



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:37 PM GMT

PDB ID : 1VY4
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in the pre-attack state of peptide bond formation containing acylated tRNA-substrates in the A and P sites.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.60 Å(reported)

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

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

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

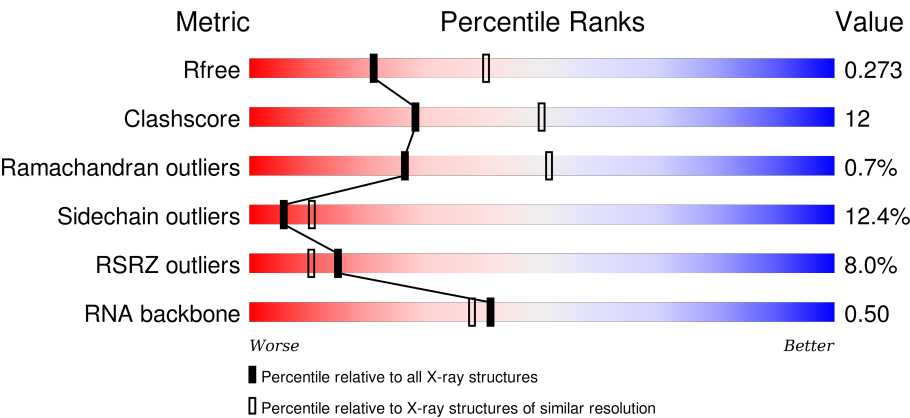
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)
RNA backbone	2183	1022 (3.00-2.20)

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

Mol	Chain	Length	Quality of chain
1	AA	1521	<div><div></div><div><div></div><div>49%</div><div>38%</div><div>11%</div><div>..</div></div></div>
1	CA	1521	<div><div>4%</div><div><div></div><div>43%</div><div>40%</div><div>14%</div><div>..</div></div></div>
2	AB	256	<div><div>11%</div><div><div></div><div>45%</div><div>37%</div><div>8%</div><div>•</div><div>10%</div></div></div>
2	CB	256	<div><div>34%</div><div><div></div><div>36%</div><div>44%</div><div>10%</div><div>•</div><div>10%</div></div></div>

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Mol	Chain	Length	Quality of chain
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
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	





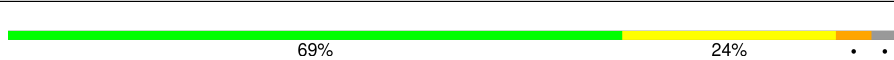
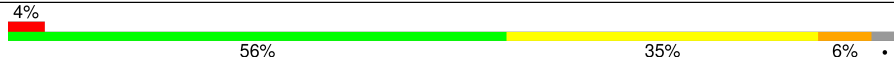
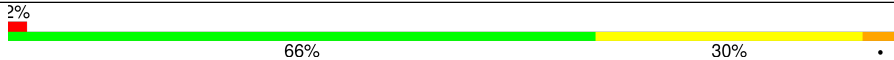
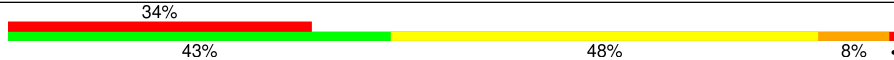
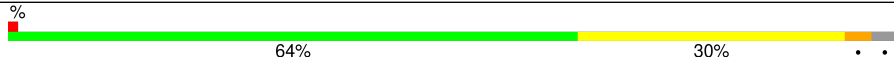
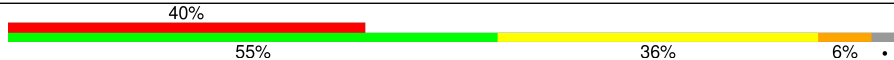
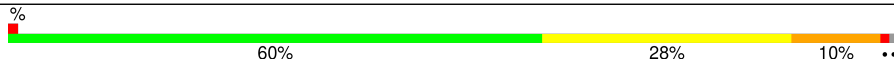
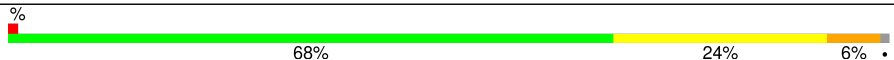


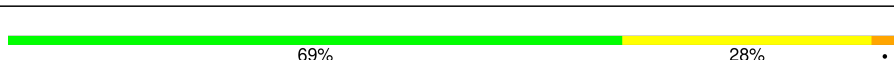
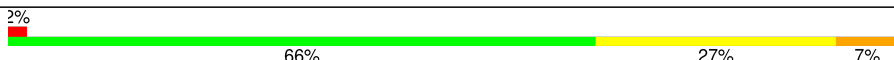
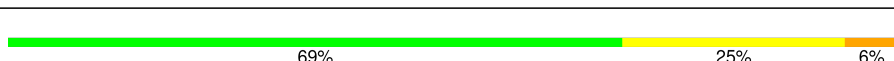
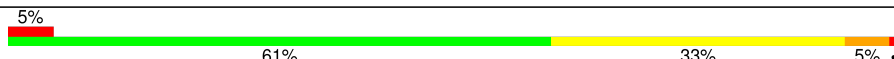
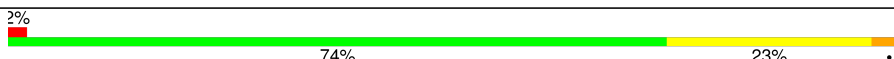

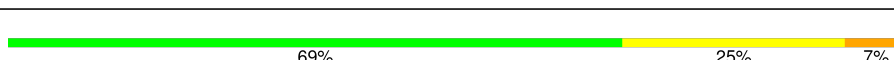
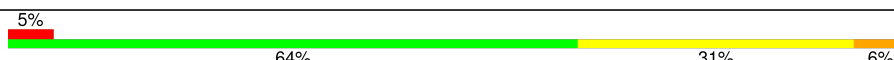
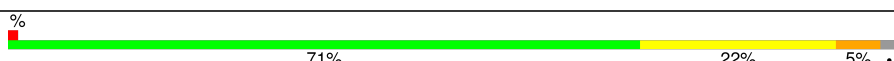
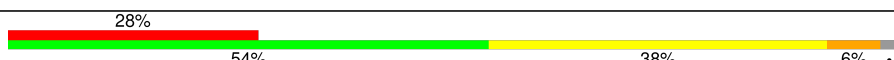
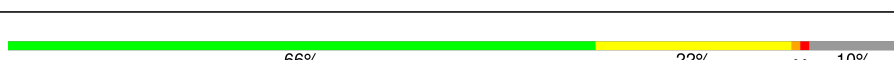
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Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AW	76	
23	CW	76	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
27	DB	121	



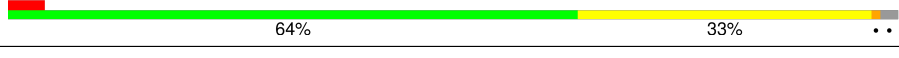
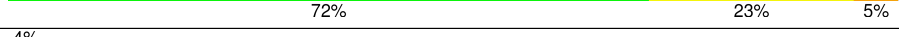
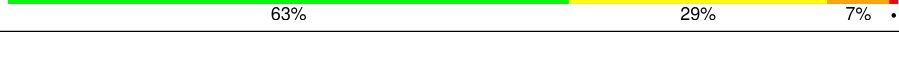
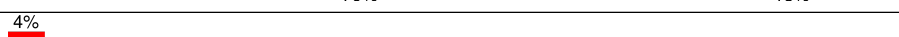
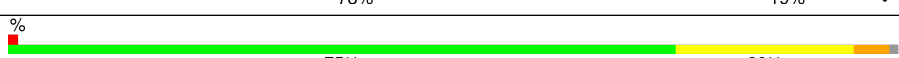



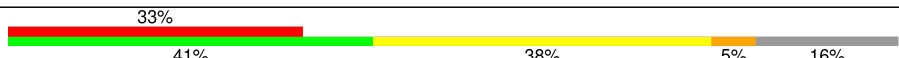




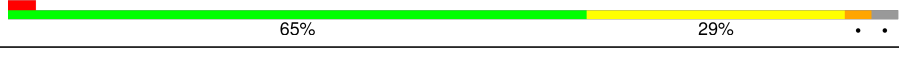

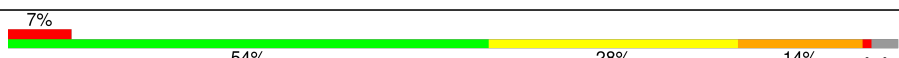


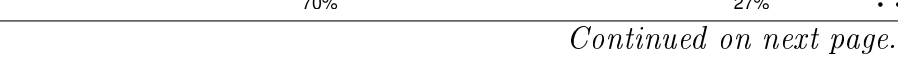


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Mol	Chain	Length	Quality of chain
28	BD	276	
28	DD	276	
29	BE	206	
29	DE	206	
30	BF	210	
30	DF	210	
31	BG	182	
31	DG	182	
32	BH	180	
32	DH	180	
33	BI	148	
33	DI	148	
34	BN	140	
34	DN	140	
35	BO	122	
35	DO	122	
36	BP	150	
36	DP	150	
37	BQ	141	
37	DQ	141	
38	BR	118	
38	DR	118	
39	BS	112	
39	DS	112	
40	BT	146	









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Mol	Chain	Length	Quality of chain
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	
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	

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Mol	Chain	Length	Quality of chain
53	B6	54	
53	D6	54	
54	B7	49	
54	D7	49	
55	B8	65	
55	D8	65	
56	B9	37	
56	D9	37	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	PSU	CY	39	-	-	X	-
57	MG	AA	1675	-	-	-	X
57	MG	AA	1687	-	-	-	X
57	MG	AA	1702	-	-	-	X
57	MG	AA	1725	-	-	-	X
57	MG	AA	1730	-	-	-	X
57	MG	AA	1756	-	-	-	X
57	MG	AA	1757	-	-	-	X
57	MG	AX	3002	-	-	-	X
57	MG	AX	3003	-	-	-	X
57	MG	BA	3007	-	-	-	X
57	MG	BA	3018	-	-	-	X
57	MG	BA	3033	-	-	-	X
57	MG	BA	3035	-	-	-	X
57	MG	BA	3037	-	-	-	X
57	MG	BA	3041	-	-	-	X
57	MG	BA	3044	-	-	-	X
57	MG	BA	3061	-	-	-	X
57	MG	BA	3070	-	-	-	X
57	MG	BA	3083	-	-	-	X
57	MG	BA	3085	-	-	-	X
57	MG	BA	3100	-	-	-	X
57	MG	BA	3103	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BA	3111	-	-	-	X
57	MG	BA	3121	-	-	-	X
57	MG	BA	3124	-	-	-	X
57	MG	BA	3135	-	-	-	X
57	MG	BA	3136	-	-	-	X
57	MG	BA	3142	-	-	-	X
57	MG	BA	3171	-	-	-	X
57	MG	BA	3174	-	-	-	X
57	MG	BA	3176	-	-	-	X
57	MG	BA	3182	-	-	-	X
57	MG	BA	3186	-	-	-	X
57	MG	BA	3200	-	-	-	X
57	MG	BA	3204	-	-	-	X
57	MG	BA	3210	-	-	-	X
57	MG	BA	3214	-	-	-	X
57	MG	BA	3215	-	-	-	X
57	MG	BA	3216	-	-	-	X
57	MG	BA	3219	-	-	-	X
57	MG	BA	3244	-	-	-	X
57	MG	BA	3256	-	-	-	X
57	MG	BA	3277	-	-	-	X
57	MG	BA	3310	-	-	-	X
57	MG	BA	3369	-	-	-	X
57	MG	BA	3400	-	-	-	X
57	MG	BA	3403	-	-	-	X
57	MG	BA	3424	-	-	-	X
57	MG	BA	3425	-	-	-	X
57	MG	BA	3456	-	-	-	X
57	MG	BA	3507	-	-	-	X
57	MG	BA	3520	-	-	-	X
57	MG	BA	3526	-	-	-	X
57	MG	BA	3529	-	-	-	X
57	MG	BA	3530	-	-	-	X
57	MG	BA	3543	-	-	-	X
57	MG	BA	3561	-	-	-	X
57	MG	BA	3591	-	-	-	X
57	MG	BA	3608	-	-	-	X
57	MG	BA	3648	-	-	-	X
57	MG	BA	3672	-	-	-	X
57	MG	BA	3674	-	-	-	X
57	MG	BA	3680	-	-	-	X
57	MG	BA	3688	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	BA	3700	-	-	-	X
57	MG	BA	3710	-	-	-	X
57	MG	BA	3716	-	-	-	X
57	MG	BA	3743	-	-	-	X
57	MG	BA	3770	-	-	-	X
57	MG	BA	3775	-	-	-	X
57	MG	BA	3795	-	-	-	X
57	MG	BA	3807	-	-	-	X
57	MG	BA	3814	-	-	-	X
57	MG	BD	3003	-	-	-	X
57	MG	BD	3007	-	-	-	X
57	MG	BD	3008	-	-	-	X
57	MG	BF	302	-	-	-	X
57	MG	BF	303	-	-	-	X
57	MG	BF	304	-	-	-	X
57	MG	BF	306	-	-	-	X
57	MG	BU	201	-	-	-	X
57	MG	BU	203	-	-	-	X
57	MG	BU	204	-	-	-	X
57	MG	BV	201	-	-	-	X
57	MG	BX	3001	-	-	-	X
57	MG	CA	3067	-	-	-	X
57	MG	CA	3130	-	-	-	X
57	MG	CA	3167	-	-	-	X
57	MG	CA	3168	-	-	-	X
57	MG	DA	3026	-	-	-	X
57	MG	DA	3027	-	-	-	X
57	MG	DA	3029	-	-	-	X
57	MG	DA	3042	-	-	-	X
57	MG	DA	3060	-	-	-	X
57	MG	DA	3070	-	-	-	X
57	MG	DA	3090	-	-	-	X
57	MG	DA	3102	-	-	-	X
57	MG	DA	3103	-	-	-	X
57	MG	DA	3105	-	-	-	X
57	MG	DA	3119	-	-	-	X
57	MG	DA	3160	-	-	-	X
57	MG	DA	3161	-	-	-	X
57	MG	DA	3169	-	-	-	X
57	MG	DA	3191	-	-	-	X
57	MG	DA	3192	-	-	-	X
57	MG	DA	3220	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	DA	3274	-	-	-	X
57	MG	DA	3323	-	-	-	X
57	MG	DA	3325	-	-	-	X
57	MG	DA	3362	-	-	-	X
57	MG	DA	3422	-	-	-	X
57	MG	DA	3456	-	-	-	X
57	MG	DA	3464	-	-	-	X
57	MG	DA	3491	-	-	-	X
57	MG	DA	3500	-	-	-	X
57	MG	DA	3503	-	-	-	X
57	MG	DA	3602	-	-	-	X
57	MG	DA	3617	-	-	-	X
57	MG	DA	3621	-	-	-	X
57	MG	DA	3624	-	-	-	X
57	MG	DA	3657	-	-	-	X
57	MG	DA	3660	-	-	-	X
57	MG	DB	3008	-	-	-	X
57	MG	DE	3001	-	-	-	X
57	MG	DF	301	-	-	-	X
57	MG	DF	305	-	-	-	X
57	MG	DQ	3003	-	-	-	X
57	MG	DU	201	-	-	-	X
57	MG	DV	201	-	-	-	X
59	ZN	B6	102	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297127 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1497	Total	C	N	O	P	0	0	0
			32185	14324	5968	10396	1497			
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
			1544	970	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
			1678	1052	333	286	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
			812	514	146	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			820	518	147	152	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
			986	626	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		
			833	519	156	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		
			966	598	200	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	84	Total	C	N	O	S	0	0	0
			661	423	122	114	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
			731	449	156	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	12	Total	C	N	O	P	0	0	0
			252	115	46	80	11			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1599	722	287	515	73	2			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1552	697	280	502	72	1			

- 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
			1635	731	296	530	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	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
25	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

- 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
			2142	1352	426	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
			1073	688	188	196	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
			1139	709	231	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
			558	352	102	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
			517	331	102	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	B4	1	Total	Mg	0	0
			1	1		
57	BA	814	Total	Mg	0	0
			814	814		
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		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AB	1	Total 1	Mg 1	0	0
57	DF	5	Total 5	Mg 5	0	0
57	B8	2	Total 2	Mg 2	0	0
57	BE	6	Total 6	Mg 6	0	0
57	AW	2	Total 2	Mg 2	0	0
57	DU	1	Total 1	Mg 1	0	0
57	AN	2	Total 2	Mg 2	0	0
57	BP	2	Total 2	Mg 2	0	0
57	AX	15	Total 15	Mg 15	0	0
57	DN	1	Total 1	Mg 1	0	0
57	CA	169	Total 169	Mg 169	0	0
57	B5	3	Total 3	Mg 3	0	0
57	BB	23	Total 23	Mg 23	0	0
57	D8	1	Total 1	Mg 1	0	0
57	AE	1	Total 1	Mg 1	0	0
57	DB	13	Total 13	Mg 13	0	0
57	CF	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	BF	11	Total 11	Mg 11	0	0
57	BX	1	Total 1	Mg 1	0	0
57	B2	1	Total 1	Mg 1	0	0

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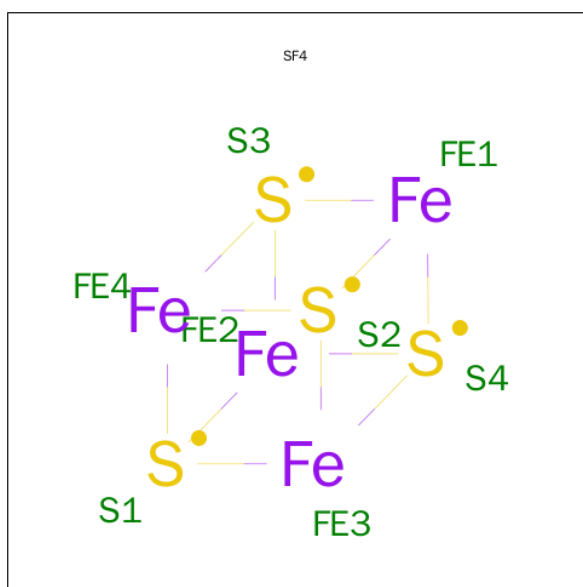
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	216	Total 216	Mg 216	0	0
57	BQ	2	Total 2	Mg 2	0	0
57	CX	2	Total 2	Mg 2	0	0
57	DV	1	Total 1	Mg 1	0	0
57	B6	2	Total 2	Mg 2	0	0
57	AM	2	Total 2	Mg 2	0	0
57	BU	4	Total 4	Mg 4	0	0
57	DR	1	Total 1	Mg 1	0	0
57	BN	3	Total 3	Mg 3	0	0
57	CT	1	Total 1	Mg 1	0	0
57	D0	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	7	Total 7	Mg 7	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	BR	2	Total 2	Mg 2	0	0
57	DA	664	Total 664	Mg 664	0	0
57	AU	1	Total 1	Mg 1	0	0
57	DW	1	Total 1	Mg 1	0	0
57	B7	5	Total 5	Mg 5	0	0
57	AL	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	BV	5	Total 5	Mg 5	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DO	2	Total 2	Mg 2	0	0
57	BO	1	Total 1	Mg 1	0	0
57	BZ	2	Total 2	Mg 2	0	0
57	DY	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	DG	1	Total 1	Mg 1	0	0
57	CD	1	Total 1	Mg 1	0	0
57	BD	10	Total 10	Mg 10	0	0
57	AT	1	Total 1	Mg 1	0	0
57	B0	2	Total 2	Mg 2	0	0
57	CE	2	Total 2	Mg 2	0	0
57	BW	4	Total 4	Mg 4	0	0
57	AY	3	Total 3	Mg 3	0	0
57	DD	4	Total 4	Mg 4	0	0
57	CK	1	Total 1	Mg 1	0	0
57	AF	1	Total 1	Mg 1	0	0
57	BH	1	Total 1	Mg 1	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	Zn	0	0
			1	1		
59	B6	1	Total	Zn	0	0
			1	1		

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

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

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	210	Total	O	0	0
			210	210		
61	AD	1	Total	O	0	0
			1	1		
61	AE	2	Total	O	0	0
			2	2		
61	AJ	1	Total	O	0	0
			1	1		
61	AL	2	Total	O	0	0
			2	2		
61	AM	2	Total	O	0	0
			2	2		
61	AV	2	Total	O	0	0
			2	2		
61	AW	4	Total	O	0	0
			4	4		
61	AX	4	Total	O	0	0
			4	4		
61	AY	1	Total	O	0	0
			1	1		
61	BA	1405	Total	O	0	1
			1406	1406		
61	BB	37	Total	O	0	0
			37	37		
61	BD	15	Total	O	0	0
			15	15		
61	BE	17	Total	O	0	0
			17	17		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BF	11	Total 11	O 11	0	0
61	BG	3	Total 3	O 3	0	0
61	BH	1	Total 1	O 1	0	0
61	BI	1	Total 1	O 1	0	0
61	BN	1	Total 1	O 1	0	0
61	BO	2	Total 2	O 2	0	0
61	BP	13	Total 13	O 13	0	0
61	BQ	4	Total 4	O 4	0	0
61	BR	2	Total 2	O 2	0	0
61	BS	2	Total 2	O 2	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	4	Total 4	O 4	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	3	Total 3	O 3	0	0
61	BX	3	Total 3	O 3	0	0
61	BZ	1	Total 1	O 1	0	0
61	B0	6	Total 6	O 6	0	0
61	B1	2	Total 2	O 2	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	4	Total 4	O 4	0	0
61	B6	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	B7	3	Total 3	O 3	0	0
61	B8	13	Total 13	O 13	0	0
61	B9	1	Total 1	O 1	0	0
61	CA	156	Total 156	O 156	0	0
61	CE	2	Total 2	O 2	0	0
61	CH	1	Total 1	O 1	0	0
61	CJ	1	Total 1	O 1	0	0
61	CK	1	Total 1	O 1	0	0
61	CL	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CW	2	Total 2	O 2	0	0
61	CX	2	Total 2	O 2	0	0
61	CY	1	Total 1	O 1	0	0
61	DA	989	Total 989	O 989	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	18	Total 18	O 18	0	0
61	DE	5	Total 5	O 5	0	0
61	DF	4	Total 4	O 4	0	0
61	DN	2	Total 2	O 2	0	0
61	DP	12	Total 12	O 12	0	0
61	DQ	1	Total 1	O 1	0	0

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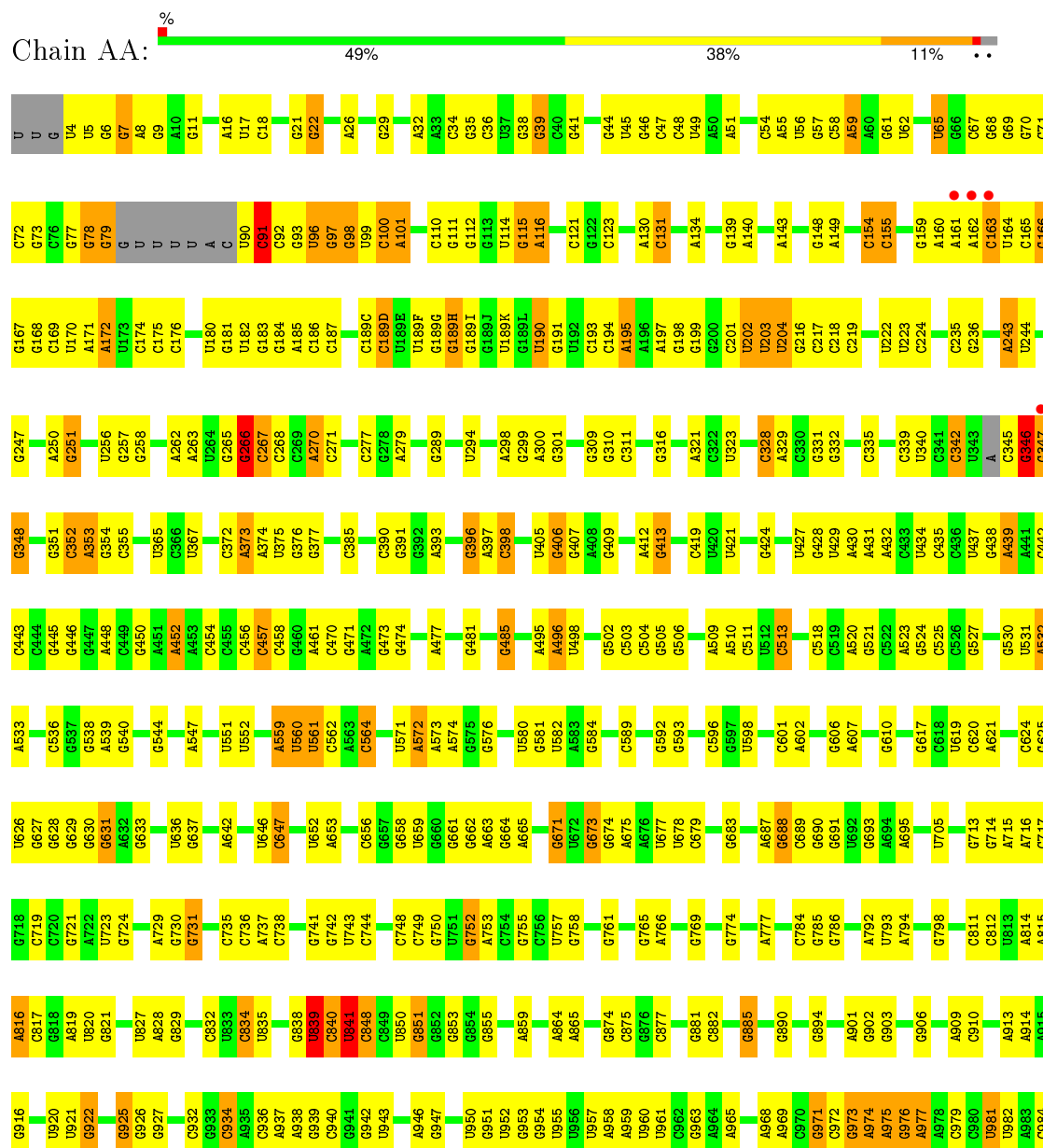
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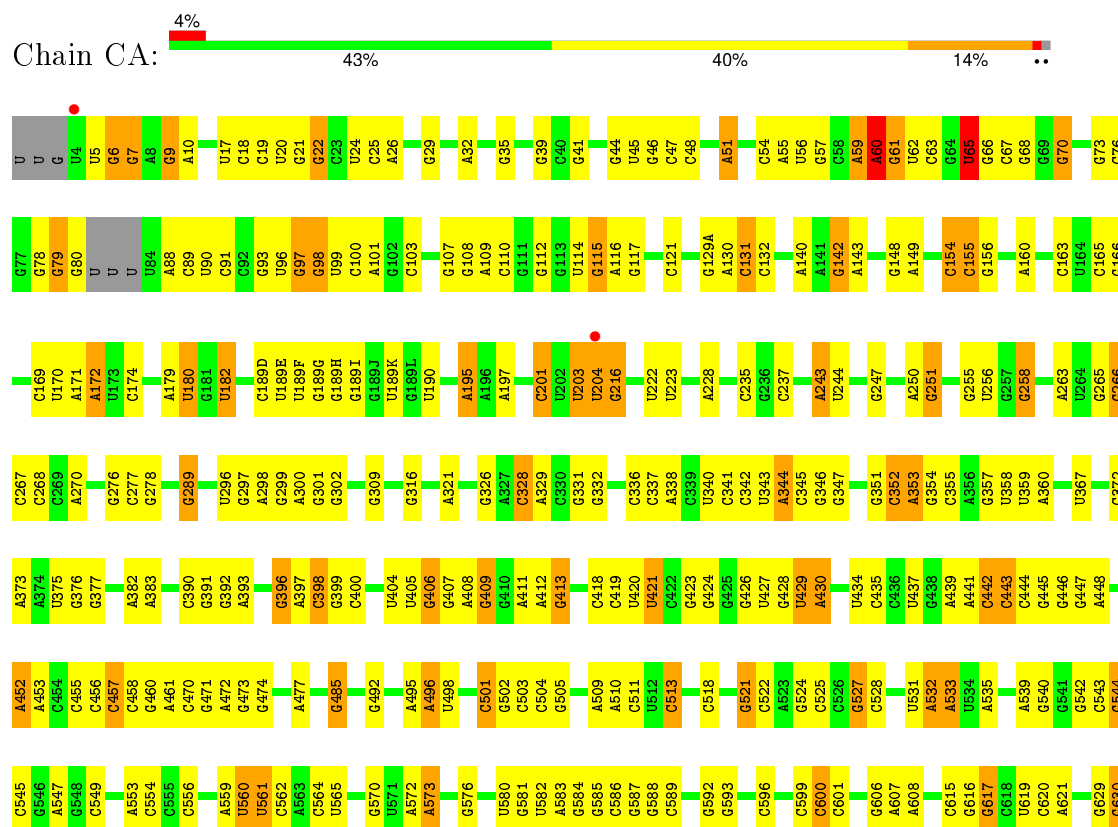
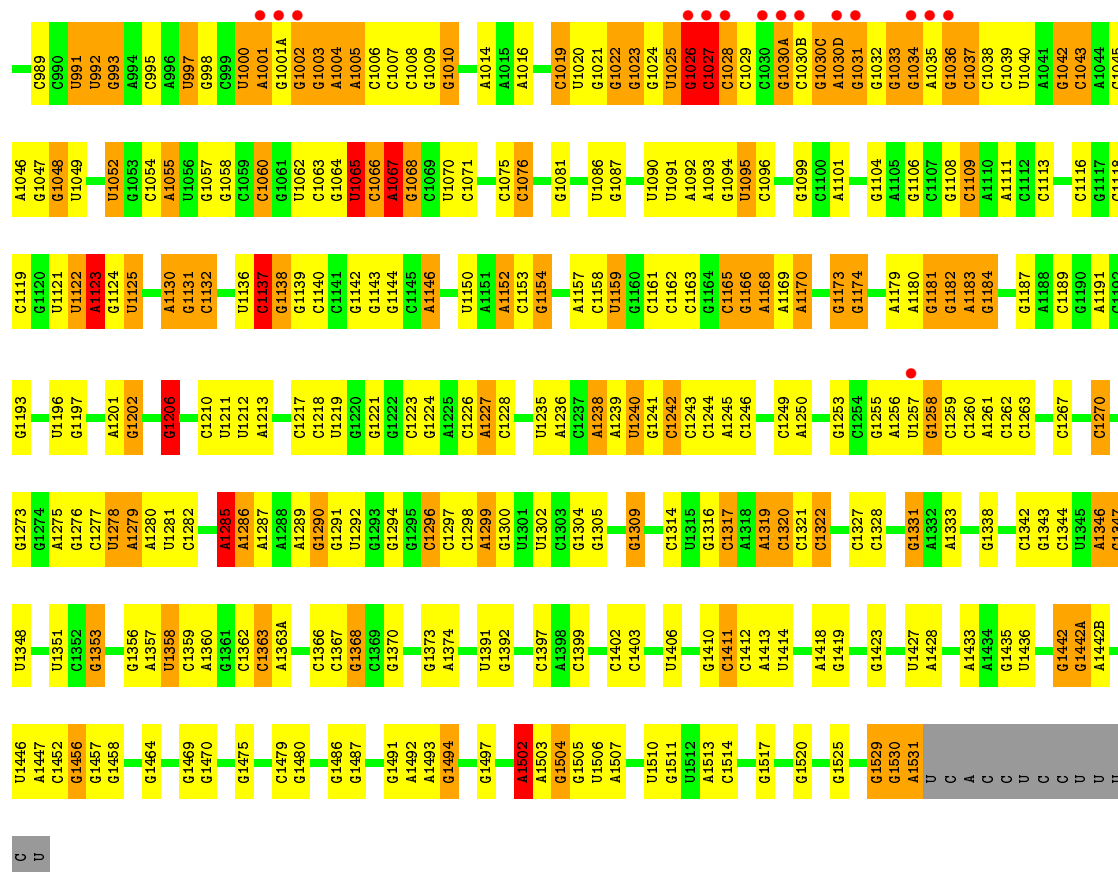
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	DT	4	Total	O	0	0
			4	4		
61	DU	1	Total	O	0	0
			1	1		
61	DV	1	Total	O	0	0
			1	1		
61	DW	1	Total	O	0	0
			1	1		
61	DX	2	Total	O	0	0
			2	2		
61	DY	1	Total	O	0	0
			1	1		
61	D0	4	Total	O	0	0
			4	4		
61	D1	1	Total	O	0	0
			1	1		
61	D3	2	Total	O	0	0
			2	2		
61	D5	1	Total	O	0	0
			1	1		
61	D6	1	Total	O	0	0
			1	1		
61	D8	3	Total	O	0	0
			3	3		

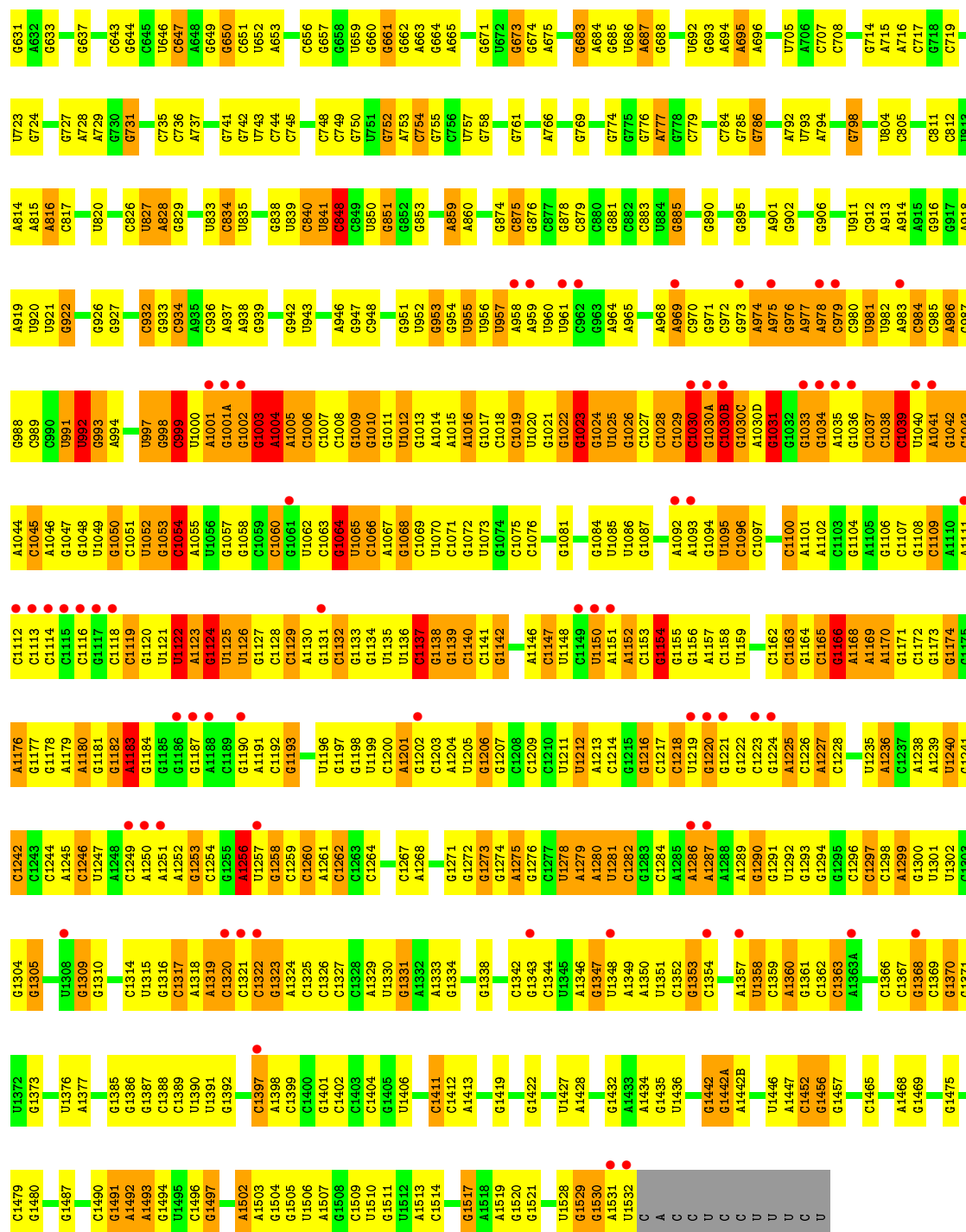
3 Residue-property plots

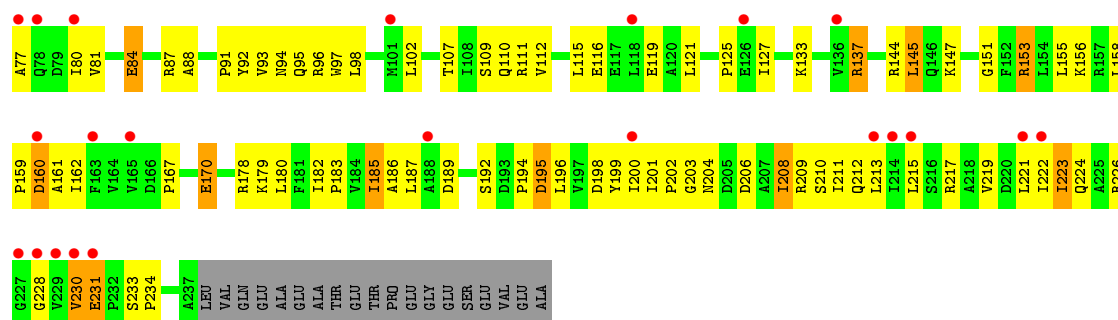
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: 16S Ribosomal RNA

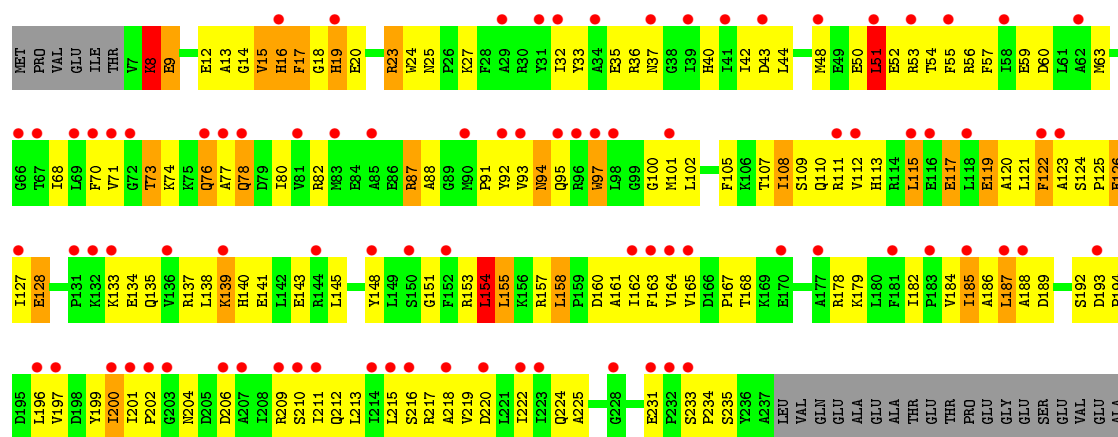




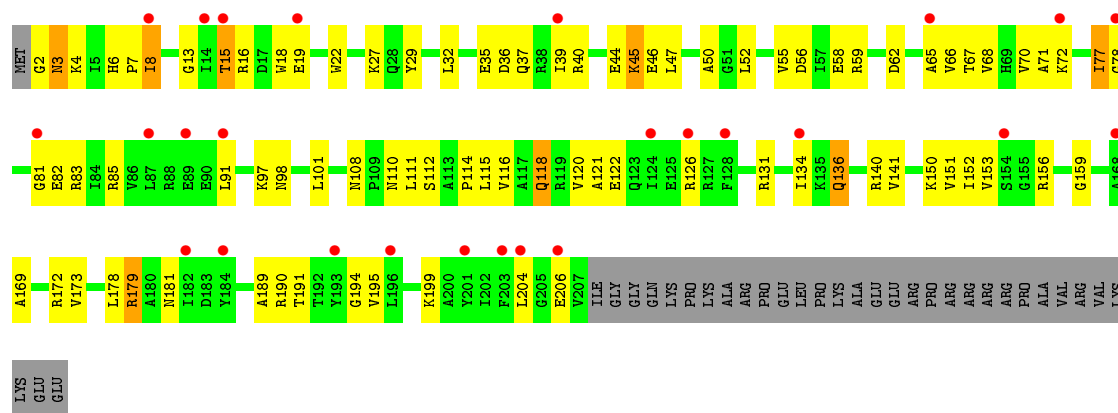




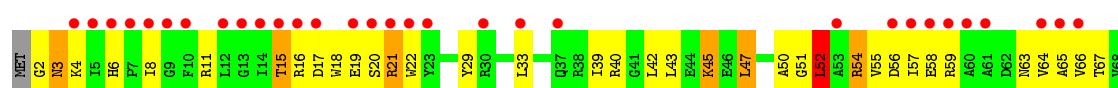
• Molecule 2: 30S ribosomal protein S2

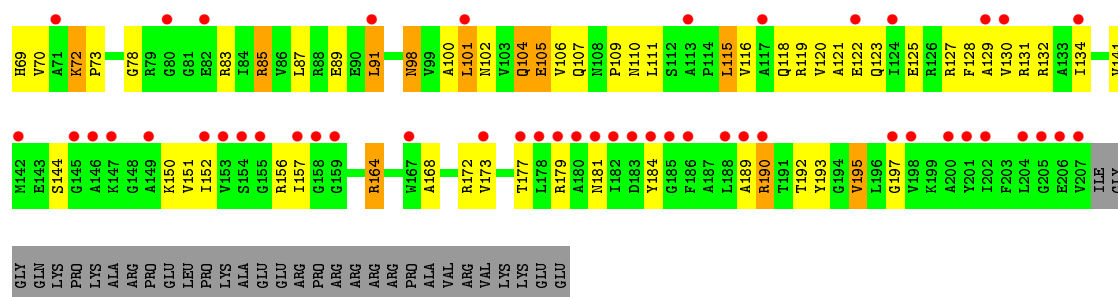


• Molecule 3: 30S ribosomal protein S3

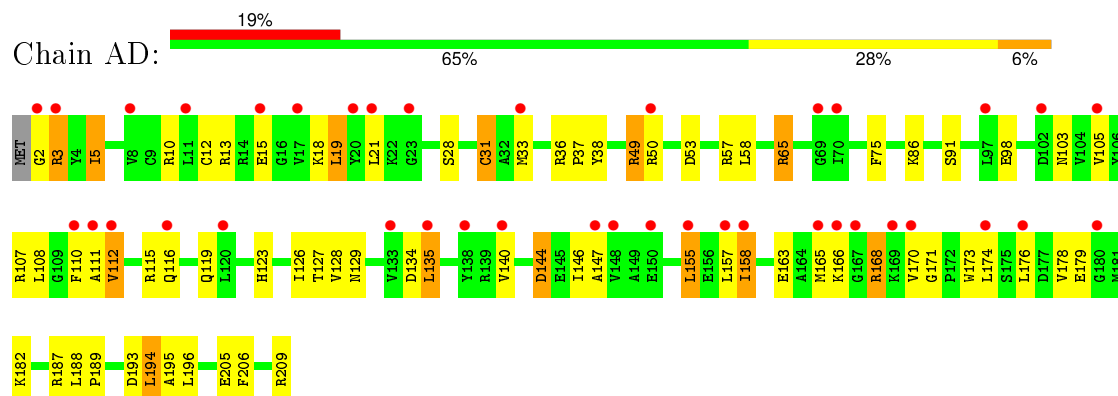


• Molecule 3: 30S ribosomal protein S3

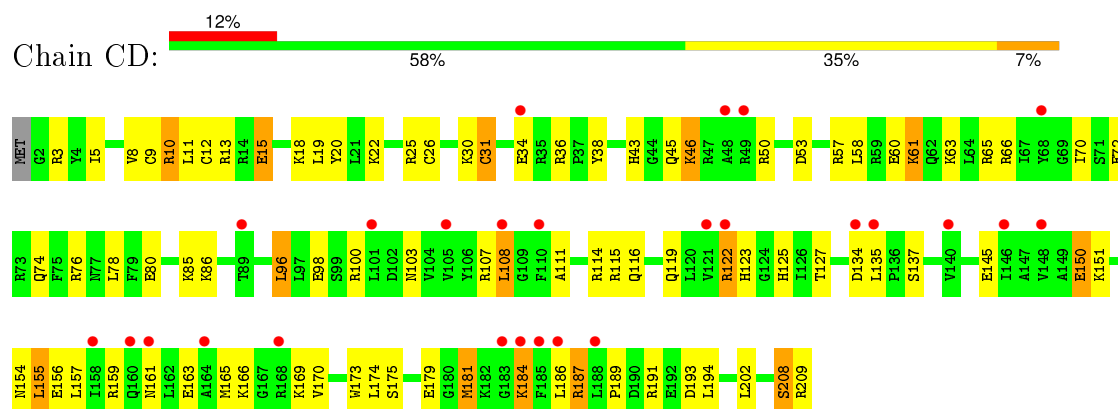




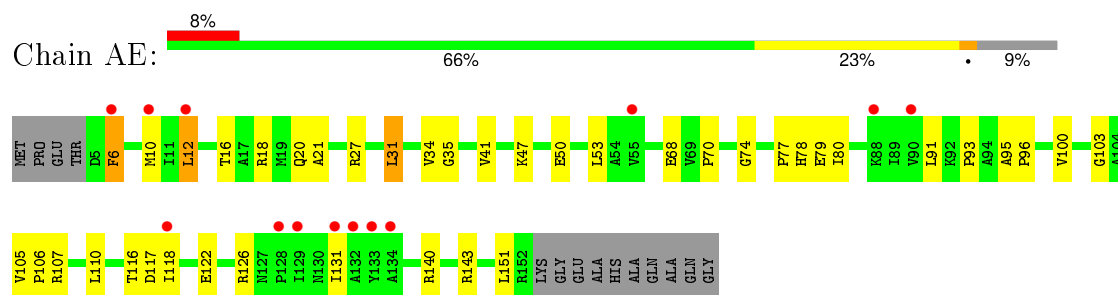
- Molecule 4: 30S ribosomal protein S4



- Molecule 4: 30S ribosomal protein S4

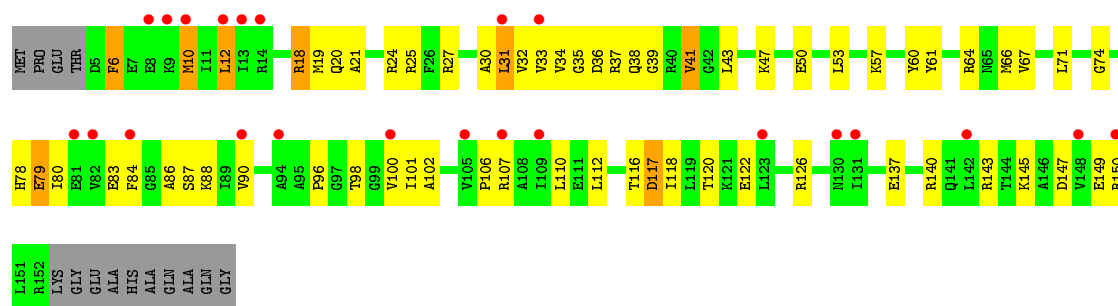


- Molecule 5: 30S ribosomal protein S5

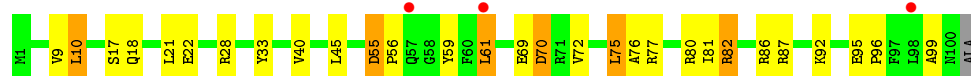


- Molecule 5: 30S ribosomal protein S5

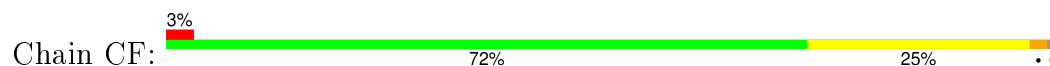




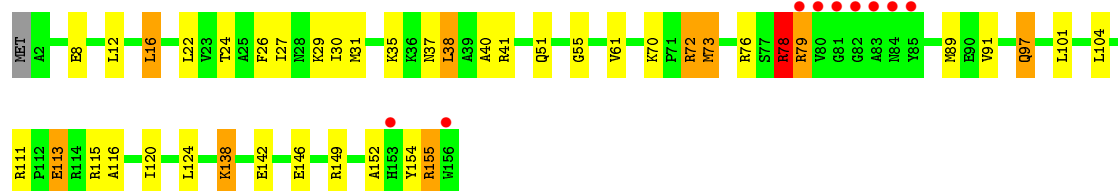
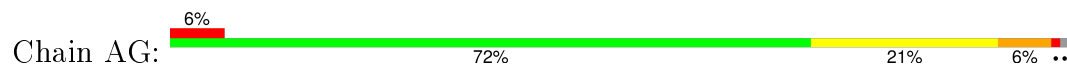
- Molecule 6: 30S ribosomal protein S6



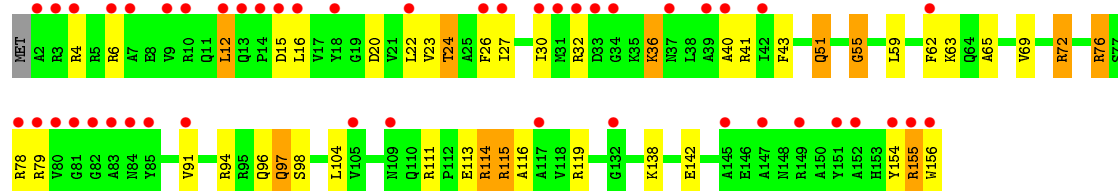
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7

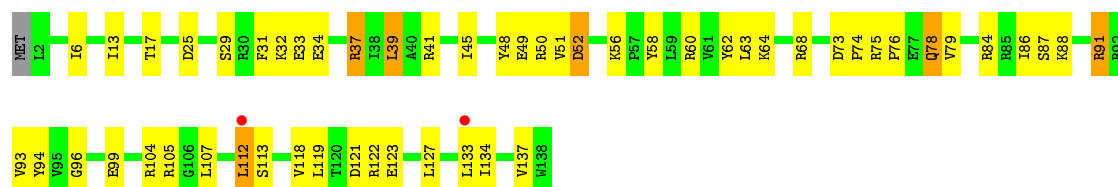


- Molecule 7: 30S ribosomal protein S7

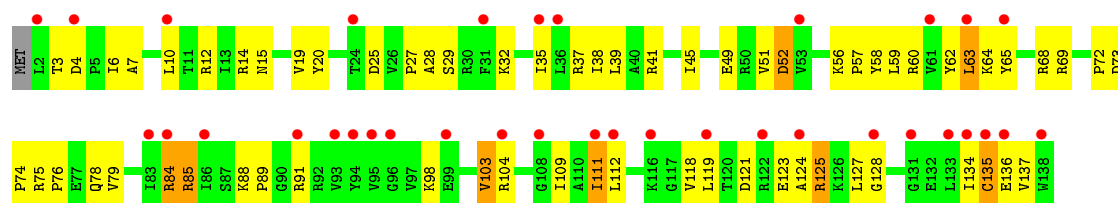


- Molecule 8: 30S ribosomal protein S8

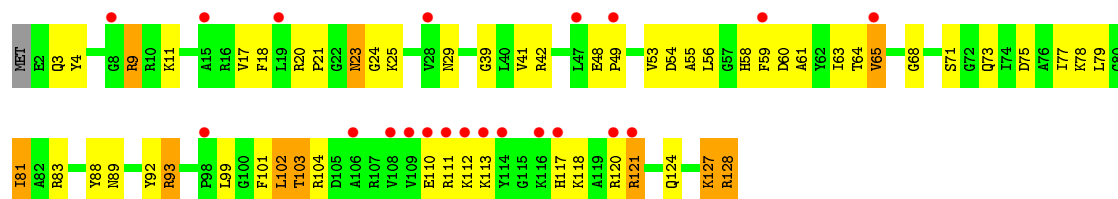




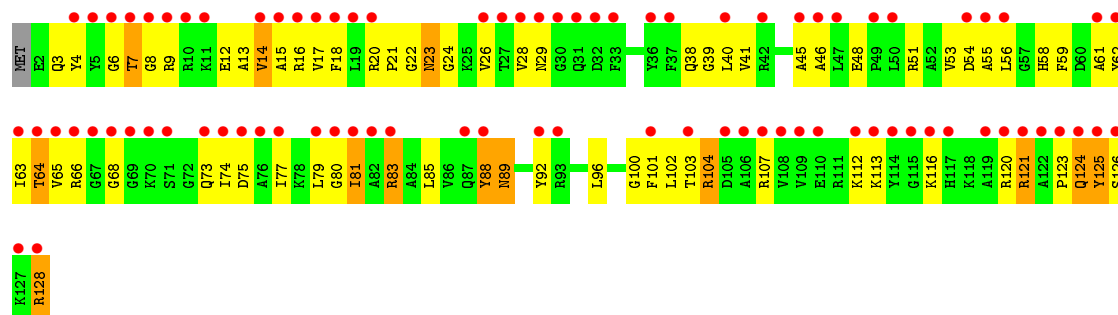
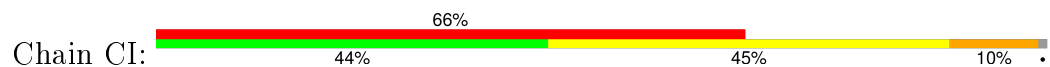
• Molecule 8: 30S ribosomal protein S8



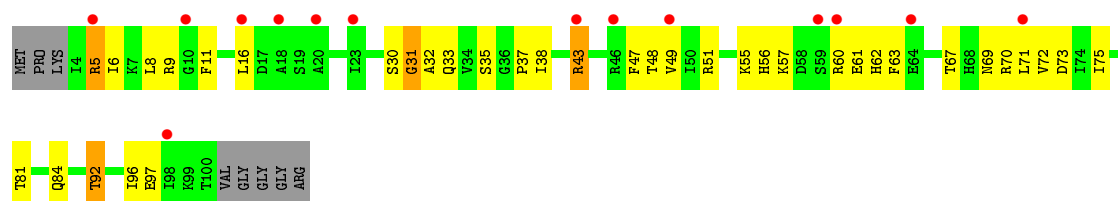
• Molecule 9: 30S ribosomal protein S9



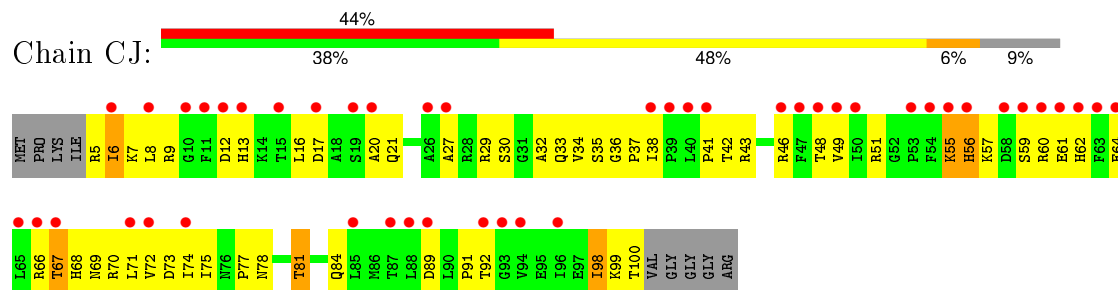
• Molecule 9: 30S ribosomal protein S9



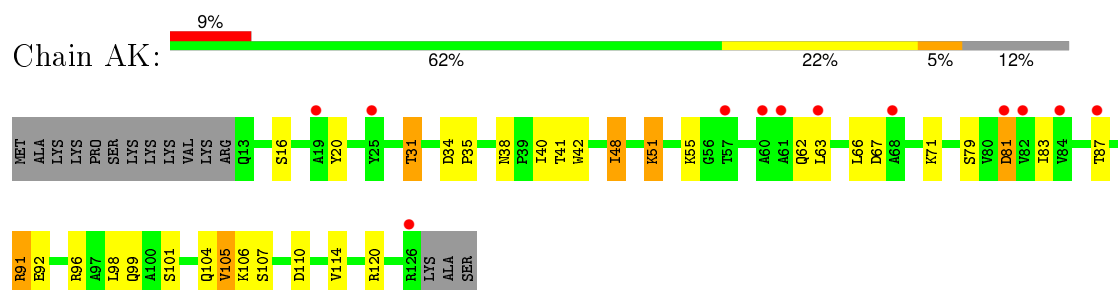
• Molecule 10: 30S ribosomal protein S10



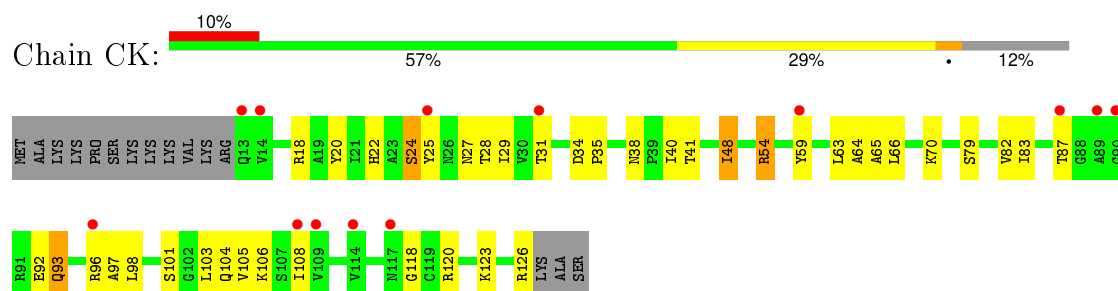
- Molecule 10: 30S ribosomal protein S10



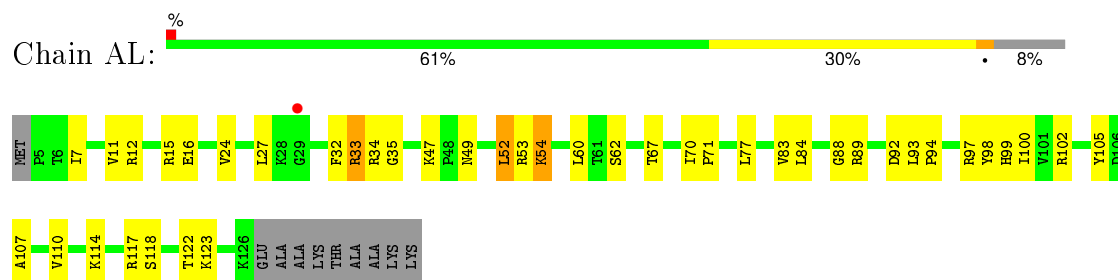
- Molecule 11: 30S ribosomal protein S11



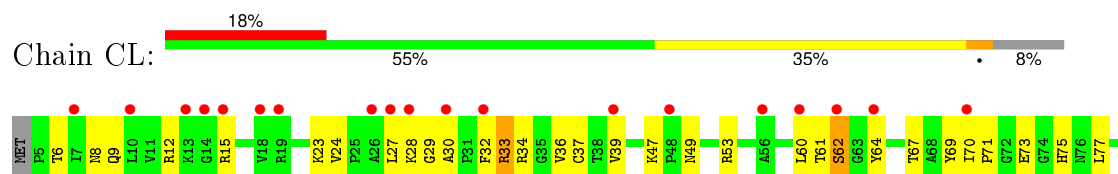
- Molecule 11: 30S ribosomal protein S11

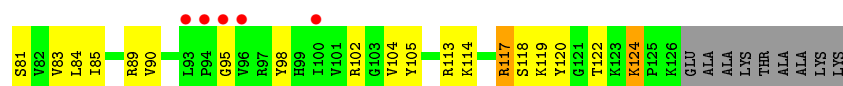


- Molecule 12: 30S ribosomal protein S12

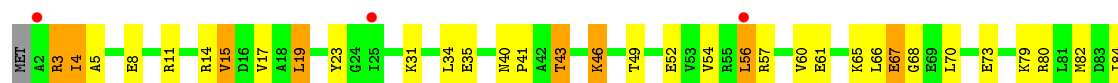


- Molecule 12: 30S ribosomal protein S12

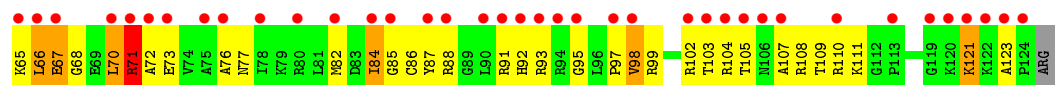




- Molecule 13: 30S ribosomal protein S13



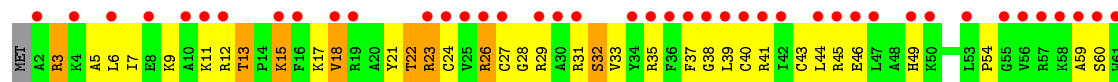
- Molecule 13: 30S ribosomal protein S13



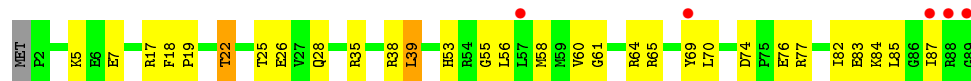
- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 15: 30S ribosomal protein S15

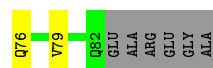
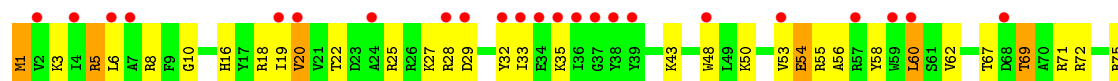


- Molecule 15: 30S ribosomal protein S15

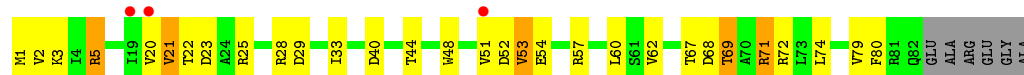




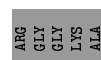
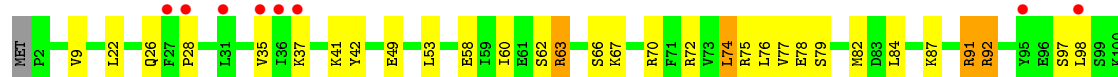
- Molecule 16: 30S ribosomal protein S16



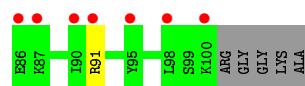
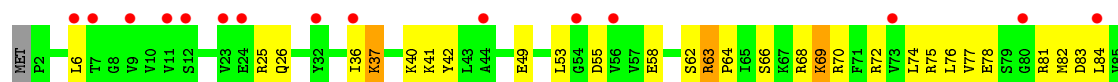
- Molecule 16: 30S ribosomal protein S16



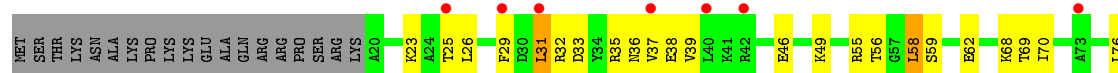
- Molecule 17: 30S ribosomal protein S17

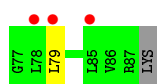


- Molecule 17: 30S ribosomal protein S17

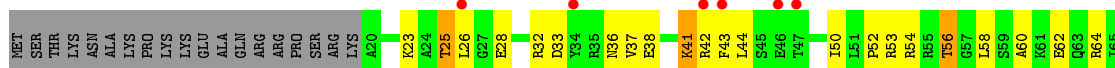


- Molecule 18: 30S ribosomal protein S18

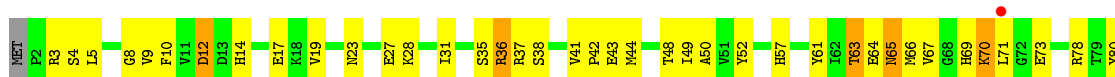
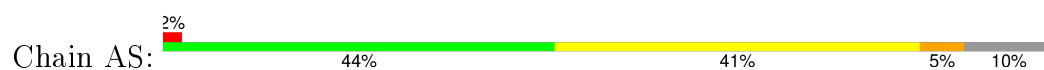




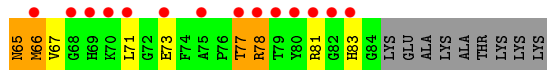
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



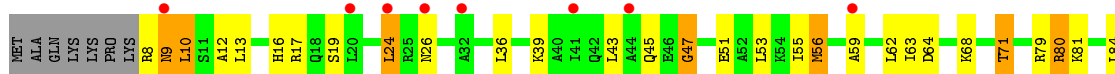
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20

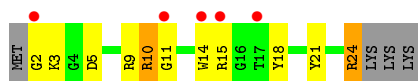


- Molecule 20: 30S ribosomal protein S20

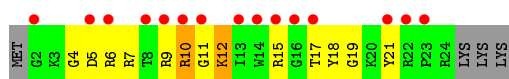




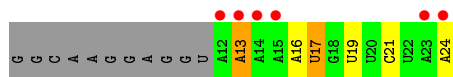
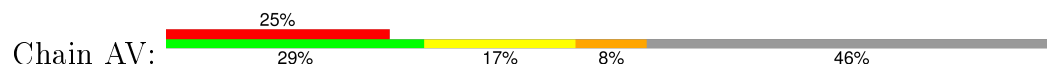
- Molecule 21: 30S ribosomal protein Thx



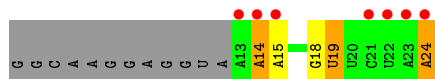
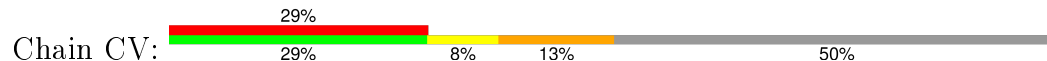
- Molecule 21: 30S ribosomal protein Thx



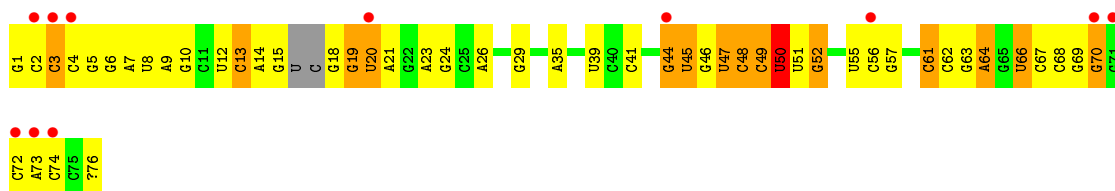
- Molecule 22: mRNA



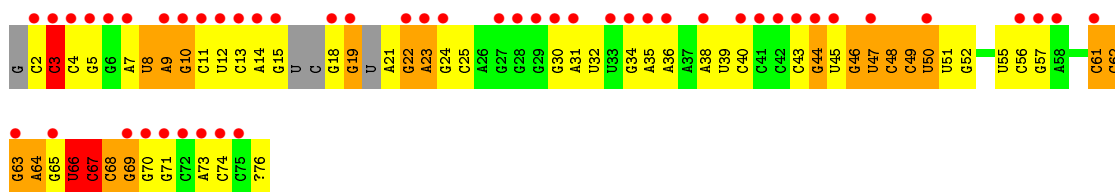
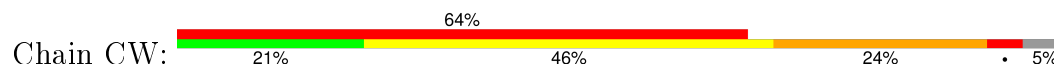
- Molecule 22: mRNA



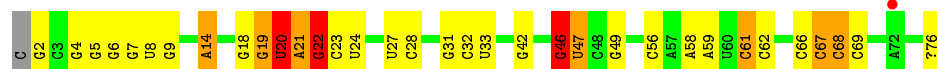
- Molecule 23: A-site tRNA



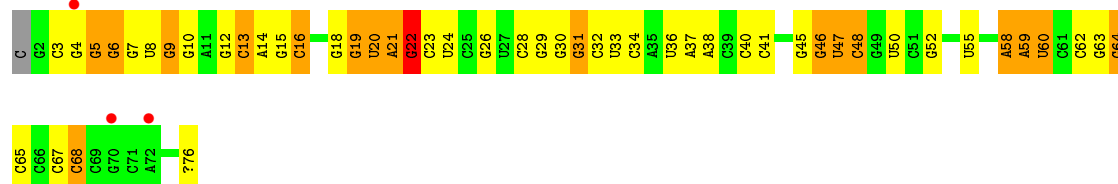
- Molecule 23: A-site tRNA



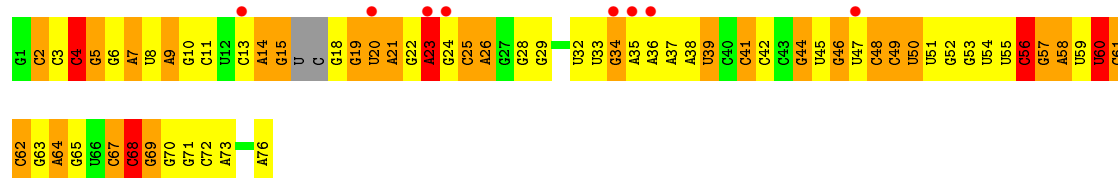
- Molecule 24: P-site tRNA



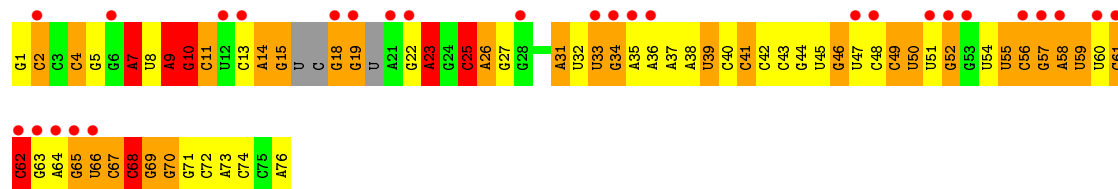
- Molecule 24: P-site tRNA



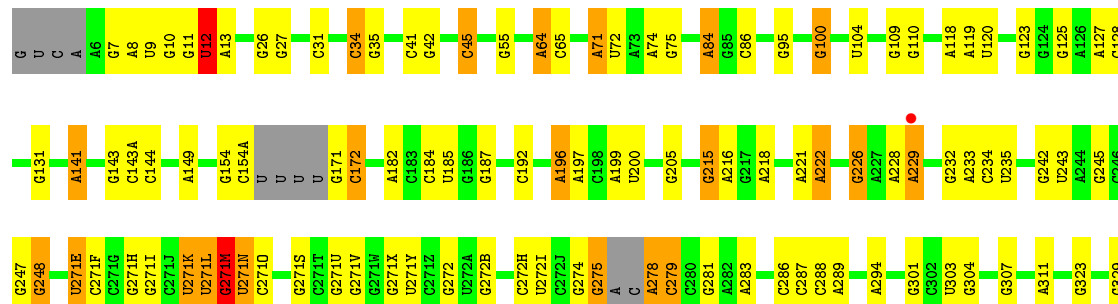
- Molecule 25: E-site tRNA



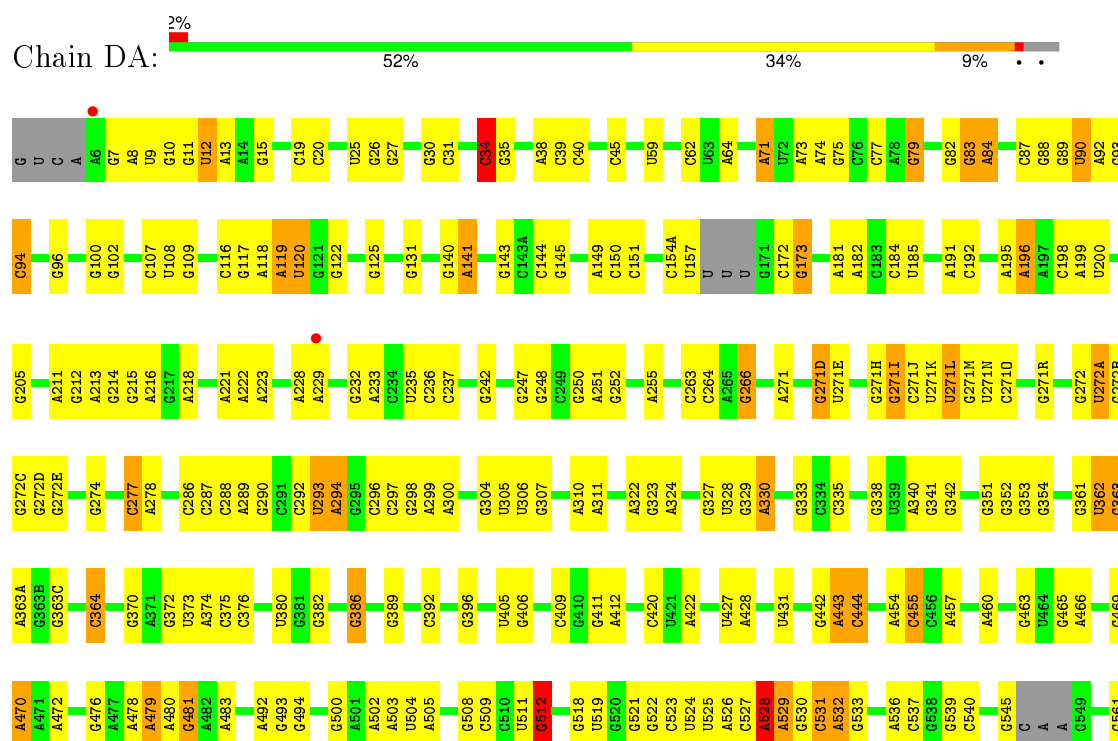
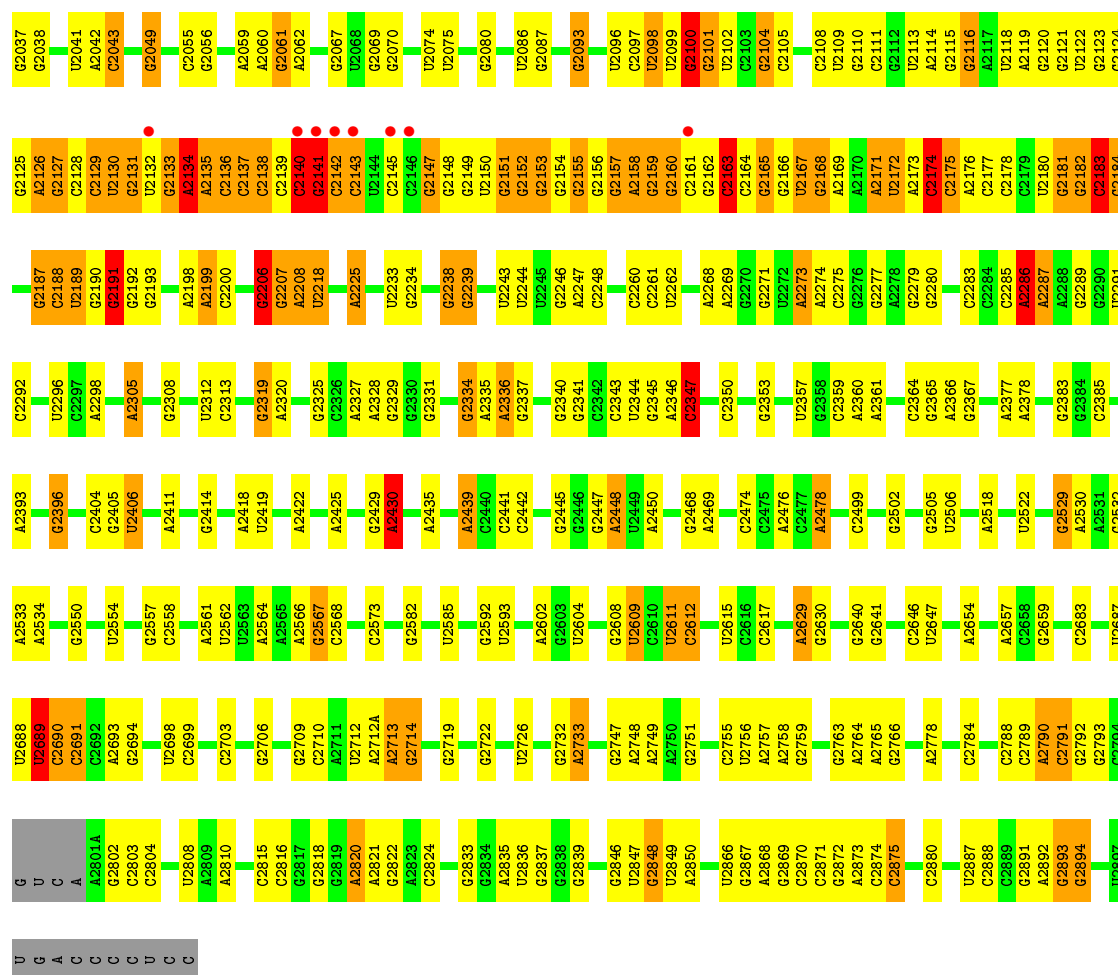
- Molecule 25: E-site tRNA



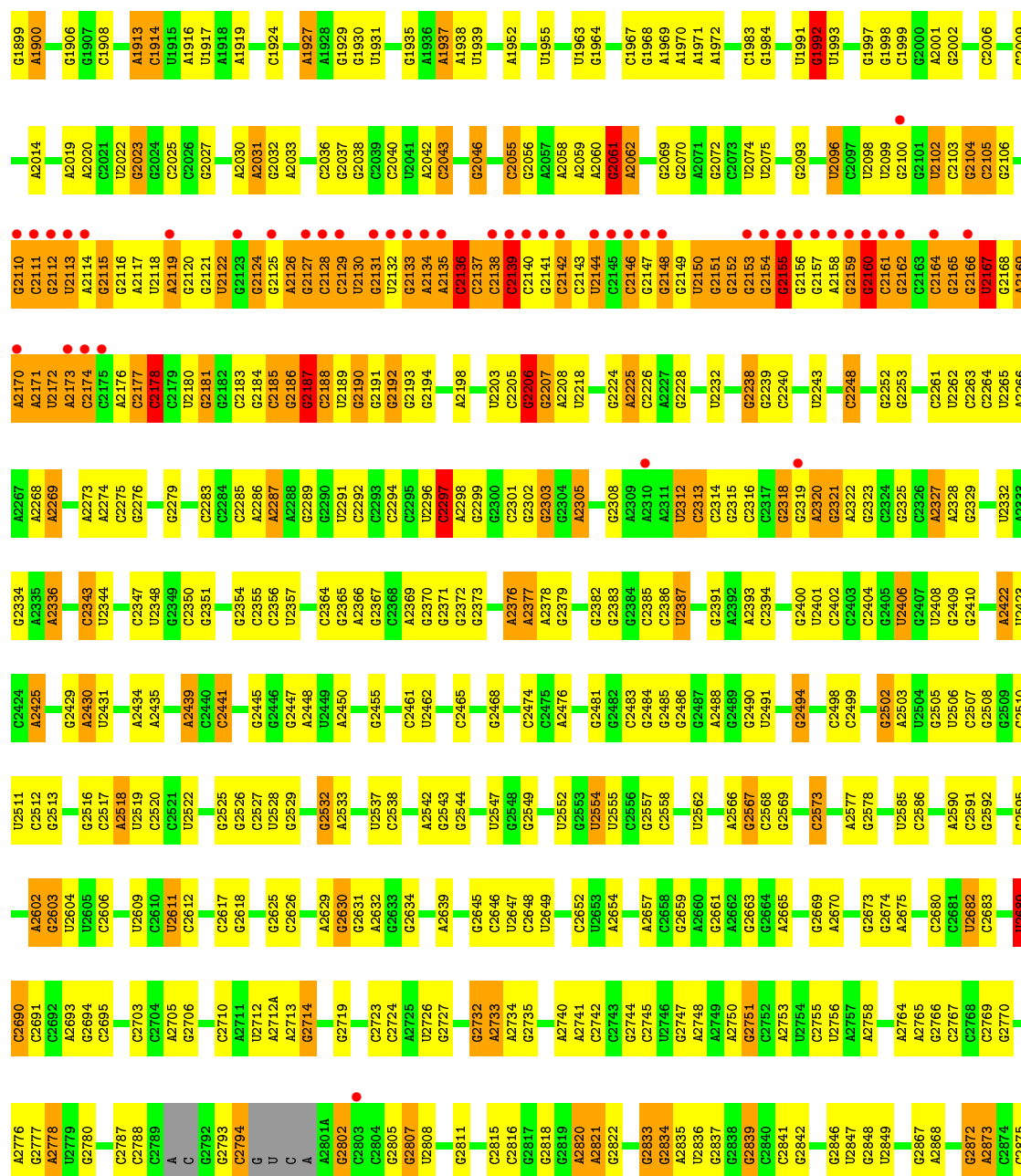
- Molecule 26: 23S Ribosomal RNA



A1783	A1689	A1419	U1273	A1143	A996	A890	G792	A575	A330
A1784	A1674	U1420	A1274	G1144	G997	G892	A793	U576	A331
A1785	G1674	G1421	A1278	C1153	C998	C893	G794	A578	C335
A1786	G1674	G1422	A1278	C1154	C999	C894	G795	C579	C352
A1791	C1683	C1428	U1292	U1155	U1000	U895	G796	C580	
A1794	C1684	C1429	C1293	A1155	A1001	A896	C797	C581	
C1795	C1686	C1430	C1297	G1164	G1002	C897	A800	G582	A359
C1796	C1687	C1431	U1300	U1165	C1005	C898	A804	G583	G360
C1797	U1688	U1542	A1301	U1166	U1006	A899	G805	A586	G361
C1798	A1689	G1434	A1302	U1167	G1008	A900	C812	C587	U362
C1799	U1689	G1441	G1303	G1170	A1009	A901	C814	U588	A363A
C1800	U1693	G1442	G1303	G1171	U1012	C804	C814	C589	G363B
A1803	G1696	A1445	G1310	A1173	C1013	U907	U813	G592	G363C
G1814	G1697	G1447	U1313	A1174	U1019	A910	U813	C601	A370
A1815	A1698	G1448	C1314	U1175	A911	A911	C814	U504	A371
G1816	G1699	G1449	C1315	G1176	A1020	A918	C817	A505	G372
G1817	A1700	G1450	C1315	A1177	A1021	A918	G818	G506	
U1818	A1701	G1451	C1315	A1178	G1022	A926	A819	A603	U380
A1825	G1702	A1452	A1342	C1179	U1025	U826	U826	C605	U383
C1958	G1703	U1453	C1345	C1180	U1026	U827	U827	U606	
U1963	U1709	G1455	C1345	G1187	A1027	G832	U828	U607	
G1964	C1710	G1467	U1352	C1201	A1028	A833	U830	G512	G386
C1967	C1711	G1467	A1353	A941	A1033	A941	G831	A515	G389
G1970	U1713	A1586	A1354	A1204	U1033	G944	U839	C516	A390
A1971	G1714	A1587	G1355	A1210	C1038	A945	U840	C517	G391
A1972	G1714	A1588	A1355	U1211	C1038	G946	A841	G526	G396
C1982	G1721	C1589	A1359	A1220	G1044	G947	U842	C527	
U1993	A1722	G1593	A1360	A1220	A1045	G948	G845	A528	G400
G1996	U1739	G1594	G1364	G1223	A1046	G952	U847	G529	U405
G1997	C1746	U1602	A1365	G1223	G1047	G953	U848	C531	G406
A2001	G1753	A1608	G1371	A1226	A1048	C955	G849	C532	G407
A2002	C1754	A1609	U1372	C1230	G1051	G956	U857	C533	
G2002	G1756	A1610	G1377	G1231	C1052	A957	U858	C534	G411
G2010	A1762	A1614	A1378	G1238	C1052	U958	U859	C536	C414
U2011	G1763	A1632	A1379	U1238	C1052	A959	C859	C537	A415
G2012	G1764	C1636	G1380	U1240	C1052	A960	A866	C543	U421
A2014	C1765	A1637	A1384	A1241	C1052	C961	G875	G545	A422
C2020	U1766	C1638	U1394	G1244	C1052	U969	C876	C	A423
C2021	C1767	U1639	A1395	G1252	C1052	C971	U877	A	A428
U2022	U1768	C1648	U1396	A1253	C1052	G972	U877	A548	
C2023	A1773	C1649	U1405	G1256	C1052	G974	U880	G549	U441
U2028	G1776	G1650	U1406	G1256	C1052	C975	G881	G558	G442
G2030	U1777	G1651	C1407	G1266	C1052	A983	G882	G563	C444
A2031	U1778	G1652	C1408	U1267	C1052	A980	G883	A	U448
G2032	U1779	A1654	C1409	A1268	C1052	G993	C884	G566	
A2033	A1780	C1653	C1409	A1269	C1052	C886	C885	U567	C451
		C1654	G3446	C1270	C1052	A887	A887	G568	
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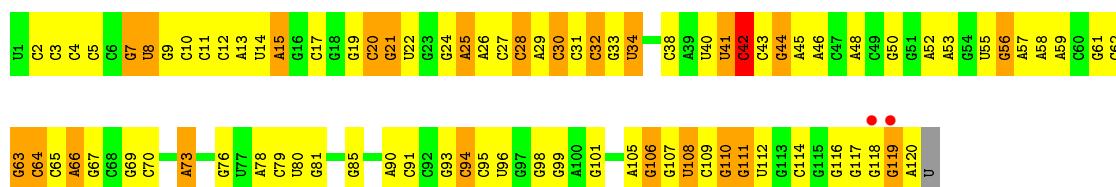


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G1793	G1667	A1567	G1488	C1291	U1205	G	G987	A901	A820	G723	G642	G563
C1794	U1795	G1568	U1489	U1292	A1210	U	C992	C902	A821	U724	A643	C564
U1796	A1669	G1569	C1293	C1293	G1211	G	G993	C903	U725	G726	C645	U565
C1797	C1575	C1576	C1407	C1297	G1212	G	C994	C904	U827	G726	A646	A567
U1798	U1576	C1408	C1408	G1297	A1213	C	C995	U905	A829	G729	G647	U568
G1799	C1577	C1409	C1409	G1298	C1218	U	C996	C908	U839	C730	G648	U569
C1800	U1578	G1410	C1410	G1299	G1219	U	A996	A909	C840	C731	G651	A571
G1801	A1579	C1411	U1300	U1300	G1220	A	G997	A910	C840	C732	C652	A572
A1902	A1580	A1412	A1301	A1301	A1220	G	A1000	A911	U847	G733	A652A	G573
A1803	U1693	G1581	G1302	G1302	G1221	A	C1005	G916	C848	A734	A652B	C574
G1804	C1694	C1582	G1303	G1303	G1221A	A	C1006	A917	A849	A735	C652C	A575
U1805	G1695	A1583	A1308	A1308	G1229	G	A1010	G921	U852	U740	G652D	U576
G1812	G1696	C1416	C1417	G1314	G1230	C	A1011	U922	C853	G741	G	G577
G1813	G1697	C1417	C1417	G1315	G1231	C	A1012	U923	C854	G741	G	C581
G1814	G1698	C1418	C1418	G1316	G1232	C	A1013	C924	C855	G748	C	G582
G1815	G1699	C1419	C1419	A1317	G1233	C	U1014	C925	C856	A751	C	A586
G1816	C1589	G1421	G1421	C1318	G1234	U	G1015	A926	U858	A752	C	C587
G1826	U1514	A1427	A1427	G1319	G1235	U	G1016	G932	C859	C753	A	U588
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A1829	G1519	C1430	C1430	C1319	G1238	U	U1019	C935	C862	A765	G	C591
C1830	U1520	U1431	U1431	G1320	G1239	A	U1020	A936	A863	G770	C	G592
U1833	C1600	G1601	G1601	U1321	G1240	A	G1021	C937	C864	G770	C	U597
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G1835	C1603	G1603	G1603	G1323	G1242	A	U1023	A941	U867	A775	G652U	G600
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G1906	A1931	A1654	A1654	U1524	G1313	U	A	C1012	C941	G801	G686	A621
G1907	A1932	A1654	A1654	U1525	G1314	U	A	C1013	C942	G801	G686	A621
G1908	A1933	A1654	A1654	U1526	G1315	U	A	C1014	C943	G801	G686	A621
G1909	A1934	A1654	A1654	U1527	G1316	U	A	C1015	C944	G801	G686	A621
G1910	A1935	A1654	A1654	U1528	G1317	U	A	C1016	C945	G801	G686	A621
G1911	A1936	A1654	A1654	U1529	G1318	U	A	C1017	C946	G801	G686	A621
G1912	A1937	A1654	A1654	U1530	G1319	U	A	C1018	C947	G801	G686	A621
G1913	A1938	A1654	A1654	U1531	G1320	U	A	C1019	C948	G801	G686	A621
G1914	A1939	A1654	A1654	U1532	G1321	U	A	C1020	C949	G801	G686	A621
G1915	A1940	A1654	A1654	U1533	G1322	U	A	C1021	C950	G801	G686	A621
G1916	A1941	A1654	A1654	U1534	G1323	U	A	C1022	C951	G801	G686	A621
G1917	A1942	A1654	A1654	U1535	G1324	U	A	C1023	C952	G801	G686	A621
G1918	A1943	A1654	A1654	U1536	G1325	U	A	C1024	C953	G801	G686	A621
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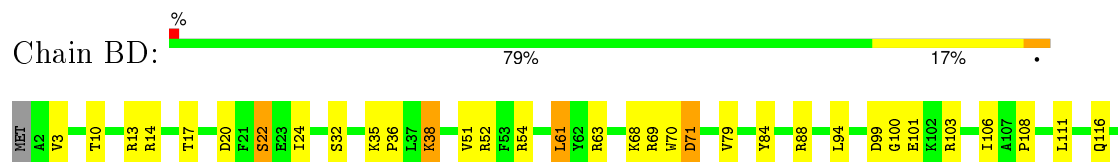


• Molecule 27: 5S Ribosomal RNA

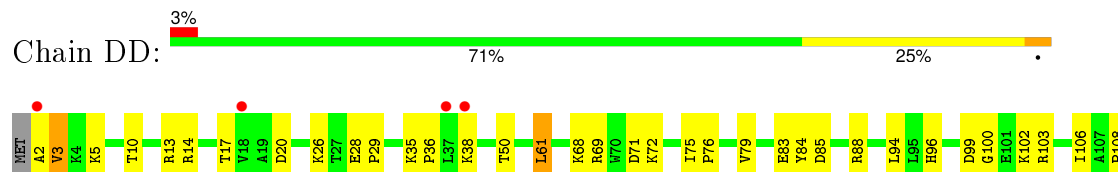




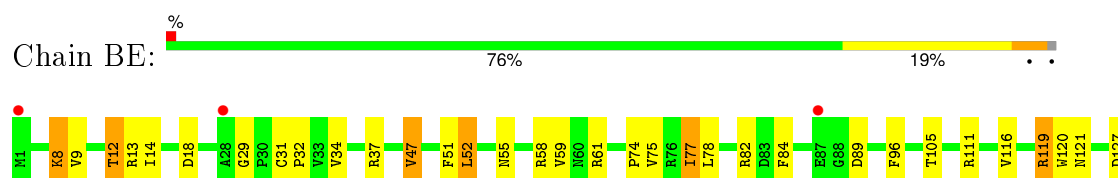
• Molecule 28: 50S ribosomal protein L2



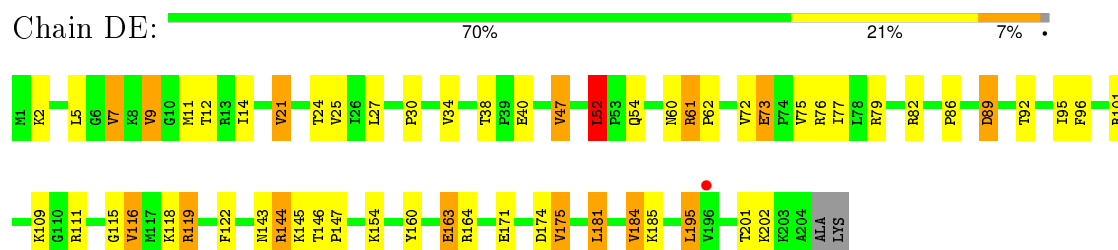
• Molecule 28: 50S ribosomal protein L2



• Molecule 29: 50S ribosomal protein L3

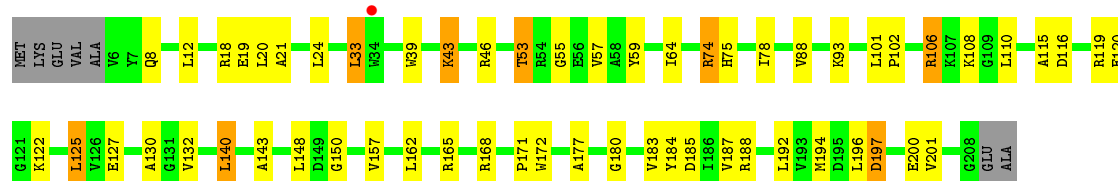


• Molecule 29: 50S ribosomal protein L3



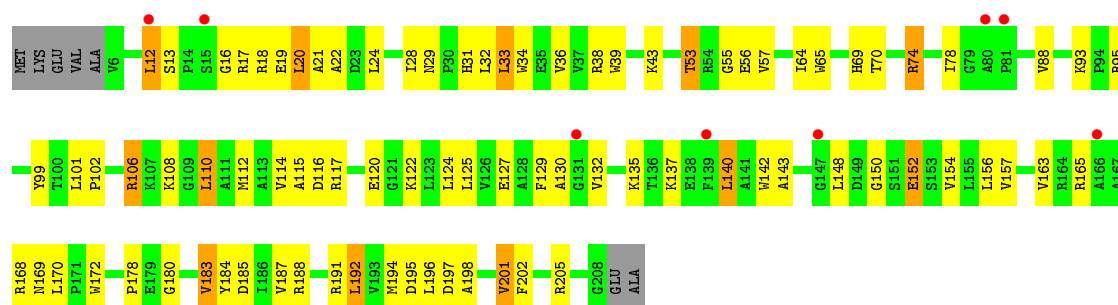
- Molecule 30: 50S ribosomal protein L4

Chain BF: 



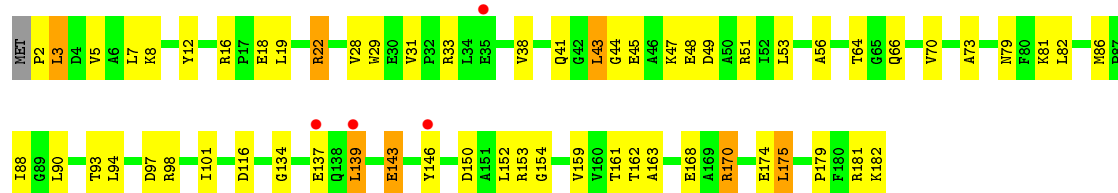
- Molecule 30: 50S ribosomal protein L4

Chain DF: 



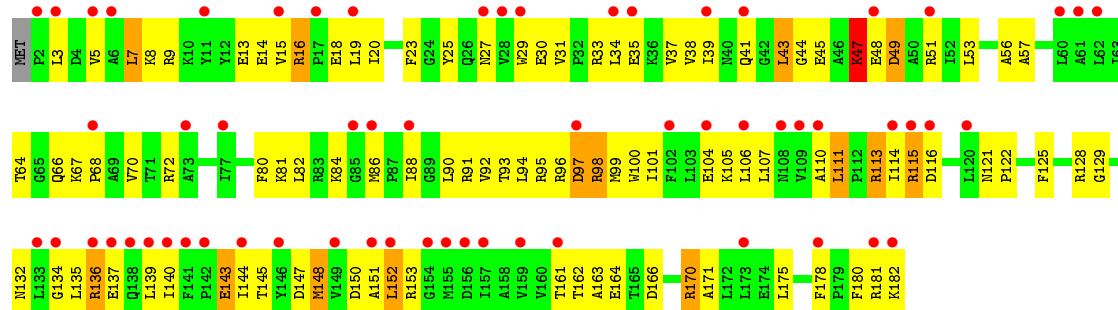
- Molecule 31: 50S ribosomal protein L5

Chain BG: 

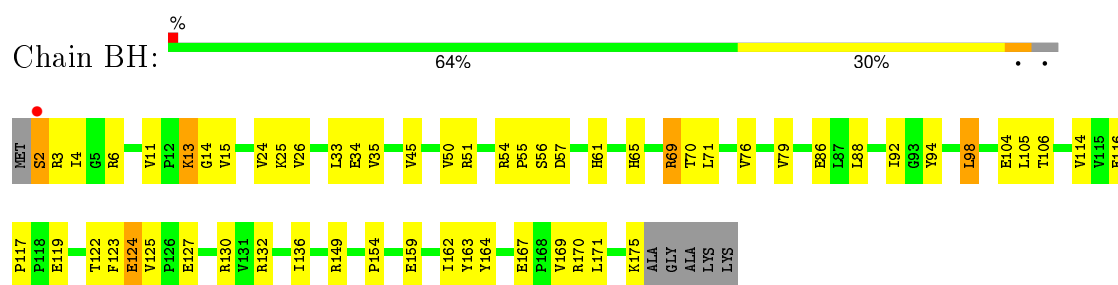


- Molecule 31: 50S ribosomal protein L5

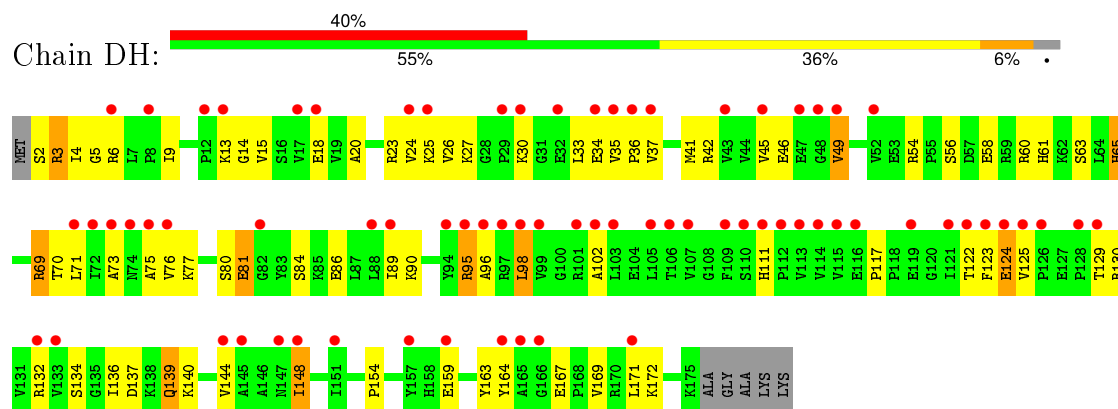
Chain DG: 



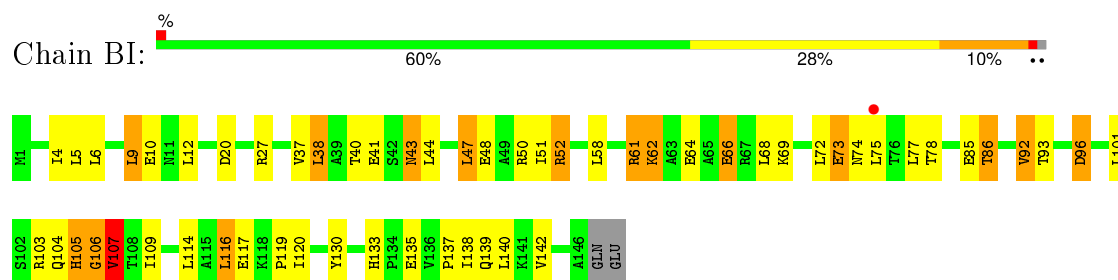
- Molecule 32: 50S ribosomal protein L6



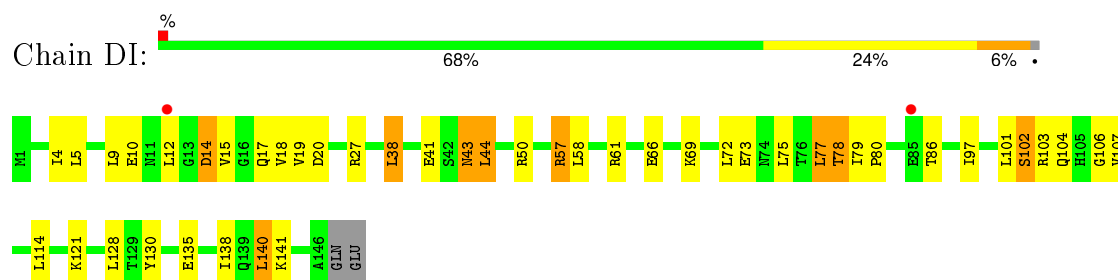
• Molecule 32: 50S ribosomal protein L6



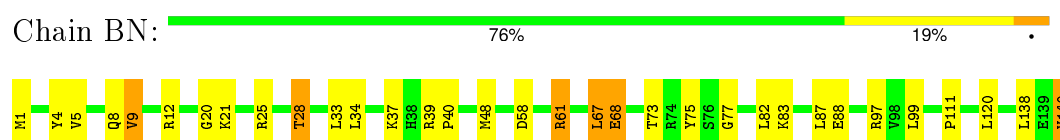
• Molecule 33: 50S ribosomal protein L9



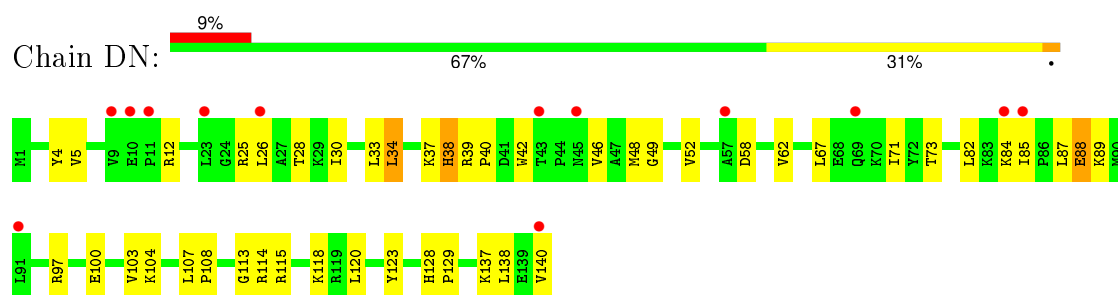
• Molecule 33: 50S ribosomal protein L9



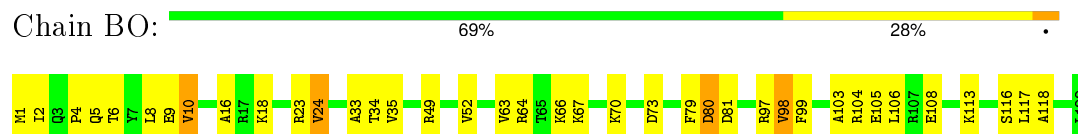
• Molecule 34: 50S ribosomal protein L13



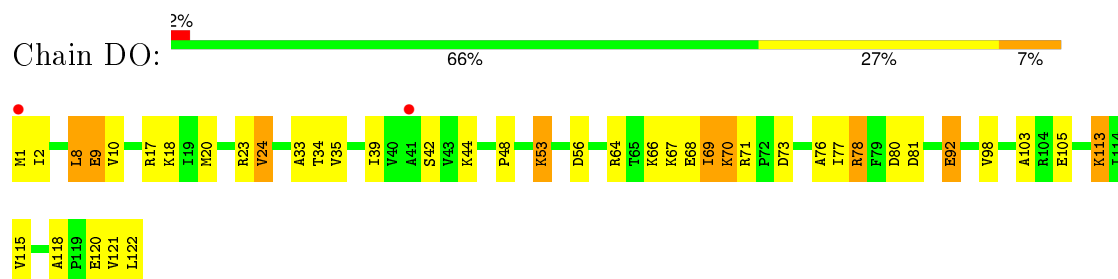
• Molecule 34: 50S ribosomal protein L13



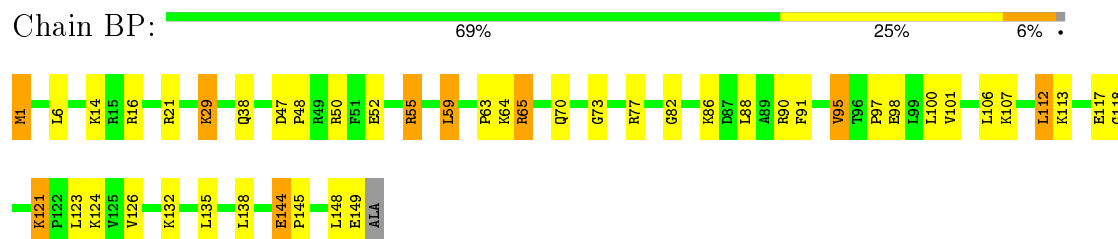
- Molecule 35: 50S ribosomal protein L14



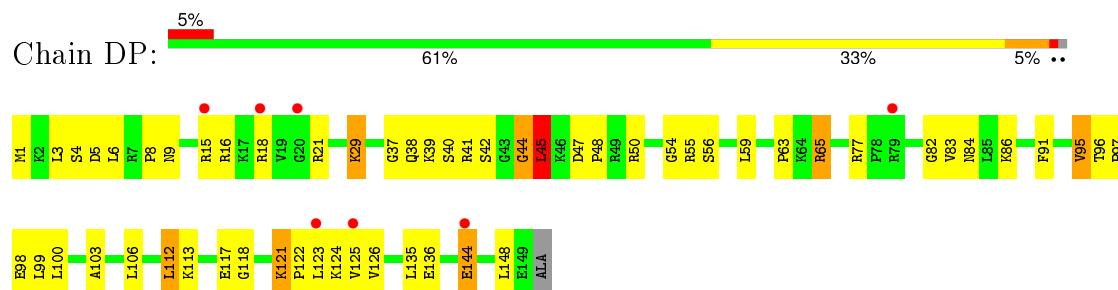
- Molecule 35: 50S ribosomal protein L14



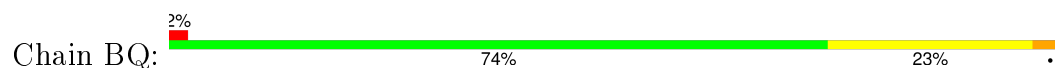
- Molecule 36: 50S ribosomal protein L15

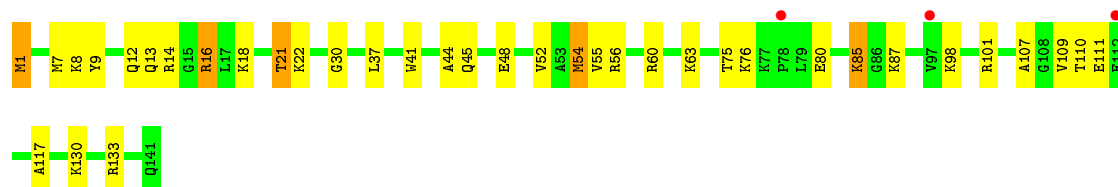


- Molecule 36: 50S ribosomal protein L15

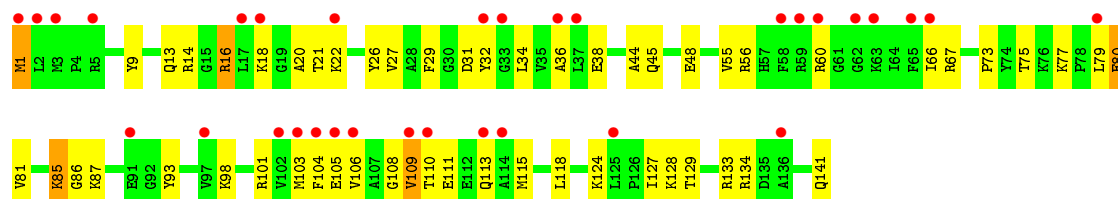


- Molecule 37: 50S ribosomal protein L16





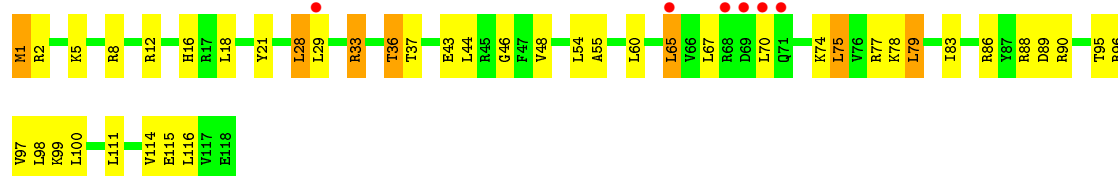
- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17



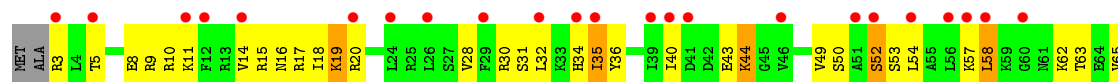
- Molecule 38: 50S ribosomal protein L17

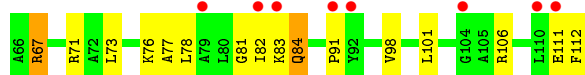


- Molecule 39: 50S ribosomal protein L18



- Molecule 39: 50S ribosomal protein L18





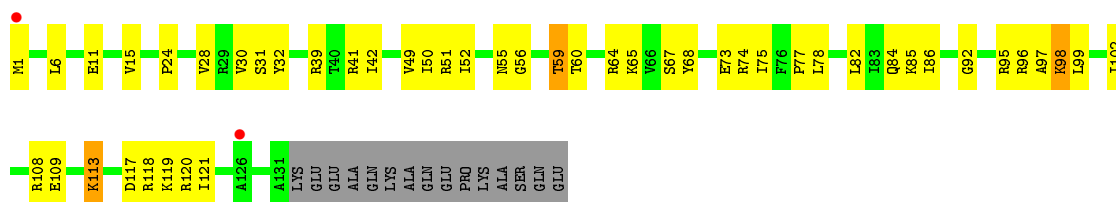
- Molecule 40: 50S ribosomal protein L19

Chain BT: 66% 22% 10%



- Molecule 40: 50S ribosomal protein L19

Chain DT: 57% 31% 10%



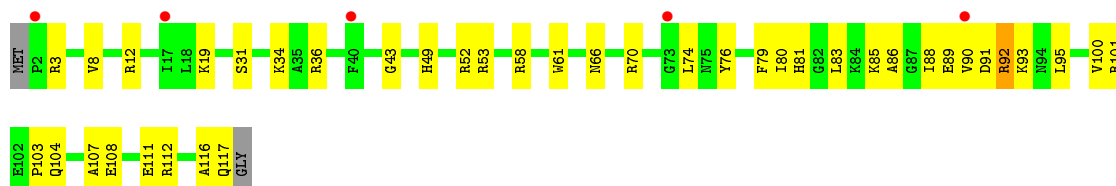
- Molecule 41: 50S ribosomal protein L20

Chain BU: 76% 21% 10%



- Molecule 41: 50S ribosomal protein L20

Chain DU: 4% 64% 33%



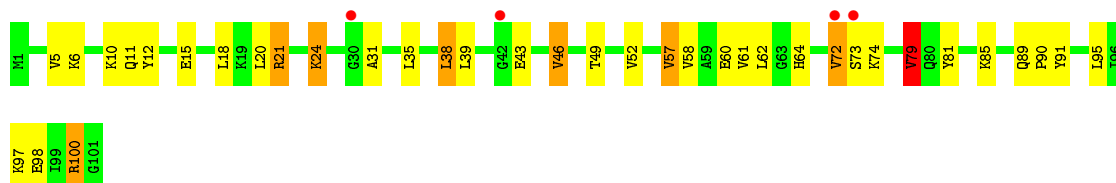
- Molecule 42: 50S ribosomal protein L21

Chain BV: 72% 23% 5%



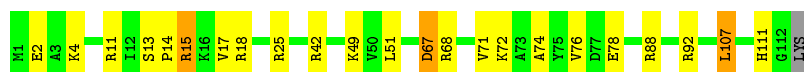
- Molecule 42: 50S ribosomal protein L21

Chain DV: 4% 63% 29% 7%



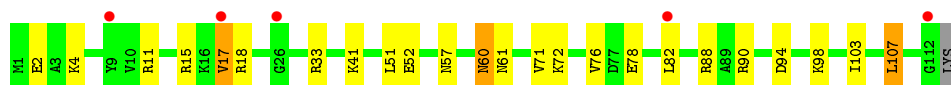
- Molecule 43: 50S ribosomal protein L22

Chain BW: 79% 18% . .



- Molecule 43: 50S ribosomal protein L22

Chain DW: 4% 78% 19% . .



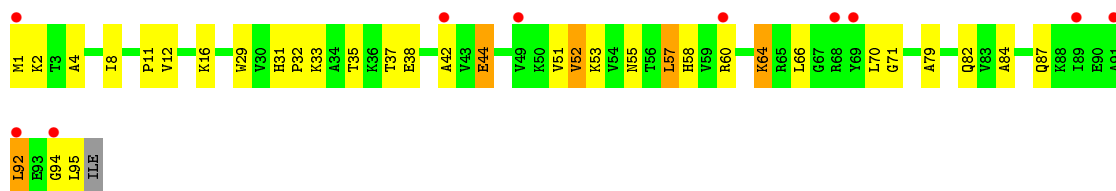
- Molecule 44: 50S ribosomal protein L23

Chain BX: 75% 20% . .



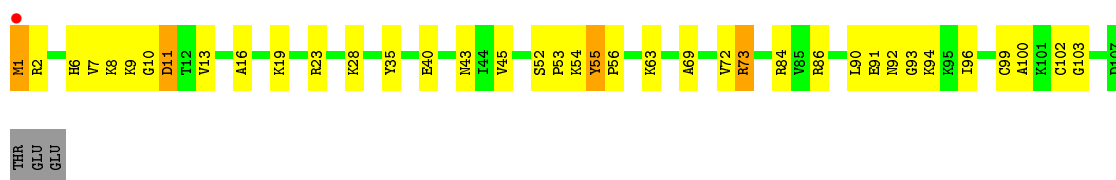
- Molecule 44: 50S ribosomal protein L23

Chain DX: 10% 64% 30% 5% .

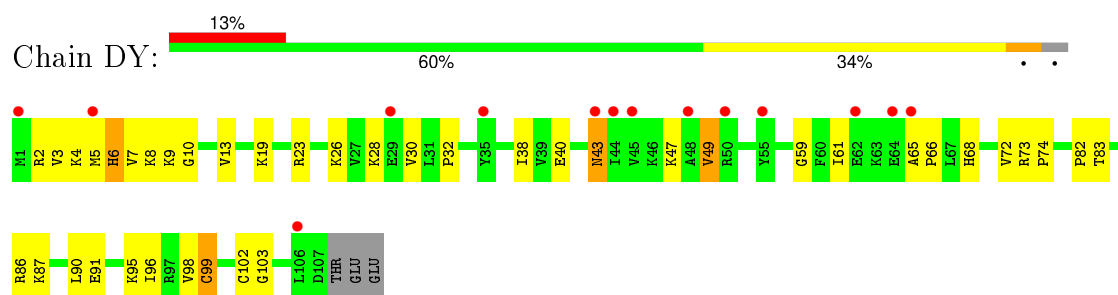


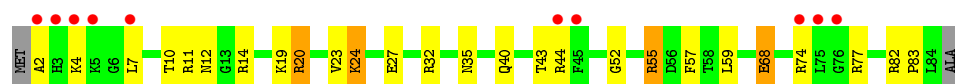
- Molecule 45: 50S ribosomal protein L24

Chain BY: 63% 31% . .

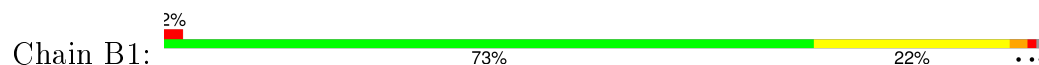


- Molecule 45: 50S ribosomal protein L24

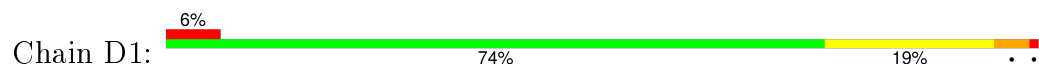




- Molecule 48: 50S ribosomal protein L28



- Molecule 48: 50S ribosomal protein L28



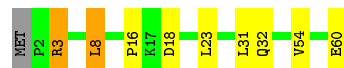
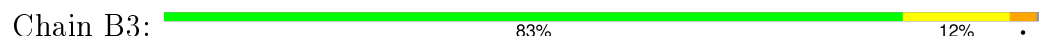
- Molecule 49: 50S ribosomal protein L29



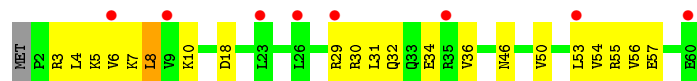
- Molecule 49: 50S ribosomal protein L29



- Molecule 50: 50S ribosomal protein L30

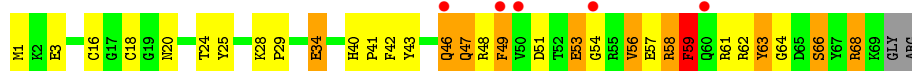


- Molecule 50: 50S ribosomal protein L30

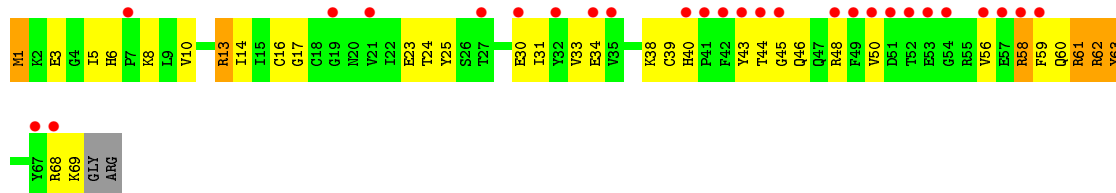
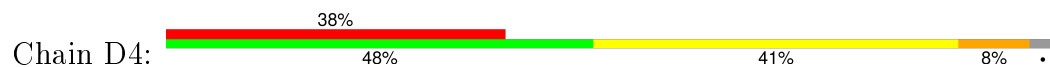


- Molecule 51: 50S ribosomal protein L31

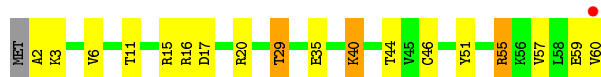




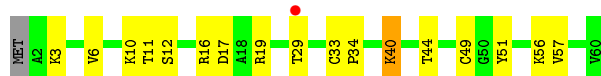
- Molecule 51: 50S ribosomal protein L31



- Molecule 52: 50S ribosomal protein L32



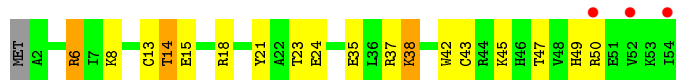
- Molecule 52: 50S ribosomal protein L32



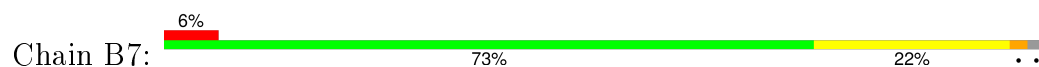
- Molecule 53: 50S ribosomal protein L33



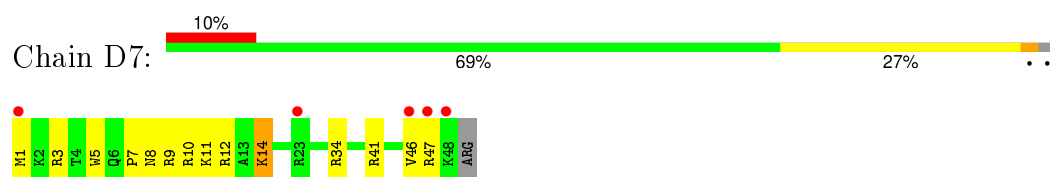
- Molecule 53: 50S ribosomal protein L33



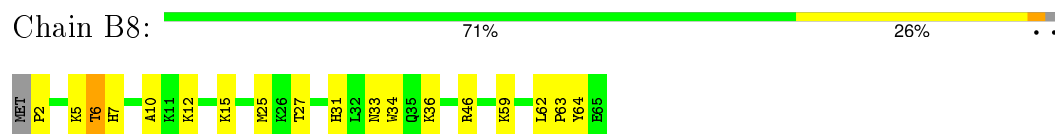
- Molecule 54: 50S ribosomal protein L34



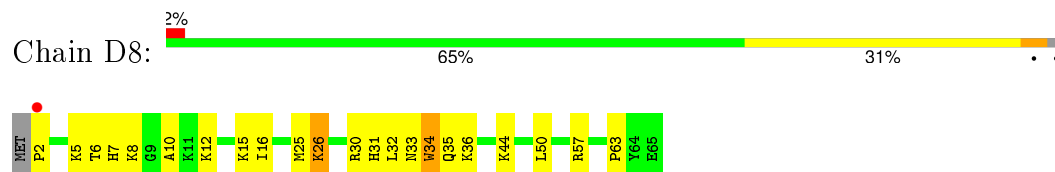
- Molecule 54: 50S ribosomal protein L34



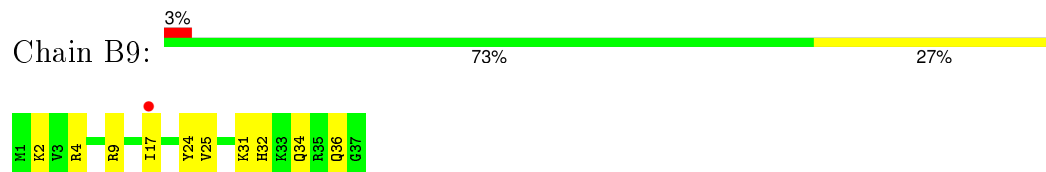
- Molecule 55: 50S ribosomal protein L35



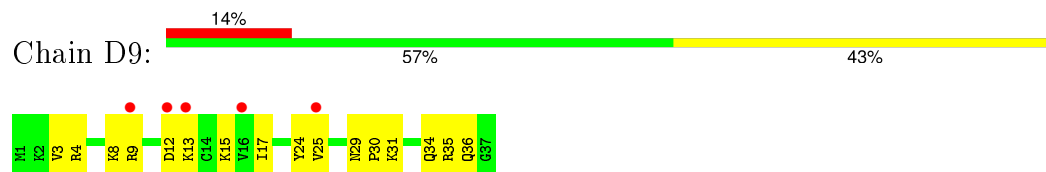
- Molecule 55: 50S ribosomal protein L35



- Molecule 56: 50S ribosomal protein L36



- Molecule 56: 50S ribosomal protein L36



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.45Å 448.85Å 619.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	151.90 – 2.60 224.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (151.90-2.60) 99.9 (224.43-2.60)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.62Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.223 , 0.264 0.235 , 0.273	Depositor DCC
R_{free} test set	88430 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 60.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 1760092 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	297127	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ZN, MIA, SF4, MG, F3N, 31H, 5MC, 4SU, 7MG, K, 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	0.38	0/36027	0.91	43/56227 (0.1%)
1	CA	0.41	8/36170 (0.0%)	1.01	101/56452 (0.2%)
2	AB	0.30	0/1881	0.62	0/2542
2	CB	0.33	0/1860	0.67	2/2518 (0.1%)
3	AC	0.27	0/1576	0.52	0/2130
3	CC	0.31	0/1568	0.61	1/2122 (0.0%)
4	AD	0.29	0/1689	0.55	0/2267
4	CD	0.30	0/1708	0.55	0/2289
5	AE	0.30	0/1145	0.54	0/1543
5	CE	0.33	0/1149	0.61	0/1548
6	AF	0.30	0/825	0.52	0/1118
6	CF	0.32	0/833	0.55	0/1128
7	AG	0.28	0/1250	0.50	0/1679
7	CG	0.27	0/1254	0.53	0/1683
8	AH	0.28	0/1108	0.52	0/1494
8	CH	0.29	0/1108	0.54	0/1494
9	AI	0.29	0/1005	0.57	0/1350
9	CI	0.31	0/997	0.64	0/1343
10	AJ	0.27	0/722	0.54	0/982
10	CJ	0.33	0/727	0.62	0/988
11	AK	0.28	0/848	0.51	0/1149
11	CK	0.28	0/848	0.53	0/1149
12	AL	0.33	0/946	0.52	0/1274
12	CL	0.30	0/946	0.58	0/1274
13	AM	0.31	0/977	0.60	0/1310
13	CM	0.31	0/961	0.62	1/1291 (0.1%)
14	AN	0.32	0/501	0.53	0/664
14	CN	0.33	0/501	0.57	0/664
15	AO	0.28	0/739	0.52	0/985
15	CO	0.29	0/739	0.54	0/985
16	AP	0.31	0/697	0.54	0/939
16	CP	0.29	0/693	0.51	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.29	0/836	0.53	0/1117
17	CQ	0.29	0/836	0.50	0/1117
18	AR	0.27	0/560	0.54	0/746
18	CR	0.29	0/560	0.56	0/746
19	AS	0.30	0/676	0.58	0/911
19	CS	0.33	0/661	0.71	0/893
20	AT	0.29	0/730	0.57	0/965
20	CT	0.28	0/733	0.55	0/969
21	AU	0.27	0/203	0.50	0/266
21	CU	0.33	0/203	0.53	0/266
22	AV	0.39	0/310	0.96	1/480 (0.2%)
22	CV	0.42	0/282	0.99	2/437 (0.5%)
23	AW	0.47	0/1577	1.20	7/2454 (0.3%)
23	CW	0.53	0/1531	1.28	9/2379 (0.4%)
24	AX	0.53	2/1700 (0.1%)	1.20	22/2650 (0.8%)
24	CX	0.46	0/1700	1.15	6/2650 (0.2%)
25	AY	0.58	0/1602	1.35	20/2493 (0.8%)
25	CY	0.59	0/1579	1.40	25/2455 (1.0%)
26	BA	0.50	1/68013 (0.0%)	0.93	91/106165 (0.1%)
26	DA	0.41	1/67542 (0.0%)	0.92	74/105428 (0.1%)
27	BB	0.41	0/2878	0.86	1/4490 (0.0%)
27	DB	0.44	0/2878	0.92	2/4490 (0.0%)
28	BD	0.37	0/2186	0.59	0/2944
28	DD	0.33	0/2192	0.57	0/2951
29	BE	0.37	0/1592	0.57	0/2149
29	DE	0.33	0/1592	0.55	0/2149
30	BF	0.34	0/1619	0.55	0/2193
30	DF	0.32	0/1615	0.55	0/2188
31	BG	0.31	0/1450	0.54	1/1959 (0.1%)
31	DG	0.33	0/1449	0.60	0/1958
32	BH	0.33	0/1356	0.54	0/1834
32	DH	0.29	0/1356	0.54	0/1834
33	BI	0.28	0/1100	0.56	0/1501
33	DI	0.29	0/1088	0.55	0/1484
34	BN	0.34	0/1144	0.53	0/1543
34	DN	0.31	0/1144	0.52	0/1543
35	BO	0.37	0/943	0.57	0/1269
35	DO	0.31	0/943	0.55	1/1269 (0.1%)
36	BP	0.35	0/1156	0.57	0/1537
36	DP	0.32	0/1152	0.61	1/1533 (0.1%)
37	BQ	0.35	0/1143	0.53	0/1527
37	DQ	0.32	0/1143	0.53	0/1527
38	BR	0.36	0/982	0.58	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.30	0/982	0.53	0/1312
39	BS	0.31	0/887	0.56	0/1180
39	DS	0.28	0/880	0.56	0/1172
40	BT	0.34	0/1105	0.56	1/1477 (0.1%)
40	DT	0.31	0/1097	0.53	0/1468
41	BU	0.39	0/977	0.56	0/1301
41	DU	0.30	0/977	0.54	0/1301
42	BV	0.36	0/782	0.58	0/1049
42	DV	0.32	0/782	0.57	1/1049 (0.1%)
43	BW	0.39	0/897	0.56	0/1205
43	DW	0.31	0/897	0.52	0/1205
44	BX	0.38	0/764	0.57	1/1025 (0.1%)
44	DX	0.33	0/764	0.58	1/1025 (0.1%)
45	BY	0.35	0/819	0.57	0/1095
45	DY	0.32	0/819	0.55	0/1095
46	BZ	0.32	0/1379	0.58	0/1873
46	DZ	0.30	0/1390	0.56	0/1890
47	B0	0.35	0/662	0.55	0/881
47	D0	0.32	0/662	0.53	0/881
48	B1	0.35	0/762	0.54	0/1014
48	D1	0.31	0/762	0.53	0/1014
49	B2	0.31	0/590	0.53	0/781
49	D2	0.28	0/590	0.46	0/781
50	B3	0.34	0/474	0.57	0/635
50	D3	0.27	0/469	0.55	0/630
51	B4	0.31	0/571	0.70	0/768
51	D4	0.32	0/545	0.67	0/737
52	B5	0.35	0/469	0.65	0/635
52	D5	0.31	0/469	0.50	0/635
53	B6	0.37	0/460	0.52	0/613
53	D6	0.29	0/456	0.49	0/608
54	B7	0.40	0/426	0.57	0/561
54	D7	0.33	0/426	0.54	0/561
55	B8	0.37	0/525	0.59	0/691
55	D8	0.32	0/525	0.51	0/691
56	B9	0.37	0/310	0.50	0/407
56	D9	0.33	0/310	0.52	0/407
All	All	0.41	12/316594 (0.0%)	0.87	415/473940 (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	2
2	CB	0	1
7	AG	0	2
20	CT	0	1
33	BI	0	1
35	BO	0	1
39	BS	0	1
51	B4	0	1
All	All	0	10

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	1154	G	N1-C2	-10.90	1.29	1.37
1	CA	1119	C	N3-C4	-10.71	1.26	1.33
1	CA	1154	G	C6-N1	-10.47	1.32	1.39
26	DA	528	A	N9-C4	-6.80	1.33	1.37
1	CA	1154	G	N7-C5	-6.78	1.35	1.39
1	CA	1119	C	C2-N3	-6.04	1.30	1.35
26	BA	1142(A)	A	N9-C4	-5.97	1.34	1.37
1	CA	1154	G	C5-C4	5.82	1.42	1.38
24	AX	22	G	N7-C5	5.60	1.42	1.39
24	AX	14	A	N7-C5	-5.36	1.36	1.39
1	CA	1154	G	C8-N7	-5.29	1.27	1.30
1	CA	1119	C	N1-C2	5.25	1.45	1.40

All (415) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	1119	C	N1-C2-O2	35.97	140.48	118.90
1	CA	1154	G	C5-C6-O6	25.44	143.86	128.60
1	CA	1154	G	N3-C2-N2	24.34	136.94	119.90
1	CA	1154	G	N1-C2-N2	-21.83	96.56	116.20
1	CA	1119	C	N3-C2-O2	-21.82	106.63	121.90
1	CA	1154	G	C5-C6-N1	-18.28	102.36	111.50
1	CA	1119	C	C2-N3-C4	17.80	128.80	119.90
1	CA	1154	G	C6-N1-C2	16.98	135.29	125.10
1	CA	1119	C	C2-N1-C1'	15.84	136.22	118.80
1	CA	1119	C	N3-C4-N4	-15.07	107.45	118.00
1	CA	1119	C	C5-C4-N4	15.04	130.73	120.20
1	CA	1119	C	C6-N1-C1'	-12.88	105.34	120.80
25	CY	66	U	C5-C4-O4	-11.57	118.96	125.90
1	CA	1154	G	C2-N3-C4	-11.37	106.22	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AX	46	G	C6-N1-C2	-11.23	118.36	125.10
1	CA	1154	G	C4-N9-C1'	10.50	140.15	126.50
26	DA	2139	C	N1-C2-O2	10.43	125.16	118.90
1	CA	1154	G	N1-C6-O6	-10.31	113.72	119.90
24	AX	14	A	C4-C5-C6	10.16	122.08	117.00
1	CA	1180	A	C5-C6-N1	-9.83	112.78	117.70
26	DA	2139	C	C2-N1-C1'	9.76	129.53	118.80
1	CA	1119	C	N1-C2-N3	-9.72	112.40	119.20
1	CA	1154	G	C8-N9-C1'	-9.27	114.95	127.00
26	DA	34	C	N1-C2-O2	9.06	124.33	118.90
24	AX	14	A	C5-N7-C8	8.99	108.39	103.90
26	DA	2102	U	N1-C2-O2	8.93	129.05	122.80
26	DA	528	A	C2-N3-C4	-8.89	106.15	110.60
25	CY	7	A	C6-N1-C2	-8.88	113.27	118.60
26	DA	2187	G	C5-C6-O6	-8.86	123.28	128.60
26	DA	2174	C	C2-N1-C1'	8.85	128.54	118.80
24	AX	22	G	C5-N7-C8	-8.78	99.91	104.30
25	AY	50	U	C5-C4-O4	8.74	131.15	125.90
1	CA	1004	A	O4'-C1'-N9	8.59	115.08	108.20
1	CA	1119	C	C5-C6-N1	8.58	125.29	121.00
26	BA	512	G	O4'-C1'-N9	8.51	115.01	108.20
24	CX	14	A	C4-C5-C6	8.43	121.22	117.00
25	AY	68	C	N1-C2-O2	8.36	123.92	118.90
26	DA	2682	U	O5'-P-OP2	-8.36	98.18	105.70
1	CA	1119	C	C4-C5-C6	-8.35	113.23	117.40
26	DA	2136	C	N1-C2-O2	8.32	123.89	118.90
25	AY	50	U	C2-N3-C4	8.32	131.99	127.00
1	CA	1180	A	C2-N3-C4	-8.29	106.46	110.60
26	BA	897	C	C5-C6-N1	8.26	125.13	121.00
26	DA	2139	C	C6-N1-C1'	-8.07	111.12	120.80
26	DA	2152	G	N1-C6-O6	8.07	124.74	119.90
26	DA	2061	G	O5'-P-OP2	-8.04	98.47	105.70
25	AY	64	A	C6-N1-C2	8.01	123.41	118.60
26	BA	2140	C	C2-N1-C1'	7.97	127.56	118.80
24	AX	22	G	C4-C5-C6	-7.92	114.05	118.80
1	AA	1027	C	N1-C2-O2	7.92	123.65	118.90
24	AX	14	A	C5-C6-N1	-7.91	113.75	117.70
25	CY	68	C	N1-C2-O2	7.88	123.62	118.90
26	DA	34	C	C2-N1-C1'	7.84	127.43	118.80
26	DA	2152	G	C5-C6-O6	-7.69	123.99	128.60
26	DA	897	C	C2-N1-C1'	7.61	127.17	118.80
25	CY	66	U	N3-C4-O4	7.57	124.69	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	79	G	C5-C6-O6	7.50	133.10	128.60
25	AY	64	A	C5-C6-N6	7.47	129.67	123.70
26	BA	2140	C	C6-N1-C2	-7.46	117.32	120.30
24	AX	46	G	N3-C2-N2	-7.39	114.72	119.90
25	CY	7	A	C5-C6-N1	7.38	121.39	117.70
1	CA	1154	G	C4-C5-C6	7.34	123.20	118.80
26	BA	1963	U	C2-N1-C1'	7.32	126.48	117.70
26	DA	2136	C	N3-C2-O2	-7.30	116.79	121.90
26	BA	999	U	O5'-P-OP2	-7.28	99.14	105.70
23	AW	50	U	C5-C6-N1	7.27	126.33	122.70
1	AA	1042	G	O4'-C1'-N9	7.24	114.00	108.20
25	AY	56	C	N1-C2-O2	7.24	123.25	118.90
26	BA	528	A	C2-N3-C4	-7.23	106.98	110.60
26	BA	12	U	C2-N1-C1'	7.20	126.34	117.70
1	CA	1137	C	O4'-C1'-N1	7.20	113.96	108.20
1	AA	997	U	C5-C4-O4	7.14	130.18	125.90
1	CA	1004	A	N1-C6-N6	-7.13	114.32	118.60
26	DA	2153	G	C5-C6-O6	-7.12	124.33	128.60
25	CY	68	C	N3-C2-O2	-7.12	116.92	121.90
1	AA	1030(B)	C	C2-N1-C1'	7.02	126.52	118.80
23	AW	70	G	C4-N9-C1'	-7.01	117.39	126.50
26	BA	897	C	C2-N1-C1'	6.97	126.47	118.80
26	BA	2140	C	N1-C2-O2	6.97	123.08	118.90
1	CA	1119	C	C6-N1-C2	-6.92	117.53	120.30
26	DA	2155	G	C6-N1-C2	6.92	129.25	125.10
26	DA	2174	C	C6-N1-C1'	-6.90	112.52	120.80
44	DX	57	LEU	CA-CB-CG	6.87	131.10	115.30
25	CY	66	U	C2-N3-C4	-6.86	122.88	127.00
26	BA	141	A	N7-C8-N9	6.84	117.22	113.80
1	AA	1067	A	P-O3'-C3'	6.84	127.91	119.70
26	BA	2269	A	O5'-P-OP1	-6.84	99.55	105.70
26	BA	2141	G	C5-C6-O6	6.83	132.70	128.60
1	CA	1225	A	C5-C6-N6	6.82	129.16	123.70
25	CY	7	A	N3-C4-N9	6.81	132.85	127.40
26	BA	1372	U	C5-C4-O4	-6.80	121.82	125.90
1	AA	1042	G	C8-N9-C1'	6.74	135.76	127.00
26	BA	330	A	C2-N3-C4	-6.73	107.23	110.60
23	AW	70	G	C8-N9-C1'	6.71	135.72	127.00
24	AX	46	G	N1-C2-N3	6.71	127.92	123.90
26	BA	1021	A	C2-N3-C4	-6.70	107.25	110.60
1	AA	1002	G	N3-C4-N9	6.69	130.01	126.00
1	CA	1150	U	C5-C4-O4	6.68	129.91	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1002	G	C4-N9-C1'	6.68	135.18	126.50
26	BA	2140	C	N3-C2-O2	-6.67	117.23	121.90
26	DA	2139	C	N3-C2-O2	-6.66	117.24	121.90
26	BA	1992	G	P-O3'-C3'	6.64	127.67	119.70
26	BA	975	C	N1-C2-O2	-6.64	114.92	118.90
25	AY	4	C	N3-C2-O2	-6.61	117.27	121.90
1	CA	1042	G	N3-C4-C5	6.58	131.89	128.60
1	CA	65	U	P-O3'-C3'	6.58	127.59	119.70
25	CY	18	G	C4-N9-C1'	6.57	135.04	126.50
1	AA	1150	U	C5-C4-O4	6.57	129.84	125.90
26	BA	1142(A)	A	C2-N3-C4	-6.56	107.32	110.60
25	CY	18	G	C8-N9-C1'	-6.55	118.48	127.00
26	BA	945	A	C2-N3-C4	-6.55	107.33	110.60
24	AX	22	G	C8-N9-C1'	6.54	135.50	127.00
1	AA	346	G	C4-N9-C1'	6.52	134.98	126.50
24	CX	14	A	C5-N7-C8	6.52	107.16	103.90
24	CX	46	G	C6-N1-C2	-6.52	121.19	125.10
26	DA	2139	C	N3-C4-C5	6.52	124.51	121.90
26	BA	1372	U	N3-C4-O4	6.52	123.96	119.40
26	DA	34	C	N3-C2-O2	-6.51	117.34	121.90
1	AA	1026	G	C8-N9-C4	-6.47	103.81	106.40
1	CA	848	C	C5-C6-N1	6.46	124.23	121.00
26	DA	2153	G	N1-C6-O6	6.45	123.77	119.90
1	CA	754	C	C2-N1-C1'	6.44	125.89	118.80
1	AA	841	U	C5-C6-N1	6.44	125.92	122.70
25	AY	4	C	C6-N1-C2	-6.43	117.73	120.30
1	CA	1030	C	C2-N1-C1'	6.41	125.84	118.80
26	DA	1614	A	O5'-P-OP1	-6.40	99.94	105.70
1	AA	1002	G	C8-N9-C1'	-6.36	118.73	127.00
26	DA	897	C	C6-N1-C1'	-6.34	113.19	120.80
44	BX	57	LEU	CA-CB-CG	6.32	129.82	115.30
26	BA	1313	U	N3-C2-O2	-6.30	117.79	122.20
25	CY	23	A	N1-C6-N6	6.30	122.38	118.60
25	AY	64	A	C5-C6-N1	-6.29	114.56	117.70
26	BA	1313	U	C2-N1-C1'	6.25	125.20	117.70
1	CA	1256	A	O4'-C1'-N9	-6.24	103.20	108.20
1	AA	839	U	P-O3'-C3'	6.23	127.18	119.70
23	CW	69	G	O4'-C1'-N9	-6.23	103.22	108.20
1	CA	1003	G	N7-C8-N9	6.22	116.21	113.10
1	AA	1042	G	C4-N9-C1'	-6.21	118.42	126.50
24	AX	22	G	C5-C6-N1	6.21	114.60	111.50
26	BA	2100	G	C5-C6-O6	-6.21	124.88	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	23	A	N1-C6-N6	-6.20	114.88	118.60
1	CA	955	U	C5-C4-O4	6.19	129.62	125.90
23	AW	70	G	N3-C4-N9	-6.18	122.29	126.00
26	BA	2848	G	O4'-C1'-N9	6.16	113.12	108.20
1	CA	984	C	C2-N3-C4	6.15	122.98	119.90
25	CY	68	C	C2-N1-C1'	6.13	125.55	118.80
1	CA	1003	G	C4-N9-C1'	6.13	134.47	126.50
13	CM	71	ARG	NE-CZ-NH1	6.12	123.36	120.30
31	BG	3	LEU	CA-CB-CG	6.12	129.38	115.30
26	BA	645	C	C2-N1-C1'	6.12	125.53	118.80
26	BA	1639	U	O5'-P-OP2	-6.12	100.20	105.70
1	AA	1027	C	N3-C2-O2	-6.10	117.63	121.90
26	BA	2615	U	O5'-P-OP1	-6.10	100.21	105.70
1	CA	1225	A	N1-C6-N6	-6.09	114.94	118.60
26	BA	1614	A	O5'-P-OP1	-6.09	100.22	105.70
26	DA	512	G	O4'-C1'-N9	6.09	113.07	108.20
1	CA	1126	U	C2-N1-C1'	6.08	125.00	117.70
26	DA	801	G	O5'-P-OP2	-6.08	100.23	105.70
25	CY	10	G	N1-C6-O6	6.06	123.53	119.90
1	CA	1452	C	C6-N1-C2	-6.05	117.88	120.30
26	DA	1992	G	C8-N9-C4	-6.05	103.98	106.40
26	BA	933	A	O4'-C1'-N9	6.02	113.02	108.20
24	AX	46	G	C5-C6-N1	6.02	114.51	111.50
1	CA	1039	C	C5-C6-N1	6.01	124.01	121.00
26	DA	2102	U	C2-N3-C4	6.00	130.60	127.00
26	BA	2163	C	C6-N1-C2	-6.00	117.90	120.30
23	CW	10	G	N3-C2-N2	-5.99	115.71	119.90
26	DA	1531	C	C2-N1-C1'	5.99	125.38	118.80
26	BA	2248	C	O5'-P-OP2	-5.98	100.31	105.70
26	DA	2187	G	N3-C4-N9	5.98	129.59	126.00
26	DA	2160	G	C5-C6-O6	5.98	132.19	128.60
26	DA	2128	C	C2-N3-C4	5.97	122.89	119.90
26	DA	2167	U	N3-C2-O2	-5.97	118.02	122.20
1	AA	991	U	P-O3'-C3'	5.95	126.83	119.70
26	BA	226	G	O4'-C1'-N9	5.94	112.95	108.20
1	CA	998	G	N9-C4-C5	5.94	107.78	105.40
26	DA	34	C	C6-N1-C1'	-5.94	113.67	120.80
24	AX	22	G	N3-C4-N9	-5.94	122.44	126.00
26	BA	1300	U	P-O3'-C3'	5.94	126.82	119.70
26	BA	31	C	O5'-P-OP1	-5.93	100.36	105.70
42	DV	38	LEU	CA-CB-CG	5.93	128.94	115.30
26	BA	330	A	N1-C2-N3	5.93	132.26	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CA	501	C	O5'-P-OP1	-5.93	100.36	105.70
26	BA	141	A	C5-N7-C8	-5.92	100.94	103.90
1	AA	1026	G	N7-C8-N9	5.91	116.06	113.10
24	AX	22	G	N1-C6-O6	-5.91	116.35	119.90
26	BA	1493	C	N1-C2-O2	5.91	122.44	118.90
1	CA	1003	G	C8-N9-C4	-5.91	104.04	106.40
1	CA	1220	G	N3-C2-N2	-5.91	115.77	119.90
26	DA	528	A	N1-C2-N3	5.91	132.25	129.30
26	BA	1176	G	OP1-P-O3'	5.90	118.17	105.20
1	CA	955	U	C2-N3-C4	5.90	130.54	127.00
26	DA	2190	G	C5-C6-O6	5.90	132.14	128.60
26	BA	141	A	O4'-C1'-N9	5.89	112.92	108.20
26	BA	1315	C	O5'-P-OP2	-5.88	100.41	105.70
1	AA	1123	A	C6-N1-C2	5.87	122.12	118.60
26	BA	2061	G	O5'-P-OP2	-5.86	100.43	105.70
25	AY	15	G	N3-C2-N2	5.85	124.00	119.90
26	BA	933	A	N7-C8-N9	5.85	116.72	113.80
1	CA	1001(A)	G	C5-C6-O6	-5.85	125.09	128.60
1	AA	1137	C	O4'-C1'-N1	-5.84	103.53	108.20
26	DA	1204	A	O4'-C1'-N9	5.84	112.87	108.20
1	CA	1166	G	N7-C8-N9	5.84	116.02	113.10
1	CA	1323	G	N3-C4-N9	5.82	129.49	126.00
1	CA	1180	A	C4-C5-C6	5.81	119.91	117.00
26	DA	2167	U	N1-C2-O2	5.81	126.87	122.80
26	BA	2789	C	C2-N1-C1'	-5.80	112.42	118.80
25	CY	4	C	N1-C2-O2	5.79	122.38	118.90
25	CY	10	G	C5-C6-O6	-5.79	125.12	128.60
1	CA	1031	G	C5-C6-O6	-5.79	125.13	128.60
24	CX	14	A	N1-C6-N6	5.78	122.07	118.60
26	BA	271(M)	G	P-O3'-C3'	5.77	126.62	119.70
26	BA	528	A	N3-C4-N9	-5.74	122.81	127.40
23	CW	66	U	P-O3'-C3'	5.74	126.58	119.70
26	BA	887	A	O4'-C1'-N9	5.73	112.79	108.20
27	DB	30	C	C6-N1-C2	-5.73	118.01	120.30
26	BA	2592	G	O5'-P-OP1	-5.71	100.56	105.70
24	AX	22	G	C4-N9-C1'	-5.71	119.08	126.50
1	AA	1052	U	N1-C2-O2	5.71	126.80	122.80
25	AY	60	U	C2-N1-C1'	5.70	124.54	117.70
1	AA	204	U	C2-N1-C1'	5.69	124.53	117.70
26	BA	975	C	C2-N1-C1'	-5.69	112.54	118.80
26	BA	1776	G	O5'-P-OP2	-5.69	100.58	105.70
26	DA	897	C	N1-C2-O2	5.69	122.31	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	548	A	P-O3'-C3'	5.69	126.52	119.70
25	CY	7	A	N3-C4-C5	-5.68	122.82	126.80
26	BA	1963	U	N1-C2-O2	5.68	126.78	122.80
26	DA	2248	C	O5'-P-OP2	-5.68	100.59	105.70
1	CA	1154	G	N3-C4-N9	5.67	129.41	126.00
26	DA	1300	U	P-O3'-C3'	5.67	126.51	119.70
24	AX	20	U	C2-N1-C1'	5.67	124.51	117.70
26	BA	1784	A	O5'-P-OP2	-5.67	100.59	105.70
1	AA	1150	U	C2-N3-C4	5.66	130.40	127.00
26	DA	2155	G	N3-C2-N2	5.66	123.86	119.90
26	DA	2102	U	N3-C2-O2	-5.65	118.24	122.20
26	BA	271(M)	G	OP1-P-O3'	5.64	117.62	105.20
26	DA	784	A	O4'-C1'-N9	5.64	112.71	108.20
1	CA	182	U	N1-C2-O2	-5.64	118.85	122.80
23	CW	36	A	C6-N1-C2	5.63	121.98	118.60
1	CA	1126	U	N1-C2-O2	5.63	126.74	122.80
25	AY	56	C	N3-C2-O2	-5.62	117.96	121.90
1	CA	1137	C	C2-N1-C1'	-5.61	112.62	118.80
1	CA	204	U	C2-N1-C1'	5.61	124.43	117.70
24	AX	22	G	N3-C4-C5	5.61	131.41	128.60
24	AX	46	G	N9-C4-C5	5.61	107.64	105.40
1	CA	1023	G	C4-N9-C1'	5.61	133.79	126.50
1	AA	346	G	O4'-C1'-N9	5.60	112.68	108.20
25	AY	68	C	C5-C6-N1	5.60	123.80	121.00
26	BA	746	A	O4'-C1'-N9	5.60	112.68	108.20
26	DA	1313	U	C2-N1-C1'	5.60	124.42	117.70
1	AA	1502	A	N1-C2-N3	5.59	132.09	129.30
25	CY	31	A	N1-C6-N6	5.58	121.95	118.60
1	AA	1206	G	C5-C6-O6	-5.58	125.25	128.60
1	CA	998	G	C6-C5-N7	5.58	133.75	130.40
25	AY	68	C	N3-C2-O2	-5.57	118.00	121.90
26	DA	1992	G	P-O3'-C3'	5.57	126.38	119.70
1	CA	1039	C	C2-N1-C1'	5.56	124.92	118.80
1	AA	91	C	C2-N1-C1'	5.56	124.91	118.80
1	CA	1047	G	N3-C4-N9	5.55	129.33	126.00
26	DA	2155	G	N1-C2-N3	-5.54	120.57	123.90
23	CW	67	C	C2-N3-C4	5.54	122.67	119.90
1	AA	1165	C	P-O3'-C3'	5.54	126.34	119.70
26	BA	1021	A	N1-C2-N3	5.53	132.06	129.30
26	BA	2593	U	N3-C4-O4	-5.53	115.53	119.40
1	CA	986	A	C6-N1-C2	-5.53	115.28	118.60
1	CA	1039	C	C5-C4-N4	-5.53	116.33	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2128	C	N1-C2-O2	5.52	122.21	118.90
26	BA	1352	U	O5'-P-OP1	-5.52	100.73	105.70
24	CX	22	G	C5-N7-C8	-5.51	101.54	104.30
1	CA	1042	G	N3-C4-N9	-5.51	122.69	126.00
1	CA	992	U	C5-C6-N1	5.50	125.45	122.70
25	CY	62	C	C2-N3-C4	5.50	122.65	119.90
26	BA	1963	U	C6-N1-C1'	-5.50	113.51	121.20
27	BB	85	G	O4'-C1'-N9	-5.49	103.81	108.20
1	CA	1180	A	N1-C2-N3	5.48	132.04	129.30
1	CA	1154	G	C5-N7-C8	5.48	107.04	104.30
26	BA	945	A	C5-N7-C8	-5.48	101.16	103.90
24	AX	14	A	C4-N9-C1'	5.47	136.16	126.30
1	CA	1030(B)	C	C6-N1-C2	-5.47	118.11	120.30
1	CA	998	G	C4-C5-N7	-5.47	108.61	110.80
26	DA	277	C	N1-C2-O2	5.47	122.18	118.90
1	AA	1065	U	P-O3'-C3'	5.47	126.26	119.70
26	DA	2160	G	C6-N1-C2	5.46	128.38	125.10
26	DA	2139	C	C5-C6-N1	5.45	123.73	121.00
40	BT	118	ARG	NE-CZ-NH1	5.45	123.02	120.30
26	BA	944	G	C4-N9-C1'	5.44	133.57	126.50
26	BA	1022	G	N3-C2-N2	-5.44	116.09	119.90
26	BA	1131	G	O4'-C1'-N9	5.44	112.55	108.20
26	DA	2187	G	C6-N1-C2	-5.43	121.84	125.10
1	AA	1131	G	C6-C5-N7	-5.43	127.14	130.40
1	CA	997	U	C5-C4-O4	5.42	129.15	125.90
26	DA	2187	G	N1-C6-O6	5.42	123.15	119.90
1	CA	1183	A	P-O3'-C3'	5.41	126.20	119.70
22	CV	19	U	C2-N3-C4	5.41	130.25	127.00
23	CW	3	C	C6-N1-C2	-5.41	118.14	120.30
1	AA	841	U	C6-N1-C2	-5.41	117.75	121.00
24	AX	14	A	C8-N9-C1'	-5.40	117.99	127.70
1	AA	1030(B)	C	N1-C2-O2	5.39	122.14	118.90
23	AW	44	G	C5-C6-O6	5.39	131.84	128.60
24	AX	46	G	C4-C5-N7	-5.39	108.64	110.80
26	BA	2167	U	C2-N1-C1'	5.39	124.16	117.70
26	BA	2134	A	C3'-C2'-C1'	5.38	105.81	101.50
1	CA	998	G	N3-C4-N9	-5.38	122.77	126.00
2	CB	154	LEU	CA-CB-CG	5.38	127.67	115.30
1	CA	942	G	C5-C6-O6	5.38	131.83	128.60
1	AA	1285	A	P-O3'-C3'	5.34	126.11	119.70
26	BA	141	A	C8-N9-C4	-5.34	103.66	105.80
23	CW	25	C	C5-C4-N4	5.34	123.94	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	DA	2153	G	C8-N9-C1'	-5.33	120.07	127.00
1	AA	925	G	C5-C6-O6	-5.33	125.40	128.60
1	CA	1123	A	C5-C6-N6	5.33	127.96	123.70
1	CA	1216	G	C4-N9-C1'	-5.33	119.58	126.50
26	DA	2153	G	N3-C4-N9	5.32	129.19	126.00
24	AX	22	G	N7-C8-N9	5.32	115.76	113.10
26	BA	1176	G	P-O3'-C3'	5.32	126.08	119.70
1	CA	1054	C	O4'-C1'-N1	5.31	112.45	108.20
3	CC	52	LEU	CA-CB-CG	5.31	127.50	115.30
26	BA	528	A	N3-C4-C5	5.30	130.51	126.80
1	CA	1122	U	C5-C4-O4	5.30	129.08	125.90
1	CA	1004	A	C6-C5-N7	5.30	136.01	132.30
26	DA	528	A	N3-C4-C5	5.30	130.51	126.80
26	DA	2153	G	N9-C4-C5	-5.30	103.28	105.40
26	DA	748	G	O4'-C1'-N9	5.29	112.43	108.20
26	BA	2347	C	N1-C2-O2	5.29	122.07	118.90
1	CA	992	U	P-O3'-C3'	5.28	126.04	119.70
26	DA	2313	C	N1-C2-O2	5.26	122.06	118.90
26	BA	2430	A	C2-N3-C4	5.26	113.23	110.60
1	CA	1220	G	N3-C4-N9	-5.25	122.85	126.00
1	CA	1452	C	C5-C6-N1	5.25	123.63	121.00
1	AA	1010	G	N3-C4-N9	5.25	129.15	126.00
1	CA	79	G	N1-C6-O6	-5.25	116.75	119.90
25	AY	23	A	C4-C5-C6	-5.25	114.38	117.00
25	CY	50	U	C5-C4-O4	5.24	129.05	125.90
26	BA	2191	G	N7-C8-N9	5.24	115.72	113.10
26	DA	2889	C	N1-C2-O2	5.24	122.05	118.90
24	CX	34	C	C2-N1-C1'	5.24	124.56	118.80
1	CA	998	G	N1-C6-O6	-5.22	116.77	119.90
26	BA	933	A	C5-N7-C8	-5.22	101.29	103.90
26	DA	2297	C	C6-N1-C2	-5.22	118.21	120.30
1	CA	687	A	P-O3'-C3'	5.21	125.96	119.70
1	AA	266	G	P-O3'-C3'	5.21	125.96	119.70
1	CA	992	U	C2-N1-C1'	5.21	123.95	117.70
1	CA	182	U	C2-N1-C1'	-5.21	111.45	117.70
26	BA	576	U	O5'-P-OP1	-5.20	101.02	105.70
22	AV	17	U	C5-C4-O4	5.20	129.02	125.90
26	BA	1416	G	O4'-C1'-N9	5.20	112.36	108.20
26	BA	2206	G	C5-C6-O6	-5.19	125.48	128.60
25	AY	50	U	N3-C4-C5	-5.19	111.49	114.60
26	DA	1937	A	O4'-C1'-N9	5.19	112.35	108.20
2	CB	51	LEU	CA-CB-CG	5.17	127.20	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BA	575	A	O5'-P-OP1	-5.17	101.05	105.70
23	CW	44	G	N3-C4-N9	5.17	129.10	126.00
26	DA	2689	U	P-O3'-C3'	5.16	125.89	119.70
35	DO	8	LEU	CA-CB-CG	5.16	127.16	115.30
1	CA	754	C	N1-C2-O2	5.16	121.99	118.90
25	CY	9	A	C4-C5-C6	-5.16	114.42	117.00
26	BA	2609	U	C2-N1-C1'	-5.15	111.52	117.70
26	BA	1107	G	N3-C4-C5	-5.15	126.02	128.60
1	CA	1012	U	N1-C2-N3	5.15	117.99	114.90
26	BA	2689	U	P-O3'-C3'	5.14	125.87	119.70
26	DA	2153	G	C6-C5-N7	-5.14	127.32	130.40
26	DA	2174	C	C5-C6-N1	5.14	123.57	121.00
36	DP	44	GLY	C-N-CA	5.14	134.54	121.70
1	CA	1030	C	C6-N1-C1'	-5.13	114.64	120.80
26	BA	826	U	OP1-P-O3'	5.13	116.49	105.20
1	CA	999	C	C2-N3-C4	5.13	122.47	119.90
26	DA	2178	C	N1-C2-O2	5.13	121.98	118.90
1	AA	1042	G	N3-C4-N9	-5.13	122.92	126.00
24	AX	14	A	C4-C5-N7	-5.12	108.14	110.70
1	CA	1124	G	N3-C4-N9	5.12	129.07	126.00
1	AA	1036	G	C4-N9-C1'	5.11	133.14	126.50
26	BA	2141	G	C6-N1-C2	5.11	128.16	125.10
25	CY	25	C	C2-N1-C1'	5.11	124.42	118.80
26	BA	2174	C	C2-N1-C1'	5.09	124.40	118.80
1	CA	1221	G	C6-N1-C2	5.09	128.16	125.10
22	CV	19	U	C5-C4-O4	5.09	128.96	125.90
1	CA	953	G	N3-C4-N9	5.09	129.06	126.00
26	BA	1021	A	C8-N9-C4	-5.09	103.77	105.80
27	DB	42	C	N1-C2-O2	5.09	121.95	118.90
25	AY	9	A	N1-C6-N6	5.08	121.65	118.60
1	CA	1166	G	C8-N9-C4	-5.08	104.37	106.40
1	CA	1064	G	P-O3'-C3'	5.08	125.79	119.70
26	DA	1038	C	C2-N1-C1'	5.07	124.38	118.80
1	CA	1126	U	C6-N1-C1'	-5.07	114.10	121.20
26	DA	2206	G	C4-N9-C1'	-5.07	119.91	126.50
26	DA	2155	G	N9-C4-C5	-5.07	103.37	105.40
23	AW	70	G	C6-C5-N7	5.06	133.44	130.40
26	BA	845	G	O4'-C1'-N9	5.06	112.25	108.20
26	DA	2174	C	N1-C2-O2	5.06	121.93	118.90
26	BA	2789	C	O4'-C1'-N1	5.06	112.25	108.20
25	CY	68	C	C6-N1-C2	-5.05	118.28	120.30
26	DA	2153	G	C4-N9-C1'	5.05	133.07	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1067	A	O4'-C1'-N9	-5.05	104.16	108.20
26	BA	1022	G	N3-C4-N9	-5.05	122.97	126.00
26	BA	2319	G	O4'-C1'-N9	5.05	112.24	108.20
23	CW	25	C	C6-N1-C1'	5.05	126.86	120.80
1	CA	65	U	OP2-P-O3'	5.04	116.30	105.20
26	BA	2183	C	N1-C2-O2	-5.04	115.88	118.90
25	AY	15	G	N1-C2-N2	-5.04	111.66	116.20
25	CY	50	U	O4'-C1'-N1	5.04	112.23	108.20
26	BA	2286	A	N7-C8-N9	5.03	116.31	113.80
1	AA	1173	G	N3-C4-N9	5.03	129.02	126.00
1	AA	1019	C	N1-C2-O2	5.03	121.92	118.90
26	DA	1558	A	P-O3'-C3'	5.03	125.73	119.70
1	CA	204	U	O4'-C1'-N1	5.03	112.22	108.20
1	AA	1026	G	N3-C4-C5	-5.02	126.09	128.60
1	CA	60	A	P-O3'-C3'	5.02	125.73	119.70
1	CA	998	G	C8-N9-C1'	5.02	133.53	127.00
25	AY	4	C	N1-C2-O2	5.02	121.91	118.90
25	CY	7	A	C6-C5-N7	-5.02	128.79	132.30
26	DA	2139	C	C4-C5-C6	-5.02	114.89	117.40
1	AA	1502	A	N7-C8-N9	5.01	116.30	113.80
25	CY	18	G	N3-C4-N9	5.01	129.01	126.00
26	BA	383	U	C2-N1-C1'	-5.00	111.70	117.70
23	AW	49	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	231	GLU	Peptide
2	AB	9	GLU	Peptide
7	AG	78	ARG	Peptide
7	AG	79	ARG	Peptide
51	B4	59	PHE	Peptide
33	BI	9	LEU	Peptide
35	BO	80	ASP	Peptide
39	BS	58	LEU	Peptide
2	CB	9	GLU	Peptide
20	CT	9	ASN	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32185	0	16245	536	0
1	CA	32312	0	16307	762	0
2	AB	1846	0	1867	81	0
2	CB	1825	0	1828	119	0
3	AC	1552	0	1546	60	0
3	CC	1544	0	1524	70	0
4	AD	1659	0	1676	56	0
4	CD	1678	0	1718	67	0
5	AE	1129	0	1185	27	0
5	CE	1133	0	1191	46	0
6	AF	812	0	804	18	0
6	CF	820	0	814	19	0
7	AG	1231	0	1238	21	0
7	CG	1235	0	1249	39	0
8	AH	1088	0	1126	35	0
8	CH	1088	0	1126	40	0
9	AI	986	0	995	43	0
9	CI	978	0	966	55	0
10	AJ	709	0	650	34	0
10	CJ	714	0	672	44	0
11	AK	833	0	836	19	0
11	CK	833	0	836	22	0
12	AL	930	0	980	27	0
12	CL	930	0	980	33	0
13	AM	966	0	1024	40	0
13	CM	950	0	988	74	0
14	AN	492	0	529	26	0
14	CN	492	0	529	34	0
15	AO	728	0	760	20	0
15	CO	728	0	760	22	0
16	AP	681	0	697	27	0
16	CP	677	0	686	22	0
17	AQ	823	0	891	26	0
17	CQ	823	0	891	19	0
18	AR	555	0	618	12	0
18	CR	555	0	618	24	0
19	AS	661	0	675	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	CS	646	0	644	40	0
20	AT	728	0	798	26	0
20	CT	731	0	807	26	0
21	AU	199	0	208	8	0
21	CU	199	0	208	9	0
22	AV	277	0	140	3	0
22	CV	252	0	130	6	0
23	AW	1599	0	830	42	0
23	CW	1552	0	794	51	0
24	AX	1635	0	839	23	0
24	CX	1635	0	839	36	0
25	AY	1581	0	805	82	0
25	CY	1561	0	796	94	0
26	BA	60729	0	30622	666	0
26	DA	60311	0	30412	876	0
27	BB	2573	0	1306	20	0
27	DB	2573	0	1306	76	0
28	BD	2136	0	2218	42	0
28	DD	2142	0	2229	58	0
29	BE	1559	0	1618	25	0
29	DE	1559	0	1618	39	0
30	BF	1584	0	1625	39	0
30	DF	1580	0	1619	60	0
31	BG	1425	0	1443	38	0
31	DG	1424	0	1434	90	0
32	BH	1330	0	1407	34	0
32	DH	1330	0	1407	44	0
33	BI	1085	0	1114	37	0
33	DI	1073	0	1106	22	0
34	BN	1117	0	1184	23	0
34	DN	1117	0	1184	26	0
35	BO	933	0	996	25	0
35	DO	933	0	996	32	0
36	BP	1139	0	1223	41	0
36	DP	1135	0	1212	52	0
37	BQ	1122	0	1179	28	0
37	DQ	1122	0	1179	40	0
38	BR	968	0	1033	22	0
38	DR	968	0	1033	28	0
39	BS	877	0	938	20	0
39	DS	870	0	923	33	0
40	BT	1091	0	1151	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	DT	1083	0	1136	37	0
41	BU	959	0	1019	18	0
41	DU	959	0	1018	30	0
42	BV	771	0	830	13	0
42	DV	771	0	830	24	0
43	BW	886	0	940	17	0
43	DW	886	0	940	13	0
44	BX	750	0	814	15	0
44	DX	750	0	814	27	0
45	BY	806	0	881	27	0
45	DY	806	0	881	30	0
46	BZ	1349	0	1355	44	0
46	DZ	1360	0	1363	70	0
47	B0	653	0	674	13	0
47	D0	653	0	674	22	0
48	B1	755	0	826	16	0
48	D1	755	0	826	18	0
49	B2	588	0	643	11	0
49	D2	588	0	643	14	0
50	B3	469	0	518	6	0
50	D3	464	0	514	13	0
51	B4	558	0	544	37	0
51	D4	532	0	503	25	0
52	B5	455	0	465	14	0
52	D5	455	0	465	13	0
53	B6	453	0	473	13	0
53	D6	449	0	469	12	0
54	B7	418	0	467	10	0
54	D7	418	0	467	13	0
55	B8	517	0	582	17	0
55	D8	517	0	582	15	0
56	B9	307	0	335	7	0
56	D9	307	0	335	11	0
57	AA	216	0	0	0	0
57	AB	1	0	0	0	0
57	AE	1	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AL	2	0	0	0	0
57	AM	2	0	0	0	0
57	AN	2	0	0	0	0
57	AT	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	AU	1	0	0	0	0
57	AW	2	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	2	0	0	0	0
57	B2	1	0	0	0	0
57	B4	1	0	0	0	0
57	B5	3	0	0	0	0
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	2	0	0	0	0
57	B9	1	0	0	0	0
57	BA	814	0	0	0	0
57	BB	23	0	0	0	0
57	BD	10	0	0	0	0
57	BE	6	0	0	0	0
57	BF	11	0	0	0	0
57	BG	2	0	0	0	0
57	BH	1	0	0	0	0
57	BN	3	0	0	0	0
57	BO	1	0	0	0	0
57	BP	2	0	0	0	0
57	BQ	2	0	0	0	0
57	BR	2	0	0	0	0
57	BU	4	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	1	0	0	0	0
57	BY	1	0	0	0	0
57	BZ	2	0	0	0	0
57	CA	169	0	0	0	0
57	CD	1	0	0	0	0
57	CE	2	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
57	CT	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	2	0	0	0	0
57	D0	1	0	0	0	0
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	DA	664	0	0	0	0
57	DB	13	0	0	0	0
57	DD	4	0	0	0	0
57	DE	7	0	0	0	0
57	DF	5	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	2	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	3	0	0	0	0
57	DR	1	0	0	0	0
57	DU	1	0	0	0	0
57	DV	1	0	0	0	0
57	DW	1	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
61	AA	210	0	0	13	0
61	AD	1	0	0	0	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	2	0	0	1	0
61	AM	2	0	0	0	0
61	AV	2	0	0	0	0
61	AW	4	0	0	0	0
61	AX	4	0	0	0	0
61	AY	1	0	0	0	0
61	B0	6	0	0	0	0
61	B1	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B3	2	0	0	0	0
61	B5	4	0	0	0	0
61	B6	2	0	0	0	0
61	B7	3	0	0	2	0
61	B8	13	0	0	0	0
61	B9	1	0	0	0	0
61	BA	1406	0	0	56	0
61	BB	37	0	0	1	0
61	BD	15	0	0	2	0
61	BE	17	0	0	4	0
61	BF	11	0	0	0	0
61	BG	3	0	0	0	0
61	BH	1	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	2	0	0	0	0
61	BP	13	0	0	0	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BS	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	4	0	0	0	0
61	BV	2	0	0	0	0
61	BW	3	0	0	1	0
61	BX	3	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	156	0	0	11	0
61	CE	2	0	0	0	0
61	CH	1	0	0	0	0
61	CJ	1	0	0	0	0
61	CK	1	0	0	0	0
61	CL	1	0	0	1	0
61	CT	1	0	0	0	0
61	CW	2	0	0	2	0
61	CX	2	0	0	0	0
61	CY	1	0	0	0	0
61	D0	4	0	0	0	0
61	D1	1	0	0	0	0
61	D3	2	0	0	0	0
61	D5	1	0	0	0	0
61	D6	1	0	0	0	0
61	D8	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	DA	989	0	0	44	0
61	DB	9	0	0	0	0
61	DD	18	0	0	3	0
61	DE	5	0	0	0	0
61	DF	4	0	0	0	0
61	DN	2	0	0	0	0
61	DP	12	0	0	4	0
61	DQ	1	0	0	0	0
61	DT	4	0	0	0	0
61	DU	1	0	0	0	0
61	DV	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	2	0	0	0	0
61	DY	1	0	0	0	0
All	All	297127	0	196404	5502	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (5502) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2139:C:N4	26:DA:2152:G:H1	1.46	1.14
1:CA:999:C:N4	1:CA:1042:G:H1	1.48	1.12
1:CA:998:G:H1	1:CA:1043:C:N4	1.51	1.09
25:AY:49:C:N4	25:AY:65:G:H1	1.51	1.09
1:CA:985:C:N4	1:CA:1220:G:H1	1.50	1.09
25:CY:7:A:N6	25:CY:66:U:H3	1.54	1.06
26:DA:2138:C:N4	26:DA:2153:G:H1	1.53	1.04
25:AY:53:G:H1	25:AY:61:C:N4	1.56	1.04
26:BA:2136:C:N4	26:BA:2155:G:H1	1.57	1.02
45:BY:92:ASN:HB2	45:BY:94:LYS:H	1.21	1.02
26:BA:2102:U:H3	26:BA:2187:G:H1	1.06	1.00
1:CA:1245:A:H61	1:CA:1292:U:H3	1.09	1.00
1:CA:985:C:H42	1:CA:1220:G:H1	0.99	0.99
1:CA:1162:C:N4	1:CA:1174:G:H1	1.60	0.99
25:CY:10:G:H1	25:CY:25:C:H42	1.09	0.98
26:BA:2499:C:OP1	61:BA:5135:HOH:O	1.83	0.97
4:CD:15:GLU:HG3	4:CD:63:LYS:HG3	1.47	0.96
26:BA:2138:C:H42	26:BA:2153:G:H1	1.09	0.96
1:CA:1000:U:H3	1:CA:1041:A:N6	1.63	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2127:G:C6	26:DA:2161:C:N4	2.34	0.95
25:CY:50:U:H3	25:CY:64:A:H61	1.02	0.95
23:AW:26:A:H61	23:AW:44:G:H1	1.06	0.94
47:B0:11:ARG:O	47:B0:14:ARG:NH2	1.99	0.94
25:AY:29:G:H1	25:AY:41:C:N4	1.65	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.64	0.94
1:CA:1025:U:H3	1:CA:1036:G:H1	1.03	0.94
25:CY:22:G:N7	25:CY:46:7MG:N2	2.14	0.94
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.31	0.94
1:CA:501:C:OP1	12:CL:124:LYS:NZ	2.01	0.93
1:CA:1162:C:H42	1:CA:1174:G:H1	1.14	0.93
40:DT:55:ASN:H	40:DT:59:THR:HG22	1.29	0.93
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.50	0.93
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.47	0.93
1:CA:838:G:H1	1:CA:848:C:H42	1.10	0.93
23:AW:19:G:H1	23:AW:56:C:H42	1.17	0.93
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.51	0.92
26:BA:2121:G:H1	26:BA:2177:C:H42	1.13	0.92
46:DZ:5:LEU:HG	46:DZ:47:VAL:HG21	1.50	0.92
25:CY:19:G:H1	25:CY:56:C:H42	1.12	0.92
25:CY:51:U:H3	25:CY:63:G:H1	1.17	0.91
23:AW:1:G:O6	23:AW:72:C:N3	2.04	0.91
26:DA:2121:G:H1	26:DA:2177:C:N4	1.68	0.91
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.04	0.91
1:CA:985:C:N3	1:CA:1220:G:N2	2.17	0.91
26:DA:2139:C:N4	26:DA:2152:G:N1	2.12	0.91
19:CS:42:PRO:HG3	51:D4:61:ARG:HG3	1.53	0.91
1:CA:1165:C:H42	1:CA:1171:G:H1	1.19	0.90
25:AY:53:G:H1	25:AY:61:C:H42	0.91	0.90
25:AY:29:G:H1	25:AY:41:C:H42	0.90	0.90
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.06	0.89
26:DA:2121:G:H1	26:DA:2177:C:H42	0.95	0.89
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.55	0.89
1:CA:1244:C:H42	1:CA:1293:G:H1	1.12	0.89
1:CA:999:C:N3	1:CA:1042:G:N2	2.21	0.89
25:AY:49:C:N3	25:AY:65:G:N2	2.21	0.89
25:CY:19:G:N2	25:CY:56:C:N3	2.20	0.89
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.89
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
1:CA:998:G:N2	1:CA:1043:C:N3	2.20	0.88
1:AA:78:G:C6	1:AA:91:C:N4	2.40	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:5:G:H1	25:AY:68:C:H42	1.16	0.88
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.55	0.88
1:AA:1316:G:H22	1:AA:1319:A:H5''	1.39	0.88
27:DB:41:U:H5	31:DG:70:VAL:H	1.22	0.88
1:AA:78:G:C2	1:AA:91:C:N3	2.43	0.87
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.36	0.87
23:AW:1:G:N1	23:AW:72:C:O2	2.07	0.87
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.06	0.87
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.08	0.87
25:CY:15:G:H22	25:CY:48:C:H42	1.16	0.87
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.55	0.87
9:AI:17:VAL:HG21	9:AI:81:ILE:HG22	1.55	0.87
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.54	0.86
1:AA:1502:A:H2	1:AA:1505:G:H1	1.21	0.86
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.06	0.86
25:CY:50:U:H3	25:CY:64:A:N6	1.74	0.86
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.57	0.86
26:DA:2139:C:N3	26:DA:2152:G:N2	2.23	0.86
26:BA:2190:G:H2'	26:BA:2191:G:H5''	1.56	0.86
26:DA:2136:C:N3	26:DA:2155:G:N2	2.24	0.86
1:AA:664:G:H22	1:AA:741:G:H1	1.23	0.86
19:AS:63:THR:H	19:AS:66:MET:HE2	1.41	0.86
1:CA:76:C:H42	1:CA:93:G:H1	0.91	0.86
26:DA:2136:C:N4	26:DA:2155:G:N1	2.24	0.85
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.10	0.85
26:DA:2807:G:N1	26:DA:2893:G:O6	2.08	0.85
26:BA:1310:G:OP2	54:B7:9:ARG:NH1	2.09	0.85
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.09	0.85
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.10	0.84
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.42	0.84
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.58	0.84
26:DA:2297:C:N3	26:DA:2321:G:N1	2.25	0.84
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.59	0.84
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.10	0.84
26:BA:2134:A:H2'	26:BA:2135:A:C8	2.13	0.84
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.10	0.84
26:DA:880:G:H22	26:DA:898:C:H1'	1.40	0.84
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.58	0.84
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	1.60	0.84
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:958:A:N6	19:CS:77:THR:O	2.11	0.84
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.11	0.83
26:DA:1039:G:O6	26:DA:1116:C:N4	2.11	0.83
1:CA:201:C:H42	1:CA:216:G:H1	1.21	0.83
42:DV:24:LYS:HG2	42:DV:64:HIS:HD2	1.43	0.83
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.11	0.83
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.59	0.83
1:CA:1286:A:H8	1:CA:1287:A:H4'	1.43	0.83
26:DA:1204:A:H2	26:DA:1241:A:H62	1.22	0.83
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.60	0.83
23:CW:49:C:N4	23:CW:65:G:O6	2.12	0.83
25:CY:31:A:N1	25:CY:39:PSU:O2	2.12	0.83
1:CA:1162:C:N3	1:CA:1174:G:N2	2.26	0.83
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.12	0.83
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.43	0.83
26:DA:2165:G:H22	26:DA:2172:U:H5	1.24	0.82
26:DA:2136:C:N4	26:DA:2155:G:H1	1.77	0.82
26:DA:652(D):C:N4	26:DA:652(U):G:O6	2.09	0.82
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.12	0.82
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.62	0.82
26:BA:2136:C:N3	26:BA:2155:G:N2	2.27	0.82
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.45	0.82
1:CA:70:G:H1	1:CA:99:U:H3	1.28	0.82
26:DA:2136:C:C4	26:DA:2155:G:N1	2.47	0.82
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.26	0.82
1:CA:975:A:H4'	1:CA:976:G:H5''	1.60	0.82
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.12	0.82
26:BA:1314:C:OP1	61:BA:4634:HOH:O	1.98	0.82
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.43	0.81
1:CA:983:A:N1	1:CA:1222:G:N2	2.28	0.81
27:DB:22:U:H3	27:DB:61:G:H1	1.24	0.81
2:AB:16:HIS:O	2:AB:18:GLY:N	2.13	0.81
1:CA:1133:G:H1	1:CA:1141:C:H42	1.24	0.81
9:CI:53:VAL:O	9:CI:55:ALA:N	2.12	0.81
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.12	0.81
25:AY:5:G:H1	25:AY:68:C:N4	1.78	0.81
1:AA:78:G:N1	1:AA:91:C:N4	2.29	0.81
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.14	0.81
1:CA:1030:C:H42	1:CA:1031:G:H1	1.24	0.81
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.46	0.81
1:CA:1000:U:H3	1:CA:1041:A:H61	0.87	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.62	0.81
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.14	0.81
28:DD:276:LYS:H	28:DD:276:LYS:HD3	1.45	0.81
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.62	0.81
25:CY:10:G:H1	25:CY:25:C:N4	1.78	0.80
23:AW:26:A:N6	23:AW:44:G:H1	1.78	0.80
26:BA:2867:G:OP2	40:BT:119:LYS:NZ	2.14	0.80
25:CY:38:A:H3'	25:CY:39:PSU:H5'	1.62	0.80
1:AA:839:U:O2'	1:AA:840:C:OP1	2.00	0.80
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.64	0.80
26:BA:1779:U:OP2	61:BA:5167:HOH:O	1.99	0.80
46:DZ:45:ASP:OD2	46:DZ:49:ARG:NH1	2.14	0.80
1:AA:90:U:H2'	1:AA:91:C:H5''	1.63	0.80
23:CW:4:C:N3	23:CW:69:G:N2	2.29	0.80
38:DR:97:VAL:HG22	38:DR:114:VAL:HG22	1.62	0.80
31:DG:145:THR:HG23	31:DG:147:ASP:H	1.46	0.80
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.15	0.80
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.15	0.80
27:DB:7:G:O6	27:DB:114:C:N4	2.14	0.80
25:AY:68:C:H2'	25:AY:69:G:H5'	1.63	0.80
25:AY:53:G:N2	25:AY:61:C:N3	2.29	0.80
26:BA:192:C:OP1	61:BA:4000:HOH:O	1.99	0.80
1:CA:878:G:H5'	8:CH:89:PRO:HG2	1.64	0.80
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.47	0.79
1:CA:838:G:H1	1:CA:848:C:N4	1.79	0.79
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.16	0.79
1:AA:347:G:O2'	1:AA:348:G:OP1	2.00	0.79
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.14	0.79
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.15	0.79
1:CA:589:C:O2	1:CA:650:G:N2	2.13	0.79
26:BA:2102:U:O2	26:BA:2187:G:N2	2.13	0.79
28:DD:238:GLY:O	61:DD:409:HOH:O	2.00	0.79
25:AY:15:G:H22	25:AY:48:C:H42	1.30	0.79
23:CW:4:C:N4	23:CW:69:G:N1	2.29	0.79
25:CY:4:C:H42	25:CY:69:G:H1	1.28	0.79
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.64	0.79
1:CA:1055:A:N7	1:CA:1200:C:N4	2.30	0.79
1:CA:1245:A:N6	1:CA:1292:U:H3	1.80	0.79
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.65	0.79
26:DA:2127:G:C2	26:DA:2161:C:N3	2.52	0.78
7:AG:38:LEU:HA	7:AG:41:ARG:HD2	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1027:C:C2	1:AA:1034:G:N1	2.52	0.78
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.17	0.78
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.65	0.78
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.64	0.78
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.29	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.66	0.78
1:CA:838:G:N2	1:CA:848:C:N3	2.30	0.78
1:CA:1028:C:N3	1:CA:1033:G:C6	2.52	0.78
1:AA:266:G:H5''	1:AA:268:C:H41	1.47	0.78
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.64	0.78
26:BA:2136:C:H42	26:BA:2155:G:H1	0.83	0.78
1:CA:664:G:H22	1:CA:741:G:H1	1.29	0.78
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.65	0.77
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.84	0.77
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.64	0.77
27:DB:20:C:N4	27:DB:63:G:O6	2.17	0.77
31:BG:12:TYR:HA	31:BG:16:ARG:HG3	1.66	0.77
1:AA:78:G:N2	1:AA:91:C:N3	2.33	0.77
26:BA:2138:C:N4	26:BA:2153:G:H1	1.81	0.77
33:BI:104:GLN:O	33:BI:106:GLY:N	2.16	0.77
44:DX:60:ARG:HH12	54:D7:47:ARG:HH22	1.30	0.77
25:AY:7:A:O2'	25:AY:49:C:H5'	1.85	0.77
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.67	0.77
23:AW:50:U:H5'	23:AW:50:U:H6	1.48	0.77
25:AY:5:G:N2	25:AY:68:C:N3	2.31	0.77
1:AA:1027:C:N3	1:AA:1034:G:C6	2.53	0.77
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.66	0.77
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.18	0.77
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.18	0.77
26:DA:2037:G:O6	61:DA:4191:HOH:O	2.02	0.77
26:BA:1689:A:H62	26:BA:1698:A:H2	1.33	0.77
1:CA:1338:G:H21	24:CX:41:C:H1'	1.49	0.77
25:CY:19:G:H1	25:CY:56:C:N4	1.82	0.77
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.02	0.77
32:DH:24:VAL:HG13	32:DH:37:VAL:HG21	1.66	0.77
26:BA:2130:U:H4'	26:BA:2133:G:H4'	1.67	0.76
1:CA:1134:G:H1	1:CA:1140:C:H42	1.29	0.76
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.67	0.76
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.67	0.76
26:DA:370:G:N7	61:DA:3786:HOH:O	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:51:U:O2	25:CY:63:G:N2	2.15	0.76
1:CA:504:C:OP1	61:CA:3202:HOH:O	2.02	0.76
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	1.65	0.76
1:CA:1128:C:O2	1:CA:1147:C:N4	2.18	0.76
39:BS:39:ILE:HB	39:BS:49:VAL:HG13	1.68	0.76
1:CA:1060:C:HO2'	10:CJ:56:HIS:HD1	1.34	0.76
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.65	0.76
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.18	0.76
26:BA:2162:G:H2'	26:BA:2163:C:H5''	1.65	0.76
24:CX:7:G:H5''	24:CX:8:4SU:H5	1.65	0.76
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.18	0.76
1:CA:1030:C:N4	1:CA:1031:G:H1	1.84	0.76
13:CM:84:ILE:O	13:CM:86:CYS:N	2.17	0.76
25:CY:49:C:H42	25:CY:65:G:H1	1.33	0.76
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.18	0.76
1:CA:76:C:N3	1:CA:93:G:N2	2.32	0.76
1:CA:694:A:HO2'	25:CY:38:A:HO2'	1.32	0.76
1:CA:1134:G:H1	1:CA:1140:C:N4	1.84	0.76
26:DA:1169:G:H1	26:DA:1180:C:H42	1.31	0.76
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.67	0.76
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.67	0.76
1:AA:998:G:H1	1:AA:1043:C:H42	1.30	0.76
26:BA:1506:C:H2'	26:BA:1507:A:H8	1.48	0.76
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.17	0.76
26:BA:587:C:OP2	36:BP:21:ARG:NH2	2.20	0.75
55:D8:32:LEU:O	55:D8:36:LYS:NZ	2.18	0.75
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.18	0.75
26:BA:2121:G:H1	26:BA:2177:C:N4	1.84	0.75
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.67	0.75
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.19	0.75
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.51	0.75
26:DA:2113:U:H3	26:DA:2170:A:H61	1.33	0.75
36:BP:124:LYS:HG3	36:BP:144:GLU:HG2	1.69	0.75
25:CY:34:G:H2'	25:CY:35:A:C8	2.21	0.75
1:CA:35:G:O2'	12:CL:118:SER:O	2.05	0.75
1:CA:1244:C:N4	1:CA:1293:G:H1	1.83	0.75
4:AD:166:LYS:NZ	4:AD:179:GLU:OE2	2.20	0.75
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.15	0.75
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.68	0.75
1:CA:1502:A:H2	1:CA:1505:G:H1	1.32	0.75
25:AY:67:C:H2'	25:AY:68:C:C6	2.21	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:68:C:H2'	25:CY:69:G:H5'	1.69	0.75
26:DA:2122:U:O4	26:DA:2176:A:N1	2.20	0.75
26:BA:2134:A:H2'	26:BA:2135:A:H8	1.49	0.75
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.19	0.75
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.20	0.75
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.19	0.75
1:CA:953:G:H5'	1:CA:965:A:H61	1.51	0.74
25:CY:38:A:C3'	25:CY:39:PSU:H5'	2.16	0.74
36:DP:42:SER:O	61:DP:303:HOH:O	2.05	0.74
3:CC:59:ARG:HG2	3:CC:64:VAL:HG13	1.68	0.74
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.20	0.74
1:CA:528:C:N4	12:CL:49:ASN:OD1	2.20	0.74
46:DZ:77:ASP:OD1	46:DZ:80:ARG:NH1	2.18	0.74
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.19	0.74
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.20	0.74
26:BA:885:C:H3'	26:BA:886:C:H5''	1.70	0.74
2:CB:125:PRO:O	2:CB:127:ILE:N	2.20	0.74
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.53	0.74
1:CA:1153:C:H42	1:CA:1154:G:H21	1.35	0.74
26:BA:279:C:H42	26:BA:361:G:H1	1.33	0.74
26:BA:1048:A:OP2	26:BA:1109:C:N4	2.21	0.74
1:AA:1007:C:N3	1:AA:1022:G:O6	2.19	0.74
1:CA:1011:G:H1	1:CA:1018:C:H42	1.33	0.74
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.19	0.74
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.19	0.74
26:BA:2353:G:N7	61:BA:4441:HOH:O	2.20	0.74
26:BA:2287:A:H62	26:BA:2344:U:H3	1.31	0.74
46:DZ:154:ASP:OD1	46:DZ:154:ASP:N	2.20	0.74
1:AA:1086:U:H3	1:AA:1099:G:H22	1.35	0.74
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.20	0.74
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.21	0.74
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.68	0.74
26:DA:2138:C:H42	26:DA:2153:G:H1	0.77	0.74
25:AY:49:C:H42	25:AY:65:G:H1	0.79	0.74
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.20	0.74
1:CA:532:A:H61	3:CC:193:TYR:HB3	1.52	0.74
26:DA:11:G:N7	61:DA:4269:HOH:O	2.21	0.74
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.70	0.74
23:CW:30:G:H1	23:CW:40:C:H42	1.34	0.74
13:CM:5:ALA:HB1	13:CM:66:LEU:HD13	1.70	0.74
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.20	0.73
24:CX:67:C:H2'	24:CX:68:C:H5'	1.69	0.73
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.68	0.73
1:CA:992:U:H6	1:CA:992:U:H5''	1.53	0.73
1:CA:1005:A:OP2	1:CA:1024:G:N2	2.19	0.73
2:CB:119:GLU:OE2	2:CB:153:ARG:NH1	2.22	0.73
26:DA:2632:A:HO2'	26:DA:2811:G:HO2'	1.32	0.73
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.68	0.73
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.70	0.73
1:CA:1054:C:C4	23:CW:34:G:H1'	2.23	0.73
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.21	0.73
52:B5:40:LYS:NZ	52:B5:44:THR:O	2.18	0.73
26:BA:993:G:OP1	41:BU:50:ARG:NH2	2.22	0.73
45:BY:92:ASN:HB2	45:BY:94:LYS:N	2.01	0.73
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.21	0.73
26:BA:847:U:OP2	61:BA:4392:HOH:O	2.06	0.73
26:BA:1602:U:O4	61:BA:4209:HOH:O	2.06	0.73
9:CI:8:GLY:HA3	9:CI:15:ALA:HB3	1.71	0.73
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.69	0.73
23:AW:18:G:O2'	23:AW:57:G:N2	2.14	0.73
56:B9:17:ILE:HG22	56:B9:24:TYR:HB2	1.70	0.73
26:BA:243:U:OP1	55:B8:6:THR:OG1	2.07	0.73
26:DA:2127:G:N1	26:DA:2161:C:C4	2.57	0.73
23:AW:19:G:N2	23:AW:56:C:N3	2.36	0.73
1:AA:812:C:N3	61:AA:4038:HOH:O	2.20	0.73
1:CA:1323:G:N2	1:CA:1361:G:O2'	2.22	0.73
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.70	0.73
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.21	0.72
26:DA:2138:C:N3	26:DA:2153:G:N2	2.34	0.72
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.06	0.72
1:AA:504:C:OP1	61:AA:4184:HOH:O	2.07	0.72
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.22	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.07	0.72
1:CA:117:G:OP2	61:CA:3236:HOH:O	2.07	0.72
26:DA:191:A:N1	61:DA:4214:HOH:O	2.22	0.72
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.54	0.72
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.69	0.72
26:DA:740:U:OP2	61:DA:4209:HOH:O	2.07	0.72
25:AY:33:U:H3'	25:AY:34:G:H5''	1.71	0.72
1:AA:975:A:H4'	1:AA:976:G:H5''	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:19:G:H1	23:CW:56:C:H42	1.37	0.72
51:B4:57:GLU:HB2	51:B4:58:ARG:HA	1.72	0.72
13:CM:5:ALA:HB3	13:CM:22:ILE:HD12	1.69	0.72
42:DV:98:GLU:OE1	42:DV:100:ARG:NH1	2.23	0.72
25:CY:7:A:H61	25:CY:66:U:H3	0.79	0.72
26:BA:65:C:O2	26:BA:456:C:N4	2.20	0.72
23:CW:50:U:O4	23:CW:64:A:N1	2.22	0.72
43:BW:15:ARG:NH1	61:BW:4002:HOH:O	2.21	0.72
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.23	0.72
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.07	0.72
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.70	0.72
25:CY:15:G:H22	25:CY:48:C:N4	1.87	0.72
26:DA:1250:G:OP2	36:DP:21:ARG:NH1	2.23	0.72
23:CW:61:C:O2'	23:CW:62:C:O5'	2.07	0.72
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.23	0.72
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.71	0.72
1:AA:934:C:OP1	61:AA:4086:HOH:O	2.08	0.71
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.22	0.71
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.71	0.71
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.23	0.71
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.72	0.71
26:BA:2049:G:N7	61:BA:5132:HOH:O	2.23	0.71
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.25	0.71
23:AW:7:A:H61	23:AW:66:U:H3	1.36	0.71
49:D2:38:GLN:HB3	49:D2:44:LEU:HB2	1.72	0.71
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.73	0.71
1:CA:1011:G:H1	1:CA:1018:C:N4	1.89	0.71
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.73	0.71
26:BA:604:G:OP2	36:BP:90:ARG:NH1	2.24	0.71
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.08	0.71
23:AW:19:G:H1	23:AW:56:C:N4	1.89	0.71
20:AT:57:ARG:HH12	20:AT:100:ILE:HD12	1.55	0.71
1:AA:1027:C:O2	1:AA:1034:G:C2	2.43	0.71
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.17	0.71
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.23	0.71
19:CS:77:THR:HG22	19:CS:78:ARG:HG2	1.71	0.71
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.71	0.71
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.23	0.71
26:BA:1140:C:O3'	34:BN:25:ARG:NH1	2.23	0.71
1:CA:1465:C:OP2	40:DT:108:ARG:NH2	2.22	0.71
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.71
26:BA:899:A:O2'	26:BA:900:A:O5'	2.08	0.71
26:DA:2788:C:OP1	29:DE:61:ARG:NH2	2.23	0.71
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.21	0.71
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.55	0.71
27:DB:5:C:H42	27:DB:116:G:H1	1.39	0.71
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.73	0.71
39:DS:15:ARG:O	39:DS:19:LYS:HD3	1.90	0.70
6:AF:70:ASP:OD1	6:AF:70:ASP:N	2.24	0.70
1:CA:1366:C:O2'	10:CJ:60:ARG:NH2	2.24	0.70
26:BA:1380:G:OP2	61:BA:5119:HOH:O	2.09	0.70
31:DG:80:PHE:O	31:DG:82:LEU:N	2.22	0.70
33:DI:72:LEU:HD21	33:DI:107:VAL:HG11	1.74	0.70
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.27	0.70
1:CA:999:C:H42	1:CA:1042:G:H1	0.74	0.70
26:BA:2448:A:OP1	61:BA:5135:HOH:O	2.09	0.70
26:DA:1038:C:H42	26:DA:1117:G:H1	1.38	0.70
26:BA:2239:G:OP2	61:BA:4313:HOH:O	2.08	0.70
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.56	0.70
26:DA:900:A:H2'	26:DA:901:A:H8	1.57	0.70
17:AQ:75:ARG:NH1	17:AQ:76:LEU:O	2.25	0.70
1:CA:993:G:O6	1:CA:1045:C:N4	2.15	0.70
26:DA:1689:A:H62	26:DA:1698:A:H2	1.40	0.70
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.72	0.70
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.57	0.70
33:DI:78:THR:O	33:DI:104:GLN:NE2	2.25	0.70
25:AY:51:U:H2'	25:AY:52:G:H8	1.56	0.70
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.74	0.70
25:AY:15:G:N1	25:AY:48:C:N3	2.39	0.70
23:CW:4:C:N4	23:CW:69:G:C6	2.59	0.70
25:AY:22:G:N7	25:AY:46:7MG:O6	2.25	0.70
1:CA:953:G:H5'	1:CA:965:A:N6	2.07	0.70
1:AA:1304:G:OP2	61:AA:4111:HOH:O	2.10	0.70
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.73	0.70
27:DB:28:C:H2'	27:DB:29:A:H8	1.57	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.72	0.70
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.24	0.70
46:DZ:44:PHE:O	46:DZ:48:PHE:N	2.21	0.70
10:CJ:5:ARG:N	10:CJ:73:ASP:HA	2.07	0.69
2:CB:161:ALA:HB1	2:CB:185:ILE:HD11	1.74	0.69
1:AA:1159:U:OP1	2:AB:133:LYS:NZ	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:812:C:N3	61:CA:3212:HOH:O	2.25	0.69
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.25	0.69
26:BA:1238:G:OP2	61:BA:4983:HOH:O	2.10	0.69
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.20	0.69
46:DZ:72:ARG:NH1	46:DZ:97:GLU:O	2.25	0.69
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.57	0.69
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.26	0.69
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.72	0.69
26:BA:1434:A:H61	26:BA:1558:A:H62	1.39	0.69
30:DF:197:ASP:OD1	30:DF:198:ALA:N	2.25	0.69
26:DA:300:A:OP1	45:DY:86:ARG:NH2	2.25	0.69
36:DP:91:PHE:O	36:DP:121:LYS:NZ	2.21	0.69
1:CA:798:G:O6	61:CA:3223:HOH:O	2.09	0.69
1:CA:1359:C:O2	61:CA:3330:HOH:O	2.09	0.69
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.69
26:BA:1297:C:OP1	61:BA:4340:HOH:O	2.09	0.69
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.25	0.69
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.75	0.69
1:CA:67:C:H2'	1:CA:68:G:C8	2.28	0.69
26:DA:987:G:O2'	26:DA:1000:A:N3	2.25	0.69
15:AO:55:GLY:HA2	15:AO:58:MET:HE2	1.73	0.69
25:CY:26:A:N1	25:CY:44:G:O6	2.26	0.69
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.25	0.69
8:CH:12:ARG:HH12	8:CH:27:PRO:HD2	1.58	0.69
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.22	0.69
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.27	0.69
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.73	0.69
23:CW:56:C:H5	26:DA:897:C:H1'	1.56	0.69
4:AD:49:ARG:HE	4:AD:49:ARG:H	1.38	0.69
1:AA:1423:G:OP1	35:BO:49:ARG:NH2	2.24	0.69
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.58	0.69
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.27	0.69
25:CY:69:G:H2'	25:CY:70:G:O4'	1.92	0.69
26:DA:878:A:N6	26:DA:899:A:O2'	2.22	0.69
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.73	0.69
19:AS:27:GLU:HB2	19:AS:28:LYS:HD2	1.74	0.69
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.75	0.69
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.57	0.69
17:CQ:53:LEU:HD23	17:CQ:82:MET:HE1	1.75	0.69
25:CY:5:G:H1	25:CY:68:C:H42	1.40	0.69
12:CL:124:LYS:HB2	12:CL:124:LYS:HZ2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.58	0.69
1:CA:1060:C:O2'	10:CJ:56:HIS:ND1	2.24	0.69
1:CA:1320:C:O4'	19:CS:73:GLU:HG2	1.93	0.69
26:BA:271(K):U:H1'	33:BI:50:ARG:HD2	1.74	0.69
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.75	0.69
1:CA:460:G:O6	1:CA:470:C:H5''	1.93	0.69
1:CA:1329:A:OP2	21:CU:7:ARG:NH2	2.22	0.69
29:BE:8:LYS:NZ	61:BE:416:HOH:O	2.18	0.69
26:DA:568:U:H5'	26:DA:945:A:N1	2.08	0.69
26:DA:89:G:H3'	26:DA:90:U:H5''	1.75	0.69
25:AY:76:A:N6	26:BA:2422:A:O4'	2.26	0.69
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.10	0.69
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.23	0.69
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.74	0.69
46:DZ:93:ASP:HA	46:DZ:131:ARG:HH22	1.57	0.69
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.26	0.69
2:AB:21:ARG:HB3	2:AB:39:ILE:HG12	1.75	0.69
23:AW:50:U:H3	23:AW:64:A:H61	1.39	0.68
26:BA:1840:G:N7	61:BA:4310:HOH:O	2.26	0.68
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.57	0.68
20:CT:43:LEU:O	20:CT:47:GLY:N	2.17	0.68
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.27	0.68
1:AA:838:G:H1	1:AA:848:C:H42	1.40	0.68
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.26	0.68
25:CY:62:C:H2'	25:CY:63:G:H8	1.58	0.68
51:D4:44:THR:O	51:D4:46:GLN:N	2.27	0.68
26:DA:741:G:OP2	61:DA:4210:HOH:O	2.12	0.68
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.26	0.68
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.40	0.68
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.20	0.68
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.57	0.68
33:BI:38:LEU:HD12	33:BI:38:LEU:H	1.58	0.68
26:BA:1714:G:H1	26:BA:1745(A):C:H42	1.41	0.68
26:DA:2128:C:H42	26:DA:2160:G:H1	1.42	0.68
8:CH:12:ARG:NH1	8:CH:27:PRO:HD2	2.09	0.68
26:DA:2689:U:H4'	26:DA:2690:C:H5'	1.75	0.68
1:AA:953:G:H5'	1:AA:965:A:H61	1.56	0.68
47:D0:40:GLN:HE21	47:D0:57:PHE:HB3	1.58	0.68
30:DF:143:ALA:HB1	30:DF:148:LEU:HB2	1.74	0.68
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.22	0.68
26:DA:2502:G:N7	61:DA:4405:HOH:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2171:A:N3	26:DA:2172:U:N3	2.41	0.68
25:AY:69:G:H2'	25:AY:70:G:O4'	1.94	0.68
1:CA:1002:G:H1	1:CA:1038:C:N4	1.91	0.68
1:CA:1166:G:H5''	1:CA:1166:G:H8	1.59	0.68
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.26	0.68
26:BA:2123:G:H1	26:BA:2175:C:H42	1.40	0.68
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.28	0.68
26:DA:1019:U:HO2'	26:DA:1021:A:H2	1.42	0.68
26:BA:1783:A:N7	61:BA:5029:HOH:O	2.27	0.68
26:BA:543:C:N4	26:BA:549:G:O6	2.18	0.68
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.59	0.68
1:AA:339:C:OP2	35:BO:97:ARG:NH1	2.26	0.68
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.26	0.68
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.75	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.93	0.68
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.76	0.68
1:AA:838:G:H1	1:AA:848:C:N4	1.91	0.68
26:BA:548:A:O2'	26:BA:549:G:OP1	2.10	0.68
27:BB:2:C:O2	27:BB:119:G:N2	2.20	0.68
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.68
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.68
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.29	0.68
26:DA:1189:A:OP2	61:DA:4174:HOH:O	2.12	0.68
1:AA:123:C:OP1	1:AA:311:C:O2'	2.11	0.68
1:CA:750:G:N3	15:CO:23:GLY:HA3	2.08	0.68
26:BA:2447:G:OP2	61:BA:4544:HOH:O	2.11	0.68
27:DB:55:U:O2'	31:DG:27:ASN:ND2	2.26	0.68
1:CA:344:A:H5''	1:CA:345:C:H5	1.59	0.68
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.26	0.68
39:DS:58:LEU:HD11	39:DS:65:VAL:HA	1.75	0.68
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.12	0.67
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.57	0.67
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.59	0.67
33:BI:106:GLY:HA2	33:BI:107:VAL:O	1.93	0.67
1:CA:1309:G:OP1	13:CM:88:ARG:NH1	2.26	0.67
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.75	0.67
26:BA:602:G:O2'	26:BA:655:A:N6	2.27	0.67
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.73	0.67
12:CL:124:LYS:HB2	12:CL:124:LYS:NZ	2.08	0.67
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.42	0.67
1:AA:572:A:OP1	61:AA:4084:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.28	0.67
26:BA:2059:A:OP2	61:BA:4315:HOH:O	2.11	0.67
24:CX:31:G:H3'	24:CX:32:5MC:HM51	1.76	0.67
25:CY:15:G:N2	25:CY:48:C:H42	1.90	0.67
19:CS:27:GLU:HB2	19:CS:28:LYS:HD3	1.77	0.67
9:AI:53:VAL:O	9:AI:55:ALA:N	2.27	0.67
1:AA:1158:C:H5	1:AA:1181:G:H1	1.42	0.67
42:DV:43:GLU:N	42:DV:43:GLU:OE2	2.27	0.67
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.27	0.67
26:DA:2121:G:N2	26:DA:2177:C:N3	2.36	0.67
1:AA:347:G:H2'	1:AA:348:G:O4'	1.94	0.67
3:CC:91:LEU:HD23	3:CC:101:LEU:HD22	1.76	0.67
26:DA:526:A:OP1	61:DA:4183:HOH:O	2.12	0.67
8:CH:4:ASP:OD2	8:CH:85:ARG:NH1	2.27	0.67
16:AP:1:MET:N	16:AP:1:MET:SD	2.62	0.67
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.77	0.67
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.77	0.67
26:DA:2518:A:OP2	61:DA:3991:HOH:O	2.12	0.67
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.77	0.67
1:CA:1310:G:OP1	13:CM:77:ASN:ND2	2.27	0.67
26:BA:1452:A:OP2	61:BA:3995:HOH:O	2.12	0.67
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.76	0.67
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.67
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.60	0.67
26:DA:2224:G:OP1	28:DD:268:ARG:NE	2.28	0.67
13:CM:121:LYS:HZ2	13:CM:121:LYS:H	1.43	0.67
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.29	0.67
1:AA:160:A:N6	1:AA:345:C:OP2	2.27	0.67
51:D4:38:LYS:O	51:D4:40:HIS:N	2.21	0.67
1:AA:67:C:H2'	1:AA:68:G:C8	2.30	0.67
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.27	0.67
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.76	0.67
26:DA:1783:A:N7	61:DA:4510:HOH:O	2.26	0.67
26:DA:2126:A:H61	26:DA:2172:U:H3'	1.60	0.67
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.58	0.67
1:AA:1022:G:H2'	1:AA:1023:G:H8	1.60	0.67
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.75	0.67
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	1.75	0.67
26:DA:2287:A:H62	26:DA:2344:U:H3	1.40	0.67
1:CA:560:U:O2'	1:CA:561:U:OP2	2.13	0.67
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.58	0.67
26:DA:2127:G:N1	26:DA:2161:C:N4	2.42	0.67
25:CY:9:A:OP2	25:CY:13:C:N4	2.26	0.67
26:DA:7:G:N2	26:DA:2896:C:O2	2.23	0.67
31:DG:13:GLU:O	31:DG:15:VAL:N	2.27	0.67
25:CY:62:C:H2'	25:CY:63:G:C8	2.30	0.66
1:CA:673:G:H2'	1:CA:674:G:C8	2.30	0.66
1:CA:951:G:OP2	13:CM:102:ARG:NH1	2.29	0.66
2:CB:87:ARG:HH21	2:CB:233:SER:HB3	1.60	0.66
27:DB:50:G:OP1	39:DS:63:THR:N	2.27	0.66
3:AC:70:VAL:HG22	3:AC:72:LYS:H	1.59	0.66
19:CS:49:ILE:HG13	19:CS:62:ILE:HD11	1.76	0.66
26:BA:971:C:OP2	61:BA:5252:HOH:O	2.11	0.66
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.30	0.66
1:CA:1155:G:H2'	1:CA:1156:G:C8	2.29	0.66
1:CA:1191:A:OP1	3:CC:3:ASN:ND2	2.28	0.66
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.60	0.66
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.27	0.66
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.76	0.66
7:CG:59:LEU:HG	7:CG:63:LYS:HE2	1.77	0.66
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.27	0.66
27:DB:76:G:N2	27:DB:101:G:O6	2.25	0.66
25:AY:6:G:O6	25:AY:7:A:N6	2.29	0.66
1:AA:1245:A:H61	1:AA:1292:U:H3	1.44	0.66
26:BA:2277:G:OP2	47:B0:10:THR:HG21	1.96	0.66
26:BA:2759:G:N7	61:BA:4108:HOH:O	2.27	0.66
13:AM:34:LEU:HD13	13:AM:41:PRO:HA	1.77	0.66
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	1.75	0.66
26:BA:123:G:OP2	61:BA:3977:HOH:O	2.14	0.66
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.30	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.13	0.66
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	1.77	0.66
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.28	0.66
26:DA:1278:A:OP1	38:DR:36:THR:HG23	1.96	0.66
20:AT:15:ARG:O	20:AT:19:SER:OG	2.13	0.66
1:CA:1348:U:H4'	9:CI:120:ARG:HD3	1.78	0.66
3:CC:150:LYS:HB2	3:CC:173:VAL:HG21	1.77	0.66
26:BA:248:G:OP1	61:BA:4977:HOH:O	2.13	0.66
26:BA:880:G:H2'	26:BA:881:G:C8	2.30	0.66
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.29	0.66
1:CA:660:G:H1	1:CA:745:C:H42	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BO:64:ARG:NH1	35:BO:81:ASP:OD1	2.29	0.66
26:BA:739:G:OP1	61:BA:5169:HOH:O	2.13	0.66
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.29	0.66
26:BA:2140:C:C2	26:BA:2151:G:N2	2.64	0.66
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.31	0.66
26:BA:2080:G:O6	61:BA:4418:HOH:O	2.12	0.66
26:BA:607:U:OP1	30:BF:102:PRO:HA	1.96	0.66
26:BA:998:C:OP1	61:BA:4644:HOH:O	2.14	0.66
1:CA:649:G:H2'	1:CA:650:G:H5''	1.78	0.65
31:DG:16:ARG:O	31:DG:20:ILE:HG13	1.95	0.65
1:AA:193:C:H2'	1:AA:194:C:H6	1.59	0.65
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.65
24:CX:9:G:O2'	24:CX:10:G:N7	2.20	0.65
1:CA:1026:G:O6	1:CA:1036:G:N2	2.28	0.65
26:BA:1174:A:H4'	26:BA:1175:U:OP1	1.95	0.65
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.30	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.30	0.65
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.77	0.65
26:BA:1754:C:H5''	40:BT:113:LYS:HE3	1.77	0.65
23:AW:5:G:H2'	23:AW:6:G:H8	1.60	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.78	0.65
26:BA:2722:G:OP2	61:BA:4098:HOH:O	2.14	0.65
1:CA:1320:C:N3	19:CS:36:ARG:NH2	2.44	0.65
1:AA:1239:A:H62	1:AA:1299:A:N6	1.94	0.65
1:CA:977:A:O2'	1:CA:981:U:N3	2.29	0.65
25:CY:4:C:N4	25:CY:69:G:H1	1.94	0.65
1:CA:1022:G:H2'	1:CA:1023:G:H8	1.60	0.65
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.70	0.65
36:DP:44:GLY:O	61:DP:301:HOH:O	2.14	0.65
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.76	0.65
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.32	0.65
25:AY:29:G:N2	25:AY:41:C:N3	2.36	0.65
26:BA:880:G:H2'	26:BA:881:G:H8	1.61	0.65
26:DA:323:G:HO2'	26:DA:1205:U:H3	1.43	0.65
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.32	0.65
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.29	0.65
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.12	0.65
26:BA:278:A:H2'	26:BA:279:C:C6	2.31	0.65
2:AB:93:VAL:HG21	2:AB:97:TRP:HD1	1.59	0.65
1:CA:954:G:H21	1:CA:1227:A:H62	1.44	0.65
1:CA:501:C:H2'	1:CA:502:G:C8	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1359:C:H1'	1:CA:1362:C:H41	1.61	0.65
23:CW:3:C:N3	23:CW:70:G:O6	2.29	0.65
26:BA:1342:A:OP2	61:BA:4209:HOH:O	2.13	0.65
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.62	0.65
26:DA:500:G:N1	26:DA:503:A:OP2	2.30	0.65
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.79	0.65
31:DG:44:GLY:O	31:DG:47:LYS:HB2	1.95	0.65
46:DZ:130:PRO:HA	46:DZ:133:ILE:HD11	1.77	0.65
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.32	0.65
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.29	0.65
1:AA:1030(D):A:N6	1:AA:1031:G:H21	1.95	0.65
26:BA:1204:A:H2	26:BA:1241:A:H62	1.43	0.65
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.78	0.65
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.79	0.65
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.32	0.65
8:CH:49:GLU:OE2	8:CH:62:TYR:OH	2.14	0.65
26:BA:2478:A:OP2	56:B9:2:LYS:NZ	2.29	0.65
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.79	0.65
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.29	0.65
26:BA:131:G:OP1	61:BA:4045:HOH:O	2.13	0.65
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.97	0.64
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.79	0.64
26:BA:882:G:N2	26:BA:895:U:O2	2.27	0.64
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.64
25:AY:51:U:H2'	25:AY:52:G:C8	2.32	0.64
27:BB:23:G:O6	61:BB:3133:HOH:O	2.10	0.64
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.61	0.64
1:AA:942:G:H21	9:AI:124:GLN:NE2	1.95	0.64
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.32	0.64
51:B4:59:PHE:HA	51:B4:61:ARG:H	1.63	0.64
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.30	0.64
26:DA:2794:C:N4	26:DA:2802:G:O6	2.30	0.64
51:D4:1:MET:HG2	51:D4:6:HIS:CD2	2.32	0.64
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	1.79	0.64
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.62	0.64
26:BA:1315:C:OP2	61:BA:4634:HOH:O	2.14	0.64
26:BA:2162:G:C2'	26:BA:2163:C:H5"	2.28	0.64
27:DB:24:G:N7	27:DB:56:G:H2'	2.12	0.64
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.30	0.64
2:CB:218:ALA:O	2:CB:222:ILE:HG23	1.97	0.64
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1648:C:OP1	61:DA:4201:HOH:O	2.14	0.64
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.33	0.64
1:CA:599:C:H2'	1:CA:600:C:H5''	1.80	0.64
2:AB:13:ALA:HB2	2:AB:44:LEU:HG	1.80	0.64
1:CA:664:G:P	18:CR:64:ARG:HH22	2.19	0.64
26:DA:528:A:O2'	26:DA:529:A:H5''	1.96	0.64
39:DS:10:ARG:NH2	39:DS:91:PRO:O	2.27	0.64
26:BA:2124:G:H1	26:BA:2174:C:H42	1.45	0.64
26:BA:744:G:OP1	61:BA:4683:HOH:O	2.15	0.64
11:CK:98:LEU:O	11:CK:101:SER:OG	2.14	0.64
1:CA:1323:G:H4'	1:CA:1363:C:C2	2.32	0.64
27:DB:66:A:H61	27:DB:109:C:H5''	1.63	0.64
26:DA:236:C:H2'	26:DA:237:C:H6	1.63	0.64
33:DI:12:LEU:HD22	33:DI:19:VAL:HG21	1.78	0.64
26:BA:1993:U:OP2	61:BA:5277:HOH:O	2.15	0.64
1:CA:1002:G:C4	1:CA:1003:G:H8	2.15	0.64
26:DA:1792:G:O2'	26:DA:1830:C:OP1	2.15	0.64
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.77	0.64
30:DF:101:LEU:HD12	30:DF:102:PRO:HD2	1.80	0.64
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	1.78	0.64
1:CA:1309:G:OP2	13:CM:99:ARG:NH2	2.28	0.64
23:AW:5:G:H2'	23:AW:6:G:C8	2.33	0.64
1:AA:195:A:OP1	20:AT:68:LYS:NZ	2.30	0.64
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.31	0.64
33:DI:102:SER:O	33:DI:106:GLY:N	2.30	0.64
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.64
45:BY:54:LYS:HA	45:BY:56:PRO:HD3	1.80	0.64
1:CA:1004:A:H2'	1:CA:1038:C:H1'	1.80	0.64
1:CA:1133:G:H1	1:CA:1141:C:N4	1.95	0.64
1:CA:1507:A:N6	1:CA:1528:U:O4	2.16	0.64
1:CA:444:C:H2'	1:CA:445:G:H8	1.62	0.64
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.62	0.64
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.30	0.64
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.64
43:BW:88:ARG:HG3	43:BW:92:ARG:HH21	1.61	0.64
1:AA:56:U:H2'	1:AA:57:G:C8	2.33	0.64
3:AC:37:GLN:NE2	14:AN:52:GLN:OE1	2.31	0.64
32:BH:86:GLU:OE2	32:BH:132:ARG:NH2	2.30	0.64
24:AX:19:G:H4'	24:AX:20:U:OP2	1.97	0.64
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.30	0.64
1:CA:1165:C:N4	1:CA:1171:G:H1	1.93	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.11	0.63
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.32	0.63
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.14	0.63
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.30	0.63
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	1.95	0.63
29:DE:101:ARG:CZ	29:DE:171:GLU:HB2	2.28	0.63
26:BA:441:U:O2	30:BF:46:ARG:NH2	2.26	0.63
23:AW:55:PSU:O3'	26:BA:897:C:H4'	1.98	0.63
25:CY:31:A:N1	25:CY:39:PSU:C2	2.65	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.32	0.63
1:AA:1027:C:C2	1:AA:1034:G:C6	2.86	0.63
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.63
1:CA:1216:G:H5''	14:CN:5:ALA:HB2	1.79	0.63
26:DA:971:C:OP2	61:DA:4615:HOH:O	2.15	0.63
1:CA:1521:G:N3	61:CA:3217:HOH:O	2.30	0.63
1:AA:894:G:N7	61:AA:4110:HOH:O	2.30	0.63
46:BZ:7:ALA:HB2	46:BZ:59:LEU:HD22	1.78	0.63
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.31	0.63
7:CG:72:ARG:HH22	7:CG:138:LYS:HZ1	1.45	0.63
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.79	0.63
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.79	0.63
1:CA:562:C:H1'	12:CL:15:ARG:HB3	1.80	0.63
25:AY:25:C:O2'	25:AY:26:A:H8	1.82	0.63
26:BA:1418:G:OP2	61:BA:4561:HOH:O	2.16	0.63
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.33	0.63
26:DA:2127:G:C2	26:DA:2161:C:C4	2.87	0.63
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.34	0.63
27:DB:19:G:H2'	27:DB:20:C:O4'	1.99	0.63
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.25	0.63
26:BA:363(A):A:H2'	26:BA:363(B):G:C8	2.34	0.63
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.31	0.63
1:CA:533:A:O2'	1:CA:535:A:OP2	2.17	0.63
3:AC:181:ASN:ND2	3:AC:204:LEU:HD12	2.13	0.63
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.30	0.63
25:AY:15:G:H22	25:AY:48:C:N4	1.96	0.63
7:CG:113:GLU:HB2	7:CG:119:ARG:HG2	1.81	0.63
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.81	0.63
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.79	0.63
16:CP:23:ASP:OD2	16:CP:25:ARG:NH1	2.32	0.63
26:BA:2683:C:OP1	40:BT:53:ARG:NH2	2.31	0.63
46:DZ:157:LEU:HD13	46:DZ:161:VAL:HG13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.13	0.63
32:DH:3:ARG:HH22	32:DH:5:GLY:H	1.47	0.63
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.80	0.63
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	1.81	0.63
20:AT:87:LYS:O	20:AT:91:LEU:HG	1.98	0.63
25:AY:5:G:N1	25:AY:68:C:N4	2.31	0.63
26:DA:1038:C:N4	26:DA:1117:G:H1	1.97	0.63
19:AS:64:GLU:O	19:AS:67:VAL:HG23	1.98	0.63
33:BI:93:THR:OG1	33:BI:96:ASP:OD1	2.17	0.63
8:AH:34:GLU:OE2	8:AH:37:ARG:NH1	2.31	0.63
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.63	0.63
1:CA:539:A:H2'	1:CA:540:G:C8	2.33	0.63
23:CW:76:F3N:OP2	61:CW:3102:HOH:O	2.15	0.63
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.30	0.63
1:CA:957:U:O2'	1:CA:959:A:N7	2.30	0.63
26:DA:2173:A:H2'	26:DA:2174:C:O4'	1.99	0.63
1:CA:1002:G:H1	1:CA:1038:C:H42	1.44	0.63
26:DA:1021:A:H62	26:DA:1141:U:H3	1.44	0.63
1:AA:1321:C:H5''	1:AA:1322:C:H2'	1.78	0.63
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.17	0.63
26:DA:1637:A:OP2	61:DA:4544:HOH:O	2.16	0.63
1:CA:1402:C:N4	22:CV:18:G:OP2	2.31	0.63
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.31	0.63
31:DG:145:THR:HG22	31:DG:148:MET:SD	2.38	0.63
1:CA:1150:U:O4	1:CA:1151:A:N6	2.32	0.63
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.31	0.63
8:CH:37:ARG:HH21	8:CH:38:ILE:HD11	1.63	0.63
26:DA:1602:U:O4	61:DA:3879:HOH:O	2.11	0.63
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.33	0.62
1:AA:1025:U:O2	1:AA:1036:G:O6	2.16	0.62
1:CA:1120:G:C6	1:CA:1154:G:N2	2.67	0.62
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.32	0.62
2:CB:216:SER:O	2:CB:220:ASP:N	2.21	0.62
23:AW:47:U:H5'	23:AW:47:U:H6	1.64	0.62
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.80	0.62
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.82	0.62
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.62	0.62
1:AA:673:G:H2'	1:AA:674:G:C8	2.34	0.62
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.31	0.62
37:DQ:67:ARG:O	37:DQ:101:ARG:NH2	2.30	0.62
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.26	0.62
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.64	0.62
13:CM:32:GLU:OE1	13:CM:59:TYR:OH	2.16	0.62
1:CA:981:U:H5'	14:CN:21:TYR:CZ	2.35	0.62
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.81	0.62
3:CC:16:ARG:NH1	3:CC:181:ASN:OD1	2.31	0.62
5:CE:36:ASP:O	5:CE:38:GLN:N	2.27	0.62
25:CY:76:A:O2'	26:DA:2394:C:N3	2.31	0.62
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.29	0.62
25:CY:31:A:C6	25:CY:39:PSU:O2	2.52	0.62
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.63	0.62
42:DV:72:VAL:HG13	42:DV:85:LYS:HB3	1.80	0.62
26:DA:322:A:OP2	30:DF:169:ASN:HB2	1.98	0.62
26:DA:902:C:H2'	26:DA:903:C:C6	2.35	0.62
36:BP:65:ARG:HG3	55:B8:25:MET:HG3	1.80	0.62
1:CA:951:G:N3	1:CA:970:C:O2'	2.29	0.62
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.33	0.62
26:DA:1890:A:OP2	61:DA:4438:HOH:O	2.16	0.62
13:CM:20:THR:HA	13:CM:25:ILE:HG22	1.81	0.62
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.80	0.62
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.81	0.62
1:CA:946:A:H2'	1:CA:947:G:C8	2.35	0.62
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.82	0.62
1:CA:975:A:N1	10:CJ:48:THR:HB	2.13	0.62
16:CP:28:ARG:NH1	16:CP:29:ASP:OD1	2.31	0.62
30:DF:122:LYS:NZ	30:DF:152:GLU:OE2	2.30	0.62
24:AX:21:A:H61	24:AX:46:G:H2'	1.64	0.62
45:DY:102:CYS:SG	45:DY:103:GLY:N	2.72	0.62
1:CA:56:U:H2'	1:CA:57:G:C8	2.35	0.62
43:DW:88:ARG:NH1	43:DW:94:ASP:OD2	2.32	0.62
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.23	0.62
1:CA:957:U:H2'	1:CA:959:A:OP2	2.00	0.62
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.64	0.62
1:AA:1414:U:H3	1:AA:1486:G:H1	1.46	0.62
26:DA:577:G:O2'	26:DA:1254:A:OP1	2.18	0.62
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.82	0.62
1:CA:661:G:H1	1:CA:744:C:H42	1.46	0.62
26:DA:658:C:H2'	26:DA:659:C:C6	2.34	0.62
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.15	0.62
1:AA:97:G:O2'	1:AA:98:G:H5''	2.00	0.62
26:DA:2096:U:H3	26:DA:2193:G:H1	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:54:C:N4	1:CA:353:A:OP2	2.32	0.62
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.81	0.62
30:DF:28:ILE:HG23	30:DF:112:MET:HE3	1.81	0.62
10:CJ:6:ILE:HG23	10:CJ:98:ILE:HG13	1.82	0.62
1:AA:984:C:H42	1:AA:1221:G:H1	1.48	0.62
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.82	0.62
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.30	0.62
3:AC:82:GLU:HG2	3:AC:85:ARG:HH21	1.63	0.62
1:CA:1404:C:O2	1:CA:1519:A:O2'	2.14	0.62
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.82	0.62
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.82	0.62
26:BA:271(L):U:OP1	33:BI:50:ARG:NH2	2.29	0.62
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.81	0.62
25:AY:25:C:O2'	25:AY:26:A:O5'	2.18	0.62
26:DA:1149:G:H2'	26:DA:1150:C:C6	2.35	0.62
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.33	0.62
33:DI:38:LEU:HD12	33:DI:38:LEU:H	1.64	0.62
26:DA:2816:C:O3'	38:DR:99:LYS:NZ	2.32	0.62
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.64	0.61
30:DF:18:ARG:NH2	30:DF:127:GLU:OE1	2.31	0.61
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.32	0.61
23:AW:76:F3N:N	24:AX:76:31H:O2'	2.33	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
26:DA:881:G:H1	26:DA:895:U:H3	1.48	0.61
37:BQ:21:THR:HG21	37:BQ:101:ARG:HB2	1.82	0.61
10:CJ:49:VAL:HG12	10:CJ:61:GLU:O	2.00	0.61
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.00	0.61
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.15	0.61
26:BA:646:A:H2'	26:BA:647:G:O4'	2.01	0.61
1:AA:62:U:OP1	1:AA:385:C:O2'	2.17	0.61
1:CA:1376:U:H3'	7:CG:94:ARG:HH21	1.65	0.61
1:CA:662:G:H2'	1:CA:663:A:C8	2.34	0.61
2:CB:101:MET:HA	2:CB:108:ILE:HG13	1.82	0.61
51:B4:53:GLU:HB3	51:B4:54:GLY:HA2	1.82	0.61
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.73	0.61
26:DA:796:C:H2'	26:DA:797:C:C6	2.34	0.61
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.81	0.61
29:BE:29:GLY:HA3	61:BE:408:HOH:O	1.99	0.61
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.83	0.61
1:CA:1397:C:OP2	5:CE:24:ARG:NH2	2.33	0.61
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1031:G:H5''	56:D9:8:LYS:HE3	1.80	0.61
27:DB:45:A:O4'	31:DG:95:ARG:NH1	2.33	0.61
26:BA:1447:G:N7	61:BA:4947:HOH:O	2.31	0.61
26:DA:1371:G:O6	61:DA:3964:HOH:O	2.12	0.61
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.34	0.61
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.81	0.61
1:CA:1297:C:OP1	13:CM:44:ARG:NH2	2.27	0.61
1:AA:139:G:N2	1:AA:224:C:O2	2.28	0.61
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.81	0.61
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.82	0.61
11:AK:91:ARG:HG3	11:AK:92:GLU:N	2.15	0.61
23:AW:26:A:N1	23:AW:44:G:N2	2.44	0.61
2:CB:16:HIS:CD2	2:CB:17:PHE:H	2.18	0.61
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.36	0.61
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.61
6:CF:61:LEU:HB3	6:CF:63:TYR:HE1	1.65	0.61
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.82	0.61
26:BA:2430:A:N3	26:BA:2430:A:H2'	2.15	0.61
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.83	0.61
1:CA:1193:G:O2'	5:CE:25:ARG:NH2	2.34	0.61
12:CL:113:ARG:NH2	61:CL:201:HOH:O	2.33	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.34	0.61
44:DX:60:ARG:HH12	54:D7:47:ARG:NH2	1.98	0.61
26:BA:1843:C:H5'	28:BD:253:GLN:NE2	2.15	0.61
8:CH:45:ILE:HG22	8:CH:63:LEU:HA	1.83	0.61
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.36	0.61
26:DA:2114:A:N6	26:DA:2119:A:N7	2.48	0.61
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.32	0.61
26:BA:2305:A:H5''	31:BG:134:GLY:HA3	1.83	0.61
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.65	0.61
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.81	0.61
10:CJ:29:ARG:HB2	10:CJ:84:GLN:HE22	1.65	0.61
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.82	0.61
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.35	0.61
25:AY:15:G:N2	25:AY:48:C:H42	1.99	0.61
1:CA:735:C:H2'	1:CA:736:C:H6	1.64	0.61
2:CB:113:HIS:O	2:CB:117:GLU:N	2.32	0.61
30:BF:8:GLN:HA	30:BF:8:GLN:HE21	1.65	0.61
1:CA:1240:U:OP2	7:CG:116:ALA:N	2.34	0.61
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.19	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1128:C:O2'	1:CA:1147:C:N3	2.23	0.61
1:AA:69:G:H2'	1:AA:70:G:C8	2.36	0.61
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.34	0.61
9:CI:3:GLN:OE1	9:CI:20:ARG:NH2	2.34	0.61
11:AK:51:LYS:HD3	11:AK:55:LYS:HE2	1.83	0.61
26:DA:1557:C:OP2	26:DA:1558:A:O2'	2.17	0.61
2:CB:13:ALA:N	2:CB:14:GLY:HA3	2.16	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.01	0.61
1:AA:1502:A:H2	1:AA:1505:G:N1	1.95	0.60
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.19	0.60
54:B7:34:ARG:NH1	54:B7:41:ARG:O	2.34	0.60
26:BA:1913:A:H4'	26:BA:1914:C:H5''	1.83	0.60
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.83	0.60
1:CA:728:A:H2'	1:CA:729:A:C8	2.36	0.60
27:BB:41:U:H5	31:BG:70:VAL:H	1.49	0.60
26:DA:1550:C:OP1	26:DA:1720:U:O2'	2.17	0.60
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.82	0.60
26:DA:821:A:N1	61:DA:4084:HOH:O	2.31	0.60
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.82	0.60
26:DA:93:G:H2'	26:DA:94:C:C6	2.36	0.60
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.20	0.60
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.82	0.60
26:DA:1250:G:N7	36:DP:18:ARG:NH2	2.49	0.60
1:CA:1329:A:H5'	13:CM:29:ARG:HD2	1.82	0.60
26:DA:2312:U:H5'	31:DG:88:ILE:HD11	1.83	0.60
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.36	0.60
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.82	0.60
14:AN:21:TYR:OH	14:AN:23:ARG:NH2	2.33	0.60
1:CA:289:G:OP2	61:CA:3236:HOH:O	2.16	0.60
1:CA:1297:C:O3'	7:CG:114:ARG:NH2	2.34	0.60
26:BA:1179:C:H2'	26:BA:1180:C:H6	1.66	0.60
1:CA:222:U:H2'	1:CA:223:U:C6	2.35	0.60
26:BA:2096:U:H3	26:BA:2193:G:H1	1.49	0.60
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.34	0.60
26:BA:2822:G:N7	61:BA:5279:HOH:O	2.32	0.60
19:AS:31:ILE:HB	19:AS:49:ILE:HG23	1.83	0.60
26:BA:288:C:H2'	26:BA:289:A:H8	1.66	0.60
26:BA:568:U:H5'	26:BA:945:A:N1	2.16	0.60
54:D7:34:ARG:NH1	54:D7:41:ARG:O	2.34	0.60
25:AY:62:C:H2'	25:AY:63:G:H8	1.66	0.60
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1135:U:H2'	1:CA:1137:C:C2	2.36	0.60
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.82	0.60
26:BA:1278:A:OP1	38:BR:36:THR:HG23	2.02	0.60
17:CQ:81:ARG:HB3	17:CQ:84:LEU:HD12	1.83	0.60
1:AA:26:A:O2'	4:AD:209:ARG:NH2	2.34	0.60
1:AA:243:A:H4'	1:AA:244:U:H5''	1.82	0.60
1:CA:501:C:H2'	1:CA:502:G:H8	1.67	0.60
25:CY:15:G:N1	25:CY:48:C:N3	2.46	0.60
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.84	0.60
1:AA:1106:G:H5''	3:AC:172:ARG:HG2	1.82	0.60
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.37	0.60
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.84	0.60
9:CI:14:VAL:HG23	9:CI:66:ARG:HB3	1.83	0.60
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.37	0.60
46:DZ:93:ASP:HA	46:DZ:131:ARG:NH2	2.17	0.60
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.01	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.00	0.60
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.35	0.60
35:DO:53:LYS:NZ	35:DO:56:ASP:OD1	2.34	0.60
26:DA:483:A:O2'	45:DY:49:VAL:O	2.10	0.60
13:CM:14:ARG:HB2	13:CM:17:VAL:HG23	1.83	0.60
1:AA:1241:G:OP1	7:AG:35:LYS:NZ	2.35	0.60
49:D2:29:LYS:HG2	49:D2:57:ILE:HD13	1.84	0.60
33:BI:104:GLN:HB3	33:BI:105:HIS:HD2	1.67	0.60
1:CA:148:G:H2'	1:CA:149:A:H8	1.66	0.60
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.02	0.60
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.83	0.60
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.13	0.60
26:BA:71:A:OP2	26:BA:71:A:H3'	2.02	0.60
26:BA:1507:A:O2'	26:BA:1508:A:O4'	2.20	0.60
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.84	0.60
23:AW:7:A:N6	23:AW:66:U:H3	2.00	0.60
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.37	0.60
1:CA:19:C:H5''	5:CE:86:ALA:HB3	1.83	0.60
18:AR:70:ILE:HG23	18:AR:79:LEU:HD12	1.84	0.60
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.37	0.60
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.84	0.60
1:CA:1456:G:N1	20:CT:51:GLU:OE2	2.30	0.60
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.67	0.60
51:D4:16:CYS:HA	51:D4:33:VAL:HB	1.83	0.60
46:DZ:59:LEU:HD11	46:DZ:69:THR:HG21	1.81	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.37	0.59
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.83	0.59
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.34	0.59
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.59
26:DA:307:G:N1	26:DA:310:A:OP2	2.33	0.59
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.84	0.59
3:CC:70:VAL:HG22	3:CC:72:LYS:H	1.66	0.59
1:AA:1125:U:H4'	10:AJ:5:ARG:HH22	1.67	0.59
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.65	0.59
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.83	0.59
26:DA:144:C:H2'	26:DA:145:G:H8	1.67	0.59
2:CB:92:TYR:N	2:CB:151:GLY:O	2.32	0.59
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.34	0.59
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.84	0.59
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.59
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.33	0.59
26:DA:2127:G:N2	26:DA:2161:C:N3	2.50	0.59
25:CY:50:U:O2	25:CY:64:A:N1	2.35	0.59
46:DZ:5:LEU:HD22	46:DZ:6:LYS:H	1.68	0.59
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.36	0.59
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.37	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.35	0.59
26:BA:1359:A:H61	26:BA:1372:U:H3	1.49	0.59
40:DT:30:VAL:HG22	40:DT:86:ILE:HG12	1.83	0.59
23:AW:9:A:OP2	23:AW:13:C:N4	2.30	0.59
11:CK:54:ARG:NH1	25:CY:39:PSU:O2'	2.35	0.59
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.32	0.59
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.84	0.59
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.67	0.59
1:AA:262:A:H2'	1:AA:263:A:C8	2.38	0.59
3:AC:50:ALA:HB1	3:AC:70:VAL:HG21	1.84	0.59
26:BA:1359:A:N6	26:BA:1372:U:H3	2.00	0.59
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.38	0.59
1:CA:646:U:H2'	1:CA:647:C:C6	2.37	0.59
26:DA:668:G:H5'	26:DA:669:G:OP2	2.01	0.59
28:BD:68:LYS:HD2	28:BD:70:TRP:CZ2	2.38	0.59
26:BA:2136:C:N4	26:BA:2155:G:N1	2.30	0.59
1:CA:986:A:N3	19:CS:52:TYR:OH	2.33	0.59
2:CB:15:VAL:HG12	2:CB:209:ARG:HB3	1.85	0.59
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:91:PHE:O	36:BP:121:LYS:NZ	2.35	0.59
39:DS:43:GLU:HB3	39:DS:44:LYS:HE2	1.82	0.59
2:CB:133:LYS:O	2:CB:137:ARG:N	2.32	0.59
39:DS:5:THR:OG1	39:DS:8:GLU:OE2	2.13	0.59
26:DA:2140:C:H2'	26:DA:2141:G:H5'	1.85	0.59
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.68	0.59
36:BP:52:GLU:OE1	36:BP:55:ARG:NH1	2.31	0.59
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.17	0.59
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.84	0.59
26:DA:2745:C:O2'	32:DH:139:GLN:O	2.20	0.59
2:CB:91:PRO:HB3	2:CB:154:LEU:HB3	1.83	0.59
40:DT:56:GLY:O	40:DT:59:THR:HG23	2.02	0.59
9:AI:17:VAL:HG23	9:AI:63:ILE:HG12	1.83	0.59
1:AA:1025:U:O2'	1:AA:1026:G:H8	1.86	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
1:CA:1298:C:P	7:CG:114:ARG:HH22	2.26	0.59
16:CP:52:ASP:O	16:CP:54:GLU:N	2.36	0.59
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.20	0.59
37:DQ:34:LEU:HB2	37:DQ:118:LEU:HD22	1.84	0.59
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.59
26:DA:481:G:O5'	45:DY:47:LYS:NZ	2.35	0.59
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.83	0.59
50:B3:3:ARG:NH1	50:B3:60:GLU:OE2	2.35	0.59
26:DA:2315:G:H2'	26:DA:2316:C:C6	2.37	0.59
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.36	0.59
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.25	0.59
26:BA:2141:G:H22	26:BA:2149:G:H22	1.51	0.59
7:CG:72:ARG:N	7:CG:142:GLU:OE2	2.30	0.59
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.38	0.59
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.02	0.59
26:BA:307:G:H21	26:BA:330:A:H62	1.49	0.59
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.37	0.59
17:AQ:9:VAL:HG21	17:AQ:84:LEU:HD13	1.84	0.59
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.84	0.59
2:CB:121:LEU:H	2:CB:125:PRO:HG2	1.68	0.59
26:BA:1478:G:O2'	26:BA:1558:A:N1	2.35	0.59
1:AA:1320:C:H5''	19:AS:70:LYS:HG3	1.84	0.59
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.51	0.59
1:CA:573:A:N3	1:CA:883:C:O2'	2.29	0.59
1:CA:1104:G:O5'	2:CB:111:ARG:HD2	2.02	0.59
36:DP:86:LYS:HB3	36:DP:118:GLY:HA3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.38	0.59
26:BA:1170:G:C2	26:BA:1171:G:H1'	2.38	0.58
2:CB:57:PHE:HE2	2:CB:185:ILE:HD12	1.67	0.58
1:CA:1120:G:C6	1:CA:1121:U:C4	2.91	0.58
2:CB:73:THR:HA	2:CB:94:ASN:O	2.02	0.58
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.84	0.58
1:AA:46:G:O2'	1:AA:365:U:O2	2.21	0.58
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.35	0.58
19:CS:38:SER:HB2	19:CS:71:LEU:HD22	1.84	0.58
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.38	0.58
1:CA:1049:U:C5	1:CA:1201:A:H5'	2.37	0.58
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.02	0.58
27:DB:11:C:OP2	27:DB:12:C:N4	2.30	0.58
13:AM:3:ARG:HG3	13:AM:4:ILE:N	2.18	0.58
2:CB:55:PHE:O	2:CB:59:GLU:N	2.25	0.58
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.51	0.58
2:AB:19:HIS:HE1	2:AB:189:ASP:HB3	1.69	0.58
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.19	0.58
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.86	0.58
26:DA:888:C:H2'	26:DA:889:C:C4	2.38	0.58
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.18	0.58
25:CY:8:4SU:H1'	25:CY:48:C:O2	2.04	0.58
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.58
13:CM:121:LYS:H	13:CM:121:LYS:NZ	2.01	0.58
46:BZ:110:GLY:N	46:BZ:144:LEU:O	2.32	0.58
2:CB:87:ARG:NH2	2:CB:233:SER:HB3	2.18	0.58
26:BA:2173:A:H3'	26:BA:2174:C:H6	1.69	0.58
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.18	0.58
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.36	0.58
1:CA:396:G:O2'	1:CA:398:C:OP1	2.11	0.58
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.85	0.58
40:BT:65:LYS:HE2	40:BT:67:SER:HB2	1.85	0.58
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.68	0.58
28:BD:79:VAL:HG21	28:BD:111:LEU:HD11	1.85	0.58
26:BA:1045:A:H1'	26:BA:1047:G:N3	2.18	0.58
25:AY:60:U:H5''	25:AY:61:C:H5	1.69	0.58
26:DA:1371:G:H2'	26:DA:1372:U:H5	1.69	0.58
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.84	0.58
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.18	0.58
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.36	0.58
1:AA:1309:G:OP2	13:AM:99:ARG:NH2	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BY:90:LEU:HD21	45:BY:96:ILE:HG12	1.85	0.58
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.03	0.58
35:DO:24:VAL:HA	35:DO:39:ILE:HG22	1.86	0.58
26:BA:880:G:N2	26:BA:898:C:N3	2.44	0.58
1:CA:1028:C:C2	1:CA:1033:G:N1	2.72	0.58
1:CA:1122:U:C4	1:CA:1123:A:N7	2.72	0.58
26:DA:362:U:O2'	26:DA:363:G:H5''	2.03	0.58
26:BA:1021:A:H62	26:BA:1141:U:H3	1.49	0.58
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.85	0.58
13:CM:92:HIS:CD2	13:CM:98:VAL:HG21	2.39	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.68	0.58
1:AA:731:G:H5'	1:AA:766:A:H4'	1.85	0.58
13:AM:11:ARG:HB2	13:AM:46:LYS:HB3	1.86	0.58
42:BV:72:VAL:HG13	42:BV:85:LYS:HB3	1.85	0.58
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.20	0.58
1:AA:1026:G:C2	1:AA:1027:C:H4'	2.38	0.58
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.37	0.58
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.86	0.58
32:DH:58:GLU:OE2	32:DH:60:ARG:NH1	2.37	0.58
5:AE:53:LEU:HD12	5:AE:53:LEU:H	1.68	0.58
26:DA:2127:G:C5	26:DA:2161:C:N4	2.71	0.58
26:BA:882:G:H1	26:BA:894:C:H42	1.50	0.58
1:AA:78:G:N2	1:AA:92:C:N3	2.51	0.58
1:AA:998:G:H1	1:AA:1043:C:N4	1.98	0.58
1:CA:148:G:H2'	1:CA:149:A:C8	2.39	0.58
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.85	0.58
46:DZ:150:LEU:H	46:DZ:172:ALA:HB3	1.68	0.58
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.68	0.58
26:DA:1412:A:H2'	26:DA:1413:G:H8	1.68	0.58
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.36	0.58
10:CJ:89:ASP:O	10:CJ:91:PRO:HD3	2.04	0.58
1:CA:328:C:H4'	1:CA:329:A:H5'	1.86	0.58
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.38	0.58
26:DA:903:C:H2'	26:DA:904:C:C6	2.38	0.58
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.18	0.58
26:BA:2404:C:O3'	36:BP:77:ARG:NH2	2.37	0.58
26:DA:858:U:H1'	26:DA:2268:A:H2'	1.84	0.58
1:CA:407:G:OP1	4:CD:115:ARG:NH2	2.35	0.58
26:DA:1166:C:H2'	26:DA:1167:U:C6	2.39	0.58
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.35	0.58
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:56:C:O4'	26:DA:2169:A:H1'	2.04	0.58
1:CA:978:A:O2'	1:CA:1321:C:N4	2.36	0.58
3:CC:65:ALA:HA	3:CC:100:ALA:HB3	1.86	0.58
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.86	0.58
2:AB:158:LEU:HD21	2:AB:180:LEU:HD13	1.86	0.58
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.58
30:BF:116:ASP:OD2	36:BP:1:MET:N	2.29	0.58
24:CX:16:C:H5'	24:CX:59:A:N1	2.19	0.58
43:DW:57:ASN:HA	43:DW:61:ASN:HD22	1.69	0.58
28:DD:28:GLU:OE2	61:DD:416:HOH:O	2.17	0.58
1:AA:72:C:H2'	1:AA:73:G:O4'	2.03	0.58
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	1.86	0.58
1:CA:964:A:N3	1:CA:969:A:O2'	2.33	0.58
1:CA:998:G:H1	1:CA:1043:C:H42	0.74	0.57
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.04	0.57
26:BA:2113:U:N3	26:BA:2114:A:N7	2.52	0.57
1:AA:1456:G:O6	20:AT:54:LYS:NZ	2.30	0.57
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.86	0.57
2:CB:52:GLU:O	2:CB:56:ARG:HG2	2.04	0.57
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.86	0.57
1:AA:21:G:OP1	61:AA:4104:HOH:O	2.17	0.57
42:DV:6:LYS:HG2	42:DV:11:GLN:HG2	1.85	0.57
26:DA:2144:U:N3	26:DA:2146:C:N3	2.52	0.57
25:CY:49:C:N3	25:CY:65:G:N2	2.46	0.57
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.86	0.57
35:BO:80:ASP:OD1	40:BT:64:ARG:NH2	2.36	0.57
26:DA:848:G:H2'	26:DA:849:A:C8	2.39	0.57
1:CA:114:U:H2'	1:CA:115:G:C8	2.39	0.57
2:CB:25:ASN:OD1	2:CB:27:LYS:HG2	2.04	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.32	0.57
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.85	0.57
23:CW:21:A:N6	23:CW:46:7MG:C4	2.72	0.57
1:AA:1392:G:H21	1:AA:1502:A:H8	1.53	0.57
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.50	0.57
23:CW:4:C:N3	23:CW:69:G:C2	2.72	0.57
1:CA:1119:C:N3	1:CA:1154:G:O6	2.36	0.57
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.37	0.57
54:B7:34:ARG:NH2	61:B7:202:HOH:O	2.36	0.57
1:CA:45:U:H2'	1:CA:46:G:C8	2.39	0.57
7:CG:27:ILE:HD13	7:CG:40:ALA:HA	1.86	0.57
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:630:G:OP2	55:B8:15:LYS:NZ	2.30	0.57
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.38	0.57
3:CC:47:LEU:O	3:CC:51:GLY:N	2.34	0.57
43:BW:68:ARG:HH11	43:BW:111:HIS:HA	1.67	0.57
2:AB:71:VAL:HG11	2:AB:170:GLU:HG2	1.86	0.57
1:CA:1097:C:H1'	1:CA:1170:A:H1'	1.86	0.57
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.20	0.57
23:CW:30:G:H1	23:CW:40:C:N4	2.03	0.57
7:CG:111:ARG:NH1	7:CG:113:GLU:OE1	2.37	0.57
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.87	0.57
26:DA:643:A:N1	26:DA:2369:A:O2'	2.36	0.57
35:DO:92:GLU:OE2	35:DO:113:LYS:HD3	2.05	0.57
42:DV:60:GLU:HB2	42:DV:97:LYS:HE2	1.85	0.57
26:BA:668:G:H5'	26:BA:669:G:OP2	2.05	0.57
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.36	0.57
26:DA:2070:G:OP2	61:DA:4461:HOH:O	2.17	0.57
26:BA:1267:U:OP1	61:BA:5075:HOH:O	2.17	0.57
1:CA:998:G:H2'	1:CA:999:C:O4'	2.04	0.57
1:CA:1168:A:H2'	1:CA:1169:A:C8	2.39	0.57
23:CW:3:C:O2	23:CW:70:G:N1	2.29	0.57
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.43	0.57
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.04	0.57
26:BA:2123:G:H1	26:BA:2175:C:N4	2.02	0.57
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.20	0.57
13:CM:93:ARG:NH1	26:DA:888:C:O5'	2.37	0.57
24:CX:55:PSU:N3	24:CX:58:A:OP2	2.26	0.57
12:AL:34:ARG:NH2	61:AL:301:HOH:O	2.36	0.57
29:DE:30:PRO:HB3	29:DE:92:THR:HG22	1.86	0.57
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.05	0.57
2:AB:137:ARG:NH1	2:AB:137:ARG:HB3	2.19	0.57
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.40	0.57
4:CD:61:LYS:NZ	4:CD:72:GLU:OE1	2.35	0.57
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.20	0.57
16:CP:57:ARG:NH2	16:CP:79:VAL:O	2.38	0.57
30:DF:195:ASP:OD1	30:DF:196:LEU:N	2.38	0.57
1:CA:444:C:H2'	1:CA:445:G:C8	2.39	0.57
1:AA:1000:U:O2	1:AA:1042:G:N2	2.37	0.57
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.86	0.57
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.38	0.57
2:CB:16:HIS:O	2:CB:18:GLY:N	2.37	0.57
1:CA:1154:G:N7	1:CA:1155:G:C4	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:33:U:H2'	25:AY:34:G:H3'	1.86	0.57
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.86	0.57
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.86	0.57
45:BY:86:ARG:HD2	45:BY:100:ALA:HA	1.87	0.57
26:DA:674:G:H1'	30:DF:74:ARG:HD3	1.85	0.57
30:DF:13:SER:OG	30:DF:16:GLY:O	2.21	0.57
6:AF:81:ILE:HD11	28:BD:125:ILE:HB	1.87	0.57
26:DA:686:G:N2	26:DA:788:A:H61	2.02	0.57
1:AA:184:G:H2'	1:AA:185:A:H8	1.70	0.57
54:B7:33:ARG:NH2	61:B7:201:HOH:O	2.38	0.57
1:CA:1001:A:H2'	1:CA:1001(A):G:C8	2.39	0.57
26:BA:892:G:H3'	26:BA:893:C:C6	2.39	0.57
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.32	0.57
1:CA:1012:U:O2	1:CA:1017:G:O6	2.23	0.57
1:AA:159:G:H2'	1:AA:161:A:OP2	2.05	0.57
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.05	0.57
26:DA:479:A:N3	26:DA:481:G:H5''	2.19	0.57
3:CC:18:TRP:H	3:CC:18:TRP:HE3	1.52	0.57
1:AA:1057:G:OP2	61:AA:4024:HOH:O	2.16	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.39	0.57
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.69	0.57
25:AY:15:G:O6	25:AY:48:C:O2	2.23	0.57
46:DZ:159:PRO:HA	46:DZ:161:VAL:N	2.20	0.57
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.23	0.57
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.86	0.57
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.70	0.57
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.15	0.57
1:CA:297:G:N2	1:CA:300:A:OP2	2.38	0.57
26:BA:1173:G:O2'	26:BA:1174:A:O4'	2.17	0.57
24:CX:21:A:N6	24:CX:46:G:H2'	2.19	0.57
26:DA:1169:G:H1	26:DA:1180:C:N4	2.01	0.57
3:CC:3:ASN:HD22	3:CC:4:LYS:HG3	1.69	0.57
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	2.05	0.57
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.37	0.57
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.05	0.57
26:BA:2357:U:OP1	47:B0:20:ARG:NH1	2.38	0.57
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.34	0.57
26:DA:614(C):A:C4	30:DF:180:GLY:HA2	2.40	0.57
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.87	0.57
1:CA:588:G:O6	1:CA:651:C:N4	2.33	0.57
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:96:THR:H	36:DP:99:LEU:CD2	2.17	0.56
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.70	0.56
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.86	0.56
45:DY:6:HIS:CD2	45:DY:7:VAL:HG23	2.40	0.56
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.86	0.56
26:DA:247:G:H4'	26:DA:386:G:C5	2.40	0.56
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.38	0.56
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.26	0.56
36:DP:99:LEU:O	36:DP:103:ALA:N	2.37	0.56
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.17	0.56
1:CA:1183:A:H5'	1:CA:1183:A:H8	1.69	0.56
26:DA:740:U:H2'	26:DA:741:G:C8	2.39	0.56
44:DX:35:THR:HG22	44:DX:38:GLU:H	1.70	0.56
13:CM:16:ASP:HB3	13:CM:34:LEU:HD11	1.87	0.56
31:DG:101:ILE:HG22	31:DG:105:LYS:HE2	1.86	0.56
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.18	0.56
26:DA:2532:G:O2'	26:DA:2657:A:N1	2.36	0.56
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.38	0.56
26:BA:222:A:H5''	26:BA:421:U:OP1	2.05	0.56
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.86	0.56
26:DA:2062:A:OP1	61:DA:3826:HOH:O	2.17	0.56
26:BA:2138:C:N3	26:BA:2153:G:N2	2.52	0.56
1:CA:1247:U:H1'	1:CA:1291:G:N2	2.20	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.86	0.56
1:AA:93:G:H2'	1:AA:96:U:O4'	2.06	0.56
1:AA:1392:G:N2	1:AA:1502:A:H8	2.03	0.56
10:CJ:55:LYS:HE3	10:CJ:56:HIS:NE2	2.20	0.56
27:DB:28:C:H2'	27:DB:29:A:C8	2.39	0.56
13:CM:29:ARG:HG3	13:CM:64:TRP:CZ3	2.39	0.56
26:DA:2184:G:H2'	26:DA:2185:C:C6	2.39	0.56
26:BA:2127:G:H21	26:BA:2173:A:H1'	1.71	0.56
26:DA:236:C:H2'	26:DA:237:C:C6	2.41	0.56
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	1.87	0.56
17:CQ:78:GLU:OE2	17:CQ:81:ARG:NH1	2.37	0.56
46:DZ:150:LEU:N	46:DZ:172:ALA:HB3	2.20	0.56
2:CB:134:GLU:HA	2:CB:137:ARG:HB2	1.87	0.56
26:DA:1412:A:H2'	26:DA:1413:G:C8	2.41	0.56
9:AI:23:ASN:ND2	9:AI:60:ASP:OD2	2.38	0.56
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.27	0.56
26:DA:614(A):U:H4'	26:DA:614(B):G:H5'	1.86	0.56
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.70	0.56
26:BA:9:U:H3	26:BA:2629:A:H2	1.54	0.56
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.36	0.56
26:BA:800:A:H8	26:BA:800:A:OP1	1.88	0.56
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.87	0.56
18:CR:43:PHE:HD1	18:CR:56:THR:HG22	1.69	0.56
13:CM:71:ARG:CG	13:CM:71:ARG:HH11	2.18	0.56
26:BA:2279:G:N7	47:B0:14:ARG:NH1	2.53	0.56
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.40	0.56
26:BA:363(A):A:H2'	26:BA:363(B):G:H8	1.71	0.56
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.68	0.56
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.88	0.56
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.41	0.56
26:BA:2839:G:H5'	38:BR:46:GLY:HA2	1.87	0.56
26:DA:518:G:H2'	26:DA:519:U:C6	2.41	0.56
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.22	0.56
2:AB:54:THR:HG23	2:AB:199:TYR:HB3	1.87	0.56
1:AA:198:G:O6	1:AA:219:C:N4	2.39	0.56
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.86	0.56
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.05	0.56
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.23	0.56
7:CG:15:ASP:HB3	7:CG:24:THR:HG23	1.86	0.56
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.20	0.56
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.23	0.56
27:DB:42:C:O2'	31:DG:67:LYS:O	2.16	0.56
1:CA:532:A:H61	3:CC:193:TYR:CB	2.16	0.56
26:DA:1231:G:H2'	26:DA:1232:G:H8	1.69	0.56
26:BA:1187:G:H5''	42:BV:81:TYR:CE1	2.39	0.56
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.87	0.56
40:BT:24:PRO:HD3	40:BT:52:ILE:HD12	1.88	0.56
26:BA:2719:G:OP2	61:BA:4851:HOH:O	2.18	0.56
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.40	0.56
23:CW:18:G:O2'	23:CW:57:G:N2	2.26	0.56
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.39	0.56
26:DA:84:A:H5'	45:DY:8:LYS:HG2	1.86	0.56
26:DA:2142:C:N3	26:DA:2149:G:O6	2.39	0.56
10:AJ:35:SER:N	10:AJ:73:ASP:O	2.33	0.56
25:AY:33:U:C3'	25:AY:34:G:H5''	2.35	0.56
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.88	0.56
26:DA:330:A:H2	26:DA:1210:A:HO2'	1.54	0.56
1:AA:45:U:H2'	1:AA:46:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.05	0.56
26:DA:2061:G:H5''	26:DA:2503:A:C2	2.40	0.56
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.87	0.56
26:BA:2130:U:O2	26:BA:2131:G:N2	2.38	0.56
13:AM:122:LYS:HD3	13:AM:123:ALA:N	2.18	0.56
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.06	0.56
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.38	0.56
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.88	0.56
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.06	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
1:CA:587:G:N2	1:CA:754:C:OP2	2.37	0.56
15:CO:17:ARG:HG3	15:CO:17:ARG:HH11	1.69	0.56
4:CD:191:ARG:NH1	4:CD:191:ARG:O	2.38	0.56
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.06	0.56
26:BA:1171:G:H3'	26:BA:1173:G:H5'	1.88	0.56
1:AA:1003:G:C2	1:AA:1004:A:N3	2.73	0.56
1:CA:1154:G:N7	1:CA:1155:G:N9	2.54	0.56
9:CI:8:GLY:O	9:CI:15:ALA:N	2.35	0.56
6:CF:50:TYR:CE2	18:CR:77:GLY:HA2	2.41	0.56
3:AC:29:TYR:OH	14:AN:54:PRO:O	2.20	0.56
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.39	0.56
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.05	0.56
25:AY:38:A:C2'	25:AY:39:PSU:H5''	2.35	0.56
1:AA:78:G:C2	1:AA:91:C:C4	2.94	0.56
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.56
37:DQ:77:LYS:NZ	37:DQ:86:GLY:O	2.39	0.56
13:CM:71:ARG:HH11	13:CM:71:ARG:HG3	1.69	0.56
9:AI:29:ASN:OD1	9:AI:65:VAL:N	2.37	0.56
5:CE:84:PHE:N	5:CE:87:SER:O	2.33	0.56
2:CB:8:LYS:HD2	2:CB:9:GLU:H	1.71	0.56
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.86	0.56
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.06	0.56
25:CY:19:G:N1	25:CY:56:C:N4	2.41	0.56
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.73	0.56
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.05	0.56
26:BA:456:C:H4'	61:BA:3937:HOH:O	2.04	0.56
1:AA:193:C:H2'	1:AA:194:C:C6	2.41	0.56
24:AX:21:A:H5'	24:AX:22:G:OP1	2.05	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.06	0.56
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:64:A:O3'	44:BX:71:GLY:HA3	2.05	0.56
26:BA:1588:C:H2'	26:BA:1589:C:C6	2.40	0.56
46:DZ:100:VAL:HG21	46:DZ:134:PRO:HG2	1.88	0.56
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.05	0.56
26:DA:1316:U:H2'	26:DA:1317:A:H8	1.71	0.56
35:BO:1:MET:HG3	35:BO:67:LYS:HG2	1.87	0.56
41:DU:76:TYR:CZ	41:DU:80:ILE:HG13	2.42	0.55
44:DX:60:ARG:NH1	54:D7:47:ARG:HH22	2.01	0.55
26:BA:278:A:O2'	26:BA:279:C:OP1	2.16	0.55
23:CW:51:U:H3	23:CW:63:G:H1	1.54	0.55
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.88	0.55
26:DA:478:A:N1	26:DA:500:G:H4'	2.21	0.55
26:DA:299:A:N1	26:DA:322:A:O2'	2.30	0.55
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.05	0.55
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.32	0.55
1:AA:946:A:H2'	1:AA:947:G:C8	2.40	0.55
26:BA:1033:U:OP1	56:B9:9:ARG:NH2	2.39	0.55
1:CA:757:U:H2'	1:CA:758:G:O4'	2.06	0.55
10:AJ:8:LEU:HB2	10:AJ:70:ARG:HB2	1.88	0.55
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.87	0.55
4:CD:43:HIS:ND1	4:CD:46:LYS:HE2	2.20	0.55
1:CA:1028:C:C4	1:CA:1033:G:O6	2.59	0.55
23:CW:44:G:H2'	23:CW:45:U:H5'	1.88	0.55
1:AA:68:G:C2	1:AA:69:G:H1'	2.42	0.55
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.88	0.55
26:BA:389:G:N1	36:BP:70:GLN:HG3	2.22	0.55
26:DA:2776:A:H4'	26:DA:2777:G:H5''	1.87	0.55
26:DA:586:A:N1	26:DA:809:G:O2'	2.31	0.55
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	1.87	0.55
27:DB:55:U:H1'	31:DG:29:TRP:CD1	2.42	0.55
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.06	0.55
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.39	0.55
1:AA:167:G:H2'	1:AA:168:G:H8	1.72	0.55
1:AA:181:G:O2'	1:AA:183:G:O6	2.18	0.55
1:AA:674:G:H2'	1:AA:675:A:H8	1.69	0.55
26:BA:2848:G:C8	40:BT:97:ALA:HB2	2.41	0.55
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.88	0.55
29:DE:163:GLU:HG2	29:DE:164:ARG:N	2.20	0.55
3:CC:56:ASP:HB2	3:CC:67:THR:HB	1.88	0.55
26:BA:588:U:H2'	26:BA:589:C:C6	2.40	0.55
1:AA:652:U:O4	1:AA:752:G:O2'	2.13	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.87	0.55
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.41	0.55
1:CA:527:G:O2'	1:CA:535:A:N1	2.34	0.55
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.41	0.55
26:DA:888:C:H5''	26:DA:889:C:OP2	2.07	0.55
18:CR:43:PHE:CD1	18:CR:56:THR:HG22	2.41	0.55
28:DD:71:ASP:HB3	28:DD:103:ARG:HH22	1.71	0.55
33:BI:114:LEU:HD12	33:BI:130:TYR:HA	1.87	0.55
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.43	0.55
10:AJ:30:SER:O	10:AJ:81:THR:HG21	2.07	0.55
1:AA:222:U:H2'	1:AA:223:U:C6	2.42	0.55
26:DA:1446:C:H42	26:DA:1465:G:H1	1.52	0.55
26:BA:535:C:O3'	41:BU:53:ARG:NH1	2.39	0.55
1:CA:420:U:O2'	1:CA:423:G:O6	2.13	0.55
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.06	0.55
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.89	0.55
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.24	0.55
26:DA:848:G:C4	26:DA:933:A:H8	2.24	0.55
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.71	0.55
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.07	0.55
40:DT:50:ILE:HA	40:DT:99:LEU:HD12	1.89	0.55
26:DA:2787:C:H1'	29:DE:62:PRO:HG3	1.88	0.55
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.26	0.55
6:CF:97:PHE:HE1	18:CR:62:GLU:HG2	1.71	0.55
26:DA:39:C:H2'	26:DA:40:C:C6	2.42	0.55
1:CA:984:C:O5'	1:CA:984:C:H6	1.88	0.55
38:DR:55:ALA:HB2	38:DR:79:LEU:HD13	1.88	0.55
1:CA:1223:C:H5''	1:CA:1224:G:H5''	1.88	0.55
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.41	0.55
1:CA:1316:G:H22	1:CA:1319:A:H5''	1.72	0.55
1:CA:1028:C:N3	1:CA:1033:G:O6	2.40	0.55
23:CW:19:G:H1	23:CW:56:C:N4	2.03	0.55
26:BA:1021:A:H8	26:BA:1022:G:H5''	1.71	0.55
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.88	0.55
26:DA:1434:A:H61	26:DA:1558:A:H62	1.54	0.55
26:BA:330:A:H2	26:BA:1210:A:H2'	1.71	0.55
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.71	0.55
2:AB:167:PRO:HG3	2:AB:186:ALA:HB1	1.88	0.55
26:DA:2126:A:N6	26:DA:2162:G:O2'	2.39	0.55
23:AW:50:U:H3	23:AW:64:A:N6	2.05	0.55
2:CB:122:PHE:CE2	2:CB:139:LYS:HG2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:87:ARG:NH1	2:CB:220:ASP:OD1	2.39	0.55
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.42	0.55
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.89	0.55
1:CA:1299:A:H2'	1:CA:1299:A:N3	2.21	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.21	0.55
26:DA:84:A:H5''	45:DY:8:LYS:HE3	1.89	0.55
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.71	0.55
1:AA:750:G:O2'	15:AO:22:THR:O	2.14	0.55
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.41	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.55
3:AC:58:GLU:HB2	3:AC:65:ALA:HB3	1.88	0.55
26:DA:528:A:C2	26:DA:2042:A:H2'	2.42	0.55
26:DA:2098:U:H3	26:DA:2191:G:H1	1.53	0.55
26:DA:2303:G:O2'	31:DG:132:ASN:HB2	2.07	0.55
26:DA:1528:A:OP2	61:DA:3982:HOH:O	2.18	0.55
27:BB:66:A:H61	27:BB:108:U:H2'	1.72	0.55
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.47	0.55
26:DA:566:U:H5''	36:DP:29:LYS:HE3	1.87	0.55
26:DA:900:A:H2'	26:DA:901:A:C8	2.41	0.55
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.42	0.55
38:DR:36:THR:HG22	38:DR:37:THR:H	1.72	0.55
50:D3:7:LYS:HB2	50:D3:34:GLU:HG3	1.89	0.55
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.89	0.55
48:D1:83:GLU:OE1	48:D1:83:GLU:N	2.39	0.55
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.06	0.55
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.88	0.55
18:CR:25:THR:O	18:CR:25:THR:OG1	2.19	0.55
1:AA:814:A:H2'	1:AA:816:A:H5''	1.89	0.55
1:AA:79:G:C2	1:AA:90:U:O2	2.60	0.55
26:BA:2190:G:C2'	26:BA:2191:G:H5''	2.34	0.55
26:DA:2298:A:H1'	26:DA:2321:G:H21	1.72	0.55
1:CA:692:U:O2'	1:CA:694:A:N7	2.34	0.55
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.71	0.55
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.21	0.55
26:DA:2848:G:C8	40:DT:97:ALA:HB2	2.42	0.55
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.42	0.55
36:DP:48:PRO:O	55:D8:57:ARG:NH2	2.37	0.55
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.38	0.55
1:AA:954:G:H21	1:AA:1227:A:H62	1.55	0.55
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.89	0.55
47:D0:32:ARG:H	47:D0:35:ASN:ND2	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:11:C:H42	23:CW:24:G:H1	1.54	0.55
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.07	0.55
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.42	0.55
26:BA:1420:U:O2'	26:BA:1421:G:OP1	2.22	0.55
1:CA:1004:A:H62	1:CA:1037:C:H2'	1.71	0.54
1:CA:1359:C:H3'	14:CN:35:ARG:HH21	1.72	0.54
1:CA:1262:C:H42	1:CA:1273:G:H1	1.53	0.54
33:BI:116:LEU:HD21	33:BI:119:PRO:HA	1.89	0.54
26:DA:297:C:H2'	26:DA:298:G:O4'	2.07	0.54
51:B4:53:GLU:HB3	51:B4:54:GLY:CA	2.37	0.54
26:BA:330:A:HO2'	26:BA:331:A:H8	1.56	0.54
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.89	0.54
26:DA:2592:G:OP1	61:DA:4233:HOH:O	2.18	0.54
26:DA:2595:G:N7	61:DA:4305:HOH:O	2.34	0.54
32:BH:154:PRO:HB3	32:BH:163:TYR:CZ	2.42	0.54
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.39	0.54
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.75	0.54
1:CA:1055:A:N3	3:CC:156:ARG:NH1	2.51	0.54
1:CA:1118:C:C2	1:CA:1119:C:H5	2.26	0.54
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.33	0.54
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.40	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:CD1	2.42	0.54
1:CA:1376:U:O5'	7:CG:94:ARG:NH2	2.40	0.54
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.54
1:AA:757:U:H2'	1:AA:758:G:O4'	2.08	0.54
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.07	0.54
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.43	0.54
24:CX:19:G:H4'	24:CX:20:U:OP2	2.07	0.54
28:DD:36:PRO:HA	28:DD:61:LEU:HD12	1.88	0.54
2:CB:63:MET:HG2	2:CB:225:ALA:HB1	1.89	0.54
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.42	0.54
26:DA:2113:U:H3	26:DA:2170:A:N6	2.03	0.54
1:CA:1165:C:N3	1:CA:1171:G:N2	2.56	0.54
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.42	0.54
31:DG:18:GLU:HG2	31:DG:175:LEU:HD21	1.89	0.54
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.37	0.54
31:DG:41:GLN:HE22	31:DG:153:ARG:HB3	1.71	0.54
38:DR:95:THR:HG22	38:DR:116:LEU:HD23	1.90	0.54
1:CA:920:U:H2'	1:CA:921:U:C6	2.41	0.54
33:DI:61:ARG:HA	33:DI:61:ARG:NE	2.22	0.54
5:AE:68:GLU:HG2	5:AE:70:PRO:HD3	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.89	0.54
1:AA:1026:G:C6	1:AA:1027:C:H1'	2.42	0.54
12:AL:97:ARG:HB2	12:AL:98:TYR:CE1	2.42	0.54
26:BA:2327:A:H2'	26:BA:2328:A:C8	2.42	0.54
1:CA:674:G:H2'	1:CA:675:A:H8	1.72	0.54
26:DA:2533:A:OP1	26:DA:2665:A:O2'	2.20	0.54
26:DA:1805:U:O2	28:DD:50:THR:HB	2.08	0.54
46:BZ:75:ASN:O	46:BZ:84:GLU:HG2	2.08	0.54
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.22	0.54
26:BA:671:C:N4	61:BA:4880:HOH:O	2.39	0.54
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.21	0.54
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.43	0.54
26:BA:620:G:N3	26:BA:620:G:H5'	2.23	0.54
1:AA:456:C:C2'	1:AA:457:C:H5'	2.37	0.54
4:CD:70:ILE:HG12	4:CD:74:GLN:HB3	1.88	0.54
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.30	0.54
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.54
1:CA:1132:C:H42	1:CA:1142:G:H1	1.55	0.54
26:BA:886:C:H4'	26:BA:886:C:OP1	2.08	0.54
1:CA:991:U:C4	1:CA:1212:U:H1'	2.42	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.73	0.54
1:CA:430:A:P	4:CD:22:LYS:HZ1	2.31	0.54
50:D3:3:ARG:HH21	50:D3:36:VAL:HG11	1.73	0.54
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.42	0.54
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.37	0.54
52:D5:49:CYS:O	52:D5:56:LYS:NZ	2.40	0.54
4:CD:150:GLU:OE2	4:CD:151:LYS:N	2.41	0.54
37:DQ:1:MET:HB2	37:DQ:44:ALA:HB1	1.89	0.54
42:BV:98:GLU:OE2	42:BV:100:ARG:NH1	2.41	0.54
26:BA:323:G:C8	30:BF:171:PRO:HG3	2.43	0.54
26:BA:614(C):A:C4	30:BF:180:GLY:HA2	2.42	0.54
30:DF:165:ARG:HG2	30:DF:168:ARG:HH21	1.73	0.54
26:DA:590:A:OP1	30:DF:95:ARG:NH1	2.41	0.54
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.55	0.54
10:AJ:5:ARG:NH2	10:AJ:73:ASP:OD2	2.24	0.54
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.88	0.54
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.72	0.54
1:CA:1348:U:OP2	1:CA:1373:G:N2	2.32	0.54
31:DG:44:GLY:N	31:DG:88:ILE:O	2.40	0.54
26:DA:954:G:H5''	37:DQ:13:GLN:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1639:U:OP1	61:DA:4007:HOH:O	2.19	0.54
23:CW:7:A:H5'	23:CW:8:4SU:H5	1.88	0.54
1:CA:266:G:H5''	1:CA:268:C:H41	1.73	0.54
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.07	0.54
37:DQ:32:TYR:HB2	37:DQ:106:VAL:HG23	1.88	0.54
26:BA:100:G:O2'	49:B2:7:ARG:NH2	2.40	0.54
24:CX:23:C:H2'	24:CX:24:U:C6	2.43	0.54
26:DA:2139:C:C4	26:DA:2153:G:C2	2.96	0.54
1:AA:1399:C:C2	1:AA:1502:A:N6	2.76	0.54
26:BA:1779:U:H2'	61:BA:5029:HOH:O	2.07	0.54
26:DA:370:G:OP2	61:DA:3787:HOH:O	2.18	0.54
1:CA:1153:C:H42	1:CA:1154:G:N2	2.04	0.54
2:CB:12:GLU:O	2:CB:15:VAL:N	2.34	0.54
25:AY:63:G:H2'	25:AY:64:A:O4'	2.08	0.54
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.38	0.54
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.08	0.54
33:DI:27:ARG:HD2	48:D1:71:TYR:CE2	2.43	0.54
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	1.89	0.54
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.88	0.54
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.41	0.54
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.72	0.54
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.08	0.54
34:BN:75:TYR:CE2	34:BN:77:GLY:HA2	2.43	0.54
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.07	0.54
1:CA:1003:G:H2'	1:CA:1004:A:H1'	1.89	0.54
1:AA:79:G:N1	1:AA:90:U:N3	2.56	0.54
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.05	0.54
26:BA:1799:G:H4'	26:BA:1800:C:H5''	1.89	0.54
1:AA:1298:C:H4'	1:AA:1299:A:H5''	1.89	0.54
26:BA:1044:G:HO2'	26:BA:1111:A:H61	1.56	0.54
26:DA:1859:A:N6	26:DA:1883:G:O2'	2.41	0.54
26:DA:2552:U:OP2	61:DA:4518:HOH:O	2.18	0.54
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.90	0.54
26:DA:305:U:H2'	26:DA:306:U:C6	2.42	0.54
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.41	0.54
26:DA:2153:G:C6	26:DA:2154:G:C6	2.96	0.54
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.90	0.54
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.89	0.54
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.88	0.54
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.34	0.54
26:DA:289:A:H2'	26:DA:290:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DH:3:ARG:NH2	32:DH:5:GLY:H	2.05	0.54
2:CB:105:PHE:CE1	2:CB:155:LEU:HD12	2.42	0.54
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.07	0.54
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.89	0.54
1:AA:560:U:O2'	1:AA:561:U:OP2	2.21	0.54
26:DA:1010:A:OP2	61:DA:4178:HOH:O	2.18	0.54
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.73	0.54
13:AM:57:ARG:O	13:AM:61:GLU:HG2	2.08	0.54
1:AA:1258:G:O2'	1:AA:1259:C:H5'	2.08	0.54
25:CY:5:G:H1	25:CY:68:C:N4	2.06	0.54
25:AY:58:A:HO2'	25:AY:60:U:H5	1.55	0.54
26:BA:2101:G:H2'	26:BA:2102:U:C6	2.43	0.54
1:AA:1316:G:N2	1:AA:1319:A:H5''	2.17	0.54
19:CS:48:THR:HG22	19:CS:61:TYR:HA	1.88	0.54
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.90	0.54
1:CA:1120:G:O6	1:CA:1154:G:N2	2.41	0.54
2:CB:115:LEU:HD11	2:CB:153:ARG:HD2	1.90	0.54
26:BA:2141:G:N7	26:BA:2151:G:N2	2.56	0.54
2:AB:69:LEU:HD12	2:AB:91:PRO:HB2	1.90	0.54
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.73	0.54
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.38	0.54
1:AA:950:U:H2'	1:AA:951:G:H8	1.73	0.54
12:AL:53:ARG:HG3	12:AL:93:LEU:HD21	1.90	0.54
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.08	0.54
9:CI:23:ASN:N	9:CI:23:ASN:HD22	2.06	0.54
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.42	0.54
26:DA:2144:U:H1'	26:DA:2148:G:N2	2.23	0.53
25:AY:19:G:H4'	25:AY:20:U:OP2	2.06	0.53
1:AA:78:G:N1	1:AA:91:C:C4	2.76	0.53
51:B4:57:GLU:CB	51:B4:58:ARG:HA	2.38	0.53
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.19	0.53
1:CA:1033:G:C2'	1:CA:1034:G:H5'	2.38	0.53
26:BA:226:G:H21	26:BA:228:A:H62	1.56	0.53
10:CJ:81:THR:HA	10:CJ:84:GLN:HB2	1.89	0.53
4:AD:173:TRP:NE1	4:AD:193:ASP:OD2	2.38	0.53
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.41	0.53
26:BA:1230:C:H2'	26:BA:1231:G:C8	2.43	0.53
5:AE:80:ILE:HG22	5:AE:91:LEU:HB2	1.89	0.53
1:CA:952:U:H2'	1:CA:953:G:C8	2.43	0.53
19:AS:65:ASN:HA	51:B4:58:ARG:HG3	1.89	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:951:G:HO2'	1:CA:972:C:H5	1.56	0.53
9:CI:6:GLY:HA3	9:CI:80:GLY:O	2.09	0.53
23:CW:50:U:H3	23:CW:64:A:H2	1.54	0.53
27:DB:28:C:OP1	39:DS:36:TYR:OH	2.16	0.53
26:BA:2142:C:O2'	26:BA:2143:C:H5'	2.08	0.53
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.42	0.53
26:BA:1019:U:HO2'	26:BA:1021:A:H2	1.55	0.53
7:CG:72:ARG:NH1	7:CG:142:GLU:OE2	2.41	0.53
61:CW:3102:HOH:O	47:D0:2:ALA:N	2.41	0.53
26:DA:144:C:H2'	26:DA:145:G:C8	2.44	0.53
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.53
6:CF:69:GLU:H	6:CF:69:GLU:CD	2.09	0.53
26:BA:1378:A:OP1	54:B7:10:ARG:NH2	2.42	0.53
1:CA:890:G:O2'	1:CA:906:G:O6	2.21	0.53
8:CH:51:VAL:HG11	8:CH:60:ARG:HH11	1.73	0.53
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.23	0.53
1:AA:202:U:O2'	1:AA:203:U:O5'	2.13	0.53
26:DA:973:A:H8	26:DA:973:A:OP1	1.92	0.53
26:BA:614(B):G:OP1	61:BA:5228:HOH:O	2.19	0.53
5:CE:6:PHE:HD1	5:CE:36:ASP:HB3	1.72	0.53
26:DA:2261:C:O2'	26:DA:2262:U:H5'	2.08	0.53
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.55	0.53
39:DS:67:ARG:O	39:DS:71:ARG:HG3	2.08	0.53
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.08	0.53
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	2.08	0.53
26:BA:642:G:H21	26:BA:646:A:H2	1.56	0.53
26:BA:197:A:N6	26:BA:2430:A:O2'	2.40	0.53
1:AA:646:U:H2'	1:AA:647:C:C6	2.43	0.53
1:CA:1250:A:N3	1:CA:1370:G:O2'	2.35	0.53
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.41	0.53
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.08	0.53
20:CT:36:LEU:HD12	20:CT:55:ILE:HG23	1.90	0.53
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.73	0.53
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.89	0.53
26:BA:2659:G:O2'	32:BH:175:LYS:NZ	2.41	0.53
26:DA:2128:C:H5'	26:DA:2173:A:N3	2.23	0.53
25:CY:70:G:H2'	25:CY:71:G:H5'	1.91	0.53
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.37	0.53
26:BA:71:A:N7	44:BX:31:HIS:HE1	2.05	0.53
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.89	0.53
1:CA:1152:A:H2'	1:CA:1153:C:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:27:LYS:O	20:AT:31:SER:OG	2.27	0.53
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.43	0.53
1:CA:1057:G:O3'	3:CC:197:GLY:HA3	2.09	0.53
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.53
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.89	0.53
3:CC:52:LEU:HD13	3:CC:118:GLN:HE22	1.73	0.53
35:DO:120:GLU:HB2	40:DT:68:TYR:HE2	1.74	0.53
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.44	0.53
46:DZ:50:GLN:OE1	46:DZ:50:GLN:N	2.34	0.53
46:BZ:28:MET:HE1	46:BZ:67:LEU:HD12	1.91	0.53
39:DS:77:ALA:HB1	39:DS:82:ILE:HB	1.89	0.53
1:AA:1270:C:OP2	21:AU:24:ARG:NH2	2.42	0.53
1:CA:243:A:H4'	1:CA:244:U:H5''	1.90	0.53
25:CY:68:C:C2'	25:CY:69:G:H5'	2.38	0.53
41:DU:92:ARG:HA	41:DU:95:LEU:HB2	1.91	0.53
1:CA:1166:G:H5'	1:CA:1168:A:OP2	2.08	0.53
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.23	0.53
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.73	0.53
1:AA:1239:A:H62	1:AA:1299:A:H62	1.57	0.53
23:CW:76:F3N:O2'	26:DA:2585:U:O4	2.15	0.53
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.73	0.53
40:DT:28:VAL:HG13	40:DT:86:ILE:HG23	1.89	0.53
26:DA:2302:G:H2'	26:DA:2303:G:H5'	1.91	0.53
26:BA:1047:G:H2'	26:BA:1110:G:H22	1.74	0.53
53:D6:35:GLU:OE2	53:D6:50:ARG:NH1	2.42	0.53
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.44	0.53
30:BF:20:LEU:HD22	30:BF:21:ALA:H	1.73	0.53
1:CA:316:G:OP2	1:CA:351:G:O2'	2.24	0.53
1:CA:97:G:O2'	1:CA:98:G:H5''	2.08	0.53
25:AY:60:U:H5''	25:AY:61:C:C5	2.43	0.53
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.73	0.53
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.73	0.53
27:DB:110:G:H2'	27:DB:111:G:H5'	1.90	0.53
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.43	0.53
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.08	0.53
26:BA:624:C:O2'	26:BA:657:U:OP1	2.24	0.53
34:DN:67:LEU:O	34:DN:88:GLU:HG2	2.08	0.53
26:BA:2887:U:H2'	26:BA:2888:C:C6	2.44	0.53
26:DA:1645:G:H5''	26:DA:1646:C:H5'	1.89	0.53
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.89	0.53
30:BF:197:ASP:OD1	30:BF:197:ASP:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BG:179:PRO:HB2	51:B4:42:PHE:HE1	1.73	0.53
32:DH:154:PRO:HB3	32:DH:163:TYR:CE2	2.43	0.53
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.41	0.53
40:DT:60:THR:HG22	40:DT:77:PRO:HA	1.90	0.53
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.09	0.53
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.09	0.53
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.53
1:CA:142:G:H2'	1:CA:143:A:C8	2.44	0.53
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.37	0.53
26:DA:2430:A:H2'	26:DA:2430:A:N3	2.23	0.53
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	1.91	0.53
26:DA:2127:G:N2	26:DA:2161:C:C2	2.77	0.53
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.73	0.53
1:CA:1119:C:C4	1:CA:1154:G:O6	2.62	0.53
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.24	0.53
27:DB:66:A:N6	27:DB:109:C:H5"	2.24	0.53
1:CA:522:C:H41	12:CL:53:ARG:NH2	2.07	0.53
23:AW:47:U:H5'	23:AW:47:U:C6	2.44	0.53
4:CD:159:ARG:O	4:CD:163:GLU:N	2.40	0.53
2:CB:70:PHE:HE1	2:CB:163:PHE:HD2	1.56	0.53
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.43	0.53
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.91	0.53
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.90	0.53
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.91	0.53
26:BA:242:G:C8	55:B8:5:LYS:HG2	2.44	0.53
31:DG:7:LEU:HD13	31:DG:104:GLU:HA	1.91	0.53
1:AA:1238:A:OP2	61:AA:4136:HOH:O	2.18	0.53
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.53
26:BA:969:U:H2'	26:BA:970:C:C6	2.44	0.53
26:DA:852:G:H2'	26:DA:853:G:C8	2.44	0.53
26:DA:8:A:H2'	26:DA:9:U:H6	1.74	0.53
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.33	0.53
1:CA:1133:G:C4	1:CA:1134:G:C8	2.97	0.53
33:BI:104:GLN:HB3	33:BI:105:HIS:CD2	2.43	0.53
1:CA:1023:G:C4	1:CA:1024:G:C8	2.97	0.53
26:DA:90:U:H1'	26:DA:92:A:C8	2.44	0.53
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.91	0.53
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.49	0.53
26:DA:601:C:OP1	30:DF:108:LYS:NZ	2.23	0.53
1:AA:877:C:H5"	8:AH:88:LYS:HD3	1.90	0.53
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2334:G:O6	47:B0:74:ARG:NH2	2.42	0.53
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.09	0.53
51:D4:58:ARG:HB3	51:D4:59:PHE:HD1	1.74	0.53
1:AA:79:G:C6	1:AA:90:U:N3	2.77	0.53
1:AA:841:U:P	1:AA:841:U:H6	2.32	0.53
27:BB:2:C:H2'	27:BB:3:C:C6	2.43	0.53
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.91	0.53
1:CA:1330:U:H4'	13:CM:23:TYR:CE1	2.43	0.53
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.43	0.53
1:AA:1241:G:C2'	1:AA:1242:C:H5'	2.38	0.53
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.44	0.53
1:CA:309:G:O2'	1:CA:607:A:N1	2.42	0.53
42:BV:14:VAL:HB	42:BV:96:ILE:HG13	1.90	0.53
8:CH:103:VAL:HG11	8:CH:136:GLU:HB2	1.91	0.53
2:CB:33:TYR:HB2	2:CB:43:ASP:HA	1.91	0.53
9:CI:29:ASN:OD1	9:CI:64:THR:HA	2.09	0.53
32:DH:26:VAL:HG21	32:DH:75:ALA:HB1	1.90	0.53
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.74	0.53
1:CA:952:U:H2'	1:CA:953:G:H8	1.73	0.52
27:DB:56:G:OP1	31:DG:27:ASN:ND2	2.42	0.52
46:DZ:111:VAL:HA	46:DZ:115:GLY:HA3	1.91	0.52
1:CA:714:G:H2'	1:CA:715:A:C8	2.44	0.52
7:CG:78:ARG:NH1	7:CG:154:TYR:O	2.41	0.52
20:CT:13:LEU:O	20:CT:17:ARG:HG3	2.09	0.52
1:CA:263:A:OP1	20:CT:79:ARG:NH1	2.41	0.52
1:AA:539:A:H2'	1:AA:540:G:C8	2.42	0.52
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.74	0.52
26:BA:1223:G:N2	26:BA:1226:A:OP2	2.35	0.52
26:BA:2611:U:C4	52:B5:3:LYS:HG2	2.44	0.52
46:DZ:33:LEU:HD21	46:DZ:90:VAL:HG21	1.90	0.52
1:CA:952:U:O2'	1:CA:965:A:N6	2.41	0.52
1:CA:975:A:H4'	1:CA:976:G:C5'	2.35	0.52
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.45	0.52
1:AA:1035:A:H8	1:AA:1035:A:O5'	1.92	0.52
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.08	0.52
26:BA:2168:G:C6	26:BA:2171:A:H8	2.27	0.52
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	1.91	0.52
23:AW:47:U:O2'	23:AW:48:C:OP1	2.23	0.52
45:DY:49:VAL:HG21	45:DY:61:ILE:HG23	1.91	0.52
26:DA:589:C:H2'	26:DA:590:A:C8	2.44	0.52
25:CY:27:G:O6	25:CY:43:C:N3	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:271(E):U:H2'	26:BA:271(F):C:C6	2.44	0.52
55:D8:26:LYS:HB2	55:D8:44:LYS:O	2.10	0.52
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.45	0.52
1:AA:714:G:H2'	1:AA:715:A:C8	2.44	0.52
53:B6:35:GLU:OE2	53:B6:50:ARG:NH1	2.43	0.52
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.09	0.52
46:DZ:6:LYS:HD2	46:DZ:8:TYR:OH	2.10	0.52
1:CA:1095:U:C4	1:CA:1096:C:C4	2.98	0.52
1:CA:1264:C:O2	1:CA:1272:G:N2	2.41	0.52
4:AD:49:ARG:NE	4:AD:49:ARG:H	2.07	0.52
26:BA:2126:A:N3	26:BA:2127:G:H1'	2.24	0.52
19:AS:48:THR:HG22	19:AS:61:TYR:HA	1.91	0.52
26:DA:885:C:H1'	26:DA:892:G:H22	1.75	0.52
1:AA:662:G:H2'	1:AA:663:A:C8	2.44	0.52
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.09	0.52
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.09	0.52
26:DA:646:A:H2'	26:DA:647:G:O4'	2.09	0.52
5:AE:79:GLU:HG3	5:AE:93:PRO:HD2	1.92	0.52
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.09	0.52
1:CA:1318:A:H5"	19:CS:3:ARG:NH2	2.20	0.52
3:AC:40:ARG:O	3:AC:44:GLU:HB2	2.10	0.52
27:DB:66:A:N6	27:DB:108:U:H3'	2.25	0.52
29:DE:111:ARG:HA	38:DR:1:MET:SD	2.50	0.52
1:CA:56:U:H2'	1:CA:57:G:H8	1.74	0.52
26:BA:2110:G:C2	26:BA:2120:G:H1'	2.44	0.52
35:BO:104:ARG:CZ	40:BT:34:VAL:HG21	2.39	0.52
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.10	0.52
1:CA:302:G:N3	1:CA:556:C:H4'	2.24	0.52
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.39	0.52
26:DA:83:G:OP1	45:DY:95:LYS:NZ	2.32	0.52
26:DA:2117:A:O2'	26:DA:2118:U:H5"	2.09	0.52
26:DA:2126:A:N6	26:DA:2172:U:H3'	2.24	0.52
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.10	0.52
1:CA:1004:A:N6	1:CA:1037:C:C2	2.77	0.52
25:CY:9:A:H5'	25:CY:46:7MG:H1'	1.91	0.52
1:CA:1286:A:N1	21:CU:18:TYR:OH	2.42	0.52
13:CM:29:ARG:HG3	13:CM:64:TRP:CH2	2.45	0.52
27:DB:110:G:C2'	27:DB:111:G:H5'	2.39	0.52
26:DA:2815:C:C5'	52:D5:29:THR:HG21	2.39	0.52
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.41	0.52
26:DA:2350:C:H2'	26:DA:2351:G:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DD:175:LEU:HD12	28:DD:185:VAL:HG21	1.92	0.52
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.92	0.52
26:DA:729:G:H5'	26:DA:730:C:H5''	1.91	0.52
1:AA:626:U:H2'	1:AA:627:G:C8	2.45	0.52
16:AP:58:TYR:O	16:AP:62:VAL:HG23	2.09	0.52
31:BG:48:GLU:HA	31:BG:51:ARG:HG2	1.91	0.52
3:CC:119:ARG:HG2	3:CC:123:GLN:HE21	1.75	0.52
25:CY:33:U:C3'	25:CY:34:G:H5''	2.40	0.52
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.09	0.52
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.32	0.52
26:BA:2173:A:H3'	26:BA:2174:C:C6	2.45	0.52
3:CC:125:GLU:HG3	3:CC:190:ARG:O	2.10	0.52
2:CB:100:GLY:O	2:CB:108:ILE:HD11	2.10	0.52
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.25	0.52
20:AT:9:ASN:O	20:AT:10:LEU:HB2	2.10	0.52
1:AA:1279:A:H4'	1:AA:1281:U:H5	1.75	0.52
1:AA:946:A:O2'	1:AA:1333:A:N3	2.35	0.52
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.44	0.52
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.91	0.52
37:BQ:30:GLY:HA2	37:BQ:107:ALA:HB2	1.92	0.52
26:DA:200:U:O4	26:DA:250:G:N2	2.43	0.52
26:BA:848:G:C4	26:BA:933:A:H8	2.26	0.52
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.49	0.52
31:BG:143:GLU:O	51:B4:28:LYS:NZ	2.32	0.52
26:BA:1028:A:H61	26:BA:1125:G:H2'	1.75	0.52
26:BA:1153:C:OP1	41:BU:92:ARG:NH1	2.43	0.52
26:DA:2155:G:H2'	26:DA:2156:G:O4'	2.10	0.52
1:CA:171:A:H2'	1:CA:172:A:C8	2.45	0.52
27:DB:17:C:O2	27:DB:67:G:N2	2.35	0.52
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.09	0.52
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.43	0.52
1:AA:950:U:H2'	1:AA:951:G:C8	2.45	0.52
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	1.91	0.52
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.52
26:DA:79:G:H1	26:DA:107:C:H42	1.58	0.52
26:DA:77:C:H42	26:DA:109:G:H1	1.57	0.52
1:AA:353:A:H5'	1:AA:353:A:H8	1.74	0.52
18:CR:70:ILE:HG23	18:CR:79:LEU:HD12	1.92	0.52
1:AA:1144:G:N2	1:AA:1146:A:H62	2.08	0.52
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.43	0.52
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:892:G:H3'	26:BA:893:C:H6	1.74	0.52
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.24	0.52
23:AW:52:G:H4'	37:BQ:56:ARG:CZ	2.39	0.52
1:CA:457:C:H2'	1:CA:458:C:H6	1.75	0.52
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.43	0.52
24:AX:21:A:N6	24:AX:46:G:H2'	2.24	0.52
1:CA:142:G:H2'	1:CA:143:A:H8	1.74	0.52
26:DA:1608:A:H1'	26:DA:1610:A:OP2	2.10	0.52
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.90	0.52
26:DA:1341:U:OP1	26:DA:1397:U:N3	2.35	0.52
26:DA:1827:C:OP2	28:DD:222:ARG:NH1	2.43	0.52
26:DA:263:C:H2'	26:DA:264:C:O4'	2.10	0.52
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	1.92	0.52
1:AA:677:U:H3	1:AA:713:G:H22	1.58	0.52
39:DS:34:HIS:ND1	39:DS:53:SER:OG	2.35	0.52
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.44	0.52
26:DA:2114:A:N6	26:DA:2115:G:H21	2.08	0.52
1:AA:1024:G:H2'	1:AA:1025:U:H5''	1.92	0.52
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.25	0.52
3:CC:22:TRP:CB	3:CC:59:ARG:HB2	2.40	0.52
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.52
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.45	0.52
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.45	0.52
25:CY:18:G:N2	25:CY:55:PSU:C4	2.77	0.52
9:AI:9:ARG:H	9:AI:79:LEU:HD23	1.75	0.52
1:CA:346:G:OP1	40:DT:41:ARG:NH2	2.42	0.52
19:CS:17:GLU:O	19:CS:21:GLU:N	2.36	0.52
26:BA:639:U:H2'	26:BA:640:C:C6	2.45	0.52
56:D9:17:ILE:HG22	56:D9:24:TYR:HB2	1.92	0.52
26:DA:637:A:H8	36:DP:117:GLU:HG3	1.75	0.52
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.25	0.52
1:AA:619:U:N3	4:AD:134:ASP:OD2	2.38	0.52
12:CL:34:ARG:HG3	12:CL:105:TYR:CE2	2.44	0.52
22:CV:14:A:C2	22:CV:15:A:C4	2.98	0.52
1:AA:347:G:HO2'	1:AA:348:G:P	2.33	0.52
28:BD:101:GLU:OE1	28:BD:103:ARG:NH1	2.42	0.52
13:AM:15:VAL:HB	13:AM:34:LEU:HD11	1.92	0.52
26:DA:93:G:H2'	26:DA:94:C:H6	1.74	0.52
6:CF:3:ARG:HD3	6:CF:64:GLN:NE2	2.25	0.52
40:DT:51:ARG:HG3	40:DT:98:LYS:HZ3	1.75	0.52
1:CA:545:C:O2'	1:CA:549:C:OP1	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.45	0.52
12:AL:77:LEU:HD21	12:AL:107:ALA:HA	1.92	0.52
20:CT:56:MET:HE3	20:CT:85:MET:HA	1.90	0.52
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.07	0.52
38:DR:74:LYS:HG2	38:DR:77:ARG:HH21	1.74	0.52
1:AA:582:U:OP1	15:AO:64:ARG:NH1	2.43	0.52
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.73	0.52
29:BE:77:ILE:HD13	29:BE:195:LEU:HD12	1.92	0.52
52:B5:55:ARG:NH1	52:B5:57:VAL:HG22	2.25	0.52
30:DF:32:LEU:O	30:DF:36:VAL:HG23	2.09	0.52
26:DA:2124:G:H1	26:DA:2174:C:H42	1.58	0.51
2:CB:135:GLN:O	2:CB:139:LYS:HB2	2.10	0.51
1:AA:1022:G:H2'	1:AA:1023:G:C8	2.44	0.51
31:DG:106:LEU:O	31:DG:111:LEU:HD22	2.10	0.51
24:CX:67:C:C2'	24:CX:68:C:H5'	2.40	0.51
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.74	0.51
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.51
23:CW:76:F3N:N	24:CX:76:31H:O2'	2.43	0.51
26:DA:956:G:H5''	37:DQ:77:LYS:HD2	1.92	0.51
1:CA:1250:A:H4'	9:CI:68:GLY:N	2.25	0.51
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.25	0.51
31:DG:48:GLU:HA	31:DG:51:ARG:HG2	1.90	0.51
8:AH:112:LEU:HA	8:AH:134:ILE:HG12	1.92	0.51
26:BA:2875:C:OP1	40:BT:3:ARG:NH1	2.42	0.51
25:AY:13:C:H2'	25:AY:14:A:C8	2.45	0.51
46:BZ:92:SER:O	46:BZ:130:PRO:HG2	2.10	0.51
46:BZ:29:TYR:HB3	46:BZ:34:ASN:HD22	1.75	0.51
26:DA:1032:A:H2	26:DA:1122:G:H22	1.59	0.51
26:BA:1345:C:OP2	61:BA:4016:HOH:O	2.18	0.51
23:AW:19:G:C5	26:BA:882:G:H4'	2.45	0.51
26:BA:2191:G:H5'	26:BA:2191:G:H8	1.74	0.51
1:CA:1359:C:H3'	14:CN:35:ARG:NH2	2.25	0.51
1:CA:1028:C:H2'	1:CA:1029:C:C6	2.45	0.51
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.11	0.51
26:DA:1721:G:N1	26:DA:1739:U:OP2	2.43	0.51
19:CS:33:THR:HG21	19:CS:71:LEU:HD21	1.91	0.51
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.10	0.51
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.45	0.51
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.45	0.51
26:DA:2645:G:N2	26:DA:2767:C:OP2	2.43	0.51
29:DE:115:GLY:O	29:DE:119:ARG:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.91	0.51
26:BA:86:C:H4'	26:BA:104:U:H1'	1.92	0.51
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.84	0.51
24:AX:66:C:H2'	24:AX:67:C:O4'	2.10	0.51
1:AA:524:G:H2'	1:AA:525:C:C6	2.46	0.51
43:BW:2:GLU:OE2	43:BW:72:LYS:HE2	2.10	0.51
24:AX:61:C:H2'	24:AX:62:C:H6	1.76	0.51
8:CH:15:ASN:O	8:CH:19:VAL:HG23	2.10	0.51
1:AA:606:G:N2	1:AA:631:G:N7	2.58	0.51
53:B6:14:THR:HG21	53:B6:48:VAL:HG22	1.92	0.51
27:DB:48:A:P	39:DS:30:ARG:HH12	2.33	0.51
27:DB:7:G:N1	27:DB:114:C:N3	2.48	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
24:CX:48:C:C2	24:CX:59:A:H1'	2.45	0.51
26:BA:2110:G:OP1	26:BA:2118:U:N3	2.27	0.51
26:BA:2751:G:C2	32:BH:2:SER:HB3	2.45	0.51
11:AK:16:SER:O	11:AK:35:PRO:HD3	2.11	0.51
27:DB:94:C:H2'	27:DB:95:C:H6	1.75	0.51
13:AM:14:ARG:HB2	13:AM:17:VAL:HG23	1.91	0.51
26:BA:41:C:H2'	26:BA:42:G:O4'	2.10	0.51
26:DA:1366:A:OP1	48:D1:3:LYS:NZ	2.30	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.58	0.51
25:CY:31:A:C2	25:CY:39:PSU:N3	2.79	0.51
1:CA:1134:G:N2	1:CA:1140:C:N3	2.54	0.51
1:AA:265:G:H2'	1:AA:267:C:H5	1.74	0.51
46:BZ:59:LEU:HD12	46:BZ:69:THR:HG21	1.92	0.51
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.91	0.51
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.58	0.51
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.46	0.51
26:DA:1325:G:OP1	26:DA:1647:G:O2'	2.15	0.51
26:DA:708:C:H42	26:DA:723:G:H1	1.57	0.51
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.92	0.51
26:BA:687:C:H5''	54:B7:2:LYS:HE2	1.91	0.51
24:AX:8:4SU:H6	24:AX:8:4SU:O5'	2.11	0.51
14:CN:6:LEU:HB3	14:CN:23:ARG:HH22	1.75	0.51
25:AY:7:A:HO2'	25:AY:49:C:H5'	1.72	0.51
46:DZ:59:LEU:HD21	46:DZ:69:THR:OG1	2.10	0.51
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.29	0.51
1:CA:1028:C:O2	1:CA:1033:G:N1	2.44	0.51
1:CA:1011:G:N2	1:CA:1018:C:N3	2.53	0.51
26:DA:528:A:C2'	26:DA:529:A:H5''	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2394:C:OP2	55:D8:30:ARG:NH1	2.43	0.51
31:DG:105:LYS:NZ	31:DG:143:GLU:OE1	2.43	0.51
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.10	0.51
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.30	0.51
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.45	0.51
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.41	0.51
26:BA:601:C:OP1	30:BF:108:LYS:HE3	2.11	0.51
26:DA:392:C:H5''	26:DA:409:C:H5''	1.93	0.51
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.10	0.51
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.26	0.51
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.46	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.40	0.51
1:CA:1120:G:C6	1:CA:1154:G:C2	2.99	0.51
13:CM:71:ARG:NH1	13:CM:71:ARG:HG3	2.25	0.51
25:AY:38:A:H2'	25:AY:39:PSU:H5''	1.91	0.51
27:DB:95:C:H2'	27:DB:96:U:C6	2.46	0.51
1:AA:309:G:O2'	1:AA:607:A:N1	2.44	0.51
26:DA:184:C:H2'	26:DA:185:U:C6	2.45	0.51
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.09	0.51
28:DD:20:ASP:OD1	28:DD:20:ASP:N	2.44	0.51
26:DA:667:U:O2	55:D8:2:PRO:HD2	2.10	0.51
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.40	0.51
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.93	0.51
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.26	0.51
25:CY:33:U:H3'	25:CY:34:G:H5''	1.92	0.51
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.92	0.51
26:BA:457:A:H5''	61:BA:3937:HOH:O	2.10	0.51
1:CA:1347:G:HO2'	1:CA:1373:G:H1	1.59	0.51
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.91	0.51
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.76	0.51
24:CX:23:C:H2'	24:CX:24:U:H6	1.75	0.51
27:DB:80:U:H2'	27:DB:81:G:C8	2.44	0.51
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.44	0.51
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.43	0.51
32:DH:30:LYS:HG3	32:DH:80:SER:O	2.10	0.51
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.44	0.51
26:DA:872:A:H2'	26:DA:873:G:C8	2.45	0.51
26:BA:2183:C:H2'	26:BA:2184:G:H8	1.76	0.51
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.45	0.51
41:DU:49:HIS:HA	41:DU:52:ARG:HB3	1.91	0.51
25:AY:68:C:C2'	25:AY:69:G:H5'	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:78:G:N2	1:AA:91:C:C2	2.79	0.51
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.32	0.51
13:CM:25:ILE:HG23	13:CM:29:ARG:HB3	1.92	0.51
1:AA:841:U:C4	1:AA:848:C:H1'	2.45	0.51
13:AM:19:LEU:HD21	13:AM:56:LEU:HD11	1.92	0.51
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.44	0.51
11:CK:101:SER:HB2	11:CK:103:LEU:HD23	1.92	0.51
2:AB:137:ARG:CZ	2:AB:137:ARG:HB3	2.41	0.51
26:DA:71:A:N7	44:DX:31:HIS:HE1	2.08	0.51
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.92	0.51
1:CA:1517:G:H1'	26:DA:1919:A:O3'	2.11	0.51
1:AA:328:C:H4'	1:AA:329:A:H5'	1.93	0.51
33:BI:140:LEU:HD22	33:BI:142:VAL:HG22	1.92	0.51
6:CF:87:ARG:HH11	6:CF:87:ARG:HB2	1.75	0.51
3:CC:63:ASN:HB2	3:CC:98:ASN:HB2	1.93	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
1:CA:1038:C:H2'	1:CA:1039:C:H5''	1.91	0.51
46:DZ:145:GLU:HG2	46:DZ:146:ILE:HD12	1.93	0.51
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.93	0.51
1:AA:1001:A:H2'	1:AA:1001(A):G:C8	2.46	0.51
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.11	0.51
1:AA:1022:G:H4'	1:AA:1022:G:OP1	2.11	0.51
1:CA:1264:C:H42	1:CA:1271:G:H1	1.58	0.51
51:B4:63:TYR:CD1	51:B4:63:TYR:N	2.77	0.51
8:CH:69:ARG:HG3	8:CH:76:PRO:HA	1.93	0.51
1:AA:1068:G:N2	1:AA:1191:A:N3	2.47	0.51
27:DB:3:C:H2'	27:DB:4:C:H6	1.76	0.51
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.46	0.51
29:BE:47:VAL:HG22	29:BE:84:PHE:O	2.11	0.51
26:DA:218:A:C2	26:DA:235:U:H4'	2.46	0.51
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.41	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
34:DN:30:ILE:HG22	34:DN:34:LEU:HD22	1.93	0.51
26:BA:880:G:N2	26:BA:898:C:C2	2.79	0.51
26:BA:893:C:O2'	26:BA:894:C:H5'	2.10	0.51
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.10	0.51
1:CA:982:U:O2	1:CA:1222:G:N1	2.43	0.51
26:BA:1048:A:P	26:BA:1109:C:H42	2.32	0.51
9:AI:48:GLU:HB3	9:AI:101:PHE:HE2	1.76	0.51
18:AR:56:THR:HB	18:AR:58:LEU:HD22	1.93	0.51
24:AX:19:G:H3'	24:AX:20:U:H6	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:96:ASP:OD1	33:BI:96:ASP:N	2.44	0.51
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.51
26:BA:907:U:HO2'	37:BQ:101:ARG:HH22	1.58	0.51
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.93	0.51
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.27	0.51
32:DH:154:PRO:HB3	32:DH:163:TYR:CZ	2.46	0.51
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.51
32:DH:20:ALA:HB3	32:DH:23:ARG:HG3	1.93	0.51
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.92	0.51
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.76	0.51
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.26	0.51
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.10	0.51
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.46	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51
1:CA:839:U:O2'	1:CA:840:C:OP1	2.27	0.51
2:CB:19:HIS:CE1	2:CB:206:ASP:HB2	2.44	0.51
40:DT:24:PRO:HD3	40:DT:52:ILE:HD12	1.93	0.51
30:DF:24:LEU:HD23	30:DF:115:ALA:HA	1.93	0.51
25:AY:28:G:H2'	25:AY:29:G:C8	2.46	0.50
1:AA:96:U:O2'	1:AA:97:G:H5'	2.11	0.50
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.14	0.50
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.44	0.50
1:CA:344:A:H4'	1:CA:345:C:OP2	2.11	0.50
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.21	0.50
21:CU:7:ARG:NH1	21:CU:21:TYR:OH	2.43	0.50
26:DA:662:G:H5''	36:DP:16:ARG:HG2	1.92	0.50
20:CT:9:ASN:O	20:CT:10:LEU:HB2	2.11	0.50
26:DA:656:G:H2'	26:DA:657:U:O4'	2.10	0.50
1:CA:735:C:H2'	1:CA:736:C:C6	2.45	0.50
8:CH:20:TYR:CE2	8:CH:76:PRO:HG2	2.46	0.50
1:AA:46:G:O6	61:AA:4164:HOH:O	2.16	0.50
23:CW:21:A:H1'	23:CW:48:C:N4	2.26	0.50
5:CE:18:ARG:HG2	5:CE:19:MET:N	2.27	0.50
1:CA:707:C:H2'	1:CA:708:C:C6	2.46	0.50
1:AA:735:C:H2'	1:AA:736:C:H6	1.76	0.50
18:CR:38:GLU:O	18:CR:41:LYS:NZ	2.45	0.50
26:DA:2103:C:C2'	26:DA:2104:G:H5'	2.40	0.50
4:CD:12:CYS:SG	4:CD:19:LEU:HB2	2.51	0.50
26:DA:1299:G:OP1	61:DA:4540:HOH:O	2.19	0.50
26:DA:2139:C:N4	26:DA:2152:G:C6	2.79	0.50
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.46	0.50
1:CA:1164:G:C2'	1:CA:1165:C:H5'	2.40	0.50
2:CB:120:ALA:O	2:CB:121:LEU:HB3	2.11	0.50
1:AA:523:A:H61	12:AL:92:ASP:HB2	1.76	0.50
1:CA:580:U:H5''	15:CO:58:MET:HG2	1.92	0.50
31:DG:5:VAL:HG22	31:DG:8:LYS:HB2	1.93	0.50
26:BA:848:G:H2'	26:BA:849:A:C8	2.46	0.50
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.29	0.50
38:BR:38:VAL:HG12	38:BR:42:LYS:HE3	1.92	0.50
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.93	0.50
26:BA:184:C:H2'	26:BA:185:U:C6	2.47	0.50
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.91	0.50
26:DA:2611:U:C4	52:D5:3:LYS:HG2	2.46	0.50
20:CT:86:ARG:NH1	20:CT:90:GLN:HE22	2.10	0.50
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.11	0.50
35:BO:34:THR:OG1	35:BO:35:VAL:N	2.43	0.50
26:BA:2133:G:O2'	26:BA:2156:G:N2	2.43	0.50
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.46	0.50
26:BA:657:U:H2'	26:BA:658:C:C6	2.45	0.50
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.11	0.50
1:CA:1007:C:H2'	1:CA:1008:C:H6	1.75	0.50
26:DA:272(A):U:H5	26:DA:272(C):G:OP1	1.95	0.50
27:DB:27:C:H5''	39:DS:54:LEU:HD21	1.94	0.50
26:DA:571:A:H5'	26:DA:2030:A:N7	2.27	0.50
26:BA:2816:C:O3'	38:BR:99:LYS:NZ	2.40	0.50
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.92	0.50
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.46	0.50
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.46	0.50
1:CA:1154:G:N7	1:CA:1155:G:C8	2.80	0.50
26:DA:361:G:O2'	26:DA:362:U:H5'	2.12	0.50
26:BA:2893:G:H4'	26:BA:2894:G:O5'	2.11	0.50
4:CD:155:LEU:O	4:CD:159:ARG:HG3	2.11	0.50
25:CY:59:U:H3'	25:CY:60:U:O2	2.12	0.50
1:AA:752:G:H4'	15:AO:69:TYR:OH	2.12	0.50
26:DA:271(R):G:H5''	48:D1:97:LEU:HD21	1.93	0.50
26:DA:873:G:N2	26:DA:905:U:C2	2.80	0.50
1:AA:551:U:H2'	1:AA:552:U:C6	2.47	0.50
53:B6:9:LEU:HD13	53:B6:51:GLU:HG3	1.92	0.50
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.47	0.50
26:BA:652(C):G:H1	26:BA:652(V):C:H42	1.59	0.50
1:CA:473:G:H2'	1:CA:474:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D3:18:ASP:N	50:D3:18:ASP:OD1	2.44	0.50
51:B4:46:GLN:O	51:B4:48:ARG:N	2.44	0.50
26:DA:866:A:H2	26:DA:867:C:C4	2.29	0.50
1:AA:642:A:N3	8:AH:113:SER:OG	2.38	0.50
25:CY:1:G:H1	25:CY:72:C:H42	1.60	0.50
26:BA:1177:A:O2'	26:BA:1178:C:O4'	2.24	0.50
1:CA:1033:G:H2'	1:CA:1034:G:H5'	1.93	0.50
3:CC:22:TRP:HB3	3:CC:59:ARG:HB2	1.93	0.50
1:CA:1119:C:OP2	9:CI:9:ARG:NH1	2.35	0.50
1:CA:344:A:H5''	1:CA:345:C:C5	2.43	0.50
25:CY:26:A:N1	25:CY:44:G:C6	2.80	0.50
26:DA:289:A:H62	26:DA:351:G:H21	1.59	0.50
20:AT:45:GLN:HA	20:AT:91:LEU:HB3	1.94	0.50
26:BA:1113:U:H2'	26:BA:1114:G:H8	1.75	0.50
26:DA:1166:C:H1'	26:DA:1184:G:N2	2.27	0.50
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.12	0.50
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.26	0.50
45:BY:16:ALA:HB2	45:BY:73:ARG:HD3	1.94	0.50
26:BA:566:U:H5''	36:BP:29:LYS:HE3	1.93	0.50
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.46	0.50
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.93	0.50
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.11	0.50
4:AD:65:ARG:HG2	4:AD:75:PHE:CD1	2.47	0.50
26:BA:2238:G:N3	26:BA:2238:G:H2'	2.25	0.50
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.44	0.50
26:DA:2528:U:O2'	26:DA:2529:G:H3'	2.12	0.50
26:DA:2252:G:H2'	26:DA:2253:G:C8	2.47	0.50
35:DO:78:ARG:HG2	40:DT:73:GLU:HB2	1.93	0.50
1:AA:186:C:H2'	1:AA:187:C:C6	2.47	0.50
13:CM:121:LYS:HZ3	23:CW:40:C:H4'	1.77	0.50
23:CW:61:C:O2'	23:CW:62:C:H6	1.95	0.50
27:DB:66:A:H61	27:DB:108:U:H3'	1.76	0.50
26:BA:2150:U:C2'	26:BA:2151:G:H5'	2.41	0.50
25:AY:25:C:C2	25:AY:26:A:C8	3.00	0.50
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.11	0.50
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.46	0.50
26:DA:601:C:O2	26:DA:605:C:H4'	2.11	0.50
1:CA:1342:C:H2'	1:CA:1343:G:C8	2.46	0.50
7:AG:78:ARG:NH2	7:AG:154:TYR:O	2.43	0.50
25:AY:44:G:H8	25:AY:44:G:OP2	1.95	0.50
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:57:ARG:NH1	51:D4:34:GLU:HA	2.27	0.50
6:CF:15:ASP:OD1	6:CF:18:GLN:N	2.24	0.50
26:DA:1038:C:N3	26:DA:1117:G:N2	2.50	0.50
4:CD:38:TYR:CZ	4:CD:45:GLN:HG3	2.47	0.50
10:CJ:27:ALA:HA	10:CJ:81:THR:CG2	2.41	0.50
2:CB:134:GLU:O	2:CB:138:LEU:HG	2.11	0.50
26:BA:222:A:H3'	26:BA:421:U:H5'	1.94	0.50
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.12	0.50
34:BN:73:THR:OG1	34:BN:82:LEU:HD11	2.11	0.50
33:DI:14:ASP:N	33:DI:17:GLN:OE1	2.44	0.50
1:CA:811:C:O2'	1:CA:901:A:N1	2.40	0.50
37:DQ:38:GLU:HG3	37:DQ:127:ILE:HB	1.94	0.50
26:DA:2001:A:H2'	26:DA:2002:G:C8	2.46	0.50
26:DA:570:G:H5''	61:DA:3844:HOH:O	2.11	0.50
26:DA:2748:A:O2'	32:DH:63:SER:O	2.18	0.50
26:BA:857:C:N4	26:BA:858:U:O4	2.45	0.50
26:BA:662:G:H5''	36:BP:16:ARG:HG2	1.94	0.50
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.94	0.50
26:DA:304:G:O6	61:DA:4181:HOH:O	2.18	0.50
1:CA:109:A:C6	1:CA:326:G:C6	3.00	0.50
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.11	0.50
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.46	0.50
25:CY:34:G:C6	25:CY:35:A:C6	3.00	0.50
1:CA:1137:C:H5''	1:CA:1138:G:OP1	2.12	0.50
24:CX:8:4SU:O2'	24:CX:21:A:N1	2.28	0.50
1:CA:457:C:H2'	1:CA:458:C:C6	2.46	0.50
1:AA:1064:G:N2	1:AA:1191:A:OP2	2.41	0.50
1:CA:1049:U:C6	1:CA:1201:A:H5'	2.47	0.50
2:AB:185:ILE:HG23	2:AB:199:TYR:HB2	1.93	0.50
26:BA:2689:U:H4'	26:BA:2690:C:H5'	1.93	0.50
33:BI:72:LEU:C	33:BI:74:ASN:H	2.14	0.50
1:AA:977:A:H1'	1:AA:982:U:O4	2.12	0.50
26:BA:84:A:H5''	45:BY:8:LYS:HG3	1.93	0.50
30:DF:137:LYS:HA	30:DF:140:LEU:HD23	1.93	0.50
29:DE:89:ASP:N	29:DE:89:ASP:OD1	2.43	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
26:DA:2240:C:OP2	61:DA:3953:HOH:O	2.19	0.50
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.47	0.50
2:AB:30:ARG:HH21	2:AB:194:PRO:HB2	1.76	0.50
1:AA:1002:G:C4	1:AA:1003:G:H1'	2.47	0.50
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:37:VAL:O	31:DG:94:LEU:N	2.41	0.50
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.43	0.50
35:DO:24:VAL:HB	35:DO:33:ALA:HB2	1.92	0.50
26:DA:1184:G:H5'	50:D3:29:ARG:HH11	1.77	0.50
26:DA:686:G:H21	26:DA:788:A:H61	1.58	0.50
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.94	0.50
26:BA:2612:C:OP2	52:B5:2:ALA:N	2.45	0.50
1:CA:1342:C:O2'	9:CI:124:GLN:HG2	2.12	0.50
23:CW:66:U:H2'	23:CW:67:C:O4'	2.12	0.50
26:BA:2846:G:H2'	26:BA:2847:U:O4'	2.11	0.50
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.92	0.50
30:DF:110:LEU:HD12	30:DF:202:PHE:CE1	2.47	0.50
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.46	0.50
26:DA:2305:A:H5''	31:DG:134:GLY:HA3	1.94	0.50
26:DA:2750:A:H8	26:DA:2750:A:OP1	1.95	0.50
1:AA:250:A:H4'	1:AA:251:G:O5'	2.10	0.50
27:BB:87:G:N2	27:BB:90:A:OP2	2.30	0.50
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.94	0.50
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.12	0.50
25:CY:4:C:H2'	25:CY:5:G:H5'	1.92	0.49
1:AA:79:G:N1	1:AA:90:U:C2	2.80	0.49
1:AA:92:C:H2'	1:AA:93:G:C8	2.47	0.49
1:CA:404:U:H5'	4:CD:122:ARG:HD3	1.94	0.49
1:CA:1316:G:O2'	1:CA:1318:A:N7	2.37	0.49
1:AA:1027:C:C4	1:AA:1034:G:O6	2.64	0.49
26:DA:2025:C:N4	61:DA:4191:HOH:O	2.45	0.49
1:CA:1128:C:H4'	1:CA:1148:U:O2	2.12	0.49
26:BA:1507:A:O2'	26:BA:1508:A:O5'	2.26	0.49
1:CA:1016:A:C5	1:CA:1017:G:H1'	2.47	0.49
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.15	0.49
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.27	0.49
26:DA:526:A:O2'	26:DA:2043:C:O2	2.24	0.49
27:DB:44:G:OP1	31:DG:98:ARG:NH2	2.45	0.49
51:B4:59:PHE:CA	51:B4:61:ARG:H	2.24	0.49
1:CA:54:C:H2'	1:CA:352:C:H41	1.77	0.49
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.12	0.49
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.47	0.49
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.12	0.49
26:BA:271(V):G:O6	61:BA:4929:HOH:O	2.19	0.49
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.11	0.49
27:DB:98:G:H2'	27:DB:99:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:47:LEU:HD13	3:AC:68:VAL:HG11	1.94	0.49
26:DA:1357:U:H2'	26:DA:1358:G:O4'	2.12	0.49
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.75	0.49
26:BA:614(A):U:H5''	61:BA:5227:HOH:O	2.12	0.49
17:AQ:28:PRO:HA	17:AQ:35:VAL:HA	1.94	0.49
26:DA:2153:G:H3'	26:DA:2154:G:H8	1.77	0.49
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.93	0.49
26:DA:900:A:O2'	26:DA:901:A:OP1	2.29	0.49
1:CA:1028:C:C2	1:CA:1033:G:C6	3.00	0.49
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.26	0.49
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.94	0.49
1:CA:1152:A:H2'	1:CA:1153:C:C6	2.46	0.49
1:AA:1007:C:O2	1:AA:1022:G:N1	2.31	0.49
1:CA:992:U:C6	1:CA:992:U:H5''	2.41	0.49
30:DF:178:PRO:HB2	30:DF:201:VAL:HG21	1.94	0.49
1:CA:954:G:H21	1:CA:1227:A:N6	2.10	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
32:DH:69:ARG:HG3	32:DH:70:THR:N	2.27	0.49
13:CM:3:ARG:HB2	51:D4:34:GLU:HG2	1.94	0.49
26:DA:141:A:C8	26:DA:1408:C:O2'	2.64	0.49
1:CA:441:A:H3'	1:CA:442:C:C6	2.48	0.49
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.60	0.49
26:DA:443:A:H5''	26:DA:444:C:OP1	2.13	0.49
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.40	0.49
1:CA:195:A:OP1	20:CT:68:LYS:NZ	2.44	0.49
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.12	0.49
1:CA:1452:C:O5'	1:CA:1452:C:H6	1.95	0.49
1:CA:65:U:H5'	1:CA:65:U:C6	2.47	0.49
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.27	0.49
26:BA:1866:C:H2'	26:BA:1876:A:O4'	2.12	0.49
26:BA:247:G:H4'	26:BA:386:G:C5	2.47	0.49
1:AA:1366:C:O2'	10:AJ:60:ARG:NH2	2.44	0.49
25:CY:61:C:H2'	25:CY:62:C:C6	2.48	0.49
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	1.94	0.49
1:CA:1324:A:H4'	1:CA:1362:C:O3'	2.12	0.49
26:BA:645:C:H5'	26:BA:646:A:OP2	2.12	0.49
51:B4:53:GLU:HG2	51:B4:56:VAL:HG22	1.94	0.49
3:CC:6:HIS:ND1	14:CN:49:HIS:HB3	2.27	0.49
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.47	0.49
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.47	0.49
2:AB:112:VAL:O	2:AB:116:GLU:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:52:LEU:HD12	29:BE:77:ILE:HD11	1.94	0.49
33:BI:6:LEU:HD11	33:BI:37:VAL:HG23	1.93	0.49
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.47	0.49
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.47	0.49
26:DA:2557:G:H2'	26:DA:2558:C:C6	2.47	0.49
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.93	0.49
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.95	0.49
35:DO:64:ARG:NH1	35:DO:81:ASP:OD1	2.45	0.49
31:BG:139:LEU:HD12	31:BG:139:LEU:H	1.75	0.49
1:CA:1249:C:O2'	9:CI:73:GLN:NE2	2.44	0.49
26:DA:2135:A:H2'	26:DA:2136:C:C5	2.47	0.49
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.42	0.49
23:CW:70:G:H2'	23:CW:71:G:H8	1.76	0.49
39:DS:58:LEU:HD21	39:DS:65:VAL:HG13	1.94	0.49
26:DA:624:C:OP1	61:DA:3854:HOH:O	2.20	0.49
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.12	0.49
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.94	0.49
1:AA:131:C:O2'	1:AA:262:A:N3	2.41	0.49
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.47	0.49
26:BA:272:G:N7	26:BA:421:U:H2'	2.27	0.49
44:DX:31:HIS:HD2	44:DX:33:LYS:H	1.59	0.49
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.45	0.49
26:DA:1509(B):A:H2'	26:DA:1510:G:H8	1.76	0.49
1:CA:814:A:H2'	1:CA:816:A:H5''	1.94	0.49
55:D8:15:LYS:HG2	55:D8:16:ILE:N	2.26	0.49
29:DE:73:GLU:OE2	29:DE:73:GLU:N	2.41	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.28	0.49
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	1.95	0.49
13:CM:60:VAL:HA	13:CM:63:THR:OG1	2.11	0.49
23:CW:68:C:H2'	23:CW:69:G:H8	1.76	0.49
13:CM:34:LEU:HD13	13:CM:41:PRO:HB3	1.94	0.49
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.77	0.49
27:DB:45:A:H2'	27:DB:46:A:C8	2.47	0.49
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.48	0.49
36:BP:121:LYS:HB3	36:BP:123:LEU:HG	1.95	0.49
10:CJ:51:ARG:O	14:CN:45:ARG:NH1	2.45	0.49
26:BA:1044:G:H5'	26:BA:1045:A:OP2	2.12	0.49
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.43	0.49
3:CC:110:ASN:O	3:CC:141:VAL:HG22	2.12	0.49
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.95	0.49
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:66:GLU:HA	33:BI:69:LYS:HB3	1.93	0.49
36:BP:138:LEU:HD23	36:BP:145:PRO:HB3	1.94	0.49
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.13	0.49
25:CY:74:C:H4'	48:D1:23:LYS:HE3	1.93	0.49
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.12	0.49
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.27	0.49
46:BZ:152:ALA:HA	46:BZ:155:LEU:HD22	1.93	0.49
1:AA:335:C:O2'	1:AA:1433:A:N3	2.41	0.49
34:BN:4:TYR:HB2	41:BU:101:ARG:NH1	2.28	0.49
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.12	0.49
26:DA:2343:C:O2'	26:DA:2373:G:O2'	2.22	0.49
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.12	0.49
26:BA:625:G:O6	36:BP:107:LYS:NZ	2.46	0.49
26:DA:2164:C:H5	26:DA:2165:G:N3	2.11	0.49
25:CY:19:G:C2	25:CY:57:G:C6	3.01	0.49
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.12	0.49
44:DX:52:VAL:HG12	44:DX:82:GLN:O	2.13	0.49
1:AA:110:C:O2'	16:AP:25:ARG:O	2.26	0.49
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.27	0.49
2:CB:105:PHE:HE1	2:CB:155:LEU:HD12	1.78	0.49
26:BA:2522:U:O2'	26:BA:2647:U:OP1	2.20	0.49
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.48	0.49
26:BA:657:U:H2'	26:BA:658:C:H6	1.77	0.49
24:AX:7:G:O2'	24:AX:49:G:H5'	2.13	0.49
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.94	0.49
5:CE:80:ILE:HD11	8:CH:104:ARG:HH21	1.77	0.49
41:BU:29:SER:OG	41:BU:30:LYS:NZ	2.40	0.49
23:AW:69:G:H2'	23:AW:69:G:N3	2.28	0.49
1:AA:1343:G:H2'	1:AA:1344:C:C6	2.47	0.49
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.48	0.49
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.44	0.49
1:CA:585:G:OP1	17:CQ:37:LYS:NZ	2.45	0.49
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.11	0.49
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.43	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.45	0.49
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.13	0.49
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.13	0.49
1:CA:343:U:H2'	1:CA:345:C:C5	2.47	0.49
25:AY:50:U:H2'	25:AY:51:U:C6	2.46	0.49
3:AC:181:ASN:HD21	3:AC:204:LEU:HD12	1.77	0.49
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1045:A:OP1	26:BA:1045:A:H4'	2.12	0.49
40:DT:24:PRO:HA	40:DT:49:VAL:HG23	1.95	0.49
26:DA:2528:U:H5''	56:D9:31:LYS:HE2	1.94	0.49
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.42	0.49
26:DA:1508:A:H4'	26:DA:1509(A):A:C5	2.47	0.49
2:AB:42:ILE:HD12	2:AB:203:GLY:HA2	1.93	0.49
39:DS:31:SER:OG	39:DS:32:LEU:N	2.46	0.49
26:BA:579:G:H2'	26:BA:580:C:C6	2.48	0.49
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.93	0.49
45:BY:28:LYS:HD2	45:BY:40:GLU:HG3	1.94	0.49
26:BA:400:G:N7	61:BA:4974:HOH:O	2.34	0.49
26:BA:2439:A:C8	26:BA:2439:A:H5'	2.48	0.49
1:AA:256:U:H2'	1:AA:257:G:H8	1.77	0.49
26:DA:854:G:H2'	26:DA:855:G:H8	1.77	0.49
1:AA:1014:A:H4'	19:AS:14:HIS:CE1	2.46	0.49
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.49
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.29	0.49
2:CB:140:HIS:O	2:CB:143:GLU:HB2	2.12	0.49
1:CA:1003:G:N2	1:CA:1025:U:O4	2.46	0.49
1:AA:346:G:C4	1:AA:347:G:H1'	2.48	0.49
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.77	0.49
1:CA:1151:A:H5'	10:CJ:41:PRO:HA	1.95	0.49
53:B6:6:ARG:HH12	53:B6:26:ASN:HB2	1.78	0.49
33:BI:109:ILE:HG23	33:BI:130:TYR:CZ	2.48	0.49
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.49
31:BG:66:GLN:HG3	51:B4:1:MET:HE1	1.94	0.49
26:DA:242:G:N2	26:DA:255:A:OP2	2.38	0.49
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.93	0.49
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.30	0.49
1:CA:834:C:H2'	1:CA:835:U:C6	2.47	0.49
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.48	0.49
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.78	0.49
42:DV:24:LYS:HG2	42:DV:64:HIS:CD2	2.35	0.49
25:CY:35:A:N6	25:CY:36:A:N1	2.61	0.49
1:CA:976:G:C8	1:CA:1362:C:N4	2.80	0.49
1:CA:589:C:N3	1:CA:650:G:N1	2.41	0.49
19:AS:27:GLU:CB	19:AS:28:LYS:HA	2.38	0.49
26:DA:1652:A:OP1	38:DR:8:ARG:NH1	2.46	0.49
26:DA:1300:U:H4'	26:DA:1301:A:H5'	1.94	0.49
13:AM:65:LYS:NZ	51:B4:53:GLU:OE1	2.45	0.49
1:CA:429:U:H1'	1:CA:430:A:H5''	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BH:154:PRO:HD3	32:BH:162:ILE:O	2.12	0.49
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.48	0.49
31:BG:170:ARG:HD3	31:BG:174:GLU:HG3	1.94	0.49
1:AA:628:G:H2'	1:AA:629:G:C8	2.48	0.49
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.41	0.49
1:CA:1010:G:N2	1:CA:1020:U:O2	2.46	0.49
1:CA:250:A:H4'	1:CA:251:G:O5'	2.12	0.49
1:AA:1137:C:H5''	1:AA:1138:G:OP1	2.13	0.49
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.49
26:DA:1657:C:H2'	26:DA:1658:C:C6	2.48	0.49
26:BA:887:A:O2'	26:BA:888:C:OP2	2.28	0.49
26:DA:1313:U:H4'	26:DA:1332:G:H4'	1.95	0.49
27:DB:20:C:H2'	27:DB:21:G:H5'	1.93	0.49
1:AA:111:G:H5''	16:AP:27:LYS:HG2	1.93	0.49
26:BA:2124:G:H1	26:BA:2174:C:N4	2.11	0.49
1:AA:262:A:C6	1:AA:263:A:C6	3.00	0.49
23:CW:21:A:N6	23:CW:46:7MG:N3	2.61	0.49
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.13	0.49
26:DA:648:G:O2'	26:DA:2351:G:OP1	2.23	0.49
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.13	0.49
24:AX:7:G:H1	24:AX:66:C:H42	1.61	0.49
1:AA:736:C:H2'	1:AA:737:A:C8	2.48	0.49
1:CA:434:U:H2'	1:CA:435:C:C6	2.48	0.49
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.94	0.49
26:DA:1339:G:N2	26:DA:1603:A:H1'	2.27	0.49
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.48	0.49
26:BA:576:U:H2'	26:BA:577:G:C8	2.47	0.49
26:DA:724:U:H2'	26:DA:725:G:O4'	2.13	0.49
39:BS:65:VAL:O	39:BS:69:VAL:HG13	2.13	0.49
32:BH:11:VAL:HG21	32:BH:50:VAL:HG23	1.94	0.49
51:B4:24:THR:OG1	51:B4:25:TYR:N	2.45	0.49
9:AI:93:ARG:HB2	9:AI:93:ARG:HH11	1.78	0.49
5:CE:12:LEU:O	5:CE:30:ALA:HA	2.13	0.49
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.48	0.49
27:DB:118:G:H2'	27:DB:119:G:H5'	1.95	0.49
19:AS:38:SER:HB2	19:AS:71:LEU:HD13	1.95	0.49
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.77	0.49
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.46	0.49
23:AW:1:G:C6	23:AW:72:C:N3	2.79	0.48
1:CA:976:G:C8	1:CA:1358:U:C2	3.01	0.48
1:AA:1027:C:C2	1:AA:1034:G:C2	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1021:A:C8	26:BA:1021:A:H3'	2.47	0.48
32:BH:86:GLU:OE2	32:BH:130:ARG:NH1	2.46	0.48
3:AC:81:GLY:O	3:AC:85:ARG:HG3	2.13	0.48
36:BP:121:LYS:O	36:BP:123:LEU:N	2.42	0.48
26:BA:1588:C:H2'	26:BA:1589:C:H6	1.78	0.48
6:AF:69:GLU:H	6:AF:69:GLU:CD	2.12	0.48
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.13	0.48
26:BA:2763:G:OP2	61:BA:4693:HOH:O	2.20	0.48
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.78	0.48
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.94	0.48
49:B2:31:GLU:HB3	49:B2:53:LEU:HD11	1.94	0.48
26:DA:539:G:H2'	26:DA:540:C:H6	1.78	0.48
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.48	0.48
26:BA:578:A:OP2	61:BA:4085:HOH:O	2.20	0.48
1:AA:1131:G:O5'	1:AA:1131:G:H8	1.96	0.48
26:DA:196:A:N3	26:DA:196:A:H2'	2.28	0.48
15:CO:26:GLU:N	15:CO:26:GLU:OE2	2.43	0.48
13:AM:80:ARG:NH2	19:AS:69:HIS:HE1	2.11	0.48
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.13	0.48
2:CB:210:SER:OG	2:CB:211:ILE:N	2.46	0.48
9:AI:77:ILE:O	9:AI:81:ILE:HG23	2.13	0.48
14:CN:29:ARG:HD3	14:CN:40:CYS:HB2	1.94	0.48
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.13	0.48
26:DA:191:A:H2'	26:DA:192:C:C6	2.48	0.48
26:BA:2141:G:C2	26:BA:2142:C:C2	3.02	0.48
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.43	0.48
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.13	0.48
26:BA:1164:G:H2'	26:BA:1165:U:C6	2.49	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.11	0.48
4:CD:175:SER:OG	4:CD:184:LYS:HB2	2.12	0.48
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.95	0.48
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.49	0.48
26:DA:2552:U:H2'	26:DA:2554:U:H5''	1.96	0.48
1:CA:834:C:H2'	1:CA:835:U:H6	1.78	0.48
4:AD:165:MET:C	4:AD:168:ARG:HH12	2.17	0.48
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.13	0.48
1:CA:936:C:H2'	1:CA:937:A:O4'	2.13	0.48
1:CA:938:A:C6	1:CA:939:G:C5	3.01	0.48
7:AG:26:PHE:O	7:AG:30:ILE:HG13	2.13	0.48
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.48
2:CB:16:HIS:CG	2:CB:17:PHE:N	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.35	0.48
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.48	0.48
54:D7:9:ARG:HE	54:D7:47:ARG:HB2	1.78	0.48
1:CA:1060:C:C5	3:CC:2:GLY:HA3	2.49	0.48
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.38	0.48
1:CA:1053:G:O5'	1:CA:1054:C:H5'	2.13	0.48
26:BA:1379:A:H4'	26:BA:1380:G:OP2	2.13	0.48
17:AQ:58:GLU:O	17:AQ:74:LEU:N	2.41	0.48
26:DA:2183:C:H2'	26:DA:2184:G:C8	2.46	0.48
26:BA:1019:U:O2'	26:BA:1021:A:H2	1.96	0.48
56:B9:2:LYS:HE2	56:B9:31:LYS:O	2.12	0.48
26:DA:1218:C:H42	26:DA:1231:G:H1	1.61	0.48
26:DA:858:U:OP1	47:D0:44:ARG:NH2	2.44	0.48
2:CB:27:LYS:HG3	2:CB:194:PRO:HD2	1.95	0.48
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.78	0.48
7:CG:20:ASP:OD2	7:CG:23:VAL:HG23	2.14	0.48
54:B7:46:VAL:HG13	54:B7:48:LYS:HE3	1.95	0.48
26:DA:223:A:O2'	26:DA:420:C:O2	2.31	0.48
45:BY:6:HIS:CD2	45:BY:6:HIS:H	2.30	0.48
26:DA:1998:G:O2'	26:DA:2724:C:O2'	2.25	0.48
26:DA:531:C:H4'	26:DA:532:A:H5''	1.95	0.48
26:BA:762:U:H5''	61:BA:4793:HOH:O	2.13	0.48
8:CH:134:ILE:HG22	8:CH:135:CYS:SG	2.54	0.48
35:DO:98:VAL:HG22	35:DO:118:ALA:HA	1.95	0.48
35:BO:24:VAL:HB	35:BO:33:ALA:HB2	1.95	0.48
1:CA:979:C:H2'	1:CA:980:C:H5'	1.95	0.48
1:CA:1126:U:O4	10:CJ:71:LEU:HD13	2.14	0.48
19:AS:19:VAL:O	19:AS:23:ASN:ND2	2.47	0.48
1:CA:1399:C:C2	1:CA:1502:A:N6	2.81	0.48
1:CA:988:G:H1	1:CA:1217:C:H42	1.60	0.48
26:DA:894:C:H2'	26:DA:895:U:C6	2.48	0.48
48:B1:85:LEU:HB3	48:B1:89:GLU:CG	2.43	0.48
26:BA:1714:G:H1	26:BA:1745(A):C:N4	2.11	0.48
27:BB:22:U:H2'	27:BB:23:G:C8	2.49	0.48
27:DB:43:C:OP1	51:D4:6:HIS:NE2	2.42	0.48
3:AC:181:ASN:HD22	3:AC:204:LEU:HB2	1.78	0.48
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.29	0.48
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.46	0.48
1:CA:736:C:H2'	1:CA:737:A:C8	2.48	0.48
23:CW:22:G:H2'	23:CW:23:A:C8	2.48	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:103:ARG:O	46:DZ:139:VAL:N	2.45	0.48
26:DA:250:G:C6	26:DA:251:A:C6	3.01	0.48
26:BA:234:C:H2'	26:BA:235:U:H6	1.79	0.48
1:CA:17:U:H2'	1:CA:18:C:C6	2.49	0.48
17:CQ:40:LYS:HD2	17:CQ:42:TYR:CZ	2.49	0.48
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.77	0.48
1:AA:963:G:H5'	61:AA:4173:HOH:O	2.12	0.48
1:AA:1525:G:OP1	11:AK:120:ARG:NH2	2.46	0.48
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.48	0.48
26:DA:2348:U:O4	26:DA:2382:G:N1	2.47	0.48
1:CA:1030:C:N3	1:CA:1031:G:N2	2.54	0.48
26:DA:2839:G:H5'	38:DR:46:GLY:CA	2.37	0.48
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.95	0.48
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.46	0.48
26:BA:900:A:H2'	26:BA:901:A:C8	2.49	0.48
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.13	0.48
26:BA:2127:G:C6	26:BA:2128:C:C4	3.01	0.48
24:AX:67:C:H2'	24:AX:68:C:H5'	1.94	0.48
26:DA:539:G:H2'	26:DA:540:C:C6	2.48	0.48
12:CL:67:THR:OG1	12:CL:95:GLY:O	2.31	0.48
26:DA:455:C:N3	26:DA:472:A:H2'	2.28	0.48
3:AC:13:GLY:HA3	14:AN:57:ARG:NH2	2.27	0.48
1:CA:203:U:OP2	1:CA:203:U:H2'	2.13	0.48
36:DP:50:ARG:HD3	55:D8:7:HIS:CD2	2.49	0.48
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.95	0.48
40:DT:109:GLU:O	40:DT:113:LYS:HB2	2.13	0.48
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.48	0.48
26:BA:1798:U:OP2	28:BD:274:ARG:NH2	2.43	0.48
1:CA:1030:C:N4	1:CA:1031:G:N1	2.58	0.48
4:AD:3:ARG:O	4:AD:5:ILE:HG22	2.12	0.48
13:CM:86:CYS:SG	13:CM:87:TYR:N	2.86	0.48
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.94	0.48
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.28	0.48
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.37	0.48
46:DZ:144:LEU:HD21	46:DZ:172:ALA:HB1	1.95	0.48
26:DA:8:A:H2'	26:DA:9:U:C6	2.49	0.48
1:CA:130:A:N3	1:CA:263:A:O2'	2.32	0.48
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.46	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.96	0.48
26:BA:1825:A:OP1	28:BD:249:PRO:HD3	2.14	0.48
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:584:G:H5'	17:AQ:91:ARG:HH22	1.78	0.48
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.33	0.48
46:DZ:40:ASP:OD2	46:DZ:42:VAL:HG12	2.14	0.48
4:AD:107:ARG:HH22	4:AD:194:LEU:HD11	1.78	0.48
41:BU:49:HIS:HA	41:BU:52:ARG:HB3	1.94	0.48
26:BA:2165:G:H1	26:BA:2172:U:H5	1.61	0.48
25:AY:35:A:H5''	25:AY:35:A:H8	1.78	0.48
13:CM:108:ARG:HD3	13:CM:108:ARG:HA	1.74	0.48
33:DI:128:LEU:O	33:DI:140:LEU:N	2.34	0.48
26:DA:597:U:H2'	26:DA:598:G:H8	1.79	0.48
1:AA:36:C:OP1	12:AL:123:LYS:NZ	2.24	0.48
26:BA:2836:U:H2'	26:BA:2837:G:C8	2.49	0.48
7:AG:73:MET:HG3	7:AG:89:MET:O	2.14	0.48
25:AY:58:A:O2'	25:AY:60:U:H5	1.96	0.48
25:CY:64:A:C2'	25:CY:65:G:H5'	2.43	0.48
25:CY:9:A:H8	25:CY:11:C:N4	2.11	0.48
46:DZ:43:GLU:O	46:DZ:47:VAL:HG23	2.13	0.48
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.43	0.48
26:DA:2036:C:H2'	26:DA:2037:G:C8	2.48	0.48
1:CA:1013:G:N2	1:CA:1015:A:H3'	2.28	0.48
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.96	0.48
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.13	0.48
51:B4:64:GLY:C	51:B4:66:SER:H	2.16	0.48
26:DA:1721:G:H2'	26:DA:1740:G:O6	2.14	0.48
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.49	0.48
26:BA:2820:A:OP2	38:BR:2:ARG:NH2	2.47	0.48
1:CA:524:G:H2'	1:CA:525:C:C6	2.49	0.48
1:AA:390:C:H2'	1:AA:391:G:C8	2.49	0.48
20:CT:16:HIS:O	20:CT:19:SER:OG	2.22	0.48
26:DA:752:A:P	54:D7:3:ARG:HH22	2.37	0.48
3:AC:45:LYS:HG3	3:AC:46:GLU:N	2.28	0.48
31:DG:57:ALA:HA	31:DG:90:LEU:HD13	1.94	0.48
1:AA:688:G:H2'	1:AA:689:C:H6	1.79	0.48
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.45	0.48
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.96	0.48
1:AA:520:A:N1	1:AA:536:C:H1'	2.28	0.48
1:AA:175:C:H2'	1:AA:176:C:C6	2.48	0.48
26:BA:2292:C:P	39:BS:17:ARG:HH12	2.35	0.48
26:DA:2144:U:H1'	26:DA:2148:G:H22	1.79	0.48
25:CY:22:G:N7	25:CY:46:7MG:C2	2.82	0.48
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:16:HIS:HD2	2:CB:204:ASN:N	2.11	0.48
32:DH:3:ARG:HB3	32:DH:3:ARG:NH1	2.29	0.48
1:CA:421:U:O2'	1:CA:423:G:N7	2.47	0.48
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.14	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.49	0.48
1:AA:1144:G:H21	1:AA:1146:A:H62	1.61	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
1:CA:442:C:H42	1:CA:492:G:H1	1.61	0.48
43:DW:33:ARG:NE	43:DW:52:GLU:OE1	2.47	0.48
1:CA:1268:A:N3	1:CA:1326:C:O2'	2.38	0.48
41:BU:108:GLU:O	41:BU:112:ARG:HG2	2.13	0.48
32:BH:104:GLU:HG3	32:BH:114:VAL:HG22	1.95	0.48
26:DA:622:G:H2'	26:DA:623:G:H8	1.78	0.48
26:DA:1899:G:N3	26:DA:1899:G:H2'	2.28	0.48
23:AW:2:C:H2'	23:AW:3:C:C6	2.48	0.48
1:CA:683:G:H2'	1:CA:684:A:C8	2.49	0.48
14:CN:24:CYS:O	14:CN:28:GLY:N	2.33	0.48
26:BA:271(H):G:H5''	48:B1:81:LYS:HE3	1.96	0.48
41:DU:108:GLU:O	41:DU:112:ARG:HG2	2.14	0.48
1:CA:1000:U:O2	1:CA:1041:A:N1	2.47	0.48
30:DF:56:GLU:OE2	30:DF:93:LYS:NZ	2.46	0.48
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.49	0.48
26:DA:340:A:H2'	26:DA:341:G:O4'	2.14	0.48
32:DH:69:ARG:O	32:DH:73:ALA:N	2.31	0.48
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.14	0.48
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.48
1:AA:574:A:HO2'	1:AA:882:C:HO2'	1.60	0.48
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.13	0.48
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.14	0.48
26:DA:1466:G:O2'	26:DA:1546:C:O2'	2.16	0.48
51:B4:16:CYS:HB3	51:B4:20:ASN:HB3	1.96	0.48
7:CG:12:LEU:HD12	7:CG:12:LEU:H	1.78	0.48
1:AA:1162:C:H42	1:AA:1174:G:H1	1.59	0.48
32:DH:122:THR:O	32:DH:134:SER:OG	2.29	0.48
1:AA:270:A:H2'	1:AA:271:C:C6	2.49	0.48
26:BA:893:C:H2'	26:BA:894:C:C6	2.49	0.48
26:DA:898:C:H2'	26:DA:899:A:C8	2.49	0.48
4:CD:53:ASP:O	4:CD:57:ARG:HG3	2.13	0.48
13:CM:4:ILE:HG22	13:CM:7:VAL:O	2.13	0.48
30:DF:116:ASP:O	30:DF:120:GLU:HG3	2.14	0.48
1:CA:991:U:H4'	1:CA:992:U:OP1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:22:G:C8	25:AY:46:7MG:O6	2.67	0.48
31:BG:41:GLN:HB2	31:BG:90:LEU:HB2	1.94	0.48
13:CM:91:ARG:NE	13:CM:97:PRO:O	2.43	0.48
26:DA:2314:C:H2'	26:DA:2315:G:H8	1.79	0.48
8:CH:119:LEU:HB3	8:CH:123:GLU:HB3	1.94	0.48
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.47	0.48
23:CW:9:A:O2'	23:CW:10:G:N7	2.47	0.48
26:BA:2336:A:H61	47:B0:43:THR:HG21	1.79	0.48
35:DO:68:GLU:OE2	35:DO:78:ARG:NH1	2.47	0.48
1:CA:1434:A:H2'	1:CA:1435:G:O4'	2.14	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.78	0.48
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.14	0.48
43:DW:82:LEU:HB2	43:DW:98:LYS:HB2	1.95	0.48
14:CN:12:ARG:HG2	14:CN:13:THR:N	2.29	0.48
26:DA:2031:A:N3	26:DA:2455:G:O2'	2.38	0.48
26:BA:774:A:N3	26:BA:774:A:H2'	2.29	0.48
11:CK:66:LEU:HB3	11:CK:70:LYS:NZ	2.29	0.48
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.14	0.48
1:CA:1162:C:N4	1:CA:1174:G:N1	2.36	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.26	0.47
10:CJ:38:ILE:HG13	10:CJ:71:LEU:HB3	1.96	0.47
27:DB:42:C:H1'	31:DG:68:PRO:HA	1.96	0.47
2:CB:153:ARG:HE	2:CB:153:ARG:HB2	1.53	0.47
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.28	0.47
30:BF:101:LEU:HD12	30:BF:102:PRO:HD2	1.95	0.47
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.49	0.47
2:CB:71:VAL:CG2	2:CB:164:VAL:HA	2.44	0.47
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	1.95	0.47
1:CA:583:A:H2'	1:CA:584:G:O4'	2.14	0.47
48:D1:76:ARG:NH1	48:D1:97:LEU:O	2.46	0.47
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.14	0.47
26:DA:1509(B):A:H2'	26:DA:1510:G:C8	2.49	0.47
43:DW:71:VAL:HA	43:DW:107:LEU:HD12	1.96	0.47
23:AW:29:G:H1	23:AW:41:C:H42	1.62	0.47
26:DA:1453:U:O4	38:DR:67:LEU:HD21	2.14	0.47
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.95	0.47
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.49	0.47
26:DA:947:G:H2'	26:DA:948:G:C8	2.49	0.47
26:DA:863:A:H2'	26:DA:864:G:H8	1.79	0.47
45:BY:45:VAL:HG23	45:BY:63:LYS:HG2	1.95	0.47
17:AQ:22:LEU:HD13	17:AQ:41:LYS:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2124:G:H1	26:DA:2174:C:N4	2.13	0.47
26:DA:2321:G:N3	26:DA:2321:G:H2'	2.28	0.47
1:CA:1502:A:H2	1:CA:1505:G:N1	2.07	0.47
1:CA:1017:G:H2'	1:CA:1018:C:C6	2.49	0.47
36:DP:21:ARG:HA	36:DP:21:ARG:HD3	1.50	0.47
1:CA:659:U:H2'	1:CA:660:G:O4'	2.14	0.47
26:BA:2142:C:H2'	26:BA:2143:C:C6	2.49	0.47
33:DI:102:SER:OG	33:DI:103:ARG:N	2.47	0.47
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.14	0.47
5:CE:6:PHE:CD1	5:CE:36:ASP:HB3	2.49	0.47
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.96	0.47
1:AA:1104:G:O5'	2:AB:111:ARG:HD2	2.14	0.47
39:DS:77:ALA:O	39:DS:81:GLY:N	2.46	0.47
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.96	0.47
26:BA:218:A:C2	26:BA:235:U:H4'	2.50	0.47
1:CA:811:C:N3	61:CA:3210:HOH:O	2.35	0.47
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.54	0.47
53:D6:21:TYR:CE1	53:D6:38:LYS:HG2	2.49	0.47
14:AN:14:PRO:HB2	14:AN:16:PHE:O	2.14	0.47
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.96	0.47
1:CA:59:A:H3'	1:CA:331:G:H22	1.79	0.47
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	1.95	0.47
32:DH:35:VAL:HG11	32:DH:71:LEU:HG	1.97	0.47
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.29	0.47
48:D1:65:SER:OG	48:D1:66:HIS:ND1	2.41	0.47
26:BA:2130:U:H1'	26:BA:2158:A:N1	2.29	0.47
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.95	0.47
1:AA:346:G:P	40:BT:41:ARG:HH22	2.36	0.47
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.47
27:DB:24:G:H4'	27:DB:25:A:C8	2.49	0.47
31:DG:111:LEU:HA	31:DG:114:ILE:HD13	1.96	0.47
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.97	0.47
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.96	0.47
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.95	0.47
26:DA:62:C:H42	26:DA:93:G:H1	1.62	0.47
26:BA:330:A:H2	26:BA:1210:A:C2'	2.26	0.47
40:DT:99:LEU:O	40:DT:102:ILE:HG12	2.14	0.47
26:DA:885:C:H2'	26:DA:886:C:H4'	1.96	0.47
39:DS:30:ARG:HD3	39:DS:98:VAL:HG22	1.97	0.47
1:CA:1267:C:H6	1:CA:1267:C:O5'	1.97	0.47
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:D2:16:LEU:HB2	49:D2:21:LEU:HD23	1.97	0.47
17:AQ:78:GLU:HG2	17:AQ:79:SER:N	2.29	0.47
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.50	0.47
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.14	0.47
15:AO:84:LYS:HD3	15:AO:84:LYS:O	2.13	0.47
45:BY:11:ASP:OD1	45:BY:11:ASP:N	2.40	0.47
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.79	0.47
25:CY:66:U:H2'	25:CY:67:C:O4'	2.14	0.47
1:CA:1004:A:H62	1:CA:1037:C:C2'	2.28	0.47
31:DG:144:ILE:HG23	31:DG:148:MET:HE1	1.96	0.47
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.45	0.47
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.47
51:B4:59:PHE:C	51:B4:61:ARG:H	2.13	0.47
2:CB:178:ARG:HH21	8:CH:74:PRO:HG3	1.80	0.47
1:CA:353:A:H8	1:CA:353:A:H5'	1.78	0.47
26:DA:1029:A:N6	26:DA:1125:G:O2'	2.44	0.47
1:CA:1225:A:OP1	13:CM:103:THR:OG1	2.30	0.47
26:BA:826:U:H4'	36:BP:55:ARG:HB2	1.96	0.47
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.15	0.47
26:DA:1639:U:C2'	26:DA:1640:C:H5''	2.42	0.47
4:CD:20:TYR:HD1	4:CD:26:CYS:HB3	1.78	0.47
39:DS:53:SER:O	39:DS:57:LYS:N	2.47	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.46	0.47
45:BY:13:VAL:HB	45:BY:72:VAL:HG13	1.95	0.47
51:B4:18:CYS:SG	51:B4:20:ASN:HB2	2.55	0.47
1:AA:1479:C:H2'	1:AA:1480:G:C8	2.49	0.47
11:CK:24:SER:OG	11:CK:25:TYR:N	2.45	0.47
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.62	0.47
26:DA:212:G:H2'	26:DA:213:A:O4'	2.13	0.47
26:DA:2136:C:H1'	26:DA:2137:C:H5'	1.96	0.47
1:AA:741:G:H2'	1:AA:742:G:O4'	2.15	0.47
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.50	0.47
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD22	1.97	0.47
44:DX:35:THR:HB	44:DX:38:GLU:HB2	1.97	0.47
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.97	0.47
26:DA:1420:U:HO2'	26:DA:1421:G:P	2.37	0.47
1:AA:952:U:H2'	1:AA:953:G:C8	2.50	0.47
1:AA:167:G:H2'	1:AA:168:G:C8	2.49	0.47
28:DD:2:ALA:O	28:DD:3:VAL:HB	2.15	0.47
26:DA:657:U:H2'	26:DA:658:C:C6	2.49	0.47
2:CB:91:PRO:HG3	2:CB:155:LEU:HD23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1316:U:H2'	26:DA:1317:A:C8	2.49	0.47
1:AA:457:C:H2'	1:AA:458:C:H6	1.79	0.47
26:DA:641:C:H42	26:DA:647:G:H1	1.62	0.47
18:CR:73:ALA:HB3	18:CR:79:LEU:HG	1.96	0.47
18:CR:41:LYS:HB3	18:CR:41:LYS:NZ	2.29	0.47
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.96	0.47
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.55	0.47
24:AX:56:C:O5'	24:AX:56:C:H6	1.97	0.47
5:CE:10:MET:HG3	5:CE:32:VAL:HG22	1.96	0.47
8:AH:33:GLU:HG2	8:AH:48:TYR:OH	2.14	0.47
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.47	0.47
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.34	0.47
2:CB:17:PHE:CD2	2:CB:44:LEU:HD11	2.49	0.47
26:DA:1019:U:O2'	26:DA:1021:A:H2	1.97	0.47
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.45	0.47
25:AY:15:G:C6	25:AY:48:C:O2	2.68	0.47
23:CW:50:U:H2'	23:CW:51:U:O4'	2.15	0.47
26:BA:2207:G:H2'	26:BA:2208:A:C2	2.50	0.47
45:DY:28:LYS:HE2	45:DY:28:LYS:HB3	1.67	0.47
26:BA:534:U:H2'	26:BA:535:C:C6	2.49	0.47
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	1.97	0.47
20:CT:56:MET:HE2	20:CT:56:MET:HB2	1.71	0.47
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	1.96	0.47
25:AY:2:C:H42	25:AY:71:G:H1	1.63	0.47
24:CX:12:G:H4'	26:DA:1908:C:O2	2.14	0.47
4:AD:12:CYS:SG	4:AD:19:LEU:HB2	2.54	0.47
33:BI:48:GLU:O	33:BI:52:ARG:HB3	2.14	0.47
28:DD:164:GLN:NE2	28:DD:176:ARG:HH22	2.12	0.47
1:CA:601:C:H42	1:CA:637:G:H1	1.63	0.47
16:AP:28:ARG:NE	16:AP:29:ASP:OD1	2.29	0.47
8:CH:84:ARG:O	8:CH:84:ARG:HG3	2.14	0.47
26:BA:2181:G:HO2'	26:BA:2182:G:P	2.37	0.47
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.13	0.47
24:CX:37:A:H2'	24:CX:38:A:O4'	2.14	0.47
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.96	0.47
50:D3:50:VAL:O	50:D3:54:VAL:HB	2.15	0.47
26:DA:2128:C:N4	26:DA:2160:G:H1	2.09	0.47
19:CS:41:VAL:O	19:CS:44:MET:HB2	2.14	0.47
1:AA:1392:G:N2	1:AA:1502:A:C8	2.83	0.47
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.55	0.47
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CV:14:A:C4	25:CY:34:G:C6	3.02	0.47
1:CA:1256:A:N1	1:CA:1278:U:H1'	2.29	0.47
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.35	0.47
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	2.15	0.47
1:CA:1392:G:H21	1:CA:1502:A:H8	1.63	0.47
26:BA:2345:G:H4'	26:BA:2346:A:H5''	1.97	0.47
1:AA:1007:C:N3	1:AA:1022:G:C6	2.83	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
26:DA:1592:C:H2'	26:DA:1593:G:H8	1.79	0.47
1:AA:162:A:H3'	1:AA:163:C:C4'	2.45	0.47
1:CA:643:C:H2'	1:CA:644:G:H8	1.79	0.47
26:DA:2547:U:O2	35:DO:23:ARG:NH2	2.47	0.47
26:BA:2140:C:C4	26:BA:2151:G:N1	2.83	0.47
1:CA:22:G:H4'	1:CA:885:G:C8	2.50	0.47
36:DP:16:ARG:HG3	61:DP:305:HOH:O	2.13	0.47
16:AP:48:TRP:HH2	16:AP:76:GLN:NE2	2.12	0.47
28:DD:26:LYS:HE2	28:DD:28:GLU:O	2.15	0.47
4:CD:22:LYS:HG3	58:CD:501:SF4:S4	2.55	0.47
8:CH:103:VAL:HG21	8:CH:109:ILE:C	2.35	0.47
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.96	0.47
27:DB:94:C:H2'	27:DB:95:C:C6	2.50	0.47
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.47
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.50	0.47
1:CA:24:U:OP1	12:CL:23:LYS:NZ	2.47	0.47
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.47	0.47
32:DH:98:LEU:HD13	32:DH:102:ALA:O	2.13	0.47
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.78	0.47
31:BG:19:LEU:HG	31:BG:175:LEU:HD23	1.97	0.47
24:AX:2:G:H2'	24:AX:2:G:N3	2.29	0.47
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.50	0.47
3:AC:62:ASP:HA	3:AC:97:LYS:HD3	1.96	0.47
30:BF:39:TRP:O	30:BF:43:LYS:HD3	2.14	0.47
13:CM:39:ILE:HG12	13:CM:52:GLU:HG2	1.96	0.47
1:AA:620:C:H2'	1:AA:621:A:O4'	2.15	0.47
50:D3:8:LEU:HD13	50:D3:31:LEU:HD23	1.97	0.47
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.15	0.47
26:BA:271(X):G:C2	26:BA:271(Y):U:O4	2.68	0.47
1:AA:564:C:O2'	8:AH:91:ARG:NH2	2.38	0.47
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.14	0.47
26:DA:1270:C:H5''	26:DA:1271:G:O5'	2.15	0.47
27:DB:70:C:H42	27:DB:107:G:H1	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.15	0.47
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.50	0.47
26:BA:2137:C:N3	26:BA:2154:G:O6	2.48	0.47
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.97	0.47
1:AA:346:G:OP1	40:BT:41:ARG:NH1	2.42	0.47
26:BA:1482:G:O6	26:BA:1507:A:N6	2.48	0.47
26:BA:2168:G:C6	26:BA:2171:A:C8	3.02	0.47
27:DB:8:U:O2'	39:DS:40:ILE:HD13	2.15	0.47
51:D4:16:CYS:SG	51:D4:17:GLY:N	2.87	0.47
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.30	0.47
26:DA:251:A:C5	26:DA:252:G:H1'	2.50	0.47
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.80	0.47
1:AA:1122:U:C4	1:AA:1123:A:N7	2.83	0.47
9:AI:4:TYR:CE2	9:AI:88:TYR:HD1	2.33	0.47
26:BA:34:C:H5''	26:BA:35:G:OP2	2.15	0.47
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.30	0.47
26:DA:2820:A:O2'	26:DA:2821:A:OP1	2.29	0.47
5:CE:145:LYS:HE3	5:CE:149:GLU:OE2	2.15	0.47
26:BA:1686:C:H2'	26:BA:1687:G:O4'	2.15	0.47
26:BA:1416:G:O2'	26:BA:1417:C:OP2	2.24	0.47
26:DA:602:G:O2'	26:DA:655:A:N6	2.48	0.47
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.47
26:DA:1127:A:H2'	26:DA:1128:A:H5''	1.97	0.47
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.97	0.47
26:DA:782:A:H5'	26:DA:783:A:N7	2.30	0.47
26:BA:784:A:N6	28:BD:229:VAL:HG11	2.30	0.47
11:CK:65:ALA:HB3	11:CK:97:ALA:HB3	1.97	0.47
26:DA:2136:C:N4	26:DA:2155:G:C6	2.82	0.47
25:CY:50:U:H2'	25:CY:51:U:C6	2.50	0.47
25:CY:35:A:H2'	25:CY:36:A:O4'	2.15	0.47
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.15	0.47
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.97	0.47
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.50	0.47
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.96	0.47
1:AA:626:U:H2'	1:AA:627:G:H8	1.78	0.47
1:CA:258:G:OP1	20:CT:86:ARG:NH1	2.48	0.47
26:DA:272:G:H4'	26:DA:272(A):U:H5''	1.97	0.47
1:AA:256:U:H2'	1:AA:257:G:C8	2.49	0.47
1:AA:1525:G:P	11:AK:120:ARG:HH22	2.37	0.47
1:AA:413:G:N2	1:AA:428:G:H1'	2.30	0.47
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:904:C:H4'	46:BZ:169:GLU:OE2	2.15	0.47
1:AA:743:U:H2'	1:AA:744:C:C6	2.50	0.47
26:DA:1600:C:OP1	44:DX:58:HIS:NE2	2.37	0.47
33:BI:47:LEU:HA	33:BI:47:LEU:HD23	1.75	0.47
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.14	0.47
2:AB:59:GLU:O	2:AB:63:MET:HG3	2.14	0.47
26:DA:2391:G:O6	26:DA:2425:A:H8	1.98	0.47
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.97	0.47
33:BI:12:LEU:HD23	33:BI:12:LEU:HA	1.79	0.47
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.24	0.47
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.42	0.47
26:DA:2153:G:C2	26:DA:2154:G:C4	3.03	0.47
26:DA:900:A:C8	26:DA:901:A:N7	2.83	0.47
26:BA:2163:C:H5'	26:BA:2163:C:C6	2.49	0.47
4:CD:103:ASN:OD1	4:CD:114:ARG:NE	2.39	0.47
1:CA:1123:A:H4'	10:CJ:37:PRO:HD2	1.96	0.47
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.96	0.47
26:BA:1745(A):C:H5'	26:BA:1746:G:OP2	2.15	0.47
2:AB:80:ILE:O	2:AB:84:GLU:HB2	2.15	0.47
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.45	0.47
3:CC:127:ARG:NH2	3:CC:192:THR:HG23	2.29	0.47
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.96	0.47
3:CC:54:ARG:H	3:CC:69:HIS:HB2	1.79	0.47
1:CA:827:U:H5''	1:CA:828:A:OP2	2.15	0.47
26:DA:613:G:O2'	26:DA:614(C):A:N1	2.40	0.47
26:BA:875:G:H2'	26:BA:876:C:O4'	2.15	0.47
6:CF:97:PHE:CE1	18:CR:62:GLU:HG2	2.50	0.47
26:BA:848:G:N9	26:BA:933:A:H8	2.11	0.47
1:CA:107:G:H2'	1:CA:108:G:O4'	2.15	0.47
26:DA:1027:A:C6	26:DA:1126:A:C4	3.03	0.47
19:AS:41:VAL:HG12	19:AS:43:GLU:H	1.80	0.47
34:DN:108:PRO:O	34:DN:113:GLY:HA3	2.15	0.47
26:DA:2841:C:H2'	26:DA:2842:G:C8	2.51	0.47
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.30	0.47
1:AA:502:G:H2'	1:AA:503:C:O4'	2.14	0.47
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.29	0.47
26:DA:955:C:OP1	37:DQ:87:LYS:HE3	2.15	0.47
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.97	0.47
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.22	0.46
25:AY:57:G:H2'	25:AY:58:A:H5'	1.97	0.46
25:AY:58:A:N6	25:AY:61:C:C2	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.46
1:AA:664:G:N2	1:AA:741:G:H1	2.03	0.46
26:BA:2134:A:HO2'	26:BA:2135:A:C5'	2.28	0.46
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.50	0.46
1:CA:1129:C:H2'	1:CA:1139:G:C5	2.49	0.46
31:DG:41:GLN:NE2	31:DG:153:ARG:HB3	2.30	0.46
1:AA:1458:G:H5''	20:AT:31:SER:HB2	1.96	0.46
24:AX:32:5MC:HM53	24:AX:33:U:O4	2.15	0.46
9:AI:79:LEU:O	9:AI:83:ARG:HG3	2.15	0.46
1:CA:447:G:O6	1:CA:485:G:O2'	2.23	0.46
26:DA:2577:A:OP2	52:D5:3:LYS:NZ	2.43	0.46
26:DA:908:C:OP2	37:DQ:22:LYS:NZ	2.48	0.46
34:DN:104:LYS:HA	34:DN:107:LEU:HD12	1.97	0.46
26:BA:1470:G:N2	26:BA:1520:G:OP2	2.36	0.46
26:DA:1628:G:H2'	26:DA:1629:U:C6	2.50	0.46
36:DP:54:GLY:O	61:DP:308:HOH:O	2.20	0.46
31:DG:107:LEU:HD21	31:DG:178:PHE:CE1	2.50	0.46
2:AB:60:ASP:OD1	2:AB:64:ARG:NH2	2.49	0.46
31:DG:122:PRO:HG3	31:DG:180:PHE:HB3	1.96	0.46
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.96	0.46
3:AC:122:GLU:O	3:AC:126:ARG:NH1	2.41	0.46
1:AA:116:A:O5'	1:AA:116:A:H8	1.97	0.46
1:AA:992:U:H4'	1:AA:993:G:H5''	1.97	0.46
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.50	0.46
1:AA:890:G:O2'	1:AA:906:G:O6	2.19	0.46
3:CC:121:ALA:HB1	3:CC:189:ALA:HB2	1.96	0.46
1:AA:1367:C:H4'	10:AJ:48:THR:HG21	1.96	0.46
20:CT:87:LYS:O	20:CT:91:LEU:HG	2.15	0.46
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.96	0.46
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.14	0.46
1:CA:1291:G:O2'	9:CI:38:GLN:HG3	2.14	0.46
26:BA:2159:G:H2'	26:BA:2160:G:C8	2.50	0.46
25:CY:35:A:C6	25:CY:36:A:C2	3.03	0.46
1:AA:405:U:H5''	1:AA:495:A:H2	1.80	0.46
1:CA:1256:A:C6	1:CA:1278:U:H1'	2.51	0.46
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.49	0.46
23:AW:50:U:H2'	23:AW:51:U:O4'	2.14	0.46
1:CA:1320:C:C1'	19:CS:73:GLU:HG2	2.46	0.46
26:BA:363(B):G:H2'	26:BA:363(C):G:H5'	1.97	0.46
47:D0:14:ARG:NH1	47:D0:14:ARG:HB2	2.30	0.46
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:110:LEU:HD13	5:AE:118:ILE:HD13	1.97	0.46
39:BS:10:ARG:O	39:BS:14:VAL:HG13	2.16	0.46
31:BG:66:GLN:HG3	51:B4:1:MET:CE	2.46	0.46
4:AD:107:ARG:NH2	4:AD:194:LEU:HD21	2.31	0.46
1:CA:59:A:H5''	1:CA:60:A:H5''	1.96	0.46
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.99	0.46
38:BR:55:ALA:HB2	38:BR:79:LEU:HD13	1.97	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.50	0.46
26:BA:839:U:H2'	26:BA:840:C:C6	2.51	0.46
1:AA:955:U:O2'	19:AS:83:HIS:HD2	1.98	0.46
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.16	0.46
26:BA:1952:A:C6	26:BA:1953:A:N1	2.83	0.46
27:BB:77:U:OP1	46:BZ:19:ARG:NH2	2.39	0.46
26:DA:293:U:H5''	26:DA:294:A:OP2	2.15	0.46
36:BP:135:LEU:HD23	36:BP:135:LEU:HA	1.71	0.46
2:AB:10:LEU:C	2:AB:12:GLU:H	2.17	0.46
43:BW:71:VAL:HA	43:BW:107:LEU:HD12	1.96	0.46
44:BX:60:ARG:HA	44:BX:75:ASP:OD2	2.16	0.46
15:AO:82:ILE:HB	15:AO:87:ILE:HB	1.96	0.46
26:DA:2127:G:OP1	26:DA:2127:G:H4'	2.15	0.46
13:CM:25:ILE:HG13	13:CM:29:ARG:HG2	1.97	0.46
1:AA:154:C:C2'	1:AA:155:C:H5'	2.45	0.46
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.98	0.46
7:CG:72:ARG:NH2	7:CG:138:LYS:HZ1	2.12	0.46
2:CB:71:VAL:HG12	2:CB:93:VAL:CG2	2.45	0.46
10:AJ:8:LEU:N	10:AJ:70:ARG:O	2.33	0.46
26:DA:1006:C:C2	26:DA:1138:G:N2	2.84	0.46
45:BY:28:LYS:HB3	45:BY:28:LYS:HE2	1.75	0.46
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.50	0.46
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.29	0.46
4:AD:18:LYS:HG2	58:AD:501:SF4:S1	2.55	0.46
26:BA:1007:C:OP1	34:BN:37:LYS:NZ	2.46	0.46
1:AA:65:U:H6	1:AA:65:U:H5'	1.80	0.46
25:AY:5:G:H2'	25:AY:6:G:C8	2.51	0.46
26:BA:2101:G:H2'	26:BA:2102:U:H6	1.80	0.46
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.15	0.46
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.30	0.46
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.50	0.46
26:BA:2162:G:C3'	26:BA:2163:C:H5''	2.46	0.46
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.80	0.46
36:DP:121:LYS:O	36:DP:123:LEU:N	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2689:U:P	26:DA:2719:G:H22	2.39	0.46
26:BA:2126:A:H4'	26:BA:2127:G:OP1	2.16	0.46
26:BA:1166:C:H2'	26:BA:1167:U:C6	2.51	0.46
24:CX:47:U:N3	24:CX:50:U:OP1	2.49	0.46
1:AA:1296:C:H5''	13:AM:14:ARG:HD2	1.96	0.46
31:BG:66:GLN:OE1	31:BG:98:ARG:NE	2.43	0.46
26:DA:242:G:C8	55:D8:5:LYS:HG2	2.51	0.46
26:BA:2562:U:O2'	35:BO:23:ARG:HD3	2.15	0.46
4:AD:187:ARG:HG2	4:AD:188:LEU:N	2.31	0.46
26:DA:2296:U:OP2	39:DS:9:ARG:NH2	2.46	0.46
31:DG:96:ARG:O	31:DG:99:MET:HB3	2.15	0.46
1:AA:316:G:OP2	1:AA:351:G:O2'	2.30	0.46
26:DA:1199:U:H2'	26:DA:1200:C:C6	2.51	0.46
26:BA:414:C:H2'	26:BA:415:A:C8	2.51	0.46
1:AA:448:A:OP2	1:AA:485:G:N1	2.33	0.46
1:AA:1090:U:H2'	1:AA:1091:U:C6	2.50	0.46
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.68	0.46
26:DA:1789:A:H2'	26:DA:1790:C:C6	2.50	0.46
9:CI:18:PHE:HD2	9:CI:62:TYR:HD2	1.63	0.46
1:CA:390:C:H2'	1:CA:391:G:C8	2.50	0.46
2:CB:87:ARG:HD3	2:CB:219:VAL:HG11	1.98	0.46
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.47	0.46
2:CB:137:ARG:HB3	2:CB:137:ARG:CZ	2.45	0.46
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.51	0.46
26:BA:2848:G:H8	40:BT:97:ALA:HB2	1.79	0.46
26:DA:852:G:H2'	26:DA:853:G:H8	1.80	0.46
26:BA:2871:C:N3	61:BA:4761:HOH:O	2.35	0.46
26:BA:234:C:H2'	26:BA:235:U:C6	2.51	0.46
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.15	0.46
30:BF:33:LEU:HB3	36:BP:6:LEU:HD21	1.98	0.46
1:AA:601:C:H2'	1:AA:602:A:C8	2.50	0.46
12:AL:52:LEU:O	12:AL:54:LYS:NZ	2.34	0.46
26:BA:1766:U:H2'	26:BA:1767:C:C6	2.51	0.46
1:CA:1390:U:H2'	1:CA:1391:U:C6	2.51	0.46
26:BA:1769:G:O2'	26:BA:1958:C:OP1	2.24	0.46
24:CX:33:U:N3	24:CX:36:U:OP2	2.48	0.46
1:AA:8:A:N6	4:AD:205:GLU:O	2.49	0.46
39:BS:110:LEU:HD12	39:BS:110:LEU:HA	1.74	0.46
23:CW:31:A:H2'	23:CW:32:PSU:O4'	2.16	0.46
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.15	0.46
1:CA:1241:G:C2'	1:CA:1242:C:H5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2712:U:OP1	26:DA:2714:G:H4'	2.16	0.46
46:DZ:5:LEU:O	46:DZ:59:LEU:HA	2.16	0.46
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.15	0.46
1:AA:1245:A:N6	1:AA:1292:U:H3	2.11	0.46
27:DB:90:A:C5	27:DB:91:C:H1'	2.51	0.46
2:AB:80:ILE:HD11	2:AB:212:GLN:CA	2.44	0.46
11:AK:91:ARG:NH1	11:AK:110:ASP:OD2	2.48	0.46
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD13	1.98	0.46
1:AA:627:G:H2'	1:AA:628:G:H8	1.81	0.46
45:BY:6:HIS:HE1	45:BY:72:VAL:O	1.99	0.46
1:AA:1286:A:H3'	1:AA:1286:A:H8	1.81	0.46
10:CJ:12:ASP:OD1	10:CJ:13:HIS:N	2.48	0.46
26:BA:2850:A:OP2	26:BA:2866:U:H5	1.98	0.46
26:DA:2648:C:H2'	26:DA:2649:U:C6	2.50	0.46
36:BP:86:LYS:HB3	36:BP:118:GLY:HA3	1.96	0.46
20:CT:26:ASN:HA	20:CT:71:THR:HG23	1.97	0.46
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.47	0.46
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.51	0.46
2:CB:76:GLN:H	2:CB:76:GLN:HG2	1.49	0.46
1:CA:841:U:H6	1:CA:841:U:OP1	1.98	0.46
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.51	0.46
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.96	0.46
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.97	0.46
25:AY:19:G:N2	25:AY:56:C:N3	2.64	0.46
2:AB:16:HIS:C	2:AB:18:GLY:H	2.14	0.46
27:DB:20:C:C2'	27:DB:21:G:H5'	2.45	0.46
5:CE:53:LEU:HD12	5:CE:53:LEU:H	1.80	0.46
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.15	0.46
4:CD:157:LEU:HD22	4:CD:161:ASN:HD21	1.80	0.46
31:DG:8:LYS:HG3	31:DG:100:TRP:CE2	2.51	0.46
13:CM:23:TYR:CE2	13:CM:70:LEU:HB3	2.50	0.46
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.46	0.46
26:BA:1047:G:H2'	26:BA:1110:G:H1	1.81	0.46
26:DA:848:G:N9	26:DA:933:A:H8	2.13	0.46
1:CA:296:U:O2'	1:CA:556:C:O2	2.25	0.46
26:DA:82:G:H5''	26:DA:296:C:H5'	1.96	0.46
32:DH:98:LEU:HD23	32:DH:125:VAL:HG23	1.97	0.46
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.51	0.46
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.15	0.46
36:BP:6:LEU:HA	36:BP:6:LEU:HD23	1.71	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.48	0.46
8:CH:111:ILE:HD11	8:CH:118:VAL:HG12	1.98	0.46
24:AX:23:C:H2'	24:AX:24:U:C6	2.51	0.46
37:DQ:108:GLY:HA3	46:DZ:116:VAL:HG13	1.96	0.46
9:CI:116:LYS:HA	9:CI:123:PRO:HD3	1.97	0.46
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.83	0.46
5:CE:39:GLY:HA2	5:CE:71:LEU:HD13	1.98	0.46
11:CK:79:SER:OG	11:CK:106:LYS:HE3	2.15	0.46
26:BA:2359:C:H2'	26:BA:2360:A:O4'	2.15	0.46
41:BU:76:TYR:CZ	41:BU:80:ILE:HG13	2.51	0.46
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.31	0.46
26:DA:1833:U:O2'	26:DA:1969:A:N1	2.38	0.46
26:DA:699:A:H4'	26:DA:1554:A:N6	2.29	0.46
1:CA:1135:U:H2'	1:CA:1137:C:N3	2.31	0.46
23:CW:4:C:C4	23:CW:69:G:N1	2.84	0.46
1:AA:1036:G:N3	1:AA:1036:G:H2'	2.31	0.46
1:CA:1392:G:N2	1:CA:1502:A:H8	2.14	0.46
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.45	0.46
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.98	0.46
1:AA:473:G:H2'	1:AA:474:G:C8	2.50	0.46
1:CA:1251:A:N1	1:CA:1354:C:O2'	2.47	0.46
1:AA:532:A:H2	1:AA:1206:G:H21	1.63	0.46
1:CA:276:G:O3'	17:CQ:68:ARG:NH1	2.48	0.46
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.30	0.46
1:CA:472:A:H5''	16:CP:80:PHE:HB3	1.98	0.46
26:DA:375:C:H2'	26:DA:376:C:C6	2.51	0.46
26:BA:45:C:OP2	26:BA:215:G:H2'	2.16	0.46
26:BA:1683:C:H2'	26:BA:1684:C:C6	2.51	0.46
33:DI:66:GLU:HA	33:DI:69:LYS:HB3	1.97	0.46
33:DI:43:ASN:C	33:DI:43:ASN:HD22	2.19	0.46
36:DP:124:LYS:HA	36:DP:144:GLU:O	2.16	0.46
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.15	0.46
26:BA:2001:A:H2'	26:BA:2002:G:C8	2.51	0.46
26:DA:2114:A:N1	26:DA:2117:A:N6	2.64	0.46
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.16	0.46
24:CX:40:C:H2'	24:CX:41:C:H6	1.81	0.46
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.50	0.46
1:CA:991:U:H3'	1:CA:1212:U:C4	2.51	0.46
36:DP:121:LYS:HD2	36:DP:123:LEU:HG	1.97	0.46
39:DS:62:LYS:HA	39:DS:65:VAL:HB	1.98	0.46
26:DA:476:G:H4'	26:DA:502:A:N1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:330:A:H2	26:BA:1210:A:O2'	1.99	0.46
1:AA:715:A:H2'	1:AA:716:A:C8	2.51	0.46
4:AD:168:ARG:H	4:AD:168:ARG:NH1	2.13	0.46
26:DA:2724:C:OP1	29:DE:118:LYS:NZ	2.33	0.46
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.51	0.46
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.15	0.46
37:BQ:1:MET:HB2	37:BQ:44:ALA:HB1	1.96	0.46
39:BS:41:ASP:OD2	39:BS:44:LYS:NZ	2.42	0.46
1:CA:1368:G:C2'	1:CA:1369:C:H5'	2.46	0.46
28:BD:10:THR:OG1	28:BD:13:ARG:HG2	2.16	0.46
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.98	0.46
2:AB:119:GLU:OE1	2:AB:153:ARG:NH2	2.49	0.46
28:DD:242:ARG:N	28:DD:242:ARG:HD3	2.31	0.46
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.16	0.46
28:DD:5:LYS:HE3	28:DD:5:LYS:HB3	1.66	0.46
26:DA:1418:G:O5'	26:DA:1418:G:H8	1.99	0.46
2:CB:23:ARG:H	2:CB:23:ARG:HG2	1.53	0.46
55:D8:8:LYS:HB3	55:D8:12:LYS:HE3	1.98	0.46
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.97	0.46
10:CJ:7:LYS:HA	10:CJ:71:LEU:HD12	1.98	0.46
2:CB:122:PHE:HA	2:CB:127:ILE:HD12	1.98	0.46
27:DB:14:U:O3'	27:DB:108:U:O2'	2.33	0.46
1:CA:1310:G:P	13:CM:88:ARG:HH22	2.39	0.46
26:BA:1021:A:H8	26:BA:1021:A:H3'	1.79	0.46
39:DS:35:ILE:HD12	39:DS:101:LEU:HD12	1.98	0.46
26:DA:2191:G:H2'	26:DA:2192:G:O4'	2.16	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
26:DA:330:A:H2	26:DA:1210:A:H2'	1.80	0.46
26:BA:1420:U:HO2'	26:BA:1421:G:P	2.38	0.46
31:BG:163:ALA:HB1	31:BG:168:GLU:HB2	1.98	0.46
26:DA:1366:A:H2'	26:DA:1367:A:O4'	2.16	0.46
26:DA:855:G:H2'	26:DA:856:C:C6	2.51	0.46
23:AW:2:C:H2'	23:AW:3:C:H6	1.81	0.46
26:DA:863:A:H2'	26:DA:864:G:C8	2.51	0.46
5:CE:41:VAL:O	5:CE:66:MET:HA	2.15	0.46
1:AA:99:U:H2'	1:AA:100:C:C6	2.50	0.46
46:BZ:70:LEU:HG	46:BZ:91:LEU:HD21	1.98	0.46
26:DA:27:G:N2	26:DA:512:G:H1'	2.31	0.46
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.15	0.46
29:DE:143:ASN:HD22	29:DE:147:PRO:HD3	1.80	0.46
44:DX:94:GLY:N	44:DX:95:LEU:HA	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.81	0.46
26:BA:879:G:O5'	26:BA:879:G:H8	1.98	0.46
40:DT:6:LEU:HA	40:DT:6:LEU:HD12	1.80	0.46
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.97	0.46
1:CA:337:C:H2'	1:CA:338:A:H8	1.81	0.46
10:CJ:5:ARG:N	10:CJ:72:VAL:O	2.48	0.45
25:CY:33:U:H2'	25:CY:35:A:OP2	2.16	0.45
26:BA:956:G:OP2	37:BQ:87:LYS:NZ	2.42	0.45
1:CA:1126:U:C4'	1:CA:1281:U:H1'	2.45	0.45
1:CA:532:A:N6	3:CC:193:TYR:HB3	2.25	0.45
1:CA:427:U:P	4:CD:13:ARG:HH22	2.39	0.45
2:CB:112:VAL:O	2:CB:115:LEU:HD23	2.17	0.45
1:AA:134:A:N1	16:AP:25:ARG:NH1	2.65	0.45
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.15	0.45
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.16	0.45
19:CS:22:LEU:O	19:CS:27:GLU:HG3	2.16	0.45
50:D3:5:LYS:HB3	50:D3:57:GLU:HG2	1.98	0.45
3:CC:50:ALA:HB1	3:CC:70:VAL:HG21	1.98	0.45
28:BD:68:LYS:O	28:BD:69:ARG:HB2	2.16	0.45
1:AA:373:A:H2'	1:AA:374:A:H8	1.80	0.45
1:AA:198:G:H2'	1:AA:199:G:H8	1.81	0.45
21:AU:18:TYR:CD1	21:AU:24:ARG:HG2	2.51	0.45
34:BN:4:TYR:HB2	41:BU:101:ARG:HH12	1.81	0.45
40:DT:42:ILE:HG12	40:DT:84:GLN:NE2	2.31	0.45
5:CE:110:LEU:HD13	5:CE:118:ILE:HD13	1.97	0.45
26:BA:2074:U:H2'	26:BA:2075:U:C6	2.51	0.45
26:DA:992:C:OP1	42:DV:74:LYS:NZ	2.33	0.45
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.51	0.45
29:DE:47:VAL:HG11	29:DE:86:PRO:HD2	1.98	0.45
1:AA:864:A:H2'	1:AA:865:A:C8	2.51	0.45
26:DA:2507:C:H5''	26:DA:2573:C:N4	2.31	0.45
26:DA:2378:A:H8	26:DA:2378:A:O5'	1.98	0.45
33:BI:61:ARG:HD2	33:BI:61:ARG:N	2.31	0.45
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.45	0.45
26:BA:1814:G:H4'	28:BD:51:VAL:HG21	1.99	0.45
26:DA:2167:U:H2'	26:DA:2167:U:O2	2.15	0.45
1:CA:1096:C:H2'	1:CA:1097:C:H6	1.81	0.45
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.16	0.45
25:AY:48:C:OP1	25:AY:48:C:H2'	2.16	0.45
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.51	0.45
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:885:C:H3'	26:BA:886:C:C5'	2.44	0.45
55:B8:6:THR:HG22	55:B8:62:LEU:HA	1.98	0.45
1:AA:166:G:H2'	1:AA:167:G:H8	1.79	0.45
26:DA:288:C:H2'	26:DA:289:A:H8	1.80	0.45
26:BA:2791:C:H2'	26:BA:2792:G:H8	1.81	0.45
1:CA:727:G:P	1:CA:742:G:H21	2.39	0.45
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.46	0.45
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.88	0.45
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.98	0.45
26:BA:2732:G:H3'	26:BA:2733:A:O4'	2.17	0.45
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.98	0.45
6:CF:87:ARG:CB	6:CF:87:ARG:HH11	2.29	0.45
1:CA:1008:C:H2'	1:CA:1009:G:O4'	2.16	0.45
26:DA:597:U:H2'	26:DA:598:G:C8	2.51	0.45
26:DA:921:G:C6	26:DA:922:U:C4	3.04	0.45
26:BA:740:U:H2'	26:BA:741:G:C8	2.51	0.45
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.98	0.45
1:AA:236:G:H5''	17:AQ:42:TYR:OH	2.16	0.45
13:AM:68:GLY:HA3	31:BG:116:ASP:OD1	2.16	0.45
29:DE:27:LEU:HD22	40:DT:1:MET:CE	2.46	0.45
1:CA:696:A:H8	1:CA:696:A:O5'	1.99	0.45
1:AA:323:U:H5'	20:AT:23:ARG:HB2	1.98	0.45
26:DA:2149:G:H5''	26:DA:2150:U:OP2	2.17	0.45
25:CY:10:G:N2	25:CY:25:C:N3	2.54	0.45
25:CY:35:A:H8	25:CY:35:A:O5'	1.98	0.45
1:AA:1038:C:O2'	1:AA:1039:C:H5'	2.17	0.45
1:CA:456:C:C2'	1:CA:457:C:H5'	2.46	0.45
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.49	0.45
1:CA:67:C:O2'	1:CA:171:A:N3	2.37	0.45
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.30	0.45
23:CW:22:G:C2	23:CW:23:A:C5	3.04	0.45
26:BA:141:A:H8	26:BA:1408:C:O2'	1.99	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.99	0.45
26:DA:271(H):G:O2'	26:DA:271(I):G:H8	2.00	0.45
30:BF:64:ILE:HG21	30:BF:78:ILE:HG23	1.96	0.45
25:AY:2:C:N4	25:AY:71:G:H1	2.14	0.45
26:BA:2180:U:H2'	26:BA:2181:G:O4'	2.17	0.45
4:AD:187:ARG:HB3	4:AD:187:ARG:HE	1.53	0.45
26:DA:1417:C:H3'	61:DA:4108:HOH:O	2.16	0.45
26:DA:2543:G:H2'	26:DA:2544:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2010:G:H5''	43:BW:42:ARG:HB2	1.97	0.45
1:CA:620:C:H2'	1:CA:621:A:O4'	2.17	0.45
9:CI:45:ALA:O	9:CI:48:GLU:HB2	2.16	0.45
2:AB:222:ILE:O	2:AB:226:ARG:HG2	2.16	0.45
19:CS:63:THR:O	19:CS:66:MET:HG3	2.16	0.45
1:AA:11:G:O2'	1:AA:506:G:N2	2.46	0.45
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.53	0.45
26:DA:1213:A:N3	26:DA:1238:G:O2'	2.46	0.45
26:BA:2747:G:O6	26:BA:2755:C:H5''	2.16	0.45
46:DZ:43:GLU:O	46:DZ:47:VAL:N	2.50	0.45
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.51	0.45
1:CA:1062:U:H2'	1:CA:1063:C:C5	2.51	0.45
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.80	0.45
31:DG:66:GLN:HE21	31:DG:92:VAL:HG23	1.82	0.45
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.85	0.45
26:DA:1654:A:OP1	38:DR:1:MET:HA	2.15	0.45
1:AA:163:C:H2'	1:AA:164:U:C6	2.51	0.45
43:BW:88:ARG:HD2	43:BW:88:ARG:HA	1.76	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.16	0.45
1:CA:110:C:O2'	16:CP:25:ARG:O	2.27	0.45
10:AJ:8:LEU:HD21	10:AJ:96:ILE:HG23	1.98	0.45
51:B4:41:PRO:HA	51:B4:47:GLN:HB3	1.98	0.45
40:DT:51:ARG:HG3	40:DT:98:LYS:NZ	2.32	0.45
1:AA:735:C:H2'	1:AA:736:C:C6	2.52	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
46:DZ:23:LYS:NZ	46:DZ:40:ASP:OD1	2.48	0.45
41:BU:76:TYR:CE1	41:BU:80:ILE:HG13	2.52	0.45
49:D2:62:THR:O	49:D2:66:GLU:HG3	2.16	0.45
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.99	0.45
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.16	0.45
35:BO:98:VAL:HG13	35:BO:117:LEU:HB3	1.97	0.45
26:DA:536:A:H2'	26:DA:537:C:C6	2.51	0.45
26:DA:2659:G:O2'	26:DA:2661:G:N7	2.38	0.45
1:CA:859:A:H2'	1:CA:860:A:O4'	2.16	0.45
1:CA:652:U:O4	1:CA:752:G:O2'	2.21	0.45
12:CL:37:CYS:SG	12:CL:81:SER:HB2	2.56	0.45
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.17	0.45
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.97	0.45
26:BA:2340:G:H2'	26:BA:2341:G:H8	1.81	0.45
13:AM:113:PRO:O	13:AM:115:LYS:NZ	2.50	0.45
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:49:GLU:OE2	8:AH:62:TYR:OH	2.26	0.45
1:AA:1055:A:H2'	3:AC:156:ARG:HD2	1.99	0.45
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.69	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.80	0.45
26:DA:2153:G:H3'	26:DA:2154:G:C8	2.51	0.45
26:BA:2191:G:C8	26:BA:2191:G:H5'	2.50	0.45
25:CY:36:A:H2'	25:CY:37:MIA:O4'	2.16	0.45
31:DG:106:LEU:HA	31:DG:110:ALA:CB	2.45	0.45
1:AA:161:A:H2'	1:AA:162:A:C8	2.52	0.45
26:DA:527:C:H4'	26:DA:528:A:O5'	2.15	0.45
1:CA:1347:G:O2'	1:CA:1373:G:N1	2.47	0.45
26:BA:1045:A:H1'	26:BA:1047:G:C2	2.51	0.45
1:CA:920:U:H2'	1:CA:921:U:H6	1.80	0.45
26:DA:71:A:H5''	26:DA:73:A:C8	2.51	0.45
26:DA:1667:G:O2'	26:DA:1991:U:O4	2.31	0.45
17:AQ:78:GLU:HG2	17:AQ:79:SER:H	1.81	0.45
33:DI:69:LYS:HG3	33:DI:73:GLU:OE1	2.16	0.45
8:AH:29:SER:OG	8:AH:32:LYS:HG3	2.17	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
42:DV:89:GLN:HA	42:DV:90:PRO:HD3	1.83	0.45
43:BW:18:ARG:NH1	43:BW:76:VAL:O	2.50	0.45
26:BA:582:G:H2'	26:BA:583:G:C8	2.52	0.45
26:DA:652:C:C2'	26:DA:652(A):A:H5'	2.46	0.45
24:CX:22:G:H8	24:CX:22:G:OP2	2.00	0.45
24:AX:4:G:H1	24:AX:69:C:H42	1.64	0.45
38:DR:70:LEU:HD13	38:DR:75:LEU:HD13	1.98	0.45
1:CA:399:G:H2'	1:CA:400:C:C6	2.51	0.45
30:DF:12:LEU:HB2	30:DF:124:LEU:HD11	1.97	0.45
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.45
28:BD:24:ILE:HD13	28:BD:84:TYR:HB2	1.99	0.45
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.80	0.45
1:CA:1320:C:H2'	1:CA:1321:C:O4'	2.17	0.45
1:CA:1121:U:C4	1:CA:1122:U:C5	3.05	0.45
9:CI:9:ARG:HA	9:CI:13:ALA:O	2.17	0.45
26:DA:2207:G:H8	26:DA:2207:G:P	2.40	0.45
23:AW:9:A:O2'	23:AW:10:G:N7	2.49	0.45
26:BA:8:A:H2'	26:BA:9:U:C6	2.52	0.45
26:DA:1527:G:H5''	26:DA:1528:A:OP1	2.16	0.45
1:CA:429:U:O3'	4:CD:22:LYS:NZ	2.45	0.45
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.57	0.45
13:CM:57:ARG:O	13:CM:61:GLU:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:175:C:H2'	1:AA:176:C:H6	1.80	0.45
28:DD:141:VAL:HG12	28:DD:164:GLN:HG3	1.99	0.45
26:BA:27:G:N2	26:BA:512:G:H1'	2.32	0.45
26:DA:2120:G:O6	26:DA:2178:C:N3	2.49	0.45
26:BA:747:U:O2	26:BA:2014:A:H1'	2.17	0.45
44:DX:44:GLU:OE2	44:DX:51:VAL:N	2.45	0.45
26:BA:2803:C:H2'	26:BA:2804:C:C6	2.51	0.45
52:D5:40:LYS:NZ	52:D5:44:THR:O	2.34	0.45
29:DE:54:GLN:HB2	29:DE:76:ARG:HG2	1.98	0.45
1:AA:850:U:H2'	1:AA:851:G:H5'	1.98	0.45
42:DV:12:TYR:CG	42:DV:20:LEU:HD21	2.52	0.45
21:CU:12:LYS:HZ2	21:CU:19:GLY:HA3	1.81	0.45
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.16	0.45
26:DA:2468:G:C4	26:DA:2481:G:C2	3.05	0.45
26:DA:2494:G:O2'	37:DQ:80:GLU:HA	2.16	0.45
1:CA:1385:G:H2'	1:CA:1386:G:C8	2.51	0.45
54:D7:5:TRP:CD1	54:D7:7:PRO:HD3	2.50	0.45
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.70	0.45
14:CN:32:SER:OG	14:CN:32:SER:O	2.28	0.45
1:AA:17:U:H2'	1:AA:18:C:C6	2.52	0.45
26:DA:1876:A:H2'	26:DA:1877:A:C8	2.52	0.45
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.31	0.45
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.97	0.45
1:CA:985:C:N4	1:CA:1220:G:N1	2.29	0.45
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.99	0.45
1:CA:1036:G:N7	1:CA:1037:C:C2	2.85	0.45
2:AB:19:HIS:CD2	2:AB:206:ASP:HB2	2.52	0.45
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.71	0.45
1:CA:660:G:H1	1:CA:745:C:N4	2.12	0.45
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.99	0.45
26:DA:848:G:C2	26:DA:933:A:H1'	2.52	0.45
1:CA:411:A:OP1	4:CD:30:LYS:HD3	2.16	0.45
1:AA:375:U:O2'	16:AP:6:LEU:O	2.32	0.45
23:CW:10:G:N2	23:CW:11:C:C2	2.84	0.45
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.52	0.45
1:AA:688:G:H2'	1:AA:689:C:C6	2.52	0.45
30:BF:125:LEU:HD12	30:BF:194:MET:HB2	1.98	0.45
1:AA:881:G:P	12:AL:12:ARG:HH22	2.40	0.45
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	2.17	0.45
24:AX:4:G:H2'	24:AX:5:G:C8	2.52	0.45
24:CX:5:G:H2'	24:CX:6:G:H5'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:48:MET:HA	2:AB:51:LEU:HD12	1.97	0.45
45:DY:90:LEU:HD11	45:DY:96:ILE:HG23	1.98	0.45
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.17	0.45
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.52	0.45
26:BA:592:G:O6	61:BA:4916:HOH:O	2.15	0.45
1:AA:407:G:O2'	4:AD:116:GLN:HG3	2.17	0.45
4:AD:144:ASP:N	4:AD:144:ASP:OD1	2.49	0.45
26:DA:620:G:H5'	26:DA:620:G:N3	2.31	0.45
26:BA:405:U:O5'	26:BA:405:U:H6	1.99	0.45
32:DH:95:ARG:HG2	32:DH:96:ALA:N	2.32	0.45
1:AA:445:G:H2'	1:AA:446:G:C8	2.52	0.45
1:CA:419:C:OP1	1:CA:513:C:O2'	2.25	0.45
26:BA:1430:C:H2'	26:BA:1431:U:C6	2.51	0.45
26:DA:2138:C:N4	26:DA:2153:G:N1	2.32	0.45
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.82	0.45
51:D4:40:HIS:O	51:D4:44:THR:N	2.24	0.45
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.37	0.45
26:BA:2168:G:O6	26:BA:2171:A:H2'	2.16	0.45
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.98	0.45
27:DB:34:U:O4	27:DB:44:G:O2'	2.29	0.45
26:BA:2312:U:OP1	31:BG:73:ALA:HA	2.17	0.45
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.17	0.45
2:CB:70:PHE:HB2	2:CB:92:TYR:CB	2.47	0.45
28:BD:70:TRP:CE2	28:BD:150:LYS:HD3	2.52	0.45
1:CA:826:C:H2'	1:CA:827:U:C6	2.51	0.45
26:DA:2328:A:H2'	26:DA:2329:G:C8	2.52	0.45
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.70	0.45
1:CA:1490:C:H2'	1:CA:1491:G:O4'	2.17	0.45
48:B1:3:LYS:HB3	48:B1:4:VAL:H	1.50	0.45
26:BA:2011:U:OP1	43:BW:42:ARG:HD3	2.17	0.45
28:BD:232:PRO:O	61:BD:3103:HOH:O	2.21	0.45
52:D5:33:CYS:HA	52:D5:34:PRO:HD3	1.85	0.45
55:B8:33:ASN:HA	55:B8:36:LYS:HD2	1.99	0.45
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.82	0.45
28:DD:171:ASP:O	28:DD:187:GLY:N	2.49	0.45
26:DA:2461:C:H2'	26:DA:2462:U:C6	2.52	0.45
1:AA:217:C:C2'	1:AA:218:C:H5'	2.46	0.45
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.52	0.45
26:DA:271(K):U:O2	33:DI:50:ARG:HG3	2.17	0.45
26:BA:675:A:C8	26:BA:804:A:C6	3.05	0.45
26:BA:95:G:O2'	49:B2:48:HIS:ND1	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BE:31:CYS:HA	29:BE:32:PRO:HD2	1.89	0.45
1:CA:1205:U:H4'	3:CC:195:VAL:HG23	1.98	0.45
34:BN:68:GLU:H	34:BN:68:GLU:HG2	1.46	0.45
4:CD:8:VAL:O	4:CD:11:LEU:HB2	2.17	0.45
32:DH:148:ILE:HG12	32:DH:148:ILE:H	1.54	0.45
26:BA:2640:G:OP1	34:BN:97:ARG:NH2	2.49	0.45
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.99	0.45
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.52	0.45
19:CS:30:LEU:HA	19:CS:48:THR:O	2.16	0.45
1:CA:982:U:H4'	1:CA:983:A:O5'	2.17	0.45
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.17	0.45
31:DG:171:ALA:O	31:DG:175:LEU:N	2.37	0.45
24:CX:10:G:N2	24:CX:26:G:H1'	2.31	0.45
26:DA:297:C:OP1	45:DY:87:LYS:HG3	2.17	0.45
26:DA:1165:U:H2'	26:DA:1166:C:C6	2.51	0.45
26:DA:2365:G:P	47:D0:55:ARG:HG2	2.57	0.45
1:CA:376:G:O2'	16:CP:5:ARG:NH2	2.50	0.45
1:CA:1253:G:H2'	1:CA:1254:C:C6	2.52	0.45
26:DA:862:G:H2'	26:DA:863:A:O4'	2.16	0.45
3:AC:156:ARG:HE	3:AC:156:ARG:HB3	1.50	0.45
26:DA:2263:C:H2'	26:DA:2264:C:O4'	2.17	0.45
26:DA:2872:G:C2	26:DA:2873:A:N6	2.85	0.45
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.44	0.45
26:BA:1501:C:O4'	28:BD:100:GLY:HA2	2.17	0.45
1:AA:678:U:H2'	1:AA:679:C:C6	2.52	0.45
3:AC:108:ASN:HB3	3:AC:111:LEU:HD12	1.99	0.45
3:CC:40:ARG:NH1	3:CC:57:ILE:HD13	2.32	0.45
1:CA:6:G:H4'	1:CA:298:A:H4'	1.98	0.45
26:DA:1287:A:C5	26:DA:1288:U:C4	3.05	0.45
26:BA:127:A:H5''	26:BA:128:C:C6	2.52	0.45
30:DF:156:LEU:HD21	30:DF:163:VAL:HG12	1.98	0.45
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	1.99	0.45
33:DI:141:LYS:HZ2	33:DI:141:LYS:HB2	1.82	0.45
26:DA:34:C:H2'	26:DA:34:C:O2	2.17	0.45
29:DE:24:THR:HG22	29:DE:184:VAL:HG12	1.98	0.45
26:BA:245:G:O5'	36:BP:73:GLY:HA2	2.16	0.45
28:BD:52:ARG:NH2	61:BD:3112:HOH:O	2.42	0.45
1:CA:502:G:C2	1:CA:503:C:C2	3.05	0.45
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.05	0.45
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.45
26:BA:587:C:P	36:BP:21:ARG:HH22	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:184:TYR:CE2	30:BF:188:ARG:HD2	2.52	0.45
13:AM:15:VAL:O	13:AM:19:LEU:HD22	2.17	0.45
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.17	0.45
26:DA:1031:G:H21	56:D9:36:GLN:HE22	1.63	0.45
2:CB:71:VAL:HG23	2:CB:71:VAL:O	2.17	0.45
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.15	0.45
26:DA:1588:C:H2'	26:DA:1589:C:H6	1.82	0.45
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.99	0.45
25:AY:13:C:H2'	25:AY:14:A:H8	1.82	0.45
44:DX:31:HIS:HA	44:DX:32:PRO:HD3	1.87	0.45
31:DG:166:ASP:O	31:DG:170:ARG:N	2.46	0.45
27:DB:73:A:C4	27:DB:105:A:C2	3.04	0.45
1:CA:65:U:H5'	1:CA:65:U:H6	1.81	0.45
1:CA:25:C:H5'	1:CA:524:G:H1'	1.98	0.45
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.45
23:CW:38:A:H5'	26:DA:1913:A:N6	2.32	0.45
26:DA:1131:G:O6	26:DA:2040:C:H1'	2.17	0.45
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.52	0.45
43:DW:2:GLU:OE2	43:DW:72:LYS:HE2	2.17	0.45
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.48	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.17	0.45
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.99	0.45
28:BD:20:ASP:OD2	28:BD:22:SER:HB2	2.17	0.45
17:CQ:63:ARG:HG2	17:CQ:64:PRO:HD2	1.99	0.45
26:BA:574:C:N3	29:BE:145:LYS:NZ	2.51	0.45
26:BA:2246:G:H2'	26:BA:2247:A:C8	2.52	0.45
1:CA:1206:G:C6	1:CA:1207:G:C5	3.05	0.45
48:B1:67:ILE:N	48:B1:68:PRO:HD2	2.31	0.45
31:BG:150:ASP:OD1	31:BG:150:ASP:N	2.46	0.45
13:AM:108:ARG:HD3	13:AM:108:ARG:HA	1.66	0.45
26:BA:11:G:H2'	26:BA:12:U:H5''	1.98	0.45
41:DU:76:TYR:HH	41:DU:92:ARG:NH1	2.12	0.44
36:BP:65:ARG:HG3	55:B8:25:MET:CG	2.46	0.44
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.51	0.44
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.44
1:CA:1120:G:N1	1:CA:1154:G:N3	2.65	0.44
1:CA:1015:A:H4'	14:CN:15:LYS:NZ	2.33	0.44
26:DA:2356:C:O3'	47:D0:20:ARG:HD3	2.17	0.44
1:AA:345:C:O5'	1:AA:345:C:H6	2.00	0.44
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.18	0.44
26:DA:971:C:H2'	26:DA:972:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:47:U:O2'	23:CW:48:C:OP1	2.29	0.44
1:CA:1084:G:C5	1:CA:1085:U:C4	3.05	0.44
1:CA:606:G:H5''	1:CA:607:A:H5'	1.99	0.44
1:AA:750:G:H1'	15:AO:22:THR:HG23	1.99	0.44
51:B4:48:ARG:HB3	51:B4:51:ASP:O	2.17	0.44
23:AW:4:C:N3	23:AW:69:G:O6	2.50	0.44
7:CG:155:ARG:HG2	7:CG:156:TRP:N	2.32	0.44
1:AA:1161:C:O2'	1:AA:1162:C:H5'	2.18	0.44
14:AN:14:PRO:HG2	14:AN:20:ALA:HB2	1.98	0.44
26:DA:1913:A:H4'	26:DA:1914:C:H5''	1.98	0.44
26:DA:2727:G:O2'	35:DO:70:LYS:NZ	2.51	0.44
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.55	0.44
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.17	0.44
45:DY:3:VAL:HB	45:DY:32:PRO:HB3	2.00	0.44
19:AS:36:ARG:NH1	19:AS:52:TYR:O	2.48	0.44
26:DA:751:A:H5'	43:DW:90:ARG:HA	1.98	0.44
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.44
26:BA:817:C:H4'	26:BA:932:G:C5	2.52	0.44
36:DP:95:VAL:HG13	36:DP:125:VAL:HG12	1.98	0.44
23:AW:61:C:H2'	23:AW:62:C:H6	1.82	0.44
1:CA:382:A:H2'	1:CA:383:A:C8	2.52	0.44
6:AF:55:ASP:HA	6:AF:56:PRO:HD3	1.84	0.44
31:DG:152:LEU:HD12	31:DG:152:LEU:H	1.82	0.44
43:DW:17:VAL:HG11	43:DW:103:ILE:HD11	1.98	0.44
1:CA:154:C:H2'	1:CA:155:C:C6	2.52	0.44
25:AY:6:G:C6	25:AY:7:A:C5	3.05	0.44
1:CA:848:C:O5'	1:CA:848:C:H6	2.00	0.44
26:BA:2130:U:H2'	26:BA:2131:G:H21	1.82	0.44
26:DA:1021:A:C8	26:DA:1021:A:H3'	2.52	0.44
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.52	0.44
2:CB:162:ILE:HG13	2:CB:162:ILE:O	2.15	0.44
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.98	0.44
46:DZ:79:ARG:HD2	46:DZ:80:ARG:NH2	2.32	0.44
27:BB:91:C:OP1	37:BQ:16:ARG:HG3	2.18	0.44
26:BA:971:C:O2'	26:BA:983:A:N3	2.40	0.44
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.51	0.44
19:AS:9:VAL:HG21	51:B4:61:ARG:HH12	1.82	0.44
30:BF:8:GLN:HA	30:BF:8:GLN:NE2	2.32	0.44
9:CI:16:ARG:HB2	9:CI:64:THR:HG23	1.99	0.44
1:AA:114:U:H1'	1:AA:353:A:H1'	1.99	0.44
1:CA:683:G:H2'	1:CA:684:A:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.50	0.44
1:AA:100:C:H2'	1:AA:101:A:C8	2.52	0.44
26:DA:921:G:H4'	26:DA:2269:A:C5	2.51	0.44
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.16	0.44
39:BS:27:SER:HA	39:BS:88:ASP:HB3	1.98	0.44
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.18	0.44
6:CF:100:ASN:HD21	18:CR:23:LYS:HG2	1.83	0.44
29:BE:149:ARG:O	61:BE:406:HOH:O	2.21	0.44
26:BA:372:G:H8	48:B1:65:SER:O	2.00	0.44
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.16	0.44
2:CB:167:PRO:HG3	2:CB:188:ALA:HB2	1.98	0.44
26:BA:2260:C:H2'	26:BA:2261:C:H6	1.82	0.44
26:BA:686:G:H8	54:B7:6:GLN:O	2.00	0.44
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.58	0.44
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.17	0.44
26:DA:774:A:N3	26:DA:774:A:H2'	2.33	0.44
9:AI:102:LEU:HD22	9:AI:102:LEU:HA	1.85	0.44
17:AQ:92:ARG:HD2	17:AQ:92:ARG:HA	1.92	0.44
33:DI:77:LEU:HD11	33:DI:97:ILE:HG23	1.99	0.44
1:AA:431:A:H2'	1:AA:432:A:O4'	2.18	0.44
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.81	0.44
26:DA:1583:A:H4'	26:DA:1586:A:C4	2.52	0.44
26:DA:776:G:H4'	26:DA:777:A:O5'	2.17	0.44
8:AH:56:LYS:HB2	8:AH:58:TYR:HE1	1.81	0.44
35:DO:76:ALA:HB3	40:DT:75:ILE:HB	1.99	0.44
3:CC:85:ARG:O	3:CC:89:GLU:HG3	2.17	0.44
25:CY:67:C:H2'	25:CY:68:C:C6	2.52	0.44
1:CA:1001(A):G:H5''	1:CA:1002:G:OP2	2.17	0.44
25:CY:51:U:N3	25:CY:63:G:N1	2.41	0.44
14:CN:40:CYS:O	14:CN:44:LEU:HB3	2.18	0.44
1:CA:1131:G:H2'	1:CA:1132:C:H6	1.82	0.44
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.83	0.44
37:DQ:134:ARG:CZ	46:DZ:122:ARG:HE	2.30	0.44
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.31	0.44
1:AA:110:C:H2'	1:AA:111:G:O4'	2.18	0.44
32:BH:124:GLU:OE1	32:BH:132:ARG:HD2	2.18	0.44
26:DA:902:C:H2'	26:DA:903:C:H6	1.82	0.44
24:AX:46:G:H5''	24:AX:47:U:OP2	2.16	0.44
26:BA:226:G:N2	26:BA:228:A:H62	2.15	0.44
1:CA:743:U:H2'	1:CA:744:C:C6	2.52	0.44
31:BG:43:LEU:HD12	31:BG:43:LEU:HA	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:45:A:H2'	27:DB:46:A:H8	1.82	0.44
1:CA:1239:A:H4'	1:CA:1240:U:H5''	1.98	0.44
19:CS:33:THR:HG22	19:CS:50:ALA:O	2.17	0.44
14:CN:45:ARG:O	14:CN:49:HIS:HD2	1.99	0.44
39:BS:6:ALA:O	39:BS:10:ARG:HB2	2.17	0.44
1:CA:715:A:H5''	1:CA:805:C:H1'	1.99	0.44
26:DA:752:A:H4'	26:DA:753:C:H5'	1.99	0.44
11:CK:66:LEU:O	11:CK:70:LYS:HD2	2.18	0.44
4:AD:18:LYS:HD2	4:AD:31:CYS:SG	2.57	0.44
2:AB:219:VAL:O	2:AB:223:ILE:HG12	2.16	0.44
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	2.00	0.44
26:DA:2441:C:OP2	26:DA:2586:C:O2'	2.31	0.44
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.99	0.44
1:CA:437:U:O2'	4:CD:125:HIS:HE1	1.99	0.44
36:DP:37:GLY:O	36:DP:40:SER:OG	2.22	0.44
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.18	0.44
1:CA:543:C:O2'	1:CA:544:G:H5'	2.17	0.44
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.53	0.44
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.51	0.44
30:BF:165:ARG:HG2	30:BF:168:ARG:HH21	1.82	0.44
31:DG:3:LEU:HD23	31:DG:3:LEU:H	1.81	0.44
26:BA:2790:A:N3	26:BA:2790:A:H2'	2.31	0.44
26:BA:796:C:H2'	26:BA:797:C:C6	2.52	0.44
26:DA:1030:G:OP2	37:DQ:128:LYS:HD3	2.17	0.44
1:CA:1004:A:C2	1:CA:1038:C:C4	3.05	0.44
26:BA:1178:C:O5'	26:BA:1178:C:H6	2.00	0.44
1:CA:1134:G:C6	1:CA:1135:U:C2	3.05	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
1:CA:1016:A:O2'	1:CA:1217:C:O2'	2.14	0.44
27:BB:91:C:OP2	37:BQ:16:ARG:NH1	2.51	0.44
33:BI:38:LEU:H	33:BI:38:LEU:CD1	2.23	0.44
26:DA:1999:C:H4'	26:DA:2723:C:O2	2.17	0.44
27:DB:33:G:N3	27:DB:50:G:N2	2.66	0.44
1:CA:994:A:C5	1:CA:1216:G:H4'	2.53	0.44
26:DA:2192:G:H5'	26:DA:2193:G:OP2	2.17	0.44
13:CM:13:LYS:HA	13:CM:44:ARG:NH1	2.33	0.44
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.17	0.44
47:D0:14:ARG:HH11	47:D0:14:ARG:HB2	1.83	0.44
26:DA:1406:U:H2'	26:DA:1407:C:C6	2.52	0.44
1:AA:21:G:H2'	1:AA:22:G:C8	2.53	0.44
1:AA:1057:G:H2'	1:AA:1058:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1085:U:H3'	1:CA:1086:U:C5	2.52	0.44
7:CG:78:ARG:CZ	7:CG:79:ARG:HH22	2.30	0.44
30:DF:187:VAL:HG12	36:DP:3:LEU:HD12	1.99	0.44
30:DF:24:LEU:HD21	30:DF:114:VAL:HG12	1.99	0.44
26:DA:2611:U:OP2	26:DA:2611:U:H3'	2.18	0.44
5:AE:27:ARG:HB2	5:AE:27:ARG:HE	1.53	0.44
1:CA:814:A:N7	1:CA:816:A:C4	2.85	0.44
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.83	0.44
34:DN:103:VAL:O	34:DN:107:LEU:HG	2.17	0.44
26:BA:1009:A:OP2	34:BN:37:LYS:NZ	2.50	0.44
1:AA:217:C:O2'	1:AA:218:C:H5'	2.17	0.44
17:AQ:60:ILE:O	17:AQ:62:SER:OG	2.34	0.44
26:DA:1129:A:N6	26:DA:2491:U:OP1	2.50	0.44
8:CH:125:ARG:HE	8:CH:125:ARG:HB2	1.49	0.44
1:AA:435:C:H6	1:AA:435:C:O5'	2.01	0.44
1:CA:90:U:O2'	1:CA:91:C:H5'	2.18	0.44
26:DA:87:C:H5''	26:DA:88:G:H5'	1.99	0.44
10:AJ:33:GLN:O	10:AJ:75:ILE:N	2.44	0.44
25:AY:57:G:H2'	25:AY:58:A:C5'	2.48	0.44
26:BA:2191:G:H2'	26:BA:2192:G:O4'	2.17	0.44
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.18	0.44
1:CA:1132:C:H2'	1:CA:1133:G:C8	2.52	0.44
1:CA:878:G:OP1	8:CH:88:LYS:HB3	2.17	0.44
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.63	0.44
52:B5:16:ARG:HD2	52:B5:20:ARG:NH1	2.31	0.44
26:DA:2286:A:H4'	26:DA:2287:A:O4'	2.17	0.44
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.37	0.44
1:CA:947:G:C6	1:CA:948:C:C4	3.06	0.44
26:DA:2274:A:C5	26:DA:2276:G:C8	3.05	0.44
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.99	0.44
30:DF:140:LEU:HD13	30:DF:170:LEU:HD21	1.99	0.44
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.18	0.44
11:CK:66:LEU:HB3	11:CK:70:LYS:HZ2	1.82	0.44
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.48	0.44
26:BA:637:A:H8	36:BP:117:GLU:HG3	1.82	0.44
26:BA:187:G:OP2	61:BA:4447:HOH:O	2.21	0.44
26:DA:1235:G:C6	26:DA:1236:G:N1	2.85	0.44
11:AK:34:ASP:HB3	11:AK:40:ILE:HD11	1.99	0.44
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.16	0.44
26:BA:2028:U:H2'	26:BA:2029:G:O4'	2.18	0.44
1:CA:1113:C:H42	1:CA:1187:G:H1	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:107:THR:O	2:AB:110:GLN:HB2	2.18	0.44
26:BA:2405:G:O2'	26:BA:2411:A:N6	2.50	0.44
1:CA:1371:G:OP1	9:CI:12:GLU:HB2	2.18	0.44
2:CB:36:ARG:O	2:CB:37:ASN:HB2	2.17	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
33:BI:62:LYS:HE3	33:BI:133:HIS:CE1	2.53	0.44
26:DA:2131:G:H5''	26:DA:2131:G:N3	2.32	0.44
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.17	0.44
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.51	0.44
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.98	0.44
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.83	0.44
1:AA:1152:A:H2'	1:AA:1153:C:H6	1.82	0.44
5:CE:57:LYS:O	5:CE:61:TYR:HD2	2.00	0.44
26:DA:2165:G:H2'	26:DA:2166:G:O4'	2.17	0.44
1:CA:1002:G:C2	1:CA:1003:G:C8	3.06	0.44
25:CY:8:4SU:S4	25:CY:14:A:N7	2.90	0.44
26:BA:2134:A:OP2	26:BA:2157:G:N2	2.50	0.44
1:CA:1286:A:H2'	1:CA:1287:A:H5'	1.99	0.44
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.30	0.44
23:CW:61:C:HO2'	23:CW:62:C:P	2.37	0.44
1:CA:1432:G:OP2	40:DT:108:ARG:HD2	2.18	0.44
26:BA:952:G:P	37:BQ:16:ARG:HH21	2.40	0.44
27:DB:33:G:C6	27:DB:34:U:C4	3.06	0.44
8:AH:119:LEU:HB3	8:AH:123:GLU:HB3	1.99	0.44
26:BA:1405:U:H2'	26:BA:1406:U:H6	1.78	0.44
7:CG:72:ARG:HH22	7:CG:138:LYS:NZ	2.15	0.44
10:CJ:69:ASN:O	10:CJ:70:ARG:HD3	2.18	0.44
1:CA:727:G:OP1	1:CA:742:G:N2	2.43	0.44
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.50	0.44
13:CM:93:ARG:HD3	26:DA:888:C:OP1	2.18	0.44
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.33	0.44
26:BA:2820:A:P	38:BR:2:ARG:HH22	2.41	0.44
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.49	0.44
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.82	0.44
25:AY:71:G:H2'	25:AY:72:C:C6	2.53	0.44
33:BI:4:ILE:HD13	33:BI:47:LEU:HG	2.00	0.44
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	1.98	0.44
46:DZ:120:ILE:HD13	46:DZ:171:ILE:HA	1.99	0.44
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.50	0.44
26:BA:1377:G:H2'	61:BA:3925:HOH:O	2.18	0.44
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:528:A:N1	26:BA:2042:A:H2'	2.32	0.44
13:AM:49:THR:OG1	13:AM:52:GLU:HG3	2.18	0.44
26:BA:764:A:H5'	28:BD:210:GLY:HA2	1.99	0.44
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	2.00	0.44
26:DA:492:A:H2'	26:DA:493:G:O4'	2.18	0.44
26:BA:281:G:O2'	26:BA:359:A:N6	2.47	0.44
26:DA:2136:C:HO2'	26:DA:2137:C:C5'	2.27	0.44
2:CB:16:HIS:CD2	2:CB:17:PHE:N	2.85	0.44
23:AW:56:C:H5	26:BA:897:C:O4'	2.00	0.44
26:DA:994:C:H1'	42:DV:10:LYS:HE3	1.98	0.44
36:DP:83:VAL:HG11	36:DP:100:LEU:HD13	1.99	0.44
46:BZ:108:PRO:HB2	46:BZ:111:VAL:HG23	1.99	0.44
17:AQ:74:LEU:HD13	17:AQ:75:ARG:HG2	2.00	0.44
26:DA:2344:U:H3'	53:D6:37:ARG:O	2.18	0.44
13:AM:60:VAL:HG12	13:AM:66:LEU:HD11	2.00	0.44
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.06	0.44
26:DA:483:A:H1'	45:DY:59:GLY:O	2.18	0.44
26:DA:2302:G:C2	26:DA:2303:G:C8	3.06	0.44
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.53	0.44
40:DT:50:ILE:HG22	40:DT:102:ILE:HD11	1.99	0.44
51:B4:40:HIS:HB3	51:B4:43:TYR:HB2	2.00	0.44
26:DA:1410:G:H2'	26:DA:1411:C:H6	1.82	0.44
26:DA:2104:G:H2'	26:DA:2105:C:C6	2.53	0.44
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.33	0.44
7:AG:72:ARG:HG3	7:AG:142:GLU:OE2	2.18	0.44
1:AA:589:C:H5''	8:AH:29:SER:HB3	1.99	0.44
26:DA:784:A:C8	26:DA:792:G:C5	3.06	0.44
31:DG:129:GLY:O	31:DG:161:THR:HB	2.18	0.44
31:BG:97:ASP:O	31:BG:101:ILE:HG13	2.17	0.44
46:DZ:99:TYR:HA	46:DZ:124:ILE:O	2.17	0.44
26:BA:1453:U:OP1	38:BR:77:ARG:NH1	2.39	0.44
1:AA:834:C:H2'	1:AA:835:U:C6	2.53	0.44
1:AA:1469:G:H2'	1:AA:1470:G:C8	2.53	0.44
38:DR:28:LEU:HD12	38:DR:48:VAL:HG21	2.00	0.44
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.99	0.44
13:AM:31:LYS:O	13:AM:35:GLU:HG3	2.18	0.44
1:AA:1223:C:H5''	1:AA:1224:G:H5''	2.00	0.44
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.73	0.44
16:AP:56:ALA:O	16:AP:60:LEU:HB2	2.18	0.44
1:AA:35:G:O2'	12:AL:118:SER:O	2.29	0.44
26:DA:2127:G:N1	26:DA:2128:C:C4	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:4:C:H3'	25:AY:5:G:H5''	2.00	0.44
1:CA:1245:A:N1	1:CA:1292:U:O2	2.51	0.44
1:CA:1291:G:C6	1:CA:1292:U:C4	3.05	0.44
1:CA:1000:U:H2'	1:CA:1001:A:H8	1.83	0.44
26:BA:892:G:N3	26:BA:892:G:H2'	2.32	0.44
26:BA:893:C:H2'	26:BA:894:C:H6	1.81	0.44
19:CS:67:VAL:H	51:D4:58:ARG:HD3	1.82	0.44
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.79	0.44
22:CV:14:A:C2	25:CY:34:G:C2	3.06	0.44
1:AA:1025:U:O2'	1:AA:1026:G:C8	2.67	0.44
33:BI:103:ARG:HG3	33:BI:104:GLN:H	1.82	0.44
1:CA:1014:A:O2'	1:CA:1219:U:H4'	2.17	0.44
2:CB:109:SER:O	2:CB:112:VAL:HB	2.17	0.44
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.87	0.44
2:AB:158:LEU:HG	2:AB:182:ILE:HD11	2.00	0.44
26:BA:2849:U:P	40:BT:95:ARG:HH12	2.40	0.44
2:CB:15:VAL:HG21	2:CB:213:LEU:HD13	1.99	0.44
26:DA:2617:C:H2'	26:DA:2618:G:O4'	2.17	0.44
10:AJ:69:ASN:O	10:AJ:70:ARG:HD3	2.17	0.44
41:DU:66:ASN:O	41:DU:70:ARG:HG3	2.18	0.44
9:CI:16:ARG:CB	9:CI:64:THR:HG23	2.47	0.44
26:BA:2693:A:H2'	26:BA:2694:G:C8	2.53	0.44
26:BA:1766:U:H2'	26:BA:1767:C:H6	1.83	0.44
1:CA:6:G:O2'	1:CA:7:G:H5'	2.17	0.44
25:CY:40:C:H2'	25:CY:41:C:C6	2.53	0.44
32:DH:18:GLU:HB3	32:DH:25:LYS:HB2	2.00	0.44
26:DA:1983:C:H4'	26:DA:2606:C:H4'	1.99	0.44
26:DA:2313:C:H4'	31:DG:91:ARG:HG3	2.00	0.44
1:CA:570:G:H1'	1:CA:820:U:C4	2.53	0.44
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.17	0.44
10:CJ:43:ARG:HB2	10:CJ:67:THR:HG23	2.00	0.44
1:AA:1130:A:H5'	9:AI:18:PHE:CE2	2.52	0.44
33:BI:43:ASN:C	33:BI:43:ASN:HD22	2.20	0.44
26:BA:2271:G:OP1	47:B0:18:ALA:HB1	2.18	0.44
1:AA:1261:A:H3'	1:AA:1262:C:C6	2.52	0.44
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	2.00	0.44
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.53	0.44
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.44
40:DT:117:ASP:O	40:DT:121:ILE:HG13	2.18	0.44
26:DA:1308:A:H2'	26:DA:1309:G:O4'	2.18	0.44
27:DB:42:C:C2	31:DG:92:VAL:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1151:A:O2'	1:CA:1152:A:H8	2.00	0.44
1:CA:1154:G:O6	1:CA:1155:G:N1	2.51	0.44
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.18	0.44
26:BA:1297:C:OP1	26:BA:2710:C:H4'	2.18	0.44
1:AA:166:G:H2'	1:AA:167:G:C8	2.53	0.44
26:DA:172:C:H2'	26:DA:173:G:H8	1.83	0.44
2:CB:71:VAL:HG22	2:CB:163:PHE:O	2.18	0.44
1:CA:44:G:H2'	1:CA:45:U:O4'	2.18	0.44
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.33	0.44
1:AA:1179:A:H4'	9:AI:103:THR:HA	2.00	0.44
26:BA:141:A:C8	26:BA:1408:C:O2'	2.68	0.44
42:BV:65:GLY:HA3	42:BV:91:TYR:CZ	2.53	0.44
26:DA:1826:G:H4'	28:DD:242:ARG:CZ	2.47	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
1:AA:1153:C:H2'	1:AA:1154:G:O4'	2.18	0.44
30:DF:39:TRP:CZ2	30:DF:43:LYS:HE2	2.52	0.44
53:D6:14:THR:HG22	53:D6:15:GLU:HG3	2.00	0.44
26:BA:2104:G:H2'	26:BA:2105:C:C6	2.53	0.44
26:DA:764:A:H5'	28:DD:210:GLY:HA2	2.00	0.44
32:BH:26:VAL:HG12	32:BH:79:VAL:HG21	1.99	0.44
5:CE:96:PRO:HA	5:CE:117:ASP:OD2	2.18	0.44
26:DA:2567:G:H2'	26:DA:2568:C:C6	2.53	0.44
26:DA:1185:C:H5''	26:DA:1186:G:OP1	2.18	0.44
7:AG:16:LEU:HD23	9:AI:41:VAL:O	2.18	0.44
28:BD:35:LYS:HB2	28:BD:36:PRO:HD2	1.99	0.44
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.17	0.44
26:DA:2439:A:H5'	26:DA:2439:A:C8	2.52	0.44
26:DA:861:A:N3	27:DB:79:C:O2'	2.43	0.44
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.53	0.44
23:AW:19:G:N1	23:AW:56:C:N4	2.53	0.43
1:CA:1226:C:C5	13:CM:104:ARG:HA	2.52	0.43
23:CW:69:G:N2	23:CW:70:G:C4	2.86	0.43
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.18	0.43
4:AD:163:GLU:O	4:AD:166:LYS:HG2	2.18	0.43
26:BA:2345:G:OP2	53:B6:38:LYS:NZ	2.46	0.43
12:AL:24:VAL:HG13	12:AL:98:TYR:HE2	1.84	0.43
45:DY:86:ARG:HB2	45:DY:98:VAL:HG23	1.99	0.43
13:CM:16:ASP:O	13:CM:20:THR:HG23	2.17	0.43
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.83	0.43
31:DG:115:ARG:NH1	31:DG:137:GLU:OE2	2.51	0.43
7:CG:22:LEU:HD13	7:CG:97:GLN:OE1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2141:G:N1	26:BA:2142:C:C2	2.86	0.43
15:CO:58:MET:O	15:CO:62:GLN:N	2.45	0.43
1:CA:954:G:H2'	1:CA:955:U:O4'	2.17	0.43
29:DE:21:VAL:HG23	29:DE:185:LYS:HD2	1.99	0.43
26:DA:298:G:H5''	26:DA:299:A:OP1	2.18	0.43
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.36	0.43
56:B9:32:HIS:O	56:B9:34:GLN:HG3	2.18	0.43
1:AA:973:G:OP1	10:AJ:57:LYS:HE3	2.18	0.43
48:D1:91:LYS:HG2	48:D1:95:LEU:HD22	2.00	0.43
4:CD:20:TYR:CD1	4:CD:26:CYS:HB3	2.52	0.43
34:DN:88:GLU:HG2	34:DN:88:GLU:H	1.56	0.43
12:CL:34:ARG:O	12:CL:61:THR:HG23	2.18	0.43
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	2.00	0.43
1:AA:1014:A:C2	1:AA:1219:U:H1'	2.53	0.43
26:BA:2561:A:H2'	26:BA:2562:U:O4'	2.17	0.43
1:CA:1177:G:H3'	1:CA:1178:G:H8	1.83	0.43
4:AD:107:ARG:HD2	4:AD:107:ARG:HA	1.78	0.43
4:AD:19:LEU:HB3	4:AD:21:LEU:HD21	2.00	0.43
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.18	0.43
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.00	0.43
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.43	0.43
26:BA:2749:A:P	32:BH:3:ARG:HH21	2.41	0.43
3:CC:111:LEU:HD11	3:CC:144:SER:O	2.17	0.43
7:AG:146:GLU:OE2	7:AG:149:ARG:NE	2.51	0.43
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.49	0.43
9:CI:4:TYR:CD2	9:CI:88:TYR:HB2	2.53	0.43
11:AK:81:ASP:OD1	11:AK:81:ASP:N	2.50	0.43
26:DA:1274:A:N3	26:DA:1297:C:H1'	2.33	0.43
9:CI:89:ASN:C	9:CI:89:ASN:HD22	2.22	0.43
5:AE:131:ILE:HD13	5:AE:131:ILE:HA	1.79	0.43
45:DY:19:LYS:HB3	45:DY:19:LYS:HE2	1.74	0.43
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.43
33:DI:44:LEU:HA	33:DI:44:LEU:HD13	1.77	0.43
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.18	0.43
26:BA:144:C:H5'	44:BX:2:LYS:HE2	2.00	0.43
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.83	0.43
26:DA:2115:G:O2'	26:DA:2167:U:O4	2.35	0.43
26:DA:2119:A:C2	26:DA:2171:A:H5'	2.46	0.43
1:CA:999:C:N4	1:CA:1042:G:N1	2.30	0.43
25:CY:71:G:H2'	25:CY:72:C:C6	2.53	0.43
26:DA:2112:G:C4	26:DA:2113:U:H1'	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:D4:46:GLN:C	51:D4:48:ARG:H	2.21	0.43
35:DO:34:THR:OG1	35:DO:35:VAL:N	2.50	0.43
36:DP:1:MET:HG2	36:DP:5:ASP:HB2	1.99	0.43
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.32	0.43
12:AL:92:ASP:O	12:AL:94:PRO:HD3	2.18	0.43
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	2.00	0.43
7:CG:113:GLU:O	7:CG:119:ARG:HD3	2.19	0.43
26:BA:228:A:H8	26:BA:229:A:H5'	1.83	0.43
13:CM:82:MET:HE2	13:CM:92:HIS:HB3	2.00	0.43
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.83	0.43
26:DA:1805:U:C2	26:DA:1813:G:N2	2.86	0.43
1:CA:448:A:O5'	1:CA:485:G:N2	2.45	0.43
1:AA:737:A:H2'	1:AA:738:C:C6	2.53	0.43
1:AA:1131:G:H22	1:AA:1143:G:H21	1.65	0.43
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.99	0.43
2:AB:219:VAL:HA	2:AB:222:ILE:HD12	2.00	0.43
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.84	0.43
21:AU:3:LYS:HB3	21:AU:14:TRP:CG	2.54	0.43
2:CB:97:TRP:HH2	2:CB:102:LEU:HD13	1.83	0.43
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.18	0.43
2:AB:208:ILE:HG13	2:AB:208:ILE:H	1.43	0.43
2:CB:53:ARG:HB3	2:CB:53:ARG:NH1	2.33	0.43
26:DA:122:G:OP1	26:DA:149:A:O2'	2.29	0.43
45:BY:52:SER:HB2	45:BY:53:PRO:HD2	2.00	0.43
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.53	0.43
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	1.99	0.43
2:AB:189:ASP:O	2:AB:192:SER:OG	2.35	0.43
1:CA:1106:G:OP1	3:CC:172:ARG:HD3	2.18	0.43
1:CA:1106:G:C6	1:CA:1107:C:C4	3.07	0.43
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.54	0.43
55:B8:6:THR:HG23	55:B8:63:PRO:HD2	2.00	0.43
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.28	0.43
1:AA:1320:C:H2'	1:AA:1321:C:O4'	2.19	0.43
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.82	0.43
26:BA:1047:G:H2'	26:BA:1110:G:N2	2.33	0.43
1:CA:1442:G:H8	1:CA:1442:G:H3'	1.84	0.43
9:CI:23:ASN:HD22	9:CI:23:ASN:H	1.66	0.43
49:B2:53:LEU:HD23	49:B2:53:LEU:HA	1.83	0.43
26:BA:563:G:H22	26:BA:578:A:H2	1.65	0.43
26:DA:493:G:H2'	26:DA:494:G:O4'	2.17	0.43
27:BB:29:A:H2'	27:BB:30:C:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:522:G:H2'	26:DA:523:C:C6	2.54	0.43
26:DA:1607:C:N4	26:DA:1622:G:OP2	2.45	0.43
4:AD:105:VAL:HG21	4:AD:126:ILE:HG13	2.00	0.43
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	1.99	0.43
38:BR:54:LEU:HD12	38:BR:54:LEU:HA	1.88	0.43
33:BI:68:LEU:HA	33:BI:68:LEU:HD23	1.77	0.43
2:AB:96:ARG:HD2	2:AB:98:LEU:HD23	2.00	0.43
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.17	0.43
26:DA:868:U:C4	26:DA:869:G:N7	2.87	0.43
34:DN:37:LYS:HG3	34:DN:42:TRP:NE1	2.33	0.43
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	2.00	0.43
26:BA:1449:A:H5'	26:BA:1450:G:OP2	2.18	0.43
26:DA:2156:G:O5'	26:DA:2156:G:H8	2.01	0.43
26:DA:880:G:N2	26:DA:898:C:H1'	2.21	0.43
1:CA:404:U:H2'	1:CA:405:U:C6	2.53	0.43
23:CW:2:C:N3	23:CW:71:G:O6	2.52	0.43
26:BA:956:G:P	37:BQ:14:ARG:HH22	2.35	0.43
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.53	0.43
1:CA:1011:G:C6	1:CA:1012:U:C2	3.06	0.43
1:CA:1304:G:C6	1:CA:1305:G:N1	2.86	0.43
26:DA:2393:A:H2'	26:DA:2394:C:O4'	2.19	0.43
25:CY:58:A:H4'	25:CY:59:U:OP1	2.18	0.43
1:AA:44:G:H2'	1:AA:45:U:O4'	2.18	0.43
29:DE:60:ASN:OD1	29:DE:62:PRO:HD2	2.18	0.43
1:CA:1342:C:H2'	1:CA:1343:G:H8	1.83	0.43
1:CA:934:C:H5	1:CA:1344:C:H2'	1.84	0.43
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.54	0.43
26:DA:862:G:O2'	27:DB:78:A:N3	2.51	0.43
9:AI:4:TYR:CD1	9:AI:88:TYR:HA	2.53	0.43
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.54	0.43
28:BD:13:ARG:HD2	28:BD:13:ARG:HA	1.82	0.43
26:DA:2519:U:O4'	26:DA:2542:A:N6	2.51	0.43
1:CA:881:G:OP2	12:CL:12:ARG:NH2	2.51	0.43
26:BA:528:A:C2	26:BA:2043:C:H4'	2.53	0.43
26:BA:813:U:H2'	26:BA:814:C:C6	2.53	0.43
2:AB:87:ARG:NE	2:AB:233:SER:HB3	2.33	0.43
46:BZ:104:PHE:HB3	46:BZ:141:VAL:HG21	1.99	0.43
26:BA:1001:A:H2'	26:BA:1002:G:O4'	2.19	0.43
26:BA:484:C:H2'	26:BA:485:C:C6	2.53	0.43
26:DA:2485:G:C2	26:DA:2486:G:C8	3.06	0.43
45:DY:43:ASN:CG	45:DY:65:ALA:HB3	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DQ:66:ILE:HG12	37:DQ:104:PHE:CE1	2.53	0.43
26:BA:954:G:H5'	37:BQ:13:GLN:HB3	2.00	0.43
20:AT:60:GLU:HG2	20:AT:81:LYS:HD3	2.00	0.43
1:AA:419:C:OP1	1:AA:513:C:O2'	2.21	0.43
19:CS:65:ASN:N	19:CS:65:ASN:OD1	2.51	0.43
26:BA:2121:G:N2	26:BA:2177:C:N3	2.50	0.43
26:DA:2036:C:H2'	26:DA:2037:G:H8	1.83	0.43
1:CA:988:G:H1'	1:CA:1014:A:N1	2.32	0.43
26:DA:2639:A:C2	26:DA:2778:A:C8	3.07	0.43
1:AA:841:U:OP2	1:AA:841:U:H6	2.02	0.43
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.19	0.43
26:DA:1652:A:O2'	26:DA:1653:G:H5'	2.17	0.43
9:AI:55:ALA:HA	9:AI:58:HIS:CD2	2.54	0.43
31:DG:43:LEU:HB3	31:DG:44:GLY:H	1.48	0.43
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	2.00	0.43
1:CA:1240:U:N3	7:CG:30:ILE:O	2.44	0.43
26:DA:647:G:H8	26:DA:647:G:O5'	2.02	0.43
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.53	0.43
26:BA:662:G:H5'	36:BP:14:LYS:O	2.18	0.43
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.19	0.43
5:CE:41:VAL:HG23	5:CE:67:VAL:HG13	2.01	0.43
11:AK:34:ASP:OD2	11:AK:38:ASN:HB2	2.19	0.43
9:AI:18:PHE:O	9:AI:61:ALA:HA	2.19	0.43
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.52	0.43
41:DU:43:GLY:HA3	42:DV:73:SER:HB3	2.01	0.43
26:DA:1847:A:H4'	26:DA:1848:A:OP2	2.18	0.43
46:BZ:79:ARG:HB3	46:BZ:80:ARG:NH1	2.33	0.43
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.42	0.43
1:CA:731:G:H5'	1:CA:766:A:H4'	2.00	0.43
26:DA:373:U:H2'	26:DA:374:A:H8	1.83	0.43
30:DF:129:PHE:HA	30:DF:142:TRP:NE1	2.33	0.43
26:BA:196:A:H2'	26:BA:196:A:N3	2.34	0.43
26:DA:949:C:H2'	26:DA:950:G:C8	2.54	0.43
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.34	0.43
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.54	0.43
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.36	0.43
1:AA:71:C:N3	1:AA:98:G:O6	2.51	0.43
1:CA:953:G:N7	13:CM:104:ARG:NH2	2.67	0.43
37:DQ:20:ALA:HB2	46:DZ:79:ARG:HG2	2.00	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
44:DX:35:THR:HG22	44:DX:37:THR:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DB:15:A:C8	27:DB:110:G:C4	3.07	0.43
26:BA:1712:C:H2'	26:BA:1713:U:O4'	2.18	0.43
26:BA:543:C:N3	26:BA:549:G:N1	2.49	0.43
1:AA:164:U:H2'	1:AA:165:C:C6	2.54	0.43
26:DA:286:C:H2'	26:DA:287:C:C6	2.54	0.43
24:AX:31:G:N7	24:AX:32:5MC:HM52	2.34	0.43
1:CA:396:G:H2'	1:CA:397:A:H5''	1.99	0.43
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	2.00	0.43
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.19	0.43
26:DA:1588:C:H2'	26:DA:1589:C:C6	2.53	0.43
1:AA:202:U:HO2'	1:AA:203:U:P	2.39	0.43
14:AN:13:THR:HA	14:AN:14:PRO:HD3	1.81	0.43
20:CT:59:ALA:O	20:CT:63:ILE:HG13	2.19	0.43
1:CA:1187:G:OP1	9:CI:113:LYS:NZ	2.50	0.43
1:CA:1187:G:H5''	9:CI:113:LYS:HE3	1.99	0.43
19:CS:13:ASP:HA	19:CS:16:LEU:HB2	2.01	0.43
1:AA:658:G:H2'	1:AA:659:U:C6	2.54	0.43
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.17	0.43
26:BA:1654:A:OP1	38:BR:1:MET:HA	2.19	0.43
44:DX:55:ASN:O	44:DX:79:ALA:HA	2.19	0.43
1:CA:553:A:H2'	1:CA:554:C:C6	2.53	0.43
26:DA:910:A:C6	26:DA:911:A:C6	3.06	0.43
1:AA:1217:C:OP1	14:AN:9:LYS:HE2	2.18	0.43
31:DG:150:ASP:OD1	31:DG:150:ASP:N	2.44	0.43
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.54	0.43
26:BA:422:A:H2'	26:BA:423:A:C8	2.53	0.43
38:DR:88:ARG:NH2	38:DR:89:ASP:OD1	2.50	0.43
26:BA:1669:A:H5''	26:BA:2550:G:OP1	2.18	0.43
26:DA:2526:G:H2'	26:DA:2527:C:H6	1.83	0.43
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.19	0.43
26:DA:2125:G:H1	26:DA:2172:U:P	2.41	0.43
25:CY:19:G:C4'	25:CY:57:G:H22	2.32	0.43
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.19	0.43
4:CD:53:ASP:HB3	4:CD:57:ARG:NH1	2.34	0.43
9:CI:22:GLY:N	9:CI:58:HIS:O	2.30	0.43
1:CA:1321:C:H3'	1:CA:1322:C:H6	1.82	0.43
1:CA:427:U:H3'	1:CA:428:G:H2'	2.01	0.43
2:AB:21:ARG:HH21	2:AB:21:ARG:H	1.65	0.43
1:CA:20:U:H2'	1:CA:21:G:O4'	2.18	0.43
1:CA:21:G:H2'	1:CA:22:G:C8	2.54	0.43
1:CA:62:U:H2'	1:CA:63:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.80	0.43
1:CA:299:G:H2'	1:CA:300:A:C8	2.53	0.43
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.18	0.43
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.19	0.43
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	2.00	0.43
1:CA:707:C:H2'	1:CA:708:C:H6	1.83	0.43
51:B4:46:GLN:O	51:B4:46:GLN:HG2	2.19	0.43
26:BA:1429:G:H2'	26:BA:1430:C:C6	2.53	0.43
28:BD:20:ASP:OD1	28:BD:20:ASP:N	2.39	0.43
1:AA:434:U:H2'	1:AA:435:C:C6	2.54	0.43
26:DA:839:U:H2'	26:DA:840:C:C6	2.53	0.43
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.83	0.43
8:CH:56:LYS:HB2	8:CH:58:TYR:HE1	1.83	0.43
11:AK:67:ASP:OD1	11:AK:71:LYS:HE3	2.18	0.43
34:DN:71:ILE:HG21	34:DN:84:LYS:HB3	2.01	0.43
26:DA:272(D):G:C2	26:DA:272(E):G:C8	3.07	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.99	0.43
46:DZ:4:ARG:HG3	46:DZ:58:VAL:HB	2.01	0.43
1:AA:1402:C:H2'	1:AA:1403:C:O4'	2.18	0.43
8:CH:124:ALA:O	8:CH:128:GLY:N	2.52	0.43
1:CA:719:C:N4	18:CR:71:LYS:NZ	2.66	0.43
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.19	0.43
26:DA:1836:C:H2'	26:DA:1837:C:H6	1.84	0.43
26:DA:2406:U:OP2	26:DA:2406:U:H2'	2.19	0.43
3:CC:104:GLN:NE2	3:CC:105:GLU:HG3	2.34	0.43
41:DU:8:VAL:O	41:DU:12:ARG:HG3	2.18	0.43
36:BP:64:LYS:HE3	55:B8:12:LYS:HD3	2.01	0.43
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.84	0.43
40:DT:92:GLY:O	40:DT:120:ARG:NH2	2.51	0.43
26:DA:2152:G:H2'	26:DA:2153:G:O4'	2.18	0.43
25:AY:3:C:H2'	25:AY:4:C:O4'	2.18	0.43
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.83	0.43
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	2.01	0.43
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.52	0.43
1:CA:1119:C:C2	1:CA:1154:G:O6	2.71	0.43
1:CA:988:G:O2'	1:CA:1014:A:N6	2.52	0.43
37:DQ:16:ARG:NH2	37:DQ:18:LYS:HD3	2.33	0.43
2:CB:73:THR:HG22	2:CB:95:GLN:O	2.18	0.43
1:AA:1362:C:H2'	1:AA:1363:C:H5''	2.01	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
26:DA:1652:A:C2'	26:DA:1653:G:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1999:C:H5'	26:DA:2723:C:O2'	2.19	0.43
1:AA:984:C:N4	1:AA:1221:G:H1	2.13	0.43
30:BF:106:ARG:HG2	30:BF:106:ARG:H	1.67	0.43
1:AA:942:G:C2	1:AA:1342:C:C2	3.06	0.43
26:DA:289:A:H62	26:DA:351:G:N2	2.15	0.43
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.52	0.43
7:CG:72:ARG:HH12	7:CG:138:LYS:NZ	2.17	0.43
25:AY:23:A:H2'	25:AY:24:G:C8	2.54	0.43
37:DQ:26:TYR:O	37:DQ:67:ARG:NH1	2.42	0.43
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.19	0.43
49:D2:32:LEU:HD12	49:D2:57:ILE:HD12	2.00	0.43
26:DA:2732:G:H3'	26:DA:2733:A:O4'	2.19	0.43
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.82	0.43
26:BA:2335:A:C8	26:BA:2337:G:C5	3.07	0.43
26:BA:2611:U:H2'	52:B5:2:ALA:O	2.19	0.43
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.19	0.43
26:DA:2031:A:C6	26:DA:2498:C:H1'	2.54	0.43
46:BZ:151:HIS:HA	46:BZ:169:GLU:O	2.19	0.43
1:CA:1368:G:OP2	9:CI:112:LYS:HG3	2.19	0.43
26:DA:2526:G:H2'	26:DA:2527:C:C6	2.53	0.43
13:CM:123:ALA:HB2	23:CW:39:PSU:H1'	2.00	0.43
26:BA:700:G:O2'	26:BA:1632:A:N3	2.43	0.43
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	2.01	0.43
26:BA:2037:G:H2'	26:BA:2038:G:C8	2.54	0.43
26:BA:476:G:H4'	26:BA:502:A:N1	2.34	0.43
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.18	0.43
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.19	0.43
26:DA:2682:U:H5'	29:DE:11:MET:O	2.19	0.43
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.83	0.43
43:BW:67:ASP:N	43:BW:67:ASP:OD1	2.50	0.43
51:B4:68:ARG:HD2	51:B4:68:ARG:HA	1.84	0.43
35:DO:69:ILE:HG12	35:DO:69:ILE:H	1.61	0.43
45:BY:19:LYS:HB3	45:BY:19:LYS:HE2	1.60	0.43
14:CN:37:PHE:HB2	14:CN:39:LEU:HB2	2.00	0.43
10:CJ:99:LYS:O	10:CJ:100:THR:OG1	2.32	0.43
26:BA:1441:G:H2'	26:BA:1442:G:H8	1.83	0.43
26:DA:2171:A:C4	26:DA:2172:U:C4	3.06	0.43
26:DA:2173:A:OP2	26:DA:2173:A:H3'	2.18	0.43
26:BA:1783:A:H5'	26:BA:2608:G:H4'	2.00	0.43
31:DG:145:THR:HG23	31:DG:147:ASP:N	2.23	0.43
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.34	0.43
31:DG:64:THR:OG1	31:DG:66:GLN:O	2.37	0.43
4:CD:13:ARG:HD2	4:CD:38:TYR:O	2.18	0.43
1:CA:1261:A:C6	1:CA:1262:C:C2	3.07	0.43
30:DF:195:ASP:HB3	30:DF:197:ASP:OD1	2.18	0.43
27:DB:15:A:OP2	27:DB:69:G:N2	2.49	0.43
1:CA:955:U:H2'	1:CA:956:U:O4'	2.19	0.43
45:BY:54:LYS:CA	45:BY:56:PRO:HD3	2.48	0.43
26:DA:1636:C:H2'	26:DA:1637:A:C8	2.54	0.43
25:CY:76:A:H62	26:DA:2422:A:C5'	2.31	0.43
26:DA:322:A:C5	26:DA:340:A:C2	3.06	0.43
26:DA:2193:G:H2'	26:DA:2194:G:H8	1.84	0.43
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.34	0.43
26:DA:2557:G:H2'	26:DA:2558:C:H6	1.83	0.43
26:DA:2693:A:H2'	26:DA:2694:G:C8	2.54	0.43
26:BA:2100:G:H1	26:BA:2189:U:H3	1.66	0.43
45:DY:5:MET:HE1	45:DY:32:PRO:HA	2.01	0.43
26:DA:2439:A:H8	26:DA:2439:A:H5'	1.84	0.43
34:BN:9:VAL:HG11	34:BN:39:ARG:HH22	1.83	0.43
5:CE:83:GLU:HA	5:CE:88:LYS:HA	2.00	0.43
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.54	0.43
4:AD:33:MET:O	4:AD:37:PRO:HB3	2.19	0.43
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.52	0.43
26:BA:1394:U:H2'	26:BA:1395:A:O4'	2.18	0.43
6:CF:91:VAL:HG11	18:CR:72:ARG:NH1	2.34	0.43
12:AL:117:ARG:HB3	12:AL:122:THR:HB	2.00	0.43
1:CA:776:G:HO2'	1:CA:777:A:H8	1.66	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.18	0.43
26:DA:2516:G:C6	26:DA:2517:C:C4	3.07	0.43
26:DA:770:G:OP2	61:DA:4255:HOH:O	2.21	0.43
1:AA:671:G:H5'	6:AF:77:ARG:HH12	1.83	0.43
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.40	0.43
1:AA:909:A:H2'	1:AA:910:C:O4'	2.19	0.43
25:CY:1:G:H2'	25:CY:2:C:C6	2.54	0.43
26:BA:2154:G:C2'	26:BA:2155:G:H5'	2.49	0.43
25:CY:51:U:H2'	25:CY:52:G:O4'	2.18	0.43
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.33	0.43
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.83	0.43
37:BQ:56:ARG:HA	37:BQ:56:ARG:HD2	1.72	0.43
27:DB:24:G:O4'	27:DB:26:A:N6	2.47	0.43
13:CM:66:LEU:O	13:CM:68:GLY:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:115:LEU:HD21	2:CB:153:ARG:NE	2.34	0.43
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.54	0.43
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.52	0.43
1:CA:1216:G:H5''	14:CN:5:ALA:CB	2.47	0.43
14:AN:23:ARG:HH11	14:AN:30:ALA:HB2	1.83	0.43
19:CS:71:LEU:HD12	19:CS:71:LEU:HA	1.91	0.43
9:AI:20:ARG:HA	9:AI:21:PRO:HD3	1.92	0.43
26:DA:2747:G:O6	26:DA:2755:C:H5''	2.19	0.43
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.59	0.43
26:DA:1010:A:H1'	26:DA:1153:C:H1'	2.00	0.43
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	2.00	0.43
1:CA:1176:A:H2'	1:CA:1177:G:H8	1.84	0.43
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.35	0.43
50:D3:46:ASN:O	50:D3:50:VAL:HG22	2.19	0.43
5:CE:110:LEU:HD13	5:CE:118:ILE:HG21	2.00	0.43
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	2.01	0.43
26:DA:2461:C:H2'	26:DA:2462:U:H6	1.84	0.43
26:DA:2740:A:H2'	26:DA:2741:A:C8	2.54	0.43
12:AL:110:VAL:O	12:AL:122:THR:OG1	2.32	0.43
26:DA:2265:U:C4	26:DA:2266:A:C5	3.07	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.19	0.43
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.19	0.43
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	2.01	0.43
26:DA:1394:U:C4	26:DA:1395:A:C5	3.07	0.43
26:BA:1005:C:O2'	34:BN:28:THR:HG21	2.19	0.43
3:AC:116:VAL:O	3:AC:120:VAL:HG23	2.19	0.43
1:CA:1112:C:N3	3:CC:177:THR:HA	2.34	0.43
3:CC:42:LEU:HA	3:CC:45:LYS:NZ	2.33	0.43
32:DH:124:GLU:OE1	32:DH:132:ARG:HD2	2.19	0.43
20:AT:29:LYS:O	20:AT:33:ILE:HG13	2.18	0.43
1:CA:1025:U:H1'	1:CA:1026:G:C8	2.54	0.42
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.53	0.42
23:AW:51:U:H2'	23:AW:52:G:C8	2.54	0.42
2:CB:122:PHE:HE2	2:CB:139:LYS:HG2	1.84	0.42
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	2.01	0.42
2:CB:115:LEU:HG	2:CB:119:GLU:OE2	2.19	0.42
1:CA:993:G:H2'	1:CA:993:G:N3	2.33	0.42
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.52	0.42
32:DH:2:SER:O	32:DH:3:ARG:HG2	2.19	0.42
3:AC:77:ILE:HG22	3:AC:81:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:82:GLU:HA	3:AC:85:ARG:NE	2.34	0.42
26:BA:1882:C:H2'	26:BA:1883:G:O4'	2.19	0.42
10:CJ:30:SER:OG	10:CJ:84:GLN:OE1	2.29	0.42
26:BA:1913:A:H4'	26:BA:1914:C:C5'	2.49	0.42
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.34	0.42
26:DA:2302:G:C6	26:DA:2303:G:N7	2.88	0.42
26:DA:2302:G:H1	26:DA:2314:C:H42	1.67	0.42
26:DA:2316:C:O2'	31:DG:128:ARG:NH1	2.52	0.42
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.48	0.42
26:DA:2591:C:H2'	26:DA:2592:G:C8	2.54	0.42
1:CA:103:C:P	20:CT:17:ARG:HH21	2.42	0.42
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.34	0.42
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.51	0.42
7:AG:70:LYS:O	7:AG:138:LYS:NZ	2.49	0.42
26:BA:2199:A:H5''	26:BA:2200:C:OP2	2.19	0.42
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.54	0.42
26:DA:272(E):G:C2	26:DA:364:C:C2	3.07	0.42
31:DG:23:PHE:HB2	31:DG:25:TYR:CE1	2.54	0.42
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	2.01	0.42
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	2.00	0.42
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.19	0.42
1:AA:294:U:OP1	1:AA:610:G:O2'	2.30	0.42
26:DA:150:C:H2'	26:DA:151:C:C6	2.54	0.42
38:DR:12:ARG:HG2	38:DR:16:HIS:ND1	2.34	0.42
28:DD:75:ILE:HA	28:DD:76:PRO:HD3	1.93	0.42
26:DA:524:U:H2'	26:DA:525:U:C6	2.54	0.42
26:DA:660:G:H5'	30:DF:99:TYR:CE2	2.53	0.42
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.48	0.42
26:BA:1504:C:H2'	26:BA:1505:C:C6	2.54	0.42
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.54	0.42
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.33	0.42
2:AB:224:GLN:HA	2:AB:228:GLY:O	2.19	0.42
26:DA:563:G:OP2	61:DA:4169:HOH:O	2.21	0.42
48:B1:62:VAL:HG22	48:B1:63:ALA:O	2.18	0.42
31:DG:135:LEU:HD13	31:DG:135:LEU:HA	1.89	0.42
35:DO:17:ARG:HD3	35:DO:17:ARG:HA	1.69	0.42
29:DE:181:LEU:HD12	29:DE:181:LEU:HA	1.76	0.42
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.81	0.42
1:CA:495:A:H4'	1:CA:496:A:OP1	2.18	0.42
42:DV:31:ALA:O	42:DV:61:VAL:HG12	2.18	0.42
1:CA:228:A:H5'	16:CP:62:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:DU:107:ALA:O	41:DU:111:GLU:HG2	2.18	0.42
45:BY:1:MET:HB2	45:BY:2:ARG:H	1.53	0.42
26:BA:1354:A:H2'	26:BA:1355:G:O4'	2.19	0.42
30:DF:31:HIS:HB2	36:DP:9:ASN:OD1	2.19	0.42
19:CS:41:VAL:HG13	19:CS:42:PRO:HD2	2.01	0.42
26:DA:1204:A:N6	26:DA:1240:U:H2'	2.34	0.42
1:AA:405:U:O4	4:AD:2:GLY:N	2.53	0.42
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
26:BA:1108:U:O2'	26:BA:1109:C:C6	2.72	0.42
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.42
31:DG:47:LYS:HE2	31:DG:47:LYS:HB3	1.56	0.42
4:CD:163:GLU:C	4:CD:165:MET:H	2.22	0.42
26:DA:1556:C:H2'	26:DA:1557:C:H6	1.84	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HD12	2.01	0.42
1:AA:373:A:H1'	1:AA:481:G:N3	2.34	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.84	0.42
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.54	0.42
1:AA:1286:A:H3'	1:AA:1286:A:C8	2.54	0.42
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.19	0.42
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	2.00	0.42
1:AA:54:C:H2'	1:AA:352:C:H41	1.84	0.42
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	2.01	0.42
3:AC:191:THR:OG1	3:AC:194:GLY:O	2.33	0.42
1:CA:850:U:H2'	1:CA:851:G:H5''	2.01	0.42
44:BX:64:LYS:HA	44:BX:64:LYS:HD3	1.83	0.42
8:AH:78:GLN:HE21	8:AH:78:GLN:HB2	1.47	0.42
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	2.01	0.42
25:AY:5:G:C2	25:AY:6:G:C4	3.07	0.42
25:AY:7:A:C6	25:AY:49:C:C4	3.07	0.42
1:AA:78:G:C2	1:AA:91:C:N4	2.87	0.42
26:BA:1177:A:H3'	26:BA:1178:C:C6	2.54	0.42
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.84	0.42
23:CW:4:C:N4	23:CW:5:G:C6	2.87	0.42
1:AA:1002:G:C6	1:AA:1003:G:N3	2.88	0.42
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.44	0.42
1:CA:1122:U:H2'	1:CA:1123:A:O4'	2.19	0.42
3:CC:39:ILE:O	3:CC:43:LEU:HG	2.19	0.42
26:BA:971:C:H2'	26:BA:972:G:O4'	2.19	0.42
24:CX:9:G:H21	24:CX:45:G:H3'	1.84	0.42
26:BA:529:A:H62	26:BA:2041:U:H3	1.67	0.42
27:DB:11:C:H3'	27:DB:12:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.34	0.42
26:DA:1188:U:C4'	42:DV:79:VAL:HG22	2.50	0.42
45:DY:7:VAL:HG21	45:DY:72:VAL:HG12	2.00	0.42
46:DZ:100:VAL:HA	46:DZ:101:PRO:HD3	1.91	0.42
1:AA:539:A:H2'	1:AA:540:G:H8	1.84	0.42
6:AF:10:LEU:HD23	6:AF:61:LEU:HD23	2.02	0.42
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.49	0.42
29:DE:96:PHE:O	29:DE:175:VAL:HG11	2.19	0.42
26:BA:1268:A:C2	26:BA:2013:A:C4	3.08	0.42
2:AB:12:GLU:HA	2:AB:213:LEU:HD11	2.01	0.42
5:AE:103:GLY:O	5:AE:106:PRO:HD2	2.19	0.42
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.34	0.42
46:DZ:28:MET:HA	46:DZ:88:PHE:O	2.18	0.42
1:AA:59:A:H3'	1:AA:331:G:H22	1.84	0.42
1:AA:530:G:O6	22:AV:21:C:H1'	2.19	0.42
27:BB:32:C:C2	27:BB:51:G:N2	2.86	0.42
1:CA:1124:G:H5'	10:CJ:36:GLY:H	1.84	0.42
26:DA:2386:C:H2'	26:DA:2387:U:C6	2.54	0.42
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.52	0.42
18:CR:44:LEU:HD23	18:CR:50:ILE:HA	2.02	0.42
45:DY:83:THR:HG21	45:DY:99:CYS:HB2	2.01	0.42
31:BG:53:LEU:HD23	31:BG:53:LEU:HA	1.84	0.42
13:CM:47:ASP:O	13:CM:48:LEU:HD23	2.18	0.42
26:DA:735:A:N7	26:DA:761:A:H2	2.17	0.42
26:DA:2705:A:H2'	26:DA:2706:G:O4'	2.20	0.42
1:CA:985:C:C2	1:CA:1220:G:N2	2.80	0.42
1:AA:1004:A:N7	1:AA:1036:G:C2	2.87	0.42
24:CX:21:A:H61	24:CX:46:G:H2'	1.84	0.42
1:CA:1320:C:H5'	1:CA:1320:C:H6	1.85	0.42
2:CB:51:LEU:HA	2:CB:54:THR:HB	2.01	0.42
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.84	0.42
26:BA:2709:G:H2'	26:BA:2710:C:C6	2.54	0.42
26:BA:171:G:O2'	26:BA:172:C:H5'	2.19	0.42
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	2.01	0.42
1:AA:1187:G:N3	14:AN:60:SER:OG	2.53	0.42
7:CG:114:ARG:HB2	7:CG:115:ARG:NH2	2.35	0.42
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.55	0.42
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.19	0.42
49:B2:3:LEU:O	49:B2:7:ARG:HG3	2.19	0.42
3:CC:134:ILE:HG22	3:CC:168:ALA:HB3	2.01	0.42
29:BE:18:ASP:HB3	40:BT:82:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1009:G:C4	1:CA:1021:G:C2	3.08	0.42
26:BA:2439:A:H5'	26:BA:2439:A:H8	1.85	0.42
27:DB:117:G:C2	27:DB:118:G:C5	3.07	0.42
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.48	0.42
26:BA:784:A:C8	26:BA:792:G:C5	3.07	0.42
1:CA:933:G:C6	1:CA:1385:G:C6	3.07	0.42
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.52	0.42
5:CE:57:LYS:HG2	5:CE:61:TYR:HE2	1.84	0.42
1:AA:658:G:H2'	1:AA:659:U:H6	1.85	0.42
1:CA:156:G:H1	1:CA:165:C:H42	1.67	0.42
26:BA:489:G:N7	43:BW:49:LYS:NZ	2.68	0.42
4:AD:176:LEU:HD12	4:AD:182:LYS:O	2.19	0.42
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.54	0.42
34:DN:123:TYR:CZ	34:DN:129:PRO:HD2	2.54	0.42
26:BA:841:A:H2'	26:BA:842:G:C8	2.54	0.42
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.54	0.42
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.18	0.42
26:BA:2347:C:O2'	53:B6:21:TYR:OH	2.35	0.42
37:DQ:73:PRO:HA	37:DQ:93:TYR:CD1	2.54	0.42
26:BA:918:A:H5''	27:BB:98:G:O2'	2.19	0.42
26:DA:2510:C:C4	26:DA:2511:U:C4	3.07	0.42
34:BN:20:GLY:HA2	34:BN:61:ARG:HD2	2.01	0.42
20:AT:13:LEU:O	20:AT:17:ARG:HG3	2.19	0.42
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.19	0.42
1:AA:79:G:C2	1:AA:90:U:C2	3.07	0.42
41:DU:92:ARG:H	41:DU:92:ARG:HG2	1.44	0.42
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.33	0.42
1:AA:1004:A:C5	1:AA:1037:C:N3	2.87	0.42
1:AA:1029:C:N4	1:AA:1030(A):G:C2	2.88	0.42
27:DB:62:C:H2'	27:DB:63:G:C8	2.55	0.42
26:DA:2130:U:H3	26:DA:2159:G:N2	2.17	0.42
27:DB:91:C:OP1	37:DQ:16:ARG:HG3	2.19	0.42
1:AA:580:U:H5''	15:AO:58:MET:HG2	2.01	0.42
1:CA:560:U:OP2	61:CA:3313:HOH:O	2.21	0.42
1:CA:911:U:O2'	1:CA:912:C:H5'	2.20	0.42
3:CC:69:HIS:HB3	3:CC:106:VAL:CG2	2.50	0.42
26:DA:954:G:O2'	26:DA:2274:A:N1	2.45	0.42
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.54	0.42
26:DA:1317:A:H2'	26:DA:1318:C:C6	2.55	0.42
1:CA:1388:C:H2'	1:CA:1389:C:C6	2.54	0.42
4:CD:150:GLU:HG3	4:CD:150:GLU:H	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:B6:50:ARG:HB2	53:B6:50:ARG:HE	1.67	0.42
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.42
26:DA:1341:U:O4	44:DX:16:LYS:HE2	2.19	0.42
9:AI:4:TYR:CE1	9:AI:88:TYR:HA	2.55	0.42
26:DA:1127:A:C2'	26:DA:1128:A:H5''	2.50	0.42
26:BA:2029:G:H2'	26:BA:2031:A:OP1	2.19	0.42
26:DA:764:A:H5'	28:DD:210:GLY:CA	2.49	0.42
36:BP:112:LEU:HA	36:BP:112:LEU:HD23	1.85	0.42
26:BA:1721:G:H3'	26:BA:1722:A:H5''	2.01	0.42
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	2.02	0.42
26:BA:2396:G:OP1	48:B1:25:LYS:NZ	2.30	0.42
1:CA:357:G:O2'	1:CA:358:U:H5'	2.18	0.42
48:D1:89:GLU:O	48:D1:93:GLU:HG2	2.19	0.42
17:CQ:62:SER:CB	17:CQ:72:ARG:HD3	2.49	0.42
26:BA:2233:U:H2'	26:BA:2234:G:C8	2.55	0.42
31:DG:53:LEU:HD23	31:DG:53:LEU:HA	1.88	0.42
26:DA:64:A:O3'	44:DX:71:GLY:HA3	2.19	0.42
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.55	0.42
26:DA:117:G:C6	26:DA:119:A:C6	3.07	0.42
3:AC:136:GLN:O	3:AC:140:ARG:HG3	2.18	0.42
32:BH:170:ARG:O	32:BH:171:LEU:HD23	2.19	0.42
12:CL:62:SER:HB2	12:CL:64:TYR:HD1	1.85	0.42
26:DA:829:A:N7	26:DA:2248:C:H5'	2.34	0.42
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.55	0.42
1:CA:1422:G:H5'	35:DO:48:PRO:HB3	2.01	0.42
20:CT:93:GLU:C	20:CT:95:ALA:H	2.23	0.42
35:BO:113:LYS:O	35:BO:116:SER:OG	2.34	0.42
26:BA:881:G:N1	26:BA:897:C:N4	2.67	0.42
9:CI:28:VAL:HA	9:CI:63:ILE:O	2.20	0.42
27:DB:31:C:H4'	31:DG:29:TRP:CZ2	2.54	0.42
27:DB:55:U:H1'	31:DG:29:TRP:HD1	1.81	0.42
27:DB:57:A:N3	31:DG:29:TRP:HB3	2.33	0.42
1:CA:1118:C:C2	1:CA:1119:C:C5	3.06	0.42
1:AA:765:G:N1	1:AA:812:C:O2'	2.42	0.42
1:AA:162:A:N7	1:AA:163:C:H1'	2.35	0.42
53:D6:18:ARG:HD2	53:D6:42:TRP:CG	2.55	0.42
2:CB:82:ARG:HG3	2:CB:92:TYR:OH	2.18	0.42
9:AI:20:ARG:O	9:AI:60:ASP:N	2.30	0.42
1:CA:921:U:O2	5:CE:19:MET:HB2	2.19	0.42
3:CC:52:LEU:HD23	3:CC:55:VAL:HG23	2.01	0.42
20:CT:56:MET:HE2	20:CT:88:VAL:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:652(C):G:H1	26:BA:652(V):C:N4	2.18	0.42
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.42
32:BH:98:LEU:HA	32:BH:98:LEU:HD12	1.91	0.42
32:DH:84:SER:HB3	32:DH:132:ARG:HH11	1.85	0.42
53:D6:13:CYS:SG	53:D6:47:THR:HG21	2.60	0.42
2:CB:107:THR:O	2:CB:110:GLN:HB3	2.19	0.42
7:AG:120:ILE:O	7:AG:124:LEU:HB2	2.20	0.42
26:DA:2228:G:OP1	28:DD:261:LYS:HE3	2.19	0.42
31:DG:121:ASN:HA	31:DG:181:ARG:HH21	1.84	0.42
26:DA:935:C:C2'	26:DA:936:C:H5'	2.50	0.42
11:CK:59:TYR:O	11:CK:63:LEU:HG	2.20	0.42
26:BA:2529:G:H5''	26:BA:2530:A:H5''	2.01	0.42
1:AA:299:G:H2'	1:AA:300:A:C8	2.55	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.85	0.42
33:BI:73:GLU:HG3	33:BI:139:GLN:O	2.19	0.42
28:DD:245:PRO:HA	28:DD:246:PRO:HD3	1.91	0.42
26:BA:775:G:C4	26:BA:794:G:C8	3.07	0.42
26:DA:925:C:H2'	26:DA:926:A:H8	1.85	0.42
26:DA:2320:A:N3	26:DA:2320:A:H2'	2.33	0.42
15:AO:85:LEU:HD23	15:AO:85:LEU:HA	1.75	0.42
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.02	0.42
26:BA:2093:G:C6	26:BA:2225:A:C8	3.08	0.42
25:AY:18:G:N2	25:AY:58:A:C8	2.88	0.42
1:CA:1002:G:N2	1:CA:1038:C:N3	2.55	0.42
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	2.00	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.06	0.42
1:CA:1357:A:N7	1:CA:1358:U:C4	2.88	0.42
1:CA:1065:U:H1'	1:CA:1066:C:OP2	2.20	0.42
1:CA:1279:A:OP2	10:CJ:9:ARG:NH1	2.53	0.42
1:CA:1126:U:H4'	1:CA:1281:U:H1'	2.01	0.42
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.55	0.42
46:BZ:108:PRO:CB	46:BZ:117:LEU:HD13	2.46	0.42
26:DA:1449:A:OP2	26:DA:1449:A:H8	2.02	0.42
26:BA:2139:C:H2'	26:BA:2140:C:H4'	2.01	0.42
31:DG:43:LEU:C	31:DG:45:GLU:H	2.21	0.42
1:AA:171:A:H2'	1:AA:172:A:C8	2.54	0.42
26:BA:1359:A:H2'	26:BA:1360:A:H5'	2.02	0.42
1:AA:396:G:O2'	1:AA:398:C:OP1	2.23	0.42
2:AB:111:ARG:HG2	2:AB:111:ARG:HH11	1.84	0.42
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.54	0.42
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:296:C:O3'	45:DY:95:LYS:NZ	2.52	0.42
26:DA:108:U:H2'	26:DA:109:G:H8	1.83	0.42
26:BA:601:C:O2'	26:BA:605:C:H5''	2.19	0.42
34:BN:4:TYR:CE2	41:BU:100:VAL:HG11	2.55	0.42
1:CA:1368:G:H2'	1:CA:1369:C:H5'	2.01	0.42
1:CA:695:A:H2'	1:CA:696:A:C8	2.55	0.42
26:DA:2055:C:H1'	29:DE:145:LYS:HE2	2.01	0.42
33:DI:77:LEU:HG	33:DI:101:LEU:HD12	2.02	0.42
5:CE:98:THR:HB	5:CE:117:ASP:HB3	2.01	0.42
46:DZ:71:VAL:HG13	46:DZ:88:PHE:CD1	2.54	0.42
34:DN:128:HIS:HA	34:DN:129:PRO:HD3	1.81	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.35	0.42
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.42
26:DA:2187:G:C6	26:DA:2188:C:N3	2.87	0.42
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.42
26:BA:1939:U:OP1	26:BA:2604:U:O2'	2.33	0.42
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.20	0.42
26:BA:2706:G:N7	61:BA:4712:HOH:O	2.37	0.42
39:BS:58:LEU:HD23	39:BS:58:LEU:HA	1.71	0.42
1:CA:779:C:O2'	11:CK:120:ARG:HD3	2.20	0.42
26:BA:895:U:H5'	26:BA:896:A:OP1	2.20	0.42
1:CA:1362:C:H2'	1:CA:1363:C:H5''	2.00	0.42
24:CX:21:A:H3'	24:CX:46:G:O6	2.19	0.42
26:DA:11:G:H2'	26:DA:12:U:H5''	2.02	0.42
30:DF:117:ARG:HH12	36:DP:1:MET:N	2.18	0.42
2:CB:95:GLN:HB2	2:CB:148:TYR:CD1	2.44	0.42
26:DA:740:U:H2'	26:DA:741:G:H8	1.81	0.42
1:AA:1304:G:C6	1:AA:1305:G:N1	2.88	0.42
26:BA:2328:A:H2'	26:BA:2329:G:H8	1.80	0.42
2:CB:70:PHE:HE1	2:CB:163:PHE:CD2	2.36	0.42
26:DA:479:A:H4'	26:DA:480:A:OP1	2.19	0.42
26:BA:1044:G:HO2'	26:BA:1111:A:N6	2.17	0.42
26:BA:1300:U:H4'	26:BA:1301:A:H5''	2.01	0.42
10:AJ:8:LEU:CD2	10:AJ:96:ILE:HG23	2.50	0.42
26:DA:1445(A):C:H2'	26:DA:1446:C:H6	1.83	0.42
1:AA:457:C:H2'	1:AA:458:C:C6	2.54	0.42
18:CR:73:ALA:CB	18:CR:79:LEU:HG	2.49	0.42
26:BA:1652:A:C2'	26:BA:1653:G:H5'	2.49	0.42
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.54	0.42
16:AP:18:ARG:NH1	16:AP:32:TYR:OH	2.52	0.42
1:CA:1268:A:H2	1:CA:1326:C:O2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1470:G:H5''	26:BA:1471:A:OP1	2.20	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.50	0.42
26:DA:271(K):U:H4'	26:DA:271(L):U:OP1	2.20	0.42
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	2.02	0.42
53:B6:8:LYS:HD3	55:B8:34:TRP:CD2	2.55	0.42
8:AH:73:ASP:OD1	8:AH:75:ARG:NH1	2.49	0.42
26:DA:1242:A:N1	36:DP:4:SER:OG	2.41	0.42
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.20	0.42
26:BA:1651:G:OP1	38:BR:40:LYS:HE3	2.20	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.01	0.42
4:AD:36:ARG:HB3	4:AD:38:TYR:CZ	2.55	0.42
26:DA:807:U:OP2	36:DP:41:ARG:NH2	2.53	0.42
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.20	0.42
28:DD:29:PRO:HA	28:DD:83:GLU:OE1	2.19	0.42
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.84	0.42
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.52	0.42
26:BA:2218:U:O4'	48:B1:52:ARG:NH2	2.53	0.42
26:BA:957:A:H5'	37:BQ:76:LYS:HG2	2.02	0.42
37:DQ:141:GLN:NE2	46:DZ:74:VAL:O	2.39	0.42
51:B4:49:PHE:HA	51:B4:49:PHE:HD1	1.72	0.42
5:CE:79:GLU:HG2	5:CE:79:GLU:O	2.18	0.42
31:BG:79:ASN:OD1	31:BG:79:ASN:N	2.52	0.42
26:DA:820:A:N3	26:DA:943:U:H4'	2.35	0.42
1:AA:636:U:H2'	1:AA:637:G:H8	1.84	0.42
26:DA:2140:C:C2	26:DA:2152:G:C2	3.07	0.42
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.55	0.42
25:AY:53:G:N1	25:AY:61:C:N4	2.38	0.42
25:CY:19:G:N3	25:CY:57:G:N1	2.68	0.42
41:DU:90:VAL:HG12	41:DU:95:LEU:HD12	2.02	0.42
25:CY:37:MIA:H2'	25:CY:38:A:O4'	2.20	0.42
1:CA:586:C:O2'	1:CA:878:G:H4'	2.19	0.42
26:DA:1371:G:H2'	26:DA:1372:U:C5	2.51	0.42
46:DZ:97:GLU:HB2	46:DZ:125:LEU:HD11	2.02	0.42
1:CA:1118:C:N1	1:CA:1119:C:H5	2.18	0.42
1:CA:456:C:H2'	1:CA:457:C:H5'	2.00	0.42
30:DF:196:LEU:HA	30:DF:196:LEU:HD23	1.86	0.42
5:AE:116:THR:HG23	5:AE:117:ASP:OD2	2.19	0.42
26:BA:171:G:C2'	26:BA:172:C:H5'	2.49	0.42
27:DB:40:U:N3	27:DB:44:G:OP2	2.48	0.42
25:AY:24:G:C6	25:AY:25:C:C4	3.08	0.42
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:76:A:N6	26:DA:2422:A:H5'	2.35	0.42
46:BZ:24:LEU:HD21	46:BZ:86:VAL:HG13	2.01	0.42
26:DA:848:G:C4	26:DA:933:A:C8	3.06	0.42
2:AB:71:VAL:CG1	2:AB:170:GLU:HG2	2.49	0.42
26:DA:644:A:C2	26:DA:2369:A:H1'	2.55	0.42
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.19	0.42
6:CF:2:ARG:HG3	6:CF:69:GLU:HG3	2.02	0.42
53:D6:35:GLU:HA	53:D6:49:HIS:O	2.20	0.42
35:DO:73:ASP:OD2	40:DT:32:TYR:OH	2.35	0.42
1:AA:627:G:O2'	1:AA:628:G:H5'	2.20	0.42
26:DA:708:C:N4	26:DA:723:G:H1	2.18	0.42
26:BA:185:U:H4'	26:BA:218:A:H4'	2.02	0.42
13:CM:3:ARG:HG2	13:CM:8:GLU:HA	2.01	0.42
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.54	0.42
5:CE:80:ILE:HA	5:CE:80:ILE:HD12	1.87	0.42
26:DA:211:A:H2'	26:DA:212:G:O4'	2.20	0.42
26:DA:1237:A:OP1	61:DA:4484:HOH:O	2.21	0.42
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.34	0.42
26:BA:2260:C:H2'	26:BA:2261:C:C6	2.55	0.42
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.55	0.42
1:AA:377:G:OP1	16:AP:3:LYS:HD3	2.20	0.42
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.20	0.42
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.35	0.42
1:AA:393:A:OP1	61:AA:4195:HOH:O	2.21	0.42
29:BE:141:ILE:HA	29:BE:154:LYS:HE2	2.02	0.42
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HD3	2.01	0.42
17:CQ:76:LEU:HD12	17:CQ:77:VAL:H	1.84	0.42
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.39	0.42
26:DA:1748:G:H2'	26:DA:1749:A:O4'	2.20	0.42
1:AA:1267:C:H6	1:AA:1267:C:O5'	2.02	0.42
1:CA:1162:C:H2'	1:CA:1163:C:O4'	2.20	0.42
1:CA:1323:G:O2'	1:CA:1362:C:O2'	2.23	0.42
1:AA:342:C:C2	1:AA:348:G:N2	2.88	0.42
2:CB:57:PHE:CE2	2:CB:185:ILE:HD12	2.50	0.42
1:CA:1011:G:H21	1:CA:1019:C:H1'	1.84	0.42
1:AA:56:U:H2'	1:AA:57:G:H8	1.79	0.42
1:AA:674:G:H2'	1:AA:675:A:C8	2.53	0.42
26:BA:1881:C:H2'	26:BA:1882:C:C6	2.55	0.42
9:CI:20:ARG:HA	9:CI:21:PRO:HD3	1.92	0.42
17:CQ:78:GLU:OE1	17:CQ:81:ARG:HD3	2.19	0.42
26:DA:847:U:OP2	61:DA:4017:HOH:O	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:193:ASP:HA	2:CB:194:PRO:HD2	1.89	0.42
12:AL:34:ARG:HG3	12:AL:105:TYR:CE2	2.55	0.42
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.20	0.42
48:D1:72:GLU:OE1	48:D1:76:ARG:NH2	2.53	0.42
26:DA:1927:A:OP1	26:DA:1927:A:H8	2.03	0.42
42:DV:21:ARG:HG2	42:DV:91:TYR:CE2	2.55	0.42
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.35	0.42
14:CN:24:CYS:HA	14:CN:38:GLY:O	2.20	0.42
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.84	0.42
32:BH:98:LEU:HD13	32:BH:125:VAL:HG23	2.00	0.42
42:BV:5:VAL:HG21	42:BV:35:LEU:HD23	2.02	0.42
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.35	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.20	0.42
1:CA:452:A:O2'	1:CA:453:A:OP2	2.34	0.42
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.20	0.42
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.46	0.42
1:AA:1210:C:C2'	1:AA:1211:U:H5'	2.50	0.42
26:DA:271(D):G:C6	26:DA:271(E):U:C4	3.08	0.42
26:DA:30:G:H2'	26:DA:31:C:O4'	2.19	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
26:DA:2110:G:H4'	26:DA:2111:C:OP2	2.20	0.42
31:DG:72:ARG:HA	31:DG:86:MET:O	2.20	0.42
31:BG:18:GLU:OE1	31:BG:22:ARG:HD3	2.20	0.42
38:DR:65:LEU:HA	38:DR:65:LEU:HD12	1.87	0.42
18:AR:25:THR:OG1	18:AR:25:THR:O	2.32	0.42
28:BD:242:ARG:HD3	28:BD:242:ARG:N	2.34	0.42
31:DG:49:ASP:N	31:DG:49:ASP:OD1	2.53	0.42
26:BA:2097:C:H2'	26:BA:2098:U:O4'	2.19	0.42
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.01	0.42
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.20	0.42
1:AA:729:A:H2'	1:AA:730:G:H8	1.84	0.42
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.08	0.42
1:AA:820:U:H4'	1:AA:821:G:OP2	2.20	0.42
26:DA:2147:G:C4	26:DA:2148:G:H1'	2.55	0.41
26:DA:2135:A:OP1	26:DA:2160:G:H1'	2.20	0.41
25:AY:5:G:H2'	25:AY:6:G:H8	1.85	0.41
28:DD:276:LYS:H	28:DD:276:LYS:CD	2.15	0.41
27:DB:19:G:H1	27:DB:64:C:H42	1.67	0.41
1:AA:1362:C:C2'	1:AA:1363:C:H5''	2.49	0.41
1:AA:841:U:C5	1:AA:848:C:H1'	2.54	0.41
31:DG:137:GLU:HB3	31:DG:139:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:981:U:O5'	1:CA:981:U:H6	2.03	0.41
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.20	0.41
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.34	0.41
26:BA:288:C:H2'	26:BA:289:A:C8	2.49	0.41
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.20	0.41
1:CA:583:A:N6	1:CA:758:G:O2'	2.53	0.41
27:DB:80:U:H2'	27:DB:81:G:H8	1.85	0.41
26:DA:2483:C:O2	37:DQ:124:LYS:NZ	2.52	0.41
26:DA:2370:G:C6	26:DA:2371:G:C6	3.07	0.41
29:DE:146:THR:HA	29:DE:147:PRO:HA	1.90	0.41
1:CA:337:C:H2'	1:CA:338:A:C8	2.54	0.41
26:BA:2405:G:O2'	26:BA:2406:U:OP1	2.29	0.41
46:BZ:104:PHE:CZ	46:BZ:119:GLU:HG2	2.55	0.41
10:CJ:16:LEU:O	10:CJ:20:ALA:N	2.34	0.41
1:CA:1072:G:H2'	1:CA:1073:U:C6	2.55	0.41
1:CA:804:U:OP1	61:CA:3206:HOH:O	2.21	0.41
26:DA:2093:G:C6	26:DA:2225:A:C8	3.08	0.41
26:DA:2100:G:C6	26:DA:2190:G:C6	3.08	0.41
26:DA:2833:G:H4'	26:DA:2834:G:OP2	2.20	0.41
45:DY:2:ARG:NH1	45:DY:4:LYS:HA	2.35	0.41
27:BB:40:U:H1'	27:BB:45:A:H61	1.84	0.41
45:DY:9:LYS:HA	45:DY:10:GLY:HA2	1.49	0.41
26:DA:812:C:H2'	26:DA:813:U:H6	1.85	0.41
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	2.01	0.41
26:DA:460:A:C2	26:DA:470:A:C4	3.08	0.41
21:AU:15:ARG:HH11	21:AU:15:ARG:HB2	1.85	0.41
47:D0:52:GLY:O	47:D0:59:LEU:HA	2.20	0.41
28:BD:61:LEU:O	28:BD:63:ARG:NH1	2.53	0.41
26:BA:26:G:H1'	26:BA:515:A:H61	1.85	0.41
1:AA:571:U:H5''	1:AA:819:A:C5	2.55	0.41
31:DG:33:ARG:O	31:DG:34:LEU:HD23	2.19	0.41
25:AY:20:U:C4'	25:AY:21:A:H5'	2.50	0.41
25:AY:21:A:H8	25:AY:21:A:OP2	2.03	0.41
2:CB:16:HIS:HD2	2:CB:204:ASN:H	1.67	0.41
25:CY:56:C:H2'	25:CY:57:G:O4'	2.20	0.41
1:AA:78:G:O2'	1:AA:79:G:H8	2.03	0.41
19:AS:65:ASN:N	19:AS:65:ASN:ND2	2.66	0.41
26:DA:2297:C:N3	26:DA:2321:G:N2	2.66	0.41
26:BA:2135:A:N6	26:BA:2156:G:O2'	2.53	0.41
26:DA:878:A:H61	26:DA:899:A:HO2'	1.59	0.41
1:CA:1133:G:N2	1:CA:1141:C:N3	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1279:A:H5''	1:CA:1280:A:OP1	2.20	0.41
1:CA:1030(A):G:H2'	1:CA:1030(B):C:H5''	2.02	0.41
1:CA:1274:G:N2	1:CA:1275:A:H62	2.17	0.41
24:CX:30:G:C6	24:CX:31:G:N7	2.89	0.41
26:BA:2150:U:H2'	26:BA:2150:U:O2	2.19	0.41
26:BA:7:G:H2'	26:BA:8:A:O4'	2.20	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.84	0.41
1:CA:266:G:H8	1:CA:266:G:H2'	1.68	0.41
13:AM:5:ALA:HA	13:AM:61:GLU:OE2	2.18	0.41
51:B4:46:GLN:N	51:B4:46:GLN:HE21	2.18	0.41
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.03	0.41
1:CA:60:A:H4'	1:CA:61:G:O5'	2.21	0.41
26:DA:373:U:H2'	26:DA:374:A:C8	2.55	0.41
32:BH:54:ARG:HA	32:BH:55:PRO:HD3	1.87	0.41
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.53	0.41
26:BA:1903:G:OP1	28:BD:241:PRO:HB2	2.20	0.41
26:DA:2875:C:H2'	26:DA:2876:G:O4'	2.20	0.41
49:D2:23:LYS:O	49:D2:27:GLU:HG3	2.20	0.41
26:BA:1515:G:H2'	26:BA:1516:C:C6	2.55	0.41
20:CT:64:ASP:OD2	20:CT:81:LYS:NZ	2.44	0.41
26:BA:2784:C:H1'	29:BE:37:ARG:NH1	2.36	0.41
26:BA:2418:A:H2'	26:BA:2419:U:C6	2.54	0.41
1:AA:690:G:C6	1:AA:691:G:C6	3.08	0.41
26:DA:732:C:H2'	26:DA:733:G:O4'	2.20	0.41
26:BA:1038:C:H42	26:BA:1117:G:H1	1.68	0.41
26:DA:382:G:OP2	61:DA:4359:HOH:O	2.22	0.41
17:AQ:87:LYS:HA	17:AQ:87:LYS:HD3	1.73	0.41
30:BF:140:LEU:HA	30:BF:140:LEU:HD13	1.86	0.41
40:BT:27:THR:HB	40:BT:90:GLN:HB3	2.01	0.41
46:DZ:96:VAL:O	46:DZ:127:LYS:HA	2.20	0.41
19:AS:12:ASP:OD1	19:AS:35:SER:HB3	2.19	0.41
13:CM:72:ALA:O	13:CM:76:ALA:N	2.48	0.41
26:DA:2137:C:C2	26:DA:2138:C:C5	3.09	0.41
1:CA:1096:C:H2'	1:CA:1097:C:C6	2.55	0.41
26:BA:2135:A:N1	26:BA:2156:G:O2'	2.44	0.41
25:CY:35:A:H3'	25:CY:36:A:C8	2.55	0.41
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.56	0.41
23:AW:52:G:H4'	37:BQ:56:ARG:NH1	2.35	0.41
46:DZ:159:PRO:HA	46:DZ:161:VAL:H	1.84	0.41
1:AA:812:C:OP1	1:AA:903:G:H1'	2.19	0.41
1:CA:1044:A:C5	1:CA:1045:C:H1'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:22:G:N7	25:AY:46:7MG:C6	2.87	0.41
1:AA:160:A:H61	1:AA:345:C:H5'	1.86	0.41
27:DB:32:C:H2'	27:DB:33:G:O4'	2.20	0.41
13:AM:56:LEU:O	13:AM:60:VAL:HG23	2.19	0.41
26:BA:2142:C:C2	26:BA:2143:C:C5	3.08	0.41
26:DA:956:G:OP2	37:DQ:14:ARG:NH2	2.53	0.41
25:CY:18:G:N2	25:CY:55:PSU:N3	2.68	0.41
2:CB:70:PHE:CD1	2:CB:163:PHE:HB3	2.55	0.41
1:CA:51:A:N7	1:CA:114:U:O2'	2.53	0.41
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.51	0.41
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.20	0.41
46:DZ:98:MET:SD	46:DZ:100:VAL:HG23	2.60	0.41
26:DA:38:A:H2'	26:DA:39:C:C6	2.55	0.41
26:DA:565:C:H4'	26:DA:1253:A:N6	2.35	0.41
26:DA:1291:C:H2'	26:DA:1292:U:C6	2.55	0.41
1:AA:456:C:H2'	1:AA:457:C:H5'	2.02	0.41
26:DA:1860:G:C6	26:DA:1883:G:N2	2.88	0.41
26:DA:2366:A:H2'	26:DA:2367:G:O4'	2.20	0.41
1:AA:114:U:H2'	1:AA:115:G:C8	2.54	0.41
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.77	0.41
26:BA:652(C):G:N2	26:BA:652(V):C:N3	2.64	0.41
34:BN:67:LEU:HD12	34:BN:67:LEU:HA	1.82	0.41
26:BA:762:U:OP1	61:BA:4794:HOH:O	2.21	0.41
4:AD:194:LEU:HD12	4:AD:195:ALA:N	2.36	0.41
30:DF:20:LEU:HD23	30:DF:20:LEU:HA	1.90	0.41
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	2.01	0.41
46:DZ:124:ILE:HD11	46:DZ:163:LEU:HD11	2.02	0.41
8:CH:58:TYR:O	8:CH:59:LEU:HD23	2.19	0.41
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.86	0.41
48:D1:86:SER:OG	48:D1:89:GLU:OE2	2.19	0.41
1:CA:617:G:H4'	16:CP:44:THR:O	2.19	0.41
30:BF:120:GLU:HB2	30:BF:122:LYS:HG2	2.01	0.41
26:DA:980:A:C4	26:DA:1136:G:O4'	2.73	0.41
1:AA:6:G:O2'	1:AA:7:G:H5'	2.20	0.41
7:CG:65:ALA:O	7:CG:69:VAL:HG23	2.20	0.41
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.68	0.41
39:BS:59:LYS:HB2	39:BS:59:LYS:HE3	1.64	0.41
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.19	0.41
1:AA:624:C:O3'	16:AP:10:GLY:HA2	2.20	0.41
49:D2:41:ILE:HG13	49:D2:43:GLN:HB2	2.02	0.41
25:AY:68:C:C4	25:AY:69:G:N7	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1290:G:C4	1:CA:1291:G:C8	3.08	0.41
1:CA:1183:A:H5'	1:CA:1183:A:C8	2.53	0.41
37:DQ:18:LYS:HE3	37:DQ:18:LYS:HB2	1.68	0.41
23:AW:66:U:H2'	23:AW:67:C:C6	2.55	0.41
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.20	0.41
30:DF:178:PRO:HB2	30:DF:201:VAL:CG2	2.49	0.41
3:CC:66:VAL:HB	3:CC:101:LEU:HA	2.02	0.41
1:CA:1412:C:H2'	1:CA:1413:A:H8	1.81	0.41
1:CA:922:G:N3	1:CA:1398:A:H2	2.19	0.41
1:CA:445:G:H2'	1:CA:446:G:C8	2.55	0.41
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.68	0.41
37:DQ:81:VAL:HB	47:D0:7:LEU:HD21	2.01	0.41
13:CM:91:ARG:HH22	13:CM:103:THR:CG2	2.33	0.41
9:CI:96:LEU:O	9:CI:100:GLY:N	2.54	0.41
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.41
1:CA:1050:G:C6	1:CA:1051:C:C4	3.09	0.41
1:CA:607:A:H2'	1:CA:608:A:O4'	2.20	0.41
32:DH:90:LYS:HD2	32:DH:163:TYR:CD1	2.54	0.41
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.35	0.41
26:DA:108:U:H2'	26:DA:109:G:C8	2.56	0.41
1:CA:839:U:H5''	1:CA:840:C:C5	2.56	0.41
29:BE:96:PHE:O	29:BE:175:VAL:HG11	2.20	0.41
34:BN:61:ARG:HE	34:BN:61:ARG:HA	1.85	0.41
32:BH:56:SER:OG	32:BH:57:ASP:N	2.54	0.41
1:CA:1114:C:O2'	14:CN:60:SER:O	2.32	0.41
26:DA:96:G:H4'	49:D2:48:HIS:CD2	2.55	0.41
31:DG:38:VAL:HG22	31:DG:93:THR:HG23	2.02	0.41
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	2.03	0.41
1:CA:1468:A:H2'	1:CA:1469:G:O4'	2.21	0.41
36:DP:97:PRO:HD3	36:DP:126:VAL:O	2.19	0.41
2:CB:32:ILE:HD13	2:CB:40:HIS:CG	2.55	0.41
26:DA:859:G:O2'	26:DA:916:G:O6	2.24	0.41
19:CS:5:LEU:HG	19:CS:5:LEU:H	1.48	0.41
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.21	0.41
3:CC:116:VAL:O	3:CC:120:VAL:HG23	2.21	0.41
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	2.02	0.41
32:DH:117:PRO:HG3	32:DH:123:PHE:CD2	2.55	0.41
1:CA:237:C:H5''	17:CQ:25:ARG:CZ	2.49	0.41
26:DA:1638:C:H5''	26:DA:2710:C:O2'	2.21	0.41
25:AY:6:G:C6	25:AY:7:A:C6	3.08	0.41
25:CY:38:A:C2'	25:CY:39:PSU:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BX:31:HIS:HA	44:BX:32:PRO:HD3	1.96	0.41
1:AA:266:G:H4'	1:AA:267:C:C5	2.55	0.41
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.21	0.41
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.31	0.41
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.88	0.41
1:AA:975:A:H4'	1:AA:976:G:C5'	2.46	0.41
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	2.03	0.41
13:AM:40:ASN:HA	13:AM:41:PRO:HD3	1.84	0.41
1:CA:1373:G:H5''	7:CG:36:LYS:HD2	2.03	0.41
25:CY:76:A:H62	26:DA:2422:A:H5'	1.86	0.41
25:AY:62:C:H2'	25:AY:63:G:C8	2.51	0.41
26:BA:1359:A:N1	26:BA:1372:U:O4	2.54	0.41
26:DA:1857:G:C6	26:DA:1858:G:C6	3.08	0.41
1:CA:411:A:C8	1:CA:413:G:C8	3.09	0.41
1:AA:374:A:C6	1:AA:375:U:C4	3.08	0.41
13:AM:54:VAL:HA	13:AM:57:ARG:HB3	2.03	0.41
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.19	0.41
26:DA:266:G:N2	26:DA:427:U:H1'	2.35	0.41
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	2.03	0.41
26:BA:27:G:C2	26:BA:512:G:N3	2.88	0.41
4:AD:111:ALA:HB1	4:AD:116:GLN:HB3	2.03	0.41
1:AA:1152:A:H2'	1:AA:1153:C:C6	2.55	0.41
11:AK:81:ASP:HB3	11:AK:107:SER:OG	2.21	0.41
26:DA:120:U:H5''	26:DA:122:G:OP2	2.20	0.41
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	2.03	0.41
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.56	0.41
46:BZ:8:TYR:HB2	46:BZ:38:TYR:CE2	2.56	0.41
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	2.02	0.41
3:CC:11:ARG:HD3	3:CC:15:THR:HG21	2.01	0.41
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.55	0.41
24:AX:27:U:H2'	24:AX:28:C:C6	2.56	0.41
26:BA:493:G:H2'	26:BA:494:G:O4'	2.20	0.41
1:CA:932:C:H4'	7:CG:4:ARG:NH2	2.35	0.41
44:BX:12:VAL:HG21	44:BX:27:THR:HG22	2.03	0.41
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.53	0.41
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.19	0.41
1:AA:971:G:N2	1:AA:1363(A):A:OP2	2.46	0.41
12:CL:33:ARG:O	12:CL:85:ILE:HG12	2.21	0.41
51:D4:60:GLN:O	51:D4:63:TYR:HE2	2.03	0.41
1:AA:1002:G:H3'	1:AA:1003:G:O4'	2.20	0.41
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1179:A:C2	1:CA:1180:A:H1'	2.55	0.41
48:B1:85:LEU:HB3	48:B1:89:GLU:HG3	2.03	0.41
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.86	0.41
26:DA:2751:G:C8	32:DH:2:SER:HA	2.56	0.41
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.55	0.41
1:AA:1241:G:O2'	1:AA:1242:C:H5'	2.20	0.41
26:DA:1446:C:N4	26:DA:1465:G:H1	2.19	0.41
26:DA:1968:G:OP1	61:DA:4233:HOH:O	2.22	0.41
5:AE:77:PRO:HG2	5:AE:78:HIS:HD2	1.85	0.41
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.20	0.41
26:DA:79:G:H1	26:DA:107:C:N4	2.19	0.41
13:CM:50:GLU:O	13:CM:50:GLU:HG3	2.20	0.41
26:DA:1754:C:OP2	40:DT:113:LYS:HE2	2.21	0.41
1:AA:992:U:H4'	1:AA:993:G:C5'	2.50	0.41
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.21	0.41
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.36	0.41
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.41
1:CA:615:C:H2'	1:CA:616:G:O4'	2.20	0.41
1:AA:1368:G:OP2	9:AI:112:LYS:HG3	2.20	0.41
26:DA:1567:A:H2'	28:DD:84:TYR:HE2	1.86	0.41
1:CA:918:A:H2'	1:CA:919:A:O4'	2.21	0.41
21:CU:6:ARG:HG2	21:CU:15:ARG:HD2	2.02	0.41
40:BT:42:ILE:HG12	40:BT:84:GLN:NE2	2.36	0.41
20:AT:59:ALA:O	20:AT:63:ILE:HG13	2.21	0.41
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.02	0.41
26:BA:109:G:H2'	26:BA:110:G:O4'	2.20	0.41
34:DN:97:ARG:HA	34:DN:100:GLU:HB2	2.03	0.41
3:AC:179:ARG:NH1	3:AC:206:GLU:OE1	2.54	0.41
26:DA:2238:G:N3	26:DA:2238:G:H2'	2.35	0.41
30:BF:196:LEU:HA	30:BF:196:LEU:HD23	1.91	0.41
45:BY:55:TYR:CD1	45:BY:55:TYR:N	2.88	0.41
26:DA:431:U:H6	26:DA:431:U:O5'	2.02	0.41
38:BR:118:GLU:H	38:BR:118:GLU:CD	2.23	0.41
39:BS:83:LYS:HB2	39:BS:83:LYS:HE2	1.88	0.41
2:AB:92:TYR:CE1	2:AB:151:GLY:HA3	2.55	0.41
31:BG:33:ARG:N	31:BG:162:THR:OG1	2.52	0.41
26:BA:1518:U:H2'	26:BA:1519:G:O4'	2.20	0.41
29:BE:59:VAL:HG21	29:BE:74:PRO:HB3	2.02	0.41
26:DA:2161:C:H2'	26:DA:2162:G:O4'	2.20	0.41
9:CI:17:VAL:HG11	9:CI:81:ILE:N	2.36	0.41
27:DB:57:A:C4	31:DG:29:TRP:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.30	0.41
26:DA:624:C:O2'	26:DA:657:U:OP1	2.36	0.41
26:DA:1012:U:C4	34:DN:25:ARG:HG2	2.56	0.41
3:CC:70:VAL:HG13	3:CC:73:PRO:HA	2.02	0.41
1:CA:1070:U:O2'	1:CA:1071:C:H5'	2.21	0.41
23:CW:11:C:N4	23:CW:24:G:H1	2.17	0.41
28:DD:61:LEU:HA	28:DD:61:LEU:HD12	1.93	0.41
26:BA:2334:G:H4'	26:BA:2335:A:OP2	2.20	0.41
25:CY:27:G:N1	25:CY:43:C:O2	2.49	0.41
26:BA:2875:C:O2'	40:BT:4:GLY:HA3	2.21	0.41
34:DN:26:LEU:O	34:DN:30:ILE:HG13	2.21	0.41
13:CM:3:ARG:CB	51:D4:34:GLU:HG2	2.50	0.41
4:AD:57:ARG:HB3	4:AD:206:PHE:HB2	2.01	0.41
32:BH:11:VAL:CG2	32:BH:50:VAL:HG23	2.50	0.41
27:DB:118:G:C2'	27:DB:119:G:H5'	2.51	0.41
2:AB:47:THR:HA	2:AB:202:PRO:HG2	2.02	0.41
1:CA:418:C:H2'	1:CA:419:C:C6	2.56	0.41
46:DZ:4:ARG:HD3	46:DZ:60:GLU:OE1	2.21	0.41
26:BA:2712:U:O2'	26:BA:2713:A:H5'	2.21	0.41
6:CF:55:ASP:HA	6:CF:56:PRO:HD3	1.83	0.41
1:CA:340:U:H2'	1:CA:341:C:C6	2.56	0.41
32:DH:15:VAL:HG23	32:DH:27:LYS:O	2.21	0.41
26:DA:1470:G:N2	26:DA:1523:U:C4	2.88	0.41
8:AH:87:SER:HB2	8:AH:93:VAL:H	1.85	0.41
1:AA:1317:C:OP1	14:AN:17:LYS:HG2	2.19	0.41
1:CA:278:G:OP2	17:CQ:41:LYS:NZ	2.36	0.41
55:D8:34:TRP:CG	55:D8:35:GLN:N	2.89	0.41
1:AA:190:U:H3'	1:AA:190:U:H6	1.85	0.41
27:BB:75:G:H5''	27:BB:75:G:H8	1.85	0.41
26:BA:143:G:H2'	26:BA:143(A):C:C6	2.55	0.41
26:BA:2366:A:H2'	26:BA:2367:G:O4'	2.21	0.41
11:CK:82:VAL:HB	11:CK:108:ILE:HG12	2.02	0.41
1:AA:4:U:O4	8:AH:105:ARG:HD3	2.20	0.41
26:BA:881:G:H1	26:BA:897:C:N4	2.19	0.41
13:CM:37:THR:HG21	13:CM:56:LEU:HA	2.03	0.41
26:BA:2131:G:H5'	26:BA:2133:G:O4'	2.21	0.41
26:DA:899:A:C2'	26:DA:900:A:H5''	2.51	0.41
1:CA:1134:G:C2	1:CA:1135:U:H1'	2.56	0.41
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	2.02	0.41
1:AA:839:U:HO2'	1:AA:840:C:P	2.35	0.41
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2287:A:H2	26:BA:2346:A:H62	1.64	0.41
1:AA:154:C:N3	1:AA:168:G:C2	2.88	0.41
1:CA:443:C:H2'	1:CA:444:C:H6	1.85	0.41
51:B4:53:GLU:HB3	51:B4:54:GLY:O	2.21	0.41
26:BA:1179:C:H2'	26:BA:1180:C:C6	2.52	0.41
14:CN:45:ARG:O	14:CN:49:HIS:CD2	2.74	0.41
26:DA:889:C:O2'	26:DA:890:A:O5'	2.36	0.41
26:DA:1165:U:H6	26:DA:1165:U:O5'	2.04	0.41
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.73	0.41
26:DA:1445(A):C:H2'	26:DA:1446:C:C6	2.56	0.41
46:DZ:50:GLN:CD	46:DZ:50:GLN:N	2.73	0.41
26:DA:637:A:C8	36:DP:117:GLU:HG3	2.55	0.41
24:AX:61:C:H2'	24:AX:62:C:C6	2.56	0.41
50:B3:16:PRO:HB2	50:B3:18:ASP:OD1	2.20	0.41
30:DF:64:ILE:HG13	30:DF:65:TRP:N	2.36	0.41
31:DG:122:PRO:HG2	31:DG:182:LYS:O	2.20	0.41
1:CA:265:G:H5'	17:CQ:64:PRO:O	2.20	0.41
1:AA:1469:G:H2'	1:AA:1470:G:H8	1.86	0.41
8:AH:75:ARG:HA	8:AH:76:PRO:HD2	1.87	0.41
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.35	0.41
8:CH:35:ILE:HG22	8:CH:39:LEU:HD23	2.03	0.41
29:DE:5:LEU:HD21	29:DE:79:ARG:HB2	2.03	0.41
1:AA:920:U:H2'	1:AA:921:U:C6	2.55	0.41
26:BA:558:G:OP1	34:BN:111:PRO:HD2	2.21	0.41
1:AA:938:A:C6	1:AA:939:G:C5	3.09	0.41
14:AN:25:VAL:HG22	14:AN:38:GLY:O	2.20	0.41
1:AA:958:A:C6	1:AA:959:A:N1	2.88	0.41
1:AA:1418:A:H2	26:BA:1948:G:N3	2.19	0.41
46:DZ:70:LEU:O	46:DZ:89:PHE:N	2.44	0.41
26:BA:2070:G:C2	26:BA:2442:C:C2	3.09	0.41
51:B4:34:GLU:HG3	51:B4:34:GLU:H	1.56	0.41
28:DD:72:LYS:HE3	28:DD:72:LYS:HB3	1.85	0.41
45:BY:91:GLU:OE2	45:BY:91:GLU:N	2.54	0.41
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.41	0.41
1:AA:995:C:H5'	14:AN:8:GLU:HG2	2.02	0.41
14:CN:22:THR:HB	14:CN:33:VAL:HG21	2.03	0.41
29:BE:119:ARG:HD2	29:BE:120:TRP:CE2	2.55	0.41
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.55	0.41
26:BA:2138:C:C2	26:BA:2154:G:C2	3.08	0.41
1:AA:925:G:H1'	1:AA:1502:A:C4	2.55	0.41
1:CA:974:A:P	14:CN:29:ARG:HH21	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:974:A:O4'	14:CN:31:ARG:HD3	2.21	0.41
26:BA:2129:C:C2	26:BA:2130:U:H5	2.39	0.41
26:BA:2156:G:H21	26:BA:2157:G:H22	1.69	0.41
26:DA:899:A:O2'	26:DA:900:A:H5''	2.21	0.41
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.55	0.41
1:AA:1026:G:N3	1:AA:1026:G:H2'	2.35	0.41
13:AM:84:ILE:CG1	13:AM:85:GLY:HA2	2.44	0.41
33:BI:106:GLY:N	33:BI:107:VAL:HG23	2.36	0.41
1:CA:1321:C:H3'	1:CA:1322:C:C6	2.56	0.41
2:CB:48:MET:HA	2:CB:51:LEU:CD2	2.51	0.41
1:CA:1011:G:C2	1:CA:1019:C:C2	3.09	0.41
39:DS:15:ARG:HB3	39:DS:19:LYS:NZ	2.36	0.41
39:DS:16:ASN:O	39:DS:19:LYS:HG2	2.21	0.41
1:AA:1305:G:OP2	21:AU:2:GLY:N	2.53	0.41
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.41	0.41
13:CM:24:GLY:C	13:CM:25:ILE:HD12	2.41	0.41
1:AA:953:G:H5'	1:AA:965:A:N6	2.31	0.41
26:DA:819:A:C4	26:DA:1189:A:C2	3.09	0.41
50:B3:31:LEU:O	50:B3:32:GLN:HB2	2.21	0.41
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.87	0.41
8:AH:118:VAL:O	8:AH:119:LEU:HD23	2.21	0.41
1:AA:1060:C:C4	3:AC:2:GLY:HA3	2.56	0.41
1:AA:1457:G:P	20:AT:39:LYS:NZ	2.94	0.41
1:CA:1401:G:OP1	22:CV:18:G:O2'	2.28	0.41
3:CC:122:GLU:HA	3:CC:125:GLU:OE1	2.21	0.41
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.54	0.41
31:DG:105:LYS:NZ	51:D4:25:TYR:O	2.53	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
16:AP:72:ARG:O	16:AP:76:GLN:N	2.30	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.20	0.41
44:DX:1:MET:N	49:D2:29:LYS:HE3	2.36	0.41
28:BD:108:PRO:HB3	28:BD:143:HIS:HE1	1.84	0.41
23:AW:9:A:H1'	23:AW:45:U:H2'	2.03	0.41
17:AQ:9:VAL:CG2	17:AQ:84:LEU:HD13	2.50	0.41
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.39	0.41
4:CD:191:ARG:HD2	4:CD:191:ARG:HA	1.94	0.41
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.56	0.41
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.21	0.41
1:CA:131:C:H2'	1:CA:132:C:C6	2.55	0.41
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.21	0.41
1:CA:875:C:O2'	8:CH:14:ARG:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:9:VAL:HA	6:AF:59:TYR:O	2.20	0.41
1:CA:1252:A:H2'	1:CA:1253:G:O4'	2.21	0.41
26:DA:854:G:H2'	26:DA:855:G:C8	2.54	0.41
35:BO:10:VAL:HG21	35:BO:16:ALA:HB3	2.03	0.41
32:DH:35:VAL:HA	32:DH:36:PRO:HD2	1.94	0.41
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.54	0.41
37:DQ:79:LEU:C	37:DQ:80:GLU:HG2	2.42	0.41
1:AA:34:C:H2'	1:AA:35:G:C8	2.56	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.56	0.41
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.20	0.41
34:BN:39:ARG:HA	34:BN:40:PRO:HD3	1.84	0.41
32:DH:84:SER:CB	32:DH:132:ARG:HH11	2.33	0.41
13:CM:47:ASP:C	13:CM:48:LEU:HD23	2.41	0.41
26:DA:116:C:H2'	26:DA:117:G:O4'	2.21	0.41
1:AA:571:U:H5''	1:AA:819:A:C4	2.56	0.41
1:CA:1529:G:H4'	1:CA:1530:G:OP2	2.21	0.41
46:DZ:70:LEU:HA	46:DZ:70:LEU:HD23	1.80	0.41
26:DA:1257:C:H2'	26:DA:1258:C:C6	2.56	0.41
26:DA:2009:G:OP1	43:DW:41:LYS:HE2	2.20	0.41
26:DA:25:U:H5'	43:DW:78:GLU:O	2.21	0.41
26:BA:947:G:H2'	26:BA:948:G:C8	2.56	0.41
29:DE:2:LYS:NZ	29:DE:95:ILE:O	2.40	0.41
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	2.02	0.41
26:BA:391:G:H1'	26:BA:411:G:O4'	2.20	0.41
26:DA:923:C:H2'	26:DA:924:C:H6	1.84	0.41
15:CO:85:LEU:HA	15:CO:85:LEU:HD23	1.82	0.41
1:AA:1427:U:H2'	1:AA:1428:A:C8	2.55	0.41
9:CI:7:THR:OG1	9:CI:83:ARG:NH1	2.54	0.41
26:BA:1352:U:OP2	61:BA:4017:HOH:O	2.22	0.41
26:BA:2641:G:H5'	34:BN:83:LYS:HE2	2.03	0.41
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.21	0.41
49:B2:13:ALA:HA	49:B2:16:LEU:HD12	2.03	0.41
53:D6:43:CYS:O	53:D6:45:LYS:HG2	2.21	0.41
31:BG:137:GLU:HG2	31:BG:152:LEU:HD22	2.03	0.41
26:BA:2788:C:OP1	29:BE:61:ARG:NH2	2.48	0.41
13:AM:94:ARG:CZ	19:AS:80:TYR:HD2	2.34	0.41
54:D7:8:ASN:HB3	54:D7:11:LYS:HB3	2.02	0.41
1:AA:981:U:H6	1:AA:981:U:O5'	2.04	0.41
35:BO:9:GLU:H	35:BO:9:GLU:HG2	1.72	0.41
28:DD:213:ARG:HD2	28:DD:213:ARG:HA	1.86	0.41
49:D2:31:GLU:O	49:D2:35:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:DI:79:ILE:HA	33:DI:80:PRO:HD2	1.90	0.41
26:DA:793:A:OP2	26:DA:2072:G:H5'	2.20	0.41
26:DA:2135:A:H61	26:DA:2157:G:N2	2.19	0.41
25:AY:5:G:C6	25:AY:6:G:C6	3.08	0.41
26:BA:2154:G:H2'	26:BA:2155:G:H5'	2.03	0.41
1:CA:1163:C:C2	1:CA:1174:G:C2	3.09	0.41
1:AA:976:G:N2	1:AA:1363:C:OP2	2.45	0.41
3:AC:8:ILE:HA	3:AC:8:ILE:HD12	1.94	0.41
26:BA:1021:A:C8	26:BA:1022:G:H5''	2.55	0.41
31:DG:56:ALA:HA	31:DG:153:ARG:HH21	1.85	0.41
51:B4:53:GLU:O	51:B4:56:VAL:HG13	2.21	0.41
31:BG:56:ALA:HA	31:BG:153:ARG:HH21	1.86	0.41
1:CA:757:U:O2'	1:CA:879:C:O2	2.38	0.41
1:CA:423:G:H3'	1:CA:423:G:N3	2.35	0.41
26:DA:1005:C:H2'	26:DA:1006:C:H6	1.83	0.41
26:DA:590:A:P	30:DF:95:ARG:HH11	2.44	0.41
26:BA:1408:C:H2'	26:BA:1409:C:C6	2.56	0.41
20:CT:36:LEU:HA	20:CT:36:LEU:HD13	1.90	0.41
26:BA:606:U:H4'	26:BA:658:C:H4'	2.03	0.41
26:DA:642:G:H21	26:DA:646:A:H2	1.68	0.41
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.52	0.41
6:AF:61:LEU:HD13	6:AF:61:LEU:HA	1.86	0.41
1:CA:1267:C:N4	1:CA:1268:A:C6	2.89	0.41
1:CA:61:G:C5	1:CA:107:G:C2	3.08	0.41
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.21	0.41
30:BF:165:ARG:HG2	30:BF:168:ARG:NH2	2.36	0.41
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	2.02	0.41
27:BB:92:C:OP1	46:BZ:79:ARG:NH1	2.54	0.41
26:BA:1477:A:C2	26:BA:1515:G:C2	3.09	0.41
26:DA:25:U:C4	26:DA:26:G:C6	3.09	0.41
24:CX:3:C:H2'	24:CX:4:G:C8	2.56	0.41
12:CL:89:ARG:HG2	12:CL:90:VAL:N	2.36	0.41
22:AV:16:A:H2'	22:AV:17:U:O4'	2.21	0.41
26:DA:1518:U:H2'	26:DA:1519:G:O4'	2.20	0.41
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.20	0.41
26:DA:706:A:H2'	26:DA:707:G:O4'	2.21	0.41
26:BA:1649:G:O2'	38:BR:107:ASP:OD2	2.32	0.41
1:AA:439:A:C8	1:AA:496:A:C6	3.09	0.41
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.21	0.41
26:BA:481:G:C4	26:BA:507:A:C2	3.09	0.41
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.21	0.41
8:CH:64:LYS:HB3	8:CH:79:VAL:HG21	2.02	0.41
26:DA:2669:G:C2	26:DA:2670:A:C8	3.09	0.41
32:DH:54:ARG:HB3	32:DH:65:HIS:CD2	2.56	0.41
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.53	0.41
26:BA:2273:A:H2'	26:BA:2274:A:C8	2.55	0.41
35:DO:20:MET:HE3	35:DO:44:LYS:HE3	2.03	0.41
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.49	0.41
37:BQ:48:GLU:O	37:BQ:52:VAL:HG23	2.20	0.41
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.56	0.40
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.56	0.40
26:BA:1171:G:N7	26:BA:1173:G:C8	2.89	0.40
26:BA:2191:G:H8	26:BA:2191:G:C5'	2.33	0.40
25:CY:36:A:C2	25:CY:37:MIA:C4	3.04	0.40
19:CS:3:ARG:NH2	19:CS:10:PHE:HB2	2.36	0.40
1:AA:1028:C:C2	1:AA:1029:C:H1'	2.56	0.40
26:DA:2037:G:O2'	26:DA:2038:G:H5'	2.22	0.40
2:CB:48:MET:HA	2:CB:51:LEU:HD21	2.02	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:N	2.35	0.40
26:BA:1107:G:N2	26:BA:1108:U:O4	2.54	0.40
26:DA:953:A:OP2	37:DQ:16:ARG:NE	2.50	0.40
1:AA:165:C:H2'	1:AA:166:G:C8	2.56	0.40
26:BA:2447:G:N2	26:BA:2450:A:OP2	2.53	0.40
26:DA:528:A:C2	26:DA:2043:C:H4'	2.57	0.40
1:AA:183:G:H1	1:AA:194:C:H42	1.69	0.40
19:AS:42:PRO:HD2	51:B4:61:ARG:HH21	1.86	0.40
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.21	0.40
26:BA:1860:G:N2	26:BA:1882:C:O2	2.49	0.40
1:AA:44:G:N7	61:AA:4044:HOH:O	2.37	0.40
42:DV:58:VAL:O	42:DV:97:LYS:N	2.45	0.40
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.46	0.40
2:AB:161:ALA:HB1	2:AB:185:ILE:HD11	2.02	0.40
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.54	0.40
26:DA:2848:G:H8	40:DT:97:ALA:HB2	1.85	0.40
30:BF:177:ALA:O	30:BF:180:GLY:N	2.45	0.40
26:BA:242:G:H5''	55:B8:64:TYR:CZ	2.57	0.40
1:CA:130:A:H1'	1:CA:263:A:O2'	2.20	0.40
29:BE:51:PHE:CD2	29:BE:52:LEU:HG	2.56	0.40
26:DA:271(H):G:O2'	26:DA:271(I):G:C8	2.74	0.40
29:DE:72:VAL:HG12	29:DE:73:GLU:O	2.21	0.40
26:DA:2694:G:C6	26:DA:2695:C:C4	3.08	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:531:C:OP1	26:DA:561:G:N1	2.50	0.40
29:BE:144:ARG:HB3	29:BE:145:LYS:H	1.53	0.40
15:CO:3:ILE:H	15:CO:3:ILE:HD13	1.86	0.40
10:CJ:42:THR:HG23	10:CJ:68:HIS:HD2	1.86	0.40
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.22	0.40
1:AA:1047:G:C2'	1:AA:1048:G:H5'	2.51	0.40
2:AB:183:PRO:HA	2:AB:198:ASP:OD2	2.21	0.40
1:CA:9:G:H2'	1:CA:10:A:C8	2.56	0.40
26:BA:274:G:H2'	26:BA:275:G:C8	2.56	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.22	0.40
1:CA:629:G:H2'	1:CA:630:G:O4'	2.21	0.40
1:CA:1325:C:H4'	21:CU:17:THR:HG21	2.02	0.40
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.21	0.40
31:BG:64:THR:HB	31:BG:94:LEU:HD21	2.03	0.40
32:BH:94:TYR:HA	32:BH:106:THR:O	2.21	0.40
46:BZ:158:PRO:HA	46:BZ:159:PRO:HD3	1.90	0.40
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.21	0.40
26:DA:195:A:H2'	26:DA:198:C:N4	2.36	0.40
45:DY:74:PRO:O	45:DY:82:PRO:HA	2.20	0.40
4:CD:179:GLU:O	4:CD:181:MET:HE2	2.21	0.40
26:DA:1479:G:C2	26:DA:1480:G:C4	3.09	0.40
36:DP:135:LEU:HA	36:DP:135:LEU:HD23	1.79	0.40
15:CO:31:LEU:HD23	15:CO:31:LEU:HA	1.89	0.40
46:BZ:76:LEU:HA	46:BZ:76:LEU:HD12	1.87	0.40
14:AN:50:LYS:HB2	14:AN:50:LYS:HE2	1.76	0.40
26:DA:2058:A:N7	61:DA:3874:HOH:O	2.37	0.40
12:CL:119:LYS:O	12:CL:120:TYR:HB2	2.21	0.40
26:BA:470:A:OP1	30:BF:59:TYR:HE1	2.03	0.40
1:CA:895:G:N7	61:CA:3246:HOH:O	2.37	0.40
26:DA:2137:C:N3	26:DA:2138:C:N4	2.68	0.40
25:AY:18:G:O6	25:AY:55:PSU:H1'	2.21	0.40
26:BA:2138:C:C4	26:BA:2154:G:C6	3.10	0.40
25:CY:9:A:H5'	25:CY:46:7MG:C1'	2.52	0.40
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	2.02	0.40
23:AW:19:G:H4'	23:AW:20:U:OP1	2.20	0.40
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.86	0.40
4:CD:108:LEU:HD12	4:CD:108:LEU:HA	1.74	0.40
26:DA:1359:A:N1	26:DA:1372:U:C4	2.89	0.40
2:CB:201:ILE:HA	2:CB:202:PRO:HD2	1.97	0.40
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.21	0.40
1:CA:1118:C:N4	1:CA:1119:C:H41	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:B5:40:LYS:HE2	52:B5:46:CYS:HA	2.04	0.40
3:AC:134:ILE:HD11	3:AC:153:VAL:HG23	2.04	0.40
27:DB:50:G:OP1	39:DS:63:THR:HG22	2.21	0.40
8:AH:123:GLU:O	8:AH:127:LEU:HD13	2.22	0.40
1:CA:981:U:H5'	14:CN:21:TYR:CE2	2.56	0.40
26:BA:1022:G:C6	26:BA:1141:U:C5	3.09	0.40
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	2.02	0.40
3:CC:70:VAL:HG22	3:CC:72:LYS:N	2.35	0.40
16:CP:69:THR:O	16:CP:72:ARG:HB2	2.22	0.40
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.40
26:BA:1421:G:C2	26:BA:1422:G:C8	3.10	0.40
26:DA:885:C:H2'	26:DA:886:C:C4'	2.51	0.40
32:DH:9:ILE:HG12	32:DH:69:ARG:HD2	2.04	0.40
1:AA:993:G:N3	1:AA:993:G:H2'	2.35	0.40
26:DA:2542:A:H4'	26:DA:2543:G:C8	2.56	0.40
26:DA:2542:A:H4'	26:DA:2543:G:H8	1.87	0.40
29:DE:52:LEU:O	29:DE:76:ARG:N	2.33	0.40
2:AB:47:THR:HG22	2:AB:51:LEU:HD11	2.03	0.40
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.21	0.40
26:DA:511:U:H4'	26:DA:1235:G:H4'	2.03	0.40
3:CC:105:GLU:OE1	3:CC:107:GLN:N	2.55	0.40
1:CA:1350:A:C2	1:CA:1351:U:C2	3.09	0.40
4:CD:76:ARG:NE	4:CD:80:GLU:OE1	2.50	0.40
2:CB:77:ALA:HB2	2:CB:165:VAL:HG11	2.03	0.40
26:DA:1482:G:C6	26:DA:1507:A:C2	3.08	0.40
36:BP:88:LEU:HD22	36:BP:95:VAL:HG21	2.03	0.40
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.20	0.40
11:CK:18:ARG:NH2	11:CK:35:PRO:O	2.49	0.40
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	2.03	0.40
27:BB:78:A:H2'	27:BB:79:C:O4'	2.21	0.40
11:CK:87:THR:O	11:CK:87:THR:OG1	2.37	0.40
26:DA:581:C:H2'	26:DA:582:G:C8	2.56	0.40
48:D1:50:ARG:NH1	48:D1:57:GLU:OE2	2.54	0.40
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.56	0.40
26:DA:2136:C:O2'	26:DA:2137:C:H6	2.05	0.40
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.22	0.40
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.36	0.40
4:CD:3:ARG:O	4:CD:5:ILE:HG22	2.21	0.40
46:DZ:97:GLU:HA	46:DZ:126:VAL:O	2.21	0.40
27:DB:57:A:O4'	31:DG:30:GLU:HG3	2.21	0.40
46:DZ:79:ARG:HD2	46:DZ:80:ARG:CZ	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:426:G:OP1	4:CD:36:ARG:NH1	2.42	0.40
1:AA:1358:U:OP2	1:AA:1359:C:N4	2.54	0.40
26:DA:587:C:OP2	36:DP:21:ARG:NH2	2.55	0.40
17:AQ:75:ARG:HH12	17:AQ:77:VAL:HA	1.86	0.40
39:DS:36:TYR:CD2	39:DS:52:SER:HB3	2.56	0.40
26:DA:2689:U:C4'	26:DA:2690:C:H5'	2.48	0.40
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	2.02	0.40
1:CA:255:G:P	17:CQ:69:LYS:HZ1	2.42	0.40
3:CC:70:VAL:N	3:CC:106:VAL:HG23	2.37	0.40
24:CX:47:U:H3'	24:CX:48:C:C5'	2.51	0.40
24:CX:58:A:O2'	24:CX:60:U:OP2	2.34	0.40
1:CA:300:A:H1'	1:CA:565:U:O2	2.20	0.40
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.21	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.21	0.40
26:BA:2331:G:O2'	47:B0:43:THR:HG22	2.21	0.40
54:D7:10:ARG:O	54:D7:14:LYS:HB2	2.22	0.40
35:BO:10:VAL:HG11	35:BO:16:ALA:HB1	2.04	0.40
2:AB:77:ALA:O	2:AB:81:VAL:HG22	2.20	0.40
26:DA:1777:U:O2'	26:DA:1778:U:H5'	2.20	0.40
7:AG:29:LYS:HD3	7:AG:29:LYS:HA	1.92	0.40
41:DU:103:PRO:O	41:DU:107:ALA:N	2.50	0.40
1:CA:9:G:H2'	1:CA:10:A:H8	1.85	0.40
42:BV:6:LYS:HG2	42:BV:11:GLN:HG2	2.03	0.40
6:AF:95:GLU:HA	6:AF:96:PRO:HD3	1.98	0.40
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.54	0.40
13:CM:95:GLY:HA2	13:CM:110:ARG:NH1	2.36	0.40
13:AM:117:VAL:HG12	13:AM:118:ALA:O	2.21	0.40
26:BA:2506:U:C2	26:BA:2585:U:O4	2.75	0.40
26:BA:1851:U:H2'	26:BA:1852:C:O4'	2.21	0.40
26:DA:1487:G:H2'	26:DA:1488:G:H5''	2.04	0.40
2:CB:197:VAL:HB	2:CB:200:ILE:HG12	2.03	0.40
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	2.03	0.40
56:D9:29:ASN:HA	56:D9:30:PRO:HD3	1.88	0.40
49:B2:64:LEU:CD2	49:B2:68:ARG:HE	2.34	0.40
38:DR:78:LYS:HE2	38:DR:83:ILE:HD11	2.04	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
36:BP:47:ASP:HA	36:BP:48:PRO:HD3	1.92	0.40
1:AA:1166:G:H5'	1:AA:1168:A:OP2	2.21	0.40
1:AA:1001:A:N1	1:AA:1040:U:O4	2.54	0.40
2:CB:42:ILE:HG21	2:CB:202:PRO:HB2	2.03	0.40
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:376:G:O2'	16:AP:5:ARG:NH2	2.54	0.40
26:DA:1653:G:H3'	38:DR:2:ARG:HD3	2.04	0.40
26:BA:2262:U:H4'	26:BA:2328:A:C2	2.56	0.40
26:DA:2224:G:H4'	26:DA:2226:C:C2	2.56	0.40
26:DA:478:A:H62	26:DA:502:A:N6	2.19	0.40
1:AA:57:G:H2'	1:AA:58:C:C6	2.57	0.40
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.57	0.40
2:CB:15:VAL:CG1	2:CB:209:ARG:HB3	2.49	0.40
14:AN:27:CYS:SG	14:AN:29:ARG:HB2	2.61	0.40
26:DA:2273:A:H2'	26:DA:2274:A:H8	1.85	0.40
1:AA:49:U:O4	1:AA:365:U:H5	2.05	0.40
24:CX:50:U:H3	24:CX:64:G:H1	1.68	0.40
1:CA:1442:G:C8	1:CA:1442:G:H3'	2.56	0.40
26:DA:2755:C:HO2'	26:DA:2756:U:H6	1.69	0.40
1:AA:1118:C:OP1	9:AI:9:ARG:NH1	2.53	0.40
1:AA:201:C:H2'	1:AA:202:U:H2'	2.03	0.40
51:B4:40:HIS:HA	51:B4:41:PRO:HD2	1.88	0.40
1:AA:737:A:OP1	6:AF:92:LYS:HG3	2.21	0.40
26:BA:335:C:H5'	45:BY:73:ARG:NH2	2.36	0.40
48:D1:23:LYS:HB2	48:D1:23:LYS:HE3	1.79	0.40
35:BO:23:ARG:HG3	35:BO:24:VAL:N	2.36	0.40
19:AS:41:VAL:O	19:AS:44:MET:HB2	2.21	0.40
29:DE:24:THR:CG2	29:DE:184:VAL:HG12	2.52	0.40
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.22	0.40
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	2.04	0.40
26:DA:469:G:H2'	26:DA:470:A:H5''	2.02	0.40
1:AA:7:G:H5''	1:AA:298:A:O4'	2.22	0.40
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.56	0.40
26:BA:286:C:H2'	26:BA:287:C:C6	2.57	0.40
35:DO:9:GLU:OE2	35:DO:18:LYS:HE3	2.21	0.40
26:DA:19:C:H2'	26:DA:20:C:H6	1.86	0.40
32:DH:77:LYS:HG3	32:DH:81:GLU:OE2	2.21	0.40
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.17	0.40
1:AA:784:C:H2'	1:AA:785:G:O4'	2.22	0.40
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.37	0.40
26:BA:303:U:O4	61:BA:4656:HOH:O	2.22	0.40
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.42	0.40
40:BT:80:SER:HA	40:BT:81:PRO:HD3	1.89	0.40
30:BF:93:LYS:HA	30:BF:93:LYS:HD3	1.91	0.40
44:DX:64:LYS:HA	44:DX:64:LYS:HD2	1.88	0.40
28:BD:38:LYS:HD2	28:BD:38:LYS:HA	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CX:28:C:H2'	24:CX:29:G:C8	2.56	0.40
24:CX:28:C:H2'	24:CX:29:G:H8	1.85	0.40
26:DA:1773:A:H5''	61:DA:4357:HOH:O	2.21	0.40
42:DV:39:LEU:HG	42:DV:46:VAL:O	2.21	0.40
26:BA:526:A:H5''	26:BA:527:C:OP1	2.21	0.40
52:D5:11:THR:HG22	52:D5:12:SER:O	2.21	0.40
26:BA:536:A:H2'	26:BA:537:C:C6	2.56	0.40
26:DA:1501:C:O4'	28:DD:100:GLY:HA2	2.21	0.40
1:CA:1065:U:P	1:CA:1190:G:H22	2.45	0.40
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.22	0.40
1:CA:1028:C:O2	1:CA:1034:G:H1'	2.21	0.40
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.57	0.40
12:AL:24:VAL:HG13	12:AL:98:TYR:CE2	2.57	0.40
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.40
8:CH:27:PRO:O	8:CH:32:LYS:HD2	2.22	0.40
38:DR:1:MET:HB2	38:DR:2:ARG:H	1.71	0.40
1:CA:643:C:H2'	1:CA:644:G:C8	2.57	0.40
26:BA:1022:G:N2	26:BA:1142(A):A:C2	2.80	0.40
26:DA:661:C:H2'	26:DA:662:G:C8	2.56	0.40
31:DG:97:ASP:O	31:DG:101:ILE:HG13	2.21	0.40
2:CB:12:GLU:C	2:CB:14:GLY:HA3	2.41	0.40
35:DO:2:ILE:HB	35:DO:33:ALA:HB3	2.03	0.40
1:CA:407:G:H5''	4:CD:115:ARG:HB3	2.03	0.40
1:AA:22:G:H4'	1:AA:885:G:C8	2.57	0.40
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.82	0.40
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.42	0.40
1:CA:1100:C:H2'	1:CA:1102:A:O5'	2.22	0.40
26:DA:1011:G:C2	26:DA:1151:G:N3	2.90	0.40
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.21	0.40
26:BA:1230:C:H2'	26:BA:1231:G:H8	1.86	0.40
1:AA:38:G:O2'	1:AA:39:G:H5''	2.21	0.40
26:DA:729:G:C6	28:DD:208:LYS:HB2	2.56	0.40
26:DA:1604:C:O2'	26:DA:1610:A:N1	2.38	0.40
31:DG:51:ARG:H	31:DG:51:ARG:HG3	1.69	0.40
26:DA:2734:A:H2'	26:DA:2735:G:O4'	2.21	0.40
1:CA:377:G:H5'	16:CP:5:ARG:NH2	2.37	0.40
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.52	0.40
26:BA:125:G:N2	54:B7:48:LYS:HA	2.36	0.40
1:AA:881:G:H2'	1:AA:882:C:O4'	2.21	0.40
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.22	0.40
2:CB:189:ASP:O	2:CB:192:SER:OG	2.40	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.44	0.40
1:AA:1261:A:H3'	1:AA:1262:C:H6	1.87	0.40
26:BA:1817:G:C6	26:BA:1818:U:C4	3.10	0.40
26:BA:484:C:H2'	26:BA:485:C:H6	1.87	0.40
53:D6:8:LYS:HD3	55:D8:34:TRP:CD2	2.56	0.40
26:DA:195:A:H2'	26:DA:198:C:H41	1.86	0.40
26:BA:303:U:H2'	26:BA:304:G:C8	2.56	0.40
26:DA:2625:G:H2'	26:DA:2626:C:O4'	2.22	0.40
29:DE:201:THR:OG1	29:DE:202:LYS:N	2.55	0.40
1:CA:179:A:C2'	1:CA:180:U:H5'	2.52	0.40
56:D9:12:ASP:OD1	56:D9:13:LYS:HG2	2.21	0.40
26:BA:1753:G:N1	26:BA:1756:G:OP2	2.53	0.40
12:AL:7:ILE:O	12:AL:11:VAL:HG23	2.21	0.40
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.85	0.40
26:BA:2147:G:H2'	26:BA:2148:G:O4'	2.22	0.40
28:BD:258:LYS:HE2	28:BD:273:ARG:CZ	2.51	0.40
26:DA:463:G:N2	26:DA:466:A:OP2	2.49	0.40
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.57	0.40
35:BO:79:PHE:CD2	40:BT:72:VAL:HG22	2.56	0.40
7:AG:97:GLN:HB2	7:AG:97:GLN:HE21	1.66	0.40
20:CT:24:LEU:HA	20:CT:24:LEU:HD13	1.71	0.40
6:CF:82:ARG:HD2	6:CF:82:ARG:HA	1.71	0.40
1:CA:408:A:H2'	1:CA:409:G:O4'	2.21	0.40
31:BG:38:VAL:HG22	31:BG:93:THR:HG23	2.03	0.40
51:D4:13:ARG:O	51:D4:30:GLU:HA	2.20	0.40
1:CA:785:G:C2'	1:CA:786:G:H5'	2.51	0.40
1:AA:719:C:H1'	18:AR:49:LYS:HB3	2.03	0.40
16:AP:54:GLU:HG3	16:AP:55:ARG:N	2.37	0.40
38:DR:96:ARG:HD3	38:DR:98:LEU:HD11	2.04	0.40
26:DA:1935:G:H1'	26:DA:1964:G:N2	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	208 (91%)	13 (6%)	8 (4%)	4	6
2	CB	229/256 (90%)	208 (91%)	14 (6%)	7 (3%)	5	8
3	AC	204/239 (85%)	193 (95%)	10 (5%)	1 (0%)	34	60
3	CC	204/239 (85%)	191 (94%)	13 (6%)	0	100	100
4	AD	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
4	CD	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	34	60
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
5	CE	146/162 (90%)	142 (97%)	3 (2%)	1 (1%)	26	51
6	AF	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
6	CF	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
7	AG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	26	51
7	CG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	26	51
8	AH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
8	CH	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
9	AI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	24	46
9	CI	125/128 (98%)	120 (96%)	4 (3%)	1 (1%)	24	46
10	AJ	95/105 (90%)	85 (90%)	8 (8%)	2 (2%)	9	16
10	CJ	94/105 (90%)	84 (89%)	6 (6%)	4 (4%)	3	4
11	AK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	21	42
11	CK	112/129 (87%)	107 (96%)	4 (4%)	1 (1%)	21	42
12	AL	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
12	CL	120/132 (91%)	117 (98%)	2 (2%)	1 (1%)	24	46
13	AM	121/126 (96%)	116 (96%)	4 (3%)	1 (1%)	24	46
13	CM	120/126 (95%)	113 (94%)	4 (3%)	3 (2%)	7	12
14	AN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
14	CN	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	AP	80/88 (91%)	78 (98%)	2 (2%)	0	100	100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	15	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
17	CQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
18	AR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
19	AS	82/93 (88%)	76 (93%)	5 (6%)	1 (1%)	16	33
19	CS	81/93 (87%)	75 (93%)	6 (7%)	0	100	100
20	AT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	2	2
20	CT	94/106 (89%)	85 (90%)	4 (4%)	5 (5%)	2	2
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
21	CU	21/27 (78%)	21 (100%)	0	0	100	100
28	BD	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	39	65
28	DD	273/276 (99%)	261 (96%)	10 (4%)	2 (1%)	26	51
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	34	60
29	DE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	34	60
30	BF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	34	60
30	DF	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	34	60
31	BG	179/182 (98%)	171 (96%)	7 (4%)	1 (1%)	30	56
31	DG	179/182 (98%)	168 (94%)	8 (4%)	3 (2%)	11	22
32	BH	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
32	DH	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
33	BI	144/148 (97%)	132 (92%)	7 (5%)	5 (4%)	4	6
33	DI	144/148 (97%)	135 (94%)	8 (6%)	1 (1%)	26	51
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
34	DN	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
36	BP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	26	51
36	DP	147/150 (98%)	139 (95%)	6 (4%)	2 (1%)	14	28
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	26	51
38	BR	116/118 (98%)	115 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	DR	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
39	BS	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
39	DS	108/112 (96%)	107 (99%)	0	1 (1%)	21	42
40	BT	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
40	DT	129/146 (88%)	126 (98%)	3 (2%)	0	100	100
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	114 (100%)	0	0	100	100
42	BV	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	19	39
42	DV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	19	39
43	BW	110/113 (97%)	110 (100%)	0	0	100	100
43	DW	110/113 (97%)	110 (100%)	0	0	100	100
44	BX	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
44	DX	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	17	36
45	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
45	DY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
46	BZ	169/206 (82%)	153 (90%)	15 (9%)	1 (1%)	30	56
46	DZ	172/206 (84%)	159 (92%)	13 (8%)	0	100	100
47	B0	81/85 (95%)	81 (100%)	0	0	100	100
47	D0	81/85 (95%)	79 (98%)	1 (1%)	1 (1%)	16	33
48	B1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	36
48	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	17	36
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%)	56 (98%)	1 (2%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	54 (81%)	9 (13%)	4 (6%)	2	2
51	D4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	3	4
52	B5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
52	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
53	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
53	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	8	15
55	B8	62/65 (95%)	62 (100%)	0	0	100	100
55	D8	62/65 (95%)	62 (100%)	0	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	11410/12128 (94%)	10945 (96%)	381 (3%)	84 (1%)	26	51

All (84) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	17	PHE
2	AB	19	HIS
2	AB	231	GLU
9	AI	54	ASP
10	AJ	56	HIS
28	BD	275	LYS
30	BF	130	ALA
33	BI	106	GLY
33	BI	107	VAL
48	B1	3	LYS
51	B4	53	GLU
51	B4	62	ARG
2	CB	8	LYS
2	CB	16	HIS
2	CB	17	PHE
2	CB	123	ALA
2	CB	126	GLU
2	CB	231	GLU
9	CI	54	ASP
10	CJ	56	HIS
10	CJ	75	ILE
13	CM	67	GLU
13	CM	85	GLY
31	DG	14	GLU
51	D4	39	CYS
51	D4	45	GLY
51	D4	62	ARG
54	D7	46	VAL
2	AB	10	LEU

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Mol	Chain	Res	Type
2	AB	16	HIS
3	AC	66	VAL
7	AG	55	GLY
10	AJ	31	GLY
19	AS	84	GLY
20	AT	10	LEU
20	AT	47	GLY
20	AT	96	GLY
20	AT	100	ILE
33	BI	105	HIS
42	BV	79	VAL
51	B4	47	GLN
2	CB	20	GLU
4	CD	46	LYS
5	CE	37	ARG
7	CG	55	GLY
10	CJ	78	ASN
20	CT	47	GLY
31	DG	81	LYS
42	DV	79	VAL
48	D1	3	LYS
13	AM	67	GLU
29	BE	52	LEU
33	BI	10	GLU
10	CJ	55	LYS
20	CT	102	GLY
28	DD	239	ARG
31	DG	47	LYS
33	DI	10	GLU
39	DS	84	GLN
2	AB	125	PRO
11	AK	105	VAL
20	CT	10	LEU
28	DD	3	VAL
29	DE	52	LEU
36	DP	45	LEU
47	D0	4	LYS
2	AB	11	LEU
31	BG	47	LYS
46	BZ	159	PRO
51	B4	59	PHE
11	CK	105	VAL

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Mol	Chain	Res	Type
30	DF	130	ALA
44	DX	2	LYS
33	BI	73	GLU
36	BP	29	LYS
36	DP	29	LYS
37	DQ	27	VAL
20	AT	102	GLY
16	CP	53	VAL
20	CT	100	ILE
13	CM	4	ILE
12	CL	30	ALA
20	CT	96	GLY
2	AB	234	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	155 (81%)	37 (19%)	2	3
2	CB	187/220 (85%)	151 (81%)	36 (19%)	2	3
3	AC	143/188 (76%)	127 (89%)	16 (11%)	7	13
3	CC	141/188 (75%)	116 (82%)	25 (18%)	2	3
4	AD	170/181 (94%)	147 (86%)	23 (14%)	5	8
4	CD	174/181 (96%)	147 (84%)	27 (16%)	3	5
5	AE	113/123 (92%)	106 (94%)	7 (6%)	23	45
5	CE	114/123 (93%)	99 (87%)	15 (13%)	5	9
6	AF	84/90 (93%)	74 (88%)	10 (12%)	6	11
6	CF	86/90 (96%)	79 (92%)	7 (8%)	15	28
7	AG	119/127 (94%)	99 (83%)	20 (17%)	2	4
7	CG	120/127 (94%)	106 (88%)	14 (12%)	7	12
8	AH	114/119 (96%)	101 (89%)	13 (11%)	7	12
8	CH	114/119 (96%)	97 (85%)	17 (15%)	4	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AI	91/99 (92%)	73 (80%)	18 (20%)	1	2
9	CI	89/99 (90%)	69 (78%)	20 (22%)	1	2
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	12	22
10	CJ	69/92 (75%)	61 (88%)	8 (12%)	7	12
11	AK	83/99 (84%)	74 (89%)	9 (11%)	8	15
11	CK	83/99 (84%)	72 (87%)	11 (13%)	5	8
12	AL	97/109 (89%)	88 (91%)	9 (9%)	11	21
12	CL	97/109 (89%)	85 (88%)	12 (12%)	6	11
13	AM	95/101 (94%)	81 (85%)	14 (15%)	4	6
13	CM	92/101 (91%)	74 (80%)	18 (20%)	1	2
14	AN	49/50 (98%)	40 (82%)	9 (18%)	2	3
14	CN	49/50 (98%)	37 (76%)	12 (24%)	1	1
15	AO	78/80 (98%)	70 (90%)	8 (10%)	9	16
15	CO	78/80 (98%)	67 (86%)	11 (14%)	4	7
16	AP	69/74 (93%)	58 (84%)	11 (16%)	3	5
16	CP	68/74 (92%)	59 (87%)	9 (13%)	5	9
17	AQ	94/97 (97%)	87 (93%)	7 (7%)	17	34
17	CQ	94/97 (97%)	84 (89%)	10 (11%)	8	15
18	AR	59/77 (77%)	50 (85%)	9 (15%)	3	5
18	CR	59/77 (77%)	46 (78%)	13 (22%)	1	2
19	AS	70/80 (88%)	59 (84%)	11 (16%)	3	5
19	CS	67/80 (84%)	54 (81%)	13 (19%)	2	3
20	AT	70/82 (85%)	60 (86%)	10 (14%)	4	7
20	CT	71/82 (87%)	62 (87%)	9 (13%)	5	10
21	AU	18/22 (82%)	15 (83%)	3 (17%)	3	4
21	CU	18/22 (82%)	15 (83%)	3 (17%)	3	4
28	BD	215/218 (99%)	196 (91%)	19 (9%)	12	24
28	DD	216/218 (99%)	200 (93%)	16 (7%)	17	34
29	BE	164/166 (99%)	145 (88%)	19 (12%)	7	12
29	DE	164/166 (99%)	141 (86%)	23 (14%)	4	7
30	BF	160/166 (96%)	142 (89%)	18 (11%)	7	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	DF	159/166 (96%)	138 (87%)	21 (13%)	5	9
31	BG	143/156 (92%)	127 (89%)	16 (11%)	7	13
31	DG	142/156 (91%)	119 (84%)	23 (16%)	3	5
32	BH	144/148 (97%)	129 (90%)	15 (10%)	9	16
32	DH	144/148 (97%)	124 (86%)	20 (14%)	4	7
33	BI	110/124 (89%)	88 (80%)	22 (20%)	1	2
33	DI	107/124 (86%)	87 (81%)	20 (19%)	2	3
34	BN	118/119 (99%)	101 (86%)	17 (14%)	4	7
34	DN	118/119 (99%)	101 (86%)	17 (14%)	4	7
35	BO	100/100 (100%)	92 (92%)	8 (8%)	15	29
35	DO	100/100 (100%)	89 (89%)	11 (11%)	8	14
36	BP	116/116 (100%)	104 (90%)	12 (10%)	9	16
36	DP	115/116 (99%)	103 (90%)	12 (10%)	9	16
37	BQ	111/111 (100%)	95 (86%)	16 (14%)	4	7
37	DQ	111/111 (100%)	97 (87%)	14 (13%)	5	10
38	BR	101/101 (100%)	83 (82%)	18 (18%)	2	3
38	DR	101/101 (100%)	86 (85%)	15 (15%)	4	6
39	BS	87/88 (99%)	79 (91%)	8 (9%)	11	21
39	DS	85/88 (97%)	74 (87%)	11 (13%)	5	9
40	BT	115/127 (91%)	107 (93%)	8 (7%)	19	37
40	DT	113/127 (89%)	105 (93%)	8 (7%)	18	36
41	BU	93/94 (99%)	86 (92%)	7 (8%)	17	33
41	DU	93/94 (99%)	87 (94%)	6 (6%)	21	42
42	BV	80/82 (98%)	70 (88%)	10 (12%)	6	10
42	DV	80/82 (98%)	67 (84%)	13 (16%)	3	5
43	BW	90/92 (98%)	83 (92%)	7 (8%)	16	30
43	DW	90/92 (98%)	84 (93%)	6 (7%)	20	40
44	BX	77/78 (99%)	72 (94%)	5 (6%)	21	42
44	DX	77/78 (99%)	70 (91%)	7 (9%)	12	22
45	BY	85/91 (93%)	77 (91%)	8 (9%)	11	20
45	DY	85/91 (93%)	78 (92%)	7 (8%)	14	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	BZ	145/179 (81%)	128 (88%)	17 (12%)	7	12
46	DZ	145/179 (81%)	127 (88%)	18 (12%)	6	11
47	B0	65/67 (97%)	61 (94%)	4 (6%)	23	45
47	D0	65/67 (97%)	59 (91%)	6 (9%)	11	21
48	B1	80/83 (96%)	72 (90%)	8 (10%)	9	18
48	D1	80/83 (96%)	71 (89%)	9 (11%)	7	13
49	B2	65/67 (97%)	59 (91%)	6 (9%)	11	21
49	D2	65/67 (97%)	60 (92%)	5 (8%)	16	31
50	B3	51/52 (98%)	47 (92%)	4 (8%)	16	30
50	D3	50/52 (96%)	47 (94%)	3 (6%)	24	47
51	B4	60/63 (95%)	51 (85%)	9 (15%)	3	6
51	D4	53/63 (84%)	38 (72%)	15 (28%)	0	1
52	B5	50/52 (96%)	46 (92%)	4 (8%)	15	29
52	D5	50/52 (96%)	48 (96%)	2 (4%)	38	67
53	B6	51/52 (98%)	45 (88%)	6 (12%)	6	12
53	D6	50/52 (96%)	47 (94%)	3 (6%)	24	47
54	B7	41/42 (98%)	39 (95%)	2 (5%)	31	57
54	D7	41/42 (98%)	39 (95%)	2 (5%)	31	57
55	B8	54/55 (98%)	50 (93%)	4 (7%)	17	34
55	D8	54/55 (98%)	50 (93%)	4 (7%)	17	34
56	B9	34/34 (100%)	33 (97%)	1 (3%)	50	77
56	D9	34/34 (100%)	33 (97%)	1 (3%)	50	77
All	All	9336/10066 (93%)	8180 (88%)	1156 (12%)	6	11

All (1156) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	15	VAL
2	AB	17	PHE
2	AB	19	HIS
2	AB	20	GLU
2	AB	21	ARG
2	AB	24	TRP

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Mol	Chain	Res	Type
2	AB	35	GLU
2	AB	48	MET
2	AB	60	ASP
2	AB	64	ARG
2	AB	67	THR
2	AB	74	LYS
2	AB	76	GLN
2	AB	84	GLU
2	AB	94	ASN
2	AB	121	LEU
2	AB	127	ILE
2	AB	137	ARG
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	160	ASP
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	195	ASP
2	AB	196	LEU
2	AB	200	ILE
2	AB	208	ILE
2	AB	209	ARG
2	AB	217	ARG
2	AB	221	LEU
2	AB	223	ILE
2	AB	230	VAL
3	AC	3	ASN
3	AC	8	ILE
3	AC	15	THR
3	AC	27	LYS
3	AC	45	LYS
3	AC	52	LEU
3	AC	77	ILE
3	AC	98	ASN
3	AC	101	LEU
3	AC	118	GLN
3	AC	131	ARG
3	AC	136	GLN

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Mol	Chain	Res	Type
3	AC	178	LEU
3	AC	179	ARG
3	AC	190	ARG
3	AC	195	VAL
4	AD	3	ARG
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	28	SER
4	AD	31	CYS
4	AD	49	ARG
4	AD	50	ARG
4	AD	58	LEU
4	AD	65	ARG
4	AD	86	LYS
4	AD	91	SER
4	AD	108	LEU
4	AD	112	VAL
4	AD	115	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	144	ASP
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	194	LEU
4	AD	196	LEU
5	AE	6	PHE
5	AE	10	MET
5	AE	12	LEU
5	AE	31	LEU
5	AE	41	VAL
5	AE	47	LYS
5	AE	151	LEU
6	AF	10	LEU
6	AF	17	SER
6	AF	28	ARG
6	AF	40	VAL
6	AF	45	LEU
6	AF	55	ASP
6	AF	61	LEU
6	AF	70	ASP

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Mol	Chain	Res	Type
6	AF	75	LEU
6	AF	82	ARG
7	AG	8	GLU
7	AG	12	LEU
7	AG	16	LEU
7	AG	24	THR
7	AG	31	MET
7	AG	38	LEU
7	AG	51	GLN
7	AG	61	VAL
7	AG	72	ARG
7	AG	73	MET
7	AG	76	ARG
7	AG	78	ARG
7	AG	79	ARG
7	AG	91	VAL
7	AG	97	GLN
7	AG	104	LEU
7	AG	113	GLU
7	AG	115	ARG
7	AG	138	LYS
7	AG	155	ARG
8	AH	25	ASP
8	AH	37	ARG
8	AH	39	LEU
8	AH	50	ARG
8	AH	52	ASP
8	AH	63	LEU
8	AH	78	GLN
8	AH	84	ARG
8	AH	91	ARG
8	AH	107	LEU
8	AH	112	LEU
8	AH	122	ARG
8	AH	137	VAL
9	AI	9	ARG
9	AI	11	LYS
9	AI	23	ASN
9	AI	42	ARG
9	AI	56	LEU
9	AI	64	THR
9	AI	65	VAL

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Mol	Chain	Res	Type
9	AI	71	SER
9	AI	75	ASP
9	AI	78	LYS
9	AI	81	ILE
9	AI	89	ASN
9	AI	93	ARG
9	AI	102	LEU
9	AI	103	THR
9	AI	121	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	9	ARG
10	AJ	16	LEU
10	AJ	43	ARG
10	AJ	84	GLN
10	AJ	92	THR
11	AK	31	THR
11	AK	48	ILE
11	AK	51	LYS
11	AK	81	ASP
11	AK	87	THR
11	AK	91	ARG
11	AK	96	ARG
11	AK	106	LYS
11	AK	114	VAL
12	AL	16	GLU
12	AL	33	ARG
12	AL	47	LYS
12	AL	52	LEU
12	AL	54	LYS
12	AL	60	LEU
12	AL	67	THR
12	AL	83	VAL
12	AL	89	ARG
13	AM	3	ARG
13	AM	4	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	43	THR
13	AM	46	LYS
13	AM	56	LEU

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Mol	Chain	Res	Type
13	AM	70	LEU
13	AM	73	GLU
13	AM	94	ARG
13	AM	98	VAL
13	AM	110	ARG
13	AM	115	LYS
13	AM	121	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	9	LYS
14	AN	12	ARG
14	AN	13	THR
14	AN	18	VAL
14	AN	32	SER
14	AN	50	LYS
15	AO	5	LYS
15	AO	7	GLU
15	AO	22	THR
15	AO	26	GLU
15	AO	38	ARG
15	AO	39	LEU
15	AO	76	GLU
15	AO	83	GLU
16	AP	1	MET
16	AP	5	ARG
16	AP	8	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	67	THR
16	AP	69	THR
16	AP	71	ARG
17	AQ	49	GLU
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	92	ARG
17	AQ	97	SER

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Mol	Chain	Res	Type
18	AR	31	LEU
18	AR	35	ARG
18	AR	37	VAL
18	AR	38	GLU
18	AR	46	GLU
18	AR	55	ARG
18	AR	58	LEU
18	AR	68	LYS
18	AR	76	LEU
19	AS	5	LEU
19	AS	12	ASP
19	AS	17	GLU
19	AS	36	ARG
19	AS	37	ARG
19	AS	63	THR
19	AS	65	ASN
19	AS	70	LYS
19	AS	78	ARG
19	AS	81	ARG
19	AS	85	LYS
20	AT	8	ARG
20	AT	13	LEU
20	AT	19	SER
20	AT	24	LEU
20	AT	31	SER
20	AT	45	GLN
20	AT	58	LYS
20	AT	60	GLU
20	AT	62	LEU
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
21	AU	24	ARG
28	BD	3	VAL
28	BD	22	SER
28	BD	32	SER
28	BD	38	LYS
28	BD	61	LEU
28	BD	71	ASP
28	BD	94	LEU
28	BD	99	ASP
28	BD	106	ILE

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Mol	Chain	Res	Type
28	BD	116	GLN
28	BD	126	GLN
28	BD	211	ARG
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	242	ARG
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG
29	BE	8	LYS
29	BE	9	VAL
29	BE	12	THR
29	BE	34	VAL
29	BE	47	VAL
29	BE	75	VAL
29	BE	77	ILE
29	BE	78	LEU
29	BE	82	ARG
29	BE	89	ASP
29	BE	116	VAL
29	BE	119	ARG
29	BE	127	ASP
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	181	LEU
29	BE	184	VAL
30	BF	12	LEU
30	BF	19	GLU
30	BF	33	LEU
30	BF	43	LYS
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	132	VAL
30	BF	140	LEU

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Mol	Chain	Res	Type
30	BF	162	LEU
30	BF	192	LEU
30	BF	197	ASP
30	BF	200	GLU
30	BF	201	VAL
31	BG	3	LEU
31	BG	7	LEU
31	BG	22	ARG
31	BG	43	LEU
31	BG	45	GLU
31	BG	49	ASP
31	BG	81	LYS
31	BG	82	LEU
31	BG	86	MET
31	BG	139	LEU
31	BG	143	GLU
31	BG	146	TYR
31	BG	159	VAL
31	BG	170	ARG
31	BG	175	LEU
31	BG	181	ARG
32	BH	2	SER
32	BH	6	ARG
32	BH	13	LYS
32	BH	45	VAL
32	BH	51	ARG
32	BH	69	ARG
32	BH	71	LEU
32	BH	76	VAL
32	BH	92	ILE
32	BH	98	LEU
32	BH	105	LEU
32	BH	116	GLU
32	BH	119	GLU
32	BH	122	THR
32	BH	124	GLU
33	BI	5	LEU
33	BI	9	LEU
33	BI	20	ASP
33	BI	38	LEU
33	BI	41	GLU
33	BI	43	ASN

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Mol	Chain	Res	Type
33	BI	47	LEU
33	BI	52	ARG
33	BI	58	LEU
33	BI	61	ARG
33	BI	62	LYS
33	BI	64	GLU
33	BI	66	GLU
33	BI	77	LEU
33	BI	78	THR
33	BI	86	THR
33	BI	92	VAL
33	BI	96	ASP
33	BI	101	LEU
33	BI	107	VAL
33	BI	116	LEU
33	BI	117	GLU
34	BN	1	MET
34	BN	5	VAL
34	BN	8	GLN
34	BN	9	VAL
34	BN	12	ARG
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	48	MET
34	BN	61	ARG
34	BN	67	LEU
34	BN	68	GLU
34	BN	87	LEU
34	BN	99	LEU
34	BN	120	LEU
34	BN	138	LEU
34	BN	140	VAL
35	BO	8	LEU
35	BO	10	VAL
35	BO	18	LYS
35	BO	24	VAL
35	BO	66	LYS
35	BO	98	VAL
35	BO	105	GLU
35	BO	108	GLU
36	BP	1	MET

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Mol	Chain	Res	Type
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	95	VAL
36	BP	98	GLU
36	BP	101	VAL
36	BP	106	LEU
36	BP	112	LEU
36	BP	121	LYS
36	BP	144	GLU
36	BP	149	GLU
37	BQ	1	MET
37	BQ	7	MET
37	BQ	8	LYS
37	BQ	16	ARG
37	BQ	21	THR
37	BQ	22	LYS
37	BQ	45	GLN
37	BQ	54	MET
37	BQ	55	VAL
37	BQ	60	ARG
37	BQ	63	LYS
37	BQ	75	THR
37	BQ	80	GLU
37	BQ	85	LYS
37	BQ	109	VAL
37	BQ	110	THR
38	BR	1	MET
38	BR	18	LEU
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	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	86	ARG
38	BR	100	LEU

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Mol	Chain	Res	Type
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	3	ARG
39	BS	20	ARG
39	BS	49	VAL
39	BS	52	SER
39	BS	59	LYS
39	BS	69	VAL
39	BS	73	LEU
39	BS	83	LYS
40	BT	28	VAL
40	BT	49	VAL
40	BT	53	ARG
40	BT	74	ARG
40	BT	78	LEU
40	BT	96	ARG
40	BT	118	ARG
40	BT	128	GLU
41	BU	8	VAL
41	BU	27	LEU
41	BU	31	SER
41	BU	74	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
42	BV	21	ARG
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	15	ARG
43	BW	17	VAL
43	BW	51	LEU
43	BW	67	ASP

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Mol	Chain	Res	Type
43	BW	107	LEU
44	BX	2	LYS
44	BX	35	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	43	ASN
45	BY	55	TYR
45	BY	73	ARG
45	BY	99	CYS
46	BZ	5	LEU
46	BZ	18	LEU
46	BZ	19	ARG
46	BZ	50	GLN
46	BZ	76	LEU
46	BZ	91	LEU
46	BZ	102	LEU
46	BZ	107	THR
46	BZ	117	LEU
46	BZ	120	ILE
46	BZ	129	SER
46	BZ	131	ARG
46	BZ	136	PHE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	169	GLU
47	B0	10	THR
47	B0	20	ARG
47	B0	55	ARG
47	B0	74	ARG
48	B1	3	LYS
48	B1	21	ARG
48	B1	23	LYS
48	B1	35	THR
48	B1	40	ARG
48	B1	59	THR
48	B1	78	LYS

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Mol	Chain	Res	Type
48	B1	95	LEU
49	B2	19	VAL
49	B2	30	ARG
49	B2	32	LEU
49	B2	40	SER
49	B2	55	ARG
49	B2	70	GLN
50	B3	3	ARG
50	B3	8	LEU
50	B3	23	LEU
50	B3	54	VAL
51	B4	3	GLU
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE
51	B4	56	VAL
51	B4	58	ARG
51	B4	63	TYR
51	B4	66	SER
51	B4	68	ARG
52	B5	6	VAL
52	B5	29	THR
52	B5	40	LYS
52	B5	55	ARG
53	B6	4	GLU
53	B6	6	ARG
53	B6	14	THR
53	B6	28	ARG
53	B6	38	LYS
53	B6	48	VAL
54	B7	9	ARG
54	B7	43	THR
55	B8	6	THR
55	B8	31	HIS
55	B8	46	ARG
55	B8	59	LYS
56	B9	4	ARG
2	CB	8	LYS
2	CB	15	VAL
2	CB	19	HIS
2	CB	23	ARG
2	CB	24	TRP

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Mol	Chain	Res	Type
2	CB	35	GLU
2	CB	50	GLU
2	CB	51	LEU
2	CB	60	ASP
2	CB	73	THR
2	CB	74	LYS
2	CB	76	GLN
2	CB	78	GLN
2	CB	87	ARG
2	CB	94	ASN
2	CB	97	TRP
2	CB	108	ILE
2	CB	115	LEU
2	CB	117	GLU
2	CB	119	GLU
2	CB	122	PHE
2	CB	124	SER
2	CB	126	GLU
2	CB	128	GLU
2	CB	139	LYS
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	158	LEU
2	CB	160	ASP
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	217	ARG
2	CB	224	GLN
2	CB	235	SER
3	CC	3	ASN
3	CC	15	THR
3	CC	17	ASP
3	CC	21	ARG
3	CC	33	LEU
3	CC	45	LYS
3	CC	47	LEU
3	CC	52	LEU
3	CC	54	ARG
3	CC	72	LYS
3	CC	85	ARG

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Mol	Chain	Res	Type
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	115	LEU
3	CC	128	PHE
3	CC	131	ARG
3	CC	151	VAL
3	CC	152	ILE
3	CC	164	ARG
3	CC	179	ARG
3	CC	190	ARG
3	CC	195	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	50	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	85	LYS
4	CD	86	LYS
4	CD	96	LEU
4	CD	107	ARG
4	CD	108	LEU
4	CD	122	ARG
4	CD	127	THR
4	CD	135	LEU
4	CD	145	GLU
4	CD	150	GLU
4	CD	155	LEU
4	CD	156	GLU
4	CD	169	LYS
4	CD	170	VAL
4	CD	181	MET
4	CD	184	LYS
4	CD	187	ARG
4	CD	194	LEU
4	CD	208	SER
5	CE	6	PHE

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Mol	Chain	Res	Type
5	CE	10	MET
5	CE	12	LEU
5	CE	18	ARG
5	CE	27	ARG
5	CE	31	LEU
5	CE	41	VAL
5	CE	47	LYS
5	CE	60	TYR
5	CE	64	ARG
5	CE	78	HIS
5	CE	79	GLU
5	CE	117	ASP
5	CE	147	ASP
5	CE	150	ARG
6	CF	17	SER
6	CF	21	LEU
6	CF	27	GLN
6	CF	28	ARG
6	CF	45	LEU
6	CF	82	ARG
6	CF	87	ARG
7	CG	6	ARG
7	CG	12	LEU
7	CG	24	THR
7	CG	32	ARG
7	CG	36	LYS
7	CG	41	ARG
7	CG	51	GLN
7	CG	72	ARG
7	CG	76	ARG
7	CG	97	GLN
7	CG	104	LEU
7	CG	114	ARG
7	CG	115	ARG
7	CG	155	ARG
8	CH	3	THR
8	CH	25	ASP
8	CH	29	SER
8	CH	52	ASP
8	CH	63	LEU
8	CH	78	GLN
8	CH	84	ARG

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Mol	Chain	Res	Type
8	CH	85	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	103	VAL
8	CH	111	ILE
8	CH	112	LEU
8	CH	125	ARG
8	CH	127	LEU
8	CH	135	CYS
8	CH	137	VAL
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN
9	CI	40	LEU
9	CI	51	ARG
9	CI	56	LEU
9	CI	64	THR
9	CI	65	VAL
9	CI	75	ASP
9	CI	81	ILE
9	CI	83	ARG
9	CI	88	TYR
9	CI	89	ASN
9	CI	102	LEU
9	CI	103	THR
9	CI	104	ARG
9	CI	121	ARG
9	CI	124	GLN
9	CI	125	TYR
9	CI	128	ARG
10	CJ	6	ILE
10	CJ	21	GLN
10	CJ	34	VAL
10	CJ	59	SER
10	CJ	67	THR
10	CJ	74	ILE
10	CJ	81	THR
10	CJ	98	ILE
11	CK	24	SER
11	CK	31	THR
11	CK	41	THR
11	CK	48	ILE

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Mol	Chain	Res	Type
11	CK	54	ARG
11	CK	92	GLU
11	CK	93	GLN
11	CK	96	ARG
11	CK	104	GLN
11	CK	123	LYS
11	CK	126	ARG
12	CL	33	ARG
12	CL	36	VAL
12	CL	39	VAL
12	CL	47	LYS
12	CL	60	LEU
12	CL	62	SER
12	CL	75	HIS
12	CL	83	VAL
12	CL	104	VAL
12	CL	114	LYS
12	CL	117	ARG
12	CL	124	LYS
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	29	ARG
13	CM	32	GLU
13	CM	44	ARG
13	CM	50	GLU
13	CM	52	GLU
13	CM	56	LEU
13	CM	63	THR
13	CM	66	LEU
13	CM	70	LEU
13	CM	71	ARG
13	CM	73	GLU
13	CM	84	ILE
13	CM	98	VAL
13	CM	105	THR
13	CM	121	LYS
14	CN	3	ARG
14	CN	7	ILE
14	CN	11	LYS
14	CN	13	THR
14	CN	15	LYS

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Mol	Chain	Res	Type
14	CN	17	LYS
14	CN	18	VAL
14	CN	22	THR
14	CN	23	ARG
14	CN	26	ARG
14	CN	32	SER
14	CN	46	GLU
15	CO	3	ILE
15	CO	4	THR
15	CO	5	LYS
15	CO	22	THR
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	48	LYS
15	CO	68	ARG
15	CO	83	GLU
15	CO	87	ILE
16	CP	1	MET
16	CP	2	VAL
16	CP	5	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	60	LEU
16	CP	67	THR
16	CP	69	THR
16	CP	71	ARG
17	CQ	36	ILE
17	CQ	37	LYS
17	CQ	49	GLU
17	CQ	55	ASP
17	CQ	63	ARG
17	CQ	69	LYS
17	CQ	74	LEU
17	CQ	75	ARG
17	CQ	83	ASP
17	CQ	91	ARG
18	CR	25	THR
18	CR	26	LEU
18	CR	28	GLU
18	CR	32	ARG
18	CR	37	VAL

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Mol	Chain	Res	Type
18	CR	41	LYS
18	CR	42	ARG
18	CR	56	THR
18	CR	58	LEU
18	CR	68	LYS
18	CR	76	LEU
18	CR	84	LYS
18	CR	87	ARG
19	CS	5	LEU
19	CS	15	LEU
19	CS	22	LEU
19	CS	30	LEU
19	CS	56	GLN
19	CS	63	THR
19	CS	64	GLU
19	CS	65	ASN
19	CS	66	MET
19	CS	77	THR
19	CS	78	ARG
19	CS	81	ARG
19	CS	83	HIS
20	CT	8	ARG
20	CT	24	LEU
20	CT	45	GLN
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	84	LEU
20	CT	93	GLU
21	CU	9	ARG
21	CU	10	ARG
21	CU	12	LYS
28	DD	61	LEU
28	DD	94	LEU
28	DD	99	ASP
28	DD	106	ILE
28	DD	113	VAL
28	DD	126	GLN
28	DD	134	ARG
28	DD	142	VAL
28	DD	211	ARG

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Mol	Chain	Res	Type
28	DD	221	VAL
28	DD	229	VAL
28	DD	242	ARG
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG
28	DD	276	LYS
29	DE	7	VAL
29	DE	9	VAL
29	DE	12	THR
29	DE	21	VAL
29	DE	34	VAL
29	DE	38	THR
29	DE	40	GLU
29	DE	47	VAL
29	DE	52	LEU
29	DE	61	ARG
29	DE	73	GLU
29	DE	75	VAL
29	DE	82	ARG
29	DE	89	ASP
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
29	DE	184	VAL
29	DE	195	LEU
30	DF	12	LEU
30	DF	17	ARG
30	DF	19	GLU
30	DF	20	LEU
30	DF	33	LEU
30	DF	53	THR
30	DF	57	VAL
30	DF	70	THR
30	DF	74	ARG
30	DF	88	VAL
30	DF	106	ARG
30	DF	110	LEU

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Mol	Chain	Res	Type
30	DF	132	VAL
30	DF	135	LYS
30	DF	140	LEU
30	DF	152	GLU
30	DF	157	VAL
30	DF	183	VAL
30	DF	192	LEU
30	DF	201	VAL
30	DF	205	ARG
31	DG	7	LEU
31	DG	9	ARG
31	DG	16	ARG
31	DG	19	LEU
31	DG	31	VAL
31	DG	35	GLU
31	DG	43	LEU
31	DG	47	LYS
31	DG	49	ASP
31	DG	84	LYS
31	DG	97	ASP
31	DG	98	ARG
31	DG	111	LEU
31	DG	113	ARG
31	DG	115	ARG
31	DG	116	ASP
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	148	MET
31	DG	152	LEU
31	DG	164	GLU
31	DG	170	ARG
32	DH	3	ARG
32	DH	6	ARG
32	DH	33	LEU
32	DH	34	GLU
32	DH	41	MET
32	DH	42	ARG
32	DH	45	VAL
32	DH	49	VAL
32	DH	65	HIS
32	DH	69	ARG

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Mol	Chain	Res	Type
32	DH	81	GLU
32	DH	95	ARG
32	DH	98	LEU
32	DH	111	HIS
32	DH	124	GLU
32	DH	136	ILE
32	DH	139	GLN
32	DH	148	ILE
32	DH	171	LEU
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	14	ASP
33	DI	15	VAL
33	DI	20	ASP
33	DI	38	LEU
33	DI	41	GLU
33	DI	43	ASN
33	DI	44	LEU
33	DI	57	ARG
33	DI	58	LEU
33	DI	75	LEU
33	DI	77	LEU
33	DI	78	THR
33	DI	86	THR
33	DI	102	SER
33	DI	114	LEU
33	DI	121	LYS
33	DI	135	GLU
33	DI	140	LEU
34	DN	5	VAL
34	DN	12	ARG
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	48	MET
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	88	GLU

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Mol	Chain	Res	Type
34	DN	89	LYS
34	DN	120	LEU
34	DN	137	LYS
34	DN	138	LEU
34	DN	140	VAL
35	DO	8	LEU
35	DO	9	GLU
35	DO	10	VAL
35	DO	24	VAL
35	DO	53	LYS
35	DO	66	LYS
35	DO	69	ILE
35	DO	70	LYS
35	DO	78	ARG
35	DO	92	GLU
35	DO	113	LYS
36	DP	15	ARG
36	DP	45	LEU
36	DP	55	ARG
36	DP	56	SER
36	DP	65	ARG
36	DP	95	VAL
36	DP	98	GLU
36	DP	106	LEU
36	DP	112	LEU
36	DP	121	LYS
36	DP	136	GLU
36	DP	144	GLU
37	DQ	1	MET
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	48	GLU
37	DQ	55	VAL
37	DQ	56	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	80	GLU
37	DQ	85	LYS
37	DQ	109	VAL
37	DQ	110	THR
37	DQ	133	ARG

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Mol	Chain	Res	Type
38	DR	1	MET
38	DR	18	LEU
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	60	LEU
38	DR	65	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	86	ARG
38	DR	100	LEU
38	DR	111	LEU
39	DS	19	LYS
39	DS	20	ARG
39	DS	35	ILE
39	DS	44	LYS
39	DS	49	VAL
39	DS	52	SER
39	DS	58	LEU
39	DS	67	ARG
39	DS	73	LEU
39	DS	78	LEU
39	DS	83	LYS
40	DT	31	SER
40	DT	59	THR
40	DT	78	LEU
40	DT	85	LYS
40	DT	96	ARG
40	DT	98	LYS
40	DT	113	LYS
40	DT	118	ARG
41	DU	31	SER
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	18	LEU

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Mol	Chain	Res	Type
42	DV	21	ARG
42	DV	24	LYS
42	DV	38	LEU
42	DV	46	VAL
42	DV	52	VAL
42	DV	57	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	95	LEU
42	DV	100	ARG
43	DW	4	LYS
43	DW	11	ARG
43	DW	17	VAL
43	DW	51	LEU
43	DW	60	ASN
43	DW	107	LEU
44	DX	44	GLU
44	DX	52	VAL
44	DX	57	LEU
44	DX	64	LYS
44	DX	66	LEU
44	DX	70	LEU
44	DX	92	LEU
45	DY	6	HIS
45	DY	23	ARG
45	DY	26	LYS
45	DY	43	ASN
45	DY	49	VAL
45	DY	91	GLU
45	DY	99	CYS
46	DZ	5	LEU
46	DZ	11	GLU
46	DZ	14	LYS
46	DZ	18	LEU
46	DZ	33	LEU
46	DZ	35	ARG
46	DZ	59	LEU
46	DZ	71	VAL
46	DZ	92	SER
46	DZ	97	GLU
46	DZ	100	VAL

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Mol	Chain	Res	Type
46	DZ	102	LEU
46	DZ	107	THR
46	DZ	120	ILE
46	DZ	131	ARG
46	DZ	136	PHE
46	DZ	154	ASP
46	DZ	157	LEU
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
47	D0	55	ARG
47	D0	68	GLU
47	D0	74	ARG
48	D1	3	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	40	ARG
48	D1	59	THR
48	D1	85	LEU
48	D1	89	GLU
48	D1	95	LEU
48	D1	97	LEU
49	D2	21	LEU
49	D2	30	ARG
49	D2	32	LEU
49	D2	55	ARG
49	D2	70	GLN
50	D3	8	LEU
50	D3	30	ARG
50	D3	55	ARG
51	D4	1	MET
51	D4	3	GLU
51	D4	5	ILE
51	D4	8	LYS
51	D4	10	VAL
51	D4	13	ARG
51	D4	14	ILE
51	D4	23	GLU
51	D4	31	ILE
51	D4	56	VAL
51	D4	58	ARG
51	D4	61	ARG

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Mol	Chain	Res	Type
51	D4	63	TYR
51	D4	68	ARG
51	D4	69	LYS
52	D5	6	VAL
52	D5	40	LYS
53	D6	6	ARG
53	D6	14	THR
53	D6	38	LYS
54	D7	1	MET
54	D7	14	LYS
55	D8	26	LYS
55	D8	31	HIS
55	D8	34	TRP
55	D8	50	LEU
56	D9	4	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (127) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	76	GLN
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	118	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	42	GLN
4	AD	77	ASN
4	AD	123	HIS
5	AE	20	GLN
5	AE	38	GLN
5	AE	73	ASN
5	AE	141	GLN
6	AF	73	ASN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	97	GLN
9	AI	23	ASN
9	AI	31	GLN
9	AI	58	HIS
9	AI	73	GLN

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Mol	Chain	Res	Type
9	AI	89	ASN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	104	GLN
12	AL	78	GLN
13	AM	92	HIS
15	AO	28	GLN
17	AQ	16	GLN
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
20	AT	9	ASN
20	AT	26	ASN
20	AT	45	GLN
20	AT	73	HIS
28	BD	164	GLN
28	BD	166	GLN
28	BD	253	GLN
30	BF	8	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
31	BG	40	ASN
33	BI	43	ASN
33	BI	105	HIS
34	BN	8	GLN
34	BN	133	GLN
36	BP	38	GLN
43	BW	60	ASN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	92	ASN
46	BZ	34	ASN
51	B4	46	GLN
56	B9	36	GLN
2	CB	16	HIS
2	CB	40	HIS
2	CB	76	GLN
2	CB	94	ASN
2	CB	224	GLN
3	CC	3	ASN

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Mol	Chain	Res	Type
3	CC	6	HIS
3	CC	28	GLN
3	CC	37	GLN
3	CC	104	GLN
3	CC	118	GLN
3	CC	123	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	161	ASN
5	CE	20	GLN
5	CE	141	GLN
6	CF	27	GLN
6	CF	73	ASN
6	CF	100	ASN
7	CG	28	ASN
8	CH	78	GLN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	73	GLN
9	CI	89	ASN
9	CI	124	GLN
10	CJ	21	GLN
10	CJ	62	HIS
10	CJ	68	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
13	CM	92	HIS
14	CN	49	HIS
15	CO	28	GLN
16	CP	16	HIS
17	CQ	16	GLN
19	CS	69	HIS
20	CT	90	GLN
28	DD	164	GLN
28	DD	253	GLN
30	DF	69	HIS
30	DF	169	ASN
30	DF	203	GLN

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Mol	Chain	Res	Type
31	DG	40	ASN
31	DG	41	GLN
31	DG	108	ASN
33	DI	43	ASN
34	DN	8	GLN
36	DP	38	GLN
37	DQ	123	HIS
39	DS	68	GLN
40	DT	43	GLN
40	DT	58	ASN
42	DV	64	HIS
43	DW	60	ASN
44	DX	31	HIS
45	DY	43	ASN
46	DZ	55	HIS
46	DZ	151	HIS
47	D0	35	ASN
49	D2	38	GLN
50	D3	32	GLN
56	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	361 (24%)	19 (1%)
1	CA	1501/1521 (98%)	370 (24%)	25 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	3 (27%)	0
23	AW	70/76 (92%)	27 (38%)	2 (2%)
23	CW	67/76 (88%)	26 (38%)	3 (4%)
24	AX	74/77 (96%)	16 (21%)	0
24	CX	74/77 (96%)	23 (31%)	0
25	AY	71/76 (93%)	37 (52%)	3 (4%)
25	CY	69/76 (90%)	36 (52%)	1 (1%)
26	BA	2812/2915 (96%)	444 (15%)	36 (1%)
26	DA	2791/2915 (95%)	563 (20%)	24 (0%)
27	BB	119/121 (98%)	13 (10%)	0
27	DB	119/121 (98%)	38 (31%)	0
All	All	9284/9620 (96%)	1960 (21%)	113 (1%)

All (1960) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	29	G
1	AA	32	A
1	AA	39	G
1	AA	41	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	55	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	100	C
1	AA	101	A
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	140	A
1	AA	143	A
1	AA	154	C
1	AA	155	C
1	AA	163	C
1	AA	166	G
1	AA	169	C
1	AA	170	U
1	AA	172	A
1	AA	174	C
1	AA	180	U
1	AA	182	U
1	AA	189(C)	C
1	AA	189(D)	C

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Mol	Chain	Res	Type
1	AA	189(F)	U
1	AA	189(G)	G
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	243	A
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	270	A
1	AA	277	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
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	396	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A

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Mol	Chain	Res	Type
1	AA	413	G
1	AA	421	U
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	457	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	477	A
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	544	G
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	564	C
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	581	G
1	AA	592	G
1	AA	593	G
1	AA	596	C
1	AA	617	G
1	AA	630	G

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Mol	Chain	Res	Type
1	AA	631	G
1	AA	633	G
1	AA	647	C
1	AA	653	A
1	AA	661	G
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	683	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	705	U
1	AA	717	C
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A
1	AA	755	G
1	AA	761	G
1	AA	774	G
1	AA	777	A
1	AA	786	G
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	798	G
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	829	G
1	AA	832	C
1	AA	834	C
1	AA	840	C
1	AA	841	U
1	AA	848	C

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Mol	Chain	Res	Type
1	AA	851	G
1	AA	853	G
1	AA	855	G
1	AA	859	A
1	AA	874	G
1	AA	875	C
1	AA	885	G
1	AA	902	G
1	AA	914	A
1	AA	916	G
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	943	U
1	AA	957	U
1	AA	960	U
1	AA	961	U
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	989	C
1	AA	992	U
1	AA	993	G
1	AA	997	U
1	AA	1000	U
1	AA	1001	A
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1010	G
1	AA	1016	A

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Mol	Chain	Res	Type
1	AA	1019	C
1	AA	1022	G
1	AA	1023	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1034	G
1	AA	1037	C
1	AA	1043	C
1	AA	1045	C
1	AA	1046	A
1	AA	1048	G
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1060	C
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1087	G
1	AA	1092	A
1	AA	1093	A
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1101	A
1	AA	1108	G
1	AA	1109	C
1	AA	1111	A
1	AA	1113	C
1	AA	1116	C
1	AA	1122	U
1	AA	1123	A

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Mol	Chain	Res	Type
1	AA	1124	G
1	AA	1125	U
1	AA	1130	A
1	AA	1132	C
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1142	G
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1159	U
1	AA	1163	C
1	AA	1165	C
1	AA	1166	G
1	AA	1168	A
1	AA	1169	A
1	AA	1170	A
1	AA	1173	G
1	AA	1174	G
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1193	G
1	AA	1196	U
1	AA	1197	G
1	AA	1201	A
1	AA	1202	G
1	AA	1206	G
1	AA	1212	U
1	AA	1213	A
1	AA	1218	C
1	AA	1227	A
1	AA	1228	C
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1242	C

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Mol	Chain	Res	Type
1	AA	1246	C
1	AA	1253	G
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1270	C
1	AA	1273	G
1	AA	1275	A
1	AA	1276	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1282	C
1	AA	1286	A
1	AA	1287	A
1	AA	1289	A
1	AA	1290	G
1	AA	1294	G
1	AA	1296	C
1	AA	1297	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1309	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1327	C
1	AA	1331	G
1	AA	1338	G
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1368	G
1	AA	1370	G
1	AA	1397	C
1	AA	1406	U

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Mol	Chain	Res	Type
1	AA	1411	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	1456	G
1	AA	1475	G
1	AA	1487	G
1	AA	1491	G
1	AA	1492	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
22	AV	13	A
22	AV	19	U
22	AV	24	A
23	AW	3	C
23	AW	8	4SU
23	AW	12	U
23	AW	13	C
23	AW	14	A
23	AW	15	G
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	23	A
23	AW	24	G
23	AW	35	A
23	AW	45	U
23	AW	46	7MG
23	AW	47	U

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Mol	Chain	Res	Type
23	AW	48	C
23	AW	49	C
23	AW	50	U
23	AW	52	G
23	AW	61	C
23	AW	63	G
23	AW	64	A
23	AW	66	U
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	6	G
24	AX	9	G
24	AX	14	A
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	22	G
24	AX	42	G
24	AX	46	G
24	AX	47	U
24	AX	58	A
24	AX	59	A
24	AX	61	C
24	AX	67	C
24	AX	68	C
25	AY	2	C
25	AY	4	C
25	AY	5	G
25	AY	7	A
25	AY	9	A
25	AY	10	G
25	AY	11	C
25	AY	14	A
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	23	A
25	AY	25	C
25	AY	26	A

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Mol	Chain	Res	Type
25	AY	32	PSU
25	AY	34	G
25	AY	39	PSU
25	AY	41	C
25	AY	42	C
25	AY	44	G
25	AY	45	U
25	AY	46	7MG
25	AY	47	U
25	AY	48	C
25	AY	49	C
25	AY	54	5MU
25	AY	56	C
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	61	C
25	AY	62	C
25	AY	67	C
25	AY	68	C
25	AY	69	G
25	AY	73	A
26	BA	10	G
26	BA	12	U
26	BA	13	A
26	BA	34	C
26	BA	45	C
26	BA	55	G
26	BA	64	A
26	BA	71	A
26	BA	72	U
26	BA	74	A
26	BA	75	G
26	BA	84	A
26	BA	100	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	149	A
26	BA	154	G
26	BA	154(A)	C

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Mol	Chain	Res	Type
26	BA	172	C
26	BA	182	A
26	BA	196	A
26	BA	199	A
26	BA	200	U
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	229	A
26	BA	232	G
26	BA	233	A
26	BA	248	G
26	BA	271(E)	U
26	BA	271(I)	G
26	BA	271(K)	U
26	BA	271(L)	U
26	BA	271(M)	G
26	BA	271(N)	U
26	BA	271(O)	C
26	BA	271(S)	G
26	BA	271(U)	G
26	BA	272(B)	G
26	BA	272(H)	C
26	BA	272(I)	U
26	BA	275	G
26	BA	279	C
26	BA	283	A
26	BA	294	A
26	BA	311	A
26	BA	329	G
26	BA	330	A
26	BA	352	G
26	BA	363	G
26	BA	363(B)	G
26	BA	370	G
26	BA	372	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	407	G

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Mol	Chain	Res	Type
26	BA	411	G
26	BA	421	U
26	BA	428	A
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	451	C
26	BA	456	C
26	BA	457	A
26	BA	470	A
26	BA	481	G
26	BA	504	U
26	BA	505	A
26	BA	509	C
26	BA	512	G
26	BA	528	A
26	BA	530	G
26	BA	531	C
26	BA	532	A
26	BA	533	G
26	BA	545	G
26	BA	549	G
26	BA	563	G
26	BA	568	U
26	BA	573	G
26	BA	575	A
26	BA	586	A
26	BA	592	G
26	BA	603	A
26	BA	604	G
26	BA	607	U
26	BA	614(B)	G
26	BA	615	G
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	652(D)	C
26	BA	652(E)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	669	G
26	BA	686	G

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Mol	Chain	Res	Type
26	BA	730	C
26	BA	740	U
26	BA	764	A
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	783	A
26	BA	784	A
26	BA	785	G
26	BA	792	G
26	BA	805	G
26	BA	812	C
26	BA	819	A
26	BA	827	U
26	BA	828	U
26	BA	830	G
26	BA	859	G
26	BA	866	A
26	BA	877	U
26	BA	880	G
26	BA	884	C
26	BA	885	C
26	BA	886	C
26	BA	887	A
26	BA	888	C
26	BA	889	C
26	BA	890	A
26	BA	892	G
26	BA	893	C
26	BA	894	C
26	BA	896	A
26	BA	897	C
26	BA	899	A
26	BA	900	A
26	BA	907	U
26	BA	910	A
26	BA	926	A
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	958	U

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Mol	Chain	Res	Type
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	983	A
26	BA	990	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C
26	BA	1022	G
26	BA	1025	G
26	BA	1026	U
26	BA	1033	U
26	BA	1038	C
26	BA	1045	A
26	BA	1046	A
26	BA	1047	G
26	BA	1048	A
26	BA	1051	G
26	BA	1107	G
26	BA	1110	G
26	BA	1112	G
26	BA	1128	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1139	G
26	BA	1170	G
26	BA	1171	G
26	BA	1173	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1177	A
26	BA	1210	A
26	BA	1211	U
26	BA	1220	A
26	BA	1244	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A

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Mol	Chain	Res	Type
26	BA	1273	U
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1314	C
26	BA	1352	U
26	BA	1359	A
26	BA	1360	A
26	BA	1365	A
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1395	A
26	BA	1416	G
26	BA	1417	C
26	BA	1421	G
26	BA	1422	G
26	BA	1428	C
26	BA	1445	A
26	BA	1449	A
26	BA	1450	G
26	BA	1455	G
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1490	A
26	BA	1493	C
26	BA	1504	C
26	BA	1508	A
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1531	C
26	BA	1539	G
26	BA	1540	U
26	BA	1542	A
26	BA	1543	C
26	BA	1554	A
26	BA	1558	A
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U

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Mol	Chain	Res	Type
26	BA	1580	A
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1648	C
26	BA	1654	A
26	BA	1674	G
26	BA	1696	G
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1722	A
26	BA	1739	U
26	BA	1746	G
26	BA	1756	G
26	BA	1762	A
26	BA	1763	G
26	BA	1764	G
26	BA	1773	A
26	BA	1780	A
26	BA	1791	A
26	BA	1800	C
26	BA	1816	G
26	BA	1828	G
26	BA	1839	G
26	BA	1847	A
26	BA	1858	G
26	BA	1861	G
26	BA	1878	G
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1919	A
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1937	A
26	BA	1938	A
26	BA	1955	U
26	BA	1963	U

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Mol	Chain	Res	Type
26	BA	1967	C
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1992	G
26	BA	1993	U
26	BA	1997	G
26	BA	2020	A
26	BA	2023	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2043	C
26	BA	2049	G
26	BA	2055	C
26	BA	2056	G
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2067	G
26	BA	2069	G
26	BA	2093	G
26	BA	2098	U
26	BA	2100	G
26	BA	2101	G
26	BA	2104	G
26	BA	2111	C
26	BA	2116	G
26	BA	2119	A
26	BA	2122	U
26	BA	2125	G
26	BA	2127	G
26	BA	2129	C
26	BA	2130	U
26	BA	2131	G
26	BA	2132	U
26	BA	2133	G
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2137	C
26	BA	2138	C

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Mol	Chain	Res	Type
26	BA	2140	C
26	BA	2141	G
26	BA	2142	C
26	BA	2143	C
26	BA	2145	C
26	BA	2147	G
26	BA	2151	G
26	BA	2152	G
26	BA	2153	G
26	BA	2155	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2161	C
26	BA	2163	C
26	BA	2164	C
26	BA	2165	G
26	BA	2166	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A
26	BA	2171	A
26	BA	2172	U
26	BA	2174	C
26	BA	2175	C
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2183	C
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2191	G
26	BA	2198	A
26	BA	2199	A
26	BA	2206	G
26	BA	2207	G
26	BA	2208	A
26	BA	2218	U
26	BA	2225	A
26	BA	2238	G

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Mol	Chain	Res	Type
26	BA	2239	G
26	BA	2268	A
26	BA	2273	A
26	BA	2275	C
26	BA	2280	G
26	BA	2283	C
26	BA	2286	A
26	BA	2287	A
26	BA	2289	G
26	BA	2298	A
26	BA	2305	A
26	BA	2308	G
26	BA	2313	C
26	BA	2320	A
26	BA	2325	G
26	BA	2334	G
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A
26	BA	2383	G
26	BA	2385	C
26	BA	2393	A
26	BA	2396	G
26	BA	2406	U
26	BA	2414	G
26	BA	2425	A
26	BA	2429	G
26	BA	2430	A
26	BA	2435	A
26	BA	2439	A
26	BA	2441	C
26	BA	2448	A
26	BA	2468	G
26	BA	2469	A
26	BA	2474	C
26	BA	2476	A
26	BA	2478	A
26	BA	2502	G
26	BA	2505	G
26	BA	2518	A

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Mol	Chain	Res	Type
26	BA	2529	G
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2582	G
26	BA	2602	A
26	BA	2609	U
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2654	A
26	BA	2689	U
26	BA	2690	C
26	BA	2691	C
26	BA	2703	C
26	BA	2712(A)	A
26	BA	2713	A
26	BA	2714	G
26	BA	2726	U
26	BA	2733	A
26	BA	2757	A
26	BA	2758	A
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A
26	BA	2790	A
26	BA	2791	C
26	BA	2793	G
26	BA	2802	G
26	BA	2808	U
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A
26	BA	2824	C
26	BA	2833	G
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2874	C

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Mol	Chain	Res	Type
26	BA	2875	C
26	BA	2880	C
26	BA	2892	A
26	BA	2893	G
26	BA	2894	G
27	BB	2	C
27	BB	45	A
27	BB	52	A
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	89	G
27	BB	106	G
27	BB	109	C
27	BB	110	G
27	BB	119	G
27	BB	120	A
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	41	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	55	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	70	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	96	U

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Mol	Chain	Res	Type
1	CA	97	G
1	CA	98	G
1	CA	100	C
1	CA	101	A
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	140	A
1	CA	142	G
1	CA	154	C
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	169	C
1	CA	170	U
1	CA	172	A
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(F)	U
1	CA	189(G)	G
1	CA	189(H)	G
1	CA	189(I)	G
1	CA	189(K)	U
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	243	A
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	270	A
1	CA	277	C
1	CA	289	G

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Mol	Chain	Res	Type
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
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	396	G
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	421	U
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	455	C
1	CA	457	C
1	CA	461	A
1	CA	471	G
1	CA	477	A
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G

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Mol	Chain	Res	Type
1	CA	527	G
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	561	U
1	CA	564	C
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	581	G
1	CA	592	G
1	CA	593	G
1	CA	596	C
1	CA	600	C
1	CA	617	G
1	CA	630	G
1	CA	631	G
1	CA	633	G
1	CA	647	C
1	CA	650	G
1	CA	653	A
1	CA	657	G
1	CA	661	G
1	CA	665	A
1	CA	671	G
1	CA	673	G
1	CA	683	G
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	705	U
1	CA	717	C
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	753	A

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Mol	Chain	Res	Type
1	CA	755	G
1	CA	761	G
1	CA	774	G
1	CA	777	A
1	CA	786	G
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	798	G
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	833	U
1	CA	834	C
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	875	C
1	CA	885	G
1	CA	902	G
1	CA	914	A
1	CA	916	G
1	CA	922	G
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	943	U
1	CA	957	U
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	973	G

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Mol	Chain	Res	Type
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	978	A
1	CA	979	C
1	CA	981	U
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	997	U
1	CA	999	C
1	CA	1001	A
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1009	G
1	CA	1010	G
1	CA	1016	A
1	CA	1019	C
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1029	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(B)	C
1	CA	1030(C)	G
1	CA	1031	G
1	CA	1033	G
1	CA	1034	G
1	CA	1037	C
1	CA	1038	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C

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Mol	Chain	Res	Type
1	CA	1045	C
1	CA	1046	A
1	CA	1050	G
1	CA	1052	U
1	CA	1053	G
1	CA	1054	C
1	CA	1060	C
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1087	G
1	CA	1092	A
1	CA	1093	A
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1100	C
1	CA	1101	A
1	CA	1108	G
1	CA	1109	C
1	CA	1111	A
1	CA	1116	C
1	CA	1122	U
1	CA	1124	G
1	CA	1125	U
1	CA	1127	G
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1142	G
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1159	U

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Mol	Chain	Res	Type
1	CA	1163	C
1	CA	1165	C
1	CA	1166	G
1	CA	1168	A
1	CA	1169	A
1	CA	1170	A
1	CA	1174	G
1	CA	1176	A
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1193	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1206	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1218	C
1	CA	1227	A
1	CA	1228	C
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1242	C
1	CA	1246	C
1	CA	1253	G
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1273	G
1	CA	1275	A
1	CA	1276	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C

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Mol	Chain	Res	Type
1	CA	1286	A
1	CA	1287	A
1	CA	1289	A
1	CA	1290	G
1	CA	1294	G
1	CA	1296	C
1	CA	1297	C
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1309	G
1	CA	1317	C
1	CA	1319	A
1	CA	1320	C
1	CA	1322	C
1	CA	1327	C
1	CA	1331	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1368	G
1	CA	1370	G
1	CA	1397	C
1	CA	1406	U
1	CA	1411	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	1456	G
1	CA	1475	G
1	CA	1487	G
1	CA	1491	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G

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Mol	Chain	Res	Type
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	19	U
22	CV	24	A
23	CW	3	C
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	13	C
23	CW	14	A
23	CW	15	G
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	35	A
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	49	C
23	CW	50	U
23	CW	52	G
23	CW	61	C
23	CW	62	C
23	CW	63	G
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	73	A
23	CW	74	C
24	CX	5	G
24	CX	6	G
24	CX	9	G

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Mol	Chain	Res	Type
24	CX	13	C
24	CX	15	G
24	CX	16	C
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	22	G
24	CX	31	G
24	CX	47	U
24	CX	48	C
24	CX	52	G
24	CX	58	A
24	CX	59	A
24	CX	60	U
24	CX	62	C
24	CX	63	G
24	CX	64	G
24	CX	65	C
24	CX	68	C
25	CY	2	C
25	CY	7	A
25	CY	9	A
25	CY	10	G
25	CY	11	C
25	CY	14	A
25	CY	15	G
25	CY	19	G
25	CY	23	A
25	CY	25	C
25	CY	26	A
25	CY	32	PSU
25	CY	33	U
25	CY	34	G
25	CY	39	PSU
25	CY	41	C
25	CY	42	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G

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Mol	Chain	Res	Type
25	CY	54	5MU
25	CY	55	PSU
25	CY	56	C
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	61	C
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	68	C
25	CY	69	G
25	CY	70	G
25	CY	73	A
26	DA	10	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
26	DA	59	U
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	79	G
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	94	C
26	DA	100	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	125	G
26	DA	140	G
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	173	G
26	DA	181	A

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Mol	Chain	Res	Type
26	DA	182	A
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	214	G
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	228	A
26	DA	229	A
26	DA	232	G
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271	A
26	DA	271(D)	G
26	DA	271(I)	G
26	DA	271(J)	C
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	292	C
26	DA	293	U
26	DA	294	A
26	DA	311	A
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	333	G
26	DA	338	G
26	DA	342	G
26	DA	352	G
26	DA	353	G
26	DA	354	G

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Mol	Chain	Res	Type
26	DA	362	U
26	DA	363	G
26	DA	363(A)	A
26	DA	363(C)	G
26	DA	364	C
26	DA	372	G
26	DA	380	U
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	405	U
26	DA	406	G
26	DA	411	G
26	DA	412	A
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	479	A
26	DA	481	G
26	DA	504	U
26	DA	505	A
26	DA	508	G
26	DA	509	C
26	DA	512	G
26	DA	521	G
26	DA	528	A
26	DA	529	A
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	545	G
26	DA	563	G
26	DA	568	U
26	DA	573	G
26	DA	575	A
26	DA	586	A

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Mol	Chain	Res	Type
26	DA	588	U
26	DA	592	G
26	DA	599	G
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	614(C)	A
26	DA	615	G
26	DA	616	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	651	G
26	DA	652(A)	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(U)	G
26	DA	669	G
26	DA	686	G
26	DA	715	G
26	DA	717	G
26	DA	726	G
26	DA	730	C
26	DA	753	C
26	DA	765	G
26	DA	774	A
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	792	G
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	828	U
26	DA	847	U
26	DA	854	G

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Mol	Chain	Res	Type
26	DA	857	C
26	DA	859	G
26	DA	866	A
26	DA	867	C
26	DA	872	A
26	DA	874	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	889	C
26	DA	890	A
26	DA	893	C
26	DA	896	A
26	DA	897	C
26	DA	898	C
26	DA	900	A
26	DA	901	A
26	DA	902	C
26	DA	903	C
26	DA	910	A
26	DA	911	A
26	DA	917	A
26	DA	923	C
26	DA	932	G
26	DA	933	A
26	DA	936	C
26	DA	938	G
26	DA	941	A
26	DA	943	U
26	DA	945	A
26	DA	946	G
26	DA	953	A
26	DA	958	U
26	DA	959	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	980	A
26	DA	983	A

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Mol	Chain	Res	Type
26	DA	996	A
26	DA	1005	C
26	DA	1006	C
26	DA	1012	U
26	DA	1013	C
26	DA	1018	C
26	DA	1020	A
26	DA	1021	A
26	DA	1022	G
26	DA	1025	G
26	DA	1026	U
26	DA	1033	U
26	DA	1034	G
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1113	U
26	DA	1114	G
26	DA	1116	C
26	DA	1121	C
26	DA	1126	A
26	DA	1128	A
26	DA	1129	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1137	G
26	DA	1139	G
26	DA	1144	G
26	DA	1159	U
26	DA	1171	G
26	DA	1204	A
26	DA	1210	A
26	DA	1211	U
26	DA	1212	G
26	DA	1220	A
26	DA	1244	G
26	DA	1247	A
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G

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Mol	Chain	Res	Type
26	DA	1272	A
26	DA	1273	U
26	DA	1292	U
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U
26	DA	1359	A
26	DA	1360	A
26	DA	1365	A
26	DA	1368	G
26	DA	1370	C
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1386	C
26	DA	1413	G
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	1435	G
26	DA	1437	C
26	DA	1445	A
26	DA	1445(A)	C
26	DA	1449	A
26	DA	1450	G
26	DA	1459	G
26	DA	1461	G
26	DA	1467	C
26	DA	1471	A
26	DA	1474	C
26	DA	1482	G
26	DA	1488	G
26	DA	1489	U
26	DA	1490	A
26	DA	1493	C
26	DA	1496	A

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Mol	Chain	Res	Type
26	DA	1497	U
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1525	G
26	DA	1531	C
26	DA	1533	G
26	DA	1539	G
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1545	A
26	DA	1547	C
26	DA	1558	A
26	DA	1559	G
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1582	C
26	DA	1584	C
26	DA	1586	A
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1616	A
26	DA	1640	C
26	DA	1648	C
26	DA	1653	G
26	DA	1654	A
26	DA	1669	A
26	DA	1674	G
26	DA	1695	G
26	DA	1696	G
26	DA	1700	A
26	DA	1701	A
26	DA	1721	G
26	DA	1722	A
26	DA	1739	U
26	DA	1740	G
26	DA	1741	A
26	DA	1743	C
26	DA	1746	G

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Mol	Chain	Res	Type
26	DA	1750	G
26	DA	1756	G
26	DA	1758	G
26	DA	1762	A
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1782	C
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1828	G
26	DA	1829	A
26	DA	1835	G
26	DA	1847	A
26	DA	1848	A
26	DA	1877	A
26	DA	1878	G
26	DA	1889	A
26	DA	1900	A
26	DA	1906	G
26	DA	1913	A
26	DA	1914	C
26	DA	1927	A
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
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

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Mol	Chain	Res	Type
26	DA	2023	G
26	DA	2027	G
26	DA	2031	A
26	DA	2032	G
26	DA	2033	A
26	DA	2043	C
26	DA	2046	G
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	2096	U
26	DA	2099	U
26	DA	2102	U
26	DA	2104	G
26	DA	2105	C
26	DA	2106	G
26	DA	2110	G
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G
26	DA	2119	A
26	DA	2122	U
26	DA	2124	G
26	DA	2126	A
26	DA	2127	G
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	2142	C

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Mol	Chain	Res	Type
26	DA	2144	U
26	DA	2146	C
26	DA	2148	G
26	DA	2150	U
26	DA	2151	G
26	DA	2154	G
26	DA	2155	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2161	C
26	DA	2162	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	2171	A
26	DA	2172	U
26	DA	2173	A
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G
26	DA	2185	C
26	DA	2186	G
26	DA	2187	G
26	DA	2188	C
26	DA	2189	U
26	DA	2192	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2225	A
26	DA	2232	U
26	DA	2238	G
26	DA	2239	G
26	DA	2243	U
26	DA	2269	A

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Mol	Chain	Res	Type
26	DA	2275	C
26	DA	2279	G
26	DA	2283	C
26	DA	2287	A
26	DA	2289	G
26	DA	2294	C
26	DA	2297	C
26	DA	2299	G
26	DA	2301	C
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G
26	DA	2312	U
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2322	A
26	DA	2325	G
26	DA	2327	A
26	DA	2334	G
26	DA	2336	A
26	DA	2343	C
26	DA	2347	C
26	DA	2354	G
26	DA	2372	G
26	DA	2376	A
26	DA	2377	A
26	DA	2383	G
26	DA	2385	C
26	DA	2387	U
26	DA	2402	C
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2423	U
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2431	U
26	DA	2434	A
26	DA	2435	A

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Mol	Chain	Res	Type
26	DA	2439	A
26	DA	2441	C
26	DA	2445	G
26	DA	2448	A
26	DA	2465	C
26	DA	2474	C
26	DA	2476	A
26	DA	2490	G
26	DA	2494	G
26	DA	2502	G
26	DA	2505	G
26	DA	2506	U
26	DA	2518	A
26	DA	2520	C
26	DA	2525	G
26	DA	2532	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2569	G
26	DA	2573	C
26	DA	2578	G
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2629	A
26	DA	2630	G
26	DA	2634	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2673	G
26	DA	2689	U
26	DA	2690	C
26	DA	2691	C
26	DA	2703	C
26	DA	2712(A)	A
26	DA	2713	A

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Mol	Chain	Res	Type
26	DA	2714	G
26	DA	2726	U
26	DA	2732	G
26	DA	2733	A
26	DA	2744	G
26	DA	2751	G
26	DA	2758	A
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2780	G
26	DA	2793	G
26	DA	2794	C
26	DA	2802	G
26	DA	2807	G
26	DA	2808	U
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2833	G
26	DA	2834	G
26	DA	2835	A
26	DA	2839	G
26	DA	2872	G
26	DA	2873	A
26	DA	2880	C
26	DA	2886	G
26	DA	2892	A
26	DA	2894	G
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	9	G
27	DB	10	C
27	DB	13	A
27	DB	15	A
27	DB	20	C
27	DB	21	G
27	DB	25	A
27	DB	28	C

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Mol	Chain	Res	Type
27	DB	30	C
27	DB	32	C
27	DB	34	U
27	DB	38	C
27	DB	41	U
27	DB	42	C
27	DB	44	G
27	DB	52	A
27	DB	53	A
27	DB	56	G
27	DB	58	A
27	DB	59	A
27	DB	63	G
27	DB	64	C
27	DB	65	C
27	DB	66	A
27	DB	73	A
27	DB	85	G
27	DB	93	G
27	DB	94	C
27	DB	106	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	112	U
27	DB	119	G
27	DB	120	A

All (113) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	839	U
1	AA	913	A

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Mol	Chain	Res	Type
1	AA	991	U
1	AA	1065	U
1	AA	1067	A
1	AA	1165	C
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
23	AW	13	C
23	AW	45	U
25	AY	19	G
25	AY	44	G
25	AY	58	A
26	BA	71	A
26	BA	196	A
26	BA	271(M)	G
26	BA	278	A
26	BA	548	A
26	BA	746	A
26	BA	774	A
26	BA	827	U
26	BA	899	A
26	BA	958	U
26	BA	960	A
26	BA	974	G
26	BA	1047	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1210	A
26	BA	1300	U
26	BA	1301	A
26	BA	1420	U
26	BA	1530	C
26	BA	1608	A
26	BA	1653	G
26	BA	1992	G
26	BA	2126	A
26	BA	2134	A
26	BA	2163	C
26	BA	2181	G
26	BA	2183	C

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Mol	Chain	Res	Type
26	BA	2187	G
26	BA	2238	G
26	BA	2406	U
26	BA	2430	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1005	A
1	CA	1027	C
1	CA	1064	G
1	CA	1065	U
1	CA	1129	C
1	CA	1183	A
1	CA	1201	A
1	CA	1212	U
1	CA	1256	A
1	CA	1331	G
1	CA	1442	G
1	CA	1492	A
23	CW	13	C
23	CW	14	A
23	CW	66	U
25	CY	46	7MG
26	DA	196	A
26	DA	271(M)	G
26	DA	277	C
26	DA	614(B)	G
26	DA	752	A
26	DA	774	A

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Mol	Chain	Res	Type
26	DA	856	C
26	DA	888	C
26	DA	900	A
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2110	G
26	DA	2126	A
26	DA	2318	G
26	DA	2422	A
26	DA	2430	A
26	DA	2689	U

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

40 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	PSU	AW	32	57,23	13,21,22	1.20	1 (7%)	18,30,33	3.32	6 (33%)
23	MIA	AW	37	23	21,31,32	1.70	2 (9%)	26,44,47	1.35	4 (15%)
23	PSU	AW	39	23	13,21,22	1.19	1 (7%)	18,30,33	3.35	6 (33%)
23	7MG	AW	46	23	19,26,27	1.05	1 (5%)	24,39,42	2.96	7 (29%)
23	5MU	AW	54	23	12,22,23	0.28	0	14,32,35	2.49	2 (14%)
23	PSU	AW	55	23	13,21,22	1.34	1 (7%)	18,30,33	3.50	6 (33%)
23	F3N	AW	76	23	27,36,37	1.51	4 (14%)	31,51,54	2.24	3 (9%)
23	4SU	AW	8	23	11,21,22	1.26	1 (9%)	13,30,33	1.15	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	5MC	AX	32	24	13,22,23	1.37	1 (7%)	15,32,35	0.89	1 (6%)
24	5MU	AX	54	24,57	12,22,23	0.34	0	14,32,35	2.34	2 (14%)
24	PSU	AX	55	24	13,21,22	1.61	2 (15%)	18,30,33	3.28	6 (33%)
24	31H	AX	76	24,57	25,34,35	1.22	3 (12%)	26,47,50	2.88	7 (26%)
24	4SU	AX	8	24	11,21,22	1.17	1 (9%)	13,30,33	1.67	1 (7%)
25	PSU	AY	32	25	13,21,22	1.02	1 (7%)	18,30,33	3.39	6 (33%)
25	MIA	AY	37	25	15,24,32	1.24	2 (13%)	16,35,47	2.02	2 (12%)
25	PSU	AY	39	25	13,21,22	1.21	1 (7%)	18,30,33	3.53	6 (33%)
25	7MG	AY	46	25	19,26,27	1.14	1 (5%)	24,39,42	3.50	10 (41%)
25	5MU	AY	54	25	12,22,23	0.36	0	14,32,35	2.53	2 (14%)
25	PSU	AY	55	25	13,21,22	1.42	1 (7%)	18,30,33	3.13	5 (27%)
25	4SU	AY	8	25	11,21,22	1.25	1 (9%)	13,30,33	1.16	1 (7%)
23	PSU	CW	32	23	13,21,22	1.25	1 (7%)	18,30,33	3.44	6 (33%)
23	MIA	CW	37	23	15,24,32	1.20	2 (13%)	16,35,47	2.10	2 (12%)
23	PSU	CW	39	23	13,21,22	1.34	1 (7%)	18,30,33	3.81	6 (33%)
23	7MG	CW	46	23	19,26,27	1.02	1 (5%)	24,39,42	2.80	7 (29%)
23	5MU	CW	54	23	12,22,23	0.35	0	14,32,35	2.62	2 (14%)
23	PSU	CW	55	23	13,21,22	1.24	1 (7%)	18,30,33	3.39	6 (33%)
23	F3N	CW	76	23	27,36,37	1.52	5 (18%)	31,51,54	2.23	2 (6%)
23	4SU	CW	8	23	11,21,22	1.21	1 (9%)	13,30,33	1.16	1 (7%)
24	5MC	CX	32	24	13,22,23	1.27	1 (7%)	15,32,35	1.06	1 (6%)
24	5MU	CX	54	24	12,22,23	0.33	0	14,32,35	2.25	2 (14%)
24	PSU	CX	55	24	13,21,22	1.32	1 (7%)	18,30,33	3.28	6 (33%)
24	31H	CX	76	24,57	25,34,35	1.27	3 (12%)	26,47,50	3.24	7 (26%)
24	4SU	CX	8	24	11,21,22	1.12	1 (9%)	13,30,33	1.67	1 (7%)
25	PSU	CY	32	25	13,21,22	1.13	1 (7%)	18,30,33	3.42	5 (27%)
25	MIA	CY	37	25	15,24,32	1.26	2 (13%)	16,35,47	2.02	2 (12%)
25	PSU	CY	39	25	13,21,22	1.65	2 (15%)	18,30,33	2.70	6 (33%)
25	7MG	CY	46	25	19,26,27	1.11	1 (5%)	24,39,42	3.04	8 (33%)
25	5MU	CY	54	25	12,22,23	0.39	0	14,32,35	2.19	2 (14%)
25	PSU	CY	55	25	13,21,22	1.01	1 (7%)	18,30,33	3.55	6 (33%)
25	4SU	CY	8	25	11,21,22	1.34	1 (9%)	13,30,33	1.16	1 (7%)

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	PSU	AW	32	57,23	-	0/7/25/26	0/2/2/2
23	MIA	AW	37	23	-	0/11/33/34	0/3/3/3
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
23	7MG	AW	46	23	-	0/7/37/38	0/3/3/3
23	5MU	AW	54	23	-	0/3/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
23	F3N	AW	76	23	-	0/15/37/38	0/4/4/4
23	4SU	AW	8	23	-	0/3/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/3/25/26	0/2/2/2
24	5MU	AX	54	24,57	-	0/3/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
24	31H	AX	76	24,57	-	1/18/40/41	0/3/3/3
24	4SU	AX	8	24	-	0/3/25/26	0/2/2/2
25	PSU	AY	32	25	-	0/7/25/26	0/2/2/2
25	MIA	AY	37	25	-	0/3/25/34	0/3/3/3
25	PSU	AY	39	25	-	0/7/25/26	0/2/2/2
25	7MG	AY	46	25	-	0/7/37/38	0/3/3/3
25	5MU	AY	54	25	-	0/3/25/26	0/2/2/2
25	PSU	AY	55	25	-	0/7/25/26	0/2/2/2
25	4SU	AY	8	25	-	0/3/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/3/25/34	0/3/3/3
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	0/7/37/38	0/3/3/3
23	5MU	CW	54	23	-	0/3/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
23	F3N	CW	76	23	-	0/15/37/38	0/4/4/4
23	4SU	CW	8	23	-	0/3/25/26	0/2/2/2
24	5MC	CX	32	24	-	0/3/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/3/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
24	31H	CX	76	24,57	-	1/18/40/41	0/3/3/3
24	4SU	CX	8	24	-	0/3/25/26	0/2/2/2
25	PSU	CY	32	25	-	0/7/25/26	0/2/2/2
25	MIA	CY	37	25	-	0/3/25/34	0/3/3/3
25	PSU	CY	39	25	-	0/7/25/26	0/2/2/2
25	7MG	CY	46	25	-	0/7/37/38	0/3/3/3
25	5MU	CY	54	25	-	0/3/25/26	0/2/2/2
25	PSU	CY	55	25	-	0/7/25/26	0/2/2/2
25	4SU	CY	8	25	-	0/3/25/26	0/2/2/2

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-6.28	1.70	1.75
24	AX	55	PSU	C5-C1'	-5.27	1.47	1.52
25	CY	39	PSU	C5-C1'	-5.18	1.47	1.52
23	AW	76	F3N	CB-CG	-4.88	1.39	1.51
25	AY	55	PSU	C5-C1'	-4.71	1.48	1.52
23	CW	76	F3N	CB-CG	-4.43	1.40	1.51
23	AW	55	PSU	C5-C1'	-4.36	1.48	1.52
23	CW	39	PSU	C5-C1'	-4.34	1.48	1.52
24	CX	55	PSU	C5-C1'	-4.29	1.48	1.52
23	CW	55	PSU	C5-C1'	-4.03	1.48	1.52
23	CW	32	PSU	C5-C1'	-4.03	1.48	1.52
25	CY	8	4SU	C4-S4	-3.99	1.59	1.67
23	AW	32	PSU	C5-C1'	-3.95	1.48	1.52
23	AW	8	4SU	C4-S4	-3.92	1.59	1.67
25	AY	8	4SU	C4-S4	-3.84	1.60	1.67
25	AY	39	PSU	C5-C1'	-3.83	1.48	1.52
23	AW	39	PSU	C5-C1'	-3.78	1.48	1.52
24	AX	8	4SU	C4-S4	-3.67	1.60	1.67
24	CX	76	31H	C5-C4	-3.64	1.32	1.40
23	CW	8	4SU	C4-S4	-3.64	1.60	1.67
24	CX	8	4SU	C4-S4	-3.56	1.60	1.67
23	CW	76	F3N	C5-C4	-3.47	1.32	1.40
25	CY	32	PSU	C5-C1'	-3.38	1.49	1.52
23	AW	76	F3N	C5-C4	-3.14	1.33	1.40
25	CY	55	PSU	C5-C1'	-3.12	1.49	1.52
24	AX	76	31H	C5-C4	-3.12	1.33	1.40
25	AY	32	PSU	C5-C1'	-3.09	1.49	1.52
24	AX	76	31H	C5-N7	-2.49	1.31	1.39
23	AW	76	F3N	C5-N7	-2.32	1.31	1.39
25	CY	39	PSU	O4'-C1'	-2.25	1.40	1.44
23	CW	76	F3N	C5-N7	-2.05	1.32	1.39
24	AX	55	PSU	O4'-C1'	-2.04	1.41	1.44
24	AX	76	31H	C3'-N3'	2.01	1.49	1.45
23	CW	76	F3N	C3'-N3'	2.02	1.49	1.45
24	CX	76	31H	C3'-N3'	2.28	1.49	1.45
23	CW	37	MIA	C2-N3	2.38	1.36	1.32
25	CY	37	MIA	C2-N3	2.43	1.36	1.32
25	AY	37	MIA	C2-N3	2.46	1.36	1.32
24	CX	76	31H	CA-N	2.60	1.48	1.45
23	CW	46	7MG	C5-C4	2.76	1.47	1.39
25	AY	46	7MG	C5-C4	3.10	1.47	1.39
23	AW	46	7MG	C5-C4	3.17	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C5-C4	3.18	1.47	1.40
25	CY	46	7MG	C5-C4	3.21	1.48	1.39
23	CW	37	MIA	C5-C4	3.33	1.48	1.40
25	AY	37	MIA	C5-C4	3.48	1.48	1.40
25	CY	37	MIA	C5-C4	3.52	1.48	1.40
23	AW	76	F3N	O4'-C1'	3.58	1.45	1.41
23	CW	76	F3N	O4'-C1'	3.70	1.45	1.41
24	CX	32	5MC	C5-C4	4.43	1.48	1.41
24	AX	32	5MC	C5-C4	4.75	1.48	1.41

All (163) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	CW	39	PSU	N1-C2-N3	-11.89	120.75	128.33
24	CX	76	31H	N3-C2-N1	-11.56	120.04	128.89
23	CW	76	F3N	N3-C2-N1	-11.54	120.06	128.89
25	CY	55	PSU	N1-C2-N3	-11.41	121.06	128.33
23	AW	76	F3N	N3-C2-N1	-11.38	120.18	128.89
24	AX	76	31H	N3-C2-N1	-11.35	120.20	128.89
25	AY	39	PSU	N1-C2-N3	-11.16	121.21	128.33
25	AY	46	7MG	C5-C4-N3	-10.87	116.23	126.82
25	AY	32	PSU	N1-C2-N3	-10.84	121.42	128.33
25	CY	32	PSU	N1-C2-N3	-10.80	121.44	128.33
23	CW	32	PSU	N1-C2-N3	-10.62	121.56	128.33
23	AW	39	PSU	N1-C2-N3	-10.42	121.68	128.33
23	AW	32	PSU	N1-C2-N3	-10.39	121.70	128.33
23	CW	55	PSU	N1-C2-N3	-10.28	121.77	128.33
24	CX	55	PSU	N1-C2-N3	-10.11	121.88	128.33
23	AW	55	PSU	N1-C2-N3	-10.07	121.91	128.33
24	AX	55	PSU	N1-C2-N3	-10.00	121.95	128.33
25	AY	55	PSU	N1-C2-N3	-9.65	122.18	128.33
23	CW	46	7MG	C5-C4-N3	-8.90	118.15	126.82
23	AW	46	7MG	C5-C4-N3	-7.81	119.21	126.82
25	CY	46	7MG	C5-C4-N3	-7.80	119.22	126.82
23	CW	37	MIA	N3-C2-N1	-7.18	123.39	128.89
25	AY	37	MIA	N3-C2-N1	-6.91	123.60	128.89
25	CY	39	PSU	N1-C2-N3	-6.84	123.97	128.33
25	CY	37	MIA	N3-C2-N1	-6.74	123.73	128.89
24	CX	76	31H	C4'-O4'-C1'	-6.13	102.99	109.72
25	AY	54	5MU	C5-C4-N3	-5.98	118.48	125.14
23	CW	54	5MU	C5-C4-N3	-5.74	118.74	125.14
23	AW	54	5MU	C5-C4-N3	-5.71	118.78	125.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CX	54	5MU	C5-C4-N3	-5.65	118.85	125.14
24	CX	8	4SU	C5-C4-N3	-5.62	118.12	123.63
24	AX	8	4SU	C5-C4-N3	-5.60	118.14	123.63
23	AW	55	PSU	C5-C1'-C2'	-5.52	105.73	115.52
23	AW	46	7MG	C5-C6-N1	-5.48	115.03	123.46
24	AX	54	5MU	C5-C4-N3	-5.46	119.06	125.14
25	CY	46	7MG	C5-C6-N1	-5.28	115.33	123.46
25	CY	54	5MU	C5-C4-N3	-5.15	119.40	125.14
24	AX	76	31H	C4'-O4'-C1'	-5.05	104.17	109.72
24	CX	76	31H	C4'-C3'-N3'	-4.93	103.33	113.61
25	CY	39	PSU	C5-C1'-C2'	-4.82	106.96	115.52
23	CW	46	7MG	C5-C6-N1	-4.67	116.28	123.46
25	AY	46	7MG	C5-C6-N1	-4.50	116.54	123.46
24	AX	76	31H	C4'-C3'-N3'	-4.29	104.66	113.61
23	CW	39	PSU	C5-C1'-C2'	-4.20	108.06	115.52
23	CW	55	PSU	C5-C6-N1	-4.08	118.63	124.39
23	CW	32	PSU	C5-C6-N1	-3.96	118.81	124.39
24	CX	55	PSU	C5-C6-N1	-3.85	118.96	124.39
24	AX	55	PSU	C5-C6-N1	-3.82	119.00	124.39
23	CW	32	PSU	C5-C1'-C2'	-3.80	108.77	115.52
23	CW	55	PSU	C5-C1'-C2'	-3.76	108.85	115.52
25	AY	39	PSU	C5-C6-N1	-3.73	119.12	124.39
25	AY	55	PSU	C5-C6-N1	-3.73	119.13	124.39
23	CW	8	4SU	C5-C4-N3	-3.70	120.01	123.63
23	AW	37	MIA	C4-C5-N7	-3.69	106.08	109.48
25	AY	32	PSU	C5-C6-N1	-3.67	119.21	124.39
25	AY	8	4SU	C5-C4-N3	-3.66	120.05	123.63
25	CY	55	PSU	C5-C1'-C2'	-3.66	109.03	115.52
23	AW	8	4SU	C5-C4-N3	-3.58	120.13	123.63
23	AW	39	PSU	C5-C6-N1	-3.47	119.49	124.39
25	CY	37	MIA	C4-C5-N7	-3.41	106.34	109.48
23	CW	39	PSU	C5-C6-N1	-3.39	119.60	124.39
23	AW	32	PSU	C5-C6-N1	-3.33	119.69	124.39
25	AY	37	MIA	C4-C5-N7	-3.27	106.47	109.48
23	CW	37	MIA	C4-C5-N7	-3.20	106.54	109.48
24	AX	76	31H	OCN-CN-N	-3.18	120.18	124.76
25	CY	8	4SU	C5-C4-N3	-3.18	120.52	123.63
23	AW	55	PSU	C5-C6-N1	-3.17	119.92	124.39
25	CY	39	PSU	C5-C6-N1	-3.16	119.94	124.39
24	CX	76	31H	OCN-CN-N	-3.13	120.25	124.76
25	AY	46	7MG	CM7-N7-C8	-2.93	112.22	120.52
25	CY	46	7MG	CM7-N7-C8	-2.85	112.44	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	37	MIA	C5-C6-N1	-2.82	117.57	120.48
23	AW	39	PSU	C5-C1'-C2'	-2.81	110.53	115.52
23	AW	46	7MG	CM7-N7-C8	-2.80	112.59	120.52
25	CY	32	PSU	C5-C6-N1	-2.78	120.47	124.39
23	AW	76	F3N	C4'-C3'-N3'	-2.76	107.85	113.61
25	AY	46	7MG	C5-C4-N9	-2.60	102.35	106.18
24	AX	55	PSU	C5-C1'-C2'	-2.56	110.97	115.52
23	AW	32	PSU	C5-C1'-C2'	-2.48	111.12	115.52
23	CW	46	7MG	CM7-N7-C8	-2.43	113.63	120.52
25	AY	39	PSU	C5-C1'-C2'	-2.40	111.26	115.52
23	CW	76	F3N	C4'-C3'-N3'	-2.39	108.61	113.61
23	AW	37	MIA	N3-C2-N1	-2.31	122.37	126.79
23	AW	46	7MG	C5-C4-N9	-2.29	102.81	106.18
25	CY	55	PSU	C5-C6-N1	-2.25	121.22	124.39
24	CX	55	PSU	C5-C1'-C2'	-2.13	111.73	115.52
25	CY	46	7MG	C5-C4-N9	-2.09	103.10	106.18
24	AX	76	31H	CA-N-CN	-2.08	119.62	122.82
23	AW	76	F3N	C2'-C1'-N9	-2.05	111.17	114.29
25	AY	32	PSU	C5-C1'-C2'	-2.00	111.97	115.52
25	AY	46	7MG	N2-C2-N3	2.06	120.61	117.20
23	CW	46	7MG	N2-C2-N1	2.06	120.61	117.20
25	AY	46	7MG	C2-N3-C4	2.09	120.64	114.53
25	AY	46	7MG	C4-N9-C1'	2.16	131.90	126.70
24	AX	32	5MC	N4-C4-N3	2.20	120.14	116.95
24	CX	76	31H	O2'-C2'-C3'	2.21	115.83	110.62
24	CX	76	31H	C2'-C3'-N3'	2.27	119.02	113.18
23	AW	46	7MG	CM7-N7-C5	2.28	131.71	124.09
23	CW	46	7MG	C2-N3-C4	2.30	121.25	114.53
25	CY	46	7MG	N2-C2-N1	2.32	121.04	117.20
25	CY	46	7MG	CM7-N7-C5	2.37	132.01	124.09
25	AY	46	7MG	CM7-N7-C5	2.38	132.04	124.09
23	AW	55	PSU	O4'-C1'-C2'	2.41	107.19	104.73
25	AY	39	PSU	O4'-C1'-C2'	2.45	107.23	104.73
24	AX	76	31H	O2'-C2'-C3'	2.47	116.46	110.62
25	CY	55	PSU	O4'-C1'-C2'	2.61	107.39	104.73
23	AW	39	PSU	O4'-C1'-C2'	2.63	107.41	104.73
23	CW	32	PSU	O4'-C1'-C2'	2.71	107.49	104.73
23	CW	39	PSU	O4'-C1'-C2'	2.72	107.50	104.73
23	CW	55	PSU	O4'-C1'-C2'	2.77	107.56	104.73
25	AY	32	PSU	O4'-C1'-C2'	2.80	107.58	104.73
25	CY	39	PSU	O4'-C1'-C2'	2.80	107.58	104.73
24	CX	32	5MC	N4-C4-N3	2.87	121.10	116.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	37	MIA	C2-N1-C6	3.02	122.22	113.35
23	AW	32	PSU	O4'-C1'-C2'	3.04	107.83	104.73
24	CX	55	PSU	O4'-C1'-C2'	3.06	107.85	104.73
24	AX	55	PSU	O4'-C1'-C2'	3.13	107.92	104.73
25	AY	55	PSU	O4'-C1'-C2'	3.14	107.94	104.73
25	CY	39	PSU	C6-N1-C2	3.22	120.64	115.47
25	CY	32	PSU	O4'-C1'-C2'	3.28	108.08	104.73
24	AX	76	31H	O4'-C1'-N9	3.29	114.99	108.10
23	AW	55	PSU	C6-N1-C2	3.70	121.42	115.47
25	CY	32	PSU	C6-N1-C2	3.84	121.65	115.47
25	CY	55	PSU	C6-N1-C2	3.87	121.70	115.47
25	AY	55	PSU	C6-N1-C2	3.89	121.72	115.47
24	AX	55	PSU	C6-N1-C2	4.06	122.00	115.47
23	AW	32	PSU	C6-N1-C2	4.07	122.01	115.47
23	CW	39	PSU	C6-N1-C2	4.10	122.06	115.47
23	AW	39	PSU	C6-N1-C2	4.12	122.09	115.47
24	CX	55	PSU	C6-N1-C2	4.15	122.15	115.47
25	AY	39	PSU	C6-N1-C2	4.29	122.36	115.47
23	CW	55	PSU	C6-N1-C2	4.39	122.53	115.47
23	CW	32	PSU	C6-N1-C2	4.43	122.59	115.47
25	AY	32	PSU	C6-N1-C2	4.45	122.63	115.47
25	AY	46	7MG	C6-N1-C2	4.57	122.28	115.94
23	CW	46	7MG	C6-N1-C2	4.60	122.32	115.94
25	CY	39	PSU	C4-N3-C2	5.15	119.70	115.25
25	CY	54	5MU	C4-N3-C2	5.72	120.19	115.25
23	CW	55	PSU	C4-N3-C2	5.91	120.36	115.25
23	AW	46	7MG	C6-N1-C2	5.95	124.19	115.94
24	CX	54	5MU	C4-N3-C2	5.98	120.41	115.25
23	CW	32	PSU	C4-N3-C2	6.09	120.51	115.25
25	CY	46	7MG	C6-N1-C2	6.14	124.47	115.94
23	CW	46	7MG	N3-C4-N9	6.20	136.05	126.75
25	AY	55	PSU	C4-N3-C2	6.35	120.74	115.25
25	AY	32	PSU	C4-N3-C2	6.36	120.75	115.25
24	CX	55	PSU	C4-N3-C2	6.40	120.78	115.25
24	AX	55	PSU	C4-N3-C2	6.48	120.85	115.25
23	AW	32	PSU	C4-N3-C2	6.49	120.86	115.25
24	AX	54	5MU	C4-N3-C2	6.54	120.90	115.25
23	AW	39	PSU	C4-N3-C2	6.69	121.03	115.25
25	AY	54	5MU	C4-N3-C2	6.85	121.17	115.25
25	CY	55	PSU	C4-N3-C2	6.89	121.20	115.25
24	CX	76	31H	O4'-C1'-N9	6.97	122.69	108.10
25	AY	39	PSU	C4-N3-C2	6.99	121.28	115.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	CY	32	PSU	C4-N3-C2	7.16	121.43	115.25
23	AW	54	5MU	C4-N3-C2	7.16	121.44	115.25
25	CY	46	7MG	N3-C4-N9	7.27	137.66	126.75
23	AW	55	PSU	C4-N3-C2	7.27	121.53	115.25
23	AW	46	7MG	N3-C4-N9	7.48	137.97	126.75
23	CW	54	5MU	C4-N3-C2	7.62	121.84	115.25
23	CW	39	PSU	C4-N3-C2	7.71	121.92	115.25
25	AY	46	7MG	N3-C4-N9	9.78	141.42	126.75

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

26 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AW	39	PSU	1	0
23	AW	55	PSU	1	0
23	AW	76	F3N	1	0
24	AX	32	5MC	2	0
24	AX	76	31H	1	0
24	AX	8	4SU	1	0
25	AY	37	MIA	1	0
25	AY	39	PSU	2	0
25	AY	46	7MG	3	0
25	AY	55	PSU	1	0
25	AY	8	4SU	1	0
23	CW	32	PSU	1	0
23	CW	39	PSU	1	0
23	CW	46	7MG	2	0
23	CW	55	PSU	1	0
23	CW	76	F3N	3	0
23	CW	8	4SU	2	0
24	CX	32	5MC	1	0
24	CX	55	PSU	1	0
24	CX	76	31H	1	0
24	CX	8	4SU	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	CY	37	MIA	3	0
25	CY	39	PSU	8	0
25	CY	46	7MG	4	0
25	CY	55	PSU	2	0
25	CY	8	4SU	2	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 2063 ligands modelled in this entry, 2061 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	501	4	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	CD	501	4	0,12,12	0.00	-	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	501	4	-	0/0/48/48	0/6/5/5
58	SF4	CD	501	4	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	AD	501	SF4	1	0
58	CD	501	SF4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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	1497/1521 (98%)	0.14	19 (1%) 79 75	41, 72, 93, 106	0
1	CA	1503/1521 (98%)	0.17	68 (4%) 37 29	43, 75, 94, 106	0
2	AB	231/256 (90%)	0.75	29 (12%) 5 3	68, 82, 89, 95	0
2	CB	231/256 (90%)	1.78	87 (37%) 0 0	68, 83, 90, 96	0
3	AC	206/239 (86%)	0.83	26 (12%) 5 3	69, 79, 87, 94	0
3	CC	206/239 (86%)	1.68	79 (38%) 0 0	70, 82, 90, 94	0
4	AD	208/209 (99%)	1.08	39 (18%) 2 1	57, 72, 81, 87	0
4	CD	208/209 (99%)	1.00	26 (12%) 5 3	60, 72, 81, 89	0
5	AE	148/162 (91%)	0.78	13 (8%) 12 8	58, 71, 81, 85	0
5	CE	148/162 (91%)	1.11	23 (15%) 3 1	60, 74, 83, 86	0
6	AF	100/101 (99%)	0.45	3 (3%) 54 47	52, 67, 75, 85	0
6	CF	100/101 (99%)	0.42	3 (3%) 54 47	57, 71, 81, 85	0
7	AG	155/156 (99%)	0.45	9 (5%) 26 20	66, 76, 85, 96	0
7	CG	155/156 (99%)	1.34	47 (30%) 1 0	68, 77, 86, 97	0
8	AH	137/138 (99%)	0.35	2 (1%) 76 71	62, 72, 79, 83	0
8	CH	137/138 (99%)	1.26	35 (25%) 1 0	64, 74, 80, 85	0
9	AI	127/128 (99%)	1.03	21 (16%) 2 1	62, 80, 87, 89	0
9	CI	127/128 (99%)	3.03	84 (66%) 0 0	69, 82, 89, 91	0
10	AJ	97/105 (92%)	0.85	14 (14%) 3 2	66, 83, 91, 92	0
10	CJ	96/105 (91%)	2.21	46 (47%) 0 0	68, 84, 91, 93	0
11	AK	114/129 (88%)	0.90	12 (10%) 8 5	51, 70, 80, 84	0
11	CK	114/129 (88%)	0.97	13 (11%) 7 4	52, 72, 81, 85	0
12	AL	122/132 (92%)	0.27	1 (0%) 87 85	41, 56, 71, 75	0
12	CL	122/132 (92%)	0.88	24 (19%) 1 1	58, 73, 82, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	0.50	7 (5%) 27 20	57, 72, 83, 88	0
13	CM	122/126 (96%)	2.04	52 (42%) 0 0	69, 85, 92, 97	0
14	AN	60/61 (98%)	1.09	8 (13%) 4 3	70, 76, 83, 84	0
14	CN	60/61 (98%)	3.12	42 (70%) 0 0	73, 79, 85, 87	0
15	AO	88/89 (98%)	0.57	5 (5%) 27 20	54, 68, 79, 83	0
15	CO	88/89 (98%)	0.59	6 (6%) 20 15	56, 70, 81, 84	0
16	AP	82/88 (93%)	1.45	23 (28%) 1 0	59, 71, 79, 84	0
16	CP	82/88 (93%)	0.69	3 (3%) 45 37	59, 70, 79, 83	0
17	AQ	99/105 (94%)	0.66	8 (8%) 15 10	57, 70, 79, 84	0
17	CQ	99/105 (94%)	1.14	22 (22%) 1 0	60, 71, 79, 84	0
18	AR	68/88 (77%)	0.80	10 (14%) 3 2	59, 69, 81, 84	0
18	CR	68/88 (77%)	0.95	11 (16%) 3 1	58, 70, 81, 85	0
19	AS	84/93 (90%)	0.36	2 (2%) 62 56	70, 81, 87, 92	0
19	CS	83/93 (89%)	2.12	39 (46%) 0 0	74, 83, 90, 94	0
20	AT	96/106 (90%)	0.40	5 (5%) 31 24	59, 71, 80, 83	0
20	CT	96/106 (90%)	0.62	8 (8%) 14 9	59, 71, 80, 83	0
21	AU	23/27 (85%)	1.23	5 (21%) 1 0	70, 75, 78, 82	0
21	CU	23/27 (85%)	2.89	15 (65%) 0 0	71, 78, 81, 82	0
22	AV	13/24 (54%)	1.97	6 (46%) 0 0	58, 77, 95, 100	0
22	CV	12/24 (50%)	2.48	7 (58%) 0 0	64, 81, 93, 95	0
23	AW	66/76 (86%)	1.15	11 (16%) 2 1	66, 95, 102, 105	0
23	CW	64/76 (84%)	3.23	49 (76%) 0 0	70, 96, 101, 106	0
24	AX	71/77 (92%)	0.09	1 (1%) 78 74	42, 73, 90, 96	0
24	CX	71/77 (92%)	0.20	3 (4%) 40 32	55, 86, 95, 98	0
25	AY	67/76 (88%)	0.59	8 (11%) 6 4	44, 97, 101, 105	0
25	CY	66/76 (86%)	1.81	28 (42%) 0 0	48, 98, 102, 103	0
26	BA	2819/2915 (96%)	0.63	19 (0%) 89 87	23, 43, 87, 106	0
26	DA	2800/2915 (96%)	-0.00	66 (2%) 62 56	27, 48, 90, 108	0
27	BB	120/121 (99%)	0.60	0 100 100	41, 64, 76, 88	0
27	DB	120/121 (99%)	0.02	2 (1%) 73 68	48, 70, 80, 91	0
28	BD	275/276 (99%)	0.49	3 (1%) 82 79	24, 41, 58, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	0.43	8 (2%) 55 48	28, 44, 61, 79	0
29	BE	204/206 (99%)	0.63	3 (1%) 76 71	23, 46, 65, 83	0
29	DE	204/206 (99%)	0.29	1 (0%) 91 90	26, 50, 67, 84	0
30	BF	203/210 (96%)	0.65	1 (0%) 91 90	25, 51, 76, 86	0
30	DF	203/210 (96%)	0.47	8 (3%) 43 35	28, 56, 78, 88	0
31	BG	181/182 (99%)	0.55	4 (2%) 65 59	55, 72, 83, 93	0
31	DG	181/182 (99%)	1.58	61 (33%) 0 0	64, 76, 85, 93	0
32	BH	174/180 (96%)	0.55	1 (0%) 90 88	50, 66, 75, 82	0
32	DH	174/180 (96%)	1.79	72 (41%) 0 0	56, 71, 79, 83	0
33	BI	146/148 (98%)	0.37	1 (0%) 89 87	49, 74, 83, 87	0
33	DI	146/148 (98%)	0.15	2 (1%) 78 74	50, 74, 83, 87	0
34	BN	140/140 (100%)	0.71	0 100 100	29, 48, 67, 79	0
34	DN	140/140 (100%)	0.84	13 (9%) 11 7	35, 53, 70, 82	0
35	BO	122/122 (100%)	0.32	0 100 100	25, 40, 57, 67	0
35	DO	122/122 (100%)	0.51	2 (1%) 74 69	44, 58, 74, 79	0
36	BP	149/150 (99%)	0.59	0 100 100	25, 55, 75, 80	0
36	DP	149/150 (99%)	0.63	7 (4%) 35 28	28, 58, 78, 83	0
37	BQ	141/141 (100%)	0.81	3 (2%) 67 61	37, 52, 68, 77	0
37	DQ	141/141 (100%)	1.27	32 (22%) 1 0	41, 58, 72, 79	0
38	BR	118/118 (100%)	0.46	0 100 100	22, 34, 50, 59	0
38	DR	118/118 (100%)	0.69	6 (5%) 32 25	38, 53, 64, 75	0
39	BS	110/112 (98%)	0.36	1 (0%) 85 83	34, 50, 64, 70	0
39	DS	110/112 (98%)	1.46	31 (28%) 1 0	70, 79, 87, 91	0
40	BT	131/146 (89%)	0.42	0 100 100	38, 51, 73, 82	0
40	DT	131/146 (89%)	0.27	2 (1%) 76 71	40, 54, 75, 81	0
41	BU	116/118 (98%)	0.47	0 100 100	17, 30, 50, 63	0
41	DU	116/118 (98%)	0.57	5 (4%) 39 31	40, 59, 79, 85	0
42	BV	101/101 (100%)	0.31	0 100 100	16, 38, 58, 68	0
42	DV	101/101 (100%)	0.36	4 (3%) 42 34	44, 73, 81, 92	0
43	BW	112/113 (99%)	0.41	0 100 100	22, 30, 49, 83	0
43	DW	112/113 (99%)	0.75	5 (4%) 37 29	35, 50, 66, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.68	1 (1%) 82 79	31, 46, 67, 83	0
44	DX	95/96 (98%)	0.74	10 (10%) 8 5	36, 50, 68, 83	0
45	BY	107/110 (97%)	0.51	1 (0%) 85 83	42, 59, 73, 84	0
45	DY	107/110 (97%)	0.81	14 (13%) 5 3	47, 61, 75, 84	0
46	BZ	171/206 (83%)	1.00	30 (17%) 2 1	40, 66, 91, 95	0
46	DZ	174/206 (84%)	1.97	68 (39%) 0 0	69, 85, 94, 101	0
47	B0	83/85 (97%)	1.00	6 (7%) 18 13	34, 50, 67, 75	0
47	D0	83/85 (97%)	1.19	10 (12%) 6 4	40, 56, 71, 76	0
48	B1	97/98 (98%)	0.51	2 (2%) 67 61	31, 49, 72, 76	0
48	D1	97/98 (98%)	0.58	6 (6%) 24 18	34, 53, 73, 78	0
49	B2	70/72 (97%)	0.45	0 100 100	33, 49, 64, 82	0
49	D2	70/72 (97%)	0.43	2 (2%) 55 48	58, 69, 78, 82	0
50	B3	59/60 (98%)	0.25	0 100 100	24, 37, 63, 74	0
50	D3	59/60 (98%)	0.97	8 (13%) 4 2	52, 65, 79, 87	0
51	B4	69/71 (97%)	0.50	5 (7%) 18 13	49, 76, 89, 91	0
51	D4	69/71 (97%)	1.78	27 (39%) 0 0	74, 89, 95, 99	0
52	B5	59/60 (98%)	0.45	1 (1%) 73 68	16, 30, 46, 68	0
52	D5	59/60 (98%)	0.33	1 (1%) 73 68	35, 49, 65, 77	0
53	B6	53/54 (98%)	0.35	0 100 100	32, 44, 57, 72	0
53	D6	53/54 (98%)	0.74	3 (5%) 27 20	49, 64, 74, 79	0
54	B7	48/49 (97%)	0.81	3 (6%) 23 17	23, 32, 58, 70	0
54	D7	48/49 (97%)	1.02	5 (10%) 8 5	26, 35, 61, 70	0
55	B8	64/65 (98%)	0.66	0 100 100	34, 42, 50, 65	0
55	D8	64/65 (98%)	0.59	1 (1%) 74 69	37, 46, 54, 65	0
56	B9	37/37 (100%)	0.99	1 (2%) 58 51	36, 51, 65, 73	0
56	D9	37/37 (100%)	0.75	5 (13%) 4 2	43, 55, 68, 76	0
All	All	20895/21748 (96%)	0.61	1680 (8%) 15 10	16, 64, 89, 108	0

All (1680) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CB	165	VAL	12.3
46	DZ	155	LEU	10.6

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Mol	Chain	Res	Type	RSRZ
13	CM	124	PRO	10.1
46	DZ	107	THR	9.2
46	DZ	171	ILE	8.7
46	DZ	114	GLY	8.7
9	CI	14	VAL	8.3
13	CM	123	ALA	8.1
9	CI	7	THR	8.1
2	CB	200	ILE	8.0
10	CJ	47	PHE	8.0
10	CJ	63	PHE	7.9
7	CG	83	ALA	7.8
9	CI	36	TYR	7.7
46	DZ	108	PRO	7.7
9	CI	76	ALA	7.7
23	CW	31	A	7.6
9	CI	106	ALA	7.5
46	BZ	106	GLY	7.4
14	CN	25	VAL	7.1
13	AM	124	PRO	7.1
14	CN	53	LEU	7.0
46	DZ	113	ALA	7.0
14	CN	38	GLY	7.0
46	BZ	107	THR	7.0
14	CN	59	ALA	6.8
1	CA	1030(B)	C	6.8
28	DD	2	ALA	6.8
13	CM	95	GLY	6.7
9	CI	79	LEU	6.7
39	DS	32	LEU	6.6
10	CJ	71	LEU	6.6
13	CM	102	ARG	6.6
13	CM	122	LYS	6.6
23	CW	71	G	6.5
46	DZ	149	SER	6.5
10	CJ	46	ARG	6.5
46	BZ	108	PRO	6.4
2	CB	92	TYR	6.4
51	D4	49	PHE	6.3
46	BZ	120	ILE	6.3
7	CG	82	GLY	6.3
9	CI	9	ARG	6.3
3	CC	13	GLY	6.3

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Mol	Chain	Res	Type	RSRZ
14	CN	39	LEU	6.3
13	CM	90	LEU	6.3
25	AY	36	A	6.2
14	CN	44	LEU	6.2
3	CC	53	ALA	6.1
19	CS	80	TYR	6.1
9	CI	80	GLY	6.1
47	B0	7	LEU	6.1
13	CM	94	ARG	6.1
14	CN	34	TYR	6.1
9	CI	123	PRO	6.1
47	D0	2	ALA	6.0
3	CC	184	TYR	6.0
26	DA	229	A	6.0
2	CB	81	VAL	6.0
46	DZ	116	VAL	6.0
51	D4	57	GLU	6.0
21	CU	6	ARG	6.0
3	CC	145	GLY	6.0
9	CI	115	GLY	6.0
46	BZ	144	LEU	6.0
5	CE	94	ALA	5.9
23	CW	3	C	5.9
8	CH	2	LEU	5.9
44	DX	92	LEU	5.9
13	AM	123	ALA	5.9
9	AI	19	LEU	5.8
2	CB	214	ILE	5.8
31	DG	140	ILE	5.8
7	AG	82	GLY	5.7
13	CM	60	VAL	5.7
13	CM	92	HIS	5.6
14	CN	35	ARG	5.6
9	CI	109	VAL	5.6
26	DA	2127	G	5.6
48	D1	2	SER	5.6
9	CI	15	ALA	5.6
3	CC	182	ILE	5.6
23	AW	71	G	5.6
3	CC	206	GLU	5.6
46	DZ	115	GLY	5.6
46	DZ	170	THR	5.6

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Mol	Chain	Res	Type	RSRZ
51	D4	40	HIS	5.5
23	CW	30	G	5.5
46	DZ	172	ALA	5.5
46	BZ	118	GLN	5.5
14	AN	2	ALA	5.5
14	CN	29	ARG	5.5
23	CW	4	C	5.5
2	CB	211	ILE	5.5
23	CW	72	C	5.5
32	DH	115	VAL	5.5
32	DH	94	TYR	5.5
26	DA	2132	U	5.5
32	DH	113	VAL	5.5
13	AM	2	ALA	5.5
25	CY	36	A	5.5
2	CB	70	PHE	5.4
2	CB	187	LEU	5.4
23	CW	56	C	5.4
54	D7	48	LYS	5.4
3	CC	8	ILE	5.4
9	AI	106	ALA	5.4
54	B7	48	LYS	5.4
9	CI	5	TYR	5.4
32	DH	102	ALA	5.4
51	D4	54	GLY	5.4
26	DA	896	A	5.4
17	CQ	80	GLY	5.4
7	CG	4	ARG	5.3
46	BZ	141	VAL	5.3
37	DQ	104	PHE	5.3
21	CU	14	TRP	5.3
9	CI	17	VAL	5.3
32	DH	107	VAL	5.3
23	CW	70	G	5.3
7	CG	81	GLY	5.3
46	DZ	143	GLY	5.3
31	DG	142	PRO	5.3
19	CS	82	GLY	5.2
47	B0	6	GLY	5.2
3	CC	71	ALA	5.2
7	AG	83	ALA	5.2
7	AG	85	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
9	CI	110	GLU	5.2
23	CW	23	A	5.2
23	CW	73	A	5.2
26	DA	2128	C	5.1
19	CS	41	VAL	5.1
26	DA	2155	G	5.1
51	D4	44	THR	5.1
21	CU	11	GLY	5.1
26	DA	2146	C	5.1
10	CJ	67	THR	5.1
19	CS	79	THR	5.1
26	DA	883	G	5.1
3	CC	12	LEU	5.1
2	CB	77	ALA	5.1
14	CN	57	ARG	5.1
21	CU	15	ARG	5.1
46	DZ	52	SER	5.1
46	DZ	141	VAL	5.1
10	CJ	49	VAL	5.0
14	CN	42	ILE	5.0
9	CI	66	ARG	5.0
31	DG	29	TRP	5.0
46	BZ	111	VAL	5.0
2	CB	164	VAL	5.0
19	CS	49	ILE	5.0
25	CY	35	A	5.0
13	CM	82	MET	5.0
14	CN	61	TRP	5.0
2	CB	196	LEU	5.0
14	CN	31	ARG	5.0
3	CC	21	ARG	4.9
46	DZ	125	LEU	4.9
2	CB	31	TYR	4.9
9	CI	114	TYR	4.9
25	CY	62	C	4.9
39	DS	58	LEU	4.9
9	CI	126	SER	4.9
47	D0	7	LEU	4.9
13	CM	4	ILE	4.9
22	CV	24	A	4.9
10	CJ	65	LEU	4.9
10	CJ	62	HIS	4.9

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Mol	Chain	Res	Type	RSRZ
47	B0	2	ALA	4.9
53	D6	54	ILE	4.9
26	BA	896	A	4.9
46	BZ	113	ALA	4.9
7	CG	156	TRP	4.9
26	DA	2160	G	4.9
9	CI	107	ARG	4.9
54	D7	46	VAL	4.9
19	CS	30	LEU	4.9
9	CI	75	ASP	4.8
46	DZ	111	VAL	4.8
23	CW	45	U	4.8
46	DZ	139	VAL	4.8
2	CB	207	ALA	4.8
5	CE	8	GLU	4.8
51	D4	52	THR	4.8
46	DZ	144	LEU	4.8
46	BZ	114	GLY	4.8
46	DZ	156	LYS	4.8
22	AV	13	A	4.8
23	CW	44	G	4.7
26	DA	2173	A	4.7
9	CI	62	TYR	4.7
31	DG	146	TYR	4.7
9	CI	61	ALA	4.7
1	CA	1115	C	4.7
31	DG	149	VAL	4.7
32	DH	106	THR	4.7
9	CI	19	LEU	4.7
2	CB	203	GLY	4.7
4	AD	138	TYR	4.7
19	CS	52	TYR	4.7
21	CU	2	GLY	4.7
9	CI	4	TYR	4.7
10	CJ	38	ILE	4.7
1	CA	1532	U	4.6
13	CM	120	LYS	4.6
1	AA	1030(B)	C	4.6
32	DH	105	LEU	4.6
31	DG	41	GLN	4.6
2	CB	152	PHE	4.6
22	CV	22	U	4.6

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Mol	Chain	Res	Type	RSRZ
1	AA	1001(A)	G	4.6
13	CM	78	ILE	4.6
51	D4	51	ASP	4.6
9	CI	116	LYS	4.6
13	CM	121	LYS	4.6
23	CW	57	G	4.6
23	AW	73	A	4.6
9	CI	108	VAL	4.6
31	DG	35	GLU	4.6
1	AA	1002	G	4.6
14	CN	58	LYS	4.6
2	CB	122	PHE	4.6
14	CN	37	PHE	4.6
31	DG	11	TYR	4.6
13	CM	66	LEU	4.5
25	CY	18	G	4.5
48	B1	98	LEU	4.5
17	AQ	27	PHE	4.5
2	CB	118	LEU	4.5
2	CB	228	GLY	4.5
3	CC	6	HIS	4.5
10	CJ	48	THR	4.5
31	BG	146	TYR	4.5
25	CY	61	C	4.5
10	CJ	50	ILE	4.5
10	CJ	10	GLY	4.5
1	CA	1220	G	4.4
9	CI	27	THR	4.4
46	DZ	119	GLU	4.4
52	B5	60	VAL	4.4
26	DA	2154	G	4.4
39	DS	56	LEU	4.4
50	D3	26	LEU	4.4
13	CM	7	VAL	4.4
7	CG	154	TYR	4.4
7	CG	80	VAL	4.4
9	CI	33	PHE	4.4
46	DZ	96	VAL	4.4
2	CB	201	ILE	4.4
26	DA	885	C	4.4
3	CC	181	ASN	4.4
23	AW	20	U	4.4

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Mol	Chain	Res	Type	RSRZ
9	CI	125	TYR	4.4
3	CC	80	GLY	4.4
25	CY	63	G	4.4
9	CI	81	ILE	4.4
2	CB	163	PHE	4.4
26	DA	2144	U	4.4
9	CI	127	LYS	4.4
7	AG	153	HIS	4.3
3	CC	207	VAL	4.3
10	CJ	60	ARG	4.3
26	BA	2145	C	4.3
9	CI	105	ASP	4.3
44	DX	68	ARG	4.3
3	CC	159	GLY	4.3
19	CS	35	SER	4.3
23	CW	5	G	4.3
3	CC	60	ALA	4.3
7	CG	84	ASN	4.3
25	CY	34	G	4.3
21	CU	8	THR	4.3
5	CE	109	ILE	4.3
32	DH	166	GLY	4.3
19	CS	14	HIS	4.3
1	CA	1030(A)	G	4.3
3	CC	204	LEU	4.3
2	CB	48	MET	4.3
7	CG	2	ALA	4.3
13	CM	87	TYR	4.3
22	AV	24	A	4.3
7	CG	79	ARG	4.3
9	AI	8	GLY	4.3
39	DS	5	THR	4.2
22	AV	12	A	4.2
1	CA	1114	C	4.2
46	BZ	112	ARG	4.2
13	CM	6	GLY	4.2
39	DS	40	ILE	4.2
10	CJ	55	LYS	4.2
16	AP	19	ILE	4.2
23	CW	28	G	4.2
23	CW	13	C	4.2
22	CV	23	A	4.2

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Mol	Chain	Res	Type	RSRZ
32	DH	48	GLY	4.2
51	D4	50	VAL	4.2
13	CM	5	ALA	4.1
25	CY	53	G	4.1
13	CM	15	VAL	4.1
14	CN	50	LYS	4.1
14	CN	41	ARG	4.1
2	AB	165	VAL	4.1
51	D4	32	TYR	4.1
3	CC	189	ALA	4.1
19	CS	69	HIS	4.1
46	BZ	146	ILE	4.1
9	CI	26	VAL	4.1
10	CJ	66	ARG	4.1
9	CI	74	ILE	4.1
2	CB	101	MET	4.1
47	D0	45	PHE	4.1
26	DA	2145	C	4.1
34	DN	140	VAL	4.1
32	DH	97	ARG	4.1
3	CC	65	ALA	4.1
8	CH	135	CYS	4.1
10	CJ	12	ASP	4.1
14	CN	47	LEU	4.1
12	CL	32	PHE	4.1
46	DZ	106	GLY	4.1
46	DZ	147	GLY	4.1
27	DB	119	G	4.1
2	CB	132	LYS	4.1
9	CI	124	GLN	4.1
1	CA	1150	U	4.0
46	DZ	152	ALA	4.0
16	AP	2	VAL	4.0
14	CN	30	ALA	4.0
32	DH	114	VAL	4.0
3	CC	14	ILE	4.0
9	CI	67	GLY	4.0
19	CS	40	ILE	4.0
31	DG	39	ILE	4.0
23	CW	69	G	4.0
26	DA	2153	G	4.0
12	CL	28	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
14	CN	36	PHE	4.0
3	AC	15	THR	4.0
9	CI	28	VAL	4.0
23	AW	44	G	4.0
9	CI	120	ARG	4.0
18	CR	87	ARG	4.0
4	AD	135	LEU	4.0
13	CM	98	VAL	4.0
26	DA	2158	A	4.0
31	DG	102	PHE	4.0
23	AW	70	G	4.0
26	DA	2156	G	4.0
13	CM	119	GLY	4.0
32	DH	98	LEU	4.0
9	AI	113	LYS	4.0
23	CW	14	A	4.0
26	BA	885	C	3.9
5	CE	90	VAL	3.9
7	CG	109	ASN	3.9
1	AA	1257	U	3.9
25	CY	64	A	3.9
45	DY	1	MET	3.9
31	DG	136	ARG	3.9
22	CV	21	C	3.9
51	D4	59	PHE	3.9
3	CC	134	ILE	3.9
46	DZ	137	ILE	3.9
13	CM	64	TRP	3.9
23	CW	2	C	3.9
25	CY	57	G	3.9
9	CI	18	PHE	3.9
14	CN	46	GLU	3.9
19	CS	10	PHE	3.9
31	DG	17	PRO	3.9
1	AA	163	C	3.9
23	AW	72	C	3.9
31	DG	19	LEU	3.9
51	B4	50	VAL	3.9
3	CC	179	ARG	3.9
9	CI	112	LYS	3.8
44	DX	89	ILE	3.8
37	DQ	32	TYR	3.8

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Mol	Chain	Res	Type	RSRZ
46	BZ	104	PHE	3.8
37	DQ	33	GLY	3.8
1	AA	1036	G	3.8
26	DA	2131	G	3.8
10	CJ	85	LEU	3.8
46	DZ	121	HIS	3.8
19	CS	32	LYS	3.8
21	CU	16	GLY	3.8
31	DG	182	LYS	3.8
1	CA	1219	U	3.8
31	DG	173	LEU	3.8
47	B0	4	LYS	3.8
23	CW	36	A	3.8
2	CB	188	ALA	3.8
10	CJ	72	VAL	3.8
7	AG	79	ARG	3.8
1	CA	1036	G	3.8
26	BA	2146	C	3.8
9	CI	101	PHE	3.8
14	CN	2	ALA	3.8
32	DH	101	ARG	3.8
30	DF	12	LEU	3.8
31	DG	133	LEU	3.8
31	DG	139	LEU	3.8
21	CU	17	THR	3.8
1	CA	1116	C	3.8
12	CL	39	VAL	3.8
2	CB	72	GLY	3.7
32	DH	111	HIS	3.7
39	DS	82	ILE	3.7
47	D0	3	HIS	3.7
9	CI	6	GLY	3.7
9	CI	122	ALA	3.7
22	CV	14	A	3.7
5	CE	10	MET	3.7
45	DY	5	MET	3.7
32	BH	2	SER	3.7
31	DG	181	ARG	3.7
54	D7	47	ARG	3.7
9	CI	64	THR	3.7
3	CC	17	ASP	3.7
9	CI	54	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
19	CS	13	ASP	3.7
3	CC	155	GLY	3.7
2	AB	221	LEU	3.7
16	AP	59	TRP	3.7
31	DG	115	ARG	3.7
1	CA	1186	G	3.7
1	CA	1321	C	3.7
2	CB	177	ALA	3.7
45	DY	65	ALA	3.7
2	CB	215	LEU	3.7
37	DQ	5	ARG	3.7
46	DZ	122	ARG	3.7
19	CS	31	ILE	3.7
10	CJ	15	THR	3.7
3	CC	16	ARG	3.7
46	DZ	118	GLN	3.7
1	CA	1001	A	3.7
1	CA	1112	C	3.7
26	DA	888	C	3.7
10	CJ	54	PHE	3.7
12	CL	18	VAL	3.6
18	AR	85	LEU	3.6
20	CT	24	LEU	3.6
23	CW	38	A	3.6
31	DG	34	LEU	3.6
26	DA	884	C	3.6
32	DH	36	PRO	3.6
1	CA	1257	U	3.6
9	AI	15	ALA	3.6
39	DS	54	LEU	3.6
46	DZ	150	LEU	3.6
26	DA	2159	G	3.6
32	DH	159	GLU	3.6
4	AD	70	ILE	3.6
31	DG	157	ILE	3.6
2	CB	202	PRO	3.6
14	AN	16	PHE	3.6
3	CC	178	LEU	3.6
7	CG	9	VAL	3.6
23	AW	3	C	3.6
9	CI	128	ARG	3.6
14	CN	56	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
19	CS	53	ASN	3.6
23	CW	10	G	3.6
2	CB	131	PRO	3.6
32	DH	96	ALA	3.6
46	DZ	51	ALA	3.6
31	DG	48	GLU	3.6
18	CR	85	LEU	3.6
46	DZ	174	VAL	3.6
43	DW	112	GLY	3.6
23	CW	41	C	3.6
3	CC	23	TYR	3.5
17	CQ	91	ARG	3.6
27	DB	118	G	3.5
9	CI	83	ARG	3.5
3	AC	128	PHE	3.5
3	CC	198	VAL	3.5
4	AD	2	GLY	3.5
38	DR	69	ASP	3.5
2	CB	232	PRO	3.5
32	DH	145	ALA	3.5
2	AB	227	GLY	3.5
5	AE	6	PHE	3.5
10	CJ	41	PRO	3.5
25	AY	34	G	3.5
12	CL	64	TYR	3.5
21	CU	10	ARG	3.5
26	BA	888	C	3.5
32	DH	72	ILE	3.5
3	AC	91	LEU	3.5
13	AM	87	TYR	3.5
47	D0	76	GLY	3.5
1	CA	1187	G	3.5
26	DA	2174	C	3.5
46	DZ	153	SER	3.5
21	CU	13	ILE	3.5
38	DR	68	ARG	3.5
46	DZ	146	ILE	3.5
4	CD	135	LEU	3.5
19	CS	75	ALA	3.5
3	AC	201	TYR	3.5
10	CJ	64	GLU	3.5
4	AD	120	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
13	CM	72	ALA	3.5
5	CE	33	VAL	3.5
25	AY	35	A	3.5
3	CC	158	GLY	3.4
7	CG	12	LEU	3.4
10	CJ	61	GLU	3.4
46	BZ	109	ALA	3.4
2	AB	230	VAL	3.4
8	CH	95	VAL	3.4
36	DP	125	VAL	3.4
48	D1	22	GLY	3.4
2	AB	118	LEU	3.4
9	CI	50	LEU	3.4
13	CM	103	THR	3.4
7	CG	40	ALA	3.4
32	DH	76	VAL	3.4
4	AD	180	GLY	3.4
14	CN	60	SER	3.4
10	CJ	88	LEU	3.4
2	CB	162	ILE	3.4
17	CQ	36	ILE	3.4
2	CB	83	MET	3.4
8	CH	122	ARG	3.4
32	DH	95	ARG	3.4
31	DG	28	VAL	3.4
7	AG	84	ASN	3.4
25	CY	52	G	3.4
32	DH	124	GLU	3.4
46	DZ	142	SER	3.4
31	DG	141	PHE	3.4
45	DY	106	LEU	3.4
4	AD	112	VAL	3.4
16	AP	38	TYR	3.4
32	DH	35	VAL	3.4
5	CE	12	LEU	3.4
12	CL	27	LEU	3.4
13	CM	93	ARG	3.4
13	CM	110	ARG	3.4
2	AB	228	GLY	3.4
1	CA	1035	A	3.4
10	CJ	27	ALA	3.4
31	DG	6	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	CA	1224	G	3.4
23	CW	22	G	3.4
4	AD	102	ASP	3.4
4	CD	134	ASP	3.4
9	AI	114	TYR	3.3
9	CI	92	TYR	3.3
51	D4	42	PHE	3.3
3	AC	8	ILE	3.3
22	AV	23	A	3.3
26	BA	2140	C	3.3
26	DA	2139	C	3.3
28	BD	276	LYS	3.3
9	CI	42	ARG	3.3
7	CG	16	LEU	3.3
23	CW	18	G	3.3
26	DA	2125	G	3.3
47	D0	5	LYS	3.3
2	CB	193	ASP	3.3
23	CW	47	U	3.3
46	BZ	149	SER	3.3
4	AD	21	LEU	3.3
19	AS	71	LEU	3.3
3	AC	39	ILE	3.3
4	CD	146	ILE	3.3
26	DA	2157	G	3.3
32	DH	125	VAL	3.3
8	CH	94	TYR	3.3
9	CI	88	TYR	3.3
23	CW	58	A	3.3
31	DG	15	VAL	3.3
10	AJ	46	ARG	3.3
46	DZ	99	TYR	3.3
23	CW	75	C	3.3
26	DA	2161	C	3.3
16	AP	7	ALA	3.3
31	DG	156	ASP	3.3
2	CB	223	ILE	3.3
4	AD	169	LYS	3.3
2	CB	197	VAL	3.3
8	CH	61	VAL	3.3
32	DH	112	PRO	3.3
23	CW	29	G	3.3

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Mol	Chain	Res	Type	RSRZ
46	BZ	143	GLY	3.3
51	D4	68	ARG	3.3
1	CA	1531	A	3.3
32	DH	144	VAL	3.3
9	AI	47	LEU	3.3
37	DQ	37	LEU	3.3
37	DQ	63	LYS	3.3
2	CB	220	ASP	3.3
1	CA	1202	G	3.3
2	AB	68	ILE	3.3
23	CW	40	C	3.2
19	CS	56	GLN	3.2
31	DG	108	ASN	3.2
2	CB	62	ALA	3.2
19	CS	83	HIS	3.2
46	BZ	164	ALA	3.2
2	AB	126	GLU	3.2
46	DZ	161	VAL	3.2
23	AW	2	C	3.2
39	DS	83	LYS	3.2
3	CC	9	GLY	3.2
2	AB	215	LEU	3.2
18	CR	26	LEU	3.2
32	DH	13	LYS	3.2
44	DX	69	TYR	3.2
14	CN	55	GLY	3.2
10	CJ	8	LEU	3.2
31	DG	60	LEU	3.2
3	CC	19	GLU	3.2
10	CJ	13	HIS	3.2
2	CB	222	ILE	3.2
14	AN	7	ILE	3.2
25	AY	20	U	3.2
10	CJ	40	LEU	3.2
7	CG	62	PHE	3.2
16	AP	35	LYS	3.2
7	CG	32	ARG	3.2
23	CW	9	A	3.2
26	DA	887	A	3.2
46	DZ	4	ARG	3.2
8	CH	131	GLY	3.2
14	AN	59	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
23	CW	74	C	3.2
46	DZ	124	ILE	3.2
3	CC	91	LEU	3.2
21	CU	5	ASP	3.2
25	CY	47	U	3.2
42	DV	73	SER	3.2
10	CJ	56	HIS	3.2
9	CI	37	PHE	3.2
32	DH	30	LYS	3.2
1	CA	1286	A	3.1
17	CQ	11	VAL	3.1
34	DN	9	VAL	3.1
51	D4	56	VAL	3.1
19	CS	70	LYS	3.1
26	DA	1026	U	3.1
39	DS	57	LYS	3.1
5	CE	81	GLU	3.1
7	AG	81	GLY	3.1
3	AC	126	ARG	3.1
13	AM	56	LEU	3.1
39	DS	35	ILE	3.1
17	CQ	9	VAL	3.1
30	DF	131	GLY	3.1
26	DA	886	C	3.1
37	DQ	114	ALA	3.1
28	BD	275	LYS	3.1
56	B9	17	ILE	3.1
32	DH	133	VAL	3.1
37	DQ	65	PHE	3.1
2	CB	29	ALA	3.1
11	CK	31	THR	3.1
13	CM	42	ALA	3.1
25	CY	12	U	3.1
1	AA	1035	A	3.1
4	AD	176	LEU	3.1
3	CC	124	ILE	3.1
26	BA	1509	C	3.1
21	CU	9	ARG	3.1
23	CW	15	G	3.1
23	CW	24	G	3.1
26	DA	2110	G	3.1
10	CJ	92	THR	3.1

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Mol	Chain	Res	Type	RSRZ
8	CH	133	LEU	3.1
33	DI	12	LEU	3.1
46	DZ	163	LEU	3.1
44	DX	94	GLY	3.1
26	DA	2896	C	3.1
25	AY	24	G	3.1
14	CN	45	ARG	3.1
9	CI	63	ILE	3.1
15	AO	87	ILE	3.1
32	DH	128	PRO	3.1
4	AD	165	MET	3.0
9	CI	10	ARG	3.0
37	DQ	103	MET	3.0
9	CI	69	GLY	3.0
31	DG	137	GLU	3.0
4	AD	20	TYR	3.0
32	DH	45	VAL	3.0
1	CA	975	A	3.0
1	CA	1111	A	3.0
1	CA	1250	A	3.0
3	AC	204	LEU	3.0
3	CC	10	PHE	3.0
17	AQ	28	PRO	3.0
19	CS	38	SER	3.0
50	D3	60	GLU	3.0
1	CA	204	U	3.0
51	D4	43	TYR	3.0
1	CA	1131	G	3.0
4	AD	3	ARG	3.0
4	CD	168	ARG	3.0
44	DX	1	MET	3.0
46	DZ	173	ALA	3.0
23	CW	42	C	3.0
26	DA	2140	C	3.0
32	DH	32	GLU	3.0
2	AB	214	ILE	3.0
8	CH	93	VAL	3.0
9	CI	65	VAL	3.0
7	CG	22	LEU	3.0
17	AQ	98	LEU	3.0
18	AR	79	LEU	3.0
19	CS	66	MET	3.0

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Mol	Chain	Res	Type	RSRZ
46	DZ	104	PHE	3.0
8	CH	86	ILE	3.0
45	DY	44	ILE	3.0
14	CN	27	CYS	3.0
8	CH	128	GLY	3.0
10	AJ	10	GLY	3.0
46	DZ	55	HIS	3.0
12	CL	60	LEU	3.0
31	DG	3	LEU	3.0
32	DH	103	LEU	3.0
23	CW	27	G	3.0
26	DA	2133	G	3.0
3	AC	72	LYS	3.0
26	DA	1509	C	3.0
37	DQ	97	VAL	3.0
39	DS	11	LYS	3.0
3	AC	193	TYR	3.0
7	CG	39	ALA	3.0
10	CJ	19	SER	3.0
46	DZ	98	MET	3.0
45	DY	29	GLU	3.0
46	BZ	169	GLU	3.0
4	CD	148	VAL	3.0
32	DH	37	VAL	3.0
45	DY	45	VAL	3.0
1	CA	1322	C	3.0
26	BA	884	C	3.0
46	DZ	3	TYR	3.0
3	AC	87	LEU	3.0
4	AD	11	LEU	3.0
3	AC	65	ALA	3.0
13	CM	76	ALA	3.0
3	CC	4	LYS	3.0
4	AD	33	MET	3.0
2	CB	66	GLY	3.0
2	CB	71	VAL	3.0
9	AI	109	VAL	3.0
37	DQ	106	VAL	3.0
56	D9	25	VAL	3.0
4	CD	188	LEU	2.9
7	CG	78	ARG	2.9
13	CM	88	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
17	AQ	31	LEU	2.9
1	AA	1031	G	2.9
14	CN	15	LYS	2.9
26	DA	2112	G	2.9
4	AD	110	PHE	2.9
9	CI	32	ASP	2.9
39	DS	12	PHE	2.9
2	CB	185	ILE	2.9
3	AC	78	GLY	2.9
3	CC	157	ILE	2.9
32	DH	148	ILE	2.9
1	CA	1151	A	2.9
9	CI	29	ASN	2.9
47	B0	3	HIS	2.9
3	CC	113	ALA	2.9
1	CA	1348	U	2.9
14	CN	24	CYS	2.9
32	DH	8	PRO	2.9
23	CW	61	C	2.9
2	AB	188	ALA	2.9
13	CM	21	TYR	2.9
4	AD	167	GLY	2.9
14	AN	15	LYS	2.9
2	CB	41	ILE	2.9
9	CI	121	ARG	2.9
26	DA	645	C	2.9
32	DH	151	ILE	2.9
50	D3	29	ARG	2.9
7	CG	91	VAL	2.9
13	CM	67	GLU	2.9
25	CY	6	G	2.9
20	CT	44	ALA	2.9
17	CQ	54	GLY	2.9
2	CB	39	ILE	2.9
8	CH	99	GLU	2.9
23	AW	56	C	2.9
12	CL	62	SER	2.9
1	CA	973	G	2.9
1	CA	1033	G	2.9
7	CG	145	ALA	2.9
46	DZ	164	ALA	2.9
2	AB	222	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
18	CR	86	VAL	2.9
31	DG	5	VAL	2.9
1	AA	1028	C	2.9
5	AE	134	ALA	2.9
31	DG	61	ALA	2.9
2	CB	170	GLU	2.9
9	CI	68	GLY	2.9
32	DH	6	ARG	2.9
32	DH	123	PHE	2.9
33	DI	85	GLU	2.9
25	CY	22	G	2.9
2	CB	90	MET	2.9
40	DT	1	MET	2.9
7	CG	30	ILE	2.9
2	CB	76	GLN	2.9
4	CD	108	LEU	2.9
9	CI	45	ALA	2.9
9	CI	103	THR	2.9
10	CJ	26	ALA	2.9
26	DA	2175	C	2.9
9	AI	112	LYS	2.9
20	CT	9	ASN	2.9
2	AB	15	VAL	2.8
2	CB	233	SER	2.8
4	AD	157	LEU	2.8
46	DZ	5	LEU	2.8
49	D2	60	LEU	2.8
9	CI	82	ALA	2.8
10	AJ	20	ALA	2.8
1	AA	162	A	2.8
22	CV	15	A	2.8
9	CI	40	LEU	2.8
38	DR	29	LEU	2.8
47	D0	75	LEU	2.8
54	B7	46	VAL	2.8
3	CC	147	LYS	2.8
25	CY	65	G	2.8
31	DG	2	PRO	2.8
31	DG	178	PHE	2.8
32	DH	116	GLU	2.8
39	DS	3	ARG	2.8
51	D4	48	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
2	AB	200	ILE	2.8
15	AO	57	LEU	2.8
7	CG	147	ALA	2.8
13	CM	80	ARG	2.8
4	CD	186	LEU	2.8
9	CI	71	SER	2.8
12	CL	10	LEU	2.8
31	BG	139	LEU	2.8
31	DG	152	LEU	2.8
32	DH	89	ILE	2.8
39	DS	52	SER	2.8
4	CD	105	VAL	2.8
21	AU	17	THR	2.8
39	DS	79	ALA	2.8
2	CB	231	GLU	2.8
7	AG	156	TRP	2.8
9	AI	117	HIS	2.8
10	CJ	74	ILE	2.8
17	CQ	23	VAL	2.8
3	CC	180	ALA	2.8
51	B4	46	GLN	2.8
26	DA	2134	A	2.8
34	DN	43	THR	2.8
37	DQ	18	LYS	2.8
54	B7	47	ARG	2.8
3	CC	101	LEU	2.8
3	CC	197	GLY	2.8
8	CH	96	GLY	2.8
18	AR	31	LEU	2.8
46	BZ	115	GLY	2.8
35	DO	1	MET	2.8
1	CA	1002	G	2.8
1	CA	1034	G	2.8
2	AB	229	VAL	2.8
9	CI	113	LYS	2.8
26	DA	614(B)	G	2.8
26	DA	2147	G	2.8
14	CN	12	ARG	2.8
46	DZ	46	LYS	2.8
53	D6	50	ARG	2.8
7	CG	7	ALA	2.8
10	AJ	18	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
3	CC	15	THR	2.8
34	DN	45	ASN	2.8
41	DU	2	PRO	2.8
22	CV	13	A	2.8
23	CW	35	A	2.8
26	DA	2138	C	2.8
4	CD	183	GLY	2.8
17	CQ	84	LEU	2.8
39	DS	34	HIS	2.8
45	DY	55	TYR	2.8
2	AB	78	GLN	2.8
13	AM	25	ILE	2.8
46	DZ	120	ILE	2.8
13	CM	104	ARG	2.8
14	CN	26	ARG	2.8
37	DQ	109	VAL	2.8
3	CC	177	THR	2.8
19	CS	77	THR	2.8
10	CJ	59	SER	2.7
51	D4	45	GLY	2.8
13	CM	23	TYR	2.7
18	AR	78	LEU	2.7
26	BA	897	C	2.7
31	DG	138	GLN	2.7
38	DR	70	LEU	2.7
36	DP	15	ARG	2.7
43	DW	9	TYR	2.7
47	B0	5	LYS	2.7
50	D3	53	LEU	2.7
26	DA	2803	C	2.7
34	DN	85	ILE	2.7
2	CB	112	VAL	2.7
3	CC	146	ALA	2.7
13	CM	50	GLU	2.7
9	AI	121	ARG	2.7
8	CH	112	LEU	2.7
34	DN	23	LEU	2.7
12	CL	13	LYS	2.7
20	AT	55	ILE	2.7
23	CW	19	G	2.7
46	DZ	47	VAL	2.7
9	AI	59	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
13	CM	97	PRO	2.7
51	D4	7	PRO	2.7
9	CI	93	ARG	2.7
1	CA	1092	A	2.7
19	CS	71	LEU	2.7
39	DS	26	LEU	2.7
8	CH	134	ILE	2.7
45	BY	1	MET	2.7
6	CF	55	ASP	2.7
10	CJ	89	ASP	2.7
1	CA	1001(A)	G	2.7
2	AB	163	PHE	2.7
8	CH	104	ARG	2.7
9	CI	8	GLY	2.7
19	CS	12	ASP	2.7
14	CN	23	ARG	2.7
19	CS	37	ARG	2.7
26	DA	2162	G	2.7
38	DR	71	GLN	2.7
14	AN	61	TRP	2.7
14	CN	6	LEU	2.7
43	DW	82	LEU	2.7
1	AA	161	A	2.7
19	CS	43	GLU	2.7
26	BA	229	A	2.7
8	CH	83	ILE	2.7
32	DH	126	PRO	2.7
9	CI	11	LYS	2.7
1	CA	1149	C	2.7
23	CW	34	G	2.7
25	AY	13	C	2.7
25	CY	48	C	2.7
4	CD	161	ASN	2.7
3	CC	190	ARG	2.7
9	CI	77	ILE	2.7
11	CK	13	GLN	2.7
3	CC	64	VAL	2.7
3	CC	183	ASP	2.7
26	BA	1026	U	2.7
46	DZ	97	GLU	2.7
5	CE	130	ASN	2.7
16	AP	4	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
9	AI	49	PRO	2.7
20	AT	20	LEU	2.6
13	CM	85	GLY	2.6
2	CB	93	VAL	2.6
23	CW	11	C	2.6
11	AK	87	THR	2.6
37	DQ	2	LEU	2.6
37	DQ	17	LEU	2.6
47	D0	74	ARG	2.6
32	DH	43	VAL	2.6
51	D4	35	VAL	2.6
11	AK	19	ALA	2.6
11	CK	59	TYR	2.6
18	AR	29	PHE	2.6
21	AU	14	TRP	2.6
1	CA	978	A	2.6
16	AP	33	ILE	2.6
16	CP	20	VAL	2.6
2	CB	144	ARG	2.6
9	CI	119	ALA	2.6
39	DS	20	ARG	2.6
45	DY	35	TYR	2.6
7	CG	33	ASP	2.6
1	CA	1221	G	2.6
2	CB	136	VAL	2.6
3	AC	124	ILE	2.6
4	AD	133	VAL	2.6
4	AD	148	VAL	2.6
4	AD	170	VAL	2.6
10	CJ	96	ILE	2.6
16	AP	36	ILE	2.6
4	AD	147	ALA	2.6
7	CG	26	PHE	2.6
32	DH	165	ALA	2.6
46	DZ	65	GLN	2.6
2	CB	16	HIS	2.6
14	CN	49	HIS	2.6
51	D4	19	GLY	2.6
56	D9	13	LYS	2.6
1	CA	979	C	2.6
16	AP	48	TRP	2.6
1	CA	1368	G	2.6

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Mol	Chain	Res	Type	RSRZ
4	AD	17	VAL	2.6
5	CE	131	ILE	2.6
11	CK	14	VAL	2.6
31	DG	151	ALA	2.6
2	CB	148	TYR	2.6
31	BG	137	GLU	2.6
4	CD	49	ARG	2.6
7	CG	6	ARG	2.6
28	DD	217	ARG	2.6
2	CB	78	GLN	2.6
15	CO	87	ILE	2.6
28	DD	276	LYS	2.6
2	AB	67	THR	2.6
7	CG	85	TYR	2.6
17	CQ	6	LEU	2.6
17	CQ	98	LEU	2.6
46	BZ	148	ASP	2.6
14	CN	40	CYS	2.6
46	DZ	112	ARG	2.6
47	D0	44	ARG	2.6
18	CR	46	GLU	2.6
22	AV	14	A	2.6
19	CS	6	LYS	2.6
47	D0	4	LYS	2.6
3	CC	202	ILE	2.6
10	CJ	53	PRO	2.6
13	AM	98	VAL	2.6
18	CR	43	PHE	2.6
31	DG	88	ILE	2.6
44	DX	49	VAL	2.6
3	CC	149	ALA	2.5
34	DN	57	ALA	2.5
2	CB	115	LEU	2.5
18	CR	47	THR	2.5
8	CH	65	TYR	2.5
1	AA	1030(A)	G	2.5
32	DH	18	GLU	2.5
2	CB	216	SER	2.5
3	CC	200	ALA	2.5
31	DG	85	GLY	2.5
31	DG	27	ASN	2.5
1	CA	1223	C	2.5

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Mol	Chain	Res	Type	RSRZ
9	CI	20	ARG	2.5
23	AW	4	C	2.5
46	BZ	121	HIS	2.5
3	CC	167	TRP	2.5
2	CB	127	ILE	2.5
2	CB	34	ALA	2.5
4	AD	105	VAL	2.5
4	AD	140	VAL	2.5
26	BA	1176	G	2.5
41	DU	73	GLY	2.5
3	CC	30	ARG	2.5
12	CL	56	ALA	2.5
19	CS	50	ALA	2.5
53	D6	52	VAL	2.5
37	DQ	79	LEU	2.5
1	CA	961	U	2.5
1	CA	1251	A	2.5
1	CA	1357	A	2.5
4	AD	150	GLU	2.5
16	AP	39	TYR	2.5
26	DA	2111	C	2.5
26	DA	2129	C	2.5
2	CB	96	ARG	2.5
21	AU	15	ARG	2.5
2	CB	133	LYS	2.5
32	DH	34	GLU	2.5
24	CX	4	G	2.5
6	CF	89	MET	2.5
8	CH	91	ARG	2.5
8	CH	138	TRP	2.5
25	CY	13	C	2.5
26	BA	2142	C	2.5
13	CM	3	ARG	2.5
3	CC	122	GLU	2.5
2	CB	69	LEU	2.5
5	CE	148	VAL	2.5
7	AG	80	VAL	2.5
32	DH	49	VAL	2.5
37	DQ	66	ILE	2.5
46	DZ	148	ASP	2.5
31	DG	62	LEU	2.5
31	DG	73	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
18	AR	25	THR	2.5
16	AP	32	TYR	2.5
7	CG	10	ARG	2.5
9	CI	30	GLY	2.5
3	CC	37	GLN	2.5
2	CB	206	ASP	2.5
4	CD	185	PHE	2.5
7	CG	37	ASN	2.5
3	AC	168	ALA	2.5
5	CE	123	LEU	2.5
11	AK	82	VAL	2.5
11	AK	84	VAL	2.5
16	AP	24	ALA	2.5
16	CP	51	VAL	2.5
17	AQ	36	ILE	2.5
32	DH	121	ILE	2.5
4	CD	89	THR	2.5
46	DZ	151	HIS	2.5
2	CB	150	SER	2.5
7	CG	155	ARG	2.5
11	CK	25	TYR	2.5
11	CK	96	ARG	2.5
25	CY	28	G	2.5
26	BA	2141	G	2.5
32	DH	74	ASN	2.5
4	AD	174	LEU	2.5
7	CG	152	ALA	2.5
10	AJ	23	ILE	2.5
11	CK	114	VAL	2.5
18	AR	40	LEU	2.5
20	CT	59	ALA	2.5
1	CA	1030	C	2.5
9	CI	70	LYS	2.5
1	CA	958	A	2.5
9	CI	117	HIS	2.5
11	AK	57	THR	2.5
31	DG	161	THR	2.5
18	AR	42	ARG	2.5
19	CS	36	ARG	2.5
3	CC	142	MET	2.5
5	AE	10	MET	2.5
29	BE	87	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
15	AO	89	GLY	2.5
42	DV	30	GLY	2.5
48	B1	2	SER	2.5
51	D4	41	PRO	2.5
10	AJ	16	LEU	2.4
46	BZ	155	LEU	2.4
2	AB	77	ALA	2.4
7	CG	42	ILE	2.4
2	CB	53	ARG	2.4
23	CW	6	G	2.4
13	CM	73	GLU	2.4
23	CW	43	C	2.4
8	CH	108	GLY	2.4
1	CA	1041	A	2.4
1	CA	1363(A)	A	2.4
26	DA	2119	A	2.4
31	DG	86	MET	2.4
37	DQ	1	MET	2.4
25	CY	51	U	2.4
7	CG	27	ILE	2.4
8	CH	124	ALA	2.4
9	CI	46	ALA	2.4
16	CP	19	ILE	2.4
17	CQ	44	ALA	2.4
39	DS	51	ALA	2.4
50	D3	9	VAL	2.4
3	AC	154	SER	2.4
17	CQ	12	SER	2.4
37	DQ	62	GLY	2.4
24	CX	70	G	2.4
25	CY	2	C	2.4
21	CU	21	TYR	2.4
3	CC	22	TRP	2.4
9	CI	49	PRO	2.4
10	CJ	11	PHE	2.4
25	CY	21	A	2.4
30	DF	139	PHE	2.4
7	CG	3	ARG	2.4
14	CN	8	GLU	2.4
38	DR	65	LEU	2.4
17	CQ	56	VAL	2.4
51	B4	60	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
2	AB	160	ASP	2.4
2	AB	101	MET	2.4
2	CB	37	ASN	2.4
1	CA	1118	C	2.4
3	AC	203	PHE	2.4
9	AI	111	ARG	2.4
12	CL	48	PRO	2.4
32	DH	71	LEU	2.4
7	CG	13	GLN	2.4
4	CD	184	LYS	2.4
10	CJ	94	VAL	2.4
14	CN	11	LYS	2.4
14	CN	18	VAL	2.4
17	CQ	87	LYS	2.4
56	D9	16	VAL	2.4
2	AB	231	GLU	2.4
9	AI	110	GLU	2.4
11	CK	117	ASN	2.4
15	CO	68	ARG	2.4
45	DY	50	ARG	2.4
2	CB	51	LEU	2.4
4	AD	97	LEU	2.4
4	CD	160	GLN	2.4
8	CH	36	LEU	2.4
11	AK	25	TYR	2.4
5	AE	132	ALA	2.4
3	AC	14	ILE	2.4
3	AC	134	ILE	2.4
4	CD	158	ILE	2.4
19	CS	68	GLY	2.4
8	CH	136	GLU	2.4
10	CJ	58	ASP	2.4
5	CE	14	ARG	2.4
15	AO	88	ARG	2.4
19	CS	81	ARG	2.4
15	AO	69	TYR	2.4
46	DZ	157	LEU	2.4
9	AI	108	VAL	2.4
30	DF	166	ALA	2.4
44	DX	91	ALA	2.4
51	D4	21	VAL	2.4
1	AA	1030	C	2.4

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Mol	Chain	Res	Type	RSRZ
11	AK	126	ARG	2.4
46	DZ	140	ASP	2.4
23	CW	12	U	2.4
1	CA	1287	A	2.4
3	CC	188	LEU	2.4
32	DH	12	PRO	2.4
31	DG	154	GLY	2.4
32	DH	164	TYR	2.4
4	AD	8	VAL	2.4
4	CD	140	VAL	2.4
5	AE	90	VAL	2.4
11	CK	89	ALA	2.4
20	CT	32	ALA	2.4
8	CH	111	ILE	2.4
17	CQ	90	ILE	2.4
30	DF	15	SER	2.4
31	DG	104	GLU	2.4
39	DS	46	VAL	2.4
2	CB	139	LYS	2.4
52	D5	29	THR	2.4
26	BA	2161	C	2.4
32	DH	147	ASN	2.4
7	CG	31	MET	2.3
8	AH	133	LEU	2.3
12	CL	94	PRO	2.3
20	AT	24	LEU	2.3
20	CT	20	LEU	2.3
41	DU	40	PHE	2.3
3	AC	206	GLU	2.3
10	AJ	64	GLU	2.3
16	AP	34	GLU	2.3
3	CC	173	VAL	2.3
9	AI	120	ARG	2.3
17	CQ	73	VAL	2.3
18	CR	84	LYS	2.3
19	AS	81	ARG	2.3
20	CT	41	ILE	2.3
20	CT	26	ASN	2.3
7	CG	14	PRO	2.3
7	CG	132	GLY	2.3
15	CO	57	LEU	2.3
46	DZ	169	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
12	CL	19	ARG	2.3
3	CC	5	ILE	2.3
31	DG	77	ILE	2.3
3	AC	89	GLU	2.3
46	BZ	119	GLU	2.3
32	DH	171	LEU	2.3
5	CE	150	ARG	2.3
3	CC	61	ALA	2.3
4	CD	164	ALA	2.3
7	CG	18	TYR	2.3
11	AK	81	ASP	2.3
35	DO	41	ALA	2.3
19	CS	60	VAL	2.3
37	DQ	102	VAL	2.3
46	DZ	105	VAL	2.3
51	D4	67	TYR	2.3
2	CB	58	ILE	2.3
31	DG	114	ILE	2.3
46	DZ	69	THR	2.3
2	CB	116	GLU	2.3
13	CM	65	LYS	2.3
1	AA	1030(D)	A	2.3
1	CA	1093	A	2.3
14	AN	14	PRO	2.3
14	CN	10	ALA	2.3
31	DG	110	ALA	2.3
3	CC	66	VAL	2.3
5	AE	133	TYR	2.3
26	DA	2142	C	2.3
12	CL	7	ILE	2.3
17	AQ	37	LYS	2.3
34	DN	10	GLU	2.3
14	CN	19	ARG	2.3
32	DH	82	GLY	2.3
16	AP	60	LEU	2.3
9	CI	73	GLN	2.3
46	DZ	154	ASP	2.3
1	CA	983	A	2.3
4	AD	166	LYS	2.3
13	CM	75	ALA	2.3
26	BA	2132	U	2.3
5	CE	105	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
32	DH	24	VAL	2.3
42	DV	72	VAL	2.3
46	DZ	128	VAL	2.3
51	D4	34	GLU	2.3
3	AC	182	ILE	2.3
10	CJ	6	ILE	2.3
37	DQ	110	THR	2.3
3	AC	81	GLY	2.3
26	BA	2143	C	2.3
31	DG	134	GLY	2.3
36	DP	20	GLY	2.3
48	D1	28	GLY	2.3
4	AD	155	LEU	2.3
46	DZ	50	GLN	2.3
2	CB	210	SER	2.3
31	DG	116	ASP	2.3
32	DH	47	GLU	2.3
1	CA	1061	G	2.3
1	CA	1117	G	2.3
13	CM	107	ALA	2.3
37	DQ	136	ALA	2.3
1	CA	4	U	2.3
1	CA	1308	U	2.3
2	CB	32	ILE	2.3
2	CB	209	ARG	2.3
3	CC	59	ARG	2.3
46	BZ	116	VAL	2.3
26	DA	652(B)	A	2.3
26	DA	2310	A	2.3
31	DG	106	LEU	2.3
31	DG	120	LEU	2.3
10	CJ	39	PRO	2.3
19	CS	73	GLU	2.3
2	AB	48	MET	2.3
16	AP	57	ARG	2.3
32	DH	132	ARG	2.3
54	D7	23	ARG	2.3
46	BZ	165	VAL	2.3
3	CC	205	GLY	2.3
6	AF	98	LEU	2.2
15	CO	31	LEU	2.2
25	AY	23	A	2.2

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Mol	Chain	Res	Type	RSRZ
5	CE	84	PHE	2.2
55	D8	2	PRO	2.2
2	CB	111	ARG	2.2
4	AD	50	ARG	2.2
9	CI	16	ARG	2.2
32	DH	73	ALA	2.2
2	AB	66	GLY	2.2
4	AD	69	GLY	2.2
17	AQ	35	VAL	2.2
32	DH	99	VAL	2.2
42	DV	42	GLY	2.2
4	AD	158	ILE	2.2
10	AJ	98	ILE	2.2
12	CL	70	ILE	2.2
12	CL	100	ILE	2.2
34	DN	69	GLN	2.2
8	CH	10	LEU	2.2
1	CA	1343	G	2.2
5	AE	128	PRO	2.2
21	CU	23	PRO	2.2
26	DA	2141	G	2.2
10	AJ	43	ARG	2.2
14	CN	4	LYS	2.2
25	CY	58	A	2.2
11	AK	60	ALA	2.2
21	AU	11	GLY	2.2
2	CB	97	TRP	2.2
18	AR	37	VAL	2.2
32	DH	52	VAL	2.2
8	CH	35	ILE	2.2
39	DS	39	ILE	2.2
1	CA	1040	U	2.2
3	AC	196	LEU	2.2
20	AT	72	LEU	2.2
34	DN	91	LEU	2.2
3	CC	186	PHE	2.2
19	CS	4	SER	2.2
31	DG	51	ARG	2.2
32	DH	29	PRO	2.2
50	D3	35	ARG	2.2
1	CA	1190	G	2.2
3	CC	129	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
39	DS	104	GLY	2.2
37	BQ	112	GLU	2.2
39	DS	111	GLU	2.2
44	DX	42	ALA	2.2
51	D4	30	GLU	2.2
1	CA	1397	C	2.2
13	CM	17	VAL	2.2
14	AN	56	VAL	2.2
26	DA	2164	C	2.2
32	DH	17	VAL	2.2
43	DW	17	VAL	2.2
10	CJ	87	THR	2.2
36	DP	79	ARG	2.2
48	D1	26	ARG	2.2
2	CB	55	PHE	2.2
23	CW	50	U	2.2
26	DA	958	U	2.2
39	DS	29	PHE	2.2
4	CD	34	GLU	2.2
12	CL	30	ALA	2.2
10	AJ	49	VAL	2.2
26	DA	2123	G	2.2
26	DA	2166	G	2.2
29	DE	196	VAL	2.2
36	DP	18	ARG	2.2
2	CB	43	ASP	2.2
1	AA	1001	A	2.2
1	CA	962	C	2.2
7	CG	151	TYR	2.2
10	AJ	71	LEU	2.2
12	CL	93	LEU	2.2
33	BI	75	LEU	2.2
4	CD	110	PHE	2.2
51	D4	53	GLU	2.2
12	CL	14	GLY	2.2
12	CL	95	GLY	2.2
8	CH	116	LYS	2.2
28	DD	18	VAL	2.2
31	DG	159	VAL	2.2
37	DQ	3	MET	2.2
8	CH	24	THR	2.2
13	CM	105	THR	2.2

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Mol	Chain	Res	Type	RSRZ
18	CR	66	LEU	2.2
36	DP	123	LEU	2.2
46	DZ	102	LEU	2.2
46	DZ	133	ILE	2.2
1	AA	1034	G	2.2
3	CC	20	SER	2.2
3	CC	201	TYR	2.2
4	AD	116	GLN	2.2
37	DQ	105	GLU	2.2
1	CA	1320	C	2.2
4	AD	23	GLY	2.2
26	DA	889	C	2.2
26	DA	6	A	2.2
19	CS	57	HIS	2.2
25	CY	33	U	2.2
28	DD	275	LYS	2.2
19	CS	78	ARG	2.2
44	DX	60	ARG	2.2
2	CB	67	THR	2.2
3	CC	56	ASP	2.2
28	BD	142	VAL	2.2
41	DU	90	VAL	2.2
46	BZ	170	THR	2.2
51	D4	27	THR	2.2
17	CQ	24	GLU	2.2
31	DG	144	ILE	2.2
32	DH	119	GLU	2.2
37	DQ	125	LEU	2.2
46	BZ	102	LEU	2.2
21	AU	2	GLY	2.2
39	DS	91	PRO	2.2
13	CM	106	ASN	2.2
34	DN	84	LYS	2.2
26	DA	2148	G	2.2
56	D9	9	ARG	2.2
32	DH	75	ALA	2.2
3	CC	58	GLU	2.2
7	CG	105	VAL	2.2
16	AP	68	ASP	2.2
37	BQ	97	VAL	2.2
2	CB	98	LEU	2.1
3	CC	33	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
3	CC	57	ILE	2.1
5	AE	12	LEU	2.1
5	CE	13	ILE	2.1
9	CI	31	GLN	2.1
16	AP	6	LEU	2.1
5	CE	9	LYS	2.1
32	DH	110	SER	2.1
14	CN	16	PHE	2.1
32	DH	109	PHE	2.1
45	DY	43	ASN	2.1
51	B4	54	GLY	2.1
2	CB	85	ALA	2.1
2	CB	123	ALA	2.1
4	CD	48	ALA	2.1
1	CA	1354	C	2.1
1	AA	1026	G	2.1
7	CG	15	ASP	2.1
4	CD	121	VAL	2.1
8	CH	53	VAL	2.1
9	CI	87	GLN	2.1
23	CW	33	U	2.1
26	DA	2897	U	2.1
17	CQ	100	LYS	2.1
23	CW	65	G	2.1
26	DA	2100	G	2.1
26	DA	2319	G	2.1
13	CM	70	LEU	2.1
39	DS	24	LEU	2.1
46	DZ	42	VAL	2.1
2	AB	80	ILE	2.1
3	CC	185	GLY	2.1
7	CG	34	GLY	2.1
12	AL	29	GLY	2.1
39	DS	60	GLY	2.1
2	CB	183	PRO	2.1
17	AQ	95	TYR	2.1
48	D1	71	TYR	2.1
7	CG	117	ALA	2.1
8	CH	4	ASP	2.1
30	DF	80	ALA	2.1
2	AB	136	VAL	2.1
4	CD	101	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
5	AE	55	VAL	2.1
11	AK	63	LEU	2.1
11	CK	87	THR	2.1
25	AY	47	U	2.1
25	CY	60	U	2.1
26	DA	2113	U	2.1
32	DH	88	LEU	2.1
25	CY	56	C	2.1
32	DH	129	THR	2.1
3	CC	152	ILE	2.1
41	DU	17	ILE	2.1
46	BZ	147	GLY	2.1
6	CF	73	ASN	2.1
7	CG	149	ARG	2.1
13	CM	113	PRO	2.1
21	CU	22	ARG	2.1
46	BZ	122	ARG	2.1
1	CA	969	A	2.1
23	CW	7	A	2.1
26	DA	2135	A	2.1
16	AP	29	ASP	2.1
5	CE	82	VAL	2.1
8	CH	63	LEU	2.1
8	CH	119	LEU	2.1
15	CO	60	VAL	2.1
16	AP	20	VAL	2.1
17	CQ	7	THR	2.1
5	AE	129	ILE	2.1
11	CK	108	ILE	2.1
25	CY	66	U	2.1
54	D7	1	MET	2.1
30	DF	81	PRO	2.1
34	DN	11	PRO	2.1
32	DH	25	LYS	2.1
2	CB	19	HIS	2.1
23	CW	63	G	2.1
10	CJ	17	ASP	2.1
4	AD	111	ALA	2.1
19	CS	24	ALA	2.1
26	DA	2114	A	2.1
26	DA	2170	A	2.1
11	CK	90	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
13	CM	71	ARG	2.1
18	CR	42	ARG	2.1
20	AT	13	LEU	2.1
51	D4	58	ARG	2.1
13	CM	63	THR	2.1
32	DH	122	THR	2.1
39	DS	14	VAL	2.1
28	DD	204	ILE	2.1
36	DP	144	GLU	2.1
8	CH	31	PHE	2.1
30	BF	34	TRP	2.1
1	AA	1027	C	2.1
4	CD	68	TYR	2.1
17	CQ	32	TYR	2.1
32	DH	157	TYR	2.1
8	CH	84	ARG	2.1
10	AJ	60	ARG	2.1
46	DZ	21	ALA	2.1
2	AB	75	LYS	2.1
10	CJ	93	GLY	2.1
15	CO	56	LEU	2.1
16	AP	37	GLY	2.1
17	CQ	86	GLU	2.1
34	DN	26	LEU	2.1
37	DQ	91	GLU	2.1
45	DY	64	GLU	2.1
50	D3	23	LEU	2.1
1	CA	1188	A	2.1
2	AB	73	THR	2.1
24	AX	72	A	2.1
13	CM	84	ILE	2.1
29	BE	1	MET	2.1
9	AI	116	LYS	2.1
18	CR	34	TYR	2.1
28	DD	38	LYS	2.1
12	CL	26	ALA	2.1
40	DT	126	ALA	2.1
46	DZ	145	GLU	2.1
9	CI	47	LEU	2.1
9	CI	56	LEU	2.1
5	CE	100	VAL	2.1
11	CK	109	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
31	DG	109	VAL	2.1
5	AE	131	ILE	2.1
31	DG	155	MET	2.1
46	BZ	124	ILE	2.1
49	D2	1	MET	2.1
24	CX	72	A	2.1
26	BA	1175	U	2.1
4	AD	15	GLU	2.1
3	AC	184	TYR	2.1
2	CB	218	ALA	2.1
10	CJ	20	ALA	2.1
11	AK	68	ALA	2.1
29	BE	28	ALA	2.1
37	DQ	36	ALA	2.1
2	AB	213	LEU	2.0
28	DD	37	LEU	2.0
39	DS	110	LEU	2.0
46	DZ	70	LEU	2.0
6	AF	57	GLN	2.0
9	AI	28	VAL	2.0
12	CL	96	VAL	2.0
16	AP	53	VAL	2.0
50	D3	6	VAL	2.0
2	CB	181	PHE	2.0
5	AE	118	ILE	2.0
37	DQ	22	LYS	2.0
37	DQ	58	PHE	2.0
10	AJ	5	ARG	2.0
37	DQ	59	ARG	2.0
37	DQ	60	ARG	2.0
1	CA	959	A	2.0
26	BA	548	A	2.0
11	AK	61	ALA	2.0
2	CB	95	GLN	2.0
5	CE	142	LEU	2.0
8	AH	112	LEU	2.0
10	AJ	59	SER	2.0
17	CQ	95	TYR	2.0
39	BS	37	ALA	2.0
39	DS	92	TYR	2.0
44	BX	34	ALA	2.0
45	DY	48	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1113	C	2.0
1	CA	1249	C	2.0
3	CC	7	PRO	2.0
9	AI	98	PRO	2.0
3	AC	19	GLU	2.0
5	CE	107	ARG	2.0
23	AW	74	C	2.0
26	DA	897	C	2.0
51	B4	49	PHE	2.0
31	BG	35	GLU	2.0
39	DS	41	ASP	2.0
30	DF	147	GLY	2.0
3	CC	117	ALA	2.0
3	CC	154	SER	2.0
5	AE	88	LYS	2.0
5	CE	31	LEU	2.0
6	AF	61	LEU	2.0
18	AR	73	ALA	2.0
25	CY	19	G	2.0
22	AV	15	A	2.0
3	CC	82	GLU	2.0
3	CC	153	VAL	2.0
4	CD	122	ARG	2.0
9	AI	65	VAL	2.0
12	CL	15	ARG	2.0
13	CM	91	ARG	2.0
37	BQ	78	PRO	2.0
56	D9	12	ASP	2.0
19	CS	8	GLY	2.0
43	DW	26	GLY	2.0
37	DQ	113	GLN	2.0
9	CI	55	ALA	2.0
16	AP	28	ARG	2.0
45	DY	62	GLU	2.0
3	CC	130	VAL	2.0
48	D1	51	VAL	2.0
1	AA	347	G	2.0
26	DA	1042	G	2.0
31	DG	68	PRO	2.0
31	DG	97	ASP	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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	PSU	AW	32	20/21	0.86	0.26	-	77,84,98,106	0
23	MIA	AW	37	29/30	0.93	0.25	-	56,65,80,82	0
23	MIA	CW	37	22/30	0.87	0.30	-	72,86,92,96	0
24	31H	AX	76	32/33	0.94	0.33	-	31,57,76,77	10
23	7MG	AW	46	24/25	0.80	0.21	-	80,97,112,135	0
25	7MG	AY	46	24/25	0.82	0.18	-	80,99,107,116	0
24	4SU	CX	8	20/21	0.80	0.13	-	84,92,105,111	0
25	PSU	CY	32	20/21	0.83	0.26	-	77,91,109,114	0
23	PSU	CW	32	20/21	0.87	0.48	-	77,86,95,106	0
23	PSU	AW	55	20/21	0.83	0.28	-	76,88,103,105	0
25	PSU	CY	55	20/21	0.75	0.41	-	86,100,107,118	0
25	PSU	AY	55	20/21	0.80	0.20	-	85,96,106,117	0
23	5MU	AW	54	21/22	0.91	0.21	-	66,80,87,93	0
24	5MC	AX	32	21/22	0.97	0.20	-	50,57,69,76	0
23	4SU	AW	8	20/21	0.84	0.17	-	83,89,107,110	0
23	PSU	AW	39	20/21	0.93	0.24	-	71,82,92,93	0
25	MIA	AY	37	22/30	0.86	0.22	-	79,89,101,116	0
24	5MU	CX	54	21/22	0.94	0.21	-	71,85,94,104	0
24	5MC	CX	32	21/22	0.95	0.18	-	63,77,85,87	0
23	F3N	CW	76	33/34	0.93	0.44	-	53,69,79,80	0
25	PSU	AY	32	20/21	0.83	0.26	-	76,92,107,110	0
24	PSU	CX	55	20/21	0.92	0.15	-	81,87,92,97	0
23	5MU	CW	54	21/22	0.86	0.23	-	76,87,97,99	0
23	PSU	CW	55	20/21	0.84	0.34	-	76,90,103,106	0
25	4SU	CY	8	20/21	0.79	0.16	-	88,102,112,128	0
23	F3N	AW	76	33/34	0.94	0.38	-	44,58,72,77	0
24	PSU	AX	55	20/21	0.94	0.16	-	52,69,77,77	0
25	4SU	AY	8	20/21	0.83	0.13	-	83,95,104,129	0
25	5MU	CY	54	21/22	0.74	0.49	-	89,99,105,136	0
23	4SU	CW	8	20/21	0.77	0.29	-	85,96,117,121	0
25	PSU	CY	39	20/21	0.81	0.27	-	86,91,104,110	0
25	MIA	CY	37	22/30	0.79	0.30	-	79,95,102,124	0
25	5MU	AY	54	21/22	0.85	0.20	-	81,89,99,128	0
24	4SU	AX	8	20/21	0.93	0.17	-	59,69,79,85	0
23	7MG	CW	46	24/25	0.73	0.33	-	81,97,101,125	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
25	7MG	CY	46	24/25	0.71	0.25	-	87,101,108,135	0
23	PSU	CW	39	20/21	0.89	0.42	-	76,85,92,95	0
24	5MU	AX	54	21/22	0.96	0.16	-	46,72,77,86	0
25	PSU	AY	39	20/21	0.86	0.25	-	84,90,102,107	0
24	31H	CX	76	32/33	0.90	0.35	-	48,68,88,99	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3770	1/1	0.97	0.44	27.31	49,49,49,49	0
57	MG	BA	3710	1/1	0.66	0.79	26.21	65,65,65,65	0
57	MG	BA	3174	1/1	0.97	0.53	25.24	38,38,38,38	0
57	MG	BA	3135	1/1	0.94	0.45	23.76	56,56,56,56	0
57	MG	BA	3214	1/1	0.96	0.50	23.57	43,43,43,43	0
57	MG	DA	3027	1/1	0.97	0.53	23.22	43,43,43,43	0
57	MG	BA	3219	1/1	0.92	0.50	19.46	58,58,58,58	0
57	MG	DA	3029	1/1	0.96	0.57	18.76	45,45,45,45	0
57	MG	BA	3033	1/1	0.97	0.40	16.53	31,31,31,31	0
57	MG	BA	3136	1/1	0.97	0.36	15.91	49,49,49,49	0
57	MG	BA	3215	1/1	0.96	0.42	14.79	37,37,37,37	0
57	MG	CA	3130	1/1	0.74	0.28	14.39	64,64,64,64	0
57	MG	BA	3103	1/1	0.85	0.35	13.36	63,63,63,63	0
57	MG	BA	3591	1/1	0.98	0.39	13.31	41,41,41,41	0
57	MG	BA	3204	1/1	0.96	0.27	12.92	67,67,67,67	0
57	MG	BA	3111	1/1	0.83	0.32	12.80	53,53,53,53	0
57	MG	BA	3018	1/1	0.86	0.40	12.66	39,39,39,39	0
57	MG	BA	3456	1/1	0.86	0.30	12.30	37,37,37,37	0
57	MG	BA	3775	1/1	0.93	0.33	12.06	39,39,39,39	0
57	MG	BA	3743	1/1	0.94	0.59	11.52	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3602	1/1	0.94	0.26	11.41	62,62,62,62	0
57	MG	DA	3102	1/1	0.95	0.32	10.88	40,40,40,40	0
57	MG	BA	3182	1/1	0.98	0.67	10.80	52,52,52,52	0
57	MG	BA	3256	1/1	0.97	0.34	10.60	34,34,34,34	0
57	MG	DA	3026	1/1	0.93	0.72	10.57	50,50,50,50	0
57	MG	DA	3500	1/1	0.87	0.35	10.41	55,55,55,55	0
57	MG	AX	3002	1/1	0.94	0.30	10.37	71,71,71,71	0
57	MG	BA	3044	1/1	0.94	0.35	10.11	43,43,43,43	0
57	MG	BA	3083	1/1	0.97	0.34	10.02	60,60,60,60	0
57	MG	BA	3171	1/1	0.90	0.32	9.99	35,35,35,35	0
57	MG	BA	3142	1/1	0.96	0.31	9.64	46,46,46,46	0
57	MG	BX	3001	1/1	0.91	0.35	9.48	44,44,44,44	0
57	MG	DU	201	1/1	0.88	0.57	9.39	58,58,58,58	0
57	MG	BA	3070	1/1	0.94	0.24	9.36	41,41,41,41	0
57	MG	BA	3100	1/1	0.94	0.25	9.27	61,61,61,61	0
57	MG	DA	3192	1/1	0.87	0.32	9.26	34,34,34,34	0
57	MG	DE	3001	1/1	0.98	0.44	9.21	31,31,31,31	0
57	MG	BF	306	1/1	0.91	0.33	8.90	49,49,49,49	0
57	MG	BA	3061	1/1	0.95	0.30	8.78	25,25,25,25	0
57	MG	BD	3003	1/1	0.91	0.30	8.72	37,37,37,37	0
57	MG	BV	201	1/1	0.94	0.36	8.67	31,31,31,31	0
57	MG	BA	3424	1/1	0.97	0.29	8.49	31,31,31,31	0
57	MG	DA	3042	1/1	0.87	0.29	8.28	49,49,49,49	0
57	MG	AA	1756	1/1	0.90	0.33	8.24	45,45,45,45	0
57	MG	DA	3624	1/1	0.75	0.48	8.23	59,59,59,59	0
57	MG	DV	201	1/1	0.88	0.50	8.23	58,58,58,58	0
57	MG	BA	3035	1/1	0.96	0.27	8.05	49,49,49,49	0
57	MG	DA	3660	1/1	0.94	0.52	7.98	46,46,46,46	0
57	MG	BA	3041	1/1	0.71	0.29	7.83	63,63,63,63	0
57	MG	BA	3561	1/1	0.87	0.26	7.57	34,34,34,34	0
57	MG	CA	3167	1/1	0.97	0.30	7.56	57,57,57,57	0
57	MG	BA	3688	1/1	0.72	0.27	7.44	61,61,61,61	0
57	MG	DF	305	1/1	0.93	0.59	7.17	45,45,45,45	0
57	MG	AA	1702	1/1	0.98	0.27	7.07	47,47,47,47	0
57	MG	DA	3464	1/1	0.93	0.30	6.86	54,54,54,54	0
57	MG	DA	3621	1/1	0.94	0.49	6.55	52,52,52,52	0
57	MG	BA	3674	1/1	0.97	0.34	6.50	48,48,48,48	0
57	MG	BA	3369	1/1	0.78	0.28	6.38	62,62,62,62	0
57	MG	BA	3680	1/1	0.73	0.32	6.32	42,42,42,42	0
57	MG	BA	3608	1/1	0.83	0.29	6.28	58,58,58,58	0
57	MG	AX	3003	1/1	0.86	0.23	5.98	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3422	1/1	0.89	0.24	5.91	62,62,62,62	0
57	MG	BA	3124	1/1	0.92	0.28	5.90	57,57,57,57	0
57	MG	DA	3617	1/1	0.86	0.25	5.89	51,51,51,51	0
57	MG	DB	3008	1/1	0.95	0.17	5.88	56,56,56,56	0
57	MG	DA	3169	1/1	0.97	0.28	5.81	41,41,41,41	0
57	MG	BA	3216	1/1	0.96	0.28	5.69	39,39,39,39	0
57	MG	AA	1757	1/1	0.95	0.25	5.60	68,68,68,68	0
57	MG	DQ	3003	1/1	0.73	0.64	5.55	62,62,62,62	0
57	MG	DA	3160	1/1	0.91	0.34	5.31	62,62,62,62	0
57	MG	CA	3067	1/1	0.98	0.24	5.29	46,46,46,46	0
57	MG	BA	3176	1/1	0.74	0.26	5.09	55,55,55,55	0
57	MG	BA	3814	1/1	0.91	0.28	5.07	39,39,39,39	0
57	MG	BF	304	1/1	0.96	0.39	5.06	41,41,41,41	0
57	MG	DA	3456	1/1	0.84	0.21	5.05	38,38,38,38	0
57	MG	DA	3119	1/1	0.92	0.26	4.99	50,50,50,50	0
57	MG	BA	3507	1/1	0.91	0.26	4.90	43,43,43,43	0
57	MG	BF	302	1/1	0.94	0.31	4.88	30,30,30,30	0
57	MG	BU	201	1/1	0.94	0.36	4.81	43,43,43,43	0
57	MG	DA	3220	1/1	0.94	0.32	4.79	50,50,50,50	0
57	MG	DA	3491	1/1	0.85	0.25	4.78	43,43,43,43	0
57	MG	DA	3060	1/1	0.94	0.28	4.65	60,60,60,60	0
57	MG	BU	204	1/1	0.98	0.31	4.59	47,47,47,47	0
57	MG	DF	301	1/1	0.92	0.31	4.59	48,48,48,48	0
57	MG	BA	3672	1/1	0.92	0.25	4.46	44,44,44,44	0
57	MG	BA	3085	1/1	0.99	0.29	4.45	31,31,31,31	0
57	MG	BA	3403	1/1	0.93	0.29	4.43	33,33,33,33	0
57	MG	BA	3186	1/1	0.97	0.27	4.12	41,41,41,41	0
57	MG	AA	1675	1/1	0.93	0.24	4.08	61,61,61,61	0
57	MG	BU	203	1/1	0.97	0.31	3.63	34,34,34,34	0
57	MG	BA	3121	1/1	0.75	0.29	3.57	42,42,42,42	0
57	MG	BD	3007	1/1	0.95	0.30	3.48	46,46,46,46	0
57	MG	AA	1687	1/1	0.91	0.21	3.47	46,46,46,46	0
57	MG	DA	3070	1/1	0.59	0.19	3.47	65,65,65,65	0
57	MG	BA	3526	1/1	0.90	0.26	3.29	41,41,41,41	0
59	ZN	B6	102	1/1	0.99	0.26	3.29	50,50,50,50	0
57	MG	DA	3657	1/1	0.79	0.45	3.26	54,54,54,54	0
57	MG	BA	3520	1/1	0.95	0.25	3.18	29,29,29,29	0
57	MG	DA	3503	1/1	0.96	0.22	2.98	38,38,38,38	0
57	MG	BA	3530	1/1	0.86	0.25	2.91	33,33,33,33	0
57	MG	DA	3103	1/1	0.98	0.22	2.90	56,56,56,56	0
57	MG	DA	3323	1/1	0.97	0.21	2.89	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3210	1/1	0.94	0.25	2.84	41,41,41,41	0
57	MG	BA	3700	1/1	0.80	0.24	2.80	36,36,36,36	0
57	MG	BA	3716	1/1	0.95	0.25	2.79	45,45,45,45	0
57	MG	BD	3008	1/1	0.98	0.30	2.74	45,45,45,45	0
57	MG	BA	3543	1/1	0.93	0.23	2.69	52,52,52,52	0
57	MG	DA	3325	1/1	0.95	0.23	2.69	45,45,45,45	0
57	MG	DA	3362	1/1	0.92	0.24	2.68	42,42,42,42	0
57	MG	BF	303	1/1	0.96	0.26	2.66	33,33,33,33	0
57	MG	CA	3168	1/1	0.95	0.20	2.66	41,41,41,41	0
57	MG	BA	3425	1/1	0.98	0.25	2.60	48,48,48,48	0
57	MG	AA	1730	1/1	0.98	0.25	2.59	27,27,27,27	0
57	MG	BA	3007	1/1	0.97	0.23	2.55	21,21,21,21	0
57	MG	DA	3191	1/1	0.79	0.30	2.52	54,54,54,54	0
57	MG	BA	3310	1/1	0.98	0.23	2.51	26,26,26,26	0
57	MG	BA	3648	1/1	0.96	0.22	2.49	58,58,58,58	0
57	MG	DA	3274	1/1	0.98	0.22	2.36	40,40,40,40	0
57	MG	BA	3529	1/1	0.89	0.25	2.32	24,24,24,24	0
57	MG	BA	3244	1/1	0.95	0.26	2.30	31,31,31,31	0
57	MG	BA	3037	1/1	0.95	0.28	2.29	42,42,42,42	0
57	MG	BA	3200	1/1	0.83	0.25	2.24	48,48,48,48	0
57	MG	AA	1725	1/1	0.96	0.22	2.24	51,51,51,51	0
57	MG	DA	3161	1/1	0.86	0.17	2.19	50,50,50,50	0
57	MG	BA	3807	1/1	0.82	0.24	2.19	66,66,66,66	0
57	MG	BA	3400	1/1	0.92	0.24	2.15	39,39,39,39	0
57	MG	BA	3795	1/1	0.96	0.25	2.10	19,19,19,19	0
57	MG	DA	3105	1/1	0.93	0.22	2.08	45,45,45,45	0
57	MG	DA	3090	1/1	0.92	0.31	2.03	50,50,50,50	0
57	MG	DA	3606	1/1	0.83	0.20	2.00	74,74,74,74	0
57	MG	DA	3213	1/1	0.97	0.18	1.97	37,37,37,37	0
57	MG	AA	1691	1/1	0.92	0.27	1.93	62,62,62,62	0
57	MG	BA	3172	1/1	0.96	0.26	1.90	40,40,40,40	0
57	MG	B7	103	1/1	0.91	0.30	1.89	40,40,40,40	0
57	MG	DA	3124	1/1	0.95	0.17	1.88	43,43,43,43	0
57	MG	DA	3167	1/1	0.94	0.21	1.88	40,40,40,40	0
57	MG	CA	3093	1/1	0.95	0.20	1.86	55,55,55,55	0
57	MG	DA	3089	1/1	0.80	0.18	1.85	52,52,52,52	0
57	MG	BA	3356	1/1	0.97	0.24	1.82	31,31,31,31	0
57	MG	B5	101	1/1	0.99	0.28	1.82	30,30,30,30	0
57	MG	CA	3050	1/1	0.82	0.19	1.80	73,73,73,73	0
57	MG	BA	3194	1/1	0.89	0.25	1.76	39,39,39,39	0
57	MG	DA	3134	1/1	0.94	0.21	1.72	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3334	1/1	0.97	0.22	1.70	57,57,57,57	0
57	MG	BA	3133	1/1	0.97	0.27	1.68	37,37,37,37	0
57	MG	DA	3247	1/1	0.94	0.16	1.66	49,49,49,49	0
57	MG	BA	3179	1/1	0.93	0.23	1.66	43,43,43,43	0
57	MG	BV	202	1/1	0.95	0.25	1.64	32,32,32,32	0
57	MG	DA	3410	1/1	0.95	0.22	1.63	40,40,40,40	0
57	MG	BA	3409	1/1	0.96	0.23	1.51	22,22,22,22	0
57	MG	BA	3226	1/1	0.96	0.22	1.50	25,25,25,25	0
57	MG	DA	3003	1/1	0.95	0.23	1.47	36,36,36,36	0
57	MG	CA	3037	1/1	0.94	0.21	1.39	53,53,53,53	0
57	MG	DA	3156	1/1	0.92	0.16	1.35	52,52,52,52	0
57	MG	BA	3798	1/1	0.93	0.24	1.30	22,22,22,22	0
57	MG	AA	1685	1/1	0.96	0.21	1.26	62,62,62,62	0
57	MG	BA	3152	1/1	0.95	0.26	1.25	23,23,23,23	0
57	MG	DA	3223	1/1	0.94	0.19	1.21	39,39,39,39	0
57	MG	BA	3277	1/1	0.95	0.43	1.20	52,52,52,52	0
57	MG	DA	3190	1/1	0.87	0.19	1.17	63,63,63,63	0
57	MG	AA	1615	1/1	0.95	0.21	1.16	51,51,51,51	0
57	MG	DA	3463	1/1	0.60	0.19	1.15	44,44,44,44	0
57	MG	BQ	3001	1/1	0.97	0.26	1.12	37,37,37,37	0
57	MG	DA	3656	1/1	0.95	0.25	1.11	41,41,41,41	0
57	MG	BA	3713	1/1	0.80	0.28	1.10	33,33,33,33	0
57	MG	BA	3373	1/1	0.94	0.22	1.07	34,34,34,34	0
57	MG	AA	1753	1/1	0.91	0.20	1.05	55,55,55,55	0
57	MG	BA	3177	1/1	0.93	0.23	1.05	46,46,46,46	0
57	MG	B9	502	1/1	0.96	0.34	1.05	46,46,46,46	0
57	MG	BA	3802	1/1	0.91	0.23	1.03	46,46,46,46	0
57	MG	BA	3576	1/1	0.97	0.24	0.96	30,30,30,30	0
57	MG	BA	3506	1/1	0.88	0.22	0.89	61,61,61,61	0
57	MG	DA	3662	1/1	0.92	0.22	0.85	50,50,50,50	0
57	MG	BA	3038	1/1	0.94	0.23	0.85	20,20,20,20	0
57	MG	DA	3264	1/1	0.97	0.18	0.80	51,51,51,51	0
57	MG	DA	3316	1/1	0.97	0.19	0.77	57,57,57,57	0
57	MG	DA	3549	1/1	0.82	0.20	0.77	49,49,49,49	0
57	MG	CA	3071	1/1	0.93	0.19	0.75	56,56,56,56	0
59	ZN	B5	103	1/1	0.99	0.21	0.73	40,40,40,40	0
57	MG	BA	3048	1/1	0.94	0.22	0.71	29,29,29,29	0
57	MG	BA	3567	1/1	0.95	0.25	0.68	32,32,32,32	0
57	MG	CA	3020	1/1	0.88	0.20	0.62	45,45,45,45	0
57	MG	DA	3194	1/1	0.88	0.16	0.60	48,48,48,48	0
57	MG	BA	3432	1/1	0.93	0.22	0.57	32,32,32,32	0
57	MG	DA	3441	1/1	0.93	0.20	0.57	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3034	1/1	0.96	0.23	0.53	35,35,35,35	0
59	ZN	D5	501	1/1	0.99	0.19	0.53	57,57,57,57	0
57	MG	DA	3232	1/1	0.89	0.19	0.53	56,56,56,56	0
57	MG	DA	3443	1/1	0.95	0.19	0.50	51,51,51,51	0
57	MG	BD	3005	1/1	0.97	0.24	0.49	44,44,44,44	0
57	MG	BA	3239	1/1	0.87	0.22	0.48	47,47,47,47	0
57	MG	BA	3187	1/1	0.94	0.22	0.44	38,38,38,38	0
57	MG	BA	3051	1/1	0.92	0.23	0.44	37,37,37,37	0
57	MG	BA	3441	1/1	0.87	0.20	0.43	39,39,39,39	0
57	MG	DA	3654	1/1	0.97	0.19	0.40	35,35,35,35	0
57	MG	BA	3308	1/1	0.96	0.23	0.38	39,39,39,39	0
57	MG	AA	1693	1/1	0.89	0.20	0.36	76,76,76,76	0
57	MG	BD	3002	1/1	0.98	0.21	0.36	28,28,28,28	0
57	MG	CA	3057	1/1	0.95	0.14	0.34	84,84,84,84	0
57	MG	DW	3001	1/1	0.96	0.21	0.33	41,41,41,41	0
57	MG	BA	3622	1/1	0.89	0.21	0.32	43,43,43,43	0
57	MG	D3	3001	1/1	0.94	0.27	0.31	63,63,63,63	0
57	MG	BA	3251	1/1	0.95	0.25	0.27	43,43,43,43	0
57	MG	DA	3023	1/1	0.87	0.14	0.25	58,58,58,58	0
57	MG	DA	3616	1/1	0.94	0.20	0.20	63,63,63,63	0
57	MG	DA	3014	1/1	0.97	0.22	0.11	44,44,44,44	0
57	MG	DA	3542	1/1	0.79	0.17	0.11	60,60,60,60	0
57	MG	AA	1613	1/1	0.84	0.18	0.08	75,75,75,75	0
57	MG	DA	3068	1/1	0.89	0.19	0.07	53,53,53,53	0
57	MG	DA	3215	1/1	0.96	0.18	0.05	40,40,40,40	0
57	MG	DA	3557	1/1	0.91	0.19	0.04	57,57,57,57	0
57	MG	CA	3096	1/1	0.97	0.18	0.03	43,43,43,43	0
57	MG	AA	1813	1/1	0.96	0.21	-0.00	38,38,38,38	0
57	MG	DA	3219	1/1	0.89	0.16	0.00	50,50,50,50	0
57	MG	CA	3061	1/1	0.80	0.21	-0.02	66,66,66,66	0
57	MG	BD	3010	1/1	0.97	0.20	-0.05	46,46,46,46	0
57	MG	DA	3178	1/1	0.98	0.17	-0.06	40,40,40,40	0
57	MG	AA	1806	1/1	0.94	0.18	-0.06	74,74,74,74	0
57	MG	BA	3793	1/1	0.98	0.22	-0.13	11,11,11,11	0
57	MG	BA	3485	1/1	0.85	0.24	-0.15	26,26,26,26	0
57	MG	AA	1672	1/1	0.99	0.17	-0.16	45,45,45,45	0
57	MG	BA	3343	1/1	0.82	0.18	-0.18	54,54,54,54	0
57	MG	CA	3046	1/1	0.94	0.18	-0.18	61,61,61,61	0
59	ZN	D6	501	1/1	0.97	0.18	-0.21	65,65,65,65	0
59	ZN	B9	501	1/1	1.00	0.23	-0.24	49,49,49,49	0
57	MG	CA	3086	1/1	0.48	0.13	-0.25	93,93,93,93	0
57	MG	BD	3004	1/1	0.97	0.20	-0.27	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3811	1/1	0.98	0.21	-0.30	48,48,48,48	0
57	MG	DA	3579	1/1	0.93	0.16	-0.30	62,62,62,62	0
57	MG	BA	3221	1/1	0.97	0.21	-0.32	29,29,29,29	0
57	MG	BA	3054	1/1	0.97	0.22	-0.33	30,30,30,30	0
57	MG	BA	3614	1/1	0.86	0.17	-0.33	53,53,53,53	0
57	MG	BA	3708	1/1	0.95	0.21	-0.35	33,33,33,33	0
57	MG	DA	3453	1/1	0.98	0.17	-0.36	54,54,54,54	0
57	MG	DB	3004	1/1	0.94	0.21	-0.36	63,63,63,63	0
57	MG	CE	202	1/1	0.26	0.19	-0.36	95,95,95,95	0
57	MG	BA	3184	1/1	0.97	0.22	-0.37	42,42,42,42	0
57	MG	BA	3686	1/1	0.93	0.19	-0.37	27,27,27,27	0
57	MG	CA	3044	1/1	0.99	0.16	-0.38	47,47,47,47	0
57	MG	BA	3280	1/1	0.94	0.21	-0.39	25,25,25,25	0
57	MG	BA	3139	1/1	0.88	0.22	-0.40	44,44,44,44	0
59	ZN	BY	501	1/1	0.95	0.18	-0.43	68,68,68,68	0
57	MG	CA	3032	1/1	0.77	0.16	-0.43	53,53,53,53	0
57	MG	DA	3465	1/1	0.94	0.17	-0.44	42,42,42,42	0
57	MG	DA	3425	1/1	0.92	0.16	-0.44	51,51,51,51	0
57	MG	DA	3072	1/1	0.90	0.17	-0.46	47,47,47,47	0
57	MG	DA	3005	1/1	0.97	0.16	-0.49	54,54,54,54	0
57	MG	BA	3314	1/1	0.92	0.18	-0.55	39,39,39,39	0
57	MG	BA	3235	1/1	0.83	0.20	-0.57	44,44,44,44	0
57	MG	DA	3637	1/1	0.85	0.14	-0.57	72,72,72,72	0
57	MG	BV	203	1/1	0.97	0.21	-0.58	23,23,23,23	0
57	MG	D8	5001	1/1	0.85	0.22	-0.61	44,44,44,44	0
57	MG	AA	1692	1/1	0.92	0.15	-0.61	65,65,65,65	0
57	MG	CT	3001	1/1	0.92	0.17	-0.64	60,60,60,60	0
57	MG	AA	1749	1/1	0.94	0.19	-0.64	50,50,50,50	0
57	MG	DA	3106	1/1	0.87	0.14	-0.65	50,50,50,50	0
57	MG	BA	3299	1/1	0.89	0.21	-0.66	60,60,60,60	0
57	MG	BA	3518	1/1	0.90	0.20	-0.69	46,46,46,46	0
57	MG	DA	3653	1/1	0.86	0.17	-0.69	33,33,33,33	0
57	MG	AA	1794	1/1	0.95	0.16	-0.72	58,58,58,58	0
57	MG	BA	3240	1/1	0.83	0.18	-0.75	53,53,53,53	0
57	MG	B7	105	1/1	0.96	0.20	-0.80	28,28,28,28	0
57	MG	AA	1695	1/1	0.84	0.20	-0.80	59,59,59,59	0
57	MG	BA	3189	1/1	0.98	0.22	-0.81	39,39,39,39	0
57	MG	CA	3042	1/1	0.91	0.13	-0.81	57,57,57,57	0
57	MG	AN	503	1/1	0.89	0.18	-0.83	52,52,52,52	0
57	MG	DA	3133	1/1	0.93	0.18	-0.83	60,60,60,60	0
57	MG	DE	3004	1/1	0.96	0.17	-0.84	31,31,31,31	0
57	MG	BA	3417	1/1	0.99	0.21	-0.84	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3261	1/1	0.95	0.21	-0.85	18,18,18,18	0
57	MG	CE	201	1/1	0.83	0.18	-0.86	65,65,65,65	0
57	MG	DA	3663	1/1	0.88	0.15	-0.86	73,73,73,73	0
57	MG	DA	3183	1/1	0.96	0.17	-0.87	41,41,41,41	0
59	ZN	AN	501	1/1	0.97	0.16	-0.90	77,77,77,77	0
57	MG	DA	3085	1/1	0.98	0.18	-0.90	28,28,28,28	0
57	MG	DA	3291	1/1	0.89	0.16	-0.92	36,36,36,36	0
57	MG	BA	3402	1/1	0.96	0.18	-0.93	27,27,27,27	0
57	MG	DA	3333	1/1	0.86	0.17	-0.94	47,47,47,47	0
57	MG	CA	3113	1/1	0.92	0.16	-0.95	47,47,47,47	0
59	ZN	DY	501	1/1	0.97	0.11	-0.95	90,90,90,90	0
57	MG	AA	1641	1/1	0.93	0.17	-0.96	65,65,65,65	0
57	MG	DB	3007	1/1	0.79	0.12	-0.96	67,67,67,67	0
57	MG	BA	3377	1/1	0.86	0.21	-0.98	51,51,51,51	0
57	MG	BA	3435	1/1	0.91	0.22	-0.98	53,53,53,53	0
57	MG	CA	3169	1/1	0.94	0.18	-0.99	62,62,62,62	0
59	ZN	D9	501	1/1	0.97	0.12	-1.02	64,64,64,64	0
57	MG	BH	201	1/1	0.97	0.20	-1.05	56,56,56,56	0
57	MG	CA	3144	1/1	0.94	0.13	-1.07	82,82,82,82	0
57	MG	DE	3002	1/1	0.95	0.16	-1.07	33,33,33,33	0
57	MG	BA	3508	1/1	0.88	0.21	-1.09	20,20,20,20	0
57	MG	BA	3334	1/1	0.94	0.21	-1.09	56,56,56,56	0
57	MG	BA	3039	1/1	0.98	0.19	-1.10	36,36,36,36	0
57	MG	DA	3595	1/1	0.93	0.13	-1.13	57,57,57,57	0
57	MG	CA	3166	1/1	0.91	0.15	-1.14	55,55,55,55	0
57	MG	DA	3411	1/1	0.84	0.18	-1.14	37,37,37,37	0
57	MG	BA	3260	1/1	0.97	0.20	-1.16	19,19,19,19	0
57	MG	BE	301	1/1	0.82	0.20	-1.18	31,31,31,31	0
57	MG	BA	3559	1/1	0.97	0.22	-1.19	26,26,26,26	0
58	SF4	AD	501	8/8	0.98	0.15	-1.24	59,68,73,79	0
57	MG	BA	3573	1/1	0.90	0.19	-1.24	41,41,41,41	0
57	MG	BA	3389	1/1	0.89	0.21	-1.24	37,37,37,37	0
57	MG	AX	3005	1/1	0.84	0.11	-1.25	65,65,65,65	0
57	MG	DA	3577	1/1	0.88	0.07	-1.25	60,60,60,60	0
57	MG	CA	3036	1/1	0.92	0.16	-1.26	73,73,73,73	0
57	MG	AB	3001	1/1	0.94	0.13	-1.26	77,77,77,77	0
57	MG	BA	3313	1/1	0.88	0.19	-1.28	38,38,38,38	0
57	MG	BA	3020	1/1	0.98	0.21	-1.31	25,25,25,25	0
57	MG	DA	3228	1/1	0.96	0.15	-1.31	44,44,44,44	0
57	MG	DA	3442	1/1	0.87	0.15	-1.31	64,64,64,64	0
57	MG	BA	3566	1/1	0.97	0.21	-1.32	31,31,31,31	0
57	MG	DA	3001	1/1	0.92	0.14	-1.35	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3258	1/1	0.96	0.16	-1.36	45,45,45,45	0
57	MG	BA	3114	1/1	0.98	0.20	-1.36	39,39,39,39	0
57	MG	DA	3040	1/1	0.97	0.14	-1.38	28,28,28,28	0
57	MG	BA	3671	1/1	0.95	0.19	-1.38	24,24,24,24	0
57	MG	DA	3528	1/1	0.92	0.14	-1.38	36,36,36,36	0
57	MG	BA	3188	1/1	0.95	0.19	-1.41	32,32,32,32	0
57	MG	AA	1814	1/1	0.91	0.15	-1.42	57,57,57,57	0
57	MG	BA	3009	1/1	0.94	0.17	-1.42	31,31,31,31	0
57	MG	BA	3487	1/1	0.74	0.13	-1.48	54,54,54,54	0
57	MG	DA	3477	1/1	0.98	0.11	-1.48	53,53,53,53	0
57	MG	BA	3704	1/1	0.90	0.18	-1.49	26,26,26,26	0
59	ZN	B4	501	1/1	0.94	0.10	-1.50	118,118,118,118	0
57	MG	CA	3142	1/1	0.95	0.18	-1.56	50,50,50,50	0
57	MG	BA	3191	1/1	0.91	0.19	-1.57	40,40,40,40	0
57	MG	DA	3216	1/1	0.96	0.15	-1.58	35,35,35,35	0
59	ZN	D4	501	1/1	0.33	0.12	-1.58	162,162,162,162	0
57	MG	BA	3541	1/1	0.92	0.20	-1.58	38,38,38,38	0
57	MG	BA	3082	1/1	0.96	0.18	-1.58	28,28,28,28	0
57	MG	DG	3001	1/1	0.86	0.14	-1.60	66,66,66,66	0
57	MG	DA	3433	1/1	0.93	0.17	-1.61	59,59,59,59	0
57	MG	BA	3382	1/1	0.98	0.12	-1.63	55,55,55,55	0
57	MG	DA	3560	1/1	0.82	0.15	-1.63	60,60,60,60	0
57	MG	CA	3094	1/1	0.81	0.08	-1.64	61,61,61,61	0
57	MG	AA	1611	1/1	0.97	0.19	-1.65	20,20,20,20	0
57	MG	BA	3045	1/1	0.97	0.17	-1.66	39,39,39,39	0
57	MG	AA	1723	1/1	0.84	0.15	-1.66	63,63,63,63	0
57	MG	CA	3110	1/1	0.87	0.12	-1.69	63,63,63,63	0
57	MG	BA	3621	1/1	0.97	0.19	-1.69	43,43,43,43	0
57	MG	DA	3340	1/1	0.97	0.14	-1.70	27,27,27,27	0
57	MG	DA	3393	1/1	0.89	0.16	-1.71	37,37,37,37	0
57	MG	AA	1740	1/1	0.98	0.17	-1.71	41,41,41,41	0
57	MG	BA	3341	1/1	0.97	0.20	-1.72	18,18,18,18	0
57	MG	DA	3371	1/1	0.93	0.17	-1.72	34,34,34,34	0
57	MG	DA	3499	1/1	0.93	0.14	-1.73	52,52,52,52	0
57	MG	AA	1747	1/1	0.88	0.15	-1.74	55,55,55,55	0
57	MG	DA	3429	1/1	0.95	0.15	-1.74	36,36,36,36	0
57	MG	DA	3087	1/1	0.84	0.18	-1.75	55,55,55,55	0
57	MG	CA	3048	1/1	0.97	0.12	-1.76	58,58,58,58	0
57	MG	BA	3387	1/1	0.97	0.20	-1.77	29,29,29,29	0
57	MG	DA	3311	1/1	0.88	0.14	-1.77	46,46,46,46	0
57	MG	AA	1779	1/1	0.96	0.14	-1.78	59,59,59,59	0
57	MG	CA	3051	1/1	0.87	0.11	-1.79	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	CA	3099	1/1	0.90	0.09	-1.79	64,64,64,64	0
57	MG	AA	1680	1/1	0.87	0.17	-1.79	51,51,51,51	0
57	MG	BB	3007	1/1	0.97	0.17	-1.80	41,41,41,41	0
57	MG	AA	1795	1/1	0.98	0.12	-1.80	55,55,55,55	0
57	MG	DA	3322	1/1	0.95	0.16	-1.82	42,42,42,42	0
57	MG	BA	3393	1/1	0.97	0.20	-1.82	23,23,23,23	0
57	MG	DA	3630	1/1	0.92	0.14	-1.86	69,69,69,69	0
57	MG	DA	3349	1/1	0.96	0.16	-1.87	34,34,34,34	0
57	MG	BA	3110	1/1	0.90	0.18	-1.88	36,36,36,36	0
57	MG	DA	3659	1/1	0.94	0.14	-1.89	41,41,41,41	0
57	MG	B5	102	1/1	0.93	0.19	-1.90	43,43,43,43	0
57	MG	DA	3331	1/1	0.95	0.15	-1.92	47,47,47,47	0
57	MG	BA	3719	1/1	0.98	0.20	-1.93	41,41,41,41	0
57	MG	BW	3003	1/1	0.95	0.15	-1.96	35,35,35,35	0
57	MG	BA	3311	1/1	0.97	0.19	-1.99	56,56,56,56	0
58	SF4	CD	501	8/8	0.98	0.14	-1.99	64,67,74,91	0
57	MG	BA	3706	1/1	0.94	0.16	-2.00	47,47,47,47	0
57	MG	BA	3358	1/1	0.91	0.18	-2.02	52,52,52,52	0
57	MG	BA	3144	1/1	0.96	0.18	-2.02	41,41,41,41	0
57	MG	BA	3448	1/1	0.97	0.18	-2.03	17,17,17,17	0
57	MG	DA	3652	1/1	0.96	0.16	-2.05	31,31,31,31	0
57	MG	DB	3003	1/1	0.82	0.10	-2.06	78,78,78,78	0
57	MG	DA	3421	1/1	0.93	0.12	-2.08	56,56,56,56	0
57	MG	DA	3607	1/1	0.82	0.14	-2.08	64,64,64,64	0
57	MG	DA	3039	1/1	0.97	0.16	-2.11	38,38,38,38	0
57	MG	B7	102	1/1	0.97	0.17	-2.12	41,41,41,41	0
57	MG	BA	3779	1/1	0.98	0.19	-2.14	17,17,17,17	0
57	MG	DA	3296	1/1	0.90	0.10	-2.15	60,60,60,60	0
57	MG	DA	3319	1/1	0.97	0.14	-2.15	33,33,33,33	0
57	MG	CA	3009	1/1	0.84	0.12	-2.15	73,73,73,73	0
57	MG	DA	3238	1/1	0.84	0.15	-2.16	48,48,48,48	0
57	MG	CA	3040	1/1	0.95	0.12	-2.18	56,56,56,56	0
57	MG	BD	3009	1/1	0.98	0.16	-2.18	37,37,37,37	0
59	ZN	CN	501	1/1	0.91	0.06	-2.19	100,100,100,100	0
57	MG	DA	3459	1/1	0.90	0.14	-2.19	49,49,49,49	0
57	MG	BA	3615	1/1	0.91	0.13	-2.21	71,71,71,71	0
57	MG	DA	3268	1/1	0.94	0.12	-2.23	41,41,41,41	0
57	MG	BA	3756	1/1	0.96	0.19	-2.25	18,18,18,18	0
57	MG	BA	3533	1/1	0.98	0.18	-2.25	23,23,23,23	0
57	MG	DA	3649	1/1	0.80	0.13	-2.26	71,71,71,71	0
57	MG	BA	3118	1/1	0.95	0.21	-2.26	35,35,35,35	0
57	MG	AA	1681	1/1	0.99	0.12	-2.29	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DQ	3001	1/1	0.92	0.08	-2.30	50,50,50,50	0
57	MG	AM	3001	1/1	0.94	0.09	-2.32	66,66,66,66	0
57	MG	CA	3106	1/1	0.94	0.13	-2.32	58,58,58,58	0
57	MG	BB	3003	1/1	0.94	0.18	-2.34	30,30,30,30	0
57	MG	BA	3131	1/1	0.88	0.19	-2.37	44,44,44,44	0
57	MG	DA	3028	1/1	0.92	0.13	-2.37	39,39,39,39	0
57	MG	BA	3806	1/1	0.92	0.17	-2.39	43,43,43,43	0
57	MG	BA	3796	1/1	0.91	0.17	-2.39	47,47,47,47	0
57	MG	DA	3420	1/1	0.80	0.11	-2.39	49,49,49,49	0
57	MG	BA	3023	1/1	0.95	0.17	-2.41	41,41,41,41	0
57	MG	BG	202	1/1	0.78	0.15	-2.43	52,52,52,52	0
57	MG	BA	3089	1/1	0.97	0.19	-2.43	36,36,36,36	0
57	MG	DA	3661	1/1	0.97	0.10	-2.44	62,62,62,62	0
57	MG	BA	3120	1/1	0.95	0.18	-2.44	45,45,45,45	0
57	MG	BA	3519	1/1	0.94	0.19	-2.45	45,45,45,45	0
57	MG	AA	1676	1/1	0.94	0.16	-2.52	58,58,58,58	0
57	MG	DA	3416	1/1	0.90	0.14	-2.52	52,52,52,52	0
57	MG	DA	3132	1/1	0.89	0.13	-2.52	43,43,43,43	0
57	MG	DA	3108	1/1	0.77	0.12	-2.55	50,50,50,50	0
57	MG	DA	3036	1/1	0.97	0.17	-2.57	35,35,35,35	0
57	MG	CA	3016	1/1	0.83	0.13	-2.57	48,48,48,48	0
57	MG	DR	3001	1/1	0.92	0.13	-2.58	49,49,49,49	0
57	MG	BA	3419	1/1	0.91	0.20	-2.59	25,25,25,25	0
57	MG	BA	3312	1/1	0.98	0.19	-2.59	31,31,31,31	0
57	MG	BA	3439	1/1	0.61	0.18	-2.60	36,36,36,36	0
57	MG	BA	3129	1/1	0.88	0.16	-2.60	54,54,54,54	0
57	MG	DD	304	1/1	0.97	0.09	-2.63	36,36,36,36	0
57	MG	DA	3186	1/1	0.92	0.15	-2.63	49,49,49,49	0
57	MG	AA	1621	1/1	0.88	0.14	-2.64	44,44,44,44	0
57	MG	DA	3619	1/1	0.82	0.15	-2.68	40,40,40,40	0
57	MG	BA	3644	1/1	0.81	0.18	-2.69	64,64,64,64	0
57	MG	BA	3315	1/1	0.97	0.18	-2.71	40,40,40,40	0
57	MG	BA	3407	1/1	0.89	0.17	-2.71	32,32,32,32	0
57	MG	BA	3694	1/1	0.90	0.19	-2.73	53,53,53,53	0
57	MG	BA	3323	1/1	0.90	0.19	-2.78	57,57,57,57	0
57	MG	BA	3762	1/1	0.96	0.18	-2.79	20,20,20,20	0
57	MG	BE	303	1/1	0.94	0.15	-2.80	43,43,43,43	0
57	MG	BA	3231	1/1	0.79	0.17	-2.81	57,57,57,57	0
57	MG	BA	3577	1/1	0.86	0.17	-2.81	58,58,58,58	0
57	MG	DA	3605	1/1	0.94	0.12	-2.82	45,45,45,45	0
57	MG	DA	3321	1/1	0.97	0.15	-2.86	29,29,29,29	0
57	MG	BA	3206	1/1	0.94	0.16	-2.89	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3388	1/1	0.91	0.20	-2.91	25,25,25,25	0
57	MG	DA	3523	1/1	0.90	0.14	-2.92	39,39,39,39	0
57	MG	DA	3347	1/1	0.88	0.14	-2.93	35,35,35,35	0
57	MG	BU	202	1/1	0.95	0.15	-2.94	40,40,40,40	0
57	MG	AA	1759	1/1	0.89	0.14	-2.95	55,55,55,55	0
57	MG	CA	3053	1/1	0.95	0.12	-2.96	41,41,41,41	0
57	MG	CA	3119	1/1	0.89	0.12	-2.97	59,59,59,59	0
57	MG	AT	3001	1/1	0.91	0.13	-2.99	63,63,63,63	0
57	MG	BN	3001	1/1	0.91	0.15	-3.00	48,48,48,48	0
57	MG	DA	3303	1/1	0.97	0.12	-3.01	43,43,43,43	0
57	MG	DF	304	1/1	0.97	0.07	-3.04	51,51,51,51	0
57	MG	AA	1776	1/1	0.95	0.16	-3.05	73,73,73,73	0
57	MG	BB	3021	1/1	0.97	0.18	-3.06	41,41,41,41	0
57	MG	AA	1631	1/1	0.78	0.14	-3.09	64,64,64,64	0
57	MG	DA	3343	1/1	0.96	0.15	-3.10	34,34,34,34	0
57	MG	BA	3395	1/1	0.94	0.20	-3.11	30,30,30,30	0
57	MG	AA	1765	1/1	0.93	0.13	-3.11	65,65,65,65	0
57	MG	DA	3418	1/1	0.86	0.07	-3.13	47,47,47,47	0
57	MG	DA	3664	1/1	0.96	0.09	-3.14	51,51,51,51	0
57	MG	BA	3012	1/1	0.94	0.17	-3.14	25,25,25,25	0
57	MG	DA	3300	1/1	0.98	0.10	-3.15	38,38,38,38	0
57	MG	DA	3327	1/1	0.91	0.15	-3.15	45,45,45,45	0
57	MG	BA	3366	1/1	0.93	0.16	-3.16	52,52,52,52	0
57	MG	DA	3229	1/1	0.97	0.12	-3.17	38,38,38,38	0
57	MG	BA	3333	1/1	0.90	0.14	-3.18	57,57,57,57	0
57	MG	BA	3509	1/1	0.94	0.18	-3.20	50,50,50,50	0
57	MG	BB	3017	1/1	0.91	0.16	-3.25	81,81,81,81	0
57	MG	DA	3625	1/1	0.81	0.10	-3.27	60,60,60,60	0
57	MG	BA	3185	1/1	0.97	0.15	-3.29	33,33,33,33	0
57	MG	BA	3253	1/1	0.86	0.20	-3.29	31,31,31,31	0
57	MG	BA	3540	1/1	0.93	0.16	-3.29	31,31,31,31	0
57	MG	BA	3158	1/1	0.95	0.17	-3.29	41,41,41,41	0
57	MG	DA	3139	1/1	0.94	0.11	-3.31	44,44,44,44	0
57	MG	DA	3552	1/1	0.89	0.13	-3.33	34,34,34,34	0
57	MG	BA	3043	1/1	0.95	0.17	-3.33	31,31,31,31	0
57	MG	DA	3109	1/1	0.96	0.13	-3.35	49,49,49,49	0
57	MG	DA	3064	1/1	0.89	0.11	-3.35	46,46,46,46	0
57	MG	DA	3013	1/1	0.98	0.13	-3.36	39,39,39,39	0
57	MG	DA	3266	1/1	0.95	0.12	-3.39	37,37,37,37	0
57	MG	BA	3348	1/1	0.92	0.18	-3.40	37,37,37,37	0
57	MG	BA	3799	1/1	0.94	0.18	-3.41	42,42,42,42	0
57	MG	DA	3037	1/1	0.97	0.12	-3.41	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3309	1/1	0.92	0.17	-3.42	65,65,65,65	0
57	MG	DA	3449	1/1	0.93	0.13	-3.43	34,34,34,34	0
57	MG	AA	1627	1/1	0.97	0.14	-3.46	54,54,54,54	0
57	MG	BA	3812	1/1	0.95	0.12	-3.46	42,42,42,42	0
57	MG	CA	3081	1/1	0.91	0.16	-3.46	44,44,44,44	0
57	MG	BA	3223	1/1	0.95	0.17	-3.46	41,41,41,41	0
57	MG	DA	3314	1/1	0.78	0.12	-3.51	43,43,43,43	0
57	MG	DA	3458	1/1	0.92	0.10	-3.52	41,41,41,41	0
57	MG	BA	3399	1/1	0.94	0.20	-3.54	41,41,41,41	0
57	MG	BA	3376	1/1	0.96	0.18	-3.54	29,29,29,29	0
57	MG	DA	3341	1/1	0.88	0.12	-3.56	55,55,55,55	0
57	MG	DA	3164	1/1	0.94	0.14	-3.57	44,44,44,44	0
57	MG	D0	101	1/1	0.91	0.13	-3.57	71,71,71,71	0
57	MG	BA	3220	1/1	0.93	0.15	-3.57	35,35,35,35	0
57	MG	AA	1644	1/1	0.82	0.12	-3.61	56,56,56,56	0
57	MG	DA	3010	1/1	0.87	0.10	-3.62	41,41,41,41	0
57	MG	BF	305	1/1	0.98	0.14	-3.62	36,36,36,36	0
57	MG	DA	3490	1/1	0.95	0.13	-3.63	33,33,33,33	0
57	MG	BD	3001	1/1	0.97	0.14	-3.65	34,34,34,34	0
57	MG	AM	3002	1/1	0.89	0.12	-3.65	68,68,68,68	0
57	MG	BA	3512	1/1	0.92	0.21	-3.66	23,23,23,23	0
57	MG	CA	3088	1/1	0.95	0.12	-3.74	43,43,43,43	0
57	MG	DA	3019	1/1	0.94	0.08	-3.79	42,42,42,42	0
57	MG	DA	3312	1/1	0.95	0.12	-3.85	42,42,42,42	0
57	MG	DA	3428	1/1	0.97	0.11	-3.88	38,38,38,38	0
57	MG	DA	3354	1/1	0.96	0.11	-3.93	41,41,41,41	0
57	MG	BA	3011	1/1	0.97	0.15	-3.93	30,30,30,30	0
57	MG	DA	3279	1/1	0.76	0.14	-3.94	36,36,36,36	0
57	MG	DA	3113	1/1	0.94	0.13	-3.95	35,35,35,35	0
57	MG	DA	3315	1/1	0.93	0.13	-3.95	44,44,44,44	0
57	MG	DA	3049	1/1	0.90	0.10	-4.00	47,47,47,47	0
57	MG	DA	3225	1/1	0.95	0.10	-4.00	55,55,55,55	0
57	MG	BA	3336	1/1	0.96	0.17	-4.03	20,20,20,20	0
57	MG	AA	1665	1/1	0.97	0.16	-4.04	55,55,55,55	0
57	MG	DA	3655	1/1	0.97	0.08	-4.05	38,38,38,38	0
57	MG	BA	3275	1/1	0.88	0.16	-4.06	66,66,66,66	0
57	MG	DA	3285	1/1	0.94	0.12	-4.08	50,50,50,50	0
57	MG	BA	3296	1/1	0.92	0.16	-4.08	55,55,55,55	0
57	MG	DA	3364	1/1	0.95	0.10	-4.09	45,45,45,45	0
57	MG	BA	3340	1/1	0.75	0.18	-4.12	27,27,27,27	0
57	MG	BA	3073	1/1	0.88	0.15	-4.12	32,32,32,32	0
57	MG	BA	3392	1/1	0.96	0.18	-4.14	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3108	1/1	0.84	0.11	-4.14	72,72,72,72	0
57	MG	BA	3527	1/1	0.93	0.19	-4.16	24,24,24,24	0
57	MG	BD	3006	1/1	0.99	0.09	-4.17	34,34,34,34	0
57	MG	CA	3029	1/1	0.89	0.11	-4.27	50,50,50,50	0
57	MG	DA	3529	1/1	0.94	0.07	-4.28	76,76,76,76	0
57	MG	BF	309	1/1	0.96	0.18	-4.29	31,31,31,31	0
57	MG	BA	3723	1/1	0.86	0.18	-4.31	30,30,30,30	0
57	MG	DA	3561	1/1	0.92	0.16	-4.32	52,52,52,52	0
57	MG	BA	3607	1/1	0.95	0.17	-4.32	36,36,36,36	0
57	MG	BA	3544	1/1	0.97	0.18	-4.34	52,52,52,52	0
57	MG	DA	3440	1/1	0.97	0.13	-4.37	36,36,36,36	0
57	MG	BA	3050	1/1	0.96	0.15	-4.37	32,32,32,32	0
57	MG	DA	3147	1/1	0.95	0.14	-4.39	44,44,44,44	0
57	MG	DA	3100	1/1	0.92	0.09	-4.41	47,47,47,47	0
57	MG	AA	1742	1/1	0.95	0.14	-4.41	52,52,52,52	0
57	MG	BA	3689	1/1	0.89	0.19	-4.43	59,59,59,59	0
57	MG	BP	3001	1/1	0.96	0.14	-4.45	34,34,34,34	0
57	MG	CA	3023	1/1	0.89	0.10	-4.45	39,39,39,39	0
57	MG	BA	3794	1/1	0.88	0.13	-4.46	37,37,37,37	0
57	MG	DA	3426	1/1	0.84	0.12	-4.48	49,49,49,49	0
57	MG	DA	3434	1/1	0.95	0.07	-4.49	60,60,60,60	0
57	MG	DA	3414	1/1	0.93	0.15	-4.51	42,42,42,42	0
57	MG	BA	3289	1/1	0.93	0.17	-4.55	49,49,49,49	0
57	MG	DE	3007	1/1	0.96	0.11	-4.59	58,58,58,58	0
57	MG	DA	3267	1/1	0.97	0.12	-4.59	44,44,44,44	0
57	MG	BA	3397	1/1	0.96	0.15	-4.61	28,28,28,28	0
57	MG	DA	3562	1/1	0.98	0.12	-4.65	31,31,31,31	0
57	MG	CA	3114	1/1	0.94	0.14	-4.65	71,71,71,71	0
57	MG	DA	3310	1/1	0.92	0.13	-4.67	35,35,35,35	0
57	MG	BA	3412	1/1	0.97	0.17	-4.67	30,30,30,30	0
57	MG	BA	3473	1/1	0.97	0.19	-4.67	28,28,28,28	0
57	MG	BR	5002	1/1	0.94	0.14	-4.75	50,50,50,50	0
57	MG	BA	3725	1/1	0.97	0.17	-4.78	31,31,31,31	0
57	MG	BA	3742	1/1	0.98	0.21	-4.78	48,48,48,48	0
57	MG	BA	3254	1/1	0.88	0.16	-4.79	33,33,33,33	0
57	MG	BA	3813	1/1	0.98	0.13	-4.80	29,29,29,29	0
57	MG	DD	302	1/1	0.87	0.14	-4.90	49,49,49,49	0
57	MG	AA	1684	1/1	0.75	0.13	-4.91	54,54,54,54	0
57	MG	BA	3486	1/1	0.96	0.13	-4.94	41,41,41,41	0
57	MG	BB	3020	1/1	0.75	0.16	-4.97	65,65,65,65	0
57	MG	DA	3522	1/1	0.88	0.11	-5.02	51,51,51,51	0
57	MG	BG	201	1/1	0.96	0.14	-5.03	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3359	1/1	0.95	0.16	-5.10	40,40,40,40	0
57	MG	DA	3246	1/1	0.96	0.06	-5.11	46,46,46,46	0
57	MG	AA	1630	1/1	0.87	0.14	-5.18	53,53,53,53	0
57	MG	BA	3380	1/1	0.96	0.15	-5.18	40,40,40,40	0
57	MG	DA	3384	1/1	0.88	0.10	-5.19	38,38,38,38	0
57	MG	DA	3318	1/1	0.62	0.10	-5.19	45,45,45,45	0
57	MG	AA	1697	1/1	0.81	0.11	-5.23	65,65,65,65	0
57	MG	DA	3439	1/1	0.90	0.12	-5.28	40,40,40,40	0
57	MG	DA	3034	1/1	0.91	0.10	-5.32	42,42,42,42	0
57	MG	DA	3526	1/1	0.94	0.12	-5.33	52,52,52,52	0
57	MG	AA	1617	1/1	0.94	0.10	-5.36	58,58,58,58	0
57	MG	AA	1619	1/1	0.90	0.11	-5.46	64,64,64,64	0
57	MG	BA	3503	1/1	0.96	0.10	-5.46	51,51,51,51	0
57	MG	BA	3737	1/1	0.91	0.16	-5.51	34,34,34,34	0
57	MG	BA	3606	1/1	0.97	0.16	-5.51	36,36,36,36	0
57	MG	BA	3585	1/1	0.96	0.16	-5.52	29,29,29,29	0
57	MG	BA	3383	1/1	0.88	0.16	-5.53	37,37,37,37	0
57	MG	DA	3581	1/1	0.98	0.07	-5.53	44,44,44,44	0
57	MG	BA	3300	1/1	0.92	0.17	-5.56	53,53,53,53	0
57	MG	BA	3665	1/1	0.98	0.17	-5.56	42,42,42,42	0
57	MG	BA	3515	1/1	0.88	0.17	-5.57	27,27,27,27	0
57	MG	BA	3327	1/1	0.47	0.17	-5.60	39,39,39,39	0
57	MG	DA	3307	1/1	0.97	0.12	-5.61	51,51,51,51	0
57	MG	BA	3805	1/1	0.87	0.13	-5.61	48,48,48,48	0
57	MG	AA	1607	1/1	0.93	0.13	-5.62	55,55,55,55	0
57	MG	DA	3489	1/1	0.97	0.09	-5.72	48,48,48,48	0
57	MG	AA	1737	1/1	0.93	0.09	-5.72	60,60,60,60	0
57	MG	AA	1735	1/1	0.97	0.12	-5.73	45,45,45,45	0
57	MG	CA	3004	1/1	0.83	0.09	-5.75	69,69,69,69	0
57	MG	DA	3397	1/1	0.83	0.15	-5.75	42,42,42,42	0
57	MG	DA	3277	1/1	0.94	0.13	-5.79	50,50,50,50	0
57	MG	AA	1655	1/1	0.79	0.12	-5.83	53,53,53,53	0
57	MG	DA	3365	1/1	0.96	0.14	-5.87	19,19,19,19	0
57	MG	BA	3548	1/1	0.97	0.13	-5.93	35,35,35,35	0
57	MG	AA	1815	1/1	0.92	0.14	-5.93	47,47,47,47	0
57	MG	BE	306	1/1	0.94	0.10	-6.00	38,38,38,38	0
57	MG	BB	3014	1/1	0.95	0.12	-6.01	67,67,67,67	0
57	MG	CA	3065	1/1	0.89	0.14	-6.04	59,59,59,59	0
57	MG	BA	3623	1/1	0.92	0.17	-6.05	43,43,43,43	0
57	MG	BA	3469	1/1	0.95	0.16	-6.07	61,61,61,61	0
57	MG	DA	3361	1/1	0.91	0.08	-6.08	33,33,33,33	0
57	MG	BA	3536	1/1	0.89	0.14	-6.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	1686	1/1	0.76	0.14	-6.09	61,61,61,61	0
57	MG	BA	3413	1/1	0.97	0.16	-6.18	37,37,37,37	0
57	MG	BV	205	1/1	0.99	0.12	-6.21	34,34,34,34	0
57	MG	BA	3494	1/1	0.97	0.11	-6.27	38,38,38,38	0
57	MG	CF	3001	1/1	0.96	0.12	-6.28	51,51,51,51	0
57	MG	DA	3532	1/1	0.90	0.13	-6.29	48,48,48,48	0
57	MG	DA	3338	1/1	0.87	0.07	-6.31	44,44,44,44	0
57	MG	BA	3736	1/1	0.97	0.16	-6.32	22,22,22,22	0
57	MG	AA	1770	1/1	0.99	0.13	-6.34	51,51,51,51	0
57	MG	BA	3365	1/1	0.87	0.13	-6.34	51,51,51,51	0
57	MG	BB	3016	1/1	0.90	0.14	-6.45	34,34,34,34	0
57	MG	BA	3234	1/1	0.96	0.12	-6.50	52,52,52,52	0
57	MG	DA	3363	1/1	0.92	0.09	-6.50	50,50,50,50	0
57	MG	BA	3371	1/1	0.98	0.10	-6.53	49,49,49,49	0
57	MG	BA	3752	1/1	0.95	0.12	-6.57	34,34,34,34	0
57	MG	DA	3214	1/1	0.96	0.08	-6.63	51,51,51,51	0
57	MG	DA	3492	1/1	0.97	0.07	-6.73	48,48,48,48	0
57	MG	BA	3036	1/1	0.91	0.12	-6.73	56,56,56,56	0
57	MG	DA	3385	1/1	0.95	0.07	-6.99	60,60,60,60	0
57	MG	BA	3225	1/1	0.85	0.13	-6.99	46,46,46,46	0
57	MG	DA	3521	1/1	0.98	0.09	-7.03	57,57,57,57	0
57	MG	BA	3346	1/1	0.86	0.10	-7.03	39,39,39,39	0
57	MG	DA	3292	1/1	0.91	0.11	-7.06	29,29,29,29	0
57	MG	B7	101	1/1	0.95	0.12	-7.21	41,41,41,41	0
57	MG	BA	3618	1/1	0.91	0.15	-7.25	35,35,35,35	0
57	MG	AA	1616	1/1	0.82	0.09	-7.33	73,73,73,73	0
57	MG	DA	3020	1/1	0.98	0.11	-7.35	26,26,26,26	0
57	MG	DA	3018	1/1	0.94	0.10	-7.35	31,31,31,31	0
57	MG	AA	1628	1/1	0.86	0.10	-7.39	65,65,65,65	0
57	MG	BF	307	1/1	0.92	0.13	-7.40	34,34,34,34	0
57	MG	DA	3282	1/1	0.93	0.10	-7.41	55,55,55,55	0
57	MG	AA	1787	1/1	0.85	0.15	-7.43	49,49,49,49	0
57	MG	BA	3714	1/1	0.94	0.12	-7.45	46,46,46,46	0
57	MG	DA	3454	1/1	0.92	0.12	-7.48	43,43,43,43	0
57	MG	BA	3410	1/1	0.90	0.16	-7.51	55,55,55,55	0
57	MG	CA	3085	1/1	0.99	0.15	-7.51	41,41,41,41	0
57	MG	DA	3593	1/1	0.91	0.08	-7.64	60,60,60,60	0
57	MG	DA	3599	1/1	0.98	0.09	-7.70	48,48,48,48	0
57	MG	BA	3804	1/1	0.94	0.16	-7.70	36,36,36,36	0
57	MG	BA	3113	1/1	0.94	0.14	-7.71	50,50,50,50	0
57	MG	BA	3643	1/1	0.96	0.12	-7.86	52,52,52,52	0
57	MG	BA	3624	1/1	0.93	0.13	-7.97	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3217	1/1	0.90	0.11	-7.99	50,50,50,50	0
57	MG	DA	3544	1/1	0.97	0.12	-8.06	53,53,53,53	0
57	MG	DA	3573	1/1	0.96	0.05	-8.08	61,61,61,61	0
57	MG	BA	3477	1/1	0.85	0.16	-8.10	68,68,68,68	0
57	MG	BA	3386	1/1	0.94	0.14	-8.30	28,28,28,28	0
57	MG	BA	3808	1/1	0.96	0.15	-8.39	38,38,38,38	0
57	MG	DA	3598	1/1	0.96	0.10	-8.47	55,55,55,55	0
57	MG	BA	3657	1/1	0.93	0.11	-8.52	38,38,38,38	0
57	MG	DA	3352	1/1	0.92	0.09	-8.56	34,34,34,34	0
57	MG	AA	1788	1/1	0.87	0.09	-8.59	75,75,75,75	0
57	MG	AA	1713	1/1	0.69	0.11	-8.61	67,67,67,67	0
57	MG	BA	3558	1/1	0.89	0.13	-8.63	51,51,51,51	0
57	MG	DA	3337	1/1	0.95	0.06	-8.64	48,48,48,48	0
57	MG	BA	3582	1/1	0.99	0.12	-8.71	31,31,31,31	0
57	MG	DA	3469	1/1	0.98	0.07	-8.77	50,50,50,50	0
57	MG	BA	3598	1/1	0.84	0.15	-8.78	33,33,33,33	0
57	MG	BA	3355	1/1	0.95	0.15	-9.20	35,35,35,35	0
57	MG	BA	3384	1/1	0.94	0.11	-9.21	45,45,45,45	0
57	MG	BA	3022	1/1	0.96	0.11	-9.23	25,25,25,25	0
57	MG	BF	308	1/1	0.96	0.08	-9.24	43,43,43,43	0
57	MG	BA	3459	1/1	0.95	0.15	-9.64	31,31,31,31	0
57	MG	DA	3280	1/1	0.85	0.09	-9.69	48,48,48,48	0
57	MG	DA	3170	1/1	0.86	0.10	-9.88	35,35,35,35	0
57	MG	BA	3583	1/1	0.99	0.15	-10.21	33,33,33,33	0
57	MG	BA	3635	1/1	0.97	0.12	-10.42	42,42,42,42	0
57	MG	BA	3330	1/1	0.92	0.15	-10.70	27,27,27,27	0
57	MG	DA	3373	1/1	0.98	0.09	-10.76	31,31,31,31	0
57	MG	DA	3283	1/1	0.94	0.07	-11.10	27,27,27,27	0
57	MG	DA	3586	1/1	0.95	0.08	-11.30	50,50,50,50	0
57	MG	BA	3021	1/1	0.98	0.12	-11.43	43,43,43,43	0
57	MG	BA	3046	1/1	0.96	0.15	-11.62	43,43,43,43	0
57	MG	BA	3059	1/1	0.94	0.14	-12.46	36,36,36,36	0
57	MG	BA	3741	1/1	0.92	0.11	-12.56	57,57,57,57	0
57	MG	BA	3587	1/1	0.92	0.11	-13.06	46,46,46,46	0
57	MG	BA	3625	1/1	0.90	0.14	-13.12	33,33,33,33	0
57	MG	BA	3525	1/1	0.86	0.16	-13.24	43,43,43,43	0
57	MG	BA	3780	1/1	0.95	0.13	-13.48	42,42,42,42	0
57	MG	BA	3434	1/1	0.97	0.11	-13.99	19,19,19,19	0
57	MG	BA	3772	1/1	0.98	0.15	-14.06	36,36,36,36	0
57	MG	DA	3252	1/1	0.95	0.07	-14.13	50,50,50,50	0
57	MG	BA	3499	1/1	0.99	0.13	-14.31	39,39,39,39	0
57	MG	DA	3011	1/1	0.96	0.07	-15.38	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3321	1/1	0.93	0.13	-16.04	53,53,53,53	0
57	MG	AA	1663	1/1	0.85	0.12	-21.27	50,50,50,50	0
57	MG	BA	3777	1/1	0.97	0.10	-22.29	41,41,41,41	0
57	MG	BA	3619	1/1	0.90	0.14	-29.83	28,28,28,28	0
57	MG	BA	3488	1/1	0.98	0.13	-35.95	20,20,20,20	0
57	MG	CA	3147	1/1	0.94	0.10	-41.86	70,70,70,70	0
57	MG	DA	3401	1/1	0.94	0.06	-	69,69,69,69	0
57	MG	DA	3497	1/1	0.82	0.19	-	58,58,58,58	0
57	MG	BA	3079	1/1	0.89	0.36	-	58,58,58,58	0
57	MG	BA	3653	1/1	0.87	0.21	-	57,57,57,57	0
57	MG	BA	3560	1/1	0.97	0.14	-	63,63,63,63	0
57	MG	BA	3247	1/1	0.93	0.17	-	29,29,29,29	0
57	MG	BE	305	1/1	0.95	0.07	-	48,48,48,48	0
57	MG	DA	3265	1/1	0.96	0.16	-	57,57,57,57	0
57	MG	CA	3137	1/1	0.89	0.15	-	78,78,78,78	0
57	MG	BA	3584	1/1	0.94	0.12	-	55,55,55,55	0
57	MG	AA	1603	1/1	0.88	0.15	-	64,64,64,64	0
57	MG	DA	3620	1/1	0.85	0.12	-	53,53,53,53	0
57	MG	BA	3760	1/1	0.97	0.17	-	50,50,50,50	0
57	MG	CA	3019	1/1	0.79	0.16	-	68,68,68,68	0
57	MG	DA	3400	1/1	0.76	0.14	-	62,62,62,62	0
57	MG	CA	3069	1/1	0.94	0.22	-	58,58,58,58	0
57	MG	DA	3498	1/1	0.95	0.17	-	35,35,35,35	0
57	MG	AX	3012	1/1	0.85	0.18	-	52,52,52,52	0
57	MG	BA	3052	1/1	0.86	0.27	-	50,50,50,50	0
57	MG	BZ	301	1/1	0.82	0.18	-	49,49,49,49	0
57	MG	BA	3224	1/1	0.77	0.30	-	59,59,59,59	0
57	MG	AA	1775	1/1	0.95	0.11	-	73,73,73,73	0
57	MG	DA	3399	1/1	0.90	0.15	-	59,59,59,59	0
57	MG	BA	3586	1/1	0.97	0.11	-	55,55,55,55	0
57	MG	DA	3121	1/1	0.96	0.10	-	40,40,40,40	0
57	MG	DA	3514	1/1	0.82	0.14	-	47,47,47,47	0
57	MG	CA	3031	1/1	0.83	0.14	-	58,58,58,58	0
57	MG	BB	3013	1/1	0.91	0.21	-	39,39,39,39	0
57	MG	BE	302	1/1	0.96	0.16	-	35,35,35,35	0
57	MG	BA	3155	1/1	0.84	0.19	-	40,40,40,40	0
57	MG	BB	3009	1/1	0.90	0.09	-	57,57,57,57	0
57	MG	BA	3266	1/1	0.89	0.10	-	44,44,44,44	0
57	MG	DE	3005	1/1	0.92	0.14	-	35,35,35,35	0
57	MG	DA	3197	1/1	0.91	0.20	-	59,59,59,59	0
57	MG	BA	3553	1/1	0.91	0.19	-	45,45,45,45	0
57	MG	BA	3782	1/1	0.98	0.16	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3022	1/1	0.92	0.45	-	60,60,60,60	0
57	MG	DA	3487	1/1	0.68	0.12	-	55,55,55,55	0
57	MG	AA	1637	1/1	0.96	0.10	-	61,61,61,61	0
57	MG	AX	3006	1/1	0.95	0.15	-	68,68,68,68	0
57	MG	DA	3479	1/1	0.91	0.10	-	42,42,42,42	0
57	MG	BA	3427	1/1	0.94	0.17	-	33,33,33,33	0
57	MG	DA	3231	1/1	0.96	0.18	-	61,61,61,61	0
57	MG	BA	3278	1/1	0.96	0.78	-	54,54,54,54	0
57	MG	DA	3572	1/1	0.90	0.19	-	65,65,65,65	0
57	MG	DA	3531	1/1	0.94	0.07	-	48,48,48,48	0
57	MG	DA	3211	1/1	0.90	0.21	-	51,51,51,51	0
57	MG	BA	3502	1/1	0.96	0.19	-	30,30,30,30	0
57	MG	AA	1653	1/1	0.97	0.23	-	54,54,54,54	0
57	MG	DA	3470	1/1	0.92	0.08	-	61,61,61,61	0
57	MG	BV	204	1/1	0.89	0.26	-	39,39,39,39	0
57	MG	DA	3097	1/1	0.74	0.14	-	47,47,47,47	0
57	MG	DA	3548	1/1	0.94	0.10	-	66,66,66,66	0
57	MG	CA	3043	1/1	0.97	0.17	-	44,44,44,44	0
57	MG	BA	3738	1/1	0.83	0.13	-	41,41,41,41	0
57	MG	AA	1704	1/1	0.88	0.13	-	57,57,57,57	0
57	MG	BA	3709	1/1	0.95	0.34	-	48,48,48,48	0
57	MG	DA	3302	1/1	0.97	0.23	-	53,53,53,53	0
57	MG	DA	3571	1/1	0.93	0.28	-	45,45,45,45	0
57	MG	CA	3052	1/1	0.86	0.12	-	71,71,71,71	0
57	MG	BA	3452	1/1	0.91	0.15	-	56,56,56,56	0
57	MG	AA	1703	1/1	0.97	0.29	-	43,43,43,43	0
57	MG	DA	3501	1/1	0.97	0.10	-	49,49,49,49	0
57	MG	DA	3587	1/1	0.93	0.12	-	51,51,51,51	0
57	MG	BA	3264	1/1	0.90	0.23	-	51,51,51,51	0
57	MG	DA	3448	1/1	0.90	0.10	-	55,55,55,55	0
57	MG	BA	3326	1/1	0.98	0.15	-	24,24,24,24	0
57	MG	DA	3395	1/1	0.81	0.17	-	58,58,58,58	0
57	MG	CA	3066	1/1	0.96	0.14	-	48,48,48,48	0
57	MG	CA	3030	1/1	0.88	0.07	-	74,74,74,74	0
57	MG	DA	3173	1/1	0.85	0.15	-	62,62,62,62	0
57	MG	AA	1722	1/1	0.98	0.18	-	57,57,57,57	0
57	MG	CA	3013	1/1	0.80	0.14	-	67,67,67,67	0
57	MG	BA	3414	1/1	0.90	0.20	-	54,54,54,54	0
57	MG	BA	3396	1/1	0.96	0.23	-	25,25,25,25	0
57	MG	DA	3370	1/1	0.97	0.13	-	59,59,59,59	0
57	MG	BA	3069	1/1	0.94	0.34	-	48,48,48,48	0
57	MG	AA	1645	1/1	0.93	0.15	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3510	1/1	0.95	0.26	-	64,64,64,64	0
57	MG	DA	3380	1/1	0.96	0.05	-	66,66,66,66	0
57	MG	DA	3237	1/1	0.89	0.12	-	59,59,59,59	0
57	MG	BA	3015	1/1	0.77	0.18	-	47,47,47,47	0
57	MG	DA	3261	1/1	0.91	0.16	-	39,39,39,39	0
57	MG	CA	3079	1/1	0.98	0.12	-	49,49,49,49	0
57	MG	DA	3589	1/1	0.95	0.08	-	29,29,29,29	0
57	MG	BA	3196	1/1	0.96	0.23	-	56,56,56,56	0
57	MG	AA	1808	1/1	0.94	0.14	-	49,49,49,49	0
57	MG	BA	3683	1/1	0.97	0.21	-	62,62,62,62	0
57	MG	DA	3626	1/1	0.87	0.11	-	81,81,81,81	0
57	MG	BA	3027	1/1	0.94	0.41	-	64,64,64,64	0
57	MG	DA	3294	1/1	0.97	0.12	-	40,40,40,40	0
57	MG	BA	3193	1/1	0.94	0.13	-	37,37,37,37	0
57	MG	BA	3062	1/1	0.85	0.30	-	59,59,59,59	0
57	MG	DA	3324	1/1	0.88	0.10	-	54,54,54,54	0
57	MG	BA	3282	1/1	0.93	0.24	-	57,57,57,57	0
57	MG	BA	3102	1/1	0.86	0.31	-	57,57,57,57	0
57	MG	DA	3209	1/1	0.99	0.09	-	49,49,49,49	0
57	MG	BA	3097	1/1	0.94	0.12	-	41,41,41,41	0
57	MG	DA	3050	1/1	0.98	0.25	-	44,44,44,44	0
57	MG	BA	3727	1/1	0.71	0.24	-	53,53,53,53	0
57	MG	BA	3667	1/1	0.72	0.24	-	58,58,58,58	0
57	MG	DA	3651	1/1	0.90	0.12	-	48,48,48,48	0
57	MG	DA	3032	1/1	0.76	0.21	-	57,57,57,57	0
57	MG	DA	3506	1/1	0.92	0.08	-	55,55,55,55	0
57	MG	BA	3391	1/1	0.97	0.15	-	41,41,41,41	0
57	MG	BA	3199	1/1	0.95	0.30	-	64,64,64,64	0
57	MG	BA	3733	1/1	0.94	0.15	-	42,42,42,42	0
57	MG	BA	3273	1/1	0.90	0.21	-	45,45,45,45	0
57	MG	AA	1772	1/1	0.99	0.20	-	47,47,47,47	0
57	MG	DA	3092	1/1	0.85	0.16	-	57,57,57,57	0
57	MG	BA	3504	1/1	0.87	0.20	-	56,56,56,56	0
57	MG	BA	3731	1/1	0.99	0.14	-	32,32,32,32	0
57	MG	CW	3001	1/1	0.89	0.19	-	66,66,66,66	0
57	MG	CA	3091	1/1	0.80	0.15	-	69,69,69,69	0
57	MG	BA	3233	1/1	0.83	0.28	-	40,40,40,40	0
57	MG	BA	3649	1/1	0.93	0.14	-	55,55,55,55	0
57	MG	DA	3435	1/1	0.86	0.12	-	44,44,44,44	0
57	MG	BA	3319	1/1	0.96	0.22	-	23,23,23,23	0
57	MG	CA	3041	1/1	0.85	0.11	-	57,57,57,57	0
57	MG	BA	3761	1/1	0.90	0.10	-	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3789	1/1	0.92	0.14	-	47,47,47,47	0
57	MG	DA	3375	1/1	0.88	0.10	-	57,57,57,57	0
57	MG	AA	1710	1/1	0.81	0.15	-	64,64,64,64	0
57	MG	DA	3505	1/1	0.90	0.08	-	51,51,51,51	0
57	MG	BA	3149	1/1	0.87	0.19	-	42,42,42,42	0
57	MG	DA	3271	1/1	0.88	0.16	-	30,30,30,30	0
57	MG	DA	3075	1/1	0.92	0.14	-	55,55,55,55	0
57	MG	AA	1652	1/1	0.89	0.23	-	62,62,62,62	0
57	MG	AA	1707	1/1	0.88	0.12	-	57,57,57,57	0
57	MG	BA	3547	1/1	0.97	0.16	-	45,45,45,45	0
57	MG	DA	3185	1/1	0.95	0.15	-	51,51,51,51	0
57	MG	AA	1719	1/1	0.96	0.16	-	63,63,63,63	0
57	MG	BA	3198	1/1	0.94	0.16	-	44,44,44,44	0
57	MG	DA	3099	1/1	0.69	0.18	-	63,63,63,63	0
57	MG	DA	3212	1/1	0.89	0.23	-	62,62,62,62	0
57	MG	BA	3768	1/1	0.92	0.13	-	57,57,57,57	0
57	MG	DA	3568	1/1	0.84	0.14	-	43,43,43,43	0
57	MG	BA	3603	1/1	0.97	0.28	-	42,42,42,42	0
57	MG	AU	101	1/1	0.97	0.12	-	56,56,56,56	0
57	MG	DA	3485	1/1	0.90	0.09	-	56,56,56,56	0
57	MG	BA	3684	1/1	0.93	0.22	-	51,51,51,51	0
57	MG	BA	3699	1/1	0.93	0.20	-	67,67,67,67	0
57	MG	DA	3650	1/1	0.80	0.14	-	61,61,61,61	0
57	MG	DA	3578	1/1	0.88	0.14	-	43,43,43,43	0
57	MG	BA	3522	1/1	0.89	0.16	-	44,44,44,44	0
57	MG	CA	3141	1/1	0.90	0.14	-	62,62,62,62	0
57	MG	CA	3126	1/1	0.90	0.09	-	45,45,45,45	0
57	MG	BA	3588	1/1	0.87	0.09	-	43,43,43,43	0
57	MG	BA	3127	1/1	0.87	0.30	-	45,45,45,45	0
57	MG	BF	310	1/1	0.82	0.23	-	56,56,56,56	0
57	MG	DN	5001	1/1	0.95	0.11	-	63,63,63,63	0
57	MG	DA	3642	1/1	0.94	0.21	-	62,62,62,62	0
57	MG	BA	3500	1/1	0.92	0.20	-	57,57,57,57	0
57	MG	BA	3803	1/1	0.90	0.34	-	55,55,55,55	0
57	MG	BB	3011	1/1	0.97	0.20	-	47,47,47,47	0
57	MG	BA	3668	1/1	0.86	0.15	-	75,75,75,75	0
57	MG	DA	3461	1/1	0.93	0.13	-	51,51,51,51	0
57	MG	BA	3363	1/1	0.95	0.17	-	52,52,52,52	0
57	MG	BA	3580	1/1	0.95	0.15	-	48,48,48,48	0
57	MG	BA	3138	1/1	0.89	0.15	-	43,43,43,43	0
57	MG	AA	1688	1/1	0.92	0.20	-	66,66,66,66	0
57	MG	DA	3530	1/1	0.82	0.14	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3486	1/1	0.89	0.13	-	57,57,57,57	0
57	MG	AA	1639	1/1	0.91	0.07	-	54,54,54,54	0
57	MG	BA	3415	1/1	0.93	0.23	-	35,35,35,35	0
57	MG	CA	3060	1/1	0.94	0.08	-	71,71,71,71	0
57	MG	AA	1677	1/1	0.98	0.21	-	43,43,43,43	0
57	MG	BA	3693	1/1	0.64	0.16	-	77,77,77,77	0
57	MG	BA	3331	1/1	0.97	0.20	-	53,53,53,53	0
57	MG	BA	3378	1/1	0.91	0.24	-	39,39,39,39	0
57	MG	DA	3520	1/1	0.79	0.11	-	57,57,57,57	0
57	MG	DA	3431	1/1	0.92	0.23	-	42,42,42,42	0
57	MG	BA	3593	1/1	0.83	0.20	-	55,55,55,55	0
57	MG	AA	1656	1/1	0.93	0.16	-	63,63,63,63	0
57	MG	BA	3230	1/1	0.87	0.33	-	58,58,58,58	0
57	MG	DA	3527	1/1	0.95	0.13	-	52,52,52,52	0
57	MG	AA	1636	1/1	0.94	0.31	-	52,52,52,52	0
57	MG	DA	3069	1/1	0.91	0.08	-	43,43,43,43	0
57	MG	BA	3774	1/1	0.95	0.32	-	27,27,27,27	0
57	MG	DA	3152	1/1	0.96	0.17	-	45,45,45,45	0
57	MG	BA	3101	1/1	0.93	0.25	-	37,37,37,37	0
57	MG	DA	3304	1/1	0.97	0.14	-	42,42,42,42	0
57	MG	DA	3144	1/1	0.97	0.23	-	41,41,41,41	0
57	MG	BA	3437	1/1	0.94	0.23	-	62,62,62,62	0
57	MG	BA	3080	1/1	0.95	0.14	-	31,31,31,31	0
57	MG	AA	1699	1/1	0.85	0.32	-	58,58,58,58	0
57	MG	DA	3195	1/1	0.98	0.13	-	42,42,42,42	0
57	MG	BA	3086	1/1	0.92	0.33	-	42,42,42,42	0
57	MG	DA	3639	1/1	0.91	0.18	-	59,59,59,59	0
57	MG	DA	3377	1/1	0.89	0.11	-	50,50,50,50	0
57	MG	CA	3165	1/1	0.93	0.09	-	42,42,42,42	0
57	MG	AA	1659	1/1	0.94	0.19	-	65,65,65,65	0
57	MG	BA	3597	1/1	0.87	0.20	-	55,55,55,55	0
57	MG	DA	3107	1/1	0.91	0.11	-	61,61,61,61	0
57	MG	DA	3002	1/1	0.79	0.14	-	64,64,64,64	0
57	MG	DA	3576	1/1	0.92	0.16	-	67,67,67,67	0
57	MG	BA	3778	1/1	0.84	0.08	-	40,40,40,40	0
57	MG	DA	3585	1/1	0.94	0.26	-	55,55,55,55	0
57	MG	DA	3142	1/1	0.94	0.13	-	51,51,51,51	0
57	MG	BA	3564	1/1	0.87	0.09	-	44,44,44,44	0
57	MG	DA	3004	1/1	0.94	0.20	-	53,53,53,53	0
57	MG	AA	1712	1/1	0.89	0.21	-	69,69,69,69	0
57	MG	BA	3016	1/1	0.75	0.27	-	67,67,67,67	0
57	MG	BA	3611	1/1	0.78	0.18	-	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3236	1/1	0.94	0.13	-	52,52,52,52	0
57	MG	CA	3135	1/1	0.90	0.06	-	59,59,59,59	0
57	MG	DA	3297	1/1	0.98	0.18	-	51,51,51,51	0
57	MG	CA	3005	1/1	0.76	0.20	-	73,73,73,73	0
57	MG	AA	1606	1/1	0.86	0.14	-	54,54,54,54	0
57	MG	BA	3325	1/1	0.89	0.15	-	45,45,45,45	0
57	MG	DA	3584	1/1	0.98	0.09	-	31,31,31,31	0
57	MG	AA	1714	1/1	0.91	0.20	-	56,56,56,56	0
57	MG	DB	3005	1/1	0.88	0.12	-	68,68,68,68	0
57	MG	DA	3451	1/1	0.89	0.08	-	55,55,55,55	0
57	MG	AA	1760	1/1	0.96	0.15	-	65,65,65,65	0
57	MG	BA	3538	1/1	0.74	0.12	-	68,68,68,68	0
57	MG	CA	3120	1/1	0.93	0.12	-	68,68,68,68	0
57	MG	BA	3599	1/1	0.93	0.16	-	60,60,60,60	0
57	MG	CA	3068	1/1	0.85	0.16	-	58,58,58,58	0
57	MG	BA	3471	1/1	0.95	0.18	-	27,27,27,27	0
57	MG	DA	3541	1/1	0.88	0.10	-	59,59,59,59	0
57	MG	AA	1690	1/1	0.93	0.42	-	52,52,52,52	0
57	MG	DA	3054	1/1	0.98	0.10	-	27,27,27,27	0
57	MG	DA	3550	1/1	0.91	0.04	-	60,60,60,60	0
57	MG	BA	3352	1/1	0.96	0.16	-	68,68,68,68	0
57	MG	DA	3383	1/1	0.99	0.13	-	28,28,28,28	0
57	MG	BA	3679	1/1	0.94	0.22	-	52,52,52,52	0
57	MG	BA	3227	1/1	0.97	0.17	-	33,33,33,33	0
57	MG	BZ	302	1/1	0.92	0.17	-	60,60,60,60	0
57	MG	DA	3407	1/1	0.92	0.08	-	58,58,58,58	0
57	MG	BA	3212	1/1	0.87	0.21	-	57,57,57,57	0
57	MG	AA	1667	1/1	0.85	0.19	-	55,55,55,55	0
57	MG	AA	1657	1/1	0.93	0.12	-	64,64,64,64	0
57	MG	DA	3484	1/1	0.96	0.07	-	46,46,46,46	0
57	MG	DA	3419	1/1	0.94	0.14	-	50,50,50,50	0
57	MG	BA	3446	1/1	0.91	0.09	-	59,59,59,59	0
57	MG	BA	3258	1/1	0.95	0.35	-	44,44,44,44	0
57	MG	DA	3041	1/1	0.78	0.18	-	60,60,60,60	0
57	MG	BA	3262	1/1	0.96	0.27	-	31,31,31,31	0
57	MG	BA	3474	1/1	0.94	0.27	-	33,33,33,33	0
57	MG	DA	3345	1/1	0.98	0.15	-	58,58,58,58	0
57	MG	BA	3663	1/1	0.92	0.20	-	50,50,50,50	0
57	MG	DA	3242	1/1	0.92	0.09	-	52,52,52,52	0
57	MG	DA	3567	1/1	0.94	0.26	-	44,44,44,44	0
57	MG	B0	3002	1/1	0.88	0.21	-	63,63,63,63	0
57	MG	DA	3061	1/1	0.76	0.22	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3013	1/1	0.96	0.20	-	28,28,28,28	0
57	MG	AX	3010	1/1	0.88	0.40	-	68,68,68,68	0
57	MG	BA	3218	1/1	0.93	0.15	-	45,45,45,45	0
57	MG	DA	3472	1/1	0.99	0.14	-	25,25,25,25	0
57	MG	DA	3631	1/1	0.94	0.12	-	49,49,49,49	0
57	MG	DA	3269	1/1	0.95	0.11	-	50,50,50,50	0
57	MG	AA	1786	1/1	0.95	0.14	-	69,69,69,69	0
57	MG	BA	3354	1/1	0.95	0.12	-	47,47,47,47	0
57	MG	AA	1609	1/1	0.91	0.13	-	63,63,63,63	0
57	MG	DA	3104	1/1	0.92	0.11	-	57,57,57,57	0
57	MG	DA	3157	1/1	0.96	0.13	-	34,34,34,34	0
57	MG	BA	3228	1/1	0.95	0.10	-	65,65,65,65	0
57	MG	BA	3453	1/1	0.81	0.28	-	50,50,50,50	0
57	MG	AA	1648	1/1	0.92	0.19	-	56,56,56,56	0
57	MG	DA	3339	1/1	0.92	0.20	-	52,52,52,52	0
57	MG	AA	1709	1/1	0.95	0.26	-	55,55,55,55	0
57	MG	BA	3166	1/1	0.90	0.18	-	33,33,33,33	0
57	MG	BA	3068	1/1	0.71	0.17	-	49,49,49,49	0
57	MG	AA	1664	1/1	0.83	0.22	-	62,62,62,62	0
57	MG	BA	3243	1/1	0.86	0.67	-	44,44,44,44	0
57	MG	BA	3596	1/1	0.94	0.17	-	59,59,59,59	0
57	MG	DB	3006	1/1	0.94	0.14	-	55,55,55,55	0
57	MG	BA	3381	1/1	0.88	0.11	-	49,49,49,49	0
57	MG	DA	3326	1/1	0.97	0.10	-	46,46,46,46	0
57	MG	CA	3102	1/1	0.82	0.16	-	71,71,71,71	0
57	MG	AA	1642	1/1	0.97	0.23	-	59,59,59,59	0
57	MG	DA	3204	1/1	0.60	0.21	-	68,68,68,68	0
57	MG	BA	3317	1/1	0.94	0.20	-	43,43,43,43	0
57	MG	DA	3244	1/1	0.90	0.27	-	55,55,55,55	0
57	MG	AA	1668	1/1	0.97	0.10	-	63,63,63,63	0
57	MG	CA	3133	1/1	0.97	0.17	-	82,82,82,82	0
57	MG	DA	3117	1/1	0.96	0.09	-	56,56,56,56	0
57	MG	BA	3542	1/1	0.92	0.16	-	44,44,44,44	0
57	MG	BA	3005	1/1	0.86	0.19	-	44,44,44,44	0
57	MG	CA	3115	1/1	0.58	0.34	-	82,82,82,82	0
57	MG	BP	3002	1/1	0.89	0.14	-	60,60,60,60	0
57	MG	DA	3390	1/1	0.86	0.10	-	58,58,58,58	0
57	MG	BA	3010	1/1	0.92	0.18	-	53,53,53,53	0
57	MG	BA	3791	1/1	0.96	0.38	-	49,49,49,49	0
57	MG	BA	3274	1/1	0.90	0.27	-	66,66,66,66	0
57	MG	BA	3740	1/1	0.91	0.19	-	65,65,65,65	0
57	MG	AA	1602	1/1	0.85	0.10	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3429	1/1	0.90	0.26	-	50,50,50,50	0
57	MG	BA	3551	1/1	0.99	0.15	-	44,44,44,44	0
57	MG	DA	3582	1/1	0.92	0.05	-	53,53,53,53	0
57	MG	DA	3289	1/1	0.88	0.16	-	52,52,52,52	0
57	MG	BA	3106	1/1	0.87	0.25	-	52,52,52,52	0
57	MG	BA	3339	1/1	0.98	0.21	-	43,43,43,43	0
57	MG	BA	3298	1/1	0.94	0.15	-	27,27,27,27	0
57	MG	BA	3209	1/1	0.91	0.24	-	48,48,48,48	0
57	MG	BA	3265	1/1	0.74	0.29	-	72,72,72,72	0
57	MG	CA	3028	1/1	0.96	0.27	-	48,48,48,48	0
57	MG	DA	3600	1/1	0.87	0.13	-	72,72,72,72	0
57	MG	DA	3379	1/1	0.84	0.09	-	46,46,46,46	0
57	MG	DA	3112	1/1	0.86	0.13	-	56,56,56,56	0
57	MG	BA	3720	1/1	0.96	0.12	-	38,38,38,38	0
57	MG	DA	3330	1/1	0.86	0.17	-	36,36,36,36	0
57	MG	DA	3008	1/1	0.85	0.12	-	45,45,45,45	0
57	MG	BA	3729	1/1	0.92	0.14	-	46,46,46,46	0
57	MG	AA	1816	1/1	0.90	0.20	-	59,59,59,59	0
57	MG	BA	3431	1/1	0.92	0.28	-	57,57,57,57	0
57	MG	AA	1732	1/1	0.98	0.20	-	63,63,63,63	0
57	MG	DA	3171	1/1	0.95	0.17	-	40,40,40,40	0
57	MG	BA	3641	1/1	0.92	0.18	-	68,68,68,68	0
57	MG	DA	3015	1/1	0.78	0.23	-	60,60,60,60	0
57	MG	DB	3009	1/1	0.94	0.14	-	58,58,58,58	0
57	MG	AA	1614	1/1	0.87	0.19	-	75,75,75,75	0
57	MG	DA	3281	1/1	0.85	0.11	-	36,36,36,36	0
57	MG	BA	3285	1/1	0.96	0.15	-	58,58,58,58	0
57	MG	BA	3480	1/1	0.94	0.18	-	47,47,47,47	0
57	MG	DA	3180	1/1	0.97	0.21	-	48,48,48,48	0
57	MG	B8	5001	1/1	0.94	0.20	-	42,42,42,42	0
57	MG	BA	3290	1/1	0.92	0.21	-	57,57,57,57	0
57	MG	DA	3408	1/1	0.98	0.23	-	55,55,55,55	0
57	MG	DA	3622	1/1	0.93	0.10	-	49,49,49,49	0
57	MG	DA	3025	1/1	0.98	0.45	-	47,47,47,47	0
57	MG	BA	3322	1/1	0.93	0.16	-	38,38,38,38	0
57	MG	DA	3614	1/1	0.91	0.14	-	55,55,55,55	0
57	MG	DA	3058	1/1	0.96	0.08	-	61,61,61,61	0
57	MG	BA	3428	1/1	0.93	0.16	-	51,51,51,51	0
57	MG	DA	3640	1/1	0.97	0.10	-	62,62,62,62	0
57	MG	BA	3205	1/1	0.96	0.43	-	57,57,57,57	0
57	MG	BA	3047	1/1	0.93	0.22	-	43,43,43,43	0
57	MG	AA	1780	1/1	0.94	0.11	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3010	1/1	0.99	0.10	-	49,49,49,49	0
57	MG	BA	3259	1/1	0.98	0.18	-	25,25,25,25	0
57	MG	BA	3267	1/1	0.98	0.30	-	61,61,61,61	0
57	MG	BA	3531	1/1	0.91	0.14	-	60,60,60,60	0
57	MG	BA	3677	1/1	0.94	0.10	-	44,44,44,44	0
57	MG	BA	3613	1/1	0.91	0.23	-	53,53,53,53	0
57	MG	BA	3654	1/1	0.96	0.11	-	59,59,59,59	0
57	MG	DA	3468	1/1	0.82	0.14	-	62,62,62,62	0
57	MG	DA	3369	1/1	0.83	0.12	-	55,55,55,55	0
57	MG	DA	3374	1/1	0.92	0.22	-	62,62,62,62	0
57	MG	CA	3025	1/1	0.93	0.24	-	53,53,53,53	0
57	MG	AA	1792	1/1	0.98	0.12	-	47,47,47,47	0
57	MG	DA	3166	1/1	0.94	0.16	-	55,55,55,55	0
57	MG	CA	3021	1/1	0.91	0.10	-	61,61,61,61	0
57	MG	BA	3385	1/1	0.97	0.23	-	30,30,30,30	0
57	MG	BA	3472	1/1	0.98	0.20	-	24,24,24,24	0
57	MG	BA	3019	1/1	0.91	0.28	-	54,54,54,54	0
57	MG	AA	1784	1/1	0.34	0.29	-	72,72,72,72	0
57	MG	DA	3329	1/1	0.95	0.10	-	47,47,47,47	0
57	MG	AA	1728	1/1	0.94	0.25	-	49,49,49,49	0
57	MG	DA	3555	1/1	0.95	0.21	-	46,46,46,46	0
57	MG	AA	1612	1/1	0.85	0.16	-	63,63,63,63	0
57	MG	DA	3566	1/1	0.92	0.18	-	37,37,37,37	0
57	MG	BA	3025	1/1	0.92	0.18	-	43,43,43,43	0
57	MG	AA	1783	1/1	0.95	0.17	-	35,35,35,35	0
57	MG	BA	3620	1/1	0.94	0.14	-	29,29,29,29	0
57	MG	BB	3019	1/1	0.83	0.20	-	70,70,70,70	0
57	MG	DA	3306	1/1	0.88	0.28	-	65,65,65,65	0
57	MG	CA	3157	1/1	0.86	0.12	-	60,60,60,60	0
57	MG	DA	3051	1/1	0.88	0.13	-	44,44,44,44	0
57	MG	BA	3145	1/1	0.84	0.25	-	48,48,48,48	0
57	MG	BA	3301	1/1	0.93	0.18	-	62,62,62,62	0
57	MG	DA	3067	1/1	0.87	0.14	-	63,63,63,63	0
57	MG	AA	1802	1/1	0.93	0.10	-	54,54,54,54	0
57	MG	BA	3049	1/1	0.84	0.19	-	46,46,46,46	0
57	MG	CA	3007	1/1	0.88	0.12	-	51,51,51,51	0
57	MG	BA	3201	1/1	0.96	0.21	-	48,48,48,48	0
57	MG	DA	3235	1/1	0.86	0.13	-	48,48,48,48	0
57	MG	DA	3403	1/1	0.91	0.09	-	49,49,49,49	0
57	MG	BA	3651	1/1	0.93	0.14	-	66,66,66,66	0
57	MG	BA	3241	1/1	0.94	0.16	-	56,56,56,56	0
57	MG	BA	3479	1/1	0.95	0.06	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3643	1/1	0.92	0.07	-	54,54,54,54	0
57	MG	AA	1796	1/1	0.97	0.07	-	64,64,64,64	0
57	MG	DA	3646	1/1	0.93	0.15	-	56,56,56,56	0
57	MG	DA	3017	1/1	0.88	0.12	-	59,59,59,59	0
57	MG	BA	3404	1/1	0.90	0.34	-	59,59,59,59	0
57	MG	DA	3603	1/1	0.87	0.06	-	65,65,65,65	0
57	MG	DA	3066	1/1	0.77	0.10	-	58,58,58,58	0
57	MG	BA	3722	1/1	0.94	0.19	-	64,64,64,64	0
57	MG	CA	3022	1/1	0.88	0.23	-	76,76,76,76	0
57	MG	BA	3563	1/1	0.92	0.12	-	50,50,50,50	0
57	MG	DA	3615	1/1	0.98	0.09	-	62,62,62,62	0
57	MG	BA	3669	1/1	0.97	0.20	-	28,28,28,28	0
57	MG	CA	3014	1/1	0.76	0.15	-	62,62,62,62	0
57	MG	DA	3251	1/1	0.94	0.15	-	40,40,40,40	0
57	MG	DA	3127	1/1	0.91	0.10	-	52,52,52,52	0
57	MG	AA	1689	1/1	0.77	0.29	-	71,71,71,71	0
57	MG	DA	3098	1/1	0.96	0.10	-	66,66,66,66	0
57	MG	BA	3718	1/1	0.99	0.17	-	47,47,47,47	0
57	MG	CA	3055	1/1	0.91	0.18	-	63,63,63,63	0
57	MG	DA	3569	1/1	0.92	0.24	-	45,45,45,45	0
57	MG	BA	3292	1/1	0.94	0.24	-	26,26,26,26	0
57	MG	CA	3105	1/1	0.97	0.12	-	75,75,75,75	0
57	MG	BA	3208	1/1	0.95	0.10	-	43,43,43,43	0
57	MG	BA	3661	1/1	0.93	0.24	-	25,25,25,25	0
57	MG	AA	1643	1/1	0.91	0.20	-	58,58,58,58	0
57	MG	AA	1807	1/1	0.95	0.07	-	68,68,68,68	0
57	MG	DA	3276	1/1	0.96	0.16	-	28,28,28,28	0
57	MG	CA	3138	1/1	0.96	0.10	-	65,65,65,65	0
57	MG	BA	3074	1/1	0.78	0.23	-	69,69,69,69	0
57	MG	DA	3016	1/1	0.79	0.09	-	66,66,66,66	0
57	MG	AA	1618	1/1	0.55	0.18	-	68,68,68,68	0
57	MG	BA	3303	1/1	0.93	0.23	-	26,26,26,26	0
57	MG	DA	3227	1/1	0.83	0.20	-	56,56,56,56	0
57	MG	DB	3010	1/1	0.83	0.13	-	75,75,75,75	0
57	MG	BA	3705	1/1	0.89	0.14	-	59,59,59,59	0
57	MG	DA	3084	1/1	0.91	0.17	-	44,44,44,44	0
57	MG	AA	1626	1/1	0.89	0.21	-	59,59,59,59	0
57	MG	BA	3670	1/1	0.81	0.18	-	54,54,54,54	0
57	MG	AA	1778	1/1	0.92	0.09	-	51,51,51,51	0
57	MG	DA	3071	1/1	0.73	0.23	-	47,47,47,47	0
57	MG	BA	3192	1/1	0.94	0.20	-	19,19,19,19	0
57	MG	BA	3238	1/1	0.95	0.48	-	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3317	1/1	0.85	0.10	-	54,54,54,54	0
57	MG	BA	3338	1/1	0.86	0.18	-	55,55,55,55	0
57	MG	AA	1736	1/1	0.96	0.10	-	49,49,49,49	0
57	MG	DA	3366	1/1	0.92	0.12	-	44,44,44,44	0
57	MG	AA	1638	1/1	0.93	0.23	-	60,60,60,60	0
57	MG	BB	3002	1/1	0.98	0.28	-	55,55,55,55	0
57	MG	BA	3126	1/1	0.91	0.23	-	36,36,36,36	0
57	MG	AA	1698	1/1	0.94	0.23	-	58,58,58,58	0
57	MG	DA	3287	1/1	0.95	0.21	-	52,52,52,52	0
57	MG	DA	3076	1/1	0.95	0.18	-	52,52,52,52	0
57	MG	DA	3415	1/1	0.85	0.18	-	43,43,43,43	0
57	MG	DA	3101	1/1	0.82	0.13	-	56,56,56,56	0
57	MG	CA	3128	1/1	0.97	0.13	-	52,52,52,52	0
57	MG	DA	3336	1/1	0.90	0.09	-	49,49,49,49	0
57	MG	BA	3178	1/1	0.95	0.17	-	32,32,32,32	0
57	MG	AA	1700	1/1	0.95	0.07	-	71,71,71,71	0
57	MG	DA	3122	1/1	0.70	0.19	-	60,60,60,60	0
57	MG	BA	3095	1/1	0.94	0.23	-	53,53,53,53	0
57	MG	DA	3021	1/1	0.89	0.17	-	50,50,50,50	0
57	MG	BA	3569	1/1	0.69	0.22	-	56,56,56,56	0
57	MG	DA	3502	1/1	0.75	0.24	-	48,48,48,48	0
57	MG	AA	1790	1/1	0.93	0.08	-	81,81,81,81	0
57	MG	DA	3446	1/1	0.90	0.14	-	50,50,50,50	0
57	MG	DA	3202	1/1	0.94	0.20	-	62,62,62,62	0
57	MG	DA	3168	1/1	0.98	0.12	-	44,44,44,44	0
57	MG	DP	201	1/1	0.87	0.21	-	69,69,69,69	0
57	MG	CA	3001	1/1	0.84	0.14	-	59,59,59,59	0
57	MG	BF	311	1/1	0.92	0.12	-	52,52,52,52	0
57	MG	DA	3335	1/1	0.93	0.25	-	49,49,49,49	0
57	MG	AA	1708	1/1	0.89	0.19	-	60,60,60,60	0
57	MG	DA	3299	1/1	0.95	0.09	-	46,46,46,46	0
57	MG	BA	3786	1/1	0.90	0.16	-	51,51,51,51	0
57	MG	AX	3008	1/1	0.88	0.15	-	76,76,76,76	0
57	MG	BA	3627	1/1	0.97	0.20	-	56,56,56,56	0
57	MG	DA	3136	1/1	0.86	0.18	-	48,48,48,48	0
57	MG	CA	3084	1/1	0.97	0.14	-	56,56,56,56	0
57	MG	BA	3128	1/1	0.91	0.19	-	42,42,42,42	0
57	MG	BA	3134	1/1	0.92	0.18	-	40,40,40,40	0
57	MG	BA	3125	1/1	0.89	0.25	-	38,38,38,38	0
57	MG	DA	3535	1/1	0.94	0.18	-	44,44,44,44	0
57	MG	DA	3024	1/1	0.80	0.41	-	61,61,61,61	0
57	MG	BA	3489	1/1	0.94	0.25	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AE	3001	1/1	0.96	0.07	-	63,63,63,63	0
57	MG	BA	3604	1/1	0.87	0.19	-	43,43,43,43	0
57	MG	DA	3088	1/1	0.86	0.25	-	50,50,50,50	0
57	MG	BA	3465	1/1	0.95	0.09	-	48,48,48,48	0
57	MG	CA	3152	1/1	0.91	0.10	-	71,71,71,71	0
57	MG	DA	3205	1/1	0.82	0.16	-	62,62,62,62	0
57	MG	BA	3466	1/1	0.96	0.17	-	51,51,51,51	0
57	MG	BA	3108	1/1	0.96	0.21	-	42,42,42,42	0
57	MG	CA	3107	1/1	0.85	0.12	-	68,68,68,68	0
57	MG	DE	3003	1/1	0.94	0.12	-	43,43,43,43	0
57	MG	BA	3293	1/1	0.95	0.11	-	58,58,58,58	0
57	MG	DA	3199	1/1	0.69	0.24	-	62,62,62,62	0
57	MG	DA	3165	1/1	0.95	0.20	-	55,55,55,55	0
57	MG	AA	1716	1/1	0.96	0.17	-	50,50,50,50	0
57	MG	BA	3394	1/1	0.94	0.28	-	40,40,40,40	0
57	MG	BA	3662	1/1	0.92	0.22	-	62,62,62,62	0
57	MG	BA	3436	1/1	0.92	0.15	-	57,57,57,57	0
57	MG	BA	3014	1/1	0.88	0.14	-	35,35,35,35	0
57	MG	BA	3590	1/1	0.96	0.15	-	33,33,33,33	0
57	MG	B5	104	1/1	0.97	0.09	-	58,58,58,58	0
57	MG	BA	3601	1/1	0.94	0.31	-	40,40,40,40	0
57	MG	BA	3305	1/1	0.92	0.15	-	46,46,46,46	0
57	MG	BA	3666	1/1	0.88	0.26	-	74,74,74,74	0
57	MG	CA	3008	1/1	0.89	0.31	-	47,47,47,47	0
57	MG	CA	3150	1/1	0.93	0.15	-	65,65,65,65	0
57	MG	DA	3376	1/1	0.74	0.11	-	51,51,51,51	0
57	MG	DA	3293	1/1	0.96	0.15	-	61,61,61,61	0
57	MG	BA	3316	1/1	0.97	0.20	-	54,54,54,54	0
57	MG	BB	3015	1/1	0.96	0.26	-	45,45,45,45	0
57	MG	BA	3555	1/1	0.94	0.19	-	50,50,50,50	0
57	MG	DA	3218	1/1	0.88	0.17	-	52,52,52,52	0
57	MG	AA	1705	1/1	0.91	0.23	-	70,70,70,70	0
57	MG	CA	3127	1/1	0.93	0.08	-	59,59,59,59	0
57	MG	BA	3257	1/1	0.81	0.18	-	43,43,43,43	0
57	MG	BA	3495	1/1	0.95	0.16	-	43,43,43,43	0
57	MG	BA	3721	1/1	0.80	0.10	-	47,47,47,47	0
57	MG	DA	3082	1/1	0.95	0.22	-	47,47,47,47	0
57	MG	BA	3658	1/1	0.90	0.12	-	61,61,61,61	0
57	MG	BA	3284	1/1	0.95	0.10	-	57,57,57,57	0
57	MG	BA	3320	1/1	0.94	0.16	-	55,55,55,55	0
57	MG	DA	3618	1/1	0.83	0.10	-	46,46,46,46	0
57	MG	DA	3044	1/1	0.96	0.18	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	1634	1/1	0.87	0.15	-	64,64,64,64	0
57	MG	BA	3250	1/1	0.86	0.21	-	68,68,68,68	0
57	MG	DA	3546	1/1	0.98	0.04	-	47,47,47,47	0
57	MG	BA	3087	1/1	0.90	0.38	-	43,43,43,43	0
57	MG	BA	3734	1/1	0.57	0.14	-	65,65,65,65	0
57	MG	BA	3675	1/1	0.94	0.26	-	56,56,56,56	0
57	MG	BA	3279	1/1	0.93	0.32	-	52,52,52,52	0
57	MG	DA	3273	1/1	0.93	0.12	-	62,62,62,62	0
57	MG	DA	3405	1/1	0.92	0.07	-	47,47,47,47	0
57	MG	DA	3208	1/1	0.88	0.16	-	54,54,54,54	0
57	MG	DA	3462	1/1	0.85	0.22	-	50,50,50,50	0
57	MG	BA	3726	1/1	0.86	0.20	-	31,31,31,31	0
57	MG	B2	3001	1/1	0.87	0.25	-	53,53,53,53	0
57	MG	BA	3351	1/1	0.94	0.19	-	45,45,45,45	0
57	MG	BA	3245	1/1	0.87	0.32	-	59,59,59,59	0
57	MG	BA	3150	1/1	0.93	0.17	-	39,39,39,39	0
57	MG	DA	3445	1/1	0.88	0.13	-	52,52,52,52	0
57	MG	BA	3455	1/1	0.95	0.14	-	52,52,52,52	0
57	MG	DA	3047	1/1	0.94	0.16	-	45,45,45,45	0
57	MG	CA	3080	1/1	0.98	0.10	-	49,49,49,49	0
57	MG	BE	304	1/1	0.93	0.23	-	23,23,23,23	0
57	MG	DA	3378	1/1	0.95	0.14	-	52,52,52,52	0
57	MG	DA	3222	1/1	0.93	0.23	-	58,58,58,58	0
57	MG	DA	3224	1/1	0.95	0.08	-	39,39,39,39	0
57	MG	BA	3130	1/1	0.96	0.46	-	48,48,48,48	0
57	MG	AA	1651	1/1	0.87	0.25	-	58,58,58,58	0
57	MG	BA	3763	1/1	0.88	0.15	-	44,44,44,44	0
57	MG	DA	3609	1/1	0.94	0.10	-	61,61,61,61	0
57	MG	CA	3129	1/1	0.88	0.13	-	69,69,69,69	0
57	MG	BA	3691	1/1	0.95	0.11	-	43,43,43,43	0
57	MG	DA	3110	1/1	0.90	0.10	-	49,49,49,49	0
57	MG	BA	3809	1/1	0.84	0.37	-	61,61,61,61	0
57	MG	BA	3521	1/1	0.96	0.22	-	40,40,40,40	0
57	MG	DA	3079	1/1	0.77	0.11	-	72,72,72,72	0
57	MG	DA	3249	1/1	0.93	0.08	-	65,65,65,65	0
57	MG	CA	3058	1/1	0.72	0.19	-	66,66,66,66	0
57	MG	AA	1605	1/1	0.88	0.15	-	50,50,50,50	0
57	MG	BB	3022	1/1	0.92	0.20	-	60,60,60,60	0
57	MG	DA	3030	1/1	0.91	0.17	-	44,44,44,44	0
57	MG	BA	3562	1/1	0.94	0.16	-	55,55,55,55	0
57	MG	BA	3638	1/1	0.88	0.17	-	65,65,65,65	0
57	MG	DA	3254	1/1	0.43	0.15	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3257	1/1	0.82	0.20	-	44,44,44,44	0
57	MG	DA	3406	1/1	0.90	0.17	-	70,70,70,70	0
57	MG	BA	3421	1/1	0.95	0.26	-	62,62,62,62	0
57	MG	DY	502	1/1	0.93	0.17	-	55,55,55,55	0
57	MG	DA	3575	1/1	0.92	0.08	-	56,56,56,56	0
57	MG	DA	3344	1/1	0.91	0.14	-	38,38,38,38	0
57	MG	DA	3475	1/1	0.94	0.17	-	56,56,56,56	0
57	MG	BA	3077	1/1	0.97	0.20	-	15,15,15,15	0
57	MG	BA	3655	1/1	0.69	0.13	-	55,55,55,55	0
57	MG	DA	3270	1/1	0.96	0.09	-	42,42,42,42	0
57	MG	DA	3172	1/1	0.86	0.21	-	61,61,61,61	0
57	MG	BA	3517	1/1	0.91	0.23	-	33,33,33,33	0
57	MG	DA	3033	1/1	0.60	0.49	-	68,68,68,68	0
57	MG	BA	3042	1/1	0.95	0.13	-	37,37,37,37	0
57	MG	CA	3148	1/1	0.89	0.15	-	68,68,68,68	0
57	MG	AA	1810	1/1	0.82	0.09	-	86,86,86,86	0
57	MG	AA	1661	1/1	0.97	0.37	-	54,54,54,54	0
57	MG	BA	3367	1/1	0.89	0.22	-	52,52,52,52	0
57	MG	BA	3104	1/1	0.99	0.19	-	24,24,24,24	0
57	MG	BA	3703	1/1	0.94	0.33	-	28,28,28,28	0
57	MG	BA	3066	1/1	0.93	0.24	-	58,58,58,58	0
57	MG	AA	1654	1/1	0.93	0.23	-	65,65,65,65	0
57	MG	DA	3396	1/1	0.93	0.17	-	46,46,46,46	0
57	MG	BA	3157	1/1	0.97	0.20	-	46,46,46,46	0
57	MG	BA	3165	1/1	0.95	0.31	-	52,52,52,52	0
57	MG	DA	3138	1/1	0.94	0.14	-	54,54,54,54	0
57	MG	BA	3785	1/1	0.93	0.14	-	56,56,56,56	0
57	MG	DA	3081	1/1	0.91	0.11	-	51,51,51,51	0
57	MG	BA	3463	1/1	0.97	0.21	-	56,56,56,56	0
57	MG	DA	3145	1/1	0.95	0.32	-	48,48,48,48	0
57	MG	DA	3055	1/1	0.90	0.14	-	53,53,53,53	0
57	MG	BA	3478	1/1	0.95	0.15	-	54,54,54,54	0
57	MG	DB	3012	1/1	0.88	0.24	-	66,66,66,66	0
57	MG	BA	3659	1/1	0.93	0.11	-	47,47,47,47	0
57	MG	AA	1799	1/1	0.92	0.11	-	78,78,78,78	0
57	MG	BA	3707	1/1	0.99	0.19	-	39,39,39,39	0
57	MG	BA	3501	1/1	0.89	0.14	-	42,42,42,42	0
57	MG	BA	3084	1/1	0.94	0.18	-	42,42,42,42	0
57	MG	DA	3540	1/1	0.94	0.06	-	50,50,50,50	0
57	MG	AA	1610	1/1	0.79	0.18	-	81,81,81,81	0
57	MG	BA	3287	1/1	0.97	0.17	-	27,27,27,27	0
57	MG	DA	3508	1/1	0.88	0.18	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3177	1/1	0.93	0.13	-	58,58,58,58	0
57	MG	DA	3125	1/1	0.89	0.14	-	56,56,56,56	0
57	MG	DA	3495	1/1	0.97	0.05	-	50,50,50,50	0
57	MG	DA	3062	1/1	0.97	0.11	-	53,53,53,53	0
57	MG	BA	3170	1/1	0.92	0.17	-	38,38,38,38	0
57	MG	BA	3535	1/1	0.91	0.20	-	39,39,39,39	0
57	MG	DA	3348	1/1	0.97	0.20	-	53,53,53,53	0
57	MG	BB	3018	1/1	0.95	0.06	-	54,54,54,54	0
57	MG	DA	3221	1/1	0.96	0.10	-	41,41,41,41	0
57	MG	BA	3361	1/1	0.96	0.08	-	56,56,56,56	0
57	MG	BA	3612	1/1	0.97	0.10	-	60,60,60,60	0
57	MG	BA	3449	1/1	0.93	0.23	-	62,62,62,62	0
57	MG	BA	3058	1/1	0.82	0.19	-	54,54,54,54	0
57	MG	DA	3150	1/1	0.87	0.16	-	50,50,50,50	0
57	MG	AA	1646	1/1	0.94	0.23	-	58,58,58,58	0
57	MG	BA	3753	1/1	0.95	0.19	-	68,68,68,68	0
57	MG	DA	3423	1/1	0.95	0.20	-	37,37,37,37	0
57	MG	DA	3248	1/1	0.97	0.11	-	58,58,58,58	0
57	MG	AA	1715	1/1	0.94	0.23	-	45,45,45,45	0
57	MG	DA	3628	1/1	0.57	0.19	-	77,77,77,77	0
57	MG	AA	1734	1/1	0.96	0.13	-	43,43,43,43	0
57	MG	AA	1696	1/1	0.84	0.10	-	83,83,83,83	0
57	MG	DA	3038	1/1	0.95	0.14	-	56,56,56,56	0
57	MG	BA	3594	1/1	0.88	0.14	-	45,45,45,45	0
57	MG	DA	3496	1/1	0.95	0.17	-	56,56,56,56	0
57	MG	CA	3139	1/1	0.86	0.36	-	81,81,81,81	0
57	MG	DA	3517	1/1	0.94	0.12	-	48,48,48,48	0
57	MG	BA	3357	1/1	0.97	0.07	-	34,34,34,34	0
57	MG	BA	3660	1/1	0.87	0.19	-	60,60,60,60	0
57	MG	DA	3563	1/1	0.93	0.10	-	70,70,70,70	0
57	MG	AA	1711	1/1	0.79	0.13	-	51,51,51,51	0
57	MG	BA	3801	1/1	0.95	0.16	-	71,71,71,71	0
57	MG	DA	3647	1/1	0.96	0.11	-	52,52,52,52	0
57	MG	AA	1803	1/1	0.97	0.12	-	46,46,46,46	0
57	MG	BA	3631	1/1	0.90	0.26	-	46,46,46,46	0
57	MG	CA	3064	1/1	0.92	0.21	-	55,55,55,55	0
57	MG	AA	1623	1/1	0.81	0.24	-	65,65,65,65	0
57	MG	BA	3757	1/1	0.93	0.18	-	43,43,43,43	0
57	MG	DA	3131	1/1	0.93	0.25	-	49,49,49,49	0
57	MG	BA	3481	1/1	0.95	0.12	-	54,54,54,54	0
57	MG	BA	3173	1/1	0.98	0.28	-	32,32,32,32	0
57	MG	BA	3568	1/1	0.96	0.23	-	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3592	1/1	0.82	0.14	-	67,67,67,67	0
57	MG	AA	1718	1/1	0.98	0.11	-	66,66,66,66	0
57	MG	BA	3539	1/1	0.98	0.14	-	42,42,42,42	0
57	MG	CA	3145	1/1	0.98	0.12	-	65,65,65,65	0
57	MG	DA	3200	1/1	0.88	0.16	-	41,41,41,41	0
57	MG	BA	3360	1/1	0.86	0.23	-	37,37,37,37	0
57	MG	DA	3295	1/1	0.95	0.20	-	67,67,67,67	0
57	MG	BA	3491	1/1	0.89	0.22	-	56,56,56,56	0
57	MG	AA	1781	1/1	0.91	0.10	-	59,59,59,59	0
57	MG	CA	3034	1/1	0.89	0.23	-	66,66,66,66	0
57	MG	BA	3213	1/1	0.95	0.15	-	43,43,43,43	0
57	MG	DA	3537	1/1	0.97	0.16	-	45,45,45,45	0
57	MG	BA	3673	1/1	0.93	0.28	-	61,61,61,61	0
57	MG	BA	3304	1/1	0.93	0.18	-	39,39,39,39	0
57	MG	DA	3243	1/1	0.90	0.12	-	48,48,48,48	0
57	MG	BW	3004	1/1	0.91	0.19	-	45,45,45,45	0
57	MG	DA	3153	1/1	0.86	0.15	-	44,44,44,44	0
57	MG	DA	3007	1/1	0.97	0.13	-	30,30,30,30	0
57	MG	DA	3638	1/1	0.96	0.09	-	47,47,47,47	0
57	MG	BA	3146	1/1	0.98	0.17	-	41,41,41,41	0
57	MG	BA	3758	1/1	0.94	0.12	-	41,41,41,41	0
57	MG	AX	3016	1/1	0.82	0.61	-	86,86,86,86	0
57	MG	AA	1733	1/1	0.94	0.12	-	50,50,50,50	0
57	MG	BA	3162	1/1	0.97	0.29	-	41,41,41,41	0
57	MG	B6	103	1/1	0.93	0.15	-	52,52,52,52	0
57	MG	BA	3800	1/1	0.99	0.18	-	29,29,29,29	0
57	MG	AX	3014	1/1	0.93	0.24	-	61,61,61,61	0
57	MG	DA	3518	1/1	0.97	0.10	-	56,56,56,56	0
57	MG	BA	3160	1/1	0.80	0.20	-	49,49,49,49	0
57	MG	DA	3263	1/1	0.96	0.13	-	65,65,65,65	0
57	MG	CA	3033	1/1	0.95	0.10	-	54,54,54,54	0
57	MG	DA	3543	1/1	0.92	0.14	-	64,64,64,64	0
57	MG	BA	3717	1/1	0.82	0.15	-	72,72,72,72	0
57	MG	DA	3203	1/1	0.97	0.18	-	53,53,53,53	0
57	MG	BA	3557	1/1	0.80	0.17	-	53,53,53,53	0
57	MG	DA	3328	1/1	0.91	0.21	-	42,42,42,42	0
57	MG	BW	3002	1/1	0.95	0.27	-	58,58,58,58	0
57	MG	DA	3648	1/1	0.81	0.07	-	62,62,62,62	0
57	MG	DA	3313	1/1	0.70	0.11	-	39,39,39,39	0
57	MG	AA	1738	1/1	0.86	0.22	-	68,68,68,68	0
57	MG	DA	3594	1/1	0.95	0.09	-	58,58,58,58	0
57	MG	BA	3450	1/1	0.94	0.25	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3642	1/1	0.88	0.18	-	64,64,64,64	0
57	MG	DA	3613	1/1	0.93	0.11	-	56,56,56,56	0
57	MG	BA	3056	1/1	0.85	0.31	-	46,46,46,46	0
57	MG	BA	3784	1/1	0.94	0.18	-	52,52,52,52	0
57	MG	DA	3163	1/1	0.98	0.21	-	34,34,34,34	0
57	MG	DA	3391	1/1	0.93	0.16	-	45,45,45,45	0
57	MG	BA	3690	1/1	0.93	0.13	-	39,39,39,39	0
57	MG	AA	1741	1/1	0.81	0.12	-	86,86,86,86	0
57	MG	DA	3120	1/1	0.97	0.33	-	56,56,56,56	0
57	MG	DA	3078	1/1	0.90	0.09	-	47,47,47,47	0
57	MG	DA	3392	1/1	0.99	0.19	-	53,53,53,53	0
57	MG	AA	1743	1/1	0.67	0.17	-	66,66,66,66	0
57	MG	CA	3153	1/1	0.88	0.11	-	69,69,69,69	0
57	MG	DA	3604	1/1	0.84	0.15	-	61,61,61,61	0
57	MG	DA	3597	1/1	0.98	0.15	-	48,48,48,48	0
57	MG	BA	3248	1/1	0.89	0.15	-	67,67,67,67	0
57	MG	DA	3381	1/1	0.98	0.15	-	40,40,40,40	0
57	MG	DA	3187	1/1	0.88	0.20	-	47,47,47,47	0
57	MG	BA	3443	1/1	0.89	0.18	-	59,59,59,59	0
57	MG	BA	3288	1/1	0.70	0.18	-	44,44,44,44	0
57	MG	BA	3783	1/1	0.96	0.15	-	37,37,37,37	0
57	MG	DQ	3002	1/1	0.90	0.16	-	47,47,47,47	0
57	MG	DA	3358	1/1	0.89	0.18	-	50,50,50,50	0
57	MG	BA	3008	1/1	0.91	0.14	-	28,28,28,28	0
57	MG	BA	3117	1/1	0.90	0.64	-	38,38,38,38	0
57	MG	BA	3438	1/1	0.96	0.20	-	35,35,35,35	0
57	MG	BA	3524	1/1	0.91	0.21	-	33,33,33,33	0
57	MG	CA	3124	1/1	0.93	0.22	-	69,69,69,69	0
57	MG	BA	3634	1/1	0.97	0.14	-	55,55,55,55	0
57	MG	BA	3306	1/1	0.96	0.17	-	15,15,15,15	0
57	MG	DA	3355	1/1	0.99	0.11	-	43,43,43,43	0
57	MG	AA	1727	1/1	0.97	0.14	-	50,50,50,50	0
57	MG	BA	3600	1/1	0.83	0.28	-	44,44,44,44	0
57	MG	BA	3272	1/1	0.66	0.26	-	64,64,64,64	0
57	MG	DA	3175	1/1	0.95	0.14	-	41,41,41,41	0
57	MG	AA	1662	1/1	0.89	0.20	-	58,58,58,58	0
57	MG	BA	3246	1/1	0.94	0.31	-	55,55,55,55	0
57	MG	AA	1650	1/1	0.83	0.15	-	74,74,74,74	0
57	MG	AA	1777	1/1	0.86	0.09	-	71,71,71,71	0
57	MG	B4	502	1/1	0.92	0.09	-	70,70,70,70	0
57	MG	CA	3109	1/1	0.86	0.15	-	74,74,74,74	0
57	MG	CA	3070	1/1	0.83	0.15	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3650	1/1	0.98	0.17	-	45,45,45,45	0
57	MG	CA	3002	1/1	0.83	0.14	-	77,77,77,77	0
57	MG	AA	1762	1/1	0.98	0.21	-	66,66,66,66	0
57	MG	DA	3512	1/1	0.86	0.12	-	37,37,37,37	0
57	MG	BA	3161	1/1	0.93	0.29	-	44,44,44,44	0
57	MG	DA	3308	1/1	0.91	0.21	-	62,62,62,62	0
57	MG	BA	3493	1/1	0.96	0.21	-	38,38,38,38	0
57	MG	DA	3612	1/1	0.80	0.08	-	58,58,58,58	0
57	MG	DA	3320	1/1	0.79	0.09	-	49,49,49,49	0
57	MG	DA	3290	1/1	0.97	0.14	-	33,33,33,33	0
57	MG	AA	1604	1/1	0.80	0.12	-	58,58,58,58	0
57	MG	BA	3423	1/1	0.83	0.16	-	69,69,69,69	0
57	MG	DA	3210	1/1	0.93	0.08	-	52,52,52,52	0
57	MG	DA	3256	1/1	0.92	0.16	-	51,51,51,51	0
57	MG	DA	3351	1/1	0.81	0.08	-	56,56,56,56	0
57	MG	BA	3232	1/1	0.86	0.24	-	49,49,49,49	0
57	MG	DA	3148	1/1	0.94	0.21	-	49,49,49,49	0
57	MG	AA	1751	1/1	0.93	0.23	-	53,53,53,53	0
57	MG	BA	3445	1/1	0.94	0.23	-	54,54,54,54	0
57	MG	BA	3203	1/1	0.88	0.34	-	61,61,61,61	0
57	MG	DA	3539	1/1	0.93	0.08	-	55,55,55,55	0
57	MG	BA	3484	1/1	0.87	0.13	-	40,40,40,40	0
57	MG	BA	3263	1/1	0.85	0.28	-	60,60,60,60	0
57	MG	AA	1801	1/1	0.91	0.09	-	71,71,71,71	0
57	MG	BA	3295	1/1	0.89	0.22	-	23,23,23,23	0
57	MG	DA	3644	1/1	0.94	0.24	-	58,58,58,58	0
57	MG	BA	3711	1/1	0.96	0.25	-	44,44,44,44	0
57	MG	CA	3090	1/1	0.83	0.17	-	76,76,76,76	0
57	MG	DA	3601	1/1	0.89	0.10	-	55,55,55,55	0
57	MG	BA	3735	1/1	0.89	0.23	-	50,50,50,50	0
57	MG	DA	3052	1/1	0.79	0.10	-	49,49,49,49	0
57	MG	AA	1798	1/1	0.91	0.11	-	62,62,62,62	0
57	MG	BA	3749	1/1	0.97	0.16	-	52,52,52,52	0
57	MG	CA	3163	1/1	0.98	0.19	-	62,62,62,62	0
57	MG	CA	3077	1/1	0.89	0.20	-	60,60,60,60	0
57	MG	DA	3634	1/1	0.73	0.14	-	68,68,68,68	0
57	MG	CA	3100	1/1	0.91	0.15	-	59,59,59,59	0
57	MG	DA	3207	1/1	0.93	0.14	-	48,48,48,48	0
57	MG	CA	3075	1/1	0.94	0.24	-	65,65,65,65	0
57	MG	AA	1789	1/1	0.85	0.15	-	60,60,60,60	0
57	MG	CA	3017	1/1	0.83	0.15	-	54,54,54,54	0
57	MG	DA	3558	1/1	0.90	0.11	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	CA	3161	1/1	0.84	0.13	-	76,76,76,76	0
57	MG	DA	3236	1/1	0.92	0.13	-	55,55,55,55	0
57	MG	BA	3153	1/1	0.95	0.15	-	45,45,45,45	0
57	MG	BA	3159	1/1	0.96	0.18	-	27,27,27,27	0
57	MG	DA	3206	1/1	0.94	0.08	-	50,50,50,50	0
57	MG	DA	3478	1/1	0.92	0.17	-	58,58,58,58	0
57	MG	BA	3460	1/1	0.92	0.11	-	52,52,52,52	0
57	MG	BA	3370	1/1	0.97	0.24	-	50,50,50,50	0
57	MG	DA	3255	1/1	0.94	0.24	-	47,47,47,47	0
57	MG	AF	3001	1/1	0.88	0.18	-	50,50,50,50	0
57	MG	BA	3747	1/1	0.85	0.24	-	55,55,55,55	0
57	MG	DA	3623	1/1	0.87	0.10	-	45,45,45,45	0
57	MG	BA	3552	1/1	0.93	0.15	-	55,55,55,55	0
57	MG	CA	3158	1/1	0.97	0.19	-	55,55,55,55	0
57	MG	BA	3116	1/1	0.95	0.35	-	46,46,46,46	0
57	MG	AA	1625	1/1	0.79	0.17	-	73,73,73,73	0
57	MG	BA	3746	1/1	0.93	0.14	-	78,78,78,78	0
57	MG	DA	3641	1/1	0.95	0.07	-	46,46,46,46	0
57	MG	DA	3346	1/1	0.95	0.14	-	49,49,49,49	0
57	MG	BA	3570	1/1	0.85	0.21	-	31,31,31,31	0
57	MG	BA	3063	1/1	0.90	0.33	-	47,47,47,47	0
57	MG	BA	3626	1/1	0.92	0.19	-	50,50,50,50	0
57	MG	BA	3759	1/1	0.79	0.13	-	70,70,70,70	0
57	MG	DA	3457	1/1	0.96	0.18	-	44,44,44,44	0
57	MG	CA	3104	1/1	0.98	0.23	-	37,37,37,37	0
57	MG	BA	3353	1/1	0.94	0.12	-	55,55,55,55	0
57	MG	BA	3788	1/1	0.94	0.24	-	44,44,44,44	0
57	MG	AA	1720	1/1	0.98	0.19	-	55,55,55,55	0
57	MG	BA	3093	1/1	0.95	0.24	-	41,41,41,41	0
57	MG	DA	3368	1/1	0.91	0.09	-	67,67,67,67	0
57	MG	DA	3387	1/1	0.96	0.10	-	59,59,59,59	0
57	MG	AA	1809	1/1	0.97	0.17	-	42,42,42,42	0
57	MG	AA	1721	1/1	0.90	0.16	-	57,57,57,57	0
57	MG	BA	3405	1/1	0.96	0.16	-	52,52,52,52	0
57	MG	DA	3413	1/1	0.90	0.20	-	62,62,62,62	0
57	MG	DA	3632	1/1	0.98	0.17	-	52,52,52,52	0
57	MG	AA	1724	1/1	0.98	0.17	-	39,39,39,39	0
57	MG	AA	1731	1/1	0.94	0.18	-	56,56,56,56	0
57	MG	BA	3697	1/1	0.93	0.18	-	41,41,41,41	0
57	MG	DA	3253	1/1	0.75	0.13	-	54,54,54,54	0
57	MG	DA	3149	1/1	0.95	0.08	-	46,46,46,46	0
57	MG	DA	3536	1/1	0.93	0.08	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3664	1/1	0.95	0.21	-	69,69,69,69	0
57	MG	BA	3702	1/1	0.49	0.12	-	39,39,39,39	0
57	MG	DA	3188	1/1	0.98	0.24	-	35,35,35,35	0
57	MG	DA	3126	1/1	0.94	0.15	-	59,59,59,59	0
57	MG	DA	3455	1/1	0.88	0.09	-	64,64,64,64	0
57	MG	AA	1673	1/1	0.94	0.13	-	48,48,48,48	0
57	MG	AA	1771	1/1	0.87	0.15	-	75,75,75,75	0
57	MG	DA	3350	1/1	0.96	0.18	-	31,31,31,31	0
57	MG	DA	3332	1/1	0.73	0.18	-	46,46,46,46	0
57	MG	DA	3570	1/1	0.90	0.16	-	43,43,43,43	0
57	MG	BA	3676	1/1	0.78	0.17	-	70,70,70,70	0
57	MG	AA	1746	1/1	0.95	0.10	-	56,56,56,56	0
57	MG	CA	3122	1/1	0.76	0.13	-	69,69,69,69	0
57	MG	DA	3080	1/1	0.92	0.10	-	49,49,49,49	0
57	MG	AA	1601	1/1	0.85	0.12	-	81,81,81,81	0
57	MG	BA	3475	1/1	0.81	0.09	-	49,49,49,49	0
57	MG	BA	3163	1/1	0.91	0.49	-	55,55,55,55	0
57	MG	DA	3524	1/1	0.90	0.17	-	52,52,52,52	0
57	MG	BA	3181	1/1	0.93	0.10	-	40,40,40,40	0
57	MG	BA	3375	1/1	0.92	0.22	-	39,39,39,39	0
57	MG	DA	3412	1/1	0.99	0.14	-	41,41,41,41	0
57	MG	AA	1805	1/1	0.94	0.07	-	48,48,48,48	0
57	MG	DA	3559	1/1	0.92	0.15	-	67,67,67,67	0
57	MG	DA	3241	1/1	0.91	0.13	-	55,55,55,55	0
57	MG	DA	3095	1/1	0.89	0.16	-	60,60,60,60	0
57	MG	AA	1793	1/1	0.96	0.17	-	63,63,63,63	0
57	MG	DA	3093	1/1	0.98	0.13	-	47,47,47,47	0
57	MG	DA	3201	1/1	0.88	0.10	-	52,52,52,52	0
57	MG	BA	3792	1/1	0.87	0.19	-	52,52,52,52	0
57	MG	BA	3739	1/1	0.98	0.11	-	21,21,21,21	0
57	MG	BA	3078	1/1	0.85	0.32	-	54,54,54,54	0
57	MG	BA	3692	1/1	0.90	0.12	-	58,58,58,58	0
57	MG	AA	1666	1/1	0.87	0.33	-	63,63,63,63	0
57	MG	BA	3379	1/1	0.89	0.18	-	35,35,35,35	0
57	MG	BA	3140	1/1	0.87	0.12	-	58,58,58,58	0
57	MG	BA	3532	1/1	0.90	0.14	-	55,55,55,55	0
57	MG	BA	3024	1/1	0.87	0.23	-	58,58,58,58	0
57	MG	BA	3687	1/1	0.84	0.18	-	64,64,64,64	0
57	MG	DA	3554	1/1	0.91	0.09	-	50,50,50,50	0
57	MG	AA	1679	1/1	0.69	0.19	-	51,51,51,51	0
57	MG	BA	3610	1/1	0.96	0.09	-	61,61,61,61	0
57	MG	DA	3473	1/1	0.96	0.22	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3088	1/1	0.88	0.17	-	43,43,43,43	0
57	MG	CX	3002	1/1	0.90	0.14	-	67,67,67,67	0
57	MG	CA	3003	1/1	0.64	0.16	-	58,58,58,58	0
57	MG	AA	1726	1/1	0.92	0.16	-	58,58,58,58	0
57	MG	BA	3324	1/1	0.95	0.15	-	60,60,60,60	0
57	MG	BA	3156	1/1	0.92	0.23	-	35,35,35,35	0
57	MG	DA	3141	1/1	0.86	0.13	-	51,51,51,51	0
57	MG	BA	3105	1/1	0.94	0.12	-	46,46,46,46	0
57	MG	BA	3426	1/1	0.92	0.15	-	46,46,46,46	0
57	MG	CA	3082	1/1	0.91	0.13	-	66,66,66,66	0
57	MG	DF	302	1/1	0.84	0.14	-	53,53,53,53	0
57	MG	DA	3367	1/1	0.93	0.17	-	49,49,49,49	0
57	MG	BA	3090	1/1	0.96	0.26	-	38,38,38,38	0
57	MG	DA	3360	1/1	0.96	0.09	-	31,31,31,31	0
57	MG	BA	3810	1/1	0.97	0.21	-	35,35,35,35	0
57	MG	AA	1774	1/1	0.95	0.17	-	51,51,51,51	0
57	MG	DO	201	1/1	0.98	0.12	-	49,49,49,49	0
57	MG	BA	3057	1/1	0.85	0.18	-	48,48,48,48	0
57	MG	AN	502	1/1	0.97	0.29	-	62,62,62,62	0
57	MG	DA	3545	1/1	0.70	0.12	-	62,62,62,62	0
57	MG	BA	3467	1/1	0.98	0.13	-	46,46,46,46	0
57	MG	DO	202	1/1	0.91	0.12	-	60,60,60,60	0
57	MG	AA	1633	1/1	0.88	0.27	-	59,59,59,59	0
57	MG	BA	3332	1/1	0.94	0.14	-	54,54,54,54	0
57	MG	DA	3275	1/1	0.86	0.14	-	65,65,65,65	0
57	MG	CA	3039	1/1	0.84	0.15	-	64,64,64,64	0
57	MG	BA	3682	1/1	0.92	0.14	-	60,60,60,60	0
57	MG	AX	3013	1/1	0.85	0.20	-	70,70,70,70	0
57	MG	AA	1758	1/1	0.99	0.09	-	37,37,37,37	0
57	MG	CA	3121	1/1	0.90	0.13	-	67,67,67,67	0
57	MG	BA	3773	1/1	0.92	0.21	-	32,32,32,32	0
57	MG	AY	3003	1/1	0.89	0.15	-	79,79,79,79	0
57	MG	DA	3288	1/1	0.94	0.16	-	39,39,39,39	0
57	MG	CA	3123	1/1	0.90	0.32	-	61,61,61,61	0
57	MG	BA	3637	1/1	0.77	0.14	-	38,38,38,38	0
57	MG	AL	201	1/1	0.72	0.13	-	63,63,63,63	0
57	MG	BA	3098	1/1	0.94	0.22	-	23,23,23,23	0
57	MG	DA	3629	1/1	0.97	0.12	-	57,57,57,57	0
57	MG	DA	3494	1/1	0.88	0.12	-	45,45,45,45	0
57	MG	AA	1658	1/1	0.86	0.14	-	64,64,64,64	0
57	MG	DA	3278	1/1	0.95	0.10	-	39,39,39,39	0
57	MG	BB	3006	1/1	0.88	0.14	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3424	1/1	0.86	0.18	-	41,41,41,41	0
57	MG	BA	3345	1/1	0.98	0.19	-	51,51,51,51	0
57	MG	BN	3003	1/1	0.93	0.21	-	38,38,38,38	0
57	MG	BA	3003	1/1	0.99	0.17	-	33,33,33,33	0
57	MG	CA	3149	1/1	0.96	0.12	-	54,54,54,54	0
57	MG	DA	3298	1/1	0.92	0.20	-	55,55,55,55	0
57	MG	BA	3797	1/1	0.96	0.31	-	51,51,51,51	0
57	MG	AA	1745	1/1	0.92	0.16	-	36,36,36,36	0
57	MG	DA	3515	1/1	0.89	0.13	-	55,55,55,55	0
57	MG	AX	3009	1/1	0.95	0.37	-	65,65,65,65	0
57	MG	BA	3440	1/1	0.96	0.20	-	35,35,35,35	0
57	MG	DA	3636	1/1	0.85	0.15	-	62,62,62,62	0
57	MG	BA	3143	1/1	0.95	0.10	-	41,41,41,41	0
57	MG	BA	3430	1/1	0.96	0.24	-	34,34,34,34	0
57	MG	BA	3470	1/1	0.91	0.11	-	57,57,57,57	0
57	MG	BF	301	1/1	0.94	0.25	-	40,40,40,40	0
57	MG	CA	3059	1/1	0.73	0.16	-	75,75,75,75	0
57	MG	DE	3006	1/1	0.97	0.21	-	38,38,38,38	0
57	MG	DA	3447	1/1	0.98	0.16	-	59,59,59,59	0
57	MG	BA	3646	1/1	0.89	0.17	-	50,50,50,50	0
57	MG	BA	3754	1/1	0.92	0.14	-	42,42,42,42	0
57	MG	AA	1682	1/1	0.85	0.26	-	59,59,59,59	0
57	MG	AA	1635	1/1	0.90	0.15	-	65,65,65,65	0
57	MG	DA	3065	1/1	0.84	0.10	-	56,56,56,56	0
57	MG	CA	3146	1/1	0.82	0.18	-	72,72,72,72	0
57	MG	AX	3004	1/1	0.91	0.13	-	61,61,61,61	0
57	MG	DA	3094	1/1	0.92	0.06	-	39,39,39,39	0
57	MG	DA	3309	1/1	0.96	0.12	-	48,48,48,48	0
57	MG	BA	3004	1/1	0.97	0.22	-	36,36,36,36	0
57	MG	DA	3151	1/1	0.92	0.13	-	37,37,37,37	0
57	MG	BA	3115	1/1	0.90	0.23	-	33,33,33,33	0
57	MG	BA	3411	1/1	0.81	0.24	-	50,50,50,50	0
57	MG	BA	3636	1/1	0.90	0.19	-	66,66,66,66	0
57	MG	DA	3564	1/1	0.94	0.16	-	53,53,53,53	0
57	MG	BA	3374	1/1	0.96	0.19	-	50,50,50,50	0
57	MG	DA	3372	1/1	0.94	0.13	-	53,53,53,53	0
57	MG	AA	1640	1/1	0.88	0.22	-	54,54,54,54	0
57	MG	BA	3329	1/1	0.89	0.10	-	60,60,60,60	0
57	MG	DA	3035	1/1	0.83	0.12	-	37,37,37,37	0
57	MG	BA	3141	1/1	0.92	0.32	-	38,38,38,38	0
57	MG	BA	3109	1/1	0.86	0.13	-	56,56,56,56	0
57	MG	BA	3168	1/1	0.95	0.24	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3647	1/1	0.91	0.08	-	53,53,53,53	0
57	MG	BA	3001	1/1	0.92	0.15	-	43,43,43,43	0
57	MG	DA	3590	1/1	0.90	0.22	-	51,51,51,51	0
57	MG	BA	3513	1/1	0.89	0.34	-	50,50,50,50	0
57	MG	DA	3608	1/1	0.94	0.09	-	57,57,57,57	0
57	MG	DA	3466	1/1	0.93	0.11	-	48,48,48,48	0
57	MG	CA	3132	1/1	0.97	0.14	-	64,64,64,64	0
57	MG	AA	1660	1/1	0.82	0.24	-	51,51,51,51	0
57	MG	DB	3011	1/1	0.89	0.26	-	67,67,67,67	0
57	MG	CA	3112	1/1	0.84	0.10	-	72,72,72,72	0
57	MG	CA	3078	1/1	0.93	0.16	-	65,65,65,65	0
57	MG	BA	3764	1/1	0.96	0.20	-	66,66,66,66	0
57	MG	AA	1797	1/1	0.92	0.17	-	59,59,59,59	0
57	MG	AA	1678	1/1	0.99	0.25	-	47,47,47,47	0
57	MG	BA	3681	1/1	0.86	0.23	-	61,61,61,61	0
57	MG	DA	3645	1/1	0.89	0.11	-	64,64,64,64	0
57	MG	BA	3765	1/1	0.90	0.24	-	49,49,49,49	0
57	MG	BA	3579	1/1	0.76	0.11	-	63,63,63,63	0
57	MG	DA	3043	1/1	0.95	0.19	-	53,53,53,53	0
57	MG	DA	3565	1/1	0.91	0.04	-	52,52,52,52	0
57	MG	BA	3064	1/1	0.94	0.22	-	45,45,45,45	0
57	MG	AA	1701	1/1	0.72	0.27	-	73,73,73,73	0
57	MG	CA	3083	1/1	0.96	0.16	-	50,50,50,50	0
57	MG	BA	3545	1/1	0.91	0.18	-	28,28,28,28	0
57	MG	DA	3128	1/1	0.94	0.28	-	56,56,56,56	0
57	MG	BA	3072	1/1	0.97	0.24	-	49,49,49,49	0
57	MG	BA	3283	1/1	0.85	0.40	-	57,57,57,57	0
57	MG	DA	3432	1/1	0.96	0.17	-	52,52,52,52	0
57	MG	BA	3523	1/1	0.86	0.21	-	41,41,41,41	0
57	MG	AA	1694	1/1	0.92	0.08	-	47,47,47,47	0
57	MG	BA	3270	1/1	0.81	0.22	-	56,56,56,56	0
57	MG	BA	3457	1/1	0.98	0.19	-	48,48,48,48	0
57	MG	BA	3724	1/1	0.96	0.18	-	20,20,20,20	0
57	MG	BA	3511	1/1	0.95	0.18	-	50,50,50,50	0
57	MG	BA	3055	1/1	0.93	0.23	-	37,37,37,37	0
57	MG	BA	3071	1/1	0.95	0.31	-	59,59,59,59	0
57	MG	BA	3031	1/1	0.96	0.27	-	36,36,36,36	0
57	MG	BR	5001	1/1	0.93	0.20	-	50,50,50,50	0
57	MG	AA	1782	1/1	0.93	0.14	-	54,54,54,54	0
57	MG	DA	3143	1/1	0.82	0.14	-	62,62,62,62	0
57	MG	AA	1683	1/1	0.94	0.13	-	62,62,62,62	0
57	MG	B0	3001	1/1	0.93	0.19	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3652	1/1	0.69	0.09	-	58,58,58,58	0
57	MG	CA	3056	1/1	0.94	0.10	-	64,64,64,64	0
57	MG	CA	3111	1/1	0.87	0.15	-	72,72,72,72	0
57	MG	DA	3009	1/1	0.94	0.17	-	61,61,61,61	0
57	MG	DA	3077	1/1	0.92	0.14	-	38,38,38,38	0
57	MG	DA	3551	1/1	0.94	0.17	-	49,49,49,49	0
57	MG	B7	104	1/1	0.84	0.27	-	62,62,62,62	0
57	MG	BB	3010	1/1	0.94	0.18	-	53,53,53,53	0
57	MG	DA	3427	1/1	0.88	0.16	-	47,47,47,47	0
57	MG	AA	1669	1/1	0.72	0.18	-	69,69,69,69	0
57	MG	AA	1752	1/1	0.93	0.14	-	48,48,48,48	0
57	MG	DA	3430	1/1	0.96	0.13	-	47,47,47,47	0
57	MG	BA	3169	1/1	0.95	0.24	-	50,50,50,50	0
57	MG	DA	3096	1/1	0.93	0.19	-	68,68,68,68	0
57	MG	AA	1769	1/1	0.95	0.19	-	50,50,50,50	0
57	MG	DA	3074	1/1	0.94	0.08	-	59,59,59,59	0
57	MG	AA	1729	1/1	0.91	0.15	-	35,35,35,35	0
57	MG	BA	3581	1/1	0.94	0.12	-	59,59,59,59	0
57	MG	BA	3698	1/1	0.97	0.11	-	47,47,47,47	0
57	MG	BA	3151	1/1	0.96	0.17	-	36,36,36,36	0
57	MG	CA	3049	1/1	0.81	0.21	-	65,65,65,65	0
57	MG	BA	3092	1/1	0.93	0.29	-	40,40,40,40	0
57	MG	BA	3482	1/1	0.96	0.16	-	51,51,51,51	0
57	MG	BA	3715	1/1	0.79	0.17	-	52,52,52,52	0
57	MG	BA	3732	1/1	0.87	0.24	-	33,33,33,33	0
57	MG	BA	3390	1/1	0.89	0.10	-	31,31,31,31	0
57	MG	BA	3537	1/1	0.95	0.08	-	43,43,43,43	0
57	MG	BA	3344	1/1	0.97	0.10	-	71,71,71,71	0
57	MG	DA	3198	1/1	0.97	0.16	-	52,52,52,52	0
57	MG	BA	3119	1/1	0.96	0.15	-	46,46,46,46	0
57	MG	DA	3174	1/1	0.76	0.19	-	52,52,52,52	0
57	MG	BA	3006	1/1	0.79	0.24	-	54,54,54,54	0
57	MG	BA	3401	1/1	0.95	0.26	-	26,26,26,26	0
57	MG	BA	3255	1/1	0.88	0.20	-	55,55,55,55	0
57	MG	AA	1785	1/1	0.94	0.11	-	72,72,72,72	0
57	MG	BA	3268	1/1	0.92	0.22	-	54,54,54,54	0
57	MG	DA	3053	1/1	0.92	0.13	-	47,47,47,47	0
57	MG	AA	1608	1/1	0.96	0.22	-	43,43,43,43	0
57	MG	BA	3190	1/1	0.97	0.28	-	54,54,54,54	0
57	MG	BA	3444	1/1	0.95	0.15	-	48,48,48,48	0
57	MG	DA	3389	1/1	0.95	0.19	-	59,59,59,59	0
57	MG	DA	3193	1/1	0.95	0.15	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3335	1/1	0.95	0.15	-	40,40,40,40	0
57	MG	AA	1773	1/1	0.96	0.10	-	61,61,61,61	0
57	MG	DA	3059	1/1	0.96	0.10	-	50,50,50,50	0
57	MG	AA	1767	1/1	0.96	0.11	-	67,67,67,67	0
57	MG	DA	3574	1/1	0.85	0.07	-	61,61,61,61	0
57	MG	CA	3089	1/1	0.90	0.23	-	74,74,74,74	0
57	MG	DA	3137	1/1	0.96	0.17	-	52,52,52,52	0
57	MG	DA	3450	1/1	0.96	0.06	-	50,50,50,50	0
57	MG	BB	3001	1/1	0.82	0.29	-	68,68,68,68	0
57	MG	DA	3556	1/1	0.90	0.13	-	55,55,55,55	0
57	MG	DA	3525	1/1	0.96	0.15	-	28,28,28,28	0
57	MG	DA	3116	1/1	0.67	0.16	-	53,53,53,53	0
57	MG	CA	3117	1/1	0.93	0.09	-	63,63,63,63	0
57	MG	BA	3318	1/1	0.86	0.16	-	54,54,54,54	0
57	MG	BA	3528	1/1	0.92	0.20	-	36,36,36,36	0
57	MG	BA	3040	1/1	0.94	0.27	-	33,33,33,33	0
57	MG	BA	3252	1/1	0.91	0.19	-	36,36,36,36	0
57	MG	B8	5002	1/1	0.86	0.30	-	53,53,53,53	0
57	MG	AA	1755	1/1	0.87	0.09	-	80,80,80,80	0
57	MG	CA	3006	1/1	0.71	0.11	-	68,68,68,68	0
57	MG	CA	3045	1/1	0.87	0.22	-	62,62,62,62	0
57	MG	BN	3002	1/1	0.82	0.20	-	51,51,51,51	0
57	MG	CA	3024	1/1	0.94	0.16	-	67,67,67,67	0
57	MG	BA	3408	1/1	0.90	0.17	-	51,51,51,51	0
57	MG	AA	1804	1/1	0.95	0.12	-	70,70,70,70	0
57	MG	CA	3074	1/1	0.95	0.14	-	60,60,60,60	0
57	MG	BA	3249	1/1	0.96	0.23	-	53,53,53,53	0
57	MG	DA	3234	1/1	0.85	0.15	-	54,54,54,54	0
57	MG	BA	3398	1/1	0.96	0.22	-	32,32,32,32	0
57	MG	CA	3026	1/1	0.90	0.21	-	66,66,66,66	0
57	MG	DB	3001	1/1	0.83	0.17	-	63,63,63,63	0
57	MG	DA	3045	1/1	0.97	0.22	-	51,51,51,51	0
57	MG	BA	3766	1/1	0.89	0.16	-	47,47,47,47	0
57	MG	BA	3294	1/1	0.94	0.16	-	43,43,43,43	0
57	MG	BA	3728	1/1	0.91	0.16	-	52,52,52,52	0
57	MG	BA	3454	1/1	0.96	0.17	-	46,46,46,46	0
57	MG	BA	3755	1/1	0.83	0.24	-	43,43,43,43	0
57	MG	BA	3589	1/1	0.94	0.22	-	59,59,59,59	0
57	MG	BA	3628	1/1	0.97	0.28	-	52,52,52,52	0
57	MG	BA	3514	1/1	0.96	0.19	-	43,43,43,43	0
57	MG	CX	3001	1/1	0.95	0.18	-	57,57,57,57	0
57	MG	BA	3359	1/1	0.88	0.06	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3605	1/1	0.96	0.18	-	47,47,47,47	0
57	MG	BA	3350	1/1	0.95	0.12	-	34,34,34,34	0
57	MG	DA	3272	1/1	0.94	0.19	-	49,49,49,49	0
57	MG	DA	3159	1/1	0.91	0.11	-	62,62,62,62	0
57	MG	DA	3012	1/1	0.94	0.11	-	43,43,43,43	0
57	MG	BA	3574	1/1	0.89	0.15	-	42,42,42,42	0
57	MG	BA	3091	1/1	0.92	0.40	-	42,42,42,42	0
57	MG	DD	303	1/1	0.93	0.34	-	51,51,51,51	0
57	MG	DA	3179	1/1	0.91	0.06	-	59,59,59,59	0
57	MG	BA	3505	1/1	0.84	0.22	-	53,53,53,53	0
57	MG	BB	3005	1/1	0.93	0.28	-	51,51,51,51	0
57	MG	AY	3001	1/1	0.88	0.32	-	63,63,63,63	0
57	MG	B6	101	1/1	0.93	0.32	-	60,60,60,60	0
57	MG	CA	3134	1/1	0.95	0.11	-	64,64,64,64	0
57	MG	DA	3357	1/1	0.92	0.13	-	33,33,33,33	0
57	MG	DA	3111	1/1	0.85	0.13	-	56,56,56,56	0
57	MG	BA	3678	1/1	0.80	0.10	-	67,67,67,67	0
57	MG	DA	3509	1/1	0.95	0.06	-	49,49,49,49	0
57	MG	BA	3730	1/1	0.78	0.17	-	68,68,68,68	0
57	MG	BA	3595	1/1	0.97	0.09	-	61,61,61,61	0
57	MG	BA	3242	1/1	0.94	0.69	-	55,55,55,55	0
57	MG	AA	1811	1/1	0.96	0.21	-	49,49,49,49	0
57	MG	CA	3151	1/1	0.91	0.10	-	64,64,64,64	0
57	MG	AX	3015	1/1	0.89	0.29	-	51,51,51,51	0
57	MG	BA	3616	1/1	0.94	0.20	-	59,59,59,59	0
57	MG	DP	202	1/1	0.89	0.09	-	49,49,49,49	0
57	MG	BA	3685	1/1	0.91	0.20	-	61,61,61,61	0
57	MG	BA	3546	1/1	0.90	0.14	-	68,68,68,68	0
57	MG	DA	3130	1/1	0.86	0.15	-	52,52,52,52	0
57	MG	AA	1744	1/1	0.96	0.17	-	44,44,44,44	0
57	MG	CA	3038	1/1	0.96	0.09	-	57,57,57,57	0
57	MG	BA	3776	1/1	0.97	0.22	-	60,60,60,60	0
57	MG	DA	3583	1/1	0.95	0.12	-	52,52,52,52	0
57	MG	BA	3645	1/1	0.91	0.18	-	47,47,47,47	0
57	MG	AA	1748	1/1	0.96	0.16	-	64,64,64,64	0
57	MG	BA	3468	1/1	0.96	0.19	-	45,45,45,45	0
57	MG	AA	1624	1/1	0.97	0.25	-	66,66,66,66	0
57	MG	BB	3023	1/1	0.97	0.16	-	47,47,47,47	0
57	MG	DA	3507	1/1	0.96	0.07	-	59,59,59,59	0
57	MG	DA	3154	1/1	0.91	0.08	-	51,51,51,51	0
57	MG	BA	3701	1/1	0.98	0.23	-	39,39,39,39	0
57	MG	BA	3060	1/1	0.83	0.22	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	AA	1649	1/1	0.94	0.18	-	28,28,28,28	0
57	MG	CA	3154	1/1	0.76	0.18	-	68,68,68,68	0
57	MG	DA	3056	1/1	0.81	0.12	-	49,49,49,49	0
57	MG	AA	1754	1/1	0.92	0.15	-	58,58,58,58	0
57	MG	BA	3148	1/1	0.93	0.28	-	38,38,38,38	0
57	MG	CA	3027	1/1	0.90	0.18	-	65,65,65,65	0
57	MG	DA	3474	1/1	0.95	0.09	-	53,53,53,53	0
57	MG	CA	3156	1/1	0.96	0.08	-	59,59,59,59	0
57	MG	BA	3291	1/1	0.96	0.26	-	53,53,53,53	0
57	MG	DA	3129	1/1	0.89	0.20	-	56,56,56,56	0
57	MG	BA	3418	1/1	0.88	0.21	-	38,38,38,38	0
57	MG	CA	3072	1/1	0.94	0.14	-	62,62,62,62	0
57	MG	BA	3029	1/1	0.86	0.27	-	36,36,36,36	0
57	MG	DA	3063	1/1	0.90	0.11	-	47,47,47,47	0
57	MG	DA	3226	1/1	0.94	0.18	-	57,57,57,57	0
57	MG	CA	3103	1/1	0.91	0.15	-	73,73,73,73	0
57	MG	DA	3260	1/1	0.91	0.17	-	39,39,39,39	0
57	MG	BA	3337	1/1	0.93	0.25	-	44,44,44,44	0
57	MG	DA	3480	1/1	0.89	0.12	-	58,58,58,58	0
57	MG	DA	3476	1/1	0.90	0.08	-	45,45,45,45	0
57	MG	DA	3031	1/1	0.91	0.14	-	42,42,42,42	0
57	MG	DD	301	1/1	0.95	0.22	-	44,44,44,44	0
57	MG	BA	3447	1/1	0.96	0.32	-	52,52,52,52	0
57	MG	AA	1800	1/1	0.93	0.13	-	59,59,59,59	0
57	MG	BA	3053	1/1	0.97	0.27	-	23,23,23,23	0
57	MG	BA	3451	1/1	0.95	0.25	-	44,44,44,44	0
57	MG	CA	3076	1/1	0.91	0.20	-	77,77,77,77	0
60	K	AX	3001	1/1	0.87	0.13	-	77,77,77,77	0
57	MG	DA	3382	1/1	0.95	0.12	-	41,41,41,41	0
57	MG	DA	3301	1/1	0.81	0.11	-	63,63,63,63	0
57	MG	CA	3092	1/1	0.99	0.24	-	51,51,51,51	0
57	MG	DB	3013	1/1	0.99	0.11	-	66,66,66,66	0
57	MG	CA	3143	1/1	0.83	0.20	-	74,74,74,74	0
57	MG	BO	5001	1/1	0.94	0.13	-	61,61,61,61	0
57	MG	DA	3547	1/1	0.98	0.08	-	48,48,48,48	0
57	MG	DA	3006	1/1	0.93	0.11	-	41,41,41,41	0
57	MG	DA	3610	1/1	0.95	0.09	-	47,47,47,47	0
57	MG	DA	3452	1/1	0.88	0.11	-	45,45,45,45	0
57	MG	DA	3239	1/1	0.89	0.14	-	49,49,49,49	0
57	MG	BA	3572	1/1	0.95	0.26	-	39,39,39,39	0
57	MG	DA	3627	1/1	0.82	0.14	-	57,57,57,57	0
57	MG	AX	3007	1/1	0.63	0.30	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3437	1/1	0.96	0.18	-	48,48,48,48	0
57	MG	BA	3222	1/1	0.89	0.14	-	42,42,42,42	0
57	MG	DA	3240	1/1	0.94	0.10	-	52,52,52,52	0
57	MG	BA	3745	1/1	0.87	0.24	-	61,61,61,61	0
57	MG	CA	3063	1/1	0.89	0.23	-	65,65,65,65	0
57	MG	BA	3639	1/1	0.97	0.18	-	49,49,49,49	0
57	MG	CA	3015	1/1	0.93	0.19	-	64,64,64,64	0
57	MG	BA	3771	1/1	0.94	0.11	-	41,41,41,41	0
57	MG	BA	3458	1/1	0.81	0.20	-	59,59,59,59	0
57	MG	BA	3347	1/1	0.82	0.19	-	38,38,38,38	0
57	MG	DA	3417	1/1	0.86	0.13	-	52,52,52,52	0
57	MG	BA	3406	1/1	0.89	0.10	-	56,56,56,56	0
57	MG	BA	3420	1/1	0.91	0.18	-	25,25,25,25	0
57	MG	CA	3140	1/1	0.96	0.16	-	57,57,57,57	0
57	MG	BA	3630	1/1	0.97	0.25	-	39,39,39,39	0
57	MG	DA	3534	1/1	0.94	0.10	-	46,46,46,46	0
57	MG	AA	1766	1/1	0.83	0.19	-	71,71,71,71	0
57	MG	BA	3229	1/1	0.79	0.24	-	52,52,52,52	0
57	MG	AA	1761	1/1	0.98	0.20	-	70,70,70,70	0
57	MG	DA	3633	1/1	0.88	0.10	-	58,58,58,58	0
57	MG	BA	3696	1/1	0.80	0.10	-	46,46,46,46	0
57	MG	DA	3118	1/1	0.86	0.16	-	39,39,39,39	0
57	MG	BA	3067	1/1	0.98	0.21	-	43,43,43,43	0
57	MG	BA	3602	1/1	0.96	0.11	-	47,47,47,47	0
57	MG	BA	3372	1/1	0.90	0.12	-	40,40,40,40	0
57	MG	BA	3342	1/1	0.97	0.29	-	67,67,67,67	0
57	MG	AA	1632	1/1	0.87	0.11	-	48,48,48,48	0
57	MG	BA	3107	1/1	0.86	0.33	-	57,57,57,57	0
57	MG	BQ	3002	1/1	0.95	0.28	-	46,46,46,46	0
57	MG	BA	3464	1/1	0.96	0.13	-	44,44,44,44	0
57	MG	DA	3123	1/1	0.84	0.16	-	54,54,54,54	0
57	MG	DA	3342	1/1	0.93	0.10	-	53,53,53,53	0
57	MG	AW	3002	1/1	0.92	0.14	-	79,79,79,79	0
57	MG	BA	3787	1/1	0.96	0.14	-	45,45,45,45	0
57	MG	DA	3471	1/1	0.89	0.32	-	54,54,54,54	0
57	MG	CA	3095	1/1	0.91	0.13	-	71,71,71,71	0
57	MG	BA	3617	1/1	0.95	0.10	-	42,42,42,42	0
57	MG	AA	1768	1/1	0.90	0.11	-	53,53,53,53	0
57	MG	DA	3086	1/1	0.76	0.11	-	47,47,47,47	0
57	MG	DA	3504	1/1	0.93	0.09	-	52,52,52,52	0
57	MG	AA	1670	1/1	0.95	0.17	-	67,67,67,67	0
57	MG	BA	3099	1/1	0.86	0.24	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3146	1/1	0.92	0.14	-	54,54,54,54	0
57	MG	BA	3422	1/1	0.94	0.16	-	36,36,36,36	0
57	MG	CA	3073	1/1	0.93	0.20	-	55,55,55,55	0
57	MG	DA	3184	1/1	0.95	0.12	-	52,52,52,52	0
57	MG	DA	3162	1/1	0.96	0.14	-	57,57,57,57	0
57	MG	AW	3001	1/1	0.84	0.11	-	59,59,59,59	0
57	MG	AA	1791	1/1	0.93	0.08	-	54,54,54,54	0
57	MG	DA	3482	1/1	0.90	0.15	-	60,60,60,60	0
57	MG	DA	3083	1/1	0.93	0.26	-	41,41,41,41	0
57	MG	BA	3571	1/1	0.85	0.24	-	28,28,28,28	0
57	MG	CA	3062	1/1	0.92	0.11	-	64,64,64,64	0
57	MG	DA	3460	1/1	0.94	0.18	-	37,37,37,37	0
57	MG	CA	3160	1/1	0.91	0.14	-	73,73,73,73	0
57	MG	BA	3002	1/1	0.83	0.28	-	53,53,53,53	0
57	MG	BA	3195	1/1	0.93	0.18	-	36,36,36,36	0
57	MG	AA	1763	1/1	0.86	0.07	-	79,79,79,79	0
57	MG	BA	3017	1/1	0.95	0.28	-	65,65,65,65	0
57	MG	DA	3057	1/1	0.63	0.20	-	44,44,44,44	0
57	MG	BA	3364	1/1	0.92	0.15	-	47,47,47,47	0
57	MG	AX	3011	1/1	0.93	0.13	-	60,60,60,60	0
57	MG	BA	3302	1/1	0.93	0.15	-	49,49,49,49	0
57	MG	DA	3404	1/1	0.95	0.08	-	43,43,43,43	0
57	MG	DA	3305	1/1	0.93	0.13	-	53,53,53,53	0
57	MG	DA	3250	1/1	0.88	0.08	-	50,50,50,50	0
57	MG	BA	3211	1/1	0.94	0.18	-	43,43,43,43	0
57	MG	BA	3656	1/1	0.85	0.17	-	45,45,45,45	0
57	MG	DA	3483	1/1	0.94	0.09	-	53,53,53,53	0
57	MG	BW	3001	1/1	0.86	0.35	-	44,44,44,44	0
57	MG	DA	3386	1/1	0.97	0.10	-	44,44,44,44	0
57	MG	DA	3481	1/1	0.92	0.13	-	40,40,40,40	0
57	MG	BA	3167	1/1	0.96	0.18	-	45,45,45,45	0
57	MG	BA	3094	1/1	0.86	0.19	-	52,52,52,52	0
57	MG	AA	1750	1/1	0.95	0.14	-	49,49,49,49	0
57	MG	BA	3175	1/1	0.85	0.29	-	57,57,57,57	0
57	MG	BA	3075	1/1	0.98	0.20	-	24,24,24,24	0
57	MG	DA	3538	1/1	0.86	0.12	-	60,60,60,60	0
57	MG	AA	1739	1/1	0.89	0.22	-	72,72,72,72	0
57	MG	CA	3035	1/1	0.92	0.11	-	53,53,53,53	0
57	MG	BA	3751	1/1	0.98	0.23	-	37,37,37,37	0
57	MG	BB	3012	1/1	0.94	0.19	-	56,56,56,56	0
57	MG	CA	3155	1/1	0.96	0.15	-	57,57,57,57	0
57	MG	DA	3091	1/1	0.90	0.20	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DF	303	1/1	0.84	0.15	-	42,42,42,42	0
57	MG	AK	3101	1/1	0.93	0.17	-	69,69,69,69	0
57	MG	DA	3048	1/1	0.93	0.12	-	59,59,59,59	0
57	MG	CA	3097	1/1	0.95	0.27	-	60,60,60,60	0
57	MG	AA	1717	1/1	0.91	0.16	-	75,75,75,75	0
57	MG	BA	3575	1/1	0.95	0.12	-	50,50,50,50	0
57	MG	DA	3245	1/1	0.98	0.08	-	58,58,58,58	0
57	MG	CA	3162	1/1	0.82	0.07	-	79,79,79,79	0
57	MG	DA	3115	1/1	0.95	0.29	-	55,55,55,55	0
57	MG	DA	3516	1/1	0.65	0.22	-	67,67,67,67	0
57	MG	CA	3131	1/1	0.90	0.24	-	69,69,69,69	0
57	MG	DA	3181	1/1	0.91	0.12	-	49,49,49,49	0
57	MG	BA	3609	1/1	0.89	0.20	-	56,56,56,56	0
57	MG	DA	3189	1/1	0.93	0.23	-	47,47,47,47	0
57	MG	BA	3462	1/1	0.93	0.11	-	53,53,53,53	0
57	MG	DA	3356	1/1	0.80	0.16	-	39,39,39,39	0
57	MG	BA	3712	1/1	0.71	0.22	-	51,51,51,51	0
57	MG	BY	502	1/1	0.91	0.24	-	46,46,46,46	0
57	MG	BA	3328	1/1	0.95	0.19	-	27,27,27,27	0
57	MG	BA	3549	1/1	0.87	0.11	-	66,66,66,66	0
57	MG	BA	3695	1/1	0.94	0.15	-	40,40,40,40	0
57	MG	BA	3183	1/1	0.82	0.48	-	49,49,49,49	0
57	MG	BA	3122	1/1	0.91	0.15	-	35,35,35,35	0
57	MG	DA	3176	1/1	0.94	0.24	-	38,38,38,38	0
57	MG	BA	3498	1/1	0.79	0.21	-	45,45,45,45	0
57	MG	AA	1706	1/1	0.96	0.22	-	60,60,60,60	0
57	MG	BA	3490	1/1	0.97	0.17	-	43,43,43,43	0
57	MG	DA	3444	1/1	0.88	0.21	-	44,44,44,44	0
57	MG	AA	1674	1/1	0.90	0.20	-	58,58,58,58	0
57	MG	AL	202	1/1	0.92	0.26	-	56,56,56,56	0
57	MG	BB	3008	1/1	0.95	0.36	-	59,59,59,59	0
57	MG	CA	3047	1/1	0.97	0.17	-	50,50,50,50	0
57	MG	DA	3658	1/1	0.90	0.49	-	62,62,62,62	0
57	MG	BA	3578	1/1	0.95	0.35	-	39,39,39,39	0
57	MG	DA	3135	1/1	0.49	0.18	-	63,63,63,63	0
57	MG	DA	3140	1/1	0.84	0.10	-	64,64,64,64	0
57	MG	BA	3065	1/1	0.88	0.31	-	50,50,50,50	0
57	MG	BA	3629	1/1	0.95	0.25	-	58,58,58,58	0
57	MG	BA	3269	1/1	0.93	0.25	-	45,45,45,45	0
57	MG	BA	3461	1/1	0.97	0.11	-	45,45,45,45	0
57	MG	BA	3123	1/1	0.93	0.09	-	43,43,43,43	0
57	MG	BA	3416	1/1	0.86	0.26	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3112	1/1	0.94	0.26	-	41,41,41,41	0
57	MG	DA	3611	1/1	0.86	0.10	-	53,53,53,53	0
57	MG	AA	1671	1/1	0.89	0.10	-	60,60,60,60	0
57	MG	AA	1764	1/1	0.85	0.10	-	66,66,66,66	0
57	MG	DA	3409	1/1	0.91	0.12	-	54,54,54,54	0
57	MG	BA	3368	1/1	0.98	0.24	-	32,32,32,32	0
57	MG	DA	3511	1/1	0.91	0.10	-	44,44,44,44	0
57	MG	DA	3388	1/1	0.90	0.14	-	47,47,47,47	0
57	MG	BA	3565	1/1	0.96	0.14	-	61,61,61,61	0
57	MG	BA	3744	1/1	0.94	0.18	-	55,55,55,55	0
57	MG	BA	3180	1/1	0.97	0.27	-	46,46,46,46	0
57	MG	BA	3633	1/1	0.86	0.18	-	57,57,57,57	0
57	MG	DA	3513	1/1	0.81	0.14	-	69,69,69,69	0
57	MG	DA	3394	1/1	0.83	0.05	-	60,60,60,60	0
57	MG	AA	1629	1/1	0.87	0.35	-	68,68,68,68	0
57	MG	BA	3032	1/1	0.95	0.21	-	33,33,33,33	0
57	MG	CA	3125	1/1	0.85	0.21	-	64,64,64,64	0
57	MG	DA	3438	1/1	0.94	0.08	-	42,42,42,42	0
57	MG	CA	3164	1/1	0.85	0.33	-	76,76,76,76	0
57	MG	AY	3002	1/1	0.93	0.31	-	52,52,52,52	0
57	MG	BA	3147	1/1	0.90	0.20	-	36,36,36,36	0
57	MG	BA	3632	1/1	0.85	0.26	-	55,55,55,55	0
57	MG	DA	3467	1/1	0.94	0.24	-	52,52,52,52	0
57	MG	BA	3271	1/1	0.86	0.18	-	60,60,60,60	0
57	MG	BA	3137	1/1	0.92	0.25	-	52,52,52,52	0
57	MG	DA	3073	1/1	0.97	0.08	-	33,33,33,33	0
57	MG	BA	3748	1/1	0.95	0.17	-	61,61,61,61	0
57	MG	DA	3519	1/1	0.86	0.14	-	58,58,58,58	0
57	MG	AA	1622	1/1	0.80	0.21	-	69,69,69,69	0
57	MG	AA	1647	1/1	0.96	0.22	-	44,44,44,44	0
57	MG	BA	3767	1/1	0.88	0.23	-	45,45,45,45	0
57	MG	DA	3635	1/1	0.94	0.11	-	43,43,43,43	0
57	MG	CA	3159	1/1	0.93	0.13	-	62,62,62,62	0
57	MG	DA	3286	1/1	0.86	0.09	-	55,55,55,55	0
57	MG	DA	3259	1/1	0.91	0.10	-	42,42,42,42	0
57	MG	BA	3592	1/1	0.86	0.09	-	65,65,65,65	0
57	MG	CD	502	1/1	0.95	0.27	-	53,53,53,53	0
57	MG	BA	3433	1/1	0.95	0.20	-	27,27,27,27	0
57	MG	DA	3155	1/1	0.92	0.24	-	53,53,53,53	0
57	MG	CK	5001	1/1	0.96	0.05	-	61,61,61,61	0
57	MG	BA	3483	1/1	0.92	0.17	-	44,44,44,44	0
57	MG	BA	3030	1/1	0.94	0.24	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	DA	3217	1/1	0.98	0.24	-	57,57,57,57	0
57	MG	BA	3276	1/1	0.95	0.40	-	44,44,44,44	0
57	MG	BA	3442	1/1	0.81	0.19	-	65,65,65,65	0
57	MG	BA	3307	1/1	0.96	0.19	-	28,28,28,28	0
57	MG	BA	3081	1/1	0.93	0.29	-	48,48,48,48	0
57	MG	DA	3553	1/1	0.92	0.07	-	72,72,72,72	0
57	MG	DA	3114	1/1	0.78	0.12	-	51,51,51,51	0
57	MG	CA	3118	1/1	0.97	0.18	-	60,60,60,60	0
57	MG	BA	3790	1/1	0.92	0.54	-	66,66,66,66	0
57	MG	BA	3750	1/1	0.98	0.22	-	46,46,46,46	0
57	MG	DA	3230	1/1	0.94	0.13	-	46,46,46,46	0
57	MG	DA	3436	1/1	0.97	0.11	-	35,35,35,35	0
57	MG	DA	3402	1/1	0.94	0.09	-	48,48,48,48	0
57	MG	BA	3028	1/1	0.94	0.20	-	37,37,37,37	0
57	MG	BA	3349	1/1	0.92	0.18	-	34,34,34,34	0
57	MG	DA	3046	1/1	0.85	0.14	-	56,56,56,56	0
57	MG	BB	3004	1/1	0.74	0.20	-	69,69,69,69	0
57	MG	BA	3096	1/1	0.90	0.18	-	60,60,60,60	0
57	MG	DA	3284	1/1	0.78	0.14	-	58,58,58,58	0
57	MG	BA	3197	1/1	0.81	0.25	-	58,58,58,58	0
57	MG	AA	1620	1/1	0.78	0.14	-	59,59,59,59	0
57	MG	BA	3554	1/1	0.89	0.09	-	51,51,51,51	0
57	MG	BA	3026	1/1	0.78	0.15	-	60,60,60,60	0
57	MG	BA	3237	1/1	0.93	0.17	-	44,44,44,44	0
57	MG	BA	3640	1/1	0.92	0.17	-	57,57,57,57	0
57	MG	BA	3154	1/1	0.63	0.21	-	52,52,52,52	0
57	MG	BA	3510	1/1	0.87	0.16	-	45,45,45,45	0
57	MG	DA	3158	1/1	0.90	0.39	-	56,56,56,56	0
57	MG	BA	3534	1/1	0.98	0.23	-	26,26,26,26	0
57	MG	CA	3087	1/1	0.87	0.07	-	57,57,57,57	0
57	MG	DA	3196	1/1	0.85	0.16	-	54,54,54,54	0
57	MG	CA	3098	1/1	0.93	0.11	-	54,54,54,54	0
57	MG	BA	3202	1/1	0.94	0.15	-	62,62,62,62	0
57	MG	BA	3076	1/1	0.96	0.38	-	42,42,42,42	0
57	MG	DA	3493	1/1	0.87	0.08	-	51,51,51,51	0
57	MG	BA	3297	1/1	0.95	0.22	-	42,42,42,42	0
57	MG	CA	3054	1/1	0.93	0.33	-	69,69,69,69	0
57	MG	BA	3281	1/1	0.81	0.28	-	50,50,50,50	0
57	MG	CA	3136	1/1	0.94	0.14	-	48,48,48,48	0
57	MG	BA	3496	1/1	0.97	0.12	-	51,51,51,51	0
57	MG	BA	3550	1/1	0.95	0.16	-	50,50,50,50	0
57	MG	CA	3011	1/1	0.85	0.25	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	BA	3164	1/1	0.77	0.22	-	46,46,46,46	0
57	MG	DA	3398	1/1	0.99	0.08	-	40,40,40,40	0
57	MG	CA	3018	1/1	0.94	0.13	-	63,63,63,63	0
57	MG	CA	3012	1/1	0.83	0.32	-	64,64,64,64	0
57	MG	BA	3476	1/1	0.99	0.16	-	48,48,48,48	0
57	MG	CA	3116	1/1	0.95	0.20	-	57,57,57,57	0
57	MG	CA	3101	1/1	0.93	0.11	-	65,65,65,65	0
57	MG	DA	3182	1/1	0.97	0.21	-	52,52,52,52	0
57	MG	DB	3002	1/1	0.94	0.26	-	63,63,63,63	0
57	MG	DA	3533	1/1	0.90	0.14	-	56,56,56,56	0
57	MG	BA	3132	1/1	0.91	0.18	-	50,50,50,50	0
57	MG	BA	3769	1/1	0.90	0.20	-	47,47,47,47	0
57	MG	DA	3596	1/1	0.73	0.19	-	69,69,69,69	0
57	MG	BA	3207	1/1	0.91	0.18	-	36,36,36,36	0
57	MG	DA	3353	1/1	0.97	0.13	-	47,47,47,47	0
57	MG	BA	3286	1/1	0.86	0.17	-	44,44,44,44	0
57	MG	BA	3781	1/1	0.91	0.16	-	56,56,56,56	0
57	MG	DA	3233	1/1	0.82	0.13	-	65,65,65,65	0
57	MG	DA	3591	1/1	0.81	0.06	-	66,66,66,66	0
57	MG	DA	3488	1/1	0.86	0.10	-	53,53,53,53	0
57	MG	BA	3556	1/1	0.94	0.07	-	46,46,46,46	0
57	MG	AA	1812	1/1	0.86	0.13	-	63,63,63,63	0
57	MG	CJ	5001	1/1	0.90	0.17	-	77,77,77,77	0
57	MG	BA	3516	1/1	0.91	0.24	-	46,46,46,46	0
57	MG	DA	3588	1/1	0.95	0.15	-	59,59,59,59	0
57	MG	BA	3492	1/1	0.96	0.12	-	38,38,38,38	0
57	MG	BA	3497	1/1	0.90	0.17	-	50,50,50,50	0
57	MG	DA	3580	1/1	0.88	0.21	-	62,62,62,62	0
57	MG	DA	3262	1/1	0.97	0.13	-	20,20,20,20	0
57	MG	BA	3362	1/1	0.97	0.22	-	47,47,47,47	0

6.5 Other polymers ⓘ

There are no such residues in this entry.