



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2014 – 04:49 AM EDT

PDB ID : 1VY7
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in the pre-attack state of peptide bond formation containing short substrate-mimic Cytidine-Cytidine-Puromycin in the A site and acylated tRNA in the P site.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.80 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>

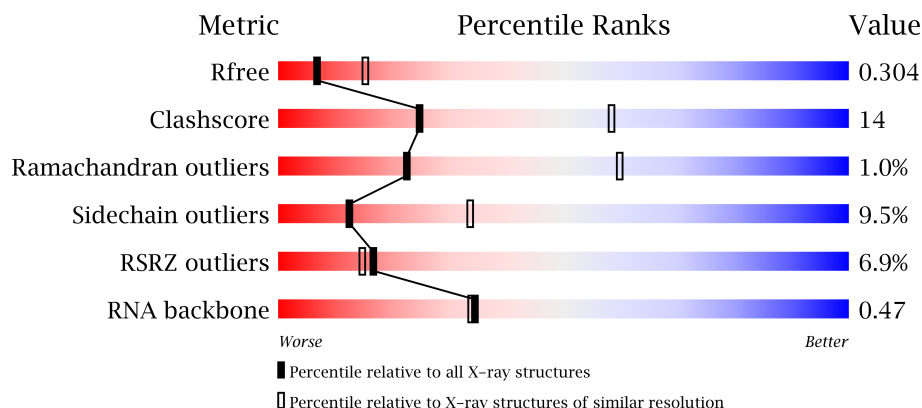
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
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) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)
RNA backbone	1838	1076 (3.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1521	
1	CA	1521	
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	

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Mol	Chain	Length	Quality of chain
6	CF	101	
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	AW	3	
23	CW	3	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	

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Mol	Chain	Length	Quality of chain
27	DB	121	
28	BD	276	
28	DD	276	
29	BE	206	
29	DE	206	
30	BF	210	
30	DF	210	
31	BG	182	
31	DG	182	
32	BH	180	
32	DH	180	
33	BI	148	
33	DI	148	
34	BN	140	
34	DN	140	
35	BO	122	
35	DO	122	
36	BP	150	
36	DP	150	
37	BQ	141	
37	DQ	141	
38	BR	118	
38	DR	118	
39	BS	112	
39	DS	112	
40	BT	146	
40	DT	146	
41	BU	118	
41	DU	118	
42	BV	101	
42	DV	101	
43	BW	113	
43	DW	113	
44	BX	96	
44	DX	96	
45	BY	110	
45	DY	110	
46	BZ	206	
46	DZ	206	
47	B0	85	
47	D0	85	
48	B1	98	

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Mol	Chain	Length	Quality of chain
48	D1	98	
49	B2	72	
49	D2	72	
50	B3	60	
50	D3	60	
51	B4	71	
51	D4	71	
52	B5	60	
52	D5	60	
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 290205 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
			32205	14333	5970	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 type Z.

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	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	6	Total	C	N	O	P	0	0	0
			129	58	24	41	6			

- Molecule 23 is a RNA chain called Cytidine-Puromycin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AW	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			
23	CW	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			

- Molecule 24 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	AX	76	Total	C	N	O	P	S	0	0	0
			1633	730	296	529	76	2			
24	CX	76	Total	C	N	O	P	S	0	0	0
			1635	731	296	530	76	2			

- Molecule 25 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	AY	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			
25	CY	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			

- Molecule 26 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BA	2819	Total	C	N	O	P	0	0	0
			60729	27026	11370	19515	2818			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

- Molecule 27 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 28 is a protein called 50S ribosomal protein L2.

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

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

- Molecule 50 is a protein called 50S ribosomal protein L30.

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

- Molecule 51 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B4	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			
51	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 52 is a protein called 50S ribosomal protein L32.

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

- Molecule 53 is a protein called 50S ribosomal protein L33.

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

- Molecule 54 is a protein called 50S ribosomal protein L34.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

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

- Molecule 56 is a protein called 50S ribosomal protein L36.

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

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	BA	720	Total	Mg	0	0
			720	720		
57	AK	1	Total	Mg	0	0
			1	1		
57	DQ	3	Total	Mg	0	0
			3	3		
57	D3	1	Total	Mg	0	0
			1	1		
57	DF	4	Total	Mg	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B8	1	Total 1	Mg 1	0	0
57	BE	7	Total 7	Mg 7	0	0
57	AW	1	Total 1	Mg 1	0	0
57	DU	4	Total 4	Mg 4	0	0
57	B1	1	Total 1	Mg 1	0	0
57	AN	2	Total 2	Mg 2	0	0
57	BP	4	Total 4	Mg 4	0	0
57	AX	11	Total 11	Mg 11	0	0
57	DN	1	Total 1	Mg 1	0	0
57	AS	1	Total 1	Mg 1	0	0
57	CA	160	Total 160	Mg 160	0	0
57	B5	2	Total 2	Mg 2	0	0
57	BB	20	Total 20	Mg 20	0	0
57	AJ	1	Total 1	Mg 1	0	0
57	D8	2	Total 2	Mg 2	0	0
57	AE	2	Total 2	Mg 2	0	0
57	DG	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	BF	10	Total 10	Mg 10	0	0
57	AV	1	Total 1	Mg 1	0	0
57	BX	1	Total 1	Mg 1	0	0

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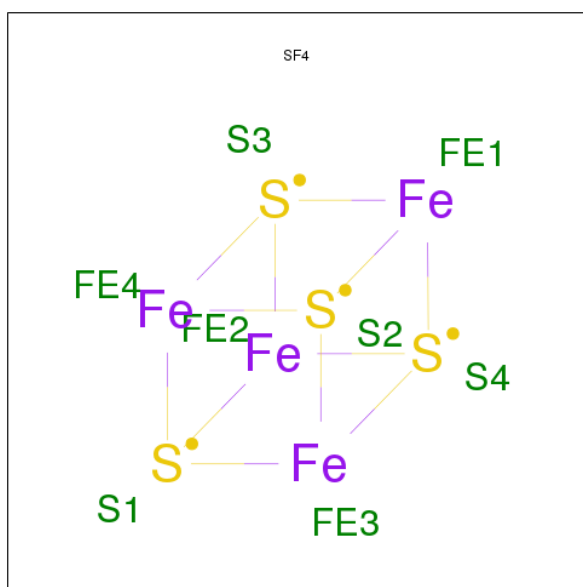
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B2	1	Total 1	Mg 1	0	0
57	AA	207	Total 207	Mg 207	0	0
57	BQ	5	Total 5	Mg 5	0	0
57	CX	2	Total 2	Mg 2	0	0
57	DV	2	Total 2	Mg 2	0	0
57	AM	1	Total 1	Mg 1	0	0
57	BU	8	Total 8	Mg 8	0	0
57	DR	2	Total 2	Mg 2	0	0
57	AD	2	Total 2	Mg 2	0	0
57	BN	6	Total 6	Mg 6	0	0
57	CT	1	Total 1	Mg 1	0	0
57	BG	2	Total 2	Mg 2	0	0
57	BY	1	Total 1	Mg 1	0	0
57	DE	4	Total 4	Mg 4	0	0
57	B3	2	Total 2	Mg 2	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	BR	3	Total 3	Mg 3	0	0
57	DA	629	Total 629	Mg 629	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DW	2	Total 2	Mg 2	0	0
57	B7	3	Total 3	Mg 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	CF	1	Total 1	Mg 1	0	0
57	BV	4	Total 4	Mg 4	0	0
57	DO	1	Total 1	Mg 1	0	0
57	BO	1	Total 1	Mg 1	0	0
57	BZ	1	Total 1	Mg 1	0	0
57	DY	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	D5	1	Total 1	Mg 1	0	0
57	BD	11	Total 11	Mg 11	0	0
57	B0	4	Total 4	Mg 4	0	0
57	CE	1	Total 1	Mg 1	0	0
57	BW	5	Total 5	Mg 5	0	0
57	DD	7	Total 7	Mg 7	0	0
57	CK	1	Total 1	Mg 1	0	0
57	AF	1	Total 1	Mg 1	0	0
57	DB	10	Total 10	Mg 10	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	B5	1	Total	Zn	0	0
			1	1		
59	B4	1	Total	Zn	0	0
			1	1		
59	CN	1	Total	Zn	0	0
			1	1		
59	BY	1	Total	Zn	0	0
			1	1		
59	B9	1	Total	Zn	0	0
			1	1		
59	DY	1	Total	Zn	0	0
			1	1		
59	D5	1	Total	Zn	0	0
			1	1		
59	D4	1	Total	Zn	0	0
			1	1		
59	AN	1	Total	Zn	0	0
			1	1		
59	D6	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	D9	1	Total 1	Zn 1	0	0
59	B6	1	Total 1	Zn 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	AX	1	Total 1	K 1	0	0
60	CX	1	Total 1	K 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	170	Total 170	O 170	0	0
61	AL	2	Total 2	O 2	0	0
61	AO	1	Total 1	O 1	0	0
61	AU	1	Total 1	O 1	0	0
61	AV	2	Total 2	O 2	0	0
61	AW	3	Total 3	O 3	0	0
61	BA	1102	Total 1102	O 1102	0	0
61	BB	36	Total 36	O 36	0	0
61	BD	8	Total 8	O 8	0	0
61	BE	13	Total 13	O 13	0	0
61	BF	4	Total 4	O 4	0	0
61	BG	3	Total 3	O 3	0	0
61	BI	1	Total 1	O 1	0	0

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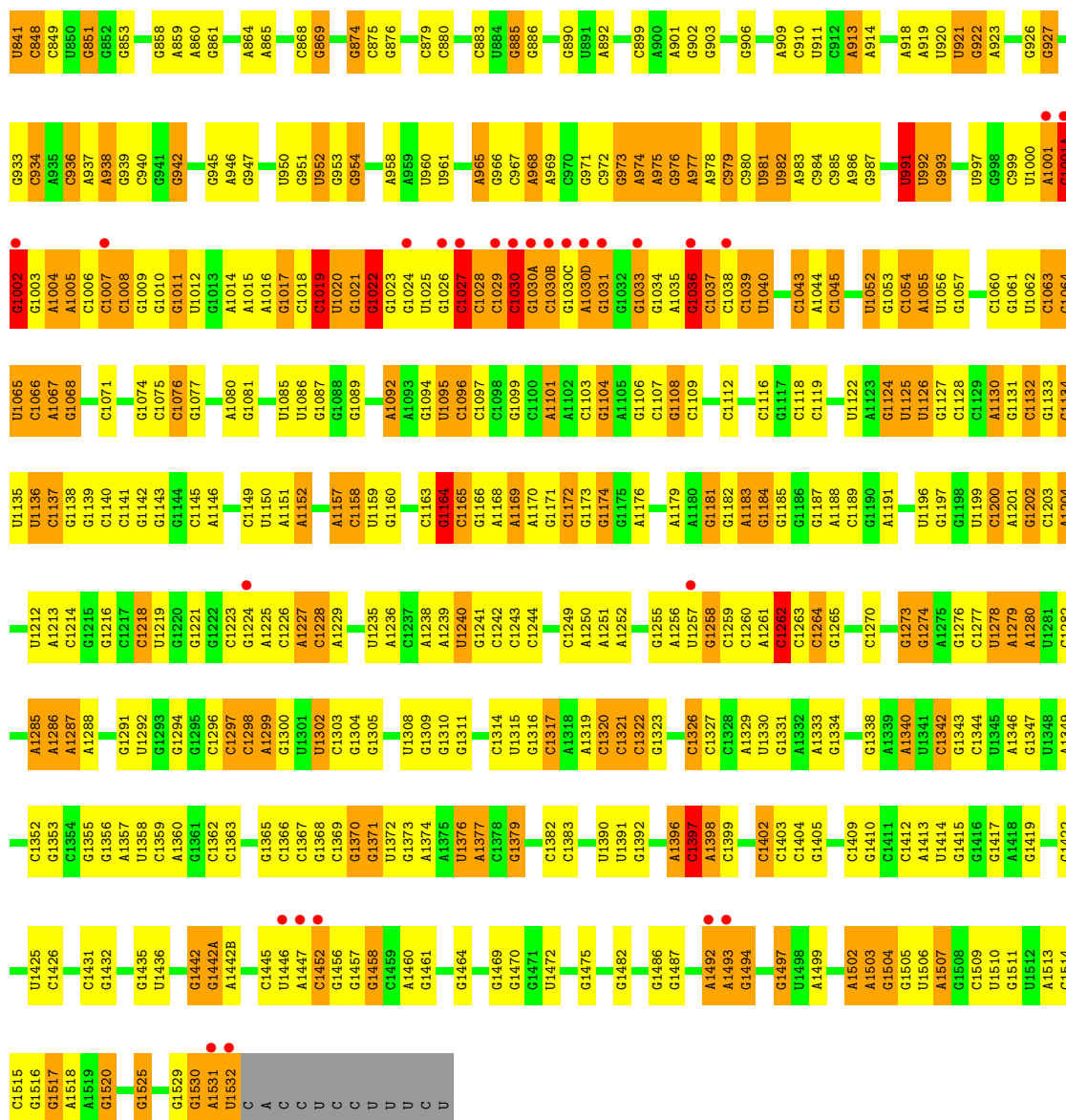
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BP	15	Total 15	O 15	0	0
61	BQ	3	Total 3	O 3	0	0
61	BR	1	Total 1	O 1	0	0
61	BS	1	Total 1	O 1	0	0
61	BT	3	Total 3	O 3	0	0
61	BU	1	Total 1	O 1	0	0
61	BV	4	Total 4	O 4	0	0
61	BW	2	Total 2	O 2	0	0
61	BX	2	Total 2	O 2	0	0
61	B0	4	Total 4	O 4	0	0
61	B1	1	Total 1	O 1	0	0
61	B3	1	Total 1	O 1	0	0
61	B5	5	Total 5	O 5	0	0
61	B7	1	Total 1	O 1	0	0
61	B8	7	Total 7	O 7	0	0
61	CA	130	Total 130	O 130	0	0
61	CE	1	Total 1	O 1	0	0
61	CJ	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	CV	1	Total 1	O 1	0	0

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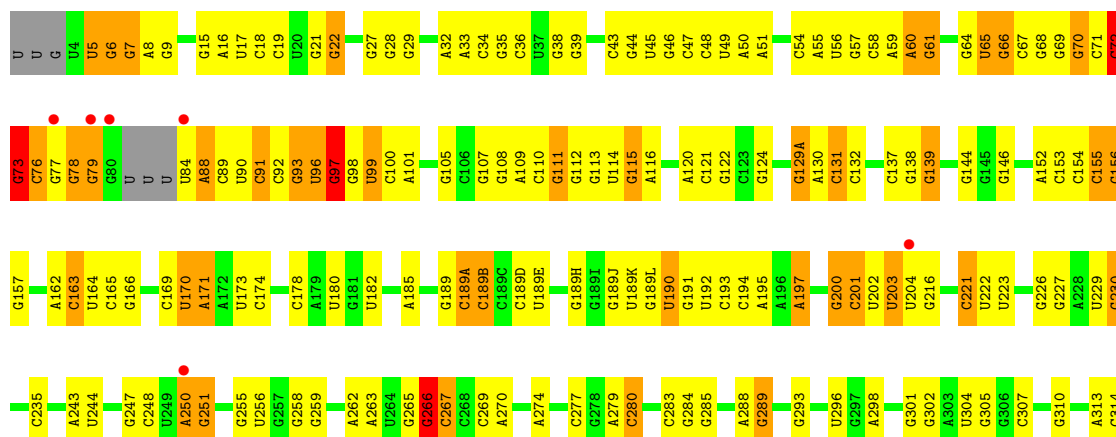
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CW	1	Total 1	O 1	0	0
61	CX	1	Total 1	O 1	0	0
61	DA	767	Total 767	O 767	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	9	Total 9	O 9	0	0
61	DE	5	Total 5	O 5	0	0
61	DF	6	Total 6	O 6	0	0
61	DN	2	Total 2	O 2	0	0
61	DP	12	Total 12	O 12	0	0
61	DR	2	Total 2	O 2	0	0
61	DT	1	Total 1	O 1	0	0
61	DU	2	Total 2	O 2	0	0
61	DV	1	Total 1	O 1	0	0
61	DX	2	Total 2	O 2	0	0
61	DY	1	Total 1	O 1	0	0
61	D0	5	Total 5	O 5	0	0
61	D1	1	Total 1	O 1	0	0
61	D3	2	Total 2	O 2	0	0
61	D7	1	Total 1	O 1	0	0
61	D8	4	Total 4	O 4	0	0



• Molecule 1: 16S Ribosomal RNA

Chain CA:

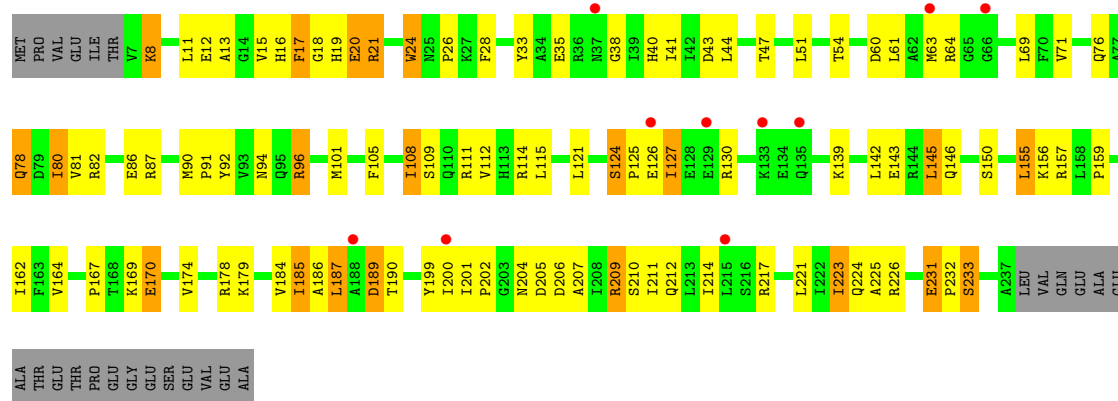


U1292	U1293	U1294	U1295	U1296	U1297	U1298	U1299	U1300	U1301	U1302	U1303	U1304	U1305	U1306	U1307	U1308	U1309	U1310	U1311	U1312	U1313	U1314	U1315	U1316	U1317	U1318	U1319	U1320	U1321	U1322	U1323	U1324	U1325	U1326	U1327	U1328	U1329	U1330	U1331	U1332	U1333	U1334	U1335	U1336	U1337	U1338	U1339	U1340	U1341	U1342	U1343	U1344	U1345	U1346	U1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355																																																																																																																																																																																																																																											
G1225	G1226	A1227	C1228	A1229	C1230	G1231	U1232	U1233	A1234	C1235	A1236	C1237	A1238	G1239	U1240	C1241	C1242	C1243	A1244	A1245	C1246	A1247	A1248	A1249	A1250	A1251	A1252	G1253	A1254	A1255	A1256	U1257	U1258	C1259	A1260	A1261	C1262	C1263	C1264	C1265	C1266	A1267	C1268	C1269	C1270	C1271	A1272	C1273	G1274	A1275	C1276	C1277	U1278	A1279	C1280	A1281	U1282	C1283	C1284	A1285	A1286	A1287	A1288	A1289	C1290	G1291																																																																																																																																																																																																																																								
G1100	A1101	A1102	C1103	C1104	A1105	C1106	C1107	C1108	C1109	A1110	A1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	U1120	U1121	U1122	A1123	C1124	U1125	U1126	C1127	C1128	C1129	A1130	C1131	C1132	C1133	C1134	U1135	U1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	C1154	U1155	C1156	A1157	C1158	U1159																																																																																																																																																																																																																																															
G1160	C1161	C1162	C1163	C1164	C1165	C1166	A1167	G1168	G1169	C1170	C1171	C1172	C1173	G1174	C1175	A1176	G1177	C1178	A1179	A1180	C1181	C1182	A1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	A1191	U1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	A1201	C1202	C1203	A1204	U1205	C1206	C1207	C1208	C1209	C1210	U1211	U1212	A1213	C1214	C1215	C1216	C1217	C1218	U1219	C1220	G1221	G1222	C1223	G1224																																																																																																																																																																																																																																										
G1034	A1035	C1036	C1037	C1038	C1039	U1040	A1041	C1042	C1043	A1044	C1045	C1046	C1047	U1048	C1049	C1050	C1051	C1052	C1053	C1054	A1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	A1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	U1090	C1091	A1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099																																																																																																																																																																																																																																									
C979	C980	U981	C982	C983	C984	C985	A986	C987	C988	C989	C990	U991	C992	C993	A994	C995	A996	U997	C998	C999	U1000	A1001	C1001A	A998	C1002	C1003	A1004	A1005	C1006	C1007	C1008	C1009	C1010	C1011	U999	C1012	C1013	A1014	C1015	A1016	C1017	C1018	C1019	U1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033																																																																																																																																																																																																																																																	
G829	G830	U831	C832	U833	C834	U835	C836	C837	C838	U839	C840	U841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903																																																																																																																																																																																																																																
U751	G752	A753	C754	G755	C756	U757	G758	A759	G760	C761	G762	C763	C764	G765	A766	C767	G768	C769	G770	C771	C772	C773	C774	C775	C776	C777	C778	C779	A780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903																																																																																																																																																		
A684	G685	U686	A687	C688	C689	G690	C691	U692	C693	A694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	A712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750																																																																																																																																																																																																																																								
C615	G616	C617	C618	U619	C620	A621	C622	C623	C624	C625	U626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750																																																																																																																																																																			
G544	C545	C546	C547	C548	C549	G550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614																																																																																																																																																																																																																																				
G460	A461	C462	C463	C464	C465	C466	C467	C468	C469	C470	C471	C472	C473	C474	C475	C476	C477	C478	C479	C480	C481	C482	C483	C484	C485	C486	C487	C488	C489	C490	C491	C492	C493	C494	C495	C496	C497	C498	C499	C500	C501	C502	C503	C504	C505	C506	C507	C508	C509	C510	C511	C512	C513	C514	C515	C516	C517	C518	C519	C520	C521	C522	C523	C524	C525	C526	C527	C528	C529	C530	C531	C532	C533	C534	C535	C536	C537	C538	C539	C540	C541	C542	C543	C544	C545	C546	C547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604	C605	C606	C607	C608	C609	C610	C611	C612	C613	C614																																																																																																																																																
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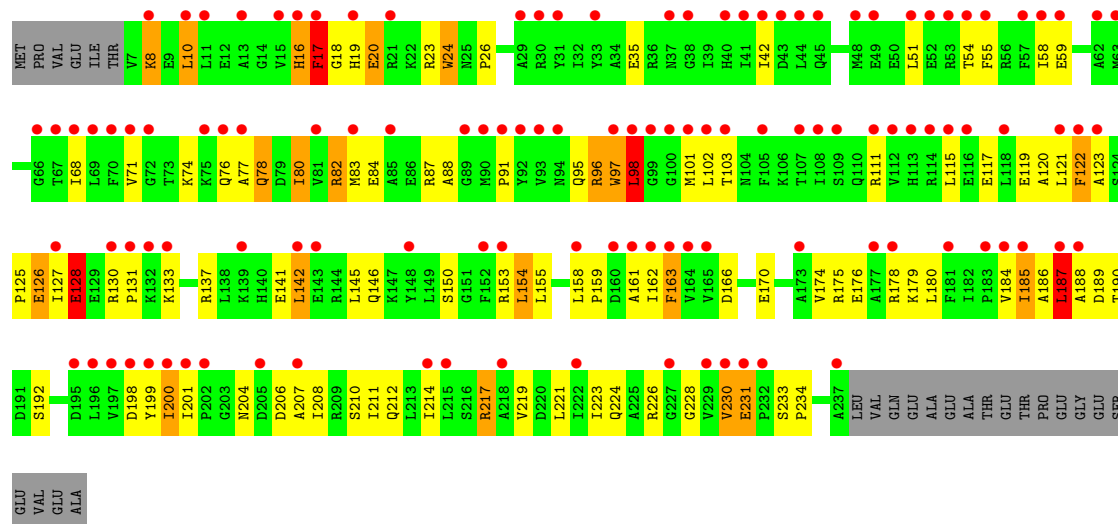
• Molecule 2: 30S ribosomal protein S2

Chain AB:



• Molecule 2: 30S ribosomal protein S2

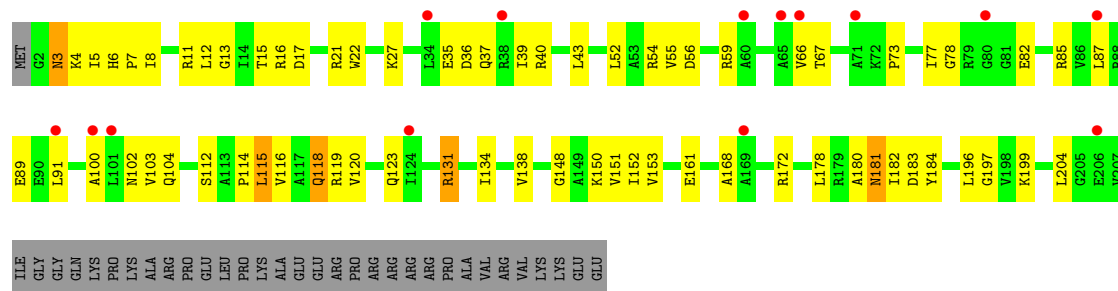
Chain CB:



• Molecule 3: 30S ribosomal protein S3

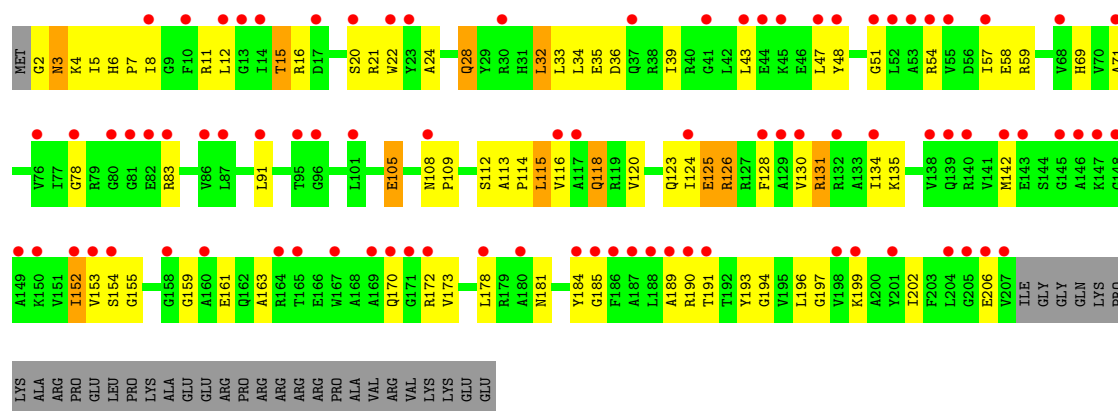
Chain AC:





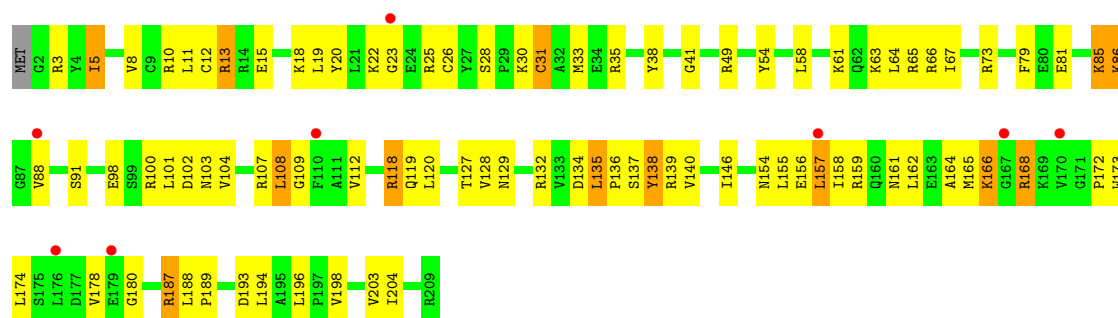
• Molecule 3: 30S ribosomal protein S3

Chain CC:



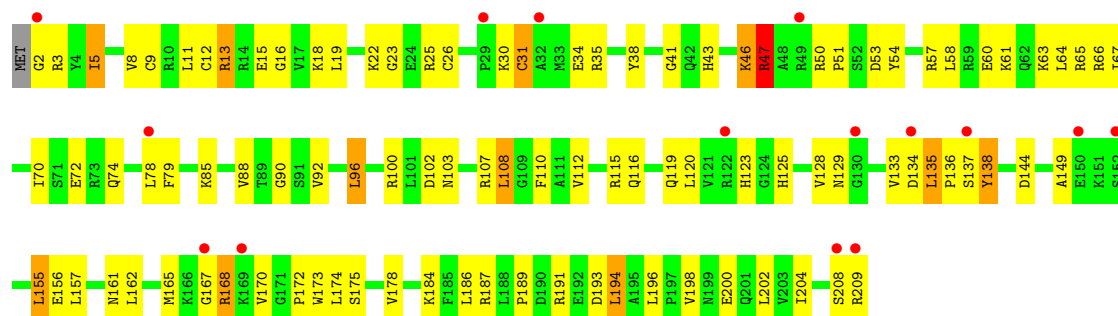
• Molecule 4: 30S ribosomal protein S4

Chain AD:

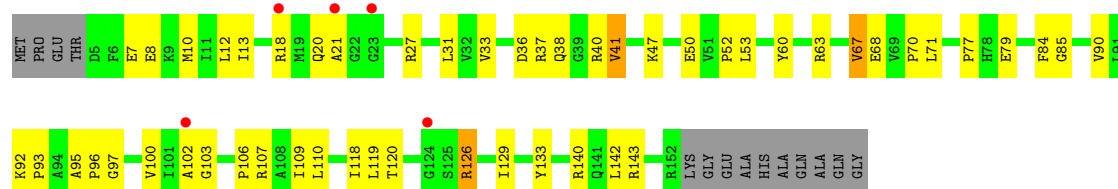


• Molecule 4: 30S ribosomal protein S4

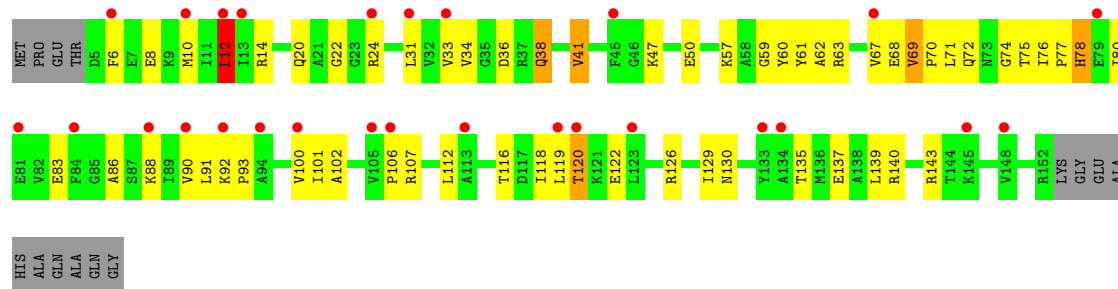
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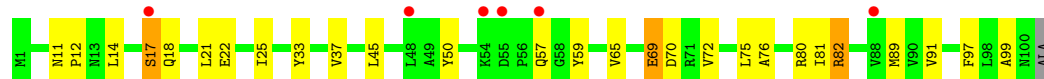
- Molecule 5: 30S ribosomal protein S5

Chain AE: 

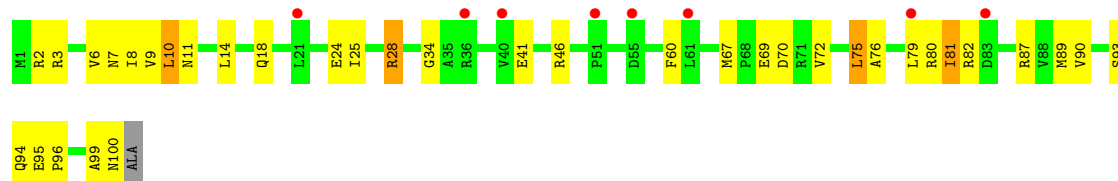
- Molecule 5: 30S ribosomal protein S5

Chain CE: 

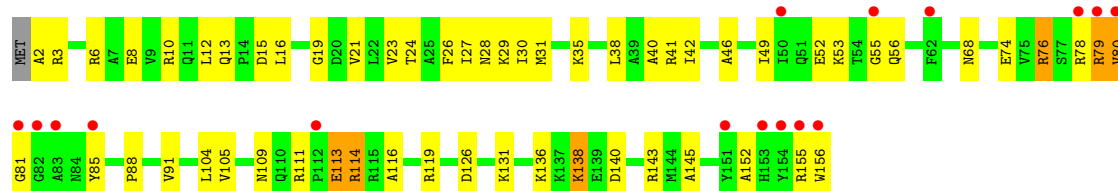
- Molecule 6: 30S ribosomal protein S6

Chain AF: 

- Molecule 6: 30S ribosomal protein S6

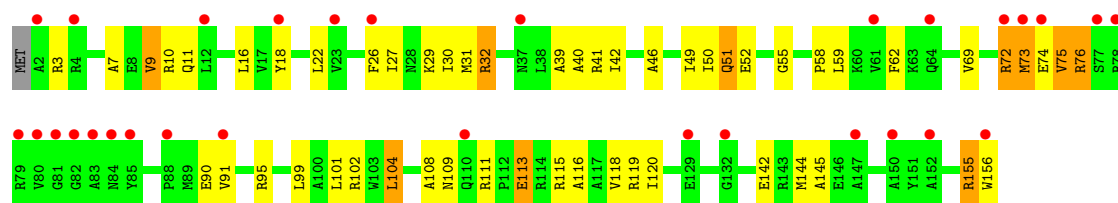
Chain CF: 

- Molecule 7: 30S ribosomal protein S7

Chain AG: 

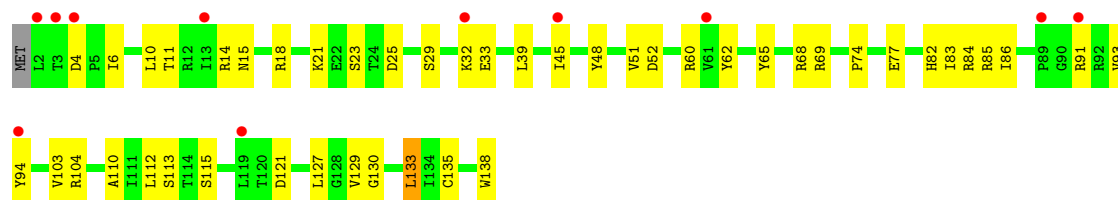
- Molecule 7: 30S ribosomal protein S7

Chain CG: 



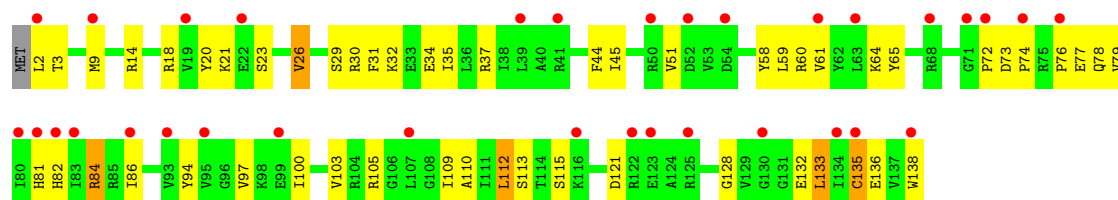
• Molecule 8: 30S ribosomal protein S8

Chain AH:



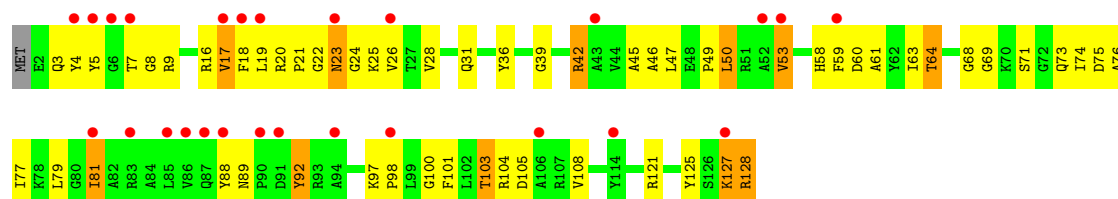
• Molecule 8: 30S ribosomal protein S8

Chain CH:



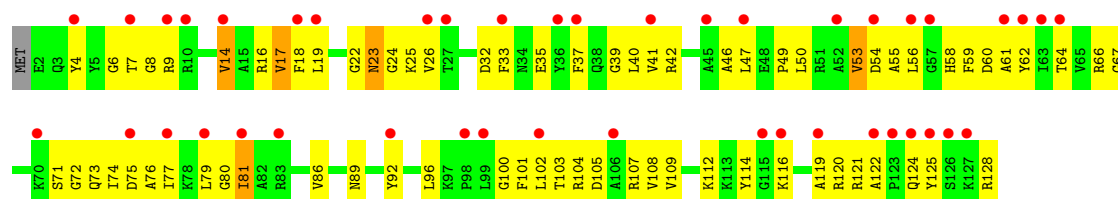
• Molecule 9: 30S ribosomal protein S9

Chain AI:



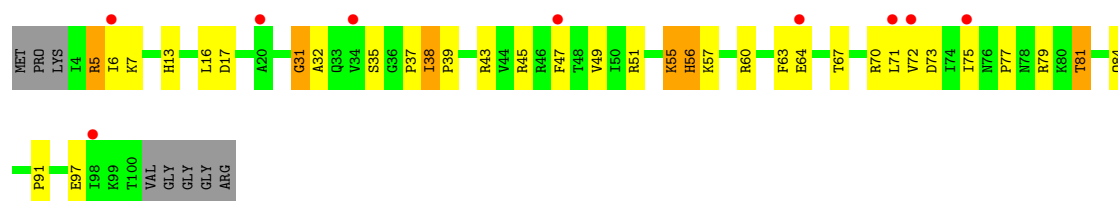
• Molecule 9: 30S ribosomal protein S9

Chain CI:



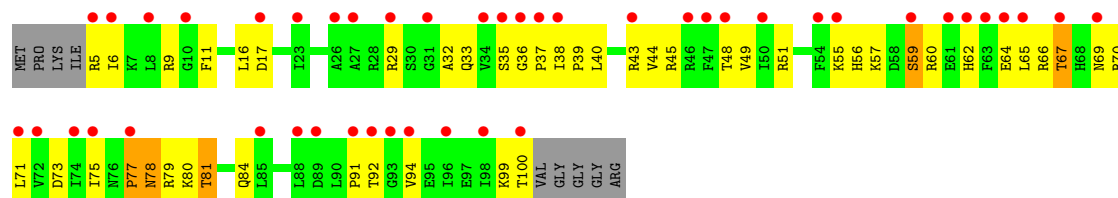
• Molecule 10: 30S ribosomal protein S10

Chain AJ:



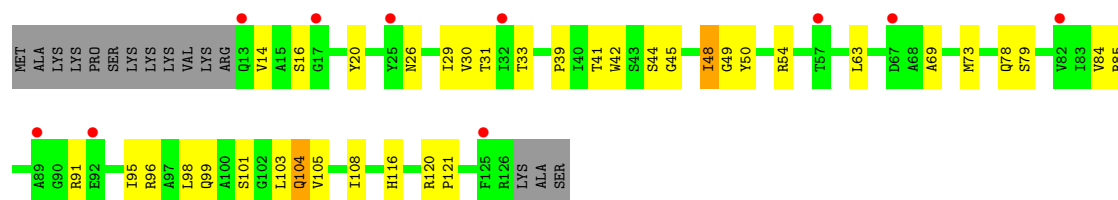
- Molecule 10: 30S ribosomal protein S10

Chain CJ:



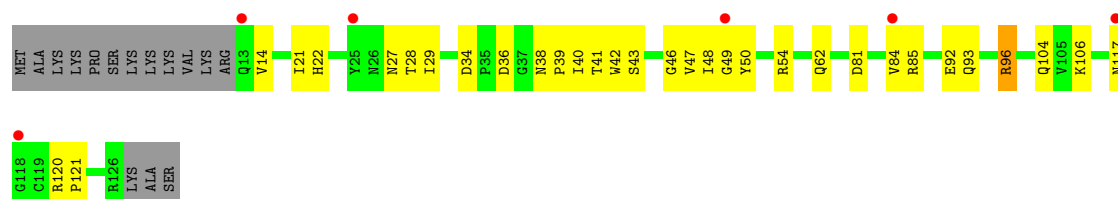
- Molecule 11: 30S ribosomal protein S11

Chain AK:



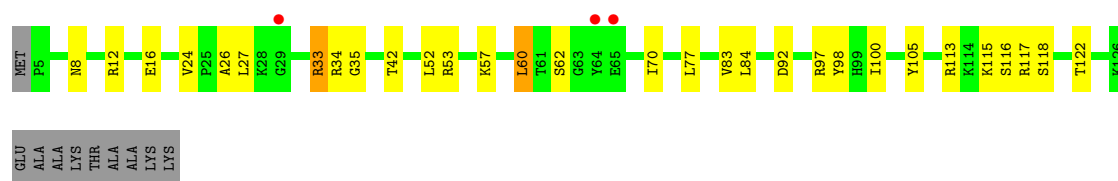
- Molecule 11: 30S ribosomal protein S11

Chain CK:



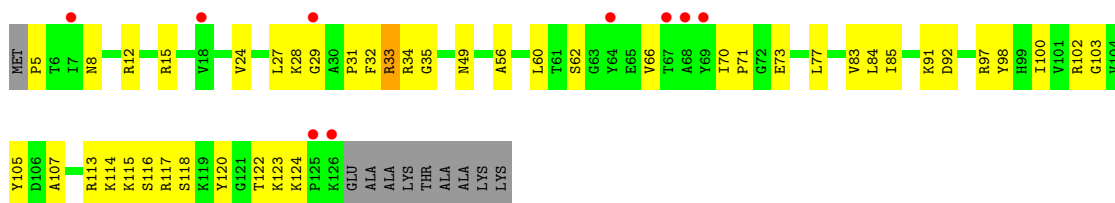
- Molecule 12: 30S ribosomal protein S12

Chain AL:



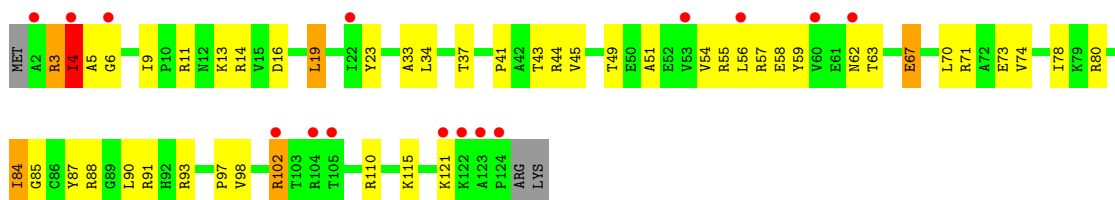
- Molecule 12: 30S ribosomal protein S12

Chain CL:



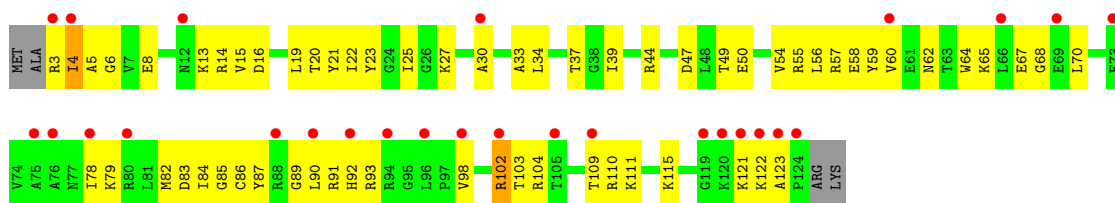
- Molecule 13: 30S ribosomal protein S13

Chain AM:



- Molecule 13: 30S ribosomal protein S13

Chain CM:



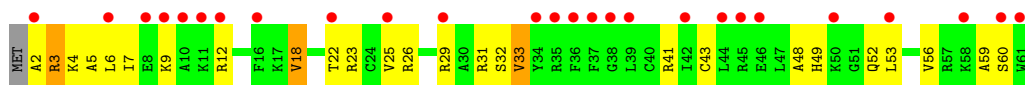
- Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:



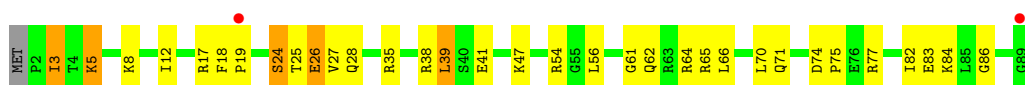
- Molecule 14: 30S ribosomal protein S14 type Z

Chain CN:



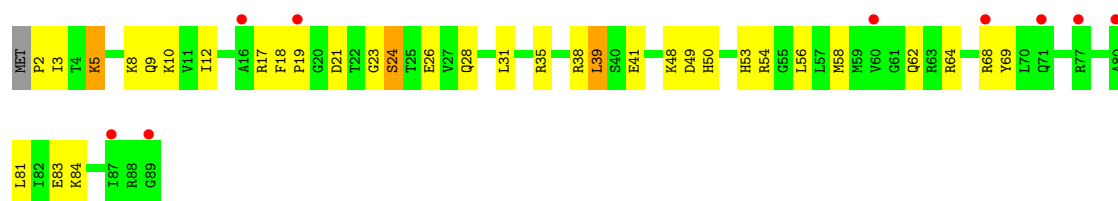
- Molecule 15: 30S ribosomal protein S15

Chain AO:



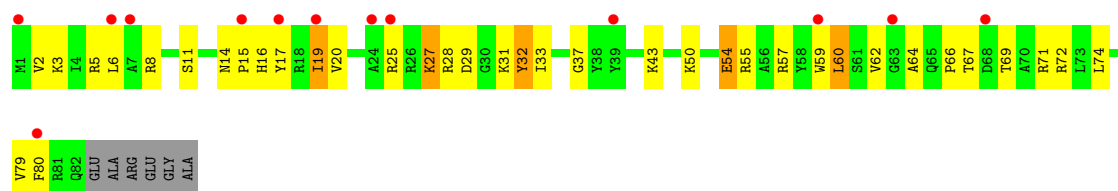
- Molecule 15: 30S ribosomal protein S15

Chain CO:



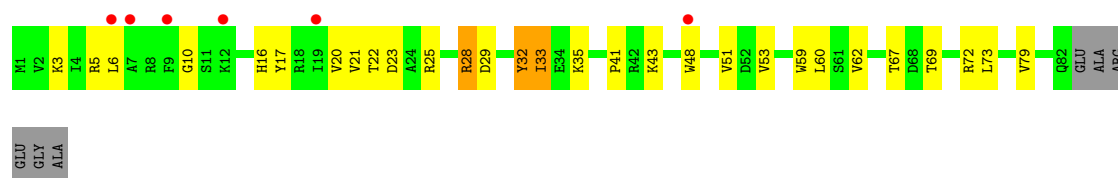
- Molecule 16: 30S ribosomal protein S16

Chain AP:



- Molecule 16: 30S ribosomal protein S16

Chain CP:



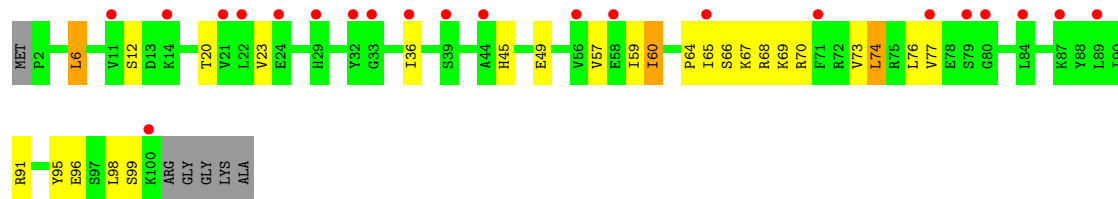
- Molecule 17: 30S ribosomal protein S17

Chain AQ:



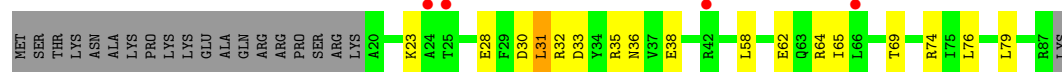
- Molecule 17: 30S ribosomal protein S17

Chain CQ:



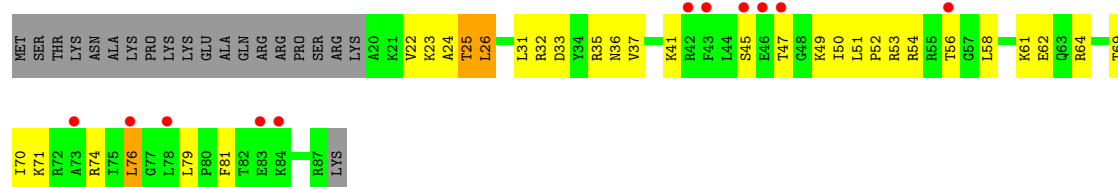
- Molecule 18: 30S ribosomal protein S18

Chain AR:



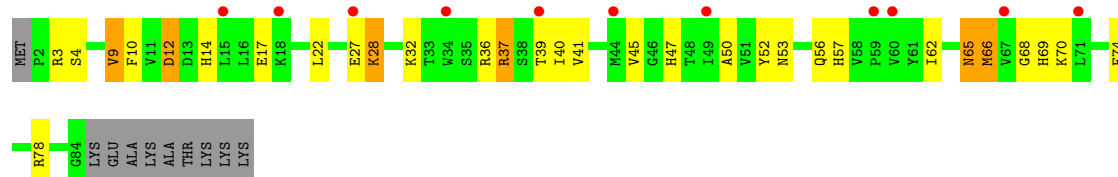
- Molecule 18: 30S ribosomal protein S18

Chain CR:



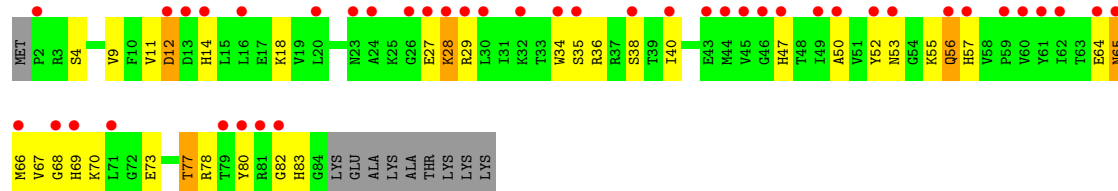
- Molecule 19: 30S ribosomal protein S19

Chain AS:



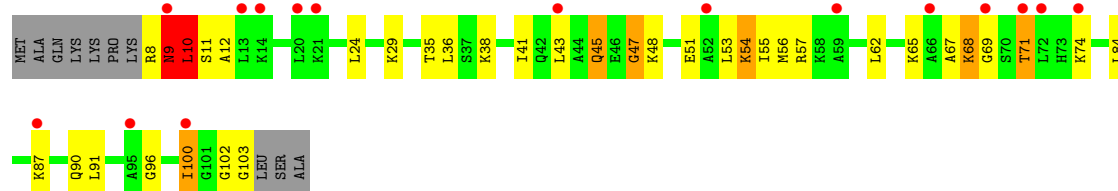
- Molecule 19: 30S ribosomal protein S19

Chain CS:



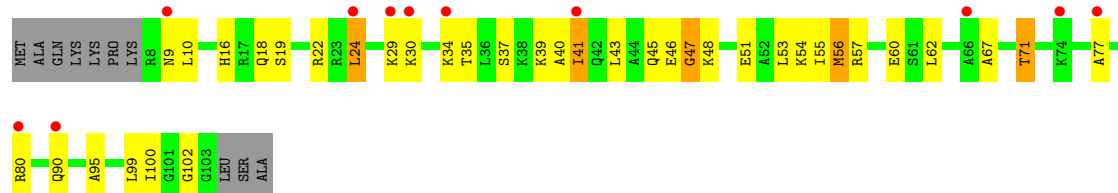
- Molecule 20: 30S ribosomal protein S20

Chain AT:



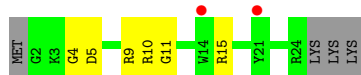
- Molecule 20: 30S ribosomal protein S20

Chain CT:



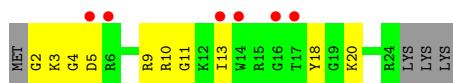
- Molecule 21: 30S ribosomal protein Thx

Chain AU:



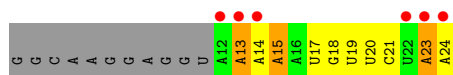
- Molecule 21: 30S ribosomal protein Thx

Chain CU:



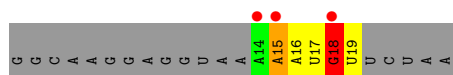
- Molecule 22: mRNA

Chain AV:



- Molecule 22: mRNA

Chain CV:



- Molecule 23: Cytidine-Puromycin

Chain AW:



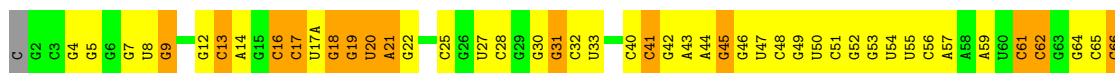
- Molecule 23: Cytidine-Puromycin

Chain CW:



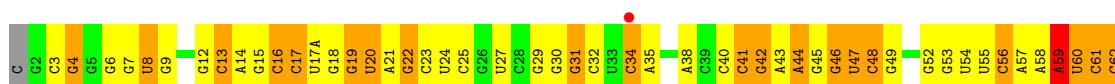
- Molecule 24: P-site tRNA

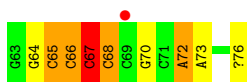
Chain AX:



- Molecule 24: P-site tRNA

Chain CX:





- Molecule 25: E-site tRNA

Chain AY:



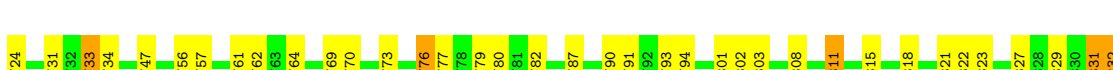
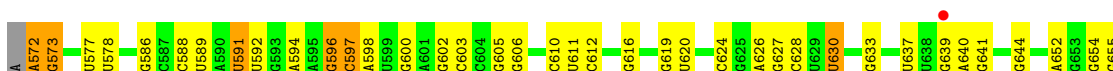
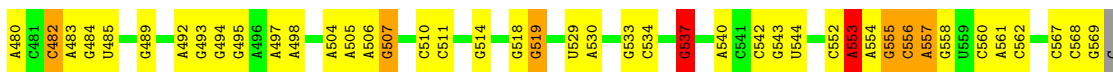
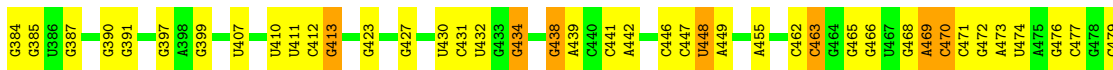
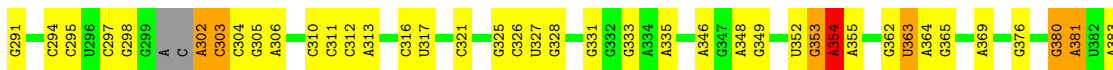
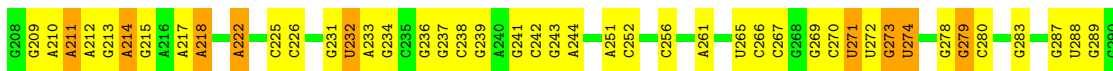
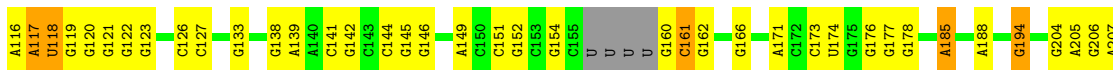
- Molecule 25: E-site tRNA

Chain CY:

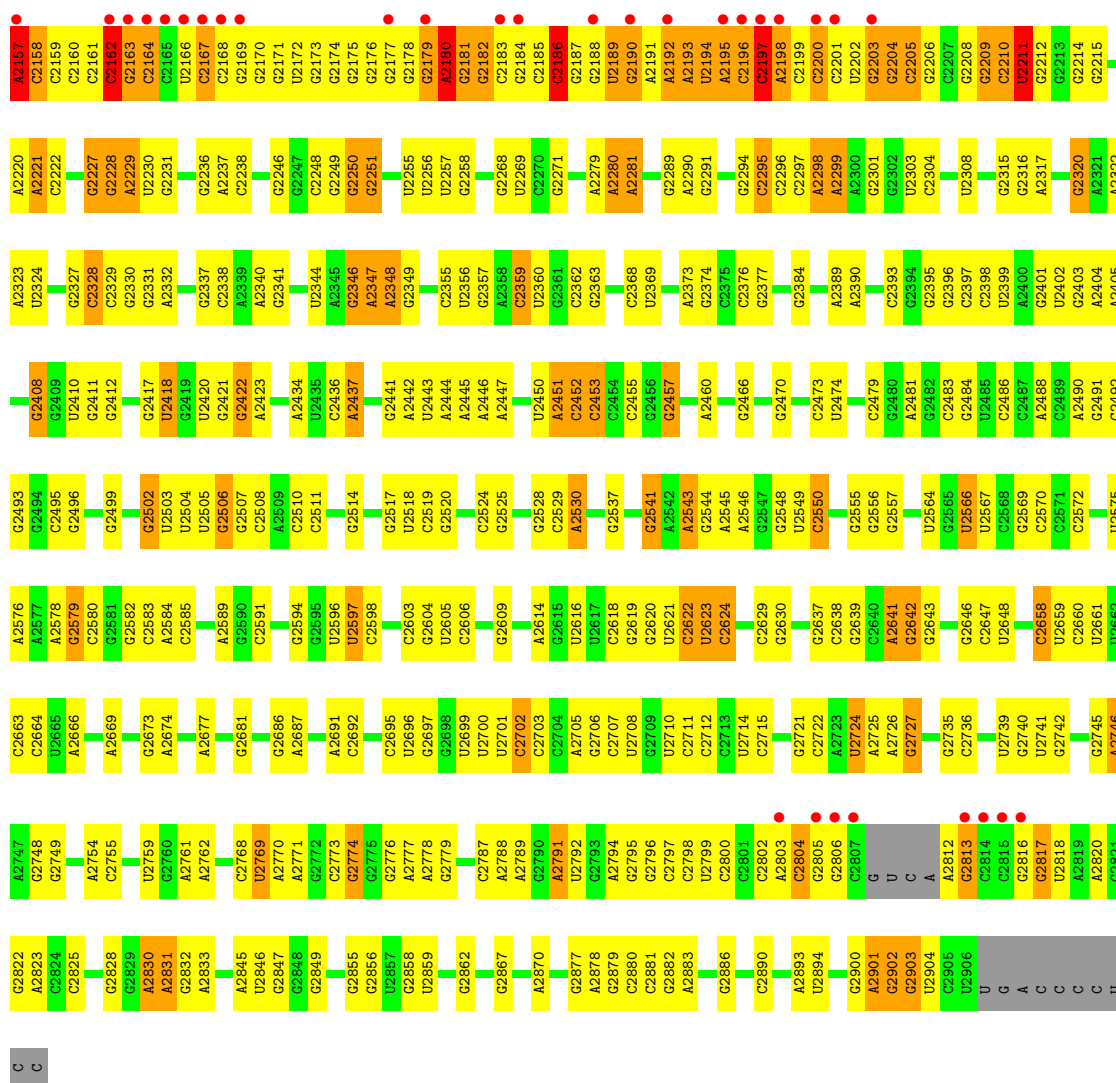


- Molecule 26: 23S Ribosomal RNA

Chain BA:

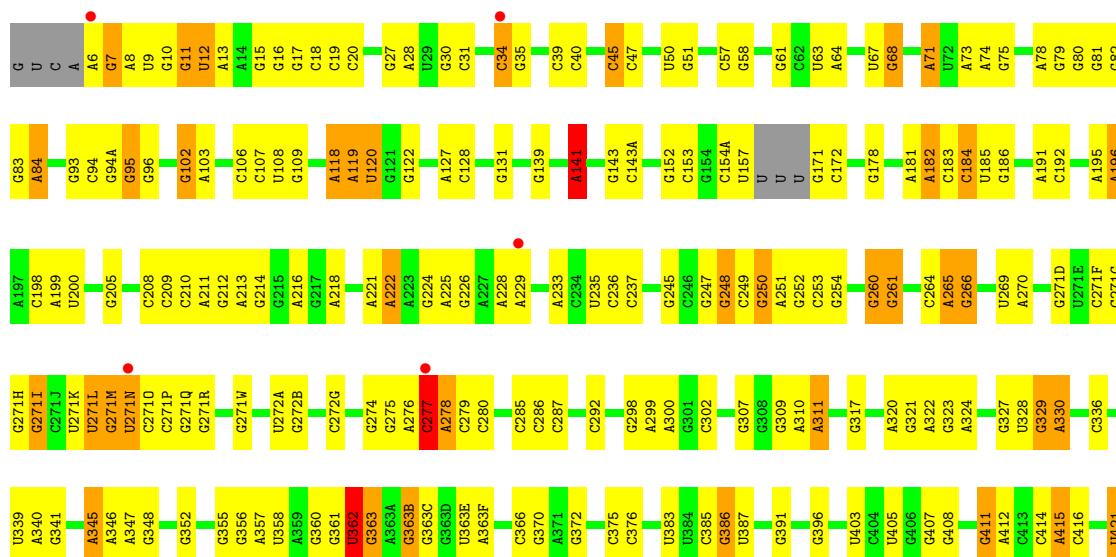


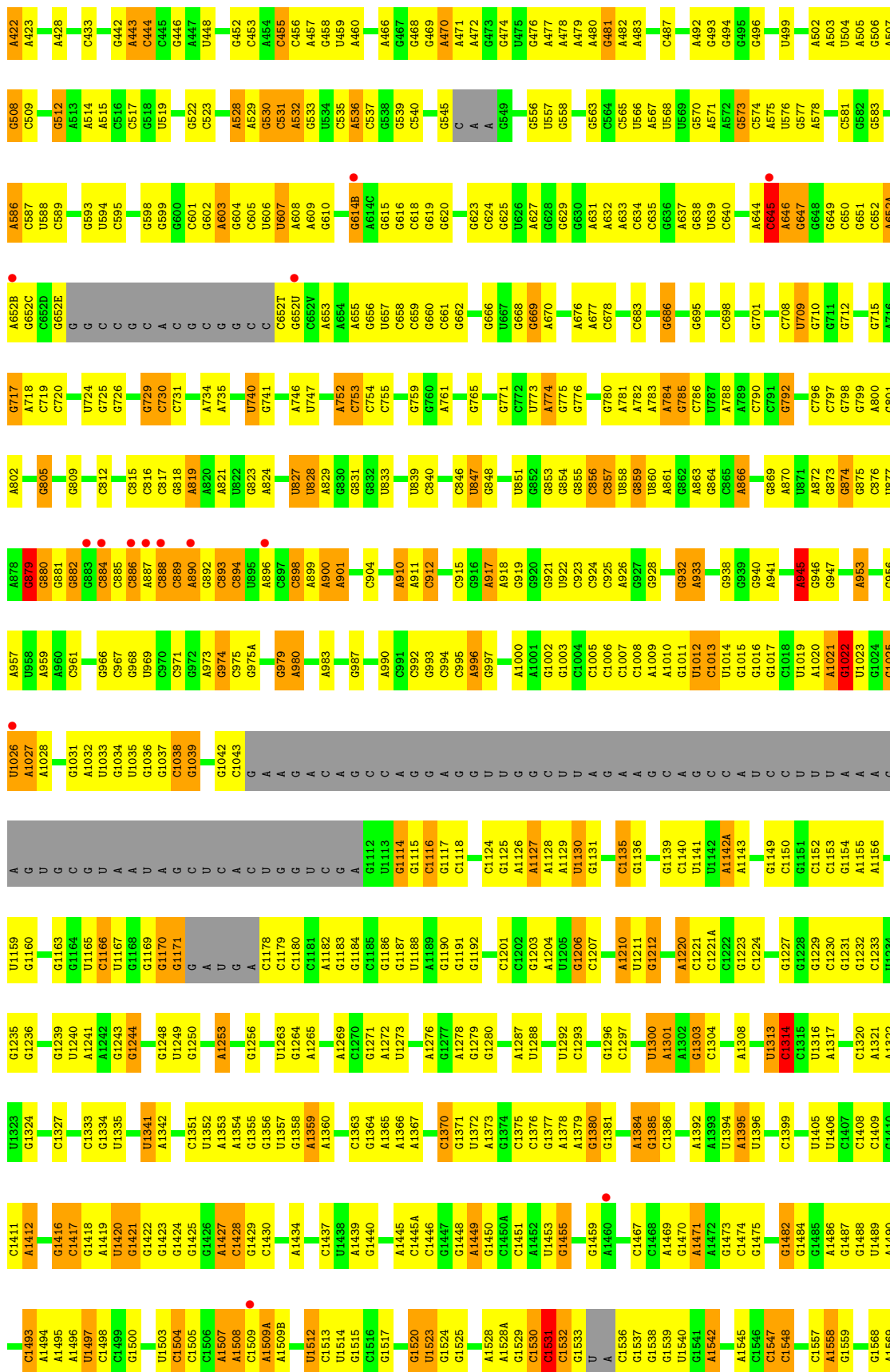
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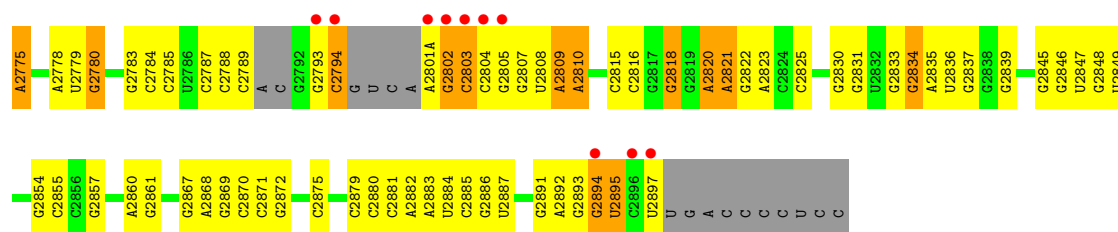
Molecule 26: 23S Ribosomal RNA

Chain DA:



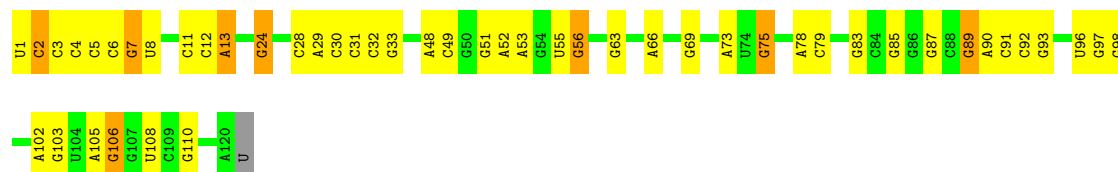






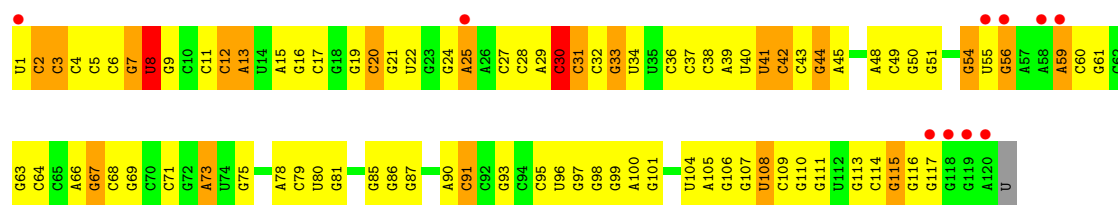
• Molecule 27: 5S Ribosomal RNA

Chain BB:



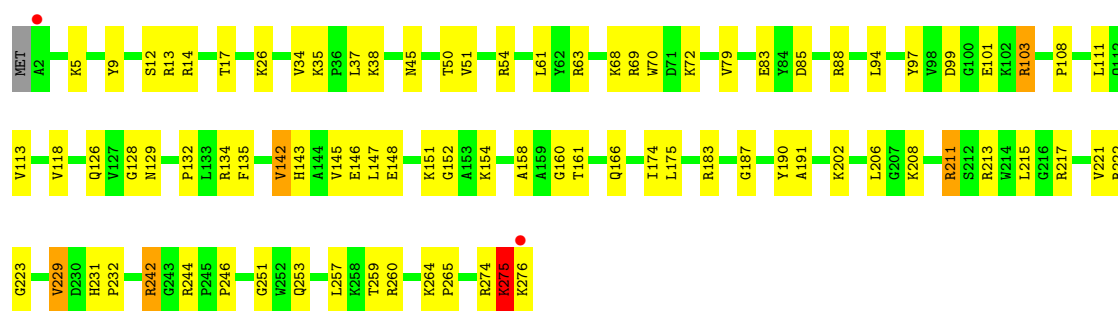
• Molecule 27: 5S Ribosomal RNA

Chain DB:



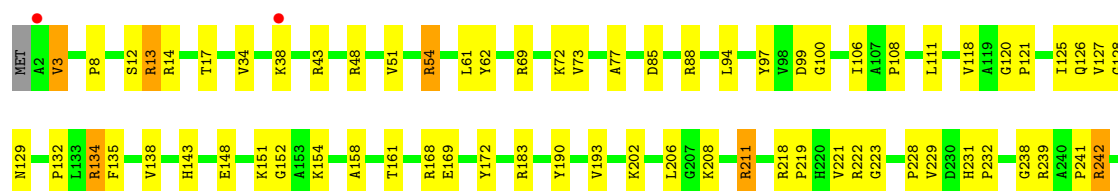
• Molecule 28: 50S ribosomal protein L2

Chain BD:



• Molecule 28: 50S ribosomal protein L2

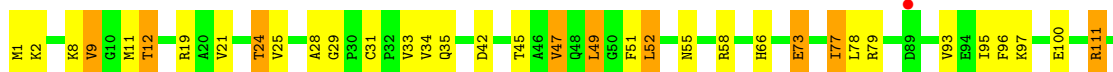
Chain DD:





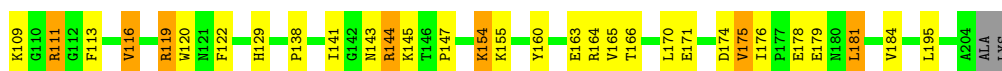
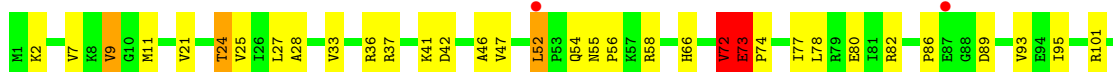
- Molecule 29: 50S ribosomal protein L3

Chain BE:



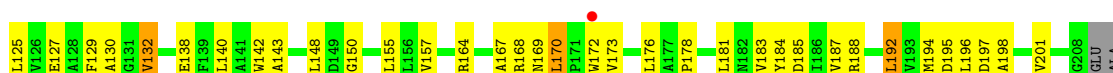
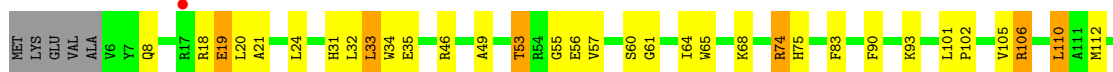
- Molecule 29: 50S ribosomal protein L3

Chain DE:



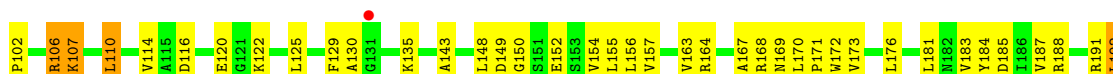
- Molecule 30: 50S ribosomal protein L4

Chain BF:



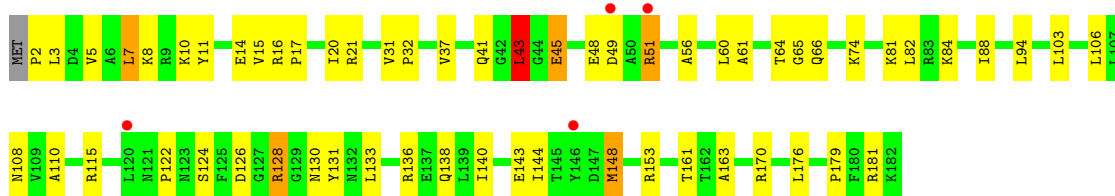
- Molecule 30: 50S ribosomal protein L4

Chain DF:



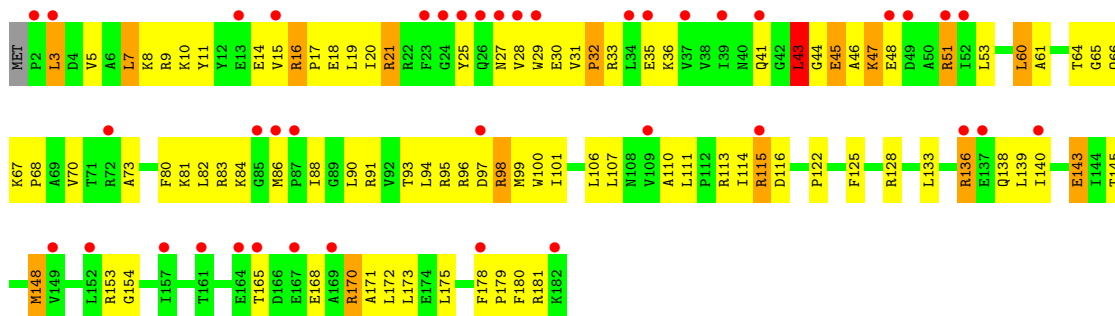
- Molecule 31: 50S ribosomal protein L5

Chain BG:



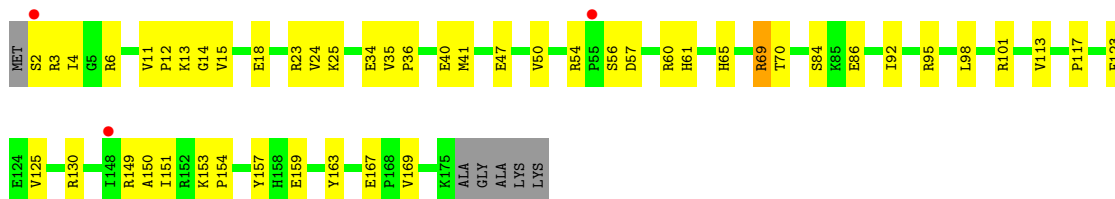
• Molecule 31: 50S ribosomal protein L5

Chain DG:



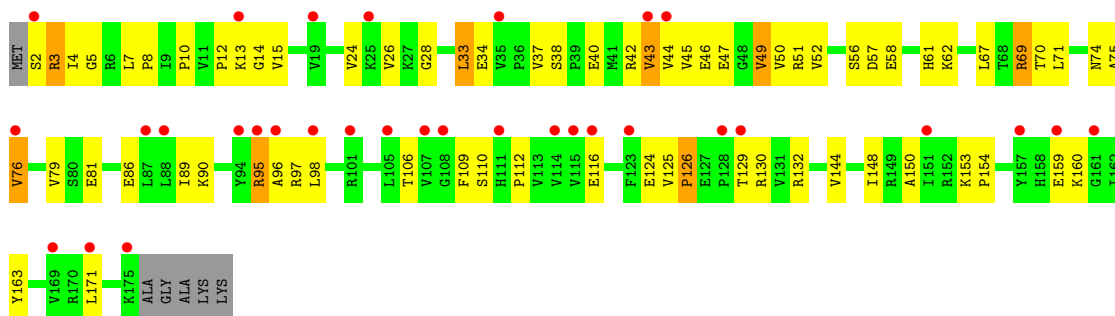
• Molecule 32: 50S ribosomal protein L6

Chain BH:



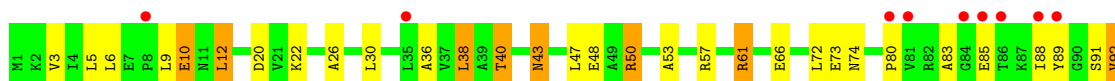
• Molecule 32: 50S ribosomal protein L6

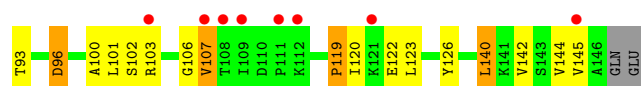
Chain DH:



• Molecule 33: 50S ribosomal protein L9

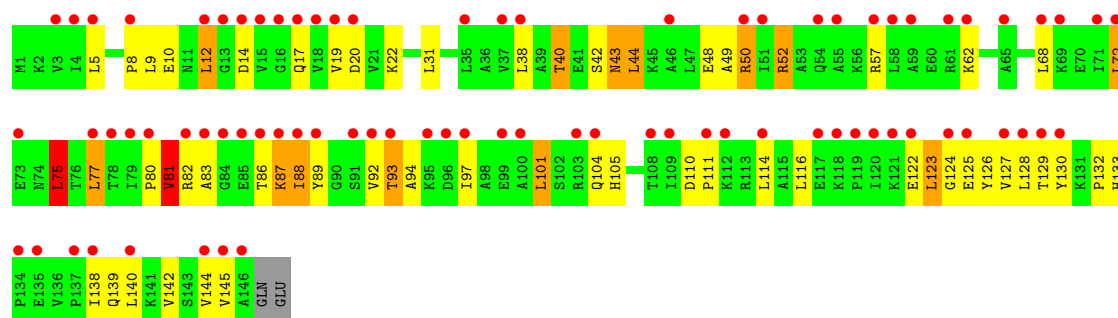
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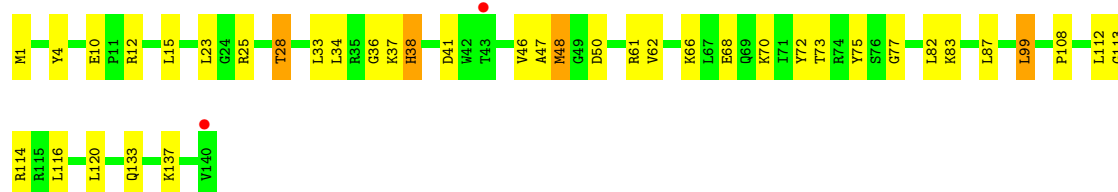
- Molecule 33: 50S ribosomal protein L9

Chain DI:



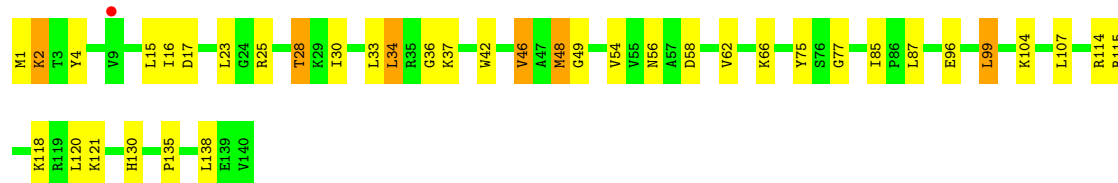
- Molecule 34: 50S ribosomal protein L13

Chain BN:



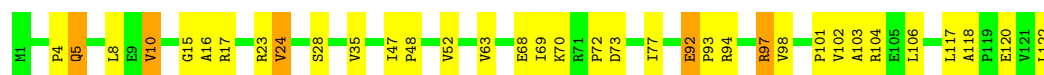
- Molecule 34: 50S ribosomal protein L13

Chain DN:



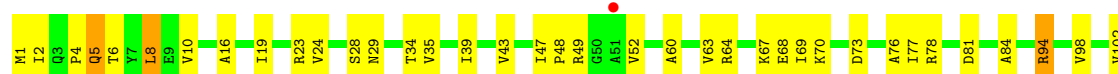
- Molecule 35: 50S ribosomal protein L14

Chain BO:



- Molecule 35: 50S ribosomal protein L14

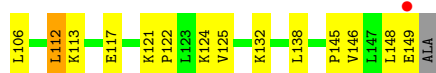
Chain DO:





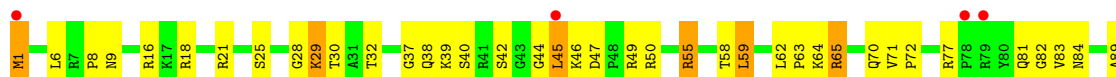
- Molecule 36: 50S ribosomal protein L15

Chain BP:



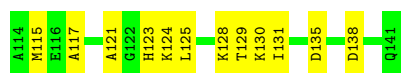
- Molecule 36: 50S ribosomal protein L15

Chain DP:



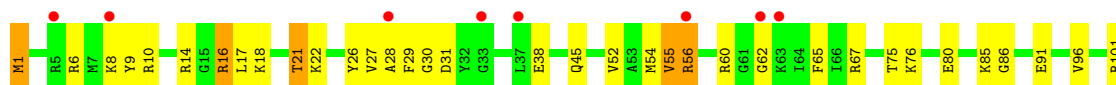
- Molecule 37: 50S ribosomal protein L16

Chain BQ:



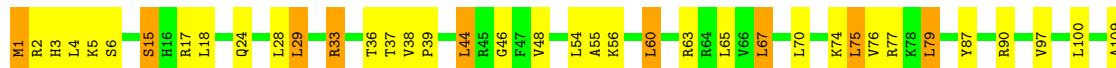
- Molecule 37: 50S ribosomal protein L16

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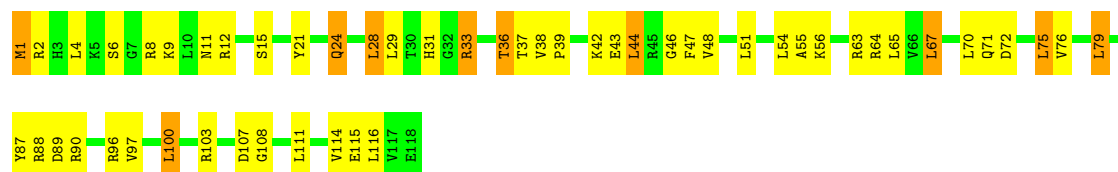
- Molecule 38: 50S ribosomal protein L17

Chain BR:



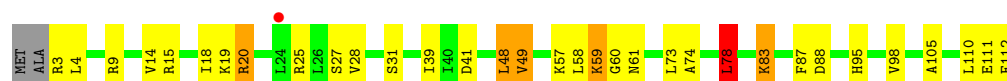
- Molecule 38: 50S ribosomal protein L17

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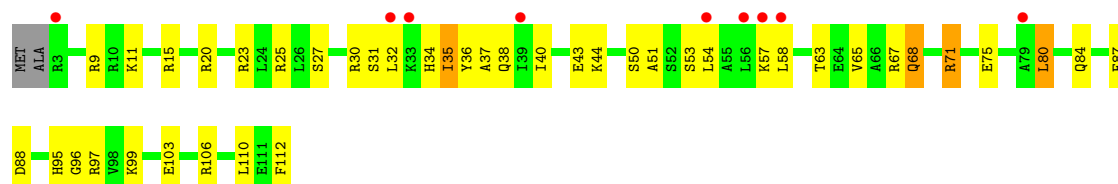
- Molecule 39: 50S ribosomal protein L18

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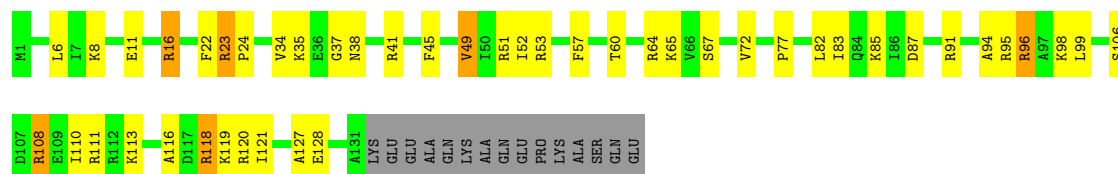
- Molecule 39: 50S ribosomal protein L18

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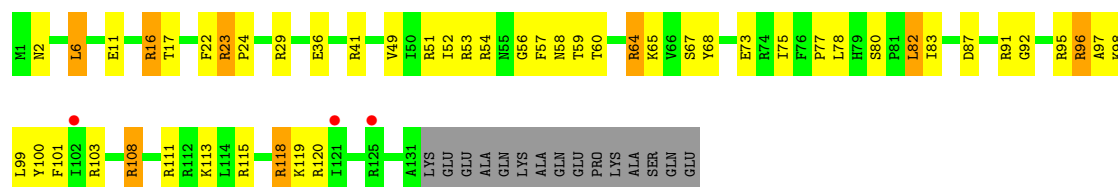
- Molecule 40: 50S ribosomal protein L19

Chain BT:



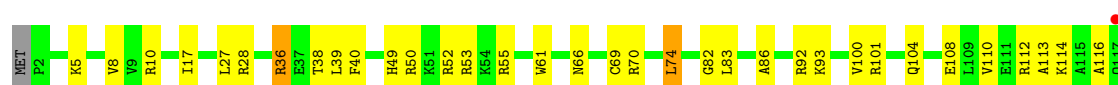
- Molecule 40: 50S ribosomal protein L19

Chain DT:



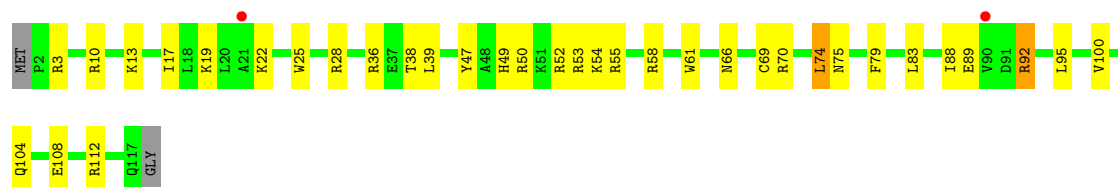
- Molecule 41: 50S ribosomal protein L20

Chain BU:



GLY

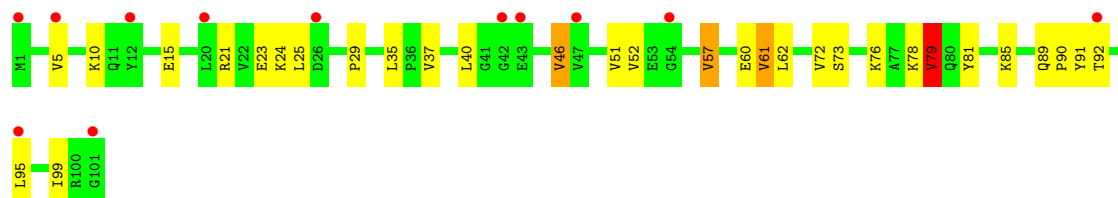
- Molecule 41: 50S ribosomal protein L20

Chain DU: 

- Molecule 42: 50S ribosomal protein L21

Chain BV: 

- Molecule 42: 50S ribosomal protein L21

Chain DV: 

- Molecule 43: 50S ribosomal protein L22

Chain BW: 

- Molecule 43: 50S ribosomal protein L22

Chain DW: 

- Molecule 44: 50S ribosomal protein L23

Chain BX: 



- Molecule 44: 50S ribosomal protein L23

Chain DX:



- Molecule 45: 50S ribosomal protein L24

Chain BY:



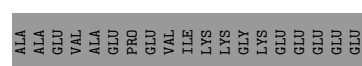
- Molecule 45: 50S ribosomal protein L24

Chain DY:



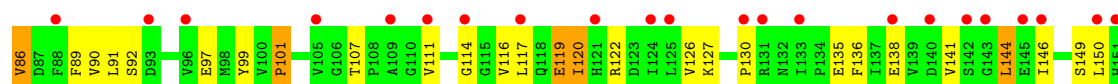
- Molecule 46: 50S ribosomal protein L25

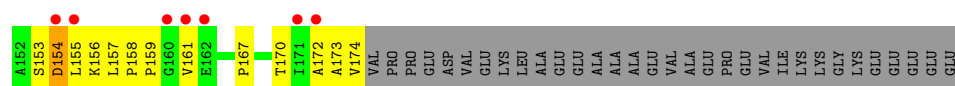
Chain BZ:



- Molecule 46: 50S ribosomal protein L25

Chain DZ:





- Molecule 47: 50S ribosomal protein L27

Chain B0:



- Molecule 47: 50S ribosomal protein L27

Chain D0:



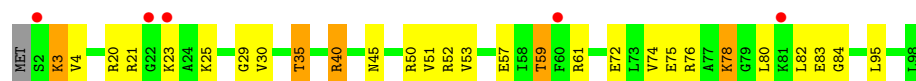
- Molecule 48: 50S ribosomal protein L28

Chain B1:



- Molecule 48: 50S ribosomal protein L28

Chain D1:



- Molecule 49: 50S ribosomal protein L29

Chain B2:



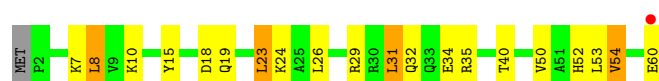
- Molecule 49: 50S ribosomal protein L29

Chain D2:



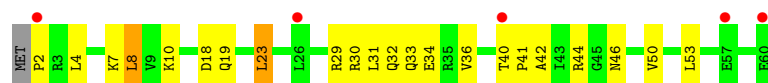
- Molecule 50: 50S ribosomal protein L30

Chain B3:



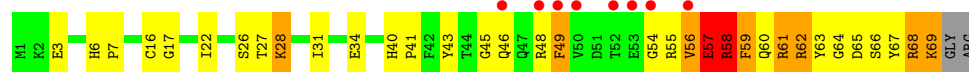
- Molecule 50: 50S ribosomal protein L30

Chain D3:



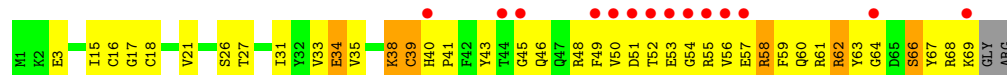
- Molecule 51: 50S ribosomal protein L31

Chain B4:



- Molecule 51: 50S ribosomal protein L31

Chain D4:



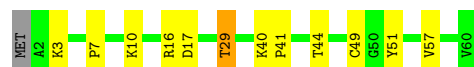
- Molecule 52: 50S ribosomal protein L32

Chain B5:



- Molecule 52: 50S ribosomal protein L32

Chain D5:



- Molecule 53: 50S ribosomal protein L33

Chain B6:



- Molecule 53: 50S ribosomal protein L33

Chain D6:



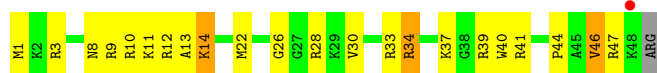
- Molecule 54: 50S ribosomal protein L34

Chain B7:



- Molecule 54: 50S ribosomal protein L34

Chain D7: 



- Molecule 55: 50S ribosomal protein L35

Chain B8: 



- Molecule 55: 50S ribosomal protein L35

Chain D8: 



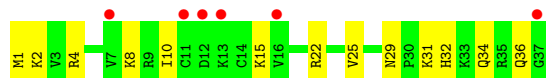
- Molecule 56: 50S ribosomal protein L36

Chain B9: 



- Molecule 56: 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	207.56Å 444.23Å 613.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	150.38 – 2.80 150.38 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.0 (150.38-2.80) 98.0 (150.38-2.80)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.82Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.234 , 0.280 0.255 , 0.304	Depositor DCC
R_{free} test set	36605 reflections (2.72%)	DCC
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 1345521 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	290205	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% 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: 5MU, MG, PPU, K, ZN, 31H, 5MC, 4SU, SF4, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.41	4/36049 (0.0%)	0.98	71/56261 (0.1%)
1	CA	0.42	7/36170 (0.0%)	1.05	147/56452 (0.3%)
2	AB	0.29	0/1881	0.59	0/2542
2	CB	0.33	0/1860	0.68	3/2518 (0.1%)
3	AC	0.28	0/1576	0.52	0/2130
3	CC	0.30	0/1566	0.58	0/2119
4	AD	0.28	0/1689	0.55	0/2267
4	CD	0.30	0/1704	0.56	0/2284
5	AE	0.29	0/1145	0.52	0/1543
5	CE	0.30	0/1149	0.58	1/1548 (0.1%)
6	AF	0.29	0/819	0.50	0/1111
6	CF	0.30	0/829	0.49	0/1123
7	AG	0.27	0/1250	0.51	0/1679
7	CG	0.29	0/1254	0.53	0/1683
8	AH	0.27	0/1108	0.51	0/1494
8	CH	0.27	0/1108	0.55	0/1494
9	AI	0.28	0/1002	0.54	0/1346
9	CI	0.30	0/997	0.56	0/1343
10	AJ	0.27	0/722	0.60	0/982
10	CJ	0.30	0/727	0.57	0/988
11	AK	0.29	0/844	0.50	0/1145
11	CK	0.27	0/848	0.50	0/1149
12	AL	0.29	0/946	0.51	0/1274
12	CL	0.29	0/946	0.56	0/1274
13	AM	0.28	0/969	0.58	0/1302
13	CM	0.29	0/961	0.57	0/1291
14	AN	0.30	0/501	0.55	0/664
14	CN	0.32	0/501	0.55	0/664
15	AO	0.27	0/739	0.53	0/985
15	CO	0.30	0/739	0.54	0/985
16	AP	0.29	0/697	0.53	0/939
16	CP	0.28	0/693	0.54	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.29	0/836	0.55	0/1117
17	CQ	0.29	0/836	0.53	0/1117
18	AR	0.27	0/560	0.48	0/746
18	CR	0.28	0/560	0.52	0/746
19	AS	0.28	0/667	0.54	0/900
19	CS	0.30	0/661	0.68	0/893
20	AT	0.27	0/730	0.58	0/965
20	CT	0.27	0/729	0.52	0/965
21	AU	0.29	0/203	0.56	0/266
21	CU	0.32	0/203	0.48	0/266
22	AV	0.49	0/310	0.95	1/480 (0.2%)
22	CV	1.15	3/144 (2.1%)	3.12	11/222 (5.0%)
23	AW	0.45	0/40	1.07	0/60
23	CW	0.35	0/40	1.09	0/60
24	AX	0.53	2/1700 (0.1%)	1.24	23/2650 (0.9%)
24	CX	0.54	0/1700	1.36	19/2650 (0.7%)
25	AY	0.33	0/115	0.82	0/176
25	CY	0.29	0/115	0.95	0/176
26	BA	0.50	4/68013 (0.0%)	0.93	70/106165 (0.1%)
26	DA	0.42	0/67542	0.94	88/105428 (0.1%)
27	BB	0.41	0/2878	0.91	2/4490 (0.0%)
27	DB	0.41	0/2878	1.00	8/4490 (0.2%)
28	BD	0.37	0/2186	0.57	0/2944
28	DD	0.34	0/2186	0.56	0/2944
29	BE	0.36	0/1592	0.53	0/2149
29	DE	0.34	0/1592	0.59	1/2149 (0.0%)
30	BF	0.35	0/1619	0.53	0/2193
30	DF	0.33	0/1615	0.56	0/2188
31	BG	0.29	0/1450	0.54	0/1959
31	DG	0.32	0/1449	0.57	0/1958
32	BH	0.30	0/1356	0.51	0/1834
32	DH	0.29	0/1356	0.51	0/1834
33	BI	0.31	0/1100	0.59	0/1501
33	DI	0.37	0/1076	0.78	4/1471 (0.3%)
34	BN	0.34	0/1144	0.54	0/1543
34	DN	0.31	0/1144	0.52	0/1543
35	BO	0.34	0/943	0.56	0/1269
35	DO	0.33	0/943	0.55	1/1269 (0.1%)
36	BP	0.35	0/1152	0.57	0/1533
36	DP	0.32	0/1152	0.63	0/1533
37	BQ	0.35	0/1143	0.59	1/1527 (0.1%)
37	DQ	0.32	0/1143	0.54	0/1527
38	BR	0.36	0/982	0.57	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.29	0/982	0.55	0/1312
39	BS	0.32	0/887	0.57	1/1180 (0.1%)
39	DS	0.29	0/880	0.57	0/1172
40	BT	0.34	0/1105	0.61	0/1477
40	DT	0.30	0/1097	0.53	0/1468
41	BU	0.35	0/977	0.53	0/1301
41	DU	0.28	0/977	0.50	0/1301
42	BV	0.36	0/782	0.55	0/1049
42	DV	0.29	0/782	0.54	0/1049
43	BW	0.35	0/897	0.53	0/1205
43	DW	0.30	0/897	0.49	0/1205
44	BX	0.39	0/764	0.58	1/1025 (0.1%)
44	DX	0.32	0/764	0.53	1/1025 (0.1%)
45	BY	0.34	0/819	0.59	0/1095
45	DY	0.30	0/819	0.55	0/1095
46	BZ	0.32	0/1379	0.58	0/1873
46	DZ	0.29	0/1390	0.54	0/1890
47	B0	0.36	0/662	0.60	0/881
47	D0	0.30	0/662	0.50	0/881
48	B1	0.32	0/762	0.53	0/1014
48	D1	0.31	0/762	0.53	0/1014
49	B2	0.32	0/590	0.57	0/781
49	D2	0.26	0/590	0.49	0/781
50	B3	0.35	0/474	0.52	0/635
50	D3	0.31	0/469	0.54	0/630
51	B4	0.34	0/565	0.70	0/761
51	D4	0.32	0/545	0.67	0/737
52	B5	0.37	0/469	0.62	1/635 (0.2%)
52	D5	0.32	0/469	0.54	0/635
53	B6	0.36	0/460	0.53	0/613
53	D6	0.34	0/456	0.51	0/608
54	B7	0.36	0/426	0.56	0/561
54	D7	0.34	0/426	0.49	0/561
55	B8	0.37	0/519	0.54	0/684
55	D8	0.31	0/525	0.50	0/691
56	B9	0.43	0/310	0.65	0/407
56	D9	0.33	0/310	0.59	0/407
All	All	0.41	20/310421 (0.0%)	0.88	455/464361 (0.1%)

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	1
7	AG	0	1
20	AT	0	1
29	DE	0	1
33	DI	0	1
39	BS	0	1
46	BZ	0	1
51	B4	0	2
51	D4	0	1
All	All	0	10

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	C6-N1	-12.37	1.30	1.39
1	AA	1172	C	N3-C4	-10.50	1.26	1.33
1	CA	1154	G	N1-C2	-10.41	1.29	1.37
1	AA	1172	C	C2-N3	-8.49	1.28	1.35
1	AA	1164	G	N1-C2	-6.91	1.32	1.37
1	CA	1154	G	N7-C5	-6.70	1.35	1.39
1	AA	1164	G	C6-N1	-6.60	1.34	1.39
22	CV	18	G	N9-C4	6.02	1.42	1.38
1	CA	1154	G	C8-N7	-5.99	1.27	1.30
22	CV	18	G	C5-C6	5.82	1.48	1.42
1	CA	1119	C	N1-C2	5.59	1.45	1.40
26	BA	1188	A	N9-C4	-5.56	1.34	1.37
26	BA	990	A	N9-C4	-5.52	1.34	1.37
1	CA	1154	G	C5-C4	5.47	1.42	1.38
22	CV	18	G	N3-C4	-5.46	1.31	1.35
1	CA	1119	C	N3-C4	-5.44	1.30	1.33
24	AX	22	G	N7-C5	5.24	1.42	1.39
26	BA	553	A	N9-C4	-5.24	1.34	1.37
26	BA	354	A	N9-C4	-5.17	1.34	1.37
24	AX	14	A	N7-C5	-5.08	1.36	1.39

All (455) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1172	C	N1-C2-O2	39.76	142.76	118.90
1	CA	1119	C	N1-C2-O2	26.84	135.00	118.90
1	AA	1172	C	N3-C2-O2	-25.31	104.18	121.90
1	CA	1154	G	C5-C6-O6	24.22	143.13	128.60
1	CA	1154	G	N1-C2-N2	-23.61	94.95	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	N3-C2-N2	23.20	136.14	119.90
1	AA	1172	C	C2-N3-C4	20.22	130.01	119.90
22	CV	18	G	C2-N3-C4	19.75	121.78	111.90
1	CA	1119	C	N3-C2-O2	-17.59	109.59	121.90
22	CV	18	G	N9-C4-C5	17.52	112.41	105.40
1	AA	1172	C	N3-C4-N4	-16.25	106.62	118.00
1	AA	1172	C	C5-C4-N4	16.18	131.53	120.20
1	CA	1119	C	C2-N1-C1'	15.95	136.34	118.80
22	CV	18	G	N3-C4-C5	-15.80	120.70	128.60
22	CV	18	G	C8-N9-C4	-15.55	100.18	106.40
22	CV	18	G	N1-C6-O6	-15.53	110.58	119.90
1	CA	1119	C	C2-N3-C4	15.35	127.57	119.90
1	CA	72	C	N1-C2-O2	14.13	127.38	118.90
22	CV	18	G	C4-C5-N7	-13.80	105.28	110.80
1	CA	1154	G	C5-C6-N1	-13.29	104.85	111.50
1	CA	1154	G	N1-C6-O6	-13.15	112.01	119.90
1	CA	1154	G	C2-N3-C4	-11.85	105.98	111.90
1	CA	1119	C	C6-N1-C1'	-11.84	106.59	120.80
26	DA	2139	C	C2-N1-C1'	11.43	131.37	118.80
1	AA	1172	C	C4-C5-C6	-11.42	111.69	117.40
1	CA	1004	A	O4'-C1'-N9	11.33	117.26	108.20
1	AA	1172	C	C5-C6-N1	11.23	126.62	121.00
27	DB	30	C	C6-N1-C2	-11.19	115.83	120.30
26	DA	1507	A	C5-C6-N1	-11.18	112.11	117.70
1	CA	1119	C	C6-N1-C2	-11.11	115.86	120.30
26	DA	2139	C	N1-C2-O2	10.94	125.47	118.90
1	CA	1154	G	C6-N1-C2	10.77	131.56	125.10
24	AX	46	G	C6-N1-C2	-10.63	118.72	125.10
1	CA	1154	G	C4-N9-C1'	10.51	140.16	126.50
1	CA	97	G	C6-N1-C2	10.34	131.30	125.10
26	BA	2083	G	O5'-P-OP2	-10.00	96.70	105.70
24	AX	14	A	C4-C5-C6	9.98	121.99	117.00
1	AA	359	U	O5'-P-OP1	-9.90	96.79	105.70
1	CA	1281	U	O4'-C1'-N1	-9.83	100.34	108.20
1	AA	1172	C	C6-N1-C2	-9.81	116.38	120.30
1	AA	1172	C	C2-N1-C1'	9.73	129.51	118.80
1	CA	1119	C	C5-C6-N1	9.70	125.85	121.00
22	CV	18	G	C5-C6-O6	9.69	134.41	128.60
26	DA	2139	C	C6-N1-C1'	-9.57	109.31	120.80
26	DA	2136	C	N1-C2-O2	9.53	124.62	118.90
1	CA	93	G	O4'-C1'-N9	9.48	115.78	108.20
1	AA	148	G	N3-C4-N9	-9.46	120.33	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1398	A	O5'-P-OP1	-9.41	97.23	105.70
26	DA	1482	G	C2-N3-C4	-9.37	107.22	111.90
26	DA	2155	G	N3-C2-N2	9.31	126.42	119.90
26	DA	1507	A	C2-N3-C4	-9.26	105.97	110.60
22	CV	18	G	C6-C5-N7	9.08	135.85	130.40
1	AA	1172	C	N1-C2-N3	-9.04	112.87	119.20
2	CB	23	ARG	NE-CZ-NH1	-9.02	115.79	120.30
26	BA	537	G	O4'-C1'-N9	9.02	115.42	108.20
1	CA	1400	C	N1-C2-O2	8.90	124.24	118.90
27	DB	30	C	N3-C2-O2	-8.87	115.69	121.90
24	CX	34	C	C2-N3-C4	-8.79	115.50	119.90
26	DA	2152	G	N1-C6-O6	8.79	125.17	119.90
1	CA	1154	G	C8-N9-C1'	-8.65	115.76	127.00
1	CA	99	U	N1-C2-O2	-8.57	116.80	122.80
1	AA	1030(B)	C	C2-N1-C1'	8.56	128.21	118.80
24	CX	34	C	C4-C5-C6	8.48	121.64	117.40
1	CA	407	G	C6-C5-N7	8.42	135.45	130.40
26	BA	1660	A	O5'-P-OP1	-8.40	98.14	105.70
26	BA	2211	U	N1-C2-O2	8.36	128.66	122.80
1	CA	407	G	N3-C4-C5	8.34	132.77	128.60
1	CA	1256	A	N1-C6-N6	8.32	123.59	118.60
1	AA	1030(B)	C	C6-N1-C2	-8.29	116.98	120.30
1	AA	1007	C	C2-N3-C4	8.27	124.03	119.90
1	CA	407	G	C4-N9-C1'	-8.26	115.77	126.50
1	CA	1154	G	N1-C2-N3	8.23	128.84	123.90
27	DB	30	C	C4-C5-C6	8.20	121.50	117.40
24	AX	14	A	C5-N7-C8	8.16	107.98	103.90
26	DA	2137	C	C5-C6-N1	8.14	125.07	121.00
24	CX	14	A	C4-C5-C6	8.12	121.06	117.00
1	CA	407	G	N3-C4-N9	-8.09	121.15	126.00
26	BA	2162	C	C2-N1-C1'	8.07	127.68	118.80
1	CA	1125	U	C5-C6-N1	8.06	126.73	122.70
1	CA	1009	G	C5-C6-O6	8.04	133.42	128.60
26	BA	354	A	C2-N3-C4	-8.03	106.58	110.60
1	CA	1400	C	C2-N1-C1'	8.02	127.63	118.80
26	DA	2152	G	C5-C6-O6	-7.99	123.81	128.60
24	AX	67	C	C2-N1-C1'	7.98	127.58	118.80
1	AA	1007	C	N1-C2-O2	7.96	123.68	118.90
1	AA	1030(B)	C	N1-C2-O2	7.88	123.63	118.90
26	DA	2121	G	N1-C6-O6	7.87	124.62	119.90
1	CA	1009	G	O5'-P-OP2	-7.83	98.65	105.70
22	CV	18	G	C6-N1-C2	-7.79	120.43	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	70	G	C5-C6-O6	7.71	133.23	128.60
1	AA	1030(B)	C	N3-C2-O2	-7.69	116.52	121.90
24	AX	22	G	N1-C6-O6	-7.67	115.30	119.90
1	CA	1009	G	N1-C6-O6	-7.62	115.33	119.90
1	CA	1400	C	C6-N1-C2	-7.59	117.26	120.30
1	CA	1007	C	C5-C6-N1	7.58	124.79	121.00
1	CA	1119	C	C5-C4-N4	7.49	125.44	120.20
1	CA	407	G	C4-C5-C6	-7.48	114.31	118.80
1	CA	97	G	N3-C4-C5	7.46	132.33	128.60
24	AX	22	G	C4-C5-C6	-7.45	114.33	118.80
26	DA	2152	G	C6-C5-N7	-7.45	125.93	130.40
1	CA	72	C	N3-C2-O2	-7.44	116.69	121.90
27	BB	89	G	O5'-P-OP2	-7.43	99.01	105.70
1	CA	1001(A)	G	N3-C4-N9	7.39	130.44	126.00
24	CX	67	C	C2-N1-C1'	7.38	126.91	118.80
26	DA	2121	G	C5-C6-O6	-7.37	124.18	128.60
26	BA	1700	G	P-O3'-C3'	7.35	128.52	119.70
24	CX	67	C	N1-C2-O2	7.30	123.28	118.90
1	CA	97	G	C5-C6-N1	-7.26	107.87	111.50
26	DA	512	G	O4'-C1'-N9	7.25	114.00	108.20
1	AA	1022	G	N3-C2-N2	7.22	124.95	119.90
1	CA	1125	U	C2-N1-C1'	7.21	126.36	117.70
26	BA	1154	U	N1-C2-O2	7.21	127.85	122.80
1	CA	1154	G	C4-C5-C6	7.20	123.12	118.80
26	BA	1068	G	N3-C4-N9	-7.18	121.69	126.00
27	DB	30	C	C2-N1-C1'	7.18	126.70	118.80
1	CA	1002	G	C5-C6-O6	7.18	132.91	128.60
1	CA	407	G	N1-C2-N2	7.18	122.66	116.20
27	DB	30	C	N3-C4-C5	-7.16	119.03	121.90
1	CA	1256	A	C5-C6-N6	-7.13	118.00	123.70
24	AX	22	G	C5-N7-C8	-7.10	100.75	104.30
26	BA	1154	U	C2-N1-C1'	7.08	126.19	117.70
26	DA	2139	C	N3-C2-O2	-7.02	116.99	121.90
22	CV	18	G	C5-C6-N1	7.00	115.00	111.50
26	DA	2136	C	N3-C2-O2	-6.96	117.03	121.90
26	BA	2162	C	C6-N1-C2	-6.93	117.53	120.30
26	BA	1154	U	N3-C2-O2	-6.91	117.36	122.20
1	CA	992	U	P-O3'-C3'	6.87	127.95	119.70
1	AA	198	G	C4-N9-C1'	6.86	135.42	126.50
1	CA	1119	C	N3-C4-C5	-6.86	119.16	121.90
1	CA	1400	C	C5-C6-N1	6.86	124.43	121.00
26	BA	354	A	N1-C2-N3	6.83	132.72	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	1067	A	C2-N3-C4	-6.81	107.19	110.60
24	CX	46	G	C6-N1-C2	-6.79	121.03	125.10
26	DA	2206	G	C4-N9-C1'	-6.76	117.71	126.50
37	BQ	56	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	CA	1001(A)	G	C4-N9-C1'	6.75	135.28	126.50
1	CA	407	G	C8-N9-C1'	6.72	135.74	127.00
1	AA	148	G	C4-N9-C1'	-6.72	117.76	126.50
1	AA	148	G	C8-N9-C1'	6.68	135.68	127.00
1	AA	1001	A	C5-C6-N6	6.67	129.04	123.70
26	DA	645	C	C2-N1-C1'	6.66	126.12	118.80
26	BA	553	A	C2-N3-C4	-6.65	107.28	110.60
26	BA	1701	A	O5'-P-OP1	-6.64	99.72	105.70
26	BA	2211	U	N3-C2-O2	-6.64	117.55	122.20
1	CA	76	C	N1-C2-O2	6.64	122.88	118.90
26	DA	2177	C	C2-N1-C1'	6.61	126.07	118.80
26	DA	2206	G	C8-N9-C1'	6.60	135.58	127.00
35	DO	8	LEU	CA-CB-CG	6.57	130.41	115.30
24	AX	22	G	N3-C4-N9	-6.56	122.07	126.00
1	AA	421	U	N1-C2-O2	6.55	127.39	122.80
26	BA	2014	G	P-O3'-C3'	6.54	127.55	119.70
26	DA	2167	U	C2-N1-C1'	6.54	125.55	117.70
26	BA	934	A	O4'-C1'-N9	6.53	113.43	108.20
26	DA	2137	C	C6-N1-C2	-6.53	117.69	120.30
1	AA	1011	G	N3-C4-C5	-6.51	125.35	128.60
1	CA	1154	G	N3-C4-N9	6.48	129.89	126.00
1	CA	1034	G	N7-C8-N9	6.47	116.34	113.10
1	AA	1019	C	C5-C6-N1	6.47	124.23	121.00
1	CA	1001(A)	G	C8-N9-C1'	-6.47	118.59	127.00
26	DA	645	C	N1-C2-O2	6.46	122.78	118.90
26	DA	2140	C	N3-C2-O2	-6.45	117.38	121.90
24	AX	67	C	C6-N1-C1'	-6.45	113.06	120.80
26	DA	2152	G	N3-C4-N9	6.44	129.87	126.00
24	CX	44	A	N1-C6-N6	6.44	122.46	118.60
24	AX	14	A	C5-C6-N1	-6.43	114.49	117.70
26	DA	2177	C	N1-C2-O2	6.43	122.75	118.90
26	DA	2167	U	N1-C2-O2	6.39	127.28	122.80
1	CA	1150	U	C5-C4-O4	6.39	129.73	125.90
26	DA	2155	G	C6-N1-C2	6.39	128.93	125.10
1	AA	148	G	N3-C4-C5	6.37	131.79	128.60
1	CA	72	C	C4-C5-C6	-6.35	114.22	117.40
1	CA	1119	C	N1-C2-N3	-6.33	114.77	119.20
1	CA	1036	G	N3-C4-N9	6.32	129.79	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	148	G	C6-C5-N7	6.30	134.18	130.40
1	CA	1018	C	C2-N1-C1'	6.28	125.71	118.80
26	DA	1507	A	C4-C5-C6	6.27	120.14	117.00
26	BA	1188	A	C2-N3-C4	-6.26	107.47	110.60
24	AX	46	G	N1-C2-N3	6.26	127.66	123.90
24	CX	34	C	N1-C2-N3	6.26	123.58	119.20
1	CA	1003	G	N7-C8-N9	6.25	116.23	113.10
1	CA	754	C	C2-N1-C1'	6.25	125.68	118.80
1	AA	421	U	N3-C2-O2	-6.25	117.83	122.20
24	AX	14	A	C8-N9-C1'	-6.22	116.50	127.70
24	AX	46	G	C5-C6-N1	6.22	114.61	111.50
1	CA	1031	G	N3-C4-N9	6.22	129.73	126.00
1	CA	1308	U	C5-C4-O4	6.22	129.63	125.90
1	AA	1011	G	N3-C4-N9	6.21	129.73	126.00
26	DA	2137	C	C2-N1-C1'	6.21	125.63	118.80
1	AA	148	G	N9-C4-C5	6.20	107.88	105.40
26	BA	12	U	C2-N1-C1'	6.20	125.14	117.70
26	DA	1699	G	N1-C6-O6	6.16	123.59	119.90
1	CA	1229	A	C6-N1-C2	6.13	122.28	118.60
1	AA	1172	C	C6-N1-C1'	-6.13	113.45	120.80
26	BA	990	A	C2-N3-C4	-6.12	107.54	110.60
1	CA	1126	U	C2-N1-C1'	6.12	125.05	117.70
26	DA	2700	C	C6-N1-C2	6.12	122.75	120.30
26	DA	2152	G	C4-N9-C1'	6.12	134.45	126.50
1	CA	93	G	C8-N9-C1'	6.12	134.95	127.00
26	DA	2160	G	N3-C4-N9	6.10	129.66	126.00
26	DA	1507	A	N1-C2-N3	6.10	132.35	129.30
24	AX	22	G	C6-C5-N7	6.09	134.05	130.40
27	DB	20	C	C2-N1-C1'	6.09	125.50	118.80
26	DA	2167	U	N3-C2-O2	-6.09	117.94	122.20
26	DA	898	C	C6-N1-C2	-6.08	117.87	120.30
1	CA	988	G	N3-C4-N9	6.08	129.65	126.00
1	CA	992	U	OP2-P-O3'	6.08	118.58	105.20
1	AA	93	G	C6-N1-C2	6.08	128.75	125.10
26	DA	2152	G	C8-N9-C1'	-6.08	119.10	127.00
26	DA	2133	G	C2-N3-C4	-6.07	108.86	111.90
1	AA	1262	C	C2-N3-C4	6.07	122.94	119.90
26	BA	1220	U	P-O3'-C3'	6.06	126.97	119.70
1	CA	1034	G	C8-N9-C4	-6.06	103.98	106.40
1	AA	1001	A	N1-C6-N6	-6.05	114.97	118.60
1	CA	1400	C	N3-C2-O2	-6.05	117.67	121.90
1	CA	1064	G	P-O3'-C3'	6.04	126.95	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1154	G	C8-N9-C4	-6.04	103.98	106.40
1	CA	1012	U	N1-C2-N3	6.04	118.52	114.90
26	DA	2152	G	N9-C4-C5	-6.04	102.99	105.40
1	AA	921	U	C2-N3-C4	6.01	130.61	127.00
1	CA	99	U	N3-C2-O2	6.01	126.41	122.20
1	CA	1154	G	N3-C4-C5	-6.01	125.60	128.60
1	AA	421	U	C2-N1-C1'	6.00	124.90	117.70
1	AA	1396	A	C6-N1-C2	5.98	122.19	118.60
1	CA	1027	C	N1-C2-O2	5.97	122.48	118.90
26	DA	893	C	C2-N1-C1'	5.94	125.34	118.80
26	DA	2150	U	N3-C2-O2	-5.94	118.04	122.20
1	CA	1355	G	N1-C6-O6	5.94	123.46	119.90
26	DA	1482	G	N1-C2-N3	5.93	127.46	123.90
26	BA	2196	C	N1-C2-O2	5.93	122.46	118.90
1	CA	1125	U	O4'-C1'-N1	5.93	112.94	108.20
24	AX	14	A	C4-N9-C1'	5.91	136.94	126.30
24	AX	14	A	N1-C6-N6	5.87	122.12	118.60
1	CA	435	C	N1-C2-O2	-5.87	115.38	118.90
1	CA	457	C	C2-N1-C1'	5.87	125.25	118.80
1	CA	1355	G	C5-C6-O6	-5.87	125.08	128.60
1	AA	198	G	C8-N9-C1'	-5.86	119.38	127.00
1	CA	1036	G	C5-C6-O6	-5.86	125.08	128.60
26	BA	1068	G	N3-C2-N2	-5.82	115.83	119.90
24	AX	22	G	C5-C6-N1	5.81	114.41	111.50
26	BA	1068	G	C4-N9-C1'	-5.81	118.95	126.50
1	AA	198	G	O4'-C1'-N9	5.80	112.84	108.20
1	CA	1216	G	N3-C4-C5	5.79	131.50	128.60
1	CA	1009	G	N9-C4-C5	5.79	107.72	105.40
1	AA	345	C	N1-C2-O2	5.79	122.37	118.90
1	CA	93	G	C4-N9-C1'	-5.78	118.98	126.50
24	CX	44	A	C5-C6-N6	-5.78	119.07	123.70
26	BA	1067	A	N1-C2-N3	5.78	132.19	129.30
1	CA	950	U	N1-C2-O2	5.78	126.84	122.80
26	BA	990	A	N1-C6-N6	5.77	122.06	118.60
26	BA	2197	C	N1-C2-O2	5.77	122.36	118.90
26	DA	1699	G	C5-C6-O6	-5.76	125.15	128.60
26	DA	893	C	N1-C2-O2	5.75	122.35	118.90
26	BA	892	G	O4'-C1'-N9	5.75	112.80	108.20
26	DA	2177	C	C6-N1-C1'	-5.75	113.90	120.80
26	BA	2122	G	C5-C6-O6	-5.72	125.17	128.60
1	CA	1273	G	C5-C6-O6	-5.72	125.17	128.60
26	DA	2178	C	C2-N1-C1'	5.71	125.08	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	DI	123	LEU	CA-CB-CG	5.70	128.41	115.30
26	DA	2152	G	C4-C5-N7	5.69	113.08	110.80
1	CA	407	G	N3-C2-N2	-5.69	115.92	119.90
26	DA	2711	A	C8-N9-C4	5.69	108.08	105.80
1	CA	97	G	N1-C2-N3	-5.68	120.49	123.90
26	BA	1577	C	P-O3'-C3'	5.68	126.51	119.70
26	DA	141	A	N7-C8-N9	5.68	116.64	113.80
26	BA	2211	U	C2-N1-C1'	5.67	124.50	117.70
26	BA	2015	U	O5'-P-OP1	-5.67	100.60	105.70
24	CX	67	C	C6-N1-C1'	-5.67	114.00	120.80
1	AA	1067	A	P-O3'-C3'	5.66	126.50	119.70
26	BA	2162	C	N1-C2-O2	5.66	122.30	118.90
26	BA	1359	U	C2-N1-C1'	5.66	124.49	117.70
1	CA	1183	A	P-O3'-C3'	5.65	126.48	119.70
24	AX	46	G	C5-C6-O6	-5.64	125.22	128.60
1	CA	1123	A	C5-C6-N6	5.63	128.21	123.70
1	AA	913	A	P-O3'-C3'	5.63	126.45	119.70
1	CA	927	G	C5-C6-O6	5.62	131.97	128.60
27	DB	20	C	C6-N1-C1'	-5.62	114.05	120.80
26	DA	945	A	O4'-C1'-N9	5.62	112.69	108.20
26	BA	2186	C	N1-C2-O2	-5.61	115.53	118.90
1	CA	1003	G	C4-N9-C1'	5.60	133.78	126.50
26	DA	1482	G	C5-C6-N1	-5.60	108.70	111.50
27	DB	8	U	C5-C6-N1	5.60	125.50	122.70
26	DA	2155	G	C5-C6-O6	5.59	131.96	128.60
27	BB	89	G	O5'-P-OP1	5.59	117.40	110.70
24	AX	22	G	C8-N9-C1'	5.58	134.25	127.00
26	DA	1531	C	C2-N1-C1'	5.58	124.94	118.80
1	CA	266	G	C4-N9-C1'	5.58	133.75	126.50
1	CA	1038	C	C2-N3-C4	5.57	122.69	119.90
1	AA	1329	A	C6-N1-C2	5.56	121.94	118.60
1	CA	1094	G	O4'-C1'-N9	5.56	112.65	108.20
26	DA	2140	C	C6-N1-C2	-5.56	118.08	120.30
1	AA	347	G	OP1-P-O3'	5.56	117.43	105.20
1	CA	1220	G	N3-C4-N9	-5.55	122.67	126.00
26	BA	2150	C	N1-C2-O2	-5.54	115.57	118.90
26	BA	2298	A	N7-C8-N9	5.53	116.57	113.80
24	CX	14	A	C4-N9-C1'	5.53	136.26	126.30
1	CA	997	U	C5-C4-O4	5.53	129.22	125.90
26	BA	553	A	C5-N7-C8	-5.52	101.14	103.90
1	AA	343	U	O4'-C1'-N1	5.52	112.62	108.20
26	DA	1647	G	O4'-C1'-N9	-5.52	103.78	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1158	C	N1-C2-O2	5.50	122.20	118.90
26	DA	1021	A	C2-N3-C4	-5.50	107.85	110.60
1	CA	1001(A)	G	N3-C4-C5	-5.49	125.85	128.60
26	DA	34	C	N1-C2-O2	5.49	122.19	118.90
24	AX	67	C	C5-C6-N1	5.48	123.74	121.00
1	CA	1256	A	C4-C5-N7	5.48	113.44	110.70
26	DA	1653	G	C4-N9-C1'	5.48	133.62	126.50
1	CA	1256	A	C6-C5-N7	-5.48	128.47	132.30
24	AX	46	G	N3-C4-C5	-5.47	125.86	128.60
39	BS	78	LEU	CA-CB-CG	5.47	127.88	115.30
26	BA	1418	U	N3-C4-O4	5.46	123.22	119.40
26	BA	1068	G	C8-N9-C1'	5.46	134.10	127.00
1	CA	1154	G	C6-C5-N7	-5.46	127.13	130.40
26	DA	1022	G	N3-C2-N2	-5.45	116.08	119.90
26	DA	2139	C	C5-C6-N1	5.45	123.73	121.00
1	AA	1030(B)	C	O4'-C1'-N1	5.45	112.56	108.20
24	CX	44	A	C6-C5-N7	-5.44	128.49	132.30
26	DA	1882	C	C5-C6-N1	5.44	123.72	121.00
1	AA	1040	U	C5-C4-O4	5.43	129.16	125.90
1	CA	1126	U	N1-C2-O2	5.43	126.60	122.80
26	BA	2162	C	N3-C2-O2	-5.42	118.10	121.90
1	CA	1036	G	N3-C4-C5	-5.41	125.89	128.60
26	BA	1218	G	O4'-C1'-N9	5.41	112.53	108.20
33	DI	72	LEU	CA-CB-CG	5.41	127.73	115.30
1	CA	84	U	C2-N1-C1'	5.40	124.18	117.70
1	CA	76	C	N3-C2-O2	-5.40	118.12	121.90
26	BA	2148	A	O4'-C1'-N9	-5.39	103.89	108.20
1	CA	1135	U	O4'-C1'-N1	5.38	112.51	108.20
26	BA	2180	A	P-O3'-C3'	5.38	126.16	119.70
1	AA	1030	C	C2-N1-C1'	5.38	124.72	118.80
1	CA	1003	G	N3-C4-C5	-5.37	125.92	128.60
26	BA	1343	C	OP1-P-O3'	5.37	117.01	105.20
26	DA	277	C	N1-C2-O2	5.37	122.12	118.90
26	BA	1426	G	O5'-P-OP2	-5.36	100.87	105.70
1	CA	73	G	N9-C1'-C2'	-5.36	106.10	112.00
26	DA	2121	G	C6-C5-N7	-5.36	127.18	130.40
26	BA	2149	G	N9-C1'-C2'	-5.36	106.10	112.00
1	AA	1040	U	C2-N3-C4	5.36	130.22	127.00
26	BA	112	U	C2-N1-C1'	5.36	124.13	117.70
26	BA	670	C	C2-N1-C1'	5.35	124.69	118.80
1	CA	1067	A	P-O3'-C3'	5.35	126.12	119.70
22	CV	18	G	C5-N7-C8	5.34	106.97	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	457	C	C6-N1-C1'	-5.34	114.39	120.80
1	CA	1329	A	C5-C6-N6	5.34	127.97	123.70
1	CA	1001(A)	G	C6-C5-N7	-5.34	127.20	130.40
1	AA	1001(A)	G	C4-N9-C1'	5.34	133.44	126.50
44	DX	57	LEU	CA-CB-CG	5.33	127.57	115.30
1	CA	1355	G	C6-C5-N7	-5.33	127.20	130.40
26	DA	879	G	C4-N9-C1'	5.33	133.43	126.50
24	CX	67	C	N3-C2-O2	-5.32	118.18	121.90
26	DA	2122	U	C5-C4-O4	-5.32	122.71	125.90
1	CA	97	G	C4-N9-C1'	-5.31	119.60	126.50
1	AA	76	C	C2-N3-C4	5.31	122.55	119.90
1	AA	347	G	P-O3'-C3'	5.30	126.06	119.70
26	BA	2157	A	N1-C6-N6	5.30	121.78	118.60
22	AV	17	U	C5-C4-O4	5.30	129.08	125.90
1	AA	991	U	OP2-P-O3'	5.29	116.84	105.20
26	BA	1068	G	N3-C4-C5	5.29	131.25	128.60
1	CA	1128	C	P-O3'-C3'	5.29	126.05	119.70
1	CA	78	G	C8-N9-C1'	5.29	133.87	127.00
26	BA	2157	A	C5-C6-N6	-5.28	119.48	123.70
5	CE	12	LEU	CA-CB-CG	5.28	127.44	115.30
24	CX	44	A	N7-C8-N9	5.28	116.44	113.80
1	AA	839	U	P-O3'-C3'	5.27	126.03	119.70
26	BA	553	A	N3-C4-N9	-5.26	123.19	127.40
26	DA	1992	G	P-O3'-C3'	5.26	126.01	119.70
1	CA	1220	G	N9-C4-C5	5.26	107.50	105.40
1	AA	921	U	C5-C4-O4	5.25	129.05	125.90
1	CA	1011	G	C4-N9-C1'	5.24	133.32	126.50
1	CA	1256	A	O4'-C1'-N9	-5.24	104.00	108.20
1	CA	1003	G	C8-N9-C4	-5.24	104.31	106.40
1	CA	1400	C	C2-N3-C4	5.23	122.52	119.90
26	DA	362	U	C5-C6-N1	5.23	125.31	122.70
1	CA	1020	U	C2-N3-C4	-5.23	123.86	127.00
26	DA	269	U	C2-N1-C1'	5.23	123.97	117.70
1	AA	1002	G	N3-C4-N9	5.22	129.13	126.00
1	CA	1400	C	O5'-P-OP2	5.22	116.96	110.70
24	AX	22	G	N7-C8-N9	5.22	115.71	113.10
24	CX	59	A	O4'-C1'-N9	5.21	112.37	108.20
1	CA	189(J)	G	O4'-C1'-N9	5.21	112.37	108.20
26	DA	277	C	P-O3'-C3'	5.21	125.95	119.70
1	CA	1002	G	N1-C6-O6	-5.20	116.78	119.90
1	AA	1030(B)	C	C6-N1-C1'	-5.20	114.56	120.80
1	CA	78	G	N9-C1'-C2'	-5.19	106.29	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2121	G	N9-C4-C5	-5.19	103.33	105.40
24	AX	14	A	N3-C4-N9	5.18	131.55	127.40
26	BA	2082	A	C8-N9-C4	5.18	107.87	105.80
24	CX	34	C	C6-N1-C2	-5.18	118.23	120.30
1	CA	1035	A	N9-C1'-C2'	-5.17	106.31	112.00
26	DA	2121	G	N3-C4-N9	5.17	129.10	126.00
1	AA	198	G	N7-C8-N9	5.17	115.69	113.10
1	AA	748	C	P-O3'-C3'	5.16	125.90	119.70
24	CX	14	A	C8-N9-C1'	-5.16	118.42	127.70
26	DA	1314	C	C2-N1-C1'	5.16	124.47	118.80
26	BA	776	G	C5-C6-O6	-5.15	125.51	128.60
29	DE	72	VAL	C-N-CA	5.14	134.55	121.70
26	BA	1311	A	O5'-P-OP2	-5.13	101.08	105.70
26	DA	2473	U	C2-N1-C1'	5.13	123.86	117.70
1	CA	1154	G	N7-C8-N9	5.13	115.67	113.10
26	BA	2724	U	O4'-C1'-N1	5.12	112.30	108.20
1	AA	1007	C	C5-C6-N1	5.12	123.56	121.00
1	CA	1213	A	O4'-C1'-N9	5.11	112.29	108.20
24	CX	59	A	C4-N9-C1'	-5.11	117.11	126.30
1	CA	1395	C	N1-C2-O2	5.11	121.96	118.90
2	CB	98	LEU	CA-CB-CG	5.11	127.05	115.30
26	BA	1221	G	P-O3'-C3'	5.10	125.82	119.70
26	BA	2157	A	N9-C4-C5	-5.10	103.76	105.80
26	DA	2184	G	C8-N9-C1'	-5.10	120.37	127.00
1	AA	1340	A	C6-N1-C2	5.10	121.66	118.60
1	AA	1036	G	N3-C2-N2	-5.09	116.33	119.90
26	DA	1313	U	C2-N1-C1'	5.09	123.81	117.70
26	DA	2140	C	C2-N1-C1'	5.09	124.40	118.80
1	CA	985	C	N1-C2-O2	-5.09	115.84	118.90
26	BA	1440	U	O5'-P-OP1	-5.09	101.12	105.70
26	BA	410	U	C2-N1-C1'	-5.08	111.60	117.70
1	CA	1018	C	C5-C6-N1	5.08	123.54	121.00
26	DA	2593	U	N3-C4-O4	-5.08	115.84	119.40
1	CA	1038	C	N3-C4-C5	-5.08	119.87	121.90
33	DI	75	LEU	CA-CB-CG	5.08	126.98	115.30
26	DA	1963	U	C2-N1-C1'	5.08	123.79	117.70
1	AA	1172	C	O4'-C1'-N1	5.08	112.26	108.20
26	BA	553	A	N3-C4-C5	5.07	130.35	126.80
26	DA	932	G	C4-N9-C1'	-5.07	119.90	126.50
1	AA	1397	C	C2-N1-C1'	5.07	124.38	118.80
1	CA	1231	G	C5-C6-O6	-5.07	125.56	128.60
26	BA	552	C	C6-N1-C2	-5.07	118.27	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	BX	57	LEU	CA-CB-CG	5.07	126.95	115.30
26	DA	2184	G	N3-C4-N9	5.07	129.04	126.00
1	AA	1027	C	C2-N3-C4	5.06	122.43	119.90
1	CA	72	C	C2-N3-C4	5.06	122.43	119.90
26	DA	2133	G	C5-C6-N1	-5.06	108.97	111.50
1	CA	1120	G	N7-C8-N9	5.06	115.63	113.10
1	CA	1256	A	N9-C4-C5	-5.05	103.78	105.80
1	CA	1273	G	N3-C4-N9	5.05	129.03	126.00
1	CA	1003	G	N3-C4-N9	5.05	129.03	126.00
26	BA	1958	A	O4'-C1'-N9	5.04	112.23	108.20
1	AA	1027	C	N3-C4-C5	-5.04	119.89	121.90
26	BA	934	A	P-O3'-C3'	5.04	125.75	119.70
26	BA	572	A	P-O3'-C3'	5.04	125.74	119.70
1	CA	1011	G	C8-N9-C1'	-5.03	120.46	127.00
26	BA	2162	C	C6-N1-C1'	-5.03	114.76	120.80
52	B5	58	LEU	CA-CB-CG	5.03	126.86	115.30
24	CX	22	G	C5-N7-C8	-5.03	101.79	104.30
1	AA	175	C	C5-C6-N1	5.03	123.51	121.00
26	DA	1507	A	N1-C6-N6	5.02	121.61	118.60
1	CA	1355	G	N3-C4-N9	5.02	129.01	126.00
33	DI	88	ILE	CB-CA-C	-5.02	101.56	111.60
1	AA	1033	G	O4'-C1'-N9	5.01	112.21	108.20
26	DA	528	A	C2-N3-C4	-5.01	108.10	110.60
1	AA	1308	U	C2-N3-C4	5.01	130.00	127.00
2	CB	187	LEU	CA-CB-CG	5.01	126.82	115.30
26	DA	2689	U	P-O3'-C3'	5.01	125.71	119.70
1	AA	266	G	P-O3'-C3'	5.01	125.71	119.70
26	BA	2131	U	C2-N1-C1'	5.01	123.71	117.70
26	DA	2122	U	C2-N3-C4	-5.00	124.00	127.00
26	DA	2176	A	C5-C6-N6	-5.00	119.70	123.70

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	8	LYS	Peptide
7	AG	79	ARG	Peptide
20	AT	9	ASN	Peptide
51	B4	57	GLU	Peptide
51	B4	58	ARG	Peptide
39	BS	58	LEU	Peptide
46	BZ	158	PRO	Peptide

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Mol	Chain	Res	Type	Group
51	D4	66	SER	Peptide
29	DE	72	VAL	Peptide
33	DI	81	VAL	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	32205	0	16255	743	1
1	CA	32312	0	16307	964	1
2	AB	1846	0	1867	74	0
2	CB	1825	0	1828	76	0
3	AC	1552	0	1546	49	0
3	CC	1542	0	1517	58	0
4	AD	1659	0	1676	74	0
4	CD	1674	0	1714	83	0
5	AE	1129	0	1184	33	0
5	CE	1133	0	1191	39	0
6	AF	806	0	793	16	0
6	CF	816	0	808	23	0
7	AG	1231	0	1238	37	0
7	CG	1235	0	1249	38	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	983	0	986	48	0
9	CI	978	0	966	53	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	38	0
11	AK	829	0	825	23	0
11	CK	833	0	836	20	0
12	AL	930	0	980	21	0
12	CL	930	0	980	33	0
13	AM	958	0	1002	37	0
13	CM	950	0	988	47	0
14	AN	492	0	529	27	0
14	CN	492	0	529	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	AO	728	0	760	22	0
15	CO	728	0	760	27	0
16	AP	681	0	697	27	0
16	CP	677	0	686	26	0
17	AQ	823	0	891	23	0
17	CQ	823	0	891	18	0
18	AR	555	0	618	11	0
18	CR	555	0	618	23	0
19	AS	652	0	662	29	0
19	CS	646	0	644	40	0
20	AT	728	0	798	27	0
20	CT	727	0	796	23	0
21	AU	199	0	208	5	0
21	CU	199	0	208	8	0
22	AV	277	0	140	7	0
22	CV	129	0	65	16	0
23	AW	74	0	51	5	0
23	CW	74	0	51	10	0
24	AX	1633	0	816	35	0
24	CX	1635	0	816	82	0
25	AY	104	0	56	3	0
25	CY	104	0	56	2	0
26	BA	60729	0	30620	950	0
26	DA	60311	0	30412	1223	1
27	BB	2573	0	1306	32	0
27	DB	2573	0	1306	87	0
28	BD	2136	0	2218	67	0
28	DD	2136	0	2218	74	0
29	BE	1559	0	1618	43	0
29	DE	1559	0	1618	56	0
30	BF	1584	0	1625	49	0
30	DF	1580	0	1619	55	0
31	BG	1425	0	1443	37	0
31	DG	1424	0	1434	73	0
32	BH	1330	0	1407	29	0
32	DH	1330	0	1407	44	0
33	BI	1085	0	1114	28	1
33	DI	1061	0	1080	50	0
34	BN	1117	0	1184	21	0
34	DN	1117	0	1184	29	0
35	BO	933	0	996	27	0
35	DO	933	0	996	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BP	1135	0	1212	53	0
36	DP	1135	0	1212	61	0
37	BQ	1122	0	1179	38	0
37	DQ	1122	0	1179	33	0
38	BR	968	0	1033	26	1
38	DR	968	0	1033	36	0
39	BS	877	0	938	28	0
39	DS	870	0	923	29	0
40	BT	1091	0	1151	37	0
40	DT	1083	0	1136	39	0
41	BU	959	0	1019	24	0
41	DU	959	0	1018	29	0
42	BV	771	0	830	21	1
42	DV	771	0	830	24	0
43	BW	886	0	940	15	0
43	DW	886	0	940	20	0
44	BX	750	0	814	24	0
44	DX	750	0	814	19	0
45	BY	806	0	881	24	0
45	DY	806	0	881	19	0
46	BZ	1349	0	1355	38	0
46	DZ	1360	0	1363	47	0
47	B0	653	0	674	20	0
47	D0	653	0	674	19	0
48	B1	755	0	826	19	0
48	D1	755	0	826	20	0
49	B2	588	0	643	8	0
49	D2	588	0	643	9	0
50	B3	469	0	518	15	0
50	D3	464	0	514	15	0
51	B4	552	0	533	32	0
51	D4	532	0	503	28	0
52	B5	455	0	465	8	0
52	D5	455	0	465	10	0
53	B6	453	0	473	13	0
53	D6	449	0	469	6	0
54	B7	418	0	467	19	0
54	D7	418	0	467	15	0
55	B8	511	0	571	29	0
55	D8	517	0	582	14	0
56	B9	307	0	335	8	0
56	D9	307	0	335	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	AA	207	0	0	0	0
57	AD	2	0	0	0	0
57	AE	2	0	0	0	0
57	AF	1	0	0	0	0
57	AJ	1	0	0	0	0
57	AK	1	0	0	0	0
57	AM	1	0	0	0	0
57	AN	2	0	0	0	0
57	AS	1	0	0	0	0
57	AV	1	0	0	0	0
57	AW	1	0	0	0	0
57	AX	11	0	0	0	0
57	B0	4	0	0	0	0
57	B1	1	0	0	0	0
57	B2	1	0	0	0	0
57	B3	2	0	0	0	0
57	B5	2	0	0	0	0
57	B7	3	0	0	0	0
57	B8	1	0	0	0	0
57	B9	1	0	0	0	0
57	BA	720	0	0	0	0
57	BB	20	0	0	0	0
57	BD	11	0	0	0	0
57	BE	7	0	0	0	0
57	BF	10	0	0	0	0
57	BG	2	0	0	0	0
57	BN	6	0	0	0	0
57	BO	1	0	0	0	0
57	BP	4	0	0	0	0
57	BQ	5	0	0	0	0
57	BR	3	0	0	0	0
57	BU	8	0	0	0	0
57	BV	4	0	0	0	0
57	BW	5	0	0	0	0
57	BX	1	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	1	0	0	0	0
57	CA	160	0	0	0	0
57	CE	1	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	CT	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	2	0	0	0	0
57	D3	1	0	0	0	0
57	D5	1	0	0	0	0
57	D8	2	0	0	0	0
57	DA	629	0	0	0	0
57	DB	10	0	0	0	0
57	DD	7	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	2	0	0	0	0
57	DU	4	0	0	0	0
57	DV	2	0	0	0	0
57	DW	2	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	1	0
58	CD	8	0	0	1	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	170	0	0	16	0
61	AL	2	0	0	1	0
61	AO	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	AW	3	0	0	0	0
61	B0	4	0	0	0	0
61	B1	1	0	0	0	0
61	B3	1	0	0	0	0
61	B5	5	0	0	0	0
61	B7	1	0	0	1	0
61	B8	7	0	0	0	0
61	BA	1102	0	0	59	0
61	BB	36	0	0	1	0
61	BD	8	0	0	1	0
61	BE	13	0	0	5	0
61	BF	4	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BP	15	0	0	1	0
61	BQ	3	0	0	0	0
61	BR	1	0	0	1	0
61	BS	1	0	0	0	0
61	BT	3	0	0	0	0
61	BU	1	0	0	1	0
61	BV	4	0	0	0	0
61	BW	2	0	0	0	0
61	BX	2	0	0	0	0
61	CA	130	0	0	8	0
61	CE	1	0	0	0	0
61	CJ	2	0	0	0	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CV	1	0	0	0	0
61	CW	1	0	0	0	0
61	CX	1	0	0	1	0
61	D0	5	0	0	1	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D7	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	767	0	0	55	0
61	DB	9	0	0	0	0
61	DD	9	0	0	3	0
61	DE	5	0	0	0	0
61	DF	6	0	0	0	0
61	DN	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DP	12	0	0	3	0
61	DR	2	0	0	1	0
61	DT	1	0	0	0	0
61	DU	2	0	0	0	0
61	DV	1	0	0	1	0
61	DX	2	0	0	0	0
61	DY	1	0	0	1	0
All	All	290205	0	193125	6241	3

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 (6241) 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	1.48	1.11
26:DA:2121:G:H1	26:DA:2177:C:N4	1.52	1.06
1:AA:1164:G:N2	1:AA:1165:C:C5	2.24	1.06
1:CA:72:C:N4	1:CA:97:G:N1	2.04	1.05
26:DA:2139:C:N4	26:DA:2152:G:H1	1.55	1.04
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.40	1.03
1:CA:1162:C:N4	1:CA:1174:G:H1	1.56	1.03
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.20	1.03
26:DA:2137:C:N4	26:DA:2154:G:H1	1.55	1.02
1:CA:1245:A:H61	1:CA:1292:U:H3	1.07	1.02
1:CA:1244:C:N4	1:CA:1293:G:H1	1.56	1.02
1:CA:76:C:C4	1:CA:93:G:N1	2.28	1.01
1:CA:1114:C:N4	1:CA:1186:G:H1	1.57	1.01
22:CV:18:G:N2	24:CX:34:C:N3	2.07	1.01
1:CA:1355:G:H1	1:CA:1367:C:H42	1.04	1.00
26:DA:2104:G:H1	26:DA:2185:C:N4	1.58	1.00
1:CA:985:C:N4	1:CA:1220:G:H1	1.60	0.99
1:CA:76:C:N4	1:CA:93:G:C6	2.31	0.99
22:CV:18:G:H1	24:CX:34:C:N4	1.60	0.99
1:AA:1164:G:N2	1:AA:1165:C:C6	2.31	0.99
26:BA:2160:C:H42	26:BA:2175:G:H1	1.04	0.99
1:CA:1000:U:H3	1:CA:1041:A:N6	1.61	0.98
26:BA:2124:U:H3	26:BA:2209:G:H1	1.11	0.98
1:CA:1000:U:H3	1:CA:1041:A:H61	0.98	0.97
24:CX:30:G:H1	24:CX:40:C:H42	1.00	0.97
1:AA:1089:G:H1	1:AA:1096:C:N4	1.62	0.97
1:CA:1133:G:H1	1:CA:1141:C:H42	1.10	0.97
1:CA:76:C:N4	1:CA:93:G:N1	2.13	0.96

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:49:G:N1	24:CX:65:C:N4	2.12	0.96
1:CA:72:C:N3	1:CA:97:G:N2	2.14	0.96
24:CX:49:G:N2	24:CX:65:C:N3	2.13	0.95
26:BA:2118:U:H3	26:BA:2215:G:H1	1.00	0.94
26:DA:2141:G:O6	26:DA:2150:U:O2	1.86	0.94
1:CA:999:C:N3	1:CA:1042:G:N2	2.16	0.94
24:AX:49:G:H1	24:AX:65:C:H42	1.16	0.93
1:CA:1262:C:H42	1:CA:1273:G:H1	1.13	0.93
1:CA:989:C:N3	1:CA:1216:G:N1	2.15	0.93
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.48	0.93
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.00	0.93
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.02	0.93
1:CA:70:G:H1	1:CA:99:U:H3	1.17	0.93
1:AA:1502:A:H2	1:AA:1505:G:H1	1.16	0.93
23:CW:76:PPU:H5''	23:CW:76:PPU:H8	1.49	0.92
26:BA:2125:C:H42	26:BA:2208:G:H1	1.11	0.92
26:DA:2141:G:C6	26:DA:2150:U:O2	2.23	0.92
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.03	0.91
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.35	0.91
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.51	0.91
22:CV:17:U:H3	24:CX:35:A:H61	1.08	0.91
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.53	0.91
26:BA:1221:G:H1'	26:BA:1222:A:H5'	1.53	0.91
1:CA:1133:G:H1	1:CA:1141:C:N4	1.69	0.91
22:CV:17:U:H3	24:CX:35:A:N6	1.70	0.90
24:AX:28:C:H42	24:AX:42:G:H1	1.19	0.90
26:DA:2139:C:N4	26:DA:2152:G:N1	2.17	0.90
1:CA:1002:G:N2	1:CA:1038:C:N3	2.18	0.89
1:CA:1027:C:C2	1:CA:1034:G:N2	2.40	0.89
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.04	0.89
1:CA:999:C:N4	1:CA:1042:G:N1	2.21	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.53	0.88
26:BA:2158:C:H42	26:BA:2177:G:H1	1.12	0.88
22:CV:18:G:H1	24:CX:34:C:H42	0.93	0.88
26:DA:2121:G:N1	26:DA:2177:C:N4	2.16	0.88
24:AX:5:G:H1	24:AX:68:C:H42	1.20	0.88
1:AA:1089:G:H1	1:AA:1096:C:H42	0.91	0.88
23:AW:76:PPU:H5''	23:AW:76:PPU:H8	1.53	0.88
26:BA:2162:C:C2	26:BA:2173:G:N2	2.41	0.88
1:CA:1244:C:N3	1:CA:1293:G:N2	2.22	0.87
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.54	0.87
24:CX:43:A:H2'	24:CX:44:A:H8	1.39	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1169:G:H1	26:DA:1180:C:H42	1.14	0.87
26:DA:1689:A:H62	26:DA:1698:A:H2	1.23	0.87
26:BA:2146:G:H1	26:BA:2196:C:H42	1.22	0.87
24:CX:30:G:H1	24:CX:40:C:N4	1.71	0.87
26:BA:1039:G:OP1	41:BU:50:ARG:NH2	2.06	0.86
27:DB:32:C:H1'	27:DB:51:G:H22	1.39	0.86
24:CX:49:G:H1	24:CX:65:C:N4	1.72	0.86
26:DA:2121:G:N2	26:DA:2177:C:N3	2.23	0.86
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.11	0.85
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.56	0.85
1:AA:677:U:H3	1:AA:713:G:H22	1.24	0.85
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.58	0.85
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.40	0.85
1:AA:78:G:N2	1:AA:91:C:N3	2.25	0.85
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.09	0.85
26:BA:2015:U:OP2	61:BA:4878:HOH:O	1.93	0.85
26:BA:2457:G:OP1	30:BF:74:ARG:NH2	2.10	0.85
1:AA:1158:C:H5	1:AA:1181:G:H1	1.19	0.85
1:AA:1164:G:O6	1:AA:1173:G:C4	2.30	0.85
1:CA:985:C:H42	1:CA:1220:G:H1	0.87	0.85
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.09	0.85
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.59	0.85
26:DA:2127:G:O6	26:DA:2161:C:N3	2.10	0.84
26:DA:1604:C:OP1	61:DA:3949:HOH:O	1.95	0.84
51:D4:51:ASP:HA	51:D4:53:GLU:HG2	1.57	0.84
26:BA:2179:G:N3	26:BA:2180:A:N6	2.24	0.84
1:CA:1047:G:HO2'	1:CA:1215:G:HO2'	1.14	0.84
26:DA:2793:G:O6	26:DA:2803:C:N4	2.10	0.84
26:BA:2122:G:H1	26:BA:2211:U:H3	1.25	0.84
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.58	0.84
26:DA:1772:G:OP1	61:DA:4123:HOH:O	1.95	0.84
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.58	0.83
1:CA:76:C:N3	1:CA:93:G:N2	2.27	0.83
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.60	0.83
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.10	0.83
1:CA:76:C:C4	1:CA:93:G:C2	2.66	0.83
24:CX:76:31H:OP1	26:DA:2439:A:N6	2.12	0.83
26:DA:731:C:OP1	61:DA:4214:HOH:O	1.94	0.83
26:BA:2142:G:H1	26:BA:2200:C:H42	1.22	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.25	0.82
26:BA:2859:U:O4	40:BT:23:ARG:NH2	2.13	0.82
1:CA:1162:C:H42	1:CA:1174:G:H1	0.85	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1114:C:H42	1:CA:1186:G:H1	0.85	0.82
1:CA:692:U:O2'	1:CA:694:A:N7	2.12	0.82
46:BZ:151:HIS:O	46:BZ:153:SER:N	2.13	0.82
1:CA:985:C:N3	1:CA:1220:G:N2	2.26	0.82
26:DA:1918:A:O2'	26:DA:1920:C:N4	2.11	0.82
26:DA:652(E):G:N2	26:DA:652(T):C:O2	2.12	0.82
26:DA:2137:C:N3	26:DA:2154:G:N2	2.25	0.82
1:AA:982:U:H5''	14:AN:6:LEU:HD21	1.62	0.82
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.44	0.82
26:DA:2114:A:N1	26:DA:2117:A:N6	2.28	0.82
26:BA:2160:C:N4	26:BA:2175:G:H1	1.76	0.82
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.82
26:DA:2104:G:H1	26:DA:2185:C:H42	0.83	0.82
1:AA:78:G:N1	1:AA:91:C:N4	2.28	0.81
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.13	0.81
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.14	0.81
1:CA:1355:G:H1	1:CA:1367:C:N4	1.76	0.81
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.12	0.81
1:AA:624:C:H2'	1:AA:625:G:H8	1.45	0.81
26:BA:2158:C:N4	26:BA:2177:G:H1	1.79	0.81
26:DA:1039:G:O6	26:DA:1116:C:N4	2.13	0.81
29:BE:121:ASN:ND2	61:BE:3108:HOH:O	2.14	0.81
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.44	0.81
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.45	0.81
1:AA:997:U:H3	1:AA:1044:A:H61	1.28	0.81
13:AM:6:GLY:O	31:BG:115:ARG:NH2	2.14	0.81
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.13	0.81
26:DA:879:G:H3'	26:DA:880:G:H8	1.46	0.81
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.13	0.81
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.14	0.80
26:BA:2125:C:N4	26:BA:2208:G:H1	1.79	0.80
1:CA:1245:A:N6	1:CA:1292:U:H3	1.79	0.80
26:BA:479:C:OP1	61:BA:4156:HOH:O	1.98	0.80
26:BA:2297:C:OP2	53:B6:6:ARG:NH1	2.13	0.80
24:CX:43:A:H2'	24:CX:44:A:C8	2.15	0.80
1:CA:1507:A:N6	1:CA:1528:U:O4	2.13	0.80
27:DB:8:U:H3	27:DB:113:G:H1	1.29	0.80
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.14	0.80
26:BA:2832:G:OP2	61:BA:4874:HOH:O	1.97	0.80
26:BA:325:G:OP2	45:BY:84:ARG:NH2	2.15	0.80
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.13	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2137:C:H42	26:DA:2154:G:H1	0.84	0.80
26:DA:2104:G:N2	26:DA:2185:C:N3	2.27	0.80
1:CA:1502:A:H2	1:CA:1505:G:H1	1.28	0.79
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.64	0.79
26:BA:1384:G:N7	44:BX:62:LYS:NZ	2.29	0.79
26:DA:1533:G:N2	26:DA:1536:C:O2	2.16	0.79
27:DB:20:C:N4	27:DB:63:G:O6	2.14	0.79
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.15	0.79
1:AA:624:C:H2'	1:AA:625:G:C8	2.18	0.79
1:CA:316:G:OP2	1:CA:351:G:O2'	2.01	0.79
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.65	0.79
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.15	0.79
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.16	0.79
27:DB:86:G:O6	27:DB:91:C:N4	2.13	0.79
26:BA:327:U:O4	61:BA:4502:HOH:O	2.01	0.79
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.65	0.79
26:BA:2802:C:O2	26:BA:2903:G:N1	2.14	0.79
26:BA:2162:C:C4	26:BA:2173:G:N1	2.51	0.78
1:CA:1400:C:H42	24:CX:34:C:H2'	1.48	0.78
26:DA:182:A:N3	26:DA:433:C:O2'	2.17	0.78
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.63	0.78
1:AA:1164:G:O6	1:AA:1173:G:C5	2.35	0.78
26:BA:656:A:OP1	36:BP:65:ARG:NH1	2.17	0.78
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.16	0.78
26:DA:847:U:O4	26:DA:933:A:N6	2.17	0.78
26:BA:1577:C:O2'	26:BA:1578:C:O5'	2.00	0.78
26:BA:2164:C:N3	26:BA:2171:G:O6	2.16	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.17	0.78
26:DA:120:U:OP2	61:DA:3738:HOH:O	2.00	0.78
26:DA:1532:C:N4	26:DA:1537:G:O6	2.14	0.78
1:CA:1007:C:N3	1:CA:1022:G:O6	2.17	0.78
1:AA:1252:A:H61	1:AA:1285:A:H61	1.28	0.78
26:BA:1480:A:H61	26:BA:1605:A:H62	1.32	0.78
1:CA:1262:C:N4	1:CA:1273:G:H1	1.81	0.78
1:AA:765:G:H1	1:AA:812:C:HO2'	1.30	0.78
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.02	0.77
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.77
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.65	0.77
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.18	0.77
26:BA:2759:U:OP2	61:BA:3988:HOH:O	2.00	0.77
26:BA:2776:G:OP2	61:BA:4535:HOH:O	2.02	0.77
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.49	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:446:G:H1	1:CA:488:C:H42	1.33	0.77
22:CV:18:G:N1	24:CX:34:C:N4	2.29	0.77
1:CA:838:G:O6	1:CA:848:C:N4	2.18	0.77
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.67	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.17	0.77
1:CA:373:A:H61	1:CA:391:G:H1'	1.48	0.77
13:CM:6:GLY:O	31:DG:115:ARG:NH2	2.18	0.77
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.67	0.77
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.18	0.77
26:DA:2116:G:N7	26:DA:2166:G:N2	2.32	0.77
1:CA:401:C:O2'	1:CA:621:A:N3	2.16	0.77
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.66	0.77
26:BA:1848:G:OP1	28:BD:88:ARG:NH2	2.18	0.77
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.18	0.77
1:CA:1029:C:N4	1:CA:1032:G:N1	2.32	0.77
1:CA:1114:C:N3	1:CA:1186:G:N2	2.31	0.77
1:CA:954:G:H21	1:CA:1227:A:H62	1.32	0.77
15:CO:17:ARG:HD3	15:CO:26:GLU:HG3	1.66	0.77
24:CX:6:G:H1	24:CX:67:C:H42	1.30	0.77
26:BA:2320:G:O6	26:BA:2323:A:N6	2.15	0.76
1:CA:1183:A:O2'	1:CA:1185:G:OP2	2.01	0.76
1:CA:1256:A:N6	1:CA:1278:U:H1'	1.98	0.76
27:DB:5:C:OP1	27:DB:61:G:O2'	2.01	0.76
26:BA:1736:A:H62	26:BA:1745:A:H2	1.30	0.76
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.68	0.76
26:DA:2141:G:O6	26:DA:2150:U:C2	2.37	0.76
28:DD:238:GLY:O	61:DD:405:HOH:O	2.03	0.76
1:AA:1089:G:N2	1:AA:1096:C:N3	2.32	0.76
24:CX:3:C:H2'	24:CX:4:G:H5''	1.67	0.76
28:DD:69:ARG:NH2	28:DD:128:GLY:O	2.18	0.76
1:AA:184:G:H2'	1:AA:185:A:H8	1.51	0.76
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.19	0.76
1:CA:1378:C:O2	7:CG:76:ARG:NH2	2.17	0.76
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.50	0.76
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.31	0.76
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.66	0.76
26:DA:1470:G:N2	26:DA:1520:G:OP2	2.17	0.76
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.50	0.76
1:AA:766:A:N6	1:AA:813:U:O2	2.18	0.76
1:CA:1356:G:H1	1:CA:1366:C:H42	1.33	0.76
16:CP:28:ARG:NH1	16:CP:29:ASP:OD2	2.19	0.76
26:DA:1143:A:OP1	34:DN:25:ARG:NH2	2.19	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.50	0.76
26:DA:586:A:N1	26:DA:809:G:O2'	2.19	0.76
1:CA:1422:G:H5''	35:DO:48:PRO:HB3	1.66	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.19	0.76
26:DA:2162:G:H4'	26:DA:2172:U:H2'	1.66	0.76
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.67	0.76
26:BA:694:G:N2	26:BA:696:C:O2	2.19	0.76
26:BA:2164:C:O2	26:BA:2171:G:N1	2.18	0.75
1:CA:457:C:N4	1:CA:474:G:O6	2.19	0.75
27:DB:32:C:H1'	27:DB:51:G:N2	2.00	0.75
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.19	0.75
1:CA:1359:C:O2'	1:CA:1361:G:N7	2.20	0.75
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.68	0.75
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.75
26:BA:1199:C:OP2	61:BA:4487:HOH:O	2.04	0.75
26:BA:2162:C:O2'	26:BA:2174:G:N2	2.19	0.75
1:AA:1422:G:H5''	35:BO:48:PRO:HB3	1.68	0.75
31:DG:80:PHE:O	31:DG:82:LEU:N	2.20	0.75
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.19	0.75
26:BA:1648:U:O4	61:BA:4096:HOH:O	2.04	0.75
26:BA:2398:C:O2'	61:BA:4897:HOH:O	2.03	0.75
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.68	0.75
26:BA:2299:A:H62	26:BA:2356:U:H3	1.34	0.75
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.21	0.75
29:DE:28:ALA:HB3	29:DE:93:VAL:HG12	1.66	0.75
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.67	0.75
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.20	0.75
1:CA:1026:G:O6	1:CA:1036:G:N2	2.19	0.75
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.68	0.75
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.03	0.75
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.17	0.75
26:DA:712:G:N2	26:DA:719:C:O2	2.17	0.75
26:BA:2308:U:OP2	39:BS:9:ARG:NH2	2.20	0.75
15:CO:64:ARG:NH2	26:DA:715:G:OP1	2.20	0.75
51:D4:38:LYS:O	51:D4:40:HIS:N	2.19	0.75
1:AA:1006:C:H42	1:AA:1023:G:H1	1.32	0.75
1:AA:1303:C:OP1	61:AA:4108:HOH:O	2.04	0.75
1:CA:627:G:H2'	1:CA:628:G:H8	1.52	0.75
26:BA:303:C:H42	26:BA:385:G:H1	1.35	0.74
26:DA:2430:A:OP2	61:DA:4174:HOH:O	2.04	0.74
27:DB:36:C:N4	27:DB:49:C:O2	2.19	0.74
26:BA:1067:A:H62	26:BA:1186:U:H3	1.34	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.19	0.74
26:BA:64:C:O2	26:BA:482:C:N4	2.19	0.74
49:D2:18:PRO:HB3	49:D2:68:ARG:HH12	1.52	0.74
26:DA:2793:G:H22	26:DA:2804:C:H1'	1.51	0.74
1:AA:1243:C:H42	1:AA:1294:G:H1	1.33	0.74
1:AA:78:G:N2	1:AA:92:C:N3	2.35	0.74
26:BA:2142:G:H1	26:BA:2200:C:N4	1.84	0.74
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.70	0.74
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.67	0.74
26:DA:678:C:N4	26:DA:799:G:O6	2.11	0.74
1:AA:448:A:O5'	1:AA:485:G:N2	2.20	0.74
26:BA:934:A:O2'	26:BA:935:C:OP2	2.04	0.74
26:BA:591:U:H5'	26:BA:990:A:N1	2.01	0.74
26:BA:9:U:H3	26:BA:2641:A:H2	1.33	0.74
26:BA:1829:U:H5'	28:BD:259:THR:HG22	1.70	0.74
1:CA:44:G:H1	1:CA:398:C:H42	1.35	0.74
26:DA:1204:A:H2	26:DA:1241:A:H62	1.33	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	1.34	0.74
26:DA:2126:A:H61	26:DA:2162:G:HO2'	1.32	0.74
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
26:BA:1417:G:N7	61:BA:4204:HOH:O	2.21	0.74
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.69	0.74
26:DA:792:G:O6	61:DA:4068:HOH:O	2.03	0.74
29:BE:28:ALA:HB3	29:BE:93:VAL:HG12	1.69	0.74
1:CA:1366:C:HO2'	10:CJ:60:ARG:HH22	1.35	0.74
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.69	0.74
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.68	0.73
24:AX:49:G:H1	24:AX:65:C:N4	1.86	0.73
26:BA:2695:C:O2	35:BO:70:LYS:NZ	2.21	0.73
26:BA:836:A:OP1	61:BA:4147:HOH:O	2.05	0.73
1:CA:532:A:O2'	1:CA:533:A:OP1	2.05	0.73
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.69	0.73
26:DA:1335:U:O4	61:DA:3860:HOH:O	2.04	0.73
26:DA:272(G):C:H42	26:DA:363(C):G:H1	1.36	0.73
26:DA:1997:G:OP2	61:DA:4145:HOH:O	2.04	0.73
26:DA:2126:A:N6	26:DA:2162:G:HO2'	1.86	0.73
1:AA:279:A:H4'	1:AA:280:C:H5''	1.69	0.73
3:CC:120:VAL:HA	3:CC:123:GLN:HE21	1.53	0.73
9:CI:17:VAL:HG11	9:CI:81:ILE:HA	1.71	0.73
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.11	0.73
1:CA:1133:G:N2	1:CA:1141:C:N3	2.36	0.73
1:CA:1103:C:H5''	2:CB:98:LEU:HD12	1.70	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.23	0.73
26:BA:542:C:OP1	52:B5:16:ARG:NH2	2.20	0.73
1:CA:1126:U:H1'	1:CA:1281:U:C2	2.23	0.73
1:CA:1244:C:H42	1:CA:1293:G:H1	0.80	0.73
33:DI:48:GLU:O	33:DI:52:ARG:NH1	2.21	0.73
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.71	0.73
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.69	0.73
26:BA:449:A:OP2	61:BA:3938:HOH:O	2.05	0.73
25:CY:76:A:O2'	26:DA:2394:C:N3	2.22	0.73
26:DA:1171:G:H22	26:DA:1178:C:H42	1.35	0.73
1:CA:1027:C:C4	1:CA:1034:G:N1	2.56	0.73
26:DA:2576:G:O2'	26:DA:2579:C:OP2	2.07	0.73
1:AA:596:C:OP2	61:AA:4068:HOH:O	2.06	0.73
26:DA:2794:C:N4	26:DA:2802:G:O6	2.17	0.73
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.22	0.73
19:AS:65:ASN:O	51:B4:58:ARG:NH1	2.21	0.73
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.21	0.73
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.69	0.73
1:CA:1053:G:N7	1:CA:1200:C:H5''	2.04	0.72
1:CA:73:G:H1	1:CA:96:U:H3	1.37	0.72
4:CD:31:CYS:HB2	58:CD:501:SF4:S3	2.29	0.72
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.21	0.72
46:BZ:69:THR:HG22	46:BZ:90:VAL:HA	1.71	0.72
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.62	0.72
26:DA:1970:A:OP1	61:DA:3907:HOH:O	2.07	0.72
26:BA:1065:U:HO2'	26:BA:1067:A:H2	1.35	0.72
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.55	0.72
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	1.71	0.72
37:DQ:22:LYS:O	46:DZ:78:LYS:NZ	2.21	0.72
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.07	0.72
1:CA:72:C:N4	1:CA:97:G:H1	1.85	0.72
1:CA:76:C:N3	1:CA:93:G:C2	2.57	0.72
26:BA:790:G:N7	61:BA:4318:HOH:O	2.22	0.72
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.71	0.72
43:BW:34:ASN:OD1	43:BW:37:ARG:NH1	2.23	0.72
12:CL:70:ILE:HG12	12:CL:100:ILE:HD12	1.72	0.72
26:DA:1851:U:O4	61:DA:4296:HOH:O	2.06	0.72
46:BZ:107:THR:HG21	46:BZ:112:ARG:HH21	1.55	0.72
1:CA:662:G:O2'	1:CA:836:G:OP1	2.07	0.72
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.70	0.72
1:CA:839:U:H5''	1:CA:840:C:H5	1.55	0.72
1:CA:839:U:OP2	1:CA:840:C:N4	2.23	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:45:U:H2'	1:AA:46:G:C8	2.25	0.72
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	1.72	0.72
16:CP:59:TRP:HA	16:CP:62:VAL:HG12	1.70	0.72
26:DA:1359:A:C6	26:DA:1372:U:C4	2.77	0.72
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.71	0.72
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.69	0.72
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.23	0.72
27:DB:29:A:C2	27:DB:30:C:H5	2.06	0.72
1:CA:1414:U:H3	1:CA:1486:G:H1	1.37	0.72
1:CA:72:C:N4	1:CA:97:G:C6	2.57	0.72
1:CA:989:C:O2	1:CA:1216:G:N2	2.19	0.72
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.70	0.72
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.72	0.71
24:CX:19:G:N2	24:CX:56:C:N3	2.37	0.71
1:AA:1305:G:H5''	21:AU:4:GLY:HA3	1.70	0.71
27:BB:8:U:O3'	39:BS:25:ARG:NH2	2.20	0.71
26:BA:2348:A:H61	47:B0:43:THR:HG22	1.55	0.71
1:AA:978:A:O2'	1:AA:1322:C:N3	2.22	0.71
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.24	0.71
36:BP:42:SER:O	61:BP:3102:HOH:O	2.06	0.71
26:DA:2127:G:N1	26:DA:2161:C:O2	2.22	0.71
27:DB:3:C:H2'	27:DB:4:C:C6	2.25	0.71
1:AA:708:C:OP1	11:AK:85:ARG:NH2	2.23	0.71
26:DA:2287:A:H62	26:DA:2344:U:H3	1.39	0.71
26:DA:2526:G:O2'	56:D9:1:MET:N	2.20	0.71
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.71	0.71
31:DG:47:LYS:HE2	31:DG:48:GLU:H	1.56	0.71
1:AA:664:G:H22	1:AA:741:G:H1	1.38	0.71
51:B4:64:GLY:O	51:B4:66:SER:N	2.23	0.71
26:BA:1219:A:H1'	26:BA:1220:U:H5''	1.73	0.71
26:BA:2825:C:H5'	52:B5:29:THR:HG21	1.71	0.71
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.55	0.71
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.24	0.71
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.72	0.71
26:DA:1637:A:OP2	61:DA:4392:HOH:O	2.07	0.71
39:BS:15:ARG:O	39:BS:19:LYS:HG2	1.91	0.71
1:CA:156:G:N2	1:CA:165:C:O2	2.19	0.71
24:CX:19:G:H1	24:CX:56:C:H42	1.39	0.71
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.23	0.71
26:BA:234:G:O6	55:B8:8:LYS:NZ	2.22	0.70
1:CA:1027:C:N3	1:CA:1034:G:C2	2.59	0.70
1:CA:1399:C:H4'	1:CA:1400:C:H5''	1.73	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:708:C:H2'	1:CA:709:G:H8	1.55	0.70
9:CI:42:ARG:NH1	9:CI:75:ASP:OD1	2.24	0.70
1:AA:1304:G:OP2	61:AA:4108:HOH:O	2.09	0.70
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.23	0.70
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.57	0.70
1:AA:221:C:H2'	1:AA:222:U:H6	1.57	0.70
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.72	0.70
26:BA:2146:G:H1	26:BA:2196:C:N4	1.88	0.70
1:CA:138:G:H2'	1:CA:139:G:H5''	1.74	0.70
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.73	0.70
1:AA:159:G:O2'	1:AA:161:A:N7	2.24	0.70
1:AA:560:U:O2'	1:AA:561:U:OP2	2.10	0.70
4:AD:13:ARG:NH1	4:AD:38:TYR:O	2.24	0.70
1:CA:76:C:C2	1:CA:93:G:N2	2.60	0.70
50:D3:7:LYS:HG3	50:D3:34:GLU:HG3	1.73	0.70
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.24	0.70
1:AA:242:C:N4	1:AA:284:G:O6	2.20	0.70
1:AA:316:G:OP2	1:AA:351:G:O2'	2.09	0.70
26:BA:176:G:OP2	61:BA:4313:HOH:O	2.08	0.70
1:AA:60:A:N1	1:AA:107:G:O2'	2.21	0.70
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.56	0.70
26:BA:1598:C:OP2	61:BA:4322:HOH:O	2.08	0.70
26:BA:2630:G:H21	29:BE:150:VAL:HG21	1.56	0.70
26:DA:1417:C:OP2	61:DA:4033:HOH:O	2.08	0.70
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.24	0.70
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.22	0.70
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.23	0.70
8:AH:21:LYS:O	8:AH:65:TYR:OH	2.08	0.70
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.72	0.70
1:AA:363:A:OP2	12:AL:34:ARG:NH1	2.24	0.70
7:CG:99:LEU:HD23	7:CG:102:ARG:HH12	1.56	0.70
7:CG:109:ASN:HA	7:CG:119:ARG:HH21	1.55	0.70
1:AA:661:G:H1	1:AA:744:C:H42	1.39	0.70
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.40	0.70
26:BA:2129:C:H42	26:BA:2204:G:H1	1.40	0.70
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.36	0.70
26:DA:1183:G:O3'	50:D3:29:ARG:NH1	2.24	0.70
26:DA:2107:C:H42	26:DA:2182:G:H1	1.40	0.70
26:DA:827:U:OP1	61:DA:4174:HOH:O	2.10	0.70
1:AA:1012:U:O2	1:AA:1017:G:O6	2.10	0.70
1:CA:1034:G:H8	1:CA:1034:G:O5'	1.73	0.70
1:CA:977:A:O2'	1:CA:981:U:N3	2.25	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1269:A:N7	61:DA:4369:HOH:O	2.25	0.70
26:DA:1300:U:H4'	26:DA:1301:A:H5''	1.74	0.70
31:DG:41:GLN:HG3	31:DG:60:LEU:HD21	1.74	0.70
1:AA:1097:C:O2'	1:AA:1169:A:N3	2.20	0.70
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.74	0.70
24:AX:5:G:H1	24:AX:68:C:N4	1.89	0.69
26:BA:1817:A:H1'	26:BA:1960:A:N6	2.07	0.69
33:BI:38:LEU:HD13	33:BI:40:THR:HG22	1.72	0.69
38:BR:15:SER:OG	61:BR:301:HOH:O	2.08	0.69
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.73	0.69
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.25	0.69
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.27	0.69
1:CA:1120:G:O6	1:CA:1154:G:N2	2.25	0.69
26:DA:1314:C:OP1	61:DA:4077:HOH:O	2.10	0.69
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.92	0.69
26:BA:261:A:N7	26:BA:283:G:N2	2.40	0.69
26:BA:355:A:N1	61:BA:4015:HOH:O	2.25	0.69
27:DB:3:C:H2'	27:DB:4:C:H6	1.55	0.69
1:AA:78:G:C2	1:AA:91:C:N3	2.60	0.69
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.24	0.69
26:BA:2769:U:O2'	61:BA:4010:HOH:O	2.10	0.69
26:DA:1333:C:OP2	61:DA:3859:HOH:O	2.10	0.69
26:DA:2198:A:O2'	26:DA:2224:G:N2	2.26	0.69
33:DI:129:THR:HG22	33:DI:139:GLN:HE22	1.57	0.69
1:AA:148:G:O6	1:AA:174:C:N4	2.25	0.69
26:BA:427:G:N7	61:BA:4780:HOH:O	2.24	0.69
1:AA:1009:G:H1	1:AA:1020:U:H3	0.76	0.69
1:AA:1086:U:H3	1:AA:1099:G:H22	1.39	0.69
26:BA:2209:G:O2'	26:BA:2210:C:OP1	2.10	0.69
26:DA:574:C:N3	29:DE:145:LYS:NZ	2.40	0.69
19:AS:12:ASP:OD2	19:AS:37:ARG:NH1	2.24	0.69
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.73	0.69
26:DA:2227:A:OP2	61:DA:4135:HOH:O	2.10	0.69
31:DG:43:LEU:HD21	31:DG:153:ARG:HG2	1.74	0.69
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.26	0.69
1:CA:701:C:OP1	1:CA:702:A:O2'	2.10	0.69
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.25	0.69
1:AA:148:G:N2	1:AA:175:C:C2	2.61	0.69
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	1.75	0.69
48:D1:50:ARG:HG2	48:D1:59:THR:HB	1.72	0.69
24:AX:28:C:N4	24:AX:42:G:H1	1.88	0.69
49:B2:28:LYS:NZ	49:B2:56:GLN:OE1	2.26	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2178:G:N2	26:BA:2180:A:H62	1.90	0.69
1:CA:870:U:OP2	61:CA:4089:HOH:O	2.10	0.69
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.73	0.69
26:BA:572:A:O2'	26:BA:573:G:OP1	2.11	0.69
26:BA:880:U:O2	36:BP:55:ARG:NH2	2.26	0.69
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.28	0.69
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.75	0.69
1:AA:1311:G:H1	1:AA:1326:C:H42	1.42	0.68
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.57	0.68
1:CA:1400:C:O4'	22:CV:18:G:N3	2.27	0.68
47:D0:14:ARG:NH1	61:D0:102:HOH:O	2.26	0.68
30:DF:110:LEU:HD21	30:DF:181:LEU:HG	1.75	0.68
26:DA:2313:C:H2'	26:DA:2314:C:H6	1.58	0.68
1:AA:78:G:H1	1:AA:91:C:N4	1.91	0.68
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.26	0.68
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.73	0.68
26:BA:2418:U:OP1	61:BA:4116:HOH:O	2.11	0.68
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.76	0.68
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.27	0.68
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.27	0.68
1:CA:72:C:C4	1:CA:97:G:N1	2.56	0.68
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.75	0.68
26:DA:1406:U:O4	26:DA:1596:A:N6	2.18	0.68
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.41	0.68
31:DG:114:ILE:HG23	31:DG:136:ARG:HH22	1.58	0.68
1:AA:789:U:O2'	1:AA:791:G:N7	2.21	0.68
1:AA:253:U:OP1	17:AQ:67:LYS:NZ	2.26	0.68
19:AS:9:VAL:HG21	51:B4:61:ARG:HH21	1.58	0.68
26:BA:1417:G:H2'	26:BA:1418:U:H5	1.59	0.68
26:BA:2412:G:O6	61:BA:4049:HOH:O	2.09	0.68
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	1.76	0.68
1:CA:376:G:H1	1:CA:387:U:H3	1.41	0.68
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.10	0.68
2:AB:19:HIS:NE2	2:AB:206:ASP:OD2	2.26	0.68
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.75	0.68
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.68
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.27	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.57	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.59	0.68
26:BA:2133:C:OP2	26:BA:2167:C:N4	2.26	0.68
26:BA:278:G:H2'	26:BA:279:G:H5''	1.74	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:397:G:OP2	61:BA:3938:HOH:O	2.12	0.68
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.04	0.68
1:CA:154:C:C2'	1:CA:155:C:H5'	2.23	0.68
16:CP:53:VAL:HG13	16:CP:79:VAL:HG22	1.76	0.68
17:CQ:60:ILE:HD12	17:CQ:74:LEU:HG	1.76	0.68
28:DD:232:PRO:O	61:DD:402:HOH:O	2.12	0.68
1:AA:159:G:N2	1:AA:162:A:OP2	2.26	0.68
26:BA:2804:C:N3	26:BA:2816:G:N2	2.36	0.68
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.27	0.68
4:CD:172:PRO:HB2	4:CD:187:ARG:HH21	1.58	0.68
12:CL:71:PRO:O	12:CL:102:ARG:NH1	2.23	0.68
26:DA:1169:G:N2	26:DA:1180:C:N3	2.40	0.68
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.27	0.68
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.28	0.68
1:AA:993:G:O6	1:AA:1045:C:N4	2.23	0.67
26:BA:1249:A:H2	26:BA:1287:A:H62	1.40	0.67
26:BA:2820:A:N6	26:BA:2900:G:O2'	2.26	0.67
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.77	0.67
1:CA:1400:C:OP2	22:CV:18:G:N1	2.26	0.67
28:DD:228:PRO:O	61:DD:401:HOH:O	2.12	0.67
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.27	0.67
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.75	0.67
1:CA:72:C:N4	1:CA:73:G:C6	2.62	0.67
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.29	0.67
26:DA:1695:G:N7	28:DD:14:ARG:NH2	2.43	0.67
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.59	0.67
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.59	0.67
26:BA:354:A:H2	26:BA:1255:A:HO2'	1.40	0.67
26:BA:2142:G:N2	26:BA:2200:C:N3	2.41	0.67
26:BA:848:G:O6	30:BF:53:THR:OG1	2.12	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:HG22	1.76	0.67
1:CA:1055:A:N7	1:CA:1200:C:N4	2.42	0.67
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.27	0.67
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.76	0.67
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.30	0.67
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.28	0.67
26:BA:2251:G:OP2	28:BD:244:ARG:NH1	2.22	0.67
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.27	0.67
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.09	0.67
1:AA:184:G:H2'	1:AA:185:A:C8	2.28	0.67
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.42	0.67
26:BA:1379:C:OP2	61:BA:4097:HOH:O	2.13	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2659:G:N2	26:DA:2662:A:OP2	2.27	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.27	0.67
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.59	0.67
1:AA:661:G:N2	1:AA:744:C:N3	2.40	0.67
1:AA:975:A:H8	1:AA:975:A:H5'	1.60	0.67
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.28	0.67
26:BA:2163:G:C2	26:BA:2164:C:H1'	2.30	0.67
26:BA:787:U:OP2	61:BA:4541:HOH:O	2.12	0.67
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.26	0.67
27:DB:49:C:OP1	39:DS:97:ARG:N	2.27	0.67
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.28	0.67
20:AT:56:MET:HG3	20:AT:84:LEU:HD22	1.76	0.67
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.77	0.67
26:DA:2136:C:O2'	26:DA:2137:C:O4'	2.11	0.67
36:BP:62:LEU:O	55:B8:13:ARG:HD3	1.95	0.67
26:BA:2346:G:O6	47:B0:74:ARG:NH2	2.28	0.67
26:BA:1296:G:OP2	36:BP:21:ARG:NH1	2.27	0.67
32:DH:124:GLU:HB2	32:DH:132:ARG:HB3	1.77	0.67
26:BA:1007:G:OP1	61:BA:4651:HOH:O	2.13	0.67
26:DA:2651:C:H42	26:DA:2669:G:H1	1.43	0.67
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.67
1:AA:103:C:O2'	1:AA:172:A:N1	2.27	0.67
1:AA:692:U:O2'	1:AA:694:A:N7	2.24	0.67
26:BA:2735:G:OP2	61:BA:3994:HOH:O	2.12	0.67
1:CA:601:C:H2'	1:CA:602:A:C8	2.30	0.67
26:DA:82:G:N1	26:DA:103:A:OP2	2.23	0.67
26:DA:1038:C:H42	26:DA:1117:G:H1	1.43	0.67
1:AA:598:U:O4	61:AA:4068:HOH:O	2.09	0.66
1:AA:652:U:O4	1:AA:752:G:O2'	2.10	0.66
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.23	0.66
1:AA:757:U:O2'	1:AA:879:C:O2	2.13	0.66
1:AA:975:A:H4'	1:AA:976:G:H5''	1.77	0.66
26:BA:154:G:O6	26:BA:161:C:N4	2.18	0.66
26:BA:2198:A:H2'	26:BA:2199:C:C6	2.30	0.66
25:AY:76:A:N6	26:BA:2434:A:O4'	2.28	0.66
1:CA:1153:C:H42	1:CA:1154:G:H21	1.41	0.66
1:CA:642:A:N3	8:CH:113:SER:OG	2.28	0.66
1:CA:1255:G:OP2	10:CJ:45:ARG:NH2	2.27	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.28	0.66
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.28	0.66
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.78	0.66
26:BA:232:U:OP1	55:B8:6:THR:OG1	2.11	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:21:G:OP1	61:CA:4042:HOH:O	2.13	0.66
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
1:CA:864:A:H5'	5:CE:86:ALA:HB2	1.77	0.66
13:CM:90:LEU:HA	13:CM:93:ARG:HD2	1.77	0.66
1:AA:56:U:H2'	1:AA:57:G:C8	2.29	0.66
1:AA:6:G:H4'	1:AA:298:A:H4'	1.77	0.66
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.77	0.66
2:CB:71:VAL:HG12	2:CB:170:GLU:HG2	1.78	0.66
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.27	0.66
26:DA:2504:U:OP2	61:DA:4075:HOH:O	2.12	0.66
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.77	0.66
26:BA:2792:U:OP1	61:BA:4671:HOH:O	2.13	0.66
26:BA:847:A:OP1	26:BA:847:A:H8	1.78	0.66
26:DA:2494:G:OP2	61:DA:4386:HOH:O	2.13	0.66
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.77	0.66
3:AC:16:ARG:NH2	3:AC:183:ASP:OD1	2.29	0.66
26:BA:2147:G:N1	26:BA:2194:U:OP1	2.29	0.66
29:BE:123:ALA:O	61:BE:3101:HOH:O	2.13	0.66
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.28	0.66
1:AA:574:A:OP2	61:AA:4006:HOH:O	2.12	0.66
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.76	0.66
1:CA:70:G:N2	1:CA:99:U:O2	2.21	0.66
26:DA:2123:G:H1	26:DA:2175:C:H42	1.43	0.66
26:DA:2141:G:O4'	26:DA:2151:G:N2	2.29	0.66
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.40	0.66
1:AA:1309:G:OP1	13:AM:88:ARG:NH1	2.29	0.66
29:BE:8:LYS:NZ	29:BE:190:GLY:O	2.24	0.66
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.42	0.66
31:DG:171:ALA:O	31:DG:175:LEU:N	2.23	0.66
42:DV:72:VAL:HG22	42:DV:85:LYS:HB3	1.78	0.66
19:AS:68:GLY:N	51:B4:58:ARG:HH21	1.94	0.66
26:DA:1665:A:OP2	61:DA:4367:HOH:O	2.14	0.66
26:DA:1993:U:OP2	61:DA:4451:HOH:O	2.13	0.66
26:DA:2736:G:N2	26:DA:2768:C:O2	2.15	0.66
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.08	0.66
26:BA:1008:U:OP1	61:BA:3878:HOH:O	2.13	0.66
26:BA:2177:G:H2'	26:BA:2178:G:O4'	1.95	0.66
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.60	0.66
26:DA:336:C:O2'	45:DY:35:TYR:OH	2.12	0.66
27:DB:22:U:H3	27:DB:61:G:H1	1.44	0.66
40:DT:51:ARG:HG3	40:DT:98:LYS:HD2	1.78	0.66
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.96	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1370:G:N7	61:BA:4100:HOH:O	2.29	0.66
1:CA:1154:G:N7	1:CA:1155:G:C8	2.64	0.66
1:CA:1400:C:C6	22:CV:18:G:N3	2.64	0.66
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.25	0.66
26:DA:2313:C:H2'	26:DA:2314:C:C6	2.31	0.66
26:DA:271(L):U:OP1	33:DI:50:ARG:NH2	2.28	0.66
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.29	0.65
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.77	0.65
26:BA:236:G:OP2	26:BA:238:C:N4	2.28	0.65
29:BE:79:ARG:NE	61:BE:3113:HOH:O	2.19	0.65
5:CE:78:HIS:HA	8:CH:105:ARG:HG3	1.77	0.65
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.76	0.65
27:DB:54:G:H21	31:DG:29:TRP:HZ2	1.42	0.65
32:DH:8:PRO:HB3	32:DH:51:ARG:HG2	1.78	0.65
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.78	0.65
24:CX:76:31H:OP2	61:CX:3101:HOH:O	2.14	0.65
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.29	0.65
7:AG:126:ASP:OD1	7:AG:131:LYS:NZ	2.29	0.65
13:AM:67:GLU:OE2	13:AM:71:ARG:NH2	2.28	0.65
26:BA:1388:A:OP2	61:BA:4096:HOH:O	2.13	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.77	0.65
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.65
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.78	0.65
26:DA:746:A:N7	61:DA:4449:HOH:O	2.29	0.65
1:AA:1262:C:N3	1:AA:1273:G:O6	2.29	0.65
20:AT:9:ASN:HD22	20:AT:10:LEU:N	1.93	0.65
26:BA:380:G:H2'	26:BA:381:A:H8	1.61	0.65
26:BA:932:C:H3'	26:BA:933:C:H5''	1.77	0.65
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.32	0.65
1:CA:1014:A:H1'	19:CS:34:TRP:HB2	1.79	0.65
1:CA:975:A:H8	1:CA:975:A:H5'	1.61	0.65
1:CA:753:A:OP1	15:CO:69:TYR:OH	2.12	0.65
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.43	0.65
26:BA:1229:G:H5'	50:B3:29:ARG:HH11	1.60	0.65
26:BA:2862:G:OP1	61:BA:4891:HOH:O	2.13	0.65
26:BA:302:A:O2'	26:BA:303:C:OP1	2.14	0.65
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.29	0.65
1:CA:903:G:OP1	61:CA:4008:HOH:O	2.14	0.65
26:DA:2698:U:H2'	26:DA:2699:C:C6	2.32	0.65
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.78	0.65
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.25	0.65
24:CX:31:G:C8	24:CX:32:5MC:HM52	2.32	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:CS:9:VAL:HB	51:D4:67:TYR:HD2	1.60	0.65
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.61	0.65
1:AA:580:U:OP2	61:AA:4021:HOH:O	2.14	0.65
1:AA:966:G:H21	9:AI:127:LYS:HZ1	1.45	0.65
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.14	0.65
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.62	0.65
1:CA:1012:U:O2	1:CA:1017:G:O6	2.14	0.65
4:CD:53:ASP:HB3	4:CD:57:ARG:HH12	1.62	0.65
24:CX:48:C:O2'	24:CX:59:A:H1'	1.97	0.65
29:DE:56:PRO:HG3	29:DE:74:PRO:HG2	1.77	0.65
26:BA:1232:G:H5''	42:BV:81:TYR:CE1	2.31	0.65
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.79	0.65
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.78	0.65
13:CM:65:LYS:HB3	51:D4:50:VAL:HG11	1.77	0.65
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.79	0.65
1:AA:1030:C:H3'	1:AA:1030(A):G:H4'	1.79	0.65
2:AB:69:LEU:HD13	2:AB:91:PRO:HB2	1.79	0.65
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.79	0.65
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.30	0.65
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.32	0.64
50:B3:10:LYS:NZ	50:B3:15:TYR:OH	2.28	0.64
9:CI:121:ARG:NH1	9:CI:122:ALA:O	2.31	0.64
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.79	0.64
26:BA:554:A:OP2	34:BN:114:ARG:NH2	2.29	0.64
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	1.79	0.64
1:CA:405:U:O4	4:CD:2:GLY:N	2.30	0.64
9:CI:112:LYS:NZ	9:CI:116:LYS:O	2.30	0.64
26:DA:458:G:O2'	26:DA:469:G:O6	2.13	0.64
35:DO:19:ILE:HG22	35:DO:43:VAL:HA	1.80	0.64
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.20	0.64
26:BA:1854:G:OP1	28:BD:54:ARG:NH1	2.31	0.64
1:CA:827:U:H2'	1:CA:859:A:H61	1.62	0.64
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.80	0.64
26:DA:1169:G:H1	26:DA:1180:C:N4	1.92	0.64
26:DA:2363:C:O2	47:D0:39:ARG:NH2	2.29	0.64
13:CM:93:ARG:HD3	26:DA:888:C:OP1	1.97	0.64
26:BA:1298:G:OP1	41:BU:36:ARG:NH2	2.30	0.64
23:AW:76:PPU:H103	26:BA:2596:U:H5'	1.78	0.64
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.97	0.64
26:DA:1971:A:N1	61:DA:3924:HOH:O	2.30	0.64
26:DA:2779:U:H4'	26:DA:2780:G:H5''	1.78	0.64
26:DA:514:A:N3	26:DA:581:C:O2'	2.26	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:86:G:N1	27:DB:91:C:N3	2.34	0.64
36:DP:42:SER:O	61:DP:302:HOH:O	2.15	0.64
2:AB:121:LEU:HD13	2:AB:126:GLU:HG2	1.80	0.64
26:BA:2180:A:N3	26:BA:2180:A:H2'	2.12	0.64
27:BB:102:A:N7	61:BB:4020:HOH:O	2.30	0.64
1:CA:600:C:H2'	1:CA:601:C:C6	2.33	0.64
24:CX:6:G:H1	24:CX:67:C:N4	1.94	0.64
1:AA:1392:G:N2	1:AA:1502:A:H8	1.95	0.64
1:AA:377:G:OP1	16:AP:3:LYS:HD2	1.97	0.64
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.24	0.64
26:BA:11:G:H2'	26:BA:12:U:H5''	1.78	0.64
26:BA:1846:A:OP2	28:BD:54:ARG:NH2	2.31	0.64
26:BA:1800:G:O2'	26:BA:1980:C:OP1	2.09	0.64
26:BA:2173:G:H2'	26:BA:2174:G:C8	2.32	0.64
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.32	0.64
14:AN:3:ARG:HH21	14:AN:3:ARG:HB3	1.62	0.64
26:BA:2754:A:OP1	56:B9:22:ARG:NH2	2.27	0.64
26:BA:1831:C:OP2	28:BD:183:ARG:NH2	2.31	0.64
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.79	0.64
26:BA:241:G:P	36:BP:50:ARG:HH12	2.21	0.64
1:CA:76:C:N4	1:CA:93:G:C2	2.66	0.64
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.79	0.64
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.29	0.64
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.32	0.64
26:DA:1276:A:O2'	38:DR:12:ARG:NH2	2.26	0.64
26:BA:2135:U:H3	26:BA:2192:A:H61	1.44	0.64
26:DA:362:U:H1'	26:DA:363:G:H5''	1.80	0.64
26:DA:910:A:N3	26:DA:2264:C:O2'	2.26	0.64
37:DQ:65:PHE:HB2	37:DQ:105:GLU:HB2	1.80	0.64
1:CA:1277:C:HO2'	1:CA:1279:A:H1'	1.63	0.64
1:CA:1395:C:O2	1:CA:1398:A:O2'	2.16	0.64
31:DG:20:ILE:HA	31:DG:25:TYR:HD1	1.63	0.64
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.80	0.64
1:AA:709:G:H2'	1:AA:710:G:H5'	1.80	0.63
26:BA:1296:G:N7	36:BP:18:ARG:NH2	2.46	0.63
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.63	0.63
1:CA:975:A:N6	1:CA:1367:C:O4'	2.26	0.63
1:CA:302:G:O2'	1:CA:556:C:H5''	1.98	0.63
1:CA:967:C:H3'	1:CA:968:A:H2'	1.79	0.63
8:CH:135:CYS:SG	8:CH:136:GLU:N	2.71	0.63
26:DA:1385:G:O2'	26:DA:1396:U:O2	2.15	0.63
1:AA:175:C:O5'	1:AA:175:C:H6	1.82	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:709:G:C2'	1:AA:710:G:H5'	2.27	0.63
26:BA:1723:A:N7	61:BA:4171:HOH:O	2.30	0.63
26:BA:2396:G:OP2	47:B0:55:ARG:NH1	2.26	0.63
1:CA:708:C:OP1	11:CK:85:ARG:NH2	2.27	0.63
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.81	0.63
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.31	0.63
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.63
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.79	0.63
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.32	0.63
1:AA:600:C:H2'	1:AA:601:C:H6	1.63	0.63
15:AO:5:LYS:HD2	15:AO:5:LYS:H	1.63	0.63
26:BA:70:A:H3'	26:BA:70:A:OP2	1.98	0.63
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.79	0.63
26:DA:1019:U:OP1	26:DA:1035:U:O2'	2.15	0.63
1:AA:96:U:O2'	1:AA:97:G:O4'	2.15	0.63
26:BA:1766:G:H2'	26:BA:1769:G:O6	1.99	0.63
26:BA:2203:G:O2'	26:BA:2204:G:OP1	2.16	0.63
1:CA:1011:G:H1	1:CA:1018:C:H42	1.47	0.63
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.62	0.63
26:DA:1356:G:OP1	61:DA:4383:HOH:O	2.16	0.63
46:DZ:10:ARG:NH2	46:DZ:26:GLY:O	2.30	0.63
1:AA:545:C:OP2	4:AD:65:ARG:NH2	2.31	0.63
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.80	0.63
26:DA:1359:A:C6	26:DA:1360:A:C5	2.87	0.63
26:DA:588:U:OP2	61:DA:3879:HOH:O	2.16	0.63
29:DE:72:VAL:HA	29:DE:73:GLU:HB3	1.80	0.63
26:BA:2163:G:N7	26:BA:2173:G:N2	2.47	0.63
26:BA:2530:A:OP2	61:BA:4227:HOH:O	2.15	0.63
31:BG:37:VAL:HG21	31:BG:103:LEU:HD21	1.80	0.63
61:BA:4874:HOH:O	38:BR:3:HIS:NE2	2.30	0.63
1:CA:419:C:OP1	1:CA:513:C:O2'	2.12	0.63
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.39	0.63
26:DA:2138:C:H2'	26:DA:2139:C:H6	1.64	0.63
26:DA:2801(A):A:N3	26:DA:2895:U:H1'	2.13	0.63
26:DA:709:U:H2'	26:DA:710:G:C8	2.34	0.63
41:DU:83:LEU:HD12	41:DU:88:ILE:HB	1.81	0.63
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.64	0.63
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.47	0.63
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.64	0.63
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.80	0.63
1:AA:148:G:N1	1:AA:175:C:N3	2.47	0.63
1:AA:835:U:H3	1:AA:851:G:H1	1.47	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.63
1:CA:60:A:OP1	1:CA:111:G:N2	2.30	0.63
4:CD:60:GLU:HG3	4:CD:198:VAL:HG13	1.80	0.63
35:DO:102:VAL:HB	35:DO:106:LEU:HD12	1.81	0.63
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.81	0.62
1:AA:826:C:O2	8:AH:15:ASN:ND2	2.32	0.62
26:BA:238:C:O2	55:B8:12:LYS:NZ	2.29	0.62
26:BA:1829:U:OP2	28:BD:274:ARG:NH2	2.32	0.62
26:DA:1429:G:H1'	26:DA:1568:G:H1'	1.81	0.62
27:DB:24:G:H5'	27:DB:25:A:H62	1.62	0.62
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.79	0.62
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	1.81	0.62
26:BA:2331:G:N2	39:BS:3:ARG:HA	2.15	0.62
26:BA:1289:G:O2'	36:BP:7:ARG:NH2	2.32	0.62
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.81	0.62
1:CA:890:G:O2'	1:CA:906:G:O6	2.15	0.62
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.79	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:HE1	1.63	0.62
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.33	0.62
1:AA:946:A:H2'	1:AA:947:G:C8	2.35	0.62
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.82	0.62
31:BG:64:THR:HB	31:BG:94:LEU:HD21	1.82	0.62
18:CR:25:THR:O	18:CR:25:THR:OG1	2.15	0.62
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.34	0.62
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.32	0.62
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	1.99	0.62
26:DA:2831:G:OP1	29:DE:58:ARG:NH2	2.29	0.62
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.63	0.62
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.82	0.62
26:BA:1360:C:OP1	61:BA:4479:HOH:O	2.15	0.62
26:BA:1760:U:H2'	26:BA:1761:G:H8	1.63	0.62
27:DB:17:C:O2	27:DB:67:G:N2	2.21	0.62
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.81	0.62
26:BA:2315:G:O6	61:BA:3888:HOH:O	2.14	0.62
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.32	0.62
37:BQ:138:ASP:OD2	46:BZ:81:ARG:NH1	2.32	0.62
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.82	0.62
4:CD:162:LEU:HA	4:CD:165:MET:HB2	1.81	0.62
24:CX:42:G:H2'	24:CX:43:A:H8	1.64	0.62
26:DA:1021:A:H62	26:DA:1141:U:H3	1.48	0.62
26:DA:1370:C:HO2'	26:DA:1811:G:HO2'	1.42	0.62
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.14	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.63	0.62
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.26	0.62
27:BB:28:C:OP1	39:BS:31:SER:OG	2.11	0.62
1:CA:975:A:H4'	1:CA:976:G:H5''	1.82	0.62
24:CX:60:U:H5'	24:CX:61:C:H5	1.63	0.62
26:DA:1230:C:H2'	26:DA:1231:G:H8	1.65	0.62
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.34	0.62
31:DG:7:LEU:HD23	31:DG:100:TRP:HE3	1.65	0.62
1:AA:1297:C:O2'	7:AG:114:ARG:NH2	2.31	0.62
1:AA:662:G:H2'	1:AA:663:A:C8	2.34	0.62
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.81	0.62
25:AY:74:C:H4'	48:B1:23:LYS:HB2	1.81	0.62
26:BA:2149:G:C6	26:BA:2184:G:N1	2.68	0.62
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.81	0.62
26:DA:1489:U:HO2'	26:DA:1490:A:H8	1.47	0.62
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.62
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.33	0.62
27:DB:55:U:H4'	31:DG:28:VAL:HG22	1.82	0.62
32:DH:97:ARG:HA	32:DH:125:VAL:HG11	1.81	0.62
26:BA:1003:U:OP2	37:BQ:14:ARG:NH1	2.33	0.62
1:CA:1240:U:C2	7:CG:32:ARG:HD3	2.34	0.62
1:CA:977:A:HO2'	1:CA:981:U:H3	1.44	0.62
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.31	0.62
1:AA:997:U:H3	1:AA:1044:A:N6	1.98	0.62
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.48	0.62
26:BA:1425:A:H4'	26:BA:1426:G:OP2	1.99	0.62
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.15	0.62
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.63	0.62
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.35	0.62
26:DA:953:A:OP1	37:DQ:18:LYS:NZ	2.33	0.62
32:DH:4:ILE:HG22	32:DH:69:ARG:HG2	1.81	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.33	0.62
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.82	0.62
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.80	0.62
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.82	0.62
1:CA:1120:G:H8	1:CA:1120:G:O5'	1.82	0.62
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.00	0.62
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	1.82	0.62
26:DA:195:A:OP1	36:DP:46:LYS:NZ	2.31	0.62
26:DA:570:G:H2'	26:DA:2030:A:C5	2.35	0.62
26:DA:2857:G:N2	26:DA:2860:A:OP2	2.31	0.62
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.35	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.28	0.62
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.35	0.61
1:AA:346:G:C4	1:AA:347:G:H1'	2.35	0.61
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	1.82	0.61
12:AL:53:ARG:NH1	12:AL:92:ASP:OD2	2.30	0.61
13:AM:37:THR:O	13:AM:55:ARG:NH1	2.31	0.61
9:CI:53:VAL:O	9:CI:55:ALA:N	2.27	0.61
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.35	0.61
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.82	0.61
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.81	0.61
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.82	0.61
1:AA:1243:C:N4	1:AA:1294:G:H1	1.98	0.61
26:BA:1473:A:H4'	26:BA:1474:C:O5'	2.01	0.61
1:CA:592:G:H1	1:CA:647:C:N4	1.97	0.61
26:DA:307:G:N7	61:DA:3912:HOH:O	2.31	0.61
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.28	0.61
6:AF:37:VAL:HA	6:AF:65:VAL:HG12	1.82	0.61
26:BA:878:G:O2'	36:BP:38:GLN:NE2	2.33	0.61
1:CA:1002:G:H1	1:CA:1038:C:H42	0.71	0.61
1:CA:659:U:C2'	1:CA:660:G:H5'	2.30	0.61
26:DA:2831:G:P	29:DE:58:ARG:HH21	2.23	0.61
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.83	0.61
26:DA:30:G:H2'	26:DA:31:C:C6	2.35	0.61
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	1.82	0.61
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.82	0.61
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.33	0.61
1:AA:958:A:N3	1:AA:985:C:O2'	2.28	0.61
1:CA:1458:G:OP1	20:CT:35:THR:OG1	2.12	0.61
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.28	0.61
3:CC:126:ARG:HG2	3:CC:126:ARG:HH11	1.65	0.61
10:CJ:81:THR:HA	10:CJ:84:GLN:HB3	1.82	0.61
23:CW:75:C:C5	23:CW:76:PPU:H93	2.36	0.61
26:DA:1528:A:OP2	26:DA:1542:A:N6	2.33	0.61
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.35	0.61
33:DI:87:LYS:HB3	33:DI:122:GLU:HA	1.83	0.61
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.32	0.61
1:AA:147:G:H1	1:AA:148:G:N2	1.99	0.61
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.32	0.61
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.83	0.61
26:BA:2014:G:N7	61:BA:4265:HOH:O	2.31	0.61
1:CA:975:A:N6	10:CJ:60:ARG:HH12	1.99	0.61
26:DA:1840:G:OP2	61:DA:4276:HOH:O	2.16	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:DG:83:ARG:N	31:DG:86:MET:SD	2.70	0.61
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.83	0.61
1:AA:600:C:H2'	1:AA:601:C:C6	2.35	0.61
26:BA:1071:G:C4	26:BA:1180:C:H1'	2.36	0.61
1:CA:1356:G:H1	1:CA:1366:C:N4	1.97	0.61
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.61
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.35	0.61
33:DI:87:LYS:HA	33:DI:123:LEU:H	1.65	0.61
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.34	0.61
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.81	0.61
43:DW:73:ALA:HB3	43:DW:106:ILE:HD12	1.82	0.61
1:AA:757:U:H2'	1:AA:758:G:O4'	2.00	0.61
3:AC:73:PRO:HB3	3:AC:103:VAL:HG11	1.82	0.61
9:AI:22:GLY:N	9:AI:58:HIS:O	2.30	0.61
26:BA:399:G:OP2	48:B1:69:LYS:HE2	2.00	0.61
26:BA:1228:G:O2'	50:B3:29:ARG:NH1	2.34	0.61
26:BA:2389:A:H2'	26:BA:2390:A:C8	2.36	0.61
1:CA:1036:G:N7	1:CA:1037:C:C2	2.68	0.61
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.36	0.61
1:CA:1229:A:O2'	24:CX:30:G:OP1	2.16	0.61
1:AA:627:G:H2'	1:AA:628:G:H8	1.66	0.61
19:AS:9:VAL:HG21	51:B4:61:ARG:NH2	2.16	0.61
51:B4:61:ARG:NH1	51:B4:62:ARG:O	2.33	0.61
26:BA:1361:C:OP2	61:BA:4479:HOH:O	2.16	0.61
26:BA:1740:U:O2'	28:BD:14:ARG:NH2	2.33	0.61
26:BA:553:A:N1	26:BA:2064:A:H2'	2.16	0.61
26:BA:2172:U:H2'	26:BA:2173:G:C8	2.36	0.61
26:BA:217:A:H8	26:BA:218:A:H5'	1.66	0.61
26:BA:2466:G:O6	61:BA:4327:HOH:O	2.10	0.61
1:CA:1423:G:OP1	35:DO:49:ARG:NH2	2.26	0.61
9:CI:37:PHE:HD1	9:CI:40:LEU:HD12	1.66	0.61
26:DA:2223:G:OP1	28:DD:172:TYR:OH	2.17	0.61
26:DA:881:G:H2'	26:DA:882:G:O4'	2.00	0.61
1:AA:171:A:H2'	1:AA:172:A:C8	2.36	0.61
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.48	0.61
26:BA:185:A:H62	36:BP:38:GLN:HE22	1.49	0.61
4:CD:64:LEU:HB2	4:CD:198:VAL:HG21	1.83	0.61
33:DI:86:THR:O	33:DI:123:LEU:HB2	2.01	0.61
1:AA:890:G:O2'	1:AA:906:G:O6	2.17	0.61
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.01	0.61
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.33	0.61
26:BA:173:C:H2'	26:BA:174:U:C6	2.36	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.33	0.61
26:DA:1324:G:N7	61:DA:3861:HOH:O	2.31	0.61
26:DA:1632:A:N7	61:DA:4171:HOH:O	2.31	0.61
26:DA:889:C:O2'	26:DA:890:A:O5'	2.18	0.61
13:AM:90:LEU:HA	13:AM:93:ARG:HD2	1.83	0.60
24:AX:16:C:O2'	24:AX:61:C:OP1	2.15	0.60
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.16	0.60
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.34	0.60
8:CH:29:SER:HB3	8:CH:32:LYS:HG3	1.82	0.60
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.35	0.60
26:DA:659:C:H2'	26:DA:660:G:H8	1.66	0.60
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.65	0.60
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.32	0.60
4:AD:172:PRO:HB2	4:AD:187:ARG:HH22	1.66	0.60
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.34	0.60
26:BA:1220:U:HO2'	26:BA:1221:G:P	2.23	0.60
26:BA:1847:G:O6	28:BD:35:LYS:NZ	2.34	0.60
31:BG:41:GLN:HE22	31:BG:153:ARG:HB3	1.66	0.60
37:BQ:77:LYS:NZ	37:BQ:86:GLY:O	2.33	0.60
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.13	0.60
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.83	0.60
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.82	0.60
26:DA:1973:G:OP1	61:DA:4133:HOH:O	2.16	0.60
27:DB:30:C:H3'	27:DB:30:C:O2	2.01	0.60
36:DP:50:ARG:HG2	55:D8:61:LEU:HD11	1.83	0.60
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.82	0.60
1:AA:309:G:O2'	1:AA:607:A:N1	2.33	0.60
1:AA:347:G:H2'	1:AA:348:G:O4'	2.00	0.60
4:AD:162:LEU:HA	4:AD:165:MET:HB2	1.83	0.60
5:AE:8:GLU:OE2	5:AE:63:ARG:NH2	2.34	0.60
26:BA:2008:A:OP1	61:BA:4252:HOH:O	2.15	0.60
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.36	0.60
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.83	0.60
1:CA:1275:A:H2'	1:CA:1276:G:O4'	2.01	0.60
1:CA:407:G:N2	1:CA:436:C:C2	2.66	0.60
26:DA:1012:U:OP1	41:DU:75:ASN:ND2	2.31	0.60
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.83	0.60
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.83	0.60
42:BV:19:LYS:HG2	42:BV:95:LEU:HD23	1.84	0.60
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.01	0.60
1:CA:986:A:O2'	19:CS:55:LYS:O	2.18	0.60
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.00	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:30:G:N2	24:CX:40:C:N3	2.40	0.60
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.01	0.60
30:DF:20:LEU:HD13	30:DF:125:LEU:HD13	1.82	0.60
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	1.84	0.60
37:DQ:85:LYS:HD3	47:D0:7:LEU:HD12	1.84	0.60
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.36	0.60
1:AA:649:G:H2'	1:AA:650:G:H8	1.66	0.60
1:AA:918:A:H2'	1:AA:919:A:C8	2.36	0.60
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.83	0.60
26:BA:1541:A:H2'	26:BA:1542:A:C8	2.36	0.60
26:BA:2543:A:H5'	32:BH:157:TYR:CZ	2.36	0.60
26:BA:1002:A:H5'	37:BQ:76:LYS:HG3	1.83	0.60
1:CA:64:G:H4'	1:CA:65:U:H3'	1.83	0.60
1:CA:757:U:O2'	1:CA:879:C:O2	2.18	0.60
18:CR:45:SER:HB3	18:CR:51:LEU:HD21	1.81	0.60
32:DH:98:LEU:HD13	32:DH:125:VAL:HG23	1.84	0.60
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.01	0.60
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.64	0.60
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.60
1:AA:473:G:H2'	1:AA:474:G:C8	2.37	0.60
1:AA:67:C:H2'	1:AA:68:G:C8	2.37	0.60
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.02	0.60
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	1.83	0.60
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.34	0.60
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.83	0.60
1:CA:1223:C:OP2	19:CS:78:ARG:NH2	2.34	0.60
1:CA:1304:G:OP1	21:CU:2:GLY:N	2.35	0.60
36:DP:63:PRO:HD3	55:D8:27:THR:HG22	1.84	0.60
26:DA:20:C:OP1	41:DU:22:LYS:NZ	2.28	0.60
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.83	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.83	0.60
2:AB:76:GLN:NE2	2:AB:206:ASP:OD1	2.35	0.60
19:AS:27:GLU:HG2	19:AS:47:HIS:NE2	2.17	0.60
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.25	0.60
26:BA:1220:U:O2'	26:BA:1221:G:O5'	2.07	0.60
26:BA:869:U:O4	26:BA:989:G:H1'	2.01	0.60
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.66	0.60
40:BT:85:LYS:NZ	40:BT:87:ASP:OD2	2.31	0.60
46:BZ:23:LYS:NZ	46:BZ:40:ASP:OD1	2.33	0.60
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.10	0.60
27:DB:49:C:H2'	27:DB:50:G:C8	2.36	0.60
1:AA:1003:G:C2	1:AA:1004:A:N3	2.70	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.83	0.60
26:BA:1211:U:H2'	26:BA:1212:C:C6	2.36	0.60
26:BA:441:C:H2'	26:BA:442:A:C8	2.37	0.60
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.01	0.60
26:DA:2736:G:N1	26:DA:2768:C:N3	2.38	0.60
29:DE:55:ASN:HB3	29:DE:58:ARG:HG3	1.84	0.60
1:AA:662:G:O2'	1:AA:836:G:OP1	2.20	0.60
4:AD:101:LEU:HB2	4:AD:138:TYR:HB3	1.84	0.60
26:BA:2108:U:H2'	26:BA:2109:G:C8	2.37	0.60
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	1.83	0.60
1:CA:999:C:N4	1:CA:1042:G:H1	1.95	0.60
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.83	0.60
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.17	0.60
26:DA:2305:A:H61	31:DG:43:LEU:HD13	1.67	0.60
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.66	0.60
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.01	0.60
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.02	0.60
1:AA:804:U:H5''	1:AA:805:C:OP2	2.02	0.60
26:BA:1271:G:OP1	42:BV:69:LYS:NZ	2.24	0.60
1:CA:27:G:H2'	1:CA:28:G:H8	1.66	0.60
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.02	0.60
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.28	0.60
26:DA:918:A:O2'	27:DB:97:G:N2	2.33	0.60
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.84	0.59
4:AD:166:LYS:HB2	4:AD:168:ARG:HH12	1.65	0.59
26:BA:1742:G:N7	28:BD:14:ARG:NH2	2.46	0.59
26:BA:715:G:H5'	26:BA:716:G:OP2	2.02	0.59
37:BQ:56:ARG:HH11	37:BQ:56:ARG:CG	2.15	0.59
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.67	0.59
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.24	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.35	0.59
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.02	0.59
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.37	0.59
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.20	0.59
26:DA:647:G:H8	26:DA:647:G:O5'	1.85	0.59
26:DA:1971:A:OP2	28:DD:242:ARG:NH2	2.35	0.59
39:DS:99:LYS:HE2	39:DS:103:GLU:OE2	2.02	0.59
1:AA:1075:C:H2'	1:AA:1076:C:H5'	1.83	0.59
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.65	0.59
26:BA:1221:G:H1'	26:BA:1222:A:C5'	2.29	0.59
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.19	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:271(M):G:H4'	26:DA:271(N):U:OP1	2.01	0.59
26:DA:657:U:H2'	26:DA:658:C:C6	2.36	0.59
29:DE:111:ARG:HA	38:DR:1:MET:HE3	1.84	0.59
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.83	0.59
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.84	0.59
1:AA:1228:C:OP1	13:AM:115:LYS:N	2.27	0.59
1:AA:148:G:N2	1:AA:175:C:O2	2.35	0.59
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.34	0.59
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.84	0.59
18:AR:31:LEU:HD12	18:AR:65:ILE:HB	1.84	0.59
24:AX:4:G:H2'	24:AX:5:G:C8	2.37	0.59
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.35	0.59
26:BA:1285:G:OP1	61:BA:4617:HOH:O	2.17	0.59
26:BA:2745:G:H3'	26:BA:2746:A:O4'	2.02	0.59
26:BA:278:G:OP1	48:B1:76:ARG:NH2	2.35	0.59
33:BI:61:ARG:HA	33:BI:61:ARG:HH11	1.68	0.59
1:CA:609:A:H2'	1:CA:610:G:H5'	1.84	0.59
1:CA:730:G:C5	1:CA:731:G:H1'	2.36	0.59
26:DA:1453:U:O2'	26:DA:1455:G:N7	2.33	0.59
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.35	0.59
26:DA:2408:U:H2'	26:DA:2409:G:H8	1.67	0.59
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.84	0.59
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.65	0.59
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.83	0.59
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.84	0.59
26:BA:1417:G:H2'	26:BA:1418:U:C5	2.37	0.59
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.84	0.59
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.34	0.59
1:CA:92:C:C2'	1:CA:93:G:H5'	2.33	0.59
3:CC:3:ASN:N	3:CC:3:ASN:OD1	2.36	0.59
1:CA:958:A:H61	19:CS:77:THR:HG23	1.65	0.59
23:CW:75:C:C4	23:CW:76:PPU:H93	2.37	0.59
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.68	0.59
26:DA:1914:C:H2'	26:DA:1915:U:C6	2.38	0.59
26:DA:84:A:H5''	45:DY:8:LYS:HG2	1.84	0.59
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.33	0.59
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.35	0.59
1:AA:763:G:C2'	1:AA:764:C:H5'	2.32	0.59
1:CA:1068:G:OP2	1:CA:1068:G:H8	1.86	0.59
1:CA:107:G:OP1	1:CA:325:A:N6	2.34	0.59
1:CA:696:A:N3	1:CA:786:G:O2'	2.29	0.59
1:CA:792:A:H4'	1:CA:793:U:H5''	1.83	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2012:G:OP2	43:DW:16:LYS:NZ	2.32	0.59
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.35	0.59
1:AA:448:A:OP2	1:AA:485:G:N1	2.22	0.59
1:AA:977:A:H2'	1:AA:978:A:H5''	1.85	0.59
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.85	0.59
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.21	0.59
26:DA:2834:G:O2'	26:DA:2883:A:N6	2.34	0.59
1:AA:1392:G:H21	1:AA:1502:A:H8	1.49	0.59
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.02	0.59
1:CA:284:G:H2'	1:CA:285:G:H8	1.68	0.59
1:CA:588:G:H4'	8:CH:2:LEU:HD12	1.83	0.59
9:CI:105:ASP:HB2	9:CI:107:ARG:HG3	1.84	0.59
36:DP:37:GLY:O	36:DP:40:SER:OG	2.21	0.59
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.83	0.59
46:DZ:24:LEU:N	46:DZ:39:VAL:O	2.35	0.59
1:AA:201:C:H42	1:AA:216:G:H1	1.50	0.59
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.68	0.59
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.37	0.59
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.38	0.59
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.33	0.59
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.36	0.59
26:DA:1301:A:H2	26:DA:1626:G:N3	2.01	0.59
26:DA:2163:C:OP1	26:DA:2165:G:N1	2.36	0.59
26:DA:2166:G:O6	26:DA:2171:A:N6	2.36	0.59
26:DA:276:A:H5''	26:DA:277:C:H5'	1.84	0.59
26:DA:578:A:OP2	61:DA:3804:HOH:O	2.16	0.59
26:DA:861:A:N3	27:DB:79:C:O2'	2.35	0.59
26:DA:892:G:H8	26:DA:892:G:O5'	1.86	0.59
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.85	0.59
33:DI:94:ALA:HA	33:DI:97:ILE:HB	1.84	0.59
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	1.83	0.59
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.84	0.59
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.68	0.59
26:BA:933:C:H4'	26:BA:933:C:OP1	2.01	0.59
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.38	0.59
18:CR:22:VAL:HB	18:CR:56:THR:HA	1.85	0.59
24:CX:49:G:C6	24:CX:65:C:N4	2.71	0.59
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.85	0.59
7:AG:15:ASP:OD1	7:AG:19:GLY:N	2.36	0.59
26:BA:1218:G:O2'	26:BA:1219:A:O5'	2.21	0.59
26:BA:2902:G:H4'	26:BA:2903:G:O5'	2.01	0.59
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:47:U:H3'	24:CX:48:C:C5'	2.32	0.59
26:DA:309:G:N3	26:DA:329:G:O2'	2.35	0.59
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.36	0.59
26:DA:2572:A:N7	29:DE:144:ARG:HD2	2.18	0.59
26:DA:336:C:HO2'	45:DY:35:TYR:HH	1.49	0.59
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.38	0.59
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.30	0.58
53:B6:34:LEU:HB2	53:B6:51:GLU:HB2	1.84	0.58
26:BA:1065:U:O2'	26:BA:1067:A:H2	1.86	0.58
26:DA:171:G:H2'	26:DA:172:C:C6	2.37	0.58
26:DA:1860:G:H1	26:DA:1882:C:H42	1.50	0.58
26:DA:2454:G:O6	61:DA:3985:HOH:O	2.15	0.58
26:DA:479:A:N3	26:DA:481:G:H5''	2.18	0.58
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.85	0.58
1:AA:1352:C:N4	61:AA:4166:HOH:O	2.33	0.58
1:AA:191:G:N2	20:AT:103:GLY:HA2	2.17	0.58
26:BA:2699:U:H2'	26:BA:2700:U:O4'	2.03	0.58
26:BA:2879:G:H2'	26:BA:2880:C:O4'	2.03	0.58
26:BA:380:G:H2'	26:BA:381:A:C8	2.37	0.58
33:BI:26:ALA:HA	33:BI:30:LEU:HB2	1.85	0.58
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.37	0.58
1:CA:1126:U:H1'	1:CA:1281:U:N3	2.18	0.58
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.38	0.58
51:D4:46:GLN:O	51:D4:48:ARG:N	2.32	0.58
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.58
26:DA:879:G:H3'	26:DA:880:G:C8	2.34	0.58
38:DR:11:ASN:ND2	61:DR:3101:HOH:O	2.34	0.58
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.15	0.58
26:BA:354:A:H2	26:BA:1255:A:H2'	1.67	0.58
26:BA:1639:G:H2'	26:BA:1640:G:C8	2.38	0.58
29:BE:47:VAL:HG13	29:BE:49:LEU:HD13	1.84	0.58
1:CA:1004:A:C6	1:CA:1037:C:C2	2.91	0.58
1:CA:1530:G:H2'	1:CA:1531:A:O4'	2.03	0.58
1:CA:978:A:OP1	1:CA:1361:G:N2	2.35	0.58
7:CG:99:LEU:HD23	7:CG:102:ARG:NH1	2.17	0.58
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.84	0.58
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.49	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.37	0.58
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.03	0.58
1:AA:613:C:H2'	1:AA:614:A:C8	2.38	0.58
5:AE:90:VAL:O	5:AE:120:THR:HA	2.04	0.58
9:AI:42:ARG:NH1	9:AI:75:ASP:OD1	2.37	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:AX:64:G:O2'	37:BQ:10:ARG:NH2	2.37	0.58
26:BA:2177:G:H3'	26:BA:2178:G:H8	1.68	0.58
1:CA:1091:U:N3	1:CA:1094:G:OP2	2.25	0.58
1:CA:1058:G:H1	1:CA:1199:U:H3	1.52	0.58
1:CA:1428:A:H2'	1:CA:1429:C:C6	2.38	0.58
1:CA:92:C:H2'	1:CA:93:G:H5'	1.83	0.58
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.38	0.58
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.21	0.58
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.84	0.58
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.38	0.58
1:AA:448:A:P	1:AA:485:G:H22	2.26	0.58
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.85	0.58
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.84	0.58
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.86	0.58
52:B5:59:GLU:HG2	52:B5:60:VAL:N	2.19	0.58
26:BA:2344:U:O4	61:BA:4724:HOH:O	2.17	0.58
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.03	0.58
33:BI:96:ASP:OD1	33:BI:96:ASP:N	2.36	0.58
1:CA:1356:G:H2'	1:CA:1357:A:C8	2.38	0.58
1:CA:953:G:H5'	1:CA:965:A:N6	2.19	0.58
2:CB:120:ALA:O	2:CB:122:PHE:N	2.35	0.58
26:DA:1531:C:H42	26:DA:1538:G:H1	1.50	0.58
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.86	0.58
28:DD:34:VAL:HB	28:DD:61:LEU:HD12	1.85	0.58
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.86	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
43:DW:18:ARG:HG3	43:DW:76:VAL:HB	1.85	0.58
1:AA:1150:U:O4	1:AA:1151:A:N6	2.37	0.58
1:AA:13:U:OP1	61:AA:4121:HOH:O	2.17	0.58
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.36	0.58
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.03	0.58
11:AK:84:VAL:HG21	11:AK:95:ILE:HD11	1.85	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
13:AM:80:ARG:NH2	51:B4:58:ARG:HD2	2.18	0.58
37:BQ:86:GLY:HA3	47:B0:10:THR:HG23	1.85	0.58
26:BA:2830:A:OP2	38:BR:2:ARG:NH2	2.36	0.58
27:BB:75:G:H8	27:BB:75:G:H5'	1.69	0.58
1:CA:592:G:H1	1:CA:647:C:H42	1.50	0.58
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.19	0.58
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.04	0.58
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.36	0.58
26:DA:251:A:C5	26:DA:252:G:H1'	2.37	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.37	0.58
26:DA:2637:U:H5''	29:DE:82:ARG:HH21	1.68	0.58
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.03	0.58
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.37	0.58
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.31	0.58
1:AA:557:G:OP1	61:AA:4060:HOH:O	2.17	0.58
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.32	0.58
9:AI:28:VAL:HG22	9:AI:63:ILE:HB	1.86	0.58
1:AA:35:G:O2'	12:AL:118:SER:O	2.17	0.58
17:AQ:6:LEU:HG	17:AQ:23:VAL:HG11	1.86	0.58
26:BA:209:G:O2'	26:BA:222:A:N3	2.34	0.58
26:BA:2761:A:H5'	32:BH:4:ILE:HD12	1.84	0.58
42:BV:72:VAL:HG22	42:BV:85:LYS:HB3	1.84	0.58
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.39	0.58
1:CA:157:G:H1	1:CA:164:U:H3	1.50	0.58
1:CA:708:C:H2'	1:CA:709:G:C8	2.36	0.58
2:CB:186:ALA:O	2:CB:201:ILE:N	2.37	0.58
24:CX:23:C:H2'	24:CX:24:U:C6	2.39	0.58
26:DA:2000:G:N7	61:DA:4004:HOH:O	2.32	0.58
26:DA:2079:U:O3'	48:D1:35:THR:OG1	2.21	0.58
33:DI:49:ALA:HA	33:DI:52:ARG:HH22	1.68	0.58
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.03	0.58
1:AA:1287:A:N1	1:AA:1370:G:N2	2.48	0.58
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.39	0.58
1:AA:984:C:H2'	1:AA:985:C:H6	1.67	0.58
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.85	0.58
54:B7:12:ARG:NH2	54:B7:44:PRO:HB3	2.19	0.58
26:BA:1976:G:O2'	26:BA:1978:U:O4	2.13	0.58
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.14	0.58
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.33	0.58
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD13	1.86	0.58
1:CA:835:U:H3	1:CA:851:G:H1	1.52	0.58
4:CD:162:LEU:HD22	4:CD:178:VAL:HG13	1.86	0.58
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.67	0.58
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.35	0.58
1:AA:1028:C:H2'	1:AA:1029:C:O4'	2.04	0.58
1:AA:613:C:H2'	1:AA:614:A:H8	1.69	0.58
36:BP:50:ARG:HH21	55:B8:7:HIS:CD2	2.21	0.58
1:CA:21:G:H2'	1:CA:22:G:C8	2.39	0.58
1:CA:27:G:H2'	1:CA:28:G:C8	2.39	0.58
1:CA:516:U:O2'	1:CA:519:C:N3	2.32	0.58
1:CA:814:A:H2'	1:CA:816:A:H5''	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.19	0.58
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.85	0.58
26:DA:1169:G:H2'	26:DA:1170:G:C8	2.38	0.58
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.69	0.58
26:DA:2301:C:H2'	26:DA:2302:G:H8	1.69	0.58
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.39	0.58
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.86	0.58
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.86	0.58
26:BA:1778:G:H2'	26:BA:1779:G:H5''	1.85	0.58
39:BS:28:VAL:HG11	39:BS:98:VAL:HG13	1.85	0.58
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.86	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.86	0.58
24:CX:64:G:H4'	37:DQ:10:ARG:NH2	2.19	0.58
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.03	0.58
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.57
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.19	0.57
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.33	0.57
26:BA:1346:U:H4'	26:BA:1347:A:C5'	2.33	0.57
26:BA:333:G:N3	26:BA:353:G:O2'	2.36	0.57
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.86	0.57
1:CA:406:G:N3	4:CD:119:GLN:NE2	2.50	0.57
1:CA:600:C:H2'	1:CA:601:C:H6	1.69	0.57
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.19	0.57
26:DA:2233:U:H2'	26:DA:2234:G:C8	2.39	0.57
26:DA:678:C:N3	26:DA:799:G:N1	2.42	0.57
26:DA:271(P):C:O3'	33:DI:42:SER:OG	2.18	0.57
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.18	0.57
1:AA:154:C:C2'	1:AA:155:C:H5'	2.33	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.40	0.57
9:AI:19:LEU:HB3	9:AI:59:PHE:CD1	2.38	0.57
26:BA:2228:G:O2'	26:BA:2229:A:OP1	2.18	0.57
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.35	0.57
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.04	0.57
1:CA:1027:C:N3	1:CA:1035:A:C2	2.72	0.57
1:CA:999:C:N4	1:CA:1042:G:C6	2.71	0.57
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.85	0.57
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.39	0.57
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.69	0.57
26:DA:528:A:C2	26:DA:2042:A:H2'	2.39	0.57
26:DA:2384:G:OP2	47:D0:55:ARG:NH2	2.37	0.57
28:DD:206:LEU:O	28:DD:211:ARG:NE	2.34	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.34	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.87	0.57
26:BA:1067:A:H3'	26:BA:1067:A:C8	2.38	0.57
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.86	0.57
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.40	0.57
1:CA:279:A:H4'	1:CA:280:C:H5''	1.85	0.57
1:CA:677:U:H3	1:CA:713:G:H22	1.52	0.57
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.37	0.57
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.37	0.57
26:DA:1814:G:H4'	28:DD:51:VAL:HG21	1.86	0.57
27:DB:42:C:O2'	31:DG:67:LYS:O	2.10	0.57
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.70	0.57
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.39	0.57
1:AA:170:U:O2'	1:AA:171:A:H5'	2.05	0.57
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.85	0.57
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.85	0.57
26:BA:1864:U:O2'	26:BA:1991:A:N1	2.29	0.57
26:BA:2130:C:H2'	26:BA:2131:U:H6	1.69	0.57
26:BA:895:G:H2'	26:BA:896:A:C8	2.40	0.57
1:CA:1029:C:N4	1:CA:1032:G:H1	2.02	0.57
1:CA:107:G:H2'	1:CA:108:G:O4'	2.05	0.57
1:CA:72:C:N4	1:CA:73:G:C5	2.72	0.57
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.04	0.57
34:DN:121:LYS:HG2	34:DN:130:HIS:NE2	2.20	0.57
42:DV:78:LYS:HB3	61:DV:301:HOH:O	2.04	0.57
1:AA:160:A:N6	1:AA:345:C:OP2	2.37	0.57
26:BA:2160:C:C2	26:BA:2176:G:C2	2.93	0.57
27:BB:29:A:H2'	27:BB:30:C:C6	2.38	0.57
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.87	0.57
1:CA:54:C:N4	1:CA:353:A:OP2	2.37	0.57
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.37	0.57
26:DA:2630:G:N2	26:DA:2788:C:O2	2.30	0.57
26:DA:57:C:H2'	26:DA:58:G:O4'	2.05	0.57
27:DB:50:G:OP1	39:DS:63:THR:N	2.37	0.57
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.03	0.57
1:AA:532:A:O2'	1:AA:533:A:OP1	2.16	0.57
26:BA:1451:U:H2'	26:BA:1452:U:C6	2.39	0.57
26:BA:2255:U:H2'	26:BA:2256:U:C6	2.39	0.57
1:CA:1027:C:C4	1:CA:1034:G:C2	2.93	0.57
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.04	0.57
1:CA:559:A:H4'	1:CA:560:U:H5''	1.87	0.57
26:DA:2284:C:OP2	53:D6:2:ALA:N	2.38	0.57
26:DA:1171:G:N2	26:DA:1178:C:H42	2.03	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.39	0.57
33:DI:87:LYS:HA	33:DI:122:GLU:HA	1.86	0.57
1:AA:1125:U:O2'	1:AA:1126:U:H5''	2.04	0.57
1:AA:984:C:H2'	1:AA:985:C:C6	2.40	0.57
9:AI:23:ASN:HB2	9:AI:25:LYS:HE3	1.86	0.57
26:BA:1346:U:H4'	26:BA:1347:A:H5''	1.85	0.57
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.38	0.57
34:BN:70:LYS:HE3	34:BN:72:TYR:CZ	2.39	0.57
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.33	0.57
26:BA:1040:C:OP1	41:BU:53:ARG:NH2	2.38	0.57
1:CA:1343:G:O2'	9:CI:121:ARG:HD2	2.04	0.57
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.85	0.57
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.29	0.57
26:DA:2136:C:H42	26:DA:2156:G:H1'	1.68	0.57
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.18	0.57
26:DA:2741:A:H61	26:DA:2763:G:H1'	1.69	0.57
27:DB:29:A:C2	27:DB:30:C:C5	2.91	0.57
1:AA:1229:A:O2'	24:AX:30:G:OP1	2.23	0.57
1:AA:250:A:H4'	1:AA:251:G:O5'	2.05	0.57
1:AA:78:G:N2	1:AA:91:C:C2	2.73	0.57
1:AA:839:U:H4'	1:AA:840:C:OP2	2.04	0.57
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.05	0.57
49:B2:22:GLU:OE2	49:B2:68:ARG:NH2	2.38	0.57
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.86	0.57
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.05	0.57
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.86	0.57
9:CI:22:GLY:N	9:CI:58:HIS:O	2.34	0.57
26:DA:1532:C:N3	26:DA:1537:G:N1	2.40	0.57
26:DA:2138:C:H2'	26:DA:2139:C:C6	2.40	0.57
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.57
26:DA:530:G:C5	26:DA:2022:U:H5''	2.39	0.57
26:DA:992:C:OP1	41:DU:47:TYR:OH	2.11	0.57
1:AA:1036:G:N3	1:AA:1036:G:H2'	2.19	0.57
1:AA:953:G:H5'	1:AA:965:A:H61	1.69	0.57
26:BA:669:A:H4'	26:BA:670:C:H5	1.70	0.57
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.38	0.57
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.86	0.57
26:DA:477:A:H2'	26:DA:478:A:C8	2.40	0.57
28:DD:51:VAL:HG11	28:DD:54:ARG:HH11	1.69	0.57
1:AA:269:C:H2'	1:AA:270:A:C8	2.39	0.57
1:AA:330:C:O2	61:AA:4093:HOH:O	2.15	0.57
1:AA:438:G:N1	1:AA:495:A:OP2	2.29	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.87	0.57
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.57
26:BA:1065:U:H3	26:BA:1188:A:H62	1.51	0.57
26:BA:1890:A:N6	26:BA:1905:G:O2'	2.37	0.57
26:BA:2045:G:H5'	26:BA:2629:C:H4'	1.86	0.57
26:BA:886:U:H2'	26:BA:887:C:C6	2.39	0.57
30:BF:195:ASP:HB3	30:BF:198:ALA:H	1.70	0.57
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.40	0.57
1:CA:473:G:H2'	1:CA:474:G:C8	2.40	0.57
1:CA:920:U:H2'	1:CA:921:U:C6	2.40	0.57
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.20	0.57
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.87	0.57
26:DA:277:C:O2'	26:DA:278:A:OP1	2.20	0.57
26:DA:286:C:H2'	26:DA:287:C:H6	1.69	0.57
26:DA:827:U:O2'	61:DA:4222:HOH:O	2.18	0.57
31:DG:47:LYS:HG2	31:DG:48:GLU:N	2.19	0.57
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.51	0.56
1:AA:1372:U:H2'	1:AA:1373:G:O4'	2.05	0.56
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.85	0.56
11:AK:48:ILE:O	11:AK:50:TYR:N	2.35	0.56
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.56
26:BA:1219:A:H4'	26:BA:1220:U:OP1	2.05	0.56
26:BA:2450:U:O2'	26:BA:2452:C:OP1	2.19	0.56
13:CM:68:GLY:HA3	31:DG:116:ASP:OD1	2.05	0.56
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.35	0.56
26:DA:387:U:OP2	48:D1:20:ARG:NH1	2.32	0.56
26:DA:536:A:H2'	26:DA:537:C:C6	2.40	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.40	0.56
26:DA:662:G:H5''	36:DP:16:ARG:HG2	1.86	0.56
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.87	0.56
36:DP:64:LYS:HA	55:D8:13:ARG:HB3	1.85	0.56
1:AA:153:C:H42	1:AA:168:G:H1	1.53	0.56
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.87	0.56
61:BA:3834:HOH:O	54:B7:34:ARG:NH2	2.38	0.56
26:BA:1819:C:OP1	28:BD:222:ARG:NH2	2.37	0.56
26:BA:36:G:N3	26:BA:476:G:O2'	2.37	0.56
26:BA:878:G:N2	36:BP:53:GLY:O	2.38	0.56
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.40	0.56
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.03	0.56
27:DB:12:C:O2'	47:D0:74:ARG:HG2	2.05	0.56
26:DA:2774:C:H2'	26:DA:2775:A:O4'	2.06	0.56
26:DA:888:C:H2'	26:DA:889:C:C4	2.40	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:889:C:O2'	26:DA:890:A:H8	1.88	0.56
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.05	0.56
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.70	0.56
20:AT:57:ARG:HH22	20:AT:100:ILE:HD11	1.70	0.56
50:B3:7:LYS:HG3	50:B3:34:GLU:HG3	1.86	0.56
26:BA:556:C:OP2	61:BA:4510:HOH:O	2.17	0.56
26:DA:752:A:H4'	26:DA:753:C:H5'	1.87	0.56
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.86	0.56
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.41	0.56
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.38	0.56
26:BA:1285:G:H2'	26:BA:1286:U:O4'	2.05	0.56
26:BA:1298:G:O6	41:BU:36:ARG:HG2	2.04	0.56
26:BA:2495:C:N3	37:BQ:124:LYS:NZ	2.48	0.56
26:BA:70:A:N7	44:BX:31:HIS:HE1	2.03	0.56
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.87	0.56
32:BH:40:GLU:OE1	32:BH:60:ARG:NH1	2.38	0.56
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.71	0.56
45:BY:86:ARG:NH1	45:BY:100:ALA:O	2.38	0.56
4:CD:155:LEU:HD22	4:CD:157:LEU:H	1.70	0.56
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.87	0.56
7:CG:9:VAL:O	7:CG:11:GLN:NE2	2.38	0.56
6:CF:2:ARG:HH22	15:CO:2:PRO:HD2	1.71	0.56
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.06	0.56
26:DA:860:U:H1'	26:DA:2268:A:H5'	1.87	0.56
1:AA:193:C:H2'	1:AA:194:C:H6	1.71	0.56
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.05	0.56
26:BA:2160:C:N3	26:BA:2175:G:N2	2.45	0.56
26:BA:2181:G:H2'	26:BA:2182:G:C8	2.41	0.56
26:BA:2660:C:H2'	26:BA:2661:U:C6	2.41	0.56
1:CA:1030:C:N4	1:CA:1032:G:O6	2.38	0.56
1:CA:93:G:H2'	1:CA:96:U:H6	1.71	0.56
3:CC:54:ARG:NH1	3:CC:54:ARG:HB3	2.21	0.56
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.69	0.56
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.33	0.56
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.39	0.56
26:DA:829:A:N7	26:DA:2248:C:H5'	2.21	0.56
26:DA:885:C:H3'	26:DA:886:C:H5''	1.87	0.56
1:AA:21:G:H2'	1:AA:22:G:C8	2.40	0.56
1:AA:858:G:O6	1:AA:869:G:H3'	2.06	0.56
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.19	0.56
26:BA:1478:C:H2'	26:BA:1479:U:O4'	2.05	0.56
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.20	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:250:A:H4'	1:CA:251:G:O5'	2.04	0.56
1:CA:93:G:O2'	1:CA:96:U:H5'	2.05	0.56
24:CX:15:G:H2'	24:CX:59:A:N6	2.21	0.56
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.05	0.56
26:DA:2301:C:H2'	26:DA:2302:G:C8	2.40	0.56
26:DA:880:G:C2	26:DA:898:C:O2	2.59	0.56
31:DG:19:LEU:HD13	31:DG:32:PRO:HG2	1.88	0.56
31:DG:46:ALA:HB2	31:DG:53:LEU:HD12	1.88	0.56
43:DW:11:ARG:HD2	43:DW:82:LEU:HD12	1.86	0.56
1:AA:542:G:H5'	4:AD:41:GLY:HA3	1.86	0.56
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.04	0.56
48:B1:3:LYS:O	48:B1:12:PRO:HD3	2.06	0.56
26:BA:1074:A:H61	26:BA:1171:G:H2'	1.70	0.56
26:BA:1896:G:OP1	61:BA:4699:HOH:O	2.17	0.56
26:BA:2022:G:OP1	38:BR:5:LYS:NZ	2.38	0.56
26:BA:2147:G:H22	26:BA:2194:U:P	2.29	0.56
26:BA:2507:G:H5''	37:BQ:82:ARG:HG2	1.85	0.56
29:BE:97:LYS:N	29:BE:100:GLU:OE1	2.29	0.56
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.87	0.56
1:CA:1399:C:H4'	1:CA:1400:C:C5'	2.35	0.56
48:D1:53:VAL:HG22	48:D1:74:VAL:HG13	1.86	0.56
26:DA:2103:C:H2'	26:DA:2104:G:H5'	1.87	0.56
26:DA:517:C:OP1	52:D5:16:ARG:NH2	2.39	0.56
26:DA:922:U:H2'	26:DA:923:C:C6	2.40	0.56
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.71	0.56
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.40	0.56
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.37	0.56
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.88	0.56
26:BA:600:G:O2'	26:BA:1300:A:OP1	2.23	0.56
26:BA:1896:G:N2	26:BA:1899:A:OP2	2.34	0.56
26:BA:242:C:O2'	61:BA:4683:HOH:O	2.17	0.56
26:BA:2702:C:OP1	38:BR:17:ARG:NH1	2.37	0.56
26:BA:922:G:H2'	26:BA:923:C:O4'	2.06	0.56
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.41	0.56
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.87	0.56
26:BA:438:G:C5	36:BP:72:PRO:HB3	2.40	0.56
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.41	0.56
1:CA:601:C:H2'	1:CA:602:A:H8	1.71	0.56
1:CA:757:U:H2'	1:CA:758:G:O4'	2.05	0.56
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.86	0.56
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.06	0.56
27:DB:2:C:O2'	27:DB:3:C:H5'	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:107:LYS:HD3	30:DF:206:ILE:HA	1.88	0.56
33:DI:97:ILE:O	33:DI:101:LEU:HB2	2.05	0.56
36:DP:121:LYS:HB3	36:DP:123:LEU:HG	1.87	0.56
26:BA:2157:A:N6	26:BA:2178:G:N2	2.54	0.56
26:BA:2303:U:H2'	26:BA:2304:C:C6	2.41	0.56
26:BA:655:G:N2	26:BA:658:A:OP2	2.30	0.56
40:BT:96:ARG:CZ	40:BT:96:ARG:HB3	2.35	0.56
1:CA:1417:G:O6	61:CA:4029:HOH:O	2.18	0.56
1:CA:598:U:H2'	1:CA:599:C:C6	2.41	0.56
1:CA:953:G:H5'	1:CA:965:A:H61	1.69	0.56
26:DA:1022:G:N7	34:DN:66:LYS:HE2	2.21	0.56
25:CY:76:A:N6	26:DA:2422:A:O4'	2.39	0.56
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.36	0.56
27:DB:1:U:O2'	27:DB:2:C:O5'	2.20	0.56
33:DI:129:THR:HG22	33:DI:139:GLN:NE2	2.20	0.56
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.40	0.56
2:AB:204:ASN:O	2:AB:210:SER:OG	2.14	0.56
14:AN:4:LYS:HA	14:AN:7:ILE:HG22	1.88	0.56
26:BA:469:A:H1'	26:BA:1246:C:O4'	2.06	0.56
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.87	0.56
4:CD:64:LEU:HA	4:CD:67:ILE:HD12	1.87	0.56
9:CI:53:VAL:HG21	9:CI:92:TYR:CZ	2.41	0.56
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.88	0.56
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.24	0.56
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.05	0.56
26:DA:11:G:H2'	26:DA:12:U:H5''	1.87	0.56
26:DA:323:G:C8	30:DF:171:PRO:HG3	2.41	0.56
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.39	0.56
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.87	0.56
46:DZ:146:ILE:HA	46:DZ:174:VAL:HG11	1.88	0.56
1:AA:1006:C:N4	1:AA:1023:G:H1	2.01	0.56
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.86	0.56
12:AL:33:ARG:HD3	12:AL:62:SER:HB3	1.88	0.56
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.38	0.56
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.21	0.56
26:BA:2096:U:H2'	26:BA:2097:U:C6	2.41	0.56
26:BA:2298:A:H4'	26:BA:2299:A:O4'	2.06	0.56
26:BA:831:A:C6	28:BD:229:VAL:HG11	2.41	0.56
26:BA:606:G:OP2	41:BU:10:ARG:HD2	2.06	0.56
26:DA:2051:A:H5'	26:DA:2578:G:O4'	2.05	0.56
26:DA:2135:A:N6	26:DA:2156:G:C2	2.74	0.56
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.41	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1106:G:H5''	3:AC:172:ARG:HG2	1.88	0.55
1:AA:1202:G:H1'	14:AN:29:ARG:HD2	1.88	0.55
1:AA:147:G:N1	1:AA:148:G:C2	2.74	0.55
1:AA:473:G:H2'	1:AA:474:G:H8	1.71	0.55
10:AJ:55:LYS:HE3	10:AJ:56:HIS:CE1	2.40	0.55
12:AL:70:ILE:HD13	12:AL:77:LEU:HD12	1.88	0.55
1:AA:1320:C:H5'	19:AS:70:LYS:HG3	1.87	0.55
26:BA:2316:G:H22	26:BA:2324:U:H3	1.54	0.55
26:BA:673:G:O2'	26:BA:2363:G:OP1	2.19	0.55
27:BB:11:C:H3'	27:BB:12:C:H6	1.69	0.55
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.55
1:CA:976:G:H22	1:CA:1363(A):A:H2'	1.71	0.55
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.05	0.55
8:CH:86:ILE:HG21	8:CH:133:LEU:HD13	1.88	0.55
3:CC:8:ILE:HG22	14:CN:49:HIS:O	2.07	0.55
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.71	0.55
26:DA:1010:A:H1'	26:DA:1153:C:H1'	1.86	0.55
26:DA:1037:G:H1	26:DA:1118:C:H42	1.54	0.55
26:DA:1710:C:H2'	26:DA:1711:C:C6	2.41	0.55
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.70	0.55
26:DA:2682:U:O2'	40:DT:58:ASN:ND2	2.39	0.55
29:DE:72:VAL:CA	29:DE:73:GLU:HB3	2.36	0.55
33:DI:52:ARG:H	33:DI:52:ARG:NH1	2.05	0.55
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.86	0.55
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.21	0.55
1:AA:636:U:H2'	1:AA:637:G:H8	1.70	0.55
22:AV:15:A:O5'	22:AV:15:A:H8	1.89	0.55
26:BA:1058:U:C5	34:BN:28:THR:HG21	2.41	0.55
26:BA:2138:G:H22	26:BA:2184:G:P	2.30	0.55
26:BA:2541:G:O6	56:B9:31:LYS:NZ	2.39	0.55
26:BA:2849:G:H5'	38:BR:46:GLY:HA2	1.87	0.55
26:BA:704:U:H2'	26:BA:705:C:C6	2.41	0.55
26:BA:630:U:OP1	30:BF:102:PRO:HA	2.06	0.55
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.41	0.55
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.39	0.55
26:DA:2802:G:H2'	26:DA:2803:C:O4'	2.06	0.55
34:DN:17:ASP:OD1	34:DN:56:ASN:ND2	2.28	0.55
1:AA:1163:C:H2'	1:AA:1164:G:H5''	1.87	0.55
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.12	0.55
1:AA:975:A:N6	10:AJ:60:ARG:HH12	2.04	0.55
26:BA:2405:A:O2'	55:B8:13:ARG:NH1	2.40	0.55
26:BA:1431:G:O2'	26:BA:1442:U:O2	2.15	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1685:C:O3'	26:BA:2721:G:N2	2.39	0.55
26:BA:514:G:O2'	43:BW:49:LYS:NZ	2.35	0.55
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.40	0.55
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.89	0.55
1:CA:877:C:O2	8:CH:3:THR:OG1	2.24	0.55
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.35	0.55
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.86	0.55
1:CA:1124:G:H5''	10:CJ:35:SER:OG	2.07	0.55
16:CP:72:ARG:HH21	16:CP:73:LEU:HD21	1.71	0.55
26:DA:2552:U:H2'	26:DA:2554:U:OP2	2.06	0.55
26:DA:618:C:H2'	26:DA:619:G:O4'	2.06	0.55
26:DA:874:G:H8	26:DA:874:G:H5'	1.72	0.55
28:DD:127:VAL:HA	28:DD:193:VAL:HG22	1.88	0.55
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.36	0.55
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.06	0.55
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.06	0.55
4:AD:109:GLY:HA3	4:AD:165:MET:HG3	1.88	0.55
26:BA:1067:A:H3'	26:BA:1067:A:H8	1.72	0.55
26:BA:1249:A:N6	26:BA:1286:U:H2'	2.21	0.55
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.21	0.55
1:CA:93:G:H2'	1:CA:96:U:C6	2.41	0.55
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.87	0.55
1:CA:406:G:O2'	4:CD:3:ARG:NH2	2.40	0.55
5:CE:8:GLU:OE2	5:CE:63:ARG:NH2	2.40	0.55
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	1.89	0.55
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.05	0.55
24:CX:16:C:H3'	24:CX:17:C:O2	2.06	0.55
24:CX:41:C:H2'	24:CX:42:G:H8	1.71	0.55
26:DA:2869:G:H2'	26:DA:2870:C:O4'	2.05	0.55
35:DO:64:ARG:NH1	35:DO:81:ASP:OD2	2.40	0.55
1:AA:70:G:H1	1:AA:99:U:H3	1.55	0.55
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.87	0.55
1:AA:562:C:N3	12:AL:16:GLU:HB3	2.22	0.55
26:BA:1218:G:N2	26:BA:1222:A:OP2	2.34	0.55
26:BA:676:G:OP1	55:B8:19:SER:OG	2.21	0.55
28:BD:118:VAL:N	28:BD:129:ASN:OD1	2.35	0.55
41:BU:17:ILE:HG23	41:BU:39:LEU:HD12	1.87	0.55
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.36	0.55
1:CA:1065:U:P	1:CA:1190:G:H22	2.29	0.55
1:CA:991:U:H3'	1:CA:1212:U:N3	2.21	0.55
23:CW:76:PPU:O	23:CW:76:PPU:H5'	2.05	0.55
24:CX:66:C:H5''	24:CX:67:C:OP2	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.37	0.55
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.20	0.55
36:DP:55:ARG:HA	61:DP:307:HOH:O	2.06	0.55
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.88	0.55
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.88	0.55
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.40	0.55
1:AA:673:G:H2'	1:AA:674:G:C8	2.42	0.55
24:AX:53:G:H3'	24:AX:54:5MU:H71	1.88	0.55
26:BA:1218:G:H22	26:BA:1222:A:P	2.28	0.55
26:BA:1766:G:H8	26:BA:1770:A:H62	1.53	0.55
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.89	0.55
46:BZ:102:LEU:HD23	46:BZ:139:VAL:HG21	1.89	0.55
1:CA:113:G:N3	1:CA:353:A:O2'	2.38	0.55
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.34	0.55
1:CA:96:U:O2'	1:CA:97:G:O4'	2.24	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.20	0.55
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.42	0.55
26:DA:796:C:H2'	26:DA:797:C:C6	2.41	0.55
26:DA:892:G:H2'	26:DA:893:C:O4'	2.07	0.55
27:DB:40:U:N3	27:DB:44:G:OP2	2.38	0.55
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.07	0.55
1:AA:28:G:O2'	1:AA:296:U:OP1	2.20	0.55
26:BA:731:G:OP1	54:B7:16:HIS:ND1	2.38	0.55
26:BA:1299:A:N6	61:BA:4106:HOH:O	2.19	0.55
26:BA:489:G:N7	61:BA:4346:HOH:O	2.33	0.55
26:BA:670:C:H5'	26:BA:671:A:OP2	2.06	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55
1:CA:1099:G:C6	1:CA:1100:C:N3	2.75	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.89	0.55
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.40	0.55
4:CD:161:ASN:O	4:CD:165:MET:N	2.39	0.55
26:DA:2102:U:H3	26:DA:2187:G:H1	1.55	0.55
26:DA:800:A:OP1	26:DA:800:A:H8	1.90	0.55
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.07	0.55
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.89	0.55
26:DA:2820:A:C6	38:DR:4:LEU:HD11	2.42	0.55
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.70	0.55
1:AA:17:U:H2'	1:AA:18:C:C6	2.42	0.55
1:AA:69:G:H2'	1:AA:70:G:C8	2.41	0.55
1:AA:838:G:H1	1:AA:848:C:H42	1.55	0.55
5:AE:7:GLU:OE1	5:AE:37:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:31:GLN:HE21	9:AI:36:TYR:HA	1.71	0.55
26:BA:831:A:H5'	26:BA:832:G:OP1	2.07	0.55
26:BA:927:G:N2	26:BA:944:C:C2	2.75	0.55
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.39	0.55
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.54	0.55
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.88	0.55
17:CQ:6:LEU:HG	17:CQ:23:VAL:HG11	1.88	0.55
49:D2:18:PRO:HB3	49:D2:68:ARG:NH1	2.20	0.55
26:DA:1497:U:H5''	26:DA:1498:C:H5	1.71	0.55
26:DA:298:G:H5''	26:DA:299:A:OP1	2.07	0.55
26:DA:729:G:H5'	26:DA:730:C:O5'	2.07	0.55
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.55
1:AA:1027:C:N3	1:AA:1034:G:C2	2.74	0.55
1:AA:659:U:C2'	1:AA:660:G:H5'	2.36	0.55
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.88	0.55
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.05	0.55
26:BA:2178:G:H21	26:BA:2180:A:H62	1.54	0.55
26:BA:605:G:H2'	26:BA:606:G:C8	2.42	0.55
1:CA:1004:A:H5''	1:CA:1025:U:C5	2.42	0.55
1:CA:1250:A:H2'	1:CA:1251:A:C8	2.42	0.55
1:CA:97:G:O2'	1:CA:98:G:O4'	2.19	0.55
3:CC:47:LEU:O	3:CC:51:GLY:N	2.40	0.55
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.89	0.55
6:CF:70:ASP:OD1	6:CF:70:ASP:N	2.37	0.55
26:DA:1434:A:H61	26:DA:1558:A:N6	2.05	0.55
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.40	0.55
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.88	0.55
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.42	0.55
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.05	0.55
1:AA:737:A:H2'	1:AA:738:C:C6	2.42	0.55
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.88	0.55
3:AC:100:ALA:O	3:AC:102:ASN:ND2	2.40	0.55
26:BA:354:A:H2	26:BA:1255:A:C2'	2.20	0.55
46:BZ:19:ARG:NH1	46:BZ:84:GLU:O	2.36	0.55
1:CA:277:C:H5''	17:CQ:68:ARG:NH2	2.22	0.55
1:CA:627:G:H2'	1:CA:628:G:C8	2.39	0.55
1:CA:804:U:H5''	1:CA:805:C:OP2	2.07	0.55
26:DA:480:A:N3	26:DA:499:U:O2'	2.33	0.55
26:DA:784:A:C5	28:DD:229:VAL:HG21	2.41	0.55
27:DB:19:G:H2'	27:DB:20:C:O4'	2.06	0.55
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.07	0.54
1:AA:527:G:O2'	1:AA:535:A:N1	2.37	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.54
2:AB:78:GLN:O	2:AB:94:ASN:ND2	2.40	0.54
26:BA:1921:G:H2'	26:BA:1921:G:N3	2.22	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.89	0.54
1:CA:979:C:H2'	1:CA:980:C:H5'	1.89	0.54
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.88	0.54
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.43	0.54
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.07	0.54
33:DI:52:ARG:H	33:DI:52:ARG:HH11	1.53	0.54
36:DP:89:ALA:O	36:DP:121:LYS:NZ	2.29	0.54
1:AA:1030:C:H5''	1:AA:1030(A):G:O5'	2.07	0.54
1:AA:1086:U:H2'	1:AA:1087:G:H8	1.72	0.54
1:AA:139:G:N2	1:AA:224:C:O2	2.40	0.54
1:AA:537:G:H5''	12:AL:113:ARG:NH1	2.23	0.54
24:AX:4:G:H2'	24:AX:5:G:H8	1.72	0.54
26:BA:734:C:H5''	54:B7:2:LYS:HE2	1.89	0.54
26:BA:1604:C:OP2	26:BA:1605:A:O2'	2.21	0.54
26:BA:2376:C:H2'	26:BA:2377:G:O4'	2.07	0.54
26:BA:2584:A:N7	29:BE:144:ARG:HD2	2.21	0.54
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.41	0.54
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.07	0.54
1:CA:49:U:O4	1:CA:365:U:H5	1.90	0.54
36:BP:121:LYS:HG3	50:D3:2:PRO:HG3	1.88	0.54
26:DA:1038:C:N4	26:DA:1117:G:H1	2.05	0.54
26:DA:1753:G:OP2	40:DT:115:ARG:NH2	2.41	0.54
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.39	0.54
26:DA:299:A:N1	26:DA:322:A:O2'	2.32	0.54
27:DB:28:C:OP1	39:DS:31:SER:OG	2.17	0.54
31:DG:32:PRO:HB3	31:DG:172:LEU:HD22	1.90	0.54
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.35	0.54
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.30	0.54
4:AD:85:LYS:HG3	4:AD:86:LYS:H	1.73	0.54
26:BA:2453:C:OP2	26:BA:2598:C:O2'	2.23	0.54
26:BA:2543:A:H5'	32:BH:157:TYR:CE1	2.42	0.54
26:BA:661:G:OP1	36:BP:132:LYS:HE2	2.07	0.54
26:BA:662:A:H5''	36:BP:117:GLU:HG2	1.89	0.54
1:CA:72:C:N4	1:CA:97:G:C2	2.73	0.54
1:CA:944:G:O2'	1:CA:1339:A:N6	2.41	0.54
24:CX:17:C:OP1	24:CX:60:U:O2'	2.24	0.54
26:DA:515:A:H1'	26:DA:581:C:H1'	1.89	0.54
26:DA:695:G:H4'	26:DA:1380:G:H5'	1.88	0.54
26:DA:2635:C:O2'	29:DE:80:GLU:OE1	2.20	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1055:A:H8	1:AA:1055:A:H5'	1.72	0.54
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.41	0.54
26:BA:1822:A:H5'	28:BD:206:LEU:HD12	1.88	0.54
26:BA:1961:U:OP1	26:BA:2616:U:O2'	2.21	0.54
29:BE:29:GLY:HA3	61:BE:3106:HOH:O	2.07	0.54
34:BN:36:GLY:HA2	34:BN:38:HIS:CE1	2.43	0.54
38:BR:33:ARG:NH1	38:BR:115:GLU:OE2	2.35	0.54
46:BZ:54:HIS:ND1	46:BZ:101:PRO:HG3	2.23	0.54
1:CA:1000:U:H2'	1:CA:1001:A:C8	2.43	0.54
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.42	0.54
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.07	0.54
1:CA:109:A:C6	1:CA:326:G:C6	2.95	0.54
1:CA:562:C:H1'	12:CL:15:ARG:HD2	1.90	0.54
13:CM:87:TYR:N	19:CS:73:GLU:O	2.40	0.54
26:DA:1023:U:OP2	61:DA:4207:HOH:O	2.18	0.54
26:DA:2370:G:H2'	26:DA:2371:G:C8	2.42	0.54
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.43	0.54
26:DA:740:U:H2'	26:DA:741:G:H8	1.72	0.54
30:DF:167:ALA:HB1	30:DF:173:VAL:HG11	1.87	0.54
40:DT:99:LEU:O	40:DT:101:PHE:N	2.40	0.54
1:AA:636:U:H2'	1:AA:637:G:C8	2.42	0.54
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.75	0.54
4:AD:102:ASP:OD1	4:AD:103:ASN:N	2.41	0.54
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.23	0.54
26:BA:354:A:HO2'	26:BA:355:A:H8	1.55	0.54
26:BA:39:C:O2	30:BF:46:ARG:NH2	2.41	0.54
26:BA:667:G:N2	26:BA:670:C:OP2	2.41	0.54
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	1.89	0.54
7:CG:69:VAL:HG21	7:CG:104:LEU:HD11	1.89	0.54
20:CT:16:HIS:O	20:CT:19:SER:OG	2.21	0.54
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.54
26:DA:2478:A:O2'	26:DA:2536:G:N2	2.40	0.54
26:DA:2818:G:OP2	38:DR:42:LYS:NZ	2.39	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
46:DZ:154:ASP:N	46:DZ:154:ASP:OD1	2.41	0.54
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.33	0.54
51:B4:55:ARG:N	51:B4:56:VAL:HA	2.23	0.54
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.23	0.54
26:BA:1827:U:H2'	26:BA:1828:C:C6	2.43	0.54
5:CE:31:LEU:HD11	5:CE:129:ILE:HA	1.89	0.54
26:DA:993:G:N2	42:DV:23:GLU:OE2	2.39	0.54
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:DD:77:ALA:HA	28:DD:97:TYR:HA	1.88	0.54
29:DE:54:GLN:OE1	29:DE:55:ASN:N	2.40	0.54
1:AA:1460:A:H2'	1:AA:1461:G:O4'	2.07	0.54
11:AK:33:THR:HG22	11:AK:39:PRO:HA	1.90	0.54
26:BA:2544:G:O2'	26:BA:2669:A:N1	2.38	0.54
1:CA:1118:C:N3	1:CA:1156:G:N2	2.56	0.54
1:CA:1403:C:N4	22:CV:18:G:OP1	2.41	0.54
1:CA:664:G:H22	1:CA:741:G:H1	1.56	0.54
3:CC:172:ARG:NH2	3:CC:206:GLU:OE1	2.40	0.54
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.89	0.54
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.22	0.54
26:DA:492:A:H2'	26:DA:493:G:O4'	2.07	0.54
26:DA:93:G:H2'	26:DA:94:C:C6	2.43	0.54
44:DX:35:THR:HG22	44:DX:38:GLU:HB2	1.90	0.54
3:AC:153:VAL:HA	3:AC:197:GLY:O	2.08	0.54
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.42	0.54
26:BA:494:G:OP2	54:B7:37:LYS:NZ	2.41	0.54
40:BT:24:PRO:HA	40:BT:49:VAL:HG22	1.89	0.54
1:CA:1027:C:N4	1:CA:1034:G:C6	2.76	0.54
1:CA:1262:C:N3	1:CA:1273:G:N2	2.49	0.54
10:CJ:38:ILE:HG13	10:CJ:38:ILE:O	2.07	0.54
26:DA:2138:C:N4	26:DA:2153:G:H1	2.03	0.54
26:DA:2544:G:H1'	26:DA:2646:C:H4'	1.89	0.54
1:AA:165:C:H2'	1:AA:166:G:C8	2.43	0.54
1:AA:791:G:N2	1:AA:1497:G:O3'	2.39	0.54
1:AA:975:A:C8	1:AA:975:A:H5'	2.41	0.54
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.72	0.54
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.41	0.54
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.90	0.54
26:BA:1153:G:N3	26:BA:1153:G:H2'	2.22	0.54
26:BA:1314:A:H2'	26:BA:1315:A:O4'	2.08	0.54
26:BA:2804:C:C2	26:BA:2816:G:N2	2.76	0.54
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.08	0.54
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.43	0.54
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.70	0.54
1:CA:1120:G:N1	1:CA:1154:G:N3	2.55	0.54
13:CM:34:LEU:HD22	13:CM:39:ILE:HB	1.90	0.54
26:DA:880:G:H2'	26:DA:880:G:N3	2.23	0.54
27:DB:105:A:OP1	46:DZ:72:ARG:NH1	2.41	0.54
26:DA:2405:G:OP1	36:DP:77:ARG:NH2	2.41	0.54
1:AA:1151:A:O2'	1:AA:1152:A:H8	1.91	0.54
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:AC:120:VAL:HA	3:AC:123:GLN:HE21	1.73	0.54
26:BA:1001:G:OP2	37:BQ:14:ARG:NH2	2.40	0.54
26:BA:2159:C:N3	26:BA:2176:G:O6	2.41	0.54
26:BA:610:C:OP2	36:BP:21:ARG:NH2	2.41	0.54
42:BV:74:LYS:HB2	42:BV:83:ARG:HB2	1.88	0.54
44:BX:54:VAL:HG22	44:BX:81:VAL:HG12	1.89	0.54
1:CA:501:C:H2'	1:CA:502:G:H8	1.72	0.54
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.72	0.54
51:D4:17:GLY:N	51:D4:33:VAL:O	2.41	0.54
26:DA:1966:A:H4'	26:DA:1967:C:OP1	2.08	0.54
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.42	0.54
36:DP:99:LEU:HA	36:DP:102:ARG:HB3	1.90	0.54
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.20	0.53
15:AO:24:SER:HB3	15:AO:27:VAL:HG23	1.89	0.53
1:AA:1505:G:O2'	22:AV:13:A:O2'	1.94	0.53
26:BA:2279:A:H5''	26:BA:2280:A:H5'	1.90	0.53
26:BA:794:U:O2	26:BA:2036:A:H1'	2.08	0.53
26:BA:932:C:H3'	26:BA:933:C:C5'	2.38	0.53
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.23	0.53
40:BT:53:ARG:NH1	40:BT:53:ARG:HB3	2.23	0.53
1:CA:792:A:H4'	1:CA:793:U:C5'	2.39	0.53
1:CA:999:C:N3	1:CA:1042:G:C2	2.76	0.53
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.41	0.53
22:CV:18:G:N2	24:CX:34:C:C2	2.75	0.53
26:DA:2162:G:H5''	26:DA:2172:U:C6	2.43	0.53
26:DA:2505:G:OP1	61:DA:3855:HOH:O	2.18	0.53
27:DB:13:A:C2	27:DB:16:G:H1'	2.43	0.53
27:DB:54:G:N2	31:DG:29:TRP:HZ2	2.04	0.53
39:DS:58:LEU:HD12	39:DS:65:VAL:HG22	1.89	0.53
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	1.89	0.53
26:BA:1093:G:N2	26:BA:1156:G:O2'	2.41	0.53
26:BA:2658:C:H2'	26:BA:2659:U:O4'	2.08	0.53
26:BA:7:G:H2'	26:BA:8:A:O4'	2.07	0.53
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.74	0.53
1:CA:154:C:H2'	1:CA:155:C:H5'	1.88	0.53
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.06	0.53
36:DP:99:LEU:O	36:DP:103:ALA:N	2.39	0.53
1:AA:1149:C:O2'	1:AA:1280:A:N1	2.31	0.53
1:AA:148:G:C2	1:AA:175:C:N3	2.77	0.53
1:AA:841:U:C5	1:AA:848:C:H1'	2.43	0.53
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.33	0.53
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.90	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.89	0.53
26:BA:2349:G:OP1	61:BA:4006:HOH:O	2.18	0.53
26:BA:2812:A:H5''	26:BA:2813:G:C8	2.43	0.53
1:CA:636:U:H2'	1:CA:637:G:H8	1.73	0.53
13:CM:62:ASN:HA	51:D4:49:PHE:HD2	1.73	0.53
1:CA:229:U:O2'	16:CP:23:ASP:OD2	2.25	0.53
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.07	0.53
26:DA:1009:A:OP2	34:DN:37:LYS:NZ	2.29	0.53
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.08	0.53
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.74	0.53
26:DA:2023:G:H1	26:DA:2040:C:H42	1.56	0.53
26:DA:2247:A:H2'	26:DA:2248:C:C6	2.44	0.53
26:DA:307:G:H21	26:DA:330:A:H62	1.55	0.53
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.90	0.53
1:AA:358:U:H2'	1:AA:359:U:C6	2.43	0.53
1:AA:460:G:N1	1:AA:470:C:H5'	2.23	0.53
1:AA:797:C:C2'	1:AA:798:G:H5'	2.38	0.53
1:AA:805:C:OP2	61:AA:4031:HOH:O	2.19	0.53
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.89	0.53
26:BA:2795:G:OP2	61:BA:4674:HOH:O	2.18	0.53
26:BA:493:G:OP1	54:B7:33:ARG:NH1	2.41	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.24	0.53
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.43	0.53
1:CA:709:G:C2'	1:CA:710:G:H5'	2.38	0.53
11:CK:43:SER:HA	11:CK:47:VAL:HG21	1.91	0.53
1:CA:377:G:OP1	16:CP:3:LYS:HD2	2.07	0.53
19:CS:27:GLU:HB3	19:CS:28:LYS:HB3	1.90	0.53
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.88	0.53
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.44	0.53
26:DA:1933:G:H2'	26:DA:1934:C:O4'	2.08	0.53
26:DA:698:C:O2'	26:DA:734:A:N6	2.42	0.53
27:DB:98:G:H2'	27:DB:99:G:O4'	2.08	0.53
46:DZ:120:ILE:HD12	46:DZ:120:ILE:H	1.72	0.53
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.32	0.53
1:AA:392:G:H2'	1:AA:393:A:H8	1.73	0.53
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.23	0.53
26:BA:1055:A:OP2	34:BN:37:LYS:NZ	2.29	0.53
26:BA:1220:U:H1'	26:BA:1221:G:OP1	2.08	0.53
1:CA:1178:G:N2	1:CA:1180:A:H3'	2.23	0.53
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.73	0.53
4:CD:173:TRP:CD2	4:CD:189:PRO:HG3	2.43	0.53
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.89	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:CQ:59:ILE:HG22	17:CQ:73:VAL:HA	1.89	0.53
26:DA:2247:A:H2'	26:DA:2248:C:H6	1.73	0.53
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.41	0.53
26:DA:623:G:H2'	26:DA:624:C:C6	2.44	0.53
26:DA:839:U:H2'	26:DA:840:C:C6	2.43	0.53
27:DB:29:A:C2	27:DB:56:G:C2	2.97	0.53
33:DI:81:VAL:O	33:DI:82:ARG:HG3	2.08	0.53
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.89	0.53
37:DQ:52:VAL:O	37:DQ:56:ARG:HB2	2.07	0.53
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.09	0.53
1:AA:947:G:N2	1:AA:1235:U:O2	2.42	0.53
1:AA:1499:A:H1'	1:AA:1520:G:H5'	1.91	0.53
2:AB:231:GLU:HB2	2:AB:232:PRO:HD3	1.91	0.53
3:AC:7:PRO:O	3:AC:11:ARG:NH1	2.42	0.53
7:AG:29:LYS:HB3	7:AG:105:VAL:HG21	1.90	0.53
11:AK:98:LEU:O	11:AK:101:SER:OG	2.15	0.53
26:BA:2053:A:C6	26:BA:2510:C:H1'	2.43	0.53
26:BA:441:C:H2'	26:BA:442:A:H8	1.73	0.53
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.08	0.53
1:CA:723:U:HO2'	1:CA:724:G:C5'	2.21	0.53
7:CG:72:ARG:NE	7:CG:142:GLU:OE2	2.42	0.53
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.09	0.53
24:CX:12:G:H4'	26:DA:1908:C:O2	2.08	0.53
26:DA:1750:G:N3	26:DA:2860:A:H2	2.06	0.53
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.35	0.53
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.44	0.53
26:DA:2659:G:N2	26:DA:2661:G:H5''	2.23	0.53
33:DI:124:GLY:O	33:DI:144:VAL:HB	2.08	0.53
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.09	0.53
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.07	0.53
1:AA:1456:G:H22	20:AT:43:LEU:HD11	1.74	0.53
24:AX:8:4SU:O2	24:AX:21:A:H2	1.91	0.53
26:BA:1633:A:H2'	26:BA:1634:C:C6	2.43	0.53
26:BA:1653:C:H4'	26:BA:1654:A:O5'	2.08	0.53
26:BA:2320:G:O2'	26:BA:2322:A:N7	2.41	0.53
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.41	0.53
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.73	0.53
53:D6:9:LEU:HA	53:D6:54:ILE:HB	1.89	0.53
26:DA:18:C:H2'	26:DA:19:C:H6	1.73	0.53
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.16	0.53
45:DY:14:LEU:N	45:DY:73:ARG:O	2.36	0.53
1:AA:542:G:P	4:AD:10:ARG:HH22	2.32	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:828:A:H2'	1:AA:829:G:O4'	2.09	0.53
17:AQ:21:VAL:N	17:AQ:42:TYR:O	2.36	0.53
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.07	0.53
26:BA:1405:A:N6	26:BA:1418:U:C2	2.76	0.53
26:BA:2707:C:H2'	26:BA:2708:U:H6	1.74	0.53
26:BA:873:U:H4'	36:BP:55:ARG:HB2	1.90	0.53
26:BA:931:C:H2'	26:BA:932:C:O4'	2.08	0.53
26:BA:2251:G:H5'	28:BD:251:GLY:HA3	1.90	0.53
33:BI:102:SER:HA	33:BI:106:GLY:HA3	1.91	0.53
33:BI:80:PRO:HA	33:BI:145:VAL:O	2.08	0.53
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.23	0.53
1:CA:1003:G:O3'	1:CA:1004:A:H4'	2.09	0.53
1:CA:1027:C:N3	1:CA:1034:G:N2	2.57	0.53
1:CA:1297:C:H4'	1:CA:1298:C:H5''	1.91	0.53
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.37	0.53
26:DA:1212:G:H1'	26:DA:1236:G:N2	2.24	0.53
26:DA:143:G:H2'	26:DA:143(A):C:C6	2.43	0.53
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.44	0.53
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.89	0.53
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.89	0.53
1:AA:1025:U:C2	1:AA:1036:G:O6	2.62	0.53
1:AA:713:G:H2'	1:AA:714:G:C8	2.43	0.53
1:AA:1189:C:H5''	3:AC:5:ILE:HD12	1.91	0.53
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.53
27:BB:30:C:H2'	27:BB:31:C:H5'	1.91	0.53
1:CA:390:C:H2'	1:CA:391:G:C8	2.44	0.53
1:CA:501:C:H2'	1:CA:502:G:C8	2.43	0.53
8:CH:103:VAL:HG21	8:CH:110:ALA:HB2	1.89	0.53
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.74	0.53
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.90	0.53
26:DA:307:G:N1	26:DA:310:A:OP2	2.38	0.53
26:DA:531:C:H4'	26:DA:532:A:H5''	1.91	0.53
26:DA:656:G:H2'	26:DA:657:U:O4'	2.09	0.53
34:DN:46:VAL:HG23	34:DN:48:MET:HG2	1.91	0.53
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.42	0.53
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.39	0.53
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.08	0.53
4:AD:162:LEU:HB3	4:AD:178:VAL:HG13	1.90	0.53
1:AA:401:C:OP2	4:AD:73:ARG:NH1	2.42	0.53
1:AA:1125:U:C4'	10:AJ:5:ARG:HH22	2.21	0.53
13:AM:80:ARG:HH21	51:B4:58:ARG:NH1	2.07	0.53
19:AS:69:HIS:H	51:B4:58:ARG:HH21	1.57	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:714:U:O2	55:B8:2:PRO:HD2	2.09	0.53
26:BA:1817:A:H1'	26:BA:1960:A:H61	1.74	0.53
26:BA:1823:G:O2'	26:BA:1861:C:OP1	2.22	0.53
26:BA:2417:G:O2'	26:BA:2423:A:N6	2.41	0.53
32:BH:101:ARG:NH2	32:BH:117:PRO:HB2	2.24	0.53
39:BS:83:LYS:HD2	39:BS:111:GLU:OE1	2.09	0.53
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.27	0.53
13:CM:4:ILE:HD11	13:CM:60:VAL:HG11	1.91	0.53
26:DA:459:U:H5''	54:D7:40:TRP:CD2	2.44	0.53
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.44	0.53
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.44	0.53
26:DA:2667:C:H1'	32:DH:109:PHE:CD1	2.44	0.53
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.07	0.53
1:AA:390:C:H2'	1:AA:391:G:C8	2.43	0.52
1:AA:581:G:N2	1:AA:760:G:N7	2.56	0.52
14:AN:29:ARG:HD3	14:AN:40:CYS:SG	2.49	0.52
26:BA:2642:G:H2'	26:BA:2643:G:C8	2.44	0.52
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.42	0.52
36:BP:95:VAL:HG13	36:BP:125:VAL:HG12	1.91	0.52
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.09	0.52
1:CA:284:G:H2'	1:CA:285:G:C8	2.44	0.52
1:CA:97:G:C2	1:CA:98:G:C4	2.97	0.52
8:CH:23:SER:HB2	8:CH:60:ARG:HG2	1.91	0.52
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.54	0.52
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.74	0.52
26:DA:571:A:N6	26:DA:2499:C:O3'	2.41	0.52
26:DA:470:A:OP1	30:DF:59:TYR:HE1	1.91	0.52
31:DG:73:ALA:HB3	31:DG:84:LYS:HA	1.91	0.52
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.91	0.52
43:DW:34:ASN:OD1	43:DW:37:ARG:NH2	2.42	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.45	0.52
1:AA:396:G:O6	61:AA:4041:HOH:O	2.18	0.52
1:AA:524:G:H2'	1:AA:525:C:C6	2.44	0.52
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.23	0.52
26:BA:1081:U:H2'	26:BA:1082:G:C8	2.44	0.52
26:BA:1617:A:H2'	26:BA:1618:A:C8	2.43	0.52
26:BA:1735:U:O2	26:BA:1747:A:H5'	2.09	0.52
26:BA:2236:G:H4'	26:BA:2238:C:C2	2.44	0.52
26:BA:34:C:H41	26:BA:473:A:H61	1.56	0.52
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.73	0.52
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.09	0.52
1:CA:1055:A:O2'	3:CC:161:GLU:O	2.24	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	1.91	0.52
51:D4:60:GLN:H	51:D4:62:ARG:HE	1.57	0.52
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.45	0.52
26:DA:2343:C:H4'	26:DA:2373:G:O3'	2.09	0.52
26:DA:2523:G:N3	26:DA:2764:A:O2'	2.42	0.52
26:DA:363(B):G:H2'	26:DA:363(C):G:C8	2.43	0.52
26:DA:900:A:H2'	26:DA:901:A:O4'	2.08	0.52
27:DB:41:U:O4	31:DG:70:VAL:HB	2.09	0.52
33:DI:77:LEU:HA	33:DI:104:GLN:OE1	2.09	0.52
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.39	0.52
37:DQ:85:LYS:HD2	37:DQ:85:LYS:N	2.24	0.52
45:DY:86:ARG:NH1	45:DY:100:ALA:O	2.42	0.52
1:AA:1164:G:N2	1:AA:1165:C:C4	2.75	0.52
1:AA:154:C:H2'	1:AA:155:C:H5'	1.90	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.73	0.52
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.52
1:AA:530:G:O6	22:AV:21:C:H1'	2.10	0.52
26:BA:1974:A:N3	26:BA:2572:C:O2'	2.40	0.52
26:BA:2221:A:OP2	26:BA:2222:C:H5	1.92	0.52
26:BA:2691:A:H4'	29:BE:165:VAL:HG11	1.92	0.52
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.73	0.52
1:CA:1216:G:H5''	14:CN:5:ALA:CB	2.39	0.52
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.45	0.52
1:CA:1370:G:N7	9:CI:109:VAL:HG11	2.24	0.52
1:CA:34:C:H2'	1:CA:35:G:H8	1.73	0.52
1:CA:662:G:H2'	1:CA:663:A:C8	2.44	0.52
16:CP:23:ASP:OD1	16:CP:25:ARG:HD3	2.09	0.52
26:DA:2035:G:P	26:DA:2036:C:H41	2.32	0.52
28:DD:152:GLY:O	28:DD:154:LYS:HG2	2.10	0.52
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.42	0.52
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.91	0.52
26:DA:537:C:OP1	34:DN:2:LYS:NZ	2.43	0.52
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.92	0.52
1:AA:299:G:H2'	1:AA:300:A:C8	2.45	0.52
1:AA:792:A:H4'	1:AA:793:U:H5''	1.92	0.52
14:AN:26:ARG:HD3	14:AN:43:CYS:SG	2.50	0.52
26:BA:1093:G:O2'	26:BA:1155:C:N4	2.42	0.52
26:BA:1361:C:O2'	26:BA:1438:A:N3	2.34	0.52
26:BA:2157:A:H61	26:BA:2178:G:N2	2.07	0.52
26:BA:326:C:OP2	45:BY:73:ARG:NH2	2.41	0.52
26:BA:843:C:H2'	26:BA:844:C:C6	2.45	0.52
26:BA:2324:U:H5'	31:BG:88:ILE:HD11	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:43:C:H2'	1:CA:44:G:O4'	2.10	0.52
1:CA:632:A:H5'	1:CA:633:G:OP2	2.09	0.52
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.91	0.52
1:CA:1305:G:H5''	21:CU:4:GLY:HA3	1.90	0.52
22:CV:15:A:H8	22:CV:15:A:O5'	1.92	0.52
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.44	0.52
26:DA:1604:C:O2'	26:DA:1610:A:N1	2.34	0.52
26:DA:253:C:OP2	55:D8:5:LYS:NZ	2.28	0.52
26:DA:275:G:H2'	26:DA:276:A:O4'	2.08	0.52
35:DO:2:ILE:HD12	35:DO:6:THR:HG21	1.91	0.52
1:AA:269:C:H2'	1:AA:270:A:H8	1.75	0.52
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.45	0.52
16:AP:57:ARG:HH21	16:AP:79:VAL:HA	1.75	0.52
28:BD:34:VAL:HG12	28:BD:63:ARG:HG3	1.91	0.52
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.30	0.52
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.92	0.52
1:CA:1011:G:H1	1:CA:1018:C:N4	2.08	0.52
1:CA:1014:A:OP1	19:CS:18:LYS:NZ	2.33	0.52
1:CA:1029:C:N4	1:CA:1032:G:C6	2.76	0.52
1:CA:1035:A:C2	1:CA:1036:G:N7	2.78	0.52
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.45	0.52
2:CB:96:ARG:CZ	2:CB:98:LEU:HD13	2.40	0.52
8:CH:112:LEU:HB3	8:CH:133:LEU:HA	1.90	0.52
26:DA:1717:G:N2	26:DA:1745:C:O2	2.43	0.52
26:DA:1779:U:H2'	61:DA:4364:HOH:O	2.09	0.52
26:DA:529:A:OP2	34:DN:114:ARG:NH2	2.41	0.52
28:DD:51:VAL:HG11	28:DD:54:ARG:NH1	2.24	0.52
1:AA:1169:A:OP2	1:AA:1169:A:H8	1.92	0.52
1:AA:1224:G:O2'	1:AA:1322:C:OP1	2.21	0.52
1:AA:861:G:HO2'	1:AA:874:G:HO2'	1.48	0.52
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.42	0.52
23:AW:76:PPU:O	23:AW:76:PPU:H5'	2.10	0.52
19:AS:69:HIS:H	51:B4:58:ARG:NH2	2.08	0.52
26:BA:1405:A:N1	26:BA:1418:U:C4	2.76	0.52
26:BA:2136:A:H2'	26:BA:2137:G:O4'	2.09	0.52
26:BA:1857:G:H4'	28:BD:242:ARG:CZ	2.39	0.52
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.91	0.52
1:CA:1124:G:H4'	1:CA:1125:U:O2	2.10	0.52
1:CA:989:C:N4	1:CA:1216:G:O6	2.43	0.52
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.10	0.52
1:CA:382:A:H2'	1:CA:383:A:C8	2.44	0.52
1:CA:745:C:OP1	1:CA:852:G:H5'	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:789:U:O2'	1:CA:791:G:N7	2.34	0.52
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.91	0.52
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.73	0.52
1:CA:1107:C:OP1	3:CC:173:VAL:N	2.42	0.52
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.10	0.52
26:DA:1032:A:O2'	26:DA:1034:G:OP2	2.24	0.52
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.45	0.52
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.09	0.52
26:DA:781:A:C8	28:DD:219:PRO:HG3	2.44	0.52
26:DA:2773:C:OP1	29:DE:166:THR:OG1	2.27	0.52
30:DF:155:LEU:HD11	30:DF:176:LEU:HD12	1.90	0.52
33:DI:88:ILE:HG22	33:DI:123:LEU:HD23	1.92	0.52
38:DR:44:LEU:HD22	38:DR:48:VAL:HG23	1.92	0.52
1:AA:1009:G:O6	1:AA:1020:U:O4	2.27	0.52
1:AA:119:A:H4'	1:AA:120:A:C8	2.45	0.52
1:AA:178:C:H2'	1:AA:179:A:H8	1.75	0.52
1:AA:966:G:H21	9:AI:127:LYS:NZ	2.07	0.52
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.09	0.52
26:BA:553:A:C2	26:BA:2064:A:H2'	2.45	0.52
26:BA:261:A:N1	26:BA:291:G:O2'	2.30	0.52
26:BA:2816:G:H2'	26:BA:2817:G:H8	1.74	0.52
1:CA:1002:G:N3	1:CA:1003:G:H8	2.07	0.52
1:CA:109:A:H2'	1:CA:326:G:N2	2.24	0.52
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.52
1:CA:190:U:H2'	1:CA:191:G:C8	2.45	0.52
1:CA:197:A:C6	1:CA:221:C:H4'	2.45	0.52
1:CA:540:G:H2'	1:CA:541:G:O4'	2.10	0.52
1:CA:604:G:H2'	1:CA:605:U:O4'	2.10	0.52
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.52
5:CE:83:GLU:HG2	5:CE:88:LYS:HG3	1.91	0.52
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	1.91	0.52
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.09	0.52
26:DA:686:G:N2	26:DA:788:A:H61	2.06	0.52
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.41	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.91	0.52
34:DN:16:ILE:HB	34:DN:54:VAL:HG22	1.91	0.52
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.91	0.52
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.92	0.52
1:AA:1005:A:C1'	1:AA:1036:G:H22	2.23	0.52
1:AA:663:A:O3'	18:AR:64:ARG:NH2	2.43	0.52
1:AA:683:G:H2'	1:AA:684:A:C8	2.44	0.52
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.91	0.52
28:BD:158:ALA:O	28:BD:161:THR:OG1	2.16	0.52
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.09	0.52
2:CB:137:ARG:O	2:CB:141:GLU:N	2.37	0.52
4:CD:128:VAL:HG12	4:CD:129:ASN:HD22	1.75	0.52
4:CD:19:LEU:HD21	4:CD:63:LYS:HG3	1.90	0.52
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.52
1:CA:1367:C:HO2'	10:CJ:48:THR:HG1	1.56	0.52
11:CK:21:ILE:HD12	11:CK:84:VAL:HG22	1.92	0.52
26:DA:2572:A:C8	29:DE:144:ARG:HD2	2.44	0.52
1:AA:1371:G:O3'	9:AI:69:GLY:HA3	2.10	0.52
26:BA:273:G:H4'	26:BA:274:U:OP1	2.10	0.52
26:BA:811:A:O4'	28:BD:213:ARG:HG3	2.10	0.52
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.91	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.78	0.52
1:CA:152:A:N6	1:CA:169:C:N3	2.56	0.52
1:CA:811:C:O2'	1:CA:901:A:N1	2.39	0.52
5:CE:143:ARG:NH1	8:CH:77:GLU:OE2	2.43	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
6:CF:7:ASN:HB2	6:CF:89:MET:HB3	1.92	0.52
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.92	0.52
26:DA:18:C:H2'	26:DA:19:C:C6	2.45	0.52
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.09	0.52
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.92	0.52
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.52
39:DS:25:ARG:NE	39:DS:88:ASP:OD2	2.29	0.52
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.92	0.52
3:AC:150:LYS:HD3	3:AC:152:ILE:HD11	1.92	0.52
4:AD:157:LEU:HD22	4:AD:161:ASN:HD21	1.75	0.52
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.40	0.52
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.92	0.52
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.09	0.52
26:BA:2290:A:H5''	47:B0:12:ASN:HD21	1.75	0.52
26:BA:1312:G:O5'	43:BW:15:ARG:NH2	2.43	0.52
26:BA:1700:G:H3'	38:BR:2:ARG:HD3	1.91	0.52
26:BA:302:A:H2'	26:BA:303:C:C6	2.45	0.52
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.39	0.52
4:CD:79:PHE:HE1	4:CD:204:ILE:HD13	1.74	0.52
1:CA:35:G:O2'	12:CL:118:SER:O	2.20	0.52
3:CC:33:LEU:HD11	14:CN:52:GLN:O	2.10	0.52
1:CA:1114:C:O2'	14:CN:60:SER:O	2.14	0.52
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.33	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2160:G:H2'	26:DA:2161:C:O4'	2.09	0.52
26:DA:2360:A:H2'	26:DA:2361:A:O4'	2.10	0.52
26:DA:2805:G:C6	26:DA:2807:G:C6	2.98	0.52
26:DA:362:U:H4'	26:DA:363:G:OP1	2.10	0.52
26:DA:817:C:H2'	26:DA:818:G:O4'	2.09	0.52
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.24	0.52
33:DI:104:GLN:O	33:DI:105:HIS:ND1	2.43	0.52
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.51
13:AM:33:ALA:O	13:AM:37:THR:OG1	2.13	0.51
24:AX:18:G:O2'	24:AX:19:G:H5'	2.09	0.51
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.93	0.51
56:B9:16:VAL:HG22	56:B9:25:VAL:HG22	1.92	0.51
26:BA:2138:G:H2'	26:BA:2139:A:C5	2.45	0.51
26:BA:2639:G:O2'	26:BA:2794:A:N1	2.35	0.51
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.90	0.51
1:CA:200:G:H2'	1:CA:201:C:O4'	2.09	0.51
1:CA:79:G:H8	1:CA:79:G:OP2	1.92	0.51
26:DA:2249:U:N3	26:DA:2253:G:OP2	2.35	0.51
26:DA:2515:C:H2'	26:DA:2516:G:H8	1.75	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.44	0.51
26:DA:271(Q):G:H2'	26:DA:271(R):G:C8	2.45	0.51
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.10	0.51
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.43	0.51
1:AA:1277:C:H1'	1:AA:1282:C:C2	2.46	0.51
4:AD:128:VAL:HG12	4:AD:129:ASN:HD22	1.75	0.51
5:AE:10:MET:HB2	5:AE:13:ILE:HD11	1.91	0.51
27:BB:11:C:H3'	27:BB:12:C:C6	2.44	0.51
39:BS:74:ALA:O	39:BS:78:LEU:HD23	2.11	0.51
1:CA:1153:C:H42	1:CA:1154:G:N2	2.08	0.51
1:CA:1191:A:OP1	3:CC:4:LYS:HG3	2.10	0.51
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.39	0.51
9:CI:53:VAL:C	9:CI:55:ALA:H	2.11	0.51
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.76	0.51
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.93	0.51
26:DA:539:G:H2'	26:DA:540:C:C6	2.44	0.51
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.46	0.51
26:DA:7:G:H2'	26:DA:8:A:H8	1.74	0.51
37:DQ:16:ARG:HG2	37:DQ:18:LYS:HE2	1.91	0.51
1:AA:649:G:H2'	1:AA:650:G:C8	2.44	0.51
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.45	0.51
37:BQ:86:GLY:HA3	47:B0:10:THR:CG2	2.41	0.51
26:BA:2374:G:OP1	55:B8:44:LYS:NZ	2.36	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2605:U:H2'	26:BA:2606:C:C6	2.45	0.51
33:BI:6:LEU:HG	33:BI:36:ALA:HA	1.93	0.51
1:CA:352:C:O2'	1:CA:354:G:OP1	2.18	0.51
1:CA:56:U:H2'	1:CA:57:G:C8	2.45	0.51
4:CD:129:ASN:HD21	4:CD:144:ASP:CG	2.13	0.51
4:CD:133:VAL:HG11	4:CD:138:TYR:HD2	1.76	0.51
7:CG:116:ALA:O	7:CG:120:ILE:HG13	2.10	0.51
26:DA:2104:G:O2'	26:DA:2105:C:O5'	2.26	0.51
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.51
26:DA:2471:C:H2'	26:DA:2472:G:O4'	2.11	0.51
27:DB:33:G:C2	27:DB:50:G:C2	2.98	0.51
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.23	0.51
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.11	0.51
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.46	0.51
1:AA:406:G:H21	4:AD:119:GLN:HE22	1.58	0.51
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.43	0.51
26:BA:1464:G:O2'	26:BA:1627:A:N6	2.42	0.51
26:BA:2156:A:H2'	26:BA:2156:A:N3	2.25	0.51
26:BA:2204:G:H2'	26:BA:2205:C:C6	2.45	0.51
26:BA:2420:U:H2'	26:BA:2421:G:C8	2.45	0.51
26:BA:909:G:O2'	27:BB:78:A:N3	2.40	0.51
30:BF:155:LEU:HD11	30:BF:176:LEU:HD12	1.92	0.51
37:BQ:110:THR:OG1	37:BQ:111:GLU:N	2.44	0.51
38:BR:70:LEU:HD13	38:BR:75:LEU:HD13	1.91	0.51
1:CA:1417:G:N2	1:CA:1482:G:H2'	2.25	0.51
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.11	0.51
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.43	0.51
1:CA:165:C:H2'	1:CA:166:G:C8	2.46	0.51
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.43	0.51
1:CA:1348:U:H5''	9:CI:119:ALA:HB3	1.93	0.51
1:CA:523:A:C2	12:CL:91:LYS:HB3	2.45	0.51
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.91	0.51
26:DA:1155:A:H5''	41:DU:55:ARG:HD3	1.92	0.51
26:DA:1783:A:N7	61:DA:4364:HOH:O	2.34	0.51
26:DA:1899:G:H2'	26:DA:1899:G:N3	2.25	0.51
26:DA:383:U:H2'	26:DA:385:C:H5	1.75	0.51
26:DA:747:U:O2	26:DA:2014:A:H1'	2.11	0.51
31:DG:145:THR:H	31:DG:148:MET:HE3	1.75	0.51
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.45	0.51
1:AA:270:A:H2'	1:AA:271:C:C6	2.46	0.51
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.46	0.51
1:AA:682:G:H1	1:AA:708:C:H42	1.57	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:20:ARG:O	9:AI:60:ASP:N	2.32	0.51
52:B5:16:ARG:HG2	52:B5:16:ARG:HH11	1.74	0.51
26:BA:1303:C:H5'	30:BF:75:HIS:CE1	2.45	0.51
26:BA:1552:C:C2'	26:BA:1553:A:H5'	2.41	0.51
26:BA:211:A:N1	26:BA:222:A:H5''	2.25	0.51
26:BA:2149:G:C6	26:BA:2184:G:C2	2.99	0.51
26:BA:588:C:H4'	26:BA:1299:A:C6	2.46	0.51
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.26	0.51
1:CA:427:U:H5'	4:CD:41:GLY:HA2	1.92	0.51
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.41	0.51
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.91	0.51
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.91	0.51
26:DA:752:A:P	54:D7:3:ARG:HH22	2.34	0.51
26:DA:1448:G:O2'	26:DA:1528(A):A:N1	2.34	0.51
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.09	0.51
26:DA:375:C:H2'	26:DA:376:C:C6	2.46	0.51
26:DA:646:A:H2'	26:DA:647:G:O4'	2.10	0.51
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.10	0.51
33:DI:122:GLU:HB2	33:DI:126:TYR:OH	2.10	0.51
40:DT:64:ARG:NH1	40:DT:103:ARG:HA	2.25	0.51
1:AA:1276:G:H2'	1:AA:1277:C:H6	1.75	0.51
1:AA:189(D):C:O2	1:AA:189(H):G:N1	2.44	0.51
1:AA:193:C:H2'	1:AA:194:C:C6	2.45	0.51
1:AA:517:G:N2	1:AA:533:A:OP2	2.39	0.51
7:AG:78:ARG:HE	7:AG:156:TRP:HE3	1.57	0.51
19:AS:68:GLY:H	51:B4:58:ARG:HE	1.59	0.51
26:BA:1072:U:H4'	26:BA:1073:A:OP1	2.10	0.51
26:BA:555:G:C5	26:BA:2044:U:H5''	2.45	0.51
26:BA:835:A:OP1	26:BA:838:C:N4	2.40	0.51
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.46	0.51
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.45	0.51
1:CA:432:A:H5''	1:CA:433:C:OP2	2.11	0.51
1:CA:448:A:O5'	1:CA:485:G:N2	2.34	0.51
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.93	0.51
11:CK:34:ASP:OD1	11:CK:36:ASP:N	2.44	0.51
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.92	0.51
50:D3:29:ARG:N	50:D3:33:GLN:OE1	2.39	0.51
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.15	0.51
27:DB:8:U:H6	27:DB:8:U:H5''	1.75	0.51
1:AA:1136:U:H5''	1:AA:1137:C:N3	2.25	0.51
1:AA:1172:C:N4	1:AA:1173:G:O6	2.44	0.51
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.41	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.91	0.51
26:BA:1718:U:HO2'	26:BA:1720:U:H5	1.57	0.51
26:BA:265:U:H2'	26:BA:266:C:C6	2.45	0.51
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.46	0.51
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.91	0.51
1:CA:376:G:H4'	16:CP:5:ARG:HD3	1.91	0.51
20:CT:29:LYS:HD2	20:CT:71:THR:HG21	1.93	0.51
26:DA:1469:A:H2'	26:DA:1470:G:O4'	2.10	0.51
26:DA:2080:G:O2'	26:DA:2081:C:H5'	2.10	0.51
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.93	0.51
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.74	0.51
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.45	0.51
1:AA:57:G:H2'	1:AA:58:C:C6	2.46	0.51
1:AA:735:C:H2'	1:AA:736:C:H6	1.76	0.51
1:AA:731:G:H5'	1:AA:766:A:H4'	1.93	0.51
1:AA:975:A:H4'	1:AA:976:G:C5'	2.38	0.51
20:AT:38:LYS:HA	20:AT:41:ILE:HD12	1.93	0.51
26:BA:119:G:H4'	26:BA:149:A:H5'	1.93	0.51
26:BA:1223:C:H2'	26:BA:1224:C:C6	2.46	0.51
26:BA:2867:G:N2	26:BA:2870:A:OP2	2.37	0.51
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.93	0.51
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.93	0.51
34:BN:47:ALA:HB2	34:BN:112:LEU:HD11	1.93	0.51
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.45	0.51
1:CA:1340:A:O2'	24:CX:31:G:O2'	2.14	0.51
1:CA:793:U:C4	1:CA:1517:G:H5''	2.46	0.51
7:CG:74:GLU:HG2	7:CG:91:VAL:HG22	1.92	0.51
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.11	0.51
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.93	0.51
26:DA:2218:U:O2	48:D1:52:ARG:NH2	2.44	0.51
26:DA:1186:G:C2	26:DA:1187:G:H1'	2.46	0.51
26:DA:2118:U:OP1	26:DA:2148:G:O2'	2.16	0.51
26:DA:632:A:H2'	26:DA:633:A:C8	2.46	0.51
26:DA:817:C:O2'	26:DA:839:U:OP1	2.25	0.51
30:DF:125:LEU:HD22	30:DF:196:LEU:HD23	1.93	0.51
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.10	0.51
1:AA:1311:G:H1	1:AA:1326:C:N4	2.09	0.51
1:AA:369:C:H42	1:AA:392:G:H1	1.59	0.51
1:AA:7:G:H5'	1:AA:298:A:O4'	2.11	0.51
1:AA:407:G:OP1	4:AD:3:ARG:NH1	2.43	0.51
1:AA:1125:U:H4'	10:AJ:5:ARG:HH12	1.76	0.51
26:BA:1074:A:N6	26:BA:1171:G:H2'	2.25	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:956:A:N1	26:BA:2289:G:H1'	2.25	0.51
26:BA:2445:A:OP2	61:BA:4119:HOH:O	2.19	0.51
15:AO:56:LEU:HD21	26:BA:762:G:C2	2.46	0.51
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.25	0.51
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.91	0.51
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.11	0.51
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.42	0.51
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.93	0.51
48:D1:80:LEU:HB3	48:D1:82:LEU:HG	1.93	0.51
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.37	0.51
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.45	0.51
26:DA:1710:C:H2'	26:DA:1711:C:H6	1.75	0.51
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.46	0.51
26:DA:2330:G:H2'	26:DA:2331:G:O4'	2.11	0.51
29:DE:179:GLU:HB3	29:DE:181:LEU:HD22	1.93	0.51
35:DO:98:VAL:HG13	35:DO:117:LEU:HB3	1.93	0.51
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.46	0.51
1:AA:345:C:H4'	1:AA:346:G:C4	2.46	0.51
1:AA:765:G:N1	1:AA:812:C:O2'	2.36	0.51
1:AA:979:C:H2'	1:AA:980:C:H5'	1.93	0.51
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.51
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.10	0.51
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.11	0.51
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.25	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.93	0.51
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.10	0.51
1:CA:1046:A:H61	1:CA:1213:A:N6	2.09	0.51
1:CA:1269:A:H2	1:CA:1312:G:N3	2.09	0.51
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.40	0.51
1:CA:413:G:N2	1:CA:428:G:H1'	2.26	0.51
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.11	0.51
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.59	0.51
1:CA:1187:G:N2	14:CN:60:SER:OG	2.36	0.51
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.11	0.51
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.31	0.51
26:DA:208:C:H2'	26:DA:209:C:C6	2.46	0.51
26:DA:2615:U:C2	52:D5:7:PRO:HA	2.46	0.51
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.11	0.51
31:DG:138:GLN:HB3	31:DG:153:ARG:O	2.11	0.51
26:DA:2728:U:H5'	35:DO:70:LYS:HZ3	1.76	0.51
41:DU:17:ILE:HG23	41:DU:39:LEU:HD12	1.92	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1255:G:H1	1:AA:1282:C:H42	1.58	0.50
1:AA:1291:G:O3'	7:AG:41:ARG:NH2	2.44	0.50
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.92	0.50
26:BA:1046:A:H62	26:BA:1200:G:H2'	1.77	0.50
26:BA:142:G:H1'	44:BX:37:THR:HG21	1.93	0.50
26:BA:206:G:OP2	61:BA:4821:HOH:O	2.19	0.50
26:BA:2623:U:C4	52:B5:3:LYS:HG2	2.45	0.50
35:BO:10:VAL:HG13	35:BO:17:ARG:C	2.31	0.50
1:CA:1288:A:H2'	1:CA:1289:A:C8	2.46	0.50
1:CA:495:A:H4'	1:CA:496:A:OP1	2.12	0.50
1:CA:839:U:H5''	1:CA:840:C:C5	2.42	0.50
1:CA:899:C:O5'	1:CA:899:C:H6	1.94	0.50
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.11	0.50
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.92	0.50
13:CM:82:MET:HE3	13:CM:92:HIS:HB3	1.91	0.50
1:CA:1014:A:P	19:CS:18:LYS:HZ1	2.34	0.50
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.12	0.50
26:DA:2171:A:H1'	26:DA:2172:U:O4'	2.11	0.50
26:DA:39:C:H2'	26:DA:40:C:C6	2.46	0.50
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.92	0.50
1:AA:1142:G:H2'	1:AA:1143:G:O4'	2.11	0.50
1:AA:1164:G:N7	1:AA:1173:G:N3	2.59	0.50
1:AA:130:A:O2'	1:AA:131:C:O5'	2.25	0.50
1:AA:339:C:H2'	1:AA:340:U:C6	2.46	0.50
26:BA:1501:U:O2'	26:BA:1502:G:N7	2.41	0.50
28:BD:97:TYR:CE1	28:BD:103:ARG:HG3	2.45	0.50
30:BF:167:ALA:HB1	30:BF:173:VAL:HG11	1.91	0.50
1:CA:1000:U:O2	1:CA:1041:A:N1	2.45	0.50
1:CA:1310:G:H1	1:CA:1327:C:H42	1.59	0.50
1:CA:438:G:OP1	4:CD:125:HIS:NE2	2.30	0.50
1:CA:763:G:C2'	1:CA:764:C:H5'	2.41	0.50
1:CA:790:A:H2'	1:CA:791:G:C8	2.46	0.50
2:CB:51:LEU:HD23	2:CB:201:ILE:HD12	1.92	0.50
4:CD:67:ILE:HD13	4:CD:196:LEU:HD23	1.94	0.50
54:D7:9:ARG:HH21	54:D7:47:ARG:HD2	1.77	0.50
26:DA:1417:C:H2'	26:DA:1418:G:O4'	2.10	0.50
26:DA:1523:U:H2'	26:DA:1524:G:O4'	2.11	0.50
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.76	0.50
26:DA:1130:U:O2	26:DA:2025:C:H5''	2.12	0.50
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.46	0.50
26:DA:2162:G:H4'	26:DA:2172:U:C2'	2.39	0.50
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.44	0.50
34:DN:15:LEU:HB2	34:DN:135:PRO:HB2	1.94	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
1:AA:631:G:H2'	1:AA:632:A:C8	2.45	0.50
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.52	0.50
19:AS:32:LYS:HE3	19:AS:57:HIS:CD2	2.46	0.50
26:BA:1539:C:C5	26:BA:2227:G:H1'	2.46	0.50
26:BA:1713:G:C2'	26:BA:1714:G:H5'	2.40	0.50
26:BA:597:C:N4	26:BA:2056:U:OP1	2.36	0.50
26:BA:2149:G:O6	26:BA:2184:G:N1	2.43	0.50
26:BA:2257:U:H5''	26:BA:2258:G:H5'	1.92	0.50
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.93	0.50
1:CA:170:U:O2'	1:CA:171:A:H5'	2.11	0.50
1:CA:791:G:C6	1:CA:792:A:N7	2.79	0.50
6:CF:99:ALA:HB2	18:CR:31:LEU:HD21	1.92	0.50
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.93	0.50
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.44	0.50
26:DA:1375:C:H2'	26:DA:1376:C:H6	1.76	0.50
31:DG:44:GLY:O	31:DG:47:LYS:HB3	2.12	0.50
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.12	0.50
1:AA:432:A:H5''	1:AA:433:C:OP2	2.10	0.50
1:AA:79:G:C2	1:AA:90:U:O2	2.64	0.50
1:AA:903:G:OP1	61:AA:4029:HOH:O	2.19	0.50
1:AA:264:U:O2'	17:AQ:64:PRO:O	2.26	0.50
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.93	0.50
26:BA:1170:C:H1'	56:B9:36:GLN:NE2	2.27	0.50
26:BA:1815:A:H4'	26:BA:1816:A:O5'	2.12	0.50
27:BB:13:A:N1	27:BB:69:G:O2'	2.33	0.50
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.43	0.50
31:BG:106:LEU:HA	31:BG:110:ALA:HB3	1.93	0.50
26:BA:2697:G:H5'	35:BO:68:GLU:OE1	2.11	0.50
46:BZ:144:LEU:HD23	46:BZ:148:ASP:HB2	1.92	0.50
1:CA:1009:G:C2	1:CA:1010:G:C8	2.99	0.50
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.59	0.50
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
13:CM:16:ASP:HB2	13:CM:30:ALA:HB1	1.93	0.50
26:DA:12:U:O2	26:DA:2626:C:H4'	2.12	0.50
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.46	0.50
26:DA:2175:C:H2'	26:DA:2176:A:O4'	2.12	0.50
27:DB:95:C:H2'	27:DB:96:U:C6	2.47	0.50
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.91	0.50
33:DI:110:ASP:HB3	33:DI:130:TYR:OH	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:DR:47:PHE:O	38:DR:51:LEU:HG	2.11	0.50
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.77	0.50
1:AA:189(C):C:H42	1:AA:189(H):G:H1	1.58	0.50
1:AA:521:G:O6	12:AL:53:ARG:NH2	2.44	0.50
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.77	0.50
26:BA:1566:U:H2'	26:BA:1567:G:O4'	2.11	0.50
26:BA:2638:C:H2'	26:BA:2639:G:O4'	2.11	0.50
26:BA:2816:G:H2'	26:BA:2817:G:C8	2.46	0.50
26:BA:211:A:H3'	26:BA:448:U:H5'	1.93	0.50
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.27	0.50
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.92	0.50
1:CA:613:C:H2'	1:CA:614:A:H8	1.75	0.50
1:CA:620:C:C2	4:CD:135:LEU:HG	2.46	0.50
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.92	0.50
9:CI:26:VAL:HG22	9:CI:61:ALA:HB3	1.93	0.50
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.47	0.50
51:D4:15:ILE:HG23	51:D4:21:VAL:HG22	1.92	0.50
27:DB:106:G:H5''	46:DZ:31:ARG:HG2	1.93	0.50
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.11	0.50
1:AA:202:U:O2'	1:AA:203:U:O5'	2.25	0.50
1:AA:451:A:N6	1:AA:480:U:H2'	2.26	0.50
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.77	0.50
26:BA:1410:G:P	48:B1:3:LYS:HG3	2.51	0.50
26:BA:864:C:OP1	61:BA:4091:HOH:O	2.19	0.50
30:BF:102:PRO:HB2	30:BF:105:VAL:HG23	1.92	0.50
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.47	0.50
2:CB:24:TRP:CZ3	2:CB:26:PRO:HA	2.46	0.50
13:CM:60:VAL:HG23	13:CM:64:TRP:HZ3	1.77	0.50
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.25	0.50
26:DA:2128:C:H5'	26:DA:2173:A:H2	1.75	0.50
26:DA:2396:G:OP1	48:D1:25:LYS:NZ	2.29	0.50
26:DA:2807:G:C6	26:DA:2808:U:C4	3.00	0.50
26:DA:995:C:OP2	41:DU:54:LYS:NZ	2.36	0.50
27:DB:24:G:H4'	27:DB:25:A:N7	2.26	0.50
33:DI:130:TYR:CE2	33:DI:132:PRO:HB3	2.46	0.50
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.12	0.50
45:DY:76:CYS:HA	45:DY:106:LEU:HD22	1.93	0.50
46:DZ:120:ILE:HD11	46:DZ:173:ALA:HB3	1.94	0.50
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.11	0.50
26:BA:2692:C:OP2	29:BE:111:ARG:NH2	2.44	0.50
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.92	0.50
33:BI:3:VAL:HG12	33:BI:38:LEU:HA	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
26:BA:2696:U:H1'	35:BO:70:LYS:HD2	1.94	0.50
1:CA:1201:A:H4'	1:CA:1202:G:O5'	2.12	0.50
1:CA:137:C:C2	1:CA:227:G:C2	3.00	0.50
1:CA:828:A:H2'	1:CA:829:G:O4'	2.12	0.50
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	1.94	0.50
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.50
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.27	0.50
26:DA:2001:A:OP1	38:DR:9:LYS:NZ	2.33	0.50
26:DA:912:C:OP1	37:DQ:9:TYR:OH	2.19	0.50
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.45	0.50
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.26	0.50
37:DQ:27:VAL:HG21	37:DQ:134:ARG:HA	1.93	0.50
1:AA:1007:C:C2'	1:AA:1008:C:H5''	2.34	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.47	0.50
24:AX:50:U:H2'	24:AX:51:C:C6	2.46	0.50
26:BA:1229:G:H5'	50:B3:29:ARG:NH1	2.26	0.50
26:BA:1342:G:OP1	26:BA:2721:G:O2'	2.21	0.50
26:BA:1899:A:H5'	26:BA:1900:G:OP2	2.12	0.50
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.50
1:CA:1162:C:N4	1:CA:1174:G:N1	2.35	0.50
1:CA:1493:A:H2'	26:DA:1913:A:H61	1.76	0.50
1:CA:17:U:H2'	1:CA:18:C:C6	2.47	0.50
1:CA:338:A:H2	1:CA:351:G:H22	1.60	0.50
1:CA:501:C:H1'	1:CA:549:C:H1'	1.94	0.50
1:CA:613:C:H2'	1:CA:614:A:C8	2.47	0.50
1:CA:407:G:H5''	4:CD:115:ARG:HB3	1.93	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50
1:CA:1400:C:N4	24:CX:35:A:C8	2.79	0.50
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.55	0.50
26:DA:1756:G:H4'	26:DA:1758:G:O4'	2.12	0.50
26:DA:184:C:H2'	26:DA:185:U:C6	2.47	0.50
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.47	0.50
26:DA:2130:U:O2	26:DA:2134:A:O2'	2.30	0.50
26:DA:271(W):G:O6	61:DA:4210:HOH:O	2.14	0.50
26:DA:366:C:H5''	26:DA:370:G:H5'	1.92	0.50
26:DA:781:A:P	28:DD:218:ARG:HH22	2.34	0.50
29:DE:77:ILE:HD12	29:DE:195:LEU:HD13	1.93	0.50
29:DE:7:VAL:HG13	29:DE:27:LEU:HB3	1.94	0.50
36:DP:25:SER:N	61:DP:311:HOH:O	2.40	0.50
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	1.92	0.50
26:BA:2050:U:H2'	26:BA:2051:G:O4'	2.11	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:611:U:H1'	30:BF:90:PHE:CG	2.47	0.50
26:BA:624:C:O2'	26:BA:628:C:H5''	2.11	0.50
26:BA:637:U:H5'	26:BA:640:A:N6	2.27	0.50
33:BI:100:ALA:HA	33:BI:103:ARG:HG2	1.93	0.50
44:BX:26:TYR:HB3	44:BX:92:LEU:HD22	1.93	0.50
1:CA:1502:A:H2	1:CA:1505:G:N1	2.03	0.50
1:CA:91:C:H2'	1:CA:92:C:C6	2.47	0.50
1:CA:1104:G:H4'	2:CB:111:ARG:HD2	1.94	0.50
18:CR:50:ILE:HG12	18:CR:70:ILE:HG21	1.93	0.50
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.50
24:CX:65:C:C4	24:CX:66:C:C4	3.00	0.50
19:CS:68:GLY:H	51:D4:58:ARG:NH1	2.10	0.50
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.12	0.50
26:DA:1581:G:H2'	26:DA:1582:C:O4'	2.11	0.50
26:DA:1889:A:N1	26:DA:2234:G:H1'	2.26	0.50
26:DA:1987:G:H2'	26:DA:1988:C:C6	2.46	0.50
26:DA:2079:U:H2'	26:DA:2080:G:O4'	2.12	0.50
26:DA:2377:A:H2'	26:DA:2378:A:C8	2.47	0.50
26:DA:2684:U:H1'	35:DO:70:LYS:HD2	1.94	0.50
26:DA:2809:A:H2'	26:DA:2810:A:C8	2.47	0.50
26:DA:469:G:C2'	26:DA:470:A:H5''	2.42	0.50
26:DA:588:U:H2'	26:DA:589:C:C6	2.47	0.50
27:DB:7:G:N3	39:DS:38:GLN:NE2	2.38	0.50
28:DD:72:LYS:HD3	28:DD:97:TYR:CE2	2.47	0.50
29:DE:36:ARG:HG2	29:DE:47:VAL:HG12	1.93	0.50
1:AA:302:G:O2'	1:AA:556:C:H5''	2.11	0.49
1:AA:664:G:P	18:AR:64:ARG:HH21	2.35	0.49
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.94	0.49
11:AK:48:ILE:HG21	11:AK:63:LEU:HB3	1.93	0.49
24:AX:49:G:N2	24:AX:65:C:N3	2.50	0.49
26:BA:1093:G:H1'	26:BA:1156:G:N2	2.27	0.49
26:BA:1189:A:OP1	34:BN:25:ARG:NH2	2.45	0.49
26:BA:2398:C:H2'	26:BA:2399:U:C6	2.47	0.49
26:BA:2575:U:H4'	35:BO:28:SER:HA	1.94	0.49
26:BA:2623:U:H6	26:BA:2623:U:H5'	1.77	0.49
26:BA:26:G:C6	26:BA:27:G:N1	2.80	0.49
26:BA:776:G:C6	28:BD:208:LYS:HB2	2.47	0.49
32:BH:12:PRO:O	32:BH:15:VAL:HG13	2.12	0.49
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.12	0.49
1:CA:696:A:H8	1:CA:696:A:O5'	1.95	0.49
2:CB:200:ILE:H	2:CB:200:ILE:HD13	1.77	0.49
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.10	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1227:A:N3	19:CS:83:HIS:HB3	2.27	0.49
31:DG:179:PRO:HG3	51:D4:43:TYR:OH	2.12	0.49
26:DA:1163:G:OP1	42:DV:24:LYS:NZ	2.34	0.49
26:DA:718:A:H3'	26:DA:719:C:H6	1.77	0.49
26:DA:71:A:H5''	26:DA:73:A:C8	2.47	0.49
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.94	0.49
27:DB:27:C:C4	27:DB:28:C:C4	3.00	0.49
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.60	0.49
26:DA:831:G:O2'	36:DP:38:GLN:NE2	2.45	0.49
1:AA:362:G:N1	1:AA:365:U:OP2	2.45	0.49
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.45	0.49
10:AJ:39:PRO:HA	10:AJ:70:ARG:HD3	1.93	0.49
26:BA:2108:U:H2'	26:BA:2109:G:H8	1.78	0.49
26:BA:2129:C:N4	26:BA:2204:G:H1	2.07	0.49
26:BA:2227:G:H5'	26:BA:2228:G:N7	2.27	0.49
26:BA:10:G:N2	26:BA:2813:G:OP1	2.31	0.49
26:BA:430:U:H4'	26:BA:431:C:H5'	1.93	0.49
1:CA:958:A:N6	19:CS:77:THR:O	2.45	0.49
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.77	0.49
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.49
15:CO:81:LEU:O	15:CO:84:LYS:HG2	2.13	0.49
23:CW:76:PPU:HM2	26:DA:2452:C:N3	2.27	0.49
26:DA:2165:G:O6	26:DA:2171:A:H8	1.95	0.49
26:DA:781:A:OP1	28:DD:218:ARG:NH2	2.45	0.49
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.44	0.49
1:AA:1024:G:C2'	1:AA:1025:U:H5'	2.41	0.49
1:AA:353:A:H8	1:AA:353:A:H5'	1.76	0.49
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.94	0.49
16:AP:19:ILE:N	16:AP:37:GLY:O	2.45	0.49
26:BA:2044:U:O2'	26:BA:2629:C:H5'	2.11	0.49
28:BD:85:ASP:OD2	28:BD:88:ARG:NH1	2.44	0.49
26:BA:1058:U:H5	34:BN:28:THR:HG21	1.77	0.49
26:BA:2877:G:OP2	40:BT:119:LYS:NZ	2.45	0.49
40:BT:45:PHE:CE2	40:BT:65:LYS:HD3	2.47	0.49
1:CA:1029:C:N3	1:CA:1032:G:C2	2.80	0.49
1:CA:89:C:H2'	1:CA:90:U:O4'	2.12	0.49
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.48	0.49
24:CX:47:U:H3'	24:CX:48:C:H5'	1.93	0.49
52:D5:41:PRO:O	52:D5:44:THR:OG1	2.24	0.49
26:DA:330:A:H2	26:DA:1210:A:H2'	1.78	0.49
26:DA:1212:G:O2'	26:DA:1235:G:O6	2.30	0.49
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2035:G:H4'	61:DA:4092:HOH:O	2.11	0.49
26:DA:2458:G:O2'	26:DA:2460:U:O4	2.21	0.49
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.76	0.49
45:DY:94:LYS:NZ	61:DY:601:HOH:O	2.44	0.49
1:AA:1068:G:N2	1:AA:1191:A:N3	2.56	0.49
1:AA:158:G:N2	1:AA:163:C:O2	2.39	0.49
1:AA:36:C:O2'	12:AL:117:ARG:NH2	2.45	0.49
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.30	0.49
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.95	0.49
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.12	0.49
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.12	0.49
26:BA:213:G:H2'	26:BA:214:A:O4'	2.12	0.49
23:AW:76:PPU:H2'	26:BA:2596:U:O2'	2.13	0.49
26:BA:2673:G:H2'	26:BA:2674:A:C8	2.47	0.49
27:BB:89:G:O6	27:BB:90:A:N6	2.46	0.49
29:BE:11:MET:HG2	29:BE:24:THR:HB	1.93	0.49
31:BG:74:LYS:O	31:BG:84:LYS:NZ	2.42	0.49
26:BA:662:A:H8	36:BP:117:GLU:HG3	1.78	0.49
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.95	0.49
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.12	0.49
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.95	0.49
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.93	0.49
26:DA:2123:G:H1	26:DA:2175:C:N4	2.10	0.49
26:DA:2783:G:H2'	26:DA:2784:C:C6	2.47	0.49
26:DA:469:G:H2'	26:DA:470:A:H5''	1.95	0.49
26:DA:774:A:N3	26:DA:774:A:H2'	2.27	0.49
26:DA:568:U:H5'	26:DA:945:A:N1	2.26	0.49
28:DD:118:VAL:N	28:DD:129:ASN:OD1	2.41	0.49
26:DA:1798:U:OP2	28:DD:274:ARG:NH2	2.45	0.49
31:DG:98:ARG:HA	31:DG:101:ILE:HB	1.93	0.49
31:DG:14:GLU:O	31:DG:17:PRO:HD2	2.12	0.49
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.93	0.49
1:AA:1494:G:H4'	26:BA:1935:A:C8	2.47	0.49
2:AB:162:ILE:O	2:AB:185:ILE:HG13	2.13	0.49
7:AG:68:ASN:O	7:AG:138:LYS:HE2	2.11	0.49
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.95	0.49
20:AT:67:ALA:C	20:AT:69:GLY:H	2.16	0.49
26:BA:1403:U:H2'	26:BA:1404:G:O4'	2.13	0.49
26:BA:2609:G:OP1	61:BA:4695:HOH:O	2.20	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.48	0.49
29:BE:2:LYS:HB2	29:BE:95:ILE:HD12	1.93	0.49
37:BQ:85:LYS:HD2	37:BQ:85:LYS:N	2.27	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1272:A:OP1	42:BV:84:LYS:HE2	2.13	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.95	0.49
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.72	0.49
1:CA:407:G:N1	1:CA:436:C:N3	2.37	0.49
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.95	0.49
8:CH:82:HIS:HB3	8:CH:138:TRP:NE1	2.26	0.49
16:CP:20:VAL:HG22	16:CP:35:LYS:HA	1.94	0.49
20:CT:46:GLU:HG2	20:CT:46:GLU:O	2.11	0.49
26:DA:1411:C:H2'	26:DA:1412:A:C8	2.47	0.49
26:DA:2808:U:H5''	26:DA:2891:G:O6	2.12	0.49
26:DA:644:A:H4'	26:DA:645:C:C5	2.46	0.49
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.12	0.49
1:AA:1038:C:H2'	1:AA:1039:C:C6	2.48	0.49
1:AA:201:C:H42	1:AA:216:G:H22	1.59	0.49
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	1.95	0.49
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.93	0.49
24:AX:40:C:C2'	24:AX:41:C:H5'	2.43	0.49
13:AM:80:ARG:HH21	51:B4:58:ARG:HH11	1.59	0.49
26:BA:1760:U:H2'	26:BA:1761:G:C8	2.46	0.49
26:BA:215:G:H21	26:BA:217:A:H62	1.59	0.49
26:BA:2859:U:H4'	26:BA:2878:A:C2	2.48	0.49
30:BF:110:LEU:HD21	30:BF:181:LEU:HG	1.93	0.49
1:CA:1004:A:N6	1:CA:1037:C:C2	2.81	0.49
1:CA:1237:C:H5''	1:CA:1238:A:O4'	2.12	0.49
1:CA:609:A:C2'	1:CA:610:G:H5'	2.42	0.49
16:CP:22:THR:HA	16:CP:33:ILE:HG12	1.94	0.49
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.78	0.49
24:CX:3:C:C2'	24:CX:4:G:H5''	2.40	0.49
26:DA:2041:U:H2'	26:DA:2042:A:C8	2.46	0.49
26:DA:2158:A:H4'	26:DA:2159:G:OP1	2.12	0.49
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.48	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.12	0.49
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.48	0.49
27:DB:6:C:C2	27:DB:116:G:N2	2.81	0.49
32:DH:70:THR:O	32:DH:74:ASN:N	2.39	0.49
1:AA:1200:C:OP1	61:AA:4099:HOH:O	2.20	0.49
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.47	0.49
1:AA:270:A:H2'	1:AA:271:C:H6	1.78	0.49
1:AA:49:U:O4	1:AA:365:U:H5	1.95	0.49
4:AD:20:TYR:CD2	4:AD:26:CYS:HB3	2.48	0.49
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.93	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1739:U:H2'	26:BA:1741:C:C5	2.48	0.49
26:BA:2172:U:H2'	26:BA:2173:G:H8	1.77	0.49
26:BA:30:G:H2'	26:BA:31:C:C6	2.47	0.49
26:BA:567:C:H2'	26:BA:568:C:C6	2.48	0.49
26:BA:992:G:H2'	26:BA:993:G:C8	2.48	0.49
38:BR:37:THR:HA	38:BR:111:LEU:HD12	1.95	0.49
1:CA:1015:A:H1'	1:CA:1219:U:H5'	1.94	0.49
1:CA:1394:A:N6	1:CA:1501:C:H5'	2.28	0.49
1:CA:539:A:H2'	1:CA:540:G:C8	2.48	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HB2	1.77	0.49
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.45	0.49
26:DA:1570:A:H2'	26:DA:1571:A:C8	2.47	0.49
26:DA:1754:C:OP1	40:DT:96:ARG:HD2	2.13	0.49
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.48	0.49
26:DA:2117:A:N1	26:DA:2171:A:N1	2.60	0.49
26:DA:2121:G:C6	26:DA:2177:C:N4	2.80	0.49
26:DA:2107:C:N4	26:DA:2182:G:H1	2.07	0.49
26:DA:2259:G:H1'	26:DA:2427:C:H2'	1.93	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.24	0.49
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.42	0.49
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.93	0.49
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.47	0.49
48:B1:50:ARG:HG2	48:B1:59:THR:HB	1.94	0.49
26:BA:484:G:C8	54:B7:37:LYS:HG2	2.48	0.49
26:BA:1851:U:C2	28:BD:202:LYS:HD3	2.47	0.49
26:BA:2149:G:H21	26:BA:2195:A:H1'	1.77	0.49
26:BA:2817:G:H2'	26:BA:2818:U:O4'	2.12	0.49
26:BA:543:G:H2'	26:BA:544:U:C6	2.47	0.49
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.94	0.49
1:CA:999:C:C4	1:CA:1042:G:N1	2.81	0.49
1:CA:22:G:H4'	1:CA:885:G:C8	2.48	0.49
1:CA:460:G:N1	1:CA:470:C:H5'	2.28	0.49
5:CE:69:VAL:HG22	5:CE:71:LEU:HD12	1.94	0.49
13:CM:33:ALA:O	13:CM:37:THR:OG1	2.19	0.49
26:DA:2173:A:C2	26:DA:2174:C:H1'	2.48	0.49
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.13	0.49
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.12	0.49
26:DA:610:G:N2	26:DA:619:G:H1'	2.27	0.49
28:DD:43:ARG:HA	28:DD:48:ARG:O	2.13	0.49
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.95	0.49
26:DA:1665:A:H4'	35:DO:67:LYS:HB2	1.94	0.49
39:DS:87:PHE:HB2	39:DS:112:PHE:CE2	2.48	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
43:DW:58:ALA:HB1	43:DW:64:MET:HB2	1.95	0.49
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.36	0.49
1:AA:509:A:N3	1:AA:543:C:O2'	2.35	0.49
1:AA:555:C:H2'	1:AA:556:C:C6	2.47	0.49
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.46	0.49
26:BA:510:C:H2'	26:BA:511:C:C6	2.48	0.49
26:BA:2740:G:O2'	35:BO:70:LYS:NZ	2.43	0.49
36:BP:124:LYS:HE3	36:BP:146:VAL:HG21	1.93	0.49
40:BT:116:ALA:HB1	40:BT:121:ILE:HD11	1.94	0.49
43:BW:68:ARG:HD3	43:BW:111:HIS:HA	1.95	0.49
1:CA:1154:G:N7	1:CA:1155:G:N7	2.61	0.49
1:CA:1235:U:O2'	1:CA:1305:G:OP1	2.28	0.49
1:CA:1314:C:H2'	1:CA:1315:U:C6	2.48	0.49
1:CA:713:G:H2'	1:CA:714:G:C8	2.46	0.49
1:CA:715:A:H2'	1:CA:716:A:C8	2.47	0.49
4:CD:108:LEU:HD23	4:CD:110:PHE:CZ	2.47	0.49
26:DA:1788:C:OP1	28:DD:222:ARG:NH2	2.45	0.49
26:DA:2103:C:C2	26:DA:2187:G:C2	3.01	0.49
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.13	0.49
27:DB:48:A:P	39:DS:30:ARG:HH12	2.36	0.49
26:DA:468:G:H5''	30:DF:60:SER:HB2	1.95	0.49
34:DN:42:TRP:HA	34:DN:48:MET:HE1	1.95	0.49
36:DP:38:GLN:HG2	36:DP:45:LEU:H	1.76	0.49
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.13	0.49
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.47	0.49
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.48	0.49
1:AA:337:C:H2'	1:AA:338:A:C8	2.48	0.49
18:AR:74:ARG:HG3	18:AR:79:LEU:HB2	1.94	0.49
26:BA:2582:G:H2'	26:BA:2583:C:O4'	2.13	0.49
26:BA:782:A:N7	26:BA:808:A:H2	2.11	0.49
26:BA:2584:A:C8	29:BE:144:ARG:HD2	2.47	0.49
30:BF:184:TYR:HE1	36:BP:3:LEU:HD21	1.77	0.49
37:BQ:63:LYS:HE2	46:BZ:118:GLN:NE2	2.27	0.49
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.45	0.49
1:CA:1260:C:OP1	1:CA:1284:C:O2'	2.26	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.47	0.49
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.94	0.49
4:CD:12:CYS:O	4:CD:16:GLY:N	2.46	0.49
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.39	0.49
7:CG:31:MET:HA	7:CG:39:ALA:HB2	1.95	0.49
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.30	0.49
26:DA:127:A:H5''	26:DA:128:C:O4'	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.77	0.49
26:DA:1688:U:H1'	26:DA:1701:A:C6	2.47	0.49
26:DA:1752:C:H2'	26:DA:1753:G:C8	2.48	0.49
26:DA:2207:G:H3'	26:DA:2208:A:H5''	1.95	0.49
28:DD:13:ARG:HD2	28:DD:13:ARG:HA	1.59	0.49
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.42	0.49
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.46	0.49
33:DI:62:LYS:HE2	33:DI:133:HIS:CD2	2.47	0.49
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.95	0.49
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.14	0.48
1:AA:401:C:H2'	1:AA:402:G:C8	2.48	0.48
26:BA:1064:C:O3'	26:BA:1166:G:N2	2.46	0.48
26:BA:2059:G:H2'	26:BA:2060:G:C8	2.48	0.48
26:BA:669:A:H4'	26:BA:670:C:C5	2.48	0.48
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.75	0.48
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.48
26:BA:2762:A:P	32:BH:3:ARG:HH21	2.36	0.48
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.31	0.48
1:CA:1244:C:N4	1:CA:1293:G:N1	2.34	0.48
1:CA:1355:G:H2'	1:CA:1356:G:C8	2.48	0.48
2:CB:142:LEU:HD21	2:CB:146:GLN:HE21	1.78	0.48
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.95	0.48
26:DA:1529:G:C6	26:DA:1530:C:N4	2.81	0.48
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.41	0.48
26:DA:2398:U:H2'	26:DA:2399:G:H8	1.77	0.48
26:DA:2579:C:H2'	26:DA:2580:U:O4'	2.13	0.48
26:DA:709:U:H2'	26:DA:710:G:H8	1.77	0.48
40:DT:64:ARG:HB2	40:DT:73:GLU:HG2	1.94	0.48
1:AA:1002:G:C6	1:AA:1003:G:C2	3.02	0.48
1:AA:1015:A:N3	1:AA:1218:C:O2'	2.44	0.48
1:AA:153:C:N4	1:AA:168:G:H1	2.10	0.48
1:AA:189:G:C6	1:AA:189(L):G:C6	3.01	0.48
1:AA:413:G:N2	1:AA:428:G:H1'	2.28	0.48
1:AA:619:U:N3	4:AD:134:ASP:OD1	2.32	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.48	0.48
9:AI:26:VAL:HG13	9:AI:61:ALA:HB3	1.94	0.48
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	1.95	0.48
26:BA:1615:G:N7	61:BD:401:HOH:O	2.35	0.48
26:BA:1971:G:C6	26:BA:1972:G:C6	3.01	0.48
26:BA:2034:G:OP1	43:BW:11:ARG:NH2	2.43	0.48
26:BA:2158:C:N3	26:BA:2177:G:N2	2.53	0.48
26:BA:989:G:H5''	26:BA:990:A:O5'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:BE:176:ILE:HB	29:BE:181:LEU:HB2	1.94	0.48
41:BU:82:GLY:HA3	41:BU:113:ALA:HB1	1.95	0.48
26:BA:572:A:H61	42:BV:19:LYS:H	1.61	0.48
1:CA:130:A:O2'	1:CA:131:C:O5'	2.29	0.48
1:CA:16:A:C2'	1:CA:17:U:H5'	2.44	0.48
1:CA:189(A):C:H2'	1:CA:189(B):C:H5'	1.94	0.48
1:CA:578:C:OP1	61:CA:4037:HOH:O	2.20	0.48
1:CA:665:A:H1'	1:CA:733:A:O4'	2.13	0.48
1:CA:800:G:H8	1:CA:800:G:O5'	1.96	0.48
1:CA:88:A:H4'	1:CA:89:C:O5'	2.13	0.48
26:DA:1421:G:C2	26:DA:1422:G:N7	2.81	0.48
26:DA:1434:A:H61	26:DA:1558:A:H62	1.60	0.48
26:DA:1860:G:C2	26:DA:1861:G:C8	3.01	0.48
26:DA:218:A:C2	26:DA:235:U:H4'	2.49	0.48
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.95	0.48
26:DA:27:G:N2	26:DA:512:G:H1'	2.29	0.48
26:DA:968:G:H2'	26:DA:969:U:C6	2.48	0.48
26:DA:968:G:H2'	26:DA:969:U:H6	1.78	0.48
1:AA:346:G:C5	1:AA:347:G:H1'	2.47	0.48
1:AA:447:G:O6	1:AA:485:G:O2'	2.27	0.48
1:AA:749:C:H2'	1:AA:750:G:H8	1.78	0.48
2:AB:15:VAL:HG11	2:AB:209:ARG:HG2	1.95	0.48
5:AE:68:GLU:OE1	5:AE:70:PRO:HG3	2.12	0.48
1:AA:728:A:C5	15:AO:54:ARG:HD2	2.49	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
26:BA:1557:A:H2'	26:BA:1558:G:O4'	2.13	0.48
26:BA:2149:G:N2	26:BA:2150:C:O2	2.46	0.48
26:BA:588:C:H4'	26:BA:1299:A:N6	2.28	0.48
26:BA:1400:A:H5''	28:BD:38:LYS:HD3	1.95	0.48
26:BA:1233:U:H4'	42:BV:79:VAL:HG22	1.96	0.48
1:CA:1038:C:H2'	1:CA:1039:C:H6	1.78	0.48
1:CA:1263:C:H2'	1:CA:1264:C:C6	2.48	0.48
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.42	0.48
1:CA:1355:G:N2	1:CA:1367:C:N3	2.53	0.48
1:CA:692:U:H2'	1:CA:694:A:OP2	2.12	0.48
1:CA:975:A:C8	1:CA:975:A:H5'	2.46	0.48
1:CA:975:A:H4'	1:CA:976:G:C5'	2.43	0.48
1:CA:993:G:H2'	1:CA:995:C:H41	1.78	0.48
1:CA:1080:A:H5'	5:CE:14:ARG:NH2	2.28	0.48
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.95	0.48
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.94	0.48
18:CR:37:VAL:HG23	18:CR:79:LEU:HD23	1.94	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1223:C:P	19:CS:78:ARG:HH21	2.36	0.48
24:CX:15:G:H2'	24:CX:59:A:H61	1.78	0.48
26:DA:1422:G:H4'	26:DA:1493:C:OP1	2.13	0.48
26:DA:2282:G:H4'	26:DA:2389:G:O2'	2.13	0.48
26:DA:1297:C:OP1	26:DA:2710:C:H4'	2.13	0.48
26:DA:345:A:N3	26:DA:347:A:N6	2.60	0.48
27:DB:5:C:O2'	27:DB:27:C:O2	2.31	0.48
30:DF:120:GLU:HB3	30:DF:122:LYS:HG2	1.95	0.48
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.47	0.48
1:AA:763:G:H2'	1:AA:764:C:H5'	1.95	0.48
26:BA:1825:U:H2'	26:BA:1826:C:C6	2.48	0.48
26:BA:2152:U:C2'	26:BA:2153:G:H21	2.26	0.48
26:BA:964:A:H5''	27:BB:98:G:O2'	2.14	0.48
29:BE:12:THR:HG21	40:BT:11:GLU:HG2	1.95	0.48
1:CA:1316:G:N2	1:CA:1319:A:OP2	2.42	0.48
1:CA:255:G:OP1	17:CQ:69:LYS:NZ	2.39	0.48
1:CA:735:C:H2'	1:CA:736:C:H6	1.77	0.48
26:DA:1754:C:N3	26:DA:2716:U:O2'	2.44	0.48
26:DA:2126:A:N6	26:DA:2163:C:O4'	2.47	0.48
26:DA:2238:G:H2'	26:DA:2238:G:N3	2.29	0.48
26:DA:598:G:H2'	26:DA:599:G:O4'	2.13	0.48
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.46	0.48
41:DU:50:ARG:HH12	42:DV:72:VAL:HA	1.79	0.48
1:AA:109:A:C6	1:AA:326:G:C6	3.01	0.48
1:AA:657:G:C2	1:AA:658:G:C8	3.02	0.48
1:AA:779:C:OP2	61:AA:4019:HOH:O	2.20	0.48
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	1.94	0.48
20:AT:43:LEU:O	20:AT:47:GLY:N	2.46	0.48
50:B3:19:GLN:OE1	50:B3:52:HIS:NE2	2.45	0.48
26:BA:1634:C:H2'	26:BA:1635:C:H6	1.78	0.48
26:BA:2184:G:H4'	26:BA:2194:U:H2'	1.95	0.48
27:BB:2:C:H2'	27:BB:3:C:C6	2.48	0.48
1:CA:1212:U:H4'	1:CA:1213:A:O5'	2.13	0.48
1:CA:1227:A:OP1	19:CS:80:TYR:OH	2.26	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H5'	1.95	0.48
1:CA:444:C:H2'	1:CA:445:G:H8	1.79	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.02	0.48
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.94	0.48
19:CS:12:ASP:OD2	19:CS:35:SER:HB3	2.12	0.48
44:DX:5:TYR:CZ	49:D2:30:ARG:HB2	2.48	0.48
26:DA:1012:U:OP2	41:DU:70:ARG:NH2	2.33	0.48
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.36	0.48
26:DA:2133:G:C2	26:DA:2157:G:N3	2.81	0.48
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.13	0.48
26:DA:7:G:H5''	34:DN:130:HIS:HE1	1.78	0.48
46:DZ:153:SER:HB3	46:DZ:167:PRO:HB3	1.96	0.48
1:AA:1239:A:H62	1:AA:1299:A:N6	2.12	0.48
1:AA:1349:A:H5''	9:AI:121:ARG:HB2	1.96	0.48
1:AA:1356:G:H2'	1:AA:1357:A:H8	1.76	0.48
1:AA:1392:G:N2	1:AA:1502:A:C8	2.77	0.48
1:AA:161:A:O5'	1:AA:161:A:H8	1.97	0.48
1:AA:186:C:H2'	1:AA:187:C:C6	2.48	0.48
1:AA:392:G:H2'	1:AA:393:A:C8	2.49	0.48
1:AA:797:C:H2'	1:AA:798:G:H5'	1.94	0.48
5:AE:102:ALA:HB1	5:AE:106:PRO:HG2	1.94	0.48
50:B3:50:VAL:O	50:B3:54:VAL:HB	2.14	0.48
26:BA:1843:A:O2'	28:BD:45:ASN:N	2.41	0.48
26:BA:591:U:H5'	26:BA:990:A:C6	2.49	0.48
33:BI:92:VAL:HG22	33:BI:120:ILE:HD12	1.95	0.48
26:BA:83:A:C5'	45:BY:8:LYS:HG2	2.44	0.48
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.95	0.48
1:CA:1078:U:H1'	5:CE:130:ASN:OD1	2.13	0.48
1:CA:1320:C:OP1	19:CS:70:LYS:HE3	2.12	0.48
1:CA:762:C:H2'	1:CA:763:G:H8	1.78	0.48
1:CA:984:C:H2'	1:CA:985:C:H6	1.79	0.48
8:CH:97:VAL:HG21	8:CH:128:GLY:HA2	1.96	0.48
13:CM:86:CYS:SG	13:CM:89:GLY:N	2.87	0.48
26:DA:1204:A:H2	26:DA:1241:A:N6	2.06	0.48
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.43	0.48
26:DA:1798:U:H5'	28:DD:259:THR:CG2	2.43	0.48
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.49	0.48
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.45	0.48
37:DQ:30:GLY:O	37:DQ:134:ARG:HD3	2.14	0.48
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.48	0.48
46:DZ:119:GLU:HG3	46:DZ:122:ARG:HH12	1.78	0.48
46:DZ:97:GLU:HA	46:DZ:127:LYS:HA	1.94	0.48
1:AA:1085:U:OP2	61:AA:4141:HOH:O	2.20	0.48
1:AA:1116:C:N3	1:AA:1184:G:O6	2.46	0.48
1:AA:1452:C:O2'	1:AA:1456:G:H5''	2.13	0.48
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.14	0.48
1:AA:44:G:C2	1:AA:45:U:H1'	2.49	0.48
4:AD:100:ARG:NH1	4:AD:137:SER:OG	2.46	0.48
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.34	0.48
26:BA:1765:U:H2'	26:BA:1766:G:O4'	2.13	0.48
26:BA:2178:G:N2	26:BA:2180:A:N6	2.60	0.48
26:BA:2596:U:H2'	26:BA:2597:U:C6	2.49	0.48
26:BA:2663:C:H2'	26:BA:2664:C:C6	2.48	0.48
26:BA:2846:U:H2'	26:BA:2847:G:C8	2.49	0.48
26:BA:510:C:H2'	26:BA:511:C:H6	1.78	0.48
26:BA:691:G:N2	26:BA:700:A:H1'	2.28	0.48
28:BD:68:LYS:HD3	28:BD:70:TRP:CH2	2.48	0.48
1:CA:953:G:H8	1:CA:953:G:O5'	1.96	0.48
8:CH:64:LYS:HD2	8:CH:79:VAL:HG21	1.96	0.48
26:DA:1815:A:H8	26:DA:1815:A:OP1	1.96	0.48
23:CW:76:PPU:H102	26:DA:2584:U:C5'	2.44	0.48
26:DA:2690:C:N4	26:DA:2713:A:H1'	2.28	0.48
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.13	0.48
26:DA:900:A:H2'	26:DA:901:A:H8	1.79	0.48
27:DB:31:C:N4	27:DB:51:G:O6	2.47	0.48
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.95	0.48
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.94	0.48
1:AA:1171:G:C2'	1:AA:1172:C:H5'	2.44	0.48
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.49	0.48
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.48	0.48
3:AC:82:GLU:HG2	3:AC:85:ARG:HH22	1.78	0.48
4:AD:22:LYS:HB2	4:AD:26:CYS:SG	2.53	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.95	0.48
17:AQ:62:SER:HB3	17:AQ:72:ARG:HD2	1.96	0.48
26:BA:2021:C:H4'	26:BA:2736:C:O2	2.14	0.48
30:BF:34:TRP:HA	36:BP:6:LEU:HD13	1.95	0.48
1:CA:222:U:H2'	1:CA:223:U:C6	2.48	0.48
1:CA:567:G:C2	1:CA:568:G:H1'	2.49	0.48
1:CA:922:G:H1	1:CA:1395:C:H42	1.62	0.48
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.95	0.48
3:CC:71:ALA:HB1	3:CC:109:PRO:HG3	1.96	0.48
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.79	0.48
24:CX:23:C:H2'	24:CX:24:U:H6	1.79	0.48
26:DA:1416:G:H1	26:DA:1582:C:H42	1.62	0.48
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.43	0.48
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.48
26:DA:277:C:HO2'	26:DA:278:A:P	2.34	0.48
26:DA:307:G:N2	26:DA:309:G:H3'	2.29	0.48
26:DA:93:G:H2'	26:DA:94:C:H6	1.78	0.48
27:DB:32:C:C2	27:DB:51:G:N1	2.81	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:DH:56:SER:OG	32:DH:57:ASP:N	2.45	0.48
37:DQ:21:THR:HG21	37:DQ:101:ARG:HD3	1.95	0.48
27:DB:117:G:O2'	39:DS:54:LEU:HD21	2.14	0.48
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.13	0.48
1:AA:292:G:N7	1:AA:293:G:H1'	2.29	0.48
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.13	0.48
12:AL:26:ALA:HB1	12:AL:60:LEU:HD23	1.95	0.48
13:AM:19:LEU:HD21	13:AM:56:LEU:HD21	1.96	0.48
26:BA:1387:U:OP2	26:BA:1440:U:O2'	2.23	0.48
26:BA:1540:A:H2'	26:BA:1541:A:C8	2.48	0.48
26:BA:2724:U:H2'	26:BA:2727:G:H5''	1.95	0.48
31:BG:16:ARG:O	31:BG:20:ILE:HG13	2.14	0.48
26:BA:2331:G:H22	39:BS:3:ARG:HA	1.77	0.48
1:CA:1002:G:H2'	1:CA:1003:G:C8	2.49	0.48
1:CA:1404:C:H2'	1:CA:1405:G:C8	2.49	0.48
1:CA:892:A:O2'	1:CA:1415:G:H4'	2.13	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.49	0.48
1:CA:659:U:H2'	1:CA:660:G:H5'	1.94	0.48
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.48
26:DA:1221:C:H2'	26:DA:1221(A):C:C6	2.48	0.48
26:DA:476:G:H4'	26:DA:502:A:N1	2.28	0.48
26:DA:7:G:H2'	26:DA:8:A:C8	2.49	0.48
27:DB:90:A:N7	27:DB:91:C:H1'	2.29	0.48
33:DI:127:VAL:HA	33:DI:140:LEU:O	2.14	0.48
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.36	0.48
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.48	0.48
1:AA:339:C:OP2	35:BO:97:ARG:HD3	2.14	0.48
4:AD:196:LEU:C	4:AD:198:VAL:H	2.17	0.48
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.96	0.48
2:AB:178:ARG:NH2	8:AH:74:PRO:HB3	2.27	0.48
9:AI:23:ASN:ND2	9:AI:23:ASN:H	2.12	0.48
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.14	0.48
15:AO:84:LYS:HD3	15:AO:84:LYS:O	2.13	0.48
26:BA:1756:U:H2'	26:BA:1757:C:C6	2.49	0.48
26:BA:2014:G:H4'	26:BA:2015:U:C5	2.49	0.48
28:BD:134:ARG:HG2	28:BD:187:GLY:O	2.14	0.48
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.79	0.48
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.14	0.48
1:CA:441:A:H3'	1:CA:442:C:C6	2.49	0.48
4:CD:173:TRP:HB2	4:CD:187:ARG:O	2.14	0.48
4:CD:90:GLY:HA3	4:CD:200:GLU:HG3	1.94	0.48
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.95	0.48
26:DA:1695:G:H8	28:DD:8:PRO:O	1.97	0.48
26:DA:1697:G:OP2	26:DA:1698:A:O2'	2.22	0.48
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.49	0.48
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.27	0.48
26:DA:2773:C:P	29:DE:166:THR:HG1	2.37	0.48
26:DA:2785:C:HO2'	29:DE:66:HIS:CE1	2.30	0.48
26:DA:577:G:H8	26:DA:577:G:O5'	1.97	0.48
26:DA:58:G:O2'	26:DA:73:A:N1	2.43	0.48
26:DA:753:C:H2'	26:DA:754:C:C6	2.49	0.48
26:DA:784:A:H5'	26:DA:785:G:OP1	2.13	0.48
33:DI:93:THR:HA	33:DI:116:LEU:HD13	1.96	0.48
1:AA:1024:G:H2'	1:AA:1024:G:N3	2.28	0.47
1:AA:1258:G:H2'	1:AA:1259:C:H6	1.78	0.47
4:AD:85:LYS:HG3	4:AD:86:LYS:N	2.28	0.47
24:AX:61:C:H2'	24:AX:62:C:H6	1.78	0.47
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.29	0.47
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.29	0.47
54:B7:24:THR:O	54:B7:28:ARG:HG3	2.13	0.47
26:BA:1338:U:H2'	26:BA:1339:C:C6	2.49	0.47
26:BA:2193:A:HO2'	26:BA:2194:U:H6	1.59	0.47
26:BA:2504:U:H2'	26:BA:2505:U:C6	2.49	0.47
26:BA:2641:A:H1'	26:BA:2642:G:H5''	1.96	0.47
26:BA:2901:A:C5	26:BA:2902:G:C6	3.02	0.47
35:BO:69:ILE:HG12	35:BO:77:ILE:HG22	1.96	0.47
26:BA:997:G:P	37:BQ:16:ARG:HH21	2.37	0.47
45:BY:6:HIS:H	45:BY:6:HIS:CD2	2.32	0.47
1:CA:1089:G:C6	1:CA:1090:U:C2	3.02	0.47
1:CA:296:U:O2'	1:CA:556:C:O2	2.30	0.47
2:CB:8:LYS:HA	2:CB:217:ARG:HE	1.79	0.47
3:CC:35:GLU:OE2	3:CC:59:ARG:NH2	2.47	0.47
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.96	0.47
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.43	0.47
7:CG:99:LEU:HA	7:CG:102:ARG:NH1	2.29	0.47
20:CT:37:SER:O	20:CT:41:ILE:HD13	2.14	0.47
26:DA:1206:G:H2'	26:DA:1207:C:C6	2.48	0.47
26:DA:1951:U:O2'	26:DA:1953:A:N7	2.43	0.47
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.49	0.47
26:DA:80:G:H2'	26:DA:81:G:O4'	2.14	0.47
29:DE:119:ARG:HD2	29:DE:120:TRP:CE2	2.49	0.47
29:DE:37:ARG:HB2	29:DE:46:ALA:N	2.29	0.47
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.58	0.47
33:DI:72:LEU:HD13	33:DI:140:LEU:HB2	1.94	0.47
1:AA:973:G:OP1	10:AJ:57:LYS:NZ	2.43	0.47
2:AB:174:VAL:HG13	2:AB:184:VAL:HG11	1.95	0.47
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.13	0.47
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.33	0.47
26:BA:83:A:H5'	45:BY:8:LYS:HG2	1.95	0.47
1:CA:1027:C:N4	1:CA:1034:G:N1	2.61	0.47
1:CA:1002:G:N2	1:CA:1039:C:C4	2.82	0.47
1:CA:66:G:OP1	1:CA:66:G:H8	1.97	0.47
1:CA:78:G:N2	1:CA:92:C:O2	2.47	0.47
1:CA:974:A:H8	1:CA:974:A:OP1	1.97	0.47
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.96	0.47
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.95	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.79	0.47
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.31	0.47
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.49	0.47
26:DA:236:C:H2'	26:DA:237:C:H6	1.79	0.47
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.49	0.47
1:AA:221:C:H2'	1:AA:222:U:C6	2.43	0.47
1:AA:381:C:H2'	1:AA:382:A:O4'	2.14	0.47
1:AA:950:U:OP2	13:AM:102:ARG:HD3	2.13	0.47
9:AI:79:LEU:HD22	9:AI:104:ARG:HB2	1.94	0.47
53:B6:14:THR:HB	53:B6:48:VAL:O	2.13	0.47
26:BA:1301:U:O5'	26:BA:1302:G:H5''	2.14	0.47
26:BA:1347:A:C8	26:BA:1349:G:C8	3.02	0.47
26:BA:2186:C:H5	26:BA:2187:G:C4	2.32	0.47
26:BA:2710:U:H2'	26:BA:2711:C:C6	2.49	0.47
40:BT:23:ARG:HG3	40:BT:120:ARG:NH1	2.29	0.47
26:BA:572:A:N6	42:BV:19:LYS:H	2.11	0.47
1:CA:1060:C:OP1	10:CJ:51:ARG:NH1	2.46	0.47
1:CA:1206:G:N7	61:CA:4001:HOH:O	2.36	0.47
1:CA:1221:G:O3'	19:CS:77:THR:HG21	2.13	0.47
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.96	0.47
1:CA:45:U:H2'	1:CA:46:G:C8	2.49	0.47
1:CA:59:A:H5''	1:CA:387:U:H5''	1.95	0.47
1:CA:605:U:C2'	1:CA:606:G:H5'	2.44	0.47
1:CA:872:A:O2'	1:CA:873:A:H3'	2.15	0.47
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.62	0.47
2:CB:184:VAL:N	2:CB:198:ASP:OD2	2.38	0.47
4:CD:31:CYS:O	4:CD:35:ARG:HG3	2.13	0.47
1:CA:1360:A:C4	14:CN:18:VAL:HG12	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:83:G:O2'	26:DA:102:G:N2	2.47	0.47
26:DA:1359:A:C6	26:DA:1360:A:C4	3.02	0.47
26:DA:236:C:H2'	26:DA:237:C:C6	2.48	0.47
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.49	0.47
26:DA:2583:G:OP2	61:DA:3952:HOH:O	2.20	0.47
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.14	0.47
38:DR:87:TYR:OH	38:DR:116:LEU:HB3	2.14	0.47
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.47
1:AA:58:C:O2'	1:AA:388:G:N7	2.37	0.47
1:AA:687:A:N1	1:AA:700:G:O2'	2.41	0.47
2:AB:28:PHE:CD1	2:AB:190:THR:HA	2.50	0.47
4:AD:164:ALA:O	4:AD:168:ARG:NH1	2.45	0.47
4:AD:187:ARG:NH1	4:AD:193:ASP:OD2	2.48	0.47
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.97	0.47
16:AP:54:GLU:HG3	16:AP:55:ARG:N	2.29	0.47
51:B4:26:SER:OG	51:B4:27:THR:N	2.47	0.47
26:BA:1320:A:N3	26:BA:1343:C:H1'	2.29	0.47
26:BA:1452:U:H2'	26:BA:1453:C:C6	2.50	0.47
26:BA:1690:G:H2'	26:BA:1691:C:O4'	2.14	0.47
26:BA:2505:U:H2'	26:BA:2506:G:O4'	2.14	0.47
26:BA:2564:U:C2	26:BA:2566:U:H5''	2.48	0.47
26:BA:2748:G:H2'	26:BA:2749:G:H8	1.78	0.47
26:BA:45:C:H2'	26:BA:46:C:C6	2.49	0.47
40:BT:108:ARG:HA	40:BT:111:ARG:NH1	2.30	0.47
26:BA:333:G:H4'	45:BY:18:GLY:HA2	1.96	0.47
46:BZ:33:LEU:HD11	46:BZ:90:VAL:HG21	1.97	0.47
1:CA:165:C:H2'	1:CA:166:G:H8	1.79	0.47
2:CB:20:GLU:HB2	2:CB:190:THR:OG1	2.14	0.47
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.14	0.47
26:DA:1170:G:H1	26:DA:1179:C:H42	1.62	0.47
26:DA:1509(A):A:N3	26:DA:1509(A):A:H5''	2.29	0.47
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.40	0.47
26:DA:191:A:N1	61:DA:4117:HOH:O	2.35	0.47
26:DA:1783:A:H5'	26:DA:2608:G:H4'	1.96	0.47
26:DA:784:A:C8	26:DA:792:G:C5	3.02	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.79	0.47
1:AA:1321:C:H5''	1:AA:1322:C:H2'	1.97	0.47
1:AA:356:A:N3	1:AA:368:U:O2'	2.42	0.47
2:AB:71:VAL:HB	2:AB:164:VAL:HG22	1.97	0.47
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.28	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:AI:100:GLY:O	9:AI:103:THR:HG23	2.14	0.47
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.97	0.47
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.96	0.47
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.44	0.47
26:BA:1381:U:OP1	44:BX:65:ARG:HD2	2.14	0.47
26:BA:1400:A:H2'	26:BA:1401:G:O4'	2.15	0.47
26:BA:1834:A:O2'	28:BD:259:THR:HG21	2.14	0.47
26:BA:2142:G:C2'	26:BA:2143:G:H5'	2.45	0.47
26:BA:2686:G:H2'	26:BA:2687:A:C8	2.50	0.47
28:BD:108:PRO:HG2	28:BD:111:LEU:HB2	1.96	0.47
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.30	0.47
40:BT:106:SER:O	40:BT:110:ILE:HG13	2.14	0.47
1:CA:1052:U:H5''	1:CA:1053:G:OP2	2.13	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.61	0.47
1:CA:6:G:H4'	1:CA:298:A:H4'	1.96	0.47
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.96	0.47
11:CK:41:THR:OG1	11:CK:42:TRP:N	2.48	0.47
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.35	0.47
26:DA:1171:G:N2	26:DA:1179:C:N3	2.61	0.47
26:DA:2140:C:H2'	26:DA:2140:C:O2	2.13	0.47
26:DA:603:A:N1	26:DA:625:G:O2'	2.37	0.47
26:DA:608:A:H2'	26:DA:609:A:C8	2.49	0.47
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.97	0.47
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.95	0.47
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.50	0.47
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.42	0.47
1:AA:1127:G:H5'	1:AA:1280:A:O2'	2.13	0.47
1:AA:411:A:OP2	4:AD:25:ARG:NH2	2.48	0.47
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.96	0.47
26:BA:1688:A:H2'	26:BA:1689:G:O4'	2.15	0.47
26:BA:2443:U:O2'	26:BA:2445:A:N7	2.36	0.47
26:BA:2637:G:H2'	26:BA:2638:C:C6	2.49	0.47
26:BA:271:U:C2	33:BI:50:ARG:HD3	2.49	0.47
26:BA:93:G:H2'	26:BA:94:G:O4'	2.15	0.47
26:BA:1834:A:H4'	28:BD:259:THR:HG23	1.96	0.47
1:CA:865:A:H5'	1:CA:1078:U:O4	2.14	0.47
1:CA:499:A:H4'	1:CA:500:G:H5'	1.97	0.47
1:CA:624:C:H2'	1:CA:625:G:H8	1.79	0.47
1:CA:721:G:H4'	1:CA:722:A:O4'	2.15	0.47
1:CA:7:G:H5'	1:CA:298:A:O4'	2.15	0.47
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	1.97	0.47
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:CX:49:G:C2	24:CX:65:C:N3	2.82	0.47
26:DA:1424:G:H2'	26:DA:1425:G:O4'	2.15	0.47
26:DA:1592:C:H2'	26:DA:1593:G:C8	2.50	0.47
26:DA:2308:G:H5''	26:DA:2310:A:OP2	2.14	0.47
26:DA:659:C:H2'	26:DA:660:G:C8	2.48	0.47
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.62	0.47
36:DP:143:GLY:O	36:DP:145:PRO:HD3	2.14	0.47
36:DP:28:GLY:O	36:DP:30:THR:N	2.48	0.47
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.97	0.47
38:DR:31:HIS:C	38:DR:33:ARG:H	2.17	0.47
40:DT:36:GLU:OE1	40:DT:41:ARG:NE	2.41	0.47
40:DT:22:PHE:HA	40:DT:91:ARG:HH12	1.78	0.47
1:AA:1112:C:C2	3:AC:178:LEU:HB2	2.49	0.47
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.48	0.47
1:AA:979:C:OP1	1:AA:1223:C:N4	2.48	0.47
1:AA:1399:C:C2	1:AA:1502:A:N6	2.82	0.47
1:AA:838:G:H1	1:AA:848:C:N4	2.13	0.47
1:AA:936:C:O2	1:AA:1382:C:N4	2.31	0.47
19:AS:39:THR:HG22	19:AS:40:ILE:O	2.15	0.47
26:BA:1223:C:H2'	26:BA:1224:C:H6	1.80	0.47
26:BA:1036:A:C6	26:BA:1231:G:H1'	2.49	0.47
26:BA:139:A:C8	26:BA:1454:C:O2'	2.65	0.47
26:BA:2125:C:N3	26:BA:2208:G:N2	2.49	0.47
26:BA:2159:C:H2'	26:BA:2160:C:C6	2.49	0.47
26:BA:231:G:O2'	26:BA:243:G:O6	2.30	0.47
26:BA:2858:G:O2'	26:BA:2877:G:N2	2.43	0.47
26:BA:2880:C:H2'	26:BA:2881:C:O4'	2.15	0.47
41:BU:36:ARG:HD2	41:BU:40:PHE:CZ	2.49	0.47
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.45	0.47
1:CA:1099:G:C5	1:CA:1100:C:N3	2.82	0.47
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.96	0.47
1:CA:545:C:O2'	1:CA:549:C:OP1	2.27	0.47
1:CA:797:C:C2'	1:CA:798:G:H5'	2.44	0.47
3:CC:32:LEU:HA	3:CC:35:GLU:HG2	1.96	0.47
7:CG:73:MET:HG3	7:CG:90:GLU:HA	1.96	0.47
10:CJ:9:ARG:HG2	10:CJ:69:ASN:OD1	2.14	0.47
26:DA:990:A:C6	26:DA:1186:G:H1'	2.50	0.47
26:DA:2220:G:H2'	26:DA:2221:G:H8	1.80	0.47
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.49	0.47
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.49	0.47
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.49	0.47
1:AA:1133:G:H2'	1:AA:1134:G:C8	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.47	0.47
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.78	0.47
1:AA:659:U:H2'	1:AA:660:G:H5'	1.96	0.47
1:AA:783:C:OP1	1:AA:1515:C:O2'	2.32	0.47
1:AA:1055:A:O2'	3:AC:161:GLU:O	2.23	0.47
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.96	0.47
26:BA:1343:C:OP1	26:BA:2722:C:H4'	2.14	0.47
26:BA:1715:A:O2'	26:BA:1721:G:N7	2.42	0.47
26:BA:1809:U:H2'	26:BA:1815:A:N6	2.30	0.47
26:BA:2748:G:H2'	26:BA:2749:G:C8	2.50	0.47
26:BA:327:U:H2'	26:BA:328:G:C8	2.49	0.47
26:BA:493:G:O6	61:BA:3834:HOH:O	2.19	0.47
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.63	0.47
1:CA:1097:C:H2'	1:CA:1098:C:O4'	2.15	0.47
1:CA:1400:C:O5'	22:CV:18:G:C2	2.68	0.47
1:CA:811:C:H4'	1:CA:901:A:H61	1.79	0.47
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.29	0.47
1:CA:584:G:H5'	17:CQ:91:ARG:NH2	2.30	0.47
1:CA:986:A:C2	19:CS:52:TYR:HE2	2.32	0.47
56:D9:2:LYS:NZ	56:D9:31:LYS:O	2.28	0.47
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.50	0.47
26:DA:2639:A:H2'	26:DA:2640:G:O4'	2.14	0.47
26:DA:411:G:C5	36:DP:72:PRO:HB3	2.50	0.47
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.50	0.47
32:DH:106:THR:HG22	32:DH:112:PRO:HB3	1.96	0.47
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.95	0.47
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.80	0.47
46:DZ:30:ASN:ND2	46:DZ:90:VAL:HB	2.29	0.47
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.50	0.47
1:AA:460:G:O5'	1:AA:460:G:H8	1.97	0.47
4:AD:31:CYS:O	4:AD:35:ARG:HG3	2.13	0.47
16:AP:66:PRO:HB2	16:AP:71:ARG:HB3	1.96	0.47
17:AQ:51:TYR:CZ	17:AQ:73:VAL:HG11	2.50	0.47
26:BA:2589:A:O4'	52:B5:3:LYS:HB2	2.13	0.47
26:BA:2182:G:H2'	26:BA:2183:C:C6	2.50	0.47
26:BA:2576:A:C2	26:BA:2659:U:H4'	2.49	0.47
26:BA:844:C:H2'	26:BA:845:G:O4'	2.15	0.47
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.47
1:CA:1281:U:P	1:CA:1282:C:H41	2.38	0.47
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.50	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.43	0.47
1:CA:76:C:N4	1:CA:96:U:N3	2.62	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.96	0.47
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.48	0.47
12:CL:113:ARG:HB3	12:CL:122:THR:HG21	1.97	0.47
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.15	0.47
26:DA:1910:G:C6	26:DA:1911:U:C4	3.02	0.47
26:DA:2398:U:H2'	26:DA:2399:G:C8	2.50	0.47
26:DA:2485:G:C2	26:DA:2486:G:C8	3.03	0.47
26:DA:2500:U:H2'	26:DA:2504:U:C5	2.50	0.47
26:DA:853:G:H2'	26:DA:854:G:H8	1.79	0.47
27:DB:78:A:C2	27:DB:100:A:C4	3.03	0.47
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.15	0.47
45:DY:12:THR:O	45:DY:75:ILE:N	2.41	0.47
1:AA:1286:A:H2'	1:AA:1287:A:H4'	1.95	0.47
1:AA:765:G:H5''	1:AA:766:A:OP1	2.15	0.47
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.47
1:AA:406:G:OP1	4:AD:5:ILE:HD11	2.14	0.47
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.97	0.47
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.54	0.47
26:BA:1075:A:OP1	37:BQ:128:LYS:NZ	2.45	0.47
26:BA:2519:C:H2'	26:BA:2520:G:O4'	2.14	0.47
26:BA:2555:G:H2'	26:BA:2556:G:C8	2.50	0.47
26:BA:37:C:H2'	26:BA:38:A:C8	2.49	0.47
26:BA:352:U:H4'	45:BY:68:HIS:CG	2.50	0.47
1:CA:1266:G:N1	1:CA:1269:A:OP2	2.47	0.47
1:CA:1271:G:H5'	1:CA:1314:C:H5''	1.95	0.47
1:CA:1398:A:OP1	1:CA:1401:G:OP1	2.33	0.47
1:CA:163:C:H2'	1:CA:164:U:O4'	2.14	0.47
1:CA:493:G:H2'	1:CA:494:U:C5	2.50	0.47
1:CA:857:C:H2'	1:CA:858:G:O4'	2.15	0.47
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.97	0.47
3:CC:54:ARG:HB2	3:CC:69:HIS:HB2	1.95	0.47
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.50	0.47
24:CX:41:C:H2'	24:CX:42:G:C8	2.49	0.47
26:DA:2199:A:H3'	26:DA:2200:C:H6	1.80	0.47
26:DA:593:G:C6	26:DA:594:U:C4	3.03	0.47
26:DA:1500:G:O2'	28:DD:100:GLY:O	2.29	0.47
30:DF:39:TRP:CD1	30:DF:101:LEU:HB2	2.49	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.14	0.47
1:AA:1276:G:H2'	1:AA:1277:C:C6	2.50	0.47
1:AA:190:U:H2'	1:AA:191:G:C8	2.50	0.47
1:AA:243:A:H4'	1:AA:244:U:H5''	1.97	0.47
1:AA:985:C:H2'	1:AA:986:A:C8	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AG:136:LYS:O	7:AG:140:ASP:HB2	2.15	0.47
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.47
8:AH:11:THR:HG23	8:AH:14:ARG:HH12	1.79	0.47
26:BA:2250:G:H2'	26:BA:2250:G:N3	2.30	0.47
26:BA:305:G:H1'	26:BA:384:G:N2	2.29	0.47
26:BA:211:A:H5''	26:BA:448:U:OP1	2.14	0.47
26:BA:916:G:H2'	26:BA:917:A:O4'	2.15	0.47
29:BE:1:MET:HE3	29:BE:199:ARG:HD2	1.97	0.47
38:BR:97:VAL:HG22	38:BR:114:VAL:HG22	1.97	0.47
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.38	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.50	0.47
1:CA:786:G:C2	1:CA:797:C:C2	3.03	0.47
11:CK:62:GLN:HB2	11:CK:93:GLN:HG3	1.95	0.47
1:CA:1358:U:H5''	14:CN:33:VAL:O	2.15	0.47
26:DA:2335:A:C8	26:DA:2337:G:C5	3.03	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
26:DA:2722:G:H5''	26:DA:2820:A:N7	2.30	0.47
27:DB:87:G:N2	27:DB:90:A:OP2	2.46	0.47
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.17	0.47
33:DI:127:VAL:HG22	33:DI:139:GLN:OE1	2.15	0.47
40:DT:77:PRO:HB2	40:DT:80:SER:HB2	1.97	0.47
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.50	0.47
1:AA:1036:G:N2	1:AA:1037:C:H1'	2.30	0.46
1:AA:1095:U:OP2	1:AA:1108:G:N1	2.43	0.46
1:AA:520:A:N1	1:AA:536:C:H1'	2.30	0.46
1:AA:841:U:H5	1:AA:848:C:H1'	1.77	0.46
1:AA:934:C:H5	1:AA:1344:C:H2'	1.79	0.46
15:AO:24:SER:OG	15:AO:25:THR:N	2.49	0.46
1:AA:134:A:H61	16:AP:25:ARG:NH1	2.13	0.46
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.49	0.46
24:AX:19:G:H4'	24:AX:20:U:OP2	2.15	0.46
26:BA:1044:C:OP1	61:BA:4488:HOH:O	2.21	0.46
26:BA:117:A:H4'	26:BA:118:U:OP1	2.16	0.46
26:BA:1404:G:O2'	26:BA:1405:A:H5''	2.15	0.46
26:BA:2142:G:H2'	26:BA:2143:G:H5'	1.97	0.46
26:BA:2576:A:OP1	26:BA:2660:C:H4'	2.16	0.46
26:BA:354:A:H2	26:BA:1255:A:O2'	1.96	0.46
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.45	0.46
28:BD:275:LYS:HB3	28:BD:276:LYS:H	1.47	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.98	0.46
1:CA:1010:G:H2'	1:CA:1011:G:C8	2.49	0.46
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:23:GLY:O	4:CD:26:CYS:HB2	2.14	0.46
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.46
1:CA:750:G:N2	15:CO:23:GLY:O	2.42	0.46
18:CR:45:SER:OG	18:CR:47:THR:HG22	2.16	0.46
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.31	0.46
26:DA:2126:A:H2	26:DA:2127:G:N3	2.12	0.46
26:DA:2134:A:O2'	26:DA:2159:G:N3	2.41	0.46
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.46
26:DA:601:C:O2'	26:DA:605:C:OP1	2.32	0.46
27:DB:42:C:O2	31:DG:93:THR:N	2.38	0.46
40:DT:23:ARG:HG3	40:DT:120:ARG:NH1	2.30	0.46
1:AA:358:U:H2'	1:AA:359:U:H6	1.80	0.46
1:AA:967:C:H3'	1:AA:968:A:H2'	1.97	0.46
4:AD:20:TYR:HA	4:AD:26:CYS:SG	2.56	0.46
11:AK:78:GLN:O	11:AK:103:LEU:HD22	2.15	0.46
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.16	0.46
19:AS:66:MET:HA	51:B4:58:ARG:NH1	2.30	0.46
26:BA:2404:A:O3'	55:B8:27:THR:HB	2.15	0.46
26:BA:2410:U:H2'	26:BA:2411:G:C8	2.51	0.46
26:BA:27:G:N2	26:BA:537:G:H1'	2.30	0.46
26:BA:2855:G:H2'	26:BA:2856:G:C8	2.50	0.46
26:BA:304:C:H2'	26:BA:305:G:O4'	2.15	0.46
26:BA:791:G:H5''	26:BA:1705:C:H5''	1.97	0.46
26:BA:879:G:N3	36:BP:53:GLY:HA3	2.30	0.46
38:BR:38:VAL:HG22	38:BR:112:ALA:HB2	1.97	0.46
1:CA:1153:C:N4	1:CA:1154:G:H21	2.10	0.46
1:CA:1166:G:H8	1:CA:1166:G:O5'	1.98	0.46
1:CA:1356:G:O5'	1:CA:1356:G:H8	1.98	0.46
1:CA:313:A:H2'	1:CA:314:C:C6	2.49	0.46
2:CB:97:TRP:CZ2	2:CB:102:LEU:HD13	2.50	0.46
14:CN:26:ARG:HD3	14:CN:43:CYS:SG	2.54	0.46
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.97	0.46
24:CX:53:G:C5	24:CX:54:5MU:H72	2.50	0.46
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.50	0.46
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.55	0.46
26:DA:2845:G:H5''	40:DT:54:ARG:O	2.15	0.46
26:DA:2886:G:H2'	26:DA:2887:U:H6	1.79	0.46
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.50	0.46
27:DB:37:C:C5	27:DB:38:C:C4	3.04	0.46
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.98	0.46
33:DI:52:ARG:HH11	33:DI:52:ARG:HG3	1.79	0.46
1:AA:107:G:H2'	1:AA:108:G:O4'	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1092:A:H5'	1:AA:1092:A:H8	1.80	0.46
1:AA:1165:C:N3	1:AA:1171:G:O6	2.49	0.46
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.36	0.46
1:AA:1404:C:H2'	1:AA:1405:G:C8	2.49	0.46
1:AA:606:G:H1'	1:AA:632:A:H61	1.80	0.46
1:AA:826:C:H2'	1:AA:827:U:C6	2.50	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.97	0.46
9:AI:47:LEU:O	9:AI:50:LEU:HG	2.15	0.46
24:AX:61:C:H2'	24:AX:62:C:C6	2.50	0.46
26:BA:1217:G:H3'	26:BA:1218:G:H5'	1.98	0.46
26:BA:1458:A:H2'	26:BA:1459:G:C8	2.50	0.46
26:BA:1506:G:H5''	26:BA:1507:A:OP2	2.16	0.46
26:BA:2228:G:H2'	26:BA:2229:A:C2	2.49	0.46
26:BA:2347:A:C8	26:BA:2349:G:C5	3.03	0.46
26:BA:278:G:C2'	26:BA:279:G:H5''	2.42	0.46
26:BA:2812:A:N3	26:BA:2904:U:H1'	2.30	0.46
26:BA:801:C:H2'	26:BA:802:C:C6	2.49	0.46
27:BB:48:A:H2'	27:BB:49:C:C6	2.50	0.46
28:BD:97:TYR:HE1	28:BD:103:ARG:HG3	1.80	0.46
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.97	0.46
1:CA:335:C:H2'	1:CA:336:C:C6	2.50	0.46
1:CA:765:G:N1	1:CA:812:C:O2'	2.40	0.46
1:CA:77:G:C5	1:CA:93:G:C2	3.04	0.46
2:CB:16:HIS:O	2:CB:18:GLY:N	2.48	0.46
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.97	0.46
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.68	0.46
17:CQ:64:PRO:HB3	17:CQ:70:ARG:NH1	2.30	0.46
26:DA:1394:U:C4	26:DA:1395:A:C5	3.03	0.46
26:DA:1486:A:H2'	26:DA:1487:G:H8	1.81	0.46
26:DA:1547:C:O2'	26:DA:1548:C:H5'	2.15	0.46
26:DA:2406:U:OP2	26:DA:2406:U:H2'	2.15	0.46
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.51	0.46
26:DA:320:A:H4'	26:DA:322:A:N7	2.30	0.46
26:DA:471:A:H2'	26:DA:472:A:O4'	2.15	0.46
26:DA:666:G:H4'	36:DP:49:ARG:NH2	2.30	0.46
26:DA:725:G:C6	26:DA:726:G:N1	2.83	0.46
26:DA:1820:U:C4	28:DD:202:LYS:HD3	2.50	0.46
36:DP:21:ARG:HA	36:DP:21:ARG:HD3	1.70	0.46
1:AA:598:U:H2'	1:AA:599:C:C6	2.50	0.46
4:AD:33:MET:HB2	58:AD:302:SF4:S2	2.55	0.46
25:AY:75:C:H5''	25:AY:76:A:OP1	2.14	0.46
26:BA:592:U:O2'	26:BA:1029:A:N1	2.41	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2149:G:O2'	26:BA:2150:C:O4'	2.34	0.46
26:BA:2184:G:C5'	26:BA:2194:U:H2'	2.46	0.46
26:BA:2357:G:N3	26:BA:2393:C:H2'	2.30	0.46
26:BA:2707:C:H2'	26:BA:2708:U:C6	2.51	0.46
26:BA:713:G:C2'	26:BA:714:U:H5'	2.45	0.46
26:BA:185:A:O2'	26:BA:852:G:O6	2.26	0.46
26:BA:873:U:C4'	36:BP:55:ARG:HB2	2.45	0.46
26:BA:63:A:C5	44:BX:66:LEU:HD12	2.50	0.46
26:BA:1387:U:O2	44:BX:80:ILE:HD12	2.15	0.46
1:CA:1055:A:H5'	1:CA:1055:A:H8	1.80	0.46
1:CA:18:C:H5'	1:CA:1079:G:H1'	1.95	0.46
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.61	0.46
1:CA:1295:G:O2'	13:CM:14:ARG:NH1	2.48	0.46
1:CA:1402:C:H2'	1:CA:1403:C:O4'	2.15	0.46
1:CA:229:U:H2'	1:CA:230:G:C8	2.51	0.46
3:CC:124:ILE:HD11	3:CC:189:ALA:HB1	1.98	0.46
20:CT:40:ALA:HB2	20:CT:55:ILE:HG22	1.97	0.46
24:CX:19:G:H1	24:CX:56:C:N4	2.09	0.46
26:DA:2017:U:O2	52:D5:10:LYS:HB2	2.15	0.46
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.48	0.46
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.80	0.46
26:DA:2823:A:OP1	29:DE:113:PHE:HB2	2.15	0.46
27:DB:32:C:N3	27:DB:33:G:C5	2.84	0.46
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.81	0.46
29:DE:72:VAL:HG22	29:DE:73:GLU:HB3	1.96	0.46
36:DP:47:ASP:OD2	36:DP:50:ARG:NH2	2.49	0.46
26:DA:1649:G:O2'	38:DR:107:ASP:OD2	2.21	0.46
46:DZ:119:GLU:HG2	46:DZ:119:GLU:H	1.49	0.46
1:AA:975:A:N6	1:AA:1367:C:O4'	2.48	0.46
1:AA:49:U:O2'	1:AA:50:A:H2'	2.14	0.46
6:AF:21:LEU:O	6:AF:25:ILE:HG12	2.15	0.46
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.15	0.46
51:B4:54:GLY:HA2	51:B4:55:ARG:HA	1.48	0.46
26:BA:1014:U:H2'	26:BA:1015:C:C6	2.51	0.46
26:BA:815:G:O2'	26:BA:1425:A:N1	2.41	0.46
26:BA:1476:C:H2'	26:BA:1477:U:C6	2.49	0.46
26:BA:2473:C:H2'	26:BA:2474:U:C6	2.51	0.46
26:BA:2524:C:H2'	26:BA:2525:G:O4'	2.15	0.46
26:BA:1814:A:H5'	26:BA:2620:G:H4'	1.97	0.46
26:BA:34:C:H41	26:BA:473:A:N6	2.14	0.46
26:BA:2116:G:OP1	33:BI:22:LYS:HD2	2.14	0.46
26:BA:412:C:O2	36:BP:71:VAL:HG21	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
42:BV:23:GLU:OE1	42:BV:89:GLN:NE2	2.47	0.46
1:CA:1038:C:H2'	1:CA:1039:C:C6	2.51	0.46
1:CA:130:A:N3	1:CA:263:A:O2'	2.37	0.46
1:CA:342:C:C2'	1:CA:343:U:H5'	2.46	0.46
1:CA:448:A:P	1:CA:485:G:H22	2.38	0.46
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.81	0.46
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.98	0.46
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.16	0.46
24:CX:49:G:N1	24:CX:65:C:C4	2.71	0.46
26:DA:1359:A:N6	26:DA:1372:U:C4	2.83	0.46
26:DA:1578:U:C2'	26:DA:1579:A:H5'	2.46	0.46
26:DA:2199:A:H3'	26:DA:2200:C:C6	2.51	0.46
26:DA:2712:U:O2'	26:DA:2713:A:H5'	2.16	0.46
27:DB:31:C:C5	27:DB:32:C:H5	2.33	0.46
27:DB:43:C:H2'	27:DB:44:G:H5''	1.98	0.46
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.97	0.46
1:AA:1025:U:O2	1:AA:1036:G:O6	2.34	0.46
1:AA:1493:A:H2'	26:BA:1935:A:N1	2.30	0.46
1:AA:674:G:H2'	1:AA:675:A:C8	2.50	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
3:AC:85:ARG:O	3:AC:89:GLU:N	2.47	0.46
4:AD:103:ASN:O	4:AD:107:ARG:HG2	2.15	0.46
4:AD:81:GLU:OE1	4:AD:139:ARG:NH1	2.36	0.46
26:BA:1825:U:H2'	26:BA:1826:C:H6	1.80	0.46
26:BA:1845:G:H4'	28:BD:51:VAL:HG21	1.98	0.46
26:BA:721:G:H1'	30:BF:74:ARG:HD3	1.97	0.46
33:BI:85:GLU:O	33:BI:123:LEU:HD12	2.15	0.46
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.35	0.46
1:CA:1456:G:O6	20:CT:54:LYS:HE3	2.15	0.46
1:CA:344:A:H4'	1:CA:345:C:OP2	2.16	0.46
1:CA:512:U:O4'	4:CD:43:HIS:HE1	1.98	0.46
6:CF:75:LEU:O	6:CF:79:LEU:HG	2.15	0.46
7:CG:29:LYS:HG3	7:CG:101:LEU:HB3	1.97	0.46
9:CI:73:GLN:HA	9:CI:76:ALA:HB3	1.98	0.46
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.97	0.46
26:DA:1353:A:H2'	26:DA:1354:A:C8	2.51	0.46
26:DA:1654:A:C1'	26:DA:2823:A:H5'	2.46	0.46
26:DA:2370:G:C6	26:DA:2371:G:C6	3.03	0.46
26:DA:2808:U:H2'	26:DA:2891:G:N1	2.30	0.46
26:DA:898:C:H2'	26:DA:899:A:O4'	2.16	0.46
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.96	0.46
29:DE:116:VAL:HG11	29:DE:138:PRO:HB3	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:DF:129:PHE:CE2	30:DF:163:VAL:HG11	2.51	0.46
31:DG:68:PRO:HG2	31:DG:90:LEU:HD22	1.97	0.46
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.47	0.46
35:DO:52:VAL:HG12	35:DO:94:ARG:NH2	2.31	0.46
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.51	0.46
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.16	0.46
1:AA:56:U:H2'	1:AA:57:G:H8	1.76	0.46
1:AA:951:G:C2'	1:AA:952:U:H5'	2.46	0.46
1:AA:976:G:C8	1:AA:1362:C:N4	2.83	0.46
2:AB:223:ILE:HA	2:AB:226:ARG:HG2	1.97	0.46
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.15	0.46
13:AM:59:TYR:O	13:AM:63:THR:OG1	2.25	0.46
26:BA:2622:C:O2	61:BA:4295:HOH:O	2.20	0.46
26:BA:2705:A:H2'	26:BA:2706:G:H8	1.80	0.46
26:BA:2658:C:OP2	26:BA:2745:G:O2'	2.34	0.46
27:BB:87:G:N2	27:BB:90:A:OP2	2.44	0.46
30:BF:8:GLN:HE22	30:BF:21:ALA:HB2	1.81	0.46
40:BT:53:ARG:CZ	40:BT:53:ARG:HB3	2.46	0.46
1:CA:1025:U:N3	1:CA:1036:G:N1	2.64	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.50	0.46
1:CA:1127:G:H5'	1:CA:1281:U:O2	2.16	0.46
1:CA:1316:G:N2	1:CA:1318:A:H3'	2.31	0.46
1:CA:269:C:H2'	1:CA:270:A:C8	2.51	0.46
1:CA:419:C:H5''	1:CA:513:C:H1'	1.98	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
1:CA:967:C:H2'	1:CA:968:A:C8	2.51	0.46
2:CB:204:ASN:O	2:CB:210:SER:OG	2.24	0.46
2:CB:19:HIS:CD2	2:CB:20:GLU:H	2.34	0.46
2:CB:82:ARG:HG2	2:CB:83:MET:N	2.31	0.46
50:D3:8:LEU:O	50:D3:32:GLN:N	2.36	0.46
26:DA:1230:C:H2'	26:DA:1231:G:C8	2.48	0.46
26:DA:2815:C:H2'	26:DA:2816:C:C6	2.51	0.46
28:DD:183:ARG:HG3	28:DD:270:ILE:HG12	1.97	0.46
41:DU:28:ARG:NH1	41:DU:38:THR:OG1	2.43	0.46
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.97	0.46
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.98	0.46
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.41	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.30	0.46
1:AA:1414:U:H3	1:AA:1486:G:H1	1.63	0.46
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.51	0.46
1:AA:309:G:H2'	1:AA:310:G:H8	1.81	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:539:A:H2'	1:AA:540:G:C8	2.50	0.46
1:AA:814:A:H2'	1:AA:816:A:H5''	1.98	0.46
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.16	0.46
8:AH:33:GLU:HG2	8:AH:48:TYR:CE2	2.50	0.46
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.98	0.46
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.81	0.46
26:BA:1405:A:C6	26:BA:1418:U:N3	2.82	0.46
26:BA:2184:G:N1	26:BA:2185:C:C4	2.84	0.46
26:BA:2201:C:H2'	26:BA:2202:U:C6	2.50	0.46
26:BA:241:G:OP1	36:BP:50:ARG:NH1	2.43	0.46
26:BA:2490:A:OP2	56:B9:2:LYS:NZ	2.41	0.46
26:BA:2736:C:H4'	38:BR:1:MET:HG3	1.98	0.46
26:BA:656:A:H2'	26:BA:657:A:O4'	2.14	0.46
28:BD:79:VAL:HG12	28:BD:113:VAL:HA	1.97	0.46
61:BA:4873:HOH:O	29:BE:162:ALA:HB3	2.16	0.46
26:BA:957:A:H2'	37:BQ:9:TYR:OH	2.16	0.46
41:BU:28:ARG:NH1	41:BU:38:THR:OG1	2.43	0.46
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.15	0.46
1:CA:838:G:C6	1:CA:848:C:N4	2.82	0.46
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.98	0.46
2:CB:97:TRP:CH2	2:CB:101:MET:HB2	2.51	0.46
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.16	0.46
26:DA:1429:G:H2'	26:DA:1430:C:C6	2.51	0.46
26:DA:1474:C:H2'	26:DA:1475:G:C8	2.51	0.46
26:DA:1851:U:C4	26:DA:1852:C:C4	3.04	0.46
26:DA:1853:A:N3	26:DA:2233:U:O2'	2.38	0.46
26:DA:195:A:H61	26:DA:198:C:H3'	1.81	0.46
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.16	0.46
26:DA:910:A:N1	26:DA:2277:G:H1'	2.31	0.46
26:DA:2741:A:OP1	56:D9:22:ARG:NH2	2.45	0.46
26:DA:2881:C:H2'	26:DA:2882:A:O4'	2.16	0.46
26:DA:30:G:H2'	26:DA:31:C:H6	1.79	0.46
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.46
26:DA:754:C:H2'	26:DA:755:C:C6	2.51	0.46
32:DH:70:THR:HG22	32:DH:74:ASN:ND2	2.31	0.46
37:DQ:26:TYR:CD1	37:DQ:28:ALA:HB2	2.51	0.46
43:DW:46:PHE:O	43:DW:50:VAL:HG23	2.16	0.46
1:AA:1065:U:H4'	1:AA:1066:C:O5'	2.15	0.46
1:AA:1165:C:N4	1:AA:1166:G:C6	2.84	0.46
1:AA:43:C:H2'	1:AA:44:G:O4'	2.15	0.46
1:AA:600:C:H5'	8:AH:129:VAL:HA	1.98	0.46
1:AA:762:C:H2'	1:AA:763:G:H8	1.80	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:927:G:H1	1:AA:1390:U:H3	1.63	0.46
4:AD:172:PRO:HB2	4:AD:187:ARG:NH2	2.31	0.46
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.98	0.46
24:AX:31:G:C8	24:AX:32:5MC:HM52	2.51	0.46
51:B4:61:ARG:HG3	51:B4:62:ARG:H	1.81	0.46
26:BA:2294:G:OP1	26:BA:2295:C:H1'	2.16	0.46
26:BA:2340:A:H2'	26:BA:2341:G:C8	2.50	0.46
32:BH:4:ILE:O	32:BH:69:ARG:HG2	2.16	0.46
40:BT:60:THR:HG22	40:BT:77:PRO:HA	1.97	0.46
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.51	0.46
1:CA:262:A:C6	1:CA:263:A:C6	3.04	0.46
1:CA:973:G:H3'	1:CA:974:A:H5''	1.97	0.46
3:CC:191:THR:HG21	3:CC:193:TYR:CZ	2.51	0.46
7:CG:75:VAL:HG13	7:CG:145:ALA:HA	1.98	0.46
24:CX:29:G:C6	24:CX:30:G:C5	3.04	0.46
26:DA:1184:G:OP1	50:D3:30:ARG:HD2	2.16	0.46
26:DA:1243:G:H2'	26:DA:1244:G:O4'	2.15	0.46
26:DA:1375:C:H2'	26:DA:1376:C:C6	2.51	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.50	0.46
26:DA:2200:C:O2	26:DA:2226:C:N4	2.49	0.46
26:DA:320:A:H4'	26:DA:322:A:C8	2.51	0.46
26:DA:566:U:H2'	26:DA:567:A:O4'	2.16	0.46
26:DA:773:U:H2'	26:DA:774:A:H5'	1.98	0.46
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.98	0.46
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.97	0.46
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.51	0.46
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.51	0.46
1:AA:189(C):C:N4	1:AA:189(H):G:H1	2.14	0.46
1:AA:600:C:O2'	1:AA:601:C:H5'	2.16	0.46
22:AV:13:A:H4'	22:AV:14:A:OP2	2.16	0.46
26:BA:976:G:O2'	50:B3:24:LYS:HD3	2.16	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:N	2.29	0.46
26:BA:1091:A:OP1	26:BA:1093:G:H5''	2.16	0.46
26:BA:2054:G:H1'	29:BE:145:LYS:HD3	1.98	0.46
34:BN:12:ARG:NH1	34:BN:38:HIS:HE2	2.14	0.46
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.16	0.46
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.15	0.46
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.33	0.46
1:CA:262:A:H2'	1:CA:263:A:C8	2.51	0.46
1:CA:634:C:H2'	1:CA:635:G:H8	1.81	0.46
1:CA:685:G:C2	1:CA:686:U:C4	3.04	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:748:C:H4'	1:CA:749:C:O5'	2.16	0.46
1:CA:98:G:C6	1:CA:99:U:C4	3.03	0.46
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.49	0.46
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.15	0.46
24:CX:22:G:H2'	24:CX:23:C:C6	2.51	0.46
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.80	0.46
26:DA:2419:U:H2'	26:DA:2420:C:C6	2.51	0.46
26:DA:2493:U:H2'	26:DA:2494:G:O4'	2.16	0.46
26:DA:576:U:H2'	26:DA:577:G:C8	2.51	0.46
26:DA:717:G:H2'	26:DA:718:A:O4'	2.17	0.46
27:DB:63:G:H2'	27:DB:64:C:C6	2.50	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.50	0.46
26:DA:784:A:C6	28:DD:229:VAL:HG21	2.51	0.46
33:DI:88:ILE:HG21	33:DI:144:VAL:CG1	2.46	0.46
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.98	0.46
1:AA:143:A:H2'	1:AA:143:A:N3	2.31	0.45
1:AA:102:G:O2'	1:AA:151:A:N3	2.31	0.45
1:AA:348:G:C2'	1:AA:349:A:H5'	2.46	0.45
1:AA:779:C:H2'	1:AA:780:A:O4'	2.16	0.45
2:AB:35:GLU:OE1	2:AB:38:GLY:HA2	2.17	0.45
1:AA:1216:G:H5''	14:AN:5:ALA:CB	2.46	0.45
24:AX:50:U:O5'	24:AX:50:U:H6	1.99	0.45
26:BA:2161:C:C2	26:BA:2175:G:C2	3.05	0.45
26:BA:1701:A:C1'	26:BA:2833:A:H5'	2.46	0.45
26:BA:769:A:H2'	26:BA:770:G:C8	2.51	0.45
30:BF:178:PRO:HB2	30:BF:201:VAL:CG2	2.47	0.45
31:BG:43:LEU:C	31:BG:45:GLU:H	2.19	0.45
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.99	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.98	0.45
26:BA:144:C:H5'	44:BX:2:LYS:HE2	1.98	0.45
1:CA:375:U:O3'	16:CP:6:LEU:HB2	2.17	0.45
1:CA:407:G:N1	1:CA:436:C:C2	2.83	0.45
1:CA:779:C:H2'	1:CA:780:A:O4'	2.16	0.45
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.16	0.45
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.17	0.45
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.45
24:CX:60:U:H3'	24:CX:61:C:H6	1.81	0.45
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.46	0.45
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.16	0.45
26:DA:2082:A:H3'	26:DA:2083:G:H8	1.81	0.45
26:DA:2133:G:O2'	26:DA:2157:G:N2	2.31	0.45
26:DA:2137:C:N4	26:DA:2154:G:N1	2.29	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:448:U:C4	26:DA:583:G:H1'	2.51	0.45
27:DB:16:G:H2'	27:DB:17:C:C6	2.51	0.45
27:DB:1:U:H2'	27:DB:2:C:C6	2.51	0.45
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.98	0.45
61:DA:4083:HOH:O	36:DP:16:ARG:HG3	2.15	0.45
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.79	0.45
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.49	0.45
1:AA:1252:A:H61	1:AA:1285:A:N6	2.05	0.45
1:AA:892:A:O2'	1:AA:1415:G:H4'	2.16	0.45
1:AA:93:G:H2'	1:AA:96:U:O4'	2.16	0.45
11:AK:45:GLY:O	11:AK:50:TYR:HB2	2.17	0.45
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.46	0.45
26:BA:1577:C:H42	26:BA:1586:G:H1	1.65	0.45
26:BA:1766:G:H5'	26:BA:1767:A:OP2	2.17	0.45
26:BA:1938:A:H2'	26:BA:1939:U:O4'	2.16	0.45
26:BA:2087:C:H2'	26:BA:2088:C:C6	2.51	0.45
26:BA:2149:G:C2	26:BA:2150:C:C2	3.04	0.45
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.73	0.45
1:CA:1202:G:H2'	1:CA:1203:C:O4'	2.16	0.45
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.17	0.45
1:CA:1371:G:C6	1:CA:1372:U:C4	3.04	0.45
1:CA:728:A:OP1	1:CA:742:G:O2'	2.34	0.45
1:CA:758:G:H5'	1:CA:880:C:H1'	1.98	0.45
1:CA:90:U:C2'	1:CA:91:C:H5'	2.46	0.45
1:CA:978:A:O2'	1:CA:1321:C:N4	2.48	0.45
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.84	0.45
7:CG:51:GLN:HB3	7:CG:51:GLN:HE21	1.64	0.45
9:CI:72:GLY:O	9:CI:76:ALA:N	2.43	0.45
3:CC:33:LEU:HD21	14:CN:53:LEU:HD22	1.97	0.45
24:CX:38:A:O5'	24:CX:38:A:H8	1.99	0.45
26:DA:184:C:H2'	26:DA:185:U:H6	1.80	0.45
26:DA:2124:G:H3'	26:DA:2125:G:H5''	1.96	0.45
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.78	0.45
34:DN:4:TYR:CE2	41:DU:100:VAL:HG11	2.51	0.45
43:DW:79:GLY:HA3	43:DW:100:THR:HG22	1.97	0.45
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.82	0.45
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.52	0.45
1:AA:22:G:H4'	1:AA:885:G:C8	2.51	0.45
1:AA:625:G:H4'	16:AP:16:HIS:HB3	1.97	0.45
1:AA:66:G:H2'	1:AA:67:C:H5'	1.98	0.45
1:AA:1152:A:OP1	10:AJ:70:ARG:NH2	2.50	0.45
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.51	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	1.99	0.45
26:BA:1217:G:H5'	26:BA:1218:G:OP2	2.16	0.45
26:BA:1686:U:O2'	26:BA:1687:C:H5'	2.17	0.45
26:BA:2097:U:OP2	26:BA:2250:G:O2'	2.28	0.45
26:BA:321:C:OP1	45:BY:87:LYS:NZ	2.42	0.45
26:BA:950:C:H2'	26:BA:951:U:C6	2.52	0.45
33:BI:106:GLY:HA2	33:BI:107:VAL:CG2	2.44	0.45
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.43	0.45
1:CA:131:C:H2'	1:CA:132:C:C6	2.51	0.45
1:CA:162:A:N3	1:CA:348:G:H4'	2.31	0.45
1:CA:72:C:N3	1:CA:97:G:C2	2.83	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
23:CW:76:PPU:N	24:CX:76:31H:N3'	2.61	0.45
24:CX:7:G:H5''	24:CX:8:4SU:H5	1.98	0.45
55:D8:9:GLY:O	55:D8:13:ARG:HG2	2.16	0.45
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.17	0.45
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.64	0.45
26:DA:1265:A:OP1	26:DA:1265:A:H8	2.00	0.45
26:DA:2016:U:H2'	26:DA:2017:U:C6	2.52	0.45
26:DA:2704:C:H2'	26:DA:2705:A:O4'	2.16	0.45
26:DA:2773:C:O2'	26:DA:2774:C:H5'	2.16	0.45
26:DA:330:A:C2	26:DA:1210:A:H2'	2.51	0.45
26:DA:608:A:OP1	30:DF:100:THR:OG1	2.25	0.45
26:DA:629:G:H5''	26:DA:650:C:O2'	2.16	0.45
26:DA:947:G:N2	26:DA:971:C:C2	2.84	0.45
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.51	0.45
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.46	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
38:DR:36:THR:HG22	38:DR:37:THR:H	1.81	0.45
39:DS:110:LEU:HD12	39:DS:110:LEU:HA	1.80	0.45
1:CA:1464:G:OP1	40:DT:108:ARG:HD3	2.16	0.45
42:DV:60:GLU:N	42:DV:95:LEU:O	2.38	0.45
45:DY:6:HIS:H	45:DY:6:HIS:CD2	2.34	0.45
1:AA:1030:C:N3	1:AA:1031:G:N2	2.65	0.45
1:AA:1225:A:H2'	1:AA:1226:C:C5	2.51	0.45
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.16	0.45
6:AF:12:PRO:HG3	6:AF:57:GLN:O	2.16	0.45
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.82	0.45
51:B4:59:PHE:HB2	51:B4:62:ARG:CZ	2.46	0.45
26:BA:1091:A:OP1	26:BA:1092:A:H3'	2.16	0.45
26:BA:1461:U:O2'	26:BA:1463:C:OP1	2.29	0.45
26:BA:2451:A:C8	26:BA:2451:A:H5'	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:842:C:H2'	26:BA:843:C:C6	2.52	0.45
26:BA:921:G:C2'	26:BA:922:G:H5'	2.46	0.45
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.17	0.45
1:CA:1176:A:H2'	1:CA:1177:G:O4'	2.16	0.45
1:CA:509:A:H2'	1:CA:510:A:C8	2.50	0.45
1:CA:5:U:H2'	1:CA:5:U:H6	1.53	0.45
3:CC:35:GLU:HG3	3:CC:36:ASP:N	2.31	0.45
1:CA:1255:G:P	10:CJ:45:ARG:HH22	2.40	0.45
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.16	0.45
13:CM:3:ARG:HB3	13:CM:8:GLU:HA	1.99	0.45
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.29	0.45
19:CS:40:ILE:HD12	19:CS:69:HIS:O	2.16	0.45
49:D2:28:LYS:HB3	49:D2:57:ILE:HG12	1.97	0.45
26:DA:2016:U:O2'	52:D5:7:PRO:O	2.33	0.45
26:DA:1011:G:H1'	26:DA:1013:C:O4'	2.16	0.45
26:DA:1613:G:C2	26:DA:1619:G:C5	3.05	0.45
26:DA:196:A:C4	26:DA:805:G:C6	3.04	0.45
26:DA:250:G:C6	26:DA:251:A:C6	3.04	0.45
26:DA:507:A:H5''	26:DA:508:G:H3'	1.98	0.45
26:DA:719:C:H2'	26:DA:720:C:C6	2.51	0.45
26:DA:815:C:H2'	26:DA:816:C:C6	2.52	0.45
26:DA:828:U:C5	26:DA:2247:A:H4'	2.52	0.45
33:DI:110:ASP:HA	33:DI:111:PRO:HD3	1.80	0.45
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.99	0.45
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.52	0.45
1:AA:429:U:H4'	1:AA:430:A:O5'	2.16	0.45
2:AB:80:ILE:HD12	2:AB:211:ILE:HG22	1.98	0.45
2:AB:82:ARG:NH1	2:AB:86:GLU:OE2	2.50	0.45
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.49	0.45
4:AD:178:VAL:C	4:AD:180:GLY:H	2.20	0.45
7:AG:140:ASP:OD1	7:AG:143:ARG:NH2	2.42	0.45
10:AJ:64:GLU:HG2	14:AN:59:ALA:HB2	1.99	0.45
13:AM:19:LEU:HA	13:AM:19:LEU:HD12	1.79	0.45
15:AO:82:ILE:O	15:AO:86:GLY:N	2.50	0.45
16:AP:6:LEU:HB3	16:AP:17:TYR:CD1	2.51	0.45
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.52	0.45
61:BA:4902:HOH:O	55:B8:42:ARG:HD2	2.15	0.45
26:BA:1002:A:N1	26:BA:2470:G:H4'	2.32	0.45
26:BA:145:G:H2'	26:BA:146:G:C8	2.51	0.45
26:BA:2189:U:H5'	26:BA:2190:G:OP2	2.17	0.45
26:BA:2490:A:H2'	26:BA:2491:G:O4'	2.16	0.45
26:BA:2703:C:O3'	26:BA:2881:C:H4'	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2830:A:P	38:BR:2:ARG:HH22	2.39	0.45
26:BA:611:U:H2'	26:BA:612:C:C6	2.51	0.45
29:BE:73:GLU:HG3	29:BE:73:GLU:H	1.60	0.45
31:BG:56:ALA:HA	31:BG:153:ARG:NH2	2.31	0.45
46:BZ:154:ASP:OD1	46:BZ:155:LEU:HD13	2.17	0.45
1:CA:1002:G:N3	1:CA:1003:G:C8	2.85	0.45
1:CA:1515:C:H2'	1:CA:1516:G:C8	2.52	0.45
1:CA:189(A):C:C2'	1:CA:189(B):C:H5'	2.46	0.45
1:CA:509:A:H5'	4:CD:54:TYR:HD1	1.81	0.45
1:CA:624:C:O2'	1:CA:625:G:H5'	2.17	0.45
1:CA:709:G:H2'	1:CA:710:G:H5'	1.98	0.45
1:CA:950:U:H2'	1:CA:951:G:H8	1.81	0.45
1:CA:976:G:OP1	14:CN:32:SER:N	2.38	0.45
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.99	0.45
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.43	0.45
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.50	0.45
26:DA:2139:C:H3'	26:DA:2140:C:H6	1.80	0.45
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.51	0.45
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.17	0.45
26:DA:2854:G:H2'	26:DA:2855:C:C6	2.50	0.45
26:DA:2886:G:H2'	26:DA:2887:U:C6	2.51	0.45
26:DA:222:A:H3'	26:DA:421:U:H5'	1.97	0.45
26:DA:71:A:H5''	26:DA:73:A:N9	2.32	0.45
26:DA:754:C:H2'	26:DA:755:C:H6	1.82	0.45
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.51	0.45
26:DA:2679:A:H4'	29:DE:165:VAL:HG11	1.98	0.45
32:DH:28:GLY:HA3	32:DH:79:VAL:HB	1.98	0.45
1:AA:1173:G:N1	1:AA:1174:G:C5	2.85	0.45
1:AA:160:A:H2'	1:AA:161:A:C8	2.52	0.45
1:AA:280:C:N3	17:AQ:39:SER:N	2.65	0.45
1:AA:599:C:H4'	8:AH:130:GLY:C	2.37	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.51	0.45
1:AA:79:G:C6	1:AA:90:U:N3	2.84	0.45
1:AA:1298:C:H2'	7:AG:114:ARG:NH1	2.31	0.45
16:AP:59:TRP:HA	16:AP:62:VAL:HG12	1.99	0.45
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.16	0.45
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.81	0.45
24:AX:13:C:O2'	26:BA:1946:C:H4'	2.15	0.45
26:BA:141:C:H2'	26:BA:142:G:O4'	2.16	0.45
26:BA:1895:U:OP1	26:BA:2422:G:O2'	2.25	0.45
26:BA:2156:A:N1	26:BA:2180:A:C8	2.85	0.45
26:BA:2348:A:H61	47:B0:43:THR:CG2	2.27	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:BD:152:GLY:O	28:BD:154:LYS:HG2	2.17	0.45
26:BA:1501:U:H1'	38:BR:60:LEU:HD21	1.98	0.45
41:BU:110:VAL:HG12	41:BU:114:LYS:HE2	1.98	0.45
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.45
1:CA:1400:C:C5	24:CX:35:A:C4	3.05	0.45
1:CA:293:G:H5'	1:CA:610:G:C2	2.52	0.45
1:CA:339:C:H2'	1:CA:340:U:C6	2.52	0.45
1:CA:34:C:H2'	1:CA:35:G:C8	2.51	0.45
1:CA:762:C:H2'	1:CA:763:G:C8	2.51	0.45
4:CD:173:TRP:CH2	4:CD:194:LEU:HD23	2.52	0.45
6:CF:6:VAL:HG13	6:CF:90:VAL:HG22	1.98	0.45
26:DA:118:A:N3	26:DA:178:G:H1'	2.32	0.45
26:DA:2152:G:H5'	26:DA:2153:G:OP2	2.17	0.45
26:DA:2427:C:OP1	61:DA:4236:HOH:O	2.21	0.45
26:DA:2701:C:H2'	26:DA:2702:U:H2'	1.99	0.45
26:DA:823:G:H2'	26:DA:824:A:C8	2.52	0.45
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.98	0.45
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.99	0.45
1:AA:1044:A:C5	1:AA:1045:C:H1'	2.52	0.45
1:AA:1095:U:P	1:AA:1108:G:H1	2.39	0.45
1:AA:1310:G:H1	1:AA:1327:C:H42	1.63	0.45
1:AA:1431:C:H2'	1:AA:1432:G:O4'	2.16	0.45
1:AA:192:U:H2'	1:AA:193:C:C6	2.52	0.45
1:AA:370:C:H2'	1:AA:371:G:C8	2.52	0.45
2:AB:92:TYR:OH	2:AB:150:SER:OG	2.34	0.45
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.16	0.45
47:B0:43:THR:HG23	47:B0:43:THR:O	2.16	0.45
26:BA:1829:U:H5'	28:BD:259:THR:CG2	2.45	0.45
26:BA:2331:G:C2	39:BS:3:ARG:HA	2.51	0.45
26:BA:2331:G:H22	39:BS:3:ARG:NE	2.15	0.45
26:BA:2798:C:H2'	26:BA:2799:U:O4'	2.17	0.45
26:BA:703:G:H2'	26:BA:704:U:O4'	2.16	0.45
28:BD:145:VAL:HG13	28:BD:191:ALA:HB2	1.99	0.45
30:BF:56:GLU:OE2	30:BF:93:LYS:NZ	2.46	0.45
32:BH:150:ALA:HA	32:BH:153:LYS:HG3	1.98	0.45
32:BH:23:ARG:HD2	32:BH:34:GLU:OE1	2.16	0.45
35:BO:63:VAL:HB	35:BO:102:VAL:HG12	1.99	0.45
36:BP:63:PRO:HB2	55:B8:30:ARG:NH2	2.32	0.45
43:BW:18:ARG:HG3	43:BW:76:VAL:HB	1.99	0.45
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.52	0.45
1:CA:791:G:N2	1:CA:1497:G:O3'	2.49	0.45
4:CD:70:ILE:HD11	4:CD:74:GLN:HB3	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.98	0.45
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.50	0.45
1:CA:1327:C:H5'	21:CU:20:LYS:HB3	1.99	0.45
24:CX:65:C:N4	24:CX:66:C:C4	2.85	0.45
50:D3:18:ASP:N	50:D3:18:ASP:OD1	2.50	0.45
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.17	0.45
26:DA:17:G:H4'	41:DU:25:TRP:NE1	2.31	0.45
26:DA:1817:G:H2'	26:DA:1818:U:H5'	1.98	0.45
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.32	0.45
26:DA:2129:C:O2'	26:DA:2130:U:H5'	2.16	0.45
26:DA:858:U:O2	26:DA:2268:A:H2'	2.17	0.45
26:DA:2312:U:H2'	26:DA:2313:C:C6	2.52	0.45
26:DA:2572:A:OP1	26:DA:2574:G:O2'	2.35	0.45
26:DA:2697:G:H2'	26:DA:2698:U:O4'	2.17	0.45
26:DA:724:U:H2'	26:DA:725:G:O4'	2.16	0.45
26:DA:856:C:HO2'	26:DA:857:C:P	2.38	0.45
32:DH:43:VAL:HG13	32:DH:52:VAL:HG22	1.99	0.45
37:DQ:62:GLY:HA2	46:DZ:116:VAL:HG21	1.99	0.45
1:AA:178:C:H2'	1:AA:179:A:C8	2.52	0.45
1:AA:397:A:N3	1:AA:397:A:H3'	2.32	0.45
1:AA:581:G:OP1	15:AO:61:GLY:HA3	2.17	0.45
3:AC:21:ARG:NH1	3:AC:56:ASP:OD2	2.50	0.45
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.31	0.45
4:AD:18:LYS:HE3	4:AD:20:TYR:OH	2.17	0.45
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.32	0.45
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.47	0.45
26:BA:1954:A:H2'	26:BA:1955:G:O4'	2.17	0.45
26:BA:217:A:H3'	26:BA:218:A:C5'	2.47	0.45
26:BA:2289:G:P	47:B0:10:THR:HG21	2.57	0.45
26:BA:596:G:O2'	26:BA:597:C:H3'	2.16	0.45
26:BA:664:U:H2'	26:BA:665:C:C6	2.52	0.45
30:BF:18:ARG:HG2	30:BF:19:GLU:H	1.81	0.45
31:BG:108:ASN:HD22	51:B4:22:ILE:HG21	1.82	0.45
31:BG:61:ALA:O	31:BG:65:GLY:N	2.39	0.45
33:BI:122:GLU:HB2	33:BI:126:TYR:OH	2.17	0.45
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.97	0.45
1:CA:1118:C:C2	1:CA:1119:C:C5	3.05	0.45
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.17	0.45
1:CA:193:C:H2'	1:CA:194:C:H6	1.82	0.45
1:CA:737:A:O2'	1:CA:738:C:H5'	2.16	0.45
1:CA:936:C:H1'	1:CA:1382:C:H42	1.80	0.45
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:CT:57:ARG:HH12	20:CT:100:ILE:HD12	1.82	0.45
24:CX:41:C:C2	24:CX:42:G:C8	3.04	0.45
26:DA:1394:U:H4'	26:DA:1603:A:H4'	1.99	0.45
26:DA:1721:G:H5'	26:DA:1722:A:H5''	1.99	0.45
26:DA:2114:A:C8	26:DA:2168:G:H1'	2.51	0.45
26:DA:2302:G:C2	26:DA:2315:G:C2	3.05	0.45
26:DA:2416:C:O2'	26:DA:2417:C:H5'	2.17	0.45
26:DA:79:G:O2'	26:DA:346:A:N3	2.35	0.45
26:DA:455:C:N3	26:DA:472:A:H2'	2.31	0.45
26:DA:940:G:O2'	61:DA:3711:HOH:O	2.18	0.45
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.16	0.45
36:DP:65:ARG:HG3	55:D8:25:MET:CG	2.47	0.45
1:AA:1133:G:H2'	1:AA:1134:G:H8	1.81	0.45
1:AA:1136:U:H5''	1:AA:1137:C:C2	2.52	0.45
1:AA:67:C:H2'	1:AA:68:G:H8	1.79	0.45
1:AA:922:G:H2'	1:AA:923:A:C8	2.52	0.45
5:AE:143:ARG:NH1	8:AH:77:GLU:OE2	2.49	0.45
1:AA:1291:G:H4'	9:AI:39:GLY:HA3	1.99	0.45
10:AJ:5:ARG:NH2	10:AJ:71:LEU:HD21	2.32	0.45
13:AM:51:ALA:HA	13:AM:54:VAL:HG22	1.98	0.45
26:BA:231:G:C8	55:B8:5:LYS:HG2	2.51	0.45
26:BA:1159:U:H2'	26:BA:1160:G:C8	2.52	0.45
26:BA:1604:C:H5''	26:BA:1605:A:OP2	2.17	0.45
26:BA:364:A:H2'	26:BA:365:G:O4'	2.17	0.45
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.99	0.45
31:BG:124:SER:HB2	31:BG:131:TYR:CE1	2.52	0.45
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.17	0.45
44:BX:65:ARG:HB2	44:BX:70:LEU:HD23	1.99	0.45
1:CA:1053:G:H4'	1:CA:1054:C:H5'	1.99	0.45
1:CA:1099:G:C2	1:CA:1100:C:O2	2.70	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.16	0.45
6:CF:2:ARG:CZ	6:CF:69:GLU:HG2	2.46	0.45
7:CG:42:ILE:HG22	7:CG:120:ILE:HD12	1.98	0.45
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.99	0.45
13:CM:82:MET:O	13:CM:93:ARG:NH2	2.48	0.45
24:CX:15:G:C4	24:CX:59:A:N6	2.85	0.45
54:D7:13:ALA:HB2	54:D7:46:VAL:HG21	1.99	0.45
26:DA:1473:G:H2'	26:DA:1474:C:O4'	2.16	0.45
26:DA:1557:C:H5''	26:DA:1558:A:OP2	2.17	0.45
26:DA:191:A:H2'	26:DA:192:C:C6	2.52	0.45
26:DA:2315:G:C6	26:DA:2316:C:N4	2.85	0.45
26:DA:265:A:C8	26:DA:266:G:H1'	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:893:C:H5'	26:DA:894:C:OP2	2.17	0.45
28:DD:77:ALA:HB2	28:DD:97:TYR:CD2	2.52	0.45
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.47	0.45
43:DW:72:LYS:N	43:DW:106:ILE:O	2.48	0.45
3:AC:16:ARG:HH22	3:AC:183:ASP:CG	2.20	0.45
6:AF:89:MET:HG2	6:AF:91:VAL:HG23	1.99	0.45
10:AJ:57:LYS:HD2	10:AJ:60:ARG:HH21	1.81	0.45
10:AJ:5:ARG:HE	10:AJ:5:ARG:HB3	1.48	0.45
26:BA:1873:G:O2'	28:BD:253:GLN:NE2	2.38	0.45
26:BA:2183:C:O2'	26:BA:2195:A:H4'	2.17	0.45
26:BA:492:A:O3'	54:B7:33:ARG:NH1	2.48	0.45
27:BB:96:U:OP1	46:BZ:14:LYS:NZ	2.49	0.45
28:BD:101:GLU:HG2	28:BD:103:ARG:HD3	1.98	0.45
1:CA:1064:G:H1'	1:CA:1065:U:OP2	2.16	0.45
1:CA:1124:G:O2'	1:CA:1145:C:C4	2.70	0.45
1:CA:1280:A:H2'	1:CA:1281:U:N3	2.31	0.45
1:CA:1405:G:H2'	1:CA:1406:U:C6	2.51	0.45
1:CA:266:G:O3'	17:CQ:67:LYS:HB2	2.16	0.45
1:CA:624:C:O2'	16:CP:10:GLY:HA2	2.16	0.45
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.98	0.45
8:CH:81:HIS:N	8:CH:138:TRP:O	2.50	0.45
8:CH:9:MET:HG3	8:CH:26:VAL:HG21	1.99	0.45
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.17	0.45
24:CX:30:G:C6	24:CX:31:G:N7	2.85	0.45
51:D4:15:ILE:N	51:D4:31:ILE:O	2.32	0.45
26:DA:1359:A:N1	26:DA:1372:U:O4	2.50	0.45
26:DA:1660:C:H2'	26:DA:1661:G:H8	1.82	0.45
26:DA:1826:G:H2'	26:DA:1827:C:C6	2.51	0.45
26:DA:1903:G:OP1	28:DD:241:PRO:HB2	2.16	0.45
26:DA:2153:G:C6	26:DA:2154:G:C6	3.05	0.45
31:DG:111:LEU:O	31:DG:114:ILE:HB	2.17	0.45
31:DG:61:ALA:O	31:DG:65:GLY:N	2.44	0.45
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.43	0.45
26:DA:2675:A:H5'	35:DO:29:ASN:O	2.17	0.45
39:DS:38:GLN:HA	39:DS:50:SER:HA	1.99	0.45
1:AA:1052:U:H5''	1:AA:1053:G:OP2	2.17	0.44
1:AA:1187:G:H2'	1:AA:1188:A:C8	2.52	0.44
1:AA:708:C:H2'	1:AA:709:G:H8	1.82	0.44
1:AA:937:A:H2'	1:AA:938:A:H5'	1.99	0.44
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.22	0.44
1:AA:1124:G:H5''	10:AJ:35:SER:OG	2.17	0.44
26:BA:1231:G:H2'	26:BA:1232:G:O4'	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:139:A:H8	26:BA:1454:C:HO2'	1.56	0.44
26:BA:1494:G:N2	26:BA:1511:C:O2	2.25	0.44
26:BA:1493:C:O2'	26:BA:1592:A:O2'	2.33	0.44
26:BA:1985:U:H4'	26:BA:1986:G:OP1	2.17	0.44
26:BA:2140:U:H4'	26:BA:2141:A:OP1	2.16	0.44
26:BA:266:C:H2'	26:BA:267:C:C6	2.52	0.44
26:BA:312:C:H2'	26:BA:313:A:H8	1.82	0.44
36:BP:98:GLU:O	36:BP:101:VAL:HB	2.16	0.44
26:BA:2479:C:H4'	37:BQ:123:HIS:CG	2.52	0.44
41:BU:50:ARG:HG2	41:BU:53:ARG:NH2	2.32	0.44
1:CA:1171:G:O2'	1:CA:1172:C:H5'	2.16	0.44
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.82	0.44
1:CA:630:G:H2'	1:CA:631:G:C8	2.52	0.44
1:CA:690:G:H8	1:CA:690:G:O5'	1.99	0.44
1:CA:707:C:H5''	11:CK:85:ARG:NH1	2.32	0.44
1:CA:922:G:H2'	1:CA:923:A:C8	2.52	0.44
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.98	0.44
2:CB:207:ALA:O	2:CB:211:ILE:HG13	2.17	0.44
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.57	0.44
1:CA:688:G:H5'	11:CK:46:GLY:C	2.37	0.44
11:CK:92:GLU:OE2	11:CK:96:ARG:NH1	2.50	0.44
20:CT:62:LEU:HD23	20:CT:62:LEU:HA	1.82	0.44
24:CX:19:G:P	24:CX:60:U:H3	2.40	0.44
26:DA:466:A:O3'	54:D7:33:ARG:NH1	2.50	0.44
26:DA:1183:G:H4'	50:D3:29:ARG:HH22	1.82	0.44
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.44
26:DA:2127:G:C6	26:DA:2161:C:N3	2.84	0.44
26:DA:2273:A:O2'	26:DA:2274:A:H5'	2.17	0.44
26:DA:2416:C:C2'	26:DA:2417:C:H5'	2.47	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44
26:DA:539:G:H2'	26:DA:540:C:H6	1.82	0.44
26:DA:601:C:O2'	26:DA:605:C:H5''	2.18	0.44
26:DA:884:C:H2'	26:DA:885:C:O4'	2.17	0.44
30:DF:164:ARG:O	30:DF:168:ARG:HB2	2.16	0.44
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.17	0.44
37:DQ:38:GLU:HB2	37:DQ:127:ILE:HG22	1.99	0.44
42:DV:85:LYS:HB2	42:DV:85:LYS:HE3	1.72	0.44
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.88	0.44
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.17	0.44
1:AA:573:A:N3	1:AA:883:C:O2'	2.41	0.44
24:AX:9:G:N3	24:AX:45:G:H2'	2.31	0.44
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:331:G:H21	26:BA:354:A:H62	1.66	0.44
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	2.00	0.44
1:CA:1417:G:H22	1:CA:1482:G:H2'	1.81	0.44
1:CA:164:U:H2'	1:CA:165:C:C6	2.52	0.44
1:CA:73:G:C6	1:CA:76:C:C5	3.05	0.44
1:CA:937:A:H2'	1:CA:938:A:H5'	1.99	0.44
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.17	0.44
14:CN:3:ARG:HD2	14:CN:4:LYS:N	2.32	0.44
17:CQ:45:HIS:HD2	17:CQ:65:ILE:HG12	1.82	0.44
24:CX:29:G:N1	24:CX:30:G:C4	2.85	0.44
51:D4:26:SER:OG	51:D4:27:THR:N	2.48	0.44
26:DA:1223:G:N2	26:DA:1227:G:C4	2.85	0.44
26:DA:1676:A:H2'	26:DA:1677:A:O4'	2.18	0.44
26:DA:2063:C:C4	26:DA:2064:C:C4	3.05	0.44
26:DA:210:C:H2'	26:DA:211:A:C8	2.52	0.44
26:DA:2552:U:C2	26:DA:2554:U:H5''	2.51	0.44
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.44
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.31	0.44
26:DA:339:U:O5'	26:DA:339:U:H6	2.00	0.44
26:DA:444:C:H4'	30:DF:49:ALA:HB2	1.99	0.44
27:DB:114:C:H2'	27:DB:115:G:O4'	2.17	0.44
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.56	0.44
1:AA:1107:C:C4	1:AA:1108:G:C8	3.05	0.44
1:AA:1262:C:N3	1:AA:1273:G:C6	2.85	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
1:AA:920:U:H2'	1:AA:921:U:C6	2.52	0.44
10:AJ:47:PHE:CZ	14:AN:37:PHE:HE1	2.36	0.44
26:BA:2203:G:HO2'	26:BA:2204:G:P	2.41	0.44
26:BA:594:A:N6	26:BA:2511:C:O3'	2.47	0.44
26:BA:2741:U:H2'	26:BA:2742:G:C8	2.53	0.44
26:BA:316:C:H2'	26:BA:317:U:C6	2.52	0.44
30:BF:129:PHE:HA	30:BF:142:TRP:NE1	2.31	0.44
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	2.00	0.44
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.50	0.44
1:CA:1261:A:C6	1:CA:1262:C:C2	3.05	0.44
1:CA:1405:G:O4'	1:CA:1519:A:H4'	2.17	0.44
1:CA:19:C:H4'	1:CA:864:A:O4'	2.17	0.44
1:CA:936:C:H2'	1:CA:937:A:O4'	2.18	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
6:CF:24:GLU:HG3	6:CF:28:ARG:HD3	1.99	0.44
6:CF:46:ARG:HB3	6:CF:60:PHE:CE1	2.51	0.44
1:CA:1216:G:OP1	14:CN:2:ALA:HA	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:D6:14:THR:O	53:D6:17:LYS:NZ	2.47	0.44
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.17	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:NH1	2.32	0.44
26:DA:1978:A:H2'	26:DA:1979:C:O4'	2.17	0.44
26:DA:2101:G:H2'	26:DA:2102:U:O4'	2.17	0.44
26:DA:2131:G:C8	26:DA:2133:G:N1	2.86	0.44
26:DA:2187:G:C2	26:DA:2188:C:C2	3.05	0.44
26:DA:248:G:O5'	26:DA:249:C:H5''	2.17	0.44
26:DA:2667:C:N3	32:DH:110:SER:OG	2.29	0.44
26:DA:854:G:H2'	26:DA:855:G:H8	1.82	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
61:DA:3809:HOH:O	30:DF:68:LYS:HE2	2.17	0.44
38:DR:72:ASP:OD2	38:DR:75:LEU:HB2	2.18	0.44
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.16	0.44
1:AA:1173:G:C6	1:AA:1174:G:C5	3.06	0.44
1:AA:499:A:H4'	1:AA:500:G:H5'	1.99	0.44
1:AA:715:A:H2'	1:AA:716:A:C8	2.53	0.44
1:AA:985:C:H2'	1:AA:986:A:H8	1.82	0.44
1:AA:986:A:H2'	1:AA:987:G:C8	2.53	0.44
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.51	0.44
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.99	0.44
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.18	0.44
24:AX:16:C:H5''	24:AX:17:C:C5	2.53	0.44
26:BA:121:G:H2'	26:BA:122:G:O4'	2.18	0.44
26:BA:1547:C:H2'	26:BA:1548:C:C6	2.52	0.44
26:BA:1824:C:H2'	26:BA:1825:U:C6	2.53	0.44
26:BA:2185:C:C4	26:BA:2186:C:O2	2.71	0.44
26:BA:310:C:H2'	26:BA:311:C:C6	2.53	0.44
26:BA:858:U:P	36:BP:29:LYS:H	2.40	0.44
26:BA:918:U:OP1	37:BQ:5:ARG:HD3	2.17	0.44
31:BG:41:GLN:HB3	31:BG:43:LEU:HD13	1.99	0.44
31:BG:7:LEU:HD23	31:BG:7:LEU:HA	1.85	0.44
1:CA:1112:C:C2	3:CC:178:LEU:HB2	2.52	0.44
1:CA:66:G:H2'	1:CA:67:C:H5'	1.98	0.44
2:CB:103:THR:HA	2:CB:180:LEU:HD11	1.99	0.44
5:CE:41:VAL:O	5:CE:67:VAL:HG13	2.17	0.44
1:CA:1400:C:N4	24:CX:34:C:H2'	2.26	0.44
26:DA:1370:C:N4	26:DA:1371:G:C6	2.86	0.44
26:DA:1359:A:C6	26:DA:1372:U:O4	2.69	0.44
26:DA:2140:C:C2	26:DA:2152:G:C2	3.05	0.44
26:DA:2151:G:H2'	26:DA:2152:G:C8	2.41	0.44
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:DE:36:ARG:NH2	29:DE:86:PRO:O	2.47	0.44
32:DH:26:VAL:HB	32:DH:33:LEU:HD12	1.99	0.44
37:DQ:1:MET:N	37:DQ:1:MET:SD	2.82	0.44
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	1.99	0.44
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	1.99	0.44
1:AA:1442(A):G:C8	40:BT:118:ARG:HG2	2.53	0.44
1:AA:222:U:H2'	1:AA:223:U:C6	2.52	0.44
3:AC:180:ALA:O	3:AC:182:ILE:N	2.51	0.44
1:AA:1366:C:HO2'	10:AJ:60:ARG:HH22	1.64	0.44
13:AM:14:ARG:HB2	13:AM:16:ASP:OD1	2.16	0.44
1:AA:110:C:O2'	16:AP:25:ARG:O	2.30	0.44
24:AX:16:C:H5''	24:AX:17:C:H5	1.83	0.44
51:B4:59:PHE:O	51:B4:62:ARG:NE	2.47	0.44
26:BA:1227:A:H2'	26:BA:1228:G:C8	2.53	0.44
26:BA:1316:C:O2'	26:BA:1695:C:OP2	2.35	0.44
26:BA:178:G:O6	26:BA:194:G:O2'	2.29	0.44
26:BA:577:U:C4	26:BA:578:U:C4	3.06	0.44
27:BB:6:C:H2'	27:BB:7:G:H5''	2.00	0.44
28:BD:38:LYS:HD2	28:BD:38:LYS:HA	1.87	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
32:BH:61:HIS:O	32:BH:65:HIS:HB2	2.18	0.44
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	1.98	0.44
36:BP:27:HIS:O	36:BP:31:ALA:HA	2.16	0.44
26:BA:1201:A:OP1	41:BU:55:ARG:HD3	2.17	0.44
41:BU:86:ALA:HB2	41:BU:116:ALA:HB2	1.98	0.44
44:BX:50:LYS:HB3	44:BX:87:GLN:HE22	1.82	0.44
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.80	0.44
1:CA:156:G:N1	1:CA:165:C:N3	2.39	0.44
1:CA:560:U:O2'	1:CA:561:U:OP2	2.32	0.44
1:CA:765:G:H5''	1:CA:766:A:OP1	2.18	0.44
1:CA:775:G:N2	1:CA:804:U:O4	2.51	0.44
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.17	0.44
10:CJ:55:LYS:HG3	10:CJ:56:HIS:N	2.31	0.44
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.44
26:DA:2357:U:OP1	47:D0:20:ARG:HD3	2.18	0.44
26:DA:469:G:O6	54:D7:37:LYS:HE2	2.17	0.44
26:DA:1224:C:O2'	42:DV:85:LYS:HA	2.18	0.44
26:DA:1333:C:H2'	26:DA:1334:G:H8	1.83	0.44
26:DA:1422:G:H1'	26:DA:1496:A:N1	2.33	0.44
26:DA:1857:G:C6	26:DA:1858:G:N1	2.86	0.44
26:DA:1963:U:H4'	26:DA:1964:G:OP1	2.17	0.44
26:DA:2137:C:C4	26:DA:2138:C:N4	2.85	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.53	0.44
26:DA:2489:G:C6	26:DA:2490:G:C6	3.06	0.44
26:DA:340:A:H2'	26:DA:341:G:O4'	2.17	0.44
26:DA:483:A:O4'	45:DY:48:ALA:HB1	2.17	0.44
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.17	0.44
1:AA:164:U:H2'	1:AA:165:C:C6	2.52	0.44
1:AA:828:A:N6	1:AA:858:G:O2'	2.51	0.44
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.99	0.44
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.81	0.44
1:AA:509:A:H5'	4:AD:54:TYR:HD2	1.82	0.44
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.98	0.44
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	2.00	0.44
8:AH:25:ASP:OD1	8:AH:60:ARG:HG3	2.17	0.44
11:AK:99:GLN:HE21	11:AK:108:ILE:HD11	1.82	0.44
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.52	0.44
26:BA:2396:G:P	47:B0:55:ARG:HH12	2.40	0.44
26:BA:1576:G:C6	26:BA:1577:C:N4	2.86	0.44
26:BA:2060:G:H2'	26:BA:2061:C:O4'	2.18	0.44
26:BA:236:G:H4'	26:BA:413:G:C5	2.52	0.44
26:BA:390:G:H2'	26:BA:391:G:C8	2.53	0.44
30:BF:74:ARG:H	30:BF:74:ARG:HG3	1.50	0.44
31:BG:16:ARG:HH21	31:BG:31:VAL:HG11	1.81	0.44
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.19	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	2.00	0.44
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.83	0.44
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.52	0.44
1:CA:616:G:C2	1:CA:617:G:C8	3.06	0.44
2:CB:210:SER:O	2:CB:214:ILE:HG12	2.18	0.44
3:CC:36:ASP:O	3:CC:39:ILE:HB	2.18	0.44
5:CE:68:GLU:OE1	5:CE:70:PRO:HG3	2.17	0.44
12:CL:34:ARG:HB3	12:CL:34:ARG:HE	1.47	0.44
12:CL:97:ARG:HB2	12:CL:98:TYR:CE2	2.52	0.44
24:CX:30:G:C4	24:CX:31:G:C8	3.05	0.44
26:DA:2230:G:H1'	48:D1:45:ASN:CG	2.38	0.44
26:DA:1126:A:H4'	26:DA:1127:A:O5'	2.18	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.18	0.44
26:DA:2024:G:N7	61:DA:3704:HOH:O	2.36	0.44
26:DA:2248:C:OP2	61:DA:3945:HOH:O	2.21	0.44
26:DA:2442:C:H2'	26:DA:2443:C:H6	1.83	0.44
26:DA:815:C:H2'	26:DA:816:C:H6	1.81	0.44
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.53	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.44
40:DT:2:ASN:O	40:DT:6:LEU:HD22	2.18	0.44
1:AA:1252:A:N6	1:AA:1285:A:H61	2.06	0.44
1:AA:1330:U:H4'	13:AM:23:TYR:CZ	2.53	0.44
1:AA:1503:A:N3	22:AV:13:A:C6	2.85	0.44
1:AA:53:A:H61	1:AA:358:U:H3	1.65	0.44
1:AA:614:A:C2'	1:AA:615:C:H5'	2.48	0.44
1:AA:938:A:C6	1:AA:939:G:C5	3.06	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.99	0.44
3:AC:27:LYS:NZ	3:AC:27:LYS:HA	2.32	0.44
4:AD:118:ARG:HG3	4:AD:136:PRO:HB3	2.00	0.44
4:AD:63:LYS:HG3	4:AD:198:VAL:HG22	2.00	0.44
5:AE:102:ALA:HB2	5:AE:120:THR:HG21	2.00	0.44
5:AE:31:LEU:HD11	5:AE:129:ILE:HA	2.00	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
11:AK:69:ALA:O	11:AK:73:MET:HG3	2.18	0.44
26:BA:1506:G:C3'	26:BA:1507:A:H5''	2.47	0.44
26:BA:2637:G:H2'	26:BA:2638:C:H6	1.83	0.44
29:BE:51:PHE:O	29:BE:77:ILE:HD12	2.18	0.44
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.18	0.44
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.52	0.44
45:BY:5:MET:HE1	45:BY:32:PRO:HA	2.00	0.44
46:BZ:117:LEU:HD23	46:BZ:119:GLU:OE1	2.18	0.44
1:CA:1038:C:O2'	1:CA:1039:C:H5'	2.17	0.44
1:CA:337:C:H2'	1:CA:338:A:H8	1.83	0.44
1:CA:976:G:O2'	1:CA:1362:C:N4	2.50	0.44
1:CA:982:U:H5	14:CN:31:ARG:HH22	1.62	0.44
2:CB:162:ILE:HG13	2:CB:162:ILE:O	2.17	0.44
5:CE:72:GLN:O	5:CE:75:THR:HG22	2.18	0.44
8:CH:14:ARG:O	8:CH:18:ARG:HD3	2.18	0.44
19:CS:9:VAL:HB	51:D4:67:TYR:CD2	2.47	0.44
24:CX:30:G:H2'	24:CX:31:G:O4'	2.17	0.44
54:D7:12:ARG:NH2	54:D7:44:PRO:HB3	2.32	0.44
26:DA:1232:G:C2	26:DA:1233:C:C2	3.05	0.44
26:DA:1321:A:H2'	26:DA:1322:A:O4'	2.17	0.44
26:DA:1470:G:H5''	26:DA:1471:A:OP1	2.17	0.44
26:DA:2138:C:N3	26:DA:2153:G:N2	2.59	0.44
26:DA:2166:G:H5'	26:DA:2167:U:O5'	2.18	0.44
26:DA:2389:G:H5''	26:DA:2390:U:O4'	2.18	0.44
26:DA:265:A:H1'	26:DA:266:G:O4'	2.18	0.44
26:DA:375:C:H2'	26:DA:376:C:H6	1.82	0.44
46:DZ:69:THR:HG22	46:DZ:90:VAL:HG13	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1010:G:N2	1:AA:1020:U:H1'	2.33	0.44
1:AA:1165:C:H2'	1:AA:1166:G:O4'	2.17	0.44
1:AA:605:U:C2'	1:AA:606:G:H5'	2.47	0.44
1:AA:90:U:O2'	1:AA:91:C:H5'	2.18	0.44
2:AB:20:GLU:O	2:AB:40:HIS:HB2	2.18	0.44
2:AB:92:TYR:HE2	2:AB:94:ASN:HB2	1.83	0.44
3:AC:118:GLN:HG2	3:AC:118:GLN:H	1.51	0.44
3:AC:39:ILE:O	3:AC:43:LEU:HG	2.17	0.44
19:AS:22:LEU:HB3	19:AS:27:GLU:HG3	2.00	0.44
48:B1:52:ARG:HH12	48:B1:57:GLU:HB2	1.83	0.44
26:BA:2187:G:H1	26:BA:2194:U:H5	1.62	0.44
26:BA:494:G:N7	54:B7:39:ARG:NH2	2.66	0.44
26:BA:654:G:N3	26:BA:664:U:O2'	2.49	0.44
26:BA:865:G:H4'	26:BA:885:C:O3'	2.17	0.44
36:BP:19:VAL:HG12	36:BP:27:HIS:HB3	2.00	0.44
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	1.99	0.44
43:BW:86:LEU:HD12	43:BW:87:PRO:HD2	2.00	0.44
46:BZ:111:VAL:O	46:BZ:112:ARG:HB2	2.17	0.44
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.17	0.44
1:CA:1121:U:C2'	1:CA:1122:U:H5'	2.47	0.44
1:CA:1286:A:H2	21:CU:18:TYR:HH	1.65	0.44
1:CA:1350:A:C5	1:CA:1351:U:C4	3.05	0.44
1:CA:683:G:H2'	1:CA:684:A:C8	2.52	0.44
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.99	0.44
3:CC:105:GLU:HG3	3:CC:105:GLU:H	1.54	0.44
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	2.00	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.18	0.44
3:CC:33:LEU:HD21	14:CN:53:LEU:CD2	2.47	0.44
26:DA:1614:A:C2	43:DW:93:ALA:HB2	2.52	0.44
26:DA:2773:C:OP1	29:DE:164:ARG:NE	2.41	0.44
27:DB:13:A:N3	27:DB:16:G:H1'	2.33	0.44
31:DG:138:GLN:NE2	31:DG:153:ARG:HB2	2.33	0.44
39:DS:15:ARG:HE	39:DS:88:ASP:CG	2.18	0.44
1:AA:418:C:H1'	1:AA:540:G:O2'	2.16	0.44
1:AA:547:A:H4'	1:AA:548:G:O5'	2.18	0.44
1:AA:679:C:C2'	1:AA:680:C:H5'	2.47	0.44
1:AA:69:G:H2'	1:AA:70:G:H8	1.83	0.44
3:AC:22:TRP:CE2	14:AN:54:PRO:HG3	2.52	0.44
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.18	0.44
9:AI:21:PRO:HA	9:AI:59:PHE:HA	2.00	0.44
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.33	0.44
19:AS:37:ARG:H	19:AS:37:ARG:HG3	1.38	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2755:C:H5''	56:B9:1:MET:HE2	2.00	0.44
26:BA:161:C:H2'	26:BA:162:G:O4'	2.18	0.44
26:BA:2018:C:H4'	26:BA:2019:G:OP1	2.16	0.44
26:BA:2155:G:N2	26:BA:2180:A:C2	2.86	0.44
26:BA:2156:A:C2'	26:BA:2156:A:N3	2.80	0.44
26:BA:756:U:H2'	26:BA:757:G:C8	2.53	0.44
37:BQ:56:ARG:HG2	37:BQ:56:ARG:HH11	1.83	0.44
43:BW:20:VAL:HG11	43:BW:44:ALA:HA	2.00	0.44
1:CA:1046:A:H61	1:CA:1213:A:H61	1.64	0.44
1:CA:486:U:H2'	1:CA:487:A:H8	1.82	0.44
1:CA:1076:C:OP1	2:CB:175:ARG:NH1	2.51	0.44
9:CI:96:LEU:HD23	9:CI:96:LEU:HA	1.84	0.44
16:CP:21:VAL:HG11	16:CP:59:TRP:NE1	2.33	0.44
1:CA:958:A:N6	19:CS:77:THR:HG23	2.32	0.44
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.79	0.44
26:DA:1007:C:C2	26:DA:1008:C:C5	3.06	0.44
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.41	0.44
26:DA:1742:G:O5'	26:DA:1742:G:H8	2.00	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.05	0.44
26:DA:2686:G:C2	26:DA:2724:C:O2	2.71	0.44
27:DB:28:C:H5''	39:DS:31:SER:HB3	1.99	0.44
35:DO:63:VAL:HG12	35:DO:106:LEU:HD11	1.99	0.44
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.99	0.44
1:AA:1134:G:C2	1:AA:1141:C:C2	3.06	0.43
1:AA:189(A):C:C2'	1:AA:189(B):C:H5'	2.48	0.43
1:AA:288:A:H2'	1:AA:289:G:H4'	1.99	0.43
1:AA:38:G:H22	1:AA:397:A:H5''	1.83	0.43
1:AA:421:U:H2'	1:AA:421:U:O2	2.16	0.43
1:AA:738:C:H2'	1:AA:739:C:C6	2.53	0.43
1:AA:993:G:N3	1:AA:993:G:H2'	2.33	0.43
4:AD:85:LYS:HG3	4:AD:86:LYS:HG2	1.99	0.43
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.54	0.43
1:AA:1503:A:N3	22:AV:13:A:N6	2.65	0.43
26:BA:2297:C:N4	53:B6:24:GLU:OE1	2.50	0.43
26:BA:2156:A:C2	26:BA:2181:G:H1'	2.52	0.43
27:BB:66:A:H61	27:BB:108:U:H2'	1.83	0.43
28:BD:134:ARG:HG3	28:BD:135:PHE:CE2	2.53	0.43
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.43
26:BA:589:U:P	36:BP:29:LYS:HZ2	2.41	0.43
39:BS:105:ALA:O	39:BS:110:LEU:HB2	2.18	0.43
44:BX:32:PRO:HA	44:BX:77:LYS:HB2	1.99	0.43
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.69	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.17	0.43
1:CA:1125:U:C3'	1:CA:1126:U:H5''	2.48	0.43
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.33	0.43
1:CA:991:U:H3'	1:CA:1212:U:H3	1.82	0.43
1:CA:164:U:H2'	1:CA:165:C:H6	1.83	0.43
1:CA:321:A:C2	1:CA:333:G:C2	3.06	0.43
1:CA:344:A:H5''	1:CA:345:C:H5	1.81	0.43
1:CA:66:G:C2'	1:CA:67:C:H5'	2.48	0.43
1:CA:763:G:H2'	1:CA:764:C:H5'	1.99	0.43
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.80	0.43
1:CA:1100:C:H5	2:CB:96:ARG:HH22	1.66	0.43
3:CC:126:ARG:HB2	3:CC:128:PHE:CE1	2.53	0.43
1:CA:881:G:P	12:CL:12:ARG:HH22	2.40	0.43
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	2.00	0.43
20:CT:24:LEU:HD12	20:CT:24:LEU:HA	1.76	0.43
37:DQ:86:GLY:HA3	47:D0:10:THR:CG2	2.48	0.43
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.43
36:DP:59:LEU:HD23	55:D8:58:ILE:HD13	2.00	0.43
56:D9:29:ASN:HB3	56:D9:32:HIS:ND1	2.33	0.43
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.53	0.43
26:DA:1264:G:O5'	26:DA:1264:G:H8	2.01	0.43
26:DA:1411:C:H2'	26:DA:1412:A:H8	1.82	0.43
26:DA:1421:G:C2	26:DA:1422:G:C8	3.06	0.43
26:DA:1484:G:O6	26:DA:1505:C:N4	2.47	0.43
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.53	0.43
26:DA:1849:G:H2'	26:DA:1850:G:H8	1.82	0.43
26:DA:200:U:O2	26:DA:386:G:N2	2.51	0.43
26:DA:839:U:H1'	26:DA:1191:G:H1'	2.00	0.43
27:DB:104:U:O3'	46:DZ:72:ARG:HD2	2.17	0.43
32:DH:12:PRO:O	32:DH:15:VAL:HG13	2.18	0.43
33:DI:87:LYS:CA	33:DI:122:GLU:HA	2.47	0.43
39:DS:95:HIS:CG	39:DS:96:GLY:N	2.86	0.43
42:DV:37:VAL:O	42:DV:51:VAL:HG23	2.18	0.43
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.18	0.43
1:AA:1168:A:C6	1:AA:1169:A:C6	3.07	0.43
1:AA:1397:C:H4'	22:AV:23:A:C2	2.53	0.43
1:AA:453:A:C5	1:AA:454:C:C4	3.06	0.43
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.53	0.43
5:AE:52:PRO:HG2	5:AE:53:LEU:HD12	1.99	0.43
9:AI:3:GLN:HG3	9:AI:20:ARG:HE	1.83	0.43
11:AK:50:TYR:HE1	11:AK:54:ARG:HE	1.64	0.43
27:BB:83:G:H4'	50:B3:52:HIS:CG	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1093:G:HO2'	26:BA:1094:A:P	2.40	0.43
26:BA:1157:A:N3	26:BA:1158:G:H1'	2.33	0.43
26:BA:1629:C:O2'	26:BA:1632:A:N3	2.51	0.43
26:BA:747:G:O2'	26:BA:1679:A:N3	2.42	0.43
26:BA:2210:C:H2'	26:BA:2211:U:O4'	2.18	0.43
26:BA:2555:G:H21	26:BA:2658:C:H5''	1.82	0.43
28:BD:145:VAL:HG11	28:BD:175:LEU:HD11	1.99	0.43
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.17	0.43
1:CA:1361:G:H8	1:CA:1361:G:O5'	2.01	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
1:CA:73:G:N1	1:CA:76:C:C5	2.86	0.43
2:CB:125:PRO:O	2:CB:127:ILE:N	2.51	0.43
4:CD:11:LEU:O	4:CD:15:GLU:HB2	2.18	0.43
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.90	0.43
1:CA:110:C:O2'	16:CP:25:ARG:O	2.31	0.43
16:CP:43:LYS:HG2	16:CP:48:TRP:CD2	2.53	0.43
24:CX:54:5MU:O4	24:CX:58:A:N7	2.51	0.43
26:DA:1263:U:C4	26:DA:1264:G:C6	3.06	0.43
26:DA:1860:G:H1	26:DA:1882:C:N4	2.16	0.43
26:DA:1959:G:C6	26:DA:1960:A:C5	3.06	0.43
26:DA:2469:A:H5''	26:DA:2470:G:OP2	2.18	0.43
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.45	0.43
26:DA:854:G:H2'	26:DA:855:G:C8	2.53	0.43
27:DB:42:C:N3	31:DG:93:THR:HB	2.33	0.43
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.52	0.43
1:AA:748:C:H4'	1:AA:749:C:O5'	2.19	0.43
2:AB:139:LYS:O	2:AB:143:GLU:HG3	2.18	0.43
6:AF:17:SER:O	6:AF:21:LEU:HG	2.18	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
7:AG:76:ARG:NH2	7:AG:156:TRP:HZ2	2.16	0.43
8:AH:103:VAL:HG21	8:AH:110:ALA:HB2	2.00	0.43
20:AT:36:LEU:HD22	20:AT:55:ILE:HG23	2.00	0.43
26:BA:602:G:H2'	26:BA:603:C:C6	2.53	0.43
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.82	0.43
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.53	0.43
42:BV:29:PRO:HA	42:BV:61:VAL:HG22	2.00	0.43
46:BZ:124:ILE:HG23	46:BZ:126:VAL:HG23	2.00	0.43
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.32	0.43
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.43
1:CA:392:G:H2'	1:CA:393:A:H8	1.82	0.43
1:CA:419:C:H5''	1:CA:513:C:C1'	2.49	0.43
1:CA:635:G:H2'	1:CA:636:U:O4'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:829:G:H1	1:CA:857:C:H42	1.65	0.43
2:CB:166:ASP:O	2:CB:170:GLU:N	2.44	0.43
1:CA:619:U:O2	4:CD:133:VAL:HA	2.18	0.43
9:CI:23:ASN:HD22	9:CI:25:LYS:H	1.67	0.43
26:DA:938:G:OP1	55:D8:52:LYS:HD2	2.18	0.43
26:DA:1028:A:H61	26:DA:1125:G:H2'	1.82	0.43
26:DA:1513:C:H2'	26:DA:1514:U:C6	2.54	0.43
26:DA:1826:G:H2'	26:DA:1827:C:H6	1.82	0.43
26:DA:185:U:H2'	26:DA:186:G:C8	2.53	0.43
26:DA:211:A:H2'	26:DA:212:G:O4'	2.18	0.43
26:DA:2483:C:N3	37:DQ:124:LYS:NZ	2.59	0.43
26:DA:271(Q):G:H2'	26:DA:271(R):G:H8	1.82	0.43
26:DA:2893:G:H4'	26:DA:2894:G:O5'	2.18	0.43
26:DA:619:G:O5'	26:DA:620:G:N2	2.51	0.43
26:DA:863:A:H2'	26:DA:864:G:C8	2.53	0.43
26:DA:900:A:O2'	26:DA:901:A:OP1	2.34	0.43
26:DA:923:C:H2'	26:DA:924:C:H6	1.83	0.43
33:DI:75:LEU:HD11	33:DI:105:HIS:CD2	2.53	0.43
43:DW:84:ARG:HG3	43:DW:98:LYS:HD2	2.00	0.43
1:AA:105:G:H2'	1:AA:106:C:C6	2.54	0.43
1:AA:1304:G:C5	1:AA:1305:G:C6	3.06	0.43
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.43
1:AA:271:C:H2'	1:AA:272:C:C6	2.53	0.43
1:AA:310:G:H5'	16:AP:31:LYS:HB2	1.99	0.43
1:AA:321:A:N7	1:AA:328:C:O2'	2.37	0.43
1:AA:593:G:C2	1:AA:594:G:C4	3.06	0.43
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.36	0.43
3:AC:16:ARG:HH22	3:AC:183:ASP:HA	1.82	0.43
1:AA:1525:G:OP2	11:AK:120:ARG:NH2	2.52	0.43
19:AS:53:ASN:OD1	19:AS:56:GLN:N	2.37	0.43
21:AU:15:ARG:HB2	21:AU:15:ARG:NH1	2.33	0.43
24:AX:7:G:O2'	24:AX:49:G:H5'	2.18	0.43
26:BA:354:A:C2	26:BA:1255:A:H2'	2.52	0.43
26:BA:1410:G:OP2	48:B1:3:LYS:HG3	2.18	0.43
26:BA:2268:G:H2'	26:BA:2269:U:O4'	2.19	0.43
26:BA:2299:A:C4	26:BA:2301:G:C8	3.07	0.43
26:BA:2804:C:H5'	26:BA:2902:G:N2	2.32	0.43
26:BA:518:G:H2'	26:BA:519:G:O4'	2.17	0.43
26:BA:560:C:O3'	41:BU:53:ARG:NH1	2.51	0.43
28:BD:72:LYS:HB3	28:BD:72:LYS:HE3	1.82	0.43
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.18	0.43
40:BT:8:LYS:HD3	40:BT:8:LYS:HA	1.79	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:BY:13:VAL:HG12	45:BY:74:PRO:HA	2.01	0.43
46:BZ:93:ASP:HB2	46:BZ:131:ARG:NH2	2.33	0.43
1:CA:1091:U:O2'	1:CA:1093:A:N7	2.46	0.43
1:CA:1104:G:C2'	1:CA:1105:A:H5'	2.48	0.43
1:CA:1055:A:H62	1:CA:1200:C:N4	2.16	0.43
1:CA:1235:U:H2'	1:CA:1236:A:O4'	2.18	0.43
1:CA:399:G:H2'	1:CA:400:C:C6	2.54	0.43
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.18	0.43
24:CX:19:G:C4	24:CX:57:A:C2	3.06	0.43
51:D4:64:GLY:C	51:D4:66:SER:H	2.22	0.43
26:DA:51:G:H1'	26:DA:119:A:N1	2.33	0.43
26:DA:1570:A:C6	26:DA:1571:A:C6	3.05	0.43
26:DA:1493:C:H41	26:DA:2206:G:C2'	2.31	0.43
26:DA:2489:G:C6	26:DA:2490:G:N1	2.87	0.43
26:DA:2492:U:H2'	26:DA:2493:U:C6	2.54	0.43
26:DA:2651:C:C2'	26:DA:2652:C:H5'	2.48	0.43
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.18	0.43
26:DA:330:A:H2	26:DA:1210:A:C2'	2.32	0.43
26:DA:523:C:H4'	26:DA:540:C:O2	2.19	0.43
26:DA:7:G:H5''	34:DN:130:HIS:CE1	2.53	0.43
26:DA:873:G:H1	26:DA:904:C:H42	1.66	0.43
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.81	0.43
28:DD:223:GLY:HA3	28:DD:231:HIS:CE1	2.54	0.43
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.18	0.43
31:DG:18:GLU:OE2	31:DG:21:ARG:NH2	2.51	0.43
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.32	0.43
46:DZ:149:SER:HB2	46:DZ:172:ALA:O	2.18	0.43
46:DZ:157:LEU:HB3	46:DZ:161:VAL:HG13	2.00	0.43
1:AA:1003:G:N1	1:AA:1004:A:N3	2.66	0.43
1:AA:1017:G:H2'	1:AA:1018:C:O4'	2.19	0.43
1:AA:182:U:H5'	1:AA:182:U:H6	1.83	0.43
1:AA:22:G:C6	1:AA:23:C:C4	3.06	0.43
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.50	0.43
1:AA:600:C:N3	1:AA:639:G:C2	2.87	0.43
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	2.01	0.43
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.00	0.43
14:AN:15:LYS:HE2	14:AN:16:PHE:CE1	2.53	0.43
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.33	0.43
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.33	0.43
26:BA:485:U:H5''	54:B7:40:TRP:CD2	2.53	0.43
23:AW:76:PPU:HD1	26:BA:2518:U:O4'	2.19	0.43
26:BA:2812:A:H1'	26:BA:2904:U:H1'	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:470:C:H4'	30:BF:49:ALA:HB2	2.00	0.43
32:BH:56:SER:OG	32:BH:57:ASP:N	2.49	0.43
36:BP:6:LEU:HD23	36:BP:6:LEU:HA	1.75	0.43
39:BS:49:VAL:HG22	39:BS:73:LEU:HD12	2.00	0.43
43:BW:51:LEU:HD23	43:BW:105:VAL:HG11	1.99	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.86	0.43
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.53	0.43
1:CA:1432:G:OP1	40:DT:108:ARG:HB2	2.17	0.43
1:CA:1507:A:H2'	1:CA:1508:G:O4'	2.19	0.43
1:CA:828:A:C2	1:CA:829:G:H1'	2.53	0.43
1:CA:77:G:C6	1:CA:93:G:C6	3.06	0.43
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.34	0.43
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.50	0.43
1:CA:1400:C:N3	24:CX:34:C:C2	2.87	0.43
26:DA:1159:U:H2'	26:DA:1160:G:H8	1.84	0.43
26:DA:1334:G:C6	26:DA:1335:U:C4	3.06	0.43
26:DA:1652:A:H2'	26:DA:1653:G:H5'	2.01	0.43
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.51	0.43
26:DA:1827:C:OP2	28:DD:222:ARG:HD2	2.18	0.43
26:DA:2341:G:H2'	26:DA:2342:C:O4'	2.17	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.81	0.43
26:DA:271(F):C:H2'	26:DA:271(G):C:C6	2.53	0.43
26:DA:2831:G:O2'	26:DA:2883:A:H2'	2.18	0.43
26:DA:753:C:H2'	26:DA:754:C:H6	1.83	0.43
32:DH:38:SER:OG	32:DH:40:GLU:HG3	2.19	0.43
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	2.00	0.43
33:DI:8:PRO:HB3	33:DI:14:ASP:OD1	2.19	0.43
26:DA:2094:G:P	33:DI:22:LYS:HD2	2.58	0.43
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	2.00	0.43
36:DP:121:LYS:O	36:DP:123:LEU:N	2.48	0.43
1:AA:99:U:H2'	1:AA:100:C:C6	2.53	0.43
1:AA:262:A:H2'	1:AA:263:A:C8	2.53	0.43
1:AA:575:G:O2'	1:AA:821:G:H5'	2.18	0.43
1:AA:991:U:O2'	1:AA:992:U:OP2	2.26	0.43
8:AH:69:ARG:HB2	8:AH:69:ARG:HE	1.52	0.43
26:BA:1167:C:H2'	26:BA:1168:G:O4'	2.18	0.43
26:BA:1188:A:C4	26:BA:1190:G:C8	3.07	0.43
26:BA:1889:G:N2	26:BA:1905:G:H2'	2.34	0.43
26:BA:2369:U:OP1	47:B0:20:ARG:NH1	2.51	0.43
27:BB:105:A:H2'	27:BB:106:G:O4'	2.18	0.43
28:BD:223:GLY:HA3	28:BD:231:HIS:CE1	2.53	0.43
30:BF:132:VAL:HA	30:BF:138:GLU:HB3	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1303:C:H4'	30:BF:83:PHE:CE1	2.52	0.43
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.53	0.43
34:BN:4:TYR:HE2	34:BN:41:ASP:HB2	1.83	0.43
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	2.00	0.43
1:CA:1272:G:C2'	1:CA:1273:G:H5'	2.48	0.43
1:CA:515:G:C5	1:CA:516:U:C4	3.06	0.43
1:CA:647:C:H2'	1:CA:648:A:H8	1.84	0.43
1:CA:971:G:O6	1:CA:1364:U:O2'	2.32	0.43
3:CC:34:LEU:HD22	14:CN:25:VAL:HG11	2.00	0.43
3:CC:54:ARG:HB3	3:CC:54:ARG:HH11	1.83	0.43
4:CD:103:ASN:O	4:CD:107:ARG:HG2	2.19	0.43
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.42	0.43
1:CA:1148:U:O2'	9:CI:66:ARG:NH1	2.51	0.43
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.17	0.43
18:CR:32:ARG:HA	18:CR:69:THR:HG21	2.01	0.43
19:CS:11:VAL:HG13	19:CS:38:SER:HB3	2.01	0.43
51:D4:40:HIS:HA	51:D4:41:PRO:HD2	1.76	0.43
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.52	0.43
26:DA:1359:A:N6	26:DA:1372:U:N3	2.67	0.43
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.51	0.43
26:DA:2378:A:H4'	39:DS:23:ARG:HD2	2.00	0.43
30:DF:93:LYS:HA	30:DF:93:LYS:HD3	1.91	0.43
31:DG:11:TYR:HA	31:DG:15:VAL:HB	2.00	0.43
36:DP:38:GLN:HG2	36:DP:45:LEU:N	2.33	0.43
42:DV:25:LEU:H	42:DV:92:THR:HG1	1.62	0.43
1:AA:1173:G:C6	1:AA:1174:G:N7	2.86	0.43
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.43
1:AA:401:C:H2'	1:AA:402:G:H8	1.83	0.43
1:AA:792:A:H4'	1:AA:793:U:C5'	2.48	0.43
13:AM:13:LYS:HA	13:AM:44:ARG:HH11	1.84	0.43
26:BA:1888:G:C6	26:BA:1889:G:C6	3.07	0.43
26:BA:174:U:H4'	26:BA:207:A:H4'	2.01	0.43
26:BA:2121:U:H2'	26:BA:2122:G:C8	2.54	0.43
26:BA:2502:G:OP2	26:BA:2502:G:H8	2.01	0.43
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.84	0.43
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	2.01	0.43
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.99	0.43
1:CA:1122:U:H2'	1:CA:1123:A:C8	2.54	0.43
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.53	0.43
1:CA:189:G:H2'	1:CA:189(A):C:C6	2.54	0.43
1:CA:243:A:H4'	1:CA:244:U:H5''	2.00	0.43
1:CA:766:A:H2'	1:CA:767:A:O4'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:96:U:O2'	1:CA:97:G:C8	2.65	0.43
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	2.00	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.80	0.43
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.54	0.43
4:CD:133:VAL:HG11	4:CD:138:TYR:CD2	2.54	0.43
1:CA:410:G:P	4:CD:30:LYS:HZ3	2.36	0.43
6:CF:8:ILE:HG22	6:CF:10:LEU:HD13	2.00	0.43
12:CL:84:LEU:HB2	12:CL:105:TYR:CE2	2.54	0.43
14:CN:4:LYS:HA	14:CN:7:ILE:HG12	2.01	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.40	0.43
19:CS:56:GLN:HE21	19:CS:56:GLN:HB3	1.59	0.43
1:CA:1222:G:H5'	19:CS:77:THR:HG21	2.00	0.43
48:D1:72:GLU:HG2	48:D1:76:ARG:HD3	2.00	0.43
26:DA:851:U:O2'	50:D3:42:ALA:O	2.29	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:1709:U:H2'	26:DA:1710:C:C6	2.54	0.43
26:DA:2274:A:C5	26:DA:2276:G:C8	3.06	0.43
26:DA:2526:G:H5'	26:DA:2742:C:O2'	2.18	0.43
26:DA:746:A:O2'	26:DA:2611:U:O2'	2.26	0.43
26:DA:466:A:N3	26:DA:683:C:H1'	2.34	0.43
26:DA:614(B):G:H1'	30:DF:44:ARG:HB2	2.00	0.43
34:DN:23:LEU:HD12	34:DN:99:LEU:HD23	2.00	0.43
36:DP:58:THR:O	36:DP:62:LEU:HG	2.18	0.43
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.53	0.43
1:AA:309:G:H1'	1:AA:608:A:C2	2.54	0.43
7:AG:23:VAL:O	7:AG:27:ILE:HG12	2.18	0.43
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.54	0.43
13:AM:91:ARG:NE	13:AM:97:PRO:O	2.51	0.43
1:AA:1316:G:H4'	14:AN:18:VAL:HG13	2.01	0.43
26:BA:2197:C:C2'	26:BA:2198:A:H5'	2.48	0.43
26:BA:251:A:H2'	26:BA:252:C:O4'	2.18	0.43
26:BA:2556:G:H2'	26:BA:2557:G:O4'	2.18	0.43
26:BA:793:A:H2'	26:BA:2624:C:H5''	1.99	0.43
26:BA:2669:A:H1'	26:BA:2677:A:N6	2.34	0.43
26:BA:287:G:N7	26:BA:448:U:H2'	2.34	0.43
33:BI:72:LEU:O	33:BI:74:ASN:N	2.48	0.43
1:CA:1005:A:H3'	1:CA:1006:C:O4'	2.19	0.43
1:CA:1007:C:H6	1:CA:1007:C:O5'	2.02	0.43
1:CA:1073:U:H2'	1:CA:1074:G:H8	1.84	0.43
1:CA:1095:U:C4	1:CA:1096:C:C4	3.07	0.43
1:CA:1277:C:O2'	1:CA:1279:A:H8	2.01	0.43
1:CA:944:G:N1	1:CA:1338:G:OP2	2.41	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1343:G:H2'	1:CA:1344:C:H6	1.80	0.43
1:CA:1352:C:N3	1:CA:1371:G:C6	2.87	0.43
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.53	0.43
1:CA:35:G:C4	1:CA:550:G:N2	2.87	0.43
1:CA:626:U:H2'	1:CA:627:G:O4'	2.19	0.43
1:CA:860:A:OP2	61:CA:4111:HOH:O	2.21	0.43
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.53	0.43
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.19	0.43
24:CX:19:G:N1	24:CX:56:C:N4	2.56	0.43
26:DA:987:G:O2'	26:DA:1000:A:N3	2.41	0.43
26:DA:1688:U:O2	26:DA:1700:A:H8	2.02	0.43
26:DA:1782:C:O2'	26:DA:2609:U:H5''	2.19	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:DA:2108:C:H2'	26:DA:2109:U:H6	1.83	0.43
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.53	0.43
26:DA:2807:G:N1	26:DA:2808:U:N3	2.67	0.43
26:DA:279:C:H2'	26:DA:280:C:C6	2.54	0.43
26:DA:557:U:H2'	26:DA:558:G:C8	2.54	0.43
26:DA:573:G:H1	26:DA:2031:A:P	2.41	0.43
26:DA:616:G:H5'	30:DF:205:ARG:HD2	2.01	0.43
26:DA:602:G:O2'	26:DA:655:A:N6	2.51	0.43
26:DA:797:C:H2'	26:DA:798:G:O4'	2.19	0.43
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.19	0.43
1:AA:173:U:C5	1:AA:198:G:H8	2.37	0.43
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.34	0.43
3:AC:138:VAL:HG23	3:AC:151:VAL:HG23	2.01	0.43
1:AA:1112:C:C4	3:AC:178:LEU:HD23	2.54	0.43
26:BA:1410:G:OP1	48:B1:2:SER:HA	2.19	0.43
26:BA:1535:U:HO2'	26:BA:1536:A:H8	1.67	0.43
26:BA:1173:A:N3	26:BA:2530:A:H5''	2.34	0.43
26:BA:2603:C:H2'	26:BA:2604:G:C8	2.54	0.43
26:BA:802:C:H2'	26:BA:803:C:H6	1.84	0.43
26:BA:891:C:C2'	26:BA:892:G:H5'	2.49	0.43
26:BA:895:G:N9	26:BA:978:A:H8	2.17	0.43
27:BB:78:A:H2'	27:BB:79:C:O4'	2.19	0.43
29:BE:167:VAL:HG12	29:BE:189:PRO:HD3	2.01	0.43
32:BH:18:GLU:HB3	32:BH:25:LYS:HB2	2.00	0.43
32:BH:35:VAL:HA	32:BH:36:PRO:HD2	1.92	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.18	0.43
1:CA:1208:C:H2'	1:CA:1209:C:O4'	2.19	0.43
1:CA:1392:G:O2'	1:CA:1393:U:H5'	2.19	0.43
1:CA:255:G:C6	1:CA:256:U:C4	3.07	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:120:LEU:HA	4:CD:120:LEU:HD23	1.88	0.43
5:CE:36:ASP:C	5:CE:38:GLN:H	2.22	0.43
1:CA:664:G:P	18:CR:64:ARG:HH21	2.42	0.43
53:D6:6:ARG:HH11	53:D6:26:ASN:HB2	1.84	0.43
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.50	0.43
26:DA:1288:U:C2	26:DA:1327:C:C2	3.07	0.43
26:DA:1359:A:N1	26:DA:1372:U:C4	2.86	0.43
26:DA:1394:U:OP1	61:DA:3949:HOH:O	2.20	0.43
26:DA:1486:A:H2'	26:DA:1487:G:C8	2.54	0.43
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.18	0.43
26:DA:2153:G:N3	26:DA:2153:G:H2'	2.33	0.43
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.84	0.43
26:DA:2352:A:N6	26:DA:2365:G:O2'	2.51	0.43
26:DA:27:G:O2'	26:DA:28:A:OP2	2.32	0.43
26:DA:422:A:H2'	26:DA:423:A:C8	2.54	0.43
26:DA:557:U:H2'	26:DA:558:G:H8	1.84	0.43
35:DO:78:ARG:HH22	40:DT:75:ILE:HD11	1.84	0.43
43:DW:13:SER:HA	43:DW:14:PRO:HD3	1.89	0.43
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.19	0.43
1:AA:1089:G:HO2'	1:AA:1170:A:H2	1.64	0.43
1:AA:408:A:H2'	1:AA:409:G:O4'	2.18	0.43
1:AA:683:G:H2'	1:AA:684:A:H8	1.84	0.43
15:AO:3:ILE:HG12	15:AO:3:ILE:O	2.19	0.43
26:BA:1355:G:H4'	54:B7:7:PRO:HB2	2.01	0.43
26:BA:2147:G:H1	26:BA:2194:U:P	2.40	0.43
26:BA:225:C:H2'	26:BA:226:C:C6	2.53	0.43
26:BA:471:C:O2'	26:BA:472:G:H5'	2.19	0.43
31:BG:148:MET:HB2	31:BG:148:MET:HE3	1.82	0.43
35:BO:120:GLU:OE1	40:BT:67:SER:OG	2.29	0.43
1:CA:1064:G:OP1	1:CA:1386:G:H4'	2.19	0.43
1:CA:1109:C:H2'	1:CA:1110:A:O4'	2.19	0.43
1:CA:1137:C:H6	1:CA:1137:C:O5'	2.02	0.43
1:CA:358:U:H2'	1:CA:359:U:C6	2.54	0.43
1:CA:417:C:H6	1:CA:417:C:O5'	2.02	0.43
1:CA:585:G:N3	1:CA:879:C:H4'	2.34	0.43
1:CA:950:U:H2'	1:CA:951:G:C8	2.53	0.43
3:CC:22:TRP:CD1	3:CC:57:ILE:HG22	2.54	0.43
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.19	0.43
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.84	0.43
26:DA:1449:A:H8	26:DA:1449:A:OP2	2.02	0.43
26:DA:171:G:H2'	26:DA:172:C:H6	1.83	0.43
26:DA:2109:U:N3	26:DA:2110:G:N7	2.66	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2706:G:O2'	38:DR:64:ARG:HD3	2.19	0.43
26:DA:355:G:H2'	26:DA:356:G:C8	2.54	0.43
26:DA:414:C:H2'	26:DA:415:A:C8	2.54	0.43
29:DE:37:ARG:NH1	29:DE:42:ASP:OD1	2.49	0.43
40:DT:59:THR:HG23	40:DT:78:LEU:CB	2.46	0.43
1:AA:201:C:N4	1:AA:216:G:H22	2.17	0.42
1:AA:300:A:H1'	1:AA:565:U:O2	2.19	0.42
1:AA:864:A:H2'	1:AA:865:A:C8	2.53	0.42
1:AA:718:G:C8	11:AK:116:HIS:HB3	2.53	0.42
13:AM:4:ILE:HA	13:AM:5:ALA:HA	1.81	0.42
20:AT:29:LYS:HB2	20:AT:71:THR:HG21	2.01	0.42
26:BA:1007:G:H4'	26:BA:2508:C:O2'	2.19	0.42
26:BA:1363:A:H2'	26:BA:1364:C:C6	2.53	0.42
26:BA:1701:A:H2'	26:BA:1702:A:H8	1.83	0.42
26:BA:1956:C:H4'	26:BA:1996:C:O3'	2.19	0.42
26:BA:239:G:OP2	55:B8:13:ARG:NH2	2.52	0.42
26:BA:2566:U:H2'	26:BA:2567:U:C6	2.53	0.42
26:BA:2569:G:H2'	26:BA:2570:C:C6	2.53	0.42
26:BA:2648:U:H1'	26:BA:2796:G:N2	2.35	0.42
26:BA:2724:U:OP1	26:BA:2727:G:H4'	2.19	0.42
26:BA:2831:A:H2'	26:BA:2832:G:O4'	2.18	0.42
26:BA:2846:U:C4	26:BA:2893:A:N6	2.87	0.42
26:BA:327:U:H2'	26:BA:328:G:H8	1.84	0.42
26:BA:875:U:H2'	26:BA:876:A:C8	2.54	0.42
26:BA:992:G:OP2	61:BA:4650:HOH:O	2.22	0.42
28:BD:146:GLU:HG2	28:BD:152:GLY:C	2.40	0.42
30:BF:106:ARG:H	30:BF:106:ARG:HG2	1.49	0.42
41:BU:10:ARG:NH2	61:BU:301:HOH:O	2.52	0.42
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.34	0.42
1:CA:1090:U:H2'	1:CA:1091:U:C6	2.53	0.42
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.18	0.42
1:CA:1512:U:H2'	1:CA:1513:A:C8	2.53	0.42
1:CA:679:C:C2'	1:CA:680:C:H5'	2.49	0.42
1:CA:1101:A:N6	2:CB:176:GLU:OE2	2.51	0.42
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.58	0.42
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.18	0.42
5:CE:93:PRO:HG2	8:CH:105:ARG:CZ	2.49	0.42
13:CM:50:GLU:HG3	13:CM:54:VAL:HG13	2.00	0.42
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.17	0.42
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.58	0.42
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.19	0.42
26:DA:2070:G:C2	26:DA:2442:C:C2	3.07	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:CW:76:PPU:H102	26:DA:2584:U:H4'	2.01	0.42
26:DA:872:A:H2'	26:DA:873:G:O4'	2.19	0.42
27:DB:43:C:C4	27:DB:45:A:C6	3.07	0.42
27:DB:68:C:H2'	27:DB:69:G:O4'	2.18	0.42
28:DD:38:LYS:HA	28:DD:38:LYS:HD2	1.83	0.42
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.32	0.42
32:DH:58:GLU:O	32:DH:62:LYS:HG3	2.19	0.42
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.19	0.42
36:DP:46:LYS:HE3	36:DP:46:LYS:HB3	1.80	0.42
42:DV:57:VAL:HG12	42:DV:99:ILE:HG12	2.00	0.42
46:DZ:91:LEU:HD23	46:DZ:130:PRO:HB3	2.01	0.42
1:AA:1322:C:H4'	1:AA:1323:G:OP1	2.20	0.42
1:AA:1355:G:H2'	1:AA:1356:G:H8	1.84	0.42
1:AA:1417:G:C6	1:AA:1482:G:C6	3.08	0.42
1:AA:266:G:H5''	1:AA:268:C:H41	1.84	0.42
1:AA:630:G:H2'	1:AA:631:G:H8	1.84	0.42
1:AA:762:C:H2'	1:AA:763:G:C8	2.55	0.42
1:AA:952:U:H2'	1:AA:953:G:C8	2.54	0.42
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	2.01	0.42
24:AX:5:G:N2	24:AX:68:C:N3	2.58	0.42
51:B4:41:PRO:HG3	51:B4:49:PHE:CE2	2.54	0.42
26:BA:1821:C:H2'	26:BA:1822:A:C5	2.54	0.42
26:BA:1851:U:C4	28:BD:160:GLY:HA3	2.54	0.42
26:BA:1859:G:H4'	26:BA:1860:A:OP1	2.18	0.42
26:BA:965:G:N2	26:BA:2281:A:OP2	2.52	0.42
26:BA:2296:C:OP1	53:B6:3:SER:OG	2.32	0.42
26:BA:2327:G:H2'	26:BA:2328:C:C6	2.55	0.42
26:BA:2619:G:H2'	26:BA:2620:G:O4'	2.19	0.42
26:BA:717:A:H4'	26:BA:718:C:O5'	2.20	0.42
26:BA:859:C:H5''	26:BA:1296:G:O2'	2.19	0.42
33:BI:140:LEU:HA	33:BI:140:LEU:HD23	1.86	0.42
35:BO:92:GLU:HG3	35:BO:93:PRO:HD2	2.00	0.42
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	2.00	0.42
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.22	0.42
46:BZ:98:MET:O	46:BZ:125:LEU:HA	2.20	0.42
46:BZ:48:PHE:CE1	46:BZ:71:VAL:HG11	2.55	0.42
1:CA:1007:C:O2	1:CA:1022:G:N1	2.31	0.42
1:CA:49:U:H3	1:CA:362:G:H1'	1.84	0.42
1:CA:524:G:H2'	1:CA:525:C:C6	2.54	0.42
1:CA:598:U:H2'	1:CA:599:C:H6	1.83	0.42
1:CA:630:G:H2'	1:CA:631:G:H8	1.84	0.42
1:CA:892:A:C6	1:CA:893:C:C4	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.17	0.42
2:CB:55:PHE:O	2:CB:59:GLU:N	2.32	0.42
4:CD:50:ARG:HA	4:CD:51:PRO:HD3	1.85	0.42
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.18	0.42
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.76	0.42
21:CU:9:ARG:O	21:CU:13:ILE:HG13	2.19	0.42
1:CA:1400:C:O4'	22:CV:18:G:H1'	2.19	0.42
24:CX:42:G:H2'	24:CX:43:A:C8	2.51	0.42
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.19	0.42
55:D8:30:ARG:HD3	55:D8:30:ARG:HA	1.57	0.42
55:D8:10:ALA:HB3	55:D8:62:LEU:HD21	2.01	0.42
26:DA:83:G:N2	26:DA:102:G:H1'	2.34	0.42
26:DA:1439:A:H2'	26:DA:1440:G:O4'	2.19	0.42
26:DA:1530:C:O2'	26:DA:1531:C:P	2.77	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.53	0.42
26:DA:2139:C:N4	26:DA:2153:G:C2	2.87	0.42
26:DA:226:G:H21	26:DA:228:A:H62	1.68	0.42
26:DA:2303:G:H2'	26:DA:2304:G:O4'	2.19	0.42
26:DA:506:G:O3'	26:DA:507:A:H8	2.02	0.42
26:DA:819:A:H5'	26:DA:973:A:N1	2.34	0.42
30:DF:149:ASP:OD1	30:DF:149:ASP:N	2.47	0.42
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.01	0.42
37:DQ:118:LEU:HB2	37:DQ:131:ILE:HD13	2.02	0.42
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.19	0.42
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.42
43:DW:69:LEU:HD22	43:DW:107:LEU:HB3	2.00	0.42
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	2.00	0.42
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.90	0.42
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.54	0.42
1:AA:1445:C:C2	1:AA:1458:G:C2	3.07	0.42
1:AA:503:C:H2'	1:AA:504:C:C6	2.54	0.42
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.20	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.19	0.42
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.83	0.42
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.84	0.42
7:AG:55:GLY:O	7:AG:56:GLN:HG3	2.19	0.42
1:AA:1202:G:O2'	14:AN:29:ARG:HG3	2.19	0.42
20:AT:10:LEU:HD23	20:AT:11:SER:H	1.83	0.42
48:B1:7:ILE:HG23	48:B1:98:LEU:HD11	2.01	0.42
26:BA:1177:G:O6	26:BA:2062:C:H1'	2.20	0.42
26:BA:133:G:C6	26:BA:145:G:C6	3.07	0.42
26:BA:1469:G:H2'	26:BA:1470:G:H8	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:1524:A:H2'	26:BA:1525:G:O4'	2.19	0.42
26:BA:1712:A:H2'	26:BA:1713:G:O4'	2.18	0.42
26:BA:2014:G:H4'	26:BA:2015:U:H5	1.84	0.42
26:BA:18:C:O2'	26:BA:577:U:OP1	2.36	0.42
26:BA:791:G:OP1	29:BE:132:HIS:ND1	2.50	0.42
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.55	0.42
34:BN:112:LEU:O	34:BN:116:LEU:HG	2.19	0.42
36:BP:138:LEU:HD23	36:BP:145:PRO:HG3	2.01	0.42
36:BP:3:LEU:HA	36:BP:3:LEU:HD12	1.84	0.42
1:CA:1400:C:H4'	22:CV:18:G:O2'	2.19	0.42
1:CA:435:C:H6	1:CA:435:C:O5'	2.01	0.42
1:CA:831:U:C2'	1:CA:832:C:H5'	2.50	0.42
3:CC:114:PRO:HA	3:CC:185:GLY:HA3	2.00	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.82	0.42
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	2.02	0.42
13:CM:60:VAL:HG23	13:CM:64:TRP:CZ3	2.53	0.42
19:CS:27:GLU:HG2	19:CS:47:HIS:CD2	2.54	0.42
24:CX:61:C:H2'	24:CX:62:C:C6	2.54	0.42
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.19	0.42
26:DA:676:A:H1'	26:DA:2443:C:H1'	2.00	0.42
26:DA:67:U:H2'	26:DA:68:G:O4'	2.19	0.42
26:DA:876:C:H2'	26:DA:877:U:O4'	2.19	0.42
27:DB:30:C:O2	27:DB:31:C:C6	2.72	0.42
29:DE:176:ILE:HG22	29:DE:178:GLU:HG2	2.01	0.42
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.07	0.42
1:AA:384:G:H2'	1:AA:385:C:C6	2.53	0.42
1:AA:730:G:C5	1:AA:731:G:H1'	2.55	0.42
1:AA:991:U:H2'	1:AA:991:U:H6	1.65	0.42
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	2.02	0.42
8:AH:86:ILE:HG12	8:AH:135:CYS:HA	2.01	0.42
8:AH:23:SER:HB3	8:AH:62:TYR:CD2	2.54	0.42
9:AI:5:TYR:HH	9:AI:7:THR:HG1	1.59	0.42
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	2.00	0.42
26:BA:2130:C:H2'	26:BA:2131:U:O4'	2.19	0.42
26:BA:2755:C:OP1	56:B9:35:ARG:HD3	2.19	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.55	0.42
26:BA:561:A:H2'	26:BA:562:C:C6	2.55	0.42
26:BA:821:A:H2'	26:BA:821:A:N3	2.35	0.42
35:BO:15:GLY:O	35:BO:47:ILE:HG12	2.19	0.42
40:BT:22:PHE:HA	40:BT:91:ARG:HH12	1.84	0.42
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.55	0.42
1:CA:38:G:H1	1:CA:397:A:H5"	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:723:U:HO2'	1:CA:724:G:H5'	1.84	0.42
1:CA:972:C:OP2	10:CJ:57:LYS:NZ	2.30	0.42
3:CC:115:LEU:O	3:CC:118:GLN:HG2	2.19	0.42
4:CD:175:SER:HB3	4:CD:186:LEU:HD21	2.01	0.42
7:CG:46:ALA:HA	7:CG:49:ILE:HD12	2.02	0.42
8:CH:94:TYR:HD1	8:CH:132:GLU:HA	1.84	0.42
8:CH:97:VAL:HA	8:CH:100:ILE:HG13	2.01	0.42
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.82	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.94	0.42
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.39	0.42
26:DA:108:U:C2	26:DA:109:G:C8	3.07	0.42
26:DA:1191:G:H2'	26:DA:1192:G:H8	1.84	0.42
26:DA:1384:A:N3	26:DA:1405:U:H1'	2.33	0.42
26:DA:208:C:H2'	26:DA:209:C:H6	1.82	0.42
26:DA:2316:C:O2'	26:DA:2317:C:H5'	2.19	0.42
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.19	0.42
27:DB:6:C:H2'	27:DB:7:G:H5''	2.00	0.42
28:DD:134:ARG:O	28:DD:168:ARG:NH2	2.52	0.42
29:DE:72:VAL:HG13	29:DE:73:GLU:O	2.19	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.31	0.42
32:DH:10:PRO:O	32:DH:76:VAL:HG21	2.19	0.42
33:DI:125:GLU:HA	33:DI:142:VAL:O	2.20	0.42
33:DI:88:ILE:HG23	33:DI:123:LEU:HA	2.00	0.42
33:DI:83:ALA:C	33:DI:89:TYR:HD2	2.23	0.42
34:DN:96:GLU:H	34:DN:96:GLU:CD	2.23	0.42
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.48	0.42
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.00	0.42
1:AA:1509:C:H2'	1:AA:1510:U:O4'	2.20	0.42
1:AA:192:U:H4'	20:AT:57:ARG:HD3	2.00	0.42
2:AB:61:LEU:HA	2:AB:61:LEU:HD12	1.85	0.42
7:AG:126:ASP:O	7:AG:131:LYS:N	2.50	0.42
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.35	0.42
16:AP:2:VAL:HG22	16:AP:64:ALA:HA	2.01	0.42
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.92	0.42
53:B6:8:LYS:HG2	55:B8:34:TRP:CD1	2.55	0.42
26:BA:1061:G:N2	26:BA:1193:C:O2	2.47	0.42
26:BA:833:C:H5''	26:BA:1811:A:C8	2.55	0.42
26:BA:2062:C:H2'	26:BA:2063:U:O4'	2.20	0.42
26:BA:310:C:H2'	26:BA:311:C:H6	1.85	0.42
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	2.01	0.42
1:CA:1089:G:C2	1:CA:1097:C:C2	3.07	0.42
1:CA:1120:G:C5	1:CA:1121:U:C5	3.07	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1513:A:C6	1:CA:1514:C:N4	2.88	0.42
1:CA:153:C:H2'	1:CA:154:C:C6	2.55	0.42
1:CA:189:G:H2'	1:CA:189(A):C:O4'	2.20	0.42
1:CA:333:G:H4'	20:CT:16:HIS:CE1	2.54	0.42
1:CA:581:G:O2'	1:CA:582:U:H5'	2.19	0.42
1:CA:625:G:H4'	16:CP:16:HIS:HB3	2.02	0.42
1:CA:838:G:C2	1:CA:849:C:C2	3.07	0.42
1:CA:71:C:H42	1:CA:98:G:H1	1.66	0.42
2:CB:96:ARG:NE	2:CB:98:LEU:HD13	2.34	0.42
3:CC:124:ILE:HD11	3:CC:189:ALA:CB	2.49	0.42
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.49	0.42
7:CG:27:ILE:O	7:CG:31:MET:N	2.53	0.42
13:CM:57:ARG:NE	51:D4:34:GLU:HB3	2.34	0.42
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.87	0.42
24:CX:31:G:C5	24:CX:32:5MC:C4	3.07	0.42
26:DA:1674:G:N2	26:DA:1677:A:N1	2.53	0.42
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.19	0.42
26:DA:2151:G:C4	26:DA:2152:G:C8	3.07	0.42
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.82	0.42
26:DA:2758:A:C4	32:DH:67:LEU:HD21	2.55	0.42
26:DA:329:G:OP1	26:DA:329:G:H8	2.02	0.42
26:DA:362:U:H3'	26:DA:362:U:OP1	2.20	0.42
26:DA:272(G):C:N4	26:DA:363(C):G:H1	2.11	0.42
33:DI:62:LYS:HE2	33:DI:133:HIS:NE2	2.34	0.42
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.19	0.42
40:DT:11:GLU:OE1	40:DT:57:PHE:HB3	2.19	0.42
1:AA:1053:G:H4'	1:AA:1054:C:H5'	2.01	0.42
1:AA:1366:C:H2'	1:AA:1367:C:H6	1.85	0.42
1:AA:194:C:O3'	20:AT:68:LYS:HD2	2.19	0.42
1:AA:399:G:H2'	1:AA:400:C:C6	2.54	0.42
6:AF:11:ASN:HB3	6:AF:14:LEU:HG	2.00	0.42
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.94	0.42
8:AH:11:THR:HG23	8:AH:14:ARG:NH1	2.34	0.42
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.01	0.42
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	2.01	0.42
13:AM:3:ARG:O	13:AM:57:ARG:NH2	2.48	0.42
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	2.01	0.42
51:B4:40:HIS:O	51:B4:43:TYR:N	2.53	0.42
26:BA:1253:C:C4	26:BA:1254:G:N7	2.88	0.42
26:BA:1331:G:N2	26:BA:1374:G:H5''	2.35	0.42
26:BA:2118:U:O4	26:BA:2215:G:O6	2.36	0.42
26:BA:2248:C:H2'	26:BA:2249:G:O4'	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2556:G:H1'	26:BA:2658:C:H4'	2.01	0.42
26:BA:504:A:C6	26:BA:506:A:C6	3.07	0.42
26:BA:956:A:H62	37:BQ:12:GLN:HA	1.85	0.42
43:BW:24:ILE:HA	43:BW:27:LYS:HG3	2.01	0.42
46:BZ:68:PRO:O	46:BZ:91:LEU:HB2	2.19	0.42
1:CA:1055:A:C8	1:CA:1206:G:C2	3.07	0.42
1:CA:1075:C:C2'	1:CA:1076:C:H5'	2.50	0.42
1:CA:1272:G:H2'	1:CA:1273:G:H5'	2.01	0.42
1:CA:1342:C:O2'	9:CI:124:GLN:HG3	2.19	0.42
1:CA:1400:C:C6	22:CV:18:G:C2	3.08	0.42
1:CA:374:A:C6	1:CA:375:U:C4	3.07	0.42
1:CA:582:U:C2	1:CA:760:G:C6	3.07	0.42
1:CA:918:A:H2'	1:CA:919:A:C8	2.53	0.42
1:CA:76:C:N4	1:CA:96:U:C2	2.88	0.42
4:CD:125:HIS:O	4:CD:149:ALA:N	2.42	0.42
1:CA:33:A:N3	12:CL:32:PHE:HE2	2.17	0.42
13:CM:44:ARG:HB2	13:CM:47:ASP:OD1	2.19	0.42
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.93	0.42
26:DA:1009:A:O5'	26:DA:1009:A:H8	2.02	0.42
26:DA:1026:U:H4'	26:DA:1027:A:OP1	2.19	0.42
26:DA:1034:G:H8	26:DA:1034:G:OP1	2.02	0.42
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.42
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.55	0.42
26:DA:2243:U:H2'	26:DA:2244:U:C6	2.54	0.42
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.83	0.42
26:DA:2662:A:H2'	26:DA:2663:G:O4'	2.19	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42
27:DB:4:C:H42	27:DB:117:G:H1	1.67	0.42
27:DB:30:C:OP2	39:DS:32:LEU:HD11	2.20	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.50	0.42
31:DG:27:ASN:HB3	31:DG:30:GLU:HB2	2.02	0.42
32:DH:126:PRO:HG2	32:DH:130:ARG:HD2	2.00	0.42
34:DN:36:GLY:HA3	34:DN:49:GLY:HA2	2.02	0.42
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.02	0.42
1:AA:112:G:OP2	16:AP:27:LYS:HD2	2.18	0.42
1:AA:486:U:H2'	1:AA:487:A:H8	1.84	0.42
1:AA:736:C:H2'	1:AA:737:A:C8	2.55	0.42
1:AA:899:C:O5'	1:AA:899:C:H6	2.02	0.42
3:AC:131:ARG:HH12	5:AE:50:GLU:HG3	1.84	0.42
16:AP:28:ARG:NH1	16:AP:29:ASP:OD2	2.45	0.42
17:AQ:64:PRO:HB3	17:AQ:70:ARG:NH1	2.34	0.42
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.83	0.42
26:BA:1470:G:H2'	26:BA:1471:G:O4'	2.19	0.42
26:BA:151:C:H2'	26:BA:152:G:H8	1.85	0.42
26:BA:1571:G:H2'	26:BA:1572:G:O4'	2.20	0.42
26:BA:2161:C:H5'	26:BA:2162:C:OP2	2.19	0.42
26:BA:2271:G:C2	26:BA:2294:G:N1	2.88	0.42
26:BA:2549:U:H2'	26:BA:2550:C:C6	2.54	0.42
26:BA:2579:G:H2'	26:BA:2580:C:C6	2.55	0.42
26:BA:287:G:O2'	26:BA:448:U:OP2	2.27	0.42
26:BA:1924:C:H5'	28:BD:246:PRO:HD3	2.01	0.42
26:BA:2797:C:O2'	29:BE:42:ASP:OD1	2.21	0.42
29:BE:49:LEU:HD12	29:BE:49:LEU:HA	1.77	0.42
30:BF:167:ALA:O	30:BF:170:LEU:HB2	2.20	0.42
31:BG:128:ARG:HE	31:BG:128:ARG:HB2	1.38	0.42
36:BP:52:GLU:HB3	36:BP:55:ARG:NH1	2.35	0.42
26:BA:999:G:H5''	37:BQ:13:GLN:HB3	2.01	0.42
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.18	0.42
40:BT:94:ALA:HB1	40:BT:99:LEU:HD21	2.01	0.42
46:BZ:150:LEU:HG	46:BZ:151:HIS:H	1.84	0.42
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.20	0.42
1:CA:1087:G:C4	1:CA:1099:G:N2	2.87	0.42
1:CA:1132:C:H42	1:CA:1142:G:H1	1.67	0.42
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.54	0.42
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.20	0.42
1:CA:514:C:N4	1:CA:515:G:O6	2.52	0.42
1:CA:1250:A:O3'	9:CI:67:GLY:HA2	2.20	0.42
18:CR:74:ARG:HB3	18:CR:81:PHE:CZ	2.55	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.54	0.42
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.53	0.42
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.01	0.42
26:DA:2099:U:H3	26:DA:2190:G:H1	1.66	0.42
26:DA:2106:G:H2'	26:DA:2107:C:O4'	2.20	0.42
26:DA:2164:C:H5''	26:DA:2165:G:C8	2.54	0.42
26:DA:2220:G:H2'	26:DA:2221:G:C8	2.55	0.42
26:DA:253:C:H2'	26:DA:254:G:O4'	2.20	0.42
26:DA:271(F):C:H2'	26:DA:271(G):C:O4'	2.20	0.42
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.54	0.42
26:DA:2787:C:H2'	26:DA:2788:C:C6	2.55	0.42
26:DA:2848:G:H1'	26:DA:2867:G:N2	2.33	0.42
26:DA:448:U:O4	26:DA:583:G:H1'	2.20	0.42
26:DA:634:C:H2'	26:DA:635:C:C6	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:866:A:H2'	26:DA:866:A:N3	2.35	0.42
26:DA:928:G:O5'	26:DA:928:G:H8	2.02	0.42
26:DA:801:G:OP2	30:DF:55:GLY:HA2	2.20	0.42
33:DI:80:PRO:HA	33:DI:145:VAL:O	2.20	0.42
39:DS:80:LEU:HD12	39:DS:80:LEU:HA	1.82	0.42
41:DU:69:CYS:HB3	41:DU:74:LEU:HD13	2.01	0.42
46:DZ:53:ILE:HG13	46:DZ:53:ILE:H	1.70	0.42
1:AA:1203:C:C2'	1:AA:1204:A:H5'	2.49	0.42
1:AA:1239:A:C4	1:AA:1298:C:N4	2.87	0.42
1:AA:495:A:H4'	1:AA:496:A:OP1	2.18	0.42
1:AA:681:C:C2	1:AA:710:G:C2	3.07	0.42
1:AA:758:G:H5'	1:AA:880:C:H1'	2.01	0.42
1:AA:840:C:H4'	1:AA:841:U:OP1	2.20	0.42
2:AB:12:GLU:HG3	2:AB:13:ALA:N	2.35	0.42
3:AC:22:TRP:CD1	3:AC:59:ARG:HD2	2.55	0.42
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.49	0.42
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.20	0.42
26:BA:1153:G:O2'	26:BA:1154:U:H5'	2.20	0.42
26:BA:1068:G:C5	26:BA:1185:C:C4	3.07	0.42
26:BA:1362:U:H2'	26:BA:1363:A:C8	2.55	0.42
26:BA:1587:U:H2'	26:BA:1588:G:O4'	2.20	0.42
26:BA:2163:G:C6	26:BA:2164:C:C2	3.07	0.42
26:BA:2146:G:N2	26:BA:2196:C:N3	2.58	0.42
26:BA:2483:C:H2'	26:BA:2484:G:O4'	2.20	0.42
27:BB:30:C:H2'	27:BB:31:C:C5'	2.49	0.42
29:BE:9:VAL:HG22	29:BE:25:VAL:HB	2.01	0.42
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.55	0.42
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.85	0.42
42:BV:89:GLN:HA	42:BV:90:PRO:HD3	1.97	0.42
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.42
44:BX:24:GLY:O	44:BX:83:VAL:HG22	2.20	0.42
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.55	0.42
1:CA:1128:C:C2	1:CA:1147:C:N4	2.87	0.42
1:CA:1252:A:H61	1:CA:1285:A:H61	1.65	0.42
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.40	0.42
1:CA:1525:G:H2'	1:CA:1526:G:O4'	2.20	0.42
1:CA:288:A:H2'	1:CA:289:G:H4'	2.01	0.42
1:CA:124:G:P	1:CA:310:G:H21	2.42	0.42
1:CA:486:U:H2'	1:CA:487:A:C8	2.55	0.42
1:CA:593:G:C6	1:CA:647:C:N3	2.88	0.42
1:CA:656:C:H2'	1:CA:657:G:O4'	2.20	0.42
1:CA:737:A:H2'	1:CA:738:C:C6	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:CD:102:ASP:OD1	4:CD:103:ASN:N	2.53	0.42
4:CD:88:VAL:O	4:CD:92:VAL:HG23	2.20	0.42
7:CG:22:LEU:HG	7:CG:62:PHE:CZ	2.55	0.42
8:CH:31:PHE:O	8:CH:35:ILE:HG13	2.20	0.42
9:CI:8:GLY:HA2	9:CI:79:LEU:HB3	2.01	0.42
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.42
26:DA:1156:A:OP1	26:DA:1156:A:H8	2.03	0.42
26:DA:1166:C:H2'	26:DA:1167:U:H6	1.84	0.42
26:DA:1598:C:O3'	44:DX:35:THR:OG1	2.37	0.42
26:DA:2078:C:C4	26:DA:2079:U:C4	3.07	0.42
26:DA:2135:A:H61	26:DA:2157:G:N2	2.18	0.42
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.84	0.42
26:DA:2162:G:O3'	26:DA:2172:U:H6	2.03	0.42
26:DA:2359:C:H2'	26:DA:2360:A:O4'	2.19	0.42
26:DA:2467:C:C4	26:DA:2468:G:C6	3.07	0.42
26:DA:2498:C:O2'	26:DA:2499:C:H5'	2.20	0.42
26:DA:2584:U:O2'	61:DA:3701:HOH:O	2.17	0.42
26:DA:1637:A:H4'	26:DA:2711:A:O2'	2.20	0.42
26:DA:2721:A:H2'	26:DA:2722:G:O4'	2.19	0.42
26:DA:321:G:C5	26:DA:341:G:H4'	2.54	0.42
26:DA:859:G:N2	26:DA:917:A:OP2	2.53	0.42
27:DB:33:G:C5	27:DB:34:U:C4	3.07	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:HG22	2.01	0.42
31:DG:33:ARG:HB2	31:DG:33:ARG:NH1	2.34	0.42
32:DH:71:LEU:O	32:DH:75:ALA:N	2.53	0.42
40:DT:73:GLU:OE1	40:DT:103:ARG:NE	2.53	0.42
26:DA:1227:G:OP1	41:DU:13:LYS:HG2	2.20	0.42
1:AA:1358:U:H2'	1:AA:1359:C:O4'	2.20	0.42
1:AA:262:A:C6	1:AA:263:A:C6	3.08	0.42
3:AC:35:GLU:O	3:AC:39:ILE:HG13	2.20	0.42
1:AA:979:C:O2	14:AN:19:ARG:HG2	2.20	0.42
1:AA:375:U:O2'	16:AP:6:LEU:O	2.36	0.42
54:B7:24:THR:HA	54:B7:25:PRO:HD3	1.96	0.42
26:BA:1357:G:N7	54:B7:9:ARG:NH2	2.67	0.42
26:BA:2163:G:N7	26:BA:2173:G:C2	2.88	0.42
26:BA:1911:A:N1	26:BA:2246:G:H1'	2.34	0.42
26:BA:2504:U:H2'	26:BA:2505:U:H6	1.85	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
26:BA:1831:C:H3'	28:BD:147:LEU:HD23	2.02	0.42
26:BA:1613:A:OP1	28:BD:211:ARG:NH1	2.53	0.42
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.52	0.42
31:BG:138:GLN:HB3	31:BG:153:ARG:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	2.02	0.42
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.85	0.42
1:CA:362:G:N1	1:CA:365:U:OP2	2.50	0.42
5:CE:90:VAL:O	5:CE:120:THR:HA	2.20	0.42
10:CJ:65:LEU:HB2	14:CN:56:VAL:HG22	2.01	0.42
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.35	0.42
26:DA:1313:U:H2'	26:DA:1610:A:C2	2.55	0.42
26:DA:1351:C:C2	26:DA:1381:G:C2	3.08	0.42
26:DA:1496:A:H2'	26:DA:1498:C:C5	2.55	0.42
26:DA:1636:C:H2'	26:DA:1637:A:H8	1.85	0.42
26:DA:2120:G:C2	26:DA:2121:G:C8	3.07	0.42
26:DA:2187:G:C5	26:DA:2188:C:C4	3.08	0.42
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.20	0.42
26:DA:846:C:H4'	26:DA:847:U:O4'	2.19	0.42
26:DA:918:A:C5	26:DA:919:G:H1'	2.55	0.42
27:DB:71:C:H1'	27:DB:107:G:N2	2.34	0.42
28:DD:158:ALA:O	28:DD:161:THR:OG1	2.30	0.42
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.53	0.42
26:DA:864:G:OP2	37:DQ:22:LYS:HE2	2.20	0.42
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.20	0.42
26:DA:1248:G:C2	41:DU:3:ARG:HD2	2.55	0.42
44:DX:54:VAL:HG22	44:DX:81:VAL:HG12	2.01	0.42
46:DZ:10:ARG:HG3	46:DZ:36:LYS:HB3	2.01	0.42
1:AA:692:U:H2'	1:AA:694:A:OP2	2.20	0.42
1:AA:841:U:O4'	1:AA:841:U:P	2.78	0.42
4:AD:120:LEU:HA	4:AD:120:LEU:HD23	1.77	0.42
1:AA:430:A:OP2	4:AD:8:VAL:HG12	2.19	0.42
13:AM:3:ARG:HH22	13:AM:11:ARG:HE	1.68	0.42
14:AN:48:ALA:HB2	14:AN:53:LEU:HD12	2.02	0.42
50:B3:8:LEU:O	50:B3:32:GLN:N	2.40	0.42
1:AA:1517:G:H1'	26:BA:1941:A:O3'	2.18	0.42
26:BA:2005:C:H4'	26:BA:2618:C:H4'	2.01	0.42
26:BA:354:A:O2'	26:BA:355:A:H8	2.02	0.42
26:BA:505:A:N3	26:BA:507:G:H5''	2.34	0.42
27:BB:103:G:O2'	46:BZ:73:GLN:NE2	2.53	0.42
27:BB:4:C:H2'	27:BB:5:C:O4'	2.19	0.42
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.91	0.42
26:BA:1702:A:H4'	29:BE:115:GLY:N	2.35	0.42
30:BF:178:PRO:HB2	30:BF:201:VAL:HG21	2.02	0.42
33:BI:10:GLU:H	33:BI:10:GLU:HG3	1.35	0.42
33:BI:83:ALA:HB2	33:BI:88:ILE:HA	2.01	0.42
39:BS:83:LYS:HB2	39:BS:83:LYS:HE2	1.92	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1026:G:N3	1:CA:1026:G:H3'	2.35	0.42
1:CA:1060:C:C5	3:CC:2:GLY:HA2	2.55	0.42
1:CA:1134:G:N3	1:CA:1134:G:H2'	2.35	0.42
1:CA:1277:C:HO2'	1:CA:1279:A:C1'	2.30	0.42
1:CA:193:C:H2'	1:CA:194:C:C6	2.55	0.42
1:CA:382:A:H2'	1:CA:383:A:H8	1.82	0.42
1:CA:45:U:OP1	1:CA:307:C:O2'	2.27	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.20	0.42
1:CA:885:G:O2'	1:CA:886:G:H5'	2.20	0.42
4:CD:134:ASP:O	4:CD:136:PRO:HD3	2.20	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.85	0.42
6:CF:14:LEU:HD22	6:CF:18:GLN:HB3	2.02	0.42
7:CG:111:ARG:HB2	7:CG:119:ARG:HD2	2.01	0.42
7:CG:50:ILE:HD11	7:CG:58:PRO:HB3	2.01	0.42
10:CJ:40:LEU:HD12	10:CJ:69:ASN:HB3	2.02	0.42
16:CP:28:ARG:HH11	16:CP:29:ASP:CG	2.20	0.42
23:CW:76:PPU:C5'	23:CW:76:PPU:H8	2.36	0.42
24:CX:72:A:H5''	24:CX:73:A:OP2	2.20	0.42
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.20	0.42
26:DA:1363:C:H2'	26:DA:1364:G:H8	1.85	0.42
26:DA:1475:G:C2	26:DA:1517:G:C2	3.08	0.42
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.85	0.42
26:DA:1973:G:H2'	26:DA:1974:C:C6	2.55	0.42
26:DA:2001:A:H2'	26:DA:2002:G:H8	1.80	0.42
26:DA:2105:C:H2'	26:DA:2106:G:C8	2.54	0.42
26:DA:2129:C:H2'	26:DA:2130:U:C6	2.55	0.42
26:DA:2376:A:H2'	26:DA:2377:A:O4'	2.20	0.42
23:CW:76:PPU:HD2	26:DA:2451:A:C4	2.54	0.42
26:DA:357:A:H2'	26:DA:358:U:C6	2.55	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.85	0.42
26:DA:407:G:H2'	26:DA:408:G:C8	2.55	0.42
26:DA:522:G:C6	26:DA:523:C:C4	3.08	0.42
26:DA:528:A:O2'	26:DA:529:A:H5'	2.19	0.42
27:DB:24:G:H5'	27:DB:25:A:N6	2.32	0.42
28:DD:12:SER:HB3	28:DD:208:LYS:HB3	2.02	0.42
29:DE:11:MET:HG2	29:DE:24:THR:HB	2.01	0.42
26:DA:2784:C:H1'	29:DE:37:ARG:HH12	1.84	0.42
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.68	0.42
33:DI:52:ARG:CG	33:DI:52:ARG:HH11	2.33	0.42
35:DO:24:VAL:HG12	35:DO:39:ILE:HG22	2.02	0.42
1:AA:1001:A:N1	1:AA:1040:U:O4	2.53	0.41
1:AA:283:C:C2'	1:AA:284:G:H5'	2.51	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:831:U:C2'	1:AA:832:C:H5'	2.50	0.41
3:AC:77:ILE:HG13	3:AC:78:GLY:N	2.35	0.41
16:AP:14:ASN:N	16:AP:15:PRO:HD3	2.35	0.41
20:AT:53:LEU:HD13	20:AT:100:ILE:O	2.20	0.41
20:AT:55:ILE:HA	20:AT:55:ILE:HD13	1.90	0.41
26:BA:1491:A:H1'	26:BA:1507:A:C2	2.55	0.41
26:BA:1495:G:H5''	26:BA:1589:A:OP2	2.20	0.41
26:BA:1654:A:H1'	26:BA:1656:A:OP2	2.20	0.41
26:BA:1779:G:H2'	26:BA:1780:A:O4'	2.20	0.41
26:BA:2164:C:N3	26:BA:2171:G:C6	2.88	0.41
26:BA:2166:U:O2'	26:BA:2167:C:H2'	2.20	0.41
26:BA:2175:G:C2	26:BA:2176:G:C8	3.07	0.41
26:BA:2368:C:OP1	47:B0:24:LYS:NZ	2.39	0.41
26:BA:2518:U:C2	26:BA:2597:U:O4	2.73	0.41
26:BA:2822:G:H2'	26:BA:2823:A:O4'	2.20	0.41
26:BA:297:C:H2'	26:BA:298:G:C8	2.55	0.41
26:BA:619:G:H2'	26:BA:620:U:O4'	2.20	0.41
29:BE:182:LEU:HD21	29:BE:198:VAL:HG11	2.02	0.41
26:BA:346:A:H3'	30:BF:169:ASN:ND2	2.35	0.41
30:BF:196:LEU:HA	30:BF:196:LEU:HD23	1.81	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.77	0.41
26:BA:709:G:H5''	36:BP:16:ARG:HG2	2.02	0.41
38:BR:118:GLU:H	38:BR:118:GLU:CD	2.23	0.41
41:BU:69:CYS:HB3	41:BU:74:LEU:HD13	2.02	0.41
44:BX:31:HIS:CD2	44:BX:33:LYS:HB2	2.55	0.41
44:BX:88:LYS:HE3	44:BX:88:LYS:HB2	1.84	0.41
1:CA:1002:G:C4	1:CA:1003:G:C8	3.08	0.41
1:CA:999:C:C2	1:CA:1042:G:N2	2.81	0.41
1:CA:1134:G:H2'	1:CA:1135:U:H5'	2.02	0.41
1:CA:1127:G:N2	1:CA:1147:C:H41	2.18	0.41
1:CA:1126:U:C2	1:CA:1281:U:O4	2.73	0.41
1:CA:1251:A:O2'	1:CA:1369:C:O2'	2.23	0.41
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.84	0.41
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.41
1:CA:683:G:C6	1:CA:684:A:C6	3.08	0.41
1:CA:712:A:N6	1:CA:713:G:C6	2.88	0.41
1:CA:894:G:C6	1:CA:895:G:C5	3.08	0.41
1:CA:926:G:H5''	1:CA:927:G:O5'	2.20	0.41
3:CC:125:GLU:HG3	3:CC:190:ARG:HG2	2.02	0.41
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.19	0.41
12:CL:103:GLY:N	12:CL:107:ALA:O	2.48	0.41
26:DA:106:C:H2'	26:DA:107:C:H6	1.84	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.59	0.41
26:DA:1721:G:H8	26:DA:1741:A:H62	1.67	0.41
26:DA:2153:G:C2	26:DA:2154:G:C4	3.08	0.41
26:DA:2120:G:N2	26:DA:2179:C:C2	2.88	0.41
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.20	0.41
26:DA:780:G:H8	26:DA:780:G:O5'	2.02	0.41
26:DA:870:A:OP1	37:DQ:6:ARG:NE	2.49	0.41
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.32	0.41
36:DP:101:VAL:HG23	36:DP:106:LEU:HD13	2.02	0.41
36:DP:96:THR:HA	36:DP:126:VAL:HB	2.01	0.41
39:DS:37:ALA:N	39:DS:51:ALA:O	2.52	0.41
40:DT:108:ARG:HA	40:DT:111:ARG:NH1	2.35	0.41
43:DW:66:GLU:HA	43:DW:69:LEU:HD12	2.02	0.41
1:AA:1007:C:N3	1:AA:1022:G:O6	2.52	0.41
1:AA:1071:C:H42	1:AA:1104:G:H1	1.68	0.41
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.41
1:AA:228:A:H2'	1:AA:229:U:O4'	2.20	0.41
1:AA:411:A:O2'	1:AA:413:G:H5'	2.20	0.41
1:AA:58:C:O5'	1:AA:58:C:H6	2.02	0.41
1:AA:626:U:H2'	1:AA:627:G:O4'	2.20	0.41
1:AA:875:C:H1'	8:AH:15:ASN:OD1	2.20	0.41
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	2.02	0.41
5:AE:33:VAL:HG21	5:AE:109:ILE:HG12	2.02	0.41
11:AK:120:ARG:HA	11:AK:121:PRO:HD3	1.86	0.41
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.20	0.41
15:AO:62:GLN:HA	15:AO:65:ARG:NH1	2.34	0.41
26:BA:2376:C:O2	47:B0:36:ILE:HD11	2.20	0.41
26:BA:2402:U:P	55:B8:35:GLN:HE22	2.44	0.41
55:B8:60:LEU:HD23	55:B8:60:LEU:HA	1.91	0.41
26:BA:1067:A:C3'	26:BA:1067:A:C8	3.00	0.41
26:BA:107:G:H2'	26:BA:108:G:O4'	2.20	0.41
26:BA:1157:A:H4'	26:BA:1158:G:OP1	2.21	0.41
26:BA:160:G:C2'	26:BA:161:C:H5'	2.50	0.41
26:BA:2036:A:H2'	26:BA:2037:A:C8	2.55	0.41
26:BA:2403:G:O6	26:BA:2437:A:H8	2.03	0.41
26:BA:312:C:H2'	26:BA:313:A:C8	2.56	0.41
26:BA:842:C:H2'	26:BA:843:C:H6	1.85	0.41
26:BA:864:C:H4'	26:BA:977:G:C5	2.55	0.41
37:BQ:57:HIS:CD2	37:BQ:117:ALA:HB2	2.55	0.41
39:BS:59:LYS:CE	39:BS:60:GLY:H	2.34	0.41
1:CA:1014:A:P	1:CA:1014:A:H8	2.43	0.41
1:CA:1118:C:H2'	1:CA:1119:C:H6	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:1245:A:N1	1:CA:1292:U:O2	2.53	0.41
1:CA:1330:U:H4'	13:CM:23:TYR:CZ	2.55	0.41
1:CA:1493:A:H2'	26:DA:1913:A:N6	2.34	0.41
1:CA:185:A:O5'	1:CA:185:A:H8	2.03	0.41
1:CA:265:G:N2	1:CA:267:C:H5'	2.35	0.41
1:CA:321:A:N7	1:CA:328:C:O2'	2.31	0.41
1:CA:348:G:O2'	1:CA:349:A:H5'	2.19	0.41
1:CA:690:G:C6	1:CA:691:G:C6	3.08	0.41
1:CA:746:A:H4'	1:CA:837:G:O2'	2.20	0.41
1:CA:909:A:H2'	1:CA:910:C:O4'	2.20	0.41
1:CA:967:C:H2'	1:CA:968:A:N7	2.34	0.41
2:CB:82:ARG:HH11	2:CB:83:MET:HE1	1.84	0.41
3:CC:131:ARG:O	3:CC:135:LYS:HB2	2.21	0.41
3:CC:159:GLY:HA2	3:CC:193:TYR:CE1	2.56	0.41
1:CA:8:A:N7	4:CD:209:ARG:HA	2.35	0.41
17:CQ:95:TYR:O	17:CQ:98:LEU:HB2	2.20	0.41
20:CT:30:LYS:O	20:CT:34:LYS:HG3	2.20	0.41
50:D3:41:PRO:HA	50:D3:44:ARG:HB3	2.01	0.41
55:D8:63:PRO:HG2	55:D8:64:TYR:CE2	2.55	0.41
26:DA:1012:U:C5	34:DN:28:THR:HG21	2.55	0.41
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.19	0.41
26:DA:1354:A:H2'	26:DA:1355:G:O4'	2.19	0.41
26:DA:1372:U:O4	26:DA:1373:A:C5	2.74	0.41
26:DA:1422:G:C4	26:DA:1423:G:C8	3.08	0.41
26:DA:1832:C:N4	26:DA:1833:U:C4	2.88	0.41
26:DA:1897:G:C6	26:DA:1898:U:C4	3.08	0.41
26:DA:2269:A:OP1	61:DA:4046:HOH:O	2.22	0.41
26:DA:271(Q):G:C2	26:DA:271(R):G:C5	3.08	0.41
26:DA:729:G:H5'	26:DA:730:C:C5'	2.50	0.41
34:DN:138:LEU:HA	34:DN:138:LEU:HD23	1.84	0.41
37:DQ:52:VAL:HA	37:DQ:55:VAL:HG12	2.03	0.41
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.70	0.41
1:AA:1172:C:C5	1:AA:1173:G:N7	2.88	0.41
1:AA:1409:C:H2'	1:AA:1410:G:H8	1.85	0.41
1:AA:636:U:H5'	17:AQ:2:PRO:HG3	2.03	0.41
1:AA:981:U:H6	1:AA:981:U:O5'	2.03	0.41
1:AA:489:C:OP1	4:AD:132:ARG:NH2	2.53	0.41
5:AE:84:PHE:CE2	5:AE:133:TYR:HD2	2.38	0.41
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.84	0.41
26:BA:1493:C:HO2'	26:BA:1592:A:HO2'	1.65	0.41
26:BA:1952:G:N2	26:BA:1990:G:H2'	2.35	0.41
26:BA:2799:U:H2'	26:BA:2800:C:C6	2.54	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2802:C:O4'	26:BA:2901:A:H2	2.04	0.41
26:BA:331:G:N2	26:BA:333:G:H3'	2.35	0.41
26:BA:861:C:H4'	26:BA:1270:C:O2	2.20	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.02	0.41
28:BD:215:LEU:HD13	28:BD:217:ARG:NH2	2.35	0.41
30:BF:31:HIS:NE2	30:BF:35:GLU:OE2	2.53	0.41
39:BS:87:PHE:HB2	39:BS:112:PHE:CE2	2.55	0.41
40:BT:35:LYS:HE3	40:BT:35:LYS:HB2	1.72	0.41
1:CA:1132:C:C4	1:CA:1133:G:N7	2.88	0.41
1:CA:304:U:H2'	1:CA:305:G:C8	2.56	0.41
1:CA:44:G:H1	1:CA:398:C:N4	2.10	0.41
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.20	0.41
1:CA:515:G:C6	1:CA:516:U:C4	3.09	0.41
1:CA:829:G:O6	61:CA:4089:HOH:O	2.19	0.41
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.20	0.41
1:CA:939:G:P	7:CG:95:ARG:HH12	2.43	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
9:CI:23:ASN:HD22	9:CI:25:LYS:HG2	1.86	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.41
26:DA:2232:U:P	48:D1:40:ARG:HH12	2.43	0.41
13:CM:65:LYS:CB	51:D4:50:VAL:HG11	2.47	0.41
26:DA:1359:A:N1	26:DA:1360:A:C5	2.88	0.41
26:DA:1529:G:O2'	26:DA:1530:C:H5'	2.20	0.41
26:DA:1688:U:H3	26:DA:1700:A:C5'	2.33	0.41
26:DA:2145:C:H2'	26:DA:2145:C:H6	1.65	0.41
26:DA:2506:U:C2	26:DA:2585:U:O4	2.73	0.41
26:DA:2588:G:H2'	26:DA:2589:A:O4'	2.19	0.41
26:DA:347:A:H2'	26:DA:348:G:H8	1.85	0.41
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.41
29:DE:122:PHE:HZ	29:DE:155:LYS:HB2	1.84	0.41
29:DE:176:ILE:HB	29:DE:181:LEU:HB2	2.02	0.41
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.41
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.19	0.41
33:DI:87:LYS:CB	33:DI:122:GLU:HA	2.49	0.41
44:DX:59:VAL:HG21	44:DX:78:LYS:HE3	2.02	0.41
46:DZ:76:LEU:HA	46:DZ:76:LEU:HD12	1.85	0.41
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.20	0.41
1:AA:1112:C:O5'	1:AA:1112:C:H6	2.03	0.41
1:AA:110:C:H2'	1:AA:111:G:O4'	2.19	0.41
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.31	0.41
1:AA:328:C:H4'	1:AA:329:A:H5'	2.02	0.41
1:AA:35:G:H2'	1:AA:36:C:C6	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:830:G:H2'	1:AA:831:U:O4'	2.21	0.41
5:AE:77:PRO:HG2	5:AE:142:LEU:HD22	2.03	0.41
8:AH:82:HIS:NE2	8:AH:84:ARG:HG2	2.35	0.41
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.38	0.41
15:AO:70:LEU:HD11	15:AO:77:ARG:HB2	2.03	0.41
19:AS:3:ARG:HH11	19:AS:10:PHE:HB2	1.86	0.41
26:BA:2289:G:OP2	47:B0:12:ASN:HB2	2.20	0.41
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.38	0.41
26:BA:1066:A:N1	26:BA:1186:U:O2'	2.40	0.41
26:BA:1091:A:OP1	26:BA:1091:A:H4'	2.20	0.41
26:BA:348:A:H2'	26:BA:349:G:O4'	2.20	0.41
28:BD:166:GLN:HB2	28:BD:174:ILE:HG22	2.02	0.41
28:BD:5:LYS:HB3	28:BD:5:LYS:HE3	1.55	0.41
29:BE:19:ARG:CZ	35:BO:72:PRO:HB3	2.50	0.41
29:BE:93:VAL:HG13	61:BE:3106:HOH:O	2.20	0.41
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	2.02	0.41
37:BQ:70:PRO:HA	37:BQ:94:VAL:O	2.20	0.41
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.56	0.41
1:CA:1153:C:N4	1:CA:1154:G:N2	2.68	0.41
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.35	0.41
1:CA:114:U:H2'	1:CA:115:G:C8	2.55	0.41
1:CA:1295:G:O3'	13:CM:14:ARG:NH1	2.53	0.41
1:CA:1494:G:H5'	26:DA:1913:A:C5	2.56	0.41
1:CA:408:A:C2	1:CA:435:C:O2	2.74	0.41
1:CA:615:C:H2'	1:CA:616:G:H8	1.85	0.41
1:CA:789:U:H2'	1:CA:791:G:OP2	2.21	0.41
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.19	0.41
1:CA:951:G:C6	1:CA:952:U:C4	3.09	0.41
5:CE:59:GLY:O	5:CE:62:ALA:HB3	2.20	0.41
5:CE:76:ILE:HB	5:CE:77:PRO:HD2	2.03	0.41
1:CA:1367:C:OP1	9:CI:114:TYR:HA	2.20	0.41
13:CM:20:THR:HA	13:CM:25:ILE:HG22	2.01	0.41
18:CR:61:LYS:HA	18:CR:64:ARG:NH1	2.36	0.41
20:CT:54:LYS:N	20:CT:100:ILE:HD11	2.34	0.41
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.35	0.41
26:DA:1303:G:C6	26:DA:1304:C:C4	3.07	0.41
26:DA:1377:G:OP2	61:DA:4242:HOH:O	2.21	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.54	0.41
26:DA:1614:A:P	26:DA:1614:A:H8	2.43	0.41
26:DA:701:G:O2'	26:DA:1631(A):A:N1	2.53	0.41
26:DA:1654:A:H1'	26:DA:2823:A:H5'	2.03	0.41
26:DA:1816:G:H3'	28:DD:62:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:2101:G:C6	26:DA:2102:U:N3	2.89	0.41
26:DA:2168:G:H5'	26:DA:2169:A:OP2	2.19	0.41
26:DA:2292:C:H2'	26:DA:2293:C:C6	2.55	0.41
26:DA:2302:G:N3	26:DA:2315:G:N2	2.68	0.41
26:DA:2245:U:O2'	26:DA:2436:G:OP2	2.19	0.41
26:DA:45:C:H2'	26:DA:47:C:C6	2.56	0.41
26:DA:853:G:H2'	26:DA:854:G:C8	2.55	0.41
26:DA:874:G:C8	26:DA:874:G:H5'	2.53	0.41
26:DA:910:A:C6	26:DA:911:A:C6	3.08	0.41
32:DH:3:ARG:HB3	32:DH:3:ARG:HH11	1.85	0.41
32:DH:45:VAL:HA	32:DH:50:VAL:HG22	2.01	0.41
36:DP:81:GLN:HB3	36:DP:106:LEU:HD23	2.02	0.41
46:DZ:156:LYS:HE3	46:DZ:156:LYS:HB3	1.55	0.41
1:AA:922:G:N3	1:AA:1398:A:H2	2.19	0.41
1:AA:345:C:H4'	1:AA:346:G:N3	2.35	0.41
1:AA:688:G:H2'	1:AA:689:C:H6	1.86	0.41
2:AB:41:ILE:HD13	2:AB:41:ILE:HA	1.95	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.03	0.41
1:AA:1379:G:N7	7:AG:2:ALA:HB3	2.35	0.41
1:AA:967:C:H4'	9:AI:125:TYR:HE1	1.85	0.41
9:AI:50:LEU:HD23	9:AI:81:ILE:CD1	2.50	0.41
14:AN:37:PHE:CE2	14:AN:53:LEU:HD13	2.55	0.41
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.35	0.41
26:BA:1063:G:N2	26:BA:1191:C:O2	2.38	0.41
26:BA:1660:A:H8	26:BA:1660:A:P	2.43	0.41
26:BA:1729:G:C4	26:BA:1788:U:C2	3.08	0.41
26:BA:905:U:O2	26:BA:2280:A:H2'	2.21	0.41
26:BA:2408:G:OP1	48:B1:25:LYS:NZ	2.34	0.41
26:BA:2789:A:C6	26:BA:2791:A:C6	3.09	0.41
26:BA:2859:U:OP2	40:BT:95:ARG:NH1	2.53	0.41
26:BA:362:G:C2'	26:BA:363:U:H5'	2.51	0.41
26:BA:904:C:OP1	47:B0:77:ARG:NH2	2.52	0.41
27:BB:24:G:O2'	27:BB:56:G:N7	2.48	0.41
29:BE:119:ARG:CG	29:BE:160:TYR:HB2	2.51	0.41
31:BG:66:GLN:HE21	31:BG:66:GLN:HB3	1.59	0.41
39:BS:110:LEU:HA	39:BS:110:LEU:HD12	1.80	0.41
1:CA:1120:G:N1	1:CA:1154:G:C2	2.88	0.41
1:CA:986:A:C6	1:CA:1220:G:C2	3.09	0.41
1:CA:1255:G:O3'	1:CA:1258:G:H1'	2.20	0.41
1:CA:1276:G:H2'	1:CA:1277:C:H6	1.85	0.41
1:CA:1327:C:H2'	1:CA:1328:C:C6	2.55	0.41
1:CA:203:U:H2'	1:CA:203:U:OP2	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:229:U:H5''	16:CP:33:ILE:HD12	2.01	0.41
1:CA:580:U:H2'	1:CA:581:G:O4'	2.20	0.41
1:CA:638:G:H2'	1:CA:639:G:O4'	2.20	0.41
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.67	0.41
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.36	0.41
48:D1:75:GLU:HA	48:D1:78:LYS:HE3	2.02	0.41
51:D4:54:GLY:HA2	51:D4:55:ARG:HA	1.53	0.41
26:DA:1114:G:H2'	26:DA:1115:G:O4'	2.20	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
26:DA:1580:A:OP2	26:DA:1580:A:H8	2.04	0.41
26:DA:16:G:H2'	26:DA:17:G:H8	1.85	0.41
26:DA:2155:G:O6	26:DA:2156:G:C2	2.74	0.41
26:DA:2467:C:OP1	56:D9:8:LYS:NZ	2.41	0.41
26:DA:2492:U:H2'	26:DA:2493:U:H6	1.84	0.41
26:DA:2515:C:H2'	26:DA:2516:G:C8	2.54	0.41
26:DA:271(H):G:O2'	26:DA:271(I):G:OP2	2.38	0.41
26:DA:363(C):G:H8	26:DA:363(C):G:O5'	2.03	0.41
26:DA:606:U:H4'	26:DA:658:C:H4'	2.01	0.41
26:DA:966:G:C6	26:DA:967:C:N4	2.89	0.41
27:DB:63:G:H2'	27:DB:64:C:H6	1.85	0.41
26:DA:2784:C:O2'	29:DE:42:ASP:OD1	2.27	0.41
13:CM:68:GLY:HA3	31:DG:116:ASP:CG	2.39	0.41
31:DG:165:THR:OG1	31:DG:168:GLU:HG3	2.21	0.41
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	2.01	0.41
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.21	0.41
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.53	0.41
36:DP:100:LEU:HD23	36:DP:100:LEU:HA	1.82	0.41
46:DZ:44:PHE:CZ	46:DZ:86:VAL:HG11	2.56	0.41
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.36	0.41
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.55	0.41
1:AA:1164:G:C5	1:AA:1173:G:C2	3.09	0.41
1:AA:782:A:H4'	1:AA:1514:C:O2'	2.21	0.41
1:AA:909:A:H2'	1:AA:910:C:O4'	2.20	0.41
1:AA:952:U:H2'	1:AA:953:G:H8	1.86	0.41
4:AD:28:SER:O	4:AD:31:CYS:HB3	2.21	0.41
7:AG:109:ASN:HA	7:AG:119:ARG:HE	1.85	0.41
7:AG:88:PRO:HB3	7:AG:145:ALA:O	2.20	0.41
7:AG:21:VAL:O	7:AG:24:THR:OG1	2.34	0.41
19:AS:45:VAL:HA	19:AS:62:ILE:HG22	2.02	0.41
26:BA:1374:G:O2'	26:BA:1375:U:H2'	2.20	0.41
26:BA:2455:C:OP1	30:BF:68:LYS:HD3	2.20	0.41
30:BF:32:LEU:HB3	30:BF:112:MET:HE1	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:BG:17:PRO:HA	31:BG:20:ILE:HD12	2.03	0.41
37:BQ:115:MET:SD	37:BQ:131:ILE:HG21	2.61	0.41
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	2.01	0.41
41:BU:61:TRP:CH2	41:BU:93:LYS:HB2	2.56	0.41
1:CA:1162:C:C2	1:CA:1175:G:C2	3.09	0.41
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.50	0.41
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.51	0.41
1:CA:866:C:C4	1:CA:867:G:H1'	2.55	0.41
9:CI:47:LEU:O	9:CI:50:LEU:HG	2.21	0.41
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	2.03	0.41
10:CJ:59:SER:O	10:CJ:60:ARG:HD3	2.21	0.41
11:CK:92:GLU:HB3	11:CK:96:ARG:NH1	2.35	0.41
12:CL:34:ARG:HG2	12:CL:35:GLY:N	2.35	0.41
26:DA:1152:C:H2'	26:DA:1153:C:H6	1.85	0.41
26:DA:1359:A:N6	26:DA:1360:A:C2	2.89	0.41
26:DA:1449:A:HO2'	26:DA:1529:G:N2	2.15	0.41
26:DA:1600:C:O2'	26:DA:1601:G:H5'	2.21	0.41
26:DA:2416:C:H2'	26:DA:2417:C:H6	1.86	0.41
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.41
26:DA:2653:U:H5''	26:DA:2654:A:OP2	2.21	0.41
26:DA:493:G:H2'	26:DA:494:G:O4'	2.20	0.41
33:DI:93:THR:HG22	33:DI:116:LEU:HD22	2.02	0.41
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	2.03	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.93	0.41
1:AA:167:G:H2'	1:AA:168:G:C8	2.54	0.41
1:AA:203:U:H2'	1:AA:203:U:OP2	2.20	0.41
1:AA:890:G:N2	1:AA:906:G:H2'	2.36	0.41
2:AB:187:LEU:HD23	2:AB:201:ILE:HB	2.02	0.41
26:BA:1159:U:H2'	26:BA:1160:G:H8	1.85	0.41
26:BA:1495:G:H1'	26:BA:1574:A:N1	2.35	0.41
26:BA:1683:C:H2'	26:BA:1684:A:C8	2.55	0.41
26:BA:1827:U:H2'	26:BA:1828:C:H6	1.84	0.41
26:BA:1884:A:H2'	26:BA:1885:A:C8	2.56	0.41
26:BA:2033:U:H2'	26:BA:2034:G:O4'	2.20	0.41
26:BA:22:C:H2'	26:BA:23:G:O4'	2.20	0.41
26:BA:2646:G:C2	26:BA:2647:C:C2	3.08	0.41
26:BA:2787:C:H2'	26:BA:2788:A:O4'	2.21	0.41
26:BA:2855:G:H2'	26:BA:2856:G:H8	1.84	0.41
26:BA:446:C:H2'	26:BA:447:C:O4'	2.20	0.41
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.02	0.41
34:BN:108:PRO:O	34:BN:113:GLY:HA3	2.20	0.41
34:BN:62:VAL:CG1	34:BN:66:LYS:HB2	2.51	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	2.03	0.41
37:BQ:54:MET:HG3	37:BQ:121:ALA:HB2	2.01	0.41
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.91	0.41
26:BA:63:A:O3'	44:BX:71:GLY:HA3	2.20	0.41
1:CA:1010:G:C4	1:CA:1011:G:C8	3.08	0.41
1:CA:1047:G:H8	1:CA:1047:G:O5'	2.04	0.41
1:CA:1067:A:O5'	1:CA:1067:A:H8	2.04	0.41
1:CA:1120:G:C6	1:CA:1154:G:C2	3.09	0.41
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.54	0.41
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	2.03	0.41
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.21	0.41
3:CC:154:SER:O	3:CC:197:GLY:N	2.49	0.41
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.52	0.41
6:CF:34:GLY:O	6:CF:67:MET:HA	2.21	0.41
11:CK:81:ASP:OD1	11:CK:106:LYS:HE2	2.20	0.41
12:CL:56:ALA:HB3	12:CL:100:ILE:HD11	2.03	0.41
1:CA:950:U:OP2	13:CM:102:ARG:HD3	2.20	0.41
16:CP:33:ILE:H	16:CP:33:ILE:HG12	1.73	0.41
1:CA:583:A:O2'	17:CQ:91:ARG:NE	2.54	0.41
48:D1:52:ARG:NH1	48:D1:57:GLU:OE2	2.53	0.41
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.67	0.41
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.40	0.41
26:DA:118:A:H1'	26:DA:178:G:O4'	2.21	0.41
26:DA:1408:C:H2'	26:DA:1409:C:C6	2.56	0.41
26:DA:141:A:H8	26:DA:1408:C:HO2'	1.58	0.41
26:DA:1647:G:P	26:DA:1647:G:H3'	2.60	0.41
26:DA:1745(A):C:H5'	26:DA:1746:G:OP2	2.20	0.41
26:DA:1850:G:H2'	26:DA:1851:U:O4'	2.20	0.41
26:DA:2250:G:O2'	26:DA:2496:C:OP1	2.32	0.41
26:DA:2711:A:OP1	26:DA:2712:U:H3'	2.20	0.41
26:DA:2787:C:H2'	26:DA:2788:C:H6	1.86	0.41
26:DA:270:A:C2	26:DA:366:C:H4'	2.56	0.41
26:DA:247:G:H4'	26:DA:386:G:C5	2.56	0.41
26:DA:649:G:H2'	26:DA:650:C:O4'	2.20	0.41
26:DA:192:C:O2'	26:DA:802:A:N3	2.50	0.41
26:DA:993:G:C6	26:DA:994:C:C4	3.08	0.41
27:DB:20:C:N4	27:DB:21:G:C6	2.88	0.41
29:DE:37:ARG:HB2	29:DE:46:ALA:H	1.85	0.41
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.56	0.41
33:DI:40:THR:HG23	33:DI:43:ASN:ND2	2.32	0.41
35:DO:77:ILE:HA	40:DT:73:GLU:O	2.21	0.41
36:DP:138:LEU:HD23	36:DP:145:PRO:HG3	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:1190:G:H5''	36:DP:32:THR:HA	2.02	0.41
1:AA:1173:G:C2	1:AA:1174:G:C4	3.08	0.41
1:AA:1250:A:C2	1:AA:1370:G:H1'	2.55	0.41
1:AA:1298:C:H4'	1:AA:1299:A:C4	2.55	0.41
1:AA:942:G:C2	1:AA:1342:C:C2	3.09	0.41
1:AA:189(B):C:H2'	1:AA:189(C):C:C6	2.56	0.41
1:AA:451:A:H61	1:AA:480:U:H2'	1.85	0.41
1:AA:37:U:O2'	1:AA:547:A:N1	2.52	0.41
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	2.03	0.41
8:AH:4:ASP:OD2	8:AH:85:ARG:NH1	2.54	0.41
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.03	0.41
44:BX:5:TYR:CE1	49:B2:30:ARG:HB2	2.55	0.41
51:B4:28:LYS:HD3	51:B4:31:ILE:HD11	2.02	0.41
51:B4:6:HIS:HA	51:B4:7:PRO:HD3	1.95	0.41
26:BA:1018:A:C8	26:BA:1233:U:C2	3.08	0.41
26:BA:121:G:O3'	26:BA:1422:C:H4'	2.20	0.41
26:BA:1276:C:H2'	26:BA:1277:G:C8	2.55	0.41
26:BA:1405:A:C2	26:BA:1418:U:C4	3.08	0.41
26:BA:2184:G:H5'	26:BA:2194:U:H2'	2.02	0.41
26:BA:279:G:H2'	26:BA:280:C:O4'	2.21	0.41
26:BA:348:A:N6	26:BA:362:G:O2'	2.49	0.41
26:BA:497:A:H2'	26:BA:498:A:O4'	2.20	0.41
26:BA:1836:U:O2	28:BD:50:THR:HB	2.21	0.41
30:BF:33:LEU:HD12	30:BF:33:LEU:HA	1.92	0.41
32:BH:3:ARG:HA	32:BH:3:ARG:NE	2.34	0.41
34:BN:23:LEU:HD12	34:BN:99:LEU:HD23	2.03	0.41
36:BP:58:THR:O	36:BP:62:LEU:HG	2.21	0.41
38:BR:74:LYS:HG2	38:BR:77:ARG:HH21	1.86	0.41
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.21	0.41
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	2.03	0.41
1:CA:1068:G:N3	1:CA:1191:A:C2	2.89	0.41
1:CA:1262:C:C2'	1:CA:1263:C:H5'	2.51	0.41
1:CA:1352:C:N4	1:CA:1370:G:H1	2.18	0.41
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.56	0.41
1:CA:527:G:O6	12:CL:49:ASN:ND2	2.53	0.41
1:CA:552:U:O2	12:CL:31:PRO:HB3	2.21	0.41
1:CA:861:G:HO2'	1:CA:874:G:HO2'	1.68	0.41
2:CB:158:LEU:HD12	2:CB:158:LEU:H	1.84	0.41
1:CA:1056:U:H4'	3:CC:163:ALA:HB2	2.02	0.41
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.56	0.41
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.21	0.41
7:CG:18:TYR:CG	7:CG:59:LEU:HD13	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:CI:32:ASP:HB3	9:CI:35:GLU:HG3	2.02	0.41
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	2.03	0.41
1:CA:667:G:O2'	15:CO:49:ASP:OD1	2.20	0.41
26:DA:1124:C:H1'	56:D9:36:GLN:NE2	2.36	0.41
26:DA:1279:G:H2'	26:DA:1280:G:O4'	2.21	0.41
26:DA:1495:A:H2'	26:DA:1496:A:C8	2.55	0.41
26:DA:152:G:H2'	26:DA:153:C:C6	2.56	0.41
26:DA:1819:A:H5''	28:DD:161:THR:HG21	2.03	0.41
26:DA:370:G:OP1	26:DA:403:U:N3	2.42	0.41
26:DA:503:A:C5	26:DA:506:G:C6	3.08	0.41
26:DA:974:G:C6	26:DA:1186:G:C6	3.09	0.41
27:DB:90:A:C5	27:DB:91:C:H1'	2.56	0.41
34:DN:62:VAL:CG1	34:DN:66:LYS:HB2	2.50	0.41
38:DR:24:GLN:HE22	38:DR:36:THR:HG21	1.86	0.41
26:DA:1341:U:O2	44:DX:80:ILE:HD12	2.21	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
1:AA:1164:G:C2'	1:AA:1165:C:H5'	2.51	0.41
1:AA:1216:G:H5''	14:AN:5:ALA:HB2	2.03	0.41
1:AA:1263:C:H2'	1:AA:1264:C:C6	2.56	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.35	0.41
2:AB:105:PHE:CZ	2:AB:155:LEU:HD12	2.55	0.41
3:AC:87:LEU:O	3:AC:91:LEU:N	2.30	0.41
4:AD:155:LEU:HD23	4:AD:156:GLU:N	2.36	0.41
8:AH:104:ARG:HG3	8:AH:138:TRP:CD2	2.56	0.41
8:AH:21:LYS:HD2	8:AH:21:LYS:HA	1.85	0.41
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.56	0.41
16:AP:8:ARG:NH2	16:AP:15:PRO:HG3	2.35	0.41
17:AQ:10:VAL:HG13	17:AQ:19:VAL:HB	2.02	0.41
48:B1:95:LEU:HA	48:B1:95:LEU:HD12	1.87	0.41
26:BA:1573:G:H5''	26:BA:1574:A:OP1	2.20	0.41
26:BA:2102:G:OP1	48:B1:35:THR:HG21	2.20	0.41
26:BA:2528:G:C6	26:BA:2529:C:C4	3.09	0.41
26:BA:2773:C:H2'	26:BA:2774:G:H5''	2.02	0.41
33:BI:43:ASN:C	33:BI:43:ASN:HD22	2.24	0.41
26:BA:234:G:O5'	36:BP:73:GLY:HA2	2.20	0.41
38:BR:38:VAL:HB	38:BR:39:PRO:HD3	2.02	0.41
26:BA:2830:A:C6	38:BR:4:LEU:HD11	2.56	0.41
39:BS:20:ARG:NH2	47:B0:48:GLY:O	2.54	0.41
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.56	0.41
1:CA:1291:G:C6	1:CA:1292:U:C4	3.08	0.41
1:CA:1381:U:H2'	1:CA:1382:C:H5'	2.03	0.41
1:CA:502:G:H2'	1:CA:503:C:O4'	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:CA:60:A:N3	1:CA:61:G:H1'	2.36	0.41
1:CA:945:G:C2	1:CA:946:A:C8	3.09	0.41
1:CA:949:A:C6	1:CA:950:U:C4	3.09	0.41
2:CB:91:PRO:HG3	2:CB:154:LEU:HD12	2.03	0.41
3:CC:24:ALA:HB1	3:CC:28:GLN:O	2.20	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.21	0.41
5:CE:93:PRO:HA	5:CE:118:ILE:HD12	2.02	0.41
9:CI:100:GLY:O	9:CI:103:THR:HG22	2.21	0.41
10:CJ:11:PHE:HE1	10:CJ:67:THR:HB	1.85	0.41
13:CM:50:GLU:O	13:CM:54:VAL:HG13	2.21	0.41
18:CR:51:LEU:HA	18:CR:52:PRO:HD3	1.90	0.41
1:CA:192:U:O2'	20:CT:60:GLU:OE2	2.22	0.41
51:D4:34:GLU:OE2	51:D4:35:VAL:HG12	2.20	0.41
54:D7:22:MET:HA	54:D7:28:ARG:HG2	2.03	0.41
54:D7:9:ARG:HE	54:D7:47:ARG:HG3	1.86	0.41
26:DA:1906:G:C8	26:DA:1929:G:H2'	2.55	0.41
26:DA:2126:A:C5	26:DA:2163:C:H1'	2.56	0.41
26:DA:2646:C:H6	26:DA:2646:C:O5'	2.04	0.41
26:DA:45:C:H2'	26:DA:47:C:H6	1.86	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.09	0.41
26:DA:573:G:O2'	26:DA:574:C:H3'	2.20	0.41
26:DA:82:G:O6	61:DA:4071:HOH:O	2.21	0.41
40:DT:56:GLY:O	40:DT:59:THR:HG22	2.21	0.41
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.41
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.56	0.41
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.69	0.41
1:AA:265:G:H5'	17:AQ:64:PRO:O	2.21	0.41
1:AA:350:G:O2'	1:AA:351:G:H5'	2.21	0.41
1:AA:407:G:N2	1:AA:436:C:C2	2.89	0.41
1:AA:472:A:H5''	16:AP:80:PHE:HB3	2.02	0.41
1:AA:738:C:H2'	1:AA:739:C:H6	1.86	0.41
1:AA:748:C:H1'	1:AA:749:C:OP2	2.20	0.41
2:AB:101:MET:HA	2:AB:108:ILE:HD12	2.02	0.41
2:AB:211:ILE:HG13	2:AB:211:ILE:H	1.66	0.41
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.85	0.41
1:AA:691:G:P	11:AK:26:ASN:HD22	2.44	0.41
11:AK:20:TYR:O	11:AK:30:VAL:HA	2.21	0.41
19:AS:36:ARG:HD2	19:AS:52:TYR:O	2.21	0.41
48:B1:97:LEU:HD23	48:B1:97:LEU:HA	1.86	0.41
26:BA:1441:A:C6	26:BA:1444:C:C2	3.09	0.41
26:BA:1739:U:O2'	26:BA:1740:U:H2'	2.20	0.41
26:BA:2190:G:O6	26:BA:2193:A:H8	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2359:C:H2'	26:BA:2360:U:C6	2.55	0.41
26:BA:2528:G:C5	26:BA:2529:C:C4	3.09	0.41
29:BE:170:LEU:HB3	29:BE:184:VAL:HG22	2.02	0.41
30:BF:60:SER:OG	30:BF:61:GLY:N	2.53	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
31:BG:41:GLN:NE2	31:BG:153:ARG:HB3	2.34	0.41
33:BI:12:LEU:HD23	33:BI:12:LEU:HA	1.79	0.41
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.34	0.41
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.89	0.41
1:CA:1005:A:H2'	1:CA:1005:A:N3	2.35	0.41
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.86	0.41
1:CA:1155:G:N7	1:CA:1156:G:C5	2.89	0.41
1:CA:1194:U:H4'	5:CE:22:GLY:O	2.21	0.41
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.54	0.41
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.20	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.62	0.41
1:CA:475:G:H2'	1:CA:476:G:C8	2.56	0.41
1:CA:522:C:H5''	12:CL:120:TYR:OH	2.21	0.41
1:CA:578:C:O2'	1:CA:728:A:N3	2.41	0.41
1:CA:968:A:H8	1:CA:968:A:O5'	2.03	0.41
5:CE:135:THR:O	5:CE:139:LEU:HG	2.21	0.41
5:CE:106:PRO:HB3	5:CE:135:THR:OG1	2.20	0.41
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.54	0.41
1:CA:764:C:H4'	15:CO:50:HIS:HB3	2.03	0.41
51:D4:61:ARG:O	51:D4:61:ARG:NE	2.53	0.41
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.53	0.41
26:DA:2142:C:H2'	26:DA:2143:C:H6	1.83	0.41
26:DA:2563:U:H4'	35:DO:28:SER:HA	2.02	0.41
26:DA:2693:A:C2	26:DA:2694:G:C8	3.09	0.41
26:DA:2884:U:C4	26:DA:2885:C:C2	3.09	0.41
26:DA:735:A:N7	26:DA:761:A:H2	2.18	0.41
26:DA:1820:U:C2	28:DD:202:LYS:HB3	2.55	0.41
29:DE:141:ILE:O	29:DE:154:LYS:HE2	2.21	0.41
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.21	0.41
30:DF:39:TRP:CG	30:DF:101:LEU:HB2	2.56	0.41
31:DG:181:ARG:HE	31:DG:181:ARG:HB3	1.78	0.41
32:DH:70:THR:HG22	32:DH:74:ASN:HD21	1.86	0.41
33:DI:114:LEU:HD11	33:DI:128:LEU:HD13	2.02	0.41
33:DI:72:LEU:HD12	33:DI:138:ILE:HG22	2.03	0.41
38:DR:100:LEU:HA	38:DR:100:LEU:HD13	1.86	0.41
1:AA:1019:C:H5''	1:AA:1019:C:H6	1.86	0.41
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1409:C:H2'	1:AA:1410:G:C8	2.56	0.41
2:AB:60:ASP:OD1	2:AB:64:ARG:NE	2.48	0.41
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.36	0.41
13:AM:91:ARG:HA	13:AM:91:ARG:HD2	1.86	0.41
15:AO:74:ASP:HA	15:AO:75:PRO:HD2	1.94	0.41
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.46	0.41
26:BA:1700:G:H4'	26:BA:1701:A:O5'	2.21	0.41
24:AX:12:G:H4'	26:BA:1930:C:O2	2.21	0.41
26:BA:1957:G:H1'	26:BA:1986:G:N2	2.35	0.41
26:BA:1696:G:C6	26:BA:2031:G:C6	3.10	0.41
26:BA:212:A:N1	26:BA:434:G:O2'	2.37	0.41
26:BA:2157:A:O5'	26:BA:2157:A:H8	2.04	0.41
26:BA:2166:U:H2'	26:BA:2168:C:C5	2.56	0.41
26:BA:2184:G:C6	26:BA:2185:C:N4	2.89	0.41
26:BA:2492:C:N4	26:BA:2493:G:C6	2.89	0.41
26:BA:856:G:C5	26:BA:857:U:C4	3.09	0.41
26:BA:921:G:H2'	26:BA:922:G:H5'	2.02	0.41
26:BA:997:G:OP1	37:BQ:16:ARG:NH2	2.54	0.41
40:BT:91:ARG:HH11	40:BT:120:ARG:NH1	2.19	0.41
1:CA:698:G:C6	1:CA:699:C:C4	3.09	0.41
1:CA:728:A:O4'	15:CO:54:ARG:NH2	2.54	0.41
1:CA:77:G:C6	1:CA:78:G:C6	3.09	0.41
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.21	0.41
6:CF:2:ARG:NE	6:CF:69:GLU:HG2	2.36	0.41
1:CA:751:U:O4'	15:CO:24:SER:HA	2.20	0.41
1:CA:1221:G:H4'	19:CS:77:THR:OG1	2.21	0.41
26:DA:1232:G:H2'	26:DA:1233:C:C6	2.56	0.41
26:DA:2514:U:H2'	26:DA:2515:C:C6	2.56	0.41
26:DA:535:C:H2'	26:DA:536:A:O4'	2.21	0.41
26:DA:565:C:C5	42:DV:78:LYS:HE3	2.56	0.41
26:DA:848:G:C2	26:DA:933:A:H1'	2.56	0.41
27:DB:59:A:H2'	27:DB:60:C:O4'	2.22	0.41
34:DN:30:ILE:O	34:DN:34:LEU:HD22	2.21	0.41
46:DZ:54:HIS:CG	46:DZ:101:PRO:HG3	2.56	0.41
1:AA:1009:G:N2	1:AA:1020:U:O2	2.44	0.40
1:AA:1226:C:P	13:AM:91:ARG:HH12	2.44	0.40
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.87	0.40
1:AA:26:A:N6	1:AA:558:G:O2'	2.52	0.40
1:AA:300:A:O2'	1:AA:564:C:O2	2.37	0.40
1:AA:78:G:C6	1:AA:91:C:N4	2.81	0.40
2:AB:231:GLU:HB2	2:AB:232:PRO:CD	2.50	0.40
8:AH:14:ARG:O	8:AH:18:ARG:HD3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.37	0.40
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.40	0.40
26:BA:1003:U:HO2'	26:BA:1004:A:P	2.43	0.40
26:BA:1577:C:HO2'	26:BA:1578:C:P	2.40	0.40
26:BA:1577:C:O2'	26:BA:1578:C:P	2.79	0.40
26:BA:2041:A:H5''	41:BU:27:LEU:HD12	2.02	0.40
26:BA:2138:G:N2	26:BA:2184:G:OP1	2.54	0.40
26:BA:242:C:OP2	55:B8:5:LYS:NZ	2.31	0.40
26:BA:2545:A:H2'	26:BA:2546:A:O4'	2.20	0.40
26:BA:733:G:N2	26:BA:835:A:H61	2.19	0.40
26:BA:895:G:N3	26:BA:978:A:H1'	2.36	0.40
28:BD:134:ARG:HG3	28:BD:135:PHE:CD2	2.56	0.40
26:BA:2697:G:H5'	35:BO:68:GLU:CD	2.41	0.40
39:BS:87:PHE:HB2	39:BS:112:PHE:CD2	2.56	0.40
1:CA:1005:A:OP2	1:CA:1024:G:N1	2.54	0.40
1:CA:1064:G:N2	1:CA:1190:G:H2'	2.36	0.40
1:CA:1304:G:C6	1:CA:1305:G:C6	3.09	0.40
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.21	0.40
1:CA:1524:C:H2'	1:CA:1525:G:O4'	2.21	0.40
1:CA:221:C:H2'	1:CA:222:U:H6	1.87	0.40
1:CA:355:C:H2'	1:CA:356:A:O4'	2.21	0.40
1:CA:512:U:OP1	4:CD:46:LYS:HE2	2.21	0.40
1:CA:92:C:N4	1:CA:93:G:N7	2.68	0.40
5:CE:41:VAL:HG22	5:CE:69:VAL:HG11	2.03	0.40
16:CP:20:VAL:HG21	16:CP:32:TYR:CD2	2.56	0.40
24:CX:60:U:H3'	24:CX:61:C:C6	2.56	0.40
51:D4:34:GLU:H	51:D4:34:GLU:CD	2.24	0.40
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.22	0.40
26:DA:1007:C:OP2	61:DA:4086:HOH:O	2.21	0.40
26:DA:565:C:H4'	26:DA:1253:A:C6	2.55	0.40
26:DA:1914:C:H2'	26:DA:1915:U:H6	1.85	0.40
26:DA:2283:C:C2	26:DA:2389:G:C2	3.08	0.40
26:DA:2793:G:H2'	26:DA:2794:C:O4'	2.21	0.40
26:DA:2808:U:O2'	26:DA:2809:A:H5'	2.20	0.40
26:DA:2882:A:OP1	38:DR:96:ARG:NE	2.48	0.40
27:DB:73:A:C4	27:DB:105:A:C2	3.09	0.40
35:DO:60:ALA:HB1	35:DO:84:ALA:HB1	2.04	0.40
43:DW:86:LEU:HA	43:DW:87:PRO:HD3	1.94	0.40
1:AA:16:A:N3	1:AA:1080:A:O2'	2.46	0.40
1:AA:937:A:C2'	1:AA:938:A:H5'	2.51	0.40
2:AB:18:GLY:HA3	2:AB:41:ILE:HD13	2.03	0.40
2:AB:90:MET:HA	2:AB:91:PRO:HD3	1.92	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:AL:42:THR:HA	12:AL:53:ARG:O	2.22	0.40
55:B8:7:HIS:HB3	55:B8:61:LEU:HB3	2.03	0.40
26:BA:1560:U:H2'	26:BA:1561:C:C6	2.56	0.40
26:BA:2151:C:N3	26:BA:2182:G:C2	2.89	0.40
26:BA:68:C:O2	26:BA:72:A:O2'	2.31	0.40
26:BA:779:C:H2'	26:BA:780:G:O4'	2.20	0.40
38:BR:109:ALA:HA	38:BR:110:PRO:HD2	1.92	0.40
38:BR:29:LEU:HA	38:BR:29:LEU:HD12	1.82	0.40
1:CA:1107:C:C4	1:CA:1108:G:C8	3.09	0.40
1:CA:1120:G:C6	1:CA:1121:U:C4	3.08	0.40
1:CA:1471:G:C2'	1:CA:1472:U:H5'	2.51	0.40
1:CA:636:U:H2'	1:CA:637:G:C8	2.55	0.40
1:CA:977:A:O3'	1:CA:980:C:N4	2.48	0.40
1:CA:97:G:N1	1:CA:98:G:C5	2.89	0.40
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.21	0.40
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.55	0.40
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	2.03	0.40
1:CA:1342:C:H4'	9:CI:125:TYR:O	2.21	0.40
9:CI:33:PHE:HZ	9:CI:46:ALA:HB3	1.86	0.40
1:CA:718:G:H5'	11:CK:117:ASN:ND2	2.36	0.40
11:CK:48:ILE:O	11:CK:50:TYR:N	2.53	0.40
12:CL:60:LEU:HD23	12:CL:66:VAL:HG22	2.02	0.40
6:CF:2:ARG:NH2	15:CO:2:PRO:HD2	2.34	0.40
15:CO:50:HIS:O	15:CO:53:HIS:HB3	2.21	0.40
26:DA:1533:G:C6	26:DA:1537:G:C6	3.09	0.40
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.21	0.40
26:DA:2125:G:N2	26:DA:2173:A:C8	2.86	0.40
26:DA:271(H):G:O6	26:DA:271(Q):G:C6	2.74	0.40
26:DA:2830:G:O2'	26:DA:2883:A:N1	2.41	0.40
26:DA:311:A:C6	26:DA:328:U:C4	3.10	0.40
26:DA:6:A:C2'	26:DA:7:G:H5'	2.50	0.40
26:DA:979:G:H5''	26:DA:980:A:H5''	2.03	0.40
26:DA:1354:A:H5''	28:DD:38:LYS:HD3	2.02	0.40
31:DG:60:LEU:HD13	31:DG:60:LEU:HA	1.89	0.40
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.51	0.40
1:AA:1368:G:C2'	1:AA:1369:C:H5'	2.51	0.40
1:AA:347:G:C6	1:AA:348:G:C5	3.09	0.40
1:AA:582:U:H2'	1:AA:583:A:C8	2.57	0.40
2:AB:126:GLU:HB3	2:AB:127:ILE:H	1.67	0.40
2:AB:155:LEU:HD11	2:AB:159:PRO:HD3	2.03	0.40
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.04	0.40
15:AO:17:ARG:HD3	15:AO:26:GLU:CD	2.41	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AQ:32:TYR:O	17:AQ:34:LYS:N	2.54	0.40
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	2.03	0.40
24:AX:43:A:H2'	24:AX:44:A:C8	2.57	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.03	0.40
48:B1:17:SER:HB2	48:B1:40:ARG:HG2	2.02	0.40
19:AS:69:HIS:N	51:B4:58:ARG:NH2	2.70	0.40
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.01	0.40
26:BA:239:G:P	55:B8:13:ARG:NH2	2.95	0.40
26:BA:1239:A:H2'	26:BA:1240:G:O4'	2.22	0.40
26:BA:1277:G:H2'	26:BA:1278:G:C8	2.56	0.40
26:BA:1616:A:H2'	26:BA:1617:A:O4'	2.21	0.40
26:BA:1822:A:C8	26:BA:1823:G:C8	3.09	0.40
26:BA:1822:A:H8	26:BA:1822:A:OP2	2.05	0.40
26:BA:1846:A:OP1	26:BA:1846:A:H8	2.05	0.40
26:BA:2163:G:N1	26:BA:2164:C:O2	2.54	0.40
26:BA:2711:C:H2'	26:BA:2712:C:O4'	2.21	0.40
26:BA:462:C:H2'	26:BA:463:C:H5'	2.03	0.40
26:BA:493:G:O2'	26:BA:843:C:O2'	2.32	0.40
26:BA:802:C:H2'	26:BA:803:C:C6	2.56	0.40
26:BA:915:U:C4	26:BA:916:G:N7	2.90	0.40
29:BE:181:LEU:HD12	29:BE:181:LEU:HA	1.83	0.40
31:BG:10:LYS:HG3	31:BG:14:GLU:OE1	2.22	0.40
45:BY:34:LYS:HG2	45:BY:34:LYS:O	2.21	0.40
1:CA:120:A:C6	1:CA:122:G:C2	3.09	0.40
1:CA:17:U:H2'	1:CA:18:C:H6	1.86	0.40
1:CA:444:C:H2'	1:CA:445:G:C8	2.57	0.40
1:CA:636:U:O2'	1:CA:637:G:H5'	2.22	0.40
1:CA:830:G:H2'	1:CA:831:U:O4'	2.21	0.40
1:CA:949:A:C5	1:CA:950:U:C4	3.10	0.40
3:CC:112:SER:O	3:CC:116:VAL:HG23	2.21	0.40
8:CH:20:TYR:HA	8:CH:65:TYR:OH	2.21	0.40
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.04	0.40
24:CX:6:G:C2	24:CX:68:C:C2	3.10	0.40
26:DA:1152:C:H2'	26:DA:1153:C:C6	2.57	0.40
26:DA:1182:A:H2'	26:DA:1183:G:C8	2.56	0.40
26:DA:1448:G:H5''	26:DA:1449:A:OP1	2.21	0.40
26:DA:2099:U:H2'	26:DA:2100:G:H8	1.86	0.40
26:DA:2154:G:C2	26:DA:2155:G:N7	2.89	0.40
26:DA:2263:C:H41	47:D0:15:ASP:HA	1.87	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.57	0.40
26:DA:360:G:H2'	26:DA:361:G:H8	1.85	0.40
26:DA:422:A:C6	26:DA:423:A:C6	3.10	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:DA:453:C:H5''	61:DA:4438:HOH:O	2.20	0.40
26:DA:638:G:H2'	26:DA:639:U:O4'	2.21	0.40
26:DA:975(A):G:H1'	26:DA:990:A:C2	2.57	0.40
29:DE:120:TRP:CD1	29:DE:155:LYS:HB3	2.57	0.40
30:DF:37:VAL:O	30:DF:41:LEU:HG	2.21	0.40
31:DG:73:ALA:O	31:DG:84:LYS:HG3	2.21	0.40
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.87	0.40
32:DH:42:ARG:HD3	32:DH:44:VAL:HG23	2.04	0.40
39:DS:43:GLU:OE1	47:D0:49:LYS:NZ	2.31	0.40
1:AA:1174:G:H8	1:AA:1174:G:H5''	1.87	0.40
1:AA:265:G:N2	1:AA:267:C:H5'	2.37	0.40
1:AA:428:G:H4'	1:AA:429:U:O5'	2.21	0.40
1:AA:875:C:C4	1:AA:876:G:N7	2.90	0.40
7:AG:26:PHE:CE2	7:AG:30:ILE:HD11	2.57	0.40
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.03	0.40
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.21	0.40
49:B2:29:LYS:HG2	49:B2:57:ILE:HD13	2.02	0.40
51:B4:48:ARG:HA	51:B4:48:ARG:CZ	2.52	0.40
51:B4:57:GLU:OE2	51:B4:58:ARG:HG3	2.21	0.40
26:BA:1098:C:O5'	26:BA:1098:C:H6	2.04	0.40
26:BA:1255:A:H4'	26:BA:1256:U:O5'	2.21	0.40
26:BA:126:C:H2'	26:BA:127:C:O4'	2.22	0.40
26:BA:185:A:H2'	26:BA:185:A:N3	2.36	0.40
26:BA:553:A:C2	26:BA:2065:C:H5'	2.56	0.40
26:BA:2073:A:H4'	29:BE:141:ILE:HG12	2.03	0.40
26:BA:2149:G:H1'	26:BA:2195:A:C2	2.56	0.40
26:BA:2329:C:H2'	26:BA:2330:G:O4'	2.21	0.40
26:BA:244:A:H1'	26:BA:411:U:C6	2.57	0.40
26:BA:495:G:O6	54:B7:37:LYS:HE2	2.21	0.40
26:BA:556:C:H4'	26:BA:557:A:H5''	2.03	0.40
27:BB:96:U:H2'	27:BB:97:G:C8	2.56	0.40
31:BG:126:ASP:HB2	31:BG:130:ASN:HB2	2.04	0.40
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	2.03	0.40
26:BA:2405:A:O2'	36:BP:60:MET:O	2.32	0.40
43:BW:33:ARG:NE	43:BW:52:GLU:OE1	2.50	0.40
1:CA:1106:G:C6	1:CA:1107:C:C4	3.09	0.40
1:CA:1409:C:H2'	1:CA:1410:G:H8	1.85	0.40
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.87	0.40
4:CD:168:ARG:HG2	4:CD:168:ARG:H	1.65	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.69	0.40
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.56	0.40
14:CN:6:LEU:HA	14:CN:6:LEU:HD12	1.95	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:CO:48:LYS:HD3	15:CO:48:LYS:HA	1.83	0.40
24:CX:22:G:H2'	24:CX:23:C:H6	1.86	0.40
50:D3:19:GLN:O	50:D3:23:LEU:HD22	2.22	0.40
26:DA:1203:G:H2'	26:DA:1241:A:N6	2.37	0.40
26:DA:1790:C:H2'	26:DA:1791:A:C5	2.56	0.40
26:DA:183:C:C2'	26:DA:184:C:H5'	2.51	0.40
26:DA:2093:G:C6	26:DA:2225:A:C8	3.10	0.40
26:DA:2104:G:O2'	26:DA:2105:C:O4'	2.36	0.40
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.21	0.40
26:DA:2151:G:N3	26:DA:2152:G:C8	2.89	0.40
26:DA:2286:A:H2'	26:DA:2286:A:N3	2.36	0.40
26:DA:260:G:C6	26:DA:261:G:C8	3.09	0.40
26:DA:660:G:C6	26:DA:661:C:C4	3.10	0.40
26:DA:466:A:H1'	26:DA:683:C:O4'	2.20	0.40
26:DA:786:C:H5''	26:DA:1780:A:N7	2.36	0.40
26:DA:873:G:H1	26:DA:904:C:N4	2.19	0.40
27:DB:16:G:O6	27:DB:66:A:H2	2.04	0.40
26:DA:2723:C:P	29:DE:109:LYS:HZ3	2.44	0.40
29:DE:119:ARG:HH11	29:DE:119:ARG:HD3	1.77	0.40
30:DF:34:TRP:CZ2	36:DP:8:PRO:HG3	2.57	0.40
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.56	0.40
37:DQ:17:LEU:HD21	37:DQ:96:VAL:HG13	2.03	0.40
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	2.03	0.40
39:DS:11:LYS:HD2	39:DS:15:ARG:NH1	2.37	0.40
39:DS:35:ILE:HG22	39:DS:53:SER:HB3	2.04	0.40
1:AA:146:G:C2	1:AA:147:G:C4	3.10	0.40
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.56	0.40
1:AA:715:A:H1'	1:AA:777:A:N1	2.35	0.40
3:AC:115:LEU:HA	3:AC:115:LEU:HD12	1.88	0.40
4:AD:86:LYS:HG2	4:AD:86:LYS:H	1.61	0.40
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.52	0.40
9:AI:97:LYS:HB3	9:AI:98:PRO:HD3	2.04	0.40
1:AA:1060:C:P	14:AN:45:ARG:HH22	2.44	0.40
16:AP:60:LEU:HD13	16:AP:60:LEU:HA	1.83	0.40
20:AT:36:LEU:HA	20:AT:36:LEU:HD23	1.84	0.40
49:B2:48:HIS:CE1	49:B2:49:LYS:HG3	2.57	0.40
50:B3:10:LYS:HB3	50:B3:53:LEU:HA	2.04	0.40
55:B8:39:LYS:HA	55:B8:42:ARG:NH1	2.37	0.40
26:BA:115:G:OP2	26:BA:117:A:O2'	2.33	0.40
26:BA:1214:G:O2'	26:BA:1215:G:H5'	2.22	0.40
26:BA:1721:G:H1'	26:BA:1723:A:N6	2.35	0.40
26:BA:2023:A:H2'	26:BA:2024:G:C8	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BA:2663:C:H2'	26:BA:2664:C:H6	1.85	0.40
26:BA:465:G:H2'	26:BA:466:G:C8	2.56	0.40
26:BA:26:G:H1'	26:BA:540:A:H61	1.86	0.40
26:BA:827:G:H1'	26:BA:832:G:C2	2.56	0.40
29:BE:35:GLN:OE1	29:BE:66:HIS:HE1	2.05	0.40
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.40
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.56	0.40
37:BQ:104:PHE:HE2	37:BQ:125:LEU:HD11	1.87	0.40
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HE2	2.04	0.40
37:BQ:12:GLN:HG2	37:BQ:73:PRO:HD2	2.03	0.40
38:BR:87:TYR:OH	38:BR:116:LEU:HB3	2.21	0.40
39:BS:41:ASP:HB2	39:BS:48:LEU:HD21	2.03	0.40
35:BO:101:PRO:HG3	40:BT:67:SER:OG	2.22	0.40
1:CA:1025:U:C4	1:CA:1036:G:O6	2.75	0.40
1:CA:1125:U:O2'	1:CA:1126:U:C2'	2.68	0.40
1:CA:1392:G:N2	1:CA:1502:A:H8	2.18	0.40
1:CA:485:G:O2'	1:CA:486:U:OP2	2.39	0.40
1:CA:538:G:H5''	12:CL:114:LYS:HB2	2.03	0.40
4:CD:46:LYS:O	4:CD:47:ARG:HB3	2.22	0.40
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.21	0.40
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	2.04	0.40
51:D4:18:CYS:HB3	51:D4:39:CYS:HB3	2.04	0.40
26:DA:1002:G:H2'	26:DA:1003:G:O4'	2.21	0.40
26:DA:996:A:N6	26:DA:1160:G:C6	2.89	0.40
26:DA:1598:C:H2'	26:DA:1599:C:C6	2.57	0.40
26:DA:2298:A:H2	26:DA:2321:G:C5	2.39	0.40
26:DA:2623:G:H4'	26:DA:2825:C:O2	2.22	0.40
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.52	0.40
26:DA:452:G:C4	26:DA:458:G:C6	3.09	0.40
26:DA:729:G:H2'	26:DA:1775:U:O2	2.20	0.40
26:DA:959:A:N3	26:DA:2457:U:O2'	2.47	0.40
27:DB:108:U:H5'	27:DB:109:C:OP2	2.22	0.40
32:DH:150:ALA:HA	32:DH:153:LYS:HG3	2.02	0.40
33:DI:44:LEU:HA	33:DI:44:LEU:HD13	1.92	0.40
34:DN:75:TYR:CE2	34:DN:77:GLY:HA2	2.56	0.40
35:DO:63:VAL:HB	35:DO:102:VAL:HG12	2.03	0.40
37:DQ:76:LYS:HB3	37:DQ:91:GLU:HG3	2.03	0.40
43:DW:86:LEU:HD22	43:DW:96:ILE:HD11	2.04	0.40
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.57	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1043:C:O2'	26:DA:2137:C:O2'[2_655]	2.08	0.12
33:BI:89:TYR:O	1:CA:357:G:O2'[3_654]	2.10	0.10
38:BR:33:ARG:NH2	42:BV:53:GLU:OE2[4_445]	2.19	0.01

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%)	204 (89%)	21 (9%)	4 (2%)	14	42
2	CB	229/256 (90%)	204 (89%)	14 (6%)	11 (5%)	4	10
3	AC	204/239 (85%)	189 (93%)	13 (6%)	2 (1%)	22	60
3	CC	204/239 (85%)	188 (92%)	15 (7%)	1 (0%)	38	76
4	AD	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	38	76
4	CD	206/209 (99%)	196 (95%)	7 (3%)	3 (2%)	15	46
5	AE	146/162 (90%)	136 (93%)	9 (6%)	1 (1%)	30	69
5	CE	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	30	69
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
7	AG	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	11	35
7	CG	153/156 (98%)	143 (94%)	9 (6%)	1 (1%)	30	69
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
8	CH	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	30	69
9	AI	125/128 (98%)	118 (94%)	7 (6%)	0	100	100
9	CI	125/128 (98%)	118 (94%)	6 (5%)	1 (1%)	27	65
10	AJ	95/105 (90%)	83 (87%)	5 (5%)	7 (7%)	2	3
10	CJ	94/105 (90%)	83 (88%)	6 (6%)	5 (5%)	3	9
11	AK	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	25	63
11	CK	112/129 (87%)	105 (94%)	6 (5%)	1 (1%)	25	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	AL	120/132 (91%)	116 (97%)	4 (3%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
13	AM	121/126 (96%)	113 (93%)	6 (5%)	2 (2%)	14	42
13	CM	120/126 (95%)	110 (92%)	9 (8%)	1 (1%)	27	65
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
15	CO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
16	AP	80/88 (91%)	75 (94%)	5 (6%)	0	100	100
16	CP	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
17	AQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
17	CQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
18	AR	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
19	AS	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
19	CS	81/93 (87%)	71 (88%)	8 (10%)	2 (2%)	9	28
20	AT	94/106 (89%)	85 (90%)	3 (3%)	6 (6%)	2	5
20	CT	94/106 (89%)	84 (89%)	6 (6%)	4 (4%)	4	13
21	AU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
21	CU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	43	80
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	30	69
29	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	38	76
29	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	22	60
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	38	76
30	DF	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	22	60
31	BG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	10	32
31	DG	179/182 (98%)	166 (93%)	9 (5%)	4 (2%)	10	32
32	BH	172/180 (96%)	161 (94%)	9 (5%)	2 (1%)	19	54
32	DH	172/180 (96%)	163 (95%)	7 (4%)	2 (1%)	19	54
33	BI	144/148 (97%)	132 (92%)	9 (6%)	3 (2%)	11	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	16	49
34	BN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
34	DN	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	30	69
35	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	27	65
35	DO	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	27	65
36	BP	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	30	69
36	DP	147/150 (98%)	133 (90%)	13 (9%)	1 (1%)	30	69
37	BQ	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
39	BS	108/112 (96%)	104 (96%)	4 (4%)	0	100	100
39	DS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	25	63
40	BT	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
40	DT	129/146 (88%)	125 (97%)	3 (2%)	1 (1%)	27	65
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
42	BV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	22	60
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	22	60
43	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
43	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
44	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
44	DX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
45	BY	105/110 (96%)	95 (90%)	10 (10%)	0	100	100
45	DY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
46	BZ	169/206 (82%)	148 (88%)	19 (11%)	2 (1%)	19	54
46	DZ	172/206 (84%)	156 (91%)	14 (8%)	2 (1%)	19	54
47	B0	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
47	D0	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	21	57
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	21	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	B2	68/72 (94%)	68 (100%)	0	0	100	100
49	D2	68/72 (94%)	68 (100%)	0	0	100	100
50	B3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	54 (81%)	8 (12%)	5 (8%)	2	3
51	D4	67/71 (94%)	53 (79%)	10 (15%)	4 (6%)	2	6
52	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
53	B6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
53	D6	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
54	B7	46/49 (94%)	46 (100%)	0	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	10	32
55	B8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
55	D8	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10783 (94%)	516 (4%)	110 (1%)	22	60

All (110) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	231	GLU
4	AD	166	LYS
7	AG	80	VAL
10	AJ	55	LYS
20	AT	10	LEU
28	BD	275	LYS
30	BF	130	ALA
31	BG	49	ASP
31	BG	51	ARG
32	BH	92	ILE
46	BZ	152	ALA
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	20	GLU

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Mol	Chain	Res	Type
2	CB	126	GLU
9	CI	54	ASP
13	CM	85	GLY
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
31	DG	81	LYS
33	DI	10	GLU
36	DP	29	LYS
48	D1	3	LYS
51	D4	39	CYS
51	D4	62	ARG
54	D7	46	VAL
10	AJ	31	GLY
10	AJ	56	HIS
10	AJ	77	PRO
11	AK	49	GLY
20	AT	47	GLY
20	AT	68	LYS
20	AT	96	GLY
48	B1	3	LYS
51	B4	45	GLY
51	B4	65	ASP
2	CB	17	PHE
2	CB	121	LEU
2	CB	128	GLU
4	CD	47	ARG
4	CD	167	GLY
7	CG	7	ALA
10	CJ	79	ARG
20	CT	47	GLY
31	DG	43	LEU
32	DH	47	GLU
33	DI	81	VAL
40	DT	100	TYR
51	D4	45	GLY
10	AJ	79	ARG
10	AJ	91	PRO
29	BE	52	LEU
31	BG	43	LEU
46	BZ	114	GLY
2	CB	122	PHE

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Mol	Chain	Res	Type
10	CJ	77	PRO
10	CJ	78	ASN
19	CS	12	ASP
19	CS	65	ASN
20	CT	102	GLY
28	DD	239	ARG
29	DE	52	LEU
29	DE	73	GLU
31	DG	32	PRO
46	DZ	101	PRO
5	AE	85	GLY
7	AG	6	ARG
7	AG	81	GLY
13	AM	67	GLU
20	AT	102	GLY
31	BG	32	PRO
35	BO	5	GLN
36	BP	29	LYS
51	B4	58	ARG
2	CB	10	LEU
2	CB	78	GLN
20	CT	95	ALA
28	DD	3	VAL
31	DG	51	ARG
32	DH	126	PRO
34	DN	2	LYS
35	DO	5	GLN
39	DS	84	GLN
51	D4	38	LYS
3	AC	181	ASN
20	AT	100	ILE
32	BH	47	GLU
33	BI	107	VAL
51	B4	57	GLU
2	CB	231	GLU
4	CD	46	LYS
5	CE	69	VAL
2	AB	78	GLN
13	AM	4	ILE
33	BI	73	GLU
8	CH	73	ASP
3	AC	66	VAL

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Mol	Chain	Res	Type
10	AJ	75	ILE
42	BV	79	VAL
10	CJ	75	ILE
42	DV	79	VAL
33	BI	119	PRO
3	CC	108	ASN
10	CJ	91	PRO
2	AB	124	SER
2	AB	125	PRO
11	CK	49	GLY
46	DZ	114	GLY

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	161 (84%)	31 (16%)	3	10
2	CB	187/220 (85%)	161 (86%)	26 (14%)	5	15
3	AC	143/188 (76%)	131 (92%)	12 (8%)	16	41
3	CC	140/188 (74%)	127 (91%)	13 (9%)	13	35
4	AD	170/181 (94%)	153 (90%)	17 (10%)	11	30
4	CD	173/181 (96%)	157 (91%)	16 (9%)	13	36
5	AE	113/123 (92%)	106 (94%)	7 (6%)	26	60
5	CE	114/123 (93%)	105 (92%)	9 (8%)	18	44
6	AF	83/90 (92%)	78 (94%)	5 (6%)	27	61
6	CF	85/90 (94%)	79 (93%)	6 (7%)	21	51
7	AG	119/127 (94%)	107 (90%)	12 (10%)	11	30
7	CG	120/127 (94%)	108 (90%)	12 (10%)	11	30
8	AH	114/119 (96%)	109 (96%)	5 (4%)	39	75
8	CH	114/119 (96%)	106 (93%)	8 (7%)	21	52
9	AI	90/99 (91%)	76 (84%)	14 (16%)	4	11
9	CI	89/99 (90%)	78 (88%)	11 (12%)	7	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	14	37
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	15	39
11	AK	82/99 (83%)	76 (93%)	6 (7%)	20	49
11	CK	83/99 (84%)	79 (95%)	4 (5%)	35	72
12	AL	97/109 (89%)	91 (94%)	6 (6%)	26	60
12	CL	97/109 (89%)	94 (97%)	3 (3%)	52	86
13	AM	93/101 (92%)	82 (88%)	11 (12%)	8	22
13	CM	92/101 (91%)	81 (88%)	11 (12%)	7	21
14	AN	49/50 (98%)	43 (88%)	6 (12%)	7	20
14	CN	49/50 (98%)	43 (88%)	6 (12%)	7	20
15	AO	78/80 (98%)	66 (85%)	12 (15%)	4	12
15	CO	78/80 (98%)	70 (90%)	8 (10%)	10	28
16	AP	69/74 (93%)	60 (87%)	9 (13%)	6	17
16	CP	68/74 (92%)	62 (91%)	6 (9%)	14	38
17	AQ	94/97 (97%)	91 (97%)	3 (3%)	51	85
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	20	48
18	AR	59/77 (77%)	54 (92%)	5 (8%)	15	41
18	CR	59/77 (77%)	54 (92%)	5 (8%)	15	41
19	AS	69/80 (86%)	61 (88%)	8 (12%)	8	23
19	CS	67/80 (84%)	62 (92%)	5 (8%)	19	47
20	AT	70/82 (85%)	60 (86%)	10 (14%)	5	14
20	CT	70/82 (85%)	63 (90%)	7 (10%)	11	30
21	AU	18/22 (82%)	16 (89%)	2 (11%)	9	25
21	CU	18/22 (82%)	17 (94%)	1 (6%)	30	64
28	BD	215/218 (99%)	201 (94%)	14 (6%)	24	57
28	DD	215/218 (99%)	200 (93%)	15 (7%)	21	52
29	BE	164/166 (99%)	144 (88%)	20 (12%)	7	20
29	DE	164/166 (99%)	147 (90%)	17 (10%)	10	28
30	BF	160/166 (96%)	145 (91%)	15 (9%)	13	34
30	DF	159/166 (96%)	146 (92%)	13 (8%)	17	43
31	BG	143/156 (92%)	128 (90%)	15 (10%)	10	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	DG	142/156 (91%)	122 (86%)	20 (14%)	5	14
32	BH	144/148 (97%)	138 (96%)	6 (4%)	40	77
32	DH	144/148 (97%)	132 (92%)	12 (8%)	16	42
33	BI	110/124 (89%)	90 (82%)	20 (18%)	2	7
33	DI	104/124 (84%)	87 (84%)	17 (16%)	3	10
34	BN	118/119 (99%)	103 (87%)	15 (13%)	6	19
34	DN	118/119 (99%)	108 (92%)	10 (8%)	15	41
35	BO	100/100 (100%)	94 (94%)	6 (6%)	27	61
35	DO	100/100 (100%)	96 (96%)	4 (4%)	42	79
36	BP	115/116 (99%)	105 (91%)	10 (9%)	15	39
36	DP	115/116 (99%)	103 (90%)	12 (10%)	10	28
37	BQ	111/111 (100%)	100 (90%)	11 (10%)	11	31
37	DQ	111/111 (100%)	100 (90%)	11 (10%)	11	31
38	BR	101/101 (100%)	82 (81%)	19 (19%)	2	7
38	DR	101/101 (100%)	84 (83%)	17 (17%)	3	9
39	BS	87/88 (99%)	79 (91%)	8 (9%)	13	36
39	DS	85/88 (97%)	75 (88%)	10 (12%)	8	22
40	BT	115/127 (91%)	106 (92%)	9 (8%)	18	45
40	DT	113/127 (89%)	103 (91%)	10 (9%)	14	38
41	BU	93/94 (99%)	86 (92%)	7 (8%)	19	47
41	DU	93/94 (99%)	88 (95%)	5 (5%)	31	66
42	BV	80/82 (98%)	68 (85%)	12 (15%)	4	12
42	DV	80/82 (98%)	72 (90%)	8 (10%)	11	30
43	BW	90/92 (98%)	84 (93%)	6 (7%)	23	55
43	DW	90/92 (98%)	82 (91%)	8 (9%)	14	38
44	BX	77/78 (99%)	74 (96%)	3 (4%)	43	80
44	DX	77/78 (99%)	72 (94%)	5 (6%)	24	57
45	BY	85/91 (93%)	77 (91%)	8 (9%)	13	34
45	DY	85/91 (93%)	78 (92%)	7 (8%)	17	43
46	BZ	145/179 (81%)	131 (90%)	14 (10%)	12	32
46	DZ	145/179 (81%)	127 (88%)	18 (12%)	7	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	B0	65/67 (97%)	62 (95%)	3 (5%)	37	73
47	D0	65/67 (97%)	62 (95%)	3 (5%)	37	73
48	B1	80/83 (96%)	72 (90%)	8 (10%)	11	30
48	D1	80/83 (96%)	73 (91%)	7 (9%)	14	38
49	B2	65/67 (97%)	56 (86%)	9 (14%)	5	15
49	D2	65/67 (97%)	59 (91%)	6 (9%)	13	36
50	B3	51/52 (98%)	45 (88%)	6 (12%)	8	22
50	D3	50/52 (96%)	47 (94%)	3 (6%)	27	61
51	B4	59/63 (94%)	47 (80%)	12 (20%)	2	5
51	D4	53/63 (84%)	46 (87%)	7 (13%)	6	16
52	B5	50/52 (96%)	48 (96%)	2 (4%)	42	79
52	D5	50/52 (96%)	48 (96%)	2 (4%)	42	79
53	B6	51/52 (98%)	44 (86%)	7 (14%)	5	15
53	D6	50/52 (96%)	48 (96%)	2 (4%)	42	79
54	B7	41/42 (98%)	38 (93%)	3 (7%)	20	49
54	D7	41/42 (98%)	38 (93%)	3 (7%)	20	49
55	B8	53/55 (96%)	49 (92%)	4 (8%)	19	47
55	D8	54/55 (98%)	53 (98%)	1 (2%)	69	94
56	B9	34/34 (100%)	31 (91%)	3 (9%)	14	38
56	D9	34/34 (100%)	33 (97%)	1 (3%)	55	88
All	All	9319/10066 (93%)	8433 (90%)	886 (10%)	12	33

All (886) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	11	LEU
2	AB	17	PHE
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP
2	AB	80	ILE
2	AB	81	VAL
2	AB	96	ARG
2	AB	108	ILE

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Mol	Chain	Res	Type
2	AB	114	ARG
2	AB	124	SER
2	AB	127	ILE
2	AB	142	LEU
2	AB	145	LEU
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	169	LYS
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	189	ASP
2	AB	200	ILE
2	AB	205	ASP
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	224	GLN
2	AB	233	SER
3	AC	3	ASN
3	AC	17	ASP
3	AC	37	GLN
3	AC	54	ARG
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	119	ARG
3	AC	131	ARG
3	AC	181	ASN
3	AC	196	LEU
3	AC	204	LEU
4	AD	5	ILE
4	AD	13	ARG
4	AD	31	CYS
4	AD	49	ARG
4	AD	58	LEU
4	AD	85	LYS
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU

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Mol	Chain	Res	Type
4	AD	118	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	138	TYR
4	AD	157	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	187	ARG
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	60	TYR
5	AE	67	VAL
5	AE	71	LEU
5	AE	126	ARG
6	AF	17	SER
6	AF	69	GLU
6	AF	70	ASP
6	AF	81	ILE
6	AF	82	ARG
7	AG	8	GLU
7	AG	10	ARG
7	AG	12	LEU
7	AG	13	GLN
7	AG	52	GLU
7	AG	53	LYS
7	AG	76	ARG
7	AG	79	ARG
7	AG	104	LEU
7	AG	113	GLU
7	AG	114	ARG
7	AG	138	LYS
8	AH	91	ARG
8	AH	112	LEU
8	AH	115	SER
8	AH	127	LEU
8	AH	133	LEU
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	50	LEU
9	AI	53	VAL

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Mol	Chain	Res	Type
9	AI	64	THR
9	AI	81	ILE
9	AI	89	ASN
9	AI	92	TYR
9	AI	103	THR
9	AI	105	ASP
9	AI	108	VAL
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	38	ILE
10	AJ	43	ARG
10	AJ	67	THR
10	AJ	81	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	96	ARG
11	AK	104	GLN
12	AL	33	ARG
12	AL	52	LEU
12	AL	57	LYS
12	AL	60	LEU
12	AL	83	VAL
12	AL	116	SER
13	AM	3	ARG
13	AM	4	ILE
13	AM	19	LEU
13	AM	43	THR
13	AM	49	THR
13	AM	73	GLU
13	AM	78	ILE
13	AM	84	ILE
13	AM	102	ARG
13	AM	110	ARG
13	AM	121	LYS
14	AN	3	ARG
14	AN	7	ILE
14	AN	18	VAL
14	AN	22	THR

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Mol	Chain	Res	Type
14	AN	23	ARG
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	24	SER
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	41	GLU
15	AO	47	LYS
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN
15	AO	83	GLU
16	AP	11	SER
16	AP	19	ILE
16	AP	27	LYS
16	AP	32	TYR
16	AP	33	ILE
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	67	THR
17	AQ	6	LEU
17	AQ	24	GLU
17	AQ	74	LEU
18	AR	28	GLU
18	AR	31	LEU
18	AR	35	ARG
18	AR	38	GLU
18	AR	76	LEU
19	AS	9	VAL
19	AS	12	ASP
19	AS	17	GLU
19	AS	28	LYS
19	AS	37	ARG
19	AS	41	VAL
19	AS	65	ASN
19	AS	66	MET
20	AT	8	ARG
20	AT	9	ASN
20	AT	10	LEU

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Mol	Chain	Res	Type
20	AT	24	LEU
20	AT	45	GLN
20	AT	54	LYS
20	AT	62	LEU
20	AT	71	THR
20	AT	74	LYS
20	AT	90	GLN
21	AU	9	ARG
21	AU	10	ARG
28	BD	37	LEU
28	BD	61	LEU
28	BD	94	LEU
28	BD	99	ASP
28	BD	103	ARG
28	BD	126	GLN
28	BD	142	VAL
28	BD	211	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	242	ARG
28	BD	257	LEU
28	BD	260	ARG
28	BD	275	LYS
29	BE	9	VAL
29	BE	12	THR
29	BE	21	VAL
29	BE	24	THR
29	BE	33	VAL
29	BE	34	VAL
29	BE	45	THR
29	BE	47	VAL
29	BE	49	LEU
29	BE	73	GLU
29	BE	77	ILE
29	BE	78	LEU
29	BE	111	ARG
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	178	GLU

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Mol	Chain	Res	Type
29	BE	181	LEU
30	BF	19	GLU
30	BF	20	LEU
30	BF	24	LEU
30	BF	33	LEU
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	132	VAL
30	BF	140	LEU
30	BF	170	LEU
30	BF	192	LEU
30	BF	197	ASP
31	BG	3	LEU
31	BG	7	LEU
31	BG	21	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	81	LYS
31	BG	82	LEU
31	BG	128	ARG
31	BG	133	LEU
31	BG	136	ARG
31	BG	140	ILE
31	BG	143	GLU
31	BG	148	MET
31	BG	170	ARG
32	BH	2	SER
32	BH	6	ARG
32	BH	41	MET
32	BH	69	ARG
32	BH	84	SER
32	BH	95	ARG
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	12	LEU
33	BI	20	ASP

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Mol	Chain	Res	Type
33	BI	38	LEU
33	BI	40	THR
33	BI	43	ASN
33	BI	47	LEU
33	BI	48	GLU
33	BI	50	ARG
33	BI	57	ARG
33	BI	61	ARG
33	BI	66	GLU
33	BI	91	SER
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	140	LEU
33	BI	142	VAL
34	BN	1	MET
34	BN	10	GLU
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	38	HIS
34	BN	46	VAL
34	BN	48	MET
34	BN	61	ARG
34	BN	68	GLU
34	BN	83	LYS
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	133	GLN
35	BO	8	LEU
35	BO	10	VAL
35	BO	24	VAL
35	BO	92	GLU
35	BO	94	ARG
35	BO	97	ARG
36	BP	42	SER
36	BP	55	ARG
36	BP	65	ARG
36	BP	70	GLN
36	BP	76	LYS
36	BP	95	VAL

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Mol	Chain	Res	Type
36	BP	106	LEU
36	BP	112	LEU
36	BP	148	LEU
36	BP	149	GLU
37	BQ	5	ARG
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	55	VAL
37	BQ	56	ARG
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	6	SER
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU
38	BR	63	ARG
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	111	LEU
39	BS	20	ARG
39	BS	48	LEU
39	BS	49	VAL
39	BS	57	LYS
39	BS	59	LYS
39	BS	61	ASN
39	BS	78	LEU
39	BS	83	LYS

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Mol	Chain	Res	Type
40	BT	6	LEU
40	BT	16	ARG
40	BT	23	ARG
40	BT	49	VAL
40	BT	64	ARG
40	BT	96	ARG
40	BT	108	ARG
40	BT	113	LYS
40	BT	118	ARG
41	BU	5	LYS
41	BU	8	VAL
41	BU	36	ARG
41	BU	74	LEU
41	BU	83	LEU
41	BU	92	ARG
41	BU	104	GLN
42	BV	6	LYS
42	BV	18	LEU
42	BV	28	GLU
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	73	SER
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	17	VAL
43	BW	23	LEU
43	BW	51	LEU
43	BW	100	THR
44	BX	57	LEU
44	BX	65	ARG
44	BX	88	LYS
45	BY	1	MET
45	BY	7	VAL
45	BY	11	ASP
45	BY	23	ARG
45	BY	31	LEU

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Mol	Chain	Res	Type
45	BY	43	ASN
45	BY	90	LEU
45	BY	91	GLU
46	BZ	5	LEU
46	BZ	6	LYS
46	BZ	19	ARG
46	BZ	58	VAL
46	BZ	61	LEU
46	BZ	72	ARG
46	BZ	76	LEU
46	BZ	107	THR
46	BZ	129	SER
46	BZ	136	PHE
46	BZ	142	SER
46	BZ	144	LEU
46	BZ	154	ASP
46	BZ	155	LEU
47	B0	7	LEU
47	B0	20	ARG
47	B0	55	ARG
48	B1	21	ARG
48	B1	35	THR
48	B1	40	ARG
48	B1	52	ARG
48	B1	75	GLU
48	B1	78	LYS
48	B1	89	GLU
48	B1	95	LEU
49	B2	3	LEU
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU
49	B2	52	ASP
49	B2	53	LEU
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	8	LEU
50	B3	23	LEU
50	B3	31	LEU
50	B3	40	THR
50	B3	54	VAL

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Mol	Chain	Res	Type
50	B3	60	GLU
51	B4	3	GLU
51	B4	28	LYS
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	56	VAL
51	B4	59	PHE
51	B4	60	GLN
51	B4	61	ARG
51	B4	67	TYR
51	B4	68	ARG
51	B4	69	LYS
52	B5	29	THR
52	B5	40	LYS
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	18	ARG
53	B6	28	ARG
53	B6	48	VAL
53	B6	52	VAL
54	B7	1	MET
54	B7	24	THR
54	B7	34	ARG
55	B8	14	VAL
55	B8	23	VAL
55	B8	31	HIS
55	B8	32	LEU
56	B9	4	ARG
56	B9	22	ARG
56	B9	27	CYS
2	CB	10	LEU
2	CB	17	PHE
2	CB	24	TRP
2	CB	35	GLU
2	CB	80	ILE
2	CB	82	ARG
2	CB	96	ARG
2	CB	97	TRP
2	CB	98	LEU
2	CB	117	GLU

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Mol	Chain	Res	Type
2	CB	119	GLU
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	150	SER
2	CB	154	LEU
2	CB	155	LEU
2	CB	163	PHE
2	CB	185	ILE
2	CB	187	LEU
2	CB	189	ASP
2	CB	200	ILE
2	CB	217	ARG
2	CB	221	LEU
2	CB	230	VAL
2	CB	233	SER
3	CC	3	ASN
3	CC	15	THR
3	CC	20	SER
3	CC	21	ARG
3	CC	28	GLN
3	CC	32	LEU
3	CC	105	GLU
3	CC	115	LEU
3	CC	118	GLN
3	CC	125	GLU
3	CC	126	ARG
3	CC	131	ARG
3	CC	152	ILE
4	CD	5	ILE
4	CD	13	ARG
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	85	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	135	LEU
4	CD	138	TYR
4	CD	155	LEU
4	CD	168	ARG

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Mol	Chain	Res	Type
4	CD	170	VAL
4	CD	191	ARG
4	CD	194	LEU
5	CE	10	MET
5	CE	12	LEU
5	CE	24	ARG
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	60	TYR
5	CE	78	HIS
5	CE	120	THR
6	CF	10	LEU
6	CF	28	ARG
6	CF	41	GLU
6	CF	75	LEU
6	CF	81	ILE
6	CF	94	GLN
7	CG	9	VAL
7	CG	10	ARG
7	CG	32	ARG
7	CG	51	GLN
7	CG	72	ARG
7	CG	73	MET
7	CG	75	VAL
7	CG	76	ARG
7	CG	104	LEU
7	CG	113	GLU
7	CG	144	MET
7	CG	155	ARG
8	CH	21	LYS
8	CH	26	VAL
8	CH	78	GLN
8	CH	84	ARG
8	CH	112	LEU
8	CH	115	SER
8	CH	133	LEU
8	CH	135	CYS
9	CI	7	THR
9	CI	14	VAL
9	CI	17	VAL
9	CI	23	ASN

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Mol	Chain	Res	Type
9	CI	53	VAL
9	CI	56	LEU
9	CI	64	THR
9	CI	81	ILE
9	CI	102	LEU
9	CI	108	VAL
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	29	ARG
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
10	CJ	100	THR
11	CK	14	VAL
11	CK	54	ARG
11	CK	96	ARG
11	CK	104	GLN
12	CL	33	ARG
12	CL	83	VAL
12	CL	124	LYS
13	CM	4	ILE
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	49	THR
13	CM	56	LEU
13	CM	70	LEU
13	CM	78	ILE
13	CM	102	ARG
13	CM	110	ARG
13	CM	121	LYS
14	CN	3	ARG
14	CN	12	ARG
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	24	SER
15	CO	38	ARG

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Mol	Chain	Res	Type
15	CO	39	LEU
15	CO	41	GLU
15	CO	83	GLU
16	CP	28	ARG
16	CP	32	TYR
16	CP	33	ILE
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	36	ILE
17	CQ	49	GLU
17	CQ	60	ILE
17	CQ	74	LEU
17	CQ	96	GLU
17	CQ	99	SER
18	CR	25	THR
18	CR	26	LEU
18	CR	35	ARG
18	CR	41	LYS
18	CR	76	LEU
19	CS	28	LYS
19	CS	56	GLN
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
20	CT	24	LEU
20	CT	41	ILE
20	CT	45	GLN
20	CT	56	MET
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
21	CU	10	ARG
28	DD	13	ARG
28	DD	54	ARG
28	DD	94	LEU
28	DD	99	ASP
28	DD	106	ILE
28	DD	126	GLN
28	DD	134	ARG
28	DD	138	VAL

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Mol	Chain	Res	Type
28	DD	169	GLU
28	DD	211	ARG
28	DD	221	VAL
28	DD	242	ARG
28	DD	257	LEU
28	DD	260	ARG
28	DD	276	LYS
29	DE	9	VAL
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	52	LEU
29	DE	72	VAL
29	DE	73	GLU
29	DE	78	LEU
29	DE	89	ASP
29	DE	111	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	144	ARG
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	181	LEU
30	DF	19	GLU
30	DF	20	LEU
30	DF	24	LEU
30	DF	33	LEU
30	DF	57	VAL
30	DF	74	ARG
30	DF	88	VAL
30	DF	106	ARG
30	DF	107	LYS
30	DF	110	LEU
30	DF	135	LYS
30	DF	170	LEU
30	DF	192	LEU
31	DG	3	LEU
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	21	ARG

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Mol	Chain	Res	Type
31	DG	35	GLU
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	47	LYS
31	DG	60	LEU
31	DG	98	ARG
31	DG	115	ARG
31	DG	128	ARG
31	DG	133	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	148	MET
31	DG	170	ARG
32	DH	2	SER
32	DH	3	ARG
32	DH	33	LEU
32	DH	34	GLU
32	DH	43	VAL
32	DH	49	VAL
32	DH	69	ARG
32	DH	76	VAL
32	DH	81	GLU
32	DH	95	ARG
32	DH	116	GLU
32	DH	171	LEU
33	DI	5	LEU
33	DI	9	LEU
33	DI	12	LEU
33	DI	20	ASP
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	50	ARG
33	DI	52	ARG
33	DI	57	ARG
33	DI	68	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	87	LYS
33	DI	92	VAL

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Mol	Chain	Res	Type
33	DI	93	THR
33	DI	101	LEU
34	DN	1	MET
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	46	VAL
34	DN	48	MET
34	DN	85	ILE
34	DN	87	LEU
34	DN	99	LEU
34	DN	120	LEU
35	DO	8	LEU
35	DO	10	VAL
35	DO	69	ILE
35	DO	94	ARG
36	DP	1	MET
36	DP	45	LEU
36	DP	55	ARG
36	DP	59	LEU
36	DP	65	ARG
36	DP	70	GLN
36	DP	83	VAL
36	DP	95	VAL
36	DP	99	LEU
36	DP	106	LEU
36	DP	112	LEU
36	DP	148	LEU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	109	VAL
37	DQ	131	ILE
38	DR	1	MET
38	DR	6	SER
38	DR	15	SER

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Mol	Chain	Res	Type
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU
38	DR	54	LEU
38	DR	63	ARG
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU
38	DR	111	LEU
39	DS	20	ARG
39	DS	35	ILE
39	DS	36	TYR
39	DS	44	LYS
39	DS	57	LYS
39	DS	67	ARG
39	DS	68	GLN
39	DS	71	ARG
39	DS	75	GLU
39	DS	80	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	23	ARG
40	DT	64	ARG
40	DT	82	LEU
40	DT	96	ARG
40	DT	108	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	36	ARG
41	DU	74	LEU
41	DU	89	GLU
41	DU	92	ARG
41	DU	104	GLN
42	DV	15	GLU
42	DV	46	VAL
42	DV	52	VAL

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Mol	Chain	Res	Type
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	73	SER
42	DV	79	VAL
43	DW	4	LYS
43	DW	11	ARG
43	DW	17	VAL
43	DW	19	LEU
43	DW	23	LEU
43	DW	51	LEU
43	DW	63	ASP
43	DW	100	THR
44	DX	1	MET
44	DX	57	LEU
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	6	HIS
45	DY	7	VAL
45	DY	19	LYS
45	DY	23	ARG
45	DY	43	ASN
45	DY	72	VAL
45	DY	90	LEU
46	DZ	5	LEU
46	DZ	11	GLU
46	DZ	18	LEU
46	DZ	19	ARG
46	DZ	50	GLN
46	DZ	61	LEU
46	DZ	72	ARG
46	DZ	74	VAL
46	DZ	76	LEU
46	DZ	86	VAL
46	DZ	107	THR
46	DZ	119	GLU
46	DZ	120	ILE
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	154	ASP
46	DZ	155	LEU

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Mol	Chain	Res	Type
46	DZ	170	THR
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	35	THR
48	D1	40	ARG
48	D1	59	THR
48	D1	78	LYS
48	D1	95	LEU
49	D2	30	ARG
49	D2	32	LEU
49	D2	45	SER
49	D2	53	LEU
49	D2	55	ARG
49	D2	70	GLN
50	D3	8	LEU
50	D3	23	LEU
50	D3	40	THR
51	D4	3	GLU
51	D4	34	GLU
51	D4	52	THR
51	D4	56	VAL
51	D4	58	ARG
51	D4	68	ARG
51	D4	69	LYS
52	D5	29	THR
52	D5	40	LYS
53	D6	6	ARG
53	D6	48	VAL
54	D7	1	MET
54	D7	14	LYS
54	D7	34	ARG
55	D8	31	HIS
56	D9	4	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (129) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	94	ASN
3	AC	6	HIS

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Mol	Chain	Res	Type
3	AC	37	GLN
3	AC	102	ASN
3	AC	104	GLN
3	AC	123	GLN
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	77	ASN
4	AD	123	HIS
4	AD	129	ASN
4	AD	161	ASN
5	AE	20	GLN
5	AE	38	GLN
6	AF	100	ASN
7	AG	13	GLN
7	AG	28	ASN
7	AG	56	GLN
7	AG	148	ASN
9	AI	23	ASN
9	AI	31	GLN
9	AI	73	GLN
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
15	AO	28	GLN
15	AO	62	GLN
19	AS	56	GLN
19	AS	57	HIS
19	AS	65	ASN
19	AS	83	HIS
20	AT	9	ASN
20	AT	45	GLN
20	AT	90	GLN
28	BD	87	ASN
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	8	GLN
30	BF	69	HIS

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Mol	Chain	Res	Type
30	BF	169	ASN
30	BF	203	GLN
31	BG	40	ASN
31	BG	108	ASN
33	BI	43	ASN
33	BI	54	GLN
33	BI	105	HIS
36	BP	38	GLN
36	BP	70	GLN
37	BQ	45	GLN
37	BQ	57	HIS
39	BS	95	HIS
40	BT	43	GLN
40	BT	123	GLN
41	BU	117	GLN
44	BX	31	HIS
45	BY	6	HIS
45	BY	43	ASN
46	BZ	73	GLN
46	BZ	118	GLN
46	BZ	132	ASN
49	B2	48	HIS
49	B2	70	GLN
51	B4	46	GLN
52	B5	23	HIS
56	B9	36	GLN
2	CB	16	HIS
2	CB	19	HIS
2	CB	40	HIS
2	CB	146	GLN
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	102	ASN
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	45	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	129	ASN
6	CF	100	ASN

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Mol	Chain	Res	Type
7	CG	28	ASN
7	CG	51	GLN
7	CG	109	ASN
9	CI	23	ASN
9	CI	58	HIS
9	CI	73	GLN
9	CI	124	GLN
10	CJ	13	HIS
10	CJ	62	HIS
12	CL	78	GLN
15	CO	28	GLN
15	CO	62	GLN
17	CQ	16	GLN
19	CS	23	ASN
19	CS	56	GLN
20	CT	45	GLN
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	143	ASN
30	DF	69	HIS
30	DF	203	GLN
31	DG	40	ASN
31	DG	41	GLN
33	DI	43	ASN
33	DI	54	GLN
33	DI	104	GLN
33	DI	133	HIS
36	DP	38	GLN
36	DP	70	GLN
37	DQ	45	GLN
37	DQ	123	HIS
38	DR	13	HIS
38	DR	71	GLN
39	DS	68	GLN
40	DT	58	ASN
40	DT	79	HIS
43	DW	60	ASN
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN
46	DZ	55	HIS

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Mol	Chain	Res	Type
56	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	407 (27%)	26 (1%)
1	CA	1501/1521 (98%)	413 (27%)	28 (1%)
22	AV	12/24 (50%)	7 (58%)	0
22	CV	5/24 (20%)	4 (80%)	0
23	AW	1/3 (33%)	0	0
23	CW	1/3 (33%)	0	0
24	AX	74/77 (96%)	26 (35%)	2 (2%)
24	CX	74/77 (96%)	31 (41%)	4 (5%)
25	AY	4/76 (5%)	1 (25%)	0
25	CY	4/76 (5%)	1 (25%)	0
26	BA	2811/2915 (96%)	529 (18%)	30 (1%)
26	DA	2791/2915 (95%)	595 (21%)	30 (1%)
27	BB	120/121 (99%)	16 (13%)	2 (1%)
27	DB	119/121 (98%)	31 (26%)	0
All	All	9012/9474 (95%)	2061 (22%)	122 (1%)

All (2061) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	15	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	50	A
1	AA	51	A
1	AA	55	A
1	AA	61	G
1	AA	68	G
1	AA	69	G
1	AA	73	G

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Mol	Chain	Res	Type
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	100	C
1	AA	101	A
1	AA	111	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
1	AA	144	G
1	AA	146	G
1	AA	155	C
1	AA	163	C
1	AA	170	U
1	AA	171	A
1	AA	173	U
1	AA	174	C
1	AA	178	C
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(B)	C
1	AA	189(D)	C
1	AA	189(H)	G
1	AA	189(J)	G
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	230	G
1	AA	247	G
1	AA	248	C
1	AA	251	G

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Mol	Chain	Res	Type
1	AA	258	G
1	AA	259	G
1	AA	266	G
1	AA	267	C
1	AA	274	A
1	AA	280	C
1	AA	283	C
1	AA	289	G
1	AA	301	G
1	AA	318	G
1	AA	320	C
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	332	G
1	AA	343	U
1	AA	346	G
1	AA	347	G
1	AA	348	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	374	A
1	AA	383	A
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	432	A

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Mol	Chain	Res	Type
1	AA	439	A
1	AA	442	C
1	AA	445	G
1	AA	452	A
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	484	G
1	AA	485	G
1	AA	495	A
1	AA	496	A
1	AA	498	U
1	AA	504	C
1	AA	505	G
1	AA	508	C
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	519	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	528	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	562	C
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	575	G
1	AA	576	G
1	AA	577	G
1	AA	581	G

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Mol	Chain	Res	Type
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	604	G
1	AA	606	G
1	AA	611	A
1	AA	615	C
1	AA	622	A
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	645	C
1	AA	646	U
1	AA	647	C
1	AA	648	A
1	AA	649	G
1	AA	653	A
1	AA	660	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	677	U
1	AA	680	C
1	AA	684	A
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	701	C
1	AA	710	G
1	AA	711	G
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	733	A
1	AA	748	C
1	AA	749	C
1	AA	752	G
1	AA	755	G
1	AA	759	A
1	AA	764	C

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Mol	Chain	Res	Type
1	AA	766	A
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	802	A
1	AA	806	C
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	832	C
1	AA	833	U
1	AA	835	U
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	849	C
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	860	A
1	AA	868	C
1	AA	869	G
1	AA	874	G
1	AA	885	G
1	AA	886	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	936	C
1	AA	938	A
1	AA	942	G
1	AA	945	G
1	AA	952	U
1	AA	954	G

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Mol	Chain	Res	Type
1	AA	960	U
1	AA	961	U
1	AA	965	A
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	979	C
1	AA	981	U
1	AA	982	U
1	AA	983	A
1	AA	992	U
1	AA	993	G
1	AA	999	C
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1011	G
1	AA	1017	G
1	AA	1019	C
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1036	G
1	AA	1037	C
1	AA	1039	C

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Mol	Chain	Res	Type
1	AA	1043	C
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1056	U
1	AA	1057	G
1	AA	1063	C
1	AA	1064	G
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1092	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1122	U
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
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1145	C
1	AA	1146	A
1	AA	1152	A
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1160	G

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Mol	Chain	Res	Type
1	AA	1164	G
1	AA	1165	C
1	AA	1169	A
1	AA	1174	G
1	AA	1176	A
1	AA	1181	G
1	AA	1183	A
1	AA	1184	G
1	AA	1185	G
1	AA	1196	U
1	AA	1197	G
1	AA	1199	U
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	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1262	C
1	AA	1264	C
1	AA	1265	G
1	AA	1270	C
1	AA	1273	G
1	AA	1274	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1286	A
1	AA	1287	A
1	AA	1296	C
1	AA	1297	C

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Mol	Chain	Res	Type
1	AA	1298	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1317	C
1	AA	1320	C
1	AA	1321	C
1	AA	1322	C
1	AA	1326	C
1	AA	1338	G
1	AA	1340	A
1	AA	1342	C
1	AA	1347	G
1	AA	1360	A
1	AA	1363	C
1	AA	1365	G
1	AA	1370	G
1	AA	1371	G
1	AA	1376	U
1	AA	1377	A
1	AA	1379	G
1	AA	1383	C
1	AA	1396	A
1	AA	1397	C
1	AA	1398	A
1	AA	1402	C
1	AA	1419	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	1457	G
1	AA	1458	G
1	AA	1472	U
1	AA	1475	G
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G

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Mol	Chain	Res	Type
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1520	G
1	AA	1525	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	15	A
22	AV	18	G
22	AV	19	U
22	AV	20	U
22	AV	23	A
22	AV	24	A
24	AX	9	G
24	AX	13	C
24	AX	16	C
24	AX	17	C
24	AX	17(A)	U
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	25	C
24	AX	27	U
24	AX	31	G
24	AX	41	C
24	AX	45	G
24	AX	47	U
24	AX	48	C
24	AX	52	G
24	AX	56	C
24	AX	59	A
24	AX	61	C
24	AX	62	C
24	AX	66	C
24	AX	67	C

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Mol	Chain	Res	Type
24	AX	68	C
24	AX	70	G
24	AX	72	A
25	AY	75	C
26	BA	7	G
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	27	G
26	BA	34	C
26	BA	45	C
26	BA	60	G
26	BA	70	A
26	BA	71	U
26	BA	73	A
26	BA	74	G
26	BA	83	A
26	BA	94	G
26	BA	100	G
26	BA	116	A
26	BA	117	A
26	BA	118	U
26	BA	120	G
26	BA	123	G
26	BA	138	G
26	BA	161	C
26	BA	166	G
26	BA	171	A
26	BA	177	G
26	BA	185	A
26	BA	188	A
26	BA	194	G
26	BA	204	G
26	BA	205	A
26	BA	210	A
26	BA	211	A
26	BA	214	A
26	BA	218	A
26	BA	222	A
26	BA	232	U
26	BA	233	A
26	BA	237	G

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Mol	Chain	Res	Type
26	BA	256	C
26	BA	269	G
26	BA	271	U
26	BA	272	U
26	BA	273	G
26	BA	274	U
26	BA	279	G
26	BA	288	U
26	BA	289	G
26	BA	294	C
26	BA	295	C
26	BA	303	C
26	BA	306	A
26	BA	335	A
26	BA	353	G
26	BA	354	A
26	BA	363	U
26	BA	369	A
26	BA	376	G
26	BA	380	G
26	BA	381	A
26	BA	383	A
26	BA	387	G
26	BA	407	U
26	BA	413	G
26	BA	423	G
26	BA	432	U
26	BA	434	G
26	BA	438	G
26	BA	439	A
26	BA	448	U
26	BA	455	A
26	BA	463	C
26	BA	468	G
26	BA	469	A
26	BA	470	C
26	BA	474	U
26	BA	477	C
26	BA	480	A
26	BA	482	C
26	BA	483	A
26	BA	507	G

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Mol	Chain	Res	Type
26	BA	519	G
26	BA	529	U
26	BA	530	A
26	BA	533	G
26	BA	534	C
26	BA	537	G
26	BA	553	A
26	BA	555	G
26	BA	556	C
26	BA	557	A
26	BA	558	G
26	BA	569	G
26	BA	573	G
26	BA	586	G
26	BA	591	U
26	BA	596	G
26	BA	597	C
26	BA	598	A
26	BA	616	G
26	BA	626	A
26	BA	627	G
26	BA	630	U
26	BA	633	G
26	BA	639	G
26	BA	641	G
26	BA	644	G
26	BA	652	A
26	BA	662	A
26	BA	670	C
26	BA	671	A
26	BA	672	G
26	BA	692	C
26	BA	693	G
26	BA	694	G
26	BA	697	C
26	BA	698	G
26	BA	714	U
26	BA	716	G
26	BA	723	A
26	BA	724	A
26	BA	733	G
26	BA	761	U

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Mol	Chain	Res	Type
26	BA	764	G
26	BA	773	G
26	BA	777	C
26	BA	811	A
26	BA	818	G
26	BA	822	G
26	BA	823	G
26	BA	829	A
26	BA	831	A
26	BA	832	G
26	BA	836	A
26	BA	839	G
26	BA	840	A
26	BA	852	G
26	BA	859	C
26	BA	866	A
26	BA	874	U
26	BA	875	U
26	BA	877	G
26	BA	906	G
26	BA	913	A
26	BA	922	G
26	BA	926	G
26	BA	927	G
26	BA	928	G
26	BA	931	C
26	BA	932	C
26	BA	933	C
26	BA	934	A
26	BA	935	C
26	BA	936	C
26	BA	937	A
26	BA	938	G
26	BA	941	U
26	BA	942	A
26	BA	943	C
26	BA	953	U
26	BA	956	A
26	BA	960	C
26	BA	976	G
26	BA	977	G
26	BA	986	A

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Mol	Chain	Res	Type
26	BA	990	A
26	BA	991	G
26	BA	998	A
26	BA	1003	U
26	BA	1004	A
26	BA	1006	C
26	BA	1019	G
26	BA	1020	C
26	BA	1021	G
26	BA	1029	A
26	BA	1042	A
26	BA	1058	U
26	BA	1059	C
26	BA	1068	G
26	BA	1072	U
26	BA	1079	U
26	BA	1084	C
26	BA	1085	G
26	BA	1086	C
26	BA	1088	G
26	BA	1091	A
26	BA	1092	A
26	BA	1153	G
26	BA	1154	U
26	BA	1155	C
26	BA	1156	G
26	BA	1157	A
26	BA	1158	G
26	BA	1174	A
26	BA	1175	A
26	BA	1176	U
26	BA	1180	C
26	BA	1181	G
26	BA	1184	G
26	BA	1186	U
26	BA	1195	G
26	BA	1201	A
26	BA	1217	G
26	BA	1218	G
26	BA	1219	A
26	BA	1220	U
26	BA	1221	G

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Mol	Chain	Res	Type
26	BA	1222	A
26	BA	1223	C
26	BA	1255	A
26	BA	1256	U
26	BA	1263	C
26	BA	1265	A
26	BA	1290	G
26	BA	1296	G
26	BA	1299	A
26	BA	1302	G
26	BA	1317	G
26	BA	1318	A
26	BA	1319	U
26	BA	1346	U
26	BA	1347	A
26	BA	1349	G
26	BA	1354	A
26	BA	1360	C
26	BA	1365	G
26	BA	1366	C
26	BA	1367	A
26	BA	1381	U
26	BA	1398	U
26	BA	1405	A
26	BA	1411	A
26	BA	1415	G
26	BA	1416	C
26	BA	1426	G
26	BA	1430	A
26	BA	1431	G
26	BA	1432	C
26	BA	1441	A
26	BA	1462	G
26	BA	1463	C
26	BA	1466	U
26	BA	1467	G
26	BA	1474	C
26	BA	1483	C
26	BA	1491	A
26	BA	1496	A
26	BA	1497	G
26	BA	1502	G

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Mol	Chain	Res	Type
26	BA	1505	C
26	BA	1506	G
26	BA	1507	A
26	BA	1514	C
26	BA	1518	A
26	BA	1525	G
26	BA	1529	G
26	BA	1536	A
26	BA	1537	G
26	BA	1538	G
26	BA	1539	C
26	BA	1542	A
26	BA	1551	C
26	BA	1553	A
26	BA	1554	A
26	BA	1555	C
26	BA	1556	A
26	BA	1561	C
26	BA	1571	G
26	BA	1578	C
26	BA	1579	C
26	BA	1588	G
26	BA	1590	C
26	BA	1594	C
26	BA	1601	A
26	BA	1602	G
26	BA	1605	A
26	BA	1613	A
26	BA	1616	A
26	BA	1625	U
26	BA	1628	G
26	BA	1631	C
26	BA	1632	A
26	BA	1654	A
26	BA	1656	A
26	BA	1691	C
26	BA	1694	G
26	BA	1695	C
26	BA	1701	A
26	BA	1711	A
26	BA	1714	G
26	BA	1721	G

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Mol	Chain	Res	Type
26	BA	1738	C
26	BA	1743	G
26	BA	1747	A
26	BA	1748	A
26	BA	1750	G
26	BA	1766	G
26	BA	1767	A
26	BA	1776	G
26	BA	1778	G
26	BA	1779	G
26	BA	1787	G
26	BA	1793	A
26	BA	1794	G
26	BA	1795	G
26	BA	1804	A
26	BA	1808	U
26	BA	1810	U
26	BA	1811	A
26	BA	1813	C
26	BA	1817	A
26	BA	1822	A
26	BA	1831	C
26	BA	1832	G
26	BA	1847	G
26	BA	1858	C
26	BA	1860	A
26	BA	1878	A
26	BA	1899	A
26	BA	1900	G
26	BA	1911	A
26	BA	1922	A
26	BA	1928	G
26	BA	1934	A
26	BA	1935	A
26	BA	1937	U
26	BA	1941	A
26	BA	1946	C
26	BA	1949	A
26	BA	1951	G
26	BA	1952	G
26	BA	1958	A
26	BA	1959	A

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Mol	Chain	Res	Type
26	BA	1960	A
26	BA	1962	U
26	BA	1963	C
26	BA	1977	U
26	BA	1985	U
26	BA	1986	G
26	BA	1989	C
26	BA	1991	A
26	BA	1992	A
26	BA	1993	A
26	BA	1994	A
26	BA	2006	G
26	BA	2013	U
26	BA	2014	G
26	BA	2015	U
26	BA	2018	C
26	BA	2019	G
26	BA	2045	G
26	BA	2049	G
26	BA	2053	A
26	BA	2054	G
26	BA	2055	A
26	BA	2057	G
26	BA	2065	C
26	BA	2073	A
26	BA	2077	C
26	BA	2078	G
26	BA	2082	A
26	BA	2083	G
26	BA	2084	A
26	BA	2091	G
26	BA	2115	G
26	BA	2118	U
26	BA	2119	C
26	BA	2122	G
26	BA	2123	G
26	BA	2124	U
26	BA	2128	G
26	BA	2139	A
26	BA	2140	U
26	BA	2141	A
26	BA	2143	G

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Mol	Chain	Res	Type
26	BA	2145	G
26	BA	2147	G
26	BA	2149	G
26	BA	2150	C
26	BA	2151	C
26	BA	2152	U
26	BA	2153	G
26	BA	2154	U
26	BA	2156	A
26	BA	2157	A
26	BA	2158	C
26	BA	2162	C
26	BA	2163	G
26	BA	2164	C
26	BA	2167	C
26	BA	2169	G
26	BA	2170	G
26	BA	2179	G
26	BA	2180	A
26	BA	2181	G
26	BA	2182	G
26	BA	2186	C
26	BA	2188	G
26	BA	2189	U
26	BA	2190	G
26	BA	2191	A
26	BA	2192	A
26	BA	2193	A
26	BA	2194	U
26	BA	2195	A
26	BA	2197	C
26	BA	2198	A
26	BA	2200	C
26	BA	2203	G
26	BA	2204	G
26	BA	2206	G
26	BA	2210	C
26	BA	2211	U
26	BA	2212	G
26	BA	2214	G
26	BA	2220	A
26	BA	2221	A

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Mol	Chain	Res	Type
26	BA	2227	G
26	BA	2228	G
26	BA	2229	A
26	BA	2230	U
26	BA	2231	G
26	BA	2237	A
26	BA	2250	G
26	BA	2251	G
26	BA	2280	A
26	BA	2281	A
26	BA	2291	G
26	BA	2295	C
26	BA	2299	A
26	BA	2317	A
26	BA	2320	G
26	BA	2328	C
26	BA	2332	A
26	BA	2337	G
26	BA	2338	C
26	BA	2346	G
26	BA	2347	A
26	BA	2348	A
26	BA	2355	C
26	BA	2359	C
26	BA	2362	C
26	BA	2373	A
26	BA	2384	G
26	BA	2395	G
26	BA	2397	C
26	BA	2401	G
26	BA	2408	G
26	BA	2418	U
26	BA	2422	G
26	BA	2436	C
26	BA	2437	A
26	BA	2441	G
26	BA	2442	A
26	BA	2444	A
26	BA	2446	A
26	BA	2447	A
26	BA	2451	A
26	BA	2452	C

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Mol	Chain	Res	Type
26	BA	2453	C
26	BA	2457	G
26	BA	2460	A
26	BA	2481	A
26	BA	2486	C
26	BA	2488	A
26	BA	2496	G
26	BA	2499	G
26	BA	2502	G
26	BA	2503	U
26	BA	2506	G
26	BA	2514	G
26	BA	2517	G
26	BA	2530	A
26	BA	2537	G
26	BA	2541	G
26	BA	2543	A
26	BA	2548	G
26	BA	2550	C
26	BA	2566	U
26	BA	2578	A
26	BA	2579	G
26	BA	2585	C
26	BA	2591	C
26	BA	2594	G
26	BA	2597	U
26	BA	2614	A
26	BA	2621	U
26	BA	2622	C
26	BA	2623	U
26	BA	2624	C
26	BA	2641	A
26	BA	2642	G
26	BA	2658	C
26	BA	2666	A
26	BA	2681	G
26	BA	2701	U
26	BA	2702	C
26	BA	2714	U
26	BA	2715	C
26	BA	2725	A
26	BA	2726	A

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Mol	Chain	Res	Type
26	BA	2727	G
26	BA	2739	U
26	BA	2746	A
26	BA	2768	C
26	BA	2770	A
26	BA	2771	A
26	BA	2774	G
26	BA	2777	A
26	BA	2778	A
26	BA	2779	G
26	BA	2791	A
26	BA	2803	A
26	BA	2804	C
26	BA	2805	G
26	BA	2806	G
26	BA	2813	G
26	BA	2817	G
26	BA	2828	G
26	BA	2830	A
26	BA	2831	A
26	BA	2845	A
26	BA	2882	G
26	BA	2883	A
26	BA	2886	G
26	BA	2890	C
26	BA	2894	U
26	BA	2901	A
26	BA	2902	G
26	BA	2903	G
27	BB	2	C
27	BB	7	G
27	BB	13	A
27	BB	24	G
27	BB	32	C
27	BB	51	G
27	BB	52	A
27	BB	53	A
27	BB	56	G
27	BB	63	G
27	BB	73	A
27	BB	75	G
27	BB	85	G

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Mol	Chain	Res	Type
27	BB	93	G
27	BB	106	G
27	BB	110	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	15	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	50	A
1	CA	51	A
1	CA	55	A
1	CA	58	C
1	CA	61	G
1	CA	66	G
1	CA	68	G
1	CA	69	G
1	CA	72	C
1	CA	73	G
1	CA	79	G
1	CA	88	A
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	100	C
1	CA	101	A
1	CA	105	G
1	CA	111	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	139	G
1	CA	144	G
1	CA	146	G

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Mol	Chain	Res	Type
1	CA	155	C
1	CA	156	G
1	CA	163	C
1	CA	170	U
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	178	C
1	CA	180	U
1	CA	182	U
1	CA	189(A)	C
1	CA	189(B)	C
1	CA	189(D)	C
1	CA	189(H)	G
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	200	G
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	226	G
1	CA	230	G
1	CA	247	G
1	CA	248	C
1	CA	251	G
1	CA	258	G
1	CA	259	G
1	CA	266	G
1	CA	267	C
1	CA	274	A
1	CA	280	C
1	CA	283	C
1	CA	289	G
1	CA	301	G
1	CA	318	G
1	CA	320	C
1	CA	321	A
1	CA	328	C

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Mol	Chain	Res	Type
1	CA	329	A
1	CA	332	G
1	CA	343	U
1	CA	344	A
1	CA	346	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	374	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	432	A
1	CA	434	U
1	CA	439	A
1	CA	442	C
1	CA	452	A
1	CA	456	C
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	484	G
1	CA	485	G
1	CA	495	A
1	CA	496	A
1	CA	498	U
1	CA	504	C
1	CA	505	G

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Mol	Chain	Res	Type
1	CA	508	C
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	519	C
1	CA	521	G
1	CA	527	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	544	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	562	C
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	575	G
1	CA	576	G
1	CA	577	G
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	604	G
1	CA	606	G
1	CA	611	A
1	CA	612	C
1	CA	615	C
1	CA	622	A
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	645	C
1	CA	646	U
1	CA	647	C
1	CA	649	G

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Mol	Chain	Res	Type
1	CA	653	A
1	CA	660	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	677	U
1	CA	680	C
1	CA	684	A
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	701	C
1	CA	710	G
1	CA	711	G
1	CA	717	C
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	733	A
1	CA	748	C
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A
1	CA	764	C
1	CA	766	A
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	802	A
1	CA	806	C
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G
1	CA	826	C
1	CA	828	A
1	CA	832	C
1	CA	833	U

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Mol	Chain	Res	Type
1	CA	835	U
1	CA	838	G
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	849	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	860	A
1	CA	868	C
1	CA	869	G
1	CA	874	G
1	CA	885	G
1	CA	886	G
1	CA	887	G
1	CA	902	G
1	CA	913	A
1	CA	914	A
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	936	C
1	CA	938	A
1	CA	942	G
1	CA	945	G
1	CA	952	U
1	CA	954	G
1	CA	960	U
1	CA	961	U
1	CA	965	A
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	979	C
1	CA	981	U

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Mol	Chain	Res	Type
1	CA	982	U
1	CA	983	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1011	G
1	CA	1017	G
1	CA	1018	C
1	CA	1020	U
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1036	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1045	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1056	U
1	CA	1057	G
1	CA	1063	C
1	CA	1064	G
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1086	U

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Mol	Chain	Res	Type
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1117	G
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1126	U
1	CA	1128	C
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1145	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1160	G
1	CA	1165	C
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1181	G
1	CA	1183	A
1	CA	1184	G
1	CA	1185	G
1	CA	1196	U
1	CA	1197	G
1	CA	1199	U

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Mol	Chain	Res	Type
1	CA	1200	C
1	CA	1202	G
1	CA	1204	A
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1264	C
1	CA	1265	G
1	CA	1270	C
1	CA	1274	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1284	C
1	CA	1287	A
1	CA	1296	C
1	CA	1297	C
1	CA	1298	C
1	CA	1300	G
1	CA	1316	G
1	CA	1317	C
1	CA	1321	C
1	CA	1322	C
1	CA	1326	C
1	CA	1338	G
1	CA	1340	A
1	CA	1342	C
1	CA	1347	G
1	CA	1360	A
1	CA	1363	C
1	CA	1365	G

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Mol	Chain	Res	Type
1	CA	1370	G
1	CA	1376	U
1	CA	1377	A
1	CA	1379	G
1	CA	1383	C
1	CA	1396	A
1	CA	1397	C
1	CA	1398	A
1	CA	1400	C
1	CA	1402	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
1	CA	1447	A
1	CA	1452	C
1	CA	1457	G
1	CA	1458	G
1	CA	1472	U
1	CA	1475	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1507	A
1	CA	1517	G
1	CA	1520	G
1	CA	1525	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	15	A
22	CV	16	A
22	CV	18	G
22	CV	19	U

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Mol	Chain	Res	Type
24	CX	4	G
24	CX	8	4SU
24	CX	9	G
24	CX	13	C
24	CX	16	C
24	CX	17	C
24	CX	17(A)	U
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	25	C
24	CX	27	U
24	CX	31	G
24	CX	41	C
24	CX	42	G
24	CX	45	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	62	C
24	CX	65	C
24	CX	66	C
24	CX	67	C
24	CX	68	C
24	CX	70	G
24	CX	72	A
25	CY	76	A
26	DA	7	G
26	DA	9	U
26	DA	10	G
26	DA	11	G
26	DA	12	U
26	DA	13	A
26	DA	15	G
26	DA	34	C
26	DA	35	G
26	DA	45	C

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Mol	Chain	Res	Type
26	DA	50	U
26	DA	61	G
26	DA	63	U
26	DA	68	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	84	A
26	DA	95	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	122	G
26	DA	131	G
26	DA	139	G
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	181	A
26	DA	182	A
26	DA	184	C
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	213	A
26	DA	214	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	224	G
26	DA	225	A
26	DA	229	A
26	DA	233	A
26	DA	245	G
26	DA	248	G
26	DA	250	G
26	DA	260	G
26	DA	261	G
26	DA	264	C
26	DA	265	A

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Mol	Chain	Res	Type
26	DA	266	G
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(O)	C
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	274	G
26	DA	277	C
26	DA	278	A
26	DA	285	C
26	DA	292	C
26	DA	302	C
26	DA	311	A
26	DA	317	G
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	345	A
26	DA	352	G
26	DA	363	G
26	DA	363(B)	G
26	DA	363(E)	U
26	DA	363(F)	A
26	DA	372	G
26	DA	386	G
26	DA	391	G
26	DA	396	G
26	DA	405	U
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	416	C
26	DA	421	U
26	DA	422	A
26	DA	428	A
26	DA	442	G
26	DA	443	A

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Mol	Chain	Res	Type
26	DA	444	C
26	DA	446	G
26	DA	455	C
26	DA	456	C
26	DA	457	A
26	DA	470	A
26	DA	474	G
26	DA	481	G
26	DA	482	A
26	DA	487	C
26	DA	496	G
26	DA	504	U
26	DA	505	A
26	DA	508	G
26	DA	509	C
26	DA	519	U
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	536	A
26	DA	545	G
26	DA	556	G
26	DA	563	G
26	DA	573	G
26	DA	575	A
26	DA	586	A
26	DA	595	C
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	615	G
26	DA	627	A
26	DA	637	A
26	DA	640	C
26	DA	645	C
26	DA	646	A
26	DA	647	G
26	DA	651	G
26	DA	652(A)	A
26	DA	652(B)	A

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Mol	Chain	Res	Type
26	DA	652(C)	G
26	DA	652(U)	G
26	DA	653	A
26	DA	669	G
26	DA	670	A
26	DA	677	A
26	DA	686	G
26	DA	708	C
26	DA	709	U
26	DA	717	G
26	DA	729	G
26	DA	730	C
26	DA	740	U
26	DA	753	C
26	DA	759	G
26	DA	765	G
26	DA	771	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C
26	DA	792	G
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	821	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	869	G
26	DA	874	G
26	DA	875	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C

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Mol	Chain	Res	Type
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	894	C
26	DA	896	A
26	DA	900	A
26	DA	901	A
26	DA	910	A
26	DA	912	C
26	DA	915	C
26	DA	917	A
26	DA	921	G
26	DA	932	G
26	DA	933	A
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	953	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	979	G
26	DA	980	A
26	DA	983	A
26	DA	996	A
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1020	A
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1027	A
26	DA	1033	U
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1116	C

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Mol	Chain	Res	Type
26	DA	1127	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1166	C
26	DA	1170	G
26	DA	1171	G
26	DA	1206	G
26	DA	1210	A
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1229	G
26	DA	1244	G
26	DA	1249	U
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1296	G
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1308	A
26	DA	1314	C
26	DA	1320	C
26	DA	1341	U
26	DA	1342	A
26	DA	1352	U
26	DA	1357	U
26	DA	1358	G
26	DA	1359	A
26	DA	1365	A
26	DA	1370	C
26	DA	1379	A
26	DA	1380	G
26	DA	1384	A

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Mol	Chain	Res	Type
26	DA	1385	G
26	DA	1386	C
26	DA	1392	A
26	DA	1395	A
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A
26	DA	1449	A
26	DA	1450	G
26	DA	1451	C
26	DA	1455	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1488	G
26	DA	1493	C
26	DA	1494	A
26	DA	1497	U
26	DA	1504	C
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1509(B)	A
26	DA	1512	U
26	DA	1520	G
26	DA	1523	U
26	DA	1525	G
26	DA	1530	C
26	DA	1531	C
26	DA	1532	C
26	DA	1542	A
26	DA	1545	A
26	DA	1547	C
26	DA	1548	C
26	DA	1558	A

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Mol	Chain	Res	Type
26	DA	1559	G
26	DA	1569	A
26	DA	1578	U
26	DA	1579	A
26	DA	1583	A
26	DA	1586	A
26	DA	1592	C
26	DA	1597	A
26	DA	1598	C
26	DA	1608	A
26	DA	1610	A
26	DA	1631	C
26	DA	1636	C
26	DA	1640	C
26	DA	1645	G
26	DA	1647	G
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1674	G
26	DA	1684	C
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1742	G
26	DA	1743	C
26	DA	1744	C
26	DA	1745(A)	C
26	DA	1746	G
26	DA	1750	G
26	DA	1756	G
26	DA	1762	A
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1791	A
26	DA	1800	C

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Mol	Chain	Res	Type
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1829	A
26	DA	1831	G
26	DA	1835	G
26	DA	1839	G
26	DA	1840	G
26	DA	1847	A
26	DA	1848	A
26	DA	1859	A
26	DA	1862	G
26	DA	1866	C
26	DA	1877	A
26	DA	1878	G
26	DA	1882	C
26	DA	1889	A
26	DA	1896	G
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A
26	DA	1914	C
26	DA	1915	U
26	DA	1929	G
26	DA	1930	G
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1940	U
26	DA	1955	U
26	DA	1960	A
26	DA	1963	U
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1984	G
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2024	G

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Mol	Chain	Res	Type
26	DA	2031	A
26	DA	2033	A
26	DA	2043	C
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2093	G
26	DA	2097	C
26	DA	2104	G
26	DA	2105	C
26	DA	2106	G
26	DA	2111	C
26	DA	2113	U
26	DA	2114	A
26	DA	2115	G
26	DA	2119	A
26	DA	2120	G
26	DA	2122	U
26	DA	2123	G
26	DA	2125	G
26	DA	2126	A
26	DA	2127	G
26	DA	2128	C
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2140	C
26	DA	2141	G
26	DA	2143	C
26	DA	2144	U
26	DA	2146	C

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Mol	Chain	Res	Type
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	G
26	DA	2164	C
26	DA	2165	G
26	DA	2166	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2175	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2189	U
26	DA	2192	G
26	DA	2193	G
26	DA	2198	A
26	DA	2200	C
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2238	G
26	DA	2239	G
26	DA	2274	A
26	DA	2275	C
26	DA	2279	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2291	U

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Mol	Chain	Res	Type
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2325	G
26	DA	2333	A
26	DA	2334	G
26	DA	2336	A
26	DA	2337	G
26	DA	2342	C
26	DA	2343	C
26	DA	2347	C
26	DA	2349	G
26	DA	2354	G
26	DA	2377	A
26	DA	2379	G
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2402	C
26	DA	2406	U
26	DA	2410	G
26	DA	2417	C
26	DA	2418	A
26	DA	2422	A
26	DA	2425	A
26	DA	2427	C
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2440	C
26	DA	2441	C
26	DA	2448	A
26	DA	2453	A
26	DA	2459	A
26	DA	2460	U
26	DA	2465	C
26	DA	2469	A
26	DA	2476	A

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Mol	Chain	Res	Type
26	DA	2477	C
26	DA	2480	C
26	DA	2484	G
26	DA	2487	G
26	DA	2490	G
26	DA	2502	G
26	DA	2505	G
26	DA	2518	A
26	DA	2529	G
26	DA	2532	G
26	DA	2535	G
26	DA	2536	G
26	DA	2542	A
26	DA	2549	G
26	DA	2554	U
26	DA	2562	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2610	C
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2627	G
26	DA	2629	A
26	DA	2630	G
26	DA	2632	A
26	DA	2634	G
26	DA	2641	G
26	DA	2652	C
26	DA	2654	A
26	DA	2660	A
26	DA	2661	G
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2702	U
26	DA	2703	C

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Mol	Chain	Res	Type
26	DA	2706	G
26	DA	2707	G
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2721	A
26	DA	2726	U
26	DA	2733	A
26	DA	2746	U
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2759	G
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2774	C
26	DA	2775	A
26	DA	2778	A
26	DA	2780	G
26	DA	2789	C
26	DA	2794	C
26	DA	2802	G
26	DA	2803	C
26	DA	2809	A
26	DA	2810	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2834	G
26	DA	2835	A
26	DA	2861	G
26	DA	2872	G
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	3	C
27	DB	7	G

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Mol	Chain	Res	Type
27	DB	8	U
27	DB	9	G
27	DB	11	C
27	DB	12	C
27	DB	13	A
27	DB	15	A
27	DB	25	A
27	DB	30	C
27	DB	31	C
27	DB	33	G
27	DB	39	A
27	DB	41	U
27	DB	42	C
27	DB	44	G
27	DB	54	G
27	DB	56	G
27	DB	59	A
27	DB	67	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	91	C
27	DB	93	G
27	DB	101	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	115	G

All (122) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	250	A
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C

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Mol	Chain	Res	Type
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1027	C
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1201	A
1	AA	1212	U
1	AA	1256	A
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1447	A
1	AA	1492	A
24	AX	16	C
24	AX	47	U
26	BA	70	A
26	BA	270	C
26	BA	271	U
26	BA	273	G
26	BA	302	A
26	BA	874	U
26	BA	1003	U
26	BA	1219	A
26	BA	1220	U
26	BA	1221	G
26	BA	1255	A
26	BA	1346	U
26	BA	1347	A
26	BA	1425	A
26	BA	1577	C
26	BA	1700	G
26	BA	1859	G
26	BA	2014	G
26	BA	2148	A
26	BA	2149	G
26	BA	2180	A
26	BA	2192	A
26	BA	2203	G
26	BA	2205	C

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Mol	Chain	Res	Type
26	BA	2209	G
26	BA	2418	U
26	BA	2451	A
26	BA	2701	U
26	BA	2769	U
26	BA	2902	G
27	BB	1	U
27	BB	52	A
1	CA	60	A
1	CA	65	U
1	CA	88	A
1	CA	96	U
1	CA	115	G
1	CA	250	A
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	748	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1442	G
1	CA	1447	A
1	CA	1492	A
24	CX	16	C
24	CX	18	G
24	CX	41	C
24	CX	46	G
26	DA	271(K)	U
26	DA	271(M)	G

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Mol	Chain	Res	Type
26	DA	277	C
26	DA	362	U
26	DA	669	G
26	DA	752	A
26	DA	774	A
26	DA	856	C
26	DA	900	A
26	DA	1026	U
26	DA	1210	A
26	DA	1395	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2104	G
26	DA	2110	G
26	DA	2282	G
26	DA	2406	U
26	DA	2422	A
26	DA	2428	G
26	DA	2439	A
26	DA	2602	A
26	DA	2689	U
26	DA	2756	U

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

12 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
23	PPU	AW	76	26,23	38,40,41	1.32	5 (13%)	54,57,60	2.32	15 (27%)
24	5MC	AX	32	24	20,22,23	1.68	4 (20%)	26,32,35	1.63	4 (15%)
24	5MU	AX	54	24	20,22,23	1.55	5 (25%)	25,32,35	2.35	4 (16%)
24	PSU	AX	55	24	19,21,22	1.85	4 (21%)	23,30,33	1.04	2 (8%)
24	31H	AX	76	24,57	30,32,35	1.15	3 (10%)	42,45,50	2.87	13 (30%)
24	4SU	AX	8	24	19,21,22	1.82	4 (21%)	23,30,33	34.02	2 (8%)
23	PPU	CW	76	26,23	38,40,41	1.26	5 (13%)	54,57,60	2.37	15 (27%)
24	5MC	CX	32	24	20,22,23	1.76	4 (20%)	26,32,35	1.46	4 (15%)
24	5MU	CX	54	24	20,22,23	1.54	4 (20%)	25,32,35	1.88	5 (20%)
24	PSU	CX	55	24	19,21,22	1.92	4 (21%)	23,30,33	1.07	3 (13%)
24	31H	CX	76	24,60,57	32,34,35	1.33	5 (15%)	44,47,50	2.56	10 (22%)
24	4SU	CX	8	24	19,21,22	1.87	4 (21%)	23,30,33	13.02	2 (8%)

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
23	PPU	AW	76	26,23	-	0/26/43/44	0/4/4/4
24	5MC	AX	32	24	-	0/6/25/26	0/2/2/2
24	5MU	AX	54	24	-	0/6/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/8/25/26	0/2/2/2
24	31H	AX	76	24,57	-	0/20/37/41	0/3/3/3
24	4SU	AX	8	24	-	0/6/25/26	0/2/2/2
23	PPU	CW	76	26,23	-	0/26/43/44	0/4/4/4
24	5MC	CX	32	24	-	0/6/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/6/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/8/25/26	0/2/2/2
24	31H	CX	76	24,60,57	-	1/23/40/41	0/3/3/3
24	4SU	CX	8	24	-	0/6/25/26	0/2/2/2

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	32	5MC	C5-C4	4.62	1.48	1.41
24	CX	32	5MC	P-OP1	4.52	1.51	1.46
24	AX	32	5MC	C5-C4	4.47	1.48	1.41
24	CX	55	PSU	P-OP1	4.42	1.51	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	55	PSU	P-OP1	4.36	1.51	1.46
24	CX	55	PSU	C5-C1'	-4.33	1.48	1.52
24	CX	8	4SU	P-OP1	4.34	1.51	1.46
24	CX	8	4SU	O2-C2	4.29	1.27	1.21
24	AX	8	4SU	O2-C2	4.29	1.27	1.21
24	AX	8	4SU	P-OP1	4.18	1.51	1.46
24	AX	32	5MC	P-OP1	4.10	1.51	1.46
24	CX	54	5MU	P-OP1	4.08	1.51	1.46
24	AX	54	5MU	P-OP1	4.05	1.51	1.46
24	CX	8	4SU	C4-S4	-3.84	1.60	1.67
23	CW	76	PPU	P-OP1	3.81	1.51	1.46
24	AX	8	4SU	C4-S4	-3.79	1.60	1.67
24	AX	55	PSU	C5-C1'	-3.79	1.48	1.52
23	AW	76	PPU	C5-C4	3.49	1.48	1.40
24	CX	55	PSU	C4-C5	3.44	1.48	1.40
24	AX	55	PSU	C4-C5	3.40	1.48	1.40
24	AX	54	5MU	C4-C5	3.30	1.48	1.40
24	CX	54	5MU	C4-C5	3.29	1.48	1.40
23	CW	76	PPU	C5-C4	3.27	1.47	1.40
23	AW	76	PPU	P-OP1	3.25	1.50	1.46
24	CX	55	PSU	O2-C2	3.24	1.26	1.21
24	CX	76	31H	C5-C4	-3.19	1.33	1.40
24	CX	8	4SU	C2-N1	3.11	1.41	1.38
23	AW	76	PPU	O5'-C5'	-3.04	1.40	1.44
24	AX	32	5MC	C2-N1	3.00	1.41	1.38
24	AX	55	PSU	O2-C2	3.00	1.25	1.21
24	AX	76	31H	C5-C4	-2.95	1.33	1.40
24	CX	32	5MC	C2-N1	2.91	1.41	1.38
24	CX	76	31H	O5'-C5'	-2.91	1.40	1.44
24	AX	54	5MU	C2-N1	2.76	1.41	1.38
24	CX	32	5MC	O2-C2	2.72	1.25	1.21
24	CX	54	5MU	O2-C2	2.70	1.25	1.21
24	AX	76	31H	C4-N9	-2.57	1.34	1.37
24	AX	32	5MC	O2-C2	2.55	1.25	1.21
23	CW	76	PPU	O5'-C5'	-2.55	1.41	1.44
23	AW	76	PPU	C6-C5	2.53	1.49	1.44
24	AX	8	4SU	C2-N1	2.45	1.41	1.38
24	CX	76	31H	C3'-N3'	2.42	1.49	1.45
23	AW	76	PPU	C4-N9	-2.36	1.34	1.37
24	CX	76	31H	C4-N9	-2.33	1.34	1.37
24	CX	76	31H	C5-N7	-2.26	1.31	1.39
24	AX	54	5MU	C4-N3	-2.22	1.33	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	CX	54	5MU	C2-N1	2.21	1.40	1.38
23	CW	76	PPU	C6-C5	2.19	1.48	1.44
23	CW	76	PPU	C4-N9	-2.14	1.34	1.37
24	AX	76	31H	C3'-N3'	2.05	1.49	1.45
24	AX	54	5MU	O2-C2	2.04	1.24	1.21

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	8	4SU	C4-N3-C2	162.91	128.57	121.60
24	CX	8	4SU	C4-N3-C2	61.90	124.25	121.60
24	AX	76	31H	N3-C2-N1	-10.48	119.67	128.89
24	CX	76	31H	N3-C2-N1	-10.33	119.81	128.89
23	CW	76	PPU	C5-C4-N3	-8.77	117.43	125.98
24	AX	76	31H	C5-C4-N3	-8.56	117.63	125.98
23	AW	76	PPU	C5-C4-N3	-8.18	118.00	125.98
24	AX	8	4SU	C2-N1-C1'	8.14	123.31	118.21
24	CX	8	4SU	C2-N1-C1'	7.51	122.92	118.21
24	AX	54	5MU	N3-C2-N1	7.46	122.20	115.97
24	AX	54	5MU	C6-N1-C2	-7.34	120.32	122.41
24	CX	76	31H	O4'-C1'-N9	7.05	123.44	108.10
24	CX	54	5MU	N3-C2-N1	6.58	121.47	115.97
23	AW	76	PPU	C5'-C4'-C3'	-6.38	104.56	115.85
24	CX	76	31H	C5-C4-N3	-6.35	119.79	125.98
23	CW	76	PPU	N3-C4-N9	6.20	136.02	125.39
23	AW	76	PPU	N3-C4-N9	5.78	135.31	125.39
24	AX	76	31H	C4'-O4'-C1'	-5.62	103.54	109.72
23	CW	76	PPU	N1-C6-N6	5.28	122.61	117.04
24	CX	32	5MC	C2-N3-C4	5.10	120.38	115.50
23	CW	76	PPU	C5'-C4'-C3'	-5.06	106.90	115.85
24	AX	76	31H	C6-C5-C4	5.03	123.20	117.55
23	CW	76	PPU	N3-C2-N1	-4.93	124.56	128.89
24	AX	32	5MC	C2-N3-C4	4.79	120.09	115.50
23	AW	76	PPU	C2-N1-C6	4.71	121.73	111.52
23	CW	76	PPU	C2-N1-C6	4.40	121.05	111.52
23	AW	76	PPU	N3-C2-N1	-4.35	125.06	128.89
24	AX	76	31H	O4'-C1'-N9	4.15	117.12	108.10
24	CX	76	31H	C5'-C4'-C3'	-3.71	109.28	115.85
24	CX	54	5MU	C5-C6-N1	-3.66	118.73	122.02
23	AW	76	PPU	N1-C6-N6	3.59	120.83	117.04
24	CX	76	31H	N3-C4-N9	3.54	131.47	125.39
24	CX	76	31H	O4'-C4'-C3'	3.52	108.91	103.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	76	31H	N3-C4-N9	3.44	131.29	125.39
24	AX	32	5MC	C6-N1-C2	3.41	121.30	118.86
23	AW	76	PPU	C4-C5-N7	-3.39	106.14	109.41
24	AX	32	5MC	C5-C6-N1	-3.35	119.01	122.02
24	AX	76	31H	C4-C5-N7	-3.27	106.25	109.41
24	AX	76	31H	O4'-C1'-C2'	-3.24	101.97	106.69
24	AX	76	31H	C5'-C4'-C3'	-3.23	110.13	115.85
23	CW	76	PPU	C9-N6-C6	-3.21	109.94	119.88
23	AW	76	PPU	C10-N6-C6	-3.21	109.95	119.88
24	CX	54	5MU	C6-N1-C2	-3.20	121.50	122.41
23	CW	76	PPU	C10-N6-C9	-3.18	105.02	115.87
24	AX	54	5MU	C5-C6-N1	-3.06	119.27	122.02
24	AX	55	PSU	C5-C1'-C2'	-2.96	110.25	115.73
24	AX	76	31H	C4'-C3'-N3'	-2.93	107.40	113.56
24	AX	76	31H	C5-C4-N9	2.88	111.07	107.09
23	AW	76	PPU	O4'-C4'-C3'	2.87	107.96	103.83
24	AX	32	5MC	N4-C4-N3	2.78	120.95	116.99
23	CW	76	PPU	C4-C5-N7	-2.74	106.76	109.41
24	AX	76	31H	C2-N3-C4	2.70	121.04	113.27
23	CW	76	PPU	C2-N3-C4	2.70	121.04	113.27
23	AW	76	PPU	C3'-N3'-C	-2.69	118.91	123.19
24	CX	55	PSU	C5-C1'-C2'	-2.60	110.90	115.73
24	CX	32	5MC	N4-C4-N3	2.56	120.64	116.99
24	AX	54	5MU	C4-N3-C2	-2.51	120.23	125.39
24	CX	54	5MU	C4-N3-C2	-2.45	120.37	125.39
24	CX	76	31H	CA-N-CN	-2.45	119.06	122.82
24	CX	76	31H	C2-N3-C4	2.39	120.14	113.27
23	CW	76	PPU	C10-N6-C6	-2.35	112.62	119.88
23	AW	76	PPU	C2-N3-C4	2.33	119.97	113.27
24	CX	76	31H	C6-C5-C4	2.32	120.15	117.55
23	AW	76	PPU	C2'-C3'-N3'	2.30	118.43	113.08
24	AX	55	PSU	C4-N3-C2	-2.29	120.72	125.36
24	CX	54	5MU	C2-N1-C1'	-2.26	116.79	118.21
24	CX	55	PSU	C4-N3-C2	-2.23	120.84	125.36
23	AW	76	PPU	C4'-C3'-N3'	-2.21	108.90	113.56
23	AW	76	PPU	P-O5'-C5'	-2.18	114.37	122.98
23	AW	76	PPU	C10-N6-C9	-2.16	108.50	115.87
23	CW	76	PPU	O4'-C4'-C3'	2.16	106.94	103.83
23	CW	76	PPU	P-O5'-C5'	-2.14	114.54	122.98
24	CX	32	5MC	C5-C6-N1	-2.10	120.13	122.02
24	CX	76	31H	C1'-C2'-C3'	2.05	106.05	102.19
24	AX	76	31H	C8-N9-C4	-2.04	105.30	106.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	76	PPU	C4'-O4'-C1'	2.03	111.95	109.72
24	CX	32	5MC	C6-N1-C2	2.02	120.31	118.86
24	CX	55	PSU	O4'-C1'-C2'	2.02	107.88	104.43
23	CW	76	PPU	C3'-N3'-C	-2.02	119.97	123.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	CX	76	31H	OCN-CN-N-CA

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1916 ligands modelled in this entry, 1914 are monoatomic - leaving 2 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	$\# Z > 2$
58	SF4	AD	302	4	12,12,12	21.81	12 (100%)	0,24,24	0.00	-
58	SF4	CD	501	4	12,12,12	21.37	12 (100%)	0,24,24	0.00	-

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
58	SF4	AD	302	4	-	0/0/48/48	0/6/5/5
58	SF4	CD	501	4	-	0/0/48/48	0/6/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	AD	302	SF4	S2-FE1	-22.57	2.18	2.33
58	CD	501	SF4	S3-FE1	-22.45	2.18	2.33
58	AD	302	SF4	S1-FE3	-22.26	2.18	2.33
58	AD	302	SF4	S2-FE4	-22.20	2.18	2.33
58	AD	302	SF4	S4-FE1	-22.09	2.18	2.33
58	AD	302	SF4	S4-FE2	-22.06	2.18	2.33
58	AD	302	SF4	S4-FE3	-21.95	2.18	2.33
58	CD	501	SF4	S3-FE4	-21.77	2.18	2.33
58	CD	501	SF4	S1-FE3	-21.76	2.18	2.33
58	AD	302	SF4	S3-FE4	-21.67	2.18	2.33
58	CD	501	SF4	S4-FE1	-21.64	2.18	2.33
58	CD	501	SF4	S4-FE3	-21.60	2.18	2.33
58	AD	302	SF4	S3-FE1	-21.60	2.18	2.33
58	AD	302	SF4	S1-FE4	-21.45	2.18	2.33
58	CD	501	SF4	S4-FE2	-21.42	2.18	2.33
58	AD	302	SF4	S1-FE2	-21.35	2.18	2.33
58	CD	501	SF4	S2-FE3	-21.33	2.18	2.33
58	AD	302	SF4	S3-FE2	-21.31	2.18	2.33
58	CD	501	SF4	S1-FE4	-21.20	2.19	2.33
58	CD	501	SF4	S2-FE1	-21.19	2.19	2.33
58	AD	302	SF4	S2-FE3	-21.12	2.19	2.33
58	CD	501	SF4	S2-FE4	-20.89	2.19	2.33
58	CD	501	SF4	S3-FE2	-20.63	2.19	2.33
58	CD	501	SF4	S1-FE2	-20.48	2.19	2.33

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	1498/1521 (98%)	0.45	34 (2%) 57 58	39, 73, 93, 105	0
1	CA	1503/1521 (98%)	0.42	60 (3%) 36 37	41, 75, 94, 106	0
2	AB	231/256 (90%)	0.29	10 (4%) 34 34	69, 82, 91, 101	0
2	CB	231/256 (90%)	2.37	120 (51%) 0 0	71, 84, 93, 101	0
3	AC	206/239 (86%)	0.57	14 (6%) 17 15	67, 79, 89, 95	0
3	CC	206/239 (86%)	2.05	86 (41%) 1 0	70, 81, 91, 95	0
4	AD	208/209 (99%)	0.44	8 (3%) 38 38	57, 74, 85, 91	0
4	CD	208/209 (99%)	0.62	15 (7%) 15 14	57, 75, 85, 92	0
5	AE	148/162 (91%)	0.43	5 (3%) 43 44	59, 71, 82, 90	0
5	CE	148/162 (91%)	0.95	27 (18%) 2 2	59, 73, 84, 91	0
6	AF	100/101 (99%)	0.55	6 (6%) 21 21	54, 69, 78, 83	0
6	CF	100/101 (99%)	0.36	8 (8%) 12 11	56, 71, 80, 83	0
7	AG	155/156 (99%)	0.49	16 (10%) 7 6	64, 76, 86, 92	0
7	CG	155/156 (99%)	1.13	30 (19%) 2 1	67, 78, 88, 92	0
8	AH	137/138 (99%)	0.52	11 (8%) 12 11	60, 72, 80, 85	0
8	CH	137/138 (99%)	1.29	33 (24%) 1 1	62, 74, 82, 85	0
9	AI	127/128 (99%)	1.06	26 (20%) 1 1	64, 83, 91, 96	0
9	CI	127/128 (99%)	1.60	43 (33%) 1 1	69, 84, 91, 98	0
10	AJ	97/105 (92%)	0.71	9 (9%) 9 7	66, 83, 92, 94	0
10	CJ	96/105 (91%)	1.87	45 (46%) 1 0	69, 85, 93, 94	0
11	AK	114/129 (88%)	0.67	10 (8%) 10 8	46, 70, 81, 85	0
11	CK	114/129 (88%)	0.33	6 (5%) 25 26	50, 71, 82, 85	0
12	AL	122/132 (92%)	0.44	3 (2%) 54 55	50, 64, 73, 81	0
12	CL	122/132 (92%)	0.55	9 (7%) 14 13	52, 65, 75, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.70	15 (12%) 5 4	58, 72, 83, 90	0
13	CM	122/126 (96%)	1.32	27 (22%) 1 1	72, 85, 93, 100	0
14	AN	60/61 (98%)	0.84	10 (16%) 2 2	65, 75, 81, 82	0
14	CN	60/61 (98%)	1.99	26 (43%) 1 0	69, 78, 83, 86	0
15	AO	88/89 (98%)	0.65	2 (2%) 57 58	54, 69, 81, 85	0
15	CO	88/89 (98%)	0.43	9 (10%) 7 6	53, 71, 82, 87	0
16	AP	82/88 (93%)	0.97	13 (15%) 3 2	59, 72, 82, 85	0
16	CP	82/88 (93%)	0.57	6 (7%) 15 13	57, 71, 81, 85	0
17	AQ	99/105 (94%)	0.58	2 (2%) 62 63	58, 71, 80, 83	0
17	CQ	99/105 (94%)	1.12	22 (22%) 1 1	56, 72, 81, 83	0
18	AR	68/88 (77%)	0.57	4 (5%) 22 21	59, 70, 80, 84	0
18	CR	68/88 (77%)	0.72	11 (16%) 2 2	60, 71, 82, 85	0
19	AS	83/93 (89%)	0.72	11 (13%) 4 3	72, 82, 89, 93	0
19	CS	83/93 (89%)	2.15	43 (51%) 0 0	73, 84, 91, 95	0
20	AT	96/106 (90%)	1.05	16 (16%) 2 2	60, 71, 83, 85	0
20	CT	96/106 (90%)	0.73	11 (11%) 5 4	56, 71, 83, 85	0
21	AU	23/27 (85%)	0.86	2 (8%) 10 9	69, 74, 79, 85	0
21	CU	23/27 (85%)	1.04	6 (26%) 1 1	71, 76, 84, 86	0
22	AV	13/24 (54%)	2.38	6 (46%) 1 0	56, 88, 93, 97	0
22	CV	6/24 (25%)	1.69	3 (50%) 0 0	59, 76, 95, 96	0
23	AW	3/3 (100%)	1.26	1 (33%) 1 1	28, 28, 30, 37	0
23	CW	3/3 (100%)	2.07	1 (33%) 1 1	42, 42, 50, 57	0
24	AX	75/77 (97%)	0.41	1 (1%) 74 75	27, 70, 84, 92	0
24	CX	75/77 (97%)	0.52	2 (2%) 52 52	30, 75, 86, 93	0
25	AY	5/76 (6%)	0.58	0 100 100	51, 76, 87, 94	0
25	CY	5/76 (6%)	2.05	3 (60%) 0 0	60, 79, 90, 91	0
26	BA	2819/2915 (96%)	0.43	55 (1%) 62 63	20, 42, 89, 107	0
26	DA	2800/2915 (96%)	0.15	79 (2%) 50 52	22, 46, 90, 107	0
27	BB	120/121 (99%)	0.33	0 100 100	37, 63, 77, 88	0
27	DB	120/121 (99%)	0.48	10 (8%) 11 10	42, 68, 80, 91	0
28	BD	275/276 (99%)	0.15	2 (0%) 84 85	21, 41, 58, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	-0.04	3 (1%) 77 78	23, 43, 61, 80	0
29	BE	204/206 (99%)	0.09	1 (0%) 88 90	21, 46, 65, 82	0
29	DE	204/206 (99%)	-0.17	2 (0%) 79 79	23, 48, 67, 84	0
30	BF	203/210 (96%)	0.14	2 (0%) 79 79	22, 51, 73, 87	0
30	DF	203/210 (96%)	0.03	5 (2%) 54 55	24, 54, 74, 86	0
31	BG	181/182 (99%)	0.15	4 (2%) 59 60	55, 70, 82, 93	0
31	DG	181/182 (99%)	1.16	40 (22%) 1 1	59, 74, 85, 93	0
32	BH	174/180 (96%)	0.14	3 (1%) 67 68	49, 65, 77, 81	0
32	DH	174/180 (96%)	1.03	32 (18%) 2 2	52, 70, 80, 84	0
33	BI	146/148 (98%)	0.75	17 (11%) 5 4	47, 81, 90, 95	0
33	DI	146/148 (98%)	3.02	79 (54%) 0 0	46, 84, 94, 99	0
34	BN	140/140 (100%)	0.22	2 (1%) 72 72	29, 49, 72, 82	0
34	DN	140/140 (100%)	-0.00	1 (0%) 84 85	33, 53, 74, 83	0
35	BO	122/122 (100%)	-0.04	0 100 100	26, 42, 61, 65	0
35	DO	122/122 (100%)	-0.01	1 (0%) 83 83	36, 57, 70, 79	0
36	BP	149/150 (99%)	0.39	4 (2%) 52 52	25, 52, 76, 85	0
36	DP	149/150 (99%)	0.41	8 (5%) 25 25	28, 54, 78, 86	0
37	BQ	141/141 (100%)	0.13	0 100 100	29, 51, 65, 78	0
37	DQ	141/141 (100%)	0.58	14 (9%) 8 6	31, 55, 69, 79	0
38	BR	118/118 (100%)	-0.11	0 100 100	23, 37, 56, 63	0
38	DR	118/118 (100%)	0.13	0 100 100	31, 50, 64, 71	0
39	BS	110/112 (98%)	0.01	1 (0%) 81 81	33, 51, 63, 76	0
39	DS	110/112 (98%)	0.58	9 (8%) 12 10	55, 76, 86, 89	0
40	BT	131/146 (89%)	-0.27	0 100 100	27, 44, 73, 86	0
40	DT	131/146 (89%)	0.13	3 (2%) 57 58	42, 59, 78, 86	0
41	BU	116/118 (98%)	-0.10	1 (0%) 81 81	18, 32, 52, 73	0
41	DU	116/118 (98%)	0.27	2 (1%) 67 68	37, 58, 75, 80	0
42	BV	101/101 (100%)	-0.10	1 (0%) 79 79	20, 43, 61, 76	0
42	DV	101/101 (100%)	0.79	12 (11%) 5 4	36, 67, 81, 87	0
43	BW	112/113 (99%)	-0.05	1 (0%) 81 81	20, 33, 51, 84	0
43	DW	112/113 (99%)	0.14	2 (1%) 65 66	32, 47, 65, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.06	1 (1%) 77 78	22, 37, 57, 82	0
44	DX	95/96 (98%)	0.64	9 (9%) 8 7	39, 59, 73, 82	0
45	BY	107/110 (97%)	0.12	1 (0%) 81 81	32, 48, 70, 81	0
45	DY	107/110 (97%)	0.85	10 (9%) 9 7	48, 68, 78, 89	0
46	BZ	171/206 (83%)	0.39	3 (1%) 65 66	40, 63, 83, 88	0
46	DZ	174/206 (84%)	1.41	48 (27%) 1 1	64, 82, 94, 97	0
47	B0	83/85 (97%)	-0.03	0 100 100	23, 38, 52, 66	0
47	D0	83/85 (97%)	0.64	5 (6%) 21 21	36, 61, 72, 81	0
48	B1	97/98 (98%)	0.14	3 (3%) 47 47	21, 42, 65, 74	0
48	D1	97/98 (98%)	0.39	5 (5%) 26 26	30, 54, 76, 82	0
49	B2	70/72 (97%)	0.05	1 (1%) 72 72	32, 48, 63, 87	0
49	D2	70/72 (97%)	0.41	1 (1%) 72 72	50, 67, 78, 83	0
50	B3	59/60 (98%)	-0.17	1 (1%) 67 68	21, 37, 62, 81	0
50	D3	59/60 (98%)	0.85	5 (8%) 11 9	44, 60, 77, 87	0
51	B4	69/71 (97%)	0.40	8 (11%) 5 4	54, 76, 91, 98	0
51	D4	69/71 (97%)	0.97	14 (20%) 1 1	80, 90, 95, 99	0
52	B5	59/60 (98%)	-0.16	1 (1%) 67 68	19, 33, 53, 65	0
52	D5	59/60 (98%)	-0.08	0 100 100	28, 48, 69, 72	0
53	B6	53/54 (98%)	-0.24	0 100 100	28, 40, 60, 64	0
53	D6	53/54 (98%)	0.51	3 (5%) 23 23	43, 59, 72, 82	0
54	B7	48/49 (97%)	-0.08	2 (4%) 35 35	18, 25, 54, 63	0
54	D7	48/49 (97%)	-0.02	1 (2%) 60 61	29, 39, 63, 81	0
55	B8	64/65 (98%)	-0.06	1 (1%) 68 69	23, 32, 46, 61	0
55	D8	64/65 (98%)	0.56	2 (3%) 47 47	37, 55, 66, 70	0
56	B9	37/37 (100%)	0.49	1 (2%) 52 52	27, 49, 67, 71	0
56	D9	37/37 (100%)	1.08	6 (16%) 2 2	46, 54, 67, 74	0
All	All	20650/21602 (95%)	0.47	1415 (6%) 17 15	18, 63, 89, 107	0

All (1415) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
33	DI	65	ALA	12.8
33	DI	111	PRO	11.9

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Mol	Chain	Res	Type	RSRZ
33	DI	119	PRO	11.9
33	DI	146	ALA	11.8
13	CM	124	PRO	10.8
33	DI	128	LEU	10.6
13	CM	123	ALA	10.0
33	DI	58	LEU	10.0
13	AM	124	PRO	9.7
33	DI	100	ALA	9.3
33	DI	85	GLU	9.3
33	DI	137	PRO	9.0
33	DI	89	TYR	8.9
33	DI	145	VAL	8.6
50	D3	2	PRO	8.6
33	DI	114	LEU	8.5
33	DI	87	LYS	8.3
1	CA	1030(B)	C	8.3
33	DI	96	ASP	8.3
3	CC	87	LEU	8.3
33	DI	99	GLU	8.1
22	AV	24	A	7.9
33	DI	118	LYS	7.8
33	DI	129	THR	7.7
33	DI	83	ALA	7.6
44	DX	92	LEU	7.2
33	DI	112	LYS	7.2
2	CB	21	ARG	7.1
33	DI	122	GLU	6.9
51	D4	45	GLY	6.7
1	CA	1532	U	6.7
3	CC	71	ALA	6.7
33	DI	86	THR	6.7
7	AG	79	ARG	6.6
33	DI	54	GLN	6.6
56	D9	12	ASP	6.6
33	DI	68	LEU	6.5
33	DI	84	GLY	6.3
31	DG	28	VAL	6.3
45	DY	1	MET	6.2
1	AA	1030(B)	C	6.2
2	CB	70	PHE	6.2
2	CB	112	VAL	6.2
14	CN	25	VAL	6.2

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Mol	Chain	Res	Type	RSRZ
10	CJ	6	ILE	6.2
13	AM	123	ALA	6.1
33	DI	109	ILE	6.0
7	CG	80	VAL	6.0
7	AG	82	GLY	5.9
3	CC	117	ALA	5.8
2	CB	29	ALA	5.8
13	CM	75	ALA	5.8
33	DI	108	THR	5.8
26	DA	2131	G	5.7
37	DQ	136	ALA	5.7
2	CB	232	PRO	5.7
2	CB	200	ILE	5.7
42	DV	1	MET	5.6
31	DG	2	PRO	5.6
2	CB	101	MET	5.6
3	CC	53	ALA	5.6
3	CC	190	ARG	5.6
7	CG	78	ARG	5.6
26	DA	2132	U	5.6
7	AG	83	ALA	5.6
3	CC	167	TRP	5.6
13	CM	119	GLY	5.6
3	CC	80	GLY	5.6
4	AD	167	GLY	5.5
26	BA	2142	G	5.5
3	CC	187	ALA	5.5
2	CB	97	TRP	5.5
14	CN	53	LEU	5.5
1	CA	1001(A)	G	5.4
33	DI	72	LEU	5.4
3	CC	170	GLN	5.4
33	DI	130	TYR	5.3
3	CC	189	ALA	5.3
7	CG	81	GLY	5.3
32	DH	115	VAL	5.3
26	DA	2116	G	5.3
33	DI	88	ILE	5.3
14	CN	37	PHE	5.2
33	DI	93	THR	5.2
26	DA	2112	G	5.2
42	DV	20	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
26	BA	2167	C	5.2
19	CS	45	VAL	5.2
36	DP	108	LYS	5.2
3	CC	146	ALA	5.2
2	CB	163	PHE	5.2
33	DI	61	ARG	5.2
5	CE	94	ALA	5.1
2	CB	45	GLN	5.1
2	CB	207	ALA	5.1
2	CB	100	GLY	5.1
2	CB	214	ILE	5.1
10	CJ	85	LEU	5.1
33	BI	84	GLY	5.1
2	CB	49	GLU	5.1
3	CC	199	LYS	5.1
26	DA	2155	G	5.1
2	CB	188	ALA	5.0
2	CB	53	ARG	5.0
2	CB	93	VAL	5.0
46	DZ	142	SER	5.0
41	BU	117	GLN	5.0
1	CA	1531	A	5.0
7	CG	83	ALA	5.0
3	CC	48	TYR	5.0
1	CA	1030(A)	G	5.0
46	DZ	114	GLY	5.0
1	AA	1257	U	4.9
9	CI	19	LEU	4.9
14	CN	22	THR	4.9
2	CB	116	GLU	4.9
43	DW	112	GLY	4.9
3	CC	37	GLN	4.9
26	DA	896	A	4.9
13	CM	121	LYS	4.9
26	DA	2142	C	4.9
46	DZ	124	ILE	4.9
13	CM	120	LYS	4.8
2	CB	102	LEU	4.8
48	B1	98	LEU	4.8
3	CC	204	LEU	4.8
14	CN	42	ILE	4.8
7	CG	84	ASN	4.8

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Mol	Chain	Res	Type	RSRZ
14	CN	8	GLU	4.8
3	CC	81	GLY	4.8
32	DH	107	VAL	4.8
19	CS	28	LYS	4.8
2	CB	77	ALA	4.8
2	CB	177	ALA	4.8
19	CS	71	LEU	4.7
9	CI	7	THR	4.7
33	DI	69	LYS	4.7
33	DI	134	PRO	4.7
16	AP	1	MET	4.7
18	CR	46	GLU	4.7
3	CC	152	ILE	4.7
26	DA	883	G	4.6
8	CH	80	ILE	4.6
2	CB	187	LEU	4.6
2	CB	123	ALA	4.6
33	DI	124	GLY	4.6
14	CN	44	LEU	4.6
47	D0	69	PHE	4.6
3	CC	165	THR	4.6
3	CC	201	TYR	4.6
11	AK	13	GLN	4.6
1	AA	1030(C)	G	4.6
2	CB	158	LEU	4.6
26	DA	2149	G	4.6
13	CM	102	ARG	4.6
26	DA	2147	G	4.5
13	AM	122	LYS	4.5
50	D3	60	GLU	4.5
1	AA	1447	A	4.5
26	DA	2173	A	4.5
8	AH	2	LEU	4.5
19	CS	16	LEU	4.5
32	DH	35	VAL	4.5
2	CB	230	VAL	4.5
3	CC	91	LEU	4.5
31	DG	29	TRP	4.4
46	DZ	171	ILE	4.4
19	CS	50	ALA	4.4
19	CS	20	LEU	4.4
2	CB	115	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
2	CB	227	GLY	4.4
27	DB	118	G	4.4
26	BA	2815	C	4.4
9	CI	64	THR	4.3
2	CB	81	VAL	4.3
3	CC	149	ALA	4.3
2	AB	188	ALA	4.3
26	DA	2133	G	4.3
2	AB	133	LYS	4.3
13	CM	122	LYS	4.3
9	AI	7	THR	4.3
46	DZ	5	LEU	4.3
26	DA	2166	G	4.3
7	AG	154	TYR	4.3
1	CA	1002	G	4.3
2	CB	11	LEU	4.3
2	CB	184	VAL	4.3
9	AI	87	GLN	4.3
2	CB	69	LEU	4.2
7	CG	82	GLY	4.2
3	CC	143	GLU	4.2
2	CB	37	ASN	4.2
26	DA	2139	C	4.2
42	DV	43	GLU	4.2
2	CB	127	ILE	4.2
46	DZ	146	ILE	4.2
9	CI	115	GLY	4.2
19	CS	32	LYS	4.2
2	CB	103	THR	4.2
19	CS	65	ASN	4.2
16	AP	7	ALA	4.2
9	AI	19	LEU	4.2
26	DA	2160	G	4.2
7	CG	79	ARG	4.2
26	BA	2168	C	4.2
8	CH	83	ILE	4.2
23	CW	76	PPU	4.2
3	CC	148	GLY	4.2
26	DA	2804	C	4.2
31	BG	49	ASP	4.2
22	AV	23	A	4.2
33	DI	17	GLN	4.2

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Mol	Chain	Res	Type	RSRZ
26	DA	2156	G	4.2
10	CJ	48	THR	4.1
33	DI	62	LYS	4.1
2	CB	201	ILE	4.1
39	DS	58	LEU	4.1
26	BA	2143	G	4.1
51	D4	52	THR	4.1
19	CS	52	TYR	4.1
20	CT	80	ARG	4.1
9	CI	41	VAL	4.1
2	CB	44	LEU	4.1
20	AT	13	LEU	4.1
19	CS	66	MET	4.1
33	DI	103	ARG	4.1
8	CH	71	GLY	4.1
5	CE	13	ILE	4.1
9	CI	26	VAL	4.1
13	CM	66	LEU	4.1
18	CR	84	LYS	4.1
2	CB	30	ARG	4.1
2	CB	83	MET	4.1
19	CS	24	ALA	4.1
2	CB	181	PHE	4.0
7	CG	85	TYR	4.0
20	AT	95	ALA	4.0
19	CS	46	GLY	4.0
8	CH	122	ARG	4.0
2	CB	185	ILE	4.0
26	DA	2138	C	4.0
43	BW	111	HIS	4.0
1	CA	80	G	4.0
46	DZ	50	GLN	4.0
2	CB	48	MET	4.0
26	DA	2125	G	4.0
9	AI	59	PHE	4.0
31	DG	85	GLY	4.0
46	BZ	105	VAL	4.0
2	CB	178	ARG	4.0
2	CB	40	HIS	4.0
3	CC	54	ARG	4.0
26	DA	2127	G	4.0
3	CC	134	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
39	DS	56	LEU	4.0
2	CB	68	ILE	3.9
3	CC	206	GLU	3.9
28	DD	2	ALA	3.9
9	CI	36	TYR	3.9
2	CB	130	ARG	3.9
33	DI	97	ILE	3.9
30	DF	21	ALA	3.9
46	DZ	143	GLY	3.9
33	BI	112	LYS	3.9
10	CJ	62	HIS	3.9
3	CC	138	VAL	3.9
32	DH	2	SER	3.9
2	CB	43	ASP	3.9
31	DG	41	GLN	3.9
33	DI	144	VAL	3.9
32	DH	88	LEU	3.8
9	AI	81	ILE	3.8
31	DG	52	ILE	3.8
11	CK	13	GLN	3.8
39	DS	57	LYS	3.8
3	AC	87	LEU	3.8
3	CC	142	MET	3.8
14	CN	11	LYS	3.8
9	CI	61	ALA	3.8
16	CP	48	TRP	3.8
2	CB	99	GLY	3.8
13	CM	78	ILE	3.8
7	CG	91	VAL	3.8
7	AG	85	TYR	3.8
26	DA	2146	C	3.8
4	AD	157	LEU	3.8
9	CI	37	PHE	3.8
2	CB	31	TYR	3.8
19	CS	35	SER	3.8
2	CB	231	GLU	3.8
2	CB	113	HIS	3.8
8	CH	82	HIS	3.8
26	BA	2132	G	3.7
14	CN	12	ARG	3.7
19	CS	79	THR	3.7
2	CB	109	SER	3.7

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Mol	Chain	Res	Type	RSRZ
9	CI	126	SER	3.7
10	CJ	74	ILE	3.7
46	DZ	4	ARG	3.7
2	CB	105	PHE	3.7
2	CB	222	ILE	3.7
8	CH	54	ASP	3.7
9	CI	63	ILE	3.7
27	DB	56	G	3.7
26	BA	2130	C	3.7
20	AT	72	LEU	3.7
5	CE	81	GLU	3.7
8	CH	81	HIS	3.7
18	AR	42	ARG	3.7
17	CQ	44	ALA	3.7
46	DZ	125	LEU	3.7
3	AC	66	VAL	3.7
9	CI	52	ALA	3.7
51	B4	50	VAL	3.7
26	DA	2140	C	3.7
33	DI	4	ILE	3.7
3	AC	80	GLY	3.7
7	CG	156	TRP	3.7
54	D7	48	LYS	3.7
13	CM	92	HIS	3.7
19	CS	47	HIS	3.7
3	CC	139	GLN	3.7
2	CB	122	PHE	3.7
2	CB	161	ALA	3.6
5	CE	90	VAL	3.6
1	AA	1532	U	3.6
9	AI	85	LEU	3.6
9	CI	79	LEU	3.6
3	CC	132	ARG	3.6
13	CM	80	ARG	3.6
2	CB	57	PHE	3.6
3	CC	180	ALA	3.6
3	CC	207	VAL	3.6
33	BI	86	THR	3.6
2	AB	37	ASN	3.6
2	CB	98	LEU	3.6
26	BA	2196	C	3.6
14	CN	50	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
26	DA	2143	C	3.6
3	CC	124	ILE	3.6
1	AA	1033	G	3.6
9	CI	70	LYS	3.6
33	BI	103	ARG	3.6
26	DA	2157	G	3.6
21	CU	14	TRP	3.6
33	DI	117	GLU	3.6
17	CQ	39	SER	3.6
31	DG	24	GLY	3.6
2	CB	52	GLU	3.6
10	CJ	17	ASP	3.6
46	DZ	140	ASP	3.6
26	DA	2154	G	3.6
49	D2	1	MET	3.6
26	DA	1509	C	3.6
2	CB	197	VAL	3.6
6	AF	55	ASP	3.6
2	CB	89	GLY	3.5
9	CI	9	ARG	3.5
14	AN	37	PHE	3.5
2	CB	90	MET	3.5
3	CC	108	ASN	3.5
9	AI	4	TYR	3.5
27	DB	58	A	3.5
45	DY	51	VAL	3.5
2	CB	131	PRO	3.5
3	CC	17	ASP	3.5
33	DI	59	ALA	3.5
2	CB	132	LYS	3.5
7	CG	18	TYR	3.5
46	DZ	93	ASP	3.5
33	BI	109	ILE	3.5
3	CC	186	PHE	3.5
10	CJ	47	PHE	3.5
1	AA	1001(A)	G	3.5
1	CA	1115	C	3.5
7	AG	156	TRP	3.5
26	DA	884	C	3.5
33	DI	82	ARG	3.5
31	DG	109	VAL	3.5
46	DZ	111	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
3	CC	57	ILE	3.5
7	CG	152	ALA	3.5
9	AI	98	PRO	3.5
51	B4	46	GLN	3.5
13	CM	105	THR	3.5
47	D0	75	LEU	3.5
9	AI	52	ALA	3.5
9	CI	106	ALA	3.5
36	DP	78	PRO	3.5
2	CB	92	TYR	3.5
2	CB	205	ASP	3.5
2	CB	229	VAL	3.5
33	BI	85	GLU	3.5
10	CJ	93	GLY	3.5
2	CB	139	LYS	3.4
19	CS	69	HIS	3.4
29	BE	89	ASP	3.4
1	AA	90	U	3.4
37	DQ	104	PHE	3.4
1	CA	1492	A	3.4
18	CR	76	LEU	3.4
1	CA	204	U	3.4
2	CB	162	ILE	3.4
27	DB	120	A	3.4
46	DZ	24	LEU	3.4
2	CB	76	GLN	3.4
3	CC	51	GLY	3.4
9	AI	5	TYR	3.4
26	DA	645	C	3.4
26	DA	2128	C	3.4
2	CB	10	LEU	3.4
2	CB	165	VAL	3.4
13	CM	4	ILE	3.4
7	AG	78	ARG	3.4
1	AA	1027	C	3.4
46	DZ	155	LEU	3.4
2	CB	15	VAL	3.4
9	CI	122	ALA	3.4
4	CD	150	GLU	3.4
26	BA	1555	C	3.4
2	CB	108	ILE	3.4
11	AK	89	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
10	CJ	92	THR	3.3
19	CS	27	GLU	3.3
1	CA	1036	G	3.3
26	DA	2894	G	3.3
3	CC	172	ARG	3.3
46	BZ	112	ARG	3.3
51	B4	49	PHE	3.3
33	DI	91	SER	3.3
33	DI	125	GLU	3.3
3	CC	47	LEU	3.3
36	BP	105	LEU	3.3
51	D4	64	GLY	3.3
2	CB	63	MET	3.3
17	CQ	32	TYR	3.3
26	BA	2201	C	3.3
6	CF	51	PRO	3.3
3	CC	76	VAL	3.3
20	AT	9	ASN	3.3
32	DH	159	GLU	3.3
2	CB	202	PRO	3.3
8	CH	74	PRO	3.3
7	CG	73	MET	3.3
8	CH	86	ILE	3.3
26	DA	229	A	3.3
2	CB	183	PRO	3.3
9	CI	57	GLY	3.3
26	BA	2133	C	3.3
26	BA	2200	C	3.3
46	DZ	105	VAL	3.3
22	AV	22	U	3.3
45	DY	55	TYR	3.3
7	CG	150	ALA	3.3
11	CK	49	GLY	3.3
2	CB	160	ASP	3.3
5	CE	88	LYS	3.3
51	B4	48	ARG	3.3
19	CS	61	TYR	3.3
31	DG	178	PHE	3.3
7	AG	81	GLY	3.3
33	DI	16	GLY	3.3
3	CC	14	ILE	3.2
12	CL	126	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
33	DI	121	LYS	3.2
2	CB	111	ARG	3.2
26	DA	2161	C	3.2
32	DH	95	ARG	3.2
46	DZ	172	ALA	3.2
1	AA	1002	G	3.2
19	CS	49	ILE	3.2
3	CC	52	LEU	3.2
10	CJ	34	VAL	3.2
46	DZ	162	GLU	3.2
3	CC	191	THR	3.2
33	DI	12	LEU	3.2
8	CH	130	GLY	3.2
6	AF	48	LEU	3.2
1	AA	1030(D)	A	3.2
26	BA	1935	A	3.2
2	CB	152	PHE	3.2
10	CJ	75	ILE	3.2
10	CJ	98	ILE	3.2
3	CC	171	GLY	3.2
51	D4	56	VAL	3.2
1	AA	1024	G	3.2
2	CB	237	ALA	3.2
26	BA	2179	G	3.2
2	AB	135	GLN	3.2
31	DG	25	TYR	3.2
19	AS	18	LYS	3.2
44	DX	89	ILE	3.2
10	AJ	34	VAL	3.2
26	DA	2110	G	3.2
2	CB	16	HIS	3.2
26	DA	34	C	3.2
26	DA	886	C	3.2
45	DY	35	TYR	3.2
19	CS	30	LEU	3.2
19	AS	67	VAL	3.2
2	AB	126	GLU	3.2
22	CV	14	A	3.2
1	CA	1202	G	3.2
26	BA	2806	G	3.2
26	DA	1026	U	3.2
26	DA	2118	U	3.2

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Mol	Chain	Res	Type	RSRZ
2	CB	67	THR	3.2
3	CC	12	LEU	3.2
3	CC	22	TRP	3.2
10	CJ	65	LEU	3.2
33	DI	79	ILE	3.2
46	DZ	96	VAL	3.1
20	AT	74	LYS	3.1
2	CB	198	ASP	3.1
48	D1	2	SER	3.1
56	D9	11	CYS	3.1
4	CD	29	PRO	3.1
18	CR	47	THR	3.1
17	CQ	65	ILE	3.1
33	DI	55	ALA	3.1
1	AA	1031	G	3.1
30	BF	17	ARG	3.1
3	CC	68	VAL	3.1
7	CG	23	VAL	3.1
31	DG	97	ASP	3.1
3	CC	145	GLY	3.1
26	DA	2803	C	3.1
26	DA	2135	A	3.1
8	CH	22	GLU	3.1
11	CK	25	TYR	3.1
14	AN	56	VAL	3.1
56	D9	13	LYS	3.1
33	DI	14	ASP	3.1
1	CA	1035	A	3.1
4	AD	176	LEU	3.1
13	CM	90	LEU	3.1
9	CI	119	ALA	3.1
18	CR	73	ALA	3.1
5	CE	79	GLU	3.1
31	DG	164	GLU	3.1
13	CM	98	VAL	3.1
26	BA	2814	C	3.1
42	DV	42	GLY	3.1
19	AS	49	ILE	3.1
2	AB	63	MET	3.1
9	AI	6	GLY	3.0
2	CB	51	LEU	3.0
32	DH	25	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	AA	204	U	3.0
26	DA	2159	G	3.0
10	AJ	64	GLU	3.0
8	AH	3	THR	3.0
33	BI	107	VAL	3.0
51	B4	56	VAL	3.0
20	CT	9	ASN	3.0
1	CA	1034	G	3.0
32	DH	128	PRO	3.0
37	DQ	137	TYR	3.0
14	CN	29	ARG	3.0
3	CC	78	GLY	3.0
27	DB	25	A	3.0
5	CE	120	THR	3.0
8	CH	2	LEU	3.0
8	CH	107	LEU	3.0
19	CS	57	HIS	3.0
4	CD	152	SER	3.0
7	AG	112	PRO	3.0
9	AI	17	VAL	3.0
3	CC	44	GLU	3.0
5	CE	10	MET	3.0
9	CI	102	LEU	3.0
22	CV	18	G	3.0
9	CI	127	LYS	3.0
8	CH	72	PRO	3.0
3	CC	158	GLY	3.0
31	DG	149	VAL	3.0
32	DH	76	VAL	3.0
47	D0	84	LEU	3.0
2	CB	41	ILE	3.0
14	CN	2	ALA	3.0
36	DP	109	GLY	3.0
12	CL	18	VAL	3.0
2	CB	142	LEU	3.0
13	AM	62	ASN	3.0
26	DA	2117	A	3.0
1	AA	1030(A)	G	3.0
9	AI	94	ALA	3.0
4	CD	130	GLY	3.0
9	CI	123	PRO	3.0
22	AV	12	A	3.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1156	G	3.0
26	BA	1221	G	3.0
26	BA	2138	G	3.0
3	CC	13	GLY	2.9
10	CJ	88	LEU	2.9
11	AK	92	GLU	2.9
11	AK	17	GLY	2.9
17	CQ	80	GLY	2.9
31	DG	51	ARG	2.9
4	AD	110	PHE	2.9
8	AH	61	VAL	2.9
32	DH	114	VAL	2.9
33	DI	38	LEU	2.9
1	CA	1493	A	2.9
7	CG	72	ARG	2.9
31	DG	136	ARG	2.9
3	CC	43	LEU	2.9
19	CS	13	ASP	2.9
33	DI	77	LEU	2.9
13	CM	94	ARG	2.9
17	CQ	29	HIS	2.9
46	BZ	106	GLY	2.9
7	CG	74	GLU	2.9
22	AV	13	A	2.9
26	DA	2170	A	2.9
3	CC	128	PHE	2.9
10	AJ	71	LEU	2.9
19	AS	15	LEU	2.9
20	CT	24	LEU	2.9
9	CI	14	VAL	2.9
16	AP	24	ALA	2.9
14	CN	46	GLU	2.9
1	CA	1212	U	2.9
7	CG	77	SER	2.9
18	AR	25	THR	2.9
19	CS	12	ASP	2.9
46	DZ	150	LEU	2.9
51	D4	44	THR	2.9
2	CB	91	PRO	2.9
3	CC	86	VAL	2.9
5	CE	67	VAL	2.9
2	CB	94	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
7	AG	153	HIS	2.9
26	BA	2134	G	2.9
26	BA	2816	G	2.9
13	AM	121	LYS	2.9
4	AD	23	GLY	2.9
46	DZ	151	HIS	2.9
5	CE	119	LEU	2.9
13	AM	56	LEU	2.9
46	DZ	41	LEU	2.9
10	CJ	72	VAL	2.9
17	CQ	77	VAL	2.9
19	CS	2	PRO	2.9
25	CY	74	C	2.9
31	DG	161	THR	2.9
41	DU	90	VAL	2.9
19	CS	68	GLY	2.9
10	CJ	96	ILE	2.9
14	AN	36	PHE	2.9
21	CU	6	ARG	2.9
37	DQ	5	ARG	2.9
10	CJ	37	PRO	2.8
16	AP	15	PRO	2.8
19	CS	60	VAL	2.8
36	BP	12	ALA	2.8
46	DZ	8	TYR	2.8
26	BA	2807	C	2.8
1	CA	1030(C)	G	2.8
26	DA	2805	G	2.8
10	CJ	63	PHE	2.8
26	DA	6	A	2.8
1	CA	1121	U	2.8
3	CC	130	VAL	2.8
8	CH	135	CYS	2.8
33	BI	89	TYR	2.8
44	DX	69	TYR	2.8
9	CI	116	LYS	2.8
16	AP	19	ILE	2.8
2	CB	164	VAL	2.8
3	CC	205	GLY	2.8
4	CD	167	GLY	2.8
5	AE	23	GLY	2.8
17	CQ	21	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
39	DS	33	LYS	2.8
9	CI	45	ALA	2.8
51	D4	40	HIS	2.8
1	CA	1017	G	2.8
3	CC	169	ALA	2.8
11	AK	25	TYR	2.8
2	CB	107	THR	2.8
8	CH	123	GLU	2.8
6	CF	55	ASP	2.8
26	BA	2197	C	2.8
2	CB	58	ILE	2.8
5	CE	12	LEU	2.8
10	CJ	71	LEU	2.8
19	CS	81	ARG	2.8
1	CA	841	U	2.8
12	CL	125	PRO	2.8
32	DH	19	VAL	2.8
33	DI	92	VAL	2.8
2	CB	33	TYR	2.8
10	CJ	55	LYS	2.8
13	CM	76	ALA	2.8
16	AP	39	TYR	2.8
31	DG	169	ALA	2.8
31	DG	182	LYS	2.8
11	AK	57	THR	2.8
3	CC	10	PHE	2.8
31	DG	23	PHE	2.8
3	CC	83	ARG	2.8
26	DA	2114	A	2.8
4	CD	208	SER	2.8
33	BI	80	PRO	2.8
2	CB	199	TYR	2.8
12	CL	64	TYR	2.8
8	AH	119	LEU	2.8
26	DA	2794	C	2.8
4	CD	134	ASP	2.8
32	DH	101	ARG	2.8
10	CJ	23	ILE	2.8
26	DA	2141	G	2.8
3	CC	188	LEU	2.8
37	DQ	121	ALA	2.8
18	CR	43	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
32	DH	123	PHE	2.7
51	D4	49	PHE	2.7
53	D6	28	ARG	2.7
10	CJ	36	GLY	2.7
33	BI	121	LYS	2.7
3	CC	20	SER	2.7
5	CE	148	VAL	2.7
32	DH	44	VAL	2.7
2	CB	196	LEU	2.7
3	CC	164	ARG	2.7
14	AN	59	ALA	2.7
17	CQ	89	LEU	2.7
40	DT	121	ILE	2.7
2	CB	55	PHE	2.7
46	DZ	121	HIS	2.7
46	DZ	154	ASP	2.7
1	CA	1119	C	2.7
26	DA	277	C	2.7
8	CH	95	VAL	2.7
6	CF	36	ARG	2.7
16	CP	19	ILE	2.7
19	AS	71	LEU	2.7
20	CT	34	LYS	2.7
21	CU	13	ILE	2.7
2	CB	148	TYR	2.7
32	DH	87	LEU	2.7
46	DZ	76	LEU	2.7
4	AD	179	GLU	2.7
14	AN	16	PHE	2.7
19	AS	27	GLU	2.7
25	CY	73	A	2.7
26	BA	2192	A	2.7
26	DA	2801(A)	A	2.7
33	DI	73	GLU	2.7
9	CI	124	GLN	2.7
26	DA	2168	G	2.7
27	DB	119	G	2.7
3	CC	116	VAL	2.7
20	AT	87	LYS	2.7
33	DI	57	ARG	2.7
26	DA	2144	U	2.7
1	CA	1038	C	2.7

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Mol	Chain	Res	Type	RSRZ
8	CH	134	ILE	2.7
25	CY	72	C	2.7
26	DA	2145	C	2.7
46	DZ	53	ILE	2.7
55	D8	65	GLU	2.7
14	CN	36	PHE	2.7
14	CN	61	TRP	2.7
1	CA	1001	A	2.7
17	CQ	100	LYS	2.7
37	DQ	63	LYS	2.7
2	CB	143	GLU	2.7
1	AA	630	G	2.7
10	AJ	47	PHE	2.7
26	DA	2123	G	2.7
42	DV	101	GLY	2.7
2	CB	75	LYS	2.7
1	CA	1257	U	2.7
2	CB	121	LEU	2.7
3	CC	8	ILE	2.7
16	AP	6	LEU	2.7
50	D3	26	LEU	2.7
2	AB	66	GLY	2.7
20	AT	21	LYS	2.7
13	AM	102	ARG	2.7
1	CA	1018	C	2.7
1	CA	1026	G	2.7
26	BA	639	G	2.7
26	BA	2147	G	2.7
2	AB	129	GLU	2.7
51	D4	57	GLU	2.7
3	CC	178	LEU	2.7
6	CF	79	LEU	2.7
32	DH	105	LEU	2.7
33	DI	18	VAL	2.7
34	BN	140	VAL	2.7
15	AO	89	GLY	2.7
33	DI	80	PRO	2.7
3	AC	65	ALA	2.7
1	AA	1030	C	2.7
39	DS	39	ILE	2.7
4	CD	209	ARG	2.7
2	CB	8	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
31	DG	3	LEU	2.6
3	CC	55	VAL	2.6
6	CF	40	VAL	2.6
8	AH	13	ILE	2.6
33	DI	15	VAL	2.6
1	AA	1224	G	2.6
42	DV	26	ASP	2.6
42	DV	12	TYR	2.6
19	CS	53	ASN	2.6
8	CH	39	LEU	2.6
17	CQ	22	LEU	2.6
4	AD	88	VAL	2.6
4	CD	137	SER	2.6
9	AI	18	PHE	2.6
19	AS	39	THR	2.6
14	CN	9	LYS	2.6
1	AA	1026	G	2.6
26	BA	2805	G	2.6
26	DA	2793	G	2.6
33	DI	35	LEU	2.6
31	DG	26	GLN	2.6
7	AG	80	VAL	2.6
13	CM	60	VAL	2.6
28	BD	2	ALA	2.6
10	CJ	43	ARG	2.6
2	CB	215	LEU	2.6
17	CQ	84	LEU	2.6
19	CS	82	GLY	2.6
46	DZ	117	LEU	2.6
3	CC	82	GLU	2.6
10	CJ	64	GLU	2.6
1	CA	250	A	2.6
11	AK	125	PHE	2.6
26	DA	2153	G	2.6
46	DZ	88	PHE	2.6
9	AI	90	PRO	2.6
21	CU	17	THR	2.6
8	CH	9	MET	2.6
23	AW	76	PPU	2.6
28	BD	276	LYS	2.6
1	CA	1039	C	2.6
46	DZ	39	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
51	D4	50	VAL	2.6
4	CD	2	GLY	2.6
37	DQ	33	GLY	2.6
7	CG	37	ASN	2.6
10	AJ	6	ILE	2.6
12	CL	7	ILE	2.6
16	AP	80	PHE	2.6
1	AA	163	C	2.6
1	CA	1028	C	2.6
1	CA	1400	C	2.6
21	CU	5	ASP	2.6
2	CB	114	ARG	2.6
10	CJ	29	ARG	2.6
13	AM	104	ARG	2.6
19	CS	34	TRP	2.6
14	AN	15	LYS	2.6
26	BA	2166	U	2.6
26	DA	271(N)	U	2.6
13	CM	109	THR	2.6
33	BI	108	THR	2.6
14	CN	34	TYR	2.6
47	D0	76	GLY	2.6
1	AA	1036	G	2.6
1	CA	1011	G	2.6
26	DA	2165	G	2.6
5	CE	100	VAL	2.6
46	DZ	133	ILE	2.6
1	CA	1219	U	2.6
27	DB	55	U	2.6
53	D6	42	TRP	2.6
14	AN	2	ALA	2.6
33	DI	140	LEU	2.6
46	DZ	55	HIS	2.6
1	AA	1492	A	2.6
1	CA	1014	A	2.6
5	CE	6	PHE	2.6
5	CE	24	ARG	2.6
8	AH	32	LYS	2.6
8	CH	41	ARG	2.6
10	AJ	72	VAL	2.6
2	CB	59	GLU	2.5
26	DA	2162	G	2.5

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Mol	Chain	Res	Type	RSRZ
16	CP	7	ALA	2.5
31	DG	86	MET	2.5
41	DU	21	ALA	2.5
8	CH	116	LYS	2.5
26	BA	2164	C	2.5
5	CE	105	VAL	2.5
32	DH	169	VAL	2.5
14	CN	58	LYS	2.5
26	DA	2802	G	2.5
31	BG	146	TYR	2.5
9	CI	81	ILE	2.5
10	CJ	50	ILE	2.5
33	BI	88	ILE	2.5
9	AI	127	LYS	2.5
10	CJ	59	SER	2.5
19	CS	59	PRO	2.5
19	CS	14	HIS	2.5
31	DG	115	ARG	2.5
2	CB	62	ALA	2.5
2	CB	42	ILE	2.5
26	BA	2188	G	2.5
26	BA	2183	C	2.5
32	BH	2	SER	2.5
18	CR	83	GLU	2.5
36	DP	110	TYR	2.5
10	CJ	100	THR	2.5
33	DI	138	ILE	2.5
45	DY	44	ILE	2.5
26	DA	2115	G	2.5
5	CE	123	LEU	2.5
26	DA	2174	C	2.5
46	DZ	25	PRO	2.5
3	CC	160	ALA	2.5
10	AJ	20	ALA	2.5
12	CL	69	TYR	2.5
45	DY	60	PHE	2.5
51	D4	69	LYS	2.5
10	AJ	75	ILE	2.5
9	AI	83	ARG	2.5
34	DN	9	VAL	2.5
45	DY	24	VAL	2.5
1	CA	1040	U	2.5

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Mol	Chain	Res	Type	RSRZ
9	CI	33	PHE	2.5
10	CJ	27	ALA	2.5
5	AE	18	ARG	2.5
11	CK	117	ASN	2.5
13	CM	12	ASN	2.5
45	DY	57	GLN	2.5
48	D1	23	LYS	2.5
5	CE	45	PHE	2.5
7	AG	155	ARG	2.5
32	DH	94	TYR	2.5
8	CH	138	TRP	2.5
11	AK	67	ASP	2.5
16	AP	59	TRP	2.5
16	AP	68	ASP	2.5
11	CK	118	GLY	2.5
4	CD	169	LYS	2.5
37	DQ	37	LEU	2.5
1	CA	949	A	2.5
1	CA	1447	A	2.5
1	AA	1446	U	2.4
2	CB	19	HIS	2.4
18	CR	42	ARG	2.4
32	DH	157	TYR	2.4
44	DX	91	ALA	2.4
11	AK	32	ILE	2.4
33	DI	104	GLN	2.4
16	AP	63	GLY	2.4
15	CO	60	VAL	2.4
3	AC	101	LEU	2.4
1	CA	79	G	2.4
1	AA	1493	A	2.4
4	CD	122	ARG	2.4
9	CI	10	ARG	2.4
7	CG	129	GLU	2.4
31	DG	49	ASP	2.4
31	DG	157	ILE	2.4
33	DI	120	ILE	2.4
46	DZ	160	GLY	2.4
33	DI	3	VAL	2.4
42	DV	92	THR	2.4
26	BA	2162	C	2.4
26	DA	2111	C	2.4

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Mol	Chain	Res	Type	RSRZ
9	CI	98	PRO	2.4
10	CJ	77	PRO	2.4
17	CQ	24	GLU	2.4
19	CS	64	GLU	2.4
31	DG	48	GLU	2.4
33	DI	135	GLU	2.4
51	B4	53	GLU	2.4
19	CS	62	ILE	2.4
20	CT	41	ILE	2.4
20	CT	77	ALA	2.4
26	DA	2148	G	2.4
2	AB	200	ILE	2.4
9	CI	62	TYR	2.4
26	DA	887	A	2.4
35	DO	51	ALA	2.4
39	DS	79	ALA	2.4
10	CJ	31	GLY	2.4
40	DT	102	ILE	2.4
13	CM	96	LEU	2.4
42	DV	95	LEU	2.4
48	B1	73	LEU	2.4
10	CJ	46	ARG	2.4
15	CO	68	ARG	2.4
36	DP	149	GLU	2.4
26	BA	696	C	2.4
3	CC	184	TYR	2.4
3	CC	45	LYS	2.4
6	CF	61	LEU	2.4
15	CO	77	ARG	2.4
26	DA	2176	A	2.4
33	DI	37	VAL	2.4
30	DF	15	SER	2.4
33	BI	8	PRO	2.4
20	AT	69	GLY	2.4
42	DV	54	GLY	2.4
1	AA	1029	C	2.4
4	CD	49	ARG	2.4
44	DX	33	LYS	2.4
4	AD	170	VAL	2.4
18	CR	78	LEU	2.4
53	D6	11	LEU	2.4
9	AI	23	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
13	CM	69	GLU	2.4
31	DG	13	GLU	2.4
26	BA	2139	A	2.4
26	DA	652(U)	G	2.4
7	CG	26	PHE	2.4
19	AS	59	PRO	2.4
21	CU	16	GLY	2.4
32	BH	148	ILE	2.4
32	DH	175	LYS	2.4
8	CH	68	ARG	2.4
39	DS	32	LEU	2.4
13	AM	60	VAL	2.4
14	AN	25	VAL	2.4
52	B5	60	VAL	2.4
26	BA	2165	C	2.4
1	CA	1275	A	2.4
3	CC	185	GLY	2.4
10	CJ	10	GLY	2.4
22	AV	14	A	2.4
26	DA	890	A	2.4
51	B4	54	GLY	2.4
1	CA	988	G	2.4
9	CI	47	LEU	2.4
36	DP	45	LEU	2.4
6	AF	88	VAL	2.4
1	AA	1007	C	2.4
13	CM	88	ARG	2.4
13	AM	22	ILE	2.4
36	BP	149	GLU	2.4
45	BY	91	GLU	2.4
55	B8	65	GLU	2.4
1	AA	1531	A	2.4
14	CN	10	ALA	2.4
7	AG	151	TYR	2.3
33	DI	19	VAL	2.3
2	CB	17	PHE	2.3
31	BG	51	ARG	2.3
31	DG	35	GLU	2.3
1	CA	1214	C	2.3
1	CA	1322	C	2.3
26	BA	1936	C	2.3
32	DH	111	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
7	AG	50	ILE	2.3
10	AJ	98	ILE	2.3
32	DH	151	ILE	2.3
46	DZ	130	PRO	2.3
2	CB	13	ALA	2.3
5	CE	134	ALA	2.3
10	CJ	26	ALA	2.3
20	AT	52	ALA	2.3
31	BG	120	LEU	2.3
46	DZ	161	VAL	2.3
9	CI	83	ARG	2.3
37	DQ	56	ARG	2.3
2	CB	38	GLY	2.3
14	CN	16	PHE	2.3
50	B3	60	GLU	2.3
10	CJ	35	SER	2.3
26	DA	614(B)	G	2.3
26	DA	2106	G	2.3
9	CI	54	ASP	2.3
10	CJ	89	ASP	2.3
17	CQ	87	LYS	2.3
3	AC	34	LEU	2.3
20	CT	66	ALA	2.3
26	BA	2129	C	2.3
3	CC	23	TYR	2.3
31	DG	15	VAL	2.3
42	DV	5	VAL	2.3
20	AT	14	LYS	2.3
33	DI	71	ILE	2.3
32	DH	171	LEU	2.3
33	DI	8	PRO	2.3
26	BA	1072	U	2.3
13	AM	2	ALA	2.3
14	CN	45	ARG	2.3
26	BA	2203	G	2.3
51	D4	55	ARG	2.3
3	CC	198	VAL	2.3
8	CH	93	VAL	2.3
10	CJ	61	GLU	2.3
16	CP	9	PHE	2.3
20	CT	30	LYS	2.3
54	B7	48	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
2	AB	215	LEU	2.3
1	CA	84	U	2.3
19	CS	44	MET	2.3
20	AT	59	ALA	2.3
20	AT	71	THR	2.3
46	DZ	145	GLU	2.3
2	CB	71	VAL	2.3
5	CE	133	TYR	2.3
26	BA	2169	G	2.3
1	AA	1038	C	2.3
3	AC	38	ARG	2.3
14	CN	60	SER	2.3
18	CR	45	SER	2.3
3	CC	147	LYS	2.3
11	AK	82	VAL	2.3
17	AQ	10	VAL	2.3
17	CQ	33	GLY	2.3
44	DX	86	GLY	2.3
1	CA	1224	G	2.3
9	AI	91	ASP	2.3
27	DB	117	G	2.3
31	DG	152	LEU	2.3
13	CM	30	ALA	2.3
33	DI	13	GLY	2.3
16	CP	6	LEU	2.3
31	DG	137	GLU	2.3
3	CC	154	SER	2.3
17	CQ	36	ILE	2.3
32	BH	55	PRO	2.3
46	DZ	83	PRO	2.3
1	CA	1019	C	2.3
1	CA	1030	C	2.3
24	CX	69	C	2.3
9	AI	106	ALA	2.3
8	AH	91	ARG	2.3
9	CI	27	THR	2.3
13	AM	105	THR	2.3
17	CQ	71	PHE	2.3
31	DG	72	ARG	2.3
31	DG	167	GLU	2.2
50	D3	57	GLU	2.2
6	CF	21	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
15	CO	71	GLN	2.2
51	D4	51	ASP	2.2
44	BX	94	GLY	2.2
48	D1	22	GLY	2.2
4	CD	32	ALA	2.2
33	DI	46	ALA	2.2
1	AA	91	C	2.2
8	CH	61	VAL	2.2
17	CQ	56	VAL	2.2
33	DI	127	VAL	2.2
51	D4	53	GLU	2.2
1	AA	216	G	2.2
26	BA	2184	G	2.2
5	CE	31	LEU	2.2
8	CH	52	ASP	2.2
9	CI	75	ASP	2.2
14	CN	39	LEU	2.2
20	AT	100	ILE	2.2
27	DB	59	A	2.2
32	DH	98	LEU	2.2
33	DI	5	LEU	2.2
37	DQ	62	GLY	2.2
8	CH	19	VAL	2.2
9	CI	18	PHE	2.2
20	AT	66	ALA	2.2
32	DH	43	VAL	2.2
45	DY	20	TYR	2.2
29	DE	52	LEU	2.2
33	BI	35	LEU	2.2
26	BA	2153	G	2.2
26	DA	2104	G	2.2
3	CC	96	GLY	2.2
7	AG	62	PHE	2.2
46	DZ	109	ALA	2.2
6	AF	54	LYS	2.2
1	CA	1116	C	2.2
7	CG	4	ARG	2.2
33	DI	51	ILE	2.2
26	BA	932	C	2.2
56	D9	37	GLY	2.2
1	AA	79	G	2.2
1	CA	1030(D)	A	2.2

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Mol	Chain	Res	Type	RSRZ
7	CG	147	ALA	2.2
10	CJ	54	PHE	2.2
26	DA	652(B)	A	2.2
10	CJ	94	VAL	2.2
17	CQ	11	VAL	2.2
9	AI	88	TYR	2.2
32	DH	13	LYS	2.2
37	DQ	130	LYS	2.2
37	DQ	135	ASP	2.2
31	DG	39	ILE	2.2
7	AG	55	GLY	2.2
1	AA	1452	C	2.2
8	CH	76	PRO	2.2
3	AC	71	ALA	2.2
9	AI	43	ALA	2.2
37	DQ	28	ALA	2.2
8	CH	125	ARG	2.2
36	BP	102	ARG	2.2
26	BA	2163	G	2.2
3	CC	41	GLY	2.2
32	DH	161	GLY	2.2
5	CE	145	LYS	2.2
24	CX	34	C	2.2
42	DV	47	VAL	2.2
54	B7	46	VAL	2.2
12	AL	64	TYR	2.2
13	CM	73	GLU	2.2
1	CA	1213	A	2.2
19	CS	26	GLY	2.2
20	CT	29	LYS	2.2
28	DD	275	LYS	2.2
48	D1	81	LYS	2.2
5	CE	84	PHE	2.2
10	CJ	91	PRO	2.2
13	CM	3	ARG	2.2
7	CG	12	LEU	2.2
9	CI	56	LEU	2.2
12	AL	65	GLU	2.2
12	CL	68	ALA	2.2
32	DH	116	GLU	2.2
39	DS	54	LEU	2.2
16	CP	12	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
20	CT	74	LYS	2.2
26	DA	2129	C	2.2
33	DI	20	ASP	2.2
7	CG	132	GLY	2.2
31	DG	140	ILE	2.2
7	CG	64	GLN	2.1
46	DZ	131	ARG	2.1
9	AI	53	VAL	2.1
14	CN	6	LEU	2.1
18	AR	24	ALA	2.1
26	BA	2177	G	2.1
26	BA	2190	G	2.1
33	BI	81	VAL	2.1
5	CE	92	LYS	2.1
26	DA	888	C	2.1
19	CS	43	GLU	2.1
48	D1	60	PHE	2.1
26	BA	2136	A	2.1
8	CH	63	LEU	2.1
10	CJ	8	LEU	2.1
3	AC	169	ALA	2.1
30	DF	6	VAL	2.1
9	CI	4	TYR	2.1
1	CA	77	G	2.1
26	BA	691	G	2.1
26	DA	2182	G	2.1
36	DP	79	ARG	2.1
33	DI	78	THR	2.1
5	CE	106	PRO	2.1
7	CG	88	PRO	2.1
36	DP	1	MET	2.1
2	CB	66	GLY	2.1
3	AC	100	ALA	2.1
6	CF	83	ASP	2.1
7	CG	2	ALA	2.1
15	CO	89	GLY	2.1
32	DH	96	ALA	2.1
2	CB	153	ARG	2.1
10	CJ	5	ARG	2.1
10	CJ	69	ASN	2.1
33	DI	50	ARG	2.1
46	DZ	82	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
14	AN	32	SER	2.1
14	AN	60	SER	2.1
26	BA	2145	G	2.1
26	BA	2813	G	2.1
2	CB	118	LEU	2.1
31	DG	87	PRO	2.1
33	BI	111	PRO	2.1
44	DX	66	LEU	2.1
30	BF	172	TRP	2.1
5	CE	113	ALA	2.1
27	DB	1	U	2.1
45	DY	16	ALA	2.1
3	CC	150	LYS	2.1
26	BA	2198	A	2.1
26	DA	2134	A	2.1
46	DZ	43	GLU	2.1
3	AC	91	LEU	2.1
3	CC	95	THR	2.1
3	CC	101	LEU	2.1
8	AH	89	PRO	2.1
18	AR	66	LEU	2.1
39	BS	24	LEU	2.1
1	CA	1024	G	2.1
3	CC	153	VAL	2.1
9	AI	26	VAL	2.1
2	CB	218	ALA	2.1
15	CO	16	ALA	2.1
26	BA	1847	G	2.1
44	DX	90	GLU	2.1
8	AH	94	TYR	2.1
9	CI	92	TYR	2.1
9	CI	125	TYR	2.1
19	CS	40	ILE	2.1
19	CS	80	TYR	2.1
20	CT	90	GLN	2.1
1	CA	412	A	2.1
1	CA	994	A	2.1
46	DZ	18	LEU	2.1
48	B1	97	LEU	2.1
10	CJ	67	THR	2.1
30	DF	131	GLY	2.1
33	DI	95	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
55	D8	45	GLY	2.1
8	CH	99	GLU	2.1
13	AM	53	VAL	2.1
19	AS	60	VAL	2.1
43	DW	85	VAL	2.1
56	D9	16	VAL	2.1
2	CB	173	ALA	2.1
5	AE	21	ALA	2.1
19	AS	34	TRP	2.1
26	DA	2897	U	2.1
13	AM	4	ILE	2.1
1	CA	1021	G	2.1
24	AX	67	C	2.1
46	DZ	44	PHE	2.1
2	CB	133	LYS	2.1
20	AT	20	LEU	2.1
40	DT	125	ARG	2.1
42	BV	71	LEU	2.1
46	DZ	72	ARG	2.1
1	AA	532	A	2.1
1	CA	1016	A	2.1
3	AC	206	GLU	2.1
14	CN	38	GLY	2.1
22	CV	15	A	2.1
26	BA	2157	A	2.1
29	DE	87	GLU	2.1
2	CB	195	ASP	2.1
8	AH	4	ASP	2.1
9	AI	86	VAL	2.1
15	AO	19	PRO	2.1
15	CO	19	PRO	2.1
44	DX	1	MET	2.1
56	B9	12	ASP	2.1
5	AE	102	ALA	2.1
19	CS	56	GLN	2.1
21	AU	14	TRP	2.1
19	CS	23	ASN	2.1
3	CC	140	ARG	2.1
47	D0	3	HIS	2.1
20	AT	43	LEU	2.1
1	CA	1190	G	2.1
46	DZ	138	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
19	CS	38	SER	2.1
51	D4	54	GLY	2.1
1	CA	958	A	2.0
31	DG	165	THR	2.0
32	DH	129	THR	2.0
34	BN	43	THR	2.0
50	D3	40	THR	2.0
51	B4	52	THR	2.0
1	CA	950	U	2.0
3	CC	129	ALA	2.0
7	CG	110	GLN	2.0
9	CI	77	ILE	2.0
10	CJ	38	ILE	2.0
46	DZ	57	ILE	2.0
8	CH	50	ARG	2.0
19	CS	29	ARG	2.0
5	CE	33	VAL	2.0
17	CQ	14	LYS	2.0
31	DG	37	VAL	2.0
6	AF	57	GLN	2.0
2	CB	85	ALA	2.0
3	CC	30	ARG	2.0
16	AP	25	ARG	2.0
16	AP	17	TYR	2.0
26	BA	2803	A	2.0
26	DA	1460	A	2.0
39	DS	3	ARG	2.0
49	B2	69	ARG	2.0
31	DG	27	ASN	2.0
46	DZ	75	ASN	2.0
2	CB	72	GLY	2.0
4	CD	78	LEU	2.0
6	AF	17	SER	2.0
28	DD	38	LYS	2.0
7	CG	61	VAL	2.0
33	BI	145	VAL	2.0
56	D9	7	VAL	2.0
3	AC	124	ILE	2.0
12	CL	67	THR	2.0
14	CN	35	ARG	2.0
15	CO	87	ILE	2.0
17	CQ	58	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
26	DA	2137	C	2.0
30	DF	26	ALA	2.0
1	AA	1001	A	2.0
1	CA	1151	A	2.0
5	AE	124	GLY	2.0
9	CI	99	LEU	2.0
12	AL	29	GLY	2.0
12	CL	29	GLY	2.0
26	BA	2195	A	2.0
32	DH	108	GLY	2.0
37	DQ	8	LYS	2.0
17	CQ	79	SER	2.0
11	CK	84	VAL	2.0
19	AS	44	MET	2.0
8	AH	45	ILE	2.0
17	AQ	65	ILE	2.0
2	CB	54	THR	2.0
3	AC	60	ALA	2.0
15	CO	80	ALA	2.0
18	CR	56	THR	2.0
26	BA	2144	U	2.0
9	AI	114	TYR	2.0
1	CA	1112	C	2.0
13	AM	6	GLY	2.0
21	AU	21	TYR	2.0
26	DA	2896	C	2.0
31	DG	34	LEU	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
23	PPU	AW	76	37/38	0.18	-	12,29,37,42	0
24	5MC	CX	32	21/22	0.20	-	68,80,88,99	0
24	PSU	AX	55	20/21	0.15	-	58,70,77,82	0
24	PSU	CX	55	20/21	0.16	-	61,72,81,89	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
24	5MU	CX	54	21/22	0.14	-	71,79,92,107	0
24	5MC	AX	32	21/22	0.17	-	46,55,75,77	0
24	5MU	AX	54	21/22	0.16	-	57,67,82,96	0
24	4SU	AX	8	20/21	0.16	-	47,59,67,84	0
24	31H	AX	76	30/33	0.24	-	14,31,55,77	8
24	31H	CX	76	32/33	0.22	-	23,42,61,84	10
24	4SU	CX	8	20/21	0.17	-	61,80,93,118	0
23	PPU	CW	76	37/38	0.21	-	27,41,53,63	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
57	MG	BA	3653	1/1	0.20	-	51,51,51,51	0
57	MG	BA	3534	1/1	0.27	-	23,23,23,23	0
57	MG	CA	3105	1/1	0.18	-	76,76,76,76	0
57	MG	BA	3007	1/1	0.10	-	39,39,39,39	0
57	MG	DA	3242	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3556	1/1	0.16	-	52,52,52,52	0
57	MG	DA	3127	1/1	0.36	-	40,40,40,40	0
57	MG	BA	3606	1/1	0.16	-	39,39,39,39	0
57	MG	DA	3366	1/1	0.15	-	40,40,40,40	0
57	MG	DA	3074	1/1	0.17	-	38,38,38,38	0
57	MG	BU	201	1/1	0.10	-	36,36,36,36	0
57	MG	BA	3442	1/1	0.11	-	51,51,51,51	0
57	MG	DE	303	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3247	1/1	0.11	-	43,43,43,43	0
57	MG	BQ	3004	1/1	0.24	-	35,35,35,35	0
57	MG	AA	3078	1/1	0.18	-	66,66,66,66	0
57	MG	B7	101	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3364	1/1	0.19	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3188	1/1	0.21	-	48,48,48,48	0
57	MG	DA	3202	1/1	0.38	-	41,41,41,41	0
57	MG	BA	3321	1/1	0.14	-	31,31,31,31	0
57	MG	AW	101	1/1	0.25	-	24,24,24,24	0
57	MG	DA	3563	1/1	0.10	-	55,55,55,55	0
59	ZN	B4	501	1/1	0.07	-	94,94,94,94	0
57	MG	CA	3098	1/1	0.07	-	76,76,76,76	0
57	MG	BA	3488	1/1	0.05	-	34,34,34,34	0
57	MG	BA	3420	1/1	0.11	-	23,23,23,23	0
57	MG	BA	3696	1/1	0.09	-	41,41,41,41	0
57	MG	DA	3156	1/1	0.14	-	46,46,46,46	0
57	MG	CA	3090	1/1	0.37	-	64,64,64,64	0
57	MG	BU	204	1/1	0.38	-	38,38,38,38	0
57	MG	BA	3657	1/1	0.11	-	55,55,55,55	0
57	MG	DA	3417	1/1	0.19	-	46,46,46,46	0
57	MG	DA	3621	1/1	0.38	-	61,61,61,61	0
57	MG	DA	3398	1/1	0.12	-	37,37,37,37	0
57	MG	CA	3003	1/1	0.12	-	74,74,74,74	0
57	MG	BF	309	1/1	0.42	-	61,61,61,61	0
57	MG	BA	3110	1/1	0.14	-	40,40,40,40	0
57	MG	DA	3322	1/1	0.17	-	51,51,51,51	0
57	MG	BA	3550	1/1	0.12	-	60,60,60,60	0
57	MG	BA	3313	1/1	0.15	-	30,30,30,30	0
57	MG	BA	3192	1/1	0.09	-	35,35,35,35	0
57	MG	BA	3602	1/1	0.34	-	65,65,65,65	0
57	MG	DA	3382	1/1	0.22	-	20,20,20,20	0
57	MG	CA	3143	1/1	0.13	-	59,59,59,59	0
57	MG	DA	3338	1/1	0.12	-	36,36,36,36	0
57	MG	BA	3650	1/1	0.10	-	49,49,49,49	0
57	MG	BA	3059	1/1	0.21	-	50,50,50,50	0
57	MG	BA	3609	1/1	0.13	-	47,47,47,47	0
57	MG	DA	3261	1/1	0.22	-	38,38,38,38	0
57	MG	BD	308	1/1	0.28	-	41,41,41,41	0
57	MG	BA	3342	1/1	0.19	-	38,38,38,38	0
57	MG	BQ	3002	1/1	0.27	-	39,39,39,39	0
57	MG	AA	3029	1/1	0.06	-	42,42,42,42	0
57	MG	DA	3050	1/1	0.13	-	48,48,48,48	0
57	MG	AA	3049	1/1	0.17	-	43,43,43,43	0
57	MG	DA	3001	1/1	0.35	-	45,45,45,45	0
57	MG	BA	3572	1/1	0.19	-	27,27,27,27	0
57	MG	DA	3056	1/1	0.08	-	35,35,35,35	0
57	MG	BA	3642	1/1	0.17	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3350	1/1	0.35	-	44,44,44,44	0
57	MG	BA	3438	1/1	0.14	-	19,19,19,19	0
57	MG	DA	3390	1/1	0.19	-	54,54,54,54	0
57	MG	BP	3002	1/1	0.25	-	32,32,32,32	0
57	MG	AA	3150	1/1	0.09	-	65,65,65,65	0
57	MG	DA	3118	1/1	0.11	-	46,46,46,46	0
57	MG	CA	3141	1/1	0.16	-	69,69,69,69	0
57	MG	DA	3133	1/1	0.10	-	52,52,52,52	0
57	MG	AA	3117	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3267	1/1	0.25	-	45,45,45,45	0
57	MG	BE	3002	1/1	0.46	-	50,50,50,50	0
57	MG	BA	3227	1/1	0.16	-	39,39,39,39	0
57	MG	DA	3046	1/1	0.30	-	50,50,50,50	0
57	MG	DA	3405	1/1	0.06	-	45,45,45,45	0
57	MG	AA	3038	1/1	0.22	-	58,58,58,58	0
57	MG	DA	3274	1/1	0.21	-	45,45,45,45	0
57	MG	CA	3001	1/1	0.09	-	53,53,53,53	0
57	MG	BA	3400	1/1	0.20	-	33,33,33,33	0
57	MG	BA	3473	1/1	0.15	-	31,31,31,31	0
57	MG	DA	3558	1/1	0.08	-	45,45,45,45	0
57	MG	DA	3210	1/1	0.37	-	57,57,57,57	0
57	MG	DA	3250	1/1	0.15	-	41,41,41,41	0
57	MG	BE	3007	1/1	0.08	-	31,31,31,31	0
57	MG	BA	3132	1/1	0.17	-	52,52,52,52	0
57	MG	BA	3369	1/1	0.14	-	57,57,57,57	0
57	MG	AA	3101	1/1	0.19	-	53,53,53,53	0
57	MG	BA	3510	1/1	0.23	-	20,20,20,20	0
57	MG	DA	3079	1/1	0.16	-	41,41,41,41	0
57	MG	BA	3112	1/1	0.23	-	58,58,58,58	0
57	MG	BA	3171	1/1	0.38	-	44,44,44,44	0
57	MG	BA	3168	1/1	0.16	-	32,32,32,32	0
57	MG	BA	3390	1/1	0.09	-	31,31,31,31	0
57	MG	DA	3280	1/1	0.18	-	49,49,49,49	0
57	MG	DA	3071	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3302	1/1	0.17	-	30,30,30,30	0
57	MG	DA	3377	1/1	0.15	-	31,31,31,31	0
57	MG	CA	3072	1/1	0.25	-	38,38,38,38	0
57	MG	BA	3559	1/1	0.16	-	36,36,36,36	0
57	MG	DA	3301	1/1	0.10	-	54,54,54,54	0
57	MG	DE	304	1/1	0.11	-	47,47,47,47	0
57	MG	AA	3153	1/1	0.08	-	46,46,46,46	0
57	MG	DA	3422	1/1	0.25	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AX	3008	1/1	0.12	-	58,58,58,58	0
57	MG	BA	3081	1/1	0.12	-	26,26,26,26	0
57	MG	DA	3282	1/1	0.19	-	36,36,36,36	0
57	MG	DR	3001	1/1	1.33	-	66,66,66,66	0
57	MG	BA	3015	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3700	1/1	0.18	-	69,69,69,69	0
57	MG	BA	3099	1/1	0.29	-	36,36,36,36	0
57	MG	AA	3170	1/1	0.15	-	70,70,70,70	0
57	MG	BA	3526	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3506	1/1	0.12	-	39,39,39,39	0
57	MG	DA	3168	1/1	0.30	-	50,50,50,50	0
60	K	CX	3001	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3317	1/1	0.19	-	42,42,42,42	0
57	MG	BA	3056	1/1	0.18	-	21,21,21,21	0
57	MG	BA	3065	1/1	0.23	-	43,43,43,43	0
57	MG	DA	3227	1/1	0.13	-	57,57,57,57	0
57	MG	DA	3506	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3437	1/1	0.20	-	52,52,52,52	0
57	MG	DA	3311	1/1	0.19	-	42,42,42,42	0
57	MG	BA	3174	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3547	1/1	0.18	-	33,33,33,33	0
57	MG	DA	3622	1/1	1.14	-	58,58,58,58	0
57	MG	BA	3360	1/1	0.17	-	60,60,60,60	0
57	MG	CA	3037	1/1	0.17	-	60,60,60,60	0
57	MG	AA	3041	1/1	0.20	-	62,62,62,62	0
57	MG	BA	3049	1/1	0.23	-	53,53,53,53	0
57	MG	BA	3374	1/1	0.14	-	48,48,48,48	0
57	MG	DA	3096	1/1	0.22	-	52,52,52,52	0
57	MG	BA	3298	1/1	0.20	-	50,50,50,50	0
57	MG	AA	3172	1/1	0.25	-	54,54,54,54	0
57	MG	DA	3076	1/1	0.17	-	53,53,53,53	0
57	MG	BA	3604	1/1	0.10	-	62,62,62,62	0
57	MG	AA	3070	1/1	0.23	-	43,43,43,43	0
57	MG	BA	3493	1/1	0.12	-	39,39,39,39	0
57	MG	DA	3262	1/1	0.07	-	39,39,39,39	0
57	MG	B8	101	1/1	0.12	-	34,34,34,34	0
57	MG	BA	3291	1/1	0.15	-	44,44,44,44	0
57	MG	DA	3061	1/1	0.26	-	36,36,36,36	0
57	MG	DA	3514	1/1	0.19	-	34,34,34,34	0
57	MG	CA	3006	1/1	0.11	-	43,43,43,43	0
57	MG	CA	3122	1/1	0.09	-	50,50,50,50	0
57	MG	DA	3605	1/1	0.09	-	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3521	1/1	0.27	-	32,32,32,32	0
57	MG	BA	3209	1/1	0.24	-	32,32,32,32	0
57	MG	BA	3119	1/1	0.21	-	41,41,41,41	0
57	MG	BA	3594	1/1	0.11	-	34,34,34,34	0
57	MG	BA	3317	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3528	1/1	0.11	-	60,60,60,60	0
57	MG	BA	3410	1/1	0.17	-	40,40,40,40	0
57	MG	DA	3440	1/1	0.26	-	44,44,44,44	0
57	MG	DA	3197	1/1	0.13	-	35,35,35,35	0
57	MG	DA	3332	1/1	0.10	-	52,52,52,52	0
57	MG	CA	3032	1/1	0.40	-	58,58,58,58	0
57	MG	DA	3490	1/1	0.07	-	62,62,62,62	0
57	MG	DA	3208	1/1	0.16	-	50,50,50,50	0
57	MG	BA	3586	1/1	0.08	-	33,33,33,33	0
57	MG	BA	3164	1/1	0.22	-	44,44,44,44	0
57	MG	DA	3566	1/1	0.08	-	40,40,40,40	0
57	MG	DD	307	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3434	1/1	0.09	-	48,48,48,48	0
57	MG	AA	3081	1/1	0.07	-	44,44,44,44	0
57	MG	CA	3114	1/1	0.23	-	96,96,96,96	0
57	MG	BA	3228	1/1	0.24	-	33,33,33,33	0
57	MG	CA	3139	1/1	0.10	-	82,82,82,82	0
57	MG	AA	3136	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3117	1/1	0.14	-	24,24,24,24	0
57	MG	BA	3472	1/1	0.10	-	39,39,39,39	0
57	MG	DA	3058	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3098	1/1	0.57	-	50,50,50,50	0
57	MG	BA	3674	1/1	0.19	-	59,59,59,59	0
57	MG	BA	3661	1/1	0.18	-	56,56,56,56	0
57	MG	DA	3095	1/1	0.23	-	45,45,45,45	0
57	MG	DU	3003	1/1	0.18	-	60,60,60,60	0
57	MG	DA	3002	1/1	0.31	-	44,44,44,44	0
57	MG	AA	3182	1/1	0.13	-	40,40,40,40	0
57	MG	D8	101	1/1	0.17	-	60,60,60,60	0
57	MG	DA	3143	1/1	0.17	-	47,47,47,47	0
57	MG	DA	3077	1/1	0.17	-	58,58,58,58	0
57	MG	BA	3045	1/1	0.16	-	33,33,33,33	0
57	MG	DB	3004	1/1	0.12	-	38,38,38,38	0
57	MG	BA	3308	1/1	0.14	-	14,14,14,14	0
57	MG	DA	3152	1/1	0.19	-	38,38,38,38	0
57	MG	DA	3425	1/1	0.12	-	40,40,40,40	0
57	MG	BA	3019	1/1	0.12	-	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3290	1/1	0.11	-	43,43,43,43	0
57	MG	DA	3629	1/1	0.27	-	40,40,40,40	0
57	MG	AX	3009	1/1	0.10	-	50,50,50,50	0
57	MG	AA	3096	1/1	0.05	-	57,57,57,57	0
57	MG	BA	3536	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3333	1/1	0.09	-	41,41,41,41	0
57	MG	CA	3052	1/1	0.07	-	61,61,61,61	0
57	MG	BA	3412	1/1	0.37	-	44,44,44,44	0
57	MG	BA	3454	1/1	0.14	-	45,45,45,45	0
57	MG	DA	3044	1/1	0.16	-	38,38,38,38	0
57	MG	BA	3273	1/1	0.17	-	30,30,30,30	0
57	MG	CA	3091	1/1	0.18	-	75,75,75,75	0
57	MG	BA	3421	1/1	0.16	-	29,29,29,29	0
57	MG	DA	3120	1/1	0.25	-	55,55,55,55	0
57	MG	CA	3021	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3124	1/1	0.21	-	30,30,30,30	0
57	MG	BA	3244	1/1	0.35	-	29,29,29,29	0
57	MG	BA	3134	1/1	0.23	-	43,43,43,43	0
57	MG	CA	3041	1/1	0.13	-	62,62,62,62	0
57	MG	BA	3675	1/1	0.11	-	41,41,41,41	0
57	MG	DA	3059	1/1	0.14	-	60,60,60,60	0
57	MG	BA	3302	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3334	1/1	0.17	-	37,37,37,37	0
57	MG	BA	3618	1/1	0.11	-	64,64,64,64	0
57	MG	AA	3006	1/1	0.08	-	62,62,62,62	0
57	MG	DA	3300	1/1	0.12	-	38,38,38,38	0
57	MG	BA	3250	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3397	1/1	0.11	-	33,33,33,33	0
57	MG	AA	3185	1/1	0.13	-	50,50,50,50	0
57	MG	DA	3591	1/1	0.08	-	69,69,69,69	0
57	MG	BA	3596	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3245	1/1	0.13	-	46,46,46,46	0
57	MG	BA	3565	1/1	0.11	-	50,50,50,50	0
57	MG	BA	3557	1/1	0.15	-	35,35,35,35	0
57	MG	DA	3099	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3330	1/1	0.14	-	49,49,49,49	0
57	MG	BA	3038	1/1	0.08	-	38,38,38,38	0
57	MG	BA	3484	1/1	0.07	-	50,50,50,50	0
59	ZN	DY	501	1/1	0.10	-	88,88,88,88	0
57	MG	BB	3012	1/1	0.15	-	33,33,33,33	0
57	MG	BF	310	1/1	0.13	-	51,51,51,51	0
57	MG	BA	3142	1/1	0.17	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BD	302	1/1	0.22	-	38,38,38,38	0
57	MG	AA	3002	1/1	0.10	-	58,58,58,58	0
57	MG	CA	3124	1/1	0.18	-	57,57,57,57	0
57	MG	BA	3677	1/1	0.24	-	30,30,30,30	0
57	MG	BA	3451	1/1	0.17	-	59,59,59,59	0
57	MG	BQ	3003	1/1	0.60	-	68,68,68,68	0
57	MG	DA	3572	1/1	0.15	-	46,46,46,46	0
57	MG	BN	3002	1/1	0.26	-	46,46,46,46	0
57	MG	DA	3387	1/1	0.16	-	29,29,29,29	0
57	MG	BA	3293	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3198	1/1	0.06	-	41,41,41,41	0
57	MG	BA	3341	1/1	0.08	-	52,52,52,52	0
57	MG	DA	3473	1/1	0.20	-	32,32,32,32	0
57	MG	DD	305	1/1	0.43	-	48,48,48,48	0
57	MG	BA	3431	1/1	0.20	-	25,25,25,25	0
57	MG	AA	3005	1/1	0.14	-	66,66,66,66	0
57	MG	BA	3079	1/1	0.24	-	55,55,55,55	0
57	MG	AX	3006	1/1	0.24	-	59,59,59,59	0
57	MG	BA	3491	1/1	0.16	-	33,33,33,33	0
57	MG	BA	3304	1/1	0.25	-	49,49,49,49	0
57	MG	DA	3540	1/1	0.07	-	43,43,43,43	0
57	MG	DA	3423	1/1	0.20	-	33,33,33,33	0
57	MG	BA	3085	1/1	0.14	-	18,18,18,18	0
57	MG	DA	3170	1/1	0.37	-	47,47,47,47	0
57	MG	CA	3062	1/1	0.09	-	73,73,73,73	0
57	MG	AA	3084	1/1	0.14	-	43,43,43,43	0
57	MG	DW	202	1/1	0.14	-	43,43,43,43	0
57	MG	AA	3175	1/1	0.31	-	61,61,61,61	0
57	MG	DA	3293	1/1	0.18	-	41,41,41,41	0
57	MG	DA	3511	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3522	1/1	0.15	-	41,41,41,41	0
57	MG	DA	3515	1/1	0.16	-	53,53,53,53	0
57	MG	DA	3166	1/1	0.17	-	47,47,47,47	0
57	MG	BA	3071	1/1	0.19	-	48,48,48,48	0
57	MG	AA	3062	1/1	0.18	-	57,57,57,57	0
57	MG	BA	3562	1/1	0.15	-	47,47,47,47	0
57	MG	AA	3089	1/1	0.22	-	61,61,61,61	0
57	MG	BA	3579	1/1	0.31	-	44,44,44,44	0
57	MG	BV	202	1/1	0.20	-	29,29,29,29	0
57	MG	AA	3022	1/1	0.06	-	57,57,57,57	0
57	MG	DA	3005	1/1	0.17	-	29,29,29,29	0
57	MG	CA	3157	1/1	0.09	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BG	3001	1/1	0.19	-	44,44,44,44	0
57	MG	CA	3018	1/1	0.11	-	47,47,47,47	0
57	MG	DA	3237	1/1	0.27	-	41,41,41,41	0
57	MG	BA	3357	1/1	0.17	-	31,31,31,31	0
57	MG	DA	3268	1/1	0.10	-	35,35,35,35	0
57	MG	BA	3091	1/1	0.22	-	56,56,56,56	0
57	MG	AX	3003	1/1	0.34	-	66,66,66,66	0
57	MG	DA	3134	1/1	0.15	-	59,59,59,59	0
57	MG	BA	3057	1/1	0.17	-	21,21,21,21	0
57	MG	DA	3371	1/1	0.20	-	47,47,47,47	0
57	MG	DA	3608	1/1	0.12	-	61,61,61,61	0
57	MG	AA	3138	1/1	0.19	-	40,40,40,40	0
57	MG	DA	3243	1/1	0.26	-	41,41,41,41	0
57	MG	AA	3013	1/1	0.10	-	53,53,53,53	0
57	MG	BA	3666	1/1	0.17	-	79,79,79,79	0
57	MG	DA	3459	1/1	0.42	-	40,40,40,40	0
57	MG	AA	3093	1/1	0.17	-	56,56,56,56	0
57	MG	DA	3386	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3173	1/1	0.32	-	42,42,42,42	0
57	MG	CA	3100	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3447	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3197	1/1	0.15	-	32,32,32,32	0
57	MG	DA	3344	1/1	0.12	-	42,42,42,42	0
57	MG	BA	3222	1/1	0.17	-	52,52,52,52	0
57	MG	DA	3414	1/1	0.12	-	37,37,37,37	0
57	MG	BA	3441	1/1	0.10	-	56,56,56,56	0
57	MG	AA	3173	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3508	1/1	0.19	-	52,52,52,52	0
57	MG	DA	3579	1/1	0.21	-	58,58,58,58	0
59	ZN	CN	501	1/1	0.07	-	101,101,101,101	0
57	MG	CA	3107	1/1	0.22	-	89,89,89,89	0
57	MG	CA	3118	1/1	0.14	-	69,69,69,69	0
57	MG	BA	3223	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3385	1/1	0.08	-	47,47,47,47	0
57	MG	BA	3348	1/1	0.11	-	17,17,17,17	0
57	MG	BA	3430	1/1	0.15	-	54,54,54,54	0
57	MG	BA	3564	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3485	1/1	0.10	-	40,40,40,40	0
57	MG	DA	3614	1/1	0.40	-	56,56,56,56	0
57	MG	BA	3270	1/1	0.37	-	47,47,47,47	0
57	MG	BA	3563	1/1	0.10	-	38,38,38,38	0
57	MG	DA	3298	1/1	0.10	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3141	1/1	0.17	-	38,38,38,38	0
57	MG	DA	3189	1/1	0.20	-	57,57,57,57	0
57	MG	CA	3127	1/1	0.29	-	76,76,76,76	0
57	MG	DA	3110	1/1	0.12	-	60,60,60,60	0
57	MG	DA	3509	1/1	0.29	-	42,42,42,42	0
57	MG	BA	3051	1/1	0.17	-	36,36,36,36	0
57	MG	BA	3624	1/1	0.09	-	26,26,26,26	0
57	MG	BA	3709	1/1	0.39	-	45,45,45,45	0
57	MG	BA	3494	1/1	0.21	-	30,30,30,30	0
57	MG	DA	3487	1/1	0.09	-	44,44,44,44	0
57	MG	DA	3543	1/1	0.15	-	61,61,61,61	0
57	MG	DA	3607	1/1	0.22	-	73,73,73,73	0
57	MG	BA	3414	1/1	0.19	-	59,59,59,59	0
57	MG	DA	3264	1/1	0.09	-	33,33,33,33	0
57	MG	CA	3138	1/1	0.15	-	66,66,66,66	0
57	MG	DA	3328	1/1	0.14	-	66,66,66,66	0
57	MG	CA	3017	1/1	0.30	-	69,69,69,69	0
57	MG	DA	3199	1/1	0.08	-	41,41,41,41	0
57	MG	DA	3620	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3373	1/1	0.20	-	43,43,43,43	0
57	MG	DA	3451	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3138	1/1	0.19	-	39,39,39,39	0
57	MG	DA	3383	1/1	0.14	-	45,45,45,45	0
57	MG	BA	3220	1/1	0.22	-	54,54,54,54	0
57	MG	BA	3509	1/1	0.31	-	34,34,34,34	0
57	MG	BA	3478	1/1	0.15	-	22,22,22,22	0
57	MG	DA	3445	1/1	0.10	-	59,59,59,59	0
57	MG	DA	3393	1/1	0.12	-	41,41,41,41	0
57	MG	CA	3094	1/1	0.10	-	80,80,80,80	0
57	MG	DA	3356	1/1	0.20	-	53,53,53,53	0
57	MG	AA	3073	1/1	0.14	-	59,59,59,59	0
57	MG	B2	3001	1/1	0.10	-	43,43,43,43	0
57	MG	CA	3075	1/1	0.14	-	48,48,48,48	0
57	MG	BA	3662	1/1	0.24	-	62,62,62,62	0
57	MG	DA	3438	1/1	0.13	-	42,42,42,42	0
57	MG	BA	3165	1/1	0.20	-	34,34,34,34	0
57	MG	CA	3020	1/1	0.14	-	51,51,51,51	0
57	MG	DA	3265	1/1	0.14	-	33,33,33,33	0
57	MG	DW	201	1/1	0.18	-	70,70,70,70	0
57	MG	BA	3585	1/1	0.15	-	45,45,45,45	0
57	MG	BA	3468	1/1	0.11	-	42,42,42,42	0
57	MG	DA	3027	1/1	0.20	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3132	1/1	0.12	-	53,53,53,53	0
57	MG	DA	3450	1/1	0.16	-	34,34,34,34	0
57	MG	DA	3113	1/1	0.21	-	42,42,42,42	0
57	MG	BA	3009	1/1	0.08	-	34,34,34,34	0
57	MG	DA	3049	1/1	0.14	-	46,46,46,46	0
57	MG	AA	3127	1/1	0.28	-	73,73,73,73	0
57	MG	DA	3349	1/1	0.16	-	35,35,35,35	0
57	MG	BA	3131	1/1	0.38	-	31,31,31,31	0
57	MG	BA	3629	1/1	0.19	-	37,37,37,37	0
57	MG	BA	3318	1/1	0.15	-	39,39,39,39	0
57	MG	BA	3537	1/1	0.17	-	35,35,35,35	0
57	MG	CA	3040	1/1	0.19	-	67,67,67,67	0
57	MG	AA	3094	1/1	0.15	-	54,54,54,54	0
57	MG	DA	3618	1/1	0.15	-	46,46,46,46	0
57	MG	AA	3151	1/1	0.16	-	72,72,72,72	0
57	MG	BA	3282	1/1	0.08	-	44,44,44,44	0
57	MG	DA	3072	1/1	0.30	-	46,46,46,46	0
57	MG	BA	3530	1/1	0.25	-	20,20,20,20	0
57	MG	DA	3070	1/1	0.19	-	35,35,35,35	0
57	MG	BA	3416	1/1	0.13	-	73,73,73,73	0
57	MG	CA	3044	1/1	0.19	-	59,59,59,59	0
57	MG	AA	3035	1/1	0.32	-	52,52,52,52	0
57	MG	DA	3130	1/1	0.21	-	55,55,55,55	0
57	MG	DA	3200	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3289	1/1	0.23	-	50,50,50,50	0
57	MG	DA	3291	1/1	0.21	-	56,56,56,56	0
57	MG	DA	3628	1/1	0.56	-	59,59,59,59	0
57	MG	BA	3047	1/1	0.20	-	44,44,44,44	0
57	MG	BA	3242	1/1	0.22	-	45,45,45,45	0
57	MG	BA	3492	1/1	0.18	-	30,30,30,30	0
57	MG	DA	3088	1/1	0.17	-	41,41,41,41	0
57	MG	DA	3533	1/1	0.56	-	47,47,47,47	0
57	MG	BA	3645	1/1	0.13	-	43,43,43,43	0
57	MG	DA	3553	1/1	0.37	-	75,75,75,75	0
57	MG	AA	3111	1/1	0.12	-	70,70,70,70	0
57	MG	AA	3120	1/1	0.08	-	53,53,53,53	0
57	MG	BA	3685	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3542	1/1	0.12	-	40,40,40,40	0
57	MG	AA	3122	1/1	0.11	-	52,52,52,52	0
57	MG	CA	3045	1/1	0.11	-	53,53,53,53	0
57	MG	AA	3063	1/1	0.12	-	89,89,89,89	0
57	MG	DA	3400	1/1	0.12	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3125	1/1	0.36	-	30,30,30,30	0
57	MG	BA	3358	1/1	0.07	-	35,35,35,35	0
57	MG	DA	3191	1/1	0.10	-	54,54,54,54	0
57	MG	CA	3147	1/1	0.12	-	56,56,56,56	0
57	MG	CT	3001	1/1	0.07	-	59,59,59,59	0
57	MG	CA	3129	1/1	0.21	-	83,83,83,83	0
57	MG	DA	3083	1/1	0.22	-	30,30,30,30	0
57	MG	BA	3225	1/1	0.08	-	45,45,45,45	0
57	MG	DA	3278	1/1	0.08	-	38,38,38,38	0
57	MG	BA	3654	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3570	1/1	0.17	-	28,28,28,28	0
57	MG	BA	3424	1/1	0.20	-	29,29,29,29	0
57	MG	CA	3120	1/1	0.24	-	72,72,72,72	0
57	MG	DA	3430	1/1	0.21	-	26,26,26,26	0
57	MG	DA	3521	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3383	1/1	0.12	-	37,37,37,37	0
57	MG	BA	3576	1/1	0.25	-	29,29,29,29	0
57	MG	DA	3180	1/1	0.31	-	41,41,41,41	0
57	MG	DA	3325	1/1	0.10	-	43,43,43,43	0
57	MG	DA	3310	1/1	0.18	-	43,43,43,43	0
57	MG	DO	5001	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3391	1/1	0.16	-	39,39,39,39	0
57	MG	BA	3701	1/1	0.18	-	17,17,17,17	0
57	MG	B0	101	1/1	0.10	-	33,33,33,33	0
57	MG	BA	3311	1/1	0.06	-	42,42,42,42	0
57	MG	CA	3081	1/1	0.12	-	67,67,67,67	0
57	MG	CA	3111	1/1	0.08	-	65,65,65,65	0
57	MG	DA	3097	1/1	0.13	-	50,50,50,50	0
57	MG	AA	3113	1/1	0.29	-	54,54,54,54	0
57	MG	CA	3068	1/1	0.07	-	53,53,53,53	0
57	MG	BA	3118	1/1	0.24	-	28,28,28,28	0
57	MG	CA	3155	1/1	0.14	-	66,66,66,66	0
57	MG	BN	3006	1/1	0.61	-	47,47,47,47	0
57	MG	BA	3356	1/1	0.11	-	36,36,36,36	0
57	MG	CA	3028	1/1	0.27	-	57,57,57,57	0
57	MG	BA	3102	1/1	0.21	-	43,43,43,43	0
57	MG	DD	302	1/1	0.15	-	50,50,50,50	0
57	MG	CA	3096	1/1	0.16	-	51,51,51,51	0
57	MG	DA	3335	1/1	0.11	-	48,48,48,48	0
57	MG	DA	3054	1/1	0.16	-	40,40,40,40	0
57	MG	CA	3026	1/1	0.11	-	59,59,59,59	0
57	MG	BA	3444	1/1	0.18	-	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3215	1/1	0.10	-	53,53,53,53	0
57	MG	DA	3397	1/1	0.07	-	46,46,46,46	0
57	MG	DA	3252	1/1	0.11	-	63,63,63,63	0
57	MG	BA	3608	1/1	0.09	-	50,50,50,50	0
57	MG	DA	3559	1/1	0.21	-	31,31,31,31	0
57	MG	AA	3007	1/1	0.18	-	47,47,47,47	0
57	MG	AA	3050	1/1	0.20	-	49,49,49,49	0
57	MG	BA	3616	1/1	0.18	-	32,32,32,32	0
57	MG	BA	3173	1/1	0.24	-	28,28,28,28	0
57	MG	CA	3154	1/1	0.18	-	68,68,68,68	0
57	MG	DA	3259	1/1	0.13	-	39,39,39,39	0
57	MG	DA	3456	1/1	0.33	-	59,59,59,59	0
57	MG	BA	3108	1/1	0.13	-	36,36,36,36	0
57	MG	DA	3493	1/1	0.11	-	53,53,53,53	0
57	MG	AA	3075	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3461	1/1	0.24	-	32,32,32,32	0
57	MG	BA	3669	1/1	0.27	-	34,34,34,34	0
57	MG	BA	3319	1/1	0.13	-	37,37,37,37	0
57	MG	CA	3035	1/1	0.20	-	63,63,63,63	0
57	MG	BA	3426	1/1	0.16	-	30,30,30,30	0
57	MG	CA	3076	1/1	0.16	-	59,59,59,59	0
57	MG	BE	3001	1/1	0.29	-	48,48,48,48	0
57	MG	BA	3268	1/1	0.15	-	45,45,45,45	0
57	MG	AA	3030	1/1	0.22	-	41,41,41,41	0
57	MG	AA	3164	1/1	0.12	-	54,54,54,54	0
57	MG	BA	3136	1/1	0.28	-	56,56,56,56	0
57	MG	DA	3319	1/1	0.31	-	45,45,45,45	0
57	MG	BA	3613	1/1	0.07	-	74,74,74,74	0
57	MG	BA	3393	1/1	0.16	-	30,30,30,30	0
57	MG	BA	3399	1/1	0.14	-	26,26,26,26	0
57	MG	BA	3116	1/1	0.28	-	54,54,54,54	0
57	MG	AX	3004	1/1	0.11	-	45,45,45,45	0
57	MG	AA	3107	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3577	1/1	0.17	-	25,25,25,25	0
57	MG	BA	3622	1/1	0.09	-	24,24,24,24	0
57	MG	DA	3157	1/1	0.16	-	44,44,44,44	0
57	MG	DA	3021	1/1	0.12	-	50,50,50,50	0
57	MG	BF	301	1/1	0.15	-	30,30,30,30	0
57	MG	BA	3247	1/1	0.14	-	37,37,37,37	0
57	MG	DA	3060	1/1	0.11	-	50,50,50,50	0
57	MG	DA	3216	1/1	0.30	-	43,43,43,43	0
57	MG	DA	3427	1/1	0.19	-	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3599	1/1	0.20	-	36,36,36,36	0
57	MG	BA	3433	1/1	0.11	-	32,32,32,32	0
57	MG	AX	3012	1/1	0.20	-	15,15,15,15	0
57	MG	BA	3384	1/1	0.27	-	19,19,19,19	0
57	MG	BA	3264	1/1	0.09	-	47,47,47,47	0
57	MG	CA	3047	1/1	0.21	-	50,50,50,50	0
57	MG	DA	3211	1/1	0.13	-	43,43,43,43	0
57	MG	BA	3702	1/1	0.12	-	41,41,41,41	0
57	MG	DA	3612	1/1	0.11	-	64,64,64,64	0
57	MG	BA	3694	1/1	0.16	-	11,11,11,11	0
57	MG	BA	3386	1/1	0.25	-	30,30,30,30	0
57	MG	BA	3205	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3483	1/1	0.31	-	41,41,41,41	0
57	MG	BA	3021	1/1	0.20	-	35,35,35,35	0
57	MG	DA	3586	1/1	0.11	-	21,21,21,21	0
57	MG	AA	3033	1/1	0.18	-	43,43,43,43	0
57	MG	BA	3289	1/1	0.12	-	41,41,41,41	0
57	MG	BA	3655	1/1	0.07	-	68,68,68,68	0
57	MG	DA	3294	1/1	0.19	-	18,18,18,18	0
57	MG	BA	3349	1/1	0.18	-	55,55,55,55	0
57	MG	AA	3163	1/1	0.13	-	70,70,70,70	0
57	MG	DA	3453	1/1	0.23	-	44,44,44,44	0
57	MG	BA	3275	1/1	0.09	-	38,38,38,38	0
57	MG	CA	3121	1/1	0.13	-	51,51,51,51	0
57	MG	AA	3183	1/1	0.16	-	43,43,43,43	0
57	MG	DA	3263	1/1	0.12	-	47,47,47,47	0
57	MG	BA	3157	1/1	0.12	-	42,42,42,42	0
57	MG	DA	3066	1/1	0.08	-	55,55,55,55	0
57	MG	AA	3130	1/1	0.15	-	52,52,52,52	0
57	MG	BA	3716	1/1	0.17	-	53,53,53,53	0
57	MG	DA	3562	1/1	0.07	-	58,58,58,58	0
57	MG	CA	3016	1/1	0.04	-	52,52,52,52	0
57	MG	CA	3110	1/1	0.18	-	56,56,56,56	0
57	MG	BN	3003	1/1	0.33	-	61,61,61,61	0
57	MG	BA	3710	1/1	0.10	-	21,21,21,21	0
57	MG	BA	3656	1/1	0.14	-	57,57,57,57	0
57	MG	DA	3443	1/1	0.17	-	27,27,27,27	0
57	MG	BA	3591	1/1	0.09	-	42,42,42,42	0
57	MG	BA	3248	1/1	0.21	-	32,32,32,32	0
57	MG	AX	3005	1/1	0.30	-	57,57,57,57	0
57	MG	DA	3100	1/1	0.15	-	38,38,38,38	0
57	MG	DA	3203	1/1	0.14	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DB	3008	1/1	0.09	-	59,59,59,59	0
57	MG	BA	3002	1/1	0.13	-	45,45,45,45	0
57	MG	BA	3423	1/1	0.26	-	26,26,26,26	0
57	MG	DA	3285	1/1	0.12	-	50,50,50,50	0
57	MG	BA	3398	1/1	0.21	-	36,36,36,36	0
57	MG	BA	3022	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3041	1/1	0.24	-	39,39,39,39	0
57	MG	BB	3002	1/1	0.19	-	44,44,44,44	0
57	MG	BA	3630	1/1	0.15	-	72,72,72,72	0
57	MG	DA	3436	1/1	0.12	-	61,61,61,61	0
57	MG	DA	3304	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3589	1/1	0.12	-	35,35,35,35	0
57	MG	AA	3205	1/1	0.24	-	48,48,48,48	0
57	MG	AA	3025	1/1	0.15	-	46,46,46,46	0
57	MG	CA	3007	1/1	0.12	-	55,55,55,55	0
57	MG	CA	3019	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3486	1/1	0.13	-	32,32,32,32	0
57	MG	AA	3156	1/1	0.13	-	86,86,86,86	0
57	MG	DA	3037	1/1	0.15	-	41,41,41,41	0
57	MG	AA	3027	1/1	0.17	-	55,55,55,55	0
57	MG	BA	3665	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3528	1/1	0.17	-	37,37,37,37	0
57	MG	BF	303	1/1	0.24	-	35,35,35,35	0
57	MG	DB	3006	1/1	0.11	-	44,44,44,44	0
57	MG	BA	3269	1/1	0.22	-	30,30,30,30	0
57	MG	AA	3009	1/1	0.07	-	40,40,40,40	0
57	MG	AA	3109	1/1	0.20	-	75,75,75,75	0
57	MG	DA	3318	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3111	1/1	0.22	-	54,54,54,54	0
57	MG	BF	305	1/1	0.14	-	33,33,33,33	0
57	MG	BA	3254	1/1	0.18	-	30,30,30,30	0
57	MG	DA	3222	1/1	0.20	-	38,38,38,38	0
57	MG	DA	3536	1/1	0.12	-	48,48,48,48	0
57	MG	DA	3560	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3240	1/1	0.29	-	52,52,52,52	0
57	MG	BA	3560	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3034	1/1	0.11	-	21,21,21,21	0
57	MG	DA	3239	1/1	0.29	-	51,51,51,51	0
57	MG	BA	3292	1/1	0.16	-	26,26,26,26	0
57	MG	DA	3260	1/1	0.21	-	43,43,43,43	0
57	MG	BA	3219	1/1	0.38	-	42,42,42,42	0
57	MG	AX	3010	1/1	0.17	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3167	1/1	0.20	-	51,51,51,51	0
57	MG	BA	3651	1/1	0.25	-	62,62,62,62	0
57	MG	BA	3427	1/1	0.14	-	23,23,23,23	0
57	MG	BA	3648	1/1	0.12	-	50,50,50,50	0
57	MG	DA	3063	1/1	0.09	-	40,40,40,40	0
57	MG	CA	3071	1/1	0.39	-	49,49,49,49	0
57	MG	DA	3164	1/1	0.06	-	44,44,44,44	0
57	MG	CA	3113	1/1	0.18	-	75,75,75,75	0
57	MG	DA	3578	1/1	0.20	-	63,63,63,63	0
57	MG	CA	3043	1/1	0.13	-	68,68,68,68	0
57	MG	DA	3031	1/1	0.10	-	36,36,36,36	0
57	MG	AA	3192	1/1	0.12	-	72,72,72,72	0
57	MG	DA	3489	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3201	1/1	0.21	-	42,42,42,42	0
57	MG	DA	3465	1/1	0.10	-	45,45,45,45	0
57	MG	BA	3330	1/1	0.16	-	14,14,14,14	0
57	MG	DA	3023	1/1	0.18	-	35,35,35,35	0
57	MG	BA	3720	1/1	0.21	-	48,48,48,48	0
57	MG	BA	3063	1/1	0.11	-	39,39,39,39	0
57	MG	BA	3084	1/1	0.14	-	37,37,37,37	0
57	MG	BA	3229	1/1	0.41	-	52,52,52,52	0
57	MG	DA	3339	1/1	0.16	-	23,23,23,23	0
57	MG	BB	3015	1/1	0.10	-	42,42,42,42	0
57	MG	CA	3053	1/1	0.13	-	59,59,59,59	0
57	MG	BA	3092	1/1	0.15	-	32,32,32,32	0
57	MG	BA	3217	1/1	0.30	-	57,57,57,57	0
57	MG	AA	3099	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3152	1/1	0.23	-	45,45,45,45	0
57	MG	CA	3027	1/1	0.07	-	62,62,62,62	0
57	MG	DA	3575	1/1	0.20	-	19,19,19,19	0
57	MG	DA	3221	1/1	0.11	-	49,49,49,49	0
57	MG	BA	3290	1/1	0.14	-	43,43,43,43	0
57	MG	BA	3107	1/1	0.23	-	49,49,49,49	0
57	MG	DA	3057	1/1	0.22	-	22,22,22,22	0
57	MG	DA	3544	1/1	0.05	-	59,59,59,59	0
57	MG	B7	103	1/1	0.19	-	51,51,51,51	0
57	MG	AA	3011	1/1	0.15	-	67,67,67,67	0
57	MG	DA	3380	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3511	1/1	0.17	-	41,41,41,41	0
57	MG	AA	3134	1/1	0.12	-	59,59,59,59	0
57	MG	BA	3670	1/1	0.09	-	25,25,25,25	0
57	MG	DA	3015	1/1	0.30	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3150	1/1	0.15	-	40,40,40,40	0
57	MG	DA	3360	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3526	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3600	1/1	0.21	-	59,59,59,59	0
57	MG	BA	3445	1/1	0.22	-	35,35,35,35	0
57	MG	DA	3258	1/1	0.24	-	32,32,32,32	0
57	MG	AA	3001	1/1	0.14	-	72,72,72,72	0
57	MG	BA	3040	1/1	0.12	-	28,28,28,28	0
57	MG	DA	3581	1/1	0.14	-	53,53,53,53	0
57	MG	CF	3001	1/1	0.15	-	51,51,51,51	0
57	MG	CW	101	1/1	0.19	-	43,43,43,43	0
57	MG	BA	3519	1/1	0.15	-	26,26,26,26	0
57	MG	DA	3408	1/1	0.10	-	44,44,44,44	0
57	MG	DA	3114	1/1	0.11	-	51,51,51,51	0
57	MG	DA	3611	1/1	0.17	-	58,58,58,58	0
57	MG	CA	3039	1/1	0.09	-	52,52,52,52	0
57	MG	DA	3454	1/1	0.25	-	28,28,28,28	0
57	MG	BE	3006	1/1	0.34	-	72,72,72,72	0
57	MG	DA	3036	1/1	0.14	-	48,48,48,48	0
57	MG	BA	3558	1/1	0.17	-	63,63,63,63	0
57	MG	BW	205	1/1	0.12	-	30,30,30,30	0
59	ZN	D9	501	1/1	0.07	-	75,75,75,75	0
57	MG	DA	3492	1/1	0.09	-	45,45,45,45	0
57	MG	BA	3200	1/1	0.21	-	39,39,39,39	0
57	MG	BA	3176	1/1	0.20	-	35,35,35,35	0
57	MG	BA	3139	1/1	0.33	-	45,45,45,45	0
57	MG	BA	3114	1/1	0.20	-	41,41,41,41	0
57	MG	BA	3546	1/1	0.24	-	27,27,27,27	0
57	MG	BA	3080	1/1	0.16	-	51,51,51,51	0
57	MG	DA	3004	1/1	0.29	-	32,32,32,32	0
57	MG	CA	3099	1/1	0.22	-	50,50,50,50	0
57	MG	DA	3106	1/1	0.17	-	52,52,52,52	0
57	MG	DA	3277	1/1	0.40	-	50,50,50,50	0
57	MG	AA	3142	1/1	0.26	-	53,53,53,53	0
57	MG	BA	3481	1/1	0.18	-	35,35,35,35	0
57	MG	BR	202	1/1	0.17	-	49,49,49,49	0
57	MG	BA	3714	1/1	0.10	-	42,42,42,42	0
57	MG	BA	3471	1/1	0.08	-	42,42,42,42	0
57	MG	AA	3058	1/1	0.14	-	48,48,48,48	0
57	MG	AA	3123	1/1	0.09	-	59,59,59,59	0
57	MG	DA	3413	1/1	0.23	-	30,30,30,30	0
57	MG	DA	3175	1/1	0.18	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3326	1/1	0.11	-	40,40,40,40	0
57	MG	DA	3508	1/1	0.10	-	58,58,58,58	0
57	MG	CA	3159	1/1	0.11	-	46,46,46,46	0
57	MG	BU	206	1/1	0.35	-	39,39,39,39	0
57	MG	BA	3183	1/1	0.25	-	50,50,50,50	0
57	MG	AD	303	1/1	0.19	-	60,60,60,60	0
57	MG	BA	3543	1/1	0.10	-	69,69,69,69	0
57	MG	AA	3044	1/1	0.11	-	46,46,46,46	0
57	MG	CA	3136	1/1	0.12	-	68,68,68,68	0
57	MG	BA	3705	1/1	0.30	-	32,32,32,32	0
57	MG	DA	3012	1/1	0.06	-	42,42,42,42	0
57	MG	BA	3039	1/1	0.14	-	27,27,27,27	0
57	MG	BA	3189	1/1	0.18	-	33,33,33,33	0
57	MG	DA	3295	1/1	0.07	-	58,58,58,58	0
57	MG	DA	3341	1/1	0.14	-	32,32,32,32	0
57	MG	DA	3407	1/1	0.23	-	67,67,67,67	0
57	MG	BQ	3005	1/1	0.17	-	39,39,39,39	0
57	MG	CA	3109	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3148	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3699	1/1	0.09	-	33,33,33,33	0
57	MG	DA	3461	1/1	0.13	-	55,55,55,55	0
57	MG	DA	3219	1/1	0.18	-	54,54,54,54	0
57	MG	DA	3283	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3113	1/1	0.22	-	57,57,57,57	0
57	MG	B7	102	1/1	0.36	-	53,53,53,53	0
57	MG	DA	3476	1/1	0.12	-	49,49,49,49	0
57	MG	DB	3003	1/1	0.07	-	76,76,76,76	0
57	MG	BA	3032	1/1	0.21	-	30,30,30,30	0
57	MG	CA	3066	1/1	0.22	-	69,69,69,69	0
57	MG	DA	3550	1/1	0.25	-	63,63,63,63	0
57	MG	AA	3068	1/1	0.12	-	64,64,64,64	0
57	MG	DA	3503	1/1	0.19	-	51,51,51,51	0
57	MG	DA	3270	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3499	1/1	0.23	-	51,51,51,51	0
57	MG	DB	3001	1/1	0.06	-	50,50,50,50	0
57	MG	AA	3140	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3343	1/1	0.15	-	37,37,37,37	0
57	MG	BA	3514	1/1	0.35	-	36,36,36,36	0
57	MG	BA	3314	1/1	0.23	-	42,42,42,42	0
57	MG	BA	3688	1/1	0.32	-	46,46,46,46	0
57	MG	DA	3094	1/1	0.18	-	38,38,38,38	0
57	MG	DA	3098	1/1	0.17	-	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3167	1/1	0.10	-	65,65,65,65	0
57	MG	DA	3616	1/1	0.14	-	28,28,28,28	0
57	MG	BA	3503	1/1	0.10	-	50,50,50,50	0
57	MG	BA	3587	1/1	0.17	-	51,51,51,51	0
57	MG	BA	3224	1/1	0.41	-	48,48,48,48	0
57	MG	BA	3678	1/1	0.14	-	49,49,49,49	0
57	MG	DA	3601	1/1	0.12	-	43,43,43,43	0
57	MG	BA	3036	1/1	0.63	-	42,42,42,42	0
57	MG	DA	3530	1/1	0.12	-	43,43,43,43	0
57	MG	DA	3207	1/1	0.22	-	39,39,39,39	0
57	MG	DA	3573	1/1	0.09	-	49,49,49,49	0
57	MG	DA	3007	1/1	0.09	-	48,48,48,48	0
57	MG	AA	3100	1/1	0.17	-	69,69,69,69	0
57	MG	AA	3004	1/1	0.20	-	61,61,61,61	0
57	MG	BA	3054	1/1	0.20	-	44,44,44,44	0
57	MG	DA	3108	1/1	0.14	-	50,50,50,50	0
57	MG	DA	3532	1/1	0.07	-	43,43,43,43	0
57	MG	BA	3090	1/1	0.20	-	50,50,50,50	0
57	MG	BD	310	1/1	0.50	-	34,34,34,34	0
57	MG	DA	3172	1/1	0.07	-	32,32,32,32	0
57	MG	AA	3155	1/1	0.18	-	65,65,65,65	0
57	MG	CA	3079	1/1	0.13	-	42,42,42,42	0
57	MG	CA	3151	1/1	0.13	-	58,58,58,58	0
57	MG	AA	3125	1/1	0.11	-	60,60,60,60	0
57	MG	BA	3031	1/1	0.11	-	51,51,51,51	0
57	MG	AA	3045	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3692	1/1	0.14	-	64,64,64,64	0
57	MG	AA	3086	1/1	0.12	-	45,45,45,45	0
57	MG	BA	3474	1/1	0.17	-	64,64,64,64	0
57	MG	BA	3668	1/1	0.15	-	39,39,39,39	0
57	MG	BA	3052	1/1	0.21	-	44,44,44,44	0
57	MG	BA	3599	1/1	0.14	-	43,43,43,43	0
57	MG	DD	306	1/1	0.37	-	44,44,44,44	0
57	MG	DA	3085	1/1	0.12	-	27,27,27,27	0
57	MG	AA	3083	1/1	0.28	-	38,38,38,38	0
57	MG	DE	302	1/1	0.59	-	51,51,51,51	0
57	MG	CJ	5001	1/1	0.10	-	51,51,51,51	0
57	MG	BA	3066	1/1	0.16	-	53,53,53,53	0
57	MG	DY	502	1/1	0.10	-	56,56,56,56	0
57	MG	AA	3121	1/1	0.09	-	66,66,66,66	0
57	MG	DA	3008	1/1	0.18	-	26,26,26,26	0
57	MG	DA	3321	1/1	0.13	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3102	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3171	1/1	0.21	-	38,38,38,38	0
57	MG	BA	3016	1/1	0.13	-	35,35,35,35	0
57	MG	BA	3235	1/1	0.18	-	52,52,52,52	0
57	MG	DA	3030	1/1	0.29	-	32,32,32,32	0
57	MG	DA	3055	1/1	0.08	-	35,35,35,35	0
57	MG	BA	3552	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3355	1/1	0.11	-	30,30,30,30	0
57	MG	BA	3204	1/1	0.14	-	61,61,61,61	0
57	MG	DA	3420	1/1	0.09	-	41,41,41,41	0
57	MG	BA	3625	1/1	0.11	-	46,46,46,46	0
57	MG	DA	3174	1/1	0.20	-	38,38,38,38	0
57	MG	DA	3494	1/1	0.17	-	56,56,56,56	0
57	MG	CA	3009	1/1	0.06	-	44,44,44,44	0
57	MG	AA	3187	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3707	1/1	0.40	-	34,34,34,34	0
57	MG	AA	3160	1/1	0.23	-	58,58,58,58	0
57	MG	CA	3022	1/1	0.24	-	55,55,55,55	0
57	MG	D5	101	1/1	0.15	-	42,42,42,42	0
57	MG	CX	3003	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3627	1/1	0.24	-	56,56,56,56	0
57	MG	AA	3195	1/1	0.09	-	58,58,58,58	0
57	MG	BA	3501	1/1	0.08	-	67,67,67,67	0
57	MG	BA	3479	1/1	0.12	-	22,22,22,22	0
57	MG	DA	3358	1/1	0.51	-	45,45,45,45	0
57	MG	BD	301	1/1	0.35	-	37,37,37,37	0
57	MG	DA	3497	1/1	0.17	-	61,61,61,61	0
57	MG	AA	3088	1/1	0.19	-	40,40,40,40	0
57	MG	DA	3345	1/1	0.17	-	28,28,28,28	0
57	MG	DA	3439	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3046	1/1	0.17	-	30,30,30,30	0
57	MG	BA	3135	1/1	0.16	-	48,48,48,48	0
57	MG	DA	3093	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3240	1/1	0.22	-	36,36,36,36	0
57	MG	DA	3053	1/1	0.23	-	50,50,50,50	0
60	K	AX	3001	1/1	0.09	-	39,39,39,39	0
57	MG	DA	3091	1/1	0.22	-	37,37,37,37	0
57	MG	BA	3372	1/1	0.09	-	58,58,58,58	0
57	MG	DA	3549	1/1	0.18	-	47,47,47,47	0
57	MG	BA	3120	1/1	0.28	-	52,52,52,52	0
57	MG	BA	3408	1/1	0.18	-	42,42,42,42	0
57	MG	DA	3223	1/1	0.08	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3389	1/1	0.12	-	57,57,57,57	0
57	MG	AF	3001	1/1	0.21	-	58,58,58,58	0
57	MG	AA	3178	1/1	0.16	-	67,67,67,67	0
57	MG	DA	3395	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3315	1/1	0.10	-	42,42,42,42	0
57	MG	DA	3220	1/1	0.16	-	54,54,54,54	0
57	MG	AA	3003	1/1	0.10	-	53,53,53,53	0
57	MG	BA	3436	1/1	0.20	-	21,21,21,21	0
57	MG	BA	3658	1/1	0.19	-	16,16,16,16	0
57	MG	AA	3161	1/1	0.19	-	28,28,28,28	0
57	MG	BA	3671	1/1	0.16	-	55,55,55,55	0
57	MG	BA	3695	1/1	0.16	-	19,19,19,19	0
57	MG	BA	3407	1/1	0.16	-	29,29,29,29	0
57	MG	BU	202	1/1	0.10	-	45,45,45,45	0
57	MG	BA	3115	1/1	0.40	-	49,49,49,49	0
57	MG	CA	3056	1/1	0.10	-	56,56,56,56	0
57	MG	CA	3106	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3332	1/1	0.20	-	29,29,29,29	0
57	MG	AA	3141	1/1	0.10	-	54,54,54,54	0
57	MG	BA	3381	1/1	0.18	-	30,30,30,30	0
57	MG	BA	3301	1/1	0.20	-	43,43,43,43	0
57	MG	DA	3122	1/1	0.12	-	58,58,58,58	0
57	MG	DA	3531	1/1	0.05	-	40,40,40,40	0
57	MG	BA	3367	1/1	0.05	-	42,42,42,42	0
57	MG	AA	3026	1/1	0.09	-	61,61,61,61	0
57	MG	DA	3308	1/1	0.14	-	52,52,52,52	0
57	MG	DA	3296	1/1	0.16	-	46,46,46,46	0
57	MG	BA	3365	1/1	0.14	-	40,40,40,40	0
57	MG	DA	3089	1/1	0.15	-	36,36,36,36	0
57	MG	DA	3551	1/1	0.08	-	57,57,57,57	0
57	MG	BW	202	1/1	0.51	-	41,41,41,41	0
57	MG	DA	3067	1/1	0.10	-	54,54,54,54	0
57	MG	CA	3117	1/1	0.12	-	100,100,100,100	0
57	MG	BE	3003	1/1	0.16	-	25,25,25,25	0
57	MG	BA	3402	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3478	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3411	1/1	0.20	-	24,24,24,24	0
57	MG	AA	3190	1/1	0.11	-	75,75,75,75	0
57	MG	BA	3531	1/1	0.27	-	20,20,20,20	0
57	MG	BF	308	1/1	0.20	-	46,46,46,46	0
57	MG	BB	3003	1/1	0.17	-	40,40,40,40	0
57	MG	AA	3196	1/1	0.12	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3187	1/1	0.20	-	39,39,39,39	0
57	MG	DA	3190	1/1	0.32	-	52,52,52,52	0
57	MG	BO	5001	1/1	0.13	-	49,49,49,49	0
57	MG	DA	3101	1/1	0.43	-	45,45,45,45	0
59	ZN	AN	501	1/1	0.12	-	71,71,71,71	0
57	MG	BA	3096	1/1	0.16	-	39,39,39,39	0
59	ZN	BY	202	1/1	0.11	-	70,70,70,70	0
57	MG	DQ	3001	1/1	0.10	-	58,58,58,58	0
57	MG	BA	3109	1/1	0.12	-	53,53,53,53	0
57	MG	BA	3070	1/1	0.24	-	44,44,44,44	0
57	MG	DA	3303	1/1	0.19	-	57,57,57,57	0
57	MG	DA	3090	1/1	0.17	-	52,52,52,52	0
57	MG	DA	3472	1/1	0.17	-	24,24,24,24	0
57	MG	DA	3051	1/1	0.08	-	54,54,54,54	0
57	MG	DA	3115	1/1	0.12	-	58,58,58,58	0
57	MG	DA	3590	1/1	0.08	-	58,58,58,58	0
57	MG	DA	3014	1/1	0.12	-	45,45,45,45	0
57	MG	CA	3070	1/1	0.27	-	42,42,42,42	0
57	MG	DA	3507	1/1	0.20	-	33,33,33,33	0
57	MG	DD	304	1/1	0.13	-	40,40,40,40	0
57	MG	DD	301	1/1	0.17	-	31,31,31,31	0
57	MG	BA	3262	1/1	0.24	-	38,38,38,38	0
57	MG	BA	3147	1/1	0.21	-	34,34,34,34	0
57	MG	DA	3460	1/1	0.10	-	57,57,57,57	0
57	MG	BA	3551	1/1	0.22	-	17,17,17,17	0
57	MG	BA	3502	1/1	0.24	-	57,57,57,57	0
57	MG	BA	3163	1/1	0.25	-	43,43,43,43	0
57	MG	BA	3713	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3363	1/1	0.18	-	35,35,35,35	0
57	MG	BU	207	1/1	0.15	-	23,23,23,23	0
58	SF4	CD	501	8/8	0.12	-	59,71,83,91	0
57	MG	DA	3589	1/1	0.10	-	52,52,52,52	0
57	MG	DV	202	1/1	0.63	-	75,75,75,75	0
57	MG	BA	3077	1/1	0.12	-	33,33,33,33	0
57	MG	BA	3690	1/1	0.12	-	49,49,49,49	0
57	MG	DA	3226	1/1	0.16	-	54,54,54,54	0
57	MG	BA	3075	1/1	0.28	-	45,45,45,45	0
57	MG	DA	3043	1/1	0.14	-	44,44,44,44	0
57	MG	BA	3284	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3614	1/1	0.10	-	64,64,64,64	0
57	MG	BA	3017	1/1	0.22	-	48,48,48,48	0
57	MG	BA	3409	1/1	0.25	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3026	1/1	0.09	-	41,41,41,41	0
57	MG	DA	3372	1/1	0.09	-	49,49,49,49	0
57	MG	BA	3340	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3582	1/1	0.15	-	24,24,24,24	0
57	MG	DA	3241	1/1	0.15	-	40,40,40,40	0
57	MG	AA	3072	1/1	0.10	-	65,65,65,65	0
57	MG	BA	3636	1/1	0.28	-	45,45,45,45	0
57	MG	DR	3002	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3442	1/1	0.24	-	34,34,34,34	0
57	MG	BA	3529	1/1	0.29	-	29,29,29,29	0
57	MG	DA	3346	1/1	0.10	-	39,39,39,39	0
57	MG	AA	3112	1/1	0.13	-	44,44,44,44	0
57	MG	BA	3515	1/1	0.15	-	44,44,44,44	0
57	MG	DA	3561	1/1	0.16	-	51,51,51,51	0
57	MG	BA	3380	1/1	0.17	-	55,55,55,55	0
57	MG	AA	3201	1/1	0.06	-	68,68,68,68	0
57	MG	DA	3541	1/1	0.09	-	40,40,40,40	0
57	MG	BA	3058	1/1	0.19	-	24,24,24,24	0
57	MG	DA	3102	1/1	0.13	-	64,64,64,64	0
57	MG	AK	3001	1/1	0.12	-	55,55,55,55	0
57	MG	BA	3687	1/1	0.13	-	30,30,30,30	0
57	MG	CA	3063	1/1	0.10	-	59,59,59,59	0
57	MG	DA	3103	1/1	0.47	-	55,55,55,55	0
57	MG	CA	3077	1/1	0.14	-	63,63,63,63	0
57	MG	AA	3180	1/1	0.21	-	61,61,61,61	0
57	MG	BA	3368	1/1	0.32	-	26,26,26,26	0
57	MG	CA	3104	1/1	0.17	-	37,37,37,37	0
57	MG	DA	3504	1/1	0.19	-	46,46,46,46	0
57	MG	AA	3206	1/1	0.06	-	62,62,62,62	0
57	MG	AA	3056	1/1	0.24	-	66,66,66,66	0
57	MG	AA	3157	1/1	0.12	-	38,38,38,38	0
57	MG	BA	3230	1/1	0.31	-	45,45,45,45	0
57	MG	DA	3235	1/1	0.26	-	48,48,48,48	0
57	MG	BA	3104	1/1	0.18	-	54,54,54,54	0
57	MG	DA	3410	1/1	0.22	-	37,37,37,37	0
57	MG	DN	5001	1/1	0.06	-	53,53,53,53	0
57	MG	DA	3512	1/1	0.10	-	24,24,24,24	0
57	MG	DA	3137	1/1	0.21	-	48,48,48,48	0
57	MG	DB	3009	1/1	0.20	-	55,55,55,55	0
57	MG	DA	3162	1/1	0.46	-	58,58,58,58	0
57	MG	BA	3181	1/1	0.23	-	49,49,49,49	0
57	MG	BA	3206	1/1	0.11	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3064	1/1	0.12	-	38,38,38,38	0
57	MG	BA	3567	1/1	0.17	-	55,55,55,55	0
57	MG	DA	3019	1/1	0.16	-	54,54,54,54	0
57	MG	AN	502	1/1	0.15	-	61,61,61,61	0
57	MG	DA	3433	1/1	0.19	-	27,27,27,27	0
57	MG	DA	3585	1/1	0.22	-	45,45,45,45	0
57	MG	BF	307	1/1	0.35	-	25,25,25,25	0
57	MG	AA	3119	1/1	0.10	-	50,50,50,50	0
57	MG	DA	3481	1/1	0.11	-	69,69,69,69	0
57	MG	DA	3353	1/1	0.12	-	42,42,42,42	0
57	MG	CA	3146	1/1	0.16	-	74,74,74,74	0
57	MG	BA	3033	1/1	0.15	-	39,39,39,39	0
57	MG	BA	3548	1/1	0.18	-	54,54,54,54	0
57	MG	BA	3245	1/1	0.28	-	37,37,37,37	0
57	MG	DA	3217	1/1	0.32	-	50,50,50,50	0
57	MG	CA	3015	1/1	0.10	-	61,61,61,61	0
57	MG	BA	3194	1/1	0.18	-	42,42,42,42	0
57	MG	DA	3092	1/1	0.08	-	29,29,29,29	0
57	MG	BA	3598	1/1	0.23	-	54,54,54,54	0
57	MG	DA	3449	1/1	0.08	-	52,52,52,52	0
57	MG	BA	3283	1/1	0.21	-	22,22,22,22	0
57	MG	AA	3065	1/1	0.09	-	48,48,48,48	0
57	MG	AA	3090	1/1	0.15	-	70,70,70,70	0
57	MG	AA	3066	1/1	0.09	-	66,66,66,66	0
57	MG	CA	3048	1/1	0.15	-	48,48,48,48	0
57	MG	DA	3253	1/1	0.20	-	34,34,34,34	0
57	MG	CA	3023	1/1	0.13	-	88,88,88,88	0
57	MG	AA	3019	1/1	0.13	-	52,52,52,52	0
57	MG	BP	3003	1/1	0.15	-	42,42,42,42	0
57	MG	BA	3190	1/1	0.20	-	24,24,24,24	0
57	MG	BA	3568	1/1	0.21	-	43,43,43,43	0
57	MG	DA	3148	1/1	0.17	-	45,45,45,45	0
57	MG	DA	3491	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3638	1/1	0.08	-	41,41,41,41	0
57	MG	DA	3020	1/1	0.16	-	32,32,32,32	0
57	MG	DA	3606	1/1	0.18	-	54,54,54,54	0
57	MG	AA	3051	1/1	0.25	-	51,51,51,51	0
57	MG	DA	3028	1/1	0.12	-	52,52,52,52	0
57	MG	DA	3081	1/1	0.25	-	45,45,45,45	0
57	MG	BA	3641	1/1	0.14	-	33,33,33,33	0
57	MG	BA	3246	1/1	0.24	-	46,46,46,46	0
57	MG	BA	3184	1/1	0.26	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3010	1/1	0.16	-	56,56,56,56	0
57	MG	DA	3045	1/1	0.11	-	39,39,39,39	0
57	MG	AA	3053	1/1	0.16	-	54,54,54,54	0
57	MG	AA	3193	1/1	0.30	-	77,77,77,77	0
57	MG	BA	3628	1/1	0.18	-	60,60,60,60	0
57	MG	AA	3115	1/1	0.30	-	38,38,38,38	0
57	MG	DA	3404	1/1	0.07	-	48,48,48,48	0
57	MG	BA	3689	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3176	1/1	0.15	-	42,42,42,42	0
57	MG	CA	3050	1/1	0.11	-	56,56,56,56	0
57	MG	BA	3082	1/1	0.15	-	57,57,57,57	0
57	MG	BA	3539	1/1	0.20	-	18,18,18,18	0
57	MG	BA	3259	1/1	0.26	-	40,40,40,40	0
57	MG	BZ	3001	1/1	0.23	-	56,56,56,56	0
57	MG	DA	3161	1/1	0.18	-	35,35,35,35	0
57	MG	BU	205	1/1	0.14	-	32,32,32,32	0
57	MG	AA	3108	1/1	0.21	-	54,54,54,54	0
57	MG	DA	3362	1/1	0.24	-	48,48,48,48	0
57	MG	BA	3504	1/1	0.23	-	33,33,33,33	0
57	MG	BA	3339	1/1	0.35	-	52,52,52,52	0
57	MG	BA	3382	1/1	0.17	-	31,31,31,31	0
59	ZN	D4	501	1/1	0.14	-	154,154,154,154	0
57	MG	DA	3276	1/1	0.13	-	56,56,56,56	0
57	MG	AA	3171	1/1	0.19	-	45,45,45,45	0
57	MG	BA	3121	1/1	0.22	-	48,48,48,48	0
57	MG	BA	3216	1/1	0.16	-	35,35,35,35	0
57	MG	DA	3537	1/1	0.20	-	45,45,45,45	0
57	MG	BA	3123	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3109	1/1	0.36	-	45,45,45,45	0
57	MG	DA	3144	1/1	0.08	-	48,48,48,48	0
57	MG	BE	3005	1/1	0.15	-	15,15,15,15	0
57	MG	BA	3048	1/1	0.12	-	44,44,44,44	0
57	MG	BA	3378	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3088	1/1	0.40	-	59,59,59,59	0
57	MG	BA	3452	1/1	0.15	-	15,15,15,15	0
57	MG	CA	3012	1/1	0.32	-	45,45,45,45	0
57	MG	DA	3034	1/1	0.22	-	46,46,46,46	0
57	MG	DA	3169	1/1	0.16	-	45,45,45,45	0
57	MG	AA	3124	1/1	0.17	-	58,58,58,58	0
57	MG	AA	3036	1/1	0.11	-	51,51,51,51	0
57	MG	AA	3095	1/1	0.11	-	44,44,44,44	0
57	MG	AA	3148	1/1	0.13	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3185	1/1	0.24	-	57,57,57,57	0
57	MG	BA	3535	1/1	0.23	-	29,29,29,29	0
57	MG	CA	3004	1/1	0.22	-	70,70,70,70	0
57	MG	DA	3367	1/1	0.14	-	24,24,24,24	0
57	MG	AA	3067	1/1	0.11	-	47,47,47,47	0
57	MG	BA	3584	1/1	0.09	-	59,59,59,59	0
57	MG	BA	3061	1/1	0.09	-	58,58,58,58	0
57	MG	DA	3013	1/1	0.16	-	43,43,43,43	0
57	MG	BA	3375	1/1	0.20	-	46,46,46,46	0
57	MG	DA	3340	1/1	0.16	-	38,38,38,38	0
57	MG	BA	3149	1/1	0.16	-	40,40,40,40	0
57	MG	DA	3539	1/1	0.20	-	52,52,52,52	0
57	MG	DA	3571	1/1	0.18	-	54,54,54,54	0
57	MG	BA	3373	1/1	0.20	-	46,46,46,46	0
57	MG	DA	3437	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3391	1/1	0.23	-	30,30,30,30	0
57	MG	BA	3419	1/1	0.21	-	58,58,58,58	0
57	MG	BA	3352	1/1	0.14	-	29,29,29,29	0
57	MG	B0	103	1/1	0.11	-	38,38,38,38	0
57	MG	BA	3111	1/1	0.26	-	51,51,51,51	0
57	MG	BA	3350	1/1	0.14	-	43,43,43,43	0
57	MG	DA	3496	1/1	0.17	-	63,63,63,63	0
57	MG	BA	3440	1/1	0.20	-	40,40,40,40	0
57	MG	BA	3146	1/1	0.17	-	47,47,47,47	0
57	MG	BA	3252	1/1	0.20	-	30,30,30,30	0
57	MG	CA	3115	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3463	1/1	0.09	-	54,54,54,54	0
57	MG	BA	3637	1/1	0.11	-	40,40,40,40	0
57	MG	DA	3254	1/1	0.25	-	42,42,42,42	0
57	MG	BA	3719	1/1	0.07	-	53,53,53,53	0
57	MG	BA	3682	1/1	0.19	-	30,30,30,30	0
57	MG	DA	3039	1/1	0.36	-	48,48,48,48	0
57	MG	BA	3322	1/1	0.16	-	40,40,40,40	0
57	MG	BA	3453	1/1	0.11	-	47,47,47,47	0
57	MG	DA	3516	1/1	0.05	-	43,43,43,43	0
57	MG	AA	3082	1/1	0.13	-	55,55,55,55	0
57	MG	DB	3005	1/1	0.18	-	54,54,54,54	0
57	MG	DA	3257	1/1	0.32	-	46,46,46,46	0
57	MG	BA	3459	1/1	0.25	-	44,44,44,44	0
57	MG	AA	3176	1/1	0.08	-	43,43,43,43	0
57	MG	BW	204	1/1	0.23	-	27,27,27,27	0
57	MG	BA	3512	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
57	MG	B9	502	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3078	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3003	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3577	1/1	0.23	-	35,35,35,35	0
57	MG	DA	3529	1/1	0.09	-	43,43,43,43	0
57	MG	DA	3178	1/1	0.17	-	39,39,39,39	0
57	MG	DA	3535	1/1	0.22	-	21,21,21,21	0
57	MG	CA	3148	1/1	0.16	-	81,81,81,81	0
57	MG	CA	3082	1/1	0.15	-	71,71,71,71	0
57	MG	CA	3029	1/1	0.14	-	48,48,48,48	0
57	MG	BA	3023	1/1	0.14	-	25,25,25,25	0
57	MG	BV	204	1/1	0.08	-	36,36,36,36	0
57	MG	CA	3064	1/1	0.15	-	64,64,64,64	0
57	MG	BA	3083	1/1	0.17	-	33,33,33,33	0
57	MG	DA	3153	1/1	0.14	-	34,34,34,34	0
57	MG	AA	3017	1/1	0.16	-	63,63,63,63	0
57	MG	BA	3256	1/1	0.08	-	36,36,36,36	0
57	MG	DA	3155	1/1	0.16	-	34,34,34,34	0
57	MG	AA	3034	1/1	0.06	-	47,47,47,47	0
57	MG	AA	3144	1/1	0.24	-	44,44,44,44	0
57	MG	BA	3187	1/1	0.13	-	35,35,35,35	0
57	MG	CA	3144	1/1	0.16	-	58,58,58,58	0
57	MG	CA	3055	1/1	0.12	-	66,66,66,66	0
57	MG	BA	3455	1/1	0.16	-	44,44,44,44	0
57	MG	CA	3031	1/1	0.09	-	55,55,55,55	0
57	MG	DA	3306	1/1	0.09	-	31,31,31,31	0
57	MG	AA	3079	1/1	0.05	-	62,62,62,62	0
57	MG	DA	3587	1/1	0.19	-	35,35,35,35	0
57	MG	BA	3237	1/1	0.16	-	36,36,36,36	0
57	MG	BA	3469	1/1	0.17	-	42,42,42,42	0
57	MG	BF	304	1/1	0.25	-	35,35,35,35	0
57	MG	DA	3003	1/1	0.15	-	56,56,56,56	0
57	MG	BA	3312	1/1	0.17	-	44,44,44,44	0
57	MG	DA	3369	1/1	0.25	-	36,36,36,36	0
57	MG	DA	3251	1/1	0.27	-	34,34,34,34	0
57	MG	DA	3625	1/1	0.24	-	57,57,57,57	0
57	MG	DA	3505	1/1	0.07	-	41,41,41,41	0
57	MG	DA	3324	1/1	0.21	-	42,42,42,42	0
57	MG	DA	3469	1/1	0.28	-	41,41,41,41	0
57	MG	DA	3192	1/1	0.20	-	31,31,31,31	0
57	MG	DA	3617	1/1	0.16	-	40,40,40,40	0
57	MG	BN	3001	1/1	0.52	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3062	1/1	0.22	-	52,52,52,52	0
57	MG	CA	3002	1/1	0.13	-	66,66,66,66	0
57	MG	BA	3706	1/1	0.27	-	27,27,27,27	0
57	MG	BA	3271	1/1	0.31	-	45,45,45,45	0
57	MG	BA	3320	1/1	0.11	-	56,56,56,56	0
57	MG	DA	3547	1/1	0.21	-	68,68,68,68	0
57	MG	DA	3163	1/1	0.19	-	43,43,43,43	0
57	MG	AA	3204	1/1	0.21	-	64,64,64,64	0
57	MG	BA	3035	1/1	0.20	-	28,28,28,28	0
57	MG	AA	3179	1/1	0.06	-	56,56,56,56	0
57	MG	DA	3119	1/1	0.17	-	52,52,52,52	0
57	MG	AA	3064	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3621	1/1	0.14	-	18,18,18,18	0
57	MG	DA	3209	1/1	0.16	-	53,53,53,53	0
57	MG	DA	3215	1/1	0.15	-	35,35,35,35	0
57	MG	DA	3513	1/1	0.13	-	49,49,49,49	0
57	MG	AA	3197	1/1	0.14	-	50,50,50,50	0
57	MG	BA	3288	1/1	0.16	-	37,37,37,37	0
57	MG	BA	3607	1/1	0.19	-	41,41,41,41	0
57	MG	BA	3523	1/1	0.13	-	31,31,31,31	0
57	MG	DA	3281	1/1	0.12	-	37,37,37,37	0
57	MG	BA	3505	1/1	0.19	-	16,16,16,16	0
57	MG	DA	3574	1/1	0.13	-	59,59,59,59	0
57	MG	BA	3432	1/1	0.25	-	35,35,35,35	0
57	MG	BA	3703	1/1	0.08	-	47,47,47,47	0
57	MG	BA	3089	1/1	0.12	-	30,30,30,30	0
57	MG	BA	3346	1/1	0.20	-	29,29,29,29	0
57	MG	DA	3603	1/1	0.09	-	40,40,40,40	0
57	MG	BA	3698	1/1	0.32	-	51,51,51,51	0
57	MG	DA	3525	1/1	0.09	-	40,40,40,40	0
57	MG	AA	3128	1/1	0.20	-	53,53,53,53	0
57	MG	BA	3191	1/1	0.06	-	22,22,22,22	0
57	MG	BA	3643	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3541	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3632	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3042	1/1	0.14	-	34,34,34,34	0
57	MG	DA	3022	1/1	0.09	-	27,27,27,27	0
57	MG	DA	3619	1/1	0.47	-	63,63,63,63	0
57	MG	AA	3177	1/1	0.15	-	66,66,66,66	0
57	MG	AA	3023	1/1	0.07	-	60,60,60,60	0
57	MG	BA	3456	1/1	0.11	-	44,44,44,44	0
57	MG	DA	3342	1/1	0.15	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3006	1/1	0.18	-	38,38,38,38	0
57	MG	BA	3401	1/1	0.26	-	31,31,31,31	0
57	MG	BA	3024	1/1	0.17	-	42,42,42,42	0
57	MG	BA	3074	1/1	0.12	-	43,43,43,43	0
57	MG	DA	3495	1/1	0.11	-	48,48,48,48	0
57	MG	CA	3013	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3026	1/1	0.23	-	36,36,36,36	0
57	MG	BB	3020	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3137	1/1	0.17	-	57,57,57,57	0
57	MG	BD	309	1/1	0.26	-	33,33,33,33	0
57	MG	DA	3316	1/1	0.12	-	39,39,39,39	0
57	MG	DA	3010	1/1	0.18	-	51,51,51,51	0
57	MG	BA	3180	1/1	0.24	-	32,32,32,32	0
57	MG	BA	3392	1/1	0.17	-	27,27,27,27	0
57	MG	BA	3069	1/1	0.18	-	48,48,48,48	0
57	MG	DA	3087	1/1	0.14	-	65,65,65,65	0
57	MG	DE	301	1/1	0.09	-	52,52,52,52	0
57	MG	AA	3166	1/1	0.19	-	70,70,70,70	0
57	MG	DA	3464	1/1	0.13	-	51,51,51,51	0
57	MG	BD	304	1/1	0.15	-	36,36,36,36	0
57	MG	BA	3376	1/1	0.18	-	21,21,21,21	0
57	MG	DA	3160	1/1	0.11	-	65,65,65,65	0
57	MG	BA	3672	1/1	0.11	-	28,28,28,28	0
57	MG	DA	3352	1/1	0.23	-	25,25,25,25	0
57	MG	DA	3184	1/1	0.09	-	44,44,44,44	0
57	MG	BA	3044	1/1	0.12	-	40,40,40,40	0
57	MG	BA	3588	1/1	0.16	-	19,19,19,19	0
57	MG	BA	3477	1/1	0.11	-	19,19,19,19	0
57	MG	BA	3207	1/1	0.15	-	55,55,55,55	0
57	MG	DA	3368	1/1	0.09	-	58,58,58,58	0
57	MG	DA	3006	1/1	0.10	-	40,40,40,40	0
57	MG	BA	3633	1/1	0.11	-	54,54,54,54	0
57	MG	AX	3011	1/1	0.32	-	73,73,73,73	0
57	MG	BA	3211	1/1	0.13	-	50,50,50,50	0
57	MG	BA	3261	1/1	0.18	-	52,52,52,52	0
57	MG	BA	3693	1/1	0.14	-	48,48,48,48	0
57	MG	BA	3338	1/1	0.08	-	50,50,50,50	0
57	MG	BA	3691	1/1	0.28	-	54,54,54,54	0
57	MG	BA	3151	1/1	0.12	-	42,42,42,42	0
57	MG	BD	306	1/1	0.27	-	30,30,30,30	0
57	MG	BB	3009	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3409	1/1	0.06	-	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3043	1/1	0.16	-	44,44,44,44	0
57	MG	DV	201	1/1	0.32	-	49,49,49,49	0
57	MG	BA	3258	1/1	0.21	-	35,35,35,35	0
57	MG	BA	3144	1/1	0.18	-	42,42,42,42	0
57	MG	BA	3715	1/1	0.12	-	33,33,33,33	0
57	MG	AA	3039	1/1	0.25	-	62,62,62,62	0
57	MG	DA	3351	1/1	0.32	-	45,45,45,45	0
57	MG	DA	3379	1/1	0.12	-	37,37,37,37	0
57	MG	AA	3169	1/1	0.14	-	48,48,48,48	0
57	MG	DA	3025	1/1	0.19	-	35,35,35,35	0
57	MG	AA	3194	1/1	0.19	-	41,41,41,41	0
57	MG	BA	3518	1/1	0.20	-	48,48,48,48	0
57	MG	BA	3030	1/1	0.11	-	44,44,44,44	0
57	MG	AA	3028	1/1	0.13	-	58,58,58,58	0
57	MG	BA	3544	1/1	0.16	-	52,52,52,52	0
57	MG	CA	3060	1/1	0.15	-	78,78,78,78	0
57	MG	BA	3415	1/1	0.19	-	61,61,61,61	0
57	MG	BA	3154	1/1	0.20	-	36,36,36,36	0
57	MG	B1	101	1/1	0.44	-	37,37,37,37	0
57	MG	DA	3231	1/1	0.25	-	33,33,33,33	0
57	MG	BA	3027	1/1	1.05	-	36,36,36,36	0
57	MG	BA	3202	1/1	0.17	-	42,42,42,42	0
57	MG	CA	3152	1/1	0.15	-	66,66,66,66	0
57	MG	BA	3156	1/1	0.16	-	43,43,43,43	0
57	MG	BB	3011	1/1	0.09	-	40,40,40,40	0
57	MG	DA	3194	1/1	0.25	-	43,43,43,43	0
57	MG	BA	3072	1/1	0.10	-	32,32,32,32	0
57	MG	BA	3635	1/1	0.10	-	59,59,59,59	0
57	MG	BA	3170	1/1	0.22	-	41,41,41,41	0
57	MG	BA	3103	1/1	0.38	-	62,62,62,62	0
57	MG	DA	3594	1/1	0.13	-	51,51,51,51	0
57	MG	BA	3428	1/1	0.15	-	54,54,54,54	0
57	MG	BA	3218	1/1	0.54	-	52,52,52,52	0
57	MG	DA	3545	1/1	0.16	-	70,70,70,70	0
57	MG	DA	3229	1/1	0.17	-	39,39,39,39	0
57	MG	DA	3150	1/1	0.29	-	41,41,41,41	0
57	MG	BA	3186	1/1	0.19	-	42,42,42,42	0
57	MG	AA	3012	1/1	0.20	-	61,61,61,61	0
57	MG	BA	3076	1/1	0.23	-	34,34,34,34	0
57	MG	DA	3255	1/1	0.28	-	34,34,34,34	0
57	MG	DA	3458	1/1	0.09	-	44,44,44,44	0
57	MG	DU	3002	1/1	0.37	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3601	1/1	0.18	-	69,69,69,69	0
57	MG	BA	3178	1/1	0.20	-	52,52,52,52	0
57	MG	BA	3470	1/1	0.13	-	69,69,69,69	0
57	MG	BA	3143	1/1	0.16	-	41,41,41,41	0
57	MG	BF	306	1/1	0.07	-	43,43,43,43	0
57	MG	BA	3253	1/1	0.22	-	28,28,28,28	0
57	MG	DA	3129	1/1	0.11	-	41,41,41,41	0
57	MG	BA	3513	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3251	1/1	0.24	-	48,48,48,48	0
57	MG	BA	3597	1/1	0.27	-	56,56,56,56	0
57	MG	BA	3106	1/1	0.22	-	24,24,24,24	0
57	MG	DA	3272	1/1	0.07	-	29,29,29,29	0
57	MG	BA	3663	1/1	0.17	-	36,36,36,36	0
57	MG	BA	3417	1/1	0.15	-	49,49,49,49	0
57	MG	DP	202	1/1	0.35	-	48,48,48,48	0
57	MG	DA	3596	1/1	0.27	-	71,71,71,71	0
57	MG	CA	3046	1/1	0.20	-	53,53,53,53	0
57	MG	BA	3140	1/1	0.17	-	26,26,26,26	0
57	MG	AA	3146	1/1	0.13	-	81,81,81,81	0
57	MG	CA	3149	1/1	0.10	-	49,49,49,49	0
57	MG	BB	3007	1/1	0.09	-	51,51,51,51	0
57	MG	CA	3085	1/1	0.30	-	71,71,71,71	0
57	MG	DA	3149	1/1	0.16	-	42,42,42,42	0
57	MG	DA	3510	1/1	0.13	-	52,52,52,52	0
57	MG	DA	3486	1/1	0.20	-	37,37,37,37	0
57	MG	BA	3610	1/1	0.22	-	60,60,60,60	0
57	MG	BA	3300	1/1	0.11	-	55,55,55,55	0
57	MG	BA	3533	1/1	0.27	-	45,45,45,45	0
57	MG	AA	3202	1/1	0.05	-	60,60,60,60	0
57	MG	DA	3501	1/1	0.20	-	47,47,47,47	0
57	MG	DA	3432	1/1	0.11	-	33,33,33,33	0
57	MG	CA	3067	1/1	0.13	-	45,45,45,45	0
57	MG	BA	3467	1/1	0.23	-	51,51,51,51	0
57	MG	DA	3470	1/1	0.13	-	34,34,34,34	0
57	MG	DA	3104	1/1	0.25	-	47,47,47,47	0
57	MG	DA	3604	1/1	0.15	-	61,61,61,61	0
57	MG	DQ	3002	1/1	0.14	-	45,45,45,45	0
57	MG	DA	3195	1/1	0.20	-	42,42,42,42	0
57	MG	AA	3199	1/1	0.14	-	58,58,58,58	0
57	MG	BA	3498	1/1	0.25	-	45,45,45,45	0
57	MG	AA	3189	1/1	0.12	-	69,69,69,69	0
57	MG	BA	3177	1/1	0.20	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	BQ	3001	1/1	0.33	-	51,51,51,51	0
57	MG	BA	3331	1/1	0.24	-	39,39,39,39	0
57	MG	AA	3077	1/1	0.20	-	52,52,52,52	0
57	MG	BA	3126	1/1	0.24	-	34,34,34,34	0
57	MG	DA	3466	1/1	0.21	-	41,41,41,41	0
57	MG	AA	3149	1/1	0.14	-	48,48,48,48	0
57	MG	DA	3064	1/1	0.24	-	52,52,52,52	0
57	MG	CA	3038	1/1	0.13	-	68,68,68,68	0
57	MG	BA	3581	1/1	0.08	-	55,55,55,55	0
57	MG	BA	3005	1/1	0.24	-	44,44,44,44	0
57	MG	BA	3037	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3107	1/1	0.19	-	39,39,39,39	0
57	MG	BA	3160	1/1	0.20	-	23,23,23,23	0
57	MG	DA	3205	1/1	0.11	-	52,52,52,52	0
57	MG	DA	3567	1/1	0.10	-	49,49,49,49	0
57	MG	DA	3376	1/1	0.25	-	40,40,40,40	0
57	MG	AA	3139	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3419	1/1	0.18	-	37,37,37,37	0
57	MG	DF	3004	1/1	0.25	-	56,56,56,56	0
57	MG	DA	3041	1/1	0.17	-	36,36,36,36	0
57	MG	BA	3595	1/1	0.20	-	52,52,52,52	0
57	MG	AA	3054	1/1	0.19	-	62,62,62,62	0
57	MG	BR	201	1/1	0.23	-	30,30,30,30	0
57	MG	BA	3060	1/1	0.24	-	59,59,59,59	0
57	MG	B0	104	1/1	0.05	-	49,49,49,49	0
57	MG	BA	3457	1/1	0.08	-	41,41,41,41	0
57	MG	AA	3133	1/1	0.16	-	59,59,59,59	0
57	MG	DA	3518	1/1	0.07	-	42,42,42,42	0
57	MG	BA	3351	1/1	0.10	-	62,62,62,62	0
57	MG	DA	3286	1/1	0.26	-	45,45,45,45	0
57	MG	AA	3131	1/1	0.17	-	56,56,56,56	0
57	MG	BA	3549	1/1	0.15	-	55,55,55,55	0
57	MG	BA	3287	1/1	0.23	-	42,42,42,42	0
57	MG	DA	3105	1/1	0.23	-	37,37,37,37	0
57	MG	BA	3466	1/1	0.23	-	57,57,57,57	0
57	MG	AA	3059	1/1	0.30	-	61,61,61,61	0
57	MG	DA	3527	1/1	0.26	-	52,52,52,52	0
57	MG	BA	3571	1/1	0.18	-	24,24,24,24	0
57	MG	CA	3101	1/1	0.13	-	41,41,41,41	0
57	MG	BA	3497	1/1	0.17	-	41,41,41,41	0
57	MG	DA	3018	1/1	0.27	-	51,51,51,51	0
57	MG	DA	3165	1/1	0.14	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3080	1/1	0.15	-	61,61,61,61	0
57	MG	AA	3116	1/1	0.20	-	41,41,41,41	0
57	MG	BA	3631	1/1	0.09	-	53,53,53,53	0
57	MG	D8	102	1/1	0.19	-	63,63,63,63	0
57	MG	DF	3001	1/1	0.12	-	36,36,36,36	0
57	MG	CA	3086	1/1	0.13	-	56,56,56,56	0
57	MG	DA	3602	1/1	0.27	-	50,50,50,50	0
57	MG	AA	3110	1/1	0.20	-	52,52,52,52	0
57	MG	BA	3155	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3233	1/1	0.31	-	55,55,55,55	0
57	MG	BA	3538	1/1	0.15	-	25,25,25,25	0
57	MG	BA	3507	1/1	0.17	-	48,48,48,48	0
57	MG	BA	3097	1/1	0.21	-	44,44,44,44	0
57	MG	BA	3199	1/1	0.22	-	60,60,60,60	0
57	MG	BA	3718	1/1	0.17	-	36,36,36,36	0
57	MG	DA	3519	1/1	0.16	-	60,60,60,60	0
57	MG	BA	3162	1/1	0.24	-	39,39,39,39	0
57	MG	AA	3106	1/1	0.07	-	53,53,53,53	0
57	MG	DA	3320	1/1	0.10	-	19,19,19,19	0
57	MG	DB	3010	1/1	0.17	-	55,55,55,55	0
57	MG	AA	3060	1/1	0.27	-	49,49,49,49	0
57	MG	DA	3177	1/1	0.31	-	29,29,29,29	0
57	MG	DA	3374	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3314	1/1	0.12	-	56,56,56,56	0
57	MG	AA	3104	1/1	0.14	-	47,47,47,47	0
57	MG	DA	3069	1/1	0.45	-	59,59,59,59	0
57	MG	DA	3457	1/1	0.20	-	45,45,45,45	0
57	MG	BA	3490	1/1	0.28	-	17,17,17,17	0
57	MG	BA	3366	1/1	0.20	-	38,38,38,38	0
57	MG	BF	302	1/1	0.15	-	59,59,59,59	0
57	MG	DA	3412	1/1	0.09	-	60,60,60,60	0
57	MG	CA	3131	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3517	1/1	0.12	-	20,20,20,20	0
57	MG	BB	3010	1/1	0.14	-	28,28,28,28	0
57	MG	DA	3179	1/1	0.20	-	50,50,50,50	0
57	MG	BA	3446	1/1	0.08	-	49,49,49,49	0
57	MG	BA	3377	1/1	0.23	-	58,58,58,58	0
57	MG	DA	3520	1/1	0.21	-	51,51,51,51	0
57	MG	BA	3068	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3448	1/1	0.23	-	36,36,36,36	0
57	MG	BY	201	1/1	0.18	-	51,51,51,51	0
57	MG	CA	3065	1/1	0.07	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3542	1/1	0.07	-	44,44,44,44	0
57	MG	BA	3482	1/1	0.13	-	56,56,56,56	0
57	MG	AA	3203	1/1	0.09	-	42,42,42,42	0
57	MG	CA	3112	1/1	0.09	-	31,31,31,31	0
57	MG	CA	3059	1/1	0.13	-	60,60,60,60	0
57	MG	DA	3154	1/1	0.17	-	40,40,40,40	0
57	MG	DA	3357	1/1	0.18	-	29,29,29,29	0
57	MG	BR	203	1/1	0.31	-	31,31,31,31	0
57	MG	BN	3004	1/1	0.61	-	49,49,49,49	0
57	MG	BB	3004	1/1	0.10	-	43,43,43,43	0
57	MG	AA	3043	1/1	0.25	-	59,59,59,59	0
57	MG	AA	3154	1/1	0.20	-	46,46,46,46	0
57	MG	BA	3053	1/1	0.22	-	33,33,33,33	0
57	MG	BA	3434	1/1	0.19	-	27,27,27,27	0
57	MG	BA	3296	1/1	0.23	-	31,31,31,31	0
57	MG	BE	3004	1/1	0.09	-	49,49,49,49	0
57	MG	BB	3005	1/1	0.17	-	42,42,42,42	0
57	MG	BA	3203	1/1	0.22	-	56,56,56,56	0
57	MG	DA	3429	1/1	0.15	-	38,38,38,38	0
57	MG	BD	303	1/1	0.29	-	42,42,42,42	0
57	MG	DA	3042	1/1	0.27	-	37,37,37,37	0
57	MG	BX	101	1/1	0.26	-	36,36,36,36	0
57	MG	CA	3137	1/1	0.16	-	81,81,81,81	0
57	MG	DA	3073	1/1	0.17	-	49,49,49,49	0
57	MG	AA	3055	1/1	0.31	-	53,53,53,53	0
57	MG	AA	3042	1/1	0.13	-	52,52,52,52	0
57	MG	BA	3325	1/1	0.10	-	38,38,38,38	0
57	MG	AA	3024	1/1	0.22	-	49,49,49,49	0
57	MG	BA	3387	1/1	0.15	-	29,29,29,29	0
57	MG	DA	3479	1/1	0.16	-	45,45,45,45	0
57	MG	BA	3681	1/1	0.16	-	42,42,42,42	0
57	MG	DA	3141	1/1	0.18	-	37,37,37,37	0
57	MG	DA	3181	1/1	0.18	-	36,36,36,36	0
57	MG	BA	3159	1/1	0.23	-	43,43,43,43	0
57	MG	DA	3233	1/1	0.24	-	41,41,41,41	0
57	MG	DA	3275	1/1	0.16	-	36,36,36,36	0
57	MG	DU	3004	1/1	0.17	-	69,69,69,69	0
57	MG	BA	3195	1/1	0.24	-	46,46,46,46	0
57	MG	DA	3288	1/1	0.22	-	32,32,32,32	0
57	MG	BV	203	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3425	1/1	0.20	-	28,28,28,28	0
57	MG	DA	3355	1/1	0.19	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3522	1/1	0.08	-	34,34,34,34	0
57	MG	BA	3580	1/1	0.26	-	13,13,13,13	0
57	MG	CA	3030	1/1	0.08	-	75,75,75,75	0
57	MG	DA	3597	1/1	0.07	-	42,42,42,42	0
57	MG	BA	3574	1/1	0.11	-	41,41,41,41	0
57	MG	B3	3001	1/1	0.10	-	43,43,43,43	0
57	MG	DQ	3003	1/1	0.24	-	59,59,59,59	0
57	MG	DA	3502	1/1	0.12	-	51,51,51,51	0
57	MG	BA	3646	1/1	0.08	-	43,43,43,43	0
57	MG	DA	3331	1/1	0.26	-	54,54,54,54	0
57	MG	BA	3464	1/1	0.20	-	26,26,26,26	0
57	MG	BA	3232	1/1	0.16	-	31,31,31,31	0
57	MG	BA	3540	1/1	0.19	-	24,24,24,24	0
57	MG	AA	3010	1/1	0.04	-	54,54,54,54	0
57	MG	DA	3401	1/1	0.11	-	36,36,36,36	0
57	MG	AX	3007	1/1	0.25	-	54,54,54,54	0
57	MG	DA	3075	1/1	0.15	-	40,40,40,40	0
57	MG	DA	3167	1/1	0.16	-	26,26,26,26	0
57	MG	BA	3305	1/1	0.15	-	45,45,45,45	0
57	MG	DA	3292	1/1	0.12	-	29,29,29,29	0
57	MG	DA	3354	1/1	0.23	-	25,25,25,25	0
57	MG	BA	3361	1/1	0.06	-	38,38,38,38	0
57	MG	BA	3133	1/1	0.19	-	29,29,29,29	0
57	MG	AA	3147	1/1	0.06	-	51,51,51,51	0
57	MG	DA	3613	1/1	0.34	-	45,45,45,45	0
57	MG	DA	3256	1/1	0.11	-	52,52,52,52	0
57	MG	BW	201	1/1	0.15	-	48,48,48,48	0
57	MG	B0	102	1/1	0.12	-	53,53,53,53	0
57	MG	CA	3005	1/1	0.13	-	81,81,81,81	0
57	MG	DA	3610	1/1	0.15	-	42,42,42,42	0
57	MG	DA	3556	1/1	0.12	-	49,49,49,49	0
57	MG	DF	3002	1/1	0.11	-	51,51,51,51	0
57	MG	DA	3384	1/1	0.08	-	41,41,41,41	0
57	MG	BA	3406	1/1	0.21	-	24,24,24,24	0
57	MG	AA	3186	1/1	0.06	-	43,43,43,43	0
57	MG	DA	3011	1/1	0.10	-	36,36,36,36	0
57	MG	DA	3146	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3087	1/1	0.19	-	44,44,44,44	0
57	MG	BA	3336	1/1	0.09	-	47,47,47,47	0
57	MG	BA	3704	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3263	1/1	0.31	-	50,50,50,50	0
57	MG	DA	3183	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
57	MG	DA	3580	1/1	0.11	-	47,47,47,47	0
57	MG	BA	3363	1/1	0.18	-	31,31,31,31	0
57	MG	DA	3084	1/1	0.15	-	42,42,42,42	0
57	MG	AA	3174	1/1	0.15	-	64,64,64,64	0
57	MG	DA	3402	1/1	0.15	-	47,47,47,47	0
57	MG	BA	3566	1/1	0.17	-	31,31,31,31	0
57	MG	BA	3094	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3484	1/1	0.09	-	41,41,41,41	0
57	MG	BA	3011	1/1	0.16	-	32,32,32,32	0
57	MG	BA	3272	1/1	0.20	-	38,38,38,38	0
57	MG	BA	3018	1/1	0.18	-	58,58,58,58	0
57	MG	BA	3012	1/1	0.14	-	38,38,38,38	0
57	MG	DA	3232	1/1	0.08	-	48,48,48,48	0
57	MG	BA	3274	1/1	0.16	-	44,44,44,44	0
57	MG	BA	3101	1/1	0.27	-	29,29,29,29	0
57	MG	DA	3116	1/1	0.20	-	36,36,36,36	0
57	MG	BA	3660	1/1	0.11	-	62,62,62,62	0
57	MG	DA	3062	1/1	0.30	-	49,49,49,49	0
57	MG	DA	3388	1/1	0.17	-	33,33,33,33	0
57	MG	BA	3213	1/1	0.15	-	48,48,48,48	0
57	MG	CA	3095	1/1	0.24	-	52,52,52,52	0
57	MG	CA	3132	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3475	1/1	0.18	-	35,35,35,35	0
57	MG	BA	3620	1/1	0.12	-	35,35,35,35	0
57	MG	BA	3182	1/1	0.18	-	36,36,36,36	0
57	MG	BA	3266	1/1	0.17	-	53,53,53,53	0
57	MG	BA	3483	1/1	0.12	-	36,36,36,36	0
57	MG	DA	3196	1/1	0.17	-	46,46,46,46	0
57	MG	BA	3337	1/1	0.14	-	51,51,51,51	0
57	MG	BA	3554	1/1	0.10	-	44,44,44,44	0
57	MG	BA	3575	1/1	0.15	-	30,30,30,30	0
57	MG	BA	3524	1/1	0.10	-	39,39,39,39	0
57	MG	AA	3048	1/1	0.16	-	42,42,42,42	0
57	MG	CA	3033	1/1	0.15	-	67,67,67,67	0
57	MG	DF	3003	1/1	0.21	-	36,36,36,36	0
57	MG	DA	3086	1/1	0.11	-	41,41,41,41	0
57	MG	AE	3002	1/1	0.15	-	61,61,61,61	0
57	MG	BA	3286	1/1	0.12	-	33,33,33,33	0
57	MG	AA	3198	1/1	0.14	-	66,66,66,66	0
59	ZN	D5	102	1/1	0.16	-	58,58,58,58	0
59	ZN	B5	102	1/1	0.15	-	41,41,41,41	0
57	MG	BA	3396	1/1	0.23	-	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	ZN	B6	501	1/1	0.14	-	43,43,43,43	0
57	MG	CA	3083	1/1	0.32	-	71,71,71,71	0
57	MG	AA	3184	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3218	1/1	0.10	-	36,36,36,36	0
57	MG	BA	3309	1/1	0.08	-	31,31,31,31	0
57	MG	BA	3388	1/1	0.16	-	31,31,31,31	0
57	MG	DA	3136	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3093	1/1	0.14	-	23,23,23,23	0
57	MG	DA	3313	1/1	0.05	-	51,51,51,51	0
57	MG	CA	3126	1/1	0.27	-	73,73,73,73	0
57	MG	DA	3047	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3520	1/1	0.17	-	46,46,46,46	0
57	MG	DD	303	1/1	0.38	-	42,42,42,42	0
57	MG	CA	3025	1/1	0.17	-	66,66,66,66	0
57	MG	BB	3019	1/1	0.15	-	62,62,62,62	0
57	MG	BA	3527	1/1	0.19	-	37,37,37,37	0
57	MG	AA	3008	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3323	1/1	0.07	-	39,39,39,39	0
57	MG	AA	3057	1/1	0.10	-	38,38,38,38	0
57	MG	AA	3018	1/1	0.16	-	62,62,62,62	0
57	MG	DA	3348	1/1	0.18	-	33,33,33,33	0
57	MG	AA	3076	1/1	0.20	-	62,62,62,62	0
57	MG	BA	3371	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3554	1/1	0.20	-	46,46,46,46	0
57	MG	BA	3626	1/1	0.22	-	48,48,48,48	0
57	MG	CA	3145	1/1	0.08	-	49,49,49,49	0
57	MG	BU	208	1/1	0.51	-	39,39,39,39	0
57	MG	BA	3489	1/1	0.22	-	36,36,36,36	0
57	MG	AA	3074	1/1	0.26	-	38,38,38,38	0
57	MG	BA	3647	1/1	0.10	-	41,41,41,41	0
57	MG	BA	3545	1/1	0.25	-	34,34,34,34	0
57	MG	BA	3238	1/1	0.25	-	26,26,26,26	0
57	MG	AA	3097	1/1	0.16	-	45,45,45,45	0
57	MG	BA	3561	1/1	0.16	-	37,37,37,37	0
57	MG	BA	3100	1/1	0.17	-	40,40,40,40	0
57	MG	BA	3449	1/1	0.14	-	31,31,31,31	0
57	MG	DA	3546	1/1	0.16	-	41,41,41,41	0
57	MG	BA	3073	1/1	0.25	-	39,39,39,39	0
57	MG	AV	3001	1/1	0.17	-	59,59,59,59	0
57	MG	BA	3169	1/1	0.13	-	40,40,40,40	0
57	MG	BA	3276	1/1	0.14	-	19,19,19,19	0
57	MG	DA	3186	1/1	0.07	-	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3474	1/1	0.20	-	52,52,52,52	0
57	MG	DA	3488	1/1	0.11	-	47,47,47,47	0
57	MG	BA	3013	1/1	0.27	-	36,36,36,36	0
57	MG	AA	3015	1/1	0.11	-	28,28,28,28	0
57	MG	BA	3328	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3095	1/1	0.22	-	29,29,29,29	0
57	MG	BD	305	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3673	1/1	0.10	-	55,55,55,55	0
57	MG	BA	3193	1/1	0.18	-	30,30,30,30	0
57	MG	CA	3097	1/1	0.22	-	43,43,43,43	0
57	MG	BA	3210	1/1	0.14	-	42,42,42,42	0
57	MG	DA	3128	1/1	0.18	-	45,45,45,45	0
57	MG	DA	3477	1/1	0.10	-	37,37,37,37	0
57	MG	AA	3165	1/1	0.16	-	47,47,47,47	0
57	MG	BA	3055	1/1	0.24	-	43,43,43,43	0
57	MG	BA	3281	1/1	0.32	-	46,46,46,46	0
57	MG	DA	3552	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3403	1/1	0.23	-	22,22,22,22	0
57	MG	AA	3162	1/1	0.09	-	40,40,40,40	0
57	MG	DA	3234	1/1	0.29	-	34,34,34,34	0
57	MG	DA	3112	1/1	0.15	-	63,63,63,63	0
57	MG	DA	3204	1/1	0.17	-	39,39,39,39	0
57	MG	BA	3138	1/1	0.24	-	57,57,57,57	0
57	MG	BA	3496	1/1	0.27	-	33,33,33,33	0
57	MG	CA	3074	1/1	0.21	-	51,51,51,51	0
57	MG	BA	3277	1/1	0.26	-	34,34,34,34	0
57	MG	DA	3249	1/1	0.18	-	48,48,48,48	0
57	MG	AM	201	1/1	0.05	-	43,43,43,43	0
57	MG	BA	3569	1/1	0.22	-	46,46,46,46	0
57	MG	BA	3344	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3249	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3212	1/1	0.28	-	24,24,24,24	0
57	MG	DA	3444	1/1	0.23	-	37,37,37,37	0
57	MG	BA	3335	1/1	0.07	-	26,26,26,26	0
57	MG	DA	3600	1/1	0.09	-	45,45,45,45	0
57	MG	AA	3181	1/1	0.07	-	82,82,82,82	0
57	MG	DA	3182	1/1	0.32	-	52,52,52,52	0
57	MG	DA	3593	1/1	0.18	-	49,49,49,49	0
57	MG	BA	3532	1/1	0.23	-	39,39,39,39	0
57	MG	DA	3441	1/1	0.25	-	43,43,43,43	0
57	MG	BA	3676	1/1	0.18	-	44,44,44,44	0
57	MG	BA	3623	1/1	0.14	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3057	1/1	0.13	-	48,48,48,48	0
57	MG	BA	3128	1/1	0.14	-	33,33,33,33	0
57	MG	BA	3605	1/1	0.21	-	44,44,44,44	0
57	MG	DA	3009	1/1	0.10	-	39,39,39,39	0
57	MG	BA	3603	1/1	0.18	-	42,42,42,42	0
57	MG	BA	3644	1/1	0.18	-	48,48,48,48	0
57	MG	BA	3050	1/1	0.09	-	44,44,44,44	0
57	MG	BA	3711	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3471	1/1	0.22	-	23,23,23,23	0
57	MG	AA	3037	1/1	0.09	-	48,48,48,48	0
57	MG	BA	3717	1/1	0.46	-	40,40,40,40	0
57	MG	DA	3033	1/1	0.15	-	46,46,46,46	0
57	MG	DA	3327	1/1	0.12	-	49,49,49,49	0
57	MG	BP	3004	1/1	0.11	-	41,41,41,41	0
57	MG	DA	3297	1/1	0.13	-	48,48,48,48	0
57	MG	CA	3011	1/1	0.25	-	39,39,39,39	0
57	MG	BA	3327	1/1	0.16	-	32,32,32,32	0
57	MG	DA	3623	1/1	0.14	-	31,31,31,31	0
57	MG	DA	3538	1/1	0.21	-	77,77,77,77	0
57	MG	BA	3234	1/1	0.37	-	39,39,39,39	0
57	MG	BA	3297	1/1	0.22	-	36,36,36,36	0
57	MG	CA	3123	1/1	0.08	-	53,53,53,53	0
57	MG	BA	3347	1/1	0.21	-	32,32,32,32	0
57	MG	BA	3267	1/1	0.34	-	33,33,33,33	0
57	MG	AA	3061	1/1	0.09	-	65,65,65,65	0
57	MG	CA	3108	1/1	0.12	-	51,51,51,51	0
57	MG	DA	3548	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3592	1/1	0.14	-	14,14,14,14	0
57	MG	DA	3416	1/1	0.06	-	46,46,46,46	0
57	MG	AX	3002	1/1	0.17	-	67,67,67,67	0
57	MG	DA	3446	1/1	0.18	-	37,37,37,37	0
57	MG	CA	3054	1/1	0.34	-	53,53,53,53	0
57	MG	DA	3029	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3458	1/1	0.13	-	40,40,40,40	0
57	MG	CA	3014	1/1	0.11	-	58,58,58,58	0
57	MG	DA	3524	1/1	0.10	-	40,40,40,40	0
57	MG	AA	3016	1/1	0.13	-	52,52,52,52	0
57	MG	CA	3073	1/1	0.05	-	57,57,57,57	0
57	MG	DA	3117	1/1	0.14	-	40,40,40,40	0
57	MG	DA	3309	1/1	0.11	-	34,34,34,34	0
57	MG	BU	203	1/1	0.23	-	35,35,35,35	0
57	MG	DA	3396	1/1	0.08	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3024	1/1	0.13	-	29,29,29,29	0
57	MG	DA	3557	1/1	0.07	-	54,54,54,54	0
57	MG	DA	3159	1/1	0.12	-	32,32,32,32	0
57	MG	BA	3418	1/1	0.21	-	26,26,26,26	0
57	MG	BA	3495	1/1	0.24	-	47,47,47,47	0
57	MG	BA	3127	1/1	0.25	-	41,41,41,41	0
57	MG	BA	3010	1/1	0.17	-	45,45,45,45	0
57	MG	BA	3329	1/1	0.15	-	21,21,21,21	0
57	MG	BA	3684	1/1	0.09	-	47,47,47,47	0
57	MG	BA	3231	1/1	0.15	-	42,42,42,42	0
57	MG	AA	3159	1/1	0.10	-	31,31,31,31	0
57	MG	BA	3480	1/1	0.23	-	50,50,50,50	0
57	MG	CA	3087	1/1	0.11	-	50,50,50,50	0
57	MG	CA	3061	1/1	0.11	-	87,87,87,87	0
57	MG	AA	3105	1/1	0.20	-	59,59,59,59	0
57	MG	BA	3450	1/1	0.08	-	45,45,45,45	0
57	MG	CA	3134	1/1	0.19	-	72,72,72,72	0
57	MG	AA	3080	1/1	0.15	-	82,82,82,82	0
57	MG	BA	3172	1/1	0.16	-	27,27,27,27	0
57	MG	BA	3198	1/1	0.19	-	45,45,45,45	0
57	MG	BA	3708	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3257	1/1	0.30	-	40,40,40,40	0
57	MG	DA	3078	1/1	0.05	-	49,49,49,49	0
57	MG	CA	3042	1/1	0.15	-	68,68,68,68	0
57	MG	DA	3370	1/1	0.12	-	72,72,72,72	0
57	MG	AA	3040	1/1	0.18	-	67,67,67,67	0
57	MG	DA	3615	1/1	0.15	-	36,36,36,36	0
57	MG	BA	3362	1/1	0.10	-	43,43,43,43	0
57	MG	BA	3583	1/1	0.10	-	54,54,54,54	0
57	MG	BA	3413	1/1	0.09	-	50,50,50,50	0
57	MG	BA	3593	1/1	0.16	-	36,36,36,36	0
57	MG	CA	3103	1/1	0.15	-	71,71,71,71	0
57	MG	BA	3475	1/1	0.07	-	31,31,31,31	0
57	MG	DA	3564	1/1	0.15	-	48,48,48,48	0
57	MG	BB	3014	1/1	0.07	-	41,41,41,41	0
57	MG	AA	3091	1/1	0.23	-	35,35,35,35	0
57	MG	BA	3307	1/1	0.27	-	31,31,31,31	0
57	MG	BB	3013	1/1	0.18	-	43,43,43,43	0
57	MG	BA	3129	1/1	0.12	-	30,30,30,30	0
57	MG	BA	3354	1/1	0.10	-	31,31,31,31	0
57	MG	BV	201	1/1	0.21	-	33,33,33,33	0
57	MG	BD	307	1/1	0.20	-	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3032	1/1	0.11	-	80,80,80,80	0
57	MG	DA	3016	1/1	0.11	-	34,34,34,34	0
57	MG	BA	3578	1/1	0.13	-	43,43,43,43	0
57	MG	AA	3143	1/1	0.14	-	32,32,32,32	0
57	MG	DA	3467	1/1	0.14	-	28,28,28,28	0
57	MG	BA	3686	1/1	0.26	-	36,36,36,36	0
57	MG	DA	3365	1/1	0.10	-	54,54,54,54	0
57	MG	AA	3114	1/1	0.29	-	57,57,57,57	0
57	MG	DA	3426	1/1	0.33	-	38,38,38,38	0
57	MG	DA	3403	1/1	0.11	-	31,31,31,31	0
57	MG	BN	3005	1/1	0.20	-	31,31,31,31	0
57	MG	CA	3034	1/1	0.23	-	49,49,49,49	0
57	MG	DA	3399	1/1	0.10	-	26,26,26,26	0
57	MG	AA	3188	1/1	0.08	-	62,62,62,62	0
57	MG	DA	3523	1/1	0.11	-	45,45,45,45	0
57	MG	DA	3452	1/1	0.16	-	40,40,40,40	0
57	MG	BB	3001	1/1	0.15	-	44,44,44,44	0
57	MG	BA	3516	1/1	0.15	-	32,32,32,32	0
57	MG	BG	3002	1/1	0.12	-	65,65,65,65	0
57	MG	CA	3119	1/1	0.10	-	74,74,74,74	0
57	MG	BA	3285	1/1	0.17	-	21,21,21,21	0
57	MG	BA	3236	1/1	0.15	-	39,39,39,39	0
57	MG	DA	3584	1/1	0.14	-	63,63,63,63	0
57	MG	CA	3142	1/1	0.19	-	55,55,55,55	0
57	MG	DA	3145	1/1	0.20	-	38,38,38,38	0
57	MG	BA	3712	1/1	0.10	-	30,30,30,30	0
57	MG	BA	3404	1/1	0.20	-	30,30,30,30	0
57	MG	DA	3375	1/1	0.22	-	30,30,30,30	0
57	MG	AA	3047	1/1	0.22	-	59,59,59,59	0
57	MG	BA	3208	1/1	0.09	-	33,33,33,33	0
57	MG	BA	3175	1/1	0.16	-	55,55,55,55	0
59	ZN	D6	501	1/1	0.15	-	64,64,64,64	0
57	MG	BA	3394	1/1	0.15	-	22,22,22,22	0
57	MG	BA	3465	1/1	0.17	-	44,44,44,44	0
57	MG	BA	3500	1/1	0.09	-	54,54,54,54	0
57	MG	DA	3121	1/1	0.11	-	39,39,39,39	0
57	MG	DA	3394	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3166	1/1	0.24	-	45,45,45,45	0
57	MG	DA	3224	1/1	0.24	-	60,60,60,60	0
57	MG	DA	3347	1/1	0.18	-	32,32,32,32	0
57	MG	DA	3279	1/1	0.27	-	50,50,50,50	0
57	MG	CA	3084	1/1	0.14	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3334	1/1	0.09	-	31,31,31,31	0
57	MG	DG	3001	1/1	0.10	-	49,49,49,49	0
57	MG	BA	3611	1/1	0.13	-	61,61,61,61	0
57	MG	DA	3499	1/1	0.12	-	47,47,47,47	0
57	MG	BA	3405	1/1	0.19	-	31,31,31,31	0
57	MG	BA	3476	1/1	0.12	-	37,37,37,37	0
57	MG	BA	3487	1/1	0.11	-	70,70,70,70	0
57	MG	BA	3460	1/1	0.15	-	43,43,43,43	0
57	MG	AA	3118	1/1	0.15	-	50,50,50,50	0
57	MG	AD	301	1/1	0.12	-	47,47,47,47	0
57	MG	BA	3395	1/1	0.16	-	19,19,19,19	0
57	MG	DA	3147	1/1	0.15	-	42,42,42,42	0
57	MG	AA	3102	1/1	0.20	-	52,52,52,52	0
57	MG	BA	3359	1/1	0.12	-	56,56,56,56	0
57	MG	BA	3573	1/1	0.13	-	29,29,29,29	0
57	MG	CA	3008	1/1	0.12	-	67,67,67,67	0
57	MG	DA	3336	1/1	0.16	-	38,38,38,38	0
57	MG	BA	3683	1/1	0.25	-	44,44,44,44	0
57	MG	DA	3626	1/1	0.19	-	38,38,38,38	0
57	MG	BA	3652	1/1	0.15	-	65,65,65,65	0
57	MG	DA	3418	1/1	0.19	-	41,41,41,41	0
57	MG	CA	3069	1/1	0.36	-	56,56,56,56	0
57	MG	DA	3035	1/1	0.15	-	45,45,45,45	0
57	MG	BA	3188	1/1	0.19	-	48,48,48,48	0
57	MG	DA	3048	1/1	0.14	-	53,53,53,53	0
57	MG	BA	3370	1/1	0.17	-	32,32,32,32	0
57	MG	AA	3126	1/1	0.15	-	52,52,52,52	0
57	MG	DA	3415	1/1	0.31	-	55,55,55,55	0
57	MG	BA	3679	1/1	0.18	-	38,38,38,38	0
57	MG	DA	3140	1/1	0.14	-	38,38,38,38	0
57	MG	BA	3443	1/1	0.23	-	38,38,38,38	0
57	MG	BA	3265	1/1	0.13	-	30,30,30,30	0
57	MG	DA	3534	1/1	0.12	-	30,30,30,30	0
58	SF4	AD	302	8/8	0.15	-	59,71,78,78	0
57	MG	DA	3455	1/1	0.32	-	34,34,34,34	0
57	MG	BA	3185	1/1	0.47	-	34,34,34,34	0
57	MG	DA	3065	1/1	0.09	-	38,38,38,38	0
57	MG	BA	3617	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3592	1/1	0.14	-	62,62,62,62	0
57	MG	AA	3020	1/1	0.17	-	62,62,62,62	0
57	MG	DA	3485	1/1	0.17	-	41,41,41,41	0
57	MG	CA	3133	1/1	0.15	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3212	1/1	0.07	-	47,47,47,47	0
57	MG	CA	3036	1/1	0.08	-	47,47,47,47	0
57	MG	DA	3206	1/1	0.19	-	37,37,37,37	0
57	MG	BA	3525	1/1	0.15	-	49,49,49,49	0
57	MG	BA	3067	1/1	0.21	-	26,26,26,26	0
57	MG	BA	3429	1/1	0.14	-	37,37,37,37	0
57	MG	DA	3378	1/1	0.13	-	33,33,33,33	0
57	MG	AA	3145	1/1	0.21	-	71,71,71,71	0
57	MG	BB	3016	1/1	0.06	-	39,39,39,39	0
57	MG	BA	3659	1/1	0.14	-	47,47,47,47	0
57	MG	AS	101	1/1	0.09	-	55,55,55,55	0
57	MG	BA	3570	1/1	0.11	-	48,48,48,48	0
57	MG	DA	3315	1/1	0.16	-	57,57,57,57	0
57	MG	DA	3555	1/1	0.14	-	70,70,70,70	0
57	MG	CA	3089	1/1	0.12	-	65,65,65,65	0
57	MG	DA	3569	1/1	0.15	-	42,42,42,42	0
57	MG	BA	3639	1/1	0.14	-	46,46,46,46	0
57	MG	AA	3129	1/1	0.15	-	37,37,37,37	0
57	MG	CA	3160	1/1	0.35	-	49,49,49,49	0
57	MG	CA	3049	1/1	0.11	-	42,42,42,42	0
57	MG	BA	3020	1/1	0.27	-	55,55,55,55	0
57	MG	CX	3002	1/1	0.27	-	75,75,75,75	0
57	MG	AA	3071	1/1	0.38	-	41,41,41,41	0
59	ZN	B9	501	1/1	0.12	-	59,59,59,59	0
57	MG	DA	3126	1/1	0.12	-	39,39,39,39	0
57	MG	AA	3031	1/1	0.11	-	41,41,41,41	0
57	MG	AA	3168	1/1	0.12	-	56,56,56,56	0
57	MG	DA	3193	1/1	0.17	-	43,43,43,43	0
57	MG	BA	3243	1/1	0.19	-	46,46,46,46	0
57	MG	AA	3158	1/1	0.09	-	72,72,72,72	0
57	MG	DA	3214	1/1	0.13	-	43,43,43,43	0
57	MG	B3	3002	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3306	1/1	0.21	-	32,32,32,32	0
57	MG	DA	3266	1/1	0.12	-	45,45,45,45	0
57	MG	DB	3002	1/1	0.07	-	75,75,75,75	0
57	MG	DA	3361	1/1	0.16	-	32,32,32,32	0
57	MG	AA	3085	1/1	0.18	-	69,69,69,69	0
57	MG	DA	3337	1/1	0.21	-	46,46,46,46	0
57	MG	BA	3295	1/1	0.14	-	56,56,56,56	0
57	MG	DA	3142	1/1	0.18	-	50,50,50,50	0
57	MG	BA	3028	1/1	0.14	-	31,31,31,31	0
57	MG	DA	3125	1/1	0.10	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	3092	1/1	0.14	-	36,36,36,36	0
57	MG	AA	3014	1/1	0.08	-	73,73,73,73	0
57	MG	DA	3312	1/1	0.19	-	30,30,30,30	0
57	MG	BA	3555	1/1	0.07	-	62,62,62,62	0
57	MG	BA	3130	1/1	0.42	-	39,39,39,39	0
57	MG	AA	3103	1/1	0.17	-	42,42,42,42	0
57	MG	DA	3246	1/1	0.30	-	57,57,57,57	0
57	MG	BA	3025	1/1	0.18	-	12,12,12,12	0
57	MG	BA	3615	1/1	0.10	-	60,60,60,60	0
57	MG	BA	3627	1/1	0.08	-	28,28,28,28	0
57	MG	BA	3310	1/1	0.18	-	43,43,43,43	0
57	MG	BA	3697	1/1	0.15	-	23,23,23,23	0
57	MG	DA	3151	1/1	0.15	-	48,48,48,48	0
57	MG	D3	3001	1/1	0.15	-	54,54,54,54	0
57	MG	DU	3001	1/1	0.62	-	56,56,56,56	0
57	MG	DA	3244	1/1	0.19	-	43,43,43,43	0
57	MG	BA	3640	1/1	0.13	-	53,53,53,53	0
57	MG	DA	3411	1/1	0.10	-	51,51,51,51	0
57	MG	DB	3007	1/1	0.08	-	55,55,55,55	0
57	MG	CA	3092	1/1	0.14	-	76,76,76,76	0
57	MG	DA	3595	1/1	0.14	-	65,65,65,65	0
57	MG	BA	3124	1/1	0.11	-	31,31,31,31	0
57	MG	BA	3299	1/1	0.21	-	27,27,27,27	0
57	MG	BA	3422	1/1	0.17	-	39,39,39,39	0
57	MG	DA	3588	1/1	0.13	-	21,21,21,21	0
57	MG	BA	3435	1/1	0.21	-	31,31,31,31	0
57	MG	BA	3582	1/1	0.15	-	23,23,23,23	0
57	MG	BA	3303	1/1	0.23	-	39,39,39,39	0
57	MG	BA	3260	1/1	0.25	-	45,45,45,45	0
57	MG	AN	503	1/1	0.14	-	61,61,61,61	0
57	MG	DA	3305	1/1	0.07	-	48,48,48,48	0
57	MG	AJ	201	1/1	0.07	-	67,67,67,67	0
57	MG	BB	3018	1/1	0.11	-	43,43,43,43	0
57	MG	BA	3553	1/1	0.19	-	41,41,41,41	0
57	MG	DA	3480	1/1	0.11	-	28,28,28,28	0
57	MG	BA	3179	1/1	0.16	-	49,49,49,49	0
57	MG	BA	3239	1/1	0.16	-	42,42,42,42	0
57	MG	BA	3014	1/1	0.09	-	46,46,46,46	0
57	MG	DA	3135	1/1	0.17	-	61,61,61,61	0
57	MG	DA	3299	1/1	0.12	-	32,32,32,32	0
57	MG	BA	3379	1/1	0.09	-	69,69,69,69	0
57	MG	DA	3359	1/1	0.13	-	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CE	3001	1/1	0.18	-	80,80,80,80	0
57	MG	DA	3609	1/1	0.25	-	55,55,55,55	0
57	MG	BA	3105	1/1	0.21	-	45,45,45,45	0
57	MG	DA	3123	1/1	0.17	-	45,45,45,45	0
57	MG	DA	3017	1/1	0.17	-	58,58,58,58	0
57	MG	AA	3132	1/1	0.21	-	67,67,67,67	0
57	MG	BA	3345	1/1	0.11	-	36,36,36,36	0
57	MG	DA	3468	1/1	0.23	-	64,64,64,64	0
57	MG	BA	3316	1/1	0.16	-	49,49,49,49	0
57	MG	DA	3225	1/1	0.12	-	42,42,42,42	0
57	MG	DA	3517	1/1	0.17	-	36,36,36,36	0
57	MG	DA	3082	1/1	0.14	-	47,47,47,47	0
57	MG	BA	3001	1/1	0.18	-	48,48,48,48	0
57	MG	BP	3001	1/1	0.40	-	49,49,49,49	0
57	MG	DA	3576	1/1	0.22	-	46,46,46,46	0
57	MG	CA	3128	1/1	0.11	-	43,43,43,43	0
57	MG	BA	3255	1/1	0.06	-	37,37,37,37	0
57	MG	CA	3125	1/1	0.14	-	64,64,64,64	0
57	MG	BA	3008	1/1	0.09	-	22,22,22,22	0
57	MG	DA	3139	1/1	0.18	-	49,49,49,49	0
57	MG	DA	3598	1/1	0.10	-	48,48,48,48	0
57	MG	BA	3612	1/1	0.20	-	58,58,58,58	0
57	MG	DA	3364	1/1	0.18	-	49,49,49,49	0
57	MG	DA	3230	1/1	0.21	-	46,46,46,46	0
57	MG	BB	3008	1/1	0.09	-	60,60,60,60	0
57	MG	DA	3213	1/1	0.28	-	51,51,51,51	0
57	MG	BW	203	1/1	0.14	-	39,39,39,39	0
57	MG	AA	3152	1/1	0.08	-	64,64,64,64	0
57	MG	BA	3326	1/1	0.13	-	40,40,40,40	0
57	MG	DA	3080	1/1	0.09	-	64,64,64,64	0
57	MG	DA	3568	1/1	0.12	-	45,45,45,45	0
57	MG	DA	3287	1/1	0.24	-	58,58,58,58	0
57	MG	DA	3482	1/1	0.21	-	31,31,31,31	0
57	MG	CA	3153	1/1	0.13	-	57,57,57,57	0
57	MG	BA	3214	1/1	0.18	-	48,48,48,48	0
57	MG	DA	3038	1/1	0.07	-	39,39,39,39	0
57	MG	BA	3619	1/1	0.14	-	54,54,54,54	0
57	MG	BA	3280	1/1	0.17	-	46,46,46,46	0
57	MG	B5	103	1/1	0.09	-	50,50,50,50	0
57	MG	BA	3634	1/1	0.24	-	58,58,58,58	0
57	MG	BA	3226	1/1	0.37	-	36,36,36,36	0
57	MG	DA	3248	1/1	0.26	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3130	1/1	0.16	-	88,88,88,88	0
57	MG	CA	3150	1/1	0.07	-	66,66,66,66	0
57	MG	BA	3029	1/1	0.18	-	53,53,53,53	0
57	MG	BA	3201	1/1	0.11	-	44,44,44,44	0
57	MG	BA	3278	1/1	0.05	-	38,38,38,38	0
57	MG	CK	3001	1/1	0.20	-	57,57,57,57	0
57	MG	DA	3228	1/1	0.26	-	49,49,49,49	0
57	MG	BA	3353	1/1	0.07	-	46,46,46,46	0
57	MG	AA	3052	1/1	0.15	-	53,53,53,53	0
57	MG	DA	3238	1/1	0.40	-	31,31,31,31	0
57	MG	DP	201	1/1	0.35	-	61,61,61,61	0
57	MG	CA	3158	1/1	0.16	-	66,66,66,66	0
57	MG	DA	3498	1/1	0.07	-	66,66,66,66	0
57	MG	BA	3333	1/1	0.09	-	58,58,58,58	0
57	MG	AA	3098	1/1	0.19	-	42,42,42,42	0
57	MG	CA	3058	1/1	0.34	-	70,70,70,70	0
57	MG	BD	311	1/1	0.40	-	60,60,60,60	0
57	MG	AA	3191	1/1	0.19	-	56,56,56,56	0
57	MG	CA	3093	1/1	0.15	-	69,69,69,69	0
57	MG	CA	3135	1/1	0.12	-	85,85,85,85	0
57	MG	DA	3424	1/1	0.09	-	56,56,56,56	0
57	MG	DA	3500	1/1	0.13	-	32,32,32,32	0
57	MG	BB	3006	1/1	0.18	-	42,42,42,42	0
57	MG	AA	3021	1/1	0.15	-	58,58,58,58	0
57	MG	BA	3664	1/1	0.11	-	66,66,66,66	0
57	MG	DA	3624	1/1	0.29	-	66,66,66,66	0
57	MG	DA	3392	1/1	0.19	-	40,40,40,40	0
57	MG	BA	3324	1/1	0.16	-	61,61,61,61	0
57	MG	DA	3307	1/1	0.16	-	51,51,51,51	0
57	MG	CA	3051	1/1	0.27	-	57,57,57,57	0
57	MG	BA	3196	1/1	0.25	-	51,51,51,51	0
57	MG	AA	3087	1/1	0.14	-	57,57,57,57	0
57	MG	BA	3145	1/1	0.13	-	41,41,41,41	0
57	MG	AA	3135	1/1	0.06	-	52,52,52,52	0
57	MG	BA	3649	1/1	0.10	-	65,65,65,65	0
57	MG	DA	3131	1/1	0.12	-	34,34,34,34	0
57	MG	AA	3207	1/1	0.08	-	57,57,57,57	0
57	MG	BA	3385	1/1	0.26	-	34,34,34,34	0
57	MG	BA	3221	1/1	0.21	-	59,59,59,59	0
57	MG	DA	3269	1/1	0.14	-	40,40,40,40	0
57	MG	BA	3279	1/1	0.23	-	48,48,48,48	0
57	MG	DA	3158	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
57	MG	BA	3153	1/1	0.07	-	53,53,53,53	0
57	MG	DA	3273	1/1	0.14	-	41,41,41,41	0
57	MG	BA	3122	1/1	0.25	-	39,39,39,39	0
57	MG	BA	3590	1/1	0.24	-	62,62,62,62	0
57	MG	DA	3431	1/1	0.15	-	56,56,56,56	0
57	MG	DA	3447	1/1	0.11	-	48,48,48,48	0
57	MG	DA	3032	1/1	0.16	-	34,34,34,34	0
57	MG	AA	3137	1/1	0.26	-	66,66,66,66	0
57	MG	BB	3017	1/1	0.08	-	28,28,28,28	0
57	MG	BA	3004	1/1	0.14	-	26,26,26,26	0
57	MG	AA	3200	1/1	0.11	-	58,58,58,58	0
57	MG	BA	3086	1/1	0.21	-	15,15,15,15	0
57	MG	AE	3001	1/1	0.31	-	85,85,85,85	0
57	MG	BA	3462	1/1	0.19	-	51,51,51,51	0
57	MG	DA	3565	1/1	0.20	-	49,49,49,49	0
57	MG	DA	3462	1/1	0.27	-	35,35,35,35	0
57	MG	BA	3294	1/1	0.22	-	37,37,37,37	0
57	MG	BA	3439	1/1	0.15	-	12,12,12,12	0
57	MG	DA	3435	1/1	0.13	-	59,59,59,59	0
57	MG	BA	3241	1/1	0.29	-	53,53,53,53	0
57	MG	DA	3583	1/1	0.12	-	44,44,44,44	0
57	MG	CA	3078	1/1	0.17	-	63,63,63,63	0
57	MG	BA	3667	1/1	0.17	-	31,31,31,31	0
57	MG	DA	3052	1/1	0.10	-	33,33,33,33	0
57	MG	CA	3140	1/1	0.06	-	48,48,48,48	0
57	MG	DA	3389	1/1	0.14	-	31,31,31,31	0
57	MG	DA	3236	1/1	0.09	-	45,45,45,45	0
57	MG	BA	3161	1/1	0.25	-	54,54,54,54	0
57	MG	DA	3406	1/1	0.14	-	62,62,62,62	0
57	MG	BA	3323	1/1	0.09	-	59,59,59,59	0
57	MG	DA	3284	1/1	0.20	-	51,51,51,51	0
57	MG	CA	3024	1/1	0.06	-	58,58,58,58	0
57	MG	B5	101	1/1	0.20	-	30,30,30,30	0
57	MG	DA	3381	1/1	0.24	-	55,55,55,55	0
57	MG	BA	3158	1/1	0.36	-	48,48,48,48	0
57	MG	CA	3116	1/1	0.34	-	74,74,74,74	0
57	MG	BA	3343	1/1	0.17	-	18,18,18,18	0
57	MG	DA	3421	1/1	0.07	-	31,31,31,31	0
57	MG	CA	3088	1/1	0.11	-	61,61,61,61	0
57	MG	AA	3069	1/1	0.12	-	75,75,75,75	0
57	MG	AA	3046	1/1	0.24	-	72,72,72,72	0
57	MG	BA	3463	1/1	0.10	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3271	1/1	0.16	-	47,47,47,47	0
57	MG	DA	3068	1/1	0.16	-	48,48,48,48	0
57	MG	BA	3448	1/1	0.08	-	42,42,42,42	0
57	MG	BA	3680	1/1	0.13	-	46,46,46,46	0
57	MG	DA	3428	1/1	0.20	-	46,46,46,46	0
57	MG	DA	3329	1/1	0.20	-	54,54,54,54	0
57	MG	CA	3156	1/1	0.04	-	57,57,57,57	0
57	MG	DA	3040	1/1	0.38	-	48,48,48,48	0

6.5 Other polymers ⓘ

There are no such residues in this entry.