342	A1278	A1419	U1212	U1212	U1151	G1089	G1029	A970	C900	A815	G734	G662	G588	G521	C436
G1343	U1280	C1420	A1213	A1213	A1151	U1090	C1030	G971	A900	A816	G735	A663	C589	C522	U437
U1281	U1281	C1344	C1214	C1214	A1152	U1091	G1030A	G972	A901	C817	G736	G664	C590	G438	G438
U1345	G1282	G1421	G1215	G1215	C1153	U1091	C1030B	C972	G902	G818	A737	A665	U591	C525	A439
A1346	G1283	C1423	G1216	G1216	G1154	A1092	G1030C	G973	G902	G818	C738	G666	G592	C526	A441
G1347	C1284	G1347	C1217	C1217	G1155	A1093	A1030D	A974	G906	C821	C739	G667	G592	G527	C442
U1348	A1285	A1428	C1218	C1218	G1156	G1094	G1031	A975	G906	G821	U740	C677	C596	C528	C443
C1352	U1286	C1352	U1219	U1219	A1157	U1095	G1032	A976	A907	C826	G741	G671	C597	U531	C444
G1353	A1287	G1353	G1220	G1220	C1158	C1096	G1033	A977	A908	U827	G742	U672	U598	G445	G445
C1354	A1288	C1354	G1221	G1221	U1159	G1097	G1034	A978	A828	U827	G742	G673	C599	A532	G446
C1354	A1289	C1354	G1222	G1222	G1160	C1100	A1035	C979	A813	A828	G742	G674	C600	A533	G447
G1290	C1223	C1354	G1223	G1223	C1161	C1100	G1036	C980	A915	G829	C745	C601	C600	U534	A448
G1291	G1224	C1354	G1224	G1224	C1162	A1101	C1037	U981	A915	G830	C749	U677	C601	A535	A452
U1292	A1225	C1354	G1225	G1225	C1163	A1102	C1038	U982	G916	U831	C749	U678	G606	C536	A453
G1293	A1226	A1227	C1163	C1163	C1103	C1103	C1039	A983	G917	C832	G750	C679	G606	G537	A453
G1361	A1227	A1227	G1166	A1227	G1166	U1104	U1040	C984	A918	U833	U751	C679	A507	G537	A453



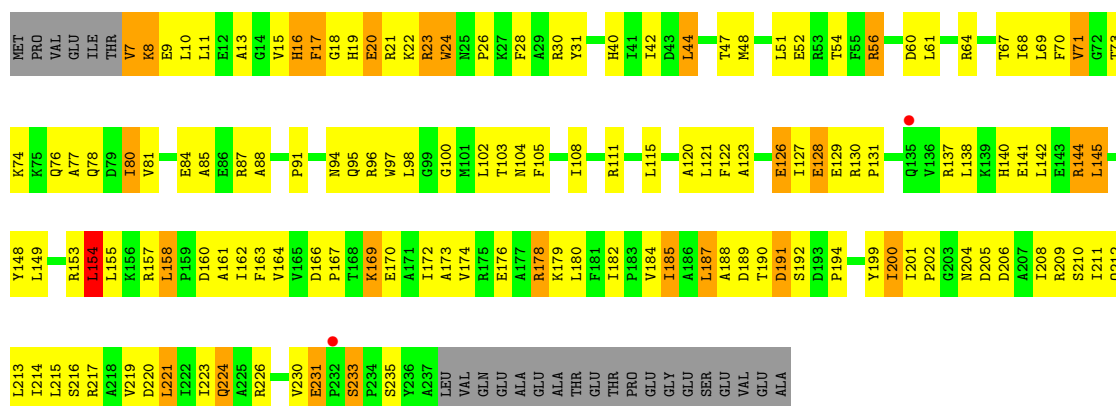
• Molecule 2: 30S Ribosomal Protein S2

Chain AB:



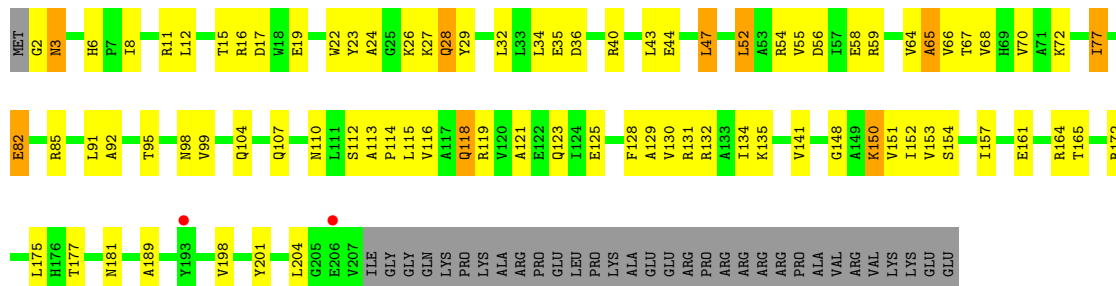
• Molecule 2: 30S Ribosomal Protein S2

Chain CB:



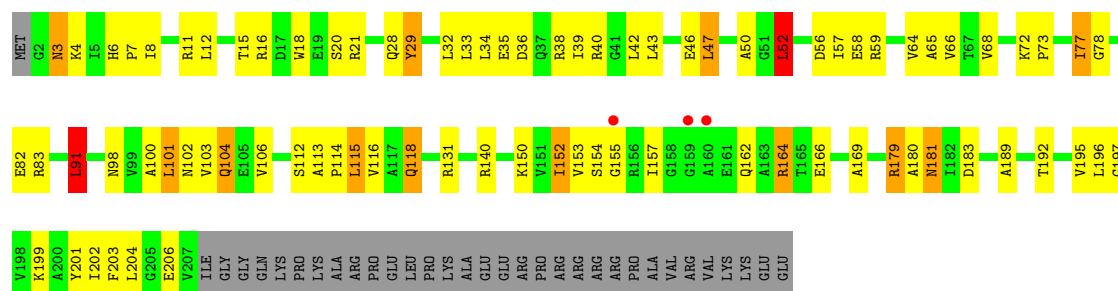
• Molecule 3: 30S Ribosomal Protein S3

Chain AC:



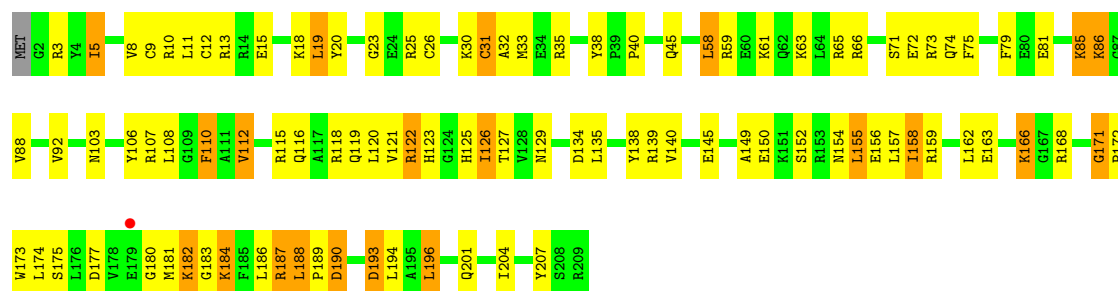
• Molecule 3: 30S Ribosomal Protein S3

Chain CC:



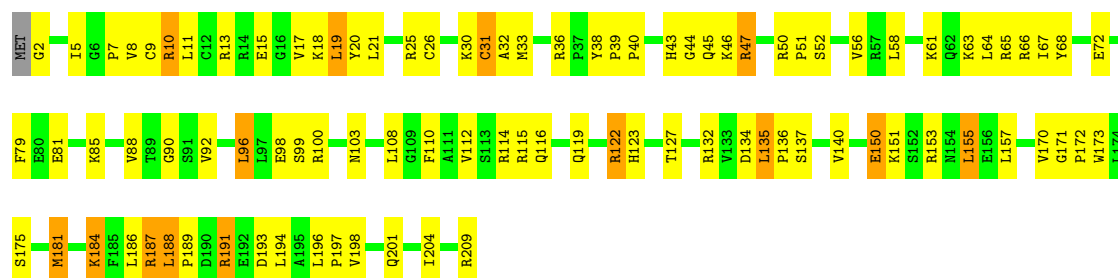
• Molecule 4: 30S Ribosomal Protein S4

Chain AD:



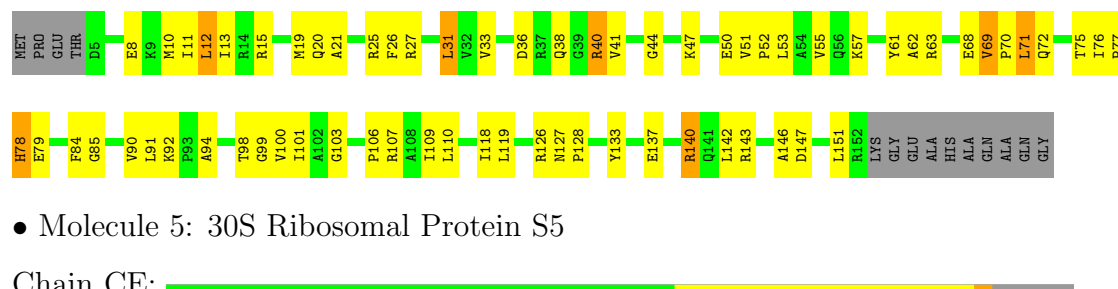
• Molecule 4: 30S Ribosomal Protein S4

Chain CD:



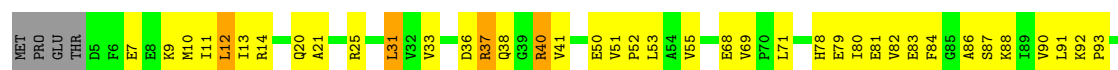
• Molecule 5: 30S Ribosomal Protein S5

Chain AE:



• Molecule 5: 30S Ribosomal Protein S5

Chain CE:





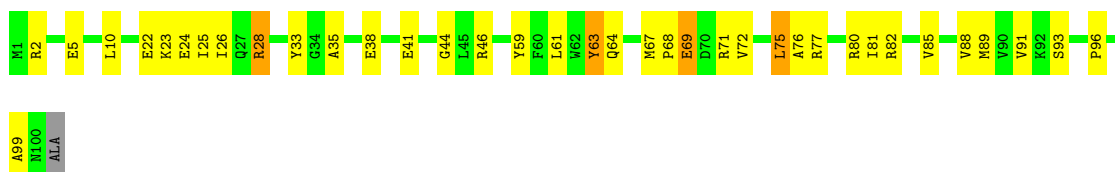
- Molecule 6: 30S Ribosomal Protein S6

Chain AF:



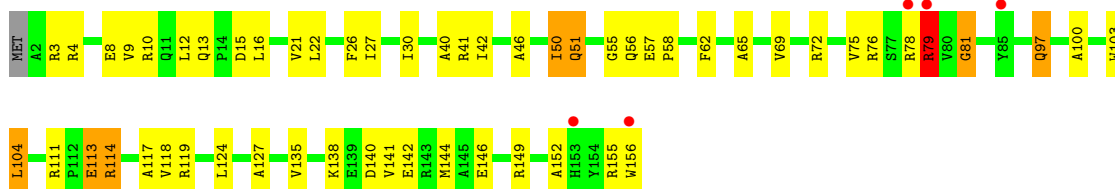
- Molecule 6: 30S Ribosomal Protein S6

Chain CF:



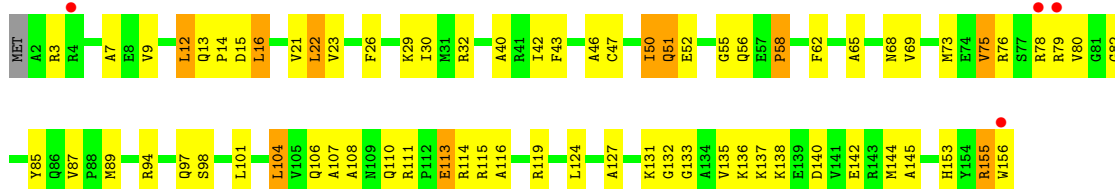
- Molecule 7: 30S Ribosomal Protein S7

Chain AG:



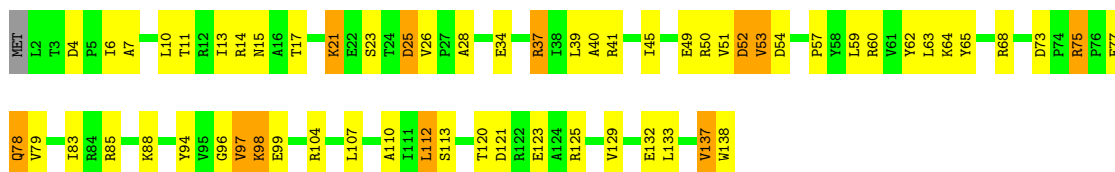
- Molecule 7: 30S Ribosomal Protein S7

Chain CG:



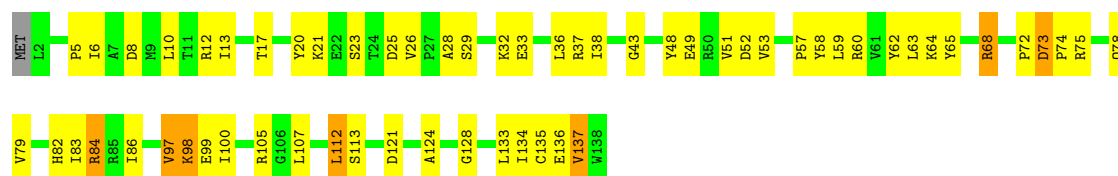
- Molecule 8: 30S Ribosomal Protein S8

Chain AH:



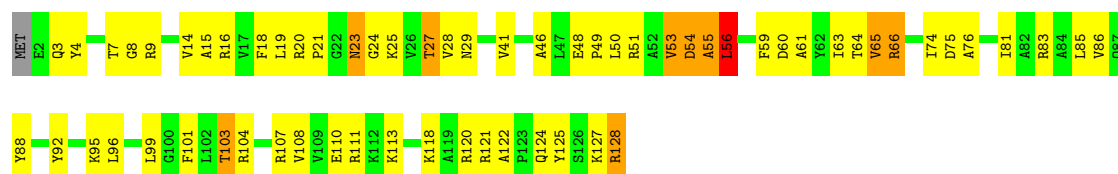
- Molecule 8: 30S Ribosomal Protein S8

Chain CH:



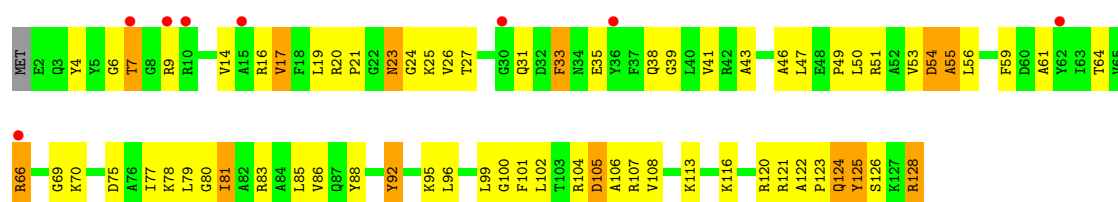
- Molecule 9: 30S Ribosomal Protein S9

Chain AI:



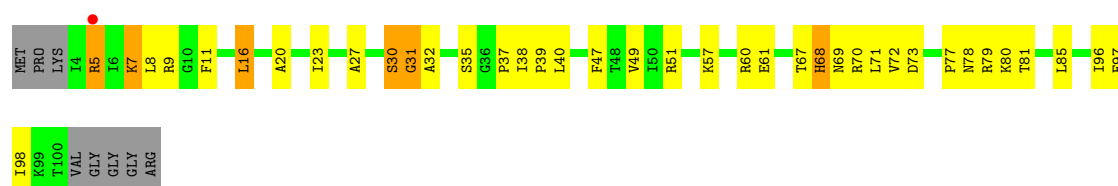
- Molecule 9: 30S Ribosomal Protein S9

Chain CI:



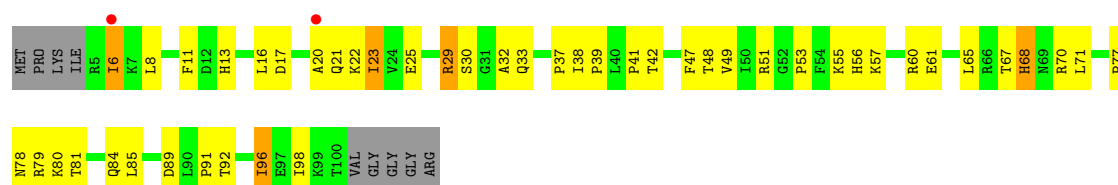
- Molecule 10: 30S Ribosomal Protein S10

Chain AJ:



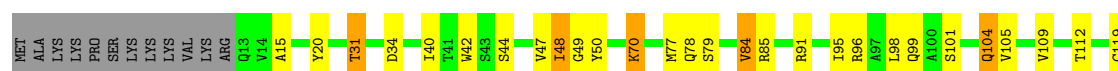
- Molecule 10: 30S Ribosomal Protein S10

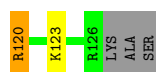
Chain CJ:



- Molecule 11: 30S Ribosomal Protein S11

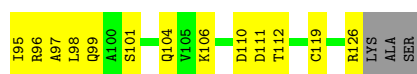
Chain AK:





• Molecule 11: 30S Ribosomal Protein S11

Chain CK:



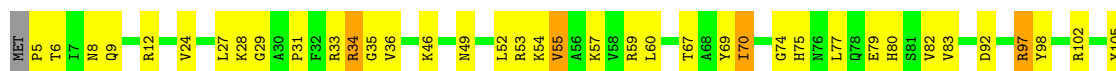
• Molecule 12: 30S Ribosomal Protein S12

Chain AL:



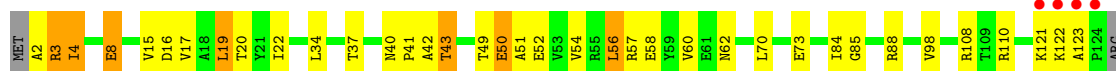
• Molecule 12: 30S Ribosomal Protein S12

Chain CL:



• Molecule 13: 30S Ribosomal Protein S13

Chain AM:



• Molecule 13: 30S Ribosomal Protein S13

Chain CM:



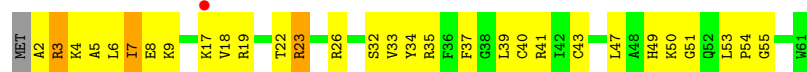
• Molecule 14: 30S Ribosomal Protein S14

Chain AN:



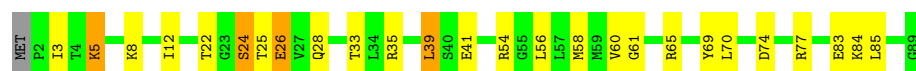
- Molecule 14: 30S Ribosomal Protein S14

Chain CN:



- Molecule 15: 30S Ribosomal Protein S15

Chain AO:



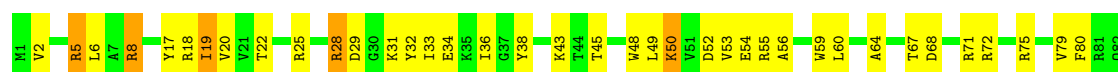
- Molecule 15: 30S Ribosomal Protein S15

Chain CO:



- Molecule 16: 30S Ribosomal Protein S16

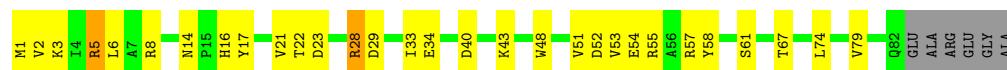
Chain AP:



GLU
ALA
ALA
ARG
GLU
GLY
ALA

- Molecule 16: 30S Ribosomal Protein S16

Chain CP:



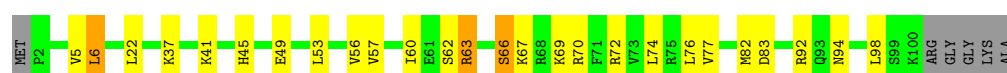
- Molecule 17: 30S Ribosomal Protein S17

Chain AQ:



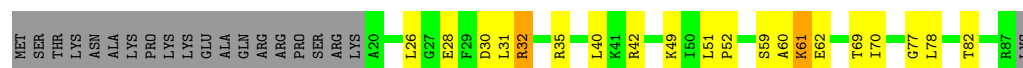
- Molecule 17: 30S Ribosomal Protein S17

Chain CQ:



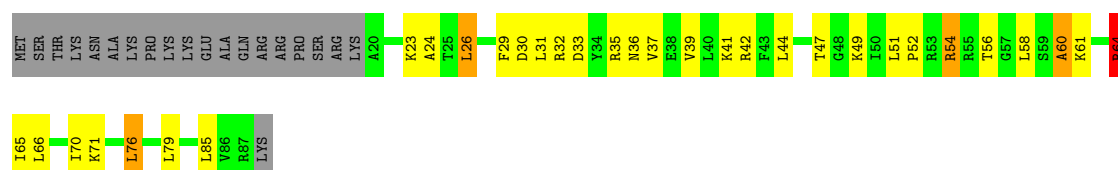
- Molecule 18: 30S Ribosomal Protein S18

Chain AR:



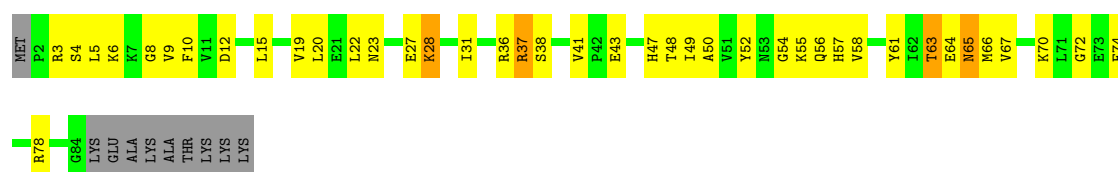
- Molecule 18: 30S Ribosomal Protein S18

Chain CR:



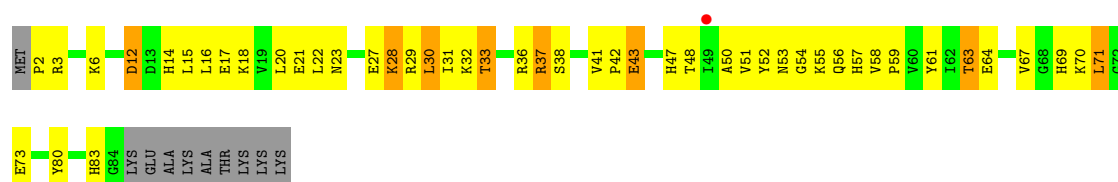
- Molecule 19: 30S Ribosomal Protein S19

Chain AS:



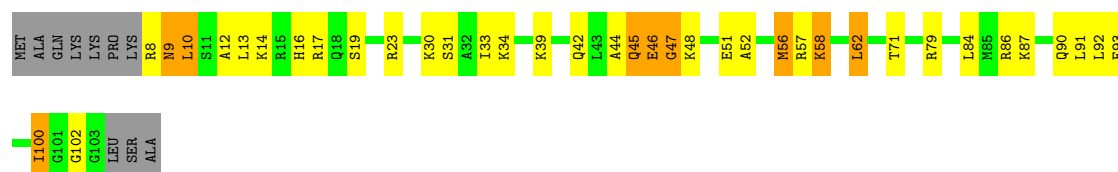
- Molecule 19: 30S Ribosomal Protein S19

Chain CS:



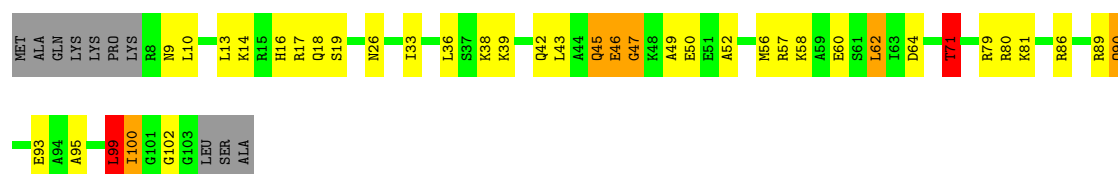
- Molecule 20: 30S Ribosomal Protein S20

Chain AT:



- Molecule 20: 30S Ribosomal Protein S20

Chain CT:



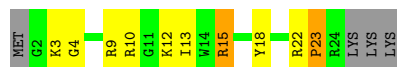
- Molecule 21: 30S Ribosomal Protein THX

Chain AU:



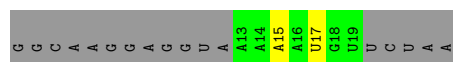
- Molecule 21: 30S Ribosomal Protein THX

Chain CU:



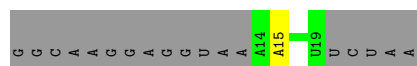
- Molecule 22: mRNA

Chain AV:



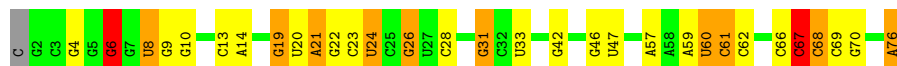
- Molecule 22: mRNA

Chain CV:



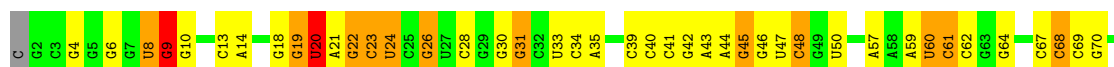
- Molecule 23: P-site tRNA

Chain AX:



- Molecule 23: P-site tRNA

Chain CX:



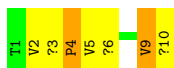
- Molecule 24: GE82832

Chain AW:



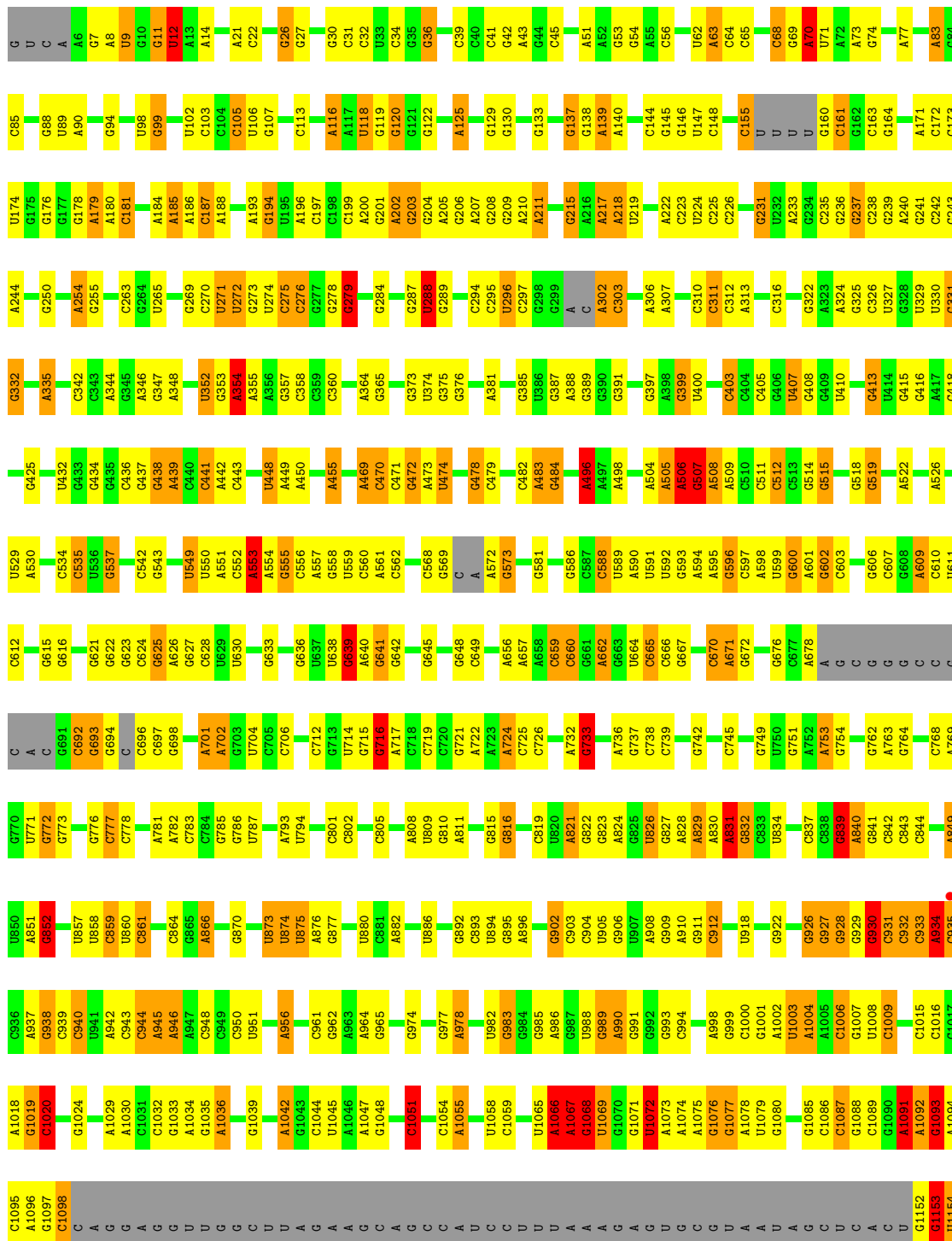
- Molecule 24: GE82832

Chain CW:

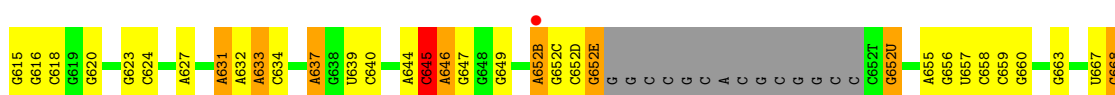


- Molecule 25: 23S Ribosomal RNA

Chain BA:

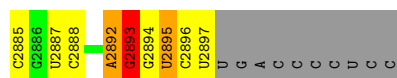


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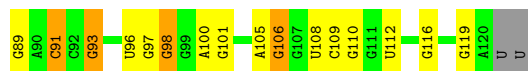
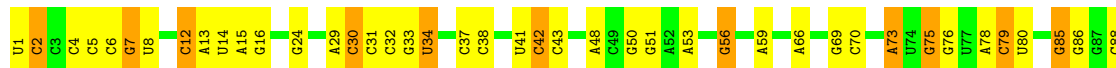
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G1653	U1576	U1507	U1431			C	C	A1010	A941	A878	U807	C736
A1654	C1577	C1432	C1432	G1358	A1284	C	C	G1011		G879	G808	C737
	U1578	A1508	U1433	A1359	A1287	A	A	U1012	A945	G880	G809	G738
A1762	A1579	C1509	A1434	A1360	U1288	G	G	C1013	G946	G881	U810	G739
G1763	A1580	A1509A		U1361		C	C	U1014	G947	G882	U811	U740
A1665		G1510	C1437	C1363	A1210	A	C	U1015	G948	G883	C812	G741
C1765	U1586	G1510	U1438	G1364	U1211	A	A	G1016	C949	C884	U813	
G1666	A1587		A1439	U1365	G1212	U	U	G1017	G950	C885	C814	U747
U1766	C1588	C1513	G1440	A1366	A1214	C	C	G1018	C951	C886	C815	G746
C1767	C1589	U1514	G1441	A1367	G1215	C	U	U1019	G952	A887	C816	G745
U1768	U1590	G1515	G1441	G1368	G1295	U	U	A1020	A953	C888	C817	C749
G1769		C1516		G1369	C1297	U	U	A1021	G954	C889	G818	A752

A	G2729	C2646	G2567	A2497	G2429	A2360	C2293	G2219	C	G2080	U2016	G1933	G1844	G1774
A2801A	G2729	U2647	G2570	C2498	A2430	A2361	C2294	G2219	U	C2081	U2017	C1934	G1845	U1775
C2802	G2732	C2648	G2570	C2499	U2431	C2364	U2295	C2225	C	A2082	G2018	G1935	G1846	U1776
C2803	A2733	U2649	U2500	G2500	A2432	G2365	U2296	C2226	C	G2083	A2019	A1936	A1847	U1777
C2805	G2734	U2650	G2501	G2502	A2433	G2365	C2297	G2227	G	C2084	A2020	A1937	A1848	U1778
G2807	G2735	A2684	G2575	G2503	A2434	G2370	A2298	G2228	G	C2085	C2021	A1938	G1849	U1779
			G2576	A2503	A2435	G2371	G2299	G2230	G	U2086	U2022	A1780	G1850	A1780
			A2577	G2504	G2436	G2372	G2302	G2230	U	G2087	G2023	C1942	U1851	C1781
			G2578	U2505	U2437	G2373	G2302	G2234	G	G2090	G2024	U1943		C1782
			G2579	G2508	A2438	G2374	G2303	G2234	G	G2090	C2025	U1946	A1854	A1783
			U2580	G2509	A2439	C2374	G2304	G2235	G	G2093	C2026	U1947	A1855	A1784
			G2581	C2510	C2440	G2375	A2305	G2238	G	G2094	G2027	C1947	G1856	A1785
			G2582	U2511	C2441	A2376	C2307	G2239	G	C2097	G2028		G1857	A1786
			G2583	C2512	C2442	A2377	G2308	G2239	G	U2098	G2029	G1954	G1858	A1787
			U2584		C2443	G2378	G2309	G2242	G	U2099	A2031	U1955	A1859	C1788
			U2585	G2516	G2444	G2379	G2310	G2242	A	G2100	G2032	U1956	G1860	A1789
			U2586	G2517	G2445	G2380	G2311	G2244	G	G2101	G2033	C1957	G1866	A1790
			A2587	G2518	A2448	G2381	U2312	U2244	C		U2034	A1960	A1876	A1791
			A2588	G2519	A2451	G2382	U2313	C2248	G		G2037	C1961	A1877	U1794
			U2589	U2519	A2451	G2383	C2314	U2249	C		G2038	C1962	G1878	U1795
			A2590	C2520	G2454	G2384	G2315	G2250	C		G2039	U1963	G1879	U1796
			G2591	G2523	G2455	A2388	G2316	G2251	G		C2040	G1964	C1880	C1797
			G2592	G2524	G2455	U2390	G2317	G2252	G		U2041	C1965	C1881	U1798
			G2595	G2525	G2458	G2391	G2318	G2253	U		A2042	A1966	G1882	G1799
						A2392	G2319	G2253	G		A2043	C1967	G1883	C1800
						A2393	G2320	U2257	A		C2044	G1968	A1884	G1801
						C2394	A2321	G2258	A		A2045	A1969	A1885	A1802
						G2397	G2324	U2261	A		G2046	A1970	C1886	A1803
						U2398	G2325	U2262	U		C2047	A1971	C1804	C1804
						G2399	C2326	G2263	A		U2048	A1972	U1805	U1805
						G2400	A2327	C2264	C		G2049	G1973		
						G2401	A2328	A2267	A		C2050	C1982	G1897	A1810
						G2402	G2329	A2268	C		A2051	C1983	U1898	G1811
						C2403	G2330	A2269	C		G2052	G1984	G1899	A1812
						G2404	G2331	A2270	C		G2053	G1985	A1900	A1815
						G2405	U2332	G2270	U		A2054		G1903	A1816
						G2406	A2333	G2271	G		C2055	U1991	G1906	G1817
						U2407	G2334	U2272	U		G2056	G1992	G1907	U1818
						G2408	A2335	A2273	G		A2057	U1993	G1907	A1819
						G2409	A2336	A2274	G		A2058	G1996	G1908	
						C2475	G2337	G2275	C		A2059	G1997		G1823
						G2410	G2338	G2276	G		A2060	G1997		
						A2411	G2339	G2277	G		G2061	G2000	A1912	G1826
						G2412		A2278	C		A2062	A1913	C1827	G1827
						G2413	C2343	A2279	C		C2063	A2001	G1828	C1828
						G2414	U2344	G2280	U		C2064	U1915	A1829	A1829
						G2415	G2345	G2281	U		C2065	A1916	C1830	C1830
						G2416	A2346	G2282	U		C2066	U1917	G1831	G1831
						C2417	G2347	G2283	U			C2006	A1918	G1832
						G2418	U2348	G2284	A		G2069	C2007	A1919	U1833
						U2419	U2349	G2285	A		G2070	C2008	U1834	U1834
						G2420	G2351	A2286	C			G2009	G1835	G1835
						G2421	G2351	A2287	C		U2074	G2010	A1927	C1836
						A2422	G2354	A2288	C		U2075	U2011	A1928	
						A2425	U2357	G2289	C		U2076	G2012	G1929	G1840
						A2426	G2358	G2290	C		U2077	A2013	G1930	U1841
						G2427	G2358	U2291	C			A2014	U1931	U1842
						G2428	C2359	G2292	C			A2015	A1932	C1843



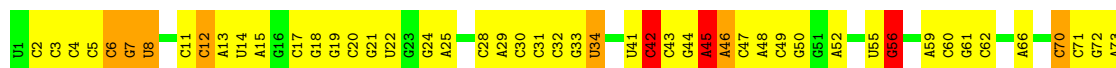
- Molecule 26: 5S Ribosomal RNA

Chain BB:



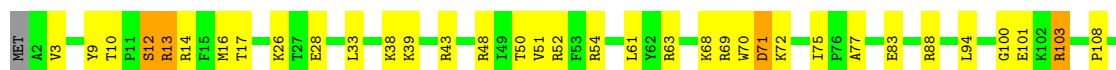
- Molecule 26: 5S Ribosomal RNA

Chain DB:



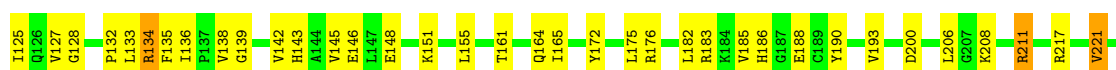
- Molecule 27: 50S Ribosomal Protein L2

Chain BD:



- Molecule 27: 50S Ribosomal Protein L2

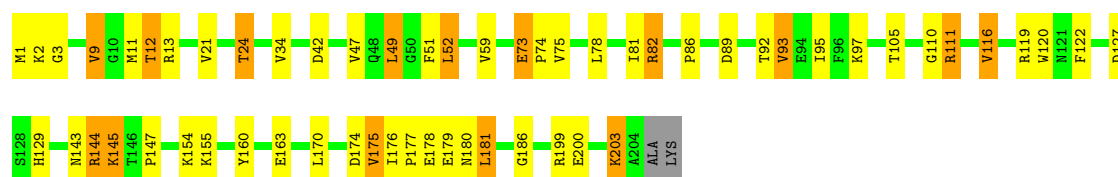
Chain DD:



- Molecule 28: 50S Ribosomal Protein L3

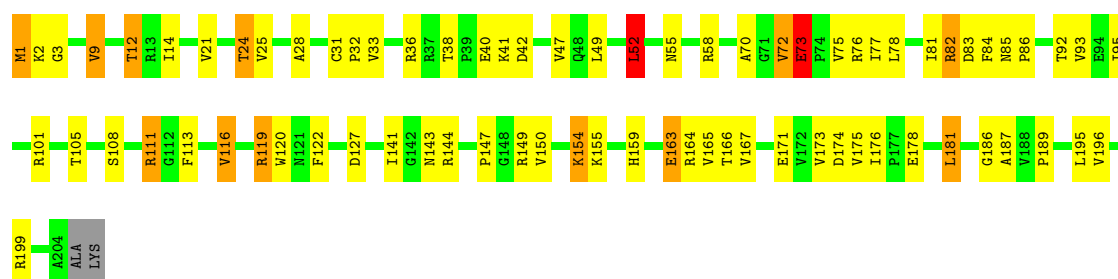
Chain BE:





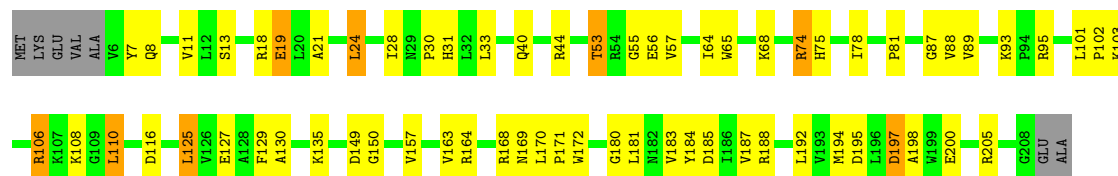
• Molecule 28: 50S Ribosomal Protein L3

Chain DE:



• Molecule 29: 50S Ribosomal Protein L4

Chain BF:



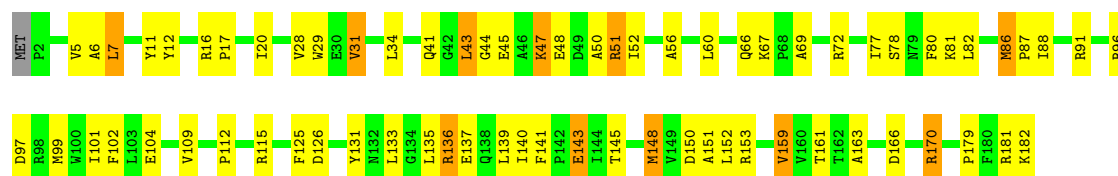
• Molecule 29: 50S Ribosomal Protein L4

Chain DF:



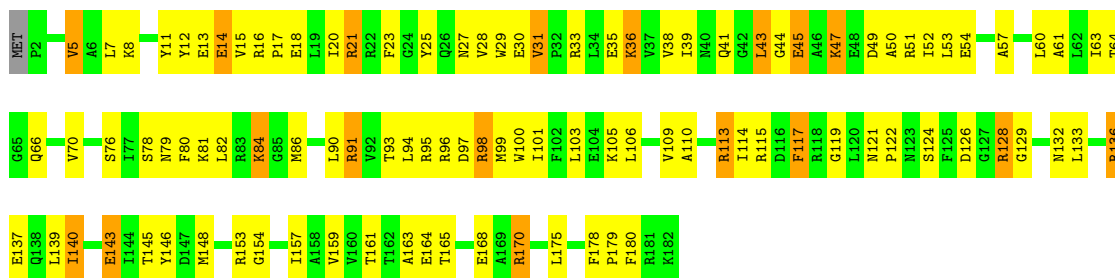
• Molecule 30: 50S Ribosomal Protein L5

Chain BG:



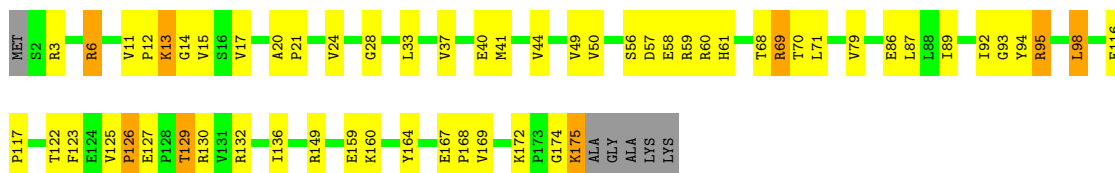
• Molecule 30: 50S Ribosomal Protein L5

Chain DG:



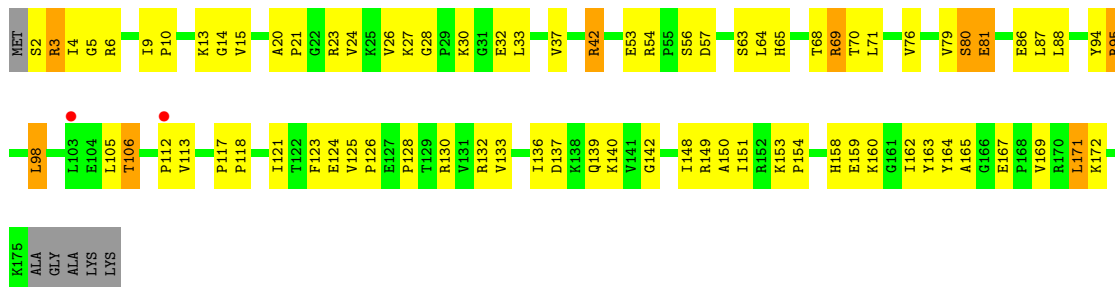
• Molecule 31: 50S Ribosomal Protein L6

Chain BH:



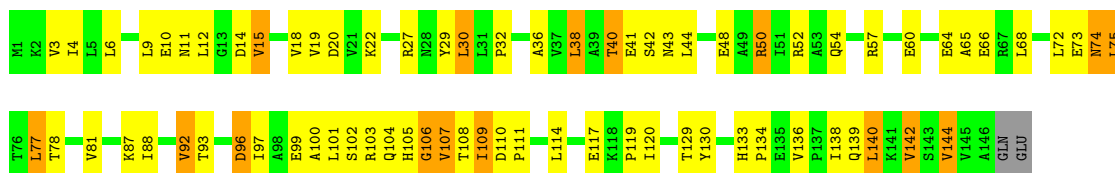
• Molecule 31: 50S Ribosomal Protein L6

Chain DH:



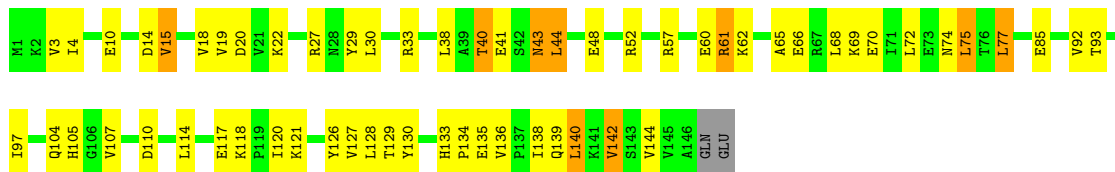
• Molecule 32: 50S Ribosomal Protein L9

Chain BI:



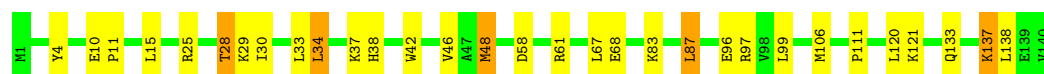
• Molecule 32: 50S Ribosomal Protein L9

Chain DI:



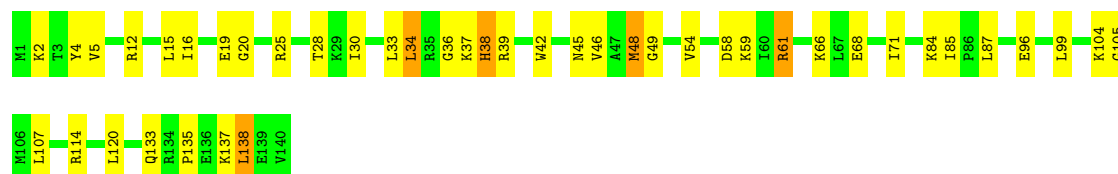
• Molecule 33: 50S Ribosomal Protein L13

Chain BN: 



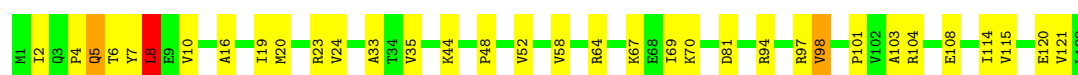
- Molecule 33: 50S Ribosomal Protein L13

Chain DN: 



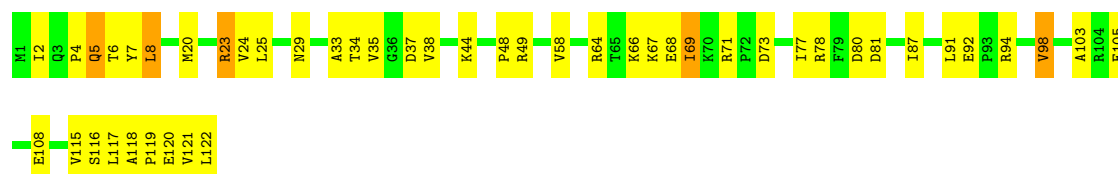
- Molecule 34: 50S Ribosomal Protein L14

Chain BO: 



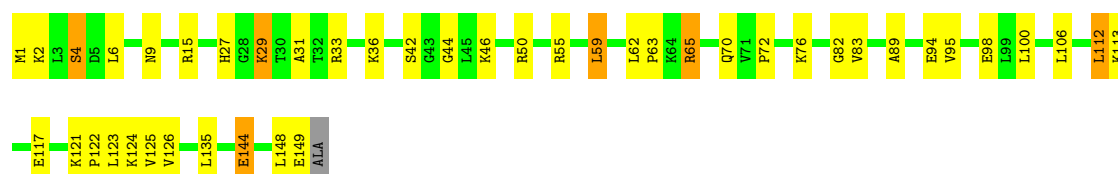
- Molecule 34: 50S Ribosomal Protein L14

Chain DO: 



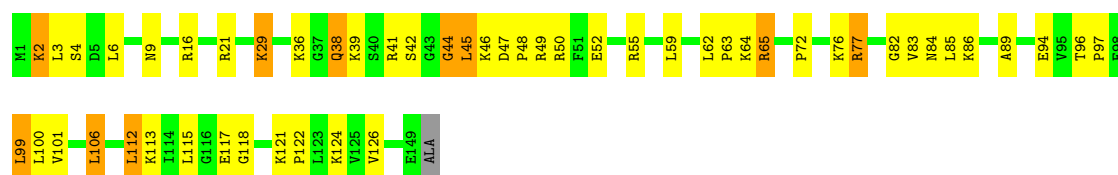
- Molecule 35: 50S Ribosomal Protein L15

Chain BP: 



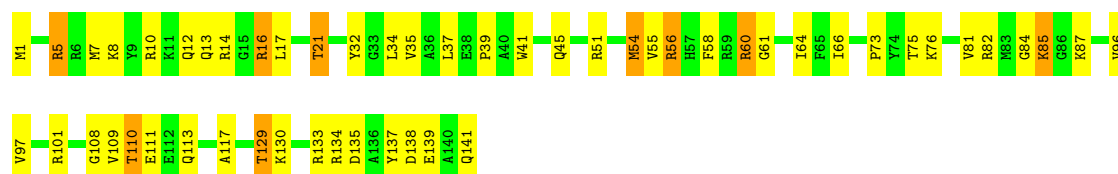
- Molecule 35: 50S Ribosomal Protein L15

Chain DP: 



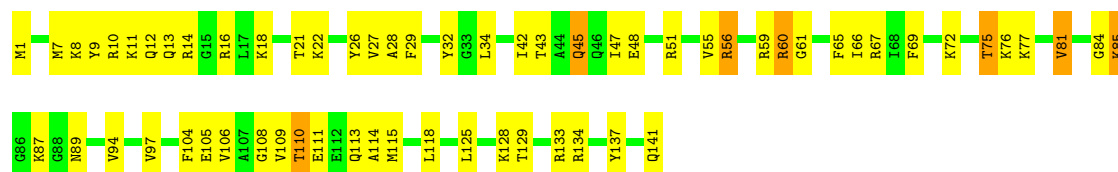
- Molecule 36: 50S Ribosomal Protein L16

Chain BQ: 



• Molecule 36: 50S Ribosomal Protein L16

Chain DQ:



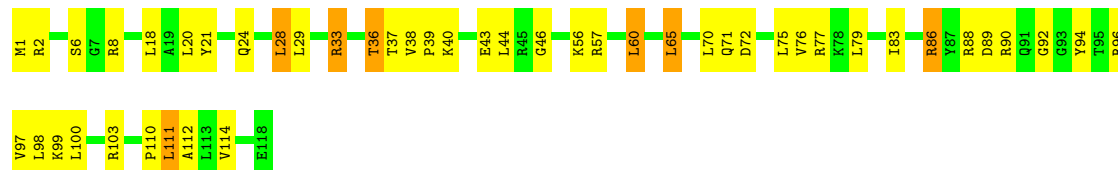
• Molecule 37: 50S Ribosomal Protein L17

Chain BR:



• Molecule 37: 50S Ribosomal Protein L17

Chain DR:



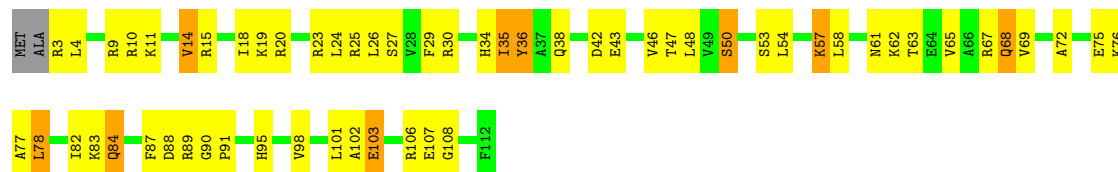
• Molecule 38: 50S Ribosomal Protein L18

Chain BS:



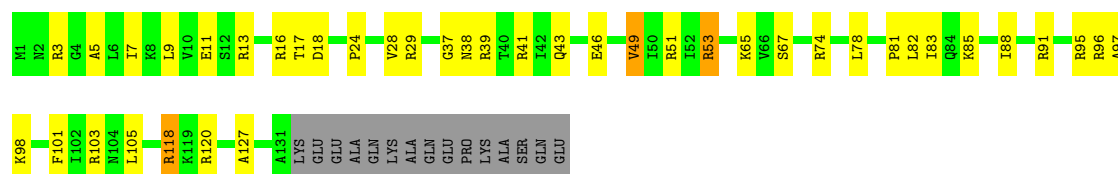
• Molecule 38: 50S Ribosomal Protein L18

Chain DS:



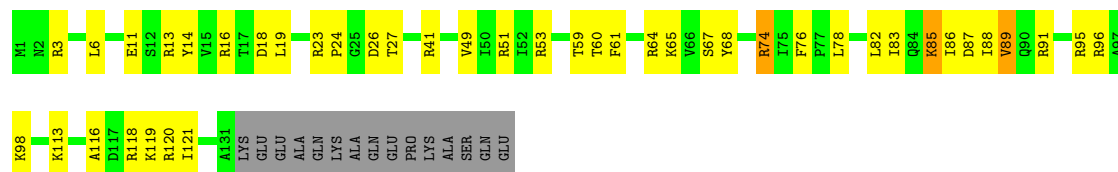
• Molecule 39: 50S Ribosomal Protein L19

Chain BT:



• Molecule 39: 50S Ribosomal Protein L19

Chain DT:



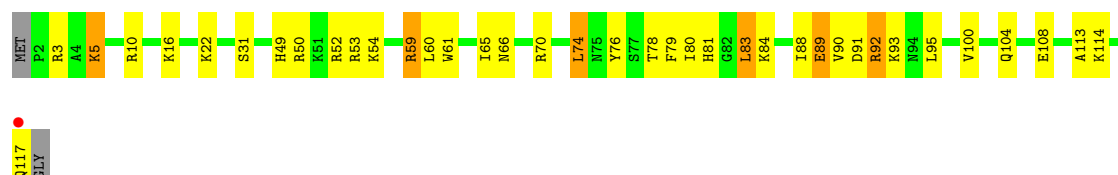
• Molecule 40: 50S Ribosomal Protein L20

Chain BU:



• Molecule 40: 50S Ribosomal Protein L20

Chain DU:



• Molecule 41: 50S Ribosomal Protein L21

Chain BV:



• Molecule 41: 50S Ribosomal Protein L21

Chain DV:



• Molecule 42: 50S Ribosomal Protein L22

Chain BW:



- Molecule 42: 50S Ribosomal Protein L22

Chain DW:



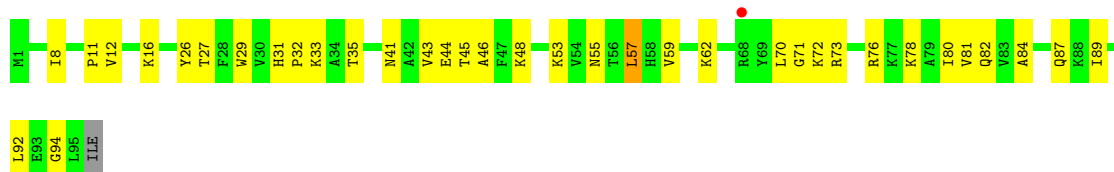
- Molecule 43: 50S Ribosomal Protein L23

Chain BX:



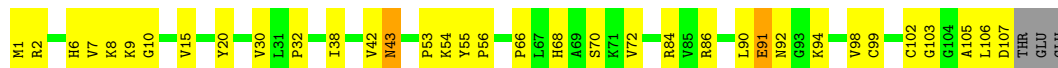
- Molecule 43: 50S Ribosomal Protein L23

Chain DX:



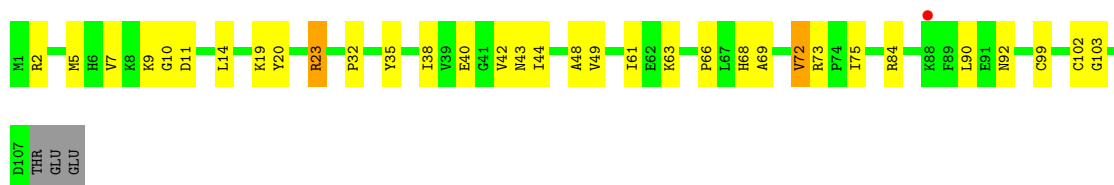
- Molecule 44: 50S Ribosomal Protein L24

Chain BY:



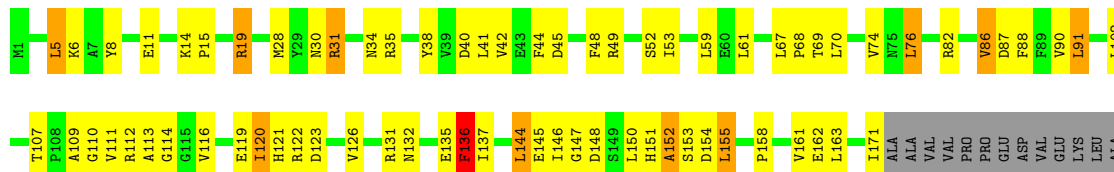
- Molecule 44: 50S Ribosomal Protein L24

Chain DY:



- Molecule 45: 50S Ribosomal Protein L25

Chain BZ:



GLU
GLU
ALA
ALA
ALA
GLU
VAL
ALA
GLU
PRO
GLU
VAL
ILE
LYS
LYS
GLY
LYS
GLU
GLU
GLU

• Molecule 45: 50S Ribosomal Protein L25

Chain DZ:

H1 L5 K6 A7 Y8 E11 G12 R19 R30 R31 R32 R33 Y38 V39 D40 L41 V42 E43 F44 D45 K46 V47 F48 R49 Q50 A51 S52 S53 S54 L61 P62 L67 P68 T69 L70 V165 V171 R72 Q73 V74 V75 L76 P83 V86 D87 V90 L91 S92 D93 E94 P95

V96 E97 P101 T107 P108 V116 H121 R122 D123 L124 L125 V128 S129 P130 R131 M132 I133 V141 L144 L150 H151 A152 S153 D154 L155 K156 L157 P158 V161 E162 L163 A164 V165 S166 P167 V174 VAL PRO GLU ASP VAL VAL LYS LEU ALA GLU ALA ALA

ALA
GLU
VAL
GLU
PRO
GLU
VAL
ILE
LYS
LYS
GLY
GLU
GLU
GLU
GLU

• Molecule 46: 50S Ribosomal Protein L27

Chain B0:

MET A2 H3 K4 K5 G6 L7 G8 T10 R11 N12 G13 R14 K19 R20 V23 E27 V30 R39 Q40 T43 K46 K49 N50 M53 G54 R55 D56 F57 T58 L59 V66 V67 E68 F69 G73 R77 L84 ALA

• Molecule 46: 50S Ribosomal Protein L27

Chain D0:

MET A2 H3 K4 K5 G6 L7 G8 T10 R11 R14 B15 S16 K19 R20 V23 K24 R25 Y26 E27 R32 Q40 T43 M53 G54 R55 D56 F57 T58 L59 E68 F69 R72 L75 G76 R82 P83 L84 ALA

• Molecule 47: 50S Ribosomal Protein L28

Chain B1:

MET S2 K3 R11 R21 G22 K23 R26 G29 K33 T34 T35 R40 N45 R50 V51 R52 T59 F60 R61 A64 S65 H66 I67 Y71 Y74 L82 L85 S86 E89 I90 K91 L95 L98

• Molecule 47: 50S Ribosomal Protein L28

Chain D1:

MET S2 K3 I7 R21 G22 K23 A24 K25 R26 G29 V30 G31 T35 K39 R40 R50 V51 R52 E57 E58 T59 F60 R61 A64 S65 H66 I67 Y71 Y72 L73 V74 A77 K78 G79 L80 E83 G84 L85 E89 K92 E93 L94 L95 L98

• Molecule 48: 50S Ribosomal Protein L29

Chain B2:

M1 K2 L3 V6 L10 L16 S17 P18 L21 R26 E27 K28 K29 R30 E31 L32 R36 F37 S40 T41 L44 S45 Q46 M47 H48 K49 D52 L53 V54 R55 V63 L64 N65 E66 K67 R68 R69 Q70 ASN ALA

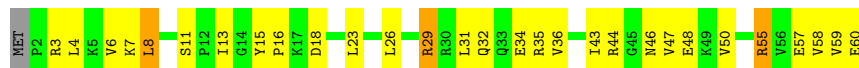
• Molecule 48: 50S Ribosomal Protein L29

Chain D2:



- Molecule 49: 50S Ribosomal Protein L30

Chain B3:



- Molecule 49: 50S Ribosomal Protein L30

Chain D3:



- Molecule 50: 50S Ribosomal Protein L31

Chain B4:



- Molecule 50: 50S Ribosomal Protein L31

Chain D4:



- Molecule 51: 50S Ribosomal Protein L32

Chain B5:



- Molecule 51: 50S Ribosomal Protein L32

Chain D5:



- Molecule 52: 50S Ribosomal Protein L33

Chain B6:



- Molecule 52: 50S Ribosomal Protein L33

Chain D6:



- Molecule 53: 50S Ribosomal Protein L34

Chain B7:



- Molecule 53: 50S Ribosomal Protein L34

Chain D7:



- Molecule 54: 50S Ribosomal Protein L35

Chain B8:



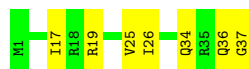
- Molecule 54: 50S Ribosomal Protein L35

Chain D8:



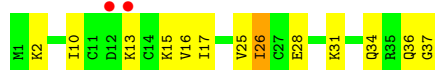
- Molecule 55: 50S Ribosomal Protein L36

Chain B9:



- Molecule 55: 50S Ribosomal Protein L36

Chain D9:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.68Å 450.64Å 622.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.68 – 3.10 49.68 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.2 (49.68-3.10) 98.2 (49.68-3.10)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	0.25	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.203 , 0.260 0.231 , 0.282	Depositor DCC
R_{free} test set	41240 reflections (3.99%)	DCC
Wilson B-factor (Å ²)	71.0	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 1034786 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	286321	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.83% 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, K, 2QZ, ZN, 2QY, MVA, 004, FME, 2R3, SF4, 2R1

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	AA	0.75	2/36038 (0.0%)	1.31	240/56244 (0.4%)
1	CA	0.75	10/36170 (0.0%)	1.36	314/56452 (0.6%)
2	AB	0.49	0/1881	0.77	1/2542 (0.0%)
2	CB	0.54	0/1860	0.79	1/2518 (0.0%)
3	AC	0.47	0/1576	0.65	0/2130
3	CC	0.51	0/1566	0.71	2/2119 (0.1%)
4	AD	0.49	0/1689	0.73	0/2267
4	CD	0.49	0/1704	0.70	1/2284 (0.0%)
5	AE	0.47	0/1145	0.70	0/1543
5	CE	0.50	0/1149	0.71	0/1548
6	AF	0.47	0/819	0.69	0/1111
6	CF	0.52	0/829	0.74	1/1123 (0.1%)
7	AG	0.48	0/1250	0.67	1/1679 (0.1%)
7	CG	0.50	0/1254	0.71	1/1683 (0.1%)
8	AH	0.45	0/1108	0.66	0/1494
8	CH	0.48	0/1108	0.69	0/1494
9	AI	0.46	0/1002	0.72	0/1346
9	CI	0.56	0/997	0.75	1/1343 (0.1%)
10	AJ	0.47	0/722	0.68	0/982
10	CJ	0.51	0/727	0.68	0/988
11	AK	0.44	0/844	0.62	0/1145
11	CK	0.46	0/848	0.66	0/1149
12	AL	0.52	0/946	0.69	0/1274
12	CL	0.51	0/946	0.73	0/1274
13	AM	0.46	0/969	0.69	0/1302
13	CM	0.49	0/961	0.66	0/1291
14	AN	0.51	0/501	0.67	0/664
14	CN	0.54	0/501	0.68	0/664
15	AO	0.47	0/739	0.72	0/985
15	CO	0.46	0/739	0.73	0/985
16	AP	0.45	0/697	0.71	0/939
16	CP	0.47	0/693	0.65	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.48	0/836	0.66	0/1117
17	CQ	0.49	0/836	0.68	0/1117
18	AR	0.49	0/560	0.72	0/746
18	CR	0.51	0/560	0.75	1/746 (0.1%)
19	AS	0.47	0/667	0.68	0/900
19	CS	0.54	0/661	0.82	2/893 (0.2%)
20	AT	0.51	0/730	0.76	0/965
20	CT	0.44	0/729	0.68	0/965
21	AU	0.45	0/203	0.65	0/266
21	CU	0.51	0/203	0.68	0/266
22	AV	0.94	0/127	1.36	2/198 (1.0%)
22	CV	0.86	0/126	1.29	0/195
23	AX	0.85	5/1813 (0.3%)	1.59	36/2825 (1.3%)
23	CX	0.88	4/1813 (0.2%)	1.81	40/2825 (1.4%)
24	AW	0.50	0/20	0.80	0/23
24	CW	0.43	0/20	0.70	0/23
25	BA	1.06	33/65892 (0.1%)	1.42	649/102850 (0.6%)
25	DA	0.79	9/65466 (0.0%)	1.39	590/102184 (0.6%)
26	BB	0.82	0/2878	1.26	11/4490 (0.2%)
26	DB	0.89	0/2878	1.39	18/4490 (0.4%)
27	BD	0.67	1/2186 (0.0%)	0.78	1/2944 (0.0%)
27	DD	0.61	2/2186 (0.1%)	0.77	1/2944 (0.0%)
28	BE	0.69	0/1592	0.75	0/2149
28	DE	0.55	0/1592	0.77	1/2149 (0.0%)
29	BF	0.69	0/1619	0.76	0/2193
29	DF	0.53	0/1615	0.77	1/2188 (0.0%)
30	BG	0.46	0/1450	0.70	0/1959
30	DG	0.55	0/1449	0.74	0/1958
31	BH	0.60	0/1356	0.70	0/1834
31	DH	0.56	0/1356	0.70	0/1834
32	BI	0.49	0/1100	0.74	1/1501 (0.1%)
32	DI	0.48	0/1076	0.77	0/1471
33	BN	0.65	0/1144	0.73	0/1543
33	DN	0.50	0/1144	0.72	0/1543
34	BO	0.65	0/943	0.73	1/1269 (0.1%)
34	DO	0.54	0/943	0.73	1/1269 (0.1%)
35	BP	0.62	0/1152	0.77	0/1533
35	DP	0.53	0/1152	0.80	1/1533 (0.1%)
36	BQ	0.64	0/1143	0.76	0/1527
36	DQ	0.60	0/1143	0.79	0/1527
37	BR	0.59	0/982	0.78	0/1312
37	DR	0.49	0/982	0.71	0/1312
38	BS	0.54	0/887	0.77	0/1180

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DS	0.47	0/880	0.72	0/1172
39	BT	0.59	0/1105	0.79	1/1477 (0.1%)
39	DT	0.50	0/1097	0.72	0/1468
40	BU	0.71	1/977 (0.1%)	0.73	0/1301
40	DU	0.54	0/977	0.71	1/1301 (0.1%)
41	BV	0.68	0/782	0.74	1/1049 (0.1%)
41	DV	0.55	0/782	0.71	0/1049
42	BW	0.74	0/897	0.74	0/1205
42	DW	0.56	0/897	0.72	0/1205
43	BX	0.66	0/764	0.96	3/1025 (0.3%)
43	DX	0.55	0/764	0.75	1/1025 (0.1%)
44	BY	0.64	0/819	0.78	0/1095
44	DY	0.54	0/819	0.74	0/1095
45	BZ	0.56	0/1379	0.75	0/1873
45	DZ	0.53	0/1390	0.71	0/1890
46	B0	0.63	0/662	0.81	2/881 (0.2%)
46	D0	0.54	0/662	0.73	0/881
47	B1	0.61	0/762	0.74	0/1014
47	D1	0.51	0/762	0.75	1/1014 (0.1%)
48	B2	0.61	0/590	0.79	0/781
48	D2	0.48	0/590	0.66	0/781
49	B3	0.70	0/474	0.76	0/635
49	D3	0.45	0/469	0.67	0/630
50	B4	0.58	0/564	0.79	0/759
50	D4	0.59	0/544	0.86	1/735 (0.1%)
51	B5	0.66	0/469	0.78	0/635
51	D5	0.53	0/469	0.74	1/635 (0.2%)
52	B6	0.67	0/460	0.64	0/613
52	D6	0.53	0/456	0.70	0/608
53	B7	0.79	0/426	0.78	0/561
53	D7	0.62	0/426	0.76	1/561 (0.2%)
54	B8	0.70	0/519	0.71	0/684
54	D8	0.55	0/525	0.75	0/691
55	B9	0.69	0/310	0.76	0/407
55	D9	0.60	0/310	0.79	0/407
All	All	0.79	67/305966 (0.0%)	1.24	1933/457396 (0.4%)

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
2	AB	0	3
4	CD	0	1
7	AG	0	1
23	CX	1	0
24	AW	0	1
24	CW	0	1
27	DD	0	1
38	BS	0	1
45	BZ	0	1
50	B4	0	1
All	All	1	11

All (67) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AX	76	A	N7-C5	-11.16	1.32	1.39
1	CA	1154	G	C6-N1	-11.02	1.31	1.39
1	CA	1154	G	N1-C2	-10.69	1.29	1.37
25	BA	1188	A	N9-C4	-10.29	1.31	1.37
1	CA	1119	C	N3-C4	-10.20	1.26	1.33
25	BA	2299	A	N9-C4	-9.27	1.32	1.37
23	CX	76	A	N7-C5	-8.97	1.33	1.39
25	BA	1067	A	N9-C4	-8.63	1.32	1.37
23	CX	76	A	C5-C6	-8.11	1.33	1.41
25	DA	528	A	N9-C4	-7.89	1.33	1.37
1	CA	1492	A	N9-C4	7.83	1.42	1.37
25	BA	1222	A	N9-C4	7.65	1.42	1.37
23	AX	76	A	C5-C6	-7.63	1.34	1.41
1	CA	1154	G	N7-C5	-7.45	1.34	1.39
25	BA	1234	A	N9-C4	-6.96	1.33	1.37
23	CX	76	A	C5-C4	-6.68	1.34	1.38
25	BA	1188	A	N3-C4	-6.67	1.30	1.34
25	DA	2287	A	N9-C4	-6.63	1.33	1.37
40	BU	69	CYS	CB-SG	-6.61	1.71	1.82
25	BA	2601	A	N9-C4	-6.59	1.33	1.37
25	DA	2207	G	N7-C5	-6.42	1.35	1.39
23	AX	22	G	N7-C5	6.40	1.43	1.39
27	DD	28	GLU	CG-CD	6.36	1.61	1.51
25	BA	1605	A	N9-C4	-6.13	1.34	1.37
25	BA	2444	A	C5-C6	-6.13	1.35	1.41
1	CA	1154	G	C5-C4	6.05	1.42	1.38
25	DA	1142(A)	A	N9-C4	-6.03	1.34	1.37
25	DA	2320	A	N9-C4	6.01	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	DA	2725	A	N9-C4	-5.99	1.34	1.37
1	CA	1154	G	N9-C4	5.94	1.42	1.38
23	AX	46	G	C6-N1	5.78	1.43	1.39
25	BA	978	A	N9-C4	-5.77	1.34	1.37
25	BA	657	A	N9-C4	-5.77	1.34	1.37
25	BA	178	G	N7-C5	-5.64	1.35	1.39
1	CA	1119	C	N1-C2	5.58	1.45	1.40
25	BA	1425	A	N9-C4	-5.57	1.34	1.37
25	BA	354	A	N9-C4	-5.49	1.34	1.37
25	BA	2527	C	N1-C6	-5.48	1.33	1.37
25	BA	552	C	N3-C4	-5.46	1.30	1.33
25	BA	782	A	N3-C4	-5.42	1.31	1.34
25	DA	530	G	N9-C8	5.42	1.41	1.37
25	BA	506	A	N7-C5	-5.42	1.36	1.39
1	CA	1154	G	C8-N7	-5.40	1.27	1.30
25	BA	2803	A	N9-C4	5.38	1.41	1.37
25	BA	1153	G	N9-C4	5.35	1.42	1.38
25	BA	2509	A	N3-C4	-5.31	1.31	1.34
25	BA	2039	U	C2-N3	-5.30	1.34	1.37
1	AA	1124	G	N9-C4	5.29	1.42	1.38
23	CX	22	G	N7-C5	5.27	1.42	1.39
1	AA	1531	A	N9-C4	5.25	1.41	1.37
27	DD	28	GLU	CB-CG	5.21	1.62	1.52
25	BA	840	A	N7-C5	-5.21	1.36	1.39
25	BA	1234	A	N3-C4	-5.20	1.31	1.34
25	DA	2599	G	C6-N1	-5.20	1.35	1.39
25	BA	840	A	C5-C6	-5.18	1.36	1.41
25	BA	1076	G	C6-N1	-5.17	1.35	1.39
25	DA	784	A	N9-C4	-5.17	1.34	1.37
25	BA	186	A	N3-C4	-5.17	1.31	1.34
1	CA	998	G	N7-C5	5.16	1.42	1.39
25	BA	781	A	N9-C4	-5.16	1.34	1.37
25	BA	1818	A	C6-N1	-5.04	1.32	1.35
27	BD	28	GLU	CG-CD	5.04	1.59	1.51
25	BA	1030	A	N9-C4	-5.02	1.34	1.37
25	BA	990	A	N9-C4	-5.02	1.34	1.37
25	BA	2598	C	N1-C6	-5.02	1.34	1.37
23	AX	14	A	N7-C5	-5.01	1.36	1.39
25	BA	2080	A	N3-C4	-5.01	1.31	1.34

All (1933) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CX	76	A	O4'-C1'-N9	38.71	139.17	108.20
1	CA	1119	C	N1-C2-O2	32.56	138.44	118.90
1	CA	1154	G	C5-C6-O6	28.63	145.78	128.60
1	CA	1154	G	N3-C2-N2	25.05	137.43	119.90
1	CA	1154	G	N1-C2-N2	-22.71	95.76	116.20
1	CA	1119	C	N3-C2-O2	-21.96	106.53	121.90
23	CX	76	A	C2-N3-C4	19.79	120.49	110.60
23	CX	76	A	N1-C2-N3	-19.05	119.78	129.30
23	AX	76	A	C2-N3-C4	18.48	119.84	110.60
23	AX	76	A	N1-C2-N3	-17.90	120.35	129.30
1	CA	1119	C	C2-N3-C4	17.09	128.45	119.90
1	CA	1154	G	C5-C6-N1	-17.07	102.97	111.50
1	CA	1119	C	C2-N1-C1'	16.03	136.44	118.80
43	BX	65	ARG	NE-CZ-NH2	15.41	128.00	120.30
23	AX	76	A	O4'-C1'-N9	15.35	120.48	108.20
1	CA	1154	G	C6-N1-C2	14.89	134.03	125.10
23	AX	8	U	C2-N3-C4	14.86	135.91	127.00
1	CA	1119	C	C5-C4-N4	14.60	130.42	120.20
1	CA	1154	G	N1-C6-O6	-14.49	111.20	119.90
25	BA	1067	A	C2-N3-C4	-14.43	103.38	110.60
1	CA	999	C	N1-C2-O2	13.32	126.89	118.90
1	CA	1154	G	C4-N9-C1'	12.75	143.07	126.50
25	DA	528	A	C2-N3-C4	-12.60	104.30	110.60
25	BA	2058	C	O5'-P-OP1	-12.50	94.45	105.70
23	CX	8	U	C2-N3-C4	12.28	134.37	127.00
1	CA	1119	C	N3-C4-N4	-12.22	109.45	118.00
1	CA	1119	C	C6-N1-C2	-12.18	115.43	120.30
25	BA	139	A	N7-C8-N9	12.11	119.86	113.80
25	DA	945	A	N1-C6-N6	11.58	125.55	118.60
25	BA	139	A	C5-N7-C8	-11.57	98.12	103.90
1	CA	1119	C	C6-N1-C1'	-11.45	107.07	120.80
43	BX	65	ARG	NE-CZ-NH1	-11.42	114.59	120.30
1	CA	1154	G	C8-N9-C1'	-11.28	112.34	127.00
25	BA	1188	A	C2-N3-C4	-11.10	105.05	110.60
1	AA	1125	U	N1-C2-O2	11.09	130.56	122.80
23	CX	76	A	N3-C4-C5	-10.90	119.17	126.80
23	CX	8	U	C5-C6-N1	10.69	128.04	122.70
26	BB	91	C	C6-N1-C2	10.59	124.53	120.30
23	AX	46	G	C6-N1-C2	-10.39	118.86	125.10
1	CA	1004	A	O4'-C1'-N9	10.33	116.47	108.20
25	BA	990	A	C5-N7-C8	-10.27	98.77	103.90
25	BA	1098	C	C6-N1-C2	-10.25	116.20	120.30
23	CX	76	A	C5-N7-C8	10.25	109.02	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2835	C	O5'-P-OP1	-10.24	96.48	105.70
23	CX	76	A	N7-C8-N9	-10.24	108.68	113.80
23	AX	76	A	N7-C8-N9	-10.15	108.72	113.80
1	AA	1125	U	N1-C2-N3	-10.09	108.85	114.90
25	DA	856	C	C6-N1-C2	-10.03	116.29	120.30
25	BA	201	G	O5'-P-OP2	-9.99	96.71	105.70
23	CX	46	G	C6-N1-C2	-9.84	119.20	125.10
1	CA	1119	C	C5-C6-N1	9.74	125.87	121.00
25	DA	1698	A	N1-C6-N6	9.70	124.42	118.60
1	CA	927	G	C5-C6-O6	9.70	134.42	128.60
25	DA	205	G	C8-N9-C4	9.64	110.26	106.40
25	BA	990	A	C2-N3-C4	-9.64	105.78	110.60
25	BA	1067	A	C5-N7-C8	-9.61	99.10	103.90
1	CA	1154	G	C5-N7-C8	9.58	109.09	104.30
25	DA	2084	C	C6-N1-C2	9.51	124.10	120.30
23	AX	76	A	C5-N7-C8	9.49	108.64	103.90
25	DA	1823	G	O5'-P-OP2	-9.46	97.19	105.70
25	BA	724	A	O5'-P-OP2	-9.43	97.22	105.70
25	BA	1440	U	O5'-P-OP1	-9.40	97.24	105.70
25	BA	1020	C	C6-N1-C2	9.38	124.05	120.30
25	BA	607	C	C6-N1-C2	9.38	124.05	120.30
25	BA	537	G	O4'-C1'-N9	9.35	115.68	108.20
25	DA	1021	A	C2-N3-C4	-9.26	105.97	110.60
23	AX	8	U	C5-C4-O4	9.26	131.45	125.90
23	AX	14	A	C5-N7-C8	9.19	108.49	103.90
25	BA	2299	A	C2-N3-C4	-9.15	106.03	110.60
1	AA	1127	G	N3-C4-N9	9.14	131.48	126.00
23	AX	22	G	C5-N7-C8	-9.09	99.76	104.30
25	DA	2253	G	N1-C6-O6	9.03	125.32	119.90
23	CX	22	G	C5-N7-C8	-9.03	99.79	104.30
25	BA	1225	C	C6-N1-C2	8.99	123.89	120.30
25	DA	2503	A	C5-C6-N6	-8.97	116.52	123.70
25	BA	354	A	C2-N3-C4	-8.94	106.13	110.60
25	BA	139	A	C8-N9-C4	-8.93	102.23	105.80
26	DB	115	G	C8-N9-C4	8.93	109.97	106.40
25	DA	2207	G	C6-C5-N7	-8.92	125.05	130.40
25	BA	1216	G	C8-N9-C4	-8.90	102.84	106.40
25	DA	915	C	C6-N1-C2	-8.87	116.75	120.30
23	AX	14	A	C4-C5-C6	8.85	121.42	117.00
25	DA	1269	A	N1-C6-N6	8.84	123.91	118.60
23	AX	76	A	N3-C4-C5	-8.83	120.62	126.80
25	DA	1204	A	C2-N3-C4	-8.80	106.20	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	934	A	O4'-C1'-N9	8.80	115.24	108.20
25	DA	970	C	N1-C2-O2	-8.78	113.63	118.90
1	CA	1154	G	C4-C5-C6	8.76	124.06	118.80
25	DA	2804	C	C6-N1-C2	-8.75	116.80	120.30
25	DA	1698	A	C6-C5-N7	-8.74	126.18	132.30
25	BA	930	G	O4'-C1'-N9	8.72	115.18	108.20
25	DA	2188	C	C6-N1-C2	-8.68	116.83	120.30
25	DA	1698	A	C2-N3-C4	-8.66	106.27	110.60
1	AA	1030(B)	C	C2-N1-C1'	8.62	128.28	118.80
25	DA	530	G	C8-N9-C4	-8.62	102.95	106.40
25	BA	1686	U	O5'-P-OP2	-8.60	97.96	105.70
1	CA	1003	G	N3-C4-C5	-8.57	124.32	128.60
25	BA	1314	A	C8-N9-C4	8.55	109.22	105.80
25	BA	1067	A	N3-C4-C5	8.55	132.79	126.80
1	AA	1036	G	C4-N9-C1'	8.55	137.61	126.50
23	CX	46	G	N3-C2-N2	-8.53	113.93	119.90
25	BA	2105	G	C5-C6-O6	-8.49	123.51	128.60
1	CA	1260	C	C6-N1-C2	-8.48	116.91	120.30
25	BA	507	G	O4'-C1'-N9	8.45	114.96	108.20
1	AA	166	G	C8-N9-C4	-8.43	103.03	106.40
25	BA	1665	G	O5'-P-OP2	-8.41	98.13	105.70
7	CG	22	LEU	CA-CB-CG	8.39	134.60	115.30
25	DA	1791	A	O5'-P-OP1	-8.39	98.15	105.70
1	CA	998	G	C6-C5-N7	8.37	135.42	130.40
1	CA	1154	G	C2-N3-C4	-8.36	107.72	111.90
25	BA	2630	G	N3-C4-C5	-8.35	124.42	128.60
25	DA	249	C	C6-N1-C2	8.34	123.64	120.30
25	DA	1489	U	N3-C2-O2	-8.34	116.36	122.20
23	AX	46	G	C5-C6-N1	8.31	115.66	111.50
1	CA	999	C	N3-C2-O2	-8.30	116.09	121.90
25	BA	1188	A	O5'-P-OP1	-8.29	98.24	105.70
25	DA	945	A	C2-N3-C4	-8.29	106.46	110.60
25	DA	528	A	N1-C2-N3	8.27	133.44	129.30
25	BA	837	C	O5'-P-OP2	-8.27	98.26	105.70
25	BA	1067	A	C5-C6-N1	-8.27	113.57	117.70
1	CA	1122	U	C2-N1-C1'	8.26	127.61	117.70
25	DA	1937	A	N1-C6-N6	8.26	123.56	118.60
25	DA	1284	A	N1-C6-N6	8.25	123.55	118.60
1	CA	1154	G	N3-C4-C5	-8.24	124.48	128.60
25	BA	2701	U	P-O3'-C3'	8.23	129.58	119.70
25	BA	1072	U	N1-C2-O2	8.23	128.56	122.80
25	BA	2830	A	N1-C6-N6	8.23	123.54	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	945	A	C6-C5-N7	-8.23	126.54	132.30
25	BA	194	G	C8-N9-C4	8.22	109.69	106.40
1	CA	1154	G	C4-C5-N7	-8.21	107.52	110.80
25	DA	37	C	C6-N1-C2	8.19	123.58	120.30
25	DA	1489	U	C2-N1-C1'	8.19	127.53	117.70
1	CA	1311	G	N3-C4-N9	-8.19	121.09	126.00
25	BA	553	A	C2-N3-C4	-8.18	106.51	110.60
1	CA	841	U	C5-C6-N1	8.18	126.79	122.70
25	BA	2298	A	N1-C2-N3	8.18	133.39	129.30
25	BA	1985	U	C2-N1-C1'	8.17	127.50	117.70
1	CA	1012	U	N1-C2-O2	-8.17	117.08	122.80
25	DA	2039	C	C6-N1-C2	-8.16	117.04	120.30
1	AA	1036	G	C8-N9-C1'	-8.15	116.41	127.00
23	AX	8	U	N1-C2-N3	-8.15	110.01	114.90
25	BA	990	A	C4-C5-N7	8.10	114.75	110.70
1	CA	1396	A	O5'-P-OP1	-8.10	98.42	105.70
25	DA	933	A	C5-N7-C8	-8.09	99.86	103.90
25	DA	1380	G	O5'-P-OP2	-8.08	98.43	105.70
25	DA	1786	A	O4'-C1'-N9	8.07	114.66	108.20
25	DA	249	C	O5'-P-OP2	-8.07	98.44	105.70
1	AA	896	C	C6-N1-C2	8.01	123.50	120.30
25	DA	1284	A	O5'-P-OP2	-8.01	98.49	105.70
25	BA	2331	G	N3-C4-C5	8.00	132.60	128.60
25	BA	133	G	N3-C4-C5	8.00	132.60	128.60
25	DA	945	A	C4-C5-N7	8.00	114.70	110.70
25	BA	254	A	N7-C8-N9	7.99	117.80	113.80
25	BA	1700	G	P-O3'-C3'	7.98	129.28	119.70
25	BA	1216	G	N7-C8-N9	7.98	117.09	113.10
25	DA	2503	A	N1-C6-N6	7.97	123.39	118.60
1	CA	1037	C	C6-N1-C2	-7.97	117.11	120.30
25	DA	330	A	C2-N3-C4	-7.96	106.62	110.60
25	BA	552	C	N3-C2-O2	-7.96	116.33	121.90
25	BA	254	A	C8-N9-C4	-7.96	102.62	105.80
1	CA	1141	C	C2-N1-C1'	-7.96	110.05	118.80
25	BA	2331	G	C2-N3-C4	-7.94	107.93	111.90
25	BA	2835	C	N1-C2-O2	-7.88	114.17	118.90
23	CX	39	C	C6-N1-C2	-7.88	117.15	120.30
25	BA	288	U	O4'-C1'-N1	7.87	114.50	108.20
25	BA	12	U	N3-C2-O2	-7.86	116.70	122.20
25	DA	898	C	C5-C6-N1	7.86	124.93	121.00
25	BA	2725	A	O5'-P-OP1	-7.85	98.64	105.70
25	BA	2830	A	C4-C5-N7	7.85	114.62	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1236	G	O5'-P-OP1	-7.85	98.64	105.70
1	CA	1149	C	C6-N1-C2	-7.84	117.16	120.30
25	DA	1934	C	C6-N1-C2	7.84	123.44	120.30
1	AA	193	C	C5-C6-N1	7.84	124.92	121.00
1	AA	1125	U	C2-N3-C4	7.84	131.70	127.00
23	AX	8	U	N1-C2-O2	7.83	128.28	122.80
23	CX	14	A	C5-N7-C8	7.79	107.79	103.90
25	DA	1640	C	N1-C2-O2	7.78	123.56	118.90
25	BA	2734	A	O5'-P-OP1	-7.77	98.71	105.70
25	BA	978	A	C5-N7-C8	-7.77	100.02	103.90
1	AA	1030(B)	C	N1-C2-O2	7.76	123.56	118.90
25	DA	2207	G	N1-C6-O6	7.76	124.56	119.90
25	BA	733	G	C5-C6-O6	-7.76	123.94	128.60
25	BA	2265	G	N1-C6-O6	7.76	124.55	119.90
1	AA	1530	G	N1-C6-O6	7.73	124.54	119.90
1	AA	1158	C	C4-C5-C6	7.71	121.25	117.40
1	CA	1017	G	C6-N1-C2	7.71	129.72	125.10
1	CA	1183	A	P-O3'-C3'	7.71	128.95	119.70
25	BA	2876	U	C5-C6-N1	-7.70	118.85	122.70
34	DO	8	LEU	CA-CB-CG	7.69	132.98	115.30
1	CA	1484	C	C6-N1-C2	7.67	123.37	120.30
25	BA	2830	A	N9-C4-C5	-7.67	102.73	105.80
1	AA	1131	G	C6-C5-N7	-7.65	125.81	130.40
25	DA	1372	U	C5-C4-O4	-7.64	121.32	125.90
25	DA	735	A	C8-N9-C4	7.64	108.85	105.80
25	DA	912	C	C6-N1-C2	-7.63	117.25	120.30
25	BA	961	C	N1-C2-O2	7.63	123.48	118.90
25	BA	484	G	N9-C4-C5	7.62	108.45	105.40
25	BA	1188	A	N3-C4-C5	7.62	132.14	126.80
25	BA	990	A	N7-C8-N9	7.62	117.61	113.80
25	DA	1118	C	C6-N1-C2	-7.62	117.25	120.30
1	CA	1133	G	C5-C6-O6	7.61	133.17	128.60
25	DA	2273	A	C8-N9-C4	7.61	108.84	105.80
25	DA	1703	G	N1-C6-O6	7.61	124.46	119.90
25	BA	2607	G	O5'-P-OP1	-7.61	98.86	105.70
1	CA	1033	G	N9-C4-C5	-7.59	102.36	105.40
25	DA	448	U	O5'-P-OP1	-7.59	98.87	105.70
25	BA	1067	A	N3-C4-N9	-7.58	121.33	127.40
25	DA	948	G	N3-C4-C5	7.58	132.39	128.60
25	BA	2250	G	O5'-P-OP1	-7.57	98.89	105.70
25	BA	139	A	C4-C5-N7	7.56	114.48	110.70
25	BA	990	A	C6-C5-N7	-7.56	127.01	132.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CX	76	A	N9-C4-C5	7.55	108.82	105.80
25	BA	1327	G	N1-C6-O6	7.54	124.42	119.90
25	BA	2092	G	N9-C4-C5	-7.51	102.40	105.40
1	CA	299	G	N1-C6-O6	7.50	124.40	119.90
25	BA	1222	A	C8-N9-C4	-7.49	102.80	105.80
1	CA	998	G	N1-C6-O6	-7.49	115.41	119.90
25	BA	1719	C	N3-C4-C5	-7.48	118.91	121.90
25	BA	2608	U	C5-C6-N1	-7.48	118.96	122.70
25	BA	1067	A	N1-C6-N6	7.48	123.09	118.60
1	AA	1137	C	C6-N1-C2	-7.48	117.31	120.30
25	DA	573	G	N1-C6-O6	-7.48	115.41	119.90
1	AA	188	C	C6-N1-C2	-7.47	117.31	120.30
25	DA	1372	U	N3-C4-O4	7.47	124.63	119.40
1	CA	927	G	N1-C6-O6	-7.47	115.42	119.90
1	CA	1054	C	C2-N1-C1'	7.45	127.00	118.80
25	BA	1093	G	N3-C4-C5	-7.44	124.88	128.60
26	DB	6	C	C6-N1-C2	7.43	123.27	120.30
25	BA	1800	G	N1-C6-O6	7.43	124.36	119.90
25	BA	2015	U	O5'-P-OP1	-7.43	99.01	105.70
1	AA	476	G	O4'-C1'-N9	7.43	114.14	108.20
25	DA	1489	U	N1-C2-O2	7.43	128.00	122.80
23	CX	76	A	C4-C5-N7	-7.42	106.99	110.70
25	BA	1153	G	N3-C4-C5	-7.42	124.89	128.60
25	BA	2262	G	O5'-P-OP2	-7.41	99.03	105.70
25	DA	2253	G	C4-C5-N7	7.40	113.76	110.80
1	AA	1124	G	C8-N9-C4	-7.40	103.44	106.40
25	BA	1093	G	N3-C4-N9	7.40	130.44	126.00
23	AX	22	G	N3-C4-N9	-7.40	121.56	126.00
25	BA	215	G	O4'-C1'-N9	7.39	114.11	108.20
23	AX	76	A	C5-C6-N1	7.39	121.39	117.70
25	BA	2081	A	C8-N9-C4	7.39	108.75	105.80
25	DA	1404	C	O5'-P-OP2	-7.38	99.06	105.70
1	CA	998	G	C4-C5-N7	-7.38	107.85	110.80
25	BA	990	A	N1-C6-N6	7.38	123.03	118.60
25	BA	1766	G	C4-C5-N7	7.36	113.74	110.80
25	DA	2805	G	N1-C6-O6	-7.35	115.49	119.90
25	DA	1022	G	N3-C4-N9	-7.34	121.59	126.00
25	BA	2515	A	N1-C2-N3	-7.33	125.64	129.30
1	AA	1124	G	N3-C4-C5	-7.33	124.94	128.60
1	CA	1154	G	N3-C4-N9	7.31	130.38	126.00
25	BA	2299	A	N3-C4-C5	7.30	131.91	126.80
25	DA	1696	G	O5'-P-OP2	-7.30	99.13	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	827	U	N3-C2-O2	7.29	127.31	122.20
1	CA	1141	C	C6-N1-C1'	7.29	129.55	120.80
25	DA	2805	G	N9-C4-C5	7.28	108.31	105.40
1	AA	738	C	C6-N1-C2	-7.27	117.39	120.30
23	AX	22	G	C4-C5-C6	-7.27	114.44	118.80
25	DA	2805	G	C4-C5-N7	-7.27	107.89	110.80
25	BA	2627	U	O5'-P-OP1	-7.25	99.17	105.70
1	CA	998	G	C5-C6-O6	7.24	132.95	128.60
25	DA	1142(A)	A	C2-N3-C4	-7.24	106.98	110.60
51	D5	58	LEU	CA-CB-CG	7.24	131.95	115.30
1	AA	728	A	O5'-P-OP2	-7.23	99.19	105.70
1	CA	927	G	C4-C5-N7	-7.23	107.91	110.80
25	DA	2261	C	C6-N1-C2	7.23	123.19	120.30
25	BA	201	G	O5'-P-OP1	7.22	119.37	110.70
25	BA	2331	G	C5-N7-C8	-7.22	100.69	104.30
25	DA	687	C	N3-C4-C5	7.21	124.78	121.90
1	AA	1030(B)	C	C6-N1-C2	-7.21	117.42	120.30
25	DA	2207	G	C4-C5-C6	7.21	123.12	118.80
25	DA	476	G	O5'-P-OP2	-7.21	99.22	105.70
25	DA	2374	C	C6-N1-C2	7.21	123.18	120.30
25	BA	2298	A	C4-C5-C6	7.20	120.60	117.00
1	AA	1028	C	C6-N1-C2	-7.19	117.42	120.30
25	DA	205	G	N7-C8-N9	-7.18	109.51	113.10
25	BA	2092	G	C8-N9-C4	7.18	109.27	106.40
25	DA	1204	A	O4'-C1'-N9	7.17	113.94	108.20
25	DA	2574	G	N1-C6-O6	7.17	124.20	119.90
25	DA	2463	C	C6-N1-C2	7.17	123.17	120.30
1	CA	1038	C	C2-N3-C4	7.16	123.48	119.90
1	CA	1492	A	C8-N9-C4	-7.16	102.94	105.80
25	BA	1054	C	N1-C2-O2	7.16	123.20	118.90
25	BA	1745	A	C2-N3-C4	-7.15	107.02	110.60
25	BA	2701	U	N3-C2-O2	-7.15	117.19	122.20
25	BA	2058	C	O5'-P-OP2	7.15	119.28	110.70
1	CA	1113	C	C6-N1-C2	-7.15	117.44	120.30
25	BA	2028	C	O5'-P-OP1	-7.15	99.27	105.70
25	BA	733	G	C4-C5-N7	7.14	113.66	110.80
25	BA	834	U	O5'-P-OP1	-7.14	99.27	105.70
25	BA	553	A	C6-N1-C2	7.14	122.88	118.60
23	AX	4	G	C8-N9-C4	7.14	109.25	106.40
25	BA	1076	G	N1-C2-N2	-7.13	109.78	116.20
25	BA	706	C	C6-N1-C2	7.12	123.15	120.30
23	CX	76	A	C4-C5-C6	7.12	120.56	117.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1605	A	C2-N3-C4	-7.11	107.04	110.60
25	BA	852	G	O5'-P-OP1	-7.11	99.31	105.70
25	BA	1077	G	N1-C6-O6	-7.10	115.64	119.90
25	DA	2588	G	O5'-P-OP1	-7.10	99.31	105.70
25	BA	2229	A	O4'-C1'-N9	7.10	113.88	108.20
25	BA	1249	A	O4'-C1'-N9	7.09	113.88	108.20
25	DA	528	A	N3-C4-C5	7.09	131.77	126.80
25	DA	2805	G	C8-N9-C4	-7.09	103.56	106.40
1	CA	1126	U	C5-C6-N1	7.08	126.24	122.70
1	AA	1026	G	C4-N9-C1'	7.07	135.69	126.50
25	DA	2321	G	N9-C4-C5	-7.07	102.57	105.40
25	BA	2556	G	N1-C6-O6	7.07	124.14	119.90
25	DA	129	C	C6-N1-C2	7.07	123.13	120.30
25	BA	1068	G	N3-C4-N9	-7.07	121.76	126.00
25	DA	1284	A	N9-C4-C5	-7.06	102.98	105.80
25	DA	2253	G	C6-C5-N7	-7.04	126.17	130.40
25	DA	2523	G	O5'-P-OP2	-7.04	99.37	105.70
25	BA	1067	A	N7-C8-N9	7.03	117.32	113.80
25	BA	103	C	O5'-P-OP2	-7.01	99.39	105.70
25	DA	2253	G	C5-C6-O6	-7.01	124.39	128.60
25	BA	473	A	O5'-P-OP1	-7.01	99.39	105.70
1	CA	927	G	N9-C4-C5	7.01	108.20	105.40
25	BA	1098	C	C5-C6-N1	7.01	124.50	121.00
1	CA	1033	G	C4-C5-N7	7.01	113.60	110.80
1	AA	1531	A	O4'-C1'-N9	-7.01	102.59	108.20
25	BA	733	G	N1-C6-O6	7.01	124.10	119.90
1	CA	1157	A	N1-C6-N6	-7.00	114.40	118.60
23	CX	14	A	C4-C5-C6	7.00	120.50	117.00
25	BA	602	G	N1-C6-O6	7.00	124.10	119.90
25	BA	2589	A	C8-N9-C4	-7.00	103.00	105.80
25	BA	122	G	O5'-P-OP2	-6.99	99.41	105.70
25	DA	2298	A	C6-N1-C2	6.99	122.79	118.60
25	DA	214	G	O4'-C1'-N9	6.98	113.78	108.20
25	BA	1871	G	N1-C6-O6	-6.98	115.71	119.90
25	BA	852	G	C5-C6-N1	6.97	114.99	111.50
25	BA	753	A	C2-N3-C4	-6.97	107.11	110.60
23	AX	46	G	C5-C6-O6	-6.97	124.42	128.60
25	BA	1006	C	O5'-P-OP2	-6.97	99.43	105.70
25	BA	2577	A	O5'-P-OP1	-6.97	99.43	105.70
25	BA	1719	C	C6-N1-C2	-6.96	117.52	120.30
25	BA	1844	G	C8-N9-C4	6.96	109.18	106.40
25	BA	819	C	C6-N1-C2	6.94	123.08	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	467	G	C8-N9-C4	6.94	109.17	106.40
1	AA	1131	G	N7-C8-N9	6.93	116.56	113.10
25	DA	2007	C	C6-N1-C2	6.93	123.07	120.30
25	DA	1204	A	N1-C6-N6	6.92	122.75	118.60
25	DA	2427	C	C6-N1-C2	6.92	123.07	120.30
25	BA	1188	A	N3-C4-N9	-6.92	121.86	127.40
25	DA	981	A	C5-C6-N6	6.91	129.23	123.70
25	BA	2081	A	N7-C8-N9	-6.91	110.34	113.80
1	CA	1259	C	C6-N1-C2	-6.91	117.53	120.30
25	BA	2804	C	C6-N1-C2	-6.90	117.54	120.30
25	DA	1339	G	O5'-P-OP1	-6.90	99.49	105.70
25	DA	1783	A	C8-N9-C4	6.90	108.56	105.80
25	DA	2298	A	N1-C2-N3	-6.90	125.85	129.30
25	BA	2331	G	C4-C5-N7	6.89	113.56	110.80
1	AA	199	G	C8-N9-C4	6.89	109.16	106.40
1	AA	383	A	C5-N7-C8	6.89	107.35	103.90
1	CA	1000	U	C5-C6-N1	6.89	126.14	122.70
25	DA	1251	C	N1-C2-O2	-6.89	114.77	118.90
25	BA	555	G	C4-C5-N7	6.88	113.55	110.80
1	CA	79	G	C5-C6-O6	6.88	132.73	128.60
1	AA	476	G	C4-N9-C1'	6.88	135.44	126.50
25	DA	1022	G	N3-C2-N2	-6.88	115.08	119.90
1	AA	1007	C	C5-C6-N1	6.88	124.44	121.00
1	CA	1119	C	N1-C2-N3	-6.88	114.39	119.20
25	DA	933	A	N7-C8-N9	6.88	117.24	113.80
25	DA	1653	G	C4-N9-C1'	6.88	135.44	126.50
1	CA	1017	G	C5-C6-O6	6.87	132.72	128.60
25	BA	2549	U	C5-C4-O4	6.87	130.02	125.90
1	CA	525	C	C5-C6-N1	6.87	124.43	121.00
1	AA	443	C	C2-N1-C1'	6.86	126.35	118.80
25	BA	1462	G	O4'-C1'-N9	6.86	113.69	108.20
1	AA	97	G	O4'-C1'-N9	6.86	113.69	108.20
1	AA	921	U	C2-N3-C4	6.85	131.11	127.00
25	DA	2689	U	P-O3'-C3'	6.85	127.92	119.70
1	AA	1397	C	O4'-C1'-N1	6.84	113.67	108.20
25	BA	1588	G	N3-C4-C5	-6.84	125.18	128.60
25	BA	2551	C	C6-N1-C2	6.84	123.03	120.30
25	DA	2829	C	C6-N1-C2	6.83	123.03	120.30
25	DA	1328	G	C5-C6-O6	-6.83	124.50	128.60
1	AA	720	C	C6-N1-C2	-6.83	117.57	120.30
25	DA	2206	G	C4-N9-C1'	-6.83	117.62	126.50
1	CA	1054	C	C6-N1-C2	-6.83	117.57	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	148	C	C6-N1-C2	6.83	123.03	120.30
1	AA	1396	A	C6-N1-C2	6.82	122.69	118.60
25	DA	2048	G	C5-C6-O6	6.82	132.69	128.60
1	CA	1163	C	C5-C6-N1	6.82	124.41	121.00
25	DA	294	A	N1-C6-N6	-6.82	114.51	118.60
25	BA	2105	G	N1-C6-O6	6.82	123.99	119.90
25	DA	1432	C	C6-N1-C2	6.82	123.03	120.30
25	DA	2345	G	C5-C6-O6	6.81	132.69	128.60
1	CA	117	G	N3-C4-N9	6.81	130.09	126.00
25	BA	555	G	N3-C4-C5	6.80	132.00	128.60
25	BA	2299	A	N3-C4-N9	-6.80	121.96	127.40
1	CA	1054	C	P-O3'-C3'	6.80	127.86	119.70
25	DA	2313	C	N1-C2-O2	6.79	122.97	118.90
1	AA	893	C	N1-C2-O2	6.79	122.97	118.90
25	DA	2751	G	N3-C4-C5	-6.79	125.21	128.60
1	AA	509	A	C8-N9-C4	-6.78	103.09	105.80
1	AA	63	C	N1-C2-O2	6.78	122.97	118.90
25	BA	824	A	N1-C2-N3	6.77	132.68	129.30
1	CA	1042	G	C6-N1-C2	6.76	129.16	125.10
25	BA	841	G	C5-C6-O6	6.76	132.65	128.60
25	BA	1314	A	N7-C8-N9	-6.75	110.42	113.80
25	BA	2444	A	N1-C6-N6	6.75	122.65	118.60
25	BA	553	A	N3-C4-C5	6.75	131.52	126.80
1	AA	1285	A	P-O3'-C3'	6.74	127.79	119.70
25	BA	2014	G	P-O3'-C3'	6.74	127.79	119.70
1	AA	1397	C	C2-N1-C1'	6.74	126.21	118.80
25	DA	524	U	O5'-P-OP2	-6.74	99.64	105.70
1	CA	1502	A	O5'-P-OP2	-6.73	99.64	105.70
25	DA	2010	G	O5'-P-OP2	6.73	118.78	110.70
25	BA	1843	A	O5'-P-OP1	-6.72	99.65	105.70
1	CA	848	C	C5-C6-N1	6.72	124.36	121.00
1	AA	1395	C	C2-N3-C4	6.72	123.26	119.90
25	DA	741	G	O5'-P-OP1	-6.72	99.65	105.70
1	CA	979	C	C6-N1-C2	-6.72	117.61	120.30
25	DA	110	G	C8-N9-C4	6.72	109.09	106.40
25	DA	1721	G	N3-C4-N9	6.71	130.03	126.00
1	CA	1258	G	O4'-C1'-N9	6.71	113.57	108.20
25	DA	2520	C	N3-C4-C5	6.71	124.58	121.90
1	CA	1003	G	N3-C4-N9	6.71	130.03	126.00
1	CA	1033	G	N1-C6-O6	6.71	123.93	119.90
25	DA	219	G	N3-C4-C5	-6.71	125.25	128.60
25	DA	1489	U	C4-C5-C6	6.70	123.72	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	CC	52	LEU	CA-CB-CG	6.70	130.72	115.30
25	DA	784	A	C8-N9-C4	6.70	108.48	105.80
1	CA	1126	U	C2-N1-C1'	6.69	125.73	117.70
1	CA	1135	U	O4'-C1'-N1	6.68	113.54	108.20
25	DA	738	G	N3-C4-C5	-6.67	125.26	128.60
1	AA	1502	A	O5'-P-OP2	-6.67	99.69	105.70
1	CA	1023	G	N3-C4-N9	6.67	130.00	126.00
26	DB	42	C	O5'-P-OP1	-6.67	99.70	105.70
1	CA	1456	G	C8-N9-C4	6.67	109.07	106.40
25	BA	1327	G	C5-C6-O6	-6.67	124.60	128.60
1	CA	1311	G	C6-C5-N7	6.67	134.40	130.40
25	BA	831	A	O4'-C1'-N9	6.66	113.53	108.20
25	DA	2360	A	C8-N9-C4	6.66	108.46	105.80
25	BA	555	G	C2-N3-C4	-6.66	108.57	111.90
25	DA	827	U	N1-C2-O2	-6.65	118.14	122.80
25	BA	1093	G	C4-N9-C1'	6.65	135.14	126.50
25	BA	2448	G	N3-C2-N2	-6.64	115.25	119.90
25	DA	1992	G	C8-N9-C4	-6.64	103.74	106.40
25	BA	43	A	C2-N3-C4	-6.64	107.28	110.60
25	DA	1281	G	O5'-P-OP2	6.64	118.67	110.70
25	DA	2286	A	N1-C6-N6	6.64	122.58	118.60
25	BA	2228	G	OP1-P-O3'	6.64	119.80	105.20
25	BA	2551	C	C5-C6-N1	-6.64	117.68	121.00
25	DA	776	G	C8-N9-C4	-6.64	103.75	106.40
25	DA	945	A	O4'-C1'-N9	6.64	113.51	108.20
25	DA	933	A	C4-C5-N7	6.63	114.02	110.70
25	DA	945	A	C5-N7-C8	-6.63	100.59	103.90
25	DA	2388	A	O4'-C1'-N9	6.63	113.50	108.20
26	DB	104	U	C6-N1-C2	6.63	124.98	121.00
25	BA	2260	C	O5'-P-OP2	-6.62	99.74	105.70
1	CA	726	C	O5'-P-OP1	-6.62	99.74	105.70
25	BA	2550	C	C6-N1-C2	6.62	122.95	120.30
25	DA	1395	A	O4'-C1'-N9	6.62	113.50	108.20
1	AA	1493	A	P-O3'-C3'	6.61	127.64	119.70
1	CA	1180	A	O4'-C1'-N9	6.61	113.48	108.20
25	BA	254	A	C5-N7-C8	-6.60	100.60	103.90
25	DA	63	U	N3-C4-O4	-6.60	114.78	119.40
25	DA	1489	U	C6-N1-C1'	-6.60	111.96	121.20
1	CA	1286	A	C8-N9-C4	-6.60	103.16	105.80
25	BA	805	C	C6-N1-C2	-6.59	117.66	120.30
1	CA	1123	A	O4'-C1'-N9	6.59	113.47	108.20
25	DA	2218	U	N3-C2-O2	-6.59	117.58	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	482	A	O5'-P-OP2	-6.59	99.77	105.70
25	DA	2050	C	C6-N1-C2	6.59	122.94	120.30
25	DA	2388	A	C2-N3-C4	6.59	113.89	110.60
25	DA	451	C	C6-N1-C2	6.59	122.94	120.30
1	AA	193	C	C6-N1-C2	-6.58	117.67	120.30
1	AA	458	C	C2-N1-C1'	6.58	126.04	118.80
25	BA	2298	A	C6-C5-N7	-6.58	127.69	132.30
25	DA	945	A	N9-C4-C5	-6.58	103.17	105.80
25	DA	2805	G	O4'-C1'-N9	6.58	113.46	108.20
25	BA	418	G	C5-C6-O6	-6.57	124.66	128.60
25	BA	148	C	C6-N1-C2	6.57	122.93	120.30
25	DA	826	U	C5-C6-N1	-6.57	119.41	122.70
25	DA	2253	G	N9-C4-C5	-6.57	102.77	105.40
1	CA	1003	G	C4-N9-C1'	6.57	135.04	126.50
1	CA	999	C	C6-N1-C1'	-6.57	112.92	120.80
25	BA	717	A	O4'-C1'-N9	-6.56	102.95	108.20
25	BA	2331	G	O4'-C1'-N9	6.55	113.44	108.20
1	CA	899	C	C6-N1-C2	6.55	122.92	120.30
1	AA	1137	C	C5-C6-N1	6.55	124.28	121.00
25	DA	2287	A	C2-N3-C4	-6.55	107.33	110.60
25	DA	2501	C	N3-C4-C5	6.55	124.52	121.90
25	BA	2054	G	N3-C4-C5	6.54	131.87	128.60
25	DA	2512	C	C6-N1-C2	6.54	122.92	120.30
1	AA	266	G	P-O3'-C3'	6.54	127.55	119.70
25	BA	1483	C	C6-N1-C2	-6.54	117.68	120.30
25	DA	2560	C	C6-N1-C2	6.54	122.92	120.30
25	BA	176	G	N1-C6-O6	6.54	123.82	119.90
25	DA	2061	G	C8-N9-C4	6.53	109.01	106.40
25	BA	666	C	C6-N1-C2	-6.51	117.69	120.30
1	AA	1127	G	C5-N7-C8	6.51	107.56	104.30
1	CA	1023	G	N3-C2-N2	6.51	124.46	119.90
25	BA	660	C	C6-N1-C2	-6.51	117.70	120.30
25	DA	1681	G	N3-C4-C5	6.50	131.85	128.60
25	BA	176	G	C4-C5-N7	6.49	113.40	110.80
1	CA	1502	A	N1-C2-N3	6.49	132.54	129.30
1	CA	1502	A	C5-N7-C8	-6.49	100.66	103.90
25	DA	1257	C	C6-N1-C2	-6.48	117.71	120.30
26	BB	98	G	O5'-P-OP2	-6.48	99.87	105.70
25	BA	781	A	N1-C6-N6	6.47	122.48	118.60
2	CB	154	LEU	CA-CB-CG	6.47	130.19	115.30
25	BA	2544	G	N1-C6-O6	6.47	123.78	119.90
25	DA	1022	G	C8-N9-C1'	6.47	135.41	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	987	G	C5-C6-O6	-6.47	124.72	128.60
23	AX	8	U	N3-C4-C5	-6.46	110.72	114.60
1	AA	382	A	N1-C6-N6	-6.46	114.72	118.60
1	AA	1125	U	C4-C5-C6	-6.46	115.83	119.70
1	CA	65	U	P-O3'-C3'	6.46	127.45	119.70
1	AA	470	C	N1-C2-O2	6.46	122.77	118.90
23	AX	22	G	N3-C4-C5	6.46	131.83	128.60
1	CA	1260	C	C5-C6-N1	6.46	124.23	121.00
25	DA	530	G	N3-C4-N9	-6.45	122.13	126.00
25	BA	1263	C	O5'-P-OP2	-6.45	99.90	105.70
25	BA	271	U	O4'-C1'-N1	6.44	113.35	108.20
25	DA	1635	G	N1-C6-O6	6.44	123.77	119.90
25	BA	2638	C	C6-N1-C2	6.44	122.88	120.30
25	DA	1142	U	N1-C2-O2	6.44	127.31	122.80
25	DA	933	A	N1-C6-N6	6.44	122.46	118.60
25	BA	2253	A	O5'-P-OP1	-6.43	99.91	105.70
1	CA	1163	C	C2-N3-C4	6.43	123.12	119.90
25	BA	139	A	O4'-C1'-N9	6.43	113.35	108.20
25	DA	2805	G	N3-C4-C5	-6.43	125.38	128.60
25	BA	1423	G	N1-C6-O6	-6.42	116.05	119.90
25	BA	1742	G	C6-C5-N7	-6.42	126.55	130.40
1	CA	1036	G	C5-C6-N1	-6.42	108.29	111.50
1	AA	1206	G	C5-C6-O6	-6.42	124.75	128.60
23	CX	46	G	C5-C6-N1	6.41	114.71	111.50
25	DA	216	A	C2-N3-C4	-6.41	107.40	110.60
1	AA	165	C	C6-N1-C2	-6.41	117.74	120.30
25	BA	2673	G	N3-C4-C5	-6.41	125.40	128.60
1	AA	532	A	OP1-P-O3'	6.40	119.29	105.20
25	DA	1021	A	N1-C2-N3	6.40	132.50	129.30
25	BA	2227	G	C4-N9-C1'	-6.40	118.18	126.50
25	BA	2891	C	C6-N1-C2	-6.40	117.74	120.30
25	DA	2544	G	N1-C6-O6	6.40	123.74	119.90
22	AV	17	U	C5-C4-O4	6.40	129.74	125.90
25	DA	2313	C	N3-C2-O2	-6.40	117.42	121.90
25	BA	2630	G	N3-C4-N9	6.40	129.84	126.00
25	BA	352	U	O5'-P-OP2	-6.40	99.94	105.70
1	AA	63	C	N3-C2-O2	-6.39	117.42	121.90
1	CA	1042	G	C8-N9-C4	6.39	108.96	106.40
43	DX	57	LEU	CA-CB-CG	6.39	130.00	115.30
1	CA	1132	C	C6-N1-C2	-6.39	117.74	120.30
25	DA	2512	C	N3-C2-O2	6.39	126.37	121.90
1	AA	458	C	N1-C2-O2	6.39	122.73	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2830	A	C6-C5-N7	-6.39	127.83	132.30
1	AA	841	U	C6-N1-C2	-6.39	117.17	121.00
25	BA	1045	U	O5'-P-OP2	-6.38	99.95	105.70
25	BA	2026	G	C2-N3-C4	-6.38	108.71	111.90
25	DA	1698	A	C4-C5-N7	6.38	113.89	110.70
25	BA	2331	G	N3-C4-N9	-6.38	122.17	126.00
25	BA	1312	G	C8-N9-C4	6.38	108.95	106.40
25	BA	1919	G	N1-C6-O6	6.38	123.73	119.90
1	CA	1033	G	C6-N1-C2	6.38	128.93	125.10
1	CA	1169	A	C4-C5-C6	6.38	120.19	117.00
25	DA	2850	A	OP1-P-OP2	-6.37	110.04	119.60
1	AA	1058	G	C5-C6-O6	-6.37	124.78	128.60
25	BA	2280	A	O5'-P-OP1	-6.36	99.97	105.70
1	AA	1024	G	C4-N9-C1'	6.36	134.76	126.50
25	DA	2574	G	C5-C6-O6	-6.36	124.78	128.60
25	BA	978	A	N7-C8-N9	6.35	116.98	113.80
25	BA	1812	C	C6-N1-C2	6.35	122.84	120.30
25	DA	63	U	C5-C4-O4	6.35	129.71	125.90
25	DA	1022	G	C4-N9-C1'	-6.35	118.24	126.50
1	CA	1511	G	N1-C6-O6	6.35	123.71	119.90
1	AA	496	A	C8-N9-C4	-6.34	103.26	105.80
25	BA	568	C	C6-N1-C2	6.34	122.84	120.30
1	CA	1122	U	C6-N1-C1'	-6.34	112.32	121.20
25	DA	31	C	C6-N1-C2	-6.34	117.76	120.30
1	AA	443	C	C6-N1-C1'	-6.34	113.19	120.80
1	CA	1012	U	N1-C2-N3	6.33	118.70	114.90
26	DB	95	C	C6-N1-C2	6.33	122.83	120.30
25	BA	2442	A	N1-C6-N6	-6.33	114.80	118.60
1	AA	800	G	C8-N9-C4	-6.33	103.87	106.40
25	BA	2701	U	C6-N1-C2	-6.33	117.20	121.00
1	CA	754	C	C2-N1-C1'	6.32	125.75	118.80
23	CX	22	G	C4-C5-C6	-6.32	115.01	118.80
25	BA	342	C	C6-N1-C2	-6.32	117.77	120.30
1	CA	1402	C	C6-N1-C2	-6.32	117.77	120.30
1	CA	1311	G	N3-C4-C5	6.32	131.76	128.60
26	DB	8	U	C5-C6-N1	6.31	125.86	122.70
35	DP	44	GLY	N-CA-C	-6.31	97.31	113.10
25	BA	2094	G	C6-C5-N7	-6.31	126.61	130.40
25	DA	1681	G	C2-N3-C4	-6.31	108.74	111.90
25	DA	2279	G	C8-N9-C4	6.31	108.92	106.40
1	AA	1054	C	P-O3'-C3'	6.31	127.27	119.70
1	CA	1391	U	C5-C4-O4	6.30	129.68	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1029	C	C2-N1-C1'	-6.30	111.87	118.80
25	BA	733	G	C6-C5-N7	-6.30	126.62	130.40
25	BA	781	A	C2-N3-C4	-6.30	107.45	110.60
1	CA	967	C	C6-N1-C2	6.30	122.82	120.30
1	CA	1227	A	N7-C8-N9	6.30	116.95	113.80
25	DA	1284	A	C5-C6-N6	-6.30	118.66	123.70
25	BA	2631	C	C6-N1-C2	6.29	122.82	120.30
1	CA	908	A	O5'-P-OP2	-6.29	100.04	105.70
25	DA	528	A	N1-C6-N6	6.29	122.38	118.60
25	DA	1363	C	C5-C6-N1	-6.29	117.85	121.00
25	BA	484	G	C8-N9-C4	-6.29	103.88	106.40
25	DA	2070	G	N1-C6-O6	-6.28	116.13	119.90
25	BA	849	A	C8-N9-C4	-6.28	103.29	105.80
1	CA	999	C	C2-N1-C1'	6.28	125.70	118.80
25	DA	1600	C	O5'-P-OP2	-6.28	100.05	105.70
1	AA	227	G	C8-N9-C4	6.27	108.91	106.40
25	DA	2617	C	O5'-P-OP1	-6.27	100.05	105.70
25	BA	1779	G	C8-N9-C4	-6.27	103.89	106.40
25	DA	2048	G	N1-C6-O6	-6.27	116.14	119.90
25	DA	271(Y)	U	O4'-C1'-N1	6.26	113.21	108.20
1	AA	383	A	C4-C5-C6	6.26	120.13	117.00
1	CA	528	C	C6-N1-C2	-6.26	117.80	120.30
25	DA	2357	U	O5'-P-OP2	-6.26	100.06	105.70
1	CA	1272	G	C5-C6-O6	6.26	132.35	128.60
25	DA	2554	U	O5'-P-OP2	-6.25	100.07	105.70
25	BA	405	C	C6-N1-C2	6.25	122.80	120.30
25	BA	474	U	N3-C2-O2	-6.25	117.82	122.20
1	CA	117	G	C8-N9-C1'	-6.25	118.87	127.00
1	CA	1500	A	N1-C6-N6	6.25	122.35	118.60
25	BA	2638	C	N3-C4-C5	6.24	124.40	121.90
1	AA	1127	G	N3-C4-C5	-6.24	125.48	128.60
26	DB	115	G	N9-C4-C5	-6.24	102.90	105.40
25	BA	2283	G	N3-C4-N9	6.24	129.74	126.00
25	DA	2406	U	O4'-C1'-N1	-6.24	103.21	108.20
1	AA	167	G	C4-N9-C1'	6.23	134.60	126.50
25	DA	1698	A	N1-C2-N3	6.23	132.41	129.30
1	AA	1127	G	C8-N9-C4	6.22	108.89	106.40
25	BA	1779	G	N7-C8-N9	6.22	116.21	113.10
25	BA	1926	G	N1-C6-O6	-6.22	116.17	119.90
1	CA	509	A	C8-N9-C4	-6.22	103.31	105.80
1	AA	175	C	C6-N1-C2	-6.21	117.81	120.30
1	AA	1067	A	P-O3'-C3'	6.21	127.16	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	5	U	C6-N1-C2	-6.21	117.27	121.00
1	CA	967	C	N3-C2-O2	6.21	126.25	121.90
25	DA	614	U	C5-C4-O4	6.21	129.63	125.90
25	DA	2751	G	C4-N9-C1'	6.21	134.57	126.50
26	BB	93	G	C8-N9-C4	-6.21	103.92	106.40
25	BA	1832	G	N1-C6-O6	6.20	123.62	119.90
1	CA	354	G	C6-C5-N7	-6.20	126.68	130.40
25	BA	1629	C	C5-C6-N1	-6.20	117.90	121.00
1	AA	1515	C	N3-C4-C5	-6.19	119.42	121.90
25	BA	77	A	N1-C6-N6	6.19	122.32	118.60
1	AA	1150	U	C2-N3-C4	6.19	130.71	127.00
25	BA	2298	A	N7-C8-N9	6.19	116.90	113.80
25	DA	566	U	C5-C6-N1	-6.19	119.61	122.70
25	DA	2520	C	C6-N1-C2	6.19	122.78	120.30
25	DA	2053	G	C8-N9-C4	6.18	108.87	106.40
25	DA	1558	A	P-O3'-C3'	6.18	127.12	119.70
1	CA	1064	G	P-O3'-C3'	6.18	127.12	119.70
25	BA	1343	C	OP1-P-O3'	6.18	118.79	105.20
1	AA	1131	G	C4-C5-N7	6.17	113.27	110.80
25	BA	595	A	N1-C6-N6	-6.17	114.90	118.60
25	DA	154(A)	C	N1-C2-O2	6.17	122.60	118.90
25	DA	1363	C	C6-N1-C2	6.17	122.77	120.30
25	DA	2298	A	N9-C4-C5	-6.16	103.33	105.80
25	BA	39	C	O5'-P-OP2	-6.16	100.16	105.70
19	CS	16	LEU	CA-CB-CG	6.16	129.47	115.30
1	AA	488	C	C6-N1-C2	-6.16	117.84	120.30
25	BA	1255	A	C8-N9-C4	-6.15	103.34	105.80
25	BA	2403	G	O4'-C1'-N9	6.15	113.12	108.20
25	DA	2591	C	C6-N1-C2	-6.15	117.84	120.30
25	DA	130	C	N3-C4-C5	6.15	124.36	121.90
1	CA	818	G	C8-N9-C4	6.15	108.86	106.40
25	BA	1067	A	C4-C5-N7	6.14	113.77	110.70
25	DA	1790	C	P-O3'-C3'	6.14	127.07	119.70
25	DA	2042	A	C8-N9-C4	6.14	108.25	105.80
25	BA	859	C	C6-N1-C2	-6.14	117.84	120.30
25	BA	842	C	N1-C2-O2	6.13	122.58	118.90
25	BA	994	C	C6-N1-C2	6.13	122.75	120.30
25	DA	75	G	C8-N9-C4	-6.13	103.95	106.40
1	AA	347	G	C4-N9-C1'	6.13	134.47	126.50
25	BA	1725	G	C8-N9-C4	-6.13	103.95	106.40
25	BA	1067	A	N1-C2-N3	6.13	132.37	129.30
25	DA	414	C	O5'-P-OP2	-6.13	100.18	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1026	G	N3-C4-C5	-6.13	125.54	128.60
1	AA	1531	A	C8-N9-C4	-6.13	103.35	105.80
1	CA	1122	U	C5-C4-O4	-6.13	122.22	125.90
25	BA	2624	C	O5'-P-OP1	-6.12	100.19	105.70
1	AA	226	G	C8-N9-C4	6.12	108.85	106.40
1	AA	536	C	O5'-P-OP2	-6.12	100.19	105.70
25	DA	2207	G	C4-N9-C1'	6.12	134.45	126.50
25	BA	892	G	O4'-C1'-N9	6.11	113.09	108.20
23	CX	46	G	N9-C4-C5	6.11	107.84	105.40
25	DA	2623	G	N1-C6-O6	6.11	123.57	119.90
1	AA	1530	G	C5-C6-O6	-6.11	124.94	128.60
25	BA	840	A	N1-C6-N6	6.11	122.26	118.60
25	BA	2298	A	C8-N9-C4	-6.10	103.36	105.80
25	DA	1239	G	N1-C6-O6	6.10	123.56	119.90
25	BA	139	A	C6-C5-N7	-6.10	128.03	132.30
25	BA	2807	C	C5-C6-N1	6.10	124.05	121.00
1	CA	1002	G	N3-C2-N2	-6.10	115.63	119.90
25	BA	590	A	C2-N3-C4	-6.09	107.55	110.60
25	BA	873	U	OP2-P-O3'	6.09	118.61	105.20
25	DA	133	C	O5'-P-OP2	-6.09	100.22	105.70
25	DA	141	A	N7-C8-N9	6.09	116.85	113.80
1	CA	894	G	N3-C4-C5	6.09	131.65	128.60
25	BA	834	U	N1-C2-N3	6.09	118.55	114.90
1	CA	1149	C	C5-C6-N1	6.08	124.04	121.00
25	DA	2084	C	C5-C6-N1	-6.08	117.96	121.00
1	CA	736	C	C6-N1-C2	-6.08	117.87	120.30
25	DA	2321	G	C8-N9-C1'	-6.08	119.09	127.00
1	AA	1030(A)	G	O4'-C1'-N9	6.08	113.06	108.20
25	DA	2218	U	N1-C2-O2	6.08	127.06	122.80
26	BB	30	C	C6-N1-C2	-6.07	117.87	120.30
1	CA	915	A	C8-N9-C4	6.07	108.23	105.80
25	DA	991	C	O5'-P-OP1	6.07	117.98	110.70
1	CA	1137	C	P-O3'-C3'	6.07	126.98	119.70
1	CA	1484	C	C5-C6-N1	-6.06	117.97	121.00
25	BA	56	C	C2-N3-C4	6.06	122.93	119.90
25	DA	1721	G	N3-C2-N2	6.06	124.14	119.90
1	CA	1154	G	O4'-C1'-N9	6.06	113.05	108.20
25	DA	1531	C	C5-C6-N1	6.06	124.03	121.00
25	BA	332	G	C6-C5-N7	-6.06	126.77	130.40
25	DA	1122	G	O5'-P-OP2	-6.06	100.25	105.70
25	BA	2077	C	C2-N3-C4	6.05	122.93	119.90
1	AA	383	A	C8-N9-C1'	-6.05	116.81	127.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1002	G	C5-C6-O6	6.05	132.23	128.60
25	BA	1298	G	N3-C2-N2	-6.05	115.67	119.90
1	AA	1030(B)	C	N3-C2-O2	-6.05	117.67	121.90
25	BA	12	U	C6-N1-C2	-6.05	117.37	121.00
25	BA	2107	C	O5'-P-OP2	-6.05	100.26	105.70
25	BA	332	G	C4-C5-N7	6.04	113.22	110.80
25	BA	552	C	N3-C4-N4	-6.04	113.77	118.00
25	DA	801	G	O5'-P-OP2	-6.04	100.26	105.70
25	BA	535	C	C6-N1-C2	-6.04	117.88	120.30
1	AA	1127	G	N9-C4-C5	-6.04	102.98	105.40
25	DA	94(A)	G	C8-N9-C4	-6.04	103.98	106.40
25	BA	254	A	C6-C5-N7	-6.03	128.08	132.30
25	DA	1653	G	C8-N9-C1'	-6.03	119.16	127.00
23	CX	8	U	N1-C2-N3	-6.03	111.28	114.90
25	BA	1718	U	N1-C2-O2	-6.03	118.58	122.80
26	BB	91	C	N3-C4-C5	6.03	124.31	121.90
25	DA	2540	C	C6-N1-C2	6.03	122.71	120.30
1	CA	299	G	N9-C4-C5	-6.03	102.99	105.40
25	DA	2335	A	O4'-C1'-N9	6.03	113.02	108.20
25	BA	588	C	N1-C2-O2	6.02	122.51	118.90
25	BA	2830	A	C5-N7-C8	-6.02	100.89	103.90
25	BA	783	C	N1-C2-O2	-6.02	115.29	118.90
1	CA	1044	A	C6-N1-C2	6.02	122.21	118.60
25	DA	461	C	N3-C2-O2	6.02	126.11	121.90
25	BA	978	A	O4'-C1'-N9	6.01	113.01	108.20
25	BA	2236	G	C8-N9-C4	6.01	108.81	106.40
25	DA	1763	G	O5'-P-OP2	-6.01	100.29	105.70
1	CA	992	U	P-O3'-C3'	6.01	126.91	119.70
25	BA	876	A	O5'-P-OP2	-6.00	100.30	105.70
25	BA	1076	G	N3-C2-N2	6.00	124.10	119.90
25	BA	2650	G	C8-N9-C4	-6.00	104.00	106.40
1	CA	1042	G	N1-C2-N3	-6.00	120.30	123.90
25	DA	482	A	C8-N9-C4	6.00	108.20	105.80
25	DA	971	C	N1-C2-O2	-6.00	115.30	118.90
25	BA	2462	A	N1-C6-N6	6.00	122.20	118.60
25	DA	141	A	C5-N7-C8	-6.00	100.90	103.90
1	AA	218	C	C6-N1-C2	-6.00	117.90	120.30
1	AA	1493	A	O5'-P-OP1	6.00	117.89	110.70
25	BA	2228	G	P-O3'-C3'	5.99	126.89	119.70
25	DA	680	G	N1-C6-O6	5.99	123.50	119.90
25	DA	2751	G	N3-C4-N9	5.99	129.59	126.00
23	CX	34	C	C6-N1-C2	-5.98	117.91	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	807	U	O5'-P-OP2	5.98	117.87	110.70
1	CA	841	U	C6-N1-C2	-5.98	117.41	121.00
23	CX	22	G	N7-C8-N9	5.97	116.09	113.10
25	DA	2090	G	N1-C6-O6	-5.97	116.32	119.90
1	AA	890	G	O4'-C1'-N9	5.97	112.97	108.20
25	BA	2110	G	N3-C4-C5	5.97	131.59	128.60
1	AA	1286	A	C8-N9-C4	-5.97	103.41	105.80
25	BA	2515	A	C2-N3-C4	5.97	113.58	110.60
25	DA	627	A	C8-N9-C4	5.96	108.19	105.80
25	BA	348	A	O5'-P-OP1	-5.96	100.33	105.70
1	AA	1131	G	N1-C6-O6	5.96	123.47	119.90
1	AA	1201	A	P-O3'-C3'	5.96	126.85	119.70
25	BA	89	U	N3-C2-O2	-5.96	118.03	122.20
1	CA	1028	C	C5-C6-N1	5.96	123.98	121.00
25	DA	53	A	C8-N9-C4	5.96	108.18	105.80
1	AA	738	C	C5-C6-N1	5.96	123.98	121.00
1	AA	1127	G	N7-C8-N9	-5.96	110.12	113.10
1	AA	1150	U	N3-C4-C5	-5.96	111.03	114.60
26	DB	74	U	C5-C4-O4	5.96	129.47	125.90
25	BA	1800	G	O5'-P-OP2	-5.96	100.34	105.70
1	AA	1007	C	C2-N1-C1'	5.95	125.35	118.80
25	DA	141	A	C2-N3-C4	-5.95	107.62	110.60
1	CA	1169	A	N1-C6-N6	5.95	122.17	118.60
25	BA	1072	U	C2-N1-C1'	5.95	124.84	117.70
25	DA	1573	G	C8-N9-C4	5.95	108.78	106.40
25	DA	2617	C	C6-N1-C2	5.95	122.68	120.30
1	CA	308	C	C6-N1-C2	5.95	122.68	120.30
25	DA	1325	G	C6-C5-N7	-5.95	126.83	130.40
25	BA	70	A	P-O3'-C3'	5.95	126.83	119.70
1	AA	92	C	C5-C6-N1	5.94	123.97	121.00
25	BA	354	A	C5-N7-C8	-5.94	100.93	103.90
26	BB	80	U	C5-C4-O4	5.94	129.47	125.90
25	DA	2351	G	N3-C4-N9	5.94	129.57	126.00
25	DA	901	A	N7-C8-N9	5.94	116.77	113.80
25	BA	1555	C	C6-N1-C2	-5.94	117.92	120.30
25	BA	2080	A	OP2-P-O3'	5.94	118.27	105.20
1	AA	476	G	C8-N9-C1'	-5.94	119.28	127.00
1	AA	1026	G	C8-N9-C1'	-5.94	119.28	127.00
25	BA	2372	A	C2-N3-C4	-5.94	107.63	110.60
1	AA	122	G	C8-N9-C4	5.93	108.77	106.40
25	DA	1129	A	N1-C6-N6	-5.93	115.04	118.60
25	DA	210	C	C2-N1-C1'	-5.93	112.28	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1673	U	C5-C4-O4	-5.93	122.34	125.90
25	BA	1072	U	N3-C2-O2	-5.92	118.05	122.20
1	CA	1312	G	N9-C4-C5	5.92	107.77	105.40
25	DA	1648	C	O5'-P-OP1	5.92	117.81	110.70
25	BA	1240	G	N9-C4-C5	5.92	107.77	105.40
25	BA	2735	G	N3-C4-N9	5.92	129.55	126.00
23	AX	8	U	C5-C6-N1	5.92	125.66	122.70
25	BA	2835	C	N3-C2-O2	5.92	126.04	121.90
25	BA	1423	G	C5-C6-O6	5.91	132.15	128.60
1	CA	916	G	C8-N9-C4	-5.91	104.03	106.40
25	DA	633	A	N1-C6-N6	5.91	122.15	118.60
25	DA	1640	C	C2-N1-C1'	5.91	125.30	118.80
25	BA	1757	C	C6-N1-C2	5.91	122.66	120.30
1	AA	383	A	C4-N9-C1'	5.91	136.93	126.30
25	DA	2351	G	N3-C4-C5	-5.91	125.65	128.60
25	BA	2026	G	OP2-P-O3'	5.90	118.19	105.20
25	DA	2805	G	C5-C6-O6	5.90	132.14	128.60
1	CA	204	U	C2-N1-C1'	5.90	124.78	117.70
7	AG	81	GLY	N-CA-C	5.90	127.85	113.10
25	BA	176	G	C6-C5-N7	-5.90	126.86	130.40
1	CA	337	C	C6-N1-C2	-5.90	117.94	120.30
25	DA	176	G	C8-N9-C4	5.90	108.76	106.40
23	CX	20	U	C2-N1-C1'	5.89	124.77	117.70
25	BA	1249	A	C2-N3-C4	-5.89	107.66	110.60
25	BA	2268	G	C4-C5-N7	5.88	113.15	110.80
1	CA	1125	U	C2-N1-C1'	5.88	124.76	117.70
25	DA	1368	G	O5'-P-OP2	-5.88	100.41	105.70
1	AA	1502	A	N7-C8-N9	5.88	116.74	113.80
25	BA	2354	C	C6-N1-C2	-5.88	117.95	120.30
25	BA	119	G	C5-C6-O6	-5.88	125.07	128.60
25	BA	670	C	C5-C6-N1	5.88	123.94	121.00
25	DA	1257	C	N3-C4-C5	-5.88	119.55	121.90
1	AA	1171	G	N3-C4-C5	-5.88	125.66	128.60
1	CA	998	G	N3-C4-N9	-5.88	122.47	126.00
25	DA	454	A	C8-N9-C4	5.88	108.15	105.80
25	BA	2601	A	C8-N9-C4	5.88	108.15	105.80
9	CI	105	ASP	CB-CG-OD1	5.88	123.59	118.30
1	AA	1181	G	C6-N1-C2	5.87	128.62	125.10
25	BA	2258	G	N9-C4-C5	-5.87	103.05	105.40
25	DA	2033	A	C2-N3-C4	5.87	113.53	110.60
25	BA	2506	G	C8-N9-C4	5.87	108.75	106.40
25	DA	2273	A	N7-C8-N9	-5.87	110.87	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1959	A	C8-N9-C4	5.87	108.15	105.80
23	AX	76	A	C5-C6-N6	-5.86	119.01	123.70
1	CA	917	G	C8-N9-C4	-5.86	104.06	106.40
25	BA	1377	A	C2-N3-C4	-5.86	107.67	110.60
25	DA	945	A	C5-C6-N6	-5.86	119.02	123.70
25	DA	1698	A	C4-C5-C6	5.85	119.93	117.00
1	AA	97	G	N3-C4-C5	-5.85	125.67	128.60
1	CA	901	A	N1-C6-N6	-5.85	115.09	118.60
1	CA	1169	A	C6-C5-N7	-5.85	128.21	132.30
25	DA	735	A	N7-C8-N9	-5.85	110.88	113.80
1	AA	1127	G	C4-C5-C6	5.84	122.31	118.80
25	DA	459	U	N3-C2-O2	-5.84	118.11	122.20
1	AA	990	C	C6-N1-C2	-5.84	117.96	120.30
25	DA	2032	G	N1-C6-O6	-5.84	116.40	119.90
25	BA	621	G	O5'-P-OP2	-5.84	100.44	105.70
25	DA	2324	C	N3-C4-C5	5.84	124.24	121.90
25	BA	279	G	N7-C8-N9	5.84	116.02	113.10
1	AA	841	U	C5-C6-N1	5.83	125.62	122.70
25	DA	948	G	C8-N9-C4	5.83	108.73	106.40
47	D1	85	LEU	CA-CB-CG	5.83	128.72	115.30
25	BA	1093	G	C8-N9-C1'	-5.83	119.42	127.00
1	AA	1054	C	N3-C2-O2	-5.83	117.82	121.90
25	BA	2105	G	N9-C4-C5	-5.83	103.07	105.40
1	CA	1311	G	C4-N9-C1'	-5.83	118.92	126.50
25	DA	2330	G	N1-C6-O6	5.83	123.40	119.90
25	BA	903	C	C6-N1-C2	-5.83	117.97	120.30
1	CA	1271	G	C5-C6-O6	-5.83	125.11	128.60
25	BA	1461	U	C5-C4-O4	5.82	129.39	125.90
1	CA	117	G	C6-C5-N7	-5.82	126.91	130.40
1	AA	1125	U	P-O3'-C3'	5.82	126.69	119.70
25	BA	2876	U	C4-C5-C6	5.82	123.19	119.70
1	CA	1286	A	N7-C8-N9	5.82	116.71	113.80
25	DA	2024	G	C8-N9-C4	5.82	108.73	106.40
25	BA	1719	C	N3-C4-N4	5.82	122.07	118.00
23	CX	18	G	N3-C4-C5	5.82	131.51	128.60
25	DA	2679	A	O5'-P-OP2	-5.82	100.47	105.70
25	DA	2287	A	N3-C4-C5	5.82	130.87	126.80
1	CA	1000	U	C2-N3-C4	5.81	130.49	127.00
1	CA	1157	A	C6-C5-N7	5.81	136.37	132.30
1	AA	884	U	O5'-P-OP2	-5.81	100.47	105.70
1	AA	1131	G	C4-N9-C1'	5.81	134.06	126.50
25	BA	1154	U	N1-C2-O2	5.81	126.87	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1663	C	C2-N3-C4	-5.81	116.99	119.90
25	BA	2729	U	N3-C2-O2	-5.81	118.13	122.20
25	DA	792	G	C5-C6-N1	5.81	114.41	111.50
1	AA	261	U	N1-C2-O2	-5.81	118.73	122.80
1	AA	1024	G	N3-C4-C5	-5.81	125.70	128.60
25	BA	555	G	C5-N7-C8	-5.81	101.40	104.30
1	CA	353	A	OP2-P-O3'	5.81	117.98	105.20
1	CA	1125	U	C5-C6-N1	5.81	125.60	122.70
25	DA	1192	G	C8-N9-C4	5.81	108.72	106.40
1	AA	904	C	C6-N1-C2	5.80	122.62	120.30
1	CA	117	G	C4-N9-C1'	5.80	134.05	126.50
1	AA	1269	A	N1-C6-N6	-5.80	115.12	118.60
25	BA	2026	G	N3-C4-C5	5.80	131.50	128.60
25	DA	901	A	C8-N9-C4	-5.80	103.48	105.80
25	BA	990	A	C5-C6-N1	-5.80	114.80	117.70
1	AA	336	C	N3-C2-O2	5.80	125.96	121.90
1	AA	421	U	N1-C2-O2	5.80	126.86	122.80
1	AA	1396	A	C5-C6-N6	5.80	128.34	123.70
25	BA	125	A	N1-C6-N6	5.80	122.08	118.60
1	CA	691	G	C8-N9-C4	5.79	108.72	106.40
23	AX	22	G	N7-C8-N9	5.79	116.00	113.10
25	DA	1682	G	C8-N9-C4	5.79	108.72	106.40
1	CA	1206	G	C5-C6-O6	-5.79	125.13	128.60
25	DA	1899	G	N9-C4-C5	-5.79	103.08	105.40
1	CA	79	G	C6-N1-C2	5.79	128.57	125.10
25	DA	205	G	N9-C4-C5	-5.79	103.09	105.40
25	BA	553	A	C4-C5-N7	5.78	113.59	110.70
25	BA	1255	A	P-O3'-C3'	5.78	126.64	119.70
25	DA	1405	U	O5'-P-OP2	-5.78	100.50	105.70
1	AA	991	U	P-O3'-C3'	5.78	126.63	119.70
1	CA	1149	C	N1-C2-O2	5.78	122.37	118.90
25	DA	1413	G	N1-C6-O6	5.78	123.37	119.90
1	AA	167	G	N7-C8-N9	5.78	115.99	113.10
25	BA	176	G	C5-N7-C8	-5.78	101.41	104.30
1	CA	1216	G	N3-C4-C5	5.78	131.49	128.60
25	DA	1325	G	N3-C4-N9	5.77	129.46	126.00
1	CA	1499	A	C8-N9-C4	5.77	108.11	105.80
25	DA	1239	G	C5-C6-O6	-5.77	125.14	128.60
25	BA	2320	G	N3-C4-C5	5.77	131.49	128.60
1	CA	1044	A	C5-C6-N6	5.77	128.32	123.70
1	AA	483	C	C6-N1-C2	5.77	122.61	120.30
25	DA	2010	G	C8-N9-C4	-5.77	104.09	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1578	C	C5-C6-N1	5.77	123.88	121.00
25	BA	1153	G	N3-C4-N9	5.76	129.46	126.00
25	BA	2065	C	N1-C2-O2	-5.76	115.44	118.90
1	CA	794	A	C8-N9-C4	-5.76	103.49	105.80
1	CA	398	C	N3-C4-N4	-5.76	113.97	118.00
25	DA	1284	A	C4-C5-N7	5.76	113.58	110.70
1	AA	1026	G	N3-C4-N9	5.76	129.46	126.00
25	BA	553	A	C5-N7-C8	-5.76	101.02	103.90
23	AX	14	A	C5-C6-N1	-5.76	114.82	117.70
25	BA	2044	U	O5'-P-OP1	-5.76	100.52	105.70
26	BB	41	U	C5-C6-N1	-5.76	119.82	122.70
25	DA	962	G	C8-N9-C4	-5.76	104.10	106.40
1	AA	1181	G	N3-C4-C5	5.76	131.48	128.60
25	BA	841	G	C4-C5-N7	-5.75	108.50	110.80
25	DA	467	G	N7-C8-N9	-5.75	110.22	113.10
25	DA	2347	C	N1-C2-O2	5.75	122.35	118.90
25	BA	2014	G	C2'-C3'-O3'	5.75	122.90	113.70
1	CA	890	G	O4'-C1'-N9	5.75	112.80	108.20
25	BA	2245	U	C5-C6-N1	-5.75	119.83	122.70
1	AA	1036	G	N3-C4-N9	5.74	129.45	126.00
1	CA	377	G	N3-C4-N9	5.74	129.45	126.00
46	B0	77	ARG	NE-CZ-NH1	-5.74	117.43	120.30
25	BA	1605	A	N1-C6-N6	5.74	122.04	118.60
23	CX	76	A	N3-C4-N9	5.74	131.99	127.40
25	DA	2281	C	O5'-P-OP1	-5.74	100.54	105.70
25	BA	1252	C	O5'-P-OP1	-5.74	100.54	105.70
25	DA	2744	G	C5-C6-O6	-5.74	125.16	128.60
1	CA	915	A	N7-C8-N9	-5.73	110.93	113.80
1	CA	721	G	N1-C6-O6	5.73	123.34	119.90
25	DA	727	A	C8-N9-C4	-5.73	103.51	105.80
25	DA	1027	A	N9-C4-C5	-5.73	103.51	105.80
1	CA	1002	G	N3-C4-N9	-5.73	122.56	126.00
25	DA	557	U	C5-C6-N1	-5.73	119.84	122.70
25	DA	308	G	O5'-P-OP2	-5.72	100.55	105.70
25	DA	981	A	N1-C6-N6	-5.72	115.17	118.60
23	AX	6	G	N1-C6-O6	5.72	123.33	119.90
25	BA	989	G	C4-N9-C1'	5.72	133.94	126.50
43	BX	57	LEU	CA-CB-CG	5.72	128.46	115.30
1	CA	1028	C	N3-C2-O2	5.72	125.90	121.90
25	DA	119	A	N1-C6-N6	5.72	122.03	118.60
25	DA	912	C	N1-C2-O2	5.72	122.33	118.90
1	AA	166	G	N7-C8-N9	5.71	115.96	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2509	G	C5-C6-N1	-5.71	108.64	111.50
1	CA	1157	A	C4-C5-N7	-5.71	107.84	110.70
25	DA	738	G	O5'-P-OP1	5.71	117.55	110.70
1	CA	997	U	C2-N3-C4	5.71	130.43	127.00
25	BA	2271	G	C8-N9-C4	-5.71	104.12	106.40
1	CA	1149	C	C2-N1-C1'	5.71	125.08	118.80
25	DA	242	G	N7-C8-N9	-5.71	110.25	113.10
25	DA	1647	G	O4'-C1'-N9	-5.71	103.63	108.20
1	AA	1531	A	N7-C8-N9	5.71	116.65	113.80
25	BA	2836	A	C8-N9-C4	5.71	108.08	105.80
19	CS	71	LEU	CA-CB-CG	5.71	128.42	115.30
25	DA	504	U	N1-C2-O2	5.71	126.79	122.80
25	BA	1694	G	O5'-P-OP1	-5.70	100.57	105.70
25	BA	1742	G	N3-C4-N9	5.70	129.42	126.00
25	DA	2271	G	N3-C4-N9	5.70	129.42	126.00
25	BA	990	A	O4'-C1'-N9	5.70	112.76	108.20
1	CA	1134	G	C8-N9-C4	-5.70	104.12	106.40
25	DA	1698	A	C5-N7-C8	-5.70	101.05	103.90
25	DA	560	C	C6-N1-C2	5.70	122.58	120.30
25	DA	991	C	O5'-P-OP2	-5.69	100.58	105.70
25	BA	295	C	O5'-P-OP2	-5.69	100.58	105.70
25	BA	1222	A	N7-C8-N9	5.69	116.65	113.80
46	B0	12	ASN	N-CA-C	5.69	126.37	111.00
1	CA	5	U	N3-C2-O2	-5.69	118.22	122.20
25	BA	2054	G	N3-C4-N9	-5.69	122.59	126.00
1	CA	754	C	N1-C2-O2	5.69	122.31	118.90
1	CA	1492	A	C2-N3-C4	5.69	113.44	110.60
25	DA	2057	A	C8-N9-C4	5.69	108.07	105.80
25	DA	2725	A	C2-N3-C4	-5.69	107.76	110.60
25	DA	1142(A)	A	N1-C2-N3	5.68	132.14	129.30
1	AA	162	A	C8-N9-C4	-5.68	103.53	105.80
1	AA	1124	G	C2-N3-C4	5.68	114.74	111.90
25	BA	2608	U	N1-C2-O2	-5.68	118.82	122.80
25	DA	193	U	N3-C4-O4	5.68	123.38	119.40
25	DA	885	C	C5-C6-N1	5.68	123.84	121.00
25	DA	2345	G	C8-N9-C4	-5.68	104.13	106.40
25	BA	1343	C	OP2-P-O3'	-5.68	92.71	105.20
25	DA	2794	C	C5-C6-N1	5.68	123.84	121.00
25	BA	2902	G	P-O3'-C3'	5.68	126.51	119.70
1	CA	266	G	N1-C6-O6	5.68	123.31	119.90
25	DA	795	C	O5'-P-OP2	-5.68	100.59	105.70
25	DA	1926	U	N3-C2-O2	-5.68	118.23	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1328	G	C4-C5-N7	5.67	113.07	110.80
1	AA	1054	C	N1-C2-O2	5.67	122.30	118.90
25	BA	2495	C	N1-C2-O2	5.67	122.30	118.90
25	BA	716	G	C8-N9-C4	5.67	108.67	106.40
25	BA	1766	G	C5-C6-O6	-5.67	125.20	128.60
25	DA	2590	A	O5'-P-OP2	5.67	117.50	110.70
25	BA	357	G	C4-N9-C1'	5.67	133.87	126.50
1	CA	1277	C	N1-C2-O2	5.67	122.30	118.90
26	DB	52	A	C8-N9-C4	-5.67	103.53	105.80
25	BA	2861	A	OP2-P-O3'	5.67	117.66	105.20
1	CA	142	G	N3-C4-C5	-5.67	125.77	128.60
25	BA	36	G	O5'-P-OP2	-5.66	100.61	105.70
25	DA	1377	G	N3-C4-C5	-5.66	125.77	128.60
25	BA	553	A	C5-C6-N1	-5.66	114.87	117.70
25	DA	1363	C	O5'-P-OP2	-5.66	100.61	105.70
25	BA	1850	A	C8-N9-C4	5.66	108.06	105.80
25	DA	2043	C	C2-N1-C1'	5.65	125.02	118.80
25	DA	2053	G	N9-C4-C5	-5.65	103.14	105.40
1	AA	71	C	N1-C2-O2	5.65	122.29	118.90
25	BA	2804	C	C5-C6-N1	5.65	123.83	121.00
25	BA	185	A	N1-C6-N6	5.65	121.99	118.60
25	BA	2056	U	N3-C4-O4	5.65	123.35	119.40
25	BA	737	G	N1-C6-O6	5.65	123.29	119.90
25	BA	1700	G	N3-C4-C5	-5.64	125.78	128.60
1	CA	557	G	N9-C4-C5	-5.64	103.14	105.40
25	DA	532	A	O4'-C1'-N9	5.64	112.72	108.20
25	DA	783	A	O5'-P-OP2	-5.64	100.62	105.70
25	DA	1997	G	N3-C4-C5	-5.64	125.78	128.60
26	DB	45	A	P-O3'-C3'	5.64	126.47	119.70
25	DA	1115	G	N3-C4-C5	5.64	131.42	128.60
25	BA	615	G	N1-C6-O6	-5.64	116.52	119.90
25	BA	1807	G	N1-C6-O6	5.64	123.28	119.90
25	DA	2061	G	N9-C4-C5	-5.64	103.14	105.40
25	BA	2522	C	C6-N1-C2	5.64	122.55	120.30
1	CA	1484	C	C2-N1-C1'	-5.64	112.60	118.80
1	CA	1272	G	N1-C6-O6	-5.63	116.52	119.90
25	DA	1455	G	N1-C6-O6	5.63	123.28	119.90
25	DA	2440	C	C5-C4-N4	5.63	124.14	120.20
25	DA	956	G	C4-N9-C1'	5.63	133.82	126.50
25	DA	781	A	N1-C6-N6	-5.63	115.22	118.60
25	BA	103	C	N1-C2-O2	5.63	122.28	118.90
25	BA	1667	U	N3-C4-C5	-5.62	111.22	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CX	8	U	N3-C4-C5	-5.62	111.23	114.60
1	AA	526	C	C6-N1-C2	5.62	122.55	120.30
25	DA	915	C	N3-C2-O2	-5.62	117.97	121.90
25	BA	1153	G	C8-N9-C4	-5.62	104.15	106.40
25	BA	2272	C	C5-C6-N1	-5.62	118.19	121.00
1	CA	1227	A	C8-N9-C4	-5.62	103.55	105.80
25	DA	768	G	N1-C6-O6	5.62	123.27	119.90
25	DA	1021	A	C5-C6-N1	-5.62	114.89	117.70
25	BA	1378	G	C4-C5-N7	5.62	113.05	110.80
1	CA	1189	C	C6-N1-C2	5.62	122.55	120.30
25	BA	2096	U	O5'-P-OP1	-5.62	100.65	105.70
25	DA	2206	G	C8-N9-C1'	5.61	134.30	127.00
25	BA	120	G	C5-C6-O6	-5.61	125.23	128.60
25	DA	971	C	N3-C4-N4	5.61	121.93	118.00
25	DA	1269	A	C5-C6-N1	-5.61	114.90	117.70
25	DA	2081	C	C6-N1-C2	5.61	122.54	120.30
29	DF	12	LEU	CA-CB-CG	5.61	128.20	115.30
1	AA	652	U	O5'-P-OP1	-5.61	100.66	105.70
25	BA	1378	G	C5-C6-O6	-5.60	125.24	128.60
25	BA	1681	A	C8-N9-C4	-5.60	103.56	105.80
25	DA	110	G	N7-C8-N9	-5.60	110.30	113.10
1	CA	399	G	C8-N9-C4	5.60	108.64	106.40
25	BA	1426	G	O5'-P-OP2	-5.60	100.66	105.70
1	CA	557	G	N3-C2-N2	5.60	123.82	119.90
25	BA	179	A	C5-N7-C8	-5.60	101.10	103.90
1	AA	340	U	C6-N1-C2	5.60	124.36	121.00
25	BA	1663	C	N3-C4-C5	5.60	124.14	121.90
40	DU	74	LEU	CA-CB-CG	5.59	128.17	115.30
25	BA	1188	A	C5-N7-C8	-5.59	101.10	103.90
1	CA	544	G	N1-C6-O6	-5.59	116.55	119.90
25	DA	956	G	N3-C4-C5	-5.59	125.80	128.60
25	BA	1068	G	N3-C2-N2	-5.59	115.99	119.90
25	BA	1390	G	N1-C6-O6	5.59	123.25	119.90
25	DA	806	C	N3-C4-C5	-5.59	119.66	121.90
25	DA	733	G	N9-C4-C5	-5.59	103.17	105.40
25	DA	912	C	C5-C6-N1	5.59	123.79	121.00
25	BA	2630	G	C6-N1-C2	-5.59	121.75	125.10
25	BA	2495	C	C5-C6-N1	5.58	123.79	121.00
25	BA	2239	A	N9-C4-C5	5.58	108.03	105.80
25	DA	2476	A	C8-N9-C4	-5.58	103.57	105.80
25	BA	1158	G	C8-N9-C4	-5.58	104.17	106.40
25	DA	242	G	C4-N9-C1'	-5.58	119.24	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2333	A	C8-N9-C4	5.58	108.03	105.80
1	CA	1042	G	N3-C4-C5	5.58	131.39	128.60
25	DA	2804	C	N3-C2-O2	-5.58	117.99	121.90
1	CA	1279	A	C5-N7-C8	-5.58	101.11	103.90
1	CA	687	A	P-O3'-C3'	5.58	126.39	119.70
25	DA	376	C	C6-N1-C2	5.58	122.53	120.30
25	BA	113	C	O5'-P-OP1	-5.57	100.68	105.70
25	BA	403	C	N3-C4-N4	-5.57	114.10	118.00
25	BA	1221	G	OP1-P-O3'	5.57	117.46	105.20
25	BA	2513	C	O4'-C1'-N1	5.57	112.66	108.20
25	BA	1152	G	O4'-C1'-N9	-5.57	103.74	108.20
25	DA	981	A	C6-N1-C2	5.57	121.94	118.60
25	DA	1328	G	N9-C4-C5	-5.57	103.17	105.40
1	CA	1051	C	N1-C2-O2	-5.57	115.56	118.90
25	BA	94	G	O5'-P-OP2	-5.57	100.69	105.70
25	DA	210	C	C6-N1-C2	5.57	122.53	120.30
1	AA	1030(B)	C	C5-C6-N1	5.57	123.78	121.00
25	BA	2641	A	O4'-C1'-N9	5.56	112.65	108.20
1	CA	1067	A	P-O3'-C3'	5.56	126.38	119.70
25	BA	514	G	C4-C5-N7	-5.56	108.58	110.80
3	CC	91	LEU	CA-CB-CG	5.56	128.09	115.30
25	DA	2771	C	O5'-P-OP1	-5.56	100.69	105.70
25	DA	2896	C	C6-N1-C2	-5.56	118.08	120.30
25	BA	2419	G	C8-N9-C1'	-5.56	119.77	127.00
25	BA	1659	G	C5-C6-O6	5.56	131.94	128.60
25	BA	2740	G	O5'-P-OP2	-5.56	100.70	105.70
25	DA	552	G	N3-C4-C5	5.56	131.38	128.60
25	DA	2464	C	C5-C6-N1	-5.56	118.22	121.00
25	BA	873	U	OP1-P-O3'	-5.55	92.99	105.20
1	AA	383	A	O4'-C1'-N9	5.55	112.64	108.20
1	CA	299	G	C6-C5-N7	-5.55	127.07	130.40
1	CA	1124	G	N3-C4-C5	-5.55	125.83	128.60
25	BA	472	G	N1-C6-O6	5.55	123.23	119.90
25	BA	105	C	C6-N1-C2	5.55	122.52	120.30
25	BA	2666	A	N1-C6-N6	5.55	121.93	118.60
25	DA	1348	G	C5-C6-O6	-5.55	125.27	128.60
1	CA	117	G	N9-C4-C5	-5.54	103.18	105.40
1	CA	1017	G	C5-C6-N1	-5.54	108.73	111.50
1	AA	1127	G	C8-N9-C1'	-5.54	119.80	127.00
1	AA	1192	C	C6-N1-C2	-5.54	118.08	120.30
25	BA	553	A	O4'-C1'-N9	-5.54	103.77	108.20
25	BA	1991	A	O5'-P-OP2	5.54	117.35	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2103	C	O5'-P-OP2	-5.54	100.71	105.70
25	DA	106	C	N1-C2-O2	5.54	122.22	118.90
1	CA	1492	A	N3-C4-C5	-5.54	122.92	126.80
25	DA	2416	C	N1-C2-O2	-5.54	115.58	118.90
25	BA	498	A	O5'-P-OP1	5.54	117.34	110.70
25	BA	1431	G	O4'-C1'-N9	5.54	112.63	108.20
25	BA	1832	G	C4-C5-N7	5.54	113.01	110.80
1	CA	365	U	C5-C6-N1	-5.54	119.93	122.70
25	DA	1213	A	C8-N9-C4	5.54	108.01	105.80
25	DA	2321	G	C6-N1-C2	5.54	128.42	125.10
1	AA	1298	C	N1-C2-O2	5.53	122.22	118.90
25	BA	1075	A	N1-C6-N6	5.53	121.92	118.60
25	BA	2061	C	C5-C6-N1	5.53	123.77	121.00
1	AA	1030(B)	C	C6-N1-C1'	-5.53	114.16	120.80
1	CA	1003	G	C8-N9-C1'	-5.53	119.81	127.00
25	BA	1746	G	C8-N9-C4	-5.53	104.19	106.40
25	DA	1769	G	C8-N9-C4	-5.53	104.19	106.40
25	DA	465	G	C5-C6-O6	-5.53	125.28	128.60
25	DA	1926	U	C5-C4-O4	5.53	129.22	125.90
25	BA	1929	G	N1-C6-O6	5.53	123.22	119.90
41	BV	82	ARG	NE-CZ-NH1	-5.53	117.54	120.30
1	CA	1279	A	N7-C8-N9	5.53	116.56	113.80
1	CA	1502	A	C4-C5-N7	5.53	113.46	110.70
25	BA	1325	G	O5'-P-OP2	-5.53	100.73	105.70
25	BA	1629	C	C6-N1-C2	5.53	122.51	120.30
1	CA	1011	G	C4-C5-N7	-5.53	108.59	110.80
1	AA	381	C	N1-C2-O2	5.52	122.21	118.90
23	CX	9	G	C4-N9-C1'	-5.52	119.32	126.50
1	AA	687	A	P-O3'-C3'	5.52	126.33	119.70
25	DA	2595	G	C8-N9-C4	5.52	108.61	106.40
1	AA	1154	G	N9-C4-C5	-5.52	103.19	105.40
25	BA	271	U	C2-N1-C1'	-5.52	111.08	117.70
25	BA	1284	G	N1-C6-O6	5.52	123.21	119.90
25	DA	277	C	C2-N1-C1'	5.52	124.87	118.80
23	AX	14	A	C4-C5-N7	-5.52	107.94	110.70
25	BA	1343	C	C6-N1-C2	5.52	122.51	120.30
25	DA	786	C	C6-N1-C2	5.52	122.51	120.30
26	DB	102	A	C8-N9-C4	5.52	108.01	105.80
25	BA	2094	G	C4-C5-N7	5.52	113.01	110.80
25	BA	990	A	C8-N9-C4	-5.51	103.59	105.80
26	BB	93	G	C6-C5-N7	-5.51	127.09	130.40
25	DA	1830	C	C6-N1-C2	5.51	122.50	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1007	C	N1-C2-O2	5.51	122.21	118.90
1	CA	1273	G	N3-C4-N9	5.51	129.31	126.00
25	BA	179	A	C5-C6-N6	-5.51	119.29	123.70
4	CD	188	LEU	CA-CB-CG	5.51	127.97	115.30
1	CA	265	G	O4'-C1'-N9	-5.50	103.80	108.20
25	DA	508	G	O5'-P-OP1	-5.50	100.75	105.70
26	DB	79	C	N3-C4-C5	-5.50	119.70	121.90
25	DA	389	G	C5-C6-O6	-5.50	125.30	128.60
25	DA	2744	G	N1-C6-O6	5.50	123.20	119.90
25	BA	179	A	C4-C5-N7	5.50	113.45	110.70
1	AA	913	A	P-O3'-C3'	5.49	126.29	119.70
23	AX	69	C	C2-N1-C1'	5.49	124.84	118.80
25	BA	68	C	OP2-P-O3'	5.49	117.29	105.20
25	DA	1665	A	C8-N9-C4	-5.49	103.60	105.80
25	BA	1078	A	C8-N9-C4	5.49	108.00	105.80
25	BA	1429	C	C5-C6-N1	5.49	123.75	121.00
1	CA	1183	A	OP1-P-O3'	5.49	117.28	105.20
1	CA	1271	G	N9-C4-C5	-5.49	103.20	105.40
25	BA	592	U	N1-C2-O2	-5.49	118.96	122.80
25	BA	2105	G	C4-C5-N7	5.49	113.00	110.80
25	BA	2622	C	O5'-P-OP1	-5.49	100.76	105.70
25	DA	1672	C	C5-C4-N4	-5.49	116.36	120.20
25	BA	902	G	N3-C4-N9	5.49	129.29	126.00
25	DA	1261	C	O5'-P-OP1	-5.49	100.76	105.70
25	BA	827	G	N3-C4-C5	-5.48	125.86	128.60
25	BA	1051	C	OP1-P-OP2	5.48	127.82	119.60
25	BA	2059	G	N3-C2-N2	5.48	123.74	119.90
28	DE	72	VAL	C-N-CA	5.48	135.41	121.70
1	CA	300	A	N1-C6-N6	-5.48	115.31	118.60
25	DA	250	G	C8-N9-C4	-5.48	104.21	106.40
1	AA	1058	G	N9-C4-C5	-5.48	103.21	105.40
25	BA	12	U	N1-C2-O2	5.48	126.64	122.80
1	CA	5	U	C2-N1-C1'	5.48	124.27	117.70
23	CX	18	G	C8-N9-C4	5.48	108.59	106.40
25	DA	917	A	OP1-P-O3'	5.48	117.25	105.20
25	BA	193	A	C8-N9-C4	5.48	107.99	105.80
1	AA	267	C	O5'-P-OP1	-5.47	100.77	105.70
25	DA	1531	C	C2-N1-C1'	5.47	124.82	118.80
25	DA	1982	C	N3-C4-C5	-5.47	119.71	121.90
1	AA	1145	C	N1-C2-O2	5.47	122.18	118.90
25	BA	2380	C	C6-N1-C2	5.47	122.49	120.30
1	CA	1022	G	N3-C4-N9	-5.47	122.72	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2054	G	C8-N9-C1'	5.47	134.11	127.00
25	BA	2601	A	N3-C4-C5	5.47	130.63	126.80
25	BA	2460	A	N1-C6-N6	5.46	121.88	118.60
1	CA	1420	C	C6-N1-C2	-5.46	118.11	120.30
25	BA	978	A	C4-C5-N7	5.46	113.43	110.70
1	CA	354	G	C4-N9-C1'	5.46	133.60	126.50
25	DA	2351	G	C4-N9-C1'	5.46	133.60	126.50
25	BA	235	C	O5'-P-OP1	-5.46	100.79	105.70
25	DA	1336	A	N1-C6-N6	-5.46	115.32	118.60
25	DA	2230	G	O5'-P-OP1	-5.46	100.79	105.70
25	DA	2252	G	N3-C4-N9	-5.46	122.72	126.00
1	AA	922	G	C6-N1-C2	5.46	128.38	125.10
25	BA	1055	A	C8-N9-C4	-5.46	103.62	105.80
25	DA	1672	C	C6-N1-C1'	-5.46	114.25	120.80
25	DA	2532	G	C5-C6-O6	-5.46	125.32	128.60
25	BA	2298	A	C4-N9-C1'	5.46	136.12	126.30
25	BA	2601	A	C4-C5-C6	-5.46	114.27	117.00
1	CA	1420	C	C5-C6-N1	5.46	123.73	121.00
1	CA	1502	A	C6-C5-N7	-5.46	128.48	132.30
25	BA	1402	G	C5-C6-O6	-5.45	125.33	128.60
25	DA	1004	C	N1-C2-O2	-5.45	115.63	118.90
25	DA	1688	U	O5'-P-OP2	-5.45	100.79	105.70
25	BA	2495	C	C2-N1-C1'	5.45	124.80	118.80
26	DB	104	U	C5-C6-N1	-5.45	119.97	122.70
25	BA	2498	G	N1-C6-O6	-5.45	116.63	119.90
25	DA	1123	C	C6-N1-C2	5.45	122.48	120.30
25	DA	1348	G	N1-C6-O6	5.45	123.17	119.90
1	CA	998	G	C4-N9-C1'	-5.45	119.42	126.50
25	DA	193	U	C5-C4-O4	-5.45	122.63	125.90
25	DA	1256	G	C4-N9-C1'	5.45	133.58	126.50
26	DB	56	G	N3-C4-C5	-5.45	125.88	128.60
25	DA	1236	G	O5'-P-OP2	5.45	117.24	110.70
1	CA	1034	G	N3-C4-N9	-5.45	122.73	126.00
1	CA	1122	U	C5-C6-N1	5.44	125.42	122.70
23	CX	76	A	C5-C6-N1	5.44	120.42	117.70
1	CA	1124	G	O4'-C1'-N9	5.44	112.56	108.20
25	BA	397	G	N9-C4-C5	-5.44	103.22	105.40
25	BA	552	C	C5-C4-N4	5.44	124.01	120.20
26	BB	79	C	C6-N1-C2	-5.44	118.12	120.30
25	DA	2623	G	C5-C6-O6	-5.44	125.33	128.60
1	AA	1058	G	N1-C6-O6	5.44	123.16	119.90
25	BA	828	A	C2-N3-C4	5.44	113.32	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1858	C	N3-C2-O2	-5.44	118.09	121.90
25	BA	1605	A	N3-C4-C5	5.44	130.61	126.80
25	BA	2830	A	C5-C6-N6	-5.44	119.35	123.70
1	CA	1290	G	C8-N9-C4	-5.44	104.22	106.40
25	BA	186	A	C5-N7-C8	-5.44	101.18	103.90
25	DA	668	G	C2-N3-C4	-5.44	109.18	111.90
1	AA	1007	C	C2-N3-C4	5.43	122.62	119.90
25	BA	1207	C	C6-N1-C2	-5.43	118.13	120.30
25	BA	1538	G	C8-N9-C4	5.43	108.57	106.40
25	DA	738	G	C4-N9-C1'	5.43	133.56	126.50
25	DA	2207	G	N3-C4-N9	5.43	129.26	126.00
25	BA	2248	C	C5-C4-N4	-5.43	116.40	120.20
25	DA	2458	G	N3-C4-N9	5.43	129.26	126.00
1	CA	1126	U	C6-N1-C2	-5.43	117.74	121.00
25	BA	993	G	N9-C4-C5	-5.43	103.23	105.40
1	AA	348	G	C5-C6-O6	-5.43	125.34	128.60
25	BA	839	G	N3-C2-N2	5.43	123.70	119.90
1	CA	525	C	N3-C4-N4	5.43	121.80	118.00
1	AA	458	C	C5-C6-N1	5.42	123.71	121.00
1	CA	1003	G	C4-C5-C6	5.42	122.06	118.80
1	CA	1227	A	C5-N7-C8	-5.42	101.19	103.90
1	CA	115	G	P-O3'-C3'	5.42	126.21	119.70
25	DA	242	G	C6-C5-N7	5.42	133.65	130.40
25	DA	1432	C	C5-C4-N4	-5.42	116.41	120.20
25	BA	125	A	C5-C6-N6	-5.42	119.36	123.70
25	DA	1769	G	N3-C4-C5	-5.42	125.89	128.60
1	AA	1530	G	C4-C5-N7	5.42	112.97	110.80
23	AX	76	A	N3-C4-N9	5.42	131.73	127.40
25	BA	1188	A	C5-C6-N1	-5.42	114.99	117.70
25	BA	2331	G	N1-C6-O6	5.42	123.15	119.90
1	CA	1028	C	N1-C2-O2	-5.42	115.65	118.90
25	DA	133	C	C6-N1-C2	5.42	122.47	120.30
25	DA	906	G	N9-C4-C5	5.42	107.57	105.40
1	AA	98	G	N7-C8-N9	5.42	115.81	113.10
25	BA	1608	G	C8-N9-C4	-5.42	104.23	106.40
26	BB	85	G	C6-C5-N7	-5.42	127.15	130.40
1	CA	794	A	N7-C8-N9	5.41	116.51	113.80
25	BA	279	G	C8-N9-C4	-5.41	104.24	106.40
25	BA	2460	A	C5-C6-N6	-5.41	119.37	123.70
1	AA	749	C	C5-C6-N1	5.41	123.70	121.00
25	BA	254	A	O4'-C1'-N9	5.41	112.53	108.20
25	BA	1985	U	C6-N1-C1'	-5.41	113.63	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	149	A	C8-N9-C4	-5.40	103.64	105.80
25	DA	242	G	C8-N9-C4	5.40	108.56	106.40
25	BA	2567	U	O5'-P-OP1	-5.40	100.84	105.70
25	BA	2896	G	C8-N9-C4	-5.40	104.24	106.40
1	CA	499	A	C8-N9-C4	5.40	107.96	105.80
1	CA	1199	U	C5-C4-O4	5.40	129.14	125.90
23	CX	22	G	N3-C4-N9	-5.40	122.76	126.00
25	BA	311	C	C6-N1-C2	5.40	122.46	120.30
25	BA	1577	C	P-O3'-C3'	5.40	126.18	119.70
25	DA	1937	A	C6-C5-N7	-5.40	128.52	132.30
25	BA	2094	G	N1-C6-O6	5.40	123.14	119.90
1	CA	993	G	N3-C4-N9	5.40	129.24	126.00
1	AA	1123	A	C6-N1-C2	5.40	121.84	118.60
1	AA	1149	C	C6-N1-C2	-5.39	118.14	120.30
25	DA	956	G	C4-C5-C6	5.39	122.04	118.80
25	DA	970	C	N3-C2-O2	5.39	125.68	121.90
25	BA	1177	G	O4'-C1'-N9	5.39	112.51	108.20
25	DA	2373	G	N1-C6-O6	5.39	123.14	119.90
34	BO	8	LEU	CA-CB-CG	5.39	127.70	115.30
25	DA	188	G	C4-C5-N7	5.39	112.96	110.80
25	DA	793	A	O5'-P-OP2	-5.39	100.85	105.70
1	CA	246	A	C8-N9-C4	5.39	107.95	105.80
1	CA	1125	U	C6-N1-C2	-5.39	117.77	121.00
1	CA	1311	G	C8-N9-C1'	5.39	134.00	127.00
23	CX	45	G	N3-C4-C5	5.39	131.29	128.60
25	DA	512	G	O4'-C1'-N9	5.39	112.51	108.20
50	D4	68	ARG	NE-CZ-NH2	5.39	122.99	120.30
1	CA	1415	G	O5'-P-OP2	-5.38	100.86	105.70
25	DA	2689	U	N3-C2-O2	-5.38	118.43	122.20
1	AA	1502	A	C6-C5-N7	-5.38	128.53	132.30
25	BA	2703	C	O5'-P-OP1	-5.38	100.86	105.70
1	CA	28	G	C8-N9-C4	-5.38	104.25	106.40
25	BA	187	C	OP2-P-O3'	5.38	117.03	105.20
25	BA	1302	G	C8-N9-C1'	-5.38	120.01	127.00
25	BA	2036	A	N1-C6-N6	5.38	121.83	118.60
25	DA	1430	C	N1-C2-O2	5.38	122.13	118.90
1	AA	115	G	P-O3'-C3'	5.38	126.15	119.70
25	BA	181	C	N3-C4-C5	5.38	124.05	121.90
1	CA	525	C	C5-C4-N4	-5.38	116.44	120.20
1	CA	913	A	P-O3'-C3'	5.37	126.15	119.70
25	BA	1304	C	C6-N1-C2	5.37	122.45	120.30
25	DA	1021	A	N1-C6-N6	5.37	121.82	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	166	G	N3-C4-C5	-5.37	125.92	128.60
1	AA	1139	G	C6-C5-N7	5.37	133.62	130.40
1	CA	502	G	OP1-P-O3'	5.37	117.01	105.20
1	CA	1366	C	C2-N3-C4	5.37	122.58	119.90
1	CA	1398	A	C8-N9-C4	5.37	107.95	105.80
25	DA	1365	A	C6-N1-C2	-5.37	115.38	118.60
25	DA	2616	C	N3-C2-O2	-5.37	118.14	121.90
25	BA	116	A	N1-C6-N6	-5.37	115.38	118.60
25	DA	530	G	N7-C8-N9	5.37	115.78	113.10
1	AA	63	C	C6-N1-C2	-5.37	118.15	120.30
25	BA	1412	A	N1-C6-N6	-5.37	115.38	118.60
25	BA	2059	G	N3-C4-N9	5.37	129.22	126.00
1	CA	354	G	N3-C4-N9	5.37	129.22	126.00
1	CA	397	A	OP2-P-O3'	5.37	117.00	105.20
25	DA	2332	U	C5-C6-N1	-5.37	120.02	122.70
25	BA	2476	C	C6-N1-C2	5.36	122.44	120.30
25	DA	179	G	C5-C6-O6	-5.36	125.38	128.60
25	DA	1607	C	N1-C2-O2	5.36	122.12	118.90
1	AA	1007	C	O4'-C1'-N1	-5.36	103.91	108.20
25	BA	716	G	N1-C6-O6	-5.36	116.68	119.90
1	CA	1312	G	N3-C4-N9	-5.36	122.78	126.00
1	AA	71	C	C5-C6-N1	5.36	123.68	121.00
1	CA	1325	C	C5-C4-N4	5.36	123.95	120.20
25	BA	2462	A	N1-C2-N3	-5.36	126.62	129.30
25	DA	2325	G	C8-N9-C4	-5.36	104.26	106.40
25	BA	1246	C	C6-N1-C2	5.36	122.44	120.30
25	BA	1543	U	N3-C4-O4	-5.36	115.65	119.40
25	BA	1298	G	C4-C5-N7	-5.35	108.66	110.80
25	BA	1919	G	C5-C6-O6	-5.35	125.39	128.60
32	BI	30	LEU	CA-CB-CG	-5.35	102.99	115.30
25	DA	907	U	C5-C6-N1	5.35	125.38	122.70
25	BA	678	A	C8-N9-C4	-5.35	103.66	105.80
25	DA	2275	C	O4'-C1'-N1	-5.35	103.92	108.20
1	AA	561	U	C6-N1-C2	5.35	124.21	121.00
25	BA	140	A	N1-C6-N6	-5.35	115.39	118.60
25	BA	1370	G	C8-N9-C4	5.35	108.54	106.40
25	BA	2265	G	C8-N9-C4	5.35	108.54	106.40
25	BA	2735	G	N3-C4-C5	-5.35	125.93	128.60
25	DA	179	G	N1-C6-O6	5.35	123.11	119.90
25	DA	1365	A	N1-C2-N3	5.35	131.97	129.30
25	DA	2503	A	N3-C4-N9	5.35	131.68	127.40
25	DA	530	G	N9-C4-C5	5.34	107.54	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1029	C	C6-N1-C1'	5.34	127.21	120.80
25	BA	145	G	O5'-P-OP2	-5.34	100.89	105.70
1	CA	1099	G	C4-C5-N7	-5.34	108.66	110.80
25	DA	116	C	C6-N1-C2	-5.34	118.16	120.30
1	AA	576	G	N1-C6-O6	5.34	123.10	119.90
25	BA	1783	C	C6-N1-C2	5.34	122.44	120.30
25	BA	1977	U	N1-C2-O2	-5.34	119.06	122.80
1	CA	1030(B)	C	C6-N1-C2	-5.34	118.16	120.30
25	DA	2540	C	C2-N1-C1'	-5.34	112.93	118.80
1	AA	561	U	N1-C2-N3	-5.34	111.70	114.90
25	DA	204	A	OP1-P-O3'	5.34	116.94	105.20
25	DA	1210	A	P-O3'-C3'	5.34	126.11	119.70
25	DA	2586	C	C5-C6-N1	5.34	123.67	121.00
26	DB	30	C	C6-N1-C2	-5.34	118.17	120.30
25	BA	2513	C	C2-N1-C1'	-5.33	112.93	118.80
25	DA	1781	C	N1-C2-O2	-5.33	115.70	118.90
1	CA	266	G	C5-N7-C8	-5.33	101.63	104.30
25	DA	1471	A	C8-N9-C4	-5.33	103.67	105.80
25	BA	1302	G	N9-C4-C5	-5.33	103.27	105.40
25	BA	2634	C	N3-C2-O2	5.33	125.63	121.90
25	BA	2734	A	C8-N9-C4	5.33	107.93	105.80
1	CA	1043	C	N3-C4-C5	-5.33	119.77	121.90
1	CA	1119	C	C4-C5-C6	-5.33	114.73	117.40
25	DA	1897	G	N1-C6-O6	5.33	123.10	119.90
25	DA	2488	A	C8-N9-C4	5.33	107.93	105.80
25	DA	2532	G	N1-C6-O6	5.33	123.10	119.90
25	BA	405	C	C5-C4-N4	-5.33	116.47	120.20
1	CA	572	A	C8-N9-C4	5.33	107.93	105.80
25	DA	811	U	C5-C6-N1	-5.33	120.04	122.70
25	BA	397	G	N3-C4-N9	5.32	129.19	126.00
25	BA	1723	A	N1-C6-N6	-5.32	115.41	118.60
25	BA	1389	G	C4-N9-C1'	5.32	133.42	126.50
1	CA	1005	A	OP1-P-O3'	5.32	116.91	105.20
1	CA	1063	C	C6-N1-C2	-5.32	118.17	120.30
1	AA	1388	C	N1-C2-O2	-5.32	115.71	118.90
25	BA	354	A	N3-C4-C5	5.32	130.52	126.80
25	BA	1298	G	N3-C4-N9	-5.32	122.81	126.00
1	CA	615	C	C6-N1-C2	-5.32	118.17	120.30
25	DA	1703	G	C6-C5-N7	-5.32	127.21	130.40
1	CA	1065	U	P-O3'-C3'	5.32	126.08	119.70
25	BA	2239	A	C8-N9-C4	-5.32	103.67	105.80
25	DA	1181	C	N1-C2-O2	5.32	122.09	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1930	G	C4-N9-C1'	-5.32	119.59	126.50
1	AA	1122	U	N3-C2-O2	-5.32	118.48	122.20
1	CA	701	C	N3-C2-O2	-5.32	118.18	121.90
25	BA	1746	G	N9-C4-C5	5.31	107.53	105.40
25	DA	1313	U	C2-N1-C1'	5.31	124.08	117.70
25	BA	2011	G	C8-N9-C4	5.31	108.52	106.40
25	DA	1204	A	C4-C5-N7	5.31	113.36	110.70
25	DA	2772	C	C6-N1-C2	5.31	122.42	120.30
1	AA	1067	A	O4'-C1'-N9	-5.31	103.95	108.20
25	BA	139	A	N1-C6-N6	5.31	121.79	118.60
25	BA	1154	U	N3-C2-O2	-5.31	118.48	122.20
1	CA	984	C	C2-N3-C4	5.31	122.55	119.90
25	DA	729	G	N1-C6-O6	5.31	123.09	119.90
25	DA	2755	C	C5-C6-N1	5.31	123.66	121.00
1	AA	1396	A	C5-C6-N1	-5.31	115.05	117.70
25	BA	2054	G	C5-N7-C8	-5.31	101.65	104.30
25	DA	1254	A	C8-N9-C4	-5.31	103.68	105.80
1	CA	1180	A	N7-C8-N9	5.31	116.45	113.80
25	BA	2036	A	N9-C4-C5	-5.30	103.68	105.80
25	BA	2370	G	N1-C6-O6	-5.30	116.72	119.90
25	BA	2518	U	O4'-C1'-N1	5.30	112.44	108.20
1	CA	783	C	N3-C4-C5	5.30	124.02	121.90
25	BA	478	G	N3-C4-C5	-5.30	125.95	128.60
25	DA	2207	G	C8-N9-C1'	-5.30	120.11	127.00
25	BA	410	U	C2-N1-C1'	-5.30	111.34	117.70
25	BA	839	G	O4'-C1'-N9	-5.30	103.96	108.20
25	DA	1142	U	N3-C2-O2	-5.30	118.49	122.20
25	BA	670	C	C2-N1-C1'	5.29	124.62	118.80
1	CA	1205	U	C6-N1-C2	-5.29	117.82	121.00
1	AA	97	G	N3-C4-N9	5.29	129.18	126.00
1	CA	400	C	C6-N1-C2	5.29	122.42	120.30
25	DA	1698	A	N9-C4-C5	-5.29	103.68	105.80
25	BA	139	A	C2-N3-C4	-5.29	107.96	110.60
25	DA	2338	G	C4-N9-C1'	-5.29	119.62	126.50
25	BA	342	C	N3-C4-C5	-5.29	119.78	121.90
25	BA	1425	A	OP2-P-O3'	5.29	116.83	105.20
1	AA	1131	G	C5-N7-C8	-5.29	101.66	104.30
25	BA	1068	G	N9-C4-C5	5.29	107.51	105.40
25	BA	1298	G	N9-C4-C5	5.29	107.51	105.40
25	BA	2495	C	C6-N1-C2	-5.29	118.19	120.30
1	CA	733	A	O5'-P-OP2	-5.29	100.94	105.70
25	DA	1831	G	C8-N9-C4	-5.29	104.29	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	557	G	C8-N9-C4	5.28	108.51	106.40
1	CA	1502	A	N7-C8-N9	5.28	116.44	113.80
1	AA	944	G	C4-N9-C1'	5.28	133.37	126.50
25	DA	1684	C	N3-C4-C5	-5.28	119.79	121.90
23	AX	46	G	N3-C2-N2	-5.28	116.20	119.90
25	DA	2479	G	N1-C6-O6	-5.28	116.73	119.90
25	BA	2262	G	C8-N9-C4	-5.28	104.29	106.40
1	CA	1163	C	N1-C2-O2	5.28	122.07	118.90
25	DA	2252	G	N3-C2-N2	-5.28	116.20	119.90
1	AA	1235	U	C6-N1-C2	-5.28	117.83	121.00
1	CA	660	G	C8-N9-C4	5.28	108.51	106.40
23	CX	24	U	C6-N1-C2	-5.28	117.83	121.00
25	DA	1653	G	C6-C5-N7	-5.28	127.23	130.40
25	BA	1954	A	O5'-P-OP1	-5.28	100.95	105.70
25	DA	1021	A	C5-N7-C8	-5.28	101.26	103.90
25	DA	1281	G	N3-C4-C5	5.27	131.24	128.60
25	BA	496	A	OP1-P-O3'	5.27	116.80	105.20
25	BA	1066	A	C8-N9-C4	-5.27	103.69	105.80
25	DA	2612	C	C6-N1-C2	5.27	122.41	120.30
1	AA	998	G	N3-C4-N9	-5.27	122.84	126.00
1	AA	1278	U	C5-C6-N1	5.27	125.33	122.70
25	BA	2858	G	O4'-C1'-N9	5.27	112.42	108.20
1	AA	422	C	O4'-C1'-N1	5.27	112.42	108.20
25	BA	1009	C	N3-C4-N4	5.27	121.69	118.00
25	DA	1212	G	C8-N9-C4	5.27	108.51	106.40
1	AA	159	G	C4-N9-C1'	-5.27	119.65	126.50
25	DA	669	G	OP1-P-OP2	-5.27	111.70	119.60
25	DA	2645	G	N3-C2-N2	5.27	123.59	119.90
25	DA	1880	C	C6-N1-C2	5.26	122.41	120.30
27	DD	275	LYS	N-CA-C	-5.26	96.79	111.00
25	BA	1421	C	OP1-P-O3'	5.26	116.78	105.20
1	CA	667	G	N3-C4-C5	5.26	131.23	128.60
1	CA	1004	A	N1-C6-N6	-5.26	115.44	118.60
25	DA	511	U	N3-C2-O2	-5.26	118.52	122.20
25	BA	2291	G	C8-N9-C4	5.26	108.50	106.40
25	BA	498	A	O5'-P-OP2	-5.26	100.97	105.70
25	BA	1444	C	OP2-P-O3'	5.26	116.77	105.20
25	DA	729	G	C4-N9-C1'	5.26	133.34	126.50
25	BA	1718	U	N3-C2-O2	5.25	125.88	122.20
1	CA	65	U	OP2-P-O3'	5.25	116.76	105.20
25	DA	1963	U	C2-N1-C1'	5.25	124.00	117.70
25	BA	1314	A	C2-N3-C4	-5.25	107.97	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1270	C	OP2-P-O3'	5.25	116.75	105.20
25	BA	2042	A	O5'-P-OP1	-5.25	100.97	105.70
1	CA	1026	G	N7-C8-N9	5.25	115.72	113.10
1	CA	1149	C	N3-C2-O2	-5.25	118.23	121.90
25	DA	2491	U	N1-C2-O2	5.25	126.47	122.80
1	CA	1312	G	C8-N9-C4	-5.25	104.30	106.40
25	DA	2057	A	N7-C8-N9	-5.25	111.18	113.80
25	DA	1899	G	OP1-P-O3'	5.24	116.73	105.20
25	BA	1308	A	N1-C6-N6	5.24	121.74	118.60
25	DA	740	U	O5'-P-OP1	5.24	116.99	110.70
1	AA	1113	C	C6-N1-C2	-5.24	118.20	120.30
25	BA	88	G	C8-N9-C4	-5.24	104.31	106.40
25	BA	193	A	N7-C8-N9	-5.24	111.18	113.80
25	BA	702	A	C8-N9-C4	-5.24	103.70	105.80
25	BA	912	C	C6-N1-C2	5.24	122.39	120.30
25	BA	12	U	C2-N1-C1'	5.24	123.98	117.70
25	DA	1997	G	N3-C4-N9	5.24	129.14	126.00
22	AV	17	U	C2-N3-C4	5.24	130.14	127.00
25	DA	71	A	N1-C6-N6	5.24	121.74	118.60
25	DA	2531	A	C8-N9-C4	5.24	107.89	105.80
25	BA	600	G	C8-N9-C4	5.23	108.49	106.40
25	DA	21	A	C8-N9-C4	5.23	107.89	105.80
1	AA	934	C	O5'-P-OP1	-5.23	100.99	105.70
1	AA	1150	U	C6-N1-C2	-5.23	117.86	121.00
25	BA	180	A	OP2-P-O3'	5.23	116.70	105.20
1	CA	354	G	C4-C5-N7	5.23	112.89	110.80
25	BA	719	C	OP2-P-O3'	5.23	116.70	105.20
25	DA	1571	A	N1-C6-N6	-5.23	115.46	118.60
25	BA	2684	G	C8-N9-C4	5.23	108.49	106.40
25	DA	116	C	C4-C5-C6	5.23	120.01	117.40
1	AA	98	G	N3-C4-N9	5.22	129.13	126.00
25	BA	827	G	C4-C5-C6	5.22	121.94	118.80
25	BA	2062	C	C6-N1-C2	5.22	122.39	120.30
25	BA	2283	G	C8-N9-C1'	-5.22	120.21	127.00
1	CA	44	G	C4-N9-C1'	5.22	133.29	126.50
25	DA	154(A)	C	C2-N1-C1'	5.22	124.55	118.80
1	AA	1531	A	C4-N9-C1'	5.22	135.70	126.30
25	DA	1372	U	C2-N1-C1'	5.22	123.97	117.70
1	CA	1080	A	N1-C6-N6	-5.22	115.47	118.60
25	DA	1880	C	C5-C6-N1	-5.22	118.39	121.00
25	DA	1992	G	C2-N3-C4	5.22	114.51	111.90
25	DA	2374	C	C5-C6-N1	-5.22	118.39	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	175	C	C5-C6-N1	5.22	123.61	121.00
1	AA	340	U	C5-C6-N1	-5.22	120.09	122.70
25	BA	194	G	O5'-P-OP2	-5.22	101.00	105.70
25	DA	2601	C	N3-C4-C5	5.22	123.99	121.90
25	BA	331	G	O5'-P-OP1	-5.21	101.01	105.70
23	CX	35	A	C5-C6-N6	5.21	127.87	123.70
1	AA	6	G	N3-C4-N9	5.21	129.13	126.00
25	DA	933	A	C6-C5-N7	-5.21	128.65	132.30
25	DA	1555	G	N1-C6-O6	5.21	123.03	119.90
25	DA	1970	A	O4'-C1'-N9	-5.21	104.03	108.20
25	BA	733	G	C5-N7-C8	-5.21	101.69	104.30
1	AA	167	G	C8-N9-C1'	-5.21	120.23	127.00
25	DA	1797	C	C5-C6-N1	-5.21	118.40	121.00
1	AA	354	G	O5'-P-OP2	-5.21	101.02	105.70
25	BA	231	G	N3-C4-C5	5.21	131.20	128.60
25	BA	2011	G	N7-C8-N9	-5.21	110.50	113.10
25	BA	2421	G	N1-C2-N2	-5.21	111.51	116.20
25	BA	989	G	C8-N9-C4	-5.20	104.32	106.40
25	BA	1725	G	N9-C4-C5	5.20	107.48	105.40
25	BA	2285	A	C8-N9-C4	-5.20	103.72	105.80
25	DA	1897	G	O5'-P-OP1	-5.20	101.02	105.70
25	BA	1187	U	C5-C6-N1	5.20	125.30	122.70
25	DA	885	C	C6-N1-C2	-5.20	118.22	120.30
25	DA	1475	G	N1-C6-O6	5.20	123.02	119.90
25	DA	2519	U	C6-N1-C2	5.20	124.12	121.00
1	AA	645	C	N1-C2-O2	5.20	122.02	118.90
25	DA	807	U	C6-N1-C2	-5.20	117.88	121.00
1	AA	1276	G	N3-C4-C5	-5.20	126.00	128.60
25	BA	1454	C	C6-N1-C2	-5.20	118.22	120.30
25	BA	1367	A	O5'-P-OP1	-5.19	101.03	105.70
25	DA	2249	U	C5-C4-O4	5.19	129.02	125.90
25	BA	665	C	N1-C2-O2	-5.19	115.79	118.90
25	BA	2227	G	C8-N9-C1'	5.19	133.75	127.00
1	CA	1141	C	C5-C4-N4	5.19	123.83	120.20
25	DA	2877	G	N3-C4-C5	5.19	131.19	128.60
53	D7	35	ARG	NE-CZ-NH1	-5.19	117.70	120.30
1	AA	339	C	C5-C6-N1	-5.19	118.41	121.00
1	CA	1226	C	C6-N1-C2	-5.19	118.22	120.30
23	CX	46	G	C8-N9-C1'	5.19	133.74	127.00
25	DA	1961	C	C2-N1-C1'	-5.19	113.09	118.80
25	DA	2010	G	O5'-P-OP1	-5.19	101.03	105.70
25	DA	2878	U	C6-N1-C2	-5.19	117.89	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	1220	U	P-O3'-C3'	5.19	125.92	119.70
23	CX	23	C	O5'-P-OP1	-5.19	101.03	105.70
25	DA	1602	U	O5'-P-OP2	5.19	116.92	110.70
1	AA	496	A	N9-C4-C5	5.18	107.87	105.80
1	AA	1127	G	C6-C5-N7	-5.18	127.29	130.40
1	CA	1397	C	C2-N1-C1'	5.18	124.50	118.80
25	DA	1679	U	C5-C4-O4	5.18	129.01	125.90
1	AA	348	G	O5'-P-OP1	5.18	116.92	110.70
25	BA	2077	C	N3-C4-C5	-5.18	119.83	121.90
25	DA	792	G	N3-C4-C5	-5.18	126.01	128.60
25	BA	1386	U	N1-C2-O2	-5.18	119.17	122.80
25	BA	2389	A	C2-N3-C4	-5.18	108.01	110.60
25	DA	188	G	C5-N7-C8	-5.18	101.71	104.30
27	BD	111	LEU	CA-CB-CG	5.18	127.21	115.30
25	DA	2227	A	N1-C6-N6	-5.18	115.49	118.60
25	DA	2540	C	O5'-P-OP2	-5.18	101.04	105.70
25	BA	1382	A	O5'-P-OP2	-5.17	101.04	105.70
25	BA	2059	G	N1-C2-N2	-5.17	111.54	116.20
1	CA	1240	U	O4'-C1'-N1	5.17	112.34	108.20
25	DA	13	A	N1-C6-N6	-5.17	115.50	118.60
25	DA	1432	C	N3-C4-N4	5.17	121.62	118.00
25	BA	242	C	C6-N1-C2	5.17	122.37	120.30
1	CA	46	G	C5-C6-O6	-5.17	125.50	128.60
1	CA	64	G	C5-C6-N1	-5.17	108.91	111.50
25	BA	1035	G	N3-C4-N9	5.17	129.10	126.00
25	DA	954	G	N1-C6-O6	-5.17	116.80	119.90
25	DA	2804	C	N1-C2-O2	5.17	122.00	118.90
23	CX	9	G	N3-C4-C5	5.17	131.19	128.60
25	DA	1215	G	OP1-P-O3'	5.17	116.57	105.20
25	BA	1154	U	C2-N1-C1'	5.17	123.90	117.70
25	BA	1852	A	C8-N9-C4	-5.17	103.73	105.80
1	CA	254	G	OP2-P-O3'	5.17	116.57	105.20
1	CA	380	G	N3-C4-N9	-5.17	122.90	126.00
1	CA	1171	G	N7-C8-N9	5.17	115.68	113.10
25	DA	34	C	C6-N1-C2	-5.17	118.23	120.30
25	BA	2594	G	C8-N9-C4	-5.17	104.33	106.40
25	BA	962	G	N3-C4-C5	-5.16	126.02	128.60
25	BA	1175	A	N1-C6-N6	-5.16	115.50	118.60
25	BA	2299	A	C5-N7-C8	-5.16	101.32	103.90
1	CA	1036	G	C4-N9-C1'	5.16	133.21	126.50
25	BA	202	A	C8-N9-C4	5.16	107.86	105.80
1	CA	1246	C	N3-C2-O2	-5.16	118.29	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CX	26	G	C6-N1-C2	5.16	128.20	125.10
25	DA	448	U	C5-C6-N1	-5.16	120.12	122.70
25	DA	2320	A	C2-N3-C4	5.16	113.18	110.60
25	BA	1985	U	C5-C6-N1	5.16	125.28	122.70
25	BA	2299	A	O4'-C1'-N9	-5.16	104.07	108.20
25	DA	512	G	C8-N9-C1'	5.16	133.71	127.00
1	AA	46	G	N1-C6-O6	5.16	122.99	119.90
25	BA	2065	C	N3-C2-O2	5.16	125.51	121.90
18	CR	64	ARG	NE-CZ-NH2	-5.16	117.72	120.30
25	DA	1204	A	C5-N7-C8	-5.16	101.32	103.90
25	BA	639	G	O4'-C1'-N9	5.15	112.32	108.20
25	DA	2512	C	N1-C2-O2	-5.15	115.81	118.90
25	BA	1076	G	N9-C4-C5	-5.15	103.34	105.40
25	BA	1222	A	C4-C5-C6	5.15	119.58	117.00
25	DA	2386	C	N3-C4-C5	5.15	123.96	121.90
25	BA	1019	G	OP1-P-OP2	5.15	127.33	119.60
25	DA	446	G	C8-N9-C4	5.15	108.46	106.40
25	DA	645	C	C6-N1-C2	-5.15	118.24	120.30
26	DB	70	C	C6-N1-C2	-5.15	118.24	120.30
25	BA	2428	C	C5-C6-N1	5.15	123.57	121.00
1	CA	800	G	OP2-P-O3'	5.15	116.53	105.20
25	DA	2483	C	C5-C6-N1	5.15	123.58	121.00
25	BA	354	A	N1-C2-N3	5.15	131.87	129.30
25	DA	737	C	C6-N1-C2	5.15	122.36	120.30
25	BA	2537	G	O5'-P-OP1	5.14	116.87	110.70
25	DA	1937	A	N9-C4-C5	-5.14	103.74	105.80
25	BA	2061	C	C6-N1-C2	-5.14	118.24	120.30
25	BA	2544	G	C5-C6-O6	-5.14	125.52	128.60
25	BA	2574	U	C5-C6-N1	-5.14	120.13	122.70
25	DA	1313	U	C5-C6-N1	5.14	125.27	122.70
25	DA	2321	G	C6-C5-N7	-5.14	127.32	130.40
1	AA	159	G	N9-C1'-C2'	-5.14	106.35	112.00
25	BA	1321	A	C5-C6-N1	-5.14	115.13	117.70
25	BA	1745	A	N1-C6-N6	5.14	121.68	118.60
25	BA	2608	U	C6-N1-C2	5.14	124.08	121.00
25	DA	1487	G	C8-N9-C4	-5.14	104.34	106.40
25	BA	332	G	C8-N9-C1'	-5.14	120.32	127.00
1	CA	299	G	C5-C6-O6	-5.14	125.52	128.60
1	AA	1506	U	N3-C4-O4	5.13	122.99	119.40
25	BA	2256	U	N3-C4-O4	-5.13	115.81	119.40
25	BA	2419	G	C4-N9-C1'	5.13	133.18	126.50
25	BA	2566	U	N1-C2-O2	-5.13	119.21	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	271(M)	G	N3-C4-C5	-5.13	126.03	128.60
25	DA	792	G	N3-C4-N9	5.13	129.08	126.00
25	BA	30	G	OP1-P-O3'	5.13	116.49	105.20
1	AA	341	C	C6-N1-C2	5.13	122.35	120.30
25	DA	90	U	C2-N1-C1'	5.13	123.86	117.70
25	DA	1124	C	N3-C4-C5	5.13	123.95	121.90
25	BA	1153	G	C2-N3-C4	5.13	114.47	111.90
1	CA	1028	C	C6-N1-C2	-5.13	118.25	120.30
1	CA	1269	A	N1-C6-N6	-5.13	115.52	118.60
25	DA	762	U	C2-N1-C1'	5.13	123.86	117.70
25	DA	1375	C	O5'-P-OP1	-5.13	101.08	105.70
25	DA	1596	A	C8-N9-C4	5.13	107.85	105.80
25	DA	2039	C	C2-N1-C1'	5.13	124.44	118.80
1	AA	578	C	C6-N1-C2	-5.13	118.25	120.30
1	AA	1150	U	C5-C6-N1	5.13	125.26	122.70
25	BA	1707	C	C6-N1-C2	-5.13	118.25	120.30
25	DA	602	G	N3-C4-N9	5.13	129.08	126.00
1	CA	893	C	C6-N1-C2	5.13	122.35	120.30
1	CA	1307	U	C5-C6-N1	5.13	125.26	122.70
25	DA	914	C	N1-C2-O2	5.13	121.97	118.90
25	DA	1718	G	C4-N9-C1'	5.13	133.16	126.50
25	DA	1966	A	N1-C6-N6	-5.13	115.53	118.60
25	DA	2591	C	N3-C4-C5	-5.13	119.85	121.90
1	CA	1519	A	C8-N9-C4	-5.12	103.75	105.80
25	DA	889	C	C6-N1-C2	-5.12	118.25	120.30
1	AA	190	U	C5-C6-N1	5.12	125.26	122.70
25	DA	1017	G	C4-N9-C1'	5.12	133.16	126.50
25	DA	2413	G	N1-C6-O6	5.12	122.97	119.90
1	AA	781	A	N9-C4-C5	-5.12	103.75	105.80
1	AA	814	A	OP1-P-O3'	5.12	116.47	105.20
1	AA	1435	G	C5-C6-N1	-5.12	108.94	111.50
25	BA	332	G	C4-N9-C1'	5.12	133.16	126.50
25	BA	725	C	C6-N1-C2	5.12	122.35	120.30
25	DA	199	A	C5-C6-N6	-5.12	119.60	123.70
25	DA	2474	C	N1-C2-O2	5.12	121.97	118.90
25	BA	2258	G	C5-C6-O6	-5.12	125.53	128.60
1	CA	1502	A	C2-N3-C4	-5.12	108.04	110.60
25	BA	861	C	C4-C5-C6	-5.12	114.84	117.40
25	DA	1115	G	C4-N9-C1'	-5.12	119.85	126.50
1	CA	1522	U	OP2-P-O3'	5.11	116.45	105.20
25	BA	2040	G	O5'-P-OP1	5.11	116.83	110.70
1	AA	1004	A	P-O3'-C3'	5.11	125.83	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1145	C	N3-C2-O2	-5.11	118.32	121.90
25	BA	2230	U	N1-C2-O2	5.11	126.38	122.80
25	DA	783	A	C4-C5-C6	5.11	119.56	117.00
25	DA	1897	G	C5-C6-O6	-5.11	125.53	128.60
25	BA	1483	C	C2-N1-C1'	5.11	124.42	118.80
25	BA	1725	G	N3-C2-N2	-5.11	116.32	119.90
1	CA	865	A	C8-N9-C4	-5.11	103.76	105.80
25	DA	912	C	N3-C2-O2	-5.11	118.33	121.90
25	DA	2893	G	N9-C4-C5	-5.11	103.36	105.40
1	AA	421	U	N3-C2-O2	-5.11	118.63	122.20
25	BA	2621	U	C6-N1-C2	5.11	124.06	121.00
1	CA	998	G	N9-C4-C5	5.11	107.44	105.40
25	DA	584	C	N1-C2-O2	-5.11	115.84	118.90
25	BA	418	G	N1-C6-O6	5.10	122.96	119.90
25	DA	188	G	C5-C6-O6	-5.10	125.54	128.60
25	BA	515	G	N1-C6-O6	5.10	122.96	119.90
25	BA	553	A	O5'-P-OP2	-5.10	101.11	105.70
25	BA	1418	U	C5-C6-N1	5.10	125.25	122.70
25	BA	1429	C	C5-C4-N4	-5.10	116.63	120.20
25	DA	389	G	N1-C6-O6	5.10	122.96	119.90
25	DA	1363	C	N3-C4-N4	-5.10	114.43	118.00
25	DA	2297	C	C5-C6-N1	5.10	123.55	121.00
1	CA	833	U	O5'-P-OP2	-5.10	101.11	105.70
25	BA	1718	U	C5-C6-N1	5.10	125.25	122.70
25	BA	2054	G	C4-N9-C1'	-5.10	119.87	126.50
25	DA	560	C	C5-C6-N1	-5.10	118.45	121.00
25	DA	1204	A	N9-C1'-C2'	5.10	120.63	114.00
1	AA	192	U	C6-N1-C2	-5.10	117.94	121.00
1	AA	348	G	N1-C6-O6	5.10	122.96	119.90
25	BA	772	G	N3-C4-C5	-5.10	126.05	128.60
25	DA	1802	A	C6-N1-C2	-5.10	115.54	118.60
1	AA	840	C	O4'-C1'-N1	-5.10	104.12	108.20
1	AA	1125	U	C6-N1-C2	5.09	124.06	121.00
25	BA	2735	G	C8-N9-C1'	-5.09	120.38	127.00
25	DA	394	A	O5'-P-OP1	-5.09	101.12	105.70
26	DB	79	C	C6-N1-C2	-5.09	118.26	120.30
1	AA	977	A	N1-C6-N6	-5.09	115.54	118.60
26	DB	60	C	C5-C6-N1	5.09	123.55	121.00
25	BA	930	G	C4-N9-C1'	-5.09	119.88	126.50
25	DA	461	C	N3-C4-N4	5.09	121.56	118.00
25	DA	1439	A	C8-N9-C4	5.09	107.84	105.80
1	CA	1017	G	N3-C4-C5	5.09	131.15	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1296	C	N3-C2-O2	5.09	125.46	121.90
25	BA	816	G	N9-C4-C5	-5.09	103.36	105.40
1	CA	1044	A	N1-C6-N6	-5.09	115.55	118.60
1	AA	167	G	C6-C5-N7	-5.09	127.35	130.40
1	AA	532	A	P-O3'-C3'	5.09	125.80	119.70
23	AX	22	G	C8-N9-C1'	5.09	133.61	127.00
25	DA	783	A	N3-C4-C5	-5.09	123.24	126.80
25	DA	2591	C	N1-C2-O2	-5.09	115.85	118.90
1	AA	220	G	C4-N9-C1'	5.08	133.11	126.50
1	AA	162	A	N7-C8-N9	5.08	116.34	113.80
25	BA	332	G	N9-C4-C5	-5.08	103.37	105.40
25	BA	2383	G	N1-C2-N3	-5.08	120.85	123.90
25	DA	1614	A	N1-C6-N6	-5.08	115.55	118.60
25	DA	2523	G	O5'-P-OP1	5.08	116.80	110.70
25	BA	1459	G	C5-C6-O6	-5.08	125.55	128.60
25	DA	729	G	C8-N9-C1'	-5.08	120.39	127.00
25	DA	1588	C	N3-C4-C5	5.08	123.93	121.90
25	BA	103	C	N3-C4-C5	5.08	123.93	121.90
25	DA	1421	G	N1-C6-O6	5.08	122.95	119.90
1	AA	1183	A	P-O3'-C3'	5.08	125.79	119.70
25	BA	893	C	C6-N1-C2	5.08	122.33	120.30
25	DA	116	C	N3-C2-O2	-5.08	118.34	121.90
25	DA	2828	C	C6-N1-C2	5.08	122.33	120.30
25	DA	1653	G	N3-C4-N9	5.08	129.05	126.00
1	AA	1397	C	C6-N1-C1'	-5.08	114.71	120.80
23	AX	24	U	N3-C2-O2	-5.08	118.65	122.20
25	BA	1153	G	O5'-P-OP2	-5.08	101.13	105.70
25	DA	1253	A	C8-N9-C4	5.08	107.83	105.80
25	DA	1340	U	C5-C4-O4	-5.08	122.86	125.90
25	BA	1417	G	C5-C6-O6	-5.07	125.56	128.60
1	CA	1034	G	N9-C4-C5	5.07	107.43	105.40
1	CA	1036	G	C8-N9-C1'	-5.07	120.41	127.00
25	DA	148	C	C5-C6-N1	-5.07	118.46	121.00
25	BA	1578	C	C2-N1-C1'	5.07	124.38	118.80
23	AX	14	A	C4-N9-C1'	5.07	135.42	126.30
25	BA	639	G	C4-C5-N7	-5.07	108.77	110.80
25	BA	1076	G	C2-N3-C4	-5.07	109.37	111.90
25	BA	1412	A	C4-C5-N7	-5.07	108.17	110.70
25	BA	1920	U	C5-C4-O4	5.07	128.94	125.90
23	CX	22	G	C8-N9-C1'	5.07	133.59	127.00
25	DA	2286	A	C6-C5-N7	-5.07	128.75	132.30
1	CA	287	U	O5'-P-OP2	-5.06	101.14	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	2347	C	N3-C2-O2	-5.06	118.36	121.90
25	DA	2519	U	C5-C6-N1	-5.06	120.17	122.70
1	CA	1020	U	N1-C2-O2	5.06	126.34	122.80
1	AA	460	G	N7-C8-N9	5.06	115.63	113.10
25	BA	2067	C	N3-C4-C5	5.06	123.92	121.90
25	BA	179	A	N1-C6-N6	5.06	121.64	118.60
25	BA	2549	U	N3-C4-O4	-5.06	115.86	119.40
25	BA	2627	U	C4-C5-C6	-5.06	116.66	119.70
25	DA	685	A	OP1-P-OP2	5.06	127.19	119.60
25	DA	2063	C	N1-C2-O2	-5.06	115.86	118.90
25	DA	2627	G	N1-C6-O6	-5.06	116.86	119.90
25	DA	2042	A	C2-N3-C4	-5.06	108.07	110.60
25	BA	829	A	C8-N9-C4	5.06	107.82	105.80
25	DA	1123	C	N3-C2-O2	5.06	125.44	121.90
25	BA	1745	A	C5-C6-N1	-5.05	115.17	117.70
25	BA	2227	G	N3-C4-C5	5.05	131.13	128.60
25	BA	2697	G	N1-C6-O6	-5.05	116.87	119.90
25	DA	985	C	C5-C6-N1	-5.05	118.47	121.00
25	DA	1620	G	O5'-P-OP2	5.05	116.77	110.70
25	DA	2338	G	C8-N9-C1'	5.05	133.57	127.00
25	BA	137	G	C8-N9-C4	5.05	108.42	106.40
25	BA	51	A	C8-N9-C4	-5.05	103.78	105.80
25	BA	107	G	C6-C5-N7	5.05	133.43	130.40
25	BA	2397	C	N3-C4-C5	5.05	123.92	121.90
1	CA	1028	C	C2-N3-C4	5.05	122.43	119.90
1	CA	1224	G	C8-N9-C4	-5.05	104.38	106.40
23	AX	67	C	N1-C2-O2	5.05	121.93	118.90
25	BA	1091	A	C8-N9-C4	5.05	107.82	105.80
25	BA	1821	C	P-O3'-C3'	5.05	125.76	119.70
1	CA	265	G	N1-C6-O6	5.05	122.93	119.90
25	DA	330	A	N3-C4-C5	5.05	130.33	126.80
26	BB	93	G	N7-C8-N9	5.05	115.62	113.10
25	DA	729	G	C6-C5-N7	-5.05	127.37	130.40
25	BA	194	G	N7-C8-N9	-5.05	110.58	113.10
25	BA	2265	G	N9-C4-C5	-5.05	103.38	105.40
1	CA	662	G	N3-C4-N9	5.05	129.03	126.00
25	DA	90	U	N3-C2-O2	-5.05	118.67	122.20
25	DA	315	G	O5'-P-OP1	5.05	116.76	110.70
25	DA	1189	A	O5'-P-OP1	5.05	116.75	110.70
25	BA	990	A	N1-C2-N3	5.04	131.82	129.30
25	DA	1022	G	N9-C4-C5	5.04	107.42	105.40
25	DA	975	C	C6-N1-C2	-5.04	118.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	DA	1899	G	N3-C4-N9	5.04	129.03	126.00
25	DA	2298	A	C4-C5-N7	5.04	113.22	110.70
25	DA	2440	C	C2-N1-C1'	-5.04	113.25	118.80
1	AA	1131	G	C5-C6-O6	-5.04	125.58	128.60
23	AX	14	A	C8-N9-C1'	-5.04	118.63	127.70
25	BA	622	G	C8-N9-C4	5.04	108.42	106.40
25	BA	1823	G	N3-C4-C5	5.04	131.12	128.60
1	CA	1264	C	C6-N1-C2	5.04	122.32	120.30
25	DA	879	G	N3-C4-C5	-5.04	126.08	128.60
1	AA	340	U	C2-N1-C1'	-5.04	111.65	117.70
6	CF	75	LEU	CA-CB-CG	5.04	126.89	115.30
25	DA	1251	C	N3-C2-O2	5.04	125.43	121.90
25	DA	1828	G	C5-C6-O6	5.04	131.62	128.60
1	AA	1286	A	O5'-P-OP1	-5.04	101.17	105.70
25	BA	1219	A	P-O3'-C3'	5.04	125.75	119.70
25	BA	2465	A	N1-C6-N6	-5.04	115.58	118.60
25	DA	2024	G	C5-C6-O6	-5.04	125.58	128.60
1	AA	1024	G	C8-N9-C1'	-5.04	120.45	127.00
25	DA	1488	G	N3-C4-C5	-5.04	126.08	128.60
25	DA	2321	G	C4-C5-N7	5.04	112.81	110.80
25	BA	2001	C	C6-N1-C2	-5.04	118.29	120.30
25	DA	374	A	N1-C6-N6	5.04	121.62	118.60
25	DA	1320	C	N1-C2-O2	-5.04	115.88	118.90
25	BA	418	G	N9-C4-C5	-5.03	103.39	105.40
25	DA	1441	G	C8-N9-C4	5.03	108.41	106.40
25	BA	666	C	N3-C4-C5	-5.03	119.89	121.90
25	DA	768	G	C5-C6-O6	-5.03	125.58	128.60
1	AA	827	U	N3-C2-O2	-5.03	118.68	122.20
25	BA	512	C	C6-N1-C2	5.03	122.31	120.30
25	BA	2610	A	C8-N9-C4	5.03	107.81	105.80
39	BT	103	ARG	NE-CZ-NH1	-5.03	117.78	120.30
1	CA	266	G	P-O3'-C3'	5.03	125.74	119.70
1	AA	30	U	OP2-P-O3'	5.03	116.26	105.20
25	BA	1366	C	C6-N1-C2	5.03	122.31	120.30
25	DA	1204	A	C5-C6-N1	-5.03	115.19	117.70
25	DA	1339	G	O5'-P-OP2	5.03	116.73	110.70
25	DA	2292	C	O5'-P-OP2	-5.03	101.18	105.70
1	AA	1395	C	N1-C2-O2	5.03	121.92	118.90
2	AB	128	GLU	N-CA-C	-5.03	97.43	111.00
25	BA	1687	C	N1-C2-O2	5.03	121.92	118.90
25	BA	2899	C	O5'-P-OP2	-5.03	101.18	105.70
1	CA	99	U	C2-N1-C1'	-5.03	111.67	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1169	A	C8-N9-C4	-5.03	103.79	105.80
1	AA	59	A	C2-N3-C4	5.02	113.11	110.60
1	AA	66	G	C5-C6-N1	-5.02	108.99	111.50
25	BA	1277	G	N3-C4-C5	5.02	131.11	128.60
25	BA	2527	C	C5-C4-N4	-5.02	116.69	120.20
25	BA	2550	C	N3-C4-C5	5.02	123.91	121.90
25	DA	1266	G	C8-N9-C4	5.02	108.41	106.40
25	BA	1177	G	N3-C2-N2	5.02	123.42	119.90
1	CA	1206	G	N1-C6-O6	5.02	122.91	119.90
1	AA	1007	C	C6-N1-C1'	-5.02	114.78	120.80
1	AA	1206	G	N1-C6-O6	5.02	122.91	119.90
25	BA	2300	A	N1-C6-N6	5.02	121.61	118.60
1	AA	975	A	O4'-C1'-N9	-5.02	104.19	108.20
25	DA	1259	G	OP2-P-O3'	5.02	116.24	105.20
1	AA	1502	A	C5-N7-C8	-5.02	101.39	103.90
25	BA	2579	G	C5-N7-C8	5.02	106.81	104.30
25	DA	1004	C	N3-C2-O2	5.02	125.41	121.90
25	BA	2843	G	N3-C4-N9	5.01	129.01	126.00
1	AA	328	C	O5'-P-OP1	-5.01	101.19	105.70
25	BA	1823	G	N3-C4-N9	-5.01	122.99	126.00
1	AA	1335	C	C6-N1-C2	5.01	122.30	120.30
25	BA	2451	A	O4'-C1'-N9	-5.01	104.19	108.20
25	BA	2906	U	C2-N1-C1'	5.01	123.72	117.70
23	CX	76	A	C5-C6-N6	-5.01	119.69	123.70
25	DA	389	G	C8-N9-C4	5.01	108.41	106.40
25	DA	2689	U	OP2-P-O3'	5.01	116.23	105.20
25	BA	1417	G	N1-C6-O6	5.01	122.91	119.90
25	BA	441	C	N3-C4-C5	5.01	123.90	121.90
25	DA	2896	C	N1-C2-O2	5.01	121.91	118.90
1	AA	1127	G	N1-C2-N2	-5.01	111.69	116.20
25	BA	120	G	N1-C6-O6	5.01	122.90	119.90
25	BA	2105	G	C8-N9-C4	5.01	108.40	106.40
1	CA	46	G	N1-C6-O6	5.00	122.90	119.90
25	DA	1703	G	C5-C6-O6	-5.00	125.60	128.60
25	BA	26	G	C6-C5-N7	-5.00	127.40	130.40
25	DA	863	A	OP2-P-O3'	5.00	116.21	105.20
1	AA	347	G	C8-N9-C1'	-5.00	120.50	127.00
25	BA	2283	G	C4-N9-C1'	5.00	133.00	126.50
1	CA	1132	C	C5-C6-N1	5.00	123.50	121.00
25	DA	461	C	N1-C2-O2	-5.00	115.90	118.90
25	DA	1432	C	N3-C2-O2	5.00	125.40	121.90
25	DA	1721	G	N3-C4-C5	-5.00	126.10	128.60

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
23	CX	76	A	C1'

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	79	ARG	Peptide
24	AW	4	PRO	Peptide
50	B4	59	PHE	Peptide
38	BS	58	LEU	Peptide
45	BZ	136	PHE	Peptide
4	CD	45	GLN	Peptide
24	CW	9	MVA	Peptide
27	DD	274	ARG	Peptide

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	AA	32196	0	16251	809	0
1	CA	32312	0	16307	915	0
2	AB	1846	0	1867	109	0
2	CB	1825	0	1828	119	0
3	AC	1552	0	1546	59	0
3	CC	1542	0	1517	66	0
4	AD	1659	0	1676	99	0
4	CD	1674	0	1714	78	0
5	AE	1129	0	1185	50	0
5	CE	1133	0	1191	45	0
6	AF	806	0	793	33	0
6	CF	816	0	808	27	0
7	AG	1231	0	1238	35	0
7	CG	1235	0	1249	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AH	1088	0	1126	48	0
8	CH	1088	0	1126	46	0
9	AI	983	0	986	54	0
9	CI	978	0	966	57	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	47	0
11	AK	829	0	825	19	0
11	CK	833	0	836	29	0
12	AL	930	0	980	28	0
12	CL	930	0	980	34	0
13	AM	958	0	1002	25	0
13	CM	950	0	988	56	0
14	AN	492	0	529	26	0
14	CN	492	0	529	29	0
15	AO	728	0	760	16	0
15	CO	728	0	760	27	0
16	AP	681	0	697	29	0
16	CP	677	0	686	28	0
17	AQ	823	0	891	21	0
17	CQ	823	0	891	19	0
18	AR	555	0	618	17	0
18	CR	555	0	618	27	0
19	AS	652	0	662	36	0
19	CS	646	0	644	56	0
20	AT	728	0	798	30	0
20	CT	727	0	796	28	0
21	AU	199	0	208	5	0
21	CU	199	0	208	7	0
22	AV	114	0	54	0	0
22	CV	113	0	54	0	0
23	AX	1623	0	823	18	0
23	CX	1623	0	824	24	0
24	AW	93	0	51	6	0
24	CW	93	0	51	7	0
25	BA	58834	0	29667	785	0
25	DA	58458	0	29482	1100	0
26	BB	2573	0	1306	38	0
26	DB	2573	0	1306	54	0
27	BD	2136	0	2218	64	0
27	DD	2136	0	2218	74	0
28	BE	1559	0	1618	38	0
28	DE	1559	0	1618	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	BF	1584	0	1625	46	0
29	DF	1580	0	1619	69	0
30	BG	1425	0	1443	45	0
30	DG	1424	0	1434	82	0
31	BH	1330	0	1407	33	0
31	DH	1330	0	1407	52	0
32	BI	1085	0	1114	42	0
32	DI	1061	0	1080	31	0
33	BN	1117	0	1183	17	0
33	DN	1117	0	1184	26	0
34	BO	933	0	996	24	0
34	DO	933	0	996	36	0
35	BP	1135	0	1212	37	0
35	DP	1135	0	1211	46	0
36	BQ	1122	0	1179	38	0
36	DQ	1122	0	1179	47	0
37	BR	968	0	1033	24	0
37	DR	968	0	1032	30	0
38	BS	877	0	938	25	0
38	DS	870	0	923	47	0
39	BT	1091	0	1151	28	0
39	DT	1083	0	1136	36	0
40	BU	959	0	1019	26	0
40	DU	959	0	1019	37	0
41	BV	771	0	830	11	0
41	DV	771	0	830	23	0
42	BW	886	0	940	9	0
42	DW	886	0	940	17	0
43	BX	750	0	814	20	0
43	DX	750	0	814	25	0
44	BY	806	0	881	25	0
44	DY	806	0	881	21	0
45	BZ	1349	0	1355	47	0
45	DZ	1360	0	1363	48	0
46	B0	653	0	674	25	0
46	D0	653	0	674	23	0
47	B1	755	0	826	19	0
47	D1	755	0	826	26	0
48	B2	588	0	643	18	0
48	D2	588	0	643	20	0
49	B3	469	0	518	17	0
49	D3	464	0	514	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	B4	551	0	532	38	0
50	D4	531	0	502	32	0
51	B5	455	0	465	13	0
51	D5	455	0	465	11	0
52	B6	453	0	473	10	0
52	D6	449	0	469	10	0
53	B7	418	0	466	9	0
53	D7	418	0	467	9	0
54	B8	511	0	571	27	0
54	D8	517	0	582	27	0
55	B9	307	0	335	5	0
55	D9	307	0	335	10	0
56	AA	221	0	0	0	0
56	AD	1	0	0	0	0
56	AF	1	0	0	0	0
56	AK	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	2	0	0	0	0
56	AV	1	0	0	0	0
56	AX	9	0	0	0	0
56	B0	4	0	0	0	0
56	B1	1	0	0	0	0
56	B2	1	0	0	0	0
56	B3	3	0	0	0	0
56	B4	1	0	0	0	0
56	B5	1	0	0	0	0
56	B7	4	0	0	0	0
56	B8	3	0	0	0	0
56	B9	1	0	0	0	0
56	BA	738	0	0	0	0
56	BB	18	0	0	0	0
56	BD	12	0	0	0	0
56	BE	10	0	0	0	0
56	BF	8	0	0	0	0
56	BG	4	0	0	0	0
56	BN	6	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	5	0	0	0	0
56	BR	4	0	0	0	0
56	BU	8	0	0	0	0
56	BV	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BW	5	0	0	0	0
56	BX	1	0	0	0	0
56	BY	1	0	0	0	0
56	BZ	1	0	0	0	0
56	CA	172	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CQ	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	3	0	0	0	0
56	D0	1	0	0	0	0
56	D3	1	0	0	0	0
56	D5	2	0	0	0	0
56	D8	1	0	0	0	0
56	DA	653	0	0	0	0
56	DB	12	0	0	0	0
56	DD	8	0	0	0	0
56	DE	6	0	0	0	0
56	DF	6	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	1	0	0	0	0
56	DQ	5	0	0	0	0
56	DR	2	0	0	0	0
56	DV	4	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AD	8	0	0	1	0
57	CD	8	0	0	1	0
58	AN	1	0	0	0	0
58	B4	1	0	0	0	0
58	B5	1	0	0	0	0
58	B6	1	0	0	0	0
58	B9	1	0	0	0	0
58	BY	1	0	0	0	0
58	CN	1	0	0	0	0
58	D4	1	0	0	0	0
58	D5	1	0	0	0	0
58	D6	1	0	0	0	0
58	D9	1	0	0	0	0
58	DY	1	0	0	0	0
59	AX	10	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	CX	10	0	10	2	0
60	BA	1	0	0	0	0
60	DA	1	0	0	0	0
61	AA	148	0	0	27	0
61	AD	1	0	0	0	0
61	AE	3	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	1	0	0	0	0
61	AP	1	0	0	0	0
61	AU	1	0	0	0	0
61	AV	1	0	0	0	0
61	AX	1	0	0	0	0
61	B0	4	0	0	0	0
61	B1	2	0	0	0	0
61	B5	3	0	0	1	0
61	B7	1	0	0	1	0
61	B8	8	0	0	1	0
61	BA	1092	0	0	113	0
61	BB	26	0	0	0	0
61	BD	8	0	0	1	0
61	BE	9	0	0	4	0
61	BF	4	0	0	0	0
61	BG	1	0	0	0	0
61	BN	3	0	0	0	0
61	BO	2	0	0	0	0
61	BP	15	0	0	3	0
61	BQ	3	0	0	1	0
61	BR	1	0	0	0	0
61	BT	1	0	0	0	0
61	BU	4	0	0	0	0
61	BV	2	0	0	0	0
61	BW	2	0	0	0	0
61	BX	4	0	0	1	0
61	CA	187	0	0	24	0
61	CE	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CX	2	0	0	0	0
61	D0	5	0	0	1	0
61	D1	1	0	0	0	0
61	D7	2	0	0	0	0
61	D8	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DA	902	0	0	120	0
61	DB	7	0	0	0	0
61	DD	8	0	0	0	0
61	DE	13	0	0	1	0
61	DF	5	0	0	0	0
61	DO	1	0	0	0	0
61	DP	14	0	0	0	0
61	DQ	3	0	0	1	0
61	DU	4	0	0	0	0
61	DV	1	0	0	0	0
61	DX	2	0	0	0	0
61	DY	2	0	0	0	0
All	All	286321	0	191060	6362	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 14.

All (6362) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1002:G:H1	1:CA:1038:C:N4	1.42	1.16
1:AA:348:G:H2'	1:AA:349:A:H5'	1.36	1.04
1:AA:1125:U:N3	1:AA:1127:G:N7	2.06	1.03
39:BT:16:ARG:NH2	39:BT:83:ILE:O	1.92	1.02
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.40	1.02
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.41	1.01
1:CA:1162:C:H42	1:CA:1174:G:H1	1.02	1.00
25:DA:1019:U:HO2'	25:DA:1021:A:H2	1.01	1.00
1:AA:1129:C:N4	1:AA:1143:G:H1	1.59	0.99
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.43	0.98
25:DA:2206:G:H3'	25:DA:2207:G:C8	1.98	0.98
1:CA:1007:C:N3	1:CA:1022:G:N2	2.12	0.97
30:BG:41:GLN:HG3	30:BG:60:LEU:HD11	1.48	0.96
38:DS:35:ILE:HD11	38:DS:101:LEU:HD12	1.47	0.96
1:CA:998:G:H1	1:CA:1043:C:H42	1.14	0.95
25:BA:9:U:H3	25:BA:2641:A:H2	1.15	0.95
30:BG:66:GLN:HG2	50:B4:1:MET:HE3	1.44	0.95
10:CJ:8:LEU:HB2	10:CJ:70:ARG:HB2	1.49	0.95
1:CA:1163:C:H42	1:CA:1173:G:H1	1.07	0.94
25:DA:1689:A:H62	25:DA:1698:A:H2	1.15	0.93
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.05	0.93
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.50	0.92
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.49	0.92

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1002:G:N2	1:CA:1038:C:N3	2.16	0.92
1:AA:1129:C:H42	1:AA:1143:G:H1	0.95	0.91
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.02	0.91
25:DA:1648:C:OP1	61:DA:4111:HOH:O	1.88	0.91
1:CA:999:C:N4	1:CA:1042:G:N1	2.17	0.91
26:DB:22:U:H3	26:DB:61:G:H1	1.18	0.91
1:CA:1007:C:N4	1:CA:1022:G:N1	2.19	0.91
1:AA:201:C:H42	1:AA:216:G:H1	1.11	0.90
25:DA:1204:A:H2	25:DA:1241:A:H62	1.19	0.90
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.02	0.90
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.52	0.90
28:BE:110:GLY:O	61:BE:406:HOH:O	1.89	0.90
50:D4:53:GLU:HG2	50:D4:55:ARG:H	1.34	0.90
1:CA:1153:C:H42	1:CA:1154:G:H21	1.17	0.90
25:DA:526:A:OP1	61:DA:4572:HOH:O	1.89	0.90
25:DA:195:A:N7	61:DA:4175:HOH:O	2.04	0.89
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.54	0.89
44:BY:54:LYS:HA	44:BY:56:PRO:HD3	1.52	0.89
25:DA:566:U:H5''	35:DP:29:LYS:HE3	1.55	0.88
25:DA:2615:U:OP1	61:DA:3943:HOH:O	1.91	0.88
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.53	0.88
25:DA:740:U:OP2	61:DA:4117:HOH:O	1.92	0.88
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.55	0.88
1:CA:1163:C:N4	1:CA:1173:G:H1	1.72	0.88
1:CA:999:C:N4	1:CA:1042:G:C6	2.42	0.88
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.06	0.88
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.05	0.87
1:CA:563:A:N6	61:CA:4065:HOH:O	2.06	0.87
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.56	0.87
25:DA:981:A:OP1	61:DA:4033:HOH:O	1.92	0.86
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.37	0.86
25:BA:1395:A:OP1	61:BA:4761:HOH:O	1.93	0.86
25:BA:1686:U:OP1	61:BA:4272:HOH:O	1.93	0.86
16:AP:53:VAL:HG13	16:AP:79:VAL:HG13	1.57	0.86
25:BA:537:G:N7	61:BA:4621:HOH:O	2.07	0.86
25:DA:2592:G:OP1	61:DA:4137:HOH:O	1.93	0.86
25:DA:323:G:HO2'	25:DA:1205:U:H3	1.23	0.86
25:DA:1153:C:OP1	40:DU:92:ARG:NH1	2.09	0.86
25:DA:1268:A:OP1	61:DA:3940:HOH:O	1.93	0.86
25:DA:2807:G:N1	25:DA:2893:G:O6	2.09	0.86
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.08	0.86
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.54	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:B3:8:LEU:HD13	49:B3:31:LEU:HD23	1.58	0.85
13:AM:2:ALA:N	13:AM:8:GLU:OE1	2.09	0.85
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.57	0.85
1:CA:1493:A:H1'	25:DA:1913:A:H62	1.39	0.85
25:DA:770:G:OP2	61:DA:4148:HOH:O	1.94	0.85
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.09	0.85
25:BA:303:C:H42	25:BA:385:G:H1	1.24	0.85
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.09	0.85
25:DA:2879:C:OP2	61:DA:4045:HOH:O	1.95	0.85
1:CA:1502:A:H2	1:CA:1505:G:H1	1.24	0.85
25:BA:2720:G:O6	61:BA:4017:HOH:O	1.93	0.85
25:BA:1500:A:OP2	61:BA:3907:HOH:O	1.95	0.85
2:AB:21:ARG:HB3	2:AB:39:ILE:HA	1.57	0.84
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.41	0.84
1:CA:1162:C:N4	1:CA:1174:G:H1	1.74	0.84
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.09	0.84
25:BA:894:U:O4	25:BA:978:A:N6	2.10	0.84
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.59	0.84
25:BA:1577:C:O2'	25:BA:1578:C:O5'	1.96	0.84
25:DA:1271:G:OP2	61:DA:4112:HOH:O	1.96	0.84
25:DA:1021:A:H62	25:DA:1141:U:H3	1.22	0.84
25:DA:2632:A:HO2'	25:DA:2811:G:HO2'	1.17	0.84
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.40	0.84
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.11	0.84
1:CA:1122:U:O4	1:CA:1151:A:N1	2.11	0.83
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.11	0.83
25:BA:1736:A:H62	25:BA:1745:A:H2	1.24	0.83
1:AA:1314:C:OP2	19:AS:4:SER:OG	1.94	0.83
25:BA:2587:C:OP2	61:BA:4081:HOH:O	1.96	0.83
30:DG:113:ARG:NH1	30:DG:139:LEU:O	2.12	0.83
4:AD:149:ALA:HB3	4:AD:152:SER:HB2	1.60	0.83
1:CA:999:C:C4	1:CA:1042:G:N1	2.47	0.83
32:BI:129:THR:HG22	32:BI:139:GLN:HE22	1.42	0.83
1:CA:599:C:H2'	1:CA:600:C:H5''	1.61	0.83
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.51	0.83
1:AA:166:G:H2'	1:AA:167:G:C8	2.14	0.83
30:DG:11:TYR:CZ	30:DG:16:ARG:HD3	2.14	0.83
25:BA:2585:C:OP1	61:BA:4081:HOH:O	1.97	0.82
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.61	0.82
35:DP:96:THR:H	35:DP:99:LEU:HD21	1.44	0.82
36:DQ:81:VAL:HB	46:D0:7:LEU:HD21	1.59	0.82
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.11	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2748:A:H5'	31:DH:4:ILE:HD12	1.59	0.82
1:CA:64:G:H4'	1:CA:65:U:H3'	1.61	0.82
1:CA:972:C:OP1	61:CA:4184:HOH:O	1.95	0.82
46:D0:53:MET:HG3	46:D0:59:LEU:HD23	1.61	0.82
1:CA:1492:A:N3	25:DA:1913:A:N6	2.28	0.82
16:CP:1:MET:SD	16:CP:3:LYS:NZ	2.51	0.82
31:DH:98:LEU:HD22	31:DH:125:VAL:HG23	1.62	0.82
2:CB:178:ARG:HH22	8:CH:68:ARG:HH12	1.25	0.82
1:AA:1158:C:H5	1:AA:1181:G:H1	1.26	0.82
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.79	0.82
32:DI:72:LEU:HD21	32:DI:107:VAL:HG11	1.60	0.82
3:AC:134:ILE:HD11	3:AC:153:VAL:HG23	1.62	0.82
1:CA:1003:G:N2	1:CA:1025:U:O4	2.13	0.82
25:BA:237:G:OP1	61:BA:4880:HOH:O	1.96	0.81
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.59	0.81
23:CX:50:U:H3	23:CX:64:G:H1	1.28	0.81
27:DD:71:ASP:HB2	27:DD:103:ARG:HH22	1.45	0.81
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.13	0.81
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.12	0.81
1:AA:189(B):C:N4	1:AA:189(I):G:O6	2.11	0.81
25:DA:2243:U:OP1	61:DA:4350:HOH:O	1.98	0.81
1:CA:376:G:H5''	16:CP:5:ARG:HD3	1.63	0.81
25:BA:1503:G:OP2	61:BA:3908:HOH:O	1.99	0.81
38:BS:59:LYS:HE3	38:BS:60:GLY:H	1.44	0.81
1:CA:1007:C:N4	1:CA:1022:G:H1	1.77	0.81
2:CB:15:VAL:HG21	2:CB:213:LEU:HD12	1.62	0.81
25:DA:20:C:OP1	40:DU:22:LYS:NZ	2.12	0.81
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.61	0.81
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.63	0.81
25:BA:1683:C:OP2	61:BA:4524:HOH:O	1.99	0.81
25:DA:1782:C:OP1	61:DA:4383:HOH:O	1.99	0.81
25:BA:1462:G:N2	25:BA:1629:C:O2	2.11	0.81
26:BB:42:C:OP1	30:BG:67:LYS:NZ	2.13	0.81
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	1.62	0.80
25:BA:1036:A:OP2	61:BA:4503:HOH:O	1.99	0.80
1:AA:1124:G:O2'	1:AA:1145:C:N4	2.14	0.80
23:CX:4:G:H1	23:CX:69:C:H42	1.28	0.80
1:AA:1414:U:H3	1:AA:1486:G:H1	1.28	0.80
25:DA:570:G:O6	61:DA:4475:HOH:O	1.99	0.80
1:CA:975:A:H4'	1:CA:976:G:H5''	1.63	0.80
1:CA:953:G:H5'	1:CA:965:A:H61	1.47	0.80
25:DA:2022:U:OP1	61:DA:4084:HOH:O	1.99	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:768:A:OP2	61:CA:4023:HOH:O	1.98	0.80
1:CA:608:A:OP2	61:CA:4182:HOH:O	1.99	0.80
1:AA:1304:G:OP2	61:AA:4087:HOH:O	1.97	0.80
25:DA:198:C:OP2	61:DA:4175:HOH:O	1.99	0.80
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.15	0.80
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.62	0.80
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.00	0.80
1:AA:421:U:O2'	1:AA:423:G:N7	2.14	0.80
25:DA:1352:U:OP1	61:DA:3785:HOH:O	1.98	0.80
25:DA:2052:G:O2'	61:DA:3729:HOH:O	1.99	0.80
25:BA:238:C:O2	54:B8:12:LYS:NZ	2.14	0.80
9:AI:64:THR:HG23	9:AI:66:ARG:HH21	1.47	0.80
1:CA:444:C:H2'	1:CA:445:G:H8	1.48	0.80
1:CA:1030(A):G:N1	1:CA:1030(D):A:OP2	2.13	0.80
25:DA:2037:G:O6	61:DA:4103:HOH:O	2.00	0.80
25:BA:1694:G:OP1	61:BA:4516:HOH:O	1.99	0.80
1:AA:166:G:H2'	1:AA:167:G:H8	1.47	0.79
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.14	0.79
1:AA:1502:A:H2	1:AA:1505:G:H1	1.25	0.79
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.16	0.79
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.64	0.79
35:BP:50:ARG:HH21	54:B8:7:HIS:HD2	1.28	0.79
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.65	0.79
1:AA:509:A:OP2	61:AA:4088:HOH:O	2.01	0.79
1:CA:673:G:H2'	1:CA:674:G:C8	2.16	0.79
20:CT:57:ARG:HH22	20:CT:100:ILE:HD12	1.46	0.79
29:BF:53:THR:HG23	29:BF:55:GLY:H	1.48	0.79
1:AA:1145:C:H4'	1:AA:1146:A:H5'	1.65	0.79
25:BA:831:A:OP2	61:BA:4454:HOH:O	1.99	0.79
35:BP:36:LYS:O	61:BP:304:HOH:O	1.99	0.79
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.45	0.79
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.15	0.79
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.01	0.79
25:BA:2804:C:H2'	25:BA:2805:G:H8	1.47	0.79
1:AA:1492:A:N3	25:BA:1935:A:N6	2.31	0.79
25:BA:2299:A:H62	25:BA:2356:U:H3	1.28	0.79
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.65	0.79
1:AA:165:C:H2'	1:AA:166:G:C8	2.18	0.79
25:BA:241:G:OP1	35:BP:50:ARG:NH1	2.16	0.79
30:BG:161:THR:HG22	30:BG:163:ALA:H	1.48	0.79
1:CA:939:G:H1	1:CA:1344:C:H42	1.27	0.79
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.64	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1001:G:O6	61:BA:3865:HOH:O	2.00	0.78
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.16	0.78
25:DA:1250:G:OP1	61:DA:4455:HOH:O	2.00	0.78
25:BA:2614:A:OP1	61:BA:4815:HOH:O	2.01	0.78
1:AA:97:G:O2'	1:AA:98:G:O4'	2.00	0.78
25:DA:1159:U:H2'	25:DA:1160:G:H8	1.48	0.78
1:CA:1005:A:H1'	1:CA:1036:G:H1	1.49	0.78
1:CA:289:G:OP2	61:CA:4053:HOH:O	2.01	0.78
39:BT:95:ARG:HH11	39:BT:95:ARG:HG2	1.47	0.78
25:BA:988:U:OP2	61:BA:4601:HOH:O	2.01	0.78
25:DA:2005:A:OP1	61:DA:4386:HOH:O	2.01	0.78
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.28	0.78
25:BA:455:A:OP1	61:BA:3961:HOH:O	2.00	0.78
1:CA:1142:G:H3'	1:CA:1143:G:H8	1.47	0.78
1:AA:1124:G:HO2'	1:AA:1145:C:N4	1.82	0.78
25:DA:1997:G:OP2	61:DA:4560:HOH:O	2.01	0.78
25:BA:611:U:OP2	61:BA:4160:HOH:O	2.01	0.78
25:BA:1018:A:OP2	61:BA:4046:HOH:O	2.01	0.78
25:BA:535:C:OP1	61:BA:4621:HOH:O	2.00	0.77
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.50	0.77
25:DA:271(A):A:N7	25:DA:271(W):G:N2	2.32	0.77
25:BA:1404:G:OP2	61:BA:4219:HOH:O	2.02	0.77
4:CD:13:ARG:HB2	4:CD:40:PRO:HD3	1.66	0.77
1:AA:289:G:OP2	61:AA:4071:HOH:O	2.02	0.77
39:BT:65:LYS:HE2	39:BT:67:SER:HB2	1.66	0.77
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.16	0.77
28:BE:93:VAL:HG21	28:BE:180:ASN:HA	1.67	0.77
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.66	0.77
25:DA:1604:C:OP1	61:DA:3956:HOH:O	2.03	0.77
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.50	0.77
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.18	0.77
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.66	0.77
25:BA:808:A:OP1	61:BA:4592:HOH:O	2.01	0.77
25:DA:2032:G:N7	61:DA:3886:HOH:O	2.16	0.77
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.67	0.77
32:DI:110:ASP:N	32:DI:130:TYR:OH	2.16	0.77
1:CA:1133:G:H1	1:CA:1141:C:H42	1.33	0.77
25:BA:1717:C:OP1	61:BA:3893:HOH:O	2.02	0.77
25:BA:2227:G:H3'	25:BA:2228:G:C8	2.19	0.77
1:CA:1048:G:OP1	14:CN:3:ARG:NH2	2.18	0.77
1:AA:1128:C:O2	1:AA:1147:C:N4	2.17	0.77
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.18	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.18	0.77
25:BA:11:G:H2'	25:BA:12:U:H5'	1.65	0.77
1:AA:1126:U:H5	10:AJ:71:LEU:HD22	1.49	0.76
1:CA:677:U:H3	1:CA:713:G:H22	1.33	0.76
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.67	0.76
25:BA:1016:C:OP2	61:BA:4637:HOH:O	2.04	0.76
25:DA:1488:G:C6	25:DA:1489:U:H5	2.03	0.76
1:AA:1492:A:O2'	25:BA:1935:A:N1	2.18	0.76
1:AA:642:A:N3	8:AH:113:SER:OG	2.17	0.76
1:CA:352:C:OP2	61:CA:4051:HOH:O	2.02	0.76
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.18	0.76
25:DA:120:U:OP2	61:DA:3744:HOH:O	2.03	0.76
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.19	0.76
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.65	0.76
26:DB:44:G:OP1	30:DG:98:ARG:NH2	2.19	0.76
25:DA:2805:G:H2'	25:DA:2807:G:H8	1.51	0.76
1:AA:167:G:H2'	1:AA:168:G:H8	1.49	0.76
25:BA:2604:G:O2'	61:BA:4655:HOH:O	1.99	0.76
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.49	0.76
25:DA:1253:A:N7	61:DA:3854:HOH:O	2.18	0.76
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.67	0.76
25:BA:667:G:H21	25:BA:671:A:H2	1.34	0.76
1:CA:610:G:O6	61:CA:4180:HOH:O	2.04	0.76
25:DA:801:G:OP2	61:DA:3762:HOH:O	2.02	0.76
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.18	0.76
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.32	0.76
25:BA:934:A:H4'	25:BA:935:C:H5	1.51	0.76
1:AA:803:G:OP1	61:AA:4050:HOH:O	2.03	0.76
25:BA:1431:G:O2'	25:BA:1442:U:O2	2.03	0.76
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.19	0.76
43:BX:31:HIS:HD2	43:BX:33:LYS:H	1.29	0.76
43:DX:11:PRO:HB3	43:DX:92:LEU:HD11	1.66	0.76
26:BB:31:C:O2	26:BB:53:A:N6	2.19	0.76
1:AA:975:A:H4'	1:AA:976:G:H5''	1.67	0.76
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.66	0.76
25:BA:2331:G:H22	38:BS:3:ARG:HE	1.34	0.75
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.20	0.75
1:CA:323:U:OP1	20:CT:26:ASN:ND2	2.18	0.75
1:CA:999:C:N3	1:CA:1042:G:N2	2.34	0.75
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.68	0.75
25:DA:2371:G:O6	61:DA:3975:HOH:O	2.03	0.75
20:AT:9:ASN:HB3	20:AT:10:LEU:HD12	1.69	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:87:ARG:HH21	2:AB:219:VAL:HG12	1.51	0.75
1:AA:348:G:H2'	1:AA:349:A:C5'	2.16	0.75
29:BF:13:SER:HA	29:BF:127:GLU:HG3	1.66	0.75
25:BA:2331:G:H22	38:BS:3:ARG:NE	1.85	0.75
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.19	0.75
15:CO:14:GLU:OE2	15:CO:84:LYS:NZ	2.20	0.75
25:DA:1762:A:N1	61:DA:4178:HOH:O	2.18	0.75
25:DA:1412:A:H2'	25:DA:1413:G:C8	2.21	0.75
25:BA:2732:G:OP2	61:BA:4645:HOH:O	2.03	0.75
1:AA:954:G:H21	1:AA:1227:A:H62	1.30	0.75
1:AA:165:C:H2'	1:AA:166:G:H8	1.52	0.75
1:AA:474:G:H2'	1:AA:475:G:H8	1.51	0.75
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.52	0.75
25:DA:1376:C:OP2	61:DA:3757:HOH:O	2.05	0.75
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.20	0.75
25:BA:880:U:O2	35:BP:55:ARG:NH2	2.20	0.75
25:BA:2510:C:OP2	61:BA:4510:HOH:O	2.05	0.75
1:AA:180:U:O2	1:AA:196:A:N6	2.19	0.75
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.67	0.74
25:BA:945:A:O2'	25:BA:946:A:O5'	2.05	0.74
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.67	0.74
25:BA:1065:U:H3	25:BA:1188:A:H62	1.36	0.74
25:DA:2049:G:OP2	61:DA:3941:HOH:O	2.05	0.74
32:BI:77:LEU:HB3	32:BI:142:VAL:HG12	1.68	0.74
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.19	0.74
25:DA:452:G:OP2	61:DA:4105:HOH:O	2.04	0.74
25:BA:2059:G:N7	61:BA:4504:HOH:O	2.20	0.74
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.35	0.74
25:DA:1315:C:OP2	61:DA:4076:HOH:O	2.05	0.74
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.32	0.74
7:AG:62:PHE:HA	7:AG:124:LEU:HD22	1.70	0.74
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.69	0.74
25:BA:1356:G:OP2	53:B7:9:ARG:NH1	2.20	0.74
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.20	0.74
39:DT:26:ASP:OD1	39:DT:120:ARG:NH2	2.21	0.74
1:CA:1223:C:H5''	1:CA:1224:G:H5'	1.68	0.74
25:BA:2365:G:N7	61:BA:4327:HOH:O	2.19	0.74
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.68	0.74
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.20	0.74
25:BA:591:U:O4	61:BA:4046:HOH:O	2.05	0.74
3:CC:32:LEU:HD12	3:CC:59:ARG:HH12	1.53	0.74
1:AA:574:A:OP2	61:AA:4004:HOH:O	2.04	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2287:A:H62	25:DA:2344:U:H3	1.31	0.74
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.21	0.74
25:BA:130:G:O6	61:BA:4550:HOH:O	2.04	0.74
1:CA:1153:C:H42	1:CA:1154:G:N2	1.86	0.74
8:AH:49:GLU:HG2	8:AH:62:TYR:HE2	1.53	0.74
25:DA:848:G:H2'	25:DA:849:A:C8	2.22	0.74
25:DA:832:G:OP1	61:DA:4165:HOH:O	2.06	0.74
1:CA:998:G:H1	1:CA:1043:C:N4	1.83	0.73
1:AA:1054:C:OP1	61:AA:4053:HOH:O	2.04	0.73
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.21	0.73
1:CA:804:U:OP1	61:CA:4020:HOH:O	2.06	0.73
25:BA:1513:G:HO2'	25:BA:1593:C:HO2'	1.33	0.73
1:AA:1162:C:H42	1:AA:1174:G:H1	1.35	0.73
25:BA:874:U:OP1	61:BA:4633:HOH:O	2.05	0.73
1:CA:504:C:OP1	61:CA:4009:HOH:O	2.05	0.73
25:BA:1809:U:O2	61:BA:4722:HOH:O	2.05	0.73
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.24	0.73
25:DA:2248:C:OP2	61:DA:3945:HOH:O	2.06	0.73
2:CB:163:PHE:HD1	2:CB:185:ILE:HG13	1.53	0.73
25:DA:919:G:N2	25:DA:2269:A:OP2	2.21	0.73
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.53	0.73
1:AA:184:G:H2'	1:AA:185:A:H8	1.54	0.73
25:DA:963:U:OP2	61:DA:4173:HOH:O	2.04	0.73
1:CA:316:G:OP2	1:CA:351:G:O2'	2.06	0.73
25:BA:2227:G:H5'	25:BA:2228:G:N7	2.03	0.73
43:BX:31:HIS:CD2	43:BX:33:LYS:H	2.07	0.73
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.89	0.73
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.02	0.73
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.71	0.73
1:AA:812:C:N3	61:AA:4028:HOH:O	2.22	0.73
2:CB:91:PRO:HG2	2:CB:155:LEU:HD23	1.71	0.73
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.21	0.73
1:CA:959:A:HO2'	1:CA:984:C:HO2'	1.37	0.73
25:BA:985:G:OP1	61:BA:4728:HOH:O	2.07	0.73
1:CA:664:G:P	18:CR:64:ARG:HH22	2.10	0.73
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.87	0.73
50:D4:38:LYS:O	50:D4:40:HIS:N	2.21	0.73
25:DA:1817:G:OP1	27:DD:88:ARG:NH2	2.21	0.73
1:AA:262:A:H2'	1:AA:263:A:C8	2.24	0.73
13:CM:27:LYS:HA	13:CM:27:LYS:HE2	1.69	0.73
25:DA:900:A:H2'	25:DA:901:A:C8	2.24	0.73
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.20	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.20	0.73
1:CA:989:C:N4	1:CA:1216:G:O6	2.17	0.73
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.22	0.73
25:BA:1398:U:OP2	61:BA:3932:HOH:O	2.05	0.73
1:AA:558:G:OP1	61:AA:4042:HOH:O	2.07	0.73
1:AA:266:G:H5''	1:AA:268:C:H41	1.53	0.73
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.70	0.73
30:DG:80:PHE:O	30:DG:82:LEU:N	2.20	0.73
40:DU:83:LEU:HD12	40:DU:88:ILE:HD12	1.70	0.72
30:BG:48:GLU:HA	30:BG:51:ARG:HE	1.53	0.72
25:DA:2749:A:H1'	31:DH:63:SER:HB3	1.71	0.72
1:CA:1251:A:HO2'	1:CA:1369:C:HO2'	1.32	0.72
1:AA:601:C:H2'	1:AA:602:A:C8	2.24	0.72
2:CB:52:GLU:HG2	2:CB:56:ARG:HH22	1.54	0.72
46:D0:27:GLU:HG3	46:D0:68:GLU:HA	1.71	0.72
25:BA:2745:G:OP1	28:BE:203:LYS:NZ	2.17	0.72
11:AK:15:ALA:HB1	11:AK:78:GLN:HB2	1.69	0.72
1:AA:1028:C:H42	1:AA:1033:G:H1	1.36	0.72
1:CA:1003:G:H1	1:CA:1035:A:H61	1.37	0.72
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.71	0.72
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.35	0.72
25:DA:963:U:OP1	61:DA:3740:HOH:O	2.08	0.72
1:AA:864:A:OP1	61:AA:4127:HOH:O	2.08	0.72
15:AO:56:LEU:O	15:AO:60:VAL:HG23	1.88	0.72
25:BA:2019:G:OP2	61:BA:4565:HOH:O	2.07	0.72
25:DA:574:C:OP1	61:DA:3788:HOH:O	2.08	0.72
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.72	0.72
1:AA:972:C:OP1	61:AA:4123:HOH:O	2.08	0.72
1:AA:881:G:P	12:AL:12:ARG:HH22	2.12	0.72
38:BS:15:ARG:O	38:BS:19:LYS:HG2	1.89	0.72
25:DA:1876:A:H2'	25:DA:1877:A:C8	2.24	0.72
25:BA:1695:C:OP1	61:BA:4516:HOH:O	2.07	0.72
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.72	0.72
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.63	0.72
25:DA:1670:C:OP1	61:DA:3750:HOH:O	2.07	0.72
25:DA:400:G:O6	61:DA:4274:HOH:O	2.06	0.72
1:AA:346:G:O6	1:AA:348:G:N2	2.23	0.72
27:DD:71:ASP:CB	27:DD:103:ARG:HH22	2.03	0.72
1:CA:1135:U:O2'	1:CA:1137:C:O2	2.05	0.72
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.72	0.72
50:B4:57:GLU:HB3	50:B4:58:ARG:HA	1.71	0.72
7:CG:68:ASN:ND2	7:CG:127:ALA:O	2.19	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.22	0.72
30:DG:136:ARG:HH11	30:DG:137:GLU:H	1.37	0.72
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.72	0.72
32:BI:48:GLU:HG2	32:BI:52:ARG:HH22	1.55	0.71
25:DA:731:C:OP1	61:DA:4224:HOH:O	2.08	0.71
51:B5:17:ASP:OD2	61:B5:602:HOH:O	2.07	0.71
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.70	0.71
30:BG:16:ARG:NE	30:BG:31:VAL:HG11	2.05	0.71
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.22	0.71
1:CA:693:G:H2'	1:CA:694:A:C8	2.25	0.71
1:AA:1027:C:O2'	1:AA:1034:G:N2	2.23	0.71
35:BP:50:ARG:HH21	54:B8:7:HIS:CD2	2.09	0.71
25:DA:89:G:H3'	25:DA:90:U:H5''	1.71	0.71
26:BB:48:A:H4'	38:BS:95:HIS:HD2	1.53	0.71
25:BA:1679:A:OP2	61:BA:4622:HOH:O	2.07	0.71
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.08	0.71
25:BA:2804:C:H2'	25:BA:2805:G:C8	2.24	0.71
25:DA:600:G:N3	61:DA:3733:HOH:O	2.23	0.71
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.22	0.71
25:BA:1379:C:OP2	61:BA:4121:HOH:O	2.07	0.71
25:DA:11:G:H2'	25:DA:12:U:H5'	1.71	0.71
10:AJ:7:LYS:HE2	10:AJ:9:ARG:HH12	1.55	0.71
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.24	0.71
2:CB:96:ARG:HD2	2:CB:98:LEU:HD22	1.72	0.71
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.23	0.71
1:AA:1036:G:H5'	1:AA:1037:C:H5	1.55	0.71
25:DA:2267:A:H5''	25:DA:2268:A:H5'	1.71	0.71
25:DA:819:A:OP2	25:DA:1187:G:N2	2.19	0.71
46:B0:40:GLN:HE21	46:B0:57:PHE:HB3	1.55	0.71
1:CA:21:G:OP1	61:CA:4062:HOH:O	2.07	0.71
25:BA:2228:G:O2'	25:BA:2229:A:OP1	2.07	0.71
1:CA:148:G:H2'	1:CA:149:A:H8	1.54	0.71
49:D3:8:LEU:HD13	49:D3:31:LEU:HD23	1.73	0.71
25:DA:1665:A:OP2	61:DA:4385:HOH:O	2.08	0.71
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.23	0.71
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.19	0.71
36:DQ:34:LEU:HD11	36:DQ:129:THR:HB	1.73	0.71
1:CA:1189:C:O2	61:CA:4087:HOH:O	2.08	0.71
1:AA:1223:C:H5''	1:AA:1224:G:H5'	1.72	0.71
4:AD:15:GLU:HG3	4:AD:63:LYS:HE2	1.72	0.71
25:BA:597:C:OP1	61:BA:3998:HOH:O	2.09	0.71
31:DH:159:GLU:HG3	31:DH:169:VAL:HG11	1.72	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.23	0.70
46:D0:14:ARG:NH1	61:D0:202:HOH:O	2.23	0.70
3:CC:73:PRO:HB3	3:CC:103:VAL:HG11	1.70	0.70
1:CA:954:G:H21	1:CA:1227:A:H62	1.39	0.70
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.26	0.70
25:DA:1488:G:C6	25:DA:1489:U:C5	2.78	0.70
25:DA:2819:G:N7	61:DA:4006:HOH:O	2.24	0.70
30:BG:102:PHE:HE1	30:BG:141:PHE:HE2	1.37	0.70
1:AA:411:A:OP1	4:AD:30:LYS:NZ	2.19	0.70
25:DA:287:C:H2'	25:DA:288:C:H6	1.56	0.70
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.25	0.70
1:AA:17:U:H2'	1:AA:18:C:C6	2.26	0.70
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.72	0.70
1:AA:167:G:H2'	1:AA:168:G:C8	2.26	0.70
1:CA:1142:G:H3'	1:CA:1143:G:C8	2.26	0.70
9:AI:53:VAL:O	9:AI:55:ALA:N	2.21	0.70
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.24	0.70
25:BA:932:C:H3'	25:BA:933:C:H5''	1.73	0.70
25:BA:322:G:N7	61:BA:3883:HOH:O	2.23	0.70
25:DA:1310:G:OP2	53:D7:9:ARG:NH1	2.21	0.70
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.09	0.70
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.25	0.70
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.56	0.70
25:BA:2862:G:OP1	61:BA:4875:HOH:O	2.10	0.70
10:AJ:78:ASN:O	10:AJ:80:LYS:N	2.25	0.70
1:CA:572:A:OP1	61:CA:4046:HOH:O	2.10	0.70
35:BP:33:ARG:O	61:BP:301:HOH:O	2.07	0.70
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.24	0.70
1:AA:221:C:H2'	1:AA:222:U:H6	1.54	0.70
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.24	0.70
25:DA:1235:G:OP1	61:DA:4361:HOH:O	2.08	0.70
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.73	0.70
25:BA:1055:A:OP2	33:BN:37:LYS:NZ	2.19	0.70
25:DA:827:U:OP1	61:DA:4180:HOH:O	2.08	0.70
1:AA:1129:C:N3	1:AA:1143:G:N2	2.37	0.70
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.27	0.70
1:CA:811:C:N4	61:CA:4026:HOH:O	2.25	0.70
25:BA:147:U:O4	61:BA:4550:HOH:O	2.06	0.70
25:BA:2101:U:O4	61:BA:4300:HOH:O	2.09	0.70
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.73	0.70
50:D4:68:ARG:HG3	50:D4:68:ARG:HH21	1.54	0.70
45:DZ:93:ASP:O	45:DZ:131:ARG:NH1	2.23	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.74	0.70
25:DA:2705:A:OP2	61:DA:4123:HOH:O	2.08	0.70
25:DA:2206:G:H3'	25:DA:2207:G:H8	1.56	0.70
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	1.90	0.70
36:DQ:48:GLU:OE1	36:DQ:51:ARG:NH2	2.24	0.70
36:BQ:10:ARG:NH1	61:BQ:302:HOH:O	2.25	0.70
1:AA:148:G:HO2'	1:AA:149:A:H8	1.40	0.70
25:BA:70:A:N7	43:BX:31:HIS:HE1	1.90	0.69
1:CA:1269:A:N1	1:CA:1312:G:O2'	2.24	0.69
25:BA:284:G:O6	61:BA:4714:HOH:O	2.09	0.69
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.73	0.69
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.74	0.69
25:BA:1249:A:H2	25:BA:1287:A:H62	1.40	0.69
2:CB:77:ALA:HB2	2:CB:211:ILE:HD13	1.73	0.69
25:BA:9:U:N3	25:BA:2641:A:H2	1.89	0.69
20:CT:49:ALA:HB3	20:CT:99:LEU:HD22	1.74	0.69
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.27	0.69
1:AA:1292:U:OP2	7:AG:41:ARG:NH2	2.24	0.69
1:CA:1002:G:H2'	1:CA:1003:G:C8	2.27	0.69
25:BA:388:A:H2'	25:BA:389:G:C8	2.27	0.69
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.27	0.69
25:DA:1671:U:HO2'	25:DA:1673:U:H5	1.40	0.69
25:DA:993:G:OP1	40:DU:50:ARG:NH2	2.25	0.69
25:DA:1803:A:O2'	27:DD:259:THR:HG21	1.92	0.69
5:AE:100:VAL:HG22	5:AE:118:ILE:HG22	1.74	0.69
52:D6:13:CYS:SG	52:D6:47:THR:HG21	2.33	0.69
2:CB:178:ARG:HH22	8:CH:68:ARG:NH1	1.91	0.69
31:BH:56:SER:OG	31:BH:57:ASP:N	2.26	0.69
25:DA:1017:G:N7	61:DA:4208:HOH:O	2.25	0.69
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.58	0.69
25:DA:1637:A:OP2	61:DA:4412:HOH:O	2.10	0.69
25:BA:2457:G:OP1	29:BF:74:ARG:NH2	2.26	0.69
25:BA:1831:C:OP1	27:BD:264:LYS:NZ	2.24	0.69
25:BA:1480:A:H61	25:BA:1605:A:H62	1.40	0.69
1:CA:503:C:OP2	12:CL:116:SER:HB3	1.93	0.69
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.26	0.69
1:AA:1025:U:O2	1:AA:1036:G:O6	2.11	0.69
25:DA:1509(B):A:H2'	25:DA:1510:G:C8	2.28	0.69
1:CA:652:U:O4	1:CA:752:G:O2'	2.10	0.69
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.58	0.69
25:DA:2682:U:OP2	61:DA:3802:HOH:O	2.09	0.69
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.74	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.25	0.69
25:DA:1430:C:H2'	25:DA:1431:U:H6	1.57	0.69
4:CD:15:GLU:HG2	4:CD:63:LYS:HB3	1.75	0.69
25:DA:1143:A:OP1	33:DN:25:ARG:NH2	2.26	0.69
25:BA:2101:U:O3'	47:B1:35:THR:OG1	2.11	0.69
29:DF:185:ASP:HA	29:DF:188:ARG:HD3	1.75	0.69
44:BY:102:CYS:SG	44:BY:103:GLY:N	2.66	0.69
1:CA:532:A:O2'	1:CA:533:A:OP1	2.11	0.69
25:BA:1648:U:O4	61:BA:4117:HOH:O	2.08	0.69
25:DA:649:G:H4'	54:D8:46:ARG:HH22	1.57	0.69
19:AS:9:VAL:HG21	50:B4:61:ARG:HH22	1.57	0.69
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.26	0.69
25:BA:551:A:OP1	61:BA:4499:HOH:O	2.11	0.69
28:DE:72:VAL:HG22	28:DE:73:GLU:HG2	1.75	0.69
18:CR:54:ARG:HH11	18:CR:54:ARG:HB2	1.58	0.69
1:AA:596:C:OP2	61:AA:4043:HOH:O	2.11	0.69
1:CA:837:G:H1	1:CA:849:C:H42	1.41	0.69
4:AD:120:LEU:HB3	4:AD:126:ILE:HD11	1.73	0.69
25:BA:2619:G:O3'	61:BA:4188:HOH:O	2.11	0.69
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.75	0.69
1:AA:1003:G:N2	1:AA:1038:C:N3	2.41	0.68
28:DE:72:VAL:HG13	28:DE:73:GLU:O	1.93	0.68
1:CA:891:U:OP2	61:CA:4083:HOH:O	2.11	0.68
9:CI:24:GLY:HA2	9:CI:59:PHE:O	1.93	0.68
29:DF:195:ASP:OD1	29:DF:196:LEU:N	2.26	0.68
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.58	0.68
25:DA:2016:U:H2'	25:DA:2017:U:C6	2.29	0.68
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.74	0.68
6:AF:69:GLU:O	6:AF:72:VAL:HG12	1.93	0.68
25:DA:1963:U:O2'	61:DA:4441:HOH:O	2.11	0.68
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	1.73	0.68
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.56	0.68
1:AA:839:U:O2'	1:AA:840:C:OP1	2.11	0.68
25:BA:272:U:H4'	32:BI:50:ARG:HH12	1.58	0.68
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.75	0.68
25:BA:1315:A:N7	61:BA:4265:HOH:O	2.25	0.68
1:AA:21:G:OP1	61:AA:4080:HOH:O	2.10	0.68
1:AA:35:G:O2'	12:AL:118:SER:O	2.12	0.68
1:AA:1125:U:O2'	1:AA:1126:U:OP2	2.10	0.68
10:AJ:5:ARG:NE	10:AJ:73:ASP:OD1	2.25	0.68
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.12	0.68
25:BA:2460:A:OP2	61:BA:4510:HOH:O	2.11	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2552:U:H2'	25:DA:2554:U:OP2	1.93	0.68
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.76	0.68
61:DA:4599:HOH:O	46:D0:4:LYS:NZ	2.24	0.68
1:CA:1003:G:H1	1:CA:1035:A:N6	1.91	0.68
25:BA:1576:G:C6	25:BA:1577:C:N4	2.61	0.68
25:BA:1815:A:OP2	61:BA:4519:HOH:O	2.10	0.68
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.76	0.68
44:DY:102:CYS:SG	44:DY:103:GLY:N	2.67	0.68
2:CB:144:ARG:NH1	2:CB:148:TYR:OH	2.26	0.68
50:D4:44:THR:O	50:D4:46:GLN:N	2.27	0.68
39:BT:24:PRO:HA	39:BT:49:VAL:HG22	1.74	0.68
25:BA:1463:C:O2'	25:BA:1633:A:N3	2.27	0.68
19:CS:42:PRO:HG3	50:D4:61:ARG:HG2	1.75	0.68
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.28	0.68
47:D1:50:ARG:HG2	47:D1:59:THR:HB	1.76	0.68
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.74	0.68
13:CM:3:ARG:HE	13:CM:4:ILE:HG22	1.58	0.68
25:BA:927:G:N2	25:BA:944:C:N3	2.41	0.68
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.27	0.68
1:CA:1193:G:O2'	5:CE:25:ARG:NH2	2.27	0.68
25:DA:639:U:H2'	25:DA:640:C:C6	2.29	0.68
12:CL:57:LYS:HG2	12:CL:67:THR:HG22	1.73	0.68
27:DD:132:PRO:HG2	27:DD:135:PHE:HD2	1.57	0.68
1:AA:836:G:OP2	18:AR:61:LYS:NZ	2.27	0.68
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.76	0.68
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.27	0.68
25:DA:1200:C:H5'	61:DA:3770:HOH:O	1.94	0.68
1:CA:735:C:H2'	1:CA:736:C:H6	1.58	0.68
1:CA:419:C:OP1	1:CA:513:C:O2'	2.10	0.68
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.74	0.68
1:AA:661:G:H1	1:AA:744:C:H42	1.39	0.68
1:CA:646:U:H2'	1:CA:647:C:C6	2.29	0.68
25:DA:2393:A:H5''	35:DP:63:PRO:HB3	1.76	0.68
25:DA:2394:C:OP2	54:D8:30:ARG:NH1	2.27	0.68
25:BA:1047:A:OP2	61:BA:3917:HOH:O	2.11	0.68
29:BF:8:GLN:NE2	29:BF:21:ALA:HB2	2.09	0.68
2:CB:210:SER:O	2:CB:214:ILE:HG12	1.94	0.68
1:AA:664:G:H22	1:AA:741:G:H1	1.39	0.68
1:CA:460:G:O6	1:CA:470:C:H5''	1.93	0.68
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.26	0.68
1:AA:1086:U:H3	1:AA:1099:G:H22	1.42	0.68
25:BA:2734:A:N7	61:BA:4015:HOH:O	2.27	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:278:G:OP2	17:AQ:92:ARG:NH2	2.27	0.68
25:DA:2287:A:N6	25:DA:2344:U:H3	1.92	0.68
1:CA:474:G:H2'	1:CA:475:G:H8	1.58	0.68
25:BA:2212:G:H2'	25:BA:2213:G:O4'	1.93	0.68
25:DA:2427:C:OP1	61:DA:4257:HOH:O	2.11	0.68
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.26	0.68
1:AA:342:C:N3	1:AA:343:U:H5	1.92	0.67
61:BE:406:HOH:O	37:BR:3:HIS:NE2	2.27	0.67
5:CE:9:LYS:HB2	5:CE:112:LEU:HD11	1.76	0.67
25:DA:652(D):C:H42	25:DA:652(U):G:H1	1.42	0.67
25:BA:335:A:OP2	61:BA:4497:HOH:O	2.11	0.67
25:DA:1607:C:N4	25:DA:1622:G:OP2	2.27	0.67
1:AA:59:A:H3'	1:AA:331:G:H22	1.59	0.67
25:BA:1361:C:OP2	61:BA:4471:HOH:O	2.12	0.67
46:D0:24:LYS:HA	46:D0:24:LYS:HE2	1.76	0.67
47:D1:65:SER:HG	47:D1:66:HIS:HD1	1.39	0.67
1:CA:1042:G:O2'	1:CA:1043:C:O4'	2.12	0.67
1:CA:382:A:H2'	1:CA:383:A:C8	2.28	0.67
1:AA:946:A:H2'	1:AA:947:G:C8	2.28	0.67
25:DA:2006:C:OP2	61:DA:4388:HOH:O	2.12	0.67
25:DA:962:G:OP1	61:DA:4173:HOH:O	2.12	0.67
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.76	0.67
47:D1:77:ALA:HA	47:D1:80:LEU:HD13	1.77	0.67
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.74	0.67
1:CA:565:U:OP2	61:CA:4054:HOH:O	2.13	0.67
25:BA:2081:A:OP2	61:BA:4212:HOH:O	2.12	0.67
9:AI:4:TYR:HB2	9:AI:19:LEU:HB2	1.77	0.67
25:BA:2361:G:OP1	61:BA:3947:HOH:O	2.12	0.67
25:DA:588:U:OP2	61:DA:3873:HOH:O	2.11	0.67
25:DA:994:C:OP2	40:DU:54:LYS:NZ	2.28	0.67
1:CA:1251:A:O2'	1:CA:1369:C:O2'	2.08	0.67
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.10	0.67
50:D4:62:ARG:O	50:D4:64:GLY:N	2.28	0.67
25:DA:272:G:H4'	25:DA:272(A):U:H5''	1.74	0.67
25:DA:2431:U:OP2	61:DA:3860:HOH:O	2.12	0.67
51:B5:16:ARG:NH1	51:B5:17:ASP:OD1	2.28	0.67
23:CX:73:A:H5''	23:CX:74:C:H5'	1.77	0.67
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.43	0.67
25:BA:1391:C:OP2	61:BA:3931:HOH:O	2.10	0.67
25:BA:2460:A:OP1	61:BA:4034:HOH:O	2.11	0.67
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.28	0.67
1:AA:1108:G:O6	61:AA:4120:HOH:O	2.10	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:754:C:H2'	25:DA:755:C:H6	1.60	0.67
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.29	0.67
25:DA:1971:A:OP1	61:DA:3909:HOH:O	2.13	0.67
25:BA:324:A:OP2	44:BY:86:ARG:NH2	2.28	0.67
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.10	0.67
1:CA:1226:C:N4	13:CM:104:ARG:HG3	2.10	0.67
1:CA:117:G:OP2	61:CA:4053:HOH:O	2.13	0.67
25:DA:2430:A:OP2	61:DA:4180:HOH:O	2.12	0.67
9:CI:33:PHE:HE1	9:CI:43:ALA:HB1	1.59	0.67
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.28	0.67
25:BA:2420:U:OP2	61:BA:4137:HOH:O	2.13	0.67
30:DG:16:ARG:O	30:DG:20:ILE:HG13	1.95	0.67
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.27	0.67
25:DA:1359:A:H2'	25:DA:1360:A:H5'	1.77	0.67
32:DI:104:GLN:O	32:DI:105:HIS:ND1	2.28	0.67
6:AF:68:PRO:HB2	6:AF:71:ARG:HG3	1.77	0.67
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.20	0.67
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.30	0.67
14:AN:37:PHE:HB3	14:AN:39:LEU:HD12	1.76	0.67
1:CA:1004:A:C6	1:CA:1037:C:C2	2.82	0.66
23:CX:64:G:H4'	36:DQ:10:ARG:HH21	1.59	0.66
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.31	0.66
27:BD:132:PRO:HG2	27:BD:135:PHE:HD2	1.60	0.66
1:CA:1170:A:O2'	1:CA:1171:G:O4'	2.12	0.66
45:BZ:69:THR:HG22	45:BZ:90:VAL:HA	1.77	0.66
25:BA:2897:U:H2'	25:BA:2898:C:C6	2.30	0.66
25:DA:602:G:O2'	25:DA:655:A:N6	2.28	0.66
25:BA:449:A:OP2	61:BA:3954:HOH:O	2.13	0.66
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.30	0.66
25:BA:1007:G:OP1	61:BA:4616:HOH:O	2.12	0.66
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.14	0.66
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.27	0.66
1:AA:1422:G:H5''	34:BO:48:PRO:HB3	1.77	0.66
1:AA:1321:C:H5''	1:AA:1322:C:H2'	1.77	0.66
25:DA:1652:A:OP1	37:DR:8:ARG:NH1	2.28	0.66
45:DZ:108:PRO:HG3	45:DZ:141:VAL:HB	1.77	0.66
33:DN:42:TRP:HA	33:DN:48:MET:HE1	1.78	0.66
25:DA:1606:G:OP1	61:DA:4577:HOH:O	2.13	0.66
33:DN:20:GLY:HA2	33:DN:61:ARG:HE	1.58	0.66
25:BA:2600:G:OP2	61:BA:4789:HOH:O	2.14	0.66
25:DA:2685:G:O6	61:DA:3896:HOH:O	2.09	0.66
48:B2:16:LEU:O	48:B2:67:LYS:NZ	2.27	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:773:U:OP1	61:DA:4405:HOH:O	2.12	0.66
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.28	0.66
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.76	0.66
23:CX:23:C:H2'	23:CX:24:U:C6	2.30	0.66
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.10	0.66
1:AA:243:A:H4'	1:AA:244:U:H5''	1.77	0.66
25:DA:1301:A:OP1	61:DA:4411:HOH:O	2.13	0.66
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.29	0.66
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.30	0.66
29:DF:18:ARG:NH2	29:DF:127:GLU:OE1	2.28	0.66
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.78	0.66
29:DF:13:SER:HA	29:DF:127:GLU:HG3	1.77	0.66
25:BA:2817:G:N1	25:BA:2902:G:O6	2.19	0.66
25:DA:1774:C:OP1	61:DA:3936:HOH:O	2.13	0.66
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.11	0.66
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.61	0.66
42:BW:12:ILE:HD13	42:BW:17:VAL:HG13	1.77	0.66
25:BA:2324:U:H5'	30:BG:88:ILE:HD11	1.78	0.66
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.13	0.66
1:AA:407:G:H5''	4:AD:115:ARG:HB3	1.78	0.66
2:AB:166:ASP:HB3	2:AB:169:LYS:HB2	1.78	0.66
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.60	0.66
1:CA:1120:G:O6	1:CA:1154:G:N2	2.29	0.66
1:AA:117:G:OP2	61:AA:4071:HOH:O	2.14	0.66
50:D4:61:ARG:O	50:D4:61:ARG:NH1	2.28	0.66
27:BD:108:PRO:HD2	27:BD:111:LEU:HG	1.78	0.66
25:DA:818:G:OP2	61:DA:3837:HOH:O	2.13	0.66
4:CD:43:HIS:HA	4:CD:46:LYS:HG3	1.77	0.66
25:DA:2070:G:OP2	61:DA:4339:HOH:O	2.13	0.66
25:BA:1091:A:OP1	25:BA:1091:A:H4'	1.94	0.65
1:CA:539:A:H2'	1:CA:540:G:C8	2.31	0.65
25:DA:900:A:H2'	25:DA:901:A:H8	1.61	0.65
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.30	0.65
10:CJ:29:ARG:HB2	10:CJ:84:GLN:HE22	1.60	0.65
26:DB:75:G:N2	45:DZ:87:ASP:OD1	2.28	0.65
1:CA:1236:A:O2'	1:CA:1304:G:H4'	1.96	0.65
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.28	0.65
25:DA:1313:U:OP1	61:DA:3981:HOH:O	2.15	0.65
2:CB:47:THR:O	2:CB:51:LEU:N	2.27	0.65
25:BA:839:G:OP2	61:BA:4064:HOH:O	2.13	0.65
19:CS:15:LEU:HD12	19:CS:18:LYS:HD2	1.79	0.65
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.31	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:CJ:42:THR:HG21	10:CJ:68:HIS:HD2	1.61	0.65
1:CA:56:U:H2'	1:CA:57:G:C8	2.31	0.65
35:BP:59:LEU:HD11	54:B8:10:ALA:HB2	1.78	0.65
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.78	0.65
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.78	0.65
25:DA:411:G:OP1	61:DA:3857:HOH:O	2.14	0.65
1:CA:333:G:H4'	20:CT:16:HIS:CE1	2.30	0.65
28:DE:14:ILE:HD11	28:DE:173:VAL:HG11	1.76	0.65
25:BA:601:A:OP2	61:BA:4002:HOH:O	2.14	0.65
2:AB:15:VAL:HB	2:AB:209:ARG:HG2	1.79	0.65
30:DG:25:TYR:HB3	30:DG:30:GLU:HB2	1.79	0.65
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.77	0.65
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.30	0.65
25:BA:2832:G:OP2	61:BE:406:HOH:O	2.13	0.65
1:AA:1198:G:OP2	61:AA:4053:HOH:O	2.14	0.65
44:BY:98:VAL:HG12	44:BY:105:ALA:HA	1.78	0.65
4:AD:31:CYS:SG	4:AD:32:ALA:N	2.69	0.65
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	1.79	0.65
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.32	0.65
1:AA:159:G:H2'	1:AA:161:A:OP2	1.97	0.65
25:DA:31:C:OP1	61:DA:4153:HOH:O	2.14	0.65
25:BA:950:C:H2'	25:BA:951:U:C6	2.32	0.65
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.77	0.65
2:AB:87:ARG:NH1	2:AB:233:SER:OG	2.30	0.65
1:AA:1095:U:OP1	1:AA:1108:G:N2	2.30	0.65
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.12	0.65
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.78	0.65
8:CH:49:GLU:HG2	8:CH:62:TYR:HE2	1.62	0.65
25:BA:849:A:OP1	61:BA:4293:HOH:O	2.13	0.65
25:BA:2349:G:OP1	61:BA:4028:HOH:O	2.13	0.65
35:BP:44:GLY:O	61:BP:302:HOH:O	2.14	0.65
23:CX:40:C:H2'	23:CX:41:C:H6	1.62	0.65
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.62	0.65
1:CA:558:G:OP1	61:CA:4171:HOH:O	2.14	0.65
53:B7:33:ARG:NH2	61:B7:4001:HOH:O	2.30	0.65
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.14	0.65
32:DI:77:LEU:HB3	32:DI:142:VAL:HG12	1.79	0.65
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.32	0.65
25:BA:2442:A:OP2	61:BA:4633:HOH:O	2.14	0.65
1:AA:659:U:H2'	1:AA:660:G:H8	1.62	0.65
1:AA:673:G:H2'	1:AA:674:G:C8	2.32	0.65
25:DA:370:G:OP1	25:DA:403:U:N3	2.24	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	1.77	0.64
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.26	0.64
4:AD:173:TRP:NE1	4:AD:193:ASP:OD1	2.29	0.64
25:BA:1398:U:OP1	61:BA:3990:HOH:O	2.15	0.64
25:DA:1430:C:H2'	25:DA:1431:U:C6	2.32	0.64
17:CQ:22:LEU:HD13	17:CQ:41:LYS:HG3	1.79	0.64
43:BX:92:LEU:C	43:BX:94:GLY:H	2.00	0.64
1:CA:353:A:H8	1:CA:353:A:H5'	1.62	0.64
39:DT:65:LYS:HE2	39:DT:67:SER:HB2	1.79	0.64
25:DA:2680:C:H1'	28:DE:187:ALA:HB1	1.78	0.64
54:B8:6:THR:HG22	54:B8:63:PRO:HD2	1.79	0.64
25:BA:589:U:H5''	35:BP:29:LYS:HE3	1.79	0.64
1:CA:662:G:O2'	1:CA:836:G:OP1	2.14	0.64
25:DA:2708:G:H1'	37:DR:71:GLN:HE22	1.62	0.64
5:AE:137:GLU:HG2	5:AE:140:ARG:HH11	1.63	0.64
2:AB:210:SER:O	2:AB:214:ILE:HG12	1.97	0.64
30:DG:129:GLY:O	30:DG:161:THR:HB	1.97	0.64
25:DA:143:G:H2'	25:DA:143(A):C:C6	2.32	0.64
37:BR:28:LEU:HD12	37:BR:48:VAL:HG21	1.79	0.64
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.78	0.64
25:BA:1848:G:OP1	27:BD:88:ARG:NH2	2.30	0.64
25:DA:455:C:N3	25:DA:472:A:H2'	2.12	0.64
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.32	0.64
1:CA:69:G:H2'	1:CA:70:G:H8	1.62	0.64
1:CA:1154:G:N7	1:CA:1155:G:C4	2.66	0.64
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.61	0.64
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.62	0.64
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.79	0.64
45:DZ:153:SER:OG	45:DZ:154:ASP:OD1	2.14	0.64
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.28	0.64
25:DA:524:U:H2'	25:DA:525:U:C6	2.33	0.64
25:DA:2062:A:OP1	61:DA:3798:HOH:O	2.14	0.64
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	1.77	0.64
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.32	0.64
19:CS:37:ARG:O	19:CS:70:LYS:NZ	2.28	0.64
1:AA:457:C:H2'	1:AA:458:C:C6	2.33	0.64
1:AA:476:G:H2'	1:AA:477:A:O4'	1.98	0.64
20:CT:86:ARG:O	20:CT:90:GLN:HB2	1.98	0.64
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.12	0.64
1:AA:56:U:H2'	1:AA:57:G:C8	2.33	0.64
1:AA:123:C:OP1	1:AA:311:C:O2'	2.13	0.64
23:AX:6:G:H1	23:AX:67:C:H42	1.45	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:CJ:16:LEU:HD13	10:CJ:70:ARG:HG2	1.78	0.64
50:D4:64:GLY:C	50:D4:66:SER:H	2.01	0.64
25:BA:2405:A:H5'	35:BP:63:PRO:HB3	1.79	0.64
59:CX:101:FME:HCN	25:DA:2451:A:H2	1.62	0.64
4:CD:92:VAL:O	4:CD:96:LEU:HD22	1.97	0.64
28:DE:150:VAL:HG13	28:DE:154:LYS:HG3	1.79	0.64
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.16	0.64
25:DA:1776:G:OP2	61:DA:3756:HOH:O	2.14	0.64
1:CA:1133:G:H1	1:CA:1141:C:N4	1.95	0.64
1:CA:1015:A:H2'	1:CA:1016:A:C8	2.33	0.64
1:AA:193:C:H2'	1:AA:194:C:H6	1.61	0.64
1:CA:1312:G:N7	19:CS:2:PRO:HG2	2.12	0.64
1:AA:161:A:H2'	1:AA:162:A:C8	2.32	0.64
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.78	0.64
25:DA:1973:G:OP1	61:DA:4138:HOH:O	2.15	0.64
37:DR:97:VAL:HG22	37:DR:114:VAL:HG22	1.79	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.31	0.64
1:CA:814:A:H2'	1:CA:816:A:H5''	1.78	0.64
1:AA:1494:G:HO2'	25:BA:1934:A:HO2'	1.43	0.64
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.28	0.64
1:AA:1042:G:O2'	1:AA:1043:C:O4'	2.14	0.64
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.31	0.64
25:DA:586:A:N1	25:DA:809:G:O2'	2.25	0.64
1:AA:1530:G:H2'	1:AA:1531:A:O4'	1.97	0.64
25:DA:594:U:H3	25:DA:663:G:H1	1.44	0.64
25:BA:1997:G:OP2	61:BA:4529:HOH:O	2.15	0.64
25:DA:1604:C:OP2	61:DA:4392:HOH:O	2.15	0.64
25:DA:2781:A:H5''	25:DA:2782:G:H5'	1.79	0.64
37:BR:53:HIS:ND1	37:BR:94:TYR:OH	2.30	0.64
26:DB:11:C:OP2	26:DB:12:C:N4	2.27	0.64
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.80	0.64
16:AP:19:ILE:HD13	16:AP:36:ILE:HG13	1.78	0.64
1:AA:630:G:H2'	1:AA:631:G:H8	1.62	0.64
2:CB:16:HIS:CB	2:CB:204:ASN:HB3	2.24	0.64
25:DA:2298:A:C6	25:DA:2321:G:N1	2.66	0.64
25:BA:778:C:OP2	61:BA:4592:HOH:O	2.15	0.64
28:DE:73:GLU:HG3	28:DE:73:GLU:O	1.96	0.64
19:CS:64:GLU:HB2	50:D4:59:PHE:HE1	1.62	0.64
3:AC:36:ASP:O	3:AC:40:ARG:HG3	1.98	0.64
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.79	0.64
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.30	0.64
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.13	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.28	0.63
25:BA:641:G:OP1	29:BF:40:GLN:NE2	2.24	0.63
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.31	0.63
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.33	0.63
25:DA:365:C:OP2	61:DA:4447:HOH:O	2.15	0.63
36:DQ:59:ARG:O	36:DQ:61:GLY:N	2.23	0.63
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.80	0.63
13:CM:22:ILE:HB	13:CM:25:ILE:HD13	1.79	0.63
1:AA:518:C:O2'	1:AA:530:G:N2	2.31	0.63
1:CA:404:U:H5'	4:CD:122:ARG:HD3	1.80	0.63
1:CA:953:G:H5'	1:CA:965:A:N6	2.13	0.63
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.14	0.63
5:CE:78:HIS:HE1	5:CE:143:ARG:H	1.45	0.63
1:AA:945:G:OP2	61:AA:4057:HOH:O	2.15	0.63
1:CA:59:A:H3'	1:CA:331:G:H22	1.62	0.63
25:BA:2369:U:OP1	46:B0:20:ARG:NH1	2.31	0.63
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.80	0.63
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.13	0.63
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.34	0.63
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.29	0.63
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.13	0.63
25:BA:53:G:O2'	53:B7:35:ARG:HD3	1.98	0.63
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.63	0.63
25:BA:2701:U:H4'	25:BA:2702:C:O5'	1.97	0.63
1:CA:405:U:O4	4:CD:2:GLY:N	2.32	0.63
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.81	0.63
25:DA:1667:G:O2'	25:DA:1991:U:O4	2.13	0.63
50:B4:24:THR:OG1	50:B4:25:TYR:N	2.31	0.63
25:DA:1766:U:H2'	25:DA:1767:C:H6	1.63	0.63
25:DA:2816:C:O3'	37:DR:99:LYS:NZ	2.32	0.63
1:CA:1320:C:H5'	19:CS:70:LYS:HG3	1.80	0.63
2:CB:56:ARG:HB3	2:CB:56:ARG:HH11	1.63	0.63
25:BA:560:C:O3'	40:BU:53:ARG:NH1	2.31	0.63
2:CB:87:ARG:HE	2:CB:233:SER:HB3	1.63	0.63
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.33	0.63
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	1.80	0.63
1:AA:333:G:H4'	20:AT:16:HIS:CE1	2.33	0.63
26:DB:14:U:OP2	26:DB:70:C:O2'	2.14	0.63
25:DA:298:G:H5''	25:DA:299:A:OP1	1.98	0.63
4:CD:31:CYS:SG	4:CD:33:MET:N	2.71	0.63
25:BA:1701:A:OP2	61:BA:4089:HOH:O	2.15	0.63
25:DA:568:U:H5'	25:DA:945:A:N1	2.14	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1145:C:H4'	1:CA:1146:A:H5'	1.81	0.63
12:AL:79:GLU:HB3	12:AL:80:HIS:HD2	1.64	0.63
40:DU:92:ARG:HA	40:DU:95:LEU:HB2	1.81	0.63
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.80	0.63
2:AB:62:ALA:HB2	2:AB:222:ILE:HG22	1.80	0.63
25:BA:1044:C:OP1	61:BA:4480:HOH:O	2.15	0.63
11:CK:98:LEU:O	11:CK:101:SER:OG	2.13	0.63
25:DA:144:C:H2'	25:DA:145:G:H8	1.62	0.63
23:CX:48:C:C2	23:CX:59:A:H1'	2.34	0.63
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.31	0.63
4:AD:177:ASP:HB3	4:AD:182:LYS:HD3	1.81	0.63
25:BA:1020:C:OP1	61:BA:4060:HOH:O	2.16	0.63
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.32	0.63
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.28	0.63
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.28	0.63
1:AA:503:C:OP2	12:AL:116:SER:HB3	1.99	0.63
25:BA:599:U:OP1	61:BA:4467:HOH:O	2.15	0.63
15:AO:5:LYS:HD2	15:AO:5:LYS:H	1.63	0.63
27:DD:183:ARG:HG3	27:DD:270:ILE:HG12	1.81	0.63
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.81	0.63
25:DA:2803:C:H2'	25:DA:2804:C:H6	1.63	0.63
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.80	0.63
25:DA:1889:A:H2'	25:DA:1890:A:C8	2.33	0.63
25:DA:1721:G:H8	25:DA:1741:A:H62	1.46	0.63
2:AB:78:GLN:O	2:AB:81:VAL:HG23	1.98	0.63
5:AE:78:HIS:CD2	5:AE:142:LEU:HD23	2.34	0.63
25:DA:1688:U:O2	25:DA:1700:A:H5'	1.99	0.63
1:AA:200:G:H5'	1:AA:201:C:OP2	1.99	0.62
25:DA:1159:U:H2'	25:DA:1160:G:C8	2.32	0.62
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.34	0.62
1:CA:45:U:H2'	1:CA:46:G:C8	2.34	0.62
25:DA:2016:U:H2'	25:DA:2017:U:H6	1.64	0.62
50:D4:59:PHE:HA	50:D4:61:ARG:N	2.14	0.62
25:DA:2098:U:H2'	25:DA:2099:U:O4'	1.99	0.62
25:DA:2469:A:H4'	36:DQ:56:ARG:HD2	1.79	0.62
1:CA:585:G:OP1	17:CQ:37:LYS:NZ	2.24	0.62
1:AA:400:C:H5''	4:AD:73:ARG:HH22	1.63	0.62
29:DF:165:ARG:HG2	29:DF:168:ARG:NH2	2.14	0.62
1:AA:445:G:H2'	1:AA:446:G:C8	2.33	0.62
1:CA:1163:C:N3	1:CA:1173:G:N2	2.47	0.62
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.81	0.62
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.81	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:404:U:H5'	4:AD:122:ARG:HD2	1.81	0.62
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.63	0.62
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.15	0.62
25:BA:2367:C:H1'	46:B0:39:ARG:HH21	1.63	0.62
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.81	0.62
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.14	0.62
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.31	0.62
25:DA:2079:U:OP1	47:D1:21:ARG:NH2	2.32	0.62
25:DA:854:G:H2'	25:DA:855:G:H8	1.64	0.62
1:AA:187:C:H2'	1:AA:188:C:H6	1.65	0.62
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.32	0.62
8:AH:14:ARG:NH2	8:AH:83:ILE:O	2.33	0.62
1:AA:552:U:C2'	1:AA:553:A:H5'	2.29	0.62
1:AA:937:A:OP2	61:AA:4095:HOH:O	2.16	0.62
32:BI:40:THR:O	32:BI:44:LEU:HB2	1.99	0.62
1:AA:486:U:H2'	1:AA:487:A:C8	2.35	0.62
25:DA:62:C:H42	25:DA:93:G:H1	1.46	0.62
16:AP:43:LYS:HG2	16:AP:48:TRP:CD2	2.34	0.62
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.15	0.62
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.17	0.62
1:AA:560:U:O2'	1:AA:561:U:OP2	2.16	0.62
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.80	0.62
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.32	0.62
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.81	0.62
2:CB:163:PHE:CD1	2:CB:185:ILE:HG13	2.34	0.62
28:DE:3:GLY:HA3	28:DE:81:ILE:HD12	1.80	0.62
25:DA:333:G:H5''	25:DA:334:C:OP2	1.99	0.62
52:B6:13:CYS:SG	52:B6:47:THR:HG21	2.39	0.62
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.64	0.62
2:AB:74:LYS:NZ	2:AB:205:ASP:OD2	2.32	0.62
12:CL:49:ASN:ND2	12:CL:92:ASP:OD2	2.31	0.62
25:DA:1036:G:H1	25:DA:1119:C:H42	1.45	0.62
16:AP:53:VAL:HG22	16:AP:79:VAL:HG22	1.80	0.62
1:AA:96:U:H2'	1:AA:97:G:C8	2.35	0.62
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.46	0.62
19:AS:36:ARG:HB3	19:AS:72:GLY:HA3	1.79	0.62
3:CC:6:HIS:HB3	14:CN:49:HIS:ND1	2.14	0.62
1:CA:1108:G:O6	61:CA:4092:HOH:O	2.14	0.62
1:CA:1036:G:H5'	1:CA:1037:C:C6	2.35	0.62
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	1.81	0.62
1:CA:586:C:O2'	1:CA:878:G:H4'	1.98	0.62
16:AP:43:LYS:HG2	16:AP:48:TRP:CE2	2.35	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.80	0.62
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.35	0.62
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.12	0.62
25:DA:2584:U:O4	61:DA:3959:HOH:O	2.13	0.62
23:CX:9:G:O2'	23:CX:10:G:N7	2.23	0.62
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.33	0.62
1:AA:983:A:H1'	1:AA:1049:U:O2	2.00	0.62
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.35	0.62
1:AA:863:U:OP1	61:AA:4128:HOH:O	2.16	0.62
25:DA:658:C:H2'	25:DA:659:C:C6	2.35	0.62
1:AA:1125:U:C2	1:AA:1127:G:N7	2.68	0.62
30:DG:11:TYR:CE2	30:DG:16:ARG:HD3	2.35	0.62
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.64	0.62
9:AI:29:ASN:ND2	9:AI:65:VAL:O	2.33	0.62
45:BZ:102:LEU:HD13	45:BZ:123:ASP:HA	1.81	0.62
45:DZ:45:ASP:OD1	45:DZ:49:ARG:NH1	2.32	0.62
32:BI:72:LEU:O	32:BI:74:ASN:N	2.31	0.62
50:B4:15:ILE:HD12	50:B4:21:VAL:HG22	1.82	0.62
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	1.81	0.62
1:CA:1502:A:H2	1:CA:1505:G:N1	1.95	0.61
1:AA:460:G:O6	1:AA:470:C:H5"	2.00	0.61
1:AA:175:C:H2'	1:AA:176:C:H6	1.64	0.61
29:DF:183:VAL:O	29:DF:187:VAL:HG23	2.00	0.61
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.15	0.61
19:CS:41:VAL:HG12	19:CS:43:GLU:H	1.63	0.61
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.33	0.61
1:CA:447:G:O6	61:CA:4157:HOH:O	2.16	0.61
25:DA:579:G:H2'	25:DA:580:C:C6	2.35	0.61
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.64	0.61
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.65	0.61
1:AA:993:G:H1	1:AA:1045:C:H42	1.48	0.61
1:CA:1239:A:H62	1:CA:1299:A:H62	1.47	0.61
1:AA:1442(A):G:C8	39:BT:118:ARG:HG2	2.35	0.61
25:DA:2218:U:O2	47:D1:52:ARG:NH2	2.33	0.61
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.82	0.61
30:DG:18:GLU:OE2	30:DG:21:ARG:NH1	2.32	0.61
19:AS:64:GLU:HB2	50:B4:59:PHE:HE1	1.65	0.61
39:DT:85:LYS:NZ	39:DT:87:ASP:OD2	2.33	0.61
1:AA:1241:G:H1	1:AA:1296:C:H42	1.49	0.61
25:BA:2713:C:H2'	25:BA:2714:U:H2'	1.81	0.61
35:DP:50:ARG:HH21	35:DP:50:ARG:HG3	1.66	0.61
34:DO:119:PRO:HB2	39:DT:68:TYR:CE2	2.35	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:202:U:H3'	1:CA:203:U:H6	1.63	0.61
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	1.81	0.61
1:CA:1041:A:N6	1:CA:1042:G:O6	2.33	0.61
25:DA:1496:A:N3	25:DA:1577:C:O2'	2.32	0.61
25:BA:2412:G:O6	61:BA:4067:HOH:O	2.14	0.61
25:DA:2640:G:N7	61:DA:3808:HOH:O	2.31	0.61
25:DA:867:C:H2'	25:DA:868:U:C6	2.35	0.61
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.66	0.61
2:CB:48:MET:HA	2:CB:51:LEU:HB2	1.83	0.61
25:DA:2748:A:O2'	31:DH:63:SER:O	2.19	0.61
1:AA:1158:C:H5	1:AA:1181:G:N1	1.98	0.61
27:BD:71:ASP:CB	27:BD:103:ARG:HH22	2.13	0.61
39:DT:24:PRO:HA	39:DT:49:VAL:HG22	1.82	0.61
14:CN:37:PHE:HB3	14:CN:39:LEU:HD12	1.81	0.61
25:DA:2303:G:O2'	30:DG:132:ASN:HB2	2.01	0.61
6:AF:38:GLU:HB2	6:AF:64:GLN:HG2	1.83	0.61
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.35	0.61
25:DA:1773:A:H5''	61:DA:4248:HOH:O	1.99	0.61
11:CK:58:PRO:HG3	11:CK:89:ALA:O	2.00	0.61
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.82	0.61
1:CA:1422:G:O3'	34:DO:49:ARG:NH1	2.34	0.61
25:DA:2557:G:H2'	25:DA:2558:C:H6	1.66	0.61
28:BE:175:VAL:HG22	28:BE:177:PRO:HD3	1.82	0.61
25:DA:2404:C:O3'	35:DP:77:ARG:NH2	2.33	0.61
15:CO:88:ARG:HB3	15:CO:88:ARG:HH21	1.63	0.61
1:AA:154:C:N4	1:AA:168:G:O6	2.34	0.61
23:CX:4:G:H1	23:CX:69:C:N4	1.97	0.61
1:AA:601:C:H2'	1:AA:602:A:H8	1.63	0.61
1:CA:192:U:O2'	1:CA:193:C:H5'	2.00	0.61
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.34	0.61
15:CO:5:LYS:HD2	15:CO:5:LYS:H	1.64	0.61
25:DA:307:G:N1	25:DA:310:A:OP2	2.33	0.61
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.36	0.61
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.01	0.61
6:CF:24:GLU:HG3	6:CF:28:ARG:HH11	1.65	0.61
1:AA:1260:C:O5'	1:AA:1284:C:H4'	2.01	0.61
41:DV:5:VAL:HG11	41:DV:57:VAL:HG21	1.83	0.61
4:AD:184:LYS:HB3	4:AD:184:LYS:NZ	2.16	0.61
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.65	0.61
4:CD:17:VAL:HG11	4:CD:197:PRO:HG3	1.82	0.61
25:DA:2589:A:OP1	61:DA:4063:HOH:O	2.15	0.61
1:CA:1150:U:O4	1:CA:1151:A:N6	2.34	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.18	0.61
20:CT:57:ARG:HH12	20:CT:100:ILE:HG13	1.65	0.61
39:DT:95:ARG:HG2	39:DT:95:ARG:HH11	1.64	0.61
25:DA:948:G:OP1	61:DA:4173:HOH:O	2.16	0.61
1:CA:9:G:H2'	1:CA:10:A:H8	1.65	0.61
25:DA:867:C:H2'	25:DA:868:U:H6	1.66	0.61
25:DA:887:A:O2'	25:DA:889:C:OP2	2.18	0.61
29:DF:103:LYS:HA	29:DF:106:ARG:HG3	1.82	0.61
37:DR:36:THR:HG22	37:DR:37:THR:H	1.66	0.61
25:BA:1577:C:HO2'	25:BA:1578:C:P	2.23	0.61
25:BA:2460:A:N1	61:BA:4605:HOH:O	2.31	0.61
25:BA:787:U:OP2	61:BA:4519:HOH:O	2.16	0.61
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.30	0.61
29:DF:11:VAL:HG22	29:DF:125:LEU:HB2	1.83	0.61
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.16	0.61
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	1.82	0.61
25:DA:1900:A:OP2	61:DA:3902:HOH:O	2.16	0.61
25:DA:2845:G:H2'	25:DA:2846:G:C8	2.36	0.61
25:BA:1405:A:H61	25:BA:1418:U:H3	1.49	0.61
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.83	0.61
29:BF:65:TRP:CZ2	29:BF:75:HIS:HD2	2.19	0.61
39:DT:16:ARG:NH1	39:DT:18:ASP:OD2	2.35	0.60
25:BA:1219:A:H4'	25:BA:1220:U:OP1	2.01	0.60
25:BA:1701:A:OP1	37:BR:1:MET:HA	2.00	0.60
1:AA:552:U:H2'	1:AA:553:A:H5'	1.83	0.60
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.36	0.60
25:DA:973:A:OP2	61:DA:3814:HOH:O	2.17	0.60
6:CF:61:LEU:HB3	6:CF:63:TYR:HE1	1.65	0.60
3:CC:150:LYS:HG3	3:CC:169:ALA:HB2	1.83	0.60
26:DB:41:U:H5	30:DG:70:VAL:H	1.48	0.60
25:DA:289:A:N6	25:DA:351:G:O2'	2.34	0.60
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.16	0.60
25:BA:1231:G:H2'	25:BA:1232:G:O4'	2.01	0.60
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.32	0.60
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.65	0.60
1:AA:1026:G:H5'	1:AA:1027:C:H5''	1.83	0.60
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.35	0.60
11:CK:62:GLN:HG3	11:CK:97:ALA:HB2	1.82	0.60
16:CP:52:ASP:O	16:CP:54:GLU:N	2.32	0.60
25:DA:585:G:O2'	25:DA:1254:A:N6	2.31	0.60
25:DA:1531:C:H42	25:DA:1538:G:H1	1.49	0.60
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.01	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:201:C:N4	1:AA:216:G:H1	1.91	0.60
1:AA:1271:G:H5''	1:AA:1314:C:OP1	2.02	0.60
1:AA:881:G:OP2	12:AL:12:ARG:NH2	2.34	0.60
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.36	0.60
25:BA:272:U:H4'	32:BI:50:ARG:NH1	2.16	0.60
1:AA:827:U:H5''	1:AA:828:A:OP2	2.02	0.60
1:CA:826:C:H2'	1:CA:827:U:C6	2.35	0.60
25:DA:390:A:N6	61:DA:4490:HOH:O	2.33	0.60
45:BZ:109:ALA:HB3	45:BZ:145:GLU:HG3	1.83	0.60
25:BA:649:C:O2'	25:BA:704:U:OP1	2.19	0.60
3:CC:18:TRP:CD1	14:CN:54:PRO:HA	2.36	0.60
25:BA:1829:U:H5'	27:BD:259:THR:CG2	2.28	0.60
25:DA:2570:G:O6	61:DA:4417:HOH:O	2.12	0.60
25:DA:1125:G:H5'	55:D9:37:GLY:HA2	1.81	0.60
1:CA:67:C:H2'	1:CA:68:G:C8	2.35	0.60
1:AA:677:U:H3	1:AA:713:G:H22	1.47	0.60
25:DA:2870:C:H2'	25:DA:2871:C:O4'	2.00	0.60
5:AE:11:ILE:HB	5:AE:31:LEU:HB3	1.83	0.60
25:DA:2785:C:OP1	28:DE:41:LYS:NZ	2.17	0.60
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.66	0.60
1:AA:953:G:H5'	1:AA:965:A:H61	1.66	0.60
25:BA:594:A:O2'	41:BV:78:LYS:NZ	2.32	0.60
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.34	0.60
1:AA:1007:C:N3	1:AA:1022:G:O6	2.35	0.60
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.82	0.60
1:AA:486:U:H2'	1:AA:487:A:H8	1.65	0.60
6:CF:82:ARG:HB2	6:CF:85:VAL:HG23	1.82	0.60
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.01	0.60
28:DE:52:LEU:O	28:DE:76:ARG:N	2.24	0.60
9:AI:86:VAL:HG13	9:AI:96:LEU:HD12	1.83	0.60
43:DX:59:VAL:HG21	43:DX:78:LYS:HE3	1.84	0.60
44:DY:38:ILE:HD13	44:DY:66:PRO:HA	1.83	0.60
1:AA:691:G:H2'	1:AA:692:U:C6	2.36	0.60
25:DA:898:C:H2'	25:DA:899:A:O4'	2.02	0.60
25:BA:2227:G:H3'	25:BA:2228:G:N7	2.15	0.60
1:CA:491:G:O6	61:CA:4132:HOH:O	2.11	0.60
31:BH:3:ARG:HG2	31:BH:6:ARG:HG2	1.84	0.60
30:DG:39:ILE:HG23	30:DG:157:ILE:HG12	1.83	0.60
1:AA:383:A:C2	1:AA:384:G:H1'	2.36	0.60
25:BA:1739:U:H2'	25:BA:1741:C:C5	2.37	0.60
12:AL:59:ARG:HD3	24:AW:1:2QZ:OG1	2.02	0.60
1:CA:749:C:OP2	61:CA:4142:HOH:O	2.16	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:DP:89:ALA:O	35:DP:121:LYS:NZ	2.29	0.60
25:DA:2397:G:N2	25:DA:2420:C:H1'	2.16	0.60
30:DG:16:ARG:HE	30:DG:31:VAL:HG11	1.65	0.60
1:AA:232:G:H1'	1:AA:262:A:N1	2.17	0.60
31:BH:40:GLU:OE1	31:BH:61:HIS:NE2	2.31	0.60
1:CA:1286:A:H2	21:CU:18:TYR:HH	1.50	0.60
1:CA:69:G:H2'	1:CA:70:G:C8	2.37	0.60
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.13	0.60
28:BE:120:TRP:CE3	28:BE:155:LYS:HD3	2.37	0.60
50:D4:15:ILE:HB	50:D4:32:TYR:HD1	1.66	0.60
1:AA:322:C:O2'	20:AT:23:ARG:HD2	2.02	0.60
25:BA:1668:G:OP2	61:BA:4215:HOH:O	2.17	0.60
31:BH:92:ILE:H	31:BH:92:ILE:HD12	1.67	0.60
30:BG:170:ARG:NH2	30:BG:182:LYS:O	2.35	0.60
1:CA:939:G:H1	1:CA:1344:C:N4	1.98	0.60
1:AA:961:U:OP2	1:AA:1223:C:O2'	2.16	0.60
1:CA:735:C:H2'	1:CA:736:C:C6	2.35	0.60
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.01	0.60
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.18	0.60
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.02	0.60
36:DQ:66:ILE:HG12	36:DQ:104:PHE:CE2	2.37	0.60
1:CA:426:G:OP1	4:CD:36:ARG:NH1	2.33	0.60
25:DA:981:A:N1	25:DA:2027:G:O2'	2.28	0.60
36:DQ:34:LEU:HB2	36:DQ:118:LEU:HD22	1.83	0.60
50:B4:62:ARG:HB2	50:B4:63:TYR:HD1	1.67	0.60
1:AA:454:C:P	16:AP:75:ARG:HH22	2.24	0.60
35:DP:47:ASP:OD2	35:DP:50:ARG:NH2	2.34	0.60
25:BA:1889:G:N2	25:BA:1905:G:H2'	2.17	0.60
25:BA:278:G:H2'	25:BA:279:G:H5''	1.82	0.60
20:CT:58:LYS:HE3	20:CT:62:LEU:HD12	1.84	0.60
16:CP:14:ASN:OD1	16:CP:16:HIS:HE1	1.85	0.60
6:AF:61:LEU:HB3	6:AF:63:TYR:HE1	1.65	0.60
2:AB:163:PHE:HD1	2:AB:185:ILE:HD12	1.67	0.59
1:CA:1151:A:C5'	10:CJ:41:PRO:HA	2.32	0.59
25:BA:830:A:OP2	61:BA:4454:HOH:O	2.17	0.59
25:BA:599:U:H2'	25:BA:600:G:C8	2.36	0.59
25:BA:922:G:H1	25:BA:948:C:H42	1.49	0.59
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.84	0.59
3:CC:189:ALA:HB3	3:CC:196:LEU:HB2	1.84	0.59
34:BO:98:VAL:HG11	34:BO:114:ILE:HG23	1.84	0.59
20:AT:44:ALA:HB2	20:AT:52:ALA:HB1	1.83	0.59
25:BA:98:U:OP1	25:BA:99:G:O2'	2.14	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:443:A:H5''	25:DA:444:C:OP1	2.02	0.59
34:DO:98:VAL:HG13	34:DO:117:LEU:HB3	1.84	0.59
25:DA:704:G:H1'	25:DA:726:G:N2	2.17	0.59
11:CK:48:ILE:O	11:CK:50:TYR:N	2.33	0.59
2:CB:100:GLY:O	2:CB:104:ASN:N	2.34	0.59
25:DA:82:G:N1	25:DA:103:A:OP2	2.28	0.59
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.35	0.59
25:BA:2406:C:OP2	54:B8:30:ARG:NH1	2.35	0.59
50:D4:15:ILE:HB	50:D4:32:TYR:CD1	2.36	0.59
27:DD:108:PRO:HG2	27:DD:111:LEU:HB2	1.84	0.59
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.84	0.59
19:CS:48:THR:HG22	19:CS:61:TYR:HA	1.82	0.59
1:AA:128:G:O2'	17:AQ:3:LYS:NZ	2.34	0.59
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.02	0.59
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.84	0.59
6:CF:33:TYR:HB2	6:CF:75:LEU:HD23	1.83	0.59
48:D2:29:LYS:HG2	48:D2:57:ILE:HD13	1.84	0.59
46:B0:53:MET:HG3	46:B0:59:LEU:HD23	1.83	0.59
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.02	0.59
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.85	0.59
25:BA:139:A:H8	25:BA:1454:C:O2'	1.86	0.59
39:BT:53:ARG:HH11	39:BT:53:ARG:HB3	1.67	0.59
10:AJ:7:LYS:HB3	10:AJ:97:GLU:HB2	1.83	0.59
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.37	0.59
25:DA:1903:G:OP1	27:DD:241:PRO:HB2	2.02	0.59
19:CS:51:VAL:O	19:CS:58:VAL:N	2.30	0.59
15:CO:3:ILE:HG21	15:CO:34:LEU:HD21	1.83	0.59
25:DA:885:C:H2'	25:DA:886:C:H4'	1.84	0.59
35:BP:89:ALA:O	35:BP:121:LYS:NZ	2.29	0.59
18:AR:42:ARG:HH21	18:AR:42:ARG:HA	1.67	0.59
25:BA:2274:U:OP2	46:B0:19:LYS:NZ	2.34	0.59
25:BA:2092:G:N3	61:BA:3834:HOH:O	2.31	0.59
1:AA:501:C:H1'	1:AA:549:C:H1'	1.84	0.59
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.37	0.59
25:DA:226:G:H21	25:DA:228:A:H62	1.50	0.59
25:BA:2213:G:H5'	25:BA:2214:G:OP2	2.03	0.59
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.02	0.59
1:CA:827:U:H5''	1:CA:828:A:OP2	2.02	0.59
25:DA:799:G:O6	61:DA:4430:HOH:O	2.15	0.59
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.84	0.59
1:AA:1009:G:O6	1:AA:1020:U:O2	2.20	0.59
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.33	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1632:A:OP2	61:DA:4177:HOH:O	2.17	0.59
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.18	0.59
25:BA:1229:G:H5'	49:B3:29:ARG:NH1	2.17	0.59
26:DB:48:A:H4'	38:DS:95:HIS:HD2	1.68	0.59
1:AA:1342:C:H4'	9:AI:125:TYR:HB3	1.84	0.59
25:DA:212:G:H2'	25:DA:213:A:O4'	2.02	0.59
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.84	0.59
2:CB:7:VAL:HB	2:CB:9:GLU:HG3	1.85	0.59
10:CJ:8:LEU:HD12	10:CJ:20:ALA:HB2	1.85	0.59
1:AA:78:G:H1	1:AA:92:C:N4	2.01	0.59
4:CD:8:VAL:HB	4:CD:115:ARG:HH12	1.67	0.59
4:AD:182:LYS:HG2	4:AD:183:GLY:N	2.16	0.59
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.84	0.59
25:BA:479:C:OP1	61:BA:4179:HOH:O	2.17	0.59
25:BA:1385:G:H5''	43:BX:16:LYS:HD3	1.83	0.59
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.17	0.59
1:AA:623:C:H2'	1:AA:624:C:H6	1.68	0.59
25:BA:1897:C:H2'	25:BA:1898:A:O4'	2.02	0.59
47:D1:3:LYS:HB2	47:D1:61:ARG:HH11	1.66	0.59
1:CA:776:G:N2	1:CA:802:A:OP2	2.29	0.59
3:AC:70:VAL:HG12	3:AC:72:LYS:H	1.66	0.59
1:CA:427:U:H3'	1:CA:428:G:H2'	1.85	0.59
30:BG:12:TYR:HA	30:BG:16:ARG:HG2	1.84	0.59
1:CA:457:C:H2'	1:CA:458:C:H6	1.68	0.59
25:DA:2802:G:H2'	25:DA:2803:C:O4'	2.01	0.59
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.18	0.59
30:DG:50:ALA:O	30:DG:52:ILE:N	2.35	0.59
34:DO:77:ILE:HG13	39:DT:74:ARG:HG2	1.83	0.59
27:BD:183:ARG:HG3	27:BD:270:ILE:HG12	1.85	0.59
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.83	0.59
25:BA:1410:G:P	47:B1:3:LYS:HG3	2.43	0.59
16:AP:50:LYS:HA	16:AP:50:LYS:HE2	1.85	0.59
3:CC:114:PRO:O	3:CC:118:GLN:HG2	2.03	0.59
25:DA:2074:U:OP1	61:DA:3911:HOH:O	2.17	0.59
1:AA:1126:U:C5	10:AJ:71:LEU:HD22	2.36	0.59
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.38	0.59
1:CA:1493:A:H1'	25:DA:1913:A:N6	2.13	0.59
1:AA:433:C:H2'	1:AA:434:U:H6	1.67	0.59
25:DA:1314:C:OP1	61:DA:4076:HOH:O	2.17	0.59
1:CA:693:G:H2'	1:CA:694:A:H8	1.68	0.59
25:DA:1359:A:N1	25:DA:1372:U:O4	2.35	0.59
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.34	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.51	0.59
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.02	0.59
31:DH:30:LYS:HG3	31:DH:80:SER:O	2.02	0.59
3:CC:36:ASP:HA	3:CC:39:ILE:HD12	1.85	0.59
5:CE:36:ASP:O	5:CE:38:GLN:N	2.36	0.59
25:BA:1077:G:H21	55:B9:36:GLN:HE22	1.50	0.59
25:DA:2298:A:N1	25:DA:2321:G:C6	2.71	0.59
1:AA:174:C:H2'	1:AA:175:C:C6	2.38	0.59
1:AA:659:U:H2'	1:AA:660:G:C8	2.38	0.59
25:DA:1359:A:H61	25:DA:1372:U:H3	1.50	0.59
1:CA:1287:A:N3	1:CA:1353:G:O2'	2.32	0.59
1:CA:826:C:H2'	1:CA:827:U:H6	1.68	0.59
1:AA:715:A:H2'	1:AA:716:A:C8	2.38	0.59
1:AA:382:A:C2	1:AA:383:A:N7	2.70	0.59
1:AA:323:U:H2'	1:AA:324:G:O4'	2.02	0.59
1:AA:501:C:O2'	1:AA:549:C:O2	2.21	0.59
1:AA:913:A:OP1	12:AL:46:LYS:NZ	2.36	0.59
25:DA:1840:G:OP2	61:DA:4306:HOH:O	2.16	0.59
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.68	0.59
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.06	0.59
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.84	0.59
52:B6:14:THR:HB	52:B6:48:VAL:O	2.03	0.59
25:BA:129:G:OP1	61:BA:3963:HOH:O	2.17	0.59
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.35	0.59
1:CA:1005:A:H1'	1:CA:1036:G:N1	2.16	0.58
25:DA:2299:G:N1	25:DA:2318:G:C8	2.71	0.58
43:BX:31:HIS:CD2	43:BX:33:LYS:HB2	2.37	0.58
25:DA:143:G:H2'	25:DA:143(A):C:H6	1.66	0.58
1:AA:692:U:O2'	1:AA:694:A:N7	2.28	0.58
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.38	0.58
1:AA:833:U:H2'	1:AA:834:C:C6	2.38	0.58
25:DA:2472:G:N1	25:DA:2477:C:OP1	2.25	0.58
7:CG:76:ARG:O	7:CG:87:VAL:N	2.36	0.58
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.20	0.58
1:CA:999:C:N4	1:CA:1043:C:N3	2.51	0.58
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.32	0.58
25:BA:2745:G:P	28:BE:203:LYS:HZ1	2.26	0.58
5:CE:9:LYS:HD2	5:CE:112:LEU:HD21	1.86	0.58
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.38	0.58
4:AD:31:CYS:SG	4:AD:33:MET:N	2.74	0.58
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.21	0.58
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.36	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
42:DW:60:ASN:HD22	42:DW:60:ASN:N	2.02	0.58
5:AE:143:ARG:NH1	8:AH:77:GLU:OE1	2.36	0.58
1:CA:552:U:C2'	1:CA:553:A:H5'	2.33	0.58
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	1.86	0.58
28:DE:28:ALA:HB3	28:DE:93:VAL:HG12	1.84	0.58
7:CG:75:VAL:HG13	7:CG:145:ALA:HA	1.85	0.58
1:CA:1121:U:H2'	1:CA:1122:U:O4'	2.03	0.58
1:CA:1047:G:H1	1:CA:1210:C:H42	1.51	0.58
1:AA:600:C:H2'	1:AA:601:C:C6	2.38	0.58
1:CA:9:G:H2'	1:CA:10:A:C8	2.38	0.58
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.86	0.58
1:CA:1271:G:H5''	1:CA:1314:C:OP1	2.04	0.58
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.06	0.58
1:CA:202:U:H3'	1:CA:203:U:C6	2.38	0.58
25:DA:2314:C:H2'	25:DA:2315:G:C8	2.38	0.58
25:BA:1233:U:H4'	41:BV:79:VAL:HG22	1.84	0.58
1:AA:713:G:H2'	1:AA:714:G:C8	2.38	0.58
1:AA:737:A:H2'	1:AA:738:C:C6	2.37	0.58
2:CB:40:HIS:HB3	2:CB:190:THR:HG21	1.85	0.58
53:D7:5:TRP:CD1	53:D7:7:PRO:HD3	2.38	0.58
29:DF:137:LYS:HA	29:DF:140:LEU:HD23	1.85	0.58
25:DA:2502:G:N7	61:DA:4548:HOH:O	2.31	0.58
32:BI:4:ILE:HG12	32:BI:18:VAL:HG22	1.84	0.58
3:AC:157:ILE:HD12	3:AC:164:ARG:HB3	1.84	0.58
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.39	0.58
3:CC:180:ALA:HB1	3:CC:203:PHE:HE1	1.69	0.58
1:CA:1086:U:H3	1:CA:1099:G:H22	1.51	0.58
20:AT:45:GLN:HA	20:AT:91:LEU:HB3	1.84	0.58
11:AK:15:ALA:HA	11:AK:77:MET:HA	1.84	0.58
1:AA:1392:G:N2	1:AA:1502:A:H8	2.02	0.58
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.38	0.58
25:BA:1185:C:O3'	33:BN:25:ARG:NH1	2.36	0.58
31:BH:40:GLU:OE2	31:BH:60:ARG:NH1	2.37	0.58
25:BA:2853:G:O6	61:BA:4561:HOH:O	2.17	0.58
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.84	0.58
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.86	0.58
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.85	0.58
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.85	0.58
45:DZ:130:PRO:O	45:DZ:133:ILE:HG13	2.03	0.58
1:AA:269:C:H2'	1:AA:270:A:C8	2.37	0.58
34:DO:80:ASP:OD1	39:DT:64:ARG:NH2	2.36	0.58
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.86	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:DU:65:ILE:HD11	40:DU:95:LEU:HB3	1.86	0.58
7:AG:46:ALA:O	7:AG:50:ILE:HG23	2.04	0.58
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.84	0.58
19:AS:41:VAL:HG12	19:AS:43:GLU:H	1.68	0.58
25:DA:83:G:O2'	25:DA:102:G:N2	2.36	0.58
25:BA:2080:A:N7	61:BA:4112:HOH:O	2.32	0.58
1:CA:222:U:H2'	1:CA:223:U:C6	2.38	0.58
28:DE:9:VAL:HB	39:DT:3:ARG:HG2	1.85	0.58
1:CA:975:A:N1	10:CJ:48:THR:HB	2.19	0.58
1:AA:924:C:O2'	1:AA:1502:A:N6	2.35	0.58
34:BO:35:VAL:HG21	34:BO:69:ILE:HD13	1.85	0.58
5:AE:94:ALA:HB2	5:AE:119:LEU:HG	1.85	0.58
12:AL:36:VAL:HG22	12:AL:82:VAL:HG22	1.86	0.58
31:DH:124:GLU:HB2	31:DH:132:ARG:HB3	1.86	0.58
26:BB:6:C:H2'	26:BB:7:G:H5''	1.85	0.58
25:BA:1779:G:H5''	25:BA:1779:G:H8	1.68	0.58
53:B7:47:ARG:HH11	53:B7:47:ARG:HB3	1.67	0.58
43:BX:41:ASN:O	43:BX:45:THR:HG23	2.04	0.58
1:CA:130:A:O2'	1:CA:131:C:O5'	2.19	0.58
1:CA:1026:G:H5'	1:CA:1027:C:H5''	1.85	0.58
9:AI:16:ARG:HD3	9:AI:64:THR:HG21	1.85	0.58
1:CA:426:G:H2'	1:CA:427:U:C6	2.39	0.58
39:BT:53:ARG:NH1	39:BT:53:ARG:HB3	2.18	0.58
5:CE:78:HIS:CE1	5:CE:143:ARG:H	2.22	0.58
30:DG:38:VAL:HG22	30:DG:93:THR:HG23	1.84	0.58
25:BA:2022:G:OP1	37:BR:5:LYS:NZ	2.37	0.58
25:DA:171:G:H2'	25:DA:172:C:C6	2.39	0.58
7:AG:42:ILE:HG23	7:AG:117:ALA:HA	1.84	0.58
25:BA:2251:G:OP2	61:BA:4210:HOH:O	2.17	0.58
1:CA:913:A:OP1	12:CL:46:LYS:NZ	2.36	0.58
25:DA:7:G:H2'	25:DA:8:A:C8	2.38	0.58
1:CA:1316:G:H2'	1:CA:1318:A:OP2	2.04	0.58
25:DA:2680:C:OP2	28:DE:111:ARG:NH2	2.37	0.58
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.85	0.58
36:BQ:110:THR:HG23	36:BQ:113:GLN:OE1	2.04	0.58
32:BI:104:GLN:HG3	32:BI:105:HIS:CD2	2.38	0.58
1:CA:642:A:N3	8:CH:113:SER:OG	2.35	0.58
2:CB:30:ARG:HH21	2:CB:194:PRO:HB2	1.68	0.58
8:AH:83:ILE:HB	8:AH:137:VAL:HG13	1.86	0.58
25:BA:945:A:O2'	25:BA:946:A:H8	1.87	0.58
6:AF:10:LEU:HD23	6:AF:61:LEU:HD13	1.86	0.58
3:CC:39:ILE:O	3:CC:43:LEU:HG	2.04	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1618:A:H5'	61:DA:3986:HOH:O	2.04	0.58
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.25	0.58
2:CB:87:ARG:NE	2:CB:233:SER:HB3	2.18	0.57
5:AE:147:ASP:O	5:AE:151:LEU:HG	2.03	0.57
25:DA:1327:C:OP2	61:DA:3851:HOH:O	2.17	0.57
25:DA:1169:G:H1	25:DA:1180:C:H42	1.52	0.57
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.37	0.57
1:AA:997:U:H3	1:AA:1044:A:H61	1.52	0.57
1:AA:1521:G:N3	61:AA:4036:HOH:O	2.32	0.57
7:CG:14:PRO:HG3	7:CG:21:VAL:HG13	1.86	0.57
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.84	0.57
29:BF:53:THR:HG22	29:BF:56:GLU:HG3	1.85	0.57
1:AA:1189:C:O2	61:AA:4114:HOH:O	2.16	0.57
23:CX:23:C:H2'	23:CX:24:U:H6	1.69	0.57
1:CA:1422:G:H5''	34:DO:48:PRO:HB3	1.86	0.57
43:DX:31:HIS:HD2	43:DX:33:LYS:H	1.51	0.57
1:CA:17:U:H2'	1:CA:18:C:C6	2.39	0.57
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.85	0.57
1:CA:689:C:OP2	11:CK:55:LYS:NZ	2.35	0.57
31:BH:98:LEU:HD22	31:BH:125:VAL:HG23	1.85	0.57
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.86	0.57
1:CA:392:G:H2'	1:CA:393:A:C8	2.39	0.57
25:DA:2591:C:OP1	27:DD:239:ARG:HD2	2.03	0.57
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.04	0.57
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.04	0.57
19:AS:31:ILE:HB	19:AS:49:ILE:HG12	1.85	0.57
44:BY:54:LYS:HA	44:BY:56:PRO:CD	2.31	0.57
15:CO:54:ARG:O	15:CO:58:MET:HG3	2.04	0.57
25:DA:286:C:H2'	25:DA:287:C:C6	2.38	0.57
1:CA:1269:A:C8	1:CA:1270:C:H1'	2.38	0.57
1:CA:839:U:O2'	1:CA:840:C:OP1	2.20	0.57
1:CA:1309:G:O2'	13:CM:77:ASN:ND2	2.38	0.57
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.85	0.57
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.39	0.57
1:CA:148:G:H2'	1:CA:149:A:C8	2.37	0.57
19:CS:64:GLU:HB2	50:D4:59:PHE:CE1	2.39	0.57
1:AA:444:C:H2'	1:AA:445:G:H8	1.69	0.57
25:BA:1890:A:N6	25:BA:1905:G:O2'	2.38	0.57
7:CG:76:ARG:CZ	7:CG:89:MET:HB2	2.34	0.57
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.86	0.57
2:AB:60:ASP:OD1	2:AB:64:ARG:NE	2.35	0.57
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.68	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.85	0.57
24:AW:4:PRO:O	24:AW:6:2R1:N	2.37	0.57
29:BF:197:ASP:OD1	29:BF:197:ASP:N	2.37	0.57
37:DR:83:ILE:O	37:DR:86:ARG:HG2	2.04	0.57
25:BA:303:C:N4	25:BA:385:G:H1	1.98	0.57
1:AA:1270:C:C2'	1:AA:1271:G:H5'	2.34	0.57
25:DA:2023:G:H5'	25:DA:2617:C:H4'	1.87	0.57
25:DA:674:G:H1'	29:DF:74:ARG:HD3	1.87	0.57
1:CA:1160:G:H22	1:CA:1176:A:H2	1.52	0.57
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.87	0.57
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.87	0.57
45:DZ:39:VAL:HG21	45:DZ:44:PHE:HB2	1.85	0.57
34:DO:87:ILE:HD12	34:DO:91:LEU:HA	1.86	0.57
1:CA:785:G:C2'	1:CA:786:G:H5'	2.34	0.57
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.52	0.57
25:DA:956:G:H5'	25:DA:957:A:OP2	2.04	0.57
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.38	0.57
1:AA:347:G:H21	1:AA:348:G:H3'	1.69	0.57
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.86	0.57
25:DA:195:A:H5''	25:DA:196:A:O5'	2.03	0.57
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.15	0.57
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.34	0.57
1:AA:96:U:O2'	1:AA:97:G:H5'	2.04	0.57
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.38	0.57
3:CC:58:GLU:HB2	3:CC:65:ALA:HB3	1.86	0.57
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	1.87	0.57
1:CA:243:A:H4'	1:CA:244:U:H5''	1.85	0.57
6:AF:44:GLY:HA2	6:AF:59:TYR:CZ	2.40	0.57
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.85	0.57
2:CB:102:LEU:HD23	2:CB:182:ILE:HD12	1.86	0.57
33:DN:58:ASP:OD1	33:DN:58:ASP:N	2.34	0.57
2:CB:166:ASP:HB3	2:CB:169:LYS:HB2	1.86	0.57
25:BA:1068:G:H22	25:BA:1188:A:H2	1.47	0.57
40:DU:76:TYR:HH	40:DU:92:ARG:HH11	1.52	0.57
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.85	0.57
1:CA:706:A:H5''	11:CK:22:HIS:CE1	2.39	0.57
35:DP:86:LYS:HB3	35:DP:118:GLY:HA3	1.86	0.57
25:BA:625:G:O2'	25:BA:702:A:N6	2.38	0.57
1:CA:1125:U:HO2'	1:CA:1126:U:H2'	1.69	0.57
1:AA:1392:G:H21	1:AA:1502:A:H8	1.53	0.57
14:CN:4:LYS:HA	14:CN:7:ILE:HD13	1.87	0.57
1:AA:1162:C:N4	1:AA:1174:G:H1	2.01	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:10:G:H2'	25:DA:11:G:H8	1.70	0.57
15:CO:4:THR:HB	15:CO:5:LYS:HD2	1.87	0.57
1:AA:828:A:H2'	1:AA:829:G:O4'	2.05	0.57
25:BA:572:A:O2'	25:BA:573:G:OP1	2.21	0.57
25:BA:2786:C:H2'	25:BA:2787:C:H6	1.68	0.57
25:BA:181:C:OP1	61:BA:3915:HOH:O	2.17	0.57
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.19	0.57
1:AA:216:G:H2'	1:AA:217:C:C6	2.40	0.57
25:BA:2299:A:N6	25:BA:2356:U:H3	2.01	0.57
30:BG:47:LYS:HG3	30:BG:48:GLU:H	1.69	0.57
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	1.87	0.57
25:DA:30:G:H2'	25:DA:31:C:C6	2.40	0.57
30:DG:103:LEU:HD23	30:DG:106:LEU:HD23	1.86	0.57
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.38	0.57
25:DA:2689:U:OP2	25:DA:2719:G:N2	2.36	0.57
48:B2:1:MET:HE2	48:B2:6:VAL:HG22	1.86	0.57
25:DA:2189:U:H2'	25:DA:2190:G:C8	2.40	0.57
25:BA:2308:U:OP2	38:BS:9:ARG:NH2	2.37	0.57
30:DG:114:ILE:HB	30:DG:117:PHE:HB2	1.87	0.57
25:BA:676:G:OP1	54:B8:19:SER:OG	2.21	0.57
10:CJ:55:LYS:HG3	10:CJ:56:HIS:CD2	2.40	0.57
25:DA:38:A:H2'	25:DA:39:C:C6	2.40	0.57
25:DA:660:G:H5'	29:DF:99:TYR:CE2	2.40	0.57
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.86	0.57
28:DE:101:ARG:NH2	28:DE:171:GLU:HB2	2.19	0.57
25:DA:2312:U:C5	25:DA:2313:C:H5	2.23	0.57
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.70	0.57
2:CB:44:LEU:H	2:CB:44:LEU:HD22	1.70	0.57
1:AA:1028:C:N4	1:AA:1033:G:H1	2.00	0.57
25:DA:82:G:O6	61:DA:4494:HOH:O	2.17	0.57
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.39	0.57
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.40	0.57
35:BP:2:LYS:NZ	35:BP:4:SER:HB3	2.20	0.57
45:DZ:48:PHE:CE1	45:DZ:52:SER:HA	2.40	0.57
25:BA:311:C:H2'	25:BA:312:C:H6	1.69	0.57
25:BA:1836:U:O2	27:BD:50:THR:HB	2.04	0.57
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.37	0.57
10:CJ:8:LEU:HD23	10:CJ:96:ILE:HG23	1.87	0.56
1:CA:1157:A:N6	1:CA:1180:A:C4	2.72	0.56
1:AA:1002:G:H3'	1:AA:1003:G:H8	1.70	0.56
1:CA:1138:G:C5	1:CA:1140:C:H1'	2.40	0.56
1:AA:175:C:H2'	1:AA:176:C:C6	2.39	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1636:C:H2'	25:DA:1637:A:C8	2.40	0.56
1:CA:738:C:H2'	1:CA:739:C:H6	1.70	0.56
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.70	0.56
25:DA:71:A:H5''	25:DA:73:A:C8	2.40	0.56
45:BZ:158:PRO:O	45:BZ:161:VAL:HG12	2.04	0.56
25:BA:118:U:OP2	61:BA:3886:HOH:O	2.17	0.56
13:AM:56:LEU:O	13:AM:60:VAL:HG23	2.04	0.56
10:CJ:65:LEU:HD12	14:CN:55:GLY:O	2.05	0.56
1:AA:994:A:N1	1:AA:1047:G:H4'	2.20	0.56
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.39	0.56
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.40	0.56
1:CA:149:A:H2'	1:CA:150:C:C6	2.40	0.56
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.87	0.56
43:BX:88:LYS:NZ	43:BX:90:GLU:OE1	2.33	0.56
7:CG:106:GLN:O	7:CG:110:GLN:HG3	2.05	0.56
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.05	0.56
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.40	0.56
25:BA:692:C:H2'	25:BA:693:G:O4'	2.05	0.56
1:CA:1414:U:H3	1:CA:1486:G:H1	1.53	0.56
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.70	0.56
25:DA:1798:U:H5'	27:DD:259:THR:CG2	2.31	0.56
1:CA:1318:A:O2'	19:CS:37:ARG:HB2	2.06	0.56
1:AA:409:G:N2	1:AA:433:C:O2	2.38	0.56
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.20	0.56
25:DA:2299:G:N2	25:DA:2318:G:H8	2.02	0.56
1:AA:1025:U:C2	1:AA:1036:G:O6	2.58	0.56
1:AA:78:G:H1	1:AA:92:C:H42	1.54	0.56
1:AA:192:U:HO2'	1:AA:193:C:H6	1.52	0.56
4:CD:31:CYS:SG	4:CD:32:ALA:N	2.79	0.56
50:B4:56:VAL:HB	50:B4:60:GLN:HG3	1.88	0.56
1:AA:149:A:H2'	1:AA:150:C:C6	2.40	0.56
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	1.87	0.56
15:CO:5:LYS:CD	15:CO:5:LYS:H	2.17	0.56
13:CM:81:LEU:HD22	13:CM:88:ARG:HB3	1.86	0.56
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.04	0.56
3:CC:56:ASP:O	3:CC:57:ILE:HD12	2.05	0.56
31:BH:86:GLU:OE2	31:BH:130:ARG:HD3	2.06	0.56
8:CH:10:LEU:HD22	8:CH:83:ILE:HD11	1.85	0.56
16:CP:21:VAL:HG13	16:CP:33:ILE:HB	1.86	0.56
25:BA:2860:A:OP2	25:BA:2876:U:H5	1.89	0.56
25:DA:1470:G:H5''	25:DA:1471:A:OP1	2.05	0.56
25:BA:2431:U:O4	61:BA:4236:HOH:O	2.14	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.04	0.56
2:CB:120:ALA:O	2:CB:122:PHE:N	2.34	0.56
1:AA:532:A:O2'	1:AA:533:A:OP1	2.20	0.56
1:AA:1125:U:H1'	1:AA:1126:U:O5'	2.06	0.56
25:BA:1066:A:N1	25:BA:1186:U:O2'	2.27	0.56
1:CA:1279:A:H5''	1:CA:1280:A:OP1	2.06	0.56
25:BA:1000:C:OP1	36:BQ:87:LYS:HE3	2.05	0.56
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.40	0.56
1:AA:193:C:H2'	1:AA:194:C:C6	2.39	0.56
1:CA:1207:G:H2'	1:CA:1208:C:C6	2.39	0.56
1:CA:834:C:H2'	1:CA:835:U:C6	2.40	0.56
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	1.87	0.56
1:CA:1104:G:H5'	2:CB:111:ARG:HD2	1.86	0.56
25:BA:624:C:O2'	25:BA:628:C:OP1	2.16	0.56
25:DA:500:G:N1	25:DA:503:A:OP2	2.38	0.56
18:AR:51:LEU:HD23	18:AR:52:PRO:HD2	1.87	0.56
25:BA:2013:U:H2'	25:BA:2014:G:H5''	1.86	0.56
53:D7:26:GLY:O	53:D7:30:VAL:HG23	2.05	0.56
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.04	0.56
25:DA:479:A:N3	25:DA:481:G:H5''	2.20	0.56
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.88	0.56
28:DE:143:ASN:HD22	28:DE:147:PRO:HD3	1.70	0.56
25:DA:375:C:H2'	25:DA:376:C:C6	2.40	0.56
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.40	0.56
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.86	0.56
1:CA:1002:G:N2	1:CA:1039:C:N3	2.54	0.56
1:AA:1125:U:H3'	10:AJ:5:ARG:HH22	1.70	0.56
25:DA:1359:A:N6	25:DA:1372:U:H3	2.03	0.56
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.06	0.56
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.87	0.56
26:DB:95:C:H2'	26:DB:96:U:C6	2.40	0.56
26:BB:50:G:H5''	38:BS:61:ASN:HD22	1.69	0.56
25:BA:2694:U:OP2	61:BA:4014:HOH:O	2.17	0.56
9:CI:6:GLY:H	9:CI:17:VAL:HG12	1.70	0.56
16:AP:18:ARG:NH1	16:AP:32:TYR:OH	2.38	0.56
1:AA:1202:G:N2	14:AN:46:GLU:OE1	2.32	0.56
1:CA:38:G:H22	1:CA:397:A:H5''	1.71	0.56
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.05	0.56
25:BA:83:A:H5'	44:BY:8:LYS:HG2	1.86	0.56
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.03	0.56
23:CX:8:U:H6	23:CX:8:U:O5'	1.89	0.56
25:BA:1615:G:P	27:BD:63:ARG:HH22	2.29	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:CL:74:GLY:O	12:CL:102:ARG:NH1	2.27	0.56
25:DA:857:C:H4'	46:D0:23:VAL:HG21	1.88	0.56
25:DA:271(H):G:H2'	25:DA:271(I):G:H8	1.69	0.56
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.06	0.56
28:BE:127:ASP:OD2	61:BE:408:HOH:O	2.18	0.56
25:BA:2481:A:O2'	36:BQ:56:ARG:HD2	2.06	0.56
25:DA:988:A:N7	61:DA:3839:HOH:O	2.32	0.56
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.24	0.56
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.30	0.56
1:CA:200:G:H2'	1:CA:201:C:C6	2.41	0.56
27:BD:206:LEU:HD22	27:BD:211:ARG:HG2	1.87	0.56
1:AA:1318:A:H4'	19:AS:10:PHE:CZ	2.40	0.56
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.87	0.56
59:CX:101:FME:HCN	25:DA:2451:A:C2	2.40	0.56
17:AQ:57:VAL:HG12	17:AQ:76:LEU:HA	1.88	0.56
4:CD:103:ASN:OD1	4:CD:114:ARG:NE	2.37	0.56
48:B2:32:LEU:HD12	48:B2:36:ARG:HH11	1.69	0.56
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.39	0.56
34:BO:2:ILE:HB	34:BO:33:ALA:HB3	1.87	0.56
25:BA:1067:A:H8	25:BA:1068:G:H5''	1.69	0.56
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.41	0.56
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.41	0.56
26:DB:48:A:H2'	26:DB:49:C:C6	2.40	0.56
25:DA:172:C:H2'	25:DA:173:G:H8	1.70	0.56
31:BH:125:VAL:HG12	31:BH:127:GLU:O	2.05	0.56
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.88	0.56
25:DA:1338:G:N3	25:DA:1393:A:H2	2.04	0.56
14:AN:14:PRO:HG2	14:AN:16:PHE:O	2.06	0.56
30:BG:72:ARG:NH1	30:BG:87:PRO:HG3	2.21	0.56
1:CA:187:C:H2'	1:CA:188:C:H6	1.71	0.56
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.06	0.56
30:BG:179:PRO:HB2	50:B4:42:PHE:HE2	1.70	0.56
14:AN:21:TYR:OH	14:AN:23:ARG:NH2	2.38	0.56
25:BA:930:G:H2'	25:BA:931:C:C6	2.41	0.56
1:CA:861:G:OP1	8:CH:75:ARG:NH2	2.38	0.56
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.20	0.56
37:DR:88:ARG:NH2	37:DR:89:ASP:OD2	2.38	0.56
29:BF:185:ASP:OD1	29:BF:188:ARG:NH1	2.35	0.56
25:BA:1091:A:O2'	25:BA:1093:G:C4	2.57	0.56
1:CA:1263:C:H2'	1:CA:1264:C:C6	2.41	0.56
34:DO:68:GLU:CB	34:DO:78:ARG:HB2	2.36	0.56
1:CA:890:G:O2'	1:CA:906:G:O6	2.19	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
41:BV:21:ARG:HG2	41:BV:91:TYR:CD1	2.41	0.56
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.35	0.56
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.88	0.56
11:CK:18:ARG:NH2	11:CK:35:PRO:O	2.32	0.56
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.06	0.56
1:AA:1138:G:C6	1:AA:1140:C:H1'	2.41	0.56
25:DA:247:G:H4'	25:DA:386:G:C5	2.40	0.56
1:AA:272:C:H2'	1:AA:273:A:H8	1.71	0.56
25:DA:1815:A:OP2	27:DD:54:ARG:NH2	2.37	0.56
4:AD:155:LEU:HD22	4:AD:156:GLU:H	1.70	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.86	0.56
9:CI:53:VAL:O	9:CI:55:ALA:N	2.39	0.56
33:BN:67:LEU:HD12	33:BN:87:LEU:HD13	1.87	0.56
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.06	0.56
8:CH:84:ARG:HD2	8:CH:136:GLU:HG2	1.87	0.56
30:DG:43:LEU:HD12	30:DG:45:GLU:HG3	1.88	0.56
30:DG:12:TYR:HA	30:DG:16:ARG:HG2	1.88	0.55
25:DA:287:C:H2'	25:DA:288:C:C6	2.38	0.55
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.70	0.55
1:CA:814:A:N7	1:CA:816:A:C4	2.73	0.55
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.71	0.55
25:BA:918:U:OP1	36:BQ:5:ARG:HD3	2.06	0.55
25:DA:1309:G:HO2'	25:DA:1611:C:HO2'	1.53	0.55
25:DA:2359:C:H2'	25:DA:2360:A:O4'	2.05	0.55
25:DA:275:G:H2'	25:DA:276:A:C8	2.41	0.55
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.41	0.55
2:CB:189:ASP:HB3	2:CB:204:ASN:HA	1.89	0.55
1:CA:444:C:H2'	1:CA:445:G:C8	2.34	0.55
39:BT:95:ARG:NH1	39:BT:95:ARG:HG2	2.21	0.55
1:AA:221:C:H2'	1:AA:222:U:C6	2.38	0.55
50:D4:46:GLN:C	50:D4:48:ARG:H	2.09	0.55
30:DG:101:ILE:HG22	30:DG:105:LYS:HE2	1.87	0.55
23:CX:59:A:H2'	23:CX:60:U:H5'	1.89	0.55
32:BI:72:LEU:C	32:BI:74:ASN:H	2.09	0.55
48:B2:1:MET:N	48:B2:52:ASP:OD2	2.38	0.55
15:AO:26:GLU:OE2	15:AO:77:ARG:NE	2.39	0.55
1:CA:8:A:N6	4:CD:209:ARG:HB2	2.21	0.55
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.05	0.55
1:AA:520:A:N1	1:AA:536:C:H1'	2.21	0.55
8:AH:98:LYS:H	8:AH:98:LYS:HD3	1.71	0.55
25:BA:606:G:OP2	40:BU:10:ARG:NH1	2.36	0.55
1:CA:138:G:H8	1:CA:138:G:H5'	1.71	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:BF:101:LEU:O	29:BF:106:ARG:HD3	2.06	0.55
25:BA:7:G:H2'	25:BA:8:A:O4'	2.06	0.55
1:AA:437:U:H5'	4:AD:155:LEU:HD11	1.88	0.55
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.40	0.55
25:BA:2661:U:H2'	25:BA:2662:U:C6	2.41	0.55
25:BA:231:G:O2'	25:BA:243:G:O6	2.20	0.55
55:D9:15:LYS:HE2	55:D9:17:ILE:HD13	1.89	0.55
25:BA:645:G:H5'	25:BA:645:G:N3	2.22	0.55
61:BA:4299:HOH:O	37:BR:15:SER:HB3	2.06	0.55
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.87	0.55
25:BA:934:A:H4'	25:BA:935:C:C5	2.39	0.55
1:CA:324:G:N7	61:CA:4084:HOH:O	2.33	0.55
25:DA:286:C:H2'	25:DA:287:C:H6	1.71	0.55
2:AB:229:VAL:HG12	2:AB:230:VAL:H	1.70	0.55
25:DA:906:G:O2'	36:DQ:67:ARG:NH2	2.37	0.55
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.89	0.55
1:AA:738:C:OP1	6:AF:2:ARG:NH1	2.39	0.55
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.88	0.55
25:BA:742:G:OP1	25:BA:1426:G:O2'	2.22	0.55
25:DA:957:A:H5'	36:DQ:76:LYS:HG3	1.88	0.55
25:BA:1553:A:O2'	25:BA:1554:A:H8	1.88	0.55
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.06	0.55
25:DA:2357:U:OP1	46:D0:20:ARG:HD3	2.06	0.55
35:BP:62:LEU:O	54:B8:13:ARG:HD3	2.05	0.55
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.40	0.55
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.40	0.55
25:BA:2332:A:H2'	25:BA:2332:A:N3	2.20	0.55
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.41	0.55
25:BA:721:G:H1'	29:BF:74:ARG:HD3	1.88	0.55
25:BA:2373:A:OP1	54:B8:27:THR:OG1	2.24	0.55
1:AA:487:A:H2'	1:AA:488:C:O4'	2.06	0.55
15:CO:88:ARG:NH2	15:CO:88:ARG:HB3	2.21	0.55
1:CA:433:C:H2'	1:CA:434:U:H6	1.72	0.55
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.88	0.55
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.07	0.55
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.06	0.55
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.87	0.55
12:AL:71:PRO:HG2	12:AL:102:ARG:HG3	1.88	0.55
33:DN:96:GLU:H	33:DN:96:GLU:CD	2.10	0.55
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.07	0.55
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.07	0.55
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:219:VAL:HA	2:AB:222:ILE:HD11	1.88	0.55
1:AA:630:G:H2'	1:AA:631:G:C8	2.41	0.55
25:DA:2640:G:H1	25:DA:2774:C:H42	1.55	0.55
3:AC:130:VAL:HG21	3:AC:157:ILE:HG23	1.88	0.55
1:CA:130:A:H5'	17:CQ:63:ARG:HE	1.71	0.55
1:CA:441:A:H3'	1:CA:442:C:C6	2.40	0.55
25:DA:614(C):A:C4	29:DF:180:GLY:HA2	2.42	0.55
6:CF:99:ALA:HB1	18:CR:23:LYS:HE3	1.88	0.55
25:BA:1766:G:H3'	25:BA:1767:A:H5''	1.87	0.55
32:BI:133:HIS:ND1	32:BI:134:PRO:O	2.38	0.55
31:DH:149:ARG:NH1	31:DH:167:GLU:OE2	2.38	0.55
2:AB:163:PHE:HA	2:AB:185:ILE:HG13	1.89	0.55
1:CA:445:G:H2'	1:CA:446:G:C8	2.42	0.55
25:BA:1466:U:HO2'	25:BA:1467:G:P	2.29	0.55
25:DA:2314:C:H2'	25:DA:2315:G:H8	1.72	0.55
1:AA:833:U:H2'	1:AA:834:C:H6	1.71	0.55
26:DB:95:C:H2'	26:DB:96:U:H6	1.71	0.55
25:DA:2541:A:N7	61:DA:3938:HOH:O	2.33	0.55
54:B8:39:LYS:O	54:B8:43:GLN:HG3	2.06	0.55
1:AA:768:A:OP2	61:AA:4024:HOH:O	2.18	0.55
8:CH:112:LEU:HA	8:CH:134:ILE:HG12	1.89	0.55
16:AP:28:ARG:HG2	16:AP:29:ASP:OD1	2.05	0.55
11:CK:85:ARG:HE	11:CK:111:ASP:HB3	1.71	0.55
25:DA:1025:G:O2'	61:DA:4219:HOH:O	2.06	0.55
10:AJ:35:SER:CB	10:AJ:73:ASP:HB2	2.29	0.55
1:AA:91:C:H2'	1:AA:92:C:C6	2.42	0.55
13:CM:60:VAL:HG23	13:CM:64:TRP:CE3	2.42	0.55
1:AA:1260:C:OP1	1:AA:1284:C:O2'	2.25	0.55
25:BA:1232:G:H5''	41:BV:81:TYR:CE1	2.41	0.55
1:AA:727:G:N2	1:AA:730:G:OP2	2.39	0.55
45:BZ:48:PHE:CE1	45:BZ:52:SER:HA	2.41	0.55
1:AA:1239:A:H62	1:AA:1299:A:N6	2.05	0.55
47:D1:85:LEU:HB3	47:D1:89:GLU:HB3	1.88	0.55
25:BA:1698:G:OP1	37:BR:40:LYS:HE3	2.06	0.55
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	1.88	0.55
25:DA:1805:U:O2	27:DD:50:THR:HB	2.07	0.55
25:DA:668:G:H5'	25:DA:669:G:OP2	2.06	0.55
1:CA:927:G:H2'	1:CA:928:G:H8	1.72	0.55
4:AD:3:ARG:HE	4:AD:118:ARG:HD3	1.71	0.55
1:AA:880:C:OP1	12:AL:8:ASN:ND2	2.37	0.55
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.39	0.55
25:DA:800:A:OP1	25:DA:800:A:H8	1.90	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AX:59:A:H2'	23:AX:60:U:H5'	1.88	0.55
1:CA:1025:U:H1'	1:CA:1026:G:C8	2.42	0.55
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.22	0.55
2:AB:87:ARG:NH2	2:AB:220:ASP:OD1	2.24	0.55
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.06	0.55
1:CA:840:C:H4'	1:CA:841:U:OP1	2.06	0.55
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.39	0.55
25:DA:1889:A:N1	25:DA:2234:G:H1'	2.22	0.55
1:AA:1008:C:H42	1:AA:1021:G:H1	1.54	0.55
45:DZ:52:SER:OG	45:DZ:53:ILE:N	2.40	0.55
2:AB:30:ARG:HH21	2:AB:194:PRO:HB2	1.72	0.55
42:DW:9:TYR:H	42:DW:102:HIS:CE1	2.25	0.55
7:CG:69:VAL:HG21	7:CG:104:LEU:HD11	1.88	0.55
4:AD:107:ARG:NH2	4:AD:194:LEU:HD22	2.21	0.55
25:DA:1448:G:H4'	25:DA:1542:A:OP1	2.06	0.55
1:AA:1127:G:H1'	1:AA:1280:A:C6	2.42	0.55
25:DA:848:G:N3	25:DA:933:A:H1'	2.21	0.55
25:BA:933:C:H4'	25:BA:933:C:OP1	2.05	0.55
25:BA:1639:G:H2'	25:BA:1640:G:H8	1.72	0.55
25:DA:139(A):G:N7	61:DA:4443:HOH:O	2.33	0.55
25:DA:71:A:N7	43:DX:31:HIS:HE1	2.04	0.55
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.42	0.55
29:BF:116:ASP:OD2	35:BP:1:MET:HB2	2.07	0.55
49:D3:10:LYS:HB3	49:D3:53:LEU:HA	1.89	0.55
25:DA:1014:U:H2'	25:DA:1015:G:H8	1.72	0.55
46:B0:30:VAL:HG22	46:B0:66:VAL:HG22	1.89	0.55
1:CA:543:C:C2'	1:CA:544:G:H5'	2.36	0.55
35:DP:101:VAL:HA	35:DP:106:LEU:O	2.07	0.55
2:AB:7:VAL:HG11	2:AB:221:LEU:HD23	1.89	0.55
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.40	0.55
8:CH:68:ARG:HH11	8:CH:68:ARG:HG3	1.71	0.54
25:DA:19:C:H2'	25:DA:20:C:H6	1.71	0.54
25:DA:1427:A:H4'	25:DA:1428:C:O5'	2.07	0.54
1:CA:1216:G:H5''	14:CN:5:ALA:CB	2.37	0.54
10:AJ:47:PHE:CZ	14:AN:37:PHE:HE1	2.25	0.54
5:CE:78:HIS:CE1	5:CE:142:LEU:HA	2.42	0.54
2:AB:178:ARG:NH2	8:AH:68:ARG:HH22	2.05	0.54
20:AT:47:GLY:HA2	20:AT:48:LYS:HB2	1.89	0.54
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.30	0.54
5:AE:15:ARG:HD2	5:AE:26:PHE:CD2	2.41	0.54
21:CU:12:LYS:HB3	21:CU:22:ARG:HD2	1.89	0.54
25:DA:1651:G:OP1	37:DR:40:LYS:HE3	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.06	0.54
25:DA:1009:A:OP2	61:DA:4091:HOH:O	2.18	0.54
50:B4:63:TYR:N	50:B4:63:TYR:HD1	2.06	0.54
1:CA:192:U:H2'	1:CA:193:C:H6	1.71	0.54
1:CA:671:G:H2'	1:CA:672:U:O4'	2.07	0.54
25:BA:1405:A:N1	25:BA:1418:U:O4	2.40	0.54
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.71	0.54
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.42	0.54
1:CA:8:A:C6	4:CD:209:ARG:HB2	2.42	0.54
3:CC:116:VAL:HG21	3:CC:202:ILE:HD11	1.89	0.54
1:AA:877:C:H5''	8:AH:88:LYS:HD3	1.89	0.54
25:DA:1579:A:H2'	25:DA:1580:A:C8	2.43	0.54
37:BR:97:VAL:HG22	37:BR:114:VAL:HG22	1.89	0.54
33:BN:58:ASP:OD1	33:BN:58:ASP:N	2.37	0.54
1:AA:339:C:OP2	34:BO:97:ARG:HD3	2.07	0.54
1:CA:1025:U:N3	1:CA:1036:G:C6	2.75	0.54
1:AA:96:U:H2'	1:AA:97:G:H8	1.71	0.54
4:AD:172:PRO:HB2	4:AD:187:ARG:NH2	2.22	0.54
38:BS:11:LYS:HD2	38:BS:15:ARG:HH12	1.73	0.54
40:BU:76:TYR:HH	40:BU:92:ARG:HH11	1.50	0.54
5:CE:53:LEU:HD12	5:CE:53:LEU:H	1.73	0.54
25:BA:1553:A:O2'	25:BA:1554:A:O5'	2.25	0.54
4:AD:103:ASN:O	4:AD:107:ARG:HG2	2.07	0.54
9:CI:23:ASN:OD1	9:CI:25:LYS:HE3	2.08	0.54
52:D6:35:GLU:HG2	52:D6:50:ARG:HD3	1.88	0.54
49:B3:55:ARG:NH1	49:B3:57:GLU:OE1	2.36	0.54
25:DA:2887:U:H2'	25:DA:2888:C:C6	2.42	0.54
1:CA:1120:G:C6	1:CA:1154:G:C2	2.95	0.54
1:CA:923:A:OP1	5:CE:21:ALA:HB2	2.08	0.54
25:BA:1003:U:OP2	36:BQ:14:ARG:NH1	2.41	0.54
30:BG:16:ARG:CZ	30:BG:31:VAL:HG11	2.37	0.54
1:AA:105:G:H2'	1:AA:106:C:C6	2.43	0.54
1:AA:1010:G:N2	1:AA:1020:U:O2'	2.40	0.54
1:CA:552:U:H2'	1:CA:553:A:H5'	1.89	0.54
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.08	0.54
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.39	0.54
39:DT:116:ALA:HB1	39:DT:121:ILE:HD11	1.88	0.54
1:AA:986:A:H1'	19:AS:54:GLY:O	2.07	0.54
25:DA:2335:A:O2'	25:DA:2336:A:H5''	2.07	0.54
32:DI:117:GLU:HG3	32:DI:118:LYS:H	1.71	0.54
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.22	0.54
10:AJ:8:LEU:HB2	10:AJ:70:ARG:HB2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
50:D4:2:LYS:HB2	50:D4:5:ILE:HD13	1.89	0.54
1:CA:560:U:O2'	1:CA:561:U:OP2	2.22	0.54
25:DA:918:A:H5''	26:DB:98:G:O2'	2.08	0.54
26:BB:43:C:H5''	50:B4:1:MET:HG2	1.90	0.54
1:CA:1015:A:H2'	1:CA:1016:A:H8	1.72	0.54
4:AD:122:ARG:HA	4:AD:122:ARG:HE	1.72	0.54
4:AD:18:LYS:HD2	4:AD:31:CYS:SG	2.48	0.54
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.39	0.54
34:DO:116:SER:OG	34:DO:117:LEU:N	2.40	0.54
36:BQ:56:ARG:HG3	36:BQ:56:ARG:HH11	1.71	0.54
1:CA:250:A:H4'	1:CA:251:G:O5'	2.08	0.54
27:DD:172:TYR:CD1	27:DD:186:HIS:HA	2.43	0.54
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.06	0.54
25:BA:762:G:H2'	25:BA:763:A:O4'	2.08	0.54
21:CU:15:ARG:HB2	21:CU:15:ARG:HH11	1.72	0.54
25:BA:144:C:H5'	43:BX:2:LYS:HE2	1.89	0.54
1:CA:1154:G:N7	1:CA:1155:G:C8	2.76	0.54
25:DA:195:A:OP1	35:DP:46:LYS:NZ	2.37	0.54
1:CA:1129:C:H1'	1:CA:1130:A:N7	2.21	0.54
1:AA:190:U:H2'	1:AA:191:G:H8	1.70	0.54
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.89	0.54
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.07	0.54
1:AA:159:G:N2	1:AA:161:A:H3'	2.22	0.54
5:AE:77:PRO:HD2	5:AE:142:LEU:HD22	1.89	0.54
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.07	0.54
25:DA:348:G:H2'	25:DA:349:G:H8	1.72	0.54
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.43	0.54
44:DY:7:VAL:HG21	44:DY:72:VAL:HG12	1.90	0.54
9:CI:4:TYR:CZ	9:CI:88:TYR:HA	2.43	0.54
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.12	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HD2	1.90	0.54
26:DB:50:G:OP1	38:DS:63:THR:OG1	2.19	0.54
9:CI:4:TYR:CE2	9:CI:88:TYR:HD1	2.25	0.54
19:CS:17:GLU:O	19:CS:21:GLU:N	2.34	0.54
25:DA:1341:U:OP2	25:DA:1394:U:O2'	2.23	0.54
25:DA:607:U:OP1	29:DF:102:PRO:HA	2.08	0.54
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.43	0.54
39:BT:5:ALA:O	39:BT:9:LEU:N	2.41	0.54
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.42	0.54
28:BE:59:VAL:HG21	28:BE:74:PRO:HB3	1.90	0.54
1:AA:434:U:H2'	1:AA:435:C:C6	2.42	0.54
25:DA:1270:C:H5''	25:DA:1271:G:H5'	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:78:G:C6	1:AA:91:C:N4	2.75	0.54
34:BO:35:VAL:HG11	34:BO:103:ALA:CB	2.36	0.54
1:AA:1316:G:H2'	1:AA:1318:A:OP2	2.07	0.54
1:CA:1169:A:N7	1:CA:1170:A:C5	2.76	0.54
1:AA:186:C:H2'	1:AA:187:C:C6	2.42	0.54
1:CA:942:G:C2	1:CA:1342:C:C2	2.96	0.54
25:DA:340:A:N6	25:DA:341:G:C2	2.75	0.54
1:CA:991:U:O4	1:CA:1212:U:H1'	2.08	0.54
25:BA:1471:G:H2'	25:BA:1472:G:C8	2.43	0.54
1:AA:72:C:H2'	1:AA:73:G:O4'	2.08	0.54
38:DS:34:HIS:ND1	38:DS:53:SER:OG	2.33	0.54
5:AE:51:VAL:O	5:AE:55:VAL:HG23	2.08	0.54
25:BA:236:G:H4'	25:BA:413:G:C5	2.43	0.54
28:DE:24:THR:HG22	28:DE:186:GLY:O	2.07	0.54
1:CA:1154:G:N7	1:CA:1155:G:N9	2.55	0.54
30:BG:11:TYR:CZ	30:BG:16:ARG:HD3	2.41	0.54
25:DA:2268:A:OP1	61:DA:4048:HOH:O	2.18	0.54
4:AD:121:VAL:O	4:AD:134:ASP:HA	2.07	0.54
5:AE:76:ILE:HB	5:AE:77:PRO:HD2	1.90	0.54
25:DA:887:A:H5'	25:DA:888:C:OP1	2.07	0.54
25:BA:312:C:H2'	25:BA:313:A:H8	1.72	0.54
25:DA:2331:G:O2'	46:D0:43:THR:HG22	2.08	0.54
9:CI:4:TYR:CE1	9:CI:88:TYR:HA	2.42	0.54
25:BA:287:G:N7	25:BA:448:U:H2'	2.22	0.54
25:DA:708:C:H42	25:DA:723:G:H1	1.55	0.54
30:BG:143:GLU:OE2	50:B4:26:SER:OG	2.20	0.54
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.72	0.54
23:AX:61:C:H2'	23:AX:62:C:H6	1.72	0.54
3:CC:50:ALA:HB1	3:CC:72:LYS:O	2.08	0.54
25:DA:2706:G:N7	61:DA:4124:HOH:O	2.34	0.54
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.43	0.54
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.73	0.54
1:CA:841:U:H6	1:CA:841:U:OP1	1.91	0.54
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.07	0.54
13:CM:25:ILE:HD11	13:CM:66:LEU:HD13	1.90	0.54
25:DA:529:A:H62	25:DA:2041:U:H3	1.56	0.54
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.42	0.54
1:CA:985:C:H2'	1:CA:986:A:C8	2.43	0.54
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.41	0.54
19:AS:61:TYR:CE2	19:AS:63:THR:HG23	2.44	0.54
1:AA:69:G:H2'	1:AA:70:G:C8	2.43	0.54
3:AC:129:ALA:HB3	3:AC:132:ARG:HB2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:BQ:84:GLY:O	36:BQ:85:LYS:HB2	2.08	0.54
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.43	0.54
25:DA:997:G:OP1	40:DU:92:ARG:HG2	2.08	0.53
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.73	0.53
6:AF:69:GLU:OE1	6:AF:69:GLU:N	2.39	0.53
1:CA:737:A:H2'	1:CA:738:C:C6	2.43	0.53
25:BA:479:C:O2	25:BA:483:A:O2'	2.24	0.53
25:DA:2689:U:P	25:DA:2719:G:H22	2.31	0.53
19:CS:20:LEU:HD23	19:CS:23:ASN:HD22	1.73	0.53
25:BA:2474:U:H1'	25:BA:2503:U:O4	2.08	0.53
12:CL:36:VAL:HG22	12:CL:82:VAL:HG22	1.89	0.53
28:DE:55:ASN:O	28:DE:58:ARG:HG2	2.07	0.53
40:DU:89:GLU:HB2	41:DV:50:PRO:HB2	1.89	0.53
1:CA:276:G:H2'	1:CA:277:C:H5'	1.90	0.53
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.90	0.53
1:AA:316:G:OP2	1:AA:351:G:O2'	2.24	0.53
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.25	0.53
25:BA:2822:G:N2	25:BA:2899:C:O2	2.41	0.53
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.09	0.53
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.43	0.53
15:CO:56:LEU:O	15:CO:60:VAL:HG23	2.08	0.53
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.90	0.53
50:B4:63:TYR:CD1	50:B4:63:TYR:N	2.76	0.53
1:CA:192:U:H2'	1:CA:193:C:C6	2.43	0.53
25:BA:272:U:OP1	32:BI:50:ARG:NH2	2.42	0.53
1:AA:21:G:H2'	1:AA:22:G:C8	2.43	0.53
4:AD:116:GLN:NE2	4:AD:157:LEU:HD21	2.23	0.53
5:CE:52:PRO:HG2	5:CE:53:LEU:HD12	1.91	0.53
25:DA:1469:A:H2'	25:DA:1470:G:O4'	2.08	0.53
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.42	0.53
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.43	0.53
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.08	0.53
28:DE:119:ARG:HD2	28:DE:120:TRP:CE2	2.43	0.53
25:DA:1826:G:H4'	27:DD:242:ARG:NH1	2.23	0.53
31:DH:64:LEU:O	31:DH:68:THR:OG1	2.20	0.53
53:B7:1:MET:H3	53:B7:1:MET:HE3	1.73	0.53
23:CX:19:G:H4'	23:CX:20:U:OP2	2.09	0.53
25:BA:1985:U:H4'	25:BA:1986:G:OP1	2.08	0.53
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.43	0.53
25:BA:1346:U:H4'	25:BA:1347:A:H5'	1.91	0.53
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.26	0.53
1:CA:598:U:H2'	1:CA:599:C:C6	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:CJ:48:THR:O	14:CN:34:TYR:OH	2.27	0.53
1:CA:557:G:C6	1:CA:558:G:C6	2.96	0.53
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	1.90	0.53
35:BP:121:LYS:HG2	35:BP:122:PRO:HD2	1.91	0.53
31:DH:80:SER:OG	31:DH:81:GLU:N	2.40	0.53
18:CR:29:PHE:HE1	18:CR:31:LEU:HD13	1.72	0.53
8:AH:34:GLU:OE2	8:AH:37:ARG:NH1	2.34	0.53
31:DH:33:LEU:HD21	31:DH:136:ILE:HG13	1.90	0.53
11:AK:98:LEU:O	11:AK:101:SER:OG	2.17	0.53
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.38	0.53
1:CA:999:C:N3	1:CA:1042:G:C2	2.77	0.53
25:DA:300:A:H1'	25:DA:319:C:H1'	1.88	0.53
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.08	0.53
1:AA:262:A:C6	1:AA:263:A:C6	2.96	0.53
1:CA:1170:A:O2'	1:CA:1171:G:C8	2.61	0.53
1:CA:1305:G:H22	1:CA:1331:G:H1'	1.73	0.53
23:CX:10:G:N2	23:CX:26:G:H1'	2.24	0.53
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.43	0.53
13:CM:92:HIS:CE1	13:CM:98:VAL:HG11	2.44	0.53
26:BB:33:G:C2	26:BB:50:G:C2	2.97	0.53
30:DG:41:GLN:HB3	30:DG:43:LEU:HD22	1.91	0.53
25:DA:2831:G:OP1	28:DE:58:ARG:NH2	2.28	0.53
1:AA:545:C:H5'	4:AD:72:GLU:HG2	1.90	0.53
28:DE:163:GLU:HG2	28:DE:164:ARG:N	2.23	0.53
25:BA:2642:G:H2'	25:BA:2643:G:C8	2.43	0.53
1:CA:1128:C:H1'	1:CA:1147:C:N3	2.22	0.53
1:CA:1126:U:H4'	1:CA:1281:U:H1'	1.91	0.53
25:DA:2849:U:O4	39:DT:23:ARG:NH2	2.32	0.53
1:AA:664:G:N2	1:AA:741:G:H1	2.06	0.53
1:CA:837:G:H1	1:CA:849:C:N4	2.06	0.53
45:DZ:154:ASP:N	45:DZ:154:ASP:OD1	2.42	0.53
1:AA:991:U:N3	1:AA:1212:U:H1'	2.24	0.53
11:AK:48:ILE:O	11:AK:50:TYR:N	2.40	0.53
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.23	0.53
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	1.91	0.53
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.91	0.53
26:BB:78:A:C2	26:BB:100:A:C4	2.95	0.53
1:AA:352:C:OP2	61:AA:4067:HOH:O	2.19	0.53
25:DA:997:G:O2'	25:DA:998:C:H5'	2.08	0.53
16:CP:5:ARG:NH1	16:CP:28:ARG:HA	2.24	0.53
25:DA:2299:G:H22	25:DA:2318:G:H8	1.56	0.53
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.09	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:CQ:66:SER:OG	17:CQ:67:LYS:N	2.42	0.53
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.41	0.53
1:AA:102:G:H2'	1:AA:103:C:C6	2.43	0.53
25:BA:1405:A:N3	25:BA:1405:A:H5'	2.24	0.53
1:CA:1104:G:H4'	2:CB:111:ARG:HH11	1.73	0.53
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.44	0.53
45:DZ:53:ILE:HG22	45:DZ:71:VAL:O	2.09	0.53
25:DA:2887:U:H2'	25:DA:2888:C:H6	1.73	0.53
2:AB:35:GLU:HB2	2:AB:40:HIS:CD2	2.44	0.53
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.90	0.53
25:BA:346:A:H5'	25:BA:364:A:H1'	1.89	0.53
35:BP:124:LYS:HG3	35:BP:144:GLU:HG2	1.91	0.53
18:AR:40:LEU:HD22	18:AR:70:ILE:HG12	1.90	0.53
32:BI:108:THR:O	32:BI:109:ILE:HD12	2.09	0.53
25:BA:1293:A:OP1	29:BF:95:ARG:NH2	2.39	0.53
25:DA:1914:C:H2'	25:DA:1915:U:O4'	2.08	0.53
25:BA:1775:C:H5'	25:BA:1776:G:OP2	2.08	0.53
25:BA:776:G:H2'	25:BA:1806:U:H1'	1.90	0.53
4:AD:196:LEU:H	4:AD:196:LEU:HD12	1.73	0.53
25:DA:1946:U:H2'	25:DA:1947:C:C6	2.43	0.53
44:BY:38:ILE:HD11	44:BY:66:PRO:HG3	1.90	0.53
25:DA:2600:A:C6	25:DA:2601:C:N4	2.77	0.53
25:DA:2510:C:H4'	61:DA:4416:HOH:O	2.07	0.53
1:AA:33:A:H2'	1:AA:34:C:C6	2.44	0.53
11:AK:15:ALA:O	11:AK:79:SER:N	2.33	0.53
35:BP:65:ARG:HG3	54:B8:25:MET:HG3	1.91	0.53
2:AB:219:VAL:O	2:AB:222:ILE:HG13	2.09	0.53
1:AA:473:G:C2	1:AA:474:G:C5	2.97	0.53
25:DA:2286:A:H4'	25:DA:2287:A:O4'	2.08	0.53
1:AA:1031:G:H2'	1:AA:1032:G:H8	1.73	0.53
19:AS:22:LEU:HD13	19:AS:47:HIS:CD2	2.44	0.53
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.44	0.53
48:D2:28:LYS:HD3	48:D2:60:LEU:HD11	1.91	0.53
1:AA:652:U:O4	1:AA:752:G:O2'	2.22	0.53
28:DE:108:SER:HB3	28:DE:165:VAL:HG21	1.91	0.53
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.41	0.53
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.90	0.53
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.90	0.53
30:DG:96:ARG:O	30:DG:99:MET:HB3	2.09	0.53
25:BA:1660:A:OP1	25:BA:1663:C:N4	2.39	0.53
23:AX:23:C:H2'	23:AX:24:U:C6	2.44	0.53
1:CA:587:G:N2	1:CA:754:C:OP2	2.34	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:67:U:H2'	25:DA:68:G:O4'	2.09	0.53
1:AA:258:G:H2'	1:AA:259:G:H8	1.73	0.53
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.09	0.53
1:AA:376:G:O3'	16:AP:5:ARG:NH2	2.41	0.53
8:AH:39:LEU:HB3	8:AH:45:ILE:HD11	1.90	0.53
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.89	0.53
25:BA:1067:A:H2'	25:BA:1069:U:H5'	1.89	0.53
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.43	0.53
25:BA:139:A:C8	25:BA:1454:C:O2'	2.60	0.53
25:DA:1319:G:C6	25:DA:1320:C:N4	2.77	0.53
1:AA:243:A:C2	1:AA:246:A:C8	2.97	0.53
25:DA:2469:A:C2	25:DA:2482:G:C8	2.97	0.53
13:CM:89:GLY:O	13:CM:93:ARG:HG3	2.09	0.53
25:DA:2189:U:H2'	25:DA:2190:G:H8	1.74	0.53
25:DA:796:C:H2'	25:DA:797:C:C6	2.44	0.53
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.08	0.53
25:DA:2698:U:H2'	25:DA:2699:C:C6	2.44	0.53
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.09	0.53
18:CR:61:LYS:O	18:CR:65:ILE:HG12	2.08	0.53
25:BA:326:C:H2'	25:BA:327:U:H6	1.74	0.53
25:BA:407:U:H2'	25:BA:408:G:H8	1.73	0.53
25:DA:96:G:H4'	48:D2:48:HIS:CD2	2.43	0.53
1:AA:189(K):U:H2'	1:AA:189(L):G:C8	2.44	0.53
1:CA:1007:C:C4	1:CA:1022:G:N1	2.73	0.53
1:CA:1122:U:C4	1:CA:1151:A:N1	2.77	0.53
25:DA:2712:U:H1'	25:DA:2712(A):A:C8	2.44	0.53
32:BI:3:VAL:HG12	32:BI:38:LEU:HA	1.91	0.53
1:AA:381:C:N4	1:AA:382:A:C2	2.77	0.53
41:BV:95:LEU:HD13	41:BV:97:LYS:HD3	1.90	0.53
25:BA:2255:U:OP1	61:BA:3915:HOH:O	2.19	0.53
23:AX:59:A:C2'	23:AX:60:U:H5'	2.39	0.53
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.91	0.53
23:AX:23:C:H2'	23:AX:24:U:H6	1.74	0.53
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.09	0.53
38:DS:11:LYS:O	38:DS:15:ARG:HG3	2.09	0.53
1:AA:987:G:H1	1:AA:1218:C:H42	1.57	0.53
25:BA:1597:C:OP1	25:BA:1765:U:O2'	2.19	0.53
30:DG:63:ILE:HA	30:DG:143:GLU:HG3	1.89	0.53
1:CA:73:G:C6	1:CA:97:G:C6	2.97	0.53
1:AA:1027:C:C2	1:AA:1034:G:N1	2.69	0.53
7:CG:62:PHE:HA	7:CG:124:LEU:HD22	1.90	0.53
1:CA:954:G:H2'	1:CA:955:U:C6	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.09	0.53
13:AM:37:THR:HG21	13:AM:56:LEU:HA	1.90	0.53
25:DA:687:C:H42	25:DA:787:U:H4'	1.73	0.53
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.41	0.53
15:CO:33:THR:HG21	15:CO:85:LEU:HD22	1.91	0.53
32:BI:27:ARG:HD2	47:B1:71:TYR:CE1	2.44	0.53
25:BA:851:A:OP1	61:BA:4484:HOH:O	2.19	0.53
12:AL:60:LEU:HD21	12:AL:66:VAL:HG22	1.91	0.53
32:BI:29:TYR:O	32:BI:32:PRO:HD2	2.09	0.53
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.24	0.52
1:AA:975:A:H8	1:AA:975:A:H5'	1.74	0.52
1:CA:983:A:H2	1:CA:984:C:C6	2.26	0.52
50:D4:46:GLN:HB3	50:D4:48:ARG:HG2	1.90	0.52
1:CA:473:G:H2'	1:CA:474:G:C8	2.45	0.52
27:BD:108:PRO:HG3	27:BD:143:HIS:CE1	2.43	0.52
25:DA:475:U:C4	25:DA:481:G:O6	2.62	0.52
25:BA:1993:A:C4	27:BD:241:PRO:HD3	2.45	0.52
5:CE:90:VAL:O	5:CE:91:LEU:HD13	2.08	0.52
25:DA:1344:G:O2'	25:DA:1385:G:H2'	2.09	0.52
25:BA:1653:C:H4'	25:BA:1654:A:O5'	2.09	0.52
1:CA:850:U:H2'	1:CA:851:G:H5''	1.90	0.52
25:DA:2750:A:H8	25:DA:2750:A:OP1	1.92	0.52
1:AA:1070:U:OP1	5:AE:25:ARG:NH1	2.38	0.52
25:DA:1858:G:O6	61:DA:4292:HOH:O	2.16	0.52
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.28	0.52
1:AA:154:C:N3	1:AA:168:G:N1	2.58	0.52
2:CB:178:ARG:CZ	8:CH:74:PRO:HG3	2.40	0.52
1:AA:923:A:H2'	1:AA:924:C:C6	2.44	0.52
25:DA:10:G:H2'	25:DA:11:G:C8	2.44	0.52
25:DA:1434:A:H61	25:DA:1558:A:N6	2.07	0.52
1:AA:56:U:H2'	1:AA:57:G:H8	1.72	0.52
25:DA:2313:C:O2	25:DA:2313:C:H2'	2.09	0.52
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	1.90	0.52
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.09	0.52
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.09	0.52
25:DA:531:C:H5'	61:DA:4094:HOH:O	2.09	0.52
31:DH:105:LEU:HD11	31:DH:148:ILE:HG23	1.91	0.52
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.24	0.52
25:BA:1954:A:H2'	25:BA:1955:G:O4'	2.09	0.52
1:CA:1116:C:H2'	1:CA:1117:G:H5''	1.90	0.52
32:DI:43:ASN:C	32:DI:43:ASN:HD22	2.12	0.52
25:BA:1952:G:O2'	25:BA:1990:G:O6	2.20	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.10	0.52
1:CA:1179:A:N1	1:CA:1180:A:C8	2.78	0.52
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.75	0.52
25:DA:2454:G:H1'	61:DA:3886:HOH:O	2.08	0.52
30:BG:16:ARG:HE	30:BG:31:VAL:HG11	1.73	0.52
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.44	0.52
49:B3:59:VAL:O	49:B3:60:GLU:HG2	2.09	0.52
32:DI:126:TYR:HB2	32:DI:142:VAL:HG23	1.92	0.52
36:DQ:56:ARG:CG	36:DQ:56:ARG:HH11	2.22	0.52
1:CA:583:A:H2'	1:CA:584:G:O4'	2.09	0.52
1:AA:1256:A:H5''	1:AA:1258:G:H1'	1.92	0.52
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.91	0.52
25:DA:1219:G:H1	25:DA:1230:C:H42	1.55	0.52
40:DU:78:THR:O	40:DU:117:GLN:NE2	2.42	0.52
25:BA:1913:G:H2'	25:BA:1914:C:C6	2.45	0.52
8:AH:120:THR:H	8:AH:123:GLU:HB2	1.72	0.52
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.73	0.52
1:AA:719:C:O2'	18:AR:49:LYS:HB3	2.10	0.52
1:AA:1142:G:H3'	1:AA:1143:G:H8	1.74	0.52
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.91	0.52
1:AA:558:G:H5''	1:AA:559:A:OP2	2.10	0.52
1:CA:1131:G:OP1	9:CI:20:ARG:NH2	2.42	0.52
40:DU:79:PHE:CZ	40:DU:83:LEU:HD21	2.44	0.52
25:DA:2704:C:H2'	25:DA:2705:A:O4'	2.09	0.52
1:CA:838:G:H1	1:CA:848:C:H42	1.56	0.52
25:BA:1221:G:N2	25:BA:1223:C:OP2	2.43	0.52
25:DA:2099:U:H5'	25:DA:2100:G:OP2	2.09	0.52
25:DA:2562:U:H1'	34:DO:23:ARG:HD3	1.92	0.52
1:CA:1237:C:HO2'	1:CA:1300:G:H1	1.55	0.52
25:BA:662:A:H8	35:BP:117:GLU:HG3	1.74	0.52
47:D1:73:LEU:HB3	47:D1:94:LEU:HD22	1.91	0.52
25:DA:991:C:OP1	61:DA:4100:HOH:O	2.19	0.52
27:DD:133:LEU:HA	27:DD:136:ILE:HD12	1.90	0.52
25:DA:446:G:OP1	40:DU:3:ARG:NH1	2.39	0.52
34:DO:71:ARG:NE	34:DO:105:GLU:OE2	2.42	0.52
25:DA:184:C:H2'	25:DA:185:U:H6	1.75	0.52
34:BO:8:LEU:HB2	34:BO:19:ILE:HG13	1.91	0.52
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.91	0.52
26:BB:86:G:H1	26:BB:91:C:N4	2.08	0.52
1:AA:364:A:H2'	1:AA:365:U:C6	2.44	0.52
38:DS:26:LEU:HD22	38:DS:87:PHE:CE1	2.44	0.52
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.25	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1589:C:H2'	25:DA:1590:U:C6	2.44	0.52
1:CA:1216:G:H5''	14:CN:5:ALA:HB2	1.91	0.52
1:AA:503:C:H2'	1:AA:504:C:H6	1.74	0.52
1:CA:1310:G:H5'	13:CM:77:ASN:ND2	2.25	0.52
1:AA:985:C:H2'	1:AA:986:A:C8	2.44	0.52
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.52
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.08	0.52
4:CD:99:SER:O	4:CD:140:VAL:HG23	2.09	0.52
1:AA:100:C:H2'	1:AA:101:A:C8	2.44	0.52
1:AA:1210:C:H2'	1:AA:1211:U:H5'	1.92	0.52
25:DA:2751:G:C8	31:DH:2:SER:N	2.77	0.52
30:DG:122:PRO:HG3	30:DG:180:PHE:HB3	1.92	0.52
25:BA:2819:A:C6	25:BA:2820:A:C6	2.98	0.52
32:DI:93:THR:O	32:DI:97:ILE:HG13	2.09	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.78	0.52
38:DS:3:ARG:O	38:DS:4:LEU:HD23	2.10	0.52
1:AA:195:A:N3	1:AA:222:U:O2'	2.30	0.52
28:BE:47:VAL:HG21	28:BE:86:PRO:CD	2.38	0.52
1:AA:148:G:O2'	1:AA:149:A:H8	1.91	0.52
25:DA:271(H):G:H2'	25:DA:271(I):G:C8	2.45	0.52
25:DA:1300:U:H4'	25:DA:1301:A:H5''	1.91	0.52
25:DA:524:U:H2'	25:DA:525:U:H6	1.73	0.52
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.74	0.52
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.44	0.52
25:DA:1309:G:O2'	25:DA:1611:C:O2'	2.27	0.52
1:AA:520:A:O2'	12:AL:73:GLU:OE1	2.14	0.52
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.90	0.52
25:DA:1857:G:O2'	25:DA:1885:A:N6	2.42	0.52
25:DA:947:G:N2	25:DA:971:C:C2	2.78	0.52
41:DV:62:LEU:HD11	41:DV:95:LEU:HB2	1.91	0.52
1:CA:358:U:H2'	1:CA:359:U:H6	1.75	0.52
25:DA:468:G:H5''	29:DF:60:SER:HB2	1.90	0.52
25:DA:539:G:H2'	25:DA:540:C:H6	1.73	0.52
37:DR:38:VAL:HG22	37:DR:112:ALA:HB2	1.92	0.52
41:DV:65:GLY:HA3	41:DV:91:TYR:CZ	2.44	0.52
31:DH:56:SER:OG	31:DH:57:ASP:N	2.40	0.52
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.07	0.52
1:CA:1041:A:C6	1:CA:1042:G:C6	2.98	0.52
30:DG:82:LEU:HA	30:DG:86:MET:SD	2.49	0.52
25:BA:2897:U:H2'	25:BA:2898:C:H6	1.72	0.52
33:DN:38:HIS:ND1	33:DN:39:ARG:HG3	2.25	0.52
25:DA:2262:U:H4'	25:DA:2328:A:C2	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.57	0.52
25:BA:173:C:H2'	25:BA:174:U:C6	2.44	0.52
25:DA:592:G:O2'	54:D8:4:MET:HG3	2.09	0.52
6:CF:96:PRO:HB3	18:CR:30:ASP:CG	2.30	0.52
25:BA:1941:A:H5''	25:BA:1942:C:OP2	2.10	0.52
45:DZ:6:LYS:HE2	45:DZ:43:GLU:OE1	2.09	0.52
26:BB:76:G:N2	26:BB:101:G:O6	2.40	0.52
45:DZ:152:ALA:O	45:DZ:155:LEU:HD22	2.10	0.52
45:DZ:157:LEU:HB3	45:DZ:161:VAL:HG13	1.92	0.52
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.91	0.52
30:DG:16:ARG:NE	30:DG:31:VAL:HG11	2.25	0.52
25:BA:1717:C:O2	28:BE:129:HIS:NE2	2.34	0.52
25:BA:1814:A:OP1	61:BA:4519:HOH:O	2.18	0.52
1:CA:1207:G:H2'	1:CA:1208:C:H6	1.75	0.52
1:CA:192:U:C2'	1:CA:193:C:H5'	2.40	0.52
26:DB:19:G:H2'	26:DB:20:C:O4'	2.09	0.52
1:AA:826:C:H2'	1:AA:827:U:C6	2.44	0.52
15:AO:74:ASP:OD2	15:AO:77:ARG:HG3	2.09	0.52
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.42	0.52
25:DA:348:G:H2'	25:DA:349:G:C8	2.45	0.52
45:DZ:8:TYR:HB2	45:DZ:38:TYR:CE2	2.45	0.52
54:B8:62:LEU:HB3	54:B8:65:GLU:HG2	1.91	0.52
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.92	0.52
15:AO:33:THR:HG21	15:AO:85:LEU:HD22	1.91	0.52
4:AD:85:LYS:HG3	4:AD:86:LYS:N	2.24	0.52
6:AF:67:MET:SD	6:AF:75:LEU:HD13	2.50	0.52
26:DB:46:A:H2'	26:DB:47:C:C6	2.44	0.52
1:CA:792:A:H4'	1:CA:793:U:O5'	2.10	0.52
25:DA:323:G:O2'	25:DA:1205:U:N3	2.32	0.52
25:DA:1268:A:H2'	25:DA:1269:A:O4'	2.10	0.52
1:CA:1492:A:H2'	1:CA:1493:A:H1'	1.92	0.52
2:CB:56:ARG:NH1	2:CB:56:ARG:HB3	2.25	0.52
1:CA:1269:A:H2	1:CA:1312:G:N3	2.08	0.52
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.25	0.52
1:AA:407:G:H2'	1:AA:408:A:H8	1.74	0.52
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.45	0.52
1:CA:1063:C:H5''	1:CA:1064:G:H2'	1.92	0.52
25:DA:72:U:OP2	48:D2:29:LYS:NZ	2.33	0.52
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.40	0.52
9:AI:7:THR:O	9:AI:83:ARG:NH1	2.41	0.52
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.45	0.52
25:BA:344:A:OP1	29:BF:135:LYS:NZ	2.41	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.39	0.52
1:AA:447:G:H2'	1:AA:485:G:N2	2.25	0.52
23:AX:10:G:N2	23:AX:26:G:H1'	2.25	0.52
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.91	0.52
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.35	0.52
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.92	0.52
9:CI:78:LYS:HD3	9:CI:101:PHE:HD2	1.75	0.52
36:BQ:35:VAL:HG13	36:BQ:130:LYS:HB3	1.92	0.52
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.43	0.52
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.45	0.52
2:AB:55:PHE:HA	2:AB:58:ILE:HD12	1.92	0.52
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.42	0.52
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.92	0.52
1:CA:1309:G:H5'	13:CM:78:ILE:HD11	1.92	0.52
25:DA:154:G:O6	25:DA:172:C:N4	2.43	0.52
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.45	0.52
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.10	0.52
28:DE:120:TRP:CE3	28:DE:155:LYS:HD3	2.45	0.52
40:DU:78:THR:HG22	40:DU:117:GLN:NE2	2.24	0.52
25:DA:601:C:O2	25:DA:605:C:H4'	2.10	0.52
25:DA:864:G:C6	25:DA:865:C:N4	2.78	0.52
31:BH:24:VAL:HG13	31:BH:37:VAL:HG21	1.91	0.52
20:CT:13:LEU:O	20:CT:17:ARG:HG3	2.10	0.52
29:DF:65:TRP:CZ2	29:DF:75:HIS:HD2	2.28	0.52
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.44	0.52
31:DH:106:THR:HG23	31:DH:112:PRO:HB3	1.92	0.52
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.25	0.52
25:DA:774:A:N3	25:DA:774:A:H2'	2.25	0.52
25:BA:864:C:O2'	25:BA:886:U:H5''	2.10	0.52
26:DB:66:A:H61	26:DB:109:C:H5'	1.75	0.52
25:DA:84:A:N1	25:DA:98:G:O2'	2.41	0.52
39:DT:23:ARG:HG3	39:DT:120:ARG:NH1	2.24	0.51
1:AA:184:G:H2'	1:AA:185:A:C8	2.42	0.51
1:AA:1223:C:H5''	1:AA:1224:G:C5'	2.40	0.51
12:CL:97:ARG:HB2	12:CL:98:TYR:CE2	2.45	0.51
1:CA:652:U:O2'	1:CA:653:A:OP2	2.24	0.51
1:AA:657:G:C2	1:AA:658:G:C8	2.98	0.51
1:AA:503:C:H2'	1:AA:504:C:C6	2.46	0.51
28:BE:11:MET:HG2	28:BE:24:THR:HB	1.92	0.51
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.43	0.51
26:BB:91:C:OP2	36:BQ:16:ARG:NH1	2.42	0.51
26:DB:43:C:H5''	50:D4:1:MET:HG2	1.91	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:528:A:C2	25:DA:2042:A:H2'	2.45	0.51
27:BD:234:GLY:O	61:BD:402:HOH:O	2.19	0.51
1:CA:15:G:H2'	1:CA:16:A:H8	1.74	0.51
1:AA:396:G:O2'	1:AA:398:C:OP1	2.15	0.51
25:DA:1529:G:H2'	25:DA:1530:C:H6	1.75	0.51
39:DT:19:LEU:HD22	39:DT:86:ILE:HG13	1.92	0.51
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.40	0.51
1:CA:1517:G:H1'	25:DA:1919:A:O3'	2.10	0.51
1:CA:660:G:H1	1:CA:745:C:H42	1.58	0.51
32:DI:62:LYS:HG2	32:DI:133:HIS:NE2	2.25	0.51
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.44	0.51
25:BA:611:U:H2'	25:BA:612:C:C6	2.46	0.51
1:AA:192:U:O2'	1:AA:193:C:H6	1.92	0.51
1:CA:1227:A:H8	1:CA:1227:A:H3'	1.75	0.51
1:CA:1206:G:H4'	3:CC:192:THR:O	2.09	0.51
18:CR:52:PRO:O	18:CR:56:THR:HG23	2.10	0.51
25:BA:1378:G:OP1	61:BA:4471:HOH:O	2.19	0.51
1:CA:1311:G:H1	1:CA:1326:C:H42	1.57	0.51
25:DA:652(B):A:C2	25:DA:655:A:H1'	2.44	0.51
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.42	0.51
26:DB:6:C:H2'	26:DB:7:G:H5''	1.92	0.51
20:CT:16:HIS:O	20:CT:19:SER:OG	2.17	0.51
28:DE:141:ILE:O	28:DE:154:LYS:HE2	2.10	0.51
1:AA:502:G:C6	1:AA:503:C:C4	2.98	0.51
32:BI:72:LEU:HA	32:BI:75:LEU:HD11	1.91	0.51
43:BX:1:MET:HE1	48:B2:26:ARG:HH21	1.75	0.51
1:AA:785:G:C2'	1:AA:786:G:H5'	2.41	0.51
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.92	0.51
25:BA:2779:G:H2'	25:BA:2779:G:N3	2.24	0.51
2:CB:167:PRO:HG3	2:CB:188:ALA:HB2	1.92	0.51
9:AI:64:THR:HG23	9:AI:66:ARG:HD2	1.92	0.51
1:CA:1121:U:C4	1:CA:1122:U:C5	2.98	0.51
25:BA:895:G:H2'	25:BA:896:A:C8	2.46	0.51
1:AA:1399:C:C2	1:AA:1502:A:N6	2.78	0.51
2:AB:220:ASP:O	2:AB:223:ILE:HG12	2.10	0.51
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.28	0.51
10:CJ:22:LYS:HA	10:CJ:25:GLU:HB2	1.93	0.51
25:BA:2372:A:H8	25:BA:2372:A:O5'	1.92	0.51
3:CC:180:ALA:HB1	3:CC:203:PHE:CE1	2.46	0.51
47:B1:3:LYS:HB2	47:B1:61:ARG:NH1	2.25	0.51
45:BZ:110:GLY:O	45:BZ:113:ALA:HB3	2.10	0.51
25:DA:2474:C:H5''	25:DA:2475:C:OP2	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.45	0.51
1:AA:45:U:H2'	1:AA:46:G:C8	2.45	0.51
1:CA:344:A:H4'	1:CA:345:C:OP2	2.10	0.51
36:BQ:51:ARG:HD3	36:BQ:66:ILE:HD11	1.93	0.51
1:AA:202:U:H3'	1:AA:203:U:H6	1.75	0.51
38:DS:88:ASP:OD1	38:DS:90:GLY:N	2.43	0.51
25:BA:2889:C:OP2	61:BA:4427:HOH:O	2.19	0.51
25:DA:852:G:N2	25:DA:926:A:H1'	2.26	0.51
25:DA:1563:G:H2'	25:DA:1564:C:C6	2.45	0.51
1:AA:626:U:C2	1:AA:627:G:C8	2.98	0.51
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.92	0.51
47:B1:91:LYS:O	47:B1:95:LEU:HD22	2.11	0.51
1:CA:1004:A:H2'	1:CA:1005:A:H5'	1.92	0.51
1:AA:413:G:N2	1:AA:428:G:H1'	2.24	0.51
8:AH:25:ASP:N	8:AH:25:ASP:OD1	2.43	0.51
1:AA:674:G:H2'	1:AA:675:A:H8	1.74	0.51
25:BA:1405:A:N6	25:BA:1418:U:H3	2.09	0.51
48:B2:2:LYS:O	48:B2:6:VAL:HG23	2.11	0.51
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.35	0.51
25:DA:184:C:H2'	25:DA:185:U:C6	2.45	0.51
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.91	0.51
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	1.92	0.51
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.92	0.51
1:CA:266:G:H5'	1:CA:266:G:C8	2.46	0.51
28:BE:2:LYS:HG3	28:BE:200:GLU:HB2	1.93	0.51
1:AA:543:C:C2'	1:AA:544:G:H5'	2.41	0.51
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.44	0.51
1:CA:1001(A):G:H2'	1:CA:1002:G:O4'	2.11	0.51
4:AD:158:ILE:O	4:AD:162:LEU:N	2.42	0.51
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.45	0.51
1:AA:865:A:C2	1:AA:918:A:H4'	2.46	0.51
19:AS:65:ASN:HA	50:B4:58:ARG:HG3	1.93	0.51
25:BA:559:U:H2'	25:BA:560:C:C6	2.45	0.51
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.26	0.51
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.10	0.51
25:DA:588:U:H2'	25:DA:589:C:C6	2.45	0.51
25:DA:1766:U:H2'	25:DA:1767:C:C6	2.44	0.51
2:AB:208:ILE:HA	2:AB:211:ILE:HD12	1.91	0.51
1:AA:102:G:H2'	1:AA:103:C:H6	1.76	0.51
1:CA:392:G:H2'	1:CA:393:A:H8	1.73	0.51
5:CE:40:ARG:NH2	5:CE:68:GLU:HA	2.25	0.51
25:BA:549:U:H2'	25:BA:550:U:C6	2.46	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:146:GLU:O	7:AG:149:ARG:HB2	2.11	0.51
49:D3:16:PRO:HB2	49:D3:18:ASP:OD1	2.11	0.51
1:AA:671:G:H2'	1:AA:672:U:O4'	2.11	0.51
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.74	0.51
48:B2:44:LEU:HD23	48:B2:47:ASN:HA	1.93	0.51
1:AA:1051:C:H2'	1:AA:1052:U:C6	2.45	0.51
25:DA:1297:C:H2'	25:DA:1298:C:H6	1.76	0.51
1:CA:424:G:H2'	1:CA:425:G:H8	1.75	0.51
1:AA:1144:G:N2	1:AA:1146:A:H62	2.09	0.51
25:DA:848:G:N9	25:DA:933:A:H8	2.08	0.51
1:AA:714:G:H2'	1:AA:715:A:C8	2.46	0.51
25:BA:155:C:H6	25:BA:155:C:OP2	1.94	0.51
1:AA:1187:G:H2'	1:AA:1188:A:C8	2.45	0.51
1:AA:747:C:OP2	1:AA:748:C:N4	2.44	0.51
25:BA:1647:G:N7	61:BA:4116:HOH:O	2.35	0.51
44:DY:44:ILE:HA	44:DY:63:LYS:O	2.11	0.51
25:DA:1709:U:H2'	25:DA:1710:C:C6	2.45	0.51
25:BA:296:U:H2'	25:BA:297:C:H6	1.76	0.51
25:DA:1810:A:H2'	25:DA:1811:G:O4'	2.11	0.51
1:CA:920:U:H2'	1:CA:921:U:C6	2.45	0.51
25:BA:581:G:OP1	33:BN:111:PRO:HD2	2.11	0.51
30:BG:131:TYR:HB3	30:BG:159:VAL:HG13	1.91	0.51
13:CM:14:ARG:CZ	13:CM:42:ALA:HA	2.40	0.51
36:DQ:75:THR:HA	36:DQ:89:ASN:O	2.11	0.51
25:DA:2602:A:OP2	25:DA:2603:G:H5''	2.11	0.51
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.26	0.51
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.46	0.51
1:CA:144:G:H1	1:CA:178:C:H42	1.59	0.51
2:CB:138:LEU:HA	2:CB:141:GLU:HB3	1.92	0.51
1:AA:346:G:C6	1:AA:348:G:N2	2.78	0.51
1:CA:1316:G:O2'	1:CA:1318:A:N7	2.38	0.51
1:CA:620:C:C2	4:CD:135:LEU:HG	2.46	0.51
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.46	0.51
38:BS:11:LYS:HD2	38:BS:15:ARG:NH1	2.25	0.51
50:B4:62:ARG:HB2	50:B4:63:TYR:CD1	2.44	0.51
25:DA:411:G:C5	35:DP:72:PRO:HB3	2.46	0.51
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.35	0.51
35:BP:121:LYS:O	35:BP:123:LEU:N	2.44	0.51
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.92	0.51
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.11	0.51
25:DA:2408:U:H6	25:DA:2408:U:O5'	1.94	0.51
2:CB:24:TRP:CZ3	2:CB:26:PRO:HA	2.46	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2050:U:H2'	25:BA:2051:G:O4'	2.11	0.51
8:AH:11:THR:HG22	8:AH:15:ASN:ND2	2.25	0.51
3:CC:42:LEU:O	3:CC:46:GLU:HG2	2.11	0.51
1:CA:596:C:H2'	1:CA:597:G:H8	1.74	0.51
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.44	0.51
37:BR:26:LYS:HE2	37:BR:70:LEU:O	2.10	0.51
1:CA:1002:G:N2	1:CA:1039:C:C4	2.79	0.51
1:CA:1162:C:N3	1:CA:1174:G:N2	2.45	0.51
25:BA:8:A:H2'	25:BA:9:U:H6	1.76	0.51
25:DA:2320:A:N3	25:DA:2320:A:H2'	2.24	0.51
7:CG:107:ALA:O	7:CG:111:ARG:HG3	2.10	0.51
2:CB:84:GLU:OE1	2:CB:216:SER:HA	2.11	0.51
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.46	0.51
4:AD:18:LYS:HG2	57:AD:501:SF4:S1	2.51	0.51
1:AA:991:U:C4	1:AA:1212:U:H1'	2.46	0.51
1:AA:1442:G:H2'	1:AA:1442(A):G:H5'	1.93	0.51
12:AL:59:ARG:HD3	24:AW:10:2QY:C	2.41	0.51
3:CC:164:ARG:NH2	3:CC:166:GLU:OE1	2.44	0.51
1:AA:738:C:H2'	1:AA:739:C:C6	2.46	0.51
25:DA:1164:G:H2'	25:DA:1165:U:C6	2.46	0.51
4:AD:3:ARG:HE	4:AD:118:ARG:CD	2.24	0.51
25:DA:1529:G:H2'	25:DA:1530:C:C6	2.45	0.51
25:DA:924:C:H2'	25:DA:925:C:C6	2.46	0.51
1:CA:1260:C:HO2'	1:CA:1283:G:HO2'	1.59	0.51
25:BA:1373:C:O2'	61:BA:3810:HOH:O	2.17	0.51
25:BA:1284:G:OP2	61:BA:4767:HOH:O	2.18	0.51
25:DA:2293:C:H5'	38:DS:89:ARG:NH2	2.25	0.51
1:CA:568:G:N7	12:CL:5:PRO:HD3	2.26	0.51
1:CA:1009:G:H2'	1:CA:1010:G:O4'	2.10	0.51
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.46	0.51
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.75	0.51
1:CA:980:C:H1'	14:CN:19:ARG:HA	1.92	0.51
45:BZ:150:LEU:HB3	45:BZ:171:ILE:HD11	1.92	0.51
25:DA:903:C:H2'	25:DA:904:C:C6	2.46	0.51
2:AB:185:ILE:CG2	2:AB:199:TYR:HB2	2.41	0.51
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.46	0.51
1:CA:599:C:C2'	1:CA:600:C:H5''	2.37	0.51
1:CA:623:C:H2'	1:CA:624:C:H6	1.75	0.51
44:BY:92:ASN:HB3	44:BY:94:LYS:N	2.22	0.51
2:CB:91:PRO:HG3	2:CB:154:LEU:HD12	1.92	0.51
25:DA:817:C:H2'	25:DA:818:G:O4'	2.11	0.51
25:DA:30:G:OP2	40:DU:5:LYS:HE2	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:82:MET:HE2	13:CM:92:HIS:HB3	1.93	0.51
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.10	0.51
26:BB:86:G:H1	26:BB:91:C:H42	1.59	0.51
1:AA:542:G:P	4:AD:10:ARG:HH22	2.34	0.51
25:DA:873:G:N2	25:DA:905:U:C2	2.78	0.51
17:CQ:45:HIS:HA	17:CQ:69:LYS:HE3	1.92	0.51
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.26	0.51
25:DA:1161:C:H2'	25:DA:1162:G:H8	1.76	0.51
25:DA:909:A:H2'	25:DA:912:C:H5	1.76	0.51
25:DA:1639:U:H2'	25:DA:1640:C:H5''	1.92	0.51
25:DA:2850:A:OP2	25:DA:2866:U:H5	1.94	0.51
13:AM:49:THR:HB	13:AM:52:GLU:H	1.75	0.51
47:B1:50:ARG:HG2	47:B1:59:THR:HB	1.93	0.51
1:CA:1005:A:C2	1:CA:1026:G:C8	2.99	0.51
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.11	0.51
25:DA:1022:G:N7	33:DN:66:LYS:HE2	2.26	0.51
26:DB:21:G:H2'	26:DB:22:U:O4'	2.10	0.51
1:CA:1120:G:C6	1:CA:1121:U:C4	2.98	0.51
1:CA:1122:U:H3	1:CA:1151:A:H2	1.59	0.51
1:AA:474:G:H2'	1:AA:475:G:C8	2.40	0.51
3:CC:35:GLU:OE2	3:CC:59:ARG:NH2	2.35	0.51
1:CA:396:G:O2'	1:CA:398:C:OP1	2.22	0.51
25:BA:1008:U:OP2	61:BA:4616:HOH:O	2.19	0.51
25:DA:784:A:C5	27:DD:229:VAL:HG21	2.46	0.51
1:AA:693:G:H2'	1:AA:694:A:C8	2.46	0.51
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.26	0.51
7:CG:76:ARG:HD3	7:CG:89:MET:HG3	1.93	0.51
28:DE:92:THR:O	28:DE:95:ILE:HG23	2.11	0.51
25:BA:1549:U:H2'	25:BA:1550:C:C6	2.46	0.51
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.39	0.51
33:DN:4:TYR:CD2	40:DU:100:VAL:HG11	2.46	0.51
2:CB:60:ASP:O	2:CB:64:ARG:HG2	2.10	0.51
1:AA:394:G:H2'	1:AA:395:C:H6	1.76	0.51
30:BG:137:GLU:OE1	30:BG:139:LEU:HD11	2.11	0.51
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.26	0.51
27:BD:123:ALA:HB3	27:BD:131:LEU:HG	1.93	0.51
49:B3:44:ARG:O	49:B3:48:GLU:HG3	2.11	0.51
25:DA:1833:U:H2'	25:DA:1834:U:H6	1.75	0.51
2:CB:80:ILE:HD13	2:CB:80:ILE:O	2.11	0.50
1:CA:922:G:H2'	1:CA:923:A:C8	2.45	0.50
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.45	0.50
1:AA:1025:U:H3	1:AA:1036:G:H1	1.60	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
50:B4:63:TYR:H	50:B4:63:TYR:HD1	1.57	0.50
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.93	0.50
23:AX:6:G:H1	23:AX:67:C:N4	2.09	0.50
1:CA:758:G:N7	61:CA:4152:HOH:O	2.34	0.50
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.92	0.50
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.11	0.50
25:BA:930:G:O6	25:BA:939:C:C2	2.64	0.50
18:AR:59:SER:H	18:AR:62:GLU:HG3	1.76	0.50
25:BA:2847:G:H21	37:BR:45:ARG:HH12	1.59	0.50
1:CA:127:G:OP1	1:CA:635:G:H1'	2.11	0.50
1:CA:545:C:OP1	4:CD:61:LYS:NZ	2.42	0.50
25:BA:1846:A:OP2	27:BD:54:ARG:NH2	2.45	0.50
25:DA:1819:A:H5''	27:DD:161:THR:HG21	1.93	0.50
29:DF:154:VAL:HG22	29:DF:191:ARG:HB2	1.94	0.50
25:BA:208:G:H2'	25:BA:209:G:O4'	2.11	0.50
31:BH:94:TYR:CE2	31:BH:160:LYS:HG2	2.46	0.50
1:CA:1060:C:H4'	10:CJ:51:ARG:HB3	1.93	0.50
12:CL:34:ARG:HG3	12:CL:105:TYR:CE2	2.45	0.50
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.11	0.50
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.26	0.50
25:DA:2847:U:OP1	39:DT:98:LYS:NZ	2.42	0.50
25:DA:118:A:N3	25:DA:178:G:H1'	2.26	0.50
31:DH:117:PRO:HG3	31:DH:123:PHE:CD2	2.46	0.50
28:BE:116:VAL:HG13	28:BE:122:PHE:HB2	1.93	0.50
25:DA:1007:C:P	33:DN:37:LYS:HZ2	2.34	0.50
25:DA:2615:U:H2'	25:DA:2616:C:H6	1.77	0.50
30:DG:14:GLU:O	30:DG:17:PRO:HD2	2.11	0.50
26:BB:42:C:C6	30:BG:69:ALA:HB2	2.46	0.50
25:BA:831:A:C5	27:BD:229:VAL:HG21	2.46	0.50
1:CA:1014:A:C2	1:CA:1219:U:H1'	2.46	0.50
25:DA:1665:A:H4'	34:DO:67:LYS:HB2	1.93	0.50
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.43	0.50
30:DG:97:ASP:O	30:DG:101:ILE:HG13	2.11	0.50
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.93	0.50
25:DA:2316:C:O2'	30:DG:128:ARG:NH1	2.44	0.50
25:BA:310:C:H2'	25:BA:311:C:C6	2.46	0.50
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.10	0.50
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.92	0.50
29:BF:164:ARG:O	29:BF:168:ARG:HB2	2.11	0.50
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.11	0.50
1:CA:1241:G:H2'	1:CA:1242:C:C6	2.45	0.50
13:CM:80:ARG:HH22	19:CS:69:HIS:CE1	2.29	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
55:B9:25:VAL:HB	55:B9:34:GLN:HB2	1.93	0.50
25:DA:581:C:H2'	25:DA:582:G:C8	2.47	0.50
30:DG:36:LYS:HE3	30:DG:95:ARG:NH1	2.27	0.50
35:DP:94:GLU:HG3	35:DP:124:LYS:HD3	1.94	0.50
35:DP:2:LYS:NZ	35:DP:4:SER:OG	2.42	0.50
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.11	0.50
28:BE:34:VAL:HG21	28:BE:78:LEU:HD11	1.93	0.50
1:CA:509:A:C8	1:CA:509:A:H3'	2.45	0.50
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.26	0.50
1:CA:91:C:H2'	1:CA:92:C:C6	2.46	0.50
32:DI:134:PRO:C	32:DI:136:VAL:H	2.15	0.50
34:DO:25:LEU:HD12	34:DO:38:VAL:HG12	1.93	0.50
23:CX:44:A:C6	23:CX:45:G:C6	3.00	0.50
30:DG:13:GLU:O	30:DG:15:VAL:N	2.44	0.50
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.41	0.50
1:AA:1036:G:H5'	1:AA:1037:C:C5	2.41	0.50
1:CA:487:A:H2'	1:CA:488:C:O4'	2.11	0.50
25:DA:1187:G:H5''	41:DV:81:TYR:CE1	2.46	0.50
1:AA:946:A:O2'	1:AA:1333:A:N3	2.40	0.50
25:DA:454:A:H4'	25:DA:455:C:OP2	2.11	0.50
1:CA:689:C:OP1	11:CK:27:ASN:ND2	2.45	0.50
25:BA:239:G:H2'	25:BA:240:A:C8	2.47	0.50
5:CE:100:VAL:HG22	5:CE:118:ILE:HG22	1.92	0.50
1:AA:985:C:H2'	1:AA:986:A:H8	1.76	0.50
18:AR:59:SER:H	18:AR:62:GLU:CG	2.24	0.50
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.11	0.50
30:BG:109:VAL:C	30:BG:112:PRO:HD2	2.31	0.50
46:B0:27:GLU:HG3	46:B0:68:GLU:HA	1.92	0.50
11:AK:34:ASP:HB3	11:AK:40:ILE:HD11	1.93	0.50
27:BD:26:LYS:HB3	27:BD:83:GLU:HG2	1.93	0.50
1:AA:308:C:H2'	1:AA:309:G:C8	2.46	0.50
1:AA:261:U:OP2	20:AT:79:ARG:NH2	2.44	0.50
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.11	0.50
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.23	0.50
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.25	0.50
25:DA:465:G:C6	25:DA:466:A:N6	2.79	0.50
1:CA:1270:C:C2'	1:CA:1271:G:H5'	2.42	0.50
1:CA:300:A:H1'	1:CA:565:U:O2	2.11	0.50
9:AI:3:GLN:HG2	9:AI:20:ARG:HE	1.77	0.50
33:DN:20:GLY:HA2	33:DN:61:ARG:NE	2.27	0.50
25:BA:2062:C:H2'	25:BA:2063:U:O4'	2.12	0.50
25:BA:2377:G:O6	54:B8:39:LYS:HE3	2.11	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.93	0.50
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.46	0.50
25:BA:275:C:H2'	25:BA:276:C:C6	2.47	0.50
25:DA:250:G:H2'	25:DA:251:A:C8	2.47	0.50
19:AS:52:TYR:HA	19:AS:56:GLN:O	2.11	0.50
1:AA:684:A:H2'	1:AA:685:G:C8	2.46	0.50
1:CA:998:G:N2	1:CA:1043:C:N3	2.48	0.50
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.93	0.50
8:AH:4:ASP:OD2	8:AH:85:ARG:NH1	2.36	0.50
43:BX:31:HIS:HD2	43:BX:33:LYS:N	2.05	0.50
43:DX:92:LEU:C	43:DX:94:GLY:H	2.15	0.50
25:DA:1412:A:H2'	25:DA:1413:G:H8	1.72	0.50
25:BA:1093:G:H2'	25:BA:1156:G:H1	1.77	0.50
1:CA:757:U:H2'	1:CA:758:G:O4'	2.11	0.50
1:CA:1072:G:C6	1:CA:1073:U:C4	3.00	0.50
25:DA:2336:A:H61	46:D0:43:THR:HG21	1.76	0.50
1:CA:170:U:O2'	1:CA:171:A:H5'	2.12	0.50
25:DA:937:U:H2'	25:DA:938:G:O4'	2.12	0.50
27:DD:221:VAL:HG22	27:DD:226:MET:CE	2.42	0.50
20:CT:42:GLN:O	20:CT:45:GLN:HB3	2.11	0.50
1:CA:977:A:N3	1:CA:977:A:H2'	2.26	0.50
52:B6:11:LEU:HB2	52:B6:21:TYR:HB2	1.92	0.50
29:DF:167:ALA:O	29:DF:170:LEU:HB2	2.11	0.50
7:AG:16:LEU:HD23	9:AI:41:VAL:HG12	1.92	0.50
9:AI:48:GLU:OE2	9:AI:51:ARG:HD2	2.12	0.50
48:D2:1:MET:SD	48:D2:56:GLN:NE2	2.85	0.50
1:CA:1004:A:C8	1:CA:1005:A:H4'	2.47	0.50
10:CJ:13:HIS:O	10:CJ:17:ASP:HB2	2.12	0.50
25:DA:1697:G:OP2	25:DA:1698:A:O2'	2.24	0.50
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.11	0.50
1:AA:166:G:C4	1:AA:167:G:N7	2.79	0.50
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.46	0.50
25:BA:2211:U:H2'	25:BA:2212:G:H5'	1.92	0.50
25:DA:1359:A:N1	25:DA:1372:U:C4	2.80	0.50
1:AA:407:G:OP1	4:AD:115:ARG:HD3	2.12	0.50
1:CA:1093:A:H5''	1:CA:1094:G:OP2	2.12	0.50
1:AA:826:C:H2'	1:AA:827:U:H6	1.77	0.50
1:AA:382:A:N3	1:AA:383:A:N7	2.59	0.50
1:AA:36:C:O2'	1:AA:501:C:OP1	2.26	0.50
1:AA:738:C:H2'	1:AA:739:C:H6	1.75	0.50
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.94	0.50
41:BV:14:VAL:HA	41:BV:18:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DE:101:ARG:CZ	28:DE:171:GLU:HB2	2.41	0.50
25:DA:2262:U:OP2	46:D0:19:LYS:HD3	2.12	0.50
1:CA:276:G:C2'	1:CA:277:C:H5'	2.41	0.50
32:BI:29:TYR:C	32:BI:32:PRO:HD2	2.31	0.50
1:AA:67:C:H2'	1:AA:68:G:C8	2.46	0.50
41:DV:95:LEU:HD13	41:DV:97:LYS:HD3	1.93	0.50
25:DA:1563:G:H2'	25:DA:1564:C:H6	1.77	0.50
25:DA:2293:C:H5'	25:DA:2294:C:OP2	2.11	0.50
5:AE:98:THR:HG22	5:AE:99:GLY:O	2.12	0.50
33:BN:15:LEU:HD12	33:BN:137:LYS:HG2	1.94	0.50
25:DA:1328:G:H2'	25:DA:1330:C:C5	2.47	0.50
61:BA:3804:HOH:O	51:B5:15:ARG:HG2	2.11	0.50
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.11	0.50
11:CK:81:ASP:OD1	11:CK:106:LYS:HE2	2.12	0.50
7:CG:16:LEU:H	7:CG:16:LEU:HD22	1.77	0.50
25:BA:1153:G:H2'	25:BA:1153:G:N3	2.27	0.50
7:AG:69:VAL:HG22	7:AG:135:VAL:HG22	1.94	0.50
40:DU:66:ASN:O	40:DU:70:ARG:HG3	2.12	0.50
25:DA:1153:C:H2'	25:DA:1154:G:O4'	2.12	0.50
3:AC:58:GLU:HB2	3:AC:65:ALA:HB2	1.92	0.50
2:AB:71:VAL:HB	2:AB:164:VAL:HG13	1.93	0.50
1:CA:1095:U:P	1:CA:1108:G:H1	2.35	0.50
1:AA:491:G:H2'	1:AA:492:G:O4'	2.12	0.50
25:DA:2336:A:H61	46:D0:43:THR:CG2	2.25	0.50
45:DZ:5:LEU:HD13	45:DZ:6:LYS:O	2.12	0.50
25:DA:2293:C:H42	25:DA:2339:G:H1	1.58	0.50
46:B0:27:GLU:HA	46:B0:67:VAL:HG12	1.94	0.50
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.47	0.50
7:AG:78:ARG:HG2	7:AG:79:ARG:HB2	1.94	0.50
25:BA:179:A:N3	25:BA:726:C:O2'	2.37	0.50
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.11	0.50
2:AB:45:GLN:O	2:AB:49:GLU:HB2	2.11	0.50
25:DA:1346:G:OP2	61:DA:4263:HOH:O	2.20	0.50
13:AM:84:ILE:HG13	19:AS:74:PHE:HE1	1.75	0.50
9:CI:105:ASP:HB2	9:CI:107:ARG:HG3	1.93	0.50
27:BD:38:LYS:HE3	27:BD:39:LYS:O	2.12	0.50
1:AA:872:A:C8	1:AA:874:G:C8	3.00	0.50
38:DS:25:ARG:NH1	38:DS:42:ASP:OD1	2.41	0.50
1:AA:397:A:N3	1:AA:397:A:H3'	2.26	0.50
42:DW:35:ILE:HG23	51:D5:28:PRO:HD2	1.93	0.50
1:CA:1036:G:N7	1:CA:1037:C:C2	2.80	0.50
1:CA:715:A:H2'	1:CA:716:A:C8	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:414:A:H2'	1:AA:415:A:O4'	2.12	0.50
25:DA:2711:A:H5''	25:DA:2712:U:H5''	1.94	0.50
9:AI:19:LEU:HB3	9:AI:59:PHE:HD2	1.76	0.50
25:BA:1221:G:H1'	25:BA:1222:A:O5'	2.11	0.50
25:DA:330:A:H2	25:DA:1210:A:H2'	1.76	0.50
13:CM:93:ARG:HD3	25:DA:888:C:OP2	2.12	0.50
25:DA:1406:U:H2'	25:DA:1407:C:C6	2.46	0.50
25:DA:954:G:C5	25:DA:955:C:C5	2.99	0.50
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.94	0.50
25:BA:1712:A:H4'	34:BO:67:LYS:HB2	1.92	0.50
1:CA:153:C:H2'	1:CA:154:C:C6	2.47	0.50
25:DA:2386:C:H2'	25:DA:2387:U:C6	2.46	0.50
25:BA:225:C:H2'	25:BA:226:C:C6	2.46	0.50
29:DF:150:GLY:HA2	29:DF:172:TRP:CE3	2.47	0.50
25:BA:1855:G:OP1	27:BD:52:ARG:NH1	2.40	0.50
20:CT:43:LEU:O	20:CT:47:GLY:N	2.45	0.50
1:AA:701:C:O2	1:AA:703:G:N1	2.45	0.50
25:DA:2882:A:OP1	37:DR:96:ARG:NE	2.44	0.50
1:AA:1269:A:H2	1:AA:1312:G:N3	2.10	0.50
5:AE:90:VAL:O	5:AE:91:LEU:HD13	2.10	0.50
1:AA:1129:C:O2'	1:AA:1139:G:N7	2.33	0.50
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.77	0.50
25:BA:831:A:H5'	25:BA:832:G:OP1	2.12	0.50
1:AA:457:C:H2'	1:AA:458:C:H6	1.74	0.50
35:DP:65:ARG:HG3	54:D8:25:MET:HG3	1.93	0.50
25:DA:878:A:N6	25:DA:900:A:N7	2.60	0.50
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.08	0.50
1:AA:1224:G:O2'	1:AA:1322:C:OP1	2.29	0.50
1:AA:174:C:H2'	1:AA:175:C:H6	1.76	0.50
25:DA:754:C:H2'	25:DA:755:C:C6	2.43	0.50
27:DD:16:MET:HG3	27:DD:206:LEU:O	2.12	0.50
25:DA:2302:G:C6	25:DA:2303:G:N7	2.80	0.50
1:AA:137:C:H2'	1:AA:138:G:H5'	1.94	0.50
27:BD:10:THR:OG1	27:BD:13:ARG:HB2	2.12	0.50
32:BI:93:THR:OG1	32:BI:96:ASP:OD1	2.19	0.50
25:BA:910:A:H2'	25:BA:911:G:H8	1.77	0.50
1:AA:203:U:OP2	1:AA:203:U:H2'	2.12	0.50
25:DA:873:G:H2'	25:DA:874:G:H5''	1.94	0.50
25:DA:1453:U:OP1	37:DR:77:ARG:NH1	2.36	0.50
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	2.11	0.50
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.45	0.50
4:AD:25:ARG:HG2	4:AD:25:ARG:O	2.11	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DB:3:C:H2'	26:DB:4:C:C6	2.47	0.50
1:CA:501:C:H2'	1:CA:502:G:C8	2.47	0.50
1:AA:1145:C:H4'	1:AA:1146:A:C5'	2.41	0.49
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.12	0.49
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	1.94	0.49
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.47	0.49
1:AA:1241:G:H1	1:AA:1296:C:N4	2.10	0.49
38:DS:10:ARG:HH21	38:DS:91:PRO:HB2	1.77	0.49
11:CK:20:TYR:CE1	11:CK:83:ILE:HD12	2.46	0.49
25:BA:2899:C:H2'	25:BA:2900:G:O4'	2.12	0.49
15:CO:29:VAL:HG11	15:CO:81:LEU:HD21	1.94	0.49
25:BA:2486:C:H5''	25:BA:2487:C:OP2	2.12	0.49
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.93	0.49
4:CD:26:CYS:HA	57:CD:501:SF4:S2	2.52	0.49
1:AA:524:G:H2'	1:AA:525:C:C6	2.46	0.49
48:D2:32:LEU:HD23	48:D2:53:LEU:HB3	1.94	0.49
1:CA:999:C:C4	1:CA:1042:G:C2	2.99	0.49
1:AA:160:A:N1	1:AA:343:U:C2	2.80	0.49
27:DD:71:ASP:HB2	27:DD:103:ARG:NH2	2.22	0.49
25:DA:1996:C:H4'	25:DA:1997:G:OP1	2.11	0.49
1:CA:1047:G:H5''	14:CN:4:LYS:HD3	1.93	0.49
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.47	0.49
32:DI:140:LEU:HD13	32:DI:142:VAL:HG13	1.94	0.49
1:CA:59:A:H5''	1:CA:60:A:H5''	1.94	0.49
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.28	0.49
25:DA:1651:G:H5'	37:DR:39:PRO:HG2	1.94	0.49
1:AA:1210:C:C2'	1:AA:1211:U:H5'	2.42	0.49
25:DA:1161:C:H2'	25:DA:1162:G:C8	2.46	0.49
46:B0:27:GLU:HB2	46:B0:69:PHE:HD1	1.77	0.49
7:AG:78:ARG:HH21	7:AG:156:TRP:HB3	1.77	0.49
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.77	0.49
25:DA:608:A:H2'	25:DA:609:A:C8	2.47	0.49
7:CG:47:CYS:O	7:CG:50:ILE:HG12	2.11	0.49
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.47	0.49
1:AA:64:G:H4'	1:AA:65:U:H3'	1.93	0.49
23:AX:20:U:H5''	23:AX:21:A:OP2	2.12	0.49
8:CH:124:ALA:O	8:CH:128:GLY:N	2.44	0.49
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.45	0.49
1:AA:1492:A:H1'	25:BA:1935:A:H61	1.78	0.49
25:BA:1001:G:OP2	36:BQ:87:LYS:HE2	2.12	0.49
1:CA:691:G:H2'	1:CA:692:U:C6	2.46	0.49
1:CA:297:G:N2	1:CA:300:A:OP2	2.45	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1222:A:H3'	25:BA:1223:C:C6	2.48	0.49
29:DF:20:LEU:HD22	29:DF:21:ALA:H	1.77	0.49
32:BI:38:LEU:HB2	32:BI:40:THR:HG22	1.94	0.49
1:AA:1298:C:H4'	1:AA:1299:A:C4	2.46	0.49
1:CA:358:U:H2'	1:CA:359:U:C6	2.47	0.49
25:BA:354:A:HO2'	25:BA:355:A:H8	1.58	0.49
35:DP:84:ASN:OD1	35:DP:117:GLU:HB2	2.12	0.49
25:BA:296:U:H2'	25:BA:297:C:C6	2.46	0.49
1:AA:41:G:H2'	1:AA:42:G:C8	2.47	0.49
10:CJ:11:PHE:CE1	10:CJ:67:THR:HG22	2.47	0.49
21:AU:9:ARG:HA	21:AU:22:ARG:HB2	1.94	0.49
34:DO:2:ILE:HD12	34:DO:6:THR:HG21	1.94	0.49
47:D1:7:ILE:HG23	47:D1:98:LEU:HD11	1.93	0.49
41:BV:98:GLU:OE1	41:BV:100:ARG:HD3	2.12	0.49
20:AT:57:ARG:HH22	20:AT:100:ILE:HD12	1.77	0.49
25:DA:812:C:H2'	25:DA:813:U:H6	1.77	0.49
12:CL:54:LYS:O	12:CL:70:ILE:HG13	2.11	0.49
42:BW:18:ARG:NH1	42:BW:76:VAL:O	2.46	0.49
25:BA:2314:G:C2	25:BA:2327:G:C2	3.00	0.49
7:CG:132:GLY:O	7:CG:136:LYS:HG2	2.12	0.49
54:D8:3:LYS:HB2	54:D8:64:TYR:OH	2.11	0.49
1:CA:1057:G:C5	1:CA:1204:A:C2	3.00	0.49
1:AA:615:C:H2'	1:AA:616:G:O4'	2.12	0.49
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	1.93	0.49
26:DB:78:A:H2'	26:DB:79:C:O4'	2.12	0.49
1:CA:1025:U:O2'	1:CA:1026:G:H5''	2.12	0.49
25:DA:2592:G:N7	61:DA:3923:HOH:O	2.34	0.49
25:DA:816:C:O2'	25:DA:932:G:O6	2.31	0.49
51:B5:16:ARG:HG2	51:B5:16:ARG:HH11	1.78	0.49
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.47	0.49
50:D4:46:GLN:HG3	50:D4:48:ARG:HH21	1.77	0.49
13:CM:60:VAL:HG23	13:CM:64:TRP:HE3	1.77	0.49
25:BA:1904:C:H2'	25:BA:1905:G:O4'	2.13	0.49
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.13	0.49
29:BF:103:LYS:HA	29:BF:106:ARG:HG3	1.94	0.49
1:AA:391:G:O3'	16:AP:8:ARG:NH2	2.46	0.49
25:DA:637:A:H2'	35:DP:117:GLU:OE2	2.11	0.49
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.94	0.49
26:BB:15:A:OP1	26:BB:108:U:O2'	2.24	0.49
12:AL:25:PRO:HD2	12:AL:98:TYR:OH	2.12	0.49
29:BF:31:HIS:HB2	35:BP:9:ASN:OD1	2.12	0.49
31:DH:27:LYS:HZ3	31:DH:32:GLU:HB2	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:189(L):G:H2'	1:CA:190:U:H6	1.76	0.49
1:AA:757:U:H2'	1:AA:758:G:O4'	2.11	0.49
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.11	0.49
31:DH:3:ARG:HH22	31:DH:5:GLY:H	1.61	0.49
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.44	0.49
25:BA:2827:G:OP1	37:BR:99:LYS:HE2	2.12	0.49
33:BN:96:GLU:H	33:BN:96:GLU:CD	2.16	0.49
25:BA:1248:G:O6	61:BA:4634:HOH:O	2.19	0.49
1:CA:1240:U:OP2	7:CG:115:ARG:HA	2.12	0.49
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.20	0.49
25:DA:315:G:H2'	25:DA:316:C:C6	2.48	0.49
4:AD:30:LYS:HA	4:AD:35:ARG:HH11	1.78	0.49
25:DA:2552:U:C2	25:DA:2554:U:H5''	2.48	0.49
1:AA:1189:C:H5''	1:AA:1190:G:OP2	2.13	0.49
25:DA:2845:G:H2'	25:DA:2846:G:H8	1.75	0.49
4:CD:150:GLU:HA	4:CD:153:ARG:HE	1.77	0.49
8:CH:20:TYR:CE2	8:CH:75:ARG:HG2	2.47	0.49
1:AA:1243:C:H2'	1:AA:1244:C:H6	1.78	0.49
25:BA:407:U:H2'	25:BA:408:G:C8	2.47	0.49
25:BA:1940:A:O2'	25:BA:1942:C:N4	2.46	0.49
1:AA:394:G:H2'	1:AA:395:C:C6	2.46	0.49
25:BA:809:U:H4'	25:BA:810:G:O5'	2.12	0.49
25:BA:2398:C:O2'	61:BA:3871:HOH:O	2.20	0.49
43:DX:44:GLU:O	43:DX:48:LYS:N	2.45	0.49
1:AA:665:A:H1'	1:AA:733:A:O4'	2.12	0.49
25:DA:1614:A:C2	42:DW:93:ALA:HB2	2.47	0.49
25:DA:483:A:O2'	44:DY:49:VAL:O	2.19	0.49
25:BA:1298:G:C2	25:BA:1299:A:C2	3.01	0.49
1:AA:130:A:O2'	1:AA:131:C:O5'	2.28	0.49
40:BU:58:ARG:HA	40:BU:61:TRP:CE3	2.47	0.49
25:DA:684:G:OP1	53:D7:16:HIS:ND1	2.45	0.49
34:DO:20:MET:HE3	34:DO:44:LYS:HE3	1.95	0.49
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.33	0.49
25:BA:672:G:H8	25:BA:672:G:O5'	1.96	0.49
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.77	0.49
1:CA:1423:G:P	34:DO:49:ARG:HH12	2.34	0.49
2:AB:20:GLU:HG2	2:AB:191:ASP:HB3	1.94	0.49
25:BA:207:A:C2	25:BA:224:U:H4'	2.47	0.49
1:AA:542:G:H2'	1:AA:543:C:C6	2.47	0.49
9:CI:38:GLN:HG2	9:CI:39:GLY:N	2.27	0.49
1:AA:999:C:H2'	1:AA:1000:U:O4'	2.13	0.49
1:CA:628:G:H2'	1:CA:629:G:C8	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1919:G:H2'	25:BA:1920:U:O4'	2.13	0.49
25:BA:1825:U:H2'	25:BA:1826:C:C6	2.47	0.49
25:DA:807:U:OP1	35:DP:36:LYS:NZ	2.40	0.49
25:DA:2471:C:N4	25:DA:2476:A:O2'	2.46	0.49
1:AA:678:U:H2'	1:AA:679:C:C6	2.47	0.49
25:DA:176:G:O2'	25:DA:177:G:H5'	2.12	0.49
25:BA:2879:G:H2'	25:BA:2880:C:O4'	2.13	0.49
13:AM:50:GLU:O	13:AM:54:VAL:HG22	2.13	0.49
32:DI:70:GLU:O	32:DI:74:ASN:HB2	2.13	0.49
25:DA:1472:A:H2'	25:DA:1473:G:O4'	2.13	0.49
2:CB:221:LEU:HD13	2:CB:224:GLN:HE22	1.76	0.49
5:AE:84:PHE:CE2	5:AE:133:TYR:HD2	2.31	0.49
1:CA:1151:A:H5''	10:CJ:41:PRO:HA	1.95	0.49
1:CA:427:U:H2'	1:CA:428:G:C8	2.48	0.49
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.13	0.49
1:CA:975:A:H4'	1:CA:976:G:C5'	2.40	0.49
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.94	0.49
25:DA:1313:U:H2'	25:DA:1610:A:N1	2.27	0.49
1:CA:253:U:H2'	1:CA:254:G:H8	1.77	0.49
1:AA:1015:A:H2'	1:AA:1016:A:H8	1.78	0.49
1:AA:540:G:H2'	1:AA:541:G:O4'	2.12	0.49
25:BA:1552:C:O2'	25:BA:1553:A:H5'	2.13	0.49
25:DA:539:G:H2'	25:DA:540:C:C6	2.47	0.49
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.45	0.49
25:DA:601:C:O2'	29:DF:104:LYS:NZ	2.46	0.49
25:DA:895:U:O2'	25:DA:896:A:H2'	2.13	0.49
2:AB:98:LEU:HB2	2:AB:101:MET:SD	2.52	0.49
27:BD:175:LEU:HD12	27:BD:185:VAL:HG21	1.95	0.49
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.29	0.49
25:BA:2507:G:H5''	36:BQ:82:ARG:HG2	1.93	0.49
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.47	0.49
25:BA:1098:C:O5'	25:BA:1098:C:H6	1.96	0.49
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.28	0.49
2:CB:23:ARG:HB2	2:CB:23:ARG:NH1	2.28	0.49
25:DA:491:G:H2'	25:DA:492:A:C8	2.48	0.49
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.93	0.49
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.12	0.49
2:CB:208:ILE:HA	2:CB:211:ILE:HD12	1.95	0.49
25:DA:999:U:O2'	25:DA:1000:A:H5'	2.13	0.49
1:CA:600:C:H2'	1:CA:601:C:C6	2.48	0.49
25:BA:1317:G:OP2	61:BA:4516:HOH:O	2.20	0.49
1:AA:472:A:N6	1:AA:473:G:C2	2.80	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:191:G:C6	1:AA:192:U:C4	3.01	0.49
25:BA:2316:G:H22	25:BA:2324:U:H3	1.61	0.49
25:DA:1434:A:H61	25:DA:1558:A:H62	1.59	0.49
25:DA:2100:G:H2'	25:DA:2101:G:H5'	1.94	0.49
1:AA:445:G:H2'	1:AA:446:G:H8	1.78	0.49
25:DA:1531:C:N4	25:DA:1538:G:H1	2.10	0.49
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.48	0.49
25:BA:1810:U:H2'	61:BA:4800:HOH:O	2.11	0.49
25:DA:989:G:H4'	25:DA:990:A:OP1	2.12	0.49
27:DD:228:PRO:HD3	27:DD:235:GLY:CA	2.42	0.49
25:DA:2649:U:H2'	25:DA:2650:U:C6	2.47	0.49
49:B3:11:SER:OG	49:B3:13:ILE:HG13	2.12	0.49
1:AA:302:G:N3	1:AA:556:C:H4'	2.28	0.49
41:DV:24:LYS:HA	41:DV:92:THR:OG1	2.12	0.49
29:DF:88:VAL:HG21	29:DF:91:GLY:HA3	1.95	0.49
25:BA:821:A:H2'	25:BA:821:A:N3	2.27	0.49
1:AA:250:A:H4'	1:AA:251:G:O5'	2.13	0.49
25:BA:330:U:H2'	25:BA:331:G:O4'	2.13	0.49
14:CN:47:LEU:O	14:CN:51:GLY:N	2.44	0.49
25:BA:1521:C:H2'	25:BA:1522:G:C8	2.48	0.49
1:AA:1148:U:H2'	1:AA:1149:C:O4'	2.13	0.49
1:AA:438:G:O2'	1:AA:494:U:O4	2.23	0.49
1:CA:1129:C:H4'	9:CI:16:ARG:HH22	1.78	0.49
2:AB:20:GLU:O	2:AB:40:HIS:HB2	2.12	0.49
1:AA:542:G:H2'	1:AA:543:C:H6	1.78	0.49
1:AA:308:C:H2'	1:AA:309:G:H8	1.77	0.49
23:AX:8:U:O5'	23:AX:8:U:H6	1.95	0.49
1:CA:164:U:H2'	1:CA:165:C:C6	2.47	0.49
33:DN:104:LYS:HA	33:DN:107:LEU:HD12	1.93	0.49
40:BU:24:TYR:HB2	40:BU:29:SER:HB3	1.95	0.49
30:DG:7:LEU:HD22	30:DG:100:TRP:HE3	1.78	0.49
44:DY:35:TYR:CE2	44:DY:69:ALA:HB3	2.47	0.49
36:BQ:133:ARG:HG2	36:BQ:134:ARG:N	2.28	0.49
25:BA:1588:G:H5''	25:BA:1589:A:OP2	2.12	0.49
44:DY:14:LEU:HB2	44:DY:75:ILE:HD11	1.95	0.49
37:DR:72:ASP:O	37:DR:76:VAL:HG23	2.13	0.49
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.95	0.49
1:CA:1003:G:H2'	1:CA:1004:A:H4'	1.95	0.49
16:CP:28:ARG:HG3	16:CP:29:ASP:N	2.28	0.49
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.95	0.49
1:AA:864:A:H2'	1:AA:865:A:C8	2.47	0.49
1:CA:532:A:H2	1:CA:1207:G:H4'	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:15:ALA:HB2	9:AI:65:VAL:HG23	1.94	0.49
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.23	0.49
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.12	0.49
25:DA:1815:A:P	27:DD:54:ARG:HH22	2.36	0.49
35:DP:38:GLN:HG2	35:DP:45:LEU:H	1.78	0.49
38:DS:15:ARG:O	38:DS:19:LYS:HG2	2.12	0.49
1:AA:392:G:H2'	1:AA:393:A:H8	1.78	0.49
50:B4:20:ASN:ND2	50:B4:36:CYS:SG	2.82	0.49
1:AA:276:G:H2'	1:AA:277:C:H5'	1.95	0.49
25:DA:2740:A:C6	25:DA:2741:A:C6	3.01	0.49
25:DA:321:G:OP2	29:DF:135:LYS:HG3	2.12	0.49
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.62	0.49
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.45	0.49
25:BA:602:G:H2'	25:BA:603:C:C6	2.48	0.49
1:CA:1006:C:C4	1:CA:1007:C:C5	3.01	0.48
1:AA:1145:C:H5''	1:AA:1146:A:OP1	2.13	0.48
1:AA:435:C:H2'	1:AA:436:C:H6	1.77	0.48
1:AA:438:G:OP1	4:AD:125:HIS:NE2	2.33	0.48
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.11	0.48
25:BA:1525:G:O2'	25:BA:1605:A:N1	2.43	0.48
1:AA:1015:A:H8	1:AA:1015:A:O5'	1.96	0.48
25:DA:792:G:OP2	61:DA:3818:HOH:O	2.20	0.48
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.48	0.48
31:DH:86:GLU:OE1	31:DH:130:ARG:HD3	2.13	0.48
8:CH:83:ILE:HB	8:CH:137:VAL:HG13	1.95	0.48
25:BA:1615:G:OP2	27:BD:63:ARG:NH2	2.45	0.48
1:CA:199:G:O2'	1:CA:200:G:H5'	2.12	0.48
36:DQ:65:PHE:HB2	36:DQ:105:GLU:HB2	1.93	0.48
44:DY:49:VAL:HG21	44:DY:61:ILE:HG23	1.94	0.48
25:DA:2505:G:O6	25:DA:2576:G:H2'	2.13	0.48
1:CA:831:U:H3	1:CA:855:G:H1	1.60	0.48
7:CG:133:GLY:O	7:CG:137:LYS:N	2.45	0.48
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.94	0.48
7:CG:22:LEU:HD13	7:CG:97:GLN:OE1	2.13	0.48
25:DA:2031:A:N3	25:DA:2455:G:O2'	2.41	0.48
54:D8:62:LEU:HB3	54:D8:65:GLU:HG2	1.94	0.48
28:DE:178:GLU:OE2	28:DE:178:GLU:N	2.36	0.48
12:CL:123:LYS:H	12:CL:123:LYS:HG2	1.37	0.48
1:AA:1438:G:H2'	1:AA:1439:C:H6	1.77	0.48
34:BO:7:TYR:CE1	34:BO:20:MET:HB2	2.48	0.48
25:DA:409:C:O2'	25:DA:410:G:H5'	2.12	0.48
1:CA:1036:G:H3'	1:CA:1037:C:O4'	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:AJ:5:ARG:HH21	10:AJ:73:ASP:CG	2.17	0.48
25:BA:839:G:H5'	25:BA:840:A:H5'	1.95	0.48
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.12	0.48
25:DA:2711:A:OP2	61:DA:3973:HOH:O	2.20	0.48
4:CD:63:LYS:HG3	4:CD:198:VAL:HG22	1.95	0.48
25:BA:1314:A:H2'	25:BA:1315:A:O4'	2.13	0.48
1:CA:736:C:H2'	1:CA:737:A:C8	2.47	0.48
32:DI:75:LEU:HD11	32:DI:105:HIS:CD2	2.47	0.48
1:AA:62:U:O2'	1:AA:379:C:H1'	2.14	0.48
25:DA:2360:A:H2'	25:DA:2361:A:O4'	2.13	0.48
25:DA:2261:C:O2'	25:DA:2262:U:H5'	2.13	0.48
31:DH:94:TYR:CE2	31:DH:160:LYS:HG2	2.48	0.48
1:AA:236:G:H2'	1:AA:237:C:C6	2.47	0.48
29:DF:167:ALA:HB1	29:DF:173:VAL:HG11	1.95	0.48
37:DR:103:ARG:NH1	37:DR:110:PRO:HD3	2.28	0.48
2:CB:105:PHE:CD2	2:CB:158:LEU:HG	2.48	0.48
1:AA:293:G:C6	1:AA:294:U:C4	3.01	0.48
25:BA:1285:G:H2'	25:BA:1286:U:O4'	2.13	0.48
25:BA:2444:A:C8	47:B1:33:LYS:HD2	2.48	0.48
1:CA:730:G:C5	1:CA:731:G:H1'	2.47	0.48
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.13	0.48
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.48	0.48
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.28	0.48
25:BA:870:G:C6	25:BA:882:A:N1	2.80	0.48
25:DA:116:C:H2'	25:DA:117:G:O4'	2.12	0.48
25:DA:322:A:OP2	29:DF:169:ASN:HB2	2.13	0.48
25:DA:2391:G:O2'	25:DA:2422:A:N7	2.46	0.48
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.45	0.48
1:CA:1038:C:O2'	1:CA:1039:C:H5'	2.13	0.48
44:BY:53:PRO:HA	44:BY:56:PRO:HD3	1.94	0.48
1:AA:437:U:O3'	4:AD:125:HIS:HE1	1.96	0.48
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.49	0.48
25:BA:70:A:H3'	25:BA:70:A:OP2	2.13	0.48
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.61	0.48
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.13	0.48
1:CA:460:G:H1'	1:CA:472:A:H61	1.77	0.48
13:CM:37:THR:HG21	13:CM:56:LEU:HA	1.94	0.48
1:CA:1095:U:OP1	1:CA:1108:G:N2	2.36	0.48
3:AC:52:LEU:HA	3:AC:70:VAL:HG22	1.95	0.48
48:B2:32:LEU:HD23	48:B2:53:LEU:HB3	1.95	0.48
36:DQ:27:VAL:HG11	36:DQ:134:ARG:HG3	1.95	0.48
40:DU:113:ALA:O	40:DU:117:GLN:HG2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:DS:87:PHE:CZ	38:DS:102:ALA:HB2	2.48	0.48
1:AA:1051:C:H2'	1:AA:1052:U:H6	1.79	0.48
1:AA:1052:U:H5''	1:AA:1053:G:OP2	2.13	0.48
25:DA:328:U:H4'	44:DY:68:HIS:CD2	2.49	0.48
36:BQ:55:VAL:HG12	36:BQ:64:ILE:HD12	1.96	0.48
20:AT:56:MET:HG3	20:AT:84:LEU:HD22	1.95	0.48
1:CA:1288:A:H2'	1:CA:1289:A:C8	2.49	0.48
1:CA:48:C:OP2	61:CA:4095:HOH:O	2.20	0.48
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.48	0.48
1:CA:5:U:H5'	1:CA:6:G:C5	2.48	0.48
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.12	0.48
25:BA:794:U:O2	25:BA:2036:A:H1'	2.13	0.48
50:B4:46:GLN:HG2	50:B4:48:ARG:HG2	1.95	0.48
27:BD:72:LYS:HE3	27:BD:75:ILE:HD12	1.95	0.48
1:AA:1340:A:O2'	23:AX:31:G:O3'	2.31	0.48
25:BA:347:G:C8	29:BF:171:PRO:HG3	2.48	0.48
25:DA:2025:C:H2'	25:DA:2026:C:C6	2.49	0.48
1:CA:1005:A:H8	1:CA:1005:A:O5'	1.96	0.48
1:CA:1007:C:N4	1:CA:1022:G:C6	2.81	0.48
1:CA:1040:U:C4	1:CA:1041:A:C8	3.01	0.48
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.49	0.48
30:DG:136:ARG:HD2	30:DG:137:GLU:N	2.28	0.48
25:BA:596:G:O2'	25:BA:597:C:H3'	2.13	0.48
2:AB:12:GLU:O	2:AB:15:VAL:HG13	2.14	0.48
2:AB:15:VAL:HG11	2:AB:213:LEU:HD12	1.95	0.48
1:AA:1530:G:H4'	1:AA:1530:G:OP1	2.13	0.48
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.95	0.48
2:AB:77:ALA:O	2:AB:81:VAL:HG22	2.13	0.48
25:DA:330:A:HO2'	25:DA:331:A:H8	1.61	0.48
6:CF:24:GLU:HG3	6:CF:28:ARG:HD3	1.95	0.48
4:AD:175:SER:OG	4:AD:184:LYS:HB2	2.13	0.48
25:DA:784:A:OP2	61:DA:4063:HOH:O	2.20	0.48
1:AA:384:G:C2	1:AA:385:C:C4	3.02	0.48
25:DA:614(C):A:N3	29:DF:180:GLY:HA2	2.29	0.48
1:CA:986:A:O2'	19:CS:55:LYS:O	2.31	0.48
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.28	0.48
25:DA:2293:C:OP1	25:DA:2377:A:N6	2.46	0.48
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.35	0.48
36:BQ:54:MET:HG3	36:BQ:117:ALA:HB1	1.95	0.48
27:DD:58:HIS:HD1	27:DD:59:LYS:N	2.11	0.48
25:DA:2872:G:C2	25:DA:2873:A:N6	2.82	0.48
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1446:U:O2'	1:CA:1447:A:O5'	2.31	0.48
25:BA:2623:U:H6	25:BA:2623:U:H5'	1.79	0.48
25:DA:1520:G:H3'	25:DA:1523:U:H6	1.78	0.48
7:AG:72:ARG:HG3	7:AG:142:GLU:OE2	2.12	0.48
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.49	0.48
2:CB:97:TRP:CH2	2:CB:173:ALA:HA	2.49	0.48
32:DI:29:TYR:O	32:DI:33:ARG:HD2	2.14	0.48
1:CA:216:G:H2'	1:CA:217:C:C6	2.49	0.48
25:BA:1845:G:H4'	27:BD:51:VAL:HG21	1.96	0.48
25:DA:1449:A:H5'	25:DA:1450:G:OP2	2.14	0.48
28:BE:179:GLU:HB3	28:BE:181:LEU:HD22	1.95	0.48
33:BN:28:THR:HG22	33:BN:29:LYS:N	2.29	0.48
25:BA:2601:A:N3	61:BA:3847:HOH:O	2.35	0.48
2:CB:71:VAL:HG23	2:CB:164:VAL:HA	1.95	0.48
2:CB:127:ILE:HG12	2:CB:128:GLU:H	1.78	0.48
31:DH:113:VAL:HG11	31:DH:151:ILE:HD13	1.94	0.48
1:CA:1003:G:C6	1:CA:1004:A:C2	3.02	0.48
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.81	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.43	0.48
1:AA:926:G:C6	1:AA:1505:G:C6	3.02	0.48
34:BO:101:PRO:HG3	39:BT:67:SER:OG	2.13	0.48
31:BH:56:SER:OG	31:BH:58:GLU:HG2	2.13	0.48
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.49	0.48
1:CA:839:U:H5''	1:CA:840:C:C5	2.48	0.48
25:DA:2680:C:H5'	28:DE:189:PRO:HA	1.96	0.48
31:DH:26:VAL:HG12	31:DH:79:VAL:HG11	1.95	0.48
12:AL:36:VAL:HG23	24:AW:10:2QY:CE1	2.43	0.48
34:DO:98:VAL:HG22	34:DO:118:ALA:HA	1.95	0.48
11:CK:33:THR:HA	11:CK:39:PRO:HA	1.95	0.48
30:DG:41:GLN:NE2	30:DG:154:GLY:O	2.46	0.48
1:AA:1327:C:H2'	1:AA:1328:C:C6	2.48	0.48
52:B6:21:TYR:CE2	52:B6:38:LYS:HG2	2.48	0.48
23:AX:19:G:H4'	23:AX:20:U:OP2	2.12	0.48
30:BG:56:ALA:HA	30:BG:153:ARG:NH2	2.29	0.48
25:BA:2303:U:O2'	25:BA:2386:C:O2	2.24	0.48
25:DA:507:A:H5''	25:DA:508:G:H3'	1.95	0.48
25:DA:934:G:H2'	25:DA:935:C:H6	1.79	0.48
6:CF:68:PRO:HB2	6:CF:71:ARG:HG3	1.95	0.48
25:DA:428:A:H3'	25:DA:429:A:C8	2.48	0.48
1:CA:520:A:N1	1:CA:536:C:H1'	2.29	0.48
11:CK:19:ALA:HA	11:CK:32:ILE:HD13	1.96	0.48
1:CA:554:C:H2'	1:CA:555:C:H6	1.77	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1131:G:H8	1:AA:1131:G:O5'	1.96	0.48
3:CC:34:LEU:HG	3:CC:38:ARG:HH12	1.78	0.48
27:BD:68:LYS:HD2	27:BD:70:TRP:CH2	2.48	0.48
41:DV:30:GLY:H	41:DV:61:VAL:HG13	1.79	0.48
1:AA:620:C:H2'	1:AA:621:A:O4'	2.14	0.48
1:CA:1002:G:H1	1:CA:1038:C:H42	0.67	0.48
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.95	0.48
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.95	0.48
30:BG:102:PHE:HE1	30:BG:141:PHE:CE2	2.26	0.48
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.27	0.48
2:CB:73:THR:HB	2:CB:95:GLN:O	2.14	0.48
30:DG:101:ILE:HD13	50:D4:25:TYR:HB2	1.94	0.48
1:CA:1169:A:H8	1:CA:1169:A:H3'	1.79	0.48
10:CJ:42:THR:CG2	10:CJ:68:HIS:HD2	2.25	0.48
8:CH:49:GLU:HG2	8:CH:62:TYR:CE2	2.45	0.48
1:CA:585:G:N3	1:CA:879:C:H4'	2.29	0.48
25:BA:2343:G:O2'	25:BA:2348:A:N1	2.35	0.48
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	1.95	0.48
10:CJ:47:PHE:CZ	14:CN:37:PHE:HE1	2.32	0.48
25:DA:784:A:C8	25:DA:792:G:C5	3.01	0.48
25:DA:1666:G:OP1	34:DO:66:LYS:HE3	2.14	0.48
25:DA:1163:G:C2	25:DA:1164:G:C8	3.01	0.48
48:B2:32:LEU:HD12	48:B2:36:ARG:NH1	2.29	0.48
7:CG:78:ARG:HH21	7:CG:156:TRP:HB3	1.78	0.48
1:AA:1298:C:H2'	7:AG:114:ARG:NH1	2.28	0.48
2:AB:168:THR:OG1	2:AB:192:SER:HB3	2.13	0.48
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.95	0.48
2:AB:19:HIS:NE2	2:AB:206:ASP:OD2	2.46	0.48
12:CL:34:ARG:HG2	12:CL:35:GLY:N	2.29	0.48
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.29	0.48
13:AM:15:VAL:O	13:AM:19:LEU:HD22	2.13	0.48
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.96	0.48
10:AJ:57:LYS:HD2	10:AJ:60:ARG:HH21	1.79	0.48
9:CI:31:GLN:HB2	9:CI:35:GLU:OE2	2.13	0.48
25:BA:1537:G:O2'	27:BD:101:GLU:HB2	2.14	0.48
1:CA:270:A:H2'	1:CA:271:C:C6	2.48	0.48
42:DW:70:TYR:OH	42:DW:72:LYS:HG3	2.14	0.48
7:AG:152:ALA:HB1	7:AG:155:ARG:NH2	2.28	0.48
25:DA:180:G:H5''	25:DA:181:A:OP2	2.13	0.48
1:CA:999:C:N4	1:CA:1042:G:C2	2.81	0.48
1:CA:999:C:N4	1:CA:1043:C:C4	2.81	0.48
1:CA:1320:C:C1'	19:CS:73:GLU:HG3	2.44	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:154:C:H5	1:AA:155:C:C5	2.31	0.48
1:CA:1277:C:O2'	1:CA:1279:A:H8	1.94	0.48
1:CA:1137:C:H1'	1:CA:1138:G:C2	2.48	0.48
25:BA:217:A:H2'	25:BA:219:U:O4'	2.13	0.48
25:BA:1815:A:H5''	61:BA:4186:HOH:O	2.13	0.48
25:BA:1093:G:H2'	25:BA:1156:G:N2	2.26	0.48
25:BA:1604:C:H5''	25:BA:1605:A:OP2	2.14	0.48
1:CA:758:G:H5''	1:CA:758:G:H8	1.78	0.48
46:B0:53:MET:HG3	46:B0:59:LEU:CD2	2.43	0.48
26:DB:50:G:OP2	38:DS:62:LYS:HD3	2.13	0.48
3:AC:135:LYS:HE2	5:AE:53:LEU:HD11	1.95	0.48
1:CA:1342:C:H1'	9:CI:124:GLN:NE2	2.28	0.48
1:AA:364:A:H2'	1:AA:365:U:H6	1.79	0.48
25:DA:2094:G:OP1	32:DI:22:LYS:HD2	2.14	0.48
25:BA:438:G:C5	35:BP:72:PRO:HB3	2.49	0.48
25:DA:2489:G:C6	25:DA:2490:G:C6	3.02	0.48
32:BI:100:ALA:HA	32:BI:103:ARG:HG2	1.94	0.48
10:AJ:68:HIS:CD2	10:AJ:68:HIS:H	2.31	0.48
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.94	0.48
25:DA:78:A:H2'	25:DA:79:G:H8	1.78	0.48
25:DA:1041:C:OP1	45:DZ:46:LYS:NZ	2.43	0.48
1:CA:422:C:H4'	1:CA:423:G:C4	2.48	0.48
10:CJ:8:LEU:CD2	10:CJ:96:ILE:HG23	2.43	0.48
1:CA:1492:A:H2'	1:CA:1493:A:C1'	2.43	0.48
25:BA:1576:G:O2'	25:BA:1577:C:H5'	2.14	0.48
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.13	0.48
14:CN:7:ILE:HG12	14:CN:8:GLU:N	2.27	0.48
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.79	0.48
3:AC:32:LEU:HD22	3:AC:59:ARG:HH12	1.79	0.48
25:BA:388:A:H2'	25:BA:389:G:H8	1.77	0.48
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.46	0.48
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.44	0.48
1:CA:418:C:H2'	1:CA:419:C:C6	2.48	0.48
16:CP:51:VAL:O	16:CP:53:VAL:HG23	2.14	0.48
31:DH:20:ALA:HB3	31:DH:23:ARG:HG3	1.95	0.48
27:BD:9:TYR:CZ	27:BD:13:ARG:HG2	2.49	0.48
13:AM:84:ILE:HD12	19:AS:74:PHE:HZ	1.78	0.48
25:DA:1256:G:H5'	25:DA:1257:C:OP2	2.13	0.48
1:CA:364:A:H2'	1:CA:365:U:H6	1.79	0.48
1:AA:1206:G:C6	1:AA:1207:G:C5	3.01	0.48
25:DA:1287:A:H5''	25:DA:1288:U:OP2	2.13	0.48
25:BA:860:U:H2'	25:BA:861:C:C6	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
48:D2:10:LEU:HD22	48:D2:14:ARG:NH1	2.29	0.48
25:BA:2814:C:H2'	25:BA:2815:C:O4'	2.14	0.48
25:BA:137:G:O2'	25:BA:138:G:H5'	2.14	0.48
16:AP:52:ASP:OD1	16:AP:54:GLU:HG3	2.14	0.48
1:CA:797:C:O2'	1:CA:798:G:H5'	2.13	0.48
25:DA:1022:G:C6	25:DA:1140:C:C4	3.01	0.48
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.14	0.48
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.95	0.48
46:D0:27:GLU:HB2	46:D0:69:PHE:HD1	1.78	0.48
25:BA:1093:G:HO2'	25:BA:1094:A:H8	1.61	0.48
1:AA:430:A:OP1	4:AD:9:CYS:HB2	2.13	0.48
1:CA:192:U:O2'	20:CT:60:GLU:OE2	2.25	0.48
1:AA:658:G:H2'	1:AA:659:U:C6	2.48	0.48
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.47	0.48
45:BZ:30:ASN:ND2	45:BZ:90:VAL:HB	2.28	0.48
1:AA:1286:A:H2	21:AU:18:TYR:HH	1.60	0.48
6:CF:61:LEU:HD23	6:CF:63:TYR:OH	2.13	0.48
25:DA:892:G:H2'	25:DA:893:C:O4'	2.14	0.48
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.29	0.48
1:CA:790:A:H2'	1:CA:791:G:C8	2.49	0.48
30:BG:50:ALA:O	30:BG:52:ILE:N	2.47	0.48
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.49	0.48
25:BA:1362:U:H2'	25:BA:1363:A:C8	2.49	0.48
25:BA:905:U:O2	25:BA:2280:A:H2'	2.14	0.48
25:DA:2823:A:OP1	28:DE:159:HIS:NE2	2.42	0.48
1:AA:662:G:H2'	1:AA:663:A:C8	2.48	0.48
34:DO:64:ARG:NH1	34:DO:81:ASP:OD1	2.47	0.48
1:AA:300:A:H2'	1:AA:301:G:O4'	2.13	0.48
1:AA:300:A:O2'	1:AA:564:C:N3	2.36	0.48
34:DO:73:ASP:HB2	39:DT:82:LEU:HD13	1.96	0.48
45:BZ:152:ALA:HA	45:BZ:155:LEU:HD22	1.94	0.48
45:DZ:19:ARG:HE	45:DZ:19:ARG:HB2	1.44	0.48
40:BU:16:LYS:HE2	40:BU:16:LYS:HB3	1.55	0.48
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.13	0.48
2:CB:8:LYS:HD2	2:CB:51:LEU:HD13	1.96	0.48
25:BA:1067:A:H8	25:BA:1067:A:H3'	1.79	0.48
30:DG:11:TYR:O	30:DG:16:ARG:HG2	2.13	0.48
32:DI:110:ASP:H	32:DI:130:TYR:HH	1.55	0.48
1:AA:1028:C:H2'	1:AA:1029:C:O4'	2.14	0.48
25:DA:271(F):C:H2'	25:DA:271(G):C:H6	1.78	0.48
29:DF:164:ARG:O	29:DF:168:ARG:HB2	2.14	0.48
3:AC:113:ALA:HB3	3:AC:114:PRO:HD3	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:CF:10:LEU:HD12	6:CF:85:VAL:HA	1.94	0.48
38:DS:53:SER:OG	38:DS:54:LEU:N	2.47	0.48
1:AA:376:G:H2'	1:AA:377:G:H8	1.79	0.48
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.49	0.48
1:AA:1237:C:HO2'	1:AA:1300:G:H1	1.62	0.48
25:BA:484:G:C8	53:B7:37:LYS:HG2	2.49	0.48
42:BW:86:LEU:HD12	42:BW:87:PRO:HD2	1.96	0.48
26:BB:37:C:C5	26:BB:38:C:C5	3.02	0.48
28:DE:127:ASP:OD2	61:DE:408:HOH:O	2.19	0.48
25:DA:729:G:OP2	27:DD:13:ARG:NH1	2.45	0.48
17:CQ:62:SER:OG	17:CQ:72:ARG:HD3	2.13	0.48
25:DA:1463:C:H2'	25:DA:1464:C:H6	1.78	0.48
1:AA:1234:C:C2'	1:AA:1235:U:H5'	2.44	0.48
47:D1:64:ALA:HA	47:D1:67:ILE:HG13	1.96	0.48
2:CB:48:MET:HA	2:CB:51:LEU:HD12	1.96	0.47
4:AD:155:LEU:HD22	4:AD:156:GLU:N	2.29	0.47
1:CA:1358:U:OP2	1:CA:1359:C:H5	1.97	0.47
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.96	0.47
25:BA:777:C:OP2	61:BA:4592:HOH:O	2.20	0.47
25:BA:671:A:H2'	25:BA:672:G:O4'	2.14	0.47
25:DA:1593:G:C2	25:DA:1594:G:C4	3.02	0.47
1:CA:1262:C:H42	1:CA:1273:G:H1	1.61	0.47
1:CA:1206:G:C6	1:CA:1207:G:C5	3.03	0.47
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.79	0.47
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.13	0.47
25:BA:1220:U:OP1	25:BA:1222:A:N6	2.47	0.47
1:AA:606:G:H1'	1:AA:632:A:H61	1.79	0.47
25:DA:910:A:C5	36:DQ:13:GLN:HG3	2.49	0.47
25:DA:867:C:O2	25:DA:913:U:H5'	2.14	0.47
1:CA:785:G:H2'	1:CA:786:G:H5'	1.96	0.47
48:B2:32:LEU:CD1	48:B2:36:ARG:HH11	2.26	0.47
19:CS:27:GLU:HB2	19:CS:28:LYS:HE2	1.95	0.47
25:DA:253:C:O2'	61:DA:4187:HOH:O	2.16	0.47
25:BA:1925:G:OP1	27:BD:241:PRO:HB2	2.14	0.47
29:DF:126:VAL:HG21	29:DF:129:PHE:CZ	2.49	0.47
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.49	0.47
6:CF:44:GLY:HA2	6:CF:59:TYR:CZ	2.48	0.47
4:AD:12:CYS:SG	4:AD:19:LEU:N	2.77	0.47
27:DD:72:LYS:HB3	27:DD:75:ILE:HD12	1.96	0.47
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.79	0.47
25:BA:2087:C:H2'	25:BA:2088:C:C6	2.49	0.47
25:DA:688:U:H5'	25:DA:1780:A:C2	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:36:ARG:HG3	4:CD:38:TYR:CE2	2.49	0.47
25:BA:1686:U:O2'	25:BA:1687:C:H5'	2.14	0.47
20:CT:50:GLU:HB2	20:CT:99:LEU:HD23	1.96	0.47
25:BA:1091:A:OP1	25:BA:1092:A:H3'	2.13	0.47
29:DF:7:TYR:O	29:DF:22:ALA:N	2.46	0.47
30:DG:103:LEU:HD22	30:DG:178:PHE:HZ	1.80	0.47
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.49	0.47
1:CA:543:C:O2'	1:CA:544:G:H5'	2.14	0.47
25:BA:904:C:H4'	46:B0:23:VAL:HG21	1.96	0.47
25:DA:1463:C:H2'	25:DA:1464:C:C6	2.49	0.47
25:BA:1086:C:H2'	25:BA:1087:C:O4'	2.14	0.47
31:DH:87:LEU:HD23	31:DH:164:TYR:HA	1.96	0.47
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.49	0.47
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.62	0.47
28:BE:92:THR:O	28:BE:95:ILE:HG23	2.14	0.47
8:AH:96:GLY:H	8:AH:99:GLU:CD	2.18	0.47
1:CA:109:A:H2'	1:CA:326:G:N2	2.28	0.47
27:DD:275:LYS:HB3	27:DD:276:LYS:HA	1.96	0.47
5:AE:72:GLN:O	5:AE:75:THR:HG22	2.14	0.47
1:AA:49:U:H3	1:AA:362:G:H1'	1.80	0.47
1:AA:1127:G:H21	1:AA:1148:U:H3	1.61	0.47
1:CA:1157:A:N7	1:CA:1180:A:C6	2.82	0.47
19:AS:65:ASN:ND2	19:AS:66:MET:HG3	2.29	0.47
1:AA:146:G:H5''	1:AA:146:G:H8	1.80	0.47
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.14	0.47
1:CA:457:C:H2'	1:CA:458:C:C6	2.49	0.47
14:AN:37:PHE:CE2	14:AN:53:LEU:HD13	2.50	0.47
1:CA:577:G:C8	1:CA:816:A:C6	3.02	0.47
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.29	0.47
30:DG:114:ILE:HD12	30:DG:117:PHE:HD2	1.79	0.47
2:AB:24:TRP:HD1	2:AB:24:TRP:H	1.62	0.47
25:BA:1913:G:H2'	25:BA:1914:C:H6	1.78	0.47
1:CA:1009:G:N2	1:CA:1010:G:H1'	2.30	0.47
25:DA:1935:G:H1'	25:DA:1964:G:N2	2.29	0.47
34:BO:64:ARG:NH1	34:BO:81:ASP:OD1	2.46	0.47
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.46	0.47
25:BA:2698:G:H5'	61:BA:4643:HOH:O	2.15	0.47
1:CA:932:C:H2'	1:CA:933:G:C8	2.49	0.47
20:CT:46:GLU:HG2	20:CT:46:GLU:O	2.13	0.47
25:DA:1027:A:C6	25:DA:1126:A:C4	3.02	0.47
12:CL:79:GLU:HB3	12:CL:80:HIS:HD2	1.78	0.47
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.67	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:129(A):G:C6	1:AA:189(E):U:H4'	2.50	0.47
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.29	0.47
1:AA:1125:U:O4	1:AA:1128:C:C5	2.68	0.47
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.14	0.47
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.96	0.47
25:DA:2319:G:C2	38:DS:3:ARG:HA	2.49	0.47
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.29	0.47
19:CS:30:LEU:CD1	19:CS:32:LYS:HG3	2.41	0.47
1:AA:430:A:H2'	1:AA:431:A:O4'	2.15	0.47
25:BA:956:A:OP2	61:BA:4430:HOH:O	2.20	0.47
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.43	0.47
29:BF:7:TYR:CD2	29:BF:24:LEU:HB2	2.49	0.47
1:CA:1074:G:O2'	1:CA:1101:A:N1	2.37	0.47
27:BD:132:PRO:HA	27:BD:190:TYR:HA	1.96	0.47
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.96	0.47
29:DF:165:ARG:HG2	29:DF:168:ARG:HH21	1.79	0.47
25:DA:2303:G:H2'	25:DA:2304:G:O4'	2.14	0.47
50:D4:15:ILE:HG23	50:D4:21:VAL:HG22	1.96	0.47
14:AN:4:LYS:HD3	14:AN:7:ILE:CG2	2.44	0.47
25:BA:2643:G:N2	25:BA:2800:C:O2	2.40	0.47
25:BA:911:G:O2'	25:BA:912:C:H5'	2.14	0.47
25:DA:1528(A):A:C8	25:DA:1529:G:C8	3.03	0.47
25:DA:118:A:H1'	25:DA:178:G:O4'	2.14	0.47
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.30	0.47
25:DA:1523:U:C2	25:DA:1524:G:C8	3.01	0.47
28:BE:176:ILE:HB	28:BE:181:LEU:HB2	1.96	0.47
1:CA:554:C:H2'	1:CA:555:C:C6	2.49	0.47
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.61	0.47
25:BA:2538:G:H5'	25:BA:2755:C:O2'	2.13	0.47
49:D3:3:ARG:HH11	49:D3:60:GLU:CB	2.27	0.47
6:AF:99:ALA:O	18:AR:28:GLU:HG3	2.14	0.47
52:D6:38:LYS:NZ	52:D6:38:LYS:HB2	2.29	0.47
32:BI:110:ASP:HA	32:BI:111:PRO:HD2	1.72	0.47
3:AC:123:GLN:HG2	3:AC:128:PHE:CD2	2.50	0.47
1:CA:341:C:H6	1:CA:341:C:O5'	1.98	0.47
25:BA:2116:G:OP1	32:BI:22:LYS:HD2	2.14	0.47
25:DA:1932:A:H2'	25:DA:1933:G:O4'	2.14	0.47
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.79	0.47
25:DA:565:C:H2'	25:DA:566:U:O4'	2.15	0.47
35:DP:99:LEU:HD23	35:DP:99:LEU:H	1.79	0.47
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.96	0.47
1:CA:1133:G:N2	1:CA:1141:C:N3	2.59	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:934:A:O2'	25:BA:935:C:OP2	2.27	0.47
1:CA:954:G:H21	1:CA:1227:A:N6	2.08	0.47
25:DA:639:U:H2'	25:DA:640:C:H6	1.79	0.47
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.13	0.47
29:BF:7:TYR:HD2	29:BF:24:LEU:HB2	1.78	0.47
36:DQ:59:ARG:C	36:DQ:61:GLY:H	2.13	0.47
25:BA:2702:C:N4	25:BA:2726:A:H1'	2.29	0.47
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.95	0.47
1:CA:834:C:H2'	1:CA:835:U:H6	1.77	0.47
1:AA:1256:A:H5''	1:AA:1258:G:C1'	2.44	0.47
47:D1:3:LYS:H	47:D1:61:ARG:HH12	1.62	0.47
25:DA:1291:C:H2'	25:DA:1292:U:C6	2.49	0.47
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.14	0.47
25:BA:83:A:H5''	44:BY:8:LYS:HE3	1.97	0.47
29:DF:160:ASN:HB3	29:DF:163:VAL:HB	1.96	0.47
1:AA:685:G:C2	1:AA:686:U:C4	3.02	0.47
25:BA:1828:C:H4'	27:BD:257:LEU:O	2.15	0.47
25:DA:78:A:H2'	25:DA:79:G:C8	2.49	0.47
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.79	0.47
29:BF:110:LEU:HD12	29:BF:205:ARG:HG2	1.96	0.47
25:DA:1513:C:H2'	25:DA:1514:U:C6	2.49	0.47
5:CE:83:GLU:HG2	5:CE:88:LYS:HG3	1.95	0.47
1:AA:481:G:H1'	1:AA:483:C:N4	2.30	0.47
28:DE:195:LEU:HG	28:DE:196:VAL:N	2.30	0.47
25:BA:2795:G:OP2	61:BA:4647:HOH:O	2.20	0.47
9:AI:28:VAL:HA	9:AI:63:ILE:HB	1.97	0.47
29:BF:195:ASP:HB3	29:BF:198:ALA:H	1.78	0.47
5:AE:69:VAL:HG22	5:AE:71:LEU:HD23	1.96	0.47
25:DA:86:C:H4'	25:DA:104:U:H1'	1.96	0.47
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.79	0.47
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.29	0.47
27:DD:71:ASP:OD2	27:DD:103:ARG:NH2	2.47	0.47
30:BG:67:LYS:H	50:B4:6:HIS:CE1	2.33	0.47
25:BA:12:U:O2	25:BA:12:U:H2'	2.14	0.47
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.14	0.47
12:CL:119:LYS:O	12:CL:120:TYR:HB2	2.15	0.47
25:DA:900:A:H2'	25:DA:901:A:O4'	2.15	0.47
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.73	0.47
1:AA:674:G:H2'	1:AA:675:A:C8	2.49	0.47
6:AF:97:PHE:HD2	18:AR:31:LEU:HD23	1.80	0.47
30:DG:103:LEU:HA	30:DG:106:LEU:HB3	1.96	0.47
41:DV:5:VAL:CG1	41:DV:57:VAL:HG21	2.44	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:82:MET:CE	13:CM:92:HIS:HB3	2.45	0.47
25:BA:1517:G:C6	25:BA:1567:G:N7	2.83	0.47
1:AA:1137:C:H5''	1:AA:1138:G:OP1	2.15	0.47
36:DQ:32:TYR:CE1	36:DQ:133:ARG:HG3	2.49	0.47
26:DB:43:C:C5	26:DB:45:A:N6	2.82	0.47
25:DA:2408:U:H2'	25:DA:2409:G:C8	2.49	0.47
25:BA:1549:U:H2'	25:BA:1550:C:H6	1.79	0.47
25:BA:2325:C:C2'	25:BA:2326:C:H5'	2.45	0.47
1:CA:1292:U:C2	1:CA:1293:G:C8	3.03	0.47
25:BA:2087:C:H2'	25:BA:2088:C:H6	1.79	0.47
25:BA:2846:U:C4	25:BA:2893:A:N6	2.83	0.47
25:BA:1547:C:O4'	27:BD:100:GLY:HA2	2.15	0.47
1:AA:567:G:H1'	61:AA:4081:HOH:O	2.13	0.47
25:DA:1845:G:OP1	27:DD:258:LYS:NZ	2.43	0.47
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.15	0.47
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.66	0.47
20:AT:58:LYS:O	20:AT:62:LEU:HB2	2.14	0.47
30:DG:64:THR:HB	30:DG:94:LEU:HD11	1.96	0.47
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.96	0.47
25:DA:735:A:C6	25:DA:736:C:C2	3.03	0.47
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.49	0.47
5:AE:8:GLU:OE1	5:AE:63:ARG:NH2	2.48	0.47
16:AP:38:TYR:O	16:AP:49:LEU:HD12	2.15	0.47
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.49	0.47
39:BT:91:ARG:HH11	39:BT:120:ARG:NH1	2.12	0.47
1:CA:1119:C:N3	1:CA:1154:G:O6	2.48	0.47
25:BA:1577:C:H1'	25:BA:1578:C:OP1	2.15	0.47
1:CA:622:A:H3'	1:CA:623:C:C6	2.49	0.47
25:DA:2319:G:N2	38:DS:3:ARG:HA	2.29	0.47
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.15	0.47
1:CA:410:G:H5''	1:CA:411:A:OP1	2.14	0.47
30:BG:11:TYR:CE2	30:BG:16:ARG:HD3	2.50	0.47
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.96	0.47
25:DA:1359:A:C2	25:DA:1372:U:O4	2.68	0.47
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.49	0.47
10:CJ:25:GLU:O	10:CJ:29:ARG:HD3	2.15	0.47
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.30	0.47
1:AA:1346:A:C8	7:AG:10:ARG:NH2	2.83	0.47
35:BP:63:PRO:HB2	54:B8:30:ARG:NH2	2.30	0.47
50:B4:14:ILE:HD12	50:B4:24:THR:HG21	1.96	0.47
1:AA:676:A:H2'	1:AA:677:U:C6	2.50	0.47
5:AE:53:LEU:HD12	5:AE:53:LEU:H	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:572:A:H61	41:BV:18:LEU:HD23	1.80	0.47
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.15	0.47
31:BH:86:GLU:OE1	31:BH:132:ARG:NH1	2.45	0.47
28:DE:143:ASN:HD22	28:DE:147:PRO:CD	2.28	0.47
1:CA:985:C:H2'	1:CA:986:A:H8	1.80	0.47
24:CW:9:MVA:O	24:CW:10:2QY:CD2	2.63	0.47
25:BA:2642:G:H2'	25:BA:2643:G:H8	1.79	0.47
11:AK:44:SER:OG	11:AK:47:VAL:HG23	2.14	0.47
25:BA:908:A:H2'	25:BA:909:G:O4'	2.14	0.47
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.80	0.47
1:AA:110:C:O2'	16:AP:25:ARG:O	2.32	0.47
45:BZ:144:LEU:HD11	45:BZ:150:LEU:HD22	1.95	0.47
2:CB:127:ILE:C	2:CB:129:GLU:H	2.16	0.47
1:CA:865:A:C2	1:CA:918:A:H4'	2.50	0.47
1:CA:337:C:H2'	1:CA:338:A:C8	2.50	0.47
26:BB:29:A:C2	26:BB:30:C:C2	3.03	0.47
25:DA:2659:G:N2	25:DA:2661:G:H3'	2.30	0.47
32:DI:3:VAL:HG12	32:DI:38:LEU:HA	1.96	0.47
25:BA:399:G:H8	47:B1:65:SER:O	1.97	0.47
3:CC:140:ARG:NH1	3:CC:140:ARG:HB2	2.29	0.47
45:BZ:70:LEU:HA	45:BZ:70:LEU:HD23	1.58	0.47
25:DA:2508:G:C2	25:DA:2582:G:C6	3.02	0.47
47:D1:25:LYS:HG3	47:D1:31:GLY:HA2	1.97	0.47
49:D3:6:VAL:HG13	49:D3:56:VAL:HG13	1.96	0.47
6:CF:35:ALA:HA	6:CF:67:MET:HB3	1.96	0.47
25:DA:153:C:OP2	47:D1:92:LYS:NZ	2.46	0.47
25:DA:1197:G:H5'	25:DA:1227:G:O2'	2.14	0.47
17:AQ:10:VAL:HG13	17:AQ:19:VAL:HB	1.97	0.47
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.48	0.47
9:AI:9:ARG:HG2	9:AI:14:VAL:HG13	1.97	0.47
2:AB:162:ILE:HD11	2:AB:184:VAL:HG22	1.95	0.47
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.47
1:AA:1392:G:C2'	1:AA:1393:U:H5'	2.45	0.47
25:BA:2299:A:H2	25:BA:2358:A:H62	1.60	0.47
27:BD:16:MET:HG3	27:BD:206:LEU:O	2.15	0.47
25:DA:2078:C:C4	25:DA:2079:U:C4	3.02	0.47
25:DA:2315:G:H2'	25:DA:2316:C:C6	2.49	0.47
25:DA:1188:U:C4'	41:DV:79:VAL:HG22	2.45	0.47
25:BA:623:G:N2	25:BA:628:C:O3'	2.47	0.47
1:CA:452:A:O2'	1:CA:453:A:OP2	2.29	0.47
25:DA:2364:C:OP1	46:D0:55:ARG:NH1	2.48	0.47
1:CA:441:A:H3'	1:CA:442:C:H6	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DB:79:C:H2'	26:DB:80:U:O4'	2.15	0.47
25:DA:2538:C:H2'	25:DA:2539:C:H6	1.79	0.47
1:CA:429:U:H1'	1:CA:430:A:H5''	1.97	0.47
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.30	0.47
25:BA:1833:A:N1	25:BA:1853:G:H1'	2.30	0.47
25:BA:1759:C:H2'	25:BA:1760:U:O4'	2.15	0.47
25:BA:1496:A:H5'	25:BA:1497:G:OP2	2.14	0.47
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.14	0.47
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.30	0.47
47:B1:64:ALA:HA	47:B1:67:ILE:HG13	1.97	0.47
38:BS:24:LEU:HA	38:BS:24:LEU:HD23	1.70	0.47
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.49	0.47
1:AA:1125:U:N3	1:AA:1127:G:C5	2.68	0.47
1:CA:1154:G:C8	1:CA:1155:G:C8	3.02	0.47
1:AA:435:C:H2'	1:AA:436:C:C6	2.50	0.47
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.97	0.47
3:AC:181:ASN:ND2	3:AC:204:LEU:HD12	2.30	0.47
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.30	0.47
1:CA:957:U:H2'	1:CA:959:A:OP2	2.14	0.47
13:CM:16:ASP:N	13:CM:16:ASP:OD1	2.48	0.47
1:CA:885:G:O2'	1:CA:914:A:N1	2.38	0.47
25:BA:932:C:H3'	25:BA:933:C:C5'	2.43	0.47
1:AA:172:A:N7	1:AA:174:C:C4	2.83	0.47
1:CA:838:G:H1	1:CA:848:C:N4	2.13	0.47
6:AF:62:TRP:CH2	6:AF:64:GLN:HB2	2.50	0.47
25:DA:585:G:H2'	25:DA:1251:C:H42	1.79	0.47
24:AW:9:MVA:O	24:AW:10:2QY:CD2	2.62	0.47
3:AC:44:GLU:HG2	3:AC:52:LEU:HD22	1.97	0.47
42:DW:59:VAL:HG12	42:DW:60:ASN:HD22	1.80	0.47
29:BF:101:LEU:HD12	29:BF:102:PRO:HD2	1.97	0.47
5:CE:104:ALA:HA	5:CE:107:ARG:HB3	1.96	0.47
40:DU:89:GLU:HB2	41:DV:50:PRO:CB	2.45	0.47
1:AA:652:U:O2'	1:AA:653:A:OP2	2.26	0.47
35:DP:45:LEU:HA	35:DP:45:LEU:HD23	1.51	0.47
1:AA:276:G:C2'	1:AA:277:C:H5'	2.45	0.47
5:AE:68:GLU:HG2	5:AE:70:PRO:HG3	1.97	0.47
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.97	0.47
5:CE:84:PHE:N	5:CE:87:SER:O	2.48	0.47
40:BU:78:THR:HG22	40:BU:117:GLN:HE22	1.80	0.47
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.97	0.47
1:CA:859:A:H2'	1:CA:860:A:O4'	2.15	0.47
29:BF:150:GLY:HA2	29:BF:172:TRP:CE3	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:CG:138:LYS:HE2	7:CG:142:GLU:OE1	2.15	0.47
25:BA:2335:G:H2'	25:BA:2336:C:O4'	2.15	0.47
25:BA:553:A:C2	25:BA:2065:C:H4'	2.50	0.47
4:AD:65:ARG:HG2	4:AD:75:PHE:CD1	2.50	0.47
1:CA:78:G:H2'	1:CA:79:G:H5'	1.97	0.47
39:DT:78:LEU:O	39:DT:78:LEU:HD13	2.14	0.47
25:DA:678:C:H2'	25:DA:679:C:C6	2.50	0.47
1:CA:1492:A:H5''	1:CA:1493:A:OP2	2.15	0.47
25:DA:19:C:H2'	25:DA:20:C:C6	2.50	0.47
4:AD:173:TRP:HB2	4:AD:187:ARG:O	2.15	0.47
1:AA:458:C:H2'	1:AA:460:G:C8	2.50	0.47
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.14	0.47
25:DA:10:G:H1'	25:DA:2801(A):A:C6	2.50	0.47
25:DA:1509(B):A:H2'	25:DA:1510:G:H8	1.77	0.47
1:AA:159:G:O2'	1:AA:161:A:N7	2.35	0.47
2:AB:178:ARG:HH22	8:AH:68:ARG:HH22	1.62	0.47
43:DX:59:VAL:N	43:DX:76:ARG:O	2.33	0.47
1:AA:735:C:H2'	1:AA:736:C:H6	1.80	0.47
16:CP:21:VAL:HG22	16:CP:33:ILE:HD12	1.97	0.47
15:AO:24:SER:OG	15:AO:25:THR:N	2.48	0.47
1:AA:1140:C:H2'	1:AA:1141:C:C6	2.49	0.47
7:CG:79:ARG:HB3	7:CG:80:VAL:H	1.39	0.47
25:BA:908:A:N3	26:BB:79:C:O2'	2.41	0.47
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.78	0.47
4:CD:184:LYS:HE3	4:CD:186:LEU:HD23	1.96	0.47
25:DA:489:G:N7	42:DW:49:LYS:NZ	2.61	0.47
25:DA:2227:A:OP1	27:DD:263:ARG:HD2	2.15	0.47
1:CA:160:A:H61	1:CA:347:G:H1'	1.80	0.47
25:DA:701:G:N2	25:DA:732:C:C2	2.82	0.47
27:DD:80:ALA:HB3	27:DD:94:LEU:HD13	1.96	0.47
25:DA:922:U:H2'	25:DA:923:C:C6	2.50	0.47
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.43	0.47
18:CR:76:LEU:HD12	18:CR:76:LEU:HA	1.74	0.47
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.50	0.47
32:DI:65:ALA:O	32:DI:69:LYS:N	2.46	0.47
36:DQ:125:LEU:O	61:DQ:302:HOH:O	2.20	0.47
1:AA:499:A:N3	1:AA:546:G:N2	2.54	0.47
1:AA:342:C:N3	1:AA:348:G:O6	2.48	0.46
1:AA:1129:C:H5''	9:AI:16:ARG:HH12	1.79	0.46
1:CA:922:G:N3	1:CA:1398:A:H2	2.13	0.46
1:AA:1392:G:N2	1:AA:1502:A:C8	2.83	0.46
1:AA:93:G:O2'	1:AA:96:U:H5'	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:CO:39:LEU:HB3	15:CO:56:LEU:HD13	1.96	0.46
25:DA:1199:U:H2'	25:DA:1200:C:C6	2.50	0.46
46:B0:43:THR:O	46:B0:43:THR:HG23	2.14	0.46
1:AA:103:C:OP2	20:AT:14:LYS:NZ	2.30	0.46
1:AA:103:C:P	20:AT:17:ARG:HH21	2.38	0.46
1:AA:1442:G:HO2'	1:AA:1442(A):G:P	2.34	0.46
25:DA:2302:G:C2	25:DA:2303:G:C8	3.03	0.46
1:CA:1309:G:N2	1:CA:1329:A:H1'	2.30	0.46
1:CA:1310:G:H5'	13:CM:77:ASN:HD21	1.80	0.46
25:BA:1229:G:H5'	49:B3:29:ARG:HH12	1.80	0.46
25:DA:2312:U:C4	25:DA:2313:C:H5	2.32	0.46
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.97	0.46
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.45	0.46
1:AA:189(F):U:O2'	17:AQ:63:ARG:NH2	2.48	0.46
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.48	0.46
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.68	0.46
10:AJ:57:LYS:HD2	10:AJ:60:ARG:NH2	2.30	0.46
29:DF:29:ASN:HB3	29:DF:112:MET:HE1	1.97	0.46
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.98	0.46
16:CP:55:ARG:O	16:CP:58:TYR:HB3	2.15	0.46
25:DA:1151:G:H5''	40:DU:81:HIS:CD2	2.50	0.46
35:DP:49:ARG:NH1	54:D8:61:LEU:HD23	2.30	0.46
53:D7:24:THR:O	53:D7:28:ARG:HG3	2.15	0.46
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.14	0.46
6:AF:12:PRO:HG3	6:AF:57:GLN:O	2.15	0.46
1:CA:1068:G:N2	1:CA:1191:A:N3	2.55	0.46
10:AJ:27:ALA:HA	10:AJ:81:THR:CG2	2.45	0.46
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.15	0.46
30:DG:78:SER:OG	30:DG:79:ASN:N	2.48	0.46
13:AM:16:ASP:N	13:AM:16:ASP:OD1	2.47	0.46
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.14	0.46
25:DA:1317:A:H2'	25:DA:1318:C:C6	2.50	0.46
25:DA:75:G:H4'	48:D2:55:ARG:NH1	2.30	0.46
2:AB:97:TRP:CH2	2:AB:173:ALA:HA	2.49	0.46
1:CA:376:G:H2'	1:CA:377:G:H8	1.80	0.46
1:CA:1347:G:H22	1:CA:1373:G:H2'	1.77	0.46
1:AA:918:A:H2'	1:AA:919:A:C8	2.50	0.46
25:DA:1866:C:H2'	25:DA:1876:A:O4'	2.15	0.46
1:AA:1223:C:OP2	19:AS:78:ARG:NH2	2.45	0.46
1:CA:840:C:H5''	1:CA:841:U:H5	1.80	0.46
2:AB:174:VAL:O	2:AB:178:ARG:HB2	2.14	0.46
25:DA:333:G:N3	25:DA:333:G:H2'	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DF:36:VAL:HG11	29:DF:183:VAL:HG11	1.97	0.46
25:DA:330:A:H2	25:DA:1210:A:HO2'	1.63	0.46
25:BA:1900:G:H2'	25:BA:1901:C:C6	2.49	0.46
29:BF:106:ARG:HG2	29:BF:106:ARG:H	1.37	0.46
6:AF:35:ALA:HA	6:AF:67:MET:HB3	1.96	0.46
25:DA:924:C:H2'	25:DA:925:C:H6	1.79	0.46
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.15	0.46
25:BA:329:U:H2'	25:BA:330:U:C6	2.50	0.46
1:AA:646:U:H2'	1:AA:647:C:C6	2.50	0.46
1:AA:1457:G:P	20:AT:39:LYS:HZ1	2.38	0.46
25:DA:1669:A:H5''	25:DA:2550:G:OP1	2.15	0.46
25:BA:768:C:H2'	25:BA:769:A:C8	2.49	0.46
6:CF:5:GLU:HG3	6:CF:93:SER:OG	2.16	0.46
48:B2:37:PHE:O	48:B2:40:SER:HB3	2.14	0.46
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.14	0.46
10:CJ:57:LYS:HD2	10:CJ:60:ARG:HH21	1.81	0.46
25:DA:2348:U:O4	25:DA:2382:G:N1	2.48	0.46
25:DA:1221(A):C:C2	25:DA:1229:G:C2	3.03	0.46
1:CA:1003:G:C6	1:CA:1004:A:H2	2.34	0.46
2:CB:163:PHE:HA	2:CB:185:ILE:O	2.15	0.46
2:CB:15:VAL:CG1	2:CB:209:ARG:HB3	2.41	0.46
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.96	0.46
2:AB:55:PHE:HE1	2:AB:218:ALA:HA	1.80	0.46
40:DU:76:TYR:CZ	40:DU:80:ILE:HG13	2.51	0.46
30:DG:16:ARG:HB2	30:DG:17:PRO:HD3	1.98	0.46
1:AA:1005:A:H5'	1:AA:1038:C:H1'	1.96	0.46
30:BG:16:ARG:O	30:BG:20:ILE:HG13	2.15	0.46
25:DA:1593:G:C4	25:DA:1594:G:C8	3.03	0.46
26:DB:90:A:N7	26:DB:91:C:H1'	2.30	0.46
25:BA:335:A:C6	25:BA:352:U:C4	3.04	0.46
25:BA:324:A:P	44:BY:86:ARG:HH22	2.38	0.46
13:CM:60:VAL:HG22	13:CM:66:LEU:HD11	1.96	0.46
25:DA:1740:G:H2'	25:DA:1741:A:C8	2.51	0.46
26:DB:33:G:C2	26:DB:50:G:C2	3.04	0.46
5:CE:36:ASP:C	5:CE:38:GLN:H	2.18	0.46
1:AA:532:A:O2'	1:AA:533:A:P	2.74	0.46
29:DF:129:PHE:O	29:DF:132:VAL:HG13	2.15	0.46
25:BA:364:A:H2'	25:BA:365:G:O4'	2.15	0.46
45:BZ:120:ILE:HB	45:BZ:171:ILE:HA	1.97	0.46
25:DA:874:G:H2'	25:DA:875:G:O4'	2.15	0.46
25:BA:2314:G:N2	25:BA:2327:G:C4	2.84	0.46
1:AA:616:G:C2	1:AA:617:G:C8	3.04	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:491:G:H2'	25:DA:492:A:H8	1.80	0.46
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.50	0.46
25:DA:1668:A:H4'	25:DA:1669:A:O5'	2.14	0.46
25:BA:2389:A:H2'	25:BA:2390:A:C8	2.50	0.46
25:BA:636:G:N2	25:BA:640:A:O2'	2.48	0.46
25:DA:263:C:H2'	25:DA:264:C:O4'	2.15	0.46
25:BA:664:U:H2'	25:BA:665:C:C6	2.50	0.46
32:BI:81:VAL:HG21	32:BI:88:ILE:HD13	1.96	0.46
1:AA:1232:U:OP1	9:AI:124:GLN:HG2	2.15	0.46
40:DU:59:ARG:HB3	40:DU:59:ARG:HH11	1.80	0.46
28:BE:51:PHE:H	28:BE:75:VAL:CG1	2.27	0.46
25:BA:982:U:H2'	25:BA:983:G:O4'	2.15	0.46
25:DA:861:A:C2	25:DA:917:A:C4	3.03	0.46
10:AJ:20:ALA:HA	10:AJ:23:ILE:HG22	1.95	0.46
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.80	0.46
51:B5:42:PRO:HB2	51:B5:43:HIS:ND1	2.30	0.46
1:CA:1327:C:H2'	1:CA:1328:C:C6	2.51	0.46
25:BA:436:C:O2'	25:BA:437:G:H5'	2.16	0.46
2:CB:167:PRO:HD3	2:CB:187:LEU:O	2.15	0.46
4:AD:155:LEU:O	4:AD:158:ILE:HG12	2.15	0.46
14:CN:3:ARG:O	14:CN:7:ILE:HG23	2.15	0.46
25:BA:1592:A:H2'	25:BA:1593:C:O4'	2.16	0.46
25:BA:2658:C:OP2	25:BA:2745:G:O2'	2.19	0.46
25:DA:857:C:H2'	25:DA:858:U:C6	2.50	0.46
25:BA:926:G:H2'	25:BA:927:G:C1'	2.46	0.46
54:D8:30:ARG:HD3	54:D8:30:ARG:HA	1.69	0.46
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.15	0.46
25:DA:1358:G:O2'	25:DA:1359:A:H5''	2.15	0.46
25:BA:1217:G:H3'	25:BA:1218:G:H5'	1.98	0.46
25:DA:568:U:H5'	25:DA:945:A:C2	2.50	0.46
3:CC:6:HIS:CD2	3:CC:8:ILE:H	2.32	0.46
25:DA:656:G:H2'	25:DA:657:U:O4'	2.14	0.46
25:DA:792:G:H5''	25:DA:793:A:H5'	1.98	0.46
25:DA:888:C:H2'	25:DA:889:C:N3	2.30	0.46
25:DA:889:C:O2'	25:DA:890:A:H8	1.99	0.46
25:DA:956:G:OP1	36:DQ:87:LYS:HG3	2.16	0.46
25:BA:2225:U:O4'	27:BD:151:LYS:HE2	2.14	0.46
8:AH:39:LEU:HD12	8:AH:39:LEU:HA	1.79	0.46
1:CA:1238:A:C2	1:CA:1303:C:H4'	2.50	0.46
1:AA:391:G:C6	1:AA:392:G:C5	3.03	0.46
25:DA:1529:G:O2'	25:DA:1530:C:H5'	2.16	0.46
25:DA:1259:G:H2'	25:DA:1260:G:C8	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.16	0.46
1:CA:1240:U:O2'	7:CG:32:ARG:HD3	2.16	0.46
25:DA:1794:U:H2'	25:DA:1795:C:H6	1.80	0.46
25:BA:736:A:N3	25:BA:826:U:O2'	2.43	0.46
9:AI:121:ARG:NH1	9:AI:122:ALA:O	2.49	0.46
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.16	0.46
25:DA:647:G:H8	25:DA:647:G:O5'	1.99	0.46
25:BA:85:C:H4'	25:BA:102:U:H1'	1.97	0.46
25:DA:1142:U:H2'	25:DA:1142:U:O2	2.15	0.46
44:BY:30:VAL:O	44:BY:32:PRO:HD3	2.16	0.46
1:AA:814:A:H2'	1:AA:816:A:H5''	1.97	0.46
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.81	0.46
2:CB:47:THR:HA	2:CB:202:PRO:HG2	1.98	0.46
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.81	0.46
1:CA:1120:G:N1	1:CA:1154:G:N3	2.64	0.46
1:AA:437:U:O3'	4:AD:125:HIS:CE1	2.69	0.46
25:DA:302:C:H2'	25:DA:303:U:C6	2.50	0.46
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.96	0.46
25:DA:2287:A:O2'	25:DA:2288:A:H3'	2.15	0.46
1:AA:863:U:H2'	1:AA:865:A:OP2	2.15	0.46
1:CA:693:G:H1'	7:CG:82:GLY:HA3	1.97	0.46
29:DF:184:TYR:CE1	35:DP:3:LEU:HD21	2.50	0.46
1:AA:59:A:H5''	1:AA:60:A:H5''	1.97	0.46
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.96	0.46
5:CE:137:GLU:HG2	5:CE:140:ARG:NH1	2.29	0.46
1:AA:186:C:H2'	1:AA:187:C:H6	1.80	0.46
10:AJ:67:THR:O	10:AJ:67:THR:OG1	2.31	0.46
25:DA:2747:G:H21	25:DA:2757:A:H62	1.64	0.46
40:DU:78:THR:HG22	40:DU:117:GLN:HE21	1.81	0.46
25:BA:696:C:P	25:BA:696:C:H6	2.38	0.46
25:BA:910:A:H2'	25:BA:911:G:C8	2.50	0.46
1:CA:1240:U:C2	7:CG:32:ARG:HD2	2.50	0.46
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.50	0.46
25:DA:1506:C:H2'	25:DA:1507:A:H5'	1.98	0.46
8:AH:97:VAL:HG23	8:AH:129:VAL:O	2.16	0.46
33:DN:71:ILE:HG21	33:DN:84:LYS:HB3	1.98	0.46
13:CM:15:VAL:HG11	13:CM:48:LEU:HD21	1.96	0.46
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.49	0.46
3:CC:104:GLN:HB3	3:CC:104:GLN:HE21	1.58	0.46
25:DA:34:C:OP1	25:DA:34:C:H6	1.99	0.46
31:DH:137:ASP:HB3	31:DH:140:LYS:HB3	1.95	0.46
6:CF:38:GLU:HB2	6:CF:64:GLN:HG2	1.96	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:17:PHE:HB2	2:CB:44:LEU:CD1	2.46	0.46
1:CA:1154:G:N7	1:CA:1155:G:C5	2.83	0.46
1:CA:1154:G:O6	1:CA:1155:G:N1	2.48	0.46
29:DF:53:THR:HG23	29:DF:55:GLY:N	2.26	0.46
13:CM:3:ARG:CA	50:D4:34:GLU:HG2	2.43	0.46
1:CA:323:U:H2'	1:CA:324:G:O4'	2.16	0.46
25:DA:1589:C:H2'	25:DA:1590:U:H6	1.80	0.46
25:BA:2901:A:N6	25:BA:2902:G:N1	2.64	0.46
1:CA:1145:C:H5''	1:CA:1146:A:OP1	2.16	0.46
25:BA:922:G:H1	25:BA:948:C:N4	2.13	0.46
20:CT:33:ILE:HG13	20:CT:62:LEU:HD22	1.96	0.46
25:DA:1364:G:P	47:D1:3:LYS:HG3	2.55	0.46
19:CS:22:LEU:HB3	19:CS:27:GLU:HG3	1.97	0.46
25:DA:1341:U:OP1	25:DA:1397:U:N3	2.40	0.46
1:AA:292:G:N7	1:AA:293:G:H1'	2.31	0.46
25:BA:553:A:N1	25:BA:2064:A:H2'	2.30	0.46
9:CI:26:VAL:HG22	9:CI:61:ALA:HB3	1.97	0.46
16:CP:6:LEU:HD23	16:CP:17:TYR:CG	2.51	0.46
1:CA:25:C:H2'	1:CA:26:A:C8	2.51	0.46
1:CA:32:A:C2	1:CA:33:A:C4	3.04	0.46
25:BA:68:C:O2'	25:BA:69:G:H5'	2.16	0.46
38:DS:38:GLN:HB2	38:DS:47:THR:HG23	1.96	0.46
45:DZ:54:HIS:CG	45:DZ:101:PRO:HG3	2.51	0.46
2:AB:127:ILE:HB	2:AB:129:GLU:H	1.79	0.46
4:CD:191:ARG:O	4:CD:191:ARG:HD2	2.16	0.46
7:CG:12:LEU:H	7:CG:12:LEU:HD12	1.80	0.46
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.51	0.46
1:AA:346:G:OP1	39:BT:41:ARG:NH2	2.48	0.46
9:CI:14:VAL:HG22	9:CI:66:ARG:O	2.16	0.46
1:AA:1270:C:H2'	1:AA:1271:G:H5'	1.98	0.46
1:CA:1126:U:H6	1:CA:1281:U:O2	1.98	0.46
3:AC:58:GLU:O	3:AC:59:ARG:HG3	2.15	0.46
1:AA:865:A:H2	1:AA:918:A:H4'	1.79	0.46
30:BG:102:PHE:CE1	30:BG:141:PHE:HE2	2.25	0.46
25:DA:1324:G:C2	25:DA:1331:A:C2	3.04	0.46
25:DA:1371:G:H2'	25:DA:1372:U:H5	1.80	0.46
25:DA:1420:U:HO2'	25:DA:1421:G:P	2.39	0.46
34:DO:120:GLU:HB2	39:DT:68:TYR:HE2	1.81	0.46
24:AW:3:004:C	24:AW:4:PRO:O	2.63	0.46
36:DQ:32:TYR:OH	36:DQ:111:GLU:OE1	2.29	0.46
1:AA:877:C:OP1	8:AH:88:LYS:NZ	2.34	0.46
9:CI:99:LEU:HB3	9:CI:101:PHE:HE1	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:918:A:H2'	1:CA:919:A:C8	2.50	0.46
46:D0:82:ARG:HA	46:D0:83:PRO:HD3	1.73	0.46
25:DA:2443:C:H2'	25:DA:2444:G:H8	1.80	0.46
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.50	0.46
25:DA:2885:C:O2'	51:D5:34:PRO:HG3	2.14	0.46
43:DX:41:ASN:O	43:DX:45:THR:HG23	2.15	0.46
1:CA:232:G:H1'	1:CA:262:A:N1	2.30	0.46
51:D5:40:LYS:HD3	51:D5:41:PRO:O	2.16	0.46
5:CE:7:GLU:OE1	5:CE:37:ARG:NH2	2.47	0.46
3:CC:106:VAL:HG11	3:CC:115:LEU:HD21	1.98	0.46
36:BQ:21:THR:HG21	36:BQ:101:ARG:HB2	1.98	0.46
28:DE:36:ARG:HD3	28:DE:85:ASN:HD21	1.80	0.46
2:AB:54:THR:HG22	2:AB:58:ILE:HD11	1.97	0.46
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.98	0.46
1:CA:1491:G:H3'	1:CA:1492:A:C8	2.50	0.46
50:D4:46:GLN:HG2	50:D4:48:ARG:HE	1.81	0.46
25:DA:1198:U:H2'	25:DA:1199:U:C6	2.50	0.46
1:AA:658:G:C2	1:AA:749:C:N3	2.83	0.46
25:BA:1465:A:O2'	25:BA:1467:G:N7	2.44	0.46
5:AE:77:PRO:HG2	5:AE:78:HIS:CD2	2.51	0.46
3:AC:115:LEU:O	3:AC:118:GLN:HG2	2.15	0.46
25:DA:1773:A:C5	25:DA:1829:A:H1'	2.51	0.46
25:BA:1233:U:C2'	25:BA:1234:A:H5'	2.45	0.46
1:AA:676:A:H2'	1:AA:677:U:H6	1.79	0.46
25:BA:279:G:H5''	25:BA:279:G:H8	1.81	0.46
26:DB:31:C:C2'	26:DB:32:C:H5'	2.45	0.46
19:CS:20:LEU:HA	19:CS:23:ASN:HD22	1.81	0.46
25:BA:1662:A:H4'	25:BA:1663:C:OP2	2.15	0.46
1:CA:96:U:O2'	1:CA:97:G:H5'	2.15	0.46
30:DG:170:ARG:HH21	30:DG:180:PHE:CB	2.28	0.46
25:DA:492:A:H2'	25:DA:493:G:O4'	2.16	0.46
41:DV:64:HIS:CD2	41:DV:92:THR:HG1	2.33	0.46
1:CA:283:C:H2'	1:CA:284:G:O4'	2.15	0.46
1:CA:174:C:H2'	1:CA:175:C:H6	1.81	0.46
25:DA:32:C:O2'	25:DA:33:U:H5'	2.16	0.46
31:BH:71:LEU:HA	31:BH:71:LEU:HD12	1.70	0.46
6:CF:22:GLU:O	6:CF:26:ILE:HG13	2.16	0.46
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.16	0.46
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.98	0.46
1:CA:1118:C:H1'	1:CA:1179:A:C4	2.51	0.46
25:BA:1199:C:H2'	25:BA:1200:G:O4'	2.16	0.46
25:BA:1008:U:H2'	25:BA:1009:C:C6	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:CQ:41:LYS:NZ	17:CQ:92:ARG:HH21	2.14	0.46
1:AA:597:G:H5''	1:AA:598:U:OP2	2.16	0.46
25:DA:704:G:H1'	25:DA:726:G:H22	1.81	0.46
1:AA:736:C:H2'	1:AA:737:A:C8	2.51	0.46
25:BA:2786:C:H2'	25:BA:2787:C:C6	2.51	0.46
25:DA:1163:G:O2'	25:DA:1164:G:H5'	2.16	0.46
25:BA:160:G:O2'	25:BA:161:C:H5'	2.16	0.46
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.76	0.46
36:DQ:111:GLU:O	36:DQ:115:MET:HG2	2.16	0.46
25:DA:2831:G:P	28:DE:58:ARG:HH22	2.38	0.46
7:AG:69:VAL:HG12	7:AG:100:ALA:HA	1.96	0.46
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.98	0.46
9:AI:27:THR:O	9:AI:63:ILE:N	2.49	0.46
1:CA:89:C:H2'	1:CA:90:U:O4'	2.16	0.46
25:DA:2228:G:C6	25:DA:2229:C:C4	3.04	0.46
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.15	0.46
25:DA:1417:C:H2'	25:DA:1418:G:O4'	2.16	0.46
1:AA:1068:G:N7	1:AA:1094:G:H2'	2.31	0.46
1:AA:920:U:H2'	1:AA:921:U:C6	2.51	0.46
25:BA:1096:A:N3	25:BA:1096:A:H2'	2.30	0.46
25:BA:593:G:H2'	25:BA:2052:A:C5	2.50	0.46
40:BU:95:LEU:HA	40:BU:95:LEU:HD12	1.78	0.46
52:D6:19:ARG:N	52:D6:19:ARG:HD2	2.30	0.46
25:DA:189:G:H2'	25:DA:205:G:N2	2.30	0.46
40:BU:66:ASN:O	40:BU:70:ARG:HG3	2.15	0.46
25:DA:2207:G:H3'	25:DA:2208:A:H5''	1.98	0.46
1:CA:923:A:H2'	1:CA:924:C:C6	2.51	0.46
25:BA:1629:C:H2'	25:BA:1630:A:H8	1.81	0.46
1:AA:78:G:C2	1:AA:91:C:N3	2.84	0.46
1:CA:983:A:H3'	1:CA:983:A:N3	2.31	0.46
1:AA:658:G:H2'	1:AA:659:U:H6	1.80	0.46
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.49	0.46
32:BI:104:GLN:HG3	32:BI:105:HIS:HD2	1.80	0.46
25:DA:1885:A:H2'	25:DA:1886:C:O4'	2.17	0.46
25:BA:1854:G:OP1	27:BD:54:ARG:NH1	2.48	0.46
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.16	0.46
1:CA:1077:G:C2	1:CA:1081:G:C6	3.04	0.46
10:AJ:30:SER:O	10:AJ:81:THR:HG23	2.16	0.46
25:BA:1171:G:H5'	55:B9:37:GLY:HA2	1.98	0.46
25:DA:2354:G:OP1	46:D0:32:ARG:NH2	2.49	0.46
25:BA:1264:G:OP2	40:BU:19:LYS:HE3	2.15	0.46
28:BE:143:ASN:HD22	28:BE:147:PRO:HD3	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2461:C:H2'	25:DA:2462:U:C6	2.51	0.46
25:BA:751:G:O2'	25:BA:773:G:N2	2.35	0.46
36:DQ:108:GLY:HA3	45:DZ:116:VAL:HG13	1.96	0.46
25:BA:508:A:H5''	25:BA:509:A:OP1	2.16	0.46
33:DN:19:GLU:HA	33:DN:59:LYS:HB2	1.97	0.46
27:BD:182:LEU:HA	27:BD:182:LEU:HD23	1.65	0.46
45:DZ:70:LEU:HA	45:DZ:70:LEU:HD23	1.79	0.46
25:BA:2812:A:N3	25:BA:2904:U:H1'	2.31	0.46
44:BY:15:VAL:HG21	44:BY:42:VAL:HG11	1.99	0.46
4:AD:190:ASP:OD1	4:AD:190:ASP:N	2.49	0.45
26:BB:48:A:H4'	38:BS:95:HIS:CD2	2.42	0.45
4:AD:30:LYS:HA	4:AD:35:ARG:NH1	2.31	0.45
11:AK:99:GLN:HG3	11:AK:105:VAL:HG11	1.97	0.45
33:DN:30:ILE:O	33:DN:34:LEU:HD22	2.16	0.45
25:DA:1405:U:H2'	25:DA:1406:U:H6	1.77	0.45
3:CC:183:ASP:N	3:CC:202:ILE:O	2.46	0.45
1:CA:433:C:H2'	1:CA:434:U:C6	2.49	0.45
36:BQ:85:LYS:HD3	46:B0:7:LEU:HG	1.98	0.45
1:AA:752:G:H4'	15:AO:69:TYR:OH	2.16	0.45
4:CD:20:TYR:CD1	4:CD:26:CYS:HB3	2.51	0.45
1:CA:1243:C:H2'	1:CA:1244:C:H6	1.81	0.45
27:BD:72:LYS:HB3	27:BD:75:ILE:HD12	1.99	0.45
25:DA:77:C:O2'	48:D2:14:ARG:NH2	2.49	0.45
1:CA:931:C:H42	1:CA:1386:G:H1	1.64	0.45
11:AK:31:THR:HA	11:AK:42:TRP:HA	1.98	0.45
44:DY:19:LYS:HE2	44:DY:20:TYR:CE1	2.51	0.45
25:DA:1707:G:H2'	25:DA:1708:C:C6	2.51	0.45
36:DQ:42:ILE:HG22	36:DQ:47:ILE:HG13	1.98	0.45
1:CA:1058:G:N2	10:CJ:53:PRO:HG3	2.31	0.45
25:DA:556:G:C6	25:DA:557:U:C4	3.04	0.45
26:BB:75:G:H8	26:BB:75:G:H5''	1.80	0.45
1:AA:1424:C:H2'	1:AA:1425:U:O4'	2.15	0.45
25:DA:1783:A:H5'	25:DA:2608:G:H4'	1.98	0.45
38:DS:77:ALA:HB1	38:DS:82:ILE:HB	1.97	0.45
39:DT:61:PHE:CE1	39:DT:76:PHE:HB2	2.51	0.45
25:DA:2065:C:H2'	25:DA:2066:C:H6	1.80	0.45
42:BW:71:VAL:HA	42:BW:107:LEU:HD12	1.98	0.45
1:CA:1004:A:H3'	1:CA:1005:A:O4'	2.16	0.45
2:CB:51:LEU:HD23	2:CB:201:ILE:HD12	1.97	0.45
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.15	0.45
25:DA:858:U:O2	25:DA:2268:A:H2'	2.16	0.45
29:BF:8:GLN:OE1	29:BF:19:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.98	0.45
19:AS:38:SER:O	19:AS:70:LYS:HD3	2.17	0.45
25:DA:1266:G:O4'	42:DW:15:ARG:NH2	2.48	0.45
25:DA:776:G:C8	25:DA:793:A:C2	3.04	0.45
1:CA:1329:A:P	13:CM:28:ALA:HB3	2.57	0.45
1:CA:689:C:O4'	1:CA:704:A:H2	1.99	0.45
41:DV:62:LEU:CD1	41:DV:95:LEU:HB2	2.46	0.45
45:DZ:6:LYS:HE3	45:DZ:8:TYR:OH	2.16	0.45
25:DA:881:G:C2	25:DA:882:G:C4	3.03	0.45
25:DA:428:A:H3'	25:DA:429:A:H8	1.81	0.45
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.36	0.45
25:DA:2443:C:H2'	25:DA:2444:G:C8	2.51	0.45
29:DF:31:HIS:NE2	29:DF:35:GLU:OE2	2.49	0.45
25:DA:94(A):G:N2	48:D2:47:ASN:OD1	2.40	0.45
30:BG:97:ASP:O	30:BG:101:ILE:HG13	2.16	0.45
25:DA:1321:A:H2'	25:DA:1322:A:O4'	2.16	0.45
34:DO:4:PRO:O	34:DO:5:GLN:HB2	2.17	0.45
39:BT:29:ARG:HB2	39:BT:46:GLU:HG3	1.97	0.45
38:DS:30:ARG:HD3	38:DS:98:VAL:HG22	1.97	0.45
1:AA:958:A:C6	1:AA:959:A:N1	2.84	0.45
30:DG:61:ALA:HA	30:DG:66:GLN:O	2.15	0.45
45:BZ:136:PHE:O	45:BZ:137:ILE:HG13	2.17	0.45
27:BD:43:ARG:HA	27:BD:48:ARG:O	2.16	0.45
25:DA:57:C:H2'	25:DA:58:G:O4'	2.16	0.45
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.97	0.45
31:BH:174:GLY:O	31:BH:175:LYS:HB3	2.16	0.45
25:BA:1702:A:H3'	25:BA:1703:C:H6	1.81	0.45
1:CA:1007:C:N3	1:CA:1022:G:C2	2.83	0.45
25:DA:987:G:O2'	25:DA:1000:A:N3	2.44	0.45
29:BF:184:TYR:O	29:BF:188:ARG:HG3	2.16	0.45
1:AA:181:G:N1	1:AA:195:A:C8	2.84	0.45
3:CC:28:GLN:HB3	3:CC:32:LEU:HD23	1.96	0.45
25:DA:858:U:H1'	25:DA:2268:A:H2'	1.97	0.45
1:AA:660:G:H2'	1:AA:661:G:H8	1.82	0.45
1:CA:299:G:H2'	1:CA:300:A:C8	2.50	0.45
1:AA:1030:C:H5''	1:AA:1030(A):G:O5'	2.16	0.45
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.52	0.45
36:DQ:56:ARG:HG3	36:DQ:56:ARG:HH11	1.81	0.45
1:AA:323:U:OP1	20:AT:23:ARG:HA	2.16	0.45
1:CA:243:A:C2	1:CA:246:A:C8	3.05	0.45
1:CA:1342:C:H4'	9:CI:125:TYR:HB3	1.97	0.45
19:CS:22:LEU:HD23	19:CS:28:LYS:HA	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.72	0.45
25:DA:2335:A:C8	25:DA:2337:G:N7	2.84	0.45
1:CA:1479:C:H2'	1:CA:1480:G:C8	2.51	0.45
12:CL:117:ARG:NH2	12:CL:124:LYS:HB2	2.31	0.45
1:CA:790:A:C6	1:CA:791:G:C6	3.05	0.45
25:DA:903:C:H2'	25:DA:904:C:H6	1.80	0.45
19:AS:12:ASP:OD1	19:AS:37:ARG:HD2	2.16	0.45
20:CT:89:ARG:O	20:CT:93:GLU:HB2	2.15	0.45
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.81	0.45
5:AE:44:GLY:HA3	5:AE:62:ALA:HB2	1.99	0.45
25:BA:471:C:H2'	25:BA:472:G:O4'	2.16	0.45
1:CA:1194:U:H2'	1:CA:1195:C:C6	2.51	0.45
25:DA:2439:A:C8	25:DA:2439:A:H5'	2.50	0.45
45:BZ:28:MET:HA	45:BZ:88:PHE:O	2.16	0.45
1:AA:355:C:C4	1:AA:356:A:N7	2.84	0.45
1:AA:1082:G:H2'	1:AA:1083:U:O4'	2.16	0.45
1:AA:1035:A:H2	1:AA:1036:G:N7	2.15	0.45
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.99	0.45
31:DH:163:TYR:CE2	31:DH:169:VAL:HG22	2.52	0.45
50:B4:59:PHE:C	50:B4:61:ARG:H	2.18	0.45
1:CA:474:G:H2'	1:CA:475:G:C8	2.47	0.45
54:B8:30:ARG:HA	54:B8:30:ARG:HD3	1.58	0.45
1:CA:757:U:O2'	1:CA:879:C:O2	2.32	0.45
3:CC:179:ARG:O	3:CC:206:GLU:HA	2.16	0.45
45:DZ:45:ASP:OD2	45:DZ:49:ARG:HD2	2.16	0.45
7:CG:153:HIS:CE1	11:CK:58:PRO:HD2	2.50	0.45
1:CA:872:A:C4	1:CA:874:G:N7	2.85	0.45
25:DA:140:G:N2	25:DA:1596:A:H4'	2.31	0.45
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.99	0.45
1:CA:186:C:H2'	1:CA:187:C:C6	2.51	0.45
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.37	0.45
1:CA:927:G:H2'	1:CA:928:G:C8	2.52	0.45
25:BA:1882:U:H3	25:BA:1913:G:H1	1.64	0.45
25:BA:1825:U:H2'	25:BA:1826:C:H6	1.82	0.45
1:AA:299:G:C6	1:AA:300:A:C6	3.04	0.45
25:BA:1183:G:H2'	33:BN:106:MET:HE2	1.98	0.45
25:BA:2117:C:H2'	25:BA:2118:U:O4'	2.16	0.45
43:BX:26:TYR:CE2	43:BX:89:ILE:HG13	2.51	0.45
26:BB:32:C:C2	26:BB:51:G:N2	2.85	0.45
1:CA:35:G:C5	1:CA:36:C:C4	3.04	0.45
1:CA:35:G:C6	1:CA:36:C:N4	2.85	0.45
35:DP:52:GLU:OE2	54:D8:57:ARG:NH1	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1523:G:OP1	11:AK:123:LYS:HD2	2.16	0.45
1:CA:1186:G:O3'	9:CI:113:LYS:NZ	2.49	0.45
1:CA:685:G:C2	1:CA:686:U:C4	3.04	0.45
25:DA:747:U:O2	25:DA:2014:A:H1'	2.17	0.45
31:BH:159:GLU:HG3	31:BH:169:VAL:HG11	1.99	0.45
25:BA:270:C:H6	25:BA:270:C:O5'	1.99	0.45
32:DI:129:THR:HG22	32:DI:139:GLN:HE22	1.80	0.45
46:D0:72:ARG:O	46:D0:75:LEU:HB2	2.16	0.45
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.98	0.45
1:AA:433:C:H2'	1:AA:434:U:C6	2.49	0.45
1:CA:489:C:H2'	1:CA:490:G:H8	1.81	0.45
43:DX:26:TYR:CE2	43:DX:89:ILE:HG13	2.51	0.45
3:CC:73:PRO:O	3:CC:77:ILE:HG12	2.16	0.45
45:DZ:131:ARG:HD2	45:DZ:131:ARG:H	1.81	0.45
1:AA:1030(C):G:N7	1:AA:1031:G:N2	2.65	0.45
4:CD:43:HIS:CA	4:CD:46:LYS:HG3	2.45	0.45
5:AE:78:HIS:NE2	5:AE:142:LEU:HA	2.32	0.45
25:DA:139(A):G:O2'	25:DA:140:G:H5'	2.17	0.45
26:DB:33:G:C2'	26:DB:34:U:H5'	2.47	0.45
31:DH:20:ALA:HB3	31:DH:23:ARG:CG	2.46	0.45
1:AA:1239:A:H62	1:AA:1299:A:H62	1.64	0.45
38:DS:36:TYR:CD1	38:DS:36:TYR:N	2.85	0.45
1:AA:202:U:H3'	1:AA:203:U:C6	2.51	0.45
52:B6:11:LEU:HB3	52:B6:49:HIS:HB3	1.99	0.45
25:DA:2564:A:OP1	25:DA:2648:C:H4'	2.16	0.45
25:DA:506:G:O3'	25:DA:507:A:H8	2.00	0.45
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.52	0.45
25:DA:714:U:O2	25:DA:716:A:C8	2.70	0.45
36:BQ:34:LEU:HD11	36:BQ:129:THR:HB	1.99	0.45
34:BO:104:ARG:NH2	39:BT:43:GLN:OE1	2.50	0.45
1:AA:303:A:HO2'	1:AA:555:C:HO2'	1.57	0.45
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.51	0.45
25:DA:1927:A:H2'	25:DA:1928:A:C8	2.52	0.45
2:CB:180:LEU:HD23	2:CB:180:LEU:HA	1.69	0.45
13:CM:8:GLU:HG2	30:DG:146:TYR:HD2	1.81	0.45
14:CN:32:SER:O	14:CN:40:CYS:HA	2.17	0.45
7:AG:103:TRP:CH2	7:AG:141:VAL:HG21	2.52	0.45
45:BZ:8:TYR:HB2	45:BZ:38:TYR:CE2	2.51	0.45
8:AH:53:VAL:HG12	8:AH:54:ASP:OD1	2.16	0.45
8:AH:28:ALA:HA	8:AH:59:LEU:HG	1.98	0.45
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.16	0.45
25:DA:198:C:H5'	25:DA:2244:U:OP1	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1003:U:HO2'	25:BA:1004:A:P	2.40	0.45
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.99	0.45
7:AG:50:ILE:CD1	7:AG:58:PRO:HA	2.41	0.45
1:AA:473:G:H2'	1:AA:474:G:C8	2.52	0.45
3:AC:58:GLU:HB2	3:AC:65:ALA:CB	2.46	0.45
1:CA:959:A:O2'	1:CA:984:C:O2'	2.14	0.45
18:CR:56:THR:HB	18:CR:58:LEU:HD23	1.98	0.45
1:CA:840:C:H5''	1:CA:848:C:O2	2.17	0.45
25:BA:1314:A:C2	25:BA:2035:A:C4	3.05	0.45
29:BF:7:TYR:O	29:BF:21:ALA:HA	2.16	0.45
5:AE:137:GLU:HG2	5:AE:140:ARG:NH1	2.30	0.45
25:DA:955:C:OP1	36:DQ:87:LYS:HE3	2.16	0.45
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.16	0.45
38:DS:26:LEU:HD22	38:DS:87:PHE:CD1	2.51	0.45
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.81	0.45
28:DE:77:ILE:HD13	28:DE:195:LEU:HD13	1.98	0.45
29:DF:33:LEU:HB3	35:DP:6:LEU:HD21	1.99	0.45
25:DA:646:A:H2'	25:DA:647:G:O4'	2.16	0.45
25:DA:222:A:C2	25:DA:233:A:H5''	2.52	0.45
8:AH:121:ASP:OD1	8:AH:121:ASP:N	2.49	0.45
25:DA:2658:C:O3'	31:DH:158:HIS:HE1	1.98	0.45
25:DA:1539:G:H2'	25:DA:1540:U:C6	2.52	0.45
1:CA:881:G:P	12:CL:12:ARG:HH22	2.40	0.45
25:BA:1938:A:H2'	25:BA:1939:U:O4'	2.17	0.45
9:CI:47:LEU:HD22	9:CI:50:LEU:HD21	1.99	0.45
1:AA:1309:G:OP1	13:AM:88:ARG:NH1	2.49	0.45
45:BZ:74:VAL:HG22	45:BZ:86:VAL:HG12	1.99	0.45
37:DR:60:LEU:HA	37:DR:60:LEU:HD23	1.77	0.45
13:CM:47:ASP:N	13:CM:47:ASP:OD1	2.50	0.45
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.68	0.45
8:CH:63:LEU:HA	8:CH:63:LEU:HD13	1.85	0.45
47:B1:86:SER:N	47:B1:89:GLU:HG3	2.31	0.45
17:CQ:94:ASN:O	17:CQ:98:LEU:HD13	2.16	0.45
1:CA:1504:G:OP1	1:CA:1507:A:H4'	2.17	0.45
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.97	0.45
6:AF:81:ILE:HD11	27:BD:125:ILE:HB	1.99	0.45
27:DD:2:ALA:O	27:DD:3:VAL:HB	2.16	0.45
1:AA:1123:A:H61	1:AA:1149:C:N4	2.15	0.45
1:AA:1125:U:HO2'	1:AA:1126:U:P	2.39	0.45
2:CB:17:PHE:HB2	2:CB:44:LEU:HD12	1.97	0.45
25:DA:1138:G:H2'	25:DA:1139:G:O4'	2.16	0.45
4:CD:10:ARG:HB2	4:CD:40:PRO:HG3	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1003:G:N2	25:DA:1153:C:C2	2.84	0.45
1:CA:624:C:H2'	1:CA:625:G:H8	1.82	0.45
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.99	0.45
25:DA:2370:G:H2'	25:DA:2371:G:C8	2.51	0.45
25:DA:919:G:C6	25:DA:920:G:C5	3.05	0.45
25:DA:1876:A:H2'	25:DA:1877:A:H8	1.77	0.45
25:DA:11:G:C2'	25:DA:12:U:H5'	2.43	0.45
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.50	0.45
1:CA:584:G:H2'	1:CA:585:G:C8	2.51	0.45
43:DX:53:LYS:NZ	43:DX:55:ASN:OD1	2.32	0.45
3:CC:52:LEU:HD23	3:CC:68:VAL:HG13	1.98	0.45
25:BA:1410:G:OP2	47:B1:3:LYS:HG3	2.16	0.45
10:CJ:55:LYS:HE3	10:CJ:56:HIS:HE2	1.82	0.45
25:DA:1291:C:H2'	25:DA:1292:U:H6	1.82	0.45
5:AE:36:ASP:OD1	5:AE:38:GLN:N	2.37	0.45
20:CT:43:LEU:HB3	20:CT:52:ALA:HB2	1.99	0.45
36:BQ:54:MET:HB3	36:BQ:64:ILE:HD11	1.99	0.45
25:DA:729:G:C5	27:DD:208:LYS:HB2	2.51	0.45
25:DA:1786:A:C4	25:DA:1938:A:C6	3.04	0.45
28:BE:51:PHE:O	28:BE:75:VAL:HG13	2.16	0.45
51:D5:41:PRO:HG2	51:D5:44:THR:OG1	2.16	0.45
45:BZ:45:ASP:OD1	45:BZ:49:ARG:HD2	2.16	0.45
26:BB:14:U:OP2	26:BB:70:C:O2'	2.29	0.45
27:DD:268:ARG:HD3	27:DD:269:PHE:CE2	2.51	0.45
25:BA:561:A:H2'	25:BA:562:C:C6	2.52	0.45
25:BA:1002:A:N1	25:BA:2470:G:H4'	2.32	0.45
25:DA:2019:A:OP2	51:D5:9:LYS:NZ	2.30	0.45
25:DA:362:U:O2'	25:DA:363:G:H5'	2.17	0.45
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.78	0.45
1:AA:419:C:OP1	1:AA:513:C:O2'	2.27	0.45
1:AA:109:A:H2'	1:AA:326:G:N2	2.32	0.45
29:BF:181:LEU:HD12	29:BF:181:LEU:HA	1.71	0.45
44:BY:55:TYR:CD2	44:BY:55:TYR:N	2.84	0.45
25:BA:943:C:H6	25:BA:943:C:O5'	2.00	0.45
11:AK:70:LYS:HB2	11:AK:70:LYS:NZ	2.31	0.45
14:CN:6:LEU:HB3	14:CN:23:ARG:NH2	2.32	0.45
14:CN:2:ALA:HB1	14:CN:6:LEU:HD13	1.97	0.45
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.52	0.45
25:DA:1006:C:C2	25:DA:1138:G:N2	2.85	0.45
1:CA:1118:C:C2	1:CA:1119:C:H5	2.35	0.45
4:CD:132:ARG:NH2	4:CD:134:ASP:OD2	2.49	0.45
1:AA:1002:G:H5''	1:AA:1003:G:OP2	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:AH:7:ALA:HB2	8:AH:85:ARG:HD2	1.98	0.45
4:AD:189:PRO:HB3	4:AD:193:ASP:HB3	1.99	0.45
4:AD:5:ILE:O	4:AD:5:ILE:HD13	2.17	0.45
25:DA:1336:A:H2'	25:DA:1337:G:C8	2.52	0.45
39:DT:95:ARG:HG2	39:DT:95:ARG:NH1	2.31	0.45
25:DA:64:A:O3'	43:DX:71:GLY:HA3	2.17	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.52	0.45
27:DD:148:GLU:CB	27:DD:151:LYS:HD2	2.45	0.45
2:AB:95:GLN:HB3	2:AB:147:LYS:HZ2	1.82	0.45
1:AA:991:U:H1'	1:AA:993:G:C8	2.52	0.45
6:CF:61:LEU:HB3	6:CF:63:TYR:CE1	2.49	0.45
1:AA:1258:G:O2'	1:AA:1259:C:H5'	2.17	0.45
25:BA:2092:G:H2'	25:BA:2093:A:O4'	2.16	0.45
1:CA:130:A:H5'	17:CQ:63:ARG:NE	2.32	0.45
1:CA:130:A:OP2	17:CQ:63:ARG:NE	2.44	0.45
25:DA:2261:C:C5	46:D0:16:SER:HB3	2.52	0.45
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.99	0.45
25:BA:211:A:H5''	25:BA:448:U:OP1	2.16	0.45
25:DA:1857:G:C6	25:DA:1858:G:N1	2.85	0.45
1:AA:44:G:C2	1:AA:45:U:H1'	2.50	0.45
25:DA:1710:C:H2'	25:DA:1711:C:C6	2.51	0.45
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.51	0.45
1:AA:1511:G:H2'	1:AA:1512:U:O4'	2.17	0.45
1:AA:721:G:C6	1:AA:733:A:C2	3.04	0.45
27:DD:58:HIS:ND1	27:DD:59:LYS:N	2.65	0.45
1:CA:1403:C:H6	1:CA:1403:C:O5'	1.99	0.45
25:BA:1715:A:H4'	25:BA:1716:A:O5'	2.16	0.45
1:CA:615:C:H2'	1:CA:616:G:O4'	2.16	0.45
23:CX:67:C:C2'	23:CX:68:C:H5'	2.46	0.45
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.17	0.45
26:DB:17:C:H2'	26:DB:18:G:O4'	2.16	0.45
29:DF:120:GLU:HB3	29:DF:122:LYS:HG2	1.99	0.45
1:CA:1106:G:H2'	1:CA:1107:C:H6	1.82	0.45
25:DA:1477:A:H2'	25:DA:1478:G:O4'	2.16	0.45
35:BP:46:LYS:HB3	35:BP:46:LYS:HE3	1.77	0.45
1:AA:1285:A:O5'	1:AA:1285:A:H8	1.99	0.45
37:DR:28:LEU:HD23	37:DR:28:LEU:HA	1.85	0.45
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.49	0.45
6:AF:60:PHE:CE2	18:AR:78:LEU:HD21	2.52	0.45
25:BA:2289:G:OP2	46:B0:10:THR:HG21	2.16	0.45
26:BB:106:G:OP1	45:BZ:31:ARG:HG2	2.17	0.45
16:AP:56:ALA:O	16:AP:60:LEU:HD23	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2528:U:O2'	25:DA:2529:G:H3'	2.16	0.45
25:BA:1834:A:C8	25:BA:1835:C:C5	3.04	0.45
25:BA:2299:A:C4	25:BA:2301:G:C8	3.05	0.45
4:AD:13:ARG:HB3	4:AD:38:TYR:O	2.17	0.45
49:D3:8:LEU:O	49:D3:32:GLN:N	2.38	0.45
25:DA:652(B):A:H2	25:DA:655:A:H1'	1.82	0.45
9:CI:53:VAL:HG21	9:CI:92:TYR:OH	2.17	0.45
4:CD:17:VAL:HG11	4:CD:197:PRO:CG	2.47	0.45
26:BB:50:G:O5'	26:BB:50:G:H8	2.00	0.45
25:BA:211:A:H3'	25:BA:448:U:H5'	1.99	0.45
28:DE:119:ARG:HB3	28:DE:120:TRP:CD1	2.52	0.45
25:DA:2699:C:H2'	25:DA:2700:C:O4'	2.17	0.45
49:D3:6:VAL:HG12	49:D3:56:VAL:HG22	1.98	0.45
1:AA:921:U:O2	5:AE:19:MET:HB2	2.17	0.45
1:CA:35:G:O2'	12:CL:118:SER:O	2.34	0.45
1:AA:303:A:O2'	1:AA:555:C:O2'	2.34	0.45
1:CA:1106:G:H2'	1:CA:1107:C:C6	2.51	0.45
4:CD:79:PHE:HE1	4:CD:204:ILE:HD13	1.81	0.45
25:DA:1525:G:H2'	25:DA:1526:G:H8	1.82	0.45
25:BA:2624:C:H2'	25:BA:2625:U:H5'	1.99	0.45
25:DA:193:U:O3'	25:DA:803:U:H4'	2.17	0.45
25:DA:804:A:H5''	25:DA:805:G:OP1	2.17	0.45
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	1.99	0.45
28:DE:1:MET:HB3	28:DE:83:ASP:O	2.16	0.45
52:B6:19:ARG:NH2	52:B6:52:VAL:HG11	2.32	0.45
25:DA:587:C:OP2	35:DP:21:ARG:NH2	2.50	0.45
2:CB:81:VAL:O	2:CB:85:ALA:N	2.49	0.45
25:BA:163:C:H2'	25:BA:164:G:O4'	2.17	0.45
1:CA:1038:C:H2'	1:CA:1039:C:C6	2.52	0.45
25:DA:2242:G:H2'	25:DA:2243:U:O4'	2.17	0.45
1:CA:1136:U:O5'	1:CA:1137:C:C4	2.69	0.45
25:BA:217:A:OP1	35:BP:76:LYS:NZ	2.42	0.45
1:AA:192:U:O2'	1:AA:193:C:C6	2.68	0.45
25:DA:1817:G:H2'	25:DA:1818:U:H5'	1.98	0.45
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.32	0.45
25:BA:2211:U:C2'	25:BA:2212:G:H5'	2.47	0.45
25:DA:652(D):C:N4	25:DA:652(U):G:H1	2.10	0.45
25:DA:1652:A:C2'	25:DA:1653:G:H5'	2.47	0.45
1:AA:452:A:O2'	1:AA:453:A:OP2	2.29	0.45
2:AB:71:VAL:HA	2:AB:93:VAL:HG23	1.99	0.45
46:B0:43:THR:OG1	46:B0:46:LYS:HG2	2.16	0.45
25:BA:2274:U:P	46:B0:19:LYS:HZ3	2.40	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:254:A:H1'	25:BA:255:G:O4'	2.17	0.45
25:BA:2660:C:H2'	25:BA:2661:U:C6	2.53	0.45
25:BA:2473:C:H2'	25:BA:2474:U:C6	2.51	0.45
1:CA:1237:C:H3'	1:CA:1336:C:H41	1.82	0.45
25:BA:2784:C:H2'	25:BA:2785:C:H6	1.82	0.45
13:AM:84:ILE:N	13:AM:85:GLY:HA2	2.32	0.45
44:DY:49:VAL:CG2	44:DY:61:ILE:HG23	2.47	0.45
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.17	0.45
1:CA:1289:A:H2	1:CA:1372:U:O4'	2.00	0.45
25:DA:2002:G:OP2	61:DA:3782:HOH:O	2.21	0.45
1:CA:590:C:H2'	1:CA:591:U:C6	2.52	0.45
1:CA:1066:C:O2'	1:CA:1067:A:H5'	2.17	0.45
13:CM:87:TYR:O	13:CM:91:ARG:HG2	2.17	0.45
30:BG:115:ARG:HB3	30:BG:136:ARG:HH22	1.81	0.45
9:AI:18:PHE:O	9:AI:61:ALA:HA	2.17	0.45
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.51	0.45
25:DA:1575:C:H2'	25:DA:1576:U:H6	1.81	0.45
54:B8:54:GLU:O	54:B8:58:ILE:HG13	2.17	0.45
25:DA:453:C:O2	25:DA:457:A:O2'	2.35	0.45
27:BD:180:GLY:HA3	27:BD:275:LYS:HD2	1.98	0.45
54:D8:54:GLU:O	54:D8:58:ILE:HG13	2.17	0.45
38:DS:57:LYS:HE2	38:DS:57:LYS:HB2	1.79	0.45
40:BU:85:LYS:HE2	40:BU:85:LYS:HB3	1.78	0.45
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.99	0.45
17:AQ:26:GLN:HE21	17:AQ:37:LYS:HG2	1.81	0.45
25:BA:1321:A:N1	25:BA:1341:C:O2'	2.48	0.45
5:AE:127:ASN:HA	5:AE:128:PRO:HD3	1.85	0.45
28:DE:176:ILE:HB	28:DE:181:LEU:HB2	1.98	0.45
38:DS:23:ARG:NH2	38:DS:84:GLN:HG2	2.32	0.45
25:DA:1022:G:C5	25:DA:1140:C:C4	3.06	0.44
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.82	0.44
40:DU:65:ILE:CD1	40:DU:95:LEU:HB3	2.47	0.44
40:DU:76:TYR:HH	40:DU:92:ARG:NH1	2.15	0.44
1:CA:953:G:N7	13:CM:104:ARG:NH1	2.65	0.44
1:CA:1030(A):G:HO2'	1:CA:1030(B):C:H5	1.61	0.44
25:DA:1489:U:O3'	25:DA:1490:A:H8	2.00	0.44
1:CA:1166:G:H1'	1:CA:1171:G:H22	1.81	0.44
23:CX:40:C:H2'	23:CX:41:C:C6	2.46	0.44
25:DA:911:A:H2'	36:DQ:9:TYR:CZ	2.53	0.44
31:DH:86:GLU:CD	31:DH:130:ARG:HD3	2.38	0.44
25:DA:39:C:H2'	25:DA:40:C:C6	2.52	0.44
25:DA:614:U:H4'	25:DA:614(C):A:N6	2.32	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:B8:42:ARG:HD2	61:B8:203:HOH:O	2.17	0.44
21:CU:22:ARG:HA	21:CU:23:PRO:HD3	1.74	0.44
4:AD:61:LYS:NZ	4:AD:72:GLU:OE2	2.48	0.44
25:BA:722:A:C8	25:BA:851:A:C6	3.05	0.44
25:DA:1857:G:C6	25:DA:1858:G:C6	3.05	0.44
1:AA:1187:G:H4'	9:AI:111:ARG:NH1	2.31	0.44
1:CA:791:G:C5	1:CA:792:A:N7	2.85	0.44
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.32	0.44
7:CG:56:GLN:O	7:CG:58:PRO:HD3	2.17	0.44
1:CA:1291:G:C6	1:CA:1292:U:C4	3.05	0.44
1:CA:1192:C:OP2	3:CC:4:LYS:NZ	2.45	0.44
25:DA:1540:U:O2'	25:DA:1541:G:H5'	2.17	0.44
36:BQ:135:ASP:OD2	45:BZ:49:ARG:NH2	2.50	0.44
25:DA:931:G:O2'	49:D3:24:LYS:HD3	2.16	0.44
42:BW:84:ARG:HG3	42:BW:98:LYS:HD2	1.99	0.44
32:DI:27:ARG:HD2	47:D1:71:TYR:CE1	2.52	0.44
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.50	0.44
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.98	0.44
25:BA:659:C:H2'	25:BA:660:C:C6	2.52	0.44
1:AA:590:C:H2'	1:AA:591:U:H6	1.81	0.44
54:D8:34:TRP:CG	54:D8:35:GLN:N	2.85	0.44
11:CK:44:SER:OG	11:CK:47:VAL:HG23	2.17	0.44
25:BA:1032:C:C2'	25:BA:1033:G:H5'	2.47	0.44
3:CC:66:VAL:HB	3:CC:101:LEU:HA	1.99	0.44
49:B3:43:ILE:O	49:B3:47:VAL:HG23	2.18	0.44
24:CW:4:PRO:O	24:CW:5:MVA:HG23	2.17	0.44
1:CA:1005:A:H3'	1:CA:1006:C:O4'	2.17	0.44
1:CA:1119:C:C4	1:CA:1154:G:O6	2.71	0.44
1:CA:1118:C:C2	1:CA:1119:C:C5	3.06	0.44
1:AA:922:G:C6	1:AA:923:A:C6	3.04	0.44
3:CC:58:GLU:O	3:CC:59:ARG:HG3	2.16	0.44
25:BA:597:C:H1'	25:BA:2077:C:C6	2.53	0.44
9:AI:85:LEU:HB3	9:AI:92:TYR:HD2	1.82	0.44
25:DA:2714:G:P	61:DA:3973:HOH:O	2.75	0.44
4:AD:122:ARG:O	4:AD:134:ASP:HB2	2.18	0.44
6:AF:21:LEU:O	6:AF:24:GLU:HB3	2.16	0.44
1:CA:738:C:H2'	1:CA:739:C:C6	2.50	0.44
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.32	0.44
4:CD:43:HIS:ND1	4:CD:46:LYS:HE3	2.32	0.44
28:DE:150:VAL:CG1	28:DE:154:LYS:HG3	2.45	0.44
4:AD:177:ASP:OD2	4:AD:180:GLY:HA3	2.16	0.44
25:DA:1420:U:O2'	25:DA:1421:G:OP1	2.31	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:78:ILE:HD12	13:CM:92:HIS:NE2	2.32	0.44
1:AA:384:G:H2'	1:AA:385:C:C6	2.51	0.44
9:CI:51:ARG:HG2	9:CI:56:LEU:CD2	2.46	0.44
2:CB:74:LYS:HZ2	2:CB:166:ASP:HB2	1.82	0.44
8:CH:17:THR:HA	8:CH:65:TYR:HE2	1.82	0.44
25:DA:1527:G:H2'	25:DA:1542:A:N1	2.32	0.44
38:DS:36:TYR:OH	38:DS:54:LEU:HD22	2.17	0.44
1:CA:269:C:H2'	1:CA:270:A:C8	2.51	0.44
1:CA:1209:C:HO2'	1:CA:1214:C:H42	1.61	0.44
1:AA:1068:G:OP2	1:AA:1068:G:H8	2.00	0.44
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.98	0.44
36:BQ:32:TYR:OH	36:BQ:111:GLU:OE1	2.15	0.44
36:BQ:137:TYR:O	36:BQ:141:GLN:HG2	2.16	0.44
31:BH:93:GLY:O	31:BH:95:ARG:NH2	2.50	0.44
43:BX:24:GLY:O	43:BX:83:VAL:HG22	2.17	0.44
20:AT:92:LEU:HA	20:AT:92:LEU:HD23	1.80	0.44
30:BG:34:LEU:HA	30:BG:34:LEU:HD23	1.76	0.44
51:B5:48:GLU:HA	51:B5:48:GLU:OE1	2.16	0.44
10:CJ:23:ILE:HD12	10:CJ:85:LEU:HD22	2.00	0.44
25:DA:949:C:H2'	25:DA:950:G:C8	2.51	0.44
51:B5:33:CYS:HB2	51:B5:40:LYS:HD2	1.98	0.44
49:B3:46:ASN:O	49:B3:50:VAL:HG22	2.17	0.44
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.81	0.44
2:CB:7:VAL:HG12	2:CB:8:LYS:HG2	1.99	0.44
10:CJ:16:LEU:HD23	10:CJ:16:LEU:HA	1.88	0.44
25:BA:11:G:C2'	25:BA:12:U:H5'	2.42	0.44
1:CA:811:C:O2'	1:CA:901:A:N1	2.48	0.44
1:CA:671:G:N2	1:CA:735:C:O2	2.49	0.44
30:DG:110:ALA:HA	30:DG:140:ILE:O	2.17	0.44
3:CC:150:LYS:HD2	3:CC:201:TYR:HD2	1.82	0.44
6:CF:72:VAL:O	6:CF:75:LEU:HB3	2.18	0.44
1:CA:1339:A:H2'	1:CA:1340:A:O4'	2.18	0.44
25:BA:1778:G:H2'	25:BA:1779:G:H5''	1.99	0.44
25:DA:953:A:O2'	25:DA:954:G:H5'	2.18	0.44
25:BA:701:A:H2	25:BA:702:A:C2	2.36	0.44
30:DG:114:ILE:HD12	30:DG:117:PHE:CD2	2.52	0.44
14:AN:13:THR:HA	14:AN:14:PRO:HD3	1.85	0.44
1:CA:186:C:H2'	1:CA:187:C:H6	1.83	0.44
1:AA:272:C:H2'	1:AA:273:A:C8	2.52	0.44
7:CG:78:ARG:NH2	7:CG:79:ARG:HH22	2.16	0.44
31:DH:149:ARG:NH1	31:DH:154:PRO:HG2	2.32	0.44
25:DA:1448:G:H1'	25:DA:1528:A:N1	2.33	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:341:G:H2'	25:DA:342:G:O4'	2.17	0.44
19:AS:48:THR:HG22	19:AS:61:TYR:HA	1.99	0.44
18:CR:36:ASN:OD1	18:CR:39:VAL:HG23	2.17	0.44
6:AF:1:MET:HA	6:AF:67:MET:O	2.18	0.44
32:BI:93:THR:H	32:BI:96:ASP:CG	2.21	0.44
52:D6:11:LEU:HA	52:D6:11:LEU:HD23	1.80	0.44
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.51	0.44
8:AH:121:ASP:HB2	8:AH:125:ARG:NH1	2.31	0.44
36:BQ:135:ASP:O	36:BQ:139:GLU:HG3	2.17	0.44
1:AA:109:A:C6	1:AA:326:G:C6	3.06	0.44
25:DA:2044:C:C2	25:DA:2625:G:C2	3.05	0.44
45:DZ:11:GLU:HB3	45:DZ:12:GLY:H	1.53	0.44
3:AC:26:LYS:HA	14:AN:36:PHE:CE1	2.52	0.44
3:AC:26:LYS:HA	14:AN:36:PHE:HE1	1.81	0.44
33:DN:16:ILE:HB	33:DN:54:VAL:HG22	1.99	0.44
1:CA:7:G:O2'	5:CE:120:THR:O	2.35	0.44
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.32	0.44
25:BA:1709:C:H1'	25:BA:2699:U:H5''	1.99	0.44
35:DP:62:LEU:O	54:D8:13:ARG:HD3	2.17	0.44
1:AA:977:A:H1'	1:AA:982:U:O4	2.17	0.44
36:DQ:77:LYS:HE3	36:DQ:84:GLY:O	2.17	0.44
48:D2:3:LEU:HD23	48:D2:3:LEU:HA	1.72	0.44
33:BN:138:LEU:HA	33:BN:138:LEU:HD23	1.53	0.44
25:BA:288:U:H2'	25:BA:288:U:H6	1.56	0.44
25:DA:583:G:OP2	40:DU:10:ARG:NH1	2.50	0.44
25:DA:1223:G:N2	25:DA:1226:A:OP2	2.44	0.44
1:CA:1001(A):G:N3	1:CA:1002:G:H1'	2.32	0.44
2:CB:9:GLU:HA	2:CB:48:MET:SD	2.58	0.44
25:DA:1005:C:H4'	25:DA:1012:U:C6	2.52	0.44
2:AB:47:THR:O	2:AB:51:LEU:N	2.40	0.44
30:DG:11:TYR:HA	30:DG:15:VAL:HB	2.00	0.44
7:AG:56:GLN:O	7:AG:58:PRO:HD3	2.17	0.44
1:CA:1223:C:H5''	1:CA:1224:G:C5'	2.43	0.44
1:AA:410:G:H5''	1:AA:411:A:OP1	2.17	0.44
25:BA:2101:U:OP1	47:B1:21:ARG:NH2	2.51	0.44
1:AA:149:A:H2'	1:AA:150:C:H6	1.81	0.44
50:D4:46:GLN:HG3	50:D4:48:ARG:NH2	2.32	0.44
25:BA:927:G:C2	25:BA:928:G:C8	3.05	0.44
25:DA:2708:G:H1'	37:DR:71:GLN:NE2	2.32	0.44
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.83	0.44
1:CA:1091:U:H2'	1:CA:1093:A:OP2	2.18	0.44
25:BA:2348:A:H61	46:B0:43:THR:HG21	1.81	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:70:VAL:HA	30:DG:90:LEU:HD23	2.00	0.44
25:DA:2745:C:C4	25:DA:2746:U:C4	3.04	0.44
45:BZ:120:ILE:HD13	45:BZ:120:ILE:N	2.33	0.44
25:DA:2881:C:H2'	25:DA:2882:A:O4'	2.18	0.44
1:CA:189(L):G:H2'	1:CA:190:U:C6	2.52	0.44
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.53	0.44
25:DA:2734:A:H2'	25:DA:2735:G:O4'	2.17	0.44
25:DA:1041:C:H42	25:DA:1114:G:H1	1.64	0.44
25:BA:768:C:H2'	25:BA:769:A:H8	1.82	0.44
28:BE:51:PHE:CD2	28:BE:52:LEU:HG	2.51	0.44
29:BF:28:ILE:O	29:BF:30:PRO:HD3	2.17	0.44
25:BA:41:C:H2'	25:BA:42:G:O4'	2.17	0.44
1:CA:633:G:H2'	1:CA:634:C:C6	2.53	0.44
25:DA:192:C:O2'	25:DA:802:A:N3	2.44	0.44
25:BA:2042:A:O2'	25:BA:2043:C:H5'	2.17	0.44
31:BH:87:LEU:HD23	31:BH:164:TYR:HA	1.99	0.44
25:BA:2425:G:H2'	25:BA:2426:G:O4'	2.18	0.44
8:CH:98:LYS:HE3	8:CH:98:LYS:HB2	1.66	0.44
37:BR:65:LEU:HD13	37:BR:65:LEU:HA	1.59	0.44
55:D9:2:LYS:HE2	55:D9:31:LYS:O	2.17	0.44
3:AC:43:LEU:HD21	3:AC:91:LEU:HD13	1.99	0.44
50:B4:40:HIS:HA	50:B4:41:PRO:HD2	1.84	0.44
25:DA:675:A:C6	25:DA:676:A:C6	3.05	0.44
50:D4:16:CYS:SG	50:D4:17:GLY:N	2.90	0.44
1:AA:144:G:H1	1:AA:178:C:H42	1.64	0.44
1:CA:1024:G:H2'	1:CA:1024:G:N3	2.33	0.44
1:CA:1004:A:C6	1:CA:1038:C:C6	3.06	0.44
1:CA:1346:A:H5''	9:CI:120:ARG:HH12	1.83	0.44
1:CA:620:C:H2'	1:CA:621:A:O4'	2.17	0.44
25:DA:2318:G:N2	38:DS:3:ARG:NH1	2.66	0.44
7:AG:50:ILE:HD11	7:AG:58:PRO:CA	2.40	0.44
13:CM:16:ASP:HB3	13:CM:34:LEU:CD1	2.46	0.44
25:BA:2340:A:H2'	25:BA:2341:G:H8	1.83	0.44
25:BA:1044:C:OP2	40:BU:92:ARG:NH2	2.51	0.44
25:DA:652(D):C:H2'	25:DA:652(E):G:O4'	2.17	0.44
1:AA:1030(B):C:H2'	1:AA:1030(C):G:H5'	2.00	0.44
25:DA:817:C:O2'	25:DA:839:U:H5''	2.18	0.44
20:AT:16:HIS:O	20:AT:19:SER:OG	2.24	0.44
26:DB:70:C:H2'	26:DB:71:C:H6	1.83	0.44
41:DV:35:LEU:HB2	41:DV:57:VAL:HG23	1.99	0.44
1:CA:66:G:C2	1:CA:67:C:C6	3.05	0.44
7:CG:26:PHE:CE2	7:CG:30:ILE:HD11	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:BZ:161:VAL:HG13	45:BZ:161:VAL:O	2.18	0.44
1:CA:397:A:H3'	1:CA:397:A:N3	2.32	0.44
7:CG:69:VAL:HG21	7:CG:104:LEU:CD1	2.48	0.44
29:DF:102:PRO:HB2	29:DF:105:VAL:HG23	2.00	0.44
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.17	0.44
25:BA:851:A:H5''	25:BA:852:G:OP1	2.17	0.44
1:AA:392:G:H2'	1:AA:393:A:C8	2.53	0.44
1:CA:1259:C:C4	1:CA:1260:C:H1'	2.53	0.44
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.51	0.44
32:BI:99:GLU:O	32:BI:103:ARG:NH1	2.50	0.44
25:BA:2116:G:P	32:BI:22:LYS:HD2	2.57	0.44
1:AA:500:G:N2	1:AA:546:G:H1'	2.32	0.44
25:BA:640:A:C4	29:BF:180:GLY:HA2	2.53	0.44
25:BA:1096:A:H3'	25:BA:1097:G:H8	1.82	0.44
25:BA:1002:A:H5'	36:BQ:76:LYS:HG3	1.98	0.44
2:AB:145:LEU:O	2:AB:149:LEU:HB2	2.18	0.44
1:AA:1289:A:N1	1:AA:1371:G:O2'	2.42	0.44
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	1.98	0.44
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.65	0.44
25:BA:2410:U:H2'	25:BA:2411:G:C8	2.53	0.44
44:BY:20:TYR:CE1	44:BY:43:ASN:HA	2.52	0.44
25:BA:2418:U:OP1	61:BA:4136:HOH:O	2.21	0.44
15:AO:54:ARG:O	15:AO:58:MET:HG3	2.17	0.44
36:DQ:137:TYR:CE1	45:DZ:83:PRO:HG3	2.52	0.44
25:BA:2545:A:H2'	25:BA:2546:A:O4'	2.17	0.44
25:BA:964:A:H5''	26:BB:98:G:O2'	2.18	0.44
30:BG:43:LEU:HB3	30:BG:44:GLY:H	1.52	0.44
1:CA:1036:G:N7	1:CA:1037:C:O2	2.51	0.44
2:CB:16:HIS:CB	2:CB:210:SER:HB3	2.42	0.44
25:DA:2318:G:H21	38:DS:3:ARG:HD3	1.83	0.44
1:AA:457:C:H2'	1:AA:458:C:C5	2.53	0.44
1:CA:692:U:O2'	1:CA:694:A:N7	2.37	0.44
2:CB:96:ARG:NH1	2:CB:98:LEU:HD13	2.33	0.44
40:BU:50:ARG:HG2	40:BU:53:ARG:NH2	2.33	0.44
25:BA:927:G:C2'	25:BA:928:G:H5'	2.48	0.44
1:CA:472:A:C2	1:CA:473:G:H1'	2.53	0.44
16:AP:75:ARG:HA	16:AP:80:PHE:HD2	1.82	0.44
1:AA:1346:A:C8	1:AA:1348:U:O2	2.71	0.44
25:DA:1721:G:H8	25:DA:1741:A:N6	2.12	0.44
1:AA:444:C:H2'	1:AA:445:G:C8	2.50	0.44
25:DA:311:A:C8	25:DA:332:A:N7	2.85	0.44
1:AA:62:U:OP1	1:AA:385:C:O2'	2.35	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DB:31:C:H4'	30:DG:29:TRP:CZ2	2.52	0.44
25:BA:939:C:O2'	25:BA:940:C:H5'	2.16	0.44
30:DG:170:ARG:HD3	30:DG:170:ARG:C	2.38	0.44
13:AM:49:THR:HG22	13:AM:51:ALA:H	1.82	0.44
25:DA:1027:A:N6	25:DA:1126:A:C4	2.86	0.44
29:DF:33:LEU:HD22	29:DF:112:MET:HE3	2.00	0.44
25:DA:2461:C:H2'	25:DA:2462:U:H6	1.83	0.44
25:DA:108:U:H2'	25:DA:109:G:C8	2.52	0.44
7:CG:40:ALA:HB1	9:CI:41:VAL:HG21	1.98	0.44
7:CG:42:ILE:HD13	7:CG:116:ALA:HB3	1.99	0.44
31:BH:28:GLY:HA3	31:BH:79:VAL:HB	2.00	0.44
2:CB:172:ILE:O	2:CB:176:GLU:HG3	2.18	0.44
14:AN:26:ARG:NH2	14:AN:47:LEU:HD21	2.33	0.44
44:DY:90:LEU:HD23	44:DY:92:ASN:HB2	1.99	0.44
25:DA:815:C:C2	25:DA:1193:G:C2	3.05	0.44
2:AB:113:HIS:HA	2:AB:116:GLU:HB2	2.00	0.44
1:CA:1380:U:C4	7:CG:3:ARG:HG2	2.52	0.44
1:CA:292:G:C5	1:CA:293:G:H1'	2.53	0.44
12:AL:57:LYS:HG2	12:AL:65:GLU:OE2	2.18	0.44
4:AD:188:LEU:H	4:AD:188:LEU:HD23	1.82	0.44
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.98	0.44
1:CA:407:G:N2	1:CA:436:C:C2	2.86	0.44
16:AP:6:LEU:HD23	16:AP:17:TYR:CD2	2.52	0.44
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.53	0.44
2:AB:163:PHE:HA	2:AB:185:ILE:O	2.17	0.44
13:AM:4:ILE:HB	13:AM:57:ARG:HG3	1.99	0.44
1:CA:767:A:H2'	1:CA:768:A:O4'	2.16	0.44
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.18	0.44
26:BB:31:C:H4'	30:BG:29:TRP:CH2	2.51	0.44
1:AA:1291:G:H2'	1:AA:1292:U:C6	2.53	0.44
4:CD:64:LEU:HD22	4:CD:198:VAL:HG11	1.99	0.44
45:DZ:141:VAL:O	45:DZ:144:LEU:HB2	2.18	0.44
35:BP:59:LEU:HD21	54:B8:10:ALA:HA	1.99	0.44
1:CA:60:A:N6	1:CA:110:C:N3	2.64	0.44
25:DA:2556:C:H2'	25:DA:2557:G:O4'	2.18	0.44
25:BA:648:G:H2'	25:BA:649:C:C6	2.52	0.44
25:BA:254:A:C8	25:BA:255:G:H1'	2.53	0.44
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.18	0.44
11:CK:85:ARG:HA	11:CK:112:THR:OG1	2.17	0.44
1:AA:376:G:H2'	1:AA:377:G:C8	2.52	0.44
45:DZ:5:LEU:HD22	45:DZ:6:LYS:H	1.83	0.44
25:BA:276:C:O3'	32:BI:42:SER:OG	2.36	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2410:G:H2'	25:DA:2411:A:O4'	2.17	0.44
25:DA:2294:C:OP2	38:DS:89:ARG:NH2	2.41	0.44
7:CG:131:LYS:HG2	7:CG:132:GLY:H	1.83	0.44
28:BE:181:LEU:HD12	28:BE:181:LEU:HA	1.79	0.44
1:CA:430:A:H2'	1:CA:431:A:O4'	2.18	0.44
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.50	0.44
35:DP:64:LYS:HA	54:D8:13:ARG:HB3	2.00	0.44
25:BA:442:A:H2'	25:BA:443:C:C6	2.53	0.44
25:DA:984:A:H5''	25:DA:985:C:H5	1.81	0.44
4:AD:20:TYR:HD1	4:AD:26:CYS:HB3	1.82	0.44
46:D0:40:GLN:HE21	46:D0:57:PHE:HB3	1.83	0.44
25:DA:460:A:P	53:D7:41:ARG:HH22	2.41	0.44
3:AC:47:LEU:HD12	3:AC:68:VAL:HG11	1.98	0.44
26:BB:12:C:H2'	46:B0:73:GLY:HA3	1.99	0.44
1:AA:720:C:H6	1:AA:720:C:O5'	2.01	0.44
8:CH:36:LEU:HA	8:CH:36:LEU:HD23	1.89	0.44
20:AT:34:LYS:HE2	20:AT:34:LYS:HB2	1.69	0.44
3:AC:77:ILE:H	3:AC:77:ILE:HG12	1.70	0.44
1:AA:799:G:H5''	1:AA:799:G:H8	1.82	0.44
5:CE:51:VAL:O	5:CE:55:VAL:HG23	2.17	0.44
1:AA:1060:C:N4	3:AC:2:GLY:HA3	2.32	0.44
1:CA:1005:A:H2	1:CA:1026:G:C8	2.36	0.44
1:AA:1125:U:O2'	1:AA:1126:U:P	2.75	0.44
4:CD:39:PRO:O	4:CD:44:GLY:HA3	2.18	0.44
1:CA:1277:C:HO2'	1:CA:1279:A:H1'	1.83	0.44
1:CA:922:G:C6	1:CA:923:A:C6	3.05	0.44
1:CA:1142:G:C2	1:CA:1143:G:H1'	2.52	0.44
1:AA:456:C:H2'	1:AA:457:C:C6	2.53	0.44
1:AA:1198:G:C6	1:AA:1199:U:C4	3.06	0.44
3:AC:58:GLU:H	3:AC:65:ALA:HB3	1.83	0.44
25:DA:1115:G:OP2	25:DA:1115:G:H8	2.01	0.44
25:DA:2251:G:OP1	61:DA:4599:HOH:O	2.21	0.44
25:BA:926:G:H2'	25:BA:927:G:O4'	2.17	0.44
9:CI:53:VAL:C	9:CI:55:ALA:H	2.20	0.44
25:BA:2850:C:H4'	37:BR:53:HIS:CE1	2.53	0.44
13:CM:82:MET:O	13:CM:93:ARG:NH2	2.51	0.44
3:CC:33:LEU:HD21	14:CN:53:LEU:CD2	2.48	0.44
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.52	0.44
1:AA:532:A:H5'	3:AC:161:GLU:OE2	2.18	0.44
1:AA:1073:U:H2'	1:AA:1074:G:C8	2.53	0.44
36:DQ:27:VAL:O	36:DQ:29:PHE:N	2.51	0.44
25:DA:863:A:O2'	25:DA:864:G:H5'	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:875:G:C2	25:DA:903:C:C2	3.06	0.44
2:CB:230:VAL:HG13	2:CB:231:GLU:O	2.18	0.44
1:CA:933:G:C6	1:CA:1385:G:C6	3.05	0.44
25:BA:2336:C:H5''	25:BA:2337:G:H5'	2.00	0.44
1:CA:1068:G:H8	1:CA:1068:G:OP2	2.00	0.44
1:AA:1456:G:N1	20:AT:51:GLU:OE1	2.51	0.44
26:DB:42:C:O2'	30:DG:66:GLN:HG2	2.18	0.44
27:BD:145:VAL:HG12	27:BD:146:GLU:O	2.18	0.44
3:AC:175:LEU:HD21	3:AC:201:TYR:CE2	2.52	0.44
52:B6:9:LEU:HD21	52:B6:25:LYS:HB3	1.98	0.44
27:DD:77:ALA:HB2	27:DD:97:TYR:CD2	2.52	0.44
20:CT:14:LYS:O	20:CT:18:GLN:HG3	2.18	0.44
10:AJ:40:LEU:HB2	10:AJ:69:ASN:HB3	2.00	0.44
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.99	0.44
11:AK:85:ARG:HA	11:AK:112:THR:OG1	2.18	0.44
33:BN:30:ILE:HG22	33:BN:34:LEU:HD22	2.00	0.44
1:AA:1134:G:N3	1:AA:1134:G:H2'	2.33	0.44
25:DA:55:G:H2'	25:DA:56:A:H8	1.83	0.44
1:AA:1084:G:C5	1:AA:1085:U:C4	3.06	0.44
31:DH:150:ALA:HA	31:DH:153:LYS:HG3	2.00	0.44
25:BA:2614:A:N7	46:B0:3:HIS:CE1	2.86	0.44
1:AA:78:G:N1	1:AA:91:C:N4	2.66	0.44
1:CA:713:G:H2'	1:CA:714:G:C8	2.53	0.44
1:AA:600:C:H2'	1:AA:601:C:H6	1.83	0.44
25:BA:1091:A:H2'	25:BA:1091:A:N3	2.31	0.44
25:BA:1157:A:N3	25:BA:1158:G:H1'	2.33	0.44
25:BA:2214:G:H5'	25:BA:2215:G:OP2	2.18	0.44
25:DA:271(F):C:H2'	25:DA:271(G):C:C6	2.52	0.44
1:CA:1324:A:H5'	1:CA:1362:C:O2'	2.18	0.44
31:BH:126:PRO:HB2	31:BH:127:GLU:H	1.51	0.44
1:AA:539:A:H2'	1:AA:540:G:C8	2.52	0.44
19:CS:28:LYS:HD2	19:CS:47:HIS:HA	2.00	0.44
12:CL:36:VAL:HG23	24:CW:10:2QY:CE1	2.47	0.44
7:CG:51:GLN:HB3	7:CG:51:GLN:HE21	1.63	0.44
25:DA:2854:G:H2'	25:DA:2855:C:C6	2.52	0.44
25:BA:2830:A:OP1	37:BR:2:ARG:NH2	2.51	0.44
1:CA:165:C:O5'	1:CA:165:C:H6	2.01	0.44
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.18	0.44
39:DT:88:ILE:HG21	39:DT:91:ARG:NE	2.33	0.44
1:AA:8:A:H5'	5:AE:101:ILE:HG22	2.00	0.44
20:AT:42:GLN:NE2	20:AT:46:GLU:OE2	2.51	0.44
3:CC:153:VAL:HA	3:CC:197:GLY:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AF:48:LEU:HD22	18:AR:77:GLY:HA3	1.99	0.44
25:BA:1749:G:H2'	25:BA:1750:G:O4'	2.17	0.44
38:BS:103:GLU:O	38:BS:107:GLU:HG3	2.18	0.44
37:BR:72:ASP:OD2	37:BR:75:LEU:HB2	2.18	0.44
4:AD:106:TYR:HE2	4:AD:112:VAL:O	2.01	0.44
25:BA:1805:C:O5'	25:BA:1805:C:H6	2.01	0.44
33:DN:138:LEU:HA	33:DN:138:LEU:HD23	1.75	0.44
1:AA:1164:G:H2'	1:AA:1165:C:H6	1.82	0.44
4:AD:88:VAL:O	4:AD:92:VAL:HG23	2.18	0.44
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.57	0.44
1:CA:142:G:H2'	1:CA:143:A:C8	2.53	0.44
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.46	0.44
1:AA:346:G:H3'	1:AA:346:G:N3	2.33	0.43
25:BA:1188:A:C4	25:BA:1190:G:C8	3.05	0.43
39:DT:16:ARG:HD2	39:DT:18:ASP:OD1	2.18	0.43
1:CA:926:G:C6	1:CA:1505:G:C6	3.06	0.43
1:AA:10:A:OP2	5:AE:126:ARG:HD2	2.17	0.43
15:CO:54:ARG:O	15:CO:57:LEU:HB2	2.18	0.43
19:AS:50:ALA:HA	19:AS:58:VAL:O	2.18	0.43
25:BA:2804:C:H6	25:BA:2804:C:OP2	2.01	0.43
1:CA:1017:G:H2'	1:CA:1018:C:O4'	2.17	0.43
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.18	0.43
8:AH:25:ASP:HA	8:AH:60:ARG:HA	1.99	0.43
1:AA:404:U:H2'	1:AA:405:U:C6	2.53	0.43
29:DF:196:LEU:HA	29:DF:196:LEU:HD23	1.66	0.43
1:CA:380:G:C2	1:CA:384:G:C6	3.06	0.43
27:DD:206:LEU:HD23	27:DD:206:LEU:HA	1.68	0.43
27:DD:206:LEU:CD2	27:DD:211:ARG:HG2	2.46	0.43
17:CQ:41:LYS:HZ2	17:CQ:92:ARG:HH21	1.65	0.43
25:BA:588:C:H2'	25:BA:589:U:O4'	2.18	0.43
8:AH:94:TYR:HD1	8:AH:132:GLU:HA	1.83	0.43
25:DA:1991:U:H2'	25:DA:1992:G:H5''	1.99	0.43
23:CX:59:A:C2'	23:CX:60:U:H5'	2.47	0.43
1:AA:106:C:O2'	1:AA:379:C:H5''	2.17	0.43
25:DA:1384:A:N3	25:DA:1405:U:H1'	2.32	0.43
25:DA:479:A:O2'	25:DA:481:G:H5'	2.18	0.43
26:BB:33:G:C2'	26:BB:34:U:H5'	2.47	0.43
1:CA:93:G:O2'	1:CA:96:U:H5'	2.18	0.43
25:BA:174:U:H4'	25:BA:207:A:H4'	2.00	0.43
14:AN:45:ARG:HG2	14:AN:49:HIS:HD2	1.83	0.43
5:CE:84:PHE:CE2	5:CE:133:TYR:HD2	2.36	0.43
1:CA:89:C:C4	1:CA:90:U:C5	3.05	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.53	0.43
25:BA:1319:U:H4'	25:BA:1321:A:OP2	2.18	0.43
5:CE:102:ALA:HB2	5:CE:120:THR:HG21	2.00	0.43
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.18	0.43
25:BA:171:A:H2'	25:BA:172:C:O4'	2.18	0.43
25:BA:31:C:C4	25:BA:32:C:C5	3.05	0.43
1:CA:579:G:C6	1:CA:580:U:C4	3.06	0.43
25:DA:2197:U:H1'	25:DA:2198:A:C8	2.53	0.43
30:DG:54:GLU:O	30:DG:57:ALA:HB3	2.17	0.43
25:DA:271(S):G:C2'	25:DA:271(T):C:H5'	2.47	0.43
25:DA:644:A:H4'	25:DA:645:C:N4	2.33	0.43
45:DZ:67:LEU:HA	45:DZ:68:PRO:HD3	1.64	0.43
25:BA:1874:C:H6	25:BA:1874:C:O5'	2.01	0.43
40:DU:16:LYS:HB3	40:DU:16:LYS:HE2	1.78	0.43
4:AD:110:PHE:CD1	4:AD:110:PHE:N	2.86	0.43
25:DA:1942:C:OP2	25:DA:1943:U:O2'	2.20	0.43
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.53	0.43
25:DA:777:A:H2'	25:DA:778:G:H8	1.83	0.43
25:BA:1617:A:H2'	25:BA:1618:A:C8	2.53	0.43
25:DA:1268:A:C2	25:DA:2013:A:C4	3.06	0.43
1:AA:432:A:OP2	1:AA:433:C:N4	2.43	0.43
1:CA:1133:G:C2'	1:CA:1134:G:H8	2.30	0.43
1:CA:1224:G:O2'	1:CA:1322:C:OP1	2.26	0.43
1:AA:428:G:O4'	1:AA:430:A:C8	2.72	0.43
36:BQ:12:GLN:HG2	36:BQ:73:PRO:HD2	2.00	0.43
28:DE:70:ALA:O	28:DE:72:VAL:N	2.42	0.43
1:CA:848:C:H2'	1:CA:849:C:O4'	2.18	0.43
2:AB:230:VAL:HG22	2:AB:231:GLU:H	1.83	0.43
25:DA:910:A:H2'	25:DA:2264:C:O2'	2.18	0.43
25:DA:657:U:H2'	25:DA:658:C:C6	2.52	0.43
35:DP:47:ASP:HA	35:DP:48:PRO:HD3	1.80	0.43
25:DA:307:G:H21	25:DA:330:A:H62	1.66	0.43
25:DA:2274:A:C5	25:DA:2276:G:C8	3.05	0.43
25:DA:880:G:N2	25:DA:898:C:H1'	2.33	0.43
36:DQ:66:ILE:HG12	36:DQ:104:PHE:HE2	1.82	0.43
3:CC:155:GLY:O	3:CC:157:ILE:HG13	2.19	0.43
25:BA:1899:A:H5'	25:BA:1900:G:OP2	2.18	0.43
19:CS:20:LEU:HA	19:CS:23:ASN:ND2	2.34	0.43
1:CA:1237:C:O2'	1:CA:1300:G:N1	2.43	0.43
1:CA:245:C:O2	1:CA:283:C:N3	2.51	0.43
3:CC:12:LEU:HA	3:CC:16:ARG:HB3	2.00	0.43
38:BS:35:ILE:HG12	38:BS:101:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DF:123:LEU:HD12	29:DF:124:LEU:N	2.32	0.43
18:CR:66:LEU:O	18:CR:70:ILE:HG13	2.18	0.43
25:BA:400:U:H1'	25:BA:450:A:N3	2.34	0.43
1:CA:960:U:O2	1:CA:960:U:H2'	2.17	0.43
25:BA:733:G:OP2	25:BA:733:G:H4'	2.18	0.43
43:BX:40:LYS:HE2	61:BX:3103:HOH:O	2.17	0.43
32:BI:10:GLU:O	32:BI:12:LEU:N	2.51	0.43
25:BA:1072:U:H4'	25:BA:1073:A:OP1	2.18	0.43
25:BA:1042:A:H4'	40:BU:91:ASP:OD2	2.17	0.43
17:AQ:50:LYS:HD2	17:AQ:51:TYR:CZ	2.53	0.43
2:CB:187:LEU:HD13	2:CB:205:ASP:HA	2.01	0.43
1:CA:1119:C:H2'	1:CA:1120:G:H8	1.82	0.43
1:AA:1034:G:H5''	1:AA:1035:A:OP2	2.18	0.43
1:CA:1134:G:H2'	1:CA:1135:U:H5'	2.00	0.43
39:DT:53:ARG:HD3	39:DT:60:THR:OG1	2.18	0.43
1:AA:180:U:O2'	1:AA:181:G:H5'	2.18	0.43
1:AA:414:A:C5	1:AA:431:A:C2	3.06	0.43
9:AI:53:VAL:C	9:AI:55:ALA:H	2.17	0.43
50:B4:62:ARG:C	50:B4:64:GLY:HA2	2.38	0.43
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.83	0.43
25:DA:2776:A:C6	25:DA:2782:G:H1'	2.54	0.43
29:DF:11:VAL:HG21	29:DF:20:LEU:HB2	1.99	0.43
1:AA:400:C:H5''	4:AD:73:ARG:NH2	2.32	0.43
2:CB:100:GLY:HA2	2:CB:103:THR:OG1	2.18	0.43
16:CP:74:LEU:HD23	16:CP:79:VAL:HG11	2.00	0.43
5:AE:52:PRO:HG2	5:AE:53:LEU:HD12	1.99	0.43
25:BA:2307:C:C2'	25:BA:2308:U:H5'	2.48	0.43
45:BZ:126:VAL:HG13	45:BZ:161:VAL:HG23	1.99	0.43
19:CS:28:LYS:CB	19:CS:29:ARG:HA	2.48	0.43
1:AA:375:U:C2	1:AA:376:G:C8	3.06	0.43
1:CA:791:G:C6	1:CA:792:A:N7	2.86	0.43
1:AA:584:G:H1	1:AA:757:U:H3	1.65	0.43
31:DH:54:ARG:HD3	31:DH:65:HIS:ND1	2.34	0.43
1:AA:1234:C:O2'	1:AA:1235:U:H5'	2.19	0.43
25:BA:2671:G:O2'	31:BH:175:LYS:NZ	2.50	0.43
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.18	0.43
37:BR:38:VAL:HB	37:BR:39:PRO:HD3	2.00	0.43
49:D3:7:LYS:HG3	49:D3:34:GLU:HG3	2.00	0.43
25:BA:1541:A:C6	25:BA:1542:A:C6	3.06	0.43
3:AC:24:ALA:HB1	3:AC:28:GLN:O	2.19	0.43
29:BF:81:PRO:HA	29:BF:87:GLY:O	2.17	0.43
25:BA:2858:G:C8	39:BT:97:ALA:HB2	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:22:LEU:HD13	7:AG:97:GLN:OE1	2.18	0.43
40:DU:61:TRP:CH2	40:DU:93:LYS:HB2	2.53	0.43
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.33	0.43
5:CE:148:VAL:HG21	8:CH:107:LEU:HD12	2.00	0.43
25:BA:843:C:H2'	25:BA:844:C:C6	2.54	0.43
55:D9:13:LYS:HD3	55:D9:28:GLU:OE2	2.17	0.43
25:DA:1907:G:C2	25:DA:1908:C:C2	3.07	0.43
25:DA:2494:G:C4	25:DA:2495:G:C8	3.06	0.43
32:DI:48:GLU:OE2	32:DI:52:ARG:HD3	2.18	0.43
4:AD:129:ASN:OD1	4:AD:145:GLU:N	2.45	0.43
9:CI:128:ARG:NH2	23:CX:33:U:OP2	2.50	0.43
32:DI:61:ARG:HA	32:DI:61:ARG:HD3	1.81	0.43
54:D8:50:LEU:HD23	54:D8:50:LEU:HA	1.75	0.43
27:BD:77:ALA:O	27:BD:116:GLN:HG3	2.18	0.43
25:BA:609:A:H5'	29:BF:89:VAL:HG21	1.99	0.43
10:CJ:89:ASP:O	10:CJ:91:PRO:HD3	2.18	0.43
32:DI:92:VAL:CG2	32:DI:120:ILE:HB	2.48	0.43
1:AA:1125:U:C3'	10:AJ:5:ARG:HH22	2.30	0.43
1:CA:1122:U:C4	1:CA:1123:A:N7	2.87	0.43
25:DA:999:U:H3'	25:DA:1154:G:O6	2.19	0.43
45:DZ:30:ASN:ND2	45:DZ:90:VAL:HB	2.33	0.43
1:AA:1502:A:H2	1:AA:1505:G:N1	2.04	0.43
1:AA:1162:C:H2'	1:AA:1163:C:C6	2.53	0.43
1:AA:170:U:O2'	1:AA:171:A:H5'	2.17	0.43
46:D0:24:LYS:O	46:D0:25:ARG:HD3	2.18	0.43
16:AP:68:ASP:O	16:AP:71:ARG:HG2	2.17	0.43
1:AA:630:G:O2'	1:AA:631:G:H5'	2.18	0.43
11:CK:99:GLN:C	11:CK:101:SER:H	2.21	0.43
29:DF:36:VAL:HG11	29:DF:183:VAL:CG1	2.48	0.43
4:AD:184:LYS:HB3	4:AD:184:LYS:HZ2	1.83	0.43
6:CF:25:ILE:CD1	6:CF:82:ARG:HH21	2.31	0.43
47:B1:3:LYS:HB2	47:B1:61:ARG:HH11	1.83	0.43
1:AA:442:C:H5'	1:AA:443:C:OP2	2.18	0.43
26:DB:46:A:C5	26:DB:47:C:C4	3.06	0.43
9:CI:46:ALA:HA	9:CI:78:LYS:HB2	2.01	0.43
45:BZ:150:LEU:HB3	45:BZ:171:ILE:CD1	2.48	0.43
27:DD:221:VAL:HG22	27:DD:226:MET:HE3	2.00	0.43
7:CG:94:ARG:O	7:CG:97:GLN:HB3	2.19	0.43
1:AA:298:A:C6	1:AA:299:G:C2	3.06	0.43
25:DA:729:G:C6	27:DD:208:LYS:HB2	2.53	0.43
53:D7:22:MET:HA	53:D7:28:ARG:HG2	2.00	0.43
1:CA:1105:A:C2	1:CA:1106:G:N7	2.86	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:118:LEU:HD11	2:AB:141:GLU:HG2	2.01	0.43
51:B5:40:LYS:HE2	51:B5:40:LYS:HB2	1.88	0.43
25:DA:644:A:H4'	25:DA:645:C:C4	2.53	0.43
25:BA:715:G:H5'	25:BA:716:G:OP2	2.18	0.43
8:CH:33:GLU:HG2	8:CH:48:TYR:CE2	2.53	0.43
25:BA:1721:G:H1'	25:BA:1723:A:N6	2.33	0.43
19:CS:12:ASP:OD2	19:CS:38:SER:OG	2.36	0.43
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.99	0.43
12:AL:77:LEU:HD21	12:AL:107:ALA:HA	1.99	0.43
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.19	0.43
48:B2:63:VAL:O	48:B2:66:GLU:HB2	2.18	0.43
6:AF:92:LYS:HB2	6:AF:92:LYS:HE2	1.83	0.43
33:BN:38:HIS:HD1	33:BN:38:HIS:H	1.66	0.43
25:DA:2249:U:O4	61:DA:3947:HOH:O	2.21	0.43
12:CL:75:HIS:ND1	12:CL:77:LEU:HB2	2.33	0.43
1:CA:1038:C:C2'	1:CA:1039:C:H5'	2.49	0.43
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.53	0.43
1:CA:401:C:H1'	1:CA:622:A:H1'	2.01	0.43
1:AA:147:G:C6	1:AA:148:G:C5	3.07	0.43
30:DG:25:TYR:HB3	30:DG:30:GLU:CB	2.47	0.43
1:AA:631:G:H2'	1:AA:632:A:H8	1.82	0.43
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.18	0.43
1:CA:688:G:H5'	11:CK:46:GLY:C	2.39	0.43
25:DA:1784:A:H4'	25:DA:1785:A:O5'	2.19	0.43
19:CS:31:ILE:HG22	19:CS:33:THR:HG22	2.00	0.43
26:DB:46:A:H2'	26:DB:47:C:H6	1.84	0.43
1:CA:545:C:H5'	4:CD:72:GLU:CB	2.49	0.43
25:DA:483:A:O4'	44:DY:48:ALA:HB1	2.18	0.43
25:BA:1183:G:H2'	25:BA:1184:G:O4'	2.18	0.43
1:CA:35:G:C5	1:CA:36:C:N4	2.86	0.43
8:AH:110:ALA:HB3	8:AH:121:ASP:HB3	2.00	0.43
25:BA:2768:C:C4	55:B9:19:ARG:NH1	2.86	0.43
25:DA:1970:A:OP2	61:DA:3905:HOH:O	2.20	0.43
25:DA:1859:A:N6	25:DA:1883:G:O2'	2.52	0.43
1:AA:353:A:H5'	1:AA:353:A:H8	1.84	0.43
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.99	0.43
26:BB:73:A:C4	26:BB:105:A:C2	3.06	0.43
25:BA:1324:A:OP1	37:BR:36:THR:HG22	2.18	0.43
26:BB:66:A:H61	26:BB:109:C:H5'	1.82	0.43
1:CA:683:G:C6	1:CA:684:A:C5	3.07	0.43
1:AA:416:G:C6	1:AA:417:C:C4	3.06	0.43
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
47:B1:82:LEU:HA	47:B1:85:LEU:HD12	2.01	0.43
53:B7:24:THR:HG22	53:B7:26:GLY:N	2.32	0.43
37:DR:92:GLY:HA2	37:DR:94:TYR:CZ	2.54	0.43
1:AA:1142:G:H3'	1:AA:1143:G:C8	2.53	0.43
26:DB:5:C:OP1	26:DB:61:G:O2'	2.34	0.43
1:CA:1151:A:C4	1:CA:1152:A:N7	2.87	0.43
25:DA:517:C:OP1	51:D5:16:ARG:NH2	2.51	0.43
1:AA:93:G:H2'	1:AA:96:U:O4'	2.19	0.43
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.32	0.43
7:AG:50:ILE:O	7:AG:50:ILE:HD12	2.19	0.43
31:DH:169:VAL:HG12	31:DH:171:LEU:HD22	2.00	0.43
1:CA:1312:G:O6	19:CS:2:PRO:HD2	2.18	0.43
50:B4:59:PHE:HA	50:B4:61:ARG:HG2	2.00	0.43
25:DA:1955:U:O4	25:DA:2554:U:H5	2.01	0.43
50:D4:62:ARG:HD3	50:D4:62:ARG:H	1.83	0.43
1:AA:246:A:N1	1:AA:278:G:O2'	2.39	0.43
1:AA:1030:C:H3'	1:AA:1030(A):G:H4'	2.01	0.43
23:AX:66:C:H2'	23:AX:67:C:O4'	2.17	0.43
23:AX:6:G:N2	23:AX:68:C:C2	2.86	0.43
1:AA:598:U:H2'	1:AA:599:C:H6	1.84	0.43
30:DG:179:PRO:HG3	50:D4:43:TYR:OH	2.18	0.43
1:CA:1093:A:N3	1:CA:1109:C:O2'	2.47	0.43
13:CM:88:ARG:HG3	13:CM:98:VAL:HG12	2.00	0.43
1:CA:1071:C:H2'	1:CA:1072:G:H8	1.84	0.43
7:AG:27:ILE:CD1	7:AG:40:ALA:HA	2.47	0.43
28:DE:147:PRO:HB2	28:DE:149:ARG:HG2	2.01	0.43
34:BO:2:ILE:HG23	34:BO:6:THR:HG21	2.01	0.43
25:BA:2661:U:H2'	25:BA:2662:U:H6	1.84	0.43
55:D9:17:ILE:HG21	55:D9:26:ILE:HD11	2.01	0.43
25:DA:2330:G:H2'	25:DA:2331:G:O4'	2.18	0.43
10:CJ:11:PHE:CD1	10:CJ:67:THR:HG22	2.54	0.43
47:D1:95:LEU:O	47:D1:98:LEU:HB2	2.18	0.43
3:AC:123:GLN:HG2	3:AC:128:PHE:HD2	1.84	0.43
13:CM:15:VAL:O	13:CM:19:LEU:HD22	2.19	0.43
3:CC:12:LEU:HD23	3:CC:12:LEU:HA	1.86	0.43
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.19	0.43
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.53	0.43
25:DA:2636:U:H1'	25:DA:2783:G:N2	2.34	0.43
26:BB:24:G:N7	26:BB:56:G:H2'	2.34	0.43
23:CX:61:C:H2'	23:CX:62:C:H6	1.82	0.43
1:AA:6:G:O2'	1:AA:7:G:H5'	2.18	0.43
25:BA:2306:C:OP2	38:BS:89:ARG:NH2	2.46	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:724:G:C2	1:CA:725:G:C8	3.06	0.43
1:CA:500:G:C6	1:CA:546:G:C2	3.07	0.43
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.54	0.43
25:DA:271(X):G:C2	25:DA:271(Y):U:O4	2.71	0.43
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.52	0.43
49:B3:18:ASP:N	49:B3:18:ASP:OD1	2.51	0.43
32:BI:87:LYS:HE3	32:BI:87:LYS:HB2	1.85	0.43
49:B3:4:LEU:O	49:B3:36:VAL:HA	2.18	0.43
4:CD:52:SER:O	4:CD:56:VAL:HG23	2.19	0.43
25:BA:403:C:H42	25:BA:425:G:H1	1.65	0.43
10:CJ:16:LEU:HD13	10:CJ:70:ARG:CG	2.47	0.43
25:DA:2027:G:H2'	25:DA:2028:U:O4'	2.19	0.43
1:AA:436:C:H5''	4:AD:156:GLU:OE2	2.19	0.43
35:DP:96:THR:N	35:DP:99:LEU:HD21	2.24	0.43
1:CA:1125:U:H2'	1:CA:1127:G:N7	2.34	0.43
1:CA:445:G:H2'	1:CA:446:G:H8	1.83	0.43
1:CA:1015:A:C6	1:CA:1016:A:C6	3.07	0.43
27:BD:206:LEU:HD23	27:BD:206:LEU:HA	1.78	0.43
25:DA:702:G:C2	25:DA:731:C:C2	3.06	0.43
42:DW:14:PRO:HG2	42:DW:78:GLU:CG	2.46	0.43
25:DA:31:C:H5'	25:DA:1239:G:OP1	2.19	0.43
1:CA:1323:G:H4'	1:CA:1363:C:N3	2.32	0.43
1:CA:1052:U:H5''	1:CA:1053:G:OP2	2.17	0.43
25:DA:154:G:C6	25:DA:173:G:C6	3.07	0.43
25:DA:952:G:C6	25:DA:953:A:N7	2.87	0.43
26:DB:28:C:H2'	26:DB:29:A:O4'	2.19	0.43
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	2.00	0.43
25:DA:863:A:H2'	25:DA:864:G:C8	2.53	0.43
25:DA:863:A:OP1	36:DQ:22:LYS:HG3	2.18	0.43
1:AA:625:G:O2'	1:AA:626:U:H5'	2.17	0.43
12:CL:34:ARG:HB3	12:CL:34:ARG:HE	1.37	0.43
21:AU:22:ARG:HA	21:AU:23:PRO:HD3	1.65	0.43
25:DA:242:G:H5''	54:D8:64:TYR:CE2	2.54	0.43
31:DH:3:ARG:NH1	31:DH:3:ARG:HB3	2.34	0.43
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.54	0.43
10:AJ:81:THR:O	10:AJ:85:LEU:HG	2.18	0.43
1:AA:1343:G:O2'	9:AI:121:ARG:HD2	2.19	0.43
3:CC:112:SER:O	3:CC:115:LEU:HB2	2.19	0.43
25:BA:1095:C:H2'	25:BA:1096:A:H8	1.84	0.43
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.58	0.43
25:DA:108:U:H2'	25:DA:109:G:H8	1.84	0.43
6:AF:82:ARG:HB3	6:AF:85:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.49	0.43
25:BA:2843:G:H4'	25:BA:2844:G:OP2	2.19	0.43
25:DA:1475:G:C2	25:DA:1517:G:C2	3.06	0.43
25:BA:1558:G:H2'	25:BA:1559:C:C6	2.54	0.43
25:DA:844:C:C5	25:DA:845:G:C6	3.06	0.43
25:DA:2645:G:H4'	25:DA:2732:G:O3'	2.19	0.43
25:BA:199:C:H2'	25:BA:200:A:C8	2.54	0.43
1:AA:389:A:C6	1:AA:390:C:H1'	2.53	0.43
25:DA:2464:C:C2	25:DA:2487:G:C2	3.07	0.43
17:CQ:56:VAL:O	17:CQ:77:VAL:HB	2.19	0.43
2:AB:124:SER:HB3	2:AB:125:PRO:HA	2.01	0.43
1:CA:937:A:H1'	1:CA:1379:G:N2	2.34	0.43
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.50	0.43
25:BA:1034:A:H8	25:BA:1034:A:O5'	2.02	0.43
25:DA:763:G:H1'	25:DA:765:G:O4'	2.18	0.43
26:BB:96:U:H2'	26:BB:97:G:C8	2.54	0.43
25:BA:316:C:C2	25:BA:373:G:C2	3.07	0.43
25:DA:1462:C:H4'	25:DA:2703:C:H5'	2.00	0.43
4:CD:67:ILE:HG22	4:CD:68:TYR:CD1	2.54	0.43
45:DZ:121:HIS:HB3	45:DZ:123:ASP:O	2.18	0.43
1:CA:1005:A:N6	1:CA:1024:G:O2'	2.51	0.43
25:DA:1005:C:C2	25:DA:1143:A:C5	3.06	0.43
1:CA:1178:G:H2'	1:CA:1180:A:OP2	2.18	0.43
25:DA:2318:G:H21	38:DS:3:ARG:CD	2.31	0.43
1:AA:975:A:H4'	1:AA:976:G:C5'	2.44	0.43
1:CA:961:U:OP2	1:CA:1223:C:O2'	2.31	0.43
7:CG:111:ARG:HB2	7:CG:119:ARG:HD2	2.00	0.43
1:AA:637:G:C6	1:AA:638:G:C5	3.06	0.43
7:CG:65:ALA:HB3	7:CG:124:LEU:HD23	2.01	0.43
50:D4:59:PHE:HA	50:D4:60:GLN:C	2.39	0.43
1:CA:473:G:O2'	1:CA:474:G:H5'	2.19	0.43
9:AI:19:LEU:HB3	9:AI:59:PHE:CD2	2.52	0.43
3:AC:12:LEU:HD11	14:AN:51:GLY:CA	2.48	0.43
26:DB:11:C:H3'	26:DB:12:C:C6	2.54	0.43
25:BA:866:A:C4	25:BA:1234:A:C2	3.06	0.43
25:DA:898:C:H6	25:DA:898:C:H3'	1.84	0.43
19:CS:23:ASN:OD1	19:CS:47:HIS:NE2	2.51	0.43
1:CA:452:A:C2	1:CA:453:A:C4	3.06	0.43
1:AA:1187:G:H2'	1:AA:1188:A:H8	1.84	0.43
25:DA:537:C:H2'	25:DA:538:G:O4'	2.19	0.43
45:DZ:161:VAL:O	45:DZ:161:VAL:HG13	2.19	0.43
32:BI:93:THR:O	32:BI:97:ILE:HG13	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2094:G:P	32:DI:22:LYS:HD2	2.59	0.43
25:DA:706:A:H2'	25:DA:707:G:O4'	2.19	0.43
25:DA:2409:G:H2'	25:DA:2410:G:O4'	2.18	0.43
25:BA:1854:G:N2	61:BA:3835:HOH:O	2.41	0.43
1:CA:1385:G:C6	1:CA:1386:G:C5	3.07	0.43
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.17	0.43
28:DE:1:MET:O	28:DE:84:PHE:HB2	2.19	0.43
25:BA:2418:U:H2'	25:BA:2418:U:OP2	2.19	0.43
25:DA:2494:G:C5	25:DA:2495:G:N7	2.87	0.43
1:AA:113:G:H2'	1:AA:114:U:C6	2.54	0.43
2:AB:180:LEU:O	2:AB:181:PHE:HB2	2.18	0.43
8:CH:37:ARG:NH2	8:CH:38:ILE:HG12	2.34	0.43
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.19	0.43
36:BQ:58:PHE:HB3	36:BQ:61:GLY:O	2.18	0.43
25:DA:616:G:C2	25:DA:618:C:C2	3.06	0.43
25:DA:1759:A:H4'	25:DA:2715:C:O4'	2.19	0.43
25:DA:2563:U:O2	25:DA:2565:A:H8	2.01	0.43
1:AA:312:C:H2'	1:AA:313:A:H8	1.83	0.43
25:DA:2679:A:C2	25:DA:2729:G:C2	3.07	0.43
33:BN:48:MET:H	33:BN:48:MET:HG3	1.70	0.43
25:DA:1578:U:H2'	25:DA:1578:U:O2	2.18	0.43
40:BU:104:GLN:CD	40:BU:104:GLN:H	2.22	0.43
1:CA:1157:A:N6	1:CA:1180:A:N3	2.67	0.43
1:AA:433:C:H6	1:AA:433:C:O5'	2.02	0.43
1:AA:601:C:O2	1:AA:637:G:N2	2.27	0.43
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.54	0.43
25:DA:1665:A:C4'	34:DO:67:LYS:HB2	2.48	0.43
5:CE:12:LEU:HD22	5:CE:13:ILE:N	2.33	0.43
30:DG:23:PHE:HB2	30:DG:25:TYR:CZ	2.53	0.43
1:AA:161:A:H2'	1:AA:162:A:H8	1.82	0.43
1:AA:357:G:O2'	1:AA:358:U:H5'	2.19	0.43
25:BA:1766:G:H3'	25:BA:1767:A:C5'	2.47	0.43
28:DE:163:GLU:HG2	28:DE:164:ARG:H	1.83	0.43
8:AH:40:ALA:HA	8:AH:45:ILE:HG13	2.00	0.43
25:DA:536:A:H2'	25:DA:537:C:C6	2.54	0.43
36:BQ:37:LEU:HD21	36:BQ:130:LYS:HE2	2.00	0.43
1:AA:625:G:C2'	1:AA:626:U:H5'	2.48	0.43
25:DA:1711:C:H2'	25:DA:1712:C:C6	2.53	0.43
1:AA:309:G:H1'	1:AA:608:A:C2	2.54	0.43
37:DR:96:ARG:HD3	37:DR:98:LEU:HD11	2.00	0.43
12:AL:85:ILE:HD12	12:AL:98:TYR:HB3	2.00	0.43
25:DA:881:G:H1	25:DA:895:U:H3	1.67	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2648:C:H2'	25:DA:2649:U:C6	2.54	0.43
25:DA:322:A:P	29:DF:169:ASN:HB2	2.59	0.43
1:AA:298:A:H5''	1:AA:299:G:OP2	2.18	0.43
36:DQ:42:ILE:HD13	36:DQ:97:VAL:CG2	2.49	0.43
1:AA:958:A:C2	19:AS:55:LYS:HB2	2.54	0.43
45:BZ:44:PHE:CZ	45:BZ:86:VAL:HG11	2.53	0.43
3:CC:16:ARG:HA	3:CC:16:ARG:HD2	1.80	0.43
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	2.01	0.43
39:DT:88:ILE:HG13	39:DT:91:ARG:NH2	2.34	0.43
4:AD:23:GLY:HA3	4:AD:112:VAL:HB	2.01	0.43
25:BA:1073:A:C2	25:BA:2500:A:H5'	2.53	0.43
1:AA:114:U:H1'	1:AA:353:A:H1'	2.00	0.43
29:BF:11:VAL:HG22	29:BF:125:LEU:HB2	2.00	0.43
25:DA:1332:G:OP1	61:DA:4077:HOH:O	2.21	0.43
25:DA:2000:G:N7	61:DA:4008:HOH:O	2.36	0.43
25:BA:1176:U:O2	25:BA:2047:C:H5''	2.19	0.43
42:BW:20:VAL:O	42:BW:23:LEU:HB2	2.19	0.43
30:BG:150:ASP:OD2	30:BG:151:ALA:N	2.52	0.43
39:BT:81:PRO:HG2	39:BT:82:LEU:HD12	2.01	0.43
1:AA:327:A:C4	1:AA:329:A:C8	3.07	0.43
45:BZ:19:ARG:HB2	45:BZ:19:ARG:HE	1.65	0.43
28:BE:73:GLU:HG3	28:BE:73:GLU:H	1.54	0.43
3:AC:34:LEU:O	3:AC:34:LEU:HD12	2.19	0.43
29:BF:149:ASP:OD1	29:BF:149:ASP:N	2.45	0.43
44:BY:91:GLU:CD	44:BY:91:GLU:N	2.72	0.43
25:BA:302:A:H8	25:BA:302:A:P	2.42	0.43
1:CA:402:G:C2'	1:CA:403:C:H5'	2.49	0.43
31:DH:95:ARG:HB2	31:DH:128:PRO:HB2	2.01	0.43
1:AA:1443:G:C2	1:AA:1460:A:N3	2.87	0.43
1:AA:901:A:C5	1:AA:902:G:H1'	2.54	0.43
25:DA:196:A:H2'	25:DA:196:A:N3	2.34	0.43
30:DG:16:ARG:HA	30:DG:16:ARG:HD2	1.69	0.43
50:B4:59:PHE:HA	50:B4:61:ARG:H	1.83	0.43
5:CE:11:ILE:HB	5:CE:31:LEU:HB3	2.00	0.43
25:DA:854:G:H2'	25:DA:855:G:C8	2.48	0.43
25:DA:2302:G:C6	25:DA:2315:G:C6	3.06	0.43
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.27	0.43
11:CK:48:ILE:C	11:CK:50:TYR:H	2.21	0.43
25:DA:1169:G:O5'	25:DA:1169:G:H8	2.01	0.43
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.18	0.43
7:CG:101:LEU:O	7:CG:104:LEU:HB2	2.18	0.43
25:DA:538:G:H2'	25:DA:539:G:H8	1.83	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:601:C:O2'	25:DA:605:C:H5''	2.19	0.43
1:AA:309:G:O2'	1:AA:607:A:N1	2.48	0.43
13:AM:40:ASN:OD1	13:AM:42:ALA:HB3	2.19	0.43
25:BA:2830:A:O2'	25:BA:2831:A:OP1	2.37	0.43
1:CA:80:G:N2	1:CA:90:U:H1'	2.34	0.43
25:DA:2310:A:H61	30:DG:79:ASN:ND2	2.17	0.43
25:DA:55:G:H2'	25:DA:56:A:C8	2.54	0.43
5:CE:92:LYS:HA	5:CE:93:PRO:HD2	1.84	0.43
25:DA:1638:C:H5''	25:DA:2710:C:O2'	2.19	0.43
34:DO:34:THR:O	34:DO:37:ASP:HB2	2.19	0.43
45:BZ:5:LEU:O	45:BZ:59:LEU:HA	2.19	0.43
25:BA:2490:A:H2'	25:BA:2491:G:O4'	2.19	0.43
13:CM:97:PRO:HB3	13:CM:101:GLN:OE1	2.19	0.43
32:BI:65:ALA:HB1	32:BI:136:VAL:HG11	1.99	0.43
27:DD:139:GLY:H	27:DD:165:ILE:HB	1.84	0.43
15:CO:82:ILE:HB	15:CO:87:ILE:HB	2.01	0.43
31:BH:89:ILE:O	31:BH:129:THR:HG22	2.19	0.43
1:CA:1375:A:O2'	7:CG:29:LYS:NZ	2.50	0.43
25:BA:1752:G:C6	25:BA:1753:U:C4	3.07	0.43
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.54	0.43
1:AA:687:A:N3	1:AA:688:G:H1'	2.33	0.43
25:BA:64:C:H2'	25:BA:65:C:H6	1.83	0.43
26:BB:1:U:H2'	26:BB:2:C:C6	2.53	0.43
25:DA:2675:A:H4'	34:DO:29:ASN:ND2	2.34	0.43
30:DG:76:SER:CB	30:DG:84:LYS:H	2.32	0.43
4:CD:19:LEU:O	4:CD:21:LEU:N	2.51	0.43
16:AP:22:THR:HA	16:AP:33:ILE:HG12	2.00	0.43
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.19	0.43
25:DA:927:G:H2'	25:DA:928:G:C8	2.53	0.43
25:BA:2070:G:C5	25:BA:2071:G:C8	3.07	0.43
48:D2:35:LEU:HA	48:D2:35:LEU:HD23	1.80	0.43
54:D8:22:VAL:CG2	54:D8:59:LYS:HG3	2.48	0.43
4:AD:45:GLN:HB3	4:AD:45:GLN:HE21	1.59	0.43
1:CA:261:U:C5	20:CT:79:ARG:CZ	3.02	0.43
12:CL:55:VAL:HG12	12:CL:69:TYR:HA	2.01	0.43
36:BQ:39:PRO:HA	36:BQ:97:VAL:O	2.19	0.43
1:AA:1362:C:H2'	1:AA:1363:C:H5''	2.00	0.43
25:DA:2257:U:H2'	25:DA:2258:C:C6	2.54	0.43
1:AA:1129:C:H1'	1:AA:1130:A:N7	2.34	0.42
9:AI:64:THR:CG2	9:AI:66:ARG:HD2	2.49	0.42
30:DG:109:VAL:O	30:DG:113:ARG:HB2	2.19	0.42
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.33	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DG:33:ARG:O	30:DG:161:THR:HG23	2.18	0.42
1:CA:939:G:H2'	1:CA:940:C:C6	2.54	0.42
25:BA:2331:G:C8	25:BA:2332:A:C2	3.07	0.42
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.19	0.42
1:CA:1445:C:C2	1:CA:1458:G:C2	3.07	0.42
1:AA:453:A:C5	1:AA:454:C:C4	3.07	0.42
1:CA:491:G:C2	1:CA:492:G:C4	3.07	0.42
25:DA:879:G:C8	25:DA:880:G:C8	3.07	0.42
3:AC:44:GLU:HG2	3:AC:52:LEU:CD2	2.49	0.42
33:DN:96:GLU:N	33:DN:96:GLU:OE2	2.46	0.42
7:CG:69:VAL:HG22	7:CG:135:VAL:HG22	2.01	0.42
26:DB:28:C:OP1	38:DS:36:TYR:OH	2.34	0.42
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.82	0.42
1:CA:1317:C:OP1	14:CN:17:LYS:HG2	2.19	0.42
25:BA:1712:A:C4'	34:BO:67:LYS:HB2	2.49	0.42
1:CA:414:A:C5	1:CA:431:A:C2	3.07	0.42
29:DF:31:HIS:HB2	35:DP:9:ASN:OD1	2.19	0.42
25:BA:1702:A:H3'	25:BA:1703:C:C6	2.53	0.42
8:AH:73:ASP:OD2	8:AH:75:ARG:NH1	2.52	0.42
30:BG:96:ARG:O	30:BG:99:MET:HB3	2.19	0.42
26:BB:4:C:H2'	26:BB:5:C:O4'	2.19	0.42
25:DA:272(B):G:H2'	25:DA:272(C):G:C8	2.54	0.42
29:DF:138:GLU:O	29:DF:141:ALA:HB3	2.19	0.42
25:BA:771:U:H2'	25:BA:772:G:O4'	2.18	0.42
25:DA:2076:U:O5'	25:DA:2076:U:H6	2.02	0.42
1:AA:1445:C:C4	1:AA:1446:U:C4	3.07	0.42
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	2.00	0.42
2:AB:54:THR:HG23	2:AB:199:TYR:HB3	2.00	0.42
4:AD:13:ARG:HB2	4:AD:40:PRO:HD3	2.00	0.42
25:DA:1412:A:C2	25:DA:1591:G:C2	3.07	0.42
25:BA:2442:A:N3	25:BA:2442:A:H2'	2.33	0.42
51:B5:16:ARG:O	51:B5:20:ARG:HG3	2.19	0.42
4:AD:15:GLU:OE2	4:AD:66:ARG:NH1	2.52	0.42
1:AA:410:G:N1	1:AA:431:A:OP2	2.48	0.42
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	2.00	0.42
5:CE:10:MET:HG2	5:CE:13:ILE:HD11	2.00	0.42
1:CA:382:A:H2'	1:CA:383:A:H8	1.78	0.42
25:DA:754:C:H4'	25:DA:1272:A:N6	2.34	0.42
23:CX:22:G:H2'	23:CX:23:C:C6	2.54	0.42
28:DE:14:ILE:HB	39:DT:14:TYR:CE2	2.54	0.42
25:DA:945:A:C4	25:DA:2448:A:C2	3.07	0.42
25:BA:311:C:H2'	25:BA:312:C:C6	2.51	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1338:G:N7	43:DX:62:LYS:NZ	2.64	0.42
54:B8:39:LYS:HA	54:B8:42:ARG:NH1	2.34	0.42
10:AJ:16:LEU:HD21	10:AJ:70:ARG:CG	2.49	0.42
30:DG:121:ASN:HB3	30:DG:124:SER:HB2	2.00	0.42
25:DA:2408:U:H2'	25:DA:2409:G:H8	1.84	0.42
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.54	0.42
34:DO:7:TYR:CZ	34:DO:44:LYS:HG3	2.54	0.42
2:CB:23:ARG:HB2	2:CB:23:ARG:HH11	1.82	0.42
25:DA:77:C:H5''	48:D2:10:LEU:HD21	2.01	0.42
26:BB:37:C:C5	26:BB:38:C:C4	3.06	0.42
25:DA:1514:U:H2'	25:DA:1515:G:C8	2.55	0.42
25:DA:1515:G:H2'	25:DA:1516:C:C6	2.55	0.42
38:BS:6:ALA:O	38:BS:10:ARG:HB2	2.18	0.42
4:AD:110:PHE:HD1	4:AD:110:PHE:N	2.16	0.42
45:BZ:15:PRO:O	45:BZ:19:ARG:HB2	2.19	0.42
1:AA:1446:U:O2'	1:AA:1447:A:O5'	2.38	0.42
1:CA:339:C:H2'	1:CA:340:U:C6	2.54	0.42
42:DW:46:PHE:O	42:DW:50:VAL:HG23	2.19	0.42
29:DF:37:VAL:HA	29:DF:40:GLN:HB2	2.00	0.42
25:BA:21:A:H2'	25:BA:22:C:O4'	2.19	0.42
20:AT:30:LYS:HA	20:AT:33:ILE:HD12	2.00	0.42
34:BO:115:VAL:HG13	34:BO:121:VAL:HG21	2.00	0.42
1:AA:1100:C:O2'	1:AA:1102:A:OP1	2.34	0.42
25:DA:2193:G:H2'	25:DA:2194:G:C8	2.54	0.42
17:CQ:5:VAL:O	17:CQ:6:LEU:HD13	2.19	0.42
25:DA:532:A:N7	25:DA:2021:C:O2'	2.42	0.42
12:AL:6:THR:HG23	12:AL:9:GLN:OE1	2.19	0.42
1:AA:317:G:C6	1:AA:318:G:C5	3.07	0.42
45:DZ:7:ALA:O	45:DZ:62:PRO:HD3	2.19	0.42
13:CM:23:TYR:CD2	13:CM:70:LEU:HD13	2.54	0.42
1:CA:1205:U:O2'	3:CC:195:VAL:HG23	2.19	0.42
25:BA:873:U:H2'	25:BA:875:U:O4'	2.19	0.42
25:DA:768:G:C6	25:DA:769:G:C5	3.07	0.42
1:AA:39:G:C6	1:AA:40:C:C4	3.07	0.42
2:CB:187:LEU:HD23	2:CB:201:ILE:HG22	2.00	0.42
1:CA:1122:U:C5	1:CA:1123:A:N7	2.88	0.42
1:AA:1006:C:H2'	1:AA:1007:C:O4'	2.19	0.42
36:BQ:14:ARG:HG2	36:BQ:41:TRP:HH2	1.83	0.42
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.54	0.42
4:AD:119:GLN:HG2	4:AD:123:HIS:NE2	2.35	0.42
25:BA:2695:C:OP1	39:BT:53:ARG:NH2	2.52	0.42
1:CA:9:G:O6	1:CA:558:G:H2'	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:AL:24:VAL:CG1	12:AL:27:LEU:HD22	2.44	0.42
29:DF:184:TYR:O	29:DF:188:ARG:HG3	2.20	0.42
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.19	0.42
50:D4:64:GLY:C	50:D4:66:SER:N	2.71	0.42
25:DA:652(D):C:C2'	25:DA:652(E):G:H5'	2.49	0.42
9:AI:3:GLN:CG	9:AI:20:ARG:HE	2.32	0.42
1:CA:448:A:P	1:CA:485:G:H22	2.42	0.42
47:D1:52:ARG:NH2	47:D1:57:GLU:HB2	2.34	0.42
1:CA:833:U:H2'	1:CA:834:C:C6	2.54	0.42
25:DA:289:A:H2'	25:DA:290:G:C8	2.54	0.42
45:BZ:111:VAL:HG12	45:BZ:112:ARG:N	2.34	0.42
25:DA:660:G:H5'	29:DF:99:TYR:CD2	2.55	0.42
25:BA:1766:G:H8	25:BA:1770:A:H62	1.66	0.42
25:BA:287:G:O2'	25:BA:448:U:OP2	2.26	0.42
25:DA:934:G:H2'	25:DA:935:C:C6	2.55	0.42
25:DA:180:G:H5''	25:DA:181:A:P	2.59	0.42
25:DA:1167:U:O2	25:DA:1183:G:N2	2.52	0.42
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	2.02	0.42
33:BN:42:TRP:CE3	40:BU:63:VAL:HG11	2.54	0.42
1:CA:19:C:H5''	5:CE:86:ALA:HB3	2.02	0.42
1:AA:310:G:H5''	16:AP:31:LYS:HB2	2.02	0.42
25:DA:837:C:N3	25:DA:941:A:N6	2.67	0.42
43:BX:12:VAL:HG22	43:BX:29:TRP:CE2	2.54	0.42
50:B4:8:LYS:HB3	50:B4:8:LYS:HE2	1.70	0.42
25:DA:2275:C:H5'	25:DA:2275:C:H6	1.84	0.42
38:DS:69:VAL:O	38:DS:72:ALA:HB3	2.18	0.42
3:AC:64:VAL:HG13	3:AC:99:VAL:HA	2.01	0.42
25:DA:760:G:H2'	25:DA:761:A:O4'	2.19	0.42
7:AG:51:GLN:O	7:AG:55:GLY:HA2	2.19	0.42
1:AA:1114:C:H42	1:AA:1186:G:H1	1.67	0.42
1:AA:1091:U:H2'	1:AA:1093:A:OP2	2.19	0.42
1:CA:1005:A:H1'	1:CA:1036:G:C6	2.55	0.42
1:CA:1023:G:C4	1:CA:1024:G:C8	3.07	0.42
1:CA:1120:G:C6	1:CA:1154:G:N2	2.87	0.42
1:CA:540:G:H2'	1:CA:541:G:O4'	2.19	0.42
25:BA:895:G:O6	25:BA:974:G:H2'	2.20	0.42
25:DA:2298:A:C8	25:DA:2299:G:C8	3.07	0.42
1:AA:922:G:H2'	1:AA:923:A:C8	2.54	0.42
1:CA:1210:C:H2'	1:CA:1211:U:H5''	2.01	0.42
1:AA:1316:G:N2	1:AA:1318:A:H3'	2.34	0.42
1:CA:473:G:H2'	1:CA:474:G:H8	1.81	0.42
1:AA:1086:U:C2'	1:AA:1087:G:H5'	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:383:A:H5''	1:CA:384:G:OP2	2.20	0.42
9:CI:33:PHE:CE1	9:CI:43:ALA:HB1	2.46	0.42
8:AH:104:ARG:HG3	8:AH:138:TRP:CD2	2.54	0.42
25:DA:2419:U:H2'	25:DA:2420:C:C6	2.54	0.42
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.19	0.42
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.84	0.42
25:DA:2477:C:N4	55:D9:10:ILE:HG23	2.34	0.42
31:BH:17:VAL:HG21	31:BH:50:VAL:HG21	2.01	0.42
30:BG:86:MET:HA	30:BG:87:PRO:HD3	1.90	0.42
25:BA:776:G:OP2	27:BD:13:ARG:NH1	2.45	0.42
1:CA:97:G:O2'	1:CA:98:G:O4'	2.35	0.42
9:CI:99:LEU:HB3	9:CI:101:PHE:CE1	2.54	0.42
34:DO:2:ILE:HB	34:DO:33:ALA:HB3	2.01	0.42
1:AA:998:G:H2'	1:AA:999:C:C6	2.55	0.42
1:CA:590:C:H2'	1:CA:591:U:H6	1.84	0.42
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	2.00	0.42
25:DA:1418:G:O5'	25:DA:1418:G:H8	2.03	0.42
1:CA:35:G:H2'	1:CA:36:C:C6	2.55	0.42
4:CD:90:GLY:HA2	4:CD:204:ILE:HD11	2.01	0.42
25:BA:2760:G:C2	25:BA:2769:U:C5	3.07	0.42
16:AP:6:LEU:HB3	16:AP:17:TYR:CD2	2.54	0.42
25:DA:1517:G:C6	25:DA:1518:U:C4	3.07	0.42
25:DA:836:G:H2'	25:DA:837:C:C6	2.53	0.42
29:DF:110:LEU:HD21	29:DF:181:LEU:HG	2.00	0.42
31:DH:88:LEU:HD23	31:DH:165:ALA:HA	2.01	0.42
39:BT:7:ILE:O	39:BT:11:GLU:HG3	2.19	0.42
27:DD:134:ARG:NH1	27:DD:188:GLU:OE2	2.51	0.42
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.20	0.42
51:D5:48:GLU:O	51:D5:60:VAL:HG11	2.20	0.42
25:DA:871:U:H5''	36:DQ:69:PHE:CE2	2.54	0.42
1:AA:1524:C:OP1	11:AK:120:ARG:NH1	2.50	0.42
38:DS:24:LEU:HD23	38:DS:24:LEU:HA	1.88	0.42
16:AP:34:GLU:OE2	16:AP:55:ARG:NH2	2.39	0.42
1:AA:1405:G:O4'	1:AA:1519:A:H4'	2.20	0.42
38:DS:78:LEU:HD11	38:DS:108:GLY:O	2.18	0.42
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.80	0.42
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.54	0.42
1:AA:1129:C:N4	1:AA:1143:G:N1	2.40	0.42
1:CA:1179:A:C6	1:CA:1180:A:C8	3.07	0.42
25:DA:319:C:N4	25:DA:320:A:C6	2.87	0.42
1:CA:622:A:H3'	1:CA:623:C:H6	1.84	0.42
16:CP:5:ARG:HH12	16:CP:28:ARG:HA	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2298:A:N6	25:DA:2321:G:H1	2.18	0.42
1:AA:1486:G:H2'	1:AA:1487:G:C1'	2.50	0.42
25:DA:2005:A:H5''	25:DA:2006:C:OP2	2.20	0.42
1:CA:973:G:H3'	1:CA:974:A:H5''	2.01	0.42
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.18	0.42
25:DA:829:A:N7	25:DA:2248:C:H5'	2.35	0.42
25:DA:900:A:C2'	25:DA:901:A:H8	2.32	0.42
50:B4:53:GLU:O	50:B4:56:VAL:HG13	2.20	0.42
25:DA:1636:C:H2'	25:DA:1637:A:H8	1.80	0.42
1:CA:460:G:C6	1:CA:470:C:H5''	2.53	0.42
19:AS:19:VAL:O	19:AS:22:LEU:HB2	2.19	0.42
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.20	0.42
25:BA:2245:U:H2'	25:BA:2246:G:C8	2.54	0.42
1:CA:391:G:C6	1:CA:392:G:C5	3.07	0.42
25:DA:1815:A:P	27:DD:54:ARG:NH2	2.92	0.42
34:BO:10:VAL:HG21	34:BO:16:ALA:HB3	2.01	0.42
5:CE:40:ARG:HH21	5:CE:68:GLU:HA	1.82	0.42
25:DA:608:A:C6	25:DA:609:A:C6	3.07	0.42
25:DA:2740:A:C6	25:DA:2764:A:C8	3.07	0.42
25:BA:904:C:N4	25:BA:905:U:O4	2.52	0.42
35:DP:6:LEU:HA	35:DP:6:LEU:HD23	1.76	0.42
26:BB:16:G:C6	26:BB:69:G:C2	3.08	0.42
25:DA:1790:C:H5''	25:DA:1791:A:OP1	2.19	0.42
45:DZ:95:PRO:HA	45:DZ:129:SER:HA	2.00	0.42
25:DA:442:G:O4'	29:DF:46:ARG:HG3	2.19	0.42
1:AA:575:G:O2'	1:AA:821:G:H5'	2.19	0.42
38:DS:103:GLU:O	38:DS:107:GLU:HG3	2.20	0.42
1:CA:373:A:H2'	1:CA:374:A:H8	1.84	0.42
25:DA:576:U:H2'	25:DA:577:G:C8	2.55	0.42
37:BR:83:ILE:O	37:BR:86:ARG:HG2	2.20	0.42
35:DP:83:VAL:O	35:DP:115:LEU:N	2.44	0.42
45:DZ:122:ARG:HH11	45:DZ:122:ARG:HG2	1.84	0.42
28:BE:49:LEU:HA	28:BE:49:LEU:HD12	1.89	0.42
47:B1:98:LEU:HA	47:B1:98:LEU:HD23	1.88	0.42
4:CD:110:PHE:N	4:CD:110:PHE:CD1	2.87	0.42
45:DZ:150:LEU:HD12	45:DZ:150:LEU:HA	1.58	0.42
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.91	0.42
25:DA:2055:C:H5'	25:DA:2056:G:O5'	2.19	0.42
1:AA:448:A:H2'	1:AA:449:C:C6	2.54	0.42
1:CA:1002:G:N3	1:CA:1003:G:N7	2.67	0.42
1:CA:999:C:C2	1:CA:1042:G:N2	2.87	0.42
25:DA:14:A:C6	25:DA:526:A:C2	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:158:ILE:HB	4:AD:162:LEU:HD12	2.01	0.42
25:DA:994:C:O2'	25:DA:996:A:OP1	2.30	0.42
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.54	0.42
25:DA:1510:G:O5'	25:DA:1510:G:H8	2.03	0.42
1:CA:837:G:H2'	1:CA:838:G:C8	2.55	0.42
1:CA:735:C:H5'	18:CR:71:LYS:HD3	2.00	0.42
1:AA:1346:A:H5''	9:AI:120:ARG:NH1	2.34	0.42
1:AA:1041:A:C2'	1:AA:1042:G:H5'	2.49	0.42
1:CA:1145:C:H4'	1:CA:1146:A:C5'	2.48	0.42
15:AO:5:LYS:CD	15:AO:5:LYS:H	2.31	0.42
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	2.01	0.42
25:DA:172:C:H2'	25:DA:173:G:C8	2.52	0.42
1:AA:271:C:H2'	1:AA:272:C:C6	2.54	0.42
29:DF:32:LEU:HD11	29:DF:105:VAL:HG13	2.00	0.42
26:DB:24:G:H4'	26:DB:25:A:N7	2.35	0.42
25:BA:354:A:H2	25:BA:1255:A:O2'	2.02	0.42
14:AN:45:ARG:HG2	14:AN:49:HIS:CD2	2.53	0.42
23:AX:19:G:C5	23:AX:57:A:C2	3.07	0.42
1:CA:1057:G:C4	1:CA:1204:A:C2	3.07	0.42
1:CA:881:G:H2'	1:CA:882:C:O4'	2.19	0.42
25:DA:2046:G:H2'	25:DA:2047:U:C6	2.53	0.42
4:CD:81:GLU:O	4:CD:85:LYS:HB2	2.20	0.42
25:DA:1844:C:OP1	27:DD:257:LEU:HD23	2.19	0.42
29:DF:51:THR:HG23	29:DF:92:PRO:HG2	2.01	0.42
13:AM:20:THR:C	13:AM:22:ILE:H	2.21	0.42
25:BA:196:A:H2'	25:BA:197:C:O4'	2.18	0.42
30:BG:125:PHE:HB3	30:BG:166:ASP:OD1	2.20	0.42
26:DB:15:A:O4'	26:DB:110:G:C8	2.73	0.42
30:BG:145:THR:OG1	30:BG:148:MET:SD	2.73	0.42
25:DA:2399:G:C6	25:DA:2400:G:C5	3.07	0.42
25:BA:1308:A:OP1	42:BW:99:ARG:NH1	2.49	0.42
25:BA:2703:C:O3'	25:BA:2881:C:H4'	2.20	0.42
25:DA:1479:G:C6	25:DA:1480:G:C5	3.08	0.42
48:B2:3:LEU:HA	48:B2:3:LEU:HD23	1.76	0.42
27:BD:33:LEU:HA	27:BD:33:LEU:HD23	1.81	0.42
1:CA:1002:G:N2	1:CA:1038:C:C2	2.82	0.42
1:CA:1002:G:H5''	1:CA:1003:G:OP2	2.19	0.42
1:CA:1002:G:C2	1:CA:1038:C:N3	2.83	0.42
1:AA:341:C:O2'	1:AA:342:C:H5'	2.20	0.42
39:BT:16:ARG:HD2	39:BT:18:ASP:OD1	2.20	0.42
2:CB:69:LEU:HD12	2:CB:70:PHE:H	1.84	0.42
25:DA:2319:G:H22	38:DS:3:ARG:HE	1.68	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1001:A:N6	1:AA:1001(A):G:O6	2.53	0.42
1:CA:149:A:H2'	1:CA:150:C:H6	1.83	0.42
49:B3:3:ARG:HD3	49:B3:60:GLU:OE2	2.20	0.42
1:CA:811:C:H4'	1:CA:900:A:N6	2.34	0.42
1:CA:1158:C:H2'	1:CA:1160:G:H5'	2.02	0.42
4:AD:121:VAL:HA	4:AD:126:ILE:HG13	2.01	0.42
1:AA:840:C:H4'	1:AA:841:U:OP1	2.20	0.42
9:AI:4:TYR:CZ	9:AI:88:TYR:HD1	2.38	0.42
43:BX:92:LEU:C	43:BX:94:GLY:N	2.71	0.42
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.35	0.42
1:CA:1239:A:H62	1:CA:1299:A:N6	2.16	0.42
1:AA:1047:G:O3'	14:AN:4:LYS:HB2	2.20	0.42
25:DA:2510:C:C4	25:DA:2511:U:C4	3.08	0.42
1:AA:68:G:H22	1:AA:101:A:H2	1.67	0.42
30:DG:170:ARG:HD3	30:DG:170:ARG:O	2.19	0.42
26:DB:45:A:H2'	26:DB:46:A:H8	1.84	0.42
25:DA:864:G:OP2	36:DQ:22:LYS:HE2	2.20	0.42
1:AA:1236:A:H2'	1:AA:1237:C:C6	2.55	0.42
1:AA:1438:G:H2'	1:AA:1439:C:C6	2.54	0.42
1:CA:865:A:H2	1:CA:918:A:H4'	1.83	0.42
25:DA:2348:U:OP2	54:D8:42:ARG:NH2	2.52	0.42
3:AC:23:TYR:CG	3:AC:24:ALA:N	2.87	0.42
2:AB:102:LEU:HB3	2:AB:180:LEU:CD1	2.50	0.42
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.42
25:DA:1425:G:H2'	25:DA:1426:G:O4'	2.19	0.42
25:DA:1654:A:O2'	28:DE:113:PHE:O	2.30	0.42
1:CA:189:G:C5	1:CA:189(A):C:C4	3.07	0.42
31:DH:42:ARG:NH1	31:DH:53:GLU:OE2	2.52	0.42
25:DA:2009:G:O2'	25:DA:2010:G:H5'	2.20	0.42
2:CB:28:PHE:CD1	2:CB:31:TYR:HB2	2.55	0.42
27:DD:145:VAL:HG12	27:DD:146:GLU:O	2.18	0.42
25:BA:2887:G:O2'	25:BA:2888:U:H5'	2.18	0.42
25:DA:824:A:H2'	25:DA:825:C:O4'	2.19	0.42
25:BA:416:G:N1	35:BP:70:GLN:HG3	2.34	0.42
31:DH:118:PRO:HD2	31:DH:121:ILE:HB	2.00	0.42
38:DS:68:GLN:HE21	38:DS:68:GLN:HA	1.85	0.42
2:AB:156:LYS:HB3	2:AB:156:LYS:HE2	1.81	0.42
25:DA:2307:G:H8	25:DA:2307:G:OP1	2.03	0.42
2:CB:78:GLN:O	2:CB:94:ASN:ND2	2.52	0.42
25:DA:530:G:O4'	25:DA:530:G:N3	2.53	0.42
1:CA:938:A:N6	1:CA:939:G:C6	2.88	0.42
25:DA:1375:C:H2'	25:DA:1376:C:H6	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:32:LEU:HD22	3:AC:59:ARG:NH1	2.34	0.42
20:CT:39:LYS:HB2	20:CT:39:LYS:HE3	1.90	0.42
50:D4:60:GLN:HA	50:D4:62:ARG:HG2	2.02	0.42
31:BH:167:GLU:HA	31:BH:168:PRO:HD3	1.86	0.42
1:CA:947:G:H2'	1:CA:948:C:O4'	2.20	0.42
25:BA:950:C:H2'	25:BA:951:U:H6	1.83	0.42
25:BA:589:U:OP1	35:BP:29:LYS:HD2	2.19	0.42
25:DA:13:A:N1	25:DA:525:U:H2'	2.34	0.42
19:CS:50:ALA:HA	19:CS:58:VAL:O	2.20	0.42
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.20	0.42
6:AF:63:TYR:CD1	6:AF:63:TYR:N	2.88	0.42
25:DA:1364:G:OP2	47:D1:3:LYS:HG3	2.20	0.42
26:BB:6:C:C2	26:BB:116:G:N2	2.88	0.42
25:DA:2590:A:O2'	25:DA:2591:C:H5'	2.20	0.42
16:CP:21:VAL:CG1	16:CP:34:GLU:HB3	2.50	0.42
25:BA:83:A:C5'	44:BY:8:LYS:HG2	2.49	0.42
30:DG:45:GLU:C	30:DG:47:LYS:H	2.23	0.42
25:DA:1015:G:O2'	25:DA:1016:G:H5'	2.20	0.42
1:CA:991:U:C4	1:CA:1212:U:H1'	2.54	0.42
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.19	0.42
9:CI:95:LYS:HA	9:CI:99:LEU:HD13	2.00	0.42
1:CA:15:G:H2'	1:CA:16:A:C8	2.53	0.42
1:CA:741:G:H2'	1:CA:742:G:O4'	2.20	0.42
29:DF:154:VAL:HG22	29:DF:191:ARG:CB	2.49	0.42
25:BA:2326:C:H2'	25:BA:2327:G:C8	2.55	0.42
1:CA:1292:U:O2'	1:CA:1293:G:H5'	2.20	0.42
27:DD:13:ARG:HD2	27:DD:13:ARG:HA	1.43	0.42
2:AB:141:GLU:O	2:AB:145:LEU:HB2	2.20	0.42
1:CA:683:G:H2'	1:CA:684:A:C8	2.55	0.42
25:DA:9:U:O4	25:DA:2629:A:H2	2.02	0.42
28:BE:3:GLY:HA3	28:BE:81:ILE:HD12	2.01	0.42
1:CA:1522:U:H2'	1:CA:1523:G:H8	1.84	0.42
25:BA:1273:G:OP1	40:BU:13:LYS:HG2	2.19	0.42
1:CA:176:C:H2'	1:CA:177:C:C6	2.54	0.42
8:CH:5:PRO:O	8:CH:8:ASP:HB3	2.19	0.42
2:CB:20:GLU:HG3	2:CB:191:ASP:HB3	2.02	0.42
48:B2:18:PRO:HA	48:B2:21:LEU:HB2	2.02	0.42
25:BA:753:A:H2'	25:BA:754:G:O4'	2.20	0.42
2:AB:119:GLU:OE2	2:AB:153:ARG:NH2	2.53	0.42
25:DA:571:A:N6	25:DA:2499:C:O3'	2.53	0.42
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	2.02	0.42
54:D8:26:LYS:HG2	54:D8:48:PHE:CD1	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1057:G:OP2	61:AA:4014:HOH:O	2.22	0.42
35:BP:135:LEU:HD23	35:BP:135:LEU:HA	1.86	0.42
38:BS:58:LEU:HD23	38:BS:58:LEU:HA	1.83	0.42
1:AA:1503:A:OP1	1:AA:1503:A:H8	2.03	0.42
27:DD:127:VAL:HA	27:DD:193:VAL:HG22	2.01	0.42
25:DA:959:A:C6	25:DA:960:A:C6	3.08	0.42
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.19	0.42
25:DA:2298:A:N7	25:DA:2299:G:C4	2.88	0.42
25:BA:1629:C:C2	25:BA:1630:A:C8	3.08	0.42
1:CA:951:G:C6	1:CA:952:U:C4	3.08	0.42
1:CA:677:U:H1'	11:CK:119:CYS:SG	2.60	0.42
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.42
40:DU:79:PHE:O	40:DU:83:LEU:HD22	2.20	0.42
1:AA:657:G:C2	1:AA:750:G:C5	3.08	0.42
1:CA:472:A:H2'	1:CA:473:G:O4'	2.20	0.42
6:AF:96:PRO:HB3	18:AR:30:ASP:CG	2.39	0.42
25:DA:144:C:H2'	25:DA:145:G:C8	2.50	0.42
30:DG:128:ARG:HE	30:DG:128:ARG:HB2	1.55	0.42
1:AA:1256:A:C2	1:AA:1277:C:N4	2.88	0.42
1:AA:1277:C:H1'	1:AA:1282:C:C2	2.55	0.42
25:BA:1898:A:H2'	25:BA:1899:A:C8	2.54	0.42
1:AA:357:G:C2	1:AA:358:U:C5	3.08	0.42
25:BA:2860:A:C2	25:BA:2861:A:C4	3.08	0.42
19:CS:27:GLU:HG2	19:CS:47:HIS:HE2	1.83	0.42
1:AA:352:C:O2'	1:AA:354:G:OP1	2.28	0.42
25:DA:537:C:H1'	33:DN:45:ASN:HD21	1.85	0.42
23:AX:19:G:C4	23:AX:57:A:C2	3.07	0.42
25:BA:1522:G:N2	25:BA:1565:G:C4	2.87	0.42
1:CA:576:G:N2	1:CA:760:G:OP2	2.53	0.42
34:BO:7:TYR:CZ	34:BO:44:LYS:HG3	2.55	0.42
25:BA:2623:U:H2'	51:B5:2:ALA:O	2.20	0.42
1:CA:160:A:H2'	1:CA:161:A:C8	2.55	0.42
1:AA:589:C:O2'	1:AA:590:C:H5'	2.20	0.42
1:AA:977:A:H2'	1:AA:978:A:H5''	2.01	0.42
1:AA:1060:C:H41	3:AC:2:GLY:HA3	1.85	0.42
6:CF:80:ARG:NH1	6:CF:88:VAL:O	2.53	0.42
32:BI:6:LEU:HG	32:BI:36:ALA:HA	2.01	0.42
1:AA:66:G:O3'	1:AA:199:G:H4'	2.20	0.42
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.49	0.42
25:DA:2821:A:C2	25:DA:2822:G:C4	3.08	0.42
25:BA:1370:G:C4	25:BA:1374:G:O6	2.72	0.42
45:BZ:67:LEU:HA	45:BZ:68:PRO:HD3	1.72	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:244:A:C2	25:DA:255:A:C4	3.08	0.42
25:BA:1387:U:OP1	25:BA:1443:U:N3	2.47	0.42
25:DA:459:U:H4'	53:D7:40:TRP:CZ3	2.55	0.42
25:DA:1912:A:C8	25:DA:1918:A:C2	3.08	0.42
25:BA:439:A:O5'	25:BA:439:A:H8	2.03	0.42
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.55	0.42
17:AQ:27:PHE:CZ	17:AQ:36:ILE:HD11	2.55	0.42
25:DA:595:C:H2'	25:DA:596:G:O4'	2.19	0.42
4:CD:135:LEU:O	4:CD:137:SER:N	2.53	0.42
1:CA:952:U:O2'	1:CA:965:A:N6	2.52	0.42
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.53	0.42
25:BA:831:A:C8	25:BA:839:G:C5	3.08	0.42
1:AA:1162:C:H2'	1:AA:1163:C:H6	1.85	0.42
1:AA:192:U:C2	1:AA:193:C:C5	3.08	0.42
3:AC:22:TRP:CD1	3:AC:59:ARG:HD2	2.54	0.42
1:CA:1188:A:H2'	1:CA:1189:C:O4'	2.19	0.42
1:CA:1270:C:H2'	1:CA:1271:G:H5'	2.02	0.42
1:AA:22:G:H2'	1:AA:23:C:C6	2.55	0.42
16:AP:71:ARG:O	16:AP:75:ARG:N	2.30	0.42
25:BA:1224:C:O2'	25:BA:1225:C:H5'	2.20	0.42
1:AA:673:G:N2	1:AA:674:G:C2	2.88	0.42
1:AA:55:A:C5	1:AA:56:U:C5	3.08	0.42
1:CA:59:A:H5''	1:CA:60:A:C5'	2.49	0.42
1:CA:1298:C:H4'	1:CA:1299:A:C4	2.54	0.42
25:DA:776:G:C8	25:DA:793:A:N3	2.88	0.42
1:AA:1277:C:H2'	1:AA:1279:A:C8	2.53	0.42
31:DH:130:ARG:HH11	31:DH:132:ARG:NH2	2.18	0.42
19:CS:29:ARG:O	19:CS:31:ILE:HG13	2.19	0.42
25:BA:374:U:H2'	25:BA:375:G:O4'	2.20	0.42
36:DQ:133:ARG:HG2	36:DQ:134:ARG:N	2.34	0.42
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.20	0.42
24:CW:9:MVA:HN3	24:CW:10:2QY:CE2	2.49	0.42
41:DV:58:VAL:O	41:DV:97:LYS:N	2.38	0.42
9:CI:96:LEU:HA	9:CI:96:LEU:HD23	1.92	0.42
1:AA:684:A:H2'	1:AA:685:G:H8	1.84	0.42
1:CA:1228:C:H4'	13:CM:116:THR:HA	2.01	0.42
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	2.02	0.42
27:DD:228:PRO:HD3	27:DD:235:GLY:HA3	2.02	0.42
25:DA:1575:C:H2'	25:DA:1576:U:C6	2.55	0.42
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.88	0.42
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	2.02	0.42
3:AC:175:LEU:HD21	3:AC:201:TYR:HE2	1.85	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:DI:14:ASP:OD1	32:DI:15:VAL:N	2.53	0.42
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	2.01	0.42
25:BA:2673:G:H2'	25:BA:2674:A:C8	2.55	0.42
25:BA:2677:A:C2	25:BA:2678:C:C2	3.08	0.42
25:BA:738:C:O2'	25:BA:739:C:H5'	2.20	0.42
51:D5:49:CYS:SG	51:D5:51:TYR:HB2	2.59	0.42
37:BR:117:VAL:HG12	37:BR:118:GLU:N	2.34	0.42
25:DA:1275:A:N1	25:DA:1295:C:O2'	2.39	0.42
49:B3:26:LEU:O	49:B3:35:ARG:NE	2.51	0.42
39:BT:101:PHE:HD2	39:BT:105:LEU:HD11	1.84	0.42
25:BA:2517:G:O6	25:BA:2588:G:H2'	2.19	0.42
40:BU:112:ARG:H	40:BU:112:ARG:HG2	1.53	0.42
25:DA:1024:G:O5'	25:DA:1024:G:H8	2.02	0.42
34:DO:69:ILE:HD13	34:DO:69:ILE:H	1.85	0.42
28:BE:178:GLU:OE2	28:BE:178:GLU:N	2.47	0.42
25:BA:2450:U:O2'	25:BA:2452:C:OP1	2.30	0.42
1:CA:226:G:C2	1:CA:227:G:C8	3.08	0.42
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.19	0.42
1:AA:1308:U:H5''	13:AM:98:VAL:CG2	2.49	0.42
25:DA:597:U:H2'	25:DA:598:G:C8	2.55	0.42
1:AA:890:G:O2'	1:AA:906:G:O6	2.31	0.42
25:BA:2797:C:O2'	28:BE:42:ASP:OD1	2.22	0.42
25:DA:190:A:OP2	47:D1:39:LYS:HE3	2.19	0.42
25:BA:801:C:H2'	25:BA:802:C:C6	2.55	0.42
25:DA:1138:G:O2'	33:DN:105:GLY:HA3	2.20	0.41
1:CA:922:G:H2'	1:CA:923:A:H8	1.85	0.41
34:BO:120:GLU:OE1	39:BT:67:SER:OG	2.27	0.41
10:CJ:49:VAL:HG23	14:CN:41:ARG:HD2	2.00	0.41
43:BX:31:HIS:HD2	43:BX:33:LYS:HB2	1.84	0.41
2:AB:219:VAL:HA	2:AB:222:ILE:CD1	2.49	0.41
25:DA:848:G:C4	25:DA:933:A:H8	2.38	0.41
25:DA:30:G:H2'	25:DA:31:C:H6	1.84	0.41
4:CD:88:VAL:O	4:CD:92:VAL:HG23	2.20	0.41
1:AA:503:C:O2'	1:AA:504:C:H5'	2.20	0.41
1:CA:447:G:H2'	1:CA:485:G:N2	2.35	0.41
25:DA:884:C:H5'	25:DA:885:C:OP2	2.20	0.41
1:AA:622:A:H3'	1:AA:623:C:C6	2.55	0.41
45:BZ:111:VAL:C	45:BZ:113:ALA:N	2.71	0.41
25:BA:310:C:H2'	25:BA:311:C:H6	1.85	0.41
25:BA:312:C:H2'	25:BA:313:A:C8	2.53	0.41
25:DA:275:G:H2'	25:DA:276:A:H8	1.83	0.41
1:AA:767:A:H2'	1:AA:768:A:O4'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:721:C:H2'	25:DA:722:A:C8	2.55	0.41
31:BH:37:VAL:HG13	31:BH:68:THR:CG2	2.50	0.41
25:DA:1833:U:O2'	25:DA:1969:A:N1	2.37	0.41
13:CM:80:ARG:O	13:CM:84:ILE:HG23	2.20	0.41
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.55	0.41
1:CA:1245:A:H61	1:CA:1292:U:H3	1.68	0.41
25:DA:489:G:H2'	25:DA:491:G:O4'	2.20	0.41
1:CA:1105:A:C2	1:CA:1106:G:C8	3.08	0.41
11:CK:43:SER:HA	11:CK:47:VAL:HG21	2.02	0.41
10:CJ:23:ILE:HD13	10:CJ:23:ILE:HA	1.74	0.41
35:DP:85:LEU:HG	35:DP:115:LEU:O	2.20	0.41
4:CD:110:PHE:N	4:CD:110:PHE:HD1	2.18	0.41
43:DX:46:ALA:O	48:D2:30:ARG:NH2	2.50	0.41
25:DA:2376:A:N3	38:DS:106:ARG:NH2	2.60	0.41
15:CO:76:GLU:HA	15:CO:76:GLU:OE1	2.20	0.41
25:DA:623:G:C2	25:DA:624:C:C2	3.08	0.41
36:DQ:43:THR:OG1	36:DQ:45:GLN:HG2	2.20	0.41
25:DA:2758:A:C2	25:DA:2759:G:H1'	2.55	0.41
25:DA:1366:A:H2'	25:DA:1367:A:O4'	2.20	0.41
25:BA:202:A:H2'	25:BA:203:G:O4'	2.19	0.41
25:BA:2798:C:H2'	25:BA:2799:U:C6	2.55	0.41
21:CU:9:ARG:O	21:CU:13:ILE:HG13	2.20	0.41
1:CA:61:G:C5	1:CA:107:G:C2	3.08	0.41
12:AL:124:LYS:HA	12:AL:125:PRO:HD3	1.77	0.41
44:BY:1:MET:HE2	44:BY:1:MET:HB2	1.89	0.41
35:BP:6:LEU:HA	35:BP:6:LEU:HD23	1.71	0.41
4:AD:81:GLU:OE2	4:AD:139:ARG:NH2	2.53	0.41
32:DI:127:VAL:O	32:DI:128:LEU:HD23	2.19	0.41
25:BA:518:G:H2'	25:BA:519:G:O4'	2.20	0.41
25:DA:1339:G:H5''	43:DX:16:LYS:HD3	2.01	0.41
1:CA:538:G:OP2	12:CL:115:LYS:HB2	2.18	0.41
25:DA:1954:G:N2	25:DA:1956:U:C2	2.89	0.41
25:DA:1032:A:O3'	55:D9:16:VAL:HG11	2.19	0.41
25:DA:590:A:H2'	25:DA:591:C:C6	2.54	0.41
42:DW:31:GLU:O	42:DW:34:ASN:HB2	2.20	0.41
1:AA:342:C:N3	1:AA:348:G:C6	2.87	0.41
49:B3:31:LEU:HD23	49:B3:31:LEU:HA	1.88	0.41
25:DA:1782:C:O4'	25:DA:2609:U:C2	2.73	0.41
1:AA:1004:A:C8	1:AA:1037:C:C2	3.09	0.41
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.19	0.41
15:CO:15:PHE:CZ	15:CO:84:LYS:HG2	2.55	0.41
1:CA:557:G:N1	1:CA:558:G:C2	2.88	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:44:G:H2'	1:CA:45:U:O4'	2.20	0.41
4:CD:8:VAL:HA	4:CD:11:LEU:HD13	2.02	0.41
25:DA:2070:G:C2	25:DA:2442:C:C2	3.08	0.41
25:DA:843:G:C2	25:DA:936:C:C2	3.08	0.41
30:DG:178:PHE:HA	30:DG:179:PRO:HD2	1.87	0.41
45:BZ:121:HIS:HB3	45:BZ:123:ASP:O	2.20	0.41
1:CA:833:U:H2'	1:CA:834:C:H6	1.85	0.41
25:BA:1889:G:H21	25:BA:1905:G:H2'	1.84	0.41
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.55	0.41
26:DB:33:G:C6	26:DB:34:U:C4	3.08	0.41
30:DG:117:PHE:CE1	30:DG:119:GLY:HA2	2.55	0.41
38:BS:61:ASN:O	38:BS:65:VAL:HG23	2.19	0.41
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.48	0.41
1:CA:137:C:H2'	1:CA:138:G:H5'	2.00	0.41
1:CA:991:U:H3'	1:CA:1212:U:N3	2.35	0.41
23:CX:19:G:C4	23:CX:57:A:C2	3.08	0.41
8:AH:34:GLU:CD	8:AH:37:ARG:HH22	2.23	0.41
1:AA:545:C:H5'	4:AD:72:GLU:CB	2.51	0.41
27:DD:68:LYS:O	27:DD:69:ARG:HB2	2.20	0.41
31:DH:123:PHE:CD1	31:DH:133:VAL:HG22	2.56	0.41
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.20	0.41
25:DA:1026:U:H4'	25:DA:1027:A:OP1	2.20	0.41
25:BA:2285:A:O2'	25:BA:2286:A:H5'	2.20	0.41
1:CA:407:G:O2'	4:CD:116:GLN:HG3	2.20	0.41
25:DA:442:G:H21	29:DF:48:THR:HB	1.86	0.41
1:AA:20:U:H1'	1:AA:916:G:N2	2.34	0.41
53:D7:12:ARG:NH2	53:D7:44:PRO:HB3	2.35	0.41
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.20	0.41
3:CC:11:ARG:HB3	3:CC:15:THR:HB	2.00	0.41
27:DD:232:PRO:HG2	27:DD:248:SER:O	2.20	0.41
43:DX:72:LYS:HG2	43:DX:73:ARG:O	2.20	0.41
6:CF:89:MET:HG2	6:CF:91:VAL:HG23	2.02	0.41
1:AA:1325:C:O2'	1:AA:1326:C:H5'	2.19	0.41
36:DQ:141:GLN:NE2	45:DZ:74:VAL:O	2.42	0.41
25:DA:2416:C:H2'	25:DA:2417:C:H6	1.85	0.41
25:DA:2058:A:N7	61:DA:3842:HOH:O	2.37	0.41
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.24	0.41
4:AD:138:TYR:HE1	4:AD:140:VAL:HA	1.85	0.41
25:BA:233:A:C2	25:BA:244:A:C4	3.08	0.41
25:DA:826:U:H5''	25:DA:2428:G:O3'	2.20	0.41
41:DV:40:LEU:HD11	41:DV:55:ALA:HB2	2.01	0.41
25:DA:1399:C:O2'	25:DA:1400:G:H5'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:AJ:38:ILE:HA	10:AJ:39:PRO:HD3	1.85	0.41
39:BT:16:ARG:NH1	39:BT:18:ASP:OD2	2.53	0.41
1:CA:1151:A:C2	1:CA:1152:A:C5	3.08	0.41
1:CA:1155:G:N7	1:CA:1156:G:C5	2.88	0.41
25:DA:2892:A:H2'	25:DA:2893:G:H5'	2.02	0.41
25:BA:895:G:N9	25:BA:978:A:H8	2.18	0.41
25:DA:2319:G:H4'	25:DA:2320:A:OP1	2.19	0.41
1:CA:663:A:C2'	1:CA:664:G:H5'	2.49	0.41
1:AA:1001(A):G:C5	1:AA:1002:G:C8	3.08	0.41
1:CA:445:G:C6	1:CA:490:G:C6	3.09	0.41
1:AA:1162:C:C2	1:AA:1175:G:C2	3.09	0.41
25:DA:674:G:C1'	29:DF:74:ARG:HD3	2.50	0.41
50:B4:56:VAL:HB	50:B4:57:GLU:H	1.65	0.41
25:BA:324:A:H2'	25:BA:358:C:H1'	2.02	0.41
3:AC:19:GLU:HB3	3:AC:40:ARG:HH21	1.85	0.41
13:CM:29:ARG:NH1	13:CM:64:TRP:HB3	2.35	0.41
1:CA:1309:G:H2'	1:CA:1310:G:O4'	2.20	0.41
19:AS:31:ILE:O	19:AS:49:ILE:HG23	2.20	0.41
25:DA:254:G:N7	54:D8:5:LYS:HE2	2.35	0.41
25:DA:340:A:H2'	25:DA:341:G:O4'	2.19	0.41
47:D1:23:LYS:HB2	47:D1:23:LYS:HE3	1.70	0.41
25:BA:1775:C:H6	25:BA:1775:C:H5''	1.85	0.41
1:AA:258:G:N3	1:AA:259:G:C8	2.89	0.41
25:BA:694:G:N1	25:BA:696:C:O2	2.53	0.41
45:DZ:5:LEU:HD22	45:DZ:6:LYS:N	2.35	0.41
25:DA:2517:C:C6	25:DA:2542:A:N7	2.88	0.41
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.20	0.41
25:DA:1639:U:C2'	25:DA:1640:C:H5''	2.51	0.41
23:AX:8:U:O2	23:AX:21:A:H2	2.03	0.41
41:DV:25:LEU:H	41:DV:92:THR:HG1	1.65	0.41
25:DA:2030:A:H4'	25:DA:2031:A:C8	2.55	0.41
25:DA:79:G:C4	25:DA:80:G:C8	3.08	0.41
25:DA:729:G:O5'	27:DD:208:LYS:NZ	2.54	0.41
39:BT:88:ILE:HG21	39:BT:91:ARG:NE	2.35	0.41
25:BA:442:A:H2'	25:BA:443:C:H6	1.85	0.41
1:AA:1085:U:OP2	61:AA:4121:HOH:O	2.22	0.41
25:BA:1722:C:H2'	25:BA:1723:A:O4'	2.20	0.41
16:AP:55:ARG:HA	16:AP:55:ARG:HD2	1.89	0.41
1:AA:575:G:HO2'	1:AA:821:G:H5'	1.85	0.41
4:AD:71:SER:OG	4:AD:74:GLN:HB2	2.21	0.41
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	2.03	0.41
18:CR:35:ARG:O	18:CR:37:VAL:N	2.51	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:BI:102:SER:HA	32:BI:106:GLY:HA3	2.01	0.41
37:DR:21:TYR:OH	37:DR:43:GLU:HG2	2.21	0.41
25:BA:2038:U:H1'	51:B5:6:VAL:HG13	2.02	0.41
1:AA:1039:C:N4	1:AA:1040:U:O4	2.53	0.41
17:CQ:53:LEU:HD23	17:CQ:82:MET:HE1	2.01	0.41
36:DQ:106:VAL:HG21	36:DQ:114:ALA:HB1	2.02	0.41
36:DQ:72:LYS:HB3	36:DQ:94:VAL:HG23	2.01	0.41
37:DR:65:LEU:HA	37:DR:65:LEU:HD12	1.65	0.41
48:D2:21:LEU:HA	48:D2:21:LEU:HD23	1.86	0.41
35:DP:16:ARG:HH11	35:DP:16:ARG:HD2	1.73	0.41
55:B9:17:ILE:HD12	55:B9:17:ILE:HA	1.81	0.41
48:B2:10:LEU:HD23	48:B2:10:LEU:HA	1.90	0.41
31:DH:71:LEU:HA	31:DH:71:LEU:HD12	1.78	0.41
25:BA:2455:C:OP1	29:BF:68:LYS:HD3	2.20	0.41
1:CA:964:A:N3	1:CA:969:A:O2'	2.34	0.41
1:CA:1001:A:N6	1:CA:1001(A):G:O6	2.53	0.41
2:CB:213:LEU:HD22	2:CB:214:ILE:HD13	2.02	0.41
1:CA:1120:G:H8	1:CA:1120:G:O5'	2.02	0.41
30:DG:17:PRO:HA	30:DG:20:ILE:HD12	2.01	0.41
4:CD:100:ARG:HG2	4:CD:137:SER:HA	2.01	0.41
25:DA:2023:G:H4'	25:DA:2617:C:O3'	2.20	0.41
25:DA:996:A:H4'	40:DU:91:ASP:OD2	2.20	0.41
4:AD:190:ASP:H	4:AD:193:ASP:HB2	1.86	0.41
1:CA:558:G:H5''	1:CA:559:A:OP2	2.20	0.41
26:DB:90:A:C5	26:DB:91:C:H1'	2.56	0.41
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	2.02	0.41
25:DA:1313:U:H2'	25:DA:1610:A:C2	2.55	0.41
19:AS:22:LEU:HD13	19:AS:47:HIS:HD2	1.85	0.41
25:DA:1364:G:C8	47:D1:3:LYS:HD2	2.55	0.41
26:DB:33:G:N3	26:DB:50:G:C2	2.88	0.41
2:CB:192:SER:O	2:CB:194:PRO:HD3	2.20	0.41
25:BA:469:A:H5''	25:BA:470:C:OP1	2.19	0.41
1:AA:258:G:H2'	1:AA:259:G:C8	2.55	0.41
35:DP:38:GLN:O	35:DP:39:LYS:CB	2.69	0.41
25:BA:223:C:H2'	25:BA:224:U:C6	2.56	0.41
1:CA:727:G:N2	1:CA:730:G:OP2	2.51	0.41
25:BA:2303:U:OP1	25:BA:2392:C:O2'	2.25	0.41
5:CE:81:GLU:OE1	5:CE:88:LYS:HE2	2.20	0.41
1:CA:1077:G:N1	1:CA:1081:G:C6	2.89	0.41
1:CA:865:A:H5'	1:CA:1078:U:O4	2.20	0.41
50:B4:68:ARG:HB3	50:B4:69:LYS:H	1.43	0.41
8:AH:28:ALA:HB3	8:AH:57:PRO:HB2	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1349:A:OP2	9:AI:118:LYS:HE3	2.20	0.41
54:D8:56:GLU:HA	54:D8:59:LYS:HE3	2.02	0.41
18:CR:26:LEU:HA	18:CR:26:LEU:HD13	1.93	0.41
39:BT:101:PHE:CD2	39:BT:105:LEU:HD11	2.56	0.41
28:DE:166:THR:HG21	28:DE:199:ARG:HH22	1.85	0.41
30:BG:6:ALA:HB3	30:BG:104:GLU:OE2	2.20	0.41
29:BF:129:PHE:CD2	29:BF:163:VAL:HG21	2.56	0.41
1:CA:1266:G:N2	1:CA:1268:A:H3'	2.35	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.21	0.41
42:DW:79:GLY:CA	42:DW:100:THR:HG22	2.51	0.41
25:BA:1506:G:H5''	25:BA:1507:A:OP2	2.20	0.41
35:BP:27:HIS:O	35:BP:31:ALA:HA	2.19	0.41
25:DA:45:C:H2'	25:DA:47:C:C6	2.56	0.41
1:CA:971:G:OP1	1:CA:971:G:H3'	2.19	0.41
1:CA:438:G:O2'	1:CA:494:U:O4	2.32	0.41
34:BO:4:PRO:O	34:BO:5:GLN:HB2	2.20	0.41
1:CA:328:C:H4'	1:CA:329:A:H5'	2.02	0.41
2:CB:7:VAL:HB	2:CB:8:LYS:H	1.72	0.41
1:CA:1179:A:C6	1:CA:1180:A:N7	2.89	0.41
1:CA:1127:G:H2'	1:CA:1128:C:C6	2.55	0.41
43:DX:26:TYR:HB3	43:DX:92:LEU:CD2	2.51	0.41
20:CT:26:ASN:OD1	20:CT:71:THR:HG23	2.21	0.41
25:BA:1155:C:C5	25:BA:1156:G:C6	3.09	0.41
1:CA:1227:A:C3'	1:CA:1227:A:C8	3.03	0.41
1:CA:1264:C:C2	1:CA:1272:G:N2	2.88	0.41
1:AA:404:U:H2'	1:AA:405:U:H6	1.86	0.41
25:BA:1047:A:H2'	25:BA:1048:G:O4'	2.20	0.41
28:DE:167:VAL:HG11	28:DE:189:PRO:HD3	2.02	0.41
5:AE:31:LEU:HA	5:AE:31:LEU:HD23	1.80	0.41
5:AE:78:HIS:CE1	8:AH:104:ARG:NH1	2.89	0.41
30:DG:18:GLU:HG2	30:DG:175:LEU:HD21	2.01	0.41
6:AF:62:TRP:CD1	18:AR:35:ARG:HD2	2.56	0.41
25:DA:2472:G:H2'	25:DA:2475:C:H42	1.85	0.41
4:CD:153:ARG:HB2	4:CD:181:MET:SD	2.61	0.41
25:BA:1530:G:N2	25:BA:1552:C:C2	2.88	0.41
46:D0:19:LYS:NZ	46:D0:19:LYS:H	2.18	0.41
44:BY:106:LEU:O	44:BY:107:ASP:HB2	2.20	0.41
25:DA:705:A:H2'	25:DA:706:A:O4'	2.21	0.41
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.41
26:DB:3:C:H2'	26:DB:4:C:H6	1.84	0.41
25:BA:1520:G:C6	25:BA:1521:C:N3	2.89	0.41
1:CA:325:A:H2'	1:CA:326:G:O4'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:919:A:O2'	1:CA:1080:A:N1	2.50	0.41
16:CP:55:ARG:O	16:CP:58:TYR:N	2.51	0.41
19:AS:20:LEU:HD13	50:B4:69:LYS:HE2	2.03	0.41
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.35	0.41
1:AA:512:U:H2'	1:AA:513:C:C6	2.56	0.41
13:CM:91:ARG:HA	13:CM:91:ARG:HD2	1.93	0.41
36:BQ:137:TYR:HB3	45:BZ:76:LEU:HD21	2.01	0.41
25:DA:1790:C:O3'	25:DA:1791:A:C8	2.73	0.41
2:AB:36:ARG:C	2:AB:38:GLY:H	2.23	0.41
25:DA:343:C:H2'	25:DA:344:G:H8	1.85	0.41
30:BG:77:ILE:HG21	30:BG:80:PHE:CD2	2.56	0.41
3:AC:152:ILE:O	3:AC:198:VAL:HA	2.20	0.41
9:AI:128:ARG:NH2	23:AX:33:U:OP2	2.53	0.41
1:CA:1460:A:H2'	1:CA:1461:G:O4'	2.21	0.41
33:BN:10:GLU:OE1	33:BN:11:PRO:HD2	2.21	0.41
25:DA:632:A:H2'	25:DA:633:A:C8	2.55	0.41
1:CA:868:C:H2'	1:CA:869:G:O4'	2.21	0.41
1:CA:53:A:N6	1:CA:54:C:C4	2.88	0.41
4:CD:171:GLY:HA2	4:CD:172:PRO:HD3	1.93	0.41
25:DA:372:G:O2'	25:DA:373:U:OP2	2.37	0.41
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	2.01	0.41
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.80	0.41
40:BU:18:LEU:HD23	40:BU:18:LEU:HA	1.89	0.41
25:DA:2297:C:C6	25:DA:2297:C:H3'	2.55	0.41
38:BS:110:LEU:HD12	38:BS:110:LEU:HA	1.70	0.41
25:DA:966:G:C6	25:DA:967:C:N4	2.88	0.41
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.41
25:DA:301:G:C4	25:DA:302:C:C5	3.08	0.41
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.35	0.41
36:BQ:41:TRP:CD1	36:BQ:96:VAL:HG22	2.55	0.41
4:AD:59:ARG:NH2	4:AD:66:ARG:NH1	2.68	0.41
4:CD:15:GLU:CG	4:CD:63:LYS:HB3	2.46	0.41
25:DA:1788:C:H2'	25:DA:1789:A:O4'	2.20	0.41
45:BZ:151:HIS:C	45:BZ:153:SER:N	2.73	0.41
19:CS:41:VAL:HG12	19:CS:43:GLU:N	2.30	0.41
25:DA:2640:G:H1	25:DA:2774:C:N4	2.17	0.41
1:CA:749:C:O2'	1:CA:750:G:H5'	2.20	0.41
1:AA:538:G:O2'	1:AA:539:A:H5'	2.21	0.41
11:CK:33:THR:OG1	11:CK:34:ASP:O	2.31	0.41
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.36	0.41
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.55	0.41
25:DA:1580:A:OP2	25:DA:1580:A:H8	2.04	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:376:G:OP1	16:AP:5:ARG:HB2	2.20	0.41
43:DX:84:ALA:O	43:DX:87:GLN:HG3	2.21	0.41
25:DA:705:A:H1'	27:DD:9:TYR:CE1	2.55	0.41
23:CX:43:A:C2	23:CX:44:A:C4	3.09	0.41
12:CL:80:HIS:HD1	24:CW:6:2R1:CG2	2.31	0.41
25:BA:999:G:N3	25:BA:2286:A:C2	2.88	0.41
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.61	0.41
38:DS:29:PHE:CD1	38:DS:30:ARG:N	2.89	0.41
25:DA:1525:G:H2'	25:DA:1526:G:C8	2.56	0.41
24:CW:4:PRO:HA	24:CW:5:MVA:HN1	1.33	0.41
53:B7:24:THR:HG22	53:B7:26:GLY:H	1.86	0.41
29:DF:110:LEU:HA	29:DF:110:LEU:HD23	1.79	0.41
17:AQ:62:SER:CB	17:AQ:72:ARG:HD3	2.49	0.41
1:CA:1111:A:H2'	1:CA:1112:C:C6	2.56	0.41
2:CB:200:ILE:O	2:CB:200:ILE:HG12	2.21	0.41
19:AS:15:LEU:HD12	19:AS:15:LEU:HA	1.96	0.41
47:B1:11:ARG:HD2	47:B1:11:ARG:HH11	1.70	0.41
2:AB:137:ARG:NH1	2:AB:137:ARG:HB3	2.36	0.41
25:DA:1854:A:H2'	25:DA:1855:G:O4'	2.20	0.41
25:BA:1421:C:H2'	25:BA:1422:C:H6	1.85	0.41
1:AA:628:G:H2'	1:AA:629:G:C8	2.55	0.41
25:BA:2555:G:H2'	25:BA:2556:G:C8	2.55	0.41
1:CA:1039:C:N4	1:CA:1040:U:O4	2.54	0.41
2:CB:185:ILE:HA	2:CB:199:TYR:O	2.21	0.41
26:DB:5:C:OP1	26:DB:62:C:H5'	2.21	0.41
25:DA:2320:A:H4'	25:DA:2321:G:N7	2.36	0.41
1:CA:664:G:P	18:CR:64:ARG:HH12	2.44	0.41
25:DA:1487:G:H2'	25:DA:1488:G:H8	1.85	0.41
1:CA:10:A:O2'	1:CA:11:G:H5'	2.20	0.41
1:CA:955:U:O2'	19:CS:83:HIS:HD2	2.03	0.41
1:CA:647:C:C2'	1:CA:648:A:H5'	2.50	0.41
45:DZ:144:LEU:HD23	45:DZ:144:LEU:HA	1.89	0.41
13:CM:20:THR:C	13:CM:22:ILE:H	2.23	0.41
25:DA:910:A:C6	25:DA:911:A:C6	3.08	0.41
25:DA:784:A:H5'	25:DA:785:G:OP1	2.20	0.41
3:CC:18:TRP:NE1	14:CN:53:LEU:O	2.53	0.41
1:AA:1258:G:H1	1:AA:1277:C:H42	1.68	0.41
43:DX:31:HIS:HA	43:DX:32:PRO:HD3	1.87	0.41
15:CO:64:ARG:HH11	15:CO:68:ARG:NH2	2.17	0.41
25:BA:816:G:H5'	25:BA:1425:A:N6	2.36	0.41
25:DA:375:C:H2'	25:DA:376:C:H6	1.84	0.41
7:CG:69:VAL:HG12	7:CG:69:VAL:O	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2328:A:H2'	25:DA:2329:G:C8	2.56	0.41
25:DA:2337:G:C2	25:DA:2338:G:C8	3.08	0.41
25:DA:1341:U:H3'	25:DA:1397:U:O2	2.21	0.41
1:CA:991:U:N3	1:CA:1212:U:O2	2.53	0.41
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.21	0.41
13:AM:49:THR:OG1	13:AM:52:GLU:OE1	2.28	0.41
30:BG:139:LEU:HG	30:BG:139:LEU:H	1.53	0.41
9:AI:23:ASN:ND2	9:AI:25:LYS:HE3	2.36	0.41
31:DH:3:ARG:NH2	31:DH:5:GLY:H	2.19	0.41
1:CA:1245:A:H2'	1:CA:1246:C:C6	2.56	0.41
1:AA:1339:A:H2'	1:AA:1340:A:O4'	2.21	0.41
25:DA:2488:A:O2'	25:DA:2489:G:H5'	2.21	0.41
25:BA:1362:U:H2'	25:BA:1363:A:H8	1.85	0.41
24:CW:3:004:O	24:CW:6:2R1:N	2.53	0.41
25:BA:642:G:H5'	29:BF:205:ARG:HD2	2.02	0.41
40:DU:81:HIS:O	40:DU:84:LYS:HB3	2.21	0.41
1:CA:1191:A:OP1	3:CC:4:LYS:HG3	2.20	0.41
25:DA:811:U:H2'	35:DP:21:ARG:HA	2.02	0.41
26:DB:83:G:H5''	49:D3:52:HIS:CE1	2.55	0.41
25:BA:1505:C:H4'	25:BA:1506:G:O5'	2.19	0.41
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.21	0.41
25:DA:2467:C:C5	25:DA:2468:G:C6	3.08	0.41
37:DR:33:ARG:NH2	51:D5:57:VAL:O	2.49	0.41
49:B3:15:TYR:HA	49:B3:16:PRO:HD3	1.88	0.41
1:AA:1508:G:H2'	1:AA:1509:C:O4'	2.21	0.41
7:AG:104:LEU:HD13	7:AG:104:LEU:HA	1.88	0.41
41:DV:43:GLU:N	41:DV:43:GLU:OE2	2.54	0.41
48:D2:8:LYS:HA	48:D2:8:LYS:HD2	1.92	0.41
32:BI:30:LEU:HD23	32:BI:30:LEU:HA	1.70	0.41
25:DA:2836:U:C4	25:DA:2883:A:N6	2.88	0.41
25:DA:1850:G:C6	25:DA:1851:U:C4	3.09	0.41
51:B5:35:GLU:HG3	51:B5:51:TYR:CD2	2.56	0.41
23:CX:30:G:C4	23:CX:31:G:C8	3.09	0.41
10:CJ:8:LEU:HB3	10:CJ:16:LEU:CD2	2.51	0.41
1:CA:541:G:H2'	1:CA:542:G:H8	1.85	0.41
4:CD:38:TYR:HA	4:CD:39:PRO:HD3	1.92	0.41
13:AM:3:ARG:CG	13:AM:8:GLU:HA	2.51	0.41
10:CJ:6:ILE:HD13	10:CJ:98:ILE:HD11	2.02	0.41
25:DA:1486:A:O2'	25:DA:1487:G:H5'	2.21	0.41
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.31	0.41
25:DA:932:G:H4'	25:DA:933:A:O5'	2.21	0.41
25:BA:1051:C:O2	25:BA:1189:A:C6	2.74	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2120:U:C4	25:BA:2121:U:C5	3.09	0.41
10:CJ:21:GLN:O	10:CJ:25:GLU:HG2	2.20	0.41
3:AC:12:LEU:HD23	3:AC:12:LEU:HA	1.96	0.41
2:AB:71:VAL:HG13	2:AB:93:VAL:HG21	2.02	0.41
3:CC:180:ALA:HA	3:CC:206:GLU:HB3	2.02	0.41
50:B4:15:ILE:HB	50:B4:32:TYR:CD1	2.55	0.41
1:CA:202:U:O2'	1:CA:203:U:O5'	2.19	0.41
1:CA:1442:G:H2'	1:CA:1442(A):G:H5'	2.02	0.41
1:CA:437:U:C5'	4:CD:155:LEU:HD11	2.50	0.41
25:DA:2590:A:OP2	27:DD:238:GLY:HA2	2.20	0.41
7:CG:26:PHE:CD2	7:CG:30:ILE:HD11	2.56	0.41
9:CI:54:ASP:O	9:CI:56:LEU:N	2.44	0.41
27:DD:182:LEU:HA	27:DD:182:LEU:HD23	1.90	0.41
14:AN:12:ARG:HG2	14:AN:13:THR:N	2.35	0.41
30:DG:43:LEU:HB3	30:DG:44:GLY:H	1.48	0.41
1:CA:1387:G:H2'	1:CA:1388:C:H6	1.84	0.41
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.20	0.41
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.56	0.41
38:DS:19:LYS:H	38:DS:19:LYS:HG2	1.59	0.41
25:BA:1652:G:H5''	25:BA:1653:C:OP1	2.21	0.41
25:DA:1274:A:N3	25:DA:1297:C:H1'	2.35	0.41
30:BG:137:GLU:HG2	30:BG:152:LEU:HD22	2.03	0.41
11:CK:81:ASP:OD1	11:CK:106:LYS:HB2	2.21	0.41
1:AA:872:A:C4	1:AA:874:G:N7	2.88	0.41
31:DH:3:ARG:CD	31:DH:54:ARG:HH12	2.34	0.41
25:DA:990:A:N1	25:DA:1186:G:O2'	2.52	0.41
50:B4:18:CYS:SG	50:B4:20:ASN:HB2	2.61	0.41
41:DV:31:ALA:O	41:DV:61:VAL:HG12	2.20	0.41
52:D6:21:TYR:CE1	52:D6:38:LYS:HG2	2.55	0.41
1:AA:178:C:H2'	1:AA:179:A:O4'	2.21	0.41
1:CA:292:G:N7	1:CA:293:G:H1'	2.35	0.41
34:DO:29:ASN:OD1	34:DO:29:ASN:N	2.54	0.41
25:BA:771:U:C4	25:BA:772:G:C5	3.09	0.41
13:AM:17:VAL:O	13:AM:20:THR:OG1	2.19	0.41
25:BA:1821:C:H5''	25:BA:1822:A:OP1	2.20	0.41
39:DT:27:THR:O	39:DT:89:VAL:HG22	2.20	0.41
25:DA:2638:G:P	28:DE:82:ARG:NH2	2.94	0.41
44:DY:5:MET:HE1	44:DY:32:PRO:HA	2.03	0.41
44:BY:68:HIS:CE1	44:BY:70:SER:HB3	2.56	0.41
25:DA:1664:A:OP1	61:DA:4384:HOH:O	2.21	0.41
25:BA:2219:U:H1'	25:BA:2220:A:C8	2.55	0.41
1:CA:678:U:H2'	1:CA:679:C:C6	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1649:G:C2'	25:DA:1650:G:H5'	2.51	0.41
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.86	0.41
51:D5:19:ARG:HH11	51:D5:19:ARG:HD2	1.74	0.41
30:BG:7:LEU:HD23	30:BG:7:LEU:HA	1.85	0.41
25:DA:527:C:H5'	25:DA:527:C:O2	2.21	0.41
48:B2:41:ILE:HG12	48:B2:41:ILE:H	1.67	0.41
8:CH:97:VAL:O	8:CH:100:ILE:HG13	2.21	0.41
25:BA:785:G:C6	25:BA:786:G:C2	3.07	0.41
28:DE:31:CYS:HA	28:DE:32:PRO:HD2	1.83	0.41
1:AA:1366:C:H2'	1:AA:1367:C:C6	2.56	0.41
10:AJ:38:ILE:HG13	10:AJ:71:LEU:HB3	2.03	0.41
1:CA:1154:G:H8	1:CA:1154:G:H2'	1.35	0.41
1:CA:1493:A:O2'	1:CA:1494:G:O5'	2.34	0.41
1:CA:601:C:C2	1:CA:638:G:N2	2.88	0.41
30:DG:11:TYR:O	30:DG:16:ARG:N	2.49	0.41
1:CA:1256:A:H2	1:CA:1277:C:H42	1.67	0.41
1:CA:952:U:C5	13:CM:104:ARG:NH1	2.89	0.41
1:AA:1304:G:C6	1:AA:1305:G:N1	2.89	0.41
1:AA:509:A:O4'	4:AD:58:LEU:HD12	2.21	0.41
1:CA:939:G:N2	1:CA:1344:C:N3	2.59	0.41
13:CM:3:ARG:C	13:CM:3:ARG:HD2	2.41	0.41
1:CA:1047:G:H1	1:CA:1210:C:N4	2.16	0.41
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.22	0.41
3:CC:59:ARG:HG3	3:CC:64:VAL:HA	2.03	0.41
25:BA:215:G:H21	25:BA:217:A:H62	1.67	0.41
25:BA:146:G:C6	25:BA:147:U:C4	3.09	0.41
25:DA:878:A:C6	25:DA:900:A:N7	2.89	0.41
1:AA:741:G:H2'	1:AA:742:G:O4'	2.21	0.41
40:DU:88:ILE:HG22	40:DU:90:VAL:HG23	2.03	0.41
2:CB:52:GLU:HG2	2:CB:56:ARG:NH2	2.30	0.41
2:CB:56:ARG:CB	2:CB:56:ARG:HH11	2.31	0.41
2:CB:219:VAL:O	2:CB:223:ILE:HG23	2.21	0.41
1:CA:22:G:H4'	1:CA:885:G:C8	2.56	0.41
1:AA:146:G:C4	1:AA:147:G:C8	3.08	0.41
4:CD:196:LEU:O	4:CD:198:VAL:N	2.46	0.41
25:BA:2119:C:H2'	25:BA:2120:U:O4'	2.21	0.41
25:DA:1607:C:H5''	25:DA:1608:A:H5'	2.03	0.41
25:DA:1533:G:C2	25:DA:1537:G:C6	3.08	0.41
43:BX:92:LEU:O	43:BX:94:GLY:N	2.51	0.41
1:CA:353:A:C8	1:CA:353:A:H5'	2.49	0.41
19:AS:22:LEU:O	19:AS:27:GLU:HG3	2.21	0.41
4:CD:88:VAL:HG13	5:CE:97:GLY:HA2	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2627:G:N3	25:DA:2781:A:H2	2.19	0.41
19:CS:58:VAL:HA	19:CS:59:PRO:HD2	1.80	0.41
2:AB:71:VAL:HG12	2:AB:170:GLU:HG2	2.03	0.41
25:DA:1739:U:O2'	25:DA:1740:G:H8	2.04	0.41
2:AB:211:ILE:H	2:AB:211:ILE:HG13	1.69	0.41
25:DA:2274:A:C6	25:DA:2276:G:C8	3.09	0.41
33:DN:36:GLY:HA3	33:DN:49:GLY:HA2	2.03	0.41
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.85	0.41
1:AA:129:U:H5'	17:AQ:3:LYS:HZ3	1.86	0.41
26:DB:48:A:H4'	38:DS:95:HIS:CD2	2.53	0.41
1:AA:138:G:H2'	1:AA:139:G:O4'	2.21	0.41
27:DD:182:LEU:O	27:DD:271:ILE:N	2.47	0.41
14:AN:46:GLU:O	14:AN:50:LYS:HG3	2.21	0.41
8:CH:20:TYR:HE2	8:CH:75:ARG:HG2	1.85	0.41
1:AA:1136:U:H5''	1:AA:1137:C:C4	2.56	0.41
9:CI:23:ASN:HD22	9:CI:23:ASN:H	1.68	0.41
26:DB:24:G:N7	26:DB:56:G:H2'	2.35	0.41
11:AK:44:SER:O	11:AK:48:ILE:HD13	2.21	0.41
45:DZ:5:LEU:HG	45:DZ:47:VAL:HG21	2.03	0.41
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.85	0.41
26:DB:43:C:C4	26:DB:45:A:C6	3.08	0.41
25:DA:863:A:H2'	25:DA:864:G:H8	1.86	0.41
25:DA:2516:G:C6	25:DA:2517:C:C4	3.09	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.20	0.41
30:BG:109:VAL:HG13	50:B4:33:VAL:HG11	2.03	0.41
1:AA:872:A:C5	1:AA:874:G:C8	3.09	0.41
41:BV:98:GLU:CD	41:BV:100:ARG:HH11	2.24	0.41
25:DA:2505:G:H2'	25:DA:2576:G:O6	2.20	0.41
25:BA:870:G:C6	25:BA:882:A:C6	3.09	0.41
1:CA:589:C:O2'	1:CA:590:C:H5'	2.21	0.41
27:DD:12:SER:HB3	27:DD:208:LYS:HB3	2.03	0.41
1:CA:919:A:H8	1:CA:919:A:O5'	2.03	0.41
16:CP:58:TYR:O	16:CP:61:SER:N	2.52	0.41
40:BU:19:LYS:O	40:BU:22:LYS:HG3	2.21	0.41
50:B4:40:HIS:O	50:B4:43:TYR:N	2.54	0.41
25:BA:441:C:O2'	25:BA:442:A:H5'	2.21	0.41
1:AA:1084:G:H2'	1:AA:1085:U:C5	2.56	0.41
1:CA:500:G:N2	1:CA:546:G:H1'	2.36	0.41
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.54	0.41
1:CA:1330:U:O3'	13:CM:23:TYR:HE1	2.04	0.41
29:DF:110:LEU:HD11	29:DF:181:LEU:HD23	2.03	0.41
25:BA:415:G:O2'	25:BA:416:G:N7	2.43	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2416:C:O5'	25:DA:2416:C:H6	2.04	0.41
3:CC:11:ARG:HD3	3:CC:15:THR:HB	2.02	0.41
45:DZ:125:LEU:HG	45:DZ:164:ALA:HB3	2.01	0.41
27:DD:175:LEU:HD12	27:DD:185:VAL:HG21	2.03	0.41
25:DA:1348:G:O6	25:DA:1349:A:N6	2.54	0.41
1:CA:454:C:OP2	1:CA:455:C:N4	2.52	0.41
25:DA:2840:C:H2'	25:DA:2841:C:C6	2.56	0.41
9:CI:106:ALA:O	9:CI:108:VAL:HG23	2.21	0.41
43:DX:27:THR:OG1	43:DX:80:ILE:HG12	2.21	0.41
25:DA:335:C:H4'	44:DY:73:ARG:CD	2.51	0.41
1:AA:1058:G:H2'	1:AA:1059:C:O4'	2.20	0.41
30:DG:91:ARG:HB3	30:DG:91:ARG:HE	1.53	0.41
34:BO:108:GLU:HG3	34:BO:108:GLU:H	1.63	0.41
17:AQ:81:ARG:HD2	17:AQ:81:ARG:HA	1.86	0.41
33:DN:114:ARG:HD2	33:DN:114:ARG:HH11	1.75	0.41
25:DA:1804:C:O5'	25:DA:1804:C:H6	2.02	0.41
25:BA:496:A:H5''	25:BA:496:A:C8	2.56	0.41
13:AM:108:ARG:HA	13:AM:108:ARG:HD3	1.83	0.41
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.20	0.41
32:BI:14:ASP:OD1	32:BI:15:VAL:N	2.54	0.41
3:AC:82:GLU:O	3:AC:85:ARG:HB2	2.21	0.41
45:DZ:156:LYS:NZ	45:DZ:158:PRO:HD3	2.35	0.41
25:BA:26:G:C6	25:BA:27:G:N1	2.88	0.41
52:D6:5:VAL:O	52:D6:27:LYS:HG2	2.21	0.41
45:BZ:119:GLU:OE2	45:BZ:122:ARG:NH1	2.54	0.41
37:DR:20:LEU:O	37:DR:24:GLN:HG3	2.21	0.41
1:AA:857:C:H2'	1:AA:858:G:O4'	2.21	0.41
25:BA:1830:G:O2'	27:BD:181:GLU:OE2	2.29	0.41
25:BA:2240:G:C5	25:BA:2241:C:C4	3.09	0.41
48:B2:65:ASN:OD1	48:B2:69:ARG:NH1	2.39	0.41
1:AA:717:C:H6	1:AA:717:C:H5''	1.86	0.41
30:DG:53:LEU:HA	30:DG:53:LEU:HD23	1.84	0.41
1:AA:1168:A:C6	1:AA:1169:A:C6	3.09	0.41
1:CA:505:G:C6	1:CA:535:A:C2	3.09	0.41
1:CA:1233:G:H2'	1:CA:1234:C:C6	2.55	0.41
7:AG:65:ALA:HB1	7:AG:127:ALA:HB3	2.02	0.41
1:AA:1125:U:H2'	1:AA:1125:U:OP2	2.21	0.41
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.33	0.41
25:BA:2710:U:H2'	25:BA:2711:C:C6	2.56	0.41
1:CA:1492:A:H2'	25:DA:1913:A:H62	1.84	0.41
25:DA:994:C:H1'	41:DV:10:LYS:HE3	2.03	0.41
1:AA:475:G:O2'	1:AA:476:G:H5'	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2287:A:C4	25:DA:2289:G:C8	3.09	0.41
25:DA:2801(A):A:N3	25:DA:2895:U:H1'	2.36	0.41
1:CA:20:U:H2'	1:CA:21:G:O4'	2.21	0.41
1:CA:955:U:H2'	1:CA:956:U:O4'	2.21	0.41
32:DI:104:GLN:O	32:DI:105:HIS:CG	2.73	0.41
25:DA:855:G:H2'	25:DA:856:C:C6	2.56	0.41
25:DA:658:C:H2'	25:DA:659:C:H6	1.85	0.41
1:AA:991:U:H1'	1:AA:993:G:H8	1.86	0.41
1:AA:827:U:H2'	1:AA:859:A:H61	1.85	0.41
25:DA:2746:U:H2'	25:DA:2747:G:H5'	2.01	0.41
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.56	0.41
25:BA:1210:G:H2'	25:BA:1211:U:C6	2.56	0.41
45:BZ:52:SER:OG	45:BZ:53:ILE:N	2.54	0.41
1:AA:1216:G:N2	1:AA:1217:C:C2	2.89	0.41
1:CA:991:U:H3'	1:CA:1212:U:C4	2.56	0.41
26:BB:78:A:H2'	26:BB:79:C:O4'	2.21	0.41
15:CO:81:LEU:HD11	15:CO:85:LEU:HD12	2.02	0.41
36:BQ:16:ARG:HG3	36:BQ:17:LEU:H	1.86	0.41
7:CG:46:ALA:O	7:CG:50:ILE:HG23	2.21	0.41
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.20	0.41
25:BA:1024:G:C2	25:BA:1032:C:C2	3.09	0.41
1:AA:1371:G:C6	1:AA:1372:U:C4	3.08	0.41
45:BZ:14:LYS:HA	45:BZ:15:PRO:HD3	1.95	0.41
1:CA:263:A:OP1	20:CT:79:ARG:NH1	2.54	0.41
25:DA:2193:G:H2'	25:DA:2194:G:H8	1.87	0.41
25:DA:623:G:C6	25:DA:624:C:C4	3.09	0.41
25:DA:2416:C:O2'	25:DA:2417:C:H5'	2.21	0.41
44:DY:5:MET:HB2	44:DY:5:MET:HE2	1.91	0.41
25:DA:1334:G:H2'	25:DA:1335:U:C6	2.56	0.41
2:AB:197:VAL:HB	2:AB:200:ILE:CG2	2.51	0.41
31:BH:117:PRO:HG3	31:BH:123:PHE:CD2	2.56	0.41
26:DB:114:C:H4'	38:DS:46:VAL:HG22	2.02	0.41
2:CB:137:ARG:HB3	2:CB:137:ARG:NH1	2.36	0.41
25:BA:1908:C:O5'	25:BA:1908:C:H6	2.04	0.41
54:B8:50:LEU:HA	54:B8:50:LEU:HD23	1.94	0.41
38:DS:61:ASN:O	38:DS:65:VAL:HG23	2.21	0.41
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.92	0.41
3:AC:150:LYS:HG2	3:AC:151:VAL:N	2.36	0.41
13:CM:107:ALA:HB3	13:CM:111:LYS:HE3	2.03	0.41
1:AA:1127:G:C2'	1:AA:1128:C:H5'	2.50	0.40
2:CB:13:ALA:C	2:CB:15:VAL:H	2.25	0.40
25:BA:1067:A:C3'	25:BA:1067:A:C8	3.04	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:DU:80:ILE:HD13	40:DU:80:ILE:HA	1.91	0.40
45:DZ:33:LEU:HD21	45:DZ:90:VAL:HG21	2.03	0.40
1:AA:1314:C:N4	1:AA:1315:U:O4	2.54	0.40
1:CA:401:C:O2'	1:CA:621:A:N3	2.47	0.40
32:DI:72:LEU:HB2	32:DI:138:ILE:HG21	2.03	0.40
1:CA:446:G:H1	1:CA:488:C:H42	1.70	0.40
29:BF:56:GLU:OE2	29:BF:93:LYS:NZ	2.47	0.40
25:BA:1431:G:H4'	25:BA:1432:C:OP1	2.21	0.40
25:DA:1682:G:H1'	25:DA:1762:A:C6	2.57	0.40
25:DA:1590:U:H2'	25:DA:1591:G:C8	2.57	0.40
1:AA:266:G:H5'	1:AA:266:G:C8	2.56	0.40
25:DA:89:G:C3'	25:DA:90:U:H5''	2.44	0.40
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.44	0.40
4:CD:11:LEU:HD23	4:CD:66:ARG:HB3	2.03	0.40
18:CR:51:LEU:HA	18:CR:52:PRO:HD3	1.94	0.40
19:CS:63:THR:OG1	19:CS:64:GLU:N	2.54	0.40
1:AA:933:G:C6	1:AA:1385:G:C6	3.09	0.40
1:CA:1074:G:C2	1:CA:1075:C:C2	3.09	0.40
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.22	0.40
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.85	0.40
1:AA:407:G:O2'	4:AD:116:GLN:HG3	2.21	0.40
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.56	0.40
25:DA:1957:C:O2'	25:DA:1985:G:H1'	2.22	0.40
2:AB:78:GLN:NE2	2:AB:95:GLN:OE1	2.54	0.40
25:BA:922:G:O2'	45:BZ:151:HIS:CE1	2.74	0.40
19:CS:41:VAL:CG1	19:CS:43:GLU:H	2.29	0.40
6:AF:37:VAL:HG12	6:AF:38:GLU:N	2.36	0.40
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.55	0.40
35:DP:121:LYS:HG2	35:DP:122:PRO:HD2	2.03	0.40
28:DE:2:LYS:HB2	28:DE:95:ILE:HD12	2.03	0.40
44:DY:40:GLU:O	44:DY:42:VAL:HG23	2.21	0.40
25:BA:815:G:C6	25:BA:816:G:C5	3.08	0.40
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	2.03	0.40
25:DA:2361:A:P	54:D8:27:THR:HG1	2.44	0.40
31:DH:149:ARG:HA	31:DH:162:ILE:HG21	2.03	0.40
29:DF:101:LEU:HD12	29:DF:102:PRO:HD2	2.03	0.40
1:CA:1220:G:H2'	1:CA:1221:G:O4'	2.20	0.40
54:B8:16:ILE:HD11	54:B8:62:LEU:HD12	2.02	0.40
9:CI:96:LEU:O	9:CI:100:GLY:N	2.54	0.40
1:AA:44:G:H2'	1:AA:45:U:O4'	2.20	0.40
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.35	0.40
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:684:A:C6	1:AA:685:G:C6	3.09	0.40
7:AG:79:ARG:HH21	7:AG:79:ARG:HB2	1.85	0.40
1:AA:584:G:O6	61:AA:4012:HOH:O	2.20	0.40
25:DA:1131:G:C2	25:DA:1132:A:C4	3.10	0.40
5:AE:69:VAL:HA	5:AE:70:PRO:HD3	1.72	0.40
7:CG:155:ARG:NH1	7:CG:155:ARG:HB3	2.36	0.40
25:DA:2228:G:C5	25:DA:2229:C:C4	3.09	0.40
47:B1:86:SER:H	47:B1:89:GLU:HG3	1.85	0.40
25:DA:1195:G:O2'	25:DA:1226:A:N1	2.46	0.40
25:BA:1541:A:H2'	25:BA:1542:A:C8	2.55	0.40
32:DI:60:GLU:CB	32:DI:61:ARG:HH21	2.34	0.40
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	2.02	0.40
25:BA:496:A:OP1	25:BA:496:A:H4'	2.20	0.40
25:BA:2564:U:C2	25:BA:2566:U:H5'	2.56	0.40
25:DA:2716:U:O2'	25:DA:2717:G:H5'	2.20	0.40
31:DH:9:ILE:HA	31:DH:10:PRO:HD2	1.94	0.40
5:CE:152:ARG:HG3	8:CH:43:GLY:O	2.21	0.40
27:DD:164:GLN:NE2	27:DD:176:ARG:HH22	2.19	0.40
25:BA:2718:G:C2	25:BA:2719:G:H1'	2.56	0.40
25:DA:1801:G:H3'	25:DA:1802:A:H5'	2.03	0.40
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.36	0.40
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.21	0.40
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	2.02	0.40
48:B2:48:HIS:CE1	48:B2:49:LYS:HG3	2.56	0.40
1:CA:233:C:H6	1:CA:233:C:O5'	2.04	0.40
25:BA:857:U:O5'	25:BA:857:U:H6	2.04	0.40
45:BZ:91:LEU:HD13	45:BZ:91:LEU:HA	1.88	0.40
28:BE:9:VAL:HB	39:BT:3:ARG:HG2	2.02	0.40
25:BA:639:G:N2	29:BF:44:ARG:O	2.53	0.40
25:DA:227:A:C2	25:DA:2407:G:H1'	2.56	0.40
1:CA:236:G:C6	1:CA:237:C:C4	3.09	0.40
25:DA:2436:G:C6	25:DA:2437:U:C4	3.10	0.40
25:DA:1022:G:C6	25:DA:1140:C:N3	2.90	0.40
1:AA:1139:G:N2	1:AA:1143:G:C6	2.89	0.40
2:AB:55:PHE:CE1	2:AB:218:ALA:HA	2.56	0.40
1:CA:1178:G:N3	1:CA:1180:A:H2	2.19	0.40
35:DP:46:LYS:HE3	35:DP:46:LYS:HB3	1.90	0.40
25:DA:300:A:H1'	25:DA:319:C:C1'	2.51	0.40
1:CA:598:U:H2'	1:CA:599:C:H6	1.86	0.40
25:DA:2298:A:N1	25:DA:2321:G:C2	2.88	0.40
1:CA:1226:C:H6	13:CM:103:THR:OG1	2.04	0.40
25:DA:530:G:C5	25:DA:2022:U:H5''	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:489:C:H2'	1:CA:490:G:C8	2.57	0.40
25:BA:1316:C:H5''	25:BA:1317:G:O5'	2.21	0.40
1:AA:92:C:H2'	1:AA:93:G:C8	2.56	0.40
25:DA:996:A:N6	25:DA:1160:G:C6	2.90	0.40
1:CA:1014:A:N3	1:CA:1219:U:H1'	2.36	0.40
1:CA:522:C:H5''	12:CL:120:TYR:OH	2.21	0.40
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.03	0.40
1:CA:458:C:C2	1:CA:460:G:C8	3.10	0.40
25:DA:1971:A:C4	27:DD:241:PRO:HD3	2.57	0.40
30:DG:25:TYR:CD2	30:DG:30:GLU:HB3	2.57	0.40
34:DO:35:VAL:HG11	34:DO:103:ALA:CB	2.50	0.40
1:CA:1063:C:H3'	1:CA:1064:G:H2'	2.04	0.40
26:DB:32:C:C4	26:DB:33:G:N7	2.89	0.40
28:DE:93:VAL:O	28:DE:95:ILE:N	2.54	0.40
20:AT:45:GLN:HE21	20:AT:45:GLN:HB3	1.60	0.40
3:CC:113:ALA:CB	3:CC:202:ILE:HG13	2.50	0.40
1:AA:491:G:C4	1:AA:492:G:C8	3.09	0.40
1:CA:986:A:H1'	19:CS:54:GLY:O	2.21	0.40
48:D2:48:HIS:O	48:D2:52:ASP:HB2	2.20	0.40
12:AL:60:LEU:HA	12:AL:60:LEU:HD13	1.93	0.40
1:AA:237:C:OP2	17:AQ:40:LYS:NZ	2.48	0.40
1:AA:670:G:C4	1:AA:671:G:C8	3.09	0.40
20:CT:10:LEU:HD12	20:CT:10:LEU:HA	1.88	0.40
1:CA:1244:C:H42	1:CA:1293:G:H1	1.68	0.40
25:BA:2354:C:O2'	25:BA:2386:C:H5''	2.20	0.40
7:AG:152:ALA:HB1	7:AG:155:ARG:HH21	1.86	0.40
25:BA:2075:G:OP1	28:BE:144:ARG:HG2	2.20	0.40
54:D8:38:GLY:O	54:D8:42:ARG:HB2	2.20	0.40
44:DY:19:LYS:HB3	44:DY:19:LYS:HE2	1.91	0.40
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	2.03	0.40
54:D8:9:GLY:O	54:D8:13:ARG:HG2	2.20	0.40
1:AA:1164:G:H2'	1:AA:1165:C:C6	2.56	0.40
1:AA:1164:G:O2'	1:AA:1165:C:H5'	2.21	0.40
25:DA:1032:A:H2	25:DA:1122:G:H22	1.70	0.40
41:DV:40:LEU:HB2	41:DV:46:VAL:HG22	2.02	0.40
52:B6:40:CYS:HA	52:B6:41:PRO:HD3	1.85	0.40
25:DA:699:A:H4'	25:DA:1554:A:N6	2.36	0.40
12:AL:88:GLY:O	12:AL:99:HIS:HD2	2.04	0.40
25:DA:324:A:N6	25:DA:338:G:O2'	2.50	0.40
25:DA:2282:G:H4'	25:DA:2389:G:O2'	2.21	0.40
36:BQ:108:GLY:HA3	45:BZ:116:VAL:HG13	2.03	0.40
1:AA:1110:A:OP2	61:AA:4115:HOH:O	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1465:C:H2'	1:CA:1466:C:O4'	2.21	0.40
25:BA:505:A:N3	25:BA:507:G:H5''	2.37	0.40
25:DA:282:A:N6	25:DA:284:U:C2	2.89	0.40
25:DA:112:U:H2'	25:DA:113:G:O4'	2.21	0.40
1:AA:341:C:C2'	1:AA:342:C:H5'	2.51	0.40
1:AA:1127:G:H22	1:AA:1147:C:N4	2.20	0.40
25:BA:2832:G:O2'	25:BA:2834:C:OP2	2.31	0.40
1:CA:1122:U:C4	1:CA:1123:A:C5	3.09	0.40
40:DU:76:TYR:CE1	40:DU:80:ILE:HG13	2.57	0.40
25:BA:1736:A:N6	25:BA:1745:A:H2	2.04	0.40
1:AA:78:G:N2	1:AA:91:C:N3	2.69	0.40
4:AD:171:GLY:HA2	4:AD:172:PRO:HD3	1.95	0.40
4:AD:173:TRP:HA	4:AD:186:LEU:HB2	2.02	0.40
1:AA:477:A:O2'	1:AA:479:C:H5'	2.22	0.40
1:AA:184:G:O4'	1:AA:224:C:H4'	2.21	0.40
1:AA:864:A:O5'	1:AA:864:A:H8	2.05	0.40
25:DA:2267:A:H5''	25:DA:2268:A:C5'	2.47	0.40
1:AA:1321:C:H3'	1:AA:1322:C:H6	1.86	0.40
25:BA:2701:U:OP2	25:BA:2882:G:N2	2.47	0.40
25:DA:310:A:HO2'	25:DA:311:A:P	2.44	0.40
38:DS:10:ARG:O	38:DS:14:VAL:HG13	2.22	0.40
17:AQ:60:ILE:HG12	17:AQ:61:GLU:N	2.36	0.40
1:AA:1277:C:H2'	1:AA:1279:A:H8	1.85	0.40
25:BA:1900:G:H2'	25:BA:1901:C:H6	1.86	0.40
25:BA:2430:A:H2'	25:BA:2431:U:O4'	2.21	0.40
25:DA:2329:G:H2'	25:DA:2330:G:O4'	2.22	0.40
35:BP:94:GLU:HG3	35:BP:124:LYS:HB3	2.03	0.40
30:DG:121:ASN:HA	30:DG:122:PRO:HD3	1.89	0.40
1:AA:731:G:OP1	1:AA:766:A:H1'	2.20	0.40
25:DA:724:U:H2'	25:DA:725:G:O4'	2.21	0.40
25:DA:248:G:H5'	25:DA:250:G:N7	2.35	0.40
11:CK:104:GLN:HG2	11:CK:106:LYS:HG2	2.02	0.40
34:DO:7:TYR:CE1	34:DO:20:MET:HB2	2.57	0.40
25:DA:392:C:H5''	25:DA:409:C:H5''	2.03	0.40
39:BT:91:ARG:HH11	39:BT:120:ARG:HH11	1.68	0.40
25:DA:2536:G:C5	25:DA:2537:U:C5	3.09	0.40
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.56	0.40
25:DA:94(A):G:H2'	25:DA:95:G:O4'	2.21	0.40
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.36	0.40
1:CA:340:U:C2	1:CA:350:G:N2	2.89	0.40
25:DA:45:C:H2'	25:DA:47:C:H6	1.86	0.40
25:BA:26:G:C6	25:BA:27:G:C6	3.09	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:1753:G:H2'	25:DA:1755:A:OP2	2.22	0.40
1:CA:41:G:H2'	1:CA:42:G:C8	2.56	0.40
1:CA:654:G:H2'	1:CA:655:A:O4'	2.21	0.40
27:BD:127:VAL:HA	27:BD:193:VAL:HG22	2.04	0.40
36:DQ:110:THR:HG23	36:DQ:113:GLN:OE1	2.21	0.40
18:CR:44:LEU:HD11	18:CR:79:LEU:HB3	2.02	0.40
25:BA:2428:C:H6	25:BA:2428:C:O5'	2.04	0.40
3:AC:92:ALA:HA	3:AC:95:THR:CB	2.51	0.40
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.49	0.40
1:AA:633:G:H2'	1:AA:634:C:C6	2.57	0.40
30:DG:165:THR:HG23	30:DG:168:GLU:OE2	2.21	0.40
25:DA:870:A:C2	25:DA:908:C:C2	3.09	0.40
1:CA:1003:G:H2'	1:CA:1004:A:C4'	2.52	0.40
1:AA:1122:U:C4	1:AA:1123:A:N7	2.89	0.40
1:CA:1150:U:C4	1:CA:1151:A:N6	2.89	0.40
25:BA:1686:U:H4'	25:BA:2711:C:H4'	2.02	0.40
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	2.04	0.40
8:AH:6:ILE:O	8:AH:10:LEU:HG	2.21	0.40
50:B4:59:PHE:CA	50:B4:61:ARG:H	2.34	0.40
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	2.03	0.40
1:AA:1030:C:N4	1:AA:1031:G:C6	2.90	0.40
1:CA:1166:G:H2'	1:CA:1169:A:OP2	2.22	0.40
28:DE:14:ILE:HB	39:DT:14:TYR:CZ	2.56	0.40
25:DA:30:G:H2'	25:DA:31:C:O4'	2.21	0.40
25:DA:143:G:C6	25:DA:143(A):C:C4	3.10	0.40
6:CF:82:ARG:NH1	6:CF:82:ARG:HB3	2.36	0.40
1:CA:551:U:H2'	1:CA:552:U:C6	2.56	0.40
25:DA:2745:C:H4'	31:DH:142:GLY:O	2.20	0.40
1:CA:688:G:H2'	1:CA:689:C:H6	1.85	0.40
31:BH:11:VAL:HA	31:BH:12:PRO:HD3	1.94	0.40
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.56	0.40
25:BA:1857:G:H4'	27:BD:242:ARG:CZ	2.51	0.40
26:DB:98:G:C5	26:DB:99:G:C8	3.09	0.40
28:DE:105:THR:HG21	28:DE:164:ARG:CZ	2.51	0.40
25:BA:346:A:OP2	29:BF:169:ASN:HB2	2.21	0.40
1:AA:235:C:H2'	1:AA:236:G:H8	1.87	0.40
1:CA:596:C:H2'	1:CA:597:G:C8	2.54	0.40
1:CA:1317:C:H42	14:CN:19:ARG:HH21	1.69	0.40
1:AA:583:A:N6	1:AA:758:G:O2'	2.54	0.40
37:DR:70:LEU:O	37:DR:72:ASP:N	2.55	0.40
1:CA:1371:G:O3'	9:CI:69:GLY:HA3	2.21	0.40
25:DA:1131:G:C8	25:DA:2025:C:H4'	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.21	0.40
25:DA:1288:U:O2'	25:DA:1647:G:N2	2.55	0.40
4:AD:65:ARG:HG2	4:AD:75:PHE:CG	2.57	0.40
1:CA:79:G:H1	1:CA:90:U:H3	1.70	0.40
39:DT:59:THR:HG23	39:DT:78:LEU:HB2	2.03	0.40
1:CA:708:C:H2'	1:CA:709:G:H8	1.86	0.40
53:B7:24:THR:O	53:B7:28:ARG:HG3	2.22	0.40
1:AA:1443:G:C2	1:AA:1460:A:C2	3.09	0.40
15:CO:74:ASP:OD1	15:CO:76:GLU:HB2	2.21	0.40
25:DA:373:U:H2'	25:DA:374:A:H8	1.86	0.40
52:D6:25:LYS:HE3	52:D6:27:LYS:HA	2.04	0.40
45:DZ:96:VAL:N	45:DZ:128:VAL:O	2.45	0.40
1:CA:363:A:C5	12:CL:31:PRO:HD2	2.57	0.40
46:B0:49:LYS:O	46:B0:50:ASN:HB2	2.22	0.40
37:BR:109:ALA:O	37:BR:111:LEU:HD22	2.22	0.40
25:BA:105:C:H2'	25:BA:106:U:H6	1.85	0.40
28:DE:12:THR:HG21	39:DT:11:GLU:OE2	2.21	0.40
1:CA:194:C:H5''	1:CA:195:A:OP2	2.22	0.40
25:DA:2580:U:C5	25:DA:2581:G:C6	3.09	0.40
25:BA:2528:G:C6	25:BA:2529:C:N4	2.89	0.40
40:BU:98:LEU:HA	40:BU:98:LEU:HD23	1.80	0.40
8:AH:78:GLN:HE21	8:AH:78:GLN:HB2	1.65	0.40
38:BS:36:TYR:CD1	38:BS:36:TYR:N	2.90	0.40
5:AE:27:ARG:HB2	5:AE:27:ARG:HE	1.45	0.40
2:AB:215:LEU:HD23	2:AB:215:LEU:HA	1.86	0.40
1:AA:256:U:H2'	1:AA:257:G:C8	2.57	0.40
25:BA:511:C:H2'	25:BA:512:C:C6	2.56	0.40
28:DE:38:THR:O	28:DE:42:ASP:N	2.40	0.40
1:AA:1247:U:H2'	1:AA:1248:A:O4'	2.22	0.40
45:BZ:34:ASN:O	45:BZ:35:ARG:HD2	2.21	0.40
25:BA:2650:G:P	28:BE:82:ARG:HH22	2.45	0.40
1:CA:1003:G:C2'	1:CA:1004:A:H4'	2.52	0.40
25:BA:1394:G:O6	25:BA:1395:A:N6	2.55	0.40
25:DA:2748:A:C6	25:DA:2749:A:C5	3.10	0.40
1:AA:1005:A:H5''	1:AA:1006:C:OP2	2.20	0.40
10:CJ:49:VAL:HG12	10:CJ:61:GLU:O	2.22	0.40
1:CA:1272:G:C5	1:CA:1273:G:C8	3.10	0.40
1:AA:1095:U:P	1:AA:1108:G:H1	2.43	0.40
25:DA:1301:A:C8	25:DA:1303:G:C8	3.09	0.40
25:BA:2372:A:C2	25:BA:2373:A:H1'	2.56	0.40
2:AB:95:GLN:HB3	2:AB:147:LYS:NZ	2.36	0.40
13:CM:90:LEU:HD23	13:CM:93:ARG:NE	2.37	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:DR:37:THR:HA	37:DR:111:LEU:HD12	2.02	0.40
1:AA:828:A:N6	1:AA:829:G:C2	2.90	0.40
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.54	0.40
1:AA:676:A:H2	11:AK:119:CYS:SG	2.44	0.40
25:BA:2274:U:O2'	25:BA:2275:C:H5'	2.21	0.40
1:CA:1086:U:H2'	1:CA:1087:G:O4'	2.21	0.40
41:BV:18:LEU:O	41:BV:95:LEU:HD23	2.22	0.40
25:BA:938:G:C2	25:BA:939:C:C2	3.10	0.40
25:BA:1698:G:N2	25:BA:2029:C:C2	2.90	0.40
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.86	0.40
1:AA:69:G:H2'	1:AA:70:G:H8	1.82	0.40
4:AD:61:LYS:HD2	4:AD:207:TYR:OH	2.21	0.40
18:AR:40:LEU:HD23	18:AR:40:LEU:HA	1.72	0.40
1:CA:1183:A:H5'	1:CA:1183:A:H8	1.85	0.40
19:CS:36:ARG:NH1	19:CS:53:ASN:HA	2.37	0.40
8:CH:86:ILE:HG12	8:CH:135:CYS:HA	2.04	0.40
2:AB:19:HIS:HE1	2:AB:189:ASP:CB	2.35	0.40
14:AN:3:ARG:HH21	14:AN:3:ARG:CB	2.34	0.40
46:B0:27:GLU:HB2	46:B0:69:PHE:CD1	2.56	0.40
1:AA:41:G:H2'	1:AA:42:G:H8	1.87	0.40
25:DA:1416:G:HO2'	25:DA:1417:C:H5	1.65	0.40
39:DT:61:PHE:CZ	39:DT:76:PHE:HB2	2.57	0.40
1:AA:1367:C:N3	1:AA:1368:G:C8	2.90	0.40
25:DA:1842:G:H2'	25:DA:1843:C:O4'	2.22	0.40
25:BA:2310:A:H2'	25:BA:2311:G:O4'	2.21	0.40
25:DA:478:A:C6	25:DA:480:A:C6	3.09	0.40
25:BA:1781:G:O2'	25:BA:2870:A:N1	2.48	0.40
25:DA:1171:G:H1	25:DA:1178:C:H42	1.69	0.40
25:BA:504:A:C6	25:BA:506:A:C6	3.09	0.40
49:B3:7:LYS:HG3	49:B3:34:GLU:HG3	2.04	0.40
5:AE:57:LYS:HD3	5:AE:61:TYR:HE2	1.87	0.40
45:BZ:163:LEU:HA	45:BZ:163:LEU:HD12	1.87	0.40
50:B4:9:LEU:HA	50:B4:9:LEU:HD23	1.96	0.40
25:BA:218:A:H3'	25:BA:218:A:C8	2.57	0.40
32:BI:140:LEU:HA	32:BI:140:LEU:HD23	1.71	0.40
1:AA:1079:G:C6	1:AA:1080:A:N6	2.90	0.40
16:AP:59:TRP:HB3	16:AP:64:ALA:HB2	2.04	0.40
25:DA:2433:A:H5"	25:DA:2434:A:OP1	2.21	0.40
17:AQ:58:GLU:O	17:AQ:74:LEU:N	2.43	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	
2	AB	229/256 (90%)	200 (87%)	23 (10%)	6 (3%)	8	41
2	CB	229/256 (90%)	201 (88%)	18 (8%)	10 (4%)	4	25
3	AC	204/239 (85%)	179 (88%)	22 (11%)	3 (2%)	15	57
3	CC	204/239 (85%)	178 (87%)	24 (12%)	2 (1%)	22	68
4	AD	206/209 (99%)	182 (88%)	22 (11%)	2 (1%)	22	68
4	CD	206/209 (99%)	185 (90%)	18 (9%)	3 (2%)	15	57
5	AE	146/162 (90%)	127 (87%)	15 (10%)	4 (3%)	8	39
5	CE	146/162 (90%)	133 (91%)	10 (7%)	3 (2%)	11	48
6	AF	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
6	CF	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
7	AG	153/156 (98%)	137 (90%)	14 (9%)	2 (1%)	18	60
7	CG	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	30	76
8	AH	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	30	76
9	AI	125/128 (98%)	111 (89%)	10 (8%)	4 (3%)	6	35
9	CI	125/128 (98%)	112 (90%)	11 (9%)	2 (2%)	14	55
10	AJ	95/105 (90%)	85 (90%)	7 (7%)	3 (3%)	6	35
10	CJ	94/105 (90%)	86 (92%)	7 (7%)	1 (1%)	21	65
11	AK	112/129 (87%)	98 (88%)	13 (12%)	1 (1%)	25	71
11	CK	112/129 (87%)	99 (88%)	12 (11%)	1 (1%)	25	71
12	AL	120/132 (91%)	116 (97%)	4 (3%)	0	100	100
12	CL	120/132 (91%)	112 (93%)	8 (7%)	0	100	100
13	AM	121/126 (96%)	106 (88%)	15 (12%)	0	100	100
13	CM	120/126 (95%)	104 (87%)	14 (12%)	2 (2%)	14	54
14	AN	58/61 (95%)	54 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	AO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
15	CO	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	19	62
16	AP	80/88 (91%)	69 (86%)	11 (14%)	0	100	100
16	CP	80/88 (91%)	70 (88%)	10 (12%)	0	100	100
17	AQ	97/105 (92%)	91 (94%)	6 (6%)	0	100	100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
18	AR	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	15	57
18	CR	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	15	57
19	AS	81/93 (87%)	74 (91%)	7 (9%)	0	100	100
19	CS	81/93 (87%)	69 (85%)	12 (15%)	0	100	100
20	AT	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	3	21
20	CT	94/106 (89%)	85 (90%)	3 (3%)	6 (6%)	2	15
21	AU	21/27 (78%)	17 (81%)	4 (19%)	0	100	100
21	CU	21/27 (78%)	18 (86%)	1 (5%)	2 (10%)	1	7
24	AW	3/10 (30%)	1 (33%)	0	2 (67%)	0	0
24	CW	3/10 (30%)	1 (33%)	1 (33%)	1 (33%)	0	0
27	BD	273/276 (99%)	259 (95%)	13 (5%)	1 (0%)	43	84
27	DD	273/276 (99%)	257 (94%)	13 (5%)	3 (1%)	21	65
28	BE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	38	81
28	DE	202/206 (98%)	194 (96%)	6 (3%)	2 (1%)	22	68
29	BF	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	38	81
29	DF	201/210 (96%)	189 (94%)	10 (5%)	2 (1%)	22	68
30	BG	179/182 (98%)	163 (91%)	13 (7%)	3 (2%)	14	54
30	DG	179/182 (98%)	160 (89%)	13 (7%)	6 (3%)	6	32
31	BH	172/180 (96%)	161 (94%)	10 (6%)	1 (1%)	33	78
31	DH	172/180 (96%)	159 (92%)	11 (6%)	2 (1%)	19	62
32	BI	144/148 (97%)	122 (85%)	17 (12%)	5 (4%)	6	32
32	DI	144/148 (97%)	123 (85%)	17 (12%)	4 (3%)	8	39
33	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
33	DN	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	30	76

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	BO	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	27	74
34	DO	120/122 (98%)	117 (98%)	2 (2%)	1 (1%)	27	74
35	BP	147/150 (98%)	132 (90%)	14 (10%)	1 (1%)	30	76
35	DP	147/150 (98%)	133 (90%)	12 (8%)	2 (1%)	16	58
36	BQ	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	30	76
36	DQ	139/141 (99%)	129 (93%)	8 (6%)	2 (1%)	16	58
37	BR	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	25	71
37	DR	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
38	BS	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	25	71
38	DS	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	25	71
39	BT	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	27	74
39	DT	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
40	BU	114/118 (97%)	114 (100%)	0	0	100	100
40	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
41	BV	99/101 (98%)	91 (92%)	7 (7%)	1 (1%)	22	68
41	DV	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	22	68
42	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
42	DW	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
43	BX	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	21	65
43	DX	93/96 (97%)	87 (94%)	6 (6%)	0	100	100
44	BY	105/110 (96%)	95 (90%)	10 (10%)	0	100	100
44	DY	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
45	BZ	169/206 (82%)	150 (89%)	17 (10%)	2 (1%)	19	62
45	DZ	172/206 (84%)	157 (91%)	15 (9%)	0	100	100
46	B0	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	19	62
46	D0	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
47	B1	95/98 (97%)	93 (98%)	0	2 (2%)	11	48
47	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	21	65
48	B2	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
48	D2	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
49	B3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	D3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
50	B4	67/71 (94%)	50 (75%)	9 (13%)	8 (12%)	1	4
50	D4	67/71 (94%)	50 (75%)	8 (12%)	9 (13%)	0	2
51	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	B6	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
52	D6	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
53	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
53	D7	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	10	46
54	B8	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
54	D8	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
55	B9	35/37 (95%)	35 (100%)	0	0	100	100
55	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11415/12148 (94%)	10525 (92%)	749 (7%)	141 (1%)	19	62

All (141) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	17	PHE
2	AB	125	PRO
3	AC	65	ALA
3	AC	107	GLN
4	AD	166	LYS
7	AG	4	ARG
9	AI	54	ASP
9	AI	56	LEU
10	AJ	31	GLY
10	AJ	79	ARG
18	AR	60	ALA
20	AT	10	LEU
27	BD	275	LYS
29	BF	130	ALA
30	BG	51	ARG
30	BG	126	ASP
31	BH	126	PRO
32	BI	73	GLU
36	BQ	60	ARG

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Mol	Chain	Res	Type
38	BS	60	GLY
47	B1	3	LYS
50	B4	49	PHE
50	B4	55	ARG
50	B4	68	ARG
2	CB	16	HIS
2	CB	126	GLU
2	CB	231	GLU
3	CC	91	LEU
3	CC	181	ASN
7	CG	7	ALA
13	CM	106	ASN
20	CT	95	ALA
20	CT	99	LEU
27	DD	239	ARG
29	DF	21	ALA
29	DF	130	ALA
30	DG	14	GLU
30	DG	47	LYS
30	DG	51	ARG
30	DG	81	LYS
30	DG	126	ASP
31	DH	126	PRO
32	DI	10	GLU
35	DP	38	GLN
36	DQ	28	ALA
36	DQ	60	ARG
47	D1	3	LYS
50	D4	39	CYS
50	D4	45	GLY
50	D4	55	ARG
50	D4	63	TYR
53	D7	46	VAL
2	AB	16	HIS
2	AB	19	HIS
4	AD	171	GLY
5	AE	85	GLY
5	AE	140	ARG
9	AI	95	LYS
11	AK	49	GLY
20	AT	47	GLY
32	BI	11	ASN

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Mol	Chain	Res	Type
32	BI	106	GLY
34	BO	5	GLN
41	BV	79	VAL
46	B0	13	GLY
50	B4	47	GLN
50	B4	56	VAL
50	B4	66	SER
2	CB	8	LYS
2	CB	10	LEU
2	CB	17	PHE
2	CB	20	GLU
2	CB	121	LEU
2	CB	123	ALA
9	CI	54	ASP
9	CI	55	ALA
10	CJ	79	ARG
11	CK	49	GLY
31	DH	80	SER
33	DN	2	LYS
34	DO	5	GLN
41	DV	79	VAL
50	D4	38	LYS
50	D4	60	GLN
50	D4	62	ARG
2	AB	128	GLU
9	AI	55	ALA
20	AT	102	GLY
35	BP	29	LYS
37	BR	45	ARG
43	BX	93	GLU
45	BZ	152	ALA
50	B4	57	GLU
50	B4	62	ARG
2	CB	21	ARG
5	CE	146	ALA
13	CM	10	PRO
20	CT	47	GLY
21	CU	3	LYS
28	DE	52	LEU
32	DI	30	LEU
32	DI	135	GLU
38	DS	84	GLN

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Mol	Chain	Res	Type
50	D4	49	PHE
3	AC	66	VAL
20	AT	71	THR
24	AW	7	PRO
28	BE	52	LEU
32	BI	107	VAL
39	BT	127	ALA
4	CD	47	ARG
5	CE	37	ARG
21	CU	23	PRO
24	CW	4	PRO
27	DD	3	VAL
28	DE	73	GLU
7	AG	81	GLY
30	BG	47	LYS
32	BI	117	GLU
4	CD	136	PRO
15	CO	88	ARG
18	CR	60	ALA
20	CT	71	THR
20	CT	102	GLY
35	DP	45	LEU
5	AE	146	ALA
10	AJ	77	PRO
47	B1	45	ASN
8	CH	73	ASP
30	DG	117	PHE
32	DI	85	GLU
50	D4	29	PRO
2	AB	231	GLU
24	AW	4	PRO
20	AT	100	ILE
20	CT	100	ILE
27	DD	238	GLY
5	AE	69	VAL
45	BZ	114	GLY
5	CE	69	VAL
4	CD	7	PRO

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	147 (77%)	45 (23%)	1	5
2	CB	187/220 (85%)	152 (81%)	35 (19%)	2	9
3	AC	143/188 (76%)	125 (87%)	18 (13%)	7	24
3	CC	140/188 (74%)	122 (87%)	18 (13%)	6	24
4	AD	170/181 (94%)	145 (85%)	25 (15%)	4	18
4	CD	173/181 (96%)	152 (88%)	21 (12%)	7	27
5	AE	113/123 (92%)	104 (92%)	9 (8%)	17	55
5	CE	114/123 (93%)	107 (94%)	7 (6%)	26	67
6	AF	83/90 (92%)	76 (92%)	7 (8%)	16	52
6	CF	85/90 (94%)	79 (93%)	6 (7%)	21	61
7	AG	119/127 (94%)	100 (84%)	19 (16%)	3	13
7	CG	120/127 (94%)	102 (85%)	18 (15%)	4	17
8	AH	114/119 (96%)	98 (86%)	16 (14%)	5	21
8	CH	114/119 (96%)	102 (90%)	12 (10%)	10	35
9	AI	90/99 (91%)	76 (84%)	14 (16%)	4	14
9	CI	89/99 (90%)	75 (84%)	14 (16%)	4	14
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	14	45
10	CJ	69/92 (75%)	64 (93%)	5 (7%)	21	60
11	AK	82/99 (83%)	73 (89%)	9 (11%)	9	34
11	CK	83/99 (84%)	77 (93%)	6 (7%)	21	60
12	AL	97/109 (89%)	90 (93%)	7 (7%)	21	60
12	CL	97/109 (89%)	87 (90%)	10 (10%)	10	36
13	AM	93/101 (92%)	82 (88%)	11 (12%)	8	29
13	CM	92/101 (91%)	80 (87%)	12 (13%)	6	23
14	AN	49/50 (98%)	41 (84%)	8 (16%)	3	12
14	CN	49/50 (98%)	42 (86%)	7 (14%)	5	19
15	AO	78/80 (98%)	69 (88%)	9 (12%)	8	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	CO	78/80 (98%)	66 (85%)	12 (15%)	4	15
16	AP	69/74 (93%)	60 (87%)	9 (13%)	6	23
16	CP	68/74 (92%)	63 (93%)	5 (7%)	20	59
17	AQ	94/97 (97%)	89 (95%)	5 (5%)	32	72
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	20	59
18	AR	59/77 (77%)	55 (93%)	4 (7%)	22	62
18	CR	59/77 (77%)	52 (88%)	7 (12%)	8	27
19	AS	69/80 (86%)	63 (91%)	6 (9%)	15	49
19	CS	67/80 (84%)	57 (85%)	10 (15%)	4	17
20	AT	70/82 (85%)	61 (87%)	9 (13%)	6	24
20	CT	70/82 (85%)	60 (86%)	10 (14%)	5	19
21	AU	18/22 (82%)	14 (78%)	4 (22%)	1	6
21	CU	18/22 (82%)	16 (89%)	2 (11%)	9	33
24	AW	3/3 (100%)	2 (67%)	1 (33%)	0	0
24	CW	3/3 (100%)	2 (67%)	1 (33%)	0	0
27	BD	215/218 (99%)	198 (92%)	17 (8%)	18	55
27	DD	215/218 (99%)	190 (88%)	25 (12%)	8	30
28	BE	164/166 (99%)	142 (87%)	22 (13%)	6	22
28	DE	164/166 (99%)	144 (88%)	20 (12%)	7	26
29	BF	160/166 (96%)	143 (89%)	17 (11%)	10	35
29	DF	159/166 (96%)	145 (91%)	14 (9%)	14	49
30	BG	143/156 (92%)	123 (86%)	20 (14%)	5	21
30	DG	142/156 (91%)	116 (82%)	26 (18%)	2	10
31	BH	144/148 (97%)	129 (90%)	15 (10%)	10	36
31	DH	144/148 (97%)	131 (91%)	13 (9%)	14	47
32	BI	110/124 (89%)	82 (74%)	28 (26%)	1	2
32	DI	104/124 (84%)	86 (83%)	18 (17%)	3	11
33	BN	118/119 (99%)	103 (87%)	15 (13%)	6	24
33	DN	118/119 (99%)	102 (86%)	16 (14%)	5	21
34	BO	100/100 (100%)	94 (94%)	6 (6%)	27	67
34	DO	100/100 (100%)	91 (91%)	9 (9%)	14	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	BP	115/116 (99%)	102 (89%)	13 (11%)	9	32
35	DP	115/116 (99%)	104 (90%)	11 (10%)	12	42
36	BQ	111/111 (100%)	94 (85%)	17 (15%)	4	15
36	DQ	111/111 (100%)	96 (86%)	15 (14%)	6	22
37	BR	101/101 (100%)	83 (82%)	18 (18%)	2	10
37	DR	101/101 (100%)	85 (84%)	16 (16%)	4	14
38	BS	87/88 (99%)	77 (88%)	10 (12%)	8	31
38	DS	85/88 (97%)	70 (82%)	15 (18%)	3	10
39	BT	115/127 (91%)	104 (90%)	11 (10%)	12	42
39	DT	113/127 (89%)	105 (93%)	8 (7%)	21	61
40	BU	93/94 (99%)	83 (89%)	10 (11%)	9	34
40	DU	93/94 (99%)	82 (88%)	11 (12%)	8	29
41	BV	80/82 (98%)	69 (86%)	11 (14%)	5	21
41	DV	80/82 (98%)	71 (89%)	9 (11%)	9	32
42	BW	90/92 (98%)	79 (88%)	11 (12%)	7	26
42	DW	90/92 (98%)	80 (89%)	10 (11%)	9	33
43	BX	77/78 (99%)	73 (95%)	4 (5%)	32	73
43	DX	77/78 (99%)	74 (96%)	3 (4%)	43	83
44	BY	85/91 (93%)	79 (93%)	6 (7%)	21	61
44	DY	85/91 (93%)	79 (93%)	6 (7%)	21	61
45	BZ	145/179 (81%)	121 (83%)	24 (17%)	3	12
45	DZ	145/179 (81%)	126 (87%)	19 (13%)	6	23
46	B0	65/67 (97%)	61 (94%)	4 (6%)	26	66
46	D0	65/67 (97%)	59 (91%)	6 (9%)	13	45
47	B1	80/83 (96%)	72 (90%)	8 (10%)	11	38
47	D1	80/83 (96%)	73 (91%)	7 (9%)	14	49
48	B2	65/67 (97%)	56 (86%)	9 (14%)	5	21
48	D2	65/67 (97%)	57 (88%)	8 (12%)	7	26
49	B3	51/52 (98%)	44 (86%)	7 (14%)	5	21
49	D3	50/52 (96%)	43 (86%)	7 (14%)	5	21
50	B4	59/63 (94%)	48 (81%)	11 (19%)	2	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	D4	53/63 (84%)	45 (85%)	8 (15%)	4	16
51	B5	50/52 (96%)	45 (90%)	5 (10%)	11	38
51	D5	50/52 (96%)	45 (90%)	5 (10%)	11	38
52	B6	51/52 (98%)	45 (88%)	6 (12%)	8	29
52	D6	50/52 (96%)	46 (92%)	4 (8%)	17	55
53	B7	41/42 (98%)	37 (90%)	4 (10%)	12	40
53	D7	41/42 (98%)	39 (95%)	2 (5%)	35	76
54	B8	53/55 (96%)	49 (92%)	4 (8%)	19	58
54	D8	54/55 (98%)	50 (93%)	4 (7%)	20	59
55	B9	34/34 (100%)	33 (97%)	1 (3%)	55	88
55	D9	34/34 (100%)	33 (97%)	1 (3%)	55	88
All	All	9325/10072 (93%)	8209 (88%)	1116 (12%)	7	27

All (1116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP
2	AB	49	GLU
2	AB	53	ARG
2	AB	56	ARG
2	AB	67	THR
2	AB	71	VAL
2	AB	80	ILE
2	AB	81	VAL
2	AB	87	ARG
2	AB	96	ARG
2	AB	109	SER
2	AB	112	VAL
2	AB	114	ARG
2	AB	116	GLU
2	AB	126	GLU

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Mol	Chain	Res	Type
2	AB	128	GLU
2	AB	142	LEU
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	158	LEU
2	AB	170	GLU
2	AB	178	ARG
2	AB	185	ILE
2	AB	187	LEU
2	AB	190	THR
2	AB	196	LEU
2	AB	200	ILE
2	AB	208	ILE
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	222	ILE
2	AB	226	ARG
2	AB	233	SER
3	AC	3	ASN
3	AC	17	ASP
3	AC	27	LYS
3	AC	28	GLN
3	AC	29	TYR
3	AC	47	LEU
3	AC	52	LEU
3	AC	54	ARG
3	AC	77	ILE
3	AC	82	GLU
3	AC	98	ASN
3	AC	104	GLN
3	AC	118	GLN
3	AC	119	ARG
3	AC	131	ARG
3	AC	150	LYS
3	AC	154	SER
3	AC	165	THR
4	AD	5	ILE

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Mol	Chain	Res	Type
4	AD	19	LEU
4	AD	31	CYS
4	AD	58	LEU
4	AD	85	LYS
4	AD	86	LYS
4	AD	110	PHE
4	AD	112	VAL
4	AD	122	ARG
4	AD	126	ILE
4	AD	127	THR
4	AD	135	LEU
4	AD	150	GLU
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	181	MET
4	AD	182	LYS
4	AD	184	LYS
4	AD	187	ARG
4	AD	188	LEU
4	AD	190	ASP
4	AD	193	ASP
4	AD	196	LEU
4	AD	201	GLN
5	AE	10	MET
5	AE	12	LEU
5	AE	31	LEU
5	AE	40	ARG
5	AE	41	VAL
5	AE	47	LYS
5	AE	71	LEU
5	AE	78	HIS
5	AE	79	GLU
6	AF	46	ARG
6	AF	55	ASP
6	AF	63	TYR
6	AF	69	GLU
6	AF	74	ASP
6	AF	82	ARG
6	AF	94	GLN
7	AG	8	GLU
7	AG	9	VAL

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Mol	Chain	Res	Type
7	AG	12	LEU
7	AG	13	GLN
7	AG	15	ASP
7	AG	21	VAL
7	AG	50	ILE
7	AG	51	GLN
7	AG	57	GLU
7	AG	75	VAL
7	AG	76	ARG
7	AG	79	ARG
7	AG	97	GLN
7	AG	104	LEU
7	AG	113	GLU
7	AG	114	ARG
7	AG	138	LYS
7	AG	140	ASP
7	AG	144	MET
8	AH	21	LYS
8	AH	23	SER
8	AH	25	ASP
8	AH	26	VAL
8	AH	37	ARG
8	AH	50	ARG
8	AH	52	ASP
8	AH	53	VAL
8	AH	63	LEU
8	AH	75	ARG
8	AH	78	GLN
8	AH	97	VAL
8	AH	98	LYS
8	AH	107	LEU
8	AH	112	LEU
8	AH	137	VAL
9	AI	23	ASN
9	AI	27	THR
9	AI	53	VAL
9	AI	54	ASP
9	AI	56	LEU
9	AI	60	ASP
9	AI	65	VAL
9	AI	66	ARG
9	AI	75	ASP

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Mol	Chain	Res	Type
9	AI	81	ILE
9	AI	103	THR
9	AI	108	VAL
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	16	LEU
10	AJ	30	SER
10	AJ	68	HIS
10	AJ	96	ILE
11	AK	31	THR
11	AK	48	ILE
11	AK	70	LYS
11	AK	84	VAL
11	AK	95	ILE
11	AK	96	ARG
11	AK	104	GLN
11	AK	109	VAL
11	AK	120	ARG
12	AL	6	THR
12	AL	33	ARG
12	AL	46	LYS
12	AL	55	VAL
12	AL	67	THR
12	AL	70	ILE
12	AL	86	ARG
13	AM	3	ARG
13	AM	4	ILE
13	AM	8	GLU
13	AM	19	LEU
13	AM	43	THR
13	AM	50	GLU
13	AM	56	LEU
13	AM	70	LEU
13	AM	73	GLU
13	AM	110	ARG
13	AM	121	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	18	VAL

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Mol	Chain	Res	Type
14	AN	22	THR
14	AN	23	ARG
14	AN	32	SER
14	AN	33	VAL
15	AO	3	ILE
15	AO	5	LYS
15	AO	22	THR
15	AO	24	SER
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	83	GLU
15	AO	84	LYS
16	AP	2	VAL
16	AP	5	ARG
16	AP	8	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	28	ARG
16	AP	45	THR
16	AP	50	LYS
16	AP	67	THR
17	AQ	14	LYS
17	AQ	53	LEU
17	AQ	60	ILE
17	AQ	63	ARG
17	AQ	74	LEU
18	AR	26	LEU
18	AR	32	ARG
18	AR	61	LYS
18	AR	82	THR
19	AS	5	LEU
19	AS	6	LYS
19	AS	28	LYS
19	AS	37	ARG
19	AS	63	THR
19	AS	65	ASN
20	AT	8	ARG
20	AT	9	ASN
20	AT	13	LEU
20	AT	31	SER
20	AT	45	GLN

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Mol	Chain	Res	Type
20	AT	46	GLU
20	AT	56	MET
20	AT	58	LYS
20	AT	62	LEU
21	AU	7	ARG
21	AU	9	ARG
21	AU	10	ARG
21	AU	15	ARG
24	AW	2	VAL
27	BD	3	VAL
27	BD	12	SER
27	BD	13	ARG
27	BD	61	LEU
27	BD	71	ASP
27	BD	94	LEU
27	BD	103	ARG
27	BD	138	VAL
27	BD	142	VAL
27	BD	155	LEU
27	BD	211	ARG
27	BD	217	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	242	ARG
27	BD	257	LEU
27	BD	260	ARG
28	BE	1	MET
28	BE	9	VAL
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	49	LEU
28	BE	73	GLU
28	BE	82	ARG
28	BE	89	ASP
28	BE	93	VAL
28	BE	97	LYS
28	BE	111	ARG
28	BE	116	VAL
28	BE	119	ARG
28	BE	144	ARG
28	BE	145	LYS

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Mol	Chain	Res	Type
28	BE	154	LYS
28	BE	163	GLU
28	BE	170	LEU
28	BE	175	VAL
28	BE	181	LEU
28	BE	203	LYS
29	BF	19	GLU
29	BF	24	LEU
29	BF	33	LEU
29	BF	53	THR
29	BF	57	VAL
29	BF	64	ILE
29	BF	74	ARG
29	BF	78	ILE
29	BF	88	VAL
29	BF	106	ARG
29	BF	108	LYS
29	BF	110	LEU
29	BF	125	LEU
29	BF	170	LEU
29	BF	192	LEU
29	BF	197	ASP
29	BF	200	GLU
30	BG	5	VAL
30	BG	7	LEU
30	BG	28	VAL
30	BG	31	VAL
30	BG	43	LEU
30	BG	45	GLU
30	BG	78	SER
30	BG	81	LYS
30	BG	82	LEU
30	BG	86	MET
30	BG	91	ARG
30	BG	133	LEU
30	BG	135	LEU
30	BG	136	ARG
30	BG	140	ILE
30	BG	143	GLU
30	BG	148	MET
30	BG	159	VAL
30	BG	170	ARG

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Mol	Chain	Res	Type
30	BG	181	ARG
31	BH	6	ARG
31	BH	13	LYS
31	BH	15	VAL
31	BH	41	MET
31	BH	44	VAL
31	BH	49	VAL
31	BH	59	ARG
31	BH	69	ARG
31	BH	95	ARG
31	BH	98	LEU
31	BH	116	GLU
31	BH	122	THR
31	BH	129	THR
31	BH	172	LYS
31	BH	175	LYS
32	BI	9	LEU
32	BI	15	VAL
32	BI	19	VAL
32	BI	20	ASP
32	BI	38	LEU
32	BI	40	THR
32	BI	41	GLU
32	BI	43	ASN
32	BI	50	ARG
32	BI	54	GLN
32	BI	57	ARG
32	BI	60	GLU
32	BI	64	GLU
32	BI	66	GLU
32	BI	68	LEU
32	BI	74	ASN
32	BI	75	LEU
32	BI	77	LEU
32	BI	78	THR
32	BI	92	VAL
32	BI	96	ASP
32	BI	101	LEU
32	BI	107	VAL
32	BI	109	ILE
32	BI	114	LEU
32	BI	140	LEU

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Mol	Chain	Res	Type
32	BI	142	VAL
32	BI	144	VAL
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	68	GLU
33	BN	83	LYS
33	BN	87	LEU
33	BN	97	ARG
33	BN	99	LEU
33	BN	120	LEU
33	BN	121	LYS
33	BN	133	GLN
33	BN	137	LYS
34	BO	8	LEU
34	BO	23	ARG
34	BO	24	VAL
34	BO	58	VAL
34	BO	94	ARG
34	BO	98	VAL
35	BP	4	SER
35	BP	15	ARG
35	BP	42	SER
35	BP	59	LEU
35	BP	65	ARG
35	BP	83	VAL
35	BP	95	VAL
35	BP	98	GLU
35	BP	106	LEU
35	BP	112	LEU
35	BP	125	VAL
35	BP	144	GLU
35	BP	149	GLU
36	BQ	1	MET
36	BQ	5	ARG
36	BQ	7	MET
36	BQ	8	LYS
36	BQ	16	ARG
36	BQ	21	THR

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Mol	Chain	Res	Type
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	56	ARG
36	BQ	60	ARG
36	BQ	75	THR
36	BQ	81	VAL
36	BQ	85	LYS
36	BQ	109	VAL
36	BQ	110	THR
36	BQ	129	THR
36	BQ	138	ASP
37	BR	1	MET
37	BR	6	SER
37	BR	18	LEU
37	BR	28	LEU
37	BR	29	LEU
37	BR	33	ARG
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	86	ARG
37	BR	91	GLN
37	BR	100	LEU
37	BR	111	LEU
38	BS	14	VAL
38	BS	20	ARG
38	BS	36	TYR
38	BS	43	GLU
38	BS	48	LEU
38	BS	50	SER
38	BS	59	LYS
38	BS	61	ASN
38	BS	78	LEU
38	BS	103	GLU
39	BT	13	ARG
39	BT	17	THR
39	BT	28	VAL

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Mol	Chain	Res	Type
39	BT	39	ARG
39	BT	49	VAL
39	BT	53	ARG
39	BT	74	ARG
39	BT	78	LEU
39	BT	85	LYS
39	BT	96	ARG
39	BT	118	ARG
40	BU	8	VAL
40	BU	31	SER
40	BU	36	ARG
40	BU	60	LEU
40	BU	74	LEU
40	BU	83	LEU
40	BU	92	ARG
40	BU	95	LEU
40	BU	104	GLN
40	BU	117	GLN
41	BV	10	LYS
41	BV	18	LEU
41	BV	21	ARG
41	BV	51	VAL
41	BV	52	VAL
41	BV	61	VAL
41	BV	62	LEU
41	BV	72	VAL
41	BV	79	VAL
41	BV	95	LEU
41	BV	100	ARG
42	BW	11	ARG
42	BW	15	ARG
42	BW	17	VAL
42	BW	23	LEU
42	BW	27	LYS
42	BW	51	LEU
42	BW	60	ASN
42	BW	63	ASP
42	BW	67	ASP
42	BW	100	THR
42	BW	107	LEU
43	BX	2	LYS
43	BX	57	LEU

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Mol	Chain	Res	Type
43	BX	66	LEU
43	BX	70	LEU
44	BY	2	ARG
44	BY	7	VAL
44	BY	43	ASN
44	BY	72	VAL
44	BY	90	LEU
44	BY	91	GLU
45	BZ	5	LEU
45	BZ	6	LYS
45	BZ	11	GLU
45	BZ	19	ARG
45	BZ	31	ARG
45	BZ	40	ASP
45	BZ	41	LEU
45	BZ	42	VAL
45	BZ	61	LEU
45	BZ	76	LEU
45	BZ	82	ARG
45	BZ	86	VAL
45	BZ	87	ASP
45	BZ	91	LEU
45	BZ	107	THR
45	BZ	120	ILE
45	BZ	131	ARG
45	BZ	132	ASN
45	BZ	135	GLU
45	BZ	136	PHE
45	BZ	144	LEU
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	162	GLU
46	B0	7	LEU
46	B0	10	THR
46	B0	20	ARG
46	B0	55	ARG
47	B1	21	ARG
47	B1	26	ARG
47	B1	35	THR
47	B1	40	ARG
47	B1	52	ARG
47	B1	59	THR

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Mol	Chain	Res	Type
47	B1	89	GLU
47	B1	95	LEU
48	B2	28	LYS
48	B2	30	ARG
48	B2	41	ILE
48	B2	45	SER
48	B2	52	ASP
48	B2	53	LEU
48	B2	55	ARG
48	B2	64	LEU
48	B2	70	GLN
49	B3	6	VAL
49	B3	8	LEU
49	B3	23	LEU
49	B3	29	ARG
49	B3	32	GLN
49	B3	55	ARG
49	B3	58	VAL
50	B4	5	ILE
50	B4	28	LYS
50	B4	34	GLU
50	B4	46	GLN
50	B4	49	PHE
50	B4	56	VAL
50	B4	58	ARG
50	B4	61	ARG
50	B4	63	TYR
50	B4	68	ARG
50	B4	69	LYS
51	B5	6	VAL
51	B5	29	THR
51	B5	40	LYS
51	B5	58	LEU
51	B5	60	VAL
52	B6	4	GLU
52	B6	6	ARG
52	B6	14	THR
52	B6	38	LYS
52	B6	48	VAL
52	B6	49	HIS
53	B7	1	MET
53	B7	23	ARG

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Mol	Chain	Res	Type
53	B7	43	THR
53	B7	47	ARG
54	B8	14	VAL
54	B8	29	LYS
54	B8	31	HIS
54	B8	32	LEU
55	B9	26	ILE
2	CB	7	VAL
2	CB	11	LEU
2	CB	22	LYS
2	CB	23	ARG
2	CB	24	TRP
2	CB	44	LEU
2	CB	56	ARG
2	CB	67	THR
2	CB	71	VAL
2	CB	80	ILE
2	CB	108	ILE
2	CB	115	LEU
2	CB	126	GLU
2	CB	128	GLU
2	CB	140	HIS
2	CB	142	LEU
2	CB	144	ARG
2	CB	145	LEU
2	CB	153	ARG
2	CB	154	LEU
2	CB	157	ARG
2	CB	158	LEU
2	CB	160	ASP
2	CB	169	LYS
2	CB	178	ARG
2	CB	185	ILE
2	CB	187	LEU
2	CB	191	ASP
2	CB	200	ILE
2	CB	217	ARG
2	CB	221	LEU
2	CB	224	GLN
2	CB	226	ARG
2	CB	233	SER
2	CB	235	SER

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Mol	Chain	Res	Type
3	CC	3	ASN
3	CC	20	SER
3	CC	29	TYR
3	CC	47	LEU
3	CC	52	LEU
3	CC	77	ILE
3	CC	82	GLU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	115	LEU
3	CC	118	GLN
3	CC	131	ARG
3	CC	152	ILE
3	CC	154	SER
3	CC	162	GLN
3	CC	164	ARG
3	CC	179	ARG
4	CD	10	ARG
4	CD	19	LEU
4	CD	31	CYS
4	CD	47	ARG
4	CD	58	LEU
4	CD	65	ARG
4	CD	96	LEU
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	150	GLU
4	CD	155	LEU
4	CD	157	LEU
4	CD	170	VAL
4	CD	181	MET
4	CD	184	LYS
4	CD	187	ARG
4	CD	188	LEU
4	CD	191	ARG
4	CD	194	LEU
4	CD	201	GLN
5	CE	12	LEU
5	CE	31	LEU
5	CE	40	ARG

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Mol	Chain	Res	Type
5	CE	41	VAL
5	CE	71	LEU
5	CE	79	GLU
5	CE	82	VAL
6	CF	23	LYS
6	CF	28	ARG
6	CF	41	GLU
6	CF	46	ARG
6	CF	63	TYR
6	CF	69	GLU
7	CG	9	VAL
7	CG	12	LEU
7	CG	13	GLN
7	CG	15	ASP
7	CG	16	LEU
7	CG	50	ILE
7	CG	51	GLN
7	CG	52	GLU
7	CG	58	PRO
7	CG	73	MET
7	CG	75	VAL
7	CG	85	TYR
7	CG	104	LEU
7	CG	113	GLU
7	CG	114	ARG
7	CG	140	ASP
7	CG	144	MET
7	CG	155	ARG
8	CH	21	LYS
8	CH	23	SER
8	CH	25	ASP
8	CH	53	VAL
8	CH	68	ARG
8	CH	78	GLN
8	CH	84	ARG
8	CH	97	VAL
8	CH	98	LYS
8	CH	99	GLU
8	CH	112	LEU
8	CH	137	VAL
9	CI	7	THR
9	CI	17	VAL

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Mol	Chain	Res	Type
9	CI	23	ASN
9	CI	27	THR
9	CI	33	PHE
9	CI	66	ARG
9	CI	75	ASP
9	CI	81	ILE
9	CI	86	VAL
9	CI	92	TYR
9	CI	102	LEU
9	CI	124	GLN
9	CI	125	TYR
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	23	ILE
10	CJ	29	ARG
10	CJ	68	HIS
10	CJ	96	ILE
11	CK	54	ARG
11	CK	79	SER
11	CK	84	VAL
11	CK	95	ILE
11	CK	96	ARG
11	CK	126	ARG
12	CL	33	ARG
12	CL	34	ARG
12	CL	52	LEU
12	CL	55	VAL
12	CL	59	ARG
12	CL	60	LEU
12	CL	70	ILE
12	CL	83	VAL
12	CL	97	ARG
12	CL	123	LYS
13	CM	3	ARG
13	CM	4	ILE
13	CM	8	GLU
13	CM	19	LEU
13	CM	27	LYS
13	CM	47	ASP
13	CM	56	LEU
13	CM	70	LEU
13	CM	104	ARG

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Mol	Chain	Res	Type
13	CM	106	ASN
13	CM	110	ARG
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	33	VAL
14	CN	50	LYS
15	CO	3	ILE
15	CO	5	LYS
15	CO	7	GLU
15	CO	10	LYS
15	CO	22	THR
15	CO	24	SER
15	CO	26	GLU
15	CO	39	LEU
15	CO	54	ARG
15	CO	76	GLU
15	CO	83	GLU
15	CO	84	LYS
16	CP	2	VAL
16	CP	5	ARG
16	CP	8	ARG
16	CP	28	ARG
16	CP	67	THR
17	CQ	6	LEU
17	CQ	49	GLU
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	66	SER
17	CQ	74	LEU
17	CQ	83	ASP
18	CR	26	LEU
18	CR	32	ARG
18	CR	41	LYS
18	CR	42	ARG
18	CR	54	ARG
18	CR	64	ARG
18	CR	76	LEU
19	CS	6	LYS

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Mol	Chain	Res	Type
19	CS	12	ASP
19	CS	28	LYS
19	CS	30	LEU
19	CS	33	THR
19	CS	37	ARG
19	CS	43	GLU
19	CS	56	GLN
19	CS	63	THR
19	CS	71	LEU
20	CT	36	LEU
20	CT	38	LYS
20	CT	45	GLN
20	CT	46	GLU
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
20	CT	99	LEU
21	CU	10	ARG
21	CU	15	ARG
24	CW	2	VAL
27	DD	13	ARG
27	DD	32	SER
27	DD	61	LEU
27	DD	69	ARG
27	DD	88	ARG
27	DD	94	LEU
27	DD	103	ARG
27	DD	106	ILE
27	DD	113	VAL
27	DD	116	GLN
27	DD	134	ARG
27	DD	138	VAL
27	DD	142	VAL
27	DD	155	LEU
27	DD	200	ASP
27	DD	211	ARG
27	DD	217	ARG
27	DD	221	VAL
27	DD	229	VAL
27	DD	242	ARG

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Mol	Chain	Res	Type
27	DD	257	LEU
27	DD	259	THR
27	DD	260	ARG
27	DD	274	ARG
27	DD	276	LYS
28	DE	1	MET
28	DE	9	VAL
28	DE	12	THR
28	DE	21	VAL
28	DE	24	THR
28	DE	33	VAL
28	DE	40	GLU
28	DE	49	LEU
28	DE	52	LEU
28	DE	73	GLU
28	DE	75	VAL
28	DE	78	LEU
28	DE	82	ARG
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	154	LYS
28	DE	163	GLU
28	DE	181	LEU
29	DF	12	LEU
29	DF	19	GLU
29	DF	20	LEU
29	DF	24	LEU
29	DF	33	LEU
29	DF	74	ARG
29	DF	106	ARG
29	DF	107	LYS
29	DF	108	LYS
29	DF	110	LEU
29	DF	135	LYS
29	DF	137	LYS
29	DF	192	LEU
29	DF	200	GLU
30	DG	5	VAL
30	DG	21	ARG
30	DG	28	VAL

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Mol	Chain	Res	Type
30	DG	31	VAL
30	DG	35	GLU
30	DG	36	LYS
30	DG	43	LEU
30	DG	45	GLU
30	DG	49	ASP
30	DG	60	LEU
30	DG	84	LYS
30	DG	91	ARG
30	DG	98	ARG
30	DG	113	ARG
30	DG	115	ARG
30	DG	128	ARG
30	DG	133	LEU
30	DG	136	ARG
30	DG	140	ILE
30	DG	143	GLU
30	DG	145	THR
30	DG	148	MET
30	DG	153	ARG
30	DG	159	VAL
30	DG	164	GLU
30	DG	170	ARG
31	DH	3	ARG
31	DH	6	ARG
31	DH	15	VAL
31	DH	42	ARG
31	DH	69	ARG
31	DH	76	VAL
31	DH	81	GLU
31	DH	95	ARG
31	DH	98	LEU
31	DH	106	THR
31	DH	139	GLN
31	DH	171	LEU
31	DH	172	LYS
32	DI	15	VAL
32	DI	19	VAL
32	DI	20	ASP
32	DI	40	THR
32	DI	41	GLU
32	DI	43	ASN

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Mol	Chain	Res	Type
32	DI	44	LEU
32	DI	57	ARG
32	DI	61	ARG
32	DI	66	GLU
32	DI	68	LEU
32	DI	75	LEU
32	DI	77	LEU
32	DI	114	LEU
32	DI	121	LYS
32	DI	140	LEU
32	DI	142	VAL
32	DI	144	VAL
33	DN	5	VAL
33	DN	12	ARG
33	DN	33	LEU
33	DN	34	LEU
33	DN	38	HIS
33	DN	46	VAL
33	DN	48	MET
33	DN	61	ARG
33	DN	68	GLU
33	DN	85	ILE
33	DN	87	LEU
33	DN	99	LEU
33	DN	120	LEU
33	DN	133	GLN
33	DN	137	LYS
33	DN	138	LEU
34	DO	8	LEU
34	DO	23	ARG
34	DO	24	VAL
34	DO	58	VAL
34	DO	69	ILE
34	DO	92	GLU
34	DO	94	ARG
34	DO	98	VAL
34	DO	108	GLU
35	DP	2	LYS
35	DP	29	LYS
35	DP	42	SER
35	DP	55	ARG
35	DP	59	LEU

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Mol	Chain	Res	Type
35	DP	65	ARG
35	DP	76	LYS
35	DP	77	ARG
35	DP	99	LEU
35	DP	106	LEU
35	DP	112	LEU
36	DQ	1	MET
36	DQ	7	MET
36	DQ	8	LYS
36	DQ	11	LYS
36	DQ	16	ARG
36	DQ	21	THR
36	DQ	45	GLN
36	DQ	55	VAL
36	DQ	56	ARG
36	DQ	60	ARG
36	DQ	75	THR
36	DQ	81	VAL
36	DQ	85	LYS
36	DQ	109	VAL
36	DQ	110	THR
37	DR	1	MET
37	DR	6	SER
37	DR	18	LEU
37	DR	28	LEU
37	DR	29	LEU
37	DR	33	ARG
37	DR	36	THR
37	DR	44	LEU
37	DR	57	ARG
37	DR	60	LEU
37	DR	65	LEU
37	DR	75	LEU
37	DR	79	LEU
37	DR	86	ARG
37	DR	100	LEU
37	DR	111	LEU
38	DS	14	VAL
38	DS	20	ARG
38	DS	35	ILE
38	DS	36	TYR
38	DS	43	GLU

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Mol	Chain	Res	Type
38	DS	48	LEU
38	DS	50	SER
38	DS	57	LYS
38	DS	58	LEU
38	DS	67	ARG
38	DS	68	GLN
38	DS	75	GLU
38	DS	78	LEU
38	DS	83	LYS
38	DS	103	GLU
39	DT	6	LEU
39	DT	13	ARG
39	DT	74	ARG
39	DT	85	LYS
39	DT	89	VAL
39	DT	96	ARG
39	DT	113	LYS
39	DT	118	ARG
40	DU	5	LYS
40	DU	31	SER
40	DU	59	ARG
40	DU	60	LEU
40	DU	74	LEU
40	DU	83	LEU
40	DU	89	GLU
40	DU	92	ARG
40	DU	104	GLN
40	DU	108	GLU
40	DU	114	LYS
41	DV	15	GLU
41	DV	18	LEU
41	DV	21	ARG
41	DV	52	VAL
41	DV	57	VAL
41	DV	62	LEU
41	DV	72	VAL
41	DV	79	VAL
41	DV	95	LEU
42	DW	11	ARG
42	DW	15	ARG
42	DW	17	VAL
42	DW	23	LEU

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Mol	Chain	Res	Type
42	DW	27	LYS
42	DW	51	LEU
42	DW	60	ASN
42	DW	63	ASP
42	DW	100	THR
42	DW	107	LEU
43	DX	35	THR
43	DX	57	LEU
43	DX	70	LEU
44	DY	2	ARG
44	DY	11	ASP
44	DY	23	ARG
44	DY	43	ASN
44	DY	72	VAL
44	DY	99	CYS
45	DZ	5	LEU
45	DZ	11	GLU
45	DZ	19	ARG
45	DZ	31	ARG
45	DZ	33	LEU
45	DZ	40	ASP
45	DZ	41	LEU
45	DZ	50	GLN
45	DZ	61	LEU
45	DZ	72	ARG
45	DZ	76	LEU
45	DZ	86	VAL
45	DZ	87	ASP
45	DZ	91	LEU
45	DZ	107	THR
45	DZ	154	ASP
45	DZ	155	LEU
45	DZ	162	GLU
45	DZ	165	VAL
46	D0	7	LEU
46	D0	10	THR
46	D0	19	LYS
46	D0	20	ARG
46	D0	24	LYS
46	D0	55	ARG
47	D1	21	ARG
47	D1	26	ARG

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Mol	Chain	Res	Type
47	D1	35	THR
47	D1	40	ARG
47	D1	52	ARG
47	D1	59	THR
47	D1	78	LYS
48	D2	28	LYS
48	D2	30	ARG
48	D2	40	SER
48	D2	45	SER
48	D2	52	ASP
48	D2	53	LEU
48	D2	55	ARG
48	D2	70	GLN
49	D3	6	VAL
49	D3	8	LEU
49	D3	23	LEU
49	D3	24	LYS
49	D3	30	ARG
49	D3	32	GLN
49	D3	44	ARG
50	D4	5	ILE
50	D4	44	THR
50	D4	56	VAL
50	D4	58	ARG
50	D4	61	ARG
50	D4	63	TYR
50	D4	68	ARG
50	D4	69	LYS
51	D5	29	THR
51	D5	33	CYS
51	D5	40	LYS
51	D5	48	GLU
51	D5	58	LEU
52	D6	6	ARG
52	D6	9	LEU
52	D6	38	LYS
52	D6	48	VAL
53	D7	1	MET
53	D7	48	LYS
54	D8	14	VAL
54	D8	26	LYS
54	D8	29	LYS

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Mol	Chain	Res	Type
54	D8	31	HIS
55	D9	26	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (113) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	40	HIS
3	AC	6	HIS
3	AC	28	GLN
3	AC	104	GLN
3	AC	118	GLN
3	AC	136	GLN
3	AC	181	ASN
4	AD	45	GLN
5	AE	20	GLN
5	AE	56	GLN
5	AE	141	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	148	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	34	ASN
9	AI	89	ASN
10	AJ	13	HIS
10	AJ	56	HIS
11	AK	93	GLN
12	AL	78	GLN
12	AL	99	HIS
13	AM	92	HIS
15	AO	28	GLN
15	AO	62	GLN
16	AP	13	HIS
17	AQ	16	GLN
17	AQ	26	GLN
19	AS	23	ASN
19	AS	47	HIS
19	AS	65	ASN
19	AS	69	HIS
20	AT	9	ASN
20	AT	45	GLN

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Mol	Chain	Res	Type
20	AT	90	GLN
27	BD	253	GLN
29	BF	69	HIS
29	BF	169	ASN
29	BF	203	GLN
31	BH	158	HIS
32	BI	43	ASN
32	BI	139	GLN
35	BP	38	GLN
36	BQ	45	GLN
39	BT	123	GLN
40	BU	117	GLN
41	BV	80	GLN
43	BX	31	HIS
44	BY	6	HIS
44	BY	43	ASN
45	BZ	32	HIS
45	BZ	151	HIS
46	B0	3	HIS
48	B2	38	GLN
48	B2	70	GLN
49	B3	32	GLN
55	B9	36	GLN
2	CB	19	HIS
2	CB	40	HIS
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	37	GLN
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	45	GLN
4	CD	74	GLN
4	CD	125	HIS
5	CE	20	GLN
5	CE	78	HIS
5	CE	141	GLN
7	CG	51	GLN
8	CH	78	GLN
9	CI	31	GLN

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Mol	Chain	Res	Type
9	CI	58	HIS
10	CJ	68	HIS
11	CK	22	HIS
11	CK	93	GLN
12	CL	78	GLN
13	CM	77	ASN
15	CO	28	GLN
16	CP	16	HIS
19	CS	65	ASN
19	CS	69	HIS
20	CT	16	HIS
27	DD	87	ASN
27	DD	164	GLN
27	DD	253	GLN
28	DE	85	ASN
29	DF	69	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	40	ASN
30	DG	79	ASN
31	DH	139	GLN
31	DH	158	HIS
32	DI	43	ASN
35	DP	38	GLN
36	DQ	45	GLN
37	DR	13	HIS
37	DR	71	GLN
38	DS	68	GLN
39	DT	123	GLN
41	DV	64	HIS
43	DX	31	HIS
44	DY	43	ASN
46	D0	3	HIS
48	D2	38	GLN
55	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1522 (98%)	393 (26%)	25 (1%)
1	CA	1502/1522 (98%)	388 (25%)	31 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	AV	4/24 (16%)	1 (25%)	0
22	CV	4/24 (16%)	1 (25%)	0
23	AX	75/77 (97%)	16 (21%)	0
23	CX	75/77 (97%)	16 (21%)	0
25	BA	2722/2915 (93%)	508 (18%)	40 (1%)
25	DA	2704/2915 (92%)	535 (19%)	37 (1%)
26	BB	119/122 (97%)	18 (15%)	0
26	DB	119/122 (97%)	24 (20%)	1 (0%)
All	All	8819/9320 (94%)	1900 (21%)	134 (1%)

All (1900) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	G
1	AA	9	G
1	AA	15	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	44	G
1	AA	47	C
1	AA	48	C
1	AA	50	A
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	63	C
1	AA	69	G
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	101	A
1	AA	102	G
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	129(A)	G
1	AA	131	C

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Mol	Chain	Res	Type
1	AA	138	G
1	AA	141	A
1	AA	142	G
1	AA	143	A
1	AA	144	G
1	AA	149	A
1	AA	163	C
1	AA	165	C
1	AA	166	G
1	AA	171	A
1	AA	173	U
1	AA	174	C
1	AA	180	U
1	AA	181	G
1	AA	182	U
1	AA	189(D)	C
1	AA	189(F)	U
1	AA	190	U
1	AA	193	C
1	AA	194	C
1	AA	195	A
1	AA	197	A
1	AA	199	G
1	AA	201	C
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	220	G
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	269	C
1	AA	277	C
1	AA	281	G
1	AA	289	G
1	AA	298	A
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G

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Mol	Chain	Res	Type
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	349	A
1	AA	351	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	383	A
1	AA	388	G
1	AA	396	G
1	AA	397	A
1	AA	398	C
1	AA	403	C
1	AA	406	G
1	AA	409	G
1	AA	411	A
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	415	A
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	461	A
1	AA	471	G
1	AA	474	G
1	AA	484	G
1	AA	485	G
1	AA	492	G
1	AA	496	A
1	AA	498	U

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Mol	Chain	Res	Type
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	536	C
1	AA	544	G
1	AA	547	A
1	AA	553	A
1	AA	559	A
1	AA	561	U
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	592	G
1	AA	596	C
1	AA	597	G
1	AA	606	G
1	AA	626	U
1	AA	630	G
1	AA	631	G
1	AA	633	G
1	AA	639	G
1	AA	641	U
1	AA	649	G
1	AA	650	G
1	AA	651	C
1	AA	653	A
1	AA	665	A
1	AA	673	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	704	A

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Mol	Chain	Res	Type
1	AA	711	G
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	755	G
1	AA	760	G
1	AA	774	G
1	AA	777	A
1	AA	786	G
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	802	A
1	AA	806	C
1	AA	812	C
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	818	G
1	AA	821	G
1	AA	827	U
1	AA	828	A
1	AA	829	G
1	AA	836	G
1	AA	839	U
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	855	G
1	AA	858	G
1	AA	859	A
1	AA	870	U
1	AA	873	A
1	AA	876	G
1	AA	902	G
1	AA	914	A
1	AA	916	G
1	AA	922	G
1	AA	926	G

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Mol	Chain	Res	Type
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	942	G
1	AA	958	A
1	AA	960	U
1	AA	961	U
1	AA	967	C
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	982	U
1	AA	983	A
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	999	C
1	AA	1000	U
1	AA	1001	A
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1006	C
1	AA	1007	C
1	AA	1009	G
1	AA	1011	G
1	AA	1013	G
1	AA	1014	A
1	AA	1019	C
1	AA	1020	U
1	AA	1022	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C

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Mol	Chain	Res	Type
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1031	G
1	AA	1033	G
1	AA	1035	A
1	AA	1036	G
1	AA	1037	C
1	AA	1039	C
1	AA	1042	G
1	AA	1043	C
1	AA	1052	U
1	AA	1053	G
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1070	U
1	AA	1076	C
1	AA	1081	G
1	AA	1087	G
1	AA	1091	U
1	AA	1092	A
1	AA	1093	A
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1109	C
1	AA	1119	C
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1128	C
1	AA	1130	A
1	AA	1132	C
1	AA	1134	G
1	AA	1135	U

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Mol	Chain	Res	Type
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1141	C
1	AA	1145	C
1	AA	1146	A
1	AA	1151	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1159	U
1	AA	1160	G
1	AA	1161	C
1	AA	1166	G
1	AA	1173	G
1	AA	1176	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1189	C
1	AA	1193	G
1	AA	1196	U
1	AA	1197	G
1	AA	1200	C
1	AA	1202	G
1	AA	1204	A
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1223	C
1	AA	1224	G
1	AA	1227	A
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1250	A
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1259	C
1	AA	1260	C

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Mol	Chain	Res	Type
1	AA	1262	C
1	AA	1270	C
1	AA	1271	G
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1282	C
1	AA	1283	G
1	AA	1284	C
1	AA	1286	A
1	AA	1287	A
1	AA	1294	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1311	G
1	AA	1314	C
1	AA	1317	C
1	AA	1320	C
1	AA	1322	C
1	AA	1323	G
1	AA	1338	G
1	AA	1340	A
1	AA	1343	G
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1354	C
1	AA	1358	U
1	AA	1360	A
1	AA	1361	G
1	AA	1363	C
1	AA	1370	G
1	AA	1377	A
1	AA	1379	G
1	AA	1393	U
1	AA	1396	A

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Mol	Chain	Res	Type
1	AA	1397	C
1	AA	1402	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1457	G
1	AA	1469	G
1	AA	1487	G
1	AA	1489	G
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	15	A
23	AX	6	G
23	AX	9	G
23	AX	13	C
23	AX	19	G
23	AX	21	A
23	AX	26	G
23	AX	28	C
23	AX	31	G
23	AX	42	G
23	AX	47	U
23	AX	60	U
23	AX	61	C
23	AX	67	C

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Mol	Chain	Res	Type
23	AX	68	C
23	AX	70	G
23	AX	76	A
25	BA	9	U
25	BA	11	G
25	BA	12	U
25	BA	14	A
25	BA	34	C
25	BA	36	G
25	BA	45	C
25	BA	54	G
25	BA	62	U
25	BA	63	A
25	BA	70	A
25	BA	71	U
25	BA	73	A
25	BA	74	G
25	BA	83	A
25	BA	90	A
25	BA	99	G
25	BA	116	A
25	BA	118	U
25	BA	120	G
25	BA	125	A
25	BA	155	C
25	BA	161	C
25	BA	185	A
25	BA	187	C
25	BA	188	A
25	BA	194	G
25	BA	203	G
25	BA	204	G
25	BA	205	A
25	BA	206	G
25	BA	210	A
25	BA	211	A
25	BA	217	A
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	250	G
25	BA	263	C

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Mol	Chain	Res	Type
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	275	C
25	BA	276	C
25	BA	279	G
25	BA	288	U
25	BA	289	G
25	BA	294	C
25	BA	296	U
25	BA	303	C
25	BA	306	A
25	BA	307	A
25	BA	332	G
25	BA	335	A
25	BA	353	G
25	BA	354	A
25	BA	360	C
25	BA	376	G
25	BA	381	A
25	BA	387	G
25	BA	391	G
25	BA	399	G
25	BA	407	U
25	BA	413	G
25	BA	432	U
25	BA	434	G
25	BA	438	G
25	BA	439	A
25	BA	448	U
25	BA	455	A
25	BA	469	A
25	BA	470	C
25	BA	474	U
25	BA	478	G
25	BA	482	C
25	BA	483	A
25	BA	496	A
25	BA	505	A

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Mol	Chain	Res	Type
25	BA	506	A
25	BA	507	G
25	BA	508	A
25	BA	515	G
25	BA	519	G
25	BA	522	A
25	BA	526	A
25	BA	529	U
25	BA	530	A
25	BA	534	C
25	BA	543	G
25	BA	549	U
25	BA	554	A
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	569	G
25	BA	573	G
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	609	A
25	BA	610	C
25	BA	616	G
25	BA	625	G
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	633	G
25	BA	638	U
25	BA	639	G
25	BA	641	G
25	BA	659	C
25	BA	662	A
25	BA	670	C
25	BA	671	A
25	BA	692	C
25	BA	693	G
25	BA	697	C
25	BA	698	G
25	BA	701	A

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Mol	Chain	Res	Type
25	BA	712	C
25	BA	716	G
25	BA	724	A
25	BA	733	G
25	BA	745	C
25	BA	749	G
25	BA	764	G
25	BA	777	C
25	BA	811	A
25	BA	822	G
25	BA	823	G
25	BA	826	U
25	BA	829	A
25	BA	831	A
25	BA	832	G
25	BA	839	G
25	BA	852	G
25	BA	858	U
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	877	G
25	BA	902	G
25	BA	906	G
25	BA	926	G
25	BA	927	G
25	BA	928	G
25	BA	929	G
25	BA	930	G
25	BA	931	C
25	BA	932	C
25	BA	933	C
25	BA	934	A
25	BA	935	C
25	BA	937	A
25	BA	938	G
25	BA	940	C
25	BA	942	A
25	BA	944	C
25	BA	945	A
25	BA	946	A

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Mol	Chain	Res	Type
25	BA	956	A
25	BA	965	G
25	BA	977	G
25	BA	983	G
25	BA	986	A
25	BA	989	G
25	BA	990	A
25	BA	991	G
25	BA	998	A
25	BA	1003	U
25	BA	1004	A
25	BA	1006	C
25	BA	1015	C
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1036	A
25	BA	1042	A
25	BA	1051	C
25	BA	1058	U
25	BA	1059	C
25	BA	1066	A
25	BA	1067	A
25	BA	1068	G
25	BA	1069	U
25	BA	1072	U
25	BA	1076	G
25	BA	1079	U
25	BA	1080	G
25	BA	1085	G
25	BA	1087	C
25	BA	1088	G
25	BA	1089	C
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1153	G
25	BA	1154	U
25	BA	1156	G
25	BA	1158	G
25	BA	1168	G
25	BA	1174	A

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Mol	Chain	Res	Type
25	BA	1175	A
25	BA	1176	U
25	BA	1180	C
25	BA	1181	G
25	BA	1184	G
25	BA	1186	U
25	BA	1187	U
25	BA	1188	A
25	BA	1189	A
25	BA	1195	G
25	BA	1202	A
25	BA	1210	G
25	BA	1216	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1223	C
25	BA	1225	C
25	BA	1229	G
25	BA	1255	A
25	BA	1256	U
25	BA	1263	C
25	BA	1266	C
25	BA	1296	G
25	BA	1298	G
25	BA	1299	A
25	BA	1302	G
25	BA	1311	A
25	BA	1317	G
25	BA	1318	A
25	BA	1319	U
25	BA	1321	A
25	BA	1346	U
25	BA	1347	A
25	BA	1359	U
25	BA	1360	C
25	BA	1367	A
25	BA	1384	G
25	BA	1398	U

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Mol	Chain	Res	Type
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1416	C
25	BA	1417	G
25	BA	1418	U
25	BA	1426	G
25	BA	1430	A
25	BA	1431	G
25	BA	1432	C
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U
25	BA	1467	G
25	BA	1468	G
25	BA	1474	C
25	BA	1487	G
25	BA	1491	A
25	BA	1496	A
25	BA	1507	A
25	BA	1514	C
25	BA	1518	A
25	BA	1519	A
25	BA	1525	G
25	BA	1529	G
25	BA	1536	A
25	BA	1539	C
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1569	U
25	BA	1574	A
25	BA	1578	C
25	BA	1579	C
25	BA	1589	A
25	BA	1590	C
25	BA	1592	A
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1628	G

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Mol	Chain	Res	Type
25	BA	1631	C
25	BA	1632	A
25	BA	1654	A
25	BA	1655	A
25	BA	1656	A
25	BA	1660	A
25	BA	1686	U
25	BA	1694	G
25	BA	1695	C
25	BA	1696	G
25	BA	1701	A
25	BA	1711	A
25	BA	1721	G
25	BA	1722	C
25	BA	1735	U
25	BA	1742	G
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1766	G
25	BA	1767	A
25	BA	1768	U
25	BA	1769	G
25	BA	1776	G
25	BA	1777	G
25	BA	1779	G
25	BA	1787	G
25	BA	1791	A
25	BA	1794	G
25	BA	1795	G
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1822	A
25	BA	1831	C
25	BA	1832	G
25	BA	1843	A
25	BA	1847	G
25	BA	1860	A
25	BA	1870	G
25	BA	1878	A
25	BA	1879	A

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Mol	Chain	Res	Type
25	BA	1899	A
25	BA	1900	G
25	BA	1911	A
25	BA	1922	A
25	BA	1928	G
25	BA	1935	A
25	BA	1936	C
25	BA	1941	A
25	BA	1951	G
25	BA	1952	G
25	BA	1953	U
25	BA	1954	A
25	BA	1958	A
25	BA	1960	A
25	BA	1963	C
25	BA	1977	U
25	BA	1985	U
25	BA	1987	C
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2042	A
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2065	C
25	BA	2071	G
25	BA	2074	G
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A
25	BA	2091	G
25	BA	2115	G
25	BA	2121	U
25	BA	2122	G

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Mol	Chain	Res	Type
25	BA	2212	G
25	BA	2214	G
25	BA	2217	C
25	BA	2220	A
25	BA	2227	G
25	BA	2228	G
25	BA	2229	A
25	BA	2230	U
25	BA	2237	A
25	BA	2246	G
25	BA	2250	G
25	BA	2251	G
25	BA	2260	C
25	BA	2264	G
25	BA	2280	A
25	BA	2281	A
25	BA	2285	A
25	BA	2287	C
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2306	C
25	BA	2308	U
25	BA	2317	A
25	BA	2320	G
25	BA	2326	C
25	BA	2332	A
25	BA	2337	G
25	BA	2339	A
25	BA	2346	G
25	BA	2347	A
25	BA	2348	A
25	BA	2353	G
25	BA	2355	C
25	BA	2359	C
25	BA	2362	C
25	BA	2366	G
25	BA	2373	A
25	BA	2384	G
25	BA	2388	A
25	BA	2391	G
25	BA	2395	G

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Mol	Chain	Res	Type
25	BA	2397	C
25	BA	2401	G
25	BA	2412	G
25	BA	2418	U
25	BA	2422	G
25	BA	2430	A
25	BA	2434	A
25	BA	2435	U
25	BA	2436	C
25	BA	2437	A
25	BA	2441	G
25	BA	2442	A
25	BA	2443	U
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C
25	BA	2459	G
25	BA	2460	A
25	BA	2480	G
25	BA	2481	A
25	BA	2486	C
25	BA	2488	A
25	BA	2490	A
25	BA	2510	C
25	BA	2514	G
25	BA	2517	G
25	BA	2518	U
25	BA	2530	A
25	BA	2532	C
25	BA	2537	G
25	BA	2541	G
25	BA	2547	G
25	BA	2566	U
25	BA	2578	A
25	BA	2579	G
25	BA	2594	G
25	BA	2614	A
25	BA	2615	G
25	BA	2621	U
25	BA	2622	C
25	BA	2623	U
25	BA	2624	C

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Mol	Chain	Res	Type
25	BA	2632	C
25	BA	2641	A
25	BA	2642	G
25	BA	2653	G
25	BA	2666	A
25	BA	2674	A
25	BA	2690	C
25	BA	2691	A
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2714	U
25	BA	2715	C
25	BA	2719	G
25	BA	2725	A
25	BA	2726	A
25	BA	2727	G
25	BA	2739	U
25	BA	2746	A
25	BA	2764	G
25	BA	2770	A
25	BA	2771	A
25	BA	2777	A
25	BA	2778	A
25	BA	2779	G
25	BA	2782	C
25	BA	2788	A
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2807	C
25	BA	2813	G
25	BA	2816	G
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2843	G
25	BA	2845	A
25	BA	2849	G
25	BA	2876	U
25	BA	2882	G
25	BA	2883	A

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Mol	Chain	Res	Type
25	BA	2884	C
25	BA	2890	C
25	BA	2893	A
25	BA	2899	C
25	BA	2901	A
25	BA	2903	G
25	BA	2906	U
26	BB	2	C
26	BB	7	G
26	BB	12	C
26	BB	13	A
26	BB	34	U
26	BB	42	C
26	BB	56	G
26	BB	59	A
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	88	C
26	BB	89	G
26	BB	93	G
26	BB	106	G
26	BB	110	G
26	BB	112	U
26	BB	119	G
1	CA	7	G
1	CA	9	G
1	CA	15	G
1	CA	22	G
1	CA	32	A
1	CA	39	G
1	CA	44	G
1	CA	47	C
1	CA	48	C
1	CA	50	A
1	CA	51	A
1	CA	59	A
1	CA	63	C
1	CA	65	U
1	CA	66	G
1	CA	69	G
1	CA	77	G

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Mol	Chain	Res	Type
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	101	A
1	CA	102	G
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	129(A)	G
1	CA	131	C
1	CA	138	G
1	CA	142	G
1	CA	144	G
1	CA	163	C
1	CA	165	C
1	CA	166	G
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	181	G
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	190	U
1	CA	193	C
1	CA	194	C
1	CA	195	A
1	CA	197	A
1	CA	199	G
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	220	G
1	CA	247	G

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Mol	Chain	Res	Type
1	CA	251	G
1	CA	258	G
1	CA	265	G
1	CA	266	G
1	CA	267	C
1	CA	269	C
1	CA	277	C
1	CA	281	G
1	CA	289	G
1	CA	298	A
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	346	G
1	CA	351	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	383	A
1	CA	388	G
1	CA	396	G
1	CA	397	A
1	CA	398	C
1	CA	403	C
1	CA	406	G
1	CA	409	G
1	CA	411	A
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	415	A
1	CA	422	C
1	CA	424	G
1	CA	427	U
1	CA	429	U
1	CA	430	A

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Mol	Chain	Res	Type
1	CA	439	A
1	CA	442	C
1	CA	452	A
1	CA	461	A
1	CA	471	G
1	CA	474	G
1	CA	484	G
1	CA	485	G
1	CA	492	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	536	C
1	CA	544	G
1	CA	547	A
1	CA	553	A
1	CA	559	A
1	CA	561	U
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	592	G
1	CA	596	C
1	CA	597	G
1	CA	600	C
1	CA	606	G
1	CA	626	U
1	CA	630	G
1	CA	631	G
1	CA	633	G
1	CA	639	G

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Mol	Chain	Res	Type
1	CA	641	U
1	CA	650	G
1	CA	651	C
1	CA	653	A
1	CA	665	A
1	CA	673	G
1	CA	680	C
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	711	G
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	752	G
1	CA	755	G
1	CA	760	G
1	CA	774	G
1	CA	777	A
1	CA	786	G
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	802	A
1	CA	806	C
1	CA	812	C
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	818	G
1	CA	821	G
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	836	G
1	CA	839	U
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	855	G
1	CA	858	G

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Mol	Chain	Res	Type
1	CA	859	A
1	CA	873	A
1	CA	876	G
1	CA	902	G
1	CA	914	A
1	CA	916	G
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	935	A
1	CA	942	G
1	CA	958	A
1	CA	960	U
1	CA	961	U
1	CA	967	C
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	982	U
1	CA	983	A
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	995	C
1	CA	1001	A
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1007	C
1	CA	1011	G
1	CA	1013	G
1	CA	1014	A
1	CA	1019	C

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Mol	Chain	Res	Type
1	CA	1020	U
1	CA	1022	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1031	G
1	CA	1033	G
1	CA	1035	A
1	CA	1036	G
1	CA	1037	C
1	CA	1039	C
1	CA	1041	A
1	CA	1042	G
1	CA	1043	C
1	CA	1052	U
1	CA	1053	G
1	CA	1054	C
1	CA	1055	A
1	CA	1063	C
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1070	U
1	CA	1076	C
1	CA	1081	G
1	CA	1087	G
1	CA	1089	G
1	CA	1091	U
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1109	C
1	CA	1117	G
1	CA	1119	C

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Mol	Chain	Res	Type
1	CA	1120	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1128	C
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1134	G
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1141	C
1	CA	1145	C
1	CA	1146	A
1	CA	1147	C
1	CA	1151	A
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1159	U
1	CA	1160	G
1	CA	1161	C
1	CA	1163	C
1	CA	1171	G
1	CA	1173	G
1	CA	1176	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1189	C
1	CA	1193	G
1	CA	1196	U
1	CA	1197	G
1	CA	1200	C
1	CA	1202	G
1	CA	1204	A
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A

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Mol	Chain	Res	Type
1	CA	1214	C
1	CA	1223	C
1	CA	1224	G
1	CA	1227	A
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1250	A
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1259	C
1	CA	1260	C
1	CA	1262	C
1	CA	1270	C
1	CA	1271	G
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1283	G
1	CA	1284	C
1	CA	1287	A
1	CA	1297	C
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1311	G
1	CA	1314	C
1	CA	1317	C
1	CA	1320	C
1	CA	1322	C
1	CA	1323	G
1	CA	1338	G
1	CA	1340	A
1	CA	1343	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1354	C

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Mol	Chain	Res	Type
1	CA	1358	U
1	CA	1360	A
1	CA	1361	G
1	CA	1363	C
1	CA	1370	G
1	CA	1377	A
1	CA	1379	G
1	CA	1393	U
1	CA	1396	A
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1447	A
1	CA	1456	G
1	CA	1457	G
1	CA	1469	G
1	CA	1487	G
1	CA	1489	G
1	CA	1493	A
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1519	A
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	15	A
23	CX	6	G
23	CX	9	G
23	CX	13	C
23	CX	19	G
23	CX	20	U
23	CX	21	A

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Mol	Chain	Res	Type
23	CX	28	C
23	CX	31	G
23	CX	42	G
23	CX	47	U
23	CX	48	C
23	CX	60	U
23	CX	61	C
23	CX	68	C
23	CX	70	G
23	CX	76	A
25	DA	8	A
25	DA	10	G
25	DA	12	U
25	DA	15	G
25	DA	32	C
25	DA	34	C
25	DA	35	G
25	DA	36	G
25	DA	41	C
25	DA	45	C
25	DA	55	G
25	DA	61	G
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	83	G
25	DA	84	A
25	DA	90	U
25	DA	95	G
25	DA	100	G
25	DA	102	G
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	125	G
25	DA	133	C
25	DA	141	A
25	DA	149	A
25	DA	154(A)	C
25	DA	157	U
25	DA	173	G
25	DA	180	G

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Mol	Chain	Res	Type
25	DA	181	A
25	DA	182	A
25	DA	188	G
25	DA	196	A
25	DA	199	A
25	DA	205	G
25	DA	214	G
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	225	A
25	DA	229	A
25	DA	233	A
25	DA	248	G
25	DA	250	G
25	DA	266	G
25	DA	267	C
25	DA	271(E)	U
25	DA	271(H)	G
25	DA	271(J)	C
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	271(T)	C
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	277	C
25	DA	278	A
25	DA	292	C
25	DA	304	G
25	DA	311	A
25	DA	312	G
25	DA	324	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	333	G
25	DA	338	G
25	DA	339	U
25	DA	342	G

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Mol	Chain	Res	Type
25	DA	348	G
25	DA	351	G
25	DA	352	G
25	DA	363	G
25	DA	363(C)	G
25	DA	386	G
25	DA	396	G
25	DA	399	G
25	DA	405	U
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	415	A
25	DA	428	A
25	DA	437	G
25	DA	438	G
25	DA	443	A
25	DA	444	C
25	DA	454	A
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	480	A
25	DA	481	G
25	DA	504	U
25	DA	505	A
25	DA	509	C
25	DA	524	U
25	DA	527	C
25	DA	528	A
25	DA	529	A
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	545	G
25	DA	563	G
25	DA	568	U
25	DA	573	G
25	DA	575	A
25	DA	586	A

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Mol	Chain	Res	Type
25	DA	587	C
25	DA	592	G
25	DA	603	A
25	DA	604	G
25	DA	606	U
25	DA	607	U
25	DA	610	G
25	DA	614(B)	G
25	DA	614(C)	A
25	DA	615	G
25	DA	631	A
25	DA	634	C
25	DA	637	A
25	DA	645	C
25	DA	646	A
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	652(E)	G
25	DA	652(U)	G
25	DA	669	G
25	DA	670	A
25	DA	686	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	747	U
25	DA	749	C
25	DA	752	A
25	DA	753	C
25	DA	765	G
25	DA	771	G
25	DA	775	G
25	DA	776	G
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	790	C
25	DA	792	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U

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Mol	Chain	Res	Type
25	DA	854	G
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	867	C
25	DA	869	G
25	DA	871	U
25	DA	874	G
25	DA	878	A
25	DA	879	G
25	DA	880	G
25	DA	884	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C
25	DA	890	A
25	DA	895	U
25	DA	896	A
25	DA	897	C
25	DA	898	C
25	DA	899	A
25	DA	900	A
25	DA	901	A
25	DA	910	A
25	DA	911	A
25	DA	913	U
25	DA	914	C
25	DA	917	A
25	DA	923	C
25	DA	926	A
25	DA	932	G
25	DA	938	G
25	DA	941	A
25	DA	945	A
25	DA	946	G
25	DA	953	A
25	DA	957	A
25	DA	958	U
25	DA	959	A
25	DA	961	C
25	DA	974	G

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Mol	Chain	Res	Type
25	DA	975	C
25	DA	983	A
25	DA	996	A
25	DA	1010	A
25	DA	1012	U
25	DA	1013	C
25	DA	1020	A
25	DA	1022	G
25	DA	1023	U
25	DA	1025	G
25	DA	1027	A
25	DA	1033	U
25	DA	1034	G
25	DA	1038	C
25	DA	1039	G
25	DA	1040	C
25	DA	1041	C
25	DA	1043	C
25	DA	1114	G
25	DA	1115	G
25	DA	1118	C
25	DA	1119	C
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1142(A)	A
25	DA	1155	A
25	DA	1170	G
25	DA	1171	G
25	DA	1186	G
25	DA	1204	A
25	DA	1205	U
25	DA	1210	A
25	DA	1211	U
25	DA	1219	G
25	DA	1220	A
25	DA	1230	C
25	DA	1249	U
25	DA	1253	A
25	DA	1256	G
25	DA	1271	G

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Mol	Chain	Res	Type
25	DA	1272	A
25	DA	1273	U
25	DA	1284	A
25	DA	1287	A
25	DA	1300	U
25	DA	1301	A
25	DA	1313	U
25	DA	1314	C
25	DA	1315	C
25	DA	1321	A
25	DA	1332	G
25	DA	1345	C
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1366	A
25	DA	1368	G
25	DA	1370	C
25	DA	1380	G
25	DA	1384	A
25	DA	1385	G
25	DA	1386	C
25	DA	1395	A
25	DA	1403	C
25	DA	1410	G
25	DA	1411	C
25	DA	1416	G
25	DA	1417	C
25	DA	1419	A
25	DA	1420	U
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1437	C
25	DA	1445	A
25	DA	1445(A)	C
25	DA	1449	A
25	DA	1450	G
25	DA	1455	G
25	DA	1459	G
25	DA	1466	G
25	DA	1467	C

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Mol	Chain	Res	Type
25	DA	1471	A
25	DA	1482	G
25	DA	1490	A
25	DA	1492	G
25	DA	1493	C
25	DA	1495	A
25	DA	1496	A
25	DA	1497	U
25	DA	1504	C
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1531	C
25	DA	1541	G
25	DA	1542	A
25	DA	1543	C
25	DA	1547	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1580	A
25	DA	1586	A
25	DA	1588	C
25	DA	1595	G
25	DA	1598	C
25	DA	1603	A
25	DA	1608	A
25	DA	1609	A
25	DA	1610	A
25	DA	1613	G
25	DA	1618	A
25	DA	1625	C
25	DA	1631(A)	A
25	DA	1632	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1674	G
25	DA	1676	A

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Mol	Chain	Res	Type
25	DA	1682	G
25	DA	1696	G
25	DA	1700	A
25	DA	1701	A
25	DA	1703	G
25	DA	1718	G
25	DA	1721	G
25	DA	1722	A
25	DA	1740	G
25	DA	1746	G
25	DA	1756	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A
25	DA	1782	C
25	DA	1786	A
25	DA	1791	A
25	DA	1800	C
25	DA	1801	G
25	DA	1812	A
25	DA	1816	G
25	DA	1823	G
25	DA	1829	A
25	DA	1835	G
25	DA	1836	C
25	DA	1847	A
25	DA	1848	A
25	DA	1860	G
25	DA	1877	A
25	DA	1878	G
25	DA	1881	C
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1926	U
25	DA	1929	G
25	DA	1930	G
25	DA	1931	U
25	DA	1936	A

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Mol	Chain	Res	Type
25	DA	1938	A
25	DA	1955	U
25	DA	1960	A
25	DA	1963	U
25	DA	1966	A
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1984	G
25	DA	1993	U
25	DA	1997	G
25	DA	2005	A
25	DA	2020	A
25	DA	2021	C
25	DA	2023	G
25	DA	2031	A
25	DA	2032	G
25	DA	2033	A
25	DA	2034	U
25	DA	2039	C
25	DA	2043	C
25	DA	2049	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2069	G
25	DA	2076	U
25	DA	2082	A
25	DA	2093	G
25	DA	2097	C
25	DA	2099	U
25	DA	2101	G
25	DA	2189	U
25	DA	2192	G
25	DA	2193	G
25	DA	2198	A
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A

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Mol	Chain	Res	Type
25	DA	2218	U
25	DA	2219	G
25	DA	2225	A
25	DA	2235	G
25	DA	2238	G
25	DA	2239	G
25	DA	2243	U
25	DA	2251	G
25	DA	2267	A
25	DA	2268	A
25	DA	2269	A
25	DA	2275	C
25	DA	2278	A
25	DA	2279	G
25	DA	2283	C
25	DA	2286	A
25	DA	2287	A
25	DA	2289	G
25	DA	2291	U
25	DA	2298	A
25	DA	2303	G
25	DA	2305	A
25	DA	2308	G
25	DA	2312	U
25	DA	2318	G
25	DA	2319	G
25	DA	2320	A
25	DA	2321	G
25	DA	2325	G
25	DA	2327	A
25	DA	2334	G
25	DA	2335	A
25	DA	2336	A
25	DA	2343	C
25	DA	2347	C
25	DA	2348	U
25	DA	2359	C
25	DA	2376	A
25	DA	2383	G
25	DA	2384	G
25	DA	2385	C
25	DA	2388	A

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Mol	Chain	Res	Type
25	DA	2391	G
25	DA	2401	U
25	DA	2402	C
25	DA	2406	U
25	DA	2410	G
25	DA	2413	G
25	DA	2414	G
25	DA	2422	A
25	DA	2425	A
25	DA	2429	G
25	DA	2430	A
25	DA	2434	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2448	A
25	DA	2465	C
25	DA	2468	G
25	DA	2469	A
25	DA	2474	C
25	DA	2476	A
25	DA	2487	G
25	DA	2492	U
25	DA	2497	A
25	DA	2502	G
25	DA	2505	G
25	DA	2518	A
25	DA	2520	C
25	DA	2525	G
25	DA	2529	G
25	DA	2549	G
25	DA	2554	U
25	DA	2566	A
25	DA	2567	G
25	DA	2586	C
25	DA	2602	A
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2615	U
25	DA	2629	A
25	DA	2630	G

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Mol	Chain	Res	Type
25	DA	2632	A
25	DA	2654	A
25	DA	2663	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2717	G
25	DA	2726	U
25	DA	2733	A
25	DA	2751	G
25	DA	2752	C
25	DA	2757	A
25	DA	2758	A
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2779	U
25	DA	2780	G
25	DA	2789	C
25	DA	2793	G
25	DA	2802	G
25	DA	2803	C
25	DA	2804	C
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2872	G
25	DA	2879	C
25	DA	2880	C
25	DA	2892	A
25	DA	2893	G
25	DA	2894	G
25	DA	2895	U
25	DA	2897	U
26	DB	2	C

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Mol	Chain	Res	Type
26	DB	7	G
26	DB	8	U
26	DB	12	C
26	DB	13	A
26	DB	34	U
26	DB	42	C
26	DB	45	A
26	DB	46	A
26	DB	56	G
26	DB	59	A
26	DB	72	G
26	DB	73	A
26	DB	75	G
26	DB	85	G
26	DB	88	C
26	DB	89	G
26	DB	90	A
26	DB	93	G
26	DB	106	G
26	DB	110	G
26	DB	112	U
26	DB	116	G
26	DB	119	G

All (134) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	97	G
1	AA	115	G
1	AA	148	G
1	AA	266	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	793	U
1	AA	913	A
1	AA	991	U
1	AA	1027	C
1	AA	1042	G
1	AA	1054	C

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Mol	Chain	Res	Type
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1125	U
1	AA	1165	C
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
25	BA	70	A
25	BA	99	G
25	BA	184	A
25	BA	185	A
25	BA	273	G
25	BA	302	A
25	BA	553	A
25	BA	716	G
25	BA	732	A
25	BA	793	A
25	BA	811	A
25	BA	821	A
25	BA	874	U
25	BA	945	A
25	BA	990	A
25	BA	1003	U
25	BA	1019	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1425	A
25	BA	1466	U
25	BA	1507	A
25	BA	1577	C
25	BA	1654	A
25	BA	1655	A
25	BA	1700	G
25	BA	1793	A
25	BA	2014	G
25	BA	2228	G
25	BA	2347	A

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Mol	Chain	Res	Type
25	BA	2418	U
25	BA	2434	A
25	BA	2442	A
25	BA	2623	U
25	BA	2701	U
25	BA	2763	A
25	BA	2769	U
25	BA	2902	G
1	CA	4	U
1	CA	5	U
1	CA	65	U
1	CA	97	G
1	CA	115	G
1	CA	204	U
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	793	U
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1005	A
1	CA	1027	C
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1137	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1299	A
1	CA	1442	G
1	CA	1531	A
25	DA	195	A
25	DA	249	C
25	DA	271(M)	G

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Mol	Chain	Res	Type
25	DA	277	C
25	DA	310	A
25	DA	503	A
25	DA	528	A
25	DA	620	G
25	DA	669	G
25	DA	685	A
25	DA	752	A
25	DA	827	U
25	DA	856	C
25	DA	900	A
25	DA	1026	U
25	DA	1210	A
25	DA	1378	A
25	DA	1379	A
25	DA	1395	A
25	DA	1420	U
25	DA	1427	A
25	DA	1530	C
25	DA	1543	C
25	DA	1558	A
25	DA	1559	G
25	DA	1608	A
25	DA	1653	G
25	DA	1790	C
25	DA	1992	G
25	DA	2318	G
25	DA	2335	A
25	DA	2406	U
25	DA	2439	A
25	DA	2611	U
25	DA	2689	U
25	DA	2750	A
25	DA	2756	U
26	DB	45	A

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	2QZ	AW	1	24	8,8,9	6.07	2 (25%)	7,10,12	4.48	1 (14%)
24	2QY	AW	10	24	12,13,14	1.40	2 (16%)	13,16,18	2.74	4 (30%)
24	004	AW	3	24	10,10,11	6.58	3 (30%)	10,12,14	4.25	1 (10%)
24	MVA	AW	5	24	7,7,8	6.69	2 (28%)	5,8,10	1.83	1 (20%)
24	2R1	AW	6	24	9,10,11	2.24	4 (44%)	10,13,15	42.20	3 (30%)
24	2R3	AW	8	24	14,14,15	5.64	1 (7%)	16,18,20	1.98	7 (43%)
24	MVA	AW	9	24	7,7,8	5.33	2 (28%)	5,8,10	1.19	1 (20%)
24	2QZ	CW	1	24	8,8,9	6.20	2 (25%)	7,10,12	3.96	2 (28%)
24	2QY	CW	10	24	12,13,14	1.42	3 (25%)	13,16,18	2.11	2 (15%)
24	004	CW	3	24	10,10,11	5.93	3 (30%)	10,12,14	2.35	1 (10%)
24	MVA	CW	5	24	7,7,8	6.83	3 (42%)	5,8,10	1.21	1 (20%)
24	2R1	CW	6	24	9,10,11	2.27	3 (33%)	10,13,15	25.54	3 (30%)
24	2R3	CW	8	24	14,14,15	5.57	1 (7%)	16,18,20	1.81	6 (37%)
24	MVA	CW	9	24	7,7,8	6.38	3 (42%)	5,8,10	1.71	2 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	2QZ	AW	1	24	-	1/8/10/12	0/0/0/0
24	2QY	AW	10	24	-	1/5/8/10	0/1/1/1
24	004	AW	3	24	-	0/4/6/8	0/1/1/1
24	MVA	AW	5	24	-	1/6/8/10	0/0/0/0
24	2R1	AW	6	24	-	0/4/14/16	0/0/1/1
24	2R3	AW	8	24	-	0/10/12/14	0/1/1/1
24	MVA	AW	9	24	-	0/6/8/10	0/0/0/0
24	2QZ	CW	1	24	-	1/8/10/12	0/0/0/0
24	2QY	CW	10	24	-	0/5/8/10	0/1/1/1
24	004	CW	3	24	-	0/4/6/8	0/1/1/1
24	MVA	CW	5	24	-	0/6/8/10	0/0/0/0
24	2R1	CW	6	24	-	0/4/14/16	0/0/1/1
24	2R3	CW	8	24	-	0/10/12/14	0/1/1/1
24	MVA	CW	9	24	-	0/6/8/10	0/0/0/0

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AW	8	2R3	O-C	20.93	1.25	1.11
24	CW	8	2R3	O-C	20.69	1.25	1.11
24	AW	3	004	O-C	19.96	1.25	1.11
24	CW	5	MVA	O-C	17.69	1.23	1.11
24	AW	5	MVA	O-C	17.46	1.23	1.11
24	CW	1	2QZ	O-C	17.27	1.23	1.11
24	CW	3	004	O-C	17.26	1.23	1.11
24	AW	1	2QZ	O-C	16.80	1.23	1.11
24	CW	9	MVA	O-C	15.76	1.22	1.11
24	AW	9	MVA	O-C	13.82	1.20	1.11
24	CW	3	004	CB-CA	-5.74	1.49	1.52
24	CW	9	MVA	CB-CA	5.43	1.58	1.54
24	CW	6	2R1	CA-N	5.29	1.46	1.35
24	AW	3	004	CA-C	5.15	1.55	1.48
24	AW	6	2R1	CA-N	4.86	1.45	1.35
24	CW	3	004	CA-C	4.52	1.54	1.48
24	AW	1	2QZ	CA-C	3.08	1.55	1.49
24	CW	6	2R1	CG2-CB	-3.06	1.48	1.51
24	AW	10	2QY	CA-N	3.02	1.49	1.37
24	CW	10	2QY	CG-CB	3.00	1.53	1.46
24	CW	10	2QY	O-C	2.82	1.25	1.18
24	AW	3	004	CB-CA	-2.79	1.51	1.52
24	CW	6	2R1	O-C	2.72	1.25	1.18
24	AW	10	2QY	O-C	2.71	1.25	1.18
24	AW	6	2R1	O-C	2.70	1.25	1.18
24	AW	5	MVA	CA-C	2.64	1.54	1.49
24	CW	10	2QY	CA-N	2.62	1.47	1.37
24	CW	5	MVA	CB-CA	2.57	1.56	1.54
24	AW	6	2R1	CG2-CB	-2.38	1.49	1.51
24	CW	9	MVA	CA-C	2.38	1.54	1.49
24	AW	9	MVA	CA-C	2.37	1.54	1.49
24	CW	1	2QZ	CA-C	2.16	1.53	1.49
24	CW	5	MVA	CA-C	2.08	1.53	1.49
24	AW	6	2R1	OD1-CG1	2.02	1.55	1.42

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AW	6	2R1	CG1-CB-CA	132.32	125.12	119.61
24	CW	6	2R1	CG1-CB-CA	79.57	122.92	119.61
24	AW	6	2R1	OD2-CG2-CB	-16.77	88.98	112.43
24	CW	6	2R1	OD2-CG2-CB	-13.56	93.46	112.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AW	3	004	C-CA-N	-13.05	111.79	113.27
24	AW	1	2QZ	OG1-CB-CG2	11.36	142.97	109.72
24	CW	1	2QZ	OG1-CB-CG2	9.89	138.68	109.72
24	CW	3	004	C-CA-N	6.90	114.05	113.27
24	AW	10	2QY	CB-CA-N	6.48	132.28	121.57
24	CW	10	2QY	CB-CA-N	5.54	130.73	121.57
24	AW	10	2QY	CN-N-CA	-5.24	107.83	124.32
24	CW	10	2QY	CN-N-CA	-4.80	109.22	124.32
24	AW	10	2QY	CG-CB-CA	-3.91	123.86	130.63
24	CW	8	2R3	CB-CA-N	3.66	116.44	109.41
24	AW	8	2R3	OB-CB-CA	3.58	114.47	107.48
24	AW	5	MVA	CN-N-CA	3.52	124.49	114.39
24	AW	6	2R1	CG2-CB-CA	-3.51	118.45	123.55
24	AW	8	2R3	CB-CA-N	3.41	115.95	109.41
24	AW	8	2R3	CE2-CD2-CG	2.92	124.22	121.20
24	CW	8	2R3	CO-OH-CZ	-2.90	110.78	117.54
24	AW	8	2R3	C-CA-N	-2.80	107.38	111.94
24	AW	9	MVA	CN-N-CA	2.62	121.93	114.39
24	CW	8	2R3	CD2-CE2-CZ	-2.58	116.43	119.75
24	CW	9	MVA	CG2-CB-CA	2.55	114.26	111.38
24	CW	1	2QZ	CG2-CB-CA	-2.46	108.02	112.17
24	CW	8	2R3	CE2-CD2-CG	2.43	123.71	121.20
24	CW	9	MVA	CN-N-CA	2.32	121.07	114.39
24	CW	6	2R1	CB-CA-N	-2.26	120.04	123.13
24	AW	8	2R3	CD2-CE2-CZ	-2.18	116.95	119.75
24	CW	8	2R3	C-CA-N	-2.17	108.41	111.94
24	AW	10	2QY	CD2-CG-CD1	2.16	120.96	117.66
24	CW	8	2R3	OB-CB-CA	2.14	111.64	107.48
24	AW	8	2R3	CO-OH-CZ	-2.12	112.62	117.54
24	AW	8	2R3	CD1-CE1-CZ	2.09	122.43	119.75
24	CW	5	MVA	CB-CA-N	2.08	115.01	111.12

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	AW	1	2QZ	C-CA-N-CN1
24	CW	1	2QZ	C-CA-N-CN1
24	AW	5	MVA	CB-CA-N-CN
24	AW	10	2QY	CB-CA-N-CN

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1991 ligands modelled in this entry, 1987 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
57	SF4	AD	501	4	12,12,12	22.94	12 (100%)	0,24,24	0.00	-
59	FME	AX	101	23	9,9,10	6.44	3 (33%)	6,9,11	1.55	2 (33%)
57	SF4	CD	501	4	12,12,12	21.98	12 (100%)	0,24,24	0.00	-
59	FME	CX	101	23	9,9,10	6.95	3 (33%)	6,9,11	1.27	1 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SF4	AD	501	4	-	0/0/48/48	0/6/5/5
59	FME	AX	101	23	-	1/7/9/11	0/0/0/0
57	SF4	CD	501	4	-	0/0/48/48	0/6/5/5
59	FME	CX	101	23	-	1/7/9/11	0/0/0/0

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AD	501	SF4	S1-FE2	-24.75	2.16	2.33
57	AD	501	SF4	S3-FE4	-24.11	2.17	2.33
57	CD	501	SF4	S4-FE3	-24.04	2.17	2.33
57	CD	501	SF4	S2-FE1	-23.63	2.17	2.33
57	AD	501	SF4	S2-FE1	-23.62	2.17	2.33
57	AD	501	SF4	S4-FE1	-23.44	2.17	2.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	CD	501	SF4	S2-FE3	-23.41	2.17	2.33
57	CD	501	SF4	S3-FE4	-23.29	2.17	2.33
57	AD	501	SF4	S1-FE3	-23.22	2.17	2.33
57	AD	501	SF4	S1-FE4	-23.16	2.17	2.33
57	AD	501	SF4	S2-FE3	-23.11	2.17	2.33
57	AD	501	SF4	S4-FE3	-23.10	2.17	2.33
57	CD	501	SF4	S1-FE3	-22.72	2.18	2.33
57	AD	501	SF4	S3-FE2	-22.69	2.18	2.33
57	CD	501	SF4	S4-FE1	-22.38	2.18	2.33
57	CD	501	SF4	S1-FE2	-21.66	2.18	2.33
57	AD	501	SF4	S3-FE1	-21.56	2.18	2.33
57	CD	501	SF4	S3-FE1	-21.24	2.19	2.33
57	AD	501	SF4	S2-FE4	-21.11	2.19	2.33
57	AD	501	SF4	S4-FE2	-21.11	2.19	2.33
57	CD	501	SF4	S2-FE4	-21.08	2.19	2.33
57	CD	501	SF4	S4-FE2	-21.08	2.19	2.33
59	CX	101	FME	O-C	20.50	1.25	1.11
57	CD	501	SF4	S1-FE4	-20.12	2.19	2.33
59	AX	101	FME	O-C	18.92	1.24	1.11
57	CD	501	SF4	S3-FE2	-18.38	2.20	2.33
59	AX	101	FME	CA-C	2.82	1.55	1.49
59	CX	101	FME	CA-N	2.59	1.49	1.46
59	CX	101	FME	CA-C	2.46	1.54	1.49
59	AX	101	FME	CA-N	2.27	1.48	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AX	101	FME	CA-N-CN	-2.85	118.44	122.82
59	CX	101	FME	CA-N-CN	-2.17	119.49	122.82
59	AX	101	FME	CB-CA-N	2.10	114.90	111.26

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	AX	101	FME	O1-CN-N-CA
59	CX	101	FME	O1-CN-N-CA

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1498/1522 (98%)	-0.25	26 (1%) 67 15	36, 80, 103, 123	0
1	CA	1503/1522 (98%)	-0.27	22 (1%) 70 16	38, 80, 103, 122	0
2	AB	231/256 (90%)	-0.10	1 (0%) 90 45	71, 88, 98, 107	0
2	CB	231/256 (90%)	0.09	2 (0%) 81 25	71, 89, 99, 108	0
3	AC	206/239 (86%)	0.04	2 (0%) 79 23	74, 87, 96, 108	0
3	CC	206/239 (86%)	0.19	3 (1%) 70 16	75, 89, 98, 106	0
4	AD	208/209 (99%)	-0.02	1 (0%) 88 39	62, 80, 92, 99	0
4	CD	208/209 (99%)	-0.14	0 100 100	61, 79, 92, 99	0
5	AE	148/162 (91%)	-0.23	0 100 100	53, 73, 83, 96	0
5	CE	148/162 (91%)	-0.19	0 100 100	54, 74, 85, 98	0
6	AF	100/101 (99%)	-0.17	0 100 100	60, 78, 89, 92	0
6	CF	100/101 (99%)	-0.22	0 100 100	62, 79, 89, 94	0
7	AG	155/156 (99%)	0.17	5 (3%) 45 7	74, 85, 97, 104	0
7	CG	155/156 (99%)	0.18	4 (2%) 53 8	76, 86, 99, 105	0
8	AH	137/138 (99%)	-0.09	0 100 100	60, 75, 83, 90	0
8	CH	137/138 (99%)	-0.08	0 100 100	61, 76, 83, 90	0
9	AI	127/128 (99%)	0.27	0 100 100	70, 92, 99, 103	0
9	CI	127/128 (99%)	0.72	8 (6%) 19 3	69, 93, 100, 105	0
10	AJ	97/105 (92%)	0.34	1 (1%) 79 23	71, 93, 101, 106	0
10	CJ	96/105 (91%)	0.34	2 (2%) 60 11	75, 95, 102, 107	0
11	AK	114/129 (88%)	-0.24	0 100 100	53, 74, 88, 93	0
11	CK	114/129 (88%)	-0.16	0 100 100	54, 76, 88, 93	0
12	AL	122/132 (92%)	-0.14	0 100 100	56, 68, 80, 86	0
12	CL	122/132 (92%)	-0.11	0 100 100	55, 68, 79, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.21	4 (3%)	44	6	67, 83, 95, 104	0
13	CM	122/126 (96%)	0.41	7 (5%)	23	3	77, 91, 101, 105	0
14	AN	60/61 (98%)	0.07	1 (1%)	67	15	74, 85, 95, 97	0
14	CN	60/61 (98%)	0.34	1 (1%)	67	15	77, 88, 95, 100	0
15	AO	88/89 (98%)	-0.20	0	100	100	59, 73, 87, 94	0
15	CO	88/89 (98%)	-0.05	0	100	100	58, 73, 87, 95	0
16	AP	82/88 (93%)	0.22	0	100	100	66, 77, 88, 95	0
16	CP	82/88 (93%)	-0.05	0	100	100	66, 76, 89, 93	0
17	AQ	99/105 (94%)	0.00	0	100	100	59, 73, 84, 87	0
17	CQ	99/105 (94%)	-0.06	0	100	100	60, 73, 84, 85	0
18	AR	68/88 (77%)	0.13	0	100	100	66, 76, 86, 90	0
18	CR	68/88 (77%)	0.26	0	100	100	67, 77, 87, 89	0
19	AS	83/93 (89%)	0.39	0	100	100	79, 91, 100, 105	0
19	CS	83/93 (89%)	0.53	1 (1%)	75	20	82, 92, 102, 106	0
20	AT	96/106 (90%)	0.07	0	100	100	62, 75, 88, 91	0
20	CT	96/106 (90%)	0.01	0	100	100	62, 75, 86, 94	0
21	AU	23/27 (85%)	0.82	1 (4%)	34	5	76, 87, 90, 91	0
21	CU	23/27 (85%)	0.65	0	100	100	77, 87, 91, 92	0
22	AV	7/24 (29%)	0.03	0	100	100	61, 73, 97, 100	0
22	CV	6/24 (25%)	0.52	0	100	100	64, 75, 94, 103	0
23	AX	76/77 (98%)	-0.15	0	100	100	48, 79, 96, 101	0
23	CX	76/77 (98%)	-0.06	0	100	100	47, 81, 98, 101	0
24	AW	6/10 (60%)	-0.24	0	100	100	78, 83, 93, 96	0
24	CW	6/10 (60%)	-0.14	0	100	100	67, 77, 87, 96	0
25	BA	2731/2915 (93%)	-0.35	9 (0%)	91	53	24, 44, 86, 114	0
25	DA	2714/2915 (93%)	-0.54	13 (0%)	88	39	27, 48, 87, 118	0
26	BB	120/122 (98%)	-0.46	0	100	100	41, 68, 81, 96	0
26	DB	120/122 (98%)	-0.36	0	100	100	47, 73, 86, 98	0
27	BD	275/276 (99%)	-0.32	0	100	100	24, 41, 62, 85	0
27	DD	275/276 (99%)	-0.31	0	100	100	25, 44, 63, 86	0
28	BE	204/206 (99%)	-0.27	0	100	100	22, 45, 68, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
28	DE	204/206 (99%)	-0.31	0	100	100	24, 47, 70, 90	0
29	BF	203/210 (96%)	-0.24	0	100	100	24, 53, 77, 97	0
29	DF	203/210 (96%)	-0.29	0	100	100	25, 56, 79, 96	0
30	BG	181/182 (99%)	-0.25	0	100	100	61, 76, 89, 100	0
30	DG	181/182 (99%)	-0.01	0	100	100	65, 79, 91, 100	0
31	BH	174/180 (96%)	-0.22	0	100	100	49, 67, 81, 85	0
31	DH	174/180 (96%)	0.27	2 (1%)	77	22	54, 72, 85, 89	0
32	BI	146/148 (98%)	-0.11	0	100	100	49, 77, 88, 94	0
32	DI	146/148 (98%)	0.01	0	100	100	49, 78, 88, 94	0
33	BN	140/140 (100%)	-0.29	0	100	100	33, 48, 71, 78	0
33	DN	140/140 (100%)	-0.32	0	100	100	35, 52, 73, 81	0
34	BO	122/122 (100%)	-0.33	0	100	100	23, 40, 61, 76	0
34	DO	122/122 (100%)	-0.31	0	100	100	37, 53, 71, 80	0
35	BP	149/150 (99%)	-0.25	0	100	100	25, 54, 77, 83	0
35	DP	149/150 (99%)	-0.07	0	100	100	27, 57, 81, 87	0
36	BQ	141/141 (100%)	-0.23	0	100	100	36, 52, 68, 79	0
36	DQ	141/141 (100%)	-0.32	0	100	100	38, 55, 71, 81	0
37	BR	118/118 (100%)	-0.34	0	100	100	20, 35, 52, 64	0
37	DR	118/118 (100%)	-0.27	0	100	100	36, 52, 68, 84	0
38	BS	110/112 (98%)	-0.32	0	100	100	35, 54, 71, 85	0
38	DS	110/112 (98%)	0.13	0	100	100	65, 81, 92, 95	0
39	BT	131/146 (89%)	-0.34	0	100	100	31, 45, 75, 92	0
39	DT	131/146 (89%)	-0.30	0	100	100	45, 59, 80, 90	0
40	BU	116/118 (98%)	-0.45	0	100	100	21, 31, 52, 63	0
40	DU	116/118 (98%)	-0.29	1 (0%)	81	25	36, 61, 78, 92	0
41	BV	101/101 (100%)	-0.33	0	100	100	27, 53, 73, 80	0
41	DV	101/101 (100%)	-0.20	0	100	100	29, 58, 78, 80	0
42	BW	112/113 (99%)	-0.33	0	100	100	27, 38, 62, 92	0
42	DW	112/113 (99%)	-0.19	0	100	100	30, 42, 64, 94	0
43	BX	95/96 (98%)	-0.30	0	100	100	29, 47, 72, 81	0
43	DX	95/96 (98%)	-0.19	1 (1%)	77	22	33, 51, 73, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BY	107/110 (97%)	-0.10	0 100 100	39, 61, 80, 89	0
44	DY	107/110 (97%)	0.15	1 (0%) 81 25	43, 65, 82, 92	0
45	BZ	171/206 (83%)	-0.25	0 100 100	53, 71, 85, 96	0
45	DZ	174/206 (84%)	-0.08	0 100 100	58, 74, 87, 95	0
46	B0	83/85 (97%)	-0.07	6 (7%) 15 2	25, 39, 80, 108	0
46	D0	83/85 (97%)	0.20	4 (4%) 29 4	42, 66, 86, 104	0
47	B1	97/98 (98%)	-0.23	0 100 100	27, 44, 74, 83	0
47	D1	97/98 (98%)	-0.21	0 100 100	35, 58, 79, 86	0
48	B2	70/72 (97%)	-0.35	0 100 100	35, 48, 64, 90	0
48	D2	70/72 (97%)	-0.21	0 100 100	59, 74, 83, 92	0
49	B3	59/60 (98%)	-0.29	0 100 100	24, 38, 63, 85	0
49	D3	59/60 (98%)	0.19	0 100 100	45, 62, 80, 90	0
50	B4	69/71 (97%)	-0.13	0 100 100	60, 85, 103, 105	0
50	D4	69/71 (97%)	0.12	1 (1%) 72 17	82, 96, 106, 112	0
51	B5	59/60 (98%)	-0.42	0 100 100	14, 36, 59, 74	0
51	D5	59/60 (98%)	-0.37	0 100 100	31, 50, 72, 82	0
52	B6	53/54 (98%)	-0.27	0 100 100	43, 53, 68, 75	0
52	D6	53/54 (98%)	-0.22	0 100 100	45, 56, 69, 73	0
53	B7	48/49 (97%)	-0.19	0 100 100	24, 32, 62, 84	0
53	D7	48/49 (97%)	-0.18	1 (2%) 60 11	26, 35, 63, 86	0
54	B8	64/65 (98%)	-0.23	0 100 100	31, 42, 51, 64	0
54	D8	64/65 (98%)	-0.21	0 100 100	34, 46, 56, 66	0
55	B9	37/37 (100%)	0.08	0 100 100	43, 53, 71, 77	0
55	D9	37/37 (100%)	0.47	2 (5%) 25 4	46, 58, 73, 78	0
All	All	20468/21468 (95%)	-0.22	133 (0%) 86 36	14, 65, 95, 123	0

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	8.7
13	CM	123	ALA	7.7
13	AM	123	ALA	6.0
13	AM	124	PRO	5.9
1	CA	1030(B)	C	5.9

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Mol	Chain	Res	Type	RSRZ
13	CM	122	LYS	5.5
7	CG	78	ARG	4.9
46	B0	3	HIS	4.9
1	CA	1532	U	4.7
1	AA	1000	U	4.4
1	AA	1030(B)	C	4.4
9	CI	36	TYR	4.4
1	CA	1001(A)	G	4.3
13	AM	122	LYS	4.0
1	AA	202	U	3.9
1	AA	1036	G	3.9
1	CA	1002	G	3.8
7	AG	78	ARG	3.8
7	AG	79	ARG	3.8
25	DA	229	A	3.7
1	AA	1001(A)	G	3.7
46	B0	7	LEU	3.6
1	AA	1001	A	3.5
46	D0	3	HIS	3.5
25	BA	1555	C	3.5
13	CM	121	LYS	3.5
7	CG	79	ARG	3.4
1	AA	1028	C	3.4
9	CI	9	ARG	3.4
9	CI	30	GLY	3.4
1	AA	1002	G	3.4
1	AA	1030(C)	G	3.3
1	CA	1035	A	3.3
1	AA	1037	C	3.3
1	AA	204	U	3.3
1	CA	1030(C)	G	3.2
25	BA	2815	C	3.2
1	CA	1036	G	3.2
25	BA	2814	C	3.2
25	DA	2802	G	3.2
1	CA	1026	G	3.2
13	CM	120	LYS	3.1
25	BA	2807	C	3.1
1	CA	1034	G	3.0
25	DA	2793	G	3.0
19	CS	49	ILE	3.0
1	CA	1531	A	3.0

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Mol	Chain	Res	Type	RSRZ
2	AB	133	LYS	3.0
25	DA	652(B)	A	3.0
1	CA	1257	U	2.9
46	B0	5	LYS	2.8
25	DA	2803	C	2.8
3	AC	206	GLU	2.8
25	BA	935	C	2.8
13	AM	121	LYS	2.8
3	CC	159	GLY	2.8
1	AA	201	C	2.8
1	CA	1001	A	2.8
46	B0	6	GLY	2.8
1	CA	1040	U	2.8
1	CA	1030(A)	G	2.8
1	CA	1286	A	2.7
9	CI	62	TYR	2.7
1	AA	1026	G	2.7
3	CC	155	GLY	2.7
1	CA	1037	C	2.7
55	D9	13	LYS	2.7
25	BA	1221	G	2.6
1	AA	1257	U	2.6
50	D4	68	ARG	2.5
1	AA	1044	A	2.5
7	AG	85	TYR	2.5
25	DA	1509	C	2.5
40	DU	117	GLN	2.5
10	AJ	5	ARG	2.5
1	AA	1030	C	2.4
14	CN	17	LYS	2.4
7	AG	153	HIS	2.4
9	CI	7	THR	2.4
46	B0	8	GLY	2.4
9	CI	66	ARG	2.4
3	CC	160	ALA	2.4
7	CG	156	TRP	2.4
1	CA	1493	A	2.4
46	D0	8	GLY	2.4
1	AA	1029	C	2.4
25	BA	2806	G	2.4
1	AA	1137	C	2.4
25	DA	2188	C	2.4

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Mol	Chain	Res	Type	RSRZ
46	D0	76	GLY	2.4
7	AG	156	TRP	2.4
1	CA	1038	C	2.3
1	AA	1007	C	2.3
1	CA	1003	G	2.3
7	CG	4	ARG	2.3
1	AA	999	C	2.3
1	AA	1531	A	2.3
10	CJ	6	ILE	2.3
1	AA	1039	C	2.3
9	CI	10	ARG	2.2
9	CI	15	ALA	2.2
55	D9	12	ASP	2.2
1	CA	1030(D)	A	2.2
14	AN	17	LYS	2.2
25	DA	2794	C	2.2
13	CM	102	ARG	2.2
25	BA	2816	G	2.2
46	D0	5	LYS	2.2
53	D7	48	LYS	2.2
25	DA	2801(A)	A	2.2
43	DX	68	ARG	2.2
1	AA	1020	U	2.2
31	DH	103	LEU	2.2
1	AA	1031	G	2.1
4	AD	179	GLU	2.1
2	CB	232	PRO	2.1
1	CA	1033	G	2.1
1	AA	1038	C	2.1
10	CJ	20	ALA	2.1
46	B0	4	LYS	2.1
25	DA	2805	G	2.1
31	DH	112	PRO	2.1
1	AA	1027	C	2.1
44	DY	88	LYS	2.1
21	AU	18	TYR	2.1
3	AC	193	TYR	2.0
25	DA	879	G	2.0
25	DA	888	C	2.0
13	CM	110	ARG	2.0
25	DA	2792	G	2.0
2	CB	135	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1029	C	2.0
25	BA	2813	G	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
24	2R3	CW	8	14/15	0.11	-	47,70,74,79	0
24	MVA	CW	5	8/9	0.19	-	51,78,86,88	0
24	MVA	AW	9	8/9	0.24	-	65,78,87,91	0
24	2QZ	AW	1	9/10	0.23	-	58,64,81,82	0
24	MVA	CW	9	8/9	0.20	-	61,72,80,84	0
24	2QY	AW	10	13/14	0.13	-	55,67,75,79	0
24	2R1	AW	6	10/11	0.12	-	68,82,98,104	0
24	2R3	AW	8	14/15	0.13	-	54,79,87,90	0
24	MVA	AW	5	8/9	0.19	-	66,87,90,90	0
24	2QZ	CW	1	9/10	0.22	-	57,72,81,93	0
24	004	CW	3	10/11	0.14	-	60,76,84,86	0
24	2R1	CW	6	10/11	0.11	-	79,86,90,94	0
24	2QY	CW	10	13/14	0.14	-	55,69,84,94	0
24	004	AW	3	10/11	0.13	-	71,89,99,106	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(\AA^2)	Q<0.9
56	MG	CA	3155	1/1	0.14	-	71,71,71,71	0
56	MG	DB	3002	1/1	0.27	-	56,56,56,56	0
56	MG	DA	3246	1/1	0.17	-	24,24,24,24	0
56	MG	AA	3074	1/1	0.38	-	47,47,47,47	0
56	MG	BA	3041	1/1	0.37	-	32,32,32,32	0
56	MG	AA	3151	1/1	0.07	-	41,41,41,41	0
56	MG	BA	3001	1/1	0.16	-	69,69,69,69	0
56	MG	DA	3304	1/1	0.10	-	35,35,35,35	0
56	MG	DA	3499	1/1	0.14	-	46,46,46,46	0
56	MG	BA	3249	1/1	0.22	-	40,40,40,40	0
56	MG	BA	3251	1/1	0.21	-	61,61,61,61	0
56	MG	BA	3481	1/1	0.22	-	38,38,38,38	0
56	MG	DA	3369	1/1	0.14	-	47,47,47,47	0
56	MG	BA	3643	1/1	0.27	-	43,43,43,43	0
56	MG	BA	3404	1/1	0.15	-	35,35,35,35	0
56	MG	BA	3106	1/1	0.12	-	48,48,48,48	0
56	MG	BA	3004	1/1	0.12	-	24,24,24,24	0
56	MG	BA	3194	1/1	0.18	-	55,55,55,55	0
56	MG	AA	3023	1/1	0.17	-	65,65,65,65	0
56	MG	DA	3082	1/1	0.10	-	19,19,19,19	0
56	MG	BA	3586	1/1	0.19	-	29,29,29,29	0
56	MG	CA	3099	1/1	0.32	-	65,65,65,65	0
56	MG	DA	3089	1/1	0.38	-	57,57,57,57	0
56	MG	AA	3202	1/1	0.23	-	76,76,76,76	0
56	MG	DA	3190	1/1	0.12	-	37,37,37,37	0
56	MG	BA	3712	1/1	0.10	-	58,58,58,58	0
56	MG	BA	3162	1/1	0.19	-	23,23,23,23	0
56	MG	DF	303	1/1	0.34	-	43,43,43,43	0
56	MG	BA	3299	1/1	0.23	-	9,9,9,9	0
56	MG	BA	3241	1/1	0.38	-	63,63,63,63	0
56	MG	DA	3523	1/1	0.07	-	55,55,55,55	0
56	MG	DA	3595	1/1	0.18	-	72,72,72,72	0
56	MG	DA	3511	1/1	0.07	-	65,65,65,65	0
56	MG	BA	3053	1/1	0.34	-	39,39,39,39	0
56	MG	DA	3549	1/1	0.26	-	52,52,52,52	0
56	MG	AX	110	1/1	0.19	-	42,42,42,42	0
56	MG	BE	309	1/1	0.26	-	25,25,25,25	0
56	MG	DB	3004	1/1	0.15	-	68,68,68,68	0
56	MG	BA	3018	1/1	0.40	-	40,40,40,40	0
56	MG	BA	3113	1/1	0.08	-	32,32,32,32	0
56	MG	BA	3574	1/1	0.07	-	54,54,54,54	0
56	MG	DA	3612	1/1	0.14	-	39,39,39,39	0
56	MG	BA	3208	1/1	0.24	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3150	1/1	0.10	-	59,59,59,59	0
56	MG	DA	3323	1/1	0.18	-	30,30,30,30	0
56	MG	BA	3223	1/1	0.60	-	47,47,47,47	0
56	MG	CA	3015	1/1	0.35	-	51,51,51,51	0
56	MG	BA	3246	1/1	0.22	-	46,46,46,46	0
56	MG	DA	3481	1/1	0.28	-	47,47,47,47	0
56	MG	BA	3050	1/1	0.16	-	21,21,21,21	0
56	MG	BA	3312	1/1	0.09	-	58,58,58,58	0
56	MG	DA	3351	1/1	0.40	-	35,35,35,35	0
56	MG	BA	3242	1/1	0.33	-	48,48,48,48	0
58	ZN	DY	501	1/1	0.05	-	83,83,83,83	0
56	MG	AA	3021	1/1	0.23	-	76,76,76,76	0
56	MG	BE	306	1/1	0.44	-	46,46,46,46	0
56	MG	BA	3178	1/1	0.25	-	48,48,48,48	0
56	MG	BA	3119	1/1	0.25	-	58,58,58,58	0
56	MG	AA	3177	1/1	0.16	-	80,80,80,80	0
56	MG	BB	3006	1/1	0.24	-	39,39,39,39	0
56	MG	DA	3070	1/1	0.25	-	44,44,44,44	0
56	MG	BA	3459	1/1	0.21	-	31,31,31,31	0
56	MG	AA	3131	1/1	0.48	-	56,56,56,56	0
56	MG	BA	3294	1/1	0.29	-	37,37,37,37	0
56	MG	BA	3713	1/1	0.12	-	66,66,66,66	0
56	MG	BA	3135	1/1	0.16	-	42,42,42,42	0
56	MG	DA	3027	1/1	0.42	-	39,39,39,39	0
56	MG	AA	3087	1/1	0.43	-	72,72,72,72	0
56	MG	DA	3149	1/1	0.06	-	47,47,47,47	0
56	MG	DA	3017	1/1	0.18	-	46,46,46,46	0
56	MG	BA	3075	1/1	0.23	-	45,45,45,45	0
56	MG	BA	3719	1/1	0.24	-	25,25,25,25	0
56	MG	DA	3111	1/1	0.20	-	53,53,53,53	0
56	MG	DA	3495	1/1	0.23	-	39,39,39,39	0
56	MG	BA	3490	1/1	0.23	-	38,38,38,38	0
56	MG	BA	3056	1/1	0.41	-	44,44,44,44	0
56	MG	DA	3610	1/1	0.25	-	54,54,54,54	0
56	MG	BA	3128	1/1	0.30	-	40,40,40,40	0
56	MG	BA	3327	1/1	0.17	-	38,38,38,38	0
56	MG	BA	3254	1/1	0.16	-	59,59,59,59	0
56	MG	D5	101	1/1	0.44	-	53,53,53,53	0
56	MG	AA	3123	1/1	0.46	-	39,39,39,39	0
56	MG	DA	3095	1/1	0.24	-	61,61,61,61	0
59	FME	CX	101	10/11	0.58	-	71,82,97,105	0
56	MG	BA	3594	1/1	0.32	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3040	1/1	0.34	-	51,51,51,51	0
56	MG	AA	3103	1/1	0.20	-	38,38,38,38	0
56	MG	BA	3027	1/1	0.16	-	45,45,45,45	0
56	MG	BD	305	1/1	0.24	-	48,48,48,48	0
56	MG	DA	3505	1/1	0.06	-	65,65,65,65	0
56	MG	DA	3164	1/1	0.27	-	48,48,48,48	0
56	MG	BB	3016	1/1	0.12	-	21,21,21,21	0
56	MG	DA	3454	1/1	0.29	-	55,55,55,55	0
56	MG	BA	3191	1/1	0.18	-	52,52,52,52	0
56	MG	BA	3715	1/1	0.13	-	47,47,47,47	0
56	MG	DA	3456	1/1	0.13	-	47,47,47,47	0
56	MG	AA	3133	1/1	0.36	-	63,63,63,63	0
56	MG	AX	106	1/1	0.15	-	73,73,73,73	0
56	MG	BA	3686	1/1	0.13	-	25,25,25,25	0
56	MG	AA	3160	1/1	0.29	-	52,52,52,52	0
56	MG	BA	3700	1/1	0.12	-	67,67,67,67	0
56	MG	BA	3470	1/1	0.20	-	54,54,54,54	0
56	MG	BA	3488	1/1	0.34	-	35,35,35,35	0
56	MG	BA	3569	1/1	0.18	-	19,19,19,19	0
56	MG	DA	3036	1/1	0.30	-	35,35,35,35	0
56	MG	AA	3092	1/1	0.47	-	50,50,50,50	0
56	MG	BA	3396	1/1	0.18	-	22,22,22,22	0
56	MG	B7	103	1/1	0.92	-	48,48,48,48	0
56	MG	DA	3541	1/1	0.26	-	35,35,35,35	0
56	MG	BA	3533	1/1	0.15	-	32,32,32,32	0
56	MG	CA	3004	1/1	0.24	-	96,96,96,96	0
56	MG	DA	3566	1/1	0.15	-	71,71,71,71	0
56	MG	BA	3193	1/1	0.70	-	52,52,52,52	0
56	MG	AA	3053	1/1	0.34	-	49,49,49,49	0
56	MG	DA	3401	1/1	0.28	-	58,58,58,58	0
56	MG	AA	3128	1/1	0.21	-	68,68,68,68	0
56	MG	DV	202	1/1	0.80	-	63,63,63,63	0
56	MG	BA	3253	1/1	0.17	-	51,51,51,51	0
56	MG	DQ	204	1/1	0.16	-	43,43,43,43	0
56	MG	CA	3152	1/1	0.39	-	55,55,55,55	0
56	MG	DA	3178	1/1	0.36	-	43,43,43,43	0
56	MG	DD	308	1/1	0.16	-	55,55,55,55	0
56	MG	BA	3402	1/1	0.24	-	71,71,71,71	0
56	MG	CA	3112	1/1	0.23	-	59,59,59,59	0
56	MG	BW	203	1/1	0.28	-	45,45,45,45	0
56	MG	CA	3140	1/1	0.16	-	73,73,73,73	0
56	MG	DA	3065	1/1	0.22	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3130	1/1	0.45	-	43,43,43,43	0
56	MG	DA	3441	1/1	0.34	-	53,53,53,53	0
56	MG	BA	3549	1/1	0.21	-	27,27,27,27	0
56	MG	DA	3144	1/1	0.40	-	36,36,36,36	0
56	MG	AA	3034	1/1	0.17	-	48,48,48,48	0
56	MG	CE	3002	1/1	0.07	-	55,55,55,55	0
56	MG	DA	3421	1/1	0.21	-	34,34,34,34	0
56	MG	AA	3204	1/1	0.13	-	54,54,54,54	0
56	MG	AA	3024	1/1	0.17	-	53,53,53,53	0
56	MG	BA	3644	1/1	0.15	-	43,43,43,43	0
56	MG	BA	3116	1/1	0.19	-	31,31,31,31	0
56	MG	B5	502	1/1	0.11	-	54,54,54,54	0
56	MG	DA	3121	1/1	0.26	-	48,48,48,48	0
56	MG	BA	3167	1/1	0.33	-	39,39,39,39	0
56	MG	BA	3124	1/1	0.17	-	39,39,39,39	0
56	MG	DA	3571	1/1	0.13	-	46,46,46,46	0
56	MG	BP	203	1/1	0.68	-	29,29,29,29	0
56	MG	BA	3333	1/1	0.12	-	49,49,49,49	0
58	ZN	B9	501	1/1	0.10	-	48,48,48,48	0
56	MG	BA	3104	1/1	0.32	-	45,45,45,45	0
56	MG	DA	3615	1/1	0.40	-	60,60,60,60	0
56	MG	BA	3540	1/1	0.24	-	34,34,34,34	0
56	MG	BA	3391	1/1	0.14	-	48,48,48,48	0
56	MG	BA	3081	1/1	0.10	-	14,14,14,14	0
56	MG	DA	3232	1/1	0.23	-	50,50,50,50	0
56	MG	BA	3638	1/1	0.25	-	37,37,37,37	0
56	MG	BA	3301	1/1	0.13	-	56,56,56,56	0
56	MG	DA	3363	1/1	0.09	-	57,57,57,57	0
56	MG	BA	3716	1/1	0.11	-	27,27,27,27	0
56	MG	BA	3252	1/1	0.17	-	55,55,55,55	0
56	MG	DA	3476	1/1	0.20	-	45,45,45,45	0
56	MG	DA	3606	1/1	0.12	-	58,58,58,58	0
56	MG	BA	3108	1/1	0.14	-	55,55,55,55	0
56	MG	DA	3334	1/1	0.17	-	49,49,49,49	0
56	MG	BA	3090	1/1	0.18	-	46,46,46,46	0
56	MG	BA	3118	1/1	0.18	-	39,39,39,39	0
56	MG	AA	3088	1/1	0.33	-	63,63,63,63	0
56	MG	AX	109	1/1	0.08	-	43,43,43,43	0
60	K	DA	3231	1/1	0.29	-	96,96,96,96	0
56	MG	BA	3140	1/1	0.18	-	64,64,64,64	0
56	MG	BA	3679	1/1	0.38	-	27,27,27,27	0
56	MG	BA	3697	1/1	0.14	-	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3107	1/1	0.29	-	55,55,55,55	0
56	MG	CA	3169	1/1	0.17	-	57,57,57,57	0
56	MG	BA	3274	1/1	0.15	-	52,52,52,52	0
56	MG	BA	3534	1/1	0.12	-	41,41,41,41	0
56	MG	AA	3081	1/1	0.24	-	41,41,41,41	0
56	MG	BA	3581	1/1	0.10	-	51,51,51,51	0
56	MG	DA	3546	1/1	0.12	-	44,44,44,44	0
56	MG	AA	3216	1/1	0.14	-	58,58,58,58	0
56	MG	DA	3025	1/1	0.34	-	44,44,44,44	0
56	MG	BA	3381	1/1	0.10	-	37,37,37,37	0
56	MG	BA	3248	1/1	0.27	-	43,43,43,43	0
56	MG	DA	3151	1/1	0.29	-	60,60,60,60	0
56	MG	AA	3162	1/1	0.24	-	74,74,74,74	0
56	MG	DA	3594	1/1	0.34	-	47,47,47,47	0
56	MG	BA	3288	1/1	0.24	-	61,61,61,61	0
56	MG	BA	3365	1/1	0.14	-	20,20,20,20	0
56	MG	DA	3411	1/1	0.16	-	21,21,21,21	0
56	MG	DA	3307	1/1	0.28	-	37,37,37,37	0
56	MG	BA	3087	1/1	0.51	-	61,61,61,61	0
56	MG	AA	3112	1/1	0.17	-	51,51,51,51	0
56	MG	AA	3082	1/1	0.27	-	39,39,39,39	0
56	MG	CA	3063	1/1	0.11	-	61,61,61,61	0
56	MG	DA	3236	1/1	0.20	-	46,46,46,46	0
56	MG	BW	204	1/1	0.37	-	35,35,35,35	0
56	MG	DA	3413	1/1	0.23	-	53,53,53,53	0
56	MG	CA	3032	1/1	0.18	-	42,42,42,42	0
56	MG	CA	3028	1/1	0.40	-	43,43,43,43	0
56	MG	DA	3455	1/1	0.19	-	60,60,60,60	0
56	MG	AA	3069	1/1	0.12	-	84,84,84,84	0
56	MG	CA	3055	1/1	0.27	-	62,62,62,62	0
56	MG	BA	3065	1/1	0.41	-	50,50,50,50	0
56	MG	DA	3352	1/1	0.41	-	47,47,47,47	0
56	MG	CA	3057	1/1	0.24	-	49,49,49,49	0
56	MG	DA	3423	1/1	0.14	-	29,29,29,29	0
56	MG	BB	3002	1/1	0.20	-	59,59,59,59	0
56	MG	BA	3006	1/1	0.26	-	42,42,42,42	0
56	MG	AA	3039	1/1	0.20	-	60,60,60,60	0
56	MG	CA	3127	1/1	0.25	-	79,79,79,79	0
56	MG	BA	3061	1/1	0.47	-	51,51,51,51	0
56	MG	DA	3459	1/1	0.11	-	33,33,33,33	0
56	MG	DA	3488	1/1	0.05	-	46,46,46,46	0
56	MG	BA	3080	1/1	0.46	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3447	1/1	0.13	-	37,37,37,37	0
56	MG	BA	3625	1/1	0.13	-	51,51,51,51	0
56	MG	CA	3041	1/1	0.68	-	75,75,75,75	0
56	MG	BA	3455	1/1	0.13	-	47,47,47,47	0
56	MG	DA	3191	1/1	0.49	-	47,47,47,47	0
56	MG	BA	3539	1/1	0.16	-	35,35,35,35	0
56	MG	DA	3258	1/1	0.17	-	32,32,32,32	0
56	MG	AX	107	1/1	0.24	-	66,66,66,66	0
56	MG	BA	3261	1/1	0.28	-	34,34,34,34	0
56	MG	BD	307	1/1	0.19	-	43,43,43,43	0
56	MG	DA	3326	1/1	0.20	-	33,33,33,33	0
56	MG	BE	302	1/1	0.21	-	33,33,33,33	0
56	MG	AA	3209	1/1	0.31	-	70,70,70,70	0
56	MG	CA	3110	1/1	0.19	-	97,97,97,97	0
56	MG	BB	3014	1/1	0.12	-	69,69,69,69	0
56	MG	DA	3467	1/1	0.08	-	35,35,35,35	0
56	MG	CA	3019	1/1	0.07	-	49,49,49,49	0
56	MG	DA	3196	1/1	0.32	-	44,44,44,44	0
56	MG	AA	3015	1/1	0.13	-	73,73,73,73	0
56	MG	DA	3001	1/1	0.32	-	78,78,78,78	0
56	MG	DE	305	1/1	0.74	-	65,65,65,65	0
56	MG	DA	3439	1/1	0.18	-	28,28,28,28	0
56	MG	BU	208	1/1	0.93	-	56,56,56,56	0
56	MG	AA	3001	1/1	0.21	-	68,68,68,68	0
56	MG	BA	3409	1/1	0.21	-	27,27,27,27	0
56	MG	DA	3632	1/1	0.19	-	71,71,71,71	0
56	MG	BA	3271	1/1	0.14	-	36,36,36,36	0
56	MG	CA	3105	1/1	0.08	-	79,79,79,79	0
56	MG	DA	3184	1/1	0.33	-	45,45,45,45	0
56	MG	AA	3026	1/1	0.18	-	41,41,41,41	0
56	MG	BA	3629	1/1	0.14	-	47,47,47,47	0
56	MG	DA	3277	1/1	0.25	-	49,49,49,49	0
56	MG	BA	3069	1/1	0.41	-	41,41,41,41	0
56	MG	BA	3400	1/1	0.18	-	24,24,24,24	0
56	MG	DA	3212	1/1	0.09	-	48,48,48,48	0
56	MG	AA	3173	1/1	0.23	-	32,32,32,32	0
56	MG	BA	3278	1/1	0.17	-	34,34,34,34	0
56	MG	DA	3465	1/1	0.17	-	49,49,49,49	0
56	MG	DA	3135	1/1	0.21	-	50,50,50,50	0
56	MG	DA	3031	1/1	0.28	-	55,55,55,55	0
56	MG	BA	3688	1/1	0.10	-	54,54,54,54	0
56	MG	BA	3179	1/1	0.21	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3104	1/1	0.27	-	62,62,62,62	0
56	MG	B4	3001	1/1	0.24	-	100,100,100,100	0
56	MG	DA	3309	1/1	0.18	-	33,33,33,33	0
56	MG	BA	3567	1/1	0.22	-	37,37,37,37	0
56	MG	BA	3685	1/1	0.09	-	67,67,67,67	0
56	MG	AA	3156	1/1	0.19	-	62,62,62,62	0
56	MG	BA	3472	1/1	0.08	-	30,30,30,30	0
56	MG	BQ	201	1/1	0.51	-	61,61,61,61	0
56	MG	BA	3528	1/1	0.22	-	33,33,33,33	0
56	MG	BA	3012	1/1	0.16	-	40,40,40,40	0
56	MG	BA	3491	1/1	0.18	-	23,23,23,23	0
56	MG	CA	3091	1/1	0.15	-	72,72,72,72	0
56	MG	BA	3503	1/1	0.29	-	31,31,31,31	0
56	MG	BA	3291	1/1	0.17	-	41,41,41,41	0
56	MG	BQ	203	1/1	0.22	-	58,58,58,58	0
56	MG	AD	502	1/1	0.39	-	43,43,43,43	0
56	MG	AA	3067	1/1	0.40	-	87,87,87,87	0
56	MG	CA	3097	1/1	0.13	-	48,48,48,48	0
56	MG	B7	102	1/1	0.25	-	40,40,40,40	0
56	MG	DA	3448	1/1	0.07	-	57,57,57,57	0
56	MG	BA	3489	1/1	0.14	-	43,43,43,43	0
56	MG	DA	3186	1/1	0.45	-	53,53,53,53	0
56	MG	BA	3036	1/1	0.17	-	38,38,38,38	0
56	MG	DO	5001	1/1	0.12	-	35,35,35,35	0
56	MG	CA	3023	1/1	0.13	-	37,37,37,37	0
56	MG	BA	3667	1/1	0.09	-	63,63,63,63	0
56	MG	BA	3660	1/1	0.34	-	71,71,71,71	0
56	MG	CA	3133	1/1	0.06	-	49,49,49,49	0
56	MG	BA	3133	1/1	0.23	-	32,32,32,32	0
56	MG	DA	3366	1/1	0.37	-	36,36,36,36	0
56	MG	DA	3327	1/1	0.18	-	29,29,29,29	0
56	MG	BA	3550	1/1	0.24	-	45,45,45,45	0
56	MG	AA	3071	1/1	0.34	-	60,60,60,60	0
56	MG	BA	3627	1/1	0.20	-	50,50,50,50	0
56	MG	BV	204	1/1	0.19	-	20,20,20,20	0
56	MG	CA	3134	1/1	0.12	-	82,82,82,82	0
56	MG	BA	3484	1/1	0.16	-	54,54,54,54	0
56	MG	CA	3088	1/1	0.24	-	43,43,43,43	0
56	MG	BA	3026	1/1	0.43	-	36,36,36,36	0
56	MG	DA	3648	1/1	0.14	-	52,52,52,52	0
56	MG	BA	3462	1/1	0.10	-	52,52,52,52	0
56	MG	BA	3597	1/1	0.34	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3240	1/1	0.23	-	51,51,51,51	0
56	MG	BA	3482	1/1	0.17	-	72,72,72,72	0
56	MG	DA	3553	1/1	0.34	-	70,70,70,70	0
56	MG	BN	3001	1/1	0.74	-	54,54,54,54	0
56	MG	DB	3011	1/1	0.34	-	55,55,55,55	0
56	MG	AA	3076	1/1	0.31	-	66,66,66,66	0
56	MG	DA	3324	1/1	0.26	-	40,40,40,40	0
56	MG	BD	312	1/1	0.84	-	80,80,80,80	0
56	MG	BA	3446	1/1	0.12	-	49,49,49,49	0
56	MG	BA	3474	1/1	0.22	-	42,42,42,42	0
56	MG	BD	302	1/1	0.34	-	58,58,58,58	0
56	MG	CA	3102	1/1	0.09	-	41,41,41,41	0
56	MG	DA	3285	1/1	0.21	-	55,55,55,55	0
56	MG	BA	3738	1/1	0.29	-	59,59,59,59	0
56	MG	BA	3100	1/1	0.23	-	48,48,48,48	0
56	MG	AA	3002	1/1	0.19	-	57,57,57,57	0
56	MG	AA	3022	1/1	0.25	-	48,48,48,48	0
56	MG	DA	3078	1/1	0.20	-	44,44,44,44	0
56	MG	B7	104	1/1	0.13	-	51,51,51,51	0
56	MG	DA	3640	1/1	0.68	-	56,56,56,56	0
56	MG	CA	3080	1/1	0.15	-	55,55,55,55	0
56	MG	CA	3126	1/1	0.23	-	61,61,61,61	0
56	MG	BA	3367	1/1	0.09	-	50,50,50,50	0
56	MG	CA	3039	1/1	0.35	-	72,72,72,72	0
56	MG	DA	3302	1/1	0.17	-	22,22,22,22	0
56	MG	DA	3564	1/1	0.74	-	61,61,61,61	0
56	MG	DA	3464	1/1	0.61	-	50,50,50,50	0
56	MG	BA	3202	1/1	0.27	-	41,41,41,41	0
56	MG	CA	3136	1/1	0.20	-	45,45,45,45	0
56	MG	AA	3014	1/1	0.19	-	28,28,28,28	0
56	MG	DA	3247	1/1	0.09	-	31,31,31,31	0
56	MG	BE	301	1/1	0.50	-	43,43,43,43	0
56	MG	BA	3717	1/1	0.21	-	57,57,57,57	0
56	MG	DA	3555	1/1	0.13	-	41,41,41,41	0
56	MG	BA	3226	1/1	0.29	-	32,32,32,32	0
56	MG	DA	3322	1/1	0.14	-	55,55,55,55	0
56	MG	DA	3313	1/1	0.13	-	52,52,52,52	0
56	MG	BA	3126	1/1	0.21	-	24,24,24,24	0
56	MG	CA	3090	1/1	0.16	-	73,73,73,73	0
56	MG	AA	3064	1/1	0.17	-	79,79,79,79	0
56	MG	AA	3179	1/1	0.27	-	34,34,34,34	0
56	MG	DA	3311	1/1	0.10	-	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3515	1/1	0.06	-	56,56,56,56	0
56	MG	CA	3144	1/1	0.56	-	63,63,63,63	0
56	MG	BA	3681	1/1	0.14	-	40,40,40,40	0
56	MG	BA	3354	1/1	0.14	-	74,74,74,74	0
56	MG	AA	3104	1/1	0.17	-	37,37,37,37	0
56	MG	AA	3099	1/1	0.44	-	60,60,60,60	0
56	MG	DA	3122	1/1	0.14	-	62,62,62,62	0
56	MG	DA	3561	1/1	0.16	-	45,45,45,45	0
56	MG	AA	3150	1/1	0.27	-	46,46,46,46	0
56	MG	BB	3012	1/1	0.17	-	56,56,56,56	0
56	MG	BA	3541	1/1	0.22	-	30,30,30,30	0
56	MG	BN	3006	1/1	0.13	-	24,24,24,24	0
56	MG	DA	3654	1/1	0.19	-	52,52,52,52	0
56	MG	DA	3254	1/1	0.23	-	30,30,30,30	0
56	MG	DA	3368	1/1	0.11	-	39,39,39,39	0
56	MG	DA	3046	1/1	0.20	-	56,56,56,56	0
56	MG	BA	3458	1/1	0.12	-	29,29,29,29	0
56	MG	DA	3028	1/1	0.06	-	35,35,35,35	0
56	MG	BA	3382	1/1	0.13	-	51,51,51,51	0
56	MG	DA	3219	1/1	0.16	-	60,60,60,60	0
56	MG	AA	3142	1/1	0.26	-	38,38,38,38	0
56	MG	DA	3417	1/1	0.15	-	34,34,34,34	0
56	MG	DA	3043	1/1	0.45	-	54,54,54,54	0
56	MG	BA	3476	1/1	0.13	-	40,40,40,40	0
56	MG	DA	3379	1/1	0.22	-	28,28,28,28	0
56	MG	BR	203	1/1	0.20	-	15,15,15,15	0
56	MG	BA	3532	1/1	0.19	-	34,34,34,34	0
56	MG	BA	3257	1/1	0.33	-	38,38,38,38	0
56	MG	BA	3495	1/1	0.36	-	84,84,84,84	0
56	MG	DA	3494	1/1	0.09	-	78,78,78,78	0
56	MG	BA	3587	1/1	0.20	-	23,23,23,23	0
56	MG	DA	3038	1/1	0.15	-	39,39,39,39	0
56	MG	DA	3280	1/1	0.20	-	57,57,57,57	0
56	MG	BA	3115	1/1	0.29	-	36,36,36,36	0
56	MG	BA	3184	1/1	0.40	-	49,49,49,49	0
56	MG	BA	3255	1/1	0.18	-	41,41,41,41	0
56	MG	BA	3353	1/1	0.30	-	57,57,57,57	0
56	MG	BA	3121	1/1	0.27	-	57,57,57,57	0
56	MG	DA	3106	1/1	0.17	-	41,41,41,41	0
56	MG	BA	3282	1/1	0.41	-	49,49,49,49	0
56	MG	BA	3595	1/1	0.19	-	41,41,41,41	0
56	MG	AA	3080	1/1	0.17	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3624	1/1	0.24	-	52,52,52,52	0
56	MG	BA	3334	1/1	0.28	-	73,73,73,73	0
56	MG	DA	3428	1/1	0.27	-	51,51,51,51	0
56	MG	BA	3330	1/1	0.18	-	39,39,39,39	0
56	MG	CA	3073	1/1	0.31	-	55,55,55,55	0
56	MG	BA	3170	1/1	0.61	-	48,48,48,48	0
56	MG	CA	3131	1/1	0.11	-	55,55,55,55	0
56	MG	BA	3316	1/1	0.16	-	28,28,28,28	0
56	MG	DA	3158	1/1	0.37	-	57,57,57,57	0
56	MG	DA	3373	1/1	0.24	-	29,29,29,29	0
56	MG	DA	3550	1/1	0.16	-	53,53,53,53	0
56	MG	CA	3156	1/1	0.16	-	70,70,70,70	0
56	MG	DA	3453	1/1	0.39	-	61,61,61,61	0
56	MG	DA	3129	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3582	1/1	0.10	-	52,52,52,52	0
56	MG	DA	3222	1/1	0.13	-	71,71,71,71	0
56	MG	BA	3572	1/1	0.20	-	36,36,36,36	0
56	MG	CA	3067	1/1	0.30	-	80,80,80,80	0
56	MG	DA	3482	1/1	0.14	-	55,55,55,55	0
56	MG	BA	3201	1/1	0.31	-	36,36,36,36	0
56	MG	AA	3168	1/1	0.34	-	68,68,68,68	0
56	MG	BA	3479	1/1	0.11	-	56,56,56,56	0
56	MG	CA	3165	1/1	0.09	-	40,40,40,40	0
56	MG	AA	3038	1/1	0.33	-	66,66,66,66	0
56	MG	DA	3355	1/1	0.26	-	18,18,18,18	0
56	MG	DA	3256	1/1	0.18	-	63,63,63,63	0
56	MG	CA	3011	1/1	0.30	-	42,42,42,42	0
56	MG	AA	3097	1/1	0.23	-	43,43,43,43	0
56	MG	BA	3297	1/1	1.47	-	53,53,53,53	0
56	MG	B2	101	1/1	0.40	-	40,40,40,40	0
56	MG	CA	3035	1/1	0.23	-	52,52,52,52	0
56	MG	DA	3591	1/1	0.23	-	58,58,58,58	0
56	MG	BA	3439	1/1	0.15	-	34,34,34,34	0
56	MG	DA	3493	1/1	0.14	-	29,29,29,29	0
56	MG	DA	3003	1/1	0.36	-	56,56,56,56	0
56	MG	BA	3062	1/1	0.34	-	42,42,42,42	0
56	MG	CA	3093	1/1	0.06	-	53,53,53,53	0
56	MG	CA	3016	1/1	0.48	-	76,76,76,76	0
56	MG	DA	3384	1/1	0.12	-	23,23,23,23	0
56	MG	DA	3475	1/1	0.10	-	36,36,36,36	0
59	FME	AX	101	10/11	0.44	-	48,75,97,113	0
56	MG	DA	3187	1/1	0.49	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3444	1/1	0.14	-	43,43,43,43	0
56	MG	BU	205	1/1	0.32	-	42,42,42,42	0
56	MG	DA	3442	1/1	0.16	-	40,40,40,40	0
56	MG	BA	3142	1/1	0.72	-	46,46,46,46	0
56	MG	DA	3452	1/1	0.17	-	56,56,56,56	0
56	MG	DA	3156	1/1	0.57	-	29,29,29,29	0
56	MG	DA	3405	1/1	0.10	-	47,47,47,47	0
58	ZN	AN	102	1/1	0.11	-	90,90,90,90	0
56	MG	BA	3487	1/1	0.13	-	31,31,31,31	0
56	MG	DW	201	1/1	0.32	-	46,46,46,46	0
56	MG	BA	3412	1/1	0.18	-	26,26,26,26	0
56	MG	DA	3625	1/1	0.10	-	35,35,35,35	0
56	MG	BA	3077	1/1	0.20	-	39,39,39,39	0
56	MG	BA	3247	1/1	0.81	-	68,68,68,68	0
56	MG	DA	3193	1/1	0.21	-	65,65,65,65	0
56	MG	BA	3259	1/1	0.49	-	27,27,27,27	0
56	MG	CA	3162	1/1	0.22	-	46,46,46,46	0
56	MG	BA	3032	1/1	0.19	-	49,49,49,49	0
56	MG	CA	3074	1/1	0.20	-	54,54,54,54	0
56	MG	AA	3186	1/1	0.06	-	49,49,49,49	0
56	MG	DA	3055	1/1	0.24	-	48,48,48,48	0
56	MG	CA	3002	1/1	0.06	-	62,62,62,62	0
56	MG	CA	3151	1/1	0.24	-	80,80,80,80	0
56	MG	CA	3095	1/1	0.12	-	39,39,39,39	0
56	MG	BA	3044	1/1	0.29	-	42,42,42,42	0
56	MG	BA	3702	1/1	0.13	-	56,56,56,56	0
56	MG	DA	3593	1/1	0.25	-	73,73,73,73	0
56	MG	BA	3157	1/1	0.45	-	63,63,63,63	0
56	MG	AA	3107	1/1	0.26	-	44,44,44,44	0
56	MG	DA	3468	1/1	0.14	-	48,48,48,48	0
56	MG	DA	3039	1/1	0.35	-	59,59,59,59	0
56	MG	CA	3060	1/1	0.37	-	43,43,43,43	0
56	MG	DA	3367	1/1	0.24	-	42,42,42,42	0
56	MG	BA	3655	1/1	0.18	-	52,52,52,52	0
56	MG	BA	3600	1/1	0.18	-	47,47,47,47	0
56	MG	BA	3302	1/1	0.14	-	27,27,27,27	0
56	MG	BA	3375	1/1	0.22	-	31,31,31,31	0
56	MG	BA	3730	1/1	0.67	-	45,45,45,45	0
56	MG	BA	3307	1/1	0.23	-	33,33,33,33	0
56	MG	DF	305	1/1	0.78	-	39,39,39,39	0
56	MG	DY	502	1/1	0.09	-	60,60,60,60	0
56	MG	AA	3050	1/1	0.48	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3252	1/1	0.12	-	45,45,45,45	0
56	MG	DA	3002	1/1	0.20	-	55,55,55,55	0
56	MG	DA	3643	1/1	0.68	-	53,53,53,53	0
56	MG	DA	3614	1/1	0.21	-	48,48,48,48	0
56	MG	BA	3019	1/1	0.18	-	39,39,39,39	0
56	MG	DA	3331	1/1	0.10	-	34,34,34,34	0
56	MG	AA	3056	1/1	0.19	-	39,39,39,39	0
56	MG	DA	3177	1/1	0.07	-	33,33,33,33	0
56	MG	BA	3153	1/1	0.33	-	35,35,35,35	0
56	MG	CA	3086	1/1	0.22	-	80,80,80,80	0
56	MG	DA	3040	1/1	0.11	-	42,42,42,42	0
56	MG	BA	3608	1/1	0.16	-	68,68,68,68	0
56	MG	BA	3310	1/1	0.16	-	13,13,13,13	0
56	MG	BA	3692	1/1	0.37	-	36,36,36,36	0
56	MG	DA	3221	1/1	0.19	-	49,49,49,49	0
56	MG	BA	3410	1/1	0.13	-	27,27,27,27	0
56	MG	BA	3438	1/1	0.21	-	30,30,30,30	0
56	MG	CA	3062	1/1	0.23	-	57,57,57,57	0
56	MG	BA	3147	1/1	0.23	-	46,46,46,46	0
56	MG	DA	3601	1/1	0.12	-	77,77,77,77	0
56	MG	BB	3001	1/1	0.17	-	54,54,54,54	0
56	MG	BO	201	1/1	0.15	-	70,70,70,70	0
56	MG	DA	3068	1/1	0.30	-	55,55,55,55	0
56	MG	DA	3638	1/1	0.30	-	62,62,62,62	0
56	MG	DA	3018	1/1	0.51	-	48,48,48,48	0
56	MG	DA	3650	1/1	0.60	-	48,48,48,48	0
56	MG	BA	3721	1/1	0.08	-	25,25,25,25	0
56	MG	BA	3204	1/1	0.39	-	25,25,25,25	0
56	MG	DA	3119	1/1	0.15	-	44,44,44,44	0
56	MG	DF	306	1/1	0.28	-	50,50,50,50	0
56	MG	DA	3317	1/1	0.11	-	32,32,32,32	0
56	MG	DA	3472	1/1	0.15	-	36,36,36,36	0
56	MG	DA	3103	1/1	0.87	-	48,48,48,48	0
56	MG	BA	3699	1/1	0.54	-	56,56,56,56	0
56	MG	DA	3338	1/1	0.13	-	29,29,29,29	0
56	MG	BA	3622	1/1	0.53	-	77,77,77,77	0
56	MG	BA	3139	1/1	0.28	-	51,51,51,51	0
56	MG	DA	3312	1/1	0.28	-	43,43,43,43	0
56	MG	BA	3029	1/1	0.40	-	53,53,53,53	0
56	MG	DA	3080	1/1	0.12	-	44,44,44,44	0
56	MG	BE	307	1/1	0.26	-	39,39,39,39	0
56	MG	DA	3227	1/1	0.13	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
56	MG	BA	3163	1/1	0.18	-	50,50,50,50	0
56	MG	AA	3046	1/1	0.14	-	73,73,73,73	0
56	MG	AA	3148	1/1	0.20	-	66,66,66,66	0
56	MG	AA	3200	1/1	0.26	-	68,68,68,68	0
56	MG	DA	3530	1/1	0.16	-	49,49,49,49	0
56	MG	DA	3054	1/1	0.11	-	51,51,51,51	0
56	MG	DA	3604	1/1	0.18	-	54,54,54,54	0
56	MG	BA	3519	1/1	0.15	-	39,39,39,39	0
56	MG	BA	3422	1/1	0.22	-	42,42,42,42	0
56	MG	AA	3143	1/1	0.10	-	45,45,45,45	0
56	MG	DA	3424	1/1	0.22	-	30,30,30,30	0
56	MG	BA	3607	1/1	0.47	-	53,53,53,53	0
56	MG	DA	3297	1/1	0.14	-	57,57,57,57	0
56	MG	AA	3054	1/1	0.24	-	45,45,45,45	0
56	MG	BA	3669	1/1	0.26	-	75,75,75,75	0
56	MG	DA	3265	1/1	0.25	-	51,51,51,51	0
56	MG	BA	3656	1/1	0.12	-	33,33,33,33	0
56	MG	DA	3596	1/1	0.08	-	67,67,67,67	0
56	MG	AA	3221	1/1	0.10	-	64,64,64,64	0
56	MG	BA	3535	1/1	0.18	-	37,37,37,37	0
56	MG	BA	3093	1/1	0.21	-	25,25,25,25	0
56	MG	BA	3394	1/1	0.13	-	49,49,49,49	0
56	MG	DA	3161	1/1	0.30	-	60,60,60,60	0
56	MG	BA	3529	1/1	0.21	-	35,35,35,35	0
56	MG	DA	3199	1/1	0.12	-	42,42,42,42	0
56	MG	AA	3164	1/1	0.38	-	69,69,69,69	0
56	MG	BQ	202	1/1	0.29	-	28,28,28,28	0
56	MG	BA	3445	1/1	0.21	-	25,25,25,25	0
56	MG	AA	3012	1/1	0.15	-	56,56,56,56	0
56	MG	BA	3374	1/1	0.21	-	44,44,44,44	0
56	MG	DA	3274	1/1	0.11	-	52,52,52,52	0
56	MG	DA	3132	1/1	0.75	-	54,54,54,54	0
56	MG	BA	3078	1/1	0.28	-	17,17,17,17	0
56	MG	BA	3185	1/1	0.21	-	47,47,47,47	0
56	MG	DA	3004	1/1	0.20	-	29,29,29,29	0
56	MG	DA	3173	1/1	0.43	-	39,39,39,39	0
56	MG	BA	3348	1/1	0.20	-	64,64,64,64	0
56	MG	CA	3026	1/1	0.08	-	52,52,52,52	0
56	MG	DA	3079	1/1	0.21	-	37,37,37,37	0
56	MG	BA	3578	1/1	0.31	-	54,54,54,54	0
56	MG	BA	3514	1/1	0.14	-	37,37,37,37	0
56	MG	AA	3055	1/1	0.20	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3407	1/1	0.23	-	21,21,21,21	0
56	MG	BA	3573	1/1	0.14	-	56,56,56,56	0
56	MG	AA	3145	1/1	0.26	-	63,63,63,63	0
56	MG	BA	3161	1/1	0.69	-	49,49,49,49	0
56	MG	AN	101	1/1	0.20	-	63,63,63,63	0
56	MG	DA	3275	1/1	0.10	-	38,38,38,38	0
56	MG	BA	3361	1/1	0.25	-	34,34,34,34	0
56	MG	BE	308	1/1	0.17	-	52,52,52,52	0
56	MG	DA	3162	1/1	0.17	-	71,71,71,71	0
56	MG	DD	302	1/1	0.22	-	46,46,46,46	0
56	MG	CA	3111	1/1	0.12	-	64,64,64,64	0
56	MG	DA	3629	1/1	0.16	-	19,19,19,19	0
56	MG	CA	3034	1/1	0.23	-	65,65,65,65	0
56	MG	BF	303	1/1	0.21	-	36,36,36,36	0
56	MG	DA	3134	1/1	0.23	-	46,46,46,46	0
56	MG	CA	3164	1/1	0.39	-	49,49,49,49	0
56	MG	BA	3691	1/1	0.37	-	49,49,49,49	0
56	MG	AA	3083	1/1	0.08	-	65,65,65,65	0
56	MG	DA	3592	1/1	0.18	-	65,65,65,65	0
56	MG	AA	3049	1/1	0.50	-	51,51,51,51	0
58	ZN	CN	501	1/1	0.11	-	108,108,108,108	0
56	MG	BF	306	1/1	0.19	-	37,37,37,37	0
56	MG	DA	3030	1/1	0.33	-	51,51,51,51	0
56	MG	BA	3726	1/1	0.42	-	47,47,47,47	0
56	MG	AA	3100	1/1	0.69	-	40,40,40,40	0
56	MG	DA	3139	1/1	0.17	-	40,40,40,40	0
56	MG	BA	3114	1/1	0.34	-	51,51,51,51	0
56	MG	AA	3161	1/1	0.13	-	72,72,72,72	0
56	MG	BA	3565	1/1	0.10	-	55,55,55,55	0
56	MG	BP	204	1/1	0.19	-	55,55,55,55	0
56	MG	BA	3451	1/1	0.29	-	28,28,28,28	0
56	MG	AA	3201	1/1	0.12	-	67,67,67,67	0
56	MG	BA	3633	1/1	0.10	-	58,58,58,58	0
56	MG	DA	3225	1/1	0.15	-	45,45,45,45	0
56	MG	BA	3398	1/1	0.12	-	41,41,41,41	0
56	MG	AX	108	1/1	0.22	-	61,61,61,61	0
56	MG	BA	3457	1/1	0.10	-	57,57,57,57	0
56	MG	BA	3345	1/1	0.21	-	33,33,33,33	0
56	MG	BA	3509	1/1	0.16	-	27,27,27,27	0
56	MG	CA	3147	1/1	0.27	-	66,66,66,66	0
56	MG	BA	3362	1/1	0.09	-	43,43,43,43	0
56	MG	DA	3042	1/1	0.26	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3435	1/1	0.21	-	24,24,24,24	0
56	MG	DA	3608	1/1	0.28	-	57,57,57,57	0
56	MG	BA	3433	1/1	0.22	-	39,39,39,39	0
56	MG	DA	3215	1/1	0.31	-	29,29,29,29	0
56	MG	DA	3192	1/1	0.12	-	47,47,47,47	0
56	MG	BA	3144	1/1	0.28	-	74,74,74,74	0
56	MG	BA	3319	1/1	0.17	-	25,25,25,25	0
56	MG	BA	3105	1/1	0.45	-	34,34,34,34	0
56	MG	BA	3709	1/1	0.12	-	86,86,86,86	0
56	MG	DA	3558	1/1	0.19	-	37,37,37,37	0
56	MG	DA	3627	1/1	0.20	-	43,43,43,43	0
56	MG	DA	3374	1/1	0.05	-	37,37,37,37	0
56	MG	DB	3008	1/1	0.08	-	45,45,45,45	0
56	MG	DA	3589	1/1	0.18	-	59,59,59,59	0
56	MG	DA	3182	1/1	0.15	-	32,32,32,32	0
56	MG	BA	3366	1/1	0.09	-	63,63,63,63	0
56	MG	AA	3170	1/1	0.19	-	101,101,101,101	0
56	MG	CA	3113	1/1	0.26	-	77,77,77,77	0
56	MG	CA	3047	1/1	0.14	-	63,63,63,63	0
56	MG	DA	3230	1/1	0.14	-	62,62,62,62	0
56	MG	BF	301	1/1	0.59	-	45,45,45,45	0
56	MG	CA	3121	1/1	0.29	-	53,53,53,53	0
56	MG	DA	3242	1/1	0.23	-	35,35,35,35	0
56	MG	BQ	204	1/1	0.17	-	12,12,12,12	0
56	MG	DA	3321	1/1	0.23	-	41,41,41,41	0
56	MG	BA	3063	1/1	0.25	-	43,43,43,43	0
56	MG	BA	3718	1/1	0.38	-	57,57,57,57	0
56	MG	AA	3098	1/1	0.31	-	72,72,72,72	0
56	MG	DA	3244	1/1	0.30	-	29,29,29,29	0
56	MG	BA	3125	1/1	0.20	-	39,39,39,39	0
56	MG	BA	3584	1/1	0.18	-	22,22,22,22	0
56	MG	AA	3198	1/1	0.12	-	87,87,87,87	0
56	MG	DA	3484	1/1	0.25	-	51,51,51,51	0
56	MG	DA	3176	1/1	0.28	-	39,39,39,39	0
56	MG	BA	3338	1/1	0.20	-	50,50,50,50	0
56	MG	BF	308	1/1	0.25	-	28,28,28,28	0
56	MG	DA	3517	1/1	0.20	-	50,50,50,50	0
56	MG	AA	3091	1/1	0.13	-	75,75,75,75	0
56	MG	AA	3190	1/1	0.32	-	67,67,67,67	0
56	MG	BA	3486	1/1	0.06	-	38,38,38,38	0
56	MG	CA	3014	1/1	0.18	-	50,50,50,50	0
56	MG	DA	3419	1/1	0.17	-	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3373	1/1	0.28	-	36,36,36,36	0
56	MG	DB	3012	1/1	0.29	-	59,59,59,59	0
56	MG	BA	3507	1/1	0.08	-	68,68,68,68	0
56	MG	AA	3155	1/1	0.15	-	70,70,70,70	0
56	MG	AA	3208	1/1	0.35	-	46,46,46,46	0
56	MG	AA	3206	1/1	0.07	-	70,70,70,70	0
56	MG	DA	3519	1/1	0.14	-	44,44,44,44	0
56	MG	BA	3710	1/1	0.20	-	48,48,48,48	0
56	MG	DD	305	1/1	0.66	-	49,49,49,49	0
56	MG	DA	3479	1/1	0.23	-	57,57,57,57	0
56	MG	CA	3107	1/1	0.12	-	60,60,60,60	0
56	MG	BA	3623	1/1	0.24	-	47,47,47,47	0
56	MG	CA	3027	1/1	0.16	-	57,57,57,57	0
56	MG	DA	3399	1/1	0.18	-	41,41,41,41	0
56	MG	DA	3283	1/1	0.16	-	33,33,33,33	0
56	MG	CA	3005	1/1	0.29	-	54,54,54,54	0
56	MG	BA	3552	1/1	0.23	-	29,29,29,29	0
56	MG	BA	3020	1/1	0.11	-	45,45,45,45	0
56	MG	BA	3545	1/1	0.24	-	47,47,47,47	0
56	MG	AA	3172	1/1	0.07	-	53,53,53,53	0
56	MG	DA	3267	1/1	0.16	-	61,61,61,61	0
56	MG	DA	3229	1/1	0.14	-	40,40,40,40	0
56	MG	BA	3152	1/1	0.34	-	46,46,46,46	0
56	MG	DA	3200	1/1	0.18	-	42,42,42,42	0
56	MG	DA	3616	1/1	0.21	-	62,62,62,62	0
56	MG	BA	3576	1/1	0.26	-	23,23,23,23	0
56	MG	DB	3009	1/1	0.36	-	40,40,40,40	0
56	MG	BA	3428	1/1	0.12	-	45,45,45,45	0
56	MG	DA	3072	1/1	0.14	-	41,41,41,41	0
56	MG	DA	3233	1/1	0.19	-	42,42,42,42	0
56	MG	DA	3086	1/1	0.29	-	43,43,43,43	0
56	MG	DA	3291	1/1	0.26	-	35,35,35,35	0
56	MG	BA	3303	1/1	0.17	-	35,35,35,35	0
56	MG	DQ	201	1/1	0.35	-	48,48,48,48	0
56	MG	BA	3442	1/1	0.15	-	12,12,12,12	0
56	MG	B1	3001	1/1	0.86	-	54,54,54,54	0
56	MG	CA	3154	1/1	0.16	-	49,49,49,49	0
56	MG	AA	3063	1/1	0.31	-	61,61,61,61	0
56	MG	DA	3090	1/1	0.29	-	47,47,47,47	0
56	MG	BA	3092	1/1	0.26	-	51,51,51,51	0
56	MG	CA	3072	1/1	0.23	-	38,38,38,38	0
56	MG	DA	3114	1/1	0.18	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3387	1/1	0.13	-	56,56,56,56	0
56	MG	DA	3118	1/1	0.09	-	39,39,39,39	0
56	MG	CA	3141	1/1	0.25	-	70,70,70,70	0
56	MG	BA	3230	1/1	0.50	-	46,46,46,46	0
56	MG	BA	3536	1/1	0.13	-	27,27,27,27	0
56	MG	BA	3143	1/1	0.32	-	40,40,40,40	0
56	MG	DA	3370	1/1	0.17	-	38,38,38,38	0
56	MG	BU	207	1/1	0.19	-	40,40,40,40	0
56	MG	DA	3133	1/1	0.16	-	33,33,33,33	0
56	MG	BD	303	1/1	0.24	-	42,42,42,42	0
56	MG	DA	3460	1/1	0.35	-	50,50,50,50	0
56	MG	DA	3600	1/1	0.07	-	45,45,45,45	0
56	MG	BA	3122	1/1	0.25	-	52,52,52,52	0
56	MG	DA	3102	1/1	0.26	-	41,41,41,41	0
56	MG	AA	3030	1/1	0.30	-	69,69,69,69	0
56	MG	AA	3078	1/1	0.28	-	42,42,42,42	0
56	MG	BA	3494	1/1	0.32	-	18,18,18,18	0
56	MG	BA	3324	1/1	0.17	-	36,36,36,36	0
56	MG	BA	3668	1/1	0.13	-	38,38,38,38	0
56	MG	BA	3030	1/1	0.42	-	51,51,51,51	0
56	MG	BA	3222	1/1	0.30	-	25,25,25,25	0
56	MG	DA	3611	1/1	0.08	-	42,42,42,42	0
56	MG	CA	3132	1/1	0.11	-	70,70,70,70	0
56	MG	BA	3577	1/1	0.10	-	52,52,52,52	0
56	MG	BA	3048	1/1	0.23	-	31,31,31,31	0
56	MG	BD	310	1/1	0.31	-	48,48,48,48	0
56	MG	DA	3535	1/1	0.19	-	33,33,33,33	0
56	MG	BA	3173	1/1	0.61	-	37,37,37,37	0
56	MG	BA	3452	1/1	0.25	-	47,47,47,47	0
56	MG	DA	3398	1/1	0.15	-	35,35,35,35	0
56	MG	BA	3192	1/1	0.53	-	58,58,58,58	0
56	MG	DA	3310	1/1	0.20	-	53,53,53,53	0
56	MG	DA	3015	1/1	0.23	-	49,49,49,49	0
56	MG	DA	3409	1/1	0.13	-	32,32,32,32	0
56	MG	DE	301	1/1	0.61	-	51,51,51,51	0
56	MG	DA	3058	1/1	0.43	-	47,47,47,47	0
56	MG	DA	3463	1/1	0.34	-	43,43,43,43	0
56	MG	DA	3051	1/1	0.12	-	46,46,46,46	0
56	MG	CA	3100	1/1	0.13	-	60,60,60,60	0
56	MG	BA	3187	1/1	0.66	-	50,50,50,50	0
56	MG	BA	3296	1/1	0.23	-	46,46,46,46	0
56	MG	DA	3362	1/1	0.12	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3520	1/1	0.15	-	34,34,34,34	0
56	MG	DA	3120	1/1	0.78	-	51,51,51,51	0
56	MG	CA	3089	1/1	0.17	-	52,52,52,52	0
56	MG	AA	3192	1/1	0.09	-	57,57,57,57	0
56	MG	BA	3244	1/1	0.47	-	65,65,65,65	0
56	MG	AA	3035	1/1	0.40	-	71,71,71,71	0
56	MG	B7	101	1/1	0.18	-	43,43,43,43	0
56	MG	BA	3357	1/1	0.15	-	49,49,49,49	0
56	MG	BA	3277	1/1	0.35	-	45,45,45,45	0
56	MG	BA	3551	1/1	0.21	-	25,25,25,25	0
56	MG	BA	3197	1/1	0.27	-	39,39,39,39	0
56	MG	BA	3372	1/1	0.17	-	38,38,38,38	0
56	MG	DA	3578	1/1	0.40	-	49,49,49,49	0
56	MG	AA	3108	1/1	0.34	-	67,67,67,67	0
56	MG	CX	102	1/1	0.06	-	61,61,61,61	0
56	MG	BA	3054	1/1	0.25	-	46,46,46,46	0
56	MG	DA	3635	1/1	0.31	-	58,58,58,58	0
56	MG	BA	3195	1/1	0.32	-	47,47,47,47	0
56	MG	AA	3084	1/1	0.33	-	78,78,78,78	0
56	MG	BU	202	1/1	0.35	-	32,32,32,32	0
56	MG	BA	3571	1/1	0.08	-	65,65,65,65	0
56	MG	DA	3576	1/1	0.14	-	38,38,38,38	0
56	MG	AA	3093	1/1	0.60	-	88,88,88,88	0
56	MG	DA	3525	1/1	0.58	-	70,70,70,70	0
56	MG	BA	3436	1/1	0.09	-	37,37,37,37	0
56	MG	BA	3145	1/1	0.37	-	38,38,38,38	0
56	MG	BA	3735	1/1	0.20	-	45,45,45,45	0
56	MG	DA	3573	1/1	0.28	-	40,40,40,40	0
56	MG	DB	3010	1/1	0.20	-	73,73,73,73	0
56	MG	DA	3432	1/1	0.24	-	66,66,66,66	0
56	MG	DA	3091	1/1	0.39	-	44,44,44,44	0
56	MG	CA	3149	1/1	0.17	-	74,74,74,74	0
56	MG	DA	3357	1/1	0.22	-	56,56,56,56	0
56	MG	BA	3599	1/1	0.29	-	46,46,46,46	0
56	MG	BA	3298	1/1	0.36	-	49,49,49,49	0
56	MG	BA	3671	1/1	0.27	-	57,57,57,57	0
56	MG	DA	3238	1/1	0.10	-	61,61,61,61	0
56	MG	BA	3648	1/1	0.30	-	49,49,49,49	0
56	MG	DA	3380	1/1	0.15	-	26,26,26,26	0
56	MG	DA	3547	1/1	0.09	-	41,41,41,41	0
56	MG	AA	3073	1/1	0.06	-	46,46,46,46	0
56	MG	DA	3197	1/1	0.43	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3457	1/1	0.12	-	37,37,37,37	0
56	MG	AA	3013	1/1	0.24	-	78,78,78,78	0
56	MG	BA	3215	1/1	0.18	-	69,69,69,69	0
56	MG	BA	3331	1/1	0.18	-	47,47,47,47	0
56	MG	BR	204	1/1	0.64	-	43,43,43,43	0
56	MG	BA	3238	1/1	0.16	-	51,51,51,51	0
56	MG	BA	3180	1/1	0.87	-	43,43,43,43	0
56	MG	CA	3081	1/1	0.10	-	72,72,72,72	0
56	MG	BA	3557	1/1	0.26	-	31,31,31,31	0
56	MG	AA	3048	1/1	0.20	-	57,57,57,57	0
56	MG	BA	3311	1/1	0.27	-	42,42,42,42	0
56	MG	DA	3062	1/1	0.32	-	55,55,55,55	0
56	MG	BA	3049	1/1	0.36	-	35,35,35,35	0
56	MG	DA	3056	1/1	0.38	-	43,43,43,43	0
56	MG	BA	3290	1/1	0.25	-	49,49,49,49	0
56	MG	DA	3316	1/1	0.16	-	58,58,58,58	0
56	MG	DA	3165	1/1	0.23	-	44,44,44,44	0
56	MG	AA	3020	1/1	0.12	-	77,77,77,77	0
56	MG	BA	3183	1/1	0.24	-	48,48,48,48	0
56	MG	BA	3342	1/1	0.16	-	31,31,31,31	0
56	MG	AA	3027	1/1	0.06	-	55,55,55,55	0
56	MG	CA	3012	1/1	0.10	-	49,49,49,49	0
56	MG	BA	3067	1/1	0.34	-	53,53,53,53	0
56	MG	DG	3001	1/1	0.14	-	63,63,63,63	0
56	MG	DA	3260	1/1	0.10	-	40,40,40,40	0
56	MG	BA	3465	1/1	0.13	-	40,40,40,40	0
56	MG	BA	3548	1/1	0.21	-	50,50,50,50	0
56	MG	BA	3262	1/1	0.23	-	56,56,56,56	0
56	MG	CA	3161	1/1	0.13	-	54,54,54,54	0
56	MG	DA	3538	1/1	0.17	-	44,44,44,44	0
56	MG	BA	3684	1/1	0.16	-	58,58,58,58	0
56	MG	CA	3049	1/1	0.25	-	53,53,53,53	0
56	MG	DA	3415	1/1	0.21	-	56,56,56,56	0
56	MG	DA	3644	1/1	0.07	-	42,42,42,42	0
56	MG	DA	3016	1/1	0.26	-	37,37,37,37	0
56	MG	DA	3211	1/1	0.09	-	51,51,51,51	0
56	MG	CA	3160	1/1	0.14	-	59,59,59,59	0
56	MG	AA	3047	1/1	0.29	-	61,61,61,61	0
56	MG	BA	3003	1/1	0.15	-	43,43,43,43	0
56	MG	BA	3385	1/1	0.22	-	26,26,26,26	0
56	MG	BA	3198	1/1	0.16	-	52,52,52,52	0
56	MG	BA	3405	1/1	0.13	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3587	1/1	0.14	-	64,64,64,64	0
56	MG	B8	103	1/1	0.17	-	24,24,24,24	0
56	MG	BA	3363	1/1	0.13	-	39,39,39,39	0
56	MG	BA	3388	1/1	0.15	-	34,34,34,34	0
56	MG	BA	3527	1/1	0.17	-	64,64,64,64	0
56	MG	DA	3526	1/1	0.20	-	54,54,54,54	0
56	MG	DA	3064	1/1	0.40	-	50,50,50,50	0
56	MG	DA	3617	1/1	0.18	-	58,58,58,58	0
56	MG	AA	3077	1/1	0.44	-	65,65,65,65	0
56	MG	BA	3524	1/1	0.25	-	55,55,55,55	0
56	MG	BA	3408	1/1	0.15	-	24,24,24,24	0
56	MG	DA	3208	1/1	0.99	-	43,43,43,43	0
56	MG	DA	3301	1/1	0.14	-	45,45,45,45	0
56	MG	AA	3163	1/1	0.17	-	28,28,28,28	0
56	MG	AA	3210	1/1	0.05	-	40,40,40,40	0
56	MG	BA	3615	1/1	0.20	-	36,36,36,36	0
56	MG	DA	3140	1/1	0.34	-	54,54,54,54	0
56	MG	BA	3698	1/1	0.21	-	41,41,41,41	0
56	MG	BA	3651	1/1	0.14	-	45,45,45,45	0
56	MG	DA	3101	1/1	0.37	-	48,48,48,48	0
56	MG	AA	3004	1/1	0.11	-	55,55,55,55	0
56	MG	AA	3144	1/1	0.08	-	48,48,48,48	0
56	MG	CA	3163	1/1	0.23	-	65,65,65,65	0
56	MG	DA	3568	1/1	0.09	-	42,42,42,42	0
56	MG	AA	3139	1/1	0.33	-	56,56,56,56	0
56	MG	CA	3048	1/1	0.20	-	62,62,62,62	0
56	MG	BA	3172	1/1	0.92	-	48,48,48,48	0
56	MG	BA	3555	1/1	0.18	-	53,53,53,53	0
56	MG	BA	3411	1/1	0.14	-	38,38,38,38	0
56	MG	CA	3051	1/1	0.10	-	63,63,63,63	0
56	MG	BA	3390	1/1	0.20	-	30,30,30,30	0
56	MG	BA	3635	1/1	0.09	-	78,78,78,78	0
56	MG	CA	3153	1/1	0.12	-	83,83,83,83	0
56	MG	DA	3356	1/1	0.12	-	27,27,27,27	0
56	MG	DA	3350	1/1	0.04	-	32,32,32,32	0
56	MG	DA	3404	1/1	0.13	-	47,47,47,47	0
56	MG	DA	3185	1/1	0.61	-	52,52,52,52	0
56	MG	BA	3347	1/1	0.27	-	25,25,25,25	0
56	MG	DA	3203	1/1	0.14	-	41,41,41,41	0
56	MG	DA	3014	1/1	0.20	-	34,34,34,34	0
56	MG	BA	3463	1/1	0.18	-	55,55,55,55	0
56	MG	BA	3341	1/1	0.09	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DQ	202	1/1	0.23	-	34,34,34,34	0
56	MG	DA	3137	1/1	0.26	-	56,56,56,56	0
56	MG	BA	3196	1/1	0.76	-	56,56,56,56	0
56	MG	DA	3354	1/1	0.15	-	27,27,27,27	0
56	MG	DA	3296	1/1	0.09	-	31,31,31,31	0
56	MG	AA	3214	1/1	0.29	-	75,75,75,75	0
56	MG	BA	3546	1/1	0.29	-	48,48,48,48	0
56	MG	BA	3621	1/1	0.33	-	74,74,74,74	0
56	MG	AA	3068	1/1	0.08	-	66,66,66,66	0
56	MG	BB	3013	1/1	0.11	-	39,39,39,39	0
56	MG	BA	3662	1/1	0.14	-	39,39,39,39	0
56	MG	BA	3613	1/1	0.28	-	76,76,76,76	0
56	MG	DV	201	1/1	0.32	-	55,55,55,55	0
56	MG	CA	3075	1/1	0.20	-	76,76,76,76	0
56	MG	DA	3605	1/1	0.13	-	44,44,44,44	0
56	MG	BA	3034	1/1	0.41	-	52,52,52,52	0
56	MG	BA	3232	1/1	0.11	-	29,29,29,29	0
56	MG	BA	3460	1/1	0.13	-	33,33,33,33	0
56	MG	CA	3170	1/1	0.45	-	50,50,50,50	0
56	MG	BA	3647	1/1	0.11	-	34,34,34,34	0
56	MG	AA	3041	1/1	0.17	-	49,49,49,49	0
56	MG	BA	3522	1/1	0.13	-	49,49,49,49	0
56	MG	DA	3477	1/1	0.10	-	49,49,49,49	0
56	MG	AA	3199	1/1	0.13	-	88,88,88,88	0
56	MG	DA	3033	1/1	0.26	-	39,39,39,39	0
56	MG	AA	3101	1/1	0.16	-	56,56,56,56	0
56	MG	AA	3115	1/1	0.10	-	48,48,48,48	0
56	MG	BA	3304	1/1	0.19	-	49,49,49,49	0
56	MG	BA	3134	1/1	0.34	-	47,47,47,47	0
56	MG	CA	3066	1/1	0.11	-	55,55,55,55	0
56	MG	DA	3210	1/1	0.16	-	40,40,40,40	0
56	MG	AA	3122	1/1	0.54	-	44,44,44,44	0
56	MG	BA	3654	1/1	0.17	-	25,25,25,25	0
56	MG	DA	3391	1/1	0.14	-	41,41,41,41	0
56	MG	BA	3305	1/1	0.13	-	44,44,44,44	0
56	MG	CA	3013	1/1	0.11	-	51,51,51,51	0
56	MG	BA	3015	1/1	0.34	-	44,44,44,44	0
56	MG	AA	3042	1/1	0.33	-	44,44,44,44	0
56	MG	DA	3537	1/1	0.20	-	65,65,65,65	0
56	MG	BA	3371	1/1	0.17	-	15,15,15,15	0
56	MG	BA	3432	1/1	0.17	-	60,60,60,60	0
56	MG	DA	3063	1/1	0.13	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3469	1/1	0.17	-	47,47,47,47	0
56	MG	CA	3003	1/1	0.14	-	66,66,66,66	0
56	MG	CA	3109	1/1	0.14	-	83,83,83,83	0
56	MG	DA	3022	1/1	0.22	-	45,45,45,45	0
56	MG	DA	3116	1/1	0.30	-	39,39,39,39	0
56	MG	DA	3047	1/1	0.08	-	34,34,34,34	0
56	MG	BA	3216	1/1	0.26	-	41,41,41,41	0
56	MG	BA	3002	1/1	0.20	-	54,54,54,54	0
56	MG	BA	3694	1/1	0.36	-	56,56,56,56	0
56	MG	DA	3057	1/1	0.19	-	52,52,52,52	0
56	MG	AA	3135	1/1	0.20	-	41,41,41,41	0
56	MG	BA	3295	1/1	0.54	-	75,75,75,75	0
56	MG	BA	3559	1/1	0.14	-	48,48,48,48	0
56	MG	BQ	205	1/1	0.42	-	49,49,49,49	0
56	MG	BA	3160	1/1	0.66	-	53,53,53,53	0
56	MG	DA	3249	1/1	0.21	-	28,28,28,28	0
56	MG	CA	3166	1/1	0.17	-	59,59,59,59	0
56	MG	DA	3575	1/1	0.19	-	43,43,43,43	0
56	MG	BA	3335	1/1	0.18	-	35,35,35,35	0
56	MG	DA	3206	1/1	0.28	-	42,42,42,42	0
56	MG	BA	3508	1/1	0.16	-	34,34,34,34	0
56	MG	BA	3306	1/1	0.14	-	48,48,48,48	0
56	MG	BB	3009	1/1	0.14	-	48,48,48,48	0
56	MG	DA	3359	1/1	0.22	-	46,46,46,46	0
56	MG	BD	306	1/1	0.53	-	46,46,46,46	0
56	MG	AA	3118	1/1	0.35	-	52,52,52,52	0
56	MG	DA	3383	1/1	0.08	-	56,56,56,56	0
56	MG	DA	3438	1/1	0.52	-	70,70,70,70	0
56	MG	BA	3355	1/1	0.19	-	64,64,64,64	0
56	MG	DA	3008	1/1	0.28	-	51,51,51,51	0
56	MG	BA	3427	1/1	0.10	-	48,48,48,48	0
56	MG	DA	3295	1/1	0.23	-	39,39,39,39	0
56	MG	DA	3514	1/1	0.11	-	39,39,39,39	0
56	MG	DA	3294	1/1	0.08	-	47,47,47,47	0
56	MG	AA	3106	1/1	0.26	-	56,56,56,56	0
56	MG	AA	3075	1/1	0.11	-	52,52,52,52	0
56	MG	BA	3156	1/1	0.35	-	56,56,56,56	0
56	MG	DA	3544	1/1	0.11	-	51,51,51,51	0
56	MG	BV	202	1/1	0.48	-	56,56,56,56	0
56	MG	CA	3078	1/1	0.31	-	46,46,46,46	0
56	MG	DA	3245	1/1	0.14	-	37,37,37,37	0
56	MG	DA	3406	1/1	0.09	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3630	1/1	0.26	-	52,52,52,52	0
56	MG	BA	3064	1/1	0.22	-	39,39,39,39	0
56	MG	DA	3349	1/1	0.14	-	54,54,54,54	0
56	MG	BA	3563	1/1	0.22	-	37,37,37,37	0
56	MG	DA	3136	1/1	0.12	-	49,49,49,49	0
56	MG	CA	3007	1/1	0.58	-	68,68,68,68	0
56	MG	DA	3270	1/1	0.22	-	36,36,36,36	0
56	MG	DA	3532	1/1	0.09	-	57,57,57,57	0
56	MG	AA	3194	1/1	0.16	-	54,54,54,54	0
56	MG	CA	3142	1/1	0.19	-	59,59,59,59	0
58	ZN	D4	501	1/1	0.08	-	153,153,153,153	0
56	MG	DA	3466	1/1	0.14	-	56,56,56,56	0
56	MG	DA	3400	1/1	0.19	-	42,42,42,42	0
56	MG	BA	3512	1/1	0.21	-	40,40,40,40	0
56	MG	AN	103	1/1	0.41	-	60,60,60,60	0
56	MG	BA	3448	1/1	0.10	-	29,29,29,29	0
56	MG	BA	3110	1/1	0.31	-	55,55,55,55	0
56	MG	AA	3165	1/1	0.16	-	23,23,23,23	0
56	MG	AA	3220	1/1	0.12	-	40,40,40,40	0
58	ZN	D5	103	1/1	0.06	-	70,70,70,70	0
56	MG	BA	3729	1/1	0.46	-	46,46,46,46	0
56	MG	DA	3207	1/1	0.12	-	58,58,58,58	0
56	MG	DF	302	1/1	0.25	-	43,43,43,43	0
56	MG	BA	3091	1/1	0.59	-	45,45,45,45	0
56	MG	BA	3628	1/1	0.18	-	41,41,41,41	0
56	MG	BA	3537	1/1	0.36	-	31,31,31,31	0
56	MG	BA	3420	1/1	0.30	-	33,33,33,33	0
56	MG	BA	3217	1/1	0.08	-	28,28,28,28	0
56	MG	DA	3141	1/1	0.14	-	62,62,62,62	0
56	MG	DA	3451	1/1	0.08	-	49,49,49,49	0
56	MG	BA	3211	1/1	0.30	-	38,38,38,38	0
56	MG	BA	3045	1/1	0.30	-	34,34,34,34	0
56	MG	CA	3020	1/1	0.18	-	47,47,47,47	0
56	MG	BA	3325	1/1	0.17	-	58,58,58,58	0
56	MG	BB	3010	1/1	0.25	-	40,40,40,40	0
56	MG	DA	3098	1/1	1.35	-	43,43,43,43	0
56	MG	DA	3223	1/1	0.24	-	66,66,66,66	0
56	MG	DA	3364	1/1	0.20	-	32,32,32,32	0
56	MG	BA	3076	1/1	0.21	-	41,41,41,41	0
56	MG	AA	3011	1/1	1.09	-	55,55,55,55	0
56	MG	DE	306	1/1	0.14	-	32,32,32,32	0
56	MG	BA	3352	1/1	0.11	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3109	1/1	0.53	-	66,66,66,66	0
56	MG	BA	3332	1/1	0.19	-	39,39,39,39	0
56	MG	DA	3041	1/1	0.47	-	57,57,57,57	0
56	MG	DF	304	1/1	0.28	-	44,44,44,44	0
56	MG	BA	3359	1/1	0.20	-	23,23,23,23	0
56	MG	DA	3006	1/1	0.15	-	42,42,42,42	0
56	MG	BA	3506	1/1	0.14	-	30,30,30,30	0
56	MG	BA	3141	1/1	0.28	-	43,43,43,43	0
56	MG	DA	3298	1/1	0.32	-	37,37,37,37	0
56	MG	DA	3049	1/1	0.32	-	58,58,58,58	0
56	MG	BA	3631	1/1	0.12	-	78,78,78,78	0
56	MG	DA	3443	1/1	0.15	-	53,53,53,53	0
56	MG	BA	3349	1/1	0.25	-	43,43,43,43	0
56	MG	BA	3609	1/1	0.12	-	46,46,46,46	0
56	MG	BA	3728	1/1	0.48	-	32,32,32,32	0
56	MG	DA	3377	1/1	0.28	-	59,59,59,59	0
56	MG	DA	3201	1/1	0.13	-	48,48,48,48	0
56	MG	DA	3024	1/1	0.48	-	65,65,65,65	0
56	MG	DA	3393	1/1	0.20	-	41,41,41,41	0
56	MG	BA	3344	1/1	0.10	-	30,30,30,30	0
56	MG	BA	3419	1/1	0.13	-	24,24,24,24	0
56	MG	DA	3218	1/1	0.18	-	62,62,62,62	0
56	MG	AA	3146	1/1	0.22	-	48,48,48,48	0
56	MG	BB	3003	1/1	0.24	-	43,43,43,43	0
56	MG	BA	3203	1/1	0.27	-	32,32,32,32	0
56	MG	BB	3017	1/1	0.20	-	64,64,64,64	0
56	MG	DA	3340	1/1	0.14	-	47,47,47,47	0
56	MG	DA	3358	1/1	0.17	-	46,46,46,46	0
56	MG	BA	3235	1/1	0.29	-	47,47,47,47	0
56	MG	BA	3328	1/1	0.24	-	42,42,42,42	0
56	MG	BA	3616	1/1	0.12	-	33,33,33,33	0
56	MG	BA	3526	1/1	0.18	-	19,19,19,19	0
56	MG	BA	3560	1/1	0.20	-	61,61,61,61	0
56	MG	DA	3271	1/1	0.20	-	37,37,37,37	0
56	MG	CA	3025	1/1	0.20	-	94,94,94,94	0
56	MG	DA	3143	1/1	0.22	-	46,46,46,46	0
58	ZN	D6	501	1/1	0.12	-	61,61,61,61	0
58	ZN	B6	501	1/1	0.13	-	49,49,49,49	0
56	MG	DA	3586	1/1	0.09	-	29,29,29,29	0
56	MG	D8	5001	1/1	0.32	-	47,47,47,47	0
56	MG	BA	3500	1/1	0.17	-	37,37,37,37	0
56	MG	DA	3626	1/1	0.07	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3598	1/1	0.30	-	66,66,66,66	0
56	MG	BA	3270	1/1	0.31	-	50,50,50,50	0
56	MG	DA	3584	1/1	0.11	-	61,61,61,61	0
56	MG	BD	304	1/1	0.50	-	58,58,58,58	0
56	MG	BA	3322	1/1	0.25	-	22,22,22,22	0
56	MG	BA	3499	1/1	0.17	-	55,55,55,55	0
56	MG	BA	3009	1/1	0.17	-	25,25,25,25	0
56	MG	DE	302	1/1	0.36	-	44,44,44,44	0
56	MG	AA	3124	1/1	0.10	-	57,57,57,57	0
56	MG	BA	3568	1/1	0.22	-	47,47,47,47	0
56	MG	AA	3090	1/1	0.17	-	68,68,68,68	0
56	MG	DA	3378	1/1	0.14	-	45,45,45,45	0
56	MG	CA	3050	1/1	0.13	-	43,43,43,43	0
56	MG	BD	301	1/1	0.25	-	28,28,28,28	0
56	MG	DA	3458	1/1	0.15	-	71,71,71,71	0
56	MG	BA	3358	1/1	0.07	-	33,33,33,33	0
56	MG	AA	3176	1/1	0.12	-	63,63,63,63	0
56	MG	DA	3220	1/1	0.11	-	37,37,37,37	0
56	MG	DA	3094	1/1	0.18	-	26,26,26,26	0
56	MG	DA	3123	1/1	0.23	-	59,59,59,59	0
56	MG	DA	3152	1/1	0.23	-	50,50,50,50	0
56	MG	BB	3011	1/1	0.18	-	37,37,37,37	0
56	MG	BA	3393	1/1	0.19	-	38,38,38,38	0
56	MG	DA	3551	1/1	0.10	-	52,52,52,52	0
56	MG	BA	3150	1/1	0.48	-	34,34,34,34	0
56	MG	AA	3154	1/1	0.07	-	63,63,63,63	0
56	MG	BA	3610	1/1	0.22	-	40,40,40,40	0
56	MG	DA	3255	1/1	0.19	-	40,40,40,40	0
56	MG	AA	3180	1/1	0.37	-	66,66,66,66	0
56	MG	BA	3212	1/1	0.30	-	43,43,43,43	0
56	MG	DA	3093	1/1	0.20	-	53,53,53,53	0
56	MG	DA	3235	1/1	0.20	-	50,50,50,50	0
56	MG	DA	3613	1/1	0.15	-	54,54,54,54	0
56	MG	DA	3412	1/1	0.29	-	30,30,30,30	0
56	MG	BA	3732	1/1	0.47	-	61,61,61,61	0
56	MG	DA	3498	1/1	0.14	-	56,56,56,56	0
56	MG	BA	3483	1/1	0.25	-	53,53,53,53	0
56	MG	BA	3337	1/1	0.17	-	23,23,23,23	0
56	MG	BP	202	1/1	0.12	-	40,40,40,40	0
56	MG	DA	3490	1/1	0.10	-	39,39,39,39	0
56	MG	BA	3575	1/1	0.19	-	51,51,51,51	0
56	MG	DA	3287	1/1	0.26	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3010	1/1	0.38	-	70,70,70,70	0
56	MG	AA	3196	1/1	0.32	-	65,65,65,65	0
56	MG	BA	3010	1/1	0.18	-	32,32,32,32	0
56	MG	BA	3096	1/1	0.38	-	62,62,62,62	0
56	MG	BA	3071	1/1	0.30	-	55,55,55,55	0
56	MG	CA	3098	1/1	0.25	-	46,46,46,46	0
56	MG	DA	3382	1/1	0.13	-	25,25,25,25	0
56	MG	DA	3131	1/1	0.20	-	54,54,54,54	0
56	MG	DA	3179	1/1	0.23	-	46,46,46,46	0
56	MG	BA	3510	1/1	0.23	-	40,40,40,40	0
56	MG	DA	3372	1/1	0.11	-	45,45,45,45	0
56	MG	DA	3343	1/1	0.19	-	41,41,41,41	0
56	MG	BA	3088	1/1	0.34	-	56,56,56,56	0
56	MG	BA	3658	1/1	0.27	-	79,79,79,79	0
56	MG	BA	3498	1/1	0.14	-	39,39,39,39	0
56	MG	BA	3734	1/1	0.24	-	45,45,45,45	0
56	MG	BA	3205	1/1	0.18	-	40,40,40,40	0
56	MG	AA	3211	1/1	0.22	-	36,36,36,36	0
56	MG	DA	3572	1/1	0.09	-	53,53,53,53	0
56	MG	BA	3072	1/1	0.30	-	45,45,45,45	0
56	MG	DA	3146	1/1	0.16	-	34,34,34,34	0
56	MG	DA	3060	1/1	0.28	-	55,55,55,55	0
56	MG	BA	3705	1/1	0.05	-	39,39,39,39	0
56	MG	BA	3505	1/1	0.19	-	59,59,59,59	0
56	MG	DA	3394	1/1	0.17	-	47,47,47,47	0
56	MG	BA	3492	1/1	0.27	-	23,23,23,23	0
56	MG	DA	3084	1/1	0.28	-	70,70,70,70	0
56	MG	BA	3225	1/1	0.33	-	62,62,62,62	0
56	MG	BA	3553	1/1	0.12	-	31,31,31,31	0
56	MG	BA	3739	1/1	0.80	-	50,50,50,50	0
56	MG	BA	3214	1/1	0.09	-	53,53,53,53	0
56	MG	DA	3414	1/1	0.20	-	49,49,49,49	0
56	MG	CA	3104	1/1	0.20	-	62,62,62,62	0
56	MG	BA	3580	1/1	0.10	-	58,58,58,58	0
56	MG	AA	3219	1/1	0.18	-	57,57,57,57	0
56	MG	BA	3329	1/1	0.13	-	29,29,29,29	0
56	MG	DA	3649	1/1	0.23	-	24,24,24,24	0
56	MG	DA	3336	1/1	0.12	-	27,27,27,27	0
56	MG	B0	101	1/1	0.18	-	36,36,36,36	0
56	MG	BA	3619	1/1	0.28	-	40,40,40,40	0
56	MG	DA	3205	1/1	0.09	-	38,38,38,38	0
56	MG	DA	3261	1/1	0.22	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3395	1/1	0.20	-	25,25,25,25	0
56	MG	AA	3134	1/1	0.35	-	70,70,70,70	0
56	MG	DA	3365	1/1	0.05	-	40,40,40,40	0
56	MG	CA	3071	1/1	0.09	-	63,63,63,63	0
56	MG	BA	3042	1/1	0.62	-	47,47,47,47	0
56	MG	DA	3250	1/1	0.13	-	31,31,31,31	0
56	MG	DB	3003	1/1	0.13	-	63,63,63,63	0
56	MG	BA	3708	1/1	0.22	-	40,40,40,40	0
56	MG	DA	3125	1/1	0.50	-	48,48,48,48	0
56	MG	BA	3350	1/1	0.24	-	47,47,47,47	0
56	MG	DA	3284	1/1	0.12	-	68,68,68,68	0
56	MG	DA	3473	1/1	0.29	-	32,32,32,32	0
56	MG	DA	3486	1/1	0.12	-	38,38,38,38	0
56	MG	BA	3579	1/1	0.23	-	63,63,63,63	0
56	MG	BA	3240	1/1	0.18	-	28,28,28,28	0
56	MG	DA	3521	1/1	0.12	-	62,62,62,62	0
56	MG	AX	104	1/1	0.14	-	76,76,76,76	0
56	MG	CA	3021	1/1	0.22	-	53,53,53,53	0
56	MG	DA	3607	1/1	0.10	-	45,45,45,45	0
56	MG	BA	3074	1/1	0.08	-	42,42,42,42	0
56	MG	AA	3121	1/1	0.56	-	51,51,51,51	0
56	MG	DA	3385	1/1	0.15	-	35,35,35,35	0
56	MG	CA	3101	1/1	0.15	-	70,70,70,70	0
56	MG	DA	3228	1/1	0.27	-	45,45,45,45	0
56	MG	BA	3676	1/1	0.21	-	51,51,51,51	0
56	MG	BA	3673	1/1	0.19	-	53,53,53,53	0
56	MG	DA	3497	1/1	0.22	-	60,60,60,60	0
56	MG	BA	3227	1/1	0.32	-	32,32,32,32	0
56	MG	BA	3653	1/1	0.13	-	69,69,69,69	0
56	MG	DA	3543	1/1	0.16	-	42,42,42,42	0
56	MG	BA	3562	1/1	0.10	-	73,73,73,73	0
56	MG	DA	3390	1/1	0.11	-	42,42,42,42	0
56	MG	DA	3071	1/1	0.48	-	46,46,46,46	0
56	MG	DA	3430	1/1	0.26	-	55,55,55,55	0
56	MG	BA	3406	1/1	0.15	-	28,28,28,28	0
56	MG	DA	3345	1/1	0.09	-	31,31,31,31	0
56	MG	CA	3085	1/1	0.30	-	43,43,43,43	0
56	MG	BA	3137	1/1	0.29	-	42,42,42,42	0
56	MG	BA	3286	1/1	0.22	-	32,32,32,32	0
56	MG	BA	3340	1/1	0.14	-	57,57,57,57	0
56	MG	BA	3220	1/1	0.13	-	57,57,57,57	0
56	MG	BA	3129	1/1	0.23	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BF	307	1/1	0.44	-	47,47,47,47	0
56	MG	BA	3218	1/1	0.22	-	62,62,62,62	0
56	MG	DA	3554	1/1	0.18	-	70,70,70,70	0
56	MG	BA	3323	1/1	0.14	-	23,23,23,23	0
56	MG	DA	3637	1/1	0.27	-	48,48,48,48	0
56	MG	DA	3332	1/1	0.12	-	33,33,33,33	0
56	MG	AA	3040	1/1	0.12	-	55,55,55,55	0
56	MG	DA	3478	1/1	0.25	-	46,46,46,46	0
56	MG	BA	3585	1/1	0.17	-	51,51,51,51	0
56	MG	BA	3229	1/1	0.14	-	22,22,22,22	0
56	MG	DA	3303	1/1	0.18	-	47,47,47,47	0
56	MG	DA	3641	1/1	0.36	-	61,61,61,61	0
56	MG	DA	3318	1/1	0.10	-	45,45,45,45	0
56	MG	AA	3189	1/1	0.09	-	77,77,77,77	0
56	MG	CA	3069	1/1	0.10	-	69,69,69,69	0
56	MG	BD	309	1/1	0.14	-	42,42,42,42	0
56	MG	DA	3167	1/1	0.24	-	48,48,48,48	0
56	MG	DA	3166	1/1	0.11	-	32,32,32,32	0
56	MG	BA	3703	1/1	0.21	-	31,31,31,31	0
56	MG	BA	3723	1/1	0.13	-	49,49,49,49	0
56	MG	BA	3530	1/1	0.29	-	31,31,31,31	0
56	MG	D5	102	1/1	0.57	-	55,55,55,55	0
56	MG	BA	3086	1/1	0.42	-	49,49,49,49	0
56	MG	CA	3108	1/1	0.24	-	52,52,52,52	0
56	MG	BA	3683	1/1	0.22	-	60,60,60,60	0
56	MG	DA	3032	1/1	0.15	-	46,46,46,46	0
56	MG	CA	3146	1/1	0.18	-	69,69,69,69	0
56	MG	BG	3003	1/1	0.17	-	42,42,42,42	0
56	MG	CA	3070	1/1	0.34	-	55,55,55,55	0
56	MG	BA	3733	1/1	0.10	-	27,27,27,27	0
56	MG	DA	3619	1/1	0.25	-	48,48,48,48	0
56	MG	DA	3308	1/1	0.34	-	30,30,30,30	0
56	MG	DA	3264	1/1	0.32	-	49,49,49,49	0
56	MG	DA	3083	1/1	0.23	-	41,41,41,41	0
56	MG	BA	3219	1/1	0.20	-	65,65,65,65	0
56	MG	BA	3714	1/1	0.25	-	58,58,58,58	0
56	MG	BA	3267	1/1	0.16	-	41,41,41,41	0
56	MG	BA	3693	1/1	0.15	-	64,64,64,64	0
56	MG	BA	3207	1/1	0.21	-	35,35,35,35	0
56	MG	BA	3642	1/1	0.27	-	51,51,51,51	0
56	MG	AA	3051	1/1	0.45	-	73,73,73,73	0
56	MG	BA	3028	1/1	0.20	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3037	1/1	0.31	-	67,67,67,67	0
56	MG	AV	101	1/1	0.19	-	36,36,36,36	0
56	MG	BA	3561	1/1	0.19	-	24,24,24,24	0
56	MG	AA	3009	1/1	0.28	-	79,79,79,79	0
56	MG	BN	3004	1/1	0.37	-	66,66,66,66	0
56	MG	BA	3068	1/1	0.40	-	54,54,54,54	0
56	MG	BA	3521	1/1	0.12	-	49,49,49,49	0
56	MG	BA	3525	1/1	0.23	-	43,43,43,43	0
56	MG	DA	3539	1/1	0.18	-	53,53,53,53	0
56	MG	DA	3226	1/1	0.22	-	50,50,50,50	0
56	MG	BA	3283	1/1	0.17	-	17,17,17,17	0
56	MG	BA	3245	1/1	0.36	-	47,47,47,47	0
56	MG	BA	3051	1/1	0.15	-	20,20,20,20	0
56	MG	DA	3621	1/1	0.13	-	54,54,54,54	0
56	MG	BZ	3001	1/1	0.29	-	61,61,61,61	0
56	MG	BA	3423	1/1	0.07	-	26,26,26,26	0
56	MG	DA	3059	1/1	0.10	-	46,46,46,46	0
56	MG	DA	3435	1/1	0.23	-	46,46,46,46	0
56	MG	CA	3024	1/1	0.46	-	65,65,65,65	0
56	MG	DA	3181	1/1	0.30	-	36,36,36,36	0
56	MG	BA	3265	1/1	0.10	-	20,20,20,20	0
56	MG	DA	3567	1/1	0.17	-	62,62,62,62	0
56	MG	DA	3630	1/1	0.19	-	40,40,40,40	0
56	MG	DA	3510	1/1	0.23	-	63,63,63,63	0
56	MG	BA	3603	1/1	0.08	-	39,39,39,39	0
56	MG	BA	3617	1/1	0.23	-	62,62,62,62	0
56	MG	DA	3282	1/1	0.10	-	36,36,36,36	0
56	MG	AA	3167	1/1	0.18	-	67,67,67,67	0
56	MG	DA	3346	1/1	0.24	-	29,29,29,29	0
56	MG	AA	3174	1/1	0.23	-	33,33,33,33	0
56	MG	BA	3101	1/1	0.14	-	35,35,35,35	0
56	MG	CA	3042	1/1	0.55	-	85,85,85,85	0
56	MG	BA	3626	1/1	0.12	-	43,43,43,43	0
56	MG	BA	3107	1/1	0.20	-	40,40,40,40	0
56	MG	BA	3544	1/1	0.22	-	27,27,27,27	0
56	MG	CA	3167	1/1	0.08	-	78,78,78,78	0
56	MG	BA	3464	1/1	0.09	-	43,43,43,43	0
56	MG	DA	3528	1/1	0.09	-	56,56,56,56	0
56	MG	DA	3044	1/1	0.12	-	46,46,46,46	0
56	MG	BA	3016	1/1	0.24	-	33,33,33,33	0
56	MG	BA	3343	1/1	0.18	-	40,40,40,40	0
58	ZN	D9	501	1/1	0.04	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3356	1/1	0.26	-	56,56,56,56	0
56	MG	BA	3711	1/1	0.17	-	86,86,86,86	0
56	MG	BN	3002	1/1	0.32	-	56,56,56,56	0
56	MG	AA	3185	1/1	0.28	-	46,46,46,46	0
56	MG	BA	3014	1/1	0.69	-	34,34,34,34	0
56	MG	DB	3001	1/1	0.25	-	68,68,68,68	0
56	MG	DA	3508	1/1	0.21	-	38,38,38,38	0
56	MG	DA	3534	1/1	0.16	-	45,45,45,45	0
56	MG	BU	204	1/1	0.39	-	44,44,44,44	0
56	MG	DA	3371	1/1	0.07	-	44,44,44,44	0
56	MG	AA	3062	1/1	0.10	-	32,32,32,32	0
56	MG	AA	3019	1/1	0.44	-	74,74,74,74	0
56	MG	DD	307	1/1	0.54	-	38,38,38,38	0
56	MG	DA	3628	1/1	0.20	-	63,63,63,63	0
56	MG	BA	3639	1/1	0.15	-	50,50,50,50	0
56	MG	BA	3421	1/1	0.11	-	36,36,36,36	0
56	MG	BA	3046	1/1	0.14	-	29,29,29,29	0
56	MG	CA	3129	1/1	0.16	-	45,45,45,45	0
56	MG	BA	3637	1/1	0.36	-	33,33,33,33	0
56	MG	BA	3592	1/1	0.16	-	28,28,28,28	0
56	MG	AA	3217	1/1	0.70	-	67,67,67,67	0
56	MG	DF	301	1/1	0.47	-	32,32,32,32	0
56	MG	BA	3070	1/1	0.14	-	35,35,35,35	0
56	MG	BA	3132	1/1	0.23	-	35,35,35,35	0
56	MG	DA	3189	1/1	0.14	-	55,55,55,55	0
56	MG	BA	3123	1/1	0.34	-	69,69,69,69	0
56	MG	BA	3136	1/1	0.23	-	58,58,58,58	0
56	MG	DA	3503	1/1	0.19	-	71,71,71,71	0
56	MG	BA	3604	1/1	0.10	-	72,72,72,72	0
56	MG	DA	3504	1/1	0.06	-	44,44,44,44	0
56	MG	DA	3470	1/1	0.28	-	52,52,52,52	0
56	MG	BA	3336	1/1	0.21	-	54,54,54,54	0
56	MG	BA	3426	1/1	0.24	-	51,51,51,51	0
56	MG	BA	3281	1/1	0.19	-	52,52,52,52	0
56	MG	BA	3399	1/1	0.20	-	18,18,18,18	0
56	MG	BA	3645	1/1	0.09	-	56,56,56,56	0
56	MG	BA	3146	1/1	0.28	-	52,52,52,52	0
56	MG	DA	3422	1/1	0.12	-	38,38,38,38	0
56	MG	DA	3007	1/1	0.24	-	30,30,30,30	0
56	MG	DA	3652	1/1	0.40	-	60,60,60,60	0
56	MG	DA	3099	1/1	0.29	-	44,44,44,44	0
56	MG	BA	3517	1/1	0.09	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3262	1/1	0.22	-	44,44,44,44	0
56	MG	AA	3094	1/1	0.19	-	68,68,68,68	0
56	MG	DA	3075	1/1	0.30	-	44,44,44,44	0
56	MG	BA	3318	1/1	0.12	-	33,33,33,33	0
56	MG	BA	3379	1/1	0.24	-	22,22,22,22	0
56	MG	AA	3138	1/1	0.54	-	37,37,37,37	0
56	MG	AA	3184	1/1	0.09	-	72,72,72,72	0
56	MG	DA	3112	1/1	0.41	-	54,54,54,54	0
56	MG	AA	3178	1/1	0.20	-	65,65,65,65	0
56	MG	CA	3040	1/1	0.33	-	42,42,42,42	0
56	MG	BA	3672	1/1	0.28	-	48,48,48,48	0
56	MG	BA	3634	1/1	0.67	-	63,63,63,63	0
56	MG	DA	3204	1/1	0.41	-	34,34,34,34	0
56	MG	BA	3233	1/1	0.22	-	47,47,47,47	0
56	MG	BA	3263	1/1	0.24	-	79,79,79,79	0
56	MG	BA	3111	1/1	0.41	-	53,53,53,53	0
56	MG	DA	3293	1/1	0.27	-	53,53,53,53	0
56	MG	BB	3004	1/1	0.25	-	54,54,54,54	0
57	SF4	CD	501	8/8	0.13	-	64,75,91,95	0
56	MG	BA	3031	1/1	0.78	-	41,41,41,41	0
56	MG	AA	3110	1/1	0.24	-	48,48,48,48	0
56	MG	AA	3187	1/1	0.04	-	62,62,62,62	0
56	MG	BA	3159	1/1	0.33	-	48,48,48,48	0
56	MG	AA	3018	1/1	0.30	-	38,38,38,38	0
56	MG	BA	3602	1/1	0.09	-	35,35,35,35	0
56	MG	DA	3315	1/1	0.08	-	31,31,31,31	0
56	MG	DA	3188	1/1	0.38	-	47,47,47,47	0
56	MG	BA	3287	1/1	0.19	-	53,53,53,53	0
56	MG	AA	3052	1/1	0.24	-	60,60,60,60	0
56	MG	BA	3605	1/1	0.32	-	59,59,59,59	0
56	MG	BA	3035	1/1	0.10	-	37,37,37,37	0
56	MG	DA	3286	1/1	0.18	-	62,62,62,62	0
56	MG	AA	3169	1/1	0.13	-	76,76,76,76	0
56	MG	DA	3581	1/1	0.73	-	73,73,73,73	0
56	MG	DA	3599	1/1	0.23	-	72,72,72,72	0
56	MG	DA	3171	1/1	0.24	-	39,39,39,39	0
56	MG	BA	3538	1/1	0.15	-	36,36,36,36	0
56	MG	BA	3293	1/1	0.18	-	45,45,45,45	0
56	MG	DA	3126	1/1	0.37	-	43,43,43,43	0
56	MG	BA	3516	1/1	0.09	-	47,47,47,47	0
56	MG	CA	3145	1/1	0.07	-	43,43,43,43	0
56	MG	DA	3273	1/1	0.13	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BN	3003	1/1	0.40	-	59,59,59,59	0
56	MG	DA	3290	1/1	0.07	-	42,42,42,42	0
56	MG	BA	3166	1/1	0.54	-	59,59,59,59	0
56	MG	CA	3018	1/1	0.28	-	54,54,54,54	0
56	MG	AA	3136	1/1	0.09	-	62,62,62,62	0
56	MG	DA	3020	1/1	0.29	-	52,52,52,52	0
56	MG	BA	3424	1/1	0.17	-	15,15,15,15	0
56	MG	DA	3420	1/1	0.15	-	51,51,51,51	0
56	MG	BA	3234	1/1	0.30	-	55,55,55,55	0
56	MG	AA	3058	1/1	0.18	-	50,50,50,50	0
56	MG	BA	3017	1/1	0.56	-	44,44,44,44	0
56	MG	BA	3117	1/1	0.25	-	25,25,25,25	0
56	MG	DA	3563	1/1	0.17	-	64,64,64,64	0
56	MG	DA	3403	1/1	0.13	-	28,28,28,28	0
56	MG	CA	3096	1/1	0.09	-	60,60,60,60	0
56	MG	AA	3181	1/1	0.29	-	57,57,57,57	0
56	MG	CA	3128	1/1	0.26	-	41,41,41,41	0
56	MG	DA	3292	1/1	0.21	-	37,37,37,37	0
56	MG	CA	3119	1/1	0.20	-	64,64,64,64	0
56	MG	DA	3272	1/1	0.29	-	27,27,27,27	0
56	MG	BA	3501	1/1	0.24	-	59,59,59,59	0
56	MG	CA	3123	1/1	0.14	-	77,77,77,77	0
56	MG	DA	3281	1/1	0.25	-	42,42,42,42	0
56	MG	BA	3437	1/1	0.15	-	42,42,42,42	0
56	MG	AA	3070	1/1	0.11	-	75,75,75,75	0
56	MG	BA	3650	1/1	0.16	-	45,45,45,45	0
56	MG	AK	3001	1/1	0.22	-	45,45,45,45	0
56	MG	DA	3569	1/1	0.19	-	37,37,37,37	0
56	MG	BF	302	1/1	0.30	-	46,46,46,46	0
56	MG	DA	3474	1/1	0.09	-	61,61,61,61	0
56	MG	AA	3195	1/1	0.17	-	71,71,71,71	0
56	MG	BA	3339	1/1	0.22	-	43,43,43,43	0
56	MG	BA	3564	1/1	0.07	-	52,52,52,52	0
56	MG	BA	3418	1/1	0.14	-	27,27,27,27	0
56	MG	DA	3153	1/1	0.25	-	38,38,38,38	0
56	MG	CA	3076	1/1	0.32	-	40,40,40,40	0
56	MG	BG	3002	1/1	0.11	-	42,42,42,42	0
56	MG	CE	3001	1/1	0.33	-	68,68,68,68	0
56	MG	BA	3737	1/1	0.25	-	60,60,60,60	0
56	MG	BA	3272	1/1	0.33	-	7,7,7,7	0
56	MG	DA	3209	1/1	0.14	-	41,41,41,41	0
56	MG	DA	3248	1/1	0.27	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DB	3007	1/1	0.25	-	45,45,45,45	0
56	MG	BA	3228	1/1	0.26	-	63,63,63,63	0
56	MG	DN	5001	1/1	0.14	-	75,75,75,75	0
56	MG	DA	3446	1/1	0.12	-	52,52,52,52	0
56	MG	AA	3212	1/1	0.14	-	79,79,79,79	0
56	MG	AA	3025	1/1	0.13	-	69,69,69,69	0
56	MG	B3	101	1/1	0.15	-	28,28,28,28	0
56	MG	BA	3511	1/1	0.17	-	39,39,39,39	0
56	MG	DA	3172	1/1	0.45	-	51,51,51,51	0
56	MG	DA	3381	1/1	0.27	-	47,47,47,47	0
56	MG	AA	3117	1/1	0.23	-	71,71,71,71	0
56	MG	DA	3408	1/1	0.23	-	37,37,37,37	0
56	MG	BA	3037	1/1	0.20	-	31,31,31,31	0
56	MG	DA	3077	1/1	0.27	-	50,50,50,50	0
56	MG	BA	3055	1/1	0.20	-	44,44,44,44	0
56	MG	BA	3531	1/1	0.28	-	38,38,38,38	0
56	MG	BA	3558	1/1	0.21	-	35,35,35,35	0
56	MG	AA	3158	1/1	0.24	-	44,44,44,44	0
56	MG	CA	3135	1/1	0.52	-	76,76,76,76	0
56	MG	BA	3102	1/1	0.28	-	52,52,52,52	0
56	MG	CA	3125	1/1	0.15	-	72,72,72,72	0
56	MG	DA	3529	1/1	0.08	-	63,63,63,63	0
56	MG	DA	3557	1/1	0.11	-	45,45,45,45	0
56	MG	BA	3485	1/1	0.29	-	44,44,44,44	0
56	MG	BA	3513	1/1	0.11	-	45,45,45,45	0
56	MG	BA	3590	1/1	0.13	-	64,64,64,64	0
56	MG	BA	3058	1/1	0.41	-	38,38,38,38	0
57	SF4	AD	501	8/8	0.14	-	59,72,92,96	0
56	MG	BD	311	1/1	0.53	-	45,45,45,45	0
56	MG	BA	3084	1/1	0.17	-	33,33,33,33	0
56	MG	DA	3397	1/1	0.18	-	41,41,41,41	0
56	MG	DA	3288	1/1	0.18	-	47,47,47,47	0
56	MG	AA	3045	1/1	0.32	-	61,61,61,61	0
56	MG	CA	3043	1/1	0.32	-	49,49,49,49	0
56	MG	DA	3342	1/1	0.12	-	52,52,52,52	0
56	MG	BA	3441	1/1	0.24	-	25,25,25,25	0
56	MG	AA	3017	1/1	0.28	-	55,55,55,55	0
56	MG	BA	3079	1/1	0.27	-	42,42,42,42	0
56	MG	DQ	203	1/1	0.31	-	57,57,57,57	0
56	MG	CX	103	1/1	0.27	-	60,60,60,60	0
56	MG	BA	3112	1/1	0.09	-	38,38,38,38	0
56	MG	BA	3095	1/1	0.39	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3158	1/1	0.23	-	76,76,76,76	0
56	MG	AX	105	1/1	0.66	-	56,56,56,56	0
56	MG	BA	3210	1/1	0.09	-	34,34,34,34	0
56	MG	BA	3308	1/1	0.08	-	44,44,44,44	0
56	MG	BA	3097	1/1	0.19	-	33,33,33,33	0
56	MG	DA	3500	1/1	0.19	-	50,50,50,50	0
56	MG	DA	3314	1/1	0.20	-	64,64,64,64	0
56	MG	DW	202	1/1	0.44	-	58,58,58,58	0
56	MG	CA	3143	1/1	0.09	-	87,87,87,87	0
56	MG	DA	3634	1/1	0.15	-	51,51,51,51	0
56	MG	CA	3115	1/1	0.11	-	55,55,55,55	0
56	MG	BA	3675	1/1	0.12	-	49,49,49,49	0
56	MG	BA	3260	1/1	0.18	-	22,22,22,22	0
56	MG	DA	3023	1/1	0.33	-	52,52,52,52	0
56	MG	AA	3003	1/1	0.30	-	63,63,63,63	0
56	MG	BA	3570	1/1	0.12	-	61,61,61,61	0
56	MG	DA	3559	1/1	0.19	-	46,46,46,46	0
56	MG	DA	3524	1/1	0.11	-	28,28,28,28	0
56	MG	CA	3138	1/1	0.25	-	72,72,72,72	0
56	MG	DA	3097	1/1	0.27	-	61,61,61,61	0
56	MG	DA	3392	1/1	0.18	-	35,35,35,35	0
56	MG	DA	3081	1/1	0.20	-	48,48,48,48	0
56	MG	DA	3168	1/1	0.39	-	48,48,48,48	0
56	MG	DE	303	1/1	0.11	-	41,41,41,41	0
56	MG	BA	3120	1/1	0.07	-	51,51,51,51	0
56	MG	DA	3145	1/1	0.42	-	65,65,65,65	0
56	MG	DA	3590	1/1	0.18	-	80,80,80,80	0
56	MG	BW	202	1/1	0.17	-	34,34,34,34	0
56	MG	BA	3313	1/1	0.26	-	36,36,36,36	0
56	MG	BA	3680	1/1	0.38	-	37,37,37,37	0
56	MG	DA	3533	1/1	0.09	-	68,68,68,68	0
56	MG	AA	3197	1/1	0.40	-	69,69,69,69	0
56	MG	DA	3127	1/1	0.07	-	48,48,48,48	0
56	MG	BA	3724	1/1	0.18	-	58,58,58,58	0
56	MG	BA	3158	1/1	0.60	-	64,64,64,64	0
56	MG	DA	3183	1/1	0.12	-	54,54,54,54	0
56	MG	BA	3275	1/1	0.22	-	46,46,46,46	0
56	MG	BA	3598	1/1	0.11	-	56,56,56,56	0
56	MG	AA	3153	1/1	0.14	-	45,45,45,45	0
56	MG	BA	3736	1/1	0.23	-	48,48,48,48	0
56	MG	BA	3066	1/1	0.23	-	44,44,44,44	0
56	MG	AA	3215	1/1	0.10	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3250	1/1	0.17	-	45,45,45,45	0
56	MG	BA	3566	1/1	0.10	-	53,53,53,53	0
56	MG	BA	3155	1/1	0.39	-	57,57,57,57	0
56	MG	BA	3186	1/1	0.15	-	53,53,53,53	0
56	MG	DA	3105	1/1	0.34	-	48,48,48,48	0
56	MG	DA	3050	1/1	0.58	-	31,31,31,31	0
56	MG	AA	3191	1/1	0.13	-	71,71,71,71	0
56	MG	BA	3401	1/1	0.11	-	42,42,42,42	0
56	MG	DA	3234	1/1	0.22	-	33,33,33,33	0
56	MG	BA	3073	1/1	0.89	-	41,41,41,41	0
56	MG	CA	3017	1/1	0.23	-	42,42,42,42	0
56	MG	BA	3556	1/1	0.33	-	27,27,27,27	0
56	MG	CA	3009	1/1	0.13	-	47,47,47,47	0
56	MG	CA	3106	1/1	0.31	-	64,64,64,64	0
56	MG	BA	3175	1/1	0.27	-	48,48,48,48	0
56	MG	DA	3108	1/1	0.52	-	37,37,37,37	0
56	MG	DA	3325	1/1	0.16	-	36,36,36,36	0
56	MG	BA	3417	1/1	0.17	-	18,18,18,18	0
56	MG	DA	3214	1/1	0.27	-	64,64,64,64	0
56	MG	BA	3190	1/1	0.20	-	42,42,42,42	0
56	MG	DA	3213	1/1	0.23	-	44,44,44,44	0
56	MG	BA	3285	1/1	0.14	-	32,32,32,32	0
56	MG	DA	3347	1/1	0.16	-	62,62,62,62	0
56	MG	DA	3501	1/1	0.20	-	23,23,23,23	0
56	MG	AA	3028	1/1	0.47	-	60,60,60,60	0
56	MG	AA	3060	1/1	0.54	-	60,60,60,60	0
56	MG	BY	201	1/1	0.33	-	58,58,58,58	0
56	MG	DA	3507	1/1	0.15	-	54,54,54,54	0
56	MG	BA	3236	1/1	0.20	-	36,36,36,36	0
56	MG	BA	3103	1/1	0.12	-	53,53,53,53	0
56	MG	AA	3119	1/1	0.37	-	63,63,63,63	0
56	MG	CA	3010	1/1	0.10	-	32,32,32,32	0
56	MG	DA	3269	1/1	0.12	-	48,48,48,48	0
56	MG	DA	3276	1/1	0.22	-	36,36,36,36	0
56	MG	AA	3203	1/1	0.14	-	63,63,63,63	0
56	MG	BA	3652	1/1	0.21	-	64,64,64,64	0
56	MG	DA	3319	1/1	0.17	-	53,53,53,53	0
56	MG	DA	3515	1/1	0.27	-	48,48,48,48	0
56	MG	DA	3169	1/1	0.42	-	57,57,57,57	0
56	MG	BA	3392	1/1	0.24	-	56,56,56,56	0
56	MG	DA	3259	1/1	0.16	-	47,47,47,47	0
56	MG	AA	3137	1/1	0.21	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DQ	205	1/1	0.44	-	55,55,55,55	0
56	MG	DA	3329	1/1	0.16	-	53,53,53,53	0
56	MG	BA	3475	1/1	0.20	-	36,36,36,36	0
56	MG	DA	3623	1/1	0.16	-	53,53,53,53	0
56	MG	CA	3084	1/1	0.14	-	64,64,64,64	0
56	MG	DA	3066	1/1	0.40	-	53,53,53,53	0
56	MG	DA	3548	1/1	0.14	-	37,37,37,37	0
56	MG	BA	3440	1/1	0.37	-	38,38,38,38	0
56	MG	AA	3043	1/1	0.52	-	74,74,74,74	0
56	MG	DA	3348	1/1	0.30	-	37,37,37,37	0
56	MG	DA	3052	1/1	0.21	-	23,23,23,23	0
56	MG	BA	3677	1/1	0.25	-	67,67,67,67	0
56	MG	DA	3516	1/1	0.15	-	40,40,40,40	0
56	MG	DA	3061	1/1	0.41	-	52,52,52,52	0
56	MG	DA	3646	1/1	0.07	-	38,38,38,38	0
56	MG	DA	3202	1/1	0.31	-	42,42,42,42	0
56	MG	CA	3052	1/1	0.13	-	39,39,39,39	0
56	MG	AA	3066	1/1	0.27	-	38,38,38,38	0
56	MG	BA	3273	1/1	0.40	-	42,42,42,42	0
56	MG	AX	102	1/1	0.23	-	74,74,74,74	0
56	MG	BA	3461	1/1	0.24	-	36,36,36,36	0
56	MG	AA	3125	1/1	0.16	-	47,47,47,47	0
56	MG	B8	102	1/1	0.10	-	60,60,60,60	0
56	MG	BA	3690	1/1	0.17	-	53,53,53,53	0
56	MG	DA	3631	1/1	0.16	-	56,56,56,56	0
56	MG	DA	3026	1/1	0.21	-	37,37,37,37	0
56	MG	BE	305	1/1	0.69	-	42,42,42,42	0
56	MG	BA	3687	1/1	0.22	-	38,38,38,38	0
56	MG	DA	3096	1/1	0.16	-	60,60,60,60	0
56	MG	BA	3039	1/1	0.14	-	42,42,42,42	0
56	MG	DA	3011	1/1	0.42	-	45,45,45,45	0
56	MG	CA	3045	1/1	0.09	-	54,54,54,54	0
56	MG	CA	3077	1/1	0.21	-	53,53,53,53	0
56	MG	BA	3403	1/1	0.21	-	41,41,41,41	0
56	MG	AA	3089	1/1	0.43	-	78,78,78,78	0
56	MG	BA	3209	1/1	0.39	-	40,40,40,40	0
56	MG	AA	3057	1/1	0.08	-	37,37,37,37	0
56	MG	BA	3380	1/1	0.13	-	53,53,53,53	0
56	MG	AA	3044	1/1	0.22	-	66,66,66,66	0
56	MG	BD	308	1/1	0.34	-	23,23,23,23	0
56	MG	DA	3588	1/1	0.18	-	40,40,40,40	0
56	MG	BA	3177	1/1	0.22	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3082	1/1	0.08	-	47,47,47,47	0
56	MG	DA	3574	1/1	0.17	-	56,56,56,56	0
56	MG	BA	3456	1/1	0.08	-	52,52,52,52	0
56	MG	BA	3664	1/1	0.28	-	68,68,68,68	0
56	MG	BU	203	1/1	0.30	-	33,33,33,33	0
56	MG	BA	3011	1/1	0.08	-	37,37,37,37	0
56	MG	D0	101	1/1	0.13	-	63,63,63,63	0
56	MG	BA	3008	1/1	0.15	-	50,50,50,50	0
56	MG	AA	3175	1/1	0.14	-	76,76,76,76	0
56	MG	DD	304	1/1	0.23	-	35,35,35,35	0
56	MG	BA	3416	1/1	0.25	-	42,42,42,42	0
56	MG	BA	3450	1/1	0.26	-	46,46,46,46	0
56	MG	BA	3360	1/1	0.18	-	38,38,38,38	0
56	MG	BF	304	1/1	0.07	-	35,35,35,35	0
56	MG	BA	3098	1/1	0.15	-	35,35,35,35	0
56	MG	AA	3036	1/1	0.25	-	71,71,71,71	0
56	MG	DA	3150	1/1	0.19	-	64,64,64,64	0
56	MG	BA	3430	1/1	0.29	-	49,49,49,49	0
56	MG	BA	3547	1/1	0.19	-	31,31,31,31	0
56	MG	B8	101	1/1	0.52	-	49,49,49,49	0
56	MG	BA	3082	1/1	0.28	-	41,41,41,41	0
56	MG	DA	3485	1/1	0.09	-	38,38,38,38	0
56	MG	BA	3266	1/1	0.32	-	46,46,46,46	0
56	MG	DA	3037	1/1	0.33	-	35,35,35,35	0
56	MG	AA	3188	1/1	0.25	-	53,53,53,53	0
56	MG	CA	3120	1/1	0.19	-	58,58,58,58	0
56	MG	BA	3151	1/1	0.07	-	52,52,52,52	0
56	MG	DA	3620	1/1	0.20	-	71,71,71,71	0
56	MG	BA	3280	1/1	0.66	-	69,69,69,69	0
56	MG	DA	3216	1/1	0.17	-	31,31,31,31	0
56	MG	BA	3386	1/1	0.15	-	58,58,58,58	0
56	MG	BA	3477	1/1	0.11	-	25,25,25,25	0
56	MG	BA	3171	1/1	0.33	-	40,40,40,40	0
58	ZN	B4	3002	1/1	0.06	-	165,165,165,165	0
56	MG	AA	3061	1/1	0.21	-	82,82,82,82	0
56	MG	DA	3170	1/1	0.74	-	57,57,57,57	0
56	MG	BA	3636	1/1	0.10	-	36,36,36,36	0
56	MG	BA	3471	1/1	0.17	-	51,51,51,51	0
56	MG	AA	3105	1/1	0.21	-	46,46,46,46	0
56	MG	DA	3433	1/1	0.19	-	48,48,48,48	0
56	MG	DA	3330	1/1	0.18	-	37,37,37,37	0
56	MG	BA	3666	1/1	0.30	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AM	3001	1/1	0.08	-	65,65,65,65	0
56	MG	DA	3579	1/1	0.17	-	23,23,23,23	0
56	MG	BA	3731	1/1	0.37	-	55,55,55,55	0
56	MG	BA	3606	1/1	0.21	-	25,25,25,25	0
56	MG	DA	3436	1/1	0.08	-	62,62,62,62	0
56	MG	DA	3622	1/1	0.09	-	55,55,55,55	0
56	MG	DA	3009	1/1	0.12	-	31,31,31,31	0
56	MG	DA	3536	1/1	0.18	-	80,80,80,80	0
56	MG	CA	3029	1/1	0.21	-	59,59,59,59	0
56	MG	AA	3037	1/1	0.41	-	61,61,61,61	0
56	MG	DA	3019	1/1	0.12	-	30,30,30,30	0
56	MG	DA	3092	1/1	0.52	-	39,39,39,39	0
56	MG	DA	3487	1/1	0.18	-	57,57,57,57	0
56	MG	AA	3029	1/1	0.62	-	52,52,52,52	0
56	MG	CA	3033	1/1	0.18	-	68,68,68,68	0
56	MG	CA	3087	1/1	0.18	-	41,41,41,41	0
56	MG	DA	3128	1/1	0.21	-	52,52,52,52	0
56	MG	AA	3205	1/1	0.17	-	61,61,61,61	0
56	MG	B0	102	1/1	0.57	-	40,40,40,40	0
56	MG	DA	3239	1/1	0.23	-	39,39,39,39	0
56	MG	DA	3556	1/1	0.07	-	56,56,56,56	0
56	MG	DA	3502	1/1	0.10	-	65,65,65,65	0
56	MG	BA	3518	1/1	0.12	-	41,41,41,41	0
56	MG	AX	103	1/1	0.08	-	66,66,66,66	0
56	MG	DA	3160	1/1	0.15	-	44,44,44,44	0
56	MG	BA	3284	1/1	0.11	-	54,54,54,54	0
56	MG	BV	203	1/1	1.06	-	46,46,46,46	0
56	MG	BA	3013	1/1	0.08	-	40,40,40,40	0
56	MG	BA	3466	1/1	0.14	-	61,61,61,61	0
56	MG	BE	304	1/1	0.09	-	49,49,49,49	0
56	MG	DA	3386	1/1	0.16	-	56,56,56,56	0
56	MG	DA	3100	1/1	0.47	-	56,56,56,56	0
56	MG	DA	3496	1/1	0.14	-	53,53,53,53	0
56	MG	DA	3449	1/1	0.10	-	43,43,43,43	0
56	MG	BA	3047	1/1	0.47	-	47,47,47,47	0
56	MG	CA	3038	1/1	0.43	-	70,70,70,70	0
56	MG	BA	3583	1/1	0.21	-	27,27,27,27	0
56	MG	AA	3086	1/1	0.28	-	51,51,51,51	0
56	MG	BA	3213	1/1	0.05	-	41,41,41,41	0
56	MG	CA	3114	1/1	0.24	-	82,82,82,82	0
56	MG	DA	3651	1/1	0.60	-	52,52,52,52	0
56	MG	DA	3257	1/1	0.11	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	CA	3031	1/1	0.40	-	53,53,53,53	0
56	MG	AA	3031	1/1	0.23	-	41,41,41,41	0
56	MG	BA	3268	1/1	0.18	-	46,46,46,46	0
56	MG	AA	3079	1/1	1.09	-	74,74,74,74	0
56	MG	DA	3427	1/1	0.57	-	60,60,60,60	0
56	MG	BW	205	1/1	0.38	-	41,41,41,41	0
56	MG	CA	3172	1/1	0.14	-	51,51,51,51	0
56	MG	BA	3620	1/1	0.12	-	47,47,47,47	0
56	MG	DA	3396	1/1	0.22	-	35,35,35,35	0
56	MG	BA	3243	1/1	0.16	-	48,48,48,48	0
56	MG	AA	3126	1/1	0.15	-	54,54,54,54	0
58	ZN	BY	202	1/1	0.08	-	71,71,71,71	0
56	MG	BA	3231	1/1	0.49	-	38,38,38,38	0
56	MG	AA	3182	1/1	0.12	-	49,49,49,49	0
56	MG	BA	3493	1/1	0.36	-	15,15,15,15	0
56	MG	BA	3384	1/1	0.35	-	60,60,60,60	0
56	MG	BA	3060	1/1	0.39	-	40,40,40,40	0
56	MG	BA	3237	1/1	0.54	-	51,51,51,51	0
56	MG	BA	3189	1/1	0.17	-	54,54,54,54	0
56	MG	BA	3149	1/1	0.58	-	40,40,40,40	0
56	MG	AA	3102	1/1	0.06	-	64,64,64,64	0
56	MG	BA	3127	1/1	0.38	-	50,50,50,50	0
56	MG	DA	3636	1/1	0.14	-	61,61,61,61	0
56	MG	DA	3522	1/1	0.17	-	61,61,61,61	0
56	MG	BA	3364	1/1	0.23	-	29,29,29,29	0
56	MG	BA	3449	1/1	0.12	-	21,21,21,21	0
56	MG	DA	3045	1/1	0.36	-	41,41,41,41	0
56	MG	BA	3174	1/1	0.08	-	48,48,48,48	0
56	MG	AA	3152	1/1	0.09	-	19,19,19,19	0
56	MG	DA	3580	1/1	0.14	-	46,46,46,46	0
56	MG	BB	3007	1/1	0.08	-	47,47,47,47	0
56	MG	BA	3083	1/1	0.23	-	63,63,63,63	0
56	MG	AA	3132	1/1	0.32	-	76,76,76,76	0
56	MG	BA	3468	1/1	0.18	-	30,30,30,30	0
56	MG	CA	3094	1/1	0.18	-	43,43,43,43	0
56	MG	AA	3005	1/1	0.15	-	66,66,66,66	0
56	MG	BA	3443	1/1	0.16	-	26,26,26,26	0
56	MG	DA	3480	1/1	0.09	-	52,52,52,52	0
56	MG	DA	3299	1/1	0.20	-	40,40,40,40	0
56	MG	DA	3450	1/1	0.13	-	43,43,43,43	0
56	MG	DA	3531	1/1	0.10	-	57,57,57,57	0
56	MG	DA	3175	1/1	0.19	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3266	1/1	0.24	-	43,43,43,43	0
56	MG	DA	3570	1/1	0.24	-	28,28,28,28	0
56	MG	CA	3124	1/1	0.15	-	61,61,61,61	0
56	MG	DA	3224	1/1	0.17	-	47,47,47,47	0
56	MG	CA	3044	1/1	0.23	-	63,63,63,63	0
56	MG	BA	3351	1/1	0.06	-	30,30,30,30	0
56	MG	BA	3663	1/1	0.27	-	56,56,56,56	0
56	MG	DA	3012	1/1	0.22	-	57,57,57,57	0
56	MG	BA	3618	1/1	0.28	-	46,46,46,46	0
56	MG	DA	3110	1/1	0.13	-	49,49,49,49	0
56	MG	AA	3147	1/1	0.41	-	61,61,61,61	0
56	MG	BE	310	1/1	0.27	-	50,50,50,50	0
56	MG	CA	3064	1/1	0.13	-	58,58,58,58	0
56	MG	BN	3005	1/1	0.85	-	52,52,52,52	0
56	MG	DA	3540	1/1	0.23	-	54,54,54,54	0
56	MG	CA	3103	1/1	0.18	-	83,83,83,83	0
56	MG	BA	3279	1/1	0.22	-	48,48,48,48	0
56	MG	BA	3022	1/1	0.33	-	52,52,52,52	0
56	MG	BA	3582	1/1	0.21	-	25,25,25,25	0
56	MG	BA	3292	1/1	0.21	-	63,63,63,63	0
56	MG	BA	3043	1/1	0.20	-	52,52,52,52	0
56	MG	DA	3124	1/1	0.13	-	67,67,67,67	0
56	MG	BA	3407	1/1	0.18	-	15,15,15,15	0
56	MG	DA	3426	1/1	0.15	-	74,74,74,74	0
56	MG	DA	3489	1/1	0.18	-	36,36,36,36	0
56	MG	AA	3072	1/1	0.29	-	79,79,79,79	0
56	MG	BA	3165	1/1	0.34	-	53,53,53,53	0
56	MG	DV	204	1/1	0.22	-	41,41,41,41	0
56	MG	BA	3425	1/1	0.34	-	36,36,36,36	0
56	MG	AA	3032	1/1	0.35	-	57,57,57,57	0
56	MG	BA	3264	1/1	0.17	-	30,30,30,30	0
56	MG	BA	3454	1/1	0.10	-	22,22,22,22	0
56	MG	BR	202	1/1	0.27	-	27,27,27,27	0
56	MG	AA	3218	1/1	0.54	-	65,65,65,65	0
56	MG	DA	3115	1/1	0.10	-	63,63,63,63	0
56	MG	DA	3447	1/1	0.06	-	56,56,56,56	0
56	MG	DA	3376	1/1	0.07	-	31,31,31,31	0
56	MG	DA	3142	1/1	0.24	-	33,33,33,33	0
56	MG	DA	3483	1/1	0.19	-	49,49,49,49	0
56	MG	CA	3159	1/1	0.58	-	91,91,91,91	0
56	MG	DA	3243	1/1	0.21	-	67,67,67,67	0
56	MG	BA	3434	1/1	0.12	-	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3006	1/1	0.08	-	78,78,78,78	0
56	MG	CA	3022	1/1	0.04	-	70,70,70,70	0
56	MG	DA	3048	1/1	0.40	-	37,37,37,37	0
56	MG	AA	3149	1/1	0.09	-	50,50,50,50	0
56	MG	DA	3339	1/1	0.09	-	37,37,37,37	0
56	MG	DA	3337	1/1	0.09	-	27,27,27,27	0
56	MG	BA	3670	1/1	0.15	-	59,59,59,59	0
56	MG	CA	3148	1/1	0.23	-	68,68,68,68	0
56	MG	BA	3038	1/1	0.53	-	51,51,51,51	0
56	MG	BA	3138	1/1	0.16	-	46,46,46,46	0
56	MG	BA	3309	1/1	0.14	-	46,46,46,46	0
56	MG	DA	3194	1/1	0.14	-	48,48,48,48	0
56	MG	DA	3279	1/1	0.29	-	63,63,63,63	0
56	MG	AA	3171	1/1	0.25	-	72,72,72,72	0
56	MG	DA	3069	1/1	0.11	-	51,51,51,51	0
56	MG	DA	3148	1/1	0.25	-	47,47,47,47	0
56	MG	AA	3085	1/1	0.30	-	69,69,69,69	0
56	MG	BA	3321	1/1	0.16	-	29,29,29,29	0
56	MG	CF	3001	1/1	0.24	-	55,55,55,55	0
56	MG	DD	301	1/1	0.46	-	46,46,46,46	0
56	MG	D3	101	1/1	0.43	-	63,63,63,63	0
56	MG	CA	3006	1/1	0.15	-	77,77,77,77	0
56	MG	BA	3596	1/1	0.11	-	51,51,51,51	0
56	MG	DA	3013	1/1	0.09	-	47,47,47,47	0
56	MG	BA	3727	1/1	0.57	-	68,68,68,68	0
56	MG	DA	3159	1/1	0.24	-	51,51,51,51	0
56	MG	BA	3199	1/1	0.48	-	36,36,36,36	0
56	MG	BA	3496	1/1	0.43	-	57,57,57,57	0
56	MG	DA	3353	1/1	0.11	-	62,62,62,62	0
56	MG	BA	3413	1/1	0.13	-	20,20,20,20	0
56	MG	AA	3016	1/1	0.06	-	63,63,63,63	0
56	MG	BA	3289	1/1	0.34	-	60,60,60,60	0
56	MG	AA	3157	1/1	0.08	-	35,35,35,35	0
56	MG	BA	3181	1/1	0.35	-	38,38,38,38	0
56	MG	DA	3603	1/1	0.17	-	55,55,55,55	0
56	MG	DV	203	1/1	0.78	-	54,54,54,54	0
56	MG	DA	3237	1/1	0.18	-	45,45,45,45	0
56	MG	BA	3387	1/1	0.08	-	48,48,48,48	0
56	MG	CA	3059	1/1	0.28	-	51,51,51,51	0
56	MG	BG	3004	1/1	0.04	-	62,62,62,62	0
56	MG	AA	3130	1/1	0.22	-	46,46,46,46	0
56	MG	DA	3653	1/1	0.34	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3113	1/1	0.63	-	43,43,43,43	0
56	MG	BA	3317	1/1	0.15	-	40,40,40,40	0
56	MG	DA	3416	1/1	0.08	-	44,44,44,44	0
56	MG	DA	3217	1/1	0.47	-	54,54,54,54	0
56	MG	BA	3326	1/1	0.09	-	41,41,41,41	0
56	MG	DA	3361	1/1	0.11	-	61,61,61,61	0
56	MG	BA	3701	1/1	0.13	-	32,32,32,32	0
56	MG	CA	3054	1/1	0.34	-	48,48,48,48	0
56	MG	DA	3445	1/1	0.24	-	39,39,39,39	0
56	MG	BA	3478	1/1	0.13	-	29,29,29,29	0
56	MG	BA	3444	1/1	0.12	-	74,74,74,74	0
56	MG	BA	3661	1/1	0.15	-	68,68,68,68	0
56	MG	DA	3647	1/1	0.40	-	66,66,66,66	0
56	MG	DA	3520	1/1	0.20	-	51,51,51,51	0
56	MG	AA	3096	1/1	0.28	-	44,44,44,44	0
56	MG	CT	3001	1/1	0.40	-	57,57,57,57	0
56	MG	BA	3397	1/1	0.19	-	28,28,28,28	0
56	MG	CA	3068	1/1	0.11	-	41,41,41,41	0
56	MG	CA	3061	1/1	0.26	-	46,46,46,46	0
56	MG	BB	3005	1/1	0.27	-	61,61,61,61	0
56	MG	DA	3147	1/1	0.13	-	53,53,53,53	0
56	MG	DA	3029	1/1	0.13	-	61,61,61,61	0
56	MG	DA	3609	1/1	0.34	-	64,64,64,64	0
56	MG	BA	3725	1/1	0.11	-	49,49,49,49	0
56	MG	BA	3612	1/1	0.13	-	37,37,37,37	0
56	MG	BA	3480	1/1	0.20	-	17,17,17,17	0
56	MG	BA	3368	1/1	0.20	-	35,35,35,35	0
56	MG	BA	3258	1/1	0.23	-	40,40,40,40	0
56	MG	BA	3378	1/1	0.12	-	20,20,20,20	0
56	MG	CX	104	1/1	0.12	-	40,40,40,40	0
56	MG	AA	3007	1/1	0.16	-	82,82,82,82	0
56	MG	BB	3015	1/1	0.11	-	37,37,37,37	0
56	MG	BA	3320	1/1	0.28	-	57,57,57,57	0
56	MG	DA	3602	1/1	0.18	-	52,52,52,52	0
56	MG	AA	3127	1/1	0.17	-	62,62,62,62	0
56	MG	BA	3414	1/1	0.21	-	19,19,19,19	0
56	MG	CA	3118	1/1	0.09	-	37,37,37,37	0
56	MG	DA	3395	1/1	0.22	-	34,34,34,34	0
56	MG	DA	3157	1/1	1.06	-	62,62,62,62	0
56	MG	AA	3113	1/1	0.34	-	68,68,68,68	0
56	MG	BA	3649	1/1	0.20	-	66,66,66,66	0
56	MG	DA	3251	1/1	0.12	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3148	1/1	0.32	-	52,52,52,52	0
58	ZN	B5	501	1/1	0.10	-	54,54,54,54	0
56	MG	B9	502	1/1	0.25	-	49,49,49,49	0
56	MG	AA	3114	1/1	0.49	-	66,66,66,66	0
56	MG	BA	3154	1/1	0.16	-	61,61,61,61	0
56	MG	BA	3221	1/1	0.29	-	44,44,44,44	0
56	MG	BA	3588	1/1	0.21	-	48,48,48,48	0
56	MG	DA	3471	1/1	0.12	-	37,37,37,37	0
56	MG	BA	3094	1/1	0.85	-	61,61,61,61	0
56	MG	BA	3057	1/1	0.28	-	35,35,35,35	0
56	MG	BA	3085	1/1	0.49	-	48,48,48,48	0
56	MG	BA	3176	1/1	0.18	-	38,38,38,38	0
56	MG	DA	3087	1/1	0.18	-	49,49,49,49	0
56	MG	CA	3130	1/1	0.08	-	65,65,65,65	0
56	MG	BA	3589	1/1	0.15	-	51,51,51,51	0
56	MG	BA	3377	1/1	0.12	-	32,32,32,32	0
56	MG	B3	102	1/1	0.13	-	59,59,59,59	0
56	MG	BA	3168	1/1	0.27	-	42,42,42,42	0
56	MG	DA	3085	1/1	0.13	-	36,36,36,36	0
56	MG	AA	3141	1/1	0.21	-	48,48,48,48	0
56	MG	DA	3138	1/1	0.20	-	42,42,42,42	0
56	MG	BA	3383	1/1	0.17	-	38,38,38,38	0
56	MG	DA	3341	1/1	0.19	-	23,23,23,23	0
56	MG	BA	3182	1/1	0.29	-	51,51,51,51	0
56	MG	BA	3665	1/1	0.20	-	39,39,39,39	0
56	MG	DA	3335	1/1	0.27	-	38,38,38,38	0
56	MG	AA	3193	1/1	0.12	-	60,60,60,60	0
56	MG	BA	3021	1/1	0.25	-	42,42,42,42	0
56	MG	BA	3502	1/1	0.23	-	43,43,43,43	0
56	MG	DA	3305	1/1	0.10	-	33,33,33,33	0
56	MG	BA	3542	1/1	0.22	-	19,19,19,19	0
56	MG	DA	3429	1/1	0.19	-	44,44,44,44	0
56	MG	AA	3095	1/1	0.24	-	58,58,58,58	0
56	MG	DA	3344	1/1	0.10	-	26,26,26,26	0
56	MG	CA	3058	1/1	0.09	-	40,40,40,40	0
56	MG	DA	3642	1/1	0.12	-	35,35,35,35	0
56	MG	DA	3440	1/1	0.28	-	33,33,33,33	0
56	MG	BA	3188	1/1	0.15	-	37,37,37,37	0
56	MG	DA	3431	1/1	0.11	-	41,41,41,41	0
56	MG	CA	3053	1/1	1.40	-	73,73,73,73	0
56	MG	BA	3689	1/1	0.23	-	39,39,39,39	0
56	MG	CA	3116	1/1	0.21	-	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3116	1/1	0.56	-	52,52,52,52	0
56	MG	DA	3306	1/1	0.18	-	33,33,33,33	0
56	MG	AA	3120	1/1	0.67	-	71,71,71,71	0
56	MG	BA	3720	1/1	0.19	-	33,33,33,33	0
56	MG	DD	306	1/1	1.12	-	44,44,44,44	0
56	MG	BA	3523	1/1	0.14	-	48,48,48,48	0
56	MG	AA	3008	1/1	0.34	-	54,54,54,54	0
56	MG	AA	3033	1/1	0.37	-	64,64,64,64	0
56	MG	BA	3641	1/1	0.11	-	45,45,45,45	0
56	MG	BA	3591	1/1	0.38	-	48,48,48,48	0
56	MG	DA	3010	1/1	0.16	-	39,39,39,39	0
56	MG	CA	3008	1/1	0.75	-	53,53,53,53	0
56	MG	BA	3005	1/1	0.17	-	36,36,36,36	0
56	MG	DA	3117	1/1	0.18	-	53,53,53,53	0
56	MG	DA	3053	1/1	0.17	-	42,42,42,42	0
56	MG	DA	3542	1/1	0.18	-	32,32,32,32	0
56	MG	CA	3083	1/1	0.09	-	39,39,39,39	0
56	MG	DA	3268	1/1	0.15	-	40,40,40,40	0
56	MG	BA	3369	1/1	0.21	-	45,45,45,45	0
56	MG	BA	3007	1/1	0.21	-	35,35,35,35	0
56	MG	BA	3659	1/1	0.18	-	46,46,46,46	0
56	MG	AF	3001	1/1	0.16	-	61,61,61,61	0
56	MG	AA	3159	1/1	0.29	-	57,57,57,57	0
56	MG	DA	3289	1/1	0.13	-	26,26,26,26	0
56	MG	DA	3583	1/1	0.20	-	48,48,48,48	0
56	MG	DA	3491	1/1	0.16	-	56,56,56,56	0
56	MG	DA	3597	1/1	0.21	-	47,47,47,47	0
56	MG	DA	3512	1/1	0.24	-	61,61,61,61	0
56	MG	BU	201	1/1	0.71	-	39,39,39,39	0
56	MG	BW	201	1/1	0.77	-	53,53,53,53	0
56	MG	CA	3046	1/1	0.33	-	53,53,53,53	0
56	MG	BX	3001	1/1	0.32	-	55,55,55,55	0
60	K	BA	3300	1/1	0.31	-	100,100,100,100	0
56	MG	DB	3006	1/1	0.15	-	42,42,42,42	0
56	MG	BA	3706	1/1	0.44	-	63,63,63,63	0
56	MG	DA	3195	1/1	0.10	-	50,50,50,50	0
56	MG	DA	3562	1/1	0.10	-	61,61,61,61	0
56	MG	BA	3640	1/1	0.20	-	60,60,60,60	0
56	MG	BB	3008	1/1	0.22	-	35,35,35,35	0
56	MG	CA	3137	1/1	0.14	-	48,48,48,48	0
56	MG	DA	3241	1/1	0.21	-	15,15,15,15	0
56	MG	CA	3079	1/1	0.14	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3035	1/1	0.18	-	56,56,56,56	0
56	MG	AA	3213	1/1	0.17	-	29,29,29,29	0
56	MG	DA	3088	1/1	0.14	-	46,46,46,46	0
56	MG	DA	3300	1/1	0.15	-	37,37,37,37	0
56	MG	DA	3174	1/1	0.24	-	41,41,41,41	0
56	MG	BA	3682	1/1	0.16	-	38,38,38,38	0
56	MG	DA	3180	1/1	0.18	-	46,46,46,46	0
56	MG	DA	3418	1/1	0.17	-	29,29,29,29	0
56	MG	BA	3109	1/1	0.08	-	36,36,36,36	0
56	MG	B0	103	1/1	0.84	-	59,59,59,59	0
56	MG	DA	3410	1/1	0.23	-	69,69,69,69	0
56	MG	DA	3360	1/1	0.23	-	41,41,41,41	0
56	MG	BA	3099	1/1	0.19	-	44,44,44,44	0
56	MG	DA	3074	1/1	0.18	-	54,54,54,54	0
56	MG	DE	304	1/1	0.20	-	41,41,41,41	0
56	MG	BA	3611	1/1	0.26	-	52,52,52,52	0
56	MG	DA	3545	1/1	0.59	-	75,75,75,75	0
56	MG	DA	3461	1/1	0.22	-	41,41,41,41	0
56	MG	DA	3198	1/1	0.28	-	48,48,48,48	0
56	MG	DA	3527	1/1	0.09	-	46,46,46,46	0
56	MG	DA	3437	1/1	0.14	-	49,49,49,49	0
56	MG	BE	303	1/1	0.15	-	29,29,29,29	0
56	MG	DR	202	1/1	0.16	-	37,37,37,37	0
56	MG	BA	3453	1/1	0.19	-	18,18,18,18	0
56	MG	DD	303	1/1	0.20	-	19,19,19,19	0
56	MG	AA	3111	1/1	0.18	-	95,95,95,95	0
56	MG	BA	3389	1/1	0.12	-	48,48,48,48	0
56	MG	BA	3722	1/1	0.17	-	32,32,32,32	0
56	MG	CA	3056	1/1	0.12	-	64,64,64,64	0
56	MG	DA	3506	1/1	0.06	-	59,59,59,59	0
56	MG	CA	3168	1/1	0.36	-	77,77,77,77	0
56	MG	DA	3154	1/1	0.62	-	45,45,45,45	0
56	MG	BA	3200	1/1	0.26	-	25,25,25,25	0
56	MG	BA	3554	1/1	0.19	-	31,31,31,31	0
56	MG	BA	3269	1/1	0.63	-	34,34,34,34	0
56	MG	BA	3169	1/1	0.56	-	46,46,46,46	0
56	MG	BA	3224	1/1	0.74	-	64,64,64,64	0
56	MG	BA	3415	1/1	0.23	-	27,27,27,27	0
56	MG	DA	3333	1/1	0.25	-	58,58,58,58	0
56	MG	DA	3253	1/1	0.17	-	42,42,42,42	0
56	MG	BF	305	1/1	0.34	-	35,35,35,35	0
56	MG	DA	3624	1/1	0.34	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	DA	3155	1/1	0.17	-	50,50,50,50	0
56	MG	BA	3256	1/1	0.20	-	58,58,58,58	0
56	MG	AA	3183	1/1	0.09	-	42,42,42,42	0
56	MG	DA	3618	1/1	0.09	-	39,39,39,39	0
56	MG	BA	3497	1/1	0.13	-	62,62,62,62	0
56	MG	DA	3560	1/1	0.12	-	34,34,34,34	0
56	MG	BA	3024	1/1	0.41	-	35,35,35,35	0
56	MG	BA	3467	1/1	0.05	-	40,40,40,40	0
56	MG	BA	3707	1/1	0.20	-	36,36,36,36	0
56	MG	DA	3639	1/1	0.29	-	15,15,15,15	0
56	MG	DA	3513	1/1	0.21	-	49,49,49,49	0
56	MG	DA	3163	1/1	0.18	-	39,39,39,39	0
56	MG	BA	3370	1/1	0.20	-	54,54,54,54	0
56	MG	BA	3614	1/1	0.41	-	30,30,30,30	0
56	MG	BA	3593	1/1	0.14	-	74,74,74,74	0
56	MG	B0	104	1/1	0.11	-	43,43,43,43	0
56	MG	BA	3315	1/1	0.10	-	37,37,37,37	0
56	MG	BB	3018	1/1	0.18	-	60,60,60,60	0
56	MG	DA	3389	1/1	0.25	-	27,27,27,27	0
56	MG	BA	3632	1/1	0.25	-	57,57,57,57	0
56	MG	BA	3704	1/1	0.17	-	85,85,85,85	0
56	MG	DA	3005	1/1	0.22	-	42,42,42,42	0
56	MG	CA	3171	1/1	0.31	-	67,67,67,67	0
56	MG	BG	3001	1/1	0.15	-	64,64,64,64	0
56	MG	BR	201	1/1	0.54	-	51,51,51,51	0
56	MG	DA	3375	1/1	0.15	-	60,60,60,60	0
56	MG	BA	3543	1/1	0.30	-	52,52,52,52	0
56	MG	AA	3166	1/1	0.17	-	48,48,48,48	0
56	MG	CA	3122	1/1	0.05	-	47,47,47,47	0
56	MG	BA	3131	1/1	0.77	-	54,54,54,54	0
56	MG	DR	201	1/1	0.56	-	65,65,65,65	0
56	MG	B3	103	1/1	0.59	-	41,41,41,41	0
56	MG	BA	3276	1/1	0.28	-	40,40,40,40	0
56	MG	AA	3207	1/1	0.28	-	45,45,45,45	0
56	MG	DA	3034	1/1	0.15	-	40,40,40,40	0
56	MG	BA	3346	1/1	0.22	-	37,37,37,37	0
56	MG	BU	206	1/1	0.38	-	60,60,60,60	0
56	MG	DA	3278	1/1	0.19	-	47,47,47,47	0
56	MG	DA	3462	1/1	0.10	-	55,55,55,55	0
56	MG	BA	3678	1/1	0.16	-	53,53,53,53	0
56	MG	CQ	201	1/1	0.18	-	56,56,56,56	0
56	MG	CA	3001	1/1	0.13	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	AA	3065	1/1	0.27	-	60,60,60,60	0
56	MG	BA	3695	1/1	0.16	-	15,15,15,15	0
56	MG	BA	3601	1/1	0.29	-	64,64,64,64	0
56	MG	DA	3509	1/1	0.18	-	55,55,55,55	0
56	MG	DA	3577	1/1	0.24	-	44,44,44,44	0
56	MG	BA	3473	1/1	0.12	-	51,51,51,51	0
56	MG	AA	3129	1/1	0.31	-	77,77,77,77	0
56	MG	DA	3263	1/1	0.18	-	31,31,31,31	0
56	MG	DA	3552	1/1	0.12	-	34,34,34,34	0
56	MG	DA	3633	1/1	0.20	-	54,54,54,54	0
56	MG	BA	3646	1/1	0.24	-	52,52,52,52	0
56	MG	BA	3025	1/1	0.23	-	28,28,28,28	0
56	MG	CA	3030	1/1	0.48	-	73,73,73,73	0
56	MG	DA	3067	1/1	0.52	-	43,43,43,43	0
56	MG	DA	3585	1/1	0.15	-	62,62,62,62	0
56	MG	DA	3425	1/1	0.10	-	27,27,27,27	0
56	MG	DA	3492	1/1	0.35	-	68,68,68,68	0
56	MG	DA	3518	1/1	0.16	-	40,40,40,40	0
56	MG	CA	3139	1/1	0.29	-	75,75,75,75	0
56	MG	BA	3696	1/1	0.25	-	39,39,39,39	0
56	MG	DA	3130	1/1	0.14	-	32,32,32,32	0
56	MG	DB	3005	1/1	0.24	-	43,43,43,43	0
56	MG	DA	3434	1/1	0.26	-	49,49,49,49	0
56	MG	DA	3565	1/1	0.09	-	57,57,57,57	0
56	MG	BA	3164	1/1	0.74	-	56,56,56,56	0
56	MG	BA	3239	1/1	0.09	-	33,33,33,33	0
56	MG	BA	3314	1/1	0.17	-	24,24,24,24	0
56	MG	CA	3092	1/1	0.12	-	47,47,47,47	0
56	MG	CA	3117	1/1	0.12	-	68,68,68,68	0
56	MG	BA	3657	1/1	0.16	-	56,56,56,56	0
56	MG	BA	3429	1/1	0.13	-	20,20,20,20	0
56	MG	BA	3059	1/1	0.61	-	45,45,45,45	0
56	MG	BA	3504	1/1	0.28	-	41,41,41,41	0
56	MG	BA	3431	1/1	0.22	-	17,17,17,17	0
56	MG	AA	3109	1/1	0.35	-	65,65,65,65	0
56	MG	AA	3059	1/1	1.09	-	54,54,54,54	0
56	MG	BA	3033	1/1	0.40	-	35,35,35,35	0
56	MG	AA	3140	1/1	0.12	-	70,70,70,70	0
56	MG	DA	3328	1/1	0.15	-	28,28,28,28	0
56	MG	BA	3052	1/1	0.25	-	29,29,29,29	0
56	MG	BA	3469	1/1	0.09	-	38,38,38,38	0
56	MG	CA	3157	1/1	0.13	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	BA	3089	1/1	0.44	-	61,61,61,61	0
56	MG	DA	3320	1/1	0.18	-	30,30,30,30	0
56	MG	BV	201	1/1	0.38	-	53,53,53,53	0
56	MG	CA	3065	1/1	0.23	-	75,75,75,75	0
56	MG	BP	201	1/1	0.69	-	40,40,40,40	0
56	MG	DA	3645	1/1	0.09	-	30,30,30,30	0
56	MG	BA	3023	1/1	0.14	-	66,66,66,66	0
56	MG	BA	3376	1/1	0.07	-	48,48,48,48	0
56	MG	DA	3402	1/1	0.09	-	61,61,61,61	0
56	MG	BA	3206	1/1	0.34	-	57,57,57,57	0
56	MG	CA	3036	1/1	0.65	-	68,68,68,68	0
56	MG	DA	3076	1/1	0.53	-	44,44,44,44	0
56	MG	DA	3073	1/1	0.16	-	44,44,44,44	0
56	MG	BA	3674	1/1	0.16	-	55,55,55,55	0
56	MG	DA	3388	1/1	0.15	-	54,54,54,54	0
56	MG	DA	3021	1/1	0.14	-	35,35,35,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.